

Supplemental Figures and Tables

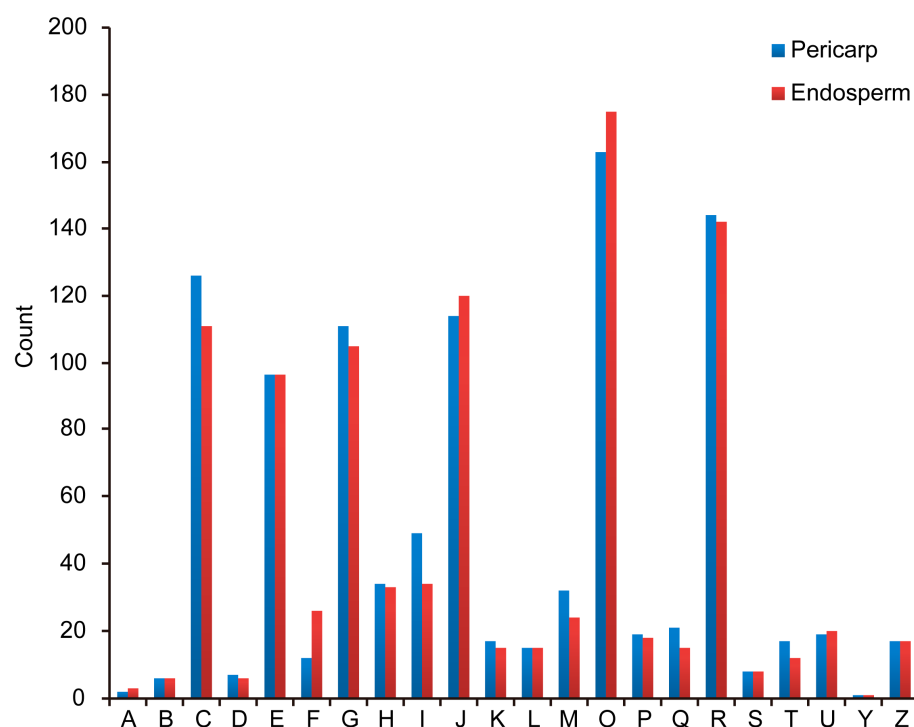


Figure S1. Cluster of orthologous groups (COG) analysis of pericarp and endosperm in Dan232.

A, RNA processing and modification; B, Chromatin structure and dynamics; C, Energy production and conversion; D, Cell cycle control, cell division, chromosome partitioning; E, Amino acid transport and metabolism; F, Nucleotide transport and metabolism; G, Carbohydrate transport and metabolism; H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; J, Translation, ribosomal structure and biogenesis; K, Transcription; L, Replication, recombination and repair; M, Cell wall/membrane/envelope biogenesis; O, Posttranslational modification, protein turnover, chaperones; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis, transport and catabolism; R, General function prediction only; S, Function unknown; T, Signal transduction mechanisms; U, Intracellular trafficking, secretion, and vesicular transport; Y, Nuclear structure; Z, Cytoskeleton.

Table S1. The quantitation of identified proteins in endosperm and pericarp using iTRAQ.

Id	Identified Proteins	Accession Number	Molecular Weight	N1	D1	D2	D3	D4	D5	D6	D7	D8
1	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01 (+1)	103 kDa	Ref	-0.5	0.3	-1.9	-1.9	Reference Missing	2.7	1.8	1.1
2	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01 (+1)	92 kDa	Ref	-1.2	-1.1	-2	-0.4	Reference Missing	Reference Missing	-0.4	Reference Missing
3	seq=translation; coord=9:22100864..22105552:1; parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302	GRMZM2G064302_P01	48 kDa	Ref	-0.7	-0.7	-0.6	-0.3	0.5	0.9	1.2	1.3
4	seq=translation; coord=1:176837841..176844200:1; parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751	GRMZM2G149751_P01 (+2)	84 kDa	Ref	-0.7	Value Missing	-0.8	-0.6	-1.4	-1.9	-2.1	-2
5	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01 (+2)	32 kDa	Ref	-0.3	0.4	0	0.5	0.4	0.3	0.5	0.8
6	seq=translation; coord=1:296477860..296482170:1; parent_transcript=GRMZM2G040369_T01; parent_gene=GRMZM2G040369	GRMZM2G040369_P01 (+3)	94 kDa	Ref	-0.5	-1	-1	-0.5	-0.6	0.5	0.3	0.2
7	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	57 kDa	Ref	0.1	0.9	0.7	0	0.6	1.3	Reference Missing	Reference Missing
8	seq=translation; coord=1:197267922..197271011:1; parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423	GRMZM2G175423_P01	39 kDa	Ref	-0.9	0.6	-0.6	-0.3	Reference Missing	Reference Missing	1.8	Reference Missing
9	seq=translation; coord=3:126460606..126465045:-1; parent_transcript=GRMZM2G340251_T01; parent_gene=GRMZM2G340251	GRMZM2G340251_P01 (+2)	71 kDa	Ref	Reference Missing	-0.1	-0.3	0	1.9	1.6	1.4	1.5
10	seq=translation; coord=3:207616747..207621242:-1; parent_transcript=GRMZM2G041275_T01; parent_gene=GRMZM2G041275	GRMZM2G041275_P01	59 kDa	Ref	Reference Missing	No Values	No Values	Reference Missing	-4.1	Value Missing	-5.3	Value Missing
11	seq=translation; coord=5:167751373..167752582:1; parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111	GRMZM2G326111_P01	18 kDa	Ref	-0.4	-0.8	-1.5	-2.2	-1.8	Value Missing	-3.2	-3.1
12	seq=translation; coord=4:240050091..240053865:1; parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007	GRMZM2G415007_P01	73 kDa	Ref	-0.2	-0.3	0.1	-0.1	0.1	0.2	0.7	0.9

13	seq=translation; coord=3:165722970..165725581:1; parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823	GRMZM2G057823_P01	39 kDa	Ref	-0.5	-0.5	0.2	0.4	0.4	1.6	2.1	2.6
14	seq=translation; coord=4:198369976..198374059:-1; parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631	GRMZM2G012631_P01	80 kDa	Ref	-0.1	-0.4	-0.2	-0.5	-0.5	-0.1	-0.6	-0.6
15	seq=translation; coord=4:21135870..21139019:1; parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295	GRMZM2G015295_P01 (+1)	53 kDa	Ref	-0.8	0	-0.3	0.3	0.1	-0.7	-1	-0.3
16	seq=translation; coord=6:39891824..39893787:1; parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883	GRMZM2G174883_P01	53 kDa	Ref	-1.1	-0.4	-1	-1.3	Reference Missing	Reference Missing	2.4	2
17	seq=translation; coord=4:28118892..28124783:1; parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	87 kDa	Ref	-0.7	-0.5	-0.5	-0.4	-0.7	-0.3	-0.2	-0.2
18	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	38 kDa	Ref	Reference Missing	1	Reference Missing	0.7	-0.5	-1.6	-0.7	0.2
19	seq=translation; coord=9:138424253..138428598:1; parent_transcript=GRMZM2G054300_T01; parent_gene=GRMZM2G054300	GRMZM2G054300_P01 (+1)	27 kDa	Ref	-0.2	-0.2	0	-0.8	-1.2	-0.9	-1.4	-0.8
20	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	109 kDa	Ref	-0.1	-0.8	-0.4	0.2	-0.9	-0.1	-0.3	0.2
21	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01 (+2)	36 kDa	Ref	0.1	0.4	0.4	0.8	2.9	Reference Missing	Reference Missing	1.8
22	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02 (+1)	52 kDa	Ref	-0.6	-0.3	-0.6	-0.5	-0.4	0.5	0.4	0.9
23	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01 (+1)	71 kDa	Ref	-1	-0.7	-0.7	-1.3	0.1	Reference Missing	0.6	0.5
24	seq=translation; coord=3:187441065..187444892:-1; parent_transcript=GRMZM2G071790_T01; parent_gene=GRMZM2G071790	GRMZM2G071790_P01 (+4)	55 kDa	Ref	1.1	0.3	-0.9	-1.2	-0.4	-2.4	-2.7	-3.2
25	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	61 kDa	Ref	-0.8	-0.6	-1	-0.5	-1.5	-1.2	-1.2	-0.9

26	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	38 kDa	Ref	-0.2	0	-0.9	-0.7	Reference Missing	Reference Missing	Reference Missing	1.7
27	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01 (+1)	27 kDa	Ref	-0.8	Value Missing	-0.5	-0.9	-1.6	-4	-3	-2.9
28	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03 (+2)	67 kDa	Ref	-0.2	1.2	-0.6	-0.8	1.5	2.6	2.1	1.1
29	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01 (+3)	42 kDa	Ref	-1.1	-0.9	-0.8	-1.3	0.6	1	0.6	0.8
30	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	29 kDa	Ref	0.2	0.2	0.4	Reference Missing	1.5	1.8	3.3	4.4
31	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	75 kDa	Ref	-1.5	-1.4	-1.7	-1.3	-1.5	Reference Missing	Reference Missing	-0.5
32	seq=translation; coord=2:209289645..209292956:-1; parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696	GRMZM2G113696_P01 (+1)	17 kDa	Ref	-1.1	-1.5	-1.7	Value Missing	0.6	0.2	0	-0.1
33	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02 (+1)	17 kDa	Ref	Value Missing	1.1	2	2.2	-4.2	-4	Value Missing	-2.1
34	seq=translation; coord=5:9471280..9475018:-1; parent_transcript=GRMZM2G152466_T01; parent_gene=GRMZM2G152466	GRMZM2G152466_P01 (+6)	50 kDa	Ref	0.6	-0.2	-1.7	-1.8	0.3	-1.1	-1.6	-2.7
35	seq=translation; coord=1:278130299..278132841:1; parent_transcript=GRMZM2G328500_T01; parent_gene=GRMZM2G328500	GRMZM2G328500_P01 (+2)	56 kDa	Ref	-0.9	-0.3	Value Missing	-0.7	-3.9	Value Missing	Value Missing	-5.4
36	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518	GRMZM2G428518_P01	97 kDa	Ref	-1.4	-0.8	0.6	-0.9	-3.9	-0.8	-0.6	0.4
37	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371	GRMZM2G048371_P01 (+1)	48 kDa	Ref	0.2	0.1	0	-0.1	-0.3	0.2	0.7	0.9
38	seq=translation; coord=5:18767810..18770458:1; parent_transcript=GRMZM2G087326_T01; parent_gene=GRMZM2G087326	GRMZM2G087326_P01	41 kDa	Ref	Value Missing	Value Missing	Value Missing	0	No Values	No Values	No Values	No Values

39	seq=translation; coord=8:134521573..134531903:1; parent_transcript=GRMZM2G067985_T04; parent_gene=GRMZM2G067985	GRMZM2G067985_P04 (+13)	47 kDa	Ref	0	0.1	-0.4	-0.2	0.5	-0.2	-0.7	-1.5
40	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	53 kDa	Ref	0.8	0.4	1.5	1.1	-3.1	-5.1	-4.4	-4.4
41	seq=translation; coord=10:1135114..1145295:1; parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576	GRMZM2G057576_P01	193 kDa	Ref	0.3	0	-0.6	-0.1	0.5	-0.4	-0.8	-1.8
42	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	50 kDa	Ref	-0.2	-0.1	-0.5	-0.2	0.1	0.6	0.6	1.1
43	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	36 kDa	Ref	-0.4	-0.3	-0.8	-0.6	-1.5	-2.4	-1.8	-1.4
44	seq=translation; coord=6:87119198..87122939:1; parent_transcript=GRMZM2G027995_T01; parent_gene=GRMZM2G027995	GRMZM2G027995_P01 (+1)	47 kDa	Ref	-1.4	-1.8	-1	-0.1	-0.4	0	-1.9	-1.2
45	seq=translation; coord=9:87062457..87064566:1; parent_transcript=GRMZM2G153541_T06; parent_gene=GRMZM2G153541	GRMZM2G153541_P06	49 kDa	Ref	1	1.3	0.6	0.8	3	3.1	3.1	2.3
46	seq=translation; coord=9:122220190..122226863:-1; parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908	GRMZM2G152908_P01	93 kDa	Ref	1.3	1.6	-0.7	-1	1.7	2.2	Reference Missing	0
47	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	34 kDa	Ref	0.7	1.9	1.6	2	1.1	2.2	3.2	4.2
48	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	23 kDa	Ref	-0.6	-0.9	-1.4	-2	-1.2	-1.5	Value Missing	-2.1
49	seq=translation; coord=8:170762955..170767680:-1; parent_transcript=GRMZM5G833389_T02; parent_gene=GRMZM5G833389	GRMZM5G833389_P02	61 kDa	Ref	-0.2	-0.6	0.1	-0.1	0.2	-0.3	-0.5	-1.2
50	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	50 kDa	Ref	0.5	0.8	0.9	2.4	Reference Missing	-0.6	0.9	2.7
51	seq=translation; coord=5:59268337..59270968:1; parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521	GRMZM2G084521_P01 (+1)	23 kDa	Ref	-0.9	-1.2	-1.4	-1.6	-1.1	-0.6	-0.2	0

52	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01 (+1)	69 kDa	Ref	0	-0.1	-0.7	-0.2	0.9	0.1	-0.1	-0.4
53	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	63 kDa	Ref	-0.8	0	0	0	-1.1	0.1	0.4	0.7
54	seq=translation; coord=7:24410021..24413947:-1; parent_transcript=GRMZM2G358059_T01; parent_gene=GRMZM2G358059	GRMZM2G358059_P01	48 kDa	Ref	-1.1	-1	-1.5	-1.6	-2.5	-3.2	-3.3	-3.7
55	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	48 kDa	Ref	0.7	-0.1	-0.2	-0.9	-0.4	-0.6	Reference Missing	Reference Missing
56	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	93 kDa	Ref	0.1	0	-0.4	-0.3	1.2	0.6	0.3	0.5
57	seq=translation; coord=5:32089861..32094927:-1; parent_transcript=AC233949.1_FGT004; parent_gene=AC233949.1_FG004	AC233949.1_FGP004	94 kDa	Ref	0.2	-0.4	0.2	-0.1	-0.2	0.2	0.1	-0.3
58	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	74 kDa	Ref	-0.3	-1	0	-0.4	Reference Missing	-1.4	-1.8	-2
59	seq=translation; coord=5:21697782..21703415:1; parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815	GRMZM2G153815_P01	73 kDa	Ref	-0.4	-0.5	-0.4	-0.5	0	-0.9	-0.8	-0.6
60	seq=translation; coord=2:71110426..71138423:1; parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933	GRMZM2G024933_P02	17 kDa	Ref	-1.2	-0.6	-0.6	-0.5	-1	0.3	0.7	Reference Missing
61	seq=translation; coord=1:45512802..45515978:-1; parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01 (+1)	65 kDa	Ref	-0.7	-0.4	-0.7	-0.3	-1.4	-1.7	-1	-0.9
62	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01 (+1)	36 kDa	Ref	0	-0.5	-1.1	-0.4	1.6	-0.1	-0.1	-0.9
63	seq=translation; coord=6:104066600..104071298:1; parent_transcript=GRMZM2G122871_T01; parent_gene=GRMZM2G122871	GRMZM2G122871_P01	47 kDa	Ref	0.5	1.1	-0.2	0.2	1	1.8	0.9	1.5
64	seq=translation; coord=5:189820639..189827796:1; parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688	GRMZM2G162688_P01	65 kDa	Ref	1.3	1.3	0.9	-0.2	2.3	2.1	2.2	3.3

65	seq=translation; coord=8:147686846..147691734:-1; parent_transcript=GRMZM2G432128_T01; parent_gene=GRMZM2G432128	GRMZM2G432128_P01	46 kDa	Ref	-1.8	-1.3	-0.9	-0.5	-1.6	-1.9	-1.9	-1.4
66	seq=translation; coord=6:74407967..74410838:1; parent_transcript=GRMZM2G108780_T01; parent_gene=GRMZM2G108780	GRMZM2G108780_P01	14 kDa	Ref	Value Missing	-0.3	-0.6	-1.4	-3	-3	Value Missing	Value Missing
67	seq=translation; coord=1:273983281..273986931:-1; parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658	GRMZM2G442658_P02 (+1)	41 kDa	Ref	0	0.7	0.2	0.9	1.3	1.3	1.5	1.2
68	seq=translation; coord=1:178476591..178478157:-1; parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603	GRMZM2G080603_P01 (+2)	15 kDa	Ref	0.6	0.5	0.3	-0.6	0.4	-0.3	-0.3	0.5
69	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	33 kDa	Ref	-0.4	0.7	0	0.3	-5.4	Reference Missing	Reference Missing	-1.6
70	seq=translation; coord=6:165631098..165635858:-1; parent_transcript=GRMZM2G154595_T01; parent_gene=GRMZM2G154595	GRMZM2G154595_P01	35 kDa	Ref	-0.1	Value Missing	-0.2	Value Missing	-3.5	-3.9	-3.5	-3.3
71	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	108 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.6	0.7	0.9
72	seq=translation; coord=2:5064059..5067153:-1; parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886	GRMZM2G081886_P01	65 kDa	Ref	-0.5	-0.5	-0.4	0	1.2	0.2	-0.1	-0.1
73	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	96 kDa	Ref	0	0.9	1.5	2.2	No Values	No Values	No Values	No Values
74	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01 (+2)	53 kDa	Ref	0	-0.3	0.3	0.3	3.8	3.8	3.8	2.6
75	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	36 kDa	Ref	-1.2	0.6	-0.3	-1.1	-3.9	-3.7	Reference Missing	-4
76	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	17 kDa	Ref	-1.1	-2.6	-2.8	-3	-1	0.1	0.1	-0.2
77	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	23 kDa	Ref	0.2	0.2	0.3	-1.2	-3.6	-1.8	-1.8	-0.2

78	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01 (+1)	35 kDa	Ref	-0.2	-0.5	-0.5	-0.4	-1	-2.8	-3.5	-3.8
79	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	54 kDa	Ref	-0.9	-0.7	-1	-0.2	0.5	0.9	0.5	1.2
80	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01 (+1)	40 kDa	Ref	1.8	1.6	1.1	0.6	-0.2	-0.3	-0.4	1.9
81	seq=translation; coord=4:13395375..13398777:-1; parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346	GRMZM2G098346_P01	41 kDa	Ref	-0.3	0.3	-0.4	0.3	-1.6	-0.4	-1.4	-1.1
82	seq=translation; coord=2:41302953..41306124:-1; parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499	GRMZM2G102499_P02 (+2)	32 kDa	Ref	1.9	1.5	2	1.2	0.6	-1.4	-1.2	2
83	seq=translation; coord=7:168785597..168786938:1; parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761	GRMZM2G129761_P01	28 kDa	Ref	0.2	2.1	0.5	1.1	-1.9	Reference Missing	-1.1	Reference Missing
84	seq=translation; coord=3:186793464..186794596:-1; parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	23 kDa	Ref	0.3	0.3	Reference Missing	4.4	1.8	2.7	3.5	Reference Missing
85	seq=translation; coord=4:105179813..105180991:-1; parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388	GRMZM2G162388_P01	18 kDa	Ref	Value Missing	-2.8	-3.1	Value Missing	Value Missing	-4.4	-4.5	-4.8
86	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01 (+2)	35 kDa	Ref	-0.8	-0.5	-0.4	-0.5	-0.2	1.2	1.9	2.7
87	seq=translation; coord=9:129274385..129278107:-1; parent_transcript=GRMZM2G058522_T01; parent_gene=GRMZM2G058522	GRMZM2G058522_P01 (+5)	15 kDa	Ref	-1	-1	-1	-1.3	Value Missing	Value Missing	Value Missing	Value Missing
88	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	71 kDa	Ref	-0.3	0.1	0.1	-0.7	1	2.2	2.5	2.4
89	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	61 kDa	Ref	0.1	-0.1	-0.3	-0.3	-1.3	-1.8	-1.8	-2.2
90	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	81 kDa	Ref	-1.1	-0.4	-1.9	-2.6	-0.3	-1.9	-1.4	-1.4

91	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01 (+1)	64 kDa	Ref	Value Missing	Value Missing	-1.9	-2.2	-2.1	-1.9	Reference Missing	-2.5
92	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	38 kDa	Ref	1	1.2	0.8	0	4.1	1.3	1.4	1.7
93	seq=translation; coord=4:58954361..58960521:-1; parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506	GRMZM2G068506_P01	52 kDa	Ref	-2.1	-1.7	-0.8	-1.3	-4.6	-2.6	Reference Missing	-2.5
94	seq=translation; coord=6:83777893..83783487:1; parent_transcript=GRMZM2G141931_T01; parent_gene=GRMZM2G141931	GRMZM2G141931_P01	93 kDa	Ref	0.5	0.2	0.5	0.1	No Values	No Values	No Values	No Values
95	seq=translation; coord=5:155951379..155960766:1; parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875	GRMZM2G027875_P01	96 kDa	Ref	-0.2	-0.5	-0.6	-0.3	-0.1	-0.2	-0.1	0.2
96	seq=translation; coord=4:160954463..160955623:1; parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515	GRMZM2G342515_P01	17 kDa	Ref	0.5	-0.1	0.2	0	-0.9	-5.1	Value Missing	-4.5
97	seq=translation; coord=3:202432697..202435947:1; parent_transcript=GRMZM2G055276_T01; parent_gene=GRMZM2G055276	GRMZM2G055276_P01	40 kDa	Ref	2	0.5	0.7	0.4	Reference Missing	Reference Missing	Reference Missing	Reference Missing
98	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	63 kDa	Ref	-0.8	-0.6	-1.4	-1.2	0.4	0.1	0.1	0.6
99	seq=translation; coord=4:220508652..220512101:1; parent_transcript=GRMZM2G027378_T01; parent_gene=GRMZM2G027378	GRMZM2G027378_P01 (+1)	17 kDa	Ref	-0.7	-0.7	-0.6	-1.9	-0.9	-0.3	-0.7	-0.5
100	seq=translation; coord=5:29990567..29996686:1; parent_transcript=GRMZM2G167505_T01; parent_gene=GRMZM2G167505	GRMZM2G167505_P01 (+2)	45 kDa	Ref	0.2	-0.4	-0.3	-1.2	-0.2	-2.4	-1.6	-0.8
101	seq=translation; coord=5:186517098..186522957:-1; parent_transcript=GRMZM2G540538_T01; parent_gene=GRMZM2G540538	GRMZM2G540538_P01	37 kDa	Ref	-1.4	-0.6	-0.5	-0.1	0.2	-0.4	-0.8	-0.3
102	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	73 kDa	Ref	0.1	0	1.1	Reference Missing	1.6	Reference Missing	2.7	3.1
103	seq=translation; coord=1:177027402..177032403:1; parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887	GRMZM2G005887_P01 (+2)	34 kDa	Ref	0.5	0.7	0.8	0.6	-1	-0.1	-0.2	-0.3

104	seq=translation; coord=2:33534101..33535449:1; parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943	GRMZM2G051943_P01	29 kDa	Ref	0.3	0.4	1.8	Reference Missing	Reference Missing	-1.7	0.1	Reference Missing
105	seq=translation; coord=1:292089538..292095812:-1; parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056	GRMZM2G347056_P01	66 kDa	Ref	-0.4	-0.3	-0.6	-0.1	0	-1.2	-1.2	-1
106	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	55 kDa	Ref	-0.5	-0.8	-0.7	0	2.9	2.9	2.9	2.8
107	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	40 kDa	Ref	-0.3	1.1	0.7	1.6	-1.8	-2.1	-2.2	-2.5
108	seq=translation; coord=6:122797861..122838407:1; parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505	GRMZM2G032505_P02 (+1)	47 kDa	Ref	0.1	-0.3	0.1	-0.2	-0.5	0.8	0.2	-0.5
109	seq=translation; coord=3:151819389..151821475:1; parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032	GRMZM2G125032_P01	36 kDa	Ref	0.1	Value Missing	0.4	1.7	0	0	1.6	2.5
110	seq=translation; coord=3:56281784..56287937:1; parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106	GRMZM2G136106_P01	60 kDa	Ref	-0.1	0.8	0.2	0.7	1.5	1.3	1.1	1.2
111	seq=translation; coord=5:213541443..213545321:-1; parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958	GRMZM2G178958_P01	62 kDa	Ref	-0.3	-0.5	-0.5	-0.5	-0.9	-1.4	-1	-1.2
112	seq=translation; coord=10:142329418..142336291:1; parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182	GRMZM2G114182_P01	150 kDa	Ref	-0.3	-0.6	-0.5	-1.1	0.2	0.3	0.2	-0.2
113	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	45 kDa	Ref	0	0.3	0.1	0.5	0.3	-0.1	-0.3	-0.5
114	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628	GRMZM2G032628_P01	91 kDa	Ref	-0.9	-0.6	-1.9	-1.5	-1.9	-1.1	Reference Missing	-2.7
115	seq=translation; coord=8:21816689..21823022:1; parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049	GRMZM2G032049_P01	90 kDa	Ref	0.3	-0.4	-0.3	-0.9	-4.9	-3.3	-3.2	-2.7
116	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	61 kDa	Ref	-1.2	-0.4	-0.7	-0.6	-2.2	-2.5	-2.5	-2.7

117	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771	GRMZM2G005771_P01 (+1)	18 kDa	Ref	-1.5	-0.9	-0.7	-0.9	-2.1	-1.7	-1.4	-1.2
118	seq=translation; coord=10:1725712..1731899:-1; parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062	GRMZM2G130062_P01	67 kDa	Ref	-0.7	0.5	-0.1	0.8	-6.1	-5.1	-4.9	-4.5
119	seq=translation; coord=3:31898226..31901626:-1; parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304	GRMZM2G120304_P01 (+1)	33 kDa	Ref	0.5	-0.2	-0.2	-0.5	-1.5	-2.1	-1.7	-1.7
120	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01 (+1)	19 kDa	Ref	0	-0.6	0.8	-0.7	-0.9	0.2	-0.1	1.1
121	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01 (+2)	35 kDa	Ref	1.2	1.4	0.6	0.7	0.2	-0.2	-0.6	-0.9
122	seq=translation; coord=3:146522696..146524904:-1; parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342	GRMZM2G103342_P01	38 kDa	Ref	0.2	0	1.7	3.6	No Values	No Values	No Values	No Values
123	seq=translation; coord=2:16219232..16221297:1; parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752	GRMZM2G003752_P01	44 kDa	Ref	-0.5	0	-1.1	-1.2	0	-0.9	0	0.4
124	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	101 kDa	Ref	-0.9	-1.3	-1	-1.3	-4.7	-2.6	-2.5	-2.3
125	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01 (+6)	26 kDa	Ref	-0.7	-1.1	-1.4	-2	0.8	0.8	Reference Missing	1.3
126	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	47 kDa	Ref	-0.3	-0.2	-0.4	0	1.5	0.6	0.3	0.8
127	seq=translation; coord=8:158089079..158099475:-1; parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988	GRMZM2G180988_P02 (+1)	108 kDa	Ref	-0.4	-0.6	-0.6	-0.6	-0.1	0	-0.1	-0.6
128	seq=translation; coord=2:167237699..167240039:1; parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855	GRMZM2G352855_P01 (+3)	49 kDa	Ref	0.4	0.8	1.7	2.6	No Values	No Values	No Values	No Values
129	seq=translation; coord=7:10287294..10291100:1; parent_transcript=GRMZM2G100403_T02; parent_gene=GRMZM2G100403	GRMZM2G100403_P02	44 kDa	Ref	0.7	0.5	0.6	0.4	1.1	0.4	0.4	-0.6

130	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01 (+1)	23 kDa	Ref	-0.8	-1	-0.1	-0.5	-1.5	-0.8	-0.9	-0.1
131	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01 (+1)	43 kDa	Ref	0.7	-0.1	-0.2	-1.3	0	-1.4	-1.7	-1.5
132	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	48 kDa	Ref	0.2	0.1	0.2	0.8	-0.4	0.1	0.1	0
133	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	20 kDa	Ref	-0.9	-0.3	0	-0.7	-4.1	-2.6	-1.9	-1.1
134	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	99 kDa	Ref	0	-0.3	-0.7	-0.2	1.7	1.9	2	2.2
135	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667	GRMZM2G140667_P01 (+1)	31 kDa	Ref	0.2	0.1	0.1	-0.4	-2	-1	-1	-0.8
136	seq=translation; coord=6:145087390..145092201:1; parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301	GRMZM2G179301_P02 (+1)	26 kDa	Ref	-0.2	-0.1	0.1	-0.4	-0.7	0.4	1.1	1.8
137	seq=translation; coord=1:79067709..79069201:-1; parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	14 kDa	Ref	0.4	-0.5	1.5	-0.1	-2.8	-2.3	-1.8	0.5
138	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04 (+2)	36 kDa	Ref	-0.6	-0.9	-0.8	-1.2	-4.6	-5.1	-5.8	-6.2
139	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01 (+1)	41 kDa	Ref	0.2	0.4	0.4	0.7	-4	-4.3	-4.3	-4.6
140	seq=translation; coord=5:15546617..15552849:-1; parent_transcript=GRMZM2G112149_T01; parent_gene=GRMZM2G112149	GRMZM2G112149_P01 (+2)	85 kDa	Ref	-0.2	-0.1	0.3	0.4	No Values	No Values	No Values	No Values
141	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	57 kDa	Ref	2.5	1.8	1.8	1.3	Reference Missing	Reference Missing	Reference Missing	0.7
142	seq=translation; coord=7:18473070..18475522:1; parent_transcript=GRMZM2G168149_T01; parent_gene=GRMZM2G168149	GRMZM2G168149_P01	30 kDa	Ref	0.7	0.5	-0.2	0.6	3.6	2.9	2.7	1.9

143	seq=translation; coord=6:44382950..44385913:-1; parent_transcript=GRMZM2G087570_T01; parent_gene=GRMZM2G087570	GRMZM2G087570_P01	26 kDa	Ref	-0.3	0	-0.1	-0.7	-1.2	-1.2	-1	-0.7
144	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	75 kDa	Ref	-0.1	0.3	0.6	1.4	No Values	No Values	No Values	No Values
145	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01 (+2)	54 kDa	Ref	-0.6	-0.4	-0.9	-0.6	1	-0.1	0	-0.2
146	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01 (+1)	54 kDa	Ref	-0.4	-0.3	-0.5	0.1	-0.9	-0.7	-1.5	-1.9
147	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005 (+1)	63 kDa	Ref	-0.1	-0.2	-0.3	-0.2	0	-0.1	0	-0.3
148	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	17 kDa	Ref	-1.6	-1.1	-0.6	-1.8	-0.9	1.5	2	3.1
149	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185	GRMZM2G110185_P02 (+1)	48 kDa	Ref	0.1	-0.1	-0.2	-0.1	-0.2	0.4	0.2	-0.5
150	seq=translation; coord=2:106286427..106287698:1; parent_transcript=GRMZM2G045809_T01; parent_gene=GRMZM2G045809	GRMZM2G045809_P01	25 kDa	Ref	0.8	2.3	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
151	seq=translation; coord=7:165383929..165386707:-1; parent_transcript=GRMZM2G031545_T01; parent_gene=GRMZM2G031545	GRMZM2G031545_P01 (+2)	25 kDa	Ref	-1	-1.5	-0.3	-1.3	-0.5	0.1	0.1	0.7
152	seq=translation; coord=6:125241154..125242106:-1; parent_transcript=GRMZM2G357296_T01; parent_gene=GRMZM2G357296	GRMZM2G357296_P01	18 kDa	Ref	0.4	0.2	-0.1	-0.3	0.4	-1.7	-1	-2.4
153	seq=translation; coord=9:98777728..98779013:-1; parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921	GRMZM2G036921_P01	24 kDa	Ref	-1.3	-1	-1.5	-2.3	-1.4	-1.6	-1.5	-1.6
154	seq=translation; coord=3:146602562..146604776:1; parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430	GRMZM2G171430_P01	10 kDa	Ref	-0.7	-0.9	-1.3	-2.4	-0.4	0.9	0.6	0.6
155	seq=translation; coord=4:149167730..149173878:1; parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850	GRMZM2G063850_P01	65 kDa	Ref	1	1	0.7	0	-0.7	-1.6	-2	-0.3

156	seq=translation; coord=5:1488844..1491571:1; parent_transcript=GRMZM2G125271_T01; parent_gene=GRMZM2G125271	GRMZM2G125271_P01	30 kDa	Ref	No Values	No Values	No Values	No Values	1	1.4	0.9	0.2
157	seq=translation; coord=9:142495842..142498679:-1; parent_transcript=GRMZM2G067303_T01; parent_gene=GRMZM2G067303	GRMZM2G067303_P01 (+3)	14 kDa	Ref	0.9	0.5	0.1	-0.7	1.8	1	1	0.2
158	seq=translation; coord=8:162236975..162239554:-1; parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118	GRMZM2G042118_P01	16 kDa	Ref	0.4	-0.7	-0.4	-1	3	0	0.7	0.3
159	seq=translation; coord=1:258363419..258365809:1; parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919	GRMZM2G067919_P02	65 kDa	Ref	0.2	0.6	1.3	3.5	-1	-1.2	Reference Missing	Reference Missing
160	seq=translation; coord=8:18231012..18236007:-1; parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639	GRMZM2G107639_P01 (+1)	44 kDa	Ref	-0.4	-0.1	-0.2	-0.3	-0.9	-0.1	0.1	0.2
161	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	53 kDa	Ref	0.1	0.2	-0.3	0.1	1.6	1.5	1.3	1.1
162	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	23 kDa	Ref	-0.2	-0.7	-0.3	-1.3	Value Missing	-1	-1	0.4
163	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01 (+1)	29 kDa	Ref	0.4	1.7	1.9	1.9	0	0	0.5	0.8
164	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01 (+2)	19 kDa	Ref	-0.9	-1	-1.9	-2.2	0.2	-1.1	-1.2	-1.2
165	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441	GRMZM2G078441_P01	71 kDa	Ref	0.2	1.5	0.7	1	-0.2	Reference Missing	1.3	1.5
166	seq=translation; coord=3:218323126..218325508:1; parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903	GRMZM2G176903_P01 (+1)	38 kDa	Ref	0.4	0.1	0.1	0	1	0.9	1.1	1.5
167	seq=translation; coord=5:205777032..205781614:-1; parent_transcript=GRMZM2G140150_T01; parent_gene=GRMZM2G140150	GRMZM2G140150_P01	43 kDa	Ref	1.3	0.3	1.2	0.4	No Values	No Values	No Values	No Values
168	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	57 kDa	Ref	0	0	0	-0.1	1.6	2.1	1.3	1.2

169	seq=translation; coord=6:161659850..161663090:-1; parent_transcript=GRMZM2G121186_T01; parent_gene=GRMZM2G121186	GRMZM2G121186_P01	43 kDa	Ref	0.4	0.3	0.2	-0.4	0	-0.9	-0.9	-0.2
170	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01 (+3)	74 kDa	Ref	-1.5	-1.8	-1.8	-2.1	1.4	-0.1	-0.5	-0.8
171	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01 (+1)	44 kDa	Ref	0.2	-0.2	0.2	-0.1	-0.7	0.1	-0.3	0
172	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	16 kDa	Ref	2	Reference Missing	1.3	1.4	2.6	1.6	1.4	1.1
173	seq=translation; coord=3:230606444..230608235:-1; parent_transcript=GRMZM2G010868_T01; parent_gene=GRMZM2G010868	GRMZM2G010868_P01 (+1)	12 kDa	Ref	1.4	2.1	2.2	2.1	Value Missing	Value Missing	Value Missing	-3.5
174	seq=translation; coord=1:192400083..192403759:1; parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585	GRMZM2G096585_P03 (+2)	62 kDa	Ref	-1.3	-1.5	-1.4	-2.2	-1.4	-1.8	-1.6	-0.9
175	seq=translation; coord=4:183449044..183455471:-1; parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818	GRMZM2G111818_P01 (+1)	117 kDa	Ref	-0.3	-0.6	-1	-0.5	-0.6	-0.8	-1.1	-0.7
176	seq=translation; coord=4:163768734..163771529:1; parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186	GRMZM2G135186_P01 (+2)	42 kDa	Ref	1.6	1.8	0.9	1.6	2.1	0.1	-0.1	-0.8
177	seq=translation; coord=1:234775005..234780894:-1; parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120	GRMZM2G416120_P01	61 kDa	Ref	-0.8	-0.8	-0.2	-0.4	Reference Missing	-2.8	Reference Missing	-3
178	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	60 kDa	Ref	-0.7	-0.8	-0.6	-1.3	-2	-1.2	-1.1	-1.1
179	seq=translation; coord=1:293163457..293166106:1; parent_transcript=GRMZM2G060702_T02; parent_gene=GRMZM2G060702	GRMZM2G060702_P02	16 kDa	Ref	-1.9	-2.1	-0.9	-1.2	No Values	No Values	No Values	No Values
180	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	28 kDa	Ref	-0.4	-0.8	-0.9	-1.7	-1.2	-1.1	-0.2	-0.1
181	seq=translation; coord=7:174283500..174287760:-1; parent_transcript=GRMZM2G430600_T01; parent_gene=GRMZM2G430600	GRMZM2G430600_P01 (+1)	36 kDa	Ref	0.4	-0.3	0.6	-0.1	-2.3	-1.5	-1.4	0.8

182	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	38 kDa	Ref	-0.6	-0.5	0.2	0.1	0.8	1.8	2.3	2.8
183	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	41 kDa	Ref	0	2	1.5	2.3	No Values	No Values	No Values	No Values
184	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	43 kDa	Ref	0.8	0.8	0.9	0.7	-0.1	-0.5	-0.2	0.1
185	seq=translation; coord=9:148111509..148115129:1; parent_transcript=GRMZM2G145258_T01; parent_gene=GRMZM2G145258	GRMZM2G145258_P01	30 kDa	Ref	0.7	0.9	0.3	0.6	2.1	1.2	1	1
186	seq=translation; coord=6:124803945..124805261:1; parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812	GRMZM2G084812_P01	32 kDa	Ref	0.1	0.5	-1	-1.9	-1.7	-1.5	-1.1	-0.8
187	seq=translation; coord=6:164551086..164552313:1; parent_transcript=GRMZM2G021794_T01; parent_gene=GRMZM2G021794	GRMZM2G021794_P01	28 kDa	Ref	-1.1	-0.7	-1.2	-1.7	-2.2	-2.9	-3.1	-2.9
188	seq=translation; coord=1:278183921..278192926:-1; parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158	GRMZM2G074158_P01 (+1)	110 kDa	Ref	-0.2	-0.7	-1	0.5	-6.8	-5.5	-5.5	-5.8
189	seq=translation; coord=4:215212969..215240759:1; parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123	GRMZM2G094123_P01	58 kDa	Ref	0.3	0.3	-0.2	-0.3	-2.3	-2	-2.2	-2.2
190	seq=translation; coord=4:237610321..237618962:-1; parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384	GRMZM2G155384_P02	97 kDa	Ref	0.6	0.2	-0.2	0.4	2.3	1.2	1.1	0.7
191	seq=translation; coord=5:215817786..215821620:-1; parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768	GRMZM5G848768_P02	48 kDa	Ref	-0.4	0	0.3	1	0.6	1	1.4	1.5
192	seq=translation; coord=9:150090384..150093179:-1; parent_transcript=GRMZM2G099657_T01; parent_gene=GRMZM2G099657	GRMZM2G099657_P01 (+2)	33 kDa	Ref	-0.2	-0.6	-1.4	-0.7	1.9	-2.4	0.2	-0.3
193	seq=translation; coord=3:113472963..113480259:-1; parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347	GRMZM2G093347_P01 (+1)	24 kDa	Ref	-1.3	-1.4	-1.3	-1.1	0.8	0.5	0.1	0
194	seq=translation; coord=2:231986102..231987473:-1; parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206	GRMZM2G053206_P01	39 kDa	Ref	-0.3	0.2	1.2	Reference Missing	0.7	2.6	4.6	4.8

195	seq=translation; coord=3:201684716..201689628:-1; parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724	GRMZM2G159724_P01 (+1)	66 kDa	Ref	-0.4	-0.3	0.8	1.8	Value Missing	Value Missing	Value Missing	Value Missing
196	seq=translation; coord=5:153543150..153551579:1; parent_transcript=GRMZM2G177781_T01; parent_gene=GRMZM2G177781	GRMZM2G177781_P01 (+1)	70 kDa	Ref	-0.6	-1.1	-1.2	-1.8	-2	-2.4	-2.2	-2.5
197	seq=translation; coord=5:215289055..215297830:1; parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449	GRMZM5G806449_P01 (+1)	53 kDa	Ref	-0.7	-0.4	-0.2	0.3	0.5	-0.3	0.1	0.5
198	seq=translation; coord=4:2762573..2764339:1; parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541	GRMZM2G126541_P01	54 kDa	Ref	-0.3	0	1.1	2.1	No Values	No Values	No Values	No Values
199	seq=translation; coord=9:33125819..33139794:1; parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675	GRMZM2G058675_P02	59 kDa	Ref	-0.7	-0.4	-0.6	-0.1	-3.8	-3.4	-3.2	-3.2
200	seq=translation; coord=1:228251511..228256942:-1; parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455	GRMZM2G346455_P05 (+1)	46 kDa	Ref	1.4	1.7	0.9	1.2	0.3	1.6	2.2	2.6
201	seq=translation; coord=10:144060305..144061413:1; parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313	GRMZM5G895313_P01	20 kDa	Ref	0.3	-0.1	-0.5	-1.1	0.6	-0.9	-0.8	-1.3
202	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	56 kDa	Ref	-2.1	Value Missing	-2.1	-1.8	-3.1	-3.5	-3.4	-3.2
203	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01 (+1)	105 kDa	Ref	0.7	0.8	0.8	1.6	6.3	5.4	6.3	Value Missing
204	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01 (+11)	45 kDa	Ref	1	0.2	-0.6	-0.3	2	0.6	-0.1	-1.3
205	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	40 kDa	Ref	-0.8	-1.1	-0.4	-1.2	-1	-0.9	-0.6	1.2
206	seq=translation; coord=8:39208505..39211382:-1; parent_transcript=GRMZM2G335657_T01; parent_gene=GRMZM2G335657	GRMZM2G335657_P01	53 kDa	Ref	-0.4	0	0	0.4	2.3	1.2	1.2	0.9
207	seq=translation; coord=9:132550417..132551258:1; parent_transcript=GRMZM2G404249_T01; parent_gene=GRMZM2G404249	GRMZM2G404249_P01 (+1)	17 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	1.4	2.5	3.4

208	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	38 kDa	Ref	0	0.6	1	2.4	No Values	No Values	No Values	No Values
209	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	46 kDa	Ref	0.4	0.4	0.3	0.5	1.3	0.3	0.3	1.3
210	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01 (+1)	39 kDa	Ref	0.4	1.4	0.2	1	2	2.5	3.6	4.3
211	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01 (+1)	16 kDa	Ref	0	-0.6	0.1	-1.3	-1	-2.1	-1.9	-1.9
212	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02 (+1)	14 kDa	Ref	-0.4	-0.2	-0.4	-0.6	-0.8	0.2	0.4	0.7
213	seq=translation; coord=5:63800401..63802605:-1; parent_transcript=GRMZM5G834758_T02; parent_gene=GRMZM5G834758	GRMZM5G834758_P02 (+1)	17 kDa	Ref	1.9	1	1.2	1.2	2.2	0.9	0.8	1.3
214	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01 (+1)	12 kDa	Ref	-0.9	-1.3	-1.4	-2.3	-3.1	-2.4	-2	-1.8
215	seq=translation; coord=3:210506972..210508715:1; parent_transcript=GRMZM2G022931_T01; parent_gene=GRMZM2G022931	GRMZM2G022931_P01	25 kDa	Ref	-1	-1	-1.1	-1.4	-5.1	-5.9	Value Missing	-4.8
216	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01 (+2)	68 kDa	Ref	0	0	-0.3	0.1	1.2	1.1	1.3	0.9
217	seq=translation; coord=4:153394405..153398468:1; parent_transcript=GRMZM2G135893_T01; parent_gene=GRMZM2G135893	GRMZM2G135893_P01	27 kDa	Ref	0	-0.1	-0.3	-0.6	-0.6	-1	-1	-0.3
218	seq=translation; coord=3:112198031..112206945:-1; parent_transcript=GRMZM2G086882_T01; parent_gene=GRMZM2G086882	GRMZM2G086882_P01	26 kDa	Ref	1.9	1.6	2	0.6	-0.3	0	-0.1	1.1
219	seq=translation; coord=7:54363440..54365032:-1; parent_transcript=GRMZM2G032766_T01; parent_gene=GRMZM2G032766	GRMZM2G032766_P01	42 kDa	Ref	1.4	0.8	2.2	2	1.9	1.1	1.4	0.7
220	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	50 kDa	Ref	-1.7	-2	-2.5	-2.5	-4.6	-5.2	-4.3	-4.6

221	seq=translation; coord=6:165013896..165020496:1; parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757	GRMZM2G065757_P01 (+1)	55 kDa	Ref	0.6	1	0.5	2.2	-4	Reference Missing	-4.1	-3.5
222	seq=translation; coord=10:18124892..18142878:-1; parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271	GRMZM2G082271_P01	110 kDa	Ref	0	-0.2	-0.4	-0.2	-0.1	0	-0.2	-0.5
223	seq=translation; coord=4:3210119..3212030:-1; parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054	GRMZM2G085054_P02	49 kDa	Ref	0	-0.1	0	-0.6	-1.2	-1.1	-1	-0.8
224	seq=translation; coord=3:8299415..8303114:-1; parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898	GRMZM2G314898_P01	46 kDa	Ref	-1.1	-0.8	-1.1	-0.2	-2.6	-2.3	-2	-2.1
225	seq=translation; coord=6:140347883..140348297:-1; parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002	AC233879.1_FGP002	10 kDa	Ref	Reference Missing	1.5	Reference Missing	Reference Missing	-4.4	-4.3	-3.9	-3.6
226	seq=translation; coord=10:4673451..4676086:-1; parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762	GRMZM2G003762_P03	25 kDa	Ref	-0.8	-0.6	-0.7	-1.1	-0.9	-0.6	-1.3	-1.6
227	seq=translation; coord=6:145987055..145988456:-1; parent_transcript=GRMZM2G306345_T01; parent_gene=GRMZM2G306345	GRMZM2G306345_P01	21 kDa	Ref	-0.3	1.1	-0.9	-1	Reference Missing	0.2	1.5	-0.6
228	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	24 kDa	Ref	0.3	0.8	3	4.7	0.5	Reference Missing	2.7	4.3
229	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01 (+1)	49 kDa	Ref	0.8	0.5	0.9	1.2	2.6	-0.4	0.2	0.5
230	seq=translation; coord=9:139405932..139410290:-1; parent_transcript=GRMZM2G165357_T01; parent_gene=GRMZM2G165357	GRMZM2G165357_P01 (+1)	39 kDa	Ref	0.4	0.8	0.2	-0.2	1.5	0.9	1.3	1.6
231	seq=translation; coord=10:148968847..148972562:1; parent_transcript=GRMZM2G104613_T01; parent_gene=GRMZM2G104613	GRMZM2G104613_P01	43 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
232	seq=translation; coord=4:128262885..128265210:1; parent_transcript=GRMZM2G008748_T02; parent_gene=GRMZM2G008748	GRMZM2G008748_P02	24 kDa	Ref	0.9	1.3	1.2	0.1	1	0.5	0	0.7
233	seq=translation; coord=1:298408224..298413579:-1; parent_transcript=GRMZM2G022269_T01; parent_gene=GRMZM2G022269	GRMZM2G022269_P01 (+1)	48 kDa	Ref	-0.5	-0.2	0.1	Value Missing	-5.4	-5.9	-5.7	-6.6

234	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	43 kDa	Ref	0.5	0.5	0.3	0	1.1	0.6	0.5	0.9
235	seq=translation; coord=10:82668664..82669799:-1; parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137	GRMZM2G121137_P01	12 kDa	Ref	-2.6	-3	0	-3.1	0.4	0.5	0.5	0.2
236	seq=translation; coord=1:275835279..275836493:-1; parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857	GRMZM2G025857_P01	27 kDa	Ref	0	1.2	0.3	0.8	-3.2	Reference Missing	-3	-3.5
237	seq=translation; coord=8:129620163..129623583:1; parent_transcript=GRMZM2G117198_T01; parent_gene=GRMZM2G117198	GRMZM2G117198_P01 (+1)	43 kDa	Ref	0.6	0.7	0.4	0.5	6.1	3.8	4.1	3.8
238	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	54 kDa	Ref	0.6	1.2	0.7	1.1	2.6	2.9	2.8	4.3
239	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	55 kDa	Ref	-0.8	-1.5	-1.1	-0.5	-2.9	-1.6	-1.5	-1.3
240	seq=translation; coord=10:109798193..109804126:1; parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041	GRMZM2G151041_P01 (+1)	116 kDa	Ref	-0.1	0.2	-0.3	0.4	-2	-1.8	-1.5	-1.5
241	seq=translation; coord=1:263143605..263149463:1; parent_transcript=GRMZM2G079668_T01; parent_gene=GRMZM2G079668	GRMZM2G079668_P01 (+1)	73 kDa	Ref	No Values	No Values	No Values	No Values	0	0.8	0.2	0
242	seq=translation; coord=3:41741731..41743930:-1; parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	36 kDa	Ref	-0.1	0.8	0.2	-0.2	0.9	-1.2	-0.9	-0.7
243	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01 (+9)	25 kDa	Ref	0.3	-0.2	-0.6	-1	0.5	-0.1	-0.2	-1.2
244	seq=translation; coord=5:199786088..199787380:1; parent_transcript=GRMZM2G054201_T01; parent_gene=GRMZM2G054201	GRMZM2G054201_P01 (+4)	18 kDa	Ref	0.7	0.5	0.7	0.4	-1.2	-0.9	-1.3	-1.3
245	seq=translation; coord=4:176858064..176868636:-1; parent_transcript=GRMZM2G149281_T01; parent_gene=GRMZM2G149281	GRMZM2G149281_P01 (+3)	23 kDa	Ref	-1.8	-1.6	-1.8	-2.9	-4.3	-4.5	Value Missing	-5.2
246	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	45 kDa	Ref	-0.4	-0.4	-0.4	-0.2	-0.6	-1.1	-1.4	-1.7

247	seq=translation; coord=1:12248908..12249912:-1; parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236	GRMZM2G472236_P01	28 kDa	Ref	-1.5	-0.7	-1	Value Missing	-2.1	-2.4	-2.1	-0.3
248	seq=translation; coord=2:205943881..205945286:-1; parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295	GRMZM2G099295_P01	35 kDa	Ref	0.1	-0.8	-0.3	0.2	-1.7	-3	-2.9	-3.1
249	seq=translation; coord=1:77258356..77350693:1; parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523	GRMZM2G020523_P01	35 kDa	Ref	-0.3	1.2	1.1	0.8	1	-0.9	0	0.1
250	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01 (+3)	58 kDa	Ref	0.3	0.4	0.5	0.1	-0.9	-0.6	-0.5	-0.6
251	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P01 (+6)	36 kDa	Ref	-0.7	-0.5	-1	-0.7	-2.1	-1.5	-1.4	-1.5
252	seq=translation; coord=6:135883373..135887597:1; parent_transcript=GRMZM2G059991_T01; parent_gene=GRMZM2G059991	GRMZM2G059991_P01	26 kDa	Ref	0.3	0.2	0.5	0.4	1.3	0.7	0.9	1.6
253	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	57 kDa	Ref	0.3	0.7	0.2	0.7	1.7	1.8	1.5	1.3
254	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	87 kDa	Ref	-0.5	-0.8	-0.7	-0.6	-0.9	-0.3	-0.7	-0.8
255	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01 (+1)	50 kDa	Ref	-0.1	-0.1	-0.5	-0.2	-0.4	-0.3	-0.3	-0.1
256	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	34 kDa	Ref	1.5	1.6	1.4	0.9	2.6	1.2	0.6	0.9
257	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01 (+3)	67 kDa	Ref	0.7	0.4	-0.1	0.8	0.7	-1.3	-1.3	-1.3
258	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	28 kDa	Ref	-0.3	-0.6	-0.4	-0.8	-8.5	-8.4	-8.4	-7.8
259	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	94 kDa	Ref	0.3	0	-0.6	-1.3	-0.6	-0.8	-0.3	-0.5

260	seq=translation; coord=7:137455248..137460051:1; parent_transcript=GRMZM2G115757_T01; parent_gene=GRMZM2G115757	GRMZM2G115757_P01 (+1)	16 kDa	Ref	-1	-1.4	-1.2	-1.8	-4.9	-5.7	-5.2	-5.3
261	seq=translation; coord=1:66023613..66026784:-1; parent_transcript=GRMZM2G078876_T01; parent_gene=GRMZM2G078876	GRMZM2G078876_P01	17 kDa	Ref	-0.1	-0.2	-0.3	-0.3	-3.4	Value Missing	Value Missing	-5.1
262	seq=translation; coord=10:145479598..145483674:-1; parent_transcript=GRMZM2G073465_T03; parent_gene=GRMZM2G073465	GRMZM2G073465_P03	51 kDa	Ref	-0.9	-1.5	-0.1	1.3	-4.9	-6.1	-5.8	-5
263	seq=translation; coord=6:9203729..9206286:-1; parent_transcript=GRMZM2G066460_T01; parent_gene=GRMZM2G066460	GRMZM2G066460_P01	34 kDa	Ref	No Values	No Values	No Values	No Values	1	0.1	-0.6	-0.6
264	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	50 kDa	Ref	-1.6	-1.6	-1.4	-0.9	-2.2	-2.3	-1.9	-1.6
265	seq=translation; coord=1:203587258..203590599:-1; parent_transcript=GRMZM2G106928_T01; parent_gene=GRMZM2G106928	GRMZM2G106928_P01	21 kDa	Ref	-0.5	Value Missing	-0.6	-1.1	-0.7	-0.2	0.3	0.6
266	seq=translation; coord=7:160032302..160036034:1; parent_transcript=GRMZM2G083243_T01; parent_gene=GRMZM2G083243	GRMZM2G083243_P01 (+1)	50 kDa	Ref	0.2	0.2	-0.9	-0.4	0.5	-0.5	-0.3	-1.4
267	seq=translation; coord=3:24095213..24095931:-1; parent_transcript=GRMZM2G011523_T01; parent_gene=GRMZM2G011523	GRMZM2G011523_P01 (+2)	10 kDa	Ref	0	2.1	2.7	1.1	Value Missing	Value Missing	0.2	0.1
268	seq=translation; coord=6:161966268..161967646:1; parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475	GRMZM2G096475_P01	19 kDa	Ref	0.2	0.4	1.9	2.5	-1.4	Value Missing	Value Missing	Reference Missing
269	seq=translation; coord=2:86767115..86790532:1; parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313	GRMZM2G028313_P01 (+1)	58 kDa	Ref	-0.2	-0.2	-0.5	-0.2	-0.2	-0.2	-0.3	-0.6
270	seq=translation; coord=1:94680007..94684730:-1; parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576	GRMZM2G178576_P02 (+1)	18 kDa	Ref	-1.4	-1.5	-1.5	-2.1	1.5	2.3	2.9	3.5
271	seq=translation; coord=10:75695843..75698244:1; parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352	GRMZM2G099352_P03	26 kDa	Ref	-0.6	-0.8	-0.4	-0.2	0.9	1	0.6	0
272	seq=translation; coord=3:19924648..19927549:1; parent_transcript=GRMZM2G169182_T01; parent_gene=GRMZM2G169182	GRMZM2G169182_P01 (+1)	70 kDa	Ref	No Values	No Values	No Values	No Values	-0.7	0.2	0.1	-0.2

273	seq=translation; coord=8:168745391..168749427:1; parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206	GRMZM2G146206_P04	27 kDa	Ref	2.5	2.8	2.5	2.4	-1.5	Reference Missing	-1.8	-1.3
274	seq=translation; coord=2:48112888..48133114:1; parent_transcript=GRMZM2G053019_T01; parent_gene=GRMZM2G053019	GRMZM2G053019_P01	47 kDa	Ref	No Values	No Values	No Values	No Values	1.3	1.2	1.3	1.5
275	seq=translation; coord=10:4694280..4699187:-1; parent_transcript=GRMZM2G004534_T01; parent_gene=GRMZM2G004534	GRMZM2G004534_P01	57 kDa	Ref	0	-0.1	-0.1	0.5	1.7	0.5	0.4	1.1
276	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	32 kDa	Ref	0.2	-0.2	0.5	-0.6	0.5	1.2	1	0.8
277	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G094074_P01 (+6)	16 kDa	Ref	0.7	1.1	0.7	-0.1	1.5	1.1	0.6	0.1
278	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	31 kDa	Ref	-1	-1.2	-0.7	-2	-0.1	-0.3	-0.3	-0.3
279	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01 (+2)	42 kDa	Ref	-0.1	0.7	0.6	1.9	-0.7	-0.2	-0.5	-1.3
280	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110	GRMZM2G017110_P02 (+1)	56 kDa	Ref	Value Missing	-2.5	-2.4	-2.3	-1.2	-0.7	-1	-0.9
281	seq=translation; coord=1:56160677..56162858:-1; parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916	GRMZM2G054916_P01	54 kDa	Ref	Reference Missing	0.5	0.4	1.4	Reference Missing	1.2	Reference Missing	Reference Missing
282	seq=translation; coord=4:26893142..26901172:1; parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900	GRMZM2G093900_P01	56 kDa	Ref	0.8	0.2	-0.1	0.2	-0.4	1	0	0.2
283	seq=translation; coord=8:37409326..37412866:1; parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416	GRMZM2G002416_P01	50 kDa	Ref	-0.2	-0.5	-0.5	-0.3	0.1	-0.6	-0.9	-1.3
284	seq=translation; coord=2:58586007..58596234:1; parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054	GRMZM2G073054_P01 (+1)	93 kDa	Ref	-0.7	-1	-1.4	-1.7	3.3	3.3	3.5	3.2
285	seq=translation; coord=1:2801080..2803977:-1; parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881	GRMZM2G041881_P01	18 kDa	Ref	1.4	1.7	1	0.4	1.3	Reference Missing	0.2	0.8

286	seq=translation; coord=10:110621503..110626726:1; parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=8:9901033..9904862:-1;	GRMZM2G079538_P01 (+3)	49 kDa	Ref	0	0.4	0.5	0.6	0.7	0.8	0.3	0.1
287	parent_transcript=GRMZM2G069195_T01; parent_gene=GRMZM2G069195 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G069195_P01	42 kDa	Ref	-0.3	-0.5	-0.4	-0.3	-0.9	-0.9	-1.2	-1
288	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:222203896..222206239:-1;	GRMZM2G318780_P02	92 kDa	Ref	1.4	2.3	1.3	Reference Missing	-0.9	-0.2	-0.2	-0.5
289	parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269 seq=translation; coord=10:132619525..132621315:1;	GRMZM2G320269_P01	39 kDa	Ref	0.5	-0.4	-0.8	-1.5	-0.3	-1.6	-1.6	-1.9
290	parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855 seq=translation; coord=8:162019785..16202395:1;	GRMZM2G468855_P02	33 kDa	Ref	-0.9	-0.9	1.4	Value Missing	Reference Missing	-2.5	-3	-3.7
291	parent_transcript=GRMZM2G053898_T01; parent_gene=GRMZM2G053898 seq=translation; coord=8:173117675..173120538:1;	GRMZM2G053898_P01 (+3)	10 kDa	Ref	2.2	1.5	1.6	-0.1	-0.3	0.4	0.3	Reference Missing
292	parent_transcript=GRMZM2G116273_T01; parent_gene=GRMZM2G116273 seq=translation; coord=1:250061761..250067450:1;	GRMZM2G116273_P01	24 kDa	Ref	-1.1	-0.8	0	0.1	-2.1	-0.7	-0.5	0.4
293	parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470 seq=translation; coord=9:130484606..130489460:-1;	GRMZM2G157470_P01	38 kDa	Ref	1.2	1	0.9	0.1	0.2	-0.7	Value Missing	-1.8
294	parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092 seq=translation; coord=4:236362229..236373144:1;	GRMZM2G436092_P01 (+3)	29 kDa	Ref	-0.9	-1	-1.4	-1.2	0.1	-1.4	-1.6	-2.1
295	parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629 seq=translation; coord=7:131783728..131787563:1;	GRMZM2G168629_P01 (+1)	134 kDa	Ref	0.3	0.4	0.3	0.3	0.3	0.5	0.3	-0.3
296	parent_transcript=GRMZM2G069651_T01; parent_gene=GRMZM2G069651 seq=translation; coord=8:171565757..171566487:-1;	GRMZM2G069651_P01	80 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.5	-1	-1.1
297	parent_transcript=GRMZM2G091054_T01; parent_gene=GRMZM2G091054 seq=translation; coord=5:63317874..63324803:-1;	GRMZM2G091054_P01	12 kDa	Ref	1.5	1.2	1	0	Reference Missing	0.9	1.2	1.2
298	parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01 (+1)	93 kDa	Ref	-0.8	-0.8	-0.7	-0.6	-3.1	-2.7	-2.3	-1.9

299	seq=translation; coord=1:233228509..233231671:-1; parent_transcript=GRMZM2G134747_T01; parent_gene=GRMZM2G134747	GRMZM2G134747_P01	19 kDa	Ref	-0.7	-0.9	-0.3	-1.2	-1.3	-0.3	-0.3	-0.2
300	seq=translation; coord=6:92813319..92815990:-1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02 (+1)	50 kDa	Ref	0.7	0.2	-0.5	-0.7	1.2	0.6	0.7	-0.2
301	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01 (+1)	42 kDa	Ref	-0.6	-1.3	-1.6	-1.9	-0.5	-1.7	-1.7	-2.3
302	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	56 kDa	Ref	0.3	-0.3	-0.3	-0.8	0.3	0.6	1	0.7
303	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	47 kDa	Ref	0.6	0.6	0.6	0.6	1.6	1.3	1.5	1.3
304	seq=translation; coord=5:77434003..77436424:1; parent_transcript=GRMZM5G805485_T01; parent_gene=GRMZM5G805485	GRMZM5G805485_P01	68 kDa	Ref	0.6	0	0.7	-0.1	0.9	1.1	0.6	0.7
305	seq=translation; coord=3:220506759..220509488:1; parent_transcript=GRMZM2G116135_T01; parent_gene=GRMZM2G116135	GRMZM2G116135_P01	24 kDa	Ref	0.8	0.3	-0.1	-0.7	1.5	0.7	1.5	-0.8
306	seq=translation; coord=6:39092081..39092901:1; parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806	GRMZM2G012806_P01	10 kDa	Ref	-0.6	-0.8	-0.7	-0.6	Reference Missing	-2.7	-2	-2.4
307	seq=translation; coord=10:55753301..55756434:-1; parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087	GRMZM2G127087_P01 (+1)	66 kDa	Ref	0.4	0.1	2.1	3.7	No Values	No Values	No Values	No Values
308	seq=translation; coord=8:142871869..142875661:-1; parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738	GRMZM2G134738_P01 (+1)	18 kDa	Ref	1.8	0.8	1.4	0.7	-0.6	-0.9	-2.3	-1.6
309	seq=translation; coord=2:3098932..3104990:1; parent_transcript=GRMZM2G071333_T01; parent_gene=GRMZM2G071333	GRMZM2G071333_P01	123 kDa	Ref	-0.2	-0.5	-0.7	-0.5	2.2	2.3	2.4	2
310	seq=translation; coord=1:177045380..177050536:-1; parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742	GRMZM2G094742_P03	9 kDa	Ref	-0.1	0.6	-0.5	-0.7	1.3	1.4	1.6	1.9
311	seq=translation; coord=2:29943554..29946951:-1; parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295	GRMZM2G150295_P01	14 kDa	Ref	0	-0.8	-1.4	-2.1	0.1	-0.2	-1	0.5

312	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	34 kDa	Ref	-0.7	0.3	0.6	0.2	No Values	No Values	No Values	No Values
313	seq=translation; coord=3:1711864..1714237:1; parent_transcript=GRMZM2G123558_T01; parent_gene=GRMZM2G123558	GRMZM2G123558_P01 (+1)	23 kDa	Ref	Reference Missing	2.3	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
314	seq=translation; coord=4:230101062..230104782:-1; parent_transcript=GRMZM2G134582_T01; parent_gene=GRMZM2G134582	GRMZM2G134582_P01 (+1)	47 kDa	Ref	0.9	1.2	0.8	0.6	0.6	0.8	0.7	0.7
315	seq=translation; coord=7:124381997..124386923:1; parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173	GRMZM2G389173_P01	47 kDa	Ref	0.5	0.8	0.8	0.5	1.4	1.3	Reference Missing	Reference Missing
316	seq=translation; coord=2:7091727..7098725:-1; parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758	GRMZM2G379758_P01	106 kDa	Ref	0.6	0.3	0	0.5	-0.4	-1.1	-1.2	-2.3
317	seq=translation; coord=8:150358554..150362799:-1; parent_transcript=GRMZM2G055936_T01; parent_gene=GRMZM2G055936	GRMZM2G055936_P01	17 kDa	Ref	-1.7	-1.8	-1	-2.3	-1.5	-0.6	-0.7	-0.3
318	seq=translation; coord=7:172711231..172713259:1; parent_transcript=GRMZM2G063617_T01; parent_gene=GRMZM2G063617	GRMZM2G063617_P01	15 kDa	Ref	0.8	1	1	0.6	-0.7	-1	-1.2	-2
319	seq=translation; coord=5:84934242..84936493:1; parent_transcript=GRMZM2G010321_T01; parent_gene=GRMZM2G010321	GRMZM2G010321_P01	17 kDa	Ref	-2	-1.8	-2.1	-3	-3.7	-6.4	-5.9	-6.6
320	seq=translation; coord=10:132006574..132009975:-1; parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714	GRMZM2G164714_P02	52 kDa	Ref	-0.2	-0.2	0.1	-0.2	-3.6	-2.9	-2.8	-3
321	seq=translation; coord=2:71086139..71088448:-1; parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176	GRMZM2G112176_P01 (+1)	16 kDa	Ref	0.2	0	-0.3	-0.3	-3	-1.4	-0.9	-0.3
322	seq=translation; coord=1:76732179..76733770:-1; parent_transcript=GRMZM2G077316_T01; parent_gene=GRMZM2G077316	GRMZM2G077316_P01	26 kDa	Ref	-0.5	0	-0.4	-0.3	-2	-1.6	-1.7	-2
323	seq=translation; coord=8:157452514..157453996:-1; parent_transcript=GRMZM2G059299_T01; parent_gene=GRMZM2G059299	GRMZM2G059299_P01	49 kDa	Ref	Reference Missing	1.5	2	Reference Missing	-6.1	Reference Missing	Reference Missing	-2.3
324	seq=translation; coord=2:197582100..197595530:1; parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870	GRMZM2G117870_P01	120 kDa	Ref	0.5	0.1	0	0.3	-0.2	-0.3	-0.6	0

325	seq=translation; coord=4:233024312..233031203:1; parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817	GRMZM2G165817_P01 (+1)	45 kDa	Ref	-0.4	-0.7	-0.2	-0.3	-0.5	0.6	0.3	0.2
326	seq=translation; coord=1:216050547..216055495:-1; parent_transcript=GRMZM2G016189_T01; parent_gene=GRMZM2G016189	GRMZM2G016189_P01	49 kDa	Ref	0.2	0	0.3	0.6	-2.4	-2.1	-1.4	-0.9
327	seq=translation; coord=8:38410669..38412926:1; parent_transcript=GRMZM2G054123_T01; parent_gene=GRMZM2G054123	GRMZM2G054123_P01 (+4)	43 kDa	Ref	-0.3	0.2	-0.1	0.3	-1.1	-4.3	-3.9	-4
328	seq=translation; coord=9:139187765..139188857:1; parent_transcript=GRMZM2G305046_T01; parent_gene=GRMZM2G305046	GRMZM2G305046_P01 (+1)	17 kDa	Ref	1.8	0.9	1.3	1	No Values	No Values	No Values	No Values
329	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	21 kDa	Ref	-0.1	-0.2	0.1	0.2	-5.2	-4.3	-4.5	-4.5
330	seq=translation; coord=8:135138380..135140767:-1; parent_transcript=GRMZM2G076544_T01; parent_gene=GRMZM2G076544	GRMZM2G076544_P01	26 kDa	Ref	-1.2	-1.2	-1.4	-1.8	-1.6	-0.8	-1.3	-1.6
331	seq=translation; coord=5:169454598..169459090:1; parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300	GRMZM2G139300_P01	67 kDa	Ref	0.4	0.5	0.7	1.5	4.7	5.7	5.9	4.8
332	seq=translation; coord=3:173015163..173022969:-1; parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281	GRMZM2G038281_P01 (+1)	94 kDa	Ref	-1.1	-1.5	-1.9	-1.8	-1.8	-1.7	-2.2	-2.3
333	seq=translation; coord=2:82394515..82407013:1; parent_transcript=GRMZM5G858094_T01; parent_gene=GRMZM5G858094	GRMZM5G858094_P01 (+1)	257 kDa	Ref	0	-0.2	-0.7	-0.5	0.9	0.5	0.5	-0.2
334	seq=translation; coord=8:74938636..74939549:-1; parent_transcript=GRMZM2G045664_T01; parent_gene=GRMZM2G045664	GRMZM2G045664_P01	18 kDa	Ref	-1.7	-0.6	-1	-1.5	-1	-0.7	-2	-0.8
335	seq=translation; coord=3:26352719..26355885:1; parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916	GRMZM2G410916_P02	67 kDa	Ref	-1.1	-0.4	-1.7	-2.1	-2.2	-2	-1.6	-2
336	seq=translation; coord=6:165704660..165707098:-1; parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604	GRMZM2G354604_P01 (+2)	26 kDa	Ref	-0.1	-0.1	-0.4	-0.2	0.8	0.1	0	-0.4
337	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01 (+1)	11 kDa	Ref	-0.5	-1.3	-0.7	-1.1	Value Missing	-0.1	Value Missing	0.5

338	seq=translation; coord=6:31411848..31415600:-1; parent_transcript=GRMZM2G099186_T02; parent_gene=GRMZM2G099186	GRMZM2G099186_P02 (+1)	35 kDa	Ref	0.8	0.9	0.2	0.3	0.9	0	0.1	-0.7
339	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	16 kDa	Ref	-1.1	-1.5	-1.2	-2.2	-4.4	-4.4	-4.2	-4.5
340	seq=translation; coord=2:61490885..61494711:-1; parent_transcript=GRMZM2G134668_T02; parent_gene=GRMZM2G134668	GRMZM2G134668_P02	60 kDa	Ref	1.1	1	1	1.3	3.8	2.2	2.2	1.8
341	seq=translation; coord=1:58418770..58420264:-1; parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290	GRMZM2G075290_P01	38 kDa	Ref	-0.1	0.6	0.6	0.1	4.7	5.4	5.5	4.9
342	seq=translation; coord=7:171733893..171737098:-1; parent_transcript=GRMZM2G025992_T01; parent_gene=GRMZM2G025992	GRMZM2G025992_P01 (+3)	22 kDa	Ref	-0.8	-1.1	-0.9	-1.4	-2.1	-2	-1.3	-0.9
343	seq=translation; coord=4:217021920..217028774:-1; parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578	GRMZM2G180578_P01	56 kDa	Ref	0.4	0	-0.6	-0.4	3.3	1.2	0.6	1.3
344	seq=translation; coord=3:226624022..226632817:-1; parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086	GRMZM2G017086_P01 (+1)	54 kDa	Ref	0.1	-0.3	-0.2	-0.2	0.5	0	0	-0.4
345	seq=translation; coord=2:183929119..183934914:-1; parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284	GRMZM2G399284_P01 (+1)	26 kDa	Ref	-0.4	-0.6	-0.2	-0.6	0.8	1.5	2	2
346	seq=translation; coord=4:170332797..170339707:-1; parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410	GRMZM2G008410_P01	37 kDa	Ref	-0.5	-0.8	-0.7	-0.9	-0.8	-1.6	-1.6	-1.3
347	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	48 kDa	Ref	0.5	0.6	0.7	0.5	-0.8	-0.3	0.3	-0.4
348	seq=translation; coord=8:171852196..171855863:-1; parent_transcript=GRMZM2G159643_T01; parent_gene=GRMZM2G159643	GRMZM2G159643_P01	22 kDa	Ref	1.1	1.5	1.4	2.2	No Values	No Values	No Values	No Values
349	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	56 kDa	Ref	0	0.2	-0.5	0.4	0.9	2	1.4	1.1
350	seq=translation; coord=1:246702682..246710172:-1; parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589	GRMZM2G146589_P01 (+3)	69 kDa	Ref	0.7	1.1	0.5	0.4	2.5	1.5	1.3	2.5

351	seq=translation; coord=7:123475099..123479587:1; parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944	GRMZM5G824944_P01 (+1)	68 kDa	Ref	0.1	-0.2	-0.4	0.2	-0.1	0.2	0.2	0.5
352	seq=translation; coord=1:220892398..220897302:-1; parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022	GRMZM2G078022_P03 (+2)	23 kDa	Ref	-0.5	-0.5	-1.1	-1.2	-1.9	-3.7	-3.9	-3.7
353	seq=translation; coord=7:136570996..136574421:1; parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386	GRMZM2G074386_P01	24 kDa	Ref	-0.2	-0.2	0	0.3	0.2	-0.3	0	-0.2
354	seq=translation; coord=1:20418930..20420739:-1; parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367	GRMZM2G134367_P01	47 kDa	Ref	-0.1	-1.1	-0.7	-1.1	-2.5	-2.4	-2.7	-3.1
355	seq=translation; coord=8:79300397..79307702:1; parent_transcript=GRMZM2G073774_T01; parent_gene=GRMZM2G073774	GRMZM2G073774_P01 (+2)	59 kDa	Ref	0	0.2	-0.3	-0.3	-2.2	-2.4	-2.4	-2.7
356	seq=translation; coord=6:75746632..75749530:-1; parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528	GRMZM2G130528_P01	40 kDa	Ref	0.8	2.6	1.9	3	2.3	1.8	2.9	3.4
357	seq=translation; coord=1:200480447..200483616:-1; parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018	GRMZM2G157018_P01	20 kDa	Ref	1.7	0.9	1.9	0.6	No Values	No Values	No Values	No Values
358	seq=translation; coord=9:48437559..48441823:-1; parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811	GRMZM2G049811_P01	41 kDa	Ref	-0.5	0	0	0.3	-1.6	-0.8	-1.5	-1.1
359	seq=translation; coord=1:180400813..180406565:-1; parent_transcript=GRMZM2G085474_T01; parent_gene=GRMZM2G085474	GRMZM2G085474_P01 (+1)	41 kDa	Ref	0.2	-0.4	-0.9	-0.4	0.3	-1.2	-1.5	-2.3
360	seq=translation; coord=9:139511132..139514364:1; parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532	GRMZM2G366532_P01 (+1)	72 kDa	Ref	-0.4	0.5	0.5	Reference Missing	-0.4	0.7	1.2	1.5
361	seq=translation; coord=4:38181649..38185320:-1; parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430	GRMZM2G103430_P01 (+4)	51 kDa	Ref	-0.3	-0.6	-0.9	-0.5	-1.3	-1.6	-2.5	-2.9
362	seq=translation; coord=4:53954699..53962275:1; parent_transcript=GRMZM2G423027_T01; parent_gene=GRMZM2G423027	GRMZM2G423027_P01 (+1)	25 kDa	Ref	-0.3	-0.2	-0.1	-1.1	-2.5	-1.6	-0.5	0
363	seq=translation; coord=4:237508371..237511930:-1; parent_transcript=GRMZM2G166035_T01; parent_gene=GRMZM2G166035	GRMZM2G166035_P01 (+1)	31 kDa	Ref	-0.8	-1	-1.1	-0.5	-4.5	-4.1	-3.9	-3.9

364	seq=translation; coord=5:199376854..199379060:1; parent_transcript=GRMZM2G027741_T01; parent_gene=GRMZM2G027741	GRMZM2G027741_P01 (+3)	29 kDa	Ref	0	-0.2	0	-0.5	-2.5	-2.4	-2	-0.5
365	seq=translation; coord=3:161953049..161955801:1; parent_transcript=GRMZM2G153991_T01; parent_gene=GRMZM2G153991	GRMZM2G153991_P01	16 kDa	Ref	-0.8	-0.8	-1	-1.6	-2.1	-1.6	-2.3	-2.1
366	seq=translation; coord=6:161454531..161462066:-1; parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087	GRMZM2G090087_P02 (+1)	61 kDa	Ref	-0.8	-0.8	-0.8	-0.5	4.9	4.7	5	5
367	seq=translation; coord=7:23715448..23717527:-1; parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030	GRMZM2G097030_P01	51 kDa	Ref	-0.3	Value Missing	Value Missing	Value Missing	-5.5	-5.1	-5.7	-6.2
368	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	33 kDa	Ref	2.2	1.2	0.9	1.2	2.7	3.7	4.5	4.6
369	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01 (+2)	78 kDa	Ref	-0.7	-0.7	-1.4	-1	1.3	0.7	0.5	-0.3
370	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	15 kDa	Ref	0.1	-0.1	0.3	-0.1	0.4	-0.4	-1.3	-1.9
371	seq=translation; coord=1:60163114..60165406:1; parent_transcript=GRMZM2G000923_T01; parent_gene=GRMZM2G000923	GRMZM2G000923_P01 (+2)	23 kDa	Ref	0.8	0.6	0.6	0	1.8	0.8	1.2	1.6
372	seq=translation; coord=9:107209042..107212141:1; parent_transcript=GRMZM2G172357_T01; parent_gene=GRMZM2G172357	GRMZM2G172357_P01 (+3)	15 kDa	Ref	0	-0.4	0.9	-1.1	-4.2	-3.9	-4.2	-3.5
373	seq=translation; coord=1:293135180..293138761:1; parent_transcript=GRMZM2G061900_T01; parent_gene=GRMZM2G061900	GRMZM2G061900_P01 (+3)	24 kDa	Ref	0.4	0.5	-0.4	-0.3	0.9	-1.5	-1.5	-2.2
374	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	40 kDa	Ref	-0.1	0.7	0.4	1.3	-1.4	0	0.3	0.8
375	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	29 kDa	Ref	0.7	1.2	0.9	0.2	0.1	0.8	0.6	0.8
376	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01 (+1)	16 kDa	Ref	2	2.3	1.5	1.6	0	-0.7	-0.3	-0.1

377	seq=translation; coord=4:239151749..239155703:-1; parent_transcript=GRMZM2G024310_T01; parent_gene=GRMZM2G024310	GRMZM2G024310_P01	28 kDa	Ref	1.4	0.8	1.5	0.6	No Values	No Values	No Values	No Values
378	seq=translation; coord=9:145346839..145349218:-1; parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225	GRMZM2G067225_P01	53 kDa	Ref	1	0.6	1	1.7	No Values	No Values	No Values	No Values
379	seq=translation; coord=5:163984090..163986394:1; parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008	GRMZM2G143008_P01	69 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.5	1.2	0.9
380	seq=translation; coord=2:232101270..232109417:-1; parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034	GRMZM2G036034_P01 (+1)	99 kDa	Ref	-0.9	-1.1	-1.2	-1.1	2.6	1.4	2.5	2.8
381	seq=translation; coord=1:26684241..26696594:-1; parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628	GRMZM2G099628_P02	89 kDa	Ref	-1	-1	-0.7	-1.2	-1.3	-0.9	-0.8	-0.8
382	seq=translation; coord=3:12189233..12194178:1; parent_transcript=GRMZM2G054559_T01; parent_gene=GRMZM2G054559	GRMZM2G054559_P01 (+1)	92 kDa	Ref	-0.5	-0.5	-0.7	-0.1	3.2	2.6	2.8	3.2
383	seq=translation; coord=2:31644513..31646214:-1; parent_transcript=GRMZM2G083253_T02; parent_gene=GRMZM2G083253	GRMZM2G083253_P02 (+6)	17 kDa	Ref	-0.5	-0.4	-0.9	-1.5	0.1	0.9	0.6	-0.6
384	seq=translation; coord=7:150542721..150550925:1; parent_transcript=GRMZM2G138220_T01; parent_gene=GRMZM2G138220	GRMZM2G138220_P01 (+1)	21 kDa	Ref	-0.7	-0.7	-0.4	-0.8	-1.7	-1.6	-1.3	-1.3
385	seq=translation; coord=9:37790950..37793111:1; parent_transcript=GRMZM2G118873_T01; parent_gene=GRMZM2G118873	GRMZM2G118873_P01 (+2)	25 kDa	Ref	3.3	-0.8	-0.8	-1	4	Value Missing	-0.4	-0.4
386	seq=translation; coord=2:220832499..220836411:-1; parent_transcript=GRMZM2G148769_T01; parent_gene=GRMZM2G148769	GRMZM2G148769_P01 (+1)	35 kDa	Ref	-1.1	-1.4	-0.9	Value Missing	-4.4	-2.9	-2.9	-1.3
387	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	19 kDa	Ref	0.7	0.5	-0.5	-0.7	-4.8	-4.8	-4.9	-2.7
388	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	89 kDa	Ref	No Values	No Values	No Values	No Values	1	0.6	0.1	0.1
389	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	64 kDa	Ref	-0.8	-1.5	-0.6	-1	No Values	No Values	No Values	No Values

390	seq=translation; coord=8:162756043..162756672:-1; parent_transcript=GRMZM2G170969_T01; parent_gene=GRMZM2G170969	GRMZM2G170969_P01	10 kDa	Ref	2.7	2.4	3.7	2.6	No Values	No Values	No Values	No Values
391	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	66 kDa	Ref	-0.8	-1	0	-0.1	-1.3	0	0	-0.2
392	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	53 kDa	Ref	-0.4	-0.5	0	-0.3	0.6	0.7	0.9	0.9
393	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01 (+3)	28 kDa	Ref	0.3	-0.4	-0.7	-0.5	2	0.9	0.3	-0.8
394	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01 (+1)	239 kDa	Ref	0.1	0.1	0.2	0.7	1.7	1.2	1.3	1.2
395	seq=translation; coord=5:154983595..154988021:1; parent_transcript=GRMZM2G167356_T01; parent_gene=GRMZM2G167356	GRMZM2G167356_P01 (+1)	39 kDa	Ref	-1.4	-1.8	-1.2	-2	-2	-3.4	-2.8	-4
396	seq=translation; coord=4:28340661..28347586:1; parent_transcript=GRMZM2G426591_T01; parent_gene=GRMZM2G426591	GRMZM2G426591_P01 (+2)	49 kDa	Ref	Value Missing	-0.4	-0.3	-0.7	-0.5	-0.4	Value Missing	-1.4
397	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01 (+1)	22 kDa	Ref	0.6	0.1	0.1	-0.1	0.9	Reference Missing	1.4	0.7
398	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	28 kDa	Ref	0.8	2.6	1.3	1.5	-1.2	Reference Missing	-0.6	1.5
399	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01 (+2)	55 kDa	Ref	-0.2	0.1	-0.1	0.1	-0.6	-0.7	-0.3	-0.5
400	seq=translation; coord=4:175134158..175138628:1; parent_transcript=GRMZM2G070239_T01; parent_gene=GRMZM2G070239	GRMZM2G070239_P01 (+1)	19 kDa	Ref	-0.3	-0.3	-1	-0.8	0.6	-0.4	-0.4	-0.8
401	seq=translation; coord=4:179822113..179823382:-1; parent_transcript=GRMZM2G007729_T02; parent_gene=GRMZM2G007729	GRMZM2G007729_P02	24 kDa	Ref	Reference Missing	-1.2	Reference Missing	-1.2	-0.4	-1	-1.9	-0.8
402	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	19 kDa	Ref	-2.3	Value Missing	-1.7	-2.4	-2.8	-1.5	-2.9	-2.1

403	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	11 kDa	Ref	-0.8	-1.1	-0.7	-2	-4	-1.4	-1.5	-0.2
404	seq=translation; coord=3:215654139..215663757:-1; parent_transcript=GRMZM2G125193_T01; parent_gene=GRMZM2G125193	GRMZM2G125193_P01	26 kDa	Ref	0.8	0	1.1	-0.3	0.3	0.9	0.2	1.8
405	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01 (+1)	44 kDa	Ref	-1.7	-1.5	-1.8	-1.1	-4.9	-4.5	-5	-5.3
406	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	62 kDa	Ref	-1	-0.9	-1.6	-1.8	-0.4	Reference Missing	Reference Missing	0.8
407	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	16 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	0.4	2.1
408	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	52 kDa	Ref	0.1	-0.4	-0.6	-0.5	0.7	0.1	0.1	-0.1
409	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	38 kDa	Ref	0	0	-0.3	-0.9	0.6	-0.9	-1.4	-0.9
410	seq=translation; coord=5:75935116..75939320:-1; parent_transcript=GRMZM2G019121_T01; parent_gene=GRMZM2G019121	GRMZM2G019121_P01	61 kDa	Ref	0.4	0.3	0.4	0.2	0.3	0	-0.1	-0.2
411	seq=translation; coord=6:158451653..158457625:-1; parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396	GRMZM2G176396_P01 (+2)	42 kDa	Ref	-0.1	-0.3	-0.3	0.1	-0.8	0	-0.2	0.6
412	seq=translation; coord=5:163209220..163228678:1; parent_transcript=GRMZM2G012690_T01; parent_gene=GRMZM2G012690	GRMZM2G012690_P01	47 kDa	Ref	-1.1	-1.3	-1.2	-2.2	-1.2	-2	-2.3	-1.9
413	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	133 kDa	Ref	0.9	0.2	0.5	-0.1	1.1	-0.3	-0.5	-0.6
414	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	16 kDa	Ref	1	0.9	0.6	0	-2.1	-2.7	-3.2	-2.4
415	seq=translation; coord=7:165243551..165244574:-1; parent_transcript=GRMZM2G030731_T01; parent_gene=GRMZM2G030731	GRMZM2G030731_P01 (+1)	16 kDa	Ref	1	0.6	0.2	0.3	1.4	0.3	-0.6	-1.2

416	seq=translation; coord=2:192576240..192582957:1; parent_transcript=GRMZM2G097226_T01; parent_gene=GRMZM2G097226	GRMZM2G097226_P01 (+1)	40 kDa	Ref	-0.1	0	0	0.2	5.7	5.5	5.9	5.6
417	seq=translation; coord=4:230189571..230193924:-1; parent_transcript=GRMZM2G161969_T01; parent_gene=GRMZM2G161969	GRMZM2G161969_P01	40 kDa	Ref	0	-0.1	0	-0.1	2.2	1.5	1.6	2
418	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	50 kDa	Ref	0	-0.3	-0.6	-0.3	0.8	0.8	0.7	0.5
419	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01 (+1)	122 kDa	Ref	0.1	-0.3	-0.8	-0.4	0.8	-0.4	-0.7	-1.1
420	seq=translation; coord=2:133839420..133842192:1; parent_transcript=GRMZM2G111143_T01; parent_gene=GRMZM2G111143	GRMZM2G111143_P01 (+2)	49 kDa	Ref	-0.3	Value Missing	0.1	0.4	1.1	0.4	1.6	Reference Missing
421	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	38 kDa	Ref	-0.5	-0.3	-0.2	0	-3.3	-2.7	-2.1	-1.6
422	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	26 kDa	Ref	0.6	1.9	0.8	1.2	-2.3	Reference Missing	-0.6	-0.2
423	seq=translation; coord=3:132396184..132400373:-1; parent_transcript=GRMZM2G063949_T01; parent_gene=GRMZM2G063949	GRMZM2G063949_P01 (+2)	44 kDa	Ref	0.1	-0.1	-0.4	-0.4	-2.4	-1.7	-1.6	-1.4
424	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263	GRMZM2G079263_P01 (+2)	52 kDa	Ref	-3.1	-1.2	-1.5	-1.8	-4.2	Value Missing	Value Missing	Value Missing
425	seq=translation; coord=5:142403718..142405631:1; parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436	GRMZM2G412436_P01	62 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	2.1
426	seq=translation; coord=3:47448537..47463984:-1; parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101	GRMZM2G011101_P01 (+1)	105 kDa	Ref	0	Value Missing	-0.2	Value Missing	0.4	-0.1	-0.8	-1.2
427	seq=translation; coord=9:143165107..143170341:1; parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01 (+3)	42 kDa	Ref	0	0	-0.2	-0.1	1.1	0.6	0.9	0.9
428	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	100 kDa	Ref	0.3	-0.4	-0.3	-0.3	-1.1	-1.7	-1.4	Reference Missing

429	seq=translation; coord=1:290265297..290286811:1; parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664	GRMZM2G082664_P01	52 kDa	Ref	0.6	0.8	0.9	0.9	2.6	2.5	2.6	2.2
430	seq=translation; coord=5:10855539..10861668:-1; parent_transcript=GRMZM2G109383_T01; parent_gene=GRMZM2G109383	GRMZM2G109383_P01	71 kDa	Ref	-0.7	-0.3	-0.9	-1	-2.1	-1.8	-1.3	-1.4
431	seq=translation; coord=2:160150779..160152270:1; parent_transcript=GRMZM2G304548_T01; parent_gene=GRMZM2G304548	GRMZM2G304548_P01	20 kDa	Ref	No Values	No Values	No Values	No Values	1.2	Reference Missing	0.1	-0.1
432	seq=translation; coord=1:192404194..192408778:-1; parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806	GRMZM2G096806_P01	115 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.3	0.7	0.2
433	seq=translation; coord=2:139185152..139187472:-1; parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292	GRMZM2G047292_P01	54 kDa	Ref	No Values	Reference Missing	Reference Missing	Reference Missing	-8.1	-7.6	-7.3	-7.2
434	seq=translation; coord=5:47578824..47582423:1; parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967	GRMZM2G085967_P01 (+1)	35 kDa	Ref	0.3	0.7	-1.3	-1.8	-1.6	-2.3	-1.7	-2.7
435	seq=translation; coord=6:1338452..1339388:-1; parent_transcript=GRMZM2G122357_T01; parent_gene=GRMZM2G122357	GRMZM2G122357_P01	14 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0	Reference Missing	0.6
436	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	61 kDa	Ref	-0.4	-0.5	-0.4	-0.2	-0.4	0.1	-0.5	-0.7
437	seq=translation; coord=4:125089612..125098586:-1; parent_transcript=GRMZM2G157019_T01; parent_gene=GRMZM2G157019	GRMZM2G157019_P01	28 kDa	Ref	-0.6	-1.2	-1.3	-1.3	0.7	0.7	0.1	0.3
438	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	45 kDa	Ref	-0.8	-0.9	0	0.1	-0.2	-0.1	0	0.5
439	seq=translation; coord=3:3887574..3888713:1; parent_transcript=GRMZM2G093405_T01; parent_gene=GRMZM2G093405	GRMZM2G093405_P01 (+1)	24 kDa	Ref	1	1.3	0.4	-0.6	0.7	0.9	0.6	0.7
440	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01 (+8)	104 kDa	Ref	0.2	0	-0.4	-0.3	2.2	1.7	0.9	0.4
441	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	49 kDa	Ref	0.1	0.3	0.1	-0.4	4.1	Reference Missing	5.1	3.9

442	seq=translation; coord=8:116533013..116535098:1; parent_transcript=GRMZM2G009936_T01; parent_gene=GRMZM2G009936	GRMZM2G009936_P01 (+2)	13 kDa	Ref	1.3	1.3	0.5	-0.3	1.3	-0.3	-0.3	-0.7
443	seq=translation; coord=1:62530194..62532719:1; parent_transcript=GRMZM2G577677_T01; parent_gene=GRMZM2G577677	GRMZM2G577677_P01	15 kDa	Ref	0.1	-0.3	-0.6	-1.1	-0.2	-0.2	0.2	-0.3
444	seq=translation; coord=9:106627644..106628551:-1; parent_transcript=GRMZM2G361699_T01; parent_gene=GRMZM2G361699	GRMZM2G361699_P01	12 kDa	Ref	0.3	0.1	-0.1	-0.3	-4	-2.8	Reference Missing	-2.6
445	seq=translation; coord=7:116376688..116380988:1; parent_transcript=GRMZM2G116689_T01; parent_gene=GRMZM2G116689	GRMZM2G116689_P01 (+1)	17 kDa	Ref	0.7	-0.2	1	0.4	-1.2	0.1	-0.8	0.6
446	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01 (+17)	24 kDa	Ref	0.2	0.1	-0.2	-0.3	1.8	1.4	0.6	0.3
447	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620	GRMZM2G035620_P01	31 kDa	Ref	Value Missing	-0.5	Value Missing	Value Missing	-3.4	-2.2	-2	-1.3
448	seq=translation; coord=1:38637065..38637541:1; parent_transcript=AC208204.3_FGT006; parent_gene=AC208204.3_FG006	AC208204.3_FGP006 (+1)	18 kDa	Ref	-0.5	0.8	1.1	-0.2	-0.3	Reference Missing	2	2.9
449	seq=translation; coord=3:168695539..168699190:1; parent_transcript=GRMZM2G156861_T02; parent_gene=GRMZM2G156861	GRMZM2G156861_P02	98 kDa	Ref	1.6	2.2	0.5	0.9	No Values	No Values	No Values	No Values
450	seq=translation; coord=4:193146957..193151153:1; parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551	GRMZM5G821551_P02 (+1)	70 kDa	Ref	-0.7	-0.9	-1.1	-1.2	-3	-3.2	-3.4	-3.7
451	seq=translation; coord=1:221739264..221743951:-1; parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163	GRMZM2G450163_P01	67 kDa	Ref	-0.4	-0.2	-0.3	-0.5	0.2	0.8	0.7	0.5
452	seq=translation; coord=6:4896839..4897613:-1; parent_transcript=GRMZM2G391364_T01; parent_gene=GRMZM2G391364	GRMZM2G391364_P01	17 kDa	Ref	0.6	0.1	1	-0.6	0	1.1	1	2.3
453	seq=translation; coord=5:185405145..185408787:1; parent_transcript=GRMZM2G148387_T01; parent_gene=GRMZM2G148387	GRMZM2G148387_P01	14 kDa	Ref	0.2	-1.5	0.3	0	-5	-4.5	-4.1	-3.2
454	seq=translation; coord=3:141261688..141325830:1; parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584	GRMZM2G073584_P02	102 kDa	Ref	-0.2	0	-0.5	0.3	-1.6	-0.7	-1.5	-1.2

455	seq=translation; coord=10:148228962..148233420:1; parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714	GRMZM2G008714_P01 (+1)	66 kDa	Ref	-0.9	-0.5	-0.1	0.5	5.1	4.8	4.9	4.7
456	seq=translation; coord=5:213904655..213909590:1; parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910	GRMZM5G836910_P01	50 kDa	Ref	No Values	No Values	No Values	No Values	0.4	1.4	Reference Missing	Reference Missing
457	seq=translation; coord=1:91875822..91877199:-1; parent_transcript=GRMZM2G176595_T01; parent_gene=GRMZM2G176595	GRMZM2G176595_P01	30 kDa	Ref	0.8	1.1	1.9	1.7	No Values	No Values	No Values	No Values
458	seq=translation; coord=10:23213183..23215664:1; parent_transcript=GRMZM2G036427_T01; parent_gene=GRMZM2G036427	GRMZM2G036427_P01 (+1)	18 kDa	Ref	0.7	1.8	2	1.9	No Values	No Values	No Values	No Values
459	seq=translation; coord=9:136016928..136020802:-1; parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	63 kDa	Ref	-1	-0.2	-0.5	-0.5	-0.4	0.2	-0.3	-0.7
460	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	39 kDa	Ref	2	1.7	1.5	1.1	Reference Missing	Reference Missing	1.3	1.4
461	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01 (+1)	40 kDa	Ref	-1.2	-1.1	-1	-0.7	0.8	1.7	0.5	0.5
462	seq=translation; coord=2:176644918..176648601:1; parent_transcript=GRMZM2G150616_T01; parent_gene=GRMZM2G150616	GRMZM2G150616_P01	29 kDa	Ref	0.3	0.4	0.3	0.3	2.7	0.1	-0.2	-1
463	seq=translation; coord=4:154624996..154627067:1; parent_transcript=GRMZM2G156785_T01; parent_gene=GRMZM2G156785	GRMZM2G156785_P01 (+2)	15 kDa	Ref	2.4	1	0.7	0.2	3.8	2.5	2.7	2
464	seq=translation; coord=9:23256308..23260236:-1; parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993	GRMZM2G024993_P01 (+1)	67 kDa	Ref	-0.3	0.6	0.2	0.3	-1.5	-2.3	Reference Missing	-0.9
465	seq=translation; coord=4:37762302..37763543:-1; parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050	GRMZM2G112050_P01 (+2)	16 kDa	Ref	1.2	1.1	0.5	0.2	Reference Missing	Reference Missing	3.2	2.9
466	seq=translation; coord=9:28603999..28607933:1; parent_transcript=GRMZM2G153969_T01; parent_gene=GRMZM2G153969	GRMZM2G153969_P01	18 kDa	Ref	-1.1	-1.1	-1.1	-2.2	-0.7	-3.9	-3.2	-4
467	seq=translation; coord=3:197406823..197407784:-1; parent_transcript=GRMZM2G010762_T01; parent_gene=GRMZM2G010762	GRMZM2G010762_P01	23 kDa	Ref	1.2	0.9	2.4	1.9	0.8	-0.7	2.4	3.1

	seq=translation; coord=1:7192641..7198439:-1;											
468	parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158 seq=translation; coord=2:110896551..110900469:-1;	GRMZM2G057158_P01 (+1)	56 kDa	Ref	0.1	-0.3	0	-1	-0.4	-0.5	-0.8	-0.6
469	parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894 seq=translation; coord=8:116617793..116620719:-1;	GRMZM2G033894_P01	46 kDa	Ref	0.5	0.1	0.3	0.1	0.1	-0.5	-0.8	-1
470	parent_transcript=GRMZM5G802801_T01; parent_gene=GRMZM5G802801 seq=translation; coord=2:125696253..125710943:1;	GRMZM5G802801_P01	71 kDa	Ref	No Values	No Values	No Values	No Values	-0.7	0.6	0.2	0.4
471	parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316 seq=translation; coord=6:120018887..120020772:1;	GRMZM5G877316_P02 (+1)	47 kDa	Ref	0.7	0.3	0	0.3	-0.2	0.3	-0.5	-0.6
472	parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404 seq=translation; coord=2:60415730..60417474:1;	GRMZM2G383404_P01	52 kDa	Ref	0.4	1.4	0.6	0.4	No Values	No Values	No Values	No Values
473	parent_transcript=GRMZM2G085260_T01; parent_gene=GRMZM2G085260 seq=translation; coord=10:22319764..22321055:-1;	GRMZM2G085260_P01	34 kDa	Ref	No Values	No Values	No Values	No Values	0	1	1.6	3.3
474	parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283 seq=translation; coord=5:208194750..208197747:1;	GRMZM2G075283_P01	17 kDa	Ref	0.3	0.2	2.2	2.9	No Values	No Values	No Values	No Values
475	parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950 seq=translation; coord=2:1436938..1441569:-1;	GRMZM2G061950_P01	35 kDa	Ref	0.1	-0.4	0.1	-0.4	No Values	No Values	No Values	No Values
476	parent_transcript=GRMZM2G019500_T01; parent_gene=GRMZM2G019500 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G019500_P01	32 kDa	Ref	0.8	0.4	0.5	-0.4	-6.3	-7.1	-7.5	-7.4
477	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=1:236088923..236128384:-1;	GRMZM2G066650_P01	96 kDa	Ref	-0.6	-0.5	0.3	0	1.1	0.8	-0.2	-0.2
478	parent_transcript=GRMZM2G053764_T01; parent_gene=GRMZM2G053764 seq=translation; coord=4:233821047..233828196:1;	GRMZM2G053764_P01 (+3)	42 kDa	Ref	-0.8	0	-0.6	-0.8	-0.5	-0.4	0.1	-0.5
479	parent_transcript=GRMZM2G064023_T01; parent_gene=GRMZM2G064023 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G064023_P01 (+3)	52 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	0.3	-0.4	-0.3
480	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094	GRMZM2G328094_P01	39 kDa	Ref	0.1	-0.2	-0.6	-0.2	0	-0.3	-0.3	-0.3

481	seq=translation; coord=5:215477924..215482853:1; parent_transcript=GRMZM2G078396_T01; parent_gene=GRMZM2G078396 seq=translation; coord=3:6926705..6931400:-1;	GRMZM2G078396_P01 (+4)	15 kDa	Ref	1.1	1.2	0.7	0.9	1.6	0.9	0.5	-0.6
482	parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646 seq=translation; coord=7:19072056..19090250:-1;	GRMZM2G166646_P01	54 kDa	Ref	1.7	0.7	1.3	0.8	3.7	2.3	2.4	1.5
483	parent_transcript=GRMZM2G462325_T01; parent_gene=GRMZM2G462325 seq=translation; coord=1:273865741..273870770:-1;	GRMZM2G462325_P01	49 kDa	Ref	No Values	No Values	No Values	No Values	1.3	1.2	1	0.3
484	parent_transcript=GRMZM2G416388_T01; parent_gene=GRMZM2G416388 seq=translation; coord=1:52807627..52810251:-1;	GRMZM2G416388_P01 (+3)	22 kDa	Ref	-1.2	-1.3	-0.6	-1.1	-2.7	-2	-2.2	-2.1
485	parent_transcript=GRMZM2G018728_T01; parent_gene=GRMZM2G018728 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G018728_P01	14 kDa	Ref	-0.6	-1.3	-1.6	-2.1	-4.4	-3.4	-3.7	-2.6
486	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=8:162579348..162580103:-1;	GRMZM2G401328_P01	19 kDa	Ref	-0.4	-0.7	0.3	0.9	-3	-2.3	-1	-0.4
487	parent_transcript=GRMZM2G030717_T01; parent_gene=GRMZM2G030717 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G030717_P01	16 kDa	Ref	-0.1	0.6	1	0.8	Reference Missing	Reference Missing	Reference Missing	4
488	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=7:168744978..168747272:1;	GRMZM2G005552_P01	38 kDa	Ref	-0.1	-0.5	-0.2	-0.3	Value Missing	Value Missing	Value Missing	Value Missing
489	parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757 seq=translation; coord=4:131010547..131027664:-1;	GRMZM2G039757_P01	72 kDa	Ref	-0.1	0.4	0.9	1.3	5.8	5.8	6.8	7.1
490	parent_transcript=GRMZM2G006672_T02; parent_gene=GRMZM2G006672 seq=translation; coord=7:159130478..159136959:-1;	GRMZM2G006672_P02	40 kDa	Ref	0.4	0.3	0.3	1.1	Reference Missing	Reference Missing	0.9	Reference Missing
491	parent_transcript=GRMZM2G107562_T01; parent_gene=GRMZM2G107562 seq=translation; coord=2:22990515..22995670:1;	GRMZM2G107562_P01	18 kDa	Ref	-1	-1	-1.2	-1.4	-2.6	-2.4	-3	-2.9
492	parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G122937_P01 (+1)	22 kDa	Ref	2.3	1.6	2	0.3	No Values	No Values	No Values	No Values
493	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401	GRMZM2G015401_P01 (+1)	39 kDa	Ref	0.9	0.7	0.2	1.2	2.4	0.1	0	-1.1

494	seq=translation; coord=7:127859191..127864034:-1; parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614	GRMZM2G140614_P01 (+1)	68 kDa	Ref	0.1	0	-0.1	0	3.4	2.8	3.1	2.6
495	seq=translation; coord=1:217021624..217059348:1; parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542	GRMZM2G090542_P01	98 kDa	Ref	-0.1	-0.1	-0.1	0	0.4	-0.3	0.1	0
496	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	59 kDa	Ref	-0.2	-0.1	-0.3	0.3	-0.6	-0.4	0.3	0.7
497	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01 (+1)	136 kDa	Ref	0.2	0.1	-0.1	-0.2	1.2	0.6	0.4	-0.2
498	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G180930_T02; parent_gene=GRMZM2G180930	GRMZM2G180930_P02 (+1)	36 kDa	Ref	-0.1	0.1	-0.4	-0.1	-0.9	-1	-0.9	-0.5
499	seq=translation; coord=2:233428481..233430995:-1; parent_transcript=GRMZM2G018607_T01; parent_gene=GRMZM2G018607	GRMZM2G018607_P01	78 kDa	Ref	1.8	2.1	2.1	1.1	Reference Missing	1.1	3.4	Reference Missing
500	seq=translation; coord=6:56216948..56219146:-1; parent_transcript=GRMZM2G385287_T01; parent_gene=GRMZM2G385287	GRMZM2G385287_P01	21 kDa	Ref	0	-0.1	-0.1	-0.3	0.8	0.6	0.1	-0.3
501	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01 (+1)	23 kDa	Ref	-0.3	-0.1	-0.5	-0.2	1.5	1.6	1.6	1.7
502	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01 (+1)	110 kDa	Ref	-0.7	-1.2	-0.9	-0.7	0.4	0.9	0.7	1.3
503	seq=translation; coord=6:138057377..138059762:-1; parent_transcript=GRMZM2G078985_T01; parent_gene=GRMZM2G078985	GRMZM2G078985_P01 (+2)	22 kDa	Ref	0.6	0	1	0.1	-0.4	0.7	0.1	0.2
504	seq=translation; coord=6:108069110..108070157:1; parent_transcript=GRMZM2G073150_T01; parent_gene=GRMZM2G073150	GRMZM2G073150_P01	16 kDa	Ref	1.2	0.9	1.5	0.3	2	2.1	1.2	2.3
505	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	40 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.1	1.2	3
506	seq=translation; coord=3:186781963..186783499:-1; parent_transcript=GRMZM2G460860_T01; parent_gene=GRMZM2G460860	GRMZM2G460860_P01	35 kDa	Ref	Reference Missing	Reference Missing	Reference Missing	Reference Missing	-3.1	-4.5	Reference Missing	-6

507	seq=translation; coord=8:69592559..69594672:1; parent_transcript=GRMZM2G001514_T01; parent_gene=GRMZM2G001514	GRMZM2G001514_P01	29 kDa	Ref	-1.5	-0.8	-1.6	-2.1	-1.8	-2.6	-2.6	-3.3
508	seq=translation; coord=6:142310594..142315324:-1; parent_transcript=GRMZM2G137535_T01; parent_gene=GRMZM2G137535	GRMZM2G137535_P01 (+1)	35 kDa	Ref	0.2	-0.1	1.5	3	No Values	No Values	No Values	No Values
509	seq=translation; coord=5:169817842..169818381:1; parent_transcript=AC233850.1_FGT002; parent_gene=AC233850.1_FG002	AC233850.1_FGP002	19 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
510	seq=translation; coord=6:69568276..69571793:-1; parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775	GRMZM2G152775_P04	26 kDa	Ref	-1.2	-0.8	-0.8	-0.7	-1.1	-1.7	-1.6	-1.9
511	seq=translation; coord=4:193735481..193760758:1; parent_transcript=AC215244.3_FGT002; parent_gene=AC215244.3_FG002	AC215244.3_FGP002	36 kDa	Ref	2.7	2.9	2.3	2	2	2	1.6	3.6
512	seq=translation; coord=2:2326285..2329820:1; parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541	GRMZM2G077541_P01 (+1)	41 kDa	Ref	-0.2	0	0	0.1	-1.2	-0.8	Reference Missing	-0.1
513	seq=translation; coord=7:41731651..41795285:-1; parent_transcript=GRMZM2G069676_T02; parent_gene=GRMZM2G069676	GRMZM2G069676_P02 (+1)	59 kDa	Ref	-0.3	0	0.1	-0.1	-0.6	-0.3	0.9	0.7
514	seq=translation; coord=6:165533613..165537241:1; parent_transcript=GRMZM5G829778_T01; parent_gene=GRMZM5G829778	GRMZM5G829778_P01	46 kDa	Ref	-0.2	0.1	0.2	0.2	0.8	0.9	1.3	1.6
515	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407	GRMZM2G139407_P01 (+1)	52 kDa	Ref	-0.4	-0.3	-0.5	-0.3	-0.4	-1.3	-0.8	-0.7
516	seq=translation; coord=4:83505768..83508091:1; parent_transcript=GRMZM2G068455_T01; parent_gene=GRMZM2G068455	GRMZM2G068455_P01 (+2)	42 kDa	Ref	-0.1	0.1	0.2	0.2	-1.6	-0.7	-0.6	-0.7
517	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050	GRMZM2G093050_P01 (+1)	112 kDa	Ref	1.7	1	1	0.6	1.7	0.6	0.2	-0.3
518	seq=translation; coord=1:215329050..215330533:1; parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133	GRMZM2G106133_P02	20 kDa	Ref	Reference Missing	1.8	1.2	1.3	1.3	-0.3	0	-0.3
519	seq=translation; coord=5:215493131..215497186:1; parent_transcript=GRMZM5G824600_T03; parent_gene=GRMZM5G824600	GRMZM5G824600_P03	41 kDa	Ref	-0.4	-0.4	-0.6	0.3	-2.7	-3.2	-3.2	-3.3

520	seq=translation; coord=7:46478537..46482054:1; parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129	GRMZM2G011129_P01	33 kDa	Ref	-0.3	-0.7	-0.4	-1.4	-0.6	-1.3	-0.8	-0.7
521	seq=translation; coord=1:10991438..10998924:-1; parent_transcript=GRMZM2G056870_T01; parent_gene=GRMZM2G056870	GRMZM2G056870_P01	26 kDa	Ref	-0.6	-1.1	1	-0.3	No Values	No Values	No Values	No Values
522	seq=translation; coord=3:223089120..223091094:-1; parent_transcript=GRMZM2G042008_T01; parent_gene=GRMZM2G042008	GRMZM2G042008_P01	50 kDa	Ref	1.3	0.7	0.3	1.1	5.3	2.7	2.7	1.5
523	seq=translation; coord=3:190774183..190777585:1; parent_transcript=GRMZM2G062373_T01; parent_gene=GRMZM2G062373	GRMZM2G062373_P01 (+1)	27 kDa	Ref	1.1	1	0.6	-0.2	-0.1	0.4	0.7	1
524	seq=translation; coord=7:148082947..148083258:1; parent_transcript=AC196961.2_FGT003; parent_gene=AC196961.2_FG003	AC196961.2_FGP003 (+20)	11 kDa	Ref	1.8	0.6	0.3	-0.8	2.7	-1.6	-1	-0.2
525	seq=translation; coord=10:85640717..85645627:1; parent_transcript=GRMZM2G394500_T01; parent_gene=GRMZM2G394500	GRMZM2G394500_P01 (+1)	38 kDa	Ref	0	1.7	1.7	1.7	No Values	No Values	No Values	No Values
526	seq=translation; coord=1:41376931..41378234:-1; parent_transcript=GRMZM2G172574_T01; parent_gene=GRMZM2G172574	GRMZM2G172574_P01	15 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	Reference Missing	2.1	3.5
527	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	83 kDa	Ref	0.1	-0.4	Value Missing	-0.1	0.8	Reference Missing	-0.1	-0.3
528	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	33 kDa	Ref	0.8	0.9	0.7	1.2	2.2	0.9	0.6	-0.6
529	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G019236_T01; parent_gene=GRMZM2G019236	GRMZM2G019236_P01 (+2)	118 kDa	Ref	-0.8	-1.3	-1.7	-0.7	-0.3	-0.4	-0.1	-0.6
530	seq=translation; coord=7:41420177..41423983:-1; parent_transcript=GRMZM2G014914_T01; parent_gene=GRMZM2G014914	GRMZM2G014914_P01 (+1)	30 kDa	Ref	1.1	0.8	0.1	0.5	3.2	3	2.4	1.4
531	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	46 kDa	Ref	1.1	0.8	0.9	1.5	1.6	2.5	3	3.5
532	seq=translation; coord=8:12989704..12991151:-1; parent_transcript=GRMZM2G097900_T01; parent_gene=GRMZM2G097900	GRMZM2G097900_P01	21 kDa	Ref	0.6	0	-0.3	-0.5	-0.3	0.4	0.3	0.9

533	seq=translation; coord=1:224236124..224244611:-1; parent_transcript=GRMZM2G031572_T01; parent_gene=GRMZM2G031572	GRMZM2G031572_P01	56 kDa	Ref	-2.1	-2.6	-2.5	-2.2	Value Missing	0.3	-0.5	-0.4
534	seq=translation; coord=8:101408887..101413622:1; parent_transcript=GRMZM2G033799_T01; parent_gene=GRMZM2G033799	GRMZM2G033799_P01 (+2)	49 kDa	Ref	-0.1	-0.1	0	0.3	-1.1	-0.4	-0.4	-0.3
535	seq=translation; coord=1:8135964..8147853:-1; parent_transcript=GRMZM2G176397_T01; parent_gene=GRMZM2G176397	GRMZM2G176397_P01 (+1)	74 kDa	Ref	-0.6	-0.7	-0.7	-0.7	1.9	1.5	1.7	1.9
536	seq=translation; coord=3:136407818..136421472:1; parent_transcript=GRMZM2G168510_T02; parent_gene=GRMZM2G168510	GRMZM2G168510_P02	32 kDa	Ref	-0.6	-0.3	-0.5	-0.8	0.4	-0.4	-1	-0.9
537	seq=translation; coord=8:21615163..21616013:1; parent_transcript=GRMZM2G034157_T01; parent_gene=GRMZM2G034157	GRMZM2G034157_P01	18 kDa	Ref	0.5	0.6	Reference Missing	Reference Missing	-1.2	Reference Missing	Reference Missing	2.9
538	seq=translation; coord=5:125802058..125817596:1; parent_transcript=GRMZM2G038126_T01; parent_gene=GRMZM2G038126	GRMZM2G038126_P01 (+3)	53 kDa	Ref	0	Value Missing	Value Missing	-0.6	-6.4	-5.5	-5.7	-6.7
539	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	34 kDa	Ref	0.6	1.1	1.3	3.4	-4.5	Reference Missing	Reference Missing	Reference Missing
540	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	41 kDa	Ref	-0.7	-0.9	-1.2	-1.4	-1	-1.3	-1.3	-1.7
541	seq=translation; coord=5:46946530..46947446:-1; parent_transcript=AC209987.4_FGT010; parent_gene=AC209987.4_FG010	AC209987.4_FGP010	26 kDa	Ref	-0.2	-0.2	1	2.1	-2.4	-1.3	-0.4	0.3
542	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014	AC209206.3_FGP014	60 kDa	Ref	0.3	0.3	0.8	1.5	No Values	No Values	No Values	No Values
543	seq=translation; coord=1:228643379..228644379:-1; parent_transcript=GRMZM2G153208_T01; parent_gene=GRMZM2G153208	GRMZM2G153208_P01	24 kDa	Ref	-0.5	1.5	1.3	1.8	No Values	No Values	No Values	No Values
544	seq=translation; coord=4:231475847..231481286:1; parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362	GRMZM2G107362_P02 (+3)	47 kDa	Ref	-0.3	-0.4	-0.4	-0.4	-0.8	-0.1	-0.1	-0.8
545	seq=translation; coord=5:18452211..18455290:-1; parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996	GRMZM2G066996_P01	42 kDa	Ref	-1.3	-1.4	-0.9	-0.6	0.8	1	1.2	1.6

	seq=translation; coord=9:8196377..8197429:-1;											
546	parent_transcript=GRMZM2G150656_T03; parent_gene=GRMZM2G150656 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G150656_P03	13 kDa	Ref	-1.6	-1.9	-1.7	-2.6	-2.8	-2.6	-1.9	-1.4
547	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=8:158113092..158118053:-1;	GRMZM2G393671_P01	26 kDa	Ref	-0.7	-0.8	-0.4	-0.8	-1.7	-1.2	-1.2	-0.2
548	parent_transcript=GRMZM2G109472_T01; parent_gene=GRMZM2G109472 seq=translation; coord=7:170244063..170247650:1;	GRMZM2G109472_P01 (+1)	51 kDa	Ref	-0.8	-0.9	-1.3	-1.1	0.8	1.1	1.1	1.5
549	parent_transcript=GRMZM2G024484_T01; parent_gene=GRMZM2G024484 seq=translation; coord=9:7615635..7616809:-1;	GRMZM2G024484_P01 (+2)	55 kDa	Ref	0.7	0.7	-0.1	0.3	1.2	0.1	0.5	0.4
550	parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880 seq=translation; coord=2:1928487..1932811:-1;	GRMZM5G898880_P01	35 kDa	Ref	-0.9	-0.4	-0.7	-0.2	-0.3	-0.4	-0.1	-0.1
551	parent_transcript=GRMZM2G407347_T01; parent_gene=GRMZM2G407347 seq=translation; coord=1:68430654..68436197:1;	GRMZM2G407347_P01 (+1)	27 kDa	Ref	-0.8	-0.4	-0.1	-1	-4	-4.1	-4.2	-4.4
552	parent_transcript=GRMZM5G866758_T02; parent_gene=GRMZM5G866758 seq=translation; coord=4:14930698..14950684:-1;	GRMZM5G866758_P02	41 kDa	Ref	-0.1	-0.1	-0.5	0	-0.7	-0.8	-0.7	-1
553	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=1:39213217..39219522:-1;	GRMZM2G151050_P01 (+1)	63 kDa	Ref	Reference Missing	Reference Missing	Reference Missing	0.9	Reference Missing	Reference Missing	Reference Missing	Reference Missing
554	parent_transcript=GRMZM2G141799_T01; parent_gene=GRMZM2G141799 seq=translation; coord=4:53078446..53083109:-1;	GRMZM2G141799_P01	29 kDa	Ref	-0.9	-0.9	-1	-0.8	2.4	2.4	2.8	2.9
555	parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708 seq=translation; coord=8:83335717..83339016:1;	GRMZM2G134708_P01	46 kDa	Ref	-0.3	-0.4	-0.1	0.3	6.8	5	4.7	Value Missing
556	parent_transcript=GRMZM2G104025_T01; parent_gene=GRMZM2G104025 seq=translation; coord=5:67403566..67405443:1;	GRMZM2G104025_P01 (+1)	21 kDa	Ref	0.5	0.5	0.3	0.2	-0.1	-0.6	-1.3	-1.8
557	parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929 seq=translation; coord=9:133421526..133422671:1;	GRMZM2G128929_P01	38 kDa	Ref	0.3	0.4	0.3	0.3	0.9	0.8	0.8	0.3
558	parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	38 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	-1.1	-0.4	0.8

559	seq=translation; coord=1:293793122..293796213:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02 (+1)	41 kDa	Ref	1	0.8	0.9	0.6	-1.3	-1.5	-1.8	-0.2
560	seq=translation; coord=5:85252669..85257667:1; parent_transcript=GRMZM2G104632_T01; parent_gene=GRMZM2G104632	GRMZM2G104632_P01	43 kDa	Ref	0.4	0.2	-0.3	-0.1	1.5	1.2	1.4	0.7
561	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	33 kDa	Ref	1.7	1.2	1.1	0.8	4.4	4.3	4.6	3.5
562	seq=translation; coord=6:75510288..75518697:1; parent_transcript=GRMZM2G060870_T01; parent_gene=GRMZM2G060870	GRMZM2G060870_P01 (+1)	23 kDa	Ref	-1.2	-1.8	-1.2	-1.4	-2.3	-2	-2.2	-0.8
563	seq=translation; coord=8:14389329..14393515:-1; parent_transcript=GRMZM2G018177_T01; parent_gene=GRMZM2G018177	GRMZM2G018177_P01	27 kDa	Ref	0.1	0.7	0.4	0.3	-0.4	-0.5	0.3	0.6
564	seq=translation; coord=1:3000161..3000884:-1; parent_transcript=GRMZM2G137329_T01; parent_gene=GRMZM2G137329	GRMZM2G137329_P01	10 kDa	Ref	2.3	3.4	2.6	2.3	0.9	0.7	0.3	Reference Missing
565	seq=translation; coord=4:217521316..217523853:1; parent_transcript=GRMZM2G066222_T01; parent_gene=GRMZM2G066222	GRMZM2G066222_P01 (+2)	10 kDa	Ref	0.8	0.4	0.1	0.7	-1.2	-3.5	-3.4	-3.7
566	seq=translation; coord=8:148264071..148273363:1; parent_transcript=GRMZM2G030167_T01; parent_gene=GRMZM2G030167	GRMZM2G030167_P01	27 kDa	Ref	0.2	1	1	0	-1.4	-0.8	-0.9	-0.3
567	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	34 kDa	Ref	-0.4	-0.5	-0.2	-0.8	1.6	1.7	1.4	1.5
568	seq=translation; coord=9:124034244..124040497:-1; parent_transcript=GRMZM2G162968_T01; parent_gene=GRMZM2G162968	GRMZM2G162968_P01	109 kDa	Ref	-0.4	-0.6	-0.1	-0.9	0.2	1	1	1.2
569	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	44 kDa	Ref	2	1.9	2.4	1.4	-2.3	-3.4	-3.4	-3.8
570	seq=translation; coord=4:69841345..69843586:1; parent_transcript=GRMZM2G100225_T01; parent_gene=GRMZM2G100225	GRMZM2G100225_P01 (+1)	28 kDa	Ref	0.8	0.1	1.1	0	1.6	1.7	1.5	1.7
571	seq=translation; coord=6:157770836..157775279:1; parent_transcript=GRMZM2G424053_T02; parent_gene=GRMZM2G424053	GRMZM2G424053_P02	14 kDa	Ref	-1.7	-1.7	-1.1	-1.3	-1.4	-1.6	-1.5	-0.2

572	seq=translation; coord=2:190158113..190161171:-1; parent_transcript=GRMZM2G365374_T01; parent_gene=GRMZM2G365374	GRMZM2G365374_P01	73 kDa	Ref	-0.4	-0.1	0.8	-0.3	-0.1	-2.3	-2.6	-2.9
573	seq=translation; coord=1:167851430..167863929:-1; parent_transcript=GRMZM2G130034_T01; parent_gene=GRMZM2G130034	GRMZM2G130034_P01 (+1)	50 kDa	Ref	2.9	3	2	2.4	-2.9	-2.7	Reference Missing	-2.9
574	seq=translation; coord=1:233560736..233562244:-1; parent_transcript=GRMZM2G001850_T01; parent_gene=GRMZM2G001850	GRMZM2G001850_P01	21 kDa	Ref	-1.3	-1.9	-1.3	-1.6	-0.4	-2.2	-2.2	-2.8
575	seq=translation; coord=6:43621161..43627397:1; parent_transcript=GRMZM2G025214_T02; parent_gene=GRMZM2G025214	GRMZM2G025214_P02	40 kDa	Ref	No Values	No Values	No Values	No Values	0.4	0.4	0.1	0.1
576	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	81 kDa	Ref	0.4	0.2	0.1	0.2	4.6	3.5	2.9	2.8
577	seq=translation; coord=9:94249084..94255465:1; parent_transcript=AC211394.4_FGT004; parent_gene=AC211394.4_FG004	AC211394.4_FGP004	55 kDa	Ref	0	0.8	0.9	0.4	No Values	No Values	No Values	No Values
578	seq=translation; coord=6:115546691..115548383:1; parent_transcript=GRMZM2G156310_T01; parent_gene=GRMZM2G156310	GRMZM2G156310_P01	35 kDa	Ref	0.4	0.3	0.1	0.1	No Values	No Values	No Values	No Values
579	seq=translation; coord=10:96759871..96761276:-1; parent_transcript=GRMZM2G330635_T01; parent_gene=GRMZM2G330635	GRMZM2G330635_P01	25 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	1.5	1.8	1.9
580	seq=translation; coord=6:107821435..107825807:-1; parent_transcript=GRMZM2G135498_T01; parent_gene=GRMZM2G135498	GRMZM2G135498_P01	49 kDa	Ref	1.2	1.2	0.3	1.1	1.2	1.1	Reference Missing	-0.6
581	seq=translation; coord=4:201542946..201547734:-1; parent_transcript=GRMZM2G381744_T01; parent_gene=GRMZM2G381744	GRMZM2G381744_P01	59 kDa	Ref	-1.1	-1.1	-0.9	-1	0.5	0.1	-0.3	-0.9
582	seq=translation; coord=1:247547660..247549896:1; parent_transcript=GRMZM2G027451_T02; parent_gene=GRMZM2G027451	GRMZM2G027451_P02 (+3)	24 kDa	Ref	1.1	0.8	-0.1	0.4	1.1	1.4	0.9	-0.4
583	seq=translation; coord=4:39092198..39097412:-1; parent_transcript=GRMZM2G158153_T01; parent_gene=GRMZM2G158153	GRMZM2G158153_P01 (+1)	73 kDa	Ref	0.9	0.4	0.3	-0.1	0.8	0	-0.1	-0.1
584	seq=translation; coord=1:99538428..99539066:-1; parent_transcript=AC194914.3_FGT002; parent_gene=AC194914.3_FG002	AC194914.3_FGP002	23 kDa	Ref	-0.3	-0.7	-0.2	-0.1	-2	-0.7	-0.6	-1.1

585	seq=translation; coord=6:137412311..137414138:-1; parent_transcript=AC233866.1_FGT006; parent_gene=AC233866.1_FG006	AC233866.1_FGP006 (+3)	49 kDa	Ref	No Values	No Values	No Values	No Values	No Values	No Values	No Values	No Values
586	seq=translation; coord=4:236107257..236109295:-1; parent_transcript=GRMZM2G051208_T01; parent_gene=GRMZM2G051208	GRMZM2G051208_P01	17 kDa	Ref	-0.7	-0.8	-0.8	-1.4	-1.5	-3.4	-2	-3.4
587	seq=translation; coord=5:168671806..168673715:1; parent_transcript=GRMZM2G113332_T01; parent_gene=GRMZM2G113332	GRMZM2G113332_P01	11 kDa	Ref	2.4	1.5	0.8	-0.5	2.5	2.7	3.1	2.9
588	seq=translation; coord=4:194761789..194765861:1; parent_transcript=GRMZM2G149150_T01; parent_gene=GRMZM2G149150	GRMZM2G149150_P01	50 kDa	Ref	Reference Missing	1.4	Reference Missing	0.3	-2.6	-3.1	-3	-3.2
589	seq=translation; coord=9:25922353..25927460:1; parent_transcript=GRMZM2G083716_T01; parent_gene=GRMZM2G083716	GRMZM2G083716_P01 (+3)	64 kDa	Ref	-1.9	-1.3	-0.3	-1.3	-0.6	0	-0.6	-0.8
590	seq=translation; coord=7:86433388..86439128:-1; parent_transcript=GRMZM2G473001_T01; parent_gene=GRMZM2G473001	GRMZM2G473001_P01	110 kDa	Ref	0.1	-0.9	-0.9	-0.9	Value Missing	2.9	Value Missing	2.3
591	seq=translation; coord=3:179988293..179993427:-1; parent_transcript=GRMZM2G014136_T01; parent_gene=GRMZM2G014136	GRMZM2G014136_P01	76 kDa	Ref	-0.4	-0.7	-0.8	-0.1	3.2	2.9	3	3
592	seq=translation; coord=5:14853348..14857185:-1; parent_transcript=GRMZM2G066191_T01; parent_gene=GRMZM2G066191	GRMZM2G066191_P01 (+1)	50 kDa	Ref	0.1	0.6	-0.5	-0.5	1.3	0.2	0.1	-1
593	seq=translation; coord=7:25903581..25911265:1; parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958	GRMZM2G016958_P01	48 kDa	Ref	-0.2	0.3	0.6	0.7	-4.9	-3.8	Reference Missing	-3.3
594	seq=translation; coord=10:93684085..93687059:-1; parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699	GRMZM5G833699_P01	82 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	2	2.4	2.5
595	seq=translation; coord=7:39873483..39874398:1; parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560	GRMZM5G896560_P01	24 kDa	Ref	2.9	3.1	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
596	seq=translation; coord=2:220539596..220543690:1; parent_transcript=GRMZM2G163421_T01; parent_gene=GRMZM2G163421	GRMZM2G163421_P01	57 kDa	Ref	0.4	1	0.3	0	-2	-2.5	-2.7	-2.2
597	seq=translation; coord=10:119822322..119823346:-1; parent_transcript=GRMZM2G096695_T01; parent_gene=GRMZM2G096695	GRMZM2G096695_P01	16 kDa	Ref	1.2	1.1	0.5	0.3	-3.2	-2.5	-2.6	-1.9

598	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01 (+1)	36 kDa	Ref	1.4	1.2	1.2	1	2.8	2.2	1.8	2.2
599	seq=translation; coord=2:207032350..207038547:1; parent_transcript=GRMZM2G039251_T01; parent_gene=GRMZM2G039251	GRMZM2G039251_P01 (+1)	34 kDa	Ref	0	-0.4	-0.6	0.2	-0.3	-1.3	-1	-0.9
600	seq=translation; coord=7:116285614..116288886:-1; parent_transcript=GRMZM2G160770_T01; parent_gene=GRMZM2G160770	GRMZM2G160770_P01	23 kDa	Ref	0.3	-0.4	0	-1.3	-1.8	-0.4	-0.9	-0.5
601	seq=translation; coord=1:296201923..296204120:1; parent_transcript=GRMZM5G874478_T01; parent_gene=GRMZM5G874478	GRMZM5G874478_P01 (+2)	22 kDa	Ref	1.3	1.1	0.6	0.6	2.8	1.4	Reference Missing	1.7
602	seq=translation; coord=2:189276282..189278019:-1; parent_transcript=GRMZM2G004138_T01; parent_gene=GRMZM2G004138	GRMZM2G004138_P01	31 kDa	Ref	0	0.2	1.8	-0.2	-2.9	-1.9	-1.3	-1
603	seq=translation; coord=1:204681269..204683434:-1; parent_transcript=GRMZM2G057608_T01; parent_gene=GRMZM2G057608	GRMZM2G057608_P01 (+5)	12 kDa	Ref	1.9	2	1.2	1.2	1.8	-0.8	-1.2	-0.9
604	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	62 kDa	Ref	0	-0.1	-0.5	-0.3	-4	-4.3	-4.5	-4.2
605	seq=translation; coord=4:63419630..63429299:-1; parent_transcript=GRMZM2G075775_T01; parent_gene=GRMZM2G075775	GRMZM2G075775_P01	23 kDa	Ref	-0.8	-1	-1.7	-1.6	-1.8	-2.5	-3.3	-3.3
606	seq=translation; coord=1:193791442..193794419:-1; parent_transcript=GRMZM2G148744_T01; parent_gene=GRMZM2G148744	GRMZM2G148744_P01 (+2)	19 kDa	Ref	0.7	1.1	0.8	0.5	No Values	Reference Missing	No Values	Reference Missing
607	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01 (+4)	15 kDa	Ref	-2.8	-2.5	-1.7	-2.1	-0.3	-2.8	-2.7	-2.9
608	seq=translation; coord=3:33565292..33570884:-1; parent_transcript=GRMZM2G328893_T01; parent_gene=GRMZM2G328893	GRMZM2G328893_P01	32 kDa	Ref	0	0	0	0	4.9	6.4	4.6	4.9
609	seq=translation; coord=9:92916278..92921897:-1; parent_transcript=GRMZM2G326472_T01; parent_gene=GRMZM2G326472	GRMZM2G326472_P01 (+2)	110 kDa	Ref	-0.5	-1.2	-1.7	-1.9	-1.5	-0.8	-0.6	-0.7
610	seq=translation; coord=5:146886556..146888542:-1; parent_transcript=GRMZM2G014444_T01; parent_gene=GRMZM2G014444	GRMZM2G014444_P01 (+4)	20 kDa	Ref	-0.1	-0.4	-0.2	0.1	0.1	-0.7	-1.1	-1.5

611	seq=translation; coord=1:35919768..35937067:-1; parent_transcript=GRMZM2G174589_T01; parent_gene=GRMZM2G174589	GRMZM2G174589_P01	63 kDa	Ref	0	0.1	-0.5	-0.1	-3.1	-3.3	-3.2	-3.9
612	seq=translation; coord=4:183698889..183701902:1; parent_transcript=GRMZM2G088847_T01; parent_gene=GRMZM2G088847	GRMZM2G088847_P01 (+5)	12 kDa	Ref	-1.6	Value Missing	-0.9	Value Missing	-3	-1.6	-1.7	-1.6
613	seq=translation; coord=5:191366452..191369776:1; parent_transcript=GRMZM5G840002_T01; parent_gene=GRMZM5G840002	GRMZM5G840002_P01 (+2)	26 kDa	Ref	-1.4	-0.6	-0.5	-1	-2.9	-2.5	-2.9	-3.3
614	seq=translation; coord=3:213298401..213303662:1; parent_transcript=GRMZM2G033515_T01; parent_gene=GRMZM2G033515	GRMZM2G033515_P01	46 kDa	Ref	Value Missing	Value Missing	Value Missing	-3.7	Value Missing	Value Missing	Value Missing	Value Missing
615	seq=translation; coord=3:158348059..158355046:1; parent_transcript=GRMZM2G139617_T01; parent_gene=GRMZM2G139617	GRMZM2G139617_P01	55 kDa	Ref	1.3	Reference Missing	Reference Missing	-0.3	4.3	3.8	6.5	4.3
616	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01 (+1)	108 kDa	Ref	Reference Missing	No Values	No Values	No Values	-7.7	-9.1	-8.9	-9.9
617	seq=translation; coord=2:2487249..2492988:-1; parent_transcript=GRMZM2G104430_T01; parent_gene=GRMZM2G104430	GRMZM2G104430_P01 (+1)	51 kDa	Ref	1	1.4	1.1	0.9	-2.3	-1.6	-1.5	-1.5
618	seq=translation; coord=4:110069837..110073965:1; parent_transcript=GRMZM2G139680_T01; parent_gene=GRMZM2G139680	GRMZM2G139680_P01	28 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	-0.4	-0.4	-0.1
619	seq=translation; coord=7:13844415..13850805:1; parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898	GRMZM2G001898_P01	43 kDa	Ref	0	0.1	-0.1	0.1	7.4	6.5	6.2	6
620	seq=translation; coord=3:218835389..218837093:-1; parent_transcript=GRMZM2G074097_T01; parent_gene=GRMZM2G074097	GRMZM2G074097_P01	37 kDa	Ref	-0.7	-1.3	-1.6	-2.2	-0.4	-2.2	-1.5	-1.9
621	seq=translation; coord=1:7566145..7569296:1; parent_transcript=GRMZM2G410991_T01; parent_gene=GRMZM2G410991	GRMZM2G410991_P01	37 kDa	Ref	-1.1	0	0.2	0.5	No Values	No Values	No Values	No Values
622	seq=translation; coord=1:8972308..8976833:-1; parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932	GRMZM2G046932_P01	81 kDa	Ref	0.5	-0.2	-0.4	0	0.3	0.7	0.3	-0.2
623	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01 (+4)	60 kDa	Ref	0.1	-0.3	-0.4	-0.3	-0.1	-0.7	-1	-1.2

624	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01 (+2)	69 kDa	Ref	0.7	0.6	0.3	1.3	2.7	1.1	0.9	1.2
625	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	27 kDa	Ref	-1	-0.8	0.1	0.7	0.3	0.5	0.7	1.5
626	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01 (+2)	40 kDa	Ref	0.8	0.3	0.4	-0.2	2.6	2.3	1.6	1.4
627	seq=translation; coord=1:214719298..214723588:1; parent_transcript=GRMZM2G058702_T01; parent_gene=GRMZM2G058702	GRMZM2G058702_P01 (+1)	49 kDa	Ref	-0.4	-0.8	-0.7	-0.2	4.8	3.7	3.6	3.3
628	seq=translation; coord=2:190424050..190431552:1; parent_transcript=GRMZM2G446050_T01; parent_gene=GRMZM2G446050	GRMZM2G446050_P01	170 kDa	Ref	-0.7	-0.8	-1	-1.1	-0.5	-1.7	-2.2	-2.8
629	seq=translation; coord=9:150809669..150813518:1; parent_transcript=GRMZM2G169384_T01; parent_gene=GRMZM2G169384	GRMZM2G169384_P01	44 kDa	Ref	1.3	1.1	0.9	0.1	1.3	-1	-1	-0.6
630	seq=translation; coord=4:54122481..54127439:-1; parent_transcript=GRMZM2G070422_T01; parent_gene=GRMZM2G070422	GRMZM2G070422_P01 (+1)	39 kDa	Ref	-0.1	-0.3	-0.1	-0.4	0.1	-1	-1.2	-1.9
631	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01 (+2)	61 kDa	Ref	-0.9	-0.2	-0.1	-0.1	-3	-2.8	-2.5	-2.7
632	seq=translation; coord=6:113343612..113346307:1; parent_transcript=GRMZM2G168119_T01; parent_gene=GRMZM2G168119	GRMZM2G168119_P01	35 kDa	Ref	1.1	0.6	1	0	2.9	2.7	2.6	5.2
633	seq=translation; coord=10:29873986..29885675:1; parent_transcript=GRMZM2G042089_T01; parent_gene=GRMZM2G042089	GRMZM2G042089_P01 (+2)	57 kDa	Ref	0.1	-0.1	-0.5	-0.1	0.5	-0.3	-0.6	-1.1
634	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	79 kDa	Ref	-0.4	-0.7	-1.3	-0.3	4.9	4.1	5.8	4.8
635	seq=translation; coord=9:129405892..129410419:1; parent_transcript=GRMZM2G125148_T01; parent_gene=GRMZM2G125148	GRMZM2G125148_P01 (+2)	62 kDa	Ref	0.5	-0.6	-0.4	-0.9	-1.1	-4.1	-3.3	-3.7
636	seq=translation; coord=7:13173972..13176516:-1; parent_transcript=GRMZM2G144653_T02; parent_gene=GRMZM2G144653	GRMZM2G144653_P02	13 kDa	Ref	-1.8	-1.6	-1.2	-1.5	0.5	0.3	0.3	3.2

637	seq=translation; coord=1:154077677..154081800:1; parent_transcript=GRMZM2G056039_T01; parent_gene=GRMZM2G056039 seq=translation; coord=4:9677072..9677727:-1;	GRMZM2G056039_P01	71 kDa	Ref	0.9	0.6	0.6	0.2	-0.7	-0.7	-0.8	-1.2
638	parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675 seq=translation; coord=1:25625764..25630712:-1; parent_transcript=GRMZM2G091563_T01; parent_gene=GRMZM2G091563 seq=translation; coord=5:23016144..23019861:1;	GRMZM2G419675_P01 (+1)	16 kDa	Ref	-0.1	1.7	2.1	2.3	0.2	-0.1	-0.3	0
639	parent_transcript=GRMZM2G091563_T01; parent_gene=GRMZM2G091563 seq=translation; coord=5:23016144..23019861:1; parent_transcript=GRMZM2G030169_T01; parent_gene=GRMZM2G030169 seq=translation; coord=8:8351675..8357336:1;	GRMZM2G091563_P01	58 kDa	Ref	0.2	Value Missing	0.7	-0.3	No Values	No Values	No Values	No Values
640	parent_transcript=GRMZM2G030169_T01; parent_gene=GRMZM2G030169 seq=translation; coord=4:12082697..12084089:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153 seq=translation; coord=3:128521980..128525993:1;	GRMZM2G030169_P01 (+3)	42 kDa	Ref	0.1	0.2	-0.6	0.2	-0.5	-1.4	-1.6	-2.5
641	parent_transcript=GRMZM2G132796_T01; parent_gene=GRMZM2G132796 seq=translation; coord=4:12082697..12084089:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153 seq=translation; coord=3:128521980..128525993:1;	GRMZM2G132796_P01	68 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
642	parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153 seq=translation; coord=3:128521980..128525993:1; parent_transcript=GRMZM2G034083_T01; parent_gene=GRMZM2G034083 seq=translation; coord=1:298687651..298689984:1;	GRMZM2G358153_P01	31 kDa	Ref	0.2	0	1.2	2.9	4.2	5	5.2	6
643	parent_transcript=GRMZM2G034083_T01; parent_gene=GRMZM2G034083 seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637 seq=translation; coord=7:1266505..1269350:-1;	GRMZM2G034083_P01	47 kDa	Ref	-1.1	-0.8	-0.7	-0.6	No Values	No Values	No Values	No Values
644	parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637 seq=translation; coord=7:1266505..1269350:-1; parent_transcript=GRMZM2G420743_T01; parent_gene=GRMZM2G420743 seq=translation; coord=1:172122450..172128491:-1;	GRMZM5G821637_P05	38 kDa	Ref	1.8	1.6	0.7	-0.2	No Values	No Values	No Values	No Values
645	parent_transcript=GRMZM2G420743_T01; parent_gene=GRMZM2G420743 seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262 seq=translation; coord=1:167864280..167870604:1;	GRMZM2G420743_P01	26 kDa	Ref	-0.3	0.8	0	0.6	No Values	No Values	No Values	No Values
646	parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262 seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095 seq=translation; coord=1:230179502..230183279:1;	GRMZM2G029262_P01 (+2)	39 kDa	Ref	-0.2	-0.2	-0.4	-0.4	0.8	0.4	0.3	0.3
647	parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095 seq=translation; coord=1:230179502..230183279:1; parent_transcript=GRMZM2G131577_T01; parent_gene=GRMZM2G131577 seq=translation; coord=2:212180089..212183936:-1;	GRMZM2G130095_P01 (+1)	54 kDa	Ref	1.4	0.7	1.1	0.5	0.4	-1.2	Reference Missing	-1.3
648	parent_transcript=GRMZM2G131577_T01; parent_gene=GRMZM2G131577 seq=translation; coord=2:212180089..212183936:-1; parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160	GRMZM2G131577_P01 (+1)	18 kDa	Ref	No Values	No Values	No Values	No Values	No Values	No Values	No Values	No Values
649	parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160	GRMZM2G365160_P01 (+1)	59 kDa	Ref	1	1	0.6	1.1	2.1	1.6	1.2	0.8

650	seq=translation; coord=4:33112293..33117947:1; parent_transcript=GRMZM2G104907_T01; parent_gene=GRMZM2G104907	GRMZM2G104907_P01	27 kDa	Ref	-0.5	-1.1	-0.9	-1.4	-1.2	-2.7	-2.6	-3.2
651	seq=translation; coord=3:168523033..168526394:1; parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845	GRMZM2G086845_P01	35 kDa	Ref	-0.5	-0.8	-0.3	-0.6	-0.3	0.2	0.3	0.3
652	seq=translation; coord=4:63703567..63707582:1; parent_transcript=GRMZM2G024959_T01; parent_gene=GRMZM2G024959	GRMZM2G024959_P01 (+1)	45 kDa	Ref	-0.5	-0.8	-0.1	-0.3	0.8	1.7	1.5	0.8
653	seq=translation; coord=4:165966482..165969746:-1; parent_transcript=GRMZM2G125268_T01; parent_gene=GRMZM2G125268	GRMZM2G125268_P01	59 kDa	Ref	-0.5	-1.1	-1.7	-1.5	-2.5	-1.1	-0.6	-0.6
654	seq=translation; coord=10:142067983..142070677:1; parent_transcript=GRMZM2G019325_T01; parent_gene=GRMZM2G019325	GRMZM2G019325_P01 (+1)	18 kDa	Ref	0.3	-0.4	-1.3	-0.6	0.1	-0.7	-1	-1.9
655	seq=translation; coord=2:196050685..196097541:1; parent_transcript=GRMZM2G058105_T01; parent_gene=GRMZM2G058105	GRMZM2G058105_P01	35 kDa	Ref	0.4	0	-0.6	-0.7	1.6	0.9	0.8	0.3
656	seq=translation; coord=10:4243574..4244555:-1; parent_transcript=GRMZM5G898755_T01; parent_gene=GRMZM5G898755	GRMZM5G898755_P01 (+1)	12 kDa	Ref	2	0.8	-0.4	-1	-5.1	-5.4	-5.4	-5.3
657	seq=translation; coord=10:76402669..76405224:1; parent_transcript=GRMZM2G079908_T01; parent_gene=GRMZM2G079908	GRMZM2G079908_P01 (+2)	13 kDa	Ref	2.9	1.4	2.2	0.3	-1.2	-0.8	-1.1	0.5
658	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	29 kDa	Ref	0.3	1	1.4	1.8	-1.1	-1	-0.2	0.1
659	seq=translation; coord=4:229408072..229414150:-1; parent_transcript=GRMZM2G162992_T02; parent_gene=GRMZM2G162992	GRMZM2G162992_P02	71 kDa	Ref	0.2	-0.3	-0.4	-1	-0.9	-1.7	-1.1	-2
660	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P01 (+6)	72 kDa	Ref	0.6	0.2	1.1	1.2	1.2	1.1	2.8	2.9
661	seq=translation; coord=1:214899491..214901246:-1; parent_transcript=AC217050.4_FGT006; parent_gene=AC217050.4_FG006	AC217050.4_FGP006	29 kDa	Ref	2.1	1.5	2	1.5	0.9	-1.2	-1.5	1.4
662	seq=translation; coord=UNKNOWN:5070241..5074601:-1; parent_transcript=GRMZM2G351125_T01; parent_gene=GRMZM2G351125	GRMZM2G351125_P01	146 kDa	Ref	1.1	1	0.8	0.8	-4.9	-5.4	-6.2	-5.8

663	seq=translation; coord=4:197713557..197717259:-1; parent_transcript=GRMZM2G050218_T01; parent_gene=GRMZM2G050218	GRMZM2G050218_P01	40 kDa	Ref	-0.2	-0.8	-0.8	-1.2	3.4	1.6	1.6	1.7
664	seq=translation; coord=9:14322326..14327546:-1; parent_transcript=GRMZM2G014240_T01; parent_gene=GRMZM2G014240	GRMZM2G014240_P01	80 kDa	Ref	1.3	1.5	0.3	1.2	3.5	1.3	0.9	0.2
665	seq=translation; coord=10:1152679..1158648:-1; parent_transcript=GRMZM2G057441_T01; parent_gene=GRMZM2G057441	GRMZM2G057441_P01	117 kDa	Ref	-0.2	-0.4	-0.7	0	-1.6	-2.2	-2	-1.7
666	seq=translation; coord=5:193849196..193850728:-1; parent_transcript=GRMZM2G147014_T01; parent_gene=GRMZM2G147014	GRMZM2G147014_P01	31 kDa	Ref	0.4	1.2	1.8	1.3	No Values	No Values	No Values	No Values
667	seq=translation; coord=8:25334083..25343016:1; parent_transcript=GRMZM2G373928_T01; parent_gene=GRMZM2G373928	GRMZM2G373928_P01 (+1)	19 kDa	Ref	-0.7	-0.9	-0.9	-1	5.9	6.5	6.2	Value Missing
668	seq=translation; coord=4:147218569..147222484:-1; parent_transcript=GRMZM2G070343_T01; parent_gene=GRMZM2G070343	GRMZM2G070343_P01 (+2)	19 kDa	Ref	-0.2	-0.6	0.8	-0.6	-2.9	-1.4	-1.6	0.3
669	seq=translation; coord=8:136129273..136131879:-1; parent_transcript=GRMZM2G100146_T01; parent_gene=GRMZM2G100146	GRMZM2G100146_P01	33 kDa	Ref	No Values	No Values	No Values	No Values	0.5	-0.9	-1.5	-1.5
670	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	79 kDa	Ref	No Values	No Values	No Values	No Values	0.9	0.9	0.4	0.8
671	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	54 kDa	Ref	-1.1	-1.5	-1.7	-1.5	No Values	No Values	No Values	No Values
672	seq=translation; coord=8:118103124..118103722:-1; parent_transcript=AC197705.4_FGT003; parent_gene=AC197705.4_FG003	AC197705.4_FGP003	19 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.1	1.1	3.9
673	seq=translation; coord=3:59325157..59327502:1; parent_transcript=GRMZM2G107228_T01; parent_gene=GRMZM2G107228	GRMZM2G107228_P01	38 kDa	Ref	0.3	0.1	Reference Missing	1.7	No Values	No Values	No Values	No Values
674	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	51 kDa	Ref	0	0	0.3	1.2	0.7	-0.1	0.3	0.6
675	seq=translation; coord=6:49040773..49051761:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	67 kDa	Ref	-0.4	-0.5	-0.8	-0.5	0.5	1	0.9	0.4

676	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G014805_T01; parent_gene=GRMZM2G014805	GRMZM2G014805_P01	132 kDa	Ref	-0.7	-0.9	-0.9	-0.7	-0.4	-0.9	-1	-1.1
677	seq=translation; coord=1:175294828..175302644:-1; parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365	GRMZM2G022365_P01	43 kDa	Ref	1.1	0.1	0.4	0.6	1.5	1.8	1.5	1.2
678	seq=translation; coord=7:155957641..155960914:1; parent_transcript=GRMZM2G173863_T01; parent_gene=GRMZM2G173863	GRMZM2G173863_P01 (+1)	22 kDa	Ref	0.5	0	0	-1	-0.8	-2.1	-2.6	-1.6
679	seq=translation; coord=5:9900674..9908640:1; parent_transcript=GRMZM2G096596_T01; parent_gene=GRMZM2G096596	GRMZM2G096596_P01	52 kDa	Ref	-1.2	-1.2	-0.8	-1.1	0.2	-0.8	-0.4	-1.2
680	seq=translation; coord=2:222875577..222883048:1; parent_transcript=GRMZM2G172101_T01; parent_gene=GRMZM2G172101	GRMZM2G172101_P01 (+2)	52 kDa	Ref	0.2	0.6	0.4	0.5	-0.9	-0.3	-0.1	0
681	seq=translation; coord=8:138510107..138515042:1; parent_transcript=GRMZM2G700683_T01; parent_gene=GRMZM2G700683	GRMZM2G700683_P01	127 kDa	Ref	No Values	No Values	No Values	No Values	0.8	0.7	0.4	0.2
682	seq=translation; coord=7:6064236..6068299:1; parent_transcript=GRMZM2G025977_T01; parent_gene=GRMZM2G025977	GRMZM2G025977_P01 (+2)	40 kDa	Ref	0.6	0.5	1	0.5	-5.7	-5	-4.9	-5.5
683	seq=translation; coord=1:12146189..12150797:1; parent_transcript=GRMZM2G000823_T01; parent_gene=GRMZM2G000823	GRMZM2G000823_P01	52 kDa	Ref	-0.4	-0.5	0	-0.1	1.9	3.1	3.1	3.3
684	seq=translation; coord=8:116620898..116625716:1; parent_transcript=GRMZM5G874500_T02; parent_gene=GRMZM5G874500	GRMZM5G874500_P02 (+1)	65 kDa	Ref	0.5	0.2	-0.1	-0.3	-1.3	-0.9	-0.9	-1.2
685	seq=translation; coord=2:233433323..233435947:-1; parent_transcript=GRMZM2G018197_T01; parent_gene=GRMZM2G018197	GRMZM2G018197_P01	44 kDa	Ref	1	0.6	0.4	0.5	1.9	0.8	0.4	-0.5
686	seq=translation; coord=3:8746797..8754263:1; parent_transcript=GRMZM2G120271_T01; parent_gene=GRMZM2G120271	GRMZM2G120271_P01	28 kDa	Ref	0.1	-0.2	0.1	-0.8	-0.4	-0.8	-0.7	-1.5
687	seq=translation; coord=1:288732967..288734700:1; parent_transcript=GRMZM2G164020_T01; parent_gene=GRMZM2G164020	GRMZM2G164020_P01 (+1)	38 kDa	Ref	-0.2	-1.4	-1.4	-3	-3.1	-4.2	-4.1	-5
688	seq=translation; coord=7:39219675..39225654:-1; parent_transcript=GRMZM2G471269_T04; parent_gene=GRMZM2G471269	GRMZM2G471269_P04	56 kDa	Ref	0.5	1.1	1.1	2	0.8	2.1	2.2	2.8

689	seq=translation; coord=2:176000645..176001838:1; parent_transcript=GRMZM2G046961_T01; parent_gene=GRMZM2G046961	GRMZM2G046961_P01	18 kDa	Ref	0.3	-0.3	-0.6	-0.9	-1.4	-1.8	-1.6	-2
690	seq=translation; coord=3:135219277..135223126:-1; parent_transcript=GRMZM2G150521_T01; parent_gene=GRMZM2G150521	GRMZM2G150521_P01	25 kDa	Ref	-0.5	-1	-0.8	-1.3	-1.2	-3.1	-2.7	-3.5
691	seq=translation; coord=8:78643850..78648764:1; parent_transcript=GRMZM5G892645_T01; parent_gene=GRMZM5G892645	GRMZM5G892645_P01 (+3)	49 kDa	Ref	-0.4	-1.2	-1.4	-0.9	0.4	-0.4	-0.7	-1
692	seq=translation; coord=2:108630218..108681539:-1; parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043	GRMZM2G158043_P02	106 kDa	Ref	-1.8	-1.3	-1.2	-1.9	Value Missing	-6.9	-6.6	-6.7
693	seq=translation; coord=10:124299211..124301978:1; parent_transcript=GRMZM2G173878_T01; parent_gene=GRMZM2G173878	GRMZM2G173878_P01 (+1)	23 kDa	Ref	0.5	0.4	0	0.6	4.8	3.9	3.8	4.1
694	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	30 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.8	0.7	0
695	seq=translation; coord=5:203926164..203934465:-1; parent_transcript=GRMZM2G150172_T01; parent_gene=GRMZM2G150172	GRMZM2G150172_P01	18 kDa	Ref	1.3	1.8	1.6	1.4	No Values	No Values	No Values	No Values
696	seq=translation; coord=5:112928080..112930204:-1; parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081	GRMZM2G144081_P01 (+1)	47 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	2.9	0.8	0
697	seq=translation; coord=3:8884623..8885815:-1; parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810	GRMZM2G083810_P01	18 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.2	0.7	2.6
698	seq=translation; coord=10:102318701..102320375:-1; parent_transcript=AC204711.3_FGT003; parent_gene=AC204711.3_FG003	AC204711.3_FGP003	16 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	Reference Missing	0.7
699	seq=translation; coord=6:31707585..31709218:-1; parent_transcript=GRMZM2G050412_T01; parent_gene=GRMZM2G050412	GRMZM2G050412_P01	34 kDa	Ref	2.4	1	0.6	0.7	No Values	No Values	No Values	No Values
700	seq=translation; coord=9:128714706..128721565:1; parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124	GRMZM2G095124_P01	99 kDa	Ref	-0.1	0	-0.6	-0.5	-0.2	-0.7	-0.7	-0.8
701	seq=translation; coord=2:214832665..214852459:1; parent_transcript=GRMZM2G035985_T01; parent_gene=GRMZM2G035985	GRMZM2G035985_P01 (+1)	122 kDa	Ref	-0.1	-0.4	-0.8	-0.5	1.8	0.7	0.3	-0.2

702	seq=translation; coord=4:234901650..234908817:1; parent_transcript=GRMZM2G143462_T01; parent_gene=GRMZM2G143462	GRMZM2G143462_P01 (+5)	40 kDa	Ref	0	-1	-0.9	-0.8	-1.7	-1.8	-2	-1.6
703	seq=translation; coord=2:212405484..212408361:-1; parent_transcript=GRMZM5G879278_T02; parent_gene=GRMZM5G879278	GRMZM5G879278_P02 (+2)	35 kDa	Ref	Reference Missing	Reference Missing	Reference Missing	Reference Missing	Reference Missing	Reference Missing	Reference Missing	0.2
704	seq=translation; coord=6:157814627..157816731:-1; parent_transcript=GRMZM2G097040_T01; parent_gene=GRMZM2G097040	GRMZM2G097040_P01	18 kDa	Ref	0.7	0.8	0.8	0.2	0.6	0.1	0.4	0.4
705	seq=translation; coord=5:120784559..120792367:1; parent_transcript=GRMZM2G093359_T01; parent_gene=GRMZM2G093359	GRMZM2G093359_P01 (+1)	49 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
706	seq=translation; coord=3:185834707..185839417:-1; parent_transcript=GRMZM2G003385_T01; parent_gene=GRMZM2G003385	GRMZM2G003385_P01 (+1)	60 kDa	Ref	0	-0.2	-0.5	0.2	2.3	2.7	2.2	1.5
707	seq=translation; coord=5:188243871..188290615:-1; parent_transcript=GRMZM5G824831_T01; parent_gene=GRMZM5G824831	GRMZM5G824831_P01 (+7)	26 kDa	Ref	0.1	-0.4	-0.3	-0.1	-1.8	-1.9	-1.5	-1.4
708	seq=translation; coord=2:32257322..32262715:1; parent_transcript=GRMZM2G157061_T01; parent_gene=GRMZM2G157061	GRMZM2G157061_P01	86 kDa	Ref	2.7	2.3	2.6	1.8	-0.4	-1	-0.4	-1.4
709	seq=translation; coord=6:112268596..112280791:-1; parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687	GRMZM2G553687_P01	204 kDa	Ref	0.2	0.9	-0.4	0.1	2.3	2.3	1.9	1.1
710	seq=translation; coord=3:34547144..34558771:1; parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012	EF517601.1_FGP012	87 kDa	Ref	-0.8	-0.8	-0.3	-0.4	-2	-1.5	-1.9	-1.8
711	seq=translation; coord=3:162825591..162831818:-1; parent_transcript=GRMZM2G133173_T01; parent_gene=GRMZM2G133173	GRMZM2G133173_P01	77 kDa	Ref	0.6	0.4	0.5	0.4	-0.2	-1.4	-1.4	-2.1
712	seq=translation; coord=1:143622295..143626633:1; parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526	GRMZM2G152526_P01	37 kDa	Ref	0.8	0.3	0.3	-0.4	3.3	2.1	2.2	2.4
713	seq=translation; coord=10:90200523..90201913:-1; parent_transcript=GRMZM2G132093_T01; parent_gene=GRMZM2G132093	GRMZM2G132093_P01	25 kDa	Ref	-0.6	-0.1	1.3	1.3	0.3	0.5	0.6	-0.1
714	seq=translation; coord=5:12565068..12568390:1; parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566	GRMZM2G111566_P01	23 kDa	Ref	-1.2	-1.5	-0.4	-0.2	-4.2	-4.7	-4.8	-3.7

715	seq=translation; coord=9:22655251..22657461:1; parent_transcript=GRMZM2G092296_T01; parent_gene=GRMZM2G092296 seq=translation; coord=9:6307326..6312829:-1;	GRMZM2G092296_P01	14 kDa	Ref	0.2	0.2	0	-0.6	1	0.6	0.8	0.4
716	parent_transcript=GRMZM2G082198_T01; parent_gene=GRMZM2G082198 seq=translation; coord=7:120200894..120203011:1; parent_transcript=GRMZM2G138727_T01; parent_gene=GRMZM2G138727 seq=translation; coord=2:34985296..34990180:-1; parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219 seq=translation;	GRMZM2G082198_P01	23 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	-0.3	-1.1	-0.3
717	parent_transcript=GRMZM2G138727_T01; parent_gene=GRMZM2G138727 seq=translation; coord=2:34985296..34990180:-1; parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219 seq=translation;	GRMZM2G138727_P01	24 kDa	Ref	1.1	2.2	1	0.6	2	Reference Missing	Value Missing	Value Missing
718	parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219 seq=translation; coord=2:17796828..17799226:-1; parent_transcript=GRMZM2G101408_T01; parent_gene=GRMZM2G101408 seq=translation;	GRMZM2G021219_P01	41 kDa	Ref	-0.1	-0.1	0.3	0.5	6.9	Value Missing	Value Missing	7.3
719	parent_transcript=GRMZM2G101408_T01; parent_gene=GRMZM2G101408 seq=translation; coord=6:86343600..86346720:-1; parent_transcript=GRMZM2G082823_T01; parent_gene=GRMZM2G082823 seq=translation;	GRMZM2G101408_P01 (+2)	16 kDa	Ref	2.7	1.7	2.3	1.1	1.2	1.5	1.4	0.4
720	parent_transcript=GRMZM2G082823_T01; parent_gene=GRMZM2G082823 seq=translation; coord=8:160297692..160299701:-1; parent_transcript=GRMZM2G105005_T01; parent_gene=GRMZM2G105005 seq=translation;	GRMZM2G082823_P01	80 kDa	Ref	0.9	Value Missing	-0.1	-0.1	1.6	2.1	2	1.1
721	parent_transcript=GRMZM2G105005_T01; parent_gene=GRMZM2G105005 seq=translation; coord=5:14072358..14073760:-1; parent_transcript=GRMZM2G165901_T01; parent_gene=GRMZM2G165901 seq=translation;	GRMZM2G105005_P01 (+2)	37 kDa	Ref	0.7	0.9	1.2	2	-0.6	0.4	0.6	1.8
722	parent_transcript=GRMZM2G165901_T01; parent_gene=GRMZM2G165901 seq=translation; coord=4:136936001..136939330:1; parent_transcript=GRMZM2G044684_T01; parent_gene=GRMZM2G044684 seq=translation;	GRMZM2G165901_P01	16 kDa	Ref	0.5	-1	0.2	0.5	2.1	-1.8	-0.2	0.1
723	parent_transcript=GRMZM2G044684_T01; parent_gene=GRMZM2G044684 seq=translation; coord=9:64028902..64031969:1; parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898 seq=translation;	GRMZM2G044684_P01	36 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0	-0.4	2
724	parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898 seq=translation; coord=3:202766518..202768685:-1; parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation;	GRMZM2G469898_P01 (+1)	43 kDa	Ref	1.2	0.3	-0.6	-0.6	No Values	No Values	No Values	No Values
725	parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation; coord=2:189488589..189490512:-1; parent_transcript=GRMZM2G081017_T01; parent_gene=GRMZM2G081017 seq=translation;	GRMZM2G181135_P01	54 kDa	Ref	-0.1	0.5	1.5	2.3	No Values	No Values	No Values	No Values
726	parent_transcript=GRMZM2G081017_T01; parent_gene=GRMZM2G081017 seq=translation; coord=8:118165588..118167724:1; parent_transcript=AC197705.4_FGT001; parent_gene=AC197705.4_FG001	GRMZM2G081017_P01 (+3)	33 kDa	Ref	0.1	0.6	0.4	0.7	No Values	No Values	No Values	No Values
727	parent_transcript=AC197705.4_FGT001; parent_gene=AC197705.4_FG001	AC197705.4_FGP001	65 kDa	Ref	No Values	No Values	No Values	No Values	2.1	1.2	1.6	1.3

728	seq=translation; coord=8:87034106..87038095:-1; parent_transcript=GRMZM2G007404_T01; parent_gene=GRMZM2G007404	GRMZM2G007404_P01 (+1)	48 kDa	Ref	0.1	0.3	0.3	0.3	No Values	No Values	No Values	No Values
729	seq=translation; coord=1:262889860..262892469:1; parent_transcript=GRMZM2G024131_T01; parent_gene=GRMZM2G024131	GRMZM2G024131_P01 (+1)	50 kDa	Ref	No Values	No Values	No Values	No Values	2.3	3.2	3	2.1
730	seq=translation; coord=3:204689100..204690354:1; parent_transcript=GRMZM2G425629_T02; parent_gene=GRMZM2G425629	GRMZM2G425629_P02	24 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	3.5
731	seq=translation; coord=2:223290295..223311152:1; parent_transcript=GRMZM2G172369_T03; parent_gene=GRMZM2G172369	GRMZM2G172369_P03	114 kDa	Ref	0.3	0.1	-0.2	0.7	No Values	No Values	No Values	No Values
732	seq=translation; coord=9:151682948..151683563:1; parent_transcript=GRMZM2G428040_T01; parent_gene=GRMZM2G428040	GRMZM2G428040_P01	13 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.9	1.3	Reference Missing
733	seq=translation; coord=10:87090618..87092722:1; parent_transcript=GRMZM2G123029_T01; parent_gene=GRMZM2G123029	GRMZM2G123029_P01 (+4)	32 kDa	Ref	0.3	0.6	1.3	2	No Values	No Values	No Values	No Values
734	seq=translation; coord=4:233120026..233126298:-1; parent_transcript=GRMZM2G049839_T01; parent_gene=GRMZM2G049839	GRMZM2G049839_P01 (+1)	45 kDa	Ref	0.1	0.6	0.4	0.3	1.8	1.7	2	2.3
735	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	96 kDa	Ref	0	-0.8	-0.9	-1.2	-1.2	-1	-1.7	-1.8
736	seq=translation; coord=3:217464401..217471380:-1; parent_transcript=GRMZM2G105019_T01; parent_gene=GRMZM2G105019	GRMZM2G105019_P01	40 kDa	Ref	-0.4	-0.2	-0.5	-0.7	-0.9	-0.2	-0.3	-0.5
737	seq=translation; coord=3:111553578..111570930:1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01 (+1)	401 kDa	Ref	0.4	0.5	0	0.4	0.7	0.3	0.4	-0.5
738	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G136296_T01; parent_gene=GRMZM2G136296	GRMZM2G136296_P01 (+1)	99 kDa	Ref	-0.2	0	-0.4	-0.3	-2.2	-2.6	-2.8	-2.9
739	seq=translation; coord=8:115478841..115482432:1; parent_transcript=GRMZM2G111411_T01; parent_gene=GRMZM2G111411	GRMZM2G111411_P01	24 kDa	Ref	0	-0.4	0	Value Missing	-1.2	-2.7	-3.5	-2.8
740	seq=translation; coord=3:1479593..1481033:-1; parent_transcript=GRMZM5G825437_T04; parent_gene=GRMZM5G825437	GRMZM5G825437_P04	15 kDa	Ref	-0.1	-0.5	-0.2	-0.5	-1.4	-2.5	-1.5	-1

741	seq=translation; coord=8:16994084..16999444:-1; parent_transcript=GRMZM2G025215_T01; parent_gene=GRMZM2G025215	GRMZM2G025215_P01	59 kDa	Ref	1.5	0.9	1.4	1.1	3.4	3.2	2.5	3.2
742	seq=translation; coord=4:127851768..127857102:1; parent_transcript=GRMZM2G018416_T01; parent_gene=GRMZM2G018416	GRMZM2G018416_P01	82 kDa	Ref	Value Missing	0.6	-0.2	0.1	-0.8	-2.5	-2.2	-1.7
743	seq=translation; coord=9:18896527..18899443:1; parent_transcript=GRMZM2G102596_T01; parent_gene=GRMZM2G102596	GRMZM2G102596_P01 (+2)	30 kDa	Ref	0.8	0.6	0.4	0.7	1.3	0.8	-0.1	-0.4
744	seq=translation; coord=1:5952987..5954672:1; parent_transcript=GRMZM2G065718_T01; parent_gene=GRMZM2G065718	GRMZM2G065718_P01	41 kDa	Ref	-0.7	0.4	-1	-1.3	-1	-2.2	-2.2	-2
745	seq=translation; coord=3:133888888..133893638:1; parent_transcript=GRMZM2G116204_T01; parent_gene=GRMZM2G116204	GRMZM2G116204_P01	22 kDa	Ref	0	-0.7	-1.3	-0.6	-0.1	0.7	0.7	1.2
746	seq=translation; coord=3:9805845..9808735:-1; parent_transcript=GRMZM2G083418_T01; parent_gene=GRMZM2G083418	GRMZM2G083418_P01	35 kDa	Ref	2.7	2.3	1.8	1.9	Reference Missing	3.3	3.4	Reference Missing
747	seq=translation; coord=10:148849233..148855901:1; parent_transcript=GRMZM2G406074_T01; parent_gene=GRMZM2G406074	GRMZM2G406074_P01	25 kDa	Ref	0.2	-0.1	0.1	-0.1	1.8	2.6	1.6	2.4
748	seq=translation; coord=2:146194741..146200435:-1; parent_transcript=GRMZM2G537291_T01; parent_gene=GRMZM2G537291	GRMZM2G537291_P01	68 kDa	Ref	-1	-1	-0.7	-1.2	-0.4	-0.8	-1	-1.5
749	seq=translation; coord=9:93447494..93469121:-1; parent_transcript=GRMZM2G348666_T01; parent_gene=GRMZM2G348666	GRMZM2G348666_P01 (+1)	133 kDa	Ref	-0.2	-0.2	-0.6	0.2	-3.3	-3.2	-3.2	-3.6
750	seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898	GRMZM5G876898_P01 (+1)	44 kDa	Ref	-0.6	0.1	-0.1	-0.1	-4.1	Reference Missing	Reference Missing	-3.8
751	seq=translation; coord=1:67644786..67647420:1; parent_transcript=GRMZM2G051879_T01; parent_gene=GRMZM2G051879	GRMZM2G051879_P01 (+13)	15 kDa	Ref	1.7	1.7	1	0.3	-3.5	-6.5	-6.2	-4.8
752	seq=translation; coord=1:68543805..68546269:-1; parent_transcript=GRMZM2G077991_T01; parent_gene=GRMZM2G077991	GRMZM2G077991_P01 (+3)	16 kDa	Ref	0.6	0.3	-1.2	-1.6	1.6	Value Missing	-3.3	Value Missing
753	seq=translation; coord=10:8848146..8849526:-1; parent_transcript=GRMZM2G136910_T01; parent_gene=GRMZM2G136910	GRMZM2G136910_P01	16 kDa	Ref	-2.4	-2.7	-2	-2.2	1.1	0.1	0.6	-0.2

754	seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693	GRMZM2G049693_P01 (+1)	66 kDa	Ref	Reference Missing	Reference Missing	0.2	1.3	-2.4	-3.7	-3.3	-2.7
755	seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G160925_P01	41 kDa	Ref	0	-0.1	-0.1	-0.1	-0.3	-0.8	-0.8	-1
756	seq=translation; coord=1:279565504..279568174:1; parent_transcript=GRMZM2G047456_T02; parent_gene=GRMZM2G047456	GRMZM2G047456_P02 (+2)	34 kDa	Ref	-1.1	-0.5	-0.5	-0.7	-0.8	-2.7	-2.1	-1.3
757	seq=translation; coord=8:143279539..143283510:-1; parent_transcript=GRMZM2G050270_T01; parent_gene=GRMZM2G050270	GRMZM2G050270_P01	46 kDa	Ref	-0.6	-0.7	-1	-0.6	-0.5	-1.2	-1	-1
758	seq=translation; coord=5:193157657..193165368:1; parent_transcript=AC211737.3_FGT012; parent_gene=AC211737.3_FG012	AC211737.3_FGP012	75 kDa	Ref	-0.4	-0.7	-0.2	0	6.4	6.5	7.6	Value Missing
759	seq=translation; coord=4:237521017..237524915:-1; parent_transcript=GRMZM2G165917_T01; parent_gene=GRMZM2G165917	GRMZM2G165917_P01 (+3)	49 kDa	Ref	0.6	0.6	1	0.1	3.9	1.9	1.9	2.6
760	seq=translation; coord=5:69096740..69101545:-1; parent_transcript=GRMZM2G020146_T01; parent_gene=GRMZM2G020146	GRMZM2G020146_P01	57 kDa	Ref	-1.4	-1.7	-1.4	-1	0.2	1.1	3.1	2.8
761	seq=translation; coord=10:96835856..96839456:-1; parent_transcript=GRMZM2G021170_T01; parent_gene=GRMZM2G021170	GRMZM2G021170_P01	29 kDa	Ref	-1	-1.9	-1.5	Value Missing	-2.9	-3	-4	-4.3
762	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	39 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.8	0.9	1.2
763	seq=translation; coord=6:153256043..153259238:1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	36 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	1.2	1.8	3.2
764	seq=translation; coord=6:156534704..156535855:-1; parent_transcript=GRMZM2G410134_T01; parent_gene=GRMZM2G410134	GRMZM2G410134_P01	22 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0.3	Reference Missing	-0.7
765	seq=translation; coord=6:157582700..157589894:1; parent_transcript=GRMZM2G006377_T01; parent_gene=GRMZM2G006377	GRMZM2G006377_P01	49 kDa	Ref	0.3	0.6	1.3	1.7	No Values	No Values	No Values	No Values
766	seq=translation; coord=6:63919594..63950390:1; parent_transcript=GRMZM2G052812_T02; parent_gene=GRMZM2G052812	GRMZM2G052812_P02 (+1)	37 kDa	Ref	-0.4	0.2	0.2	0.5	No Values	No Values	No Values	No Values

767	seq=translation; coord=1:41468889..41473581:1; parent_transcript=GRMZM2G044027_T01; parent_gene=GRMZM2G044027	GRMZM2G044027_P01 (+1)	39 kDa	Ref	0.6	1.3	0.7	-0.2	No Values	No Values	No Values	No Values
768	seq=translation; coord=8:17872894..17877539:1; parent_transcript=GRMZM2G080722_T01; parent_gene=GRMZM2G080722	GRMZM2G080722_P01	20 kDa	Ref	0	0	0	-0.3	-1.4	-1.6	-2.5	-2.2
769	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	41 kDa	Ref	0.8	-0.4	-1	-0.6	-2	-3	-2.5	-2.8
770	seq=translation; coord=6:148590842..148593721:1; parent_transcript=GRMZM2G033641_T01; parent_gene=GRMZM2G033641	GRMZM2G033641_P01	68 kDa	Ref	0.9	0.8	1.3	1.4	2.7	1.3	1.2	1
771	seq=translation; coord=6:168917945..168919116:1; parent_transcript=GRMZM5G833747_T01; parent_gene=GRMZM5G833747	GRMZM5G833747_P01 (+2)	17 kDa	Ref	-1.5	-1.8	-1.8	-2	1.9	2.6	3.2	3.6
772	seq=translation; coord=1:41535916..41540223:-1; parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329	GRMZM2G157329_P01 (+1)	27 kDa	Ref	0.8	0.2	0.3	0.3	3.6	4.2	3.8	2.3
773	seq=translation; coord=5:19123690..19126862:1; parent_transcript=GRMZM2G074898_T01; parent_gene=GRMZM2G074898	GRMZM2G074898_P01 (+8)	18 kDa	Ref	1.1	0.4	-0.3	0	1.7	0.7	0.4	-0.6
774	seq=translation; coord=2:38192410..38194128:1; parent_transcript=GRMZM2G121700_T01; parent_gene=GRMZM2G121700	GRMZM2G121700_P01	32 kDa	Ref	-1.1	-0.8	-1.2	-1.6	-1.8	-1.9	-1.9	-1.8
775	seq=translation; coord=2:17348097..17355999:-1; parent_transcript=GRMZM2G145968_T01; parent_gene=GRMZM2G145968	GRMZM2G145968_P01	14 kDa	Ref	2.2	2	1.8	1.3	2.7	2	2.5	2.3
776	seq=translation; coord=5:180669231..180673418:1; parent_transcript=GRMZM2G139614_T01; parent_gene=GRMZM2G139614	GRMZM2G139614_P01	56 kDa	Ref	3.3	2.8	2.6	2.2	Reference Missing	Reference Missing	Reference Missing	Reference Missing
777	seq=translation; coord=7:10575103..10576227:-1; parent_transcript=GRMZM2G328171_T01; parent_gene=GRMZM2G328171	GRMZM2G328171_P01	33 kDa	Ref	-0.2	-0.1	-0.5	0	3.7	4.6	5.5	6.4
778	seq=translation; coord=4:199076122..199077395:-1; parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720	GRMZM2G177720_P01	17 kDa	Ref	-0.1	-0.1	-0.5	-0.3	0.2	0.3	-0.2	Reference Missing
779	seq=translation; coord=2:24608141..24615659:1; parent_transcript=GRMZM2G061928_T01; parent_gene=GRMZM2G061928	GRMZM2G061928_P01 (+2)	24 kDa	Ref	No Values	No Values	No Values	No Values	0.3	-0.2	-0.9	0.1

780	seq=translation; coord=4:195054129..195060931:1; parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406	GRMZM2G084406_P02	66 kDa	Ref	-0.1	0.4	0.5	0.4	-5.5	-5.9	-5.8	-5.8
781	seq=translation; coord=6:98313412..98316578:1; parent_transcript=GRMZM2G110402_T01; parent_gene=GRMZM2G110402	GRMZM2G110402_P01 (+2)	24 kDa	Ref	1.1	0.4	0.5	-0.1	-2.3	-2.7	-2.4	-3.1
782	seq=translation; coord=3:151293748..151299116:1; parent_transcript=GRMZM2G030902_T01; parent_gene=GRMZM2G030902	GRMZM2G030902_P01 (+7)	40 kDa	Ref	-1.4	-1.5	-2.1	-2.7	-2.7	-4.5	-4.6	-5.5
783	seq=translation; coord=1:293644603..293647117:-1; parent_transcript=GRMZM2G068244_T01; parent_gene=GRMZM2G068244	GRMZM2G068244_P01	28 kDa	Ref	-0.8	-1.1	-0.2	-1.2	-4.4	-4.2	Reference Missing	-2.8
784	seq=translation; coord=10:103630422..103635991:-1; parent_transcript=GRMZM2G359298_T01; parent_gene=GRMZM2G359298	GRMZM2G359298_P01	83 kDa	Ref	0.8	1.8	1.9	0.6	-0.2	0.2	1.6	0.7
785	seq=translation; coord=8:171328319..171331663:-1; parent_transcript=GRMZM2G172932_T01; parent_gene=GRMZM2G172932	GRMZM2G172932_P01 (+2)	50 kDa	Ref	0.7	-0.1	-0.9	-1.1	-0.3	-1.7	-1.8	-2.9
786	seq=translation; coord=1:16603599..16606666:-1; parent_transcript=GRMZM2G016511_T01; parent_gene=GRMZM2G016511	GRMZM2G016511_P01	27 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	0	-0.1	-0.6
787	seq=translation; coord=5:212248891..212249987:1; parent_transcript=GRMZM2G098167_T01; parent_gene=GRMZM2G098167	GRMZM2G098167_P01	18 kDa	Ref	0.9	1.4	1.3	0.4	5.2	5.1	5.4	6
788	seq=translation; coord=7:7118087..7119389:-1; parent_transcript=GRMZM2G320298_T01; parent_gene=GRMZM2G320298	GRMZM2G320298_P01	35 kDa	Ref	-1.5	-0.7	-1.2	0.2	0.5	1.6	1.7	0.8
789	seq=translation; coord=6:147724800..147731064:1; parent_transcript=GRMZM2G070199_T01; parent_gene=GRMZM2G070199	GRMZM2G070199_P01	12 kDa	Ref	1.9	2.3	2.2	0.9	0.4	Value Missing	-0.8	-1
790	seq=translation; coord=4:7172367..7173014:-1; parent_transcript=GRMZM2G132162_T01; parent_gene=GRMZM2G132162	GRMZM2G132162_P01	10 kDa	Ref	1.7	1.6	4.3	-0.1	2.3	1.7	1.4	0.6
791	seq=translation; coord=7:152391333..152401606:1; parent_transcript=GRMZM2G325008_T01; parent_gene=GRMZM2G325008	GRMZM2G325008_P01 (+4)	70 kDa	Ref	-0.1	0.6	0	0.2	2.2	1.2	1.5	1.6
792	seq=translation; coord=5:31178435..31182856:-1; parent_transcript=GRMZM2G102639_T01; parent_gene=GRMZM2G102639	GRMZM2G102639_P01 (+1)	39 kDa	Ref	-0.6	-0.5	-0.5	-0.5	0.2	-0.5	-0.4	-0.9

793	seq=translation; coord=3:221273481..221276486:-1; parent_transcript=GRMZM2G051764_T01; parent_gene=GRMZM2G051764	GRMZM2G051764_P01 (+2)	37 kDa	Ref	0.2	0.5	0.5	0.7	-4.6	-4	-3.7	-4.5
794	seq=translation; coord=1:14103040..14104304:1; parent_transcript=GRMZM5G850455_T01; parent_gene=GRMZM5G850455	GRMZM5G850455_P01 (+2)	21 kDa	Ref	1.2	0.1	-0.1	-0.2	-0.9	Value Missing	-4.5	-4.2
795	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290	GRMZM2G066290_P01 (+1)	63 kDa	Ref	No Values	No Values	No Values	No Values	0.5	-0.3	-0.8	-0.9
796	seq=translation; coord=2:36456199..36464613:-1; parent_transcript=GRMZM2G130230_T01; parent_gene=GRMZM2G130230	GRMZM2G130230_P01 (+2)	58 kDa	Ref	-0.7	-1.3	-0.7	-0.5	No Values	No Values	No Values	No Values
797	seq=translation; coord=9:149239142..149244150:1; parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528	GRMZM2G004528_P03 (+1)	56 kDa	Ref	No Values	No Values	No Values	No Values	2	0.4	0.2	0.2
798	seq=translation; coord=4:237868446..237932504:1; parent_transcript=GRMZM2G092627_T01; parent_gene=GRMZM2G092627	GRMZM2G092627_P01	155 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.5	0.6	-0.2
799	seq=translation; coord=5:128105440..128107392:-1; parent_transcript=GRMZM2G071089_T01; parent_gene=GRMZM2G071089	GRMZM2G071089_P01	25 kDa	Ref	3.6	2.6	1.8	0.5	No Values	No Values	No Values	No Values
800	seq=translation; coord=3:52892215..52895069:-1; parent_transcript=GRMZM2G033226_T01; parent_gene=GRMZM2G033226	GRMZM2G033226_P01	20 kDa	Ref	-0.2	-0.3	-0.8	-0.4	No Values	No Values	No Values	No Values
801	seq=translation; coord=2:224904656..224907978:1; parent_transcript=GRMZM2G408768_T01; parent_gene=GRMZM2G408768	GRMZM2G408768_P01	29 kDa	Ref	1.4	0.9	1.1	0.9	No Values	No Values	No Values	No Values
802	seq=translation; coord=1:298431972..298436349:1; parent_transcript=GRMZM2G021742_T01; parent_gene=GRMZM2G021742	GRMZM2G021742_P01	32 kDa	Ref	0.1	0.2	0.1	0.2	-0.7	-1.9	-1.8	-0.9
803	seq=translation; coord=4:100154058..100157650:1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01 (+1)	44 kDa	Ref	-0.3	-0.6	-0.5	-1.2	-0.4	-1.3	-0.6	-0.9
804	seq=translation; coord=9:86866692..86874101:-1; parent_transcript=GRMZM2G022275_T01; parent_gene=GRMZM2G022275	GRMZM2G022275_P01 (+1)	53 kDa	Ref	-0.2	-0.4	-0.8	-0.5	No Values	No Values	No Values	No Values
805	seq=translation; coord=8:155644343..155646847:-1; parent_transcript=GRMZM2G151252_T01; parent_gene=GRMZM2G151252	GRMZM2G151252_P01 (+2)	16 kDa	Ref	0.9	0.9	0.1	0.2	-0.2	-1.5	-1.4	-1.6

806	seq=translation; coord=7:108281609..108388418:-1; parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=4:2112375..2118463:-1;	GRMZM2G700188_P04 (+1)	43 kDa	Ref	0.8	1	0.2	0.5	0.9	Reference Missing	1.7	1.3
807	parent_transcript=GRMZM2G057450_T01; parent_gene=GRMZM2G057450 seq=translation; coord=7:166387724..166390583:1;	GRMZM2G057450_P01 (+6)	60 kDa	Ref	0.5	0.3	0.4	0.3	-2.5	-3	-3.2	-3.3
808	parent_transcript=GRMZM2G054136_T01; parent_gene=GRMZM2G054136 seq=translation; coord=6:167112832..167116884:-1;	GRMZM2G054136_P01 (+6)	29 kDa	Ref	1	0.8	0.3	0.4	1.7	0.5	0.1	-0.2
809	parent_transcript=GRMZM2G144372_T01; parent_gene=GRMZM2G144372 seq=translation; coord=3:230441023..230443000:1;	GRMZM2G144372_P01	43 kDa	Ref	-0.5	-0.2	-0.7	-0.8	-2.9	-2.7	-2.8	-2.8
810	parent_transcript=GRMZM2G353103_T01; parent_gene=GRMZM2G353103 seq=translation; coord=8:5159968..5162055:1;	GRMZM2G353103_P01 (+1)	17 kDa	Ref	0.9	0.4	0.3	0.5	1.6	1.7	0.8	1.5
811	parent_transcript=GRMZM2G044128_T01; parent_gene=GRMZM2G044128 seq=translation; coord=2:235441754..235443878:-1;	GRMZM2G044128_P01	64 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Value Missing	Value Missing	Value Missing
812	parent_transcript=GRMZM2G082974_T01; parent_gene=GRMZM2G082974 seq=translation; coord=1:275223498..275227310:-1;	GRMZM2G082974_P01	17 kDa	Ref	-0.4	-1.7	-2.6	-3	0	-0.5	-0.8	-0.7
813	parent_transcript=GRMZM2G169671_T01; parent_gene=GRMZM2G169671 seq=translation; coord=5:115978543..115983314:-1;	GRMZM2G169671_P01	27 kDa	Ref	0.1	-0.2	-0.5	-0.4	-0.6	-1	-0.7	-1
814	parent_transcript=GRMZM2G452633_T01; parent_gene=GRMZM2G452633 seq=translation; coord=7:16096163..16099019:1;	GRMZM2G452633_P01 (+2)	40 kDa	Ref	2.6	2	1.1	0.7	2.4	-0.8	-1.1	-1.3
815	parent_transcript=GRMZM2G170044_T01; parent_gene=GRMZM2G170044 seq=translation; coord=3:188328660..188331609:-1;	GRMZM2G170044_P01	21 kDa	Ref	-0.3	0.4	0.6	0.3	-1.6	-3	-3.1	-2
816	parent_transcript=GRMZM2G047274_T01; parent_gene=GRMZM2G047274 seq=translation; coord=10:38522742..38534648:1;	GRMZM2G047274_P01	46 kDa	Ref	0.7	0.9	0.9	0.9	4.1	2.3	1.7	0.9
817	parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406 seq=translation; coord=10:3062645..3066771:-1;	GRMZM2G010406_P01 (+2)	53 kDa	Ref	0.1	0.1	-0.4	-0.3	-1.2	-1.5	-1.4	-1.5
818	parent_transcript=GRMZM2G068465_T01; parent_gene=GRMZM2G068465	GRMZM2G068465_P01 (+3)	56 kDa	Ref	1.6	0.8	1.2	0.6	Reference Missing	Reference Missing	Reference Missing	Reference Missing

819	seq=translation; coord=2:21258086..21262803:1; parent_transcript=GRMZM2G019919_T01; parent_gene=GRMZM2G019919	GRMZM2G019919_P01 (+2)	89 kDa	Ref	0.6	0.1	-0.3	-0.5	0.5	-0.9	-0.8	-1.1
820	seq=translation; coord=6:150509782..150519705:1; parent_transcript=GRMZM2G118037_T01; parent_gene=GRMZM2G118037	GRMZM2G118037_P01	14 kDa	Ref	2	1.4	1.5	0.3	-1.9	-1.1	-1	0.2
821	seq=translation; coord=8:134463276..134464095:1; parent_transcript=GRMZM2G028393_T01; parent_gene=GRMZM2G028393	GRMZM2G028393_P01 (+1)	8 kDa	Ref	0.5	1.1	1.7	1.3	-2.7	-1.4	-0.8	0.1
822	seq=translation; coord=1:292879723..292882219:-1; parent_transcript=AC225147.4_FGT002; parent_gene=AC225147.4_FG002	AC225147.4_FGP002 (+5)	16 kDa	Ref	0.6	0.2	-1.1	-0.8	-1.7	-2.5	-2.8	-4
823	seq=translation; coord=8:15778520..15799328:1; parent_transcript=GRMZM2G097775_T01; parent_gene=GRMZM2G097775	GRMZM2G097775_P01 (+1)	47 kDa	Ref	0	0.1	0.2	0.1	-0.5	Value Missing	-3.9	-3.8
824	seq=translation; coord=8:113008265..113010860:-1; parent_transcript=GRMZM2G044947_T01; parent_gene=GRMZM2G044947	GRMZM2G044947_P01 (+2)	40 kDa	Ref	0.3	0.7	0.3	0.5	-1	-2.1	-2.9	-2.7
825	seq=translation; coord=6:129086004..129087221:1; parent_transcript=GRMZM2G447795_T01; parent_gene=GRMZM2G447795	GRMZM2G447795_P01	35 kDa	Ref	0.4	0.2	0.4	1.2	2.3	2.5	3.7	4.4
826	seq=translation; coord=1:84413344..84417967:1; parent_transcript=GRMZM2G083173_T01; parent_gene=GRMZM2G083173	GRMZM2G083173_P01 (+1)	80 kDa	Ref	1.7	1.4	1	1.8	4.4	2.1	2.3	1.3
827	seq=translation; coord=4:14570220..14574637:-1; parent_transcript=GRMZM5G840928_T01; parent_gene=GRMZM5G840928	GRMZM5G840928_P01 (+2)	44 kDa	Ref	-0.2	-0.1	0.4	0.6	-1.1	-0.2	-1.1	-1
828	seq=translation; coord=6:88903392..88908316:-1; parent_transcript=GRMZM2G150256_T01; parent_gene=GRMZM2G150256	GRMZM2G150256_P01	52 kDa	Ref	0.1	-0.2	-0.1	0.1	No Values	No Values	No Values	No Values
829	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	84 kDa	Ref	1	0.1	-0.5	-1.6	No Values	No Values	No Values	No Values
830	seq=translation; coord=8:171412337..171415029:-1; parent_transcript=GRMZM2G012160_T01; parent_gene=GRMZM2G012160	GRMZM2G012160_P01	15 kDa	Ref	0.8	0.5	3.5	2.7	No Values	No Values	No Values	No Values
831	seq=translation; coord=3:213775068..213778961:1; parent_transcript=GRMZM2G047298_T01; parent_gene=GRMZM2G047298	GRMZM2G047298_P01	42 kDa	Ref	0	-0.2	-1.8	-1.5	No Values	No Values	No Values	No Values

832	seq=translation; coord=2:33498879..33500909:-1; parent_transcript=GRMZM2G051898_T01; parent_gene=GRMZM2G051898	GRMZM2G051898_P01	40 kDa	Ref	0.8	0.8	Reference Missing	2.8	No Values	No Values	No Values	No Values
833	seq=translation; coord=4:182566741..182604691:1; parent_transcript=GRMZM2G439339_T04; parent_gene=GRMZM2G439339	GRMZM2G439339_P04 (+1)	226 kDa	Ref	No Values	No Values	No Values	No Values	0.7	0.6	0.1	-0.2
834	seq=translation; coord=7:173600066..173601522:1; parent_transcript=GRMZM2G348125_T01; parent_gene=GRMZM2G348125	GRMZM2G348125_P01 (+1)	23 kDa	Ref	-0.1	0.3	2	0.3	No Values	No Values	No Values	No Values
835	seq=translation; coord=1:240863375..240866448:1; parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434	GRMZM2G124434_P01	43 kDa	Ref	-0.9	-0.6	-0.7	-0.3	0.2	-0.7	-1	-1.2
836	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01 (+2)	34 kDa	Ref	0.3	0	-0.1	0	0.8	0.8	1	0.3
837	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	55 kDa	Ref	-0.2	0.4	0.3	0.8	-0.5	-0.1	0.4	-0.1
838	seq=translation; coord=1:226551729..226556786:-1; parent_transcript=GRMZM2G131769_T01; parent_gene=GRMZM2G131769	GRMZM2G131769_P01	54 kDa	Ref	-1.3	-1.4	-1.1	-1.6	2	1.7	1.9	1.5
839	seq=translation; coord=2:224332394..224344331:1; parent_transcript=GRMZM2G169095_T01; parent_gene=GRMZM2G169095	GRMZM2G169095_P01	71 kDa	Ref	-0.1	-0.4	-0.9	-0.3	1.8	1.3	1.2	1
840	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	55 kDa	Ref	0.8	0.8	2.7	5.5	-0.6	0.3	1.5	1.5
841	seq=translation; coord=1:22629310..22633408:1; parent_transcript=GRMZM2G055025_T01; parent_gene=GRMZM2G055025	GRMZM2G055025_P01	29 kDa	Ref	0.6	0.4	0.4	0.9	2.6	0.7	1.1	0.4
842	seq=translation; coord=1:5345118..5348832:1; parent_transcript=GRMZM2G119494_T01; parent_gene=GRMZM2G119494	GRMZM2G119494_P01	50 kDa	Ref	-0.7	-0.7	-0.6	-0.4	-3.5	-2.8	-2.3	-2.4
843	seq=translation; coord=5:175584484..175585836:1; parent_transcript=GRMZM2G049675_T01; parent_gene=GRMZM2G049675	GRMZM2G049675_P01 (+1)	35 kDa	Ref	-0.6	-0.2	-0.2	0.8	1.7	2.7	1.3	1.4
844	seq=translation; coord=1:250092343..250095992:-1; parent_transcript=GRMZM2G364069_T01; parent_gene=GRMZM2G364069	GRMZM2G364069_P01	47 kDa	Ref	1	0.5	1	0.7	-1.9	-3.2	-3.3	-3.1

845	seq=translation; coord=1:65994545..65996015:-1; parent_transcript=GRMZM2G004298_T01; parent_gene=GRMZM2G004298	GRMZM2G004298_P01 (+5)	23 kDa	Ref	0.6	-0.3	0.6	1.4	0.3	-1	0.2	0
846	seq=translation; coord=1:274494460..274510748:-1; parent_transcript=GRMZM2G396451_T02; parent_gene=GRMZM2G396451	GRMZM2G396451_P02 (+1)	161 kDa	Ref	0.1	-0.4	-0.5	-0.3	-0.6	-1.9	-2	-2.1
847	seq=translation; coord=7:159001810..159027357:-1; parent_transcript=GRMZM2G081155_T01; parent_gene=GRMZM2G081155	GRMZM2G081155_P01 (+2)	70 kDa	Ref	-0.2	-0.1	-0.4	0	-1.6	-1.8	-2.3	-2.4
848	seq=translation; coord=2:62991591..62998602:-1; parent_transcript=GRMZM2G171688_T01; parent_gene=GRMZM2G171688	GRMZM2G171688_P01	76 kDa	Ref	-0.4	-1.3	-0.6	-0.6	-1.5	0	0.2	0
849	seq=translation; coord=5:13253262..13257697:-1; parent_transcript=GRMZM2G076524_T01; parent_gene=GRMZM2G076524	GRMZM2G076524_P01 (+1)	34 kDa	Ref	0.3	0.5	0.7	-0.7	-0.6	-0.2	-0.2	-0.1
850	seq=translation; coord=8:2052922..2061036:1; parent_transcript=GRMZM2G052875_T01; parent_gene=GRMZM2G052875	GRMZM2G052875_P01 (+1)	69 kDa	Ref	0.2	0	0.4	0.4	0	-0.5	-0.2	0.1
851	seq=translation; coord=1:194657095..194659202:-1; parent_transcript=GRMZM2G083725_T01; parent_gene=GRMZM2G083725	GRMZM2G083725_P01 (+1)	19 kDa	Ref	Reference Missing	0.4	0.1	-0.3	1.6	1.1	1.2	0.6
852	seq=translation; coord=3:154973863..154975444:-1; parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246	GRMZM2G146246_P02	24 kDa	Ref	-1.1	-0.8	0	-1.5	-1.7	-1	-1.3	0.4
853	seq=translation; coord=1:174313373..174317518:1; parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565	GRMZM2G088565_P01	42 kDa	Ref	0.9	0.5	0.2	0.5	-0.7	-0.9	-1.3	-1.7
854	seq=translation; coord=7:137275571..137279379:1; parent_transcript=GRMZM2G458164_T01; parent_gene=GRMZM2G458164	GRMZM2G458164_P01	52 kDa	Ref	0.6	0	0.1	0.5	4.5	3.4	4.1	5.3
855	seq=translation; coord=1:296874949..296877709:-1; parent_transcript=GRMZM2G035017_T01; parent_gene=GRMZM2G035017	GRMZM2G035017_P01	30 kDa	Ref	1.4	1.9	1.4	1.6	1	1.8	-0.3	-0.2
856	seq=translation; coord=2:160538409..160543692:1; parent_transcript=GRMZM2G151549_T01; parent_gene=GRMZM2G151549	GRMZM2G151549_P01 (+1)	51 kDa	Ref	0.3	-0.2	0.4	-0.4	0	-1	-0.4	-1
857	seq=translation; coord=3:205620317..205627720:1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01 (+1)	47 kDa	Ref	0.1	-0.5	-0.3	-0.5	-2.1	-2.5	-2.8	-2.7

858	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01 (+1)	33 kDa	Ref	3.1	2.2	1.6	0.8	-0.8	-1.2	-1.8	-2.4
859	seq=translation; coord=7:155559747..155562921:1; parent_transcript=GRMZM2G108285_T01; parent_gene=GRMZM2G108285	GRMZM2G108285_P01	25 kDa	Ref	-0.8	-1	0.3	0.7	-2	-1.1	-1.9	0.3
860	seq=translation; coord=8:13369483..13372340:-1; parent_transcript=GRMZM2G119361_T01; parent_gene=GRMZM2G119361	GRMZM2G119361_P01 (+1)	70 kDa	Ref	-0.3	1	-0.3	0.2	-9	-8.3	-8.7	-8.7
861	seq=translation; coord=1:296017136..296022027:1; parent_transcript=GRMZM2G053458_T01; parent_gene=GRMZM2G053458	GRMZM2G053458_P01 (+1)	16 kDa	Ref	-0.6	-1.6	-1	-1.5	0.5	Value Missing	-0.2	Value Missing
862	seq=translation; coord=4:1508758..1509325:-1; parent_transcript=GRMZM2G107302_T01; parent_gene=GRMZM2G107302	GRMZM2G107302_P01	10 kDa	Ref	1.2	0.5	0.7	-1.1	Reference Missing	-2.7	-1.5	-2.8
863	seq=translation; coord=10:4071331..4073937:-1; parent_transcript=GRMZM2G129804_T01; parent_gene=GRMZM2G129804	GRMZM2G129804_P01	26 kDa	Ref	-1.4	-0.8	-0.7	-1.7	-1.2	-0.6	-0.3	-0.3
864	seq=translation; coord=1:216692560..216696036:1; parent_transcript=GRMZM2G167669_T01; parent_gene=GRMZM2G167669	GRMZM2G167669_P01	55 kDa	Ref	0.6	0.2	-1.3	-0.5	Value Missing	7.4	7.8	Value Missing
865	seq=translation; coord=1:262391932..262394279:1; parent_transcript=GRMZM2G063503_T02; parent_gene=GRMZM2G063503	GRMZM2G063503_P02	10 kDa	Ref	-1.4	-2.3	-0.8	-2.2	0.4	0.8	-0.2	2.3
866	seq=translation; coord=5:62197397..62202236:1; parent_transcript=GRMZM2G152111_T01; parent_gene=GRMZM2G152111	GRMZM2G152111_P01 (+4)	25 kDa	Ref	-0.4	-0.5	-1	-1	1.1	0	-0.8	-1.2
867	seq=translation; coord=8:39126474..39127702:1; parent_transcript=GRMZM2G047732_T01; parent_gene=GRMZM2G047732	GRMZM2G047732_P01 (+1)	18 kDa	Ref	0.5	-0.1	-0.2	-0.4	-2	-2.9	-4.8	-4.7
868	seq=translation; coord=5:1122734..1125202:1; parent_transcript=GRMZM2G034326_T01; parent_gene=GRMZM2G034326	GRMZM2G034326_P01 (+3)	17 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.5	0.4	0
869	seq=translation; coord=5:202050924..202059781:1; parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040	GRMZM2G020040_P01 (+1)	104 kDa	Ref	-0.2	0	0	-0.5	No Values	No Values	No Values	No Values
870	seq=translation; coord=1:221648603..221653196:1; parent_transcript=GRMZM2G163437_T01; parent_gene=GRMZM2G163437	GRMZM2G163437_P01 (+1)	56 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	2.5	2.9	2.9

871	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	57 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.5	0.5
872	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	59 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	-0.1	0.3	0.9
873	seq=translation; coord=9:77151999..77153846:1; parent_transcript=GRMZM2G080839_T01; parent_gene=GRMZM2G080839	GRMZM2G080839_P01	58 kDa	Ref	0.6	0.6	1.7	3.3	No Values	No Values	No Values	No Values
874	seq=translation; coord=4:9657544..9658965:-1; parent_transcript=GRMZM2G117989_T01; parent_gene=GRMZM2G117989	GRMZM2G117989_P01 (+5)	18 kDa	Ref	0.1	0	4.1	4.2	No Values	No Values	No Values	No Values
875	seq=translation; coord=5:6444041..6445037:1; parent_transcript=GRMZM2G077034_T01; parent_gene=GRMZM2G077034	GRMZM2G077034_P01	10 kDa	Ref	0.4	0.7	0.8	0.9	No Values	No Values	No Values	No Values
876	seq=translation; coord=5:193174093..193205154:1; parent_transcript=GRMZM5G883741_T02; parent_gene=GRMZM5G883741	GRMZM5G883741_P02	66 kDa	Ref	-0.3	-0.7	-0.6	-0.3	No Values	No Values	No Values	No Values
877	seq=translation; coord=1:27178033..27184068:-1; parent_transcript=GRMZM5G891739_T01; parent_gene=GRMZM5G891739	GRMZM5G891739_P01	17 kDa	Ref	-0.5	-0.8	-0.5	-0.7	-2	-1.4	-0.7	-1
878	seq=translation; coord=9:11741082..11743899:1; parent_transcript=GRMZM2G177098_T03; parent_gene=GRMZM2G177098	GRMZM2G177098_P03	13 kDa	Ref	0.5	0.1	-0.3	0	2	1.6	1.2	0.8
879	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	143 kDa	Ref	0.1	-0.4	0.2	-0.5	-3.6	-4	-4.1	-4.3
880	seq=translation; coord=2:164667085..164668830:-1; parent_transcript=AC210204.3_FGT002; parent_gene=AC210204.3_FG002	AC210204.3_FGP002	34 kDa	Ref	0.5	0.2	1.4	1	1.3	2	2.3	2.1
881	seq=translation; coord=5:171688070..171693270:-1; parent_transcript=GRMZM2G000278_T01; parent_gene=GRMZM2G000278	GRMZM2G000278_P01 (+4)	42 kDa	Ref	0.7	0.5	-0.1	0.2	2.4	1.7	1.6	1.5
882	seq=translation; coord=10:5718777..5728532:-1; parent_transcript=GRMZM2G020446_T01; parent_gene=GRMZM2G020446	GRMZM2G020446_P01	53 kDa	Ref	-0.5	-0.8	-0.9	-0.2	1.4	0.3	1.6	-0.5
883	seq=translation; coord=1:67436204..67440532:-1; parent_transcript=GRMZM2G107473_T01; parent_gene=GRMZM2G107473	GRMZM2G107473_P01	30 kDa	Ref	1.1	1.6	0.9	Reference Missing	0.5	0	-0.2	-0.8

884	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	191 kDa	Ref	0.5	0.4	-0.3	0.2	2.2	-0.1	-0.3	-0.8
885	seq=translation; coord=1:300990204..300994789:1; parent_transcript=GRMZM2G122267_T01; parent_gene=GRMZM2G122267	GRMZM2G122267_P01 (+1)	63 kDa	Ref	-0.5	-0.6	-0.4	-0.2	-1.6	-1.8	-1.6	-1.3
886	seq=translation; coord=4:162075480..162081835:-1; parent_transcript=GRMZM2G042502_T01; parent_gene=GRMZM2G042502	GRMZM2G042502_P01 (+2)	67 kDa	Ref	0.6	-0.3	-0.9	-0.3	4.1	3.4	3.4	3.7
887	seq=translation; coord=3:158520150..158525636:-1; parent_transcript=GRMZM2G081102_T01; parent_gene=GRMZM2G081102	GRMZM2G081102_P01 (+6)	24 kDa	Ref	1.1	1.2	0.1	-0.1	0.4	-0.4	-0.6	-1.4
888	seq=translation; coord=5:4422815..4424855:1; parent_transcript=GRMZM2G130544_T02; parent_gene=GRMZM2G130544	GRMZM2G130544_P02	18 kDa	Ref	0.4	0.6	0.4	0.2	No Values	No Values	No Values	No Values
889	seq=translation; coord=10:17606896..17610628:1; parent_transcript=GRMZM2G009448_T01; parent_gene=GRMZM2G009448	GRMZM2G009448_P01	26 kDa	Ref	-0.6	-1.3	-1.5	-1.8	5.8	3.6	4.2	3.3
890	seq=translation; coord=1:213095235..213096735:1; parent_transcript=GRMZM2G161274_T02; parent_gene=GRMZM2G161274	GRMZM2G161274_P02	25 kDa	Ref	1.1	1.2	2.6	4.5	-0.6	-0.8	-0.1	3.1
891	seq=translation; coord=10:128106169..128112118:-1; parent_transcript=GRMZM2G098577_T01; parent_gene=GRMZM2G098577	GRMZM2G098577_P01	87 kDa	Ref	1.4	1.4	1.3	0.7	0.3	-0.1	-0.5	0
892	seq=translation; coord=1:289108489..289111192:-1; parent_transcript=GRMZM2G053023_T01; parent_gene=GRMZM2G053023	GRMZM2G053023_P01 (+1)	15 kDa	Ref	-1.6	-1.8	-1.4	-1.6	-1.8	-1.8	-1.9	-0.1
893	seq=translation; coord=9:1634017..1638812:-1; parent_transcript=GRMZM2G143862_T01; parent_gene=GRMZM2G143862	GRMZM2G143862_P01	32 kDa	Ref	-0.1	-0.2	-0.8	0.2	-4.4	-4.8	-5.1	-5
894	seq=translation; coord=9:126016122..126022567:1; parent_transcript=GRMZM2G170843_T01; parent_gene=GRMZM2G170843	GRMZM2G170843_P01 (+1)	51 kDa	Ref	-0.1	-0.3	-0.2	-0.9	-1.8	-1.2	-0.6	-0.2
895	seq=translation; coord=5:70685080..70691262:-1; parent_transcript=GRMZM2G120578_T01; parent_gene=GRMZM2G120578	GRMZM2G120578_P01 (+1)	42 kDa	Ref	-0.1	-0.2	-0.4	-0.4	1.4	0	0.5	0
896	seq=translation; coord=1:190997916..191004927:1; parent_transcript=GRMZM2G084149_T01; parent_gene=GRMZM2G084149	GRMZM2G084149_P01	51 kDa	Ref	1.5	1.6	1.9	1.3	6.3	5.5	5.7	5.3

897	seq=translation; coord=5:83557023..83560095:1; parent_transcript=AC234515.1_FGT003; parent_gene=AC234515.1_FG003	AC234515.1_FGP003	50 kDa	Ref	0.1	-0.6	-1.6	-1.6	-2	Value Missing	Value Missing	Value Missing
898	seq=translation; coord=8:79074521..79075661:-1; parent_transcript=GRMZM2G125893_T01; parent_gene=GRMZM2G125893	GRMZM2G125893_P01	15 kDa	Ref	-0.2	0.2	0.1	-0.8	0.6	1.1	1.5	1.8
899	seq=translation; coord=2:19443026..19444255:1; parent_transcript=GRMZM2G132777_T01; parent_gene=GRMZM2G132777	GRMZM2G132777_P01	35 kDa	Ref	-1	-1.7	-1.3	-1.6	-3.3	-3.2	-3.1	-3.3
900	seq=translation; coord=3:224922109..224926422:1; parent_transcript=GRMZM2G064753_T01; parent_gene=GRMZM2G064753	GRMZM2G064753_P01	18 kDa	Ref	1.2	0.4	0.5	0.1	No Values	No Values	No Values	No Values
901	seq=translation; coord=2:184451593..184456789:1; parent_transcript=GRMZM5G820822_T01; parent_gene=GRMZM5G820822	GRMZM5G820822_P01	27 kDa	Ref	No Values	No Values	No Values	No Values	No Values	No Values	No Values	No Values
902	seq=translation; coord=7:104173693..104176328:-1; parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160	GRMZM2G032160_P01	82 kDa	Ref	0.1	0	0.6	1.3	No Values	No Values	No Values	No Values
903	seq=translation; coord=2:6820716..6853179:1; parent_transcript=GRMZM2G138782_T01; parent_gene=GRMZM2G138782	GRMZM2G138782_P01	67 kDa	Ref	1.6	1.3	1.2	1.3	No Values	No Values	No Values	No Values
904	seq=translation; coord=2:24834408..24836108:-1; parent_transcript=GRMZM2G108153_T01; parent_gene=GRMZM2G108153	GRMZM2G108153_P01	35 kDa	Ref	1.6	0.7	Reference Missing	2.4	No Values	No Values	No Values	No Values
905	seq=translation; coord=8:125902255..125906710:1; parent_transcript=GRMZM2G059693_T01; parent_gene=GRMZM2G059693	GRMZM2G059693_P01 (+2)	58 kDa	Ref	1.6	1.1	-0.4	-0.3	No Values	No Values	No Values	No Values
906	seq=translation; coord=7:151190045..151192101:1; parent_transcript=GRMZM2G155911_T01; parent_gene=GRMZM2G155911	GRMZM2G155911_P01	52 kDa	Ref	-0.8	0	0.1	0.3	No Values	No Values	No Values	No Values
907	seq=translation; coord=7:129358205..129362749:-1; parent_transcript=GRMZM5G843748_T02; parent_gene=GRMZM5G843748	GRMZM5G843748_P02	38 kDa	Ref	-0.1	-0.2	0.4	0.8	No Values	No Values	No Values	No Values
908	seq=translation; coord=5:77916981..77922073:1; parent_transcript=GRMZM2G097207_T01; parent_gene=GRMZM2G097207	GRMZM2G097207_P01	53 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.5	0.3	0.7
909	seq=translation; coord=10:86984445..86986672:1; parent_transcript=GRMZM2G028104_T01; parent_gene=GRMZM2G028104	GRMZM2G028104_P01	47 kDa	Ref	0.5	1.5	1.4	2.7	No Values	No Values	No Values	No Values

910	seq=translation; coord=7:137518004..137519265:-1; parent_transcript=GRMZM2G066202_T01; parent_gene=GRMZM2G066202	GRMZM2G066202_P01	27 kDa	Ref	1.3	0.6	1.1	0.2	No Values	No Values	No Values	No Values
911	seq=translation; coord=9:41048627..41058528:-1; parent_transcript=GRMZM2G538535_T01; parent_gene=GRMZM2G538535	GRMZM2G538535_P01	49 kDa	Ref	0.5	0.2	1.2	1.8	No Values	No Values	No Values	No Values
912	seq=translation; coord=1:232041908..232053896:-1; parent_transcript=GRMZM2G148323_T01; parent_gene=GRMZM2G148323	GRMZM2G148323_P01	62 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.4	0.1	-0.1
913	seq=translation; coord=2:2338643..2346346:-1; parent_transcript=GRMZM2G077744_T01; parent_gene=GRMZM2G077744	GRMZM2G077744_P01 (+3)	16 kDa	Ref	1.1	1.4	1.4	0.8	0.7	-0.9	-0.8	-1.3
914	seq=translation; coord=2:196218998..196222283:1; parent_transcript=GRMZM2G042604_T01; parent_gene=GRMZM2G042604	GRMZM2G042604_P01 (+3)	27 kDa	Ref	0.1	0	0.4	0	-1.3	-0.4	-0.4	0.1
915	seq=translation; coord=8:18214060..18227316:1; parent_transcript=GRMZM2G107696_T01; parent_gene=GRMZM2G107696	GRMZM2G107696_P01 (+1)	93 kDa	Ref	-0.3	0.1	-0.1	-0.4	-1.7	-1.7	-1.3	-1.4
916	seq=translation; coord=9:115668526..115674221:1; parent_transcript=GRMZM5G818887_T01; parent_gene=GRMZM5G818887	GRMZM5G818887_P01	35 kDa	Ref	0.1	0.2	0	0.3	-0.1	0.7	0.7	0.4
917	seq=translation; coord=1:248590498..248595499:-1; parent_transcript=GRMZM5G830403_T02; parent_gene=GRMZM5G830403	GRMZM5G830403_P02 (+2)	36 kDa	Ref	0.5	-0.9	-0.6	-1.3	0	-1.1	Value Missing	Value Missing
918	seq=translation; coord=7:155961862..155967544:-1; parent_transcript=GRMZM2G173910_T01; parent_gene=GRMZM2G173910	GRMZM2G173910_P01	32 kDa	Ref	0.1	-0.1	-0.4	-0.6	-0.3	-1	-1.1	-1.3
919	seq=translation; coord=5:15703665..15718967:1; parent_transcript=AC197122.3_FGT003; parent_gene=AC197122.3_FG003	AC197122.3_FGP003	65 kDa	Ref	0	-0.3	-0.4	-0.5	-1.4	-2.1	-2.9	-2.4
920	seq=translation; coord=6:117850410..117855773:-1; parent_transcript=GRMZM2G074454_T01; parent_gene=GRMZM2G074454	GRMZM2G074454_P01	57 kDa	Ref	-0.3	-0.6	-1.2	-0.6	0.9	1.2	1.1	0.3
921	seq=translation; coord=8:83396432..83400437:1; parent_transcript=GRMZM2G131249_T02; parent_gene=GRMZM2G131249	GRMZM2G131249_P02	29 kDa	Ref	-0.5	-0.7	-0.6	-0.6	0.5	-0.6	-0.2	0.1
922	seq=translation; coord=6:167006647..167019258:1; parent_transcript=AC233870.1_FGT006; parent_gene=AC233870.1_FG006	AC233870.1_FGP006	23 kDa	Ref	0	-0.3	0.2	-0.6	2.2	1.1	1.3	0.9

923	seq=translation; coord=8:3347680..3350552:1; parent_transcript=GRMZM2G013461_T01; parent_gene=GRMZM2G013461	GRMZM2G013461_P01 (+1)	27 kDa	Ref	0.6	0.2	0.9	-0.2	2	3.1	3.7	3.4
924	seq=translation; coord=9:134504096..134514418:-1; parent_transcript=GRMZM2G051613_T01; parent_gene=GRMZM2G051613	GRMZM2G051613_P01 (+1)	19 kDa	Ref	0	-0.3	-0.1	-0.9	-1.1	-2.2	-2.5	-2.4
925	seq=translation; coord=2:232093952..232099171:1; parent_transcript=GRMZM2G035807_T01; parent_gene=GRMZM2G035807	GRMZM2G035807_P01 (+3)	68 kDa	Ref	1.1	0.7	0.3	1	2.4	0.6	0.4	-0.2
926	seq=translation; coord=1:66948065..66952666:-1; parent_transcript=GRMZM2G152925_T01; parent_gene=GRMZM2G152925	GRMZM2G152925_P01	19 kDa	Ref	2.5	2.2	2.6	2	No Values	No Values	No Values	No Values
927	seq=translation; coord=8:143277512..143279395:-1; parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072	GRMZM2G050072_P01	45 kDa	Ref	-0.1	0.2	-0.1	0.1	0.8	0.9	1	1.2
928	seq=translation; coord=10:25975417..25980229:-1; parent_transcript=GRMZM2G014376_T01; parent_gene=GRMZM2G014376	GRMZM2G014376_P01 (+2)	58 kDa	Ref	0	0	-0.5	-0.2	3.9	4.8	5	4.3
929	seq=translation; coord=1:264743594..264751569:1; parent_transcript=GRMZM2G002687_T01; parent_gene=GRMZM2G002687	GRMZM2G002687_P01	46 kDa	Ref	-1.5	-1.7	-1.3	-1.7	-0.6	-0.3	0.3	0.4
930	seq=translation; coord=4:170517685..170521446:-1; parent_transcript=GRMZM2G150648_T03; parent_gene=GRMZM2G150648	GRMZM2G150648_P03 (+2)	32 kDa	Ref	1.2	0.3	0.1	0.4	Reference Missing	0.2	-0.1	Value Missing
931	seq=translation; coord=4:174901704..174907176:-1; parent_transcript=GRMZM2G039263_T01; parent_gene=GRMZM2G039263	GRMZM2G039263_P01 (+2)	59 kDa	Ref	-1.1	Value Missing	Value Missing	Value Missing	-5	-5.5	Value Missing	-6.2
932	seq=translation; coord=1:226171571..226174821:1; parent_transcript=GRMZM5G882228_T02; parent_gene=GRMZM5G882228	GRMZM5G882228_P02	23 kDa	Ref	0.2	0.2	0.5	0.4	-4.1	-5.7	-5.7	-5.8
933	seq=translation; coord=3:19453334..19462209:1; parent_transcript=GRMZM2G088834_T03; parent_gene=GRMZM2G088834	GRMZM2G088834_P03 (+1)	48 kDa	Ref	1.6	1.9	1.7	1.5	1.3	1.3	1.1	0.4
934	seq=translation; coord=2:170263508..170267458:-1; parent_transcript=GRMZM2G074687_T01; parent_gene=GRMZM2G074687	GRMZM2G074687_P01	48 kDa	Ref	1.2	1.2	0.9	0.5	0.4	-1	-0.6	-0.8
935	seq=translation; coord=1:94486908..94489534:1; parent_transcript=GRMZM2G052666_T01; parent_gene=GRMZM2G052666	GRMZM2G052666_P01	28 kDa	Ref	0.1	0	0.7	0.1	1	1.8	2.2	2.1

936	seq=translation; coord=3:47497754..47499644:-1; parent_transcript=GRMZM2G123407_T01; parent_gene=GRMZM2G123407	GRMZM2G123407_P01	24 kDa	Ref	-1.2	-1.2	-1.6	-2.6	-1.4	-1.2	-1	-1.7
937	seq=translation; coord=1:277739114..277741150:1; parent_transcript=GRMZM2G090422_T01; parent_gene=GRMZM2G090422	GRMZM2G090422_P01	24 kDa	Ref	0.6	0.2	0.1	0.1	3	2.1	2.3	1.7
938	seq=translation; coord=4:229500502..229510053:1; parent_transcript=GRMZM2G069631_T01; parent_gene=GRMZM2G069631	GRMZM2G069631_P01 (+5)	58 kDa	Ref	0.1	-0.1	-0.1	-0.1	0.1	-0.4	-0.5	-0.5
939	seq=translation; coord=2:30905783..30911404:-1; parent_transcript=GRMZM2G352129_T01; parent_gene=GRMZM2G352129	GRMZM2G352129_P01	72 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	0.7	0.4
940	seq=translation; coord=1:84814341..84815071:1; parent_transcript=GRMZM2G402564_T01; parent_gene=GRMZM2G402564	GRMZM2G402564_P01	8 kDa	Ref	No Values	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing
941	seq=translation; coord=2:53844493..53846005:1; parent_transcript=GRMZM2G044132_T01; parent_gene=GRMZM2G044132	GRMZM2G044132_P01	28 kDa	Ref	0.9	1.8	2.7	3.7	No Values	No Values	No Values	No Values
942	seq=translation; coord=5:183144788..183149469:1; parent_transcript=GRMZM2G007647_T01; parent_gene=GRMZM2G007647	GRMZM2G007647_P01	52 kDa	Ref	No Values	No Values	No Values	No Values	1.9	1.5	0.7	0.3
943	seq=translation; coord=5:6445850..6453287:-1; parent_transcript=GRMZM2G076885_T01; parent_gene=GRMZM2G076885	GRMZM2G076885_P01	41 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	0.1	-0.7
944	seq=translation; coord=8:144270470..144273473:-1; parent_transcript=GRMZM2G024315_T01; parent_gene=GRMZM2G024315	GRMZM2G024315_P01	38 kDa	Ref	0.1	0.1	0.9	1.2	No Values	No Values	No Values	No Values
945	seq=translation; coord=3:30996380..30997528:1; parent_transcript=AC226235.2_FGT001; parent_gene=AC226235.2_FG001	AC226235.2_FGP001	33 kDa	Ref	-1.8	-1.9	-1.1	-1.9	No Values	No Values	No Values	No Values
946	seq=translation; coord=5:65417067..65419686:1; parent_transcript=GRMZM2G112805_T01; parent_gene=GRMZM2G112805	GRMZM2G112805_P01	30 kDa	Ref	Reference Missing	2	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
947	seq=translation; coord=2:34740703..34741540:1; parent_transcript=AC155352.2_FGT010; parent_gene=AC155352.2_FG010	AC155352.2_FGP010 (+2)	14 kDa	Ref	1.1	1.3	1	0.5	No Values	No Values	No Values	No Values
948	seq=translation; coord=10:4776409..4777145:-1; parent_transcript=GRMZM2G031033_T01; parent_gene=GRMZM2G031033	GRMZM2G031033_P01	16 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.2	0.6	-0.1

949	seq=translation; coord=6:14560251..14563314:-1; parent_transcript=GRMZM2G076943_T01; parent_gene=GRMZM2G076943 seq=translation; coord=4:1482217..1485577:-1;	GRMZM2G076943_P01	76 kDa	Ref	1.4	2.2	1	1.4	No Values	No Values	No Values	No Values
950	parent_transcript=GRMZM2G107082_T01; parent_gene=GRMZM2G107082 seq=translation; coord=5:181383017..181386545:1;	GRMZM2G107082_P01	47 kDa	Ref	0.1	0.1	-0.1	0.1	No Values	No Values	No Values	No Values
951	parent_transcript=GRMZM2G029583_T02; parent_gene=GRMZM2G029583 seq=translation; coord=1:297509820..297513009:-1;	GRMZM2G029583_P02 (+1)	44 kDa	Ref	0.8	0.1	0.2	0.7	0.3	-2.5	-2.3	-1.3
952	parent_transcript=GRMZM5G898915_T01; parent_gene=GRMZM5G898915 seq=translation; coord=4:26128851..26131595:1;	GRMZM5G898915_P01	37 kDa	Ref	-0.6	-0.6	-0.9	-0.8	0.7	0.8	0.7	0.8
953	parent_transcript=GRMZM2G024482_T02; parent_gene=GRMZM2G024482 seq=translation; coord=2:82246568..82258715:1;	GRMZM2G024482_P02	24 kDa	Ref	-0.5	-0.3	-0.7	-0.6	2.1	2.3	2.6	2.8
954	parent_transcript=GRMZM2G125310_T01; parent_gene=GRMZM2G125310 seq=translation; coord=10:70222469..70228198:-1;	GRMZM2G125310_P01 (+1)	25 kDa	Ref	-0.2	0.1	-0.3	-0.5	-1.7	-1.1	-0.7	-0.4
955	parent_transcript=GRMZM2G103287_T01; parent_gene=GRMZM2G103287 seq=translation; coord=7:8520216..8522520:-1;	GRMZM2G103287_P01 (+1)	37 kDa	Ref	0.1	0	-0.3	-0.1	-0.9	-0.8	-0.6	-0.2
956	parent_transcript=GRMZM2G024354_T01; parent_gene=GRMZM2G024354 seq=translation; coord=1:225492875..225495179:1;	GRMZM2G024354_P01	24 kDa	Ref	1	-0.1	-1.7	-1.2	0	-1.2	-2.2	-3.2
957	parent_transcript=GRMZM2G056431_T01; parent_gene=GRMZM2G056431 seq=translation; coord=10:69423694..69433754:-1;	GRMZM2G056431_P01 (+1)	13 kDa	Ref	1.8	1.7	1.9	1.4	4.2	4.3	4.6	4.7
958	parent_transcript=GRMZM2G145870_T01; parent_gene=GRMZM2G145870 seq=translation; coord=4:5375612..5380694:1;	GRMZM2G145870_P01 (+1)	42 kDa	Ref	-0.8	-0.8	-0.5	-0.2	-1.6	-1.7	-1.6	-1.1
959	parent_transcript=GRMZM2G154169_T01; parent_gene=GRMZM2G154169 seq=translation; coord=9:110247484..110252966:-1;	GRMZM2G154169_P01	23 kDa	Ref	0.9	0.9	1	0.8	0.7	Reference Missing	0.2	0.2
960	parent_transcript=GRMZM2G174444_T01; parent_gene=GRMZM2G174444 seq=translation; coord=5:29321627..29325204:1;	GRMZM2G174444_P01 (+1)	12 kDa	Ref	-0.8	-0.5	0.1	-0.3	0.7	0.1	0.5	1
961	parent_transcript=GRMZM2G158277_T01; parent_gene=GRMZM2G158277	GRMZM2G158277_P01 (+2)	30 kDa	Ref	0.6	0.4	0.7	0	0.7	-0.1	-0.3	-0.5

962	seq=translation; coord=8:21874081..21876830:1; parent_transcript=GRMZM2G033283_T01; parent_gene=GRMZM2G033283	GRMZM2G033283_P01	21 kDa	Ref	0	-0.1	-0.4	-0.1	-1.1	-1.2	-1.2	-0.7
963	seq=translation; coord=6:158946942..158950117:1; parent_transcript=GRMZM2G044368_T01; parent_gene=GRMZM2G044368	GRMZM2G044368_P01 (+3)	23 kDa	Ref	-0.3	-0.4	-0.2	-0.2	0.7	0	-0.2	-0.4
964	seq=translation; coord=2:46344346..46345626:-1; parent_transcript=AC206968.3_FGT003; parent_gene=AC206968.3_FG003	AC206968.3_FGP003	48 kDa	Ref	-1.1	-1	-0.8	-0.9	-2.8	-3.4	-3.4	-3.2
965	seq=translation; coord=6:130963745..130976059:-1; parent_transcript=GRMZM2G361605_T01; parent_gene=GRMZM2G361605	GRMZM2G361605_P01 (+1)	94 kDa	Ref	-0.4	-0.6	-0.8	-0.8	No Values	No Values	No Values	No Values
966	seq=translation; coord=5:160443383..160458679:1; parent_transcript=GRMZM2G052435_T03; parent_gene=GRMZM2G052435	GRMZM2G052435_P03	119 kDa	Ref	No Values	No Values	No Values	No Values	0.8	-0.3	-0.5	-0.1
967	seq=translation; coord=7:170026036..170029198:1; parent_transcript=GRMZM2G055527_T01; parent_gene=GRMZM2G055527	GRMZM2G055527_P01	11 kDa	Ref	-0.6	-1	-0.9	-2.1	2.6	3.1	3	3
968	seq=translation; coord=4:45262758..45263990:-1; parent_transcript=GRMZM2G071575_T01; parent_gene=GRMZM2G071575	GRMZM2G071575_P01	19 kDa	Ref	1.2	0.9	0.6	0.4	-0.6	-0.9	-0.8	-1.4
969	seq=translation; coord=3:57145425..57150481:1; parent_transcript=GRMZM2G033644_T01; parent_gene=GRMZM2G033644	GRMZM2G033644_P01	57 kDa	Ref	-1.2	-0.8	-0.9	-0.5	Value Missing	0.7	1	-0.1
970	seq=translation; coord=10:79271116..79273839:-1; parent_transcript=GRMZM2G032564_T01; parent_gene=GRMZM2G032564	GRMZM2G032564_P01 (+5)	14 kDa	Ref	0.8	0.1	-0.9	-0.5	0	-1.2	-1.6	-2.5
971	seq=translation; coord=2:217631963..217637147:1; parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425	GRMZM2G109425_P01 (+1)	59 kDa	Ref	-1	-0.6	-0.6	0.3	-3.2	-3.2	-3.4	-3.8
972	seq=translation; coord=8:122751582..122753805:1; parent_transcript=GRMZM2G154936_T01; parent_gene=GRMZM2G154936	GRMZM2G154936_P01 (+2)	18 kDa	Ref	2.1	1.6	1.3	1.1	1	-3.8	-3.4	-3.8
973	seq=translation; coord=10:35583589..35590383:1; parent_transcript=GRMZM2G009443_T01; parent_gene=GRMZM2G009443	GRMZM2G009443_P01 (+1)	102 kDa	Ref	0.8	Value Missing	0.2	0.6	Reference Missing	Reference Missing	Reference Missing	Reference Missing
974	seq=translation; coord=8:1370962..1373972:-1; parent_transcript=GRMZM2G042636_T01; parent_gene=GRMZM2G042636	GRMZM2G042636_P01 (+6)	50 kDa	Ref	1.4	0.2	-1.1	-1.4	1.6	-0.7	-0.9	-1.9

975	seq=translation; coord=4:93237748..93253880:1; parent_transcript=GRMZM2G451443_T01; parent_gene=GRMZM2G451443	GRMZM2G451443_P01	63 kDa	Ref	0.3	0.1	-0.1	-0.3	Reference Missing	-0.5	-0.8	-1
976	seq=translation; coord=5:24616889..24618887:-1; parent_transcript=GRMZM2G032910_T01; parent_gene=GRMZM2G032910	GRMZM2G032910_P01 (+1)	35 kDa	Ref	-0.5	-0.3	-0.2	0.8	2.6	2.6	3	3.1
977	seq=translation; coord=1:12987102..12993471:1; parent_transcript=GRMZM2G172322_T01; parent_gene=GRMZM2G172322	GRMZM2G172322_P01 (+1)	59 kDa	Ref	-0.1	-0.2	0.2	0.3	1.5	1.4	1.9	2.2
978	seq=translation; coord=4:54600217..54609072:-1; parent_transcript=GRMZM2G098496_T01; parent_gene=GRMZM2G098496	GRMZM2G098496_P01 (+1)	32 kDa	Ref	0.8	0.8	1.5	0.4	-1	-0.7	-1.1	1.7
979	seq=translation; coord=3:148834092..148846161:-1; parent_transcript=GRMZM2G047310_T02; parent_gene=GRMZM2G047310	GRMZM2G047310_P02	108 kDa	Ref	-0.6	-0.7	-0.8	-0.6	2.3	2	2.5	1.7
980	seq=translation; coord=5:155530969..155538363:-1; parent_transcript=GRMZM2G015132_T01; parent_gene=GRMZM2G015132	GRMZM2G015132_P01	58 kDa	Ref	-0.2	-0.4	-0.4	0.3	-0.1	-1	-1.2	-0.8
981	seq=translation; coord=8:98594898..98599276:-1; parent_transcript=GRMZM2G114954_T01; parent_gene=GRMZM2G114954	GRMZM2G114954_P01 (+3)	12 kDa	Ref	1	-0.9	1.2	0.2	-2.9	-2.9	-3.7	-3.1
982	seq=translation; coord=8:9919345..9920090:-1; parent_transcript=AC204893.3_FGT001; parent_gene=AC204893.3_FG001	AC204893.3_FGP001 (+1)	13 kDa	Ref	-1.6	-1.7	-2.6	-3.5	-4	-5.6	-5.8	-5.8
983	seq=translation; coord=8:159703050..159707801:1; parent_transcript=GRMZM2G122607_T01; parent_gene=GRMZM2G122607	GRMZM2G122607_P01	48 kDa	Ref	Reference Missing	0.6	Reference Missing	0.4	2.7	3.1	2.9	2.2
984	seq=translation; coord=4:161027635..161031592:-1; parent_transcript=GRMZM2G156068_T01; parent_gene=GRMZM2G156068	GRMZM2G156068_P01 (+1)	26 kDa	Ref	-0.8	-0.3	0.1	0	0.8	1.3	1.2	0.8
985	seq=translation; coord=3:88528132..88533870:-1; parent_transcript=GRMZM2G476933_T01; parent_gene=GRMZM2G476933	GRMZM2G476933_P01	29 kDa	Ref	0.5	-0.3	-0.2	-0.6	0.8	0	-0.2	-0.7
986	seq=translation; coord=1:56223520..56226018:1; parent_transcript=GRMZM2G062425_T01; parent_gene=GRMZM2G062425	GRMZM2G062425_P01 (+1)	28 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.4	-1.1	-1.2
987	seq=translation; coord=2:207265904..207268967:1; parent_transcript=AC194970.5_FGT009; parent_gene=AC194970.5_FG009	AC194970.5_FGP009	52 kDa	Ref	1.7	0.9	1.4	0.1	-1.6	-1.8	-2.1	-2.5

988	seq=translation; coord=3:224163656..224168718:-1; parent_transcript=GRMZM2G339540_T04; parent_gene=GRMZM2G339540	GRMZM2G339540_P04 (+1)	70 kDa	Ref	0.3	0.8	0.4	0.9	No Values	No Values	No Values	No Values
989	seq=translation; coord=7:154714410..154723867:1; parent_transcript=GRMZM2G375593_T01; parent_gene=GRMZM2G375593	GRMZM2G375593_P01	104 kDa	Ref	No Values	No Values	No Values	No Values	1	1.1	0.5	0.5
990	seq=translation; coord=7:7507005..7510800:-1; parent_transcript=GRMZM2G143330_T01; parent_gene=GRMZM2G143330	GRMZM2G143330_P01	36 kDa	Ref	No Values	No Values	No Values	No Values	0.9	1	0.8	0.3
991	seq=translation; coord=7:124863398..124868735:1; parent_transcript=GRMZM2G067265_T01; parent_gene=GRMZM2G067265	GRMZM2G067265_P01 (+1)	54 kDa	Ref	No Values	No Values	No Values	No Values	0.2	Reference Missing	0.6	1
992	seq=translation; coord=1:289786005..289788499:1; parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833	GRMZM2G168833_P01	21 kDa	Ref	-0.1	0.7	1.3	2.5	No Values	No Values	No Values	No Values
993	seq=translation; coord=5:159290030..159322686:-1; parent_transcript=GRMZM2G386155_T01; parent_gene=GRMZM2G386155	GRMZM2G386155_P01 (+1)	54 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.6	1.8	1.8
994	seq=translation; coord=6:103857605..103858686:-1; parent_transcript=GRMZM2G335618_T01; parent_gene=GRMZM2G335618	GRMZM2G335618_P01	26 kDa	Ref	-0.7	-0.7	-0.3	0.7	No Values	No Values	No Values	No Values
995	seq=translation; coord=2:42784980..42792494:1; parent_transcript=GRMZM2G065073_T02; parent_gene=GRMZM2G065073	GRMZM2G065073_P02	61 kDa	Ref	0.4	0.7	0.9	1.3	No Values	No Values	No Values	No Values
996	seq=translation; coord=8:607069..619737:1; parent_transcript=GRMZM2G077233_T01; parent_gene=GRMZM2G077233	GRMZM2G077233_P01 (+4)	55 kDa	Ref	0.5	0	0.9	3	No Values	No Values	No Values	No Values
997	seq=translation; coord=3:184434264..184435351:1; parent_transcript=GRMZM2G126397_T01; parent_gene=GRMZM2G126397	GRMZM2G126397_P01	13 kDa	Ref	3.1	0.4	0.3	0.1	No Values	No Values	No Values	No Values
998	seq=translation; coord=5:168890072..168891220:-1; parent_transcript=GRMZM2G115491_T01; parent_gene=GRMZM2G115491	GRMZM2G115491_P01	25 kDa	Ref	0.2	0.8	0.7	1.1	No Values	No Values	No Values	No Values
999	seq=translation; coord=8:5023676..5024789:1; parent_transcript=GRMZM2G095164_T01; parent_gene=GRMZM2G095164	GRMZM2G095164_P01 (+1)	13 kDa	Ref	5	4.1	4.5	3.4	No Values	No Values	No Values	No Values
1000	seq=translation; coord=4:35209593..35215535:1; parent_transcript=GRMZM2G145972_T02; parent_gene=GRMZM2G145972	GRMZM2G145972_P02	65 kDa	Ref	0.9	0.8	1.4	2.5	No Values	No Values	No Values	No Values

1001	seq=translation; coord=9:143036859..143040005:-1; parent_transcript=GRMZM2G149809_T01; parent_gene=GRMZM2G149809	GRMZM2G149809_P01 (+1)	32 kDa	Ref	0.4	0.8	2.6	3.3	No Values	No Values	No Values	No Values
1002	seq=translation; coord=3:147969444..147972018:1; parent_transcript=GRMZM2G701801_T02; parent_gene=GRMZM2G701801	GRMZM2G701801_P02	22 kDa	Ref	0.4	0.4	0.8	1.1	No Values	No Values	No Values	No Values
1003	seq=translation; coord=8:159254849..159263818:-1; parent_transcript=GRMZM2G046558_T02; parent_gene=GRMZM2G046558	GRMZM2G046558_P02	32 kDa	Ref	-0.2	-0.4	0	-0.6	-3.1	-3	-3.4	-2.6
1004	seq=translation; coord=9:64132094..64145762:1; parent_transcript=GRMZM2G072909_T01; parent_gene=GRMZM2G072909	GRMZM2G072909_P01	47 kDa	Ref	-1.1	-1.2	-1.4	-1.1	0.2	0.6	-0.4	-0.1
1005	seq=translation; coord=4:194605171..194610906:-1; parent_transcript=GRMZM2G097043_T01; parent_gene=GRMZM2G097043	GRMZM2G097043_P01	88 kDa	Ref	1.1	0.4	0.8	0.3	-1.4	-0.7	-0.9	-0.8
1006	seq=translation; coord=1:3830541..3834833:1; parent_transcript=GRMZM2G085909_T01; parent_gene=GRMZM2G085909	GRMZM2G085909_P01	58 kDa	Ref	-1.1	-1.1	-0.6	-0.9	-2.1	-2	-2.3	-3.1
1007	seq=translation; coord=2:212802942..212807188:1; parent_transcript=GRMZM2G141510_T01; parent_gene=GRMZM2G141510	GRMZM2G141510_P01	47 kDa	Ref	0.3	0.2	-0.4	-0.3	1.5	1.2	1.5	0.9
1008	seq=translation; coord=8:10870907..10877056:1; parent_transcript=GRMZM2G030384_T01; parent_gene=GRMZM2G030384	GRMZM2G030384_P01	66 kDa	Ref	0.1	-0.2	-0.4	0.1	-2.9	-2.8	-2.4	-2.1
1009	seq=translation; coord=10:141573795..141580886:-1; parent_transcript=GRMZM2G156145_T01; parent_gene=GRMZM2G156145	GRMZM2G156145_P01	110 kDa	Ref	0.3	0.4	0.3	0.1	-0.3	-0.8	-0.7	-1.3
1010	seq=translation; coord=6:161231386..161234113:-1; parent_transcript=GRMZM2G159032_T01; parent_gene=GRMZM2G159032	GRMZM2G159032_P01 (+2)	33 kDa	Ref	-0.4	-1	-1.2	-1	-0.7	-3	-3.1	-3
1011	seq=translation; coord=5:183882422..183889051:-1; parent_transcript=GRMZM2G142088_T01; parent_gene=GRMZM2G142088	GRMZM2G142088_P01 (+1)	87 kDa	Ref	0.4	-0.5	-1.2	-0.7	-0.7	-2.7	-3.9	-3.4
1012	seq=translation; coord=5:204089494..204100246:-1; parent_transcript=GRMZM2G029186_T01; parent_gene=GRMZM2G029186	GRMZM2G029186_P01 (+3)	146 kDa	Ref	-0.6	-0.6	-1	-1	-4.1	-4.1	-4.5	-4.6
1013	seq=translation; coord=5:74450298..74452700:-1; parent_transcript=GRMZM5G831200_T01; parent_gene=GRMZM5G831200	GRMZM5G831200_P01	55 kDa	Ref	-0.3	-0.5	-0.6	-1	-3.7	-1.9	-0.6	-1

1014	seq=translation; coord=3:133205499..133209390:-1; parent_transcript=GRMZM2G136262_T01; parent_gene=GRMZM2G136262	GRMZM2G136262_P01	15 kDa	Ref	-0.5	-0.6	-0.3	-0.6	-1.3	-1.1	-1	-0.9
1015	seq=translation; coord=6:131028969..131032495:1; parent_transcript=GRMZM2G133631_T01; parent_gene=GRMZM2G133631	GRMZM2G133631_P01 (+5)	22 kDa	Ref	0.1	0.2	0.2	-0.1	3.2	3.3	3.4	3
1016	seq=translation; coord=6:140465764..140469654:1; parent_transcript=AC213884.3_FGT001; parent_gene=AC213884.3_FG001	AC213884.3_FGP001	24 kDa	Ref	0.2	0.2	0.5	-0.2	No Values	No Values	No Values	No Values
1017	seq=translation; coord=10:23245983..23251624:-1; parent_transcript=GRMZM2G013478_T01; parent_gene=GRMZM2G013478	GRMZM2G013478_P01	24 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.3	0.3	0.9
1018	seq=translation; coord=9:153591547..153607432:1; parent_transcript=GRMZM2G051219_T01; parent_gene=GRMZM2G051219	GRMZM2G051219_P01 (+1)	41 kDa	Ref	-2.3	-1.7	-1.3	-2.1	No Values	No Values	No Values	No Values
1019	seq=translation; coord=4:235606747..235623515:-1; parent_transcript=GRMZM2G119482_T01; parent_gene=GRMZM2G119482	GRMZM2G119482_P01	56 kDa	Ref	Reference Missing	0.1	Reference Missing	0.8	-3	-2.4	-2.5	-2.9
1020	seq=translation; coord=6:102399027..102412128:1; parent_transcript=GRMZM2G106427_T01; parent_gene=GRMZM2G106427	GRMZM2G106427_P01 (+3)	35 kDa	Ref	0.2	0.2	0.2	0.1	1.6	1.4	1.4	1.1
1021	seq=translation; coord=1:46061768..46066293:1; parent_transcript=GRMZM2G058138_T01; parent_gene=GRMZM2G058138	GRMZM2G058138_P01 (+2)	38 kDa	Ref	1	1	0.1	1	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1022	seq=translation; coord=4:102065832..102092090:1; parent_transcript=GRMZM2G028766_T01; parent_gene=GRMZM2G028766	GRMZM2G028766_P01 (+1)	47 kDa	Ref	-0.5	-0.5	-1.4	-2.1	-3.4	-4	-4.1	-3.8
1023	seq=translation; coord=5:176347442..176349538:1; parent_transcript=GRMZM2G056629_T01; parent_gene=GRMZM2G056629	GRMZM2G056629_P01	41 kDa	Ref	2.3	2.3	1.8	1.4	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1024	seq=translation; coord=6:160040980..160045154:-1; parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036	GRMZM2G005036_P01	54 kDa	Ref	0.7	0.6	0.2	1	5.3	3.6	3.6	3.1
1025	seq=translation; coord=1:274275100..274280175:1; parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283	GRMZM2G135283_P03 (+1)	57 kDa	Ref	0.1	-0.4	-0.3	0.2	5	5.5	5.4	4.6
1026	seq=translation; coord=1:191893507..191894902:1; parent_transcript=GRMZM2G427451_T01; parent_gene=GRMZM2G427451	GRMZM2G427451_P01	25 kDa	Ref	-0.4	-0.9	-2.3	-3.3	-0.5	-1	-0.9	-0.6

1027	seq=translation; coord=1:56746484..56752553:1; parent_transcript=GRMZM2G010823_T01; parent_gene=GRMZM2G010823	GRMZM2G010823_P01	54 kDa	Ref	0.4	0.3	0	0.5	1	0.6	0.4	0.1
1028	seq=translation; coord=8:116304892..116311147:-1; parent_transcript=GRMZM2G055489_T01; parent_gene=GRMZM2G055489	GRMZM2G055489_P01 (+2)	47 kDa	Ref	0.1	-0.1	-0.3	-0.1	1.6	1.8	2.2	2.2
1029	seq=translation; coord=5:56740173..56751799:1; parent_transcript=GRMZM2G115939_T01; parent_gene=GRMZM2G115939	GRMZM2G115939_P01 (+2)	21 kDa	Ref	-0.2	-0.3	-0.4	-0.6	-0.8	-0.6	-0.8	-0.6
1030	seq=translation; coord=4:163464001..163467089:-1; parent_transcript=GRMZM2G072612_T01; parent_gene=GRMZM2G072612	GRMZM2G072612_P01 (+1)	39 kDa	Ref	0.1	-0.2	0.1	0.9	1.2	1.9	2.3	2.9
1031	seq=translation; coord=10:106434010..106436707:-1; parent_transcript=GRMZM2G139512_T01; parent_gene=GRMZM2G139512	GRMZM2G139512_P01 (+3)	29 kDa	Ref	0.2	-0.4	-0.1	0.8	-0.8	-0.2	-0.6	-0.5
1032	seq=translation; coord=7:164069905..164076083:1; parent_transcript=GRMZM2G136918_T01; parent_gene=GRMZM2G136918	GRMZM2G136918_P01 (+4)	31 kDa	Ref	-1	-1.4	-0.7	-1.4	-1.9	-0.3	0	-0.3
1033	seq=translation; coord=10:148101348..148102945:1; parent_transcript=GRMZM5G892522_T01; parent_gene=GRMZM5G892522	GRMZM5G892522_P01	19 kDa	Ref	-1.6	-1.6	-1.2	-1.6	-3.8	-2.8	-2.5	0
1034	seq=translation; coord=4:154310162..154311883:-1; parent_transcript=GRMZM2G373522_T01; parent_gene=GRMZM2G373522	GRMZM2G373522_P01	31 kDa	Ref	2.3	2	2.2	2.5	3.1	2.4	2.1	2.3
1035	seq=translation; coord=5:113730181..113780006:1; parent_transcript=GRMZM2G056661_T01; parent_gene=GRMZM2G056661	GRMZM2G056661_P01 (+1)	222 kDa	Ref	No Values	No Values	No Values	No Values	1.5	0.3	0.8	-1.9
1036	seq=translation; coord=8:173103213..173107748:1; parent_transcript=GRMZM2G124365_T01; parent_gene=GRMZM2G124365	GRMZM2G124365_P01	35 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.4	-0.7	1.7
1037	seq=translation; coord=1:60216405..60219476:-1; parent_transcript=GRMZM2G144995_T01; parent_gene=GRMZM2G144995	GRMZM2G144995_P01 (+1)	61 kDa	Ref	No Values	No Values	No Values	No Values	1.1	0.5	0.7	-1.1
1038	seq=translation; coord=5:64107900..64117086:1; parent_transcript=GRMZM2G145088_T01; parent_gene=GRMZM2G145088	GRMZM2G145088_P01	131 kDa	Ref	-0.2	-0.4	-0.6	-0.6	No Values	No Values	No Values	No Values
1039	seq=translation; coord=4:238325251..238328383:-1; parent_transcript=GRMZM2G060567_T01; parent_gene=GRMZM2G060567	GRMZM2G060567_P01	26 kDa	Ref	2.6	2.5	2.5	1.4	No Values	No Values	No Values	No Values

1040	seq=translation; coord=7:106230652..106231840:1; parent_transcript=GRMZM2G025646_T01; parent_gene=GRMZM2G025646	GRMZM2G025646_P01 (+1)	15 kDa	Ref	No Values	No Values	No Values	No Values	3.2	2.9	2.3	1.6
1041	seq=translation; coord=3:22814532..22820273:-1; parent_transcript=GRMZM2G009282_T01; parent_gene=GRMZM2G009282	GRMZM2G009282_P01	102 kDa	Ref	1.1	0.1	-0.7	0.7	No Values	No Values	No Values	No Values
1042	seq=translation; coord=2:130291275..130295558:-1; parent_transcript=GRMZM2G118800_T01; parent_gene=GRMZM2G118800	GRMZM2G118800_P01	52 kDa	Ref	1.4	0.5	0.9	1.9	No Values	No Values	No Values	No Values
1043	seq=translation; coord=4:172748163..172754261:1; parent_transcript=GRMZM2G178398_T01; parent_gene=GRMZM2G178398	GRMZM2G178398_P01	99 kDa	Ref	0.8	0.5	0.2	0.1	No Values	No Values	No Values	No Values
1044	seq=translation; coord=5:182124005..182130631:-1; parent_transcript=GRMZM2G137409_T01; parent_gene=GRMZM2G137409	GRMZM2G137409_P01	82 kDa	Ref	0.1	0.2	1.4	2.2	No Values	No Values	No Values	No Values
1045	seq=translation; coord=1:293041177..293042705:-1; parent_transcript=GRMZM2G155329_T01; parent_gene=GRMZM2G155329	GRMZM2G155329_P01	24 kDa	Ref	-0.1	-0.3	1.2	2.1	No Values	No Values	No Values	No Values
1046	seq=translation; coord=7:156569238..156573041:1; parent_transcript=GRMZM2G153162_T02; parent_gene=GRMZM2G153162	GRMZM2G153162_P02	101 kDa	Ref	No Values	No Values	No Values	No Values	0.1	-0.9	-0.5	-1
1047	seq=translation; coord=3:123772202..123775285:1; parent_transcript=GRMZM2G164868_T01; parent_gene=GRMZM2G164868	GRMZM2G164868_P01 (+1)	58 kDa	Ref	No Values	No Values	No Values	No Values	0.8	-1.5	-0.4	-0.7
1048	seq=translation; coord=4:163261154..163272206:1; parent_transcript=GRMZM2G014994_T01; parent_gene=GRMZM2G014994	GRMZM2G014994_P01	18 kDa	Ref	0.5	-0.4	-1.2	-2	No Values	No Values	No Values	No Values
1049	seq=translation; coord=10:12167272..12169103:-1; parent_transcript=GRMZM2G094375_T01; parent_gene=GRMZM2G094375	GRMZM2G094375_P01 (+1)	47 kDa	Ref	0.5	0.3	1	2	No Values	No Values	No Values	No Values
1050	seq=translation; coord=3:231890529..231892088:-1; parent_transcript=GRMZM2G175076_T01; parent_gene=GRMZM2G175076	GRMZM2G175076_P01	24 kDa	Ref	0.1	-0.2	1.6	2.4	No Values	No Values	No Values	No Values
1051	seq=translation; coord=6:166587013..166592611:1; parent_transcript=GRMZM2G027955_T01; parent_gene=GRMZM2G027955	GRMZM2G027955_P01 (+2)	59 kDa	Ref	-1.2	-1.4	-2	-2.2	1.6	1.7	1.2	1.2
1052	seq=translation; coord=2:36317292..36319768:1; parent_transcript=GRMZM2G102183_T01; parent_gene=GRMZM2G102183	GRMZM2G102183_P01 (+2)	47 kDa	Ref	0.2	0.4	-0.1	1	0.4	0.6	Reference Missing	Reference Missing

1053	seq=translation; coord=4:173177749..173179720:-1; parent_transcript=GRMZM2G054012_T01; parent_gene=GRMZM2G054012	GRMZM2G054012_P01 (+3)	7 kDa	Ref	1	0.3	-0.3	-0.8	1.6	0.4	0.5	0
1054	seq=translation; coord=10:63619774..63622627:-1; parent_transcript=GRMZM2G368861_T01; parent_gene=GRMZM2G368861	GRMZM2G368861_P01	9 kDa	Ref	0.3	3.9	3	1.8	0.7	0.5	0.6	-0.2
1055	seq=translation; coord=1:191987932..191990561:1; parent_transcript=AC197246.3_FGT003; parent_gene=AC197246.3_FG003	AC197246.3_FGP003 (+4)	16 kDa	Ref	0.2	0	0	0.4	-3.1	-2.8	-3	-3.9
1056	seq=translation; coord=10:127861555..127867760:-1; parent_transcript=GRMZM2G096705_T01; parent_gene=GRMZM2G096705	GRMZM2G096705_P01	49 kDa	Ref	0.3	-0.3	-0.4	-0.6	0.9	-1.2	-0.8	-0.6
1057	seq=translation; coord=7:82007091..82010522:1; parent_transcript=GRMZM2G056501_T01; parent_gene=GRMZM2G056501	GRMZM2G056501_P01 (+2)	18 kDa	Ref	-1	-1	-1	-1.6	-0.8	-0.3	-1.1	-0.8
1058	seq=translation; coord=2:189443283..189447454:1; parent_transcript=GRMZM2G112165_T01; parent_gene=GRMZM2G112165	GRMZM2G112165_P01	80 kDa	Ref	-2.1	-2.5	-2.6	-2.3	1.3	1	1.2	1.3
1059	seq=translation; coord=8:127487910..127490998:1; parent_transcript=GRMZM2G150485_T01; parent_gene=GRMZM2G150485	GRMZM2G150485_P01 (+2)	33 kDa	Ref	-1	-0.6	-1	-1.2	3	2.8	2.9	1.6
1060	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	30 kDa	Ref	1.4	1.1	0.4	0.9	-1.2	-1.7	-1.7	-1.6
1061	seq=translation; coord=1:27094498..27098727:1; parent_transcript=GRMZM2G163129_T01; parent_gene=GRMZM2G163129	GRMZM2G163129_P01	103 kDa	Ref	0	-0.5	-0.4	-0.3	-0.8	-1.2	-0.8	-0.7
1062	seq=translation; coord=6:109292609..109296377:1; parent_transcript=GRMZM2G048194_T01; parent_gene=GRMZM2G048194	GRMZM2G048194_P01 (+1)	41 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	-1.4	-1.6	-2.2
1063	seq=translation; coord=8:78073258..78079706:1; parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418	GRMZM2G023418_P01	144 kDa	Ref	1	-0.2	0.4	-0.1	-1	-2	-1.9	-2.5
1064	seq=translation; coord=9:150816519..150821326:-1; parent_transcript=GRMZM2G169365_T01; parent_gene=GRMZM2G169365	GRMZM2G169365_P01	39 kDa	Ref	0.3	-0.6	-0.5	-0.7	-3.6	-3.5	-2.7	-2.6
1065	seq=translation; coord=2:193416339..193419729:-1; parent_transcript=GRMZM2G023080_T01; parent_gene=GRMZM2G023080	GRMZM2G023080_P01 (+3)	29 kDa	Ref	-0.1	-0.6	-0.2	-0.4	0.2	0.7	-0.5	0.1

1066	seq=translation; coord=5:30771033..30772796:1; parent_transcript=GRMZM2G026216_T01; parent_gene=GRMZM2G026216	GRMZM2G026216_P01 (+3)	19 kDa	Ref	1.1	1	0	0.3	1.1	0.8	0.4	-0.7
1067	seq=translation; coord=5:215656610..215661825:1; parent_transcript=GRMZM2G143651_T01; parent_gene=GRMZM2G143651	GRMZM2G143651_P01	50 kDa	Ref	2.1	1.6	1.1	2.1	Reference Missing	Reference Missing	Reference Missing	Value Missing
1068	seq=translation; coord=6:28127232..28129613:1; parent_transcript=GRMZM2G165815_T02; parent_gene=GRMZM2G165815	GRMZM2G165815_P02	23 kDa	Ref	0.6	0.3	0.5	-0.7	-0.9	0.2	-0.5	1.7
1069	seq=translation; coord=8:154456893..154470550:1; parent_transcript=GRMZM2G316113_T01; parent_gene=GRMZM2G316113	GRMZM2G316113_P01 (+2)	155 kDa	Ref	0.2	-0.4	-0.9	0.6	-0.5	-1.4	-1.1	-1.1
1070	seq=translation; coord=6:24549898..24554957:-1; parent_transcript=GRMZM2G111579_T01; parent_gene=GRMZM2G111579	GRMZM2G111579_P01	57 kDa	Ref	-0.7	-0.9	-0.4	-0.1	-0.8	-0.1	0.1	-0.1
1071	seq=translation; coord=5:163610246..163620614:1; parent_transcript=GRMZM2G360589_T01; parent_gene=GRMZM2G360589	GRMZM2G360589_P01	46 kDa	Ref	-0.8	-0.7	-0.6	0.3	-1.4	-0.5	-1.3	-1.5
1072	seq=translation; coord=2:76993674..76995064:1; parent_transcript=GRMZM2G069523_T01; parent_gene=GRMZM2G069523	GRMZM2G069523_P01	28 kDa	Ref	0	-0.2	0.2	0.2	0.9	0.6	1.1	0.7
1073	seq=translation; coord=4:240105137..240108983:1; parent_transcript=GRMZM2G079348_T01; parent_gene=GRMZM2G079348	GRMZM2G079348_P01 (+3)	79 kDa	Ref	-1.5	-2.6	-2.2	-1.3	-1.8	-2.1	-2.3	-2.7
1074	seq=translation; coord=5:3195909..3207226:1; parent_transcript=GRMZM2G071071_T01; parent_gene=GRMZM2G071071	GRMZM2G071071_P01	72 kDa	Ref	1	1.2	0.4	0.9	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1075	seq=translation; coord=8:94750778..94753384:1; parent_transcript=GRMZM2G147221_T01; parent_gene=GRMZM2G147221	GRMZM2G147221_P01	59 kDa	Ref	-1	Value Missing	-1.4	Value Missing	5	4.5	4.2	4.6
1076	seq=translation; coord=6:6269340..6271805:-1; parent_transcript=GRMZM2G134134_T02; parent_gene=GRMZM2G134134	GRMZM2G134134_P02	40 kDa	Ref	-0.2	-0.1	-0.2	0.2	-2.1	-2.4	-2.2	-2.1
1077	seq=translation; coord=9:19034931..19038665:-1; parent_transcript=GRMZM5G877388_T02; parent_gene=GRMZM5G877388	GRMZM5G877388_P02	14 kDa	Ref	-1.3	-1.4	-1.3	-1.7	-2.2	-3.1	-2.8	-3.5
1078	seq=translation; coord=1:34664608..34673432:1; parent_transcript=GRMZM2G058870_T01; parent_gene=GRMZM2G058870	GRMZM2G058870_P01	198 kDa	Ref	1.1	0.9	0.1	0.4	0.7	-0.7	-1.3	-1.5

1079	seq=translation; coord=5:6688332..6691221:1; parent_transcript=GRMZM5G862540_T01; parent_gene=GRMZM5G862540	GRMZM5G862540_P01 (+1)	53 kDa	Ref	-0.6	-0.7	-1	-0.6	0.2	Value Missing	-1.5	-0.5
1080	seq=translation; coord=9:57980157..57982564:1; parent_transcript=GRMZM2G066111_T01; parent_gene=GRMZM2G066111	GRMZM2G066111_P01 (+3)	24 kDa	Ref	1.2	1.2	0.4	1.2	2.1	0.4	0.1	-0.4
1081	seq=translation; coord=3:87798819..87808953:-1; parent_transcript=GRMZM2G009593_T01; parent_gene=GRMZM2G009593	GRMZM2G009593_P01 (+2)	106 kDa	Ref	0	0.7	-0.1	-0.2	-4.7	-5	-5.5	-5.5
1082	seq=translation; coord=2:196359627..196363692:-1; parent_transcript=GRMZM2G573867_T01; parent_gene=GRMZM2G573867	GRMZM2G573867_P01 (+1)	48 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	-0.3	-0.3	-0.4
1083	seq=translation; coord=1:49207907..49216831:1; parent_transcript=GRMZM2G140432_T01; parent_gene=GRMZM2G140432	GRMZM2G140432_P01	95 kDa	Ref	0.6	-0.1	0.9	-0.3	No Values	No Values	No Values	No Values
1084	seq=translation; coord=5:214501921..21450506:1; parent_transcript=GRMZM2G008728_T02; parent_gene=GRMZM2G008728	GRMZM2G008728_P02	34 kDa	Ref	0	0.1	0.5	0.2	No Values	No Values	No Values	No Values
1085	seq=translation; coord=1:298585659..298587727:-1; parent_transcript=GRMZM2G058568_T03; parent_gene=GRMZM2G058568	GRMZM2G058568_P03 (+1)	57 kDa	Ref	0.4	0.1	0.4	0.4	No Values	No Values	No Values	No Values
1086	seq=translation; coord=9:116241684..116244580:-1; parent_transcript=GRMZM2G013002_T01; parent_gene=GRMZM2G013002	GRMZM2G013002_P01	32 kDa	Ref	1.1	0.8	0.6	1.1	No Values	No Values	No Values	No Values
1087	seq=translation; coord=9:107790531..107797125:1; parent_transcript=GRMZM2G055320_T01; parent_gene=GRMZM2G055320	GRMZM2G055320_P01	68 kDa	Ref	-0.9	-0.8	-1.2	-1.6	No Values	No Values	No Values	No Values
1088	seq=translation; coord=8:143676986..143682414:1; parent_transcript=GRMZM2G107757_T01; parent_gene=GRMZM2G107757	GRMZM2G107757_P01 (+2)	25 kDa	Ref	Reference Missing	2.3	1.9	1.3	No Values	No Values	No Values	No Values
1089	seq=translation; coord=3:147676601..147679180:-1; parent_transcript=GRMZM2G479112_T01; parent_gene=GRMZM2G479112	GRMZM2G479112_P01	57 kDa	Ref	-0.1	0.1	0.1	0.8	No Values	No Values	No Values	No Values
1090	seq=translation; coord=8:8472359..8474789:1; parent_transcript=GRMZM2G021614_T01; parent_gene=GRMZM2G021614	GRMZM2G021614_P01 (+1)	19 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	1.1	1.6	2.1
1091	seq=translation; coord=6:123432811..123435820:-1; parent_transcript=GRMZM2G127160_T01; parent_gene=GRMZM2G127160	GRMZM2G127160_P01 (+1)	47 kDa	Ref	No Values	No Values	No Values	No Values	2.1	0.6	0.6	0.2

1092	seq=translation; coord=9:7614057..7616811:1; parent_transcript=GRMZM2G079949_T01; parent_gene=GRMZM2G079949	GRMZM2G079949_P01	35 kDa	Ref	-0.3	-0.2	-0.1	0.3	No Values	No Values	No Values	No Values
1093	seq=translation; coord=5:188857165..188858944:1; parent_transcript=GRMZM2G170017_T01; parent_gene=GRMZM2G170017	GRMZM2G170017_P01	34 kDa	Ref	Reference Missing	0.1	3.7	5.5	No Values	No Values	No Values	No Values
1094	seq=translation; coord=6:160034201..160039816:-1; parent_transcript=GRMZM2G004932_T01; parent_gene=GRMZM2G004932	GRMZM2G004932_P01	63 kDa	Ref	0.6	0.1	0.1	1.1	No Values	No Values	No Values	No Values
1095	seq=translation; coord=1:38548724..38550734:-1; parent_transcript=GRMZM2G012566_T02; parent_gene=GRMZM2G012566	GRMZM2G012566_P02	18 kDa	Ref	1.4	1.8	1	0	No Values	No Values	No Values	No Values
1096	seq=translation; coord=4:53673036..53676735:-1; parent_transcript=GRMZM2G032367_T01; parent_gene=GRMZM2G032367	GRMZM2G032367_P01 (+5)	34 kDa	Ref	1.3	1.2	1.8	1.8	No Values	No Values	No Values	No Values
1097	seq=translation; coord=1:258447609..258448792:1; parent_transcript=GRMZM2G039639_T01; parent_gene=GRMZM2G039639	GRMZM2G039639_P01	24 kDa	Ref	-0.1	-0.5	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
1098	seq=translation; coord=1:7406938..7408184:1; parent_transcript=GRMZM2G099454_T02; parent_gene=GRMZM2G099454	GRMZM2G099454_P02 (+3)	28 kDa	Ref	1.3	2.1	1.2	2.5	No Values	No Values	No Values	No Values
1099	seq=translation; coord=5:49897243..49899430:-1; parent_transcript=GRMZM2G177828_T01; parent_gene=GRMZM2G177828	GRMZM2G177828_P01	14 kDa	Ref	4.9	4.5	3.2	1.8	No Values	No Values	No Values	No Values
1100	seq=translation; coord=8:2199781..2200562:-1; parent_transcript=GRMZM2G353266_T01; parent_gene=GRMZM2G353266	GRMZM2G353266_P01	14 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	-0.2	-0.1	0
1101	seq=translation; coord=7:3483732..3484794:1; parent_transcript=GRMZM2G465226_T01; parent_gene=GRMZM2G465226	GRMZM2G465226_P01	17 kDa	Ref	0.3	0	-0.2	-0.1	No Values	No Values	No Values	No Values
1102	seq=translation; coord=7:29542055..29544356:-1; parent_transcript=GRMZM5G872934_T01; parent_gene=GRMZM5G872934	GRMZM5G872934_P01	31 kDa	Ref	0.3	1.3	1.5	1.6	No Values	No Values	No Values	No Values
1103	seq=translation; coord=2:12351628..12357486:-1; parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728	GRMZM2G125728_P01 (+1)	63 kDa	Ref	0.5	0.3	-0.1	-0.2	Reference Missing	2.8	2.8	2.6
1104	seq=translation; coord=2:236283794..236288865:1; parent_transcript=GRMZM2G103955_T02; parent_gene=GRMZM2G103955	GRMZM2G103955_P02	49 kDa	Ref	1.5	0.9	0.7	0.2	3.2	1.1	0.8	-0.6

1105	seq=translation; coord=1:194210583..194219751:1; parent_transcript=GRMZM2G171111_T02; parent_gene=GRMZM2G171111	GRMZM2G171111_P02 (+1)	27 kDa	Ref	-0.8	-0.4	-0.6	-0.4	0.7	0.3	0.7	0.7
1106	seq=translation; coord=2:115064269..115065362:-1; parent_transcript=GRMZM2G008649_T01; parent_gene=GRMZM2G008649	GRMZM2G008649_P01 (+1)	25 kDa	Ref	No Values	No Values	No Values	No Values	-1.7	-2	-2.2	-2.3
1107	seq=translation; coord=3:193091877..193119714:1; parent_transcript=GRMZM2G071441_T01; parent_gene=GRMZM2G071441	GRMZM2G071441_P01 (+1)	113 kDa	Ref	0.3	0.6	-0.1	0.3	1.8	1.9	1.3	1.1
1108	seq=translation; coord=5:1526460..1528840:-1; parent_transcript=GRMZM2G448001_T01; parent_gene=GRMZM2G448001	GRMZM2G448001_P01	74 kDa	Ref	-0.1	0.5	1	1.7	-2.6	-0.8	0	0.6
1109	seq=translation; coord=5:14752854..14761623:1; parent_transcript=GRMZM2G553314_T01; parent_gene=GRMZM2G553314	GRMZM2G553314_P01	84 kDa	Ref	-0.2	-0.5	-0.3	-0.1	-2	-2	-2.3	-2.4
1110	seq=translation; coord=1:67523715..67533727:-1; parent_transcript=GRMZM2G410479_T01; parent_gene=GRMZM2G410479	GRMZM2G410479_P01	169 kDa	Ref	-0.1	-0.3	-0.8	-0.1	1.8	1.7	0.4	0.5
1111	seq=translation; coord=7:156205011..156210949:-1; parent_transcript=GRMZM5G890190_T01; parent_gene=GRMZM5G890190	GRMZM5G890190_P01 (+1)	28 kDa	Ref	0	-0.2	-0.4	-0.7	-3.3	-3.9	-4.3	-4.2
1112	seq=translation; coord=4:201936215..201938145:1; parent_transcript=GRMZM2G325118_T01; parent_gene=GRMZM2G325118	GRMZM2G325118_P01	46 kDa	Ref	0.8	3	4.3	3.9	0	Value Missing	0.2	Reference Missing
1113	seq=translation; coord=9:130498884..130500159:1; parent_transcript=GRMZM2G134107_T01; parent_gene=GRMZM2G134107	GRMZM2G134107_P01	14 kDa	Ref	0.7	1.1	1	0.5	3.4	3	3	2.4
1114	seq=translation; coord=2:8578099..8582568:-1; parent_transcript=GRMZM2G012628_T01; parent_gene=GRMZM2G012628	GRMZM2G012628_P01	47 kDa	Ref	-0.5	-0.4	-0.7	-1	1	0.1	-0.6	-0.3
1115	seq=translation; coord=7:11441042..11445373:-1; parent_transcript=GRMZM2G401308_T02; parent_gene=GRMZM2G401308	GRMZM2G401308_P02	22 kDa	Ref	0.6	-0.2	-1.2	-1.9	-1	-2.1	-2.1	-2.1
1116	seq=translation; coord=3:44223365..44228905:-1; parent_transcript=GRMZM2G003883_T01; parent_gene=GRMZM2G003883	GRMZM2G003883_P01	55 kDa	Ref	-0.9	-1	-0.5	-0.4	2.4	1.3	1.1	0.5
1117	seq=translation; coord=8:29610407..29612711:1; parent_transcript=GRMZM2G067522_T01; parent_gene=GRMZM2G067522	GRMZM2G067522_P01	16 kDa	Ref	0.2	0.3	0.7	-0.1	-2.7	-1.7	-1.7	-3.6

1118	seq=translation; coord=4:17087184..17096848:1; parent_transcript=GRMZM2G045987_T01; parent_gene=GRMZM2G045987	GRMZM2G045987_P01	86 kDa	Ref	0.1	-0.2	-0.5	-0.1	-2	-2.5	-2.9	-3.2
1119	seq=translation; coord=10:11749519..11756094:-1; parent_transcript=GRMZM2G036534_T01; parent_gene=GRMZM2G036534	GRMZM2G036534_P01	48 kDa	Ref	Value Missing	1	0.9	0.9	-2.1	Reference Missing	-3.7	-3.7
1120	seq=translation; coord=4:187884467..187890415:-1; parent_transcript=GRMZM2G119175_T01; parent_gene=GRMZM2G119175	GRMZM2G119175_P01 (+1)	57 kDa	Ref	-0.2	-0.2	-0.8	-0.2	2.4	1.9	0.7	0.7
1121	seq=translation; coord=7:154188635..154191068:-1; parent_transcript=GRMZM2G056369_T01; parent_gene=GRMZM2G056369	GRMZM2G056369_P01	63 kDa	Ref	0.3	1.1	0.1	0.4	2.6	Reference Missing	Reference Missing	Reference Missing
1122	seq=translation; coord=5:30994200..30995891:-1; parent_transcript=GRMZM2G111477_T01; parent_gene=GRMZM2G111477	GRMZM2G111477_P01	21 kDa	Ref	-1	-0.6	-0.1	-0.8	-2.6	-2.2	-1.8	-2
1123	seq=translation; coord=4:140347561..140350401:1; parent_transcript=GRMZM2G079817_T01; parent_gene=GRMZM2G079817	GRMZM2G079817_P01	59 kDa	Ref	-0.4	-0.6	-0.1	0.4	2	2.3	2.6	2.8
1124	seq=translation; coord=1:189145769..189150346:-1; parent_transcript=GRMZM2G088627_T01; parent_gene=GRMZM2G088627	GRMZM2G088627_P01	49 kDa	Ref	1.4	1.6	1.2	1.4	2.7	1.4	1.4	2.8
1125	seq=translation; coord=6:151454748..151457344:-1; parent_transcript=GRMZM2G059314_T01; parent_gene=GRMZM2G059314	GRMZM2G059314_P01	41 kDa	Ref	-0.2	-0.2	-0.4	-0.8	2.2	2	2.3	3.4
1126	seq=translation; coord=5:13726531..13727525:-1; parent_transcript=GRMZM2G129083_T01; parent_gene=GRMZM2G129083	GRMZM2G129083_P01	16 kDa	Ref	1.5	1.8	2.7	2.2	1.4	-0.5	-0.4	-0.9
1127	seq=translation; coord=9:22677939..22681262:-1; parent_transcript=GRMZM5G877500_T01; parent_gene=GRMZM5G877500	GRMZM5G877500_P01	42 kDa	Ref	-0.7	-0.5	-0.5	-0.1	1.4	1.2	0.9	0.9
1128	seq=translation; coord=3:160397311..160408336:1; parent_transcript=GRMZM2G129155_T01; parent_gene=GRMZM2G129155	GRMZM2G129155_P01 (+1)	90 kDa	Ref	1.1	0.1	-0.3	1.1	2.3	1.1	1.9	1.1
1129	seq=translation; coord=1:132810230..132856187:1; parent_transcript=GRMZM2G019673_T01; parent_gene=GRMZM2G019673	GRMZM2G019673_P01 (+2)	80 kDa	Ref	-0.4	-0.4	-0.1	0.6	-0.4	-0.6	-0.7	-1
1130	seq=translation; coord=4:237676754..237682663:-1; parent_transcript=GRMZM2G117346_T01; parent_gene=GRMZM2G117346	GRMZM2G117346_P01 (+5)	142 kDa	Ref	3.8	3.3	2.9	2.6	Reference Missing	Reference Missing	Reference Missing	Reference Missing

1131	seq=translation; coord=2:45890416..45891705:-1; parent_transcript=GRMZM2G152141_T01; parent_gene=GRMZM2G152141	GRMZM2G152141_P01	19 kDa	Ref	-1.6	-1.3	-1.6	-1.3	Value Missing	3.3	Value Missing	Value Missing
1132	seq=translation; coord=8:135417381..135418239:1; parent_transcript=GRMZM2G175273_T01; parent_gene=GRMZM2G175273	GRMZM2G175273_P01	8 kDa	Ref	2.3	2.1	1.9	0.9	No Values	No Values	No Values	No Values
1133	seq=translation; coord=4:183588190..183591209:-1; parent_transcript=GRMZM2G325575_T01; parent_gene=GRMZM2G325575	GRMZM2G325575_P01	37 kDa	Ref	-0.2	0.7	0.4	1	1	1.1	0.9	2.2
1134	seq=translation; coord=6:115639609..115647217:-1; parent_transcript=GRMZM2G008556_T01; parent_gene=GRMZM2G008556	GRMZM2G008556_P01 (+3)	68 kDa	Ref	0.8	-0.1	0	-0.5	3.1	2.6	2.8	3.2
1135	seq=translation; coord=3:196019180..196024451:1; parent_transcript=GRMZM2G324886_T01; parent_gene=GRMZM2G324886	GRMZM2G324886_P01	25 kDa	Ref	0.4	-0.3	-0.5	-1.1	-4.3	-3.2	-4.5	-3.9
1136	seq=translation; coord=4:168987228..168990822:1; parent_transcript=GRMZM2G018947_T01; parent_gene=GRMZM2G018947	GRMZM2G018947_P01 (+2)	46 kDa	Ref	-1.1	-1.4	-1.2	-0.7	-4.3	-4.9	-5.6	-5.8
1137	seq=translation; coord=8:157966228..157972830:-1; parent_transcript=GRMZM2G016827_T02; parent_gene=GRMZM2G016827	GRMZM2G016827_P02	33 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	Reference Missing	0.1	0.4
1138	seq=translation; coord=8:2349948..2353138:1; parent_transcript=GRMZM2G027728_T01; parent_gene=GRMZM2G027728	GRMZM2G027728_P01 (+1)	12 kDa	Ref	0.8	1	0.4	0.3	0.1	-0.7	-1	-1
1139	seq=translation; coord=7:1306578..1314769:-1; parent_transcript=GRMZM2G120563_T06; parent_gene=GRMZM2G120563	GRMZM2G120563_P06 (+1)	44 kDa	Ref	-0.7	-1.9	-1.8	-1.2	-0.9	-0.6	-0.5	0.1
1140	seq=translation; coord=1:197854710..197858129:-1; parent_transcript=GRMZM2G021816_T01; parent_gene=GRMZM2G021816	GRMZM2G021816_P01	39 kDa	Ref	-0.6	-0.7	-0.3	-0.9	No Values	No Values	No Values	No Values
1141	seq=translation; coord=3:134285297..134289508:1; parent_transcript=GRMZM2G047434_T01; parent_gene=GRMZM2G047434	GRMZM2G047434_P01	38 kDa	Ref	No Values	No Values	No Values	No Values	1	-1.9	-1.3	-1.3
1142	seq=translation; coord=6:76236848..76238660:1; parent_transcript=GRMZM2G051338_T01; parent_gene=GRMZM2G051338	GRMZM2G051338_P01	20 kDa	Ref	-0.3	0	1.9	0.7	No Values	No Values	No Values	No Values
1143	seq=translation; coord=2:20765568..20767537:1; parent_transcript=GRMZM2G337229_T01; parent_gene=GRMZM2G337229	GRMZM2G337229_P01	16 kDa	Ref	-0.5	2.1	0.7	0.4	No Values	No Values	No Values	No Values

1144	seq=translation; coord=3:221235623..221241542:1; parent_transcript=GRMZM2G149321_T01; parent_gene=GRMZM2G149321	GRMZM2G149321_P01	53 kDa	Ref	No Values	No Values	No Values	No Values	0.7	-0.6	0.6	-1.6
1145	seq=translation; coord=1:264855610..264864472:-1; parent_transcript=AC217401.3_FGT002; parent_gene=AC217401.3_FG002	AC217401.3_FGP002	63 kDa	Ref	-0.1	-0.4	-0.6	0.5	No Values	No Values	No Values	No Values
1146	seq=translation; coord=1:269493908..269506409:1; parent_transcript=GRMZM5G826838_T01; parent_gene=GRMZM5G826838	GRMZM5G826838_P01	55 kDa	Ref	0.1	0.2	0.3	0.3	No Values	No Values	No Values	No Values
1147	seq=translation; coord=9:12103632..12110868:-1; parent_transcript=GRMZM2G467169_T01; parent_gene=GRMZM2G467169	GRMZM2G467169_P01 (+1)	107 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	1.4	0.8
1148	seq=translation; coord=1:278837830..278839720:1; parent_transcript=GRMZM2G118809_T01; parent_gene=GRMZM2G118809	GRMZM2G118809_P01 (+1)	57 kDa	Ref	0.3	0.1	Reference Missing	Reference Missing	No Values	No Values	No Values	No Values
1149	seq=translation; coord=9:138771755..138777249:1; parent_transcript=GRMZM2G162426_T01; parent_gene=GRMZM2G162426	GRMZM2G162426_P01	116 kDa	Ref	0.5	0	-0.4	0.2	No Values	No Values	No Values	No Values
1150	seq=translation; coord=1:276433043..276437555:-1; parent_transcript=GRMZM2G100084_T01; parent_gene=GRMZM2G100084	GRMZM2G100084_P01	53 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.8	0.9	1
1151	seq=translation; coord=4:177628395..177630803:-1; parent_transcript=GRMZM2G126732_T01; parent_gene=GRMZM2G126732	GRMZM2G126732_P01 (+1)	41 kDa	Ref	0.6	1.5	2	1.8	No Values	No Values	No Values	No Values
1152	seq=translation; coord=9:26817670..26821498:1; parent_transcript=GRMZM2G475293_T01; parent_gene=GRMZM2G475293	GRMZM2G475293_P01 (+1)	27 kDa	Ref	No Values	No Values	No Values	No Values	-1.2	-0.5	-0.3	1.4
1153	seq=translation; coord=3:166381506..166384595:-1; parent_transcript=GRMZM2G359397_T01; parent_gene=GRMZM2G359397	GRMZM2G359397_P01 (+2)	51 kDa	Ref	No Values	No Values	No Values	No Values	0.8	1.7	2	2
1154	seq=translation; coord=2:199547128..199550293:1; parent_transcript=GRMZM5G868679_T01; parent_gene=GRMZM5G868679	GRMZM5G868679_P01	69 kDa	Ref	0.2	0.2	0.4	1	No Values	No Values	No Values	No Values
1155	seq=translation; coord=4:11466211..11470058:-1; parent_transcript=GRMZM2G085711_T02; parent_gene=GRMZM2G085711	GRMZM2G085711_P02	50 kDa	Ref	No Values	No Values	No Values	No Values	0.6	1.5	1.9	2.5
1156	seq=translation; coord=7:7954180..7955128:1; parent_transcript=GRMZM2G021149_T01; parent_gene=GRMZM2G021149	GRMZM2G021149_P01 (+1)	28 kDa	Ref	0.3	0.1	0.2	0.1	No Values	No Values	No Values	No Values

1157	seq=translation; coord=7:152772009..152776227:1; parent_transcript=GRMZM2G108849_T02; parent_gene=GRMZM2G108849	GRMZM2G108849_P02 (+2)	23 kDa	Ref	0.4	0.1	0.3	1.3	No Values	No Values	No Values	No Values
1158	seq=translation; coord=10:144683393..144689170:-1; parent_transcript=GRMZM2G136895_T01; parent_gene=GRMZM2G136895	GRMZM2G136895_P01	81 kDa	Ref	0	-0.1	0.3	0.4	No Values	No Values	No Values	No Values
1159	seq=translation; coord=3:91357080..91360381:-1; parent_transcript=GRMZM2G077415_T01; parent_gene=GRMZM2G077415	GRMZM2G077415_P01	24 kDa	Ref	-0.4	0.1	-0.2	0	No Values	No Values	No Values	No Values
1160	seq=translation; coord=7:149132369..149134157:-1; parent_transcript=GRMZM2G077673_T01; parent_gene=GRMZM2G077673	GRMZM2G077673_P01	38 kDa	Ref	-0.5	0	-0.2	0.2	No Values	No Values	No Values	No Values
1161	seq=translation; coord=4:184547632..184552118:-1; parent_transcript=GRMZM2G347541_T01; parent_gene=GRMZM2G347541	GRMZM2G347541_P01 (+1)	69 kDa	Ref	No Values	No Values	No Values	No Values	0.3	-0.2	-0.1	0.1
1162	seq=translation; coord=7:1269463..1270529:-1; parent_transcript=GRMZM2G420733_T01; parent_gene=GRMZM2G420733	GRMZM2G420733_P01	25 kDa	Ref	-0.2	0.3	0.2	-0.4	No Values	No Values	No Values	No Values
1163	seq=translation; coord=3:207473256..207484650:-1; parent_transcript=GRMZM2G073045_T01; parent_gene=GRMZM2G073045	GRMZM2G073045_P01	38 kDa	Ref	-0.3	-0.3	-0.3	-0.5	No Values	No Values	No Values	No Values
1164	seq=translation; coord=6:124736591..124745000:-1; parent_transcript=GRMZM2G148709_T01; parent_gene=GRMZM2G148709	GRMZM2G148709_P01 (+3)	73 kDa	Ref	-0.1	-0.4	-0.5	-0.5	-0.1	-0.6	-0.4	-0.8
1165	seq=translation; coord=7:160059330..160068443:-1; parent_transcript=GRMZM5G887631_T01; parent_gene=GRMZM5G887631	GRMZM5G887631_P01	79 kDa	Ref	0	-0.6	0	0.5	-1.1	0.3	-0.2	-0.8
1166	seq=translation; coord=9:87461648..87475465:-1; parent_transcript=GRMZM2G047564_T03; parent_gene=GRMZM2G047564	GRMZM2G047564_P03 (+1)	46 kDa	Ref	-0.4	-0.6	-0.4	-0.3	0.1	-0.2	-0.3	0.3
1167	seq=translation; coord=5:211206297..211209456:-1; parent_transcript=GRMZM2G151440_T01; parent_gene=GRMZM2G151440	GRMZM2G151440_P01 (+1)	42 kDa	Ref	-0.3	-0.1	-0.2	-0.2	-1.7	-1.5	-1.5	-1.6
1168	seq=translation; coord=4:230556470..230569433:1; parent_transcript=GRMZM2G038195_T01; parent_gene=GRMZM2G038195	GRMZM2G038195_P01 (+3)	35 kDa	Ref	-0.3	-0.2	-0.3	-0.2	-0.1	-0.3	-0.6	-1
1169	seq=translation; coord=6:133205650..133225934:-1; parent_transcript=GRMZM2G076006_T03; parent_gene=GRMZM2G076006	GRMZM2G076006_P03	38 kDa	Ref	-0.3	-0.1	0	0.4	-0.7	-0.5	0	0.5

1170	seq=translation; coord=6:81686909..81693610:1; parent_transcript=GRMZM2G103266_T01; parent_gene=GRMZM2G103266	GRMZM2G103266_P01 (+2)	78 kDa	Ref	0.6	0.8	1	0.8	-1.5	-1.2	-0.7	-0.5
1171	seq=translation; coord=9:59939835..59941693:-1; parent_transcript=GRMZM2G471357_T01; parent_gene=GRMZM2G471357	GRMZM2G471357_P01 (+1)	33 kDa	Ref	Value Missing	0.6	Value Missing	0.2	-3.6	-3.7	-2.5	-1.4
1172	seq=translation; coord=7:168913721..168922316:-1; parent_transcript=GRMZM2G026991_T01; parent_gene=GRMZM2G026991	GRMZM2G026991_P01	249 kDa	Ref	0.5	0	-0.4	-0.3	0.8	-0.5	-0.9	-1.4
1173	seq=translation; coord=2:179742429..179748543:1; parent_transcript=GRMZM2G105772_T01; parent_gene=GRMZM2G105772	GRMZM2G105772_P01 (+1)	42 kDa	Ref	1.3	1.2	0.9	1.2	-0.5	Reference Missing	-0.3	Reference Missing
1174	seq=translation; coord=3:225222066..225226693:-1; parent_transcript=GRMZM2G049866_T01; parent_gene=GRMZM2G049866	GRMZM2G049866_P01 (+1)	45 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	0.1	-1.2	-1.2
1175	seq=translation; coord=5:194043178..194045076:1; parent_transcript=GRMZM2G013821_T01; parent_gene=GRMZM2G013821	GRMZM2G013821_P01 (+1)	15 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	-1.9	-1.8	-2
1176	seq=translation; coord=1:292988864..292997657:1; parent_transcript=GRMZM2G155580_T01; parent_gene=GRMZM2G155580	GRMZM2G155580_P01 (+2)	68 kDa	Ref	0.6	0	-0.5	-0.3	-2.2	-2.2	-2.3	-2.5
1177	seq=translation; coord=6:140312649..140313648:-1; parent_transcript=GRMZM2G162659_T01; parent_gene=GRMZM2G162659	GRMZM2G162659_P01	12 kDa	Ref	0	-0.1	-0.3	0.9	-1.3	-1.1	Reference Missing	-0.6
1178	seq=translation; coord=5:157517807..157521679:-1; parent_transcript=GRMZM2G057642_T02; parent_gene=GRMZM2G057642	GRMZM2G057642_P02 (+1)	38 kDa	Ref	1.1	0.4	0.1	0.1	1.4	-0.1	-0.2	-0.7
1179	seq=translation; coord=3:1481217..1482997:-1; parent_transcript=GRMZM2G087103_T02; parent_gene=GRMZM2G087103	GRMZM2G087103_P02 (+2)	36 kDa	Ref	-2	-0.3	-1.6	-1.6	-1.6	0.9	1.2	0.4
1180	seq=translation; coord=1:74628405..74631787:1; parent_transcript=GRMZM2G130121_T01; parent_gene=GRMZM2G130121	GRMZM2G130121_P01	74 kDa	Ref	Reference Missing	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing	Reference Missing	-2.3
1181	seq=translation; coord=9:150085751..150089143:1; parent_transcript=GRMZM2G100120_T01; parent_gene=GRMZM2G100120	GRMZM2G100120_P01 (+5)	26 kDa	Ref	0.3	0.2	0	-0.1	0.1	-0.9	-0.9	-1.1
1182	seq=translation; coord=8:157386210..157395665:-1; parent_transcript=GRMZM2G133926_T01; parent_gene=GRMZM2G133926	GRMZM2G133926_P01	47 kDa	Ref	-1.2	-0.4	-0.6	-0.6	-0.2	-1.3	-1.7	-1.8

1183	seq=translation; coord=3:39476674..39479631:1; parent_transcript=GRMZM2G132465_T01; parent_gene=GRMZM2G132465	GRMZM2G132465_P01 (+4)	47 kDa	Ref	-0.2	-0.6	-0.7	-0.8	-3.6	-4.3	-4	-4.4
1184	seq=translation; coord=3:182713971..182717776:-1; parent_transcript=GRMZM2G504401_T01; parent_gene=GRMZM2G504401	GRMZM2G504401_P01	27 kDa	Ref	-0.7	-0.4	-0.4	-0.8	-2.2	-1.2	-0.8	-0.8
1185	seq=translation; coord=7:165748301..165751201:-1; parent_transcript=GRMZM2G053999_T01; parent_gene=GRMZM2G053999	GRMZM2G053999_P01	36 kDa	Ref	-0.1	-0.1	-0.2	0.3	2.4	0.9	0.9	0.8
1186	seq=translation; coord=1:273298297..273299437:-1; parent_transcript=GRMZM2G481194_T01; parent_gene=GRMZM2G481194	GRMZM2G481194_P01	21 kDa	Ref	-0.1	-0.4	-0.8	-1.1	0.6	0.6	0.6	0.5
1187	seq=translation; coord=4:162677644..162687691:1; parent_transcript=GRMZM2G020775_T01; parent_gene=GRMZM2G020775	GRMZM2G020775_P01	47 kDa	Ref	-1.2	-0.9	-1.1	-1	1.4	0.8	1	0.3
1188	seq=translation; coord=1:269035042..269037767:1; parent_transcript=GRMZM2G047055_T01; parent_gene=GRMZM2G047055	GRMZM2G047055_P01 (+4)	42 kDa	Ref	0.4	-0.4	-1.3	-0.8	2.1	0.7	-0.1	-0.6
1189	seq=translation; coord=3:186233588..186237469:1; parent_transcript=GRMZM2G133213_T01; parent_gene=GRMZM2G133213	GRMZM2G133213_P01	31 kDa	Ref	1.1	1.1	1.1	2.3	3.9	1.8	2.3	1.6
1190	seq=translation; coord=4:197674970..197676500:1; parent_transcript=GRMZM2G301908_T01; parent_gene=GRMZM2G301908	GRMZM2G301908_P01	27 kDa	Ref	0	-0.9	-1.4	-1.6	2.6	2.5	2.6	2.4
1191	seq=translation; coord=9:4832748..4841265:1; parent_transcript=GRMZM2G124288_T01; parent_gene=GRMZM2G124288	GRMZM2G124288_P01 (+1)	68 kDa	Ref	1.3	0.9	1	0.7	3.7	2.4	2.7	2.4
1192	seq=translation; coord=7:52251311..52252353:1; parent_transcript=GRMZM2G027198_T01; parent_gene=GRMZM2G027198	GRMZM2G027198_P01	18 kDa	Ref	-0.1	0.4	1.9	3	0.5	0	0.8	0.4
1193	seq=translation; coord=6:128560617..128567071:1; parent_transcript=GRMZM2G027723_T01; parent_gene=GRMZM2G027723	GRMZM2G027723_P01 (+2)	121 kDa	Ref	-1.7	-1.6	-2.7	-3.1	0.9	Value Missing	Value Missing	Value Missing
1194	seq=translation; coord=7:14459963..14466085:-1; parent_transcript=GRMZM2G104325_T01; parent_gene=GRMZM2G104325	GRMZM2G104325_P01	105 kDa	Ref	1.6	1.2	Reference Missing	0.6	No Values	No Values	No Values	No Values
1195	seq=translation; coord=7:158136732..158153170:1; parent_transcript=GRMZM2G107654_T01; parent_gene=GRMZM2G107654	GRMZM2G107654_P01	53 kDa	Ref	0.1	-0.4	-0.2	-0.3	-0.3	-0.6	-0.5	-0.5

1196	seq=translation; coord=8:157237785..157240528:-1; parent_transcript=GRMZM2G446960_T01; parent_gene=GRMZM2G446960	GRMZM2G446960_P01	20 kDa	Ref	1.2	0.9	0.4	0.4	No Values	No Values	No Values	No Values
1197	seq=translation; coord=5:31131578..31135872:-1; parent_transcript=GRMZM2G110201_T01; parent_gene=GRMZM2G110201	GRMZM2G110201_P01	48 kDa	Ref	-0.3	-0.5	-0.5	-0.8	No Values	No Values	No Values	No Values
1198	seq=translation; coord=6:2438893..2441433:1; parent_transcript=GRMZM2G024303_T01; parent_gene=GRMZM2G024303	GRMZM2G024303_P01	44 kDa	Ref	0.4	0.5	0.3	1.2	No Values	No Values	No Values	No Values
1199	seq=translation; coord=5:98993016..98997371:-1; parent_transcript=GRMZM5G844562_T01; parent_gene=GRMZM5G844562	GRMZM5G844562_P01 (+1)	39 kDa	Ref	-0.2	0.6	0.7	1.5	No Values	No Values	No Values	No Values
1200	seq=translation; coord=2:23469563..23473424:1; parent_transcript=GRMZM2G177923_T01; parent_gene=GRMZM2G177923	GRMZM2G177923_P01	83 kDa	Ref	-0.7	-0.5	-0.4	0.3	No Values	No Values	No Values	No Values
1201	seq=translation; coord=10:123811073..123815007:1; parent_transcript=GRMZM2G064159_T01; parent_gene=GRMZM2G064159	GRMZM2G064159_P01	42 kDa	Ref	0.1	-0.2	0.2	0.1	No Values	No Values	No Values	No Values
1202	seq=translation; coord=3:168695539..168839001:1; parent_transcript=GRMZM2G156861_T03; parent_gene=GRMZM2G156861	GRMZM2G156861_P03	98 kDa	Ref	0.7	Reference Missing	Reference Missing	-0.1	No Values	No Values	No Values	No Values
1203	seq=translation; coord=6:143138266..143147623:1; parent_transcript=GRMZM2G305851_T01; parent_gene=GRMZM2G305851	GRMZM2G305851_P01	41 kDa	Ref	1.7	1.6	1	1.7	No Values	No Values	No Values	No Values
1204	seq=translation; coord=4:18573473..18575395:-1; parent_transcript=GRMZM2G440208_T01; parent_gene=GRMZM2G440208	GRMZM2G440208_P01	54 kDa	Ref	No Values	No Values	No Values	No Values	1	0.7	0.4	0.4
1205	seq=translation; coord=7:143292623..143296263:1; parent_transcript=GRMZM2G109405_T01; parent_gene=GRMZM2G109405	GRMZM2G109405_P01 (+2)	43 kDa	Ref	0.2	0.3	0.3	0.6	No Values	No Values	No Values	No Values
1206	seq=translation; coord=9:89703050..89707450:1; parent_transcript=GRMZM2G442551_T01; parent_gene=GRMZM2G442551	GRMZM2G442551_P01 (+1)	91 kDa	Ref	0.4	0.3	-0.1	0.3	No Values	No Values	No Values	No Values
1207	seq=translation; coord=8:173066444..173072416:1; parent_transcript=GRMZM2G424857_T01; parent_gene=GRMZM2G424857	GRMZM2G424857_P01	50 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0	Reference Missing	Reference Missing
1208	seq=translation; coord=7:126805106..126806657:1; parent_transcript=GRMZM5G826321_T01; parent_gene=GRMZM5G826321	GRMZM5G826321_P01	34 kDa	Ref	-0.8	-1	-0.9	-1.2	No Values	No Values	No Values	No Values

1209	seq=translation; coord=7:131436732..131438757:1; parent_transcript=GRMZM2G018108_T01; parent_gene=GRMZM2G018108	GRMZM2G018108_P01	50 kDa	Ref	0.5	1.5	2.2	2.9	No Values	No Values	No Values	No Values
1210	seq=translation; coord=5:201664982..201667877:1; parent_transcript=GRMZM2G170602_T01; parent_gene=GRMZM2G170602	GRMZM2G170602_P01	42 kDa	Ref	0.2	0	0.7	2.4	No Values	No Values	No Values	No Values
1211	seq=translation; coord=5:3285681..3289943:1; parent_transcript=GRMZM2G017532_T01; parent_gene=GRMZM2G017532	GRMZM2G017532_P01	21 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	1.1	0.9	2.7
1212	seq=translation; coord=4:180245812..180247211:1; parent_transcript=GRMZM2G448883_T01; parent_gene=GRMZM2G448883	GRMZM2G448883_P01	33 kDa	Ref	2	2.2	2.3	3	No Values	No Values	No Values	No Values
1213	seq=translation; coord=4:238055009..238057832:-1; parent_transcript=AC233922.1_FGT005; parent_gene=AC233922.1_FG005	AC233922.1_FGP005	40 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.6	1.6	0.7
1214	seq=translation; coord=8:17966967..17971201:-1; parent_transcript=GRMZM2G175171_T01; parent_gene=GRMZM2G175171	GRMZM2G175171_P01	60 kDa	Ref	0.3	-0.1	0.4	1	No Values	No Values	No Values	No Values
1215	seq=translation; coord=1:228560968..228564785:1; parent_transcript=GRMZM5G888696_T02; parent_gene=GRMZM5G888696	GRMZM5G888696_P02	68 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.3	-0.2
1216	seq=translation; coord=6:161451718..161452634:-1; parent_transcript=GRMZM2G090245_T01; parent_gene=GRMZM2G090245	GRMZM2G090245_P01	23 kDa	Ref	Reference Missing	0.4	0.5	Reference Missing	No Values	No Values	No Values	No Values
1217	seq=translation; coord=2:43428306..43433991:1; parent_transcript=GRMZM2G031028_T02; parent_gene=GRMZM2G031028	GRMZM2G031028_P02	34 kDa	Ref	-0.8	-0.7	-0.4	-0.5	No Values	No Values	No Values	No Values
1218	seq=translation; coord=3:206531676..206533642:1; parent_transcript=GRMZM2G050570_T01; parent_gene=GRMZM2G050570	GRMZM2G050570_P01	58 kDa	Ref	-0.1	-0.3	-0.7	-0.7	0.5	0.5	0.4	0.4
1219	seq=translation; coord=6:115289930..115298874:1; parent_transcript=GRMZM2G157462_T01; parent_gene=GRMZM2G157462	GRMZM2G157462_P01	100 kDa	Ref	0.6	0.5	0.5	0.7	0.9	0.4	0.2	-0.2
1220	seq=translation; coord=6:127249169..127252532:1; parent_transcript=GRMZM2G018020_T01; parent_gene=GRMZM2G018020	GRMZM2G018020_P01	28 kDa	Ref	0.5	0.3	-0.4	-0.5	1.5	-0.3	-1.6	-1.2
1221	seq=translation; coord=6:126779719..126784379:1; parent_transcript=GRMZM2G159369_T01; parent_gene=GRMZM2G159369	GRMZM2G159369_P01	40 kDa	Ref	0	0.2	0	0.1	-1.3	-2.1	-1.9	-0.3

1222	seq=translation; coord=1:218981641..218987465:-1; parent_transcript=GRMZM5G895175_T01; parent_gene=GRMZM5G895175	GRMZM5G895175_P01	85 kDa	Ref	1.2	0.3	0.4	-0.3	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1223	seq=translation; coord=7:10365682..10368158:1; parent_transcript=GRMZM2G018074_T01; parent_gene=GRMZM2G018074	GRMZM2G018074_P01	78 kDa	Ref	0.7	0.8	0.9	0.3	3.6	3.6	4.3	3.4
1224	seq=translation; coord=9:12323292..12327304:-1; parent_transcript=GRMZM2G151923_T01; parent_gene=GRMZM2G151923	GRMZM2G151923_P01 (+4)	21 kDa	Ref	0.7	0.6	0.3	0.2	0.5	-0.6	-0.9	-1.4
1225	seq=translation; coord=8:171187220..171190525:-1; parent_transcript=GRMZM2G028346_T01; parent_gene=GRMZM2G028346	GRMZM2G028346_P01 (+3)	25 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0	-0.2	-0.5
1226	seq=translation; coord=9:7578400..7585814:1; parent_transcript=GRMZM2G120302_T01; parent_gene=GRMZM2G120302	GRMZM2G120302_P01	79 kDa	Ref	0.4	0	0.4	0.5	-2.5	-2.5	-2.9	-2.6
1227	seq=translation; coord=UNKNOWN:5634502..5650723:1; parent_transcript=GRMZM2G011070_T01; parent_gene=GRMZM2G011070	GRMZM2G011070_P01	135 kDa	Ref	0.4	0.4	0	0.1	1.1	1.4	1	0.9
1228	seq=translation; coord=8:156372419..156374495:-1; parent_transcript=GRMZM2G073622_T01; parent_gene=GRMZM2G073622	GRMZM2G073622_P01 (+2)	24 kDa	Ref	-1.9	-1.5	-1.5	-2	0.5	0.6	0.1	-0.1
1229	seq=translation; coord=4:175739965..175751055:-1; parent_transcript=GRMZM2G181362_T01; parent_gene=GRMZM2G181362	GRMZM2G181362_P01 (+1)	116 kDa	Ref	-1.3	-0.4	-1.2	-0.4	-1.5	-0.6	-0.9	-1.1
1230	seq=translation; coord=2:173380725..173391388:-1; parent_transcript=GRMZM2G106213_T01; parent_gene=GRMZM2G106213	GRMZM2G106213_P01 (+1)	56 kDa	Ref	-0.2	-0.8	-1.2	-1.1	0.1	1.2	1.2	0.9
1231	seq=translation; coord=6:148703816..148706201:1; parent_transcript=AC235543.1_FGT003; parent_gene=AC235543.1_FG003	AC235543.1_FGP003	19 kDa	Ref	1.3	1	0.8	0.5	2.5	2.7	2.6	1.9
1232	seq=translation; coord=4:223661025..223669104:-1; parent_transcript=GRMZM2G068489_T01; parent_gene=GRMZM2G068489	GRMZM2G068489_P01 (+2)	21 kDa	Ref	1	-0.5	0.1	0	No Values	Reference Missing	Reference Missing	Reference Missing
1233	seq=translation; coord=4:214239084..214241779:1; parent_transcript=GRMZM2G126190_T01; parent_gene=GRMZM2G126190	GRMZM2G126190_P01 (+2)	42 kDa	Ref	0.4	-0.3	-0.3	-0.2	No Values	No Values	No Values	No Values
1234	seq=translation; coord=2:25300018..25310642:1; parent_transcript=GRMZM5G827171_T01; parent_gene=GRMZM5G827171	GRMZM5G827171_P01 (+2)	48 kDa	Ref	0.8	0.5	0.3	-0.1	2	0.9	0.9	0.7

1235	seq=translation; coord=7:33992878..33998025:-1; parent_transcript=GRMZM2G051771_T01; parent_gene=GRMZM2G051771	GRMZM2G051771_P01 (+1)	31 kDa	Ref	-0.5	-0.5	-0.5	0	1.7	2	2.1	3.1
1236	seq=translation; coord=2:2545896..2547904:1; parent_transcript=GRMZM2G010257_T01; parent_gene=GRMZM2G010257	GRMZM2G010257_P01 (+14)	11 kDa	Ref	0.3	-0.9	-0.1	0.6	-1	-2	-3.5	-3
1237	seq=translation; coord=8:70525339..70528822:1; parent_transcript=GRMZM2G413652_T01; parent_gene=GRMZM2G413652	GRMZM2G413652_P01 (+1)	30 kDa	Ref	No Values	No Values	No Values	No Values	-1.4	-1.3	-1.6	-1.5
1238	seq=translation; coord=1:289192462..289217741:1; parent_transcript=GRMZM5G825524_T01; parent_gene=GRMZM5G825524	GRMZM5G825524_P01 (+2)	91 kDa	Ref	-0.5	-0.7	-0.5	-0.4	2.8	1.2	Value Missing	1.4
1239	seq=translation; coord=1:2038186..2040079:1; parent_transcript=GRMZM2G164696_T01; parent_gene=GRMZM2G164696	GRMZM2G164696_P01 (+1)	50 kDa	Ref	1.3	-0.3	-0.2	-0.9	-0.2	-2.7	-3.1	-3.9
1240	seq=translation; coord=6:160675824..160684398:1; parent_transcript=GRMZM2G587327_T01; parent_gene=GRMZM2G587327	GRMZM2G587327_P01	81 kDa	Ref	No Values	No Values	No Values	No Values	0.9	-0.8	-1.2	-1.6
1241	seq=translation; coord=9:139381433..139385689:-1; parent_transcript=GRMZM2G166767_T01; parent_gene=GRMZM2G166767	GRMZM2G166767_P01 (+1)	76 kDa	Ref	0	-0.6	-0.8	-0.5	No Values	No Values	No Values	No Values
1242	seq=translation; coord=5:181396172..181399390:-1; parent_transcript=GRMZM2G031496_T01; parent_gene=GRMZM2G031496	GRMZM2G031496_P01 (+1)	37 kDa	Ref	0.3	-0.4	0.9	0	No Values	No Values	No Values	No Values
1243	seq=translation; coord=1:268558195..268564501:-1; parent_transcript=GRMZM2G000622_T01; parent_gene=GRMZM2G000622	GRMZM2G000622_P01	155 kDa	Ref	No Values	No Values	No Values	No Values	0.8	-0.1	-0.2	-0.4
1244	seq=translation; coord=4:41369510..41378299:1; parent_transcript=GRMZM2G138060_T01; parent_gene=GRMZM2G138060	GRMZM2G138060_P01	88 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.5	-0.1
1245	seq=translation; coord=9:119710257..119715669:-1; parent_transcript=GRMZM2G151387_T01; parent_gene=GRMZM2G151387	GRMZM2G151387_P01 (+1)	80 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0	-0.2	-0.2
1246	seq=translation; coord=5:74640062..74641850:-1; parent_transcript=GRMZM2G017249_T01; parent_gene=GRMZM2G017249	GRMZM2G017249_P01	64 kDa	Ref	0.9	0.5	0.4	0.9	No Values	No Values	No Values	No Values
1247	seq=translation; coord=4:5455601..5457606:1; parent_transcript=GRMZM2G154523_T01; parent_gene=GRMZM2G154523	GRMZM2G154523_P01	44 kDa	Ref	1.2	2.8	2.1	2.4	No Values	No Values	No Values	No Values

1248	seq=translation; coord=2:3805095..3807781:-1; parent_transcript=GRMZM2G173341_T01; parent_gene=GRMZM2G173341	GRMZM2G173341_P01 (+2)	39 kDa	Ref	-1.3	-1.1	-1.4	-0.9	No Values	No Values	No Values	No Values
1249	seq=translation; coord=3:213896741..213905427:1; parent_transcript=GRMZM2G466833_T01; parent_gene=GRMZM2G466833	GRMZM2G466833_P01	44 kDa	Ref	No Values	No Values	No Values	No Values	0.1	-0.1	-0.2	0.3
1250	seq=translation; coord=10:19475272..19481312:1; parent_transcript=GRMZM2G181227_T01; parent_gene=GRMZM2G181227	GRMZM2G181227_P01	43 kDa	Ref	-0.9	-0.5	1.1	1.7	No Values	No Values	No Values	No Values
1251	seq=translation; coord=4:42919325..42920272:1; parent_transcript=GRMZM2G154578_T01; parent_gene=GRMZM2G154578	GRMZM2G154578_P01	25 kDa	Ref	-0.2	0	-0.9	-1	No Values	No Values	No Values	No Values
1252	seq=translation; coord=4:81250432..81251801:-1; parent_transcript=GRMZM2G004878_T01; parent_gene=GRMZM2G004878	GRMZM2G004878_P01	19 kDa	Ref	2.7	0.9	0.1	-0.1	No Values	No Values	No Values	No Values
1253	seq=translation; coord=6:142082329..142086400:1; parent_transcript=AC215201.3_FGT005; parent_gene=AC215201.3_FG005	AC215201.3_FGP005	63 kDa	Ref	No Values	No Values	No Values	No Values	-0.5	0.8	1.2	1.3
1254	seq=translation; coord=1:34386070..34400519:-1; parent_transcript=GRMZM2G102483_T02; parent_gene=GRMZM2G102483	GRMZM2G102483_P02 (+1)	42 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	-0.1	Reference Missing	Reference Missing
1255	seq=translation; coord=4:237941870..237948667:1; parent_transcript=GRMZM2G139341_T01; parent_gene=GRMZM2G139341	GRMZM2G139341_P01 (+1)	73 kDa	Ref	No Values	No Values	No Values	No Values	2.2	1.4	1.3	0.2
1256	seq=translation; coord=1:285124791..285129572:-1; parent_transcript=GRMZM2G058584_T01; parent_gene=GRMZM2G058584	GRMZM2G058584_P01 (+1)	51 kDa	Ref	No Values	No Values	No Values	No Values	1.4	1.2	2.2	2.1
1257	seq=translation; coord=6:154130608..154132782:-1; parent_transcript=GRMZM2G361064_T01; parent_gene=GRMZM2G361064	GRMZM2G361064_P01	26 kDa	Ref	0	0.4	0.3	0.6	No Values	No Values	No Values	No Values
1258	seq=translation; coord=6:39088029..39088716:1; parent_transcript=GRMZM2G012928_T01; parent_gene=GRMZM2G012928	GRMZM2G012928_P01	8 kDa	Ref	No Values	No Values	No Values	No Values	0	Reference Missing	Reference Missing	Reference Missing
1259	seq=translation; coord=4:12818434..12823201:-1; parent_transcript=GRMZM2G139441_T01; parent_gene=GRMZM2G139441	GRMZM2G139441_P01 (+1)	45 kDa	Ref	1	0.3	0.1	0.1	-1.4	-1.3	-2.8	-2.2
1260	seq=translation; coord=6:114177100..114187293:-1; parent_transcript=GRMZM2G010960_T01; parent_gene=GRMZM2G010960	GRMZM2G010960_P01	157 kDa	Ref	1.4	2	1.8	1.4	1.6	2.2	2.5	1.7

1261	seq=translation; coord=8:48994683..48999789:-1; parent_transcript=GRMZM2G083836_T01; parent_gene=GRMZM2G083836	GRMZM2G083836_P01 (+1)	63 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.1	0.1	-0.6
1262	seq=translation; coord=2:176238563..176244250:1; parent_transcript=GRMZM2G098076_T01; parent_gene=GRMZM2G098076	GRMZM2G098076_P01 (+1)	69 kDa	Ref	No Values	No Values	No Values	No Values	1.1	0.1	-0.3	0.3
1263	seq=translation; coord=1:234254283..234259941:1; parent_transcript=GRMZM2G445905_T01; parent_gene=GRMZM2G445905	GRMZM2G445905_P01 (+1)	24 kDa	Ref	Value Missing	0.6	Value Missing	0.5	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1264	seq=translation; coord=3:217231435..217244458:-1; parent_transcript=AC198725.4_FGT007; parent_gene=AC198725.4_FG007	AC198725.4_FGP007	114 kDa	Ref	No Values	No Values	No Values	Reference Missing	-3.3	-3.5	-4.8	-4.3
1265	seq=translation; coord=8:138088772..138094325:-1; parent_transcript=GRMZM2G018901_T01; parent_gene=GRMZM2G018901	GRMZM2G018901_P01 (+1)	20 kDa	Ref	-1.1	-1.1	-1.4	-0.6	-0.8	-1	-0.9	-0.8
1266	seq=translation; coord=8:15548387..15551947:-1; parent_transcript=GRMZM2G038821_T01; parent_gene=GRMZM2G038821	GRMZM2G038821_P01	69 kDa	Ref	No Values	No Values	No Values	Reference Missing	-7.1	-6.6	-5.9	-5.9
1267	seq=translation; coord=8:14541175..14542451:-1; parent_transcript=GRMZM2G052869_T02; parent_gene=GRMZM2G052869	GRMZM2G052869_P02 (+1)	6 kDa	Ref	0.1	1.7	0.8	-0.7	-0.4	-0.6	0.5	-0.7
1268	seq=translation; coord=2:208530771..208535295:-1; parent_transcript=GRMZM2G090274_T01; parent_gene=GRMZM2G090274	GRMZM2G090274_P01 (+1)	49 kDa	Ref	0.4	-0.2	-0.1	-0.1	0.8	1	0	-0.4
1269	seq=translation; coord=4:187295953..187301881:-1; parent_transcript=GRMZM2G055538_T01; parent_gene=GRMZM2G055538	GRMZM2G055538_P01 (+2)	21 kDa	Ref	0.8	0.3	0.3	0.1	-0.3	-1.7	-1.8	-1.6
1270	seq=translation; coord=1:250554600..250557666:-1; parent_transcript=GRMZM2G020142_T01; parent_gene=GRMZM2G020142	GRMZM2G020142_P01 (+1)	41 kDa	Ref	0.1	0.2	-0.9	-0.1	0.4	0.3	-1.2	-2
1271	seq=translation; coord=5:213944858..213947602:-1; parent_transcript=GRMZM2G469111_T01; parent_gene=GRMZM2G469111	GRMZM2G469111_P01	74 kDa	Ref	1.3	1.3	0.4	0.9	1.7	-0.5	-1	-2.3
1272	seq=translation; coord=5:76210306..76210828:1; parent_transcript=AC192244.3_FGT001; parent_gene=AC192244.3_FG001	AC192244.3_FGP001	13 kDa	Ref	-0.1	-0.2	0.5	0.1	-0.3	0.1	0.4	0.1
1273	seq=translation; coord=6:87790147..87797085:1; parent_transcript=GRMZM2G156099_T01; parent_gene=GRMZM2G156099	GRMZM2G156099_P01 (+2)	79 kDa	Ref	0.3	0.3	-0.4	-0.1	1.7	0.6	1.2	1

1274	seq=translation; coord=6:163428972..163435944:-1; parent_transcript=GRMZM2G149717_T01; parent_gene=GRMZM2G149717	GRMZM2G149717_P01 (+1)	73 kDa	Ref	0.8	0.4	0.4	0.4	5.2	6.2	5.9	5.3
1275	seq=translation; coord=4:53963570..53966108:-1; parent_transcript=GRMZM2G123234_T01; parent_gene=GRMZM2G123234	GRMZM2G123234_P01	31 kDa	Ref	No Values	No Values	No Values	No Values	-1	-1.7	-1	-2
1276	seq=translation; coord=2:209110460..209113041:-1; parent_transcript=GRMZM2G378106_T01; parent_gene=GRMZM2G378106	GRMZM2G378106_P01 (+1)	67 kDa	Ref	-0.9	-0.6	-0.2	0.1	No Values	No Values	No Values	No Values
1277	seq=translation; coord=10:125125070..125130397:1; parent_transcript=GRMZM2G065292_T01; parent_gene=GRMZM2G065292	GRMZM2G065292_P01	82 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.6	0.6	0.5
1278	seq=translation; coord=6:112003443..112007827:-1; parent_transcript=GRMZM2G073700_T01; parent_gene=GRMZM2G073700	GRMZM2G073700_P01	35 kDa	Ref	No Values	No Values	No Values	No Values	1.2	0.8	0.8	0.9
1279	seq=translation; coord=7:162255747..162259720:1; parent_transcript=GRMZM2G167932_T01; parent_gene=GRMZM2G167932	GRMZM2G167932_P01 (+1)	49 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	-1.7	-1.6	-1.6
1280	seq=translation; coord=4:162903711..162910128:1; parent_transcript=GRMZM2G453424_T03; parent_gene=GRMZM2G453424	GRMZM2G453424_P03 (+4)	23 kDa	Ref	No Values	No Values	No Values	No Values	0.2	-0.2	-0.8	-0.7
1281	seq=translation; coord=5:183319186..183326822:-1; parent_transcript=GRMZM2G014750_T01; parent_gene=GRMZM2G014750	GRMZM2G014750_P01 (+1)	52 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.5	-0.7	-0.9
1282	seq=translation; coord=9:131582315..131589080:-1; parent_transcript=GRMZM2G006178_T01; parent_gene=GRMZM2G006178	GRMZM2G006178_P01 (+3)	68 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.4	0.4	-0.2
1283	seq=translation; coord=5:18992634..18995244:-1; parent_transcript=GRMZM2G045192_T01; parent_gene=GRMZM2G045192	GRMZM2G045192_P01 (+2)	27 kDa	Ref	-0.7	-0.7	-0.1	-0.6	No Values	No Values	No Values	No Values
1284	seq=translation; coord=9:30842366..30844467:1; parent_transcript=GRMZM2G060163_T01; parent_gene=GRMZM2G060163	GRMZM2G060163_P01	39 kDa	Ref	No Values	No Values	No Values	No Values	3.2	-0.6	0.1	-1
1285	seq=translation; coord=6:149942002..149944565:-1; parent_transcript=GRMZM2G161534_T01; parent_gene=GRMZM2G161534	GRMZM2G161534_P01	39 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	0.9	1.1
1286	seq=translation; coord=1:295450010..295457140:-1; parent_transcript=GRMZM2G458549_T01; parent_gene=GRMZM2G458549	GRMZM2G458549_P01 (+1)	64 kDa	Ref	-0.3	-0.4	-0.4	0.1	No Values	No Values	No Values	No Values

1287	seq=translation; coord=2:28117445..28120590:1; parent_transcript=GRMZM2G441347_T01; parent_gene=GRMZM2G441347	GRMZM2G441347_P01	76 kDa	Ref	0.2	0.4	0.1	0	No Values	No Values	No Values	No Values
1288	seq=translation; coord=6:164983203..164994562:1; parent_transcript=GRMZM2G101515_T01; parent_gene=GRMZM2G101515	GRMZM2G101515_P01	91 kDa	Ref	No Values	No Values	No Values	No Values	1	-0.1	-0.8	-1.3
1289	seq=translation; coord=8:173177746..173180822:1; parent_transcript=GRMZM2G074028_T01; parent_gene=GRMZM2G074028	GRMZM2G074028_P01 (+4)	16 kDa	Ref	1.4	1.2	1.2	1.3	No Values	No Values	No Values	No Values
1290	seq=translation; coord=2:22504092..22513426:-1; parent_transcript=GRMZM2G070863_T01; parent_gene=GRMZM2G070863	GRMZM2G070863_P01	65 kDa	Ref	No Values	No Values	No Values	No Values	1	0.4	0.4	2.3
1291	seq=translation; coord=7:13851997..13853595:1; parent_transcript=GRMZM2G108076_T01; parent_gene=GRMZM2G108076	GRMZM2G108076_P01	12 kDa	Ref	0.2	0.4	0.4	0.9	No Values	No Values	No Values	No Values
1292	seq=translation; coord=3:36465309..36469955:-1; parent_transcript=GRMZM2G038606_T01; parent_gene=GRMZM2G038606	GRMZM2G038606_P01 (+3)	19 kDa	Ref	1.6	1.1	0.9	0	No Values	No Values	No Values	No Values
1293	seq=translation; coord=3:198588979..198593726:-1; parent_transcript=GRMZM2G042818_T01; parent_gene=GRMZM2G042818	GRMZM2G042818_P01	43 kDa	Ref	-0.3	0.2	-0.1	0.2	No Values	No Values	No Values	No Values
1294	seq=translation; coord=2:196329725..196336472:-1; parent_transcript=GRMZM2G050193_T01; parent_gene=GRMZM2G050193	GRMZM2G050193_P01 (+1)	61 kDa	Ref	1	1	0.7	0.9	No Values	No Values	No Values	No Values
1295	seq=translation; coord=4:176500156..176502218:1; parent_transcript=GRMZM2G091189_T01; parent_gene=GRMZM2G091189	GRMZM2G091189_P01	26 kDa	Ref	No Values	No Values	No Values	No Values	1	0	-0.8	-0.7
1296	seq=translation; coord=1:260939345..260957939:1; parent_transcript=GRMZM2G104542_T01; parent_gene=GRMZM2G104542	GRMZM2G104542_P01	64 kDa	Ref	Reference Missing	Reference Missing	0.2	Reference Missing	No Values	No Values	No Values	No Values
1297	seq=translation; coord=5:216598113..216599835:1; parent_transcript=GRMZM2G145133_T01; parent_gene=GRMZM2G145133	GRMZM2G145133_P01 (+1)	48 kDa	Ref	-1	-0.6	-0.9	-0.8	No Values	No Values	No Values	No Values
1298	seq=translation; coord=3:39292213..39295100:1; parent_transcript=GRMZM2G145449_T01; parent_gene=GRMZM2G145449	GRMZM2G145449_P01	21 kDa	Ref	-2.5	-3.1	-2.7	-2.2	No Values	No Values	No Values	No Values
1299	seq=translation; coord=9:150649384..150656114:-1; parent_transcript=GRMZM2G172523_T01; parent_gene=GRMZM2G172523	GRMZM2G172523_P01 (+2)	60 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.5	0.7	0.9

1300	seq=translation; coord=4:185694322..185697081:1; parent_transcript=GRMZM5G840955_T01; parent_gene=GRMZM5G840955	GRMZM5G840955_P01	33 kDa	Ref	1.4	1	1.2	1.6	No Values	No Values	No Values	No Values
1301	seq=translation; coord=8:157100232..157101209:-1; parent_transcript=GRMZM2G168552_T01; parent_gene=GRMZM2G168552	GRMZM2G168552_P01	20 kDa	Ref	0.4	0	2.3	-0.2	No Values	No Values	No Values	No Values
1302	seq=translation; coord=1:3714426..3715519:1; parent_transcript=GRMZM2G030173_T01; parent_gene=GRMZM2G030173	GRMZM2G030173_P01	27 kDa	Ref	-0.2	-0.2	-0.4	-1	No Values	No Values	No Values	No Values
1303	seq=translation; coord=7:18222228..18224357:1; parent_transcript=GRMZM2G094928_T01; parent_gene=GRMZM2G094928	GRMZM2G094928_P01 (+1)	12 kDa	Ref	1.3	0.8	1.4	0.3	No Values	No Values	No Values	No Values
1304	seq=translation; coord=3:4757467..4758786:-1; parent_transcript=GRMZM2G055434_T01; parent_gene=GRMZM2G055434	GRMZM2G055434_P01	23 kDa	Ref	No Values	No Values	No Values	No Values	2.6	0.1	1.3	0.7
1305	seq=translation; coord=1:299124462..299129776:-1; parent_transcript=GRMZM2G176612_T02; parent_gene=GRMZM2G176612	GRMZM2G176612_P02	45 kDa	Ref	3.3	3	2.3	1.2	-1.5	-2.3	-2.1	-2.4
1306	seq=translation; coord=10:16487570..16504336:1; parent_transcript=GRMZM2G028307_T02; parent_gene=GRMZM2G028307	GRMZM2G028307_P02	73 kDa	Ref	-0.1	-0.3	0	0.4	1	0.6	0.7	1
1307	seq=translation; coord=1:165814484..165965196:1; parent_transcript=GRMZM2G003595_T01; parent_gene=GRMZM2G003595	GRMZM2G003595_P01 (+2)	7 kDa	Ref	3.3	2.9	2.4	1.4	4.9	4.5	4.3	3.9
1308	seq=translation; coord=2:9503022..9507292:-1; parent_transcript=GRMZM2G040397_T01; parent_gene=GRMZM2G040397	GRMZM2G040397_P01 (+1)	45 kDa	Ref	0.6	0.3	0.3	0.5	0.1	-0.9	-1.3	-1.3
1309	seq=translation; coord=2:56806976..56810257:1; parent_transcript=GRMZM2G119689_T01; parent_gene=GRMZM2G119689	GRMZM2G119689_P01 (+2)	66 kDa	Ref	-0.1	-0.6	0.5	-0.4	-0.8	-2.3	-1.6	-2.7
1310	seq=translation; coord=9:99409919..99416720:1; parent_transcript=GRMZM2G033555_T01; parent_gene=GRMZM2G033555	GRMZM2G033555_P01 (+2)	38 kDa	Ref	-0.4	-0.8	-0.7	-0.3	1.5	1.6	1.3	1.3
1311	seq=translation; coord=8:4108305..4111250:-1; parent_transcript=GRMZM2G028156_T01; parent_gene=GRMZM2G028156	GRMZM2G028156_P01 (+3)	88 kDa	Ref	0	0.3	0	-0.1	0.3	-0.2	-0.1	-0.6
1312	seq=translation; coord=2:198568661..198574971:1; parent_transcript=GRMZM2G081571_T04; parent_gene=GRMZM2G081571	GRMZM2G081571_P04 (+1)	36 kDa	Ref	-1	-0.7	-0.8	-0.4	-2.1	-0.9	-0.7	-0.6

1313	seq=translation; coord=3:159873679..159879241:-1; parent_transcript=GRMZM2G105531_T01; parent_gene=GRMZM2G105531	GRMZM2G105531_P01	22 kDa	Ref	0.8	0.3	1	0.4	1.7	0.7	0.9	0.5
1314	seq=translation; coord=6:161446540..161449925:1; parent_transcript=GRMZM2G115049_T01; parent_gene=GRMZM2G115049	GRMZM2G115049_P01	29 kDa	Ref	1.3	0.5	0.4	0.8	1.1	-1.9	-1.2	-1.5
1315	seq=translation; coord=9:83796519..83798959:1; parent_transcript=GRMZM2G140179_T01; parent_gene=GRMZM2G140179	GRMZM2G140179_P01	74 kDa	Ref	Reference Missing	Reference Missing	Reference Missing	Reference Missing	0.4	-2.3	-4.8	-5
1316	seq=translation; coord=7:169836954..169839970:-1; parent_transcript=GRMZM2G037177_T01; parent_gene=GRMZM2G037177	GRMZM2G037177_P01	26 kDa	Ref	0	0.1	0	0.4	2.9	2.2	1.6	1.4
1317	seq=translation; coord=8:174419193..174424343:1; parent_transcript=GRMZM2G118462_T01; parent_gene=GRMZM2G118462	GRMZM2G118462_P01 (+2)	102 kDa	Ref	No Values	No Values	No Values	No Values	1	0.6	0.6	0.2
1318	seq=translation; coord=4:186948838..186952130:-1; parent_transcript=GRMZM2G357595_T01; parent_gene=GRMZM2G357595	GRMZM2G357595_P01	31 kDa	Ref	0.5	0.4	0	0.7	No Values	No Values	No Values	No Values
1319	seq=translation; coord=3:37865603..37869803:1; parent_transcript=GRMZM2G069208_T01; parent_gene=GRMZM2G069208	GRMZM2G069208_P01 (+2)	33 kDa	Ref	No Values	No Values	No Values	No Values	1.3	1.6	1	0.8
1320	seq=translation; coord=3:7078308..7082094:1; parent_transcript=GRMZM2G104081_T01; parent_gene=GRMZM2G104081	GRMZM2G104081_P01 (+2)	54 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	0.9	0.5	-0.5
1321	seq=translation; coord=10:61378667..61384801:1; parent_transcript=GRMZM2G143568_T01; parent_gene=GRMZM2G143568	GRMZM2G143568_P01	69 kDa	Ref	0	-0.4	-0.6	-0.2	No Values	No Values	No Values	No Values
1322	seq=translation; coord=2:12023721..12027357:-1; parent_transcript=GRMZM2G156365_T02; parent_gene=GRMZM2G156365	GRMZM2G156365_P02 (+4)	33 kDa	Ref	0.7	0.1	-1.1	-1.5	No Values	No Values	No Values	No Values
1323	seq=translation; coord=5:18170761..18172340:1; parent_transcript=GRMZM2G060940_T01; parent_gene=GRMZM2G060940	GRMZM2G060940_P01 (+2)	40 kDa	Ref	No Values	No Values	No Values	No Values	1	2.1	Reference Missing	1.1
1324	seq=translation; coord=3:127303985..127310112:-1; parent_transcript=AC182617.3_FGT001; parent_gene=AC182617.3_FG001	AC182617.3_FGP001 (+4)	38 kDa	Ref	No Values	No Values	No Values	No Values	0.4	0.3	0.1	-0.1
1325	seq=translation; coord=7:132157014..132162257:1; parent_transcript=GRMZM2G068862_T01; parent_gene=GRMZM2G068862	GRMZM2G068862_P01	44 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.4	0.1	0.5

1326	seq=translation; coord=4:120394113..120399917:1; parent_transcript=GRMZM2G153984_T01; parent_gene=GRMZM2G153984	GRMZM2G153984_P01	31 kDa	Ref	-0.3	-0.3	-0.3	-0.3	No Values	No Values	No Values	No Values
1327	seq=translation; coord=2:130522633..130525928:-1; parent_transcript=GRMZM2G128268_T01; parent_gene=GRMZM2G128268	GRMZM2G128268_P01	45 kDa	Ref	1.3	-0.7	-0.2	-0.1	No Values	No Values	No Values	No Values
1328	seq=translation; coord=3:173472565..173475730:-1; parent_transcript=GRMZM2G081652_T01; parent_gene=GRMZM2G081652	GRMZM2G081652_P01	62 kDa	Ref	0.8	0.2	0.5	0.6	No Values	No Values	No Values	No Values
1329	seq=translation; coord=1:205090665..205094372:1; parent_transcript=GRMZM2G144387_T01; parent_gene=GRMZM2G144387	GRMZM2G144387_P01 (+1)	25 kDa	Ref	0.9	1.1	1.3	0.3	No Values	No Values	No Values	No Values
1330	seq=translation; coord=10:98135181..98154139:1; parent_transcript=AC197672.3_FGT002; parent_gene=AC197672.3_FG002	AC197672.3_FGP002	257 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	-0.5	Reference Missing	-0.3
1331	seq=translation; coord=9:9638146..9648092:-1; parent_transcript=GRMZM2G033130_T01; parent_gene=GRMZM2G033130	GRMZM2G033130_P01 (+4)	104 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1332	seq=translation; coord=9:99437276..99441674:1; parent_transcript=GRMZM2G034069_T01; parent_gene=GRMZM2G034069	GRMZM2G034069_P01	35 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.4	0	0
1333	seq=translation; coord=9:146299403..146305484:1; parent_transcript=GRMZM2G051782_T01; parent_gene=GRMZM2G051782	GRMZM2G051782_P01	50 kDa	Ref	No Values	No Values	No Values	No Values	0.3	1.6	1.3	0.8
1334	seq=translation; coord=1:283086410..283088116:1; parent_transcript=GRMZM2G065083_T01; parent_gene=GRMZM2G065083	GRMZM2G065083_P01	15 kDa	Ref	No Values	No Values	No Values	No Values	0	0	0.5	0.7
1335	seq=translation; coord=5:184168891..184173292:1; parent_transcript=GRMZM2G071846_T01; parent_gene=GRMZM2G071846	GRMZM2G071846_P01	24 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0.6	0.5	-0.3
1336	seq=translation; coord=2:189499850..189501644:1; parent_transcript=GRMZM2G080466_T01; parent_gene=GRMZM2G080466	GRMZM2G080466_P01 (+3)	14 kDa	Ref	2.9	2	2.7	3.3	No Values	No Values	No Values	No Values
1337	seq=translation; coord=1:183983464..183984705:-1; parent_transcript=GRMZM2G080724_T01; parent_gene=GRMZM2G080724	GRMZM2G080724_P01	27 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.2	-0.8	-0.3
1338	seq=translation; coord=2:29975938..29981822:1; parent_transcript=GRMZM2G082581_T01; parent_gene=GRMZM2G082581	GRMZM2G082581_P01	36 kDa	Ref	No Values	No Values	No Values	No Values	0	-0.2	-0.1	0.3

1339	seq=translation; coord=8:137403695..137407159:-1; parent_transcript=GRMZM2G106960_T01; parent_gene=GRMZM2G106960	GRMZM2G106960_P01	23 kDa	Ref	-1.6	-1.7	-1.4	-1.4	No Values	No Values	No Values	No Values
1340	seq=translation; coord=5:13615570..13621897:1; parent_transcript=GRMZM2G161222_T03; parent_gene=GRMZM2G161222	GRMZM2G161222_P03	58 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1341	seq=translation; coord=9:92025063..92027986:-1; parent_transcript=GRMZM2G316232_T01; parent_gene=GRMZM2G316232	GRMZM2G316232_P01	57 kDa	Ref	No Values	No Values	No Values	No Values	1.6	0.9	0.2	0.3
1342	seq=translation; coord=10:117993529..118000841:-1; parent_transcript=GRMZM2G353213_T01; parent_gene=GRMZM2G353213	GRMZM2G353213_P01 (+1)	35 kDa	Ref	No Values	No Values	No Values	No Values	-0.5	-0.9	-0.5	0
1343	seq=translation; coord=9:137069559..137072594:-1; parent_transcript=GRMZM2G053652_T01; parent_gene=GRMZM2G053652	GRMZM2G053652_P01 (+1)	22 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1344	seq=translation; coord=1:297376727..297379573:-1; parent_transcript=GRMZM2G369815_T01; parent_gene=GRMZM2G369815	GRMZM2G369815_P01 (+1)	42 kDa	Ref	2	-1	-2.5	-2.3	No Values	No Values	No Values	No Values
1345	seq=translation; coord=4:159862612..159866537:1; parent_transcript=GRMZM2G050371_T01; parent_gene=GRMZM2G050371	GRMZM2G050371_P01	40 kDa	Ref	No Values	No Values	No Values	No Values	-1	-1.3	-1.3	-1
1346	seq=translation; coord=8:17388792..17393555:-1; parent_transcript=GRMZM2G061969_T01; parent_gene=GRMZM2G061969	GRMZM2G061969_P01	92 kDa	Ref	-0.1	-0.3	-0.7	-0.4	No Values	No Values	No Values	No Values
1347	seq=translation; coord=5:215652783..215654639:1; parent_transcript=GRMZM2G143627_T01; parent_gene=GRMZM2G143627	GRMZM2G143627_P01 (+1)	13 kDa	Ref	1.4	0.5	1.2	-0.4	No Values	No Values	No Values	No Values
1348	seq=translation; coord=1:286506118..286513080:-1; parent_transcript=GRMZM2G141473_T01; parent_gene=GRMZM2G141473	GRMZM2G141473_P01	146 kDa	Ref	0	0	0.9	2.3	No Values	No Values	No Values	No Values
1349	seq=translation; coord=5:18753627..18756558:1; parent_transcript=GRMZM2G138572_T01; parent_gene=GRMZM2G138572	GRMZM2G138572_P01	19 kDa	Ref	0.8	-0.2	1	-0.8	No Values	No Values	No Values	No Values
1350	seq=translation; coord=2:26769801..26771736:1; parent_transcript=GRMZM2G474575_T01; parent_gene=GRMZM2G474575	GRMZM2G474575_P01	23 kDa	Ref	No Values	No Values	No Values	No Values	-1.1	-0.2	1.1	2.4
1351	seq=translation; coord=7:110983097..110986540:-1; parent_transcript=GRMZM2G048277_T01; parent_gene=GRMZM2G048277	GRMZM2G048277_P01 (+2)	16 kDa	Ref	-0.4	0.1	-0.3	Value Missing	-2.8	-5	-6.2	-5.9

1352	seq=translation; coord=8:42281387..42289748:-1; parent_transcript=GRMZM2G145595_T01; parent_gene=GRMZM2G145595	GRMZM2G145595_P01	60 kDa	Ref	0.1	0.6	0.3	0.5	-2.4	-2.7	-2.8	-3.1
1353	seq=translation; coord=1:31242217..31244585:-1; parent_transcript=GRMZM2G116846_T01; parent_gene=GRMZM2G116846	GRMZM2G116846_P01	36 kDa	Ref	-0.7	-0.1	-1.2	-0.7	2.4	2.2	1.9	1.9
1354	seq=translation; coord=1:292354165..292360031:-1; parent_transcript=GRMZM2G151967_T01; parent_gene=GRMZM2G151967	GRMZM2G151967_P01	59 kDa	Ref	0	-0.2	-0.1	0.4	4.4	2.5	2.8	3.7
1355	seq=translation; coord=7:4538433..4546019:1; parent_transcript=GRMZM2G480002_T01; parent_gene=GRMZM2G480002	GRMZM2G480002_P01	187 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.2	0.7	0.7
1356	seq=translation; coord=5:21571290..21578409:-1; parent_transcript=GRMZM2G073934_T01; parent_gene=GRMZM2G073934	GRMZM2G073934_P01	53 kDa	Ref	0.8	0.5	0.1	0.4	No Values	No Values	No Values	No Values
1357	seq=translation; coord=1:298331067..29833316:1; parent_transcript=GRMZM2G023242_T01; parent_gene=GRMZM2G023242	GRMZM2G023242_P01 (+2)	17 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.2	-0.2	0.3
1358	seq=translation; coord=2:25913684..25932129:1; parent_transcript=GRMZM2G376731_T01; parent_gene=GRMZM2G376731	GRMZM2G376731_P01	99 kDa	Ref	No Values	No Values	No Values	No Values	0.9	-0.7	-0.9	-0.9
1359	seq=translation; coord=5:14176514..14178456:-1; parent_transcript=GRMZM5G858249_T01; parent_gene=GRMZM5G858249	GRMZM5G858249_P01	33 kDa	Ref	0.4	0.7	1.3	2	No Values	No Values	No Values	No Values
1360	seq=translation; coord=3:135084015..135105483:1; parent_transcript=GRMZM2G326116_T01; parent_gene=GRMZM2G326116	GRMZM2G326116_P01	35 kDa	Ref	-1.7	-1.6	-0.9	-1.1	No Values	No Values	No Values	No Values
1361	seq=translation; coord=6:110695290..110707260:1; parent_transcript=GRMZM2G412611_T01; parent_gene=GRMZM2G412611	GRMZM2G412611_P01	164 kDa	Ref	-0.8	-0.8	-0.4	-0.9	No Values	No Values	No Values	No Values
1362	seq=translation; coord=3:1767353..1776209:-1; parent_transcript=GRMZM2G123499_T01; parent_gene=GRMZM2G123499	GRMZM2G123499_P01 (+1)	74 kDa	Ref	0.1	0.1	-0.2	0.2	No Values	No Values	No Values	No Values
1363	seq=translation; coord=1:122162499..122163689:1; parent_transcript=AC202185.4_FGT004; parent_gene=AC202185.4_FG004	AC202185.4_FGP004	23 kDa	Ref	-0.2	0	1.6	0.3	No Values	No Values	No Values	No Values
1364	seq=translation; coord=2:71785920..71790206:-1; parent_transcript=GRMZM2G000980_T01; parent_gene=GRMZM2G000980	GRMZM2G000980_P01 (+1)	80 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	1	Reference Missing	1.1

1365	seq=translation; coord=5:17058108..17064678:1; parent_transcript=GRMZM2G018943_T01; parent_gene=GRMZM2G018943	GRMZM2G018943_P01 (+1)	80 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.1	0.2	-0.3
1366	seq=translation; coord=6:112137413..112140985:1; parent_transcript=GRMZM2G064993_T01; parent_gene=GRMZM2G064993	GRMZM2G064993_P01	38 kDa	Ref	0.5	-0.3	0.1	-0.2	No Values	No Values	No Values	No Values
1367	seq=translation; coord=5:59290440..59291930:-1; parent_transcript=GRMZM2G084942_T01; parent_gene=GRMZM2G084942	GRMZM2G084942_P01 (+1)	40 kDa	Ref	0.8	0.8	0.7	0.9	No Values	No Values	No Values	No Values
1368	seq=translation; coord=5:209693887..209699045:1; parent_transcript=GRMZM2G101463_T01; parent_gene=GRMZM2G101463	GRMZM2G101463_P01	56 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.9	0.6	0.3
1369	seq=translation; coord=3:184059147..184065670:1; parent_transcript=GRMZM2G118363_T01; parent_gene=GRMZM2G118363	GRMZM2G118363_P01	67 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
1370	seq=translation; coord=9:140970479..140979075:-1; parent_transcript=GRMZM2G119627_T01; parent_gene=GRMZM2G119627	GRMZM2G119627_P01	54 kDa	Ref	No Values	No Values	No Values	No Values	-1.6	-1.3	-1.7	-1.7
1371	seq=translation; coord=6:111182254..111183500:-1; parent_transcript=GRMZM2G122302_T01; parent_gene=GRMZM2G122302	GRMZM2G122302_P01	20 kDa	Ref	0.1	1.6	0.6	-0.5	No Values	No Values	No Values	No Values
1372	seq=translation; coord=8:85844666..85847518:-1; parent_transcript=GRMZM2G132130_T01; parent_gene=GRMZM2G132130	GRMZM2G132130_P01	29 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.4	-0.2	0.4
1373	seq=translation; coord=1:256071969..256085112:1; parent_transcript=GRMZM2G150772_T02; parent_gene=GRMZM2G150772	GRMZM2G150772_P02	179 kDa	Ref	-0.4	-0.3	-1.1	-1.1	No Values	No Values	No Values	No Values
1374	seq=translation; coord=6:111253708..111260162:-1; parent_transcript=GRMZM2G329306_T01; parent_gene=GRMZM2G329306	GRMZM2G329306_P01	43 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	-0.6	0.5	-0.9
1375	seq=translation; coord=10:136292132..136296887:1; parent_transcript=GRMZM2G414915_T01; parent_gene=GRMZM2G414915	GRMZM2G414915_P01	82 kDa	Ref	-0.7	-0.7	-1.2	-1.2	No Values	No Values	No Values	No Values
1376	seq=translation; coord=6:140865431..140872714:-1; parent_transcript=GRMZM2G442057_T01; parent_gene=GRMZM2G442057	GRMZM2G442057_P01	47 kDa	Ref	No Values	No Values	No Values	No Values	1.3	0.6	Reference Missing	0.8
1377	seq=translation; coord=10:10725550..10730964:1; parent_transcript=GRMZM2G014397_T02; parent_gene=GRMZM2G014397	GRMZM2G014397_P02 (+1)	34 kDa	Ref	1.2	1.5	1.7	1.7	No Values	No Values	No Values	No Values

1378	seq=translation; coord=1:257994567..257995838:-1; parent_transcript=GRMZM2G044762_T01; parent_gene=GRMZM2G044762	GRMZM2G044762_P01 (+1)	23 kDa	Ref	No Values	No Values	No Values	No Values	0.3	-0.2	0	-0.4
1379	seq=translation; coord=1:152164284..152165382:1; parent_transcript=GRMZM2G132077_T01; parent_gene=GRMZM2G132077	GRMZM2G132077_P01	18 kDa	Ref	0.6	-0.3	-0.3	0.1	No Values	No Values	No Values	No Values
1380	seq=translation; coord=3:124642615..124647335:-1; parent_transcript=GRMZM2G098397_T01; parent_gene=GRMZM2G098397	GRMZM2G098397_P01 (+3)	63 kDa	Ref	0.2	0.2	0.1	0.7	No Values	No Values	No Values	No Values
1381	seq=translation; coord=8:23799793..23801891:-1; parent_transcript=GRMZM5G861077_T01; parent_gene=GRMZM5G861077	GRMZM5G861077_P01	66 kDa	Ref	-0.3	-0.1	-0.4	0.2	No Values	No Values	No Values	No Values
1382	seq=translation; coord=7:174339610..174341979:-1; parent_transcript=GRMZM2G424205_T01; parent_gene=GRMZM2G424205	GRMZM2G424205_P01	26 kDa	Ref	-0.7	-1.2	-0.4	0.2	No Values	No Values	No Values	No Values
1383	seq=translation; coord=8:121435529..121437647:-1; parent_transcript=GRMZM2G042865_T01; parent_gene=GRMZM2G042865	GRMZM2G042865_P01 (+1)	51 kDa	Ref	-0.2	-0.4	-0.4	-0.4	No Values	No Values	No Values	No Values
1384	seq=translation; coord=8:76128223..76129850:1; parent_transcript=AC231180.2_FGT006; parent_gene=AC231180.2_FG006	AC231180.2_FGP006	48 kDa	Ref	0.6	-0.2	-1.4	-1.6	No Values	No Values	No Values	No Values
1385	seq=translation; coord=7:25812344..25817942:1; parent_transcript=GRMZM2G003789_T01; parent_gene=GRMZM2G003789	GRMZM2G003789_P01	47 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0.1	0.7	0.5
1386	seq=translation; coord=1:171489898..171496325:1; parent_transcript=GRMZM2G019926_T02; parent_gene=GRMZM2G019926	GRMZM2G019926_P02 (+2)	35 kDa	Ref	0	0.2	-0.1	0.7	No Values	No Values	No Values	No Values
1387	seq=translation; coord=2:8914517..8917818:-1; parent_transcript=GRMZM2G076239_T02; parent_gene=GRMZM2G076239	GRMZM2G076239_P02 (+3)	40 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.6	1.4	0.9
1388	seq=translation; coord=3:205146239..205150759:-1; parent_transcript=GRMZM2G098569_T01; parent_gene=GRMZM2G098569	GRMZM2G098569_P01	41 kDa	Ref	0.7	0.5	0.6	1.1	No Values	No Values	No Values	No Values
1389	seq=translation; coord=6:105434141..105436791:1; parent_transcript=GRMZM2G403076_T01; parent_gene=GRMZM2G403076	GRMZM2G403076_P01	62 kDa	Ref	0.8	-0.1	0.3	2.2	No Values	No Values	No Values	No Values
1390	seq=translation; coord=4:18676199..18682894:1; parent_transcript=GRMZM2G574782_T01; parent_gene=GRMZM2G574782	GRMZM2G574782_P01	57 kDa	Ref	0.3	0.2	0.4	0.3	No Values	No Values	No Values	No Values

1391	seq=translation; coord=8:152750732..152754708:1; parent_transcript=GRMZM5G823017_T01; parent_gene=GRMZM5G823017	GRMZM5G823017_P01 (+2)	46 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	-1.4	-0.3	-0.1
1392	seq=translation; coord=8:118191461..118195143:-1; parent_transcript=AC197705.4_FGT007; parent_gene=AC197705.4_FG007	AC197705.4_FGP007	57 kDa	Ref	No Values	No Values	No Values	No Values	1.2	-1	-0.8	-2
1393	seq=translation; coord=8:29145636..29147578:-1; parent_transcript=GRMZM2G007151_T01; parent_gene=GRMZM2G007151	GRMZM2G007151_P01 (+1)	21 kDa	Ref	1.8	1.7	2.7	1	No Values	No Values	No Values	No Values
1394	seq=translation; coord=3:2080450..2084636:1; parent_transcript=GRMZM2G153181_T01; parent_gene=GRMZM2G153181	GRMZM2G153181_P01	61 kDa	Ref	1.5	0.5	0.1	0.6	No Values	No Values	No Values	No Values
1395	seq=translation; coord=5:58525626..58534933:-1; parent_transcript=GRMZM2G397247_T04; parent_gene=GRMZM2G397247	GRMZM2G397247_P04	46 kDa	Ref	0.3	0	0.4	0.2	No Values	No Values	No Values	No Values
1396	seq=translation; coord=1:210463083..210467521:1; parent_transcript=GRMZM2G073814_T02; parent_gene=GRMZM2G073814	GRMZM2G073814_P02	65 kDa	Ref	-0.4	-1.7	-1	-0.4	No Values	No Values	No Values	No Values
1397	seq=translation; coord=10:16517475..16520678:1; parent_transcript=GRMZM2G091819_T01; parent_gene=GRMZM2G091819	GRMZM2G091819_P01	44 kDa	Ref	No Values	No Values	No Values	No Values	2.7	0.3	0	-1.5
1398	seq=translation; coord=4:151648685..151655399:1; parent_transcript=GRMZM2G145226_T01; parent_gene=GRMZM2G145226	GRMZM2G145226_P01	25 kDa	Ref	No Values	No Values	No Values	No Values	-1.6	-0.8	-0.5	-0.6
1399	seq=translation; coord=1:287289676..287296815:-1; parent_transcript=GRMZM2G178415_T01; parent_gene=GRMZM2G178415	GRMZM2G178415_P01 (+3)	44 kDa	Ref	-0.6	-0.1	-0.3	-0.4	No Values	No Values	No Values	No Values
1400	seq=translation; coord=8:64567512..64568715:-1; parent_transcript=GRMZM2G075796_T01; parent_gene=GRMZM2G075796	GRMZM2G075796_P01	21 kDa	Ref	0.4	0.1	0.5	-0.1	No Values	No Values	No Values	No Values
1401	seq=translation; coord=5:6157585..6167807:-1; parent_transcript=GRMZM2G171588_T01; parent_gene=GRMZM2G171588	GRMZM2G171588_P01 (+2)	36 kDa	Ref	1.1	0.4	0.2	0	No Values	No Values	No Values	No Values

Table S2. The peptides of identified proteins using iTRAQ.

Id	Protein Name	Accession Numbers	Assigned	Unique	Sequence	Prob	Modifications	Ion Score	Identity Score
1	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	aETSPEDVGGMHAAAGILTER	95%	n+304 (+304)	84.15	25.00
2	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	aETSPEDVGGmHAAAGILTER	95%	n+304 (+304), Oxidation (+16)	48.54	25.00
3	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	aLPPGLWAEVL DGLR	95%	n+304 (+304)	59.90	26.05
4	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	aMDGLSVTIR	95%	n+304 (+304)	38.70	25.00
5	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	eLcSETGANQEDALAR	95%	n+304 (+304), Carbamidomethyl (+57)	93.42	25.00
6	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	eLVSYK	88%	n+304 (+304), K+304 (+304)	27.63	26.32
7	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	eMQDIEFTVQESR	95%	n+304 (+304)	51.51	25.00
8	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	emQDIEFTVQESR	95%	n+304 (+304), Oxidation (+16)	44.89	25.00
9	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	fIPIYLAQGILQHDPFEVLDQR	95%	n+304 (+304)	55.80	25.15
10	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	fLDMFGNVVM DIPHALFEEK	95%	n+304 (+304), K+304 (+304)	34.23	25.47
11	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	fLDmFGNVVM DIPHALFEEK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	33.23	25.00
12	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	fLDMFGNVVM DIPHALFEEK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	46.80	25.04
13	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	fLDmFGNVVM DIPHALFEEK	95%	n+304 (+304), Oxidation (+16), Oxidation (+16), K+304 (+304)	38.67	25.00
14	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	iAVDMVNEGLVER	95%	n+304 (+304)	56.80	26.73
15	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	iAVDmVNEGLVER	95%	n+304 (+304), Oxidation (+16)	49.13	25.37
16	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	iGTMIEIPR	86%	n+304 (+304)	26.90	26.59

17	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	IGISYPELTEMQAR	95%	n+304 (+304)	42.94	25.00
18	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	IGISYPELTEmQAR	95%	n+304 (+304), Oxidation (+16)	54.35	25.00
19	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	ILDPLHEFLPEGNVVEIVR	95%	n+304 (+304)	48.29	25.55
20	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	ISEVNPMLGFR	89%	n+304 (+304)	27.22	25.73
21	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	nDTDLTATDLk	95%	n+304 (+304), K+304 (+304)	31.03	25.16
22	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	nNGAEGIGLcR	95%	n+304 (+304), Carbamidomethyl (+57)	31.09	25.00
23	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	nVYVEAk	91%	n+304 (+304), K+304 (+304)	28.08	26.24
24	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	qLELAVLAVFDSWESPR	95%	n+304 (+304)	39.73	25.66
25	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	qMIMAPTVELR	95%	n+304 (+304)	33.07	26.15
26	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	qmIMAPTVELR	95%	n+304 (+304), Oxidation (+16)	34.08	25.09
27	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	qPLSPALSGDLGTFMSWVDDVRk	95%	n+304 (+304), K+304 (+304)	34.50	25.00
28	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	rFLDMFGNVVMDIPHALFEEK	95%	n+304 (+304), K+304 (+304)	52.78	25.00
29	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	rPLLSVR	95%	n+304 (+304)	29.87	25.00
30	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	sGAAVSMPPGMMDTVNLGLNDQVAAGLAAK	95%	n+304 (+304), K+304 (+304)	57.89	25.00
31	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	sVILVR	94%	n+304 (+304)	31.34	25.00
32	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	tGLDYVScSPFR	95%	n+304 (+304), Carbamidomethyl (+57)	41.27	25.00
33	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	vLANADTPEDALAAR	95%	n+304 (+304)	84.55	25.54
34	seq=translation; coord=8:107003965..107014830:1; parent_transcript=GRMZM2G097457_T01; parent_gene=GRMZM2G097457	GRMZM2G097457_P01,GRMZM2G097457_P02	TRUE	TRUE	wVEEYMGAAIGDPR	94%	n+304 (+304)	31.32	25.00

35	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	aADILVNFFDk	95%	n+304 (+304), K+304 (+304)	54.96	26.91
36	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	aDPSYWDk	94%	n+304 (+304), K+304 (+304)	27.05	25.00
37	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	aLENEMLLR	92%	n+304 (+304)	29.01	26.18
38	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	aLENEmLLR	93%	n+304 (+304), Oxidation (+16)	28.72	25.51
39	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	dTVGQYESHIAFTLPGLYR	95%	n+304 (+304)	78.26	25.30
40	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	eLANLVIVAGDHGk	95%	n+304 (+304), K+304 (+304)	66.03	25.00
41	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	eMQAKPDLIIGNYSdGNLVATLLAHk	95%	n+304 (+304), K+304 (+304)	34.51	25.00
42	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	eSLYPLLNFLk	95%	n+304 (+304), K+304 (+304)	36.54	25.00
43	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fDVWPYLETYTEDVSSEImk	95%	n+304 (+304), K+304 (+304)	33.47	25.00
44	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fDVWPyLETYTEDVSSEImk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	28.53	25.00
45	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fDVWPYLETYTEDVSSEImk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	57.47	25.00
46	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fNIVSPGADMSVYYPYTETDk	95%	n+304 (+304), K+304 (+304)	38.41	25.00
47	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fNIVSPGADMSVYYPYTETDkR	95%	n+304 (+304), K+304 (+304)	45.01	25.00
48	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	fNIVSPGADmSVYYPYTETDkR	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	32.83	25.00
49	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	gTTMMLNDR	95%	n+304 (+304)	29.71	25.00
50	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	gTTmMLNDR	94%	n+304 (+304), Oxidation (+16)	28.99	25.00
51	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713 seq=translation; coord=9:11496011..11502772:1;	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	gTTmMLNDR	95%	n+304 (+304), Oxidation (+16)	31.56	25.00
52	parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	gWGDTAk	94%	n+304 (+304), K+304 (+304)	29.40	25.00

53	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	hQLLAEFDALFDSDk	95%	n+304 (+304), K+304 (+304)	43.06	25.00
54	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	hQLLAEFDALFDSDkEk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	37.10	25.75
55	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	kAEYLLSVQDTPYSEFNHR	95%	K+304 (+304), n+304 (+304)	43.05	25.00
56	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	IFQDKESLYPLLNFLk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.47	25.00
57	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	IGATFSSHPNELIALFSR	95%	n+304 (+304)	68.82	25.89
58	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	IGVTQcTIAHALEk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.46	25.01
59	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	ILPDAAGTTcGQR	85%	n+304 (+304), Carbamidomethyl (+57)	25.05	25.00
60	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	ITAFHPEIEELYSVDENSEHK	95%	n+304 (+304), K+304 (+304)	37.51	25.00
61	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	mYSLIDEYk	95%	n+304 (+304), K+304 (+304)	43.83	25.00
62	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	nMTGLVEMYGk	95%	n+304 (+304), K+304 (+304)	42.22	25.05
63	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	nmTGLVEMYGk	93%	n+304 (+304), Oxidation (+16), K+304 (+304)	28.72	25.00
64	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	qQGLDITPk	95%	n+304 (+304), K+304 (+304)	36.03	25.69
65	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	sLASQVPLSFD	95%	n+304 (+304)	30.22	25.19
66	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	tkYPNSDIYLDk	94%	n+304 (+304), K+304 (+304), K+304 (+304)	27.79	25.45
67	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	vIGTEHTDIIR	95%	n+304 (+304)	32.67	26.43
68	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	vNVSELAVEELSVSEYLAfk	95%	n+304 (+304), K+304 (+304)	44.70	25.25
69	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	yAPFEDILR	94%	n+304 (+304)	30.83	25.00
70	seq=translation; coord=9:11496011..11502772:1; parent_transcript=GRMZM2G089713_T01; parent_gene=GRMZM2G089713	GRMZM2G089713_P01,GRMZM2G089713_P02	TRUE	TRUE	yIEMFYALK	95%	n+304 (+304), K+304 (+304)	34.41	25.67

71	seq=translation; coord=9:22100864..22105552:1; parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	aGWGVMMASHR	95%	n+304 (+304)	49.48	25.00
72	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	aVSNVNNIIGPAIVGk	93%	n+304 (+304), K+304 (+304)	27.13	25.00
73	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	aVTITWVvk	95%	n+304 (+304), K+304 (+304)	32.04	25.76
74	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	gAVPSGASTGIYEALER	95%	n+304 (+304)	72.41	25.47
75	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	gNPTVEVDVGLSDGSYAR	95%	n+304 (+304)	93.58	25.00
76	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	gNPTVEVDVGLSDGSyAR	95%	n+304 (+304), iTRAQ8plex (+304)	36.35	25.09
77	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	iEELGDAAVYAGAk	95%	n+304 (+304), K+304 (+304)	31.25	25.85
78	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	iEELGDAAVyAGAk	94%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	28.00	25.72
79	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	IAMQEFMILPTGASSFk	95%	n+304 (+304), K+304 (+304)	39.90	25.81
80	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	IaMQEFMILPTGASSFk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	42.45	25.75
81	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	IAMQEFmILPTGASSFk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	38.48	25.88
82	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	ITDEIGQk	95%	n+304 (+304), K+304 (+304)	37.01	25.69
83	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	mGVEVYHNLk	95%	n+304 (+304), K+304 (+304)	43.63	26.16
84	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	sGETEDTFIADLSVGLSTGQIk	95%	n+304 (+304), K+304 (+304)	56.38	25.16
85	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	tcNALLLk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.81	25.00
86	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	vNQIGSVTESIEAVR	95%	n+304 (+304)	70.85	25.30
87	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	vQIVGDDLLVTNPTR	95%	n+304 (+304)	31.29	26.71
88	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302	GRMZM2G064302_P01	TRUE	TRUE	vVIGMDVAASEFFGEK	95%	n+304 (+304), K+304 (+304)	61.37	25.38

89	seq=translation; coord=9:22100864..22105552:1; parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=9:22100864..22105552:1;	GRMZM2G064302_P01	TRUE	TRUE	vVIGMDVAASEFFGEK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	34.42	25.40
90	parent_transcript=GRMZM2G064302_T01; parent_gene=GRMZM2G064302 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G064302_P01	TRUE	TRUE	vVIGMDVAASEFFGEKDK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	45.72	26.12
91	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	aAGASWIQFDEPTLVLDLSDK	95%	n+304 (+304), K+304 (+304)	63.94	25.55
92	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	aEHAFYLDWAVHSFR	95%	n+304 (+304)	58.42	25.00
93	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	eVIAELk	94%	n+304 (+304), K+304 (+304)	28.71	25.00
94	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	gFLLSLSSILPVYk	95%	n+304 (+304), K+304 (+304)	32.68	25.00
95	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	gTQTLGLVTSAGFPAGk	95%	n+304 (+304), K+304 (+304)	50.73	25.00
96	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	iPSAEIADR	95%	n+304 (+304)	32.83	25.13
97	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	iSEEEYVTAIk	95%	n+304 (+304), K+304 (+304)	37.64	25.77
98	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	INLPILPTTTIGSFQQTVELR	95%	n+304 (+304)	36.48	25.00
99	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	nIWADDLATSLSLTQSLEAVVGk	95%	n+304 (+304), K+304 (+304)	59.25	25.00
100	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	qMADAGIk	95%	n+304 (+304), K+304 (+304)	35.37	26.50
101	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	sTAEDLEK	95%	n+304 (+304), K+304 (+304)	32.28	25.51
102	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	tLTSLSSVTAYGFDLVR	95%	n+304 (+304)	63.90	25.37
103	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	tLTSLSSVTAYGFDLVR	95%	n+304 (+304), iTRAQ8plex (+304)	30.46	25.73
104	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	vVEVDALak	95%	n+304 (+304), K+304 (+304)	44.89	26.14
105	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751 seq=translation; coord=1:176837841..176844200:1;	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	wFDTNYHFIVPELGPNTk	95%	n+304 (+304), K+304 (+304)	33.31	25.00
106	parent_transcript=GRMZM2G149751_T01; parent_gene=GRMZM2G149751	GRMZM2G149751_P01,GRMZM2G149751_P03, GRMZM2G149751_P05	TRUE	TRUE	ySWTGGEIGFDTYFSMAR	95%	n+304 (+304), iTRAQ8plex (+304)	32.96	25.00

107	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	aGIALNDHFik	95%	n+304 (+304), K+304 (+304)	34.23	25.00
108	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	gASYEEIk	95%	n+304 (+304), K+304 (+304)	35.27	26.06
109	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	gIMGYVEEDLVSTDFTGDSR	95%	n+304 (+304)	42.80	25.00
110	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	gImGYVEEDLVSTDFTGDSR	95%	n+304 (+304), Oxidation (+16)	32.48	25.00
111	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	gIMGyVEEDLVSTDFTGDSR	95%	n+304 (+304), iTRAQ8plex (+304)	32.72	25.00
112	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	hSDIALk	95%	n+304 (+304), K+304 (+304)	28.78	25.00
113	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	tLLFGEkPVTVFgIR	94%	n+304 (+304), K+304 (+304)	30.25	25.00
114	seq=translation; coord=6:6898695..6903246:-1; parent_transcript=GRMZM2G180625_T01; parent_gene=GRMZM2G180625	GRMZM2G180625_P01,GRMZM2G180625_P02, GRMZM2G180625_P03	TRUE	TRUE	viHDNFGIIEGLMTTVHAITATQk	95%	n+304 (+304), K+304 (+304)	32.71	25.00
115	seq=translation; coord=1:296477860..296482170:1; parent_transcript=GRMZM2G040369_T01; parent_gene=GRMZM2G040369	GRMZM2G040369_P01,GRMZM2G040369_P02, GRMZM2G095851_P01,GRMZM2G095851_P02	TRUE	TRUE	aFLPVIESFGFSSQLR	95%	n+304 (+304)	61.54	25.91
116	seq=translation; coord=1:296477860..296482170:1; parent_transcript=GRMZM2G040369_T01; parent_gene=GRMZM2G040369	GRMZM2G040369_P01,GRMZM2G040369_P02, GRMZM2G095851_P01,GRMZM2G095851_P02	TRUE	TRUE	eQMTPLSEFEDk	95%	n+304 (+304), K+304 (+304)	35.90	25.00
117	seq=translation; coord=1:296477860..296482170:1; parent_transcript=GRMZM2G040369_T01; parent_gene=GRMZM2G040369	GRMZM2G040369_P01,GRMZM2G040369_P02, GRMZM2G095851_P01,GRMZM2G095851_P02	TRUE	TRUE	eQMTPLSEFEDkL	95%	n+304 (+304), K+304 (+304)	41.41	25.02
118	seq=translation; coord=1:296477860..296482170:1; parent_transcript=GRMZM2G040369_T01; parent_gene=GRMZM2G040369	GRMZM2G040369_P01,GRMZM2G040369_P02, GRMZM2G095851_P01,GRMZM2G095851_P02	TRUE	TRUE	fGVDETk	86%	n+304 (+304), K+304 (+304)	26.19	26.10
119	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	aAAAPVkdEL	94%	n+304 (+304), K+304 (+304)	30.52	25.16
120	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	dFDVAALMk	95%	n+304 (+304), K+304 (+304)	36.54	26.68
121	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	fIDASTIPR	88%	n+304 (+304)	26.32	25.00
122	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	kLAPEYENAAk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.89	25.00
123	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	IAPEYENAAk	95%	n+304 (+304), K+304 (+304)	30.42	25.54
124	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481	GRMZM2G091481_P01	TRUE	TRUE	IAPILDEAATTLQSDEEVIAk	95%	n+304 (+304), K+304 (+304)	38.57	25.00

125	seq=translation; coord=4:14854376..14859167:-1; parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=4:14854376..14859167:-1;	GRMZM2G091481_P01	TRUE	TRUE	mDATANDVPSEFDVQGYPTLYFVTPSGk	95%	n+304 (+304), K+304 (+304)	31.68	25.00
126	parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=4:14854376..14859167:-1;	GRMZM2G091481_P01	TRUE	TRUE	mDATANDVPSEFDVQGYPTLYFVTPSGk	95%	Oxidation (+16), n+304 (+304), K+304 (+304)	36.09	25.00
127	parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=4:14854376..14859167:-1;	GRMZM2G091481_P01	TRUE	TRUE	nPDNHPYLMk	95%	n+304 (+304), K+304 (+304)	31.09	25.00
128	parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=4:14854376..14859167:-1;	GRMZM2G091481_P01	TRUE	TRUE	sAYSAAEEFk	95%	n+304 (+304), K+304 (+304)	53.40	25.00
129	parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=4:14854376..14859167:-1;	GRMZM2G091481_P01	TRUE	TRUE	tADDIVDFIk	95%	n+304 (+304), K+304 (+304)	33.75	26.53
130	parent_transcript=GRMZM2G091481_T01; parent_gene=GRMZM2G091481 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G091481_P01	TRUE	TRUE	vVVDNVDHDFVfk	95%	n+304 (+304), K+304 (+304)	29.77	25.76
131	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	aAMGSDIDVSLDcAGFSk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.54	25.00
132	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	aAmGSDIDVSLDcAGFSk	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304)	73.41	25.00
133	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	aGVGPETGVLVVGAGPIGLVSLAAR	95%	n+304 (+304)	42.20	25.00
134	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	aVGlcGSDVHYLR	95%	n+304 (+304), Carbamidomethyl (+57)	56.07	25.16
135	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	dTWPLcIDFLR	95%	n+304 (+304), Carbamidomethyl (+57)	32.72	25.00
136	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	dVEEAFEVSAR	95%	n+304 (+304)	36.62	25.00
137	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	eVDVVGVR	95%	n+304 (+304)	36.37	25.00
138	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	gAQGSDAAGGEVEENMAAWLVAK	95%	n+304 (+304), K+304 (+304)	77.37	25.00
139	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	iAHFVVK	91%	n+304 (+304), K+304 (+304)	26.11	25.00
140	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	IPVGPYDVR	95%	n+304 (+304)	33.40	25.25
141	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	rAGVGPETGVLVVGAGPIGLVSLAAR	95%	n+304 (+304)	54.61	25.00
142	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423	GRMZM2G175423_P01	TRUE	TRUE	sLGADAAVR	95%	n+304 (+304)	36.93	26.63

143	seq=translation; coord=1:197267922..197271011:1; parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	vALEPGVScWR	95%	n+304 (+304), Carbamidomethyl (+57)	35.09	25.00
144	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	vcLVGMGHNEMTLPLTAAAR	95%	n+304 (+304), Carbamidomethyl (+57)	47.28	25.00
145	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	vcLVGmGHNEMTLPLTAAAR	95%	n+304 (+304), Carbamidomethyl (+57), Oxidation (+16)	35.06	25.00
146	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	vcLVGMGHNEmTLPLTAAAR	95%	Carbamidomethyl (+57), Oxidation (+16)	54.34	25.00
147	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	vVVVDVDDHR	95%	n+304 (+304)	50.75	25.47
148	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=1:197267922..197271011:1;	GRMZM2G175423_P01	TRUE	TRUE	ykDTWPLcIDFLR	94%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	29.13	25.99
149	parent_transcript=GRMZM2G175423_T01; parent_gene=GRMZM2G175423 seq=translation; coord=3:126460606..126465045:-1;	GRMZM2G175423_P01	TRUE	TRUE	yNLcEDMk	88%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.10	25.00
150	parent_transcript=GRMZM2G340251_T01; parent_gene=GRMZM2G340251 seq=translation; coord=3:126460606..126465045:-1;	GRMZM2G340251_P01,GRMZM2G340251_P02, GRMZM2G340251_P03	TRUE	TRUE	kiEDIAAIAISWLDANQLAEDEFEDk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.25	25.00
151	parent_transcript=GRMZM2G340251_T01; parent_gene=GRMZM2G340251 seq=translation; coord=3:126460606..126465045:-1;	GRMZM2G340251_P01,GRMZM2G340251_P02, GRMZM2G340251_P03	TRUE	TRUE	mYQGAGEDMGGAGGMDPADAGSGGPGPk	95%	n+304 (+304), K+304 (+304)	85.45	25.00
152	parent_transcript=GRMZM2G340251_T01; parent_gene=GRMZM2G340251 seq=translation; coord=3:2076216747..207621242:-1;	GRMZM2G340251_P01,GRMZM2G340251_P02, GRMZM2G340251_P03	TRUE	TRUE	nSLENYSYNMR	95%	n+304 (+304)	37.71	25.00
153	parent_transcript=GRMZM2G041275_T01; parent_gene=GRMZM2G041275 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G041275_P01	TRUE	TRUE	fDEGLPPILTAEVLDNNIR	95%	n+304 (+304)	59.91	25.25
154	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	hVVFGQVVEGMDVVk	95%	n+304 (+304), K+304 (+304)	60.28	25.01
155	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	hVVFGQVVEGmDVVk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	41.29	25.84
156	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	vADcGQLS	95%	n+304 (+304), Carbamidomethyl (+57)	51.57	25.00
157	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	vFFDMTVGGAPAGR	95%	n+304 (+304)	49.09	25.00
158	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	vFFDmTVGGAPAGR	95%	n+304 (+304), Oxidation (+16)	49.58	25.00
159	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111 seq=translation; coord=5:167751373..167752582:1;	GRMZM2G326111_P01	TRUE	TRUE	viPEFMcQGQDFTR	95%	n+304 (+304), Carbamidomethyl (+57)	74.65	25.00
160	parent_transcript=GRMZM2G326111_T01; parent_gene=GRMZM2G326111	GRMZM2G326111_P01	TRUE	TRUE	viPEFmcQGQDFTR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	64.65	25.00

161	seq=translation; coord=4:240050091..240053865:1; parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	aMEDAGLEK	95%	n+304 (+304), K+304 (+304)	48.21	25.00
162	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	dAGVIAGLNVAR	95%	n+304 (+304)	42.06	26.62
163	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	dILLLDVAPLTGLIETVGGVMTK	95%	n+304 (+304), K+304 (+304)	41.60	25.00
164	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	dILLLDVAPLTGLIETVGGVmTk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	47.82	25.00
165	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	eAEFEAEEDk	95%	n+304 (+304), K+304 (+304)	51.02	25.00
166	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	eALEWLDNQSAAEK	95%	n+304 (+304), K+304 (+304)	57.75	25.00
167	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	eALEWLDNQSAAEKEDYEK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	30.81	25.00
168	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	eVEAVcNPIVSAVYQR	95%	n+304 (+304), Carbamidomethyl (+57)	66.19	25.00
169	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	fEELNNDLFR	95%	n+304 (+304)	33.48	25.00
170	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	iMEYFIK	95%	n+304 (+304), K+304 (+304)	37.24	25.29
171	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	iNDAVVTVPAYFNDAGR	95%	n+304 (+304)	52.12	25.00
172	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	iTPSWVAFTDSEK	95%	n+304 (+304)	47.75	25.00
173	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	IkEVEAVcNPIVSAVYQR	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	44.46	25.00
174	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	nQLETYYVNMk	93%	n+304 (+304), K+304 (+304)	27.40	25.07
175	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	sGGAPGGDADGGVDDHDEL	95%	n+304 (+304)	38.42	25.00
176	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	sQIHEIVLVGGSTR	95%	n+304 (+304)	41.57	26.16
177	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	sQVFTTYQDQQTTSIQVFEGEK	90%	n+304 (+304)	26.49	25.00
178	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007	GRMZM2G415007_P01	TRUE	TRUE	tIFDVk	90%	n+304 (+304), K+304 (+304)	27.25	25.53

179	seq=translation; coord=4:240050091..240053865:1; parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	vEIESLFDGTDSEPLTR	95%	n+304 (+304)	64.01	25.00
180	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	vFSPEEISAMILGk	95%	n+304 (+304), K+304 (+304)	49.46	25.66
181	parent_transcript=GRMZM2G415007_T01; parent_gene=GRMZM2G415007 seq=translation; coord=4:240050091..240053865:1;	GRMZM2G415007_P01	TRUE	TRUE	vFSPEEISAmILGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	34.64	25.47
182	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	kPWSLSFSFGR	94%	K+304 (+304), n+304 (+304)	26.16	25.87
183	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	kVTPEVIAEYTVR	91%	K+304 (+304), n+304 (+304)	27.74	25.00
184	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	nLNAMNk	89%	n+304 (+304), K+304 (+304)	28.67	26.70
185	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	tVPAAPVAVVFLSGGQSEEEATR	95%	n+304 (+304)	32.80	25.38
186	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	vENLEK	91%	n+304 (+304), K+304 (+304)	30.55	27.77
187	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=3:165722970..165725581:1;	GRMZM2G057823_P01	TRUE	TRUE	vTPEVIAEYTVR	95%	n+304 (+304)	44.81	25.00
188	parent_transcript=GRMZM2G057823_T01; parent_gene=GRMZM2G057823 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G057823_P01	TRUE	TRUE	vTPEVIAEyTVR	94%	n+304 (+304), iTRAQ8plex (+304)	29.97	25.31
189	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	aNNTLTIIDSGIGMTk	91%	n+304 (+304), K+304 (+304)	27.39	26.25
190	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	eVSHewQLVnk	95%	n+304 (+304), K+304 (+304)	32.29	25.74
191	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	gYEVLFMVDAIDeYSIGQLk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	37.92	25.00
192	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	hNDDEQYVWESQAGGSFTVAR	95%	n+304 (+304)	43.38	25.00
193	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	hSEFISYPISLWIEk	95%	n+304 (+304), K+304 (+304)	29.92	25.51
194	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	KTMEINPENAIEMEELR	95%	K+304 (+304), n+304 (+304)	72.86	25.73
195	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	IDESEDEK	95%	n+304 (+304), K+304 (+304)	41.39	25.00
196	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631	GRMZM2G012631_P01	TRUE	TRUE	mTLYLkDDQLEYLEER	93%	n+304 (+304), K+304 (+304)	27.05	25.37

197	seq=translation; coord=4:198369976..198374059:-1; parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:198369976..198374059:-1;	GRMZM2G012631_P01	TRUE	TRUE	tMEINPENAI MEELR	95%	n+304 (+304)	44.66	25.00
198	parent_transcript=GRMZM2G012631_T01; parent_gene=GRMZM2G012631 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G012631_P01	TRUE	TRUE	tmEINPENAI MEELR	95%	n+304 (+304), Oxidation (+16)	57.21	25.00
199	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	aEEDYEK	95%	n+304 (+304), K+304 (+304)	38.20	25.00
200	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	aTDVMIAGk	95%	n+304 (+304), K+304 (+304)	41.31	26.61
201	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	dIIMVDHMR	95%	n+304 (+304)	65.07	25.00
202	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	dLSQADFGR	93%	n+304 (+304)	29.43	25.00
203	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	dSAAVFAWk	95%	n+304 (+304), K+304 (+304)	35.13	26.69
204	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	gcAAAlk	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.11	26.54
205	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	gETLEEWwCTER	95%	n+304 (+304), Carbamidomethyl (+57)	46.24	25.00
206	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	hSLPDGLMR	95%	n+304 (+304)	36.87	25.04
207	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	iPDPESTDNAEFk	95%	n+304 (+304), K+304 (+304)	30.77	25.00
208	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	iVLTIIR	95%	n+304 (+304)	30.38	25.00
209	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IEIELAEVEMPGLMAcR	95%	n+304 (+304), Carbamidomethyl (+57)	63.81	25.00
210	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IEIELAEVEmpGLMAcR	91%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	26.22	25.00
211	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IEIELAEVEMPGLmAcR	94%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	30.24	25.00
212	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IEIELAEVEmpGLmAcR	95%	n+304 (+304), Oxidation (+16), Oxidation (+16), Carbamidomethyl (+57)	40.36	25.00
213	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IVGVSEETTTGVk	95%	n+304 (+304), K+304 (+304)	66.77	26.56
214	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	IYQMQUETGALLFPAINVNDsvTk	95%	n+304 (+304), K+304 (+304)	77.73	25.22

215	seq=translation; coord=4:21135870..21139019:1; parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	nNAIVcNIGHFDNEIDMLGLETYPGVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	50.74	25.00
216	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	vAALHLGk	95%	n+304 (+304), K+304 (+304)	33.11	25.00
217	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	vAVVcGYGDVGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	58.88	25.88
218	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=4:21135870..21139019:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	wcScNIFSTQDHAAAAIAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	51.69	25.00
219	parent_transcript=GRMZM2G015295_T01; parent_gene=GRMZM2G015295 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G015295_P01,GRMZM2G015295_P02	TRUE	TRUE	wVFPETNTGIIVLAEGR	95%	n+304 (+304)	53.80	25.20
220	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	aGQLLIVPQGYLVATk	95%	n+304 (+304), K+304 (+304)	48.21	25.00
221	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	aQGEFGQYIAFETNPDTMVSHVAGk	95%	n+304 (+304), K+304 (+304)	98.46	25.00
222	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	eLTcAGIFAVR	95%	n+304 (+304), Carbamidomethyl (+57)	65.08	25.00
223	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	fLLAGGFSk	95%	n+304 (+304), K+304 (+304)	36.79	25.00
224	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	fLSEALGVSMHVAEK	95%	n+304 (+304), K+304 (+304)	31.18	25.67
225	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	fPVLNLVQMSAVR	95%	n+304 (+304)	37.06	25.43
226	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	gQPHFAENIFk	95%	n+304 (+304), K+304 (+304)	36.09	26.56
227	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	hNVcAMEVR	95%	n+304 (+304), Carbamidomethyl (+57)	31.54	25.00
228	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	kHELAVLTPAGSGSYQQGQAGSAQQ	94%	K+304 (+304), n+304 (+304)	25.82	25.72
229	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	IDQADVYSPGAGR	95%	n+304 (+304)	40.33	25.00
230	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	IDQADVYSPGAGR	95%	n+304 (+304), iTRAQ8plex (+304)	38.05	25.00
231	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	IEALEPR	88%	n+304 (+304)	27.04	26.39
232	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883	GRMZM2G174883_P01	TRUE	TRUE	nSVLSDLPAAVIASSYAISMEEAAELK	95%	n+304 (+304), K+304 (+304)	37.01	25.00

233	seq=translation; coord=6:39891824..39893787:1; parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	nSVLSDLPAAVIASSYAISmEEAAELK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	49.15	25.12
234	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	vDLYQDAIMSPFWNFNAHSAMYGIR	95%	n+304 (+304)	79.93	25.00
235	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	vQSEAGSVQyFSR	95%	n+304 (+304)	49.26	25.00
236	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=6:39891824..39893787:1;	GRMZM2G174883_P01	TRUE	TRUE	vQSEAGSVQyFSR	95%	n+304 (+304), iTRAQ8plex (+304)	41.27	25.62
237	parent_transcript=GRMZM2G174883_T01; parent_gene=GRMZM2G174883 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G174883_P01	TRUE	TRUE	vVVDAMGLLLPR	95%	n+304 (+304)	60.02	25.16
238	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	aGEDADSLGLTGHHER	95%	n+304 (+304)	72.80	25.00
239	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	aTIANMSPEYGATMGFFPVDHVTLDyLk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	32.16	25.00
240	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	dIW PSTEEIAQVQSSVLPDMfk	95%	n+304 (+304), K+304 (+304)	29.46	25.71
241	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	dMTMSPPGPSTVvk	94%	n+304 (+304), K+304 (+304)	28.99	25.35
242	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	fDFHGQPAEMk	95%	n+304 (+304), K+304 (+304)	29.46	25.00
243	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	fVEFYGEGMGk	95%	n+304 (+304), K+304 (+304)	46.64	25.00
244	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	gNPMWNQLTVPEASLYSWDSk	95%	n+304 (+304), K+304 (+304)	59.68	25.00
245	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	iNPLVPVDLVIDHSVQVDVAR	95%	n+304 (+304)	88.50	25.08
246	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	iYSSYLELNLDEVEPSMSGPk	95%	n+304 (+304), K+304 (+304)	40.66	25.00
247	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	iYSSYLELNLDEVEPSMSGPk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	29.44	25.00
248	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	ISVFDAAMR	89%	n+304 (+304)	26.89	25.00
249	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801 seq=translation; coord=4:28118892..28124783:1;	GRMZM2G020801_P01	TRUE	TRUE	mFVDYNEPPTER	95%	n+304 (+304)	44.68	25.00
250	parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	TRUE	TRUE	sFTcIVR	87%	n+304 (+304), Carbamidomethyl (+57)	25.69	25.00

251	seq=translation; coord=4:28118892..28124783:1; parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	TRUE	TRUE	sGVTATDLVLTVTQMLR	95%	n+304 (+304)	32.62	26.02
252	seq=translation; coord=4:28118892..28124783:1; parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	TRUE	TRUE	sGVTATDLVLTVTQmLR	95%	n+304 (+304), Oxidation (+16)	59.22	25.95
253	seq=translation; coord=4:28118892..28124783:1; parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	TRUE	TRUE	sQNAVQANMELEFSR	95%	n+304 (+304)	83.53	25.00
254	seq=translation; coord=4:28118892..28124783:1; parent_transcript=GRMZM2G020801_T01; parent_gene=GRMZM2G020801	GRMZM2G020801_P01	TRUE	TRUE	tSLAPSGSVVTK	95%	n+304 (+304), K+304 (+304)	37.98	25.45
255	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	aDEGFSATVR	90%	n+304 (+304)	27.24	25.00
256	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	dEEGNPAFALVNK	95%	n+304 (+304), K+304 (+304)	46.60	25.44
257	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	dEEGYPAFALVNR	95%	n+304 (+304)	58.94	25.00
258	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	dGNVVLAPANPR	95%	n+304 (+304)	61.90	25.21
259	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	dGTNIVLWk	95%	n+304 (+304), K+304 (+304)	33.76	26.71
260	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	fGGGGEPTVR	91%	n+304 (+304)	27.70	25.00
261	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	gDNQSWk	91%	n+304 (+304), K+304 (+304)	28.32	25.00
262	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	gHGGVHDGTTVVLWEWak	95%	n+304 (+304), K+304 (+304)	36.42	25.49
263	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	iLPWGDEAYAGGSSAANAPR	95%	n+304 (+304)	94.97	25.00
264	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	iLPWGDEAYAGGSSAANAPR	95%	n+304 (+304), iTRAQ8plex (+304)	29.08	25.09
265	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	IVPFNPEYQDESVLWTESGDVGK	95%	n+304 (+304), K+304 (+304)	50.61	25.00
266	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	IVPYNPGYQDESVLWTESR	95%	n+304 (+304)	41.74	25.00
267	seq=translation; coord=1:53621183..53623074:-1; parent_transcript=GRMZM2G020940_T01; parent_gene=GRMZM2G020940	GRMZM2G020940_P01	TRUE	TRUE	IVPyNPGYQDESVLWTESR	93%	n+304 (+304), iTRAQ8plex (+304)	27.69	25.40
268	seq=translation; coord=9:138424253..138428598:1; parent_transcript=GRMZM2G054300_T01; parent_gene=GRMZM2G054300	GRMZM2G054300_P01,GRMZM2G054300_P04	TRUE	TRUE	cPAELAHGANAGLDIAVR	95%	Carbamidomethyl (+57), n+304 (+304)	62.68	25.00

269	seq=translation; coord=9:138424253..138428598:1; parent_transcript=GRMZM2G054300_T01; parent_gene=GRMZM2G054300 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G054300_P01,GRMZM2G054300_P04	TRUE	TRUE	nYPTVSAEYSEAVEk	95%	n+304 (+304), K+304 (+304)	44.91	25.00
270	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	aLMDEMAVVATk	94%	n+304 (+304), K+304 (+304)	31.29	25.81
271	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	eEVFDAlk	95%	n+304 (+304), K+304 (+304)	32.16	26.25
272	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	eFVQEcyELSAEYENDRDEAR	95%	n+304 (+304), Carbamidomethyl (+57)	37.05	25.00
273	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	eLLQVAGHk	95%	n+304 (+304), K+304 (+304)	39.52	25.00
274	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	eMYNEWPFFR	92%	n+304 (+304)	28.89	25.00
275	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	eSYITTLNVcQAYTLk	90%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.96	25.58
276	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	fHLPVWLFGAAIk	95%	n+304 (+304), K+304 (+304)	30.83	25.00
277	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	fLDILQLHGPHLR	95%	n+304 (+304)	32.19	25.29
278	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	gDPGIAAVYDk	95%	n+304 (+304), K+304 (+304)	50.60	25.90
279	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	iRDPSFQVSPQPLSk	95%	n+304 (+304), K+304 (+304)	32.50	25.00
280	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	iADLEAAPAAVAR	95%	n+304 (+304)	38.40	26.47
281	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	iLVADDLQSFGEQLR	95%	n+304 (+304)	58.88	25.00
282	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	iVEYDALLVDR	95%	n+304 (+304)	36.60	25.00
283	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	qVSTFGLALVk	95%	n+304 (+304), K+304 (+304)	48.47	25.00
284	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	rQDWLLSELR	95%	n+304 (+304)	35.01	26.34
285	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542 seq=translation; coord=5:144808460..144816059:-1;	GRMZM2G069542_P01	TRUE	TRUE	rTPPTPQDEMR	95%	n+304 (+304)	29.44	25.00
286	parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	sATPETEYGR	95%	n+304 (+304)	42.81	25.00

287	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	sIVFQEPR	91%	n+304 (+304)	28.29	25.38
288	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	sLcAcGdkPIADGSLDLFLR	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	25.86	25.67
289	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	tPPTPQDEMRR	95%	n+304 (+304)	33.52	25.00
290	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	vLGDVRR	92%	n+304 (+304)	28.96	25.00
291	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	vTLDLLEMVFAK	95%	n+304 (+304), K+304 (+304)	37.03	25.00
292	seq=translation; coord=5:144808460..144816059:-1; parent_transcript=GRMZM2G069542_T01; parent_gene=GRMZM2G069542	GRMZM2G069542_P01	TRUE	TRUE	vTVQGEVIEHSFGEEllcFR	95%	n+304 (+304), Carbamidomethyl (+57)	42.29	25.00
293	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	aEAEGSLK	87%	n+304 (+304), K+304 (+304)	27.80	26.93
294	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	dAPMFVVGvNEK	95%	n+304 (+304), K+304 (+304)	41.29	25.76
295	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	eVAVFGcR	95%	n+304 (+304), Carbamidomethyl (+57)	35.11	25.00
296	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	fGIVEGLMTTVHAITATQK	95%	n+304 (+304), K+304 (+304)	40.03	25.00
297	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	fGIVEGLmTTVHAITATQK	94%	n+304 (+304), Oxidation (+16), K+304 (+304)	26.22	25.00
298	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	gILGyVEEDLVSTDFQGDSR	92%	n+304 (+304)	28.55	25.00
299	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	gILGyVEEDLVSTDFQGDSR	95%	n+304 (+304), iTRAQ8plex (+304)	43.27	25.00
300	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	IVSWYDNEWGYSTR	95%	n+304 (+304)	54.65	25.00
301	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	IVSWyDNEWGYSTR	95%	n+304 (+304), iTRAQ8plex (+304)	52.49	25.00
302	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	nPEEIPWGSVGAeyVVSTGVFTDQEK	95%	n+304 (+304), K+304 (+304)	47.06	25.00
303	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	sATYDEIK	95%	n+304 (+304), K+304 (+304)	40.37	26.77

304	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	sDINIVSNAScTTNcLAPLAK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	37.15	25.00
305	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	tLLFGEK	89%	n+304 (+304), K+304 (+304)	26.99	25.19
306	seq=translation; coord=4:133103720..133107109:1; parent_transcript=GRMZM2G071630_T01; parent_gene=GRMZM2G071630	GRMZM2G071630_P01,GRMZM2G176307_P01, GRMZM2G176307_P02	TRUE	TRUE	tVDGPSSk	91%	n+304 (+304), K+304 (+304)	28.20	25.16
307	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	eYVFVANSNDNLGAIVDIK	95%	n+304 (+304), K+304 (+304)	67.57	25.38
308	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	eyVFVANSNDNLGAIVDIK	94%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	25.35	25.00
309	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	iFNTNNLWVNLK	95%	n+304 (+304), K+304 (+304)	37.38	25.15
310	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	IEIPDGDVLENk	95%	n+304 (+304), K+304 (+304)	32.31	25.68
311	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	IEIPDGDVLENkDVNGPEDL	91%	n+304 (+304), K+304 (+304)	25.77	25.00
312	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	nGFTFLDLIVIQIESLNkk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	31.13	25.00
313	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	sGFISLVSr	95%	n+304 (+304)	33.35	25.00
314	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	sVIEVR	87%	n+304 (+304)	26.65	25.76
315	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	vQLLEIAQVPDEHVNEfk	95%	n+304 (+304), K+304 (+304)	35.38	25.63
316	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	yGcNVPLLLMNSFNTHDDTQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.05	25.00
317	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	yLSGEAEQIEWSk	95%	n+304 (+304), K+304 (+304)	47.81	25.54
318	seq=translation; coord=7:146491263..146498155:-1; parent_transcript=GRMZM2G032003_T02; parent_gene=GRMZM2G032003	GRMZM2G032003_P02,GRMZM2G032003_P05	TRUE	TRUE	yLSGEAEQIEWSk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	45.29	25.89
319	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	aGGMQQPMPMGQQQVFPR	95%	n+304 (+304)	49.31	25.00
320	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	aLYDTFcAFGNILSck	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	66.31	25.00

321	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	aLyDTFcAFGNILSck	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	30.26	25.00
322	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	eLFAEYGNITSck	92%	Carbamidomethyl (+57), n+304 (+304)	26.63	25.00
323	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	eNVSSNik	95%	n+304 (+304), K+304 (+304)	32.28	26.47
324	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	fQNTNLyLk	95%	n+304 (+304), K+304 (+304)	37.14	25.47
325	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	fSNVYvk	86%	n+304 (+304), K+304 (+304)	25.26	25.00
326	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	gYGFVQFEK	95%	n+304 (+304), K+304 (+304)	47.49	25.00
327	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	iATDPSGESR	94%	n+304 (+304)	30.68	25.00
328	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	IMLGENLyPLVEQLER	95%	n+304 (+304)	40.70	25.40
329	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	ImLGENLyPLVEQLER	95%	n+304 (+304), Oxidation (+16)	33.42	25.55
330	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	IMLGENLyPLVEQLER	94%	n+304 (+304), iTRAQ8plex (+304)	27.42	25.07
331	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	nLEENIDDEK	95%	n+304 (+304), K+304 (+304)	51.00	25.00
332	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	nLEENIDDEKLR	95%	n+304 (+304), K+304 (+304)	32.79	25.53
333	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	nLSDTVTDELK	95%	n+304 (+304), K+304 (+304)	72.93	25.00
334	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	nVQEVAek	95%	n+304 (+304), K+304 (+304)	32.83	25.34
335	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	sAQHLQSQNVSTEQQLANLSLNDGVVSS	95%	n+304 (+304)	42.68	25.00
336	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829 seq=translation; coord=2:162466718..162472431:1;	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	sGTGNIFik	95%	n+304 (+304), K+304 (+304)	44.07	26.22
337	parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	sLGAYVYNNYNNQGDAAAR	95%	n+304 (+304)	89.41	25.00

338	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	sLGyAYVYNNQGDAAAR	90%	n+304 (+304), iTRAQ8plex (+304)	25.03	25.00
339	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	vAEAMEVLR	94%	n+304 (+304)	30.69	25.22
340	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	vFVGPFVR	95%	n+304 (+304)	34.90	25.00
341	seq=translation; coord=2:162466718..162472431:1; parent_transcript=GRMZM2G102829_T01; parent_gene=GRMZM2G102829	GRMZM2G102829_P01,GRMZM2G102829_P02	TRUE	TRUE	yGTITSAVVMR	95%	n+304 (+304)	34.37	25.37
342	seq=translation; coord=3:187441065..187444892:-1; parent_transcript=GRMZM2G071790_T01; parent_gene=GRMZM2G071790	GRMZM2G071790_P01,GRMZM2G071790_P02, GRMZM2G071790_P03,GRMZM2G071790_P04, GRMZM2G071790_P05	TRUE	TRUE	yTGNSDLQLER	95%	n+304 (+304)	39.48	25.00
343	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	TRUE	TRUE	aTGAFILTASHNPGPGPTEDFGIK	93%	n+304 (+304), K+304 (+304)	25.18	25.02
344	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	TRUE	TRUE	dSQEALAPLVDVALK	95%	n+304 (+304), K+304 (+304)	42.63	25.00
345	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	TRUE	TRUE	gLFTVTk	95%	n+304 (+304), K+304 (+304)	36.92	25.00
346	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	TRUE	TRUE	vTVFQQPHYLQNFVQSTFNALPADQVK	95%	n+304 (+304), K+304 (+304)	33.70	25.00
347	seq=translation; coord=1:267887520..267894179:1; parent_transcript=GRMZM2G023289_T03; parent_gene=GRMZM2G023289	GRMZM2G023289_P03	TRUE	TRUE	vYIEQYEK	95%	n+304 (+304), K+304 (+304)	34.25	25.16
348	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	aGVALNcLEAPLDVDIPGGGR	95%	n+304 (+304), Carbamidomethyl (+57)	48.74	25.28
349	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	aISPEVLQASFNTTPEMEK	95%	n+304 (+304), K+304 (+304)	50.01	25.71
350	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	aWDLPEPDAAR	95%	n+304 (+304)	38.07	25.00
351	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	aYGGDGGAYYEWSPADLPMLAVASIGAAK	95%	n+304 (+304), K+304 (+304)	44.05	25.00
352	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	ayGGDGGAYYEWSPADLPMLAVASIGAAK	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	38.45	25.00
353	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	aYGGDGGAYYEWSPADLPMLAVASIGAAK	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.00	25.00
354	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	iADASGMEWFSIITTPNPVFSHLAGK	95%	n+304 (+304), K+304 (+304)	61.17	25.00
355	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	iADASGmEWFSIITTPNPVFSHLAGK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	30.06	25.35

356	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	iEGGSLFIVPR	95%	n+304 (+304)	37.00	25.02
357	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	IPASAAALPAPSPQDR	95%	n+304 (+304)	68.69	25.54
358	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	ISLAAGGLSLPSYSDSAk	95%	n+304 (+304), K+304 (+304)	63.14	25.26
359	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	IVSSQPASGIVk	95%	n+304 (+304), K+304 (+304)	49.28	25.13
360	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	rLDSEIFFAPSSN	95%	n+304 (+304)	33.78	25.00
361	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	vAYVLQGVGTcGLVLPEATk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	75.32	25.00
362	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	vQVVGPDGR	94%	n+304 (+304)	30.74	25.00
363	seq=translation; coord=6:34438543..34440508:1; parent_transcript=GRMZM2G034724_T01; parent_gene=GRMZM2G034724	GRMZM2G034724_P01	TRUE	TRUE	vVVLNTANLPLVR	95%	n+304 (+304)	39.99	25.00
364	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	aLLGESNEFVGDKVAYALSQGLk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	31.60	25.00
365	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	eLAAQPDVDGFLVGGASLkPEFIDIINAATVk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.72	25.00
366	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	kGGAFTGEVSAEMLVNLGVPPVVILGHSEr	95%	K+304 (+304), n+304 (+304)	28.95	25.00
367	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	qEFHVAAQNcWVvk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.34	25.76
368	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	qEFHVAAQNcWVvk	90%	Pyro-cmC (-17), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.24	25.00
369	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	tLNEGQVPPSDVVEVVSPYPVFLPVvk	95%	n+304 (+304), K+304 (+304)	30.04	25.00
370	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	tNASPEVAESTR	95%	n+304 (+304)	50.41	25.00
371	seq=translation; coord=3:17824258..17828243:1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	vAYALSQGLk	95%	n+304 (+304), K+304 (+304)	47.66	25.00
372	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G030784_T01; parent_gene=GRMZM2G030784	GRMZM2G030784_P01,GRMZM2G030784_P02	TRUE	TRUE	vIAcVGETLEQR	95%	n+304 (+304), Carbamidomethyl (+57)	64.10	25.00
373	parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	aAILVR	95%	n+304 (+304)	30.65	25.00

374	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	aETSPEDVGGMHAAVGILTER	95%	n+304 (+304)	69.85	25.00
375	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	aETSPEDVGGmHAAVGILTER	95%	n+304 (+304), Oxidation (+16)	60.40	25.00
376	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	eLVGQYk	91%	n+304 (+304), K+304 (+304)	28.16	25.92
377	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	eMQDIEFTVQENR	95%	n+304 (+304)	56.01	25.00
378	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	emQDIEFTVQENR	95%	n+304 (+304), Oxidation (+16)	62.98	25.00
379	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	fLDMFGNVVMDIPR	95%	n+304 (+304)	30.55	25.00
380	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	fLDmFGNVVMDIPR	95%	n+304 (+304), Oxidation (+16)	50.21	25.00
381	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	fLDMFGNVVmDIPR	95%	n+304 (+304), Oxidation (+16)	45.79	25.00
382	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	iAVDMVNEGLVEPR	95%	n+304 (+304)	71.96	26.15
383	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	kQLELAVLAVFNSWESPR	95%	K+304 (+304), n+304 (+304)	33.08	25.00
384	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	IVTIGGHVLR	95%	n+304 (+304)	52.11	25.00
385	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	nDTDLTASDLk	95%	n+304 (+304), K+304 (+304)	41.72	25.44
386	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	nLMPQAYDELVENcNILESHYk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	77.36	25.00
387	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	qLELAVLAVFNSWESPR	95%	n+304 (+304)	50.76	26.24
388	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	qMIMAPTLELR	95%	n+304 (+304)	33.90	25.54
389	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	rFLDMFGNVVMDIPR	95%	n+304 (+304)	57.75	25.24
390	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	sGAAVSMPGMMMDTVNLNLGNDEVAAGLAak	95%	n+304 (+304), K+304 (+304)	56.23	25.00
391	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	sLFEEK	88%	n+304 (+304), K+304 (+304)	26.76	25.44

392	seq=translation; coord=6:145987055..145992446:-1; parent_transcript=GRMZM2G306345_T03; parent_gene=GRMZM2G306345	GRMZM2G306345_P03,GRMZM2G306345_P04, GRMZM2G306345_P05	TRUE	TRUE	vLANADTPDDALTAR	95%	n+304 (+304)	84.22	25.00
393	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	aDLNVLPDDAQK	95%	n+304 (+304), K+304 (+304)	32.64	25.26
394	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	eLDYLVGAVANPk	95%	n+304 (+304), K+304 (+304)	30.50	26.64
395	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	eLDyLVGAVANPk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	30.61	25.00
396	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	faADAESk	91%	n+304 (+304), K+304 (+304)	28.16	25.15
397	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	faAGTEAIAk	95%	n+304 (+304), K+304 (+304)	38.84	25.61
398	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	gVSLLLPTDIVVADk	95%	n+304 (+304), K+304 (+304)	48.42	25.00
399	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	iGVIESLLak	95%	n+304 (+304), K+304 (+304)	47.54	25.00
400	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	iVPATAIPDDWMGLDVGPDATk	90%	n+304 (+304), K+304 (+304)	25.78	25.44
401	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	IAAALPEGGVLLLENVR	95%	n+304 (+304)	74.29	25.00
402	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	IAELTTTk	95%	n+304 (+304), K+304 (+304)	31.46	26.41
403	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	IELATSLIEk	92%	n+304 (+304), K+304 (+304)	26.06	25.00
404	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	sVGTLGGEADLk	92%	n+304 (+304), K+304 (+304)	28.48	25.84
405	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	tFDEALDTTk	95%	n+304 (+304), K+304 (+304)	56.77	26.36
406	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	vDILILGGGMIYTFyk	95%	n+304 (+304), K+304 (+304)	48.28	25.00
407	seq=translation; coord=5:84822215..84825942:1; parent_transcript=GRMZM2G382914_T01; parent_gene=GRMZM2G382914	GRMZM2G382914_P01,GRMZM2G382914_P02, GRMZM2G382914_P03,GRMZM2G382914_P04	TRUE	TRUE	vDILILGGGMIYTFyk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	32.75	25.00
408	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	aALWFWMNSVHGVVPQGFGATTR	95%	n+304 (+304)	44.52	25.00
409	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	aIGFDGLGDPGR	92%	n+304 (+304)	29.16	25.00

410	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633 seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	aYPGFAHGGSQVGK	95%	n+304 (+304), K+304 (+304)	36.48	25.26
411	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	dAVVAFK	89%	n+304 (+304), K+304 (+304)	27.99	26.40
412	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	fGYcGTTDEYcGDGcQSGPcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	32.75	25.00
413	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	fGycGTTDEYcGDGcQSGPcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	29.86	25.00
414	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	fGYcGTTDEYcGDGcQSGPcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	35.81	25.00
415	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633 seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	qLGVDPGPNLTc	95%	n+304 (+304), Carbamidomethyl (+57)	36.58	25.00
416	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633 seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633	GRMZM2G005633_P02	TRUE	TRUE	sAFLSAVk	94%	n+304 (+304), K+304 (+304)	28.65	25.00
417	seq=translation; coord=10:127370249..127371829:-1; parent_transcript=GRMZM2G005633_T02; parent_gene=GRMZM2G005633 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G005633_P02	TRUE	TRUE	sNAYcDPTK	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.36	25.00
418	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	aVVTVPAYFNDSQR	95%	n+304 (+304)	53.26	25.00
419	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	dAISGGSTQSmk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	39.25	25.00
420	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	dVVLLDVTPLSLGLETLGGMtK	95%	n+304 (+304), K+304 (+304)	60.98	25.00
421	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	dVVLLDVTPLSLGLETLGGMtK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	65.27	25.00
422	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	hIeATLSR	94%	n+304 (+304)	28.41	26.07
423	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	iPAVQELVR	87%	n+304 (+304)	25.59	25.00
424	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500	GRMZM2G001500_P02	TRUE	TRUE	iVDWLASNfK	95%	n+304 (+304), K+304 (+304)	47.90	26.53

425	seq=translation; coord=10:21722658..21727770:1; parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1;	GRMZM2G001500_P02	TRUE	TRUE	ISLSDLDEVILVGGSTR	95%	n+304 (+304)	51.28	25.39
426	parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1;	GRMZM2G001500_P02	TRUE	TRUE	mAEEVDDEAk	93%	Oxidation (+16), n+304 (+304), K+304 (+304)	28.33	25.00
427	parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1;	GRMZM2G001500_P02	TRUE	TRUE	mELSTLTQANISLPFITATADGPK	95%	n+304 (+304), K+304 (+304)	36.73	25.01
428	parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1;	GRMZM2G001500_P02	TRUE	TRUE	mVEEADk	94%	Oxidation (+16), n+304 (+304), K+304 (+304)	27.70	25.00
429	parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=10:21722658..21727770:1;	GRMZM2G001500_P02	TRUE	TRUE	nQADSVVYQTEk	95%	n+304 (+304), K+304 (+304)	64.79	25.00
430	parent_transcript=GRMZM2G001500_T02; parent_gene=GRMZM2G001500 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G001500_P02	TRUE	TRUE	vVGIDLGTTSAVAAMEGGKPTVVTNAEGAR	95%	n+304 (+304), K+304 (+304)	28.88	25.00
431	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	dDLRLPTDELVAQIk	93%	n+304 (+304), K+304 (+304)	26.34	25.00
432	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	dLVVTVQSAMGEEQIcAlk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.68	25.01
433	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	dLVVTVQSAmGEEQIcAlk	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304)	48.72	25.49
434	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	eGFESGk	86%	n+304 (+304), K+304 (+304)	26.19	25.89
435	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	IPDELVAQIk	95%	n+304 (+304), K+304 (+304)	32.90	25.37
436	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	tEYQLIDISEDGFVSLTSDGNTk	95%	n+304 (+304), K+304 (+304)	55.83	25.00
437	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	tEyQLIDISEDGFVSLTSDGNTk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	35.50	25.00
438	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	tEYQLIDISEDGFVSLTSDGNTKDDLr	95%	n+304 (+304), K+304 (+304)	38.48	25.00
439	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=2:209289645..209292956:-1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	tYPQAGTVR	89%	n+304 (+304)	26.78	25.00
440	parent_transcript=GRMZM2G113696_T01; parent_gene=GRMZM2G113696 seq=translation; coord=1:47172055..47173158:1;	GRMZM2G113696_P01,GRMZM2G144030_P01	TRUE	TRUE	tyPQAGTVR	95%	n+304 (+304), iTRAQ8plex (+304)	30.56	26.21
441	parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524 seq=translation; coord=1:47172055..47173158:1;	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	eSVTAIFk	95%	n+304 (+304), K+304 (+304)	34.17	26.23
442	parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	gAEAYLVANPDAYN	95%	n+304 (+304)	68.92	25.00

443	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	gAEAYLVANPDAYN	94%	n+304 (+304), iTRAQ8plex (+304)	31.33	25.00
444	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	gAEAYLVANPDAYN	95%	n+304 (+304), iTRAQ8plex (+304)	42.98	25.00
445	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	IEFLDADk	90%	n+304 (+304), K+304 (+304)	26.38	26.13
446	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	ILPGVEVk	95%	n+304 (+304), K+304 (+304)	37.96	25.00
447	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	nTLIEGGGIGVAIETATSHIK	95%	n+304 (+304), K+304 (+304)	96.76	25.00
448	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	qFNFTSVMPFsFMk	95%	n+304 (+304), K+304 (+304)	30.06	25.25
449	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	qFNFTSVMPFsFMk	93%	n+304 (+304), Oxidation (+16), K+304 (+304)	27.31	25.00
450	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	qFNFTSVMPFsFmk	92%	n+304 (+304), Oxidation (+16), K+304 (+304)	26.69	25.00
451	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	qFNFTSVMPFsFmk	94%	n+304 (+304), Oxidation (+16), Oxidation (+16), K+304 (+304)	28.55	25.00
452	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	vASHVVASAQPVEGDGGVGSVR	95%	n+304 (+304)	87.41	25.00
453	seq=translation; coord=1:47172055..47173158:1; parent_transcript=GRMZM2G112524_T02; parent_gene=GRMZM2G112524	GRMZM2G112524_P02,GRMZM2G112538_P01	TRUE	TRUE	vEPAAGGGSVVk	91%	n+304 (+304), K+304 (+304)	28.28	25.33
454	seq=translation; coord=5:9471280..9475018:-1; parent_transcript=GRMZM2G152466_T01; parent_gene=GRMZM2G152466	GRMZM2G152466_P01,GRMZM2G152466_P03, GRMZM2G153292_P01,GRMZM2G153292_P02, GRMZM2G153292_P03,GRMZM2G153292_P04, GRMZM2G153292_P08	TRUE	TRUE	aVFVDLEPTVIDEVR	95%	n+304 (+304)	64.68	25.99
455	seq=translation; coord=5:9471280..9475018:-1; parent_transcript=GRMZM2G152466_T01; parent_gene=GRMZM2G152466	GRMZM2G152466_P01,GRMZM2G152466_P03, GRMZM2G153292_P01,GRMZM2G153292_P02, GRMZM2G153292_P03,GRMZM2G153292_P04, GRMZM2G153292_P08	TRUE	TRUE	aYHEQLSVAEITNSAFEPSSMMak	95%	n+304 (+304), K+304 (+304)	36.64	25.00
456	seq=translation; coord=5:9471280..9475018:-1; parent_transcript=GRMZM2G152466_T01; parent_gene=GRMZM2G152466	GRMZM2G152466_P01,GRMZM2G152466_P03, GRMZM2G153292_P01,GRMZM2G153292_P02, GRMZM2G153292_P03,GRMZM2G153292_P04, GRMZM2G153292_P08	TRUE	TRUE	tIGGGDDAFNTFFSETGAGk	95%	n+304 (+304), K+304 (+304)	44.29	25.00
457	seq=translation; coord=1:278130299..278132841:1; parent_transcript=GRMZM2G328500_T01; parent_gene=GRMZM2G328500	GRMZM2G328500_P01,GRMZM2G328500_P02, GRMZM2G328500_P03	TRUE	TRUE	gAHLcILTEWDEFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.15	25.05
458	seq=translation; coord=1:278130299..278132841:1; parent_transcript=GRMZM2G328500_T01; parent_gene=GRMZM2G328500	GRMZM2G328500_P01,GRMZM2G328500_P02, GRMZM2G328500_P03	TRUE	TRUE	iSSVNAISALcEATGANVTEVAYAVGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.45	25.31
459	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518	GRMZM2G428518_P01	TRUE	TRUE	dEATYGVDR	93%	n+304 (+304)	28.09	25.00

460	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518 seq=translation; coord=6:91630823..91634799:1;	GRMZM2G428518_P01	TRUE	TRUE	gVLVSPVLEPGATTVEAYFPAGR	95%	n+304 (+304)	52.48	25.33
461	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518 seq=translation; coord=6:91630823..91634799:1;	GRMZM2G428518_P01	TRUE	TRUE	gVLVSPVLEPGATTVEAYFPAGR	95%	n+304 (+304), iTRAQ8plex (+304)	53.77	25.00
462	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518 seq=translation; coord=6:91630823..91634799:1;	GRMZM2G428518_P01	TRUE	TRUE	wIQLGAFYPFAR	94%	n+304 (+304)	31.70	26.13
463	seq=translation; coord=6:91630823..91634799:1; parent_transcript=GRMZM2G428518_T01; parent_gene=GRMZM2G428518 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G428518_P01	TRUE	TRUE	wIQLGAFyPFAR	93%	n+304 (+304), iTRAQ8plex (+304)	26.81	25.30
464	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	aAVPSGASTGVYEALRL	95%	n+304 (+304)	61.54	26.04
465	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	dPTAQTEIDNFMVQLDGTK	95%	n+304 (+304), K+304 (+304)	32.54	25.00
466	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	gNPTVEVDVFcSDGTFAR	92%	n+304 (+304), Carbamidomethyl (+57)	26.35	25.00
467	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	iEELGAIYVYAGAK	95%	n+304 (+304), K+304 (+304)	37.70	25.17
468	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	IAMQEFMILPTGAASFk	95%	n+304 (+304), K+304 (+304)	50.33	25.45
469	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	IAMQEFmILPTGAASFk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	30.84	25.44
470	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	mGVEVYHHLk	95%	n+304 (+304), K+304 (+304)	28.82	25.19
471	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	mTEEIGEQQVIGDILLVTNPTR	95%	n+304 (+304)	31.43	25.11
472	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	scNALLK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.91	25.15
473	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	sFVSEYPIVSIEDPFQDDWVHYAK	95%	n+304 (+304), K+304 (+304)	41.14	25.00
474	seq=translation; coord=1:125074232..125080812:-1; parent_transcript=GRMZM2G048371_T01; parent_gene=GRMZM2G048371 seq=translation; coord=1:125074232..125080812:-1;	GRMZM2G048371_P01,GRMZM2G048371_P03	TRUE	TRUE	sGETEDTFIADLAVGLSTGQIK	95%	n+304 (+304), K+304 (+304)	54.23	25.69
475	seq=translation; coord=5:18767810..18770458:1; parent_transcript=GRMZM2G087326_T01; parent_gene=GRMZM2G087326	GRMZM2G087326_P01	TRUE	TRUE	vNQIGSVTESIEAVk	95%	n+304 (+304), K+304 (+304)	44.52	25.76
476					IGDAMVWTWIEAWDELNPAGPAAGk	95%	n+304 (+304), K+304 (+304)	51.17	25.42

477	seq=translation; coord=8:134521573..134531903:1; parent_transcript=GRMZM2G067985_T04; parent_gene=GRMZM2G067985	GRMZM2G067985_P04,GRMZM2G067985_P05, GRMZM2G067985_P06,GRMZM2G067985_P09, GRMZM2G067985_P10,GRMZM2G067985_P12, GRMZM2G067985_P15,GRMZM2G104017_P02, GRMZM2G104017_P03,GRMZM2G104017_P04, GRMZM2G110378_P01,GRMZM2G110378_P02, GRMZM2G110378_P04,GRMZM2G110378_P05	TRUE	TRUE	eEYDESGPAIVHR	95%	n+304 (+304)	72.35	25.00
478	seq=translation; coord=8:134521573..134531903:1; parent_transcript=GRMZM2G067985_T04; parent_gene=GRMZM2G067985	GRMZM2G067985_P04,GRMZM2G067985_P05, GRMZM2G067985_P06,GRMZM2G067985_P09, GRMZM2G067985_P10,GRMZM2G067985_P12, GRMZM2G067985_P15,GRMZM2G104017_P02, GRMZM2G104017_P03,GRMZM2G104017_P04, GRMZM2G110378_P01,GRMZM2G110378_P02, GRMZM2G110378_P04,GRMZM2G110378_P05	TRUE	TRUE	IAYIALDYEQELETak	95%	n+304 (+304), K+304 (+304)	61.48	25.75
479	seq=translation; coord=8:134521573..134531903:1; parent_transcript=GRMZM2G067985_T04; parent_gene=GRMZM2G067985	GRMZM2G067985_P04,GRMZM2G067985_P05, GRMZM2G067985_P06,GRMZM2G067985_P09, GRMZM2G067985_P10,GRMZM2G067985_P12, GRMZM2G067985_P15,GRMZM2G104017_P02, GRMZM2G104017_P03,GRMZM2G104017_P04, GRMZM2G110378_P01,GRMZM2G110378_P02, GRMZM2G110378_P04,GRMZM2G110378_P05	TRUE	TRUE	IayIALDYEQELETak	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	39.89	25.00
480	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	aNAGcNGGLMDYAFQYIAk	90%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.59	25.00
481	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	aVAHQPVSAIEASGSHFQFYSEGVSFGR	95%	n+304 (+304)	41.62	25.00
482	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	cGTELDHGVAAVGYGVTADGtK	89%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	25.15	25.00
483	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	dQGQcGScWAFSTIAAVEGINAik	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	50.59	25.00
484	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	dVPASVDWR	93%	n+304 (+304)	29.71	25.00
485	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	eGHcGIAMEASYPVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	65.01	25.00
486	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	eGHcGIaMEASYPVk	95%	n+304 (+304), Carbamidomethyl (+57), Oxidation (+16), K+304 (+304)	34.38	25.00
487	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	fGDMTADEFR	95%	n+304 (+304)	35.11	25.00
488	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217	GRMZM2G456217_P01	TRUE	TRUE	fGDmTADEFR	92%	n+304 (+304), Oxidation (+16)	28.90	25.00

489	seq=translation; coord=1:205422404..205424254:-1; parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	gAVTDVvk	87%	n+304 (+304), K+304 (+304)	28.48	28.19
490	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	hGGVAAEDAYPYR	95%	n+304 (+304)	49.45	25.00
491	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	hGGVAAEDAYPyR	91%	n+304 (+304), iTRAQ8plex (+304)	28.38	25.00
492	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	kSPAPVVTIDGYEDVPANDESALK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	40.73	25.00
493	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	IIHEFNr	89%	n+304 (+304)	25.01	25.00
494	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	nSWGPEWGEk	95%	n+304 (+304), K+304 (+304)	43.94	25.00
495	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	qGSSASASSFYADAR	93%	n+304 (+304)	29.43	25.00
496	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	qGSSASASSFMyADAR	95%	Pyro-cmC (-17), n+304 (+304), iTRAQ8plex (+304)	37.89	25.00
497	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=1:205422404..205424254:-1;	GRMZM2G456217_P01	TRUE	TRUE	sPAPVVTIDGYEDVPANDESALK	95%	n+304 (+304), K+304 (+304)	63.46	25.31
498	parent_transcript=GRMZM2G456217_T01; parent_gene=GRMZM2G456217 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G456217_P01	TRUE	TRUE	vHAVVDEdGSSHDEL	95%	n+304 (+304)	46.86	25.00
499	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aAEEANVYNdLVk	95%	n+304 (+304), K+304 (+304)	43.67	25.21
500	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aDDAAHFLdVIR	95%	n+304 (+304)	50.80	25.02
501	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aFMTADLPHELlELk	94%	n+304 (+304), K+304 (+304)	25.67	25.15
502	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aHMGIFTELGVLYAR	95%	n+304 (+304)	66.61	25.28
503	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aHMGIFTELGVLYAR	95%	n+304 (+304), iTRAQ8plex (+304)	29.40	25.80
504	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aNLPGAENLVVQR	95%	n+304 (+304)	53.25	26.33
505	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	aVHFYLQEHpDLINDMLNLVLR	95%	n+304 (+304)	37.60	25.56
506	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576	GRMZM2G057576_P01	TRUE	TRUE	eAAELAAESpQGllR	95%	n+304 (+304)	56.86	26.27

507	seq=translation; coord=10:1135114..1145295:1; parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	eALTLTSLGIAPQVF/TFTHVTESEK	95%	n+304 (+304), K+304 (+304)	29.03	25.00
508	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	eGLVSEAIESFIR	95%	n+304 (+304)	31.75	25.00
509	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	eVcFACVDAEEFR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	64.97	25.00
510	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	fGFVPDLTHLYLTNNMLR	95%	n+304 (+304)	34.23	25.00
511	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	fNLNVQAVDVLDDNIR	95%	n+304 (+304)	62.18	25.21
512	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	fQELFAQTk	95%	n+304 (+304), K+304 (+304)	38.14	25.00
513	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	gcFSELIALMESGLGLER	95%	n+304 (+304), Carbamidomethyl (+57)	44.20	25.00
514	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	gNMQLFSVDQQR	95%	n+304 (+304)	35.52	25.00
515	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	gQcDDELINVTNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	41.37	25.00
516	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	iiYAFISNWAK	95%	n+304 (+304), K+304 (+304)	30.48	25.40
517	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	INAFESLELSR	95%	n+304 (+304)	41.82	25.00
518	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	qVGYPDYLFLLQTILR	95%	n+304 (+304)	39.16	25.44
519	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	qVGyTPDYLFLLQTILR	95%	n+304 (+304), iTRAQ8plex (+304)	34.79	25.00
520	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	rDPTLAVVAYR	89%	n+304 (+304)	25.20	25.13
521	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	sHQMPEQVFWk	95%	n+304 (+304), K+304 (+304)	33.03	26.21
522	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	tANLANNQIINYR	95%	n+304 (+304)	55.34	25.90
523	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	tVDNDLALK	95%	n+304 (+304), K+304 (+304)	37.70	26.41
524	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576	GRMZM2G057576_P01	TRUE	TRUE	vDGELIFAYAK	95%	n+304 (+304), K+304 (+304)	37.24	25.54

525	seq=translation; coord=10:1135114..1145295:1; parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	vEEDAVWSQVak	95%	n+304 (+304), K+304 (+304)	36.47	25.93
526	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	vLQPENeyR	88%	n+304 (+304)	26.35	25.00
527	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	vNPGNAPLVVGQLLDDeCPEDFIK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	64.03	25.42
528	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	vVGNEPSTLIcFASK	95%	Carbamidomethyl (+57), K+304 (+304)	30.11	25.80
529	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=10:1135114..1145295:1;	GRMZM2G057576_P01	TRUE	TRUE	wLVLIgiAPGAPERQLVk	95%	n+304 (+304), K+304 (+304)	31.20	25.00
530	parent_transcript=GRMZM2G057576_T01; parent_gene=GRMZM2G057576 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G057576_P01	TRUE	TRUE	yKEAAELAAESpQGLLR	95%	n+304 (+304), K+304 (+304)	58.37	26.01
531	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	aEQMLINNPsr	95%	n+304 (+304)	42.17	25.00
532	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	dSEMFNEWTLElk	95%	n+304 (+304), K+304 (+304)	30.60	25.00
533	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	eYLPITGLAEFNk	95%	n+304 (+304), K+304 (+304)	31.95	25.56
534	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	eYLPITGLAEFNk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	33.96	25.00
535	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	gTPGDWSHIik	95%	n+304 (+304), K+304 (+304)	36.52	26.52
536	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	iSMAGLSMR	95%	n+304 (+304)	40.37	25.00
537	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	lIFGADSPAIQENR	95%	n+304 (+304)	63.48	25.74
538	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	mFVADGGELLMAQSYak	95%	n+304 (+304), K+304 (+304)	55.63	25.00
539	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	mFVADGGELLmAQSYak	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	47.72	25.22
540	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	qEYHIYMTSDGR	91%	Pyro-cmC (-17), n+304 (+304)	27.15	25.00
541	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712 seq=translation; coord=3:195313538..195319148:1;	GRMZM2G094712_P01	TRUE	TRUE	qIGMFTFTGLNSEQVAFMR	95%	n+304 (+304)	85.83	25.00
542	parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	qQLFNAlk	95%	n+304 (+304), K+304 (+304)	37.73	26.35

543	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	rAEQMLINNP SR	91%	n+304 (+304)	27.19	26.23
544	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	sLLPFFDSAYQGFASGSLDK	95%	n+304 (+304), K+304 (+304)	48.61	25.56
545	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	sLLPFFDSAYQGFASGSLDKDAQSVR	95%	n+304 (+304), K+304 (+304)	52.96	25.00
546	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	tEEGkPLVLNVVR	95%	n+304 (+304), K+304 (+304)	29.98	25.00
547	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	tIYIPQPTWGNHPk	92%	n+304 (+304), K+304 (+304)	28.23	25.49
548	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	tVPHLADAIHAAVTQLk	95%	n+304 (+304), K+304 (+304)	31.69	25.00
549	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	vATVQCcLSGTGSLR	95%	n+304 (+304), Carbamidomethyl (+57)	47.32	25.00
550	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	vFTLSGLNVR	95%	n+304 (+304)	32.61	25.00
551	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	vGGEFLAR	88%	n+304 (+304)	26.95	26.29
552	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	vkEYLPITGLAEFNk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	28.18	25.00
553	seq=translation; coord=3:195313538..195319148:1; parent_transcript=GRMZM2G094712_T01; parent_gene=GRMZM2G094712	GRMZM2G094712_P01	TRUE	TRUE	vNLGVGAYR	88%	n+304 (+304)	26.20	25.00
554	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	eFAPSIPEk	94%	n+304 (+304), K+304 (+304)	30.85	26.71
555	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	eLVSDDEWLNGEFTTVQQR	91%	n+304 (+304)	25.06	25.00
556	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	gAAIik	92%	n+304 (+304), K+304 (+304)	28.69	27.28
557	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	iVQGLPIDEF SR	95%	n+304 (+304)	45.26	25.44
558	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	kMDATAQELTEEK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	39.66	25.53
559	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	INVQVSDVk	95%	n+304 (+304), K+304 (+304)	30.61	26.60
560	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359	GRMZM2G415359_P02	TRUE	TRUE	mDATAQELTEEK	95%	n+304 (+304), K+304 (+304)	40.59	25.00

561	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=1:231336278..231341950:-1;	GRMZM2G415359_P02	TRUE	TRUE	mELVDAAFPLLk	95%	n+304 (+304), K+304 (+304)	34.48	25.75
562	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=1:231336278..231341950:-1;	GRMZM2G415359_P02	TRUE	TRUE	mELVDAAFPLLk	90%	Oxidation (+16), n+304 (+304), K+304 (+304)	26.20	25.63
563	seq=translation; coord=1:231336278..231341950:-1; parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=1:231336278..231341950:-1;	GRMZM2G415359_P02	TRUE	TRUE	sQASALEAHAAPNck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.27	25.02
564	parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=1:231336278..231341950:-1;	GRMZM2G415359_P02	TRUE	TRUE	vLVTGAAGQIGYALVPMIAR	95%	n+304 (+304)	50.37	25.00
565	parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=1:231336278..231341950:-1;	GRMZM2G415359_P02	TRUE	TRUE	vLVTGAAGQIGyALVPMIAR	95%	n+304 (+304), iTRAQ8plex (+304)	35.40	25.00
566	parent_transcript=GRMZM2G415359_T02; parent_gene=GRMZM2G415359 seq=translation; coord=6:87119198..87122939:1;	GRMZM2G415359_P02	TRUE	TRUE	vLVVANPANTNALILk	95%	n+304 (+304), K+304 (+304)	61.82	25.00
567	parent_transcript=GRMZM2G027995_T01; parent_gene=GRMZM2G027995 seq=translation; coord=6:87119198..87122939:1;	GRMZM2G027995_P01,GRMZM2G027995_P02	TRUE	TRUE	dQIYDIFQLLPsk	95%	n+304 (+304), K+304 (+304)	40.66	25.15
568	parent_transcript=GRMZM2G027995_T01; parent_gene=GRMZM2G027995 seq=translation; coord=6:87119198..87122939:1;	GRMZM2G027995_P01,GRMZM2G027995_P02	TRUE	TRUE	gFkDQIYDIFQLLPsk	94%	n+304 (+304), K+304 (+304), K+304 (+304)	25.32	25.00
569	parent_transcript=GRMZM2G027995_T01; parent_gene=GRMZM2G027995 seq=translation; coord=9:87062457..87064566:1;	GRMZM2G027995_P01,GRMZM2G027995_P02	TRUE	TRUE	iLASGVHVVVGTPGR	95%	n+304 (+304)	41.55	25.31
570	parent_transcript=GRMZM2G153541_T06; parent_gene=GRMZM2G153541 seq=translation; coord=9:87062457..87064566:1;	GRMZM2G153541_P06	TRUE	TRUE	mVPTkPMVVETFSQYPPLGR	95%	n+304 (+304), K+304 (+304)	37.98	25.00
571	parent_transcript=GRMZM2G153541_T06; parent_gene=GRMZM2G153541 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G153541_P06	TRUE	TRUE	tHINIVIGHVDSGk	95%	n+304 (+304), K+304 (+304)	27.76	25.56
572	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	aMENEMLLR	95%	n+304 (+304)	32.36	25.00
573	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	aSALLVDFFDk	95%	n+304 (+304), K+304 (+304)	44.72	25.88
574	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	dGAFEDVLR	95%	n+304 (+304)	40.63	25.00
575	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	dTVGQYESHMAFTMPGLYR	95%	n+304 (+304)	44.52	25.00
576	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	eSMYPLLNFLR	93%	n+304 (+304)	29.70	25.05
577	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	fNIVSPGADLSIYFPYTESHK	95%	n+304 (+304), K+304 (+304)	61.23	25.48
578	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908	GRMZM2G152908_P01	TRUE	TRUE	gMLQPHQIIAEYNNAIPEAER	95%	n+304 (+304)	47.03	25.00

579	seq=translation; coord=9:122220190..122226863:-1; parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	gMTMMLNDR	91%	n+304 (+304)	28.10	25.00
580	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	iGDSLSAHPNELVAVFTR	92%	n+304 (+304)	27.90	25.91
581	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	IFHDkESMYPLLNFLR	94%	n+304 (+304), K+304 (+304)	26.77	25.75
582	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	IkDGAfEDVLR	95%	n+304 (+304), K+304 (+304)	37.59	26.00
583	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	ILPDATGTTcGQR	95%	n+304 (+304), Carbamidomethyl (+57)	38.44	25.00
584	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	nLTGLVELYGR	95%	n+304 (+304)	40.54	25.00
585	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	qcGLDITPk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.24	25.53
586	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	tMASTVPLAVEGEPSSk	95%	n+304 (+304), K+304 (+304)	30.39	25.28
587	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	vLGTEHcHILR	95%	n+304 (+304), Carbamidomethyl (+57)	38.99	25.11
588	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	vNVSELAVEELR	95%	n+304 (+304)	65.16	25.98
589	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=9:122220190..122226863:-1;	GRMZM2G152908_P01	TRUE	TRUE	vPEYLQFk	95%	n+304 (+304), K+304 (+304)	30.98	25.48
590	parent_transcript=GRMZM2G152908_T01; parent_gene=GRMZM2G152908 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G152908_P01	TRUE	TRUE	yLEMLYAlk	95%	n+304 (+304), K+304 (+304)	37.58	25.88
591	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G162359_P01	TRUE	TRUE	aDNYGGFMIWDR	95%	n+304 (+304)	42.11	25.00
592	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G162359_P01	TRUE	TRUE	aLDTGIFER	95%	n+304 (+304)	43.91	25.00
593	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G162359_P01	TRUE	TRUE	eAcDSGLYTMVIMSFLDVyGPQR	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)	27.93	25.00
594	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G162359_P01	TRUE	TRUE	fYVGLTASEmTHGWVHPk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	29.46	25.00
595	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359 seq=translation; coord=7:10651271..10653006:1;	GRMZM2G162359_P01	TRUE	TRUE	gSPADRYDVLALeLAK	95%	n+304 (+304), K+304 (+304)	34.20	25.66
596	parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	iYDDADcEAR	95%	n+304 (+304), Carbamidomethyl (+57)	48.61	25.00

597	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	nVYDVAPSAQk	95%	n+304 (+304), K+304 (+304)	45.95	25.51
598	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	rPFGDAWLDGVDLFLER	95%	n+304 (+304)	58.09	25.00
599	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	wHLAWDEWTAAYPATR	95%	n+304 (+304)	62.16	25.00
600	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	wHLAWDEWTAAYPATR	95%	n+304 (+304), iTRAQ8plex (+304)	29.97	25.00
601	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	yDVLALELAK	95%	n+304 (+304), K+304 (+304)	33.41	25.31
602	seq=translation; coord=7:10651271..10653006:1; parent_transcript=GRMZM2G162359_T01; parent_gene=GRMZM2G162359	GRMZM2G162359_P01	TRUE	TRUE	yDVLALELAK	94%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	25.37	25.00
603	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	aVDVTGPDGSFVR	95%	n+304 (+304)	53.84	25.01
604	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	cGEPGHMAR	95%	Carbamidomethyl (+57), n+304 (+304)	30.80	25.00
605	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	dcPSADGGGGYGGGGYGGGGYGGGGGGGGGcFk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	34.57	25.00
606	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	dcSSGGGGYGGGGGGGGGcYnCGQAGHMAR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304),	174.05	25.00
607	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	dcSSGGGGYGGGGGGGGGcYnCGQAGHMAR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), iTRAQ8plex (+304), Carbamidomethyl (+57) n+304 (+304),	34.83	25.00
608	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	dcSSGGGGYGGGGGGGGGcYnCGQAGHmAR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Oxidation (+16) n+304 (+304),	39.47	25.00
609	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	dcSSGGGGYGGGGGGGGGcYnCGQAGHmAR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), iTRAQ8plex (+304), Carbamidomethyl (+57), Oxidation (+16)	27.90	25.00
610	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	fGGGGGGGGDR	95%	n+304 (+304)	46.31	25.00
611	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	scYNcGEAGHIAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	74.37	25.00

612	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768	GRMZM2G389768_P01	TRUE	TRUE	scyNcGEAGHIAR	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304), Carbamidomethyl (+57) n+304 (+304),	37.07	25.00
613	seq=translation; coord=4:238121524..238123238:-1; parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768 seq=translation; coord=4:238121524..238123238:-1;	GRMZM2G389768_P01	TRUE	TRUE	sGGGGGPGAcYk	95%	Carbamidomethyl (+57), n+304 (+304)	38.82	25.00
614	parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768 seq=translation; coord=4:238121524..238123238:-1;	GRMZM2G389768_P01	TRUE	TRUE	sLAEGEEVEFSVSEGDGDR	95%	n+304 (+304)	102.09	25.00
615	parent_transcript=GRMZM2G389768_T01; parent_gene=GRMZM2G389768 seq=translation; coord=4:238121524..238123238:-1;	GRMZM2G389768_P01	TRUE	TRUE	sYGGSWGGGR	90%	n+304 (+304)	27.23	25.00
616	seq=translation; coord=8:170762955..170767680:-1; parent_transcript=GRMZM5G833389_T02; parent_gene=GRMZM5G833389	GRMZM5G833389_P02	TRUE	TRUE	aLEIAEK	91%	n+304 (+304), K+304 (+304)	28.16	25.92
617	seq=translation; coord=8:170762955..170767680:-1; parent_transcript=GRMZM5G833389_T02; parent_gene=GRMZM5G833389	GRMZM5G833389_P02	TRUE	TRUE	aLEYADFDNFDR	95%	n+304 (+304)	53.24	25.00
618	seq=translation; coord=8:170762955..170767680:-1; parent_transcript=GRMZM5G833389_T02; parent_gene=GRMZM5G833389	GRMZM5G833389_P02	TRUE	TRUE	eSFESGTLHLIGLLSDGGVHSR	95%	n+304 (+304)	61.07	25.69
619	seq=translation; coord=8:170762955..170767680:-1; parent_transcript=GRMZM5G833389_T02; parent_gene=GRMZM5G833389	GRMZM5G833389_P02	TRUE	TRUE	iILDAVEQVGGIYLVTDHGHNAEDMVk	94%	n+304 (+304), K+304 (+304)	25.53	25.00
620	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	aFLQPSHYDADEVMFVk	94%	n+304 (+304), K+304 (+304)	25.06	25.00
621	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	eGEGVIVLLR	95%	n+304 (+304)	43.22	26.09
622	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	fTHELLEDAVGNYR	95%	n+304 (+304)	32.46	25.00
623	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	gEITTASEEQIR	95%	n+304 (+304)	59.98	25.00
624	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	gSMMAFSYNTR	95%	n+304 (+304)	35.72	25.00
625	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	iAIVLk	94%	n+304 (+304), K+304 (+304)	27.89	25.00
626	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	ILAFGADEEQQVDR	95%	n+304 (+304)	64.97	25.00
627	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	ILDMDVGLANIAR	88%	n+304 (+304)	27.77	26.50
628	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703	GRMZM2G026703_P01	TRUE	TRUE	vAELEAAPR	95%	n+304 (+304)	34.89	27.43

629	seq=translation; coord=1:287062939..287065014:-1; parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703 seq=translation; coord=1:287062939..287065014:-1;	GRMZM2G026703_P01	TRUE	TRUE	vFLAGNSALQk	95%	n+304 (+304), K+304 (+304)	40.15	25.53
630	parent_transcript=GRMZM2G026703_T01; parent_gene=GRMZM2G026703 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G026703_P01	TRUE	TRUE	vVMLLSPVVSTSGR	95%	n+304 (+304)	47.97	25.54
631	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	dLTEVTHk	95%	n+304 (+304), K+304 (+304)	36.22	25.00
632	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	gGESIYGLk	92%	n+304 (+304), K+304 (+304)	28.53	26.64
633	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	hTGPGLLSMANAGR	95%	n+304 (+304)	39.18	25.00
634	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	iIPSFMLQGGDFLTGDGR	95%	n+304 (+304)	41.94	25.00
635	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	iVMGLFGk	92%	n+304 (+304), K+304 (+304)	28.60	25.00
636	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=5:59268337..59270968:1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	vLSGMDVVYk	95%	n+304 (+304), K+304 (+304)	40.14	25.47
637	parent_transcript=GRMZM2G084521_T01; parent_gene=GRMZM2G084521 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G084521_P01,GRMZM2G084521_P03	TRUE	TRUE	vYFDIEIDGkPAGR	92%	n+304 (+304), K+304 (+304)	27.63	26.12
638	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	dALAESDk	90%	n+304 (+304), K+304 (+304)	27.90	25.25
639	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	dMGYNVSMADSTSR	95%	n+304 (+304)	72.53	25.00
640	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	fDPDFIDIR	95%	n+304 (+304)	34.18	25.00
641	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	fEDPAEGEALVGK	95%	n+304 (+304), K+304 (+304)	43.05	25.00
642	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	fTMLQTWVPR	95%	n+304 (+304)	32.82	25.00
643	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	kVSGPVVVADGMGGAAMYELVR	95%	K+304 (+304), n+304 (+304)	56.35	25.00
644	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	IAADTPLLTGQR	95%	n+304 (+304)	34.65	26.52
645	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857 seq=translation; coord=4:235443029..235449150:-1;	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	IAEMPADSGYPAYLAAR	95%	n+304 (+304)	74.50	25.00
646	parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	IGDLFYR	92%	n+304 (+304)	28.59	25.00

647	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	IYDLTTGFR	94%	n+304 (+304)	30.30	25.00
648	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	sGDVYIPR	95%	n+304 (+304)	37.38	25.00
649	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	tTLVANTSNNMPVAAR	95%	n+304 (+304)	59.66	25.91
650	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	vGHDNLIGEIIR	95%	n+304 (+304)	39.63	26.53
651	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	vLDALFPSVLGGTcAIPGAFGcGk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	44.96	25.91
652	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	vSGPVVVADGMGGAAMYELVR	95%	n+304 (+304)	69.24	25.00
653	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	vTTFEDSEK	95%	n+304 (+304), K+304 (+304)	43.80	25.60
654	seq=translation; coord=4:235443029..235449150:-1; parent_transcript=GRMZM2G421857_T01; parent_gene=GRMZM2G421857	GRMZM2G421857_P01,GRMZM2G421857_P02	TRUE	TRUE	ySNSEAVVYVGcGER	93%	n+304 (+304), Carbamidomethyl (+57)	29.56	25.00
655	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	eNQTIQSVLGTSTR	95%	n+304 (+304)	58.71	25.40
656	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	gIPSLVAIGPTGQTVSR	95%	n+304 (+304)	49.21	25.26
657	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	IEILA EK	90%	n+304 (+304), K+304 (+304)	25.56	25.00
658	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	mPWLAI PQGDIk	95%	n+304 (+304), K+304 (+304)	37.33	25.00
659	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	mPWLAVPFSDSEGR	95%	n+304 (+304)	59.36	25.00
660	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	nEEAFNEYFAk	95%	n+304 (+304), K+304 (+304)	34.82	25.00
661	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	sFEVV FASADR	95%	n+304 (+304)	34.37	25.00
662	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	sFEVV FASADRNEEAFNEYFAk	95%	n+304 (+304), K+304 (+304)	32.00	25.00
663	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324	GRMZM2G048324_P01	TRUE	TRUE	sQLMIHGADAPFTEER	95%	n+304 (+304)	36.22	25.00

664	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324 seq=translation; coord=1:70424654..70429257:1;	GRMZM2G048324_P01	TRUE	TRUE	tVLVYFSak	95%	n+304 (+304), K+304 (+304)	45.12	25.69
665	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324 seq=translation; coord=1:70424654..70429257:1;	GRMZM2G048324_P01	TRUE	TRUE	vPISELEGk	95%	n+304 (+304), K+304 (+304)	31.02	26.13
666	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324 seq=translation; coord=1:70424654..70429257:1;	GRMZM2G048324_P01	TRUE	TRUE	vPVSELVGk	95%	n+304 (+304), K+304 (+304)	46.28	25.00
667	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324 seq=translation; coord=1:70424654..70429257:1;	GRMZM2G048324_P01	TRUE	TRUE	vSGIPHLVILDak	95%	n+304 (+304), K+304 (+304)	34.29	25.00
668	seq=translation; coord=1:70424654..70429257:1; parent_transcript=GRMZM2G048324_T01; parent_gene=GRMZM2G048324 seq=translation; coord=7:24410021..24413947:-1;	GRMZM2G048324_P01	TRUE	TRUE	yFELSSLPTLVIGPDGk	95%	n+304 (+304), K+304 (+304)	40.62	25.00
669	seq=translation; coord=7:24410021..24413947:-1; parent_transcript=GRMZM2G358059_T01; parent_gene=GRMZM2G358059 seq=translation; coord=7:24410021..24413947:-1;	GRMZM2G358059_P01	TRUE	TRUE	aAFDEAEk	93%	n+304 (+304), K+304 (+304)	28.26	26.00
670	seq=translation; coord=7:24410021..24413947:-1; parent_transcript=GRMZM2G358059_T01; parent_gene=GRMZM2G358059 seq=translation; coord=7:24410021..24413947:-1;	GRMZM2G358059_P01	TRUE	TRUE	fGGDTSYSIMFGPDicGYSTk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	59.50	25.00
671	seq=translation; coord=7:24410021..24413947:-1; parent_transcript=GRMZM2G358059_T01; parent_gene=GRMZM2G358059 seq=translation; coord=7:24410021..24413947:-1;	GRMZM2G358059_P01	TRUE	TRUE	kFGGDTSYSIMFGPDicGYSTk	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.83	25.00
672	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	ILGGGDVDQk	87%	n+304 (+304), K+304 (+304)	26.82	26.29
673	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	aDGDTVk	93%	n+304 (+304), K+304 (+304)	30.85	27.15
674	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	aINGDVSTLASDGsk	95%	n+304 (+304), K+304 (+304)	33.45	25.87
675	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	aPLSVYLIDAVLLPR	95%	n+304 (+304)	55.34	25.00
676	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	aPLSVyLIDAVLLPR	95%	n+304 (+304), iTRAQ8plex (+304)	34.94	25.00
677	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	aQGSDDGIVNITVFPDGR	95%	n+304 (+304)	87.74	25.26
678	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	eQPYYIAVLQVR	95%	n+304 (+304)	32.30	25.59
679	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	eQPYYIAVLQVR	90%	n+304 (+304), iTRAQ8plex (+304)	26.48	25.09
680	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610 seq=translation; coord=9:36545543..36547162:1;	GRMZM2G144610_P01	TRUE	TRUE	eQPYYIAVLQVR	90%	n+304 (+304), iTRAQ8plex (+304)	26.74	25.28
681	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	iSSASASAATVTK	95%	n+304 (+304), K+304 (+304)	35.23	25.74

682	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	IGSIQGGFAQAASLYQASGK	95%	n+304 (+304), K+304 (+304)	65.90	25.08
683	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	IQLDDLQR	92%	n+304 (+304)	30.59	26.77
684	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	sTVTVLAVDNAVMAR	95%	n+304 (+304)	69.28	25.47
685	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	sTVTVLAVDNAVMAR	95%	n+304 (+304), Oxidation (+16)	29.67	25.40
686	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	tLLDkAPLSVYLIDAVLLPR	95%	n+304 (+304), K+304 (+304)	38.70	25.00
687	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	vAAFTPSGSPSNR	89%	n+304 (+304)	26.95	25.47
688	seq=translation; coord=9:36545543..36547162:1; parent_transcript=GRMZM2G144610_T01; parent_gene=GRMZM2G144610	GRMZM2G144610_P01	TRUE	TRUE	viYLHVLLDYFDAAK	95%	n+304 (+304), K+304 (+304)	29.45	25.00
689	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	aVLDAATIAGLQPLR	95%	n+304 (+304)	63.07	25.48
690	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	fEHIDMSEK	93%	n+304 (+304), K+304 (+304)	27.22	25.00
691	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	mDTDDAPSDPAVASDVNMQEPK	95%	n+304 (+304), K+304 (+304)	61.61	25.00
692	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	rEEFEQISASVLER	95%	n+304 (+304)	35.21	25.20
693	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	tFTSTQLLAMVLSNLK	95%	n+304 (+304), K+304 (+304)	35.68	25.00
694	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	vGDPIELR	95%	n+304 (+304)	33.67	26.69
695	seq=translation; coord=6:130343970..130350095:1; parent_transcript=GRMZM2G023232_T01; parent_gene=GRMZM2G023232	GRMZM2G023232_P01	TRUE	TRUE	vLTFFK	92%	n+304 (+304), K+304 (+304)	25.71	25.00
696	seq=translation; coord=5:32089861..32094927:-1; parent_transcript=AC233949.1_FGT004; parent_gene=AC233949.1_FG004	AC233949.1_FGP004	TRUE	TRUE	aPHFEESMK	95%	n+304 (+304), K+304 (+304)	29.69	25.00
697	seq=translation; coord=5:32089861..32094927:-1; parent_transcript=AC233949.1_FGT004; parent_gene=AC233949.1_FG004	AC233949.1_FGP004	TRUE	TRUE	dFSTAILER	94%	n+304 (+304)	30.96	25.00
698	seq=translation; coord=5:32089861..32094927:-1; parent_transcript=AC233949.1_FGT004; parent_gene=AC233949.1_FG004	AC233949.1_FGP004	TRUE	TRUE	dTicIVLADETCEEPk	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	27.64	25.00

699	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	aTPAVPVGGcYR	95%	n+304 (+304), Carbamidomethyl (+57)	31.29	25.00
700	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	aVLDSVQAcIFTGYWEDVGTIK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.37	25.24
701	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	dALLDLLK	92%	n+304 (+304), K+304 (+304)	26.64	25.00
702	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	dSVMMGADTYETEEASK	95%	n+304 (+304), K+304 (+304)	55.81	25.00
703	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	fDFYDPK	91%	n+304 (+304), K+304 (+304)	25.32	25.00
704	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	fWVLEDYYSHK	95%	n+304 (+304), K+304 (+304)	72.39	25.74
705	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	gIQEADHPEEGYYIR	95%	n+304 (+304)	47.27	25.00
706	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	hVEDDADITIScAPVDESR	95%	n+304 (+304), Carbamidomethyl (+57)	33.70	25.00
707	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	iFVMSQFNSTSLNR	95%	n+304 (+304)	58.13	25.00
708	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	mNYMELVQk	95%	n+304 (+304), K+304 (+304)	46.75	25.25
709	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	nATINDGSVI	95%	n+304 (+304)	35.43	25.00
710	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	nVVITNSk	93%	n+304 (+304), K+304 (+304)	29.92	26.62
711	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	sFFDANLALTEQPSk	95%	n+304 (+304), K+304 (+304)	33.05	25.77
712	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	sGIVVILK	95%	n+304 (+304), K+304 (+304)	39.65	25.00
713	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	siDNIVILSGDQLYR	95%	n+304 (+304)	65.65	25.76
714	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	tPFFTAPR	91%	n+304 (+304)	25.21	25.00
715	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	vAATTQcILTSDAcPETLHSQTQSSR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	69.35	25.00
716	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899	GRMZM2G429899_P01	TRUE	TRUE	vETNFLSYAIDDAQk	95%	n+304 (+304), K+304 (+304)	66.06	25.83

717	seq=translation; coord=3:216414684..216424048:-1; parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899 seq=translation; coord=3:216414684..216424048:-1;	GRMZM2G429899_P01	TRUE	TRUE	vSAIILGGGTGSQLPFLTSTR	95%	n+304 (+304)	32.25	25.89
718	parent_transcript=GRMZM2G429899_T01; parent_gene=GRMZM2G429899 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G429899_P01	TRUE	TRUE	yPYLASMGIVFk	95%	n+304 (+304), K+304 (+304)	39.71	25.50
719	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	aAGNEVIGIDLGTNScVSVMEGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.60	25.00
720	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	aLIDIR	95%	n+304 (+304)	30.25	25.00
721	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	dkIPAEVASEIEAAIADLR	95%	n+304 (+304), K+304 (+304)	60.29	25.00
722	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	eTAESYLgk	95%	n+304 (+304), K+304 (+304)	34.13	25.97
723	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	eVDEVLVGGMTR	95%	n+304 (+304)	45.08	25.00
724	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	fESLVHNLIER	95%	n+304 (+304)	54.54	26.40
725	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	hLNITLTR	95%	n+304 (+304)	33.56	25.39
726	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	iPAEVASEIEAAIADLR	95%	n+304 (+304)	47.45	25.92
727	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	mVQEAEHLAQk	95%	n+304 (+304), K+304 (+304)	39.30	25.74
728	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	qAVTNPQNTFFGTk	95%	n+304 (+304), K+304 (+304)	37.07	25.68
729	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	qEMASDDIEk	95%	n+304 (+304), K+304 (+304)	55.41	25.00
730	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	qYSPSQVGAFVLtk	93%	n+304 (+304), K+304 (+304)	27.63	25.00
731	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	sQVFSTAADNQTQVGIR	95%	n+304 (+304)	74.47	25.04
732	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	sSGLSEADIQk	95%	n+304 (+304), K+304 (+304)	69.89	25.30
733	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815 seq=translation; coord=5:21697782..21703415:1;	GRMZM2G153815_P01	TRUE	TRUE	tTPSVVAFTQk	95%	n+304 (+304), K+304 (+304)	32.59	25.00
734	parent_transcript=GRMZM2G153815_T01; parent_gene=GRMZM2G153815	GRMZM2G153815_P01	TRUE	TRUE	vQEVVSEIFGk	95%	n+304 (+304), K+304 (+304)	41.19	26.04

735	seq=translation; coord=2:71110426..71138423:1; parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	aFADAGADVLFIDALASVEEmk	95%	n+304 (+304), K+304 (+304)	44.89	25.99
736	seq=translation; coord=2:71110426..71138423:1; parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	aFADAGADVLFIDALASVEEmk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	36.93	25.16
737	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	aMQDALVAIk	95%	n+304 (+304), K+304 (+304)	46.42	26.57
738	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	dGGVPPPSVLPSFQEIk	95%	n+304 (+304), K+304 (+304)	30.16	25.44
739	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	eSGSDIVIVAR	93%	n+304 (+304)	30.06	25.61
740	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	kESGSDIVIVAR	93%	K+304 (+304), n+304 (+304)	29.72	26.25
741	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	IVVYPLSLVGVSMR	95%	n+304 (+304)	49.75	25.35
742	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	IVVyPLSLVGVSMR	94%	n+304 (+304), iTRAQ8plex (+304)	29.01	25.00
743	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	qAISHDEALWR	95%	n+304 (+304)	44.91	25.00
744	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=2:71110426..71138423:1;	GRMZM2G024933_P02	TRUE	TRUE	qAISHDEALWR	86%	Pyro-cmC (-17), n+304 (+304)	25.45	25.00
745	parent_transcript=GRMZM2G024933_T02; parent_gene=GRMZM2G024933 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G024933_P02	TRUE	TRUE	tPILSPAEEIEIGFR	95%	n+304 (+304)	71.47	25.66
746	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	aFVDMVDASGYAVMPSAk	95%	n+304 (+304), K+304 (+304)	64.67	25.00
747	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	dcLcFIEVIAHk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	47.88	26.32
748	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	dPVPFFLTPr	91%	n+304 (+304)	26.58	25.65
749	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	eFLSELAk	93%	n+304 (+304), K+304 (+304)	28.32	26.22
750	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186 seq=translation; coord=1:45512802..45515978:-1;	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	iFVPEGQPLESEPNEPLR	95%	n+304 (+304)	47.87	25.58
751	parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	IVGccNELNAGYAADGYAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	37.93	25.00

752	seq=translation; coord=1:45512802..45515978:-1; parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	IVGccNELNAGyAADGYAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), iTRAQ8plex (+304)	33.69	25.00
753	seq=translation; coord=1:45512802..45515978:-1; parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	mGLEAAVEATVEFLNk	95%	n+304 (+304), K+304 (+304)	36.57	25.37
754	seq=translation; coord=1:45512802..45515978:-1; parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	mGLEAAVEATVEFLNk	95%	Oxidation (+16), n+304 (+304), K+304 (+304)	33.51	25.77
755	seq=translation; coord=1:45512802..45515978:-1; parent_transcript=GRMZM2G087186_T01; parent_gene=GRMZM2G087186	GRMZM2G087186_P01,GRMZM2G087186_P02	TRUE	TRUE	mLTGDSAVIAETGDSWFNCqk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.09	25.00
756	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	dGVTLWLDLAEGk	95%	n+304 (+304), K+304 (+304)	35.54	25.61
757	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	dVLSVAFSVDNR	95%	n+304 (+304)	33.46	25.31
758	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	fSPNTFQPTIVSGSWDR	95%	n+304 (+304)	73.17	25.00
759	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	fVGHEk	90%	n+304 (+304), K+304 (+304)	25.58	25.00
760	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	IWDLSTGLTTR	95%	n+304 (+304)	37.83	25.21
761	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	IWNTLGEck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.25	25.16
762	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	IYSLDAGSIHSLcFSPNR	95%	n+304 (+304), Carbamidomethyl (+57)	71.33	25.00
763	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	vWNLTNck	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.23	26.18
764	seq=translation; coord=6:162882094..162884481:1; parent_transcript=GRMZM2G038032_T01; parent_gene=GRMZM2G038032	GRMZM2G038032_P01,GRMZM2G040477_P01	TRUE	TRUE	yWLcAATQDSVc	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.76	25.31
765	seq=translation; coord=6:104066600..104071298:1; parent_transcript=GRMZM2G122871_T01; parent_gene=GRMZM2G122871	GRMZM2G122871_P01	TRUE	TRUE	aLIAEYSGIk	95%	n+304 (+304), K+304 (+304)	54.83	25.61
766	seq=translation; coord=6:104066600..104071298:1; parent_transcript=GRMZM2G122871_T01; parent_gene=GRMZM2G122871	GRMZM2G122871_P01	TRUE	TRUE	IGYLPYVSTTEETAISLk	95%	n+304 (+304), K+304 (+304)	71.41	25.72
767	seq=translation; coord=6:104066600..104071298:1; parent_transcript=GRMZM2G122871_T01; parent_gene=GRMZM2G122871	GRMZM2G122871_P01	TRUE	TRUE	IGYLPYVSTTEETAISLkR	95%	n+304 (+304), K+304 (+304)	32.48	25.00
768	seq=translation; coord=6:104066600..104071298:1; parent_transcript=GRMZM2G122871_T01; parent_gene=GRMZM2G122871	GRMZM2G122871_P01	TRUE	TRUE	mLVIGSEPPFk	95%	n+304 (+304), K+304 (+304)	35.54	25.85

769	seq=translation; coord=5:189820639..189827796:1; parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	aGLEDaK	87%	n+304 (+304), K+304 (+304)	28.07	27.57
770	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	aLEHDDDISYLTNR	95%	n+304 (+304)	41.58	25.00
771	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	aMETYQAGLK	95%	n+304 (+304), K+304 (+304)	51.87	25.74
772	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	aYLNPDFMQMLR	95%	n+304 (+304)	47.91	25.00
773	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	ayLNPDFMQMLR	92%	n+304 (+304), iTRAQ8plex (+304)	26.55	25.00
774	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	dFDIAIETYQk	91%	n+304 (+304), K+304 (+304)	26.87	25.73
775	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	dFEAAIQHYTk	94%	n+304 (+304), K+304 (+304)	28.51	25.33
776	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	eVEPEPEPEPMDFTDEEK	95%	n+304 (+304), K+304 (+304)	30.06	25.00
777	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	gLALDPSNEGLk	95%	n+304 (+304), K+304 (+304)	32.38	25.00
778	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	qVLNDFQENPR	95%	n+304 (+304)	35.56	25.00
779	parent_transcript=GRMZM2G162688_T01; parent_gene=GRMZM2G162688 seq=translation; coord=5:189820639..189827796:1;	GRMZM2G162688_P01	TRUE	TRUE	rGPSGPDAIGQMFQGPWLWSK	95%	n+304 (+304), K+304 (+304)	30.57	25.16
780	parent_transcript=GRMZM2G432128_T01; parent_gene=GRMZM2G432128 seq=translation; coord=8:147686846..147691734:-1;	GRMZM2G432128_P01	TRUE	TRUE	aFAEASMTTAYEK	95%	n+304 (+304), K+304 (+304)	38.76	25.00
781	parent_transcript=GRMZM2G432128_T01; parent_gene=GRMZM2G432128 seq=translation; coord=8:147686846..147691734:-1;	GRMZM2G432128_P01	TRUE	TRUE	IEAAcVETVESGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.31	25.45
782	parent_transcript=GRMZM2G432128_T01; parent_gene=GRMZM2G432128 seq=translation; coord=6:74407967..74410838:1;	GRMZM2G432128_P01	TRUE	TRUE	IILPFLDLDIK	95%	n+304 (+304), K+304 (+304)	45.61	25.00
783	parent_transcript=GRMZM2G108780_T01; parent_gene=GRMZM2G108780 seq=translation; coord=6:74407967..74410838:1;	GRMZM2G108780_P01	TRUE	TRUE	kTGMSLIIGVYDEPMTPGQcNMVVER	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	63.08	25.00
784	parent_transcript=GRMZM2G108780_T01; parent_gene=GRMZM2G108780 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G108780_P01	TRUE	TRUE	tGMSLIIGVYDEPMTPGQcNMVVER	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	30.65	25.00
785	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	gSTVAVFGLGAVGLAAEGAR	95%	n+304 (+304)	104.91	25.29
786	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	gVMIADGk	95%	n+304 (+304), K+304 (+304)	34.51	26.61

787	seq=translation; coord=1:273983281..273986931:-1; parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	iFGHEAGGIIIESVGEGVTDVAPGDHVLVFTGEck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	53.33	25.00
788	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	iIGVDLNPSR	95%	n+304 (+304)	33.76	26.95
789	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	sAESNMCDLLR	95%	n+304 (+304), Carbamidomethyl (+57)	47.66	25.00
790	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	sAESNmCDLLR	88%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	26.04	25.00
791	seq=translation; coord=1:273983281..273986931:-1; parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	sVEcTGNINAMIQAFecVHDGWGVAVLVGVPHk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	44.66	25.00
792	seq=translation; coord=1:273983281..273986931:-1; parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	tDLPNVVELYMK	94%	n+304 (+304), K+304 (+304)	31.78	26.21
793	parent_transcript=GRMZM2G442658_T02; parent_gene=GRMZM2G442658 seq=translation; coord=1:273983281..273986931:-1;	GRMZM2G442658_P02,GRMZM2G442658_P04	TRUE	TRUE	tHPMNFLLNER	95%	n+304 (+304)	31.05	25.00
794	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=1:178476591..178478157:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	dGGGGYGGGGYGGGGYGGGGYGGGGNR	95%	n+304 (+304)	114.03	25.00
795	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=1:178476591..178478157:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	dGGGGYGGGGYGGGGYGGGGYGGGGNR	95%	n+304 (+304), iTRAQ8plex (+304)	40.59	25.00
796	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=1:178476591..178478157:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	gFGFVTFSTEEAMR	95%	n+304 (+304)	59.81	25.00
797	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=1:178476591..178478157:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	gFGFVTFSTEEAmR	95%	n+304 (+304), Oxidation (+16)	51.00	25.00
798	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=1:178476591..178478157:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	gGGYGNSDGNWR	95%	n+304 (+304)	50.61	25.00
799	parent_transcript=GRMZM2G080603_T01; parent_gene=GRMZM2G080603 seq=translation; coord=8:109163217..109164387:-1;	GRMZM2G080603_P01,GRMZM2G080603_P03, GRMZM2G080603_P04	TRUE	TRUE	nITVNEAQSR	95%	n+304 (+304)	37.12	25.47
800	parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536 seq=translation; coord=8:109163217..109164387:-1;	GRMZM2G063536_P01	TRUE	TRUE	aAFEWADHPTAVIPDMQk	95%	n+304 (+304), K+304 (+304)	42.05	25.00
801	parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536 seq=translation; coord=8:109163217..109164387:-1;	GRMZM2G063536_P01	TRUE	TRUE	aVNDLAK	93%	n+304 (+304), K+304 (+304)	28.82	25.65
802	parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536 seq=translation; coord=8:109163217..109164387:-1;	GRMZM2G063536_P01	TRUE	TRUE	dGDTHLLGDNP	95%	n+304 (+304)	57.46	25.00
803	parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	gIFQPVLPEk	95%	n+304 (+304), K+304 (+304)	36.76	25.00

804	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	gLETVTMGR	93%	n+304 (+304)	28.17	25.00
805	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	kVPELWFYTELK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	27.10	25.00
806	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	IVVMVcEGLR	90%	n+304 (+304), Carbamidomethyl (+57)	27.06	25.00
807	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	mDNLYLVGFR	92%	n+304 (+304)	28.44	25.00
808	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	mDNLYLVGFR	95%	Oxidation (+16), n+304 (+304)	32.67	25.00
809	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	tPGGVWWEFGk	95%	n+304 (+304), K+304 (+304)	32.52	25.44
810	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	tSSITLAIR	95%	n+304 (+304)	33.07	25.00
811	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	vPELWFYTELK	95%	n+304 (+304), K+304 (+304)	40.91	25.58
812	seq=translation; coord=8:109163217..109164387:-1; parent_transcript=GRMZM2G063536_T01; parent_gene=GRMZM2G063536	GRMZM2G063536_P01	TRUE	TRUE	yQDLIGNk	95%	n+304 (+304), K+304 (+304)	34.28	26.34
813	seq=translation; coord=6:165631098..165635858:-1; parent_transcript=GRMZM2G154595_T01; parent_gene=GRMZM2G154595	GRMZM2G154595_P01	TRUE	TRUE	gFMGDDQLGEALEGSDVVIIPAGVPR	95%	n+304 (+304)	62.81	25.00
814	seq=translation; coord=6:165631098..165635858:-1; parent_transcript=GRMZM2G154595_T01; parent_gene=GRMZM2G154595	GRMZM2G154595_P01	TRUE	TRUE	hcPNALVNMIISNPVNSTVPIAAEVfk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.21	25.00
815	seq=translation; coord=6:165631098..165635858:-1; parent_transcript=GRMZM2G154595_T01; parent_gene=GRMZM2G154595	GRMZM2G154595_P01	TRUE	TRUE	nGVEEVLGLGELNEFEk	95%	n+304 (+304), K+304 (+304)	41.93	25.43
816	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	dLPPSAIGEGSGFDAK	95%	n+304 (+304), K+304 (+304)	38.74	25.75
817	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	eFGTVYLGDK	95%	n+304 (+304), K+304 (+304)	44.89	25.37
818	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	gEIVLAQFSVDNSWNR	95%	n+304 (+304)	57.72	25.00
819	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	gFAVSnk	92%	n+304 (+304), K+304 (+304)	29.87	26.95
820	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	gGEQNSYLAELLR	95%	n+304 (+304)	56.62	25.00
821	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002	AC207890.3_FGP002	TRUE	TRUE	nVAYSVISAGWAR	95%	n+304 (+304)	41.18	25.00

822	seq=translation; coord=4:94432879..94438375:1; parent_transcript=AC207890.3_FGT002; parent_gene=AC207890.3_FG002 seq=translation; coord=2:5064059..5067153:-1;	AC207890.3_FGP002	TRUE	TRUE	tALQNLEQFQDk	94%	n+304 (+304), K+304 (+304)	28.60	26.46
823	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	aLDSGVVAQAALDVFTk	95%	n+304 (+304), K+304 (+304)	45.67	25.00
824	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	eFANVDCsYGLSPEDLR	95%	n+304 (+304), Carbamidomethyl (+57)	60.42	25.00
825	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	ePPAADNk	95%	n+304 (+304), K+304 (+304)	29.23	25.47
826	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	fPSAISETGEITVEGR	95%	n+304 (+304)	90.55	25.00
827	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	gELASAVNAPMPVPAEVLSELPFVVLAEK	95%	n+304 (+304), K+304 (+304)	39.53	25.00
828	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	gGVIDEELVR	95%	n+304 (+304)	45.98	25.90
829	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	gLIEPISSVFVNLVNADFTAK	95%	n+304 (+304), K+304 (+304)	43.32	25.00
830	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	hAVMAIGVDEEPSk	95%	n+304 (+304), K+304 (+304)	44.33	25.42
831	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	iGEIPAIEEFVFLk	95%	n+304 (+304), K+304 (+304)	47.03	25.00
832	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	iSLcDALIVR	93%	n+304 (+304), Carbamidomethyl (+57)	29.71	25.13
833	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	IAVQLVAGGGGik	95%	n+304 (+304), K+304 (+304)	42.34	25.00
834	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	IGAAGLALLR	95%	n+304 (+304)	29.09	25.00
835	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	mLNDEAFak	95%	n+304 (+304), K+304 (+304)	37.15	25.85
836	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=2:5064059..5067153:-1;	GRMZM2G081886_P01	TRUE	TRUE	nIAQADASLk	95%	n+304 (+304), K+304 (+304)	48.50	26.38
837	parent_transcript=GRMZM2G081886_T01; parent_gene=GRMZM2G081886 seq=translation; coord=1:264200949..264205758:1;	GRMZM2G081886_P01	TRUE	TRUE	tLAILGFGk	95%	n+304 (+304), K+304 (+304)	34.70	25.00
838	parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130 seq=translation; coord=1:264200949..264205758:1;	GRMZM2G109130_P01	TRUE	TRUE	aITQGIIPAVR	95%	n+304 (+304)	61.50	25.73
839	parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	dLLPAGGDYLLk	95%	n+304 (+304), K+304 (+304)	32.38	25.61

840	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	dTPEWTS DAR	95%	n+304 (+304)	34.73	25.00
841	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	eVLAGVNPMVITR	95%	n+304 (+304)	38.22	26.44
842	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	fGVTFDWEVEk	95%	n+304 (+304), K+304 (+304)	40.23	25.94
843	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	fMPFLIDVNNLEGNFiYATR	95%	n+304 (+304), iTRAQ8plex (+304)	39.90	25.66
844	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	gAVTFVANSWVYPAGk	95%	n+304 (+304), K+304 (+304)	33.35	25.25
845	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	gDEELQAWWk	95%	n+304 (+304), K+304 (+304)	31.11	25.00
846	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	gVAVADPSSPYk	95%	n+304 (+304), K+304 (+304)	38.93	25.37
847	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	iQALED MR	94%	n+304 (+304)	31.84	26.03
848	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	IFPLQLVk	89%	n+304 (+304), K+304 (+304)	25.01	25.00
849	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	IPIPQIIQEDk	95%	n+304 (+304), K+304 (+304)	41.85	25.00
850	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	ISLVEQIYVPR	95%	n+304 (+304)	49.25	25.00
851	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	nLEGLTVQQALDGNR	95%	n+304 (+304)	52.74	25.51
852	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	sWNFTEQGLPADLVk	95%	n+304 (+304), K+304 (+304)	45.13	25.58
853	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	tITLDDVPGR	95%	n+304 (+304)	55.27	25.77
854	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	vGAEANLEQWLTSPLSLTTGESk	94%	n+304 (+304), K+304 (+304)	28.70	25.00
855	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	vYTPASSGV EAWVWQLAk	95%	n+304 (+304), K+304 (+304)	59.51	26.20
856	seq=translation; coord=1:264200949..264205758:1; parent_transcript=GRMZM2G109130_T01; parent_gene=GRMZM2G109130	GRMZM2G109130_P01	TRUE	TRUE	yALGMSSVVYk	94%	n+304 (+304), K+304 (+304)	28.57	25.33
857	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01,GRMZM2G127798_P02, GRMZM2G127798_P03	TRUE	TRUE	aEGNLPVYGFHPASFVk	95%	n+304 (+304), K+304 (+304)	40.57	25.21

858	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01,GRMZM2G127798_P02, GRMZM2G127798_P03	TRUE	TRUE	aYDRNPGLASLLVDPEFAQEIMDR	91%	n+304 (+304)	25.78	25.00
859	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01,GRMZM2G127798_P02, GRMZM2G127798_P03	TRUE	TRUE	iFQGDYYSTGSPVdk	95%	n+304 (+304), K+304 (+304)	54.01	25.00
860	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01,GRMZM2G127798_P02, GRMZM2G127798_P03	TRUE	TRUE	nPGLASLLVDPEFAQEIMDR	95%	n+304 (+304)	65.80	25.00
861	seq=translation; coord=6:57744396..57747092:-1; parent_transcript=GRMZM2G127798_T01; parent_gene=GRMZM2G127798	GRMZM2G127798_P01,GRMZM2G127798_P02, GRMZM2G127798_P03	TRUE	TRUE	yVEDIVlk	90%	n+304 (+304), K+304 (+304)	25.34	25.11
862	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	cSYNYSSSSNLk	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	46.89	25.00
863	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	lIQPSScQVLQQCcHDLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	70.90	25.00
864	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	ncHEFLR	95%	n+304 (+304), Carbamidomethyl (+57)	32.25	25.00
865	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	qQcSPLVMPFLQSR	95%	n+304 (+304), Carbamidomethyl (+57)	34.64	25.00
866	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	qQcSPLVmPFLQSR	95%	n+304 (+304), Carbamidomethyl (+57), Oxidation (+16)	50.10	25.00
867	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	qQQPQQPQQYQQGQEk	95%	n+304 (+304), K+304 (+304)	40.36	25.17
868	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	qQQPQQPQQYQQGQEk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	48.57	25.00
869	seq=translation; coord=7:120173851..120175165:1; parent_transcript=GRMZM2G138689_T01; parent_gene=GRMZM2G138689	GRMZM2G138689_P01	TRUE	TRUE	sQQQQcHcQEQQQTTR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	30.81	25.00
870	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	aEGEGGAVVSWAMEFDk	95%	n+304 (+304), K+304 (+304)	54.64	25.00
871	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	aEGEGGAVVSWAmEFdk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	32.63	25.00
872	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	aNDQVPDPDVik	95%	n+304 (+304), K+304 (+304)	40.08	26.02
873	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	dSTELFPk	93%	n+304 (+304), K+304 (+304)	30.70	25.53
874	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	iFPEQYk	87%	n+304 (+304), K+304 (+304)	25.92	25.19

875	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	IETADDENK	95%	n+304 (+304), K+304 (+304)	39.11	25.00
876	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	slETVEGDGk	94%	n+304 (+304), K+304 (+304)	31.46	26.04
877	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	tFHDLDYLLK	95%	n+304 (+304), K+304 (+304)	30.67	26.07
878	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	tFHDLDYLLKN	94%	n+304 (+304), K+304 (+304)	25.81	25.68
879	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	vELVVEVk	95%	n+304 (+304), K+304 (+304)	31.53	25.00
880	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	vVSYSVVDGELADFYK	95%	n+304 (+304), K+304 (+304)	40.78	25.47
881	seq=translation; coord=2:40588194..40589174:-1; parent_transcript=GRMZM2G102356_T01; parent_gene=GRMZM2G102356	GRMZM2G102356_P01	TRUE	TRUE	yTEAVPMLTFak	95%	n+304 (+304), K+304 (+304)	35.24	25.97
882	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	aAAGNPDTLGDCPFsqR	95%	n+304 (+304), Carbamidomethyl (+57)	56.54	25.00
883	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	aLLDELQALDDHLK	95%	n+304 (+304), K+304 (+304)	41.09	25.31
884	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	cIADSDVITQVIEek	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	35.44	25.31
885	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	fPTPSLVTPPEYASVGsk	95%	n+304 (+304), K+304 (+304)	41.00	25.62
886	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	iFPAFVk	86%	n+304 (+304), K+304 (+304)	25.16	25.00
887	seq=translation; coord=8:133171791..133174888:1; parent_transcript=GRMZM5G855672_T02; parent_gene=GRMZM5G855672	GRMZM5G855672_P02	TRUE	TRUE	iFHLQIALEHfK	95%	n+304 (+304), K+304 (+304)	49.59	25.00
888	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	aAGVLCsyDPNVR	95%	n+304 (+304), Carbamidomethyl (+57)	39.15	25.00
889	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	aPGGAPANVAcAIak	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.94	25.44
890	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	eGILSIWk	93%	n+304 (+304), K+304 (+304)	31.69	26.66
891	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	fGDDEFghMLVNIlk	95%	n+304 (+304), K+304 (+304)	31.65	25.43
892	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	gAIPALPTVATAQDLIAk	95%	n+304 (+304), K+304 (+304)	52.60	25.00

893	seq=translation; coord=6:3570233..3573134:1; parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	IGGSSAFVgk	95%	n+304 (+304), K+304 (+304)	28.35	25.54
894	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	ILVVTGDGk	95%	n+304 (+304), K+304 (+304)	35.69	25.28
895	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	IPLWSPDAAR	90%	n+304 (+304)	27.64	25.28
896	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	nPSADMLLTEAELDLGLVR	95%	n+304 (+304)	77.12	26.25
897	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	nVLSLWFDGLk	95%	n+304 (+304), K+304 (+304)	57.87	25.69
898	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	tALAFVTLk	95%	n+304 (+304), K+304 (+304)	31.53	25.00
899	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=6:3570233..3573134:1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	vFHYGSISLISEPcR	95%	n+304 (+304), Carbamidomethyl (+57)	59.59	25.00
900	parent_transcript=GRMZM2G051677_T01; parent_gene=GRMZM2G051677 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G051677_P01,GRMZM2G051677_P02	TRUE	TRUE	vSDDEVAFLTR	95%	n+304 (+304)	38.02	25.00
901	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	aGLMVQQQVSAR	95%	n+304 (+304)	40.83	25.83
902	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	eAGSDSWk	91%	n+304 (+304), K+304 (+304)	26.84	25.00
903	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	eAIEINNSVPQGLSSSIFTk	95%	n+304 (+304), K+304 (+304)	30.42	25.68
904	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	eEHQFLAELGLAQR	95%	n+304 (+304)	51.98	25.51
905	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	eELFGPVLVVMk	95%	n+304 (+304), K+304 (+304)	42.34	25.05
906	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	gAPTTLITIAMTk	95%	n+304 (+304), K+304 (+304)	29.25	25.00
907	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	gTLLGPLHTPASK	94%	n+304 (+304), K+304 (+304)	27.94	25.00
908	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	iLFGGSAIESEGNFVQPTIVEITPSAPVVK	95%	n+304 (+304), K+304 (+304)	65.01	25.00
909	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440 seq=translation; coord=2:184127551..184138715:-1;	GRMZM2G130440_P02	TRUE	TRUE	iPLVSFTGSTR	95%	n+304 (+304)	40.58	25.20
910	parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	iVASVLEK	95%	n+304 (+304), K+304 (+304)	31.22	25.00

911	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	IILHENIYQTLFDQLVEVYK	95%	n+304 (+304), K+304 (+304)	39.87	25.00
912	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	IVSLEMGk	93%	n+304 (+304), K+304 (+304)	29.16	27.02
913	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	qIGDALR	91%	n+304 (+304)	27.81	25.00
914	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	sVLFAAVGTAGQR	95%	n+304 (+304)	44.77	25.51
915	seq=translation; coord=2:184127551..184138715:-1; parent_transcript=GRMZM2G130440_T02; parent_gene=GRMZM2G130440	GRMZM2G130440_P02	TRUE	TRUE	tWMAIPAPk	91%	n+304 (+304), K+304 (+304)	28.56	25.42
916	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	aEAQAAYDk	95%	n+304 (+304), K+304 (+304)	48.94	25.43
917	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	aMEAISEGk	95%	n+304 (+304), K+304 (+304)	50.35	26.54
918	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	dANAALINPDSAK	95%	n+304 (+304), K+304 (+304)	54.43	25.00
919	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	dFVEAck	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.81	25.31
920	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	dYLQSLGAK	94%	n+304 (+304), K+304 (+304)	29.46	26.51
921	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	gFPGGMPGGGFPR	95%	n+304 (+304)	31.69	25.00
922	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	gMAYAMLGk	95%	n+304 (+304), K+304 (+304)	34.01	25.00
923	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	iPAAAPSFESPk	95%	n+304 (+304), K+304 (+304)	33.23	25.54
924	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	kNPSLLADPNLSFFR	95%	K+304 (+304), n+304 (+304)	28.54	25.19
925	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	mGNPSVEVTEENR	95%	n+304 (+304)	75.29	25.00
926	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	mGNPSVEVTEENR	95%	Oxidation (+16), n+304 (+304)	38.08	25.00
927	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	nPSLLADPNLSFFR	95%	n+304 (+304)	38.86	25.04
928	seq=translation; coord=4:241239335..241241698:1; parent_transcript=GRMZM2G134806_T01; parent_gene=GRMZM2G134806	GRMZM2G134806_P01,GRMZM2G134806_P02	TRUE	TRUE	wEEAAHDLHTASNMDYDEEINAVLk	92%	n+304 (+304), K+304 (+304)	26.47	25.00

929	seq=translation; coord=4:13395375..13398777:-1; parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	eLELEk	85%	n+304 (+304), K+304 (+304)	26.10	26.09
930	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	fITHSVPFSEINTAFDLMLk	95%	n+304 (+304), K+304 (+304)	29.76	25.68
931	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	gSTVAIFGLGAVGLAAMEGAR	95%	n+304 (+304)	79.12	25.00
932	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	gVMIGDGk	93%	n+304 (+304), K+304 (+304)	31.03	26.48
933	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	iIGVDINPAk	90%	n+304 (+304), K+304 (+304)	25.43	25.00
934	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	iLGHEAGGIVESVGEGVT LAPGDHVL PVFTG Eck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.13	25.00
935	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	iLYTALcHTDVYFWEAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	50.37	26.04
936	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	iNPEAPLdk	95%	n+304 (+304), K+304 (+304)	36.08	25.00
937	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	sEESNMcdLLR	95%	n+304 (+304), Carbamidomethyl (+57)	54.92	25.00
938	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	sEESNmcDLLR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	34.67	25.00
939	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	tDLPNVVEMYmk	95%	n+304 (+304), K+304 (+304)	40.33	25.43
940	parent_transcript=GRMZM2G098346_T01; parent_gene=GRMZM2G098346 seq=translation; coord=4:13395375..13398777:-1;	GRMZM2G098346_P01	TRUE	TRUE	tDLPNVVEMYmk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	38.67	25.00
941	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499 seq=translation; coord=2:41302953..41306124:-1;	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	dAAENTMVAYk	95%	n+304 (+304), K+304 (+304)	68.97	25.00
942	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499 seq=translation; coord=2:41302953..41306124:-1;	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	dNLTlWTSdISEDPAEEIR	95%	n+304 (+304)	45.42	25.00
943	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499 seq=translation; coord=2:41302953..41306124:-1;	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	icDGILk	86%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.40	27.00
944	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499 seq=translation; coord=2:41302953..41306124:-1;	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	iETELTk	95%	n+304 (+304), K+304 (+304)	36.02	25.00
945	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499 seq=translation; coord=2:41302953..41306124:-1;	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	tVDSEELTVEER	95%	n+304 (+304)	42.87	25.00
946	parent_transcript=GRMZM2G102499_T02; parent_gene=GRMZM2G102499	GRMZM2G102499_P02,GRMZM2G102499_P03, GRMZM2G102499_P04	TRUE	TRUE	yEEMVEFMek	95%	n+304 (+304), K+304 (+304)	30.93	25.00

947	seq=translation; coord=7:168785597..168786938:1; parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	aLHVVPDk	95%	n+304 (+304), K+304 (+304)	31.13	25.90
948	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	aVDSLTAak	95%	n+304 (+304), K+304 (+304)	34.86	25.00
949	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	dVEAYGgk	95%	n+304 (+304), K+304 (+304)	29.21	25.42
950	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	iHDYVGDGYAIIFSHPADFTPvcTTEMAAMAGYAK	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.81	25.00
951	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	ILGIScDDVESHr	95%	n+304 (+304), Carbamidomethyl (+57)	64.68	25.00
952	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	ISFLYPATTGR	87%	n+304 (+304)	26.92	26.31
953	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	mFPQGFETADLPsk	95%	n+304 (+304), K+304 (+304)	32.61	25.51
954	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	mFPQGFETADLPsk	95%	Oxidation (+16), n+304 (+304), K+304 (+304)	39.97	25.02
955	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	mFPQGFETADLPskk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	30.17	26.50
956	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	nMDEVLR	92%	n+304 (+304)	28.44	25.00
957	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	qLNMVDPDEk	95%	n+304 (+304), K+304 (+304)	42.37	25.09
958	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	qLNMVDPDEkDAAGR	95%	n+304 (+304), K+304 (+304)	45.87	25.00
959	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	qLNMVDPDEkDAAGR	91%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.33	25.00
960	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=7:168785597..168786938:1;	GRMZM2G129761_P01	TRUE	TRUE	vATPANWkPGEcAVIAPGVSDDEAR	94%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	28.17	25.22
961	parent_transcript=GRMZM2G129761_T01; parent_gene=GRMZM2G129761 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G129761_P01	TRUE	TRUE	vTFPILADPAR	94%	n+304 (+304)	30.38	26.41
962	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	TRUE	TRUE	aDINAQcPAAlk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304), n+304 (+304), Carbamidomethyl (+57),	41.35	25.35
963	seq=translation; coord=3:186793464..186794596:-1; parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	TRUE	TRUE	aDINAQcPAAlkVPGGcASAcEk	94%	K+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	26.17	25.00

964	seq=translation; coord=3:186793464..186794596:-1; parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	TRUE	TRUE	gTcQTGDcGGALAcTVSGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304),	78.55	25.00
965	seq=translation; coord=3:186793464..186794596:-1; parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	IcPDAYSyAk	95%	Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	38.60	25.00
966	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	IGGDTYccR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57)	35.59	25.00
967	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	nTLWPAALPGGGAR	95%	n+304 (+304)	37.75	25.00
968	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	tGcSFDGSGR	95%	n+304 (+304), Carbamidomethyl (+57)	40.39	25.00
969	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	tPATLAEYTLNR	95%	n+304 (+304)	40.02	25.00
970	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474 seq=translation; coord=3:186793464..186794596:-1;	GRMZM2G092474_P01	TRUE	TRUE	tPATLAEyTLNR	95%	n+304 (+304), iTRAQ8plex (+304)	31.98	26.75
971	parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	TRUE	TRUE	tWTVQVPAGTAHAR	95%	n+304 (+304)	33.74	25.43
972	seq=translation; coord=3:186793464..186794596:-1; parent_transcript=GRMZM2G092474_T01; parent_gene=GRMZM2G092474	GRMZM2G092474_P01	TRUE	TRUE	vPGGcASAcEk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	43.46	25.00
973	seq=translation; coord=4:105179813..105180991:-1; parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388 seq=translation; coord=4:105179813..105180991:-1;	GRMZM2G162388_P01	TRUE	TRUE	hVVFQGVVEGMEVvk	95%	n+304 (+304), K+304 (+304)	104.78	25.02
974	parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388 seq=translation; coord=4:105179813..105180991:-1;	GRMZM2G162388_P01	TRUE	TRUE	hVVFQGVVEGmEVvk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	50.72	25.79
975	parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388 seq=translation; coord=4:105179813..105180991:-1;	GRMZM2G162388_P01	TRUE	TRUE	vAdcGQL	95%	n+304 (+304), Carbamidomethyl (+57)	35.97	25.00
976	parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388 seq=translation; coord=4:105179813..105180991:-1;	GRMZM2G162388_P01	TRUE	TRUE	viPQFmcQGGDFTR	95%	n+304 (+304), Carbamidomethyl (+57)	52.32	25.00
977	parent_transcript=GRMZM2G162388_T01; parent_gene=GRMZM2G162388 seq=translation; coord=4:105179813..105180991:-1;	GRMZM2G162388_P01	TRUE	TRUE	viPQFmcQGGDFTR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	45.71	25.00
978	parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192 seq=translation; coord=10:60080812..60087313:-1;	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	aAEAVVDWHk	95%	n+304 (+304), K+304 (+304)	41.15	25.77
979	parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192 seq=translation; coord=10:60080812..60087313:-1;	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	aDTPEPLcQVMLR	95%	n+304 (+304), Carbamidomethyl (+57)	50.39	25.00
980	parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	gGSTVIAFAQDPDGyMFELIQR	95%	n+304 (+304), iTRAQ8plex (+304)	30.61	25.04

981	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	gNAYAQAIGTNDVYK	95%	n+304 (+304), K+304 (+304)	49.32	25.37
982	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	iASFVDPDGWk	95%	n+304 (+304), K+304 (+304)	29.50	25.00
983	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	mLHAVYR	95%	n+304 (+304)	30.34	26.71
984	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	qPGPLPGINTk	95%	n+304 (+304), K+304 (+304)	46.79	25.00
985	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	qPGPLPGINTk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	32.43	25.00
986	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	sAEAVDLATk	95%	n+304 (+304), K+304 (+304)	54.68	25.55
987	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	vLVNDNTDFLk	95%	n+304 (+304), K+304 (+304)	51.74	25.73
988	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	yDIGTGFGHFAIANDDVYK	95%	n+304 (+304), K+304 (+304)	40.51	25.00
989	seq=translation; coord=10:60080812..60087313:-1; parent_transcript=GRMZM2G181192_T01; parent_gene=GRMZM2G181192	GRMZM2G181192_P01,GRMZM2G181192_P02, GRMZM2G181192_P03	TRUE	TRUE	yTIAMLGYADEDk	95%	n+304 (+304), K+304 (+304)	31.69	25.00
990	seq=translation; coord=9:129274385..129278107:-1; parent_transcript=GRMZM2G058522_T01; parent_gene=GRMZM2G058522	GRMZM2G058522_P01,GRMZM2G058522_P04, GRMZM2G058522_P05,GRMZM2G058522_P06, GRMZM2G058522_P08,GRMZM2G058522_P09	TRUE	TRUE	aVAVLGSSDGVk	95%	n+304 (+304), K+304 (+304)	61.57	26.31
991	seq=translation; coord=9:129274385..129278107:-1; parent_transcript=GRMZM2G058522_T01; parent_gene=GRMZM2G058522	GRMZM2G058522_P01,GRMZM2G058522_P04, GRMZM2G058522_P05,GRMZM2G058522_P06, GRMZM2G058522_P08,GRMZM2G058522_P09	TRUE	TRUE	eHGAPEDENR	95%	n+304 (+304)	43.28	25.00
992	seq=translation; coord=9:129274385..129278107:-1; parent_transcript=GRMZM2G058522_T01; parent_gene=GRMZM2G058522	GRMZM2G058522_P01,GRMZM2G058522_P04, GRMZM2G058522_P05,GRMZM2G058522_P06, GRMZM2G058522_P08,GRMZM2G058522_P09	TRUE	TRUE	hAGDLGNVTAGADGVANINVTDSQIPLTGPNSIIGR	95%	n+304 (+304)	54.53	25.00
993	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	TRUE	TRUE	kIEDAVDGAISWLSNQLAEVEEFEDk	94%	K+304 (+304), n+304 (+304), K+304 (+304)	25.51	25.00
994	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	TRUE	TRUE	mYQGEAGMGAAAGMDEADAPSGSGAGPk	95%	n+304 (+304), K+304 (+304)	92.74	25.00
995	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	TRUE	TRUE	mYQGEAGMGAAAGMDEADAPSGSGAGPk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	51.62	25.00
996	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	TRUE	TRUE	sEGPAIGDLGTTYScVGWVQHDR	95%	n+304 (+304), Carbamidomethyl (+57)	102.07	25.00
997	seq=translation; coord=8:168955391..168958754:-1; parent_transcript=GRMZM2G310431_T01; parent_gene=GRMZM2G310431	GRMZM2G310431_P01	TRUE	TRUE	tTPSYVGFTDTER	95%	n+304 (+304)	58.06	25.00

998	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	eLFEFLPNTIQEQLMLER	95%	n+304 (+304)	41.58	25.40
999	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	eVPTSFGFDTAck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.91	25.00
1000	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	gGPAGIMk	86%	n+304 (+304), K+304 (+304)	26.43	25.94
1001	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	iYSEMIGNVMTDAR	95%	n+304 (+304)	64.40	25.00
1002	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	ILHALPLPSVLR	95%	n+304 (+304)	32.71	25.00
1003	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	nQGGFDMicSGR	95%	n+304 (+304), Carbamidomethyl (+57)	31.61	25.00
1004	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	yVELTSDFVYPYR	95%	n+304 (+304)	48.99	25.00
1005	seq=translation; coord=6:115191842..115198242:-1; parent_transcript=GRMZM2G059151_T01; parent_gene=GRMZM2G059151	GRMZM2G059151_P01	TRUE	TRUE	yVELTSDFVyPYR	92%	n+304 (+304), iTRAQ8plex (+304)	27.19	26.03
1006	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	aPVIVAk	94%	n+304 (+304), K+304 (+304)	30.40	25.00
1007	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	dLSGIMITVEHAAFMAEK	95%	n+304 (+304), K+304 (+304)	37.28	25.68
1008	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	gGFSGLFPDSSDFAYR	95%	n+304 (+304)	47.16	25.00
1009	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	iLGTISSPDTVMWcDVR	95%	n+304 (+304), Carbamidomethyl (+57)	34.97	25.00
1010	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	IGFGVVDAVvk	95%	n+304 (+304), K+304 (+304)	40.34	25.00
1011	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	qFITDYISSPEVNFLTISGR	95%	n+304 (+304)	33.62	25.08
1012	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	sSFTSQVTTINDLk	93%	n+304 (+304), K+304 (+304)	28.43	25.73
1013	seq=translation; coord=5:179010381..179015571:1; parent_transcript=GRMZM2G013324_T01; parent_gene=GRMZM2G013324	GRMZM2G013324_P01	TRUE	TRUE	ySLVYMIEEGVR	95%	n+304 (+304)	39.27	25.00
1014	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	dLITILEDAlR	95%	n+304 (+304)	37.47	25.80
1015	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	dSTTIVGDGTTQEEVnk	95%	n+304 (+304), K+304 (+304)	57.00	25.00

1016	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	eEVGLSLDK	95%	n+304 (+304), K+304 (+304)	37.64	26.89
1017	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	eLHFNk	95%	n+304 (+304), K+304 (+304)	28.48	25.00
1018	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	kSQYLDIATLTGGTVIR	95%	K+304 (+304), n+304 (+304)	27.33	25.43
1019	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	nQIEATEQEYER	93%	n+304 (+304)	29.58	25.00
1020	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	sAENNLVSVEGMQFDR	95%	n+304 (+304)	55.10	25.00
1021	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	sGyPILIVAEIDIEQEALATLVVNR	95%	n+304 (+304), iTRAQ8plex (+304)	46.42	25.00
1022	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	tFITSDAVVVDAK	95%	n+304 (+304), K+304 (+304)	40.13	26.37
1023	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	tNDLAGDGTTSVVLAQGMITEGVK	95%	n+304 (+304), K+304 (+304)	47.85	25.69
1024	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	vDAIIETLENDEQk	95%	n+304 (+304), K+304 (+304)	44.89	26.11
1025	seq=translation; coord=4:240742463..240747734:-1; parent_transcript=GRMZM2G015989_T01; parent_gene=GRMZM2G015989	GRMZM2G015989_P01,GRMZM2G015989_P02	TRUE	TRUE	yGYNAATGEYEDLMAAGIIDPTk	95%	n+304 (+304), K+304 (+304)	51.13	25.00
1026	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	aGGEDYSLTVR	95%	n+304 (+304)	37.34	25.00
1027	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	aHGGVHDGTEIVLWk	95%	n+304 (+304), K+304 (+304)	57.86	25.19
1028	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	aNENYcLAVR	95%	n+304 (+304), Carbamidomethyl (+57)	37.89	25.00
1029	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	dEYQHWWk	95%	n+304 (+304), K+304 (+304)	34.35	25.00
1030	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	dGAVVLAPVNPk	95%	n+304 (+304), K+304 (+304)	30.71	25.00
1031	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	gENQSWk	89%	n+304 (+304), K+304 (+304)	26.52	25.00
1032	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	IAPFSPDQEDASVLWTESk	95%	n+304 (+304), K+304 (+304)	35.56	25.00
1033	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380	GRMZM2G469380_P02	TRUE	TRUE	IVPYNPDYQDESVLWTESR	95%	n+304 (+304)	37.31	25.00

1034	seq=translation; coord=7:173553684..173555507:-1; parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380 seq=translation; coord=7:173553684..173555507:-1;	GRMZM2G469380_P02	TRUE	TRUE	vkDEEGMPAFALVNk	95%	n+304 (+304), K+304 (+304)	31.02	25.28
1035	parent_transcript=GRMZM2G469380_T02; parent_gene=GRMZM2G469380 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G469380_P02	TRUE	TRUE	vRDEEGYPAFALVNk	95%	n+304 (+304), K+304 (+304)	43.35	26.19
1036	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	aMMVDTTILGLDDVR	87%	n+304 (+304)	26.19	25.65
1037	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	aSPPPWNTAAEQPIPk	95%	n+304 (+304), K+304 (+304)	36.75	26.01
1038	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	aYGSNIGGYk	95%	n+304 (+304), K+304 (+304)	36.80	25.47
1039	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	eQFPEANDFGSEVIPGATSIGk	95%	n+304 (+304), K+304 (+304)	46.49	25.00
1040	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	eTNADITVAALPMDEk	95%	n+304 (+304), K+304 (+304)	57.93	25.38
1041	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	fAPIYTQPR	89%	n+304 (+304)	26.15	25.28
1042	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	gGIPIGIGk	91%	n+304 (+304), K+304 (+304)	25.86	25.00
1043	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=4:58954361..58960521:-1;	GRMZM2G068506_P01	TRUE	TRUE	iNHSVVGLR	93%	n+304 (+304)	27.40	26.14
1044	parent_transcript=GRMZM2G068506_T01; parent_gene=GRMZM2G068506 seq=translation; coord=6:83777893..83783487:1;	GRMZM2G068506_P01	TRUE	TRUE	nEGFVEVLAAQSPDNPNWFQGTADAVR	95%	n+304 (+304)	52.91	25.00
1045	parent_transcript=GRMZM2G141931_T01; parent_gene=GRMZM2G141931 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G141931_P01	TRUE	TRUE	aLESENVDSVk	95%	n+304 (+304), K+304 (+304)	50.54	25.48
1046	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	aAYVALMQTVSk	95%	n+304 (+304), K+304 (+304)	31.00	25.43
1047	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	aEADLGNVLk	95%	n+304 (+304), K+304 (+304)	51.36	25.68
1048	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	eTALLFDEMHSAAANK	95%	n+304 (+304), K+304 (+304)	28.01	25.21
1049	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	eVLNFILSPEVR	95%	n+304 (+304)	49.16	25.00
1050	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	fLIDFLEPFALK	95%	n+304 (+304), K+304 (+304)	30.99	25.00
1051	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875	GRMZM2G027875_P01	TRUE	TRUE	gTLTLALAELGHEATINEAVR	95%	n+304 (+304)	69.11	25.00

1052	seq=translation; coord=5:155951379..155960766:1; parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	iNAQWVvk	94%	n+304 (+304), K+304 (+304)	29.13	25.00
1053	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	iTLEVPSETIALSNMPVIEEK	95%	n+304 (+304), K+304 (+304)	31.35	25.00
1054	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	kFLIDFLEPFALK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	29.15	25.00
1055	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	IDALAGSHPIEVDINHVDEIDEIDFAISYR	95%	n+304 (+304)	26.51	25.00
1056	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	INVNQTSFYR	93%	n+304 (+304)	30.05	25.00
1057	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	mDMVAIPDFAAGAMENyGLVTYR	95%	n+304 (+304), iTRAQ8plex (+304)	31.89	25.00
1058	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	mLQNYLGAEVFQNSLAAYIK	95%	n+304 (+304), K+304 (+304)	46.42	25.07
1059	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	nMAVTQFEPADAR	95%	n+304 (+304)	42.04	25.00
1060	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	nQDAIFLLR	93%	n+304 (+304)	29.79	25.00
1061	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	rFNVFLEDR	95%	n+304 (+304)	42.22	25.45
1062	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	tEDLWAALEEGSGPEVR	95%	n+304 (+304)	32.86	25.00
1063	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=5:155951379..155960766:1;	GRMZM2G027875_P01	TRUE	TRUE	tLMHSWtk	95%	n+304 (+304), K+304 (+304)	30.97	26.12
1064	parent_transcript=GRMZM2G027875_T01; parent_gene=GRMZM2G027875 seq=translation; coord=4:160954463..160955623:1;	GRMZM2G027875_P01	TRUE	TRUE	vSYDEELAAR	92%	n+304 (+304)	28.57	25.00
1065	parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515 seq=translation; coord=4:160954463..160955623:1;	GRMZM2G342515_P01	TRUE	TRUE	aMSIMNSFINDIFEK	95%	n+304 (+304), K+304 (+304)	43.14	25.61
1066	parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515 seq=translation; coord=4:160954463..160955623:1;	GRMZM2G342515_P01	TRUE	TRUE	amSIMNSFINDIFEK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	46.44	25.01
1067	parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515 seq=translation; coord=4:160954463..160955623:1;	GRMZM2G342515_P01	TRUE	TRUE	hAVSEGtK	95%	n+304 (+304), K+304 (+304)	48.59	25.00
1068	parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515 seq=translation; coord=4:160954463..160955623:1;	GRMZM2G342515_P01	TRUE	TRUE	IVLPGELak	95%	n+304 (+304), K+304 (+304)	35.80	25.00
1069	parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515	GRMZM2G342515_P01	TRUE	TRUE	qVHPDIGISSk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	34.51	25.00

1070	seq=translation; coord=4:160954463..160955623:1; parent_transcript=GRMZM2G342515_T01; parent_gene=GRMZM2G342515	GRMZM2G342515_P01	TRUE	TRUE	vAEEEPSEK	93%	n+304 (+304), K+304 (+304)	30.31	25.50
1071	seq=translation; coord=3:202432697..202435947:1; parent_transcript=GRMZM2G055276_T01; parent_gene=GRMZM2G055276	GRMZM2G055276_P01	TRUE	TRUE	nVEFADDSEPPR	95%	n+304 (+304)	30.31	25.00
1072	seq=translation; coord=3:202432697..202435947:1; parent_transcript=GRMZM2G055276_T01; parent_gene=GRMZM2G055276	GRMZM2G055276_P01	TRUE	TRUE	qGEQNDAPAADENk	95%	n+304 (+304), K+304 (+304)	39.03	25.00
1073	seq=translation; coord=3:202432697..202435947:1; parent_transcript=GRMZM2G055276_T01; parent_gene=GRMZM2G055276	GRMZM2G055276_P01	TRUE	TRUE	qGEQNDAPAADENkDNK	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304), K+304 (+304)	33.44	25.00
1074	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	dLFLLPEAFk	95%	n+304 (+304), K+304 (+304)	32.11	25.00
1075	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	eGLPAFPMGk	95%	n+304 (+304), K+304 (+304)	34.79	25.61
1076	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	fDYILTQQAFVTVdk	95%	n+304 (+304), K+304 (+304)	33.45	25.40
1077	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	gHSYSEIINESLIESVDSLNPFMHAR	95%	n+304 (+304)	56.17	25.00
1078	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	gILLGAVHGMVEALFR	95%	n+304 (+304)	69.03	25.00
1079	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	gILLGAVHGmVEALFR	95%	n+304 (+304), Oxidation (+16)	33.23	25.40
1080	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	gMLEVYNSLITEEGk	95%	n+304 (+304), K+304 (+304)	50.90	26.23
1081	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	gVAFMVdNcSTTAR	95%	n+304 (+304), Carbamidomethyl (+57)	59.41	25.00
1082	seq=translation; coord=3:213623450..213627174:-1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	nTVESITGIIsk	95%	n+304 (+304), K+304 (+304)	34.25	25.00
1083	seq=translation; coord=4:220508652..220512101:1; parent_transcript=GRMZM2G004382_T01; parent_gene=GRMZM2G004382	GRMZM2G004382_P01	TRUE	TRUE	qIGVIGWGSQGPAAQNLr	95%	n+304 (+304)	67.06	25.49
1084	seq=translation; coord=4:220508652..220512101:1; parent_transcript=GRMZM2G027378_T01; parent_gene=GRMZM2G027378	GRMZM2G027378_P01,GRMZM2G071010_P01	TRUE	TRUE	dYTMENILTQLk	95%	n+304 (+304), K+304 (+304)	32.05	26.54
1085	seq=translation; coord=4:220508652..220512101:1; parent_transcript=GRMZM2G027378_T01; parent_gene=GRMZM2G027378	GRMZM2G027378_P01,GRMZM2G071010_P01	TRUE	TRUE	fGLLANWQR	85%	n+304 (+304)	25.05	25.00
1086	seq=translation; coord=4:220508652..220512101:1; parent_transcript=GRMZM2G027378_T01; parent_gene=GRMZM2G027378	GRMZM2G027378_P01,GRMZM2G071010_P01	TRUE	TRUE	tLGSSGAGSSVVVPR	95%	n+304 (+304)	90.40	25.13
1087	seq=translation; coord=5:29990567..29996686:1; parent_transcript=GRMZM2G167505_T01; parent_gene=GRMZM2G167505	GRMZM2G167505_P01,GRMZM2G167505_P02, GRMZM2G167505_P03	TRUE	TRUE	gFGFITDSEDAVDR	95%	n+304 (+304)	35.57	25.00

1088	seq=translation; coord=5:29990567..29996686:1; parent_transcript=GRMZM2G167505_T01; parent_gene=GRMZM2G167505	GRMZM2G167505_P01,GRMZM2G167505_P02, GRMZM2G167505_P03	TRUE	TRUE	gFGFVVFADPAAVDR	95%	n+304 (+304)	59.53	25.00
1089	seq=translation; coord=5:29990567..29996686:1; parent_transcript=GRMZM2G167505_T01; parent_gene=GRMZM2G167505	GRMZM2G167505_P01,GRMZM2G167505_P02, GRMZM2G167505_P03	TRUE	TRUE	qYFETFGIVTDVVVMYDQNTQRPR	95%	n+304 (+304)	29.50	25.00
1090	seq=translation; coord=5:186517098..186522957:-1; parent_transcript=GRMZM2G540538_T01; parent_gene=GRMZM2G540538	GRMZM2G540538_P01	TRUE	TRUE	gWETENIEEIALK	95%	n+304 (+304), K+304 (+304)	32.76	25.43
1091	seq=translation; coord=5:186517098..186522957:-1; parent_transcript=GRMZM2G540538_T01; parent_gene=GRMZM2G540538	GRMZM2G540538_P01	TRUE	TRUE	hLPMYDELASK	95%	n+304 (+304), K+304 (+304)	41.67	25.53
1092	seq=translation; coord=5:186517098..186522957:-1; parent_transcript=GRMZM2G540538_T01; parent_gene=GRMZM2G540538	GRMZM2G540538_P01	TRUE	TRUE	sNVEYIAGGATQNSIR	95%	n+304 (+304)	34.09	25.00
1093	seq=translation; coord=5:186517098..186522957:-1; parent_transcript=GRMZM2G540538_T01; parent_gene=GRMZM2G540538	GRMZM2G540538_P01	TRUE	TRUE	vLPYADYIFGNETEAK	95%	n+304 (+304), K+304 (+304)	61.22	25.56
1094	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	aAYPIEYIPNAK	95%	n+304 (+304), K+304 (+304)	30.63	26.65
1095	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	dGAASTFAAALSEEER	95%	n+304 (+304)	70.96	25.00
1096	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	dGDVALFFGLSGTGK	95%	n+304 (+304), K+304 (+304)	55.31	25.38
1097	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	eMVLGTQYAGEMK	95%	n+304 (+304), K+304 (+304)	40.43	26.20
1098	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	fGAVLENVVFDEHTR	95%	n+304 (+304)	46.54	25.00
1099	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	fTHVLYNLSPAELYEQAik	95%	n+304 (+304), K+304 (+304)	36.48	25.02
1100	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	gLFGVMHYLMPK	95%	n+304 (+304), K+304 (+304)	43.28	26.02
1101	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	gSFITSGALATLSGAK	95%	n+304 (+304), K+304 (+304)	35.31	25.00
1102	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	gSPNIEMDEHTFLTNR	95%	n+304 (+304)	60.16	25.00
1103	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	gVPSEILDPINTWTDK	95%	n+304 (+304), K+304 (+304)	48.77	25.51
1104	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	nFEVFASYK	95%	n+304 (+304), K+304 (+304)	29.62	25.72
1105	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932	GRMZM5G870932_P01	TRUE	TRUE	nVILLAcDAFGVLPVSK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.79	25.00

1106	seq=translation; coord=9:141825338..141830182:1; parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932 seq=translation; coord=9:141825338..141830182:1;	GRMZM5G870932_P01	TRUE	TRUE	qQLQSISASLASLTR	95%	n+304 (+304)	55.89	25.08
1107	parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932 seq=translation; coord=9:141825338..141830182:1;	GRMZM5G870932_P01	TRUE	TRUE	tEVFGLIEIPEIK	95%	n+304 (+304), K+304 (+304)	37.39	25.98
1108	parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932 seq=translation; coord=9:141825338..141830182:1;	GRMZM5G870932_P01	TRUE	TRUE	vFVNDQFLNWDPENR	95%	n+304 (+304)	38.00	25.00
1109	parent_transcript=GRMZM5G870932_T01; parent_gene=GRMZM5G870932 seq=translation; coord=1:177027402..177032403:1;	GRMZM5G870932_P01	TRUE	TRUE	yGATGWLVTGWSSGGR	95%	n+304 (+304)	75.98	25.00
1110	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	dVTELIGHTPLVYLNk	95%	n+304 (+304), K+304 (+304)	38.81	25.00
1111	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	eGLLVGISSGAAAAA AVR	95%	n+304 (+304)	86.87	25.45
1112	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	eQNPNVk	94%	n+304 (+304), K+304 (+304)	27.66	25.00
1113	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	iDGLVSGIGTGGTITGTGR	95%	n+304 (+304)	83.75	25.34
1114	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	IFVVVFPsfGER	95%	n+304 (+304)	33.75	26.36
1115	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	ITLTPASMSMER	90%	n+304 (+304)	27.36	25.00
1116	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=1:177027402..177032403:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	tPNSYILQQFENPANPk	95%	n+304 (+304), K+304 (+304)	47.61	26.11
1117	parent_transcript=GRMZM2G005887_T01; parent_gene=GRMZM2G005887 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G005887_P01,GRMZM2G005887_P02, GRMZM2G005887_P05	TRUE	TRUE	yLSSVLFQSiK	95%	n+304 (+304), K+304 (+304)	29.33	25.00
1118	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	nQAGSGcEGK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.11	25.00
1119	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	sAFLSAVNAYPGFAHGGTEVEGK	95%	n+304 (+304), K+304 (+304)	66.35	25.00
1120	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	sNAYcDASNR	95%	n+304 (+304), Carbamidomethyl (+57)	36.89	25.00
1121	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	tALWFWMNNVHR	95%	n+304 (+304)	39.67	25.00
1122	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	vAQDAVIAFk	95%	n+304 (+304), K+304 (+304)	44.95	25.51
1123	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943	GRMZM2G051943_P01	TRUE	TRUE	vAQDAVIAFKTALWFWMNNVHR	95%	n+304 (+304), K+304 (+304)	34.53	25.00

1124	seq=translation; coord=2:33534101..33535449:1; parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=2:33534101..33535449:1;	GRMZM2G051943_P01	TRUE	TRUE	vDPGNLTc	90%	n+304 (+304), Carbamidomethyl (+57)	26.36	25.00
1125	parent_transcript=GRMZM2G051943_T01; parent_gene=GRMZM2G051943 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G051943_P01	TRUE	TRUE	vMPQGFgATIR	95%	n+304 (+304)	31.95	25.00
1126	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	aFPSLTyIAVnK	95%	n+304 (+304), K+304 (+304)	33.85	25.00
1127	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	aYLEFFcAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.85	25.00
1128	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	fTNFcQGk	92%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.60	25.00
1129	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	fVQVEGGfAcALDLVQHIR	95%	n+304 (+304), Carbamidomethyl (+57)	95.77	25.28
1130	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	gWGcMFPEGDSSR	95%	n+304 (+304), Carbamidomethyl (+57)	46.78	25.00
1131	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	iDHALETik	92%	n+304 (+304), K+304 (+304)	29.25	25.00
1132	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	iDDQLVNINQk	95%	n+304 (+304), K+304 (+304)	57.98	25.12
1133	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	iLEAAGDGR	95%	n+304 (+304)	36.09	25.50
1134	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	iPSEITAALDPikDNEEA VR	93%	n+304 (+304), K+304 (+304)	27.64	25.00
1135	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	IQEEWAVPLk	95%	n+304 (+304), K+304 (+304)	39.62	25.00
1136	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	ITSPWSELDGLQPETk	95%	n+304 (+304), K+304 (+304)	55.97	25.29
1137	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	sAIGILMNLGLIEESk	95%	n+304 (+304), K+304 (+304)	57.10	25.00
1138	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	sDSPTVGWGGPGGYVYQk	95%	n+304 (+304), K+304 (+304)	57.13	25.00
1139	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=1:292089538..292095812:-1;	GRMZM2G347056_P01	TRUE	TRUE	tEEGVENL FER	95%	n+304 (+304)	53.47	25.00
1140	parent_transcript=GRMZM2G347056_T01; parent_gene=GRMZM2G347056 seq=translation; coord=7:155357370..155360570:1;	GRMZM2G347056_P01	TRUE	TRUE	tLGWDQYPHGR	95%	n+304 (+304)	38.59	25.00
1141	parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	aAAEEAGHPewDLPDDAGTYNDTPeK	95%	n+304 (+304), K+304 (+304)	31.80	25.00

1142	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	aEIPIEEILEVAQPk	95%	n+304 (+304), K+304 (+304)	67.32	25.00
1143	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	aSMNFTcAEMR	91%	n+304 (+304), Carbamidomethyl (+57)	28.10	25.00
1144	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	eGLNLAcENALNR	95%	n+304 (+304), Carbamidomethyl (+57)	57.24	25.00
1145	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	ePGVYDWSAYR	94%	n+304 (+304)	30.94	25.00
1146	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	fFLTWYSNk	93%	n+304 (+304), K+304 (+304)	28.72	26.25
1147	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	IVQEAGLk	93%	n+304 (+304), K+304 (+304)	32.75	27.85
1148	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	mHANLDYNPNVDPVAPLER	95%	n+304 (+304)	41.01	25.00
1149	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	sAPEELVQQVLSAGWR	95%	n+304 (+304)	51.50	25.31
1150	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	sGLTNIEYLTLGVDDQPLFHGR	95%	n+304 (+304)	77.78	25.45
1151	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	sGLTNIEyLTLGVDDQPLFHGR	95%	n+304 (+304), iTRAQ8plex (+304)	42.96	25.69
1152	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	vSDELFEQNYTTFk	89%	n+304 (+304), K+304 (+304)	25.11	25.00
1153	seq=translation; coord=7:155357370..155360570:1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	yDATAYNTILR	95%	n+304 (+304)	34.13	25.00
1154	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=GRMZM2G058310_T01; parent_gene=GRMZM2G058310	GRMZM2G058310_P01	TRUE	TRUE	yPSYPQSQGWVFPVGGEFicYDk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.35	25.00
1155	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	TRUE	TRUE	aALAPEEVVAR	95%	n+304 (+304)	46.45	25.90
1156	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	TRUE	TRUE	aQGVFHVDMIMLAHNPGGk	95%	n+304 (+304), K+304 (+304)	34.29	26.74
1157	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	TRUE	TRUE	dAVLDGGIPFNk	91%	n+304 (+304), K+304 (+304)	26.84	25.95
1158	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	TRUE	TRUE	gAGFSGFk	92%	n+304 (+304), K+304 (+304)	27.61	26.00
1159	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004	AC196475.3_FGP004	TRUE	TRUE	hVGGMDFASVPAGDAILMk	95%	n+304 (+304), K+304 (+304)	39.01	25.17

1160	seq=translation; coord=4:32249665..32251536:-1; parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	ILASYDVVR	95%	n+304 (+304)	37.03	25.00
1161	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	mPAAPGDPAAAAAMVDR	94%	n+304 (+304)	31.00	25.00
1162	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	nAIELGLLEVLQk	95%	n+304 (+304), K+304 (+304)	63.35	25.00
1163	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	vIVVcVLPVNTTEATPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.83	25.54
1164	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	vLMESWYYLk	94%	n+304 (+304), K+304 (+304)	29.04	25.60
1165	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	wILHDWSDAHcATLLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.05	25.69
1166	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=4:32249665..32251536:-1;	AC196475.3_FGP004	TRUE	TRUE	wLTPNEDGVSMaALALMNQDk	95%	n+304 (+304), K+304 (+304)	35.73	25.19
1167	parent_transcript=AC196475.3_FGT004; parent_gene=AC196475.3_FG004 seq=translation; coord=6:122797861..122838407:1;	AC196475.3_FGP004	TRUE	TRUE	wLTPNEDGVSmAALALMNQDk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	33.43	25.51
1168	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	aDILDPALMR	95%	n+304 (+304)	42.25	25.93
1169	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	aPcIIFIDEIDAIGTk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.44	25.28
1170	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	dATEVTHEDFNEGIVQVQak	95%	n+304 (+304), K+304 (+304)	37.96	25.22
1171	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	dSYLIDTLPSEYDSR	95%	n+304 (+304)	31.51	25.00
1172	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	kMNVNPDVNFEELAR	95%	K+304 (+304), n+304 (+304)	41.23	25.91
1173	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	IAGPQLVQMFIDGAK	95%	n+304 (+304), K+304 (+304)	39.98	26.24
1174	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	qIQELVEAIVLPMTHk	95%	n+304 (+304), K+304 (+304)	45.95	25.00
1175	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=6:122797861..122838407:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	qIQELVEAIVLPMTHk	92%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	27.52	25.00
1176	parent_transcript=GRMZM2G032505_T02; parent_gene=GRMZM2G032505 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G032505_P02,GRMZM2G032505_P03	TRUE	TRUE	tMLELLNQLDGFSSDER	95%	n+304 (+304)	35.75	25.00
1177	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032	GRMZM2G125032_P01	TRUE	TRUE	dISLGATFQPGTTVR	95%	n+304 (+304)	63.17	25.07

1178	seq=translation; coord=3:151819389..151821475:1; parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	fDVVANSFPSSGSFAQGyMADVAR	95%	n+304 (+304), iTRAQ8plex (+304)	41.42	25.00
1179	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	nLDAALAR	94%	n+304 (+304)	31.07	25.68
1180	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	rTGPLETFVFAMFNENQk	95%	n+304 (+304), K+304 (+304)	29.42	25.00
1181	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	sASFADSWVQSNVRPYPAVGik	95%	n+304 (+304), K+304 (+304)	30.20	25.00
1182	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	tGPLETFVFAMFNENQk	95%	n+304 (+304), K+304 (+304)	41.18	25.00
1183	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	vVSESGWPSAGGFGASVDNAR	95%	n+304 (+304)	62.64	25.00
1184	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:151819389..151821475:1;	GRMZM2G125032_P01	TRUE	TRUE	yLAGTGAPLLANVYPYFAYR	95%	n+304 (+304)	29.78	25.00
1185	parent_transcript=GRMZM2G125032_T01; parent_gene=GRMZM2G125032 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G125032_P01	TRUE	TRUE	yVAVGNEVQGDTR	95%	n+304 (+304)	62.03	25.00
1186	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	aGAYmENVEVGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	52.10	25.00
1187	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	aSTADLASPAGR	95%	n+304 (+304)	44.17	25.00
1188	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	aTMEHVMTVLAAITNQYTcLDGFAYQSGGR	95%	n+304 (+304), Carbamidomethyl (+57)	29.17	25.00
1189	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	aTmEHVMTVLAAITNQYTcLDGFAYQSGGR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	49.16	25.00
1190	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	dGSGDYTTVAAAATAAPTNSk	95%	n+304 (+304), K+304 (+304)	29.32	25.00
1191	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	dLTIENSAGPSk	95%	n+304 (+304), K+304 (+304)	44.68	26.05
1192	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	eDPNQNTGISIQR	95%	n+304 (+304)	40.56	25.00
1193	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	hVIYik	95%	n+304 (+304), K+304 (+304)	35.03	27.90
1194	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	hVNLMFVGDGIGk	95%	n+304 (+304), K+304 (+304)	45.99	26.41
1195	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106	GRMZM2G136106_P01	TRUE	TRUE	lAINDcLELLSTTMDELr	90%	n+304 (+304), Carbamidomethyl (+57)	27.51	25.00

1196	seq=translation; coord=3:56281784..56287937:1; parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	IAINDcLELLSTTmDELR	95%	n+304 (+304), Carbamidomethyl (+57), Oxidation (+16)	33.19	25.00
1197	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	mVSNsLAMAK	95%	n+304 (+304), K+304 (+304)	40.99	26.07
1198	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	nVVDGYTTFR	95%	n+304 (+304)	37.73	25.00
1199	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	sATVAVVGNNFLAR	95%	n+304 (+304)	70.75	25.02
1200	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=3:56281784..56287937:1;	GRMZM2G136106_P01	TRUE	TRUE	vAAAADLAAQSSTk	95%	n+304 (+304), K+304 (+304)	94.00	25.99
1201	parent_transcript=GRMZM2G136106_T01; parent_gene=GRMZM2G136106 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G136106_P01	TRUE	TRUE	vGADLSAFYR	95%	n+304 (+304)	40.26	25.00
1202	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	dIEFSEWk	95%	n+304 (+304), K+304 (+304)	29.53	25.00
1203	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	eVAAASEVSGEk	95%	n+304 (+304), K+304 (+304)	52.01	25.98
1204	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	gDILAVAVTEk	95%	n+304 (+304), K+304 (+304)	45.29	25.66
1205	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	gLTFDSGGYNIk	95%	n+304 (+304), K+304 (+304)	33.00	25.33
1206	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	IAGQGfK	91%	n+304 (+304), K+304 (+304)	26.43	25.97
1207	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	IPLEESYWESMk	90%	n+304 (+304), K+304 (+304)	27.40	25.74
1208	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	ITAAAVASGTVLGLYEDSR	95%	n+304 (+304)	31.14	25.94
1209	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	ITLADALVYAcNQGVEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.84	25.08
1210	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	qGGSITAALFLk	95%	n+304 (+304), K+304 (+304)	32.50	25.00
1211	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	qVDIIGLGSAGEVDQk	95%	n+304 (+304), K+304 (+304)	65.01	25.60
1212	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	tIEVNNTDAEGR	95%	n+304 (+304)	38.65	25.00
1213	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958	GRMZM2G178958_P01	TRUE	TRUE	vGLIGLGSQAPSTAAASR	94%	n+304 (+304)	29.02	25.58

1214	seq=translation; coord=5:213541443..213545321:-1; parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=5:213541443..213545321:-1;	GRMZM2G178958_P01	TRUE	TRUE	vQWMHIDMAGPVWSDk	94%	n+304 (+304), K+304 (+304)	26.07	25.00
1215	parent_transcript=GRMZM2G178958_T01; parent_gene=GRMZM2G178958 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G178958_P01	TRUE	TRUE	yANDLSSGVIFGR	95%	n+304 (+304)	33.14	25.00
1216	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	aASLEAVVEAASEK	95%	n+304 (+304), K+304 (+304)	49.91	25.83
1217	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	aEELQLQVAALK	95%	n+304 (+304), K+304 (+304)	34.29	25.29
1218	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	aQLVLEALSQk	95%	n+304 (+304), K+304 (+304)	47.61	25.00
1219	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	aSQLSDDLEAYQTK	95%	n+304 (+304), K+304 (+304)	54.63	25.00
1220	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	dLTEAENk	95%	n+304 (+304), K+304 (+304)	49.33	25.00
1221	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	gVEEELEQYR	88%	n+304 (+304)	26.15	25.00
1222	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	iLDLEAQIQAMHAAEQALK	95%	n+304 (+304), K+304 (+304)	45.43	25.01
1223	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	iQEIEAELDSSADk	95%	n+304 (+304), K+304 (+304)	28.23	25.44
1224	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	iQQEAAVSAER	95%	n+304 (+304)	35.37	25.43
1225	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	IEEEMNVdk	95%	n+304 (+304), K+304 (+304)	50.97	25.00
1226	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	IETELTTVLEELQAK	95%	n+304 (+304), K+304 (+304)	44.56	25.00
1227	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	IQLAYSk	95%	n+304 (+304), K+304 (+304)	31.95	25.00
1228	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	IVMVDELQEk	95%	n+304 (+304), K+304 (+304)	38.17	25.79
1229	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	mLELAQSNMk	95%	n+304 (+304), K+304 (+304)	30.34	26.41
1230	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182 seq=translation; coord=10:142329418..142336291:1;	GRMZM2G114182_P01	TRUE	TRUE	qITLSEik	95%	n+304 (+304), K+304 (+304)	36.83	25.00
1231	parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182	GRMZM2G114182_P01	TRUE	TRUE	tLDGMIEHK	95%	n+304 (+304), K+304 (+304)	28.83	25.43

1232	seq=translation; coord=10:142329418..142336291:1; parent_transcript=GRMZM2G114182_T01; parent_gene=GRMZM2G114182	GRMZM2G114182_P01	TRUE	TRUE	vVQEALELSk	95%	n+304 (+304), K+304 (+304)	35.28	25.21
1233	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	aGALYDTIDASGGYYVcPVDk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	54.54	25.00
1234	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	aSIYNAMPLAGVEk	95%	n+304 (+304), K+304 (+304)	43.13	26.18
1235	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	fGVIYAGAQk	95%	n+304 (+304), K+304 (+304)	45.02	25.00
1236	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	fSAASVAWSGk	92%	n+304 (+304), K+304 (+304)	28.90	26.22
1237	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	gVYNFAAGPATLPLSVLk	95%	n+304 (+304), K+304 (+304)	43.56	25.00
1238	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	kAGALYDTIDASGGYYVcPVDk	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.90	25.00
1239	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	kDLIGAAQIPVMLDFk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.38	25.00
1240	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	IVAFMk	90%	n+304 (+304), K+304 (+304)	25.35	25.00
1241	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	nVGPSGVTTIAVR	95%	n+304 (+304)	53.46	25.68
1242	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	qFIAEAAk	95%	n+304 (+304), K+304 (+304)	35.05	25.93
1243	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	sGILVADMSSNfcSkPVDVSR	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.34	25.00
1244	seq=translation; coord=1:12140829..12142573:1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	sHMNVPTLAK	95%	n+304 (+304), K+304 (+304)	28.96	26.05
1245	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G300801_T01; parent_gene=GRMZM2G300801	GRMZM2G300801_P01	TRUE	TRUE	yTALPPFDAIAQNPEAR	95%	n+304 (+304)	49.47	25.00
1246	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628	GRMZM2G032628_P01	TRUE	TRUE	aVMVPEGENGLASR	95%	n+304 (+304)	57.87	25.00
1247	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628	GRMZM2G032628_P01	TRUE	TRUE	iFQIDPMLQGYk	95%	n+304 (+304), K+304 (+304)	31.08	25.58
1248	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628	GRMZM2G032628_P01	TRUE	TRUE	IFNYGNWEVLR	95%	n+304 (+304)	30.05	25.00
1249	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628	GRMZM2G032628_P01	TRUE	TRUE	mGDIVHTLTNR	95%	n+304 (+304)	41.63	25.00

1250	seq=translation; coord=5:168451664..168468750:-1; parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628 seq=translation; coord=5:168451664..168468750:-1;	GRMZM2G032628_P01	TRUE	TRUE	vVLDSAGLFGGFSR	95%	n+304 (+304)	57.07	25.00
1251	parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628 seq=translation; coord=5:168451664..168468750:-1;	GRMZM2G032628_P01	TRUE	TRUE	vVPPPSDGQk	95%	n+304 (+304), K+304 (+304)	42.24	25.77
1252	parent_transcript=GRMZM2G032628_T01; parent_gene=GRMZM2G032628 seq=translation; coord=5:168451664..168468750:-1;	GRMZM2G032628_P01	TRUE	TRUE	ySVQAPGEIPYDGIYDPPEEVK	92%	n+304 (+304), K+304 (+304)	25.76	25.00
1253	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	aEYDPLk	93%	n+304 (+304), K+304 (+304)	29.72	26.27
1254	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	aGPALPLEALLALGLDQR	95%	n+304 (+304)	48.30	25.00
1255	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	aMFIDFLak	95%	n+304 (+304), K+304 (+304)	40.46	25.12
1256	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	dAYAVPSLATAVLGDK	95%	n+304 (+304), K+304 (+304)	40.82	25.79
1257	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	fDDTNPEAEk	95%	n+304 (+304), K+304 (+304)	55.13	25.00
1258	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	gLIAEGAATLR	95%	n+304 (+304)	33.56	26.40
1259	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	gVLHWWAEPAPGVEPLk	95%	n+304 (+304), K+304 (+304)	41.56	25.00
1260	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	gVSSTAINSFIR	95%	n+304 (+304)	42.07	25.71
1261	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	IAEILGpk	95%	n+304 (+304), K+304 (+304)	29.74	25.00
1262	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	IFMSENPAELEDWLGDNLNPHSK	95%	n+304 (+304), K+304 (+304)	30.66	25.00
1263	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	ILTLAGLR	87%	n+304 (+304)	25.25	25.00
1264	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	INISNTVMSk	93%	n+304 (+304), K+304 (+304)	28.15	26.59
1265	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	mWPDASDTDASSHk	95%	n+304 (+304), K+304 (+304)	37.68	25.00
1266	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049 seq=translation; coord=8:21816689..21823022:1;	GRMZM2G032049_P01	TRUE	TRUE	nMSDLIAYR	95%	n+304 (+304)	35.68	25.00
1267	parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049	GRMZM2G032049_P01	TRUE	TRUE	sTVTDVLEENMEAIk	91%	n+304 (+304), K+304 (+304)	26.63	25.80

1268	seq=translation; coord=8:21816689..21823022:1; parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049	GRMZM2G032049_P01	TRUE	TRUE	vWITNLEEGk	95%	n+304 (+304), K+304 (+304)	39.77	25.00
1269	seq=translation; coord=8:21816689..21823022:1; parent_transcript=GRMZM2G032049_T01; parent_gene=GRMZM2G032049	GRMZM2G032049_P01	TRUE	TRUE	wVDGWDDPR	87%	n+304 (+304)	25.18	25.00
1270	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	aIELADPMENAGASLIR	95%	n+304 (+304)	75.37	25.00
1271	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	aLLQDIAIVTGAIEYQSk	95%	n+304 (+304), K+304 (+304)	61.85	25.16
1272	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	aLVAPAALIAHNAGVEGEVIVDk	95%	n+304 (+304), K+304 (+304)	45.39	25.00
1273	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	aPLIIAEDVSGEALATLVINK	95%	n+304 (+304), K+304 (+304)	40.17	25.00
1274	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	aVAAISAGNDEFVGTMI AEAIK	95%	n+304 (+304), K+304 (+304)	74.68	25.08
1275	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	dLGLLVEDTTVEQLGIAR	95%	n+304 (+304)	85.59	25.30
1276	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	eIAFDQGSR	95%	n+304 (+304)	29.93	25.00
1277	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	eIIPLEQTTQLR	95%	n+304 (+304)	70.90	25.00
1278	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	eTLDDPEER	95%	n+304 (+304)	35.83	25.00
1279	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	IAAAVGVTLGPR	95%	n+304 (+304)	39.23	25.21
1280	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	IGADI IQk	89%	n+304 (+304), K+304 (+304)	25.79	25.00
1281	seq=translation; coord=1:299988513..299993142:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	IGMLSITSGANPVSVk	95%	n+304 (+304), K+304 (+304)	41.62	25.29
1282	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G434173_T01; parent_gene=GRMZM2G434173	GRMZM2G434173_P01	TRUE	TRUE	vGASTEAELEDR	95%	n+304 (+304)	68.29	25.00
1283	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771	GRMZM2G005771_P01, GRMZM2G005771_P02	TRUE	TRUE	aLQPIFIYGR	95%	n+304 (+304)	34.57	25.40
1284	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771	GRMZM2G005771_P01, GRMZM2G005771_P02	TRUE	TRUE	hVPVNIAGTR	95%	n+304 (+304)	43.60	25.00
1285	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771	GRMZM2G005771_P01, GRMZM2G005771_P02	TRUE	TRUE	icDGEWLYADPDGILVSR	95%	n+304 (+304), Carbamidomethyl (+57)	41.65	25.00

1286	seq=translation; coord=5:65023010..65024952:-1; parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771 seq=translation; coord=5:65023010..65024952:-1;	GRMZM2G005771_P01,GRMZM2G005771_P02	TRUE	TRUE	qVFAGPIVTLk	95%	n+304 (+304), K+304 (+304)	44.43	25.00
1287	parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771 seq=translation; coord=5:65023010..65024952:-1;	GRMZM2G005771_P01,GRMZM2G005771_P02	TRUE	TRUE	vLVVDGGGSMR	95%	n+304 (+304)	39.42	25.00
1288	parent_transcript=GRMZM2G005771_T01; parent_gene=GRMZM2G005771 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G005771_P01,GRMZM2G005771_P02	TRUE	TRUE	vYEDNVLVR	95%	n+304 (+304)	32.44	25.00
1289	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	aGATTLNIPDTVGYNLPYEFgk	95%	n+304 (+304), K+304 (+304)	41.27	25.61
1290	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	aNTPGIEk	92%	n+304 (+304), K+304 (+304)	27.73	25.00
1291	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	eFLYHILGEVIk	95%	n+304 (+304), K+304 (+304)	32.46	25.00
1292	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	eLLDGLYTGDISR	95%	n+304 (+304)	39.03	25.00
1293	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	eYSMTSVTEGIDAIATTR	95%	n+304 (+304)	90.58	25.00
1294	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	eySMTSVTEGIDAIATTR	95%	n+304 (+304), iTRAQ8plex (+304)	65.44	25.20
1295	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	sFSGSGASMDIVVSSVR	92%	n+304 (+304)	26.12	25.00
1296	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=10:1725712..1731899:-1;	GRMZM2G130062_P01	TRUE	TRUE	sLGcTDVEFSPEDAGR	95%	n+304 (+304), Carbamidomethyl (+57)	59.75	25.00
1297	parent_transcript=GRMZM2G130062_T01; parent_gene=GRMZM2G130062 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G130062_P01	TRUE	TRUE	vVVTGDVSNNak	95%	n+304 (+304), K+304 (+304)	47.39	26.04
1298	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	aGEDQYSLASR	95%	n+304 (+304)	41.13	25.00
1299	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	dGTALVLWEWcEGDNQR	95%	n+304 (+304), Carbamidomethyl (+57)	75.54	25.00
1300	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	dVGdGFR	86%	n+304 (+304)	25.48	25.00
1301	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	gPPPPVYGGYGQPPPPDPYGR	93%	n+304 (+304)	27.39	25.00
1302	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304 seq=translation; coord=3:31898226..31901626:-1;	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	hNPDSLDESVLWTESR	95%	n+304 (+304)	95.75	25.00
1303	parent_transcript=GRMZM2G120304_T01; parent_gene=GRMZM2G120304	GRMZM2G120304_P01,GRMZM2G120304_P02	TRUE	TRUE	rGPPPPVYGGYGQPPPPDPYGR	95%	n+304 (+304)	44.22	25.00

1304	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	aGSDDVGAASANSTAASGEDLk	95%	n+304 (+304), K+304 (+304)	80.87	25.00
1305	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	gLLDLTcQTVADMIk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	45.03	26.27
1306	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	nDFTPEEEEEIR	95%	n+304 (+304)	52.45	25.00
1307	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	nDFTPEEEEEIRR	94%	n+304 (+304)	28.44	25.00
1308	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	nWDADFVk	86%	n+304 (+304), K+304 (+304)	25.08	25.00
1309	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	sSDGEEFEVEEAVAMESQTIR	95%	n+304 (+304)	57.99	25.00
1310	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	vDQATLFDLILAANYLNik	95%	n+304 (+304), K+304 (+304)	40.80	25.00
1311	seq=translation; coord=4:20543360..20550099:-1; parent_transcript=GRMZM2G101446_T01; parent_gene=GRMZM2G101446	GRMZM2G101446_P01,GRMZM2G101446_P02	TRUE	TRUE	vIEYcNk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.97	25.66
1312	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	aDLVVDVLik	95%	n+304 (+304), K+304 (+304)	43.62	25.00
1313	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	dFGSAVWDMIR	95%	n+304 (+304)	49.44	25.00
1314	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	dIQPGSIIPYLVr	93%	n+304 (+304)	29.27	25.00
1315	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	gTGYTIk	86%	n+304 (+304), K+304 (+304)	25.95	25.48
1316	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	iDVDTPFGNMk	95%	n+304 (+304), K+304 (+304)	43.07	25.20
1317	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	iPVSLVFDIik	94%	n+304 (+304), K+304 (+304)	28.34	25.00
1318	seq=translation; coord=1:297016125..297019051:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	nPNPVPiPLVDIDYLI DSGR	95%	n+304 (+304)	61.58	25.42
1319	seq=translation; coord=3:146522696..146524904:-1; parent_transcript=GRMZM2G352415_T01; parent_gene=GRMZM2G352415	GRMZM2G352415_P01,GRMZM2G352415_P02, GRMZM2G352415_P03	TRUE	TRUE	vLLVDVPIIGr	95%	n+304 (+304)	38.25	25.00
1320	seq=translation; coord=3:146522696..146524904:-1; parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342	GRMZM2G103342_P01	TRUE	TRUE	eFLASAVr	91%	n+304 (+304)	28.35	25.08
1321	seq=translation; coord=3:146522696..146524904:-1; parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342	GRMZM2G103342_P01	TRUE	TRUE	eSVALGGGPAYk	95%	n+304 (+304), K+304 (+304)	54.86	26.28

1322	seq=translation; coord=3:146522696..146524904:-1; parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	iNLDTVTLVALSGGHTVGIAHcGSFDNR	95%	n+304 (+304), Carbamidomethyl (+57)	37.84	25.00
1323	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	IFPTQDPTLNk	95%	n+304 (+304), K+304 (+304)	45.40	25.97
1324	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	mGQVNVLTGSQGQVR	95%	n+304 (+304)	64.91	25.77
1325	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	qNVGLAAALIR	95%	n+304 (+304)	68.15	25.00
1326	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	vPTLLSFLAK	95%	n+304 (+304), K+304 (+304)	56.05	25.00
1327	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	vVScADIVALAAR	95%	n+304 (+304), Carbamidomethyl (+57)	54.62	25.68
1328	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=3:146522696..146524904:-1;	GRMZM2G103342_P01	TRUE	TRUE	yPPLAPGLSFDFYk	95%	n+304 (+304), K+304 (+304)	52.28	25.87
1329	parent_transcript=GRMZM2G103342_T01; parent_gene=GRMZM2G103342 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G103342_P01	TRUE	TRUE	yYVDLLNR	91%	n+304 (+304)	28.95	25.69
1330	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	aLTLFAPNDDAFk	95%	n+304 (+304), K+304 (+304)	45.09	26.10
1331	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	dLPDLsk	91%	n+304 (+304), K+304 (+304)	28.44	25.11
1332	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	iPTLASTAAGk	95%	n+304 (+304), K+304 (+304)	68.54	26.30
1333	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	lIVSSGVvk	95%	n+304 (+304), K+304 (+304)	32.20	25.00
1334	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	lLTLLDYFDEk	95%	n+304 (+304), K+304 (+304)	46.41	25.44
1335	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	lLTLLDYFDEkk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	33.18	25.00
1336	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	ITSADLVALQYHALPQYAPk	95%	n+304 (+304), K+304 (+304)	50.20	25.00
1337	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=2:16219232..16221297:1;	GRMZM2G003752_P01	TRUE	TRUE	vAFASAAPGak	95%	n+304 (+304), K+304 (+304)	38.13	25.38
1338	parent_transcript=GRMZM2G003752_T01; parent_gene=GRMZM2G003752 seq=translation; coord=6:160621048..160624717:1;	GRMZM2G003752_P01	TRUE	TRUE	yDLAVASSGDEVTLDTGVdk	95%	n+304 (+304), K+304 (+304)	78.65	25.00
1339	parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	aHVAVFNTLLQLVDDGR	93%	n+304 (+304)	29.59	26.53

1340	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	aLAEQFLDDENLLVR	95%	n+304 (+304)	44.94	25.16
1341	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	dLVMQEVVR	95%	n+304 (+304)	32.27	25.48
1342	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	eELQFTLQEAER	95%	n+304 (+304)	47.89	25.00
1343	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	gDSHLAVDQLLGLLEDQSI/SDcLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.09	25.00
1344	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	gDVPSNLLDVR	93%	n+304 (+304)	28.72	25.42
1345	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	iDMSEYMEQHSVAR	95%	n+304 (+304)	65.11	25.00
1346	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	IDEIVFDPLSHEQLR	95%	n+304 (+304)	52.58	25.66
1347	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	IIALDMGALVAGAK	95%	n+304 (+304), K+304 (+304)	32.71	25.00
1348	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	qAITGASGGDGAAGDSFER	95%	n+304 (+304)	96.05	25.00
1349	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	rEELQFTLQEAER	95%	n+304 (+304)	31.15	25.00
1350	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	tEGSMDAANLFKPMILAR	95%	n+304 (+304), K+304 (+304)	33.55	25.76
1351	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	vQLDSQP EEIDNLER	95%	n+304 (+304)	64.81	25.00
1352	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	vVGQTEAVSAVAEAVLR	95%	n+304 (+304)	56.32	26.07
1353	seq=translation; coord=6:160621048..160624717:1; parent_transcript=GRMZM2G360681_T01; parent_gene=GRMZM2G360681	GRMZM2G360681_P01	TRUE	TRUE	yGALQEIDAAISK	95%	n+304 (+304), K+304 (+304)	61.86	25.48
1354	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	aATVVTPk	94%	n+304 (+304), K+304 (+304)	29.35	25.00
1355	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	eDDIIGILETDDVvk	95%	n+304 (+304), K+304 (+304)	47.04	26.21
1356	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	gADGTAYIVLR	95%	n+304 (+304)	47.24	25.00

1357	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	iAVDIETGAQVVYSK	95%	n+304 (+304), K+304 (+304)	51.63	25.00
1358	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	qPLSVSAGSTVLYSK	91%	n+304 (+304), K+304 (+304)	25.93	25.00
1359	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	qPLSVSAGSTVLYSK	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	31.29	25.00
1360	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	rQPLSVSAGSTVLYSK	94%	n+304 (+304), K+304 (+304)	25.69	25.00
1361	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	tPGGLILTETTK	95%	n+304 (+304), K+304 (+304)	37.77	25.00
1362	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	tVGGILLPSTAQTkPQGGEVVAVGAGR	95%	n+304 (+304), K+304 (+304)	38.05	25.00
1363	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	yAGTEVEFNDSk	95%	n+304 (+304), K+304 (+304)	28.78	25.00
1364	seq=translation; coord=9:11079860..11085004:-1; parent_transcript=GRMZM2G127609_T01; parent_gene=GRMZM2G127609	GRMZM2G127609_P01,GRMZM2G127609_P02, GRMZM2G127609_P03,GRMZM2G127609_P04, GRMZM2G127609_P06,GRMZM2G127609_P07, GRMZM2G127609_P08	TRUE	TRUE	yAGTEVEFNDSk	94%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.53	25.91
1365	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	dGLQFASK	95%	n+304 (+304), K+304 (+304)	34.93	26.16
1366	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	eSGEPVPEYDYLpYfYSR	95%	n+304 (+304), iTRAQ8plex (+304)	31.72	25.00
1367	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	IPGFYVcVSGSGEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	49.17	25.00
1368	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	ITDFGTQGADSNILYLR	95%	n+304 (+304)	32.60	25.00
1369	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	IVAAIQAk	95%	n+304 (+304), K+304 (+304)	40.47	25.45
1370	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	qGVkPGLAIIsk	86%	Pyro-cmC (-17), n+304 (+304), K+304 (+304), K+304 (+304)	25.37	25.00
1371	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881	GRMZM2G084881_P01	TRUE	TRUE	sFDLAWQFYGDNVGETILFGSDPTSSkPk	94%	n+304 (+304), K+304 (+304), K+304 (+304)	25.85	25.00

1372	seq=translation; coord=2:165615333..165620418:-1; parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881 seq=translation; coord=2:165615333..165620418:-1;	GRMZM2G084881_P01	TRUE	TRUE	tLTSAGANFTYEILLIATGSSVIK	95%	n+304 (+304), K+304 (+304)	34.60	25.00
1373	parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881 seq=translation; coord=2:165615333..165620418:-1;	GRMZM2G084881_P01	TRUE	TRUE	tQPPVANLEELk	95%	n+304 (+304), K+304 (+304)	47.43	25.00
1374	parent_transcript=GRMZM2G084881_T01; parent_gene=GRMZM2G084881 seq=translation; coord=2:165615333..165620418:-1;	GRMZM2G084881_P01	TRUE	TRUE	vLGAFLEGGSPDENk	95%	n+304 (+304), K+304 (+304)	57.77	25.26
1375	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=8:158089079..158099475:-1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	aAAVAALSSVLTAEQSGSSENLR	95%	n+304 (+304)	71.36	25.05
1376	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=8:158089079..158099475:-1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	dAAVDGAPSDTDGAVAETR	95%	n+304 (+304)	83.74	25.00
1377	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=8:158089079..158099475:-1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	eEETTENVGEATFSYDR	95%	n+304 (+304)	102.32	25.00
1378	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=8:158089079..158099475:-1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	ePPQFVALFQPMILk	95%	n+304 (+304), K+304 (+304)	36.70	25.00
1379	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=8:158089079..158099475:-1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	gATGETYTTGIALIR	95%	n+304 (+304)	72.42	25.00
1380	parent_transcript=GRMZM2G180988_T02; parent_gene=GRMZM2G180988 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G180988_P02,GRMZM2G180988_P03	TRUE	TRUE	sTTPVNEEVPLLEGGGk	95%	n+304 (+304), K+304 (+304)	29.31	25.08
1381	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	aVILGHSGFGMVALEFVR	95%	n+304 (+304)	50.64	26.05
1382	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	eLMELVEAASER	95%	n+304 (+304)	57.39	25.00
1383	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	iNLISVLAFek	95%	n+304 (+304), K+304 (+304)	34.11	25.00
1384	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	IQAPLVVTR	95%	n+304 (+304)	36.58	25.98
1385	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	IVLVAPTLPGGFLEPVR	95%	n+304 (+304)	36.30	25.00
1386	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	mGSFAAPMVPMTYISGVGNR	91%	n+304 (+304)	25.77	25.00
1387	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=2:167237699..167240039:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	sFESAIVNFPSPAVFGR	95%	n+304 (+304)	35.41	25.63
1388	parent_transcript=GRMZM2G352855_T01; parent_gene=GRMZM2G352855 seq=translation; coord=7:10287294..10291100:1;	GRMZM2G352855_P01,GRMZM2G352855_P03, GRMZM2G352855_P04,GRMZM2G352855_P05	TRUE	TRUE	yAPSPGQTSEVYSR	95%	n+304 (+304)	58.86	25.00
1389	parent_transcript=GRMZM2G100403_T02; parent_gene=GRMZM2G100403	GRMZM2G100403_P02	TRUE	TRUE	fVIWTQSAFNk	95%	n+304 (+304), K+304 (+304)	51.29	25.87

1390	seq=translation; coord=7:10287294..10291100:1; parent_transcript=GRMZM2G100403_T02; parent_gene=GRMZM2G100403	GRMZM2G100403_P02	TRUE	TRUE	iESVPEMPLVISDSAESIEK	95%	n+304 (+304), K+304 (+304)	48.26	25.95
1391	seq=translation; coord=7:10287294..10291100:1; parent_transcript=GRMZM2G100403_T02; parent_gene=GRMZM2G100403	GRMZM2G100403_P02	TRUE	TRUE	tMVSDSDYTEFENFSK	94%	n+304 (+304), K+304 (+304)	28.72	25.00
1392	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	dQDDQWIR	87%	n+304 (+304)	25.63	25.00
1393	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	eEVIQAWYMDSEEDQR	93%	n+304 (+304)	29.81	25.00
1394	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	eFIPLDk	90%	n+304 (+304), K+304 (+304)	26.63	25.26
1395	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	fTLDSDNyIK	95%	n+304 (+304), K+304 (+304)	51.52	25.00
1396	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	gYSYMDicDVcPEk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	56.77	25.00
1397	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	INADDWENDENLk	95%	n+304 (+304), K+304 (+304)	47.85	25.00
1398	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	INADDWENDENLkk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	32.41	25.48
1399	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	ISELGILSWR	95%	n+304 (+304)	35.66	25.33
1400	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	nFFEEHLHTDEEIR	95%	n+304 (+304)	38.78	25.00
1401	seq=translation; coord=1:12514731..12519380:1; parent_transcript=GRMZM2G165998_T01; parent_gene=GRMZM2G165998	GRMZM2G165998_P01,GRMZM2G165998_P03	TRUE	TRUE	ycLESGSYFDVR	95%	n+304 (+304), Carbamidomethyl (+57)	61.86	25.00
1402	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	aGLVNAlk	95%	n+304 (+304), K+304 (+304)	34.16	25.00
1403	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	eTFDTSDLNASLPAAAAALSIEDR	93%	n+304 (+304)	28.07	25.00
1404	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	gVPDFWLtAMk	89%	n+304 (+304), K+304 (+304)	28.03	26.11
1405	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	IDFFFDtNPFFk	95%	n+304 (+304), K+304 (+304)	40.24	26.04
1406	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	IYEPLYtk	95%	n+304 (+304), K+304 (+304)	30.54	25.00

1407	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	tNEVLSEEIQER	95%	n+304 (+304)	46.01	25.00
1408	seq=translation; coord=9:19393494..19397648:-1; parent_transcript=GRMZM2G140051_T01; parent_gene=GRMZM2G140051	GRMZM2G140051_P01,GRMZM2G140051_P02	TRUE	TRUE	tYHMVDEDDPILEK	95%	n+304 (+304), K+304 (+304)	40.29	25.00
1409	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	aGcLSILcEDEMQAVAVk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	59.21	25.00
1410	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	dPILGVTEAFLADPSSDk	95%	n+304 (+304), K+304 (+304)	39.10	25.95
1411	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	eISHQFk	91%	n+304 (+304), K+304 (+304)	25.24	25.00
1412	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	gLDFSGLMNEIk	95%	n+304 (+304), K+304 (+304)	39.41	25.69
1413	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	hFPFFDMAYQGFASGDPER	95%	n+304 (+304)	58.49	25.00
1414	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	hFPFFDMAYQGFASGDPER	95%	n+304 (+304), iTRAQ8plex (+304)	47.29	25.00
1415	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	iAGLNMEYLPMGGSVk	95%	n+304 (+304), K+304 (+304)	51.78	25.85
1416	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	iSMAGVTTGNVGYLANAIHEVTkPN	95%	n+304 (+304), K+304 (+304)	59.90	25.00
1417	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	kHFPFFDMAYQGFASGDPER	95%	K+304 (+304), n+304 (+304)	30.08	25.00
1418	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	lAYGEDSDFIk	95%	n+304 (+304), K+304 (+304)	55.50	25.00
1419	seq=translation; coord=5:146841857..146847013:-1; parent_transcript=GRMZM2G146677_T01; parent_gene=GRMZM2G146677	GRMZM2G146677_P01	TRUE	TRUE	lFADFQk	92%	n+304 (+304), K+304 (+304)	28.68	26.35
1420	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	nAPDGSFFLLHAcAHNPTGVDPTEEQWR	93%	n+304 (+304), Carbamidomethyl (+57)	25.10	25.00
1421	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	dPAAAPVAVGPGAEGAPPSQLPR	95%	n+304 (+304)	71.98	25.31
1422	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	hHLAFSVADYDGFVTGLk	95%	n+304 (+304), K+304 (+304)	28.83	25.88
1423	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	iPSPTYSGFQVAVLR	95%	n+304 (+304)	44.06	25.38

1424	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	IAAFYEAVLGFER	95%	n+304 (+304)	31.85	25.34
1425	seq=translation; coord=1:258878414..258878962:1; parent_transcript=GRMZM2G704005_T01; parent_gene=GRMZM2G704005	GRMZM2G704005_P01	TRUE	TRUE	IPSSPDVALHLIER	95%	n+304 (+304)	91.78	25.91
1426	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	aGEDADSLGLTGR	95%	n+304 (+304)	45.37	25.00
1427	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	cILMDNTGVPVVDLAAMR	95%	Carbamidomethyl (+57), n+304 (+304)	33.27	25.00
1428	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	dGVTTTIDIVLTMTQMLR	90%	n+304 (+304)	28.47	25.88
1429	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	dIWPSNQEIDEVVSVQTHLFk	95%	n+304 (+304), K+304 (+304)	33.21	25.13
1430	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	eALYPWEDR	95%	n+304 (+304)	43.70	25.00
1431	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	iIDWENTSPk	95%	n+304 (+304), K+304 (+304)	43.81	25.39
1432	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	iNPLIPDAVIDHAVR	95%	n+304 (+304)	50.50	25.08
1433	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	IAEIPFkPAR	94%	n+304 (+304), K+304 (+304)	28.25	25.00
1434	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	IYVYDAAMk	95%	n+304 (+304), K+304 (+304)	36.55	25.75
1435	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	tSLTPGSVVATEYlk	95%	n+304 (+304), K+304 (+304)	40.31	25.00
1436	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	vDVAGTYDALDR	95%	n+304 (+304)	44.23	25.00
1437	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	vLLESAIR	89%	n+304 (+304)	26.96	25.00
1438	seq=translation; coord=10:96330046..96338713:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	vYDSIMER	95%	n+304 (+304)	34.08	25.00
1439	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM5G858454_T02; parent_gene=GRMZM5G858454	GRMZM5G858454_P02	TRUE	TRUE	wNQLPVPk	95%	n+304 (+304), K+304 (+304)	34.74	25.37
1440	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	aYPTVNEDYlk	95%	n+304 (+304), K+304 (+304)	36.60	26.15
1441	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	eLLSGEk	92%	n+304 (+304), K+304 (+304)	29.41	26.76

1442	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=2:218589206..218592127:-1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	IAWHSAGTFDVBATk	92%	n+304 (+304), K+304 (+304)	27.62	25.73
1443	parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=2:218589206..218592127:-1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	nPAEQAHGANAGLEIAIR	95%	n+304 (+304)	42.17	25.92
1444	seq=translation; coord=2:218589206..218592127:-1; parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=2:218589206..218592127:-1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	qDkPEPPPEGR	91%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	25.38	25.00
1445	parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=2:218589206..218592127:-1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	qVFSTQMGLSDQDIVALSGGHTLGR	95%	n+304 (+304)	93.33	25.00
1446	parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=2:218589206..218592127:-1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	sGFEGAWTSNPLIFDNSYFk	90%	n+304 (+304), K+304 (+304)	25.69	25.00
1447	parent_transcript=GRMZM2G140667_T01; parent_gene=GRMZM2G140667 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G140667_P01,GRMZM2G140667_P02	TRUE	TRUE	yAADEDAFFADYAEHLK	95%	n+304 (+304), K+304 (+304)	45.28	25.00
1448	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	aAVVLVADVFGFEAPIMR	95%	n+304 (+304)	42.76	26.55
1449	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	aAVVLVADVFGFEAPImR	92%	n+304 (+304), Oxidation (+16)	26.70	26.04
1450	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	aYVAGPEDSk	95%	n+304 (+304), K+304 (+304)	38.19	25.81
1451	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	gFEETk	87%	n+304 (+304), K+304 (+304)	27.48	26.67
1452	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	iFPGVAHGWSVR	95%	n+304 (+304)	50.39	25.95
1453	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	qVIGAlk	95%	n+304 (+304), K+304 (+304)	29.04	25.00
1454	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=6:145087390..145092201:1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	sAEeAFADMLDWFNk	95%	n+304 (+304), K+304 (+304)	49.03	25.00
1455	parent_transcript=GRMZM2G179301_T02; parent_gene=GRMZM2G179301 seq=translation; coord=1:79067709..79069201:-1;	GRMZM2G179301_P02,GRMZM2G179301_P03	TRUE	TRUE	vVDSFGGLk	95%	n+304 (+304), K+304 (+304)	35.95	25.62
1456	parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925 seq=translation; coord=1:79067709..79069201:-1;	GRMZM2G148925_P01	TRUE	TRUE	gEQQVVSgMNYR	95%	n+304 (+304)	49.70	25.00
1457	parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925 seq=translation; coord=1:79067709..79069201:-1;	GRMZM2G148925_P01	TRUE	TRUE	gEQQVVSgMNYR	95%	n+304 (+304), Oxidation (+16)	39.32	25.00
1458	parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925 seq=translation; coord=1:79067709..79069201:-1;	GRMZM2G148925_P01	TRUE	TRUE	IAADGLR	93%	n+304 (+304)	30.15	25.87
1459	parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	TRUE	TRUE	IYVDAADPAGR	93%	n+304 (+304)	29.66	25.00

1460	seq=translation; coord=1:79067709..79069201:-1; parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	TRUE	TRUE	qLASFPVPR	95%	n+304 (+304)	35.09	26.01
1461	seq=translation; coord=1:79067709..79069201:-1; parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	TRUE	TRUE	tVPYVAVVYEQVWTR	95%	n+304 (+304)	43.88	26.01
1462	seq=translation; coord=1:79067709..79069201:-1; parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	TRUE	TRUE	tVPYVAVVYEQVWTR	95%	n+304 (+304), iTRAQ8plex (+304)	32.45	25.45
1463	seq=translation; coord=1:79067709..79069201:-1; parent_transcript=GRMZM2G148925_T01; parent_gene=GRMZM2G148925	GRMZM2G148925_P01	TRUE	TRUE	tVPYVAVVYEQVWTR	95%	n+304 (+304), iTRAQ8plex (+304)	56.35	25.49
1464	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	aQEETYGSSGYGYGR	95%	n+304 (+304)	33.95	25.00
1465	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	kASEEDEGAFGSGGYR	95%	K+304 (+304), n+304 (+304)	34.44	25.00
1466	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	kNEEQSYGSGGYGYEK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	34.10	25.00
1467	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	kPQVEESYGSEYSGFGR	95%	K+304 (+304), n+304 (+304)	38.82	25.00
1468	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	qEESYSGSYGR	95%	n+304 (+304)	36.52	25.00
1469	seq=translation; coord=6:113557759..113560731:-1; parent_transcript=GRMZM2G701082_T04; parent_gene=GRMZM2G701082	GRMZM2G701082_P04,GRMZM2G701082_P05, GRMZM2G701082_P06	TRUE	TRUE	tPQVEESYGSGYGR	95%	n+304 (+304)	52.52	25.00
1470	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	aVLDTAIANR	90%	n+304 (+304)	28.17	25.81
1471	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	eSALVQEV	93%	n+304 (+304)	29.32	25.00
1472	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	IAFAVGDSGDGcAGSMAAEAYAAR	95%	n+304 (+304), Carbamidomethyl (+57)	40.63	25.00
1473	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	IAFAVGDSGDGcAGSMAAEyAAR	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)	41.64	25.00
1474	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	IGNEASIR	93%	n+304 (+304)	31.36	26.61
1475	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	mDAVTLVIHNPGEEDPacGPLIDGVAIR	95%	n+304 (+304), Carbamidomethyl (+57)	64.32	25.00
1476	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	mDAVTLVIHNPGEEDPacGPLIDGVAIR	95%	Oxidation (+16), n+304 (+304), Carbamidomethyl (+57)	72.23	25.00
1477	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	qGDMLLVPPQGAHAVR	95%	n+304 (+304)	41.61	26.16

1478	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	qGDMLLVVPQGAHAVR	95%	Pyro-cmC (-17), n+304 (+304)	47.91	25.00
1479	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	qGDmLLVVPQGAHAVR	95%	n+304 (+304), Oxidation (+16)	38.80	25.87
1480	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	qGDmLLVVPQGAHAVR	95%	Pyro-cmC (-17), n+304 (+304), Oxidation (+16)	57.40	25.00
1481	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	wETSGFVEYIESGHk	95%	n+304 (+304), K+304 (+304)	57.23	25.00
1482	seq=translation; coord=3:224673584..224677732:1; parent_transcript=GRMZM2G034985_T01; parent_gene=GRMZM2G034985	GRMZM2G034985_P01,GRMZM2G034985_P03	TRUE	TRUE	yVDAAHFAVPQGAR	95%	n+304 (+304)	35.93	25.48
1483	seq=translation; coord=5:15546617..15552849:-1; parent_transcript=GRMZM2G112149_T01; parent_gene=GRMZM2G112149	GRMZM2G112149_P01,GRMZM2G112149_P02, GRMZM2G112149_P03	TRUE	TRUE	aAGASWIQLDEPTLVk	95%	n+304 (+304), K+304 (+304)	47.84	25.40
1484	seq=translation; coord=5:15546617..15552849:-1; parent_transcript=GRMZM2G112149_T01; parent_gene=GRMZM2G112149	GRMZM2G112149_P01,GRMZM2G112149_P02, GRMZM2G112149_P03	TRUE	TRUE	dEVYFAANAAQASR	95%	n+304 (+304)	80.40	25.00
1485	seq=translation; coord=5:15546617..15552849:-1; parent_transcript=GRMZM2G112149_T01; parent_gene=GRMZM2G112149	GRMZM2G112149_P01,GRMZM2G112149_P02, GRMZM2G112149_P03	TRUE	TRUE	nIWADDLAASLTLHSLEAVAGk	95%	n+304 (+304), K+304 (+304)	30.05	25.00
1486	seq=translation; coord=5:15546617..15552849:-1; parent_transcript=GRMZM2G112149_T01; parent_gene=GRMZM2G112149	GRMZM2G112149_P01,GRMZM2G112149_P02, GRMZM2G112149_P03	TRUE	TRUE	sSAEDLEk	94%	n+304 (+304), K+304 (+304)	30.54	25.00
1487	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	fTPAPADSGR	89%	n+304 (+304)	26.14	25.00
1488	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	gLTHEEMMLPTGPR	95%	n+304 (+304)	48.41	25.00
1489	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	gTTLSEFTTFGAAAAQR	95%	n+304 (+304)	63.98	25.16
1490	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	iDVELEHR	95%	n+304 (+304)	44.36	25.40
1491	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	iSMLESQLEQLSR	95%	n+304 (+304)	47.06	25.75
1492	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	sSDLDMTSR	91%	n+304 (+304)	26.76	25.00
1493	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	vNPFGDakPR	95%	n+304 (+304), K+304 (+304)	41.71	25.37
1494	seq=translation; coord=2:37325095..37329643:1; parent_transcript=GRMZM2G163471_T01; parent_gene=GRMZM2G163471	GRMZM2G163471_P01	TRUE	TRUE	vTTLAPTSLGEEPQATVVDRPR	95%	n+304 (+304)	33.35	25.67
1495	seq=translation; coord=7:18473070..18475522:1; parent_transcript=GRMZM2G168149_T01; parent_gene=GRMZM2G168149	GRMZM2G168149_P01	TRUE	TRUE	tYGFLTPEFWAETk	95%	n+304 (+304), K+304 (+304)	48.94	25.29

1496	seq=translation; coord=6:44382950..44385913:-1; parent_transcript=GRMZM2G087570_T01; parent_gene=GRMZM2G087570	GRMZM2G087570_P01	TRUE	TRUE	hVVFQGVVEGMDIVR	95%	n+304 (+304)	62.61	25.11
1497	seq=translation; coord=6:44382950..44385913:-1; parent_transcript=GRMZM2G087570_T01; parent_gene=GRMZM2G087570	GRMZM2G087570_P01	TRUE	TRUE	iVIGLYGDDVPQTAENFR	95%	n+304 (+304)	77.56	25.17
1498	seq=translation; coord=6:44382950..44385913:-1; parent_transcript=GRMZM2G087570_T01; parent_gene=GRMZM2G087570	GRMZM2G087570_P01	TRUE	TRUE	iVIGLYGDDVPQTAENFR	91%	n+304 (+304), iTRAQ8plex (+304)	26.20	25.79
1499	seq=translation; coord=6:44382950..44385913:-1; parent_transcript=GRMZM2G087570_T01; parent_gene=GRMZM2G087570	GRMZM2G087570_P01	TRUE	TRUE	IIESQETDR	93%	n+304 (+304)	30.03	25.00
1500	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	aVLPQEVEAAR	95%	n+304 (+304)	33.63	26.63
1501	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	dGPALQVELLR	95%	n+304 (+304)	40.74	26.20
1502	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	eAVFTYAEDAASGSLPLMQk	95%	n+304 (+304), K+304 (+304)	54.97	25.26
1503	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	eELGcVFLTGER	95%	n+304 (+304), Carbamidomethyl (+57)	49.17	25.00
1504	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	eLISAIDR	95%	n+304 (+304)	32.84	25.49
1505	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	iAGIEGGFFk	95%	n+304 (+304), K+304 (+304)	45.34	25.00
1506	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	IAIANIGk	92%	n+304 (+304), K+304 (+304)	28.58	25.00
1507	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	IVDPMLEcLk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.70	25.90
1508	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	vAVAEGTAPVANR	95%	n+304 (+304)	34.28	26.07
1509	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	vFVGISQGk	95%	n+304 (+304), K+304 (+304)	29.96	25.00
1510	seq=translation; coord=5:186677004..186680745:-1; parent_transcript=GRMZM2G074604_T01; parent_gene=GRMZM2G074604	GRMZM2G074604_P01	TRUE	TRUE	vLTMNPSGELSSAR	95%	n+304 (+304)	41.77	25.00
1511	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	aVVGEELSSDLLYLEFLDKFER	95%	n+304 (+304), K+304 (+304)	70.27	25.47
1512	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	gYPGYMYTDLATIYER	90%	n+304 (+304)	27.19	25.00
1513	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	gyPGYMYTDLATIYER	95%	n+304 (+304), iTRAQ8plex (+304)	41.22	25.00

1514	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	hVLVILTDMSSYADALR	95%	n+304 (+304)	50.23	25.24
1515	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	iALTTAEYLAYEcGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	53.53	25.09
1516	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	iPLFSAAGLPHNEIAAQicR	95%	n+304 (+304), Carbamidomethyl (+57)	50.48	26.07
1517	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	nIFQSLDLAWTLR	95%	n+304 (+304)	56.73	25.07
1518	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	qIYPPINVLPSLSR	95%	n+304 (+304)	33.21	25.76
1519	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	sAIGEGMTR	87%	n+304 (+304)	26.11	25.19
1520	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	tPVSLDMLGR	94%	n+304 (+304)	32.01	25.72
1521	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	tVSGVAGPLVLDk	95%	n+304 (+304), K+304 (+304)	46.79	25.00
1522	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	vTLFLNLANDPTIER	95%	n+304 (+304)	72.30	25.47
1523	seq=translation; coord=9:78409591..78421558:1; parent_transcript=GRMZM2G094497_T01; parent_gene=GRMZM2G094497	GRMZM2G094497_P01,GRMZM2G181151_P01, GRMZM2G181151_P02	TRUE	TRUE	yTTVQFTGEVLk	95%	n+304 (+304), K+304 (+304)	52.94	25.00
1524	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	fLILPSLLSGR	95%	n+304 (+304)	34.45	25.00
1525	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	gGPQMIQLSLDGk	95%	n+304 (+304), K+304 (+304)	35.00	26.32
1526	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	gPGYATPLEAMEk	89%	n+304 (+304), K+304 (+304)	26.18	25.00
1527	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	gSDVVVYTDGQEQQYNVPQVk	95%	n+304 (+304), K+304 (+304)	39.51	25.00
1528	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	qTLDLGDGTGLLPLEVR	95%	n+304 (+304)	46.37	25.40
1529	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	tMISSSWGAPAAFR	95%	n+304 (+304)	44.03	25.00
1530	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	wDEQFFGDLDVk	95%	n+304 (+304), K+304 (+304)	30.97	25.00
1531	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	wEkPGHSPLFGYDFWYQPR	95%	n+304 (+304), K+304 (+304)	37.81	25.00

1532	seq=translation; coord=3:161729177..161732426:-1; parent_transcript=GRMZM2G103812_T01; parent_gene=GRMZM2G103812	GRMZM2G103812_P01,GRMZM2G103812_P02	TRUE	TRUE	yLYFVNWLHGDIR	95%	n+304 (+304)	42.06	25.17
1533	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	eAGMVGFR	88%	n+304 (+304)	26.41	25.00
1534	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	ecALLTDGR	92%	n+304 (+304), Carbamidomethyl (+57)	28.92	25.00
1535	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	fNTVGVSDAISMGR	95%	n+304 (+304)	70.56	25.00
1536	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	gGPGMPPEMLTPTSAIMGAGLGK	95%	n+304 (+304), K+304 (+304)	47.74	25.51
1537	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	sQGASQAVLYGVGLTDADLR	95%	n+304 (+304)	81.93	25.15
1538	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	viDVLTEQQLEER	95%	n+304 (+304)	62.90	25.67
1539	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	wTPPPYk	94%	n+304 (+304), K+304 (+304)	30.15	26.09
1540	seq=translation; coord=1:204259324..204264422:-1; parent_transcript=AC234528.1_FGT005; parent_gene=AC234528.1_FG005	AC234528.1_FGP005,GRMZM2G014069_P01	TRUE	TRUE	yLLELLk	90%	n+304 (+304), K+304 (+304)	25.27	25.00
1541	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	dVVLTGR	92%	n+304 (+304)	29.79	25.55
1542	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	eIALWFPEGVAQWk	95%	n+304 (+304), K+304 (+304)	49.47	25.69
1543	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	gDYAVEVGR	94%	n+304 (+304)	30.45	25.00
1544	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	gLIGDIISR	95%	n+304 (+304)	41.20	25.00
1545	seq=translation; coord=7:149915726..149918129:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	iIGATRPWEAAPGTIR	91%	n+304 (+304)	28.99	25.65
1546	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G134797_T02; parent_gene=GRMZM2G134797	GRMZM2G134797_P02	TRUE	TRUE	kEIALWFPEGVAQWk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	27.03	25.00
1547	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G110185_P02; parent_gene=GRMZM2G110185	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	acIVFFDEVDAIGGAR	95%	n+304 (+304), Carbamidomethyl (+57)	66.66	25.00
1548	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G110185_P02; parent_gene=GRMZM2G110185	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	eSDTGLAPPSQWDLVSDk	92%	n+304 (+304), K+304 (+304)	27.92	25.00
1549	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G110185_P02; parent_gene=GRMZM2G110185	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	fDDGVGGDNEVQR	91%	n+304 (+304)	27.71	25.00

1550	seq=translation; coord=5:212375127..212379000:-1; parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	gVLcYGGPGTGk	90%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.93	26.36
1551	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	iISPNTDDAk	95%	n+304 (+304), K+304 (+304)	36.54	26.01
1552	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	qMMQEEQLQVAR	95%	n+304 (+304)	42.47	25.00
1553	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	sVcTEAGMYAIR	95%	n+304 (+304), Carbamidomethyl (+57)	36.39	25.00
1554	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	tMLEIVNQLDGF DAR	95%	n+304 (+304)	53.61	25.00
1555	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=5:212375127..212379000:-1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	vSPTDIEEGMR	95%	n+304 (+304)	40.28	25.00
1556	parent_transcript=GRMZM2G110185_T02; parent_gene=GRMZM2G110185 seq=translation; coord=2:106286427..106287698:1;	GRMZM2G110185_P02,GRMZM2G181359_P01	TRUE	TRUE	yQIQIPLPPk	89%	n+304 (+304), K+304 (+304)	25.05	25.00
1557	parent_transcript=GRMZM2G045809_T01; parent_gene=GRMZM2G045809 seq=translation; coord=2:106286427..106287698:1;	GRMZM2G045809_P01	TRUE	TRUE	dPMAVTPDDFFNAAMIIDk	95%	n+304 (+304), K+304 (+304)	28.06	25.00
1558	parent_transcript=GRMZM2G045809_T01; parent_gene=GRMZM2G045809 seq=translation; coord=7:165383929..165386707:-1;	GRMZM2G045809_P01	TRUE	TRUE	kLIDWLQSQFWD TNY	95%	K+304 (+304), n+304 (+304)	39.84	25.53
1559	parent_transcript=GRMZM2G031545_T01; parent_gene=GRMZM2G031545 seq=translation; coord=7:165383929..165386707:-1;	GRMZM2G031545_P01,GRMZM2G031545_P02, GRMZM2G031545_P04	TRUE	TRUE	ISGITAEGQGVk	93%	n+304 (+304), K+304 (+304)	28.80	26.40
1560	parent_transcript=GRMZM2G031545_T01; parent_gene=GRMZM2G031545 seq=translation; coord=6:125241154..125242106:-1;	GRMZM2G031545_P01,GRMZM2G031545_P02, GRMZM2G031545_P04	TRUE	TRUE	wFNHIDALVR	95%	n+304 (+304)	51.71	25.77
1561	parent_transcript=GRMZM2G357296_T01; parent_gene=GRMZM2G357296 seq=translation; coord=6:125241154..125242106:-1;	GRMZM2G357296_P01	TRUE	TRUE	ecPNTEcGAGVFMANHFDR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	65.46	25.00
1562	parent_transcript=GRMZM2G357296_T01; parent_gene=GRMZM2G357296 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G357296_P01	TRUE	TRUE	ISVLQFYk	95%	n+304 (+304), K+304 (+304)	32.18	25.00
1563	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	aMGVELDLSdkPVGLGVR	95%	n+304 (+304), K+304 (+304)	36.81	25.00
1564	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	amGVELDLSdkPVGLGVR	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	32.31	25.11
1565	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	aVASSASAAPAAAAk	95%	n+304 (+304), K+304 (+304)	46.91	26.83
1566	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	gVDTVAcvSVNDAFVMR	95%	n+304 (+304), Carbamidomethyl (+57)	69.77	25.00
1567	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921	GRMZM2G036921_P01	TRUE	TRUE	hLPGFVak	95%	n+304 (+304), K+304 (+304)	42.07	25.00

1568	seq=translation; coord=9:98777728..98779013:-1; parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	vVLFVPGAFTPTcTQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.89	25.16
1569	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	yALLAEDGVVk	95%	n+304 (+304), K+304 (+304)	64.92	26.01
1570	parent_transcript=GRMZM2G036921_T01; parent_gene=GRMZM2G036921 seq=translation; coord=9:98777728..98779013:-1;	GRMZM2G036921_P01	TRUE	TRUE	yALLAEDGVVk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	38.44	25.00
1571	parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430 seq=translation; coord=3:146602562..146604776:1;	GRMZM2G171430_P01	TRUE	TRUE	iILTSDPk	95%	n+304 (+304), K+304 (+304)	29.70	25.75
1572	parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430 seq=translation; coord=3:146602562..146604776:1;	GRMZM2G171430_P01	TRUE	TRUE	vFSVPEAAPFTAVLk	95%	n+304 (+304), K+304 (+304)	31.57	25.00
1573	parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430 seq=translation; coord=3:146602562..146604776:1;	GRMZM2G171430_P01	TRUE	TRUE	vPPQTSaiITNDGIGINPQQSAGNVFLk	95%	n+304 (+304), K+304 (+304)	33.89	25.00
1574	parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430 seq=translation; coord=3:146602562..146604776:1;	GRMZM2G171430_P01	TRUE	TRUE	yAAEEFk	92%	n+304 (+304), K+304 (+304)	26.43	25.00
1575	parent_transcript=GRMZM2G171430_T01; parent_gene=GRMZM2G171430 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G171430_P01	TRUE	TRUE	yAAEEFkVPPQTSaiITNDGIGINPQQSAGNVFLk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	28.17	25.00
1576	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	aLELDDDISYLTNR	95%	n+304 (+304)	64.72	25.00
1577	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	aVETYQAGLk	90%	n+304 (+304), K+304 (+304)	26.31	25.69
1578	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	aYLNEPDFMHMMR	95%	n+304 (+304)	58.31	25.00
1579	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	ayLNEPDFMHMMR	95%	n+304 (+304), iTRAQ8plex (+304)	28.05	25.00
1580	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	dFDIAIETFQk	95%	n+304 (+304), K+304 (+304)	37.33	26.24
1581	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	gLLEDPsNEGLk	95%	n+304 (+304), K+304 (+304)	48.68	25.07
1582	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	gSSGPDAIGQMFQGPPELWSk	95%	n+304 (+304), K+304 (+304)	39.01	25.00
1583	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	qQQQQQTPPSETk	95%	n+304 (+304), K+304 (+304)	33.84	26.17
1584	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=4:149167730..149173878:1;	GRMZM2G063850_P01	TRUE	TRUE	qVLIDFQENPSAAQEHLk	95%	n+304 (+304), K+304 (+304)	64.57	25.65
1585	parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850	GRMZM2G063850_P01	TRUE	TRUE	qVLIDFQENPSAAQEHLk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	38.36	25.00

1586	seq=translation; coord=4:149167730..149173878:1; parent_transcript=GRMZM2G063850_T01; parent_gene=GRMZM2G063850 seq=translation; coord=5:1488844..1491571:1;	GRMZM2G063850_P01	TRUE	TRUE	rGSSGPDaIGQMfQGPELWSK	95%	n+304 (+304), K+304 (+304)	29.67	25.00
1587	parent_transcript=GRMZM2G125271_T01; parent_gene=GRMZM2G125271 seq=translation; coord=5:1488844..1491571:1;	GRMZM2G125271_P01	TRUE	TRUE	dAAAQAAANA	95%	n+304 (+304)	53.03	25.00
1588	parent_transcript=GRMZM2G125271_T01; parent_gene=GRMZM2G125271 seq=translation; coord=9:142495842..142498679:-1;	GRMZM2G125271_P01	TRUE	TRUE	gSFETIHVEDSLGHQFATR	95%	n+304 (+304)	50.93	25.00
1589	parent_transcript=GRMZM2G067303_T01; parent_gene=GRMZM2G067303 seq=translation; coord=9:142495842..142498679:-1;	GRMZM2G067303_P01,GRMZM2G067303_P02, GRMZM2G170336_P01,GRMZM2G170336_P02	TRUE	TRUE	IGVEDAPELQLNR	95%	n+304 (+304)	40.01	25.00
1590	parent_transcript=GRMZM2G067303_T01; parent_gene=GRMZM2G067303 seq=translation; coord=8:162236975..162239554:-1;	GRMZM2G067303_P01,GRMZM2G067303_P02, GRMZM2G170336_P01,GRMZM2G170336_P02	TRUE	TRUE	vIDLISSPDVVK	95%	n+304 (+304), K+304 (+304)	42.50	25.00
1591	parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118 seq=translation; coord=8:162236975..162239554:-1;	GRMZM2G042118_P01	TRUE	TRUE	eAFSSFGEVTEAR	95%	n+304 (+304)	44.14	25.00
1592	parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118 seq=translation; coord=8:162236975..162239554:-1;	GRMZM2G042118_P01	TRUE	TRUE	eAISAMDGk	95%	n+304 (+304), K+304 (+304)	36.54	25.90
1593	parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118 seq=translation; coord=8:162236975..162239554:-1;	GRMZM2G042118_P01	TRUE	TRUE	gFGFVNYSDDAAK	95%	n+304 (+304), K+304 (+304)	47.76	25.00
1594	parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118 seq=translation; coord=8:162236975..162239554:-1;	GRMZM2G042118_P01	TRUE	TRUE	gGGGYGGGGYGGGGYGGGGYGGGGYGGGSQSYDA	95%	n+304 (+304), iTRAQ8plex (+304)	44.08	25.00
1595	parent_transcript=GRMZM2G042118_T01; parent_gene=GRMZM2G042118 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G042118_P01	TRUE	TRUE	IFIGGLDWGVDDVK	95%	n+304 (+304), K+304 (+304)	50.38	26.35
1596	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	aEEVDEVLGSR	95%	n+304 (+304)	44.26	25.00
1597	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	aLSFASK	88%	n+304 (+304), K+304 (+304)	26.22	25.73
1598	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	dSNLQIVcFEVHADR	95%	n+304 (+304), Carbamidomethyl (+57)	70.26	25.00
1599	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	iLHTISVPGEFQFFGPGGR	95%	n+304 (+304)	52.36	26.20
1600	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	ISPGTAFVVPAGHPFVAVASR	95%	n+304 (+304)	45.87	25.56
1601	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	nPESLSSFSk	92%	n+304 (+304), K+304 (+304)	27.47	25.53
1602	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	qGHVFPVAPAGAVTYLANTDGR	95%	n+304 (+304)	86.91	25.00
1603	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919	GRMZM2G067919_P02	TRUE	TRUE	qGHVFPVAPAGAVTYLANTDGR	95%	Pyro-cmC (-17), n+304 (+304)	92.28	25.00

1604	seq=translation; coord=1:258363419..258365809:1; parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	qGHVFPAPAGAVTyLANTDGR	95%	Pyro-cmC (-17), n+304 (+304), iTRAQ8plex (+304)	30.21	25.00
1605	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	sEEEEESSEEQEEAGQGYHTIR	95%	n+304 (+304)	80.50	25.00
1606	parent_transcript=GRMZM2G067919_T02; parent_gene=GRMZM2G067919 seq=translation; coord=1:258363419..258365809:1;	GRMZM2G067919_P02	TRUE	TRUE	vFLAGADNVLQK	95%	n+304 (+304), K+304 (+304)	54.06	25.00
1607	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	aLLVEALSPLGEDNVK	95%	n+304 (+304), K+304 (+304)	50.16	25.00
1608	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	aVETDAPVMVik	95%	n+304 (+304), K+304 (+304)	42.16	26.71
1609	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	dVMSLAQGVVYWQPPESAMDK	95%	n+304 (+304), K+304 (+304)	30.50	25.00
1610	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	gGEGAIYLVAK	95%	n+304 (+304), K+304 (+304)	49.47	25.29
1611	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	iQELLR	90%	n+304 (+304)	27.42	25.00
1612	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	IALYSLEAGPEWIK	95%	n+304 (+304), K+304 (+304)	44.24	25.00
1613	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	IPDScSDDFEAVR	95%	n+304 (+304), Carbamidomethyl (+57)	68.19	25.00
1614	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	rGLQLVTDGMVQ	95%	n+304 (+304)	39.54	25.71
1615	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	tLHPDWDWLEK	95%	n+304 (+304), K+304 (+304)	32.77	26.16
1616	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	vGYIAFPNEADGFHDQLLK	94%	n+304 (+304), K+304 (+304)	28.76	25.62
1617	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	vQDNIPIcASIIGQR	95%	n+304 (+304), Carbamidomethyl (+57)	48.93	26.04
1618	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=8:18231012..18236007:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	vSFGGLK	95%	n+304 (+304), K+304 (+304)	29.83	26.19
1619	parent_transcript=GRMZM2G107639_T01; parent_gene=GRMZM2G107639 seq=translation; coord=5:37229486..37234332:-1;	GRMZM2G107639_P01,GRMZM2G107639_P02	TRUE	TRUE	yGSDDGLPELR	92%	n+304 (+304)	28.48	25.00
1620	parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064 seq=translation; coord=5:37229486..37234332:-1;	GRMZM2G088064_P03	TRUE	TRUE	aFHEAFLAEYRD	95%	n+304 (+304)	40.39	25.00
1621	parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	aLEDAFNk	95%	n+304 (+304), K+304 (+304)	33.72	26.18

1622	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	aLVVINPGNPTGQVLAEDNQYDIVk	95%	n+304 (+304), K+304 (+304)	34.83	25.00
1623	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	dAIAAGIMSR	95%	n+304 (+304)	32.38	25.00
1624	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	eVLALcDHPcLLEk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	38.37	26.28
1625	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	gEIVIHAQR	91%	n+304 (+304)	26.55	26.14
1626	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	gGYMEITGFSAPVR	95%	n+304 (+304)	65.54	25.00
1627	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	lLESTGIVVVPGSGFGQVPGTWHIR	95%	n+304 (+304)	65.44	25.00
1628	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	nEGLVLLADEVQYENIYVDNk	95%	n+304 (+304), K+304 (+304)	64.68	25.20
1629	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	rGGYMEITGFSAPVR	95%	n+304 (+304)	51.41	25.44
1630	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	sLFSADAI SR	95%	n+304 (+304)	37.22	25.00
1631	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	tGWGLEISDLk	94%	n+304 (+304), K+304 (+304)	31.21	25.98
1632	seq=translation; coord=5:37229486..37234332:-1; parent_transcript=GRMZM2G088064_T03; parent_gene=GRMZM2G088064	GRMZM2G088064_P03	TRUE	TRUE	vGDES YASYk	95%	n+304 (+304), K+304 (+304)	42.79	25.00
1633	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	TRUE	TRUE	aATGkPDTLGDCpFSQR	93%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	27.78	25.00
1634	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	TRUE	TRUE	aLLDELQALDEHLk	95%	n+304 (+304), K+304 (+304)	72.83	25.00
1635	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	TRUE	TRUE	fPTPSLTVPEYASVGSk	95%	n+304 (+304), K+304 (+304)	59.25	25.98
1636	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	TRUE	TRUE	iFPAFITFLk	95%	n+304 (+304), K+304 (+304)	36.98	25.00
1637	seq=translation; coord=6:34430048..34433142:1; parent_transcript=GRMZM2G035502_T01; parent_gene=GRMZM2G035502	GRMZM2G035502_P01	TRUE	TRUE	iFHLQVALEHFk	95%	n+304 (+304), K+304 (+304)	32.34	25.00
1638	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	aGYFVVVPDFLk	95%	n+304 (+304), K+304 (+304)	37.03	25.44

1639	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	aVcLSHPYSVTADDMk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.83	25.00
1640	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	aVVLASDVFGYEAPLLR	95%	n+304 (+304)	67.00	25.67
1641	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	aVVLASDVFGYEAPLLR	95%	n+304 (+304), iTRAQ8plex (+304)	31.84	25.19
1642	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	aYVSGAASSSR	95%	n+304 (+304)	39.60	25.00
1643	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	fVHVLR	92%	n+304 (+304)	26.88	25.24
1644	seq=translation; coord=4:70066543..70068959:-1; parent_transcript=GRMZM2G073079_T01; parent_gene=GRMZM2G073079	GRMZM2G073079_P01,GRMZM2G076348_P01	TRUE	TRUE	iFQGVHGFACR	95%	n+304 (+304), Carbamidomethyl (+57)	46.10	25.00
1645	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	mEAVGSQSGATAESVR	95%	n+304 (+304), K+304 (+304)	42.77	25.00
1646	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	mEAVGSQSGATAESVR	95%	Oxidation (+16), n+304 (+304)	36.93	25.00
1647	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	vFFDILIGk	95%	n+304 (+304), K+304 (+304)	32.20	25.00
1648	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	vIPGFMcQGQDFTR	95%	n+304 (+304), Carbamidomethyl (+57)	37.70	25.00
1649	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	vVDGYAVVDk	95%	n+304 (+304), K+304 (+304)	46.88	25.76
1650	seq=translation; coord=7:8218240..8220274:1; parent_transcript=GRMZM2G170397_T01; parent_gene=GRMZM2G170397	GRMZM2G170397_P01,GRMZM2G170397_P02, GRMZM2G170397_P03	TRUE	TRUE	vVMELFADk	95%	n+304 (+304), K+304 (+304)	31.26	26.51
1651	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441	GRMZM2G078441_P01	TRUE	TRUE	eGDVFVVPR	95%	n+304 (+304)	33.22	25.00
1652	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441	GRMZM2G078441_P01	TRUE	TRUE	eSTILPcVScAEELAEk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	54.16	25.00
1653	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441	GRMZM2G078441_P01	TRUE	TRUE	eSTILPcVScAEELAEAEER	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	55.00	25.00
1654	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441	GRMZM2G078441_P01	TRUE	TRUE	gDVYNFEQGSILYIQSPNASR	95%	n+304 (+304), iTRAQ8plex (+304)	42.49	25.00

1656	seq=translation; coord=9:148445803..148448625:-1; parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	gFETDVLRL	95%	n+304 (+304)	32.06	25.00
1657	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	gkVTSIEESESQSSLEVER	95%	n+304 (+304), K+304 (+304)	85.94	25.00
1658	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	gSVLQAIGk	95%	n+304 (+304), K+304 (+304)	41.32	25.00
1659	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	vkEGDVFVVPR	95%	n+304 (+304), K+304 (+304)	33.04	25.00
1660	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	vLALALGQR	87%	n+304 (+304)	25.67	25.00
1661	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=9:148445803..148448625:-1;	GRMZM2G078441_P01	TRUE	TRUE	vTSIEESESQSSLEVER	95%	n+304 (+304)	85.84	25.00
1662	parent_transcript=GRMZM2G078441_T01; parent_gene=GRMZM2G078441 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G078441_P01	TRUE	TRUE	vVAESEAGSVSAVDVADAAGTAYR	95%	n+304 (+304)	99.04	25.00
1663	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	fGIGQGAAGMTVcGTPEYVR	95%	n+304 (+304), Carbamidomethyl (+57)	54.49	25.00
1664	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	fTTESLEk	91%	n+304 (+304), K+304 (+304)	28.26	25.37
1665	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	gITFFDTSDAYGPR	95%	n+304 (+304)	62.68	25.00
1666	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	iEDLak	91%	n+304 (+304), K+304 (+304)	27.36	26.90
1667	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	kYQcSPAQLALAWVLR	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	61.29	25.00
1668	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	IDAGYIDLYyQHR	95%	n+304 (+304), iTRAQ8plex (+304)	27.78	25.25
1669	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=3:218323126..218325508:1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	IGFGcMGLTGTYNAPLGDEAAVAHVAFR	95%	n+304 (+304), Carbamidomethyl (+57)	74.65	25.00
1670	parent_transcript=GRMZM2G176903_T01; parent_gene=GRMZM2G176903 seq=translation; coord=5:205777032..205781614:-1;	GRMZM2G176903_P01,GRMZM2G176903_P02	TRUE	TRUE	yQcSPAQLALAWVLR	95%	n+304 (+304), Carbamidomethyl (+57)	60.09	25.74
1671	parent_transcript=GRMZM2G140150_T01; parent_gene=GRMZM2G140150 seq=translation; coord=5:63564993..63569468:1;	GRMZM2G140150_P01	TRUE	TRUE	gFNVESFGPDR	95%	n+304 (+304)	46.25	25.00
1672	parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212 seq=translation; coord=5:63564993..63569468:1;	GRMZM2G088212_P01	TRUE	TRUE	aPGVQTPVIVR	87%	n+304 (+304)	25.63	25.00
1673	parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	dEEVNYFPSR	95%	n+304 (+304)	38.09	25.00

1674	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	eGNFDLVGNMMPVFFIR	95%	n+304 (+304)	48.78	25.00
1675	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	gFFEVDHVSHTCADFLR	95%	n+304 (+304), Carbamidomethyl (+57)	57.04	25.00
1676	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	hMEGFGVNTYTLINR	95%	n+304 (+304)	63.66	25.00
1677	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	hMEGFGVNTYTLINR	94%	n+304 (+304), iTRAQ8plex (+304)	26.28	26.01
1678	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	IGPNYMLPVPNApk	91%	n+304 (+304), K+304 (+304)	25.39	25.09
1679	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	tNLQENWR	92%	n+304 (+304)	28.71	25.07
1680	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	tWPEDIPLQPVGR	93%	n+304 (+304)	28.08	25.60
1681	seq=translation; coord=5:63564993..63569468:1; parent_transcript=GRMZM2G088212_T01; parent_gene=GRMZM2G088212	GRMZM2G088212_P01	TRUE	TRUE	wVDALTDPR	95%	n+304 (+304)	32.87	25.00
1682	seq=translation; coord=6:161659850..161663090:-1; parent_transcript=GRMZM2G121186_T01; parent_gene=GRMZM2G121186	GRMZM2G121186_P01	TRUE	TRUE	eSAAETPEEQk	95%	n+304 (+304), K+304 (+304)	30.78	25.00
1683	seq=translation; coord=6:161659850..161663090:-1; parent_transcript=GRMZM2G121186_T01; parent_gene=GRMZM2G121186	GRMZM2G121186_P01	TRUE	TRUE	hTDVLENLEPk	95%	n+304 (+304), K+304 (+304)	57.35	26.00
1684	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	aAAVAAAPAAVPk	93%	n+304 (+304), K+304 (+304)	26.24	25.00
1685	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	aEFDDVk	95%	n+304 (+304), K+304 (+304)	33.06	25.47
1686	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	aLELSGSDIGGGYELYVDEakPR	95%	n+304 (+304), K+304 (+304)	76.67	25.00
1687	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	aPAATik	91%	n+304 (+304), K+304 (+304)	29.82	27.95
1688	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	eFFEDVGEVVDVR	95%	n+304 (+304)	56.04	25.00
1689	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	fPTHDDGNR	95%	n+304 (+304)	32.51	25.00
1690	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	gFcYVEFVSAAAAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	43.23	25.00
1691	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	gMAYIDFk	95%	n+304 (+304), K+304 (+304)	39.88	25.00

1692	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	gNSSSIFIR	94%	n+304 (+304)	29.06	25.00
1693	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	nLSEDEIR	95%	n+304 (+304)	33.21	25.00
1694	seq=translation; coord=4:27749082..27753340:1; parent_transcript=GRMZM2G131943_T01; parent_gene=GRMZM2G131943	GRMZM2G131943_P01,GRMZM2G131943_P02, GRMZM2G131943_P03,GRMZM2G131943_P04	TRUE	TRUE	sGNDGSFQk	94%	n+304 (+304), K+304 (+304)	27.90	25.39
1695	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	aFEDAEITHVDDTVDPVR	95%	n+304 (+304)	81.20	25.00
1696	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	aPQAAGAIHTDFER	95%	n+304 (+304)	63.19	25.00
1697	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	aVDGIFHVLR	95%	n+304 (+304)	57.58	25.76
1698	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	dMETISEELR	95%	n+304 (+304)	33.44	25.00
1699	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	gAHAGDGLGNAFLSHIR	95%	n+304 (+304)	48.25	25.20
1700	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	gFicAEVMk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	35.18	26.53
1701	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	iGIVGLPNVGk	95%	n+304 (+304), K+304 (+304)	39.73	25.00
1702	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	IVDMPEDAAk	94%	n+304 (+304), K+304 (+304)	28.42	25.00
1703	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	sEVPAYLEVTDIAGLIR	95%	n+304 (+304)	39.21	26.19
1704	seq=translation; coord=10:61794133..61802175:-1; parent_transcript=GRMZM2G146115_T01; parent_gene=GRMZM2G146115	GRMZM2G146115_P01,GRMZM2G146115_P02	TRUE	TRUE	tGFAAIHLYFFTAGPDEVk	95%	n+304 (+304), K+304 (+304)	30.63	25.40
1705	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	TRUE	TRUE	dLDQVAGR	86%	n+304 (+304)	25.34	25.00
1706	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	TRUE	TRUE	dVNPHEFVk	95%	n+304 (+304), K+304 (+304)	41.19	25.53
1707	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	TRUE	TRUE	eLPPYDPDWYYIR	95%	n+304 (+304)	38.75	25.00
1708	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	TRUE	TRUE	eLPPYDPDWYyIR	91%	n+304 (+304), iTRAQ8plex (+304)	25.16	25.00
1709	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775	GRMZM5G881775_P02	TRUE	TRUE	mELPEWVDIVk	95%	n+304 (+304), K+304 (+304)	36.21	25.71

1710	seq=translation; coord=9:123775912..123778018:1; parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775 seq=translation; coord=9:123775912..123778018:1;	GRMZM5G881775_P02	TRUE	TRUE	nILQQLQEMGIIDVDPk	95%	n+304 (+304), K+304 (+304)	52.66	25.00
1711	parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775 seq=translation; coord=9:123775912..123778018:1;	GRMZM5G881775_P02	TRUE	TRUE	qGIGVGGFQk	95%	n+304 (+304), K+304 (+304)	51.35	25.12
1712	parent_transcript=GRMZM5G881775_T02; parent_gene=GRMZM5G881775 seq=translation; coord=9:123775912..123778018:1;	GRMZM5G881775_P02	TRUE	TRUE	qGIGVGGFQk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	33.88	25.60
1713	parent_transcript=GRMZM2G010868_T01; parent_gene=GRMZM2G010868 seq=translation; coord=3:230606444..230608235:-1;	GRMZM2G010868_P01,GRMZM2G010868_P02	TRUE	TRUE	gTGSGPSASccSGVR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	31.32	25.00
1714	parent_transcript=GRMZM2G010868_T01; parent_gene=GRMZM2G010868 seq=translation; coord=3:230606444..230608235:-1;	GRMZM2G010868_P01,GRMZM2G010868_P02	TRUE	TRUE	gVSGLNAGNAASIPSk	95%	n+304 (+304), K+304 (+304)	78.07	25.81
1715	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	aLEIDPDNR	94%	n+304 (+304)	30.93	25.00
1716	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	dGYFcPALAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.12	25.47
1717	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	gWDQGIk	91%	n+304 (+304), K+304 (+304)	28.61	26.39
1718	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	IEDGTVVSk	90%	n+304 (+304), K+304 (+304)	26.40	26.18
1719	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	IGQGQVIk	91%	n+304 (+304), K+304 (+304)	27.71	25.00
1720	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	IQDGAFTK	95%	n+304 (+304), K+304 (+304)	44.10	26.15
1721	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	tDEEEVIAGLDR	95%	n+304 (+304)	54.56	25.00
1722	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	vLELDSQNVk	95%	n+304 (+304), K+304 (+304)	40.38	26.15
1723	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	vQAYIQLADLELAEADIK	95%	n+304 (+304), K+304 (+304)	77.72	25.35
1724	parent_transcript=GRMZM2G096585_T03; parent_gene=GRMZM2G096585 seq=translation; coord=1:192400083..192403759:1;	GRMZM2G096585_P03,GRMZM2G096585_P04, GRMZM2G096585_P06	TRUE	TRUE	yIEYDTSFSEDEK	95%	n+304 (+304), K+304 (+304)	33.05	25.00
1725	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:183449044..183455471:-1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	aETFGIPIPDWAK	95%	n+304 (+304), K+304 (+304)	42.39	26.00
1726	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:183449044..183455471:-1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	fPIAGSADDAQk	95%	n+304 (+304), K+304 (+304)	38.35	25.95
1727	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	IIDLAINETLGESK	95%	n+304 (+304), K+304 (+304)	72.24	25.00

1728	seq=translation; coord=4:183449044..183455471:-1; parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:183449044..183455471:-1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	IQELNNAVIITITGDLTK	95%	n+304 (+304), K+304 (+304)	50.95	25.00
1729	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:183449044..183455471:-1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	sTVAATAAMTINPELHVEALQNR	95%	n+304 (+304)	64.33	25.61
1730	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:183449044..183455471:-1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	tLPPGFHNMPIQFEK	94%	n+304 (+304), K+304 (+304)	26.21	25.56
1731	parent_transcript=GRMZM2G111818_T01; parent_gene=GRMZM2G111818 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G111818_P01,GRMZM2G111818_P04	TRUE	TRUE	tPTEVNAFLSNPGGYATAAR	95%	n+304 (+304)	41.10	25.00
1732	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	dEGFSSLWR	95%	n+304 (+304)	36.94	25.00
1733	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	glADcFk	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.34	25.54
1734	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	nFMIDFMMGGVSAAVSk	95%	n+304 (+304), K+304 (+304)	57.14	25.00
1735	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	sDGIAGLYR	94%	n+304 (+304)	30.85	25.00
1736	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=4:163768734..163771529:1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	sSLDAFQQILk	95%	n+304 (+304), K+304 (+304)	36.74	25.00
1737	parent_transcript=GRMZM2G135186_T01; parent_gene=GRMZM2G135186 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G135186_P01,GRMZM2G135186_P02, GRMZM2G135186_P03	TRUE	TRUE	tIkDEGFSSLWR	95%	n+304 (+304), K+304 (+304)	32.29	25.82
1738	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	aIFTEGck	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.17	25.87
1739	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	eGVITIADGNTLYNELEVVEGMk	95%	n+304 (+304), K+304 (+304)	75.67	25.54
1740	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	gISMAVDVAVTNLk	95%	n+304 (+304), K+304 (+304)	48.04	25.00
1741	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	gVEELADAVk	95%	n+304 (+304), K+304 (+304)	46.85	25.66
1742	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	nVVIEQSFGAPk	95%	n+304 (+304), K+304 (+304)	40.29	25.67
1743	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	qRPLLIVAEDVESEALGTLIInk	94%	n+304 (+304), K+304 (+304)	25.31	25.00
1744	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120 seq=translation; coord=1:234775005..234780894:-1;	GRMZM2G416120_P01	TRUE	TRUE	sVAAGMNAMDLR	95%	n+304 (+304)	40.85	25.00
1745	parent_transcript=GRMZM2G416120_T01; parent_gene=GRMZM2G416120	GRMZM2G416120_P01	TRUE	TRUE	vLEMALK	95%	n+304 (+304), K+304 (+304)	28.34	25.00

1746	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	eIFQNPEFLR	89%	n+304 (+304)	25.92	25.00
1747	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	eVVAGScDVPAPQQR	95%	n+304 (+304), Carbamidomethyl (+57)	51.56	25.00
1748	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	fTVQTDLGATVGGFk	95%	n+304 (+304), K+304 (+304)	49.48	25.58
1749	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	nLMESNPQMR	95%	n+304 (+304)	32.42	25.00
1750	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	nMIMSNPQMR	95%	n+304 (+304)	32.54	25.00
1751	seq=translation; coord=1:84919829..84924586:-1; parent_transcript=GRMZM2G136769_T01; parent_gene=GRMZM2G136769	GRMZM2G136769_P01	TRUE	TRUE	qLTSPETLQQLLLFQQSLLGQLGQHQPQNQGR	95%	n+304 (+304)	54.29	25.00
1752	seq=translation; coord=1:293163457..293166106:1; parent_transcript=GRMZM2G060702_T02; parent_gene=GRMZM2G060702	GRMZM2G060702_P02	TRUE	TRUE	aTSYDDFTNSLPENDcR	95%	n+304 (+304), Carbamidomethyl (+57)	55.51	25.00
1753	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	dSAFAAlk	91%	n+304 (+304), K+304 (+304)	27.48	26.41
1754	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	gGITVFPk	95%	n+304 (+304), K+304 (+304)	36.50	25.20
1755	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	rGGITVFPk	95%	n+304 (+304), K+304 (+304)	28.30	25.00
1756	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	sLLcHALPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.97	25.00
1757	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	vLLPMQIFk	95%	n+304 (+304), K+304 (+304)	32.85	25.00
1758	seq=translation; coord=4:198559982..198560791:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	vLLPmQIFk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	46.82	25.00
1759	seq=translation; coord=7:174283500..174287760:-1; parent_transcript=AC234156.1_FGT005; parent_gene=AC234156.1_FG005	AC234156.1_FGP005	TRUE	TRUE	yYSLAEFDR	95%	n+304 (+304)	37.48	25.00
1760	seq=translation; coord=7:174283500..174287760:-1; parent_transcript=GRMZM2G430600_T01; parent_gene=GRMZM2G430600	GRMZM2G430600_P01,GRMZM2G430600_P02	TRUE	TRUE	eADVdGDGQINyEEFVk	95%	n+304 (+304), K+304 (+304)	58.01	25.00
1761	seq=translation; coord=7:174283500..174287760:-1; parent_transcript=GRMZM2G430600_T01; parent_gene=GRMZM2G430600	GRMZM2G430600_P01,GRMZM2G430600_P02	TRUE	TRUE	eADVdGDGQINyEEFVk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	28.36	25.00
1762	seq=translation; coord=7:174283500..174287760:-1; parent_transcript=GRMZM2G430600_T01; parent_gene=GRMZM2G430600	GRMZM2G430600_P01,GRMZM2G430600_P02	TRUE	TRUE	vLcLHGFR	94%	n+304 (+304), Carbamidomethyl (+57)	28.93	25.76
1763	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	kPWALSFSGR	94%	K+304 (+304), n+304 (+304)	26.20	25.38

1764	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	KVTPEVIAQYTVR	95%	K+304 (+304), n+304 (+304)	40.71	25.00
1765	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	tVPAAVPAVFLSGGQSEEEATLNLNAMNk	95%	n+304 (+304), K+304 (+304)	69.63	25.00
1766	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	vTPEVIAQYTVR	95%	n+304 (+304)	42.42	25.01
1767	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	vTPEVIAQyTVR	94%	n+304 (+304), iTRAQ8plex (+304)	29.01	25.00
1768	seq=translation; coord=8:163307256..163309969:-1; parent_transcript=GRMZM2G066024_T01; parent_gene=GRMZM2G066024	GRMZM2G066024_P01	TRUE	TRUE	yADELlIk	95%	n+304 (+304), K+304 (+304)	34.79	26.69
1769	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	TRUE	TRUE	gANMAITGATAMDAPFFR	95%	n+304 (+304)	69.88	25.00
1770	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	TRUE	TRUE	gANmAITGATAMDAPFFR	86%	n+304 (+304), Oxidation (+16)	25.36	25.00
1771	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	TRUE	TRUE	kGANMAITGATAMDAPFFR	95%	K+304 (+304), n+304 (+304)	60.34	25.20
1772	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	TRUE	TRUE	nPGSYGFSSVFQAccGSGGGk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	47.66	25.00
1773	seq=translation; coord=9:18329697..18331617:-1; parent_transcript=AC231745.1_FGT003; parent_gene=AC231745.1_FG003	AC231745.1_FGP003	TRUE	TRUE	vIPDFLcSR	88%	n+304 (+304), Carbamidomethyl (+57)	26.01	25.00
1774	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	aDQQMLIYQGk	95%	n+304 (+304), K+304 (+304)	43.69	26.26
1775	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	aIDYLYSGIPENVEAQPVAR	95%	n+304 (+304)	38.70	25.43
1776	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	aPATLAQPAAPVAPAASVAR	95%	n+304 (+304)	93.15	25.00
1777	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	aSSSGASTATTak	94%	n+304 (+304), K+304 (+304)	27.67	25.65
1778	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	eLVLEVFFAcNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.38	25.74
1779	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	gTNFEIASPDASVADVk	95%	n+304 (+304), K+304 (+304)	46.09	25.00
1780	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417	GRMZM2G035417_P01	TRUE	TRUE	iIETTQGQSTYR	95%	n+304 (+304)	34.17	25.00

1781	seq=translation; coord=9:106398227..106409066:1; parent_transcript=GRMZM2G035417_T01; parent_gene=GRMZM2G035417 seq=translation; coord=9:148111509..148115129:1;	GRMZM2G035417_P01	TRUE	TRUE	IIQENQAEFLR	95%	n+304 (+304)	41.84	25.16
1782	parent_transcript=GRMZM2G145258_T01; parent_gene=GRMZM2G145258 seq=translation; coord=6:124803945..124805261:1;	GRMZM2G145258_P01	TRUE	TRUE	IERPVEGDEAGQEVAABE	95%	n+304 (+304)	36.26	25.00
1783	parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812 seq=translation; coord=6:124803945..124805261:1;	GRMZM2G084812_P01	TRUE	TRUE	dDDPLAVYAcSk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	41.39	25.00
1784	parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812	GRMZM2G084812_P01	TRUE	TRUE	dDTVLTDDTTVVTSTIQATVR	95%	n+304 (+304)	48.54	25.22
1785	seq=translation; coord=6:124803945..124805261:1; parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812	GRMZM2G084812_P01	TRUE	TRUE	dTALTVCfPVDAAVAAfMpk	95%	n+304 (+304), Carbamidomethyl (+57), Oxidation (+16), K+304 (+304)	32.65	25.00
1786	seq=translation; coord=6:124803945..124805261:1; parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812 seq=translation; coord=6:124803945..124805261:1;	GRMZM2G084812_P01	TRUE	TRUE	sFAGLLAADPk	95%	n+304 (+304), K+304 (+304)	50.91	26.14
1787	parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812 seq=translation; coord=6:124803945..124805261:1;	GRMZM2G084812_P01	TRUE	TRUE	tAILLYHAVPDYYSMQFLK	95%	n+304 (+304), K+304 (+304)	49.31	25.77
1788	parent_transcript=GRMZM2G084812_T01; parent_gene=GRMZM2G084812 seq=translation; coord=6:164551086..164552313:1;	GRMZM2G084812_P01	TRUE	TRUE	vTTLATTSVAK	93%	n+304 (+304), K+304 (+304)	27.08	25.00
1789	parent_transcript=GRMZM2G021794_T01; parent_gene=GRMZM2G021794 seq=translation; coord=6:164551086..164552313:1;	GRMZM2G021794_P01	TRUE	TRUE	aLkDEQFSEFR	94%	n+304 (+304), K+304 (+304)	31.12	25.37
1790	parent_transcript=GRMZM2G021794_T01; parent_gene=GRMZM2G021794 seq=translation; coord=6:164551086..164552313:1;	GRMZM2G021794_P01	TRUE	TRUE	dEQFSEFR	95%	n+304 (+304)	32.83	25.00
1791	parent_transcript=GRMZM2G021794_T01; parent_gene=GRMZM2G021794 seq=translation; coord=6:164551086..164552313:1;	GRMZM2G021794_P01	TRUE	TRUE	fYLSMLGTLGK	95%	n+304 (+304), K+304 (+304)	28.41	25.93
1792	parent_transcript=GRMZM2G021794_T01; parent_gene=GRMZM2G021794 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G021794_P01	TRUE	TRUE	fYLSmLGTLSGK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	35.98	25.81
1793	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	aDYFLVGK	95%	n+304 (+304), K+304 (+304)	42.58	25.35
1794	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	aGESLNWEDFPK	95%	n+304 (+304), K+304 (+304)	37.80	25.00
1795	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	aLTNAINLEITGEYAEALK	94%	n+304 (+304), K+304 (+304)	26.06	25.34
1796	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	aVAHDVPIPGYK	95%	n+304 (+304), K+304 (+304)	29.54	25.77
1797	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	dFPSYIEcQEK	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.36	25.00

1798	seq=translation; coord=1:278183921..278192926:-1; parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	dGQEEIAENWLEMgyPWEVVr	95%	n+304 (+304), iTRAQ8plex (+304)	40.03	25.00
1799	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	dIWDISPAILP	95%	n+304 (+304)	60.53	26.34
1800	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	dVQGPVSPAELPSVLNSIGSSAIASNIK	95%	n+304 (+304), K+304 (+304)	44.59	25.00
1801	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	eEVGEENFFLFGAEAEIAGLR	95%	n+304 (+304)	83.67	25.00
1802	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	fADNEDLHSEWR	95%	n+304 (+304)	41.43	25.00
1803	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	fcNPALSALISK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	35.21	25.63
1804	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	gLSWSEAWSITER	95%	n+304 (+304)	64.17	25.00
1805	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	iLMDVik	90%	n+304 (+304), K+304 (+304)	27.47	25.85
1806	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	mSILNTAGSSk	95%	n+304 (+304), K+304 (+304)	44.73	26.44
1807	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	qLLNILGIVYR	95%	n+304 (+304)	33.11	25.00
1808	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	sGVFGTYSYDELMSLEGNEGYGR	95%	n+304 (+304), iTRAQ8plex (+304)	29.82	25.00
1809	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	sGVFGTYSYDELMSLEGNEGYGR	94%	n+304 (+304), iTRAQ8plex (+304)	25.31	25.00
1810	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	tGYIVSPDAMFDVQVK	95%	n+304 (+304), K+304 (+304)	43.88	25.60
1811	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=1:278183921..278192926:-1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	wIGSDDWVLNTDK	95%	n+304 (+304), K+304 (+304)	33.69	25.00
1812	parent_transcript=GRMZM2G074158_T01; parent_gene=GRMZM2G074158 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G074158_P01,GRMZM2G074158_P02	TRUE	TRUE	wSLDIMQK	90%	n+304 (+304), K+304 (+304)	27.63	26.04
1813	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	eEADEEVLIQILELYR	95%	n+304 (+304)	78.34	25.00
1814	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	eFLWQEGHTAFATK	95%	n+304 (+304), K+304 (+304)	42.29	25.00
1815	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123	GRMZM2G094123_P01	TRUE	TRUE	eMVWQNSWAYTTR	95%	n+304 (+304)	47.84	25.00

1816	seq=translation; coord=4:215212969..215240759:1; parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	fAGGLYTSVEAFIPNTGR	95%	n+304 (+304)	90.62	25.00
1817	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	gAcESTVYTLDSQSGIR	92%	n+304 (+304), Carbamidomethyl (+57)	26.94	25.00
1818	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	iYEEFLAVPVSk	95%	n+304 (+304), K+304 (+304)	32.85	25.00
1819	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	lILAPWcDEEEIEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.67	26.25
1820	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	sIGVMVMTHGDDk	95%	n+304 (+304), K+304 (+304)	45.17	25.00
1821	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:215212969..215240759:1;	GRMZM2G094123_P01	TRUE	TRUE	vDIPVTNLVEEVk	95%	n+304 (+304), K+304 (+304)	45.49	25.00
1822	parent_transcript=GRMZM2G094123_T01; parent_gene=GRMZM2G094123 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G094123_P01	TRUE	TRUE	vLLDEIQk	95%	n+304 (+304), K+304 (+304)	34.70	25.00
1823	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	aVPLALGILciSNPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	62.16	25.00
1824	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	lLPVALGLLYLGk	95%	n+304 (+304), K+304 (+304)	33.87	25.00
1825	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	mLLTVDEDLkPLSPVPR	94%	n+304 (+304), K+304 (+304)	25.46	25.00
1826	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	nLAGEIAQEFQk	95%	n+304 (+304), K+304 (+304)	35.94	25.63
1827	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	sEAELAEPiIR	95%	n+304 (+304)	40.92	26.50
1828	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	vGQAVDVVGQAGRpk	95%	n+304 (+304), K+304 (+304)	28.19	25.00
1829	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	vNVMDTLsr	88%	n+304 (+304)	26.24	25.00
1830	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=4:237610321..237618962:-1;	GRMZM2G155384_P02	TRUE	TRUE	ycDVTLMsLAYAGTGNVlk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.78	25.00
1831	parent_transcript=GRMZM2G155384_T02; parent_gene=GRMZM2G155384 seq=translation; coord=5:215817786..215821620:-1;	GRMZM2G155384_P02	TRUE	TRUE	yIPLTPVLEGFVIlk	95%	n+304 (+304), K+304 (+304)	50.30	25.00
1832	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	dGTTTAGNSSQVSDGAGAVLLmk	95%	n+304 (+304), K+304 (+304)	32.16	25.20
1833	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768	GRMZM5G848768_P02	TRUE	TRUE	dTYPEDLLTVVlk	95%	n+304 (+304), K+304 (+304)	31.07	25.69

1834	seq=translation; coord=5:215817786..215821620:-1; parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	gDAVDGLSNVR	88%	n+304 (+304)	26.09	25.00
1835	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	iNPADIGDIVVGTVLPGSQR	95%	n+304 (+304)	60.94	25.65
1836	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	mAALFAGFPETVPVR	95%	n+304 (+304)	76.69	25.00
1837	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	sFAAVGVDPAVMGVGPAPAIPAAVK	95%	n+304 (+304), K+304 (+304)	38.81	25.00
1838	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=5:215817786..215821620:-1;	GRMZM5G848768_P02	TRUE	TRUE	sSSFGDDVVVVAAYR	95%	n+304 (+304)	56.86	25.00
1839	parent_transcript=GRMZM5G848768_T02; parent_gene=GRMZM5G848768 seq=translation; coord=9:150090384..150093179:-1;	GRMZM5G848768_P02	TRUE	TRUE	sSSFGDDVVVVAAYR	95%	n+304 (+304), iTRAQ8plex (+304)	38.16	25.39
1840	parent_transcript=GRMZM2G099657_T01; parent_gene=GRMZM2G099657 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G099657_P01,GRMZM2G126821_P01, GRMZM2G145308_P01	TRUE	TRUE	nSIGcLFWLLAR	95%	n+304 (+304), Carbamidomethyl (+57)	47.43	25.00
1841	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	aLVVDDLIATGGTLcAAVK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.80	25.00
1842	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	dTIDLFVER	95%	n+304 (+304)	32.63	25.00
1843	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	gFIFGPPIALAIGAK	95%	n+304 (+304), K+304 (+304)	32.96	25.00
1844	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	kLPGEVISEEYSLEYGTDk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	45.54	25.12
1845	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=3:113472963..113480259:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	IAGIASSIR	95%	n+304 (+304)	40.53	25.00
1846	parent_transcript=GRMZM2G093347_T01; parent_gene=GRMZM2G093347 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G093347_P01,GRMZM2G131907_P01	TRUE	TRUE	IGDRPVFVLVEADA	95%	n+304 (+304)	34.08	25.80
1847	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	aFDAAAAGPNFPWMSR	95%	n+304 (+304)	75.60	25.00
1848	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	aFDAAAAGPNFPWmSR	95%	n+304 (+304), Oxidation (+16)	55.92	25.00
1849	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	dASTSLYTAPlk	95%	n+304 (+304), K+304 (+304)	38.51	25.81
1850	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	dGHPLVLDLTSPVISLATcASSK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.43	25.05
1851	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206	GRMZM2G053206_P01	TRUE	TRUE	gDFTTmLAGTAPLHAGAGAGPGYYVSTGIAVEQAR	95%	n+304 (+304), Oxidation (+16)	59.35	25.00

1852	seq=translation; coord=2:231986102..231987473:-1; parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	sTSGDSVGVVAFGGGPLFFVPPDR	95%	n+304 (+304)	38.57	25.00
1853	parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=2:231986102..231987473:-1;	GRMZM2G053206_P01	TRUE	TRUE	vAAVAPFDR	93%	n+304 (+304)	30.39	25.87
1854	seq=translation; coord=2:231986102..231987473:-1; parent_transcript=GRMZM2G053206_T01; parent_gene=GRMZM2G053206 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G053206_P01	TRUE	TRUE	vAlcLPSDGR	95%	n+304 (+304), Carbamidomethyl (+57)	34.32	25.13
1855	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	aTGQEYTDFLQEFMTAVk	95%	n+304 (+304), K+304 (+304)	70.41	25.00
1856	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	gLLPPAIVSQELQER	95%	n+304 (+304)	47.24	25.91
1857	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	iWLVDsk	93%	n+304 (+304), K+304 (+304)	28.73	26.53
1858	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	ILIDNVEELLPIVYPTVGEAcQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	58.78	25.00
1859	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	vHDDMLLAASEALAQVTEENFEK	95%	n+304 (+304), K+304 (+304)	75.54	25.00
1860	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	vLIQFEDFANHNAFDLLAR	95%	n+304 (+304)	43.01	25.26
1861	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=3:201684716..201689628:-1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	yAEScMYSPIYR	95%	n+304 (+304), Carbamidomethyl (+57)	52.58	25.00
1862	parent_transcript=GRMZM2G159724_T01; parent_gene=GRMZM2G159724 seq=translation; coord=5:153543150..153551579:1;	GRMZM2G159724_P01,GRMZM2G159724_P03	TRUE	TRUE	yMALMDLQEGNER	95%	n+304 (+304)	60.31	25.00
1863	parent_transcript=GRMZM2G177781_T01; parent_gene=GRMZM2G177781 seq=translation; coord=5:153543150..153551579:1;	GRMZM2G177781_P01,GRMZM2G177781_P02	TRUE	TRUE	eVIAEADAGSSGAVSGGR	95%	n+304 (+304)	86.51	25.00
1864	parent_transcript=GRMZM2G177781_T01; parent_gene=GRMZM2G177781 seq=translation; coord=5:153543150..153551579:1;	GRMZM2G177781_P01,GRMZM2G177781_P02	TRUE	TRUE	qLVAEVTSENR	94%	n+304 (+304)	30.05	25.59
1865	parent_transcript=GRMZM2G177781_T01; parent_gene=GRMZM2G177781 seq=translation; coord=5:153543150..153551579:1;	GRMZM2G177781_P01,GRMZM2G177781_P02	TRUE	TRUE	qVELSGNPEQISK	95%	n+304 (+304), K+304 (+304)	36.24	25.83
1866	parent_transcript=GRMZM2G177781_T01; parent_gene=GRMZM2G177781 seq=translation; coord=5:215289055..215297830:1;	GRMZM2G177781_P01,GRMZM2G177781_P02	TRUE	TRUE	qVELSGNPEQISK	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	31.86	25.00
1867	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	aIVASNLEGR	95%	n+304 (+304)	36.04	25.44
1868	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	gEELIADVFLFATGR	95%	n+304 (+304)	36.72	25.55
1869	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	gMGAEVDLFYR	95%	n+304 (+304)	31.72	25.00

1870	seq=translation; coord=5:215289055..215297830:1; parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	iNLTPVALMEATcFAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.37	25.43
1871	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	INLQAAGVEIDR	95%	n+304 (+304)	47.30	26.72
1872	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	tSAPSVWAVGVDVTNR	95%	n+304 (+304)	67.71	25.00
1873	parent_transcript=GRMZM5G806449_T01; parent_gene=GRMZM5G806449 seq=translation; coord=5:215289055..215297830:1;	GRMZM5G806449_P01,GRMZM5G806449_P03	TRUE	TRUE	vVTDkGEELIADVVLATGR	95%	n+304 (+304), K+304 (+304)	32.80	25.00
1874	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	aAGFMNDAGVR	91%	n+304 (+304)	28.01	25.00
1875	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	aRPLFLTGESYAGk	95%	n+304 (+304), K+304 (+304)	41.29	25.33
1876	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	dAPAPPWELVSAVVVAALHDDVMk	95%	n+304 (+304), K+304 (+304)	31.35	25.00
1877	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	dAQGVVVSVEALLR	95%	n+304 (+304)	62.59	25.90
1878	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	eAAAMQAEAAALAAAGR	95%	n+304 (+304)	88.81	25.00
1879	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	eAVDAWFR	91%	n+304 (+304)	27.95	25.00
1880	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	eLDWDGLAAFR	95%	n+304 (+304)	48.31	25.00
1881	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=4:2762573..2764339:1;	GRMZM2G126541_P01	TRUE	TRUE	rDAPAPPWELVSAVVVAALHDDVMk	95%	n+304 (+304), K+304 (+304)	48.17	25.00
1882	parent_transcript=GRMZM2G126541_T01; parent_gene=GRMZM2G126541 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G126541_P01	TRUE	TRUE	rEAAAMQAEAAALAAAGR	93%	n+304 (+304)	28.35	25.69
1883	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	fADLIEk	92%	n+304 (+304), K+304 (+304)	26.59	25.00
1884	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	gFYIQTIFSDVQDGMk	95%	n+304 (+304), K+304 (+304)	64.38	25.15
1885	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	gVEQGPGPIDDEQFNk	95%	n+304 (+304), K+304 (+304)	45.47	25.00
1886	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	iAQEEIFGPVQSILk	95%	n+304 (+304), K+304 (+304)	54.95	25.00
1887	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675	GRMZM2G058675_P02	TRUE	TRUE	iILELAak	95%	n+304 (+304), K+304 (+304)	37.97	25.00

1888	seq=translation; coord=9:33125819..33139794:1; parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	ILHEAGLPEGVNVNVSGFGPTAGAAALASHMDVDk	95%	n+304 (+304), K+304 (+304)	34.28	25.00
1889	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	tAEQTPLSALYISK	95%	n+304 (+304), K+304 (+304)	29.55	25.00
1890	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	tGEVIAHVAEGDAEDINR	95%	n+304 (+304)	61.83	25.00
1891	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	tVTLELGGk	95%	n+304 (+304), K+304 (+304)	35.29	26.39
1892	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=9:33125819..33139794:1;	GRMZM2G058675_P02	TRUE	TRUE	yGVDGGATLVTGGDR	95%	n+304 (+304)	35.85	25.00
1893	parent_transcript=GRMZM2G058675_T02; parent_gene=GRMZM2G058675 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G058675_P02	TRUE	TRUE	yGVDGGATLVTGGDR	95%	n+304 (+304), iTRAQ8plex (+304)	40.07	26.10
1894	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	aLADYVHAK	95%	n+304 (+304), K+304 (+304)	36.08	26.44
1895	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	aMSQQTMGILNSEVIQVNSQGAQGk	95%	n+304 (+304), K+304 (+304)	56.46	25.00
1896	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	aPLLIgCDVR	89%	n+304 (+304), Carbamidomethyl (+57)	27.38	25.56
1897	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	dYQGSFVANR	93%	n+304 (+304)	29.66	25.00
1898	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	gIFFSLcEWGR	95%	n+304 (+304), Carbamidomethyl (+57)	36.56	25.00
1899	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	qNPATWAGGMGNSWR	95%	n+304 (+304)	50.67	25.00
1900	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	qTADALVNTGLAK	95%	n+304 (+304), K+304 (+304)	42.57	26.19
1901	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	tFSSWGIDYlk	95%	n+304 (+304), K+304 (+304)	36.34	26.02
1902	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=1:228251511..228256942:-1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	tDDIADNWGSMTSR	95%	n+304 (+304)	81.64	25.00
1903	parent_transcript=GRMZM2G346455_T05; parent_gene=GRMZM2G346455 seq=translation; coord=10:144060305..144061413:1;	GRMZM2G346455_P05,GRMZM2G346455_P06	TRUE	TRUE	tDDIADNWGSMTSR	95%	n+304 (+304), Oxidation (+16)	37.87	25.00
1904	parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313 seq=translation; coord=10:144060305..144061413:1;	GRMZM5G895313_P01	TRUE	TRUE	dcSQGGGyGGGGGGGR	95%	n+304 (+304), Carbamidomethyl (+57)	43.20	25.00
1905	parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313	GRMZM5G895313_P01	TRUE	TRUE	dcSQGGGyGGGGGGGR	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)	27.37	25.00

1906	seq=translation; coord=10:144060305..144061413:1; parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313	GRMZM5G895313_P01	TRUE	TRUE	gYGGGGGYGGGYGGGGGGGGR	95%	n+304 (+304)	93.86	25.00
1907	seq=translation; coord=10:144060305..144061413:1; parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313	GRMZM5G895313_P01	TRUE	TRUE	gYGGGGGYGGGyGGGGGGGGR	94%	n+304 (+304), iTRAQ8plex (+304)	27.96	25.00
1908	seq=translation; coord=10:144060305..144061413:1; parent_transcript=GRMZM5G895313_T01; parent_gene=GRMZM5G895313	GRMZM5G895313_P01	TRUE	TRUE	sLNDGDAVEYTVGSGNDGR	95%	n+304 (+304)	79.57	25.00
1909	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	TRUE	TRUE	aVAHQPVSVIAEAGGR	95%	n+304 (+304)	61.78	25.61
1910	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	TRUE	TRUE	eFQLYk	92%	n+304 (+304), K+304 (+304)	28.71	25.00
1911	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	TRUE	TRUE	gAVAPVk	90%	n+304 (+304), K+304 (+304)	25.41	25.00
1912	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	TRUE	TRUE	vVSIDGFEDVPENDEK	95%	n+304 (+304), K+304 (+304)	47.03	25.00
1913	seq=translation; coord=2:2548940..2552572:1; parent_transcript=GRMZM2G010435_T01; parent_gene=GRMZM2G010435	GRMZM2G010435_P01	TRUE	TRUE	wGEDGYIR	91%	n+304 (+304)	27.89	25.00
1914	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	aDIGIAVADATDAAR	95%	n+304 (+304)	55.22	25.28
1915	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	eIHFLPFNPVDk	95%	n+304 (+304), K+304 (+304)	36.57	26.70
1916	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	eSPGGPWQFVGLLPLFDPPR	95%	n+304 (+304)	49.59	25.42
1917	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	gAPEQILDLCk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	43.60	25.35
1918	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	hIVGMTGDGVNDAPALK	95%	n+304 (+304), K+304 (+304)	52.75	26.68
1919	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	IGDIVPADAR	91%	n+304 (+304)	29.72	26.36
1920	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	nEAVDLENIPIEEVFELk	94%	n+304 (+304), K+304 (+304)	26.03	25.07
1921	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	nkESPGGPWQFVGLLPLFDPPR	89%	n+304 (+304), K+304 (+304)	25.32	25.31
1922	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	nLVEVFck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.36	25.43

1923	seq=translation; coord=2:4299718..4306692:-1; parent_transcript=GRMZM2G019404_T01; parent_gene=GRMZM2G019404	GRMZM2G019404_P01,GRMZM2G019404_P02	TRUE	TRUE	wGEQEAAILVPGDIISIK	95%	n+304 (+304), K+304 (+304)	37.92	25.56
1924	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	aGQETHDASTEFDR	95%	n+304 (+304)	34.61	25.00
1925	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	dEMIDIIGVtk	95%	n+304 (+304), K+304 (+304)	47.85	26.00
1926	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	dITPMGGFPHYGIVk	95%	n+304 (+304), K+304 (+304)	31.02	26.78
1927	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	eIQLQLEk	95%	n+304 (+304), K+304 (+304)	48.97	26.28
1928	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	eVPDVAVFQk	95%	n+304 (+304), K+304 (+304)	52.36	26.45
1929	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	gDYLMIk	93%	n+304 (+304), K+304 (+304)	29.05	26.44
1930	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	gYEGVVTR	86%	n+304 (+304)	25.25	25.00

1931	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	IALEEIK	86%	n+304 (+304), K+304 (+304)	25.28	25.00
1932	seq=translation; coord=2:51927314..51930580:1; parent_transcript=GRMZM2G109677_T01; parent_gene=GRMZM2G109677	GRMZM2G109677_P01,GRMZM2G109677_P02, GRMZM2G109677_P04,GRMZM2G132968_P02, GRMZM2G135727_P01,GRMZM2G135727_P02, GRMZM2G324314_P01,GRMZM2G324314_P03, GRMZM2G324314_P04,GRMZM5G801409_P02, GRMZM5G801409_P03,GRMZM5G801409_P04	TRUE	TRUE	vAcIGAWHPAR	95%	n+304 (+304), Carbamidomethyl (+57)	52.17	25.00
1933	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	aDEFIik	95%	n+304 (+304), K+304 (+304)	37.87	25.05
1934	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	eVLSSMEEEEADk	95%	n+304 (+304), K+304 (+304)	35.26	25.00
1935	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	eVLSSMEEEEADkLSGSAAR	94%	n+304 (+304), K+304 (+304)	28.50	25.00
1936	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	iASLDVLak	95%	n+304 (+304), K+304 (+304)	37.61	25.00
1937	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	IAPEYER	86%	n+304 (+304)	25.40	25.00
1938	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	IATIPSSVVLTPTETFDIVLDETk	95%	n+304 (+304), K+304 (+304)	35.26	25.00
1939	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	IDEGVVIANLDADk	93%	n+304 (+304), K+304 (+304)	28.80	26.56
1940	seq=translation; coord=3:64458994..64462315:1; parent_transcript=GRMZM2G128171_T02; parent_gene=GRMZM2G128171	GRMZM2G128171_P02	TRUE	TRUE	tAEALAEFLNTEGGTNVk	95%	n+304 (+304), K+304 (+304)	53.38	25.21
1941	seq=translation; coord=8:39208505..39211382:-1; parent_transcript=GRMZM2G335657_T01; parent_gene=GRMZM2G335657	GRMZM2G335657_P01	TRUE	TRUE	aAQLGLk	95%	n+304 (+304), K+304 (+304)	31.99	25.00
1942	seq=translation; coord=8:39208505..39211382:-1; parent_transcript=GRMZM2G335657_T01; parent_gene=GRMZM2G335657	GRMZM2G335657_P01	TRUE	TRUE	gTLGGTcLNVGcIPSk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	57.54	25.73
1943	seq=translation; coord=8:39208505..39211382:-1; parent_transcript=GRMZM2G335657_T01; parent_gene=GRMZM2G335657	GRMZM2G335657_P01	TRUE	TRUE	tEEQVTALGIPYR	95%	n+304 (+304)	36.85	25.00
1944	seq=translation; coord=9:132550417..132551258:1; parent_transcript=GRMZM2G404249_T01; parent_gene=GRMZM2G404249	GRMZM2G404249_P01,GRMZM5G899188_P01	TRUE	TRUE	eLAGAYAFVVDMPGLSTGDIR	95%	n+304 (+304)	55.62	25.00
1945	seq=translation; coord=9:132550417..132551258:1; parent_transcript=GRMZM2G404249_T01; parent_gene=GRMZM2G404249	GRMZM2G404249_P01,GRMZM5G899188_P01	TRUE	TRUE	eLAGAYAFVVDMPGLSTGDIR	95%	n+304 (+304), iTRAQ8plex (+304)	33.45	25.00

1946	seq=translation; coord=9:132550417..132551258:1; parent_transcript=GRMZM2G404249_T01; parent_gene=GRMZM2G404249	GRMZM2G404249_P01,GRMZM5G899188_P01	TRUE	TRUE	mFGLETPR	92%	n+304 (+304)	27.39	25.00
1947	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	aLVDSFVR	92%	n+304 (+304)	28.70	25.00
1948	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	aYAFLLk	95%	n+304 (+304), K+304 (+304)	42.78	25.00
1949	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	dSIPNSPSLR	89%	n+304 (+304)	26.95	25.00
1950	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	dSVVLTGGLGYk	95%	n+304 (+304), K+304 (+304)	50.82	25.00
1951	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	fFDVVDR	93%	n+304 (+304)	29.34	25.00
1952	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	gcDGSVLIDSTANNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.26	25.00
1953	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	mGQIEVLTGTQGEIR	95%	n+304 (+304)	55.07	25.33
1954	seq=translation; coord=6:125154676..125157008:1; parent_transcript=GRMZM2G450233_T01; parent_gene=GRMZM2G450233	GRMZM2G450233_P01	TRUE	TRUE	mHFHDcFVR	95%	n+304 (+304), Carbamidomethyl (+57)	37.68	25.00
1955	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	aISSSSAYDDQFk	95%	n+304 (+304), K+304 (+304)	54.18	25.00
1956	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	dAESAYWELVIk	95%	n+304 (+304), K+304 (+304)	47.72	26.11
1957	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	gVTSNPTIFQk	95%	n+304 (+304), K+304 (+304)	56.93	25.56
1958	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	iGTPEALALR	91%	n+304 (+304)	29.71	26.54
1959	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	IGIDWEEVGk	95%	n+304 (+304), K+304 (+304)	30.42	25.48
1960	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	ILWASTGVk	94%	n+304 (+304), K+304 (+304)	30.32	25.00
1961	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	qLELEGVDSFk	95%	n+304 (+304), K+304 (+304)	37.82	26.13
1962	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	sFDSLLVSLQEk	95%	n+304 (+304), K+304 (+304)	33.33	25.84
1963	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	tVDANVSEAEVGYSALEk	95%	n+304 (+304), K+304 (+304)	44.24	25.60

1964	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	vDTLIDk	87%	n+304 (+304), K+304 (+304)	25.87	25.00
1965	seq=translation; coord=8:160390396..160393378:1; parent_transcript=GRMZM2G134256_T01; parent_gene=GRMZM2G134256	GRMZM2G134256_P01	TRUE	TRUE	vTSVASFFVSR	88%	n+304 (+304)	27.06	25.68
1966	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	aLSLQLADR	89%	n+304 (+304)	28.76	27.02
1967	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	aVcLCfAK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	30.54	26.50
1968	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	eGATVAFTFVR	95%	n+304 (+304)	35.98	25.01
1969	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	eSIGDVTEADLER	89%	n+304 (+304)	25.08	25.00
1970	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	iDVVVNNAEQYER	95%	n+304 (+304)	83.91	25.00
1971	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	tNIFYFLVSk	95%	n+304 (+304), K+304 (+304)	44.22	25.59
1972	seq=translation; coord=2:210034645..210036617:1; parent_transcript=GRMZM2G339994_T01; parent_gene=GRMZM2G339994	GRMZM2G339994_P01,GRMZM2G339994_P02	TRUE	TRUE	vALVTGGDSIGIR	95%	n+304 (+304)	51.25	26.45
1973	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	fDELMAAAAEER	95%	n+304 (+304)	56.33	25.00
1974	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	iEIILGk	95%	n+304 (+304), K+304 (+304)	30.47	25.00
1975	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	nLTVTGDAASGGEGQR	95%	n+304 (+304)	49.13	25.00
1976	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	sDKFDELMAAAAEER	95%	n+304 (+304), K+304 (+304)	40.84	25.00
1977	seq=translation; coord=3:11894936..11898354:1; parent_transcript=GRMZM2G096240_T01; parent_gene=GRMZM2G096240	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	tSTVEINDESR	95%	n+304 (+304)	35.02	25.00
1978	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G096240_P01,GRMZM2G098335_P01	TRUE	TRUE	vVEEIAEGVk	95%	n+304 (+304), K+304 (+304)	42.61	26.39
1979	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02,GRMZM2G407249_P01	TRUE	TRUE	aALVGLYQETSMLTFEGQk	95%	n+304 (+304), K+304 (+304)	79.01	25.26
1980	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02,GRMZM2G407249_P01	TRUE	TRUE	aALVGLYQETSmlTFEGQk	89%	n+304 (+304), Oxidation (+16), K+304 (+304)	25.59	25.48

1981	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02,GRMZM2G407249_P01	TRUE	TRUE	aFVEHYR	95%	n+304 (+304)	36.74	25.00
1982	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02,GRMZM2G407249_P01	TRUE	TRUE	fQGPSAIAGk	95%	n+304 (+304), K+304 (+304)	38.00	25.93
1983	seq=translation; coord=4:44859117..44861815:-1; parent_transcript=GRMZM2G006953_T02; parent_gene=GRMZM2G006953	GRMZM2G006953_P02,GRMZM2G407249_P01	TRUE	TRUE	fSQAFHLLPAAGSFFVQNDMFR	95%	n+304 (+304)	45.38	25.00
1984	seq=translation; coord=5:63800401..63802605:-1; parent_transcript=GRMZM5G834758_T02; parent_gene=GRMZM5G834758	GRMZM5G834758_P02,GRMZM5G834758_P03	TRUE	TRUE	aIAAYNk	92%	n+304 (+304), K+304 (+304)	27.12	25.40
1985	seq=translation; coord=5:63800401..63802605:-1; parent_transcript=GRMZM5G834758_T02; parent_gene=GRMZM5G834758	GRMZM5G834758_P02,GRMZM5G834758_P03	TRUE	TRUE	aPSAFFVFMEEFR	95%	n+304 (+304)	43.55	25.00
1986	seq=translation; coord=5:63800401..63802605:-1; parent_transcript=GRMZM5G834758_T02; parent_gene=GRMZM5G834758	GRMZM5G834758_P02,GRMZM5G834758_P03	TRUE	TRUE	rAPSAFFVFMEEFR	95%	n+304 (+304)	60.28	25.00
1987	seq=translation; coord=5:63800401..63802605:-1; parent_transcript=GRMZM5G834758_T02; parent_gene=GRMZM5G834758	GRMZM5G834758_P02,GRMZM5G834758_P03	TRUE	TRUE	rAPSAFFVFmEEFR	95%	n+304 (+304), Oxidation (+16)	41.61	25.00
1988	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01,GRMZM2G015784_P03	TRUE	TRUE	dPGQQPFSFSIGQGSVIK	95%	n+304 (+304), K+304 (+304)	45.08	25.50
1989	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01,GRMZM2G015784_P03	TRUE	TRUE	gWDEGVMTMQVGEVAR	95%	n+304 (+304)	62.09	25.00
1990	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01,GRMZM2G015784_P03	TRUE	TRUE	gWDEGVmTMQVGEVAR	95%	n+304 (+304), Oxidation (+16)	69.14	25.00
1991	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01,GRMZM2G015784_P03	TRUE	TRUE	gWDEGVMTmQVGEVAR	95%	n+304 (+304), Oxidation (+16)	64.93	25.00
1992	seq=translation; coord=5:209262549..209264524:-1; parent_transcript=GRMZM2G015784_T01; parent_gene=GRMZM2G015784	GRMZM2G015784_P01,GRMZM2G015784_P03	TRUE	TRUE	gWDEGVmTmQVGEVAR	93%	n+304 (+304), Oxidation (+16), Oxidation (+16)	29.92	25.00
1993	seq=translation; coord=3:210506972..210508715:1; parent_transcript=GRMZM2G022931_T01; parent_gene=GRMZM2G022931	GRMZM2G022931_P01	TRUE	TRUE	gGQFTMFMR	95%	n+304 (+304)	32.48	25.00
1994	seq=translation; coord=3:210506972..210508715:1; parent_transcript=GRMZM2G022931_T01; parent_gene=GRMZM2G022931	GRMZM2G022931_P01	TRUE	TRUE	gGQFTmFMR	90%	n+304 (+304), Oxidation (+16)	27.18	25.00
1995	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G022931_T01; parent_gene=GRMZM2G022931	GRMZM2G022931_P01	TRUE	TRUE	vLLPLELFGAk	95%	n+304 (+304), K+304 (+304)	42.18	25.00
1996	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	aFGGQSLDFGk	95%	n+304 (+304), K+304 (+304)	50.96	26.55
1997	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	aSNILATGGYGR	86%	n+304 (+304)	25.57	25.17
1998	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	aVIELENYGLPFSR	95%	n+304 (+304)	57.91	25.00

1999	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	IGANSLDIVVFR	95%	n+304 (+304)	66.38	25.00
2000	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	IPGISETAAIFAGVDVTK	94%	n+304 (+304), K+304 (+304)	27.99	25.00
2001	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	sMTMEIR	88%	n+304 (+304)	26.32	25.00
2002	seq=translation; coord=7:4234486..4239316:1; parent_transcript=GRMZM2G064799_T01; parent_gene=GRMZM2G064799	GRMZM2G064799_P01,GRMZM2G064799_P02, GRMZM2G079888_P01	TRUE	TRUE	vMQNNAAVFR	93%	n+304 (+304)	29.71	25.00
2003	seq=translation; coord=4:153394405..153398468:1; parent_transcript=GRMZM2G135893_T01; parent_gene=GRMZM2G135893	GRMZM2G135893_P01	TRUE	TRUE	gSLFGDNIK	92%	n+304 (+304), K+304 (+304)	29.66	26.18
2004	seq=translation; coord=3:112198031..112206945:-1; parent_transcript=GRMZM2G086882_T01; parent_gene=GRMZM2G086882	GRMZM2G086882_P01	TRUE	TRUE	gELVSDDLVVGIIDEAMk	95%	n+304 (+304), K+304 (+304)	52.85	25.29
2005	seq=translation; coord=3:112198031..112206945:-1; parent_transcript=GRMZM2G086882_T01; parent_gene=GRMZM2G086882	GRMZM2G086882_P01	TRUE	TRUE	IEAFHR	95%	n+304 (+304)	32.25	25.09
2006	seq=translation; coord=3:112198031..112206945:-1; parent_transcript=GRMZM2G086882_T01; parent_gene=GRMZM2G086882	GRMZM2G086882_P01	TRUE	TRUE	ILIGPPGSGk	95%	n+304 (+304), K+304 (+304)	42.73	25.00
2007	seq=translation; coord=3:112198031..112206945:-1; parent_transcript=GRMZM2G086882_T01; parent_gene=GRMZM2G086882	GRMZM2G086882_P01	TRUE	TRUE	vLNFAIDDAVLEER	95%	n+304 (+304)	91.69	25.89
2008	seq=translation; coord=7:54363440..54365032:-1; parent_transcript=GRMZM2G032766_T01; parent_gene=GRMZM2G032766	GRMZM2G032766_P01	TRUE	TRUE	dVLDDAGIGGk	95%	n+304 (+304), K+304 (+304)	56.55	26.19
2009	seq=translation; coord=7:54363440..54365032:-1; parent_transcript=GRMZM2G032766_T01; parent_gene=GRMZM2G032766	GRMZM2G032766_P01	TRUE	TRUE	vDLNNGENPTWDEK	90%	n+304 (+304), K+304 (+304)	25.54	25.00
2010	seq=translation; coord=7:54363440..54365032:-1; parent_transcript=GRMZM2G032766_T01; parent_gene=GRMZM2G032766	GRMZM2G032766_P01	TRUE	TRUE	veENLER	91%	n+304 (+304)	27.96	25.00
2011	seq=translation; coord=7:54363440..54365032:-1; parent_transcript=GRMZM2G032766_T01; parent_gene=GRMZM2G032766	GRMZM2G032766_P01	TRUE	TRUE	yYDPNPYPAPAGYANAGTR	95%	n+304 (+304)	30.77	25.00
2012	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	TRUE	TRUE	eADGSVk	91%	n+304 (+304), K+304 (+304)	26.75	25.77
2013	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	TRUE	TRUE	fGQGECSAYLFPDIYTDGR	94%	n+304 (+304)	30.23	25.00
2014	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	TRUE	TRUE	iSVQGI DAVLFAPDDAk	95%	n+304 (+304), K+304 (+304)	64.45	25.28
2015	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	TRUE	TRUE	IVSEGYVLTVLAPNDEAMAR	93%	n+304 (+304)	27.31	25.00
2016	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825	GRMZM2G027825_P01	TRUE	TRUE	IVSEGYVLTVLAPNDEAMAR	95%	n+304 (+304), iTRAQ8plex (+304)	45.21	25.24

2017	seq=translation; coord=5:4664985..4668821:1; parent_transcript=GRMZM2G027825_T01; parent_gene=GRMZM2G027825 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G027825_P01	TRUE	TRUE	sLQALLLVHVLPSR	95%	n+304 (+304)	37.28	25.00
2018	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	dQEFIATk	95%	n+304 (+304), K+304 (+304)	52.11	26.12
2019	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	ePGLTFMVAk	94%	n+304 (+304), K+304 (+304)	29.79	26.11
2020	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	fTVIFDTGSSNLWVPSSk	95%	n+304 (+304), K+304 (+304)	32.61	25.33
2021	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	gyWQFNMGDVLVDGk	93%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	25.64	25.49
2022	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	hADEGEGGEIVFGGMDSSHYk	95%	n+304 (+304), K+304 (+304)	49.16	25.00
2023	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	iGAAGVVSQeck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	51.12	25.56
2024	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	IPSPMGESAVDcGSLASMPDIAFTIGGk	95%	Carbamidomethyl (+57), K+304 (+304)	38.45	25.00
2025	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	nyMNAQYFGEIGVGSPPQk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	33.93	25.54
2026	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	qGLISDPVFSFWFNR	93%	n+304 (+304)	29.29	25.00
2027	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=6:165013896..165020496:1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	tQELILNYINQLcER	95%	n+304 (+304), Carbamidomethyl (+57)	47.85	25.47
2028	parent_transcript=GRMZM2G065757_T01; parent_gene=GRMZM2G065757 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G065757_P01,GRMZM2G065757_P02	TRUE	TRUE	tVVSQYQQQLDLLLAETQPAk	95%	n+304 (+304), K+304 (+304)	43.06	25.00
2029	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	aFALLSEEGIAk	95%	n+304 (+304), K+304 (+304)	55.03	25.72
2030	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	aSQLEGALLEk	91%	n+304 (+304), K+304 (+304)	25.88	25.77
2031	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	aVFGEIYPDPVR	95%	n+304 (+304)	30.18	25.00
2032	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	eAMALANSIASMk	92%	n+304 (+304), K+304 (+304)	25.91	25.24
2033	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	gFNASMEEAR	95%	n+304 (+304)	41.75	25.00
2034	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271	GRMZM2G082271_P01	TRUE	TRUE	gLPIMLFSTDEASNk	95%	n+304 (+304), K+304 (+304)	48.02	26.07

2035	seq=translation; coord=10:18124892..18142878:-1; parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	gSIVLPEk	88%	n+304 (+304), K+304 (+304)	26.72	25.34
2036	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	IEDELR	89%	n+304 (+304)	25.83	25.00
2037	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	sGLDAAIPAAR	95%	n+304 (+304)	33.02	25.00
2038	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	tLIAPNHTcTHMLNFALR	95%	n+304 (+304), Carbamidomethyl (+57)	38.51	25.22
2039	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	vLDWLTPSIAPLk	95%	n+304 (+304), K+304 (+304)	32.10	25.00
2040	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=10:18124892..18142878:-1;	GRMZM2G082271_P01	TRUE	TRUE	wAWELLTQVYk	95%	n+304 (+304), K+304 (+304)	30.38	26.06
2041	parent_transcript=GRMZM2G082271_T01; parent_gene=GRMZM2G082271 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G082271_P01	TRUE	TRUE	wPSSPVVPVDDPTLLFANAGMNQFkPVFLGTAAPDSPLGR	95%	n+304 (+304), K+304 (+304)	26.97	25.00
2042	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	aPDPADYPADYR	95%	n+304 (+304)	34.06	25.00
2043	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	dDMSVPVYAVAPLNk	95%	n+304 (+304), K+304 (+304)	65.12	25.22
2044	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	gFESGALPDGVEDR	95%	n+304 (+304)	52.36	25.00
2045	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	gIDESAGSDLTNLVHLINsY	95%	n+304 (+304), iTRAQ8plex (+304)	65.57	25.00
2046	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	gVGITVFHTAGAR	95%	n+304 (+304)	53.61	26.95
2047	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	kDDAVAEAPPYR	95%	K+304 (+304), n+304 (+304)	31.25	25.09
2048	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	IMGGSEEGEGIR	95%	n+304 (+304)	40.02	25.00
2049	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=4:3210119..3212030:-1;	GRMZM2G085054_P02	TRUE	TRUE	ISALLSAADGEAGEAGGR	95%	n+304 (+304)	62.65	25.00
2050	parent_transcript=GRMZM2G085054_T02; parent_gene=GRMZM2G085054 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G085054_P02	TRUE	TRUE	vGTEVAGDQLER	95%	n+304 (+304)	52.36	25.00
2051	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	aLAFFYPLAGR	95%	n+304 (+304)	39.83	25.63
2052	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898	GRMZM2G314898_P01	TRUE	TRUE	aLALDPAAEVk	95%	n+304 (+304), K+304 (+304)	43.56	25.00

2053	seq=translation; coord=3:8299415..8303114:-1; parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	gLVESMHIFR	95%	n+304 (+304)	51.39	26.24
2054	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	iSEGPVkBASATPEETLPLAWVDR	95%	n+304 (+304), K+304 (+304)	38.82	25.35
2055	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	lCFFASVR	85%	n+304 (+304), Carbamidomethyl (+57)	25.05	25.00
2056	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	sGAGEAPAVIR	92%	n+304 (+304)	29.03	25.00
2057	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=3:8299415..8303114:-1;	GRMZM2G314898_P01	TRUE	TRUE	vLASSLVEVVDIIR	95%	n+304 (+304)	43.07	25.00
2058	parent_transcript=GRMZM2G314898_T01; parent_gene=GRMZM2G314898 seq=translation; coord=6:140347883..140348297:-1;	GRMZM2G314898_P01	TRUE	TRUE	vLPVWHR	95%	n+304 (+304)	28.40	25.00
2059	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	eGETVVPGGTGGk	95%	n+304 (+304), K+304 (+304)	38.23	25.09
2060	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	eGVSIDESk	92%	n+304 (+304), K+304 (+304)	28.76	25.00
2061	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	eQLGQQGYSEMgk	95%	n+304 (+304), K+304 (+304)	63.67	25.00
2062	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	eQLGQQGYSEmGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	31.49	25.00
2063	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	gGLSTTDESgGER	95%	n+304 (+304)	51.98	25.00
2064	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=6:140347883..140348297:-1;	AC233879.1_FGP002	TRUE	TRUE	rEQLGQQGYSEMgk	94%	n+304 (+304), K+304 (+304)	31.79	25.60
2065	parent_transcript=AC233879.1_FGT002; parent_gene=AC233879.1_FG002 seq=translation; coord=10:4673451..4676086:-1;	AC233879.1_FGP002	TRUE	TRUE	sVEAQEHAEGR	95%	n+304 (+304)	38.40	25.00
2066	parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762 seq=translation; coord=10:4673451..4676086:-1;	GRMZM2G003762_P03	TRUE	TRUE	dEVFcLFEGVLDNLGR	95%	n+304 (+304), Carbamidomethyl (+57)	65.47	25.00
2067	parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762 seq=translation; coord=10:4673451..4676086:-1;	GRMZM2G003762_P03	TRUE	TRUE	gANEVLLVIEAYk	95%	n+304 (+304), K+304 (+304)	42.96	25.00
2068	parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762 seq=translation; coord=10:4673451..4676086:-1;	GRMZM2G003762_P03	TRUE	TRUE	sLAPFPQGcFYsNALGGLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.27	25.88
2069	parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762 seq=translation; coord=10:4673451..4676086:-1;	GRMZM2G003762_P03	TRUE	TRUE	sTNSLLVASDPEGR	95%	n+304 (+304)	45.20	25.00
2070	parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762	GRMZM2G003762_P03	TRUE	TRUE	vTAVPADEEEIcGATfk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.95	25.00

2071	seq=translation; coord=10:4673451..4676086:-1; parent_transcript=GRMZM2G003762_T03; parent_gene=GRMZM2G003762	GRMZM2G003762_P03	TRUE	TRUE	vVEGSTVLTALH	95%	n+304 (+304)	61.03	26.57
2072	seq=translation; coord=6:145987055..145988456:-1; parent_transcript=GRMZM2G306345_T01; parent_gene=GRMZM2G306345	GRMZM2G306345_P01	TRUE	TRUE	aGLDYVScSPFR	95%	n+304 (+304), Carbamidomethyl (+57)	56.26	25.00
2073	seq=translation; coord=6:145987055..145988456:-1; parent_transcript=GRMZM2G306345_T01; parent_gene=GRMZM2G306345	GRMZM2G306345_P01	TRUE	TRUE	fIPVYLAQGILQHDPFEVLDQR	95%	n+304 (+304)	54.50	25.19
2074	seq=translation; coord=6:145987055..145988456:-1; parent_transcript=GRMZM2G306345_T01; parent_gene=GRMZM2G306345	GRMZM2G306345_P01	TRUE	TRUE	vGTMIEIPR	94%	n+304 (+304)	31.11	25.69
2075	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	aPNTLAEYALK	95%	n+304 (+304), K+304 (+304)	43.86	26.26
2076	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	dDATSTFTcPAGTNYK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	49.86	25.00
2077	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	gQcPDAYSYPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.53	25.00
2078	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	iTAPAGTTAAR	91%	n+304 (+304)	29.12	26.24
2079	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	tGdcGGVLQcTGyGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	62.59	25.00
2080	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	tGdcGGVLQcTGyGR	90%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), iTRAQ8plex (+304)	25.50	25.00
2081	seq=translation; coord=7:160215143..160216461:-1; parent_transcript=GRMZM2G374971_T01; parent_gene=GRMZM2G374971	GRMZM2G374971_P01	TRUE	TRUE	vVFcP	95%	n+304 (+304), Carbamidomethyl (+57)	33.17	25.81
2082	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	aDEAYcLTVR	94%	n+304 (+304), Carbamidomethyl (+57)	30.98	25.00
2083	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	dAEGQPAFALINR	95%	n+304 (+304)	38.63	25.00
2084	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	dEFQHWVk	94%	n+304 (+304), K+304 (+304)	28.04	25.42
2085	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	IVPYNAEYLDESVLWTESHVgk	95%	n+304 (+304), K+304 (+304)	36.39	25.00
2086	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	IVPYNPEyVDESVLWTESR	95%	n+304 (+304)	55.25	25.00
2087	seq=translation; coord=2:217342775..217345487:1; parent_transcript=GRMZM2G003409_T01; parent_gene=GRMZM2G003409	GRMZM2G003409_P01,GRMZM2G003409_P04	TRUE	TRUE	IVPYNPEyVDESVLWTESR	89%	n+304 (+304), iTRAQ8plex (+304)	25.25	25.04

2088	seq=translation; coord=9:139405932..139410290:-1; parent_transcript=GRMZM2G165357_T01; parent_gene=GRMZM2G165357	GRMZM2G165357_P01,GRMZM2G165357_P02	TRUE	TRUE	iLVTGGAGFIGSHLVDk	95%	n+304 (+304), K+304 (+304)	40.27	25.00
2089	seq=translation; coord=9:139405932..139410290:-1; parent_transcript=GRMZM2G165357_T01; parent_gene=GRMZM2G165357	GRMZM2G165357_P01,GRMZM2G165357_P02	TRUE	TRUE	sFcYVADMVDGLik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	42.19	25.00
2090	seq=translation; coord=9:139405932..139410290:-1; parent_transcript=GRMZM2G165357_T01; parent_gene=GRMZM2G165357	GRMZM2G165357_P01,GRMZM2G165357_P02	TRUE	TRUE	tGPINLGNPGEFTMLEAENVk	95%	n+304 (+304), K+304 (+304)	41.03	26.12
2091	seq=translation; coord=10:148968847..148972562:1; parent_transcript=GRMZM2G104613_T01; parent_gene=GRMZM2G104613	GRMZM2G104613_P01	TRUE	TRUE	dVLSFAGALEGVELR	95%	n+304 (+304)	69.58	25.40
2092	seq=translation; coord=10:148968847..148972562:1; parent_transcript=GRMZM2G104613_T01; parent_gene=GRMZM2G104613	GRMZM2G104613_P01	TRUE	TRUE	rIEAAVTETLNHGFR	95%	n+304 (+304)	37.07	26.47
2093	seq=translation; coord=4:128262885..128265210:1; parent_transcript=GRMZM2G008748_T02; parent_gene=GRMZM2G008748	GRMZM2G008748_P02	TRUE	TRUE	aAAAVEPk	94%	n+304 (+304), K+304 (+304)	31.08	25.00
2094	seq=translation; coord=4:128262885..128265210:1; parent_transcript=GRMZM2G008748_T02; parent_gene=GRMZM2G008748	GRMZM2G008748_P02	TRUE	TRUE	aIEAVPELk	94%	n+304 (+304), K+304 (+304)	30.88	25.00
2095	seq=translation; coord=4:128262885..128265210:1; parent_transcript=GRMZM2G008748_T02; parent_gene=GRMZM2G008748	GRMZM2G008748_P02	TRUE	TRUE	aVDSALik	95%	n+304 (+304), K+304 (+304)	42.73	25.43
2096	seq=translation; coord=4:128262885..128265210:1; parent_transcript=GRMZM2G008748_T02; parent_gene=GRMZM2G008748	GRMZM2G008748_P02	TRUE	TRUE	sGLLLISGPFk	95%	n+304 (+304), K+304 (+304)	33.16	25.00
2097	seq=translation; coord=1:298408224..298413579:-1; parent_transcript=GRMZM2G022269_T01; parent_gene=GRMZM2G022269	GRMZM2G022269_P01,GRMZM2G022269_P03	TRUE	TRUE	qLDkPFLMPIEDVFSIQGR	95%	n+304 (+304), K+304 (+304)	42.60	25.16
2098	seq=translation; coord=1:298408224..298413579:-1; parent_transcript=GRMZM2G022269_T01; parent_gene=GRMZM2G022269	GRMZM2G022269_P01,GRMZM2G022269_P03	TRUE	TRUE	qLDkPFLMPIEDVFSIQGR	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	31.23	25.77
2099	seq=translation; coord=1:298408224..298413579:-1; parent_transcript=GRMZM2G022269_T01; parent_gene=GRMZM2G022269	GRMZM2G022269_P01,GRMZM2G022269_P03	TRUE	TRUE	tGEDVEILGLAQTGPLk	94%	n+304 (+304), K+304 (+304)	27.29	25.00
2100	seq=translation; coord=1:298408224..298413579:-1; parent_transcript=GRMZM2G022269_T01; parent_gene=GRMZM2G022269	GRMZM2G022269_P01,GRMZM2G022269_P03	TRUE	TRUE	vELLGEMk	95%	n+304 (+304), K+304 (+304)	34.60	25.31
2101	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	TRUE	TRUE	aGDVLAAANTAAEVAMR	95%	n+304 (+304)	70.67	25.91
2102	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	TRUE	TRUE	aWLAGTk	95%	n+304 (+304), K+304 (+304)	32.88	25.37
2103	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	TRUE	TRUE	eLDLSSNDVVtk	95%	n+304 (+304), K+304 (+304)	54.50	25.63
2104	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	TRUE	TRUE	eQTGNVyk	94%	n+304 (+304), K+304 (+304)	31.58	27.18
2105	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001	AC233895.1_FGP001	TRUE	TRUE	fIFSEISQk	95%	n+304 (+304), K+304 (+304)	29.44	25.17

2106	seq=translation; coord=6:140407545..140410127:1; parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001 seq=translation; coord=6:140407545..140410127:1;	AC233895.1_FGP001	TRUE	TRUE	iVDLcEk	86%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.63	26.40
2107	parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001 seq=translation; coord=6:140407545..140410127:1;	AC233895.1_FGP001	TRUE	TRUE	iVEGVLSHQLk	95%	n+304 (+304), K+304 (+304)	40.35	25.00
2108	parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001 seq=translation; coord=6:140407545..140410127:1;	AC233895.1_FGP001	TRUE	TRUE	qFVIDGNk	88%	n+304 (+304), K+304 (+304)	26.95	26.53
2109	parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001 seq=translation; coord=6:140407545..140410127:1;	AC233895.1_FGP001	TRUE	TRUE	sIEDNAEIk	95%	n+304 (+304), K+304 (+304)	58.00	26.25
2110	parent_transcript=AC233895.1_FGT001; parent_gene=AC233895.1_FG001 seq=translation; coord=10:82668664..82669799:-1;	AC233895.1_FGP001	TRUE	TRUE	vAAAYDck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.23	26.04
2111	parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137 seq=translation; coord=10:82668664..82669799:-1;	GRMZM2G121137_P01	TRUE	TRUE	aVPNLDMEcIR	95%	n+304 (+304), Carbamidomethyl (+57)	49.62	25.19
2112	parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137 seq=translation; coord=10:82668664..82669799:-1;	GRMZM2G121137_P01	TRUE	TRUE	aVPNLDMEcIR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	50.30	25.00
2113	parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137 seq=translation; coord=10:82668664..82669799:-1;	GRMZM2G121137_P01	TRUE	TRUE	gPVTAPSYTDDccVAIR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304), iTRAQ8plex	60.82	25.00
2114	parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137 seq=translation; coord=10:82668664..82669799:-1;	GRMZM2G121137_P01	TRUE	TRUE	gPVTAPSYTDDccVAIR	95%	(+304), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304), K+304	33.53	25.00
2115	parent_transcript=GRMZM2G121137_T01; parent_gene=GRMZM2G121137 seq=translation; coord=10:82668664..82669799:-1;	GRMZM2G121137_P01	TRUE	TRUE	IkGPVTAPSYTDDccVAIR	95%	(+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	50.67	25.51
2116	parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857 seq=translation; coord=1:275835279..275836493:-1;	GRMZM2G025857_P01	TRUE	TRUE	aQTAcPVADAGATVTETELAGR	95%	n+304 (+304), Carbamidomethyl (+57)	105.41	25.00
2117	parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857 seq=translation; coord=1:275835279..275836493:-1;	GRMZM2G025857_P01	TRUE	TRUE	fGDVLVDVGELADQPVAAPR	95%	n+304 (+304)	49.39	25.00
2118	parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857 seq=translation; coord=1:275835279..275836493:-1;	GRMZM2G025857_P01	TRUE	TRUE	gGPAAVLQSAATVNAR	95%	n+304 (+304)	66.67	25.44
2119	parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857 seq=translation; coord=1:275835279..275836493:-1;	GRMZM2G025857_P01	TRUE	TRUE	IQAAEQSVLGGTQk	95%	n+304 (+304), K+304 (+304)	43.90	26.01
2120	parent_transcript=GRMZM2G025857_T01; parent_gene=GRMZM2G025857 seq=translation; coord=8:129620163..129623583:1;	GRMZM2G025857_P01	TRUE	TRUE	mVSPAPVAMTDPPGALEK	95%	n+304 (+304), K+304 (+304)	40.51	25.53
2121	parent_transcript=GRMZM2G117198_T01; parent_gene=GRMZM2G117198 seq=translation; coord=8:129620163..129623583:1;	GRMZM2G117198_P01,GRMZM2G117198_P02	TRUE	TRUE	aNVDYEk	95%	n+304 (+304), K+304 (+304)	30.05	25.47
2122	parent_transcript=GRMZM2G117198_T01; parent_gene=GRMZM2G117198	GRMZM2G117198_P01,GRMZM2G117198_P02	TRUE	TRUE	eHVikPVIPEQYLDEK	93%	n+304 (+304), K+304 (+304), K+304 (+304)	25.01	25.00

2123	seq=translation; coord=8:129620163..129623583:1; parent_transcript=GRMZM2G117198_T01; parent_gene=GRMZM2G117198	GRMZM2G117198_P01,GRMZM2G117198_P02	TRUE	TRUE	IcDQVSDAVLDAcLAEDPDSk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	34.10	25.00
2124	seq=translation; coord=8:129620163..129623583:1; parent_transcript=GRMZM2G117198_T01; parent_gene=GRMZM2G117198	GRMZM2G117198_P01,GRMZM2G117198_P02	TRUE	TRUE	tQVTVEYR	91%	n+304 (+304)	28.22	25.00
2125	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	aHFEFMEK	95%	n+304 (+304), K+304 (+304)	30.81	25.59
2126	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	aLEVTHYLGGENYVFWGGR	95%	n+304 (+304)	30.30	25.00
2127	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	eLDHLANFLQAAVDYk	95%	n+304 (+304), K+304 (+304)	47.10	25.19
2128	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	eSTDVEDLFLAHISGMDTLAR	95%	n+304 (+304)	48.03	25.00
2129	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	fSVAFWHTFR	95%	n+304 (+304)	49.59	25.00
2130	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	gTGADPFPGAPTk	95%	n+304 (+304), K+304 (+304)	36.99	25.71
2131	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	IIEDGSLDALVR	95%	n+304 (+304)	36.19	26.16
2132	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	qELAEILFHSAL	95%	n+304 (+304)	39.44	25.63
2133	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	qLQGETNIkPLWGTAQLFMHPR	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	36.60	25.21
2134	seq=translation; coord=2:215654249..215658893:-1; parent_transcript=GRMZM2G005493_T01; parent_gene=GRMZM2G005493	GRMZM2G005493_P01	TRUE	TRUE	yQSFDSEIGALIEAGk	95%	n+304 (+304), K+304 (+304)	44.90	25.11
2135	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	TRUE	TRUE	aGALAVVDGR	95%	n+304 (+304)	31.39	25.21
2136	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	TRUE	TRUE	aLDILFILHAEHEMNCSTAAVR	95%	n+304 (+304), Carbamidomethyl (+57)	55.40	25.00
2137	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	TRUE	TRUE	aMGFPTEFFPVLFAIPR	95%	n+304 (+304)	50.82	25.39
2138	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	TRUE	TRUE	dPLIEVAIALEK	95%	n+304 (+304), K+304 (+304)	39.69	25.00
2139	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588	GRMZM2G135588_P01	TRUE	TRUE	kLADEVFSIVGR	89%	K+304 (+304), n+304 (+304)	25.16	25.00

2140	seq=translation; coord=5:149458858..149463589:-1; parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588 seq=translation; coord=5:149458858..149463589:-1;	GRMZM2G135588_P01	TRUE	TRUE	IADEVFSIVGR	95%	n+304 (+304)	46.80	25.00
2141	parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588 seq=translation; coord=5:149458858..149463589:-1;	GRMZM2G135588_P01	TRUE	TRUE	IAGRPPVLPNTLSYSENFYMLDSLGDGR	95%	n+304 (+304)	42.49	25.00
2142	parent_transcript=GRMZM2G135588_T01; parent_gene=GRMZM2G135588 seq=translation; coord=5:149458858..149463589:-1;	GRMZM2G135588_P01	TRUE	TRUE	mLNEIGSMENIPDFIVGVK	95%	n+304 (+304), K+304 (+304)	32.03	25.61
2143	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	aAHLGVESIVIGMPHR	95%	n+304 (+304)	34.44	25.02
2144	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	aWEADPSSVDESWDNFFR	95%	n+304 (+304)	67.65	25.00
2145	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	dRIETVNPMDITYDR	93%	n+304 (+304)	27.76	25.00
2146	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	dWLSAYWTGfK	91%	n+304 (+304), K+304 (+304)	28.64	25.38
2147	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	fGLEGAETLIPGMk	95%	n+304 (+304), K+304 (+304)	35.13	26.34
2148	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	IIWSTQFESFLATk	95%	n+304 (+304), K+304 (+304)	34.20	25.60
2149	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	INVLGNVVR	95%	n+304 (+304)	29.74	25.00
2150	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	ITDSFLDGTSSVYLEELQR	95%	n+304 (+304)	61.55	25.00
2151	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=10:109798193..109804126:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	sNLSEFDDLGHGPGFDk	93%	n+304 (+304), K+304 (+304)	25.05	25.00
2152	parent_transcript=GRMZM2G151041_T01; parent_gene=GRMZM2G151041 seq=translation; coord=1:263143605..263149463:1;	GRMZM2G151041_P01,GRMZM2G151041_P02	TRUE	TRUE	vYYELDEER	95%	n+304 (+304)	41.02	25.00
2153	parent_transcript=GRMZM2G079668_T01; parent_gene=GRMZM2G079668 seq=translation; coord=1:263143605..263149463:1;	GRMZM2G079668_P01,GRMZM2G079668_P02	TRUE	TRUE	mELSSLTQTNMSLPFITATADGPK	95%	n+304 (+304), K+304 (+304)	76.47	25.63
2154	parent_transcript=GRMZM2G079668_T01; parent_gene=GRMZM2G079668 seq=translation; coord=3:41741731..41743930:-1;	GRMZM2G079668_P01,GRMZM2G079668_P02	TRUE	TRUE	qVSYLVIR	95%	n+304 (+304)	33.03	25.00
2155	parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648 seq=translation; coord=3:41741731..41743930:-1;	GRMZM2G144648_P01	TRUE	TRUE	acPGVVScADIVALAAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	68.14	25.47
2156	parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648 seq=translation; coord=3:41741731..41743930:-1;	GRMZM2G144648_P01	TRUE	TRUE	aSLWQVETGR	86%	n+304 (+304)	25.84	25.66
2157	parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	TRUE	TRUE	dAVSYQfK	92%	n+304 (+304), K+304 (+304)	29.13	25.00

2158	seq=translation; coord=3:41741731..41743930:-1; parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	TRUE	TRUE	gcDASILLDTAQSEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.64	25.08
2159	seq=translation; coord=3:41741731..41743930:-1; parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	TRUE	TRUE	nScPSVDSIVR	95%	n+304 (+304), Carbamidomethyl (+57)	36.21	25.00
2160	seq=translation; coord=3:41741731..41743930:-1; parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	TRUE	TRUE	sVTWAQVAANPALPAR	95%	n+304 (+304)	49.27	25.61
2161	seq=translation; coord=3:41741731..41743930:-1; parent_transcript=GRMZM2G144648_T01; parent_gene=GRMZM2G144648	GRMZM2G144648_P01	TRUE	TRUE	tAAPNLVGGYEVIDAIK	95%	n+304 (+304), K+304 (+304)	67.74	25.07
2162	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	aDGYILEGK	95%	n+304 (+304), K+304 (+304)	37.89	26.52
2163	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	eLEFYMK	95%	n+304 (+304), K+304 (+304)	34.77	25.00
2164	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	iLDVVYNASNNEVLR	95%	n+304 (+304)	48.17	26.19
2165	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	kDNAEGQEVEAAEETk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	41.17	25.66
2166	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	IDTGNYSWGSEAVTR	95%	n+304 (+304)	66.48	25.00
2167	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	qWYLTHYGVDIGR	95%	n+304 (+304)	50.56	25.05
2168	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	qWyLTHYGVDIGR	91%	Pyro-cmC (-17), n+304 (+304), iTRAQ8plex (+304)	25.53	25.00

2169	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	sAIVQVDAAPfk	95%	n+304 (+304), K+304 (+304)	50.38	26.05
2170	seq=translation; coord=4:232510364..232513106:1; parent_transcript=GRMZM2G030228_T01; parent_gene=GRMZM2G030228	GRMZM2G030228_P01,GRMZM2G030228_P02, GRMZM2G030228_P03,GRMZM2G051848_P01, GRMZM2G063700_P01,GRMZM2G063700_P02, GRMZM2G336875_P01,GRMZM2G360677_P01, GRMZM2G360677_P02,GRMZM2G360677_P03	TRUE	TRUE	tLDPHIEEQFGSGR	95%	n+304 (+304)	48.72	25.00
2171	seq=translation; coord=5:199786088..199787380:1; parent_transcript=GRMZM2G054201_T01; parent_gene=GRMZM2G054201	GRMZM2G054201_P01,GRMZM2G054201_P02, GRMZM2G054201_P03,GRMZM2G121075_P01, GRMZM2G121075_P02	TRUE	TRUE	hSGNISLDDVIEIAR	95%	n+304 (+304)	47.70	25.22
2172	seq=translation; coord=4:176858064..176868636:-1; parent_transcript=GRMZM2G149281_T01; parent_gene=GRMZM2G149281	GRMZM2G149281_P01,GRMZM2G149281_P02, GRMZM2G149281_P03,GRMZM2G149281_P04	TRUE	TRUE	aIFAPYSLk	94%	n+304 (+304), K+304 (+304)	27.19	25.00
2173	seq=translation; coord=4:176858064..176868636:-1; parent_transcript=GRMZM2G149281_T01; parent_gene=GRMZM2G149281	GRMZM2G149281_P01,GRMZM2G149281_P02, GRMZM2G149281_P03,GRMZM2G149281_P04	TRUE	TRUE	iSPAFVLFFDcSEEDMEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	62.62	25.00
2174	seq=translation; coord=4:176858064..176868636:-1; parent_transcript=GRMZM2G149281_T01; parent_gene=GRMZM2G149281	GRMZM2G149281_P01,GRMZM2G149281_P02, GRMZM2G149281_P03,GRMZM2G149281_P04	TRUE	TRUE	vTVVFLGPGSGSk	95%	n+304 (+304), K+304 (+304)	50.29	25.00
2175	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	aSDLDIASVLGMGFpk	95%	n+304 (+304), K+304 (+304)	48.44	25.93
2176	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	dIYADAFGER	87%	n+304 (+304)	25.51	25.00
2177	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	dVDMVIEAVIEK	95%	n+304 (+304), K+304 (+304)	33.75	26.82
2178	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	eVNPQFLQR	89%	n+304 (+304)	26.78	25.25
2179	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	nLSDSLVDLMVK	95%	n+304 (+304), K+304 (+304)	63.49	26.41
2180	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	tIAGNLEGLVk	95%	n+304 (+304), K+304 (+304)	55.04	25.56
2181	seq=translation; coord=4:221070736..221076802:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	tSPQAILDLITIGk	95%	n+304 (+304), K+304 (+304)	36.62	25.00
2182	seq=translation; coord=1:12248908..12249912:-1; parent_transcript=GRMZM5G854613_T01; parent_gene=GRMZM5G854613	GRMZM5G854613_P01	TRUE	TRUE	vMDENNVIR	91%	n+304 (+304)	28.76	25.61
2183	seq=translation; coord=1:12248908..12249912:-1; parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236	GRMZM2G472236_P01	TRUE	TRUE	aTLGDVLANATAR	95%	n+304 (+304)	57.16	26.54
2184	seq=translation; coord=1:12248908..12249912:-1; parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236	GRMZM2G472236_P01	TRUE	TRUE	gGPAAAMQSAATANER	95%	n+304 (+304)	74.55	25.00

2185	seq=translation; coord=1:12248908..12249912:-1; parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236 seq=translation; coord=1:12248908..12249912:-1;	GRMZM2G472236_P01	TRUE	TRUE	iVTEFVAGQAVGQyLAR	95%	n+304 (+304), iTRAQ8plex (+304)	32.86	25.00
2186	parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236 seq=translation; coord=1:12248908..12249912:-1;	GRMZM2G472236_P01	TRUE	TRUE	mGAVGHDQATDATAVQGVTVSETR	95%	n+304 (+304)	81.65	25.00
2187	parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236 seq=translation; coord=1:12248908..12249912:-1;	GRMZM2G472236_P01	TRUE	TRUE	sDAAAIQAAEAR	95%	n+304 (+304)	59.34	25.00
2188	parent_transcript=GRMZM2G472236_T01; parent_gene=GRMZM2G472236 seq=translation; coord=1:12248908..12249912:-1;	GRMZM2G472236_P01	TRUE	TRUE	vTIGEALeATALAAGDAPVER	95%	n+304 (+304)	47.88	25.48
2189	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	dDARDEINTVDLSHNR	95%	n+304 (+304)	27.29	25.00
2190	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	dIHALLSVk	92%	n+304 (+304), K+304 (+304)	26.48	25.00
2191	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	gLDSVDLSSNR	95%	n+304 (+304)	37.28	25.00
2192	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	gQIPSAVGGLTELmSLTLFR	95%	n+304 (+304)	56.96	26.13
2193	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	gQIPSAVGGLTELmSLTLFR	95%	n+304 (+304), Oxidation (+16)	65.75	25.22
2194	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	hNQLTGPIAGLVQGQFR	95%	n+304 (+304)	33.76	25.37
2195	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	ITGGIPAAAFADLPsLR	95%	n+304 (+304)	63.22	26.42
2196	parent_transcript=GRMZM2G099295_T01; parent_gene=GRMZM2G099295 seq=translation; coord=2:205943881..205945286:-1;	GRMZM2G099295_P01	TRUE	TRUE	IVFPPELTyLDLSHNLIR	95%	n+304 (+304)	63.58	25.01
2197	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523 seq=translation; coord=1:77258356..77350693:1;	GRMZM2G020523_P01	TRUE	TRUE	dSVAQLGGPSWAVPLGR	95%	n+304 (+304)	80.08	26.28
2198	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523 seq=translation; coord=1:77258356..77350693:1;	GRMZM2G020523_P01	TRUE	TRUE	gAGPNAGSLR	93%	n+304 (+304)	30.10	25.00
2199	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523 seq=translation; coord=1:77258356..77350693:1;	GRMZM2G020523_P01	TRUE	TRUE	gFDVIdNIk	95%	n+304 (+304), K+304 (+304)	37.12	26.11
2200	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523 seq=translation; coord=1:77258356..77350693:1;	GRMZM2G020523_P01	TRUE	TRUE	gLsSTMVAlSGAHTVGR	95%	n+304 (+304)	57.69	25.00
2201	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523 seq=translation; coord=1:77258356..77350693:1;	GRMZM2G020523_P01	TRUE	TRUE	mGSISPLTGTDGEIR	95%	n+304 (+304)	54.24	25.00
2202	parent_transcript=GRMZM2G020523_T01; parent_gene=GRMZM2G020523	GRMZM2G020523_P01	TRUE	TRUE	tAVSTAVLLEPR	95%	n+304 (+304)	50.03	25.59

2203	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	eGQMVDIR	86%	n+304 (+304)	25.24	25.00
2204	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	iQAVIESGVFPR	95%	n+304 (+304)	46.41	26.20
2205	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	IVELLMHPASASVLIPALR	95%	n+304 (+304)	56.07	25.00
2206	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	sPPIEEVISTGVVPR	95%	n+304 (+304)	46.54	26.04
2207	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	tVGNIVTGDDMQTQcVIDNQALPcLLNLLTTNHk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Carbamidomethyl (+57),	26.39	25.00
2208	seq=translation; coord=6:127495800..127501815:-1; parent_transcript=GRMZM2G009845_T01; parent_gene=GRMZM2G009845	GRMZM2G009845_P01,GRMZM2G009845_P02, GRMZM2G088088_P01,GRMZM2G088088_P02	TRUE	TRUE	yLVAQGcIkPLcDLLVcPDPR	95%	K+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	32.77	25.00
2209	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P01,GRMZM2G046804_P02, GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	aGIALNDHFVc	95%	n+304 (+304), K+304 (+304)	34.42	25.02
2210	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	gASYEDIK	95%	n+304 (+304), K+304 (+304)	35.67	26.13
2211	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	gIMGYAEEDLVSTDFLGDSR	95%	n+304 (+304)	32.16	25.00
2212	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	hSDITLk	91%	n+304 (+304), K+304 (+304)	25.97	25.00
2213	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	tLLFGDkPVTVFgIR	95%	n+304 (+304), K+304 (+304)	36.53	25.00
2214	seq=translation; coord=4:36880092..36884475:-1; parent_transcript=GRMZM2G046804_T01; parent_gene=GRMZM2G046804	GRMZM2G046804_P04,GRMZM2G046804_P05, GRMZM2G046804_P06,GRMZM2G046804_P07, GRMZM2G046804_P08 GRMZM2G046804_P01,GRMZM2G046804_P02,	TRUE	TRUE	vHDFNGIVEGLMTTVHAITATQk	95%	n+304 (+304), K+304 (+304)	27.88	25.00
2215	seq=translation; coord=6:135883373..135887597:1; parent_transcript=GRMZM2G059991_T01; parent_gene=GRMZM2G059991	GRMZM2G059991_P01	TRUE	TRUE	aLEQLDTAVSk	95%	n+304 (+304), K+304 (+304)	36.28	26.89
2216	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	aNAVAIGNYLMSk	95%	n+304 (+304), K+304 (+304)	58.30	25.45
2217	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	fADSFDMPGFTLESmk	95%	n+304 (+304), K+304 (+304)	55.05	25.00

2218	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	iGAPAMTSR	95%	n+304 (+304)	32.74	25.15
2219	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	IIcGG SAYPR	94%	n+304 (+304), Carbamidomethyl (+57)	28.32	25.00
2220	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	nAVFGDSSALSPGGVR	95%	n+304 (+304)	34.04	25.00
2221	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	vSAATGYIDYek	91%	n+304 (+304), K+304 (+304)	26.76	25.50
2222	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	yYGGNDVIDEIE NLcR	95%	n+304 (+304), Carbamidomethyl (+57)	49.55	25.00
2223	seq=translation; coord=4:20772978..20777200:-1; parent_transcript=GRMZM2G078143_T01; parent_gene=GRMZM2G078143	GRMZM2G078143_P01	TRUE	TRUE	yYGGNDVIDEIE NLcR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	34.42	25.00
2224	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	dSGSPEANDLTHWDLTFW SER	95%	n+304 (+304)	62.54	25.00
2225	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	eAVLSGVALEDEQR	95%	n+304 (+304)	76.30	25.48
2226	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	fSE NVLDATk	95%	n+304 (+304), K+304 (+304)	35.35	26.20
2227	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	gI EPTWak	89%	n+304 (+304), K+304 (+304)	25.95	25.00
2228	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	gREPSPEPLLR	95%	n+304 (+304)	42.82	26.87
2229	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	gVEWDAVELPSQFMENWcYHk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.00	25.00
2230	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	IEGELEELEk	95%	n+304 (+304), K+304 (+304)	42.56	25.00
2231	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	IEVIWGMVDHLk	95%	n+304 (+304), K+304 (+304)	26.64	25.00
2232	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	qDEGFVAGIR	89%	n+304 (+304)	27.05	25.00
2233	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	tQVLAPLPEDR	89%	n+304 (+304)	28.33	26.69
2234	seq=translation; coord=5:216695478..216702082:-1; parent_transcript=GRMZM2G133919_T01; parent_gene=GRMZM2G133919	GRMZM2G133919_P01	TRUE	TRUE	vMDGLFLAHk	95%	n+304 (+304), K+304 (+304)	34.70	26.10
2235	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	aVDGSYVFSk	95%	n+304 (+304), K+304 (+304)	37.13	25.00

2236	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	dYNVDMVPk	95%	n+304 (+304), K+304 (+304)	33.03	25.28
2237	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	ecILSGLLSVDGLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	46.85	25.61
2238	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	IYSESLAR	90%	n+304 (+304)	26.47	25.00
2239	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	sPLMGLFEK	95%	n+304 (+304), K+304 (+304)	33.04	25.74
2240	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	vEFDMEGk	94%	n+304 (+304), K+304 (+304)	31.97	25.73
2241	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	yGLSDDTVDFIGHALALHR	95%	n+304 (+304)	63.77	25.07
2242	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	yGLSDDTVDFIGHALALHR	95%	n+304 (+304), iTRAQ8plex (+304)	34.28	25.35
2243	seq=translation; coord=8:103922075..103930908:-1; parent_transcript=GRMZM2G435373_T01; parent_gene=GRMZM2G435373	GRMZM2G435373_P01,GRMZM2G435373_P02	TRUE	TRUE	yLDEPALDTVk	95%	n+304 (+304), K+304 (+304)	39.55	26.51
2244	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	aLLDVGLIR	94%	n+304 (+304)	30.29	25.00
2245	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	dITAQIISASIAGDMVLASAYSHELPR	95%	n+304 (+304)	79.74	25.56
2246	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	dITAQIISASIAGDMVLASaYsHELPR	95%	n+304 (+304), iTRAQ8plex (+304)	42.75	25.09
2247	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	gALDGGDLIPHSEk	94%	n+304 (+304), K+304 (+304)	29.52	26.05
2248	seq=translation; coord=3:168231994..168235001:-1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	gIEADDMEALYk	93%	n+304 (+304), K+304 (+304)	27.62	25.42
2249	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM5G815894_T03; parent_gene=GRMZM5G815894	GRMZM5G815894_P03	TRUE	TRUE	nLAEETPEK	95%	n+304 (+304), K+304 (+304)	36.20	25.00
2250	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	aTIFPHNVGLGATR	95%	n+304 (+304)	49.29	26.02
2251	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	gFVISDWEGIDR	95%	n+304 (+304)	41.13	25.00
2252	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	iDDAVYR	90%	n+304 (+304)	27.65	25.00
2253	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	iGEATALEVR	94%	n+304 (+304)	32.49	26.19

2254	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	iGQMTQIER	89%	n+304 (+304)	26.58	25.00
2255	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	sLVLLk	95%	n+304 (+304), K+304 (+304)	32.74	25.00
2256	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	sSYAPLLPLPk	95%	n+304 (+304), K+304 (+304)	50.88	25.02
2257	seq=translation; coord=1:276305013..276310701:1; parent_transcript=GRMZM2G147687_T01; parent_gene=GRMZM2G147687	GRMZM2G147687_P01,GRMZM2G147687_P02, GRMZM2G147687_P03,GRMZM2G147687_P04	TRUE	TRUE	sVDQLPMNVGDAHYDPLFPFGFLTTk	95%	n+304 (+304), K+304 (+304)	47.31	25.00
2258	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	aAAAAEEPEEAK	95%	n+304 (+304), K+304 (+304)	51.45	25.00
2259	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	aQDLAQPLVGAQIPFk	95%	n+304 (+304), K+304 (+304)	64.16	25.00
2260	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	eEEFDSFTSTk	95%	n+304 (+304), K+304 (+304)	35.68	25.00
2261	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	iGIAVDLSDESFAVvk	95%	n+304 (+304), K+304 (+304)	55.14	25.94
2262	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	ISAAQAVAAIQPTSPR	95%	n+304 (+304)	53.97	26.28
2263	seq=translation; coord=6:156819019..156827574:1; parent_transcript=GRMZM2G701221_T01; parent_gene=GRMZM2G701221	GRMZM2G701221_P01	TRUE	TRUE	yPDDAFGDELR	95%	n+304 (+304)	64.26	25.00
2264	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	TRUE	TRUE	eAALSSDQk	94%	n+304 (+304), K+304 (+304)	30.99	26.30
2265	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	TRUE	TRUE	eFQVNDGFPFSIALSWk	95%	n+304 (+304), K+304 (+304)	29.33	25.00
2266	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	TRUE	TRUE	fGHIDISEk	95%	n+304 (+304), K+304 (+304)	38.93	25.05
2267	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	TRUE	TRUE	hTDPVLLVSDLk	95%	n+304 (+304), K+304 (+304)	28.81	25.00
2268	seq=translation; coord=8:90052293..90060254:-1; parent_transcript=GRMZM2G063676_T01; parent_gene=GRMZM2G063676	GRMZM2G063676_P01	TRUE	TRUE	kFSDPELQSDLASFPFR	95%	K+304 (+304), n+304 (+304)	50.61	25.73
2269	seq=translation; coord=7:137455248..137460051:1; parent_transcript=GRMZM2G115757_T01; parent_gene=GRMZM2G115757	GRMZM2G063676_P01	TRUE	TRUE	vINECSEVENWLR	95%	n+304 (+304), Carbamidomethyl (+57)	66.22	25.00
2270	seq=translation; coord=7:137455248..137460051:1; parent_transcript=GRMZM2G115757_T01; parent_gene=GRMZM2G115757	GRMZM2G115757_P01,GRMZM2G115757_P02	TRUE	TRUE	gDPIEFELGTGQVIk	95%	n+304 (+304), K+304 (+304)	51.54	25.29
2271	seq=translation; coord=7:137455248..137460051:1; parent_transcript=GRMZM2G115757_T01; parent_gene=GRMZM2G115757	GRMZM2G115757_P01,GRMZM2G115757_P02	TRUE	TRUE	ITDGTVFDSSYER	95%	n+304 (+304)	66.76	25.00

2272	seq=translation; coord=7:137455248..137460051:1; parent_transcript=GRMZM2G115757_T01; parent_gene=GRMZM2G115757	GRMZM2G115757_P01,GRMZM2G115757_P02	TRUE	TRUE	sGDVSELQIGVk	95%	n+304 (+304), K+304 (+304)	67.43	26.23
2273	seq=translation; coord=1:66023613..66026784:-1; parent_transcript=GRMZM2G078876_T01; parent_gene=GRMZM2G078876	GRMZM2G078876_P01	TRUE	TRUE	rPSAAccGEVk	94%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	27.36	25.00
2274	seq=translation; coord=1:66023613..66026784:-1; parent_transcript=GRMZM2G078876_T01; parent_gene=GRMZM2G078876	GRMZM2G078876_P01	TRUE	TRUE	rVLALPGAcGASNAAFsk	95%	Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	48.98	25.39
2275	seq=translation; coord=1:66023613..66026784:-1; parent_transcript=GRMZM2G078876_T01; parent_gene=GRMZM2G078876	GRMZM2G078876_P01	TRUE	TRUE	tAVASPVIVGcLcSLAGSNSSNLGFPIDmk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	49.31	25.00
2276	seq=translation; coord=1:66023613..66026784:-1; parent_transcript=GRMZM2G078876_T01; parent_gene=GRMZM2G078876	GRMZM2G078876_P01	TRUE	TRUE	vLALPGAcGASNAAFsk	95%	Carbamidomethyl (+57), K+304 (+304)	68.55	25.85
2277	seq=translation; coord=10:145479598..145483674:-1; parent_transcript=GRMZM2G073465_T03; parent_gene=GRMZM2G073465	GRMZM2G073465_P03	TRUE	TRUE	aVANQPISVAIEAGGR	95%	n+304 (+304)	67.62	25.61
2278	seq=translation; coord=10:145479598..145483674:-1; parent_transcript=GRMZM2G073465_T03; parent_gene=GRMZM2G073465	GRMZM2G073465_P03	TRUE	TRUE	vVTIDSYEDVPANSEK	95%	n+304 (+304), K+304 (+304)	42.72	25.00
2279	seq=translation; coord=6:9203729..9206286:-1; parent_transcript=GRMZM2G066460_T01; parent_gene=GRMZM2G066460	GRMZM2G066460_P01	TRUE	TRUE	fAFAAPVAAGDSGAAAApK	95%	n+304 (+304), K+304 (+304)	61.88	25.26
2280	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	gFESGALPDGVEDEVr	90%	n+304 (+304)	25.37	25.00
2281	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	gIGIGVDVDETASPR	95%	n+304 (+304)	66.56	25.00
2282	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	gLAITVFHSGALDPADYPADYr	95%	n+304 (+304)	49.23	25.00
2283	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	tDLTDLVDLIK	95%	n+304 (+304), K+304 (+304)	37.44	25.80
2284	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	vDTSDL EEFAELLAR	95%	n+304 (+304)	74.65	25.00
2285	seq=translation; coord=1:180306606..180308510:1; parent_transcript=GRMZM2G161335_T01; parent_gene=GRMZM2G161335	GRMZM2G161335_P01	TRUE	TRUE	vGT ELVGEQLER	92%	n+304 (+304)	29.00	25.30
2286	seq=translation; coord=1:203587258..203590599:-1; parent_transcript=GRMZM2G106928_T01; parent_gene=GRMZM2G106928	GRMZM2G106928_P01	TRUE	TRUE	aFVVHELED DLGk	95%	n+304 (+304), K+304 (+304)	33.36	26.33
2287	seq=translation; coord=1:203587258..203590599:-1; parent_transcript=GRMZM2G106928_T01; parent_gene=GRMZM2G106928	GRMZM2G106928_P01	TRUE	TRUE	gASEVEGVVTLTQDDGPTTVNVR	91%	n+304 (+304)	27.72	25.00
2288	seq=translation; coord=1:203587258..203590599:-1; parent_transcript=GRMZM2G106928_T01; parent_gene=GRMZM2G106928	GRMZM2G106928_P01	TRUE	TRUE	hAGDLGNIVANAEGIAEATIVDTQIPLTGPNSVVGR	95%	n+304 (+304)	33.49	25.00

2289	seq=translation; coord=1:203587258..203590599:-1; parent_transcript=GRMZM2G106928_T01; parent_gene=GRMZM2G106928 seq=translation; coord=7:160032302..160036034:1;	GRMZM2G106928_P01	TRUE	TRUE	IACGVVGLTPL	95%	n+304 (+304), Carbamidomethyl (+57)	72.81	27.13
2290	parent_transcript=GRMZM2G083243_T01; parent_gene=GRMZM2G083243 seq=translation; coord=7:160032302..160036034:1;	GRMZM2G083243_P01,GRMZM2G099167_P01	TRUE	TRUE	aYHEQLSVPEITNAVFEPSSMMAK	95%	n+304 (+304), K+304 (+304)	26.47	25.00
2291	parent_transcript=GRMZM2G083243_T01; parent_gene=GRMZM2G083243 seq=translation; coord=7:160032302..160036034:1;	GRMZM2G083243_P01,GRMZM2G099167_P01	TRUE	TRUE	IISQISSLTTS LR	95%	n+304 (+304)	34.42	25.00
2292	parent_transcript=GRMZM2G083243_T01; parent_gene=GRMZM2G083243	GRMZM2G083243_P01,GRMZM2G099167_P01	TRUE	TRUE	tVQFVDWcPTGfk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	35.77	25.00
2293	seq=translation; coord=3:24095213..24095931:-1; parent_transcript=GRMZM2G011523_T01; parent_gene=GRMZM2G011523	GRMZM2G011523_P01,GRMZM2G011523_P02, GRMZM2G011523_P04	TRUE	TRUE	dFLPENCgck	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	30.48	25.00
2294	seq=translation; coord=3:24095213..24095931:-1; parent_transcript=GRMZM2G011523_T01; parent_gene=GRMZM2G011523	GRMZM2G011523_P01,GRMZM2G011523_P02, GRMZM2G011523_P04	TRUE	TRUE	ncVPVSTdk	90%	Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Carbamidomethyl (+57),	27.44	25.00
2295	seq=translation; coord=3:24095213..24095931:-1; parent_transcript=GRMZM2G011523_T01; parent_gene=GRMZM2G011523	GRMZM2G011523_P01,GRMZM2G011523_P02, GRMZM2G011523_P04	TRUE	TRUE	qcWcGEcTSWSGVWtcDDLLTk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	46.79	25.00
2296	seq=translation; coord=6:161966268..161967646:1; parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aADAAGHAAGk	89%	n+304 (+304), K+304 (+304)	26.08	25.91
2297	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aADAMEAAk	95%	n+304 (+304), K+304 (+304)	49.35	25.00
2298	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aAEAGQYAk	95%	n+304 (+304), K+304 (+304)	52.66	26.09
2299	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aGETTEAAk	92%	n+304 (+304), K+304 (+304)	27.03	25.59
2300	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aSDTGSYLgk	95%	n+304 (+304), K+304 (+304)	55.84	25.54
2301	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	aSYQAGETk	95%	n+304 (+304), K+304 (+304)	37.63	26.39
2302	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	dAVMSTLGMGGDDk	95%	n+304 (+304), K+304 (+304)	61.04	25.00
2303	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=6:161966268..161967646:1;	GRMZM2G096475_P01	TRUE	TRUE	dAVMSTLGMGGDDk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	38.64	25.00
2304	parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475	GRMZM2G096475_P01	TRUE	TRUE	sGGVIQQATEQV k	95%	n+304 (+304), K+304 (+304)	43.42	26.18

2305	seq=translation; coord=6:161966268..161967646:1; parent_transcript=GRMZM2G096475_T01; parent_gene=GRMZM2G096475 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G096475_P01	TRUE	TRUE	tGQAVGATk	95%	n+304 (+304), K+304 (+304)	45.84	27.63
2306	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	dVQFLPSGLVGTNMk	92%	n+304 (+304), K+304 (+304)	27.00	25.11
2307	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	eGDSLIMPnk	95%	n+304 (+304), K+304 (+304)	31.29	25.53
2308	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	eIQSSLQSLk	95%	n+304 (+304), K+304 (+304)	40.53	25.84
2309	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	fTILDAPGHk	95%	n+304 (+304), K+304 (+304)	56.94	25.16
2310	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	hLNVVFIGHVDAGk	95%	n+304 (+304), K+304 (+304)	39.80	25.20
2311	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	iQVNNLlclEk	92%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.67	25.21
2312	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	IVVVINK	93%	n+304 (+304), K+304 (+304)	26.83	25.00
2313	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	slcSWWDGPcLFVLDR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	61.82	25.00
2314	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=2:86767115..86790532:1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	sTTGGQILFLSGQVDDR	95%	n+304 (+304)	83.47	25.00
2315	parent_transcript=GRMZM2G028313_T01; parent_gene=GRMZM2G028313 seq=translation; coord=1:94680007..94684730:-1;	GRMZM2G028313_P01,GRMZM2G028313_P03	TRUE	TRUE	vIGLNLDsk	95%	n+304 (+304), K+304 (+304)	43.74	26.28
2316	parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576 seq=translation; coord=1:94680007..94684730:-1;	GRMZM2G178576_P02,GRMZM2G178576_P03	TRUE	TRUE	eIALWFPEGPADWQSSQHPWIYk	95%	n+304 (+304), K+304 (+304)	29.82	25.00
2317	parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576 seq=translation; coord=1:94680007..94684730:-1;	GRMZM2G178576_P02,GRMZM2G178576_P03	TRUE	TRUE	gDFAVDIGR	95%	n+304 (+304)	39.05	25.00
2318	parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576 seq=translation; coord=1:94680007..94684730:-1;	GRMZM2G178576_P02,GRMZM2G178576_P03	TRUE	TRUE	gLIGEISR	95%	n+304 (+304)	34.71	25.00
2319	parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576 seq=translation; coord=1:94680007..94684730:-1;	GRMZM2G178576_P02,GRMZM2G178576_P03	TRUE	TRUE	iIGATNPLASEPGTIR	95%	n+304 (+304)	59.34	26.54
2320	parent_transcript=GRMZM2G178576_T02; parent_gene=GRMZM2G178576 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G178576_P02,GRMZM2G178576_P03	TRUE	TRUE	kIIGATNPLASEPGTIR	95%	K+304 (+304), n+304 (+304)	51.16	25.00
2321	parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G099352_P03	TRUE	TRUE	dEDEPRPPVLAPPEV	95%	n+304 (+304)	48.04	25.00
2322	parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352	GRMZM2G099352_P03	TRUE	TRUE	eLAEDGYSGVEVR	95%	n+304 (+304)	40.47	25.00

2323	seq=translation; coord=10:75695843..75698244:1; parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G099352_P03	TRUE	TRUE	fKdGYMISSGQPVNEYIDSAVR	95%	n+304 (+304), K+304 (+304)	34.57	25.04
2324	parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G099352_P03	TRUE	TRUE	fVSDGVFYAELNEMLTR	95%	n+304 (+304)	65.24	25.00
2325	parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G099352_P03	TRUE	TRUE	gLcAIAQAESLR	95%	n+304 (+304), Carbamidomethyl (+57)	50.56	26.09
2326	parent_transcript=GRMZM2G099352_T03; parent_gene=GRMZM2G099352 seq=translation; coord=10:75695843..75698244:1;	GRMZM2G099352_P03	TRUE	TRUE	iMLDWDPk	91%	n+304 (+304), K+304 (+304)	29.05	25.89
2327	parent_transcript=GRMZM2G169182_T01; parent_gene=GRMZM2G169182 seq=translation; coord=3:19924648..19927549:1;	GRMZM2G169182_P01,GRMZM2G169182_P02	TRUE	TRUE	gGDSWDEFPSSAAAAAAGGGGR	95%	n+304 (+304)	80.48	25.00
2328	parent_transcript=GRMZM2G169182_T01; parent_gene=GRMZM2G169182 seq=translation; coord=3:19924648..19927549:1;	GRMZM2G169182_P01,GRMZM2G169182_P02	TRUE	TRUE	IQAGAAAAAVGTGR	95%	n+304 (+304)	52.51	26.39
2329	parent_transcript=GRMZM2G169182_T01; parent_gene=GRMZM2G169182 seq=translation; coord=3:19924648..19927549:1;	GRMZM2G169182_P01,GRMZM2G169182_P02	TRUE	TRUE	qDVPPVVDPTNR	95%	n+304 (+304)	41.24	25.00
2330	parent_transcript=GRMZM2G169182_T01; parent_gene=GRMZM2G169182 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G169182_P01,GRMZM2G169182_P02	TRUE	TRUE	sGVTNSAPTEDQR	95%	n+304 (+304)	43.01	25.00
2331	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	aLLGESSDFVADk	95%	n+304 (+304), K+304 (+304)	58.08	25.88
2332	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	eAGTTMDVVAAQTK	89%	n+304 (+304), K+304 (+304)	27.56	25.89
2333	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	eAGTTmDVVAAQTK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	29.71	25.44
2334	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	iSDWTNIVLAYEPVWAI GTGk	95%	n+304 (+304), K+304 (+304)	38.88	25.16
2335	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	kGGAFTGEISAEMLVNLQVPWVILGHSER	95%	K+304 (+304), n+304 (+304)	28.12	25.00
2336	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	vATPAQAQEVHDGLR	95%	n+304 (+304)	52.56	25.25
2337	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	vAYALTQGLk	95%	n+304 (+304), K+304 (+304)	28.28	25.12
2338	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=8:168745391..168749427:1;	GRMZM2G146206_P04	TRUE	TRUE	vIAcIGETLEQR	95%	n+304 (+304), Carbamidomethyl (+57)	43.08	25.38
2339	parent_transcript=GRMZM2G146206_T04; parent_gene=GRMZM2G146206 seq=translation; coord=2:48112888..48133114:1;	GRMZM2G146206_P04	TRUE	TRUE	wLHSNVSPAVAE LTR	95%	n+304 (+304)	50.87	25.49
2340	parent_transcript=GRMZM2G053019_T01; parent_gene=GRMZM2G053019	GRMZM2G053019_P01	TRUE	TRUE	dLQSSLEMV DVK	95%	n+304 (+304), K+304 (+304)	51.45	26.28

2341	seq=translation; coord=2:48112888..48133114:1; parent_transcript=GRMZM2G053019_T01; parent_gene=GRMZM2G053019	GRMZM2G053019_P01	TRUE	TRUE	gPTESSQSGPMLSJETIEK	95%	n+304 (+304), K+304 (+304)	44.23	25.17
2342	seq=translation; coord=2:48112888..48133114:1; parent_transcript=GRMZM2G053019_T01; parent_gene=GRMZM2G053019	GRMZM2G053019_P01	TRUE	TRUE	nMGSPDQWDNR	95%	n+304 (+304)	46.45	25.00
2343	seq=translation; coord=10:4694280..4699187:-1; parent_transcript=GRMZM2G004534_T01; parent_gene=GRMZM2G004534	GRMZM2G004534_P01	TRUE	TRUE	iENVEGLNHFDEILAEADGILSR	95%	n+304 (+304)	43.20	25.33
2344	seq=translation; coord=10:4694280..4699187:-1; parent_transcript=GRMZM2G004534_T01; parent_gene=GRMZM2G004534	GRMZM2G004534_P01	TRUE	TRUE	IGDLSQTQIFak	95%	n+304 (+304), K+304 (+304)	31.63	25.21
2345	seq=translation; coord=10:4694280..4699187:-1; parent_transcript=GRMZM2G004534_T01; parent_gene=GRMZM2G004534	GRMZM2G004534_P01	TRUE	TRUE	yRPSMPVLSVVIPR	95%	n+304 (+304)	32.02	25.00
2346	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	aEESAASGDPLAMASK	94%	n+304 (+304), K+304 (+304)	27.98	25.00
2347	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	ePDLELFR	90%	n+304 (+304)	28.33	25.97
2348	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	gFGFVNFVHR	95%	n+304 (+304)	37.82	25.00
2349	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	gGAVLMVcR	86%	n+304 (+304), Carbamidomethyl (+57)	25.30	25.00
2350	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	ITMVSTEEILLRPR	95%	n+304 (+304)	37.31	25.80
2351	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	vEWATPRPN	95%	n+304 (+304)	35.25	25.00
2352	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	VTNLS EDTREPDLLELFR	91%	n+304 (+304)	26.35	25.34
2353	seq=translation; coord=4:37224780..37227724:1; parent_transcript=GRMZM2G064133_T01; parent_gene=GRMZM2G064133	GRMZM2G064133_P01	TRUE	TRUE	wGELEEDDGGDLDFLLPPR	95%	n+304 (+304)	46.81	25.00
2354	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G094074_P01,GRMZM2G094074_P02, GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02	TRUE	TRUE	aDRDESSPYAAMLAQDVAQR	95%	n+304 (+304)	57.24	25.00
2355	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G094074_P01,GRMZM2G094074_P02, GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02	TRUE	TRUE	eENVTLGPTVR	95%	n+304 (+304)	35.08	26.45
2356	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02	TRUE	TRUE	eLGITALHIK	95%	n+304 (+304), K+304 (+304)	30.13	25.00

2357	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G094074_P01,GRMZM2G094074_P02, GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02 GRMZM2G094074_P01,GRMZM2G094074_P02, GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02	TRUE	TRUE	iEDVTPVPPTDSTR	95%	n+304 (+304)	43.60	25.00
2358	seq=translation; coord=6:90306950..90312408:-1; parent_transcript=GRMZM2G094074_T01; parent_gene=GRMZM2G094074	GRMZM2G100462_P02,GRMZM2G100462_P03, GRMZM2G120432_P01,GRMZM2G120432_P02, GRMZM5G805627_P02	TRUE	TRUE	tPGPGAQSALR	93%	n+304 (+304)	30.58	25.79
2359	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	TRUE	TRUE	sSVLMDVKPWDETDMK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	35.69	25.35
2360	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	TRUE	TRUE	sVQMEGLTWGASK	95%	n+304 (+304), K+304 (+304)	37.60	26.09
2361	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	TRUE	TRUE	tYVSGDSITK	95%	n+304 (+304), K+304 (+304)	49.78	25.91
2362	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	TRUE	TRUE	vFAAVPSKPGAEPNAAR	95%	n+304 (+304), K+304 (+304)	31.46	25.00
2363	seq=translation; coord=7:171631430..171634129:1; parent_transcript=GRMZM2G439201_T02; parent_gene=GRMZM2G439201	GRMZM2G439201_P02	TRUE	TRUE	wYETVSAAVASR	93%	n+304 (+304)	29.87	25.00
2364	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	dAYVGDEAQAK	95%	n+304 (+304), K+304 (+304)	67.82	25.00
2365	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	gYSLTSAER	95%	n+304 (+304)	31.68	25.00
2366	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	lAYVALDYEQELETAR	95%	n+304 (+304)	70.07	25.00
2367	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	lAYVALDYEQELETAR	95%	n+304 (+304), iTRAQ8plex (+304)	45.45	25.13
2368	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	sYEMPDGQVITIGSER	95%	n+304 (+304)	54.00	25.00
2369	seq=translation; coord=8:100394854..100398658:-1; parent_transcript=GRMZM2G126010_T01; parent_gene=GRMZM2G126010	GRMZM2G126010_P01,GRMZM2G126010_P02, GRMZM2G126010_P03	TRUE	TRUE	syEMPDGQVITIGSER	95%	n+304 (+304), iTRAQ8plex (+304)	47.12	25.00
2370	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	dAGVPLVAFSLR	95%	n+304 (+304)	47.86	25.00
2371	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	eAAQQIISDEMLDGNPR	95%	n+304 (+304)	80.51	25.00
2372	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	fGWIVPAYTMPADAEHVAVLR	95%	n+304 (+304)	65.29	25.04
2373	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	fSVFDVSENLR	95%	n+304 (+304)	41.67	25.00

2374	seq=translation; coord=1:198230317..198233618:-1; parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110 seq=translation; coord=1:198230317..198233618:-1;	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	gScQIIAQYYQLIR	95%	n+304 (+304), Carbamidomethyl (+57)	46.71	25.98
2375	parent_transcript=GRMZM2G017110_T02; parent_gene=GRMZM2G017110 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G017110_P02,GRMZM2G017110_P03	TRUE	TRUE	nIMENcQENAAILR	95%	n+304 (+304), Carbamidomethyl (+57)	58.78	25.00
2376	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	aGPFEFFGFTTSAR	95%	n+304 (+304)	35.61	25.00
2377	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	eGLMHIGFITMEPk	94%	n+304 (+304), K+304 (+304)	29.26	25.53
2378	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	gLFLHR	95%	n+304 (+304)	36.43	27.04
2379	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	mGDVLHIDAGSTFYMVNPGk	95%	n+304 (+304), K+304 (+304)	32.03	25.00
2380	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	nRPQFLVGASSVLR	95%	n+304 (+304)	44.56	25.02
2381	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	tLFVPQYLDSSITLFVQR	95%	n+304 (+304)	64.76	25.53
2382	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=1:56160677..56162858:-1;	GRMZM2G054916_P01	TRUE	TRUE	tMLGPEIAAAGGAR	95%	n+304 (+304)	49.36	25.54
2383	parent_transcript=GRMZM2G054916_T01; parent_gene=GRMZM2G054916 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G054916_P01	TRUE	TRUE	vVESEGGQVR	88%	n+304 (+304)	26.70	25.59
2384	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	aFSGSPIVGEIR	95%	n+304 (+304)	44.46	25.04
2385	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	eGPETIAAFIAEPMGAGGVILPPk	93%	n+304 (+304), K+304 (+304)	26.39	25.00
2386	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	gHSM LAPFTAGWQSTDVHPLVIER	95%	n+304 (+304)	56.87	25.00
2387	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	gLGLILGTEFVDNk	95%	n+304 (+304), K+304 (+304)	29.58	25.00
2388	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	KYDILLIADEVITAFGR	95%	K+304 (+304), n+304 (+304)	27.40	25.00
2389	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	IPDETEEEFSTR	95%	n+304 (+304)	40.16	25.00
2390	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=4:26893142..26901172:1;	GRMZM2G093900_P01	TRUE	TRUE	sPNDPFPAEWGVGSIFGAeEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	43.24	25.00
2391	parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900	GRMZM2G093900_P01	TRUE	TRUE	tTkPSLDLANDILSMFTAR	95%	n+304 (+304), K+304 (+304)	29.04	25.00

2392	seq=translation; coord=4:26893142..26901172:1; parent_transcript=GRMZM2G093900_T01; parent_gene=GRMZM2G093900 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G093900_P01	TRUE	TRUE	vAGDSIMLSPLIMTPNEVEEIIISK	95%	n+304 (+304), K+304 (+304)	29.75	25.02
2393	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G002416_P01	TRUE	TRUE	aGkDLVSSLVSGLLTIGPR	95%	n+304 (+304), K+304 (+304)	43.59	25.00
2394	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G002416_P01	TRUE	TRUE	dLVSSLVSGLLTIGPR	95%	n+304 (+304)	42.26	25.00
2395	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G002416_P01	TRUE	TRUE	fGGAIDDAAR	95%	n+304 (+304)	40.35	25.00
2396	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G002416_P01	TRUE	TRUE	mMVVLGELGGkDEYSLVEALK	95%	n+304 (+304), K+304 (+304)	38.16	25.00
2397	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=8:37409326..37412866:1;	GRMZM2G002416_P01	TRUE	TRUE	sGGELESAQAK	94%	n+304 (+304), K+304 (+304)	28.12	25.43
2398	parent_transcript=GRMZM2G002416_T01; parent_gene=GRMZM2G002416 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G002416_P01	TRUE	TRUE	vQkPVVAWVSGTcAR	90%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	26.48	25.79
2399	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	aAIDQHEGGLDAFSR	95%	n+304 (+304)	33.01	25.00
2400	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	aPLVEEKPR	90%	n+304 (+304), K+304 (+304)	25.54	25.00
2401	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	gMQEFDQAMQHLEGk	95%	n+304 (+304), K+304 (+304)	31.07	25.00
2402	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	iVLSDDDGLFGGFSR	95%	n+304 (+304)	48.64	25.00
2403	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	iYEIDPMLEGFR	95%	n+304 (+304)	55.37	25.00
2404	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	qSDEYWEMGDIVHTLTNR	95%	n+304 (+304)	61.18	25.00
2405	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=2:58586007..58596234:1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	vIIFER	90%	n+304 (+304)	27.44	25.00
2406	parent_transcript=GRMZM2G073054_T01; parent_gene=GRMZM2G073054 seq=translation; coord=1:2801080..2803977:-1;	GRMZM2G073054_P01,GRMZM2G073054_P02	TRUE	TRUE	vIPPPGDGQR	95%	n+304 (+304)	31.48	25.00
2407	parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881 seq=translation; coord=1:2801080..2803977:-1;	GRMZM2G041881_P01	TRUE	TRUE	dDIVIQFNPK	95%	n+304 (+304), K+304 (+304)	48.95	25.76
2408	parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881 seq=translation; coord=1:2801080..2803977:-1;	GRMZM2G041881_P01	TRUE	TRUE	eVPEAEPEEK	90%	n+304 (+304), K+304 (+304)	27.70	25.53
2409	parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881	GRMZM2G041881_P01	TRUE	TRUE	sLQDLLPTIINQLGPDNLENLk	95%	n+304 (+304), K+304 (+304)	39.55	25.00

2410	seq=translation; coord=1:2801080..2803977:-1; parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881 seq=translation; coord=1:2801080..2803977:-1;	GRMZM2G041881_P01	TRUE	TRUE	sLQDLLPTIINQLGPDNLENLkR	92%	n+304 (+304), K+304 (+304)	26.85	25.00
2411	parent_transcript=GRMZM2G041881_T01; parent_gene=GRMZM2G041881 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G041881_P01	TRUE	TRUE	vQASIPANTWVVGVPQTK	93%	n+304 (+304), K+304 (+304)	27.64	25.11
2412	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	dADTMNFADIEK	95%	n+304 (+304), K+304 (+304)	44.07	25.00
2413	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	dSQNTFAMLSTFNEVDMTNLMk	95%	n+304 (+304), K+304 (+304)	54.82	25.00
2414	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	gLVPVPIR	87%	n+304 (+304)	25.80	25.00
2415	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	IGLMScFvk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.56	25.00
2416	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	IIASEGDTVTPGTK	95%	n+304 (+304), K+304 (+304)	51.97	26.02
2417	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=10:110621503..110626726:1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	ILLDI	90%	n+304 (+304)	29.99	28.69
2418	parent_transcript=GRMZM2G079538_T01; parent_gene=GRMZM2G079538 seq=translation; coord=8:9901033..9904862:-1;	GRMZM2G079538_P01,GRMZM2G079538_P02, GRMZM2G079538_P03,GRMZM5G807639_P03	TRUE	TRUE	tSPSEPQLPPk	95%	n+304 (+304), K+304 (+304)	36.61	26.11
2419	parent_transcript=GRMZM2G069195_T01; parent_gene=GRMZM2G069195 seq=translation; coord=8:9901033..9904862:-1;	GRMZM2G069195_P01	TRUE	TRUE	aAAGSYSDELVSTak	95%	n+304 (+304), K+304 (+304)	48.74	25.00
2420	parent_transcript=GRMZM2G069195_T01; parent_gene=GRMZM2G069195 seq=translation; coord=8:9901033..9904862:-1;	GRMZM2G069195_P01	TRUE	TRUE	ISSIGLDNTEPNR	95%	n+304 (+304)	44.82	26.01
2421	parent_transcript=GRMZM2G069195_T01; parent_gene=GRMZM2G069195 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G069195_P01	TRUE	TRUE	yTGEGESDEak	95%	n+304 (+304), K+304 (+304)	53.49	25.00
2422	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G318780_P02	TRUE	TRUE	aLAEGPFLDVLr	95%	n+304 (+304)	34.61	25.53
2423	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G318780_P02	TRUE	TRUE	aLENEMVLR	88%	n+304 (+304)	26.13	25.69
2424	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G318780_P02	TRUE	TRUE	dcLEPLLDFLR	94%	n+304 (+304), Carbamidomethyl (+57)	28.45	25.00
2425	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G318780_P02	TRUE	TRUE	fNIVSPGADMSIYFPHTek	95%	n+304 (+304), K+304 (+304)	56.98	25.00
2426	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780 seq=translation; coord=1:56785163..56792250:-1;	GRMZM2G318780_P02	TRUE	TRUE	gILQPHHILDALDEVQGSgGR	95%	n+304 (+304)	47.48	25.40
2427	parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780	GRMZM2G318780_P02	TRUE	TRUE	IMTLAGVYGFWk	95%	n+304 (+304), K+304 (+304)	34.76	25.39

2428	seq=translation; coord=1:56785163..56792250:-1; parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780	GRMZM2G318780_P02	TRUE	TRUE	IPADTPYSQFAYK	95%	n+304 (+304), K+304 (+304)	35.29	25.17
2429	seq=translation; coord=1:56785163..56792250:-1; parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780	GRMZM2G318780_P02	TRUE	TRUE	nELVALLSk	95%	n+304 (+304), K+304 (+304)	45.27	25.00
2430	seq=translation; coord=1:56785163..56792250:-1; parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780	GRMZM2G318780_P02	TRUE	TRUE	nITGLVEAFak	95%	n+304 (+304), K+304 (+304)	34.69	25.00
2431	seq=translation; coord=1:56785163..56792250:-1; parent_transcript=GRMZM2G318780_T02; parent_gene=GRMZM2G318780	GRMZM2G318780_P02	TRUE	TRUE	nTVGQYESHTAFTLPGLYR	95%	n+304 (+304)	57.94	25.00
2432	seq=translation; coord=1:222203896..222206239:-1; parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269	GRMZM2G320269_P01	TRUE	TRUE	aLFHSDEALLR	95%	n+304 (+304)	32.39	26.51
2433	seq=translation; coord=1:222203896..222206239:-1; parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269	GRMZM2G320269_P01	TRUE	TRUE	dGNLYQVETGR	95%	n+304 (+304)	43.23	25.00
2434	seq=translation; coord=1:222203896..222206239:-1; parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269	GRMZM2G320269_P01	TRUE	TRUE	dScPDAEAVVR	95%	n+304 (+304), Carbamidomethyl (+57)	52.15	25.00
2435	seq=translation; coord=1:222203896..222206239:-1; parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269	GRMZM2G320269_P01	TRUE	TRUE	dSDPTLDGAYAAELR	95%	n+304 (+304)	41.54	25.00
2436	seq=translation; coord=1:222203896..222206239:-1; parent_transcript=GRMZM2G320269_T01; parent_gene=GRMZM2G320269	GRMZM2G320269_P01	TRUE	TRUE	nLPDSMDGIR	95%	n+304 (+304)	33.44	25.00
2437	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	dFEAGAlk	93%	n+304 (+304), K+304 (+304)	30.47	27.12
2438	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	gAAAVEELADAGLSGVVFHQLEVTDQAQSIAR	95%	n+304 (+304)	73.78	25.00
2439	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	gMDAFQMAELMR	95%	n+304 (+304)	69.08	25.00
2440	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	gWPTEFAAYk	95%	n+304 (+304), K+304 (+304)	38.18	25.38
2441	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	IDELLSTFLR	88%	n+304 (+304)	27.89	26.59
2442	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	nVTEALLPLLLQASSSGGGR	92%	n+304 (+304)	27.83	25.94
2443	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	vALLPEGGPTGAFFALGk	95%	n+304 (+304), K+304 (+304)	57.43	25.00
2444	seq=translation; coord=10:132619525..132621315:1; parent_transcript=GRMZM2G468855_T02; parent_gene=GRMZM2G468855	GRMZM2G468855_P02	TRUE	TRUE	vVNVSSDFGLLR	95%	n+304 (+304)	50.24	25.74
2445	seq=translation; coord=8:162019785..162023951:1; parent_transcript=GRMZM2G053898_T01; parent_gene=GRMZM2G053898	GRMZM2G053898_P01,GRMZM2G053898_P02, GRMZM2G082390_P01,GRMZM2G082390_P02	TRUE	TRUE	gQDGNVFFFR	95%	n+304 (+304)	34.62	25.00

2446	seq=translation; coord=8:162019785..162023951:1; parent_transcript=GRMZM2G053898_T01; parent_gene=GRMZM2G053898	GRMZM2G053898_P01,GRMZM2G053898_P02, GRMZM2G082390_P01,GRMZM2G082390_P02	TRUE	TRUE	IMNAYcDR	86%	n+304 (+304), Carbamidomethyl (+57)	25.43	25.00
2447	seq=translation; coord=8:162019785..162023951:1; parent_transcript=GRMZM2G053898_T01; parent_gene=GRMZM2G053898	GRMZM2G053898_P01,GRMZM2G053898_P02, GRMZM2G082390_P01,GRMZM2G082390_P02	TRUE	TRUE	qSVDMAIAFLFDGR	95%	n+304 (+304)	89.83	25.00
2448	seq=translation; coord=8:173117675..173120538:1; parent_transcript=GRMZM2G116273_T01; parent_gene=GRMZM2G116273	GRMZM2G116273_P01	TRUE	TRUE	IYGAVMSWNVTR	95%	n+304 (+304)	38.40	25.00
2449	seq=translation; coord=8:173117675..173120538:1; parent_transcript=GRMZM2G116273_T01; parent_gene=GRMZM2G116273	GRMZM2G116273_P01	TRUE	TRUE	nPFGQVPALQDGDLYLFESR	95%	n+304 (+304)	56.21	25.00
2450	seq=translation; coord=8:173117675..173120538:1; parent_transcript=GRMZM2G116273_T01; parent_gene=GRMZM2G116273	GRMZM2G116273_P01	TRUE	TRUE	nPFGQVPALQDGDLYLFESR	95%	n+304 (+304), iTRAQ8plex (+304)	34.47	25.00
2451	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	aANcDEGQIQPGASAVR	95%	n+304 (+304), Carbamidomethyl (+57)	64.80	25.00
2452	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	aASTTELPAPSGWTK	95%	n+304 (+304), K+304 (+304)	64.66	25.82
2453	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	aHPGGPASSEFDWGTSDTPR	95%	n+304 (+304)	92.13	25.00
2454	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	aTESPEGEK	95%	n+304 (+304), K+304 (+304)	30.66	25.00
2455	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	eVAPAVDATEETEK	95%	n+304 (+304), K+304 (+304)	52.53	25.49
2456	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	eVPNADAAEK	95%	n+304 (+304), K+304 (+304)	37.15	25.60
2457	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	fEVIFVSPTGEEVK	95%	n+304 (+304), K+304 (+304)	60.15	25.63
2458	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	gAENSGQPNTGSQEPK	95%	n+304 (+304), K+304 (+304)	36.41	25.00
2459	seq=translation; coord=1:250061761..250067450:1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	gTDVEMK	91%	n+304 (+304), K+304 (+304)	28.95	26.22
2460	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G157470_T01; parent_gene=GRMZM2G157470	GRMZM2G157470_P01	TRUE	TRUE	qLTQYLK	92%	n+304 (+304), K+304 (+304)	27.52	25.00
2461	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	aGDVcFSEVYR	95%	n+304 (+304), Carbamidomethyl (+57)	42.74	25.00
2462	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	dAEEAIAGR	95%	n+304 (+304)	32.09	25.00
2463	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	eGGGTVGIVDYNYYDMK	95%	n+304 (+304), K+304 (+304)	57.16	25.00

2464	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	eVEDLFYk	95%	n+304 (+304), K+304 (+304)	35.76	25.62
2465	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	iVDIDLk	92%	n+304 (+304), K+304 (+304)	26.45	25.00
2466	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	kAGDVCfSEVYR	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	28.99	25.01
2467	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	tIYVGNLPGDIR	95%	n+304 (+304)	40.07	25.89
2468	seq=translation; coord=9:130484606..130489460:-1; parent_transcript=GRMZM2G436092_T01; parent_gene=GRMZM2G436092	GRMZM2G436092_P01,GRMZM2G436092_P02, GRMZM2G436092_P03,GRMZM2G436092_P05	TRUE	TRUE	vLVTGLPSSASWQDLk	95%	n+304 (+304), K+304 (+304)	49.18	25.00
2469	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	aTLQVVQLLk	95%	n+304 (+304), K+304 (+304)	31.90	25.00
2470	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	aTVAlAik	95%	n+304 (+304), K+304 (+304)	41.37	25.29
2471	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	cPSAVLAVLDSIVEPIEk	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	38.44	25.00
2472	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	eYSLQALSFMLR	95%	n+304 (+304)	50.10	25.71
2473	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	gLLPEILPLLYDQTVIk	95%	n+304 (+304), K+304 (+304)	64.16	25.00
2474	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	iLLSLAPQLIk	95%	n+304 (+304), K+304 (+304)	38.05	25.00
2475	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	ITITVLQQLLEDASGDVSGLAVk	95%	n+304 (+304), K+304 (+304)	43.66	25.00
2476	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	mDIFNTFIELLR	95%	n+304 (+304)	48.00	26.09
2477	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	yLPFILDQIDNQKk	95%	n+304 (+304), K+304 (+304)	34.33	25.35
2478	seq=translation; coord=4:236362229..236373144:1; parent_transcript=GRMZM2G168629_T01; parent_gene=GRMZM2G168629	GRMZM2G168629_P01,GRMZM2G168629_P04	TRUE	TRUE	yMATSDLLSELNk	95%	n+304 (+304), K+304 (+304)	39.45	25.09
2479	seq=translation; coord=7:131783728..131787563:1; parent_transcript=GRMZM2G069651_T01; parent_gene=GRMZM2G069651	GRMZM2G069651_P01	TRUE	TRUE	aSNTLSIIDSGIGMTk	95%	n+304 (+304), K+304 (+304)	38.15	25.72
2480	seq=translation; coord=7:131783728..131787563:1; parent_transcript=GRMZM2G069651_T01; parent_gene=GRMZM2G069651	GRMZM2G069651_P01	TRUE	TRUE	eDQLEYLEER	95%	n+304 (+304)	41.07	25.00
2481	seq=translation; coord=8:171565757..171566487:-1; parent_transcript=GRMZM2G091054_T01; parent_gene=GRMZM2G091054	GRMZM2G091054_P01	TRUE	TRUE	tYVMFPANPk	93%	n+304 (+304), K+304 (+304)	30.28	25.66

2482	seq=translation; coord=8:171565757..171566487:-1; parent_transcript=GRMZM2G091054_T01; parent_gene=GRMZM2G091054	GRMZM2G091054_P01	TRUE	TRUE	vPPSDAccGVik	88%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	26.41	25.07
2483	seq=translation; coord=8:171565757..171566487:-1; parent_transcript=GRMZM2G091054_T01; parent_gene=GRMZM2G091054	GRMZM2G091054_P01	TRUE	TRUE	vVcMEk	91%	Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	26.08	25.82
2484	seq=translation; coord=8:171565757..171566487:-1; parent_transcript=GRMZM2G091054_T01; parent_gene=GRMZM2G091054	GRMZM2G091054_P01	TRUE	TRUE	vVYVAEQck	95%	Carbamidomethyl (+57), K+304 (+304)	33.12	26.35
2485	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	eFADNVLP	95%	n+304 (+304)	31.05	25.69
2486	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	fGAPYDGVHWDPPASER	95%	n+304 (+304)	40.08	25.00
2487	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	fGVWSik	94%	n+304 (+304), K+304 (+304)	28.91	26.79
2488	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	fLHGGVWVDR	95%	n+304 (+304)	33.17	25.19
2489	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	gDLVFVFNHPk	95%	n+304 (+304), K+304 (+304)	38.84	25.65
2490	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	gDVDHLPIYDLDPk	91%	n+304 (+304), K+304 (+304)	26.14	25.87
2491	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	gSIEENEGSLESFSk	95%	n+304 (+304), K+304 (+304)	55.38	25.00
2492	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	qWSLVDTDHLR	95%	n+304 (+304)	48.72	25.00
2493	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	rQWSLVDTDHLR	95%	n+304 (+304)	33.97	25.00
2494	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	vALDSDALVFGGHGR	95%	n+304 (+304)	49.03	25.37
2495	seq=translation; coord=5:63317874..63324803:-1; parent_transcript=GRMZM2G088753_T01; parent_gene=GRMZM2G088753	GRMZM2G088753_P01,GRMZM2G088753_P02	TRUE	TRUE	yMNAFDQAMNALDER	95%	n+304 (+304)	56.09	25.00
2496	seq=translation; coord=1:233228509..233231671:-1; parent_transcript=GRMZM2G134747_T01; parent_gene=GRMZM2G134747	GRMZM2G134747_P01	TRUE	TRUE	aALPTLTDDLIELMMQPPFR	95%	n+304 (+304)	33.20	25.45
2497	seq=translation; coord=1:233228509..233231671:-1; parent_transcript=GRMZM2G134747_T01; parent_gene=GRMZM2G134747	GRMZM2G134747_P01	TRUE	TRUE	aALPTLTDDLIELMmQPPFR	95%	n+304 (+304), Oxidation (+16)	41.30	25.65
2498	seq=translation; coord=1:233228509..233231671:-1; parent_transcript=GRMZM2G134747_T01; parent_gene=GRMZM2G134747	GRMZM2G134747_P01	TRUE	TRUE	aDTPPALR	95%	n+304 (+304)	36.06	25.42

2499	seq=translation; coord=1:233228509..233231671:-1; parent_transcript=GRMZM2G134747_T01; parent_gene=GRMZM2G134747	GRMZM2G134747_P01	TRUE	TRUE	tFSGIAAETGLTNVYVAQLLR	93%	n+304 (+304)	28.14	25.87
2500	seq=translation; coord=6:92813319..92815990:-1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02,GRMZM2G043822_P03	TRUE	TRUE	aLTVPELTQQMWDSk	95%	n+304 (+304), K+304 (+304)	59.15	26.75
2501	seq=translation; coord=6:92813319..92815990:-1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02,GRMZM2G043822_P03	TRUE	TRUE	iNVVYNEASGGR	95%	n+304 (+304)	46.53	25.00
2502	seq=translation; coord=6:92813319..92815990:-1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02,GRMZM2G043822_P03	TRUE	TRUE	ISTPTFGDLNHLISATMSGVTccLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	33.19	25.00
2503	seq=translation; coord=6:92813319..92815990:-1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02,GRMZM2G043822_P03	TRUE	TRUE	sGPFGQIFRPDNFVFGQSGAGNNWAK	95%	n+304 (+304), K+304 (+304)	33.94	25.00
2504	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G043822_T02; parent_gene=GRMZM2G043822	GRMZM2G043822_P02,GRMZM2G043822_P03	TRUE	TRUE	sSVcDIPPIGLk	92%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.61	25.00
2505	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01,GRMZM2G104481_P04	TRUE	TRUE	gFGFVTFESEDAVER	95%	n+304 (+304)	63.87	25.00
2506	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01,GRMZM2G104481_P04	TRUE	TRUE	gFGFVTFSDPSVLDR	95%	n+304 (+304)	47.32	25.00
2507	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01,GRMZM2G104481_P04	TRUE	TRUE	gLAEAVGNVDAGGEDER	95%	n+304 (+304)	100.09	25.00
2508	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01,GRMZM2G104481_P04	TRUE	TRUE	gLAEAVGNVDAGGEDERDADSSGGDASGk	95%	n+304 (+304), K+304 (+304)	31.99	25.00
2509	seq=translation; coord=9:59153476..59160133:1; parent_transcript=GRMZM2G104481_T01; parent_gene=GRMZM2G104481	GRMZM2G104481_P01,GRMZM2G104481_P04	TRUE	TRUE	iFVGGIPPSLTEDk	95%	n+304 (+304), K+304 (+304)	33.20	25.53
2510	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	aSAYWFR	90%	n+304 (+304)	26.41	25.00
2511	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	fGIVYVDFNTLER	95%	n+304 (+304)	38.99	25.97
2512	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	gANWLGLLSR	93%	n+304 (+304)	29.81	25.33
2513	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	gSADYIGINEYTSYMK	95%	n+304 (+304), K+304 (+304)	41.98	25.00
2514	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	hWFTFNEPR	95%	n+304 (+304)	47.81	25.00
2515	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	iVALLGYDTGSNPPQR	95%	n+304 (+304)	59.41	25.89
2516	parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE					

2517	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	mADLFTDYADFcFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.04	25.00
2518	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	mADLFTDYADFcFk	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), K+304 (+304)	27.38	25.00
2519	seq=translation; coord=1:264798453..264802516:-1; parent_transcript=GRMZM2G118003_T03; parent_gene=GRMZM2G118003	GRMZM2G118003_P03	TRUE	TRUE	sYIGQLk	91%	n+304 (+304), K+304 (+304)	25.73	25.69
2520	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	aMLSLPASK	95%	n+304 (+304), K+304 (+304)	43.48	26.93
2521	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	eHEDVELLAR	95%	n+304 (+304)	47.40	25.00
2522	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	gDSIGGVVTciAR	95%	n+304 (+304), Carbamidomethyl (+57)	43.24	25.00
2523	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	gLSPVPFDk	94%	n+304 (+304), K+304 (+304)	33.10	26.98
2524	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	iPLTEADMQVELDR	95%	n+304 (+304)	43.34	25.43
2525	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	mIAAIDTVR	95%	n+304 (+304)	31.17	25.00
2526	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	sGVEILAFVsk	95%	n+304 (+304), K+304 (+304)	29.48	25.00
2527	seq=translation; coord=1:35455268..35465683:-1; parent_transcript=GRMZM2G164562_T01; parent_gene=GRMZM2G164562	GRMZM2G164562_P01	TRUE	TRUE	vHQVLPEDAVDYETVTLIHIESNIVR	95%	n+304 (+304)	43.55	25.26
2528	seq=translation; coord=5:77434003..77436424:1; parent_transcript=GRMZM5G805485_T01; parent_gene=GRMZM5G805485	GRMZM5G805485_P01	TRUE	TRUE	aSYAALQAWk	95%	n+304 (+304), K+304 (+304)	45.38	25.71
2529	seq=translation; coord=5:77434003..77436424:1; parent_transcript=GRMZM5G805485_T01; parent_gene=GRMZM5G805485	GRMZM5G805485_P01	TRUE	TRUE	fVGGFPEVVLSPALR	95%	n+304 (+304)	48.07	25.04
2530	seq=translation; coord=5:77434003..77436424:1; parent_transcript=GRMZM5G805485_T01; parent_gene=GRMZM5G805485	GRMZM5G805485_P01	TRUE	TRUE	IEGAVPAGVcALASLR	95%	n+304 (+304), Carbamidomethyl (+57)	47.14	26.55
2531	seq=translation; coord=3:220506759..220509488:1; parent_transcript=GRMZM5G805485_T01; parent_gene=GRMZM5G805485	GRMZM5G805485_P01	TRUE	TRUE	IQGQLPSAIANMAAVQELDVAR	95%	n+304 (+304)	60.72	26.09
2532	seq=translation; coord=3:220506759..220509488:1; parent_transcript=GRMZM2G116135_T01; parent_gene=GRMZM2G116135	GRMZM2G116135_P01	TRUE	TRUE	ePTAPVAAPAPSTGVpk	95%	n+304 (+304), K+304 (+304)	35.57	25.00
2533	seq=translation; coord=6:39092081..39092901:1; parent_transcript=GRMZM2G116135_T01; parent_gene=GRMZM2G116135	GRMZM2G116135_P01	TRUE	TRUE	vWLDPNVESEISMANSR	95%	n+304 (+304)	49.02	25.00
2534	parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806	GRMZM2G012806_P01	TRUE	TRUE	dMPNAYIQVLPGSPVTLRLRPDR	95%	n+304 (+304)	30.44	25.66

2535	seq=translation; coord=6:39092081..39092901:1; parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806 seq=translation; coord=6:39092081..39092901:1;	GRMZM2G012806_P01	TRUE	TRUE	dmPNAYIQVLPVGSPVTLDLRPDR	95%	n+304 (+304), Oxidation (+16)	30.05	25.00
2536	parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806 seq=translation; coord=6:39092081..39092901:1;	GRMZM2G012806_P01	TRUE	TRUE	eATETIlk	95%	n+304 (+304), K+304 (+304)	40.19	25.04
2537	parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806 seq=translation; coord=6:39092081..39092901:1;	GRMZM2G012806_P01	TRUE	TRUE	iFVDTVAMTPTVG	95%	n+304 (+304)	52.03	25.00
2538	parent_transcript=GRMZM2G012806_T01; parent_gene=GRMZM2G012806 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G012806_P01	TRUE	TRUE	kTSWPEVVGMSIk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	33.60	25.00
2539	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	dFYMYLLk	93%	n+304 (+304), K+304 (+304)	28.37	26.19
2540	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	dQYGNFIEVDTR	95%	n+304 (+304)	55.02	25.00
2541	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	dYIPIYek	91%	n+304 (+304), K+304 (+304)	28.88	25.72
2542	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	eLTEDSWk	88%	n+304 (+304), K+304 (+304)	26.35	25.12
2543	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	fMIEQGLAlk	95%	n+304 (+304), K+304 (+304)	30.72	25.55
2544	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	gSHDVPEIVDLIITLQR	95%	n+304 (+304)	49.95	26.60
2545	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	iMEWVMSDAELVk	95%	n+304 (+304), K+304 (+304)	44.77	25.39
2546	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	IEHLESPIAEVSSALDTPLFR	95%	n+304 (+304)	45.71	25.44
2547	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	INFNLLQLLYSELk	95%	n+304 (+304), K+304 (+304)	39.02	25.00
2548	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	sILEFAk	93%	n+304 (+304), K+304 (+304)	27.33	25.00
2549	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	sLLSYNAAYLR	95%	n+304 (+304)	43.35	26.02
2550	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=10:55753301..55756434:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	tVDYMYk	86%	n+304 (+304), K+304 (+304)	25.34	25.00
2551	parent_transcript=GRMZM2G127087_T01; parent_gene=GRMZM2G127087 seq=translation; coord=8:142871869..142875661:-1;	GRMZM2G127087_P01,GRMZM2G127087_P03	TRUE	TRUE	tVLEFAR	91%	n+304 (+304)	28.37	25.00
2552	parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	eELEAELQGk	95%	n+304 (+304), K+304 (+304)	45.01	25.04

2553	seq=translation; coord=8:142871869..142875661:-1; parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738 seq=translation; coord=8:142871869..142875661:-1;	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	eEPAVIESYYNk	95%	n+304 (+304), K+304 (+304)	37.80	25.38
2554	parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738 seq=translation; coord=8:142871869..142875661:-1;	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	fDMDSPVGPFGTk	95%	n+304 (+304), K+304 (+304)	51.09	25.00
2555	parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738 seq=translation; coord=8:142871869..142875661:-1;	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	rFMDSPVGPFGTk	95%	n+304 (+304), K+304 (+304)	39.16	25.91
2556	parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738 seq=translation; coord=8:142871869..142875661:-1;	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	vEDVMPiATGLER	95%	n+304 (+304)	44.99	25.94
2557	parent_transcript=GRMZM2G134738_T01; parent_gene=GRMZM2G134738 seq=translation; coord=2:3098932..3104990:1;	GRMZM2G134738_P01,GRMZM2G134738_P02	TRUE	TRUE	vEDVMPiATGLERELEAEELQgk	95%	n+304 (+304), K+304 (+304)	33.03	25.09
2558	parent_transcript=GRMZM2G071333_T01; parent_gene=GRMZM2G071333 seq=translation; coord=2:3098932..3104990:1;	GRMZM2G071333_P01	TRUE	TRUE	sFGLDDEEIAR	89%	n+304 (+304)	26.85	25.00
2559	parent_transcript=GRMZM2G071333_T01; parent_gene=GRMZM2G071333 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G071333_P01	TRUE	TRUE	yQWEIMk	93%	n+304 (+304), K+304 (+304)	29.02	25.77
2560	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G094742_P03	TRUE	TRUE	gNVTPDAVLQTVSk	95%	n+304 (+304), K+304 (+304)	48.13	26.14
2561	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G094742_P03	TRUE	TRUE	mEGVESYDVIDIMEQk	95%	n+304 (+304), K+304 (+304)	60.92	25.00
2562	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G094742_P03	TRUE	TRUE	mEGVESYDVIDIMEQk	95%	Oxidation (+16), n+304 (+304), K+304 (+304)	41.30	25.00
2563	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G094742_P03	TRUE	TRUE	mEGVESYDVIDImEQk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	38.03	25.00
2564	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=1:177045380..177050536:-1;	GRMZM2G094742_P03	TRUE	TRUE	tSFWEAEAVTSESATPAGATA	95%	n+304 (+304)	62.45	25.00
2565	parent_transcript=GRMZM2G094742_T03; parent_gene=GRMZM2G094742 seq=translation; coord=2:29943554..29946951:-1;	GRMZM2G094742_P03	TRUE	TRUE	vGMScEGcVGAVk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	50.27	25.00
2566	parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295 seq=translation; coord=2:29943554..29946951:-1;	GRMZM2G150295_P01	TRUE	TRUE	eIVASAPLVVFSk	95%	n+304 (+304), K+304 (+304)	48.02	25.00
2567	parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295 seq=translation; coord=2:29943554..29946951:-1;	GRMZM2G150295_P01	TRUE	TRUE	gITSSTSSPTSSPESR	95%	n+304 (+304)	87.93	25.00
2568	parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295 seq=translation; coord=2:29943554..29946951:-1;	GRMZM2G150295_P01	TRUE	TRUE	hIGGcDDTMALNNDGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	54.91	25.00
2569	parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295	GRMZM2G150295_P01	TRUE	TRUE	IVPLLTEAGAIAGSASK	95%	n+304 (+304), K+304 (+304)	34.08	25.00

2570	seq=translation; coord=2:29943554..29946951:-1; parent_transcript=GRMZM2G150295_T01; parent_gene=GRMZM2G150295	GRMZM2G150295_P01	TRUE	TRUE	tScPFcVR	88%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	26.38	25.00
2571	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	gFHVdGcEASAEAR	95%	n+304 (+304), Carbamidomethyl (+57)	48.25	25.00
2572	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	lYSSLWNADDWATR	95%	n+304 (+304)	67.12	25.00
2573	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	nYVPTWAQDHIHYIDGGR	95%	n+304 (+304)	38.85	25.00
2574	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	tDWSNAPFVASYR	92%	n+304 (+304)	29.02	25.00
2575	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	yGAAVPPEcAR	93%	n+304 (+304), Carbamidomethyl (+57)	29.52	25.00
2576	seq=translation; coord=4:191578887..191581169:1; parent_transcript=GRMZM2G004699_T01; parent_gene=GRMZM2G004699	GRMZM2G004699_P01	TRUE	TRUE	yTIYNYcTDR	93%	n+304 (+304), Carbamidomethyl (+57)	29.73	25.00
2577	seq=translation; coord=3:1711864..1714237:1; parent_transcript=GRMZM2G123558_T01; parent_gene=GRMZM2G123558	GRMZM2G123558_P01,GRMZM2G123558_P02	TRUE	TRUE	eVAVEEK	95%	n+304 (+304), K+304 (+304)	38.35	25.73
2578	seq=translation; coord=3:1711864..1714237:1; parent_transcript=GRMZM2G123558_T01; parent_gene=GRMZM2G123558	GRMZM2G123558_P01,GRMZM2G123558_P02	TRUE	TRUE	sGTSPLLPAlTlFDK	95%	n+304 (+304), K+304 (+304)	32.92	25.00
2579	seq=translation; coord=3:1711864..1714237:1; parent_transcript=GRMZM2G123558_T01; parent_gene=GRMZM2G123558	GRMZM2G123558_P01,GRMZM2G123558_P02	TRUE	TRUE	vVEAYEASPEVvk	94%	n+304 (+304), K+304 (+304)	28.59	25.55
2580	seq=translation; coord=4:230101062..230104782:-1; parent_transcript=GRMZM2G134582_T01; parent_gene=GRMZM2G134582	GRMZM2G134582_P01,GRMZM2G320497_P01	TRUE	TRUE	iPVLETPDGPVFESNAIAR	95%	n+304 (+304)	37.96	26.03
2581	seq=translation; coord=4:230101062..230104782:-1; parent_transcript=GRMZM2G134582_T01; parent_gene=GRMZM2G134582	GRMZM2G134582_P01,GRMZM2G320497_P01	TRUE	TRUE	mILDDWk	95%	n+304 (+304), K+304 (+304)	30.61	25.21
2582	seq=translation; coord=4:230101062..230104782:-1; parent_transcript=GRMZM2G134582_T01; parent_gene=GRMZM2G134582	GRMZM2G134582_P01,GRMZM2G320497_P01	TRUE	TRUE	qAEAVPLVPQk	95%	n+304 (+304), K+304 (+304)	37.25	25.00
2583	seq=translation; coord=4:230101062..230104782:-1; parent_transcript=GRMZM2G134582_T01; parent_gene=GRMZM2G134582	GRMZM2G134582_P01,GRMZM2G320497_P01	TRUE	TRUE	tLIAAEYSGVvk	95%	n+304 (+304), K+304 (+304)	53.32	25.71
2584	seq=translation; coord=7:124381997..124386923:1; parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173	GRMZM2G389173_P01	TRUE	TRUE	dEIIEFVvk	95%	n+304 (+304), K+304 (+304)	45.98	26.17
2585	seq=translation; coord=7:124381997..124386923:1; parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173	GRMZM2G389173_P01	TRUE	TRUE	dLWIVEFFAPWcGHck	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	33.19	25.00
2586	seq=translation; coord=7:124381997..124386923:1; parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173	GRMZM2G389173_P01	TRUE	TRUE	dVkpIVEFALSQVvk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.76	25.00

2587	seq=translation; coord=7:124381997..124386923:1; parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	gNLPLNDAPTVVASEPWDGk	95%	n+304 (+304), K+304 (+304)	32.08	25.77
2588	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	gVATVAALDADAHQALAEYGIk	95%	n+304 (+304), K+304 (+304)	41.03	25.24
2589	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	nFDELVVk	88%	n+304 (+304), K+304 (+304)	27.56	26.34
2590	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	qLAPAWEk	95%	n+304 (+304), K+304 (+304)	32.04	25.00
2591	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	vEGFPTILVFGADk	95%	n+304 (+304), K+304 (+304)	33.91	25.00
2592	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=7:124381997..124386923:1;	GRMZM2G389173_P01	TRUE	TRUE	vEGFPTILVFGADkESFPYQGAR	95%	n+304 (+304), K+304 (+304)	27.32	25.00
2593	parent_transcript=GRMZM2G389173_T01; parent_gene=GRMZM2G389173 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G389173_P01	TRUE	TRUE	yLELLLSVAEk	95%	n+304 (+304), K+304 (+304)	31.01	25.00
2594	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	aFSVINSLEIWk	91%	n+304 (+304), K+304 (+304)	25.84	25.00
2595	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	aGLINEAHGcLTelySTGR	95%	n+304 (+304), Carbamidomethyl (+57)	52.61	25.00
2596	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	eEPLFLVVAQNVQDYLER	95%	n+304 (+304)	73.83	25.44
2597	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	eEPLFLVVAQNVQDyLER	95%	n+304 (+304), iTRAQ8plex (+304)	38.64	25.00
2598	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	eHVLEMLELk	95%	n+304 (+304), K+304 (+304)	35.48	25.71
2599	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	eLLAQGVQQSR	95%	n+304 (+304)	33.16	26.88
2600	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	gPSPFVVIPEAVHR	95%	n+304 (+304)	39.47	25.33
2601	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	IQGLLFQMADk	95%	n+304 (+304), K+304 (+304)	36.50	25.98
2602	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	IREEPLFLVVAQNVQDYLER	95%	n+304 (+304)	32.79	25.39
2603	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=2:7091727..7098725:-1;	GRMZM2G379758_P01	TRUE	TRUE	IREEPLFLVVAQNVQDyLER	94%	n+304 (+304), iTRAQ8plex (+304)	25.17	25.00
2604	parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758	GRMZM2G379758_P01	TRUE	TRUE	tLMDGLMFLIYk	95%	n+304 (+304), K+304 (+304)	35.62	26.28

2605	seq=translation; coord=2:7091727..7098725:-1; parent_transcript=GRMZM2G379758_T01; parent_gene=GRMZM2G379758 seq=translation; coord=8:150358554..150362799:-1;	GRMZM2G379758_P01	TRUE	TRUE	wQDNFVSSQGR	94%	n+304 (+304)	29.11	25.00
2606	parent_transcript=GRMZM2G055936_T01; parent_gene=GRMZM2G055936 seq=translation; coord=8:150358554..150362799:-1;	GRMZM2G055936_P01	TRUE	TRUE	aLDLELDLTdk	95%	n+304 (+304), K+304 (+304)	53.58	25.79
2607	parent_transcript=GRMZM2G055936_T01; parent_gene=GRMZM2G055936 seq=translation; coord=8:150358554..150362799:-1;	GRMZM2G055936_P01	TRUE	TRUE	fLADGSGAYTk	95%	n+304 (+304), K+304 (+304)	67.55	25.12
2608	parent_transcript=GRMZM2G055936_T01; parent_gene=GRMZM2G055936 seq=translation; coord=8:150358554..150362799:-1;	GRMZM2G055936_P01	TRUE	TRUE	gVDEILLISVNDPFVMk	95%	n+304 (+304), K+304 (+304)	41.36	25.21
2609	parent_transcript=GRMZM2G055936_T01; parent_gene=GRMZM2G055936 seq=translation; coord=7:172711231..172713259:1;	GRMZM2G055936_P01	TRUE	TRUE	vILFGVPGAFTPTcSNQHVPGFITQAEQLK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.97	25.00
2610	parent_transcript=GRMZM2G063617_T01; parent_gene=GRMZM2G063617 seq=translation; coord=7:172711231..172713259:1;	GRMZM2G063617_P01	TRUE	TRUE	aGNLGDSVTISR	95%	n+304 (+304)	55.42	25.13
2611	parent_transcript=GRMZM2G063617_T01; parent_gene=GRMZM2G063617 seq=translation; coord=5:84934242..84936493:1;	GRMZM2G063617_P01	TRUE	TRUE	iMEVASLEk	95%	n+304 (+304), K+304 (+304)	29.97	25.22
2612	parent_transcript=GRMZM2G010321_T01; parent_gene=GRMZM2G010321 seq=translation; coord=5:84934242..84936493:1;	GRMZM2G010321_P01	TRUE	TRUE	fcEEEDNH	95%	n+304 (+304), Carbamidomethyl (+57)	50.89	25.00
2613	parent_transcript=GRMZM2G010321_T01; parent_gene=GRMZM2G010321 seq=translation; coord=5:84934242..84936493:1;	GRMZM2G010321_P01	TRUE	TRUE	ISNSGDLNSLMDDDk	95%	n+304 (+304), K+304 (+304)	34.05	25.00
2614	parent_transcript=GRMZM2G010321_T01; parent_gene=GRMZM2G010321 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G010321_P01	TRUE	TRUE	ISNSGDLNSLMDDDkYSK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	40.00	25.00
2615	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	aFADAGADVLFIDALASR	95%	n+304 (+304)	80.95	25.11
2616	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	gFINAGFAGIILEDQVSPk	95%	n+304 (+304), K+304 (+304)	52.34	25.20
2617	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	iIAYPLSLIGVSMR	95%	n+304 (+304)	40.31	25.42
2618	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	iIPGLAGANIMER	95%	n+304 (+304)	33.23	26.62
2619	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	iPAGFLEGMTR	95%	n+304 (+304)	31.23	25.00
2620	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	iPPPSLPTFEEIk	95%	n+304 (+304), K+304 (+304)	32.82	25.30
2621	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=10:132006574..132009975:-1;	GRMZM2G164714_P02	TRUE	TRUE	IGLPDVGLISYGENIDQGR	95%	n+304 (+304)	36.84	25.55
2622	parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714	GRMZM2G164714_P02	TRUE	TRUE	tPILSPVELEEIGYk	95%	n+304 (+304), K+304 (+304)	39.38	25.67

2623	seq=translation; coord=10:132006574..132009975:-1; parent_transcript=GRMZM2G164714_T02; parent_gene=GRMZM2G164714 seq=translation; coord=2:71086139..71088448:-1;	GRMZM2G164714_P02	TRUE	TRUE	vLEMPGAHQAPAcYDALSAR	95%	n+304 (+304), Carbamidomethyl (+57)	38.36	25.00
2624	parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176 seq=translation; coord=2:71086139..71088448:-1;	GRMZM2G112176_P01,GRMZM2G112176_P02	TRUE	TRUE	iLATPGAHQAPccYDALGAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	30.69	25.00
2625	parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176 seq=translation; coord=2:71086139..71088448:-1;	GRMZM2G112176_P01,GRMZM2G112176_P02	TRUE	TRUE	IGLPDVGLISYGEMVDQGR	95%	n+304 (+304)	66.66	25.00
2626	parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176 seq=translation; coord=2:71086139..71088448:-1;	GRMZM2G112176_P01,GRMZM2G112176_P02	TRUE	TRUE	IGLPDVGLISyGEMVDQGR	91%	n+304 (+304), iTRAQ8plex (+304)	26.01	25.58
2627	parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176 seq=translation; coord=2:71086139..71088448:-1;	GRMZM2G112176_P01,GRMZM2G112176_P02	TRUE	TRUE	IGLPDVGLISYGE mVDQGR	95%	n+304 (+304), Oxidation (+16)	54.38	25.22
2628	parent_transcript=GRMZM2G112176_T01; parent_gene=GRMZM2G112176 seq=translation; coord=1:76732179..76733770:-1;	GRMZM2G112176_P01,GRMZM2G112176_P02	TRUE	TRUE	sGESPAALR	88%	n+304 (+304)	25.69	25.00
2629	parent_transcript=GRMZM2G077316_T01; parent_gene=GRMZM2G077316 seq=translation; coord=8:157452514..157453996:-1;	GRMZM2G077316_P01	TRUE	TRUE	vQELYVYEINER	95%	n+304 (+304)	59.17	25.00
2630	parent_transcript=GRMZM2G059299_T01; parent_gene=GRMZM2G059299 seq=translation; coord=8:157452514..157453996:-1;	GRMZM2G059299_P01	TRUE	TRUE	dGNLLLLDAR	95%	n+304 (+304)	52.97	26.91
2631	parent_transcript=GRMZM2G059299_T01; parent_gene=GRMZM2G059299 seq=translation; coord=8:157452514..157453996:-1;	GRMZM2G059299_P01	TRUE	TRUE	gSPVGEGAAAELTAAGDLVLR	95%	n+304 (+304)	74.27	26.42
2632	parent_transcript=GRMZM2G059299_T01; parent_gene=GRMZM2G059299 seq=translation; coord=2:197582100..197595530:1;	GRMZM2G059299_P01	TRUE	TRUE	IVSLPLGLAYFNDPATSLR	95%	n+304 (+304)	37.59	25.89
2633	parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870 seq=translation; coord=2:197582100..197595530:1;	GRMZM2G117870_P01	TRUE	TRUE	eAFTMDEQR	87%	n+304 (+304)	25.23	25.00
2634	parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870 seq=translation; coord=2:197582100..197595530:1;	GRMZM2G117870_P01	TRUE	TRUE	IENEMDIVLDAVNk	89%	n+304 (+304), K+304 (+304)	25.84	25.71
2635	parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870 seq=translation; coord=2:197582100..197595530:1;	GRMZM2G117870_P01	TRUE	TRUE	ILHPFMPFVTEELWQR	95%	n+304 (+304)	79.97	25.53
2636	parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870 seq=translation; coord=2:197582100..197595530:1;	GRMZM2G117870_P01	TRUE	TRUE	nESDANLEAQk	95%	n+304 (+304), K+304 (+304)	37.85	25.00
2637	parent_transcript=GRMZM2G117870_T01; parent_gene=GRMZM2G117870 seq=translation; coord=4:233024312..233031203:1;	GRMZM2G117870_P01	TRUE	TRUE	vPAWYVTLEDDLdk	89%	n+304 (+304), K+304 (+304)	26.14	26.05
2638	parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817 seq=translation; coord=4:233024312..233031203:1;	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	dHQPCiIFMDEIDAIGGR	95%	n+304 (+304), Carbamidomethyl (+57)	29.38	25.00
2639	parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817 seq=translation; coord=4:233024312..233031203:1;	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	eSIELPLMNPELFLR	94%	n+304 (+304)	29.97	26.32
2640	parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	nVcTEAGMAAIR	87%	n+304 (+304), Carbamidomethyl (+57)	25.76	25.00

2641	seq=translation; coord=4:233024312..233031203:1; parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	sLSQSVGQIIGEVLRPLDNER	95%	n+304 (+304)	35.08	25.00
2642	seq=translation; coord=4:233024312..233031203:1; parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	tLMELLNQLDGFDELGk	95%	n+304 (+304), K+304 (+304)	44.07	25.62
2643	seq=translation; coord=4:233024312..233031203:1; parent_transcript=GRMZM2G165817_T01; parent_gene=GRMZM2G165817	GRMZM2G165817_P01,GRMZM2G171604_P01	TRUE	TRUE	vVLDMTTLTIMR	95%	n+304 (+304)	35.98	25.29
2644	seq=translation; coord=1:216050547..216055495:-1; parent_transcript=GRMZM2G016189_T01; parent_gene=GRMZM2G016189	GRMZM2G016189_P01	TRUE	TRUE	eLGEGGIDNYLSVk	95%	n+304 (+304), K+304 (+304)	44.59	26.12
2645	seq=translation; coord=1:216050547..216055495:-1; parent_transcript=GRMZM2G016189_T01; parent_gene=GRMZM2G016189	GRMZM2G016189_P01	TRUE	TRUE	IGPVVSEGGYQEK	95%	n+304 (+304), K+304 (+304)	50.98	26.52
2646	seq=translation; coord=1:216050547..216055495:-1; parent_transcript=GRMZM2G016189_T01; parent_gene=GRMZM2G016189	GRMZM2G016189_P01	TRUE	TRUE	rEPIGVVGLITPWNYPLLMATWk	95%	n+304 (+304), K+304 (+304)	36.07	25.00
2647	seq=translation; coord=1:216050547..216055495:-1; parent_transcript=GRMZM2G016189_T01; parent_gene=GRMZM2G016189	GRMZM2G016189_P01	TRUE	TRUE	rLPVVNPTEAHIGEIPAGTAEDVDAAVAAAR	95%	n+304 (+304)	61.49	25.00
2648	seq=translation; coord=8:38410669..38412926:1; parent_transcript=GRMZM2G054123_T01; parent_gene=GRMZM2G054123	GRMZM2G054123_P01,GRMZM2G054123_P02, GRMZM2G054123_P03,GRMZM2G054123_P04, GRMZM2G054123_P05	TRUE	TRUE	eIGFTSDDVGLDADR	95%	n+304 (+304)	79.55	25.00
2649	seq=translation; coord=8:38410669..38412926:1; parent_transcript=GRMZM2G054123_T01; parent_gene=GRMZM2G054123	GRMZM2G054123_P01,GRMZM2G054123_P02, GRMZM2G054123_P03,GRMZM2G054123_P04, GRMZM2G054123_P05	TRUE	TRUE	lCDQVSDAVLDACLAQDPDSk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	44.80	25.00
2650	seq=translation; coord=8:38410669..38412926:1; parent_transcript=GRMZM2G054123_T01; parent_gene=GRMZM2G054123	GRMZM2G054123_P01,GRMZM2G054123_P02, GRMZM2G054123_P03,GRMZM2G054123_P04, GRMZM2G054123_P05	TRUE	TRUE	tQVTVEYVNEGGAMVPVR	95%	n+304 (+304)	52.30	25.00
2651	seq=translation; coord=9:139187765..139188857:1; parent_transcript=GRMZM2G305046_T01; parent_gene=GRMZM2G305046	GRMZM2G305046_P01,GRMZM2G305046_P02	TRUE	TRUE	ILGGVTIAHGGVLPNINPVLLPk	95%	n+304 (+304), K+304 (+304)	37.48	25.00
2652	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	TRUE	TRUE	dQWSPALTLk	95%	n+304 (+304), K+304 (+304)	35.98	26.09
2653	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	TRUE	TRUE	dYPTFAATAR	95%	n+304 (+304)	33.31	25.00
2654	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	TRUE	TRUE	IVEMGFPEQVR	94%	n+304 (+304)	28.00	25.00
2655	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	TRUE	TRUE	sASTGMEEK	95%	n+304 (+304), K+304 (+304)	27.88	25.00
2656	seq=translation; coord=8:160396937..160401812:1; parent_transcript=GRMZM2G134176_T01; parent_gene=GRMZM2G134176	GRMZM2G134176_P01	TRUE	TRUE	sVDGDENMALEK	95%	n+304 (+304), K+304 (+304)	38.90	25.00
2657	seq=translation; coord=8:135138380..135140767:-1; parent_transcript=GRMZM2G076544_T01; parent_gene=GRMZM2G076544	GRMZM2G076544_P01	TRUE	TRUE	hVVFQQVLEGMDVVSLESQETDR	95%	n+304 (+304)	99.64	25.00

2658	seq=translation; coord=8:135138380..135140767:-1; parent_transcript=GRMZM2G076544_T01; parent_gene=GRMZM2G076544 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G076544_P01	TRUE	TRUE	iVIGLYGDDVPQTTFENFR	95%	n+304 (+304)	38.96	25.00
2659	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	aEAFDPAYDDDAQK	95%	n+304 (+304), K+304 (+304)	30.73	25.00
2660	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	dASDPLLR	86%	n+304 (+304)	25.24	25.00
2661	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	gMALVYR	87%	n+304 (+304)	26.29	25.54
2662	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	gWAGIHAIPR	95%	n+304 (+304)	33.95	25.00
2663	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	gWYHLFYQYNPK	95%	n+304 (+304), K+304 (+304)	35.53	25.44
2664	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	qLLQWPIHEVEK	90%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	27.75	25.31
2665	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=5:169454598..169459090:1;	GRMZM2G139300_P01	TRUE	TRUE	tFYDPVER	90%	n+304 (+304)	27.61	25.00
2666	parent_transcript=GRMZM2G139300_T01; parent_gene=GRMZM2G139300 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G139300_P01	TRUE	TRUE	vLMcTDPTK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	38.14	25.00
2667	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	acLNTNScTVSLTDESFGK	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	34.00	25.00
2668	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	dAGLLLLLR	92%	n+304 (+304)	28.57	25.00
2669	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	dLcPGVTK	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.02	25.71
2670	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	fASLGNPSGTcR	86%	n+304 (+304), Carbamidomethyl (+57)	25.22	25.00
2671	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	gGSVQNYVVYHGGTNFGR	95%	n+304 (+304)	43.46	25.00
2672	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	iWTENWPGWFQTFGESNPHRPEDVAFVAR	95%	n+304 (+304)	29.43	25.00
2673	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=3:173015163..173022969:-1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	nQPLTWYK	91%	n+304 (+304), K+304 (+304)	29.15	25.84
2674	parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	sFTTYIVDMMK	95%	n+304 (+304), K+304 (+304)	35.18	25.02

2675	seq=translation; coord=3:173015163..173022969:-1; parent_transcript=GRMZM2G038281_T01; parent_gene=GRMZM2G038281 seq=translation; coord=2:82394515..82407013:1;	GRMZM2G038281_P01,GRMZM2G038281_P02	TRUE	TRUE	vNVDVPQGDDPVGIDMQSMGk	95%	n+304 (+304), K+304 (+304)	46.95	25.00
2676	parent_transcript=GRMZM5G858094_T01; parent_gene=GRMZM5G858094 seq=translation; coord=2:82394515..82407013:1;	GRMZM5G858094_P01,GRMZM5G858094_P02	TRUE	TRUE	dIIENLSYGSEk	95%	n+304 (+304), K+304 (+304)	43.59	25.15
2677	parent_transcript=GRMZM5G858094_T01; parent_gene=GRMZM5G858094 seq=translation; coord=2:82394515..82407013:1;	GRMZM5G858094_P01,GRMZM5G858094_P02	TRUE	TRUE	eDAFFETVTNLACeR	95%	n+304 (+304), Carbamidomethyl (+57)	34.80	25.00
2678	parent_transcript=GRMZM2G045664_T01; parent_gene=GRMZM2G045664 seq=translation; coord=8:74938636..74939549:-1;	GRMZM2G045664_P01	TRUE	TRUE	eVASGTMPPDPGWIAASGSTALEIPak	95%	n+304 (+304), K+304 (+304)	55.20	25.47
2679	parent_transcript=GRMZM2G045664_T01; parent_gene=GRMZM2G045664 seq=translation; coord=8:74938636..74939549:-1;	GRMZM2G045664_P01	TRUE	TRUE	IPicEVITYTLR	90%	n+304 (+304), Carbamidomethyl (+57)	27.63	25.00
2680	parent_transcript=GRMZM2G045664_T01; parent_gene=GRMZM2G045664 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G045664_P01	TRUE	TRUE	vPYDFLVSLVR	92%	n+304 (+304)	30.52	26.58
2681	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G410916_P02	TRUE	TRUE	dTVIVEER	95%	n+304 (+304)	34.76	25.66
2682	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G410916_P02	TRUE	TRUE	gDVQLVMANAAPWWLVk	95%	n+304 (+304), K+304 (+304)	46.02	25.55
2683	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G410916_P02	TRUE	TRUE	iTEVTVR	93%	n+304 (+304)	29.57	25.00
2684	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G410916_P02	TRUE	TRUE	ILLNLDAVVR	95%	n+304 (+304)	32.77	25.00
2685	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=3:26352719..26355885:1;	GRMZM2G410916_P02	TRUE	TRUE	sDlcDLAGDVR	95%	n+304 (+304), Carbamidomethyl (+57)	40.42	25.00
2686	parent_transcript=GRMZM2G410916_T02; parent_gene=GRMZM2G410916 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G410916_P02	TRUE	TRUE	sLDGLATPDFTR	95%	n+304 (+304)	45.23	25.00
2687	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	dGYYIHGQcAIIMFDVTSR	95%	n+304 (+304), Carbamidomethyl (+57)	55.10	25.00
2688	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	dGYYIHGQcAIIMFDVTSR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	44.26	25.00
2689	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	fYcWDTAGQEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.63	25.00
2690	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	hLTGEFEk	95%	n+304 (+304), K+304 (+304)	32.33	25.79
2691	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604 seq=translation; coord=6:165704660..165707098:-1;	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	IVIVGDGGTGk	95%	n+304 (+304), K+304 (+304)	33.06	25.48
2692	parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	nLQYYEISak	95%	n+304 (+304), K+304 (+304)	32.09	25.16

2693	seq=translation; coord=6:165704660..165707098:-1; parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	sNYNFEKPFPLYLAR	95%	n+304 (+304), K+304 (+304)	31.50	25.85
2694	seq=translation; coord=6:165704660..165707098:-1; parent_transcript=GRMZM2G354604_T01; parent_gene=GRMZM2G354604	GRMZM2G354604_P01,GRMZM2G354604_P02, GRMZM2G354604_P03	TRUE	TRUE	vcENIPIVLcGNk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	44.09	26.25
2695	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01,GRMZM2G013652_P03	TRUE	TRUE	aGNLIPVALk	95%	n+304 (+304), K+304 (+304)	39.27	25.00
2696	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01,GRMZM2G013652_P03	TRUE	TRUE	eGDTVLLPEYGGTEV	95%	n+304 (+304), K+304 (+304)	35.35	25.25
2697	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01,GRMZM2G013652_P03	TRUE	TRUE	eHDILGTLVD	95%	n+304 (+304)	43.18	25.00
2698	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01,GRMZM2G013652_P03	TRUE	TRUE	eYLLFR	87%	n+304 (+304)	25.54	25.00
2699	seq=translation; coord=7:169267359..169269362:1; parent_transcript=GRMZM2G013652_T01; parent_gene=GRMZM2G013652	GRMZM2G013652_P01,GRMZM2G013652_P03	TRUE	TRUE	vVAVGPGER	88%	n+304 (+304)	28.28	27.28
2700	seq=translation; coord=6:31411848..31415600:-1; parent_transcript=GRMZM2G099186_T02; parent_gene=GRMZM2G099186	GRMZM2G099186_P02,GRMZM2G175419_P01	TRUE	TRUE	dADDAQYNLDGR	95%	n+304 (+304)	50.99	25.00
2701	seq=translation; coord=6:31411848..31415600:-1; parent_transcript=GRMZM2G099186_T02; parent_gene=GRMZM2G099186	GRMZM2G099186_P02,GRMZM2G175419_P01	TRUE	TRUE	dLEYLFSk	95%	n+304 (+304), K+304 (+304)	35.61	25.45
2702	seq=translation; coord=6:31411848..31415600:-1; parent_transcript=GRMZM2G099186_T02; parent_gene=GRMZM2G099186	GRMZM2G099186_P02,GRMZM2G175419_P01	TRUE	TRUE	dYAFIEFSDPR	94%	n+304 (+304)	30.42	25.00
2703	seq=translation; coord=6:31411848..31415600:-1; parent_transcript=GRMZM2G099186_T02; parent_gene=GRMZM2G099186	GRMZM2G099186_P02,GRMZM2G175419_P01	TRUE	TRUE	iIVEFAK	92%	n+304 (+304), K+304 (+304)	28.98	25.00
2704	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	TRUE	TRUE	gLEDTDFLNNMDPFVILTcR	95%	n+304 (+304), Carbamidomethyl (+57)	40.60	25.00
2705	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	TRUE	TRUE	gLEDTDFLNNmDPFVILTcR	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57)	43.09	25.00
2706	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	TRUE	TRUE	IALTFTPAAETR	95%	n+304 (+304)	53.05	25.49
2707	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	TRUE	TRUE	IEVLLVSAk	95%	n+304 (+304), K+304 (+304)	41.49	25.00
2708	seq=translation; coord=10:148535505..148536885:1; parent_transcript=GRMZM2G011513_T01; parent_gene=GRMZM2G011513	GRMZM2G011513_P01	TRUE	TRUE	rPDDNEEGPPYSSWS	95%	n+304 (+304)	47.05	25.00
2709	seq=translation; coord=2:61490885..61494711:-1; parent_transcript=GRMZM2G134668_T02; parent_gene=GRMZM2G134668	GRMZM2G134668_P02	TRUE	TRUE	dGTVVLQFEVR	95%	n+304 (+304)	46.39	25.65

2710	seq=translation; coord=2:61490885..61494711:-1; parent_transcript=GRMZM2G134668_T02; parent_gene=GRMZM2G134668 seq=translation; coord=2:61490885..61494711:-1;	GRMZM2G134668_P02	TRUE	TRUE	eLDEPVTlk	95%	n+304 (+304), K+304 (+304)	42.90	25.55
2711	parent_transcript=GRMZM2G134668_T02; parent_gene=GRMZM2G134668 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G134668_P02	TRUE	TRUE	iLVDGEEK	95%	n+304 (+304), K+304 (+304)	30.65	26.59
2712	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	iVAEFLQEVGHIR	95%	n+304 (+304)	78.05	26.95
2713	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	IALGGPPPVGAR	89%	n+304 (+304)	26.56	25.00
2714	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	IGAEGAicTNVLSADR	89%	n+304 (+304), Carbamidomethyl (+57)	25.14	25.00
2715	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	ILAGLLGVEAAQDAVFR	95%	n+304 (+304)	54.27	25.31
2716	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	rLGAEGAicTNVLSADR	95%	n+304 (+304), Carbamidomethyl (+57)	46.89	25.61
2717	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=1:58418770..58420264:-1;	GRMZM2G075290_P01	TRUE	TRUE	tPAELLSILYLTGDER	92%	n+304 (+304)	28.41	26.48
2718	parent_transcript=GRMZM2G075290_T01; parent_gene=GRMZM2G075290 seq=translation; coord=7:171733893..171737098:-1;	GRMZM2G075290_P01	TRUE	TRUE	vMDEAFGTR	91%	n+304 (+304)	27.91	25.00
2719	parent_transcript=GRMZM2G025992_T01; parent_gene=GRMZM2G025992 seq=translation; coord=7:171733893..171737098:-1;	GRMZM2G025992_P01,GRMZM2G025992_P03, GRMZM2G025992_P04,GRMZM2G025992_P05	TRUE	TRUE	aVAVLAGTDVvk	95%	n+304 (+304), K+304 (+304)	54.69	25.29
2720	parent_transcript=GRMZM2G025992_T01; parent_gene=GRMZM2G025992 seq=translation; coord=4:217021920..217028774:-1;	GRMZM2G025992_P01,GRMZM2G025992_P03, GRMZM2G025992_P04,GRMZM2G025992_P05	TRUE	TRUE	hAGDLGNVTAGEDGVNVNITDSQIPLAGPHSIIGR	95%	n+304 (+304)	31.87	25.00
2721	parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578 seq=translation; coord=4:217021920..217028774:-1;	GRMZM2G180578_P01	TRUE	TRUE	dELGQETLLNLLLR	95%	n+304 (+304)	70.62	26.05
2722	parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578 seq=translation; coord=4:217021920..217028774:-1;	GRMZM2G180578_P01	TRUE	TRUE	hMAEDDDDDF	95%	n+304 (+304)	38.36	25.00
2723	parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578 seq=translation; coord=4:217021920..217028774:-1;	GRMZM2G180578_P01	TRUE	TRUE	iSLADIak	93%	n+304 (+304), K+304 (+304)	27.07	25.00
2724	parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578 seq=translation; coord=4:217021920..217028774:-1;	GRMZM2G180578_P01	TRUE	TRUE	vGDLELFR	92%	n+304 (+304)	29.07	25.00
2725	parent_transcript=GRMZM2G180578_T01; parent_gene=GRMZM2G180578 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G180578_P01	TRUE	TRUE	yLFYLGk	95%	n+304 (+304), K+304 (+304)	30.36	25.00
2726	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	dDADWSTLGvk	95%	n+304 (+304), K+304 (+304)	61.44	25.00
2727	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	eLFPGIEIDTSQPPIVFk	95%	n+304 (+304), K+304 (+304)	30.48	25.48

2728	seq=translation; coord=3:226624022..226632817:-1; parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	IMMIGTADEIVK	95%	n+304 (+304), K+304 (+304)	30.43	25.51
2729	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	qLFGIDLVSr	94%	n+304 (+304)	31.13	25.00
2730	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	qLTGVYDLVAVLTHK	95%	n+304 (+304), K+304 (+304)	59.63	25.00
2731	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	qLTGVYDLVAVLTHK	91%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.66	26.60
2732	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=3:226624022..226632817:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	sALLSYSDTVR	95%	n+304 (+304)	38.68	26.05
2733	parent_transcript=GRMZM2G017086_T01; parent_gene=GRMZM2G017086 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G017086_P01,GRMZM2G017086_P03	TRUE	TRUE	wIEFDDDNPNIR	95%	n+304 (+304)	44.66	25.00
2734	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	eDDIIGILSDDDVK	95%	n+304 (+304), K+304 (+304)	50.95	25.01
2735	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	gEDGEYIVLR	94%	n+304 (+304)	30.31	25.00
2736	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	iEISVPVGAQVVYSK	94%	n+304 (+304), K+304 (+304)	30.73	25.00
2737	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	nPLSITPGSNVMYSK	95%	n+304 (+304), K+304 (+304)	36.39	26.74
2738	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=2:183929119..183934914:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	sDGGILLPVSVQTRPQGGEIVAVGEGR	92%	n+304 (+304)	26.79	25.00
2739	parent_transcript=GRMZM2G399284_T01; parent_gene=GRMZM2G399284 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G399284_P01,GRMZM2G399284_P03	TRUE	TRUE	yAGSEfKGEDGEYIVLR	93%	n+304 (+304), K+304 (+304)	27.66	25.26
2740	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G008410_P01	TRUE	TRUE	aMELILEK	95%	n+304 (+304), K+304 (+304)	36.53	25.82
2741	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G008410_P01	TRUE	TRUE	fLVSNtAAGcIIgK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	46.86	25.65
2742	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G008410_P01	TRUE	TRUE	gDYISGTSDR	90%	n+304 (+304)	26.57	25.00
2743	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G008410_P01	TRUE	TRUE	iIMVSGLFDEVMK	95%	n+304 (+304), K+304 (+304)	60.31	25.20
2744	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410 seq=translation; coord=4:170332797..170339707:-1;	GRMZM2G008410_P01	TRUE	TRUE	sPASNEAQESLTIGIADEHIGAVVGR	95%	n+304 (+304)	90.16	25.00
2745	parent_transcript=GRMZM2G008410_T01; parent_gene=GRMZM2G008410	GRMZM2G008410_P01	TRUE	TRUE	vTITGTPEAIR	91%	n+304 (+304)	27.86	25.00

2746	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	aDMDALPLQESVEWEHK	95%	n+304 (+304), K+304 (+304)	54.21	25.00
2747	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	dRPFFPPTINSPELHDFFNNAVAGEMVGSR	95%	n+304 (+304)	38.35	25.00
2748	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	eADPLDSQVVTVGk	95%	n+304 (+304), K+304 (+304)	54.78	26.30
2749	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	ePAFADWMVGVr	95%	n+304 (+304)	48.21	25.00
2750	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	fQGGGAFNVPDSVTIGGTFR	95%	n+304 (+304)	35.09	25.40
2751	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	hPFAVTGVVATVGTGGPPFVALR	95%	n+304 (+304)	43.85	25.00
2752	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	iEEVIVSQASVQR	95%	n+304 (+304)	30.54	25.51
2753	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	iHENPELGYEEFQTSSELVR	95%	n+304 (+304)	53.97	25.00
2754	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	qQPAATADk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	35.78	25.00
2755	seq=translation; coord=3:218785554..218795824:-1; parent_transcript=GRMZM2G090779_T01; parent_gene=GRMZM2G090779	GRMZM2G090779_P01	TRUE	TRUE	qQPAATADkAETHDEL	91%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	26.98	25.00
2756	seq=translation; coord=8:171852196..171855863:-1; parent_transcript=GRMZM2G159643_T01; parent_gene=GRMZM2G159643	GRMZM2G159643_P01	TRUE	TRUE	IAEEIQk	86%	n+304 (+304), K+304 (+304)	27.33	27.19
2757	seq=translation; coord=8:171852196..171855863:-1; parent_transcript=GRMZM2G159643_T01; parent_gene=GRMZM2G159643	GRMZM2G159643_P01	TRUE	TRUE	tWQVPETLPEEVLGk	95%	n+304 (+304), K+304 (+304)	40.54	25.84
2758	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	aLADSPIIGEIR	95%	n+304 (+304)	45.31	26.05
2759	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	kYDILFIADDEVITAFGR	95%	K+304 (+304), n+304 (+304)	42.05	25.00
2760	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	IATNLENLILk	95%	n+304 (+304), K+304 (+304)	31.60	25.00
2761	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	sPTDLFPAEWGVGAIFGEcQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.84	25.00
2762	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	tTkPSLDLAQEILSMFTAR	95%	n+304 (+304), K+304 (+304)	34.14	25.00
2763	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886	GRMZM5G817886_P02	TRUE	TRUE	yHLPGETEEDFATR	95%	n+304 (+304), iTRAQ8plex (+304)	39.39	25.00

2764	seq=translation; coord=2:10210584..10215840:-1; parent_transcript=GRMZM5G817886_T02; parent_gene=GRMZM5G817886 seq=translation; coord=1:246702682..246710172:-1;	GRMZM5G817886_P02	TRUE	TRUE	yLDSLGLWcTALGGSEPR	95%	n+304 (+304), Carbamidomethyl (+57)	29.59	25.00
2765	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	aSAADDDMDPTQYYENR	95%	n+304 (+304)	34.52	25.00
2766	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	fPVGISVPEYIEk	90%	n+304 (+304), K+304 (+304)	25.37	25.00
2767	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	gEGSAVPVPWTPGMGR	95%	n+304 (+304)	44.46	25.00
2768	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	IFFYDLYGGGMk	95%	n+304 (+304), K+304 (+304)	49.76	25.26
2769	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	ITDVAEcLAGR	94%	n+304 (+304), Carbamidomethyl (+57)	31.32	25.00
2770	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=1:246702682..246710172:-1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	ITMLLTDSQNIk	95%	n+304 (+304), K+304 (+304)	30.69	25.00
2771	parent_transcript=GRMZM2G146589_T01; parent_gene=GRMZM2G146589 seq=translation; coord=7:123475099..123479587:1;	GRMZM2G146589_P01,GRMZM2G146589_P02, GRMZM2G146589_P03,GRMZM2G146589_P04	TRUE	TRUE	tSELDEAEFSk	93%	n+304 (+304), K+304 (+304)	26.36	25.00
2772	parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944 seq=translation; coord=7:123475099..123479587:1;	GRMZM5G824944_P01,GRMZM5G824944_P02	TRUE	TRUE	hFADIMFR	95%	n+304 (+304)	32.15	25.00
2773	parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944 seq=translation; coord=7:123475099..123479587:1;	GRMZM5G824944_P01,GRMZM5G824944_P02	TRUE	TRUE	IDIDPESITWR	95%	n+304 (+304)	31.86	25.01
2774	parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944 seq=translation; coord=7:123475099..123479587:1;	GRMZM5G824944_P01,GRMZM5G824944_P02	TRUE	TRUE	sGEPITADDLGVGGALTVMk	95%	n+304 (+304), K+304 (+304)	49.19	25.00
2775	parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944 seq=translation; coord=7:123475099..123479587:1;	GRMZM5G824944_P01,GRMZM5G824944_P02	TRUE	TRUE	tDPNELTPDEIR	95%	n+304 (+304)	53.38	25.00
2776	parent_transcript=GRMZM5G824944_T01; parent_gene=GRMZM5G824944 seq=translation; coord=1:220892398..220897302:-1;	GRMZM5G824944_P01,GRMZM5G824944_P02	TRUE	TRUE	vLLSVLDELk	95%	n+304 (+304), K+304 (+304)	43.96	25.00
2777	parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022 seq=translation; coord=1:220892398..220897302:-1;	GRMZM2G078022_P01,GRMZM2G078022_P02, GRMZM2G078022_P03	TRUE	TRUE	aPHFVk	95%	n+304 (+304), K+304 (+304)	37.84	25.00
2778	parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022 seq=translation; coord=1:220892398..220897302:-1;	GRMZM2G078022_P01,GRMZM2G078022_P02, GRMZM2G078022_P03	TRUE	TRUE	aVEAEETESAETk	95%	n+304 (+304), K+304 (+304)	77.29	25.00
2779	parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022 seq=translation; coord=1:220892398..220897302:-1;	GRMZM2G078022_P01,GRMZM2G078022_P02, GRMZM2G078022_P03	TRUE	TRUE	sIFcIVEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.36	26.88
2780	parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022 seq=translation; coord=1:220892398..220897302:-1;	GRMZM2G078022_P01,GRMZM2G078022_P02, GRMZM2G078022_P03	TRUE	TRUE	vNLDPDGVFTFSGSAGTNlyElk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.11	25.00
2781	parent_transcript=GRMZM2G078022_T03; parent_gene=GRMZM2G078022	GRMZM2G078022_P01,GRMZM2G078022_P02, GRMZM2G078022_P03	TRUE	TRUE	vYITVQLPDAk	95%	n+304 (+304), K+304 (+304)	39.89	25.00

2782	seq=translation; coord=7:136570996..136574421:1; parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386 seq=translation; coord=7:136570996..136574421:1;	GRMZM2G074386_P01	TRUE	TRUE	dVFASATER	93%	n+304 (+304)	30.01	25.00
2783	parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386 seq=translation; coord=7:136570996..136574421:1;	GRMZM2G074386_P01	TRUE	TRUE	eYIDLR	95%	n+304 (+304)	30.64	25.00
2784	parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386 seq=translation; coord=7:136570996..136574421:1;	GRMZM2G074386_P01	TRUE	TRUE	fFPYYAFNVLGGLDSEGK	95%	n+304 (+304), K+304 (+304)	61.99	25.17
2785	parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386 seq=translation; coord=7:136570996..136574421:1;	GRMZM2G074386_P01	TRUE	TRUE	ISVGYSILTR	95%	n+304 (+304)	34.71	27.23
2786	parent_transcript=GRMZM2G074386_T01; parent_gene=GRMZM2G074386 seq=translation; coord=1:20418930..20420739:-1;	GRMZM2G074386_P01	TRUE	TRUE	mScPAMAQLSNTLYYK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.19	25.22
2787	parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367 seq=translation; coord=1:20418930..20420739:-1;	GRMZM2G134367_P01	TRUE	TRUE	vAGAAADLLHAASQYGK	95%	n+304 (+304), K+304 (+304)	34.49	25.00
2788	parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367 seq=translation; coord=1:20418930..20420739:-1;	GRMZM2G134367_P01	TRUE	TRUE	yEDEDYR	90%	n+304 (+304)	27.34	25.00
2789	parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367 seq=translation; coord=1:20418930..20420739:-1;	GRMZM2G134367_P01	TRUE	TRUE	yEEDDEYR	95%	n+304 (+304)	31.69	25.00
2790	parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367 seq=translation; coord=1:20418930..20420739:-1;	GRMZM2G134367_P01	TRUE	TRUE	yEEEGYK	95%	n+304 (+304), K+304 (+304)	41.95	25.00
2791	parent_transcript=GRMZM2G134367_T01; parent_gene=GRMZM2G134367 seq=translation; coord=8:79300397..79307702:1;	GRMZM2G134367_P01	TRUE	TRUE	yEQEDNYK	93%	n+304 (+304), K+304 (+304)	29.38	25.00
2792	parent_transcript=GRMZM2G073774_T01; parent_gene=GRMZM2G073774 seq=translation; coord=8:79300397..79307702:1;	GRMZM2G073774_P01,GRMZM2G152958_P01, GRMZM2G152958_P02	TRUE	TRUE	aLGVDILTVGTIVGK	95%	n+304 (+304), K+304 (+304)	60.34	25.00
2793	parent_transcript=GRMZM2G073774_T01; parent_gene=GRMZM2G073774 seq=translation; coord=8:79300397..79307702:1;	GRMZM2G073774_P01,GRMZM2G152958_P01, GRMZM2G152958_P02	TRUE	TRUE	gFVPVDER	95%	n+304 (+304)	41.58	25.55
2794	parent_transcript=GRMZM2G073774_T01; parent_gene=GRMZM2G073774 seq=translation; coord=8:79300397..79307702:1;	GRMZM2G073774_P01,GRMZM2G152958_P01, GRMZM2G152958_P02	TRUE	TRUE	gLLENINVTQR	95%	n+304 (+304)	65.56	26.11
2795	parent_transcript=GRMZM2G073774_T01; parent_gene=GRMZM2G073774 seq=translation; coord=6:75746632..75749530:-1;	GRMZM2G073774_P01,GRMZM2G152958_P01, GRMZM2G152958_P02	TRUE	TRUE	IMLAHAASAQGISVVEQISGK	95%	n+304 (+304), K+304 (+304)	27.25	25.00
2796	parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528 seq=translation; coord=6:75746632..75749530:-1;	GRMZM2G130528_P01	TRUE	TRUE	eGANMAITGATAMDAPFFR	95%	n+304 (+304)	43.89	25.00
2797	parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528 seq=translation; coord=6:75746632..75749530:-1;	GRMZM2G130528_P01	TRUE	TRUE	eGANmAITGATAMDAPFFR	95%	n+304 (+304), Oxidation (+16)	73.73	25.00
2798	parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528	GRMZM2G130528_P01	TRUE	TRUE	eGANMAITGATAmDAPFFR	95%	n+304 (+304), Oxidation (+16)	33.47	25.00

2799	seq=translation; coord=6:75746632..75749530:-1; parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528	GRMZM2G130528_P01	TRUE	TRUE	nPGSYGFSTAFQTccGSGGGk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	54.83	25.00
2800	seq=translation; coord=6:75746632..75749530:-1; parent_transcript=GRMZM2G130528_T01; parent_gene=GRMZM2G130528 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G130528_P01	TRUE	TRUE	vIPDFLcSk	95%	Carbamidomethyl (+57), K+304 (+304), K+304 (+304)	36.40	26.05
2801	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G157018_P01	TRUE	TRUE	eAFESIEIPk	95%	n+304 (+304), K+304 (+304)	45.02	25.34
2802	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G157018_P01	TRUE	TRUE	eLAEMEEMR	87%	n+304 (+304)	25.87	25.00
2803	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G157018_P01	TRUE	TRUE	fDAVIAELk	95%	n+304 (+304), K+304 (+304)	31.60	25.07
2804	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G157018_P01	TRUE	TRUE	fSQEPQPIDWEYR	95%	n+304 (+304)	33.74	25.00
2805	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=1:200480447..200483616:-1;	GRMZM2G157018_P01	TRUE	TRUE	iTMTADDYFek	95%	n+304 (+304), K+304 (+304)	34.88	25.00
2806	parent_transcript=GRMZM2G157018_T01; parent_gene=GRMZM2G157018 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G157018_P01	TRUE	TRUE	tIIDWDGMAk	95%	n+304 (+304), K+304 (+304)	69.12	25.08
2807	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G049811_P01	TRUE	TRUE	fEEDLDAMLpk	95%	n+304 (+304), K+304 (+304)	54.89	25.59
2808	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G049811_P01	TRUE	TRUE	gEDFPVQNYIVk	95%	n+304 (+304), K+304 (+304)	76.26	25.98
2809	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G049811_P01	TRUE	TRUE	hIEDMHVLITPFHPAYVTAER	95%	n+304 (+304)	27.20	25.00
2810	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G049811_P01	TRUE	TRUE	IQIDPELEk	95%	n+304 (+304), K+304 (+304)	36.40	25.15
2811	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=9:48437559..48441823:-1;	GRMZM2G049811_P01	TRUE	TRUE	nFLPGYQQVVQGEWNVAGIAHR	95%	n+304 (+304)	61.57	25.39
2812	parent_transcript=GRMZM2G049811_T01; parent_gene=GRMZM2G049811 seq=translation; coord=1:180400813..180406565:-1;	GRMZM2G049811_P01	TRUE	TRUE	nPNFVGcVEGALGIR	95%	n+304 (+304), Carbamidomethyl (+57)	67.25	25.51
2813	parent_transcript=GRMZM2G085474_T01; parent_gene=GRMZM2G085474 seq=translation; coord=1:180400813..180406565:-1;	GRMZM2G085474_P01,GRMZM2G085474_P04	TRUE	TRUE	dSGAFAWEIVPIEVPVGR	95%	n+304 (+304)	50.87	26.14
2814	parent_transcript=GRMZM2G085474_T01; parent_gene=GRMZM2G085474 seq=translation; coord=1:180400813..180406565:-1;	GRMZM2G085474_P01,GRMZM2G085474_P04	TRUE	TRUE	eDQDAFAIQSNQR	95%	n+304 (+304)	55.17	25.00
2815	parent_transcript=GRMZM2G085474_T01; parent_gene=GRMZM2G085474	GRMZM2G085474_P01,GRMZM2G085474_P04	TRUE	TRUE	tPLGGFLGALSSLPATk	95%	n+304 (+304), K+304 (+304)	44.72	25.00

2816	seq=translation; coord=9:139511132..139514364:1; parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532 seq=translation; coord=9:139511132..139514364:1;	GRMZM2G366532_P01,GRMZM2G366532_P02	TRUE	TRUE	dAGVIAGLNVTR	93%	n+304 (+304)	31.72	26.51
2817	parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532 seq=translation; coord=9:139511132..139514364:1;	GRMZM2G366532_P01,GRMZM2G366532_P02	TRUE	TRUE	fDPSVQADMk	95%	n+304 (+304), K+304 (+304)	40.85	25.00
2818	parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532 seq=translation; coord=9:139511132..139514364:1;	GRMZM2G366532_P01,GRMZM2G366532_P02	TRUE	TRUE	sINPDEAVAYGAAVQAAILSSEGNGK	95%	n+304 (+304), K+304 (+304)	71.85	25.43
2819	parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532 seq=translation; coord=9:139511132..139514364:1;	GRMZM2G366532_P01,GRMZM2G366532_P02	TRUE	TRUE	sQIHVVVLVGGSTR	95%	n+304 (+304)	30.62	26.59
2820	parent_transcript=GRMZM2G366532_T01; parent_gene=GRMZM2G366532 seq=translation; coord=9:139511132..139514364:1;	GRMZM2G366532_P01,GRMZM2G366532_P02	TRUE	TRUE	wLDGNQLAEAEFEDk	95%	n+304 (+304), K+304 (+304)	51.16	25.00
2821	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	dITEEDLR	95%	n+304 (+304)	31.97	25.00
2822	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	gFAFVTFMDk	95%	n+304 (+304), K+304 (+304)	33.57	25.00
2823	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	gPDVAGGGPEDEER	95%	n+304 (+304)	92.52	25.00
2824	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	gPGVINIEMFk	95%	n+304 (+304), K+304 (+304)	52.68	26.28
2825	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	mVPMVLPDGR	95%	n+304 (+304)	31.15	25.07
2826	parent_transcript=GRMZM2G103430_T01; parent_gene=GRMZM2G103430 seq=translation; coord=4:38181649..38185320:-1;	GRMZM2G103430_P01,GRMZM2G103430_P02, GRMZM2G103430_P03,GRMZM2G103430_P04, GRMZM2G103430_P05	TRUE	TRUE	vDGSQTLTVSWAEPk	95%	n+304 (+304), K+304 (+304)	45.51	25.98
2827	parent_transcript=GRMZM2G423027_T01; parent_gene=GRMZM2G423027 seq=translation; coord=4:53954699..53962275:1;	GRMZM2G423027_P01,GRMZM2G423027_P07	TRUE	TRUE	mVIPVGTVFQELk	95%	n+304 (+304), K+304 (+304)	51.13	25.00
2828	parent_transcript=GRMZM2G423027_T01; parent_gene=GRMZM2G423027 seq=translation; coord=4:53954699..53962275:1;	GRMZM2G423027_P01,GRMZM2G423027_P07	TRUE	TRUE	vAEVMEAIRDR	95%	n+304 (+304)	36.30	25.50
2829	parent_transcript=GRMZM2G166035_T01; parent_gene=GRMZM2G166035 seq=translation; coord=4:237508371..237511930:-1;	GRMZM2G166035_P01,GRMZM2G166035_P02	TRUE	TRUE	aSMEDFYEAR	95%	n+304 (+304)	43.11	25.00
2830	parent_transcript=GRMZM2G166035_T01; parent_gene=GRMZM2G166035 seq=translation; coord=5:199376854..199379060:1;	GRMZM2G166035_P01,GRMZM2G166035_P02	TRUE	TRUE	vGMFGVYDGHGGVR	95%	n+304 (+304)	57.79	25.00
2831	parent_transcript=GRMZM2G027741_T01; parent_gene=GRMZM2G027741 seq=translation; coord=5:199376854..199379060:1;	GRMZM2G027741_P01,GRMZM2G027741_P02, GRMZM2G027741_P03,GRMZM2G027741_P04	TRUE	TRUE	aFSEVAAER	95%	n+304 (+304)	31.98	25.00
2832	parent_transcript=GRMZM2G027741_T01; parent_gene=GRMZM2G027741 seq=translation; coord=5:199376854..199379060:1;	GRMZM2G027741_P01,GRMZM2G027741_P02, GRMZM2G027741_P03,GRMZM2G027741_P04	TRUE	TRUE	aLMLIEAWGESGDELr	93%	n+304 (+304)	29.68	25.00
2833	parent_transcript=GRMZM2G027741_T01; parent_gene=GRMZM2G027741	GRMZM2G027741_P01,GRMZM2G027741_P02, GRMZM2G027741_P03,GRMZM2G027741_P04	TRUE	TRUE	vDSVELIR	91%	n+304 (+304)	28.95	25.69

2834	seq=translation; coord=5:199376854..199379060:1; parent_transcript=GRMZM2G027741_T01; parent_gene=GRMZM2G027741 seq=translation; coord=3:161953049..161955801:1;	GRMZM2G027741_P01,GRMZM2G027741_P02, GRMZM2G027741_P03,GRMZM2G027741_P04	TRUE	TRUE	vQYLSLVLETTIVk	93%	n+304 (+304), K+304 (+304)	27.20	25.00
2835	parent_transcript=GRMZM2G153991_T01; parent_gene=GRMZM2G153991 seq=translation; coord=3:161953049..161955801:1;	GRMZM2G153991_P01	TRUE	TRUE	gTLTDGVSFDDSSYDR	95%	n+304 (+304)	73.86	25.00
2836	parent_transcript=GRMZM2G153991_T01; parent_gene=GRMZM2G153991 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G153991_P01	TRUE	TRUE	sGDVTELQIGVvk	95%	n+304 (+304), K+304 (+304)	34.39	26.09
2837	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	aAHMLGQPAVLDFFAk	95%	n+304 (+304), K+304 (+304)	29.82	25.87
2838	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	fLENFcGDQVR	93%	n+304 (+304), Carbamidomethyl (+57)	30.13	25.00
2839	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	gAGIGTPEAIk	95%	n+304 (+304), K+304 (+304)	56.30	25.17
2840	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	IEDAGFDWk	95%	n+304 (+304), K+304 (+304)	29.54	25.00
2841	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	ILHDCGLPAEDMDFINS DGAVMNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.23	25.00
2842	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	ILLEANPk	91%	n+304 (+304), K+304 (+304)	27.75	25.00
2843	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	sGNFELVTk	95%	n+304 (+304), K+304 (+304)	33.78	26.58
2844	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=6:161454531..161462066:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	sYQQALAEVQVSQk	95%	n+304 (+304), K+304 (+304)	36.02	25.58
2845	parent_transcript=GRMZM2G090087_T02; parent_gene=GRMZM2G090087 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G090087_P02,GRMZM2G090087_P03	TRUE	TRUE	yLMYGDISAk	95%	n+304 (+304), K+304 (+304)	34.46	25.51
2846	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G097030_P01	TRUE	TRUE	aDGAATLLSMLATPR	95%	n+304 (+304)	29.85	25.15
2847	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G097030_P01	TRUE	TRUE	eVAcVVVDGQWYk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	44.18	25.30
2848	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G097030_P01	TRUE	TRUE	IDEVVPGLEPLR	95%	n+304 (+304)	41.40	26.56
2849	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G097030_P01	TRUE	TRUE	IMAGELGPQGPR	90%	n+304 (+304)	27.48	25.85
2850	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030 seq=translation; coord=7:23715448..23717527:-1;	GRMZM2G097030_P01	TRUE	TRUE	vAVPALVLR	95%	n+304 (+304)	31.33	25.00
2851	parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030	GRMZM2G097030_P01	TRUE	TRUE	vDGSDDETVLR	95%	n+304 (+304)	46.03	25.00

2852	seq=translation; coord=7:23715448..23717527:-1; parent_transcript=GRMZM2G097030_T01; parent_gene=GRMZM2G097030	GRMZM2G097030_P01	TRUE	TRUE	vVMFPFPFWSHINQMLQLGK	95%	n+304 (+304), K+304 (+304)	31.23	25.00
2853	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	eVSGTYGAFEGATTLTSLR	95%	n+304 (+304)	68.81	25.17
2854	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	gPDASLVAR	95%	n+304 (+304)	33.09	25.51
2855	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	iGLWGGPGGSAQDITAERPPQR	95%	n+304 (+304)	34.31	25.00
2856	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	IVDAIGVYLR	95%	n+304 (+304)	39.07	25.00
2857	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	vQGITSEIGNAHQLFVVVFDTR	95%	n+304 (+304)	77.45	25.30
2858	seq=translation; coord=6:31868128..31869802:-1; parent_transcript=GRMZM2G163406_T01; parent_gene=GRMZM2G163406	GRMZM2G163406_P01	TRUE	TRUE	yVSDFPVYDGR	95%	n+304 (+304)	46.13	25.00
2859	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01,GRMZM2G375504_P02, GRMZM2G375504_P03	TRUE	TRUE	aDLLVLLSDVDGLYGPPEPGSk	95%	n+304 (+304), K+304 (+304)	47.78	25.19
2860	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01,GRMZM2G375504_P02, GRMZM2G375504_P03	TRUE	TRUE	aPGLDDILLSLk	94%	n+304 (+304), K+304 (+304)	28.58	25.00
2861	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01,GRMZM2G375504_P02, GRMZM2G375504_P03	TRUE	TRUE	iLLDIADALEQNEDLIR	95%	n+304 (+304)	38.82	25.62
2862	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01,GRMZM2G375504_P02, GRMZM2G375504_P03	TRUE	TRUE	IcETVESLLDLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.10	25.50
2863	seq=translation; coord=8:95715355..95726032:1; parent_transcript=GRMZM2G375504_T01; parent_gene=GRMZM2G375504	GRMZM2G375504_P01,GRMZM2G375504_P02, GRMZM2G375504_P03	TRUE	TRUE	IDDVIDLVIPR	95%	n+304 (+304)	50.16	26.34
2864	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	TRUE	TRUE	aALSDFDR	95%	n+304 (+304)	37.87	25.00
2865	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	TRUE	TRUE	aLVDAPDMVR	93%	n+304 (+304)	29.76	25.00
2866	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	TRUE	TRUE	aMEEADVk	95%	n+304 (+304), K+304 (+304)	37.29	25.42
2867	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	TRUE	TRUE	IVVIVDVVDQNR	95%	n+304 (+304)	78.08	25.69
2868	seq=translation; coord=7:147132517..147134161:-1; parent_transcript=GRMZM2G168330_T02; parent_gene=GRMZM2G168330	GRMZM2G168330_P02	TRUE	TRUE	wENSSWGk	89%	n+304 (+304), K+304 (+304)	25.81	25.00
2869	seq=translation; coord=1:60163114..60165406:1; parent_transcript=GRMZM2G000923_T01; parent_gene=GRMZM2G000923	GRMZM2G000923_P01,GRMZM2G000923_P02, GRMZM2G465333_P01	TRUE	TRUE	dIELVMTQASVSRPk	93%	n+304 (+304), K+304 (+304)	27.85	25.24

2870	seq=translation; coord=1:60163114..60165406:1; parent_transcript=GRMZM2G000923_T01; parent_gene=GRMZM2G000923	GRMZM2G000923_P01,GRMZM2G000923_P02, GRMZM2G465333_P01	TRUE	TRUE	iEDLSSQLQTQAAEQFk	95%	n+304 (+304), K+304 (+304)	44.20	25.80
2871	seq=translation; coord=1:60163114..60165406:1; parent_transcript=GRMZM2G000923_T01; parent_gene=GRMZM2G000923	GRMZM2G000923_P01,GRMZM2G000923_P02, GRMZM2G465333_P01	TRUE	TRUE	sPNSDTYVIFGEAk	95%	n+304 (+304), K+304 (+304)	38.31	25.74
2872	seq=translation; coord=1:60163114..60165406:1; parent_transcript=GRMZM2G000923_T01; parent_gene=GRMZM2G000923	GRMZM2G000923_P01,GRMZM2G000923_P02, GRMZM2G465333_P01	TRUE	TRUE	tAQTAEEELATQIEQQk	95%	n+304 (+304), K+304 (+304)	65.30	26.31
2873	seq=translation; coord=9:107209042..107212141:1; parent_transcript=GRMZM2G172357_T01; parent_gene=GRMZM2G172357	GRMZM2G172357_P01,GRMZM2G172357_P02, GRMZM2G172357_P05,GRMZM2G172357_P06	TRUE	TRUE	eDGSEIQDALLEIVGR	95%	n+304 (+304)	52.86	25.01
2874	seq=translation; coord=9:107209042..107212141:1; parent_transcript=GRMZM2G172357_T01; parent_gene=GRMZM2G172357	GRMZM2G172357_P01,GRMZM2G172357_P02, GRMZM2G172357_P05,GRMZM2G172357_P06	TRUE	TRUE	ILNIGVk	93%	n+304 (+304), K+304 (+304)	27.22	25.00
2875	seq=translation; coord=9:107209042..107212141:1; parent_transcript=GRMZM2G172357_T01; parent_gene=GRMZM2G172357	GRMZM2G172357_P01,GRMZM2G172357_P02, GRMZM2G172357_P05,GRMZM2G172357_P06	TRUE	TRUE	tVPQVFVHGk	95%	n+304 (+304), K+304 (+304)	30.83	25.00
2876	seq=translation; coord=1:293135180..293138761:1; parent_transcript=GRMZM2G061900_T01; parent_gene=GRMZM2G061900	GRMZM2G061900_P01,GRMZM2G061900_P02, GRMZM2G156476_P01,GRMZM2G156476_P02	TRUE	TRUE	aDYDYLIK	90%	n+304 (+304), K+304 (+304)	25.53	25.00
2877	seq=translation; coord=1:293135180..293138761:1; parent_transcript=GRMZM2G061900_T01; parent_gene=GRMZM2G061900	GRMZM2G061900_P01,GRMZM2G061900_P02, GRMZM2G156476_P01,GRMZM2G156476_P02	TRUE	TRUE	gQALADEYGik	95%	n+304 (+304), K+304 (+304)	44.31	25.49
2878	seq=translation; coord=1:293135180..293138761:1; parent_transcript=GRMZM2G061900_T01; parent_gene=GRMZM2G061900	GRMZM2G061900_P01,GRMZM2G061900_P02, GRMZM2G156476_P01,GRMZM2G156476_P02	TRUE	TRUE	tNLNVEQVFFSIAR	95%	n+304 (+304)	42.70	25.25
2879	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	aLWFSPTNDGYSGTGYGLPR	95%	n+304 (+304), iTRAQ8plex (+304)	28.78	25.00
2880	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	aPTDPLPk	95%	n+304 (+304), K+304 (+304)	32.76	25.76
2881	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	aVISNMEk	95%	n+304 (+304), K+304 (+304)	34.37	26.58
2882	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	gADLFFR	95%	n+304 (+304)	33.18	25.00
2883	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	iFISELLVDELTTQSQEIIHK	95%	n+304 (+304), K+304 (+304)	38.19	25.00
2884	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	ILLPQFk	93%	n+304 (+304), K+304 (+304)	28.36	25.00
2885	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	INSEGILK	95%	n+304 (+304), K+304 (+304)	41.50	25.49
2886	seq=translation; coord=1:234307913..234320907:1; parent_transcript=GRMZM2G008607_T01; parent_gene=GRMZM2G008607	GRMZM2G008607_P01	TRUE	TRUE	sYIEFAER	92%	n+304 (+304)	27.48	25.00
2887	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	aLAADDRVEIcQLPVGdGVTLcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	31.64	25.44

2888	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	eGPALPVLDDLIAEEK	95%	n+304 (+304), K+304 (+304)	39.83	25.71
2889	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	hPWNLMTTSADEGQFLNMLIK	95%	n+304 (+304), K+304 (+304)	29.19	25.00
2890	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	sDDLQYILDTSVYPR	95%	n+304 (+304)	53.92	25.00
2891	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	sDDLQYILDTSVYPR	95%	n+304 (+304), iTRAQ8plex (+304)	30.36	25.21
2892	seq=translation; coord=6:79193305..79195490:1; parent_transcript=GRMZM2G127948_T01; parent_gene=GRMZM2G127948	GRMZM2G127948_P01	TRUE	TRUE	vElcQLPVG DGVTLCr	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	66.78	25.77
2893	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	aSALPASccSGVvk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	41.37	25.25
2894	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	cGVSVGFPIsmSTDcNk	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	59.85	25.00
2895	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	cGVSVGFPIsmSTDcNk	95%	Carbamidomethyl (+57), n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304)	41.13	25.00
2896	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	sLANSvk	87%	n+304 (+304), K+304 (+304)	26.41	25.85
2897	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	sVNMGT VATIPGk	92%	n+304 (+304), K+304 (+304)	27.73	26.15
2898	seq=translation; coord=3:231823510..231824603:1; parent_transcript=GRMZM2G107839_T01; parent_gene=GRMZM2G107839	GRMZM2G107839_P01,GRMZM2G107839_P02	TRUE	TRUE	sVNmGT VATIPGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	43.79	26.00
2899	seq=translation; coord=4:216707047..216710020:-1; parent_transcript=GRMZM2G091715_T01; parent_gene=GRMZM2G091715	GRMZM2G091715_P01,GRMZM2G091715_P03, GRMZM2G175818_P02	TRUE	TRUE	qLALPDHTEVcGESk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	49.50	25.51
2900	seq=translation; coord=4:216707047..216710020:-1; parent_transcript=GRMZM2G091715_T01; parent_gene=GRMZM2G091715	GRMZM2G091715_P01,GRMZM2G091715_P03, GRMZM2G175818_P02	TRUE	TRUE	qLALPDHTEVcGESk	95%	Pyro-cmC (-17), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.17	25.00
2901	seq=translation; coord=4:239151749..239155703:-1; parent_transcript=GRMZM2G024310_T01; parent_gene=GRMZM2G024310	GRMZM2G024310_P01	TRUE	TRUE	nMATLMAEFdk	95%	n+304 (+304), K+304 (+304)	48.29	25.00
2902	seq=translation; coord=9:145346839..145349218:-1; parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225	GRMZM2G067225_P01	TRUE	TRUE	dRLDFYFQGQdk	95%	n+304 (+304), K+304 (+304)	27.25	25.00
2903	seq=translation; coord=9:145346839..145349218:-1; parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225	GRMZM2G067225_P01	TRUE	TRUE	dVPGSYGLPLVGAVR	95%	n+304 (+304)	36.90	25.99
2904	seq=translation; coord=9:145346839..145349218:-1; parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225	GRMZM2G067225_P01	TRUE	TRUE	kDLLVESHDAVFQVR	95%	K+304 (+304), n+304 (+304)	37.18	25.30

2905	seq=translation; coord=9:145346839..145349218:-1; parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	kGEMLFGYQPcAtk	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.27	26.62
2906	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	mNVPPGPFMAR	89%	n+304 (+304)	26.63	25.00
2907	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	sFPVLFDMdk	95%	n+304 (+304), K+304 (+304)	38.77	25.55
2908	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	sNFSSLLATVEAELak	95%	n+304 (+304), K+304 (+304)	36.10	25.80
2909	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	sVWVESLR	94%	n+304 (+304)	32.11	25.72
2910	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=9:145346839..145349218:-1;	GRMZM2G067225_P01	TRUE	TRUE	vFGDTAGDFVPDR	95%	n+304 (+304)	51.01	25.00
2911	parent_transcript=GRMZM2G067225_T01; parent_gene=GRMZM2G067225 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G067225_P01	TRUE	TRUE	vVAVLDAk	88%	n+304 (+304), K+304 (+304)	28.58	27.10
2912	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	aDLLLALGVR	95%	n+304 (+304)	31.91	25.00
2913	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	diQQQMAVPVWDkPMSLPGYIAR	95%	n+304 (+304), K+304 (+304)	30.74	25.26
2914	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	dVFAYPGGASMEIHQALTR	95%	n+304 (+304)	72.80	25.00
2915	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	hNYLVLDVDDIPR	95%	n+304 (+304)	58.19	25.43
2916	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	iVHVDIDPAEIGk	94%	n+304 (+304), K+304 (+304)	25.53	25.00
2917	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	kGADILVESLER	95%	K+304 (+304), n+304 (+304)	29.82	25.97
2918	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	IALQGMNALLEGSTSk	95%	n+304 (+304), K+304 (+304)	36.98	25.72
2919	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	IPKPPATELLEQVLR	95%	n+304 (+304), K+304 (+304)	39.71	25.00
2920	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	mIGTDAFQETPIVEVTR	95%	n+304 (+304)	65.82	25.01
2921	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=5:163984090..163986394:1;	GRMZM2G143008_P01	TRUE	TRUE	mLETPGPYLLDIIVPHQEHLVPMIPSGGAFk	95%	n+304 (+304), K+304 (+304)	26.17	25.00
2922	parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008	GRMZM2G143008_P01	TRUE	TRUE	sPVIANHLFR	95%	n+304 (+304)	57.29	25.73

2923	seq=translation; coord=5:163984090..163986394:1; parent_transcript=GRMZM2G143008_T01; parent_gene=GRMZM2G143008 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G143008_P01	TRUE	TRUE	vFVLNNQHLMGVVQWEDR	95%	n+304 (+304)	67.71	25.45
2924	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	aIVDSIIILIR	95%	n+304 (+304)	36.77	25.00
2925	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	eLSPSADEVIIIVTSSLMk	95%	n+304 (+304), K+304 (+304)	37.63	25.00
2926	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	eLTPAITVLQLFLSSSkPVLR	95%	n+304 (+304), K+304 (+304)	39.88	25.00
2927	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	iIDSTLLTQIER	95%	n+304 (+304)	59.16	25.00
2928	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	ILSSIEPFADFGk	95%	n+304 (+304), K+304 (+304)	39.81	25.81
2929	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	ILYLLNQGDFTK	95%	n+304 (+304), K+304 (+304)	43.14	25.00
2930	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=2:232101270..232109417:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	nAWENMDPETER	95%	n+304 (+304)	32.19	25.00
2931	parent_transcript=GRMZM2G036034_T01; parent_gene=GRMZM2G036034 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G036034_P01,GRMZM2G178618_P01	TRUE	TRUE	sSAPVELTEAETEYSNVVvk	95%	n+304 (+304), K+304 (+304)	32.25	25.29
2932	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	dTDHLFLELPLLR	95%	n+304 (+304)	50.67	26.26
2933	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	gIGVFGNDAk	95%	n+304 (+304), K+304 (+304)	30.79	25.99
2934	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	hPDADSLYVEEIDVGEDTPR	95%	n+304 (+304)	42.37	25.00
2935	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	sPWDFVPAGHR	95%	n+304 (+304)	37.77	25.00
2936	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	vELVEPPESAAGVER	95%	n+304 (+304)	63.27	25.67
2937	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=1:26684241..26696594:-1;	GRMZM2G099628_P02	TRUE	TRUE	vTFAGYSGEPEASLSGk	95%	n+304 (+304), K+304 (+304)	49.11	25.75
2938	parent_transcript=GRMZM2G099628_T02; parent_gene=GRMZM2G099628 seq=translation; coord=3:12189233..12194178:1;	GRMZM2G099628_P02	TRUE	TRUE	wGVVPVPEk	95%	n+304 (+304), K+304 (+304)	28.72	25.71
2939	parent_transcript=GRMZM2G054559_T01; parent_gene=GRMZM2G054559 seq=translation; coord=3:12189233..12194178:1;	GRMZM2G054559_P01,GRMZM2G054559_P08	TRUE	TRUE	eTWNVQLFR	90%	n+304 (+304)	27.26	25.00
2940	parent_transcript=GRMZM2G054559_T01; parent_gene=GRMZM2G054559	GRMZM2G054559_P01,GRMZM2G054559_P08	TRUE	TRUE	iVSFIGGIDLcDGR	95%	n+304 (+304), Carbamidomethyl (+57)	31.98	25.00

2941	seq=translation; coord=3:12189233..12194178:1; parent_transcript=GRMZM2G054559_T01; parent_gene=GRMZM2G054559	GRMZM2G054559_P01,GRMZM2G054559_P08	TRUE	TRUE	qEGEYEPEEHPEPDTDIYR	95%	n+304 (+304)	39.28	25.00
2942	seq=translation; coord=3:12189233..12194178:1; parent_transcript=GRMZM2G054559_T01; parent_gene=GRMZM2G054559	GRMZM2G054559_P01,GRMZM2G054559_P08	TRUE	TRUE	sIDGGAAGFGFPETPEEAAR	95%	n+304 (+304)	56.64	25.00
2943	seq=translation; coord=2:31644513..31646214:-1; parent_transcript=GRMZM2G083253_T02; parent_gene=GRMZM2G083253	GRMZM2G083253_P02,GRMZM2G083253_P04, GRMZM2G083253_P05,GRMZM2G083253_P06, GRMZM2G166659_P01,GRMZM2G166659_P04, GRMZM2G166659_P05	TRUE	TRUE	iEDNNTLVFIVDLK	95%	n+304 (+304), K+304 (+304)	32.50	25.09
2944	seq=translation; coord=2:31644513..31646214:-1; parent_transcript=GRMZM2G083253_T02; parent_gene=GRMZM2G083253	GRMZM2G083253_P02,GRMZM2G083253_P04, GRMZM2G083253_P05,GRMZM2G083253_P06, GRMZM2G166659_P01,GRMZM2G166659_P04, GRMZM2G166659_P05	TRUE	TRUE	IDQYQILK	95%	n+304 (+304), K+304 (+304)	32.72	25.00
2945	seq=translation; coord=2:31644513..31646214:-1; parent_transcript=GRMZM2G083253_T02; parent_gene=GRMZM2G083253	GRMZM2G083253_P02,GRMZM2G083253_P04, GRMZM2G083253_P05,GRMZM2G083253_P06, GRMZM2G166659_P01,GRMZM2G166659_P04, GRMZM2G166659_P05	TRUE	TRUE	ITPDYDALDVANK	95%	n+304 (+304), K+304 (+304)	47.28	25.77
2946	seq=translation; coord=7:150542721..150550925:1; parent_transcript=GRMZM2G138220_T01; parent_gene=GRMZM2G138220	GRMZM2G138220_P01,GRMZM2G171628_P01	TRUE	TRUE	aEAQIGVDVHSALNAALTG	95%	n+304 (+304)	44.76	25.00
2947	seq=translation; coord=7:150542721..150550925:1; parent_transcript=GRMZM2G138220_T01; parent_gene=GRMZM2G138220	GRMZM2G138220_P01,GRMZM2G171628_P01	TRUE	TRUE	gLAEFTAK	93%	n+304 (+304), K+304 (+304)	29.39	26.80
2948	seq=translation; coord=7:150542721..150550925:1; parent_transcript=GRMZM2G138220_T01; parent_gene=GRMZM2G138220	GRMZM2G138220_P01,GRMZM2G171628_P01	TRUE	TRUE	IGSASTDLEK	95%	n+304 (+304), K+304 (+304)	41.85	26.23
2949	seq=translation; coord=7:150542721..150550925:1; parent_transcript=GRMZM2G138220_T01; parent_gene=GRMZM2G138220	GRMZM2G138220_P01,GRMZM2G171628_P01	TRUE	TRUE	ITVNFVLPYK	95%	n+304 (+304), K+304 (+304)	31.77	25.00
2950	seq=translation; coord=9:37790950..37793111:1; parent_transcript=GRMZM2G118873_T01; parent_gene=GRMZM2G118873	GRMZM2G118873_P01,GRMZM2G118873_P02, GRMZM2G121308_P02	TRUE	TRUE	sGSTNLQAPLSVR	95%	n+304 (+304)	58.20	25.89
2951	seq=translation; coord=9:37790950..37793111:1; parent_transcript=GRMZM2G118873_T01; parent_gene=GRMZM2G118873	GRMZM2G118873_P01,GRMZM2G118873_P02, GRMZM2G121308_P02	TRUE	TRUE	sWGAUVWQYK	91%	n+304 (+304), K+304 (+304)	27.37	26.30
2952	seq=translation; coord=9:37790950..37793111:1; parent_transcript=GRMZM2G118873_T01; parent_gene=GRMZM2G118873	GRMZM2G118873_P01,GRMZM2G118873_P02, GRMZM2G121308_P02	TRUE	TRUE	vLVASNVIPAGWQPGR	95%	n+304 (+304)	69.77	25.77
2953	seq=translation; coord=2:220832499..220836411:-1; parent_transcript=GRMZM2G148769_T01; parent_gene=GRMZM2G148769	GRMZM2G148769_P01,GRMZM2G148769_P02	TRUE	TRUE	gAFTAVLSGGSLIEALR	95%	n+304 (+304)	90.91	25.37
2954	seq=translation; coord=2:220832499..220836411:-1; parent_transcript=GRMZM2G148769_T01; parent_gene=GRMZM2G148769	GRMZM2G148769_P01,GRMZM2G148769_P02	TRUE	TRUE	wHVFWVDER	95%	n+304 (+304)	40.90	25.00
2955	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	TRUE	TRUE	aNNLVFVSGVLGLNPETR	95%	n+304 (+304)	30.12	25.55
2956	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	TRUE	TRUE	aPPALGPYSQAIK	95%	n+304 (+304), K+304 (+304)	33.34	25.00
2957	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	TRUE	TRUE	sTYQVAALPLNAR	95%	n+304 (+304)	50.00	25.25

2958	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	TRUE	TRUE	tTIMLADLQDFNk	90%	n+304 (+304), K+304 (+304)	26.05	25.49
2959	seq=translation; coord=7:153098952..153101687:1; parent_transcript=GRMZM2G117642_T02; parent_gene=GRMZM2G117642	GRMZM2G117642_P02	TRUE	TRUE	yFPVPAPAR	87%	n+304 (+304)	25.58	25.47
2960	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	aQTLGDTSSLEFMR	95%	n+304 (+304)	48.49	25.00
2961	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	aVELLYEAALISSGYTPSPAELGGk	95%	n+304 (+304), K+304 (+304)	34.28	25.00
2962	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	dIEVLYLIEPIDEVAIQNLQTYk	95%	n+304 (+304), K+304 (+304)	31.82	25.00
2963	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	gVVDSDNLPLNVSR	95%	n+304 (+304)	49.65	25.49
2964	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	iFEINPDHPIIk	91%	n+304 (+304), K+304 (+304)	25.50	25.00
2965	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	iYEMMAIALGGR	95%	n+304 (+304)	42.55	25.00
2966	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	tAPFLEk	95%	n+304 (+304), K+304 (+304)	32.57	26.22
2967	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	vFISDDFDGELFPR	95%	n+304 (+304)	50.52	25.00
2968	seq=translation; coord=4:197363864..197368446:-1; parent_transcript=GRMZM2G002220_T01; parent_gene=GRMZM2G002220	GRMZM2G002220_P01	TRUE	TRUE	yWDWELANETKPIWMR	93%	n+304 (+304), K+304 (+304)	26.66	25.00
2969	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	eMGMDAYR	88%	n+304 (+304)	26.22	25.00
2970	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	iGLAFDVMGR	95%	n+304 (+304)	43.50	25.00
2971	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	iGLAFDVmGR	87%	n+304 (+304), Oxidation (+16)	25.93	25.00
2972	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	sIVEDYTYFak	95%	n+304 (+304), K+304 (+304)	36.95	25.00
2973	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	vPYGTSFLDk	95%	n+304 (+304), K+304 (+304)	30.48	26.03
2974	seq=translation; coord=10:34232717..34238135:1; parent_transcript=GRMZM2G016890_T01; parent_gene=GRMZM2G016890	GRMZM2G016890_P01	TRUE	TRUE	yGIVYVDR	89%	n+304 (+304)	26.81	25.00
2975	seq=translation; coord=8:162756043..162756672:-1; parent_transcript=GRMZM2G170969_T01; parent_gene=GRMZM2G170969	GRMZM2G170969_P01	TRUE	TRUE	aIPSAcNLPNAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	54.00	25.50

2976	seq=translation; coord=8:162756043..162756672:-1; parent_transcript=GRMZM2G170969_T01; parent_gene=GRMZM2G170969	GRMZM2G170969_P01	TRUE	TRUE	nADFGcLcSNYWnk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	53.99	25.00
2977	seq=translation; coord=8:162756043..162756672:-1; parent_transcript=GRMZM2G170969_T01; parent_gene=GRMZM2G170969	GRMZM2G170969_P01	TRUE	TRUE	nTPYAScAk	93%	Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	29.31	25.00
2978	seq=translation; coord=8:162756043..162756672:-1; parent_transcript=GRMZM2G170969_T01; parent_gene=GRMZM2G170969	GRMZM2G170969_P01	TRUE	TRUE	qcAScSSGAPSQGccDALR	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	70.74	25.00
2979	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	eTDIVDWFIPVVK	95%	n+304 (+304), K+304 (+304)	34.47	26.00
2980	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	IAEEFGPEWAMQHIIQVLEK	95%	n+304 (+304), K+304 (+304)	42.05	25.62
2981	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	IGALcMQWLEDK	92%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	27.46	25.94
2982	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	mTILQAISLLAPVMGAETcQk	95%	Carbamidomethyl (+57), K+304 (+304)	52.54	25.00
2983	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	sALASVIMGMAPVLGk	95%	n+304 (+304), K+304 (+304)	35.70	25.20
2984	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	sLPVILDQSVVEK	95%	n+304 (+304), K+304 (+304)	32.23	25.00
2985	seq=translation; coord=9:24144173..24150987:-1; parent_transcript=GRMZM2G122135_T03; parent_gene=GRMZM2G122135	GRMZM2G122135_P03	TRUE	TRUE	tEIMSFDDLTDQDDQDSVR	95%	n+304 (+304)	35.05	25.00
2986	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	aSGATWYTAVPTIHQIILDR	95%	n+304 (+304)	40.20	25.34
2987	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	aVGQELAVLDEEGR	95%	n+304 (+304)	78.39	25.00
2988	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	fGWFHTGDIGVDDQGYVR	95%	n+304 (+304)	43.10	25.00
2989	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	fGWFHTGDIGVDDQGYVR	95%	n+304 (+304), iTRAQ8plex (+304)	27.27	25.00
2990	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	fSASTFWADMR	95%	n+304 (+304)	40.01	25.00
2991	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	gNPEANEAAGR	95%	n+304 (+304)	48.79	25.00
2992	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	IELTHAALDALVDAAAAR	95%	n+304 (+304)	64.30	26.16

2993	seq=translation; coord=8:163654067..163656422:-1; parent_transcript=GRMZM2G333861_T01; parent_gene=GRMZM2G333861	GRMZM2G333861_P01	TRUE	TRUE	scSASLAPAILER	95%	n+304 (+304), Carbamidomethyl (+57)	48.20	25.00
2994	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	aMIGQVAGGGR	95%	n+304 (+304)	34.21	25.50
2995	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	aTlSIGNVLPLR	95%	n+304 (+304)	39.12	25.00
2996	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	gAPLak	92%	n+304 (+304), K+304 (+304)	25.86	25.00
2997	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	gIPEGAVVcNVEHHVGDR	95%	n+304 (+304), Carbamidomethyl (+57)	71.59	25.00
2998	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	gVVTdVIHDPGR	95%	n+304 (+304)	46.42	25.11
2999	seq=translation; coord=3:127004080..127006073:-1; parent_transcript=GRMZM2G067456_T01; parent_gene=GRMZM2G067456	GRMZM2G067456_P01,GRMZM2G072729_P01, GRMZM2G072729_P02,GRMZM2G077851_P01	TRUE	TRUE	rATLSIGNVLPLR	95%	n+304 (+304)	52.67	25.00
3000	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	aLPNPGDYHWR	93%	n+304 (+304)	27.53	25.00
3001	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	dILSDFDNLLPk	95%	n+304 (+304), K+304 (+304)	47.02	26.61
3002	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	eGYTILVLSDR	95%	n+304 (+304)	50.34	25.67
3003	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	iPEFNELVHQNR	95%	n+304 (+304)	60.64	25.00
3004	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	mEPLPDGSMNPR	87%	n+304 (+304)	25.61	25.00
3005	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	mGHFVTVFER	95%	n+304 (+304)	39.18	25.00
3006	seq=translation; coord=3:208332821..208344531:1; parent_transcript=GRMZM2G085078_T01; parent_gene=GRMZM2G085078	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	sLLDSNLEDGk	91%	n+304 (+304), K+304 (+304)	26.38	25.44
3007	seq=translation; coord=5:154983595..154988021:1; parent_transcript=GRMZM2G167356_T01; parent_gene=GRMZM2G167356	GRMZM2G085078_P01,GRMZM2G085078_P02	TRUE	TRUE	vAESLGHVILGWR	92%	n+304 (+304)	27.59	25.68
3008	seq=translation; coord=5:154983595..154988021:1; parent_transcript=GRMZM2G167356_T01; parent_gene=GRMZM2G167356	GRMZM2G167356_P01,GRMZM2G167356_P02	TRUE	TRUE	dGASGYGDAGGEDVR	92%	n+304 (+304)	28.70	25.00
3009	seq=translation; coord=5:154983595..154988021:1; parent_transcript=GRMZM2G167356_T01; parent_gene=GRMZM2G167356	GRMZM2G167356_P01,GRMZM2G167356_P02	TRUE	TRUE	gFGFVTFESEDsVER	95%	n+304 (+304)	74.87	25.00
3010	seq=translation; coord=4:28340661..28347586:1; parent_transcript=GRMZM2G426591_T01; parent_gene=GRMZM2G426591	GRMZM2G426591_P01,GRMZM2G426591_P03, GRMZM2G426591_P04	TRUE	TRUE	qVFTPYGDVVHVk	95%	n+304 (+304), K+304 (+304)	40.11	25.80

3011	seq=translation; coord=4:28340661..28347586:1; parent_transcript=GRMZM2G426591_T01; parent_gene=GRMZM2G426591	GRMZM2G426591_P01,GRMZM2G426591_P03, GRMZM2G426591_P04	TRUE	TRUE	qVFTPYGDDVHVk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	48.23	25.30
3012	seq=translation; coord=4:28340661..28347586:1; parent_transcript=GRMZM2G426591_T01; parent_gene=GRMZM2G426591	GRMZM2G426591_P01,GRMZM2G426591_P03, GRMZM2G426591_P04	TRUE	TRUE	sSAEEALVILQGLTVGGQNVr	95%	n+304 (+304)	62.41	25.85
3013	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01,GRMZM2G108348_P03	TRUE	TRUE	hIDFSLSSPFGGPGAGR	95%	n+304 (+304)	46.43	25.00
3014	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01,GRMZM2G108348_P03	TRUE	TRUE	iFEGEALLR	90%	n+304 (+304)	27.56	25.00
3015	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01,GRMZM2G108348_P03	TRUE	TRUE	kASGGGDAGDEDEE	95%	K+304 (+304), n+304 (+304)	54.89	25.00
3016	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01,GRMZM2G108348_P03	TRUE	TRUE	IDYVLALTAENFLAR	95%	n+304 (+304)	31.76	25.42
3017	seq=translation; coord=3:135594596..135597030:-1; parent_transcript=GRMZM2G108348_T01; parent_gene=GRMZM2G108348	GRMZM2G108348_P01,GRMZM2G108348_P03	TRUE	TRUE	qIVNVPSFMVR	91%	n+304 (+304)	28.40	25.19
3018	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	aDVEAPEEHPGQADYWLR	95%	n+304 (+304)	54.21	25.00
3019	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	gFAVDVVPHEMk	95%	n+304 (+304), K+304 (+304)	31.34	25.91
3020	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	IIGVEYIVSR	95%	n+304 (+304)	36.38	25.00
3021	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	IPLGAPALMVSPQADPAAAVRPDLVR	90%	n+304 (+304)	25.23	25.00
3022	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	vLDMGAAAMQSLRPVrk	95%	n+304 (+304), K+304 (+304)	28.41	25.65
3023	seq=translation; coord=3:197717130..197718439:-1; parent_transcript=GRMZM2G043521_T01; parent_gene=GRMZM2G043521	GRMZM2G043521_P01	TRUE	TRUE	yGLSTEELR	90%	n+304 (+304)	26.64	25.00
3024	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	dFcLEQNIk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.82	25.26
3025	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	eGQIYLASPyTAAASALTGYVTDP	95%	n+304 (+304), iTRAQ8plex (+304)	28.48	25.00
3026	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	fVLDGEMPPYLLAk	95%	n+304 (+304), K+304 (+304)	31.64	25.12
3027	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	sMEFVGSTVESLTMEER	95%	n+304 (+304)	90.94	25.00
3028	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	tEDFLAAAk	95%	n+304 (+304), K+304 (+304)	37.28	26.40

3029	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	tSVDYQPVYSDAEAR	95%	n+304 (+304)	72.66	25.00
3030	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	vPTFLVPATQk	95%	n+304 (+304), K+304 (+304)	31.40	25.00
3031	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	vVIIPDHYIFTSER	95%	n+304 (+304)	55.21	25.00
3032	seq=translation; coord=5:72919285..72923425:-1; parent_transcript=GRMZM2G370852_T01; parent_gene=GRMZM2G370852	GRMZM2G370852_P01,GRMZM2G370852_P02, GRMZM2G370852_P03	TRUE	TRUE	vWMDVYSLPVPGSGGk	95%	n+304 (+304), K+304 (+304)	40.45	25.84
3033	seq=translation; coord=4:175134158..175138628:1; parent_transcript=GRMZM2G070239_T01; parent_gene=GRMZM2G070239	GRMZM2G070239_P01,GRMZM2G070239_P02	TRUE	TRUE	kPPGFADFDDR	95%	K+304 (+304), n+304 (+304)	35.23	25.83
3034	seq=translation; coord=4:175134158..175138628:1; parent_transcript=GRMZM2G070239_T01; parent_gene=GRMZM2G070239	GRMZM2G070239_P01,GRMZM2G070239_P02	TRUE	TRUE	vTSGELEDEFr	95%	n+304 (+304)	60.44	25.00
3035	seq=translation; coord=4:175134158..175138628:1; parent_transcript=GRMZM2G070239_T01; parent_gene=GRMZM2G070239	GRMZM2G070239_P01,GRMZM2G070239_P02	TRUE	TRUE	vYVGnLDAR	90%	n+304 (+304)	27.68	25.00
3036	seq=translation; coord=4:179822113..179823382:-1; parent_transcript=GRMZM2G007729_T02; parent_gene=GRMZM2G007729	GRMZM2G007729_P02	TRUE	TRUE	dYAVPSLFSDIFR	95%	n+304 (+304)	39.40	25.00
3037	seq=translation; coord=4:179822113..179823382:-1; parent_transcript=GRMZM2G007729_T02; parent_gene=GRMZM2G007729	GRMZM2G007729_P02	TRUE	TRUE	dYAVPSLFSDIFRDPLSAPHISGR	95%	n+304 (+304)	32.94	25.07
3038	seq=translation; coord=4:179822113..179823382:-1; parent_transcript=GRMZM2G007729_T02; parent_gene=GRMZM2G007729	GRMZM2G007729_P02	TRUE	TRUE	ILNLVDDLAVAAPGR	95%	n+304 (+304)	49.90	25.85
3039	seq=translation; coord=4:179822113..179823382:-1; parent_transcript=GRMZM2G007729_T02; parent_gene=GRMZM2G007729	GRMZM2G007729_P02	TRUE	TRUE	vDMPGLGk	95%	n+304 (+304), K+304 (+304)	30.81	25.15
3040	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	dDASVVfAYYk	95%	n+304 (+304), K+304 (+304)	42.56	25.38
3041	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	dLQFFVGESMk	95%	n+304 (+304), K+304 (+304)	39.43	25.45
3042	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	mLVYQDLLSGDELLSDSFTYk	95%	n+304 (+304), K+304 (+304)	49.58	25.00
3043	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	mLVYQDLLSGDELLSDSFTYk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	28.07	25.00
3044	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	nLTAVLEPEk	95%	n+304 (+304), K+304 (+304)	32.74	25.04
3045	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	sFVSYIk	95%	n+304 (+304), K+304 (+304)	37.42	25.00
3046	seq=translation; coord=5:68020016..68022909:-1; parent_transcript=GRMZM2G108474_T01; parent_gene=GRMZM2G108474	GRMZM2G108474_P01	TRUE	TRUE	vVDIVDTFR	95%	n+304 (+304)	38.65	25.00

3047	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	TRUE	TRUE	aYDGTDPskPIYVSVR	95%	n+304 (+304), K+304 (+304)	42.03	25.91
3048	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	TRUE	TRUE	dEADVSGDLSGLTDk	95%	n+304 (+304), K+304 (+304)	55.21	25.00
3049	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	TRUE	TRUE	gFYGPGGAYAVFAGR	95%	n+304 (+304)	54.23	25.00
3050	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	TRUE	TRUE	gFyGPGGAYAVFAGR	95%	n+304 (+304), iTRAQ8plex (+304)	47.88	25.74
3051	seq=translation; coord=5:213336713..213337573:1; parent_transcript=GRMZM2G119782_T01; parent_gene=GRMZM2G119782	GRMZM2G119782_P01	TRUE	TRUE	yPVVAR	87%	n+304 (+304)	25.04	25.00
3052	seq=translation; coord=3:215654139..215663757:-1; parent_transcript=GRMZM2G125193_T01; parent_gene=GRMZM2G125193	GRMZM2G125193_P01	TRUE	TRUE	eAMDKGELVSDNLVVGIIDEAMk	95%	n+304 (+304), K+304 (+304)	29.95	25.00
3053	seq=translation; coord=3:215654139..215663757:-1; parent_transcript=GRMZM2G125193_T01; parent_gene=GRMZM2G125193	GRMZM2G125193_P01	TRUE	TRUE	gELVSDNLVVGIIDEAMk	95%	n+304 (+304), K+304 (+304)	57.31	25.90
3054	seq=translation; coord=3:215654139..215663757:-1; parent_transcript=GRMZM2G125193_T01; parent_gene=GRMZM2G125193	GRMZM2G125193_P01	TRUE	TRUE	vLNFAIDDAILEER	95%	n+304 (+304)	74.86	25.35
3055	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	aVAMFQALAVk	95%	n+304 (+304), K+304 (+304)	52.83	25.00
3056	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	dDSALVASMR	95%	n+304 (+304)	33.07	25.00
3057	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	dWSTGAGDLVEPVAR	95%	n+304 (+304)	66.62	25.00
3058	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	IWDEAQADAGYTVLTPTPHLDLGPR	95%	n+304 (+304)	73.51	25.01
3059	seq=translation; coord=7:134970635..134972839:-1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	sVTGLELPVQPVHTLlcYWK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.08	25.33
3060	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G052266_T01; parent_gene=GRMZM2G052266	GRMZM2G052266_P01,GRMZM2G052266_P02	TRUE	TRUE	vLLLER	95%	n+304 (+304)	29.99	25.00
3061	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	TRUE	TRUE	fDYILTQQAFVAVDk	95%	n+304 (+304), K+304 (+304)	34.18	25.95
3062	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	TRUE	TRUE	gILLGAVHGIVEALFR	95%	n+304 (+304)	74.97	25.00
3063	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	TRUE	TRUE	gILLGAVHGIVEALFRR	94%	n+304 (+304)	25.28	25.00
3064	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	TRUE	TRUE	rYTEQGMDEESAYk	95%	n+304 (+304), K+304 (+304)	36.00	25.00

3065	seq=translation; coord=3:202362837..202365659:1; parent_transcript=GRMZM2G161868_T01; parent_gene=GRMZM2G161868	GRMZM2G161868_P01	TRUE	TRUE	yTEQGMDEESAYk	95%	n+304 (+304), K+304 (+304)	49.78	25.00
3066	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	TRUE	TRUE	dAGRDWDIDYEMR	91%	n+304 (+304)	25.22	25.00
3067	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	TRUE	TRUE	dWDIDYEMR	95%	n+304 (+304)	39.86	25.00
3068	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	TRUE	TRUE	tVASGTVPDPGSLAGDGATTR	95%	n+304 (+304)	47.03	25.00
3069	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	TRUE	TRUE	vGLTVDLPPVVGk	95%	n+304 (+304), K+304 (+304)	60.08	25.00
3070	seq=translation; coord=8:60632430..60633244:-1; parent_transcript=GRMZM2G050607_T01; parent_gene=GRMZM2G050607	GRMZM2G050607_P01	TRUE	TRUE	vPYDFLVSLAk	95%	n+304 (+304), K+304 (+304)	34.99	25.00
3071	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	aHLLFDLHQAVDGLR	94%	n+304 (+304)	25.90	25.35
3072	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	aIGDLIGVVK	95%	n+304 (+304), K+304 (+304)	38.19	25.00
3073	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	iEELVGVPVHYIGVGPGR	95%	n+304 (+304)	56.66	25.47
3074	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	IDVLSGLSEIk	95%	n+304 (+304), K+304 (+304)	37.50	25.00
3075	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	IEPFIADTVHVLNESIk	95%	n+304 (+304), K+304 (+304)	33.37	25.63
3076	seq=translation; coord=1:15773796..15778609:-1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	IVDVLAPR	90%	n+304 (+304)	28.63	25.99
3077	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G119852_T01; parent_gene=GRMZM2G119852	GRMZM2G119852_P01	TRUE	TRUE	vSSLTQVSGVLGSQWGDEGk	95%	n+304 (+304), K+304 (+304)	65.53	25.25
3078	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	TRUE	TRUE	fcSDFTASDGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.85	25.00
3079	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	TRUE	TRUE	gVPFTTSAGPcR	95%	n+304 (+304), Carbamidomethyl (+57)	52.17	25.00
3080	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	TRUE	TRUE	iADkESEcDISILNIQVGLIR	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	42.61	25.09
3081	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	TRUE	TRUE	ISAADNDVFATVHPFVIR	95%	n+304 (+304)	76.20	25.84
3082	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345	GRMZM2G166345_P02	TRUE	TRUE	qHALLDNLNQELSQk	95%	n+304 (+304), K+304 (+304)	48.82	25.22

3083	seq=translation; coord=8:170316262..170329055:1; parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345 seq=translation; coord=8:170316262..170329055:1;	GRMZM2G166345_P02	TRUE	TRUE	qHALLDNLNQELSQk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	45.83	25.43
3084	parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345 seq=translation; coord=8:170316262..170329055:1;	GRMZM2G166345_P02	TRUE	TRUE	sVLLGDGfK	95%	n+304 (+304), K+304 (+304)	33.34	26.16
3085	parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345 seq=translation; coord=8:170316262..170329055:1;	GRMZM2G166345_P02	TRUE	TRUE	wMDYIQNTVGAGTTLQk	94%	n+304 (+304), K+304 (+304)	29.14	26.04
3086	parent_transcript=GRMZM2G166345_T02; parent_gene=GRMZM2G166345 seq=translation; coord=5:75935116..75939320:-1;	GRMZM2G166345_P02	TRUE	TRUE	ycSPDDLtNR	94%	n+304 (+304), Carbamidomethyl (+57)	30.94	25.00
3087	parent_transcript=GRMZM2G019121_T01; parent_gene=GRMZM2G019121 seq=translation; coord=5:75935116..75939320:-1;	GRMZM2G019121_P01	TRUE	TRUE	aiPTLPINLEDAAR	95%	n+304 (+304)	38.40	26.56
3088	parent_transcript=GRMZM2G019121_T01; parent_gene=GRMZM2G019121 seq=translation; coord=5:75935116..75939320:-1;	GRMZM2G019121_P01	TRUE	TRUE	aTTQQVEIQVR	95%	n+304 (+304)	43.86	26.51
3089	parent_transcript=GRMZM2G019121_T01; parent_gene=GRMZM2G019121 seq=translation; coord=5:75935116..75939320:-1;	GRMZM2G019121_P01	TRUE	TRUE	gEEIISGAQR	88%	n+304 (+304)	27.64	26.16
3090	parent_transcript=GRMZM2G019121_T01; parent_gene=GRMZM2G019121 seq=translation; coord=6:158451653..158457625:-1;	GRMZM2G019121_P01	TRUE	TRUE	qMAISGGFER	90%	n+304 (+304)	26.38	25.00
3091	parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396 seq=translation; coord=6:158451653..158457625:-1;	GRMZM2G176396_P01,GRMZM2G176396_P02, GRMZM2G176396_P03	TRUE	TRUE	aWPEAEfK	89%	n+304 (+304), K+304 (+304)	26.82	25.19
3092	parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396 seq=translation; coord=6:158451653..158457625:-1;	GRMZM2G176396_P01,GRMZM2G176396_P02, GRMZM2G176396_P03	TRUE	TRUE	dFIPEDER	89%	n+304 (+304)	25.79	25.00
3093	parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396 seq=translation; coord=6:158451653..158457625:-1;	GRMZM2G176396_P01,GRMZM2G176396_P02, GRMZM2G176396_P03	TRUE	TRUE	gEDDEFSLAFAR	95%	n+304 (+304)	43.61	25.00
3094	parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396 seq=translation; coord=6:158451653..158457625:-1;	GRMZM2G176396_P01,GRMZM2G176396_P02, GRMZM2G176396_P03	TRUE	TRUE	gFLPSDSFLLDNVdk	95%	n+304 (+304), K+304 (+304)	38.75	25.12
3095	parent_transcript=GRMZM2G176396_T01; parent_gene=GRMZM2G176396 seq=translation; coord=5:163209220..163228678:1;	GRMZM2G176396_P01,GRMZM2G176396_P02, GRMZM2G176396_P03	TRUE	TRUE	rGEDDEFSLAFAR	95%	n+304 (+304)	61.19	25.00
3096	parent_transcript=GRMZM2G012690_T01; parent_gene=GRMZM2G012690 seq=translation; coord=5:163209220..163228678:1;	GRMZM2G012690_P01	TRUE	TRUE	eVLTLEGMGFSTAR	95%	n+304 (+304)	49.71	25.00
3097	parent_transcript=GRMZM2G012690_T01; parent_gene=GRMZM2G012690 seq=translation; coord=5:163209220..163228678:1;	GRMZM2G012690_P01	TRUE	TRUE	IEGDEFLLAR	95%	n+304 (+304)	40.64	25.56
3098	parent_transcript=GRMZM2G012690_T01; parent_gene=GRMZM2G012690 seq=translation; coord=4:161070624..161077204:-1;	GRMZM2G012690_P01	TRUE	TRUE	vGNLHGIEFLcGFek	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.71	25.31
3099	parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875 seq=translation; coord=4:161070624..161077204:-1;	GRMZM2G015875_P01	TRUE	TRUE	dFELELER	95%	n+304 (+304)	33.94	25.00
3100	parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	eQEESLQEWek	95%	n+304 (+304), K+304 (+304)	32.46	25.00

3101	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	gWTGWSTPTPANQR	95%	n+304 (+304)	46.24	25.00
3102	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	kLWSFFTT	93%	K+304 (+304), n+304 (+304)	28.72	26.19
3103	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	mILGEVFEEK	95%	n+304 (+304), K+304 (+304)	40.77	26.54
3104	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	qTAGAVTDAPGER	95%	n+304 (+304)	50.99	25.00
3105	seq=translation; coord=4:161070624..161077204:-1; parent_transcript=GRMZM2G015875_T01; parent_gene=GRMZM2G015875	GRMZM2G015875_P01	TRUE	TRUE	tDDQGDTVk	95%	n+304 (+304), K+304 (+304)	38.27	25.00
3106	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	TRUE	TRUE	aYGELPDTLR	95%	n+304 (+304)	33.85	25.00
3107	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	TRUE	TRUE	eDGQEYAQVTR	95%	n+304 (+304)	42.16	25.00
3108	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	TRUE	TRUE	kVWIAAGDIVLVGLR	95%	K+304 (+304), n+304 (+304)	48.57	25.00
3109	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	TRUE	TRUE	vWIAAGDIVLVGLR	87%	n+304 (+304)	25.88	25.00
3110	seq=translation; coord=6:71732900..71733812:-1; parent_transcript=GRMZM2G101859_T01; parent_gene=GRMZM2G101859	GRMZM2G101859_P01	TRUE	TRUE	yMNDEAR	89%	n+304 (+304)	26.09	25.00
3111	seq=translation; coord=7:165243551..165244574:-1; parent_transcript=GRMZM2G030731_T01; parent_gene=GRMZM2G030731	GRMZM2G030731_P01,GRMZM2G096123_P01	TRUE	TRUE	aAGGAVVLTa	88%	n+304 (+304)	28.25	27.12
3112	seq=translation; coord=7:165243551..165244574:-1; parent_transcript=GRMZM2G030731_T01; parent_gene=GRMZM2G030731	GRMZM2G030731_P01,GRMZM2G096123_P01	TRUE	TRUE	aPQIDVTQFGYFk	95%	n+304 (+304), K+304 (+304)	53.11	25.66
3113	seq=translation; coord=7:165243551..165244574:-1; parent_transcript=GRMZM2G030731_T01; parent_gene=GRMZM2G030731	GRMZM2G030731_P01,GRMZM2G096123_P01	TRUE	TRUE	fYcPAVNIER	95%	n+304 (+304), Carbamidomethyl (+57)	32.31	25.00
3114	seq=translation; coord=2:192576240..192582957:1; parent_transcript=GRMZM2G097226_T01; parent_gene=GRMZM2G097226	GRMZM2G097226_P01,GRMZM2G097226_P02	TRUE	TRUE	mVGyALQAAEILSk	95%	n+304 (+304), K+304 (+304)	45.31	25.21
3115	seq=translation; coord=2:192576240..192582957:1; parent_transcript=GRMZM2G097226_T01; parent_gene=GRMZM2G097226	GRMZM2G097226_P01,GRMZM2G097226_P02	TRUE	TRUE	vLTPYSSEDAR	86%	n+304 (+304)	25.39	25.00
3116	seq=translation; coord=4:230189571..230193924:-1; parent_transcript=GRMZM2G161969_T01; parent_gene=GRMZM2G161969	GRMZM2G161969_P01	TRUE	TRUE	aDIEDYLak	95%	n+304 (+304), K+304 (+304)	39.40	26.39
3117	seq=translation; coord=4:230189571..230193924:-1; parent_transcript=GRMZM2G161969_T01; parent_gene=GRMZM2G161969	GRMZM2G161969_P01	TRUE	TRUE	aQPEPSQPk	95%	n+304 (+304), K+304 (+304)	35.72	26.61
3118	seq=translation; coord=4:230189571..230193924:-1; parent_transcript=GRMZM2G161969_T01; parent_gene=GRMZM2G161969	GRMZM2G161969_P01	TRUE	TRUE	eAFAAPGLGYVDIPNAQIR	95%	n+304 (+304)	31.76	25.37

3119	seq=translation; coord=4:230189571..230193924:-1; parent_transcript=GRMZM2G161969_T01; parent_gene=GRMZM2G161969	GRMZM2G161969_P01	TRUE	TRUE	gLGTIAEEVk	95%	n+304 (+304), K+304 (+304)	58.27	25.42
3120	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	TRUE	TRUE	aAHLK	93%	n+304 (+304), K+304 (+304)	26.52	25.00
3121	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	TRUE	TRUE	aNVVTPGTGFGPGGEGFVR	95%	n+304 (+304)	91.29	25.01
3122	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	TRUE	TRUE	IQAGYLFPEIAR	95%	n+304 (+304)	41.01	26.23
3123	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	TRUE	TRUE	nAPYVWVHFPGR	95%	n+304 (+304)	55.93	25.00
3124	seq=translation; coord=1:46852658..46861936:1; parent_transcript=GRMZM2G010328_T01; parent_gene=GRMZM2G010328	GRMZM2G010328_P01	TRUE	TRUE	nSWDVFAEILEK	95%	n+304 (+304), K+304 (+304)	51.14	25.60
3125	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	dLSQPIDVTLDDATVAAFYGTGSK	95%	n+304 (+304), K+304 (+304)	32.39	25.00
3126	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	dLYAEAAAQR	95%	n+304 (+304)	47.47	25.00
3127	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	eSEVLSLFATIINK	95%	n+304 (+304), K+304 (+304)	40.46	25.00
3128	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	fFALQVLESVIK	95%	n+304 (+304), K+304 (+304)	37.02	25.00
3129	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	fLVMVIR	87%	n+304 (+304)	25.17	25.00
3130	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	ILSEEIFDFSR	95%	n+304 (+304)	46.37	25.00
3131	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	INIILVQVLK	95%	n+304 (+304), K+304 (+304)	49.72	25.00
3132	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	IVIDSINWAFR	95%	n+304 (+304)	31.78	25.98
3133	seq=translation; coord=5:741455..752529:1; parent_transcript=GRMZM2G022258_T01; parent_gene=GRMZM2G022258	GRMZM2G022258_P01,GRMZM2G022258_P02	TRUE	TRUE	nIAETGLSLLLEILK	95%	n+304 (+304), K+304 (+304)	32.57	25.00
3134	seq=translation; coord=2:133839420..133842192:1; parent_transcript=GRMZM2G111143_T01; parent_gene=GRMZM2G111143	GRMZM2G111143_P01,GRMZM2G111143_P02, GRMZM2G111143_P03	TRUE	TRUE	aEAGQVGVGPPEAR	95%	n+304 (+304)	39.06	25.00
3135	seq=translation; coord=2:133839420..133842192:1; parent_transcript=GRMZM2G111143_T01; parent_gene=GRMZM2G111143	GRMZM2G111143_P01,GRMZM2G111143_P02, GRMZM2G111143_P03	TRUE	TRUE	nFGIFNTDLTPK	93%	n+304 (+304), K+304 (+304)	29.22	26.80
3136	seq=translation; coord=2:133839420..133842192:1; parent_transcript=GRMZM2G111143_T01; parent_gene=GRMZM2G111143	GRMZM2G111143_P01,GRMZM2G111143_P02, GRMZM2G111143_P03	TRUE	TRUE	tFETYVFSLFDENQKPGPVAER	95%	n+304 (+304), K+304 (+304)	30.27	25.00

3137	seq=translation; coord=2:133839420..133842192:1; parent_transcript=GRMZM2G111143_T01; parent_gene=GRMZM2G111143	GRMZM2G111143_P01,GRMZM2G111143_P02, GRMZM2G111143_P03	TRUE	TRUE	yDLGLLR	90%	n+304 (+304)	27.25	25.00
3138	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	gGIPicFPQFSNFGNLEPHGFAR	95%	n+304 (+304), Carbamidomethyl (+57)	78.13	25.00
3139	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	iSDISEVR	94%	n+304 (+304)	30.82	25.25
3140	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	IELSAVPSSYSGQLDPDR	95%	n+304 (+304)	31.42	25.00
3141	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	sTEQGDAIVFESELD	95%	n+304 (+304)	60.90	25.00
3142	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	vALSPGGDLMLTSR	95%	n+304 (+304)	59.92	25.40
3143	seq=translation; coord=2:4174237..4178923:-1; parent_transcript=GRMZM2G039588_T03; parent_gene=GRMZM2G039588	GRMZM2G039588_P03	TRUE	TRUE	vEGLETLDYLDNLQDR	95%	n+304 (+304)	76.88	25.00
3144	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	TRUE	TRUE	eVDLPASTTAGAGR	95%	n+304 (+304)	53.48	25.00
3145	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	TRUE	TRUE	gDALPLGLPQIMMVLR	95%	n+304 (+304)	37.17	25.65
3146	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	TRUE	TRUE	gGVLFMPGVPGVVER	95%	n+304 (+304)	39.05	26.00
3147	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	TRUE	TRUE	qcLIFDGPAGAR	95%	n+304 (+304), Carbamidomethyl (+57)	40.96	25.00
3148	seq=translation; coord=4:155907661..155908892:-1; parent_transcript=GRMZM2G044627_T01; parent_gene=GRMZM2G044627	GRMZM2G044627_P01	TRUE	TRUE	tIHFWQVDR	95%	n+304 (+304)	32.82	25.00
3149	seq=translation; coord=3:132396184..132400373:-1; parent_transcript=GRMZM2G063949_T01; parent_gene=GRMZM2G063949	GRMZM2G063949_P01,GRMZM2G167872_P01, GRMZM2G167872_P02	TRUE	TRUE	dAIEAVVLMENPAR	95%	n+304 (+304)	45.16	25.39
3150	seq=translation; coord=3:132396184..132400373:-1; parent_transcript=GRMZM2G063949_T01; parent_gene=GRMZM2G063949	GRMZM2G063949_P01,GRMZM2G167872_P01, GRMZM2G167872_P02	TRUE	TRUE	mDFIPGVDGPSEGVPR	95%	n+304 (+304)	48.68	25.00
3151	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263	GRMZM2G079263_P01,GRMZM2G079263_P02, GRMZM2G079263_P03	TRUE	TRUE	gTSATPQAIISAcSDAVPcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	73.77	25.00
3152	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263	GRMZM2G079263_P01,GRMZM2G079263_P02, GRMZM2G079263_P03	TRUE	TRUE	sAGTVVPPScLAR	95%	n+304 (+304), Carbamidomethyl (+57)	41.86	26.13
3153	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263	GRMZM2G079263_P01,GRMZM2G079263_P02, GRMZM2G079263_P03	TRUE	TRUE	sWQGGTGfAR	90%	n+304 (+304)	27.53	25.00
3154	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263	GRMZM2G079263_P01,GRMZM2G079263_P02, GRMZM2G079263_P03	TRUE	TRUE	tTDMVEDVk	95%	n+304 (+304), K+304 (+304)	35.21	25.99

3155	seq=translation; coord=6:162010397..162015714:1; parent_transcript=GRMZM2G079263_T01; parent_gene=GRMZM2G079263 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G079263_P01,GRMZM2G079263_P02, GRMZM2G079263_P03	TRUE	TRUE	vYQIWPVQLSGPck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	51.28	25.79
3156	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	aAGATADYASAK	95%	n+304 (+304), K+304 (+304)	52.92	25.59
3157	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	aEDVTWR	90%	n+304 (+304)	26.26	25.00
3158	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	dLTAGAAGTTMEYAK	95%	n+304 (+304), K+304 (+304)	58.24	25.31
3159	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	dTAWDAAGGMAQR	95%	n+304 (+304)	41.59	25.00
3160	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	dVTLATGETAAEYAK	95%	n+304 (+304), K+304 (+304)	28.84	25.97
3161	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	dVTLSTGETAAEYAK	95%	n+304 (+304), K+304 (+304)	72.84	25.04
3162	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	eTGAAAGQGVk	95%	n+304 (+304), K+304 (+304)	67.10	26.12
3163	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	gGGDENTTVVGDVLEAVGATVVGLAK	95%	n+304 (+304), K+304 (+304)	39.80	25.00
3164	parent_transcript=GRMZM2G412436_T01; parent_gene=GRMZM2G412436 seq=translation; coord=5:142403718..142405631:1;	GRMZM2G412436_P01	TRUE	TRUE	glVAGEEELVPVGGEK	95%	n+304 (+304), K+304 (+304)	71.18	25.00
3165	parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101 seq=translation; coord=3:47448537..47463984:-1;	GRMZM2G011101_P01,GRMZM2G378906_P01	TRUE	TRUE	aLPEMILicQNLr	95%	n+304 (+304), Carbamidomethyl (+57)	45.76	25.98
3166	parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101 seq=translation; coord=3:47448537..47463984:-1;	GRMZM2G011101_P01,GRMZM2G378906_P01	TRUE	TRUE	dVMVGVMMDVLR	90%	n+304 (+304)	27.33	25.00
3167	parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101 seq=translation; coord=3:47448537..47463984:-1;	GRMZM2G011101_P01,GRMZM2G378906_P01	TRUE	TRUE	kVLDLVLDTLTPR	95%	K+304 (+304), n+304 (+304)	61.99	25.00
3168	parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101 seq=translation; coord=3:47448537..47463984:-1;	GRMZM2G011101_P01,GRMZM2G378906_P01	TRUE	TRUE	IPHGDQLIPDAPELVER	95%	n+304 (+304)	42.78	25.63
3169	parent_transcript=GRMZM2G011101_T01; parent_gene=GRMZM2G011101 seq=translation; coord=9:143165107..143170341:1;	GRMZM2G011101_P01,GRMZM2G378906_P01	TRUE	TRUE	ISEPEVLEPLVPSVLANLEHR	95%	n+304 (+304)	67.48	25.00
3170	parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671 seq=translation; coord=9:143165107..143170341:1;	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	dLLASLSHQGEQEK	95%	n+304 (+304), K+304 (+304)	28.54	25.20
3171	parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671 seq=translation; coord=9:143165107..143170341:1;	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	fQAQADAVNLIcGAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	44.20	26.54
3172	parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	iIAFIGSPVik	95%	n+304 (+304), K+304 (+304)	37.08	25.00

3173	seq=translation; coord=9:143165107..143170341:1; parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	ISMEEER	86%	n+304 (+304)	25.09	25.00
3174	seq=translation; coord=9:143165107..143170341:1; parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	tQSNPENTVGVMITMAGk	93%	n+304 (+304), K+304 (+304)	27.56	25.00
3175	seq=translation; coord=9:143165107..143170341:1; parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	vLEATMicIDNSEWMR	95%	n+304 (+304), Carbamidomethyl (+57)	29.04	25.00
3176	seq=translation; coord=9:143165107..143170341:1; parent_transcript=GRMZM2G147671_T01; parent_gene=GRMZM2G147671	GRMZM2G147671_P01,GRMZM2G147671_P02, GRMZM2G165926_P01,GRMZM2G165926_P02	TRUE	TRUE	vLVTPTSDLGk	95%	n+304 (+304), K+304 (+304)	36.64	25.11
3177	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	aiTLPQGGEIMDMMEVADPDVAHVAVR	95%	n+304 (+304)	84.75	25.00
3178	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	dDALLDFYNk	95%	n+304 (+304), K+304 (+304)	37.82	25.00
3179	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	dQEFSDDLGCk	89%	n+304 (+304), Carbamidomethyl (+57)	26.10	25.00
3180	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	dWFLQLTk	93%	n+304 (+304), K+304 (+304)	27.78	25.71
3181	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	eLAVQLk	92%	n+304 (+304), K+304 (+304)	29.47	26.73
3182	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	eLAVQLkDALLAAV	95%	n+304 (+304), K+304 (+304), K+304 (+304)	42.84	25.00
3183	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	fLGEIVLQLDk	95%	n+304 (+304), K+304 (+304)	39.57	25.00
3184	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	iWTPAQDLPk	93%	n+304 (+304), K+304 (+304)	26.81	25.00
3185	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	kPSYLFALVAGQLGcR	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	29.75	25.09
3186	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	iLSHPAFDLR	95%	n+304 (+304)	44.51	25.01
3187	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	iVLASPETATDGDYAAILGVVGHEYFHNWGTGNR	95%	n+304 (+304)	47.29	25.00
3188	seq=translation; coord=1:202752380..202764238:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	tLVLPk	89%	n+304 (+304), K+304 (+304)	27.09	26.15
3189	seq=translation; coord=1:290265297..290286811:1; parent_transcript=GRMZM2G389233_T03; parent_gene=GRMZM2G389233	GRMZM2G389233_P03	TRUE	TRUE	wFALQATSEIPGNVANVQk	95%	n+304 (+304), K+304 (+304)	45.01	25.47
3190	seq=translation; coord=1:290265297..290286811:1; parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664	GRMZM2G082664_P01	TRUE	TRUE	dDTYEDIPNSQIR	95%	n+304 (+304)	35.95	25.00

3191	seq=translation; coord=1:290265297..290286811:1; parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664 seq=translation; coord=1:290265297..290286811:1;	GRMZM2G082664_P01	TRUE	TRUE	dVQVGQPIAVTVEDVEDIK	95%	n+304 (+304), K+304 (+304)	29.57	25.48
3192	parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664 seq=translation; coord=1:290265297..290286811:1;	GRMZM2G082664_P01	TRUE	TRUE	dVVLDPLLAFR	95%	n+304 (+304)	38.87	25.16
3193	parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664 seq=translation; coord=1:290265297..290286811:1;	GRMZM2G082664_P01	TRUE	TRUE	eEQSTESAPQNK	95%	n+304 (+304), K+304 (+304)	32.50	25.00
3194	parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664 seq=translation; coord=1:290265297..290286811:1;	GRMZM2G082664_P01	TRUE	TRUE	gDVLAAIk	95%	n+304 (+304), K+304 (+304)	33.19	26.56
3195	parent_transcript=GRMZM2G082664_T01; parent_gene=GRMZM2G082664 seq=translation; coord=5:10855539..10861668:-1;	GRMZM2G082664_P01	TRUE	TRUE	vVNVSEQSSTVSR	95%	n+304 (+304)	45.90	25.00
3196	parent_transcript=GRMZM2G109383_T01; parent_gene=GRMZM2G109383 seq=translation; coord=5:10855539..10861668:-1;	GRMZM2G109383_P01	TRUE	TRUE	aTGAFILTASHNPGGPK	95%	n+304 (+304), K+304 (+304)	46.92	25.26
3197	parent_transcript=GRMZM2G109383_T01; parent_gene=GRMZM2G109383 seq=translation; coord=5:10855539..10861668:-1;	GRMZM2G109383_P01	TRUE	TRUE	dSQDALAPLVDVAlk	95%	n+304 (+304), K+304 (+304)	42.25	25.38
3198	parent_transcript=GRMZM2G109383_T01; parent_gene=GRMZM2G109383 seq=translation; coord=5:10855539..10861668:-1;	GRMZM2G109383_P01	TRUE	TRUE	vTVFQQPHYLQNFVQSTFNALPVDQVR	95%	n+304 (+304)	41.22	25.13
3199	parent_transcript=GRMZM2G109383_T01; parent_gene=GRMZM2G109383 seq=translation; coord=2:160150779..160152270:1;	GRMZM2G109383_P01	TRUE	TRUE	vYIEQYER	94%	n+304 (+304)	29.07	25.00
3200	parent_transcript=GRMZM2G304548_T01; parent_gene=GRMZM2G304548 seq=translation; coord=2:160150779..160152270:1;	GRMZM2G304548_P01	TRUE	TRUE	eLADIPAYcR	95%	n+304 (+304), Carbamidomethyl (+57)	39.56	25.00
3201	parent_transcript=GRMZM2G304548_T01; parent_gene=GRMZM2G304548 seq=translation; coord=2:160150779..160152270:1;	GRMZM2G304548_P01	TRUE	TRUE	eLADIPAYcR	89%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	27.20	26.03
3202	parent_transcript=GRMZM2G304548_T01; parent_gene=GRMZM2G304548 seq=translation; coord=2:160150779..160152270:1;	GRMZM2G304548_P01	TRUE	TRUE	IEDLPGcPR	89%	n+304 (+304), Carbamidomethyl (+57)	26.20	25.00
3203	parent_transcript=GRMZM2G304548_T01; parent_gene=GRMZM2G304548 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G304548_P01	TRUE	TRUE	IPWPEIk	87%	n+304 (+304), K+304 (+304)	25.25	25.00
3204	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	dGSGQQDWNSPAR	95%	n+304 (+304)	57.70	25.00
3205	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	eLAVDPTSSIGTMGNIGNAEDK	95%	n+304 (+304), K+304 (+304)	28.88	25.00
3206	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	IASEEIIFTSNR	95%	n+304 (+304)	31.08	25.17
3207	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	mcEETMSGPTLDk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.69	25.00
3208	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806	GRMZM2G096806_P01	TRUE	TRUE	mHDEEVNEDLSR	95%	n+304 (+304)	43.66	25.00

3209	seq=translation; coord=1:192404194..192408778:-1; parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	qNENTNVMEEEER	95%	n+304 (+304)	65.54	25.00
3210	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	sSADLASVEV	95%	n+304 (+304), K+304 (+304)	44.50	25.54
3211	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	sVENTTVEGk	95%	n+304 (+304), K+304 (+304)	29.44	26.21
3212	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	sVGTGDDLLQSGk	95%	n+304 (+304), K+304 (+304)	62.06	26.11
3213	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	tDDGTLTTVATQYSEK	93%	n+304 (+304), K+304 (+304)	26.37	25.00
3214	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=1:192404194..192408778:-1;	GRMZM2G096806_P01	TRUE	TRUE	vLLADk	94%	n+304 (+304), K+304 (+304)	29.33	26.88
3215	parent_transcript=GRMZM2G096806_T01; parent_gene=GRMZM2G096806 seq=translation; coord=2:139185152..139187472:-1;	GRMZM2G096806_P01	TRUE	TRUE	vTVEDTTSR	95%	n+304 (+304)	32.84	25.00
3216	parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292 seq=translation; coord=2:139185152..139187472:-1;	GRMZM2G047292_P01	TRUE	TRUE	aPPNVNLRPAGAGVADGGAASGAFLGAR	95%	n+304 (+304)	31.21	25.00
3217	parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292 seq=translation; coord=2:139185152..139187472:-1;	GRMZM2G047292_P01	TRUE	TRUE	aVNPSGIEEGLQSLR	95%	n+304 (+304)	59.38	26.29
3218	parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292 seq=translation; coord=2:139185152..139187472:-1;	GRMZM2G047292_P01	TRUE	TRUE	fLIIDDGWQETVDEIK	95%	n+304 (+304), K+304 (+304)	51.36	26.01
3219	parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292 seq=translation; coord=2:139185152..139187472:-1;	GRMZM2G047292_P01	TRUE	TRUE	gSLYALVLPVLDGGFR	95%	n+304 (+304)	35.00	26.45
3220	parent_transcript=GRMZM2G047292_T01; parent_gene=GRMZM2G047292 seq=translation; coord=5:47578824..47582423:1;	GRMZM2G047292_P01	TRUE	TRUE	vDVQNVLETLGR	95%	n+304 (+304)	40.33	26.57
3221	parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967 seq=translation; coord=5:47578824..47582423:1;	GRMZM2G085967_P01,GRMZM2G085967_P02	TRUE	TRUE	aHIPHAPDVASTLLR	95%	n+304 (+304)	49.44	26.10
3222	parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967 seq=translation; coord=5:47578824..47582423:1;	GRMZM2G085967_P01,GRMZM2G085967_P02	TRUE	TRUE	dSVGIGGPFWSVPTGR	95%	n+304 (+304)	72.27	25.95
3223	parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967 seq=translation; coord=5:47578824..47582423:1;	GRMZM2G085967_P01,GRMZM2G085967_P02	TRUE	TRUE	eGFYDYScPQAEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.54	25.00
3224	parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967 seq=translation; coord=5:47578824..47582423:1;	GRMZM2G085967_P01,GRMZM2G085967_P02	TRUE	TRUE	gGPDDADPSLDPLYAAk	94%	n+304 (+304), K+304 (+304)	27.96	25.08
3225	parent_transcript=GRMZM2G085967_T01; parent_gene=GRMZM2G085967 seq=translation; coord=10:4165442..4166593:-1;	GRMZM2G085967_P01,GRMZM2G085967_P02	TRUE	TRUE	gLQSDAALITDAAsk	95%	n+304 (+304), K+304 (+304)	60.18	25.59
3226	parent_transcript=GRMZM2G101958_T01; parent_gene=GRMZM2G101958	GRMZM2G101958_P01	TRUE	TRUE	nAAAGVSGLNAGNAASIPSk	95%	n+304 (+304), K+304 (+304)	99.23	25.66

3227	seq=translation; coord=6:1338452..1339388:-1; parent_transcript=GRMZM2G122357_T01; parent_gene=GRMZM2G122357	GRMZM2G122357_P01	TRUE	TRUE	iADSQPVDLFAAAR	95%	n+304 (+304)	64.33	25.39
3228	seq=translation; coord=6:1338452..1339388:-1; parent_transcript=GRMZM2G122357_T01; parent_gene=GRMZM2G122357	GRMZM2G122357_P01	TRUE	TRUE	nAVIAESEPVDPASAR	95%	n+304 (+304)	81.31	25.19
3229	seq=translation; coord=6:1338452..1339388:-1; parent_transcript=GRMZM2G122357_T01; parent_gene=GRMZM2G122357	GRMZM2G122357_P01	TRUE	TRUE	qGMAEPTAGGR	95%	n+304 (+304)	32.46	25.00
3230	seq=translation; coord=6:1338452..1339388:-1; parent_transcript=GRMZM2G122357_T01; parent_gene=GRMZM2G122357	GRMZM2G122357_P01	TRUE	TRUE	vAGDDEMLR	95%	n+304 (+304)	44.02	25.00
3231	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	acGAVIVNRPEELQESDVGTR	94%	n+304 (+304), Carbamidomethyl (+57)	28.00	25.00
3232	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	aLDDAIAVLdk	95%	n+304 (+304), K+304 (+304)	35.97	26.46
3233	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	gLSDLAIHLYLsk	95%	n+304 (+304), K+304 (+304)	32.29	25.98
3234	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	iDDIVSGik	94%	n+304 (+304), K+304 (+304)	27.20	25.00
3235	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	kIGDEFFSFIVDck	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.22	25.00
3236	seq=translation; coord=1:25381004..25387870:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	nLQDAMSVAR	86%	n+304 (+304)	25.06	25.00
3237	seq=translation; coord=4:125089612..125098586:-1; parent_transcript=GRMZM2G069765_T01; parent_gene=GRMZM2G069765	GRMZM2G069765_P01	TRUE	TRUE	wPYEAAALAFEAIpR	95%	n+304 (+304)	75.58	25.79
3238	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G157019_T01; parent_gene=GRMZM2G157019	GRMZM2G157019_P01	TRUE	TRUE	tYIFADDGTTik	95%	n+304 (+304), K+304 (+304)	46.85	25.43
3239	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	aILVNIFGGImk	95%	n+304 (+304), K+304 (+304)	53.88	25.00
3240	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	aILVNIFGGImk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	42.05	25.00
3241	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	glTDEDAak	94%	n+304 (+304), K+304 (+304)	28.14	25.00
3242	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	IHGgTPANFLDVGGsASEGQVVEAfK	95%	n+304 (+304), K+304 (+304)	69.73	25.00
3243	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	INFDDNAAFR	95%	n+304 (+304)	36.20	25.00
3244	seq=translation; coord=5:186082222..186092865:1; parent_transcript=GRMZM2G064695_T04; parent_gene=GRMZM2G064695	GRMZM2G064695_P04	TRUE	TRUE	INIHEYQGAELMGk	95%	n+304 (+304), K+304 (+304)	52.83	25.72

3245	seq=translation; coord=3:3887574..3888713:1; parent_transcript=GRMZM2G093405_T01; parent_gene=GRMZM2G093405	GRMZM2G093405_P01,GRMZM2G093405_P02	TRUE	TRUE	fGGFVADADVGEQAAR	95%	n+304 (+304)	68.85	25.00
3246	seq=translation; coord=3:3887574..3888713:1; parent_transcript=GRMZM2G093405_T01; parent_gene=GRMZM2G093405	GRMZM2G093405_P01,GRMZM2G093405_P02	TRUE	TRUE	rADPASPYTVAQYNSPFEFTGR	95%	n+304 (+304)	66.03	25.00
3247	seq=translation; coord=3:3887574..3888713:1; parent_transcript=GRMZM2G093405_T01; parent_gene=GRMZM2G093405	GRMZM2G093405_P01,GRMZM2G093405_P02	TRUE	TRUE	rFGGFVADADVGEQAAR	95%	n+304 (+304)	57.53	25.00
3248	seq=translation; coord=3:3887574..3888713:1; parent_transcript=GRMZM2G093405_T01; parent_gene=GRMZM2G093405	GRMZM2G093405_P01,GRMZM2G093405_P02	TRUE	TRUE	tGFLQLFDYIQGk	95%	n+304 (+304), K+304 (+304)	51.40	25.51
3249	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05 GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04,	TRUE	TRUE	eLGScDLYPQSLR	95%	n+304 (+304), Carbamidomethyl (+57)	40.78	25.00
3250	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05 GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04,	TRUE	TRUE	gMLEEALEIATDTNYR	95%	n+304 (+304)	47.42	25.00
3251	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05 GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04,	TRUE	TRUE	gMLEEALEIATDTNyR	95%	n+304 (+304), iTRAQ8plex (+304)	36.50	25.75
3252	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05 GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04,	TRUE	TRUE	kQWVVAGADDMFIR	95%	K+304 (+304), n+304 (+304)	36.64	25.17
3253	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05 GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04,	TRUE	TRUE	sFEVTDLPVR	94%	n+304 (+304)	31.33	25.34
3254	seq=translation; coord=5:157277567..157288178:1; parent_transcript=GRMZM2G124886_T01; parent_gene=GRMZM2G124886	GRMZM2G124886_P01,GRMZM2G124886_P02, GRMZM2G124886_P03,GRMZM2G124886_P04, GRMZM2G141587_P01,GRMZM2G141587_P02, GRMZM2G141587_P03,GRMZM2G141587_P04, GRMZM2G141587_P05	TRUE	TRUE	vPEIVALWk	95%	n+304 (+304), K+304 (+304)	33.96	25.00
3255	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	TRUE	TRUE	aICTEAGLLALR	95%	n+304 (+304), Carbamidomethyl (+57)	55.76	25.99
3256	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	TRUE	TRUE	IPNVAPLSk	92%	n+304 (+304), K+304 (+304)	28.95	25.00
3257	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	TRUE	TRUE	mTLADDVNLEEFVMTk	95%	n+304 (+304), K+304 (+304)	48.89	25.00
3258	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	TRUE	TRUE	tMLELLNQLDGFDSR	95%	n+304 (+304)	34.75	25.00

3259	seq=translation; coord=7:174582270..174585306:-1; parent_transcript=GRMZM2G056569_T01; parent_gene=GRMZM2G056569	GRMZM2G056569_P01	TRUE	TRUE	vLSVVGILQDEVPDPMVSMk	95%	n+304 (+304), K+304 (+304)	30.81	25.00
3260	seq=translation; coord=8:116533013..116535098:1; parent_transcript=GRMZM2G009936_T01; parent_gene=GRMZM2G009936	GRMZM2G009936_P01,GRMZM2G009936_P02, GRMZM2G009936_P03	TRUE	TRUE	eVAGFAPYEK	91%	n+304 (+304), K+304 (+304)	30.01	26.88
3261	seq=translation; coord=8:116533013..116535098:1; parent_transcript=GRMZM2G009936_T01; parent_gene=GRMZM2G009936	GRMZM2G009936_P01,GRMZM2G009936_P02, GRMZM2G009936_P03	TRUE	TRUE	sGLFVGINK	94%	n+304 (+304), K+304 (+304)	28.13	25.00
3262	seq=translation; coord=1:62530194..62532719:1; parent_transcript=GRMZM2G577677_T01; parent_gene=GRMZM2G577677	GRMZM2G577677_P01	TRUE	TRUE	fYGDGVYNcAGcGTPLYk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	48.32	25.00
3263	seq=translation; coord=1:62530194..62532719:1; parent_transcript=GRMZM2G577677_T01; parent_gene=GRMZM2G577677	GRMZM2G577677_P01	TRUE	TRUE	gTELPGTGEYNk	95%	n+304 (+304), K+304 (+304)	51.07	25.83
3264	seq=translation; coord=1:62530194..62532719:1; parent_transcript=GRMZM2G577677_T01; parent_gene=GRMZM2G577677	GRMZM2G577677_P01	TRUE	TRUE	vLSPEQFR	95%	n+304 (+304)	43.83	25.44
3265	seq=translation; coord=9:106627644..106628551:-1; parent_transcript=GRMZM2G361699_T01; parent_gene=GRMZM2G361699	GRMZM2G361699_P01	TRUE	TRUE	dGSVEALLSGDPAK	95%	n+304 (+304), K+304 (+304)	29.83	25.69
3266	seq=translation; coord=9:106627644..106628551:-1; parent_transcript=GRMZM2G361699_T01; parent_gene=GRMZM2G361699	GRMZM2G361699_P01	TRUE	TRUE	dWTASTAESLGLAGWVR	95%	n+304 (+304)	61.59	25.00
3267	seq=translation; coord=9:106627644..106628551:-1; parent_transcript=GRMZM2G361699_T01; parent_gene=GRMZM2G361699	GRMZM2G361699_P01	TRUE	TRUE	iEDMITR	87%	n+304 (+304)	25.61	25.37
3268	seq=translation; coord=9:106627644..106628551:-1; parent_transcript=GRMZM2G361699_T01; parent_gene=GRMZM2G361699	GRMZM2G361699_P01	TRUE	TRUE	vTGVGFR	91%	n+304 (+304)	26.82	25.00
3269	seq=translation; coord=7:116376688..116380988:1; parent_transcript=GRMZM2G116689_T01; parent_gene=GRMZM2G116689	GRMZM2G116689_P01,GRMZM2G116689_P03	TRUE	TRUE	eIEIDIEPTDSIDR	95%	n+304 (+304)	45.70	25.00
3270	seq=translation; coord=7:116376688..116380988:1; parent_transcript=GRMZM2G116689_T01; parent_gene=GRMZM2G116689	GRMZM2G116689_P01,GRMZM2G116689_P03	TRUE	TRUE	tITLEVESSDTVDNVk	95%	n+304 (+304), K+304 (+304)	32.18	25.51
3271	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01,GRMZM2G015361_P03, GRMZM2G015361_P05,GRMZM2G015361_P06, GRMZM2G015361_P07,GRMZM2G105996_P01, GRMZM2G157596_P01,GRMZM2G157596_P02, GRMZM2G157596_P03,GRMZM2G157596_P04, GRMZM2G157596_P05,GRMZM2G357399_P01, GRMZM2G357399_P02,GRMZM2G395844_P01, GRMZM2G395844_P02,GRMZM2G395844_P03, GRMZM2G395844_P04,GRMZM5G836182_P01	TRUE	TRUE	dAVLLVFANK	95%	n+304 (+304), K+304 (+304)	49.25	25.00

3272	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01,GRMZM2G015361_P03, GRMZM2G015361_P05,GRMZM2G015361_P06, GRMZM2G015361_P07,GRMZM2G105996_P01, GRMZM2G157596_P01,GRMZM2G157596_P02, GRMZM2G157596_P03,GRMZM2G157596_P04, GRMZM2G157596_P05,GRMZM2G357399_P01, GRMZM2G357399_P02,GRMZM2G395844_P01, GRMZM2G395844_P02,GRMZM2G395844_P03, GRMZM2G395844_P04,GRMZM5G836182_P01	TRUE	TRUE	ILMVGLDAAGk	95%	n+304 (+304), K+304 (+304)	52.87	25.20
3273	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01,GRMZM2G015361_P03, GRMZM2G015361_P05,GRMZM2G015361_P06, GRMZM2G015361_P07,GRMZM2G105996_P01, GRMZM2G157596_P01,GRMZM2G157596_P02, GRMZM2G157596_P03,GRMZM2G157596_P04, GRMZM2G157596_P05,GRMZM2G357399_P01, GRMZM2G357399_P02,GRMZM2G395844_P01, GRMZM2G395844_P02,GRMZM2G395844_P03, GRMZM2G395844_P04,GRMZM5G836182_P01	TRUE	TRUE	IGEIVTTIPTIGFNVETVEYk	95%	n+304 (+304), K+304 (+304)	36.61	25.00
3274	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01,GRMZM2G015361_P03, GRMZM2G015361_P05,GRMZM2G015361_P06, GRMZM2G015361_P07,GRMZM2G105996_P01, GRMZM2G157596_P01,GRMZM2G157596_P02, GRMZM2G157596_P03,GRMZM2G157596_P04, GRMZM2G157596_P05,GRMZM2G357399_P01, GRMZM2G357399_P02,GRMZM2G395844_P01, GRMZM2G395844_P02,GRMZM2G395844_P03, GRMZM2G395844_P04,GRMZM5G836182_P01	TRUE	TRUE	mLNEDELr	91%	n+304 (+304)	28.24	25.00
3275	seq=translation; coord=8:4232302..4235855:1; parent_transcript=GRMZM2G015361_T01; parent_gene=GRMZM2G015361	GRMZM2G015361_P01,GRMZM2G015361_P03, GRMZM2G015361_P05,GRMZM2G015361_P06, GRMZM2G015361_P07,GRMZM2G105996_P01, GRMZM2G157596_P01,GRMZM2G157596_P02, GRMZM2G157596_P03,GRMZM2G157596_P04, GRMZM2G157596_P05,GRMZM2G357399_P01, GRMZM2G357399_P02,GRMZM2G395844_P01, GRMZM2G395844_P02,GRMZM2G395844_P03, GRMZM2G395844_P04,GRMZM5G836182_P01	TRUE	TRUE	nISFTVWDVGGQDk	95%	n+304 (+304), K+304 (+304)	36.61	25.59
3276	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620	GRMZM2G035620_P01	TRUE	TRUE	aLIPDLyR	87%	n+304 (+304)	25.25	25.00
3277	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620	GRMZM2G035620_P01	TRUE	TRUE	eDTTFDAYVVGk	95%	n+304 (+304), K+304 (+304)	29.19	25.00
3278	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620	GRMZM2G035620_P01	TRUE	TRUE	gMGLTDENQEAVDLAWSR	95%	n+304 (+304)	79.62	25.00
3279	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620	GRMZM2G035620_P01	TRUE	TRUE	vALDVAEAQHLMEGLDWQGAVk	95%	n+304 (+304), K+304 (+304)	64.22	25.00

3280	seq=translation; coord=3:228250718..228270546:-1; parent_transcript=GRMZM2G035620_T01; parent_gene=GRMZM2G035620 seq=translation; coord=1:38637065..38637541:1;	GRMZM2G035620_P01	TRUE	TRUE	vALDVAEAQHLmEGLDWQGAVk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	49.74	25.00
3281	parent_transcript=AC208204.3_FGT006; parent_gene=AC208204.3_FG006 seq=translation; coord=1:38637065..38637541:1;	AC208204.3_FGP006,GRMZM2G046382_P01	TRUE	TRUE	tSSETAAAFAGAR	95%	n+304 (+304)	33.38	25.00
3282	parent_transcript=AC208204.3_FGT006; parent_gene=AC208204.3_FG006 seq=translation; coord=7:130426898..130428254:1;	AC208204.3_FGP006,GRMZM2G046382_P01	TRUE	TRUE	vVEDGNVLQISGER	95%	n+304 (+304)	70.45	25.00
3283	parent_transcript=GRMZM2G133053_T01; parent_gene=GRMZM2G133053 seq=translation; coord=3:168695539..168699190:1;	GRMZM2G133053_P01	TRUE	TRUE	gDVVTIATAASAPAR	95%	n+304 (+304)	71.91	26.21
3284	parent_transcript=GRMZM2G156861_T02; parent_gene=GRMZM2G156861 seq=translation; coord=3:168695539..168699190:1;	GRMZM2G156861_P02	TRUE	TRUE	aWMSDEEFAR	95%	n+304 (+304)	35.98	25.00
3285	parent_transcript=GRMZM2G156861_T02; parent_gene=GRMZM2G156861 seq=translation; coord=3:168695539..168699190:1;	GRMZM2G156861_P02	TRUE	TRUE	dTMNINALAR	86%	n+304 (+304)	25.25	25.00
3286	parent_transcript=GRMZM2G156861_T02; parent_gene=GRMZM2G156861 seq=translation; coord=3:168695539..168699190:1;	GRMZM2G156861_P02	TRUE	TRUE	eTLAGVNPLIIR	95%	n+304 (+304)	33.33	25.00
3287	parent_transcript=GRMZM2G156861_T02; parent_gene=GRMZM2G156861 seq=translation; coord=4:193146957..193151153:1;	GRMZM2G156861_P02	TRUE	TRUE	IPDIPALEEFR	94%	n+304 (+304)	31.41	25.59
3288	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=4:193146957..193151153:1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	fVDVADLEFLMFPR	95%	n+304 (+304)	37.39	25.07
3289	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=4:193146957..193151153:1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	iLAILDLsAEELGAK	95%	n+304 (+304), K+304 (+304)	69.72	25.00
3290	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=4:193146957..193151153:1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	IFYIPSFk	93%	n+304 (+304), K+304 (+304)	27.49	26.11
3291	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=4:193146957..193151153:1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	mVLEALEAMSEK	95%	n+304 (+304), K+304 (+304)	34.93	25.56
3292	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=4:193146957..193151153:1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	sEEELQNVFR	93%	n+304 (+304)	28.71	25.00
3293	parent_transcript=GRMZM5G821551_T02; parent_gene=GRMZM5G821551 seq=translation; coord=1:221739264..221743951:-1;	GRMZM5G821551_P02,GRMZM5G821551_P03	TRUE	TRUE	vYLFLTSLGIDk	90%	n+304 (+304), K+304 (+304)	25.41	25.00
3294	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	aSSFLDDFYR	95%	n+304 (+304)	40.10	25.00
3295	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	aYNPQSLLYGFGGTEGLFANK	95%	n+304 (+304), K+304 (+304)	35.88	25.37
3296	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	gSTPSNFDcDYAYALGR	95%	n+304 (+304), Carbamidomethyl (+57)	57.92	25.00
3297	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163	GRMZM2G450163_P01	TRUE	TRUE	IPPcLQGPTVR	88%	n+304 (+304), Carbamidomethyl (+57)	26.56	25.53

3298	seq=translation; coord=1:221739264..221743951:-1; parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	ITLMEIISK	95%	n+304 (+304), K+304 (+304)	32.93	25.00
3299	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	tLEITDDVLASYk	95%	n+304 (+304), K+304 (+304)	63.46	25.50
3300	parent_transcript=GRMZM2G450163_T01; parent_gene=GRMZM2G450163 seq=translation; coord=1:221739264..221743951:-1;	GRMZM2G450163_P01	TRUE	TRUE	vGVVFSGR	91%	n+304 (+304)	28.42	25.00
3301	parent_transcript=GRMZM2G391364_T01; parent_gene=GRMZM2G391364 seq=translation; coord=6:4896839..4897613:-1;	GRMZM2G391364_P01	TRUE	TRUE	dLTEDQIASMR	95%	n+304 (+304)	34.99	25.00
3302	parent_transcript=GRMZM2G391364_T01; parent_gene=GRMZM2G391364 seq=translation; coord=6:4896839..4897613:-1;	GRMZM2G391364_P01	TRUE	TRUE	iAPSELGVLMR	93%	n+304 (+304)	31.69	26.74
3303	parent_transcript=GRMZM2G391364_T01; parent_gene=GRMZM2G391364 seq=translation; coord=6:4896839..4897613:-1;	GRMZM2G391364_P01	TRUE	TRUE	IEAHEFDEWIR	95%	n+304 (+304)	56.34	25.00
3304	parent_transcript=GRMZM2G391364_T01; parent_gene=GRMZM2G391364 seq=translation; coord=5:185405145..185408787:1;	GRMZM2G391364_P01	TRUE	TRUE	yDDFILR	91%	n+304 (+304)	28.15	25.00
3305	parent_transcript=GRMZM2G148387_T01; parent_gene=GRMZM2G148387 seq=translation; coord=5:185405145..185408787:1;	GRMZM2G148387_P01	TRUE	TRUE	eIIASSPVDLALR	95%	n+304 (+304)	39.83	25.51
3306	parent_transcript=GRMZM2G148387_T01; parent_gene=GRMZM2G148387 seq=translation; coord=5:185405145..185408787:1;	GRMZM2G148387_P01	TRUE	TRUE	IVPLLTEAGAIVTAR	95%	n+304 (+304)	59.09	25.00
3307	parent_transcript=GRMZM2G148387_T01; parent_gene=GRMZM2G148387 seq=translation; coord=3:141261688..141325830:1;	GRMZM2G148387_P01	TRUE	TRUE	tVPNVFVk	90%	n+304 (+304), K+304 (+304)	26.50	25.00
3308	parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584 seq=translation; coord=3:141261688..141325830:1;	GRMZM2G073584_P02	TRUE	TRUE	aTPEMWPSLIak	95%	n+304 (+304), K+304 (+304)	35.29	26.33
3309	parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584 seq=translation; coord=3:141261688..141325830:1;	GRMZM2G073584_P02	TRUE	TRUE	dISDYLSYTTR	95%	n+304 (+304)	37.77	25.00
3310	parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584 seq=translation; coord=3:141261688..141325830:1;	GRMZM2G073584_P02	TRUE	TRUE	dVPGIEFR	95%	n+304 (+304)	30.99	25.35
3311	parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584 seq=translation; coord=3:141261688..141325830:1;	GRMZM2G073584_P02	TRUE	TRUE	gFLPSLTIDQIR	95%	n+304 (+304)	38.41	25.17
3312	parent_transcript=GRMZM2G073584_T02; parent_gene=GRMZM2G073584 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G073584_P02	TRUE	TRUE	IVAAEGLFLFLR	95%	n+304 (+304)	43.14	25.00
3313	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	aALIVVLTR	95%	n+304 (+304)	33.20	25.00
3314	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	aTSESTEIVILEAALK	92%	n+304 (+304), K+304 (+304)	27.75	25.99
3315	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	eTDAFMVAR	86%	n+304 (+304)	25.37	25.00

3316	seq=translation; coord=10:148228962..148233420:1; parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	gLIPLLAEGSAK	95%	n+304 (+304), K+304 (+304)	53.66	25.50
3317	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	iGVASVIK	93%	n+304 (+304), K+304 (+304)	27.60	25.00
3318	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=10:148228962..148233420:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	iLADLDR	93%	n+304 (+304)	31.40	27.07
3319	parent_transcript=GRMZM2G008714_T01; parent_gene=GRMZM2G008714 seq=translation; coord=5:213904655..213909590:1;	GRMZM2G008714_P01,GRMZM2G150098_P01	TRUE	TRUE	sAPLPMSPLESSAVR	95%	n+304 (+304)	62.37	25.74
3320	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=5:213904655..213909590:1;	GRMZM5G836910_P01	TRUE	TRUE	eYLPiEGLAAFNK	95%	n+304 (+304), K+304 (+304)	42.47	26.22
3321	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=5:213904655..213909590:1;	GRMZM5G836910_P01	TRUE	TRUE	fEGVPMAPDPiLGVSEAFK	95%	n+304 (+304), K+304 (+304)	30.07	25.91
3322	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=5:213904655..213909590:1;	GRMZM5G836910_P01	TRUE	TRUE	iADVIQEK	95%	n+304 (+304), K+304 (+304)	38.19	25.00
3323	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=5:213904655..213909590:1;	GRMZM5G836910_P01	TRUE	TRUE	iSLAGLSLAK	95%	n+304 (+304), K+304 (+304)	45.92	25.00
3324	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=5:213904655..213909590:1;	GRMZM5G836910_P01	TRUE	TRUE	iVANVVGDPMTFGEWk	95%	n+304 (+304), K+304 (+304)	69.51	25.63
3325	parent_transcript=GRMZM5G836910_T01; parent_gene=GRMZM5G836910 seq=translation; coord=1:91875822..91877199:-1;	GRMZM5G836910_P01	TRUE	TRUE	qEMELMAGR	94%	n+304 (+304)	28.97	25.00
3326	parent_transcript=GRMZM2G176595_T01; parent_gene=GRMZM2G176595 seq=translation; coord=1:91875822..91877199:-1;	GRMZM2G176595_P01	TRUE	TRUE	gTNQYPFSSMTScGNEPIfK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.28	25.00
3327	parent_transcript=GRMZM2G176595_T01; parent_gene=GRMZM2G176595 seq=translation; coord=1:91875822..91877199:-1;	GRMZM2G176595_P01	TRUE	TRUE	hAGIIDMQFR	95%	n+304 (+304)	44.79	25.00
3328	parent_transcript=GRMZM2G176595_T01; parent_gene=GRMZM2G176595 seq=translation; coord=10:23213183..23215664:1;	GRMZM2G176595_P01	TRUE	TRUE	nVIPANYIPDVDYR	95%	n+304 (+304)	46.09	25.00
3329	parent_transcript=GRMZM2G036427_T01; parent_gene=GRMZM2G036427 seq=translation; coord=10:23213183..23215664:1;	GRMZM2G036427_P01,GRMZM2G036427_P04	TRUE	TRUE	gLcTQASDAVFEALEGDAR	95%	n+304 (+304), Carbamidomethyl (+57)	74.10	25.00
3330	parent_transcript=GRMZM2G036427_T01; parent_gene=GRMZM2G036427 seq=translation; coord=9:136016928..136020802:-1;	GRMZM2G036427_P01,GRMZM2G036427_P04	TRUE	TRUE	nVLcEAVER	95%	n+304 (+304), Carbamidomethyl (+57)	37.34	25.00
3331	parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417 seq=translation; coord=9:136016928..136020802:-1;	GRMZM2G152417_P01	TRUE	TRUE	aNAEFAGGWYHSGDLGVk	95%	n+304 (+304), K+304 (+304)	27.91	25.02
3332	parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417 seq=translation; coord=9:136016928..136020802:-1;	GRMZM2G152417_P01	TRUE	TRUE	dIDDLPR	90%	n+304 (+304)	27.55	25.00
3333	parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	TRUE	TRUE	nDANYALTPLWFLER	92%	n+304 (+304)	26.81	25.00

3334	seq=translation; coord=9:136016928..136020802:-1; parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	TRUE	TRUE	sVIFGPLPk	95%	n+304 (+304), K+304 (+304)	35.40	25.00
3335	seq=translation; coord=9:136016928..136020802:-1; parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	TRUE	TRUE	vLCAHPAVLEVSVVAR	95%	n+304 (+304), Carbamidomethyl (+57)	45.21	25.74
3336	seq=translation; coord=9:136016928..136020802:-1; parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	TRUE	TRUE	wGESPCAFVTLk	87%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.31	25.53
3337	seq=translation; coord=9:136016928..136020802:-1; parent_transcript=GRMZM2G152417_T01; parent_gene=GRMZM2G152417	GRMZM2G152417_P01	TRUE	TRUE	yIAMEGLDVDPk	95%	n+304 (+304), K+304 (+304)	70.37	25.93
3338	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	dFGDADAHGFEGGYGGGGGGFGDGGVAR	95%	n+304 (+304)	66.84	25.00
3339	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	dGDEVFIk	95%	n+304 (+304), K+304 (+304)	34.99	26.24
3340	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	eMTLEEYEk	95%	n+304 (+304), K+304 (+304)	48.52	25.00
3341	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	gPAAAPAIEDQAQFPALA	95%	n+304 (+304)	45.73	25.00
3342	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	rDFGDADAHGFEGGYGGGGGGFGDGGVAR	95%	n+304 (+304)	64.89	25.00
3343	seq=translation; coord=8:77429944..77433319:1; parent_transcript=GRMZM2G464401_T01; parent_gene=GRMZM2G464401	GRMZM2G464401_P01	TRUE	TRUE	sLSINEFLkPAEGER	95%	n+304 (+304), K+304 (+304)	46.29	25.89
3344	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01,GRMZM2G018566_P02	TRUE	TRUE	aTLFPGDGIGPEIAESVk	95%	n+304 (+304), K+304 (+304)	56.55	25.42
3345	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01,GRMZM2G018566_P02	TRUE	TRUE	nLANPTALMLSAVMMLR	95%	n+304 (+304)	50.17	26.03
3346	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01,GRMZM2G018566_P02	TRUE	TRUE	qVFNVAGVPIEWEEHYVGTEVDPR	95%	n+304 (+304)	59.85	25.00
3347	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01,GRMZM2G018566_P02	TRUE	TRUE	tESFLTWESLESVR	95%	n+304 (+304)	44.45	25.00
3348	seq=translation; coord=3:43991720..43996960:1; parent_transcript=GRMZM2G018566_T01; parent_gene=GRMZM2G018566	GRMZM2G018566_P01,GRMZM2G018566_P02	TRUE	TRUE	yDDVNLVTIR	95%	n+304 (+304)	32.69	25.31
3349	seq=translation; coord=2:176644918..176648601:1; parent_transcript=GRMZM2G150616_T01; parent_gene=GRMZM2G150616	GRMZM2G150616_P01	TRUE	TRUE	aVAVGADISLDTATGNLTK	95%	n+304 (+304), K+304 (+304)	48.83	25.90
3350	seq=translation; coord=4:154624996..154627067:1; parent_transcript=GRMZM2G156785_T01; parent_gene=GRMZM2G156785	GRMZM2G156785_P01,GRMZM2G156785_P03, GRMZM2G156785_P04	TRUE	TRUE	qEYQAQHPGNk	95%	n+304 (+304), K+304 (+304)	37.69	25.79
3351	seq=translation; coord=4:154624996..154627067:1; parent_transcript=GRMZM2G156785_T01; parent_gene=GRMZM2G156785	GRMZM2G156785_P01,GRMZM2G156785_P03, GRMZM2G156785_P04	TRUE	TRUE	sMSEQEk	90%	n+304 (+304), K+304 (+304)	25.22	25.00

3352	seq=translation; coord=4:154624996..154627067:1; parent_transcript=GRMZM2G156785_T01; parent_gene=GRMZM2G156785 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G156785_P01,GRMZM2G156785_P03, GRMZM2G156785_P04	TRUE	TRUE	sVAAVSk	95%	n+304 (+304), K+304 (+304)	29.20	26.07
3353	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	eALQAEVGLPVDR	95%	n+304 (+304)	59.36	26.22
3354	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	fAFSDYPELNLPER	95%	n+304 (+304)	58.89	25.00
3355	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	fNAALAHHIMAGADVLAVTSR	95%	n+304 (+304)	43.63	26.07
3356	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	fSLlcQAALAPR	91%	n+304 (+304), Carbamidomethyl (+57)	28.73	25.61
3357	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	sSFDIDGYEKPVETR	95%	n+304 (+304), K+304 (+304)	26.68	25.00
3358	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	vFVDHPLFLER	95%	n+304 (+304)	49.02	26.50
3359	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=9:23256308..23260236:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	vLTVSPYYAEELISGIAR	95%	n+304 (+304)	43.06	26.06
3360	parent_transcript=GRMZM2G024993_T01; parent_gene=GRMZM2G024993 seq=translation; coord=4:37762302..37763543:-1;	GRMZM2G024993_P01,GRMZM2G024993_P06	TRUE	TRUE	vVGTPAYEEMVR	95%	n+304 (+304)	37.12	25.00
3361	parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050 seq=translation; coord=4:37762302..37763543:-1;	GRMZM2G112050_P01,GRMZM2G158034_P01, GRMZM2G158034_P04	TRUE	TRUE	aHGLAPEIPEDLYFLIK	95%	n+304 (+304), K+304 (+304)	42.89	25.00
3362	parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050 seq=translation; coord=4:37762302..37763543:-1;	GRMZM2G112050_P01,GRMZM2G158034_P01, GRMZM2G158034_P04	TRUE	TRUE	dQHGIPLVk	90%	n+304 (+304), K+304 (+304)	25.32	25.00
3363	parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050 seq=translation; coord=4:37762302..37763543:-1;	GRMZM2G112050_P01,GRMZM2G158034_P01, GRMZM2G158034_P04	TRUE	TRUE	gISSALPYk	92%	n+304 (+304), K+304 (+304)	28.65	25.00
3364	parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050 seq=translation; coord=4:37762302..37763543:-1;	GRMZM2G112050_P01,GRMZM2G158034_P01, GRMZM2G158034_P04	TRUE	TRUE	kGQMPSQIGVLLR	95%	K+304 (+304), n+304 (+304)	36.74	25.00
3365	parent_transcript=GRMZM2G112050_T01; parent_gene=GRMZM2G112050 seq=translation; coord=9:28603999..28607933:1;	GRMZM2G112050_P01,GRMZM2G158034_P01, GRMZM2G158034_P04	TRUE	TRUE	tPPTWLk	90%	n+304 (+304), K+304 (+304)	28.08	25.99
3366	parent_transcript=GRMZM2G153969_T01; parent_gene=GRMZM2G153969 seq=translation; coord=9:28603999..28607933:1;	GRMZM2G153969_P01	TRUE	TRUE	iEVTQPADFk	95%	n+304 (+304), K+304 (+304)	33.91	26.38
3367	parent_transcript=GRMZM2G153969_T01; parent_gene=GRMZM2G153969 seq=translation; coord=9:28603999..28607933:1;	GRMZM2G153969_P01	TRUE	TRUE	nEQVDLLkPDTTVIFR	95%	n+304 (+304), K+304 (+304)	31.97	25.00
3368	parent_transcript=GRMZM2G153969_T01; parent_gene=GRMZM2G153969 seq=translation; coord=3:197406823..197407784:-1;	GRMZM2G153969_P01	TRUE	TRUE	vAEcLVGDSTGTVLVTAR	95%	n+304 (+304), Carbamidomethyl (+57)	96.56	25.84
3369	parent_transcript=GRMZM2G010762_T01; parent_gene=GRMZM2G010762	GRMZM2G010762_P01	TRUE	TRUE	dGWVLDPTESYNHWAGR	95%	n+304 (+304)	37.25	25.00

3370	seq=translation; coord=3:197406823..197407784:-1; parent_transcript=GRMZM2G010762_T01; parent_gene=GRMZM2G010762	GRMZM2G010762_P01	TRUE	TRUE	IYIIVMAVR	89%	n+304 (+304)	27.54	25.93
3371	seq=translation; coord=3:197406823..197407784:-1; parent_transcript=GRMZM2G010762_T01; parent_gene=GRMZM2G010762	GRMZM2G010762_P01	TRUE	TRUE	sGPFFFISSDEER	95%	n+304 (+304)	66.88	25.00
3372	seq=translation; coord=1:7192641..7198439:-1; parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158	GRMZM2G057158_P01,GRMZM2G057158_P02	TRUE	TRUE	aDLGATVGTfK	95%	n+304 (+304), K+304 (+304)	49.00	25.93
3373	seq=translation; coord=1:7192641..7198439:-1; parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158	GRMZM2G057158_P01,GRMZM2G057158_P02	TRUE	TRUE	aIVADScDVPAPQQR	95%	n+304 (+304), Carbamidomethyl (+57)	57.06	25.00
3374	seq=translation; coord=1:7192641..7198439:-1; parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158	GRMZM2G057158_P01,GRMZM2G057158_P02	TRUE	TRUE	eIMNMPLMQNLMNSPELIR	95%	n+304 (+304)	67.44	25.00
3375	seq=translation; coord=1:7192641..7198439:-1; parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158	GRMZM2G057158_P01,GRMZM2G057158_P02	TRUE	TRUE	eMIQNPEFIR	95%	n+304 (+304)	30.06	25.00
3376	seq=translation; coord=1:7192641..7198439:-1; parent_transcript=GRMZM2G057158_T01; parent_gene=GRMZM2G057158	GRMZM2G057158_P01,GRMZM2G057158_P02	TRUE	TRUE	nPDLAHVLDPSIMR	95%	n+304 (+304)	29.63	25.00
3377	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	aAQAAAAHPAVTR	95%	n+304 (+304)	52.21	25.00
3378	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	aTSDPEIWK	95%	n+304 (+304), K+304 (+304)	34.71	25.00
3379	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	eEALELYEDMVLGR	95%	n+304 (+304)	73.77	25.00
3380	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	gFGIGPDGK	95%	n+304 (+304), K+304 (+304)	29.43	26.34
3381	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	KIDDVVEEAVEFADASPHPPR	95%	K+304 (+304), n+304 (+304)	84.54	25.25
3382	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	IPIVFVNNLWAIMSHIR	95%	n+304 (+304)	35.84	25.00
3383	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	rGEGPTLVeCETRY	95%	n+304 (+304), Carbamidomethyl (+57)	44.73	25.00
3384	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	sVMAELFGK	90%	n+304 (+304), K+304 (+304)	27.30	26.68
3385	seq=translation; coord=2:110896551..110900469:-1; parent_transcript=GRMZM2G033894_T01; parent_gene=GRMZM2G033894	GRMZM2G033894_P01	TRUE	TRUE	yIIQNLA TESElk	95%	n+304 (+304), K+304 (+304)	57.66	25.43
3386	seq=translation; coord=8:116617793..116620719:-1; parent_transcript=GRMZM5G802801_T01; parent_gene=GRMZM5G802801	GRMZM5G802801_P01	TRUE	TRUE	mYQGAGADMGAAGMDEDA PAAGSAAGPk	95%	n+304 (+304), K+304 (+304)	65.62	25.00
3387	seq=translation; coord=8:116617793..116620719:-1; parent_transcript=GRMZM5G802801_T01; parent_gene=GRMZM5G802801	GRMZM5G802801_P01	TRUE	TRUE	myQGAGADMGAAGMDEDA PAAGSAAGPk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	54.08	25.00

3388	seq=translation; coord=8:116617793..116620719:-1; parent_transcript=GRMZM5G802801_T01; parent_gene=GRMZM5G802801	GRMZM5G802801_P01	TRUE	TRUE	qFSAAEISSMVLTK	95%	n+304 (+304), K+304 (+304)	39.08	26.09
3389	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	eNTLDDLIALLk	95%	n+304 (+304), K+304 (+304)	39.67	25.00
3390	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	gIVLSFITEFFk	95%	n+304 (+304), K+304 (+304)	35.42	25.28
3391	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	IAIFTALAFSQk	95%	n+304 (+304), K+304 (+304)	27.97	25.00
3392	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	ISGLPPETVFQPLLk	95%	n+304 (+304), K+304 (+304)	30.11	25.00
3393	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	mEDNLLDFFPSAk	95%	n+304 (+304), K+304 (+304)	51.53	25.00
3394	seq=translation; coord=2:125696253..125710943:1; parent_transcript=GRMZM5G877316_T02; parent_gene=GRMZM5G877316	GRMZM5G877316_P02,GRMZM5G877316_P03	TRUE	TRUE	slESSDLNFSR	93%	n+304 (+304)	29.53	25.00
3395	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	aEQGSDIGDVIDIPGVcR	95%	n+304 (+304), Carbamidomethyl (+57)	67.37	25.00
3396	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	aWVDQEALLk	95%	n+304 (+304), K+304 (+304)	38.44	26.19
3397	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	eIAAGLEASnCR	95%	n+304 (+304), Carbamidomethyl (+57)	32.29	25.00
3398	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	kAEQGS DIGDVIDIPGVcR	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	43.32	25.00
3399	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	sAHLGLPIAGAAPR	95%	n+304 (+304)	54.91	25.00
3400	seq=translation; coord=6:120018887..120020772:1; parent_transcript=GRMZM2G383404_T01; parent_gene=GRMZM2G383404	GRMZM2G383404_P01	TRUE	TRUE	sVVYVAFGNR	88%	n+304 (+304)	26.22	25.24
3401	seq=translation; coord=2:60415730..60417474:1; parent_transcript=GRMZM2G085260_T01; parent_gene=GRMZM2G085260	GRMZM2G085260_P01	TRUE	TRUE	gFPRPLLDISAANFGk	95%	n+304 (+304), K+304 (+304)	32.50	25.24
3402	seq=translation; coord=2:60415730..60417474:1; parent_transcript=GRMZM2G085260_T01; parent_gene=GRMZM2G085260	GRMZM2G085260_P01	TRUE	TRUE	kLLAGLLAVESAQDAVIR	95%	K+304 (+304), n+304 (+304)	83.27	25.00
3403	seq=translation; coord=2:60415730..60417474:1; parent_transcript=GRMZM2G085260_T01; parent_gene=GRMZM2G085260	GRMZM2G085260_P01	TRUE	TRUE	lLAGLLAVESAQDAVIR	95%	n+304 (+304)	81.84	25.31
3404	seq=translation; coord=2:60415730..60417474:1; parent_transcript=GRMZM2G085260_T01; parent_gene=GRMZM2G085260	GRMZM2G085260_P01	TRUE	TRUE	vPSYAGGVAEITAR	95%	n+304 (+304)	50.64	25.39
3405	seq=translation; coord=5:56842476..56843934:-1; parent_transcript=GRMZM2G077208_T02; parent_gene=GRMZM2G077208	GRMZM2G077208_P02,GRMZM2G37770_P01	TRUE	TRUE	qHSGEIEASAATPYELQR	95%	n+304 (+304)	62.17	25.00

3406	seq=translation; coord=5:56842476..56843934:-1; parent_transcript=GRMZM2G077208_T02; parent_gene=GRMZM2G077208	GRMZM2G077208_P02,GRMZM2G378770_P01	TRUE	TRUE	qHSGEIEASAATPYELQR	95%	Pyro-cmC (-17), n+304 (+304)	75.41	25.00
3407	seq=translation; coord=5:56842476..56843934:-1; parent_transcript=GRMZM2G077208_T02; parent_gene=GRMZM2G077208	GRMZM2G077208_P02,GRMZM2G378770_P01	TRUE	TRUE	qHSGEIEASAATPYELQR	94%	n+304 (+304), iTRAQ8plex (+304)	26.23	25.00
3408	seq=translation; coord=5:56842476..56843934:-1; parent_transcript=GRMZM2G077208_T02; parent_gene=GRMZM2G077208	GRMZM2G077208_P02,GRMZM2G378770_P01	TRUE	TRUE	qHSGEIEASAATPYELQR	95%	Pyro-cmC (-17), n+304 (+304), iTRAQ8plex (+304)	37.95	25.00
3409	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	acAGYVDAVEVDGDGGPGSVTTMk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.35	25.00
3410	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	IDGAPLAPEDEAR	95%	n+304 (+304)	53.32	25.00
3411	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	mVEAYLVAHPEDEFA	95%	n+304 (+304)	32.71	25.00
3412	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	tEVLQGGTVSAQLR	94%	n+304 (+304)	31.63	26.17
3413	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	vEAGEGAcVAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	79.17	25.00
3414	seq=translation; coord=10:22319764..22321055:-1; parent_transcript=GRMZM2G075283_T01; parent_gene=GRMZM2G075283	GRMZM2G075283_P01	TRUE	TRUE	vVALDAAAR	95%	n+304 (+304)	35.41	28.73
3415	seq=translation; coord=5:208194750..208197747:1; parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950	GRMZM2G061950_P01	TRUE	TRUE	aYSDEEIIIR	92%	n+304 (+304)	29.24	25.00
3416	seq=translation; coord=5:208194750..208197747:1; parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950	GRMZM2G061950_P01	TRUE	TRUE	IALGGMGTDDEDLTR	95%	n+304 (+304)	81.15	25.00
3417	seq=translation; coord=5:208194750..208197747:1; parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950	GRMZM2G061950_P01	TRUE	TRUE	IIISILahr	95%	n+304 (+304)	45.12	25.00
3418	seq=translation; coord=5:208194750..208197747:1; parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950	GRMZM2G061950_P01	TRUE	TRUE	ILVPLVSAYR	89%	n+304 (+304)	26.93	25.00
3419	seq=translation; coord=5:208194750..208197747:1; parent_transcript=GRMZM2G061950_T01; parent_gene=GRMZM2G061950	GRMZM2G061950_P01	TRUE	TRUE	sLEEDVAAHVTDGDFR	95%	n+304 (+304)	51.41	25.00
3420	seq=translation; coord=10:101520598..101521474:1; parent_transcript=GRMZM2G166141_T01; parent_gene=GRMZM2G166141	GRMZM2G166141_P01	TRUE	TRUE	dPMAVTPDDFFNPAMIIGk	95%	n+304 (+304), K+304 (+304)	62.40	25.00
3421	seq=translation; coord=10:101520598..101521474:1; parent_transcript=GRMZM2G166141_T01; parent_gene=GRMZM2G166141	GRMZM2G166141_P01	TRUE	TRUE	dPmAVTPDDFFNPAMIIGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	32.48	25.00
3422	seq=translation; coord=10:101520598..101521474:1; parent_transcript=GRMZM2G166141_T01; parent_gene=GRMZM2G166141	GRMZM2G166141_P01	TRUE	TRUE	dPMAVTPDDFFNPAmIIGk	92%	n+304 (+304), Oxidation (+16), K+304 (+304)	26.90	25.00
3423	seq=translation; coord=10:101520598..101521474:1; parent_transcript=GRMZM2G166141_T01; parent_gene=GRMZM2G166141	GRMZM2G166141_P01	TRUE	TRUE	dPmAVTPDDFFNPAmIIGk	95%	n+304 (+304), Oxidation (+16), Oxidation (+16), K+304 (+304)	32.07	25.00

3424	seq=translation; coord=2:1436938..1441569:-1; parent_transcript=GRMZM2G019500_T01; parent_gene=GRMZM2G019500 seq=translation; coord=2:1436938..1441569:-1;	GRMZM2G019500_P01	TRUE	TRUE	dGAAAPANDAK	93%	n+304 (+304), K+304 (+304)	27.37	25.13
3425	parent_transcript=GRMZM2G019500_T01; parent_gene=GRMZM2G019500 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G019500_P01	TRUE	TRUE	eEGILLR	95%	n+304 (+304)	32.68	25.09
3426	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G066650_P01	TRUE	TRUE	gLLQLTLTSSVASAR	95%	n+304 (+304)	30.05	25.00
3427	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G066650_P01	TRUE	TRUE	iLPFcDGIMTQLLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	49.94	26.16
3428	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G066650_P01	TRUE	TRUE	IATDMQDIFNITAK	95%	n+304 (+304), K+304 (+304)	43.61	25.37
3429	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G066650_P01	TRUE	TRUE	qALPALVPMLETLLk	95%	n+304 (+304), K+304 (+304)	33.32	25.00
3430	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=3:126628409..126636305:-1;	GRMZM2G066650_P01	TRUE	TRUE	tQLLMPFAPHIIQLDALYNGk	95%	n+304 (+304), K+304 (+304)	31.55	25.00
3431	parent_transcript=GRMZM2G066650_T01; parent_gene=GRMZM2G066650 seq=translation; coord=1:236088923..236128384:-1;	GRMZM2G066650_P01	TRUE	TRUE	tVGDDIVPLVMPFVEENITk	95%	n+304 (+304), K+304 (+304)	40.92	25.40
3432	parent_transcript=GRMZM2G053764_T01; parent_gene=GRMZM2G053764 seq=translation; coord=1:236088923..236128384:-1;	GRMZM2G053764_P01,GRMZM2G053764_P02, GRMZM2G053764_P04,GRMZM2G146374_P02	TRUE	TRUE	gPAESIYQGGVWk	95%	n+304 (+304), K+304 (+304)	36.27	25.92
3433	parent_transcript=GRMZM2G053764_T01; parent_gene=GRMZM2G053764 seq=translation; coord=1:236088923..236128384:-1;	GRMZM2G053764_P01,GRMZM2G053764_P02, GRMZM2G053764_P04,GRMZM2G146374_P02	TRUE	TRUE	sPSIGFINK	92%	n+304 (+304), K+304 (+304)	27.46	25.00
3434	parent_transcript=GRMZM2G053764_T01; parent_gene=GRMZM2G053764 seq=translation; coord=4:233821047..233828196:1;	GRMZM2G053764_P01,GRMZM2G053764_P02, GRMZM2G053764_P04,GRMZM2G146374_P02	TRUE	TRUE	vELPDAYPYk	95%	n+304 (+304), K+304 (+304)	48.10	26.19
3435	parent_transcript=GRMZM2G064023_T01; parent_gene=GRMZM2G064023 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G064023_P01,GRMZM2G064023_P02, GRMZM2G064023_P03,GRMZM2G064023_P04	TRUE	TRUE	gMIGMLWETSLLDPEEGIR	95%	n+304 (+304)	35.67	25.00
3436	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G328094_P01	TRUE	TRUE	aLIGLFHGR	95%	n+304 (+304)	43.66	25.53
3437	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G328094_P01	TRUE	TRUE	eSYTAAFPVPGDTITGYGVAR	95%	n+304 (+304)	87.00	25.00
3438	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G328094_P01	TRUE	TRUE	eYVEGYPR	88%	n+304 (+304)	26.35	25.00
3439	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G328094_P01	TRUE	TRUE	iAVcGLISQYNLADGEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.55	25.02
3440	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094 seq=translation; coord=8:6456722..6458297:1;	GRMZM2G328094_P01	TRUE	TRUE	kGETVFVSAASGAVGQLVGQFAR	95%	K+304 (+304), n+304 (+304)	43.29	25.00
3441	parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094	GRMZM2G328094_P01	TRUE	TRUE	ITGAEPAGSVLVR	95%	n+304 (+304)	45.46	26.95

3442	seq=translation; coord=8:6456722..6458297:1; parent_transcript=GRMZM2G328094_T01; parent_gene=GRMZM2G328094	GRMZM2G328094_P01	TRUE	TRUE	vVSSSDPR	89%	n+304 (+304)	26.86	25.00
3443	seq=translation; coord=5:215477924..215482853:1; parent_transcript=GRMZM2G078396_T01; parent_gene=GRMZM2G078396	GRMZM2G078396_P01,GRMZM2G102230_P01, GRMZM2G123495_P01,GRMZM2G150058_P01, GRMZM2G171181_P01	TRUE	TRUE	gSAITGPIGk	95%	n+304 (+304), K+304 (+304)	50.82	25.51
3444	seq=translation; coord=5:215477924..215482853:1; parent_transcript=GRMZM2G078396_T01; parent_gene=GRMZM2G078396	GRMZM2G078396_P01,GRMZM2G102230_P01, GRMZM2G123495_P01,GRMZM2G150058_P01, GRMZM2G171181_P01	TRUE	TRUE	mSLGLPVAATVncADNTGAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	56.27	25.13
3445	seq=translation; coord=5:215477924..215482853:1; parent_transcript=GRMZM2G078396_T01; parent_gene=GRMZM2G078396	GRMZM2G078396_P01,GRMZM2G102230_P01, GRMZM2G123495_P01,GRMZM2G150058_P01, GRMZM2G171181_P01	TRUE	TRUE	nLYISVk	95%	n+304 (+304), K+304 (+304)	34.12	25.00
3446	seq=translation; coord=5:215477924..215482853:1; parent_transcript=GRMZM2G078396_T01; parent_gene=GRMZM2G078396	GRMZM2G078396_P01,GRMZM2G102230_P01, GRMZM2G123495_P01,GRMZM2G150058_P01, GRMZM2G171181_P01	TRUE	TRUE	vMPAVIVR	93%	n+304 (+304)	28.38	25.00
3447	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	dITSVAEK	95%	n+304 (+304), K+304 (+304)	34.04	26.71
3448	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	INADVLEQFITENYTASR	95%	n+304 (+304)	59.47	25.00
3449	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	IVNEFDQIk	95%	n+304 (+304), K+304 (+304)	36.71	26.78
3450	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	sSGGFWTWLTGAR	95%	n+304 (+304)	50.79	25.00
3451	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	tMAFTTTANR	88%	n+304 (+304)	26.23	25.00
3452	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	tYMPeMVEVLIDcVR	95%	n+304 (+304), Carbamidomethyl (+57)	32.21	25.00
3453	seq=translation; coord=3:6926705..6931400:-1; parent_transcript=GRMZM2G166646_T01; parent_gene=GRMZM2G166646	GRMZM2G166646_P01	TRUE	TRUE	tyMPeMVEVLIDcVR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	50.17	25.00
3454	seq=translation; coord=7:19072056..19090250:-1; parent_transcript=GRMZM2G462325_T01; parent_gene=GRMZM2G462325	GRMZM2G462325_P01	TRUE	TRUE	IASPPSLTGSaislSVSMQAR	95%	n+304 (+304)	71.27	25.00
3455	seq=translation; coord=1:273865741..273870770:-1; parent_transcript=GRMZM2G416388_T01; parent_gene=GRMZM2G416388	GRMZM2G416388_P01,GRMZM2G416388_P02, GRMZM2G416388_P03,GRMZM2G416388_P06	TRUE	TRUE	gFETATVADVLk	95%	n+304 (+304), K+304 (+304)	44.63	26.24
3456	seq=translation; coord=1:273865741..273870770:-1; parent_transcript=GRMZM2G416388_T01; parent_gene=GRMZM2G416388	GRMZM2G416388_P01,GRMZM2G416388_P02, GRMZM2G416388_P03,GRMZM2G416388_P06	TRUE	TRUE	hIPVIDGTGMLGMVSGIDVVR	95%	n+304 (+304)	56.63	25.43
3457	seq=translation; coord=1:273865741..273870770:-1; parent_transcript=GRMZM2G416388_T01; parent_gene=GRMZM2G416388	GRMZM2G416388_P01,GRMZM2G416388_P02, GRMZM2G416388_P03,GRMZM2G416388_P06	TRUE	TRUE	siAGIVTER	92%	n+304 (+304)	29.85	25.93
3458	seq=translation; coord=1:273865741..273870770:-1; parent_transcript=GRMZM2G416388_T01; parent_gene=GRMZM2G416388	GRMZM2G416388_P01,GRMZM2G416388_P02, GRMZM2G416388_P03,GRMZM2G416388_P06	TRUE	TRUE	vLQAMQLMTENR	95%	n+304 (+304)	55.70	25.17
3459	seq=translation; coord=1:52807627..52810251:-1; parent_transcript=GRMZM2G018728_T01; parent_gene=GRMZM2G018728	GRMZM2G018728_P01	TRUE	TRUE	dINPQAPTHILIIPk	95%	n+304 (+304), K+304 (+304)	31.79	25.00

3460	seq=translation; coord=1:52807627..52810251:-1; parent_transcript=GRMZM2G018728_T01; parent_gene=GRMZM2G018728 seq=translation; coord=1:52807627..52810251:-1;	GRMZM2G018728_P01	TRUE	TRUE	eAALAAVLDDSPITFDK	95%	n+304 (+304), K+304 (+304)	72.28	26.10
3461	parent_transcript=GRMZM2G018728_T01; parent_gene=GRMZM2G018728 seq=translation; coord=1:52807627..52810251:-1;	GRMZM2G018728_P01	TRUE	TRUE	eIPSTVVVEDEK	95%	n+304 (+304), K+304 (+304)	41.62	25.90
3462	parent_transcript=GRMZM2G018728_T01; parent_gene=GRMZM2G018728 seq=translation; coord=1:52807627..52810251:-1;	GRMZM2G018728_P01	TRUE	TRUE	qEGLEDGYR	92%	n+304 (+304)	27.52	25.00
3463	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	fGEVTGGEEQVVSgMNYk	95%	n+304 (+304), K+304 (+304)	43.19	25.00
3464	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	fGEVTGGEEQVVSgMNYk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	56.21	25.00
3465	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	fGEVTGGEEQVVSgMNYk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	29.95	25.17
3466	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	IVLDATDADGk	95%	n+304 (+304), K+304 (+304)	55.17	25.87
3467	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	vAAYGAFVYEQSWTNTR	95%	n+304 (+304)	57.30	25.00
3468	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=1:79131877..79132681:-1;	GRMZM2G401328_P01	TRUE	TRUE	vAAYGAFVYEQSWTNTR	95%	n+304 (+304), iTRAQ8plex (+304)	37.11	25.49
3469	parent_transcript=GRMZM2G401328_T01; parent_gene=GRMZM2G401328 seq=translation; coord=8:162579348..162580103:-1;	GRMZM2G401328_P01	TRUE	TRUE	vAAYGAFVYEQSWTNTR	95%	n+304 (+304), iTRAQ8plex (+304)	31.60	25.47
3470	parent_transcript=GRMZM2G030717_T01; parent_gene=GRMZM2G030717 seq=translation; coord=8:162579348..162580103:-1;	GRMZM2G030717_P01	TRUE	TRUE	dVEGDGEVQELGR	95%	n+304 (+304)	39.12	25.00
3471	parent_transcript=GRMZM2G030717_T01; parent_gene=GRMZM2G030717 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G030717_P01	TRUE	TRUE	vFDAVVVVKPWLDSR	95%	n+304 (+304), K+304 (+304)	40.69	25.00
3472	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G005552_P01	TRUE	TRUE	aWDLPEADAAALVSSQPASGIVR	95%	n+304 (+304)	30.69	25.09
3473	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G005552_P01	TRUE	TRUE	dREGVALNcLEAPLDVDPGGGR	95%	n+304 (+304), Carbamidomethyl (+57)	42.94	25.00
3474	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G005552_P01	TRUE	TRUE	iADASGMEWFSIITPNPIFSLAGk	95%	n+304 (+304), K+304 (+304)	32.04	25.00
3475	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G005552_P01	TRUE	TRUE	rLDSEIFFAPPSN	95%	n+304 (+304)	38.17	25.00
3476	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552 seq=translation; coord=8:133178452..133180059:1;	GRMZM2G005552_P01	TRUE	TRUE	vEGGFLFIVPR	95%	n+304 (+304)	63.99	25.00
3477	parent_transcript=GRMZM2G005552_T01; parent_gene=GRMZM2G005552	GRMZM2G005552_P01	TRUE	TRUE	vVVLNTANLPLVK	95%	n+304 (+304), K+304 (+304)	41.08	25.00

3478	seq=translation; coord=7:168744978..168747272:1; parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757	GRMZM2G039757_P01	TRUE	TRUE	aADDGWWSVFR	93%	n+304 (+304)	29.29	25.00
3479	seq=translation; coord=7:168744978..168747272:1; parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757	GRMZM2G039757_P01	TRUE	TRUE	aLETEVAVFR	90%	n+304 (+304)	27.55	25.00
3480	seq=translation; coord=7:168744978..168747272:1; parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757	GRMZM2G039757_P01	TRUE	TRUE	ePDLFYTTWSPTER	95%	n+304 (+304)	52.99	25.00
3481	seq=translation; coord=7:168744978..168747272:1; parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757	GRMZM2G039757_P01	TRUE	TRUE	gGWPAWHGDAALFFHR	95%	n+304 (+304)	43.78	25.00
3482	seq=translation; coord=7:168744978..168747272:1; parent_transcript=GRMZM2G039757_T01; parent_gene=GRMZM2G039757	GRMZM2G039757_P01	TRUE	TRUE	nLYVVDTAR	91%	n+304 (+304)	27.86	25.00
3483	seq=translation; coord=4:131010547..131027664:-1; parent_transcript=GRMZM2G006672_T02; parent_gene=GRMZM2G006672	GRMZM2G006672_P02	TRUE	TRUE	aNPVALLSSAMMLR	95%	n+304 (+304)	42.27	25.20
3484	seq=translation; coord=4:131010547..131027664:-1; parent_transcript=GRMZM2G006672_T02; parent_gene=GRMZM2G006672	GRMZM2G006672_P02	TRUE	TRUE	aNPVALLSSAmMLR	91%	n+304 (+304), Oxidation (+16)	26.22	25.21
3485	seq=translation; coord=4:131010547..131027664:-1; parent_transcript=GRMZM2G006672_T02; parent_gene=GRMZM2G006672	GRMZM2G006672_P02	TRUE	TRUE	aNPVALLSSAmMLR	90%	n+304 (+304), Oxidation (+16)	25.56	25.24
3486	seq=translation; coord=4:131010547..131027664:-1; parent_transcript=GRMZM2G006672_T02; parent_gene=GRMZM2G006672	GRMZM2G006672_P02	TRUE	TRUE	hDNVDIVVIR	95%	n+304 (+304)	44.77	25.93
3487	seq=translation; coord=7:159130478..159136959:-1; parent_transcript=GRMZM2G107562_T01; parent_gene=GRMZM2G107562	GRMZM2G107562_P01	TRUE	TRUE	qFHNVLAVSk	95%	n+304 (+304), K+304 (+304)	38.70	25.95
3488	seq=translation; coord=7:159130478..159136959:-1; parent_transcript=GRMZM2G107562_T01; parent_gene=GRMZM2G107562	GRMZM2G107562_P01	TRUE	TRUE	qFHNVLAVSk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	41.74	25.01
3489	seq=translation; coord=7:159130478..159136959:-1; parent_transcript=GRMZM2G107562_T01; parent_gene=GRMZM2G107562	GRMZM2G107562_P01	TRUE	TRUE	qIVIGDTVVFYnk	95%	n+304 (+304), K+304 (+304)	49.65	25.30
3490	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	aEYAEK	89%	n+304 (+304), K+304 (+304)	28.06	26.57
3491	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	aLAIVEK	95%	n+304 (+304), K+304 (+304)	30.77	25.00
3492	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	aNIEAEK	91%	n+304 (+304), K+304 (+304)	30.94	27.59
3493	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	aWEENEK	95%	n+304 (+304), K+304 (+304)	40.26	25.00
3494	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	eDVADDK	95%	n+304 (+304), K+304 (+304)	36.75	25.00
3495	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	IIGcFGA	86%	n+304 (+304), Carbamidomethyl (+57)	25.47	25.00

3496	seq=translation; coord=2:22990515..22995670:1; parent_transcript=GRMZM2G122937_T01; parent_gene=GRMZM2G122937 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G122937_P01,GRMZM2G122937_P03	TRUE	TRUE	vSAILSWENTK	95%	n+304 (+304), K+304 (+304)	39.45	26.12
3497	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	fASFETIVELIYk	95%	n+304 (+304), K+304 (+304)	35.76	25.12
3498	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	gATVGDAVK	94%	n+304 (+304), K+304 (+304)	32.21	26.23
3499	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	gLSDGLPk	92%	n+304 (+304), K+304 (+304)	29.08	25.00
3500	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	gWVPPTLLGYSAQGack	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	51.92	26.03
3501	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=5:210169906..210174618:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	sEGVLGLYk	95%	n+304 (+304), K+304 (+304)	45.01	25.61
3502	parent_transcript=GRMZM2G015401_T01; parent_gene=GRMZM2G015401 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G015401_P01,GRMZM2G152827_P01	TRUE	TRUE	siSSGFGILLk	95%	n+304 (+304), K+304 (+304)	42.14	25.00
3503	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	aAGEVLALQk	95%	n+304 (+304), K+304 (+304)	37.91	25.99
3504	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	dRPAGHDWELEPGVTCGDYLFQMLQGTR	95%	n+304 (+304), Carbamidomethyl (+57)	39.78	25.00
3505	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	eGVHNFVTFIEVLR	95%	n+304 (+304)	35.89	26.11
3506	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	iLAFSQDVVSGk	95%	n+304 (+304), K+304 (+304)	37.99	25.79
3507	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=7:127859191..127864034:-1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	mGFTEDFLR	95%	n+304 (+304)	32.06	25.00
3508	parent_transcript=GRMZM2G140614_T01; parent_gene=GRMZM2G140614 seq=translation; coord=1:217021624..217059348:1;	GRMZM2G140614_P01,GRMZM2G140614_P02	TRUE	TRUE	tSEMSAVGLLPAALQGIDIK	95%	n+304 (+304), K+304 (+304)	67.94	25.00
3509	parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542 seq=translation; coord=1:217021624..217059348:1;	GRMZM2G090542_P01	TRUE	TRUE	aVEVTEFFAGQVkpPSFER	95%	n+304 (+304), K+304 (+304)	29.05	25.42
3510	parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542 seq=translation; coord=1:217021624..217059348:1;	GRMZM2G090542_P01	TRUE	TRUE	fALDVAVK	91%	n+304 (+304), K+304 (+304)	25.52	25.00
3511	parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542 seq=translation; coord=1:217021624..217059348:1;	GRMZM2G090542_P01	TRUE	TRUE	fHIFFEDGk	94%	n+304 (+304), K+304 (+304)	28.97	25.77
3512	parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542 seq=translation; coord=1:217021624..217059348:1;	GRMZM2G090542_P01	TRUE	TRUE	fLVLNAAELDVDR	95%	n+304 (+304)	67.04	25.00
3513	parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542	GRMZM2G090542_P01	TRUE	TRUE	ITLEVPSDLVALSNMPVAK	95%	n+304 (+304), K+304 (+304)	29.06	25.00

3514	seq=translation; coord=1:217021624..217059348:1; parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542	GRMZM2G090542_P01	TRUE	TRUE	nMAVTQFEAADAR	95%	n+304 (+304)	36.20	25.00
3515	seq=translation; coord=1:217021624..217059348:1; parent_transcript=GRMZM2G090542_T01; parent_gene=GRMZM2G090542	GRMZM2G090542_P01	TRUE	TRUE	sSSLISDFIESIVPR	95%	n+304 (+304)	62.17	25.15
3516	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	dLTIANTAGPDAHQAFAFR	95%	n+304 (+304)	80.26	25.00
3517	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	eAVAAAPDYGDGAFVVHVk	95%	n+304 (+304), K+304 (+304)	80.40	25.09
3518	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	eTVSVPWEk	93%	n+304 (+304), K+304 (+304)	30.59	25.58
3519	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	IPPAVSTak	95%	n+304 (+304), K+304 (+304)	39.57	25.00
3520	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	tDPAQPTGIVLSR	94%	n+304 (+304)	32.59	26.43
3521	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	tNVVLVGDMGk	87%	n+304 (+304), K+304 (+304)	26.94	26.43
3522	seq=translation; coord=3:171894936..171898201:1; parent_transcript=GRMZM2G167637_T01; parent_gene=GRMZM2G167637	GRMZM2G167637_P01	TRUE	TRUE	vHVDAYSVASFIQGEHWIPR	95%	n+304 (+304)	26.98	25.53
3523	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	dVScPycGSR	88%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	26.38	25.00
3524	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	gFPEVALHFVk	95%	n+304 (+304), K+304 (+304)	49.60	26.19
3525	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	gIFEGGLDATGR	95%	n+304 (+304)	34.73	25.00
3526	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	gWNESASPNVR	89%	n+304 (+304)	26.69	25.00
3527	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	IVLASAMALcFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.93	25.59
3528	seq=translation; coord=1:267609498..267614894:-1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	sALFVAPTPGIPVSIWTQR	95%	n+304 (+304)	41.55	25.00
3529	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G010054_T01; parent_gene=GRMZM2G010054	GRMZM2G010054_P01,GRMZM2G149406_P01	TRUE	TRUE	tVSPADDILR	95%	n+304 (+304)	39.85	26.62
3530	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G180930_T02; parent_gene=GRMZM2G180930	GRMZM2G180930_P02,GRMZM2G180930_P03	TRUE	TRUE	gGPTSVVIYDIHALQER	95%	n+304 (+304)	46.90	25.33
3531	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G180930_T02; parent_gene=GRMZM2G180930	GRMZM2G180930_P02,GRMZM2G180930_P03	TRUE	TRUE	hVVIVDDLVSQGGTLR	95%	n+304 (+304)	47.82	26.34

3532	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G180930_T02; parent_gene=GRMZM2G180930	GRMZM2G180930_P02,GRMZM2G180930_P03	TRUE	TRUE	sFDDGFNPLFINK	95%	n+304 (+304), K+304 (+304)	30.31	25.51
3533	seq=translation; coord=5:202811453..202814808:1; parent_transcript=GRMZM2G180930_T02; parent_gene=GRMZM2G180930	GRMZM2G180930_P02,GRMZM2G180930_P03	TRUE	TRUE	vEEEGDVATAFTLAR	95%	n+304 (+304)	56.17	25.00
3534	seq=translation; coord=2:233428481..233430995:-1; parent_transcript=GRMZM2G018607_T01; parent_gene=GRMZM2G018607	GRMZM2G018607_P01	TRUE	TRUE	sALEAVVADEELTALR	95%	n+304 (+304)	40.60	26.21
3535	seq=translation; coord=2:233428481..233430995:-1; parent_transcript=GRMZM2G018607_T01; parent_gene=GRMZM2G018607	GRMZM2G018607_P01	TRUE	TRUE	vPGSSADDGAVDDNVR	95%	n+304 (+304)	49.15	25.00
3536	seq=translation; coord=6:56216948..56219146:-1; parent_transcript=GRMZM2G385287_T01; parent_gene=GRMZM2G385287	GRMZM2G385287_P01	TRUE	TRUE	hLNLDLFLQEGGR	95%	n+304 (+304)	58.07	25.22
3537	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01,GRMZM2G075719_P02	TRUE	TRUE	dLGVMFIETSAK	95%	n+304 (+304), K+304 (+304)	42.46	26.01
3538	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01,GRMZM2G075719_P02	TRUE	TRUE	dSSVAVIVFDVASR	95%	n+304 (+304)	38.31	25.85
3539	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01,GRMZM2G075719_P02	TRUE	TRUE	iAALPGMETLSSAK	95%	n+304 (+304), K+304 (+304)	39.73	25.00
3540	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01,GRMZM2G075719_P02	TRUE	TRUE	qEDMVDVNL	93%	n+304 (+304)	30.12	25.00
3541	seq=translation; coord=7:150418464..150423441:1; parent_transcript=GRMZM2G075719_T01; parent_gene=GRMZM2G075719	GRMZM2G075719_P01,GRMZM2G075719_P02	TRUE	TRUE	wIDEVR	89%	n+304 (+304)	26.82	25.13
3542	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01,GRMZM2G110714_P02	TRUE	TRUE	fLDILQLHGEDIR	95%	n+304 (+304)	40.55	25.77
3543	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01,GRMZM2G110714_P02	TRUE	TRUE	hTDVMDAITEYLGIGSYR	95%	n+304 (+304)	56.29	25.00
3544	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01,GRMZM2G110714_P02	TRUE	TRUE	ILVSEDLWALGAR	95%	n+304 (+304)	44.85	25.24
3545	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01,GRMZM2G110714_P02	TRUE	TRUE	ISDDDKLVEYDALLDR	95%	n+304 (+304), K+304 (+304)	30.80	25.55
3546	seq=translation; coord=8:173702854..173715423:1; parent_transcript=GRMZM2G110714_T01; parent_gene=GRMZM2G110714	GRMZM2G110714_P01,GRMZM2G110714_P02	TRUE	TRUE	sVADGSLDLFLR	95%	n+304 (+304)	55.72	25.95
3547	seq=translation; coord=6:138057377..138059762:-1; parent_transcript=GRMZM2G078985_T01; parent_gene=GRMZM2G078985	GRMZM2G078985_P01,GRMZM2G156673_P01, GRMZM2G156673_P02	TRUE	TRUE	hTLEIHLITDANPIQVVDAIINSGPR	95%	n+304 (+304)	37.64	25.00
3548	seq=translation; coord=6:138057377..138059762:-1; parent_transcript=GRMZM2G078985_T01; parent_gene=GRMZM2G078985	GRMZM2G078985_P01,GRMZM2G156673_P01, GRMZM2G156673_P02	TRUE	TRUE	qAVDISPLR	91%	n+304 (+304)	30.46	27.16
3549	seq=translation; coord=6:138057377..138059762:-1; parent_transcript=GRMZM2G078985_T01; parent_gene=GRMZM2G078985	GRMZM2G078985_P01,GRMZM2G156673_P01, GRMZM2G156673_P02	TRUE	TRUE	tIAeCLADELINAak	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	51.63	26.78

3550	seq=translation; coord=6:138057377..138059762:-1; parent_transcript=GRMZM2G078985_T01; parent_gene=GRMZM2G078985	GRMZM2G078985_P01,GRMZM2G156673_P01, GRMZM2G156673_P02	TRUE	TRUE	vNQAIYLLTTGAR	95%	n+304 (+304)	36.23	25.00
3551	seq=translation; coord=6:108069110..108070157:1; parent_transcript=GRMZM2G073150_T01; parent_gene=GRMZM2G073150	GRMZM2G073150_P01	TRUE	TRUE	qAEVSSVPAYGRPQYGGPR	88%	Pyro-cmC (-17), n+304 (+304)	25.98	25.00
3552	seq=translation; coord=6:108069110..108070157:1; parent_transcript=GRMZM2G073150_T01; parent_gene=GRMZM2G073150	GRMZM2G073150_P01	TRUE	TRUE	sALEVEEIR	95%	n+304 (+304)	39.27	26.14
3553	seq=translation; coord=6:108069110..108070157:1; parent_transcript=GRMZM2G073150_T01; parent_gene=GRMZM2G073150	GRMZM2G073150_P01	TRUE	TRUE	vDKETMEMLAALGMADLPGVER	95%	n+304 (+304), K+304 (+304)	45.62	25.00
3554	seq=translation; coord=6:108069110..108070157:1; parent_transcript=GRMZM2G073150_T01; parent_gene=GRMZM2G073150	GRMZM2G073150_P01	TRUE	TRUE	vLEEVSILPSk	95%	n+304 (+304), K+304 (+304)	33.18	25.05
3555	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	TRUE	TRUE	gkPYYADLLDLFNEVEFK	95%	n+304 (+304), K+304 (+304)	26.14	25.08
3556	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	TRUE	TRUE	lIADIEAQPSIAVQk	95%	n+304 (+304), K+304 (+304)	54.64	25.00
3557	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	TRUE	TRUE	mVDYNVLGgk	95%	n+304 (+304), K+304 (+304)	36.08	26.32
3558	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	TRUE	TRUE	tLkEELLTDPAFEFTEESR	95%	n+304 (+304), K+304 (+304)	43.92	25.53
3559	seq=translation; coord=8:63271714..63275991:-1; parent_transcript=GRMZM2G168681_T01; parent_gene=GRMZM2G168681	GRMZM2G168681_P01	TRUE	TRUE	vPQVGliaANDGIILR	95%	n+304 (+304)	70.96	25.00
3560	seq=translation; coord=3:186781963..186783499:-1; parent_transcript=GRMZM2G460860_T01; parent_gene=GRMZM2G460860	GRMZM2G460860_P01	TRUE	TRUE	gGILGLLAGWAAR	95%	n+304 (+304)	44.39	25.00
3561	seq=translation; coord=3:186781963..186783499:-1; parent_transcript=GRMZM2G460860_T01; parent_gene=GRMZM2G460860	GRMZM2G460860_P01	TRUE	TRUE	lIAVGNAADAINEAR	95%	n+304 (+304)	65.81	26.01
3562	seq=translation; coord=3:186781963..186783499:-1; parent_transcript=GRMZM2G460860_T01; parent_gene=GRMZM2G460860	GRMZM2G460860_P01	TRUE	TRUE	vSVVALR	95%	n+304 (+304)	36.13	25.00
3563	seq=translation; coord=8:69592559..69594672:1; parent_transcript=GRMZM2G001514_T01; parent_gene=GRMZM2G001514	GRMZM2G001514_P01	TRUE	TRUE	dDQFSEfk	95%	n+304 (+304), K+304 (+304)	38.24	25.00
3564	seq=translation; coord=8:69592559..69594672:1; parent_transcript=GRMZM2G001514_T01; parent_gene=GRMZM2G001514	GRMZM2G001514_P01	TRUE	TRUE	fYSLsMLGTLDGk	95%	n+304 (+304), K+304 (+304)	33.63	25.49
3565	seq=translation; coord=6:142310594..142315324:-1; parent_transcript=GRMZM2G001514_T01; parent_gene=GRMZM2G001514	GRMZM2G001514_P01	TRUE	TRUE	fYSLsMLGTLDGk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	36.76	26.19
3566	seq=translation; coord=6:142310594..142315324:-1; parent_transcript=GRMZM2G137535_T01; parent_gene=GRMZM2G137535	GRMZM2G137535_P01,GRMZM2G137535_P02	TRUE	TRUE	eSGVEQNWGLFYPNMQHvyPISF	95%	n+304 (+304), iTRAQ8plex (+304)	33.92	25.00
3567	seq=translation; coord=6:142310594..142315324:-1; parent_transcript=GRMZM2G137535_T01; parent_gene=GRMZM2G137535	GRMZM2G137535_P01,GRMZM2G137535_P02	TRUE	TRUE	gYMGpVLQFLAR	95%	n+304 (+304)	37.82	25.00

3568	seq=translation; coord=6:142310594..142315324:-1; parent_transcript=GRMZM2G137535_T01; parent_gene=GRMZM2G137535 seq=translation; coord=5:169817842..169818381:1;	GRMZM2G137535_P01,GRMZM2G137535_P02	TRUE	TRUE	hPGAITYLFSMFNENQk	95%	n+304 (+304), K+304 (+304)	44.06	25.00
3569	parent_transcript=AC233850.1_FGT002; parent_gene=AC233850.1_FG002 seq=translation; coord=5:169817842..169818381:1;	AC233850.1_FGP002	TRUE	TRUE	IYDAAEMAFAEAYDGINR	95%	n+304 (+304)	56.04	25.00
3570	parent_transcript=AC233850.1_FGT002; parent_gene=AC233850.1_FG002 seq=translation; coord=5:169817842..169818381:1;	AC233850.1_FGP002	TRUE	TRUE	IyDAAEMAFAEAYDGINR	95%	n+304 (+304), iTRAQ8plex (+304)	72.37	25.00
3571	parent_transcript=AC233850.1_FGT002; parent_gene=AC233850.1_FG002 seq=translation; coord=5:169817842..169818381:1;	AC233850.1_FGP002	TRUE	TRUE	IYDAAEMAFAEAYDGINR	95%	n+304 (+304), iTRAQ8plex (+304)	46.59	25.00
3572	parent_transcript=AC233850.1_FGT002; parent_gene=AC233850.1_FG002 seq=translation; coord=6:69568276..69571793:-1;	AC233850.1_FGP002	TRUE	TRUE	vAADVGVATAGDAVYDIk	95%	n+304 (+304), K+304 (+304)	95.70	25.87
3573	parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775 seq=translation; coord=6:69568276..69571793:-1;	GRMZM2G152775_P04	TRUE	TRUE	eGMSQEEAEk	95%	n+304 (+304), K+304 (+304)	41.62	25.00
3574	parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775 seq=translation; coord=6:69568276..69571793:-1;	GRMZM2G152775_P04	TRUE	TRUE	iTQLTDNVVYcR	95%	n+304 (+304), Carbamidomethyl (+57)	41.79	25.00
3575	parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775 seq=translation; coord=6:69568276..69571793:-1;	GRMZM2G152775_P04	TRUE	TRUE	ILAYQNk	91%	n+304 (+304), K+304 (+304)	27.77	25.00
3576	parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775 seq=translation; coord=6:69568276..69571793:-1;	GRMZM2G152775_P04	TRUE	TRUE	nMLQAGMIVGGWdk	95%	n+304 (+304), K+304 (+304)	47.02	25.61
3577	parent_transcript=GRMZM2G152775_T04; parent_gene=GRMZM2G152775 seq=translation; coord=4:193735481..193760758:1;	GRMZM2G152775_P04	TRUE	TRUE	sGSAADTQVISDYVR	95%	n+304 (+304)	33.85	25.00
3578	parent_transcript=AC215244.3_FGT002; parent_gene=AC215244.3_FG002 seq=translation; coord=4:193735481..193760758:1;	AC215244.3_FGP002	TRUE	TRUE	qGLPPAGFSNPFDGSMQSLNDPSIk	95%	n+304 (+304), K+304 (+304)	48.99	25.00
3579	parent_transcript=AC215244.3_FGT002; parent_gene=AC215244.3_FG002 seq=translation; coord=4:193735481..193760758:1;	AC215244.3_FGP002	TRUE	TRUE	vMENPQFMTMAER	95%	n+304 (+304)	57.81	25.00
3580	parent_transcript=AC215244.3_FGT002; parent_gene=AC215244.3_FG002 seq=translation; coord=2:2326285..2329820:1;	AC215244.3_FGP002	TRUE	TRUE	yWNDPDTLQk	95%	n+304 (+304), K+304 (+304)	38.72	25.00
3581	parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541 seq=translation; coord=2:2326285..2329820:1;	GRMZM2G077541_P01,GRMZM2G077541_P02	TRUE	TRUE	aPEYLAMDEk	93%	n+304 (+304), K+304 (+304)	27.62	25.00
3582	parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541 seq=translation; coord=2:2326285..2329820:1;	GRMZM2G077541_P01,GRMZM2G077541_P02	TRUE	TRUE	gHNFTLNASFDEITASEYDGLVIPGGR	95%	n+304 (+304)	42.09	25.00
3583	parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541 seq=translation; coord=2:2326285..2329820:1;	GRMZM2G077541_P01,GRMZM2G077541_P02	TRUE	TRUE	gHNFTLNASFDEITASEYDGLVIPGGR	95%	n+304 (+304), iTRAQ8plex (+304)	27.01	25.00
3584	parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541 seq=translation; coord=2:2326285..2329820:1;	GRMZM2G077541_P01,GRMZM2G077541_P02	TRUE	TRUE	INVLLGGGTWLEPDIHR	95%	n+304 (+304)	74.32	25.89
3585	parent_transcript=GRMZM2G077541_T01; parent_gene=GRMZM2G077541	GRMZM2G077541_P01,GRMZM2G077541_P02	TRUE	TRUE	wEEDPTMAk	95%	n+304 (+304), K+304 (+304)	32.95	25.00

3586	seq=translation; coord=7:41731651..41795285:-1; parent_transcript=GRMZM2G069676_T02; parent_gene=GRMZM2G069676 seq=translation; coord=7:41731651..41795285:-1;	GRMZM2G069676_P02,GRMZM2G069676_P03	TRUE	TRUE	aDLGIIFDQDVDR	95%	n+304 (+304)	32.77	25.00
3587	seq=translation; coord=7:41731651..41795285:-1; parent_transcript=GRMZM2G069676_T02; parent_gene=GRMZM2G069676 seq=translation; coord=7:41731651..41795285:-1;	GRMZM2G069676_P02,GRMZM2G069676_P03	TRUE	TRUE	aIAAAFAAWLLNK	95%	n+304 (+304), K+304 (+304)	31.47	25.00
3588	seq=translation; coord=7:41731651..41795285:-1; parent_transcript=GRMZM2G069676_T02; parent_gene=GRMZM2G069676 seq=translation; coord=7:41731651..41795285:-1;	GRMZM2G069676_P02,GRMZM2G069676_P03	TRUE	TRUE	gVVTNVDDYMSIYASDLVQAVR	95%	n+304 (+304)	30.47	25.29
3589	seq=translation; coord=7:41731651..41795285:-1; parent_transcript=GRMZM2G069676_T02; parent_gene=GRMZM2G069676 seq=translation; coord=6:165533613..165537241:1;	GRMZM2G069676_P02,GRMZM2G069676_P03	TRUE	TRUE	IGLAVLAAVNEFPALDVTALNK	95%	n+304 (+304), K+304 (+304)	31.70	25.00
3590	seq=translation; coord=6:165533613..165537241:1; parent_transcript=GRMZM5G829778_T01; parent_gene=GRMZM5G829778 seq=translation; coord=6:165533613..165537241:1;	GRMZM5G829778_P01	TRUE	TRUE	IIFPFVDLDIK	95%	n+304 (+304), K+304 (+304)	38.92	25.00
3591	seq=translation; coord=6:165533613..165537241:1; parent_transcript=GRMZM5G829778_T01; parent_gene=GRMZM5G829778 seq=translation; coord=6:165533613..165537241:1;	GRMZM5G829778_P01	TRUE	TRUE	sHYLNTEEFIDAVADELR	95%	n+304 (+304)	44.08	25.00
3592	seq=translation; coord=6:165533613..165537241:1; parent_transcript=GRMZM5G829778_T01; parent_gene=GRMZM5G829778 seq=translation; coord=6:165533613..165537241:1;	GRMZM5G829778_P01	TRUE	TRUE	sHyLNTEEFIDAVADELR	95%	n+304 (+304), iTRAQ8plex (+304)	27.18	25.00
3593	seq=translation; coord=6:165533613..165537241:1; parent_transcript=GRMZM5G829778_T01; parent_gene=GRMZM5G829778 seq=translation; coord=10:106428641..106433063:1;	GRMZM5G829778_P01	TRUE	TRUE	yFDLGLPHR	95%	n+304 (+304)	48.44	25.00
3594	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407 seq=translation; coord=10:106428641..106433063:1;	GRMZM2G139407_P01,GRMZM2G139407_P02	TRUE	TRUE	eFVQSFFLAPQEK	95%	n+304 (+304), K+304 (+304)	29.41	25.53
3595	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407 seq=translation; coord=10:106428641..106433063:1;	GRMZM2G139407_P01,GRMZM2G139407_P02	TRUE	TRUE	gYFVLNDILR	95%	n+304 (+304)	42.19	26.43
3596	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407 seq=translation; coord=10:106428641..106433063:1;	GRMZM2G139407_P01,GRMZM2G139407_P02	TRUE	TRUE	IGRPSGTGDDGMETVTSMDAINDK	95%	n+304 (+304), K+304 (+304)	32.06	25.00
3597	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407 seq=translation; coord=10:106428641..106433063:1;	GRMZM2G139407_P01,GRMZM2G139407_P02	TRUE	TRUE	sLPLNATPQQLEEEFK	90%	n+304 (+304), K+304 (+304)	27.45	25.93
3598	seq=translation; coord=10:106428641..106433063:1; parent_transcript=GRMZM2G139407_T01; parent_gene=GRMZM2G139407 seq=translation; coord=4:83505768..83508091:1;	GRMZM2G139407_P01,GRMZM2G139407_P02	TRUE	TRUE	sLPLNATPQQLEEEFKR	90%	n+304 (+304), K+304 (+304)	26.73	26.32
3599	seq=translation; coord=4:83505768..83508091:1; parent_transcript=GRMZM2G068455_T01; parent_gene=GRMZM2G068455 seq=translation; coord=4:83505768..83508091:1;	GRMZM2G068455_P01,GRMZM2G068455_P02, GRMZM2G068455_P03	TRUE	TRUE	gIAFVNk	90%	n+304 (+304), K+304 (+304)	27.82	26.20
3600	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G068455_T01; parent_gene=GRMZM2G068455 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G068455_P01,GRMZM2G068455_P02, GRMZM2G068455_P03	TRUE	TRUE	vAVLGAAGGIGQLGLLVK	95%	n+304 (+304), K+304 (+304)	47.56	25.00
3601	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	aPDSAPVAQPPR	95%	n+304 (+304)	46.93	25.15
3602	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	dLQLIASSVLLAALSVSPYDKK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	36.16	25.00
3603	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	dLYNLEHEFLPLDLASK	94%	n+304 (+304), K+304 (+304)	26.81	26.48

3604	seq=translation; coord=3:7404885..7413183:1; parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	dRPDLTAPESLQLYLDTR	95%	n+304 (+304)	77.43	25.13
3605	parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	qSALQALHDLITsk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.92	25.58
3606	parent_transcript=GRMZM2G093050_T01; parent_gene=GRMZM2G093050 seq=translation; coord=3:7404885..7413183:1;	GRMZM2G093050_P01,GRMZM2G093050_P02	TRUE	TRUE	tMDYLER	94%	n+304 (+304)	30.58	25.00
3607	parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133 seq=translation; coord=1:215329050..215330533:1;	GRMZM2G106133_P02	TRUE	TRUE	aGAPDAPPk	94%	n+304 (+304), K+304 (+304)	32.27	26.65
3608	parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133 seq=translation; coord=1:215329050..215330533:1;	GRMZM2G106133_P02	TRUE	TRUE	dPNAPAPAPk	95%	n+304 (+304), K+304 (+304)	35.51	26.25
3609	parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133 seq=translation; coord=1:215329050..215330533:1;	GRMZM2G106133_P02	TRUE	TRUE	eSGELVFLk	95%	n+304 (+304), K+304 (+304)	29.27	25.04
3610	parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133 seq=translation; coord=1:215329050..215330533:1;	GRMZM2G106133_P02	TRUE	TRUE	sPLEAAVk	95%	n+304 (+304), K+304 (+304)	37.67	25.00
3611	parent_transcript=GRMZM2G106133_T02; parent_gene=GRMZM2G106133 seq=translation; coord=5:215493131..215497186:1;	GRMZM2G106133_P02	TRUE	TRUE	vRPAVPSETAAA	88%	n+304 (+304)	27.73	26.50
3612	parent_transcript=GRMZM5G824600_T03; parent_gene=GRMZM5G824600 seq=translation; coord=5:215493131..215497186:1;	GRMZM5G824600_P03	TRUE	TRUE	gTAFGGFk	90%	n+304 (+304), K+304 (+304)	27.14	25.00
3613	parent_transcript=GRMZM5G824600_T03; parent_gene=GRMZM5G824600 seq=translation; coord=5:215493131..215497186:1;	GRMZM5G824600_P03	TRUE	TRUE	gWGTSVIVGVAASGQEIATRPFLVTGR	95%	n+304 (+304)	28.12	25.00
3614	parent_transcript=GRMZM5G824600_T03; parent_gene=GRMZM5G824600 seq=translation; coord=5:215493131..215497186:1;	GRMZM5G824600_P03	TRUE	TRUE	nFGVTEFVNPk	95%	n+304 (+304), K+304 (+304)	57.90	25.93
3615	parent_transcript=GRMZM5G824600_T03; parent_gene=GRMZM5G824600 seq=translation; coord=7:46478537..46482054:1;	GRMZM5G824600_P03	TRUE	TRUE	vIGIDIDNk	95%	n+304 (+304), K+304 (+304)	34.07	27.23
3616	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129 seq=translation; coord=7:46478537..46482054:1;	GRMZM2G011129_P01	TRUE	TRUE	gFGFVTMASQDELDDAIALDGQSLDGR	95%	n+304 (+304)	36.92	25.00
3617	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129 seq=translation; coord=7:46478537..46482054:1;	GRMZM2G011129_P01	TRUE	TRUE	gFGFVTMSTVEEAk	95%	n+304 (+304), K+304 (+304)	36.44	25.25
3618	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129 seq=translation; coord=7:46478537..46482054:1;	GRMZM2G011129_P01	TRUE	TRUE	iYVGNLPWQVDDSR	95%	n+304 (+304)	42.81	25.00
3619	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129 seq=translation; coord=7:46478537..46482054:1;	GRMZM2G011129_P01	TRUE	TRUE	IAQLFDQAGVVEVAEViYnR	95%	n+304 (+304), iTRAQ8plex (+304)	43.77	25.00
3620	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129 seq=translation; coord=7:46478537..46482054:1;	GRMZM2G011129_P01	TRUE	TRUE	IVELFSEHGk	95%	n+304 (+304), K+304 (+304)	43.95	26.33
3621	parent_transcript=GRMZM2G011129_T01; parent_gene=GRMZM2G011129	GRMZM2G011129_P01	TRUE	TRUE	vYVGNLPYDVDSER	95%	n+304 (+304)	66.99	25.00

3622	seq=translation; coord=1:10991438..10998924:-1; parent_transcript=GRMZM2G056870_T01; parent_gene=GRMZM2G056870	GRMZM2G056870_P01	TRUE	TRUE	eLTLQEAETIALSILK	95%	n+304 (+304), K+304 (+304)	41.09	25.00
3623	seq=translation; coord=3:223089120..223091094:-1; parent_transcript=GRMZM2G042008_T01; parent_gene=GRMZM2G042008	GRMZM2G042008_P01	TRUE	TRUE	gGLSFPTQISR	95%	n+304 (+304)	37.35	25.00
3624	seq=translation; coord=3:223089120..223091094:-1; parent_transcript=GRMZM2G042008_T01; parent_gene=GRMZM2G042008	GRMZM2G042008_P01	TRUE	TRUE	gGVIVDSGTSVTR	95%	n+304 (+304)	53.21	25.00
3625	seq=translation; coord=3:190774183..190777585:1; parent_transcript=GRMZM2G042008_T01; parent_gene=GRMZM2G042008	GRMZM2G042008_P01	TRUE	TRUE	vALGcGHDNEGLFVAAAGLLGLGR	95%	n+304 (+304), Carbamidomethyl (+57)	55.80	25.22
3626	seq=translation; coord=3:190774183..190777585:1; parent_transcript=GRMZM2G062373_T01; parent_gene=GRMZM2G062373	GRMZM2G062373_P01,GRMZM2G062373_P02	TRUE	TRUE	aQDLAQLPLVDAQIPFk	94%	n+304 (+304), K+304 (+304)	31.45	25.55
3627	seq=translation; coord=3:190774183..190777585:1; parent_transcript=GRMZM2G062373_T01; parent_gene=GRMZM2G062373	GRMZM2G062373_P01,GRMZM2G062373_P02	TRUE	TRUE	ISTSadAPASVR	92%	n+304 (+304)	29.72	25.90
3628	seq=translation; coord=9:136867378..136869080:1; parent_transcript=GRMZM2G030293_T01; parent_gene=GRMZM2G030293	GRMZM2G030293_P01,GRMZM2G030293_P02, GRMZM2G124143_P01,GRMZM2G124143_P02, GRMZM2G124143_P03,GRMZM2G455828_P01, GRMZM2G455828_P02,GRMZM2G455828_P03, GRMZM2G455828_P04 AC196961.2_FGP003,ALZ1Z565.3_FGP001,ALZ 33865.1_FGP001,GRMZM2G016232_P01,GRMZ M2G016232_P02,GRMZM2G063896_P01,GRMZ M2G063896_P02,GRMZM2G072855_P01,GRMZ M2G073275_P01,GRMZM2G084195_P01,GRMZ M2G143780_P01,GRMZM2G143780_P02,GRMZ M2G143780_P03,GRMZM2G149178_P01,GRMZ M2G181153_P01,GRMZM2G332838_P01,GRMZ M2G332838_P02,GRMZM2G349651_P01,GRMZ M2G349651_P02,GRMZM2G421279_P01,GRMZ M2G479684_P01 AC196961.2_FGP003,ALZ1Z565.3_FGP001,ALZ 33865.1_FGP001,GRMZM2G016232_P01,GRMZ M2G016232_P02,GRMZM2G063896_P01,GRMZ M2G063896_P02,GRMZM2G072855_P01,GRMZ M2G073275_P01,GRMZM2G084195_P01,GRMZ M2G143780_P01,GRMZM2G143780_P02,GRMZ M2G143780_P03,GRMZM2G149178_P01,GRMZ M2G181153_P01,GRMZM2G332838_P01,GRMZ M2G332838_P02,GRMZM2G349651_P01,GRMZ M2G349651_P02,GRMZM2G421279_P01,GRMZ M2G479684_P01	TRUE	TRUE	eGDILTLESER	95%	n+304 (+304)	79.55	25.00
3629	seq=translation; coord=7:148082947..148083258:1; parent_transcript=AC196961.2_FGT003; parent_gene=AC196961.2_FG003	GRMZM2G016232_P01,GRMZ M2G016232_P02,GRMZM2G063896_P01,GRMZ M2G063896_P02,GRMZM2G072855_P01,GRMZ M2G073275_P01,GRMZM2G084195_P01,GRMZ M2G143780_P01,GRMZM2G143780_P02,GRMZ M2G143780_P03,GRMZM2G149178_P01,GRMZ M2G181153_P01,GRMZM2G332838_P01,GRMZ M2G332838_P02,GRMZM2G349651_P01,GRMZ M2G349651_P02,GRMZM2G421279_P01,GRMZ M2G479684_P01 AC196961.2_FGP003,ALZ1Z565.3_FGP001,ALZ 33865.1_FGP001,GRMZM2G016232_P01,GRMZ M2G016232_P02,GRMZM2G063896_P01,GRMZ M2G063896_P02,GRMZM2G072855_P01,GRMZ M2G073275_P01,GRMZM2G084195_P01,GRMZ M2G143780_P01,GRMZM2G143780_P02,GRMZ M2G143780_P03,GRMZM2G149178_P01,GRMZ M2G181153_P01,GRMZM2G332838_P01,GRMZ M2G332838_P02,GRMZM2G349651_P01,GRMZ M2G349651_P02,GRMZM2G421279_P01,GRMZ M2G479684_P01	TRUE	TRUE	dAVTYTEHAR	95%	n+304 (+304)	49.18	25.00
3630	seq=translation; coord=7:148082947..148083258:1; parent_transcript=AC196961.2_FGT003; parent_gene=AC196961.2_FG003	GRMZM2G016232_P01,GRMZ M2G016232_P02,GRMZM2G063896_P01,GRMZ M2G063896_P02,GRMZM2G072855_P01,GRMZ M2G073275_P01,GRMZM2G084195_P01,GRMZ M2G143780_P01,GRMZM2G143780_P02,GRMZ M2G143780_P03,GRMZM2G149178_P01,GRMZ M2G181153_P01,GRMZM2G332838_P01,GRMZ M2G332838_P02,GRMZM2G349651_P01,GRMZ M2G349651_P02,GRMZM2G421279_P01,GRMZ M2G479684_P01	TRUE	TRUE	dNIQGITkPAIR	95%	n+304 (+304), K+304 (+304)	37.66	25.54

3631	seq=translation; coord=7:148082947..148083258:1; parent_transcript=AC196961.2_FGT003; parent_gene=AC196961.2_FG003	AC196961.2_FGP003,AC112565.3_FGP001,AC112565.3_FGP001,GRMZM2G016232_P01,GRMZM2G016232_P02,GRMZM2G063896_P01,GRMZM2G063896_P02,GRMZM2G072855_P01,GRMZM2G073275_P01,GRMZM2G084195_P01,GRMZM2G143780_P01,GRMZM2G143780_P02,GRMZM2G143780_P03,GRMZM2G149178_P01,GRMZM2G181153_P01,GRMZM2G332838_P01,GRMZM2G332838_P02,GRMZM2G349651_P01,GRMZM2G349651_P02,GRMZM2G421279_P01,GRMZM2G421279_P02,GRMZM2G421279_P03,GRMZM2G421279_P04,GRMZM2G421279_P05,GRMZM2G421279_P06,GRMZM2G421279_P07,GRMZM2G421279_P08,GRMZM2G421279_P09,GRMZM2G421279_P10,GRMZM2G421279_P11,GRMZM2G421279_P12,GRMZM2G421279_P13,GRMZM2G421279_P14,GRMZM2G421279_P15,GRMZM2G421279_P16,GRMZM2G421279_P17,GRMZM2G421279_P18,GRMZM2G421279_P19,GRMZM2G421279_P20,GRMZM2G421279_P21,GRMZM2G421279_P22,GRMZM2G421279_P23,GRMZM2G421279_P24,GRMZM2G421279_P25,GRMZM2G421279_P26,GRMZM2G421279_P27,GRMZM2G421279_P28,GRMZM2G421279_P29,GRMZM2G421279_P30,GRMZM2G421279_P31,GRMZM2G421279_P32,GRMZM2G421279_P33,GRMZM2G421279_P34,GRMZM2G421279_P35,GRMZM2G421279_P36,GRMZM2G421279_P37,GRMZM2G421279_P38,GRMZM2G421279_P39,GRMZM2G421279_P40,GRMZM2G421279_P41,GRMZM2G421279_P42,GRMZM2G421279_P43,GRMZM2G421279_P44,GRMZM2G421279_P45,GRMZM2G421279_P46,GRMZM2G421279_P47,GRMZM2G421279_P48,GRMZM2G421279_P49,GRMZM2G421279_P50,GRMZM2G421279_P51,GRMZM2G421279_P52,GRMZM2G421279_P53,GRMZM2G421279_P54,GRMZM2G421279_P55,GRMZM2G421279_P56,GRMZM2G421279_P57,GRMZM2G421279_P58,GRMZM2G421279_P59,GRMZM2G421279_P60,GRMZM2G421279_P61,GRMZM2G421279_P62,GRMZM2G421279_P63,GRMZM2G421279_P64,GRMZM2G421279_P65,GRMZM2G421279_P66,GRMZM2G421279_P67,GRMZM2G421279_P68,GRMZM2G421279_P69,GRMZM2G421279_P70,GRMZM2G421279_P71,GRMZM2G421279_P72,GRMZM2G421279_P73,GRMZM2G421279_P74,GRMZM2G421279_P75,GRMZM2G421279_P76,GRMZM2G421279_P77,GRMZM2G421279_P78,GRMZM2G421279_P79,GRMZM2G421279_P80,GRMZM2G421279_P81,GRMZM2G421279_P82,GRMZM2G421279_P83,GRMZM2G421279_P84,GRMZM2G421279_P85,GRMZM2G421279_P86,GRMZM2G421279_P87,GRMZM2G421279_P88,GRMZM2G421279_P89,GRMZM2G421279_P90,GRMZM2G421279_P91,GRMZM2G421279_P92,GRMZM2G421279_P93,GRMZM2G421279_P94,GRMZM2G421279_P95,GRMZM2G421279_P96,GRMZM2G421279_P97,GRMZM2G421279_P98,GRMZM2G421279_P99,GRMZM2G421279_P100,GRMZM2G421279_P101,GRMZM2G421279_P102,GRMZM2G421279_P103,GRMZM2G421279_P104,GRMZM2G421279_P105,GRMZM2G421279_P106,GRMZM2G421279_P107,GRMZM2G421279_P108,GRMZM2G421279_P109,GRMZM2G421279_P110,GRMZM2G421279_P111,GRMZM2G421279_P112,GRMZM2G421279_P113,GRMZM2G421279_P114,GRMZM2G421279_P115,GRMZM2G421279_P116,GRMZM2G421279_P117,GRMZM2G421279_P118,GRMZM2G421279_P119,GRMZM2G421279_P120,GRMZM2G421279_P121,GRMZM2G421279_P122,GRMZM2G421279_P123,GRMZM2G421279_P124,GRMZM2G421279_P125,GRMZM2G421279_P126,GRMZM2G421279_P127,GRMZM2G421279_P128,GRMZM2G421279_P129,GRMZM2G421279_P130,GRMZM2G421279_P131,GRMZM2G421279_P132,GRMZM2G421279_P133,GRMZM2G421279_P134,GRMZM2G421279_P135,GRMZM2G421279_P136,GRMZM2G421279_P137,GRMZM2G421279_P138,GRMZM2G421279_P139,GRMZM2G421279_P140,GRMZM2G421279_P141,GRMZM2G421279_P142,GRMZM2G421279_P143,GRMZM2G421279_P144,GRMZM2G421279_P145,GRMZM2G421279_P146,GRMZM2G421279_P147,GRMZM2G421279_P148,GRMZM2G421279_P149,GRMZM2G421279_P150,GRMZM2G421279_P151,GRMZM2G421279_P152,GRMZM2G421279_P153,GRMZM2G421279_P154,GRMZM2G421279_P155,GRMZM2G421279_P156,GRMZM2G421279_P157,GRMZM2G421279_P158,GRMZM2G421279_P159,GRMZM2G421279_P160,GRMZM2G421279_P161,GRMZM2G421279_P162,GRMZM2G421279_P163,GRMZM2G421279_P164,GRMZM2G421279_P165,GRMZM2G421279_P166,GRMZM2G421279_P167,GRMZM2G421279_P168,GRMZM2G421279_P169,GRMZM2G421279_P170,GRMZM2G421279_P171,GRMZM2G421279_P172,GRMZM2G421279_P173,GRMZM2G421279_P174,GRMZM2G421279_P175,GRMZM2G421279_P176,GRMZM2G421279_P177,GRMZM2G421279_P178,GRMZM2G421279_P179,GRMZM2G421279_P180,GRMZM2G421279_P181,GRMZM2G421279_P182,GRMZM2G421279_P183,GRMZM2G421279_P184,GRMZM2G421279_P185,GRMZM2G421279_P186,GRMZM2G421279_P187,GRMZM2G421279_P188,GRMZM2G421279_P189,GRMZM2G421279_P190,GRMZM2G421279_P191,GRMZM2G421279_P192,GRMZM2G421279_P193,GRMZM2G421279_P194,GRMZM2G421279_P195,GRMZM2G421279_P196,GRMZM2G421279_P197,GRMZM2G421279_P198,GRMZM2G421279_P199,GRMZM2G421279_P200,GRMZM2G421279_P201,GRMZM2G421279_P202,GRMZM2G421279_P203,GRMZM2G421279_P204,GRMZM2G421279_P205,GRMZM2G421279_P206,GRMZM2G421279_P207,GRMZM2G421279_P208,GRMZM2G421279_P209,GRMZM2G421279_P210,GRMZM2G421279_P211,GRMZM2G421279_P212,GRMZM2G421279_P213,GRMZM2G421279_P214,GRMZM2G421279_P215,GRMZM2G421279_P216,GRMZM2G421279_P217,GRMZM2G421279_P218,GRMZM2G421279_P219,GRMZM2G421279_P220,GRMZM2G421279_P221,GRMZM2G421279_P222,GRMZM2G421279_P223,GRMZM2G421279_P224,GRMZM2G421279_P225,GRMZM2G421279_P226,GRMZM2G421279_P227,GRMZM2G421279_P228,GRMZM2G421279_P229,GRMZM2G421279_P230,GRMZM2G421279_P231,GRMZM2G421279_P232,GRMZM2G421279_P233,GRMZM2G421279_P234,GRMZM2G421279_P235,GRMZM2G421279_P236,GRMZM2G421279_P237,GRMZM2G421279_P238,GRMZM2G421279_P
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3641	seq=translation; coord=1:41376931..41378234:-1; parent_transcript=GRMZM2G172574_T01; parent_gene=GRMZM2G172574	GRMZM2G172574_P01	TRUE	TRUE	eTDELSGAVQLPDSSAAGR	95%	n+304 (+304)	110.85	25.00
3642	seq=translation; coord=1:41376931..41378234:-1; parent_transcript=GRMZM2G172574_T01; parent_gene=GRMZM2G172574	GRMZM2G172574_P01	TRUE	TRUE	IAYIILYVR	88%	n+304 (+304)	25.73	25.00
3643	seq=translation; coord=1:41376931..41378234:-1; parent_transcript=GRMZM2G172574_T01; parent_gene=GRMZM2G172574	GRMZM2G172574_P01	TRUE	TRUE	wAELESGATTIAFTPLHQR	95%	n+304 (+304)	61.46	25.50
3644	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	dIPIEVLELENk	95%	n+304 (+304), K+304 (+304)	39.77	25.34
3645	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	eVEVEEVVDVR	95%	n+304 (+304)	37.44	25.00
3646	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	iIAFAWEpk	95%	n+304 (+304), K+304 (+304)	37.04	25.77
3647	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	kYEQEDQDAFNQLSEQDR	95%	K+304 (+304), n+304 (+304)	33.26	25.00
3648	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	sHIFAVNLLDDFEk	95%	n+304 (+304), K+304 (+304)	29.03	26.03
3649	seq=translation; coord=1:96834561..96839284:-1; parent_transcript=GRMZM2G174757_T01; parent_gene=GRMZM2G174757	GRMZM2G174757_P01	TRUE	TRUE	vVLNIFDVR	95%	n+304 (+304)	37.34	25.00
3650	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	aMALNMGMLASYDQSVELFR	95%	n+304 (+304)	47.91	25.00
3651	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	gLSAGLLR	93%	n+304 (+304)	30.02	25.00
3652	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	iAPHVMMTWIFLNQIQk	95%	n+304 (+304), K+304 (+304)	45.45	25.00
3653	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	iQLGEGSAGQVTR	95%	n+304 (+304)	38.79	25.99
3654	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	iSADEGVLALWk	95%	n+304 (+304), K+304 (+304)	35.55	26.01
3655	seq=translation; coord=6:131159543..131163430:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	mQADSTLPAAQR	91%	n+304 (+304)	26.75	25.00
3656	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G051630_T01; parent_gene=GRMZM2G051630	GRMZM2G051630_P01	TRUE	TRUE	nMLANEGVR	94%	n+304 (+304)	29.47	25.00
3657	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G019236_T01; parent_gene=GRMZM2G019236	GRMZM2G019236_P01,GRMZM2G019236_P03, GRMZM2G019236_P05	TRUE	TRUE	ILPLYTLALVk	95%	n+304 (+304), K+304 (+304)	28.87	25.00
3658	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G019236_T01; parent_gene=GRMZM2G019236	GRMZM2G019236_P01,GRMZM2G019236_P03, GRMZM2G019236_P05	TRUE	TRUE	ILVFQSVLPSLGIGLSAR	95%	n+304 (+304)	34.51	25.00

3659	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G019236_T01; parent_gene=GRMZM2G019236	GRMZM2G019236_P01,GRMZM2G019236_P03, GRMZM2G019236_P05	TRUE	TRUE	rVPTDIDLPAIDSDk	95%	n+304 (+304), K+304 (+304)	30.66	25.53
3660	seq=translation; coord=4:19423579..19439397:-1; parent_transcript=GRMZM2G019236_T01; parent_gene=GRMZM2G019236	GRMZM2G019236_P01,GRMZM2G019236_P03, GRMZM2G019236_P05	TRUE	TRUE	yADLETQFAcFLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	45.66	25.31
3661	seq=translation; coord=7:41420177..41423983:-1; parent_transcript=GRMZM2G014914_T01; parent_gene=GRMZM2G014914	GRMZM2G014914_P01,GRMZM2G014914_P02	TRUE	TRUE	aFQSAFYDR	92%	n+304 (+304)	28.57	25.00
3662	seq=translation; coord=7:41420177..41423983:-1; parent_transcript=GRMZM2G014914_T01; parent_gene=GRMZM2G014914	GRMZM2G014914_P01,GRMZM2G014914_P02	TRUE	TRUE	dSHVPVLAPLPIGFAVFMVHLATIPVTGTGINPAR	94%	n+304 (+304)	28.23	25.00
3663	seq=translation; coord=7:41420177..41423983:-1; parent_transcript=GRMZM2G014914_T01; parent_gene=GRMZM2G014914	GRMZM2G014914_P01,GRMZM2G014914_P02	TRUE	TRUE	sLGAAVIYNk	95%	n+304 (+304), K+304 (+304)	41.70	25.00
3664	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	aAWHELIER	95%	n+304 (+304)	32.85	25.15
3665	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	aTVPVWak	95%	n+304 (+304), K+304 (+304)	33.64	25.00
3666	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	aVHPIALak	90%	n+304 (+304), K+304 (+304)	25.67	25.00
3667	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	eHNFSSIEEFR	91%	n+304 (+304)	26.18	25.00
3668	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	iLIGSIMEEYNk	95%	n+304 (+304), K+304 (+304)	35.64	25.73
3669	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	lCAELQDFMR	95%	n+304 (+304), Carbamidomethyl (+57)	31.91	25.00
3670	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	mGAAVGQDcDLLEEVcGWINEk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	42.42	25.00
3671	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	mTPNITDITQPAR	95%	n+304 (+304)	46.19	25.33
3672	seq=translation; coord=5:205338436..205344337:-1; parent_transcript=GRMZM2G181505_T01; parent_gene=GRMZM2G181505	GRMZM2G181505_P01	TRUE	TRUE	sGCEGVSAINTIMSVGINLk	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.15	25.97
3673	seq=translation; coord=8:12989704..12991151:-1; parent_transcript=GRMZM2G097900_T01; parent_gene=GRMZM2G097900	GRMZM2G097900_P01	TRUE	TRUE	aAFAVYDADGDGR	95%	n+304 (+304)	69.88	25.00
3674	seq=translation; coord=8:12989704..12991151:-1; parent_transcript=GRMZM2G097900_T01; parent_gene=GRMZM2G097900	GRMZM2G097900_P01	TRUE	TRUE	dGFVDLGEFR	95%	n+304 (+304)	44.16	25.00
3675	seq=translation; coord=8:12989704..12991151:-1; parent_transcript=GRMZM2G097900_T01; parent_gene=GRMZM2G097900	GRMZM2G097900_P01	TRUE	TRUE	iSPSELAAVSR	95%	n+304 (+304)	36.86	25.29

3676	seq=translation; coord=8:12989704..12991151:-1; parent_transcript=GRMZM2G097900_T01; parent_gene=GRMZM2G097900	GRMZM2G097900_P01	TRUE	TRUE	iTAAELGSLVAR	95%	n+304 (+304)	34.78	25.00
3677	seq=translation; coord=1:224236124..224244611:-1; parent_transcript=GRMZM2G031572_T01; parent_gene=GRMZM2G031572	GRMZM2G031572_P01	TRUE	TRUE	aALQEITGLVDGQLQSGR	95%	n+304 (+304)	58.80	25.16
3678	seq=translation; coord=1:224236124..224244611:-1; parent_transcript=GRMZM2G031572_T01; parent_gene=GRMZM2G031572	GRMZM2G031572_P01	TRUE	TRUE	nVFEGEVYPDFMTNLYGGGTGIAGSk	95%	n+304 (+304), K+304 (+304)	36.00	25.00
3679	seq=translation; coord=1:224236124..224244611:-1; parent_transcript=GRMZM2G031572_T01; parent_gene=GRMZM2G031572	GRMZM2G031572_P01	TRUE	TRUE	qALFDLAVFR	87%	n+304 (+304)	26.84	25.95
3680	seq=translation; coord=1:224236124..224244611:-1; parent_transcript=GRMZM2G031572_T01; parent_gene=GRMZM2G031572	GRMZM2G031572_P01	TRUE	TRUE	yYFLDYR	95%	n+304 (+304)	33.87	25.00
3681	seq=translation; coord=8:101408887..101413622:1; parent_transcript=GRMZM2G033799_T01; parent_gene=GRMZM2G033799	GRMZM2G033799_P01,GRMZM2G033799_P02, GRMZM2G033799_P03	TRUE	TRUE	eLLEEIAAIVR	88%	n+304 (+304)	26.39	25.22
3682	seq=translation; coord=8:101408887..101413622:1; parent_transcript=GRMZM2G033799_T01; parent_gene=GRMZM2G033799	GRMZM2G033799_P01,GRMZM2G033799_P02, GRMZM2G033799_P03	TRUE	TRUE	tMAITDQATALR	86%	n+304 (+304)	25.50	25.25
3683	seq=translation; coord=1:8135964..8147853:-1; parent_transcript=GRMZM2G176397_T01; parent_gene=GRMZM2G176397	GRMZM2G176397_P01,GRMZM2G176397_P02	TRUE	TRUE	mFVDHSQVDAER	95%	n+304 (+304)	53.61	25.00
3684	seq=translation; coord=1:8135964..8147853:-1; parent_transcript=GRMZM2G176397_T01; parent_gene=GRMZM2G176397	GRMZM2G176397_P01,GRMZM2G176397_P02	TRUE	TRUE	sNLAGMGIPLcYk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.44	25.51
3685	seq=translation; coord=3:136407818..136421472:1; parent_transcript=GRMZM2G168510_T02; parent_gene=GRMZM2G168510	GRMZM2G168510_P02	TRUE	TRUE	eSNcPVVADVTHALQQPAGR	95%	n+304 (+304), Carbamidomethyl (+57)	67.53	25.00
3686	seq=translation; coord=3:136407818..136421472:1; parent_transcript=GRMZM2G168510_T02; parent_gene=GRMZM2G168510	GRMZM2G168510_P02	TRUE	TRUE	IAGNPVMVMcER	95%	n+304 (+304), Carbamidomethyl (+57)	35.79	25.00
3687	seq=translation; coord=3:136407818..136421472:1; parent_transcript=GRMZM2G168510_T02; parent_gene=GRMZM2G168510	GRMZM2G168510_P02	TRUE	TRUE	IGIPLVfk	95%	n+304 (+304), K+304 (+304)	35.90	25.00
3688	seq=translation; coord=3:136407818..136421472:1; parent_transcript=GRMZM2G168510_T02; parent_gene=GRMZM2G168510	GRMZM2G168510_P02	TRUE	TRUE	vADIIQIPAFLCr	95%	n+304 (+304), Carbamidomethyl (+57)	42.54	26.28
3689	seq=translation; coord=8:21615163..21616013:1; parent_transcript=GRMZM2G034157_T01; parent_gene=GRMZM2G034157	GRMZM2G034157_P01	TRUE	TRUE	eLPGAYAFVVDMPGLGTGDIR	94%	n+304 (+304)	28.28	25.00
3690	seq=translation; coord=8:21615163..21616013:1; parent_transcript=GRMZM2G034157_T01; parent_gene=GRMZM2G034157	GRMZM2G034157_P01	TRUE	TRUE	eLPGAYAFVVDMPGLGTGDIR	95%	n+304 (+304), iTRAQ8plex (+304)	35.86	25.00
3691	seq=translation; coord=5:125802058..125817596:1; parent_transcript=GRMZM2G034157_T01; parent_gene=GRMZM2G034157	GRMZM2G034157_P01	TRUE	TRUE	vLVVSGER	89%	n+304 (+304)	26.84	25.33
3692	seq=translation; coord=5:125802058..125817596:1; parent_transcript=GRMZM2G038126_T01; parent_gene=GRMZM2G038126	GRMZM2G038126_P01,GRMZM2G038126_P02, GRMZM2G090904_P01,GRMZM2G090904_P02	TRUE	TRUE	eNAPAIIFIDEVDIAIATAR	95%	n+304 (+304)	42.82	25.00
3693	seq=translation; coord=5:125802058..125817596:1; parent_transcript=GRMZM2G038126_T01; parent_gene=GRMZM2G038126	GRMZM2G038126_P01,GRMZM2G038126_P02, GRMZM2G090904_P01,GRMZM2G090904_P02	TRUE	TRUE	mNLSDEVLEDYVSRPdk	95%	n+304 (+304), K+304 (+304)	31.30	25.00

3694	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	TRUE	TRUE	aQETLSQTADAAAEK	95%	n+304 (+304), K+304 (+304)	39.73	25.28
3695	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	TRUE	TRUE	eAAEAASESGAEAHER	95%	n+304 (+304)	84.94	25.00
3696	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	TRUE	TRUE	eTAGDAAAGASNK	95%	n+304 (+304), K+304 (+304)	59.72	25.00
3697	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	TRUE	TRUE	iSEGLGLK	93%	n+304 (+304), K+304 (+304)	28.64	25.47
3698	seq=translation; coord=1:14449794..14451164:-1; parent_transcript=GRMZM2G063287_T01; parent_gene=GRMZM2G063287	GRMZM2G063287_P01	TRUE	TRUE	vAGPDVAAVDgk	95%	n+304 (+304), K+304 (+304)	35.95	25.05
3699	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	aAGEPLTIEIIVDPpk	95%	n+304 (+304), K+304 (+304)	35.01	25.00
3700	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	aFDLLQgk	93%	n+304 (+304), K+304 (+304)	27.09	25.00
3701	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	dSDEVcLPSLELLFGR	95%	n+304 (+304), Carbamidomethyl (+57)	53.00	25.00
3702	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	lAcLLScGAGTGVGAAWR	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	27.53	25.00
3703	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	vAPVFPR	90%	n+304 (+304)	27.22	25.00
3704	seq=translation; coord=1:19327055..19329850:-1; parent_transcript=GRMZM2G154007_T01; parent_gene=GRMZM2G154007	GRMZM2G154007_P01	TRUE	TRUE	vEPGSTVAIFGLGSVGLAVVQGak	95%	n+304 (+304), K+304 (+304)	47.33	25.00
3705	seq=translation; coord=5:46946530..46947446:-1; parent_transcript=AC209987.4_FGT010; parent_gene=AC209987.4_FG010	AC209987.4_FGP010	TRUE	TRUE	fDDGSTVFTFDR	95%	n+304 (+304)	38.07	25.00
3706	seq=translation; coord=5:46946530..46947446:-1; parent_transcript=AC209987.4_FGT010; parent_gene=AC209987.4_FG010	AC209987.4_FGP010	TRUE	TRUE	fQIGDQLLFVYPK	95%	n+304 (+304), K+304 (+304)	35.67	25.42
3707	seq=translation; coord=5:46946530..46947446:-1; parent_transcript=AC209987.4_FGT010; parent_gene=AC209987.4_FG010	AC209987.4_FGP010	TRUE	TRUE	sGAFFVSGNEAScR	95%	n+304 (+304), Carbamidomethyl (+57)	72.12	25.00
3708	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014	AC209206.3_FGP014	TRUE	TRUE	aQQIDQNLmIMYR	95%	n+304 (+304)	41.16	25.00
3709	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014	AC209206.3_FGP014	TRUE	TRUE	dPLFFAHHGNI DR	95%	n+304 (+304)	29.63	25.00
3710	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014	AC209206.3_FGP014	TRUE	TRUE	fGlcDLLDDIGADGdk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.93	25.00
3711	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014	AC209206.3_FGP014	TRUE	TRUE	fYLYFHER	95%	n+304 (+304)	30.43	25.00

3712	seq=translation; coord=10:137458157..137460537:-1; parent_transcript=AC209206.3_FGT014; parent_gene=AC209206.3_FG014 seq=translation; coord=1:228643379..228644379:-1;	AC209206.3_FGP014	TRUE	TRUE	rDPAHQPPFTLDLDYDGTEPTIPR	95%	n+304 (+304)	27.98	25.00
3713	parent_transcript=GRMZM2G153208_T01; parent_gene=GRMZM2G153208 seq=translation; coord=1:228643379..228644379:-1;	GRMZM2G153208_P01	TRUE	TRUE	dGYTDDFFAQILGk	95%	n+304 (+304), K+304 (+304)	29.46	25.00
3714	parent_transcript=GRMZM2G153208_T01; parent_gene=GRMZM2G153208 seq=translation; coord=1:228643379..228644379:-1;	GRMZM2G153208_P01	TRUE	TRUE	fDQAVGLDYAk	95%	n+304 (+304), K+304 (+304)	70.06	25.59
3715	parent_transcript=GRMZM2G153208_T01; parent_gene=GRMZM2G153208 seq=translation; coord=1:228643379..228644379:-1;	GRMZM2G153208_P01	TRUE	TRUE	tVQQLWQDYk	95%	n+304 (+304), K+304 (+304)	44.76	25.29
3716	parent_transcript=GRMZM2G153208_T01; parent_gene=GRMZM2G153208 seq=translation; coord=1:228643379..228644379:-1;	GRMZM2G153208_P01	TRUE	TRUE	wDQGYDVTAR	91%	n+304 (+304)	28.25	25.00
3717	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	aVcTEAGMFALR	90%	n+304 (+304), Carbamidomethyl (+57)	26.37	25.00
3718	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	eHAPSIIIFMDEIDSIGSAR	95%	n+304 (+304)	62.29	25.00
3719	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	eLFVMAR	94%	n+304 (+304)	30.30	25.00
3720	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	iDILDQALLRPGR	92%	n+304 (+304)	26.16	25.00
3721	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	tMLELLNQLDGFEASnk	95%	n+304 (+304), K+304 (+304)	74.14	25.88
3722	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=4:231475847..231481286:1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	vDPLVNLmk	95%	n+304 (+304), K+304 (+304)	40.00	25.00
3723	parent_transcript=GRMZM2G107362_T02; parent_gene=GRMZM2G107362 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G107362_P02,GRMZM2G107362_P04, GRMZM2G137528_P01,GRMZM2G137528_P02	TRUE	TRUE	vPDSTYDMIGGLDQqIk	95%	n+304 (+304), K+304 (+304)	38.22	25.58
3724	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G066996_P01	TRUE	TRUE	aDTQSVDFQk	95%	n+304 (+304), K+304 (+304)	31.87	25.68
3725	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G066996_P01	TRUE	TRUE	eDLTGvvLFVGHVVNPLLAP	95%	n+304 (+304)	33.48	25.00
3726	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G066996_P01	TRUE	TRUE	iSFGFEASELLk	95%	n+304 (+304), K+304 (+304)	54.00	25.31
3727	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G066996_P01	TRUE	TRUE	iVLGNALYFk	95%	n+304 (+304), K+304 (+304)	45.80	25.00
3728	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=5:18452211..18455290:-1;	GRMZM2G066996_P01	TRUE	TRUE	sFTMPQDFVADHPFMFLIR	95%	n+304 (+304)	46.53	25.00
3729	parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996	GRMZM2G066996_P01	TRUE	TRUE	sFVEVNEEGTEAAAAAATVVLR	95%	n+304 (+304)	50.70	25.00

3730	seq=translation; coord=5:18452211..18455290:-1; parent_transcript=GRMZM2G066996_T01; parent_gene=GRMZM2G066996 seq=translation; coord=9:8196377..8197429:-1;	GRMZM2G066996_P01	TRUE	TRUE	vAFADGVFVDSLk	95%	n+304 (+304), K+304 (+304)	54.07	26.17
3731	parent_transcript=GRMZM2G150656_T03; parent_gene=GRMZM2G150656 seq=translation; coord=9:8196377..8197429:-1;	GRMZM2G150656_P03	TRUE	TRUE	iGVDEEIFVVDLk	95%	n+304 (+304), K+304 (+304)	43.44	25.75
3732	parent_transcript=GRMZM2G150656_T03; parent_gene=GRMZM2G150656 seq=translation; coord=9:8196377..8197429:-1;	GRMZM2G150656_P03	TRUE	TRUE	kIGVDEEIFVVDLk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	34.39	25.00
3733	parent_transcript=GRMZM2G150656_T03; parent_gene=GRMZM2G150656 seq=translation; coord=9:8196377..8197429:-1;	GRMZM2G150656_P03	TRUE	TRUE	sAQLLELMR	92%	n+304 (+304)	29.01	25.43
3734	parent_transcript=GRMZM2G150656_T03; parent_gene=GRMZM2G150656 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G150656_P03	TRUE	TRUE	vGLVYQLNIAPk	95%	n+304 (+304), K+304 (+304)	33.89	25.00
3735	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G393671_P01	TRUE	TRUE	aRPEAVASGAAAMVSSLQALATLVPGLAYIHAGPVLR	95%	n+304 (+304)	44.29	25.00
3736	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G393671_P01	TRUE	TRUE	eGVEVAQLVEk	95%	n+304 (+304), K+304 (+304)	67.34	26.32
3737	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G393671_P01	TRUE	TRUE	vAAATQAAGDAk	91%	n+304 (+304), K+304 (+304)	26.92	25.98
3738	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=7:165014609..165016387:1;	GRMZM2G393671_P01	TRUE	TRUE	vkEGVEVAQLVEk	94%	n+304 (+304), K+304 (+304), K+304 (+304)	27.96	25.00
3739	parent_transcript=GRMZM2G393671_T01; parent_gene=GRMZM2G393671 seq=translation; coord=8:158113092..158118053:-1;	GRMZM2G393671_P01	TRUE	TRUE	vSFGENFSPAR	95%	n+304 (+304)	33.16	25.00
3740	parent_transcript=GRMZM2G109472_T01; parent_gene=GRMZM2G109472 seq=translation; coord=8:158113092..158118053:-1;	GRMZM2G109472_P01,GRMZM2G109472_P03	TRUE	TRUE	aEGLVVADAVVVVDR	95%	n+304 (+304)	51.27	26.15
3741	parent_transcript=GRMZM2G109472_T01; parent_gene=GRMZM2G109472 seq=translation; coord=8:158113092..158118053:-1;	GRMZM2G109472_P01,GRMZM2G109472_P03	TRUE	TRUE	IFELMETk	95%	n+304 (+304), K+304 (+304)	30.35	25.50
3742	parent_transcript=GRMZM2G109472_T01; parent_gene=GRMZM2G109472 seq=translation; coord=7:170244063..170247650:1;	GRMZM2G109472_P01,GRMZM2G109472_P03	TRUE	TRUE	tHVDILSDFTPDFGsk	95%	n+304 (+304), K+304 (+304)	27.53	25.00
3743	parent_transcript=GRMZM2G024484_T01; parent_gene=GRMZM2G024484 seq=translation; coord=7:170244063..170247650:1;	GRMZM2G024484_P01,GRMZM2G040209_P01,GRMZM2G040209_P02	TRUE	TRUE	eGTPWLWMIMER	95%	n+304 (+304)	35.79	25.00
3744	parent_transcript=GRMZM2G024484_T01; parent_gene=GRMZM2G024484 seq=translation; coord=7:170244063..170247650:1;	GRMZM2G024484_P01,GRMZM2G040209_P01,GRMZM2G040209_P02	TRUE	TRUE	gGWDNLLAVIPGGSSVPLLPk	95%	n+304 (+304), K+304 (+304)	31.60	25.00
3745	parent_transcript=GRMZM2G024484_T01; parent_gene=GRMZM2G024484 seq=translation; coord=7:170244063..170247650:1;	GRMZM2G024484_P01,GRMZM2G040209_P01,GRMZM2G040209_P02	TRUE	TRUE	hlcDDVLMYDALK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.58	25.00
3746	parent_transcript=GRMZM2G024484_T01; parent_gene=GRMZM2G024484 seq=translation; coord=9:7615635..7616809:-1;	GRMZM2G024484_P01,GRMZM2G040209_P01,GRMZM2G040209_P02	TRUE	TRUE	rGPEWFASFGR	95%	n+304 (+304)	43.99	25.00
3747	parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880	GRMZM5G898880_P01	TRUE	TRUE	aSAAGALPDGVTIR	95%	n+304 (+304)	49.14	26.61

3748	seq=translation; coord=9:7615635..7616809:-1; parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880 seq=translation; coord=9:7615635..7616809:-1;	GRMZM5G898880_P01	TRUE	TRUE	fVVSdTVGLDDPR	95%	n+304 (+304)	50.51	25.00
3749	parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880 seq=translation; coord=9:7615635..7616809:-1;	GRMZM5G898880_P01	TRUE	TRUE	IPAAyDDAWAALR	95%	n+304 (+304)	41.43	25.39
3750	parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880 seq=translation; coord=9:7615635..7616809:-1;	GRMZM5G898880_P01	TRUE	TRUE	vLVcVAENDFLK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	45.18	25.00
3751	parent_transcript=GRMZM5G898880_T01; parent_gene=GRMZM5G898880 seq=translation; coord=2:1928487..1932811:-1;	GRMZM5G898880_P01	TRUE	TRUE	vNPFVDDAAR	95%	n+304 (+304)	37.58	25.00
3752	parent_transcript=GRMZM2G407347_T01; parent_gene=GRMZM2G407347 seq=translation; coord=2:1928487..1932811:-1;	GRMZM2G407347_P01,GRMZM2G407347_P04	TRUE	TRUE	aVGDLAAAAEVSR	95%	n+304 (+304)	49.79	25.85
3753	parent_transcript=GRMZM2G407347_T01; parent_gene=GRMZM2G407347 seq=translation; coord=2:1928487..1932811:-1;	GRMZM2G407347_P01,GRMZM2G407347_P04	TRUE	TRUE	eQLVAEIR	95%	n+304 (+304)	34.53	26.32
3754	parent_transcript=GRMZM2G407347_T01; parent_gene=GRMZM2G407347 seq=translation; coord=2:1928487..1932811:-1;	GRMZM2G407347_P01,GRMZM2G407347_P04	TRUE	TRUE	IELTAEQINNPQSAcGScGLGDAFR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	35.05	25.00
3755	parent_transcript=GRMZM2G407347_T01; parent_gene=GRMZM2G407347 seq=translation; coord=1:68430654..68436197:1;	GRMZM2G407347_P01,GRMZM2G407347_P04	TRUE	TRUE	IPFEDASVGAVLAVIK	95%	n+304 (+304), K+304 (+304)	48.14	25.00
3756	parent_transcript=GRMZM5G866758_T02; parent_gene=GRMZM5G866758 seq=translation; coord=1:68430654..68436197:1;	GRMZM5G866758_P02	TRUE	TRUE	dSGAFAWEIIPVQVPVGR	89%	n+304 (+304)	27.46	25.97
3757	parent_transcript=GRMZM5G866758_T02; parent_gene=GRMZM5G866758 seq=translation; coord=1:68430654..68436197:1;	GRMZM5G866758_P02	TRUE	TRUE	eDQDAFAIQSNER	95%	n+304 (+304)	34.75	25.00
3758	parent_transcript=GRMZM5G866758_T02; parent_gene=GRMZM5G866758 seq=translation; coord=4:14930698..14950684:-1;	GRMZM5G866758_P02	TRUE	TRUE	tPMGGFLGALSPLPATk	95%	n+304 (+304), K+304 (+304)	31.88	25.00
3759	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=4:14930698..14950684:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	aPWEAQAAAGSLPPPPAR	95%	n+304 (+304)	97.35	25.35
3760	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=4:14930698..14950684:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	dLVDFak	93%	n+304 (+304), K+304 (+304)	28.28	26.27
3761	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=4:14930698..14950684:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	gIVDVLDEMLNALDHR	95%	n+304 (+304)	51.08	25.53
3762	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=4:14930698..14950684:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	iLSLIDTWQVAFGGPSGk	95%	n+304 (+304), K+304 (+304)	69.96	25.00
3763	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=4:14930698..14950684:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	rPVYTEASSVDYLSGDSYk	95%	n+304 (+304), K+304 (+304)	32.29	25.00
3764	parent_transcript=GRMZM2G151050_T01; parent_gene=GRMZM2G151050 seq=translation; coord=1:39213217..39219522:-1;	GRMZM2G151050_P01,GRMZM2G151050_P02	TRUE	TRUE	vQILTLYVLETLsk	95%	n+304 (+304), K+304 (+304)	33.20	25.00
3765	parent_transcript=GRMZM2G141799_T01; parent_gene=GRMZM2G141799	GRMZM2G141799_P01	TRUE	TRUE	aNSVAPWYITSLTEGILANK	95%	n+304 (+304), K+304 (+304)	45.52	25.00

3766	seq=translation; coord=1:39213217..39219522:-1; parent_transcript=GRMZM2G141799_T01; parent_gene=GRMZM2G141799	GRMZM2G141799_P01	TRUE	TRUE	aVVEELAAALGAHVHTcSR	95%	n+304 (+304), Carbamidomethyl (+57)	68.87	25.04
3767	seq=translation; coord=1:39213217..39219522:-1; parent_transcript=GRMZM2G141799_T01; parent_gene=GRMZM2G141799	GRMZM2G141799_P01	TRUE	TRUE	gFSVTGSVcDLSEr	95%	n+304 (+304), Carbamidomethyl (+57)	53.94	25.00
3768	seq=translation; coord=1:39213217..39219522:-1; parent_transcript=GRMZM2G141799_T01; parent_gene=GRMZM2G141799	GRMZM2G141799_P01	TRUE	TRUE	nFEEQVVSr	95%	n+304 (+304)	32.54	25.00
3769	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	aQPPVADVQAlk	95%	n+304 (+304), K+304 (+304)	31.63	25.00
3770	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	eSGESVAEYDYPyFYSR	95%	n+304 (+304), iTRAQ8plex (+304)	37.43	25.00
3771	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	gYLFQNAAR	93%	n+304 (+304)	29.69	25.00
3772	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	IFIGQAADek	95%	n+304 (+304), K+304 (+304)	46.06	25.87
3773	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	ITDFGVQGAESNNILYLR	95%	n+304 (+304)	39.64	25.00
3774	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	tLTSAAAETFTYELLIATGSSVIK	95%	n+304 (+304), K+304 (+304)	30.48	25.00
3775	seq=translation; coord=4:53078446..53083109:-1; parent_transcript=GRMZM2G134708_T01; parent_gene=GRMZM2G134708	GRMZM2G134708_P01	TRUE	TRUE	vVGVFLEGGSAEENQAIAR	95%	n+304 (+304)	77.15	25.58
3776	seq=translation; coord=8:83335717..83339016:1; parent_transcript=GRMZM2G104025_T01; parent_gene=GRMZM2G104025	GRMZM2G104025_P01,GRMZM5G803952_P03	TRUE	TRUE	aPLGENTVLLR	95%	n+304 (+304)	33.03	25.85
3777	seq=translation; coord=8:83335717..83339016:1; parent_transcript=GRMZM2G104025_T01; parent_gene=GRMZM2G104025	GRMZM2G104025_P01,GRMZM5G803952_P03	TRUE	TRUE	iVNAGGEcLTfDQLALR	95%	n+304 (+304), Carbamidomethyl (+57)	46.35	25.28
3778	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	aGVQGVAEEMELTEEEAK	95%	n+304 (+304), K+304 (+304)	68.65	25.00
3779	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	gEMLDLQHAAAFLLPR	95%	n+304 (+304)	62.44	25.00
3780	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	gFHGIPDGNDVFLSLPAR	95%	n+304 (+304)	44.35	25.50
3781	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	gSDLVIVTAGAR	95%	n+304 (+304)	31.90	25.20
3782	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	gyTswAIGYsvASLAASLLR	95%	n+304 (+304), iTRAQ8plex (+304)	31.66	25.00
3783	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	vIGSGTnLDSSR	94%	n+304 (+304)	30.88	25.20

3784	seq=translation; coord=5:67403566..67405443:1; parent_transcript=GRMZM2G128929_T01; parent_gene=GRMZM2G128929	GRMZM2G128929_P01	TRUE	TRUE	vSVIGAGNVGMAIAQTILTR	95%	n+304 (+304)	37.47	25.00
3785	seq=translation; coord=2:4834198..4840631:-1; parent_transcript=GRMZM2G033219_T01; parent_gene=GRMZM2G033219	GRMZM2G033219_P01,GRMZM2G033219_P02, GRMZM2G143480_P01,GRMZM2G143480_P02, GRMZM2G143480_P03	TRUE	TRUE	gAEAALTAIEMASLFR	95%	n+304 (+304)	56.85	25.00
3786	seq=translation; coord=7:159911588..159920834:-1; parent_transcript=GRMZM2G305211_T02; parent_gene=GRMZM2G305211	GRMZM2G305211_P02	TRUE	TRUE	tNVSPEVAESTR	95%	n+304 (+304)	50.01	25.00
3787	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	aASVYFEeK	95%	n+304 (+304), K+304 (+304)	38.46	25.49
3788	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	dYTADk	92%	n+304 (+304), K+304 (+304)	28.36	25.68
3789	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	eQQGQGLLGALGNVTGAik	95%	n+304 (+304), K+304 (+304)	56.21	25.00
3790	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	gAAGGGGILESVQEGAR	95%	n+304 (+304)	100.38	25.00
3791	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	ITLGQQQHVDVR	95%	n+304 (+304)	65.35	26.15
3792	seq=translation; coord=9:133421526..133422671:1; parent_transcript=GRMZM2G704475_T02; parent_gene=GRMZM2G704475	GRMZM2G704475_P02	TRUE	TRUE	tSETAEATk	95%	n+304 (+304), K+304 (+304)	29.99	25.11
3793	seq=translation; coord=1:293793122..293796213:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02,GRMZM2G459811_P03	TRUE	TRUE	aAEVVSTIVQNNPk	95%	n+304 (+304), K+304 (+304)	29.44	25.54
3794	seq=translation; coord=1:293793122..293796213:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02,GRMZM2G459811_P03	TRUE	TRUE	aLGAISLIR	95%	n+304 (+304)	36.35	25.00
3795	seq=translation; coord=1:293793122..293796213:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02,GRMZM2G459811_P03	TRUE	TRUE	aLNLIQYLLHNYk	95%	n+304 (+304), K+304 (+304)	28.54	25.00
3796	seq=translation; coord=1:293793122..293796213:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02,GRMZM2G459811_P03	TRUE	TRUE	eAALGGLLELAR	95%	n+304 (+304)	73.99	25.90
3797	seq=translation; coord=5:85252669..85257667:1; parent_transcript=GRMZM2G459811_T02; parent_gene=GRMZM2G459811	GRMZM2G459811_P02,GRMZM2G459811_P03	TRUE	TRUE	gLVVLPGEDAPQQPPDVAGk	93%	n+304 (+304), K+304 (+304)	27.04	25.00
3798	seq=translation; coord=5:85252669..85257667:1; parent_transcript=GRMZM2G104632_T01; parent_gene=GRMZM2G104632	GRMZM2G104632_P01	TRUE	TRUE	dDIEVVAVNDPFIDAK	95%	n+304 (+304), K+304 (+304)	44.58	25.55
3799	seq=translation; coord=5:85252669..85257667:1; parent_transcript=GRMZM2G104632_T01; parent_gene=GRMZM2G104632	GRMZM2G104632_P01	TRUE	TRUE	gAAQNIIPSSTGAak	95%	n+304 (+304), K+304 (+304)	58.73	25.00
3800	seq=translation; coord=5:85252669..85257667:1; parent_transcript=GRMZM2G104632_T01; parent_gene=GRMZM2G104632	GRMZM2G104632_P01	TRUE	TRUE	vLDLIAHMALVSAk	95%	n+304 (+304), K+304 (+304)	33.32	25.00
3801	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	eLVPTDGEHVDASVIR	95%	n+304 (+304)	48.45	25.80

3802	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	ILTGETISSAAPQEPVPIR	92%	n+304 (+304)	26.91	26.01
3803	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	nDVDAIFEQAR	95%	n+304 (+304)	35.51	25.00
3804	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	sAGVVVDDSQPFTSIQLR	95%	n+304 (+304)	78.29	25.01
3805	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	sGMLVQDPTR	92%	n+304 (+304)	29.06	25.43
3806	seq=translation; coord=10:123440513..123444639:1; parent_transcript=GRMZM2G134539_T01; parent_gene=GRMZM2G134539	GRMZM2G134539_P01	TRUE	TRUE	tLGGGPSPDESATAAPASAAPAASR	95%	n+304 (+304)	48.11	25.00
3807	seq=translation; coord=6:75510288..75518697:1; parent_transcript=GRMZM2G060870_T01; parent_gene=GRMZM2G060870	GRMZM2G060870_P01,GRMZM2G060870_P02	TRUE	TRUE	aMDFLVELFR	95%	n+304 (+304)	35.79	26.05
3808	seq=translation; coord=6:75510288..75518697:1; parent_transcript=GRMZM2G060870_T01; parent_gene=GRMZM2G060870	GRMZM2G060870_P01,GRMZM2G060870_P02	TRUE	TRUE	eNHEFLASVGLDDMk	95%	n+304 (+304), K+304 (+304)	31.68	25.00
3809	seq=translation; coord=6:75510288..75518697:1; parent_transcript=GRMZM2G060870_T01; parent_gene=GRMZM2G060870	GRMZM2G060870_P01,GRMZM2G060870_P02	TRUE	TRUE	fGAAMAIVk	95%	n+304 (+304), K+304 (+304)	29.75	25.76
3810	seq=translation; coord=6:75510288..75518697:1; parent_transcript=GRMZM2G060870_T01; parent_gene=GRMZM2G060870	GRMZM2G060870_P01,GRMZM2G060870_P02	TRUE	TRUE	qILPVLdk	95%	n+304 (+304), K+304 (+304)	36.53	25.00
3811	seq=translation; coord=8:14389329..14393515:-1; parent_transcript=GRMZM2G018177_T01; parent_gene=GRMZM2G018177	GRMZM2G018177_P01	TRUE	TRUE	dWSNVVLAYEPVWAIGTGk	95%	n+304 (+304), K+304 (+304)	32.93	25.01
3812	seq=translation; coord=8:14389329..14393515:-1; parent_transcript=GRMZM2G018177_T01; parent_gene=GRMZM2G018177	GRMZM2G018177_P01	TRUE	TRUE	iNVSPEVSESTR	95%	n+304 (+304)	38.08	25.60
3813	seq=translation; coord=8:14389329..14393515:-1; parent_transcript=GRMZM2G018177_T01; parent_gene=GRMZM2G018177	GRMZM2G018177_P01	TRUE	TRUE	qEFQVAAQNcWVvk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.73	26.05
3814	seq=translation; coord=8:14389329..14393515:-1; parent_transcript=GRMZM2G018177_T01; parent_gene=GRMZM2G018177	GRMZM2G018177_P01	TRUE	TRUE	vAFALSQGLk	95%	n+304 (+304), K+304 (+304)	35.46	25.00
3815	seq=translation; coord=1:3000161..3000884:-1; parent_transcript=GRMZM2G137329_T01; parent_gene=GRMZM2G137329	GRMZM2G137329_P01	TRUE	TRUE	aQQGcFcQFVvk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) K+304 (+304), n+304	58.31	25.00
3816	seq=translation; coord=1:3000161..3000884:-1; parent_transcript=GRMZM2G137329_T01; parent_gene=GRMZM2G137329	GRMZM2G137329_P01	TRUE	TRUE	kVVAScGVSVP R	92%	(+304), Carbamidomethyl (+57)	26.76	25.21
3817	seq=translation; coord=1:3000161..3000884:-1; parent_transcript=GRMZM2G137329_T01; parent_gene=GRMZM2G137329	GRMZM2G137329_P01	TRUE	TRUE	vVAScGVSVP R	95%	n+304 (+304), Carbamidomethyl (+57)	47.54	25.67
3818	seq=translation; coord=4:217521316..217523853:1; parent_transcript=GRMZM2G066222_T01; parent_gene=GRMZM2G066222	GRMZM2G066222_P01,GRMZM2G132121_P02, GRMZM2G377600_P01	TRUE	TRUE	ITEGcSFR	87%	n+304 (+304), Carbamidomethyl (+57)	25.06	25.00

3819	seq=translation; coord=4:217521316..217523853:1; parent_transcript=GRMZM2G066222_T01; parent_gene=GRMZM2G066222	GRMZM2G066222_P01,GRMZM2G132121_P02, GRMZM2G377600_P01	TRUE	TRUE	IVQSPNSFFMDV	95%	n+304 (+304), K+304 (+304)	38.99	25.76
3820	seq=translation; coord=4:217521316..217523853:1; parent_transcript=GRMZM2G066222_T01; parent_gene=GRMZM2G066222	GRMZM2G066222_P01,GRMZM2G132121_P02, GRMZM2G377600_P01	TRUE	TRUE	vLQNDIDLNNPPAELEK	95%	n+304 (+304), K+304 (+304)	48.60	25.00
3821	seq=translation; coord=8:148264071..148273363:1; parent_transcript=GRMZM2G030167_T01; parent_gene=GRMZM2G030167	GRMZM2G030167_P01	TRUE	TRUE	dLIQGLLR	95%	n+304 (+304)	32.21	25.00
3822	seq=translation; coord=8:148264071..148273363:1; parent_transcript=GRMZM2G030167_T01; parent_gene=GRMZM2G030167	GRMZM2G030167_P01	TRUE	TRUE	iVFESTLDAR	95%	n+304 (+304)	35.41	25.00
3823	seq=translation; coord=8:148264071..148273363:1; parent_transcript=GRMZM2G030167_T01; parent_gene=GRMZM2G030167	GRMZM2G030167_P01	TRUE	TRUE	vLQAQDDLNVK	95%	n+304 (+304), K+304 (+304)	73.00	26.01
3824	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	aPIGEEAEGR	95%	n+304 (+304)	57.51	25.00
3825	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	dLGYTAEMVYK	95%	n+304 (+304), K+304 (+304)	47.37	25.00
3826	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	gYFDLLIK	89%	n+304 (+304), K+304 (+304)	25.20	25.00
3827	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	IGLDVAScLITR	95%	n+304 (+304), Carbamidomethyl (+57)	41.37	26.06
3828	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	nPNDNTQVSLIYANVSPDILLK	95%	n+304 (+304), K+304 (+304)	29.74	25.56
3829	seq=translation; coord=3:11529201..11534274:1; parent_transcript=GRMZM2G061830_T02; parent_gene=GRMZM2G061830	GRMZM2G061830_P02	TRUE	TRUE	vYPDGK	90%	n+304 (+304), K+304 (+304)	29.16	26.92
3830	seq=translation; coord=9:124034244..124040497:-1; parent_transcript=GRMZM2G162968_T01; parent_gene=GRMZM2G162968	GRMZM2G162968_P01	TRUE	TRUE	iTQQEFTEMAWQAIVSSPEVAK	95%	n+304 (+304), K+304 (+304)	36.11	25.72
3831	seq=translation; coord=9:124034244..124040497:-1; parent_transcript=GRMZM2G162968_T01; parent_gene=GRMZM2G162968	GRMZM2G162968_P01	TRUE	TRUE	IIALDMGALIAGAK	95%	n+304 (+304), K+304 (+304)	31.89	25.00
3832	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	TRUE	TRUE	gGVIMDVVTPEQAR	95%	n+304 (+304)	51.90	25.48
3833	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	TRUE	TRUE	iAAPYDLVMQTK	95%	n+304 (+304), K+304 (+304)	50.66	26.33
3834	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	TRUE	TRUE	IAEEAGAcAVMALER	95%	n+304 (+304), Carbamidomethyl (+57)	55.37	25.00
3835	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	TRUE	TRUE	mSDPGLIR	87%	n+304 (+304)	25.75	25.72
3836	seq=translation; coord=7:1284259..1285978:1; parent_transcript=GRMZM2G120652_T01; parent_gene=GRMZM2G120652	GRMZM2G120652_P01	TRUE	TRUE	sMDDDEVFAYAK	95%	n+304 (+304), K+304 (+304)	42.84	25.00

3837	seq=translation; coord=4:69841345..69843586:1; parent_transcript=GRMZM2G100225_T01; parent_gene=GRMZM2G100225	GRMZM2G100225_P01,GRMZM2G100225_P02	TRUE	TRUE	aAAVPESVLR	92%	n+304 (+304)	30.68	27.26
3838	seq=translation; coord=6:157770836..157775279:1; parent_transcript=GRMZM2G424053_T02; parent_gene=GRMZM2G424053	GRMZM2G424053_P02	TRUE	TRUE	aMAPIFADMAK	95%	n+304 (+304), K+304 (+304)	44.51	25.43
3839	seq=translation; coord=6:157770836..157775279:1; parent_transcript=GRMZM2G424053_T02; parent_gene=GRMZM2G424053	GRMZM2G424053_P02	TRUE	TRUE	tIAEQFSVEAMPTFLFMR	95%	n+304 (+304)	33.21	25.00
3840	seq=translation; coord=6:157770836..157775279:1; parent_transcript=GRMZM2G424053_T02; parent_gene=GRMZM2G424053	GRMZM2G424053_P02	TRUE	TRUE	vDVDEMK	94%	n+304 (+304), K+304 (+304)	30.63	25.19
3841	seq=translation; coord=2:190158113..190161171:-1; parent_transcript=GRMZM2G365374_T01; parent_gene=GRMZM2G365374	GRMZM2G365374_P01	TRUE	TRUE	eIDEVLLVGGMTR	91%	n+304 (+304)	27.82	25.00
3842	seq=translation; coord=2:190158113..190161171:-1; parent_transcript=GRMZM2G365374_T01; parent_gene=GRMZM2G365374	GRMZM2G365374_P01	TRUE	TRUE	eIESAVSDLR	89%	n+304 (+304)	26.79	25.00
3843	seq=translation; coord=2:190158113..190161171:-1; parent_transcript=GRMZM2G365374_T01; parent_gene=GRMZM2G365374	GRMZM2G365374_P01	TRUE	TRUE	fESLVNLIER	95%	n+304 (+304)	37.26	25.22
3844	seq=translation; coord=1:167851430..167863929:-1; parent_transcript=GRMZM2G130034_T01; parent_gene=GRMZM2G130034	GRMZM2G130034_P01,GRMZM2G130034_P02	TRUE	TRUE	eDAVGNIIFGR	95%	n+304 (+304)	31.30	25.00
3845	seq=translation; coord=1:167851430..167863929:-1; parent_transcript=GRMZM2G130034_T01; parent_gene=GRMZM2G130034	GRMZM2G130034_P01,GRMZM2G130034_P02	TRUE	TRUE	IMAGIEELAQLR	94%	n+304 (+304)	31.44	26.19
3846	seq=translation; coord=1:167851430..167863929:-1; parent_transcript=GRMZM2G130034_T01; parent_gene=GRMZM2G130034	GRMZM2G130034_P01,GRMZM2G130034_P02	TRUE	TRUE	INLEDLHSVFLK	95%	n+304 (+304), K+304 (+304)	30.00	25.47
3847	seq=translation; coord=1:167851430..167863929:-1; parent_transcript=GRMZM2G130034_T01; parent_gene=GRMZM2G130034	GRMZM2G130034_P01,GRMZM2G130034_P02	TRUE	TRUE	sLEVIMFTSEEPTR	95%	n+304 (+304)	45.40	25.00
3848	seq=translation; coord=1:233560736..233562244:-1; parent_transcript=GRMZM2G001850_T01; parent_gene=GRMZM2G001850	GRMZM2G001850_P01	TRUE	TRUE	gFDTSGGEDQIR	95%	n+304 (+304)	38.72	25.00
3849	seq=translation; coord=1:233560736..233562244:-1; parent_transcript=GRMZM2G001850_T01; parent_gene=GRMZM2G001850	GRMZM2G001850_P01	TRUE	TRUE	iDMATER	94%	n+304 (+304)	31.32	25.00
3850	seq=translation; coord=6:43621161..43627397:1; parent_transcript=GRMZM2G025214_T02; parent_gene=GRMZM2G025214	GRMZM2G025214_P02	TRUE	TRUE	dSQLAAQFQEIPDLK	95%	n+304 (+304), K+304 (+304)	38.80	25.91
3851	seq=translation; coord=6:43621161..43627397:1; parent_transcript=GRMZM2G025214_T02; parent_gene=GRMZM2G025214	GRMZM2G025214_P02	TRUE	TRUE	vIGTLGSLSDGTVHVR	95%	n+304 (+304)	71.61	25.00
3852	seq=translation; coord=5:1033053..1037664:1; parent_transcript=GRMZM2G313678_T01; parent_gene=GRMZM2G313678	GRMZM2G313678_P01,GRMZM2G313678_P02	TRUE	TRUE	aFLMPIEDVFSIQGR	95%	n+304 (+304)	36.16	25.00
3853	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	TRUE	TRUE	aLSEVAGALLPYDSLAVR	94%	n+304 (+304)	28.83	25.42
3854	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	TRUE	TRUE	aNVILPSSAFSEK	95%	n+304 (+304), K+304 (+304)	44.48	25.38

3855	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	TRUE	TRUE	fATEVAGVQDLGMLGR	95%	n+304 (+304)	38.85	25.34
3856	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	TRUE	TRUE	gTETIDVTDAVGSNIR	95%	n+304 (+304)	44.83	25.00
3857	seq=translation; coord=5:10781545..10785536:1; parent_transcript=GRMZM2G145854_T01; parent_gene=GRMZM2G145854	GRMZM2G145854_P01	TRUE	TRUE	vELPPNPEDALEVFDGHAVR	95%	n+304 (+304)	53.89	25.00
3858	seq=translation; coord=9:94249084..94255465:1; parent_transcript=AC211394.4_FGT004; parent_gene=AC211394.4_FG004	AC211394.4_FGP004	TRUE	TRUE	fYNPQPDYSAFR	95%	n+304 (+304)	38.43	25.00
3859	seq=translation; coord=9:94249084..94255465:1; parent_transcript=AC211394.4_FGT004; parent_gene=AC211394.4_FG004	AC211394.4_FGP004	TRUE	TRUE	sAPVYITVGDGGNQEGLASR	95%	n+304 (+304)	90.86	25.00
3860	seq=translation; coord=9:94249084..94255465:1; parent_transcript=AC211394.4_FGT004; parent_gene=AC211394.4_FG004	AC211394.4_FGP004	TRUE	TRUE	tHAIYQWNR	95%	n+304 (+304)	29.21	25.00
3861	seq=translation; coord=6:115546691..115548383:1; parent_transcript=AC211394.4_FGT004; parent_gene=AC211394.4_FG004	AC211394.4_FGP004	TRUE	TRUE	vDLVFAGHVHAYER	95%	n+304 (+304)	27.75	25.67
3862	seq=translation; coord=6:115546691..115548383:1; parent_transcript=GRMZM2G156310_T01; parent_gene=GRMZM2G156310	GRMZM2G156310_P01	TRUE	TRUE	aLEWVAASGGDPWLSR	94%	n+304 (+304)	27.89	25.00
3863	seq=translation; coord=6:115546691..115548383:1; parent_transcript=GRMZM2G156310_T01; parent_gene=GRMZM2G156310	GRMZM2G156310_P01	TRUE	TRUE	dVVIDSDAGLYVR	95%	n+304 (+304)	48.26	25.00
3864	seq=translation; coord=10:96759871..96761276:-1; parent_transcript=GRMZM2G156310_T01; parent_gene=GRMZM2G156310	GRMZM2G156310_P01	TRUE	TRUE	vLVcGAELDSLPR	95%	n+304 (+304), Carbamidomethyl (+57)	57.37	25.76
3865	seq=translation; coord=10:96759871..96761276:-1; parent_transcript=GRMZM2G330635_T01; parent_gene=GRMZM2G330635	GRMZM2G330635_P01	TRUE	TRUE	aVFGLPPLRP	93%	n+304 (+304)	26.75	25.02
3866	seq=translation; coord=10:96759871..96761276:-1; parent_transcript=GRMZM2G330635_T01; parent_gene=GRMZM2G330635	GRMZM2G330635_P01	TRUE	TRUE	eLTLGLWASPFVLR	95%	n+304 (+304)	38.20	25.00
3867	seq=translation; coord=10:96759871..96761276:-1; parent_transcript=GRMZM2G330635_T01; parent_gene=GRMZM2G330635	GRMZM2G330635_P01	TRUE	TRUE	qAVAALETLEQAFR	95%	n+304 (+304)	64.71	25.77
3868	seq=translation; coord=6:107821435..107825807:-1; parent_transcript=GRMZM2G330635_T01; parent_gene=GRMZM2G330635	GRMZM2G330635_P01	TRUE	TRUE	tAEEMAEAAAR	94%	n+304 (+304)	29.01	25.00
3869	seq=translation; coord=6:107821435..107825807:-1; parent_transcript=GRMZM2G135498_T01; parent_gene=GRMZM2G135498	GRMZM2G135498_P01	TRUE	TRUE	dGFMVMEGAGVLVMSLEHAMk	95%	n+304 (+304), K+304 (+304)	51.45	25.17
3870	seq=translation; coord=4:201542946..201547734:-1; parent_transcript=GRMZM2G135498_T01; parent_gene=GRMZM2G135498	GRMZM2G135498_P01	TRUE	TRUE	ILVGESGIGPIDR	95%	n+304 (+304)	42.89	25.91
3871	seq=translation; coord=4:201542946..201547734:-1; parent_transcript=GRMZM2G381744_T01; parent_gene=GRMZM2G381744	GRMZM2G381744_P01	TRUE	TRUE	gSTDLSILDDLER	95%	n+304 (+304)	78.55	25.00
3872	parent_gene=GRMZM2G381744	GRMZM2G381744_P01	TRUE	TRUE	nPANFNVDNVR	95%	n+304 (+304)	49.50	25.00

3873	seq=translation; coord=4:201542946..201547734:-1; parent_transcript=GRMZM2G381744_T01; parent_gene=GRMZM2G381744	GRMZM2G381744_P01	TRUE	TRUE	tIEILEDLVEK	95%	n+304 (+304), K+304 (+304)	35.26	26.06
3874	seq=translation; coord=4:201542946..201547734:-1; parent_transcript=GRMZM2G381744_T01; parent_gene=GRMZM2G381744	GRMZM2G381744_P01	TRUE	TRUE	vIVSGAAVGDMAHFcER	95%	n+304 (+304), Carbamidomethyl (+57)	48.89	25.00
3875	seq=translation; coord=1:247547660..247549896:1; parent_transcript=GRMZM2G027451_T02; parent_gene=GRMZM2G027451	GRMZM2G027451_P02,GRMZM2G027451_P03, GRMZM2G027451_P04,GRMZM2G087233_P01	TRUE	TRUE	dAFHLR	91%	n+304 (+304)	25.29	25.00
3876	seq=translation; coord=1:247547660..247549896:1; parent_transcript=GRMZM2G027451_T02; parent_gene=GRMZM2G027451	GRMZM2G027451_P02,GRMZM2G027451_P03, GRMZM2G027451_P04,GRMZM2G087233_P01	TRUE	TRUE	eNVSSEALEAAR	95%	n+304 (+304)	44.59	25.00
3877	seq=translation; coord=1:247547660..247549896:1; parent_transcript=GRMZM2G027451_T02; parent_gene=GRMZM2G027451	GRMZM2G027451_P02,GRMZM2G027451_P03, GRMZM2G027451_P04,GRMZM2G087233_P01	TRUE	TRUE	vDIGQVLLSVR	95%	n+304 (+304)	33.93	26.22
3878	seq=translation; coord=4:39092198..39097412:-1; parent_transcript=GRMZM2G158153_T01; parent_gene=GRMZM2G158153	GRMZM2G158153_P01,GRMZM2G158153_P02	TRUE	TRUE	gVSPQPGGGAAYGAGGQWTA	93%	n+304 (+304), iTRAQ8plex (+304)	26.32	25.00
3879	seq=translation; coord=4:39092198..39097412:-1; parent_transcript=GRMZM2G158153_T01; parent_gene=GRMZM2G158153	GRMZM2G158153_P01,GRMZM2G158153_P02	TRUE	TRUE	iQLIPQHPPPEGVLTTER	94%	n+304 (+304)	28.73	25.58
3880	seq=translation; coord=4:39092198..39097412:-1; parent_transcript=GRMZM2G158153_T01; parent_gene=GRMZM2G158153	GRMZM2G158153_P01,GRMZM2G158153_P02	TRUE	TRUE	sVIAEAEAGGSPALIAR	95%	n+304 (+304)	77.70	25.84
3881	seq=translation; coord=1:99538428..99539066:-1; parent_transcript=AC194914.3_FGT002; parent_gene=AC194914.3_FG002	AC194914.3_FGP002	TRUE	TRUE	eVSVISGLPASTSTER	95%	n+304 (+304)	72.80	25.49
3882	seq=translation; coord=1:99538428..99539066:-1; parent_transcript=AC194914.3_FGT002; parent_gene=AC194914.3_FG002	AC194914.3_FGP002	TRUE	TRUE	iHAPPEAVWAVVR	95%	n+304 (+304)	54.03	25.47
3883	seq=translation; coord=1:99538428..99539066:-1; parent_transcript=AC194914.3_FGT002; parent_gene=AC194914.3_FG002	AC194914.3_FGP002	TRUE	TRUE	IDLLDDAAR	94%	n+304 (+304)	29.70	25.77
3884	seq=translation; coord=1:99538428..99539066:-1; parent_transcript=AC194914.3_FGT002; parent_gene=AC194914.3_FG002	AC194914.3_FGP002	TRUE	TRUE	IFADTVIR	93%	n+304 (+304)	29.61	25.00
3885	seq=translation; coord=4:236107257..236109295:-1; parent_transcript=GRMZM2G051208_T01; parent_gene=GRMZM2G051208	GRMZM2G051208_P01	TRUE	TRUE	fcEEEDGH	95%	n+304 (+304), Carbamidomethyl (+57)	33.60	25.00
3886	seq=translation; coord=4:236107257..236109295:-1; parent_transcript=GRMZM2G051208_T01; parent_gene=GRMZM2G051208	GRMZM2G051208_P01	TRUE	TRUE	ISDSGELSSLMGDGdk	95%	n+304 (+304), K+304 (+304)	48.00	25.00
3887	seq=translation; coord=5:168671806..168673715:1; parent_transcript=GRMZM2G113332_T01; parent_gene=GRMZM2G113332	GRMZM2G113332_P01	TRUE	TRUE	mEGVETFDIDLk	95%	n+304 (+304), K+304 (+304)	49.72	25.09
3888	seq=translation; coord=5:168671806..168673715:1; parent_transcript=GRMZM2G113332_T01; parent_gene=GRMZM2G113332	GRMZM2G113332_P01	TRUE	TRUE	vAMScEGcAGAVR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	44.88	25.00
3889	seq=translation; coord=4:194761789..194765861:1; parent_transcript=GRMZM2G149150_T01; parent_gene=GRMZM2G149150	GRMZM2G149150_P01	TRUE	TRUE	aGSAAESSENEAESQSTSADR	90%	n+304 (+304)	25.28	25.00
3890	seq=translation; coord=4:194761789..194765861:1; parent_transcript=GRMZM2G149150_T01; parent_gene=GRMZM2G149150	GRMZM2G149150_P01	TRUE	TRUE	IAEIALTDPk	92%	n+304 (+304), K+304 (+304)	27.93	25.44

3891	seq=translation; coord=4:194761789..194765861:1; parent_transcript=GRMZM2G149150_T01; parent_gene=GRMZM2G149150	GRMZM2G149150_P01	TRUE	TRUE	vQVLQTEATTLAQLTMLQR	95%	n+304 (+304)	72.17	25.17
3892	seq=translation; coord=3:18219856..18221974:1; parent_transcript=AC233872.1_FGT003; parent_gene=AC233872.1_FG003	AC233872.1_FGP003	TRUE	TRUE	dMIAIEGPDFNDLDENLQR	95%	n+304 (+304)	80.35	25.00
3893	seq=translation; coord=3:18219856..18221974:1; parent_transcript=AC233872.1_FGT003; parent_gene=AC233872.1_FG003	AC233872.1_FGP003	TRUE	TRUE	dMIAIEGPDFNDLDENLQR	95%	n+304 (+304), iTRAQ8plex (+304)	40.53	25.00
3894	seq=translation; coord=9:25922353..25927460:1; parent_transcript=GRMZM2G083716_T01; parent_gene=GRMZM2G083716	GRMZM2G083716_P01,GRMZM2G083716_P02, GRMZM2G083716_P03,GRMZM2G083716_P04	TRUE	TRUE	aLVEELR	95%	n+304 (+304)	36.47	25.09
3895	seq=translation; coord=9:25922353..25927460:1; parent_transcript=GRMZM2G083716_T01; parent_gene=GRMZM2G083716	GRMZM2G083716_P01,GRMZM2G083716_P02, GRMZM2G083716_P03,GRMZM2G083716_P04	TRUE	TRUE	dLINVLEEAIR	95%	n+304 (+304)	47.80	26.07
3896	seq=translation; coord=7:86433388..86439128:-1; parent_transcript=GRMZM2G473001_T01; parent_gene=GRMZM2G473001	GRMZM2G473001_P01	TRUE	TRUE	aLLDEMAVVATEEYR	95%	n+304 (+304)	82.37	25.00
3897	seq=translation; coord=7:86433388..86439128:-1; parent_transcript=GRMZM2G473001_T01; parent_gene=GRMZM2G473001	GRMZM2G473001_P01	TRUE	TRUE	fLDILQLDHGDDLk	95%	n+304 (+304), K+304 (+304)	49.73	25.00
3898	seq=translation; coord=7:86433388..86439128:-1; parent_transcript=GRMZM2G473001_T01; parent_gene=GRMZM2G473001	GRMZM2G473001_P01	TRUE	TRUE	IATPETEYGR	95%	n+304 (+304)	42.65	25.00
3899	seq=translation; coord=7:86433388..86439128:-1; parent_transcript=GRMZM2G473001_T01; parent_gene=GRMZM2G473001	GRMZM2G473001_P01	TRUE	TRUE	INPGSEYAPGLEDTLILTMk	90%	n+304 (+304), K+304 (+304)	26.26	25.76
3900	seq=translation; coord=3:179988293..179993427:-1; parent_transcript=GRMZM2G014136_T01; parent_gene=GRMZM2G014136	GRMZM2G014136_P01	TRUE	TRUE	eNLLNLVADVLPDGR	95%	n+304 (+304)	50.71	25.72
3901	seq=translation; coord=3:179988293..179993427:-1; parent_transcript=GRMZM2G014136_T01; parent_gene=GRMZM2G014136	GRMZM2G014136_P01	TRUE	TRUE	fAAFLSPLTLGR	95%	n+304 (+304)	37.16	26.65
3902	seq=translation; coord=3:179988293..179993427:-1; parent_transcript=GRMZM2G014136_T01; parent_gene=GRMZM2G014136	GRMZM2G014136_P01	TRUE	TRUE	gIETIATYDSETR	95%	n+304 (+304)	47.03	25.00
3903	seq=translation; coord=5:14853348..14857185:-1; parent_transcript=GRMZM2G066191_T01; parent_gene=GRMZM2G066191	GRMZM2G066191_P01,GRMZM2G066191_P03	TRUE	TRUE	aVLMLEPGTMESIR	95%	n+304 (+304)	62.10	25.00
3904	seq=translation; coord=5:14853348..14857185:-1; parent_transcript=GRMZM2G066191_T01; parent_gene=GRMZM2G066191	GRMZM2G066191_P01,GRMZM2G066191_P03	TRUE	TRUE	fWEVlcGEHcVDSTGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	66.59	25.00
3905	seq=translation; coord=5:14853348..14857185:-1; parent_transcript=GRMZM2G066191_T01; parent_gene=GRMZM2G066191	GRMZM2G066191_P01,GRMZM2G066191_P03	TRUE	TRUE	ySGTSSQQLELER	87%	n+304 (+304)	25.62	25.00
3906	seq=translation; coord=7:25903581..25911265:1; parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958	GRMZM2G016958_P01	TRUE	TRUE	aDMDALPLQLVDWEHK	95%	n+304 (+304), K+304 (+304)	28.89	25.02
3907	seq=translation; coord=7:25903581..25911265:1; parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958	GRMZM2G016958_P01	TRUE	TRUE	eIDPLQAAVVSVTFMk	92%	n+304 (+304), K+304 (+304)	26.68	25.00
3908	seq=translation; coord=7:25903581..25911265:1; parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958	GRMZM2G016958_P01	TRUE	TRUE	eVAEAMLGQDk	95%	n+304 (+304), K+304 (+304)	48.46	25.74

3909	seq=translation; coord=7:25903581..25911265:1; parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958 seq=translation; coord=7:25903581..25911265:1;	GRMZM2G016958_P01	TRUE	TRUE	gGDAYNVIPESASFGGTFR	95%	n+304 (+304)	76.08	25.00
3910	parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958 seq=translation; coord=7:25903581..25911265:1;	GRMZM2G016958_P01	TRUE	TRUE	gGHAAGPQDAVDPIVAASSAIVSLQLLVAR	95%	n+304 (+304)	44.37	25.00
3911	parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958 seq=translation; coord=7:25903581..25911265:1;	GRMZM2G016958_P01	TRUE	TRUE	IRPYPATVNDEGMYR	95%	n+304 (+304)	55.24	25.00
3912	parent_transcript=GRMZM2G016958_T01; parent_gene=GRMZM2G016958 seq=translation; coord=7:25903581..25911265:1;	GRMZM2G016958_P01	TRUE	TRUE	IVFQPGEEGYGGAYHVLR	95%	n+304 (+304)	51.90	25.00
3913	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=10:93684085..93687059:-1;	GRMZM5G833699_P01	TRUE	TRUE	aILFVPR	93%	n+304 (+304)	29.27	25.91
3914	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=10:93684085..93687059:-1;	GRMZM5G833699_P01	TRUE	TRUE	aVENSPLER	95%	n+304 (+304)	34.12	25.00
3915	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=10:93684085..93687059:-1;	GRMZM5G833699_P01	TRUE	TRUE	dIYYITGESR	90%	n+304 (+304)	26.56	25.00
3916	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=10:93684085..93687059:-1;	GRMZM5G833699_P01	TRUE	TRUE	eVSHEWVQInk	95%	n+304 (+304), K+304 (+304)	30.61	25.93
3917	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=10:93684085..93687059:-1;	GRMZM5G833699_P01	TRUE	TRUE	gVVDSDDLPLNISR	95%	n+304 (+304)	49.60	25.00
3918	parent_transcript=GRMZM5G833699_T01; parent_gene=GRMZM5G833699 seq=translation; coord=7:39873483..39874398:1;	GRMZM5G833699_P01	TRUE	TRUE	tLSIIDSGVGMTk	95%	n+304 (+304), K+304 (+304)	53.44	25.85
3919	parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560 seq=translation; coord=7:39873483..39874398:1;	GRMZM5G896560_P01	TRUE	TRUE	gFGFGFGk	95%	n+304 (+304), K+304 (+304)	31.87	25.08
3920	parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560 seq=translation; coord=7:39873483..39874398:1;	GRMZM5G896560_P01	TRUE	TRUE	gGGIGHGMGGGFGk	95%	n+304 (+304), K+304 (+304)	40.70	25.12
3921	parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560 seq=translation; coord=7:39873483..39874398:1;	GRMZM5G896560_P01	TRUE	TRUE	gGGIGHGmGGGFGk	94%	n+304 (+304), Oxidation (+16), K+304 (+304)	28.51	25.00
3922	parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560 seq=translation; coord=7:39873483..39874398:1;	GRMZM5G896560_P01	TRUE	TRUE	gGGLGGGIGHGLGGGYGk	95%	n+304 (+304), K+304 (+304)	43.76	25.24
3923	parent_transcript=GRMZM5G896560_T01; parent_gene=GRMZM5G896560 seq=translation; coord=2:220539596..220543690:1;	GRMZM5G896560_P01	TRUE	TRUE	gGGLGGGYGk	95%	n+304 (+304), K+304 (+304)	67.06	25.83
3924	parent_transcript=GRMZM2G163421_T01; parent_gene=GRMZM2G163421 seq=translation; coord=2:220539596..220543690:1;	GRMZM2G163421_P01	TRUE	TRUE	eFSGTEFTNFMELAEk	95%	n+304 (+304), K+304 (+304)	52.68	25.00
3925	parent_transcript=GRMZM2G163421_T01; parent_gene=GRMZM2G163421 seq=translation; coord=2:220539596..220543690:1;	GRMZM2G163421_P01	TRUE	TRUE	gDASVEGPLIR	95%	n+304 (+304)	34.46	26.50
3926	parent_transcript=GRMZM2G163421_T01; parent_gene=GRMZM2G163421	GRMZM2G163421_P01	TRUE	TRUE	iYIVGIFk	95%	n+304 (+304), K+304 (+304)	34.85	25.00

3927	seq=translation; coord=2:220539596..220543690:1; parent_transcript=GRMZM2G163421_T01; parent_gene=GRMZM2G163421	GRMZM2G163421_P01	TRUE	TRUE	vVVADNIHVVfk	95%	n+304 (+304), K+304 (+304)	38.44	25.00
3928	seq=translation; coord=10:119822322..119823346:-1; parent_transcript=GRMZM2G096695_T01; parent_gene=GRMZM2G096695	GRMZM2G096695_P01	TRUE	TRUE	vYPEGHGEEFVEIGAGDLVVPk	95%	n+304 (+304), K+304 (+304)	41.36	25.38
3929	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01,GRMZM2G002440_P02	TRUE	TRUE	sLLDVADNLSR	95%	n+304 (+304)	41.49	25.74
3930	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01,GRMZM2G002440_P02	TRUE	TRUE	sVGASTGASSEANNVPGTEk	95%	n+304 (+304), K+304 (+304)	54.40	25.17
3931	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01,GRMZM2G002440_P02	TRUE	TRUE	sYAEMENVLAR	95%	n+304 (+304)	40.41	25.00
3932	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01,GRMZM2G002440_P02	TRUE	TRUE	vGYMLHDR	95%	n+304 (+304)	44.46	25.00
3933	seq=translation; coord=4:65004377..65017210:-1; parent_transcript=GRMZM2G002440_T01; parent_gene=GRMZM2G002440	GRMZM2G002440_P01,GRMZM2G002440_P02	TRUE	TRUE	vLRPAEVGVTEGGPTEEEPEE	95%	n+304 (+304)	43.16	25.00
3934	seq=translation; coord=2:207032350..207038547:1; parent_transcript=GRMZM2G039251_T01; parent_gene=GRMZM2G039251	GRMZM2G039251_P01,GRMZM2G072054_P01	TRUE	TRUE	eAGVTVVESPAK	95%	n+304 (+304), K+304 (+304)	48.44	26.40
3935	seq=translation; coord=2:207032350..207038547:1; parent_transcript=GRMZM2G039251_T01; parent_gene=GRMZM2G039251	GRMZM2G039251_P01,GRMZM2G072054_P01	TRUE	TRUE	iGSTMFEIFk	95%	n+304 (+304), K+304 (+304)	38.53	25.43
3936	seq=translation; coord=2:207032350..207038547:1; parent_transcript=GRMZM2G039251_T01; parent_gene=GRMZM2G039251	GRMZM2G039251_P01,GRMZM2G072054_P01	TRUE	TRUE	vIcQGITGk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.32	25.93
3937	seq=translation; coord=7:116285614..116288886:-1; parent_transcript=GRMZM2G160770_T01; parent_gene=GRMZM2G160770	GRMZM2G160770_P01	TRUE	TRUE	fGNVEAGDQLQER	95%	n+304 (+304)	68.61	25.00
3938	seq=translation; coord=7:116285614..116288886:-1; parent_transcript=GRMZM2G160770_T01; parent_gene=GRMZM2G160770	GRMZM2G160770_P01	TRUE	TRUE	gALEAEMDAIIAR	95%	n+304 (+304)	56.18	25.63
3939	seq=translation; coord=7:116285614..116288886:-1; parent_transcript=GRMZM2G160770_T01; parent_gene=GRMZM2G160770	GRMZM2G160770_P01	TRUE	TRUE	gLLGcHFR	95%	n+304 (+304), Carbamidomethyl (+57)	48.50	26.25
3940	seq=translation; coord=7:116285614..116288886:-1; parent_transcript=GRMZM2G160770_T01; parent_gene=GRMZM2G160770	GRMZM2G160770_P01	TRUE	TRUE	sDIDIPNVLAQR	95%	n+304 (+304)	33.93	26.55
3941	seq=translation; coord=1:296201923..296204120:1; parent_transcript=GRMZM5G874478_T01; parent_gene=GRMZM5G874478	GRMZM5G874478_P01,GRMZM5G874478_P02, GRMZM5G874478_P03	TRUE	TRUE	cFIGNLSWSTTDESlk	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	65.28	25.00
3942	seq=translation; coord=1:296201923..296204120:1; parent_transcript=GRMZM5G874478_T01; parent_gene=GRMZM5G874478	GRMZM5G874478_P01,GRMZM5G874478_P02, GRMZM5G874478_P03	TRUE	TRUE	fGNLTEAk	95%	n+304 (+304), K+304 (+304)	34.37	26.62
3943	seq=translation; coord=1:296201923..296204120:1; parent_transcript=GRMZM5G874478_T01; parent_gene=GRMZM5G874478	GRMZM5G874478_P01,GRMZM5G874478_P02, GRMZM5G874478_P03	TRUE	TRUE	gFGFVTfDEk	95%	n+304 (+304), K+304 (+304)	50.44	25.00
3944	seq=translation; coord=2:189276282..189278019:-1; parent_transcript=GRMZM2G004138_T01; parent_gene=GRMZM2G004138	GRMZM2G004138_P01	TRUE	TRUE	eFNAVAADPR	95%	n+304 (+304)	48.25	25.00

3945	seq=translation; coord=2:189276282..189278019:-1; parent_transcript=GRMZM2G004138_T01; parent_gene=GRMZM2G004138	GRMZM2G004138_P01	TRUE	TRUE	sQPLYQYILESTVFPR	95%	n+304 (+304)	60.61	25.69
3946	seq=translation; coord=2:189276282..189278019:-1; parent_transcript=GRMZM2G004138_T01; parent_gene=GRMZM2G004138	GRMZM2G004138_P01	TRUE	TRUE	vGLALPVLDQMVAEEGNk	95%	n+304 (+304), K+304 (+304)	34.17	25.00
3947	seq=translation; coord=1:204681269..204683434:-1; parent_transcript=GRMZM2G057608_T01; parent_gene=GRMZM2G057608	GRMZM2G057608_P01,GRMZM2G057608_P04, GRMZM2G057608_P05,GRMZM2G084868_P02, GRMZM2G084868_P03,GRMZM2G139349_P01	TRUE	TRUE	qITPSILSER	95%	n+304 (+304)	40.43	26.33
3948	seq=translation; coord=1:204681269..204683434:-1; parent_transcript=GRMZM2G057608_T01; parent_gene=GRMZM2G057608	GRMZM2G057608_P01,GRMZM2G057608_P04, GRMZM2G057608_P05,GRMZM2G084868_P02, GRMZM2G084868_P03,GRMZM2G139349_P01	TRUE	TRUE	vNNAVLFDQATYDk	95%	n+304 (+304), K+304 (+304)	50.76	25.79
3949	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	TRUE	TRUE	aSAIAGFVSANK	95%	n+304 (+304), K+304 (+304)	36.67	25.67
3950	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	TRUE	TRUE	aVLAFLDTLSGAHSDELAASR	95%	n+304 (+304)	61.28	25.25
3951	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	TRUE	TRUE	IFHIDAAk	91%	n+304 (+304), K+304 (+304)	25.10	25.00
3952	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	TRUE	TRUE	ILFVFVER	95%	n+304 (+304)	32.07	26.60
3953	seq=translation; coord=4:241233055..241239106:-1; parent_transcript=GRMZM2G134889_T01; parent_gene=GRMZM2G134889	GRMZM2G134889_P01	TRUE	TRUE	yDVQGFPTILFFIDGVPR	95%	n+304 (+304)	35.79	25.13
3954	seq=translation; coord=4:63419630..63429299:-1; parent_transcript=GRMZM2G075775_T01; parent_gene=GRMZM2G075775	GRMZM2G075775_P01	TRUE	TRUE	aSSVSDNQGLGcIALQYik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	83.94	25.37
3955	seq=translation; coord=4:63419630..63429299:-1; parent_transcript=GRMZM2G075775_T01; parent_gene=GRMZM2G075775	GRMZM2G075775_P01	TRUE	TRUE	IVAcQSQYLAPAEAFGVLLVNDak	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	51.38	25.00
3956	seq=translation; coord=1:193791442..193794419:-1; parent_transcript=GRMZM2G148744_T01; parent_gene=GRMZM2G148744	GRMZM2G148744_P01,GRMZM2G148744_P02, GRMZM2G702426_P01	TRUE	TRUE	gLDVDNLYVSHIQVNQAQk	95%	n+304 (+304), K+304 (+304)	56.34	25.00
3957	seq=translation; coord=1:193791442..193794419:-1; parent_transcript=GRMZM2G148744_T01; parent_gene=GRMZM2G148744	GRMZM2G148744_P01,GRMZM2G148744_P02, GRMZM2G702426_P01	TRUE	TRUE	yLEDVIAHk	95%	n+304 (+304), K+304 (+304)	34.32	25.98
3958	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01,GRMZM2G063340_P03, GRMZM2G063340_P04,GRMZM2G139900_P01, GRMZM2G139900_P02	TRUE	TRUE	aLcAEHNHVLTVPAAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.59	25.00
3959	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01,GRMZM2G063340_P03, GRMZM2G063340_P04,GRMZM2G139900_P01, GRMZM2G139900_P02	TRUE	TRUE	dYGEESEGLNIVQEVVk	95%	n+304 (+304), K+304 (+304)	30.55	25.00
3960	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01,GRMZM2G063340_P03, GRMZM2G063340_P04,GRMZM2G139900_P01, GRMZM2G139900_P02	TRUE	TRUE	hAAQLcVLAEdcDQPDYVk	94%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	25.47	25.00
3961	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01,GRMZM2G063340_P03, GRMZM2G063340_P04,GRMZM2G139900_P01, GRMZM2G139900_P02	TRUE	TRUE	tLGEWAGLck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.16	26.22

3962	seq=translation; coord=7:21276565..21279263:-1; parent_transcript=GRMZM2G063340_T01; parent_gene=GRMZM2G063340	GRMZM2G063340_P01,GRMZM2G063340_P03, GRMZM2G063340_P04,GRMZM2G139900_P01, GRMZM2G139900_P02	TRUE	TRUE	vVGcScVVVk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	52.10	26.51
3963	seq=translation; coord=3:33565292..33570884:-1; parent_transcript=GRMZM2G328893_T01; parent_gene=GRMZM2G328893	GRMZM2G328893_P01	TRUE	TRUE	aFGAELVLTDAak	95%	n+304 (+304), K+304 (+304)	39.45	25.00
3964	seq=translation; coord=3:33565292..33570884:-1; parent_transcript=GRMZM2G328893_T01; parent_gene=GRMZM2G328893	GRMZM2G328893_P01	TRUE	TRUE	iQGIGAGFVPR	95%	n+304 (+304)	46.19	25.82
3965	seq=translation; coord=3:33565292..33570884:-1; parent_transcript=GRMZM2G328893_T01; parent_gene=GRMZM2G328893	GRMZM2G328893_P01	TRUE	TRUE	IIVVVFPSFGER	95%	n+304 (+304)	45.03	25.83
3966	seq=translation; coord=3:33565292..33570884:-1; parent_transcript=GRMZM2G328893_T01; parent_gene=GRMZM2G328893	GRMZM2G328893_P01	TRUE	TRUE	vHYETTGPFIWEDSk	95%	n+304 (+304), K+304 (+304)	37.50	25.00
3967	seq=translation; coord=9:92916278..92921897:-1; parent_transcript=GRMZM2G326472_T01; parent_gene=GRMZM2G326472	GRMZM2G326472_P01,GRMZM2G326472_P02, GRMZM2G326472_P03	TRUE	TRUE	gVSLPDLGR	92%	n+304 (+304)	29.91	26.13
3968	seq=translation; coord=9:92916278..92921897:-1; parent_transcript=GRMZM2G326472_T01; parent_gene=GRMZM2G326472	GRMZM2G326472_P01,GRMZM2G326472_P02, GRMZM2G326472_P03	TRUE	TRUE	IADAYGGATGPHFAV	95%	n+304 (+304), K+304 (+304)	39.12	26.32
3969	seq=translation; coord=9:92916278..92921897:-1; parent_transcript=GRMZM2G326472_T01; parent_gene=GRMZM2G326472	GRMZM2G326472_P01,GRMZM2G326472_P02, GRMZM2G326472_P03	TRUE	TRUE	vFIFPILDAAGSGAAGGEDLETGNFDSGLR	95%	n+304 (+304)	31.17	25.00
3970	seq=translation; coord=5:146886556..146888542:-1; parent_transcript=GRMZM2G014444_T01; parent_gene=GRMZM2G014444	GRMZM2G014444_P01,GRMZM2G014444_P02, GRMZM2G014444_P04,GRMZM2G018770_P01, GRMZM2G018770_P02	TRUE	TRUE	aMQLLESGLk	95%	n+304 (+304), K+304 (+304)	57.37	25.20
3971	seq=translation; coord=5:146886556..146888542:-1; parent_transcript=GRMZM2G014444_T01; parent_gene=GRMZM2G014444	GRMZM2G014444_P01,GRMZM2G014444_P02, GRMZM2G014444_P04,GRMZM2G018770_P01, GRMZM2G018770_P02	TRUE	TRUE	IVLNISVGESGDR	95%	n+304 (+304)	43.36	26.36
3972	seq=translation; coord=5:146886556..146888542:-1; parent_transcript=GRMZM2G014444_T01; parent_gene=GRMZM2G014444	GRMZM2G014444_P01,GRMZM2G014444_P02, GRMZM2G014444_P04,GRMZM2G018770_P01, GRMZM2G018770_P02	TRUE	TRUE	vLEQLSGQTPVFSk	95%	n+304 (+304), K+304 (+304)	45.56	25.07
3973	seq=translation; coord=1:35919768..35937067:-1; parent_transcript=GRMZM2G174589_T01; parent_gene=GRMZM2G174589	GRMZM2G174589_P01	TRUE	TRUE	dFPLGDLPLMEVLR	95%	n+304 (+304)	37.34	26.42
3974	seq=translation; coord=1:35919768..35937067:-1; parent_transcript=GRMZM2G174589_T01; parent_gene=GRMZM2G174589	GRMZM2G174589_P01	TRUE	TRUE	dVQSPEDIVAAER	95%	n+304 (+304)	43.17	25.00
3975	seq=translation; coord=1:35919768..35937067:-1; parent_transcript=GRMZM2G174589_T01; parent_gene=GRMZM2G174589	GRMZM2G174589_P01	TRUE	TRUE	IVFPGVGAFGSAMDVLR	95%	n+304 (+304)	56.10	25.77
3976	seq=translation; coord=4:183698889..183701902:1; parent_transcript=GRMZM2G088847_T01; parent_gene=GRMZM2G088847	GRMZM2G088847_P01,GRMZM2G088847_P02, GRMZM2G088847_P03,GRMZM2G088847_P04, GRMZM2G088847_P05,GRMZM2G088847_P07	TRUE	TRUE	ISAGIASILESk	95%	n+304 (+304), K+304 (+304)	41.66	25.00
3977	seq=translation; coord=4:183698889..183701902:1; parent_transcript=GRMZM2G088847_T01; parent_gene=GRMZM2G088847	GRMZM2G088847_P01,GRMZM2G088847_P02, GRMZM2G088847_P03,GRMZM2G088847_P04, GRMZM2G088847_P05,GRMZM2G088847_P07	TRUE	TRUE	sVANIIGkPEAYVMVVLk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.13	25.00
3978	seq=translation; coord=5:191366452..191369776:1; parent_transcript=GRMZM5G840002_T01; parent_gene=GRMZM5G840002	GRMZM5G840002_P01,GRMZM5G840002_P02, GRMZM5G840002_P03	TRUE	TRUE	IkPIGDAGPVIEAGGIFAYAR	95%	n+304 (+304), K+304 (+304)	52.61	25.00

3979	seq=translation; coord=5:191366452..191369776:1; parent_transcript=GRMZM5G840002_T01; parent_gene=GRMZM5G840002	GRMZM5G840002_P01,GRMZM5G840002_P02, GRMZM5G840002_P03	TRUE	TRUE	nSVATGEVYPLELTDVGAWk	95%	n+304 (+304), K+304 (+304)	39.56	25.39
3980	seq=translation; coord=5:191366452..191369776:1; parent_transcript=GRMZM5G840002_T01; parent_gene=GRMZM5G840002	GRMZM5G840002_P01,GRMZM5G840002_P02, GRMZM5G840002_P03	TRUE	TRUE	yAIHVGGANFGcGSSR	95%	n+304 (+304), Carbamidomethyl (+57)	47.76	25.00
3981	seq=translation; coord=3:213298401..213303662:1; parent_transcript=GRMZM2G033515_T01; parent_gene=GRMZM2G033515	GRMZM2G033515_P01	TRUE	TRUE	IIFPFLDLDIK	95%	n+304 (+304), K+304 (+304)	34.91	25.00
3982	seq=translation; coord=3:158348059..158355046:1; parent_transcript=GRMZM2G139617_T01; parent_gene=GRMZM2G139617	GRMZM2G139617_P01	TRUE	TRUE	eVDFNTATLADILR	95%	n+304 (+304)	61.70	25.00
3983	seq=translation; coord=3:158348059..158355046:1; parent_transcript=GRMZM2G139617_T01; parent_gene=GRMZM2G139617	GRMZM2G139617_P01	TRUE	TRUE	ILEFLESPcVTR	95%	n+304 (+304), Carbamidomethyl (+57)	49.53	25.00
3984	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	eQVAALVSAQVQQMLAAyAANR	95%	n+304 (+304), iTRAQ8plex (+304)	41.98	25.34
3985	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	ILcESAVLLDAAAAQLWGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.55	25.00
3986	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	ILDSIVTLLSR	90%	n+304 (+304)	26.39	25.00
3987	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	IRDEDEELFeCNWVEYVR	95%	n+304 (+304), Carbamidomethyl (+57)	66.32	25.00
3988	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	nPDFNHYLFEALAAVIGR	95%	n+304 (+304)	37.64	25.68
3989	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	tGEQDPALLPAFEASLFPVLQR	95%	n+304 (+304)	31.69	25.53
3990	seq=translation; coord=1:268251834..268259468:1; parent_transcript=GRMZM5G881950_T01; parent_gene=GRMZM5G881950	GRMZM5G881950_P01,GRMZM5G881950_P02	TRUE	TRUE	vLGIANIAGQIVHEITAR	95%	n+304 (+304)	75.73	25.00
3991	seq=translation; coord=2:2487249..2492988:-1; parent_transcript=GRMZM2G104430_T01; parent_gene=GRMZM2G104430	GRMZM2G104430_P01,GRMZM2G104430_P02	TRUE	TRUE	fAPPPAAALGDAMLHGFGVGEDDDVR	95%	n+304 (+304)	83.84	25.00
3992	seq=translation; coord=2:2487249..2492988:-1; parent_transcript=GRMZM2G104430_T01; parent_gene=GRMZM2G104430	GRMZM2G104430_P01,GRMZM2G104430_P02	TRUE	TRUE	iAVEDEDEELAR	95%	n+304 (+304)	38.50	25.00
3993	seq=translation; coord=2:2487249..2492988:-1; parent_transcript=GRMZM2G104430_T01; parent_gene=GRMZM2G104430	GRMZM2G104430_P01,GRMZM2G104430_P02	TRUE	TRUE	ILEDLLPYLDk	95%	n+304 (+304), K+304 (+304)	38.78	25.00
3994	seq=translation; coord=4:110069837..110073965:1; parent_transcript=GRMZM2G139680_T01; parent_gene=GRMZM2G139680	GRMZM2G139680_P01	TRUE	TRUE	aFGVLIPDQGIAlR	94%	n+304 (+304)	29.55	25.04
3995	seq=translation; coord=4:110069837..110073965:1; parent_transcript=GRMZM2G139680_T01; parent_gene=GRMZM2G139680	GRMZM2G139680_P01	TRUE	TRUE	aPDFEAEAVFDQEFINvk	95%	n+304 (+304), K+304 (+304)	44.65	25.00
3996	seq=translation; coord=4:110069837..110073965:1; parent_transcript=GRMZM2G139680_T01; parent_gene=GRMZM2G139680	GRMZM2G139680_P01	TRUE	TRUE	aSVVDDLPLVGnk	95%	n+304 (+304), K+304 (+304)	35.64	25.90

3997	seq=translation; coord=7:13844415..13850805:1; parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=7:13844415..13850805:1;	GRMZM2G001898_P01	TRUE	TRUE	aDEHVDVTNPATQEVVSR	95%	n+304 (+304)	61.94	25.00
3998	parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=7:13844415..13850805:1;	GRMZM2G001898_P01	TRUE	TRUE	dAWGQDVFR	95%	n+304 (+304)	36.02	25.00
3999	parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=7:13844415..13850805:1;	GRMZM2G001898_P01	TRUE	TRUE	dPGAAMMLAELAMEAGLPk	95%	n+304 (+304), K+304 (+304)	50.23	25.00
4000	parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=7:13844415..13850805:1;	GRMZM2G001898_P01	TRUE	TRUE	iPLTTADEfk	95%	n+304 (+304), K+304 (+304)	39.51	26.64
4001	parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=7:13844415..13850805:1;	GRMZM2G001898_P01	TRUE	TRUE	ILIGGEFVESR	91%	n+304 (+304)	28.24	25.00
4002	parent_transcript=GRMZM2G001898_T01; parent_gene=GRMZM2G001898 seq=translation; coord=3:218835389..218837093:-1;	GRMZM2G001898_P01	TRUE	TRUE	nHAILPDADRDATLNALIAAGFGAAGQR	95%	n+304 (+304)	37.96	25.19
4003	parent_transcript=GRMZM2G074097_T01; parent_gene=GRMZM2G074097 seq=translation; coord=3:218835389..218837093:-1;	GRMZM2G074097_P01	TRUE	TRUE	aLDMNAAEDEIVR	95%	n+304 (+304)	66.24	25.00
4004	parent_transcript=GRMZM2G074097_T01; parent_gene=GRMZM2G074097 seq=translation; coord=1:7566145..7569296:1;	GRMZM2G074097_P01	TRUE	TRUE	eVVPGMIVTGMEVAEIDGAPR	95%	n+304 (+304)	81.00	25.00
4005	parent_transcript=GRMZM2G410991_T01; parent_gene=GRMZM2G410991 seq=translation; coord=1:7566145..7569296:1;	GRMZM2G410991_P01	TRUE	TRUE	gDDPPGIAAR	89%	n+304 (+304)	26.80	25.00
4006	parent_transcript=GRMZM2G410991_T01; parent_gene=GRMZM2G410991 seq=translation; coord=1:7566145..7569296:1;	GRMZM2G410991_P01	TRUE	TRUE	iPLPcTcDQVDGADVMHFAYSVAk	92%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	26.51	25.00
4007	parent_transcript=GRMZM2G410991_T01; parent_gene=GRMZM2G410991 seq=translation; coord=1:43678296..43681497:1;	GRMZM2G410991_P01	TRUE	TRUE	tSLQQGQILDVPLPVck	95%	Carbamidomethyl (+57), K+304 (+304)	50.07	25.47
4008	parent_transcript=GRMZM2G137839_T01; parent_gene=GRMZM2G137839 seq=translation; coord=1:8972308..8976833:-1;	GRMZM2G137839_P01	TRUE	TRUE	nYPTVSAEYSEAVDk	95%	n+304 (+304), K+304 (+304)	40.12	25.00
4009	parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932 seq=translation; coord=1:8972308..8976833:-1;	GRMZM2G046932_P01	TRUE	TRUE	eALNEVVAAAFVGk	95%	n+304 (+304), K+304 (+304)	33.56	25.97
4010	parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932 seq=translation; coord=1:8972308..8976833:-1;	GRMZM2G046932_P01	TRUE	TRUE	IMEMAESlik	95%	n+304 (+304), K+304 (+304)	39.30	25.51
4011	parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932 seq=translation; coord=1:8972308..8976833:-1;	GRMZM2G046932_P01	TRUE	TRUE	INMVYTLlsk	95%	n+304 (+304), K+304 (+304)	30.77	25.00
4012	parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932 seq=translation; coord=1:8972308..8976833:-1;	GRMZM2G046932_P01	TRUE	TRUE	vDALIQFILQQGASK	91%	n+304 (+304), K+304 (+304)	26.30	25.00
4013	parent_transcript=GRMZM2G046932_T01; parent_gene=GRMZM2G046932	GRMZM2G046932_P01	TRUE	TRUE	vYPTYDFAcPFVDALEGVTHALR	95%	n+304 (+304), Carbamidomethyl (+57)	42.07	25.00

4014	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	eLAVSIEGk	95%	n+304 (+304), K+304 (+304)	32.72	26.28
4015	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	gGVTSISNDGATIMR	94%	n+304 (+304)	30.63	25.08
4016	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	iLVDIaK	95%	n+304 (+304), K+304 (+304)	29.84	25.00
4017	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	lAIGDLGTQYFADR	95%	n+304 (+304)	34.21	25.00
4018	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	ILDIVHPAAK	95%	n+304 (+304), K+304 (+304)	31.47	25.00
4019	seq=translation; coord=4:237041435..237046635:-1; parent_transcript=GRMZM2G009871_T01; parent_gene=GRMZM2G009871	GRMZM2G009871_P01,GRMZM2G009871_P02, GRMZM2G009871_P03,GRMZM2G009871_P04, GRMZM2G009871_P05	TRUE	TRUE	nSTVVPGGGAIDMEISK	95%	n+304 (+304), K+304 (+304)	37.26	25.47
4020	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01,GRMZM2G033208_P02, GRMZM2G033208_P03	TRUE	TRUE	vTEEDLQR	95%	n+304 (+304)	33.90	25.00
4021	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01,GRMZM2G033208_P02, GRMZM2G033208_P03	TRUE	TRUE	eSVLPAAVTAR	94%	n+304 (+304)	32.69	26.50
4022	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01,GRMZM2G033208_P02, GRMZM2G033208_P03	TRUE	TRUE	fEALGWHTIWVk	95%	n+304 (+304), K+304 (+304)	30.95	25.49
4023	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01,GRMZM2G033208_P02, GRMZM2G033208_P03	TRUE	TRUE	qNLGWPYDTFFVPEDVk	95%	n+304 (+304), K+304 (+304)	36.87	25.00
4024	seq=translation; coord=9:22779373..22783918:1; parent_transcript=GRMZM2G033208_T01; parent_gene=GRMZM2G033208	GRMZM2G033208_P01,GRMZM2G033208_P02, GRMZM2G033208_P03	TRUE	TRUE	sIITGELPTGWVDALPk	95%	n+304 (+304), K+304 (+304)	59.33	25.00
4025	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	eVLPSPPLTSASEPPPLFDGTTTR	95%	n+304 (+304)	42.68	26.07
4026	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	fQILYSNIk	95%	n+304 (+304), K+304 (+304)	35.58	25.00
4027	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	gESLDLVk	94%	n+304 (+304), K+304 (+304)	30.44	26.77
4028	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	iDAYTQTk	95%	n+304 (+304), K+304 (+304)	36.06	26.07
4029	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	iVAIDLADRPAWYk	95%	n+304 (+304), K+304 (+304)	27.50	25.60
4030	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE	IDPQFLLEQTk	95%	n+304 (+304), K+304 (+304)	36.60	25.05
4031	seq=translation; coord=9:138752306..138754760:1; parent_transcript=GRMZM2G162486_T01; parent_gene=GRMZM2G162486	GRMZM2G162486_P01	TRUE	TRUE					

4032	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01,GRMZM2G152688_P02, GRMZM2G152688_P03	TRUE	TRUE	eLSAEAAASLVEELNR	95%	n+304 (+304)	42.84	25.77
4033	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01,GRMZM2G152688_P02, GRMZM2G152688_P03	TRUE	TRUE	gELANFEVRPR	91%	n+304 (+304)	26.90	25.81
4034	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01,GRMZM2G152688_P02, GRMZM2G152688_P03	TRUE	TRUE	gNLELLEQR	95%	n+304 (+304)	35.15	26.30
4035	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01,GRMZM2G152688_P02, GRMZM2G152688_P03	TRUE	TRUE	gYPDTHLLEPR	91%	n+304 (+304)	25.82	25.00
4036	seq=translation; coord=3:230900751..230906058:-1; parent_transcript=GRMZM2G152688_T01; parent_gene=GRMZM2G152688	GRMZM2G152688_P01,GRMZM2G152688_P02, GRMZM2G152688_P03	TRUE	TRUE	nMLSMAQEIEQMR	95%	n+304 (+304)	61.85	25.00
4037	seq=translation; coord=1:214719298..214723588:1; parent_transcript=GRMZM2G058702_T01; parent_gene=GRMZM2G058702	GRMZM2G058702_P01,GRMZM2G117786_P01	TRUE	TRUE	iVWSWAGEGDR	95%	n+304 (+304)	33.50	25.00
4038	seq=translation; coord=1:214719298..214723588:1; parent_transcript=GRMZM2G058702_T01; parent_gene=GRMZM2G058702	GRMZM2G058702_P01,GRMZM2G117786_P01	TRUE	TRUE	iVYGADLAAFLQTFK	95%	n+304 (+304), K+304 (+304)	48.60	25.00
4039	seq=translation; coord=1:214719298..214723588:1; parent_transcript=GRMZM2G058702_T01; parent_gene=GRMZM2G058702	GRMZM2G058702_P01,GRMZM2G117786_P01	TRUE	TRUE	IDIYLLSQNWk	95%	n+304 (+304), K+304 (+304)	35.90	25.42
4040	seq=translation; coord=1:214719298..214723588:1; parent_transcript=GRMZM2G058702_T01; parent_gene=GRMZM2G058702	GRMZM2G058702_P01,GRMZM2G117786_P01	TRUE	TRUE	nMVESLAVPAFR	95%	n+304 (+304)	42.10	25.56
4041	seq=translation; coord=2:190424050..190431552:1; parent_transcript=GRMZM2G446050_T01; parent_gene=GRMZM2G446050	GRMZM2G446050_P01	TRUE	TRUE	dLAFADANVAPLHLQR	95%	n+304 (+304)	83.77	25.00
4042	seq=translation; coord=2:190424050..190431552:1; parent_transcript=GRMZM2G446050_T01; parent_gene=GRMZM2G446050	GRMZM2G446050_P01	TRUE	TRUE	scSAAVESEVIR	95%	n+304 (+304), Carbamidomethyl (+57)	47.60	25.00
4043	seq=translation; coord=2:190424050..190431552:1; parent_transcript=GRMZM2G446050_T01; parent_gene=GRMZM2G446050	GRMZM2G446050_P01	TRUE	TRUE	tVDFIDEITAESNFk	95%	n+304 (+304), K+304 (+304)	33.12	25.28
4044	seq=translation; coord=9:150809669..150813518:1; parent_transcript=GRMZM2G169384_T01; parent_gene=GRMZM2G169384	GRMZM2G169384_P01	TRUE	TRUE	gGSPPGPPPPYR	95%	n+304 (+304)	33.09	25.00
4045	seq=translation; coord=9:150809669..150813518:1; parent_transcript=GRMZM2G169384_T01; parent_gene=GRMZM2G169384	GRMZM2G169384_P01	TRUE	TRUE	tLAQVVGSEEEAR	95%	n+304 (+304)	57.11	25.66
4046	seq=translation; coord=4:54122481..54127439:-1; parent_transcript=GRMZM2G070422_T01; parent_gene=GRMZM2G070422	GRMZM2G070422_P01,GRMZM2G070422_P02	TRUE	TRUE	aISSEcGPQGLPIDLR	95%	n+304 (+304), Carbamidomethyl (+57)	54.04	25.00
4047	seq=translation; coord=4:54122481..54127439:-1; parent_transcript=GRMZM2G070422_T01; parent_gene=GRMZM2G070422	GRMZM2G070422_P01,GRMZM2G070422_P02	TRUE	TRUE	eVVESVR	88%	n+304 (+304)	26.34	25.00
4048	seq=translation; coord=4:54122481..54127439:-1; parent_transcript=GRMZM2G070422_T01; parent_gene=GRMZM2G070422	GRMZM2G070422_P01,GRMZM2G070422_P02	TRUE	TRUE	mIEYSYVNPALQk	95%	n+304 (+304), K+304 (+304)	31.72	25.15
4049	seq=translation; coord=4:54122481..54127439:-1; parent_transcript=GRMZM2G070422_T01; parent_gene=GRMZM2G070422	GRMZM2G070422_P01,GRMZM2G070422_P02	TRUE	TRUE	vNTISAGPLGSR	93%	n+304 (+304)	30.78	26.43

4050	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	aAMLQGVNDLADAVk	95%	n+304 (+304), K+304 (+304)	62.58	25.65
4051	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	aPLMTIAANAGIDGAIVIGk	95%	n+304 (+304), K+304 (+304)	33.39	25.00
4052	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	eIGDLIsk	95%	n+304 (+304), K+304 (+304)	35.72	26.70
4053	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	eVSFGVGAR	89%	n+304 (+304)	26.14	25.00
4054	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	hNLDDMAVMTGGEVISEER	95%	n+304 (+304)	42.87	25.00
4055	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	kPLLIVAEDVEGDALSMLVLNk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	30.32	25.00
4056	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	lIEQEDLSLGYDAAk	95%	n+304 (+304), K+304 (+304)	31.23	26.30
4057	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	tALQDAASVSLMATTEAAVSELPATk	95%	n+304 (+304), K+304 (+304)	35.98	25.00
4058	seq=translation; coord=6:161725359..161731090:-1; parent_transcript=GRMZM2G074790_T01; parent_gene=GRMZM2G074790	GRMZM2G074790_P01,GRMZM2G074790_P02, GRMZM2G074790_P03	TRUE	TRUE	tLDNELEAVQGMk	95%	n+304 (+304), K+304 (+304)	29.25	26.26
4059	seq=translation; coord=6:113343612..113346307:1; parent_transcript=GRMZM2G168119_T01; parent_gene=GRMZM2G168119	GRMZM2G168119_P01	TRUE	TRUE	fVVFDLk	95%	n+304 (+304), K+304 (+304)	32.63	25.00
4060	seq=translation; coord=6:113343612..113346307:1; parent_transcript=GRMZM2G168119_T01; parent_gene=GRMZM2G168119	GRMZM2G168119_P01	TRUE	TRUE	qMGLPTSDEMQk	95%	n+304 (+304), K+304 (+304)	37.95	25.00
4061	seq=translation; coord=6:113343612..113346307:1; parent_transcript=GRMZM2G168119_T01; parent_gene=GRMZM2G168119	GRMZM2G168119_P01	TRUE	TRUE	vDDcFWSIEDGR	95%	n+304 (+304), Carbamidomethyl (+57)	49.53	25.00
4062	seq=translation; coord=6:113343612..113346307:1; parent_transcript=GRMZM2G168119_T01; parent_gene=GRMZM2G168119	GRMZM2G168119_P01	TRUE	TRUE	vTAMAAAVR	95%	n+304 (+304)	36.66	25.00
4063	seq=translation; coord=10:29873986..29885675:1; parent_transcript=GRMZM2G042089_T01; parent_gene=GRMZM2G042089	GRMZM2G042089_P01,GRMZM2G042089_P03, GRMZM2G143354_P01	TRUE	TRUE	iEGLLAAPk	95%	n+304 (+304), K+304 (+304)	35.86	25.00
4064	seq=translation; coord=10:29873986..29885675:1; parent_transcript=GRMZM2G042089_T01; parent_gene=GRMZM2G042089	GRMZM2G042089_P01,GRMZM2G042089_P03, GRMZM2G143354_P01	TRUE	TRUE	nSVLEWSILLIDQSNR	94%	n+304 (+304)	30.30	26.30
4065	seq=translation; coord=10:29873986..29885675:1; parent_transcript=GRMZM2G042089_T01; parent_gene=GRMZM2G042089	GRMZM2G042089_P01,GRMZM2G042089_P03, GRMZM2G143354_P01	TRUE	TRUE	qSNILEDLDTLR	95%	n+304 (+304)	59.29	25.00
4066	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	aMSLVTVGLDYER	95%	n+304 (+304)	78.78	25.00
4067	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	dIVEMVFFPVINEAcR	95%	n+304 (+304), Carbamidomethyl (+57)	28.57	25.00

4068	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	eATSFQELLFSDTck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	56.74	25.00
4069	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	gIPLSAPtk	95%	n+304 (+304), K+304 (+304)	35.90	25.00
4070	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	ISEkDIVEMVFFPVINEAcR	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	30.23	25.72
4071	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	sMAGVTPDPELMk	94%	n+304 (+304), K+304 (+304)	28.44	25.00
4072	seq=translation; coord=8:40257571..40264535:-1; parent_transcript=GRMZM2G132903_T01; parent_gene=GRMZM2G132903	GRMZM2G132903_P01	TRUE	TRUE	vAILGGGLMGSGIATAMVLSNYPVLLk	95%	n+304 (+304), K+304 (+304)	68.12	25.00
4073	seq=translation; coord=9:129405892..129410419:1; parent_transcript=GRMZM2G125148_T01; parent_gene=GRMZM2G125148	GRMZM2G125148_P01,GRMZM2G125148_P03, GRMZM2G125148_P04	TRUE	TRUE	eAPAGEGDGEk	95%	n+304 (+304), K+304 (+304)	56.77	25.37
4074	seq=translation; coord=9:129405892..129410419:1; parent_transcript=GRMZM2G125148_T01; parent_gene=GRMZM2G125148	GRMZM2G125148_P01,GRMZM2G125148_P03, GRMZM2G125148_P04	TRUE	TRUE	eVEEEPVVAAASEVk	95%	n+304 (+304), K+304 (+304)	29.05	25.68
4075	seq=translation; coord=7:13173972..13176516:-1; parent_transcript=GRMZM2G144653_T02; parent_gene=GRMZM2G144653	GRMZM2G144653_P02	TRUE	TRUE	aIAPLFVEHak	95%	n+304 (+304), K+304 (+304)	56.87	25.00
4076	seq=translation; coord=7:13173972..13176516:-1; parent_transcript=GRMZM2G144653_T02; parent_gene=GRMZM2G144653	GRMZM2G144653_P02	TRUE	TRUE	eVTAAYEVEAMPTFHFVk	95%	n+304 (+304), K+304 (+304)	52.65	25.65
4077	seq=translation; coord=7:13173972..13176516:-1; parent_transcript=GRMZM2G144653_T02; parent_gene=GRMZM2G144653	GRMZM2G144653_P02	TRUE	TRUE	fTQVVFk	94%	n+304 (+304), K+304 (+304)	27.71	25.00
4078	seq=translation; coord=1:154077677..154081800:1; parent_transcript=GRMZM2G056039_T01; parent_gene=GRMZM2G056039	GRMZM2G056039_P01	TRUE	TRUE	kIEDAIDAAISWLDANQLAEAEFDDk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.73	25.00
4079	seq=translation; coord=1:154077677..154081800:1; parent_transcript=GRMZM2G056039_T01; parent_gene=GRMZM2G056039	GRMZM2G056039_P01	TRUE	TRUE	mYQGAGADMGGSGGMDADAPAGSGGPGPk	95%	n+304 (+304), K+304 (+304)	104.53	25.00
4080	seq=translation; coord=4:9677072..9677727:-1; parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675	GRMZM2G419675_P01,GRMZM2G454556_P01	TRUE	TRUE	gYQMGHLDVDyQFVGc	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	32.65	25.00
4081	seq=translation; coord=4:9677072..9677727:-1; parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675	GRMZM2G419675_P01,GRMZM2G454556_P01	TRUE	TRUE	qQYGWTAfFcGPSGPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.22	25.00
4082	seq=translation; coord=4:9677072..9677727:-1; parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675	GRMZM2G419675_P01,GRMZM2G454556_P01	TRUE	TRUE	qQYGWTAfFcGPSGPk	95%	Pyro-cmC (-17), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.39	25.00
4083	seq=translation; coord=4:9677072..9677727:-1; parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675	GRMZM2G419675_P01,GRMZM2G454556_P01	TRUE	TRUE	qQyGWTAfFcGPSGPk	95%	Pyro-cmC (-17), n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), K+304 (+304)	60.24	25.00
4084	seq=translation; coord=4:9677072..9677727:-1; parent_transcript=GRMZM2G419675_T01; parent_gene=GRMZM2G419675	GRMZM2G419675_P01,GRMZM2G454556_P01	TRUE	TRUE	vGAYcATWDAGkPPSWR	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.43	25.00

4085	seq=translation; coord=1:25625764..25630712:-1; parent_transcript=GRMZM2G091563_T01; parent_gene=GRMZM2G091563	GRMZM2G091563_P01	TRUE	TRUE	aMEVLSDILQNSNLDQAR	95%	n+304 (+304)	30.33	25.00
4086	seq=translation; coord=5:23016144..23019861:1; parent_transcript=GRMZM2G030169_T01; parent_gene=GRMZM2G030169	GRMZM2G030169_P01,GRMZM2G030169_P02, GRMZM2G030169_P03,GRMZM2G082484_P01	TRUE	TRUE	IAYVALDYEQELETak	95%	n+304 (+304), K+304 (+304)	42.74	25.88
4087	seq=translation; coord=8:8351675..8357336:1; parent_transcript=GRMZM2G132796_T01; parent_gene=GRMZM2G132796	GRMZM2G132796_P01	TRUE	TRUE	vAEPLLPDPLPDPPSR	95%	n+304 (+304)	40.29	25.63
4088	seq=translation; coord=4:12082697..12084089:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153	GRMZM2G358153_P01	TRUE	TRUE	IPGLFIWSADSSk	93%	n+304 (+304), K+304 (+304)	28.33	25.90
4089	seq=translation; coord=4:12082697..12084089:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153	GRMZM2G358153_P01	TRUE	TRUE	tGNVTGLSPDQGIGSAk	95%	n+304 (+304), K+304 (+304)	42.94	25.75
4090	seq=translation; coord=4:12082697..12084089:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153	GRMZM2G358153_P01	TRUE	TRUE	yETEAQQIIANH	95%	n+304 (+304)	67.12	25.00
4091	seq=translation; coord=3:128521980..128525993:1; parent_transcript=GRMZM2G358153_T01; parent_gene=GRMZM2G358153	GRMZM2G358153_P01	TRUE	TRUE	yGLDGVDDVDyEHFADGADVNTFVecIGR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	39.50	25.00
4092	seq=translation; coord=3:128521980..128525993:1; parent_transcript=GRMZM2G034083_T01; parent_gene=GRMZM2G034083	GRMZM2G034083_P01	TRUE	TRUE	eEEVLQYAR	92%	n+304 (+304)	28.50	25.00
4093	seq=translation; coord=3:128521980..128525993:1; parent_transcript=GRMZM2G034083_T01; parent_gene=GRMZM2G034083	GRMZM2G034083_P01	TRUE	TRUE	sGLVALNLDLAQVR	95%	n+304 (+304)	53.24	25.12
4094	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM2G034083_T01; parent_gene=GRMZM2G034083	GRMZM2G034083_P01	TRUE	TRUE	wGNIVFPLPFGR	95%	n+304 (+304)	32.57	25.12
4095	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	aGPSAPGGAPPNPFDFTMMNLLNDPSIK	95%	n+304 (+304), K+304 (+304)	32.51	25.00
4096	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	dcVALLIESGAAVTLQNLDGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	61.55	25.00
4097	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	dPAFTEMAEQLQk	95%	n+304 (+304), K+304 (+304)	53.25	25.00
4098	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	IGSALMQDPAMSAMLGGLTNPAHK	95%	n+304 (+304), K+304 (+304)	38.63	25.25
4099	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	INNQDDVLk	95%	n+304 (+304), K+304 (+304)	46.97	25.42
4100	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	qQQQLDPQk	92%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.44	25.00
4101	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	yVATMQQLMQNPQFVAMAER	95%	n+304 (+304)	49.97	25.00
4102	seq=translation; coord=1:298687651..298689984:1; parent_transcript=GRMZM5G821637_T05; parent_gene=GRMZM5G821637	GRMZM5G821637_P05	TRUE	TRUE	yWNDPEALQk	88%	n+304 (+304), K+304 (+304)	26.81	25.67

4103	seq=translation; coord=7:1266505..1269350:-1; parent_transcript=GRMZM2G420743_T01; parent_gene=GRMZM2G420743	GRMZM2G420743_P01	TRUE	TRUE	eLAVVGGTGGLR	95%	n+304 (+304)	33.01	25.83
4104	seq=translation; coord=7:1266505..1269350:-1; parent_transcript=GRMZM2G420743_T01; parent_gene=GRMZM2G420743	GRMZM2G420743_P01	TRUE	TRUE	gASGYVLWTTAK	95%	n+304 (+304), K+304 (+304)	29.95	26.05
4105	seq=translation; coord=7:1266505..1269350:-1; parent_transcript=GRMZM2G420743_T01; parent_gene=GRMZM2G420743	GRMZM2G420743_P01	TRUE	TRUE	tFGDTVAIDDLVTDGPGVGADSRPVGR	95%	n+304 (+304)	30.46	25.00
4106	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	aFSAAVSALGIYNk	95%	n+304 (+304), K+304 (+304)	49.82	25.67
4107	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	aSGYDVESSASSDAILk	95%	n+304 (+304), K+304 (+304)	29.75	25.55
4108	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	eNINTQTHQLIDAR	95%	n+304 (+304)	54.74	25.00
4109	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	IQPHLLWSLDQVk	95%	n+304 (+304), K+304 (+304)	31.50	25.00
4110	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	nPLQEYQVAHIPGALFFDVGISDR	95%	n+304 (+304)	50.49	25.00
4111	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	vLDASWYMPAEQR	95%	n+304 (+304)	46.14	25.00
4112	seq=translation; coord=1:172122450..172128491:-1; parent_transcript=GRMZM2G029262_T01; parent_gene=GRMZM2G029262	GRMZM2G029262_P01,GRMZM2G029262_P03, GRMZM2G029262_P04	TRUE	TRUE	vWVLDGGLPQWR	95%	n+304 (+304)	34.12	26.04
4113	seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095	GRMZM2G130095_P01,GRMZM2G130095_P03	TRUE	TRUE	aVELIASHLR	95%	n+304 (+304)	50.47	26.16
4114	seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095	GRMZM2G130095_P01,GRMZM2G130095_P03	TRUE	TRUE	dEPDTELPPAVDGLLR	95%	n+304 (+304)	68.60	25.00
4115	seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095	GRMZM2G130095_P01,GRMZM2G130095_P03	TRUE	TRUE	iTDGLETETDQPQR	91%	n+304 (+304)	28.10	25.00
4116	seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095	GRMZM2G130095_P01,GRMZM2G130095_P03	TRUE	TRUE	ILVPASQAGSLIGk	95%	n+304 (+304), K+304 (+304)	52.58	25.00
4117	seq=translation; coord=1:167864280..167870604:1; parent_transcript=GRMZM2G130095_T01; parent_gene=GRMZM2G130095	GRMZM2G130095_P01,GRMZM2G130095_P03	TRUE	TRUE	sVLP LFETQIk	95%	n+304 (+304), K+304 (+304)	41.90	25.00
4118	seq=translation; coord=2:212180089..212183936:-1; parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160	GRMZM2G365160_P01,GRMZM2G365160_P02	TRUE	TRUE	gVANPLGIk	95%	n+304 (+304), K+304 (+304)	42.49	25.00
4119	seq=translation; coord=2:212180089..212183936:-1; parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160	GRMZM2G365160_P01,GRMZM2G365160_P02	TRUE	TRUE	tRPFDSILAEVR	95%	n+304 (+304)	42.86	25.17
4120	seq=translation; coord=2:212180089..212183936:-1; parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160	GRMZM2G365160_P01,GRMZM2G365160_P02	TRUE	TRUE	tVTFDLSDR	95%	n+304 (+304)	31.75	25.00

4121	seq=translation; coord=2:212180089..212183936:-1; parent_transcript=GRMZM2G365160_T01; parent_gene=GRMZM2G365160 seq=translation; coord=4:33112293..33117947:1;	GRMZM2G365160_P01,GRMZM2G365160_P02	TRUE	TRUE	vTQWNLDFMDHNEQGDR	95%	n+304 (+304)	58.21	25.00
4122	parent_transcript=GRMZM2G104907_T01; parent_gene=GRMZM2G104907 seq=translation; coord=4:33112293..33117947:1;	GRMZM2G104907_P01	TRUE	TRUE	fLVQSVVAPAGITVvk	95%	n+304 (+304), K+304 (+304)	42.66	25.00
4123	parent_transcript=GRMZM2G104907_T01; parent_gene=GRMZM2G104907 seq=translation; coord=4:33112293..33117947:1;	GRMZM2G104907_P01	TRUE	TRUE	sTcDVVVTMQAQR	95%	n+304 (+304), Carbamidomethyl (+57)	59.11	25.00
4124	parent_transcript=GRMZM2G104907_T01; parent_gene=GRMZM2G104907 seq=translation; coord=3:168523033..168526394:1;	GRMZM2G104907_P01	TRUE	TRUE	vDPLELR	93%	n+304 (+304)	33.06	28.24
4125	parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845 seq=translation; coord=3:168523033..168526394:1;	GRMZM2G086845_P01	TRUE	TRUE	gAIPSLPTEAEVLQLIEk	95%	n+304 (+304), K+304 (+304)	48.37	25.00
4126	parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845 seq=translation; coord=3:168523033..168526394:1;	GRMZM2G086845_P01	TRUE	TRUE	IGDDEFGR	93%	n+304 (+304)	29.38	25.00
4127	parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845 seq=translation; coord=3:168523033..168526394:1;	GRMZM2G086845_P01	TRUE	TRUE	IGGGAAFVGk	95%	n+304 (+304), K+304 (+304)	39.21	27.03
4128	parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845 seq=translation; coord=3:168523033..168526394:1;	GRMZM2G086845_P01	TRUE	TRUE	tQILSIWDQADIVk	95%	n+304 (+304), K+304 (+304)	37.57	25.00
4129	parent_transcript=GRMZM2G086845_T01; parent_gene=GRMZM2G086845 seq=translation; coord=4:63703567..63707582:1;	GRMZM2G086845_P01	TRUE	TRUE	vQQVDTTGAGDAFVGALLQR	95%	n+304 (+304)	37.08	25.48
4130	parent_transcript=GRMZM2G024959_T01; parent_gene=GRMZM2G024959 seq=translation; coord=4:63703567..63707582:1;	GRMZM2G024959_P01,GRMZM2G102927_P01	TRUE	TRUE	fNLIADMMMLDEAIk	95%	n+304 (+304), K+304 (+304)	45.70	25.62
4131	parent_transcript=GRMZM2G024959_T01; parent_gene=GRMZM2G024959 seq=translation; coord=4:63703567..63707582:1;	GRMZM2G024959_P01,GRMZM2G102927_P01	TRUE	TRUE	nAITSQGPGTAVEFALALVEk	95%	n+304 (+304), K+304 (+304)	37.78	25.01
4132	parent_transcript=GRMZM2G024959_T01; parent_gene=GRMZM2G024959 seq=translation; coord=4:63703567..63707582:1;	GRMZM2G024959_P01,GRMZM2G102927_P01	TRUE	TRUE	vLVPVAAGTEPIEAATTADVLNR	93%	n+304 (+304)	27.21	25.15
4133	parent_transcript=GRMZM2G024959_T01; parent_gene=GRMZM2G024959 seq=translation; coord=4:165966482..165969746:-1;	GRMZM2G024959_P01,GRMZM2G102927_P01	TRUE	TRUE	vVVDGNLITSR	92%	n+304 (+304)	29.22	25.68
4134	parent_transcript=GRMZM2G125268_T01; parent_gene=GRMZM2G125268 seq=translation; coord=4:165966482..165969746:-1;	GRMZM2G125268_P01	TRUE	TRUE	dGVEQGQPQIDGEQFNk	95%	n+304 (+304), K+304 (+304)	71.36	25.00
4135	parent_transcript=GRMZM2G125268_T01; parent_gene=GRMZM2G125268 seq=translation; coord=4:165966482..165969746:-1;	GRMZM2G125268_P01	TRUE	TRUE	fADLIER	87%	n+304 (+304)	25.53	25.00
4136	parent_transcript=GRMZM2G125268_T01; parent_gene=GRMZM2G125268 seq=translation; coord=10:142067983..142070677:1;	GRMZM2G125268_P01	TRUE	TRUE	vAEGDSEDIDR	95%	n+304 (+304)	66.66	25.00
4137	parent_transcript=GRMZM2G019325_T01; parent_gene=GRMZM2G019325 seq=translation; coord=10:142067983..142070677:1;	GRMZM2G019325_P01,GRMZM2G044800_P01	TRUE	TRUE	eAIEGTyIDk	95%	n+304 (+304), K+304 (+304)	59.37	26.19
4138	parent_transcript=GRMZM2G019325_T01; parent_gene=GRMZM2G019325	GRMZM2G019325_P01,GRMZM2G044800_P01	TRUE	TRUE	sIGLGfK	87%	n+304 (+304), K+304 (+304)	25.65	25.00

4139	seq=translation; coord=10:142067983..142070677:1; parent_transcript=GRMZM2G019325_T01; parent_gene=GRMZM2G019325	GRMZM2G019325_P01,GRMZM2G044800_P01	TRUE	TRUE	vIPAGSAAAGk	95%	n+304 (+304), K+304 (+304)	51.42	25.00
4140	seq=translation; coord=2:196050685..196097541:1; parent_transcript=GRMZM2G058105_T01; parent_gene=GRMZM2G058105	GRMZM2G058105_P01	TRUE	TRUE	aLQDAEELEVAAR	95%	n+304 (+304)	49.16	25.34
4141	seq=translation; coord=2:196050685..196097541:1; parent_transcript=GRMZM2G058105_T01; parent_gene=GRMZM2G058105	GRMZM2G058105_P01	TRUE	TRUE	gLSADALASLPSVTYk	95%	n+304 (+304), K+304 (+304)	29.63	25.00
4142	seq=translation; coord=2:196050685..196097541:1; parent_transcript=GRMZM2G058105_T01; parent_gene=GRMZM2G058105	GRMZM2G058105_P01	TRUE	TRUE	lMALAGLSDWR	93%	n+304 (+304)	30.10	25.39
4143	seq=translation; coord=10:4243574..4244555:-1; parent_transcript=GRMZM5G898755_T01; parent_gene=GRMZM5G898755	GRMZM5G898755_P01,GRMZM5G898755_P02	TRUE	TRUE	cGVSVGVPISTVDcTk	95%	Carbamidomethyl (+57), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.62	25.40
4144	seq=translation; coord=10:4243574..4244555:-1; parent_transcript=GRMZM5G898755_T01; parent_gene=GRMZM5G898755	GRMZM5G898755_P01,GRMZM5G898755_P02	TRUE	TRUE	lGGVSMANAAANIPsk	95%	n+304 (+304), K+304 (+304)	78.63	25.85
4145	seq=translation; coord=10:4243574..4244555:-1; parent_transcript=GRMZM5G898755_T01; parent_gene=GRMZM5G898755	GRMZM5G898755_P01,GRMZM5G898755_P02	TRUE	TRUE	qATcNcLk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	31.69	25.00
4146	seq=translation; coord=10:76402669..76405224:1; parent_transcript=GRMZM2G079908_T01; parent_gene=GRMZM2G079908	GRMZM2G079908_P01,GRMZM2G079908_P02, GRMZM2G079908_P04	TRUE	TRUE	gLQEEFEEHAek	95%	n+304 (+304), K+304 (+304)	71.70	25.00
4147	seq=translation; coord=10:76402669..76405224:1; parent_transcript=GRMZM2G079908_T01; parent_gene=GRMZM2G079908	GRMZM2G079908_P01,GRMZM2G079908_P02, GRMZM2G079908_P04	TRUE	TRUE	lILYGLYk	95%	n+304 (+304), K+304 (+304)	41.67	25.00
4148	seq=translation; coord=10:76402669..76405224:1; parent_transcript=GRMZM2G079908_T01; parent_gene=GRMZM2G079908	GRMZM2G079908_P01,GRMZM2G079908_P02, GRMZM2G079908_P04	TRUE	TRUE	qATVGDVNTDRPGIFYQk	90%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	25.68	25.00
4149	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	TRUE	TRUE	aAPSMSDAAMGk	95%	n+304 (+304), K+304 (+304)	54.80	25.00
4150	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	TRUE	TRUE	aLSEGGFEk	94%	n+304 (+304), K+304 (+304)	31.01	25.73
4151	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	TRUE	TRUE	iATVEPVTmk	95%	n+304 (+304), K+304 (+304)	29.29	25.00
4152	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	TRUE	TRUE	qMGPPAAPGAHPENQEAAAR	95%	Pyro-cmC (-17), n+304 (+304)	74.39	25.00
4153	seq=translation; coord=10:14302293..14305526:1; parent_transcript=GRMZM2G106622_T01; parent_gene=GRMZM2G106622	GRMZM2G106622_P01	TRUE	TRUE	qmGPPAAPGAHPENQEAAAR	95%	Pyro-cmC (-17), n+304 (+304), Oxidation (+16)	76.31	25.00
4154	seq=translation; coord=4:229408072..229414150:-1; parent_transcript=GRMZM2G162992_T02; parent_gene=GRMZM2G162992	GRMZM2G162992_P02	TRUE	TRUE	eVLAEADAGSSGAGSGGR	95%	n+304 (+304)	58.73	25.00
4155	seq=translation; coord=4:229408072..229414150:-1; parent_transcript=GRMZM2G162992_T02; parent_gene=GRMZM2G162992	GRMZM2G162992_P02	TRUE	TRUE	qLISEVTSENR	86%	n+304 (+304)	25.66	25.29

4156	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08 GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08	TRUE	TRUE	aFVSEYAVWR	95%	n+304 (+304)	40.06	25.00
4157	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08 GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08	TRUE	TRUE	dVLDSLEFAR	95%	n+304 (+304)	33.70	25.00
4158	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08 GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08	TRUE	TRUE	gSLLASLAEAAFLTGLEK	95%	n+304 (+304), K+304 (+304)	49.35	25.00
4159	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08 GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08	TRUE	TRUE	gVVWLDQVSLMPEDTYK	95%	n+304 (+304), K+304 (+304)	36.62	26.41
4160	seq=translation; coord=3:230006629..230017669:-1; parent_transcript=GRMZM2G006130_T01; parent_gene=GRMZM2G006130	GRMZM2G006130_P01,GRMZM2G006130_P02, GRMZM2G006130_P03,GRMZM2G006130_P04, GRMZM2G006130_P06,GRMZM2G006130_P07, GRMZM2G006130_P08	TRUE	TRUE	tELISMLLDLkPR	95%	n+304 (+304), K+304 (+304)	28.85	25.00
4161	seq=translation; coord=1:214899491..214901246:-1; parent_transcript=AC217050.4_FGT006; parent_gene=AC217050.4_FG006 seq=translation; coord=1:214899491..214901246:-1;	AC217050.4_FGP006	TRUE	TRUE	eSAESTMMAYk	95%	n+304 (+304), K+304 (+304)	31.88	25.00
4162	parent_transcript=AC217050.4_FGT006; parent_gene=AC217050.4_FG006 seq=translation; coord=1:214899491..214901246:-1;	AC217050.4_FGP006	TRUE	TRUE	tVDVEELTVEER	95%	n+304 (+304)	65.02	25.00
4163	parent_transcript=GRMZM2G351125_T01; parent_gene=GRMZM2G351125 seq=translation; coord=UNKNOWN:5070241..5074601:-1;	GRMZM2G351125_P01	TRUE	TRUE	eAPEESTk	95%	n+304 (+304), K+304 (+304)	27.86	25.01
4164	parent_transcript=GRMZM2G351125_T01; parent_gene=GRMZM2G351125 seq=translation; coord=UNKNOWN:5070241..5074601:-1;	GRMZM2G351125_P01	TRUE	TRUE	eVEVFSLR	95%	n+304 (+304)	43.05	25.00
4165	parent_transcript=GRMZM2G351125_T01; parent_gene=GRMZM2G351125 seq=translation; coord=4:197713557..197717259:-1;	GRMZM2G351125_P01	TRUE	TRUE	sPPLPFLSSLLQSR	95%	n+304 (+304)	51.81	25.00
4166	parent_transcript=GRMZM2G050218_T01; parent_gene=GRMZM2G050218 seq=translation; coord=4:197713557..197717259:-1;	GRMZM2G050218_P01	TRUE	TRUE	dTTDATFVR	95%	n+304 (+304)	31.68	25.00
4167	parent_transcript=GRMZM2G050218_T01; parent_gene=GRMZM2G050218 seq=translation; coord=4:197713557..197717259:-1;	GRMZM2G050218_P01	TRUE	TRUE	gFGFITYSDPAVVdk	94%	n+304 (+304), K+304 (+304)	29.01	25.82
4168	parent_transcript=GRMZM2G050218_T01; parent_gene=GRMZM2G050218 seq=translation; coord=9:14322326..14327546:-1;	GRMZM2G050218_P01	TRUE	TRUE	ISSYGGVGDFFGGAYGR	95%	n+304 (+304)	33.75	25.00
4169	parent_transcript=GRMZM2G014240_T01; parent_gene=GRMZM2G014240 seq=translation; coord=9:14322326..14327546:-1;	GRMZM2G014240_P01	TRUE	TRUE	aADVGDALVGk	95%	n+304 (+304), K+304 (+304)	53.19	26.21
4170	parent_transcript=GRMZM2G014240_T01; parent_gene=GRMZM2G014240 seq=translation; coord=9:14322326..14327546:-1;	GRMZM2G014240_P01	TRUE	TRUE	aGYADSLIEEEGLNDHNVVVk	95%	n+304 (+304), K+304 (+304)	60.16	25.00
4171	parent_transcript=GRMZM2G014240_T01; parent_gene=GRMZM2G014240	GRMZM2G014240_P01	TRUE	TRUE	nIPEDDPR	95%	n+304 (+304)	37.80	25.00

4172	seq=translation; coord=10:1152679..1158648:-1; parent_transcript=GRMZM2G057441_T01; parent_gene=GRMZM2G057441	GRMZM2G057441_P01	TRUE	TRUE	aETFGIPIGWAK	95%	n+304 (+304), K+304 (+304)	51.71	25.83
4173	seq=translation; coord=10:1152679..1158648:-1; parent_transcript=GRMZM2G057441_T01; parent_gene=GRMZM2G057441	GRMZM2G057441_P01	TRUE	TRUE	aVLNPMAMFGGIVGQEVVk	95%	n+304 (+304), K+304 (+304)	60.85	25.97
4174	seq=translation; coord=10:1152679..1158648:-1; parent_transcript=GRMZM2G057441_T01; parent_gene=GRMZM2G057441	GRMZM2G057441_P01	TRUE	TRUE	IIDLAIISINETLGDSk	95%	n+304 (+304), K+304 (+304)	59.08	25.00
4175	seq=translation; coord=5:193849196..193850728:-1; parent_transcript=GRMZM2G147014_T01; parent_gene=GRMZM2G147014	GRMZM2G147014_P01	TRUE	TRUE	sSAEEADHK	93%	n+304 (+304), K+304 (+304)	27.08	25.00
4176	seq=translation; coord=5:193849196..193850728:-1; parent_transcript=GRMZM2G147014_T01; parent_gene=GRMZM2G147014	GRMZM2G147014_P01	TRUE	TRUE	vTVSEPEk	89%	n+304 (+304), K+304 (+304)	27.67	26.05
4177	seq=translation; coord=8:25334083..25343016:1; parent_transcript=GRMZM2G373928_T01; parent_gene=GRMZM2G373928	GRMZM2G373928_P01,GRMZM2G373928_P02	TRUE	TRUE	iIGDVDPFVR	95%	n+304 (+304)	33.17	25.85
4178	seq=translation; coord=8:25334083..25343016:1; parent_transcript=GRMZM2G373928_T01; parent_gene=GRMZM2G373928	GRMZM2G373928_P01,GRMZM2G373928_P02	TRUE	TRUE	vVFLLFQQLGR	95%	n+304 (+304)	36.78	25.20
4179	seq=translation; coord=4:147218569..147222484:-1; parent_transcript=GRMZM2G070343_T01; parent_gene=GRMZM2G070343	GRMZM2G070343_P01,GRMZM2G070343_P02, GRMZM2G070343_P03	TRUE	TRUE	dSVIGAVPESTLVTcIdk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	41.29	26.25
4180	seq=translation; coord=4:147218569..147222484:-1; parent_transcript=GRMZM2G070343_T01; parent_gene=GRMZM2G070343	GRMZM2G070343_P01,GRMZM2G070343_P02, GRMZM2G070343_P03	TRUE	TRUE	INTDENPDIAQFGIR	95%	n+304 (+304)	83.42	25.00
4181	seq=translation; coord=4:147218569..147222484:-1; parent_transcript=GRMZM2G070343_T01; parent_gene=GRMZM2G070343	GRMZM2G070343_P01,GRMZM2G070343_P02, GRMZM2G070343_P03	TRUE	TRUE	sIPTMMIFk	93%	n+304 (+304), K+304 (+304)	27.34	25.00
4182	seq=translation; coord=2:2803488..2806329:1; parent_transcript=GRMZM2G102471_T01; parent_gene=GRMZM2G102471	GRMZM2G102471_P01,GRMZM2G102471_P03, GRMZM2G102471_P04,GRMZM2G102471_P06, GRMZM2G132759_P01,GRMZM2G132759_P02, GRMZM2G132759_P03,GRMZM2G132759_P04, GRMZM2G132759_P06,GRMZM2G165511_P01, GRMZM5G866947_P03,GRMZM5G866947_P04, GRMZM5G866947_P05	TRUE	TRUE	eQWSPALTISK	94%	n+304 (+304), K+304 (+304)	33.02	26.68
4183	seq=translation; coord=8:136129273..136131879:-1; parent_transcript=GRMZM2G100146_T01; parent_gene=GRMZM2G100146	GRMZM2G100146_P01	TRUE	TRUE	aVAATAsk	95%	n+304 (+304), K+304 (+304)	36.93	25.44
4184	seq=translation; coord=8:136129273..136131879:-1; parent_transcript=GRMZM2G100146_T01; parent_gene=GRMZM2G100146	GRMZM2G100146_P01	TRUE	TRUE	IAIGTLSIDk	95%	n+304 (+304), K+304 (+304)	37.29	25.00
4185	seq=translation; coord=8:136129273..136131879:-1; parent_transcript=GRMZM2G100146_T01; parent_gene=GRMZM2G100146	GRMZM2G100146_P01	TRUE	TRUE	tTSVFFSGYk	92%	n+304 (+304), K+304 (+304)	28.25	25.68
4186	seq=translation; coord=8:136129273..136131879:-1; parent_transcript=GRMZM2G100146_T01; parent_gene=GRMZM2G100146	GRMZM2G100146_P01	TRUE	TRUE	vATPPAQk	91%	n+304 (+304), K+304 (+304)	26.93	25.00
4187	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	aLTLMESPAAEALIVk	95%	n+304 (+304), K+304 (+304)	59.01	25.00

4188	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	aVVDDILPPAFLSNAK	95%	n+304 (+304), K+304 (+304)	33.79	25.00
4189	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	dGLDDLALDIPDAR	95%	n+304 (+304)	67.72	25.00
4190	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	eASEEcLVSSSQMMK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.94	25.00
4191	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	eMASVLLPSLMELFSSEDIak	95%	n+304 (+304), K+304 (+304)	37.57	25.00
4192	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	iAVQNAETQSLASPR	95%	n+304 (+304)	36.93	26.09
4193	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	IIETDAEAcLDR	95%	n+304 (+304), Carbamidomethyl (+57)	45.39	25.00
4194	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	tLNLLQEcFGEGITINQMTk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	67.16	25.40
4195	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	vAESLDDLILDIPSak	95%	n+304 (+304), K+304 (+304)	52.92	25.00
4196	seq=translation; coord=6:6317365..6323357:-1; parent_transcript=GRMZM2G412470_T02; parent_gene=GRMZM2G412470	GRMZM2G412470_P02	TRUE	TRUE	vRDGLDDLALDIPDAR	95%	n+304 (+304)	51.26	25.65
4197	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	TRUE	TRUE	dVADADALVSSLSGSAK	95%	n+304 (+304), K+304 (+304)	35.83	25.95
4198	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	TRUE	TRUE	KVWWQFYGDNVGEAVEVGNFDPk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	53.46	25.04
4199	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	TRUE	TRUE	IQAATSVEDALEIAR	95%	n+304 (+304)	66.86	25.38
4200	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	TRUE	TRUE	tSVPGIFAIGDVAAFLPk	95%	n+304 (+304), K+304 (+304)	42.68	25.00
4201	seq=translation; coord=10:82038497..82043288:1; parent_transcript=GRMZM5G828229_T02; parent_gene=GRMZM5G828229	GRMZM5G828229_P02	TRUE	TRUE	vATFWIDSDSR	90%	n+304 (+304)	27.28	25.00
4202	seq=translation; coord=8:118103124..118103722:-1; parent_transcript=AC197705.4_FGT003; parent_gene=AC197705.4_FG003	AC197705.4_FGP003	TRUE	TRUE	dMSPPLEWYGVPEGAR	95%	n+304 (+304)	54.46	25.00
4203	seq=translation; coord=8:118103124..118103722:-1; parent_transcript=AC197705.4_FGT003; parent_gene=AC197705.4_FG003	AC197705.4_FGP003	TRUE	TRUE	dQLGGLQEGVNDWk	95%	n+304 (+304), K+304 (+304)	66.96	25.28
4204	seq=translation; coord=8:118103124..118103722:-1; parent_transcript=AC197705.4_FGT003; parent_gene=AC197705.4_FG003	AC197705.4_FGP003	TRUE	TRUE	kDMSPPLEWYGVPEGAR	95%	K+304 (+304), n+304 (+304)	61.85	25.00
4205	seq=translation; coord=3:59325157..59327502:1; parent_transcript=GRMZM2G107228_T01; parent_gene=GRMZM2G107228	GRMZM2G107228_P01	TRUE	TRUE	aAVEQScPQTVScADIVAFaAR	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	30.09	25.00

4206	seq=translation; coord=3:59325157..59327502:1; parent_transcript=GRMZM2G107228_T01; parent_gene=GRMZM2G107228	GRMZM2G107228_P01	TRUE	TRUE	ILPLNLGLFFSDNQLR	95%	n+304 (+304)	60.34	25.59
4207	seq=translation; coord=3:59325157..59327502:1; parent_transcript=GRMZM2G107228_T01; parent_gene=GRMZM2G107228	GRMZM2G107228_P01	TRUE	TRUE	mGNIQVLTGTQGQIR	95%	n+304 (+304)	47.92	25.69
4208	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	gMFEDVNIILVGDHGMVGTcDR	95%	n+304 (+304), Carbamidomethyl (+57)	75.36	25.00
4209	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	iPPIIGLVGEGYk	95%	n+304 (+304), K+304 (+304)	41.64	25.00
4210	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	kLVFLEELAPWIELk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.56	25.00
4211	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	ISKPVLLISSDGFR	95%	n+304 (+304), K+304 (+304)	37.14	25.00
4212	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	IVFLEELAPWIELk	95%	n+304 (+304), K+304 (+304)	47.25	25.00
4213	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	sDWVLSVTPLLAIRPPDGVSPAEEVAK	95%	n+304 (+304), K+304 (+304)	33.74	25.00
4214	seq=translation; coord=3:5595065..5596815:-1; parent_transcript=GRMZM2G143165_T01; parent_gene=GRMZM2G143165	GRMZM2G143165_P01	TRUE	TRUE	tiFAAHGPR	95%	n+304 (+304)	45.73	25.89
4215	seq=translation; coord=6:49040773..49051761:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	TRUE	TRUE	fLHIIENSPVYPVIYDSNR	95%	n+304 (+304)	67.13	25.28
4216	seq=translation; coord=6:49040773..49051761:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	TRUE	TRUE	iFEVGDVVMLDSSR	94%	n+304 (+304)	31.33	25.00
4217	seq=translation; coord=6:49040773..49051761:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	TRUE	TRUE	mDVLLSDILGPISQDEK	95%	n+304 (+304), K+304 (+304)	57.25	25.21
4218	seq=translation; coord=6:49040773..49051761:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	TRUE	TRUE	vSGFEEIMGLVDSIVk	95%	n+304 (+304), K+304 (+304)	38.79	25.00
4219	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G700926_T01; parent_gene=GRMZM2G700926	GRMZM2G700926_P01	TRUE	TRUE	yDLLcLEGLAR	95%	n+304 (+304), Carbamidomethyl (+57)	33.12	25.00
4220	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G014805_T01; parent_gene=GRMZM2G014805	GRMZM2G014805_P01	TRUE	TRUE	dPNQNQQIQNFGDPFLMVIR	95%	n+304 (+304)	39.00	25.00
4221	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G014805_T01; parent_gene=GRMZM2G014805	GRMZM2G014805_P01	TRUE	TRUE	fTWITIESFSR	92%	n+304 (+304)	28.72	25.00
4222	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G014805_T01; parent_gene=GRMZM2G014805	GRMZM2G014805_P01	TRUE	TRUE	lLEVfYHk	95%	n+304 (+304), K+304 (+304)	32.16	25.20
4223	seq=translation; coord=3:106336887..106353717:1; parent_transcript=GRMZM2G014805_T01; parent_gene=GRMZM2G014805	GRMZM2G014805_P01	TRUE	TRUE	vELSNPDTELR	95%	n+304 (+304)	34.17	25.00

4224	seq=translation; coord=1:175294828..175302644:-1; parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=1:175294828..175302644:-1;	GRMZM2G022365_P01	TRUE	TRUE	aHPGGPAASDFDWGTGDTPR	95%	n+304 (+304)	85.81	25.00
4225	parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=1:175294828..175302644:-1;	GRMZM2G022365_P01	TRUE	TRUE	dAETGQDAPSEDGtK	95%	n+304 (+304), K+304 (+304)	43.33	25.00
4226	parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=1:175294828..175302644:-1;	GRMZM2G022365_P01	TRUE	TRUE	eAPETEEAk	95%	n+304 (+304), K+304 (+304)	29.24	25.00
4227	parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=1:175294828..175302644:-1;	GRMZM2G022365_P01	TRUE	TRUE	IVAESAADAVAAPAPETk	95%	n+304 (+304), K+304 (+304)	39.72	25.22
4228	parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=1:175294828..175302644:-1;	GRMZM2G022365_P01	TRUE	TRUE	sEIVFVSPGTGEEIk	95%	n+304 (+304), K+304 (+304)	31.64	25.95
4229	parent_transcript=GRMZM2G022365_T01; parent_gene=GRMZM2G022365 seq=translation; coord=7:155957641..155960914:1;	GRMZM2G022365_P01	TRUE	TRUE	vFDSPEGEk	91%	n+304 (+304), K+304 (+304)	29.40	26.07
4230	parent_transcript=GRMZM2G173863_T01; parent_gene=GRMZM2G173863 seq=translation; coord=7:155957641..155960914:1;	GRMZM2G173863_P01,GRMZM2G173863_P02	TRUE	TRUE	gILVQDQEPGVILFDIGLAHk	95%	n+304 (+304), K+304 (+304)	27.99	25.00
4231	parent_transcript=GRMZM2G173863_T01; parent_gene=GRMZM2G173863 seq=translation; coord=7:155957641..155960914:1;	GRMZM2G173863_P01,GRMZM2G173863_P02	TRUE	TRUE	gVEGLSQEELFVWLVPk	95%	n+304 (+304), K+304 (+304)	42.15	25.05
4232	parent_transcript=GRMZM2G173863_T01; parent_gene=GRMZM2G173863 seq=translation; coord=5:9900674..9908640:1;	GRMZM2G173863_P01,GRMZM2G173863_P02	TRUE	TRUE	gVESYTLDESTGLLEAR	95%	n+304 (+304)	43.99	25.00
4233	parent_transcript=GRMZM2G096596_T01; parent_gene=GRMZM2G096596 seq=translation; coord=5:9900674..9908640:1;	GRMZM2G096596_P01	TRUE	TRUE	sDPAIMAYDEFVAAEAVGR	95%	n+304 (+304)	32.09	25.00
4234	parent_transcript=GRMZM2G096596_T01; parent_gene=GRMZM2G096596 seq=translation; coord=5:9900674..9908640:1;	GRMZM2G096596_P01	TRUE	TRUE	sVADSLPALAWVAVFLGk	95%	n+304 (+304), K+304 (+304)	34.53	25.00
4235	parent_transcript=GRMZM2G096596_T01; parent_gene=GRMZM2G096596 seq=translation; coord=5:9900674..9908640:1;	GRMZM2G096596_P01	TRUE	TRUE	tLAIDDcDSR	95%	n+304 (+304), Carbamidomethyl (+57)	50.48	25.00
4236	parent_transcript=GRMZM2G096596_T01; parent_gene=GRMZM2G096596 seq=translation; coord=2:222875577..222883048:1;	GRMZM2G096596_P01	TRUE	TRUE	wVVENQVGk	94%	n+304 (+304), K+304 (+304)	29.31	25.83
4237	parent_transcript=GRMZM2G172101_T01; parent_gene=GRMZM2G172101 seq=translation; coord=2:222875577..222883048:1;	GRMZM2G172101_P01,GRMZM2G172101_P02, GRMZM2G172101_P03	TRUE	TRUE	aLQPYMGGIEFLPFk	95%	n+304 (+304), K+304 (+304)	32.61	25.87
4238	parent_transcript=GRMZM2G172101_T01; parent_gene=GRMZM2G172101 seq=translation; coord=2:222875577..222883048:1;	GRMZM2G172101_P01,GRMZM2G172101_P02, GRMZM2G172101_P03	TRUE	TRUE	fASVELVDEVIALDk	95%	n+304 (+304), K+304 (+304)	37.96	25.65
4239	parent_transcript=GRMZM2G172101_T01; parent_gene=GRMZM2G172101 seq=translation; coord=8:138510107..138515042:1;	GRMZM2G172101_P01,GRMZM2G172101_P02, GRMZM2G172101_P03	TRUE	TRUE	iYPAELPIk	90%	n+304 (+304), K+304 (+304)	26.70	25.44
4240	parent_transcript=GRMZM2G700683_T01; parent_gene=GRMZM2G700683 seq=translation; coord=8:138510107..138515042:1;	GRMZM2G700683_P01	TRUE	TRUE	aLAEEGYEVVLVNSNPATIMTDPGLAHR	95%	n+304 (+304)	85.63	25.00
4241	parent_transcript=GRMZM2G700683_T01; parent_gene=GRMZM2G700683	GRMZM2G700683_P01	TRUE	TRUE	vPIITVDGAR	95%	n+304 (+304)	40.43	26.13

4242	seq=translation; coord=7:6064236..6068299:1; parent_transcript=GRMZM2G025977_T01; parent_gene=GRMZM2G025977	GRMZM2G025977_P01,GRMZM2G025977_P02, GRMZM2G025977_P03	TRUE	TRUE	aVLAASGAEVVIGEVER	95%	n+304 (+304)	57.67	26.50
4243	seq=translation; coord=7:6064236..6068299:1; parent_transcript=GRMZM2G025977_T01; parent_gene=GRMZM2G025977	GRMZM2G025977_P01,GRMZM2G025977_P02, GRMZM2G025977_P03	TRUE	TRUE	dENPPDDPATITGEPDSIAMLHK	95%	n+304 (+304), K+304 (+304)	75.06	25.00
4244	seq=translation; coord=7:6064236..6068299:1; parent_transcript=GRMZM2G025977_T01; parent_gene=GRMZM2G025977	GRMZM2G025977_P01,GRMZM2G025977_P02, GRMZM2G025977_P03	TRUE	TRUE	dGVLDADAVVLALGPWSGR	95%	n+304 (+304)	44.40	26.46
4245	seq=translation; coord=7:6064236..6068299:1; parent_transcript=GRMZM2G025977_T01; parent_gene=GRMZM2G025977	GRMZM2G025977_P01,GRMZM2G025977_P02, GRMZM2G025977_P03	TRUE	TRUE	iVDLEPFSPAR	95%	n+304 (+304)	33.11	26.50
4246	seq=translation; coord=1:12146189..12150797:1; parent_transcript=GRMZM2G000823_T01; parent_gene=GRMZM2G000823	GRMZM2G000823_P01	TRUE	TRUE	iQAITLPMILTPPYk	95%	n+304 (+304), K+304 (+304)	29.88	25.00
4247	seq=translation; coord=1:12146189..12150797:1; parent_transcript=GRMZM2G000823_T01; parent_gene=GRMZM2G000823	GRMZM2G000823_P01	TRUE	TRUE	sWADVEEEEEAK	95%	n+304 (+304), K+304 (+304)	47.45	25.00
4248	seq=translation; coord=1:12146189..12150797:1; parent_transcript=GRMZM2G000823_T01; parent_gene=GRMZM2G000823	GRMZM2G000823_P01	TRUE	TRUE	vLISTDVLAR	95%	n+304 (+304)	31.70	25.00
4249	seq=translation; coord=8:116620898..116625716:1; parent_transcript=GRMZM5G874500_T02; parent_gene=GRMZM5G874500	GRMZM5G874500_P02,GRMZM5G874500_P03	TRUE	TRUE	aGLTEEQLQEIEQR	95%	n+304 (+304)	83.58	25.00
4250	seq=translation; coord=8:116620898..116625716:1; parent_transcript=GRMZM5G874500_T02; parent_gene=GRMZM5G874500	GRMZM5G874500_P02,GRMZM5G874500_P03	TRUE	TRUE	ISILGLMPSSSLAEVLk	95%	n+304 (+304), K+304 (+304)	57.06	25.00
4251	seq=translation; coord=8:116620898..116625716:1; parent_transcript=GRMZM5G874500_T02; parent_gene=GRMZM5G874500	GRMZM5G874500_P02,GRMZM5G874500_P03	TRUE	TRUE	nPADFALWk	95%	n+304 (+304), K+304 (+304)	30.27	25.93
4252	seq=translation; coord=8:116620898..116625716:1; parent_transcript=GRMZM5G874500_T02; parent_gene=GRMZM5G874500	GRMZM5G874500_P02,GRMZM5G874500_P03	TRUE	TRUE	qPEDIYIALIALETELk	95%	n+304 (+304), K+304 (+304)	34.26	25.29
4253	seq=translation; coord=2:233433323..233435947:-1; parent_transcript=GRMZM2G018197_T01; parent_gene=GRMZM2G018197	GRMZM2G018197_P01	TRUE	TRUE	fVIWTESAfk	95%	n+304 (+304), K+304 (+304)	29.33	25.42
4254	seq=translation; coord=2:233433323..233435947:-1; parent_transcript=GRMZM2G018197_T01; parent_gene=GRMZM2G018197	GRMZM2G018197_P01	TRUE	TRUE	iETVPEMPLVISDSAESIEk	95%	n+304 (+304), K+304 (+304)	36.18	25.00
4255	seq=translation; coord=3:8746797..8754263:1; parent_transcript=GRMZM2G120271_T01; parent_gene=GRMZM2G120271	GRMZM2G120271_P01	TRUE	TRUE	dGIPEcGLLQncLEELATR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	50.06	25.00
4256	seq=translation; coord=3:8746797..8754263:1; parent_transcript=GRMZM2G120271_T01; parent_gene=GRMZM2G120271	GRMZM2G120271_P01	TRUE	TRUE	dVEGASTQWDDIQR	95%	n+304 (+304)	64.55	25.00
4257	seq=translation; coord=3:8746797..8754263:1; parent_transcript=GRMZM2G120271_T01; parent_gene=GRMZM2G120271	GRMZM2G120271_P01	TRUE	TRUE	iISTDciPNYPDR	95%	n+304 (+304), Carbamidomethyl (+57)	54.76	25.00
4258	seq=translation; coord=1:288732967..288734700:1; parent_transcript=GRMZM2G164020_T01; parent_gene=GRMZM2G164020	GRMZM2G164020_P01,GRMZM2G164020_P02	TRUE	TRUE	aNPTHPPYAEMISEAVTSLk	95%	n+304 (+304), K+304 (+304)	35.46	25.00
4259	seq=translation; coord=1:288732967..288734700:1; parent_transcript=GRMZM2G164020_T01; parent_gene=GRMZM2G164020	GRMZM2G164020_P01,GRMZM2G164020_P02	TRUE	TRUE	ILLGQLk	94%	n+304 (+304), K+304 (+304)	30.30	25.00

4260	seq=translation; coord=1:288732967..288734700:1; parent_transcript=GRMZM2G164020_T01; parent_gene=GRMZM2G164020 seq=translation; coord=7:39219675..39225654:-1;	GRMZM2G164020_P01,GRMZM2G164020_P02	TRUE	TRUE	tGSSQYAIak	95%	n+304 (+304), K+304 (+304)	60.63	25.88
4261	parent_transcript=GRMZM2G471269_T04; parent_gene=GRMZM2G471269 seq=translation; coord=7:39219675..39225654:-1;	GRMZM2G471269_P04	TRUE	TRUE	iVPFLGQMISEGIELGR	95%	n+304 (+304)	37.21	25.37
4262	parent_transcript=GRMZM2G471269_T04; parent_gene=GRMZM2G471269 seq=translation; coord=7:39219675..39225654:-1;	GRMZM2G471269_P04	TRUE	TRUE	sLNFPVVDWR	95%	n+304 (+304)	35.73	25.50
4263	parent_transcript=GRMZM2G471269_T04; parent_gene=GRMZM2G471269 seq=translation; coord=7:39219675..39225654:-1;	GRMZM2G471269_P04	TRUE	TRUE	vSHILFVDSVPVGAGFSFSR	95%	n+304 (+304)	36.93	26.33
4264	parent_transcript=GRMZM2G471269_T04; parent_gene=GRMZM2G471269 seq=translation; coord=7:39219675..39225654:-1;	GRMZM2G471269_P04	TRUE	TRUE	wILDRPL	87%	n+304 (+304)	28.21	27.34
4265	parent_transcript=GRMZM2G046961_T01; parent_gene=GRMZM2G046961 seq=translation; coord=2:176000645..176001838:1;	GRMZM2G046961_P01	TRUE	TRUE	aEEDTVVVGEQPR	95%	n+304 (+304)	38.64	25.00
4266	parent_transcript=GRMZM2G046961_T01; parent_gene=GRMZM2G046961 seq=translation; coord=3:135219277..135223126:-1;	GRMZM2G046961_P01	TRUE	TRUE	gGGYEDAVVVGGR	95%	n+304 (+304)	52.99	25.00
4267	parent_transcript=GRMZM2G150521_T01; parent_gene=GRMZM2G150521 seq=translation; coord=3:135219277..135223126:-1;	GRMZM2G150521_P01	TRUE	TRUE	gFGFVYTSSEEASAAITALDGk	94%	n+304 (+304), K+304 (+304)	25.65	25.00
4268	parent_transcript=GRMZM2G150521_T01; parent_gene=GRMZM2G150521 seq=translation; coord=3:135219277..135223126:-1;	GRMZM2G150521_P01	TRUE	TRUE	IFVGISYQTDHSLR	95%	n+304 (+304)	75.20	25.00
4269	parent_transcript=GRMZM2G150521_T01; parent_gene=GRMZM2G150521 seq=translation; coord=8:78643850..78648764:1;	GRMZM2G150521_P01	TRUE	TRUE	yGQVIEAR	88%	n+304 (+304)	26.06	25.00
4270	parent_transcript=GRMZM5G892645_T01; parent_gene=GRMZM5G892645 seq=translation; coord=8:78643850..78648764:1;	GRMZM5G892645_P01,GRMZM5G892645_P02, GRMZM5G892645_P04,GRMZM5G892645_P05	TRUE	TRUE	fMQDPMIYVDDEAk	95%	n+304 (+304), K+304 (+304)	30.24	25.00
4271	parent_transcript=GRMZM5G892645_T01; parent_gene=GRMZM5G892645 seq=translation; coord=8:78643850..78648764:1;	GRMZM5G892645_P01,GRMZM5G892645_P02, GRMZM5G892645_P04,GRMZM5G892645_P05	TRUE	TRUE	gLAIITVSSASDSVLNQVQER	95%	n+304 (+304)	43.84	25.00
4272	parent_transcript=GRMZM5G892645_T01; parent_gene=GRMZM5G892645 seq=translation; coord=2:108630218..108681539:-1;	GRMZM5G892645_P01,GRMZM5G892645_P02, GRMZM5G892645_P04,GRMZM5G892645_P05	TRUE	TRUE	iLVATDLVGR	95%	n+304 (+304)	38.00	25.00
4273	parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043 seq=translation; coord=2:108630218..108681539:-1;	GRMZM2G158043_P02	TRUE	TRUE	gSYASNPDPGSR	95%	n+304 (+304)	30.47	25.00
4274	parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043 seq=translation; coord=2:108630218..108681539:-1;	GRMZM2G158043_P02	TRUE	TRUE	hDIIAALDk	94%	n+304 (+304), K+304 (+304)	26.54	25.65
4275	parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043 seq=translation; coord=2:108630218..108681539:-1;	GRMZM2G158043_P02	TRUE	TRUE	iYLYGEGWNFGEVAENQR	94%	n+304 (+304)	27.33	25.00
4276	parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043 seq=translation; coord=2:108630218..108681539:-1;	GRMZM2G158043_P02	TRUE	TRUE	IIVDLLNWAVNYk	94%	n+304 (+304), K+304 (+304)	29.07	25.00
4277	parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043	GRMZM2G158043_P02	TRUE	TRUE	IIVDLLNWAVNyk	94%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.17	25.00

4278	seq=translation; coord=2:108630218..108681539:-1; parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043	GRMZM2G158043_P02	TRUE	TRUE	ITTASDIVQR	95%	n+304 (+304)	41.37	25.15
4279	seq=translation; coord=2:108630218..108681539:-1; parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043	GRMZM2G158043_P02	TRUE	TRUE	tPMDLSIDER	95%	n+304 (+304)	45.13	25.00
4280	seq=translation; coord=2:108630218..108681539:-1; parent_transcript=GRMZM2G158043_T02; parent_gene=GRMZM2G158043	GRMZM2G158043_P02	TRUE	TRUE	vELQPENDGLPSSVTQk	95%	n+304 (+304), K+304 (+304)	31.20	25.35
4281	seq=translation; coord=10:124299211..124301978:1; parent_transcript=GRMZM2G173878_T01; parent_gene=GRMZM2G173878	GRMZM2G173878_P01,GRMZM2G330430_P02	TRUE	TRUE	eTFNHLASWLEDAR	93%	n+304 (+304)	29.43	25.00
4282	seq=translation; coord=10:124299211..124301978:1; parent_transcript=GRMZM2G173878_T01; parent_gene=GRMZM2G173878	GRMZM2G173878_P01,GRMZM2G330430_P02	TRUE	TRUE	fQPVHDLTIGVEFGAR	95%	n+304 (+304)	35.65	26.16
4283	seq=translation; coord=10:124299211..124301978:1; parent_transcript=GRMZM2G173878_T01; parent_gene=GRMZM2G173878	GRMZM2G173878_P01,GRMZM2G330430_P02	TRUE	TRUE	gAAGALLVYDITR	95%	n+304 (+304)	34.12	25.48
4284	seq=translation; coord=10:124299211..124301978:1; parent_transcript=GRMZM2G173878_T01; parent_gene=GRMZM2G173878	GRMZM2G173878_P01,GRMZM2G330430_P02	TRUE	TRUE	IQIWDTAGQESFR	95%	n+304 (+304)	49.51	25.00
4285	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	dLALGLASQTVLGAATMVSQTGk	95%	n+304 (+304), K+304 (+304)	83.24	25.00
4286	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	gTLISAVVAAAk	95%	n+304 (+304), K+304 (+304)	33.94	25.00
4287	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	gVAASGVLPAASAIR	95%	n+304 (+304)	36.43	25.50
4288	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	mQDLQDWSGQR	95%	n+304 (+304)	34.44	25.00
4289	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	qVLLQLRPR	95%	n+304 (+304)	29.66	25.00
4290	seq=translation; coord=3:150265213..150269134:1; parent_transcript=GRMZM2G068665_T01; parent_gene=GRMZM2G068665	GRMZM2G068665_P01	TRUE	TRUE	qVLLQLRPR	93%	Pyro-cmC (-17), n+304 (+304)	28.11	25.00
4291	seq=translation; coord=5:203926164..203934465:-1; parent_transcript=GRMZM2G150172_T01; parent_gene=GRMZM2G150172	GRMZM2G150172_P01	TRUE	TRUE	fPASQccAALk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	42.47	25.00
4292	seq=translation; coord=5:203926164..203934465:-1; parent_transcript=GRMZM2G150172_T01; parent_gene=GRMZM2G150172	GRMZM2G150172_P01	TRUE	TRUE	mGLScADVPR	95%	n+304 (+304), Carbamidomethyl (+57)	47.04	25.00
4293	seq=translation; coord=8:65969534..65973268:1; parent_transcript=GRMZM2G021331_T01; parent_gene=GRMZM2G021331	GRMZM2G021331_P01	TRUE	TRUE	yDEGLPPILTALEVLDNDR	95%	n+304 (+304)	61.64	25.63
4294	seq=translation; coord=8:65969534..65973268:1; parent_transcript=GRMZM2G021331_T01; parent_gene=GRMZM2G021331	GRMZM2G021331_P01	TRUE	TRUE	yDEGLPPILTALEVLDNDR	95%	n+304 (+304), iTRAQ8plex (+304)	44.84	25.04

4295	seq=translation; coord=5:112928080..112930204:-1; parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081 seq=translation; coord=5:112928080..112930204:-1;	GRMZM2G144081_P01,GRMZM2G144081_P02	TRUE	TRUE	dEGPSELYR	95%	n+304 (+304)	44.89	25.00
4296	parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081 seq=translation; coord=5:112928080..112930204:-1;	GRMZM2G144081_P01,GRMZM2G144081_P02	TRUE	TRUE	dVYDNVAHAFVk	95%	n+304 (+304), K+304 (+304)	43.41	26.32
4297	parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081 seq=translation; coord=5:112928080..112930204:-1;	GRMZM2G144081_P01,GRMZM2G144081_P02	TRUE	TRUE	iPIPTPLVAGALAGFASTLcTYPMELIK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.25	25.00
4298	parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081 seq=translation; coord=5:112928080..112930204:-1;	GRMZM2G144081_P01,GRMZM2G144081_P02	TRUE	TRUE	qQQLGDLSLR	95%	n+304 (+304)	38.37	26.41
4299	parent_transcript=GRMZM2G144081_T01; parent_gene=GRMZM2G144081 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G144081_P01,GRMZM2G144081_P02	TRUE	TRUE	rPGADVGPVATLLIGSAAGAIASSATFPLEVAR	95%	n+304 (+304)	35.34	25.00
4300	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G083810_P01	TRUE	TRUE	eLPGAYAFVVDMPGLGTGDIK	93%	n+304 (+304), K+304 (+304)	27.13	25.43
4301	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G083810_P01	TRUE	TRUE	fVLPDNADMDk	93%	n+304 (+304), K+304 (+304)	28.31	25.01
4302	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G083810_P01	TRUE	TRUE	kFVLPDNADMDk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	35.65	25.40
4303	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G083810_P01	TRUE	TRUE	mFGLETPLMVALQHLLDVPDGDAGAGGdk	95%	n+304 (+304), K+304 (+304)	28.14	25.00
4304	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=3:8884623..8885815:-1;	GRMZM2G083810_P01	TRUE	TRUE	mFGLETPLMVALQHLLDVPDGDAGAGGdk	95%	Oxidation (+16), n+304 (+304), K+304 (+304)	27.66	25.00
4305	parent_transcript=GRMZM2G083810_T01; parent_gene=GRMZM2G083810 seq=translation; coord=10:102318701..102320375:-1;	GRMZM2G083810_P01	TRUE	TRUE	mFGLETPLmVALQHLLDVPDGDAGAGGdk	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	29.92	25.00
4306	parent_transcript=AC204711.3_FGT003; parent_gene=AC204711.3_FG003 seq=translation; coord=10:102318701..102320375:-1;	AC204711.3_FGP003	TRUE	TRUE	nIEGGYTAWVESGLAVk	95%	n+304 (+304), K+304 (+304)	66.57	25.65
4307	parent_transcript=AC204711.3_FGT003; parent_gene=AC204711.3_FG003 seq=translation; coord=10:102318701..102320375:-1;	AC204711.3_FGP003	TRUE	TRUE	sELAcADLMAAGFR	95%	n+304 (+304), Carbamidomethyl (+57)	54.43	25.00
4308	parent_transcript=AC204711.3_FGT003; parent_gene=AC204711.3_FG003 seq=translation; coord=6:31707585..31709218:-1;	AC204711.3_FGP003	TRUE	TRUE	sGHVEDSLNVPYLFFTSQGR	95%	n+304 (+304)	42.14	25.00
4309	parent_transcript=GRMZM2G050412_T01; parent_gene=GRMZM2G050412 seq=translation; coord=6:31707585..31709218:-1;	GRMZM2G050412_P01	TRUE	TRUE	aGVAVDSIEFTYTDAGQR	95%	n+304 (+304)	92.10	25.00
4310	parent_transcript=GRMZM2G050412_T01; parent_gene=GRMZM2G050412 seq=translation; coord=6:31707585..31709218:-1;	GRMZM2G050412_P01	TRUE	TRUE	eVSGTYGAFEGAITLSLR	95%	n+304 (+304)	59.59	25.69
4311	parent_transcript=GRMZM2G050412_T01; parent_gene=GRMZM2G050412 seq=translation; coord=10:99379756..99383298:1;	GRMZM2G050412_P01	TRUE	TRUE	vTDSPPVYDGR	95%	n+304 (+304)	37.29	25.00
4312	parent_transcript=GRMZM2G177203_T02; parent_gene=GRMZM2G177203	GRMZM2G177203_P02	TRUE	TRUE	nLVVPIIGETNLAAGR	95%	n+304 (+304)	38.76	25.00

4313	seq=translation; coord=9:128714706..128721565:1; parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=9:128714706..128721565:1;	GRMZM2G095124_P01	TRUE	TRUE	aSFLEAWk	94%	n+304 (+304), K+304 (+304)	29.64	26.33
4314	parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=9:128714706..128721565:1;	GRMZM2G095124_P01	TRUE	TRUE	eMVPLFFEAMEALTk	95%	n+304 (+304), K+304 (+304)	42.77	25.98
4315	parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=9:128714706..128721565:1;	GRMZM2G095124_P01	TRUE	TRUE	iPLHVFFGEDGk	95%	n+304 (+304), K+304 (+304)	38.09	26.02
4316	parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=9:128714706..128721565:1;	GRMZM2G095124_P01	TRUE	TRUE	IAASNVFFIAk	95%	n+304 (+304), K+304 (+304)	33.49	25.00
4317	parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=9:128714706..128721565:1;	GRMZM2G095124_P01	TRUE	TRUE	mAPPLVTLTSAEPIQYVALR	95%	n+304 (+304)	29.00	25.00
4318	parent_transcript=GRMZM2G095124_T01; parent_gene=GRMZM2G095124 seq=translation; coord=2:214832665..214852459:1;	GRMZM2G095124_P01	TRUE	TRUE	sQPDLAILAVNTFVk	95%	n+304 (+304), K+304 (+304)	49.47	25.00
4319	parent_transcript=GRMZM2G035985_T01; parent_gene=GRMZM2G035985 seq=translation; coord=2:214832665..214852459:1;	GRMZM2G035985_P01,GRMZM2G035985_P02	TRUE	TRUE	iGIYNLEFSGLYATGDVAGAPVRPR	95%	n+304 (+304)	62.79	25.26
4320	parent_transcript=GRMZM2G035985_T01; parent_gene=GRMZM2G035985 seq=translation; coord=2:214832665..214852459:1;	GRMZM2G035985_P01,GRMZM2G035985_P02	TRUE	TRUE	ILNVGDTLAATLcYlcAGNIDk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	43.48	25.02
4321	parent_transcript=GRMZM2G035985_T01; parent_gene=GRMZM2G035985 seq=translation; coord=4:234901650..234908817:1;	GRMZM2G035985_P01,GRMZM2G035985_P02	TRUE	TRUE	tYVDLLQDLMEk	95%	n+304 (+304), K+304 (+304)	28.85	25.00
4322	parent_transcript=GRMZM2G143462_T01; parent_gene=GRMZM2G143462 seq=translation; coord=4:234901650..234908817:1;	GRMZM2G143462_P01,GRMZM2G143462_P02, GRMZM2G143462_P03,GRMZM2G143462_P04, GRMZM2G143462_P05,GRMZM2G143462_P06	TRUE	TRUE	nIEEIQGk	94%	n+304 (+304), K+304 (+304)	31.03	25.62
4323	parent_transcript=GRMZM2G143462_T01; parent_gene=GRMZM2G143462 seq=translation; coord=4:234901650..234908817:1;	GRMZM2G143462_P01,GRMZM2G143462_P02, GRMZM2G143462_P03,GRMZM2G143462_P04, GRMZM2G143462_P05,GRMZM2G143462_P06	TRUE	TRUE	nVDTIINQLMEMGGGSWDkDk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	60.87	25.53
4324	parent_transcript=GRMZM2G143462_T01; parent_gene=GRMZM2G143462 seq=translation; coord=4:234901650..234908817:1;	GRMZM2G143462_P01,GRMZM2G143462_P02, GRMZM2G143462_P03,GRMZM2G143462_P04, GRMZM2G143462_P05,GRMZM2G143462_P06	TRUE	TRUE	vNEDGFLVVMLSk	95%	n+304 (+304), K+304 (+304)	37.12	25.60
4325	parent_transcript=GRMZM2G143462_T01; parent_gene=GRMZM2G143462 seq=translation; coord=2:212405484..212408361:-1;	GRMZM2G143462_P01,GRMZM2G143462_P02, GRMZM2G143462_P03,GRMZM2G143462_P04, GRMZM2G143462_P05,GRMZM2G143462_P06	TRUE	TRUE	vQPNDTIMAVk	95%	n+304 (+304), K+304 (+304)	48.20	26.02
4326	parent_transcript=GRMZM5G879278_T02; parent_gene=GRMZM5G879278 seq=translation; coord=2:212405484..212408361:-1;	GRMZM5G879278_P02,GRMZM5G879278_P03, GRMZM5G879278_P04	TRUE	TRUE	eLSGTLLSEDDSk	95%	n+304 (+304), K+304 (+304)	34.20	26.17
4327	parent_transcript=GRMZM5G879278_T02; parent_gene=GRMZM5G879278 seq=translation; coord=2:212405484..212408361:-1;	GRMZM5G879278_P02,GRMZM5G879278_P03, GRMZM5G879278_P04	TRUE	TRUE	FTDLAGNIFk	95%	n+304 (+304), K+304 (+304)	43.59	25.01
4328	parent_transcript=GRMZM5G879278_T02; parent_gene=GRMZM5G879278	GRMZM5G879278_P02,GRMZM5G879278_P03, GRMZM5G879278_P04	TRUE	TRUE	gDETPPGTAEk	93%	n+304 (+304), K+304 (+304)	26.68	25.00

4329	seq=translation; coord=6:157814627..157816731:-1; parent_transcript=GRMZM2G097040_T01; parent_gene=GRMZM2G097040	GRMZM2G097040_P01	TRUE	TRUE	eIEETLLEHLGVk	95%	n+304 (+304), K+304 (+304)	30.67	25.00
4330	seq=translation; coord=6:157814627..157816731:-1; parent_transcript=GRMZM2G097040_T01; parent_gene=GRMZM2G097040	GRMZM2G097040_P01	TRUE	TRUE	rVVEIVEMLR	95%	n+304 (+304)	42.54	25.00
4331	seq=translation; coord=6:157814627..157816731:-1; parent_transcript=GRMZM2G097040_T01; parent_gene=GRMZM2G097040	GRMZM2G097040_P01	TRUE	TRUE	vVEIVEMLR	91%	n+304 (+304)	28.71	25.33
4332	seq=translation; coord=5:120784559..120792367:1; parent_transcript=GRMZM2G093359_T01; parent_gene=GRMZM2G093359	GRMZM2G093359_P01,GRMZM2G093359_P02	TRUE	TRUE	sFVEVAAGSHFPIQNLPGVFR	95%	n+304 (+304)	56.96	25.38
4333	seq=translation; coord=3:185834707..185839417:-1; parent_transcript=GRMZM2G003385_T01; parent_gene=GRMZM2G003385	GRMZM2G003385_P01,GRMZM2G003385_P02	TRUE	TRUE	aLQIAEk	89%	n+304 (+304), K+304 (+304)	29.89	28.03
4334	seq=translation; coord=3:185834707..185839417:-1; parent_transcript=GRMZM2G003385_T01; parent_gene=GRMZM2G003385	GRMZM2G003385_P01,GRMZM2G003385_P02	TRUE	TRUE	eEYVEVPSDSGITFNVAPk	95%	n+304 (+304), K+304 (+304)	37.78	25.80
4335	seq=translation; coord=5:188243871..188290615:-1; parent_transcript=GRMZM5G824831_T01; parent_gene=GRMZM5G824831	GRMZM5G824831_P01,GRMZM5G824831_P02, GRMZM5G824831_P03,GRMZM5G824831_P04, GRMZM5G824831_P05,GRMZM5G824831_P06, GRMZM5G824831_P07,GRMZM5G824831_P08	TRUE	TRUE	eGYEGQISSNNIEIGIIR	95%	n+304 (+304)	64.44	25.00
4336	seq=translation; coord=5:188243871..188290615:-1; parent_transcript=GRMZM5G824831_T01; parent_gene=GRMZM5G824831	GRMZM5G824831_P01,GRMZM5G824831_P02, GRMZM5G824831_P03,GRMZM5G824831_P04, GRMZM5G824831_P05,GRMZM5G824831_P06, GRMZM5G824831_P07,GRMZM5G824831_P08	TRUE	TRUE	IVQIEHALTAVGSGQTSLGik	95%	n+304 (+304), K+304 (+304)	26.98	25.00
4337	seq=translation; coord=5:188243871..188290615:-1; parent_transcript=GRMZM5G824831_T01; parent_gene=GRMZM5G824831	GRMZM5G824831_P01,GRMZM5G824831_P02, GRMZM5G824831_P03,GRMZM5G824831_P04, GRMZM5G824831_P05,GRMZM5G824831_P06, GRMZM5G824831_P07,GRMZM5G824831_P08	TRUE	TRUE	vLSPAEIKDFLEEVE	90%	n+304 (+304), K+304 (+304)	26.21	25.93
4338	seq=translation; coord=5:188243871..188290615:-1; parent_transcript=GRMZM5G824831_T01; parent_gene=GRMZM5G824831	GRMZM5G824831_P01,GRMZM5G824831_P02, GRMZM5G824831_P03,GRMZM5G824831_P04, GRMZM5G824831_P05,GRMZM5G824831_P06, GRMZM5G824831_P07,GRMZM5G824831_P08	TRUE	TRUE	yTEDMELDDAIHTAILTk	95%	n+304 (+304), K+304 (+304)	36.28	25.95
4339	seq=translation; coord=2:32257322..32262715:1; parent_transcript=GRMZM2G157061_T01; parent_gene=GRMZM2G157061	GRMZM2G157061_P01	TRUE	TRUE	eIVDVSEEILR	95%	n+304 (+304)	39.05	26.78
4340	seq=translation; coord=2:32257322..32262715:1; parent_transcript=GRMZM2G157061_T01; parent_gene=GRMZM2G157061	GRMZM2G157061_P01	TRUE	TRUE	fEALEVILk	95%	n+304 (+304), K+304 (+304)	36.90	25.00
4341	seq=translation; coord=2:32257322..32262715:1; parent_transcript=GRMZM2G157061_T01; parent_gene=GRMZM2G157061	GRMZM2G157061_P01	TRUE	TRUE	ILPQGSQAALIGk	92%	n+304 (+304), K+304 (+304)	25.87	25.00
4342	seq=translation; coord=2:32257322..32262715:1; parent_transcript=GRMZM2G157061_T01; parent_gene=GRMZM2G157061	GRMZM2G157061_P01	TRUE	TRUE	nDSTVQQQAQAQTQAQNR	95%	n+304 (+304)	28.32	25.00
4343	seq=translation; coord=6:112268596..112280791:-1; parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687	GRMZM2G553687_P01	TRUE	TRUE	acVQSADAVPALLWLLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.89	25.00

4344	seq=translation; coord=6:112268596..112280791:-1; parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687 seq=translation; coord=6:112268596..112280791:-1;	GRMZM2G553687_P01	TRUE	TRUE	aDMGPEGQYSTLQVLVNILEHPEcR	95%	n+304 (+304), Carbamidomethyl (+57)	38.80	25.00
4345	parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687 seq=translation; coord=6:112268596..112280791:-1;	GRMZM2G553687_P01	TRUE	TRUE	dTAFGAVGSHSQAVPILVSLLR	95%	n+304 (+304)	38.06	25.00
4346	parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687 seq=translation; coord=6:112268596..112280791:-1;	GRMZM2G553687_P01	TRUE	TRUE	ILAAALGDLFQNEGLAR	95%	n+304 (+304)	31.61	25.00
4347	parent_transcript=GRMZM2G553687_T01; parent_gene=GRMZM2G553687 seq=translation; coord=6:112268596..112280791:-1;	GRMZM2G553687_P01	TRUE	TRUE	vVQPLFSLLSk	95%	n+304 (+304), K+304 (+304)	39.31	25.00
4348	parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012 seq=translation; coord=3:34547144..34558771:1;	EF517601.1_FGP012	TRUE	TRUE	iHPMTIIAGYR	95%	n+304 (+304)	30.50	26.71
4349	parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012 seq=translation; coord=3:34547144..34558771:1;	EF517601.1_FGP012	TRUE	TRUE	iLVANTAMDTDK	93%	n+304 (+304), K+304 (+304)	27.95	26.67
4350	parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012 seq=translation; coord=3:34547144..34558771:1;	EF517601.1_FGP012	TRUE	TRUE	qAILLSATEAAEMILR	95%	n+304 (+304)	59.96	25.02
4351	parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012 seq=translation; coord=3:34547144..34558771:1;	EF517601.1_FGP012	TRUE	TRUE	sDLMNIAMTTLSSk	95%	n+304 (+304), K+304 (+304)	39.88	25.74
4352	parent_transcript=EF517601.1_FGT012; parent_gene=EF517601.1_FG012 seq=translation; coord=3:162825591..162831818:-1;	EF517601.1_FGP012	TRUE	TRUE	vLFGGGWPEMVMak	95%	n+304 (+304), K+304 (+304)	31.31	25.98
4353	parent_transcript=GRMZM2G133173_T01; parent_gene=GRMZM2G133173 seq=translation; coord=3:162825591..162831818:-1;	GRMZM2G133173_P01	TRUE	TRUE	aEIGISDNDAGAVESVQk	95%	n+304 (+304), K+304 (+304)	45.34	25.31
4354	parent_transcript=GRMZM2G133173_T01; parent_gene=GRMZM2G133173 seq=translation; coord=3:162825591..162831818:-1;	GRMZM2G133173_P01	TRUE	TRUE	aEISHIFR	95%	n+304 (+304)	45.29	26.63
4355	parent_transcript=GRMZM2G133173_T01; parent_gene=GRMZM2G133173 seq=translation; coord=1:143622295..143626633:1;	GRMZM2G133173_P01	TRUE	TRUE	vDkAEIGISDNDAGAVESVQk	95%	n+304 (+304), K+304 (+304)	35.21	25.00
4356	parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526 seq=translation; coord=1:143622295..143626633:1;	GRMZM2G152526_P01	TRUE	TRUE	dAGGYGGSSYGR	95%	n+304 (+304)	47.55	25.00
4357	parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526 seq=translation; coord=1:143622295..143626633:1;	GRMZM2G152526_P01	TRUE	TRUE	gFGFITFADPTVVDR	93%	n+304 (+304)	29.51	25.00
4358	parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526 seq=translation; coord=1:143622295..143626633:1;	GRMZM2G152526_P01	TRUE	TRUE	gFGFIVFDAEk	95%	n+304 (+304), K+304 (+304)	34.44	25.33
4359	parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526 seq=translation; coord=1:143622295..143626633:1;	GRMZM2G152526_P01	TRUE	TRUE	iFIGGLSk	95%	n+304 (+304), K+304 (+304)	32.24	25.00
4360	parent_transcript=GRMZM2G152526_T01; parent_gene=GRMZM2G152526 seq=translation; coord=10:90200523..90201913:-1;	GRMZM2G152526_P01	TRUE	TRUE	yGDIIDAVIMk	95%	n+304 (+304), K+304 (+304)	32.13	25.58
4361	parent_transcript=GRMZM2G132093_T01; parent_gene=GRMZM2G132093	GRMZM2G132093_P01	TRUE	TRUE	aLLALEEAGVDYELVPMSR	95%	n+304 (+304)	46.69	25.05

4362	seq=translation; coord=10:90200523..90201913:-1; parent_transcript=GRMZM2G132093_T01; parent_gene=GRMZM2G132093 seq=translation; coord=5:12565068..12568390:1;	GRMZM2G132093_P01	TRUE	TRUE	vPVLEDGDLTLFESR	95%	n+304 (+304)	41.25	25.40
4363	parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566 seq=translation; coord=5:12565068..12568390:1;	GRMZM2G111566_P01	TRUE	TRUE	dFAVVAADTSAVQSILVHK	95%	n+304 (+304), K+304 (+304)	44.82	25.00
4364	parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566 seq=translation; coord=5:12565068..12568390:1;	GRMZM2G111566_P01	TRUE	TRUE	gELATALR	90%	n+304 (+304)	27.03	25.71
4365	parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566 seq=translation; coord=5:12565068..12568390:1;	GRMZM2G111566_P01	TRUE	TRUE	IVVAPQNFVIK	95%	n+304 (+304), K+304 (+304)	44.89	25.00
4366	parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566 seq=translation; coord=5:12565068..12568390:1;	GRMZM2G111566_P01	TRUE	TRUE	nTIPLSTAAAANFTR	95%	n+304 (+304)	51.97	25.26
4367	parent_transcript=GRMZM2G111566_T01; parent_gene=GRMZM2G111566 seq=translation; coord=9:22655251..22657461:1;	GRMZM2G111566_P01	TRUE	TRUE	vQTFEFIQK	95%	n+304 (+304), K+304 (+304)	37.36	25.68
4368	parent_transcript=GRMZM2G092296_T01; parent_gene=GRMZM2G092296 seq=translation; coord=9:22655251..22657461:1;	GRMZM2G092296_P01	TRUE	TRUE	aGFEAGMMDPQHR	95%	n+304 (+304)	36.94	25.00
4369	parent_transcript=GRMZM2G092296_T01; parent_gene=GRMZM2G092296 seq=translation; coord=9:22655251..22657461:1;	GRMZM2G092296_P01	TRUE	TRUE	aGFEAGMmDPQHR	95%	n+304 (+304), Oxidation (+16)	48.18	25.00
4370	parent_transcript=GRMZM2G092296_T01; parent_gene=GRMZM2G092296 seq=translation; coord=9:6307326..6312829:-1;	GRMZM2G092296_P01	TRUE	TRUE	vIDLVSTPDVvk	95%	n+304 (+304), K+304 (+304)	33.09	25.00
4371	parent_transcript=GRMZM2G082198_T01; parent_gene=GRMZM2G082198 seq=translation; coord=9:6307326..6312829:-1;	GRMZM2G082198_P01	TRUE	TRUE	eMEEEAALR	95%	n+304 (+304)	32.83	25.00
4372	parent_transcript=GRMZM2G082198_T01; parent_gene=GRMZM2G082198 seq=translation; coord=9:6307326..6312829:-1;	GRMZM2G082198_P01	TRUE	TRUE	gFAYVEFVEVEAVQEAIK	95%	n+304 (+304), K+304 (+304)	61.72	25.42
4373	parent_transcript=GRMZM2G082198_T01; parent_gene=GRMZM2G082198	GRMZM2G082198_P01	TRUE	TRUE	vTILTDk	91%	n+304 (+304), K+304 (+304)	26.94	25.00
4374	seq=translation; coord=7:120200894..120203011:1; parent_transcript=GRMZM2G138727_T01; parent_gene=GRMZM2G138727	GRMZM2G138727_P01	TRUE	TRUE	hQcSPTATPYcSPQcQSLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	40.95	25.00
4375	seq=translation; coord=7:120200894..120203011:1; parent_transcript=GRMZM2G138727_T01; parent_gene=GRMZM2G138727 seq=translation; coord=7:120200894..120203011:1;	GRMZM2G138727_P01	TRUE	TRUE	qQccQQLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	34.33	25.00
4376	parent_transcript=GRMZM2G138727_T01; parent_gene=GRMZM2G138727 seq=translation; coord=2:34985296..34990180:-1;	GRMZM2G138727_P01	TRUE	TRUE	qVEPQHR	95%	n+304 (+304)	28.95	25.00
4377	parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219 seq=translation; coord=2:34985296..34990180:-1;	GRMZM2G021219_P01	TRUE	TRUE	aAATDSVQPEAAATETAAEPANR	95%	n+304 (+304)	67.66	25.00
4378	parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219	GRMZM2G021219_P01	TRUE	TRUE	iVLIPIVVAVDcPFPPSDK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.75	25.00

4379	seq=translation; coord=2:34985296..34990180:-1; parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219	GRMZM2G021219_P01	TRUE	TRUE	mAWVPYVPLEDR	92%	n+304 (+304)	28.46	25.00
4380	seq=translation; coord=2:34985296..34990180:-1; parent_transcript=GRMZM2G021219_T01; parent_gene=GRMZM2G021219	GRMZM2G021219_P01	TRUE	TRUE	nLEDLWLSAFPVGTEWENIDk	95%	n+304 (+304), K+304 (+304)	70.41	25.04
4381	seq=translation; coord=2:17796828..17799226:-1; parent_transcript=GRMZM2G101408_T01; parent_gene=GRMZM2G101408	GRMZM2G101408_P01,GRMZM2G101408_P02, GRMZM2G101408_P03	TRUE	TRUE	aFEEAELPk	95%	n+304 (+304), K+304 (+304)	51.32	25.67
4382	seq=translation; coord=2:17796828..17799226:-1; parent_transcript=GRMZM2G101408_T01; parent_gene=GRMZM2G101408	GRMZM2G101408_P01,GRMZM2G101408_P02, GRMZM2G101408_P03	TRUE	TRUE	vAEEEEYER	94%	n+304 (+304)	31.17	25.00
4383	seq=translation; coord=6:86343600..86346720:-1; parent_transcript=GRMZM2G082823_T01; parent_gene=GRMZM2G082823	GRMZM2G082823_P01	TRUE	TRUE	fVGAFPAVVLALPSLR	95%	n+304 (+304)	47.62	25.00
4384	seq=translation; coord=6:86343600..86346720:-1; parent_transcript=GRMZM2G082823_T01; parent_gene=GRMZM2G082823	GRMZM2G082823_P01	TRUE	TRUE	gPVPPAVcGLQGTLR	95%	n+304 (+304), Carbamidomethyl (+57)	48.73	25.69
4385	seq=translation; coord=8:160297692..160299701:-1; parent_transcript=GRMZM2G105005_T01; parent_gene=GRMZM2G105005	GRMZM2G105005_P01,GRMZM2G105005_P02, GRMZM2G105005_P03	TRUE	TRUE	sALDEVTDTGAFDR	95%	n+304 (+304)	52.04	25.00
4386	seq=translation; coord=8:160297692..160299701:-1; parent_transcript=GRMZM2G105005_T01; parent_gene=GRMZM2G105005	GRMZM2G105005_P01,GRMZM2G105005_P02, GRMZM2G105005_P03	TRUE	TRUE	ylcGDLTEADIR	95%	n+304 (+304), Carbamidomethyl (+57)	34.67	25.00
4387	seq=translation; coord=5:14072358..14073760:-1; parent_transcript=GRMZM2G165901_T01; parent_gene=GRMZM2G165901	GRMZM2G165901_P01	TRUE	TRUE	dGGYGGGGGYGGR	95%	n+304 (+304)	38.13	25.00
4388	seq=translation; coord=5:14072358..14073760:-1; parent_transcript=GRMZM2G165901_T01; parent_gene=GRMZM2G165901	GRMZM2G165901_P01	TRUE	TRUE	eGGGGGYGGGGGYGGR	95%	n+304 (+304)	47.42	25.00
4389	seq=translation; coord=7:5095194..5100761:-1; parent_transcript=GRMZM2G011858_T01; parent_gene=GRMZM2G011858	GRMZM2G011858_P01	TRUE	TRUE	ePYTATIVSVER	95%	n+304 (+304)	35.12	25.00
4390	seq=translation; coord=4:197062103..197070522:-1; parent_transcript=GRMZM2G016296_T01; parent_gene=GRMZM2G016296	GRMZM2G016296_P01,GRMZM2G016296_P02, GRMZM2G016296_P03,GRMZM2G016296_P04, GRMZM2G016296_P05,GRMZM2G016296_P06, GRMZM2G110143_P01,GRMZM2G110143_P02, GRMZM2G110143_P04,GRMZM2G110143_P05	TRUE	TRUE	tTADDLFLPLFER	94%	n+304 (+304)	30.76	25.00
4391	seq=translation; coord=4:136936001..136939330:1; parent_transcript=GRMZM2G044684_T01; parent_gene=GRMZM2G044684	GRMZM2G044684_P01	TRUE	TRUE	eESSEFEEGIILQEFR	95%	n+304 (+304)	64.88	25.00
4392	seq=translation; coord=4:136936001..136939330:1; parent_transcript=GRMZM2G044684_T01; parent_gene=GRMZM2G044684	GRMZM2G044684_P01	TRUE	TRUE	fGDDDP TAVEGSVAPQk	92%	n+304 (+304), K+304 (+304)	25.81	25.00
4393	seq=translation; coord=4:136936001..136939330:1; parent_transcript=GRMZM2G044684_T01; parent_gene=GRMZM2G044684	GRMZM2G044684_P01	TRUE	TRUE	vSAGPGPEk	95%	n+304 (+304), K+304 (+304)	34.11	25.49
4394	seq=translation; coord=9:64028902..64031969:1; parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898	GRMZM2G469898_P01,GRMZM2G469898_P02	TRUE	TRUE	aALQFVVNPGk	95%	n+304 (+304), K+304 (+304)	35.16	25.00
4395	seq=translation; coord=9:64028902..64031969:1; parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898	GRMZM2G469898_P01,GRMZM2G469898_P02	TRUE	TRUE	gANFAITGATALEYSFFk	95%	n+304 (+304), K+304 (+304)	67.36	25.37

4396	seq=translation; coord=9:64028902..64031969:1; parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898 seq=translation; coord=9:64028902..64031969:1;	GRMZM2G469898_P01,GRMZM2G469898_P02	TRUE	TRUE	IVVDFLAEHFGPLPPSQAk	95%	n+304 (+304), K+304 (+304)	45.53	25.00
4397	parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898 seq=translation; coord=9:64028902..64031969:1;	GRMZM2G469898_P01,GRMZM2G469898_P02	TRUE	TRUE	sLFVVGEFGGNDYNAPLFSGVPFSDVK	92%	n+304 (+304), K+304 (+304)	26.55	25.00
4398	parent_transcript=GRMZM2G469898_T01; parent_gene=GRMZM2G469898 seq=translation; coord=9:64028902..64031969:1;	GRMZM2G469898_P01,GRMZM2G469898_P02	TRUE	TRUE	tYVPLVak	94%	n+304 (+304), K+304 (+304)	30.41	25.00
4399	parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation; coord=3:202766518..202768685:-1;	GRMZM2G181135_P01	TRUE	TRUE	aYEYVQSSIMGASR	95%	n+304 (+304)	63.57	25.00
4400	parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation; coord=3:202766518..202768685:-1;	GRMZM2G181135_P01	TRUE	TRUE	ISYATTDGLFQSVLENHIR	95%	n+304 (+304)	66.86	25.00
4401	parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation; coord=3:202766518..202768685:-1;	GRMZM2G181135_P01	TRUE	TRUE	sDDDFEVLVER	95%	n+304 (+304)	50.49	25.00
4402	parent_transcript=GRMZM2G181135_T01; parent_gene=GRMZM2G181135 seq=translation; coord=3:202766518..202768685:-1;	GRMZM2G181135_P01	TRUE	TRUE	vMLANLHGEEDIFAFGHDVMR	95%	n+304 (+304)	39.10	25.00
4403	parent_transcript=GRMZM2G081017_T01; parent_gene=GRMZM2G081017 seq=translation; coord=2:189488589..189490512:-1;	GRMZM2G081017_P01,GRMZM2G174799_P01, GRMZM2G174799_P02,GRMZM2G174799_P03	TRUE	TRUE	fYSLAEfk	93%	n+304 (+304), K+304 (+304)	29.02	26.41
4404	parent_transcript=GRMZM2G081017_T01; parent_gene=GRMZM2G081017 seq=translation; coord=2:189488589..189490512:-1;	GRMZM2G081017_P01,GRMZM2G174799_P01, GRMZM2G174799_P02,GRMZM2G174799_P03	TRUE	TRUE	vGITVFPk	94%	n+304 (+304), K+304 (+304)	30.84	25.00
4405	parent_transcript=GRMZM2G081017_T01; parent_gene=GRMZM2G081017 seq=translation; coord=2:189488589..189490512:-1;	GRMZM2G081017_P01,GRMZM2G174799_P01, GRMZM2G174799_P02,GRMZM2G174799_P03	TRUE	TRUE	vLLPMQLFSk	95%	n+304 (+304), K+304 (+304)	35.25	25.00
4406	parent_transcript=AC197705.4_FGT001; parent_gene=AC197705.4_FG001 seq=translation; coord=8:118165588..118167724:1;	AC197705.4_FGP001	TRUE	TRUE	aNLEYAVEAAADFLnk	95%	n+304 (+304), K+304 (+304)	57.05	25.28
4407	parent_transcript=AC197705.4_FGT001; parent_gene=AC197705.4_FG001 seq=translation; coord=8:118165588..118167724:1;	AC197705.4_FGP001	TRUE	TRUE	eAFAAVADASGYPFAVMPAAK	95%	n+304 (+304), K+304 (+304)	54.68	25.26
4408	parent_transcript=AC197705.4_FGT001; parent_gene=AC197705.4_FG001 seq=translation; coord=8:87034106..87038095:-1;	AC197705.4_FGP001	TRUE	TRUE	mVVGDGPAFGcILMPEFLR	93%	n+304 (+304), Carbamidomethyl (+57)	28.39	25.00
4409	parent_transcript=GRMZM2G007404_T01; parent_gene=GRMZM2G007404 seq=translation; coord=8:87034106..87038095:-1;	GRMZM2G007404_P01,GRMZM2G007404_P03	TRUE	TRUE	eGLPLMVTDFR	92%	n+304 (+304)	28.91	25.00
4410	parent_transcript=GRMZM2G007404_T01; parent_gene=GRMZM2G007404 seq=translation; coord=8:87034106..87038095:-1;	GRMZM2G007404_P01,GRMZM2G007404_P03	TRUE	TRUE	gDSVIVVDNFFTGR	95%	n+304 (+304)	53.92	25.00
4411	parent_transcript=GRMZM2G007404_T01; parent_gene=GRMZM2G007404 seq=translation; coord=8:87034106..87038095:-1;	GRMZM2G007404_P01,GRMZM2G007404_P03	TRUE	TRUE	sFQYVSDLVEGLMk	95%	n+304 (+304), K+304 (+304)	67.96	25.83
4412	parent_transcript=GRMZM2G007404_T01; parent_gene=GRMZM2G007404 seq=translation; coord=1:262889860..262892469:1;	GRMZM2G007404_P01,GRMZM2G007404_P03	TRUE	TRUE	vLVTGGAGFVGSHLVDR	95%	n+304 (+304)	64.33	25.60
4413	parent_transcript=GRMZM2G024131_T01; parent_gene=GRMZM2G024131	GRMZM2G024131_P01,GRMZM2G024131_P02	TRUE	TRUE	aIGPcVPLPTAGR	91%	n+304 (+304), Carbamidomethyl (+57)	28.06	26.13

4414	seq=translation; coord=1:262889860..262892469:1; parent_transcript=GRMZM2G024131_T01; parent_gene=GRMZM2G024131	GRMZM2G024131_P01,GRMZM2G024131_P02	TRUE	TRUE	gLLAAGkPFLVVVR	95%	n+304 (+304), K+304 (+304)	28.09	25.00
4415	seq=translation; coord=1:262889860..262892469:1; parent_transcript=GRMZM2G024131_T01; parent_gene=GRMZM2G024131	GRMZM2G024131_P01,GRMZM2G024131_P02	TRUE	TRUE	nLDEFVQFVR	95%	n+304 (+304)	34.97	25.19
4416	seq=translation; coord=3:204689100..204690354:1; parent_transcript=GRMZM2G425629_T02; parent_gene=GRMZM2G425629	GRMZM2G425629_P02	TRUE	TRUE	dGAQQTGSYVAQTAEAR	95%	n+304 (+304)	111.94	25.00
4417	seq=translation; coord=3:204689100..204690354:1; parent_transcript=GRMZM2G425629_T02; parent_gene=GRMZM2G425629	GRMZM2G425629_P02	TRUE	TRUE	dTASDAAGAAGDR	95%	n+304 (+304)	57.18	25.00
4418	seq=translation; coord=3:204689100..204690354:1; parent_transcript=GRMZM2G425629_T02; parent_gene=GRMZM2G425629	GRMZM2G425629_P02	TRUE	TRUE	tGALLQQAGEK	92%	n+304 (+304), K+304 (+304)	26.85	25.75
4419	seq=translation; coord=2:223290295..223311152:1; parent_transcript=GRMZM2G172369_T03; parent_gene=GRMZM2G172369	GRMZM2G172369_P03	TRUE	TRUE	fIYVEQAFFQR	95%	n+304 (+304)	32.77	25.00
4420	seq=translation; coord=2:223290295..223311152:1; parent_transcript=GRMZM2G172369_T03; parent_gene=GRMZM2G172369	GRMZM2G172369_P03	TRUE	TRUE	tLGSSADIFAGIFPk	95%	n+304 (+304), K+304 (+304)	44.22	25.75
4421	seq=translation; coord=9:151682948..151683563:1; parent_transcript=GRMZM2G428040_T01; parent_gene=GRMZM2G428040	GRMZM2G428040_P01	TRUE	TRUE	aSATQSADGP EEQR	95%	n+304 (+304)	47.49	25.00
4422	seq=translation; coord=9:151682948..151683563:1; parent_transcript=GRMZM2G428040_T01; parent_gene=GRMZM2G428040	GRMZM2G428040_P01	TRUE	TRUE	eAYGGGMYAAEEEGGR	95%	n+304 (+304)	81.50	25.00
4423	seq=translation; coord=10:87090618..87092722:1; parent_transcript=GRMZM2G123029_T01; parent_gene=GRMZM2G123029	GRMZM2G123029_P01,GRMZM2G123029_P02, GRMZM2G123029_P03,GRMZM2G123029_P04,	TRUE	TRUE	eLILQYANQLcER	95%	n+304 (+304), Carbamidomethyl (+57)	50.05	25.28
4424	seq=translation; coord=10:87090618..87092722:1; parent_transcript=GRMZM2G123029_T01; parent_gene=GRMZM2G123029	GRMZM2G123029_P05 GRMZM2G123029_P01,GRMZM2G093574_P02, GRMZM2G125300_P01,GRMZM2G125300_P02, GRMZM2G125300_P03,GRMZM2G134109_P01, GRMZM2G134109_P02,GRMZM2G157300_P01, GRMZM2G421795_P02,GRMZM5G831474_P01	TRUE	TRUE	IPSPNGESTVScQEISK	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.21	25.00
4425	seq=translation; coord=6:136910575..136913807:-1; parent_transcript=GRMZM2G093574_T01; parent_gene=GRMZM2G093574	GRMZM2G093574_P01,GRMZM2G093574_P02, GRMZM2G125300_P01,GRMZM2G125300_P02, GRMZM2G125300_P03,GRMZM2G134109_P01, GRMZM2G134109_P02,GRMZM2G157300_P01, GRMZM2G421795_P02,GRMZM5G831474_P01	TRUE	TRUE	tVDLYVPR	91%	n+304 (+304)	28.13	25.00
4426	seq=translation; coord=4:171375805..171380259:-1; parent_transcript=GRMZM2G142661_T01; parent_gene=GRMZM2G142661	GRMZM2G142661_P01,GRMZM2G356938_P01	TRUE	TRUE	aLDVIPLLTPEVVDR	95%	n+304 (+304)	62.96	25.35
4427	seq=translation; coord=4:233120026..233126298:-1; parent_transcript=GRMZM2G049839_T01; parent_gene=GRMZM2G049839	GRMZM2G049839_P01,GRMZM2G049839_P02	TRUE	TRUE	gIAVGVGQSEILGR	95%	n+304 (+304)	68.51	25.77
4428	seq=translation; coord=4:233120026..233126298:-1; parent_transcript=GRMZM2G049839_T01; parent_gene=GRMZM2G049839	GRMZM2G049839_P01,GRMZM2G049839_P02	TRUE	TRUE	gIDENWEAALEHNPEAFAR	95%	n+304 (+304)	94.76	25.00
4429	seq=translation; coord=4:233120026..233126298:-1; parent_transcript=GRMZM2G049839_T01; parent_gene=GRMZM2G049839	GRMZM2G049839_P01,GRMZM2G049839_P02	TRUE	TRUE	ISAAGVQDGDGLVMMFSTSERPSQDGLR	95%	n+304 (+304)	35.72	25.00
4430	seq=translation; coord=4:233120026..233126298:-1; parent_transcript=GRMZM2G049839_T01; parent_gene=GRMZM2G049839	GRMZM2G049839_P01,GRMZM2G049839_P02	TRUE	TRUE	vNPDGTA VNPQAFQQHAR	95%	n+304 (+304)	40.08	25.00

4431	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	aAVAVLGLDLATLQGSSK	95%	n+304 (+304), K+304 (+304)	80.76	25.42
4432	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	aLPLLVPmLLETLLK	95%	n+304 (+304), K+304 (+304)	30.99	25.00
4433	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	aLPLLVPmLLETLLK	93%	n+304 (+304), Oxidation (+16), K+304 (+304)	26.25	25.00
4434	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	aQLMIPYATHLLQFEAVFK	95%	n+304 (+304), K+304 (+304)	33.34	25.00
4435	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	gIFEAYSGLQGIK	95%	n+304 (+304), K+304 (+304)	54.34	25.00
4436	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	tHLFHVFEFLR	95%	n+304 (+304)	35.82	26.33
4437	seq=translation; coord=6:141280696..141285603:-1; parent_transcript=GRMZM2G084767_T01; parent_gene=GRMZM2G084767	GRMZM2G084767_P01	TRUE	TRUE	vSNIPETSGIIGQLLQEIMR	95%	n+304 (+304)	76.55	25.48
4438	seq=translation; coord=3:217464401..217471380:-1; parent_transcript=GRMZM2G105019_T01; parent_gene=GRMZM2G105019	GRMZM2G105019_P01	TRUE	TRUE	aALELGSSYASGDSR	95%	n+304 (+304)	39.08	25.00
4439	seq=translation; coord=3:217464401..217471380:-1; parent_transcript=GRMZM2G105019_T01; parent_gene=GRMZM2G105019	GRMZM2G105019_P01	TRUE	TRUE	aEQVTWTTLDYSGRPk	95%	n+304 (+304), K+304 (+304)	32.06	26.60
4440	seq=translation; coord=3:217464401..217471380:-1; parent_transcript=GRMZM2G105019_T01; parent_gene=GRMZM2G105019	GRMZM2G105019_P01	TRUE	TRUE	aIELDPMMHK	95%	n+304 (+304), K+304 (+304)	29.58	25.58
4441	seq=translation; coord=3:111553578..111570930:1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01,GRMZM2G411536_P03	TRUE	TRUE	fQALDMTSQPTMIDTHR	95%	n+304 (+304)	55.56	25.00
4442	seq=translation; coord=3:111553578..111570930:1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01,GRMZM2G411536_P03	TRUE	TRUE	gVGADTIDPTFLEALPEDLR	95%	n+304 (+304)	47.97	25.25
4443	seq=translation; coord=3:111553578..111570930:1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01,GRMZM2G411536_P03	TRUE	TRUE	hILEDPHTLQAMELEIR	95%	n+304 (+304)	62.40	25.54
4444	seq=translation; coord=3:111553578..111570930:1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01,GRMZM2G411536_P03	TRUE	TRUE	IDAIFR	95%	n+304 (+304)	31.57	25.00
4445	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G411536_T01; parent_gene=GRMZM2G411536	GRMZM2G411536_P01,GRMZM2G411536_P03	TRUE	TRUE	ILLFLEFPcPSR	95%	n+304 (+304), Carbamidomethyl (+57)	35.82	25.72
4446	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G136296_T01; parent_gene=GRMZM2G136296	GRMZM2G136296_P01,GRMZM2G136296_P02	TRUE	TRUE	fYVQTVGDQR	95%	n+304 (+304)	31.99	25.00
4447	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G136296_T01; parent_gene=GRMZM2G136296	GRMZM2G136296_P01,GRMZM2G136296_P02	TRUE	TRUE	gEIVLSQFSLDNSWNR	95%	n+304 (+304)	59.01	25.00
4448	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G136296_T01; parent_gene=GRMZM2G136296	GRMZM2G136296_P01,GRMZM2G136296_P02	TRUE	TRUE	gGEQNPHLGELLR	94%	n+304 (+304)	28.47	25.00

4449	seq=translation; coord=5:167061160..167068865:-1; parent_transcript=GRMZM2G136296_T01; parent_gene=GRMZM2G136296 seq=translation; coord=8:115478841..115482432:1;	GRMZM2G136296_P01,GRMZM2G136296_P02	TRUE	TRUE	yLPPSAIGEASGFDAK	95%	n+304 (+304), K+304 (+304)	49.12	26.09
4450	parent_transcript=GRMZM2G111411_T01; parent_gene=GRMZM2G111411 seq=translation; coord=8:115478841..115482432:1;	GRMZM2G111411_P01	TRUE	TRUE	eLVEEIAESLTK	95%	n+304 (+304), K+304 (+304)	47.30	26.44
4451	parent_transcript=GRMZM2G111411_T01; parent_gene=GRMZM2G111411 seq=translation; coord=8:115478841..115482432:1;	GRMZM2G111411_P01	TRUE	TRUE	fkELVEEIAESLTK	95%	n+304 (+304), K+304 (+304)	29.69	25.00
4452	parent_transcript=GRMZM2G111411_T01; parent_gene=GRMZM2G111411 seq=translation; coord=3:1479593..1481033:-1;	GRMZM2G111411_P01	TRUE	TRUE	IEEVAVTTGEEDEDVLLDMK	95%	n+304 (+304), K+304 (+304)	72.65	25.00
4453	parent_transcript=GRMZM5G825437_T04; parent_gene=GRMZM5G825437 seq=translation; coord=3:1479593..1481033:-1;	GRMZM5G825437_P04	TRUE	TRUE	iAEcLVGDETGIVVFTAR	95%	n+304 (+304), Carbamidomethyl (+57)	42.35	25.00
4454	parent_transcript=GRMZM5G825437_T04; parent_gene=GRMZM5G825437 seq=translation; coord=3:1479593..1481033:-1;	GRMZM5G825437_P04	TRUE	TRUE	iEATEPASFTVk	95%	n+304 (+304), K+304 (+304)	31.11	25.88
4455	parent_transcript=GRMZM5G825437_T04; parent_gene=GRMZM5G825437 seq=translation; coord=8:16994084..16999444:-1;	GRMZM5G825437_P04	TRUE	TRUE	nDQVLLKPDATVILR	95%	n+304 (+304), K+304 (+304)	29.30	25.00
4456	parent_transcript=GRMZM2G025215_T01; parent_gene=GRMZM2G025215 seq=translation; coord=8:16994084..16999444:-1;	GRMZM2G025215_P01	TRUE	TRUE	eVQAGVQILR	92%	n+304 (+304)	29.78	25.63
4457	parent_transcript=GRMZM2G025215_T01; parent_gene=GRMZM2G025215 seq=translation; coord=8:16994084..16999444:-1;	GRMZM2G025215_P01	TRUE	TRUE	sNFPTVTIADIDR	95%	n+304 (+304)	32.33	25.00
4458	parent_transcript=GRMZM2G025215_T01; parent_gene=GRMZM2G025215 seq=translation; coord=4:127851768..127857102:1;	GRMZM2G025215_P01	TRUE	TRUE	vPLDDVVEK	87%	n+304 (+304), K+304 (+304)	26.34	25.43
4459	parent_transcript=GRMZM2G018416_T01; parent_gene=GRMZM2G018416 seq=translation; coord=4:127851768..127857102:1;	GRMZM2G018416_P01	TRUE	TRUE	aPAVVAK	93%	n+304 (+304), K+304 (+304)	29.46	25.00
4460	parent_transcript=GRMZM2G018416_T01; parent_gene=GRMZM2G018416 seq=translation; coord=4:127851768..127857102:1;	GRMZM2G018416_P01	TRUE	TRUE	vDGVITDFPGTAHR	95%	n+304 (+304)	43.83	25.00
4461	parent_transcript=GRMZM2G018416_T01; parent_gene=GRMZM2G018416 seq=translation; coord=4:127851768..127857102:1;	GRMZM2G018416_P01	TRUE	TRUE	yNLVYMIEESVR	86%	n+304 (+304)	25.40	25.00
4462	parent_transcript=GRMZM2G018416_T01; parent_gene=GRMZM2G018416 seq=translation; coord=9:18896527..18899443:1;	GRMZM2G018416_P01	TRUE	TRUE	yNLVYMIEESVR	90%	n+304 (+304), iTRAQ8plex (+304)	26.82	26.22
4463	parent_transcript=GRMZM2G102596_T01; parent_gene=GRMZM2G102596 seq=translation; coord=9:18896527..18899443:1;	GRMZM2G102596_P01,GRMZM2G102596_P02, GRMZM2G102596_P03	TRUE	TRUE	aSMGGYISSQTVR	95%	n+304 (+304)	35.10	25.00
4464	parent_transcript=GRMZM2G102596_T01; parent_gene=GRMZM2G102596 seq=translation; coord=9:18896527..18899443:1;	GRMZM2G102596_P01,GRMZM2G102596_P02, GRMZM2G102596_P03	TRUE	TRUE	gMGLSIGTMIAGWDEK	90%	n+304 (+304), K+304 (+304)	25.89	25.31
4465	parent_transcript=GRMZM2G102596_T01; parent_gene=GRMZM2G102596 seq=translation; coord=9:18896527..18899443:1;	GRMZM2G102596_P01,GRMZM2G102596_P02, GRMZM2G102596_P03	TRUE	TRUE	gPGLYYVDESEGAR	95%	n+304 (+304)	46.04	25.00
4466	parent_transcript=GRMZM2G102596_T01; parent_gene=GRMZM2G102596	GRMZM2G102596_P01,GRMZM2G102596_P02, GRMZM2G102596_P03	TRUE	TRUE	iIEINPYMLGTMAGGAADcQFWHR	95%	n+304 (+304), Carbamidomethyl (+57)	80.55	25.00

4467	seq=translation; coord=1:5952987..5954672:1; parent_transcript=GRMZM2G065718_T01; parent_gene=GRMZM2G065718 seq=translation; coord=1:5952987..5954672:1;	GRMZM2G065718_P01	TRUE	TRUE	aDVTVVAk	95%	n+304 (+304), K+304 (+304)	38.01	26.49
4468	seq=translation; coord=1:5952987..5954672:1; parent_transcript=GRMZM2G065718_T01; parent_gene=GRMZM2G065718 seq=translation; coord=1:5952987..5954672:1;	GRMZM2G065718_P01	TRUE	TRUE	gDDVSLDTGk	95%	n+304 (+304), K+304 (+304)	40.28	25.00
4469	parent_transcript=GRMZM2G065718_T01; parent_gene=GRMZM2G065718 seq=translation; coord=1:5952987..5954672:1;	GRMZM2G065718_P01	TRUE	TRUE	gLTLFAVNDDAFQAk	95%	n+304 (+304), K+304 (+304)	55.33	25.63
4470	parent_transcript=GRMZM2G065718_T01; parent_gene=GRMZM2G065718 seq=translation; coord=1:5952987..5954672:1;	GRMZM2G065718_P01	TRUE	TRUE	vVDQEDkNYGFSAAATPGAR	95%	n+304 (+304), K+304 (+304)	30.17	25.50
4471	parent_transcript=GRMZM2G116204_T01; parent_gene=GRMZM2G116204 seq=translation; coord=3:133888888..133893638:1;	GRMZM2G116204_P01	TRUE	TRUE	eVEVWLQTISPGQR	91%	n+304 (+304)	26.86	25.85
4472	parent_transcript=GRMZM2G116204_T01; parent_gene=GRMZM2G116204 seq=translation; coord=3:133888888..133893638:1;	GRMZM2G116204_P01	TRUE	TRUE	fPFVWDEdcFEAAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	45.89	25.00
4473	parent_transcript=GRMZM2G116204_T01; parent_gene=GRMZM2G116204 seq=translation; coord=3:133888888..133893638:1;	GRMZM2G116204_P01	TRUE	TRUE	gTLLMGSSSLk	95%	n+304 (+304), K+304 (+304)	33.49	25.00
4474	parent_transcript=GRMZM2G116204_T01; parent_gene=GRMZM2G116204 seq=translation; coord=3:9805845..9808735:-1;	GRMZM2G116204_P01	TRUE	TRUE	iFLYDDWSPHTAAVLk	95%	n+304 (+304), K+304 (+304)	48.44	26.17
4475	parent_transcript=GRMZM2G083418_T01; parent_gene=GRMZM2G083418 seq=translation; coord=3:9805845..9808735:-1;	GRMZM2G083418_P01	TRUE	TRUE	eLFWAPAPLTtk	95%	n+304 (+304), K+304 (+304)	30.04	25.29
4476	parent_transcript=GRMZM2G083418_T01; parent_gene=GRMZM2G083418 seq=translation; coord=3:9805845..9808735:-1;	GRMZM2G083418_P01	TRUE	TRUE	eTQEALDGSEETASAGPDEdTSaVDVk	95%	n+304 (+304), K+304 (+304)	59.84	25.00
4477	parent_transcript=GRMZM2G083418_T01; parent_gene=GRMZM2G083418 seq=translation; coord=10:148849233..148855901:1;	GRMZM2G083418_P01	TRUE	TRUE	INTGNVFAALESk	95%	n+304 (+304), K+304 (+304)	40.28	25.13
4478	parent_transcript=GRMZM2G406074_T01; parent_gene=GRMZM2G406074 seq=translation; coord=10:148849233..148855901:1;	GRMZM2G406074_P01	TRUE	TRUE	hFAPYLQSDPAASS	95%	n+304 (+304)	42.23	25.00
4479	parent_transcript=GRMZM2G406074_T01; parent_gene=GRMZM2G406074 seq=translation; coord=10:148849233..148855901:1;	GRMZM2G406074_P01	TRUE	TRUE	iDIPSAWQMPQGIDAGEEPR	95%	n+304 (+304)	33.64	25.00
4480	parent_transcript=GRMZM2G406074_T01; parent_gene=GRMZM2G406074 seq=translation; coord=2:146194741..146200435:-1;	GRMZM2G406074_P01	TRUE	TRUE	tNVGicLADPSLTk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	43.66	25.77
4481	parent_transcript=GRMZM2G537291_T01; parent_gene=GRMZM2G537291 seq=translation; coord=9:93447494..93469121:-1;	GRMZM2G537291_P01	TRUE	TRUE	aIDQIIQIPTVLR	95%	n+304 (+304)	42.49	25.00
4482	parent_transcript=GRMZM2G348666_T01; parent_gene=GRMZM2G348666 seq=translation; coord=9:93447494..93469121:-1;	GRMZM2G348666_P01,GRMZM2G348666_P03	TRUE	TRUE	fGWDcHGLPVEFEIDk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.95	25.00
4483	parent_transcript=GRMZM2G348666_T01; parent_gene=GRMZM2G348666 seq=translation; coord=9:93447494..93469121:-1;	GRMZM2G348666_P01,GRMZM2G348666_P03	TRUE	TRUE	fHNWLEGAR	95%	n+304 (+304)	31.01	25.00
4484	parent_transcript=GRMZM2G348666_T01; parent_gene=GRMZM2G348666	GRMZM2G348666_P01,GRMZM2G348666_P03	TRUE	TRUE	iPGVSLVGLk	92%	n+304 (+304), K+304 (+304)	25.80	25.00

4485	seq=translation; coord=9:93447494..93469121:-1; parent_transcript=GRMZM2G348666_T01; parent_gene=GRMZM2G348666 seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898 seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898	GRMZM2G348666_P01,GRMZM2G348666_P03	TRUE	TRUE	tALSNEAALDYR	95%	n+304 (+304)	51.60	25.00
4486	seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898 seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898	GRMZM5G876898_P01,GRMZM5G876898_P02	TRUE	TRUE	gAIPFLESVVADVAALR	94%	n+304 (+304)	28.70	25.00
4487	seq=translation; coord=2:8906086..8909067:-1; parent_transcript=GRMZM5G876898_T01; parent_gene=GRMZM5G876898	GRMZM5G876898_P01,GRMZM5G876898_P02	TRUE	TRUE	sLLALQGPLAAPTLLLTk	95%	n+304 (+304), K+304 (+304)	42.80	25.00
4488	seq=translation; coord=1:67644786..67647420:1; parent_transcript=GRMZM2G051879_T01; parent_gene=GRMZM2G051879	GRMZM2G051879_P01,GRMZM2G051879_P02, GRMZM2G051879_P03,GRMZM2G051879_P05, GRMZM2G118355_P01,GRMZM2G118355_P02, GRMZM2G118355_P03,GRMZM2G118355_P04, GRMZM2G171387_P01,GRMZM2G171387_P02, GRMZM2G176358_P01,GRMZM2G176358_P02, GRMZM2G176358_P03,GRMZM2G176358_P04	TRUE	TRUE	eIAQDFk	95%	n+304 (+304), K+304 (+304)	33.84	27.12
4489	seq=translation; coord=1:67644786..67647420:1; parent_transcript=GRMZM2G051879_T01; parent_gene=GRMZM2G051879	GRMZM2G051879_P01,GRMZM2G051879_P02, GRMZM2G051879_P03,GRMZM2G051879_P05, GRMZM2G118355_P01,GRMZM2G118355_P02, GRMZM2G118355_P03,GRMZM2G118355_P04, GRMZM2G171387_P01,GRMZM2G171387_P02, GRMZM2G176358_P01,GRMZM2G176358_P02, GRMZM2G176358_P03,GRMZM2G176358_P04	TRUE	TRUE	sTELLIR	89%	n+304 (+304)	26.66	25.00
4490	seq=translation; coord=1:68543805..68546269:-1; parent_transcript=GRMZM2G077991_T01; parent_gene=GRMZM2G077991 seq=translation; coord=1:68543805..68546269:-1; parent_transcript=GRMZM2G077991_T01; parent_gene=GRMZM2G077991 seq=translation; coord=10:8848146..8849526:-1; parent_transcript=GRMZM2G136910_T01; parent_gene=GRMZM2G136910 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G077991_P01,GRMZM2G077991_P02, GRMZM2G077991_P03,GRMZM2G168674_P01	TRUE	TRUE	eGTEAAPk	95%	n+304 (+304), K+304 (+304)	31.43	25.00
4491	seq=translation; coord=1:68543805..68546269:-1; parent_transcript=GRMZM2G077991_T01; parent_gene=GRMZM2G077991 seq=translation; coord=10:8848146..8849526:-1; parent_transcript=GRMZM2G136910_T01; parent_gene=GRMZM2G136910 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G077991_P01,GRMZM2G077991_P02, GRMZM2G077991_P03,GRMZM2G168674_P01	TRUE	TRUE	sTcSScGYPAAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	48.83	25.00
4492	seq=translation; coord=10:8848146..8849526:-1; parent_transcript=GRMZM2G136910_T01; parent_gene=GRMZM2G136910 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G136910_P01	TRUE	TRUE	eAEEAGGEK	95%	n+304 (+304), K+304 (+304)	36.65	25.00
4493	seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G049693_P01,GRMZM2G049693_P02	TRUE	TRUE	dQIGSFFYPPLGMQR	95%	n+304 (+304)	30.63	25.00
4494	seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G049693_P01,GRMZM2G049693_P02	TRUE	TRUE	dVYTLDFPTMPIDGPPVIR	95%	n+304 (+304)	49.55	25.00
4495	seq=translation; coord=9:28003772..28008138:1; parent_transcript=GRMZM2G049693_T01; parent_gene=GRMZM2G049693 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G049693_P01,GRMZM2G049693_P02	TRUE	TRUE	tTLSGISYSPDPTLR	95%	n+304 (+304)	68.12	26.13
4496	seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G160925_P01	TRUE	TRUE	dAGVDIDAGAEIVR	95%	n+304 (+304)	55.71	25.02
4497	seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925 seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G160925_P01	TRUE	TRUE	nDGITTTVGEALMAPTFIYVk	89%	n+304 (+304), K+304 (+304)	25.95	25.89
4498	seq=translation; coord=6:132760746..132763409:1; parent_transcript=GRMZM2G160925_T01; parent_gene=GRMZM2G160925	GRMZM2G160925_P01	TRUE	TRUE	sGLSLDDQLPR	95%	n+304 (+304)	41.79	26.04

4499	seq=translation; coord=1:279565504..279568174:1; parent_transcript=GRMZM2G047456_T02; parent_gene=GRMZM2G047456	GRMZM2G047456_P02,GRMZM2G047456_P03, GRMZM2G047456_P04	TRUE	TRUE	dVIELAGGPSYAVELGR	95%	n+304 (+304)	80.36	25.21
4500	seq=translation; coord=1:279565504..279568174:1; parent_transcript=GRMZM2G047456_T02; parent_gene=GRMZM2G047456	GRMZM2G047456_P02,GRMZM2G047456_P03, GRMZM2G047456_P04	TRUE	TRUE	gLFASDQVLFSDAR	95%	n+304 (+304)	77.45	25.00
4501	seq=translation; coord=1:279565504..279568174:1; parent_transcript=GRMZM2G047456_T02; parent_gene=GRMZM2G047456	GRMZM2G047456_P02,GRMZM2G047456_P03, GRMZM2G047456_P04	TRUE	TRUE	kVQAQPVAVGATIR	91%	K+304 (+304), n+304 (+304)	25.78	25.00
4502	seq=translation; coord=8:143279539..143283510:-1; parent_transcript=GRMZM2G050270_T01; parent_gene=GRMZM2G050270	GRMZM2G050270_P01	TRUE	TRUE	aLAVDFAPDAEVR	95%	n+304 (+304)	56.91	25.00
4503	seq=translation; coord=8:143279539..143283510:-1; parent_transcript=GRMZM2G050270_T01; parent_gene=GRMZM2G050270	GRMZM2G050270_P01	TRUE	TRUE	eASLVEIVTAIR	95%	n+304 (+304)	47.68	25.00
4504	seq=translation; coord=8:143279539..143283510:-1; parent_transcript=GRMZM2G050270_T01; parent_gene=GRMZM2G050270	GRMZM2G050270_P01	TRUE	TRUE	fLDWLSGGAk	95%	n+304 (+304), K+304 (+304)	34.68	26.13
4505	seq=translation; coord=8:143279539..143283510:-1; parent_transcript=GRMZM2G050270_T01; parent_gene=GRMZM2G050270	GRMZM2G050270_P01	TRUE	TRUE	sVVEIALDSik	95%	n+304 (+304), K+304 (+304)	38.67	25.00
4506	seq=translation; coord=5:193157657..193165368:1; parent_transcript=AC211737.3_FGT012; parent_gene=AC211737.3_FG012	AC211737.3_FGP012	TRUE	TRUE	aDADGAIVGASGAR	95%	n+304 (+304)	52.25	25.00
4507	seq=translation; coord=5:193157657..193165368:1; parent_transcript=AC211737.3_FGT012; parent_gene=AC211737.3_FG012	AC211737.3_FGP012	TRUE	TRUE	fLAHPDYDGR	95%	n+304 (+304)	39.58	25.00
4508	seq=translation; coord=5:193157657..193165368:1; parent_transcript=AC211737.3_FGT012; parent_gene=AC211737.3_FG012	AC211737.3_FGP012	TRUE	TRUE	IIYELFTDLTSR	90%	n+304 (+304)	25.94	25.72
4509	seq=translation; coord=5:193157657..193165368:1; parent_transcript=AC211737.3_FGT012; parent_gene=AC211737.3_FG012	AC211737.3_FGP012	TRUE	TRUE	IVINPSWk	86%	n+304 (+304), K+304 (+304)	25.22	25.00
4510	seq=translation; coord=4:237521017..237524915:-1; parent_transcript=GRMZM2G165917_T01; parent_gene=GRMZM2G165917	GRMZM2G165917_P01,GRMZM2G165917_P02, GRMZM2G165917_P03,GRMZM2G369939_P01	TRUE	TRUE	eVPVVLk	94%	n+304 (+304), K+304 (+304)	30.71	25.00
4511	seq=translation; coord=4:237521017..237524915:-1; parent_transcript=GRMZM2G165917_T01; parent_gene=GRMZM2G165917	GRMZM2G165917_P01,GRMZM2G165917_P02, GRMZM2G165917_P03,GRMZM2G369939_P01	TRUE	TRUE	IAGLLEVFik	95%	n+304 (+304), K+304 (+304)	34.61	25.00
4512	seq=translation; coord=5:69096740..69101545:-1; parent_transcript=GRMZM2G020146_T01; parent_gene=GRMZM2G020146	GRMZM2G020146_P01	TRUE	TRUE	aALEMLR	91%	n+304 (+304)	27.88	25.00
4513	seq=translation; coord=5:69096740..69101545:-1; parent_transcript=GRMZM2G020146_T01; parent_gene=GRMZM2G020146	GRMZM2G020146_P01	TRUE	TRUE	IcYDFSNLER	95%	n+304 (+304), Carbamidomethyl (+57)	47.00	25.00
4514	seq=translation; coord=5:69096740..69101545:-1; parent_transcript=GRMZM2G020146_T01; parent_gene=GRMZM2G020146	GRMZM2G020146_P01	TRUE	TRUE	nDFFITGESyAGHYIPAFASR	93%	n+304 (+304), iTRAQ8plex (+304)	25.07	25.00
4515	seq=translation; coord=1:254659295..254663896:1; parent_transcript=GRMZM2G038848_T01; parent_gene=GRMZM2G038848	GRMZM2G038848_P01,GRMZM2G038848_P02	TRUE	TRUE	aIIISVIDNLVk	95%	n+304 (+304), K+304 (+304)	48.16	25.00
4516	seq=translation; coord=10:96835856..96839456:-1; parent_transcript=GRMZM2G021170_T01; parent_gene=GRMZM2G021170	GRMZM2G021170_P01	TRUE	TRUE	gEPTVEELAGLLDVR	95%	n+304 (+304)	44.44	25.63

4517	seq=translation; coord=10:96835856..96839456:-1; parent_transcript=GRMZM2G021170_T01; parent_gene=GRMZM2G021170	GRMZM2G021170_P01	TRUE	TRUE	hPEADTLVVEVDVGEAEPR	95%	n+304 (+304)	36.77	25.00
4518	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	TRUE	TRUE	aVYDQYGEEGLK	95%	n+304 (+304), K+304 (+304)	51.82	25.00
4519	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	TRUE	TRUE	iPLAEALTGYTAHVTTLDGR	95%	n+304 (+304)	57.85	25.59
4520	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	TRUE	TRUE	iPLAEALTGyTAHVTTLDGR	95%	n+304 (+304), iTRAQ8plex (+304)	26.79	25.17
4521	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	TRUE	TRUE	qISEAYEVLSDPQk	95%	n+304 (+304), K+304 (+304)	59.27	26.63
4522	seq=translation; coord=6:164377053..164379535:-1; parent_transcript=GRMZM2G039886_T01; parent_gene=GRMZM2G039886	GRMZM2G039886_P01	TRUE	TRUE	sLTVPISSVIHPGYEEVVR	95%	n+304 (+304)	49.06	25.30
4523	seq=translation; coord=6:153256043..153259238:1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	TRUE	TRUE	dLQLDYLDLyLIHWPFr	95%	n+304 (+304)	55.68	25.00
4524	seq=translation; coord=6:153256043..153259238:1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	TRUE	TRUE	dLQLDYLDLyLIHWPFr	95%	n+304 (+304), iTRAQ8plex (+304)	32.72	25.05
4525	seq=translation; coord=6:153256043..153259238:1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	TRUE	TRUE	eMEGLVk	95%	n+304 (+304), K+304 (+304)	31.58	25.85
4526	seq=translation; coord=6:153256043..153259238:1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	TRUE	TRUE	sATEVWDHED	95%	n+304 (+304)	30.50	25.00
4527	seq=translation; coord=6:156534704..156535855:-1; parent_transcript=GRMZM2G169943_T01; parent_gene=GRMZM2G169943	GRMZM2G169943_P01	TRUE	TRUE	vLTGEELFVNk	95%	n+304 (+304), K+304 (+304)	47.96	26.39
4528	seq=translation; coord=6:156534704..156535855:-1; parent_transcript=GRMZM2G410134_T01; parent_gene=GRMZM2G410134	GRMZM2G410134_P01	TRUE	TRUE	dLQcWQEVQESPLDAcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	69.91	25.00
4529	seq=translation; coord=6:156534704..156535855:-1; parent_transcript=GRMZM2G410134_T01; parent_gene=GRMZM2G410134	GRMZM2G410134_P01	TRUE	TRUE	eYAAGLPMMcR	95%	n+304 (+304), Carbamidomethyl (+57)	35.65	25.00
4530	seq=translation; coord=6:156534704..156535855:-1; parent_transcript=GRMZM2G410134_T01; parent_gene=GRMZM2G410134	GRMZM2G410134_P01	TRUE	TRUE	gYEEAMPPLEk	95%	n+304 (+304), K+304 (+304)	36.67	25.30
4531	seq=translation; coord=6:157582700..157589894:1; parent_transcript=GRMZM2G410134_T01; parent_gene=GRMZM2G410134	GRMZM2G410134_P01	TRUE	TRUE	ISEPQEcSIFSGGDQy	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)	59.69	25.00
4532	seq=translation; coord=6:157582700..157589894:1; parent_transcript=GRMZM2G006377_T01; parent_gene=GRMZM2G006377	GRMZM2G006377_P01	TRUE	TRUE	dQGScGAcWSFSATGAMEGINK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	35.46	25.00
4533	seq=translation; coord=6:157582700..157589894:1; parent_transcript=GRMZM2G006377_T01; parent_gene=GRMZM2G006377	GRMZM2G006377_P01	TRUE	TRUE	tGSLVSLSEQELIDcDR	95%	n+304 (+304), Carbamidomethyl (+57)	89.34	25.00

4534	seq=translation; coord=6:63919594..63950390:1; parent_transcript=GRMZM2G052812_T02; parent_gene=GRMZM2G052812	GRMZM2G052812_P02,GRMZM2G052812_P05	TRUE	TRUE	IVDSLSEQDFR	87%	n+304 (+304)	25.75	25.00
4535	seq=translation; coord=6:63919594..63950390:1; parent_transcript=GRMZM2G052812_T02; parent_gene=GRMZM2G052812	GRMZM2G052812_P02,GRMZM2G052812_P05	TRUE	TRUE	yIGLSEASASTIR	95%	n+304 (+304)	40.13	25.56
4536	seq=translation; coord=1:41468889..41473581:1; parent_transcript=GRMZM2G044027_T01; parent_gene=GRMZM2G044027	GRMZM2G044027_P01,GRMZM2G044027_P02	TRUE	TRUE	eLINPDITVMTENTPDDPR	94%	n+304 (+304)	30.48	25.00
4537	seq=translation; coord=1:41468889..41473581:1; parent_transcript=GRMZM2G044027_T01; parent_gene=GRMZM2G044027	GRMZM2G044027_P01,GRMZM2G044027_P02	TRUE	TRUE	sFcYVADMVDGLIR	95%	n+304 (+304), Carbamidomethyl (+57)	33.52	25.00
4538	seq=translation; coord=8:17872894..17877539:1; parent_transcript=GRMZM2G080722_T01; parent_gene=GRMZM2G080722	GRMZM2G080722_P01	TRUE	TRUE	aYSNWPTFPQIFIK	90%	n+304 (+304), K+304 (+304)	25.37	25.00
4539	seq=translation; coord=8:17872894..17877539:1; parent_transcript=GRMZM2G080722_T01; parent_gene=GRMZM2G080722	GRMZM2G080722_P01	TRUE	TRUE	eLLGDIAQk	95%	n+304 (+304), K+304 (+304)	36.97	26.90
4540	seq=translation; coord=8:17872894..17877539:1; parent_transcript=GRMZM2G080722_T01; parent_gene=GRMZM2G080722	GRMZM2G080722_P01	TRUE	TRUE	gEFVGSGDIILTMHQk	95%	n+304 (+304), K+304 (+304)	43.21	26.17
4541	seq=translation; coord=8:17872894..17877539:1; parent_transcript=GRMZM2G080722_T01; parent_gene=GRMZM2G080722	GRMZM2G080722_P01	TRUE	TRUE	sSDMSFSDIVAQDvk	95%	n+304 (+304), K+304 (+304)	30.99	25.00
4542	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	TRUE	TRUE	dATSPLPGWIIESLk	95%	n+304 (+304), K+304 (+304)	31.93	25.00
4543	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	TRUE	TRUE	eSAIAQVIR	95%	n+304 (+304)	33.45	26.51
4544	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	TRUE	TRUE	nDGFEIGPQVLR	93%	n+304 (+304)	29.01	25.56
4545	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	TRUE	TRUE	vAVAPSLAPADVAVR	95%	n+304 (+304)	73.82	25.99
4546	seq=translation; coord=1:290521787..290523917:1; parent_transcript=GRMZM2G012224_T01; parent_gene=GRMZM2G012224	GRMZM2G012224_P01	TRUE	TRUE	vTDGVSLcGPVLDQVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.67	26.41
4547	seq=translation; coord=6:148590842..148593721:1; parent_transcript=GRMZM2G033641_T01; parent_gene=GRMZM2G033641	GRMZM2G033641_P01	TRUE	TRUE	aAEAEGAEeek	95%	n+304 (+304), K+304 (+304)	65.15	25.00
4548	seq=translation; coord=6:148590842..148593721:1; parent_transcript=GRMZM2G033641_T01; parent_gene=GRMZM2G033641	GRMZM2G033641_P01	TRUE	TRUE	eAMAMLk	91%	n+304 (+304), K+304 (+304)	30.40	27.04
4549	seq=translation; coord=6:148590842..148593721:1; parent_transcript=GRMZM2G033641_T01; parent_gene=GRMZM2G033641	GRMZM2G033641_P01	TRUE	TRUE	eELIWGVPLAGDDER	95%	n+304 (+304)	54.73	25.00
4550	seq=translation; coord=6:148590842..148593721:1; parent_transcript=GRMZM2G033641_T01; parent_gene=GRMZM2G033641	GRMZM2G033641_P01	TRUE	TRUE	qEAAAPAAEVVVEEEK	93%	n+304 (+304), K+304 (+304)	28.29	25.62
4551	seq=translation; coord=6:168917945..168919116:1; parent_transcript=GRMZM5G833747_T01; parent_gene=GRMZM5G833747	GRMZM5G833747_P01,GRMZM5G833747_P02, GRMZM5G833747_P03	TRUE	TRUE	gDLGVVVGR	95%	n+304 (+304)	34.97	27.40

4552	seq=translation; coord=6:168917945..168919116:1; parent_transcript=GRMZM5G833747_T01; parent_gene=GRMZM5G833747 seq=translation; coord=1:41535916..41540223:-1;	GRMZM5G833747_P01,GRMZM5G833747_P02, GRMZM5G833747_P03	TRUE	TRUE	tFIAIkPDGVQR	95%	n+304 (+304), K+304 (+304)	31.17	25.00
4553	parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329 seq=translation; coord=1:41535916..41540223:-1;	GRMZM2G157329_P01,GRMZM2G157329_P02	TRUE	TRUE	aPDAAWQHDMYPAVAAGGGGGGR	91%	n+304 (+304)	25.38	25.00
4554	parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329 seq=translation; coord=1:41535916..41540223:-1;	GRMZM2G157329_P01,GRMZM2G157329_P02	TRUE	TRUE	eLFSELGDLK	95%	n+304 (+304), K+304 (+304)	40.31	26.52
4555	parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329 seq=translation; coord=1:41535916..41540223:-1;	GRMZM2G157329_P01,GRMZM2G157329_P02	TRUE	TRUE	gTAEVVFAR	90%	n+304 (+304)	27.41	25.00
4556	parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329 seq=translation; coord=1:41535916..41540223:-1;	GRMZM2G157329_P01,GRMZM2G157329_P02	TRUE	TRUE	IYISNLDFGVSNDIik	95%	n+304 (+304), K+304 (+304)	41.86	26.06
4557	parent_transcript=GRMZM2G157329_T01; parent_gene=GRMZM2G157329	GRMZM2G157329_P01,GRMZM2G157329_P02	TRUE	TRUE	sAEELDADLEK	95%	n+304 (+304), K+304 (+304)	69.75	25.00
4558	seq=translation; coord=5:19123690..19126862:1; parent_transcript=GRMZM2G074898_T01; parent_gene=GRMZM2G074898	GRMZM2G074898_P01,GRMZM2G074898_P02, GRMZM2G074898_P03,GRMZM2G110328_P01, GRMZM2G110328_P02,GRMZM2G110328_P03, GRMZM2G142640_P01,GRMZM2G142640_P02, GRMZM2G142640_P03	TRUE	TRUE	aDSQVFLFANSk	94%	n+304 (+304), K+304 (+304)	29.33	26.02
4559	seq=translation; coord=5:19123690..19126862:1; parent_transcript=GRMZM2G074898_T01; parent_gene=GRMZM2G074898	GRMZM2G074898_P01,GRMZM2G074898_P02, GRMZM2G074898_P03,GRMZM2G110328_P01, GRMZM2G110328_P02,GRMZM2G110328_P03, GRMZM2G142640_P01,GRMZM2G142640_P02, GRMZM2G142640_P03	TRUE	TRUE	sIVGASLEVIQk	95%	n+304 (+304), K+304 (+304)	50.98	25.00
4560	seq=translation; coord=2:38192410..38194128:1; parent_transcript=GRMZM2G121700_T01; parent_gene=GRMZM2G121700	GRMZM2G121700_P01	TRUE	TRUE	aLFDLPDDAk	95%	n+304 (+304), K+304 (+304)	38.31	25.59
4561	seq=translation; coord=2:38192410..38194128:1; parent_transcript=GRMZM2G121700_T01; parent_gene=GRMZM2G121700	GRMZM2G121700_P01	TRUE	TRUE	iSIAMFLLAPk	95%	n+304 (+304), K+304 (+304)	32.73	25.00
4562	seq=translation; coord=2:38192410..38194128:1; parent_transcript=GRMZM2G121700_T01; parent_gene=GRMZM2G121700	GRMZM2G121700_P01	TRUE	TRUE	IAGSSPDESAR	95%	n+304 (+304)	43.96	25.00
4563	seq=translation; coord=2:17348097..17355999:-1; parent_transcript=GRMZM2G145968_T01; parent_gene=GRMZM2G145968	GRMZM2G145968_P01	TRUE	TRUE	eGDEAEGSNk	95%	n+304 (+304), K+304 (+304)	31.96	25.00
4564	seq=translation; coord=2:17348097..17355999:-1; parent_transcript=GRMZM2G145968_T01; parent_gene=GRMZM2G145968	GRMZM2G145968_P01	TRUE	TRUE	gLTPFFAFLAEFRPQYLEk	94%	n+304 (+304), K+304 (+304)	26.28	25.00
4565	seq=translation; coord=2:17348097..17355999:-1; parent_transcript=GRMZM2G145968_T01; parent_gene=GRMZM2G145968	GRMZM2G145968_P01	TRUE	TRUE	skSEVEDDEQDGNEDeDE	95%	n+304 (+304), K+304 (+304)	86.75	25.00
4566	seq=translation; coord=2:17348097..17355999:-1; parent_transcript=GRMZM2G145968_T01; parent_gene=GRMZM2G145968	GRMZM2G145968_P01	TRUE	TRUE	sMSDEEK	95%	n+304 (+304), K+304 (+304)	29.40	25.00
4567	seq=translation; coord=5:180669231..180673418:1; parent_transcript=GRMZM2G139614_T01; parent_gene=GRMZM2G139614	GRMZM2G139614_P01	TRUE	TRUE	dASATPTPPAEAGR	95%	n+304 (+304)	31.78	25.00

4568	seq=translation; coord=5:180669231..180673418:1; parent_transcript=GRMZM2G139614_T01; parent_gene=GRMZM2G139614 seq=translation; coord=7:10575103..10576227:-1;	GRMZM2G139614_P01	TRUE	TRUE	iTQMEEQLELLR	95%	n+304 (+304)	40.20	25.85
4569	parent_transcript=GRMZM2G328171_T01; parent_gene=GRMZM2G328171 seq=translation; coord=7:10575103..10576227:-1;	GRMZM2G328171_P01	TRUE	TRUE	rPFGDAYVDGLDFFLDR	95%	n+304 (+304)	47.79	25.00
4570	parent_transcript=GRMZM2G328171_T01; parent_gene=GRMZM2G328171 seq=translation; coord=4:199076122..199077395:-1;	GRMZM2G328171_P01	TRUE	TRUE	tPVQLSATPR	90%	n+304 (+304)	29.18	26.99
4571	parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720 seq=translation; coord=4:199076122..199077395:-1;	GRMZM2G177720_P01	TRUE	TRUE	dIEGWTAR	90%	n+304 (+304)	27.60	25.00
4572	parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720 seq=translation; coord=4:199076122..199077395:-1;	GRMZM2G177720_P01	TRUE	TRUE	qFGYIVLTTSAGIMDHEEAR	95%	n+304 (+304)	71.01	25.00
4573	parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720 seq=translation; coord=4:199076122..199077395:-1;	GRMZM2G177720_P01	TRUE	TRUE	qFGYIVLTTSAGIMDHEEAR	95%	Pyro-cmC (-17), n+304 (+304)	133.31	25.00
4574	parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720 seq=translation; coord=4:199076122..199077395:-1;	GRMZM2G177720_P01	TRUE	TRUE	sMYNAEK	92%	n+304 (+304), K+304 (+304)	25.91	25.00
4575	parent_transcript=GRMZM2G177720_T01; parent_gene=GRMZM2G177720 seq=translation; coord=2:24608141..24615659:1;	GRMZM2G177720_P01	TRUE	TRUE	vSVLNDALK	95%	n+304 (+304), K+304 (+304)	31.53	25.29
4576	parent_transcript=GRMZM2G061928_T01; parent_gene=GRMZM2G061928 seq=translation; coord=1:46126597..46129448:1;	GRMZM2G061928_P01, GRMZM2G061928_P02, GRMZM2G061928_P03	TRUE	TRUE	aIGLMPMIDQGEK	95%	n+304 (+304), K+304 (+304)	30.01	25.80
4577	parent_transcript=GRMZM2G030016_T01; parent_gene=GRMZM2G030016 seq=translation; coord=1:46126597..46129448:1;	GRMZM2G030016_P01, GRMZM2G030016_P02	TRUE	TRUE	dLYINNAIQMDVTGSR	95%	n+304 (+304)	86.34	25.00
4578	parent_transcript=GRMZM2G030016_T01; parent_gene=GRMZM2G030016 seq=translation; coord=4:195054129..195060931:1;	GRMZM2G030016_P01, GRMZM2G030016_P02	TRUE	TRUE	tLTAVHDGILEDVVYPAEIVGK	95%	n+304 (+304), K+304 (+304)	61.76	25.00
4579	parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406 seq=translation; coord=4:195054129..195060931:1;	GRMZM2G084406_P02	TRUE	TRUE	aRPPQEAITDFVSITGADEVTA VR	95%	n+304 (+304)	44.32	25.99
4580	parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406 seq=translation; coord=4:195054129..195060931:1;	GRMZM2G084406_P02	TRUE	TRUE	ePLQNDEGAVTVVVR	95%	n+304 (+304)	56.55	25.01
4581	parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406 seq=translation; coord=4:195054129..195060931:1;	GRMZM2G084406_P02	TRUE	TRUE	IQYLDFDIDISR	95%	n+304 (+304)	35.82	25.55
4582	parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406 seq=translation; coord=4:195054129..195060931:1;	GRMZM2G084406_P02	TRUE	TRUE	IQYLDFDIDISR	95%	n+304 (+304), iTRAQ8plex (+304)	28.80	25.29
4583	parent_transcript=GRMZM2G084406_T02; parent_gene=GRMZM2G084406 seq=translation; coord=6:98313412..98316578:1;	GRMZM2G084406_P02	TRUE	TRUE	tIEPAETVQR	90%	n+304 (+304)	27.62	26.23
4584	parent_transcript=GRMZM2G110402_T01; parent_gene=GRMZM2G110402 seq=translation; coord=6:98313412..98316578:1;	GRMZM2G110402_P01, GRMZM2G110402_P02, GRMZM2G110402_P03	TRUE	TRUE	iSVDASLAGAIIIGK	95%	n+304 (+304), K+304 (+304)	38.95	25.00
4585	parent_transcript=GRMZM2G110402_T01; parent_gene=GRMZM2G110402	GRMZM2G110402_P01, GRMZM2G110402_P02, GRMZM2G110402_P03	TRUE	TRUE	mPMGPGGPDGPPSPAVK	95%	n+304 (+304), K+304 (+304)	39.05	25.65

4586	seq=translation; coord=6:98313412..98316578:1; parent_transcript=GRMZM2G110402_T01; parent_gene=GRMZM2G110402	GRMZM2G110402_P01,GRMZM2G110402_P02, GRMZM2G110402_P03	TRUE	TRUE	mTNLGGPPVPAPPGR	95%	n+304 (+304)	47.59	26.38
4587	seq=translation; coord=6:98313412..98316578:1; parent_transcript=GRMZM2G110402_T01; parent_gene=GRMZM2G110402	GRMZM2G110402_P01,GRMZM2G110402_P02, GRMZM2G110402_P03	TRUE	TRUE	nIELEGTDFQIk	95%	n+304 (+304), K+304 (+304)	47.48	26.09
4588	seq=translation; coord=3:151293748..151299116:1; parent_transcript=GRMZM2G030902_T01; parent_gene=GRMZM2G030902	GRMZM2G030902_P01,GRMZM2G030902_P02, GRMZM2G030902_P03,GRMZM2G060977_P01, GRMZM2G060977_P02,GRMZM2G060977_P03, GRMZM2G060977_P04,GRMZM2G060977_P05	TRUE	TRUE	iPQSVDESMFR	95%	n+304 (+304)	36.66	25.00
4589	seq=translation; coord=3:151293748..151299116:1; parent_transcript=GRMZM2G030902_T01; parent_gene=GRMZM2G030902	GRMZM2G030902_P01,GRMZM2G030902_P02, GRMZM2G030902_P03,GRMZM2G060977_P01, GRMZM2G060977_P02,GRMZM2G060977_P03, GRMZM2G060977_P04,GRMZM2G060977_P05	TRUE	TRUE	IVVLGIPWDVDTEGLR	95%	n+304 (+304)	36.67	26.57
4590	seq=translation; coord=1:293644603..293647117:-1; parent_transcript=GRMZM2G068244_T01; parent_gene=GRMZM2G068244	GRMZM2G068244_P01	TRUE	TRUE	iGAAGDVYVADIR	95%	n+304 (+304)	31.38	25.50
4591	seq=translation; coord=1:293644603..293647117:-1; parent_transcript=GRMZM2G068244_T01; parent_gene=GRMZM2G068244	GRMZM2G068244_P01	TRUE	TRUE	IAPAVQGVDAIILTSAAPK	95%	n+304 (+304), K+304 (+304)	61.78	25.00
4592	seq=translation; coord=10:103630422..103635991:-1; parent_transcript=GRMZM2G359298_T01; parent_gene=GRMZM2G359298	GRMZM2G359298_P01	TRUE	TRUE	gEDTLDTWSEr	95%	n+304 (+304)	34.30	25.00
4593	seq=translation; coord=10:103630422..103635991:-1; parent_transcript=GRMZM2G359298_T01; parent_gene=GRMZM2G359298	GRMZM2G359298_P01	TRUE	TRUE	IDMDVDGADNSFVR	95%	n+304 (+304)	56.22	25.00
4594	seq=translation; coord=8:171328319..171331663:-1; parent_transcript=GRMZM2G172932_T01; parent_gene=GRMZM2G172932	GRMZM2G172932_P01,GRMZM2G172932_P02, GRMZM2G172932_P03	TRUE	TRUE	gLSMASTFVGNSTSIQEMFR	95%	n+304 (+304)	31.32	25.00
4595	seq=translation; coord=8:171328319..171331663:-1; parent_transcript=GRMZM2G172932_T01; parent_gene=GRMZM2G172932	GRMZM2G172932_P01,GRMZM2G172932_P02, GRMZM2G172932_P03	TRUE	TRUE	yTGTSDLQLER	95%	n+304 (+304)	48.82	25.00
4596	seq=translation; coord=1:16603599..16606666:-1; parent_transcript=GRMZM2G016511_T01; parent_gene=GRMZM2G016511	GRMZM2G016511_P01	TRUE	TRUE	aLTTEEIDQHILTAISERD	95%	n+304 (+304)	55.25	25.00
4597	seq=translation; coord=5:212248891..212249987:1; parent_transcript=GRMZM2G098167_T01; parent_gene=GRMZM2G098167	GRMZM2G098167_P01	TRUE	TRUE	eYAFVLDVPGLSk	95%	n+304 (+304), K+304 (+304)	40.64	25.26
4598	seq=translation; coord=5:212248891..212249987:1; parent_transcript=GRMZM2G098167_T01; parent_gene=GRMZM2G098167	GRMZM2G098167_P01	TRUE	TRUE	IPEDADTGGVAAR	93%	n+304 (+304)	29.33	25.00
4599	seq=translation; coord=5:212248891..212249987:1; parent_transcript=GRMZM2G098167_T01; parent_gene=GRMZM2G098167	GRMZM2G098167_P01	TRUE	TRUE	sDIQVTLEEDR	95%	n+304 (+304)	55.98	25.00
4600	seq=translation; coord=7:7118087..7119389:-1; parent_transcript=GRMZM2G320298_T01; parent_gene=GRMZM2G320298	GRMZM2G320298_P01	TRUE	TRUE	fGGSPADLAPVAVR	95%	n+304 (+304)	45.87	26.05
4601	seq=translation; coord=7:7118087..7119389:-1; parent_transcript=GRMZM2G320298_T01; parent_gene=GRMZM2G320298	GRMZM2G320298_P01	TRUE	TRUE	IPAAIDDGAAVLWLAR	89%	n+304 (+304)	26.03	25.82

4602	seq=translation; coord=6:147724800..147731064:1; parent_transcript=GRMZM2G070199_T01; parent_gene=GRMZM2G070199	GRMZM2G070199_P01	TRUE	TRUE	aDLIAYLk	93%	n+304 (+304), K+304 (+304)	28.08	25.31
4603	seq=translation; coord=6:147724800..147731064:1; parent_transcript=GRMZM2G070199_T01; parent_gene=GRMZM2G070199	GRMZM2G070199_P01	TRUE	TRUE	qSGTTAGYSYSAGNk	95%	n+304 (+304), K+304 (+304)	70.48	25.00
4604	seq=translation; coord=4:7172367..7173014:-1; parent_transcript=GRMZM2G132162_T01; parent_gene=GRMZM2G132162	GRMZM2G132162_P01	TRUE	TRUE	vLVSSNcETPTR	95%	n+304 (+304), Carbamidomethyl (+57)	42.69	25.00
4605	seq=translation; coord=4:7172367..7173014:-1; parent_transcript=GRMZM2G132162_T01; parent_gene=GRMZM2G132162	GRMZM2G132162_P01	TRUE	TRUE	vSIACDTGcNAAISR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	54.63	25.00
4606	seq=translation; coord=7:152391333..152401606:1; parent_transcript=GRMZM2G325008_T01; parent_gene=GRMZM2G325008	GRMZM2G325008_P01,GRMZM2G325008_P02, GRMZM2G325008_P03,GRMZM2G325008_P04, GRMZM2G325008_P05	TRUE	TRUE	IYDADPR	95%	n+304 (+304)	37.07	25.00
4607	seq=translation; coord=7:152391333..152401606:1; parent_transcript=GRMZM2G325008_T01; parent_gene=GRMZM2G325008	GRMZM2G325008_P01,GRMZM2G325008_P02, GRMZM2G325008_P03,GRMZM2G325008_P04, GRMZM2G325008_P05	TRUE	TRUE	yTNVFDAMLDVR	95%	n+304 (+304)	38.51	25.00
4608	seq=translation; coord=5:31178435..31182856:-1; parent_transcript=GRMZM2G102639_T01; parent_gene=GRMZM2G102639	GRMZM2G102639_P01,GRMZM2G170699_P01	TRUE	TRUE	lLYDTFSAFGVIVTNPk	95%	n+304 (+304), K+304 (+304)	51.86	25.51
4609	seq=translation; coord=5:31178435..31182856:-1; parent_transcript=GRMZM2G102639_T01; parent_gene=GRMZM2G102639	GRMZM2G102639_P01,GRMZM2G170699_P01	TRUE	TRUE	vTNLHQGYGFVEFR	94%	n+304 (+304)	28.56	25.00
4610	seq=translation; coord=3:221273481..221276486:-1; parent_transcript=GRMZM2G051764_T01; parent_gene=GRMZM2G051764	GRMZM2G051764_P01,GRMZM2G051764_P03, GRMZM2G051764_P04	TRUE	TRUE	dGLTAADHLGEDFYk	93%	n+304 (+304), K+304 (+304)	27.47	25.00
4611	seq=translation; coord=3:221273481..221276486:-1; parent_transcript=GRMZM2G051764_T01; parent_gene=GRMZM2G051764	GRMZM2G051764_P01,GRMZM2G051764_P03, GRMZM2G051764_P04	TRUE	TRUE	vIEIPGDTSVIDAVR	95%	n+304 (+304)	40.57	25.94
4612	seq=translation; coord=1:14103040..14104304:1; parent_transcript=GRMZM5G850455_T01; parent_gene=GRMZM5G850455	GRMZM5G850455_P01,GRMZM5G850455_P02, GRMZM5G850455_P03	TRUE	TRUE	aPPPDccGGLR	91%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	28.13	25.00
4613	seq=translation; coord=1:14103040..14104304:1; parent_transcript=GRMZM5G850455_T01; parent_gene=GRMZM5G850455	GRMZM5G850455_P01,GRMZM5G850455_P02, GRMZM5G850455_P03	TRUE	TRUE	tEcADQLVLGAPcLQYVQGQAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	59.86	25.00
4614	seq=translation; coord=7:24151509..24152227:1; parent_transcript=GRMZM2G046532_T01; parent_gene=GRMZM2G046532	GRMZM2G046532_P01	TRUE	TRUE	dANcANVcLTEGFTGGVck	95%	n+304 (+304), K+304 (+304)	72.20	25.00
4615	seq=translation; coord=2:5269563..5273858:1; parent_transcript=GRMZM2G166281_T01; parent_gene=GRMZM2G166281	GRMZM2G166281_P01	TRUE	TRUE	vVTIDSYEDVPANDEK	95%	n+304 (+304), K+304 (+304)	45.96	25.00
4616	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	aEDGEVWTFSVR	95%	n+304 (+304)	29.97	25.00
4617	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	aEVADVSEAVR	95%	n+304 (+304)	31.62	25.00
4618	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	gDMGAQVPLEQVPSIQQk	92%	n+304 (+304), K+304 (+304)	26.49	25.61

4619	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290 seq=translation; coord=7:10513154..10517482:1;	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	INLQWGLIPFR	95%	n+304 (+304)	53.23	25.35
4620	seq=translation; coord=7:10513154..10517482:1; parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290 seq=translation; coord=7:10513154..10517482:1;	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	qLnKPVIVASQLLESIMIEYPTPTR	95%	n+304 (+304), K+304 (+304)	57.58	25.00
4621	parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290 seq=translation; coord=7:10513154..10517482:1;	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	rLNLQWGLIPFR	95%	n+304 (+304)	37.72	25.00
4622	parent_transcript=GRMZM2G066290_T01; parent_gene=GRMZM2G066290 seq=translation; coord=7:10513154..10517482:1;	GRMZM2G066290_P01,GRMZM2G066290_P02	TRUE	TRUE	tINVNYDGFADVR	95%	n+304 (+304)	40.20	25.00
4623	seq=translation; coord=2:36456199..36464613:-1; parent_transcript=GRMZM2G130230_T01; parent_gene=GRMZM2G130230 seq=translation; coord=2:36456199..36464613:-1;	GRMZM2G130230_P01,GRMZM2G130230_P02, GRMZM2G130230_P03	TRUE	TRUE	dLDSAEELSACLGEFEEHQLYR	95%	n+304 (+304)	50.52	25.00
4624	parent_transcript=GRMZM2G130230_T01; parent_gene=GRMZM2G130230 seq=translation; coord=2:36456199..36464613:-1;	GRMZM2G130230_P01,GRMZM2G130230_P02, GRMZM2G130230_P03	TRUE	TRUE	dNIDNIQIVFR	92%	n+304 (+304)	29.49	25.77
4625	seq=translation; coord=2:36456199..36464613:-1; parent_transcript=GRMZM2G130230_T01; parent_gene=GRMZM2G130230 seq=translation; coord=9:149239142..149244150:1;	GRMZM2G130230_P01,GRMZM2G130230_P02, GRMZM2G130230_P03	TRUE	TRUE	gAPEDLSEFLQLIK	93%	n+304 (+304), K+304 (+304)	27.54	25.33
4626	parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528 seq=translation; coord=9:149239142..149244150:1;	GRMZM2G004528_P03,GRMZM2G155242_P01	TRUE	TRUE	acVGLAPENNMLEYK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.99	25.39
4627	seq=translation; coord=9:149239142..149244150:1; parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528 seq=translation; coord=9:149239142..149244150:1;	GRMZM2G004528_P03,GRMZM2G155242_P01	TRUE	TRUE	aMDEYTSEIFMGGK	95%	n+304 (+304), K+304 (+304)	46.89	25.00
4628	parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528 seq=translation; coord=9:149239142..149244150:1;	GRMZM2G004528_P03,GRMZM2G155242_P01	TRUE	TRUE	eGISWATk	95%	n+304 (+304), K+304 (+304)	32.08	27.31
4629	parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528 seq=translation; coord=9:149239142..149244150:1;	GRMZM2G004528_P03,GRMZM2G155242_P01	TRUE	TRUE	vLDIDLQk	95%	n+304 (+304), K+304 (+304)	37.50	25.00
4630	parent_transcript=GRMZM2G004528_T03; parent_gene=GRMZM2G004528 seq=translation; coord=4:237868446..237932504:1;	GRMZM2G004528_P03,GRMZM2G155242_P01	TRUE	TRUE	yGPTEIESEYR	95%	n+304 (+304)	41.74	25.00
4631	parent_transcript=GRMZM2G092627_T01; parent_gene=GRMZM2G092627 seq=translation; coord=4:237868446..237932504:1;	GRMZM2G092627_P01	TRUE	TRUE	gAAFLAGVVK	95%	n+304 (+304), K+304 (+304)	49.91	25.00
4632	parent_transcript=GRMZM2G092627_T01; parent_gene=GRMZM2G092627 seq=translation; coord=4:237868446..237932504:1;	GRMZM2G092627_P01	TRUE	TRUE	ILDVLNTPSEAVQR	94%	n+304 (+304)	30.84	26.36
4633	parent_transcript=GRMZM2G092627_T01; parent_gene=GRMZM2G092627 seq=translation; coord=4:237868446..237932504:1;	GRMZM2G092627_P01	TRUE	TRUE	IVLPSLLk	93%	n+304 (+304), K+304 (+304)	26.23	25.00
4634	parent_transcript=GRMZM2G092627_T01; parent_gene=GRMZM2G092627 seq=translation; coord=5:128105440..128107392:-1;	GRMZM2G092627_P01	TRUE	TRUE	qGIALALHSIADVLASK	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	43.09	25.00
4635	parent_transcript=GRMZM2G071089_T01; parent_gene=GRMZM2G071089 seq=translation; coord=5:128105440..128107392:-1;	GRMZM2G071089_P01	TRUE	TRUE	aAAAAELVK	95%	n+304 (+304), K+304 (+304)	41.12	26.92
4636	parent_transcript=GRMZM2G071089_T01; parent_gene=GRMZM2G071089	GRMZM2G071089_P01	TRUE	TRUE	aGPALLSGPIFATFEK	95%	n+304 (+304), K+304 (+304)	51.01	25.00

4637	seq=translation; coord=5:128105440..128107392:-1; parent_transcript=GRMZM2G071089_T01; parent_gene=GRMZM2G071089	GRMZM2G071089_P01	TRUE	TRUE	eGIDGEFQEk	95%	n+304 (+304), K+304 (+304)	50.88	25.56
4638	seq=translation; coord=5:128105440..128107392:-1; parent_transcript=GRMZM2G071089_T01; parent_gene=GRMZM2G071089	GRMZM2G071089_P01	TRUE	TRUE	vSTLLPVVAAEEPak	95%	n+304 (+304), K+304 (+304)	37.64	25.00
4639	seq=translation; coord=3:52892215..52895069:-1; parent_transcript=GRMZM2G033226_T01; parent_gene=GRMZM2G033226	GRMZM2G033226_P01	TRUE	TRUE	mLDFDFLcGR	95%	n+304 (+304), Carbamidomethyl (+57)	33.61	25.00
4640	seq=translation; coord=3:52892215..52895069:-1; parent_transcript=GRMZM2G033226_T01; parent_gene=GRMZM2G033226	GRMZM2G033226_P01	TRUE	TRUE	sAAASSMSAlk	95%	n+304 (+304), K+304 (+304)	42.07	26.54
4641	seq=translation; coord=3:52892215..52895069:-1; parent_transcript=GRMZM2G033226_T01; parent_gene=GRMZM2G033226	GRMZM2G033226_P01	TRUE	TRUE	vIIGPATVGGIQAGAFk	95%	n+304 (+304), K+304 (+304)	59.63	25.00
4642	seq=translation; coord=2:224904656..224907978:1; parent_transcript=GRMZM2G408768_T01; parent_gene=GRMZM2G408768	GRMZM2G408768_P01	TRUE	TRUE	aAQDIALADLAPTHPIR	95%	n+304 (+304)	64.37	25.54
4643	seq=translation; coord=2:224904656..224907978:1; parent_transcript=GRMZM2G408768_T01; parent_gene=GRMZM2G408768	GRMZM2G408768_P01	TRUE	TRUE	sAGGAGGGEELSVEER	95%	n+304 (+304)	61.83	25.00
4644	seq=translation; coord=2:224904656..224907978:1; parent_transcript=GRMZM2G408768_T01; parent_gene=GRMZM2G408768	GRMZM2G408768_P01	TRUE	TRUE	yEEMVEFMER	91%	n+304 (+304)	28.05	25.00
4645	seq=translation; coord=1:298431972..298436349:1; parent_transcript=GRMZM2G021742_T01; parent_gene=GRMZM2G021742	GRMZM2G021742_P01	TRUE	TRUE	IQFLSLDNTVtk	94%	n+304 (+304), K+304 (+304)	28.24	25.00
4646	seq=translation; coord=1:298431972..298436349:1; parent_transcript=GRMZM2G021742_T01; parent_gene=GRMZM2G021742	GRMZM2G021742_P01	TRUE	TRUE	ITADLIWk	95%	n+304 (+304), K+304 (+304)	27.83	25.00
4647	seq=translation; coord=1:298431972..298436349:1; parent_transcript=GRMZM2G021742_T01; parent_gene=GRMZM2G021742	GRMZM2G021742_P01	TRUE	TRUE	ITNLAEIDPLASLpk	92%	n+304 (+304), K+304 (+304)	25.87	25.00
4648	seq=translation; coord=1:298431972..298436349:1; parent_transcript=GRMZM2G021742_T01; parent_gene=GRMZM2G021742	GRMZM2G021742_P01	TRUE	TRUE	mDTDGENQEGGEADGQk	95%	n+304 (+304), K+304 (+304)	83.85	25.00
4649	seq=translation; coord=4:100154058..100157650:1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01,GRMZM2G091995_P02	TRUE	TRUE	eVSLPAPAPPTR	89%	n+304 (+304)	27.34	25.55
4650	seq=translation; coord=4:100154058..100157650:1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01,GRMZM2G091995_P02	TRUE	TRUE	gYFVLNDMFR	95%	n+304 (+304)	38.19	25.00
4651	seq=translation; coord=4:100154058..100157650:1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01,GRMZM2G091995_P02	TRUE	TRUE	IGRPASAAGAAGMDSVTTMEAIgEK	95%	n+304 (+304), K+304 (+304)	56.20	25.54
4652	seq=translation; coord=4:100154058..100157650:1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01,GRMZM2G091995_P02	TRUE	TRUE	nLPLNATETQLEDEFk	95%	n+304 (+304), K+304 (+304)	68.66	25.05
4653	seq=translation; coord=9:86866692..86874101:-1; parent_transcript=GRMZM2G091995_T01; parent_gene=GRMZM2G091995	GRMZM2G091995_P01,GRMZM2G091995_P02	TRUE	TRUE	qSPALAPVk	89%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	25.84	25.00
4654	parent_gene=GRMZM2G022275 parent_transcript=GRMZM2G022275_T01; parent_gene=GRMZM2G022275	GRMZM2G022275_P01,GRMZM2G022275_P02	TRUE	TRUE	gAVVWScclDR	91%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	28.22	25.00

4655	seq=translation; coord=9:86866692..86874101:-1; parent_transcript=GRMZM2G022275_T01; parent_gene=GRMZM2G022275 seq=translation; coord=9:86866692..86874101:-1;	GRMZM2G022275_P01,GRMZM2G022275_P02	TRUE	TRUE	IWDVR	92%	n+304 (+304)	30.61	26.79
4656	parent_transcript=GRMZM2G022275_T01; parent_gene=GRMZM2G022275 seq=translation; coord=8:155644343..155646847:-1;	GRMZM2G022275_P01,GRMZM2G022275_P02	TRUE	TRUE	vWDALTGDELHSFEHK	95%	n+304 (+304), K+304 (+304)	29.54	25.00
4657	parent_transcript=GRMZM2G151252_T01; parent_gene=GRMZM2G151252 seq=translation; coord=7:108281609..108388418:-1;	GRMZM2G151252_P01,GRMZM2G151252_P02, GRMZM2G151252_P04	TRUE	TRUE	sTGFLIYDNLESak	95%	n+304 (+304), K+304 (+304)	32.55	25.81
4658	parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=7:108281609..108388418:-1;	GRMZM2G700188_P04,GRMZM2G700188_P05	TRUE	TRUE	dDSGVLSPYFSR	92%	n+304 (+304)	28.84	25.00
4659	parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=7:108281609..108388418:-1;	GRMZM2G700188_P04,GRMZM2G700188_P05	TRUE	TRUE	gGFSDVLVASEHYVVR	95%	n+304 (+304)	29.76	25.29
4660	parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=7:108281609..108388418:-1;	GRMZM2G700188_P04,GRMZM2G700188_P05	TRUE	TRUE	hLGVVGLGGLGHVAVK	95%	n+304 (+304), K+304 (+304)	30.94	25.00
4661	parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=7:108281609..108388418:-1;	GRMZM2G700188_P04,GRMZM2G700188_P05	TRUE	TRUE	mDYVNTAMER	91%	n+304 (+304)	26.77	25.00
4662	parent_transcript=GRMZM2G700188_T04; parent_gene=GRMZM2G700188 seq=translation; coord=4:2112375..2118463:-1;	GRMZM2G700188_P04,GRMZM2G700188_P05	TRUE	TRUE	rQEAIENLGADEFLISR	95%	n+304 (+304)	54.83	25.91
4663	parent_transcript=GRMZM2G057450_T01; parent_gene=GRMZM2G057450 seq=translation; coord=4:2112375..2118463:-1;	GRMZM2G057450_P01,GRMZM2G057450_P02, GRMZM2G057450_P03,GRMZM2G057450_P04, GRMZM2G057450_P06,GRMZM5G813627_P01, GRMZM5G813627_P02	TRUE	TRUE	fAFVEMR	95%	n+304 (+304)	29.93	25.00
4664	parent_transcript=GRMZM2G057450_T01; parent_gene=GRMZM2G057450 seq=translation; coord=4:2112375..2118463:-1;	GRMZM2G057450_P01,GRMZM2G057450_P02, GRMZM2G057450_P03,GRMZM2G057450_P04, GRMZM2G057450_P06,GRMZM5G813627_P01, GRMZM5G813627_P02	TRUE	TRUE	iFVGGLPYFTEAQVR	95%	n+304 (+304)	46.22	25.00
4665	parent_transcript=GRMZM2G057450_T01; parent_gene=GRMZM2G057450 seq=translation; coord=4:2112375..2118463:-1;	GRMZM2G057450_P01,GRMZM2G057450_P02, GRMZM2G057450_P03,GRMZM2G057450_P04, GRMZM2G057450_P06,GRMZM5G813627_P01, GRMZM5G813627_P02	TRUE	TRUE	sVEEASNAMALDGIMFEGAPV	95%	n+304 (+304), K+304 (+304)	35.41	25.00
4666	parent_transcript=GRMZM2G054136_T01; parent_gene=GRMZM2G054136 seq=translation; coord=7:166387724..166390583:1;	GRMZM2G054136_P01,GRMZM2G054136_P03, GRMZM2G054136_P04,GRMZM2G054136_P05, GRMZM2G054136_P07,GRMZM2G054136_P09, GRMZM5G851698_P02	TRUE	TRUE	fNIANPSTGcQk	90%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.43	25.77
4667	parent_transcript=GRMZM2G054136_T01; parent_gene=GRMZM2G054136 seq=translation; coord=7:166387724..166390583:1;	GRMZM2G054136_P01,GRMZM2G054136_P03, GRMZM2G054136_P04,GRMZM2G054136_P05, GRMZM2G054136_P07,GRMZM2G054136_P09, GRMZM5G851698_P02	TRUE	TRUE	gcIVSQDLSVINLVIVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.67	25.00
4668	parent_transcript=GRMZM2G054136_T01; parent_gene=GRMZM2G054136 seq=translation; coord=7:166387724..166390583:1;	GRMZM2G054136_P01,GRMZM2G054136_P03, GRMZM2G054136_P04,GRMZM2G054136_P05, GRMZM2G054136_P07,GRMZM2G054136_P09, GRMZM5G851698_P02	TRUE	TRUE	iSQEVSGDALGEEFk	95%	n+304 (+304), K+304 (+304)	52.47	25.50
4669	parent_transcript=GRMZM2G054136_T01; parent_gene=GRMZM2G054136 seq=translation; coord=7:166387724..166390583:1;	GRMZM2G054136_P01,GRMZM2G054136_P03, GRMZM2G054136_P04,GRMZM2G054136_P05, GRMZM2G054136_P07,GRMZM2G054136_P09, GRMZM5G851698_P02	TRUE	TRUE	sEAAEYQk	92%	n+304 (+304), K+304 (+304)	27.24	25.75

4670	seq=translation; coord=6:167112832..167116884:-1; parent_transcript=GRMZM2G144372_T01; parent_gene=GRMZM2G144372	GRMZM2G144372_P01	TRUE	TRUE	dFEYSPEAQESR	95%	n+304 (+304)	42.22	25.00
4671	seq=translation; coord=6:167112832..167116884:-1; parent_transcript=GRMZM2G144372_T01; parent_gene=GRMZM2G144372	GRMZM2G144372_P01	TRUE	TRUE	dWLSYSETLDTFVVPR	95%	n+304 (+304)	75.59	25.26
4672	seq=translation; coord=6:167112832..167116884:-1; parent_transcript=GRMZM2G144372_T01; parent_gene=GRMZM2G144372	GRMZM2G144372_P01	TRUE	TRUE	qIEDLER	95%	n+304 (+304)	34.18	25.16
4673	seq=translation; coord=6:167112832..167116884:-1; parent_transcript=GRMZM2G144372_T01; parent_gene=GRMZM2G144372	GRMZM2G144372_P01	TRUE	TRUE	vGTLDSELLALSDDLV	95%	n+304 (+304), K+304 (+304)	59.79	25.00
4674	seq=translation; coord=3:230441023..230443000:1; parent_transcript=GRMZM2G353103_T01; parent_gene=GRMZM2G353103	GRMZM2G353103_P01,GRMZM2G377797_P01	TRUE	TRUE	aFEPILLAGR	95%	n+304 (+304)	35.78	25.92
4675	seq=translation; coord=3:230441023..230443000:1; parent_transcript=GRMZM2G353103_T01; parent_gene=GRMZM2G353103	GRMZM2G353103_P01,GRMZM2G377797_P01	TRUE	TRUE	gLVAYYQk	95%	n+304 (+304), K+304 (+304)	32.69	25.00
4676	seq=translation; coord=3:230441023..230443000:1; parent_transcript=GRMZM2G353103_T01; parent_gene=GRMZM2G353103	GRMZM2G353103_P01,GRMZM2G377797_P01	TRUE	TRUE	tLLVADPR	87%	n+304 (+304)	27.01	26.50
4677	seq=translation; coord=8:5159968..5162055:1; parent_transcript=GRMZM2G044128_T01; parent_gene=GRMZM2G044128	GRMZM2G044128_P01	TRUE	TRUE	gEAIAGIAEMTTAVMATcDHGAVSk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	35.08	25.00
4678	seq=translation; coord=2:235441754..235443878:-1; parent_transcript=GRMZM2G082974_T01; parent_gene=GRMZM2G082974	GRMZM2G082974_P01	TRUE	TRUE	dLLLTVMSSMGEEQIcAVk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.76	25.49
4679	seq=translation; coord=2:235441754..235443878:-1; parent_transcript=GRMZM2G082974_T01; parent_gene=GRMZM2G082974	GRMZM2G082974_P01	TRUE	TRUE	IPtDEALEGQIk	95%	n+304 (+304), K+304 (+304)	31.90	25.47
4680	seq=translation; coord=2:235441754..235443878:-1; parent_transcript=GRMZM2G082974_T01; parent_gene=GRMZM2G082974	GRMZM2G082974_P01	TRUE	TRUE	tEYQLIDITEDGFVSLTDSGNtk	93%	n+304 (+304), K+304 (+304)	26.60	25.00
4681	seq=translation; coord=2:235441754..235443878:-1; parent_transcript=GRMZM2G082974_T01; parent_gene=GRMZM2G082974	GRMZM2G082974_P01	TRUE	TRUE	tYPQQAGTIR	94%	n+304 (+304)	31.00	25.00
4682	seq=translation; coord=1:275223498..275227310:-1; parent_transcript=GRMZM2G169671_T01; parent_gene=GRMZM2G169671	GRMZM2G169671_P01	TRUE	TRUE	fAFILYDTLSk	95%	n+304 (+304), K+304 (+304)	40.56	26.01
4683	seq=translation; coord=1:275223498..275227310:-1; parent_transcript=GRMZM2G169671_T01; parent_gene=GRMZM2G169671	GRMZM2G169671_P01	TRUE	TRUE	sPPVAGAAAAGAGAGAGALMk	95%	n+304 (+304), K+304 (+304)	81.50	25.84
4684	seq=translation; coord=5:115978543..115983314:-1; parent_transcript=GRMZM2G452633_T01; parent_gene=GRMZM2G452633	GRMZM2G452633_P01,GRMZM2G452633_P02, GRMZM2G452633_P03	TRUE	TRUE	aTPMPsFYk	95%	n+304 (+304), K+304 (+304)	45.14	26.11
4685	seq=translation; coord=5:115978543..115983314:-1; parent_transcript=GRMZM2G452633_T01; parent_gene=GRMZM2G452633	GRMZM2G452633_P01,GRMZM2G452633_P02, GRMZM2G452633_P03	TRUE	TRUE	IPSEETcPLDATSR	95%	n+304 (+304), Carbamidomethyl (+57)	40.46	25.00
4686	seq=translation; coord=5:115978543..115983314:-1; parent_transcript=GRMZM2G452633_T01; parent_gene=GRMZM2G452633	GRMZM2G452633_P01,GRMZM2G452633_P02, GRMZM2G452633_P03	TRUE	TRUE	sISETeENTTTDQPAR	95%	n+304 (+304)	75.98	25.00
4687	seq=translation; coord=7:16096163..16099019:1; parent_transcript=GRMZM2G170044_T01; parent_gene=GRMZM2G170044	GRMZM2G170044_P01	TRUE	TRUE	dAQVFEQYAk	90%	n+304 (+304), K+304 (+304)	26.10	25.83

4688	seq=translation; coord=7:16096163..16099019:1; parent_transcript=GRMZM2G170044_T01; parent_gene=GRMZM2G170044	GRMZM2G170044_P01	TRUE	TRUE	ILDLPAGSk	95%	n+304 (+304), K+304 (+304)	31.08	25.65
4689	seq=translation; coord=7:16096163..16099019:1; parent_transcript=GRMZM2G170044_T01; parent_gene=GRMZM2G170044	GRMZM2G170044_P01	TRUE	TRUE	sSAAASTTAGAQK	95%	n+304 (+304), K+304 (+304)	39.09	26.46
4690	seq=translation; coord=3:188328660..188331609:-1; parent_transcript=GRMZM2G047274_T01; parent_gene=GRMZM2G047274	GRMZM2G047274_P01	TRUE	TRUE	fGFDEADIR	95%	n+304 (+304)	33.00	25.00
4691	seq=translation; coord=3:188328660..188331609:-1; parent_transcript=GRMZM2G047274_T01; parent_gene=GRMZM2G047274	GRMZM2G047274_P01	TRUE	TRUE	sLPLSTLIEMlk	95%	n+304 (+304), K+304 (+304)	36.46	25.00
4692	seq=translation; coord=10:38522742..38534648:1; parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406	GRMZM2G010406_P01,GRMZM2G010406_P03, GRMZM2G010406_P06	TRUE	TRUE	dLkEEFVSEIYYPcLR	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	37.45	25.00
4693	seq=translation; coord=10:38522742..38534648:1; parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406	GRMZM2G010406_P01,GRMZM2G010406_P03, GRMZM2G010406_P06	TRUE	TRUE	dLSPASLLAELNEIGGk	95%	n+304 (+304), K+304 (+304)	47.14	25.17
4694	seq=translation; coord=10:38522742..38534648:1; parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406	GRMZM2G010406_P01,GRMZM2G010406_P03, GRMZM2G010406_P06	TRUE	TRUE	eDAIEYAk	95%	n+304 (+304), K+304 (+304)	34.80	26.35
4695	seq=translation; coord=10:38522742..38534648:1; parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406	GRMZM2G010406_P01,GRMZM2G010406_P03, GRMZM2G010406_P06	TRUE	TRUE	fELTFYALNPelk	91%	n+304 (+304), K+304 (+304)	26.42	25.91
4696	seq=translation; coord=10:38522742..38534648:1; parent_transcript=GRMZM2G010406_T01; parent_gene=GRMZM2G010406	GRMZM2G010406_P01,GRMZM2G010406_P03, GRMZM2G010406_P06	TRUE	TRUE	gVYETPGGTIMAAAVR	95%	n+304 (+304)	46.75	25.02
4697	seq=translation; coord=10:3062645..3066771:-1; parent_transcript=GRMZM2G068465_T01; parent_gene=GRMZM2G068465	GRMZM2G068465_P01,GRMZM2G068465_P02, GRMZM5G899349_P01,GRMZM5G899349_P02	TRUE	TRUE	aiWTHLLR	95%	n+304 (+304)	34.74	25.00
4698	seq=translation; coord=10:3062645..3066771:-1; parent_transcript=GRMZM2G068465_T01; parent_gene=GRMZM2G068465	GRMZM2G068465_P01,GRMZM2G068465_P02, GRMZM5G899349_P01,GRMZM5G899349_P02	TRUE	TRUE	iDHDILAEMDVLYR	95%	n+304 (+304)	48.37	25.04
4699	seq=translation; coord=10:3062645..3066771:-1; parent_transcript=GRMZM2G068465_T01; parent_gene=GRMZM2G068465	GRMZM2G068465_P01,GRMZM2G068465_P02, GRMZM5G899349_P01,GRMZM5G899349_P02	TRUE	TRUE	IAEIFATIik	95%	n+304 (+304), K+304 (+304)	36.49	25.00
4700	seq=translation; coord=2:21258086..21262803:1; parent_transcript=GRMZM2G019919_T01; parent_gene=GRMZM2G019919	GRMZM2G019919_P01,GRMZM2G019919_P02, GRMZM2G019919_P03	TRUE	TRUE	IMMNPVTK	95%	n+304 (+304), K+304 (+304)	31.95	26.48
4701	seq=translation; coord=2:21258086..21262803:1; parent_transcript=GRMZM2G019919_T01; parent_gene=GRMZM2G019919	GRMZM2G019919_P01,GRMZM2G019919_P02, GRMZM2G019919_P03	TRUE	TRUE	tVFLDGLPPSWDEDR	95%	n+304 (+304)	58.73	25.00
4702	seq=translation; coord=2:21258086..21262803:1; parent_transcript=GRMZM2G019919_T01; parent_gene=GRMZM2G019919	GRMZM2G019919_P01,GRMZM2G019919_P02, GRMZM2G019919_P03	TRUE	TRUE	vFGVEVGEITEVR	95%	n+304 (+304)	40.56	25.00
4703	seq=translation; coord=2:21258086..21262803:1; parent_transcript=GRMZM2G019919_T01; parent_gene=GRMZM2G019919	GRMZM2G019919_P01,GRMZM2G019919_P02, GRMZM2G019919_P03	TRUE	TRUE	vSFADSYPPQVDDEIMAQVR	95%	n+304 (+304)	36.35	25.00
4704	seq=translation; coord=6:150509782..150519705:1; parent_transcript=GRMZM2G118037_T01; parent_gene=GRMZM2G118037	GRMZM2G118037_P01	TRUE	TRUE	nAASGFSAK	88%	n+304 (+304), K+304 (+304)	27.64	26.93
4705	seq=translation; coord=6:150509782..150519705:1; parent_transcript=GRMZM2G118037_T01; parent_gene=GRMZM2G118037	GRMZM2G118037_P01	TRUE	TRUE	qAAPAAQETAVHIVYVDRPEDADPEEFHIR	95%	Pyro-cmC (-17), n+304 (+304)	29.02	25.00

4706	seq=translation; coord=6:150509782..150519705:1; parent_transcript=GRMZM2G118037_T01; parent_gene=GRMZM2G118037	GRMZM2G118037_P01	TRUE	TRUE	tLTPVLGSEQk	90%	n+304 (+304), K+304 (+304)	28.13	25.87
4707	seq=translation; coord=8:134463276..134464095:1; parent_transcript=GRMZM2G028393_T01; parent_gene=GRMZM2G028393	GRMZM2G028393_P01,GRMZM2G028393_P02	TRUE	TRUE	iFVDIVAQTPHIG	95%	n+304 (+304)	33.13	26.79
4708	seq=translation; coord=8:134463276..134464095:1; parent_transcript=GRMZM2G028393_T01; parent_gene=GRMZM2G028393	GRMZM2G028393_P01,GRMZM2G028393_P02	TRUE	TRUE	tSWPEVVGLSVEDAk	95%	n+304 (+304), K+304 (+304)	35.69	26.20
4709	seq=translation; coord=1:292879723..292882219:-1; parent_transcript=AC225147.4_FGT002; parent_gene=AC225147.4_FG002	AC225147.4_FGP002,GRMZM2G084465_P01,G RMZM2G084465_P03,GRMZM2G110952_P12,G RMZM2G140609_P01,GRMZM2G163561_P01	TRUE	TRUE	gIVLEk	90%	n+304 (+304), K+304 (+304)	28.27	26.70
4710	seq=translation; coord=1:292879723..292882219:-1; parent_transcript=AC225147.4_FGT002; parent_gene=AC225147.4_FG002	AC225147.4_FGP002,GRMZM2G084465_P01,G RMZM2G084465_P03,GRMZM2G110952_P12,G RMZM2G140609_P01,GRMZM2G163561_P01	TRUE	TRUE	vSGVSLALFk	95%	n+304 (+304), K+304 (+304)	35.56	25.00
4711	seq=translation; coord=8:15778520..15799328:1; parent_transcript=GRMZM2G097775_T01; parent_gene=GRMZM2G097775	GRMZM2G097775_P01,GRMZM2G097775_P02	TRUE	TRUE	eGDWVcPDAScGNVNFAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	77.00	25.00
4712	seq=translation; coord=8:15778520..15799328:1; parent_transcript=GRMZM2G097775_T01; parent_gene=GRMZM2G097775	GRMZM2G097775_P01,GRMZM2G097775_P02	TRUE	TRUE	iSVVMAEk	94%	n+304 (+304), K+304 (+304)	30.27	26.87
4713	seq=translation; coord=8:15778520..15799328:1; parent_transcript=GRMZM2G097775_T01; parent_gene=GRMZM2G097775	GRMZM2G097775_P01,GRMZM2G097775_P02	TRUE	TRUE	iyISNLPPDVTVEELQELFGGIGQVGR	95%	n+304 (+304), iTRAQ8plex (+304)	27.92	25.00
4714	seq=translation; coord=8:113008265..113010860:-1; parent_transcript=GRMZM2G044947_T01; parent_gene=GRMZM2G044947	GRMZM2G044947_P01,GRMZM2G044947_P02, GRMZM2G044947_P03	TRUE	TRUE	gANMAIGATTMDFFk	95%	n+304 (+304), K+304 (+304)	55.17	25.00
4715	seq=translation; coord=8:113008265..113010860:-1; parent_transcript=GRMZM2G044947_T01; parent_gene=GRMZM2G044947	GRMZM2G044947_P01,GRMZM2G044947_P02, GRMZM2G044947_P03	TRUE	TRUE	iMYADFYTQVTHMIR	95%	n+304 (+304)	74.87	25.00
4716	seq=translation; coord=8:113008265..113010860:-1; parent_transcript=GRMZM2G044947_T01; parent_gene=GRMZM2G044947	GRMZM2G044947_P01,GRMZM2G044947_P02, GRMZM2G044947_P03	TRUE	TRUE	vIVDFLAEHFGLPLLPASK	93%	n+304 (+304), K+304 (+304)	25.08	25.00
4717	seq=translation; coord=6:129086004..129087221:1; parent_transcript=GRMZM2G447795_T01; parent_gene=GRMZM2G447795	GRMZM2G447795_P01	TRUE	TRUE	aPNYGGVMVWNR	93%	n+304 (+304)	29.69	25.00
4718	seq=translation; coord=6:129086004..129087221:1; parent_transcript=GRMZM2G447795_T01; parent_gene=GRMZM2G447795	GRMZM2G447795_P01	TRUE	TRUE	tGELTVFWGR	95%	n+304 (+304)	47.93	25.00
4719	seq=translation; coord=6:129086004..129087221:1; parent_transcript=GRMZM2G447795_T01; parent_gene=GRMZM2G447795	GRMZM2G447795_P01	TRUE	TRUE	yLYYDLLPk	95%	n+304 (+304), K+304 (+304)	30.18	26.06
4720	seq=translation; coord=1:84413344..84417967:1; parent_transcript=GRMZM2G083173_T01; parent_gene=GRMZM2G083173	GRMZM2G083173_P01,GRMZM2G083173_P02	TRUE	TRUE	gMPLEVITEFFSVGAK	95%	n+304 (+304), K+304 (+304)	33.76	25.02
4721	seq=translation; coord=1:84413344..84417967:1; parent_transcript=GRMZM2G083173_T01; parent_gene=GRMZM2G083173	GRMZM2G083173_P01,GRMZM2G083173_P02	TRUE	TRUE	gmPLEVITEFFSVGAK	95%	n+304 (+304), Oxidation (+16), K+304 (+304)	32.53	25.54
4722	seq=translation; coord=1:84413344..84417967:1; parent_transcript=GRMZM2G083173_T01; parent_gene=GRMZM2G083173	GRMZM2G083173_P01,GRMZM2G083173_P02	TRUE	TRUE	gREDVSGEMALLVEGLGVGk	95%	n+304 (+304), K+304 (+304)	29.98	25.94

4723	seq=translation; coord=1:84413344..84417967:1; parent_transcript=GRMZM2G083173_T01; parent_gene=GRMZM2G083173	GRMZM2G083173_P01,GRMZM2G083173_P02	TRUE	TRUE	sTLFPNFGSMFVSADQQQVvk	95%	n+304 (+304), K+304 (+304)	51.85	25.00
4724	seq=translation; coord=4:14570220..14574637:-1; parent_transcript=GRMZM5G840928_T01; parent_gene=GRMZM5G840928	GRMZM5G840928_P01,GRMZM5G840928_P03, GRMZM5G840928_P04	TRUE	TRUE	dPFLLEcVSNIMR	95%	n+304 (+304), Carbamidomethyl (+57)	39.40	25.00
4725	seq=translation; coord=4:14570220..14574637:-1; parent_transcript=GRMZM5G840928_T01; parent_gene=GRMZM5G840928	GRMZM5G840928_P01,GRMZM5G840928_P03, GRMZM5G840928_P04	TRUE	TRUE	vNPMTLgCiAASLLLR	95%	n+304 (+304), Carbamidomethyl (+57)	58.49	25.00
4726	seq=translation; coord=6:88903392..88908316:-1; parent_transcript=GRMZM2G150256_T01; parent_gene=GRMZM2G150256	GRMZM2G150256_P01	TRUE	TRUE	aFQLYSSGIFDGR	95%	n+304 (+304)	57.66	25.00
4727	seq=translation; coord=6:88903392..88908316:-1; parent_transcript=GRMZM2G150256_T01; parent_gene=GRMZM2G150256	GRMZM2G150256_P01	TRUE	TRUE	dQGQcGAcWAFSAVAVEGINK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	46.58	25.00
4728	seq=translation; coord=6:88903392..88908316:-1; parent_transcript=GRMZM2G150256_T01; parent_gene=GRMZM2G150256	GRMZM2G150256_P01	TRUE	TRUE	nSWGtQWGEAGYVR	95%	n+304 (+304)	53.60	25.00
4729	seq=translation; coord=6:88903392..88908316:-1; parent_transcript=GRMZM2G150256_T01; parent_gene=GRMZM2G150256	GRMZM2G150256_P01	TRUE	TRUE	vVSIDSFER	95%	n+304 (+304)	36.93	25.00
4730	seq=translation; coord=1:198219532..198222746:1; parent_transcript=GRMZM2G318475_T02; parent_gene=GRMZM2G318475	GRMZM2G318475_P02,GRMZM2G318475_P03	TRUE	TRUE	eGQPTAIVEDMR	95%	n+304 (+304)	43.23	25.00
4731	seq=translation; coord=2:210443691..210447027:-1; parent_transcript=GRMZM5G830681_T01; parent_gene=GRMZM5G830681	GRMZM5G830681_P01	TRUE	TRUE	nLDFLEMWR	95%	n+304 (+304)	38.06	25.00
4732	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	TRUE	TRUE	aMEGLASALQEMSAESR	95%	n+304 (+304)	34.84	25.00
4733	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	TRUE	TRUE	aQEVEHLIAEVTR	92%	n+304 (+304)	27.35	25.94
4734	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	TRUE	TRUE	IQQLSQLMEANR	95%	n+304 (+304)	53.62	25.04
4735	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	TRUE	TRUE	nEALSQVDDAVR	95%	n+304 (+304)	33.81	25.26
4736	seq=translation; coord=2:13403335..13406342:-1; parent_transcript=GRMZM2G354053_T01; parent_gene=GRMZM2G354053	GRMZM2G354053_P01	TRUE	TRUE	vLAELER	90%	n+304 (+304)	28.02	25.73
4737	seq=translation; coord=8:171412337..171415029:-1; parent_transcript=GRMZM2G012160_T01; parent_gene=GRMZM2G012160	GRMZM2G012160_P01	TRUE	TRUE	aNALLGFEK	95%	n+304 (+304), K+304 (+304)	41.97	25.85
4738	seq=translation; coord=8:171412337..171415029:-1; parent_transcript=GRMZM2G012160_T01; parent_gene=GRMZM2G012160	GRMZM2G012160_P01	TRUE	TRUE	dVPGNENDLHLQELAR	95%	n+304 (+304)	76.55	25.00
4739	seq=translation; coord=8:171412337..171415029:-1; parent_transcript=GRMZM2G012160_T01; parent_gene=GRMZM2G012160	GRMZM2G012160_P01	TRUE	TRUE	fAVDEHNK	95%	n+304 (+304), K+304 (+304)	42.65	25.00

4740	seq=translation; coord=8:171412337..171415029:-1; parent_transcript=GRMZM2G012160_T01; parent_gene=GRMZM2G012160 seq=translation; coord=3:213775068..213778961:1;	GRMZM2G012160_P01	TRUE	TRUE	tQVVAGTMYLYTIEVK	95%	n+304 (+304), K+304 (+304)	41.27	26.00
4741	parent_transcript=GRMZM2G047298_T01; parent_gene=GRMZM2G047298 seq=translation; coord=3:213775068..213778961:1;	GRMZM2G047298_P01	TRUE	TRUE	aALAAMSPVYLLDVTLLSQLR	95%	n+304 (+304), K+304 (+304)	51.54	25.00
4742	parent_transcript=GRMZM2G047298_T01; parent_gene=GRMZM2G047298 seq=translation; coord=3:213775068..213778961:1;	GRMZM2G047298_P01	TRUE	TRUE	sTYLVDIVEESVGR	95%	n+304 (+304)	42.34	25.74
4743	parent_transcript=GRMZM2G047298_T01; parent_gene=GRMZM2G047298 seq=translation; coord=2:33498879..33500909:-1;	GRMZM2G047298_P01	TRUE	TRUE	wVDSSVDTSR	95%	n+304 (+304)	33.18	25.00
4744	parent_transcript=GRMZM2G051898_T01; parent_gene=GRMZM2G051898 seq=translation; coord=2:33498879..33500909:-1;	GRMZM2G051898_P01	TRUE	TRUE	aVELVSGMETALVQNVATVPGLyR	95%	n+304 (+304), iTRAQ8plex (+304)	40.82	25.00
4745	parent_transcript=GRMZM2G051898_T01; parent_gene=GRMZM2G051898 seq=translation; coord=2:33498879..33500909:-1;	GRMZM2G051898_P01	TRUE	TRUE	gVLDFAAVADQTR	95%	n+304 (+304)	54.79	25.00
4746	parent_transcript=GRMZM2G051898_T01; parent_gene=GRMZM2G051898 seq=translation; coord=4:182566741..182604691:1;	GRMZM2G051898_P01	TRUE	TRUE	nAIPHWEISGYVEYIGSGQk	95%	n+304 (+304), K+304 (+304)	33.70	25.00
4747	parent_transcript=GRMZM2G439339_T04; parent_gene=GRMZM2G439339 seq=translation; coord=4:182566741..182604691:1;	GRMZM2G439339_P04,GRMZM2G439339_P05	TRUE	TRUE	ePSSNPAQAGASSEQR	95%	n+304 (+304)	29.74	25.00
4748	parent_transcript=GRMZM2G439339_T04; parent_gene=GRMZM2G439339 seq=translation; coord=4:182566741..182604691:1;	GRMZM2G439339_P04,GRMZM2G439339_P05	TRUE	TRUE	nTSTVVEAAETR	95%	n+304 (+304)	40.99	25.00
4749	parent_transcript=GRMZM2G439339_T04; parent_gene=GRMZM2G439339 seq=translation; coord=7:173600066..173601522:1;	GRMZM2G439339_P04,GRMZM2G439339_P05	TRUE	TRUE	sEAIIESFDDDR	95%	n+304 (+304)	38.87	25.00
4750	parent_transcript=GRMZM2G348125_T01; parent_gene=GRMZM2G348125 seq=translation; coord=7:173600066..173601522:1;	GRMZM2G348125_P01,GRMZM2G410766_P01	TRUE	TRUE	aLPPQPTVk	90%	n+304 (+304), K+304 (+304)	27.07	25.00
4751	parent_transcript=GRMZM2G348125_T01; parent_gene=GRMZM2G348125 seq=translation; coord=7:173600066..173601522:1;	GRMZM2G348125_P01,GRMZM2G410766_P01	TRUE	TRUE	aNPNYAMSVR	94%	n+304 (+304)	30.95	25.00
4752	parent_transcript=GRMZM2G348125_T01; parent_gene=GRMZM2G348125 seq=translation; coord=1:240863375..240866448:1;	GRMZM2G348125_P01,GRMZM2G410766_P01	TRUE	TRUE	IVPYNPDFLDESVLWTESR	92%	n+304 (+304)	26.91	25.00
4753	parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434 seq=translation; coord=1:240863375..240866448:1;	GRMZM2G124434_P01	TRUE	TRUE	eSDAWPAEPQDAYGLEk	95%	n+304 (+304), K+304 (+304)	44.37	25.00
4754	parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434 seq=translation; coord=1:240863375..240866448:1;	GRMZM2G124434_P01	TRUE	TRUE	iSITGAGGFIGSHIAR	95%	n+304 (+304)	81.48	26.82
4755	parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434 seq=translation; coord=1:240863375..240866448:1;	GRMZM2G124434_P01	TRUE	TRUE	IATEELck	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.38	26.33
4756	parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434 seq=translation; coord=1:240863375..240866448:1;	GRMZM2G124434_P01	TRUE	TRUE	nEHMTEDMFcHEFHLVDLR	95%	n+304 (+304), Carbamidomethyl (+57)	33.66	25.00
4757	parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434	GRMZM2G124434_P01	TRUE	TRUE	sFTFIDeCVEGVLR	95%	n+304 (+304), Carbamidomethyl (+57)	49.46	25.00

4758	seq=translation; coord=1:240863375..240866448:1; parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434	GRMZM2G124434_P01	TRUE	TRUE	tVTAYGEYTYAELER	95%	n+304 (+304)	67.44	25.00
4759	seq=translation; coord=1:240863375..240866448:1; parent_transcript=GRMZM2G124434_T01; parent_gene=GRMZM2G124434	GRMZM2G124434_P01	TRUE	TRUE	vVSTQAPVQLGSLR	95%	n+304 (+304)	38.96	25.00
4760	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01,GRMZM2G033626_P02, GRMZM2G467059_P03	TRUE	TRUE	aGVPMEVMGLMLGEFVDDyTVR	95%	n+304 (+304), iTRAQ8plex (+304)	38.20	25.00
4761	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01,GRMZM2G033626_P02, GRMZM2G467059_P03	TRUE	TRUE	IAIANVGR	87%	n+304 (+304)	25.79	25.00
4762	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01,GRMZM2G033626_P02, GRMZM2G467059_P03	TRUE	TRUE	IINPQTMMLGQEPR	95%	n+304 (+304)	32.23	25.42
4763	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01,GRMZM2G033626_P02, GRMZM2G467059_P03	TRUE	TRUE	mLLNLHK	95%	n+304 (+304), K+304 (+304)	32.73	25.00
4764	seq=translation; coord=3:38743793..38746868:-1; parent_transcript=GRMZM2G033626_T01; parent_gene=GRMZM2G033626	GRMZM2G033626_P01,GRMZM2G033626_P02, GRMZM2G467059_P03	TRUE	TRUE	tNEQTVQEMLNLAIK	95%	n+304 (+304), K+304 (+304)	29.80	25.35
4765	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	TRUE	TRUE	aLGFYDVVFDVAVYAPk	95%	n+304 (+304), K+304 (+304)	40.88	25.31
4766	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	TRUE	TRUE	eHLPPLLR	95%	n+304 (+304)	31.45	25.00
4767	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	TRUE	TRUE	iLGLIANPVk	95%	n+304 (+304), K+304 (+304)	31.57	25.00
4768	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	TRUE	TRUE	IDFIQGRFPR	93%	n+304 (+304)	27.55	25.19
4769	seq=translation; coord=3:71260323..71320829:1; parent_transcript=GRMZM2G314652_T02; parent_gene=GRMZM2G314652	GRMZM2G314652_P02	TRUE	TRUE	IVGYNTDYIGAISAIEDGIGGPGSk	95%	n+304 (+304), K+304 (+304)	29.48	25.00
4770	seq=translation; coord=1:226551729..226556786:-1; parent_transcript=GRMZM2G131769_T01; parent_gene=GRMZM2G131769	GRMZM2G131769_P01	TRUE	TRUE	eVGSAAELQAAVAGAR	95%	n+304 (+304)	62.03	25.28
4771	seq=translation; coord=1:226551729..226556786:-1; parent_transcript=GRMZM2G131769_T01; parent_gene=GRMZM2G131769	GRMZM2G131769_P01	TRUE	TRUE	nEEAGEPESATEk	95%	n+304 (+304), K+304 (+304)	43.10	25.00
4772	seq=translation; coord=2:224332394..224344331:1; parent_transcript=GRMZM2G169095_T01; parent_gene=GRMZM2G169095	GRMZM2G169095_P01	TRUE	TRUE	eALLWTDGR	92%	n+304 (+304)	29.21	25.09
4773	seq=translation; coord=2:224332394..224344331:1; parent_transcript=GRMZM2G169095_T01; parent_gene=GRMZM2G169095	GRMZM2G169095_P01	TRUE	TRUE	eFISGFTGSAGLALITMk	95%	n+304 (+304), K+304 (+304)	29.51	25.00
4774	seq=translation; coord=2:224332394..224344331:1; parent_transcript=GRMZM2G169095_T01; parent_gene=GRMZM2G169095	GRMZM2G169095_P01	TRUE	TRUE	iLEPHLNEQEk	95%	n+304 (+304), K+304 (+304)	35.22	26.54
4775	seq=translation; coord=2:224332394..224344331:1; parent_transcript=GRMZM2G169095_T01; parent_gene=GRMZM2G169095	GRMZM2G169095_P01	TRUE	TRUE	nPTELDGLR	89%	n+304 (+304)	26.11	25.02

4776	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	TRUE	TRUE	gSSYPcTER	86%	n+304 (+304), Carbamidomethyl (+57)	25.44	25.00
4777	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	TRUE	TRUE	iRPDGATLFLNAYR	95%	n+304 (+304)	34.36	25.66
4778	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	TRUE	TRUE	iWVFSGDtdAVVPLTATR	95%	n+304 (+304)	67.56	25.31
4779	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	TRUE	TRUE	qALILFR	85%	n+304 (+304)	25.04	25.00
4780	seq=translation; coord=6:134096678..134101001:-1; parent_transcript=GRMZM2G339091_T01; parent_gene=GRMZM2G339091	GRMZM2G339091_P01	TRUE	TRUE	ySIDALNLPTVVSWYPWYDAK	95%	n+304 (+304), K+304 (+304)	34.97	25.08
4781	seq=translation; coord=1:22629310..22633408:1; parent_transcript=GRMZM2G055025_T01; parent_gene=GRMZM2G055025	GRMZM2G055025_P01	TRUE	TRUE	aSAVAELTR	94%	n+304 (+304)	31.06	25.75
4782	seq=translation; coord=1:22629310..22633408:1; parent_transcript=GRMZM2G055025_T01; parent_gene=GRMZM2G055025	GRMZM2G055025_P01	TRUE	TRUE	fGLALALKP	95%	n+304 (+304), K+304 (+304)	28.92	25.00
4783	seq=translation; coord=1:22629310..22633408:1; parent_transcript=GRMZM2G055025_T01; parent_gene=GRMZM2G055025	GRMZM2G055025_P01	TRUE	TRUE	gPGLFSDIGk	92%	n+304 (+304), K+304 (+304)	29.99	25.75
4784	seq=translation; coord=1:22629310..22633408:1; parent_transcript=GRMZM2G055025_T01; parent_gene=GRMZM2G055025	GRMZM2G055025_P01	TRUE	TRUE	ITISTASASGLTSTAVk	95%	n+304 (+304), K+304 (+304)	62.82	25.00
4785	seq=translation; coord=1:5345118..5348832:1; parent_transcript=GRMZM2G119494_T01; parent_gene=GRMZM2G119494	GRMZM2G119494_P01	TRUE	TRUE	aEDSVAINTESAVR	95%	n+304 (+304)	68.50	25.00
4786	seq=translation; coord=1:5345118..5348832:1; parent_transcript=GRMZM2G119494_T01; parent_gene=GRMZM2G119494	GRMZM2G119494_P01	TRUE	TRUE	hWPLIAPLPsyGR	95%	n+304 (+304)	36.78	25.49
4787	seq=translation; coord=1:5345118..5348832:1; parent_transcript=GRMZM2G119494_T01; parent_gene=GRMZM2G119494	GRMZM2G119494_P01	TRUE	TRUE	ITcVSPTSAMIALGSEMSSGIR	95%	n+304 (+304), Carbamidomethyl (+57)	58.69	25.00
4788	seq=translation; coord=1:5345118..5348832:1; parent_transcript=GRMZM2G119494_T01; parent_gene=GRMZM2G119494	GRMZM2G119494_P01	TRUE	TRUE	vTEYGAVGDGR	93%	n+304 (+304)	30.04	25.00
4789	seq=translation; coord=5:175584484..175585836:1; parent_transcript=GRMZM2G049675_T01; parent_gene=GRMZM2G049675	GRMZM2G049675_P01,GRMZM2G128219_P01	TRUE	TRUE	gAVLIHPFWWGSEAVGEEPR	95%	n+304 (+304)	42.15	25.00
4790	seq=translation; coord=5:175584484..175585836:1; parent_transcript=GRMZM2G049675_T01; parent_gene=GRMZM2G049675	GRMZM2G049675_P01,GRMZM2G128219_P01	TRUE	TRUE	IAPEHPLPAGYDDcLAALK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.01	25.72
4791	seq=translation; coord=1:250092343..250095992:-1; parent_transcript=GRMZM2G049675_T01; parent_gene=GRMZM2G049675	GRMZM2G049675_P01,GRMZM2G128219_P01	TRUE	TRUE	wVLSAADPWVAAHGDLAR	95%	n+304 (+304)	92.01	25.48
4792	seq=translation; coord=1:250092343..250095992:-1; parent_transcript=GRMZM2G364069_T01; parent_gene=GRMZM2G364069	GRMZM2G364069_P01	TRUE	TRUE	qAHAAQEAYEEDDEMPGGAQR	95%	n+304 (+304)	58.38	25.00
4793	seq=translation; coord=1:250092343..250095992:-1; parent_transcript=GRMZM2G364069_T01; parent_gene=GRMZM2G364069	GRMZM2G364069_P01	TRUE	TRUE	vLEVHVEK	95%	n+304 (+304), K+304 (+304)	31.14	25.00

4794	seq=translation; coord=1:65994545..65996015:-1; parent_transcript=GRMZM2G004298_T01; parent_gene=GRMZM2G004298	GRMZM2G004298_P01,GRMZM2G004298_P02, GRMZM2G004298_P03,GRMZM2G096100_P01, GRMZM2G096100_P02,GRMZM2G096100_P03	TRUE	TRUE	gDVFVFPR	95%	n+304 (+304)	31.72	25.00
4795	seq=translation; coord=1:65994545..65996015:-1; parent_transcript=GRMZM2G004298_T01; parent_gene=GRMZM2G004298	GRMZM2G004298_P01,GRMZM2G004298_P02, GRMZM2G004298_P03,GRMZM2G096100_P01, GRMZM2G096100_P02,GRMZM2G096100_P03	TRUE	TRUE	nPGNTNNPAGSVVTAANVEK	95%	n+304 (+304), K+304 (+304)	32.07	25.58
4796	seq=translation; coord=1:274494460..274510748:-1; parent_transcript=GRMZM2G396451_T02; parent_gene=GRMZM2G396451	GRMZM2G396451_P02,GRMZM2G396451_P03	TRUE	TRUE	dSVETSPLLQYR	95%	n+304 (+304)	44.48	25.01
4797	seq=translation; coord=1:274494460..274510748:-1; parent_transcript=GRMZM2G396451_T02; parent_gene=GRMZM2G396451	GRMZM2G396451_P02,GRMZM2G396451_P03	TRUE	TRUE	eDYGELSSIAR	95%	n+304 (+304)	40.56	25.00
4798	seq=translation; coord=1:274494460..274510748:-1; parent_transcript=GRMZM2G396451_T02; parent_gene=GRMZM2G396451	GRMZM2G396451_P02,GRMZM2G396451_P03	TRUE	TRUE	vVVDEGQALIDSVTGLPk	95%	n+304 (+304), K+304 (+304)	55.88	25.00
4799	seq=translation; coord=7:159001810..159027357:-1; parent_transcript=GRMZM2G081155_T01; parent_gene=GRMZM2G081155	GRMZM2G081155_P01,GRMZM2G081155_P02, GRMZM2G081155_P03	TRUE	TRUE	fSPDAIQNVNLNLTPTVTR	95%	n+304 (+304)	71.41	25.49
4800	seq=translation; coord=7:159001810..159027357:-1; parent_transcript=GRMZM2G081155_T01; parent_gene=GRMZM2G081155	GRMZM2G081155_P01,GRMZM2G081155_P02, GRMZM2G081155_P03	TRUE	TRUE	qNVLLQLLALVGk	95%	n+304 (+304), K+304 (+304)	28.95	25.00
4801	seq=translation; coord=7:159001810..159027357:-1; parent_transcript=GRMZM2G081155_T01; parent_gene=GRMZM2G081155	GRMZM2G081155_P01,GRMZM2G081155_P02, GRMZM2G081155_P03	TRUE	TRUE	sVEQLGYIALLR	95%	n+304 (+304)	39.12	26.01
4802	seq=translation; coord=2:62991591..62998602:-1; parent_transcript=GRMZM2G171688_T01; parent_gene=GRMZM2G171688	GRMZM2G171688_P01	TRUE	TRUE	IVVESLEAMTETEALDMk	95%	n+304 (+304), K+304 (+304)	67.51	25.48
4803	seq=translation; coord=2:62991591..62998602:-1; parent_transcript=GRMZM2G171688_T01; parent_gene=GRMZM2G171688	GRMZM2G171688_P01	TRUE	TRUE	vLAILLDLTAEQLGAK	95%	n+304 (+304), K+304 (+304)	45.02	25.00
4804	seq=translation; coord=5:13253262..13257697:-1; parent_transcript=GRMZM2G076524_T01; parent_gene=GRMZM2G076524	GRMZM2G076524_P01,GRMZM2G076524_P02	TRUE	TRUE	aAEAcEEFSGTLVTLR	95%	n+304 (+304), Carbamidomethyl (+57)	86.74	25.00
4805	seq=translation; coord=5:13253262..13257697:-1; parent_transcript=GRMZM2G076524_T01; parent_gene=GRMZM2G076524	GRMZM2G076524_P01,GRMZM2G076524_P02	TRUE	TRUE	dLLAASWNELPDSLVAEAK	95%	n+304 (+304), K+304 (+304)	67.46	25.75
4806	seq=translation; coord=5:13253262..13257697:-1; parent_transcript=GRMZM2G076524_T01; parent_gene=GRMZM2G076524	GRMZM2G076524_P01,GRMZM2G076524_P02	TRUE	TRUE	mIHLk	92%	n+304 (+304), K+304 (+304)	26.16	25.00
4807	seq=translation; coord=8:2052922..2061036:1; parent_transcript=GRMZM2G052875_T01; parent_gene=GRMZM2G052875	GRMZM2G052875_P01,GRMZM2G052875_P02	TRUE	TRUE	dkEFYSFYDQcFETk	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	32.84	25.00
4808	seq=translation; coord=8:2052922..2061036:1; parent_transcript=GRMZM2G052875_T01; parent_gene=GRMZM2G052875	GRMZM2G052875_P01,GRMZM2G052875_P02	TRUE	TRUE	eQLNDDFcDcPDGTDEPGTSAcPEAK	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	48.57	25.00
4809	seq=translation; coord=8:2052922..2061036:1; parent_transcript=GRMZM2G052875_T01; parent_gene=GRMZM2G052875	GRMZM2G052875_P01,GRMZM2G052875_P02	TRUE	TRUE	tPVDLSEASR	89%	n+304 (+304)	26.86	25.00

4810	seq=translation; coord=1:194657095..194659202:-1; parent_transcript=GRMZM2G083725_T01; parent_gene=GRMZM2G083725 seq=translation; coord=1:194657095..194659202:-1;	GRMZM2G083725_P01,GRMZM2G083725_P02	TRUE	TRUE	aRPEcLcYIIQQTHTGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	39.57	25.00
4811	parent_transcript=GRMZM2G083725_T01; parent_gene=GRMZM2G083725 seq=translation; coord=3:154973863..154975444:-1;	GRMZM2G083725_P01,GRMZM2G083725_P02	TRUE	TRUE	nQVQSLGLR	90%	n+304 (+304)	29.71	27.37
4812	parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246 seq=translation; coord=3:154973863..154975444:-1;	GRMZM2G146246_P02	TRUE	TRUE	gLDFEIVPVDLTGAHK	95%	n+304 (+304), K+304 (+304)	55.75	25.48
4813	parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246 seq=translation; coord=3:154973863..154975444:-1;	GRMZM2G146246_P02	TRUE	TRUE	IYGMPLSPNVVR	95%	n+304 (+304)	32.57	25.45
4814	parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246 seq=translation; coord=3:154973863..154975444:-1;	GRMZM2G146246_P02	TRUE	TRUE	vATVLNEK	92%	n+304 (+304), K+304 (+304)	31.32	27.36
4815	parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246 seq=translation; coord=3:154973863..154975444:-1;	GRMZM2G146246_P02	TRUE	TRUE	vLDVYEAHLAR	95%	n+304 (+304)	65.50	26.30
4816	parent_transcript=GRMZM2G146246_T02; parent_gene=GRMZM2G146246 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G146246_P02	TRUE	TRUE	vLDVyEAHLAR	94%	n+304 (+304), iTRAQ8plex (+304)	25.69	25.16
4817	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G088565_P01	TRUE	TRUE	aDEAAAAAGSk	95%	n+304 (+304), K+304 (+304)	54.97	25.21
4818	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G088565_P01	TRUE	TRUE	gLAEMFGDLR	95%	n+304 (+304)	41.00	25.00
4819	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G088565_P01	TRUE	TRUE	gYDPEVIDIR	93%	n+304 (+304)	28.77	25.00
4820	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G088565_P01	TRUE	TRUE	sENPVVLFHEHLLYNLk	95%	n+304 (+304), K+304 (+304)	40.60	25.00
4821	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=1:174313373..174317518:1;	GRMZM2G088565_P01	TRUE	TRUE	sGGHELLMFELR	95%	n+304 (+304)	29.03	25.13
4822	parent_transcript=GRMZM2G088565_T01; parent_gene=GRMZM2G088565 seq=translation; coord=7:137275571..137279379:1;	GRMZM2G088565_P01	TRUE	TRUE	vLIVEEcMR	95%	n+304 (+304), Carbamidomethyl (+57)	38.92	25.00
4823	parent_transcript=GRMZM2G458164_T01; parent_gene=GRMZM2G458164 seq=translation; coord=7:137275571..137279379:1;	GRMZM2G458164_P01	TRUE	TRUE	gPIWcVLSAAASnk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.44	26.19
4824	parent_transcript=GRMZM2G458164_T01; parent_gene=GRMZM2G458164 seq=translation; coord=7:137275571..137279379:1;	GRMZM2G458164_P01	TRUE	TRUE	mPVFVFSLYNEDLkPGPGTER	95%	n+304 (+304), K+304 (+304)	29.39	25.44
4825	parent_transcript=GRMZM2G458164_T01; parent_gene=GRMZM2G458164 seq=translation; coord=7:137275571..137279379:1;	GRMZM2G458164_P01	TRUE	TRUE	vADDIPSPWR	93%	n+304 (+304)	29.26	25.00
4826	parent_transcript=GRMZM2G458164_T01; parent_gene=GRMZM2G458164 seq=translation; coord=1:296874949..296877709:-1;	GRMZM2G458164_P01	TRUE	TRUE	wVAENLVPPYPATR	95%	n+304 (+304)	36.99	25.31
4827	parent_transcript=GRMZM2G035017_T01; parent_gene=GRMZM2G035017	GRMZM2G035017_P01	TRUE	TRUE	gGFDTIHVEDSMGHQFATR	95%	n+304 (+304)	34.38	25.00

4828	seq=translation; coord=2:160538409..160543692:1; parent_transcript=GRMZM2G151549_T01; parent_gene=GRMZM2G151549	GRMZM2G151549_P01,GRMZM2G151549_P02	TRUE	TRUE	hLVFPLLEFLQER	95%	n+304 (+304)	35.19	25.80
4829	seq=translation; coord=2:160538409..160543692:1; parent_transcript=GRMZM2G151549_T01; parent_gene=GRMZM2G151549	GRMZM2G151549_P01,GRMZM2G151549_P02	TRUE	TRUE	lIEcEQVILNDPFLGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	56.42	25.39
4830	seq=translation; coord=2:160538409..160543692:1; parent_transcript=GRMZM2G151549_T01; parent_gene=GRMZM2G151549	GRMZM2G151549_P01,GRMZM2G151549_P02	TRUE	TRUE	sLEEAAPLVAFLQNPQLVQEFRPDK	95%	n+304 (+304), K+304 (+304)	29.51	25.00
4831	seq=translation; coord=2:160538409..160543692:1; parent_transcript=GRMZM2G151549_T01; parent_gene=GRMZM2G151549	GRMZM2G151549_P01,GRMZM2G151549_P02	TRUE	TRUE	yQIGPDQIEALYQYAK	95%	n+304 (+304), K+304 (+304)	59.92	25.01
4832	seq=translation; coord=9:26618156..26621708:1; parent_transcript=GRMZM2G051890_T01; parent_gene=GRMZM2G051890	GRMZM2G051890_P01	TRUE	TRUE	aEDVVSTMLAK	95%	n+304 (+304), K+304 (+304)	31.71	26.60
4833	seq=translation; coord=8:135054057..135061548:1; parent_transcript=GRMZM2G098039_T01; parent_gene=GRMZM2G098039	GRMZM2G098039_P01	TRUE	TRUE	aAGFDGELDASNIR	91%	n+304 (+304)	27.81	25.00
4834	seq=translation; coord=3:205620317..205627720:1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01,GRMZM2G157317_P03	TRUE	TRUE	aVFSADSALYEYLDGGWk	95%	n+304 (+304), K+304 (+304)	61.28	25.00
4835	seq=translation; coord=3:205620317..205627720:1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01,GRMZM2G157317_P03	TRUE	TRUE	dNPEPDDEGTEQEMGTFk	95%	n+304 (+304), K+304 (+304)	33.79	25.00
4836	seq=translation; coord=3:205620317..205627720:1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01,GRMZM2G157317_P03	TRUE	TRUE	gQTPSATPLFSfk	95%	n+304 (+304), K+304 (+304)	32.16	25.68
4837	seq=translation; coord=3:205620317..205627720:1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01,GRMZM2G157317_P03	TRUE	TRUE	mFAMTEGPVETGEENEk	95%	n+304 (+304), K+304 (+304)	39.45	25.00
4838	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G157317_T01; parent_gene=GRMZM2G157317	GRMZM2G157317_P01,GRMZM2G157317_P03	TRUE	TRUE	vVVGEPNEGScMPSEVEGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	74.56	25.00
4839	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	eLSGSDIFGPPPEIPARPLAAR	95%	n+304 (+304)	38.38	25.25
4840	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	eLSGTLEDADAK	95%	n+304 (+304), K+304 (+304)	45.73	25.22
4841	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	eMGGSgIFAEk	95%	n+304 (+304), K+304 (+304)	36.10	25.93
4842	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	eMSGSDIFADGTPAPR	95%	n+304 (+304)	59.06	25.00
4843	seq=translation; coord=10:121538895..121542946:-1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	nMELQGNVDFSLPQR	95%	n+304 (+304)	55.59	25.00
4844	seq=translation; coord=7:155559747..155562921:1; parent_transcript=GRMZM2G381267_T01; parent_gene=GRMZM2G381267	GRMZM2G381267_P01,GRMZM2G381267_P02	TRUE	TRUE	vSNPAGGPSNISFSEEPVVK	95%	n+304 (+304), K+304 (+304)	44.04	25.22
4845	parent_gene=GRMZM2G108285	GRMZM2G108285_P01	TRUE	TRUE	eSELIQENYLGVr	95%	n+304 (+304)	47.45	25.25

4846	seq=translation; coord=7:155559747..155562921:1; parent_transcript=GRMZM2G108285_T01; parent_gene=GRMZM2G108285	GRMZM2G108285_P01	TRUE	TRUE	gTLGEAVDMETIHK	95%	n+304 (+304), K+304 (+304)	47.23	25.22
4847	seq=translation; coord=7:155559747..155562921:1; parent_transcript=GRMZM2G108285_T01; parent_gene=GRMZM2G108285	GRMZM2G108285_P01	TRUE	TRUE	IVVDNFLMGWWDHVEK	95%	n+304 (+304), K+304 (+304)	56.82	25.44
4848	seq=translation; coord=7:155559747..155562921:1; parent_transcript=GRMZM2G108285_T01; parent_gene=GRMZM2G108285	GRMZM2G108285_P01	TRUE	TRUE	wGEHELDYLLFIVR	95%	n+304 (+304)	42.83	25.44
4849	seq=translation; coord=8:13369483..13372340:-1; parent_transcript=GRMZM2G119361_T01; parent_gene=GRMZM2G119361	GRMZM2G119361_P01,GRMZM2G119361_P02	TRUE	TRUE	gGDSWDEPFPSAAAAAGGGGR	95%	n+304 (+304)	98.87	25.00
4850	seq=translation; coord=8:13369483..13372340:-1; parent_transcript=GRMZM2G119361_T01; parent_gene=GRMZM2G119361	GRMZM2G119361_P01,GRMZM2G119361_P02	TRUE	TRUE	IFLFPATPESSSSLGSLDDSSk	95%	n+304 (+304), K+304 (+304)	38.73	25.00
4851	seq=translation; coord=8:13369483..13372340:-1; parent_transcript=GRMZM2G119361_T01; parent_gene=GRMZM2G119361	GRMZM2G119361_P01,GRMZM2G119361_P02	TRUE	TRUE	qEVAIVDPTNR	95%	n+304 (+304)	31.61	25.81
4852	seq=translation; coord=8:13369483..13372340:-1; parent_transcript=GRMZM2G119361_T01; parent_gene=GRMZM2G119361	GRMZM2G119361_P01,GRMZM2G119361_P02	TRUE	TRUE	vFSDDdk	93%	n+304 (+304), K+304 (+304)	28.35	25.00
4853	seq=translation; coord=1:296017136..296022027:1; parent_transcript=GRMZM2G053458_T01; parent_gene=GRMZM2G053458	GRMZM2G053458_P01,GRMZM2G053458_P02	TRUE	TRUE	aGAcStcAGk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	34.02	25.00
4854	seq=translation; coord=1:296017136..296022027:1; parent_transcript=GRMZM2G053458_T01; parent_gene=GRMZM2G053458	GRMZM2G053458_P01,GRMZM2G053458_P02	TRUE	TRUE	IVGPEGEEHEFDAPDDAYILDAEAETAGVELPYScR	95%	n+304 (+304), Carbamidomethyl (+57)	31.35	25.00
4855	seq=translation; coord=4:1508758..1509325:-1; parent_transcript=GRMZM2G107302_T01; parent_gene=GRMZM2G107302	GRMZM2G107302_P01	TRUE	TRUE	aEGSSNYASAcEPAVAPfk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	50.30	25.00
4856	seq=translation; coord=4:1508758..1509325:-1; parent_transcript=GRMZM2G107302_T01; parent_gene=GRMZM2G107302	GRMZM2G107302_P01	TRUE	TRUE	ecTDVNYDcNR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	36.75	25.00
4857	seq=translation; coord=10:4071331..4073937:-1; parent_transcript=GRMZM2G129804_T01; parent_gene=GRMZM2G129804	GRMZM2G129804_P01	TRUE	TRUE	iIDFDLPITVR	95%	n+304 (+304)	36.40	25.00
4858	seq=translation; coord=10:4071331..4073937:-1; parent_transcript=GRMZM2G129804_T01; parent_gene=GRMZM2G129804	GRMZM2G129804_P01	TRUE	TRUE	vGTNVEVDGAPWk	95%	n+304 (+304), K+304 (+304)	44.18	25.00
4859	seq=translation; coord=9:25038179..25042320:-1; parent_transcript=GRMZM2G051247_T01; parent_gene=GRMZM2G051247	GRMZM2G051247_P01	TRUE	TRUE	dTESLNASYER	95%	n+304 (+304)	36.59	25.00
4860	seq=translation; coord=1:216692560..216696036:1; parent_transcript=GRMZM2G167669_T01; parent_gene=GRMZM2G167669	GRMZM2G167669_P01	TRUE	TRUE	aILFFEGQR	92%	n+304 (+304)	27.59	25.93
4861	seq=translation; coord=1:216692560..216696036:1; parent_transcript=GRMZM2G167669_T01; parent_gene=GRMZM2G167669	GRMZM2G167669_P01	TRUE	TRUE	sAIQWGADFLLR	95%	n+304 (+304)	41.14	25.00
4862	seq=translation; coord=1:216692560..216696036:1; parent_transcript=GRMZM2G167669_T01; parent_gene=GRMZM2G167669	GRMZM2G167669_P01	TRUE	TRUE	sSPGSEAAGEAAAAAAYLVFR	95%	n+304 (+304)	35.83	25.00

4863	seq=translation; coord=1:216692560..216696036:1; parent_transcript=GRMZM2G167669_T01; parent_gene=GRMZM2G167669 seq=translation; coord=1:262391932..262394279:1;	GRMZM2G167669_P01	TRUE	TRUE	tLATQLLAASR	95%	n+304 (+304)	32.72	25.00
4864	parent_transcript=GRMZM2G063503_T02; parent_gene=GRMZM2G063503 seq=translation; coord=1:262391932..262394279:1;	GRMZM2G063503_P02	TRUE	TRUE	cANIFEALVGTLR	95%	Carbamidomethyl (+57), n+304 (+304)	46.32	25.00
4865	parent_transcript=GRMZM2G063503_T02; parent_gene=GRMZM2G063503 seq=translation; coord=1:262391932..262394279:1;	GRMZM2G063503_P02	TRUE	TRUE	fGVLFNDDR	91%	n+304 (+304)	27.87	25.00
4866	parent_transcript=GRMZM2G063503_T02; parent_gene=GRMZM2G063503 seq=translation; coord=1:262391932..262394279:1;	GRMZM2G063503_P02	TRUE	TRUE	IGQQQPDGSYk	95%	n+304 (+304), K+304 (+304)	49.99	25.84
4867	parent_transcript=GRMZM2G152111_T01; parent_gene=GRMZM2G152111 seq=translation; coord=5:62197397..62202236:1;	GRMZM2G152111_P01,GRMZM2G152111_P02, GRMZM2G152111_P03,GRMZM2G152111_P04, GRMZM2G152111_P06	TRUE	TRUE	gFAFVSMDTVEEAER	95%	n+304 (+304)	62.04	25.00
4868	parent_transcript=GRMZM2G152111_T01; parent_gene=GRMZM2G152111 seq=translation; coord=5:62197397..62202236:1;	GRMZM2G152111_P01,GRMZM2G152111_P02, GRMZM2G152111_P03,GRMZM2G152111_P04, GRMZM2G152111_P06	TRUE	TRUE	gNTLYVTGLSSR	95%	n+304 (+304)	41.15	25.00
4869	parent_transcript=GRMZM2G047732_T01; parent_gene=GRMZM2G047732 seq=translation; coord=8:39126474..39127702:1;	GRMZM2G047732_P01,GRMZM2G047732_P02	TRUE	TRUE	ecPNAEcGAGVFMANHFR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	75.01	25.00
4870	parent_transcript=GRMZM2G047732_T01; parent_gene=GRMZM2G047732 seq=translation; coord=8:39126474..39127702:1;	GRMZM2G047732_P01,GRMZM2G047732_P02	TRUE	TRUE	IAVLQFYk	91%	n+304 (+304), K+304 (+304)	25.93	25.00
4871	parent_transcript=GRMZM2G034326_T01; parent_gene=GRMZM2G034326 seq=translation; coord=5:1122734..1125202:1;	GRMZM2G034326_P01,GRMZM2G034326_P02, GRMZM2G034326_P03,GRMZM2G034326_P04	TRUE	TRUE	fNMVIAPTLNLDGTPDTGyYtQAGR	95%	n+304 (+304), iTRAQ8plex (+304)	33.36	25.13
4872	parent_transcript=GRMZM2G034326_T01; parent_gene=GRMZM2G034326 seq=translation; coord=5:1122734..1125202:1;	GRMZM2G034326_P01,GRMZM2G034326_P02, GRMZM2G034326_P03,GRMZM2G034326_P04	TRUE	TRUE	gDPSTAASFELDQR	95%	n+304 (+304)	63.46	25.00
4873	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	aIGDPILFR	95%	n+304 (+304)	34.89	25.00
4874	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	aYELPPGIPShk	92%	n+304 (+304), K+304 (+304)	27.27	25.53
4875	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	fAEYSVSGLTDASeK	94%	n+304 (+304), K+304 (+304)	28.49	25.00
4876	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	iDDIYAVELIGGATR	95%	n+304 (+304)	34.53	25.00
4877	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	ISEVQDWLYMDGEDAQANEFk	94%	n+304 (+304), K+304 (+304)	28.03	25.00
4878	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	IYLDLQk	95%	n+304 (+304), K+304 (+304)	40.87	25.00
4879	parent_transcript=GRMZM2G020040_T01; parent_gene=GRMZM2G020040 seq=translation; coord=5:202050924..202059781:1;	GRMZM2G020040_P01,GRMZM2G020040_P02	TRUE	TRUE	vDEVVSEAEk	95%	n+304 (+304), K+304 (+304)	59.35	25.15
4880	parent_transcript=GRMZM2G163437_T01; parent_gene=GRMZM2G163437	GRMZM2G163437_P01,GRMZM2G163437_P02	TRUE	TRUE	eTDGYFIk	95%	n+304 (+304), K+304 (+304)	34.09	25.34

4881	seq=translation; coord=1:221648603..221653196:1; parent_transcript=GRMZM2G163437_T01; parent_gene=GRMZM2G163437	GRMZM2G163437_P01,GRMZM2G163437_P02	TRUE	TRUE	iLNADNVQEAAAR	95%	n+304 (+304)	60.29	25.45
4882	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	TRUE	TRUE	gLTHDEMLLLPTGPR	95%	n+304 (+304)	71.49	25.00
4883	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	TRUE	TRUE	iSQLESQLEQLSR	95%	n+304 (+304)	51.05	26.37
4884	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	TRUE	TRUE	kIDIELEHR	95%	K+304 (+304), n+304 (+304)	40.81	25.00
4885	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	TRUE	TRUE	sYGGGSGFGGPGGER	95%	n+304 (+304)	49.15	25.00
4886	seq=translation; coord=10:125428223..125432495:1; parent_transcript=GRMZM2G066815_T01; parent_gene=GRMZM2G066815	GRMZM2G066815_P01	TRUE	TRUE	yPSLGSGGGFR	95%	n+304 (+304)	29.72	25.00
4887	seq=translation; coord=10:116860755..116863190:1; parent_transcript=GRMZM2G043737_T01; parent_gene=GRMZM2G043737	GRMZM2G043737_P01,GRMZM2G043737_P05, GRMZM2G050925_P01	TRUE	TRUE	sGAPAEFQPSFR	95%	n+304 (+304)	40.48	25.00
4888	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	TRUE	TRUE	aLSEAISGAVQR	95%	n+304 (+304)	34.91	26.68
4889	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	TRUE	TRUE	eVEGDGVSPR	95%	n+304 (+304)	33.07	25.00
4890	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	TRUE	TRUE	nIGVGAEEDDGAGGQAQLHR	95%	n+304 (+304)	106.64	25.00
4891	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	TRUE	TRUE	qLASTVYEK	95%	n+304 (+304), K+304 (+304)	36.01	25.00
4892	seq=translation; coord=5:23763272..23765390:-1; parent_transcript=GRMZM2G376743_T01; parent_gene=GRMZM2G376743	GRMZM2G376743_P01	TRUE	TRUE	qLASTVYEK	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	35.86	25.00
4893	seq=translation; coord=9:77151999..77153846:1; parent_transcript=GRMZM2G080839_T01; parent_gene=GRMZM2G080839	GRMZM2G080839_P01	TRUE	TRUE	dLYAFMAPYVSSNPR	90%	n+304 (+304)	25.25	25.00
4894	seq=translation; coord=9:77151999..77153846:1; parent_transcript=GRMZM2G080839_T01; parent_gene=GRMZM2G080839	GRMZM2G080839_P01	TRUE	TRUE	dVWANIFSR	95%	n+304 (+304)	36.42	25.00
4895	seq=translation; coord=9:77151999..77153846:1; parent_transcript=GRMZM2G080839_T01; parent_gene=GRMZM2G080839	GRMZM2G080839_P01	TRUE	TRUE	kYGLAIDNVLDVAVLDAR	95%	K+304 (+304), n+304 (+304)	52.97	25.00
4896	seq=translation; coord=9:77151999..77153846:1; parent_transcript=GRMZM2G080839_T01; parent_gene=GRMZM2G080839	GRMZM2G080839_P01	TRUE	TRUE	wQQVAPALPDDL FIR	87%	n+304 (+304)	26.73	26.00
4897	seq=translation; coord=4:9657544..9658965:-1; parent_transcript=GRMZM2G117989_T01; parent_gene=GRMZM2G117989	GRMZM2G117989_P01,GRMZM2G117989_P02, GRMZM2G117989_P03,GRMZM2G117989_P04, GRMZM2G117989_P05,GRMZM2G117989_P06	TRUE	TRUE	aTGASIVAR	95%	n+304 (+304)	37.08	25.02

4898	seq=translation; coord=4:9657544..9658965:-1; parent_transcript=GRMZM2G117989_T01; parent_gene=GRMZM2G117989	GRMZM2G117989_P01,GRMZM2G117989_P02, GRMZM2G117989_P03,GRMZM2G117989_P04, GRMZM2G117989_P05,GRMZM2G117989_P06	TRUE	TRUE	hGWTAfFcGPAGQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	47.83	25.00
4899	seq=translation; coord=4:9657544..9658965:-1; parent_transcript=GRMZM2G117989_T01; parent_gene=GRMZM2G117989	GRMZM2G117989_P01,GRMZM2G117989_P02, GRMZM2G117989_P03,GRMZM2G117989_P04, GRMZM2G117989_P05,GRMZM2G117989_P06	TRUE	TRUE	vSAYcATWDADkPLSWR	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.67	25.00
4900	seq=translation; coord=5:6444041..6445037:1; parent_transcript=GRMZM2G077034_T01; parent_gene=GRMZM2G077034	GRMZM2G077034_P01	TRUE	TRUE	hDDcLk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.70	25.00
4901	seq=translation; coord=5:6444041..6445037:1; parent_transcript=GRMZM2G077034_T01; parent_gene=GRMZM2G077034	GRMZM2G077034_P01	TRUE	TRUE	vSMAGSGFcDGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	52.48	25.00
4902	seq=translation; coord=5:6444041..6445037:1; parent_transcript=GRMZM2G077034_T01; parent_gene=GRMZM2G077034	GRMZM2G077034_P01	TRUE	TRUE	vSmAGSGFcDGk	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	38.00	25.00
4903	seq=translation; coord=5:6444041..6445037:1; parent_transcript=GRMZM2G077034_T01; parent_gene=GRMZM2G077034	GRMZM2G077034_P01	TRUE	TRUE	ycGlccATcNcVPSGTAGNk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	31.25	25.00
4904	seq=translation; coord=5:193174093..193205154:1; parent_transcript=GRMZM5G883741_T02; parent_gene=GRMZM5G883741	GRMZM5G883741_P02	TRUE	TRUE	eLVLFIER	92%	n+304 (+304)	28.44	25.00
4905	seq=translation; coord=5:193174093..193205154:1; parent_transcript=GRMZM5G883741_T02; parent_gene=GRMZM5G883741	GRMZM5G883741_P02	TRUE	TRUE	sIPEQLDEEVR	95%	n+304 (+304)	53.71	25.00
4906	seq=translation; coord=1:27178033..27184068:-1; parent_transcript=GRMZM5G891739_T01; parent_gene=GRMZM5G891739	GRMZM5G891739_P01	TRUE	TRUE	aVVVHADPDDLGR	95%	n+304 (+304)	36.30	25.43
4907	seq=translation; coord=1:27178033..27184068:-1; parent_transcript=GRMZM5G891739_T01; parent_gene=GRMZM5G891739	GRMZM5G891739_P01	TRUE	TRUE	gVALIGGSANSTVAGVIHFFEDPSTR	95%	n+304 (+304)	56.26	25.65
4908	seq=translation; coord=1:27178033..27184068:-1; parent_transcript=GRMZM5G891739_T01; parent_gene=GRMZM5G891739	GRMZM5G891739_P01	TRUE	TRUE	hLGLDLGNIVANEDGDAEVFIR	95%	n+304 (+304)	66.71	25.00
4909	seq=translation; coord=9:11741082..11743899:1; parent_transcript=GRMZM2G177098_T03; parent_gene=GRMZM2G177098	GRMZM2G177098_P03	TRUE	TRUE	eDVAWYAGk	95%	n+304 (+304), K+304 (+304)	47.50	25.88
4910	seq=translation; coord=9:11741082..11743899:1; parent_transcript=GRMZM2G177098_T03; parent_gene=GRMZM2G177098	GRMZM2G177098_P03	TRUE	TRUE	sNQYETTSLVQIEGVNTk	95%	n+304 (+304), K+304 (+304)	41.91	25.38
4911	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	dADGDDVVAQGGEEALEESTk	95%	n+304 (+304), K+304 (+304)	33.88	25.00
4912	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	fESAAAAAEEVEDDR	95%	n+304 (+304)	35.46	25.00
4913	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	gAAVEVNVVDk	94%	n+304 (+304), K+304 (+304)	28.53	25.22

4914	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	gELQEEEEQHDEER	95%	n+304 (+304)	67.91	25.00
4915	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	IVPEVEK	90%	n+304 (+304), K+304 (+304)	26.30	25.00
4916	seq=translation; coord=8:126595171..126599674:1; parent_transcript=GRMZM2G389118_T01; parent_gene=GRMZM2G389118	GRMZM2G389118_P01	TRUE	TRUE	qVVADVGEREEEEVEVR	95%	Pyro-cmC (-17), n+304 (+304)	37.53	25.00
4917	seq=translation; coord=2:164667085..164668830:-1; parent_transcript=AC210204.3_FGT002; parent_gene=AC210204.3_FG002	AC210204.3_FGP002	TRUE	TRUE	dVLDDAGVGGk	95%	n+304 (+304), K+304 (+304)	68.20	25.11
4918	seq=translation; coord=2:164667085..164668830:-1; parent_transcript=AC210204.3_FGT002; parent_gene=AC210204.3_FG002	AC210204.3_FGP002	TRUE	TRUE	IDDAVLVYDVVHANAAQGVkPLVGSAR	95%	n+304 (+304), K+304 (+304)	38.78	25.00
4919	seq=translation; coord=2:164667085..164668830:-1; parent_transcript=AC210204.3_FGT002; parent_gene=AC210204.3_FG002	AC210204.3_FGP002	TRUE	TRUE	IPLRDVLDDAGVGGk	95%	n+304 (+304), K+304 (+304)	28.97	25.00
4920	seq=translation; coord=5:171688070..171693270:-1; parent_transcript=GRMZM2G000278_T01; parent_gene=GRMZM2G000278	GRMZM2G000278_P01, GRMZM2G000278_P03, GRMZM2G130018_P01, GRMZM2G130018_P03	TRUE	TRUE	dIGSGNFGVAR	95%	n+304 (+304)	39.96	25.00
4921	seq=translation; coord=5:171688070..171693270:-1; parent_transcript=GRMZM2G000278_T01; parent_gene=GRMZM2G000278	GRMZM2G000278_P01, GRMZM2G000278_P03, GRMZM2G130018_P01, GRMZM2G130018_P03	TRUE	TRUE	sTVGTPAYIAPEVLSR	95%	n+304 (+304)	69.34	25.44
4922	seq=translation; coord=10:5718777..5728532:-1; parent_transcript=GRMZM2G020446_T01; parent_gene=GRMZM2G020446	GRMZM2G020446_P01	TRUE	TRUE	IQWFLDSIk	94%	n+304 (+304), K+304 (+304)	27.88	25.00
4923	seq=translation; coord=1:67436204..67440532:-1; parent_transcript=GRMZM2G107473_T01; parent_gene=GRMZM2G107473	GRMZM2G107473_P01	TRUE	TRUE	eLSGHDFADTLDSR	95%	n+304 (+304)	41.47	25.00
4924	seq=translation; coord=1:67436204..67440532:-1; parent_transcript=GRMZM2G107473_T01; parent_gene=GRMZM2G107473	GRMZM2G107473_P01	TRUE	TRUE	KVVFQQVTEEEADSLTk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	51.54	25.25
4925	seq=translation; coord=1:67436204..67440532:-1; parent_transcript=GRMZM2G107473_T01; parent_gene=GRMZM2G107473	GRMZM2G107473_P01	TRUE	TRUE	nTNASTFSFGDANTDSTPk	95%	n+304 (+304), K+304 (+304)	78.20	25.00
4926	seq=translation; coord=1:67436204..67440532:-1; parent_transcript=GRMZM2G107473_T01; parent_gene=GRMZM2G107473	GRMZM2G107473_P01	TRUE	TRUE	vVFGGQVTEEEADSLTk	95%	n+304 (+304), K+304 (+304)	30.38	25.29
4927	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	TRUE	TRUE	aMLTQMISIVFR	95%	n+304 (+304)	41.43	26.30
4928	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	TRUE	TRUE	eLLEEIYDSIVk	95%	n+304 (+304), K+304 (+304)	42.91	25.82
4929	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	TRUE	TRUE	gLIVDcIVQLIk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.64	25.00
4930	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	TRUE	TRUE	IVNILNLALPR	95%	n+304 (+304)	38.14	25.00
4931	seq=translation; coord=7:157907062..157937456:-1; parent_transcript=GRMZM2G335287_T01; parent_gene=GRMZM2G335287	GRMZM2G335287_P01	TRUE	TRUE	vLFPIFDHVR	95%	n+304 (+304)	37.88	25.44

4932	seq=translation; coord=1:300990204..300994789:1; parent_transcript=GRMZM2G122267_T01; parent_gene=GRMZM2G122267	GRMZM2G122267_P01,GRMZM2G122267_P02	TRUE	TRUE	dAAEQEAHMWR	95%	n+304 (+304)	47.76	25.00
4933	seq=translation; coord=1:300990204..300994789:1; parent_transcript=GRMZM2G122267_T01; parent_gene=GRMZM2G122267	GRMZM2G122267_P01,GRMZM2G122267_P02	TRUE	TRUE	ekEELLALVGLQSQVLR	95%	n+304 (+304), K+304 (+304)	37.25	25.00
4934	seq=translation; coord=1:300990204..300994789:1; parent_transcript=GRMZM2G122267_T01; parent_gene=GRMZM2G122267	GRMZM2G122267_P01,GRMZM2G122267_P02	TRUE	TRUE	ITETAEEAAEAASAAHTMDEQR	95%	n+304 (+304)	88.18	25.00
4935	seq=translation; coord=4:162075480..162081835:-1; parent_transcript=GRMZM2G042502_T01; parent_gene=GRMZM2G042502	GRMZM2G042502_P01,GRMZM2G123371_P01, GRMZM2G123371_P02	TRUE	TRUE	lIGFLGSDGLLAQR	95%	n+304 (+304)	75.23	25.47
4936	seq=translation; coord=3:158520150..158525636:-1; parent_transcript=GRMZM2G081102_T01; parent_gene=GRMZM2G081102	GRMZM2G081102_P01,GRMZM2G081102_P02, GRMZM2G081102_P03,GRMZM2G145280_P01, GRMZM2G145280_P02,GRMZM2G409407_P01, GRMZM2G409407_P02	TRUE	TRUE	gFTLEELK	95%	n+304 (+304), K+304 (+304)	45.80	26.22
4937	seq=translation; coord=3:158520150..158525636:-1; parent_transcript=GRMZM2G081102_T01; parent_gene=GRMZM2G081102	GRMZM2G081102_P01,GRMZM2G081102_P02, GRMZM2G081102_P03,GRMZM2G145280_P01, GRMZM2G145280_P02,GRMZM2G409407_P01, GRMZM2G409407_P02	TRUE	TRUE	sLEGLQANVQR	95%	n+304 (+304)	33.42	26.45
4938	seq=translation; coord=5:4422815..4424855:1; parent_transcript=GRMZM2G130544_T02; parent_gene=GRMZM2G130544	GRMZM2G130544_P02	TRUE	TRUE	aGELTPDELER	95%	n+304 (+304)	40.45	25.00
4939	seq=translation; coord=10:17606896..17610628:1; parent_transcript=GRMZM2G009448_T01; parent_gene=GRMZM2G009448	GRMZM2G009448_P01	TRUE	TRUE	gFGFITYTSSEEASAAITAMDGK	95%	n+304 (+304), K+304 (+304)	37.57	25.00
4940	seq=translation; coord=10:17606896..17610628:1; parent_transcript=GRMZM2G009448_T01; parent_gene=GRMZM2G009448	GRMZM2G009448_P01	TRUE	TRUE	yGQVIEAk	95%	n+304 (+304), K+304 (+304)	35.30	26.68
4941	seq=translation; coord=1:213095235..213096735:1; parent_transcript=GRMZM2G161274_T02; parent_gene=GRMZM2G161274	GRMZM2G161274_P02	TRUE	TRUE	fWGHEWEK	95%	n+304 (+304), K+304 (+304)	35.06	25.00
4942	seq=translation; coord=1:213095235..213096735:1; parent_transcript=GRMZM2G161274_T02; parent_gene=GRMZM2G161274	GRMZM2G161274_P02	TRUE	TRUE	vSDLLSSLR	94%	n+304 (+304)	30.27	25.00
4943	seq=translation; coord=2:49721009..49733282:-1; parent_transcript=GRMZM2G120517_T02; parent_gene=GRMZM2G120517	GRMZM2G120517_P02,GRMZM2G120517_P03	TRUE	TRUE	dQDLLVLPTDAALFEDPk	91%	n+304 (+304), K+304 (+304)	27.49	26.64
4944	seq=translation; coord=2:73288608..73291178:1; parent_transcript=GRMZM2G016928_T01; parent_gene=GRMZM2G016928	GRMZM2G016928_P01,GRMZM2G016928_P02, GRMZM2G088880_P01,GRMZM2G088880_P02, GRMZM2G088880_P03,GRMZM2G303374_P01, GRMZM2G303374_P03,GRMZM2G303374_P04, GRMZM2G303374_P05	TRUE	TRUE	aGGAYTMNTASAVTVR	95%	n+304 (+304)	51.55	25.00
4945	seq=translation; coord=10:128106169..128112118:-1; parent_transcript=GRMZM2G098577_T01; parent_gene=GRMZM2G098577	GRMZM2G098577_P01	TRUE	TRUE	dVINLIFEK	94%	n+304 (+304), K+304 (+304)	27.01	25.00
4946	seq=translation; coord=10:128106169..128112118:-1; parent_transcript=GRMZM2G098577_T01; parent_gene=GRMZM2G098577	GRMZM2G098577_P01	TRUE	TRUE	eLVDVSEDILR	95%	n+304 (+304)	44.86	25.91
4947	seq=translation; coord=10:128106169..128112118:-1; parent_transcript=GRMZM2G098577_T01; parent_gene=GRMZM2G098577	GRMZM2G098577_P01	TRUE	TRUE	sAQPPSANEEK	95%	n+304 (+304), K+304 (+304)	32.63	25.19

4948	seq=translation; coord=1:289108489..289111192:-1; parent_transcript=GRMZM2G053023_T01; parent_gene=GRMZM2G053023	GRMZM2G053023_P01,GRMZM2G053023_P02	TRUE	TRUE	vDVDELAELVAR	95%	n+304 (+304)	40.95	26.02
4949	seq=translation; coord=1:289108489..289111192:-1; parent_transcript=GRMZM2G053023_T01; parent_gene=GRMZM2G053023	GRMZM2G053023_P01,GRMZM2G053023_P02	TRUE	TRUE	vEAMPTFVLvk	95%	n+304 (+304), K+304 (+304)	69.88	25.00
4950	seq=translation; coord=9:1634017..1638812:-1; parent_transcript=GRMZM2G143862_T01; parent_gene=GRMZM2G143862	GRMZM2G143862_P01	TRUE	TRUE	eLFEFLPk	95%	n+304 (+304), K+304 (+304)	32.36	25.00
4951	seq=translation; coord=9:1634017..1638812:-1; parent_transcript=GRMZM2G143862_T01; parent_gene=GRMZM2G143862	GRMZM2G143862_P01	TRUE	TRUE	tIQEQLMLER	95%	n+304 (+304)	36.11	26.16
4952	seq=translation; coord=9:126016122..126022567:1; parent_transcript=GRMZM2G170843_T01; parent_gene=GRMZM2G170843	GRMZM2G170843_P01,GRMZM2G170843_P02	TRUE	TRUE	eVLSGScGVPAPQQR	95%	n+304 (+304), Carbamidomethyl (+57)	47.23	25.00
4953	seq=translation; coord=9:126016122..126022567:1; parent_transcript=GRMZM2G170843_T01; parent_gene=GRMZM2G170843	GRMZM2G170843_P01,GRMZM2G170843_P02	TRUE	TRUE	fTVQTDLGATVGAFk	95%	n+304 (+304), K+304 (+304)	55.37	25.38
4954	seq=translation; coord=5:70685080..70691262:-1; parent_transcript=GRMZM2G120578_T01; parent_gene=GRMZM2G120578	GRMZM2G120578_P01,GRMZM2G120578_P02	TRUE	TRUE	dGPPVNFILTPVNPIEEVEGATk	95%	n+304 (+304), K+304 (+304)	48.05	25.68
4955	seq=translation; coord=5:70685080..70691262:-1; parent_transcript=GRMZM2G120578_T01; parent_gene=GRMZM2G120578	GRMZM2G120578_P01,GRMZM2G120578_P02	TRUE	TRUE	sPYQEVLVFESSTYGk	95%	n+304 (+304), K+304 (+304)	30.24	25.60
4956	seq=translation; coord=5:70685080..70691262:-1; parent_transcript=GRMZM2G120578_T01; parent_gene=GRMZM2G120578	GRMZM2G120578_P01,GRMZM2G120578_P02	TRUE	TRUE	vQLHVGDAVEFLR	95%	n+304 (+304)	29.50	25.67
4957	seq=translation; coord=1:190997916..191004927:1; parent_transcript=GRMZM2G084149_T01; parent_gene=GRMZM2G084149	GRMZM2G084149_P01	TRUE	TRUE	aITSMLEIASLQAK	95%	n+304 (+304), K+304 (+304)	49.74	25.63
4958	seq=translation; coord=1:190997916..191004927:1; parent_transcript=GRMZM2G084149_T01; parent_gene=GRMZM2G084149	GRMZM2G084149_P01	TRUE	TRUE	iSALESIEER	95%	n+304 (+304)	49.21	25.00
4959	seq=translation; coord=5:83557023..83560095:1; parent_transcript=AC234515.1_FGT003; parent_gene=AC234515.1_FG003	AC234515.1_FGP003	TRUE	TRUE	IATPTFGDLNHLISATMSGVTccLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	33.76	25.00
4960	seq=translation; coord=8:79074521..79075661:-1; parent_transcript=GRMZM2G125893_T01; parent_gene=GRMZM2G125893	GRMZM2G125893_P01	TRUE	TRUE	gDLAIVVGR	91%	n+304 (+304)	31.32	27.97
4961	seq=translation; coord=8:79074521..79075661:-1; parent_transcript=GRMZM2G125893_T01; parent_gene=GRMZM2G125893	GRMZM2G125893_P01	TRUE	TRUE	wIYGVN	87%	n+304 (+304)	26.73	25.90
4962	seq=translation; coord=5:4038554..4040410:1; parent_transcript=GRMZM2G121221_T01; parent_gene=GRMZM2G121221	GRMZM2G121221_P01,GRMZM2G121221_P02, GRMZM2G121221_P03	TRUE	TRUE	ILNVQLk	93%	n+304 (+304), K+304 (+304)	29.69	25.00
4963	seq=translation; coord=2:19443026..19444255:1; parent_transcript=GRMZM2G132777_T01; parent_gene=GRMZM2G132777	GRMZM2G132777_P01	TRUE	TRUE	ILLTDLVSGILADR	93%	n+304 (+304)	29.37	25.00
4964	seq=translation; coord=2:19443026..19444255:1; parent_transcript=GRMZM2G132777_T01; parent_gene=GRMZM2G132777	GRMZM2G132777_P01	TRUE	TRUE	vTDALTMEEVEMVLVGk	95%	n+304 (+304), K+304 (+304)	42.55	25.20
4965	seq=translation; coord=3:224922109..224926422:1; parent_transcript=GRMZM2G064753_T01; parent_gene=GRMZM2G064753	GRMZM2G064753_P01	TRUE	TRUE	eELEAEK	94%	n+304 (+304), K+304 (+304)	30.50	27.08

4966	seq=translation; coord=3:224922109..224926422:1; parent_transcript=GRMZM2G064753_T01; parent_gene=GRMZM2G064753 seq=translation; coord=3:224922109..224926422:1;	GRMZM2G064753_P01	TRUE	TRUE	eEPSVVESYYNk	95%	n+304 (+304), K+304 (+304)	58.02	25.00
4967	parent_transcript=GRMZM2G064753_T01; parent_gene=GRMZM2G064753 seq=translation; coord=4:1494566..1495635:-1;	GRMZM2G064753_P01	TRUE	TRUE	fDMDPLVPFGTk	92%	n+304 (+304), K+304 (+304)	27.37	25.93
4968	parent_transcript=GRMZM2G107286_T01; parent_gene=GRMZM2G107286 seq=translation; coord=2:23473629..23477257:1;	GRMZM2G107286_P01	TRUE	TRUE	gNFLVGVGVIR	95%	n+304 (+304)	48.62	25.00
4969	parent_transcript=GRMZM2G177937_T01; parent_gene=GRMZM2G177937 seq=translation; coord=1:50087976..50089098:1;	GRMZM2G177937_P01,GRMZM2G177937_P03	TRUE	TRUE	INTDESPDIASQYGVr	95%	n+304 (+304)	78.54	25.00
4970	parent_transcript=GRMZM2G394203_T01; parent_gene=GRMZM2G394203 seq=translation; coord=1:50087976..50089098:1;	GRMZM2G394203_P01	TRUE	TRUE	gGGFGGGAGGGAGGGLGGGGGLGGEGGGYGGGAGR	95%	n+304 (+304)	59.35	25.00
4971	parent_transcript=GRMZM2G394203_T01; parent_gene=GRMZM2G394203 seq=translation; coord=7:104173693..104176328:-1;	GRMZM2G394203_P01	TRUE	TRUE	gGGFGGGAGGGAGGGLGGGGGLGGEGGGYGGGAGR	95%	n+304 (+304), iTRAQ8plex (+304)	85.75	25.00
4972	parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160 seq=translation; coord=7:104173693..104176328:-1;	GRMZM2G032160_P01	TRUE	TRUE	aDVAGLASTAITTSSYFYGk	95%	n+304 (+304), K+304 (+304)	38.57	25.79
4973	parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160 seq=translation; coord=7:104173693..104176328:-1;	GRMZM2G032160_P01	TRUE	TRUE	aTSTVVPDPSR	92%	n+304 (+304)	29.66	25.53
4974	parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160 seq=translation; coord=7:104173693..104176328:-1;	GRMZM2G032160_P01	TRUE	TRUE	dGPGELMLAHPLHLR	95%	n+304 (+304)	42.57	26.06
4975	parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160 seq=translation; coord=7:104173693..104176328:-1;	GRMZM2G032160_P01	TRUE	TRUE	vAYLPDASMEPVLDR	95%	n+304 (+304)	36.22	25.00
4976	parent_transcript=GRMZM2G032160_T01; parent_gene=GRMZM2G032160 seq=translation; coord=2:6820716..6853179:1;	GRMZM2G032160_P01	TRUE	TRUE	wGGLVTLQGLk	89%	n+304 (+304), K+304 (+304)	25.01	25.00
4977	parent_transcript=GRMZM2G138782_T01; parent_gene=GRMZM2G138782 seq=translation; coord=2:6820716..6853179:1;	GRMZM2G138782_P01	TRUE	TRUE	dLTIAGAVEQk	95%	n+304 (+304), K+304 (+304)	33.89	25.71
4978	parent_transcript=GRMZM2G138782_T01; parent_gene=GRMZM2G138782 seq=translation; coord=2:6820716..6853179:1;	GRMZM2G138782_P01	TRUE	TRUE	eLMYAEAAILDk	95%	n+304 (+304), K+304 (+304)	43.87	25.40
4979	parent_transcript=GRMZM2G138782_T01; parent_gene=GRMZM2G138782 seq=translation; coord=2:6820716..6853179:1;	GRMZM2G138782_P01	TRUE	TRUE	iVLDIIEIAHAAEk	95%	n+304 (+304), K+304 (+304)	44.74	25.00
4980	parent_transcript=GRMZM2G138782_T01; parent_gene=GRMZM2G138782 seq=translation; coord=2:24834408..24836108:-1;	GRMZM2G138782_P01	TRUE	TRUE	sLAETYLLQDEPLSk	95%	n+304 (+304), K+304 (+304)	42.00	27.33
4981	parent_transcript=GRMZM2G108153_T01; parent_gene=GRMZM2G108153 seq=translation; coord=2:24834408..24836108:-1;	GRMZM2G108153_P01	TRUE	TRUE	dAVSLSGGPSFTVPLGR	95%	n+304 (+304)	63.22	25.79
4982	parent_transcript=GRMZM2G108153_T01; parent_gene=GRMZM2G108153 seq=translation; coord=2:24834408..24836108:-1;	GRMZM2G108153_P01	TRUE	TRUE	gLPPNVGLQQEAVQLVEDIR	95%	n+304 (+304)	81.01	25.75
4983	parent_transcript=GRMZM2G108153_T01; parent_gene=GRMZM2G108153	GRMZM2G108153_P01	TRUE	TRUE	gVMLPSDQGLVSDPR	95%	n+304 (+304)	34.62	25.17

4984	seq=translation; coord=2:24834408..24836108:-1; parent_transcript=GRMZM2G108153_T01; parent_gene=GRMZM2G108153 seq=translation; coord=8:125902255..125906710:1;	GRMZM2G108153_P01	TRUE	TRUE	vHAACGPTVScADITVLATR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	47.29	25.00
4985	parent_transcript=GRMZM2G059693_T01; parent_gene=GRMZM2G059693 seq=translation; coord=8:125902255..125906710:1;	GRMZM2G059693_P01,GRMZM2G059693_P02, GRMZM2G059693_P04	TRUE	TRUE	aTGLLVPGIASHSPR	95%	n+304 (+304)	39.46	25.17
4986	parent_transcript=GRMZM2G059693_T01; parent_gene=GRMZM2G059693 seq=translation; coord=8:125902255..125906710:1;	GRMZM2G059693_P01,GRMZM2G059693_P02, GRMZM2G059693_P04	TRUE	TRUE	eGAVSLLYR	95%	n+304 (+304)	38.62	26.68
4987	parent_transcript=GRMZM2G059693_T01; parent_gene=GRMZM2G059693 seq=translation; coord=7:151190045..151192101:1;	GRMZM2G059693_P01,GRMZM2G059693_P02, GRMZM2G059693_P04	TRUE	TRUE	gAFLWAK	95%	n+304 (+304), K+304 (+304)	38.37	25.56
4988	parent_transcript=GRMZM2G155911_T01; parent_gene=GRMZM2G155911 seq=translation; coord=7:151190045..151192101:1;	GRMZM2G155911_P01	TRUE	TRUE	aPTEQLAADLDAHIR	95%	n+304 (+304)	74.18	25.74
4989	parent_transcript=GRMZM2G155911_T01; parent_gene=GRMZM2G155911 seq=translation; coord=7:151190045..151192101:1;	GRMZM2G155911_P01	TRUE	TRUE	IPAVQPPTDFHGIEEFISR	95%	n+304 (+304)	34.06	25.80
4990	parent_transcript=GRMZM2G155911_T01; parent_gene=GRMZM2G155911 seq=translation; coord=7:129358205..129362749:-1;	GRMZM2G155911_P01	TRUE	TRUE	nAVEEGSSSYSLR	95%	n+304 (+304)	32.85	25.00
4991	parent_transcript=GRMZM5G843748_T02; parent_gene=GRMZM5G843748 seq=translation; coord=7:129358205..129362749:-1;	GRMZM5G843748_P02	TRUE	TRUE	aFIEGMik	91%	n+304 (+304), K+304 (+304)	27.44	26.70
4992	parent_transcript=GRMZM5G843748_T02; parent_gene=GRMZM5G843748 seq=translation; coord=7:129358205..129362749:-1;	GRMZM5G843748_P02	TRUE	TRUE	dQDAFFR	86%	n+304 (+304)	25.16	25.00
4993	parent_transcript=GRMZM5G843748_T02; parent_gene=GRMZM5G843748 seq=translation; coord=7:129358205..129362749:-1;	GRMZM5G843748_P02	TRUE	TRUE	sFEVVDEIKDALEER	95%	n+304 (+304), K+304 (+304)	34.15	25.00
4994	parent_transcript=GRMZM5G843748_T02; parent_gene=GRMZM5G843748 seq=translation; coord=5:77916981..77922073:1;	GRMZM5G843748_P02	TRUE	TRUE	vFDNQYFEDLVALR	95%	n+304 (+304)	68.58	25.00
4995	parent_transcript=GRMZM2G097207_T01; parent_gene=GRMZM2G097207 seq=translation; coord=5:77916981..77922073:1;	GRMZM2G097207_P01	TRUE	TRUE	KSGLEVMMVGIPNDLLSTMATSMK	95%	K+304 (+304), n+304 (+304), K+304 (+304)	32.04	25.00
4996	parent_transcript=GRMZM2G097207_T01; parent_gene=GRMZM2G097207 seq=translation; coord=5:77916981..77922073:1;	GRMZM2G097207_P01	TRUE	TRUE	IFDAEEGTMSALR	95%	n+304 (+304)	48.71	25.00
4997	parent_transcript=GRMZM2G097207_T01; parent_gene=GRMZM2G097207 seq=translation; coord=10:86984445..86986672:1;	GRMZM2G097207_P01	TRUE	TRUE	sGLEVMVGIPNDLLSTMATSMk	95%	n+304 (+304), K+304 (+304)	49.15	25.13
4998	parent_transcript=GRMZM2G028104_T01; parent_gene=GRMZM2G028104 seq=translation; coord=10:86984445..86986672:1;	GRMZM2G028104_P01	TRUE	TRUE	aSGEVAAADVVDVVR	95%	n+304 (+304)	61.71	25.79
4999	parent_transcript=GRMZM2G028104_T01; parent_gene=GRMZM2G028104 seq=translation; coord=10:86984445..86986672:1;	GRMZM2G028104_P01	TRUE	TRUE	fVVVDAEGGGETR	95%	n+304 (+304)	46.82	25.00
5000	parent_transcript=GRMZM2G028104_T01; parent_gene=GRMZM2G028104 seq=translation; coord=7:137518004..137519265:-1;	GRMZM2G028104_P01	TRUE	TRUE	IDLLDLR	87%	n+304 (+304)	26.51	25.77
5001	parent_transcript=GRMZM2G066202_T01; parent_gene=GRMZM2G066202	GRMZM2G066202_P01	TRUE	TRUE	aAELAADSGGGEVR	95%	n+304 (+304)	36.60	25.00

5002	seq=translation; coord=7:137518004..137519265:-1; parent_transcript=GRMZM2G066202_T01; parent_gene=GRMZM2G066202	GRMZM2G066202_P01	TRUE	TRUE	gAQALLALK	95%	n+304 (+304), K+304 (+304)	37.47	25.00
5003	seq=translation; coord=9:41048627..41058528:-1; parent_transcript=GRMZM2G538535_T01; parent_gene=GRMZM2G538535	GRMZM2G538535_P01	TRUE	TRUE	aPAFSILDTcFEGQASQLR	95%	n+304 (+304), Carbamidomethyl (+57)	53.35	25.00
5004	seq=translation; coord=9:41048627..41058528:-1; parent_transcript=GRMZM2G538535_T01; parent_gene=GRMZM2G538535	GRMZM2G538535_P01	TRUE	TRUE	sAGLIGLAR	88%	n+304 (+304)	26.24	25.21
5005	seq=translation; coord=3:212009199..212010553:-1; parent_transcript=GRMZM2G453805_T01; parent_gene=GRMZM2G453805	GRMZM2G453805_P01	TRUE	TRUE	gIGNYGGIMVWDR	95%	n+304 (+304)	57.24	25.00
5006	seq=translation; coord=1:232041908..232053896:-1; parent_transcript=GRMZM2G148323_T01; parent_gene=GRMZM2G148323	GRMZM2G148323_P01	TRUE	TRUE	dAAALDPELLQLAELAPGALR	95%	n+304 (+304)	48.06	25.00
5007	seq=translation; coord=1:232041908..232053896:-1; parent_transcript=GRMZM2G148323_T01; parent_gene=GRMZM2G148323	GRMZM2G148323_P01	TRUE	TRUE	eVIPQFYFk	95%	n+304 (+304), K+304 (+304)	27.95	25.22
5008	seq=translation; coord=2:2338643..2346346:-1; parent_transcript=GRMZM2G077744_T01; parent_gene=GRMZM2G077744	GRMZM2G077744_P01,GRMZM2G077744_P02, GRMZM2G167262_P01,GRMZM2G167262_P02	TRUE	TRUE	acPDPTcIEIADccSHLk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	54.92	25.00
5009	seq=translation; coord=2:2338643..2346346:-1; parent_transcript=GRMZM2G077744_T01; parent_gene=GRMZM2G077744	GRMZM2G077744_P01,GRMZM2G077744_P02, GRMZM2G167262_P01,GRMZM2G167262_P02	TRUE	TRUE	iPHAIELDk	95%	n+304 (+304), K+304 (+304)	42.80	25.00
5010	seq=translation; coord=2:2338643..2346346:-1; parent_transcript=GRMZM2G077744_T01; parent_gene=GRMZM2G077744	GRMZM2G077744_P01,GRMZM2G077744_P02, GRMZM2G167262_P01,GRMZM2G167262_P02	TRUE	TRUE	qLMIQVAELVPk	95%	n+304 (+304), K+304 (+304)	40.30	25.00
5011	seq=translation; coord=2:196218998..196222283:1; parent_transcript=GRMZM2G042604_T01; parent_gene=GRMZM2G042604	GRMZM2G042604_P01,GRMZM2G138128_P01, GRMZM2G138128_P02,GRMZM2G138128_P03	TRUE	TRUE	aLLEVVEGGk	95%	n+304 (+304), K+304 (+304)	47.46	25.53
5012	seq=translation; coord=2:196218998..196222283:1; parent_transcript=GRMZM2G042604_T01; parent_gene=GRMZM2G042604	GRMZM2G042604_P01,GRMZM2G138128_P01, GRMZM2G138128_P02,GRMZM2G138128_P03	TRUE	TRUE	iAcLDTHIALAcAGLk	94%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	26.37	25.53
5013	seq=translation; coord=2:196218998..196222283:1; parent_transcript=GRMZM2G042604_T01; parent_gene=GRMZM2G042604	GRMZM2G042604_P01,GRMZM2G138128_P01, GRMZM2G138128_P02,GRMZM2G138128_P03	TRUE	TRUE	ITVEDPVTVEYITR	95%	n+304 (+304)	42.24	25.49
5014	seq=translation; coord=8:18214060..18227316:1; parent_transcript=GRMZM2G107696_T01; parent_gene=GRMZM2G107696	GRMZM2G107696_P01,GRMZM2G107696_P02	TRUE	TRUE	aAINTSNTGVEEAMNWLLSHMDDPDINDPIsk	95%	n+304 (+304), K+304 (+304)	37.42	25.00
5015	seq=translation; coord=8:18214060..18227316:1; parent_transcript=GRMZM2G107696_T01; parent_gene=GRMZM2G107696	GRMZM2G107696_P01,GRMZM2G107696_P02	TRUE	TRUE	eLDANTNYDWNr	95%	n+304 (+304)	31.73	25.00
5016	seq=translation; coord=8:18214060..18227316:1; parent_transcript=GRMZM2G107696_T01; parent_gene=GRMZM2G107696	GRMZM2G107696_P01,GRMZM2G107696_P02	TRUE	TRUE	eLNPFSGFk	95%	n+304 (+304), K+304 (+304)	32.43	26.48
5017	seq=translation; coord=8:18214060..18227316:1; parent_transcript=GRMZM2G107696_T01; parent_gene=GRMZM2G107696	GRMZM2G107696_P01,GRMZM2G107696_P02	TRUE	TRUE	qQDVLEFFLHLIDr	95%	n+304 (+304)	45.38	26.14

5018	seq=translation; coord=9:115668526..115674221:1; parent_transcript=GRMZM5G818887_T01; parent_gene=GRMZM5G818887 seq=translation; coord=9:115668526..115674221:1;	GRMZM5G818887_P01	TRUE	TRUE	gVLSVPEFILAGDNLVAK	95%	n+304 (+304), K+304 (+304)	36.15	25.00
5019	parent_transcript=GRMZM5G818887_T01; parent_gene=GRMZM5G818887 seq=translation; coord=9:115668526..115674221:1;	GRMZM5G818887_P01	TRUE	TRUE	mPLMPPELVFEDISQDHAR	95%	n+304 (+304)	48.05	25.00
5020	seq=translation; coord=9:115668526..115674221:1; parent_transcript=GRMZM5G818887_T01; parent_gene=GRMZM5G818887 seq=translation; coord=1:248590498..248595499:-1;	GRMZM5G818887_P01	TRUE	TRUE	tEEEEIPSMDTLDIGR	95%	n+304 (+304)	31.61	25.00
5021	parent_transcript=GRMZM5G830403_T02; parent_gene=GRMZM5G830403 seq=translation; coord=1:248590498..248595499:-1;	GRMZM5G830403_P02,GRMZM5G830403_P03, GRMZM5G830403_P04	TRUE	TRUE	ePAANQDADDQNk	95%	n+304 (+304), K+304 (+304)	42.62	25.00
5022	parent_transcript=GRMZM5G830403_T02; parent_gene=GRMZM5G830403 seq=translation; coord=7:155961862..155967544:-1;	GRMZM5G830403_P02,GRMZM5G830403_P03, GRMZM5G830403_P04	TRUE	TRUE	IVEVIEk	92%	n+304 (+304), K+304 (+304)	28.69	25.00
5023	parent_transcript=GRMZM2G173910_T01; parent_gene=GRMZM2G173910 seq=translation; coord=7:155961862..155967544:-1;	GRMZM2G173910_P01	TRUE	TRUE	aPYNIQINVk	91%	n+304 (+304), K+304 (+304)	25.98	25.05
5024	parent_transcript=GRMZM2G173910_T01; parent_gene=GRMZM2G173910 seq=translation; coord=7:155961862..155967544:-1;	GRMZM2G173910_P01	TRUE	TRUE	dFFVEEQPk	89%	n+304 (+304), K+304 (+304)	27.80	25.88
5025	parent_transcript=GRMZM2G173910_T01; parent_gene=GRMZM2G173910 seq=translation; coord=5:15703665..15718967:1;	GRMZM2G173910_P01	TRUE	TRUE	vNDAAAMAVVR	95%	n+304 (+304)	34.36	26.47
5026	parent_transcript=AC197122.3_FGT003; parent_gene=AC197122.3_FG003 seq=translation; coord=5:15703665..15718967:1;	AC197122.3_FGP003	TRUE	TRUE	dFLDDYVER	95%	n+304 (+304)	32.43	25.00
5027	parent_transcript=AC197122.3_FGT003; parent_gene=AC197122.3_FG003 seq=translation; coord=6:117850410..117855773:-1;	AC197122.3_FGP003	TRUE	TRUE	vEALEDMVS LAPSSLVk	95%	n+304 (+304), K+304 (+304)	47.35	25.00
5028	parent_transcript=GRMZM2G074454_T01; parent_gene=GRMZM2G074454 seq=translation; coord=6:117850410..117855773:-1;	GRMZM2G074454_P01	TRUE	TRUE	iGFIGLGAMGFGMASHLLk	95%	n+304 (+304), K+304 (+304)	33.45	25.00
5029	parent_transcript=GRMZM2G074454_T01; parent_gene=GRMZM2G074454 seq=translation; coord=8:83396432..83400437:1;	GRMZM2G074454_P01	TRUE	TRUE	lISEDPLLDLFlk	95%	n+304 (+304), K+304 (+304)	40.17	25.00
5030	parent_transcript=GRMZM2G131249_T02; parent_gene=GRMZM2G131249 seq=translation; coord=8:83396432..83400437:1;	GRMZM2G131249_P02	TRUE	TRUE	gFDPETGTVk	95%	n+304 (+304), K+304 (+304)	33.09	26.02
5031	parent_transcript=GRMZM2G131249_T02; parent_gene=GRMZM2G131249 seq=translation; coord=8:83396432..83400437:1;	GRMZM2G131249_P02	TRUE	TRUE	sGIENMLMHYVPEVk	90%	n+304 (+304), K+304 (+304)	27.55	26.90
5032	parent_transcript=GRMZM2G131249_T02; parent_gene=GRMZM2G131249 seq=translation; coord=8:83396432..83400437:1;	GRMZM2G131249_P02	TRUE	TRUE	sLFAIDGVTR	93%	n+304 (+304)	29.54	25.12
5033	parent_transcript=GRMZM2G131249_T02; parent_gene=GRMZM2G131249 seq=translation; coord=6:167006647..167019258:1;	GRMZM2G131249_P02	TRUE	TRUE	vFFGSDFTVTk	95%	n+304 (+304), K+304 (+304)	42.35	26.15
5034	parent_transcript=AC233870.1_FGT006; parent_gene=AC233870.1_FG006 seq=translation; coord=6:167006647..167019258:1;	AC233870.1_FGP006	TRUE	TRUE	aGNLVESMTADLAGEVTS AAGPVR	95%	n+304 (+304)	34.99	25.00
5035	parent_transcript=AC233870.1_FGT006; parent_gene=AC233870.1_FG006	AC233870.1_FGP006	TRUE	TRUE	sLDAEADLR	94%	n+304 (+304)	31.79	25.42

5036	seq=translation; coord=8:3347680..3350552:1; parent_transcript=GRMZM2G013461_T01; parent_gene=GRMZM2G013461 seq=translation; coord=8:3347680..3350552:1;	GRMZM2G013461_P01,GRMZM2G013461_P02	TRUE	TRUE	eNALLEFVR	94%	n+304 (+304)	31.04	25.54
5037	parent_transcript=GRMZM2G013461_T01; parent_gene=GRMZM2G013461 seq=translation; coord=8:3347680..3350552:1;	GRMZM2G013461_P01,GRMZM2G013461_P02	TRUE	TRUE	eQVVAGTLHHLTLEAVEAGR	95%	n+304 (+304)	50.54	25.62
5038	parent_transcript=GRMZM2G013461_T01; parent_gene=GRMZM2G013461 seq=translation; coord=8:3347680..3350552:1;	GRMZM2G013461_P01,GRMZM2G013461_P02	TRUE	TRUE	sNSLFPYELLEILR	95%	n+304 (+304)	41.25	26.62
5039	parent_transcript=GRMZM2G051613_T01; parent_gene=GRMZM2G051613 seq=translation; coord=9:134504096..134514418:-1;	GRMZM2G051613_P01,GRMZM2G051613_P02	TRUE	TRUE	eTTGIVGLEVPAPNR	95%	n+304 (+304)	76.26	26.02
5040	parent_transcript=GRMZM2G051613_T01; parent_gene=GRMZM2G051613 seq=translation; coord=9:134504096..134514418:-1;	GRMZM2G051613_P01,GRMZM2G051613_P02	TRUE	TRUE	IQIcQEEDDWk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.93	25.00
5041	parent_transcript=GRMZM2G035807_T01; parent_gene=GRMZM2G035807 seq=translation; coord=2:232093952..232099171:1;	GRMZM2G035807_P01,GRMZM2G092327_P01, GRMZM2G092327_P02,GRMZM2G092327_P03	TRUE	TRUE	IMDLLR	93%	n+304 (+304)	30.46	25.67
5042	parent_transcript=GRMZM2G035807_T01; parent_gene=GRMZM2G035807 seq=translation; coord=2:232093952..232099171:1;	GRMZM2G035807_P01,GRMZM2G092327_P01, GRMZM2G092327_P02,GRMZM2G092327_P03	TRUE	TRUE	tAAFcFPIISGILk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	37.68	25.00
5043	parent_transcript=GRMZM2G152925_T01; parent_gene=GRMZM2G152925 seq=translation; coord=1:66948065..66952666:-1;	GRMZM2G152925_P01	TRUE	TRUE	gEDAPEcDk	95%	Carbamidomethyl (+57), K+304 (+304)	31.87	25.00
5044	parent_transcript=GRMZM2G152925_T01; parent_gene=GRMZM2G152925 seq=translation; coord=1:66948065..66952666:-1;	GRMZM2G152925_P01	TRUE	TRUE	sLcPGEWVDR	92%	n+304 (+304), Carbamidomethyl (+57)	29.10	25.00
5045	parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072 seq=translation; coord=8:143277512..143279395:-1;	GRMZM2G050072_P01	TRUE	TRUE	aLVPPYPVAGR	86%	n+304 (+304)	25.27	25.00
5046	parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072 seq=translation; coord=8:143277512..143279395:-1;	GRMZM2G050072_P01	TRUE	TRUE	dATGQTcSTFDAVAVVfk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.77	25.00
5047	parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072 seq=translation; coord=8:143277512..143279395:-1;	GRMZM2G050072_P01	TRUE	TRUE	eASLPEVGVGVMR	95%	n+304 (+304)	33.90	26.10
5048	parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072 seq=translation; coord=8:143277512..143279395:-1;	GRMZM2G050072_P01	TRUE	TRUE	fTDWMR	87%	n+304 (+304)	25.04	25.00
5049	parent_transcript=GRMZM2G050072_T01; parent_gene=GRMZM2G050072 seq=translation; coord=8:143277512..143279395:-1;	GRMZM2G050072_P01	TRUE	TRUE	IEDLVMAQVTK	95%	n+304 (+304), K+304 (+304)	38.07	25.00
5050	parent_transcript=GRMZM2G014376_T01; parent_gene=GRMZM2G014376 seq=translation; coord=10:25975417..25980229:-1;	GRMZM2G014376_P01,GRMZM2G014376_P02, GRMZM2G014376_P03	TRUE	TRUE	eMAAEAAAAALGADVAELR	92%	n+304 (+304)	27.18	25.55
5051	parent_transcript=GRMZM2G014376_T01; parent_gene=GRMZM2G014376 seq=translation; coord=10:25975417..25980229:-1;	GRMZM2G014376_P01,GRMZM2G014376_P02, GRMZM2G014376_P03	TRUE	TRUE	IFVVIGAGGAGk	95%	n+304 (+304), K+304 (+304)	48.27	25.00
5052	parent_transcript=GRMZM2G014376_T01; parent_gene=GRMZM2G014376 seq=translation; coord=10:25975417..25980229:-1;	GRMZM2G014376_P01,GRMZM2G014376_P02, GRMZM2G014376_P03	TRUE	TRUE	sVGFNAVYVFLVDDLAK	95%	n+304 (+304), K+304 (+304)	33.53	25.07
5053	parent_transcript=GRMZM2G002687_T01; parent_gene=GRMZM2G002687	GRMZM2G002687_P01	TRUE	TRUE	aIGIFGNLEDHIGk	95%	n+304 (+304), K+304 (+304)	27.76	26.03

5054	seq=translation; coord=1:264743594..264751569:1; parent_transcript=GRMZM2G002687_T01; parent_gene=GRMZM2G002687	GRMZM2G002687_P01	TRUE	TRUE	IIAVLSEIVAR	94%	n+304 (+304)	30.27	25.00
5055	seq=translation; coord=4:170517685..170521446:-1; parent_transcript=GRMZM2G150648_T03; parent_gene=GRMZM2G150648	GRMZM2G150648_P03,GRMZM2G150648_P04, GRMZM2G150648_P05	TRUE	TRUE	aDQfKPAEQVTLEPYER	93%	n+304 (+304), K+304 (+304)	28.09	25.62
5056	seq=translation; coord=4:170517685..170521446:-1; parent_transcript=GRMZM2G150648_T03; parent_gene=GRMZM2G150648	GRMZM2G150648_P03,GRMZM2G150648_P04, GRMZM2G150648_P05	TRUE	TRUE	mLVGMVDVIFSDVAQPDQAR	95%	n+304 (+304)	89.36	25.00
5057	seq=translation; coord=4:174901704..174907176:-1; parent_transcript=GRMZM2G039263_T01; parent_gene=GRMZM2G039263	GRMZM2G039263_P01,GRMZM2G039263_P02, GRMZM2G110626_P01	TRUE	TRUE	eQLAIAEFAESLLIIPk	95%	n+304 (+304), K+304 (+304)	33.58	25.00
5058	seq=translation; coord=4:174901704..174907176:-1; parent_transcript=GRMZM2G039263_T01; parent_gene=GRMZM2G039263	GRMZM2G039263_P01,GRMZM2G039263_P02, GRMZM2G110626_P01	TRUE	TRUE	eVGDGTTSVVIAAELLk	91%	n+304 (+304), K+304 (+304)	25.37	25.00
5059	seq=translation; coord=4:174901704..174907176:-1; parent_transcript=GRMZM2G039263_T01; parent_gene=GRMZM2G039263	GRMZM2G039263_P01,GRMZM2G039263_P02, GRMZM2G110626_P01	TRUE	TRUE	iADDDVILVk	87%	n+304 (+304), K+304 (+304)	25.10	25.00
5060	seq=translation; coord=5:176387128..176391570:1; parent_transcript=GRMZM2G075637_T01; parent_gene=GRMZM2G075637	GRMZM2G075637_P01	TRUE	TRUE	rPLVVESFFSWFSDELK	95%	n+304 (+304), K+304 (+304)	30.76	25.00
5061	seq=translation; coord=1:226171571..226174821:1; parent_transcript=GRMZM5G882228_T02; parent_gene=GRMZM5G882228	GRMZM5G882228_P02	TRUE	TRUE	eEPETEPLPPVQMGEVSEEDLR	94%	n+304 (+304)	27.97	25.00
5062	seq=translation; coord=1:226171571..226174821:1; parent_transcript=GRMZM5G882228_T02; parent_gene=GRMZM5G882228	GRMZM5G882228_P02	TRUE	TRUE	gQIYDVTQSR	93%	n+304 (+304)	29.95	25.00
5063	seq=translation; coord=1:226171571..226174821:1; parent_transcript=GRMZM5G882228_T02; parent_gene=GRMZM5G882228	GRMZM5G882228_P02	TRUE	TRUE	mFYGPGGPYALFAGk	95%	n+304 (+304), K+304 (+304)	39.76	25.76
5064	seq=translation; coord=3:19453334..19462209:1; parent_transcript=GRMZM2G088834_T03; parent_gene=GRMZM2G088834	GRMZM2G088834_P03,GRMZM2G126860_P01	TRUE	TRUE	aFPLYMNALEYFk	95%	n+304 (+304), K+304 (+304)	53.15	26.79
5065	seq=translation; coord=3:19453334..19462209:1; parent_transcript=GRMZM2G088834_T03; parent_gene=GRMZM2G088834	GRMZM2G088834_P03,GRMZM2G126860_P01	TRUE	TRUE	eNAPSIIFIDEIDSLcGQR	95%	n+304 (+304), Carbamidomethyl (+57)	73.90	25.00
5066	seq=translation; coord=2:170263508..170267458:-1; parent_transcript=GRMZM2G074687_T01; parent_gene=GRMZM2G074687	GRMZM2G074687_P01	TRUE	TRUE	fGGDTTYSIMFGPDlcGYSTk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.05	25.00
5067	seq=translation; coord=2:170263508..170267458:-1; parent_transcript=GRMZM2G074687_T01; parent_gene=GRMZM2G074687	GRMZM2G074687_P01	TRUE	TRUE	ILGGDVDQk	94%	n+304 (+304), K+304 (+304)	30.24	27.29
5068	seq=translation; coord=1:94486908..94489534:1; parent_transcript=GRMZM2G052666_T01; parent_gene=GRMZM2G052666	GRMZM2G052666_P01	TRUE	TRUE	vQYDPAAck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.96	25.00
5069	seq=translation; coord=1:94486908..94489534:1; parent_transcript=GRMZM2G052666_T01; parent_gene=GRMZM2G052666	GRMZM2G052666_P01	TRUE	TRUE	yDDLDTFWAR	95%	n+304 (+304)	37.05	25.00
5070	seq=translation; coord=3:47497754..47499644:-1; parent_transcript=GRMZM2G123407_T01; parent_gene=GRMZM2G123407	GRMZM2G123407_P01	TRUE	TRUE	aYFFSGNYDGEQcESGQR	95%	n+304 (+304), Carbamidomethyl (+57)	33.26	25.00
5071	seq=translation; coord=3:47497754..47499644:-1; parent_transcript=GRMZM2G123407_T01; parent_gene=GRMZM2G123407	GRMZM2G123407_P01	TRUE	TRUE	dAVTVAVPLLEGR	95%	n+304 (+304)	65.63	26.37

5072	seq=translation; coord=1:277739114..277741150:1; parent_transcript=GRMZM2G090422_T01; parent_gene=GRMZM2G090422	GRMZM2G090422_P01	TRUE	TRUE	IGSQLEILAPIkY	95%	n+304 (+304), K+304 (+304)	63.58	25.00
5073	seq=translation; coord=1:277739114..277741150:1; parent_transcript=GRMZM2G090422_T01; parent_gene=GRMZM2G090422	GRMZM2G090422_P01	TRUE	TRUE	mVIPDAlk	90%	n+304 (+304), K+304 (+304)	25.93	25.47
5074	seq=translation; coord=1:277739114..277741150:1; parent_transcript=GRMZM2G090422_T01; parent_gene=GRMZM2G090422	GRMZM2G090422_P01	TRUE	TRUE	ycLLGELSk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.26	26.02
5075	seq=translation; coord=2:208079590..208081944:1; parent_transcript=GRMZM2G034764_T01; parent_gene=GRMZM2G034764	GRMZM2G034764_P01	TRUE	TRUE	aASETADAeVDSSR	95%	n+304 (+304)	62.37	25.00
5076	seq=translation; coord=4:229500502..229510053:1; parent_transcript=GRMZM2G069631_T01; parent_gene=GRMZM2G069631	GRMZM2G069631_P01,GRMZM2G069631_P02, GRMZM2G165418_P01,GRMZM2G165418_P02, GRMZM2G165418_P03,GRMZM2G165418_P04	TRUE	TRUE	IIDLR	86%	n+304 (+304)	25.44	25.00
5077	seq=translation; coord=4:229500502..229510053:1; parent_transcript=GRMZM2G069631_T01; parent_gene=GRMZM2G069631	GRMZM2G069631_P01,GRMZM2G069631_P02, GRMZM2G165418_P01,GRMZM2G165418_P02, GRMZM2G165418_P03,GRMZM2G165418_P04	TRUE	TRUE	vVLFER	90%	n+304 (+304)	27.38	25.00
5078	seq=translation; coord=2:232371777..232375068:-1; parent_transcript=GRMZM2G008919_T01; parent_gene=GRMZM2G008919	GRMZM2G008919_P01,GRMZM2G008919_P02, GRMZM2G008919_P03,GRMZM2G008919_P05, GRMZM2G104505_P01	TRUE	TRUE	gVMMENIEk	95%	n+304 (+304), K+304 (+304)	40.85	25.30
5079	seq=translation; coord=2:30905783..30911404:-1; parent_transcript=GRMZM2G352129_T01; parent_gene=GRMZM2G352129	GRMZM2G352129_P01	TRUE	TRUE	dAALSPAAQIGTLTSALANANPEQQR	95%	n+304 (+304)	44.12	25.71
5080	seq=translation; coord=2:30905783..30911404:-1; parent_transcript=GRMZM2G352129_T01; parent_gene=GRMZM2G352129	GRMZM2G352129_P01	TRUE	TRUE	nLDDSIGDDQLR	95%	n+304 (+304)	45.42	25.00
5081	seq=translation; coord=9:44374790..44375756:-1; parent_transcript=GRMZM2G382673_T01; parent_gene=GRMZM2G382673	GRMZM2G382673_P01	TRUE	TRUE	dPAHPWR	95%	n+304 (+304)	44.76	25.00
5082	seq=translation; coord=1:84814341..84815071:1; parent_transcript=GRMZM2G402564_T01; parent_gene=GRMZM2G402564	GRMZM2G402564_P01	TRUE	TRUE	aNcScGAScNcAScASA	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), n+304 (+304),	45.23	25.00
5083	seq=translation; coord=1:84814341..84815071:1; parent_transcript=GRMZM2G402564_T01; parent_gene=GRMZM2G402564	GRMZM2G402564_P01	TRUE	TRUE	cGcAVPcPGGk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57),	31.00	25.00
5084	seq=translation; coord=1:84814341..84815071:1; parent_transcript=GRMZM2G402564_T01; parent_gene=GRMZM2G402564	GRMZM2G402564_P01	TRUE	TRUE	eHTTcGcGEHcEcSPcTcGR	92%	Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	26.12	25.00
5085	seq=translation; coord=1:248861739..248864579:-1; parent_transcript=GRMZM2G073725_T01; parent_gene=GRMZM2G073725	GRMZM2G073725_P01	TRUE	TRUE	IGTIDPYFVk	95%	n+304 (+304), K+304 (+304)	37.06	25.07

5086	seq=translation; coord=10:143716436..143719458:-1; parent_transcript=GRMZM2G023387_T01; parent_gene=GRMZM2G023387	GRMZM2G023387_P01	TRUE	TRUE	aMPTFFLIK	93%	n+304 (+304), K+304 (+304)	27.02	25.00
5087	seq=translation; coord=2:53844493..53846005:1; parent_transcript=GRMZM2G044132_T01; parent_gene=GRMZM2G044132	GRMZM2G044132_P01	TRUE	TRUE	eHLGEMGALAAGAFALYER	95%	n+304 (+304)	62.51	25.00
5088	seq=translation; coord=2:53844493..53846005:1; parent_transcript=GRMZM2G044132_T01; parent_gene=GRMZM2G044132	GRMZM2G044132_P01	TRUE	TRUE	gTGGGGYnk	95%	n+304 (+304), K+304 (+304)	38.05	25.24
5089	seq=translation; coord=2:53844493..53846005:1; parent_transcript=GRMZM2G044132_T01; parent_gene=GRMZM2G044132	GRMZM2G044132_P01	TRUE	TRUE	sGAGDDYDSGYNSk	88%	n+304 (+304), K+304 (+304)	26.22	25.00
5090	seq=translation; coord=2:53844493..53846005:1; parent_transcript=GRMZM2G044132_T01; parent_gene=GRMZM2G044132	GRMZM2G044132_P01	TRUE	TRUE	sGNDGYDSGYNR	90%	n+304 (+304)	27.39	25.00
5091	seq=translation; coord=5:183144788..183149469:1; parent_transcript=GRMZM2G007647_T01; parent_gene=GRMZM2G007647	GRMZM2G007647_P01	TRUE	TRUE	eILDIAEIFR	95%	n+304 (+304)	44.02	25.00
5092	seq=translation; coord=5:183144788..183149469:1; parent_transcript=GRMZM2G007647_T01; parent_gene=GRMZM2G007647	GRMZM2G007647_P01	TRUE	TRUE	iAGVfAR	89%	n+304 (+304)	26.14	25.00
5093	seq=translation; coord=5:183144788..183149469:1; parent_transcript=GRMZM2G007647_T01; parent_gene=GRMZM2G007647	GRMZM2G007647_P01	TRUE	TRUE	IIDVHEVHDITHSPFAER	95%	n+304 (+304)	38.24	25.53
5094	seq=translation; coord=5:183144788..183149469:1; parent_transcript=GRMZM2G007647_T01; parent_gene=GRMZM2G007647	GRMZM2G007647_P01	TRUE	TRUE	rEILDIAEIFR	95%	n+304 (+304)	38.81	25.15
5095	seq=translation; coord=5:6445850..6453287:-1; parent_transcript=GRMZM2G076885_T01; parent_gene=GRMZM2G076885	GRMZM2G076885_P01	TRUE	TRUE	aAPGVTIIDDR	95%	n+304 (+304)	36.82	25.90
5096	seq=translation; coord=5:6445850..6453287:-1; parent_transcript=GRMZM2G076885_T01; parent_gene=GRMZM2G076885	GRMZM2G076885_P01	TRUE	TRUE	eDGPSVAIVGATGAVGQEFLLR	95%	n+304 (+304)	45.15	25.51
5097	seq=translation; coord=5:6445850..6453287:-1; parent_transcript=GRMZM2G076885_T01; parent_gene=GRMZM2G076885	GRMZM2G076885_P01	TRUE	TRUE	fPTPLEVSDkDDVAVGR	95%	n+304 (+304), K+304 (+304)	40.33	25.72
5098	seq=translation; coord=5:6445850..6453287:-1; parent_transcript=GRMZM2G076885_T01; parent_gene=GRMZM2G076885	GRMZM2G076885_P01	TRUE	TRUE	gAALNAVQIAEMLLk	95%	n+304 (+304), K+304 (+304)	37.00	25.00
5099	seq=translation; coord=8:144270470..144273473:-1; parent_transcript=GRMZM2G024315_T01; parent_gene=GRMZM2G024315	GRMZM2G024315_P01	TRUE	TRUE	eLGIGIVPYSPLGR	95%	n+304 (+304)	33.67	25.00
5100	seq=translation; coord=8:144270470..144273473:-1; parent_transcript=GRMZM2G024315_T01; parent_gene=GRMZM2G024315	GRMZM2G024315_P01	TRUE	TRUE	fAPENLEk	94%	n+304 (+304), K+304 (+304)	31.60	26.19
5101	seq=translation; coord=3:30996380..30997528:1; parent_transcript=GRMZM2G024315_T01; parent_gene=GRMZM2G024315	GRMZM2G024315_P01	TRUE	TRUE	gVTLFDTSDDVYGPLTNEILLGk	95%	n+304 (+304), K+304 (+304)	71.07	25.00
5102	seq=translation; coord=3:30996380..30997528:1; parent_transcript=AC226235.2_FGT001; parent_gene=AC226235.2_FG001	AC226235.2_FGP001	TRUE	TRUE	aVFVEEGDIATYTVLAADDP	95%	n+304 (+304)	33.82	25.00
5103	seq=translation; coord=3:30996380..30997528:1; parent_transcript=AC226235.2_FGT001; parent_gene=AC226235.2_FG001	AC226235.2_FGP001	TRUE	TRUE	ffPSEFGLDVDR	95%	n+304 (+304)	54.56	25.00

5104	seq=translation; coord=3:30996380..30997528:1; parent_transcript=AC226235.2_FGT001; parent_gene=AC226235.2_FG001 seq=translation; coord=5:65417067..65419686:1;	AC226235.2_FGP001	TRUE	TRUE	gDLYDQASLVSavk	95%	n+304 (+304), K+304 (+304)	34.86	25.84
5105	parent_transcript=GRMZM2G112805_T01; parent_gene=GRMZM2G112805 seq=translation; coord=5:65417067..65419686:1;	GRMZM2G112805_P01	TRUE	TRUE	aISELIPHEIANIEK	94%	n+304 (+304), K+304 (+304)	26.24	25.00
5106	parent_transcript=GRMZM2G112805_T01; parent_gene=GRMZM2G112805 seq=translation; coord=2:34740703..34741540:1;	GRMZM2G112805_P01	TRUE	TRUE	sQIIVDAEEFk	95%	n+304 (+304), K+304 (+304)	55.20	25.80
5107	parent_transcript=AC155352.2_FGT010; parent_gene=AC155352.2_FG010 seq=translation; coord=2:34740703..34741540:1;	AC155352.2_FGP010,GRMZM2G379898_P01,G RMZM2G379898_P02	TRUE	TRUE	aNVLGINLNLPLNLSLLVnycGR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	34.01	25.00
5108	parent_transcript=AC155352.2_FGT010; parent_gene=AC155352.2_FG010 seq=translation; coord=10:4776409..4777145:-1;	AC155352.2_FGP010,GRMZM2G379898_P01,G RMZM2G379898_P02	TRUE	TRUE	cPVDALK	90%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	25.66	25.00
5109	parent_transcript=GRMZM2G031033_T01; parent_gene=GRMZM2G031033 seq=translation; coord=10:4776409..4777145:-1;	GRMZM2G031033_P01	TRUE	TRUE	eVVVGEVEVak	95%	n+304 (+304), K+304 (+304)	28.71	25.62
5110	parent_transcript=GRMZM2G031033_T01; parent_gene=GRMZM2G031033 seq=translation; coord=6:14560251..14563314:-1;	GRMZM2G031033_P01	TRUE	TRUE	vDVAPGLLQDQk	95%	n+304 (+304), K+304 (+304)	45.32	25.20
5111	parent_transcript=GRMZM2G076943_T01; parent_gene=GRMZM2G076943 seq=translation; coord=6:14560251..14563314:-1;	GRMZM2G076943_P01	TRUE	TRUE	gATLYDDPcILR	95%	n+304 (+304), Carbamidomethyl (+57)	34.01	25.00
5112	parent_transcript=GRMZM2G076943_T01; parent_gene=GRMZM2G076943 seq=translation; coord=4:1482217..1485577:-1;	GRMZM2G076943_P01	TRUE	TRUE	sIDSLFLDLPALR	95%	n+304 (+304)	42.53	26.03
5113	parent_transcript=GRMZM2G107082_T01; parent_gene=GRMZM2G107082 seq=translation; coord=4:1482217..1485577:-1;	GRMZM2G107082_P01	TRUE	TRUE	vVLDcATADPDGR	95%	n+304 (+304), Carbamidomethyl (+57)	35.67	25.00
5114	parent_transcript=GRMZM2G107082_T01; parent_gene=GRMZM2G107082 seq=translation; coord=2:233468750..233475308:1;	GRMZM2G107082_P01	TRUE	TRUE	wGGIEFPLPFGR	95%	n+304 (+304)	33.06	25.19
5115	parent_transcript=GRMZM2G117226_T01; parent_gene=GRMZM2G117226 seq=translation; coord=5:181383017..181386545:1;	GRMZM2G117226_P01,GRMZM2G117226_P02, GRMZM2G117226_P03	TRUE	TRUE	iTEVLk	91%	n+304 (+304), K+304 (+304)	25.15	25.00
5116	parent_transcript=GRMZM2G029583_T02; parent_gene=GRMZM2G029583 seq=translation; coord=5:181383017..181386545:1;	GRMZM2G029583_P02,GRMZM2G029583_P03	TRUE	TRUE	iADAEENLGESEVR	95%	n+304 (+304)	67.08	25.00
5117	parent_transcript=GRMZM2G029583_T02; parent_gene=GRMZM2G029583 seq=translation; coord=5:181383017..181386545:1;	GRMZM2G029583_P02,GRMZM2G029583_P03	TRUE	TRUE	sFFVAFSGLTEQIk	95%	n+304 (+304), K+304 (+304)	44.12	25.66
5118	parent_transcript=GRMZM2G029583_T02; parent_gene=GRMZM2G029583 seq=translation; coord=5:181383017..181386545:1;	GRMZM2G029583_P02,GRMZM2G029583_P03	TRUE	TRUE	sLYFIR	86%	n+304 (+304)	25.07	25.00
5119	parent_transcript=GRMZM2G029583_T02; parent_gene=GRMZM2G029583 seq=translation; coord=1:297509820..297513009:-1;	GRMZM2G029583_P02,GRMZM2G029583_P03	TRUE	TRUE	vVDAPEILAVIGk	95%	n+304 (+304), K+304 (+304)	46.17	25.00
5120	parent_transcript=GRMZM5G898915_T01; parent_gene=GRMZM5G898915 seq=translation; coord=1:297509820..297513009:-1;	GRMZM5G898915_P01	TRUE	TRUE	aTYSLPEATTLR	95%	n+304 (+304)	32.63	25.45
5121	parent_transcript=GRMZM5G898915_T01; parent_gene=GRMZM5G898915	GRMZM5G898915_P01	TRUE	TRUE	gMSPYFGcIVGR	95%	n+304 (+304), Carbamidomethyl (+57)	45.03	25.00

5122	seq=translation; coord=1:297509820..297513009:-1; parent_transcript=GRMZM5G898915_T01; parent_gene=GRMZM5G898915 seq=translation; coord=1:297509820..297513009:-1;	GRMZM5G898915_P01	TRUE	TRUE	hITPVDENTIPTGEIMPVDGTPFDFTTER	95%	n+304 (+304)	35.14	25.00
5123	parent_transcript=GRMZM5G898915_T01; parent_gene=GRMZM5G898915 seq=translation; coord=4:26128851..26131595:1;	GRMZM5G898915_P01	TRUE	TRUE	vVWDVVEHk	94%	n+304 (+304), K+304 (+304)	28.27	25.35
5124	parent_transcript=GRMZM2G024482_T02; parent_gene=GRMZM2G024482 seq=translation; coord=4:26128851..26131595:1;	GRMZM2G024482_P02	TRUE	TRUE	dNFFFAGIDk	94%	n+304 (+304), K+304 (+304)	28.30	25.15
5125	parent_transcript=GRMZM2G024482_T02; parent_gene=GRMZM2G024482 seq=translation; coord=4:26128851..26131595:1;	GRMZM2G024482_P02	TRUE	TRUE	fPFLLVDR	94%	n+304 (+304)	31.28	25.00
5126	parent_transcript=GRMZM2G024482_T02; parent_gene=GRMZM2G024482 seq=translation; coord=4:26128851..26131595:1;	GRMZM2G024482_P02	TRUE	TRUE	kPVIAGDTLIMR	95%	K+304 (+304), n+304 (+304)	32.13	25.00
5127	parent_transcript=GRMZM2G024482_T02; parent_gene=GRMZM2G024482 seq=translation; coord=2:82246568..82258715:1;	GRMZM2G024482_P02	TRUE	TRUE	rFPFPSPVMDINQIR	95%	n+304 (+304)	65.26	26.25
5128	parent_transcript=GRMZM2G125310_T01; parent_gene=GRMZM2G125310 seq=translation; coord=2:82246568..82258715:1;	GRMZM2G125310_P01,GRMZM2G125310_P02	TRUE	TRUE	aTLELTHNWGTENDPEFk	95%	n+304 (+304), K+304 (+304)	35.87	25.00
5129	parent_transcript=GRMZM2G125310_T01; parent_gene=GRMZM2G125310 seq=translation; coord=2:82246568..82258715:1;	GRMZM2G125310_P01,GRMZM2G125310_P02	TRUE	TRUE	gFGHIGVTVDVHk	95%	n+304 (+304), K+304 (+304)	27.69	25.72
5130	parent_transcript=GRMZM2G125310_T01; parent_gene=GRMZM2G125310 seq=translation; coord=10:70222469..70228198:-1;	GRMZM2G125310_P01,GRMZM2G125310_P02	TRUE	TRUE	gYFLQQTMLR	89%	n+304 (+304)	26.92	25.00
5131	parent_transcript=GRMZM2G103287_T01; parent_gene=GRMZM2G103287 seq=translation; coord=10:70222469..70228198:-1;	GRMZM2G103287_P01,GRMZM2G103287_P02	TRUE	TRUE	aMQDFGDAEYk	95%	n+304 (+304), K+304 (+304)	32.49	25.00
5132	parent_transcript=GRMZM2G103287_T01; parent_gene=GRMZM2G103287 seq=translation; coord=10:70222469..70228198:-1;	GRMZM2G103287_P01,GRMZM2G103287_P02	TRUE	TRUE	fTEQGDAIVFESEVDk	95%	n+304 (+304), K+304 (+304)	41.73	25.38
5133	parent_transcript=GRMZM2G103287_T01; parent_gene=GRMZM2G103287 seq=translation; coord=10:70222469..70228198:-1;	GRMZM2G103287_P01,GRMZM2G103287_P02	TRUE	TRUE	iWPHSFEFR	91%	n+304 (+304)	25.84	25.00
5134	parent_transcript=GRMZM2G103287_T01; parent_gene=GRMZM2G103287 seq=translation; coord=7:8520216..8522520:-1;	GRMZM2G103287_P01,GRMZM2G103287_P02	TRUE	TRUE	vALGPSGDLSLTSR	95%	n+304 (+304)	61.96	25.48
5135	parent_transcript=GRMZM2G024354_T01; parent_gene=GRMZM2G024354 seq=translation; coord=1:225492875..225495179:1;	GRMZM2G024354_P01	TRUE	TRUE	yFEILVDVAHk	95%	n+304 (+304), K+304 (+304)	65.95	25.00
5136	parent_transcript=GRMZM2G056431_T01; parent_gene=GRMZM2G056431 seq=translation; coord=1:225492875..225495179:1;	GRMZM2G056431_P01,GRMZM2G056431_P02	TRUE	TRUE	aIEAVADIYGIDSIAADLk	95%	n+304 (+304), K+304 (+304)	47.46	25.34
5137	parent_transcript=GRMZM2G056431_T01; parent_gene=GRMZM2G056431 seq=translation; coord=1:225492875..225495179:1;	GRMZM2G056431_P01,GRMZM2G056431_P02	TRUE	TRUE	mTIIGEMDAVAIAk	95%	n+304 (+304), K+304 (+304)	66.27	26.29
5138	parent_transcript=GRMZM2G056431_T01; parent_gene=GRMZM2G056431 seq=translation; coord=10:69423694..69433754:-1;	GRMZM2G056431_P01,GRMZM2G056431_P02	TRUE	TRUE	vPTMTDDk	93%	n+304 (+304), K+304 (+304)	30.39	25.59
5139	parent_transcript=GRMZM2G145870_T01; parent_gene=GRMZM2G145870	GRMZM2G145870_P01,GRMZM2G145870_P02	TRUE	TRUE	aIVGLFGk	95%	n+304 (+304), K+304 (+304)	29.29	25.00

5140	seq=translation; coord=10:69423694..69433754:-1; parent_transcript=GRMZM2G145870_T01; parent_gene=GRMZM2G145870 seq=translation; coord=10:69423694..69433754:-1;	GRMZM2G145870_P01,GRMZM2G145870_P02	TRUE	TRUE	dFYGALEAAYk	95%	n+304 (+304), K+304 (+304)	66.05	25.22
5141	parent_transcript=GRMZM2G145870_T01; parent_gene=GRMZM2G145870 seq=translation; coord=4:5375612..5380694:1;	GRMZM2G145870_P01,GRMZM2G145870_P02	TRUE	TRUE	eIEEELGAPLNILEk	95%	n+304 (+304), K+304 (+304)	47.70	25.00
5142	parent_transcript=GRMZM2G154169_T01; parent_gene=GRMZM2G154169 seq=translation; coord=4:5375612..5380694:1;	GRMZM2G154169_P01	TRUE	TRUE	aAAELQQAAPADGR	92%	n+304 (+304)	27.28	25.87
5143	parent_transcript=GRMZM2G154169_T01; parent_gene=GRMZM2G154169 seq=translation; coord=4:5375612..5380694:1;	GRMZM2G154169_P01	TRUE	TRUE	qLILAILENQNLGk	95%	n+304 (+304), K+304 (+304)	62.68	25.00
5144	parent_transcript=GRMZM2G154169_T01; parent_gene=GRMZM2G154169 seq=translation; coord=4:5375612..5380694:1;	GRMZM2G154169_P01	TRUE	TRUE	qLILAILENQNLGk	92%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.51	25.91
5145	parent_transcript=GRMZM2G154169_T01; parent_gene=GRMZM2G154169 seq=translation; coord=9:110247484..110252966:-1;	GRMZM2G154169_P01	TRUE	TRUE	sATGADTEAGDVAEK	95%	n+304 (+304), K+304 (+304)	39.73	25.00
5146	parent_transcript=GRMZM2G174444_T01; parent_gene=GRMZM2G174444 seq=translation; coord=9:110247484..110252966:-1;	GRMZM2G174444_P01,GRMZM2G174444_P02	TRUE	TRUE	aiAPLVSk	94%	n+304 (+304), K+304 (+304)	27.05	25.00
5147	parent_transcript=GRMZM2G174444_T01; parent_gene=GRMZM2G174444 seq=translation; coord=9:110247484..110252966:-1;	GRMZM2G174444_P01,GRMZM2G174444_P02	TRUE	TRUE	IPAVFYTAVWcGPcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	28.84	25.00
5148	parent_transcript=GRMZM2G174444_T01; parent_gene=GRMZM2G174444 seq=translation; coord=5:29321627..29325204:1;	GRMZM2G174444_P01,GRMZM2G174444_P02	TRUE	TRUE	vDIELEGLNk	95%	n+304 (+304), K+304 (+304)	54.40	26.15
5149	parent_transcript=GRMZM2G158277_T01; parent_gene=GRMZM2G158277 seq=translation; coord=5:29321627..29325204:1;	GRMZM2G158277_P01,GRMZM2G158277_P02, GRMZM2G158277_P03	TRUE	TRUE	eSAVETVLDSSR	95%	n+304 (+304)	53.55	25.00
5150	parent_transcript=GRMZM2G158277_T01; parent_gene=GRMZM2G158277 seq=translation; coord=5:29321627..29325204:1;	GRMZM2G158277_P01,GRMZM2G158277_P02, GRMZM2G158277_P03	TRUE	TRUE	IEDPATGELFAAcFVLPGQR	95%	n+304 (+304), Carbamidomethyl (+57)	35.73	25.00
5151	parent_transcript=GRMZM2G158277_T01; parent_gene=GRMZM2G158277 seq=translation; coord=8:21874081..21876830:1;	GRMZM2G158277_P01,GRMZM2G158277_P02, GRMZM2G158277_P03	TRUE	TRUE	sPLPPPPNDPAAAR	95%	n+304 (+304)	33.07	25.98
5152	parent_transcript=GRMZM2G033283_T01; parent_gene=GRMZM2G033283 seq=translation; coord=8:21874081..21876830:1;	GRMZM2G033283_P01	TRUE	TRUE	fATGASVvk	95%	n+304 (+304), K+304 (+304)	28.89	25.00
5153	parent_transcript=GRMZM2G033283_T01; parent_gene=GRMZM2G033283	GRMZM2G033283_P01	TRUE	TRUE	gLFLFGVk	95%	n+304 (+304), K+304 (+304)	34.25	25.00
5154	seq=translation; coord=8:21874081..21876830:1; parent_transcript=GRMZM2G033283_T01; parent_gene=GRMZM2G033283	GRMZM2G033283_P01	TRUE	TRUE	vLycGVcGLPAEYcEFGPDFER	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	38.93	25.00
5155	seq=translation; coord=6:158946942..158950117:1; parent_transcript=GRMZM2G044368_T01; parent_gene=GRMZM2G044368 seq=translation; coord=6:158946942..158950117:1;	GRMZM2G044368_P01,GRMZM2G158887_P01, GRMZM5G811797_P04,GRMZM5G811797_P05	TRUE	TRUE	aTIGADFLTk	95%	n+304 (+304), K+304 (+304)	33.73	25.00
5156	parent_transcript=GRMZM2G044368_T01; parent_gene=GRMZM2G044368	GRMZM2G044368_P01,GRMZM2G158887_P01, GRMZM5G811797_P04,GRMZM5G811797_P05	TRUE	TRUE	eVQFEDR	94%	n+304 (+304)	30.87	25.00

5157	seq=translation; coord=6:158946942..158950117:1; parent_transcript=GRMZM2G044368_T01; parent_gene=GRMZM2G044368 seq=translation; coord=2:46344346..46345626:-1;	GRMZM2G044368_P01,GRMZM2G158887_P01, GRMZM5G811797_P04,GRMZM5G811797_P05	TRUE	TRUE	vIILGDSGVGk	89%	n+304 (+304), K+304 (+304)	25.15	25.00
5158	parent_transcript=AC206968.3_FGT003; parent_gene=AC206968.3_FG003 seq=translation; coord=2:46344346..46345626:-1;	AC206968.3_FGP003	TRUE	TRUE	iMVNQADDVAGIISsk	94%	n+304 (+304), K+304 (+304)	29.49	26.86
5159	parent_transcript=AC206968.3_FGT003; parent_gene=AC206968.3_FG003 seq=translation; coord=6:130963745..130976059:-1;	AC206968.3_FGP003	TRUE	TRUE	ILLVDIDLLESk	95%	n+304 (+304), K+304 (+304)	58.06	25.00
5160	parent_transcript=GRMZM2G361605_T01; parent_gene=GRMZM2G361605 seq=translation; coord=6:130963745..130976059:-1;	GRMZM2G361605_P01,GRMZM2G361605_P02	TRUE	TRUE	aVLDAATIAGLRPLR	92%	n+304 (+304)	26.38	25.00
5161	parent_transcript=GRMZM2G361605_T01; parent_gene=GRMZM2G361605 seq=translation; coord=5:160443383..160458679:1;	GRMZM2G361605_P01,GRMZM2G361605_P02	TRUE	TRUE	vINEcSEAENWLR	87%	n+304 (+304), Carbamidomethyl (+57)	25.60	25.00
5162	parent_transcript=GRMZM2G052435_T03; parent_gene=GRMZM2G052435 seq=translation; coord=5:160443383..160458679:1;	GRMZM2G052435_P03	TRUE	TRUE	eNVLGFIVQVPPLLR	95%	n+304 (+304)	60.95	25.00
5163	parent_transcript=GRMZM2G052435_T03; parent_gene=GRMZM2G052435 seq=translation; coord=7:170026036..170029198:1;	GRMZM2G052435_P03	TRUE	TRUE	gNVDQWVEHYLR	95%	n+304 (+304)	40.05	25.00
5164	parent_transcript=GRMZM2G055527_T01; parent_gene=GRMZM2G055527 seq=translation; coord=7:170026036..170029198:1;	GRMZM2G055527_P01	TRUE	TRUE	sTYFIQcEPTETALSik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	35.75	25.01
5165	parent_transcript=GRMZM2G055527_T01; parent_gene=GRMZM2G055527 seq=translation; coord=4:45262758..45263990:-1;	GRMZM2G055527_P01	TRUE	TRUE	vDNDSIVALALR	95%	n+304 (+304)	57.62	27.25
5166	parent_transcript=GRMZM2G071575_T01; parent_gene=GRMZM2G071575 seq=translation; coord=4:45262758..45263990:-1;	GRMZM2G071575_P01	TRUE	TRUE	aRPEcLcYIIQQVHAGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	29.54	25.35
5167	parent_transcript=GRMZM2G071575_T01; parent_gene=GRMZM2G071575 seq=translation; coord=3:57145425..57150481:1;	GRMZM2G071575_P01	TRUE	TRUE	dQVQSLGLR	87%	n+304 (+304)	26.69	25.97
5168	parent_transcript=GRMZM2G033644_T01; parent_gene=GRMZM2G033644 seq=translation; coord=3:57145425..57150481:1;	GRMZM2G033644_P01	TRUE	TRUE	fGSPLLNLPEVAIIALGR	95%	n+304 (+304)	33.86	25.00
5169	parent_transcript=GRMZM2G033644_T01; parent_gene=GRMZM2G033644 seq=translation; coord=10:79271116..79273839:-1;	GRMZM2G033644_P01	TRUE	TRUE	hTFLPFLIK	95%	n+304 (+304), K+304 (+304)	30.50	25.00
5170	parent_transcript=GRMZM2G032564_T01; parent_gene=GRMZM2G032564 seq=translation; coord=10:79271116..79273839:-1;	GRMZM2G032564_P01,GRMZM2G152552_P01, GRMZM2G152573_P04,GRMZM2G166963_P01, GRMZM5G820996_P01,GRMZM5G820996_P02	TRUE	TRUE	aFLVEEQk	95%	n+304 (+304), K+304 (+304)	37.81	26.48
5171	parent_transcript=GRMZM2G032564_T01; parent_gene=GRMZM2G032564 seq=translation; coord=2:217631963..217637147:1;	GRMZM2G032564_P01,GRMZM2G152552_P01, GRMZM2G152573_P04,GRMZM2G166963_P01, GRMZM5G820996_P01,GRMZM5G820996_P02	TRUE	TRUE	IVYQYTk	93%	n+304 (+304), K+304 (+304)	28.19	25.00
5172	parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425 seq=translation; coord=2:217631963..217637147:1;	GRMZM2G109425_P01,GRMZM2G109425_P02	TRUE	TRUE	aQLGVEAFEAALLVIPk	95%	n+304 (+304), K+304 (+304)	49.98	25.00
5173	parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425	GRMZM2G109425_P01,GRMZM2G109425_P02	TRUE	TRUE	fLVDFGFDVak	95%	n+304 (+304), K+304 (+304)	40.33	25.89

5174	seq=translation; coord=2:217631963..217637147:1; parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425 seq=translation; coord=2:217631963..217637147:1;	GRMZM2G109425_P01,GRMZM2G109425_P02	TRUE	TRUE	kPDEPIDLFMVEIMHMR	95%	K+304 (+304), n+304 (+304)	43.63	25.77
5175	parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425 seq=translation; coord=2:217631963..217637147:1;	GRMZM2G109425_P01,GRMZM2G109425_P02	TRUE	TRUE	mLVGGAGDLk	95%	n+304 (+304), K+304 (+304)	30.92	26.80
5176	parent_transcript=GRMZM2G109425_T01; parent_gene=GRMZM2G109425 seq=translation; coord=9:136083370..136087677:1;	GRMZM2G109425_P01,GRMZM2G109425_P02	TRUE	TRUE	tLAENSGLDTDQDIVSLQNEHDR	95%	n+304 (+304)	70.33	25.00
5177	parent_transcript=GRMZM2G124059_T01; parent_gene=GRMZM2G124059 seq=translation; coord=9:136083370..136087677:1;	GRMZM2G124059_P01	TRUE	TRUE	aQPVLLPHLLSYVEQLER	95%	n+304 (+304)	44.13	25.00
5178	parent_transcript=GRMZM2G124059_T01; parent_gene=GRMZM2G124059 seq=translation; coord=8:122751582..122753805:1;	GRMZM2G124059_P01	TRUE	TRUE	aQPVLLPHLLSYVEQLER	94%	n+304 (+304), iTRAQ8plex (+304)	25.87	25.00
5179	parent_transcript=GRMZM2G154936_T01; parent_gene=GRMZM2G154936 seq=translation; coord=8:122751582..122753805:1;	GRMZM2G154936_P01,GRMZM2G154936_P02, GRMZM2G154936_P03	TRUE	TRUE	gAdcASAsk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.47	25.00
5180	parent_transcript=GRMZM2G154936_T01; parent_gene=GRMZM2G154936 seq=translation; coord=8:122751582..122753805:1;	GRMZM2G154936_P01,GRMZM2G154936_P02, GRMZM2G154936_P03	TRUE	TRUE	tGVPDQAMQAAIDYAcAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	63.91	25.00
5181	parent_transcript=GRMZM2G154936_T01; parent_gene=GRMZM2G154936 seq=translation; coord=10:35583589..35590383:1;	GRMZM2G154936_P01,GRMZM2G154936_P02, GRMZM2G154936_P03	TRUE	TRUE	vAVcSYicNSYQSR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	60.67	25.00
5182	parent_transcript=GRMZM2G009443_T01; parent_gene=GRMZM2G009443 seq=translation; coord=10:35583589..35590383:1;	GRMZM2G009443_P01,GRMZM2G123922_P01	TRUE	TRUE	aHPDVFNMMMLQILEDGR	95%	n+304 (+304)	45.30	25.00
5183	parent_transcript=GRMZM2G009443_T01; parent_gene=GRMZM2G009443 seq=translation; coord=8:1370962..1373972:-1;	GRMZM2G042636_P01,GRMZM2G042636_P02, GRMZM2G042636_P03,GRMZM2G042636_P04, GRMZM2G133802_P01,GRMZM2G133802_P02, GRMZM2G133802_P03	TRUE	TRUE	yVGTSDLQLER	95%	n+304 (+304), K+304 (+304)	53.14	25.00
5184	parent_transcript=GRMZM2G042636_T01; parent_gene=GRMZM2G042636 seq=translation; coord=4:93237748..93253880:1;	GRMZM2G042636_P01,GRMZM2G042636_P02, GRMZM2G042636_P03,GRMZM2G042636_P04, GRMZM2G133802_P01,GRMZM2G133802_P02, GRMZM2G133802_P03	TRUE	TRUE	yVGTSDLQLER	95%	n+304 (+304)	53.70	25.28
5185	parent_transcript=GRMZM2G451443_T01; parent_gene=GRMZM2G451443 seq=translation; coord=4:93237748..93253880:1;	GRMZM2G451443_P01	TRUE	TRUE	eNILGFIVQVPPLLR	93%	n+304 (+304)	28.34	25.00
5186	parent_transcript=GRMZM2G451443_T01; parent_gene=GRMZM2G451443 seq=translation; coord=5:24616889..24618887:-1;	GRMZM2G451443_P01	TRUE	TRUE	tAAMDFVSELVR	95%	n+304 (+304)	33.67	25.00
5187	parent_transcript=GRMZM2G032910_T01; parent_gene=GRMZM2G032910 seq=translation; coord=5:24616889..24618887:-1;	GRMZM2G032910_P01,GRMZM2G032910_P02	TRUE	TRUE	dFGAMPAYEFALQHPGR	95%	n+304 (+304)	63.27	25.00
5188	parent_transcript=GRMZM2G032910_T01; parent_gene=GRMZM2G032910 seq=translation; coord=5:24616889..24618887:-1;	GRMZM2G032910_P01,GRMZM2G032910_P02	TRUE	TRUE	fPGFETAMR	93%	n+304 (+304)	30.11	25.00
5189	parent_transcript=GRMZM2G032910_T01; parent_gene=GRMZM2G032910 seq=translation; coord=5:24616889..24618887:-1;	GRMZM2G032910_P01,GRMZM2G032910_P02	TRUE	TRUE	fQVPVFMVMGEK	95%	n+304 (+304), K+304 (+304)	32.02	25.63
5190	parent_transcript=GRMZM2G032910_T01; parent_gene=GRMZM2G032910	GRMZM2G032910_P01,GRMZM2G032910_P02	TRUE	TRUE	tIYVLFAGAEIPIAk	95%	n+304 (+304), K+304 (+304)	47.04	25.00

5191	seq=translation; coord=1:12987102..12993471:1; parent_transcript=GRMZM2G172322_T01; parent_gene=GRMZM2G172322	GRMZM2G172322_P01,GRMZM2G172322_P02	TRUE	TRUE	aTSLGLPDR	92%	n+304 (+304)	30.34	26.51
5192	seq=translation; coord=1:12987102..12993471:1; parent_transcript=GRMZM2G172322_T01; parent_gene=GRMZM2G172322	GRMZM2G172322_P01,GRMZM2G172322_P02	TRUE	TRUE	gITFHTEQSPQAItk	94%	n+304 (+304), K+304 (+304)	28.06	25.00
5193	seq=translation; coord=1:12987102..12993471:1; parent_transcript=GRMZM2G172322_T01; parent_gene=GRMZM2G172322	GRMZM2G172322_P01,GRMZM2G172322_P02	TRUE	TRUE	tSVDSIWAVGDTVNR	92%	n+304 (+304)	26.99	25.00
5194	seq=translation; coord=1:12987102..12993471:1; parent_transcript=GRMZM2G172322_T01; parent_gene=GRMZM2G172322	GRMZM2G172322_P01,GRMZM2G172322_P02	TRUE	TRUE	vNLTPVALMEGGAFAK	95%	n+304 (+304), K+304 (+304)	37.53	25.45
5195	seq=translation; coord=4:54600217..54609072:-1; parent_transcript=GRMZM2G098496_T01; parent_gene=GRMZM2G098496	GRMZM2G098496_P01,GRMZM2G098496_P02	TRUE	TRUE	aTEIFEAIAR	93%	n+304 (+304)	29.89	25.01
5196	seq=translation; coord=4:54600217..54609072:-1; parent_transcript=GRMZM2G098496_T01; parent_gene=GRMZM2G098496	GRMZM2G098496_P01,GRMZM2G098496_P02	TRUE	TRUE	ILADLAASMDEGDVAK	95%	n+304 (+304), K+304 (+304)	41.93	25.08
5197	seq=translation; coord=4:54600217..54609072:-1; parent_transcript=GRMZM2G098496_T01; parent_gene=GRMZM2G098496	GRMZM2G098496_P01,GRMZM2G098496_P02	TRUE	TRUE	vAEIAAQLEQYPK	95%	n+304 (+304), K+304 (+304)	38.22	25.00
5198	seq=translation; coord=3:148834092..148846161:-1; parent_transcript=GRMZM2G047310_T02; parent_gene=GRMZM2G047310	GRMZM2G047310_P02	TRUE	TRUE	eAYLSDSEFQTVFGMTK	95%	n+304 (+304), K+304 (+304)	45.60	25.00
5199	seq=translation; coord=3:148834092..148846161:-1; parent_transcript=GRMZM2G047310_T02; parent_gene=GRMZM2G047310	GRMZM2G047310_P02	TRUE	TRUE	ePPQFVALFQPMVILK	95%	n+304 (+304), K+304 (+304)	38.22	25.00
5200	seq=translation; coord=3:148834092..148846161:-1; parent_transcript=GRMZM2G047310_T02; parent_gene=GRMZM2G047310	GRMZM2G047310_P02	TRUE	TRUE	tVSDDDVVLETTAPK	92%	n+304 (+304), K+304 (+304)	27.10	25.61
5201	seq=translation; coord=5:155530969..155538363:-1; parent_transcript=GRMZM2G015132_T01; parent_gene=GRMZM2G015132	GRMZM2G015132_P01	TRUE	TRUE	dNSLkPADYEGGTFTVSNLGGPFGIK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.94	25.00
5202	seq=translation; coord=5:155530969..155538363:-1; parent_transcript=GRMZM2G015132_T01; parent_gene=GRMZM2G015132	GRMZM2G015132_P01	TRUE	TRUE	gLGAIAEEVk	90%	n+304 (+304), K+304 (+304)	27.03	26.64
5203	seq=translation; coord=5:155530969..155538363:-1; parent_transcript=GRMZM2G015132_T01; parent_gene=GRMZM2G015132	GRMZM2G015132_P01	TRUE	TRUE	viDGAIGAEFlk	95%	n+304 (+304), K+304 (+304)	60.13	25.00
5204	seq=translation; coord=8:98594898..98599276:-1; parent_transcript=GRMZM2G114954_T01; parent_gene=GRMZM2G114954	GRMZM2G114954_P01,GRMZM2G114954_P02, GRMZM2G114954_P03,GRMZM2G114954_P04	TRUE	TRUE	IEFLLTELK	95%	n+304 (+304), K+304 (+304)	29.45	25.00
5205	seq=translation; coord=8:98594898..98599276:-1; parent_transcript=GRMZM2G114954_T01; parent_gene=GRMZM2G114954	GRMZM2G114954_P01,GRMZM2G114954_P02, GRMZM2G114954_P03,GRMZM2G114954_P04	TRUE	TRUE	vIAAYLLAVLGGNTSPTADDVk	95%	n+304 (+304), K+304 (+304)	29.98	25.00
5206	seq=translation; coord=8:9919345..9920090:-1; parent_transcript=AC204893.3_FGT001; parent_gene=AC204893.3_FG001	AC204893.3_FGP001,GRMZM2G322618_P01	TRUE	TRUE	nAAcLAEQLAR	95%	n+304 (+304), Carbamidomethyl (+57)	50.03	25.00
5207	seq=translation; coord=8:9919345..9920090:-1; parent_transcript=AC204893.3_FGT001; parent_gene=AC204893.3_FG001	AC204893.3_FGP001,GRMZM2G322618_P01	TRUE	TRUE	vPALSENk	95%	n+304 (+304), K+304 (+304)	32.78	25.11
5208	seq=translation; coord=8:159703050..159707801:1; parent_transcript=GRMZM2G122607_T01; parent_gene=GRMZM2G122607	GRMZM2G122607_P01	TRUE	TRUE	dLAADGGGAGGGGIGVVEMLFR	95%	n+304 (+304)	58.05	25.00

5209	seq=translation; coord=8:159703050..159707801:1; parent_transcript=GRMZM2G122607_T01; parent_gene=GRMZM2G122607	GRMZM2G122607_P01	TRUE	TRUE	iIVVLENk	95%	n+304 (+304), K+304 (+304)	36.11	25.00
5210	seq=translation; coord=4:161027635..161031592:-1; parent_transcript=GRMZM2G156068_T01; parent_gene=GRMZM2G156068	GRMZM2G156068_P01,GRMZM2G156068_P02	TRUE	TRUE	aIAEIFADAGFSVDVk	95%	n+304 (+304), K+304 (+304)	51.63	26.63
5211	seq=translation; coord=4:161027635..161031592:-1; parent_transcript=GRMZM2G156068_T01; parent_gene=GRMZM2G156068	GRMZM2G156068_P01,GRMZM2G156068_P02	TRUE	TRUE	aLFGGTGNYASALFLTAak	95%	n+304 (+304), K+304 (+304)	60.12	25.16
5212	seq=translation; coord=3:88528132..88533870:-1; parent_transcript=GRMZM2G476933_T01; parent_gene=GRMZM2G476933	GRMZM2G476933_P01	TRUE	TRUE	aTAADPAPGAPAE NSTDk	95%	n+304 (+304), K+304 (+304)	52.23	25.12
5213	seq=translation; coord=3:88528132..88533870:-1; parent_transcript=GRMZM2G476933_T01; parent_gene=GRMZM2G476933	GRMZM2G476933_P01	TRUE	TRUE	sDAEPAAAAAPVPGTNSDAAATDPAPGk	95%	n+304 (+304), K+304 (+304)	33.39	25.00
5214	seq=translation; coord=3:88528132..88533870:-1; parent_transcript=GRMZM2G476933_T01; parent_gene=GRMZM2G476933	GRMZM2G476933_P01	TRUE	TRUE	sDAEPAAVAAPAPETk	95%	n+304 (+304), K+304 (+304)	64.13	25.89
5215	seq=translation; coord=1:54927760..54932392:-1; parent_transcript=GRMZM2G031825_T01; parent_gene=GRMZM2G031825	GRMZM2G031825_P01,GRMZM2G031825_P02, GRMZM2G031825_P05	TRUE	TRUE	vDLPEIQAk	89%	n+304 (+304), K+304 (+304)	26.71	25.00
5216	seq=translation; coord=5:181390095..181395720:1; parent_transcript=GRMZM2G031107_T01; parent_gene=GRMZM2G031107	GRMZM2G031107_P01,GRMZM2G031107_P02	TRUE	TRUE	aAWEIFTPLLHDIDGGk	95%	n+304 (+304), K+304 (+304)	54.45	25.26
5217	seq=translation; coord=10:112583884..112587345:-1; parent_transcript=GRMZM2G022180_T02; parent_gene=GRMZM2G022180	GRMZM2G022180_P02	TRUE	TRUE	iLIDGEEK	91%	n+304 (+304), K+304 (+304)	28.86	25.84
5218	seq=translation; coord=5:66839986..66842997:-1; parent_transcript=GRMZM2G115176_T01; parent_gene=GRMZM2G115176	GRMZM2G115176_P01,GRMZM2G115176_P03, GRMZM2G115925_P01,GRMZM5G884325_P01, GRMZM5G884325_P02	TRUE	TRUE	fMIIPDMLk	90%	n+304 (+304), K+304 (+304)	26.12	25.45
5219	seq=translation; coord=6:167429613..167438752:-1; parent_transcript=GRMZM2G402002_T01; parent_gene=GRMZM2G402002	GRMZM2G402002_P01	TRUE	TRUE	iFSLPDLElIR	91%	n+304 (+304)	27.93	25.01
5220	seq=translation; coord=6:167429613..167438752:-1; parent_transcript=GRMZM2G402002_T01; parent_gene=GRMZM2G402002	GRMZM2G402002_P01	TRUE	TRUE	nFLDGLIESFLDLsR	95%	n+304 (+304)	41.13	25.00
5221	seq=translation; coord=1:56223520..56226018:1; parent_transcript=GRMZM2G062425_T01; parent_gene=GRMZM2G062425	GRMZM2G062425_P01,GRMZM2G062425_P02	TRUE	TRUE	eTAQQLLSQFEk	92%	n+304 (+304), K+304 (+304)	27.00	26.16
5222	seq=translation; coord=1:56223520..56226018:1; parent_transcript=GRMZM2G062425_T01; parent_gene=GRMZM2G062425	GRMZM2G062425_P01,GRMZM2G062425_P02	TRUE	TRUE	gDITLWSVDcATDAIVNAANER	95%	n+304 (+304), Carbamidomethyl (+57)	65.72	25.00
5223	seq=translation; coord=1:56223520..56226018:1; parent_transcript=GRMZM2G062425_T01; parent_gene=GRMZM2G062425	GRMZM2G062425_P01,GRMZM2G062425_P02	TRUE	TRUE	ISAAPGAGLLk	95%	n+304 (+304), K+304 (+304)	45.94	25.00
5224	seq=translation; coord=2:207265904..207268967:1; parent_transcript=AC194970.5_FGT009; parent_gene=AC194970.5_FG009	AC194970.5_FGP009	TRUE	TRUE	aAGLILQLIR	94%	n+304 (+304)	29.19	25.00
5225	seq=translation; coord=2:207265904..207268967:1; parent_transcript=AC194970.5_FGT009; parent_gene=AC194970.5_FG009	AC194970.5_FGP009	TRUE	TRUE	iLDIR	86%	n+304 (+304)	25.44	25.00
5226	seq=translation; coord=3:224163656..224168718:-1; parent_transcript=GRMZM2G339540_T04; parent_gene=GRMZM2G339540	GRMZM2G339540_P04,GRMZM2G339540_P05	TRUE	TRUE	aFLQQLNSGPIPTGIQk	95%	n+304 (+304), K+304 (+304)	61.97	25.00

5227	seq=translation; coord=3:224163656..224168718:-1; parent_transcript=GRMZM2G339540_T04; parent_gene=GRMZM2G339540 seq=translation; coord=3:224163656..224168718:-1;	GRMZM2G339540_P04,GRMZM2G339540_P05	TRUE	TRUE	IPGVGLVGAIPPGTLGR	95%	n+304 (+304)	41.79	25.00
5228	parent_transcript=GRMZM2G339540_T04; parent_gene=GRMZM2G339540 seq=translation; coord=7:154714410..154723867:1;	GRMZM2G339540_P04,GRMZM2G339540_P05	TRUE	TRUE	sALLAFLTATPHER	95%	n+304 (+304)	52.35	26.01
5229	parent_transcript=GRMZM2G375593_T01; parent_gene=GRMZM2G375593 seq=translation; coord=7:154714410..154723867:1;	GRMZM2G375593_P01	TRUE	TRUE	eGSETDQFWSLGGK	93%	n+304 (+304), K+304 (+304)	26.84	25.00
5230	parent_transcript=GRMZM2G375593_T01; parent_gene=GRMZM2G375593 seq=translation; coord=7:154714410..154723867:1;	GRMZM2G375593_P01	TRUE	TRUE	fIVLDFLMENLAR	95%	n+304 (+304)	29.51	26.25
5231	parent_transcript=GRMZM2G375593_T01; parent_gene=GRMZM2G375593 seq=translation; coord=7:7507005..7510800:-1;	GRMZM2G375593_P01	TRUE	TRUE	iALQLF	95%	n+304 (+304)	31.03	25.00
5232	parent_transcript=GRMZM2G143330_T01; parent_gene=GRMZM2G143330 seq=translation; coord=7:7507005..7510800:-1;	GRMZM2G143330_P01	TRUE	TRUE	iWDSETGQLLk	95%	n+304 (+304), K+304 (+304)	52.57	25.44
5233	parent_transcript=GRMZM2G143330_T01; parent_gene=GRMZM2G143330 seq=translation; coord=7:124863398..124868735:1;	GRMZM2G143330_P01	TRUE	TRUE	tIITAGEDATVR	95%	n+304 (+304)	39.93	25.35
5234	parent_transcript=GRMZM2G067265_T01; parent_gene=GRMZM2G067265 seq=translation; coord=7:124863398..124868735:1;	GRMZM2G067265_P01,GRMZM2G067265_P02	TRUE	TRUE	aPDFAVPLEEEAAVSk	95%	n+304 (+304), K+304 (+304)	41.37	25.66
5235	parent_transcript=GRMZM2G067265_T01; parent_gene=GRMZM2G067265 seq=translation; coord=7:124863398..124868735:1;	GRMZM2G067265_P01,GRMZM2G067265_P02	TRUE	TRUE	hGAINLGQGFPNFDGPDFVk	95%	n+304 (+304), K+304 (+304)	47.80	25.71
5236	parent_transcript=GRMZM2G067265_T01; parent_gene=GRMZM2G067265 seq=translation; coord=5:136560253..136565466:1;	GRMZM2G067265_P01,GRMZM2G067265_P02	TRUE	TRUE	tTIFTQMSMLAIk	94%	n+304 (+304), K+304 (+304)	27.65	25.00
5237	parent_transcript=GRMZM2G147210_T01; parent_gene=GRMZM2G147210 seq=translation; coord=3:15212255..15222203:-1;	GRMZM2G147210_P01	TRUE	TRUE	sPEDAAALIDDk	95%	n+304 (+304), K+304 (+304)	31.10	25.00
5238	parent_transcript=GRMZM2G334628_T01; parent_gene=GRMZM2G334628 seq=translation; coord=5:23838144..23838818:1;	GRMZM2G334628_P01,GRMZM2G334628_P02, GRMZM2G334628_P07	TRUE	TRUE	aNDQYLPFVIVDDSGk	95%	n+304 (+304), K+304 (+304)	33.53	25.00
5239	parent_transcript=GRMZM2G387360_T01; parent_gene=GRMZM2G387360 seq=translation; coord=1:289786005..289788499:1;	GRMZM2G387360_P01	TRUE	TRUE	aQEPcFcQYAR	87%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57) n+304 (+304),	25.49	25.00
5240	parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833	GRMZM2G168833_P01	TRUE	TRUE	aMDLPSLcSNPATFSDcPk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	28.85	25.00
5241	seq=translation; coord=1:289786005..289788499:1; parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833	GRMZM2G168833_P01	TRUE	TRUE	amDLPSLcSNPATFSDcPk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	29.81	25.00
5242	seq=translation; coord=1:289786005..289788499:1; parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833	GRMZM2G168833_P01	TRUE	TRUE	aPTPDccAGLk	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	55.27	25.00
5243	seq=translation; coord=1:289786005..289788499:1; parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833	GRMZM2G168833_P01	TRUE	TRUE	iLGMSDPAPEAIEFk	95%	n+304 (+304), K+304 (+304)	38.76	25.93

5244	seq=translation; coord=1:289786005..289788499:1; parent_transcript=GRMZM2G168833_T01; parent_gene=GRMZM2G168833 seq=translation; coord=5:159290030..159322686:-1;	GRMZM2G168833_P01	TRUE	TRUE	ImGLATcLTFVQDk	95%	n+304 (+304), Oxidation (+16), Carbamidomethyl (+57), K+304 (+304)	44.21	25.42
5245	parent_transcript=GRMZM2G386155_T01; parent_gene=GRMZM2G386155 seq=translation; coord=5:159290030..159322686:-1;	GRMZM2G386155_P01,GRMZM2G386155_P02	TRUE	TRUE	gAGHVPSDYLPEFVFAAYQR	95%	n+304 (+304)	56.18	25.00
5246	parent_transcript=GRMZM2G386155_T01; parent_gene=GRMZM2G386155 seq=translation; coord=5:159290030..159322686:-1;	GRMZM2G386155_P01,GRMZM2G386155_P02	TRUE	TRUE	mGITNQFIEYDSGQMFESLSk	95%	n+304 (+304), K+304 (+304)	59.56	25.00
5247	parent_transcript=GRMZM2G386155_T01; parent_gene=GRMZM2G386155 seq=translation; coord=5:159290030..159322686:-1;	GRMZM2G386155_P01,GRMZM2G386155_P02	TRUE	TRUE	vADLYDFLSk	95%	n+304 (+304), K+304 (+304)	33.46	25.35
5248	parent_transcript=GRMZM2G386155_T01; parent_gene=GRMZM2G386155 seq=translation; coord=6:103857605..103858686:-1;	GRMZM2G386155_P01,GRMZM2G386155_P02	TRUE	TRUE	vAVNPYSWTK	92%	n+304 (+304), K+304 (+304)	27.69	25.19
5249	parent_transcript=GRMZM2G335618_T01; parent_gene=GRMZM2G335618 seq=translation; coord=6:103857605..103858686:-1;	GRMZM2G335618_P01	TRUE	TRUE	kGLVLLDFWVSPFGQR	94%	K+304 (+304), n+304 (+304)	25.74	25.00
5250	parent_transcript=GRMZM2G335618_T01; parent_gene=GRMZM2G335618 seq=translation; coord=6:103857605..103858686:-1;	GRMZM2G335618_P01	TRUE	TRUE	ILPDAAYAR	91%	n+304 (+304)	27.77	25.00
5251	parent_transcript=GRMZM2G335618_T01; parent_gene=GRMZM2G335618 seq=translation; coord=6:103857605..103858686:-1;	GRMZM2G335618_P01	TRUE	TRUE	sDILLR	93%	n+304 (+304)	30.65	25.43
5252	parent_transcript=GRMZM2G335618_T01; parent_gene=GRMZM2G335618 seq=translation; coord=2:42784980..42792494:1;	GRMZM2G335618_P01	TRUE	TRUE	vDEFINLLk	95%	n+304 (+304), K+304 (+304)	35.49	25.00
5253	parent_transcript=GRMZM2G065073_T02; parent_gene=GRMZM2G065073 seq=translation; coord=2:42784980..42792494:1;	GRMZM2G065073_P02	TRUE	TRUE	IADGTAVVYDSR	95%	n+304 (+304)	36.70	25.00
5254	parent_transcript=GRMZM2G065073_T02; parent_gene=GRMZM2G065073 seq=translation; coord=2:42784980..42792494:1;	GRMZM2G065073_P02	TRUE	TRUE	nMDPLASVMAPR	94%	n+304 (+304)	30.75	25.00
5255	parent_transcript=GRMZM2G065073_T02; parent_gene=GRMZM2G065073 seq=translation; coord=8:607069..619737:1;	GRMZM2G065073_P02	TRUE	TRUE	qGDLTAVSDPR	95%	n+304 (+304)	45.48	25.00
5256	parent_transcript=GRMZM2G077233_T01; parent_gene=GRMZM2G077233 seq=translation; coord=8:607069..619737:1;	GRMZM2G077233_P01,GRMZM2G077233_P02, GRMZM2G077233_P03,GRMZM2G077233_P04, GRMZM2G077233_P06	TRUE	TRUE	dVFSFWLNR	95%	n+304 (+304)	37.32	25.00
5257	parent_transcript=GRMZM2G077233_T01; parent_gene=GRMZM2G077233 seq=translation; coord=8:607069..619737:1;	GRMZM2G077233_P01,GRMZM2G077233_P02, GRMZM2G077233_P03,GRMZM2G077233_P04, GRMZM2G077233_P06	TRUE	TRUE	eLILNYANQLcER	94%	n+304 (+304), Carbamidomethyl (+57)	31.25	25.00
5258	parent_transcript=GRMZM2G077233_T01; parent_gene=GRMZM2G077233 seq=translation; coord=3:184434264..184435351:1;	GRMZM2G077233_P01,GRMZM2G077233_P02, GRMZM2G077233_P03,GRMZM2G077233_P04, GRMZM2G077233_P06	TRUE	TRUE	tFTLTPEQYIVk	95%	n+304 (+304), K+304 (+304)	31.82	25.30
5259	parent_transcript=GRMZM2G126397_T01; parent_gene=GRMZM2G126397 seq=translation; coord=3:184434264..184435351:1;	GRMZM2G126397_P01	TRUE	TRUE	sLLQQANNTPDR	95%	n+304 (+304)	47.89	25.00
5260	parent_transcript=GRMZM2G126397_T01; parent_gene=GRMZM2G126397	GRMZM2G126397_P01	TRUE	TRUE	tlcGcLk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	32.22	25.82

5261	seq=translation; coord=5:168890072..168891220:-1; parent_transcript=GRMZM2G115491_T01; parent_gene=GRMZM2G115491	GRMZM2G115491_P01	TRUE	TRUE	aFGLPEELR	95%	n+304 (+304)	35.92	25.00
5262	seq=translation; coord=5:168890072..168891220:-1; parent_transcript=GRMZM2G115491_T01; parent_gene=GRMZM2G115491	GRMZM2G115491_P01	TRUE	TRUE	aTETALVLAGR	95%	n+304 (+304)	49.11	25.72
5263	seq=translation; coord=8:5023676..5024789:1; parent_transcript=GRMZM2G095164_T01; parent_gene=GRMZM2G095164	GRMZM2G095164_P01,GRMZM2G332259_P01	TRUE	TRUE	gASYYNcQPGAEANPYSR	93%	n+304 (+304), Carbamidomethyl (+57)	29.43	25.00
5264	seq=translation; coord=8:5023676..5024789:1; parent_transcript=GRMZM2G095164_T01; parent_gene=GRMZM2G095164	GRMZM2G095164_P01,GRMZM2G332259_P01	TRUE	TRUE	gcSAITQcR	92%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	29.23	25.00
5265	seq=translation; coord=4:35209593..35215535:1; parent_transcript=GRMZM2G145972_T02; parent_gene=GRMZM2G145972	GRMZM2G145972_P02	TRUE	TRUE	iSLIEAADHILTMFDk	95%	n+304 (+304), K+304 (+304)	31.55	26.06
5266	seq=translation; coord=4:35209593..35215535:1; parent_transcript=GRMZM2G145972_T02; parent_gene=GRMZM2G145972	GRMZM2G145972_P02	TRUE	TRUE	vMEDISEIFR	94%	n+304 (+304)	31.39	25.00
5267	seq=translation; coord=9:143036859..143040005:-1; parent_transcript=GRMZM2G149809_T01; parent_gene=GRMZM2G149809	GRMZM2G149809_P01,GRMZM2G149809_P02	TRUE	TRUE	gASAAVDAPAGWSGR	95%	n+304 (+304)	73.99	25.00
5268	seq=translation; coord=9:143036859..143040005:-1; parent_transcript=GRMZM2G149809_T01; parent_gene=GRMZM2G149809	GRMZM2G149809_P01,GRMZM2G149809_P02	TRUE	TRUE	tLCATDGATGR	95%	n+304 (+304), Carbamidomethyl (+57)	41.05	25.00
5269	seq=translation; coord=3:147969444..147972018:1; parent_transcript=GRMZM2G701801_T02; parent_gene=GRMZM2G701801	GRMZM2G701801_P02	TRUE	TRUE	aAAEVcEDSIPGLR	95%	n+304 (+304), Carbamidomethyl (+57)	48.71	25.00
5270	seq=translation; coord=3:147969444..147972018:1; parent_transcript=GRMZM2G701801_T02; parent_gene=GRMZM2G701801	GRMZM2G701801_P02	TRUE	TRUE	vLLSLQAFTLR	88%	n+304 (+304)	26.88	25.48
5271	seq=translation; coord=2:222675442..222682154:1; parent_transcript=GRMZM2G015933_T01; parent_gene=GRMZM2G015933	GRMZM2G015933_P01	TRUE	TRUE	vTAVIQDMR	95%	n+304 (+304)	32.88	25.11
5272	seq=translation; coord=4:20506351..20509895:1; parent_transcript=GRMZM2G112795_T01; parent_gene=GRMZM2G112795	GRMZM2G112795_P01	TRUE	TRUE	mIYDVNSPLFR	95%	n+304 (+304)	39.42	25.00
5273	seq=translation; coord=1:219892621..219901471:1; parent_transcript=GRMZM2G015925_T01; parent_gene=GRMZM2G015925	GRMZM2G015925_P01,GRMZM2G015925_P02	TRUE	TRUE	eVAELIk	87%	n+304 (+304), K+304 (+304)	26.02	25.47
5274	seq=translation; coord=8:159254849..159263818:-1; parent_transcript=GRMZM2G046558_T02; parent_gene=GRMZM2G046558	GRMZM2G046558_P02	TRUE	TRUE	aAAAHGIALVAPDTSPR	95%	n+304 (+304)	38.60	26.09
5275	seq=translation; coord=8:159254849..159263818:-1; parent_transcript=GRMZM2G046558_T02; parent_gene=GRMZM2G046558	GRMZM2G046558_P02	TRUE	TRUE	aAGAALTlR	90%	n+304 (+304)	26.53	25.00
5276	seq=translation; coord=8:159254849..159263818:-1; parent_transcript=GRMZM2G046558_T02; parent_gene=GRMZM2G046558	GRMZM2G046558_P02	TRUE	TRUE	sDWEEYDAtCLik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.91	25.00
5277	seq=translation; coord=8:159254849..159263818:-1; parent_transcript=GRMZM2G046558_T02; parent_gene=GRMZM2G046558	GRMZM2G046558_P02	TRUE	TRUE	vPTTILIDQGEADk	91%	n+304 (+304), K+304 (+304)	26.09	25.88
5278	seq=translation; coord=9:64132094..64145762:1; parent_transcript=GRMZM2G072909_T01; parent_gene=GRMZM2G072909	GRMZM2G072909_P01	TRUE	TRUE	aNVVVASLEDKLEIVASR	95%	n+304 (+304), K+304 (+304)	61.60	25.00

5279	seq=translation; coord=9:64132094..64145762:1; parent_transcript=GRMZM2G072909_T01; parent_gene=GRMZM2G072909	GRMZM2G072909_P01	TRUE	TRUE	gPGTAMEYSVILVEQLYGK	95%	n+304 (+304), K+304 (+304)	45.58	25.26
5280	seq=translation; coord=9:64132094..64145762:1; parent_transcript=GRMZM2G072909_T01; parent_gene=GRMZM2G072909	GRMZM2G072909_P01	TRUE	TRUE	mIADVLLDDALK	95%	n+304 (+304), K+304 (+304)	63.18	26.26
5281	seq=translation; coord=4:194605171..194610906:-1; parent_transcript=GRMZM2G097043_T01; parent_gene=GRMZM2G097043	GRMZM2G097043_P01	TRUE	TRUE	IDDFVASRPELVIEGDFIHLR	95%	n+304 (+304)	47.33	25.37
5282	seq=translation; coord=4:194605171..194610906:-1; parent_transcript=GRMZM2G097043_T01; parent_gene=GRMZM2G097043	GRMZM2G097043_P01	TRUE	TRUE	qIHDLQELLR	95%	Pyro-cmC (-17), n+304 (+304)	38.34	25.00
5283	seq=translation; coord=4:194605171..194610906:-1; parent_transcript=GRMZM2G097043_T01; parent_gene=GRMZM2G097043	GRMZM2G097043_P01	TRUE	TRUE	sLLHTIQQLQQELAEAR	95%	n+304 (+304)	56.67	25.75
5284	seq=translation; coord=1:3830541..3834833:1; parent_transcript=GRMZM2G085909_T01; parent_gene=GRMZM2G085909	GRMZM2G085909_P01	TRUE	TRUE	aVEILHAMAIPIELSDR	95%	n+304 (+304)	54.41	26.07
5285	seq=translation; coord=1:3830541..3834833:1; parent_transcript=GRMZM2G085909_T01; parent_gene=GRMZM2G085909	GRMZM2G085909_P01	TRUE	TRUE	gSNQLVIDEAER	95%	n+304 (+304)	73.15	25.13
5286	seq=translation; coord=1:3830541..3834833:1; parent_transcript=GRMZM2G085909_T01; parent_gene=GRMZM2G085909	GRMZM2G085909_P01	TRUE	TRUE	iAVIQFQISPPK	95%	n+304 (+304), K+304 (+304)	48.19	25.00
5287	seq=translation; coord=1:3830541..3834833:1; parent_transcript=GRMZM2G085909_T01; parent_gene=GRMZM2G085909	GRMZM2G085909_P01	TRUE	TRUE	IGGTVDDELIPGLIFDK	95%	n+304 (+304), K+304 (+304)	36.92	25.24
5288	seq=translation; coord=2:212802942..212807188:1; parent_transcript=GRMZM2G141510_T01; parent_gene=GRMZM2G141510	GRMZM2G141510_P01	TRUE	TRUE	dHEILPPLPVGFHR	94%	n+304 (+304)	27.05	25.79
5289	seq=translation; coord=2:212802942..212807188:1; parent_transcript=GRMZM2G141510_T01; parent_gene=GRMZM2G141510	GRMZM2G141510_P01	TRUE	TRUE	sALEATAPGLEAK	95%	n+304 (+304), K+304 (+304)	31.72	25.99
5290	seq=translation; coord=2:212802942..212807188:1; parent_transcript=GRMZM2G141510_T01; parent_gene=GRMZM2G141510	GRMZM2G141510_P01	TRUE	TRUE	yTVENLNDVSSDALLER	95%	n+304 (+304)	52.42	25.00
5291	seq=translation; coord=8:10870907..10877056:1; parent_transcript=GRMZM2G030384_T01; parent_gene=GRMZM2G030384	GRMZM2G030384_P01	TRUE	TRUE	aFVWDSGSTVGEGDGHK	95%	n+304 (+304), K+304 (+304)	52.01	25.00
5292	seq=translation; coord=8:10870907..10877056:1; parent_transcript=GRMZM2G030384_T01; parent_gene=GRMZM2G030384	GRMZM2G030384_P01	TRUE	TRUE	gILLAGDPK	95%	n+304 (+304), K+304 (+304)	41.57	25.00
5293	seq=translation; coord=8:10870907..10877056:1; parent_transcript=GRMZM2G030384_T01; parent_gene=GRMZM2G030384	GRMZM2G030384_P01	TRUE	TRUE	tILSTSYDGVIMR	95%	n+304 (+304)	46.25	25.63
5294	seq=translation; coord=10:141573795..141580886:-1; parent_transcript=GRMZM2G030384_T01; parent_gene=GRMZM2G030384	GRMZM2G030384_P01	TRUE	TRUE	vWDIFEDASGK	95%	n+304 (+304), K+304 (+304)	38.91	25.99
5295	seq=translation; coord=10:141573795..141580886:-1; parent_transcript=GRMZM2G156145_T01; parent_gene=GRMZM2G156145	GRMZM2G156145_P01	TRUE	TRUE	aTEEASGSTSSK	95%	n+304 (+304), K+304 (+304)	34.66	25.00
5296	seq=translation; coord=10:141573795..141580886:-1; parent_transcript=GRMZM2G156145_T01; parent_gene=GRMZM2G156145	GRMZM2G156145_P01	TRUE	TRUE	aTEEEENIDPR	95%	n+304 (+304)	56.10	25.00

5297	seq=translation; coord=10:141573795..141580886:-1; parent_transcript=GRMZM2G156145_T01; parent_gene=GRMZM2G156145	GRMZM2G156145_P01	TRUE	TRUE	IEAIVER	95%	n+304 (+304)	31.40	25.73
5298	seq=translation; coord=6:161231386..161234113:-1; parent_transcript=GRMZM2G159032_T01; parent_gene=GRMZM2G159032	GRMZM2G159032_P01,GRMZM2G159032_P03, GRMZM2G159032_P04	TRUE	TRUE	IAIGTSLVDK	95%	n+304 (+304), K+304 (+304)	30.25	25.00
5299	seq=translation; coord=6:161231386..161234113:-1; parent_transcript=GRMZM2G159032_T01; parent_gene=GRMZM2G159032	GRMZM2G159032_P01,GRMZM2G159032_P03, GRMZM2G159032_P04	TRUE	TRUE	sFISETALQAHSK	95%	n+304 (+304), K+304 (+304)	37.34	26.27
5300	seq=translation; coord=6:161231386..161234113:-1; parent_transcript=GRMZM2G159032_T01; parent_gene=GRMZM2G159032	GRMZM2G159032_P01,GRMZM2G159032_P03, GRMZM2G159032_P04	TRUE	TRUE	tTSVFFTGyK	92%	n+304 (+304), K+304 (+304)	27.85	26.40
5301	seq=translation; coord=5:183882422..183889051:-1; parent_transcript=GRMZM2G142088_T01; parent_gene=GRMZM2G142088	GRMZM2G142088_P01,GRMZM2G142088_P02	TRUE	TRUE	dVFSLVEAFK	95%	n+304 (+304), K+304 (+304)	31.54	25.00
5302	seq=translation; coord=5:183882422..183889051:-1; parent_transcript=GRMZM2G142088_T01; parent_gene=GRMZM2G142088	GRMZM2G142088_P01,GRMZM2G142088_P02	TRUE	TRUE	vAYDDGDVEVLLLR	95%	n+304 (+304)	49.25	25.45
5303	seq=translation; coord=5:204089494..204100246:-1; parent_transcript=GRMZM2G029186_T01; parent_gene=GRMZM2G029186	GRMZM2G029186_P01,GRMZM2G029186_P02, GRMZM2G029186_P03,GRMZM2G029186_P04	TRUE	TRUE	eISSLGPVVAR	94%	n+304 (+304)	32.80	26.58
5304	seq=translation; coord=5:204089494..204100246:-1; parent_transcript=GRMZM2G029186_T01; parent_gene=GRMZM2G029186	GRMZM2G029186_P01,GRMZM2G029186_P02, GRMZM2G029186_P03,GRMZM2G029186_P04	TRUE	TRUE	sSLDQTVEMISER	95%	n+304 (+304)	36.75	25.00
5305	seq=translation; coord=5:74450298..74452700:-1; parent_transcript=GRMZM5G831200_T01; parent_gene=GRMZM5G831200	GRMZM5G831200_P01	TRUE	TRUE	gGAFAAVADVALDR	93%	n+304 (+304)	27.03	25.47
5306	seq=translation; coord=5:74450298..74452700:-1; parent_transcript=GRMZM5G831200_T01; parent_gene=GRMZM5G831200	GRMZM5G831200_P01	TRUE	TRUE	IWLLFSGLAGAR	95%	n+304 (+304)	41.52	25.24
5307	seq=translation; coord=5:74450298..74452700:-1; parent_transcript=GRMZM5G831200_T01; parent_gene=GRMZM5G831200	GRMZM5G831200_P01	TRUE	TRUE	rADDGGEQTVcNcAVGLDYGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	67.46	25.00
5308	seq=translation; coord=3:133205499..133209390:-1; parent_transcript=GRMZM2G136262_T01; parent_gene=GRMZM2G136262	GRMZM2G136262_P01	TRUE	TRUE	eQLALPDGTAITGESK	95%	n+304 (+304), K+304 (+304)	49.74	25.88
5309	seq=translation; coord=3:133205499..133209390:-1; parent_transcript=GRMZM2G136262_T01; parent_gene=GRMZM2G136262	GRMZM2G136262_P01	TRUE	TRUE	IMLEAPPK	94%	n+304 (+304), K+304 (+304)	27.92	25.00
5310	seq=translation; coord=6:131028969..131032495:1; parent_transcript=GRMZM2G133631_T01; parent_gene=GRMZM2G133631	GRMZM2G133631_P01,GRMZM2G165567_P01, GRMZM2G165567_P02,GRMZM2G165567_P03, GRMZM2G165567_P04,GRMZM2G405064_P01	TRUE	TRUE	aPVHLVWELVR	95%	n+304 (+304)	49.83	25.56
5311	seq=translation; coord=6:131028969..131032495:1; parent_transcript=GRMZM2G133631_T01; parent_gene=GRMZM2G133631	GRMZM2G133631_P01,GRMZM2G165567_P01, GRMZM2G165567_P02,GRMZM2G165567_P03, GRMZM2G165567_P04,GRMZM2G405064_P01	TRUE	TRUE	gDQLEVGLSLR	86%	n+304 (+304)	25.81	25.74
5312	seq=translation; coord=3:153925171..153929056:-1; parent_transcript=GRMZM2G145715_T01; parent_gene=GRMZM2G145715	GRMZM2G145715_P01	TRUE	TRUE	nPNLANLLVDPEFAQEIIDR	95%	n+304 (+304)	48.35	25.48
5313	seq=translation; coord=6:140465764..140469654:1; parent_transcript=AC213884.3_FGT001; parent_gene=AC213884.3_FG001	AC213884.3_FGP001	TRUE	TRUE	icANHLVAPTTR	95%	n+304 (+304), Carbamidomethyl (+57)	36.81	25.43

5314	seq=translation; coord=6:140465764..140469654:1; parent_transcript=AC213884.3_FGT001; parent_gene=AC213884.3_FG001 seq=translation; coord=10:23245983..23251624:-1;	AC213884.3_FGP001	TRUE	TRUE	IEEVLVTTGEEDEDVLLDMK	95%	n+304 (+304), K+304 (+304)	45.13	25.00
5315	parent_transcript=GRMZM2G013478_T01; parent_gene=GRMZM2G013478 seq=translation; coord=10:23245983..23251624:-1;	GRMZM2G013478_P01	TRUE	TRUE	eIELWfk	92%	n+304 (+304), K+304 (+304)	25.75	25.00
5316	parent_transcript=GRMZM2G013478_T01; parent_gene=GRMZM2G013478 seq=translation; coord=9:153591547..153607432:1;	GRMZM2G013478_P01	TRUE	TRUE	kLIGATNPLQAEPGTIR	95%	K+304 (+304), n+304 (+304)	49.73	25.00
5317	parent_transcript=GRMZM2G051219_T01; parent_gene=GRMZM2G051219 seq=translation; coord=9:153591547..153607432:1;	GRMZM2G051219_P01,GRMZM2G051219_P02	TRUE	TRUE	aINTLESWIk	95%	n+304 (+304), K+304 (+304)	43.42	25.25
5318	parent_transcript=GRMZM2G051219_T01; parent_gene=GRMZM2G051219 seq=translation; coord=9:153591547..153607432:1;	GRMZM2G051219_P01,GRMZM2G051219_P02	TRUE	TRUE	gAIADALVLNAAASLLVSGk	95%	n+304 (+304), K+304 (+304)	29.72	25.00
5319	parent_transcript=GRMZM2G051219_T01; parent_gene=GRMZM2G051219 seq=translation; coord=4:235606747..235623515:-1;	GRMZM2G051219_P01,GRMZM2G051219_P02	TRUE	TRUE	iSAFLVLLR	94%	n+304 (+304)	35.95	30.23
5320	parent_transcript=GRMZM2G119482_T01; parent_gene=GRMZM2G119482 seq=translation; coord=4:235606747..235623515:-1;	GRMZM2G119482_P01	TRUE	TRUE	aFIQAVQSLk	95%	n+304 (+304), K+304 (+304)	47.98	25.00
5321	parent_transcript=GRMZM2G119482_T01; parent_gene=GRMZM2G119482 seq=translation; coord=4:235606747..235623515:-1;	GRMZM2G119482_P01	TRUE	TRUE	eEVFGPVAPLIPfk	95%	n+304 (+304), K+304 (+304)	36.69	25.00
5322	parent_transcript=GRMZM2G119482_T01; parent_gene=GRMZM2G119482 seq=translation; coord=5:214424827..214427180:1;	GRMZM2G119482_P01	TRUE	TRUE	qPVGVVGAITPWNFLAMITR	95%	n+304 (+304)	52.35	25.11
5323	parent_transcript=GRMZM2G030523_T01; parent_gene=GRMZM2G030523 seq=translation; coord=6:102399027..102412128:1;	GRMZM2G030523_P01	TRUE	TRUE	aDDGSDTVTFMFESPk	95%	n+304 (+304), K+304 (+304)	33.33	25.00
5324	parent_transcript=GRMZM2G106427_T01; parent_gene=GRMZM2G106427 seq=translation; coord=6:102399027..102412128:1;	GRMZM2G106427_P01,GRMZM2G106427_P02, GRMZM2G106427_P03,GRMZM2G106427_P04	TRUE	TRUE	qDAAQAIALVLWk	95%	n+304 (+304), K+304 (+304)	30.59	25.04
5325	parent_transcript=GRMZM2G106427_T01; parent_gene=GRMZM2G106427 seq=translation; coord=6:102399027..102412128:1;	GRMZM2G106427_P01,GRMZM2G106427_P02, GRMZM2G106427_P03,GRMZM2G106427_P04	TRUE	TRUE	sIVAEDDLQQR	95%	n+304 (+304)	46.22	25.00
5326	parent_transcript=GRMZM2G106427_T01; parent_gene=GRMZM2G106427 seq=translation; coord=6:102399027..102412128:1;	GRMZM2G106427_P01,GRMZM2G106427_P02, GRMZM2G106427_P03,GRMZM2G106427_P04	TRUE	TRUE	wQEATGESVSEVIFLsk	95%	n+304 (+304), K+304 (+304)	44.61	25.99
5327	parent_transcript=GRMZM2G058138_T01; parent_gene=GRMZM2G058138 seq=translation; coord=1:46061768..46066293:1;	GRMZM2G058138_P01,GRMZM2G058138_P02, GRMZM2G058138_P03	TRUE	TRUE	lIIVADPDAILDLTYEEK	95%	n+304 (+304), K+304 (+304)	39.72	25.00
5328	parent_transcript=GRMZM2G058138_T01; parent_gene=GRMZM2G058138 seq=translation; coord=4:102065832..102092090:1;	GRMZM2G058138_P01,GRMZM2G058138_P02, GRMZM2G058138_P03	TRUE	TRUE	vVPAVTPEVk	95%	n+304 (+304), K+304 (+304)	38.24	25.00
5329	parent_transcript=GRMZM2G028766_T01; parent_gene=GRMZM2G028766 seq=translation; coord=4:102065832..102092090:1;	GRMZM2G028766_P01,GRMZM2G028766_P02	TRUE	TRUE	eMLTDLEGMGFSTAR	95%	n+304 (+304)	76.77	25.00
5330	parent_transcript=GRMZM2G028766_T01; parent_gene=GRMZM2G028766 seq=translation; coord=5:176347442..176349538:1;	GRMZM2G028766_P01,GRMZM2G028766_P02	TRUE	TRUE	vGNLHVGFIEFLcGFek	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.23	25.72
5331	parent_transcript=GRMZM2G056629_T01; parent_gene=GRMZM2G056629	GRMZM2G056629_P01	TRUE	TRUE	rGTGGVAGYDTNYAVDGAASPSLRPVAR	95%	n+304 (+304)	48.94	25.00

5332	seq=translation; coord=5:176347442..176349538:1; parent_transcript=GRMZM2G056629_T01; parent_gene=GRMZM2G056629 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G056629_P01	TRUE	TRUE	VTNWGATLMSVILPDSk	95%	n+304 (+304), K+304 (+304)	40.13	26.23
5333	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G005036_P01	TRUE	TRUE	aVDLAAGELLEIATPGk	95%	n+304 (+304), K+304 (+304)	53.62	25.00
5334	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G005036_P01	TRUE	TRUE	eQLQNIk	95%	n+304 (+304), K+304 (+304)	34.00	25.00
5335	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G005036_P01	TRUE	TRUE	IDVSSLEEFVAEHyTAPR	95%	n+304 (+304), iTRAQ8plex (+304)	41.26	25.25
5336	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G005036_P01	TRUE	TRUE	qSSGGLFSWLLGGk	95%	n+304 (+304), K+304 (+304)	37.15	25.99
5337	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=6:160040980..160045154:-1;	GRMZM2G005036_P01	TRUE	TRUE	sSELPPLDVPLPGISIPSLPDFVEPSk	95%	n+304 (+304), K+304 (+304)	30.38	25.00
5338	parent_transcript=GRMZM2G005036_T01; parent_gene=GRMZM2G005036 seq=translation; coord=1:274275100..274280175:1;	GRMZM2G005036_P01	TRUE	TRUE	sYTPEMVEVLIDSVR	94%	n+304 (+304)	31.05	25.00
5339	parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283 seq=translation; coord=1:274275100..274280175:1;	GRMZM2G135283_P03,GRMZM2G135283_P04	TRUE	TRUE	gFVEEDFAk	95%	n+304 (+304), K+304 (+304)	32.99	25.56
5340	parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283 seq=translation; coord=1:274275100..274280175:1;	GRMZM2G135283_P03,GRMZM2G135283_P04	TRUE	TRUE	gLLEIPSENFTSVSVMQAVGSVMTNk	95%	n+304 (+304), K+304 (+304)	38.86	25.00
5341	parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283 seq=translation; coord=1:274275100..274280175:1;	GRMZM2G135283_P03,GRMZM2G135283_P04	TRUE	TRUE	gYELVSGGTDNHLVLVNLk	94%	n+304 (+304), K+304 (+304)	26.28	25.24
5342	parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283 seq=translation; coord=1:274275100..274280175:1;	GRMZM2G135283_P03,GRMZM2G135283_P04	TRUE	TRUE	iSATSIFFETMPYR	95%	n+304 (+304)	43.41	25.00
5343	parent_transcript=GRMZM2G135283_T03; parent_gene=GRMZM2G135283 seq=translation; coord=1:191893507..191894902:1;	GRMZM2G135283_P03,GRMZM2G135283_P04	TRUE	TRUE	vADFFDAAVNLALk	92%	n+304 (+304), K+304 (+304)	26.79	25.00
5344	parent_transcript=GRMZM2G427451_T01; parent_gene=GRMZM2G427451 seq=translation; coord=1:191893507..191894902:1;	GRMZM2G427451_P01	TRUE	TRUE	aSTPLDFPATDLAADAAGGk	95%	n+304 (+304), K+304 (+304)	49.57	25.00
5345	parent_transcript=GRMZM2G427451_T01; parent_gene=GRMZM2G427451 seq=translation; coord=1:191893507..191894902:1;	GRMZM2G427451_P01	TRUE	TRUE	aYAScEDLPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.22	25.00
5346	parent_transcript=GRMZM2G427451_T01; parent_gene=GRMZM2G427451 seq=translation; coord=1:56746484..56752553:1;	GRMZM2G427451_P01	TRUE	TRUE	hAFQADNLGak	95%	n+304 (+304), K+304 (+304)	50.37	25.00
5347	parent_transcript=GRMZM2G010823_T01; parent_gene=GRMZM2G010823 seq=translation; coord=1:56746484..56752553:1;	GRMZM2G010823_P01	TRUE	TRUE	eAALDLGVLTQEFHELVPPEk	95%	n+304 (+304), K+304 (+304)	48.01	25.00
5348	parent_transcript=GRMZM2G010823_T01; parent_gene=GRMZM2G010823 seq=translation; coord=1:56746484..56752553:1;	GRMZM2G010823_P01	TRUE	TRUE	mYQLAQGGTAVGTGLNTk	94%	n+304 (+304), K+304 (+304)	29.57	25.92
5349	parent_transcript=GRMZM2G010823_T01; parent_gene=GRMZM2G010823	GRMZM2G010823_P01	TRUE	TRUE	sLQNFDIGGER	95%	n+304 (+304)	39.35	25.00

5350	seq=translation; coord=8:116304892..116311147:-1; parent_transcript=GRMZM2G055489_T01; parent_gene=GRMZM2G055489	GRMZM2G055489_P01,GRMZM2G055489_P02, GRMZM2G055489_P04	TRUE	TRUE	fDLWESEGDVR	95%	n+304 (+304)	34.06	25.00
5351	seq=translation; coord=8:116304892..116311147:-1; parent_transcript=GRMZM2G055489_T01; parent_gene=GRMZM2G055489	GRMZM2G055489_P01,GRMZM2G055489_P02, GRMZM2G055489_P04	TRUE	TRUE	gQALAYLLk	95%	n+304 (+304), K+304 (+304)	35.96	25.00
5352	seq=translation; coord=5:56740173..56751799:1; parent_transcript=GRMZM2G115939_T01; parent_gene=GRMZM2G115939	GRMZM2G115939_P01,GRMZM2G115939_P02, GRMZM2G115939_P04	TRUE	TRUE	aMTGGYVGQHYFQR	94%	n+304 (+304)	28.49	25.00
5353	seq=translation; coord=5:56740173..56751799:1; parent_transcript=GRMZM2G115939_T01; parent_gene=GRMZM2G115939	GRMZM2G115939_P01,GRMZM2G115939_P02, GRMZM2G115939_P04	TRUE	TRUE	dISELNLpk	95%	n+304 (+304), K+304 (+304)	36.25	25.00
5354	seq=translation; coord=4:163464001..163467089:-1; parent_transcript=GRMZM2G072612_T01; parent_gene=GRMZM2G072612	GRMZM2G072612_P01,GRMZM2G072612_P02	TRUE	TRUE	dTGALLVMDPR	95%	n+304 (+304)	34.21	25.00
5355	seq=translation; coord=4:163464001..163467089:-1; parent_transcript=GRMZM2G072612_T01; parent_gene=GRMZM2G072612	GRMZM2G072612_P01,GRMZM2G072612_P02	TRUE	TRUE	fLDVVER	95%	n+304 (+304)	37.79	25.00
5356	seq=translation; coord=10:106434010..106436707:-1; parent_transcript=GRMZM2G139512_T01; parent_gene=GRMZM2G139512	GRMZM2G139512_P01,GRMZM2G139512_P02, GRMZM2G139512_P03,GRMZM2G139512_P04	TRUE	TRUE	aDLEFLVGLLk	95%	n+304 (+304), K+304 (+304)	59.88	25.00
5357	seq=translation; coord=10:106434010..106436707:-1; parent_transcript=GRMZM2G139512_T01; parent_gene=GRMZM2G139512	GRMZM2G139512_P01,GRMZM2G139512_P02, GRMZM2G139512_P03,GRMZM2G139512_P04	TRUE	TRUE	rPPEVSAAEGAGLPAAAGTALQALR	95%	n+304 (+304)	35.09	25.00
5358	seq=translation; coord=9:146914705..146918889:-1; parent_transcript=GRMZM2G321725_T02; parent_gene=GRMZM2G321725	GRMZM2G321725_P02	TRUE	TRUE	gLWQPFTALLGDAPSVDVvk	95%	n+304 (+304), K+304 (+304)	54.48	26.03
5359	seq=translation; coord=3:223741308..223745402:-1; parent_transcript=GRMZM2G157588_T01; parent_gene=GRMZM2G157588	GRMZM2G157588_P01	TRUE	TRUE	IETWSDSFQEAfDR	95%	n+304 (+304)	35.58	25.00
5360	seq=translation; coord=7:164069905..164076083:1; parent_transcript=GRMZM2G136918_T01; parent_gene=GRMZM2G136918	GRMZM2G136918_P01,GRMZM2G136918_P02, GRMZM2G136918_P03,GRMZM2G136918_P04, GRMZM2G136918_P05	TRUE	TRUE	aVHIAVSdMAEGLDAPtSLPAR	95%	n+304 (+304)	29.92	25.21
5361	seq=translation; coord=7:164069905..164076083:1; parent_transcript=GRMZM2G136918_T01; parent_gene=GRMZM2G136918	GRMZM2G136918_P01,GRMZM2G136918_P02, GRMZM2G136918_P03,GRMZM2G136918_P04, GRMZM2G136918_P05	TRUE	TRUE	IVWFLDk	93%	n+304 (+304), K+304 (+304)	30.14	25.00
5362	seq=translation; coord=8:161837476..161841019:1; parent_transcript=GRMZM2G180399_T01; parent_gene=GRMZM2G180399	GRMZM2G180399_P01,GRMZM5G852502_P01	TRUE	TRUE	dYADILEFLVDR	93%	n+304 (+304)	29.57	25.00
5363	seq=translation; coord=10:148101348..148102945:1; parent_transcript=GRMZM5G892522_T01; parent_gene=GRMZM5G892522	GRMZM5G892522_P01	TRUE	TRUE	IIAPVVDWASEEYDGR	95%	n+304 (+304)	53.52	25.00
5364	seq=translation; coord=10:148101348..148102945:1; parent_transcript=GRMZM5G892522_T01; parent_gene=GRMZM5G892522	GRMZM5G892522_P01	TRUE	TRUE	vYGLPTLIffk	92%	n+304 (+304), K+304 (+304)	26.87	25.00
5365	seq=translation; coord=4:154310162..154311883:-1; parent_transcript=GRMZM2G373522_T01; parent_gene=GRMZM2G373522	GRMZM2G373522_P01	TRUE	TRUE	iEDDDTk	94%	n+304 (+304), K+304 (+304)	31.13	25.00
5366	seq=translation; coord=4:154310162..154311883:-1; parent_transcript=GRMZM2G373522_T01; parent_gene=GRMZM2G373522	GRMZM2G373522_P01	TRUE	TRUE	nTQQHQGGGEQAQDQENEVvk	95%	n+304 (+304), K+304 (+304)	29.44	25.00
5367	seq=translation; coord=5:113730181..113780006:1; parent_transcript=GRMZM2G056661_T01; parent_gene=GRMZM2G056661	GRMZM2G056661_P01,GRMZM2G056661_P03	TRUE	TRUE	eLLSVIEAALLGStAPsPAQR	95%	n+304 (+304)	37.05	25.00

5368	seq=translation; coord=5:113730181..113780006:1; parent_transcript=GRMZM2G056661_T01; parent_gene=GRMZM2G056661 seq=translation; coord=7:170419371..170421238:-1;	GRMZM2G056661_P01,GRMZM2G056661_P03	TRUE	TRUE	vLDLLEVQLFR	95%	n+304 (+304)	42.26	25.00
5369	parent_transcript=GRMZM2G111672_T01; parent_gene=GRMZM2G111672 seq=translation; coord=8:173103213..173107748:1;	GRMZM2G111672_P01	TRUE	TRUE	dLAEFGTGLR	95%	n+304 (+304)	31.43	25.00
5370	parent_transcript=GRMZM2G124365_T01; parent_gene=GRMZM2G124365 seq=translation; coord=8:173103213..173107748:1;	GRMZM2G124365_P01	TRUE	TRUE	eVEVAYLLk	95%	n+304 (+304), K+304 (+304)	32.49	25.00
5371	parent_transcript=GRMZM2G124365_T01; parent_gene=GRMZM2G124365	GRMZM2G124365_P01	TRUE	TRUE	IEDSIIFGLLER	95%	n+304 (+304)	44.95	25.26
5372	seq=translation; coord=5:4495054..4499934:-1; parent_transcript=GRMZM2G007260_T01; parent_gene=GRMZM2G007260	GRMZM2G007260_P01,GRMZM2G007260_P02, GRMZM2G007260_P03,GRMZM2G007260_P04, GRMZM2G022206_P02,GRMZM2G074479_P01, GRMZM2G074479_P02,GRMZM2G074479_P03	TRUE	TRUE	ITLQFTEDYPNKPPTVR	95%	n+304 (+304), K+304 (+304)	31.18	25.65
5373	seq=translation; coord=8:28159275..28161158:-1; parent_transcript=GRMZM2G032348_T04; parent_gene=GRMZM2G032348 seq=translation; coord=2:147034275..147039199:-1;	GRMZM2G032348_P04,GRMZM2G032348_P05	TRUE	TRUE	eMVAALADGR	95%	n+304 (+304)	42.25	25.00
5374	parent_transcript=GRMZM2G095392_T01; parent_gene=GRMZM2G095392 seq=translation; coord=5:202307973..202315571:-1;	GRMZM2G095392_P01,GRMZM2G095392_P02, GRMZM2G140047_P01	TRUE	TRUE	aFDLLDMLk	95%	n+304 (+304), K+304 (+304)	35.69	25.63
5375	parent_transcript=GRMZM2G164948_T01; parent_gene=GRMZM2G164948 seq=translation; coord=1:60216405..60219476:-1;	GRMZM2G164948_P01,GRMZM2G164948_P02, GRMZM2G164948_P03	TRUE	TRUE	vSADSTTVLADAVIVATGAVAR	95%	n+304 (+304)	54.49	25.40
5376	parent_transcript=GRMZM2G144995_T01; parent_gene=GRMZM2G144995 seq=translation; coord=1:60216405..60219476:-1;	GRMZM2G144995_P01,GRMZM2G144995_P02	TRUE	TRUE	aSMGQDLSPVDLINVQQFAQR	95%	n+304 (+304)	72.12	25.00
5377	parent_transcript=GRMZM2G144995_T01; parent_gene=GRMZM2G144995 seq=translation; coord=5:64107900..64117086:1;	GRMZM2G144995_P01,GRMZM2G144995_P02	TRUE	TRUE	mNDIAPNLTSLIGEVVGAR	95%	n+304 (+304)	61.73	25.71
5378	parent_transcript=GRMZM2G145088_T01; parent_gene=GRMZM2G145088 seq=translation; coord=5:64107900..64117086:1;	GRMZM2G145088_P01	TRUE	TRUE	gSGLPQPVLQIWYADk	95%	n+304 (+304), K+304 (+304)	56.79	25.67
5379	parent_transcript=GRMZM2G145088_T01; parent_gene=GRMZM2G145088 seq=translation; coord=5:64107900..64117086:1;	GRMZM2G145088_P01	TRUE	TRUE	iSGQEAVAFFk	93%	n+304 (+304), K+304 (+304)	27.28	25.19
5380	parent_transcript=GRMZM2G145088_T01; parent_gene=GRMZM2G145088 seq=translation; coord=4:238325251..238328383:-1;	GRMZM2G145088_P01	TRUE	TRUE	ITMDEATFR	94%	n+304 (+304)	31.02	25.00
5381	parent_transcript=GRMZM2G060567_T01; parent_gene=GRMZM2G060567 seq=translation; coord=4:238325251..238328383:-1;	GRMZM2G060567_P01	TRUE	TRUE	dISSSVTAIANek	95%	n+304 (+304), K+304 (+304)	44.56	26.02
5382	parent_transcript=GRMZM2G060567_T01; parent_gene=GRMZM2G060567 seq=translation; coord=4:238325251..238328383:-1;	GRMZM2G060567_P01	TRUE	TRUE	gDDDFIPGR	88%	n+304 (+304)	26.29	25.00
5383	parent_transcript=GRMZM2G060567_T01; parent_gene=GRMZM2G060567 seq=translation; coord=4:238325251..238328383:-1;	GRMZM2G060567_P01	TRUE	TRUE	IVEEADfk	95%	n+304 (+304), K+304 (+304)	34.30	26.43
5384	parent_transcript=GRMZM2G060567_T01; parent_gene=GRMZM2G060567	GRMZM2G060567_P01	TRUE	TRUE	sESDFAEYAEIANk	95%	n+304 (+304), K+304 (+304)	43.36	25.00

5385	seq=translation; coord=7:106230652..106231840:1; parent_transcript=GRMZM2G025646_T01; parent_gene=GRMZM2G025646 seq=translation; coord=7:106230652..106231840:1;	GRMZM2G025646_P01,GRMZM2G025646_P02	TRUE	TRUE	sFGEVQGIIEHNR	95%	n+304 (+304)	60.80	25.00
5386	parent_transcript=GRMZM2G025646_T01; parent_gene=GRMZM2G025646 seq=translation; coord=7:106230652..106231840:1;	GRMZM2G025646_P01,GRMZM2G025646_P02	TRUE	TRUE	vLIQEISQNNQETR	95%	n+304 (+304)	45.10	25.37
5387	seq=translation; coord=7:106230652..106231840:1; parent_transcript=GRMZM2G025646_T01; parent_gene=GRMZM2G025646 seq=translation; coord=3:22814532..22820273:-1;	GRMZM2G025646_P01,GRMZM2G025646_P02	TRUE	TRUE	vVDLYGDMMSGSFAR	95%	n+304 (+304)	66.87	25.00
5388	parent_transcript=GRMZM2G009282_T01; parent_gene=GRMZM2G009282 seq=translation; coord=3:22814532..22820273:-1;	GRMZM2G009282_P01	TRUE	TRUE	dPFWFVAVHR	95%	n+304 (+304)	48.23	25.00
5389	parent_transcript=GRMZM2G009282_T01; parent_gene=GRMZM2G009282 seq=translation; coord=3:22814532..22820273:-1;	GRMZM2G009282_P01	TRUE	TRUE	ILAFLDk	91%	n+304 (+304), K+304 (+304)	26.27	25.00
5390	parent_transcript=GRMZM2G009282_T01; parent_gene=GRMZM2G009282 seq=translation; coord=2:130291275..130295558:-1;	GRMZM2G009282_P01	TRUE	TRUE	wIELGAFYPFSR	90%	n+304 (+304)	25.28	25.00
5391	parent_transcript=GRMZM2G118800_T01; parent_gene=GRMZM2G118800 seq=translation; coord=2:130291275..130295558:-1;	GRMZM2G118800_P01	TRUE	TRUE	fYGEDPLQSDLSR	95%	n+304 (+304)	61.71	25.00
5392	parent_transcript=GRMZM2G118800_T01; parent_gene=GRMZM2G118800 seq=translation; coord=4:172748163..172754261:1;	GRMZM2G118800_P01	TRUE	TRUE	sFAPELVASLk	95%	n+304 (+304), K+304 (+304)	34.55	25.65
5393	parent_transcript=GRMZM2G178398_T01; parent_gene=GRMZM2G178398 seq=translation; coord=4:172748163..172754261:1;	GRMZM2G178398_P01	TRUE	TRUE	aNPHADIGVDFDSINR	95%	n+304 (+304)	47.29	25.00
5394	parent_transcript=GRMZM2G178398_T01; parent_gene=GRMZM2G178398 seq=translation; coord=4:172748163..172754261:1;	GRMZM2G178398_P01	TRUE	TRUE	gLIVLDYLVAHGTER	95%	n+304 (+304)	54.93	25.19
5395	parent_transcript=GRMZM2G178398_T01; parent_gene=GRMZM2G178398 seq=translation; coord=5:182124005..182130631:-1;	GRMZM2G178398_P01	TRUE	TRUE	gLVLNLDISGPk	95%	n+304 (+304), K+304 (+304)	40.15	25.09
5396	parent_transcript=GRMZM2G137409_T01; parent_gene=GRMZM2G137409 seq=translation; coord=5:182124005..182130631:-1;	GRMZM2G137409_P01	TRUE	TRUE	aIAMEGATDALIQLik	95%	n+304 (+304), K+304 (+304)	59.39	25.00
5397	parent_transcript=GRMZM2G137409_T01; parent_gene=GRMZM2G137409 seq=translation; coord=5:182124005..182130631:-1;	GRMZM2G137409_P01	TRUE	TRUE	sAIGIGTLLMDGLGDTIR	95%	n+304 (+304)	42.93	25.00
5398	parent_transcript=GRMZM2G137409_T01; parent_gene=GRMZM2G137409 seq=translation; coord=1:293041177..293042705:-1;	GRMZM2G137409_P01	TRUE	TRUE	tLFDLQEISAEIR	95%	n+304 (+304)	39.31	25.37
5399	parent_transcript=GRMZM2G155329_T01; parent_gene=GRMZM2G155329 seq=translation; coord=1:293041177..293042705:-1;	GRMZM2G155329_P01	TRUE	TRUE	fTAIGVYLEDAAVPALAK	95%	n+304 (+304), K+304 (+304)	66.08	25.00
5400	parent_transcript=GRMZM2G155329_T01; parent_gene=GRMZM2G155329 seq=translation; coord=1:293041177..293042705:-1;	GRMZM2G155329_P01	TRUE	TRUE	lCeAVLESIGER	95%	n+304 (+304), Carbamidomethyl (+57)	40.64	25.90
5401	parent_transcript=GRMZM2G155329_T01; parent_gene=GRMZM2G155329 seq=translation; coord=7:156569238..156573041:1;	GRMZM2G155329_P01	TRUE	TRUE	tADELASDAFFR	95%	n+304 (+304)	65.25	25.00
5402	parent_transcript=GRMZM2G153162_T02; parent_gene=GRMZM2G153162	GRMZM2G153162_P02	TRUE	TRUE	iSSEPPNSASSVEDk	95%	n+304 (+304), K+304 (+304)	40.36	25.21

5403	seq=translation; coord=7:156569238..156573041:1; parent_transcript=GRMZM2G153162_T02; parent_gene=GRMZM2G153162 seq=translation; coord=3:123772202..123775285:1;	GRMZM2G153162_P02	TRUE	TRUE	tSSAPPNLDEQK	94%	n+304 (+304), K+304 (+304)	27.14	25.15
5404	parent_transcript=GRMZM2G164868_T01; parent_gene=GRMZM2G164868 seq=translation; coord=3:123772202..123775285:1;	GRMZM2G164868_P01,GRMZM2G164868_P02	TRUE	TRUE	aAVVASVAAFLESAGLSR	95%	n+304 (+304)	46.76	25.73
5405	parent_transcript=GRMZM2G164868_T01; parent_gene=GRMZM2G164868 seq=translation; coord=3:123772202..123775285:1;	GRMZM2G164868_P01,GRMZM2G164868_P02	TRUE	TRUE	aELAILNK	92%	n+304 (+304), K+304 (+304)	27.98	27.15
5406	parent_transcript=GRMZM2G164868_T01; parent_gene=GRMZM2G164868	GRMZM2G164868_P01,GRMZM2G164868_P02	TRUE	TRUE	tDAGSAPAEADGAK	95%	n+304 (+304), K+304 (+304)	37.78	25.85
5407	seq=translation; coord=4:163261154..163272206:1; parent_transcript=GRMZM2G014994_T01; parent_gene=GRMZM2G014994	GRMZM2G014994_P01	TRUE	TRUE	fPAGPccAALK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	35.57	25.00
5408	seq=translation; coord=4:163261154..163272206:1; parent_transcript=GRMZM2G014994_T01; parent_gene=GRMZM2G014994 seq=translation; coord=10:12167272..12169103:-1;	GRMZM2G014994_P01	TRUE	TRUE	qGLScADVLER	95%	n+304 (+304), Carbamidomethyl (+57)	46.26	25.00
5409	parent_transcript=GRMZM2G094375_T01; parent_gene=GRMZM2G094375 seq=translation; coord=10:12167272..12169103:-1;	GRMZM2G094375_P01,GRMZM2G094375_P02	TRUE	TRUE	aTVYGALVLRPR	95%	n+304 (+304)	37.70	25.24
5410	parent_transcript=GRMZM2G094375_T01; parent_gene=GRMZM2G094375 seq=translation; coord=3:231890529..231892088:-1;	GRMZM2G094375_P01,GRMZM2G094375_P02	TRUE	TRUE	iINAALNTPLFFK	95%	n+304 (+304), K+304 (+304)	50.11	25.00
5411	parent_transcript=GRMZM2G175076_T01; parent_gene=GRMZM2G175076 seq=translation; coord=3:231890529..231892088:-1;	GRMZM2G175076_P01	TRUE	TRUE	gSQYGVQLESSVR	95%	n+304 (+304)	50.82	25.00
5412	parent_transcript=GRMZM2G175076_T01; parent_gene=GRMZM2G175076 seq=translation; coord=6:167749462..167750447:-1;	GRMZM2G175076_P01	TRUE	TRUE	IAAADLYEDDEEEALEK	95%	n+304 (+304), K+304 (+304)	78.59	25.00
5413	parent_transcript=GRMZM5G849087_T01; parent_gene=GRMZM5G849087 seq=translation; coord=1:208529333..208544044:-1;	GRMZM5G849087_P01	TRUE	TRUE	aAAAAYDYEGDAR	95%	n+304 (+304)	59.24	25.00
5414	parent_transcript=GRMZM2G050583_T01; parent_gene=GRMZM2G050583 seq=translation; coord=1:41101054..41103817:1;	GRMZM2G050583_P01	TRUE	TRUE	aVSTAIYFLLPAGSVSR	95%	n+304 (+304)	31.12	25.68
5415	parent_transcript=GRMZM2G428391_T01; parent_gene=GRMZM2G428391 seq=translation; coord=3:203752020..203753539:1;	GRMZM2G428391_P01	TRUE	TRUE	sINPDEAVAYGAAVQAAILTGEGNEK	95%	n+304 (+304), K+304 (+304)	49.57	25.00
5416	parent_transcript=GRMZM2G380088_T01; parent_gene=GRMZM2G380088 seq=translation; coord=2:36927268..36929809:1;	GRMZM2G380088_P01	TRUE	TRUE	aAAAAGVATVQDLLPLLVPSAR	95%	n+304 (+304)	39.90	25.00
5417	parent_transcript=GRMZM2G022413_T01; parent_gene=GRMZM2G022413 seq=translation; coord=7:134007495..134008927:1;	GRMZM2G022413_P01	TRUE	TRUE	eWQDAIVTEVLPAR	95%	n+304 (+304)	39.13	25.29
5418	parent_transcript=GRMZM2G101711_T01; parent_gene=GRMZM2G101711 seq=translation; coord=7:167020090..167021470:-1;	GRMZM2G101711_P01,GRMZM2G101711_P02	TRUE	TRUE	sSASMESEVIR	89%	n+304 (+304)	26.69	25.00
5419	parent_transcript=GRMZM2G171597_T01; parent_gene=GRMZM2G171597	GRMZM2G171597_P01	TRUE	TRUE	aAGLPAAcGEDPAAFSR	95%	n+304 (+304), Carbamidomethyl (+57)	75.64	25.00

5420	seq=translation; coord=4:211079286..211080981:-1; parent_transcript=GRMZM5G889769_T01; parent_gene=GRMZM5G889769	GRMZM5G889769_P01	TRUE	TRUE	sTTVLADAVIVATGAVAR	95%	n+304 (+304)	54.14	25.00
5421	AC196426.3_FGP007-R seq=translation; coord=6:166587013..166592611:1;	AC196426.3_FGP007-R	TRUE	TRUE	mVVER	87%	n+304 (+304)	25.82	25.21
5422	parent_transcript=GRMZM2G027955_T01; parent_gene=GRMZM2G027955 seq=translation; coord=6:166587013..166592611:1;	GRMZM2G027955_P01,GRMZM2G027955_P02, GRMZM2G027955_P03	TRUE	TRUE	aIEHILISGDQLYR	95%	n+304 (+304)	33.04	25.15
5423	parent_transcript=GRMZM2G027955_T01; parent_gene=GRMZM2G027955 seq=translation; coord=6:166587013..166592611:1;	GRMZM2G027955_P01,GRMZM2G027955_P02, GRMZM2G027955_P03	TRUE	TRUE	dVLLDLLk	95%	n+304 (+304), K+304 (+304)	30.47	25.00
5424	parent_transcript=GRMZM2G027955_T01; parent_gene=GRMZM2G027955 seq=translation; coord=6:166587013..166592611:1;	GRMZM2G027955_P01,GRMZM2G027955_P02, GRMZM2G027955_P03	TRUE	TRUE	fIWVLEDYYk	95%	n+304 (+304), K+304 (+304)	31.70	25.85
5425	parent_transcript=GRMZM2G102183_T01; parent_gene=GRMZM2G102183 seq=translation; coord=2:36317292..36319768:1;	GRMZM2G102183_P01,GRMZM2G102183_P02, GRMZM2G102183_P03	TRUE	TRUE	aTVLVETLPVAFQMNEILHELr	95%	n+304 (+304)	79.79	25.26
5426	parent_transcript=GRMZM2G102183_T01; parent_gene=GRMZM2G102183 seq=translation; coord=2:36317292..36319768:1;	GRMZM2G102183_P01,GRMZM2G102183_P02, GRMZM2G102183_P03	TRUE	TRUE	dAVAGTISFR	91%	n+304 (+304)	27.78	25.00
5427	parent_transcript=GRMZM2G054012_T01; parent_gene=GRMZM2G054012 seq=translation; coord=4:173177749..173179720:-1;	GRMZM2G054012_P01,GRMZM2G096690_P01, GRMZM2G328168_P01,GRMZM5G805526_P01	TRUE	TRUE	fVTAVVGFGk	95%	n+304 (+304), K+304 (+304)	33.34	25.00
5428	parent_transcript=GRMZM2G054012_T01; parent_gene=GRMZM2G054012 seq=translation; coord=10:63619774..63622627:-1;	GRMZM2G054012_P01,GRMZM2G096690_P01, GRMZM2G328168_P01,GRMZM5G805526_P01	TRUE	TRUE	rFVTAVVGFGk	95%	n+304 (+304), K+304 (+304)	32.60	25.00
5429	parent_transcript=GRMZM2G368861_T01; parent_gene=GRMZM2G368861 seq=translation; coord=10:63619774..63622627:-1;	GRMZM2G368861_P01	TRUE	TRUE	eDGGWTAGYcHLR	95%	n+304 (+304), Carbamidomethyl (+57)	36.61	25.00
5430	parent_transcript=GRMZM2G368861_T01; parent_gene=GRMZM2G368861 seq=translation; coord=10:63619774..63622627:-1;	GRMZM2G368861_P01	TRUE	TRUE	IcSNEcVk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	35.65	25.00
5431	seq=translation; coord=1:191987932..191990561:1; parent_transcript=AC197246.3_FGT003; parent_gene=AC197246.3_FG003 seq=translation; coord=1:191987932..191990561:1;	AC197246.3_FGP003,GRMZM2G155931_P01,G RMZM2G155931_P03,GRMZM2G155931_P04,G RMZM2G155931_P05	TRUE	TRUE	aVPLLTk	91%	n+304 (+304), K+304 (+304)	27.04	25.00
5432	parent_transcript=AC197246.3_FGT003; parent_gene=AC197246.3_FG003 seq=translation; coord=10:127861555..127867760:-1;	AC197246.3_FGP003,GRMZM2G155931_P01,G RMZM2G155931_P03,GRMZM2G155931_P04,G RMZM2G155931_P05	TRUE	TRUE	fVVHNVSELELLMMHNR	95%	n+304 (+304)	59.10	25.00
5433	parent_transcript=GRMZM2G096705_T01; parent_gene=GRMZM2G096705 seq=translation; coord=10:127861555..127867760:-1;	GRMZM2G096705_P01	TRUE	TRUE	gLILAFk	95%	n+304 (+304), K+304 (+304)	37.44	25.00
5434	parent_transcript=GRMZM2G096705_T01; parent_gene=GRMZM2G096705 seq=translation; coord=7:82007091..82010522:1;	GRMZM2G096705_P01	TRUE	TRUE	gNVSEEQADAVEELk	95%	n+304 (+304), K+304 (+304)	54.29	25.00
5435	parent_transcript=GRMZM2G056501_T01; parent_gene=GRMZM2G056501 seq=translation; coord=7:82007091..82010522:1;	GRMZM2G056501_P01,GRMZM2G056501_P02, GRMZM2G056501_P06	TRUE	TRUE	dYSMEVILTHLk	95%	n+304 (+304), K+304 (+304)	36.12	26.72
5436	parent_transcript=GRMZM2G056501_T01; parent_gene=GRMZM2G056501 seq=translation; coord=2:189443283..189447454:1;	GRMZM2G056501_P01,GRMZM2G056501_P02, GRMZM2G056501_P06	TRUE	TRUE	fSVLGNWQR	89%	n+304 (+304)	26.85	25.00
5437	parent_transcript=GRMZM2G112165_T01; parent_gene=GRMZM2G112165	GRMZM2G112165_P01	TRUE	TRUE	aTNTLSIIDSGIGMTk	95%	n+304 (+304), K+304 (+304)	40.45	25.85

5438	seq=translation; coord=2:189443283..189447454:1; parent_transcript=GRMZM2G112165_T01; parent_gene=GRMZM2G112165	GRMZM2G112165_P01	TRUE	TRUE	rAPFDLFDTk	91%	n+304 (+304), K+304 (+304)	26.05	25.95
5439	seq=translation; coord=8:127487910..127490998:1; parent_transcript=GRMZM2G150485_T01; parent_gene=GRMZM2G150485	GRMZM2G150485_P01,GRMZM2G150485_P03, GRMZM2G150485_P06	TRUE	TRUE	sNIVGLPVSLLLk	95%	n+304 (+304), K+304 (+304)	32.32	25.00
5440	seq=translation; coord=8:127487910..127490998:1; parent_transcript=GRMZM2G150485_T01; parent_gene=GRMZM2G150485	GRMZM2G150485_P01,GRMZM2G150485_P03, GRMZM2G150485_P06	TRUE	TRUE	vAGYLTVPVGGVGPMTVAMLLk	94%	n+304 (+304), K+304 (+304)	28.21	25.00
5441	seq=translation; coord=7:166680013..166686364:1; parent_transcript=GRMZM2G025281_T01; parent_gene=GRMZM2G025281	GRMZM2G025281_P01,GRMZM2G025281_P02, GRMZM2G025281_P03,GRMZM2G077823_P01, GRMZM2G077823_P02,GRMZM2G077823_P03, GRMZM2G077823_P04,GRMZM2G077823_P05	TRUE	TRUE	eIMVQFAk	93%	n+304 (+304), K+304 (+304)	27.86	26.33
5442	seq=translation; coord=7:166680013..166686364:1; parent_transcript=GRMZM2G025281_T01; parent_gene=GRMZM2G025281	GRMZM2G025281_P01,GRMZM2G025281_P02, GRMZM2G025281_P03,GRMZM2G077823_P01, GRMZM2G077823_P02,GRMZM2G077823_P03, GRMZM2G077823_P04,GRMZM2G077823_P05	TRUE	TRUE	tTADDLFLPLFDk	95%	n+304 (+304), K+304 (+304)	31.12	25.00
5443	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	TRUE	TRUE	aGFVAQVGR	91%	n+304 (+304)	27.00	25.00
5444	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	TRUE	TRUE	eNNPDLAGDR	95%	n+304 (+304)	35.91	25.00
5445	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	TRUE	TRUE	qPEHVMMFLLAEMGTSGSLDGQQR	95%	n+304 (+304)	37.96	25.00
5446	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	TRUE	TRUE	tESLAVAEPALNFTGMk	95%	n+304 (+304), K+304 (+304)	40.41	25.79
5447	seq=translation; coord=2:217093149..217097528:-1; parent_transcript=GRMZM2G030646_T01; parent_gene=GRMZM2G030646	GRMZM2G030646_P01	TRUE	TRUE	tVFVNFMDLck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.66	25.15
5448	seq=translation; coord=1:27094498..27098727:1; parent_transcript=GRMZM2G163129_T01; parent_gene=GRMZM2G163129	GRMZM2G163129_P01	TRUE	TRUE	fHVPDVLLPDLEAR	95%	n+304 (+304)	47.81	25.65
5449	seq=translation; coord=1:27094498..27098727:1; parent_transcript=GRMZM2G163129_T01; parent_gene=GRMZM2G163129	GRMZM2G163129_P01	TRUE	TRUE	fVFADNk	91%	n+304 (+304), K+304 (+304)	26.02	25.66
5450	seq=translation; coord=1:27094498..27098727:1; parent_transcript=GRMZM2G163129_T01; parent_gene=GRMZM2G163129	GRMZM2G163129_P01	TRUE	TRUE	yGAVVTGDNSADWDHLk	95%	n+304 (+304), K+304 (+304)	27.76	25.00
5451	seq=translation; coord=5:210594434..210598555:-1; parent_transcript=GRMZM2G090718_T01; parent_gene=GRMZM2G090718	GRMZM2G090718_P01	TRUE	TRUE	aGDGVFHFVVEIPk	91%	n+304 (+304), K+304 (+304)	26.96	25.67
5452	seq=translation; coord=6:109292609..109296377:1; parent_transcript=GRMZM2G048194_T01; parent_gene=GRMZM2G048194	GRMZM2G048194_P01,GRMZM2G048194_P02	TRUE	TRUE	tTIEPcSGADAcPALLGYk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	54.84	25.00
5453	seq=translation; coord=6:109292609..109296377:1; parent_transcript=GRMZM2G048194_T01; parent_gene=GRMZM2G048194	GRMZM2G048194_P01,GRMZM2G048194_P02	TRUE	TRUE	vSEVAALFGADPAAVLAANALDFASPGAANR	95%	n+304 (+304)	31.37	25.35

5454	seq=translation; coord=8:78073258..78079706:1; parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418 seq=translation; coord=8:78073258..78079706:1;	GRMZM2G023418_P01	TRUE	TRUE	aEAAAPETk	95%	n+304 (+304), K+304 (+304)	30.94	25.00
5455	parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418 seq=translation; coord=8:78073258..78079706:1;	GRMZM2G023418_P01	TRUE	TRUE	dEGTAATAALVDDAEGk	95%	n+304 (+304), K+304 (+304)	32.57	25.00
5456	parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418 seq=translation; coord=8:78073258..78079706:1;	GRMZM2G023418_P01	TRUE	TRUE	iSAFDEEEAkPIVk	95%	n+304 (+304), K+304 (+304)	26.45	25.08
5457	parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418 seq=translation; coord=8:78073258..78079706:1;	GRMZM2G023418_P01	TRUE	TRUE	kDPIVLGVDDVLEGIak	95%	K+304 (+304), n+304 (+304), K+304 (+304)	39.39	25.00
5458	parent_transcript=GRMZM2G023418_T01; parent_gene=GRMZM2G023418 seq=translation; coord=8:78073258..78079706:1;	GRMZM2G023418_P01	TRUE	TRUE	ITDIVTQFk	95%	n+304 (+304), K+304 (+304)	30.00	25.00
5459	parent_transcript=GRMZM2G169365_T01; parent_gene=GRMZM2G169365 seq=translation; coord=9:150816519..150821326:-1;	GRMZM2G169365_P01	TRUE	TRUE	aADNQLFVATcAPAR	95%	n+304 (+304), Carbamidomethyl (+57)	69.19	25.00
5460	parent_transcript=GRMZM2G169365_T01; parent_gene=GRMZM2G169365 seq=translation; coord=9:150816519..150821326:-1;	GRMZM2G169365_P01	TRUE	TRUE	iHLFDIDIPGk	95%	n+304 (+304), K+304 (+304)	28.45	25.02
5461	parent_transcript=GRMZM2G169365_T01; parent_gene=GRMZM2G169365 seq=translation; coord=9:150816519..150821326:-1;	GRMZM2G169365_P01	TRUE	TRUE	rGDLYQLVDVQR	95%	n+304 (+304)	44.01	25.73
5462	parent_transcript=GRMZM2G169365_T01; parent_gene=GRMZM2G169365 seq=translation; coord=2:193416339..193419729:-1;	GRMZM2G169365_P01	TRUE	TRUE	tLTAGQSPTVVDVTDVGR	95%	n+304 (+304)	35.85	25.48
5463	parent_transcript=GRMZM2G023080_T01; parent_gene=GRMZM2G023080 seq=translation; coord=2:193416339..193419729:-1;	GRMZM2G023080_P01,GRMZM2G023080_P02, GRMZM2G040164_P01,GRMZM2G040164_P02	TRUE	TRUE	fDPLWNSLVGGVvk	95%	n+304 (+304), K+304 (+304)	30.22	25.29
5464	parent_transcript=GRMZM2G023080_T01; parent_gene=GRMZM2G023080 seq=translation; coord=5:30771033..30772796:1;	GRMZM2G023080_P01,GRMZM2G023080_P02, GRMZM2G040164_P01,GRMZM2G040164_P02	TRUE	TRUE	hSIIGASGEFSDFQEILR	95%	n+304 (+304)	80.56	25.00
5465	parent_transcript=GRMZM2G026216_T01; parent_gene=GRMZM2G026216 seq=translation; coord=5:30771033..30772796:1;	GRMZM2G026216_P01,GRMZM2G026216_P02, GRMZM2G089421_P01,GRMZM2G149257_P01	TRUE	TRUE	aIGVEINK	95%	n+304 (+304), K+304 (+304)	36.43	27.12
5466	parent_transcript=GRMZM2G026216_T01; parent_gene=GRMZM2G026216 seq=translation; coord=5:215656610..215661825:1;	GRMZM2G026216_P01,GRMZM2G026216_P02, GRMZM2G089421_P01,GRMZM2G149257_P01	TRUE	TRUE	iGDYVDVvk	89%	n+304 (+304), K+304 (+304)	26.82	25.88
5467	parent_transcript=GRMZM2G143651_T01; parent_gene=GRMZM2G143651 seq=translation; coord=5:215656610..215661825:1;	GRMZM2G143651_P01	TRUE	TRUE	iQPVVYVIDVAAAIIVNSLk	95%	n+304 (+304), K+304 (+304)	66.10	25.00
5468	parent_transcript=GRMZM2G143651_T01; parent_gene=GRMZM2G143651 seq=translation; coord=6:28127232..28129613:1;	GRMZM2G143651_P01	TRUE	TRUE	sSVSGIVATVFGATGFLGR	95%	n+304 (+304)	41.26	25.91
5469	parent_transcript=GRMZM2G165815_T02; parent_gene=GRMZM2G165815 seq=translation; coord=6:28127232..28129613:1;	GRMZM2G165815_P02	TRUE	TRUE	IDLDIER	95%	n+304 (+304)	33.35	25.29
5470	parent_transcript=GRMZM2G165815_T02; parent_gene=GRMZM2G165815 seq=translation; coord=8:154456893..154470550:1;	GRMZM2G165815_P02	TRUE	TRUE	sMEEMANEANEYR	95%	n+304 (+304)	66.35	25.00
5471	parent_transcript=GRMZM2G316113_T01; parent_gene=GRMZM2G316113	GRMZM2G316113_P01,GRMZM2G316113_P02, GRMZM2G316113_P05	TRUE	TRUE	aSVFGSSAEDGFLNVWDHEK	95%	n+304 (+304), K+304 (+304)	36.29	25.00

5472	seq=translation; coord=8:154456893..154470550:1; parent_transcript=GRMZM2G316113_T01; parent_gene=GRMZM2G316113 seq=translation; coord=6:24549898..24554957:-1;	GRMZM2G316113_P01,GRMZM2G316113_P02, GRMZM2G316113_P05	TRUE	TRUE	iIATHDSDPDLIWDVEAQPNR	95%	n+304 (+304)	33.32	25.45
5473	parent_transcript=GRMZM2G111579_T01; parent_gene=GRMZM2G111579 seq=translation; coord=6:24549898..24554957:-1;	GRMZM2G111579_P01	TRUE	TRUE	aGLALQPIATAIFANSPFK	95%	n+304 (+304), K+304 (+304)	58.23	25.00
5474	parent_transcript=GRMZM2G111579_T01; parent_gene=GRMZM2G111579 seq=translation; coord=5:163610246..163620614:1;	GRMZM2G111579_P01	TRUE	TRUE	wALSDIPIMPK	91%	n+304 (+304), K+304 (+304)	25.31	25.00
5475	parent_transcript=GRMZM2G360589_T01; parent_gene=GRMZM2G360589 seq=translation; coord=5:163610246..163620614:1;	GRMZM2G360589_P01	TRUE	TRUE	dMSAEVVDNNPYSR	95%	n+304 (+304)	49.26	25.00
5476	parent_transcript=GRMZM2G360589_T01; parent_gene=GRMZM2G360589 seq=translation; coord=2:76993674..76995064:1;	GRMZM2G360589_P01	TRUE	TRUE	gFETFLASLK	94%	n+304 (+304), K+304 (+304)	28.99	25.42
5477	parent_transcript=GRMZM2G069523_T01; parent_gene=GRMZM2G069523 seq=translation; coord=2:76993674..76995064:1;	GRMZM2G069523_P01	TRUE	TRUE	aMVTLTENAAELQHGIR	95%	n+304 (+304)	86.18	25.00
5478	parent_transcript=GRMZM2G069523_T01; parent_gene=GRMZM2G069523 seq=translation; coord=2:76993674..76995064:1;	GRMZM2G069523_P01	TRUE	TRUE	IFVEHGAHVVDADIQDEAGAR	95%	n+304 (+304)	61.61	25.22
5479	parent_transcript=GRMZM2G069523_T01; parent_gene=GRMZM2G069523 seq=translation; coord=2:76993674..76995064:1;	GRMZM2G069523_P01	TRUE	TRUE	vHDVAAAVFLASDDAR	91%	n+304 (+304)	26.72	25.69
5480	parent_transcript=GRMZM2G069523_T01; parent_gene=GRMZM2G069523 seq=translation; coord=4:240105137..240108983:1;	GRMZM2G069523_P01	TRUE	TRUE	vLAVNLVGPFLGTK	95%	n+304 (+304), K+304 (+304)	48.73	25.00
5481	parent_transcript=GRMZM2G079348_T01; parent_gene=GRMZM2G079348 seq=translation; coord=4:240105137..240108983:1;	GRMZM2G079348_P01,GRMZM2G079348_P02, GRMZM2G079348_P03,GRMZM2G079348_P04	TRUE	TRUE	cILTDEEAALVGGR	95%	Carbamidomethyl (+57), n+304 (+304)	69.28	25.00
5482	parent_transcript=GRMZM2G079348_T01; parent_gene=GRMZM2G079348 seq=translation; coord=4:240105137..240108983:1;	GRMZM2G079348_P01,GRMZM2G079348_P02, GRMZM2G079348_P03,GRMZM2G079348_P04	TRUE	TRUE	gFFEcTHDVTSLtCADFLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	39.06	25.00
5483	parent_transcript=GRMZM2G079348_T01; parent_gene=GRMZM2G079348 seq=translation; coord=5:3195909..3207226:1;	GRMZM2G079348_P01,GRMZM2G079348_P02, GRMZM2G079348_P03,GRMZM2G079348_P04	TRUE	TRUE	sIWIDLLAK	95%	n+304 (+304), K+304 (+304)	40.79	25.00
5484	parent_transcript=GRMZM2G071071_T01; parent_gene=GRMZM2G071071 seq=translation; coord=5:3195909..3207226:1;	GRMZM2G071071_P01	TRUE	TRUE	aPDQTLELTSEVVDFLR	95%	n+304 (+304)	43.50	25.60
5485	parent_transcript=GRMZM2G071071_T01; parent_gene=GRMZM2G071071 seq=translation; coord=5:3195909..3207226:1;	GRMZM2G071071_P01	TRUE	TRUE	IIAEcQAADAVVLTyAcDRPATLER	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	29.25	25.00
5486	parent_transcript=GRMZM2G071071_T01; parent_gene=GRMZM2G071071 seq=translation; coord=5:3195909..3207226:1;	GRMZM2G071071_P01	TRUE	TRUE	ISSFWLPELR	95%	n+304 (+304)	50.57	25.00
5487	parent_transcript=GRMZM2G071071_T01; parent_gene=GRMZM2G071071 seq=translation; coord=8:94750778..94753384:1;	GRMZM2G071071_P01	TRUE	TRUE	sSLIVALATEQFPENVPR	95%	n+304 (+304)	43.71	25.17
5488	parent_transcript=GRMZM2G147221_T01; parent_gene=GRMZM2G147221 seq=translation; coord=8:94750778..94753384:1;	GRMZM2G147221_P01	TRUE	TRUE	ILAVELLNEPLAPGATLDSLTR	95%	n+304 (+304)	37.48	25.00
5489	parent_transcript=GRMZM2G147221_T01; parent_gene=GRMZM2G147221	GRMZM2G147221_P01	TRUE	TRUE	tQASDWETfk	95%	n+304 (+304), K+304 (+304)	37.14	25.00

5490	seq=translation; coord=6:6269340..6271805:-1; parent_transcript=GRMZM2G134134_T02; parent_gene=GRMZM2G134134	GRMZM2G134134_P02	TRUE	TRUE	dLVVDMTNFYNQYk	95%	n+304 (+304), K+304 (+304)	37.58	25.04
5491	seq=translation; coord=9:19034931..19038665:-1; parent_transcript=GRMZM5G877388_T02; parent_gene=GRMZM5G877388	GRMZM5G877388_P02	TRUE	TRUE	KTGMSLIIGIYDEPMTPGQcNMVVER	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	41.44	25.00
5492	seq=translation; coord=9:19034931..19038665:-1; parent_transcript=GRMZM5G877388_T02; parent_gene=GRMZM5G877388	GRMZM5G877388_P02	TRUE	TRUE	tGMSLIIGlyDEPMTPGQcNMVVER	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57)	27.52	25.00
5493	seq=translation; coord=1:34664608..34673432:1; parent_transcript=GRMZM2G058870_T01; parent_gene=GRMZM2G058870	GRMZM2G058870_P01	TRUE	TRUE	iIGDFDGALTPLAR	92%	n+304 (+304)	29.70	26.22
5494	seq=translation; coord=1:34664608..34673432:1; parent_transcript=GRMZM2G058870_T01; parent_gene=GRMZM2G058870	GRMZM2G058870_P01	TRUE	TRUE	IVEIFSPFLEK	95%	n+304 (+304), K+304 (+304)	31.21	25.11
5495	seq=translation; coord=5:6688332..6691221:1; parent_transcript=GRMZM5G862540_T01; parent_gene=GRMZM5G862540	GRMZM5G862540_P01,GRMZM5G862540_P02	TRUE	TRUE	gAHGVcILTEWDEFK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.91	25.00
5496	seq=translation; coord=5:6688332..6691221:1; parent_transcript=GRMZM5G862540_T01; parent_gene=GRMZM5G862540	GRMZM5G862540_P01,GRMZM5G862540_P02	TRUE	TRUE	vVAMSFNTVAGk	91%	n+304 (+304), K+304 (+304)	26.63	25.77
5497	seq=translation; coord=4:84106470..84111628:-1; parent_transcript=GRMZM2G035268_T01; parent_gene=GRMZM2G035268	GRMZM2G035268_P01,GRMZM2G035268_P03	TRUE	TRUE	vVLIMESIADAVVQk	95%	n+304 (+304), K+304 (+304)	47.34	25.00
5498	seq=translation; coord=9:57980157..57982564:1; parent_transcript=GRMZM2G066111_T01; parent_gene=GRMZM2G066111	GRMZM2G066111_P01,GRMZM2G109418_P01, GRMZM2G470035_P01,GRMZM5G884912_P01	TRUE	TRUE	eAFLLEPR	91%	n+304 (+304)	28.66	25.77
5499	seq=translation; coord=9:57980157..57982564:1; parent_transcript=GRMZM2G066111_T01; parent_gene=GRMZM2G066111	GRMZM2G066111_P01,GRMZM2G109418_P01, GRMZM2G470035_P01,GRMZM5G884912_P01	TRUE	TRUE	eGFIVLR	88%	n+304 (+304)	25.98	25.00
5500	seq=translation; coord=3:87798819..87808953:-1; parent_transcript=GRMZM2G009593_T01; parent_gene=GRMZM2G009593	GRMZM2G009593_P01,GRMZM2G028700_P01, GRMZM2G070323_P01	TRUE	TRUE	gNHEAADINALFGFR	95%	n+304 (+304)	46.52	25.00
5501	seq=translation; coord=3:87798819..87808953:-1; parent_transcript=GRMZM2G009593_T01; parent_gene=GRMZM2G009593	GRMZM2G009593_P01,GRMZM2G028700_P01, GRMZM2G070323_P01	TRUE	TRUE	iFGDLHGQFGDLMR	95%	n+304 (+304)	27.79	25.00
5502	seq=translation; coord=3:87798819..87808953:-1; parent_transcript=GRMZM2G009593_T01; parent_gene=GRMZM2G009593	GRMZM2G009593_P01,GRMZM2G028700_P01, GRMZM2G070323_P01	TRUE	TRUE	IFNWLPLALIEK	92%	n+304 (+304), K+304 (+304)	26.97	25.00
5503	seq=translation; coord=6:126146579..126150071:1; parent_transcript=GRMZM2G341729_T01; parent_gene=GRMZM2G341729	GRMZM2G341729_P01	TRUE	TRUE	wVGLATDFSEGRS	95%	n+304 (+304)	40.35	25.00
5504	seq=translation; coord=2:196359627..196363692:-1; parent_transcript=GRMZM2G573867_T01; parent_gene=GRMZM2G573867	GRMZM2G573867_P01,GRMZM2G573867_P02	TRUE	TRUE	gVNFIIQIPTTLMAQVDSSVGKk	95%	n+304 (+304), K+304 (+304)	41.00	25.00
5505	seq=translation; coord=2:196359627..196363692:-1; parent_transcript=GRMZM2G573867_T01; parent_gene=GRMZM2G573867	GRMZM2G573867_P01,GRMZM2G573867_P02	TRUE	TRUE	vSTVVVDVLDGR	95%	n+304 (+304)	39.77	25.87
5506	seq=translation; coord=1:49207907..49216831:1; parent_transcript=GRMZM2G140432_T01; parent_gene=GRMZM2G140432	GRMZM2G140432_P01	TRUE	TRUE	eLcDLPLAEDIPITMSSVR	95%	n+304 (+304), Carbamidomethyl (+57)	38.93	25.00
5507	seq=translation; coord=1:49207907..49216831:1; parent_transcript=GRMZM2G140432_T01; parent_gene=GRMZM2G140432	GRMZM2G140432_P01	TRUE	TRUE	gSPNEFPGIGATSPLLWLAR	95%	n+304 (+304)	36.94	25.16

5508	seq=translation; coord=5:214501921..214505061:1; parent_transcript=GRMZM2G008728_T02; parent_gene=GRMZM2G008728 seq=translation; coord=5:214501921..214505061:1;	GRMZM2G008728_P02	TRUE	TRUE	eVEDHPALGEGEVLLVEAAAGVNR	95%	n+304 (+304)	50.30	25.00
5509	parent_transcript=GRMZM2G008728_T02; parent_gene=GRMZM2G008728 seq=translation; coord=9:147281001..147286520:-1;	GRMZM2G008728_P02	TRUE	TRUE	gVDVILDNIGGSYLQR	95%	n+304 (+304)	34.56	26.18
5510	parent_transcript=GRMZM2G100511_T01; parent_gene=GRMZM2G100511 seq=translation; coord=1:298585659..298587727:-1;	GRMZM2G100511_P01	TRUE	TRUE	aMEVLADILQNSNLDQAR	95%	n+304 (+304)	32.47	25.00
5511	parent_transcript=GRMZM2G058568_T03; parent_gene=GRMZM2G058568 seq=translation; coord=1:298585659..298587727:-1;	GRMZM2G058568_P03,GRMZM2G058568_P04	TRUE	TRUE	eLYLGDR	90%	n+304 (+304)	27.24	25.00
5512	parent_transcript=GRMZM2G058568_T03; parent_gene=GRMZM2G058568 seq=translation; coord=1:298585659..298587727:-1;	GRMZM2G058568_P03,GRMZM2G058568_P04	TRUE	TRUE	IGAGDPFPGSPPGAAR	86%	n+304 (+304)	25.68	25.21
5513	parent_transcript=GRMZM2G058568_T03; parent_gene=GRMZM2G058568 seq=translation; coord=9:116241684..116244580:-1;	GRMZM2G058568_P03,GRMZM2G058568_P04	TRUE	TRUE	vTDADLYAPAK	95%	n+304 (+304), K+304 (+304)	38.56	26.73
5514	parent_transcript=GRMZM2G013002_T01; parent_gene=GRMZM2G013002 seq=translation; coord=9:116241684..116244580:-1;	GRMZM2G013002_P01	TRUE	TRUE	eSWGSVWR	90%	n+304 (+304)	27.21	25.00
5515	parent_transcript=GRMZM2G013002_T01; parent_gene=GRMZM2G013002 seq=translation; coord=9:116241684..116244580:-1;	GRMZM2G013002_P01	TRUE	TRUE	vPcEFPLK	90%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.51	26.21
5516	parent_transcript=GRMZM2G013002_T01; parent_gene=GRMZM2G013002 seq=translation; coord=9:107790531..107797125:1;	GRMZM2G013002_P01	TRUE	TRUE	yHFDLSGTAFGR	95%	n+304 (+304), iTRAQ8plex (+304)	34.71	25.00
5517	parent_transcript=GRMZM2G055320_T01; parent_gene=GRMZM2G055320 seq=translation; coord=9:107790531..107797125:1;	GRMZM2G055320_P01	TRUE	TRUE	gDVVMALLR	95%	n+304 (+304)	41.44	25.15
5518	parent_transcript=GRMZM2G055320_T01; parent_gene=GRMZM2G055320 seq=translation; coord=9:107790531..107797125:1;	GRMZM2G055320_P01	TRUE	TRUE	gFQVPPAELEALLITHPEIK	95%	n+304 (+304), K+304 (+304)	64.58	25.00
5519	parent_transcript=GRMZM2G055320_T01; parent_gene=GRMZM2G055320 seq=translation; coord=8:143676986..143682414:1;	GRMZM2G055320_P01	TRUE	TRUE	ncPEFALVFLGAAR	95%	n+304 (+304), Carbamidomethyl (+57)	62.11	25.98
5520	parent_transcript=GRMZM2G107757_T01; parent_gene=GRMZM2G107757 seq=translation; coord=8:143676986..143682414:1;	GRMZM2G107757_P01,GRMZM2G107757_P02, GRMZM2G107757_P03	TRUE	TRUE	aTTETVDALR	90%	n+304 (+304)	27.80	25.50
5521	parent_transcript=GRMZM2G107757_T01; parent_gene=GRMZM2G107757 seq=translation; coord=8:143676986..143682414:1;	GRMZM2G107757_P01,GRMZM2G107757_P02, GRMZM2G107757_P03	TRUE	TRUE	INETLDMLEK	95%	n+304 (+304), K+304 (+304)	36.64	26.46
5522	parent_transcript=GRMZM2G107757_T01; parent_gene=GRMZM2G107757 seq=translation; coord=3:147676601..147679180:-1;	GRMZM2G107757_P01,GRMZM2G107757_P02, GRMZM2G107757_P03	TRUE	TRUE	IYEQQIEQLGNFQLR	95%	n+304 (+304)	54.77	25.68
5523	parent_transcript=GRMZM2G479112_T01; parent_gene=GRMZM2G479112 seq=translation; coord=3:147676601..147679180:-1;	GRMZM2G479112_P01	TRUE	TRUE	eLVSQFAVcDR	93%	n+304 (+304), Carbamidomethyl (+57)	30.14	25.00
5524	parent_transcript=GRMZM2G479112_T01; parent_gene=GRMZM2G479112 seq=translation; coord=3:147676601..147679180:-1;	GRMZM2G479112_P01	TRUE	TRUE	gFNPADVAVYR	93%	n+304 (+304)	30.05	25.00
5525	parent_transcript=GRMZM2G479112_T01; parent_gene=GRMZM2G479112	GRMZM2G479112_P01	TRUE	TRUE	vPAILVSPWIDR	95%	n+304 (+304)	42.60	25.90

5526	seq=translation; coord=8:8472359..8474789:1; parent_transcript=GRMZM2G021614_T01; parent_gene=GRMZM2G021614 seq=translation; coord=8:8472359..8474789:1;	GRMZM2G021614_P01,GRMZM2G021614_P02	TRUE	TRUE	eYLHWIVINIPGGTDAK	95%	n+304 (+304), K+304 (+304)	31.14	25.00
5527	parent_transcript=GRMZM2G021614_T01; parent_gene=GRMZM2G021614 seq=translation; coord=6:123432811..123435820:-1;	GRMZM2G021614_P01,GRMZM2G021614_P02	TRUE	TRUE	yVLVLFQEK	95%	n+304 (+304), K+304 (+304)	42.31	25.00
5528	parent_transcript=GRMZM2G127160_T01; parent_gene=GRMZM2G127160 seq=translation; coord=6:123432811..123435820:-1;	GRMZM2G127160_P01,GRMZM2G127160_P02	TRUE	TRUE	eSGGMAAALR	95%	n+304 (+304)	34.18	25.00
5529	parent_transcript=GRMZM2G127160_T01; parent_gene=GRMZM2G127160 seq=translation; coord=6:86773351..86783757:1;	GRMZM2G127160_P01,GRMZM2G127160_P02	TRUE	TRUE	vSMVDTDQAFNVFINR	95%	n+304 (+304)	62.55	25.00
5530	parent_transcript=GRMZM2G161493_T01; parent_gene=GRMZM2G161493 seq=translation; coord=9:7614057..7616811:1;	GRMZM2G161493_P01	TRUE	TRUE	vGFTVMDTWLAYAPV	95%	n+304 (+304), K+304 (+304)	42.02	25.02
5531	parent_transcript=GRMZM2G079949_T01; parent_gene=GRMZM2G079949 seq=translation; coord=9:7614057..7616811:1;	GRMZM2G079949_P01	TRUE	TRUE	dVVVDPATGLWAR	89%	n+304 (+304)	27.46	25.54
5532	parent_transcript=GRMZM2G079949_T01; parent_gene=GRMZM2G079949 seq=translation; coord=5:188857165..188858944:1;	GRMZM2G079949_P01	TRUE	TRUE	vFLAGASAGATIAHFVAVR	95%	n+304 (+304)	100.92	25.67
5533	parent_transcript=GRMZM2G170017_T01; parent_gene=GRMZM2G170017 seq=translation; coord=5:188857165..188858944:1;	GRMZM2G170017_P01	TRUE	TRUE	IDELSALFLEDYR	92%	n+304 (+304)	26.73	25.00
5534	parent_transcript=GRMZM2G170017_T01; parent_gene=GRMZM2G170017 seq=translation; coord=6:160034201..160039816:-1;	GRMZM2G170017_P01	TRUE	TRUE	tTQSAEQAEeCVR	95%	n+304 (+304), Carbamidomethyl (+57)	59.58	25.00
5535	parent_transcript=GRMZM2G004932_T01; parent_gene=GRMZM2G004932 seq=translation; coord=6:160034201..160039816:-1;	GRMZM2G004932_P01	TRUE	TRUE	ILLDIGLWLTHK	95%	n+304 (+304), K+304 (+304)	33.94	25.00
5536	parent_transcript=GRMZM2G004932_T01; parent_gene=GRMZM2G004932 seq=translation; coord=1:38548724..38550734:-1;	GRMZM2G004932_P01	TRUE	TRUE	sFGFDTAVEEAQR	95%	n+304 (+304)	62.44	25.00
5537	parent_transcript=GRMZM2G012566_T02; parent_gene=GRMZM2G012566 seq=translation; coord=1:38548724..38550734:-1;	GRMZM2G012566_P02	TRUE	TRUE	eYYDDAAPK	95%	n+304 (+304), K+304 (+304)	34.64	25.00
5538	parent_transcript=GRMZM2G012566_T02; parent_gene=GRMZM2G012566	GRMZM2G012566_P02	TRUE	TRUE	ISEDPAEER	95%	n+304 (+304)	33.82	25.00
5539	seq=translation; coord=4:53673036..53676735:-1; parent_transcript=GRMZM2G032367_T01; parent_gene=GRMZM2G032367	GRMZM2G032367_P01,GRMZM2G032367_P02, GRMZM2G032367_P03,GRMZM2G158479_P02, GRMZM2G158479_P03,GRMZM2G158479_P04	TRUE	TRUE	dLVGVAYTEETK	95%	n+304 (+304), K+304 (+304)	42.26	26.09
5540	seq=translation; coord=4:53673036..53676735:-1; parent_transcript=GRMZM2G032367_T01; parent_gene=GRMZM2G032367	GRMZM2G032367_P01,GRMZM2G032367_P02, GRMZM2G032367_P03,GRMZM2G158479_P02, GRMZM2G158479_P03,GRMZM2G158479_P04	TRUE	TRUE	dVVSFSLWAAEPEMEER	89%	n+304 (+304)	27.01	25.00
5541	seq=translation; coord=1:258447609..258448792:1; parent_transcript=GRMZM2G039639_T01; parent_gene=GRMZM2G039639	GRMZM2G039639_P01	TRUE	TRUE	cDADVTSQcPAALQAPGGcDNPcTVFk	95%	Carbamidomethyl (+57), n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	43.38	25.00

5542	seq=translation; coord=1:258447609..258448792:1; parent_transcript=GRMZM2G039639_T01; parent_gene=GRMZM2G039639 seq=translation; coord=1:7406938..7408184:1;	GRMZM2G039639_P01	TRUE	TRUE	gLcPDAYSYPk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.43	25.00
5543	parent_transcript=GRMZM2G099454_T02; parent_gene=GRMZM2G099454 seq=translation; coord=1:7406938..7408184:1;	GRMZM2G099454_P01,GRMZM2G099454_P02, GRMZM2G099454_P03,GRMZM2G099454_P04	TRUE	TRUE	fPGFGTTGDEQTR	95%	n+304 (+304)	33.26	25.00
5544	parent_transcript=GRMZM2G099454_T02; parent_gene=GRMZM2G099454 seq=translation; coord=5:49897243..49899430:-1;	GRMZM2G099454_P01,GRMZM2G099454_P02, GRMZM2G099454_P03,GRMZM2G099454_P04	TRUE	TRUE	gDSGcQGAFTYDAFIEAASK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	59.49	25.00
5545	parent_transcript=GRMZM2G177828_T01; parent_gene=GRMZM2G177828 seq=translation; coord=5:49897243..49899430:-1;	GRMZM2G177828_P01	TRUE	TRUE	eYDETLAYLQk	95%	n+304 (+304), K+304 (+304)	67.83	25.00
5546	parent_transcript=GRMZM2G177828_T01; parent_gene=GRMZM2G177828 seq=translation; coord=8:2199781..2200562:-1;	GRMZM2G177828_P01	TRUE	TRUE	gAIGGSGLk	95%	n+304 (+304), K+304 (+304)	30.17	25.68
5547	parent_transcript=GRMZM2G353266_T01; parent_gene=GRMZM2G353266 seq=translation; coord=8:2199781..2200562:-1;	GRMZM2G353266_P01	TRUE	TRUE	aGAAESEEDVMLR	95%	n+304 (+304)	65.28	25.00
5548	parent_transcript=GRMZM2G353266_T01; parent_gene=GRMZM2G353266 seq=translation; coord=7:3483732..3484794:1;	GRMZM2G353266_P01	TRUE	TRUE	gGGGILGSLQEGk	95%	n+304 (+304), K+304 (+304)	51.02	26.37
5549	parent_transcript=GRMZM2G465226_T01; parent_gene=GRMZM2G465226 seq=translation; coord=7:3483732..3484794:1;	GRMZM2G465226_P01	TRUE	TRUE	aDVGVPVSWDDTVAAYAQSYAAQR	95%	n+304 (+304)	45.88	25.00
5550	parent_transcript=GRMZM2G465226_T01; parent_gene=GRMZM2G465226 seq=translation; coord=7:3483732..3484794:1;	GRMZM2G465226_P01	TRUE	TRUE	aDVGVPVSWDDTVAAYAQSYAAQR	95%	n+304 (+304), iTRAQ8plex (+304)	48.41	25.08
5551	parent_transcript=GRMZM2G465226_T01; parent_gene=GRMZM2G465226 seq=translation; coord=7:29542055..29544356:-1;	GRMZM2G465226_P01	TRUE	TRUE	dSTAIGcAR	95%	n+304 (+304), Carbamidomethyl (+57)	35.92	25.00
5552	parent_transcript=GRMZM5G872934_T01; parent_gene=GRMZM5G872934 seq=translation; coord=7:29542055..29544356:-1;	GRMZM5G872934_P01	TRUE	TRUE	aSGEPALVASSVHcALR	95%	n+304 (+304), Carbamidomethyl (+57)	61.00	25.50
5553	parent_transcript=GRMZM5G872934_T01; parent_gene=GRMZM5G872934 seq=translation; coord=7:168251112..168255445:1;	GRMZM5G872934_P01	TRUE	TRUE	IWPDADGGGGeLLGR	95%	n+304 (+304), Carbamidomethyl (+57)	51.41	25.00
5554	parent_transcript=GRMZM2G160569_T01; parent_gene=GRMZM2G160569 seq=translation; coord=5:192259829..192267449:-1;	GRMZM2G160569_P01,GRMZM2G160569_P02, GRMZM2G160569_P03	TRUE	TRUE	iADAVGDWFFER	95%	n+304 (+304)	52.15	25.00
5555	parent_transcript=GRMZM2G004768_T01; parent_gene=GRMZM2G004768 seq=translation; coord=2:12351628..12357486:-1;	GRMZM2G004768_P01,GRMZM2G102502_P01	TRUE	TRUE	eALEELTR	89%	n+304 (+304)	27.68	25.67
5556	parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728 seq=translation; coord=2:12351628..12357486:-1;	GRMZM2G125728_P01,GRMZM2G125728_P02	TRUE	TRUE	dPFDLSSSANVGk	95%	n+304 (+304), K+304 (+304)	31.09	26.00
5557	parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728 seq=translation; coord=2:12351628..12357486:-1;	GRMZM2G125728_P01,GRMZM2G125728_P02	TRUE	TRUE	gLIDLNITAPk	95%	n+304 (+304), K+304 (+304)	45.26	25.00
5558	parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728 seq=translation; coord=2:12351628..12357486:-1;	GRMZM2G125728_P01,GRMZM2G125728_P02	TRUE	TRUE	kVNLADIGIVGGLGDGSDEk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	39.46	25.00
5559	parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728	GRMZM2G125728_P01,GRMZM2G125728_P02	TRUE	TRUE	sGIWADSLSR	89%	n+304 (+304)	26.56	25.00

5560	seq=translation; coord=2:12351628..12357486:-1; parent_transcript=GRMZM2G125728_T01; parent_gene=GRMZM2G125728	GRMZM2G125728_P01,GRMZM2G125728_P02	TRUE	TRUE	vNVDLFAEK	95%	n+304 (+304), K+304 (+304)	34.55	26.20
5561	seq=translation; coord=2:236283794..236288865:1; parent_transcript=GRMZM2G103955_T02; parent_gene=GRMZM2G103955	GRMZM2G103955_P02	TRUE	TRUE	aIEDEDFVDAVDcLSR	95%	n+304 (+304), Carbamidomethyl (+57)	66.74	25.00
5562	seq=translation; coord=2:236283794..236288865:1; parent_transcript=GRMZM2G103955_T02; parent_gene=GRMZM2G103955	GRMZM2G103955_P02	TRUE	TRUE	aLSMLEHLVEPDHR	95%	n+304 (+304)	43.01	25.25
5563	seq=translation; coord=2:236283794..236288865:1; parent_transcript=GRMZM2G103955_T02; parent_gene=GRMZM2G103955	GRMZM2G103955_P02	TRUE	TRUE	icLVYELVSk	92%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.65	25.00
5564	seq=translation; coord=1:194210583..194219751:1; parent_transcript=GRMZM2G171111_T02; parent_gene=GRMZM2G171111	GRMZM2G171111_P02,GRMZM2G171111_P04	TRUE	TRUE	ISTGDSLDMSPQDEK	95%	n+304 (+304), K+304 (+304)	46.80	25.00
5565	seq=translation; coord=1:194210583..194219751:1; parent_transcript=GRMZM2G171111_T02; parent_gene=GRMZM2G171111	GRMZM2G171111_P02,GRMZM2G171111_P04	TRUE	TRUE	rIPVPFDMYGIGAR	95%	n+304 (+304)	54.09	25.20
5566	seq=translation; coord=2:115064269..115065362:-1; parent_transcript=GRMZM2G008649_T01; parent_gene=GRMZM2G008649	GRMZM2G008649_P01,GRMZM2G008649_P01	TRUE	TRUE	aGEEDATAILGR	95%	n+304 (+304)	36.23	25.00
5567	seq=translation; coord=3:193091877..193119714:1; parent_transcript=GRMZM2G071441_T01; parent_gene=GRMZM2G071441	GRMZM2G071441_P01,GRMZM2G071441_P02	TRUE	TRUE	IFLEVHFR	95%	n+304 (+304)	44.08	25.00
5568	seq=translation; coord=3:193091877..193119714:1; parent_transcript=GRMZM2G071441_T01; parent_gene=GRMZM2G071441	GRMZM2G071441_P01,GRMZM2G071441_P02	TRUE	TRUE	sNSLLDLIEDLk	95%	n+304 (+304), K+304 (+304)	36.65	25.43
5569	seq=translation; coord=5:1526460..1528840:-1; parent_transcript=GRMZM2G448001_T01; parent_gene=GRMZM2G448001	GRMZM2G448001_P01	TRUE	TRUE	aLAVPDGGWPTWADDTTVFFHR	95%	n+304 (+304)	72.05	25.00
5570	seq=translation; coord=5:1526460..1528840:-1; parent_transcript=GRMZM2G448001_T01; parent_gene=GRMZM2G448001	GRMZM2G448001_P01	TRUE	TRUE	ITFTDDDVASVVDR	95%	n+304 (+304)	70.47	25.00
5571	seq=translation; coord=5:14752854..14761623:1; parent_transcript=GRMZM2G553314_T01; parent_gene=GRMZM2G553314	GRMZM2G553314_P01	TRUE	TRUE	iDIGVFDALK	95%	n+304 (+304), K+304 (+304)	36.01	25.00
5572	seq=translation; coord=5:14752854..14761623:1; parent_transcript=GRMZM2G553314_T01; parent_gene=GRMZM2G553314	GRMZM2G553314_P01	TRUE	TRUE	INIGGEVIK	94%	n+304 (+304), K+304 (+304)	29.46	25.90
5573	seq=translation; coord=1:67523715..67533727:-1; parent_transcript=GRMZM2G410479_T01; parent_gene=GRMZM2G410479	GRMZM2G410479_P01	TRUE	TRUE	aILESIR	93%	n+304 (+304)	29.31	25.00
5574	seq=translation; coord=1:67523715..67533727:-1; parent_transcript=GRMZM2G410479_T01; parent_gene=GRMZM2G410479	GRMZM2G410479_P01	TRUE	TRUE	INLQFLTLHDYLLR	95%	n+304 (+304)	40.53	25.00
5575	seq=translation; coord=1:67523715..67533727:-1; parent_transcript=GRMZM2G410479_T01; parent_gene=GRMZM2G410479	GRMZM2G410479_P01	TRUE	TRUE	nLIEEFVEILNSk	93%	n+304 (+304), K+304 (+304)	27.27	25.00
5576	seq=translation; coord=7:156205011..156210949:-1; parent_transcript=GRMZM5G890190_T01; parent_gene=GRMZM5G890190	GRMZM5G890190_P01,GRMZM5G890190_P02	TRUE	TRUE	aDDFASPLk	95%	n+304 (+304), K+304 (+304)	39.92	26.09
5577	seq=translation; coord=7:156205011..156210949:-1; parent_transcript=GRMZM5G890190_T01; parent_gene=GRMZM5G890190	GRMZM5G890190_P01,GRMZM5G890190_P02	TRUE	TRUE	icLEVER	87%	n+304 (+304), Carbamidomethyl (+57)	26.66	25.98

5578	seq=translation; coord=7:156205011..156210949:-1; parent_transcript=GRMZM5G890190_T01; parent_gene=GRMZM5G890190	GRMZM5G890190_P01,GRMZM5G890190_P02	TRUE	TRUE	ISLSAVIMGSk	93%	n+304 (+304), K+304 (+304)	27.29	25.00
5579	seq=translation; coord=4:201936215..201938145:1; parent_transcript=GRMZM2G325118_T01; parent_gene=GRMZM2G325118	GRMZM2G325118_P01	TRUE	TRUE	qAcEWQYGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	41.91	25.00
5580	seq=translation; coord=4:201936215..201938145:1; parent_transcript=GRMZM2G325118_T01; parent_gene=GRMZM2G325118	GRMZM2G325118_P01	TRUE	TRUE	qQcVQAcER	91%	Carbamidomethyl (+57), Carbamidomethyl (+57)	28.17	25.00
5581	seq=translation; coord=9:130498884..130500159:1; parent_transcript=GRMZM2G134107_T01; parent_gene=GRMZM2G134107	GRMZM2G134107_P01	TRUE	TRUE	aGQLGEGVTVTR	95%	n+304 (+304)	42.38	26.34
5582	seq=translation; coord=9:130498884..130500159:1; parent_transcript=GRMZM2G134107_T01; parent_gene=GRMZM2G134107	GRMZM2G134107_P01	TRUE	TRUE	iMEIATLEk	94%	n+304 (+304), K+304 (+304)	28.44	25.17
5583	seq=translation; coord=2:8578099..8582568:-1; parent_transcript=GRMZM2G012628_T01; parent_gene=GRMZM2G012628	GRMZM2G012628_P01	TRUE	TRUE	dkNSGQLQGYGFVEFTSR	95%	n+304 (+304), K+304 (+304)	33.48	25.00
5584	seq=translation; coord=2:8578099..8582568:-1; parent_transcript=GRMZM2G012628_T01; parent_gene=GRMZM2G012628	GRMZM2G012628_P01	TRUE	TRUE	qVFSPPYGEVVHVk	95%	n+304 (+304), K+304 (+304)	41.67	25.92
5585	seq=translation; coord=2:8578099..8582568:-1; parent_transcript=GRMZM2G012628_T01; parent_gene=GRMZM2G012628	GRMZM2G012628_P01	TRUE	TRUE	qVFSPPYGEVVHVk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	35.22	25.75
5586	seq=translation; coord=7:11441042..11445373:-1; parent_transcript=GRMZM2G401308_T02; parent_gene=GRMZM2G401308	GRMZM2G401308_P02	TRUE	TRUE	mIVEAIAALK	95%	n+304 (+304), K+304 (+304)	43.02	25.00
5587	seq=translation; coord=7:11441042..11445373:-1; parent_transcript=GRMZM2G401308_T02; parent_gene=GRMZM2G401308	GRMZM2G401308_P02	TRUE	TRUE	qLTVQLk	95%	n+304 (+304), K+304 (+304)	37.87	25.33
5588	seq=translation; coord=3:44223365..44228905:-1; parent_transcript=GRMZM2G003883_T01; parent_gene=GRMZM2G003883	GRMZM2G003883_P01	TRUE	TRUE	aALILVLTR	92%	n+304 (+304)	28.56	25.00
5589	seq=translation; coord=3:44223365..44228905:-1; parent_transcript=GRMZM2G003883_T01; parent_gene=GRMZM2G003883	GRMZM2G003883_P01	TRUE	TRUE	iDMIALSFVR	86%	n+304 (+304)	26.38	25.97
5590	seq=translation; coord=1:267894143..267897525:-1; parent_transcript=GRMZM2G024104_T01; parent_gene=GRMZM2G024104	GRMZM2G024104_P01,GRMZM2G024104_P02, GRMZM2G024104_P03,GRMZM2G024104_P04	TRUE	TRUE	aEEPWFGEIQEYTLQk	95%	n+304 (+304), K+304 (+304)	70.93	25.91
5591	seq=translation; coord=8:29610407..29612711:1; parent_transcript=GRMZM2G067522_T01; parent_gene=GRMZM2G067522	GRMZM2G067522_P01	TRUE	TRUE	aRPGAPAAAPSR	95%	n+304 (+304)	35.61	25.66
5592	seq=translation; coord=8:29610407..29612711:1; parent_transcript=GRMZM2G067522_T01; parent_gene=GRMZM2G067522	GRMZM2G067522_P01	TRUE	TRUE	iAEcLVGDETGAIVFTAR	95%	n+304 (+304), Carbamidomethyl (+57)	55.95	25.00
5593	seq=translation; coord=3:1297208..1299271:1; parent_transcript=GRMZM5G884242_T01; parent_gene=GRMZM5G884242	GRMZM5G884242_P01,GRMZM5G884242_P02, GRMZM5G884242_P03,GRMZM5G884242_P04, GRMZM5G884242_P05	TRUE	TRUE	aYFDSADWALGk	93%	n+304 (+304), K+304 (+304)	26.50	25.00
5594	seq=translation; coord=4:17087184..17096848:1; parent_transcript=GRMZM2G045987_T01; parent_gene=GRMZM2G045987	GRMZM2G045987_P01	TRUE	TRUE	iIALLGGPcTEGPGMIVSk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	66.26	25.43
5595	seq=translation; coord=4:17087184..17096848:1; parent_transcript=GRMZM2G045987_T01; parent_gene=GRMZM2G045987	GRMZM2G045987_P01	TRUE	TRUE	ITWNTWPR	93%	n+304 (+304)	29.32	25.63

5596	seq=translation; coord=4:17087184..17096848:1; parent_transcript=GRMZM2G045987_T01; parent_gene=GRMZM2G045987	GRMZM2G045987_P01	TRUE	TRUE	qLVSQGHVLDVFASALDQVGLAEMk	95%	n+304 (+304), K+304 (+304)	33.82	25.00
5597	seq=translation; coord=4:17087184..17096848:1; parent_transcript=GRMZM2G045987_T01; parent_gene=GRMZM2G045987	GRMZM2G045987_P01	TRUE	TRUE	vQGIIGPcTSLek	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.33	25.42
5598	seq=translation; coord=10:11749519..11756094:-1; parent_transcript=GRMZM2G036534_T01; parent_gene=GRMZM2G036534	GRMZM2G036534_P01	TRUE	TRUE	dVEAALAAPk	95%	n+304 (+304), K+304 (+304)	45.12	25.00
5599	seq=translation; coord=10:11749519..11756094:-1; parent_transcript=GRMZM2G036534_T01; parent_gene=GRMZM2G036534	GRMZM2G036534_P01	TRUE	TRUE	viYGADLAAFLQLak	95%	n+304 (+304), K+304 (+304)	35.04	25.00
5600	seq=translation; coord=4:187884467..187890415:-1; parent_transcript=GRMZM2G119175_T01; parent_gene=GRMZM2G119175	GRMZM2G119175_P01,GRMZM2G119175_P02	TRUE	TRUE	IGDLSQTLIFak	95%	n+304 (+304), K+304 (+304)	31.77	25.00
5601	seq=translation; coord=4:187884467..187890415:-1; parent_transcript=GRMZM2G119175_T01; parent_gene=GRMZM2G119175	GRMZM2G119175_P01,GRMZM2G119175_P02	TRUE	TRUE	yRPTMPVLVVIPR	95%	n+304 (+304)	40.92	25.00
5602	seq=translation; coord=7:154188635..154191068:-1; parent_transcript=GRMZM2G056369_T01; parent_gene=GRMZM2G056369	GRMZM2G056369_P01	TRUE	TRUE	eLQAIEDEWLAAAQLk	95%	n+304 (+304), K+304 (+304)	59.01	25.84
5603	seq=translation; coord=7:154188635..154191068:-1; parent_transcript=GRMZM2G056369_T01; parent_gene=GRMZM2G056369	GRMZM2G056369_P01	TRUE	TRUE	gQSLAAVLSAGMSAGk	95%	n+304 (+304), K+304 (+304)	42.36	25.97
5604	seq=translation; coord=7:154188635..154191068:-1; parent_transcript=GRMZM2G056369_T01; parent_gene=GRMZM2G056369	GRMZM2G056369_P01	TRUE	TRUE	vEHLFFAQLYHDR	95%	n+304 (+304)	27.46	25.00
5605	seq=translation; coord=5:30994200..30995891:-1; parent_transcript=GRMZM2G111477_T01; parent_gene=GRMZM2G111477	GRMZM2G111477_P01	TRUE	TRUE	gEYVDMVk	87%	n+304 (+304), K+304 (+304)	25.96	25.66
5606	seq=translation; coord=5:30994200..30995891:-1; parent_transcript=GRMZM2G111477_T01; parent_gene=GRMZM2G111477	GRMZM2G111477_P01	TRUE	TRUE	ILEQENTDLGYDAak	95%	n+304 (+304), K+304 (+304)	53.20	25.59
5607	seq=translation; coord=10:94095731..94103354:-1; parent_transcript=GRMZM2G174671_T01; parent_gene=GRMZM2G174671	GRMZM2G174671_P01,GRMZM2G174671_P04	TRUE	TRUE	IMHVISVsk	95%	n+304 (+304), K+304 (+304)	33.54	25.99
5608	seq=translation; coord=4:140347561..140350401:1; parent_transcript=GRMZM2G079817_T01; parent_gene=GRMZM2G079817	GRMZM2G079817_P01	TRUE	TRUE	aAPDLAEcLAVMQSLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	39.93	25.60
5609	seq=translation; coord=4:140347561..140350401:1; parent_transcript=GRMZM2G079817_T01; parent_gene=GRMZM2G079817	GRMZM2G079817_P01	TRUE	TRUE	aLSELIPATEk	95%	n+304 (+304), K+304 (+304)	29.53	25.16
5610	seq=translation; coord=4:140347561..140350401:1; parent_transcript=GRMZM2G079817_T01; parent_gene=GRMZM2G079817	GRMZM2G079817_P01	TRUE	TRUE	IPDLVELYLSDLNLENk	94%	n+304 (+304), K+304 (+304)	27.87	25.00
5611	seq=translation; coord=1:189145769..189150346:-1; parent_transcript=GRMZM2G079817_T01; parent_gene=GRMZM2G079817	GRMZM2G079817_P01	TRUE	TRUE	tIEELcFALADEHFR	95%	n+304 (+304), Carbamidomethyl (+57)	55.27	25.00
5612	seq=translation; coord=1:189145769..189150346:-1; parent_transcript=GRMZM2G088627_T01; parent_gene=GRMZM2G088627	GRMZM2G088627_P01	TRUE	TRUE	aEGDVVSVNFAYLk	95%	n+304 (+304), K+304 (+304)	40.99	25.43
5613	seq=translation; coord=1:189145769..189150346:-1; parent_transcript=GRMZM2G088627_T01; parent_gene=GRMZM2G088627	GRMZM2G088627_P01	TRUE	TRUE	gIGIYESIIR	95%	n+304 (+304)	33.46	25.99

5614	seq=translation; coord=1:189145769..189150346:-1; parent_transcript=GRMZM2G088627_T01; parent_gene=GRMZM2G088627	GRMZM2G088627_P01	TRUE	TRUE	IYDGSAMENLMk	94%	n+304 (+304), K+304 (+304)	28.66	25.00
5615	seq=translation; coord=6:151454748..151457344:-1; parent_transcript=GRMZM2G059314_T01; parent_gene=GRMZM2G059314	GRMZM2G059314_P01	TRUE	TRUE	aIGVSNFSSk	95%	n+304 (+304), K+304 (+304)	36.43	25.89
5616	seq=translation; coord=6:151454748..151457344:-1; parent_transcript=GRMZM2G059314_T01; parent_gene=GRMZM2G059314	GRMZM2G059314_P01	TRUE	TRUE	aNLDVFGWSLPEDLLAK	95%	n+304 (+304), K+304 (+304)	29.74	25.28
5617	seq=translation; coord=6:151454748..151457344:-1; parent_transcript=GRMZM2G059314_T01; parent_gene=GRMZM2G059314	GRMZM2G059314_P01	TRUE	TRUE	dLQTDYVDLYLMHWPVR	95%	n+304 (+304)	63.56	25.00
5618	seq=translation; coord=6:151454748..151457344:-1; parent_transcript=GRMZM2G059314_T01; parent_gene=GRMZM2G059314	GRMZM2G059314_P01	TRUE	TRUE	IADLLAVAR	95%	n+304 (+304)	40.28	25.00
5619	seq=translation; coord=5:13726531..13727525:-1; parent_transcript=GRMZM2G129083_T01; parent_gene=GRMZM2G129083	GRMZM2G129083_P01	TRUE	TRUE	cFSSYSAGk	95%	Carbamidomethyl (+57), n+304 (+304), K+304 (+304)	41.68	25.00
5620	seq=translation; coord=5:13726531..13727525:-1; parent_transcript=GRMZM2G129083_T01; parent_gene=GRMZM2G129083	GRMZM2G129083_P01	TRUE	TRUE	gGVVAPTVTcSEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304),	33.16	26.15
5621	seq=translation; coord=5:13726531..13727525:-1; parent_transcript=GRMZM2G129083_T01; parent_gene=GRMZM2G129083	GRMZM2G129083_P01	TRUE	TRUE	gYGGGGGGScTVDck	95%	Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	55.76	25.00
5622	seq=translation; coord=9:22677939..22681262:-1; parent_transcript=GRMZM5G877500_T01; parent_gene=GRMZM5G877500	GRMZM5G877500_P01	TRUE	TRUE	INVTAIDTYDDHR	95%	n+304 (+304)	48.14	25.00
5623	seq=translation; coord=9:22677939..22681262:-1; parent_transcript=GRMZM5G877500_T01; parent_gene=GRMZM5G877500	GRMZM5G877500_P01	TRUE	TRUE	tFPDYFDVLSTFvk	95%	n+304 (+304), K+304 (+304)	40.16	26.51
5624	seq=translation; coord=3:160397311..160408336:1; parent_transcript=GRMZM2G129155_T01; parent_gene=GRMZM2G129155	GRMZM2G129155_P01,GRMZM2G180335_P01	TRUE	TRUE	iFSPNVNLITLVDLPGITk	95%	n+304 (+304), K+304 (+304)	41.16	25.00
5625	seq=translation; coord=3:160397311..160408336:1; parent_transcript=GRMZM2G129155_T01; parent_gene=GRMZM2G129155	GRMZM2G129155_P01,GRMZM2G180335_P01	TRUE	TRUE	tLDEIPLDAEAVER	95%	n+304 (+304)	35.08	25.44
5626	seq=translation; coord=1:132810230..132856187:1; parent_transcript=GRMZM2G019673_T01; parent_gene=GRMZM2G019673	GRMZM2G019673_P01,GRMZM2G019673_P04, GRMZM2G019673_P05	TRUE	TRUE	eVFSALILSADILGk	95%	n+304 (+304), K+304 (+304)	46.80	25.00
5627	seq=translation; coord=1:132810230..132856187:1; parent_transcript=GRMZM2G019673_T01; parent_gene=GRMZM2G019673	GRMZM2G019673_P01,GRMZM2G019673_P04, GRMZM2G019673_P05	TRUE	TRUE	fLLDWLIEGHR	95%	n+304 (+304)	51.76	26.51
5628	seq=translation; coord=4:237676754..237682663:-1; parent_transcript=GRMZM2G117346_T01; parent_gene=GRMZM2G117346	GRMZM2G117346_P01,GRMZM2G117346_P02, GRMZM2G410393_P01,GRMZM2G410393_P03, GRMZM2G410393_P04,GRMZM2G410393_P05	TRUE	TRUE	aIGPQDVLATLLNNLk	95%	n+304 (+304), K+304 (+304)	31.53	25.00
5629	seq=translation; coord=4:237676754..237682663:-1; parent_transcript=GRMZM2G117346_T01; parent_gene=GRMZM2G117346	GRMZM2G117346_P01,GRMZM2G117346_P02, GRMZM2G410393_P01,GRMZM2G410393_P03, GRMZM2G410393_P04,GRMZM2G410393_P05	TRUE	TRUE	tSSDWDAPDATPGIGR	95%	n+304 (+304)	78.79	25.00
5630	seq=translation; coord=2:45890416..45891705:-1; parent_transcript=GRMZM2G152141_T01; parent_gene=GRMZM2G152141	GRMZM2G152141_P01	TRUE	TRUE	gYVSDMEVVGk	95%	n+304 (+304), K+304 (+304)	57.11	25.07

5631	seq=translation; coord=2:45890416..45891705:-1; parent_transcript=GRMZM2G152141_T01; parent_gene=GRMZM2G152141	GRMZM2G152141_P01	TRUE	TRUE	yIEALNVVHSAVHALATGNLR	95%	n+304 (+304)	59.20	25.56
5632	seq=translation; coord=8:135417381..135418239:1; parent_transcript=GRMZM2G175273_T01; parent_gene=GRMZM2G175273	GRMZM2G175273_P01	TRUE	TRUE	aQQAAGGTGTSTDNnk	95%	n+304 (+304), K+304 (+304)	73.24	25.07
5633	seq=translation; coord=8:135417381..135418239:1; parent_transcript=GRMZM2G175273_T01; parent_gene=GRMZM2G175273	GRMZM2G175273_P01	TRUE	TRUE	nSQDGLTPEQR	95%	n+304 (+304)	39.30	25.00
5634	seq=translation; coord=4:183588190..183591209:-1; parent_transcript=GRMZM2G325575_T01; parent_gene=GRMZM2G325575	GRMZM2G325575_P01	TRUE	TRUE	gDALYAMELALALEk	95%	n+304 (+304), K+304 (+304)	38.90	25.72
5635	seq=translation; coord=4:183588190..183591209:-1; parent_transcript=GRMZM2G325575_T01; parent_gene=GRMZM2G325575	GRMZM2G325575_P01	TRUE	TRUE	gHGVVHFDQMLLEEEA	95%	n+304 (+304)	31.07	25.00
5636	seq=translation; coord=6:115639609..115647217:-1; parent_transcript=GRMZM2G008556_T01; parent_gene=GRMZM2G008556	GRMZM2G008556_P01,GRMZM2G039325_P01, GRMZM5G832989_P01,GRMZM5G832989_P02	TRUE	TRUE	dDDMPPIEAILAPLEELk	95%	n+304 (+304), K+304 (+304)	42.17	25.42
5637	seq=translation; coord=6:115639609..115647217:-1; parent_transcript=GRMZM2G008556_T01; parent_gene=GRMZM2G008556	GRMZM2G008556_P01,GRMZM2G039325_P01, GRMZM5G832989_P01,GRMZM5G832989_P02	TRUE	TRUE	eAALLEAER	89%	n+304 (+304)	27.51	25.89
5638	seq=translation; coord=8:12273514..12274222:-1; parent_transcript=GRMZM2G156632_T01; parent_gene=GRMZM2G156632	GRMZM2G156632_P01	TRUE	TRUE	aIDINPGQLk	95%	n+304 (+304), K+304 (+304)	35.41	25.43
5639	seq=translation; coord=1:296022541..296026398:-1; parent_transcript=GRMZM2G053299_T01; parent_gene=GRMZM2G053299	GRMZM2G053299_P01	TRUE	TRUE	IAFVALDYEQLETAk	95%	n+304 (+304), K+304 (+304)	37.29	25.80
5640	seq=translation; coord=3:196019180..196024451:1; parent_transcript=GRMZM2G324886_T01; parent_gene=GRMZM2G324886	GRMZM2G324886_P01	TRUE	TRUE	dPMSGIMDLmk	93%	n+304 (+304), K+304 (+304)	27.72	25.00
5641	seq=translation; coord=3:196019180..196024451:1; parent_transcript=GRMZM2G324886_T01; parent_gene=GRMZM2G324886	GRMZM2G324886_P01	TRUE	TRUE	IELDELr	95%	n+304 (+304)	34.32	27.40
5642	seq=translation; coord=4:168987228..168990822:1; parent_transcript=GRMZM2G018947_T01; parent_gene=GRMZM2G018947	GRMZM2G018947_P01,GRMZM2G133764_P01, GRMZM2G133764_P02	TRUE	TRUE	ILVLDEADEMLSR	93%	n+304 (+304)	29.71	25.00
5643	seq=translation; coord=4:168987228..168990822:1; parent_transcript=GRMZM2G018947_T01; parent_gene=GRMZM2G018947	GRMZM2G018947_P01,GRMZM2G133764_P01, GRMZM2G133764_P02	TRUE	TRUE	vLITTDVWAR	95%	n+304 (+304)	32.54	25.04
5644	seq=translation; coord=4:168987228..168990822:1; parent_transcript=GRMZM2G018947_T01; parent_gene=GRMZM2G018947	GRMZM2G018947_P01,GRMZM2G133764_P01, GRMZM2G133764_P02	TRUE	TRUE	yLPPELQVVLISATLPHEILEMTsk	95%	n+304 (+304), K+304 (+304)	47.96	25.00
5645	seq=translation; coord=8:157966228..157972830:-1; parent_transcript=GRMZM2G016827_T02; parent_gene=GRMZM2G016827	GRMZM2G016827_P02	TRUE	TRUE	mGMEIETGDPVAFk	92%	n+304 (+304), K+304 (+304)	26.61	25.87
5646	seq=translation; coord=8:157966228..157972830:-1; parent_transcript=GRMZM2G016827_T02; parent_gene=GRMZM2G016827	GRMZM2G016827_P02	TRUE	TRUE	vAGASGEEDkQD	95%	n+304 (+304), K+304 (+304)	54.83	25.00
5647	seq=translation; coord=8:157966228..157972830:-1; parent_transcript=GRMZM2G016827_T02; parent_gene=GRMZM2G016827	GRMZM2G016827_P02	TRUE	TRUE	vVPILVGALSSQNEALYQLLSk	95%	n+304 (+304), K+304 (+304)	40.25	25.00
5648	seq=translation; coord=8:2349948..2353138:1; parent_transcript=GRMZM2G027728_T01; parent_gene=GRMZM2G027728	GRMZM2G027728_P01,GRMZM2G050460_P01	TRUE	TRUE	IQLVMk	90%	n+304 (+304), K+304 (+304)	27.62	25.00

5649	seq=translation; coord=8:2349948..2353138:1; parent_transcript=GRMZM2G027728_T01; parent_gene=GRMZM2G027728	GRMZM2G027728_P01,GRMZM2G050460_P01	TRUE	TRUE	vccLSIIDPGDSIIK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	32.28	25.19
5650	seq=translation; coord=7:1306578..1314769:-1; parent_transcript=GRMZM2G120563_T06; parent_gene=GRMZM2G120563 seq=translation; coord=7:1306578..1314769:-1;	GRMZM2G120563_P06,GRMZM2G120563_P07	TRUE	TRUE	eGVFHLR	91%	n+304 (+304)	27.04	26.01
5651	parent_transcript=GRMZM2G120563_T06; parent_gene=GRMZM2G120563 seq=translation; coord=1:197854710..197858129:-1;	GRMZM2G120563_P06,GRMZM2G120563_P07	TRUE	TRUE	gVMQILNTIIR	95%	n+304 (+304)	32.64	25.00
5652	parent_transcript=GRMZM2G021816_T01; parent_gene=GRMZM2G021816 seq=translation; coord=1:197854710..197858129:-1;	GRMZM2G021816_P01	TRUE	TRUE	diYEILMDENR	95%	n+304 (+304)	45.23	25.00
5653	parent_transcript=GRMZM2G021816_T01; parent_gene=GRMZM2G021816 seq=translation; coord=1:197854710..197858129:-1;	GRMZM2G021816_P01	TRUE	TRUE	eAVLAPAPAVEk	95%	n+304 (+304), K+304 (+304)	29.02	25.00
5654	parent_transcript=GRMZM2G021816_T01; parent_gene=GRMZM2G021816 seq=translation; coord=3:134285297..134289508:1;	GRMZM2G021816_P01	TRUE	TRUE	gDETPALR	88%	n+304 (+304)	27.09	25.77
5655	parent_transcript=GRMZM2G047434_T01; parent_gene=GRMZM2G047434 seq=translation; coord=3:134285297..134289508:1;	GRMZM2G047434_P01	TRUE	TRUE	aLDVLFETAMISSGFSPDNPAELSGk	95%	n+304 (+304), K+304 (+304)	34.96	25.00
5656	parent_transcript=GRMZM2G047434_T01; parent_gene=GRMZM2G047434 seq=translation; coord=3:134285297..134289508:1;	GRMZM2G047434_P01	TRUE	TRUE	fVDISKEDLDLGDNNNEER	95%	n+304 (+304), K+304 (+304)	41.28	25.00
5657	parent_transcript=GRMZM2G047434_T01; parent_gene=GRMZM2G047434 seq=translation; coord=7:161685025..161693219:-1;	GRMZM2G047434_P01	TRUE	TRUE	qEFSQAcDWIk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.03	25.00
5658	parent_transcript=GRMZM2G396397_T01; parent_gene=GRMZM2G396397 seq=translation; coord=6:76236848..76238660:1;	GRMZM2G396397_P01	TRUE	TRUE	vLIYSPAR	89%	n+304 (+304)	26.05	25.00
5659	parent_transcript=GRMZM2G051338_T01; parent_gene=GRMZM2G051338 seq=translation; coord=6:76236848..76238660:1;	GRMZM2G051338_P01	TRUE	TRUE	fVLVLFQQLGR	95%	n+304 (+304)	46.18	25.45
5660	parent_transcript=GRMZM2G051338_T01; parent_gene=GRMZM2G051338 seq=translation; coord=2:192412235..192414620:-1;	GRMZM2G051338_P01	TRUE	TRUE	vVGDVLPDFVR	88%	n+304 (+304)	28.13	26.92
5661	parent_transcript=GRMZM2G178968_T01; parent_gene=GRMZM2G178968 seq=translation; coord=2:20765568..20767537:1;	GRMZM2G178968_P01,GRMZM5G870752_P01	TRUE	TRUE	vTNPLFEK	95%	n+304 (+304), K+304 (+304)	37.09	25.00
5662	parent_transcript=GRMZM2G337229_T01; parent_gene=GRMZM2G337229 seq=translation; coord=2:20765568..20767537:1;	GRMZM2G337229_P01	TRUE	TRUE	gATGGGGYGDLQR	95%	n+304 (+304)	54.26	25.00
5663	parent_transcript=GRMZM2G337229_T01; parent_gene=GRMZM2G337229 seq=translation; coord=3:202257167..202260653:-1;	GRMZM2G337229_P01	TRUE	TRUE	qGAMMTALK	95%	n+304 (+304), K+304 (+304)	30.61	26.25
5664	parent_transcript=GRMZM2G116282_T02; parent_gene=GRMZM2G116282 seq=translation; coord=3:221235623..221241542:1;	GRMZM2G116282_P02	TRUE	TRUE	sLQPLSNk	91%	n+304 (+304), K+304 (+304)	26.33	25.93
5665	parent_transcript=GRMZM2G149321_T01; parent_gene=GRMZM2G149321	GRMZM2G149321_P01	TRUE	TRUE	dVAEcNEQPNccTEDER	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	59.76	25.00

5666	seq=translation; coord=3:221235623..221241542:1; parent_transcript=GRMZM2G149321_T01; parent_gene=GRMZM2G149321	GRMZM2G149321_P01	TRUE	TRUE	tVDEPSEAEER	95%	n+304 (+304)	32.45	25.00
5667	seq=translation; coord=3:226173114..226176070:1; parent_transcript=GRMZM2G015364_T01; parent_gene=GRMZM2G015364	GRMZM2G015364_P01,GRMZM2G015364_P02, GRMZM2G094595_P01,GRMZM2G094595_P02, GRMZM2G094595_P03,GRMZM2G094595_P04	TRUE	TRUE	eIDPSESGIATTAR	95%	n+304 (+304)	43.11	25.00
5668	seq=translation; coord=1:237087363..237092641:-1; parent_transcript=GRMZM2G036765_T01; parent_gene=GRMZM2G036765	GRMZM2G036765_P01	TRUE	TRUE	dYSTAILER	95%	n+304 (+304)	36.06	25.00
5669	seq=translation; coord=8:24719639..24721093:1; parent_transcript=GRMZM2G047139_T01; parent_gene=GRMZM2G047139	GRMZM2G047139_P01,GRMZM2G047139_P02	TRUE	TRUE	IVVDFIAQELGVPLPPSk	95%	n+304 (+304), K+304 (+304)	32.20	25.00
5670	seq=translation; coord=2:220468734..220469483:-1; parent_transcript=GRMZM2G081464_T01; parent_gene=GRMZM2G081464	GRMZM2G081464_P01	TRUE	TRUE	IFAIcNLPMPR	95%	n+304 (+304), Carbamidomethyl (+57)	35.93	26.02
5671	seq=translation; coord=8:154379685..154384907:1; parent_transcript=GRMZM2G102404_T01; parent_gene=GRMZM2G102404	GRMZM2G102404_P01,GRMZM2G102404_P02	TRUE	TRUE	sAGLAALVDALVAAGR	95%	n+304 (+304)	48.72	25.00
5672	seq=translation; coord=6:99761240..99767447:-1; parent_transcript=GRMZM2G112337_T03; parent_gene=GRMZM2G112337	GRMZM2G112337_P03,GRMZM2G112337_P04	TRUE	TRUE	iPAIVDTLLak	95%	n+304 (+304), K+304 (+304)	32.13	25.00
5673	seq=translation; coord=2:204757521..204759565:-1; parent_transcript=GRMZM2G142922_T01; parent_gene=GRMZM2G142922	GRMZM2G142922_P01	TRUE	TRUE	aAASFAALVAALak	95%	n+304 (+304), K+304 (+304)	34.22	25.00
5674	seq=translation; coord=2:135017876..135044554:1; parent_transcript=GRMZM2G162286_T01; parent_gene=GRMZM2G162286	GRMZM2G162286_P01	TRUE	TRUE	aLPLPPDLLDPLLLSSLR	95%	n+304 (+304)	50.50	25.00
5675	seq=translation; coord=1:264855610..264864472:-1; parent_transcript=AC217401.3_FGT002; parent_gene=AC217401.3_FG002	AC217401.3_FGP002	TRUE	TRUE	fGIVYVDFATLk	95%	n+304 (+304), K+304 (+304)	51.89	25.90
5676	seq=translation; coord=1:264855610..264864472:-1; parent_transcript=AC217401.3_FGT002; parent_gene=AC217401.3_FG002	AC217401.3_FGP002	TRUE	TRUE	gFVFGTATSAYQVEGAATSGGR	95%	n+304 (+304)	55.90	25.00
5677	seq=translation; coord=1:264855610..264864472:-1; parent_transcript=AC217401.3_FGT002; parent_gene=AC217401.3_FG002	AC217401.3_FGP002	TRUE	TRUE	iVAFLGYDk	95%	n+304 (+304), K+304 (+304)	37.52	25.00
5678	seq=translation; coord=1:264855610..264864472:-1; parent_transcript=AC217401.3_FGT002; parent_gene=AC217401.3_FG002	AC217401.3_FGP002	TRUE	TRUE	iVDIFADYADFcFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.16	25.00
5679	seq=translation; coord=1:269493908..269506409:1; parent_transcript=GRMZM5G826838_T01; parent_gene=GRMZM5G826838	GRMZM5G826838_P01	TRUE	TRUE	eAAYQIINDELMLDGNPR	92%	n+304 (+304)	26.55	25.00
5680	seq=translation; coord=1:269493908..269506409:1; parent_transcript=GRMZM5G826838_T01; parent_gene=GRMZM5G826838	GRMZM5G826838_P01	TRUE	TRUE	gSSQVIAQYYQLIR	95%	n+304 (+304)	47.95	26.66
5681	seq=translation; coord=1:269493908..269506409:1; parent_transcript=GRMZM5G826838_T01; parent_gene=GRMZM5G826838	GRMZM5G826838_P01	TRUE	TRUE	ILNDLLTk	95%	n+304 (+304), K+304 (+304)	31.38	25.00
5682	seq=translation; coord=9:121108632..12110868:-1; parent_transcript=GRMZM2G467169_T01; parent_gene=GRMZM2G467169	GRMZM2G467169_P01,GRMZM2G467169_P02	TRUE	TRUE	dDSVAILEQFFGNVLSk	95%	n+304 (+304), K+304 (+304)	57.99	25.33

5683	seq=translation; coord=9:12103632..12110868:-1; parent_transcript=GRMZM2G467169_T01; parent_gene=GRMZM2G467169	GRMZM2G467169_P01,GRMZM2G467169_P02	TRUE	TRUE	dLTLEALFGAAFMNELHSK	95%	n+304 (+304), K+304 (+304)	71.62	25.72
5684	seq=translation; coord=9:12103632..12110868:-1; parent_transcript=GRMZM2G467169_T01; parent_gene=GRMZM2G467169	GRMZM2G467169_P01,GRMZM2G467169_P02	TRUE	TRUE	sLLSMIVk	92%	n+304 (+304), K+304 (+304)	26.12	25.00
5685	seq=translation; coord=1:278837830..278839720:1; parent_transcript=GRMZM2G118809_T01; parent_gene=GRMZM2G118809	GRMZM2G118809_P01,GRMZM2G154870_P01	TRUE	TRUE	ILGADDMPHLPYLQcVLTETLR	95%	n+304 (+304), Carbamidomethyl (+57)	46.79	25.00
5686	seq=translation; coord=1:278837830..278839720:1; parent_transcript=GRMZM2G118809_T01; parent_gene=GRMZM2G118809	GRMZM2G118809_P01,GRMZM2G154870_P01	TRUE	TRUE	sMMAVLLTLQk	95%	n+304 (+304), K+304 (+304)	31.01	25.00
5687	seq=translation; coord=9:138771755..138777249:1; parent_transcript=GRMZM2G162426_T01; parent_gene=GRMZM2G162426	GRMZM2G162426_P01	TRUE	TRUE	IADIGVAMGITGEVAK	95%	n+304 (+304), K+304 (+304)	48.87	25.72
5688	seq=translation; coord=9:138771755..138777249:1; parent_transcript=GRMZM2G162426_T01; parent_gene=GRMZM2G162426	GRMZM2G162426_P01	TRUE	TRUE	tPSEcLAELGVsADR	95%	n+304 (+304), Carbamidomethyl (+57)	67.41	25.00
5689	seq=translation; coord=9:138771755..138777249:1; parent_transcript=GRMZM2G162426_T01; parent_gene=GRMZM2G162426	GRMZM2G162426_P01	TRUE	TRUE	vLQISSTLR	92%	n+304 (+304)	28.81	25.00
5690	seq=translation; coord=1:276433043..276437555:-1; parent_transcript=GRMZM2G100084_T01; parent_gene=GRMZM2G100084	GRMZM2G100084_P01	TRUE	TRUE	fIPYTMQAVk	95%	n+304 (+304), K+304 (+304)	35.51	25.47
5691	seq=translation; coord=1:276433043..276437555:-1; parent_transcript=GRMZM2G100084_T01; parent_gene=GRMZM2G100084	GRMZM2G100084_P01	TRUE	TRUE	gMGSLEAMTk	95%	n+304 (+304), K+304 (+304)	50.49	25.00
5692	seq=translation; coord=1:276433043..276437555:-1; parent_transcript=GRMZM2G100084_T01; parent_gene=GRMZM2G100084	GRMZM2G100084_P01	TRUE	TRUE	qGLQDLGADSVQSAHDLLR	95%	n+304 (+304)	45.65	25.00
5693	seq=translation; coord=4:177628395..177630803:-1; parent_transcript=GRMZM2G126732_T01; parent_gene=GRMZM2G126732	GRMZM2G126732_P01,GRMZM2G126732_P02	TRUE	TRUE	aHTDAGLLILLQDDQVSGLQLLR	95%	n+304 (+304)	31.06	25.55
5694	seq=translation; coord=4:177628395..177630803:-1; parent_transcript=GRMZM2G126732_T01; parent_gene=GRMZM2G126732	GRMZM2G126732_P01,GRMZM2G126732_P02	TRUE	TRUE	gGDGGEWVDVPPLR	95%	n+304 (+304)	45.99	25.00
5695	seq=translation; coord=4:177628395..177630803:-1; parent_transcript=GRMZM2G126732_T01; parent_gene=GRMZM2G126732	GRMZM2G126732_P01,GRMZM2G126732_P02	TRUE	TRUE	vLDLLcENLGLPGYLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	64.17	25.00
5696	seq=translation; coord=9:26817670..26821498:1; parent_transcript=GRMZM2G475293_T01; parent_gene=GRMZM2G475293	GRMZM2G475293_P01,GRMZM2G475293_P02	TRUE	TRUE	aGVAAGMPVVG VATR	95%	n+304 (+304)	48.24	26.12
5697	seq=translation; coord=9:26817670..26821498:1; parent_transcript=GRMZM2G475293_T01; parent_gene=GRMZM2G475293	GRMZM2G475293_P01,GRMZM2G475293_P02	TRUE	TRUE	sDVEAAQNLPDWELEk	95%	n+304 (+304), K+304 (+304)	34.46	25.04
5698	seq=translation; coord=9:26817670..26821498:1; parent_transcript=GRMZM2G475293_T01; parent_gene=GRMZM2G475293	GRMZM2G475293_P01,GRMZM2G475293_P02	TRUE	TRUE	sLVEAGAAALLV k	95%	n+304 (+304), K+304 (+304)	52.59	25.00
5699	seq=translation; coord=3:166381506..166384595:-1; parent_transcript=GRMZM2G359397_T01; parent_gene=GRMZM2G359397	GRMZM2G359397_P01,GRMZM2G359397_P02, GRMZM2G359397_P03	TRUE	TRUE	aSQEFLDMR	95%	n+304 (+304)	38.67	25.00
5700	seq=translation; coord=3:166381506..166384595:-1; parent_transcript=GRMZM2G359397_T01; parent_gene=GRMZM2G359397	GRMZM2G359397_P01,GRMZM2G359397_P02, GRMZM2G359397_P03	TRUE	TRUE	vLPGVHNFVATLIEGR	95%	n+304 (+304)	62.17	25.63

5701	seq=translation; coord=3:166381506..166384595:-1; parent_transcript=GRMZM2G359397_T01; parent_gene=GRMZM2G359397 seq=translation; coord=2:199547128..199550293:1;	GRMZM2G359397_P01,GRMZM2G359397_P02, GRMZM2G359397_P03	TRUE	TRUE	vSPLEIVFR	91%	n+304 (+304)	27.14	25.00
5702	parent_transcript=GRMZM5G868679_T01; parent_gene=GRMZM5G868679 seq=translation; coord=2:199547128..199550293:1;	GRMZM5G868679_P01	TRUE	TRUE	aSPLVLGHK	95%	n+304 (+304), K+304 (+304)	30.75	25.00
5703	parent_transcript=GRMZM5G868679_T01; parent_gene=GRMZM5G868679 seq=translation; coord=2:199547128..199550293:1;	GRMZM5G868679_P01	TRUE	TRUE	ILAPAGTLTFDR	95%	n+304 (+304)	39.25	25.35
5704	parent_transcript=GRMZM5G868679_T01; parent_gene=GRMZM5G868679 seq=translation; coord=4:11466211..11470058:-1;	GRMZM5G868679_P01	TRUE	TRUE	qPWLIFLAHR	94%	Pyro-cmC (-17), n+304 (+304)	31.03	25.60
5705	parent_transcript=GRMZM2G085711_T02; parent_gene=GRMZM2G085711 seq=translation; coord=4:11466211..11470058:-1;	GRMZM2G085711_P02	TRUE	TRUE	sILPLeK	92%	n+304 (+304), K+304 (+304)	26.11	25.00
5706	parent_transcript=GRMZM2G085711_T02; parent_gene=GRMZM2G085711 seq=translation; coord=4:11466211..11470058:-1;	GRMZM2G085711_P02	TRUE	TRUE	sIVPSWLMK	95%	n+304 (+304), K+304 (+304)	32.29	26.28
5707	parent_transcript=GRMZM2G085711_T02; parent_gene=GRMZM2G085711 seq=translation; coord=7:7954180..7955128:1;	GRMZM2G085711_P02	TRUE	TRUE	yAVIFDAGSTGSR	92%	n+304 (+304)	27.41	25.00
5708	parent_transcript=GRMZM2G021149_T01; parent_gene=GRMZM2G021149 seq=translation; coord=7:7954180..7955128:1;	GRMZM2G021149_P01,GRMZM2G022041_P01	TRUE	TRUE	gEEVVSMTVEGPPPPDES	91%	n+304 (+304)	25.75	25.00
5709	parent_transcript=GRMZM2G021149_T01; parent_gene=GRMZM2G021149 seq=translation; coord=7:152772009..152776227:1;	GRMZM2G021149_P01,GRMZM2G022041_P01	TRUE	TRUE	hMNLVLGDcEEFR	95%	n+304 (+304), Carbamidomethyl (+57)	46.23	25.00
5710	parent_transcript=GRMZM2G108849_T02; parent_gene=GRMZM2G108849 seq=translation; coord=7:152772009..152776227:1;	GRMZM2G108849_P02,GRMZM2G108849_P03, GRMZM2G108849_P04	TRUE	TRUE	gWGDDGYfk	95%	n+304 (+304), K+304 (+304)	39.08	25.00
5711	parent_transcript=GRMZM2G108849_T02; parent_gene=GRMZM2G108849 seq=translation; coord=10:144683393..144689170:-1;	GRMZM2G108849_P02,GRMZM2G108849_P03, GRMZM2G108849_P04	TRUE	TRUE	nGPVEVAFTVYEDFAHYK	95%	n+304 (+304), K+304 (+304)	28.26	25.00
5712	parent_transcript=GRMZM2G136895_T01; parent_gene=GRMZM2G136895 seq=translation; coord=10:144683393..144689170:-1;	GRMZM2G136895_P01	TRUE	TRUE	aMHNVLGLAGLTFWSPNINIFR	95%	n+304 (+304)	61.89	25.44
5713	parent_transcript=GRMZM2G136895_T01; parent_gene=GRMZM2G136895 seq=translation; coord=3:91357080..91360381:-1;	GRMZM2G136895_P01	TRUE	TRUE	IGVPLYEWWSEALHGVSYVGPGR	95%	n+304 (+304), iTRAQ8plex (+304)	41.57	25.00
5714	parent_transcript=GRMZM2G077415_T01; parent_gene=GRMZM2G077415 seq=translation; coord=3:91357080..91360381:-1;	GRMZM2G077415_P01	TRUE	TRUE	aNTFVGEVLGLDPR	95%	n+304 (+304)	51.42	25.22
5715	parent_transcript=GRMZM2G077415_T01; parent_gene=GRMZM2G077415 seq=translation; coord=7:149132369..149134157:-1;	GRMZM2G077415_P01	TRUE	TRUE	ILGVTTLDVVR	95%	n+304 (+304)	39.90	25.00
5716	parent_transcript=GRMZM2G077673_T01; parent_gene=GRMZM2G077673 seq=translation; coord=7:149132369..149134157:-1;	GRMZM2G077673_P01	TRUE	TRUE	dGLIISMDLNLcR	95%	n+304 (+304), Carbamidomethyl (+57)	62.26	25.00
5717	parent_transcript=GRMZM2G077673_T01; parent_gene=GRMZM2G077673 seq=translation; coord=4:184547632..184552118:-1;	GRMZM2G077673_P01	TRUE	TRUE	yNMVIVSPILER	95%	n+304 (+304)	41.99	25.13
5718	parent_transcript=GRMZM2G347541_T01; parent_gene=GRMZM2G347541	GRMZM2G347541_P01,GRMZM2G389362_P01	TRUE	TRUE	akPGAFPTLLVDR	95%	n+304 (+304), K+304 (+304)	34.39	25.00

5719	seq=translation; coord=4:184547632..184552118:-1; parent_transcript=GRMZM2G347541_T01; parent_gene=GRMZM2G347541 seq=translation; coord=7:1269463..1270529:-1;	GRMZM2G347541_P01,GRMZM2G389362_P01	TRUE	TRUE	kPWLWWDYVTDFAIR	95%	K+304 (+304), n+304 (+304)	30.87	25.55
5720	parent_transcript=GRMZM2G420733_T01; parent_gene=GRMZM2G420733 seq=translation; coord=7:1269463..1270529:-1;	GRMZM2G420733_P01	TRUE	TRUE	eIPVVGGTGTFR	94%	n+304 (+304)	29.27	25.85
5721	parent_transcript=GRMZM2G420733_T01; parent_gene=GRMZM2G420733 seq=translation; coord=3:207473256..207484650:-1;	GRMZM2G420733_P01	TRUE	TRUE	mATGYVLWk	95%	n+304 (+304), K+304 (+304)	33.36	25.08
5722	parent_transcript=GRMZM2G073045_T01; parent_gene=GRMZM2G073045 seq=translation; coord=3:207473256..207484650:-1;	GRMZM2G073045_P01	TRUE	TRUE	dASEIFR	86%	n+304 (+304)	25.30	25.00
5723	parent_transcript=GRMZM2G073045_T01; parent_gene=GRMZM2G073045 seq=translation; coord=9:154544227..154545597:-1;	GRMZM2G073045_P01	TRUE	TRUE	gTLDAIGLHPDGR	95%	n+304 (+304)	46.91	25.47
5724	parent_transcript=GRMZM2G037327_T01; parent_gene=GRMZM2G037327 seq=translation; coord=6:31648456..31650307:1;	GRMZM2G037327_P01	TRUE	TRUE	aGAGALAAPLAVGLLAGANVLAcGALEGAVMNPAP	95%	n+304 (+304), Carbamidomethyl (+57)	50.23	25.00
5725	parent_transcript=GRMZM2G025959_T01; parent_gene=GRMZM2G025959 seq=translation; coord=6:31648456..31650307:1;	GRMZM2G025959_P01	TRUE	TRUE	fVSDFPYDGR	91%	n+304 (+304)	27.84	25.00
5726	parent_transcript=GRMZM2G025959_T01; parent_gene=GRMZM2G025959 seq=translation; coord=5:3145791..3147542:-1;	GRMZM2G025959_P01	TRUE	TRUE	tIDLGDAEVVR	95%	n+304 (+304)	34.99	25.58
5727	parent_transcript=GRMZM2G332976_T01; parent_gene=GRMZM2G332976 seq=translation; coord=10:130448044..130450386:1;	GRMZM2G332976_P01,GRMZM2G332976_P02, GRMZM2G332976_P03,GRMZM2G332976_P04, GRMZM2G332976_P05	TRUE	TRUE	vcIADIQDEAGQQLR	95%	n+304 (+304), Carbamidomethyl (+57)	69.03	25.00
5728	parent_transcript=GRMZM2G018760_T01; parent_gene=GRMZM2G018760 seq=translation; coord=4:233220256..233225418:1;	GRMZM2G018760_P01	TRUE	TRUE	ISDMcGVDLGDAALR	95%	n+304 (+304), Carbamidomethyl (+57)	66.87	25.00
5729	parent_transcript=GRMZM2G029566_T01; parent_gene=GRMZM2G029566 seq=translation; coord=5:33171053..33173977:-1;	GRMZM2G029566_P01	TRUE	TRUE	sFVEVPAGSHFPIQNLPGVFVR	95%	n+304 (+304)	36.36	25.40
5730	parent_transcript=GRMZM2G042136_T01; parent_gene=GRMZM2G042136 seq=translation; coord=9:31907012..31908736:-1;	GRMZM2G042136_P01,GRMZM2G042136_P02	TRUE	TRUE	eAPEEEEEAAVGR	95%	n+304 (+304)	32.60	25.00
5731	parent_transcript=GRMZM2G105364_T01; parent_gene=GRMZM2G105364 seq=translation; coord=2:186818557..186819984:1;	GRMZM2G105364_P01	TRUE	TRUE	acLTLCnK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	46.90	25.00
5732	parent_transcript=GRMZM2G323504_T01; parent_gene=GRMZM2G323504 seq=translation; coord=7:18139415..18147659:-1;	GRMZM2G323504_P01	TRUE	TRUE	eLALVAEFVR	95%	n+304 (+304)	36.53	25.00
5733	parent_transcript=GRMZM2G122810_T01; parent_gene=GRMZM2G122810 seq=translation; coord=6:124736591..124745000:-1;	GRMZM2G122810_P01,GRMZM2G122810_P02, GRMZM2G122810_P03,GRMZM2G122810_P05	TRUE	TRUE	eIFTPMYFFLVR	87%	n+304 (+304)	25.07	25.00
5734	parent_transcript=GRMZM2G148709_T01; parent_gene=GRMZM2G148709 seq=translation; coord=6:124736591..124745000:-1;	GRMZM2G148709_P01,GRMZM2G148709_P02, GRMZM2G148709_P03,GRMZM2G148709_P04	TRUE	TRUE	gESFYNPYIPQVLEELSSk	95%	n+304 (+304), K+304 (+304)	35.79	25.00
5735	parent_transcript=GRMZM2G148709_T01; parent_gene=GRMZM2G148709	GRMZM2G148709_P01,GRMZM2G148709_P02, GRMZM2G148709_P03,GRMZM2G148709_P04	TRUE	TRUE	IVELLDEAk	95%	n+304 (+304), K+304 (+304)	36.58	26.13

5736	seq=translation; coord=6:124736591..124745000:-1; parent_transcript=GRMZM2G148709_T01; parent_gene=GRMZM2G148709	GRMZM2G148709_P01,GRMZM2G148709_P02, GRMZM2G148709_P03,GRMZM2G148709_P04	TRUE	TRUE	mFEFSNVDVLR	95%	n+304 (+304)	35.17	25.00
5737	seq=translation; coord=6:124736591..124745000:-1; parent_transcript=GRMZM2G148709_T01; parent_gene=GRMZM2G148709	GRMZM2G148709_P01,GRMZM2G148709_P02, GRMZM2G148709_P03,GRMZM2G148709_P04	TRUE	TRUE	tSHVGFGVLVLSGSGk	95%	n+304 (+304), K+304 (+304)	31.91	25.58
5738	seq=translation; coord=7:160059330..160068443:-1; parent_transcript=GRMZM5G887631_T01; parent_gene=GRMZM5G887631	GRMZM5G887631_P01	TRUE	TRUE	aAVAAMPELLR	93%	n+304 (+304)	29.68	26.15
5739	seq=translation; coord=7:160059330..160068443:-1; parent_transcript=GRMZM5G887631_T01; parent_gene=GRMZM5G887631	GRMZM5G887631_P01	TRUE	TRUE	gSFLPFFEELSMylTPMLGk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.43	25.04
5740	seq=translation; coord=7:160059330..160068443:-1; parent_transcript=GRMZM5G887631_T01; parent_gene=GRMZM5G887631	GRMZM5G887631_P01	TRUE	TRUE	iAlcIFDDVAEQcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	30.45	25.00
5741	seq=translation; coord=7:160059330..160068443:-1; parent_transcript=GRMZM5G887631_T01; parent_gene=GRMZM5G887631	GRMZM5G887631_P01	TRUE	TRUE	IPDNIMAYDNAVSALGk	95%	n+304 (+304), K+304 (+304)	54.71	25.38
5742	seq=translation; coord=9:87461648..87475465:-1; parent_transcript=GRMZM2G047564_T03; parent_gene=GRMZM2G047564	GRMZM2G047564_P03,GRMZM2G047564_P04	TRUE	TRUE	aLLEWETNPsvk	95%	n+304 (+304), K+304 (+304)	30.68	25.20
5743	seq=translation; coord=9:87461648..87475465:-1; parent_transcript=GRMZM2G047564_T03; parent_gene=GRMZM2G047564	GRMZM2G047564_P03,GRMZM2G047564_P04	TRUE	TRUE	gAPFSLcLTQk	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	25.98	25.89
5744	seq=translation; coord=9:87461648..87475465:-1; parent_transcript=GRMZM2G047564_T03; parent_gene=GRMZM2G047564	GRMZM2G047564_P03,GRMZM2G047564_P04	TRUE	TRUE	ILPYIISSFSPPk	95%	n+304 (+304), K+304 (+304)	36.14	25.00
5745	seq=translation; coord=5:211206297..211209456:-1; parent_transcript=GRMZM2G151440_T01; parent_gene=GRMZM2G151440	GRMZM2G151440_P01,GRMZM2G151440_P02	TRUE	TRUE	iGSVALADLLk	95%	n+304 (+304), K+304 (+304)	54.97	25.00
5746	seq=translation; coord=5:211206297..211209456:-1; parent_transcript=GRMZM2G151440_T01; parent_gene=GRMZM2G151440	GRMZM2G151440_P01,GRMZM2G151440_P02	TRUE	TRUE	wNLPNLPEGTEVWIk	95%	n+304 (+304), K+304 (+304)	40.76	25.00
5747	seq=translation; coord=4:230556470..230569433:1; parent_transcript=GRMZM2G038195_T01; parent_gene=GRMZM2G038195	GRMZM2G038195_P01,GRMZM2G038195_P02, GRMZM2G119546_P01,GRMZM2G119546_P02	TRUE	TRUE	aILMEEWNVQPVR	95%	n+304 (+304)	50.97	25.84
5748	seq=translation; coord=4:230556470..230569433:1; parent_transcript=GRMZM2G038195_T01; parent_gene=GRMZM2G038195	GRMZM2G038195_P01,GRMZM2G038195_P02, GRMZM2G119546_P01,GRMZM2G119546_P02	TRUE	TRUE	iQEVPHGPMcDLLWSDPDDR	95%	n+304 (+304), Carbamidomethyl (+57)	62.21	25.00
5749	seq=translation; coord=6:133205650..133225934:-1; parent_transcript=GRMZM2G076006_T03; parent_gene=GRMZM2G076006	GRMZM2G076006_P03	TRUE	TRUE	ILHVVYR	90%	n+304 (+304)	25.77	25.44
5750	seq=translation; coord=6:133205650..133225934:-1; parent_transcript=GRMZM2G076006_T03; parent_gene=GRMZM2G076006	GRMZM2G076006_P03	TRUE	TRUE	tVFVDNIDFLk	95%	n+304 (+304), K+304 (+304)	51.33	26.40
5751	seq=translation; coord=6:81686909..81693610:1; parent_transcript=GRMZM2G103266_T01; parent_gene=GRMZM2G103266	GRMZM2G103266_P01,GRMZM2G103266_P07, GRMZM2G103266_P09	TRUE	TRUE	gFIYVIAHIR	95%	n+304 (+304)	45.27	25.00
5752	seq=translation; coord=6:81686909..81693610:1; parent_transcript=GRMZM2G103266_T01; parent_gene=GRMZM2G103266	GRMZM2G103266_P01,GRMZM2G103266_P07, GRMZM2G103266_P09	TRUE	TRUE	sDPDVLHLR	95%	n+304 (+304)	63.98	25.00
5753	seq=translation; coord=9:59939835..59941693:-1; parent_transcript=GRMZM2G471357_T01; parent_gene=GRMZM2G471357	GRMZM2G471357_P01,GRMZM2G471357_P03	TRUE	TRUE	gFEVIDTIk	95%	n+304 (+304), K+304 (+304)	45.72	25.04

5754	seq=translation; coord=9:59939835..59941693:-1; parent_transcript=GRMZM2G471357_T01; parent_gene=GRMZM2G471357	GRMZM2G471357_P01,GRMZM2G471357_P03	TRUE	TRUE	IFFHDCFVQGC DGSILLDAGGEK	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	27.65	25.00
5755	seq=translation; coord=9:59939835..59941693:-1; parent_transcript=GRMZM2G471357_T01; parent_gene=GRMZM2G471357 seq=translation; coord=7:168913721..168922316:-1;	GRMZM2G471357_P01,GRMZM2G471357_P03	TRUE	TRUE	sGGDGNLAPIDVQTPVR	95%	n+304 (+304)	77.22	25.53
5756	parent_transcript=GRMZM2G026991_T01; parent_gene=GRMZM2G026991 seq=translation; coord=7:168913721..168922316:-1;	GRMZM2G026991_P01	TRUE	TRUE	gAWTELSPLDVMQMLGR	95%	n+304 (+304)	41.33	25.00
5757	parent_transcript=GRMZM2G026991_T01; parent_gene=GRMZM2G026991 seq=translation; coord=2:179742429..179748543:1;	GRMZM2G026991_P01	TRUE	TRUE	IVMLLDYEK	90%	n+304 (+304), K+304 (+304)	25.48	25.00
5758	parent_transcript=GRMZM2G105772_T01; parent_gene=GRMZM2G105772 seq=translation; coord=2:179742429..179748543:1;	GRMZM2G105772_P01,GRMZM2G105772_P02	TRUE	TRUE	aLVLEVFfAcNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	43.95	25.00
5759	parent_transcript=GRMZM2G105772_T01; parent_gene=GRMZM2G105772 seq=translation; coord=3:225222066..225226693:-1;	GRMZM2G105772_P01,GRMZM2G105772_P02	TRUE	TRUE	gSSFQIEVEPTDK	95%	n+304 (+304), K+304 (+304)	50.28	25.68
5760	parent_transcript=GRMZM2G049866_T01; parent_gene=GRMZM2G049866 seq=translation; coord=3:7599914..7604652:-1;	GRMZM2G049866_P01,GRMZM2G049866_P02	TRUE	TRUE	iFVGNPADMASER	95%	n+304 (+304)	44.85	25.00
5761	parent_transcript=GRMZM2G146644_T01; parent_gene=GRMZM2G146644 seq=translation; coord=3:7599914..7604652:-1;	GRMZM2G146644_P01	TRUE	TRUE	vPHPWLNMFVPR	95%	n+304 (+304)	41.69	25.19
5762	parent_transcript=GRMZM2G146644_T01; parent_gene=GRMZM2G146644 seq=translation; coord=5:194043178..194045076:1;	GRMZM2G146644_P01	TRUE	TRUE	yVDAGGEQVWIDVLR	95%	n+304 (+304)	32.81	25.00
5763	parent_transcript=GRMZM2G013821_T01; parent_gene=GRMZM2G013821 seq=translation; coord=5:194043178..194045076:1;	GRMZM2G013821_P01,GRMZM2G013821_P02	TRUE	TRUE	aMSDQEK	95%	n+304 (+304), K+304 (+304)	30.85	25.30
5764	parent_transcript=GRMZM2G013821_T01; parent_gene=GRMZM2G013821 seq=translation; coord=1:292988864..292997657:1;	GRMZM2G013821_P01,GRMZM2G013821_P02	TRUE	TRUE	qEYQALHPGNk	93%	n+304 (+304), K+304 (+304)	27.93	26.11
5765	parent_transcript=GRMZM2G155580_T01; parent_gene=GRMZM2G155580 seq=translation; coord=1:292988864..292997657:1;	GRMZM2G155580_P01,GRMZM2G155580_P02, GRMZM2G155580_P03	TRUE	TRUE	fQSIDTETfLEFLK	95%	n+304 (+304), K+304 (+304)	40.01	26.37
5766	parent_transcript=GRMZM2G155580_T01; parent_gene=GRMZM2G155580 seq=translation; coord=1:292988864..292997657:1;	GRMZM2G155580_P01,GRMZM2G155580_P02, GRMZM2G155580_P03	TRUE	TRUE	mVFLTPTVik	95%	n+304 (+304), K+304 (+304)	32.03	25.00
5767	parent_transcript=GRMZM2G155580_T01; parent_gene=GRMZM2G155580 seq=translation; coord=6:140312649..140313648:-1;	GRMZM2G155580_P01,GRMZM2G155580_P02, GRMZM2G155580_P03	TRUE	TRUE	vYAEGGDTVLDEAAR	95%	n+304 (+304)	85.87	25.00
5768	parent_transcript=GRMZM2G162659_T01; parent_gene=GRMZM2G162659 seq=translation; coord=6:140312649..140313648:-1;	GRMZM2G162659_P01	TRUE	TRUE	gGLSTMQESGGER	95%	n+304 (+304)	79.47	25.00
5769	parent_transcript=GRMZM2G162659_T01; parent_gene=GRMZM2G162659 seq=translation; coord=6:140312649..140313648:-1;	GRMZM2G162659_P01	TRUE	TRUE	mAEEGQTVVPGGTGGk	93%	n+304 (+304), K+304 (+304)	26.93	25.48
5770	parent_transcript=GRMZM2G162659_T01; parent_gene=GRMZM2G162659	GRMZM2G162659_P01	TRUE	TRUE	tLEAQEHlAeGR	95%	n+304 (+304)	42.40	25.00

5771	seq=translation; coord=5:157517807..157521679:-1; parent_transcript=GRMZM2G057642_T02; parent_gene=GRMZM2G057642 seq=translation; coord=5:157517807..157521679:-1;	GRMZM2G057642_P02,GRMZM2G057642_P03	TRUE	TRUE	dAFGYYGATIVSVK	95%	n+304 (+304), K+304 (+304)	54.94	25.81
5772	parent_transcript=GRMZM2G057642_T02; parent_gene=GRMZM2G057642 seq=translation; coord=3:1481217..1482997:-1;	GRMZM2G057642_P02,GRMZM2G057642_P03	TRUE	TRUE	IEDELVAAR	94%	n+304 (+304)	30.40	25.11
5773	parent_transcript=GRMZM2G087103_T02; parent_gene=GRMZM2G087103 seq=translation; coord=3:1481217..1482997:-1;	GRMZM2G087103_P02,GRMZM2G087103_P03, GRMZM2G087103_P04	TRUE	TRUE	gHGVFDTAMILDGALYELDAHLDR	95%	n+304 (+304)	85.25	25.00
5774	parent_transcript=GRMZM2G087103_T02; parent_gene=GRMZM2G087103 seq=translation; coord=1:74628405..74631787:1;	GRMZM2G087103_P02,GRMZM2G087103_P03, GRMZM2G087103_P04	TRUE	TRUE	IMPALSDLLWEDMk	95%	n+304 (+304), K+304 (+304)	52.72	25.97
5775	parent_transcript=GRMZM2G130121_T01; parent_gene=GRMZM2G130121 seq=translation; coord=1:74628405..74631787:1;	GRMZM2G130121_P01	TRUE	TRUE	aHSDVFNFLQLDDGR	95%	n+304 (+304)	57.29	25.42
5776	parent_transcript=GRMZM2G130121_T01; parent_gene=GRMZM2G130121	GRMZM2G130121_P01	TRUE	TRUE	fQQVFVDQPSVEDTISILR	95%	n+304 (+304)	45.19	25.44
5777	seq=translation; coord=9:150085751..150089143:1; parent_transcript=GRMZM2G100120_T01; parent_gene=GRMZM2G100120	GRMZM2G100120_P01,GRMZM2G100120_P02, GRMZM2G100120_P03,GRMZM2G100120_P04, GRMZM2G100120_P06,GRMZM2G100120_P07	TRUE	TRUE	gGQSQVIVLPR	95%	n+304 (+304)	38.43	26.73
5778	seq=translation; coord=9:150085751..150089143:1; parent_transcript=GRMZM2G100120_T01; parent_gene=GRMZM2G100120	GRMZM2G100120_P01,GRMZM2G100120_P02, GRMZM2G100120_P03,GRMZM2G100120_P04, GRMZM2G100120_P06,GRMZM2G100120_P07	TRUE	TRUE	vLIVLSHYLETAR	94%	n+304 (+304)	27.58	25.00
5779	seq=translation; coord=8:157386210..157395665:-1; parent_transcript=GRMZM2G133926_T01; parent_gene=GRMZM2G133926 seq=translation; coord=8:157386210..157395665:-1;	GRMZM2G133926_P01	TRUE	TRUE	aLLYMDGGQIDGNVVK	95%	n+304 (+304), K+304 (+304)	56.03	25.66
5780	parent_transcript=GRMZM2G133926_T01; parent_gene=GRMZM2G133926 seq=translation; coord=3:39476674..39479631:1;	GRMZM2G133926_P01	TRUE	TRUE	gYGYIEfk	93%	n+304 (+304), K+304 (+304)	27.67	25.83
5781	parent_transcript=GRMZM2G132465_T01; parent_gene=GRMZM2G132465 seq=translation; coord=3:39476674..39479631:1;	GRMZM2G132465_P01,GRMZM2G132465_P02, GRMZM2G132465_P03,GRMZM2G132465_P04, GRMZM2G132465_P05	TRUE	TRUE	aAGLSEVLAPVEATMEK	92%	n+304 (+304), K+304 (+304)	26.97	25.81
5782	parent_transcript=GRMZM2G132465_T01; parent_gene=GRMZM2G132465 seq=translation; coord=3:39476674..39479631:1;	GRMZM2G132465_P01,GRMZM2G132465_P02, GRMZM2G132465_P03,GRMZM2G132465_P04, GRMZM2G132465_P05	TRUE	TRUE	dAAIAHGDLVTTIR	95%	n+304 (+304)	47.51	26.40
5783	parent_transcript=GRMZM2G132465_T01; parent_gene=GRMZM2G132465 seq=translation; coord=4:53185415..53193846:1;	GRMZM2G132465_P01,GRMZM2G132465_P02, GRMZM2G132465_P03,GRMZM2G132465_P04, GRMZM2G132465_P05	TRUE	TRUE	dQLVELLR	87%	n+304 (+304)	25.36	25.29
5784	parent_transcript=GRMZM2G090241_T01; parent_gene=GRMZM2G090241 seq=translation; coord=3:182713971..182717776:-1;	GRMZM2G090241_P01	TRUE	TRUE	IYDMIDVLR	93%	n+304 (+304)	30.06	25.00
5785	parent_transcript=GRMZM2G504401_T01; parent_gene=GRMZM2G504401 seq=translation; coord=3:182713971..182717776:-1;	GRMZM2G504401_P01	TRUE	TRUE	aVEATPESFASFGQVIGASPDGDEFPGHDAQLDLRSR	95%	n+304 (+304)	45.61	25.00
5786	parent_transcript=GRMZM2G504401_T01; parent_gene=GRMZM2G504401 seq=translation; coord=7:165748301..165751201:-1;	GRMZM2G504401_P01	TRUE	TRUE	gTWHAGPLfk	94%	n+304 (+304), K+304 (+304)	28.57	25.00
5787	parent_transcript=GRMZM2G053999_T01; parent_gene=GRMZM2G053999	GRMZM2G053999_P01	TRUE	TRUE	aLEEAFNSLEGITcNk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	57.19	25.00

5788	seq=translation; coord=7:165748301..165751201:-1; parent_transcript=GRMZM2G053999_T01; parent_gene=GRMZM2G053999 seq=translation; coord=7:165748301..165751201:-1;	GRMZM2G053999_P01	TRUE	TRUE	aLVVINPGNPTGQVLVEENQk	95%	n+304 (+304), K+304 (+304)	31.80	25.00
5789	parent_transcript=GRMZM2G053999_T01; parent_gene=GRMZM2G053999 seq=translation; coord=1:273298297..273299437:-1;	GRMZM2G053999_P01	TRUE	TRUE	ILEATGIVVPGSGFGQVPGTWHFR	95%	n+304 (+304)	75.44	25.66
5790	parent_transcript=GRMZM2G481194_T01; parent_gene=GRMZM2G481194 seq=translation; coord=1:273298297..273299437:-1;	GRMZM2G481194_P01	TRUE	TRUE	aAVGVAPLR	88%	n+304 (+304)	26.07	25.00
5791	parent_transcript=GRMZM2G481194_T01; parent_gene=GRMZM2G481194 seq=translation; coord=1:273298297..273299437:-1;	GRMZM2G481194_P01	TRUE	TRUE	aRPAEVVALWVAEGR	95%	n+304 (+304)	53.60	26.50
5792	parent_transcript=GRMZM2G481194_T01; parent_gene=GRMZM2G481194 seq=translation; coord=4:162677644..162687691:1;	GRMZM2G481194_P01	TRUE	TRUE	qcGTYTQVWVR	95%	n+304 (+304), Carbamidomethyl (+57)	51.10	25.00
5793	parent_transcript=GRMZM2G020775_T01; parent_gene=GRMZM2G020775 seq=translation; coord=4:162677644..162687691:1;	GRMZM2G020775_P01	TRUE	TRUE	gLTHFDVDNFVEEVLVk	95%	n+304 (+304), K+304 (+304)	41.85	25.81
5794	parent_transcript=GRMZM2G020775_T01; parent_gene=GRMZM2G020775 seq=translation; coord=1:269035042..269037767:1;	GRMZM2G020775_P01	TRUE	TRUE	hIGQGEVVDHLWR	95%	n+304 (+304)	48.91	25.73
5795	parent_transcript=GRMZM2G047055_T01; parent_gene=GRMZM2G047055 seq=translation; coord=1:269035042..269037767:1;	GRMZM2G047055_P01,GRMZM2G047055_P02, GRMZM2G047055_P03,GRMZM2G152328_P01, GRMZM2G152328_P02	TRUE	TRUE	dLTDYLMk	95%	n+304 (+304), K+304 (+304)	42.19	25.20
5796	parent_transcript=GRMZM2G047055_T01; parent_gene=GRMZM2G047055 seq=translation; coord=3:186233588..186237469:1;	GRMZM2G047055_P01,GRMZM2G047055_P02, GRMZM2G152328_P01,GRMZM2G152328_P02	TRUE	TRUE	IAYIALDYDQEMETAK	95%	n+304 (+304), K+304 (+304)	57.64	25.00
5797	parent_transcript=GRMZM2G133213_T01; parent_gene=GRMZM2G133213 seq=translation; coord=3:186233588..186237469:1;	GRMZM2G133213_P01	TRUE	TRUE	aFGMLAGSGSITPMFQVAR	95%	n+304 (+304)	32.79	25.16
5798	parent_transcript=GRMZM2G133213_T01; parent_gene=GRMZM2G133213 seq=translation; coord=4:197674970..197676500:1;	GRMZM2G133213_P01	TRUE	TRUE	eMIQShcPAPAEDIQILR	95%	n+304 (+304), Carbamidomethyl (+57)	35.80	25.00
5799	parent_transcript=GRMZM2G301908_T01; parent_gene=GRMZM2G301908 seq=translation; coord=4:197674970..197676500:1;	GRMZM2G301908_P01	TRUE	TRUE	aFASLLDk	95%	n+304 (+304), K+304 (+304)	34.06	26.37
5800	parent_transcript=GRMZM2G301908_T01; parent_gene=GRMZM2G301908 seq=translation; coord=9:4832748..4841265:1;	GRMZM2G301908_P01	TRUE	TRUE	aSLLLHFAVPVYYTLR	95%	n+304 (+304)	36.40	25.00
5801	parent_transcript=GRMZM2G124288_T01; parent_gene=GRMZM2G124288 seq=translation; coord=9:4832748..4841265:1;	GRMZM2G124288_P01,GRMZM2G124288_P02	TRUE	TRUE	IFLYDFDLk	95%	n+304 (+304), K+304 (+304)	30.71	26.86
5802	parent_transcript=GRMZM2G124288_T01; parent_gene=GRMZM2G124288 seq=translation; coord=9:4832748..4841265:1;	GRMZM2G124288_P01,GRMZM2G124288_P02	TRUE	TRUE	IPLLPIEEVR	95%	n+304 (+304)	36.33	25.69
5803	parent_transcript=GRMZM2G124288_T01; parent_gene=GRMZM2G124288 seq=translation; coord=7:52251311..52252353:1;	GRMZM2G124288_P01,GRMZM2G124288_P02	TRUE	TRUE	sTTFVEASPVVQTQk	95%	n+304 (+304), K+304 (+304)	33.86	25.84
5804	parent_transcript=GRMZM2G027198_T01; parent_gene=GRMZM2G027198 seq=translation; coord=7:52251311..52252353:1;	GRMZM2G027198_P01	TRUE	TRUE	fHPGDQTVFk	95%	n+304 (+304), K+304 (+304)	32.51	25.97
5805	parent_transcript=GRMZM2G027198_T01; parent_gene=GRMZM2G027198	GRMZM2G027198_P01	TRUE	TRUE	tNYGTWVSSk	88%	n+304 (+304), K+304 (+304)	26.99	25.99

5806	seq=translation; coord=7:52251311..52252353:1; parent_transcript=GRMZM2G027198_T01; parent_gene=GRMZM2G027198	GRMZM2G027198_P01	TRUE	TRUE	yFicGFPGHcDAGMk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	35.47	25.00
5807	seq=translation; coord=3:2218397..2221027:-1; parent_transcript=GRMZM2G159388_T01; parent_gene=GRMZM2G159388 seq=translation; coord=1:235703411..235705133:-1;	GRMZM2G159388_P01	TRUE	TRUE	qPSFSDAATAAAEak	95%	n+304 (+304), K+304 (+304)	31.09	25.47
5808	parent_transcript=GRMZM2G118433_T01; parent_gene=GRMZM2G118433 seq=translation; coord=4:195793438..195797209:-1;	GRMZM2G118433_P01	TRUE	TRUE	IMEIVSAIASR	89%	n+304 (+304)	26.95	25.00
5809	parent_transcript=GRMZM2G163709_T01; parent_gene=GRMZM2G163709 seq=translation; coord=4:195793438..195797209:-1;	GRMZM2G163709_P01,GRMZM2G163709_P02, GRMZM2G163709_P03,GRMZM2G163709_P04	TRUE	TRUE	gLMLDTYDFDNDVWLcHSFQgk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	44.00	25.00
5810	parent_transcript=GRMZM2G163709_T01; parent_gene=GRMZM2G163709 seq=translation; coord=4:195793438..195797209:-1;	GRMZM2G163709_P01,GRMZM2G163709_P02, GRMZM2G163709_P03,GRMZM2G163709_P04	TRUE	TRUE	ILVFTSk	94%	n+304 (+304), K+304 (+304)	27.34	25.00
5811	parent_transcript=GRMZM2G000481_T01; parent_gene=GRMZM2G000481	GRMZM2G000481_P01,GRMZM2G134756_P01, GRMZM2G134756_P02	TRUE	TRUE	iWIADWFAQLNNk	95%	n+304 (+304), K+304 (+304)	36.11	25.21
5812	seq=translation; coord=6:128560617..128567071:1; parent_transcript=GRMZM2G027723_T01; parent_gene=GRMZM2G027723	GRMZM2G027723_P01,GRMZM2G112336_P01, GRMZM2G112336_P02	TRUE	TRUE	eGNQccPQck	92%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	25.72	25.00
5813	seq=translation; coord=6:128560617..128567071:1; parent_transcript=GRMZM2G027723_T01; parent_gene=GRMZM2G027723 seq=translation; coord=6:128560617..128567071:1;	GRMZM2G027723_P01,GRMZM2G112336_P01, GRMZM2G112336_P02	TRUE	TRUE	gPEWQLQGDDADLSSSAR	95%	n+304 (+304)	87.81	25.00
5814	parent_transcript=GRMZM2G027723_T01; parent_gene=GRMZM2G027723 seq=translation; coord=1:240997699..241001751:-1;	GRMZM2G027723_P01,GRMZM2G112336_P01, GRMZM2G112336_P02	TRUE	TRUE	vHGDDEEDVDLNEFNyk	95%	n+304 (+304), K+304 (+304)	51.81	25.00
5815	parent_transcript=GRMZM2G071268_T01; parent_gene=GRMZM2G071268 seq=translation; coord=7:14459963..14466085:-1;	GRMZM2G071268_P01	TRUE	TRUE	ILQEFvk	91%	n+304 (+304), K+304 (+304)	25.99	25.00
5816	parent_transcript=GRMZM2G104325_T01; parent_gene=GRMZM2G104325 seq=translation; coord=7:14459963..14466085:-1;	GRMZM2G104325_P01	TRUE	TRUE	eSPGGPWQFIGLLPLFPPR	95%	n+304 (+304)	31.53	25.94
5817	parent_transcript=GRMZM2G104325_T01; parent_gene=GRMZM2G104325 seq=translation; coord=7:14459963..14466085:-1;	GRMZM2G104325_P01	TRUE	TRUE	ILEGDPLk	87%	n+304 (+304), K+304 (+304)	26.42	25.83
5818	parent_transcript=GRMZM2G104325_T01; parent_gene=GRMZM2G104325 seq=translation; coord=7:158136732..158153170:1;	GRMZM2G104325_P01	TRUE	TRUE	tALTYLDGEGR	95%	n+304 (+304)	40.55	25.00
5819	parent_transcript=GRMZM2G107654_T01; parent_gene=GRMZM2G107654 seq=translation; coord=7:158136732..158153170:1;	GRMZM2G107654_P01	TRUE	TRUE	gEILMLNIGSMSTGAR	95%	n+304 (+304)	52.81	25.56
5820	parent_transcript=GRMZM2G107654_T01; parent_gene=GRMZM2G107654 seq=translation; coord=7:158136732..158153170:1;	GRMZM2G107654_P01	TRUE	TRUE	iDLIQESAAMNQHEAIQk	95%	n+304 (+304), K+304 (+304)	39.81	25.49
5821	parent_transcript=GRMZM2G107654_T01; parent_gene=GRMZM2G107654 seq=translation; coord=7:158136732..158153170:1;	GRMZM2G107654_P01	TRUE	TRUE	IHPLSPEVISR	92%	n+304 (+304)	26.24	25.19
5822	parent_transcript=GRMZM2G107654_T01; parent_gene=GRMZM2G107654	GRMZM2G107654_P01	TRUE	TRUE	IQLTAPVcTSR	88%	n+304 (+304), Carbamidomethyl (+57)	26.47	25.40

5823	seq=translation; coord=8:157237785..157240528:-1; parent_transcript=GRMZM2G446960_T01; parent_gene=GRMZM2G446960 seq=translation; coord=5:31131578..31135872:-1;	GRMZM2G446960_P01	TRUE	TRUE	sFLNLPSEVVPNTLk	95%	n+304 (+304), K+304 (+304)	52.59	25.00
5824	parent_transcript=GRMZM2G110201_T01; parent_gene=GRMZM2G110201 seq=translation; coord=5:31131578..31135872:-1;	GRMZM2G110201_P01	TRUE	TRUE	aGLYDIGIAAGLESMTVNk	95%	n+304 (+304), K+304 (+304)	40.93	26.14
5825	parent_transcript=GRMZM2G110201_T01; parent_gene=GRMZM2G110201 seq=translation; coord=5:31131578..31135872:-1;	GRMZM2G110201_P01	TRUE	TRUE	dTFAEDLLVPVfk	95%	n+304 (+304), K+304 (+304)	45.43	25.38
5826	parent_transcript=GRMZM2G110201_T01; parent_gene=GRMZM2G110201 seq=translation; coord=5:31131578..31135872:-1;	GRMZM2G110201_P01	TRUE	TRUE	IDPSEVGDIVVGTVLAPGSQR	95%	n+304 (+304)	37.92	25.29
5827	parent_transcript=GRMZM2G110201_T01; parent_gene=GRMZM2G110201 seq=translation; coord=6:2438893..2441433:1;	GRMZM2G110201_P01	TRUE	TRUE	rPAFADDVVIVAAYR	93%	n+304 (+304)	28.25	25.73
5828	parent_transcript=GRMZM2G024303_T01; parent_gene=GRMZM2G024303 seq=translation; coord=6:2438893..2441433:1;	GRMZM2G024303_P01	TRUE	TRUE	aFGASQVIAVDVLDEk	95%	n+304 (+304), K+304 (+304)	55.67	25.69
5829	parent_transcript=GRMZM2G024303_T01; parent_gene=GRMZM2G024303 seq=translation; coord=9:148077545..148089511:-1;	GRMZM2G024303_P01	TRUE	TRUE	gVDVAIEALGk	95%	n+304 (+304), K+304 (+304)	33.83	26.63
5830	parent_transcript=GRMZM2G030915_T01; parent_gene=GRMZM2G030915 seq=translation; coord=6:4593924..4606490:1;	GRMZM2G030915_P01,GRMZM2G030915_P02, GRMZM2G030915_P03,GRMZM2G030915_P04, GRMZM2G030915_P08	TRUE	TRUE	IERPVEGDEAVQEVAABE	95%	n+304 (+304)	43.97	25.00
5831	parent_transcript=GRMZM2G032315_T01; parent_gene=GRMZM2G032315 seq=translation; coord=6:97088034..97088919:1;	GRMZM2G032315_P01,GRMZM2G032315_P02, GRMZM2G157443_P01,GRMZM2G157443_P02, GRMZM2G157443_P05	TRUE	TRUE	vESYWPALFak	95%	n+304 (+304), K+304 (+304)	48.50	26.17
5832	parent_transcript=GRMZM2G045371_T01; parent_gene=GRMZM2G045371 seq=translation; coord=9:12571363..12580129:1;	GRMZM2G045371_P01,GRMZM2G045371_P02, GRMZM2G092975_P01,GRMZM2G117544_P01, GRMZM2G117544_P02	TRUE	TRUE	IYIGLSGLATDAQTLYQR	95%	n+304 (+304)	80.69	26.57
5833	parent_transcript=GRMZM2G128056_T01; parent_gene=GRMZM2G128056 seq=translation; coord=4:71986473..72026506:-1;	GRMZM2G128056_P01,GRMZM2G128056_P02	TRUE	TRUE	tATDSLAFLLk	95%	n+304 (+304), K+304 (+304)	35.12	25.22
5834	parent_transcript=GRMZM2G448456_T01; parent_gene=GRMZM2G448456 seq=translation; coord=1:227059090..227060674:-1;	GRMZM2G448456_P01	TRUE	TRUE	iVVLPTLAIVk	95%	n+304 (+304), K+304 (+304)	34.93	25.00
5835	parent_transcript=GRMZM5G864178_T01; parent_gene=GRMZM5G864178 seq=translation; coord=10:23388783..23392102:-1;	GRMZM5G864178_P01	TRUE	TRUE	IILPLVEAFESIk	90%	n+304 (+304), K+304 (+304)	25.55	25.00
5836	parent_transcript=GRMZM5G868647_T01; parent_gene=GRMZM5G868647 seq=translation; coord=5:209568609..209572480:-1;	GRMZM5G868647_P01	TRUE	TRUE	eAPPADFLLGGFGk	95%	n+304 (+304), K+304 (+304)	48.44	26.00
5837	parent_transcript=GRMZM2G012178_T01; parent_gene=GRMZM2G012178 seq=translation; coord=5:162834761..162837541:1;	GRMZM2G012178_P01	TRUE	TRUE	fAEIGVAEVLVNALR	95%	n+304 (+304)	29.00	25.00
5838	parent_transcript=GRMZM2G084279_T01; parent_gene=GRMZM2G084279 seq=translation; coord=5:98993016..98997371:-1;	GRMZM2G084279_P01,GRMZM2G084279_P02	TRUE	TRUE	gYVQDAFFR	95%	n+304 (+304)	44.09	25.00
5839	parent_transcript=GRMZM5G844562_T01; parent_gene=GRMZM5G844562 seq=translation; coord=5:98993016..98997371:-1;	GRMZM5G844562_P01,GRMZM5G844562_P03	TRUE	TRUE	gGILGLGGVGHMGVk	95%	n+304 (+304), K+304 (+304)	28.46	25.00
5840	parent_transcript=GRMZM5G844562_T01; parent_gene=GRMZM5G844562	GRMZM5G844562_P01,GRMZM5G844562_P03	TRUE	TRUE	hFGLTPGLR	95%	n+304 (+304)	42.18	26.25

5841	seq=translation; coord=5:98993016..98997371:-1; parent_transcript=GRMZM5G844562_T01; parent_gene=GRMZM5G844562	GRMZM5G844562_P01,GRMZM5G844562_P03	TRUE	TRUE	mGYVNEALER	92%	n+304 (+304)	28.89	25.00
5842	seq=translation; coord=5:98993016..98997371:-1; parent_transcript=GRMZM5G844562_T01; parent_gene=GRMZM5G844562	GRMZM5G844562_P01,GRMZM5G844562_P03	TRUE	TRUE	yPMVPGHEVVGEVVEVGPEVAK	95%	n+304 (+304), K+304 (+304)	35.80	25.00
5843	seq=translation; coord=2:23469563..23473424:1; parent_transcript=GRMZM2G177923_T01; parent_gene=GRMZM2G177923	GRMZM2G177923_P01	TRUE	TRUE	aLFNLFVQLR	92%	n+304 (+304)	27.91	25.95
5844	seq=translation; coord=2:23469563..23473424:1; parent_transcript=GRMZM2G177923_T01; parent_gene=GRMZM2G177923	GRMZM2G177923_P01	TRUE	TRUE	aLVSLTLDEK	95%	n+304 (+304), K+304 (+304)	45.78	25.00
5845	seq=translation; coord=2:23469563..23473424:1; parent_transcript=GRMZM2G177923_T01; parent_gene=GRMZM2G177923	GRMZM2G177923_P01	TRUE	TRUE	eLAAEAVR	95%	n+304 (+304)	33.13	26.55
5846	seq=translation; coord=2:23469563..23473424:1; parent_transcript=GRMZM2G177923_T01; parent_gene=GRMZM2G177923	GRMZM2G177923_P01	TRUE	TRUE	gQETSGEDPAVAAAYSLEYVvk	95%	n+304 (+304), K+304 (+304)	28.84	25.00
5847	seq=translation; coord=10:123811073..123815007:1; parent_transcript=GRMZM2G064159_T01; parent_gene=GRMZM2G064159	GRMZM2G064159_P01	TRUE	TRUE	aFPDHEVVMVEGGR	95%	n+304 (+304)	38.82	25.00
5848	seq=translation; coord=10:123811073..123815007:1; parent_transcript=GRMZM2G064159_T01; parent_gene=GRMZM2G064159	GRMZM2G064159_P01	TRUE	TRUE	eNAGPAQEVFAR	95%	n+304 (+304)	50.99	25.00
5849	seq=translation; coord=10:123811073..123815007:1; parent_transcript=GRMZM2G064159_T01; parent_gene=GRMZM2G064159	GRMZM2G064159_P01	TRUE	TRUE	iVEIER	90%	n+304 (+304)	27.42	25.00
5850	seq=translation; coord=3:168695539..168839001:1; parent_transcript=GRMZM2G156861_T03; parent_gene=GRMZM2G156861	GRMZM2G156861_P03	TRUE	TRUE	eILAGVNPMVLvk	95%	n+304 (+304), K+304 (+304)	34.45	25.00
5851	seq=translation; coord=3:168695539..168839001:1; parent_transcript=GRMZM2G156861_T03; parent_gene=GRMZM2G156861	GRMZM2G156861_P03	TRUE	TRUE	gDGLTPVVAIELSLPELR	95%	n+304 (+304)	35.21	25.45
5852	seq=translation; coord=3:168695539..168839001:1; parent_transcript=GRMZM2G156861_T03; parent_gene=GRMZM2G156861	GRMZM2G156861_P03	TRUE	TRUE	IYILDHHDNFMFPFLVR	95%	n+304 (+304)	33.36	25.05
5853	seq=translation; coord=6:143138266..143147623:1; parent_transcript=GRMZM2G305851_T01; parent_gene=GRMZM2G305851	GRMZM2G305851_P01	TRUE	TRUE	eALFVLAQLGR	95%	n+304 (+304)	33.36	25.51
5854	seq=translation; coord=6:143138266..143147623:1; parent_transcript=GRMZM2G305851_T01; parent_gene=GRMZM2G305851	GRMZM2G305851_P01	TRUE	TRUE	IFAVGTSASLIGTGVTNALIK	95%	n+304 (+304), K+304 (+304)	53.28	25.00
5855	seq=translation; coord=6:143138266..143147623:1; parent_transcript=GRMZM2G305851_T01; parent_gene=GRMZM2G305851	GRMZM2G305851_P01	TRUE	TRUE	ILADDLFLTK	95%	n+304 (+304), K+304 (+304)	38.01	25.00
5856	seq=translation; coord=4:18573473..18575395:-1; parent_transcript=GRMZM2G440208_T01; parent_gene=GRMZM2G440208	GRMZM2G440208_P01	TRUE	TRUE	gWNLNLAEALAR	95%	n+304 (+304)	35.19	26.10
5857	seq=translation; coord=4:18573473..18575395:-1; parent_transcript=GRMZM2G440208_T01; parent_gene=GRMZM2G440208	GRMZM2G440208_P01	TRUE	TRUE	iGLAGLATMGQNLAIAEk	95%	n+304 (+304), K+304 (+304)	67.92	25.00
5858	seq=translation; coord=4:18573473..18575395:-1; parent_transcript=GRMZM2G440208_T01; parent_gene=GRMZM2G440208	GRMZM2G440208_P01	TRUE	TRUE	wTVQQAELAVAAPTIAASLDGR	95%	n+304 (+304)	38.15	25.38

5859	seq=translation; coord=7:143292623..143296263:1; parent_transcript=GRMZM2G109405_T01; parent_gene=GRMZM2G109405	GRMZM2G109405_P01,GRMZM2G109405_P02, GRMZM2G109405_P03	TRUE	TRUE	aAFVGHHDHINDFcGk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.41	25.00
5860	seq=translation; coord=7:143292623..143296263:1; parent_transcript=GRMZM2G109405_T01; parent_gene=GRMZM2G109405	GRMZM2G109405_P01,GRMZM2G109405_P02, GRMZM2G109405_P03	TRUE	TRUE	IPWAAVIGNHDQEGTISR	95%	n+304 (+304)	62.38	25.68
5861	seq=translation; coord=7:143292623..143296263:1; parent_transcript=GRMZM2G109405_T01; parent_gene=GRMZM2G109405	GRMZM2G109405_P01,GRMZM2G109405_P02, GRMZM2G109405_P03	TRUE	TRUE	sMDAAIAPADMk	95%	n+304 (+304), K+304 (+304)	30.89	25.00
5862	seq=translation; coord=9:89703050..89707450:1; parent_transcript=GRMZM2G442551_T01; parent_gene=GRMZM2G442551	GRMZM2G442551_P01,GRMZM2G442551_P02	TRUE	TRUE	dLIAGQEIER	86%	n+304 (+304)	25.37	25.00
5863	seq=translation; coord=9:89703050..89707450:1; parent_transcript=GRMZM2G442551_T01; parent_gene=GRMZM2G442551	GRMZM2G442551_P01,GRMZM2G442551_P02	TRUE	TRUE	fFPDTQALVLGALS	95%	n+304 (+304), K+304 (+304)	46.61	25.00
5864	seq=translation; coord=9:89703050..89707450:1; parent_transcript=GRMZM2G442551_T01; parent_gene=GRMZM2G442551	GRMZM2G442551_P01,GRMZM2G442551_P02	TRUE	TRUE	iEGPAAWDVLNFEQR	95%	n+304 (+304)	53.37	25.00
5865	seq=translation; coord=8:173066444..173072416:1; parent_transcript=GRMZM2G424857_T01; parent_gene=GRMZM2G424857	GRMZM2G424857_P01	TRUE	TRUE	fPGLTHPGIVGTAPSAELNIWNER	95%	n+304 (+304)	32.13	25.21
5866	seq=translation; coord=8:173066444..173072416:1; parent_transcript=GRMZM2G424857_T01; parent_gene=GRMZM2G424857	GRMZM2G424857_P01	TRUE	TRUE	IVVPIDV	91%	n+304 (+304), K+304 (+304)	25.45	25.00
5867	seq=translation; coord=8:173066444..173072416:1; parent_transcript=GRMZM2G424857_T01; parent_gene=GRMZM2G424857	GRMZM2G424857_P01	TRUE	TRUE	wHPDIPPVADVTEGELFR	95%	n+304 (+304)	57.66	25.00
5868	seq=translation; coord=5:123202556..123206585:1; parent_transcript=GRMZM2G009479_T01; parent_gene=GRMZM2G009479	GRMZM2G009479_P01	TRUE	TRUE	aLDDAGDFFGk	95%	n+304 (+304), K+304 (+304)	30.65	25.00
5869	seq=translation; coord=7:126805106..126806657:1; parent_transcript=GRMZM5G826321_T01; parent_gene=GRMZM5G826321	GRMZM5G826321_P01	TRUE	TRUE	dVVVDSAGVYVR	95%	n+304 (+304)	34.17	25.00
5870	seq=translation; coord=7:126805106..126806657:1; parent_transcript=GRMZM5G826321_T01; parent_gene=GRMZM5G826321	GRMZM5G826321_P01	TRUE	TRUE	iNPLAAAAAPSLR	94%	n+304 (+304)	31.28	25.26
5871	seq=translation; coord=7:131436732..131438757:1; parent_transcript=GRMZM2G018108_T01; parent_gene=GRMZM2G018108	GRMZM2G018108_P01	TRUE	TRUE	gVPLQVGWGk	95%	n+304 (+304), K+304 (+304)	44.20	25.00
5872	seq=translation; coord=7:131436732..131438757:1; parent_transcript=GRMZM2G018108_T01; parent_gene=GRMZM2G018108	GRMZM2G018108_P01	TRUE	TRUE	tLAVIYDVNDQk	95%	n+304 (+304), K+304 (+304)	31.69	25.98
5873	seq=translation; coord=5:201664982..201667877:1; parent_transcript=GRMZM2G170602_T01; parent_gene=GRMZM2G170602	GRMZM2G170602_P01	TRUE	TRUE	nPSFVGcAEHALGIR	95%	n+304 (+304), Carbamidomethyl (+57)	85.59	25.00
5874	seq=translation; coord=5:201664982..201667877:1; parent_transcript=GRMZM2G170602_T01; parent_gene=GRMZM2G170602	GRMZM2G170602_P01	TRUE	TRUE	qAVGGGWDAVAHR	95%	Pyro-cmC (-17), n+304 (+304)	75.65	25.00
5875	seq=translation; coord=5:3285681..3289943:1; parent_transcript=GRMZM2G017532_T01; parent_gene=GRMZM2G017532	GRMZM2G017532_P01	TRUE	TRUE	aAVFALHVk	94%	n+304 (+304), K+304 (+304)	27.44	25.55
5876	seq=translation; coord=5:3285681..3289943:1; parent_transcript=GRMZM2G017532_T01; parent_gene=GRMZM2G017532	GRMZM2G017532_P01	TRUE	TRUE	eELNSWPEQSTR	95%	n+304 (+304)	32.87	25.00

5877	seq=translation; coord=4:180245812..180247211:1; parent_transcript=GRMZM2G448883_T01; parent_gene=GRMZM2G448883 seq=translation; coord=4:180245812..180247211:1;	GRMZM2G448883_P01	TRUE	TRUE	aINLVLTAAADVAVDGFcASR	95%	n+304 (+304), Carbamidomethyl (+57)	45.03	25.91
5878	parent_transcript=GRMZM2G448883_T01; parent_gene=GRMZM2G448883 seq=translation; coord=4:238055009..238057832:-1;	GRMZM2G448883_P01	TRUE	TRUE	aVITDFVSSLSAAPR	95%	n+304 (+304)	73.50	25.47
5879	parent_transcript=AC233922.1_FGT005; parent_gene=AC233922.1_FG005 seq=translation; coord=4:238055009..238057832:-1;	AC233922.1_FGP005	TRUE	TRUE	mkDVIGIVPGLAVILVGSR	95%	n+304 (+304), K+304 (+304)	51.98	25.00
5880	parent_transcript=AC233922.1_FGT005; parent_gene=AC233922.1_FG005 seq=translation; coord=8:17966967..17971201:-1;	AC233922.1_FGP005	TRUE	TRUE	vAGAITPVPGGVGPMTIAMLLSNTLESAR	95%	n+304 (+304)	28.83	25.00
5881	parent_transcript=GRMZM2G175171_T01; parent_gene=GRMZM2G175171 seq=translation; coord=8:17966967..17971201:-1;	GRMZM2G175171_P01	TRUE	TRUE	aTTIADIPR	95%	n+304 (+304)	33.44	26.32
5882	parent_transcript=GRMZM2G175171_T01; parent_gene=GRMZM2G175171 seq=translation; coord=1:228560968..228564785:1;	GRMZM2G175171_P01	TRUE	TRUE	INWLLHFGEPPk	95%	n+304 (+304), K+304 (+304)	36.17	25.00
5883	parent_transcript=GRMZM5G888696_P02; parent_gene=GRMZM5G888696 seq=translation; coord=1:228560968..228564785:1;	GRMZM5G888696_P02	TRUE	TRUE	aFVQQAQEVILADGk	95%	n+304 (+304), K+304 (+304)	44.61	25.38
5884	parent_transcript=GRMZM5G888696_P02; parent_gene=GRMZM5G888696 seq=translation; coord=6:161451718..161452634:-1;	GRMZM5G888696_P02	TRUE	TRUE	IENSLVQAIALLR	95%	n+304 (+304)	64.95	25.00
5885	parent_transcript=GRMZM2G090245_T01; parent_gene=GRMZM2G090245 seq=translation; coord=6:161451718..161452634:-1;	GRMZM2G090245_P01	TRUE	TRUE	dVTADDFHYGGLATPGTALKPFk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	29.00	25.00
5886	parent_transcript=GRMZM2G090245_T01; parent_gene=GRMZM2G090245 seq=translation; coord=2:43428306..43433991:1;	GRMZM2G090245_P01	TRUE	TRUE	vTNLDELQIVk	95%	n+304 (+304), K+304 (+304)	48.93	25.07
5887	parent_transcript=GRMZM2G031028_T02; parent_gene=GRMZM2G031028 seq=translation; coord=2:43428306..43433991:1;	GRMZM2G031028_P02	TRUE	TRUE	gDGSSIFVLFk	94%	n+304 (+304), K+304 (+304)	29.02	25.63
5888	parent_transcript=GRMZM2G031028_T02; parent_gene=GRMZM2G031028 seq=translation; coord=8:152747393..152749464:1;	GRMZM2G031028_P02	TRUE	TRUE	vLELITQLETR	95%	n+304 (+304)	31.79	25.00
5889	parent_transcript=GRMZM2G010987_T01; parent_gene=GRMZM2G010987 seq=translation; coord=9:24694136..24698929:-1;	GRMZM2G010987_P01	TRUE	TRUE	eGGESEATLTGLVDEWk	95%	n+304 (+304), K+304 (+304)	28.90	25.00
5890	parent_transcript=GRMZM2G048557_T01; parent_gene=GRMZM2G048557	GRMZM2G048557_P01,GRMZM2G048557_P02	TRUE	TRUE	tAQNPLEEFEVER	95%	n+304 (+304)	42.97	25.00
5891	seq=translation; coord=4:9697965..9698851:1; parent_transcript=GRMZM2G117942_T01; parent_gene=GRMZM2G117942	GRMZM2G117942_P01,GRMZM2G117971_P01	TRUE	TRUE	yGWTAfCGPAGPTGQAACgQcLLVTNTATGASITVR	95%	n+304 (+304), iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	39.59	25.00
5892	seq=translation; coord=4:26293451..26297824:1; parent_transcript=GRMZM2G004997_T02; parent_gene=GRMZM2G004997 seq=translation; coord=6:155589495..155593823:-1;	GRMZM2G004997_P02	TRUE	TRUE	dQILSGTENVTGNAR	95%	n+304 (+304)	68.76	25.00
5893	parent_transcript=GRMZM2G116258_T01; parent_gene=GRMZM2G116258	GRMZM2G116258_P01	TRUE	TRUE	qDGALLVFDEVMTGFR	95%	n+304 (+304)	54.66	25.00

5894	seq=translation; coord=4:195759880..195760460:-1; parent_transcript=GRMZM2G406552_T01; parent_gene=GRMZM2G406552	GRMZM2G406552_P01	TRUE	TRUE	tFTScGIAIPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	44.54	25.97
5895	seq=translation; coord=1:32051838..32054795:1; parent_transcript=GRMZM2G152477_T01; parent_gene=GRMZM2G152477	GRMZM2G152477_P01,GRMZM2G152477_P02, GRMZM2G152477_P03	TRUE	TRUE	gDALAQLSPVLR	95%	n+304 (+304)	53.25	26.16
5896	GRMZM2G057885_P01-R	GRMZM2G057885_P01-R	TRUE	TRUE	qTLEILk	92%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	28.82	25.00
5897	seq=translation; coord=5:2362323..2364777:-1; parent_transcript=GRMZM2G002825_T01; parent_gene=GRMZM2G002825	GRMZM2G002825_P01	TRUE	TRUE	aTSYEDFTNSLPENDcR	95%	n+304 (+304), Carbamidomethyl (+57)	37.51	25.00
5898	seq=translation; coord=10:116057034..116058081:-1; parent_transcript=GRMZM2G052100_T01; parent_gene=GRMZM2G052100	GRMZM2G052100_P01	TRUE	TRUE	hMEQLGQLGAIAAGAYALHEK	95%	n+304 (+304), K+304 (+304)	66.03	25.00
5899	seq=translation; coord=10:142505503..142509165:-1; parent_transcript=GRMZM2G054537_T01; parent_gene=GRMZM2G054537	GRMZM2G054537_P01	TRUE	TRUE	gLPGVLWVLPDSYLDVPNk	95%	n+304 (+304), K+304 (+304)	34.73	25.00
5900	seq=translation; coord=1:92464668..92465816:1; parent_transcript=GRMZM2G094639_T01; parent_gene=GRMZM2G094639	GRMZM2G094639_P01	TRUE	TRUE	IGVcANVLDLlk	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.07	25.43
5901	seq=translation; coord=1:288165266..288170829:-1; parent_transcript=GRMZM2G015436_T01; parent_gene=GRMZM2G015436	GRMZM2G015436_P01,GRMZM2G015436_P02, GRMZM2G015436_P03,GRMZM2G046191_P01	TRUE	TRUE	glIAQASEGFLYLVSavgVTGAR	95%	n+304 (+304)	62.31	26.12
5902	seq=translation; coord=6:75632814..75634590:1; parent_transcript=GRMZM5G873767_T01; parent_gene=GRMZM5G873767	GRMZM5G873767_P01	TRUE	TRUE	IVVDFLAQELGLPLPPSk	95%	n+304 (+304), K+304 (+304)	32.40	25.00
5903	seq=translation; coord=3:206531676..206533642:1; parent_transcript=GRMZM2G050570_T01; parent_gene=GRMZM2G050570	GRMZM2G050570_P01	TRUE	TRUE	aDFGSVMdVLQk	95%	n+304 (+304), K+304 (+304)	34.08	26.21
5904	seq=translation; coord=3:206531676..206533642:1; parent_transcript=GRMZM2G050570_T01; parent_gene=GRMZM2G050570	GRMZM2G050570_P01	TRUE	TRUE	ySLDEVVYR	95%	n+304 (+304)	33.20	25.00
5905	seq=translation; coord=6:115289930..115298874:1; parent_transcript=GRMZM2G157462_T01; parent_gene=GRMZM2G157462	GRMZM2G157462_P01	TRUE	TRUE	aFVPPQHfIR	95%	n+304 (+304)	32.00	27.20
5906	seq=translation; coord=6:115289930..115298874:1; parent_transcript=GRMZM2G157462_T01; parent_gene=GRMZM2G157462	GRMZM2G157462_P01	TRUE	TRUE	eVVAIASNALETfk	95%	n+304 (+304), K+304 (+304)	37.84	26.16
5907	seq=translation; coord=6:115289930..115298874:1; parent_transcript=GRMZM2G157462_T01; parent_gene=GRMZM2G157462	GRMZM2G157462_P01	TRUE	TRUE	vPNLLSGLQGk	95%	n+304 (+304), K+304 (+304)	42.60	25.00
5908	seq=translation; coord=6:127249169..127252532:1; parent_transcript=GRMZM2G018020_T01; parent_gene=GRMZM2G018020	GRMZM2G018020_P01	TRUE	TRUE	gQAWVVVFEDVASATEALK	95%	n+304 (+304), K+304 (+304)	47.46	26.14
5909	seq=translation; coord=6:127249169..127252532:1; parent_transcript=GRMZM2G018020_T01; parent_gene=GRMZM2G018020	GRMZM2G018020_P01	TRUE	TRUE	iLDVLAFk	90%	n+304 (+304), K+304 (+304)	25.42	25.00
5910	seq=translation; coord=6:126779719..126784379:1; parent_transcript=GRMZM2G159369_T01; parent_gene=GRMZM2G159369	GRMZM2G159369_P01	TRUE	TRUE	gHLNQEAGLVPSLNPLVk	92%	n+304 (+304), K+304 (+304)	26.77	25.00
5911	seq=translation; coord=6:126779719..126784379:1; parent_transcript=GRMZM2G159369_T01; parent_gene=GRMZM2G159369	GRMZM2G159369_P01	TRUE	TRUE	IASVFk	92%	n+304 (+304), K+304 (+304)	25.59	25.00

5912	seq=translation; coord=6:126779719..126784379:1; parent_transcript=GRMZM2G159369_T01; parent_gene=GRMZM2G159369 seq=translation; coord=1:218981641..218987465:-1;	GRMZM2G159369_P01	TRUE	TRUE	sVEALAEFVNSEAGTNV	95%	n+304 (+304), K+304 (+304)	42.66	25.35
5913	parent_transcript=GRMZM5G895175_T01; parent_gene=GRMZM5G895175 seq=translation; coord=1:218981641..218987465:-1;	GRMZM5G895175_P01	TRUE	TRUE	iSNMIEEWLk	95%	n+304 (+304), K+304 (+304)	36.79	25.80
5914	parent_transcript=GRMZM5G895175_T01; parent_gene=GRMZM5G895175	GRMZM5G895175_P01	TRUE	TRUE	IGFGLIGLGk	95%	n+304 (+304), K+304 (+304)	34.28	25.00
5915	seq=translation; coord=6:164260122..164263444:1; parent_transcript=GRMZM2G007122_T02; parent_gene=GRMZM2G007122	GRMZM2G007122_P02,GRMZM2G015287_P01, GRMZM2G115828_P01,GRMZM2G115828_P02, GRMZM2G115828_P03,GRMZM5G862131_P01, GRMZM5G862131_P02	TRUE	TRUE	IELFLPEEYPMAPk	95%	n+304 (+304), K+304 (+304)	41.79	26.54
5916	seq=translation; coord=6:164260122..164263444:1; parent_transcript=GRMZM2G007122_T02; parent_gene=GRMZM2G007122	GRMZM2G007122_P02,GRMZM2G015287_P01, GRMZM2G115828_P01,GRMZM2G115828_P02, GRMZM2G115828_P03,GRMZM5G862131_P01, GRMZM5G862131_P02	TRUE	TRUE	ILSEPAPGISASPEENMR	95%	n+304 (+304)	89.15	25.00
5917	seq=translation; coord=7:10365682..10368158:1; parent_transcript=GRMZM2G018074_T01; parent_gene=GRMZM2G018074 seq=translation; coord=7:10365682..10368158:1;	GRMZM2G018074_P01	TRUE	TRUE	sALEAVVADEELTALQAEQAR	95%	n+304 (+304)	73.17	25.82
5918	parent_transcript=GRMZM2G018074_T01; parent_gene=GRMZM2G018074 seq=translation; coord=9:12323292..12327304:-1;	GRMZM2G018074_P01	TRUE	TRUE	vPGSSAADGTVDNVR	95%	n+304 (+304)	71.72	25.00
5919	parent_transcript=GRMZM2G151923_T01; parent_gene=GRMZM2G151923 seq=translation; coord=9:12323292..12327304:-1;	GRMZM2G151923_P01,GRMZM2G151923_P02, GRMZM2G151923_P03,GRMZM2G151923_P04, GRMZM2G151923_P05	TRUE	TRUE	eLEDEFr	92%	n+304 (+304)	29.23	25.00
5920	parent_transcript=GRMZM2G151923_T01; parent_gene=GRMZM2G151923 seq=translation; coord=3:218727007..218745183:1;	GRMZM2G151923_P01,GRMZM2G151923_P02, GRMZM2G151923_P03,GRMZM2G151923_P04, GRMZM2G151923_P05	TRUE	TRUE	IYIGNLDPR	95%	n+304 (+304)	32.42	25.31
5921	parent_transcript=GRMZM2G047093_T01; parent_gene=GRMZM2G047093 seq=translation; coord=6:164682301..164684550:1;	GRMZM2G047093_P01	TRUE	TRUE	aNILEQLFLk	93%	n+304 (+304), K+304 (+304)	27.75	25.00
5922	parent_transcript=GRMZM2G022619_T01; parent_gene=GRMZM2G022619 seq=translation; coord=6:164682301..164684550:1;	GRMZM2G022619_P01,GRMZM2G113720_P01	TRUE	TRUE	aLPTPTDEHPk	95%	n+304 (+304), K+304 (+304)	32.38	26.33
5923	parent_transcript=GRMZM2G022619_T01; parent_gene=GRMZM2G022619 seq=translation; coord=8:171187220..171190525:-1;	GRMZM2G022619_P01,GRMZM2G113720_P01	TRUE	TRUE	sPcIQIik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.91	26.13
5924	parent_transcript=GRMZM2G028346_T01; parent_gene=GRMZM2G028346 seq=translation; coord=8:171187220..171190525:-1;	GRMZM2G028346_P01,GRMZM2G130398_P01, GRMZM2G130398_P02,GRMZM2G130398_P03	TRUE	TRUE	aAAQAAL EEMDAD	95%	n+304 (+304)	34.20	25.00
5925	parent_transcript=GRMZM2G028346_T01; parent_gene=GRMZM2G028346 seq=translation; coord=9:7578400..7585814:1;	GRMZM2G028346_P01,GRMZM2G130398_P01, GRMZM2G130398_P02,GRMZM2G130398_P03	TRUE	TRUE	dGIVLVGEk	95%	n+304 (+304), K+304 (+304)	45.14	25.00
5926	parent_transcript=GRMZM2G120302_T01; parent_gene=GRMZM2G120302 seq=translation; coord=9:7578400..7585814:1;	GRMZM2G120302_P01	TRUE	TRUE	gLpVALVEYEGEQHGFR	95%	n+304 (+304)	56.85	25.12
5927	parent_transcript=GRMZM2G120302_T01; parent_gene=GRMZM2G120302 seq=translation; coord=9:7578400..7585814:1;	GRMZM2G120302_P01	TRUE	TRUE	sPITADVVSgADR	95%	n+304 (+304)	35.86	25.60
5928	parent_transcript=GRMZM2G120302_T01; parent_gene=GRMZM2G120302	GRMZM2G120302_P01	TRUE	TRUE	tLAQEYGGGAFaVDk	95%	n+304 (+304), K+304 (+304)	35.10	25.91

5929	seq=translation; coord=UNKNOWN:5634502..5650723:1; parent_transcript=GRMZM2G011070_T01; parent_gene=GRMZM2G011070 seq=translation; coord=UNKNOWN:5634502..5650723:1;	GRMZM2G011070_P01	TRUE	TRUE	IAHEFWR	95%	n+304 (+304)	29.31	25.00
5930	parent_transcript=GRMZM2G011070_T01; parent_gene=GRMZM2G011070 seq=translation; coord=8:156372419..156374495:-1;	GRMZM2G011070_P01	TRUE	TRUE	vFHSEWIPR	95%	n+304 (+304)	33.43	25.28
5931	parent_transcript=GRMZM2G073622_T01; parent_gene=GRMZM2G073622 seq=translation; coord=8:156372419..156374495:-1;	GRMZM2G073622_P01,GRMZM2G073622_P02, GRMZM2G073622_P03	TRUE	TRUE	aAESSAEWTVk	95%	n+304 (+304), K+304 (+304)	58.84	26.20
5932	parent_transcript=GRMZM2G073622_T01; parent_gene=GRMZM2G073622 seq=translation; coord=4:175739965..175751055:-1;	GRMZM2G073622_P01,GRMZM2G073622_P02, GRMZM2G073622_P03	TRUE	TRUE	iAEcLVGDEGTGIIVFTAR	94%	n+304 (+304), Carbamidomethyl (+57)	28.21	26.18
5933	parent_transcript=GRMZM2G181362_T01; parent_gene=GRMZM2G181362 seq=translation; coord=4:175739965..175751055:-1;	GRMZM2G181362_P01,GRMZM2G181362_P02	TRUE	TRUE	aGLIDFLHGLGQR	95%	n+304 (+304)	49.16	26.27
5934	parent_transcript=GRMZM2G181362_T01; parent_gene=GRMZM2G181362 seq=translation; coord=5:169232491..169237426:1;	GRMZM2G181362_P01,GRMZM2G181362_P02	TRUE	TRUE	eLPFALEHLPNR	95%	n+304 (+304)	34.99	25.56
5935	parent_transcript=GRMZM2G073950_T01; parent_gene=GRMZM2G073950 seq=translation; coord=5:169232491..169237426:1;	GRMZM2G073950_P01	TRUE	TRUE	iVLVQELFEGHYFcQAQR	95%	n+304 (+304), Carbamidomethyl (+57)	44.06	25.00
5936	parent_transcript=GRMZM2G073950_T01; parent_gene=GRMZM2G073950 seq=translation; coord=5:39817839..39821668:1;	GRMZM2G073950_P01	TRUE	TRUE	vLLTLDGEk	95%	n+304 (+304), K+304 (+304)	33.90	25.54
5937	parent_transcript=GRMZM2G048549_T01; parent_gene=GRMZM2G048549 seq=translation; coord=2:173380725..173391388:-1;	GRMZM2G048549_P01	TRUE	TRUE	vLSDILLGMAAGLk	95%	n+304 (+304), K+304 (+304)	35.85	25.00
5938	parent_transcript=GRMZM2G106213_T01; parent_gene=GRMZM2G106213 seq=translation; coord=2:173380725..173391388:-1;	GRMZM2G106213_P01,GRMZM2G106213_P02	TRUE	TRUE	eLPYIASMGIYVFSk	95%	n+304 (+304), K+304 (+304)	48.78	25.56
5939	parent_transcript=GRMZM2G106213_T01; parent_gene=GRMZM2G106213 seq=translation; coord=2:173380725..173391388:-1;	GRMZM2G106213_P01,GRMZM2G106213_P02	TRUE	TRUE	eTDADITVAALPMDEQR	95%	n+304 (+304)	79.98	25.00
5940	parent_transcript=GRMZM2G106213_T01; parent_gene=GRMZM2G106213 seq=translation; coord=2:173380725..173391388:-1;	GRMZM2G106213_P01,GRMZM2G106213_P02	TRUE	TRUE	iINFDNVQEAVR	95%	n+304 (+304)	39.37	25.30
5941	parent_transcript=GRMZM2G106213_T01; parent_gene=GRMZM2G106213 seq=translation; coord=8:173029283..173035156:1;	GRMZM2G106213_P01,GRMZM2G106213_P02	TRUE	TRUE	sMMVDTTILGLDPER	91%	n+304 (+304)	28.21	25.00
5942	parent_transcript=GRMZM2G124047_T01; parent_gene=GRMZM2G124047 seq=translation; coord=6:148703816..148706201:1;	GRMZM2G124047_P01,GRMZM2G124047_P02	TRUE	TRUE	fAALVFAEHR	95%	n+304 (+304)	53.59	25.89
5943	parent_transcript=AC235543.1_FGT003; parent_gene=AC235543.1_FG003 seq=translation; coord=6:148703816..148706201:1;	AC235543.1_FGP003	TRUE	TRUE	IVLDGGGGVDVGGEDYVETR	95%	n+304 (+304)	47.52	25.00
5944	parent_transcript=AC235543.1_FGT003; parent_gene=AC235543.1_FG003 seq=translation; coord=4:223661025..223669104:-1;	AC235543.1_FGP003	TRUE	TRUE	sDPSVDTFAEPAADVAGDHDLPELR	95%	n+304 (+304)	82.42	25.00
5945	parent_transcript=GRMZM2G068489_T01; parent_gene=GRMZM2G068489 seq=translation; coord=4:223661025..223669104:-1;	GRMZM2G068489_P01,GRMZM2G109315_P01, GRMZM2G109315_P02	TRUE	TRUE	vLVLAGDLHIPHR	95%	n+304 (+304)	36.34	25.00
5946	parent_transcript=GRMZM2G068489_T01; parent_gene=GRMZM2G068489	GRMZM2G068489_P01,GRMZM2G109315_P01, GRMZM2G109315_P02	TRUE	TRUE	vVVVYVELIDGEVk	95%	n+304 (+304), K+304 (+304)	48.07	25.04

5947	seq=translation; coord=4:214239084..214241779:1; parent_transcript=GRMZM2G126190_T01; parent_gene=GRMZM2G126190	GRMZM2G126190_P01,GRMZM2G126190_P02, GRMZM2G126190_P03	TRUE	TRUE	IAYVALDYQELENAK	95%	n+304 (+304), K+304 (+304)	64.62	25.40
5948	seq=translation; coord=2:25300018..25310642:1; parent_transcript=GRMZM5G827171_T01; parent_gene=GRMZM5G827171	GRMZM5G827171_P01,GRMZM5G827171_P02, GRMZM5G827171_P03	TRUE	TRUE	aSLVDIAESFk	95%	n+304 (+304), K+304 (+304)	32.22	25.37
5949	seq=translation; coord=2:25300018..25310642:1; parent_transcript=GRMZM5G827171_T01; parent_gene=GRMZM5G827171	GRMZM5G827171_P01,GRMZM5G827171_P02, GRMZM5G827171_P03	TRUE	TRUE	fYAALDEINFFk	95%	n+304 (+304), K+304 (+304)	53.76	26.32
5950	seq=translation; coord=7:33992878..33998025:-1; parent_transcript=GRMZM2G051771_T01; parent_gene=GRMZM2G051771	GRMZM2G051771_P01,GRMZM2G051771_P02	TRUE	TRUE	qFFPHLAVGFEDPR	95%	n+304 (+304)	35.56	25.00
5951	seq=translation; coord=7:33992878..33998025:-1; parent_transcript=GRMZM2G051771_T01; parent_gene=GRMZM2G051771	GRMZM2G051771_P01,GRMZM2G051771_P02	TRUE	TRUE	qFFPHLAVGFEDPR	93%	Pyro-cmC (-17), n+304 (+304)	29.78	25.00
5952	seq=translation; coord=7:33992878..33998025:-1; parent_transcript=GRMZM2G051771_T01; parent_gene=GRMZM2G051771	GRMZM2G051771_P01,GRMZM2G051771_P02	TRUE	TRUE	sDYQNVMMVFQSSTYgk	95%	n+304 (+304), K+304 (+304)	50.60	25.00
5953	seq=translation; coord=7:94510636..94515443:1; parent_transcript=GRMZM2G053781_T01; parent_gene=GRMZM2G053781	GRMZM2G053781_P01,GRMZM2G053781_P02	TRUE	TRUE	aQSAGLcSSIEELDTik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	33.12	25.48
5954	seq=translation; coord=7:94510636..94515443:1; parent_transcript=GRMZM2G053781_T01; parent_gene=GRMZM2G053781	GRMZM2G053781_P01,GRMZM2G053781_P02	TRUE	TRUE	IVDAEIGLLQEDLDAATAR	95%	n+304 (+304)	43.32	25.42
5955	seq=translation; coord=6:89682252..89693247:1; parent_transcript=GRMZM2G044398_T01; parent_gene=GRMZM2G044398	GRMZM2G044398_P01,GRMZM2G044398_P02, GRMZM2G044398_P03,GRMZM2G044398_P04, GRMZM2G044398_P05,GRMZM2G044398_P06, GRMZM2G044398_P07	TRUE	TRUE	IEAILEK	93%	n+304 (+304), K+304 (+304)	27.24	25.00
5956	seq=translation; coord=9:126770546..126773822:1; parent_transcript=GRMZM2G426229_T01; parent_gene=GRMZM2G426229	GRMZM2G426229_P01	TRUE	TRUE	eIAVVFAEENR	88%	n+304 (+304)	26.38	25.40
5957	seq=translation; coord=9:126770546..126773822:1; parent_transcript=GRMZM2G426229_T01; parent_gene=GRMZM2G426229	GRMZM2G426229_P01	TRUE	TRUE	gFGFIQYFDPEDASDAk	95%	n+304 (+304), K+304 (+304)	61.47	25.00
5958	seq=translation; coord=2:2545896..2547904:1; parent_transcript=GRMZM2G010257_T01; parent_gene=GRMZM2G010257	GRMZM2G010257_P01,GRMZM2G075630_P01, GRMZM2G102891_P01,GRMZM2G102891_P02, GRMZM2G102891_P03,GRMZM2G105712_P01, GRMZM2G105712_P02,GRMZM2G105712_P03, GRMZM2G105712_P04,GRMZM2G105712_P05, GRMZM2G105712_P06,GRMZM2G119809_P01, GRMZM2G119809_P02,GRMZM2G119809_P03, GRMZM2G119809_P04 GRMZM2G010257_P01,GRMZM2G075630_P01, GRMZM2G102891_P01,GRMZM2G102891_P02, GRMZM2G102891_P03,GRMZM2G105712_P01, GRMZM2G105712_P02,GRMZM2G105712_P03, GRMZM2G105712_P04,GRMZM2G105712_P05, GRMZM2G105712_P06,GRMZM2G119809_P01, GRMZM2G119809_P02,GRMZM2G119809_P03, GRMZM2G119809_P04	TRUE	TRUE	dITELIAAGR	91%	n+304 (+304)	29.39	26.13
5959	seq=translation; coord=2:2545896..2547904:1; parent_transcript=GRMZM2G010257_T01; parent_gene=GRMZM2G010257	GRMZM2G105712_P02,GRMZM2G105712_P03, GRMZM2G105712_P04,GRMZM2G105712_P05, GRMZM2G105712_P06,GRMZM2G119809_P01, GRMZM2G119809_P02,GRMZM2G119809_P03, GRMZM2G119809_P04	TRUE	TRUE	mELLSQLSGk	95%	n+304 (+304), K+304 (+304)	34.55	25.68
5960	seq=translation; coord=8:70525339..70528822:1; parent_transcript=GRMZM2G413652_T01; parent_gene=GRMZM2G413652	GRMZM2G413652_P01,GRMZM2G413652_P06	TRUE	TRUE	aFTVGIGGPVGTGk	95%	n+304 (+304), K+304 (+304)	52.55	25.00

5961	seq=translation; coord=8:70525339..70528822:1; parent_transcript=GRMZM2G413652_T01; parent_gene=GRMZM2G413652	GRMZM2G413652_P01,GRMZM2G413652_P06	TRUE	TRUE	eLADYIIYIIDVSGGDK	94%	n+304 (+304), K+304 (+304)	27.16	25.25
5962	seq=translation; coord=8:70525339..70528822:1; parent_transcript=GRMZM2G413652_T01; parent_gene=GRMZM2G413652	GRMZM2G413652_P01,GRMZM2G413652_P06	TRUE	TRUE	hGVGVGIVGNHILQAWIEATGNK	95%	n+304 (+304), K+304 (+304)	31.73	25.00
5963	seq=translation; coord=1:289192462..289217741:1; parent_transcript=GRMZM5G825524_T01; parent_gene=GRMZM5G825524	GRMZM5G825524_P01,GRMZM5G844195_P02, GRMZM5G844195_P03	TRUE	TRUE	aQITAIHLIIGTLQR	95%	n+304 (+304)	45.24	25.00
5964	seq=translation; coord=1:289192462..289217741:1; parent_transcript=GRMZM5G825524_T01; parent_gene=GRMZM5G825524	GRMZM5G825524_P01,GRMZM5G844195_P02, GRMZM5G844195_P03	TRUE	TRUE	iEALFDLIK	91%	n+304 (+304), K+304 (+304)	25.43	25.00
5965	seq=translation; coord=1:289192462..289217741:1; parent_transcript=GRMZM5G825524_T01; parent_gene=GRMZM5G825524	GRMZM5G825524_P01,GRMZM5G844195_P02, GRMZM5G844195_P03	TRUE	TRUE	vMAVVIIQSIMK	95%	n+304 (+304), K+304 (+304)	30.10	25.00
5966	seq=translation; coord=1:2038186..2040079:1; parent_transcript=GRMZM2G164696_T01; parent_gene=GRMZM2G164696	GRMZM2G164696_P01,GRMZM2G164696_P03	TRUE	TRUE	fWEVVcAEHGIDATGR	95%	n+304 (+304), Carbamidomethyl (+57)	81.53	25.00
5967	seq=translation; coord=1:2038186..2040079:1; parent_transcript=GRMZM2G164696_T01; parent_gene=GRMZM2G164696	GRMZM2G164696_P01,GRMZM2G164696_P03	TRUE	TRUE	yGGDSLQLER	90%	n+304 (+304)	27.17	25.00
5968	seq=translation; coord=5:56776697..56780711:-1; parent_transcript=GRMZM2G116034_T01; parent_gene=GRMZM2G116034	GRMZM2G116034_P01,GRMZM2G116034_P02	TRUE	TRUE	dQIYDIFQLLPak	89%	n+304 (+304), K+304 (+304)	25.13	25.00
5969	seq=translation; coord=6:160675824..160684398:1; parent_transcript=GRMZM2G587327_T01; parent_gene=GRMZM2G587327	GRMZM2G587327_P01	TRUE	TRUE	iDINHFFSILSDIIR	95%	n+304 (+304)	37.80	25.00
5970	seq=translation; coord=6:160675824..160684398:1; parent_transcript=GRMZM2G587327_T01; parent_gene=GRMZM2G587327	GRMZM2G587327_P01	TRUE	TRUE	rFPNALAVVADSWVFTLR	95%	n+304 (+304)	39.33	25.59
5971	seq=translation; coord=7:162717116..162718128:1; parent_transcript=GRMZM2G309970_T01; parent_gene=GRMZM2G309970	GRMZM2G309970_P01,GRMZM2G378121_P01	TRUE	TRUE	aAEALLPSLSIWPPSQR	95%	n+304 (+304)	36.47	25.60
5972	seq=translation; coord=8:166372284..166377485:1; parent_transcript=GRMZM2G047214_T01; parent_gene=GRMZM2G047214	GRMZM2G047214_P01,GRMZM2G056495_P01, GRMZM2G056495_P02	TRUE	TRUE	mTMDDLIAR	94%	n+304 (+304)	28.91	25.00
5973	seq=translation; coord=9:139381433..139385689:-1; parent_transcript=GRMZM2G166767_T01; parent_gene=GRMZM2G166767	GRMZM2G166767_P01,GRMZM2G166767_P02	TRUE	TRUE	aMVEELLK	95%	n+304 (+304), K+304 (+304)	30.15	25.00
5974	seq=translation; coord=9:139381433..139385689:-1; parent_transcript=GRMZM2G166767_T01; parent_gene=GRMZM2G166767	GRMZM2G166767_P01,GRMZM2G166767_P02	TRUE	TRUE	mPISSDLSNPR	88%	n+304 (+304)	26.01	25.00
5975	seq=translation; coord=9:139381433..139385689:-1; parent_transcript=GRMZM2G166767_T01; parent_gene=GRMZM2G166767	GRMZM2G166767_P01,GRMZM2G166767_P02	TRUE	TRUE	nILITGAAGFIASHVANR	95%	n+304 (+304)	69.92	25.75
5976	seq=translation; coord=9:139381433..139385689:-1; parent_transcript=GRMZM2G166767_T01; parent_gene=GRMZM2G166767	GRMZM2G166767_P01,GRMZM2G166767_P02	TRUE	TRUE	sYLYcEDVAEAFEVVLHK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	78.01	25.00
5977	seq=translation; coord=5:181396172..181399390:-1; parent_transcript=GRMZM2G031496_T01; parent_gene=GRMZM2G031496	GRMZM2G031496_P01,GRMZM2G097190_P01	TRUE	TRUE	gPDPDVVAIVER	95%	n+304 (+304)	43.43	25.95
5978	seq=translation; coord=5:181396172..181399390:-1; parent_transcript=GRMZM2G031496_T01; parent_gene=GRMZM2G031496	GRMZM2G031496_P01,GRMZM2G097190_P01	TRUE	TRUE	vGVPVLGVVENMSGLR	95%	n+304 (+304)	45.62	25.79

5979	seq=translation; coord=1:268558195..268564501:-1; parent_transcript=GRMZM2G000622_T01; parent_gene=GRMZM2G000622	GRMZM2G000622_P01	TRUE	TRUE	dLWEETSFQLEELQR	95%	n+304 (+304)	50.39	25.00
5980	seq=translation; coord=1:268558195..268564501:-1; parent_transcript=GRMZM2G000622_T01; parent_gene=GRMZM2G000622	GRMZM2G000622_P01	TRUE	TRUE	gDPEIGMLVVk	95%	n+304 (+304), K+304 (+304)	34.02	25.45
5981	seq=translation; coord=1:268558195..268564501:-1; parent_transcript=GRMZM2G000622_T01; parent_gene=GRMZM2G000622	GRMZM2G000622_P01	TRUE	TRUE	IAVGEALTNLVWAK	95%	n+304 (+304), K+304 (+304)	51.74	25.00
5982	seq=translation; coord=2:46534345..46537526:-1; parent_transcript=AC202073.4_FGT001; parent_gene=AC202073.4_FG001	AC202073.4_FGP001,GRMZM2G113453_P01	TRUE	TRUE	vPALASVIVEALK	95%	n+304 (+304), K+304 (+304)	40.01	25.00
5983	seq=translation; coord=1:78701399..78707799:-1; parent_transcript=GRMZM2G050984_T01; parent_gene=GRMZM2G050984	GRMZM2G050984_P01	TRUE	TRUE	gFGGPQGLLIAENWIHHIATELQR	94%	n+304 (+304)	25.42	25.00
5984	seq=translation; coord=5:123629674..123636311:1; parent_transcript=GRMZM2G063851_T01; parent_gene=GRMZM2G063851	GRMZM2G063851_P01,GRMZM2G063851_P04	TRUE	TRUE	gMTGMLWETSLLDPEEGIR	95%	n+304 (+304)	29.06	25.00
5985	seq=translation; coord=3:117076600..117087785:1; parent_transcript=GRMZM2G069758_T01; parent_gene=GRMZM2G069758	GRMZM2G069758_P01,GRMZM2G069758_P02, GRMZM2G069758_P03,GRMZM2G069758_P05	TRUE	TRUE	aAELAVSSLQALLk	95%	n+304 (+304), K+304 (+304)	28.94	25.00
5986	seq=translation; coord=2:47087776..47091009:1; parent_transcript=GRMZM2G087192_T01; parent_gene=GRMZM2G087192	GRMZM2G087192_P01	TRUE	TRUE	fALEVTQAVVDEIGADk	95%	n+304 (+304), K+304 (+304)	41.54	25.69
5987	seq=translation; coord=3:17941693..17947153:-1; parent_transcript=GRMZM2G100881_T01; parent_gene=GRMZM2G100881	GRMZM2G100881_P01,GRMZM2G100881_P02	TRUE	TRUE	IPLLIEVLsk	95%	n+304 (+304), K+304 (+304)	33.55	25.00
5988	seq=translation; coord=5:207730826..207733163:-1; parent_transcript=GRMZM2G116981_T01; parent_gene=GRMZM2G116981	GRMZM2G116981_P01	TRUE	TRUE	ILPLPELLSSIASIk	95%	n+304 (+304), K+304 (+304)	35.96	25.00
5989	seq=translation; coord=4:36408206..36412230:1; parent_transcript=GRMZM2G131473_T01; parent_gene=GRMZM2G131473	GRMZM2G131473_P01,GRMZM2G131473_P02	TRUE	TRUE	sIIkPGMLMVdLcETLENMVR	95%	n+304 (+304), K+304 (+304), Carbamidomethyl (+57)	45.09	25.00
5990	seq=translation; coord=4:229898346..229903473:1; parent_transcript=GRMZM2G139643_T01; parent_gene=GRMZM2G139643	GRMZM2G139643_P01,GRMZM2G139643_P02, GRMZM2G139643_P03,GRMZM2G139643_P04, GRMZM2G139643_P05	TRUE	TRUE	vLEDDHVIDGR	95%	n+304 (+304)	55.67	25.00
5991	seq=translation; coord=5:74286010..74289403:1; parent_transcript=GRMZM2G152929_T03; parent_gene=GRMZM2G152929	GRMZM2G152929_P03	TRUE	TRUE	gEGLYDGLDWLASTLk	95%	n+304 (+304), K+304 (+304)	35.01	25.87
5992	seq=translation; coord=4:41369510..41378299:1; parent_transcript=GRMZM2G138060_T01; parent_gene=GRMZM2G138060	GRMZM2G138060_P01	TRUE	TRUE	dLVIYEMHLR	95%	n+304 (+304)	43.16	26.35
5993	seq=translation; coord=4:41369510..41378299:1; parent_transcript=GRMZM2G138060_T01; parent_gene=GRMZM2G138060	GRMZM2G138060_P01	TRUE	TRUE	eAPYDFLTDLPLDR	95%	n+304 (+304)	44.43	25.00
5994	seq=translation; coord=4:41369510..41378299:1; parent_transcript=GRMZM2G138060_T01; parent_gene=GRMZM2G138060	GRMZM2G138060_P01	TRUE	TRUE	gIEVIMDVVFNHTAEGNEk	95%	n+304 (+304), K+304 (+304)	33.10	25.00
5995	seq=translation; coord=4:41369510..41378299:1; parent_transcript=GRMZM2G138060_T01; parent_gene=GRMZM2G138060	GRMZM2G138060_P01	TRUE	TRUE	vTEEVPLDPLLNR	95%	n+304 (+304)	33.44	25.79
5996	seq=translation; coord=9:119710257..119715669:-1; parent_transcript=GRMZM2G151387_T01; parent_gene=GRMZM2G151387	GRMZM2G151387_P01,GRMZM2G151387_P02	TRUE	TRUE	aPPLQQTQSVPR	95%	n+304 (+304)	40.81	25.90

5997	seq=translation; coord=9:119710257..119715669:-1; parent_transcript=GRMZM2G151387_T01; parent_gene=GRMZM2G151387	GRMZM2G151387_P01,GRMZM2G151387_P02	TRUE	TRUE	aVQELLGk	95%	n+304 (+304), K+304 (+304)	28.49	25.28
5998	seq=translation; coord=9:119710257..119715669:-1; parent_transcript=GRMZM2G151387_T01; parent_gene=GRMZM2G151387	GRMZM2G151387_P01,GRMZM2G151387_P02	TRUE	TRUE	eVILPDSVVEAsk	95%	n+304 (+304), K+304 (+304)	44.19	25.00
5999	seq=translation; coord=9:119710257..119715669:-1; parent_transcript=GRMZM2G151387_T01; parent_gene=GRMZM2G151387	GRMZM2G151387_P01,GRMZM2G151387_P02	TRUE	TRUE	fGATEAsk	93%	n+304 (+304), K+304 (+304)	29.48	26.42
6000	seq=translation; coord=5:74640062..74641850:-1; parent_transcript=GRMZM2G017249_T01; parent_gene=GRMZM2G017249	GRMZM2G017249_P01	TRUE	TRUE	dIDISSVVLDNR	94%	n+304 (+304)	31.69	25.59
6001	seq=translation; coord=5:74640062..74641850:-1; parent_transcript=GRMZM2G017249_T01; parent_gene=GRMZM2G017249	GRMZM2G017249_P01	TRUE	TRUE	eVQQELPVSHFLMNLILGk	94%	n+304 (+304), K+304 (+304)	26.06	25.00
6002	seq=translation; coord=5:74640062..74641850:-1; parent_transcript=GRMZM2G017249_T01; parent_gene=GRMZM2G017249	GRMZM2G017249_P01	TRUE	TRUE	IVLEPLPEDk	95%	n+304 (+304), K+304 (+304)	33.53	25.00
6003	seq=translation; coord=4:5455601..5457606:1; parent_transcript=GRMZM2G154523_T01; parent_gene=GRMZM2G154523	GRMZM2G154523_P01	TRUE	TRUE	gLIPATIIAYLEak	95%	n+304 (+304), K+304 (+304)	35.06	25.00
6004	seq=translation; coord=4:5455601..5457606:1; parent_transcript=GRMZM2G154523_T01; parent_gene=GRMZM2G154523	GRMZM2G154523_P01	TRUE	TRUE	vADTVTNVIVPAFDVk	95%	n+304 (+304), K+304 (+304)	45.99	25.00
6005	seq=translation; coord=2:3805095..3807781:-1; parent_transcript=GRMZM2G173341_T01; parent_gene=GRMZM2G173341	GRMZM2G173341_P01,GRMZM2G173341_P02, GRMZM2G173341_P03	TRUE	TRUE	aADAMVEWNNLWk	95%	n+304 (+304), K+304 (+304)	64.47	25.47
6006	seq=translation; coord=2:3805095..3807781:-1; parent_transcript=GRMZM2G173341_T01; parent_gene=GRMZM2G173341	GRMZM2G173341_P01,GRMZM2G173341_P02, GRMZM2G173341_P03	TRUE	TRUE	dVLGPAMFPGLR	95%	n+304 (+304)	42.61	26.00
6007	seq=translation; coord=2:3805095..3807781:-1; parent_transcript=GRMZM2G173341_T01; parent_gene=GRMZM2G173341	GRMZM2G173341_P01,GRMZM2G173341_P02, GRMZM2G173341_P03	TRUE	TRUE	vMDDVLPPFQSLk	95%	n+304 (+304), K+304 (+304)	48.40	25.00
6008	seq=translation; coord=3:213896741..213905427:1; parent_transcript=GRMZM2G466833_T01; parent_gene=GRMZM2G466833	GRMZM2G466833_P01	TRUE	TRUE	aNLPVTDNVNVPVGGHAGITILPLFSQATPATNALSDEdik	95%	n+304 (+304), K+304 (+304)	29.32	25.00
6009	seq=translation; coord=3:213896741..213905427:1; parent_transcript=GRMZM2G466833_T01; parent_gene=GRMZM2G466833	GRMZM2G466833_P01	TRUE	TRUE	nGVEEVLGLGELSDFEk	95%	n+304 (+304), K+304 (+304)	31.35	25.09
6010	seq=translation; coord=3:213896741..213905427:1; parent_transcript=GRMZM2G466833_T01; parent_gene=GRMZM2G466833	GRMZM2G466833_P01	TRUE	TRUE	nLSTAIak	95%	n+304 (+304), K+304 (+304)	39.26	26.33
6011	seq=translation; coord=10:19475272..19481312:1; parent_transcript=GRMZM2G181227_T01; parent_gene=GRMZM2G181227	GRMZM2G181227_P01	TRUE	TRUE	iDDPQWEDLNLPAR	95%	n+304 (+304)	61.64	25.00
6012	seq=translation; coord=10:19475272..19481312:1; parent_transcript=GRMZM2G181227_T01; parent_gene=GRMZM2G181227	GRMZM2G181227_P01	TRUE	TRUE	IEQVPDEAVEQYFLR	95%	n+304 (+304)	36.09	25.00
6013	seq=translation; coord=4:42919325..42920272:1; parent_transcript=GRMZM2G154578_T01; parent_gene=GRMZM2G154578	GRMZM2G154578_P01	TRUE	TRUE	aYAAcEDLPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.14	25.00
6014	seq=translation; coord=4:42919325..42920272:1; parent_transcript=GRMZM2G154578_T01; parent_gene=GRMZM2G154578	GRMZM2G154578_P01	TRUE	TRUE	hAFQPDNLGak	95%	n+304 (+304), K+304 (+304)	39.32	25.97

6015	seq=translation; coord=4:81250432..81251801:-1; parent_transcript=GRMZM2G004878_T01; parent_gene=GRMZM2G004878	GRMZM2G004878_P01	TRUE	TRUE	eSGELVFK	95%	n+304 (+304), K+304 (+304)	35.05	26.71
6016	seq=translation; coord=4:81250432..81251801:-1; parent_transcript=GRMZM2G004878_T01; parent_gene=GRMZM2G004878	GRMZM2G004878_P01	TRUE	TRUE	vRPVVPSETAAA	89%	n+304 (+304)	28.50	26.47
6017	seq=translation; coord=6:142082329..142086400:1; parent_transcript=AC215201.3_FGT005; parent_gene=AC215201.3_FG005	AC215201.3_FGP005	TRUE	TRUE	IAGGVAVIK	95%	n+304 (+304), K+304 (+304)	35.46	25.00
6018	seq=translation; coord=6:142082329..142086400:1; parent_transcript=AC215201.3_FGT005; parent_gene=AC215201.3_FG005	AC215201.3_FGP005	TRUE	TRUE	vGAATETELED	95%	n+304 (+304)	64.41	25.00
6019	seq=translation; coord=1:34386070..34400519:-1; parent_transcript=GRMZM2G102483_T02; parent_gene=GRMZM2G102483	GRMZM2G102483_P02,GRMZM2G102483_P03	TRUE	TRUE	aEFQEALSDILLGMAAGLK	95%	n+304 (+304), K+304 (+304)	61.36	25.38
6020	seq=translation; coord=4:237941870..237948667:1; parent_transcript=GRMZM2G139341_T01; parent_gene=GRMZM2G139341	GRMZM2G139341_P01,GRMZM2G139341_P02	TRUE	TRUE	hQLLSFMDELIPTIR	95%	n+304 (+304)	68.86	26.17
6021	seq=translation; coord=4:237941870..237948667:1; parent_transcript=GRMZM2G139341_T01; parent_gene=GRMZM2G139341	GRMZM2G139341_P01,GRMZM2G139341_P02	TRUE	TRUE	sAGLQAIDEIVPTLLR	95%	n+304 (+304)	54.59	25.45
6022	seq=translation; coord=1:285124791..285129572:-1; parent_transcript=GRMZM2G058584_T01; parent_gene=GRMZM2G058584	GRMZM2G058584_P01,GRMZM2G058584_P02	TRUE	TRUE	eAFDVAYDNiYAFHVSQk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	26.37	25.00
6023	seq=translation; coord=1:285124791..285129572:-1; parent_transcript=GRMZM2G058584_T01; parent_gene=GRMZM2G058584	GRMZM2G058584_P01,GRMZM2G058584_P02	TRUE	TRUE	iDFSSIFGTVPNPIVEDVR	95%	n+304 (+304)	49.43	25.17
6024	seq=translation; coord=6:154130608..154132782:-1; parent_transcript=GRMZM2G361064_T01; parent_gene=GRMZM2G361064	GRMZM2G361064_P01	TRUE	TRUE	aGIVPVAFR	94%	n+304 (+304)	30.92	25.00
6025	seq=translation; coord=6:154130608..154132782:-1; parent_transcript=GRMZM2G361064_T01; parent_gene=GRMZM2G361064	GRMZM2G361064_P01	TRUE	TRUE	qALSFQVTASDGR	95%	n+304 (+304)	50.50	25.00
6026	seq=translation; coord=6:39088029..39088716:1; parent_transcript=GRMZM2G012928_T01; parent_gene=GRMZM2G012928	GRMZM2G012928_P01	TRUE	TRUE	dMPNANIQVLVPVGSVLTQDFRPDR	94%	n+304 (+304)	27.09	25.00
6027	seq=translation; coord=6:39088029..39088716:1; parent_transcript=GRMZM2G012928_T01; parent_gene=GRMZM2G012928	GRMZM2G012928_P01	TRUE	TRUE	eNkTSWPEVVGMSIK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	26.62	25.00
6028	seq=translation; coord=5:205237019..205240533:-1; parent_transcript=GRMZM5G872068_T01; parent_gene=GRMZM5G872068	GRMZM5G872068_P01	TRUE	TRUE	dTNWPLGWPIGGFPGPGPYcGIGAEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.18	25.00
6029	seq=translation; coord=1:292237691..292240994:1; parent_transcript=GRMZM2G129015_T01; parent_gene=GRMZM2G129015	GRMZM2G129015_P01,GRMZM2G129015_P02, GRMZM5G899149_P01	TRUE	TRUE	nIVEQAAGR	95%	n+304 (+304)	34.09	25.85
6030	seq=translation; coord=5:7724527..7726624:-1; parent_transcript=GRMZM2G050833_T01; parent_gene=GRMZM2G050833	GRMZM2G050833_P01,GRMZM2G050833_P02, GRMZM2G056231_P01,GRMZM2G149775_P01, GRMZM2G149775_P02	TRUE	TRUE	gDEELDTLIK	95%	n+304 (+304), K+304 (+304)	34.98	26.45
6031	seq=translation; coord=1:153349374..153351332:1; parent_transcript=GRMZM2G422631_T01; parent_gene=GRMZM2G422631	GRMZM2G422631_P01	TRUE	TRUE	fLSYQDTLDDATGR	95%	n+304 (+304)	43.94	25.00
6032	seq=translation; coord=5:158865959..158869458:1; parent_transcript=GRMZM2G098298_T01; parent_gene=GRMZM2G098298	GRMZM2G098298_P01	TRUE	TRUE	hLDHGVLLVGYGASGFAPIR	95%	n+304 (+304)	42.24	26.01

6033	seq=translation; coord=6:163821880..163829466:1; parent_transcript=GRMZM2G086132_T01; parent_gene=GRMZM2G086132	GRMZM2G086132_P01	TRUE	TRUE	ITPSALLSVLQQDPDVR	95%	n+304 (+304)	70.76	25.24
6034	seq=translation; coord=1:261408681..261412620:1; parent_transcript=GRMZM2G028379_T01; parent_gene=GRMZM2G028379	GRMZM2G028379_P01,GRMZM2G028379_P02, GRMZM2G028379_P03,GRMZM2G028379_P04, GRMZM2G028379_P05	TRUE	TRUE	aVDAVLGPR	86%	n+304 (+304)	25.38	25.00
6035	seq=translation; coord=8:14287038..14292775:1; parent_transcript=GRMZM2G085254_T01; parent_gene=GRMZM2G085254	GRMZM2G085254_P01,GRMZM2G085254_P02, GRMZM2G085254_P03	TRUE	TRUE	IPLIDVLSk	95%	n+304 (+304), K+304 (+304)	31.15	25.00
6036	seq=translation; coord=9:17633649..17644407:1; parent_transcript=GRMZM2G129451_T02; parent_gene=GRMZM2G129451	GRMZM2G129451_P02	TRUE	TRUE	gIDLIQLIIPDLMR	95%	n+304 (+304)	47.80	25.00
6037	seq=translation; coord=8:171439571..171440653:1; parent_transcript=AC204359.3_FGT005; parent_gene=AC204359.3_FG005	AC204359.3_FGP005,GRMZM2G130558_P01	TRUE	TRUE	aAQADEEAGSLLQER	95%	n+304 (+304)	59.26	25.00
6038	seq=translation; coord=2:37901719..37904325:1; parent_transcript=AC208221.3_FGT002; parent_gene=AC208221.3_FG002	AC208221.3_FGP002	TRUE	TRUE	vcEFVESDPPGYR	95%	n+304 (+304), Carbamidomethyl (+57)	33.04	25.00
6039	seq=translation; coord=2:221237698..221239030:-1; parent_transcript=GRMZM2G003852_T01; parent_gene=GRMZM2G003852	GRMZM2G003852_P01	TRUE	TRUE	vLPFSLLPPR	93%	n+304 (+304)	29.75	25.25
6040	seq=translation; coord=8:1099658740..109965366:-1; parent_transcript=GRMZM2G015906_T01; parent_gene=GRMZM2G015906	GRMZM2G015906_P01	TRUE	TRUE	IVDYVPLFFTK	95%	n+304 (+304), K+304 (+304)	36.66	25.69
6041	seq=translation; coord=10:125302195..125306046:-1; parent_transcript=GRMZM2G025054_T01; parent_gene=GRMZM2G025054	GRMZM2G025054_P01,GRMZM2G025054_P02	TRUE	TRUE	sLPELLAELDGLR	95%	n+304 (+304)	60.14	25.85
6042	seq=translation; coord=10:10582274..10586991:-1; parent_transcript=GRMZM2G026231_T01; parent_gene=GRMZM2G026231	GRMZM2G026231_P01,GRMZM2G087212_P01, GRMZM2G420310_P01	TRUE	TRUE	eDDDLLESLER	95%	n+304 (+304)	38.06	25.00
6043	seq=translation; coord=4:73093695..73100832:-1; parent_transcript=GRMZM2G031846_T01; parent_gene=GRMZM2G031846	GRMZM2G031846_P01,GRMZM2G031846_P02, GRMZM2G031846_P03,GRMZM2G031846_P04, GRMZM2G031846_P05	TRUE	TRUE	gFAFVTMDTLEGAR	95%	n+304 (+304)	63.74	25.00
6044	seq=translation; coord=4:51117703..5118736:1; parent_transcript=GRMZM2G044625_T01; parent_gene=GRMZM2G044625	GRMZM2G044625_P01,GRMZM2G088365_P01, GRMZM2G088441_P02,GRMZM2G346895_P01	TRUE	TRUE	qQPIVGGAIF	95%	n+304 (+304)	48.71	26.54
6045	seq=translation; coord=6:163005849..163012986:1; parent_transcript=GRMZM2G057251_T01; parent_gene=GRMZM2G057251	GRMZM2G057251_P01	TRUE	TRUE	sDLVAALPDR	86%	n+304 (+304)	26.45	26.24
6046	seq=translation; coord=9:30943220..30948556:1; parent_transcript=GRMZM2G058407_T01; parent_gene=GRMZM2G058407	GRMZM2G058407_P01,GRMZM2G348726_P01	TRUE	TRUE	vYVDSWDEFVER	95%	n+304 (+304)	74.32	25.00
6047	seq=translation; coord=2:233356514..233358701:1; parent_transcript=GRMZM2G080222_T01; parent_gene=GRMZM2G080222	GRMZM2G080222_P01,GRMZM2G080222_P02, GRMZM2G080222_P03,GRMZM2G102075_P01, GRMZM2G111172_P01,GRMZM2G111172_P02, GRMZM2G156110_P01,GRMZM2G156110_P02	TRUE	TRUE	nMIIVPEMIGSIVGVYNGk	95%	n+304 (+304), K+304 (+304)	54.92	25.00
6048	seq=translation; coord=7:136742676..136746945:1; parent_transcript=GRMZM2G083102_T01; parent_gene=GRMZM2G083102	GRMZM2G083102_P01,GRMZM2G083102_P02	TRUE	TRUE	iAPSMSSDFANLASEAER	95%	n+304 (+304)	47.35	25.00
6049	seq=translation; coord=4:60172575..60178518:1; parent_transcript=GRMZM2G085573_T01; parent_gene=GRMZM2G085573	GRMZM2G085573_P01,GRMZM2G085573_P02, GRMZM2G146948_P01,GRMZM2G146948_P02	TRUE	TRUE	vAFDDILSILR	95%	n+304 (+304)	46.47	25.08

6050	seq=translation; coord=2:116778906..116783025:1; parent_transcript=GRMZM2G092160_T02; parent_gene=GRMZM2G092160 seq=translation; coord=2:51230856..51233601:-1;	GRMZM2G092160_P02,GRMZM2G092160_P03	TRUE	TRUE	dMAEVFAVR	93%	n+304 (+304)	29.50	25.00
6051	parent_transcript=GRMZM2G131177_T01; parent_gene=GRMZM2G131177 seq=translation; coord=9:28610042..28612570:1;	GRMZM2G131177_P01	TRUE	TRUE	gITVSPDDYDSR	95%	n+304 (+304)	63.32	25.00
6052	parent_transcript=GRMZM2G154093_T01; parent_gene=GRMZM2G154093 seq=translation; coord=4:194515220..194519164:1;	GRMZM2G154093_P01,GRMZM2G154093_P02, GRMZM2G154093_P03,GRMZM2G154093_P04	TRUE	TRUE	ILVSPGEIVVIPQGLR	95%	n+304 (+304)	31.21	25.00
6053	parent_transcript=GRMZM2G077253_T01; parent_gene=GRMZM2G077253 seq=translation; coord=6:70936697..70946158:1;	GRMZM2G077253_P01	TRUE	TRUE	dLSSVSQNQDPISVAQQFLEGFASR	95%	n+304 (+304)	75.79	25.00
6054	parent_transcript=GRMZM2G080542_T01; parent_gene=GRMZM2G080542 seq=translation; coord=2:18615584..18619086:-1;	GRMZM2G080542_P01	TRUE	TRUE	ISALAGWFDVHFR	95%	n+304 (+304)	44.42	25.00
6055	parent_transcript=GRMZM2G144153_T01; parent_gene=GRMZM2G144153 seq=translation; coord=1:256085889..256086777:1;	GRMZM2G144153_P01,GRMZM2G144153_P03	TRUE	TRUE	gGLFGDSIK	95%	n+304 (+304), K+304 (+304)	48.83	26.73
6056	parent_transcript=GRMZM2G150688_T01; parent_gene=GRMZM2G150688 seq=translation; coord=10:114869410..114870649:1;	GRMZM2G150688_P01	TRUE	TRUE	dVNEcPcYR	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	29.85	25.00
6057	parent_transcript=GRMZM2G045844_T01; parent_gene=GRMZM2G045844 seq=translation; coord=4:12818434..12823201:-1;	GRMZM2G045844_P01,GRMZM5G800014_P01	TRUE	TRUE	fTHPADcTVDV	86%	n+304 (+304), Carbamidomethyl (+57)	25.07	25.00
6058	parent_transcript=GRMZM2G139441_T01; parent_gene=GRMZM2G139441 seq=translation; coord=4:12818434..12823201:-1;	GRMZM2G139441_P01,GRMZM2G139441_P02	TRUE	TRUE	eEMIETYLTak	95%	n+304 (+304), K+304 (+304)	31.79	26.05
6059	parent_transcript=GRMZM2G139441_T01; parent_gene=GRMZM2G139441 seq=translation; coord=6:114177100..114187293:-1;	GRMZM2G139441_P01,GRMZM2G139441_P02	TRUE	TRUE	gYAPQQNYAQGGQDGR	95%	n+304 (+304)	43.45	25.00
6060	parent_transcript=GRMZM2G010960_T01; parent_gene=GRMZM2G010960 seq=translation; coord=6:114177100..114187293:-1;	GRMZM2G010960_P01	TRUE	TRUE	gSEVSTEEMLELESNAK	95%	n+304 (+304), K+304 (+304)	45.07	25.00
6061	parent_transcript=GRMZM2G010960_T01; parent_gene=GRMZM2G010960 seq=translation; coord=6:114177100..114187293:-1;	GRMZM2G010960_P01	TRUE	TRUE	INkDQSELEGLSSGR	90%	n+304 (+304), K+304 (+304)	26.57	26.19
6062	parent_transcript=GRMZM2G010960_T01; parent_gene=GRMZM2G010960 seq=translation; coord=8:48994683..48999789:-1;	GRMZM2G010960_P01	TRUE	TRUE	sLDNTTEVk	95%	n+304 (+304), K+304 (+304)	41.79	26.30
6063	parent_transcript=GRMZM2G083836_T01; parent_gene=GRMZM2G083836 seq=translation; coord=8:48994683..48999789:-1;	GRMZM2G083836_P01,GRMZM2G083836_P03	TRUE	TRUE	kDDGSIAFENDFFk	95%	K+304 (+304), n+304 (+304), K+304 (+304)	31.43	25.35
6064	parent_transcript=GRMZM2G083836_T01; parent_gene=GRMZM2G083836 seq=translation; coord=8:48994683..48999789:-1;	GRMZM2G083836_P01,GRMZM2G083836_P03	TRUE	TRUE	qEISTAVDELNR	95%	n+304 (+304)	47.12	25.00
6065	parent_transcript=GRMZM2G083836_T01; parent_gene=GRMZM2G083836 seq=translation; coord=2:176238563..176244250:1;	GRMZM2G083836_P01,GRMZM2G083836_P03	TRUE	TRUE	vGELIGGSQR	91%	n+304 (+304)	27.56	25.47
6066	parent_transcript=GRMZM2G098076_T01; parent_gene=GRMZM2G098076 seq=translation; coord=2:176238563..176244250:1;	GRMZM2G098076_P01,GRMZM2G098076_P02	TRUE	TRUE	aYELLQELR	94%	n+304 (+304)	29.42	25.00
6067	parent_transcript=GRMZM2G098076_T01; parent_gene=GRMZM2G098076	GRMZM2G098076_P01,GRMZM2G098076_P02	TRUE	TRUE	gMEVVGAEAAPAEIK	91%	n+304 (+304), K+304 (+304)	26.78	26.54

6068	seq=translation; coord=2:176238563..176244250:1; parent_transcript=GRMZM2G098076_T01; parent_gene=GRMZM2G098076 seq=translation; coord=1:234254283..234259941:1;	GRMZM2G098076_P01,GRMZM2G098076_P02	TRUE	TRUE	IVDAEIASLQEDLDAATAR	95%	n+304 (+304)	44.76	25.04
6069	parent_transcript=GRMZM2G445905_T01; parent_gene=GRMZM2G445905 seq=translation; coord=1:234254283..234259941:1;	GRMZM2G445905_P01,GRMZM2G445905_P03	TRUE	TRUE	aYTFDVEEFWGLYDHVFRPSK	95%	n+304 (+304), K+304 (+304)	30.87	25.00
6070	parent_transcript=GRMZM2G445905_T01; parent_gene=GRMZM2G445905 seq=translation; coord=3:217231435..217244458:-1;	GRMZM2G445905_P01,GRMZM2G445905_P03	TRUE	TRUE	iIYTFHDDSR	94%	n+304 (+304)	27.09	25.00
6071	parent_transcript=AC198725.4_FGT007; parent_gene=AC198725.4_FG007 seq=translation; coord=3:217231435..217244458:-1;	AC198725.4_FGP007	TRUE	TRUE	dGATAFFLVEcIVNTASAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.00	25.65
6072	parent_transcript=AC198725.4_FGT007; parent_gene=AC198725.4_FG007 seq=translation; coord=8:138088772..138094325:-1;	AC198725.4_FGP007	TRUE	TRUE	vPNLVEYLVPTLTGLK	95%	n+304 (+304), K+304 (+304)	28.65	25.00
6073	parent_transcript=GRMZM2G018901_T01; parent_gene=GRMZM2G018901 seq=translation; coord=8:138088772..138094325:-1;	GRMZM2G018901_P01,GRMZM2G018901_P02	TRUE	TRUE	gYEPVEFSFGTGWk	95%	n+304 (+304), K+304 (+304)	29.35	25.00
6074	parent_transcript=GRMZM2G018901_T01; parent_gene=GRMZM2G018901 seq=translation; coord=8:15548387..15551947:-1;	GRMZM2G018901_P01,GRMZM2G018901_P02	TRUE	TRUE	sTYVTLSQVLDLPk	95%	n+304 (+304), K+304 (+304)	32.48	25.73
6075	parent_transcript=GRMZM2G038821_T01; parent_gene=GRMZM2G038821 seq=translation; coord=8:15548387..15551947:-1;	GRMZM2G038821_P01	TRUE	TRUE	hPVPFFLSPR	95%	n+304 (+304)	34.83	25.92
6076	parent_transcript=GRMZM2G038821_T01; parent_gene=GRMZM2G038821	GRMZM2G038821_P01	TRUE	TRUE	ISNQMNLEAAVEAAAAFLnk	95%	n+304 (+304), K+304 (+304)	38.67	25.00
6077	seq=translation; coord=8:14541175..14542451:-1; parent_transcript=GRMZM2G052869_T02; parent_gene=GRMZM2G052869	GRMZM2G052869_P02,GRMZM2G052869_P03	TRUE	TRUE	cGGNcQcDPcNcGk	95%	Carbamidomethyl (+57), n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	42.45	25.00
6078	seq=translation; coord=8:14541175..14542451:-1; parent_transcript=GRMZM2G052869_T02; parent_gene=GRMZM2G052869 seq=translation; coord=2:208530771..208535295:-1;	GRMZM2G052869_P02,GRMZM2G052869_P03	TRUE	TRUE	mYPDMAEQVTTTTQALIMGVAPSk	95%	n+304 (+304), K+304 (+304)	45.35	25.09
6079	parent_transcript=GRMZM2G090274_T01; parent_gene=GRMZM2G090274 seq=translation; coord=2:208530771..208535295:-1;	GRMZM2G090274_P01,GRMZM2G090274_P02	TRUE	TRUE	mSLEWFANEYk	95%	n+304 (+304), K+304 (+304)	28.86	25.68
6080	parent_transcript=GRMZM2G090274_T01; parent_gene=GRMZM2G090274 seq=translation; coord=4:187295953..187301881:-1;	GRMZM2G090274_P01,GRMZM2G090274_P02	TRUE	TRUE	tELSQSDMFDQR	93%	n+304 (+304)	29.27	25.00
6081	parent_transcript=GRMZM2G055538_T01; parent_gene=GRMZM2G055538 seq=translation; coord=4:187295953..187301881:-1;	GRMZM2G055538_P01,GRMZM2G055538_P02, GRMZM2G055538_P03	TRUE	TRUE	dAlcQELLQAR	95%	n+304 (+304), Carbamidomethyl (+57)	30.87	25.75
6082	parent_transcript=GRMZM2G055538_T01; parent_gene=GRMZM2G055538 seq=translation; coord=9:115327106..115330655:-1;	GRMZM2G055538_P01,GRMZM2G055538_P02, GRMZM2G055538_P03	TRUE	TRUE	IADEIVSLk	95%	n+304 (+304), K+304 (+304)	31.50	25.00
6083	parent_transcript=GRMZM2G119146_T01; parent_gene=GRMZM2G119146	GRMZM2G119146_P01,GRMZM2G180909_P01	TRUE	TRUE	rWPGWPGDSVFR	95%	n+304 (+304)	31.01	25.00

6084	seq=translation; coord=8:135950853..135955026:1; parent_transcript=GRMZM2G176707_T01; parent_gene=GRMZM2G176707	GRMZM2G176707_P01	TRUE	TRUE	IEFQFGTNPFfk	95%	n+304 (+304), K+304 (+304)	40.03	26.06
6085	seq=translation; coord=10:110956920..110958900:1; parent_transcript=GRMZM2G002921_T01; parent_gene=GRMZM2G002921	GRMZM2G002921_P01,GRMZM2G032878_P01, GRMZM2G032878_P02,GRMZM2G032878_P03	TRUE	TRUE	qLALPEGTEVcGSSk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	43.67	25.00
6086	seq=translation; coord=8:132520764..132524680:1; parent_transcript=GRMZM2G474658_T03; parent_gene=GRMZM2G474658	GRMZM2G474658_P03	TRUE	TRUE	dLEHLFGR	95%	n+304 (+304)	41.95	25.07
6087	seq=translation; coord=1:250554600..250557666:-1; parent_transcript=GRMZM2G020142_T01; parent_gene=GRMZM2G020142	GRMZM2G020142_P01,GRMZM5G895064_P01	TRUE	TRUE	ILFQELMAMAIAPR	95%	n+304 (+304)	37.90	25.26
6088	seq=translation; coord=1:250554600..250557666:-1; parent_transcript=GRMZM2G020142_T01; parent_gene=GRMZM2G020142	GRMZM2G020142_P01,GRMZM5G895064_P01	TRUE	TRUE	mTIGQLIEclMGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.86	26.07
6089	seq=translation; coord=7:170807791..170818840:1; parent_transcript=GRMZM2G152963_T01; parent_gene=GRMZM2G152963	GRMZM2G152963_P01,GRMZM2G152963_P02	TRUE	TRUE	iYVDLLQLMEk	95%	n+304 (+304), K+304 (+304)	51.21	25.65
6090	seq=translation; coord=7:170807791..170818840:1; parent_transcript=GRMZM2G152963_T01; parent_gene=GRMZM2G152963	GRMZM2G152963_P01,GRMZM2G152963_P02	TRUE	TRUE	IDFQSDSPDLLAAAPSPDR	94%	n+304 (+304)	28.84	25.17
6091	seq=translation; coord=6:24318884..24321111:-1; parent_transcript=GRMZM2G119583_T01; parent_gene=GRMZM2G119583	GRMZM2G119583_P01,GRMZM2G119583_P02	TRUE	TRUE	aFFASTGTEANEAik	95%	n+304 (+304), K+304 (+304)	48.27	25.34
6092	seq=translation; coord=6:24318884..24321111:-1; parent_transcript=GRMZM2G119583_T01; parent_gene=GRMZM2G119583	GRMZM2G119583_P01,GRMZM2G119583_P02	TRUE	TRUE	IVEVSFADR	87%	n+304 (+304)	25.08	25.00
6093	seq=translation; coord=5:213944858..213947602:-1; parent_transcript=GRMZM2G469111_T01; parent_gene=GRMZM2G469111	GRMZM2G469111_P01	TRUE	TRUE	dSAENLGELLMGDR	95%	n+304 (+304)	64.96	25.00
6094	seq=translation; coord=5:213944858..213947602:-1; parent_transcript=GRMZM2G469111_T01; parent_gene=GRMZM2G469111	GRMZM2G469111_P01	TRUE	TRUE	sPPLGADAFSLlk	90%	n+304 (+304), K+304 (+304)	25.84	25.48
6095	seq=translation; coord=5:76210306..76210828:1; parent_transcript=AC192244.3_FGT001; parent_gene=AC192244.3_FG001	AC192244.3_FGP001	TRUE	TRUE	IFQVEYAMEAVk	95%	n+304 (+304), K+304 (+304)	62.55	25.11
6096	seq=translation; coord=5:76210306..76210828:1; parent_transcript=AC192244.3_FGT001; parent_gene=AC192244.3_FG001	AC192244.3_FGP001	TRUE	TRUE	nEclNHFSVYEAPLPVSR	95%	n+304 (+304), Carbamidomethyl (+57)	36.48	25.00
6097	seq=translation; coord=5:76210306..76210828:1; parent_transcript=AC192244.3_FGT001; parent_gene=AC192244.3_FG001	AC192244.3_FGP001	TRUE	TRUE	vADHAGVALAGLTADGR	95%	n+304 (+304)	55.66	25.92
6098	seq=translation; coord=6:87790147..87797085:1; parent_transcript=GRMZM2G156099_T01; parent_gene=GRMZM2G156099	GRMZM2G156099_P01,GRMZM2G156099_P02, GRMZM5G817439_P01	TRUE	TRUE	dkIDAAAAEVLEPLVR	95%	n+304 (+304), K+304 (+304)	44.14	25.34
6099	seq=translation; coord=6:87790147..87797085:1; parent_transcript=GRMZM2G156099_T01; parent_gene=GRMZM2G156099	GRMZM2G156099_P01,GRMZM2G156099_P02, GRMZM5G817439_P01	TRUE	TRUE	vQADIEQLALVR	95%	n+304 (+304)	48.61	26.45
6100	seq=translation; coord=7:159777544..159783160:1; parent_transcript=GRMZM2G061156_T01; parent_gene=GRMZM2G061156	GRMZM2G061156_P01,GRMZM2G061156_P02, GRMZM2G061156_P03	TRUE	TRUE	iALTAEDNAPLVR	95%	n+304 (+304)	41.86	25.76
6101	seq=translation; coord=6:22918021..22921799:-1; parent_transcript=GRMZM2G143788_T01; parent_gene=GRMZM2G143788	GRMZM2G143788_P01	TRUE	TRUE	eFVGGAALPR	95%	n+304 (+304)	40.78	25.49

6102	seq=translation; coord=6:22918021..22921799:-1; parent_transcript=GRMZM2G143788_T01; parent_gene=GRMZM2G143788 seq=translation; coord=1:51013925..51015964:1;	GRMZM2G143788_P01	TRUE	TRUE	IVWAHIK	95%	n+304 (+304), K+304 (+304)	32.11	25.33
6103	parent_transcript=GRMZM2G018941_T01; parent_gene=GRMZM2G018941 seq=translation; coord=1:51013925..51015964:1;	GRMZM2G018941_P01,GRMZM2G018941_P02	TRUE	TRUE	aVPEDEGYR	92%	n+304 (+304)	28.66	25.00
6104	parent_transcript=GRMZM2G018941_T01; parent_gene=GRMZM2G018941 seq=translation; coord=6:163428972..163435944:-1;	GRMZM2G018941_P01,GRMZM2G018941_P02	TRUE	TRUE	eVLVGLYER	95%	n+304 (+304)	34.19	25.00
6105	parent_transcript=GRMZM2G149717_T01; parent_gene=GRMZM2G149717 seq=translation; coord=6:163428972..163435944:-1;	GRMZM2G149717_P01,GRMZM2G314647_P01	TRUE	TRUE	fTDFAAVR	94%	n+304 (+304)	30.36	25.00
6106	parent_transcript=GRMZM2G149717_T01; parent_gene=GRMZM2G149717 seq=translation; coord=6:163428972..163435944:-1;	GRMZM2G149717_P01,GRMZM2G314647_P01	TRUE	TRUE	gTDAVDILEGR	95%	n+304 (+304)	34.75	25.00
6107	parent_transcript=GRMZM2G149717_T01; parent_gene=GRMZM2G149717	GRMZM2G149717_P01,GRMZM2G314647_P01	TRUE	TRUE	sLLDHFFTELGAR	93%	n+304 (+304)	26.22	25.00
6108	seq=translation; coord=6:161877489..161879473:-1; parent_transcript=GRMZM2G394827_T01; parent_gene=GRMZM2G394827	GRMZM2G394827_P01,GRMZM2G394827_P02, GRMZM2G394827_P03,GRMZM2G394827_P04, GRMZM2G394827_P05,GRMZM2G394827_P06, GRMZM2G394827_P07,GRMZM2G394827_P08	TRUE	TRUE	ePNNLYNIHSfk	94%	n+304 (+304), K+304 (+304)	28.58	25.98
6109	seq=translation; coord=1:107847003..107851828:-1; parent_transcript=GRMZM2G179528_T01; parent_gene=GRMZM2G179528 seq=translation; coord=4:53963570..53966108:-1;	GRMZM2G179528_P01,GRMZM2G179528_P02, GRMZM2G179528_P03	TRUE	TRUE	ISYIWADDPPEVR	95%	n+304 (+304)	42.02	25.00
6110	parent_transcript=GRMZM2G123234_T01; parent_gene=GRMZM2G123234 seq=translation; coord=4:53963570..53966108:-1;	GRMZM2G123234_P01	TRUE	TRUE	aYVGNLPWQVDDSR	95%	n+304 (+304)	57.76	25.00
6111	parent_transcript=GRMZM2G123234_T01; parent_gene=GRMZM2G123234 seq=translation; coord=2:209110460..209113041:-1;	GRMZM2G123234_P01	TRUE	TRUE	gFGFVTMSTVEEADk	91%	n+304 (+304), K+304 (+304)	25.51	25.00
6112	parent_transcript=GRMZM2G378106_T01; parent_gene=GRMZM2G378106 seq=translation; coord=2:209110460..209113041:-1;	GRMZM2G378106_P01,GRMZM2G378106_P02	TRUE	TRUE	aLHFLFVk	94%	n+304 (+304), K+304 (+304)	27.95	25.00
6113	parent_transcript=GRMZM2G378106_T01; parent_gene=GRMZM2G378106 seq=translation; coord=10:125125070..125130397:1;	GRMZM2G378106_P01,GRMZM2G378106_P02	TRUE	TRUE	vVRPGTFEELMDYAISR	95%	n+304 (+304)	31.67	25.01
6114	parent_transcript=GRMZM2G065292_T01; parent_gene=GRMZM2G065292 seq=translation; coord=10:125125070..125130397:1;	GRMZM2G065292_P01	TRUE	TRUE	IDETHDAYEALLHEAESR	95%	n+304 (+304)	41.07	25.00
6115	parent_transcript=GRMZM2G065292_T01; parent_gene=GRMZM2G065292 seq=translation; coord=7:171699375..171703593:1;	GRMZM2G065292_P01	TRUE	TRUE	ISGLEILNLSNFSDLk	95%	n+304 (+304), K+304 (+304)	41.39	25.25
6116	parent_transcript=GRMZM2G136803_T01; parent_gene=GRMZM2G136803 seq=translation; coord=6:112003443..112007827:-1;	GRMZM2G136803_P01,GRMZM2G136803_P02	TRUE	TRUE	iDHILGFFR	95%	n+304 (+304)	35.43	26.31
6117	parent_transcript=GRMZM2G073700_T01; parent_gene=GRMZM2G073700 seq=translation; coord=6:112003443..112007827:-1;	GRMZM2G073700_P01	TRUE	TRUE	vFVGGLAWETPSEGLR	95%	n+304 (+304)	67.22	25.62
6118	parent_transcript=GRMZM2G073700_T01; parent_gene=GRMZM2G073700	GRMZM2G073700_P01	TRUE	TRUE	yGDILEAVVITDR	95%	n+304 (+304)	30.24	25.00

6119	seq=translation; coord=7:162255747..162259720:1; parent_transcript=GRMZM2G167932_T01; parent_gene=GRMZM2G167932	GRMZM2G167932_P01,GRMZM2G167932_P02	TRUE	TRUE	eTGGYYAFVEFEELSGVHNALK	95%	n+304 (+304), K+304 (+304)	68.26	25.00
6120	seq=translation; coord=7:162255747..162259720:1; parent_transcript=GRMZM2G167932_T01; parent_gene=GRMZM2G167932	GRMZM2G167932_P01,GRMZM2G167932_P02	TRUE	TRUE	fIQMFFLAPQEK	95%	n+304 (+304), K+304 (+304)	40.70	25.00
6121	seq=translation; coord=7:162255747..162259720:1; parent_transcript=GRMZM2G167932_T01; parent_gene=GRMZM2G167932	GRMZM2G167932_P01,GRMZM2G167932_P02	TRUE	TRUE	sDVFEGEGASHDEESk	95%	n+304 (+304), K+304 (+304)	46.98	25.00
6122	seq=translation; coord=4:162903711..162910128:1; parent_transcript=GRMZM2G453424_T03; parent_gene=GRMZM2G453424	GRMZM2G453424_P03,GRMZM2G453424_P04, GRMZM2G453424_P05,GRMZM2G453424_P06, GRMZM2G453424_P07	TRUE	TRUE	iPESFDk	93%	n+304 (+304), K+304 (+304)	27.04	25.62
6123	seq=translation; coord=4:162903711..162910128:1; parent_transcript=GRMZM2G453424_T03; parent_gene=GRMZM2G453424	GRMZM2G453424_P03,GRMZM2G453424_P04, GRMZM2G453424_P05,GRMZM2G453424_P06, GRMZM2G453424_P07	TRUE	TRUE	mLMNcEAAELLQEIHEHMAILEDPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.07	25.00
6124	seq=translation; coord=9:152490486..152495067:-1; parent_transcript=AC149475.2_FGT003; parent_gene=AC149475.2_FG003	AC149475.2_FGP003	TRUE	TRUE	eLALEEATIALSILk	93%	n+304 (+304), K+304 (+304)	27.16	25.00
6125	seq=translation; coord=2:21007540..21010895:1; parent_transcript=AC212835.3_FGT007; parent_gene=AC212835.3_FG007	AC212835.3_FGP007	TRUE	TRUE	gLVHVAIDAVEDAVR	95%	n+304 (+304)	57.64	25.00
6126	seq=translation; coord=1:81094071..81098200:1; parent_transcript=AC212979.2_FGT006; parent_gene=AC212979.2_FG006	AC212979.2_FGP006,GRMZM2G120973_P01,G RMZM2G120973_P02,GRMZM2G120973_P03,G RMZM2G120973_P04,GRMZM5G871419_P03,G RMZM5G871419_P04,GRMZM5G871419_P05	TRUE	TRUE	iLcASELIGSVIGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.60	25.24
6127	seq=translation; coord=5:27393255..27396313:1; parent_transcript=GRMZM2G001887_T01; parent_gene=GRMZM2G001887	GRMZM2G001887_P01,GRMZM2G001887_P03	TRUE	TRUE	iGVNSIPGIEEVNIFk	95%	n+304 (+304), K+304 (+304)	40.24	25.00
6128	seq=translation; coord=4:105098023..105100902:1; parent_transcript=GRMZM2G010743_T01; parent_gene=GRMZM2G010743	GRMZM2G010743_P01,GRMZM2G473463_P01, GRMZM2G473463_P03	TRUE	TRUE	ILILDQIk	95%	n+304 (+304), K+304 (+304)	29.76	25.00
6129	seq=translation; coord=9:7186959..7210629:-1; parent_transcript=GRMZM2G017257_T01; parent_gene=GRMZM2G017257	GRMZM2G017257_P01,GRMZM2G017257_P02	TRUE	TRUE	gVFEQLPEAVSLLALAR	95%	n+304 (+304)	32.43	25.00
6130	seq=translation; coord=8:154154493..154157871:1; parent_transcript=GRMZM2G023667_T02; parent_gene=GRMZM2G023667	GRMZM2G023667_P02	TRUE	TRUE	tPLQQLMNDALIVAk	95%	n+304 (+304), K+304 (+304)	46.49	25.02
6131	seq=translation; coord=7:121981747..121986892:1; parent_transcript=GRMZM2G038636_T01; parent_gene=GRMZM2G038636	GRMZM2G038636_P01	TRUE	TRUE	dAVGLVRPVSVAFEVITGFR	95%	n+304 (+304)	32.09	25.00
6132	seq=translation; coord=8:113064531..113068162:-1; parent_transcript=GRMZM2G044775_T02; parent_gene=GRMZM2G044775	GRMZM2G044775_P02,GRMZM2G044775_P03, GRMZM2G044775_P04	TRUE	TRUE	aEVEDIFDAPLEMFLk	95%	n+304 (+304), K+304 (+304)	51.10	25.39
6133	seq=translation; coord=6:151440759..151444649:1; parent_transcript=GRMZM2G059121_T01; parent_gene=GRMZM2G059121	GRMZM2G059121_P01	TRUE	TRUE	aGLALAEASSVLPATk	95%	n+304 (+304), K+304 (+304)	32.82	25.00
6134	seq=translation; coord=9:27092199..27094638:1; parent_transcript=GRMZM2G084739_T01; parent_gene=GRMZM2G084739	GRMZM2G084739_P01	TRUE	TRUE	hLNLDQLQEAGR	95%	n+304 (+304)	60.75	25.01
6135	seq=translation; coord=1:222151651..222155503:-1; parent_transcript=GRMZM2G096303_T02; parent_gene=GRMZM2G096303	GRMZM2G096303_P02	TRUE	TRUE	iSTADEWAEFQR	94%	n+304 (+304)	31.17	25.00

6136	seq=translation; coord=1:222151651..222155503:-1; parent_transcript=GRMZM2G096303_T02; parent_gene=GRMZM2G096303	GRMZM2G096303_P02	TRUE	TRUE	IADGLIYELSDGDNYPHFyGPGR	95%	n+304 (+304), iTRAQ8plex (+304)	31.01	25.00
6137	seq=translation; coord=5:123087268..123104980:1; parent_transcript=GRMZM2G145376_T01; parent_gene=GRMZM2G145376	GRMZM2G145376_P01,GRMZM2G145376_P02	TRUE	TRUE	IIFPEGMLAQLTLAQLK	95%	n+304 (+304), K+304 (+304)	46.54	25.00
6138	seq=translation; coord=4:25788335..25797883:-1; parent_transcript=GRMZM2G147726_T02; parent_gene=GRMZM2G147726	GRMZM2G147726_P02,GRMZM2G147726_P03	TRUE	TRUE	gEGLFEGLDWLSNTLk	95%	n+304 (+304), K+304 (+304)	36.31	25.21
6139	seq=translation; coord=2:12677824..12680299:-1; parent_transcript=GRMZM2G149649_T01; parent_gene=GRMZM2G149649	GRMZM2G149649_P01	TRUE	TRUE	hSGNISLDDVIEIAk	95%	n+304 (+304), K+304 (+304)	28.28	25.01
6140	seq=translation; coord=9:45186311..45202040:1; parent_transcript=GRMZM2G151414_T01; parent_gene=GRMZM2G151414	GRMZM2G151414_P01,GRMZM2G151414_P02	TRUE	TRUE	aMSLFEGVIk	95%	n+304 (+304), K+304 (+304)	35.01	25.55
6141	seq=translation; coord=6:136515921..136519080:-1; parent_transcript=GRMZM2G154218_T01; parent_gene=GRMZM2G154218	GRMZM2G154218_P01,GRMZM2G154218_P02	TRUE	TRUE	mIPTkPMVVETFSAYPLGR	95%	n+304 (+304), K+304 (+304)	35.17	25.00
6142	seq=translation; coord=10:132962163..132965961:-1; parent_transcript=GRMZM2G155543_T01; parent_gene=GRMZM2G155543	GRMZM2G155543_P01,GRMZM2G155543_P02, GRMZM2G155543_P03	TRUE	TRUE	dLLEIEPLELR	95%	n+304 (+304)	40.32	25.80
6143	seq=translation; coord=5:214842953..214846166:1; parent_transcript=GRMZM2G168335_T01; parent_gene=GRMZM2G168335	GRMZM2G168335_P01	TRUE	TRUE	fQPVINADLTDDDRk	95%	n+304 (+304), K+304 (+304)	33.42	25.00
6144	seq=translation; coord=5:214842953..214846166:1; parent_transcript=GRMZM2G168335_T01; parent_gene=GRMZM2G168335	GRMZM2G168335_P01	TRUE	TRUE	gSVDSLQLLR	95%	n+304 (+304)	40.37	25.00
6145	seq=translation; coord=2:202916878..202922719:1; parent_transcript=GRMZM2G171707_T01; parent_gene=GRMZM2G171707	GRMZM2G171707_P01	TRUE	TRUE	dGVTATDLVTVTHILR	95%	n+304 (+304)	53.67	25.28
6146	seq=translation; coord=2:202916878..202922719:1; parent_transcript=GRMZM2G171707_T01; parent_gene=GRMZM2G171707	GRMZM2G171707_P01	TRUE	TRUE	vLLQDFTGVPAlVDLASMR	95%	n+304 (+304)	50.05	25.51
6147	seq=translation; coord=1:287334203..287336597:-1; parent_transcript=GRMZM2G178341_T01; parent_gene=GRMZM2G178341	GRMZM2G178341_P01	TRUE	TRUE	aGELTPEELER	95%	n+304 (+304)	37.70	25.00
6148	seq=translation; coord=5:892571..893531:1; parent_transcript=GRMZM2G384338_T01; parent_gene=GRMZM2G384338	GRMZM2G384338_P01	TRUE	TRUE	aLAVLGLAAESAAALR	95%	n+304 (+304)	37.34	25.00
6149	seq=translation; coord=5:182450024..182455917:1; parent_transcript=GRMZM2G095194_T01; parent_gene=GRMZM2G095194	GRMZM2G095194_P01	TRUE	TRUE	fTDIADLTSLSLTk	94%	n+304 (+304), K+304 (+304)	29.17	26.22
6150	seq=translation; coord=5:182450024..182455917:1; parent_transcript=GRMZM2G095194_T01; parent_gene=GRMZM2G095194	GRMZM2G095194_P01	TRUE	TRUE	mMPNEIQFFDPk	95%	n+304 (+304), K+304 (+304)	28.18	25.00
6151	seq=translation; coord=2:225806982..225808719:-1; parent_transcript=GRMZM2G372068_T01; parent_gene=GRMZM2G372068	GRMZM2G372068_P01	TRUE	TRUE	sLPAIAAVLAELGETAR	95%	n+304 (+304)	30.72	25.00
6152	seq=translation; coord=7:168403976..168405995:-1; parent_transcript=GRMZM2G082365_T01; parent_gene=GRMZM2G082365	GRMZM2G082365_P01,GRMZM2G172956_P02	TRUE	TRUE	gEAIAIGIAEMTTAVMATcDHGAVAK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.45	25.00
6153	seq=translation; coord=9:79713849..79717604:-1; parent_transcript=GRMZM2G059580_T02; parent_gene=GRMZM2G059580	GRMZM2G059580_P02	TRUE	TRUE	aLIAAEYSGVk	94%	n+304 (+304), K+304 (+304)	30.76	25.48

6154	seq=translation; coord=5:183319186..183326822:-1; parent_transcript=GRMZM2G014750_T01; parent_gene=GRMZM2G014750 seq=translation; coord=5:183319186..183326822:-1;	GRMZM2G014750_P01,GRMZM2G014750_P02	TRUE	TRUE	dHIVTLEPVTGEAEK	95%	n+304 (+304), K+304 (+304)	35.23	25.30
6155	parent_transcript=GRMZM2G014750_T01; parent_gene=GRMZM2G014750 seq=translation; coord=5:183319186..183326822:-1;	GRMZM2G014750_P01,GRMZM2G014750_P02	TRUE	TRUE	iMETALVFAGANLEIRPk	95%	n+304 (+304), K+304 (+304)	31.87	25.00
6156	parent_transcript=GRMZM2G014750_T01; parent_gene=GRMZM2G014750 seq=translation; coord=5:183319186..183326822:-1;	GRMZM2G014750_P01,GRMZM2G014750_P02	TRUE	TRUE	mSAVLADGGLIik	95%	n+304 (+304), K+304 (+304)	55.24	25.00
6157	parent_transcript=GRMZM2G014750_T01; parent_gene=GRMZM2G014750 seq=translation; coord=9:131582315..131589080:-1;	GRMZM2G014750_P01,GRMZM2G014750_P02	TRUE	TRUE	tIAVSPLPcNVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.87	25.73
6158	parent_transcript=GRMZM2G006178_T01; parent_gene=GRMZM2G006178 seq=translation; coord=9:131582315..131589080:-1;	GRMZM2G006178_P01,GRMZM2G109121_P01, GRMZM2G109121_P02,GRMZM2G109121_P03	TRUE	TRUE	fKNPPDWQEILTYFR	95%	n+304 (+304), K+304 (+304)	28.67	25.47
6159	parent_transcript=GRMZM2G006178_T01; parent_gene=GRMZM2G006178 seq=translation; coord=9:131582315..131589080:-1;	GRMZM2G006178_P01,GRMZM2G109121_P01, GRMZM2G109121_P02,GRMZM2G109121_P03	TRUE	TRUE	fLSHLDITFR	95%	n+304 (+304)	47.11	25.00
6160	parent_transcript=GRMZM2G006178_T01; parent_gene=GRMZM2G006178 seq=translation; coord=5:18992634..18995244:-1;	GRMZM2G006178_P01,GRMZM2G109121_P01, GRMZM2G109121_P02,GRMZM2G109121_P03	TRUE	TRUE	nVGDLSGGELQR	95%	n+304 (+304)	58.84	25.00
6161	parent_transcript=GRMZM2G045192_T01; parent_gene=GRMZM2G045192 seq=translation; coord=5:18992634..18995244:-1;	GRMZM2G045192_P01,GRMZM2G045192_P02, GRMZM2G045192_P03	TRUE	TRUE	gLGLLEYDMSGLTGMTDMSHR	95%	n+304 (+304)	85.61	25.00
6162	parent_transcript=GRMZM2G045192_T01; parent_gene=GRMZM2G045192 seq=translation; coord=5:18992634..18995244:-1;	GRMZM2G045192_P01,GRMZM2G045192_P02, GRMZM2G045192_P03	TRUE	TRUE	gVDEVQEELkk	95%	n+304 (+304), K+304 (+304), K+304 (+304)	26.83	25.00
6163	parent_transcript=GRMZM2G045192_T01; parent_gene=GRMZM2G045192 seq=translation; coord=9:30842366..30844467:1;	GRMZM2G045192_P01,GRMZM2G045192_P02, GRMZM2G045192_P03	TRUE	TRUE	qNALVGELFLNYFcEGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	72.47	25.43
6164	parent_transcript=GRMZM2G060163_T01; parent_gene=GRMZM2G060163 seq=translation; coord=9:30842366..30844467:1;	GRMZM2G060163_P01	TRUE	TRUE	eIVADAVDIER	95%	n+304 (+304)	67.02	25.69
6165	parent_transcript=GRMZM2G060163_T01; parent_gene=GRMZM2G060163 seq=translation; coord=9:30842366..30844467:1;	GRMZM2G060163_P01	TRUE	TRUE	fPQIWEFYk	95%	n+304 (+304), K+304 (+304)	28.23	25.45
6166	parent_transcript=GRMZM2G060163_T01; parent_gene=GRMZM2G060163 seq=translation; coord=6:149942002..149944565:-1;	GRMZM2G060163_P01	TRUE	TRUE	ILMALGck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.89	25.44
6167	parent_transcript=GRMZM2G161534_T01; parent_gene=GRMZM2G161534 seq=translation; coord=6:149942002..149944565:-1;	GRMZM2G161534_P01	TRUE	TRUE	aLQQLLSLGFk	95%	n+304 (+304), K+304 (+304)	45.07	25.00
6168	parent_transcript=GRMZM2G161534_T01; parent_gene=GRMZM2G161534 seq=translation; coord=6:149942002..149944565:-1;	GRMZM2G161534_P01	TRUE	TRUE	IHEEMEVLDLELGk	95%	n+304 (+304), K+304 (+304)	27.13	26.09
6169	parent_transcript=GRMZM2G161534_T01; parent_gene=GRMZM2G161534 seq=translation; coord=1:295450010..295457140:-1;	GRMZM2G161534_P01	TRUE	TRUE	wAESHDWTLEk	95%	n+304 (+304), K+304 (+304)	28.52	25.17
6170	parent_transcript=GRMZM2G458549_T01; parent_gene=GRMZM2G458549 seq=translation; coord=1:295450010..295457140:-1;	GRMZM2G458549_P01,GRMZM2G458549_P02	TRUE	TRUE	ePIVPQFILk	95%	n+304 (+304), K+304 (+304)	29.87	25.00
6171	parent_transcript=GRMZM2G458549_T01; parent_gene=GRMZM2G458549	GRMZM2G458549_P01,GRMZM2G458549_P02	TRUE	TRUE	kEVAQFTcLSER	92%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	27.02	25.50

6172	seq=translation; coord=1:295450010..295457140:-1; parent_transcript=GRMZM2G458549_T01; parent_gene=GRMZM2G458549	GRMZM2G458549_P01,GRMZM2G458549_P02	TRUE	TRUE	vNLIGEHIDYEGYSLPMAIR	95%	n+304 (+304)	46.67	25.38
6173	seq=translation; coord=2:28117445..28120590:1; parent_transcript=GRMZM2G441347_T01; parent_gene=GRMZM2G441347	GRMZM2G441347_P01	TRUE	TRUE	aAGIEGGFFk	95%	n+304 (+304), K+304 (+304)	45.64	25.63
6174	seq=translation; coord=2:28117445..28120590:1; parent_transcript=GRMZM2G441347_T01; parent_gene=GRMZM2G441347	GRMZM2G441347_P01	TRUE	TRUE	aLLTAIDR	93%	n+304 (+304)	29.99	25.00
6175	seq=translation; coord=2:28117445..28120590:1; parent_transcript=GRMZM2G441347_T01; parent_gene=GRMZM2G441347	GRMZM2G441347_P01	TRUE	TRUE	dGAALQVELLR	95%	n+304 (+304)	36.99	26.91
6176	seq=translation; coord=6:164983203..164994562:1; parent_transcript=GRMZM2G101515_T01; parent_gene=GRMZM2G101515	GRMZM2G101515_P01	TRUE	TRUE	ecGMDPDETVSR	90%	n+304 (+304), Carbamidomethyl (+57)	26.44	25.00
6177	seq=translation; coord=6:164983203..164994562:1; parent_transcript=GRMZM2G101515_T01; parent_gene=GRMZM2G101515	GRMZM2G101515_P01	TRUE	TRUE	eESAPVDQIDAR	95%	n+304 (+304)	47.56	25.00
6178	seq=translation; coord=8:173177746..173180822:1; parent_transcript=GRMZM2G074028_T01; parent_gene=GRMZM2G074028	GRMZM2G074028_P01,GRMZM2G074028_P02, GRMZM2G074028_P03,GRMZM2G074028_P05, GRMZM5G898597_P01	TRUE	TRUE	aIVPTSDPETVYDIK	94%	n+304 (+304), K+304 (+304)	29.37	26.12
6179	seq=translation; coord=8:173177746..173180822:1; parent_transcript=GRMZM2G074028_T01; parent_gene=GRMZM2G074028	GRMZM2G074028_P01,GRMZM2G074028_P02, GRMZM2G074028_P03,GRMZM2G074028_P05, GRMZM5G898597_P01	TRUE	TRUE	kPWEITGPcASPEYR	95%	K+304 (+304), n+304 (+304), Carbamidomethyl (+57)	55.85	25.54
6180	seq=translation; coord=2:22504092..22513426:-1; parent_transcript=GRMZM2G070863_T01; parent_gene=GRMZM2G070863	GRMZM2G070863_P01	TRUE	TRUE	eLEQQEYYDPR	95%	n+304 (+304)	59.43	25.00
6181	seq=translation; coord=2:22504092..22513426:-1; parent_transcript=GRMZM2G070863_T01; parent_gene=GRMZM2G070863	GRMZM2G070863_P01	TRUE	TRUE	gLALEPSNEALK	95%	n+304 (+304), K+304 (+304)	38.61	25.58
6182	seq=translation; coord=7:13851997..13853595:1; parent_transcript=GRMZM2G108076_T01; parent_gene=GRMZM2G108076	GRMZM2G108076_P01	TRUE	TRUE	aESLEDAIQINR	95%	n+304 (+304)	44.82	26.22
6183	seq=translation; coord=7:13851997..13853595:1; parent_transcript=GRMZM2G108076_T01; parent_gene=GRMZM2G108076	GRMZM2G108076_P01	TRUE	TRUE	aSFAGDLNIFYGk	95%	n+304 (+304), K+304 (+304)	34.30	25.00
6184	seq=translation; coord=3:36465309..36469955:-1; parent_transcript=GRMZM2G038606_T01; parent_gene=GRMZM2G038606	GRMZM2G038606_P01,GRMZM2G038606_P02, GRMZM2G038606_P04,GRMZM2G095114_P01	TRUE	TRUE	mLPLSLlk	95%	n+304 (+304), K+304 (+304)	35.33	25.00
6185	seq=translation; coord=3:36465309..36469955:-1; parent_transcript=GRMZM2G038606_T01; parent_gene=GRMZM2G038606	GRMZM2G038606_P01,GRMZM2G038606_P02, GRMZM2G038606_P04,GRMZM2G095114_P01	TRUE	TRUE	vPDEVIDk	95%	n+304 (+304), K+304 (+304)	34.10	25.00
6186	seq=translation; coord=3:198588979..198593726:-1; parent_transcript=GRMZM2G042818_T01; parent_gene=GRMZM2G042818	GRMZM2G042818_P01	TRUE	TRUE	IPGYLGEYLALTGAR	95%	n+304 (+304)	43.67	25.56
6187	seq=translation; coord=3:198588979..198593726:-1; parent_transcript=GRMZM2G042818_T01; parent_gene=GRMZM2G042818	GRMZM2G042818_P01	TRUE	TRUE	vVYLLAQFLEk	95%	n+304 (+304), K+304 (+304)	32.03	25.00
6188	seq=translation; coord=2:196329725..196336472:-1; parent_transcript=GRMZM2G050193_T01; parent_gene=GRMZM2G050193	GRMZM2G050193_P01,GRMZM2G050193_P02	TRUE	TRUE	IHVEVIsk	95%	n+304 (+304), K+304 (+304)	36.02	25.00
6189	seq=translation; coord=2:196329725..196336472:-1; parent_transcript=GRMZM2G050193_T01; parent_gene=GRMZM2G050193	GRMZM2G050193_P01,GRMZM2G050193_P02	TRUE	TRUE	sLEGILPEIPLWVK	92%	n+304 (+304), K+304 (+304)	26.83	25.00

6190	seq=translation; coord=4:176500156..176502218:1; parent_transcript=GRMZM2G091189_T01; parent_gene=GRMZM2G091189	GRMZM2G091189_P01	TRUE	TRUE	eDDVIGILETDDVvk	95%	n+304 (+304), K+304 (+304)	45.77	25.79
6191	seq=translation; coord=4:176500156..176502218:1; parent_transcript=GRMZM2G091189_T01; parent_gene=GRMZM2G091189	GRMZM2G091189_P01	TRUE	TRUE	tPGGLLLTETAK	95%	n+304 (+304), K+304 (+304)	36.54	25.15
6192	seq=translation; coord=1:260939345..260957939:1; parent_transcript=GRMZM2G104542_T01; parent_gene=GRMZM2G104542	GRMZM2G104542_P01	TRUE	TRUE	aMPFIIGNETFek	95%	n+304 (+304), K+304 (+304)	34.45	26.29
6193	seq=translation; coord=1:260939345..260957939:1; parent_transcript=GRMZM2G104542_T01; parent_gene=GRMZM2G104542	GRMZM2G104542_P01	TRUE	TRUE	vTPEGSPFTSVVQVLSAALK	95%	n+304 (+304), K+304 (+304)	47.88	25.00
6194	seq=translation; coord=5:216598113..216599835:1; parent_transcript=GRMZM2G145133_T01; parent_gene=GRMZM2G145133	GRMZM2G145133_P01,GRMZM2G145133_P03	TRUE	TRUE	IVHlFcVVPR	95%	n+304 (+304), Carbamidomethyl (+57)	54.87	26.16
6195	seq=translation; coord=5:216598113..216599835:1; parent_transcript=GRMZM2G145133_T01; parent_gene=GRMZM2G145133	GRMZM2G145133_P01,GRMZM2G145133_P03	TRUE	TRUE	yGEAQMQAEEGLR	95%	n+304 (+304)	34.54	25.00
6196	seq=translation; coord=3:39292213..39295100:1; parent_transcript=GRMZM2G145449_T01; parent_gene=GRMZM2G145449	GRMZM2G145449_P01	TRUE	TRUE	sFNVEEAPSDfk	93%	n+304 (+304), K+304 (+304)	27.09	25.00
6197	seq=translation; coord=3:39292213..39295100:1; parent_transcript=GRMZM2G145449_T01; parent_gene=GRMZM2G145449	GRMZM2G145449_P01	TRUE	TRUE	sWDEGVATk	95%	n+304 (+304), K+304 (+304)	32.79	25.35
6198	seq=translation; coord=9:150649384..150656114:-1; parent_transcript=GRMZM2G172523_T01; parent_gene=GRMZM2G172523	GRMZM2G172523_P01,GRMZM2G172523_P02, GRMZM2G172523_P03	TRUE	TRUE	iAPFLFMPEGk	95%	n+304 (+304), K+304 (+304)	32.86	25.44
6199	seq=translation; coord=9:150649384..150656114:-1; parent_transcript=GRMZM2G172523_T01; parent_gene=GRMZM2G172523	GRMZM2G172523_P01,GRMZM2G172523_P02, GRMZM2G172523_P03	TRUE	TRUE	iDETPVWyVMDELGSAMR	95%	n+304 (+304), iTRAQ8plex (+304)	29.15	25.00
6200	seq=translation; coord=4:185694322..185697081:1; parent_transcript=GRMZM5G840955_T01; parent_gene=GRMZM5G840955	GRMZM5G840955_P01	TRUE	TRUE	iVLLPEPWTPESGLVTAALK	93%	n+304 (+304), K+304 (+304)	27.55	25.00
6201	seq=translation; coord=4:185694322..185697081:1; parent_transcript=GRMZM5G840955_T01; parent_gene=GRMZM5G840955	GRMZM5G840955_P01	TRUE	TRUE	IVSWEEGGYk	95%	n+304 (+304), K+304 (+304)	32.82	25.79
6202	seq=translation; coord=8:157100232..157101209:-1; parent_transcript=GRMZM2G168552_T01; parent_gene=GRMZM2G168552	GRMZM2G168552_P01	TRUE	TRUE	rPAYGADDcGYGGR	95%	n+304 (+304), Carbamidomethyl (+57)	28.79	25.00
6203	seq=translation; coord=8:157100232..157101209:-1; parent_transcript=GRMZM2G168552_T01; parent_gene=GRMZM2G168552	GRMZM2G168552_P01	TRUE	TRUE	tDEYYDNVDDR	95%	n+304 (+304)	33.92	25.00
6204	seq=translation; coord=8:14793941..14796834:1; parent_transcript=GRMZM2G139600_T01; parent_gene=GRMZM2G139600	GRMZM2G139600_P01	TRUE	TRUE	gALAAGVPGELAGLHAAWSR	95%	n+304 (+304)	66.93	25.82
6205	seq=translation; coord=1:3714426..3715519:1; parent_transcript=GRMZM2G030173_T01; parent_gene=GRMZM2G030173	GRMZM2G030173_P01	TRUE	TRUE	fLPgsAVATTIR	91%	n+304 (+304)	28.61	25.22
6206	seq=translation; coord=1:3714426..3715519:1; parent_transcript=GRMZM2G030173_T01; parent_gene=GRMZM2G030173	GRMZM2G030173_P01	TRUE	TRUE	iAVDYcPEAcLHER	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	43.22	25.00
6207	seq=translation; coord=7:18222228..18224357:1; parent_transcript=GRMZM2G094928_T01; parent_gene=GRMZM2G094928	GRMZM2G094928_P01,GRMZM2G094928_P03	TRUE	TRUE	aQMEAEFQR	92%	n+304 (+304)	29.12	25.00

6208	seq=translation; coord=7:18222228..18224357:1; parent_transcript=GRMZM2G094928_T01; parent_gene=GRMZM2G094928 seq=translation; coord=3:148974556..148982804:-1;	GRMZM2G094928_P01,GRMZM2G094928_P03	TRUE	TRUE	qSGIQQLAAEQEAQIVNAAR	95%	n+304 (+304)	96.44	25.55
6209	parent_transcript=GRMZM2G367026_T01; parent_gene=GRMZM2G367026 seq=translation; coord=3:4757467..4758786:-1;	GRMZM2G367026_P01,GRMZM2G367026_P02, GRMZM2G367026_P03	TRUE	TRUE	tHVDILSDFTPDFGANLR	95%	n+304 (+304)	35.95	25.00
6210	parent_transcript=GRMZM2G055434_T01; parent_gene=GRMZM2G055434 seq=translation; coord=3:4757467..4758786:-1;	GRMZM2G055434_P01	TRUE	TRUE	aGWAPNPAPFPNAWAER	95%	n+304 (+304)	39.17	25.00
6211	parent_transcript=GRMZM2G055434_T01; parent_gene=GRMZM2G055434 seq=translation; coord=2:5924234..5926085:1;	GRMZM2G055434_P01	TRUE	TRUE	IVVVVLAVR	89%	n+304 (+304)	26.15	25.00
6212	parent_transcript=GRMZM2G372074_T01; parent_gene=GRMZM2G372074	GRMZM2G372074_P01	TRUE	TRUE	IGAcVDILGNEVHIGDANvk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304) n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	47.15	25.45
6213	seq=translation; coord=3:155457171..155458057:1; parent_transcript=GRMZM2G158407_T01; parent_gene=GRMZM2G158407	GRMZM2G158407_P01	TRUE	TRUE	dcAGSciQQNLGTSGYck	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	66.29	25.00
6214	seq=translation; coord=1:88998110..89000472:-1; parent_transcript=GRMZM2G089121_T02; parent_gene=GRMZM2G089121	GRMZM2G089121_P02	TRUE	TRUE	vIPFLFELQSk	95%	n+304 (+304), K+304 (+304)	50.71	25.00
6215	seq=translation; coord=3:132847200..132850927:-1; parent_transcript=GRMZM2G155096_T01; parent_gene=GRMZM2G155096	GRMZM2G155096_P01,GRMZM2G155096_P02, GRMZM2G155096_P03,GRMZM2G155096_P04, GRMZM2G155096_P05,GRMZM2G155096_P06, GRMZM2G155096_P07,GRMZM2G155096_P08	TRUE	TRUE	sALNNEIEQLR	95%	n+304 (+304)	45.74	26.11
6216	seq=translation; coord=10:47749003..47752985:1; parent_transcript=GRMZM2G146951_T01; parent_gene=GRMZM2G146951 seq=translation; coord=3:199293031..199294186:1;	GRMZM2G146951_P01	TRUE	TRUE	vNMILDNLPLVPIQR	95%	n+304 (+304)	47.49	25.00
6217	parent_transcript=GRMZM5G818186_T01; parent_gene=GRMZM5G818186 seq=translation; coord=3:134681400..134683771:-1;	GRMZM5G818186_P01	TRUE	TRUE	aAAAAADVIFLMVGFPDVR	95%	n+304 (+304)	67.71	25.56
6218	parent_transcript=GRMZM2G110369_T01; parent_gene=GRMZM2G110369 seq=translation; coord=8:141648491..141651509:-1;	GRMZM2G110369_P01,GRMZM2G110369_P02	TRUE	TRUE	gLGVELLR	95%	n+304 (+304)	31.88	25.00
6219	parent_transcript=GRMZM2G351990_T01; parent_gene=GRMZM2G351990 seq=translation; coord=8:144537174..144540536:1;	GRMZM2G351990_P01	TRUE	TRUE	gYAALVGVPVPSMk	95%	n+304 (+304), K+304 (+304)	37.34	25.02
6220	parent_transcript=GRMZM2G052844_T01; parent_gene=GRMZM2G052844 seq=translation; coord=1:200401193..200409521:1;	GRMZM2G052844_P01,GRMZM2G052844_P02	TRUE	TRUE	vSVASFGGAGDGR	95%	n+304 (+304)	40.10	25.00
6221	parent_transcript=GRMZM2G082640_T01; parent_gene=GRMZM2G082640 seq=translation; coord=1:199870010..199870993:1;	GRMZM2G082640_P01,GRMZM2G082640_P02, GRMZM2G082640_P03	TRUE	TRUE	sDYEDGYEEEDVNSk	95%	n+304 (+304), K+304 (+304)	29.45	25.00
6222	parent_transcript=AC218900.3_FGT001; parent_gene=AC218900.3_FG001 seq=translation; coord=1:260618711..260622985:-1;	AC218900.3_FGP001,GRMZM2G064193_P01	TRUE	TRUE	dVVISPNVSAR	87%	n+304 (+304)	27.50	26.97
6223	parent_transcript=GRMZM2G083783_T01; parent_gene=GRMZM2G083783	GRMZM2G083783_P01,GRMZM2G083783_P03, GRMZM2G161242_P01,GRMZM2G161242_P02	TRUE	TRUE	gFGFVTFEDR	93%	n+304 (+304)	30.02	25.00

6224	seq=translation; coord=9:149245864..149247159:1; parent_transcript=GRMZM2G004466_T01; parent_gene=GRMZM2G004466	GRMZM2G004466_P01,GRMZM2G004466_P02	TRUE	TRUE	aLQLPAAck	89%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.12	26.14
6225	GRMZM2G017671_P02-R seq=translation; coord=5:193306422..193309271:1;	GRMZM2G017671_P02-R	TRUE	TRUE	IILVER	91%	n+304 (+304)	28.21	25.00
6226	parent_transcript=AC209208.3_FGT002; parent_gene=AC209208.3_FG002 seq=translation; coord=9:18623338..18625477:1;	AC209208.3_FGP002,GRMZM2G392975_P01,GRMZM2G392975_P02	TRUE	TRUE	sLGAAIYNR	95%	n+304 (+304)	38.14	25.00
6227	parent_transcript=GRMZM2G052562_T01; parent_gene=GRMZM2G052562 seq=translation; coord=2:74306561..74321272:-1;	GRMZM2G052562_P01,GRMZM2G052562_P02,GRMZM5G835276_P01	TRUE	TRUE	IVVDFLAEK	95%	n+304 (+304), K+304 (+304)	50.32	25.00
6228	parent_transcript=GRMZM2G082207_T01; parent_gene=GRMZM2G082207 seq=translation; coord=1:47177906..47178782:1;	GRMZM2G082207_P01,GRMZM2G082207_P02,GRMZM2G082207_P03,GRMZM2G082207_P04	TRUE	TRUE	aESPLDSFSLSLGLEK	95%	n+304 (+304), K+304 (+304)	38.31	25.29
6229	parent_transcript=GRMZM2G112488_T01; parent_gene=GRMZM2G112488 seq=translation; coord=6:151821892..151823785:-1;	GRMZM2G112488_P01	TRUE	TRUE	qFNFTSAMPFGFVK	92%	n+304 (+304), K+304 (+304)	27.75	25.87
6230	parent_transcript=GRMZM2G130746_T01; parent_gene=GRMZM2G130746 seq=translation; coord=7:163688367..163691160:-1;	GRMZM2G130746_P01,GRMZM2G130746_P02	TRUE	TRUE	ILAGVTIAHGGLVPINPVLPLK	95%	n+304 (+304), K+304 (+304)	39.24	25.00
6231	parent_transcript=GRMZM2G131167_T01; parent_gene=GRMZM2G131167 seq=translation; coord=2:23176274..23181034:-1;	GRMZM2G131167_P01,GRMZM2G131167_P03	TRUE	TRUE	dAFSEFGNVLEAR	95%	n+304 (+304)	56.61	25.00
6232	parent_transcript=GRMZM2G354909_T01; parent_gene=GRMZM2G354909 seq=translation; coord=1:36497245..36514437:1;	GRMZM2G354909_P01,GRMZM2G354909_P02	TRUE	TRUE	qVIETLLPLLQASSDGR	95%	n+304 (+304)	36.45	25.35
6233	parent_transcript=GRMZM2G372398_T01; parent_gene=GRMZM2G372398 seq=translation; coord=9:124917394..124918766:-1;	GRMZM2G372398_P01	TRUE	TRUE	aLELLGEIYAR	95%	n+304 (+304)	32.93	25.19
6234	parent_transcript=GRMZM2G415793_T01; parent_gene=GRMZM2G415793 seq=translation; coord=9:141474317..141477935:-1;	GRMZM2G415793_P01,GRMZM2G415793_P02	TRUE	TRUE	vQELYVYEMNER	95%	n+304 (+304)	51.15	25.00
6235	parent_transcript=GRMZM2G446234_T01; parent_gene=GRMZM2G446234 seq=translation; coord=5:215265820..215267607:1;	GRMZM2G446234_P01	TRUE	TRUE	gMDLLQEILQHLR	95%	n+304 (+304)	36.79	25.77
6236	parent_transcript=GRMZM5G862817_T01; parent_gene=GRMZM5G862817	GRMZM5G862817_P01,GRMZM5G862817_P04	TRUE	TRUE	IPDDLAAALGR	95%	n+304 (+304)	34.60	26.46
6237	seq=translation; coord=3:23896367..23898018:-1; parent_transcript=GRMZM2G114552_T01; parent_gene=GRMZM2G114552	GRMZM2G114552_P01,GRMZM2G114552_P02,GRMZM2G114552_P03,GRMZM2G114552_P04	TRUE	TRUE	dEERPWGEccDLAVcVcK	91%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	25.80	25.00
6238	seq=translation; coord=7:22256701..22261965:-1; parent_transcript=GRMZM2G140352_T01; parent_gene=GRMZM2G140352 seq=translation; coord=8:175624692..175630581:1;	GRMZM2G140352_P01,GRMZM2G140352_P02,GRMZM2G140352_P03,GRMZM2G140352_P04	TRUE	TRUE	gTVEVVFAR	91%	n+304 (+304)	28.22	25.00
6239	parent_transcript=AC211349.4_FGT001; parent_gene=AC211349.4_FG001 seq=translation; coord=6:95841179..95843445:-1;	AC211349.4_FGP001,GRMZM2G078756_P01	TRUE	TRUE	IAMVLFIDIPDIR	95%	n+304 (+304)	49.45	25.13
6240	parent_transcript=GRMZM2G014119_T01; parent_gene=GRMZM2G014119 seq=translation; coord=8:162534879..162538967:1;	GRMZM2G014119_P01	TRUE	TRUE	mQLFILTLTGK	95%	n+304 (+304), K+304 (+304)	32.54	25.00
6241	parent_transcript=GRMZM2G031204_T01; parent_gene=GRMZM2G031204	GRMZM2G031204_P01	TRUE	TRUE	sSDVTELQIGVK	95%	n+304 (+304), K+304 (+304)	66.93	25.45

6242	seq=translation; coord=2:230608941..230617571:-1; parent_transcript=GRMZM2G052403_T01; parent_gene=GRMZM2G052403 seq=translation; coord=3:196137228..196147873:1;	GRMZM2G052403_P01,GRMZM2G126453_P01, GRMZM2G126453_P02	TRUE	TRUE	iAPSVIFIDEVDSMLGR	95%	n+304 (+304)	34.49	25.73
6243	parent_transcript=GRMZM2G127665_T01; parent_gene=GRMZM2G127665 seq=translation; coord=2:10717934..10719159:-1;	GRMZM2G127665_P01	TRUE	TRUE	IVQDLSVIEAALR	95%	n+304 (+304)	32.59	25.43
6244	parent_transcript=GRMZM2G371375_T01; parent_gene=GRMZM2G371375 seq=translation; coord=5:67476538..67482854:1;	GRMZM2G371375_P01	TRUE	TRUE	gVAEDAADTASR	95%	n+304 (+304)	44.12	25.00
6245	parent_transcript=GRMZM2G472346_T01; parent_gene=GRMZM2G472346 seq=translation; coord=9:44334178..44336694:1;	GRMZM2G472346_P01,GRMZM2G472346_P02	TRUE	TRUE	sMLEELEGMLEIVEPQPpGKPR	89%	n+304 (+304), K+304 (+304)	25.79	25.77
6246	parent_transcript=GRMZM2G074085_T01; parent_gene=GRMZM2G074085 seq=translation; coord=9:15975038..15976941:1;	GRMZM2G074085_P01,GRMZM2G132623_P01, GRMZM2G132623_P02,GRMZM2G132623_P03	TRUE	TRUE	aMGTTDIR	92%	n+304 (+304)	28.60	25.00
6247	parent_transcript=GRMZM2G304378_T01; parent_gene=GRMZM2G304378 seq=translation; coord=1:299124462..299129776:-1;	GRMZM2G304378_P01	TRUE	TRUE	tcPIDTLk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.79	26.85
6248	parent_transcript=GRMZM2G176612_T02; parent_gene=GRMZM2G176612 seq=translation; coord=1:299124462..299129776:-1;	GRMZM2G176612_P02	TRUE	TRUE	aISSSQFFGTQNR	89%	n+304 (+304)	26.02	25.00
6249	parent_transcript=GRMZM2G176612_T02; parent_gene=GRMZM2G176612 seq=translation; coord=1:299124462..299129776:-1;	GRMZM2G176612_P02	TRUE	TRUE	fEYVENEPSADSR	95%	n+304 (+304)	32.33	25.00
6250	parent_transcript=GRMZM2G176612_T02; parent_gene=GRMZM2G176612 seq=translation; coord=10:16487570..16504336:1;	GRMZM2G176612_P02	TRUE	TRUE	iSFQASQDLSSLK	95%	n+304 (+304), K+304 (+304)	49.54	26.07
6251	parent_transcript=GRMZM2G028307_T02; parent_gene=GRMZM2G028307 seq=translation; coord=10:16487570..16504336:1;	GRMZM2G028307_P02	TRUE	TRUE	aQMALWSMTk	95%	n+304 (+304), K+304 (+304)	33.04	25.26
6252	parent_transcript=GRMZM2G028307_T02; parent_gene=GRMZM2G028307 seq=translation; coord=10:16487570..16504336:1;	GRMZM2G028307_P02	TRUE	TRUE	glISVQAVNADTPILDik	95%	n+304 (+304), K+304 (+304)	43.30	25.00
6253	parent_transcript=GRMZM2G028307_T02; parent_gene=GRMZM2G028307 seq=translation; coord=9:17315382..17321668:1;	GRMZM2G028307_P02	TRUE	TRUE	sWPDLDMLPFGWLTPSVNQGPFR	95%	n+304 (+304)	37.77	25.00
6254	parent_transcript=GRMZM5G864319_T01; parent_gene=GRMZM5G864319 seq=translation; coord=9:17315382..17321668:1;	GRMZM5G864319_P01	TRUE	TRUE	IFPLLASAYAFR	95%	n+304 (+304)	63.86	25.42
6255	parent_transcript=GRMZM5G864319_T01; parent_gene=GRMZM5G864319 seq=translation; coord=1:165814484..165965196:1;	GRMZM5G864319_P01	TRUE	TRUE	sPDLEAAVAHIQLVIVTk	95%	n+304 (+304), K+304 (+304)	28.00	25.00
6256	parent_transcript=GRMZM2G003595_T01; parent_gene=GRMZM2G003595 seq=translation; coord=1:165814484..165965196:1;	GRMZM2G003595_P01,GRMZM2G003595_P02, GRMZM2G003631_P01	TRUE	TRUE	kVEVQDQNEVGGMPSR	95%	K+304 (+304), n+304 (+304)	38.83	25.19
6257	parent_transcript=GRMZM2G003595_T01; parent_gene=GRMZM2G003595 seq=translation; coord=2:9503022..9507292:-1;	GRMZM2G003595_P01,GRMZM2G003595_P02, GRMZM2G003631_P01	TRUE	TRUE	qEEEEAIk	95%	n+304 (+304), K+304 (+304)	32.10	25.85
6258	parent_transcript=GRMZM2G040397_T01; parent_gene=GRMZM2G040397 seq=translation; coord=2:9503022..9507292:-1;	GRMZM2G040397_P01,GRMZM2G145460_P01	TRUE	TRUE	iSGAcFDAALGIPLGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	50.52	25.39
6259	parent_transcript=GRMZM2G040397_T01; parent_gene=GRMZM2G040397	GRMZM2G040397_P01,GRMZM2G145460_P01	TRUE	TRUE	IQFIYADLGDAk	95%	n+304 (+304), K+304 (+304)	44.97	25.00

6260	seq=translation; coord=2:56806976..56810257:1; parent_transcript=GRMZM2G119689_T01; parent_gene=GRMZM2G119689	GRMZM2G119689_P01,GRMZM2G119689_P02, GRMZM2G119689_P03	TRUE	TRUE	dLINWVALEPALRPSIPGDR	95%	n+304 (+304)	30.74	25.00
6261	seq=translation; coord=2:56806976..56810257:1; parent_transcript=GRMZM2G119689_T01; parent_gene=GRMZM2G119689	GRMZM2G119689_P01,GRMZM2G119689_P02, GRMZM2G119689_P03	TRUE	TRUE	gWAGIQAIPR	95%	n+304 (+304)	39.23	26.13
6262	seq=translation; coord=2:56806976..56810257:1; parent_transcript=GRMZM2G119689_T01; parent_gene=GRMZM2G119689	GRMZM2G119689_P01,GRMZM2G119689_P02, GRMZM2G119689_P03	TRUE	TRUE	qLLQWPiEEVEALR	95%	n+304 (+304)	40.73	25.82
6263	seq=translation; coord=3:182159627..182165670:-1; parent_transcript=GRMZM2G032258_T01; parent_gene=GRMZM2G032258	GRMZM2G032258_P01	TRUE	TRUE	eESEANEESTNk	95%	n+304 (+304), K+304 (+304)	32.28	25.00
6264	seq=translation; coord=3:182159627..182165670:-1; parent_transcript=GRMZM2G032258_T01; parent_gene=GRMZM2G032258	GRMZM2G032258_P01	TRUE	TRUE	iAIEDEIEDQR	95%	n+304 (+304)	32.30	25.00
6265	seq=translation; coord=3:215590446..215594988:1; parent_transcript=GRMZM2G057942_T01; parent_gene=GRMZM2G057942	GRMZM2G057942_P01	TRUE	TRUE	iPTLAIHLDR	95%	n+304 (+304)	59.69	27.11
6266	seq=translation; coord=3:215590446..215594988:1; parent_transcript=GRMZM2G057942_T01; parent_gene=GRMZM2G057942	GRMZM2G057942_P01	TRUE	TRUE	mVALFDHEEVGSDSAQGAGSPAMLDALSR	95%	n+304 (+304)	48.80	25.00
6267	seq=translation; coord=7:164948659..164953684:1; parent_transcript=GRMZM2G009538_T01; parent_gene=GRMZM2G009538	GRMZM2G009538_P01,GRMZM2G009538_P02	TRUE	TRUE	iAGGLDHLVAAGLSSLR	92%	n+304 (+304)	26.07	25.37
6268	seq=translation; coord=7:164948659..164953684:1; parent_transcript=GRMZM2G009538_T01; parent_gene=GRMZM2G009538	GRMZM2G009538_P01,GRMZM2G009538_P02	TRUE	TRUE	iQDVDDLAPLADLR	95%	n+304 (+304)	67.36	25.50
6269	seq=translation; coord=9:99409919..99416720:1; parent_transcript=GRMZM2G033555_T01; parent_gene=GRMZM2G033555	GRMZM2G033555_P01,GRMZM2G033555_P02, GRMZM2G033555_P03	TRUE	TRUE	nFVEDDVNSVYSSEK	95%	n+304 (+304), K+304 (+304)	28.84	25.00
6270	seq=translation; coord=9:99409919..99416720:1; parent_transcript=GRMZM2G033555_T01; parent_gene=GRMZM2G033555	GRMZM2G033555_P01,GRMZM2G033555_P02, GRMZM2G033555_P03	TRUE	TRUE	sVcVTGAGGFVASELVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.55	25.73
6271	seq=translation; coord=8:4108305..4111250:-1; parent_transcript=GRMZM2G028156_T01; parent_gene=GRMZM2G028156	GRMZM2G028156_P01,GRMZM2G431306_P01, GRMZM2G431306_P02,GRMZM2G431306_P03	TRUE	TRUE	eQIAGELQLPANK	95%	n+304 (+304), K+304 (+304)	30.24	25.00
6272	seq=translation; coord=8:4108305..4111250:-1; parent_transcript=GRMZM2G028156_T01; parent_gene=GRMZM2G028156	GRMZM2G028156_P01,GRMZM2G431306_P01, GRMZM2G431306_P02,GRMZM2G431306_P03	TRUE	TRUE	fVVPITGELIPISEMEEHMR	95%	n+304 (+304)	31.35	25.25
6273	seq=translation; coord=8:4108305..4111250:-1; parent_transcript=GRMZM2G028156_T01; parent_gene=GRMZM2G028156	GRMZM2G028156_P01,GRMZM2G431306_P01, GRMZM2G431306_P02,GRMZM2G431306_P03	TRUE	TRUE	tIGIHPPPDIR	95%	n+304 (+304)	33.73	25.00
6274	seq=translation; coord=2:198568661..198574971:1; parent_transcript=GRMZM2G081571_T04; parent_gene=GRMZM2G081571	GRMZM2G081571_P04,GRMZM2G081571_P05	TRUE	TRUE	aASFLSSLLGGGGGEPAATVvk	95%	n+304 (+304), K+304 (+304)	63.75	25.17
6275	seq=translation; coord=2:198568661..198574971:1; parent_transcript=GRMZM2G081571_T04; parent_gene=GRMZM2G081571	GRMZM2G081571_P04,GRMZM2G081571_P05	TRUE	TRUE	gLAVSQAPITSTGFR	95%	n+304 (+304)	55.48	25.84
6276	seq=translation; coord=3:159873679..159879241:-1; parent_transcript=GRMZM2G105531_T01; parent_gene=GRMZM2G105531	GRMZM2G105531_P01	TRUE	TRUE	aPELHLEIQR	95%	n+304 (+304)	38.40	25.00
6277	seq=translation; coord=3:159873679..159879241:-1; parent_transcript=GRMZM2G105531_T01; parent_gene=GRMZM2G105531	GRMZM2G105531_P01	TRUE	TRUE	IFFFEMAck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.80	25.17

6278	seq=translation; coord=6:161446540..161449925:1; parent_transcript=GRMZM2G115049_T01; parent_gene=GRMZM2G115049 seq=translation; coord=6:161446540..161449925:1;	GRMZM2G115049_P01	TRUE	TRUE	aILcVPFPYQk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.22	25.00
6279	parent_transcript=GRMZM2G115049_T01; parent_gene=GRMZM2G115049 seq=translation; coord=9:83796519..83798959:1;	GRMZM2G115049_P01	TRUE	TRUE	vGLSLVLkP	95%	n+304 (+304), K+304 (+304)	37.36	25.00
6280	parent_transcript=GRMZM2G140179_T01; parent_gene=GRMZM2G140179 seq=translation; coord=9:83796519..83798959:1;	GRMZM2G140179_P01	TRUE	TRUE	aLAGSGPAEAVYIYLLDLGk	95%	n+304 (+304), K+304 (+304)	50.07	25.00
6281	parent_transcript=GRMZM2G140179_T01; parent_gene=GRMZM2G140179 seq=translation; coord=7:169836954..169839970:-1;	GRMZM2G140179_P01	TRUE	TRUE	aLLADLASLVLSAYk	95%	n+304 (+304), K+304 (+304)	30.17	25.00
6282	parent_transcript=GRMZM2G037177_T01; parent_gene=GRMZM2G037177 seq=translation; coord=7:169836954..169839970:-1;	GRMZM2G037177_P01	TRUE	TRUE	iPSGEVWVGNPak	95%	n+304 (+304), K+304 (+304)	30.67	25.00
6283	parent_transcript=GRMZM2G037177_T01; parent_gene=GRMZM2G037177 seq=translation; coord=7:169836954..169839970:-1;	GRMZM2G037177_P01	TRUE	TRUE	sFDEIELEk	95%	n+304 (+304), K+304 (+304)	32.04	25.44
6284	parent_transcript=GRMZM2G037177_T01; parent_gene=GRMZM2G037177 seq=translation; coord=1:285137082..285140683:-1;	GRMZM2G037177_P01	TRUE	TRUE	tIMNIFEk	91%	n+304 (+304), K+304 (+304)	27.80	26.58
6285	parent_transcript=GRMZM2G058760_T01; parent_gene=GRMZM2G058760 seq=translation; coord=4:12777382..12783007:-1;	GRMZM2G058760_P01	TRUE	TRUE	iMLLPEEDPNATHIMIATGTGVAPFR	95%	n+304 (+304)	55.28	25.00
6286	parent_transcript=GRMZM2G139533_T01; parent_gene=GRMZM2G139533 seq=translation; coord=2:16302477..16307549:-1;	GRMZM2G139533_P01,GRMZM2G139533_P02	TRUE	TRUE	iPATLIADSAALMk	95%	n+304 (+304), K+304 (+304)	45.01	25.00
6287	parent_transcript=GRMZM2G175728_T01; parent_gene=GRMZM2G175728 seq=translation; coord=2:16302477..16307549:-1;	GRMZM2G175728_P01	TRUE	TRUE	sDPGIAAAVIAR	94%	n+304 (+304)	31.99	26.07
6288	parent_transcript=GRMZM2G175728_T01; parent_gene=GRMZM2G175728 seq=translation; coord=1:268608810..268612288:-1;	GRMZM2G175728_P01	TRUE	TRUE	sIALYATEDR	95%	n+304 (+304)	40.23	25.00
6289	parent_transcript=GRMZM2G176735_T01; parent_gene=GRMZM2G176735 seq=translation; coord=1:28446186..28450646:-1;	GRMZM2G176735_P01,GRMZM2G176735_P02	TRUE	TRUE	iAPPLVVPLLTGELILGk	93%	n+304 (+304), K+304 (+304)	27.31	25.00
6290	parent_transcript=GRMZM2G099860_T01; parent_gene=GRMZM2G099860 seq=translation; coord=6:164890857..164893003:-1;	GRMZM2G099860_P01	TRUE	TRUE	vVMLGVDMDIFk	95%	n+304 (+304), K+304 (+304)	58.87	25.75
6291	parent_transcript=GRMZM2G102779_T01; parent_gene=GRMZM2G102779 seq=translation; coord=7:43705280..43706429:-1;	GRMZM2G102779_P01	TRUE	TRUE	wTAQALLAGADMMk	91%	n+304 (+304), K+304 (+304)	26.73	25.49
6292	parent_transcript=GRMZM2G113668_T01; parent_gene=GRMZM2G113668 seq=translation; coord=7:43705280..43706429:-1;	GRMZM2G113668_P01	TRUE	TRUE	fLGVVR	91%	n+304 (+304)	26.76	25.00
6293	parent_transcript=GRMZM2G113668_T01; parent_gene=GRMZM2G113668 seq=translation; coord=10:18333983..18347671:-1;	GRMZM2G113668_P01	TRUE	TRUE	gHLAALLWYQGEADTMR	95%	n+304 (+304)	41.58	25.00
6294	parent_transcript=GRMZM2G015238_T01; parent_gene=GRMZM2G015238 seq=translation; coord=8:174419193..174424343:1;	GRMZM2G015238_P01	TRUE	TRUE	vVPLHSLk	89%	n+304 (+304), K+304 (+304)	25.04	25.00
6295	parent_transcript=GRMZM2G118462_T01; parent_gene=GRMZM2G118462	GRMZM2G118462_P01,GRMZM2G123277_P01, GRMZM2G304274_P01	TRUE	TRUE	ILAFENMLR	92%	n+304 (+304)	27.47	25.00

6296	seq=translation; coord=8:174419193..174424343:1; parent_transcript=GRMZM2G118462_T01; parent_gene=GRMZM2G118462	GRMZM2G118462_P01,GRMZM2G123277_P01, GRMZM2G304274_P01	TRUE	TRUE	tVLLGVDDMDIFk	95%	n+304 (+304), K+304 (+304)	40.32	25.99
6297	seq=translation; coord=4:186948838..186952130:-1; parent_transcript=GRMZM2G357595_T01; parent_gene=GRMZM2G357595	GRMZM2G357595_P01	TRUE	TRUE	aIEYDNFIecclTVk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	45.66	25.00
6298	seq=translation; coord=4:186948838..186952130:-1; parent_transcript=GRMZM2G357595_T01; parent_gene=GRMZM2G357595	GRMZM2G357595_P01	TRUE	TRUE	eFTSVFYSLQNWR	90%	n+304 (+304)	25.23	25.00
6299	seq=translation; coord=4:65261557..65280118:-1; parent_transcript=GRMZM2G055331_T01; parent_gene=GRMZM2G055331	GRMZM2G055331_P01	TRUE	TRUE	yFVEEVISGFDETDLyk	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	40.29	25.48
6300	seq=translation; coord=6:90530607..90532293:-1; parent_transcript=GRMZM2G016250_T01; parent_gene=GRMZM2G016250	GRMZM2G016250_P01,GRMZM2G302712_P01, GRMZM2G326066_P01,GRMZM2G366077_P01	TRUE	TRUE	IVNFTHLMPTR	95%	n+304 (+304)	53.75	25.30
6301	seq=translation; coord=5:5433227..5435612:-1; parent_transcript=AC195340.3_FGT001; parent_gene=AC195340.3_FG001	AC195340.3_FGP001	TRUE	TRUE	aFHEQLSVAEITSSAFEPASMMV	95%	n+304 (+304), K+304 (+304)	49.04	25.00
6302	seq=translation; coord=2:75419239..75423605:-1; parent_transcript=AC197056.3_FGT005; parent_gene=AC197056.3_FG005	AC197056.3_FGP005,GRMZM2G116693_P01	TRUE	TRUE	rWEVVFSEFIGTSR	93%	n+304 (+304)	28.11	25.45
6303	seq=translation; coord=6:132657599..132658828:-1; parent_transcript=AC234575.1_FGT003; parent_gene=AC234575.1_FG003	AC234575.1_FGP003,GRMZM2G120833_P01,G RMZM2G179797_P03	TRUE	TRUE	aDFGAVMDVLk	95%	n+304 (+304), K+304 (+304)	48.29	26.31
6304	seq=translation; coord=5:183309974..183317753:1; parent_transcript=GRMZM2G012841_T01; parent_gene=GRMZM2G012841	GRMZM2G012841_P01,GRMZM2G012841_P02, GRMZM2G012841_P03,GRMZM2G012841_P04, GRMZM2G012841_P05,GRMZM2G012841_P07, GRMZM2G012841_P09	TRUE	TRUE	IPHQMNFLEELR	95%	n+304 (+304)	59.98	25.45
6305	seq=translation; coord=1:207168310..207172439:-1; parent_transcript=GRMZM2G037655_T01; parent_gene=GRMZM2G037655	GRMZM2G037655_P01,GRMZM2G138881_P01, GRMZM2G138881_P02	TRUE	TRUE	rPVAVVMAWVR	95%	n+304 (+304)	54.97	26.19
6306	seq=translation; coord=8:13554391..13555376:1; parent_transcript=GRMZM2G041238_T01; parent_gene=GRMZM2G041238	GRMZM2G041238_P01,GRMZM2G108871_P01, GRMZM2G307892_P01,GRMZM2G327564_P01, GRMZM2G412848_P01	TRUE	TRUE	wVIHVER	95%	n+304 (+304)	36.15	26.50
6307	seq=translation; coord=2:191350704..191353166:1; parent_transcript=GRMZM2G047971_T02; parent_gene=GRMZM2G047971	GRMZM2G047971_P02,GRMZM2G065868_P01, GRMZM2G065868_P02,GRMZM2G065868_P03	TRUE	TRUE	fVVHNVSELELLLMHNR	95%	n+304 (+304)	67.03	25.81
6308	seq=translation; coord=2:161045370..161050327:-1; parent_transcript=GRMZM2G051367_T01; parent_gene=GRMZM2G051367	GRMZM2G051367_P01	TRUE	TRUE	ISLPPSLTGSAILSVSMQAR	95%	n+304 (+304)	35.66	25.34
6309	seq=translation; coord=2:3605933..3609654:-1; parent_transcript=GRMZM2G061745_T01; parent_gene=GRMZM2G061745	GRMZM2G061745_P01,GRMZM2G061745_P02, GRMZM2G061745_P03,GRMZM2G061745_P04, GRMZM2G368908_P01,GRMZM2G368908_P02	TRUE	TRUE	vVVHPLVLLSIVDHYNR	95%	n+304 (+304)	55.78	25.00
6310	seq=translation; coord=8:28291237..28300310:1; parent_transcript=GRMZM2G062953_T01; parent_gene=GRMZM2G062953	GRMZM2G062953_P01,GRMZM2G062953_P02	TRUE	TRUE	vLVLIDTWQDVFGGSHAR	95%	n+304 (+304)	48.13	25.65
6311	seq=translation; coord=3:127007479..127010593:-1; parent_transcript=GRMZM2G067476_T01; parent_gene=GRMZM2G067476	GRMZM2G067476_P01,GRMZM2G067476_P02, GRMZM2G067476_P03,GRMZM2G376727_P01, GRMZM2G376727_P02,GRMZM2G376727_P03, GRMZM2G376727_P04,GRMZM2G376727_P05	TRUE	TRUE	fQGSPAITYR	95%	n+304 (+304)	42.02	26.31

6312	seq=translation; coord=3:38428236..38432826:1; parent_transcript=GRMZM2G067511_T01; parent_gene=GRMZM2G067511 seq=translation; coord=4:180790322..180791225:-1;	GRMZM2G067511_P01	TRUE	TRUE	eADVDGDGQINYEDEFvk	95%	n+304 (+304), K+304 (+304)	47.07	25.00
6313	parent_transcript=GRMZM2G087137_T01; parent_gene=GRMZM2G087137 seq=translation; coord=5:191079735..191083805:1;	GRMZM2G087137_P01,GRMZM2G087137_P02	TRUE	TRUE	vAEPEEGTEALGVLDLR	95%	n+304 (+304)	46.14	25.33
6314	parent_transcript=GRMZM2G097728_T02; parent_gene=GRMZM2G097728 seq=translation; coord=6:120878064..120884267:-1;	GRMZM2G097728_P02,GRMZM2G097728_P03	TRUE	TRUE	nATNVEQAFMAMAASik	95%	n+304 (+304), K+304 (+304)	34.65	25.56
6315	parent_transcript=GRMZM2G101874_T01; parent_gene=GRMZM2G101874 seq=translation; coord=3:147745196..147752548:1;	GRMZM2G101874_P01	TRUE	TRUE	iPALVETLVSk	95%	n+304 (+304), K+304 (+304)	52.45	25.00
6316	parent_transcript=GRMZM2G109284_T01; parent_gene=GRMZM2G109284	GRMZM2G109284_P01	TRUE	TRUE	vDASGDAAEQPAADELR	95%	n+304 (+304)	48.16	25.00
6317	seq=translation; coord=4:236889764..236896376:-1; parent_transcript=GRMZM2G119640_T01; parent_gene=GRMZM2G119640	GRMZM2G119640_P01,GRMZM2G119640_P02, GRMZM2G119640_P03,GRMZM2G119640_P04, GRMZM2G119640_P06,GRMZM2G119640_P07	TRUE	TRUE	sLLEILDEK	95%	n+304 (+304), K+304 (+304)	41.91	25.00
6318	seq=translation; coord=6:147221316..147226156:1; parent_transcript=GRMZM2G121514_T01; parent_gene=GRMZM2G121514	GRMZM2G121514_P01,GRMZM2G121514_P02	TRUE	TRUE	gAPVLAGVHVAVR	95%	n+304 (+304)	49.22	25.00
6319	seq=translation; coord=6:131423962..131426896:1; parent_transcript=GRMZM2G126594_T01; parent_gene=GRMZM2G126594	GRMZM2G126594_P01,GRMZM2G126594_P02, GRMZM2G126594_P04,GRMZM2G127521_P01, GRMZM2G127521_P02	TRUE	TRUE	sYLEDVIAHk	95%	n+304 (+304), K+304 (+304)	38.94	26.33
6320	seq=translation; coord=7:144129492..144134147:-1; parent_transcript=GRMZM2G139210_T01; parent_gene=GRMZM2G139210	GRMZM2G139210_P01,GRMZM2G139210_P02, GRMZM2G139210_P03	TRUE	TRUE	aAIGIIDIVLk	95%	n+304 (+304), K+304 (+304)	53.16	25.00
6321	seq=translation; coord=2:38132179..38142127:1; parent_transcript=GRMZM2G147884_T01; parent_gene=GRMZM2G147884	GRMZM2G147884_P01,GRMZM2G147884_P02, GRMZM2G147884_P03	TRUE	TRUE	fVEAVLLEPEk	95%	n+304 (+304), K+304 (+304)	34.72	26.25
6322	seq=translation; coord=6:88898226..88901822:1; parent_transcript=GRMZM2G150209_T01; parent_gene=GRMZM2G150209	GRMZM2G150209_P01,GRMZM2G150209_P02	TRUE	TRUE	IYMVAPFLTGLk	95%	n+304 (+304), K+304 (+304)	30.04	25.00
6323	seq=translation; coord=7:167908789..167916594:-1; parent_transcript=GRMZM2G150683_T01; parent_gene=GRMZM2G150683	GRMZM2G150683_P01,GRMZM2G150683_P02, GRMZM2G150683_P03,GRMZM2G150683_P05, GRMZM2G150683_P06	TRUE	TRUE	qGADATALQAGLNWAcGQGR	95%	n+304 (+304), Carbamidomethyl (+57)	54.96	25.00
6324	seq=translation; coord=7:111657695..111660947:-1; parent_transcript=GRMZM2G159221_T01; parent_gene=GRMZM2G159221	GRMZM2G159221_P01,GRMZM2G159221_P02	TRUE	TRUE	eAAQDIIQEYLR	95%	n+304 (+304)	37.22	25.00
6325	seq=translation; coord=9:148206141..148211626:-1; parent_transcript=GRMZM2G181542_T01; parent_gene=GRMZM2G181542	GRMZM2G181542_P01	TRUE	TRUE	vAVDFIASHPQAk	95%	n+304 (+304), K+304 (+304)	31.22	25.28
6326	seq=translation; coord=5:79503885..79505592:1; parent_transcript=GRMZM2G314233_T01; parent_gene=GRMZM2G314233	GRMZM2G314233_P01	TRUE	TRUE	qNLAATFVNNAFVNAGFGk	95%	n+304 (+304), K+304 (+304)	47.24	25.00
6327	seq=translation; coord=3:162599045..162600039:1; parent_transcript=GRMZM5G846152_T01; parent_gene=GRMZM5G846152	GRMZM5G846152_P01	TRUE	TRUE	aHQLPGGLLPAGITAFR	95%	n+304 (+304)	51.33	25.60
6328	seq=translation; coord=7:146895009..146896961:-1; parent_transcript=GRMZM2G066528_T01; parent_gene=GRMZM2G066528	GRMZM2G066528_P01,GRMZM2G066528_P02, GRMZM2G066528_P03,GRMZM2G066528_P04	TRUE	TRUE	rPPSAFFVFMEEFr	94%	n+304 (+304)	28.47	25.00

6329	seq=translation; coord=5:155243219..155246765:-1; parent_transcript=GRMZM2G029559_T02; parent_gene=GRMZM2G029559 seq=translation; coord=2:4687656..4692442:1;	GRMZM2G029559_P02	TRUE	TRUE	IILDDWk	94%	n+304 (+304), K+304 (+304)	29.29	26.05
6330	parent_transcript=GRMZM2G086801_T01; parent_gene=GRMZM2G086801 seq=translation; coord=3:37865603..37869803:1;	GRMZM2G086801_P01,GRMZM2G086801_P02	TRUE	TRUE	iSALALLk	94%	n+304 (+304), K+304 (+304)	27.95	25.00
6331	parent_transcript=GRMZM2G069208_T01; parent_gene=GRMZM2G069208 seq=translation; coord=3:37865603..37869803:1;	GRMZM2G049429_P01,GRMZM2G049429_P02, GRMZM2G069208_P01	TRUE	TRUE	IVDLPPQEISGMGMSk	95%	n+304 (+304), K+304 (+304)	56.93	25.43
6332	parent_transcript=GRMZM2G069208_T01; parent_gene=GRMZM2G069208 seq=translation; coord=3:37865603..37869803:1;	GRMZM2G049429_P01,GRMZM2G049429_P02, GRMZM2G069208_P01	TRUE	TRUE	qFHEMVGHFVDIMk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	57.92	25.00
6333	parent_transcript=GRMZM2G069208_T01; parent_gene=GRMZM2G069208 seq=translation; coord=3:7078308..7082094:1;	GRMZM2G049429_P01,GRMZM2G049429_P02, GRMZM2G069208_P01	TRUE	TRUE	sSIILPLSLGk	95%	n+304 (+304), K+304 (+304)	40.87	25.00
6334	parent_transcript=GRMZM2G104081_T01; parent_gene=GRMZM2G104081 seq=translation; coord=3:7078308..7082094:1;	GRMZM2G104081_P01,GRMZM2G104081_P02, GRMZM2G104081_P03	TRUE	TRUE	aFSINDAVGEDVVVELQTAMEk	95%	n+304 (+304), K+304 (+304)	37.79	25.00
6335	parent_transcript=GRMZM2G104081_T01; parent_gene=GRMZM2G104081 seq=translation; coord=3:7078308..7082094:1;	GRMZM2G104081_P01,GRMZM2G104081_P02, GRMZM2G104081_P03	TRUE	TRUE	IAAAGLAGILMk	95%	n+304 (+304), K+304 (+304)	29.47	25.00
6336	parent_transcript=GRMZM2G104081_T01; parent_gene=GRMZM2G104081 seq=translation; coord=10:61378667..61384801:1;	GRMZM2G104081_P01,GRMZM2G104081_P02, GRMZM2G104081_P03	TRUE	TRUE	qGLDMHVAALINDAVGTLAGAR	95%	n+304 (+304)	30.39	25.82
6337	parent_transcript=GRMZM2G143568_T01; parent_gene=GRMZM2G143568 seq=translation; coord=10:61378667..61384801:1;	GRMZM2G143568_P01	TRUE	TRUE	aLFGVSTIYk	95%	n+304 (+304), K+304 (+304)	48.63	25.00
6338	parent_transcript=GRMZM2G143568_T01; parent_gene=GRMZM2G143568 seq=translation; coord=10:61378667..61384801:1;	GRMZM2G143568_P01	TRUE	TRUE	iLcPDSLIGSVIGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.59	25.00
6339	parent_transcript=GRMZM2G143568_T01; parent_gene=GRMZM2G143568 seq=translation; coord=2:12023721..12027357:-1;	GRMZM2G143568_P01	TRUE	TRUE	sAAVEAVLLLQAk	95%	n+304 (+304), K+304 (+304)	33.80	25.00
6340	parent_transcript=GRMZM2G156365_T02; parent_gene=GRMZM2G156365 seq=translation; coord=2:12023721..12027357:-1;	GRMZM2G156365_P02,GRMZM2G156365_P03, GRMZM2G156365_P04,GRMZM2G156365_P05, GRMZM2G156365_P06	TRUE	TRUE	aQNALLSGcSAGGLAAIHcDR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	80.08	25.00
6341	parent_transcript=GRMZM2G156365_T02; parent_gene=GRMZM2G156365 seq=translation; coord=2:12023721..12027357:-1;	GRMZM2G156365_P02,GRMZM2G156365_P03, GRMZM2G156365_P04,GRMZM2G156365_P05, GRMZM2G156365_P06	TRUE	TRUE	aVIDDLLTVR	95%	n+304 (+304)	32.18	25.00
6342	parent_transcript=GRMZM2G156365_T02; parent_gene=GRMZM2G156365 seq=translation; coord=5:18170761..18172340:1;	GRMZM2G156365_P02,GRMZM2G156365_P03, GRMZM2G156365_P04,GRMZM2G156365_P05, GRMZM2G156365_P06	TRUE	TRUE	tPLFILNAAYDSWQVk	95%	n+304 (+304), K+304 (+304)	44.66	25.30
6343	parent_transcript=GRMZM2G060940_T01; parent_gene=GRMZM2G060940 seq=translation; coord=5:18170761..18172340:1;	GRMZM2G060940_P01,GRMZM2G060940_P02, GRMZM2G060940_P03	TRUE	TRUE	dWGFVVVGHGVPAETVAR	95%	n+304 (+304)	43.97	25.28
6344	parent_transcript=GRMZM2G060940_T01; parent_gene=GRMZM2G060940 seq=translation; coord=5:18170761..18172340:1;	GRMZM2G060940_P01,GRMZM2G060940_P02, GRMZM2G060940_P03	TRUE	TRUE	eVYDLVPR	95%	n+304 (+304)	32.69	25.40
6345	parent_transcript=GRMZM2G060940_T01; parent_gene=GRMZM2G060940 seq=translation; coord=3:127303985..127310112:-1;	GRMZM2G060940_P01,GRMZM2G060940_P02, GRMZM2G060940_P03	TRUE	TRUE	ILELIAR	87%	n+304 (+304)	25.06	25.00
6346	parent_transcript=AC182617.3_FG001; parent_gene=AC182617.3_FG001	AC182617.3_FG001,GRMZM2G130332_P01,G RMZM2G130332_P02,GRMZM2G130332_P03,G RMZM2G130332_P04	TRUE	TRUE	aLHFVK	92%	n+304 (+304), K+304 (+304)	26.14	25.00

6347	seq=translation; coord=3:127303985..127310112:-1; parent_transcript=AC182617.3_FGT001; parent_gene=AC182617.3_FG001 seq=translation; coord=7:132157014..132162257:1;	AC182617.3_FGP001,GRMZM2G130332_P01,G RMZM2G130332_P02,GRMZM2G130332_P03,G RMZM2G130332_P04	TRUE	TRUE	yQGLGNDFIMVDNR	95%	n+304 (+304)	32.58	25.00
6348	parent_transcript=GRMZM2G068862_T01; parent_gene=GRMZM2G068862 seq=translation; coord=7:132157014..132162257:1;	GRMZM2G068862_P01	TRUE	TRUE	mAEQTLSLlk	93%	n+304 (+304), K+304 (+304)	26.65	25.09
6349	parent_transcript=GRMZM2G068862_T01; parent_gene=GRMZM2G068862 seq=translation; coord=4:120394113..120399917:1;	GRMZM2G068862_P01	TRUE	TRUE	vDVEYYAINVVVPQk	95%	n+304 (+304), K+304 (+304)	45.07	25.00
6350	parent_transcript=GRMZM2G153984_T01; parent_gene=GRMZM2G153984 seq=translation; coord=4:120394113..120399917:1;	GRMZM2G153984_P01	TRUE	TRUE	gYVDMSTVDAATStk	95%	n+304 (+304), K+304 (+304)	46.09	25.00
6351	parent_transcript=GRMZM2G153984_T01; parent_gene=GRMZM2G153984 seq=translation; coord=2:130522633..130525928:-1;	GRMZM2G153984_P01	TRUE	TRUE	sGLSPQTLDDVLDGAIANPMFk	95%	n+304 (+304), K+304 (+304)	29.84	25.00
6352	parent_transcript=GRMZM2G128268_T01; parent_gene=GRMZM2G128268 seq=translation; coord=2:130522633..130525928:-1;	GRMZM2G128268_P01	TRUE	TRUE	gSVSLVSQLk	95%	n+304 (+304), K+304 (+304)	46.79	25.00
6353	parent_transcript=GRMZM2G128268_T01; parent_gene=GRMZM2G128268 seq=translation; coord=3:173472565..173475730:-1;	GRMZM2G128268_P01	TRUE	TRUE	nVVGHCtSTNGGGFLFFGDDVVPSSR	95%	n+304 (+304), Carbamidomethyl (+57)	57.56	25.00
6354	parent_transcript=GRMZM2G081652_T01; parent_gene=GRMZM2G081652 seq=translation; coord=3:173472565..173475730:-1;	GRMZM2G081652_P01	TRUE	TRUE	aQVAADAPVEEVk	93%	n+304 (+304), K+304 (+304)	28.60	26.33
6355	parent_transcript=GRMZM2G081652_T01; parent_gene=GRMZM2G081652 seq=translation; coord=1:205090665..205094372:1;	GRMZM2G081652_P01	TRUE	TRUE	yIAPEQVPVQFGGLFk	95%	n+304 (+304), K+304 (+304)	47.60	25.00
6356	parent_transcript=GRMZM2G144387_T01; parent_gene=GRMZM2G144387 seq=translation; coord=1:205090665..205094372:1;	GRMZM2G144387_P01,GRMZM2G144387_P03	TRUE	TRUE	dAISQIVGDAk	95%	n+304 (+304), K+304 (+304)	32.10	26.78
6357	parent_transcript=GRMZM2G144387_T01; parent_gene=GRMZM2G144387 seq=translation; coord=9:25522193..25524594:-1;	GRMZM2G144387_P01,GRMZM2G144387_P03	TRUE	TRUE	vcMLGDAQHVVEAEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.86	25.00
6358	parent_transcript=GRMZM2G383540_T01; parent_gene=GRMZM2G383540 seq=translation; coord=10:85188397..85193819:-1;	GRMZM2G383540_P01,GRMZM5G808811_P01	TRUE	TRUE	qQMIDcYIQTLak	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.76	25.49
6359	parent_transcript=GRMZM2G101875_T01; parent_gene=GRMZM2G101875 seq=translation; coord=5:38567212..38578529:-1;	GRMZM2G101875_P01,GRMZM2G101875_P02	TRUE	TRUE	mTTDDVFLSFLPLAHILDR	95%	n+304 (+304)	34.58	25.00
6360	parent_transcript=GRMZM2G377341_T01; parent_gene=GRMZM2G377341 seq=translation; coord=10:98135181..98154139:1;	GRMZM2G377341_P01	TRUE	TRUE	sLAIANMVLGLk	94%	n+304 (+304), K+304 (+304)	28.22	25.00
6361	parent_transcript=AC197672.3_FGT002; parent_gene=AC197672.3_FG002 seq=translation; coord=10:98135181..98154139:1;	AC197672.3_FGP002	TRUE	TRUE	aIHliAMATPEDMR	95%	n+304 (+304)	31.25	25.24
6362	parent_transcript=AC197672.3_FGT002; parent_gene=AC197672.3_FG002 seq=translation; coord=9:9638146..9648092:-1;	AC197672.3_FGP002	TRUE	TRUE	dLFEGILQAGSAIVENLR	95%	n+304 (+304)	30.83	25.45
6363	parent_transcript=GRMZM2G033130_T01; parent_gene=GRMZM2G033130 seq=translation; coord=9:9638146..9648092:-1;	GRMZM2G033130_P01,GRMZM2G033130_P03, GRMZM2G033130_P04,GRMZM2G033130_P06, GRMZM2G152768_P01 GRMZM2G033130_P01,GRMZM2G033130_P03, GRMZM2G033130_P04,GRMZM2G033130_P06,	TRUE	TRUE	eSNMDPNETAQk	95%	n+304 (+304), K+304 (+304)	40.53	25.00
6364	parent_transcript=GRMZM2G033130_T01; parent_gene=GRMZM2G033130	GRMZM2G033130_P01,GRMZM2G033130_P03, GRMZM2G033130_P04,GRMZM2G033130_P06, GRMZM2G152768_P01	TRUE	TRUE	eVVVGHSADILDTLR	95%	n+304 (+304)	50.82	25.45

6365	seq=translation; coord=9:99437276..99441674:1; parent_transcript=GRMZM2G034069_T01; parent_gene=GRMZM2G034069	GRMZM2G034069_P01	TRUE	TRUE	dVADALLLAYEKPEASGR	95%	n+304 (+304), K+304 (+304)	44.22	26.10
6366	seq=translation; coord=9:99437276..99441674:1; parent_transcript=GRMZM2G034069_T01; parent_gene=GRMZM2G034069	GRMZM2G034069_P01	TRUE	TRUE	vADMINILk	95%	n+304 (+304), K+304 (+304)	31.94	25.45
6367	seq=translation; coord=9:146299403..146305484:1; parent_transcript=GRMZM2G051782_T01; parent_gene=GRMZM2G051782	GRMZM2G051782_P01	TRUE	TRUE	aLFVDLEPTVIDEVk	95%	n+304 (+304), K+304 (+304)	59.33	25.69
6368	seq=translation; coord=9:146299403..146305484:1; parent_transcript=GRMZM2G051782_T01; parent_gene=GRMZM2G051782	GRMZM2G051782_P01	TRUE	TRUE	qLFHPEQLISHk	95%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	29.21	25.25
6369	seq=translation; coord=1:283086410..283088116:1; parent_transcript=GRMZM2G065083_T01; parent_gene=GRMZM2G065083	GRMZM2G065083_P01	TRUE	TRUE	gNRPSLSLLPTLSAYEVGQLLSIYEHR	95%	n+304 (+304)	52.39	25.00
6370	seq=translation; coord=1:283086410..283088116:1; parent_transcript=GRMZM2G065083_T01; parent_gene=GRMZM2G065083	GRMZM2G065083_P01	TRUE	TRUE	vPENLIPHK	95%	n+304 (+304), K+304 (+304)	32.94	25.76
6371	seq=translation; coord=5:184168891..184173292:1; parent_transcript=GRMZM2G071846_T01; parent_gene=GRMZM2G071846	GRMZM2G071846_P01	TRUE	TRUE	gFIFGPAVALAIGAK	95%	n+304 (+304), K+304 (+304)	32.66	25.00
6372	seq=translation; coord=5:184168891..184173292:1; parent_transcript=GRMZM2G071846_T01; parent_gene=GRMZM2G071846	GRMZM2G071846_P01	TRUE	TRUE	hGIMFNDITLLLRPR	95%	n+304 (+304)	30.67	25.24
6373	seq=translation; coord=2:189499850..189501644:1; parent_transcript=GRMZM2G080466_T01; parent_gene=GRMZM2G080466	GRMZM2G080466_P01,GRMZM2G080466_P02, GRMZM2G080466_P03,GRMZM2G080466_P04	TRUE	TRUE	aEPAAEVAEk	95%	n+304 (+304), K+304 (+304)	40.96	25.74
6374	seq=translation; coord=2:189499850..189501644:1; parent_transcript=GRMZM2G080466_T01; parent_gene=GRMZM2G080466	GRMZM2G080466_P01,GRMZM2G080466_P02, GRMZM2G080466_P03,GRMZM2G080466_P04	TRUE	TRUE	eAEPEPAAAGEVk	95%	n+304 (+304), K+304 (+304)	52.22	25.66
6375	seq=translation; coord=1:183983464..183984705:-1; parent_transcript=GRMZM2G080724_T01; parent_gene=GRMZM2G080724	GRMZM2G080724_P01	TRUE	TRUE	tIMDADDADTDTR	95%	n+304 (+304)	54.19	25.00
6376	seq=translation; coord=1:183983464..183984705:-1; parent_transcript=GRMZM2G080724_T01; parent_gene=GRMZM2G080724	GRMZM2G080724_P01	TRUE	TRUE	vELPENVDVER	95%	n+304 (+304)	45.90	25.00
6377	seq=translation; coord=2:29975938..29981822:1; parent_transcript=GRMZM2G082581_T01; parent_gene=GRMZM2G082581	GRMZM2G082581_P01	TRUE	TRUE	aFAESSMAMALSk	95%	n+304 (+304), K+304 (+304)	29.10	25.07
6378	seq=translation; coord=2:29975938..29981822:1; parent_transcript=GRMZM2G082581_T01; parent_gene=GRMZM2G082581	GRMZM2G082581_P01	TRUE	TRUE	eFyLSTEEFIDAVAQQLR	95%	n+304 (+304), iTRAQ8plex (+304)	40.26	25.13
6379	seq=translation; coord=8:137403695..137407159:-1; parent_transcript=GRMZM2G106960_T01; parent_gene=GRMZM2G106960	GRMZM2G106960_P01	TRUE	TRUE	aLADDIGIPFLETSak	95%	n+304 (+304), K+304 (+304)	57.32	26.06
6380	seq=translation; coord=8:137403695..137407159:-1; parent_transcript=GRMZM2G106960_T01; parent_gene=GRMZM2G106960	GRMZM2G106960_P01	TRUE	TRUE	gAHGIIVVYDVTDQESFNNVk	95%	n+304 (+304), K+304 (+304)	33.11	25.54
6381	seq=translation; coord=5:13615570..13621897:1; parent_transcript=GRMZM2G161222_T03; parent_gene=GRMZM2G161222	GRMZM2G161222_P03	TRUE	TRUE	gVIFPIIFEALER	95%	n+304 (+304)	29.79	25.49
6382	seq=translation; coord=5:13615570..13621897:1; parent_transcript=GRMZM2G161222_T03; parent_gene=GRMZM2G161222	GRMZM2G161222_P03	TRUE	TRUE	IVAALFDLSDSLk	95%	n+304 (+304), K+304 (+304)	30.33	25.00

6383	seq=translation; coord=9:92025063..92027986:-1; parent_transcript=GRMZM2G316232_T01; parent_gene=GRMZM2G316232	GRMZM2G316232_P01	TRUE	TRUE	IADGAVLIVDAEAGVMVNTER	95%	n+304 (+304)	61.49	25.48
6384	seq=translation; coord=9:92025063..92027986:-1; parent_transcript=GRMZM2G316232_T01; parent_gene=GRMZM2G316232	GRMZM2G316232_P01	TRUE	TRUE	sFVEFILEPLYk	95%	n+304 (+304), K+304 (+304)	34.45	25.00
6385	seq=translation; coord=10:117993529..118000841:-1; parent_transcript=GRMZM2G353213_T01; parent_gene=GRMZM2G353213	GRMZM2G353213_P01,GRMZM2G353213_P02	TRUE	TRUE	fAFVDVSPEELQKk	95%	n+304 (+304), K+304 (+304)	32.40	25.89
6386	seq=translation; coord=10:117993529..118000841:-1; parent_transcript=GRMZM2G353213_T01; parent_gene=GRMZM2G353213	GRMZM2G353213_P01,GRMZM2G353213_P02	TRUE	TRUE	nLQSSPETVDVk	95%	n+304 (+304), K+304 (+304)	36.09	25.85
6387	seq=translation; coord=9:137069559..137072594:-1; parent_transcript=GRMZM2G053652_T01; parent_gene=GRMZM2G053652	GRMZM2G053652_P01,GRMZM2G053652_P02	TRUE	TRUE	IDTYTTVYR	95%	n+304 (+304)	30.31	25.08
6388	seq=translation; coord=9:137069559..137072594:-1; parent_transcript=GRMZM2G053652_T01; parent_gene=GRMZM2G053652	GRMZM2G053652_P01,GRMZM2G053652_P02	TRUE	TRUE	tLTAVHDGILEDDVFPAEIVGk	95%	n+304 (+304), K+304 (+304)	31.96	25.00
6389	seq=translation; coord=1:297376727..297379573:-1; parent_transcript=GRMZM2G369815_T01; parent_gene=GRMZM2G369815	GRMZM2G369815_P01,GRMZM2G369815_P02	TRUE	TRUE	aDDRDAVGcAASVNR	95%	n+304 (+304), Carbamidomethyl (+57)	29.18	25.00
6390	seq=translation; coord=1:297376727..297379573:-1; parent_transcript=GRMZM2G369815_T01; parent_gene=GRMZM2G369815	GRMZM2G369815_P01,GRMZM2G369815_P02	TRUE	TRUE	vTAFVEGLLER	95%	n+304 (+304)	43.81	25.00
6391	seq=translation; coord=3:221687099..221691249:1; parent_transcript=GRMZM2G071021_T01; parent_gene=GRMZM2G071021	GRMZM2G071021_P01	TRUE	TRUE	dIPGAAHLLR	95%	n+304 (+304)	59.41	25.00
6392	seq=translation; coord=4:159862612..159866537:1; parent_transcript=GRMZM2G050371_T01; parent_gene=GRMZM2G050371	GRMZM2G050371_P01	TRUE	TRUE	gFEPDANTVEIAR	95%	n+304 (+304)	29.82	25.00
6393	seq=translation; coord=4:159862612..159866537:1; parent_transcript=GRMZM2G050371_T01; parent_gene=GRMZM2G050371	GRMZM2G050371_P01	TRUE	TRUE	vFAHQDILDLaK	95%	n+304 (+304), K+304 (+304)	43.34	25.65
6394	seq=translation; coord=8:17388792..17393555:-1; parent_transcript=GRMZM2G061969_T01; parent_gene=GRMZM2G061969	GRMZM2G061969_P01	TRUE	TRUE	dLSDIIIPSPVMFPEDR	95%	n+304 (+304)	48.59	25.04
6395	seq=translation; coord=8:17388792..17393555:-1; parent_transcript=GRMZM2G061969_T01; parent_gene=GRMZM2G061969	GRMZM2G061969_P01	TRUE	TRUE	sIQDAYINAIR	94%	n+304 (+304)	30.59	25.00
6396	seq=translation; coord=5:215652783..215654639:1; parent_transcript=GRMZM2G143627_T01; parent_gene=GRMZM2G143627	GRMZM2G143627_P01,GRMZM2G143627_P02	TRUE	TRUE	gADPYDLk	94%	n+304 (+304), K+304 (+304)	31.83	26.35
6397	seq=translation; coord=5:215652783..215654639:1; parent_transcript=GRMZM2G143627_T01; parent_gene=GRMZM2G143627	GRMZM2G143627_P01,GRMZM2G143627_P02	TRUE	TRUE	qQENVLAESR	89%	n+304 (+304)	26.86	25.00
6398	seq=translation; coord=1:286506118..286513080:-1; parent_transcript=GRMZM2G141473_T01; parent_gene=GRMZM2G141473	GRMZM2G141473_P01	TRUE	TRUE	IPGYDSGAVcTFPEFLk	93%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	27.79	25.05
6399	seq=translation; coord=1:286506118..286513080:-1; parent_transcript=GRMZM2G141473_T01; parent_gene=GRMZM2G141473	GRMZM2G141473_P01	TRUE	TRUE	vGGGFGGk	86%	n+304 (+304), K+304 (+304)	25.97	25.85
6400	seq=translation; coord=5:18753627..18756558:1; parent_transcript=GRMZM2G138572_T01; parent_gene=GRMZM2G138572	GRMZM2G138572_P01	TRUE	TRUE	iLHAAFVPFGEVgk	95%	n+304 (+304), K+304 (+304)	32.33	25.00

6401	seq=translation; coord=5:18753627..18756558:1; parent_transcript=GRMZM2G138572_T01; parent_gene=GRMZM2G138572 seq=translation; coord=4:26401952..26408946:-1;	GRMZM2G138572_P01	TRUE	TRUE	sFGFVTFLE	89%	n+304 (+304)	27.32	25.71
6402	parent_transcript=GRMZM2G003814_T01; parent_gene=GRMZM2G003814 seq=translation; coord=1:35577459..35584230:-1;	GRMZM2G003814_P01	TRUE	TRUE	aVVYDEHGLPEQVLR	92%	n+304 (+304)	27.37	25.56
6403	parent_transcript=GRMZM2G127123_T01; parent_gene=GRMZM2G127123 seq=translation; coord=2:3969379..3974004:1;	GRMZM2G127123_P01,GRMZM2G127123_P03	TRUE	TRUE	FTPPAGDDPVAIDFTGMGk	95%	n+304 (+304), K+304 (+304)	49.48	25.25
6404	parent_transcript=GRMZM2G056572_T01; parent_gene=GRMZM2G056572 seq=translation; coord=7:155584542..155586999:1;	GRMZM2G056572_P01,GRMZM2G056572_P02, GRMZM2G056572_P03,GRMZM2G056572_P04, GRMZM2G056572_P05	TRUE	TRUE	iDcVDGQIVGLFGVDFGHGGAk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	97.74	25.09
6405	parent_transcript=GRMZM2G041381_T01; parent_gene=GRMZM2G041381 seq=translation; coord=9:37699870..37701617:1;	GRMZM2G041381_P01,GRMZM2G151826_P01	TRUE	TRUE	aIGAGAAk	95%	n+304 (+304), K+304 (+304)	34.19	25.37
6406	parent_transcript=GRMZM2G008539_T01; parent_gene=GRMZM2G008539 seq=translation; coord=4:24613100..24615973:-1;	GRMZM2G008539_P01,GRMZM2G099740_P01	TRUE	TRUE	gAVVDRDDAGELSELLGEAFLR	95%	n+304 (+304)	46.14	25.00
6407	parent_transcript=GRMZM2G101480_T01; parent_gene=GRMZM2G101480 seq=translation; coord=7:165751276..165754416:-1;	GRMZM2G101480_P01,GRMZM2G101480_P02, GRMZM2G101480_P04,GRMZM5G800112_P01, GRMZM5G800112_P02	TRUE	TRUE	rLDDDTENLAHER	95%	n+304 (+304)	38.39	25.00
6408	parent_transcript=GRMZM2G053939_T01; parent_gene=GRMZM2G053939 seq=translation; coord=4:206497947..206499008:-1;	GRMZM2G053939_P01	TRUE	TRUE	eVLSLcDHPALLDk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.17	25.60
6409	parent_transcript=GRMZM2G059706_T01; parent_gene=GRMZM2G059706 seq=translation; coord=8:104902929..104904891:1;	GRMZM2G059706_P01,GRMZM2G178199_P01	TRUE	TRUE	eMSIVGGSGk	95%	n+304 (+304), K+304 (+304)	45.23	26.23
6410	parent_transcript=GRMZM2G044440_T01; parent_gene=GRMZM2G044440 seq=translation; coord=10:2446094..2450352:1;	GRMZM2G044440_P01	TRUE	TRUE	mQIFVLMLTGk	95%	n+304 (+304), K+304 (+304)	31.47	25.45
6411	parent_transcript=GRMZM2G151977_T01; parent_gene=GRMZM2G151977 seq=translation; coord=2:26769801..26771736:1;	GRMZM2G151977_P01	TRUE	TRUE	sAGSPLSLLGR	94%	n+304 (+304)	29.64	25.19
6412	parent_transcript=GRMZM2G474575_T01; parent_gene=GRMZM2G474575 seq=translation; coord=2:26769801..26771736:1;	GRMZM2G474575_P01	TRUE	TRUE	aHAVVFQk	91%	n+304 (+304), K+304 (+304)	25.13	25.00
6413	parent_transcript=GRMZM2G474575_T01; parent_gene=GRMZM2G474575 seq=translation; coord=1:110974309..110976210:1;	GRMZM2G474575_P01	TRUE	TRUE	aWLGTTETDR	89%	n+304 (+304)	25.99	25.00
6414	parent_transcript=GRMZM2G154216_T01; parent_gene=GRMZM2G154216 seq=translation; coord=3:3459125..3462998:1;	GRMZM2G154216_P01	TRUE	TRUE	iGEDELGLGWAER	95%	n+304 (+304)	33.04	25.00
6415	parent_transcript=GRMZM2G102572_T01; parent_gene=GRMZM2G102572 seq=translation; coord=9:101389917..101393912:1;	GRMZM2G102572_P01,GRMZM2G102572_P02, GRMZM2G102572_P03	TRUE	TRUE	iLFEEVvk	94%	n+304 (+304), K+304 (+304)	28.59	25.00
6416	parent_transcript=GRMZM2G000566_T01; parent_gene=GRMZM2G000566 seq=translation; coord=8:164932122..164937568:1;	GRMZM2G000566_P01	TRUE	TRUE	aEFDWLALYR	92%	n+304 (+304)	28.46	25.00
6417	parent_transcript=GRMZM2G049269_T01; parent_gene=GRMZM2G049269 seq=translation; coord=5:159269189..159288759:1;	GRMZM2G049269_P01	TRUE	TRUE	IAAVFAEVD	90%	n+304 (+304)	27.70	25.43
6418	parent_transcript=GRMZM2G135691_T01; parent_gene=GRMZM2G135691	GRMZM2G135691_P01,GRMZM2G135691_P02	TRUE	TRUE	aYLTEELR	95%	n+304 (+304)	42.37	25.51

6419	seq=translation; coord=4:149744485..149746284:1; parent_transcript=GRMZM2G065021_T01; parent_gene=GRMZM2G065021	GRMZM2G065021_P01	TRUE	TRUE	aAAEESTEQQVVPFVR	95%	n+304 (+304)	72.73	25.00
6420	seq=translation; coord=4:143464625..143469700:-1; parent_transcript=GRMZM2G081582_T01; parent_gene=GRMZM2G081582	GRMZM2G081582_P01	TRUE	TRUE	IALAAIGk	92%	n+304 (+304), K+304 (+304)	26.46	25.00
6421	seq=translation; coord=10:84755864..84760724:-1; parent_transcript=GRMZM2G136341_T01; parent_gene=GRMZM2G136341	GRMZM2G136341_P01	TRUE	TRUE	ILEEALGk	95%	n+304 (+304), K+304 (+304)	28.53	25.00
6422	seq=translation; coord=1:5873406..5877213:1; parent_transcript=GRMZM2G105571_T01; parent_gene=GRMZM2G105571	GRMZM2G105571_P01,GRMZM2G105571_P02	TRUE	TRUE	aVAGAGVLAGYDk	95%	n+304 (+304), K+304 (+304)	33.11	25.47
6423	seq=translation; coord=1:5873406..5877213:1; parent_transcript=GRMZM2G105571_T01; parent_gene=GRMZM2G105571	GRMZM2G105571_P01,GRMZM2G105571_P02	TRUE	TRUE	dEGFVSLWR	89%	n+304 (+304)	26.56	25.00
6424	seq=translation; coord=3:59842989..59850482:-1; parent_transcript=GRMZM2G462140_T01; parent_gene=GRMZM2G462140	GRMZM2G462140_P01	TRUE	TRUE	sPFTSGIGLETLGVETDk	95%	n+304 (+304), K+304 (+304)	68.47	25.42
6425	seq=translation; coord=9:123408167..123411376:-1; parent_transcript=GRMZM2G124317_T01; parent_gene=GRMZM2G124317	GRMZM2G124317_P01,GRMZM2G124317_P02, GRMZM2G124317_P03,GRMZM2G124317_P07, GRMZM2G124317_P08,GRMZM2G124317_P09, GRMZM2G172244_P01,GRMZM2G172244_P02, GRMZM2G172244_P03	TRUE	TRUE	vHAAPGGSSSLGYLFGGN	95%	n+304 (+304)	33.97	25.12
6426	seq=translation; coord=9:123408167..123411376:-1; parent_transcript=GRMZM2G124317_T01; parent_gene=GRMZM2G124317	GRMZM2G124317_P01,GRMZM2G124317_P02, GRMZM2G124317_P03,GRMZM2G124317_P07, GRMZM2G124317_P08,GRMZM2G124317_P09, GRMZM2G172244_P01,GRMZM2G172244_P02, GRMZM2G172244_P03	TRUE	TRUE	vHAAPGGSSSLGYLFGGN	92%	n+304 (+304), iTRAQ8plex (+304)	26.28	25.38
6427	seq=translation; coord=4:172080242..172084381:1; parent_transcript=GRMZM2G075336_T01; parent_gene=GRMZM2G075336	GRMZM2G075336_P01,GRMZM2G075336_P02, GRMZM2G075336_P03	TRUE	TRUE	nLLSVVESWLR	95%	n+304 (+304)	39.15	25.28
6428	seq=translation; coord=5:179392458..179394688:1; parent_transcript=GRMZM2G003384_T01; parent_gene=GRMZM2G003384	GRMZM2G003384_P01	TRUE	TRUE	aVDAALik	95%	n+304 (+304), K+304 (+304)	42.78	26.07
6429	seq=translation; coord=1:41759285..41762638:-1; parent_transcript=GRMZM2G119886_T01; parent_gene=GRMZM2G119886	GRMZM2G119886_P01	TRUE	TRUE	eTPGSGAPAPAR	86%	n+304 (+304)	25.18	25.00
6430	seq=translation; coord=5:13048033..13051225:1; parent_transcript=AC213463.3_FGT007; parent_gene=AC213463.3_FG007	AC213463.3_FGP007,GRMZM2G038217_P01,G RMZM2G038217_P02,GRMZM2G389510_P01	TRUE	TRUE	gAISDLSGVQAK	95%	n+304 (+304), K+304 (+304)	75.27	25.33
6431	seq=translation; coord=6:162690848..162694219:1; parent_transcript=GRMZM2G017269_T01; parent_gene=GRMZM2G017269	GRMZM2G017269_P01,GRMZM2G095631_P01	TRUE	TRUE	IQELLEPLVPLIVk	95%	n+304 (+304), K+304 (+304)	39.05	25.00
6432	seq=translation; coord=2:156178938..156194571:-1; parent_transcript=GRMZM2G057910_T01; parent_gene=GRMZM2G057910	GRMZM2G057910_P01	TRUE	TRUE	dVAVLEAMLESSAk	95%	n+304 (+304), K+304 (+304)	38.53	26.23
6433	seq=translation; coord=2:3556786..3558729:1; parent_transcript=GRMZM2G062396_T01; parent_gene=GRMZM2G062396	GRMZM2G062396_P01	TRUE	TRUE	hTDPGTITLLQLVLGGQLQATR	95%	n+304 (+304)	32.30	25.00
6434	seq=translation; coord=4:63536096..63539819:-1; parent_transcript=GRMZM2G082087_T02; parent_gene=GRMZM2G082087	GRMZM2G082087_P02,GRMZM2G148281_P01, GRMZM2G148281_P02	TRUE	TRUE	gAIFFcQLWHVGR	95%	n+304 (+304), Carbamidomethyl (+57)	63.88	25.00

6435	seq=translation; coord=2:4624358..4637151:1; parent_transcript=GRMZM2G086489_T01; parent_gene=GRMZM2G086489 seq=translation; coord=1:7341979..7348599:1;	GRMZM2G086489_P01,GRMZM2G086489_P02, GRMZM2G104294_P01,GRMZM2G104294_P02	TRUE	TRUE	sLLEVMAAFPSAkPPLGVFFAAIAPR	95%	n+304 (+304), K+304 (+304)	31.32	25.00
6436	parent_transcript=GRMZM2G096020_T01; parent_gene=GRMZM2G096020 seq=translation; coord=5:9908227..9911250:-1;	GRMZM2G096020_P01,GRMZM2G096020_P02, GRMZM2G096020_P03	TRUE	TRUE	sLISMVQIIMSR	95%	n+304 (+304)	33.97	25.92
6437	parent_transcript=GRMZM2G096591_T01; parent_gene=GRMZM2G096591 seq=translation; coord=1:296260884..296265865:-1;	GRMZM2G096591_P01,GRMZM2G096591_P02	TRUE	TRUE	aFVSGLVSHLR	95%	n+304 (+304)	73.55	25.54
6438	parent_transcript=GRMZM2G113250_T01; parent_gene=GRMZM2G113250 seq=translation; coord=10:10551726..10552620:1;	GRMZM2G113250_P01	TRUE	TRUE	eQMIPLSEFEDkL	95%	n+304 (+304), K+304 (+304)	34.43	25.00
6439	parent_transcript=GRMZM2G132273_T01; parent_gene=GRMZM2G132273 seq=translation; coord=6:109829372..109834694:1;	GRMZM2G132273_P01,GRMZM2G320023_P01	TRUE	TRUE	eMAVVGGTGAFR	94%	n+304 (+304)	30.44	25.00
6440	parent_transcript=GRMZM2G136058_T01; parent_gene=GRMZM2G136058 seq=translation; coord=1:6546908..6550733:-1;	GRMZM2G136058_P01,GRMZM2G414569_P01	TRUE	TRUE	iEGVELELR	95%	n+304 (+304)	41.42	26.94
6441	parent_transcript=GRMZM2G137312_T01; parent_gene=GRMZM2G137312 seq=translation; coord=1:107185706..107188803:1;	GRMZM2G137312_P01	TRUE	TRUE	vAEFYLPWk	94%	n+304 (+304), K+304 (+304)	28.64	25.71
6442	parent_transcript=GRMZM2G144155_T01; parent_gene=GRMZM2G144155 seq=translation; coord=6:130597982..130600487:-1;	GRMZM2G144155_P01,GRMZM2G144155_P02, GRMZM2G144155_P03,GRMZM2G144155_P04	TRUE	TRUE	gIPAILGIISTQR	95%	n+304 (+304)	42.36	25.00
6443	parent_transcript=GRMZM2G149201_T01; parent_gene=GRMZM2G149201 seq=translation; coord=1:38008533..38011706:1;	GRMZM2G149201_P01	TRUE	TRUE	IVGAFFPAVVLELPALK	95%	n+304 (+304), K+304 (+304)	31.36	25.00
6444	parent_transcript=GRMZM2G151564_T01; parent_gene=GRMZM2G151564 seq=translation; coord=5:74616842..74620998:-1;	GRMZM2G151564_P01	TRUE	TRUE	gLSLLGLLR	95%	n+304 (+304)	33.17	25.00
6445	parent_transcript=GRMZM2G168762_T01; parent_gene=GRMZM2G168762 seq=translation; coord=2:30874561..30879119:-1;	GRMZM2G168762_P01	TRUE	TRUE	nMATLLAEFDk	94%	n+304 (+304), K+304 (+304)	28.49	25.58
6446	parent_transcript=GRMZM2G170101_T01; parent_gene=GRMZM2G170101 seq=translation; coord=2:233597234..233599119:1;	GRMZM2G170101_P01,GRMZM2G170101_P03	TRUE	TRUE	gFIFGPAIALAIGAk	95%	n+304 (+304), K+304 (+304)	39.40	25.00
6447	parent_transcript=GRMZM2G176394_T01; parent_gene=GRMZM2G176394 seq=translation; coord=6:157564314..157569386:1;	GRMZM2G176394_P01,GRMZM2G176394_P02, GRMZM2G176394_P03,GRMZM2G476294_P01	TRUE	TRUE	mAGTLAELVALNSGLR	95%	n+304 (+304)	50.48	25.99
6448	parent_transcript=GRMZM2G305115_T01; parent_gene=GRMZM2G305115 seq=translation; coord=2:164472793..164474499:-1;	GRMZM2G305115_P01,GRMZM2G305115_P03	TRUE	TRUE	fDDGWDSR	95%	n+304 (+304)	34.09	25.00
6449	parent_transcript=GRMZM2G341253_T01; parent_gene=GRMZM2G341253 seq=translation; coord=5:99408290..99409902:-1;	GRMZM2G341253_P01,GRMZM2G436404_P01	TRUE	TRUE	sVVADPDDLr	95%	n+304 (+304)	32.90	25.00
6450	parent_transcript=GRMZM2G417945_T01; parent_gene=GRMZM2G417945 seq=translation; coord=3:1295431..1296371:1;	GRMZM2G417945_P01	TRUE	TRUE	ILVDAlIAQFHTIDR	95%	n+304 (+304)	73.57	25.38
6451	parent_transcript=GRMZM5G860761_T02; parent_gene=GRMZM5G860761	GRMZM5G860761_P02	TRUE	TRUE	gGPcYYPDNLVSR	95%	n+304 (+304), Carbamidomethyl (+57)	36.87	25.00
6452	GRMZM2G155232_P01-R	GRMZM2G155232_P01- R,GRMZM2G301803_P03- R,GRMZM2G480712_P01-R	TRUE	TRUE	IEESLk	90%	n+304 (+304), K+304 (+304)	27.39	26.02

6453	seq=translation; coord=2:213386026..213389632:1; parent_transcript=GRMZM2G119675_T01; parent_gene=GRMZM2G119675 seq=translation; coord=2:197756965..197760720:1;	GRMZM2G119675_P01,GRMZM5G885744_P01, GRMZM5G885744_P02	TRUE	TRUE	tFDPWPVFFR	94%	n+304 (+304)	30.98	25.11
6454	parent_transcript=AC233910.1_FGT005; parent_gene=AC233910.1_FG005 seq=translation; coord=7:167230471..167241954:1;	AC233910.1_FGP005	TRUE	TRUE	IEVPDGAVFENK	95%	n+304 (+304), K+304 (+304)	31.06	25.93
6455	parent_transcript=GRMZM2G013811_T01; parent_gene=GRMZM2G013811 seq=translation; coord=7:33007300..33009101:-1;	GRMZM2G013811_P01	TRUE	TRUE	gPHGIGDLGDEALFLHWLR	95%	n+304 (+304)	66.62	25.09
6456	parent_transcript=GRMZM2G042692_T01; parent_gene=GRMZM2G042692 seq=translation; coord=3:29472800..29479329:1;	GRMZM2G042692_P01	TRUE	TRUE	IEGVGEVTVDSR	95%	n+304 (+304)	32.19	25.91
6457	parent_transcript=GRMZM2G051622_T01; parent_gene=GRMZM2G051622 seq=translation; coord=5:76624902..76632274:1;	GRMZM2G051622_P01	TRUE	TRUE	INTEESSIGLR	88%	n+304 (+304)	26.30	25.82
6458	parent_transcript=GRMZM2G054765_T01; parent_gene=GRMZM2G054765 seq=translation; coord=6:123603678..123607103:1;	GRMZM2G054765_P01	TRUE	TRUE	YLTEPAVAVILDVLR	95%	n+304 (+304)	52.16	25.00
6459	parent_transcript=GRMZM2G066612_T01; parent_gene=GRMZM2G066612 seq=translation; coord=2:124094006..124108029:-1;	GRMZM2G066612_P01,GRMZM2G159145_P01, GRMZM2G159145_P02	TRUE	TRUE	aTPTFFFLK	95%	n+304 (+304), K+304 (+304)	28.71	25.00
6460	parent_transcript=GRMZM2G075680_T01; parent_gene=GRMZM2G075680 seq=translation; coord=10:145183272..145197508:1;	GRMZM2G075680_P01	TRUE	TRUE	eSSVIYETR	95%	n+304 (+304)	30.96	25.08
6461	parent_transcript=GRMZM2G086030_T01; parent_gene=GRMZM2G086030 seq=translation; coord=5:5616049..5616896:-1;	GRMZM2G086030_P01	TRUE	TRUE	aFLHNLVFDTAIFR	95%	n+304 (+304)	30.67	25.85
6462	parent_transcript=GRMZM2G091535_T02; parent_gene=GRMZM2G091535 seq=translation; coord=5:50092687..50097671:-1;	GRMZM2G091535_P02	TRUE	TRUE	mVTPAPVAMTDPPGALEK	95%	n+304 (+304), K+304 (+304)	36.62	25.26
6463	parent_transcript=GRMZM2G113613_T01; parent_gene=GRMZM2G113613 seq=translation; coord=1:277843773..277846597:-1;	GRMZM2G113613_P01	TRUE	TRUE	rDDLSSLNPPVMEGLDALLAK	95%	n+304 (+304), K+304 (+304)	41.04	25.56
6464	parent_transcript=GRMZM2G123714_T01; parent_gene=GRMZM2G123714 seq=translation; coord=8:91831315..91844753:1;	GRMZM2G123714_P01,GRMZM2G123714_P02	TRUE	TRUE	sDLADSALQK	95%	n+304 (+304), K+304 (+304)	31.95	25.47
6465	parent_transcript=GRMZM2G124455_T01; parent_gene=GRMZM2G124455 seq=translation; coord=2:47422297..47424522:1;	GRMZM2G124455_P01	TRUE	TRUE	aLEQLDAAVAK	95%	n+304 (+304), K+304 (+304)	34.18	25.16
6466	parent_transcript=GRMZM2G151021_T01; parent_gene=GRMZM2G151021 seq=translation; coord=8:128348231..128358933:-1;	GRMZM2G151021_P01,GRMZM2G166484_P01	TRUE	TRUE	vAAQPQLVLAR	95%	n+304 (+304)	38.43	25.00
6467	parent_transcript=GRMZM2G170798_T01; parent_gene=GRMZM2G170798 seq=translation; coord=9:15978102..15983381:1;	GRMZM2G170798_P01	TRUE	TRUE	aIEGEGAI AVLDTAAGVWLDR	95%	n+304 (+304)	39.14	25.61
6468	parent_transcript=GRMZM2G304362_T01; parent_gene=GRMZM2G304362 seq=translation; coord=1:101830081..101832342:-1;	GRMZM2G304362_P01	TRUE	TRUE	sGLMAPLVAEDVYEIMK	95%	n+304 (+304), K+304 (+304)	43.61	25.93
6469	parent_transcript=GRMZM2G456626_T01; parent_gene=GRMZM2G456626 seq=translation; coord=8:143006137..143009764:-1;	GRMZM2G456626_P01	TRUE	TRUE	sLEDVAVPPAAFINQIAGGLR	95%	n+304 (+304)	66.26	26.20
6470	parent_transcript=GRMZM5G803433_T01; parent_gene=GRMZM5G803433	GRMZM5G803433_P01	TRUE	TRUE	dQLADIAAAALVSAHALDAVR	95%	n+304 (+304)	88.15	25.60

6471	seq=translation; coord=1:194570543..194573682:-1; parent_transcript=GRMZM2G136534_T01; parent_gene=GRMZM2G136534 seq=translation; coord=4:198078696..198080533:-1;	GRMZM2G136534_P01,GRMZM2G136534_P03	TRUE	TRUE	dScPGLESIVR	90%	n+304 (+304), Carbamidomethyl (+57)	27.08	25.00
6472	parent_transcript=GRMZM2G332522_T01; parent_gene=GRMZM2G332522 seq=translation; coord=7:55631624..55634493:-1;	GRMZM2G332522_P01,GRMZM2G332522_P02	TRUE	TRUE	vIAFDVSR	89%	n+304 (+304)	27.00	25.00
6473	parent_transcript=GRMZM2G058484_T01; parent_gene=GRMZM2G058484 GRMZM2G322723_P02-R	GRMZM2G058484_P01,GRMZM2G058484_P02, GRMZM2G058484_P03,GRMZM2G058484_P04	TRUE	TRUE	qMISIik	87%	Pyro-cmC (-17), n+304 (+304), K+304 (+304)	27.15	26.64
6474	GRMZM2G022787_P01-R	GRMZM2G022787_P01-R	TRUE	TRUE	ILAPDEEGk	88%	n+304 (+304), K+304 (+304)	25.54	25.00
6475	seq=translation; coord=7:110983097..110986540:-1;	GRMZM2G022787_P01-R	TRUE	TRUE	eLLEGVR	87%	n+304 (+304)	25.12	25.00
6476	parent_transcript=GRMZM2G048277_T01; parent_gene=GRMZM2G048277 seq=translation; coord=7:110983097..110986540:-1;	GRMZM2G048277_P01,GRMZM2G048277_P02, GRMZM2G048277_P03	TRUE	TRUE	kGGDLGWFP	95%	K+304 (+304), n+304 (+304)	28.78	26.47
6477	parent_transcript=GRMZM2G048277_T01; parent_gene=GRMZM2G048277 seq=translation; coord=7:110983097..110986540:-1;	GRMZM2G048277_P01,GRMZM2G048277_P02, GRMZM2G048277_P03	TRUE	TRUE	mAGPFQEVAFNTPEGTVSAPFk	95%	n+304 (+304), K+304 (+304)	30.67	25.00
6478	parent_transcript=GRMZM2G048277_T01; parent_gene=GRMZM2G048277 seq=translation; coord=8:42281387..42289748:-1;	GRMZM2G048277_P01,GRMZM2G048277_P02, GRMZM2G048277_P03	TRUE	TRUE	sADGLGTcTYV	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	65.77	25.00
6479	parent_transcript=GRMZM2G145595_T01; parent_gene=GRMZM2G145595 seq=translation; coord=8:42281387..42289748:-1;	GRMZM2G145595_P01	TRUE	TRUE	aLGVDILTIGITIVGk	95%	n+304 (+304), K+304 (+304)	44.02	25.00
6480	parent_transcript=GRMZM2G145595_T01; parent_gene=GRMZM2G145595 seq=translation; coord=10:107762378..107767126:1;	GRMZM2G145595_P01	TRUE	TRUE	vGFDPNEITAR	95%	n+304 (+304)	37.70	25.00
6481	parent_transcript=GRMZM2G028945_T01; parent_gene=GRMZM2G028945 seq=translation; coord=10:107762378..107767126:1;	GRMZM2G028945_P01,GRMZM2G104649_P03, GRMZM2G104649_P04	TRUE	TRUE	ISWVDIFEEIPIk	95%	n+304 (+304), K+304 (+304)	39.15	25.92
6482	parent_transcript=GRMZM2G028945_T01; parent_gene=GRMZM2G028945	GRMZM2G028945_P01,GRMZM2G104649_P03, GRMZM2G104649_P04	TRUE	TRUE	vVQMEGLAVLk	95%	n+304 (+304), K+304 (+304)	33.57	25.00
6483	seq=translation; coord=1:31242217..31244585:-1; parent_transcript=GRMZM2G116846_T01; parent_gene=GRMZM2G116846	GRMZM2G116846_P01	TRUE	TRUE	aALEEAcPGVVScADILAI	93%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	27.49	25.39
6484	seq=translation; coord=1:31242217..31244585:-1; parent_transcript=GRMZM2G116846_T01; parent_gene=GRMZM2G116846 seq=translation; coord=1:31242217..31244585:-1;	GRMZM2G116846_P01	TRUE	TRUE	fGAVGLDDTDLVALSGAHTFGR	95%	n+304 (+304)	76.00	25.00
6485	parent_transcript=GRMZM2G116846_T01; parent_gene=GRMZM2G116846 seq=translation; coord=1:292354165..292360031:-1;	GRMZM2G116846_P01	TRUE	TRUE	rGTLQSDQELLSTPGAPTAPIVGR	95%	n+304 (+304)	29.14	25.00
6486	parent_transcript=GRMZM2G151967_T01; parent_gene=GRMZM2G151967 seq=translation; coord=1:292354165..292360031:-1;	GRMZM2G151967_P01	TRUE	TRUE	aSASAVAFGLGSLGk	95%	n+304 (+304), K+304 (+304)	39.46	25.00
6487	parent_transcript=GRMZM2G151967_T01; parent_gene=GRMZM2G151967 seq=translation; coord=1:292354165..292360031:-1;	GRMZM2G151967_P01	TRUE	TRUE	dVVQSMEEAIIR	88%	n+304 (+304)	27.67	26.22
6488	parent_transcript=GRMZM2G151967_T01; parent_gene=GRMZM2G151967 seq=translation; coord=2:110482584..110497021:-1;	GRMZM2G151967_P01	TRUE	TRUE	vSSFFLGLLSQk	95%	n+304 (+304), K+304 (+304)	30.46	25.17
6489	parent_transcript=GRMZM2G081745_T01; parent_gene=GRMZM2G081745	GRMZM2G081745_P01,GRMZM2G081745_P03, GRMZM2G143725_P01,GRMZM2G143725_P02	TRUE	TRUE	fLPLYILAick	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.12	25.00

6490	seq=translation; coord=2:110482584..110497021:-1; parent_transcript=GRMZM2G081745_T01; parent_gene=GRMZM2G081745 seq=translation; coord=1:287631317..287634834:1;	GRMZM2G081745_P01,GRMZM2G081745_P03, GRMZM2G143725_P01,GRMZM2G143725_P02	TRUE	TRUE	gGYADVSLDER	94%	n+304 (+304)	31.02	25.00
6491	parent_transcript=GRMZM2G052471_T01; parent_gene=GRMZM2G052471 seq=translation; coord=3:35659936..35665816:1;	GRMZM2G052471_P01,GRMZM2G099474_P01	TRUE	TRUE	gPEEEGPK	94%	n+304 (+304), K+304 (+304)	29.28	25.90
6492	parent_transcript=GRMZM2G091119_T01; parent_gene=GRMZM2G091119 seq=translation; coord=3:35659936..35665816:1;	GRMZM2G091119_P01	TRUE	TRUE	tMGATGGINVFAQMIDDAEGLEK	95%	n+304 (+304), K+304 (+304)	72.43	25.00
6493	parent_transcript=GRMZM2G091119_T01; parent_gene=GRMZM2G091119 seq=translation; coord=2:197623496..197625443:1;	GRMZM2G091119_P01	TRUE	TRUE	tVGNIVTGDDQQTQcIIDHQALPR	95%	n+304 (+304), Carbamidomethyl (+57)	98.16	25.00
6494	parent_transcript=GRMZM2G162284_T01; parent_gene=GRMZM2G162284 seq=translation; coord=1:17933389..17954778:-1;	GRMZM2G162284_P01,GRMZM2G162284_P02, GRMZM2G162284_P03	TRUE	TRUE	rPPTAFFVFMEEFR	95%	n+304 (+304)	51.59	25.00
6495	parent_transcript=GRMZM2G059020_T01; parent_gene=GRMZM2G059020 seq=translation; coord=1:17933389..17954778:-1;	GRMZM2G059020_P01	TRUE	TRUE	iLIFFQTK	94%	n+304 (+304), K+304 (+304)	27.97	25.00
6496	parent_transcript=GRMZM2G059020_T01; parent_gene=GRMZM2G059020 seq=translation; coord=2:203135392..203142289:1;	GRMZM2G059020_P01	TRUE	TRUE	tVMVVELIK	95%	n+304 (+304), K+304 (+304)	39.28	25.00
6497	parent_transcript=GRMZM2G001820_T01; parent_gene=GRMZM2G001820 seq=translation; coord=2:177496379..177510526:-1;	GRMZM2G001820_P01	TRUE	TRUE	eLLLFYK	95%	n+304 (+304), K+304 (+304)	27.74	25.00
6498	parent_transcript=GRMZM2G034848_T01; parent_gene=GRMZM2G034848 seq=translation; coord=2:177496379..177510526:-1;	GRMZM2G034848_P01	TRUE	TRUE	iGMDVAASEFLTK	92%	n+304 (+304), K+304 (+304)	27.55	25.75
6499	parent_transcript=GRMZM2G034848_T01; parent_gene=GRMZM2G034848 seq=translation; coord=1:205410478..205412879:1;	GRMZM2G034848_P01	TRUE	TRUE	sGETEDNFIADLAVGLASGQIK	95%	n+304 (+304), K+304 (+304)	35.74	26.03
6500	parent_transcript=GRMZM2G158462_T01; parent_gene=GRMZM2G158462 seq=translation; coord=7:4538433..4546019:1;	GRMZM2G158462_P01	TRUE	TRUE	eELDDAISALDQGQLDGRPLR	90%	n+304 (+304)	25.36	25.00
6501	parent_transcript=GRMZM2G480002_T01; parent_gene=GRMZM2G480002 seq=translation; coord=7:4538433..4546019:1;	GRMZM2G480002_P01	TRUE	TRUE	hDLTDDTEELFWGSPiR	95%	n+304 (+304)	32.29	25.00
6502	parent_transcript=GRMZM2G480002_T01; parent_gene=GRMZM2G480002 seq=translation; coord=5:21571290..21578409:-1;	GRMZM2G480002_P01	TRUE	TRUE	yTSVPSDDSTSLGFR	95%	n+304 (+304)	40.85	25.00
6503	parent_transcript=GRMZM2G073934_T01; parent_gene=GRMZM2G073934 seq=translation; coord=5:21571290..21578409:-1;	GRMZM2G073934_P01	TRUE	TRUE	dALLEEAck	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	28.85	25.25
6504	parent_transcript=GRMZM2G073934_T01; parent_gene=GRMZM2G073934 seq=translation; coord=4:194340222..194342295:-1;	GRMZM2G073934_P01	TRUE	TRUE	sMLPLPYLk	95%	n+304 (+304), K+304 (+304)	36.40	25.00
6505	parent_transcript=AC190609.3_FGT002; parent_gene=AC190609.3_FG002	AC190609.3_FGP002,GRMZM2G069594_P01,G RMZM2G069594_P02,GRMZM2G069594_P03,G RMZM2G069594_P04,GRMZM2G069594_P06	TRUE	TRUE	dLLTAR	95%	n+304 (+304)	33.65	25.00
6506	seq=translation; coord=4:194340222..194342295:-1; parent_transcript=AC190609.3_FGT002; parent_gene=AC190609.3_FG002	AC190609.3_FGP002,GRMZM2G069594_P01,G RMZM2G069594_P02,GRMZM2G069594_P03,G RMZM2G069594_P04,GRMZM2G069594_P06	TRUE	TRUE	yLYTLcVFDAEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.63	25.05

6507	seq=translation; coord=2:63944481..63944981:-1; parent_transcript=AC196489.3_FGT002; parent_gene=AC196489.3_FG002 seq=translation; coord=1:63573932..63578006:1;	AC196489.3_FGP002	TRUE	TRUE	hSGNIGLDDVVEIAR	95%	n+304 (+304)	81.69	25.80
6508	parent_transcript=AC216247.3_FGT005; parent_gene=AC216247.3_FG005 seq=translation; coord=5:82556313..82561535:-1;	AC216247.3_FGP005,GRMZM2G117746_P01	TRUE	TRUE	mILGFAEGFPTMLk	95%	n+304 (+304), K+304 (+304)	37.98	25.50
6509	parent_transcript=GRMZM2G006144_T01; parent_gene=GRMZM2G006144	GRMZM2G006144_P01	TRUE	TRUE	nMVEFFDLLLSPASk	95%	n+304 (+304), K+304 (+304)	36.76	25.60
6510	seq=translation; coord=8:145082985..145087859:1; parent_transcript=GRMZM2G025387_T01; parent_gene=GRMZM2G025387	GRMZM2G025387_P01,GRMZM2G025387_P02, GRMZM2G058305_P01,GRMZM2G058305_P02, GRMZM5G856738_P01,GRMZM5G856738_P02, GRMZM5G856738_P03 GRMZM2G025387_P01,GRMZM2G025387_P02,	TRUE	TRUE	eIIAEVDTDHDGR	95%	n+304 (+304)	53.28	25.00
6511	seq=translation; coord=8:145082985..145087859:1; parent_transcript=GRMZM2G025387_T01; parent_gene=GRMZM2G025387	GRMZM2G058305_P01,GRMZM2G058305_P02, GRMZM5G856738_P01,GRMZM5G856738_P02, GRMZM5G856738_P03 GRMZM2G041694_P01,GRMZM2G041694_P02,	TRUE	TRUE	ITAAEILNHPWIR	95%	n+304 (+304)	70.26	26.12
6512	seq=translation; coord=6:162486424..162491946:-1; parent_transcript=GRMZM2G041694_T01; parent_gene=GRMZM2G041694 seq=translation; coord=8:1141430..1145642:1;	GRMZM2G041694_P01,GRMZM2G109743_P01, GRMZM2G109743_P02	TRUE	TRUE	aSILLIQDAAPHLR	95%	n+304 (+304)	33.49	26.38
6513	parent_transcript=GRMZM2G063244_T01; parent_gene=GRMZM2G063244 seq=translation; coord=1:287818241..287821189:-1;	GRMZM2G063244_P01,GRMZM2G167521_P01, GRMZM2G393515_P01,GRMZM2G398275_P01	TRUE	TRUE	iVIGLGEVVPk	95%	n+304 (+304), K+304 (+304)	38.05	25.00
6514	parent_transcript=GRMZM2G068952_T01; parent_gene=GRMZM2G068952 seq=translation; coord=3:225893665..225898677:-1;	GRMZM2G068952_P01	TRUE	TRUE	fVIWTEcAFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	38.02	26.00
6515	parent_transcript=GRMZM2G090647_T01; parent_gene=GRMZM2G090647 seq=translation; coord=8:117297233..117299896:1;	GRMZM2G090647_P01,GRMZM2G090647_P02, GRMZM2G090647_P03,GRMZM2G090647_P05, GRMZM2G090647_P06	TRUE	TRUE	sISVVGADGTSPSR	95%	n+304 (+304)	55.57	25.00
6516	parent_transcript=GRMZM2G095905_T01; parent_gene=GRMZM2G095905 seq=translation; coord=4:143082898..143087846:-1;	GRMZM2G095905_P01	TRUE	TRUE	gGFQVADLVWGk	95%	n+304 (+304), K+304 (+304)	56.04	26.21
6517	parent_transcript=GRMZM2G135132_T01; parent_gene=GRMZM2G135132 seq=translation; coord=10:149089396..149092794:1;	GRMZM2G135132_P01	TRUE	TRUE	gWETENVEEIALk	95%	n+304 (+304), K+304 (+304)	39.86	26.09
6518	parent_transcript=GRMZM2G136283_T01; parent_gene=GRMZM2G136283 seq=translation; coord=1:189637097..189642534:-1;	GRMZM2G136283_P01	TRUE	TRUE	eFIADVDDFAHk	95%	n+304 (+304), K+304 (+304)	61.02	25.95
6519	parent_transcript=GRMZM2G141784_T01; parent_gene=GRMZM2G141784 seq=translation; coord=10:148424594..148425826:-1;	GRMZM2G141784_P01,GRMZM2G141784_P02	TRUE	TRUE	INVADIEATLSHvcQMVLQDSSAR	95%	n+304 (+304), Carbamidomethyl (+57)	44.23	25.00
6520	parent_transcript=GRMZM2G142802_T01; parent_gene=GRMZM2G142802 seq=translation; coord=10:148424594..148425826:-1;	GRMZM2G142802_P01	TRUE	TRUE	dLAGAFVVFVDSR	95%	n+304 (+304)	33.55	25.37
6521	parent_transcript=GRMZM2G142802_T01; parent_gene=GRMZM2G142802 seq=translation; coord=8:112147822..112150640:-1;	GRMZM2G142802_P01	TRUE	TRUE	mFcGLDHIYcVFLGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	35.65	25.00
6522	parent_transcript=GRMZM2G153569_T01; parent_gene=GRMZM2G153569 seq=translation; coord=9:44480056..44486772:-1;	GRMZM2G153569_P01,GRMZM2G153569_P02, GRMZM2G153569_P03	TRUE	TRUE	wFNHIDALLR	95%	n+304 (+304)	49.96	27.01
6523	parent_transcript=GRMZM2G158595_T01; parent_gene=GRMZM2G158595	GRMZM2G158595_P01,GRMZM2G158595_P02	TRUE	TRUE	IVAWSDSVADLLDLHK	95%	n+304 (+304), K+304 (+304)	39.76	25.19

6524	seq=translation; coord=6:162189576..162190621:1; parent_transcript=GRMZM2G174906_T01; parent_gene=GRMZM2G174906	GRMZM2G174906_P01,GRMZM2G174906_P02	TRUE	TRUE	IHNLADEMEALR	95%	n+304 (+304)	47.34	25.00
6525	seq=translation; coord=4:37569961..37571464:1; parent_transcript=GRMZM2G324643_T01; parent_gene=GRMZM2G324643	GRMZM2G324643_P01,GRMZM2G324643_P02	TRUE	TRUE	dLTEEQIASMR	95%	n+304 (+304)	46.16	25.00
6526	seq=translation; coord=4:37569961..37571464:1; parent_transcript=GRMZM2G324643_T01; parent_gene=GRMZM2G324643	GRMZM2G324643_P01,GRMZM2G324643_P02	TRUE	TRUE	IEVHEFDEWIR	95%	n+304 (+304)	55.81	25.00
6527	seq=translation; coord=6:129879767..129880816:-1; parent_transcript=GRMZM2G441656_T01; parent_gene=GRMZM2G441656	GRMZM2G441656_P01	TRUE	TRUE	sASGMSGDPK	95%	n+304 (+304), K+304 (+304)	30.73	25.00
6528	seq=translation; coord=5:211975266..211979302:1; parent_transcript=GRMZM5G801436_T01; parent_gene=GRMZM5G801436	GRMZM5G801436_P01	TRUE	TRUE	iSPAFVLFFDcSEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	61.55	25.95
6529	seq=translation; coord=1:22937896..22938573:-1; parent_transcript=GRMZM5G863656_T01; parent_gene=GRMZM5G863656	GRMZM5G863656_P01	TRUE	TRUE	IERPVEGDEAMQEVAABE	95%	n+304 (+304)	44.39	25.00
6530	seq=translation; coord=2:230286713..230300365:-1; parent_transcript=GRMZM2G131443_T01; parent_gene=GRMZM2G131443	GRMZM2G131443_P01,GRMZM2G131443_P02, GRMZM2G131443_P03	TRUE	TRUE	iSPIVDMMTLLK	95%	n+304 (+304), K+304 (+304)	29.36	25.24
6531	seq=translation; coord=6:137824502..137828918:-1; parent_transcript=GRMZM2G170365_T01; parent_gene=GRMZM2G170365	GRMZM2G170365_P01,GRMZM2G170365_P02, GRMZM2G170365_P03,GRMZM2G170365_P04	TRUE	TRUE	aGDVcFTDVYR	95%	n+304 (+304), Carbamidomethyl (+57)	42.51	25.00
6532	seq=translation; coord=1:298331067..298333316:1; parent_transcript=GRMZM2G023242_T01; parent_gene=GRMZM2G023242	GRMZM2G023242_P01,GRMZM2G023242_P03, GRMZM2G023242_P04	TRUE	TRUE	dDLVIQFLNPK	95%	n+304 (+304), K+304 (+304)	49.71	25.99
6533	seq=translation; coord=1:298331067..298333316:1; parent_transcript=GRMZM2G023242_T01; parent_gene=GRMZM2G023242	GRMZM2G023242_P01,GRMZM2G023242_P03, GRMZM2G023242_P04	TRUE	TRUE	IQDVLPGIINQLGPDNMEHLK	95%	n+304 (+304), K+304 (+304)	30.50	25.31
6534	seq=translation; coord=1:298331067..298333316:1; parent_transcript=GRMZM2G023242_T01; parent_gene=GRMZM2G023242	GRMZM2G023242_P01,GRMZM2G023242_P03, GRMZM2G023242_P04	TRUE	TRUE	vQASIAANTWVVGSPQTK	95%	n+304 (+304), K+304 (+304)	33.92	25.60
6535	seq=translation; coord=2:25913684..25932129:1; parent_transcript=GRMZM2G376731_T01; parent_gene=GRMZM2G376731	GRMZM2G376731_P01	TRUE	TRUE	iLyDALGTLADAVGAELNQAK	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	40.76	25.00
6536	seq=translation; coord=2:25913684..25932129:1; parent_transcript=GRMZM2G376731_T01; parent_gene=GRMZM2G376731	GRMZM2G376731_P01	TRUE	TRUE	IQEFLTVAak	93%	n+304 (+304), K+304 (+304)	26.83	25.00
6537	seq=translation; coord=2:25913684..25932129:1; parent_transcript=GRMZM2G376731_T01; parent_gene=GRMZM2G376731	GRMZM2G376731_P01	TRUE	TRUE	vAGWIELFQALHK	94%	n+304 (+304), K+304 (+304)	25.05	25.00
6538	seq=translation; coord=5:14176514..14178456:-1; parent_transcript=GRMZM5G858249_T01; parent_gene=GRMZM5G858249	GRMZM5G858249_P01	TRUE	TRUE	aHAAYAVNQLYQAAGR	89%	n+304 (+304)	25.06	25.00
6539	seq=translation; coord=5:14176514..14178456:-1; parent_transcript=GRMZM5G858249_T01; parent_gene=GRMZM5G858249	GRMZM5G858249_P01	TRUE	TRUE	aSATLTSDDPsYGACvYTGgGQ	95%	n+304 (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)	34.15	25.00
6540	seq=translation; coord=5:14176514..14178456:-1; parent_transcript=GRMZM5G858249_T01; parent_gene=GRMZM5G858249	GRMZM5G858249_P01	TRUE	TRUE	hPWNcDFR	95%	n+304 (+304), Carbamidomethyl (+57)	31.51	25.00
6541	seq=translation; coord=3:135084015..135105483:1; parent_transcript=GRMZM2G326116_T01; parent_gene=GRMZM2G326116	GRMZM2G326116_P01	TRUE	TRUE	fIPSEFGMDPSK	95%	n+304 (+304), K+304 (+304)	30.59	25.33

6542	seq=translation; coord=3:135084015..135105483:1; parent_transcript=GRMZM2G326116_T01; parent_gene=GRMZM2G326116 seq=translation; coord=5:145524164..145526605:-1;	GRMZM2G326116_P01	TRUE	TRUE	iHIPADEFLASMK	95%	n+304 (+304), K+304 (+304)	29.18	26.17
6543	parent_transcript=GRMZM2G405459_T01; parent_gene=GRMZM2G405459 seq=translation; coord=6:110695290..110707260:1;	GRMZM2G405459_P01,GRMZM2G405459_P02	TRUE	TRUE	sQVEAAcPGTVScADILALAAR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	36.78	25.00
6544	parent_transcript=GRMZM2G412611_T01; parent_gene=GRMZM2G412611 seq=translation; coord=6:110695290..110707260:1;	GRMZM2G412611_P01	TRUE	TRUE	aPEAPESDESK	95%	n+304 (+304), K+304 (+304)	36.17	25.00
6545	parent_transcript=GRMZM2G412611_T01; parent_gene=GRMZM2G412611 seq=translation; coord=3:1767353..1776209:-1;	GRMZM2G412611_P01	TRUE	TRUE	iEIDDPGVHAEFLIFDETQNK	95%	n+304 (+304), K+304 (+304)	27.20	25.59
6546	parent_transcript=GRMZM2G123499_T01; parent_gene=GRMZM2G123499 seq=translation; coord=3:1767353..1776209:-1;	GRMZM2G123499_P01,GRMZM2G123499_P02	TRUE	TRUE	dALQIFFAEASK	94%	n+304 (+304), K+304 (+304)	28.59	25.43
6547	parent_transcript=GRMZM2G123499_T01; parent_gene=GRMZM2G123499 seq=translation; coord=6:47529651..47533455:-1;	GRMZM2G123499_P01,GRMZM2G123499_P02	TRUE	TRUE	sFLSELSEVVGIGSASIK	95%	n+304 (+304), K+304 (+304)	35.23	25.17
6548	parent_transcript=GRMZM2G017671_T01; parent_gene=GRMZM2G017671 seq=translation; coord=1:122162499..122163689:1;	GRMZM2G017671_P01,GRMZM2G017671_P03	TRUE	TRUE	dLTAAELVSELWNAGIK	95%	n+304 (+304), K+304 (+304)	47.59	25.00
6549	parent_transcript=AC202185.4_FGT004; parent_gene=AC202185.4_FG004 seq=translation; coord=1:122162499..122163689:1;	AC202185.4_FGP004	TRUE	TRUE	sPAGGGVAEYGSQSQQSR	95%	n+304 (+304)	36.80	25.00
6550	parent_transcript=AC202185.4_FGT004; parent_gene=AC202185.4_FG004 seq=translation; coord=2:71785920..71790206:-1;	AC202185.4_FGP004	TRUE	TRUE	tDLHPFNIPAFVLVHPVAPR	95%	n+304 (+304)	32.01	25.59
6551	parent_transcript=GRMZM2G000980_T01; parent_gene=GRMZM2G000980 seq=translation; coord=2:71785920..71790206:-1;	GRMZM2G000980_P01,GRMZM2G034313_P01	TRUE	TRUE	dFAAEMDPEVHALNAR	95%	n+304 (+304)	48.65	25.00
6552	parent_transcript=GRMZM2G000980_T01; parent_gene=GRMZM2G000980 seq=translation; coord=5:17058108..17064678:1;	GRMZM2G000980_P01,GRMZM2G034313_P01	TRUE	TRUE	eYPGYNFIGLIIGPR	95%	n+304 (+304)	43.06	25.84
6553	parent_transcript=GRMZM2G018943_T01; parent_gene=GRMZM2G018943 seq=translation; coord=5:17058108..17064678:1;	GRMZM2G018943_P01,GRMZM2G018943_P02	TRUE	TRUE	dVPQAASTLASEK	95%	n+304 (+304), K+304 (+304)	39.22	25.85
6554	parent_transcript=GRMZM2G018943_T01; parent_gene=GRMZM2G018943 seq=translation; coord=6:112137413..112140985:1;	GRMZM2G018943_P01,GRMZM2G018943_P02	TRUE	TRUE	IDIVSEIGDDDSWSR	95%	n+304 (+304)	52.64	25.00
6555	parent_transcript=GRMZM2G064993_T01; parent_gene=GRMZM2G064993 seq=translation; coord=6:112137413..112140985:1;	GRMZM2G064993_P01	TRUE	TRUE	aYAEAYGEELLR	95%	n+304 (+304)	51.11	25.00
6556	parent_transcript=GRMZM2G064993_T01; parent_gene=GRMZM2G064993 seq=translation; coord=5:59290440..59291930:-1;	GRMZM2G064993_P01	TRUE	TRUE	sITDEISGDFER	95%	n+304 (+304)	43.51	25.00
6557	parent_transcript=GRMZM2G084942_T01; parent_gene=GRMZM2G084942 seq=translation; coord=5:59290440..59291930:-1;	GRMZM2G084942_P01,GRMZM2G084942_P02	TRUE	TRUE	aDAFLNIFER	95%	n+304 (+304)	35.95	25.00
6558	parent_transcript=GRMZM2G084942_T01; parent_gene=GRMZM2G084942 seq=translation; coord=5:209693887..209699045:1;	GRMZM2G084942_P01,GRMZM2G084942_P02	TRUE	TRUE	IFDGLHDVLR	95%	n+304 (+304)	51.05	25.58
6559	parent_transcript=GRMZM2G101463_T01; parent_gene=GRMZM2G101463	GRMZM2G101463_P01	TRUE	TRUE	aILGDAFDVGMK	95%	n+304 (+304), K+304 (+304)	50.51	26.47

6560	seq=translation; coord=5:209693887..209699045:1; parent_transcript=GRMZM2G101463_T01; parent_gene=GRMZM2G101463 seq=translation; coord=3:184059147..184065670:1;	GRMZM2G101463_P01	TRUE	TRUE	gSPEAQLVA AISPEGASK	95%	n+304 (+304), K+304 (+304)	41.26	25.00
6561	parent_transcript=GRMZM2G118363_T01; parent_gene=GRMZM2G118363 seq=translation; coord=3:184059147..184065670:1;	GRMZM2G118363_P01	TRUE	TRUE	iLLLLDSWQEAFGGPGSK	95%	n+304 (+304), K+304 (+304)	34.64	25.00
6562	parent_transcript=GRMZM2G118363_T01; parent_gene=GRMZM2G118363 seq=translation; coord=9:140970479..140979075:-1;	GRMZM2G118363_P01	TRUE	TRUE	nVTDLLNDMVYALNPSPDR	95%	n+304 (+304)	41.22	25.00
6563	parent_transcript=GRMZM2G119627_T01; parent_gene=GRMZM2G119627 seq=translation; coord=9:140970479..140979075:-1;	GRMZM2G119627_P01	TRUE	TRUE	aGDLTIADVESLLNSYK	95%	n+304 (+304), K+304 (+304)	42.60	25.07
6564	parent_transcript=GRMZM2G119627_T01; parent_gene=GRMZM2G119627 seq=translation; coord=6:111182254..111183500:-1;	GRMZM2G119627_P01	TRUE	TRUE	aPDPEkDSTAIQEFLENMEGAFR	95%	n+304 (+304), K+304 (+304)	31.34	25.00
6565	parent_transcript=GRMZM2G122302_T01; parent_gene=GRMZM2G122302 seq=translation; coord=6:111182254..111183500:-1;	GRMZM2G122302_P01	TRUE	TRUE	vGDSLEfk	95%	n+304 (+304), K+304 (+304)	35.56	26.28
6566	parent_transcript=GRMZM2G122302_T01; parent_gene=GRMZM2G122302 seq=translation; coord=8:85844666..85847518:-1;	GRMZM2G122302_P01	TRUE	TRUE	yTVGDASGWTTTGDYATWASGK	95%	n+304 (+304), K+304 (+304)	34.83	25.00
6567	parent_transcript=GRMZM2G132130_T01; parent_gene=GRMZM2G132130 seq=translation; coord=8:85844666..85847518:-1;	GRMZM2G132130_P01	TRUE	TRUE	fSVVFGSLLSER	95%	n+304 (+304)	54.84	26.35
6568	parent_transcript=GRMZM2G132130_T01; parent_gene=GRMZM2G132130	GRMZM2G132130_P01	TRUE	TRUE	vFAHAAPIFFER	95%	n+304 (+304)	61.70	26.10
6569	seq=translation; coord=1:256071969..256085112:1; parent_transcript=GRMZM2G150772_T02; parent_gene=GRMZM2G150772	GRMZM2G150772_P02	TRUE	TRUE	fSALSAPGcVlcGMGSik	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	39.03	25.21
6570	seq=translation; coord=1:256071969..256085112:1; parent_transcript=GRMZM2G150772_T02; parent_gene=GRMZM2G150772 seq=translation; coord=6:111253708..111260162:-1;	GRMZM2G150772_P02	TRUE	TRUE	iAVALLQEIAR	95%	n+304 (+304)	33.57	25.00
6571	parent_transcript=GRMZM2G329306_T01; parent_gene=GRMZM2G329306 seq=translation; coord=6:111253708..111260162:-1;	GRMZM2G329306_P01	TRUE	TRUE	fEDENFVLK	95%	n+304 (+304), K+304 (+304)	36.00	26.60
6572	parent_transcript=GRMZM2G329306_T01; parent_gene=GRMZM2G329306 seq=translation; coord=10:136292132..136296887:1;	GRMZM2G329306_P01	TRUE	TRUE	IGDSSGALLDADFALR	95%	n+304 (+304)	47.57	25.50
6573	parent_transcript=GRMZM2G414915_T01; parent_gene=GRMZM2G414915 seq=translation; coord=10:136292132..136296887:1;	GRMZM2G414915_P01	TRUE	TRUE	IGIRSPVVAAAFSSR	95%	n+304 (+304)	31.96	25.40
6574	parent_transcript=GRMZM2G414915_T01; parent_gene=GRMZM2G414915 seq=translation; coord=6:140865431..140872714:-1;	GRMZM2G414915_P01	TRUE	TRUE	sLcLEGLQPHEVAGK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	42.04	25.35
6575	parent_transcript=GRMZM2G442057_T01; parent_gene=GRMZM2G442057 seq=translation; coord=6:140865431..140872714:-1;	GRMZM2G442057_P01	TRUE	TRUE	KYDTALEVLSGDLGSLGR	95%	K+304 (+304), n+304 (+304)	51.72	25.37
6576	parent_transcript=GRMZM2G442057_T01; parent_gene=GRMZM2G442057	GRMZM2G442057_P01	TRUE	TRUE	vRPIWDAVDSR	91%	n+304 (+304)	26.96	26.52

6577	seq=translation; coord=10:10725550..10730964:1; parent_transcript=GRMZM2G014397_T02; parent_gene=GRMZM2G014397	GRMZM2G014397_P02,GRMZM2G014397_P03	TRUE	TRUE	dQDTFFEDYAEAHAK	95%	n+304 (+304), K+304 (+304)	55.85	25.00
6578	seq=translation; coord=10:10725550..10730964:1; parent_transcript=GRMZM2G014397_T02; parent_gene=GRMZM2G014397	GRMZM2G014397_P02,GRMZM2G014397_P03	TRUE	TRUE	vDVAIEPQCPEGR	95%	n+304 (+304), Carbamidomethyl (+57)	31.55	25.00
6579	seq=translation; coord=1:257994567..257995838:-1; parent_transcript=GRMZM2G044762_T01; parent_gene=GRMZM2G044762	GRMZM2G044762_P01,GRMZM2G044762_P02	TRUE	TRUE	aLVPTDLSVAIPHGTyAR	94%	n+304 (+304), iTRAQ8plex (+304)	25.76	25.00
6580	seq=translation; coord=1:257994567..257995838:-1; parent_transcript=GRMZM2G044762_T01; parent_gene=GRMZM2G044762	GRMZM2G044762_P01,GRMZM2G044762_P02	TRUE	TRUE	hSIDVGAGVIDADYR	95%	n+304 (+304)	41.49	25.00
6581	seq=translation; coord=1:152164284..152165382:1; parent_transcript=GRMZM2G132077_T01; parent_gene=GRMZM2G132077	GRMZM2G132077_P01	TRUE	TRUE	iIYcNPHV	94%	n+304 (+304), Carbamidomethyl (+57)	30.66	25.00
6582	seq=translation; coord=1:152164284..152165382:1; parent_transcript=GRMZM2G132077_T01; parent_gene=GRMZM2G132077	GRMZM2G132077_P01	TRUE	TRUE	sHAEFPVcWWTGR	95%	n+304 (+304), Carbamidomethyl (+57)	43.38	25.00
6583	seq=translation; coord=3:124642615..124647335:-1; parent_transcript=GRMZM2G098397_T01; parent_gene=GRMZM2G098397	GRMZM2G098397_P01,GRMZM2G098397_P02, GRMZM2G098397_P03,GRMZM2G098397_P04	TRUE	TRUE	aSVLNLDLTNPLLAK	95%	n+304 (+304), K+304 (+304)	51.76	25.00
6584	seq=translation; coord=3:124642615..124647335:-1; parent_transcript=GRMZM2G098397_T01; parent_gene=GRMZM2G098397	GRMZM2G098397_P01,GRMZM2G098397_P02, GRMZM2G098397_P03,GRMZM2G098397_P04	TRUE	TRUE	eFIEYTVLk	92%	n+304 (+304), K+304 (+304)	26.86	25.00
6585	seq=translation; coord=2:45957407..45958283:1; parent_transcript=GRMZM2G028640_T01; parent_gene=GRMZM2G028640	GRMZM2G028640_P01	TRUE	TRUE	vYPDGHGEEFVEIAAGDLVVPk	93%	n+304 (+304), K+304 (+304)	25.13	25.00
6586	seq=translation; coord=5:12291230..12291790:-1; parent_transcript=AC206941.2_FGT002; parent_gene=AC206941.2_FG002	AC206941.2_FGP002	TRUE	TRUE	tAQAGQAIQGR	95%	n+304 (+304)	47.82	25.98
6587	seq=translation; coord=9:80565232..80569476:-1; parent_transcript=GRMZM2G027385_T01; parent_gene=GRMZM2G027385	GRMZM2G027385_P01,GRMZM2G027385_P03, GRMZM2G081583_P02,GRMZM2G081583_P04	TRUE	TRUE	sTPeMWpGLLQk	89%	n+304 (+304), K+304 (+304)	26.36	26.30
6588	seq=translation; coord=8:23799793..23801891:-1; parent_transcript=GRMZM5G861077_T01; parent_gene=GRMZM5G861077	GRMZM5G861077_P01	TRUE	TRUE	iFGVWLSGAELLR	91%	n+304 (+304)	28.40	25.00
6589	seq=translation; coord=8:23799793..23801891:-1; parent_transcript=GRMZM5G861077_T01; parent_gene=GRMZM5G861077	GRMZM5G861077_P01	TRUE	TRUE	yVGTdGcYFR	93%	n+304 (+304), Carbamidomethyl (+57)	29.34	25.00
6590	seq=translation; coord=2:231282768..231284403:-1; parent_transcript=AC148152.3_FGT005; parent_gene=AC148152.3_FG005	AC148152.3_FGP005	TRUE	TRUE	sVTFPDFIAk	93%	n+304 (+304), K+304 (+304)	28.97	26.23
6591	seq=translation; coord=7:174339610..174341979:-1; parent_transcript=GRMZM2G424205_T01; parent_gene=GRMZM2G424205	GRMZM2G424205_P01	TRUE	TRUE	gGGFGGGAGGGFGGGk	95%	n+304 (+304), K+304 (+304)	38.30	25.00
6592	seq=translation; coord=7:174339610..174341979:-1; parent_transcript=GRMZM2G424205_T01; parent_gene=GRMZM2G424205	GRMZM2G424205_P01	TRUE	TRUE	gGGFGGGk	87%	n+304 (+304), K+304 (+304)	25.68	25.02
6593	seq=translation; coord=8:121435529..121437647:-1; parent_transcript=GRMZM2G042865_T01; parent_gene=GRMZM2G042865	GRMZM2G042865_P01,GRMZM2G082037_P01	TRUE	TRUE	fLEPGGPGEAAR	87%	n+304 (+304)	25.55	25.00
6594	seq=translation; coord=8:121435529..121437647:-1; parent_transcript=GRMZM2G042865_T01; parent_gene=GRMZM2G042865	GRMZM2G042865_P01,GRMZM2G082037_P01	TRUE	TRUE	IVTDVLGIGER	95%	n+304 (+304)	36.52	25.26

6595	seq=translation; coord=8:18448251..18451290:-1; parent_transcript=GRMZM2G336815_T01; parent_gene=GRMZM2G336815 seq=translation; coord=1:11301152..11301835:-1;	GRMZM2G336815_P01	TRUE	TRUE	iFGMEHWHALR	95%	n+304 (+304)	26.09	25.00
6596	parent_transcript=AC209858.4_FGT004; parent_gene=AC209858.4_FG004 seq=translation; coord=8:163002198..163002947:1;	AC209858.4_FGP004	TRUE	TRUE	rLDLSASPLADPEAATFASPR	95%	n+304 (+304)	47.44	25.34
6597	parent_transcript=GRMZM2G022958_T01; parent_gene=GRMZM2G022958 seq=translation; coord=8:37807066..37810916:-1;	GRMZM2G022958_P01	TRUE	TRUE	vEEDINTctGEVHER	95%	n+304 (+304), Carbamidomethyl (+57)	93.10	25.00
6598	parent_transcript=GRMZM2G061088_T01; parent_gene=GRMZM2G061088 seq=translation; coord=1:38124980..38130704:-1;	GRMZM2G061088_P01	TRUE	TRUE	gFDVIDAAk	95%	n+304 (+304), K+304 (+304)	33.24	25.58
6599	parent_transcript=GRMZM2G161337_T01; parent_gene=GRMZM2G161337 seq=translation; coord=10:74848346..74854487:1;	GRMZM2G161337_P01,GRMZM2G161337_P02	TRUE	TRUE	eHIMAGDIFQIVLSQR	95%	n+304 (+304)	46.31	25.73
6600	parent_transcript=GRMZM2G106974_T01; parent_gene=GRMZM2G106974 seq=translation; coord=1:193865451..193869209:1;	GRMZM2G106974_P01	TRUE	TRUE	ILHPFMPYVTEELWQR	95%	n+304 (+304)	47.14	25.00
6601	parent_transcript=GRMZM2G114739_T01; parent_gene=GRMZM2G114739 seq=translation; coord=8:117552021..117572795:1;	GRMZM2G114739_P01	TRUE	TRUE	ISDVLELVGIPk	90%	n+304 (+304), K+304 (+304)	25.48	25.00
6602	parent_transcript=GRMZM2G051050_T01; parent_gene=GRMZM2G051050 seq=translation; coord=1:46134883..46138910:-1;	GRMZM2G051050_P01,GRMZM2G094951_P01, GRMZM2G096470_P01,GRMZM2G096470_P02	TRUE	TRUE	aDELETALMEMVk	94%	n+304 (+304), K+304 (+304)	29.30	25.56
6603	parent_transcript=GRMZM2G029543_T01; parent_gene=GRMZM2G029543 seq=translation; coord=8:119902616..119903381:-1;	GRMZM2G029543_P01	TRUE	TRUE	viAGILk	94%	n+304 (+304), K+304 (+304)	27.63	25.00
6604	parent_transcript=GRMZM2G005557_T01; parent_gene=GRMZM2G005557 seq=translation; coord=7:2997300..3007755:-1;	GRMZM2G005557_P01	TRUE	TRUE	ITEEEADAMLR	94%	n+304 (+304)	30.58	25.00
6605	parent_transcript=GRMZM2G044060_T01; parent_gene=GRMZM2G044060 seq=translation; coord=7:2997300..3007755:-1;	GRMZM2G044060_P01,GRMZM2G044060_P02	TRUE	TRUE	iGEVVDGPGEEAQQQVHDGVR	95%	n+304 (+304)	87.98	25.00
6606	parent_transcript=GRMZM2G044060_T01; parent_gene=GRMZM2G044060 seq=translation; coord=3:90023131..90026648:1;	GRMZM2G044060_P01,GRMZM2G044060_P02	TRUE	TRUE	IPAIVNVlk	93%	n+304 (+304), K+304 (+304)	26.21	25.00
6607	parent_transcript=GRMZM2G135599_T01; parent_gene=GRMZM2G135599 seq=translation; coord=5:210751187..210752748:-1;	GRMZM2G135599_P01,GRMZM2G135599_P02, GRMZM2G450424_P01,GRMZM2G450424_P03, GRMZM2G450424_P05	TRUE	TRUE	viLFPFFHR	92%	n+304 (+304)	26.52	25.00
6608	parent_transcript=GRMZM2G083886_T01; parent_gene=GRMZM2G083886 seq=translation; coord=5:210751187..210752748:-1;	GRMZM2G083886_P01	TRUE	TRUE	IEHGALPQTDVLADALAGk	95%	n+304 (+304), K+304 (+304)	28.82	25.00
6609	parent_transcript=GRMZM2G083886_T01; parent_gene=GRMZM2G083886 seq=translation; coord=4:79156649..79162538:-1;	GRMZM2G083886_P01	TRUE	TRUE	sVAPLPQk	92%	n+304 (+304), K+304 (+304)	28.58	25.00
6610	parent_transcript=GRMZM2G702490_T01; parent_gene=GRMZM2G702490 seq=translation; coord=7:2584958..2590700:-1;	GRMZM2G702490_P01	TRUE	TRUE	hiPLIFLQNITGFMVGSk	95%	n+304 (+304), K+304 (+304)	44.74	25.00
6611	parent_transcript=GRMZM2G043383_T01; parent_gene=GRMZM2G043383 seq=translation; coord=7:2584958..2590700:-1;	GRMZM2G043383_P01,GRMZM2G043383_P02, GRMZM2G070542_P01,GRMZM2G070542_P02	TRUE	TRUE	qQQILLATQVVk	93%	n+304 (+304), K+304 (+304)	26.69	25.00
6612	parent_transcript=GRMZM2G043383_T01; parent_gene=GRMZM2G043383	GRMZM2G043383_P01,GRMZM2G043383_P02, GRMZM2G070542_P01,GRMZM2G070542_P02	TRUE	TRUE	sQDYEIGDGTGVVVMAGALLEQAEK	90%	n+304 (+304), K+304 (+304)	25.93	25.31

6613	seq=translation; coord=8:104770563..104774039:-1; parent_transcript=GRMZM2G334899_T01; parent_gene=GRMZM2G334899	GRMZM2G334899_P01	TRUE	TRUE	yMGTSDEVQLER	95%	n+304 (+304)	34.09	25.00
6614	seq=translation; coord=8:10755838..10761776:-1; parent_transcript=GRMZM2G119345_T01; parent_gene=GRMZM2G119345	GRMZM2G119345_P01,GRMZM2G119345_P02	TRUE	TRUE	mGLLQVAINTAMAALTk	94%	n+304 (+304), K+304 (+304)	28.24	25.00
6615	seq=translation; coord=2:60272199..60277574:-1; parent_transcript=GRMZM2G157269_T01; parent_gene=GRMZM2G157269	GRMZM2G157269_P01	TRUE	TRUE	gPIMIEWFk	95%	n+304 (+304), K+304 (+304)	36.61	26.22
6616	seq=translation; coord=2:183342461..183343536:1; parent_transcript=GRMZM2G060429_T01; parent_gene=GRMZM2G060429	GRMZM2G060429_P01	TRUE	TRUE	hQcSPAATPYGSPQcQALQQCcHQIR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	31.55	25.00
6617	seq=translation; coord=5:206910875..206915210:-1; parent_transcript=GRMZM2G105539_T01; parent_gene=GRMZM2G105539	GRMZM2G105539_P01,GRMZM2G105539_P02	TRUE	TRUE	gVPALNFLGDILWk	95%	n+304 (+304), K+304 (+304)	32.50	25.00
6618	seq=translation; coord=3:196592864..196598555:-1; parent_transcript=GRMZM2G055857_T01; parent_gene=GRMZM2G055857	GRMZM2G055857_P01,GRMZM2G055857_P02, GRMZM2G055857_P03,GRMZM2G055857_P04	TRUE	TRUE	sIFEPLPLIIGR	95%	n+304 (+304)	33.25	25.00
6619	seq=translation; coord=4:11823842..11828550:1; parent_transcript=GRMZM2G017804_T01; parent_gene=GRMZM2G017804	GRMZM2G017804_P01,GRMZM2G017804_P02	TRUE	TRUE	mLDLNPMIIAQLk	92%	n+304 (+304), K+304 (+304)	27.00	25.59
6620	seq=translation; coord=2:161123950..161130108:1; parent_transcript=GRMZM2G018241_T01; parent_gene=GRMZM2G018241	GRMZM2G018241_P01,GRMZM2G111642_P01, GRMZM2G111642_P02,GRMZM2G111642_P03, GRMZM2G111642_P04,GRMZM2G424832_P01, GRMZM2G424832_P02	TRUE	TRUE	dGTQAcPQck	91%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	25.86	25.00
6621	seq=translation; coord=1:111589370..111591480:1; parent_transcript=GRMZM2G033930_T01; parent_gene=GRMZM2G033930	GRMZM2G033930_P01	TRUE	TRUE	eMFGDDVLGALNik	95%	n+304 (+304), K+304 (+304)	35.45	25.02
6622	seq=translation; coord=2:195920737..195924614:-1; parent_transcript=GRMZM2G002807_T01; parent_gene=GRMZM2G002807	GRMZM2G002807_P01,GRMZM5G852968_P02, GRMZM5G852968_P03	TRUE	TRUE	vIAcIGELLEER	86%	n+304 (+304), Carbamidomethyl (+57)	25.88	25.42
6623	seq=translation; coord=2:49056549..49061498:-1; parent_transcript=GRMZM2G003565_T03; parent_gene=GRMZM2G003565	GRMZM2G003565_P03	TRUE	TRUE	yAIVPDENVr	95%	n+304 (+304)	39.07	25.56
6624	seq=translation; coord=4:55258880..55260891:-1; parent_transcript=GRMZM2G005046_T01; parent_gene=GRMZM2G005046	GRMZM2G005046_P01,GRMZM2G129266_P01, GRMZM2G129266_P02	TRUE	TRUE	fDLTLGLLWk	95%	n+304 (+304), K+304 (+304)	29.37	25.00
6625	seq=translation; coord=9:151763726..151772001:-1; parent_transcript=GRMZM2G009808_T01; parent_gene=GRMZM2G009808	GRMZM2G009808_P01	TRUE	TRUE	sNLAGMGIIPlcFk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	63.74	25.79
6626	seq=translation; coord=8:172976483..172980420:-1; parent_transcript=GRMZM2G027535_T01; parent_gene=GRMZM2G027535	GRMZM2G027535_P01,GRMZM2G027535_P02	TRUE	TRUE	tWLDPLFVDDR	95%	n+304 (+304)	32.50	25.00
6627	seq=translation; coord=1:88848897..88849748:-1; parent_transcript=GRMZM2G037255_T01; parent_gene=GRMZM2G037255	GRMZM2G037255_P01	TRUE	TRUE	IGVcANVLGLVk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	46.35	25.00
6628	seq=translation; coord=8:144588215..144595174:1; parent_transcript=GRMZM2G037694_T01; parent_gene=GRMZM2G037694	GRMZM2G037694_P01,GRMZM2G037694_P02	TRUE	TRUE	iVLEALPAVLLFEK	95%	n+304 (+304), K+304 (+304)	37.29	25.00
6629	seq=translation; coord=2:177646906..177651736:-1; parent_transcript=GRMZM2G039155_T01; parent_gene=GRMZM2G039155	GRMZM2G039155_P01,GRMZM2G039155_P02, GRMZM2G039155_P03,GRMZM2G039155_P05, GRMZM2G065355_P01	TRUE	TRUE	iDELEQSINDLk	95%	n+304 (+304), K+304 (+304)	33.39	26.04

6630	seq=translation; coord=6:144596360..144598543:-1; parent_transcript=GRMZM2G042797_T01; parent_gene=GRMZM2G042797	GRMZM2G042797_P01	TRUE	TRUE	vAAVWLDGAELLR	95%	n+304 (+304)	39.92	25.34
6631	seq=translation; coord=1:41956891..41966584:-1; parent_transcript=GRMZM2G044237_T01; parent_gene=GRMZM2G044237	GRMZM2G044237_P01,GRMZM2G044237_P02, GRMZM2G044237_P03,GRMZM2G044237_P04	TRUE	TRUE	IDISLGVIPLMk	95%	n+304 (+304), K+304 (+304)	42.40	25.00
6632	seq=translation; coord=2:35876928..35877532:1; parent_transcript=GRMZM2G054046_T01; parent_gene=GRMZM2G054046	GRMZM2G054046_P01,GRMZM2G096546_P01	TRUE	TRUE	gPTDVLVHDFQFEVEQVLSR	95%	n+304 (+304)	35.48	25.25
6633	seq=translation; coord=1:5530739..5532411:1; parent_transcript=GRMZM2G055704_T01; parent_gene=GRMZM2G055704	GRMZM2G055704_P01,GRMZM2G055704_P02	TRUE	TRUE	mTVIGTVDPVQVVSk	95%	n+304 (+304), K+304 (+304)	53.12	25.00
6634	seq=translation; coord=4:208244723..208251169:1; parent_transcript=GRMZM2G060800_T01; parent_gene=GRMZM2G060800	GRMZM2G060800_P01,GRMZM2G060800_P02	TRUE	TRUE	sFAPELVASFk	95%	n+304 (+304), K+304 (+304)	28.82	25.01
6635	seq=translation; coord=6:35595648..35597164:1; parent_transcript=GRMZM2G062197_T01; parent_gene=GRMZM2G062197	GRMZM2G062197_P01,GRMZM2G062197_P02, GRMZM2G137930_P01,GRMZM2G137930_P02, GRMZM2G137930_P03,GRMZM2G137930_P04	TRUE	TRUE	alGLMPMIDQGEADDk	95%	n+304 (+304), K+304 (+304)	51.86	25.00
6636	seq=translation; coord=3:151971037..151972416:1; parent_transcript=GRMZM2G065585_T01; parent_gene=GRMZM2G065585	GRMZM2G065585_P01	TRUE	TRUE	rPGPIETYIFAMFNEDQk	94%	n+304 (+304), K+304 (+304)	26.30	25.00
6637	seq=translation; coord=7:105219462..105221560:-1; parent_transcript=GRMZM2G074781_T01; parent_gene=GRMZM2G074781	GRMZM2G074781_P01	TRUE	TRUE	eLTDWLLWLk	94%	n+304 (+304), K+304 (+304)	29.83	26.13
6638	seq=translation; coord=2:232964582..232968333:-1; parent_transcript=GRMZM2G082931_T01; parent_gene=GRMZM2G082931	GRMZM2G082931_P01	TRUE	TRUE	gFGFVTFSEPR	95%	n+304 (+304)	36.04	25.00
6639	seq=translation; coord=2:150834303..150835528:1; parent_transcript=GRMZM2G094589_T01; parent_gene=GRMZM2G094589	GRMZM2G094589_P01	TRUE	TRUE	iPGEVAIFGVFR	95%	n+304 (+304)	30.52	25.02
6640	seq=translation; coord=2:135956633..135961656:1; parent_transcript=GRMZM2G094699_T01; parent_gene=GRMZM2G094699	GRMZM2G094699_P01	TRUE	TRUE	ITEPELLEPLVPSILANLEHR	95%	n+304 (+304)	44.58	25.00
6641	seq=translation; coord=1:32308316..32321893:-1; parent_transcript=GRMZM2G099528_T01; parent_gene=GRMZM2G099528	GRMZM2G099528_P01,GRMZM2G099528_P02	TRUE	TRUE	IMcTSEicTAEER	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	48.41	25.00
6642	seq=translation; coord=6:45613410..45627830:1; parent_transcript=GRMZM2G104377_T03; parent_gene=GRMZM2G104377	GRMZM2G104377_P03	TRUE	TRUE	fLDMWEPAILAik	95%	n+304 (+304), K+304 (+304)	31.34	25.00
6643	seq=translation; coord=1:199112157..199114320:1; parent_transcript=GRMZM2G113191_T01; parent_gene=GRMZM2G113191	GRMZM2G113191_P01	TRUE	TRUE	mQSPIDLAR	95%	n+304 (+304)	39.53	26.10
6644	seq=translation; coord=4:235758732..235759487:-1; parent_transcript=GRMZM2G115340_T01; parent_gene=GRMZM2G115340	GRMZM2G115340_P01,GRMZM2G179248_P01	TRUE	TRUE	IGAcMcTk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	32.98	25.00
6645	seq=translation; coord=5:59978801..59980128:1; parent_transcript=GRMZM2G116167_T01; parent_gene=GRMZM2G116167	GRMZM2G116167_P01,GRMZM2G116167_P02	TRUE	TRUE	aFGVAPEQGLVLAR	95%	n+304 (+304)	38.19	25.25
6646	seq=translation; coord=4:191950335..191955467:1; parent_transcript=GRMZM2G117614_T01; parent_gene=GRMZM2G117614	GRMZM2G117614_P01,GRMZM2G117614_P02, GRMZM2G117614_P03,GRMZM2G117614_P04	TRUE	TRUE	vcLGNLVGMPVVVVPTGLk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.50	25.00

6647	seq=translation; coord=4:74457132..74460979:1; parent_transcript=GRMZM2G117755_T01; parent_gene=GRMZM2G117755	GRMZM2G117755_P01,GRMZM2G117755_P02, GRMZM2G150762_P01,GRMZM2G150762_P02, GRMZM2G150762_P03,GRMZM2G150762_P04, GRMZM2G150762_P05	TRUE	TRUE	eQIQSYVFDVIR	95%	n+304 (+304)	43.07	25.24
6648	seq=translation; coord=5:34609536..34613247:-1; parent_transcript=GRMZM2G120579_T01; parent_gene=GRMZM2G120579	GRMZM2G120579_P01	TRUE	TRUE	IGDLLDTMSALK	95%	n+304 (+304), K+304 (+304)	31.33	25.94
6649	seq=translation; coord=1:222130457..222134768:1; parent_transcript=GRMZM2G149946_T01; parent_gene=GRMZM2G149946	GRMZM2G149946_P01,GRMZM2G149946_P02, GRMZM2G149946_P03	TRUE	TRUE	IADSMAEFIESR	95%	n+304 (+304)	36.11	25.00
6650	seq=translation; coord=6:104494543..104508487:-1; parent_transcript=GRMZM2G159744_T01; parent_gene=GRMZM2G159744	GRMZM2G159744_P01,GRMZM2G159744_P02	TRUE	TRUE	mGcVILSFLEK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.51	25.77
6651	GRMZM2G172322_P01-R seq=translation; coord=5:130658345..130666795:1;	GRMZM2G172322_P01-R	TRUE	TRUE	aLAGQk	95%	n+304 (+304), K+304 (+304)	31.48	26.72
6652	parent_transcript=GRMZM2G179981_T01; parent_gene=GRMZM2G179981 seq=translation; coord=8:78358305..78366485:-1;	GRMZM2G179981_P01	TRUE	TRUE	sIGIELIPLETSVk	95%	n+304 (+304), K+304 (+304)	34.85	25.00
6653	parent_transcript=GRMZM2G451483_T01; parent_gene=GRMZM2G451483 seq=translation; coord=2:167362256..167363675:1;	GRMZM2G451483_P01	TRUE	TRUE	mTLNQLLVELDGFk	95%	n+304 (+304), K+304 (+304)	32.46	25.81
6654	parent_transcript=GRMZM5G872070_T01; parent_gene=GRMZM5G872070 seq=translation; coord=3:224460656..224464191:-1;	GRMZM5G872070_P01	TRUE	TRUE	glFYGDLSLcETVR	95%	n+304 (+304), Carbamidomethyl (+57)	59.11	25.00
6655	parent_transcript=GRMZM5G874955_T01; parent_gene=GRMZM5G874955 seq=translation; coord=1:40222143..40226699:1;	GRMZM5G874955_P01	TRUE	TRUE	gMILPFVPLSLTFDNK	95%	n+304 (+304), K+304 (+304)	45.34	25.00
6656	parent_transcript=GRMZM2G174644_T01; parent_gene=GRMZM2G174644 seq=translation; coord=1:50252957..50255269:1;	GRMZM2G174644_P01	TRUE	TRUE	sGVVLDLVPPLTk	90%	n+304 (+304), K+304 (+304)	25.33	25.00
6657	parent_transcript=GRMZM2G033491_T01; parent_gene=GRMZM2G033491 seq=translation; coord=6:109592211..109594652:-1;	GRMZM2G033491_P01	TRUE	TRUE	aIEVAEAIVR	87%	n+304 (+304)	26.44	25.71
6658	parent_transcript=GRMZM2G008456_T01; parent_gene=GRMZM2G008456 seq=translation; coord=6:6432070..6436373:-1;	GRMZM2G008456_P01	TRUE	TRUE	eMIMQALTELr	95%	n+304 (+304)	31.51	25.00
6659	parent_transcript=GRMZM2G009661_T01; parent_gene=GRMZM2G009661 seq=translation; coord=6:365874..371557:-1;	GRMZM2G009661_P01,GRMZM2G009661_P02, GRMZM2G369912_P01,GRMZM2G369912_P02	TRUE	TRUE	vLPIIFPALER	90%	n+304 (+304)	26.44	25.00
6660	parent_transcript=GRMZM2G021784_T01; parent_gene=GRMZM2G021784 seq=translation; coord=1:183447693..183452321:1;	GRMZM2G021784_P01,GRMZM2G021784_P02, GRMZM2G451366_P01,GRMZM2G451366_P02, GRMZM2G451366_P03	TRUE	TRUE	sALVAPLLDLPLSLFR	95%	n+304 (+304)	27.78	25.00
6661	parent_transcript=GRMZM2G042371_T01; parent_gene=GRMZM2G042371 seq=translation; coord=4:236083133..236088143:-1;	GRMZM2G042371_P01	TRUE	TRUE	vFEAPLSFLk	92%	n+304 (+304), K+304 (+304)	26.14	25.00
6662	parent_transcript=GRMZM2G051004_T01; parent_gene=GRMZM2G051004 seq=translation; coord=1:295996730..296001956:1;	GRMZM2G051004_P01	TRUE	TRUE	vLDLIAHMALVSAAAK	95%	n+304 (+304), K+304 (+304)	28.22	25.00
6663	parent_transcript=GRMZM2G053916_T01; parent_gene=GRMZM2G053916 seq=translation; coord=8:70944999..70971683:1;	GRMZM2G053916_P01,GRMZM2G053916_P06	TRUE	TRUE	iVAPDLYMAFGVSGAIQHLAQMRR	95%	n+304 (+304)	70.79	25.95
6664	parent_transcript=GRMZM2G058913_T01; parent_gene=GRMZM2G058913	GRMZM2G058913_P01,GRMZM2G130586_P01, GRMZM2G130586_P02,GRMZM2G130586_P03	TRUE	TRUE	ecGMDPDEAVSR	95%	n+304 (+304), Carbamidomethyl (+57)	37.22	25.00

6665	seq=translation; coord=3:227412676..227417690:-1; parent_transcript=GRMZM2G066101_T01; parent_gene=GRMZM2G066101 seq=translation; coord=3:229845805..229849321:1;	GRMZM2G066101_P01,GRMZM2G327032_P01, GRMZM2G327032_P02	TRUE	TRUE	fDLIYLIDk	95%	n+304 (+304), K+304 (+304)	31.34	25.00
6666	parent_transcript=GRMZM2G078592_T01; parent_gene=GRMZM2G078592 seq=translation; coord=1:183993561..184006197:1;	GRMZM2G078592_P01,GRMZM2G096972_P01	TRUE	TRUE	tNVDMVTGQLSDTR	95%	n+304 (+304)	45.50	25.00
6667	parent_transcript=GRMZM2G080775_T01; parent_gene=GRMZM2G080775 seq=translation; coord=7:120201746..120203011:1;	GRMZM2G080775_P01,GRMZM2G115855_P01	TRUE	TRUE	gLLSEAVLALEAEVLk	94%	n+304 (+304), K+304 (+304)	27.58	25.00
6668	parent_transcript=GRMZM2G138727_T02; parent_gene=GRMZM2G138727 seq=translation; coord=4:24085992..24091476:1;	GRMZM2G138727_P02	TRUE	TRUE	gAVGGADSAATDGDVRPAAADSMPLR	95%	n+304 (+304)	30.41	25.00
6669	parent_transcript=GRMZM2G162859_T01; parent_gene=GRMZM2G162859 seq=translation; coord=3:176257536..176261095:1;	GRMZM2G162859_P01,GRMZM2G162859_P02, GRMZM5G812289_P01,GRMZM5G812289_P02	TRUE	TRUE	eADkPIDELLALLR	95%	n+304 (+304), K+304 (+304)	26.82	25.00
6670	parent_transcript=GRMZM2G164141_T01; parent_gene=GRMZM2G164141 seq=translation; coord=3:201894260..201901554:1;	GRMZM2G164141_P01,GRMZM2G164141_P02, GRMZM2G164141_P03	TRUE	TRUE	tTQSGFEGFVTDR	95%	n+304 (+304)	32.84	25.00
6671	parent_transcript=GRMZM2G167856_T01; parent_gene=GRMZM2G167856 seq=translation; coord=5:91582816..91615388:1;	GRMZM2G167856_P01	TRUE	TRUE	wVGTLFALK	95%	n+304 (+304), K+304 (+304)	39.11	25.00
6672	parent_transcript=GRMZM2G174785_T01; parent_gene=GRMZM2G174785 seq=translation; coord=4:228030455..228034349:-1;	GRMZM2G133308_P01,GRMZM2G133308_P02, GRMZM2G174785_P01,GRMZM2G174785_P02	TRUE	TRUE	gNPLFDLFLNLk	95%	n+304 (+304), K+304 (+304)	31.31	25.00
6673	parent_transcript=GRMZM2G345055_T01; parent_gene=GRMZM2G345055 seq=translation; coord=6:134303791..134311555:1;	GRMZM2G345055_P01,GRMZM2G345055_P02	TRUE	TRUE	dALEEQGYTEDEIEER	95%	n+304 (+304)	34.40	25.00
6674	parent_transcript=GRMZM2G424783_T01; parent_gene=GRMZM2G424783 seq=translation; coord=6:91630823..91633819:1;	GRMZM2G424783_P01,GRMZM2G424783_P02	TRUE	TRUE	yLVGVPPVLLDFIR	91%	n+304 (+304)	25.39	25.00
6675	parent_transcript=GRMZM2G428518_T03; parent_gene=GRMZM2G428518 seq=translation; coord=9:68025092..68028223:1;	GRMZM2G428518_P03	TRUE	TRUE	ILPYMYTLMYEAHTTGAPIAR	95%	n+304 (+304)	83.17	25.54
6676	parent_transcript=GRMZM2G442129_T01; parent_gene=GRMZM2G442129 seq=translation; coord=10:95762835..95768339:-1;	GRMZM2G442129_P01,GRMZM5G839924_P01	TRUE	TRUE	vVSEPIEMTQEFR	86%	n+304 (+304)	25.12	25.00
6677	parent_transcript=GRMZM2G154509_T01; parent_gene=GRMZM2G154509	GRMZM2G154509_P01,GRMZM2G154509_P02, GRMZM2G154509_P04,GRMZM2G160184_P01, GRMZM2G160184_P03,GRMZM2G160184_P04	TRUE	TRUE	fMDWLWTR	92%	n+304 (+304)	29.00	25.00
6678	GRMZM2G178261_P04-R seq=translation; coord=5:216495038..216502228:-1;	GRMZM2G178261_P04-R	TRUE	TRUE	vVVLHMLfk	91%	n+304 (+304), K+304 (+304)	25.20	25.00
6679	parent_transcript=GRMZM2G013890_T01; parent_gene=GRMZM2G013890 seq=translation; coord=4:186487329..186488873:1;	GRMZM2G013890_P01	TRUE	TRUE	eFLNTVVTDILHLHGR	95%	n+304 (+304)	56.55	25.54
6680	parent_transcript=GRMZM2G022799_T01; parent_gene=GRMZM2G022799 seq=translation; coord=6:166051912..166055277:1;	GRMZM2G022799_P01	TRUE	TRUE	acGAFSAALQVVLAHPAPLTNR	95%	n+304 (+304), Carbamidomethyl (+57)	45.45	25.39
6681	parent_transcript=GRMZM2G026013_T02; parent_gene=GRMZM2G026013 seq=translation; coord=6:166051912..166055277:1;	GRMZM2G026013_P02,GRMZM2G026013_P04	TRUE	TRUE	eDLVQSAVSFLk	95%	n+304 (+304), K+304 (+304)	40.29	25.67
6682	parent_transcript=GRMZM2G026013_T02; parent_gene=GRMZM2G026013	GRMZM2G026013_P02,GRMZM2G026013_P04	TRUE	TRUE	vEPEAGPVAPVVPR	95%	n+304 (+304)	34.88	25.05

6683	seq=translation; coord=10:14974709..14978322:1; parent_transcript=GRMZM2G081541_T01; parent_gene=GRMZM2G081541	GRMZM2G081541_P01	TRUE	TRUE	aAELLFGLGFNk	95%	n+304 (+304), K+304 (+304)	45.93	25.00
6684	seq=translation; coord=6:89823772..89828523:1; parent_transcript=GRMZM2G082322_T01; parent_gene=GRMZM2G082322	GRMZM2G082322_P01,GRMZM2G082322_P02	TRUE	TRUE	IPFAPALAEAlk	95%	n+304 (+304), K+304 (+304)	34.35	25.01
6685	seq=translation; coord=3:27391353..27395051:1; parent_transcript=GRMZM2G089365_T01; parent_gene=GRMZM2G089365	GRMZM2G089365_P01	TRUE	TRUE	aAAGSYSELISTAk	95%	n+304 (+304), K+304 (+304)	33.65	25.24
6686	seq=translation; coord=3:27391353..27395051:1; parent_transcript=GRMZM2G089365_T01; parent_gene=GRMZM2G089365	GRMZM2G089365_P01	TRUE	TRUE	ISSIGLDNTEVNR	95%	n+304 (+304)	36.64	25.20
6687	seq=translation; coord=10:141350790..141353378:1; parent_transcript=GRMZM2G094051_T01; parent_gene=GRMZM2G094051	GRMZM2G094051_P01,GRMZM2G094051_P03, GRMZM2G094051_P04	TRUE	TRUE	iPLSNNQVIEGLGk	95%	n+304 (+304), K+304 (+304)	33.59	25.19
6688	seq=translation; coord=1:27626302..27631083:1; parent_transcript=GRMZM2G111324_T01; parent_gene=GRMZM2G111324	GRMZM2G111324_P01,GRMZM2G111324_P02, GRMZM5G824920_P01	TRUE	TRUE	mLQAALDWAcGPGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.29	25.39
6689	seq=translation; coord=6:81614390..81617700:-1; parent_transcript=GRMZM2G121354_T01; parent_gene=GRMZM2G121354	GRMZM2G121354_P01,GRMZM2G132060_P01, GRMZM2G132060_P02	TRUE	TRUE	mDIDYQVLHDAFFk	95%	n+304 (+304), K+304 (+304)	37.04	25.21
6690	seq=translation; coord=10:123373488..123378767:-1; parent_transcript=GRMZM2G135470_T01; parent_gene=GRMZM2G135470	GRMZM2G135470_P01	TRUE	TRUE	sPLIVFDDIGDIDk	95%	n+304 (+304), K+304 (+304)	42.00	25.80
6691	seq=translation; coord=9:8943775..8956824:1; parent_transcript=GRMZM2G142072_T01; parent_gene=GRMZM2G142072	GRMZM2G142072_P01,GRMZM2G171488_P01, GRMZM2G171488_P02	TRUE	TRUE	iLDMVILak	95%	n+304 (+304), K+304 (+304)	33.07	25.00
6692	seq=translation; coord=6:93327267..93330462:-1; parent_transcript=GRMZM2G143767_T01; parent_gene=GRMZM2G143767	GRMZM2G143767_P01	TRUE	TRUE	aAAATADAGGPTIFDk	95%	n+304 (+304), K+304 (+304)	37.73	26.18
6693	seq=translation; coord=8:120773908..120778906:-1; parent_transcript=GRMZM2G083016_T01; parent_gene=GRMZM2G083016	GRMZM2G083016_P01	TRUE	TRUE	iGVIESLLEk	95%	n+304 (+304), K+304 (+304)	28.77	25.00
6694	seq=translation; coord=7:149250816..149253354:1; parent_transcript=GRMZM2G084757_T01; parent_gene=GRMZM2G084757	GRMZM2G084757_P01,GRMZM2G084757_P02, GRMZM2G180724_P01	TRUE	TRUE	yFEIILVDVAHTAIR	95%	n+304 (+304), iTRAQ8plex (+304)	28.90	25.00
6695	seq=translation; coord=5:180632305..180634311:1; parent_transcript=GRMZM2G106061_T01; parent_gene=GRMZM2G106061	GRMZM2G106061_P01,GRMZM2G407996_P01, GRMZM2G407996_P02	TRUE	TRUE	iVVFLNk	94%	n+304 (+304), K+304 (+304)	26.98	25.00
6696	seq=translation; coord=5:180632305..180634311:1; parent_transcript=GRMZM2G106061_T01; parent_gene=GRMZM2G106061	GRMZM2G106061_P01,GRMZM2G407996_P01, GRMZM2G407996_P02	TRUE	TRUE	tTLTAALTMVLASVGGsAPk	95%	n+304 (+304), K+304 (+304)	40.31	25.00
6697	seq=translation; coord=8:76128223..76129850:1; parent_transcript=AC231180.2_FGT006; parent_gene=AC231180.2_FG006	AC231180.2_FGP006	TRUE	TRUE	gAWMSVASFGAR	95%	n+304 (+304)	38.43	25.00
6698	seq=translation; coord=8:76128223..76129850:1; parent_transcript=AC231180.2_FGT006; parent_gene=AC231180.2_FG006	AC231180.2_FGP006	TRUE	TRUE	gDGQTLNTGAFAR	95%	n+304 (+304)	33.22	25.00
6699	seq=translation; coord=7:25812344..25817942:1; parent_transcript=GRMZM2G003789_T01; parent_gene=GRMZM2G003789	GRMZM2G003789_P01	TRUE	TRUE	aDMDALPVQELVDWEHk	95%	n+304 (+304), K+304 (+304)	87.16	25.44
6700	seq=translation; coord=7:25812344..25817942:1; parent_transcript=GRMZM2G003789_T01; parent_gene=GRMZM2G003789	GRMZM2G003789_P01	TRUE	TRUE	eIDPLQGAVVSVTLK	95%	n+304 (+304), K+304 (+304)	39.13	25.00

6701	seq=translation; coord=1:171489898..171496325:1; parent_transcript=GRMZM2G019926_T02; parent_gene=GRMZM2G019926	GRMZM2G019926_P02,GRMZM2G019926_P03, GRMZM2G019926_P04	TRUE	TRUE	gLVDTHFIER	95%	n+304 (+304)	32.25	26.11
6702	seq=translation; coord=1:171489898..171496325:1; parent_transcript=GRMZM2G019926_T02; parent_gene=GRMZM2G019926	GRMZM2G019926_P02,GRMZM2G019926_P03, GRMZM2G019926_P04	TRUE	TRUE	gSVLAPMAGLVVk	95%	n+304 (+304), K+304 (+304)	35.75	25.00
6703	seq=translation; coord=2:8914517..8917818:-1; parent_transcript=GRMZM2G076239_T02; parent_gene=GRMZM2G076239	GRMZM2G076239_P02,GRMZM2G076239_P03, GRMZM2G076239_P04,GRMZM2G076239_P05	TRUE	TRUE	aIAVTVDAPR	95%	n+304 (+304)	40.15	27.02
6704	seq=translation; coord=2:8914517..8917818:-1; parent_transcript=GRMZM2G076239_T02; parent_gene=GRMZM2G076239	GRMZM2G076239_P02,GRMZM2G076239_P03, GRMZM2G076239_P04,GRMZM2G076239_P05	TRUE	TRUE	rVPVFLDGGIR	95%	n+304 (+304)	48.54	25.00
6705	seq=translation; coord=3:205146239..205150759:-1; parent_transcript=GRMZM2G098569_T01; parent_gene=GRMZM2G098569	GRMZM2G098569_P01	TRUE	TRUE	IEEVFHEYER	95%	n+304 (+304)	31.96	25.00
6706	seq=translation; coord=3:205146239..205150759:-1; parent_transcript=GRMZM2G098569_T01; parent_gene=GRMZM2G098569	GRMZM2G098569_P01	TRUE	TRUE	vPQVGLIAVNDGIILR	95%	n+304 (+304)	31.76	25.00
6707	seq=translation; coord=6:105434141..105436791:1; parent_transcript=GRMZM2G403076_T01; parent_gene=GRMZM2G403076	GRMZM2G403076_P01	TRUE	TRUE	sQRPEAFVVDLSSLR	95%	n+304 (+304)	51.47	25.49
6708	seq=translation; coord=6:105434141..105436791:1; parent_transcript=GRMZM2G403076_T01; parent_gene=GRMZM2G403076	GRMZM2G403076_P01	TRUE	TRUE	wQEAPALPEDLFIR	95%	n+304 (+304)	39.23	25.56
6709	seq=translation; coord=4:18676199..18682894:1; parent_transcript=GRMZM2G574782_T01; parent_gene=GRMZM2G574782	GRMZM2G574782_P01	TRUE	TRUE	IIVMSPSGVQk	95%	n+304 (+304), K+304 (+304)	38.01	25.16
6710	seq=translation; coord=4:18676199..18682894:1; parent_transcript=GRMZM2G574782_T01; parent_gene=GRMZM2G574782	GRMZM2G574782_P01	TRUE	TRUE	qLQGHIWR	95%	Pyro-cmC (-17), n+304 (+304)	46.66	25.00
6711	seq=translation; coord=8:152750732..152754708:1; parent_transcript=GRMZM5G823017_T01; parent_gene=GRMZM5G823017	GRMZM5G823017_P01,GRMZM5G823017_P02, GRMZM5G823017_P03	TRUE	TRUE	aEGTEAESGGDk	95%	n+304 (+304), K+304 (+304)	33.11	25.00
6712	seq=translation; coord=8:152750732..152754708:1; parent_transcript=GRMZM5G823017_T01; parent_gene=GRMZM5G823017	GRMZM5G823017_P01,GRMZM5G823017_P02, GRMZM5G823017_P03	TRUE	TRUE	aVFTADSALYEYLDGGWk	95%	n+304 (+304), K+304 (+304)	65.30	25.45
6713	seq=translation; coord=8:118191461..118195143:-1; parent_transcript=AC197705.4_FGT007; parent_gene=AC197705.4_FG007	AC197705.4_FGP007	TRUE	TRUE	IHDLDIFDAVk	94%	n+304 (+304), K+304 (+304)	27.71	25.05
6714	seq=translation; coord=8:118191461..118195143:-1; parent_transcript=AC197705.4_FGT007; parent_gene=AC197705.4_FG007	AC197705.4_FGP007	TRUE	TRUE	tQDELIEAEVAELLR	95%	n+304 (+304)	76.58	25.68
6715	seq=translation; coord=8:29145636..29147578:-1; parent_transcript=GRMZM2G007151_T01; parent_gene=GRMZM2G007151	GRMZM2G007151_P01,GRMZM2G007151_P02	TRUE	TRUE	aAAAGFFk	94%	n+304 (+304), K+304 (+304)	27.95	25.00
6716	seq=translation; coord=8:29145636..29147578:-1; parent_transcript=GRMZM2G007151_T01; parent_gene=GRMZM2G007151	GRMZM2G007151_P01,GRMZM2G007151_P02	TRUE	TRUE	sGASPLSPAIFILDk	95%	n+304 (+304), K+304 (+304)	29.60	25.00
6717	seq=translation; coord=3:2080450..2084636:1; parent_transcript=GRMZM2G153181_T01; parent_gene=GRMZM2G153181	GRMZM2G153181_P01	TRUE	TRUE	fEEMIGELEK	95%	n+304 (+304), K+304 (+304)	40.96	25.40
6718	seq=translation; coord=3:2080450..2084636:1; parent_transcript=GRMZM2G153181_T01; parent_gene=GRMZM2G153181	GRMZM2G153181_P01	TRUE	TRUE	iLLYILk	93%	n+304 (+304), K+304 (+304)	27.56	25.00

6719	seq=translation; coord=5:58525626..58534933:-1; parent_transcript=GRMZM2G397247_T04; parent_gene=GRMZM2G397247	GRMZM2G397247_P04	TRUE	TRUE	aGADVVSFSPDMMMDGR	95%	n+304 (+304)	57.62	25.00
6720	seq=translation; coord=5:58525626..58534933:-1; parent_transcript=GRMZM2G397247_T04; parent_gene=GRMZM2G397247	GRMZM2G397247_P04	TRUE	TRUE	dVGVNSFVLFPk	93%	n+304 (+304), K+304 (+304)	28.15	25.91
6721	seq=translation; coord=1:210463083..210467521:1; parent_transcript=GRMZM2G073814_T02; parent_gene=GRMZM2G073814	GRMZM2G073814_P02	TRUE	TRUE	aLGVVELVSFDEAIAR	92%	n+304 (+304)	27.26	25.72
6722	seq=translation; coord=1:210463083..210467521:1; parent_transcript=GRMZM2G073814_T02; parent_gene=GRMZM2G073814	GRMZM2G073814_P02	TRUE	TRUE	ISEAGLAVLR	95%	n+304 (+304)	43.26	25.00
6723	seq=translation; coord=10:16517475..16520678:1; parent_transcript=GRMZM2G091819_T01; parent_gene=GRMZM2G091819	GRMZM2G091819_P01	TRUE	TRUE	ySTSVEScEYDEASGR	95%	n+304 (+304), Carbamidomethyl (+57)	74.46	25.00
6724	seq=translation; coord=10:16517475..16520678:1; parent_transcript=GRMZM2G091819_T01; parent_gene=GRMZM2G091819	GRMZM2G091819_P01	TRUE	TRUE	yVDDYVER	91%	n+304 (+304)	26.76	25.00
6725	seq=translation; coord=4:151648685..151655399:1; parent_transcript=GRMZM2G145226_T01; parent_gene=GRMZM2G145226	GRMZM2G145226_P01	TRUE	TRUE	iAENPNSMNFNVMAISk	95%	n+304 (+304), K+304 (+304)	67.52	25.55
6726	seq=translation; coord=4:151648685..151655399:1; parent_transcript=GRMZM2G145226_T01; parent_gene=GRMZM2G145226	GRMZM2G145226_P01	TRUE	TRUE	IVEGSYFEk	91%	n+304 (+304), K+304 (+304)	25.10	25.07
6727	seq=translation; coord=1:287289676..287296815:-1; parent_transcript=GRMZM2G178415_T01; parent_gene=GRMZM2G178415	GRMZM2G178415_P01,GRMZM2G178415_P02, GRMZM2G178415_P05,GRMZM2G178415_P06	TRUE	TRUE	gVLFATEALLAEHGk	95%	n+304 (+304), K+304 (+304)	67.07	25.61
6728	seq=translation; coord=1:287289676..287296815:-1; parent_transcript=GRMZM2G178415_T01; parent_gene=GRMZM2G178415	GRMZM2G178415_P01,GRMZM2G178415_P02, GRMZM2G178415_P05,GRMZM2G178415_P06	TRUE	TRUE	sLLIPFR	90%	n+304 (+304)	27.63	25.00
6729	seq=translation; coord=8:64567512..64568715:-1; parent_transcript=GRMZM2G075796_T01; parent_gene=GRMZM2G075796	GRMZM2G075796_P01	TRUE	TRUE	IHDAADEIESLR	90%	n+304 (+304)	27.37	25.00
6730	seq=translation; coord=8:64567512..64568715:-1; parent_transcript=GRMZM2G075796_T01; parent_gene=GRMZM2G075796	GRMZM2G075796_P01	TRUE	TRUE	IQDLLAAEk	95%	n+304 (+304), K+304 (+304)	33.11	26.70
6731	seq=translation; coord=9:143391688..143394080:-1; parent_transcript=GRMZM2G140799_T01; parent_gene=GRMZM2G140799	GRMZM2G140799_P01	TRUE	TRUE	aYPLADAQLTMGILDIIQQAANYk	95%	n+304 (+304), K+304 (+304)	61.94	25.00
6732	seq=translation; coord=1:35239930..35250741:-1; parent_transcript=GRMZM2G030422_T01; parent_gene=GRMZM2G030422	GRMZM2G030422_P01,GRMZM2G030422_P02, GRMZM2G030422_P03	TRUE	TRUE	dGESHLVEWNESEGAVk	95%	n+304 (+304), K+304 (+304)	36.35	25.00
6733	seq=translation; coord=5:74642485..74645616:-1; parent_transcript=GRMZM2G017229_T01; parent_gene=GRMZM2G017229	GRMZM2G017229_P01	TRUE	TRUE	eTSEGTEEDDAAk	95%	n+304 (+304), K+304 (+304)	50.56	25.00
6734	seq=translation; coord=1:7456720..7458916:-1; parent_transcript=GRMZM2G092719_T01; parent_gene=GRMZM2G092719	GRMZM2G092719_P01	TRUE	TRUE	nSIGcLFWLLSR	95%	n+304 (+304), Carbamidomethyl (+57)	35.74	26.04
6735	seq=translation; coord=5:6157585..6167807:-1; parent_transcript=GRMZM2G171588_T01; parent_gene=GRMZM2G171588	GRMZM2G171588_P01,GRMZM2G171588_P02, GRMZM5G886709_P01	TRUE	TRUE	eQVDLFLAEVAAk	94%	n+304 (+304), K+304 (+304)	28.50	25.37
6736	seq=translation; coord=5:6157585..6167807:-1; parent_transcript=GRMZM2G171588_T01; parent_gene=GRMZM2G171588	GRMZM2G171588_P01,GRMZM2G171588_P02, GRMZM5G886709_P01	TRUE	TRUE	IcSLSPALQEFVGASELAR	89%	n+304 (+304), Carbamidomethyl (+57)	25.17	25.00

6737	seq=translation; coord=4:162265417..162267770:-1; parent_transcript=GRMZM2G064960_T01; parent_gene=GRMZM2G064960 seq=translation; coord=6:163979437..163984362:1;	GRMZM2G064960_P01,GRMZM2G064960_P02	TRUE	TRUE	dPDQEPPAPASAAEAek	95%	n+304 (+304), K+304 (+304)	40.33	25.00
6738	parent_transcript=GRMZM2G150257_T01; parent_gene=GRMZM2G150257 seq=translation; coord=5:3067129..3072217:1;	GRMZM2G150257_P01	TRUE	TRUE	eQVDLLVSQLQALGAR	95%	n+304 (+304)	39.81	25.15
6739	parent_transcript=GRMZM2G057329_T01; parent_gene=GRMZM2G057329 seq=translation; coord=5:144281597..144283761:-1;	GRMZM2G057329_P01	TRUE	TRUE	vLGDGLLVVR	95%	n+304 (+304)	30.55	25.00
6740	parent_transcript=GRMZM2G049390_T01; parent_gene=GRMZM2G049390 seq=translation; coord=4:38821429..38825409:1;	GRMZM2G049390_P01,GRMZM2G049390_P03	TRUE	TRUE	eLELLSDGANVYk	95%	n+304 (+304), K+304 (+304)	65.86	25.28
6741	parent_transcript=GRMZM2G159250_T01; parent_gene=GRMZM2G159250 seq=translation; coord=1:1665098..1666489:1;	GRMZM2G159250_P01,GRMZM2G159250_P02	TRUE	TRUE	aIETVQANFNTVR	95%	n+304 (+304)	35.35	25.00
6742	parent_transcript=GRMZM2G474194_T01; parent_gene=GRMZM2G474194 seq=translation; coord=1:205574134..205574917:-1;	GRMZM2G474194_P01	TRUE	TRUE	vPcQYPGLTVTFHIER	92%	n+304 (+304), Carbamidomethyl (+57)	27.25	25.75
6743	parent_transcript=GRMZM2G015588_T01; parent_gene=GRMZM2G015588	GRMZM2G015588_P01,GRMZM2G095579_P01, GRMZM2G095579_P02	TRUE	TRUE	gVLDYLGVEITR	95%	n+304 (+304)	33.36	25.07
6744	seq=translation; coord=1:189474106..189481738:1; parent_transcript=GRMZM2G004582_T01; parent_gene=GRMZM2G004582	GRMZM2G004582_P01,GRMZM2G004582_P02, GRMZM2G004582_P03,GRMZM2G004582_P04, GRMZM2G004582_P05,GRMZM2G004582_P07, GRMZM2G004582_P08,GRMZM2G039359_P04	TRUE	TRUE	IVLAAAILHR	95%	n+304 (+304)	69.79	25.00
6745	seq=translation; coord=6:162306497..162311290:-1; parent_transcript=GRMZM2G170400_T01; parent_gene=GRMZM2G170400 seq=translation; coord=8:8281951..8288329:1;	GRMZM2G170400_P01	TRUE	TRUE	eAGHVLALDFIESVIk	95%	n+304 (+304), K+304 (+304)	31.41	25.00
6746	parent_transcript=GRMZM5G860137_T01; parent_gene=GRMZM5G860137 seq=translation; coord=10:141964000..141969154:-1;	GRMZM5G860137_P01,GRMZM5G860137_P02	TRUE	TRUE	tPIGALLGSLSSLPATk	95%	n+304 (+304), K+304 (+304)	47.30	25.00
6747	parent_transcript=GRMZM2G028929_T01; parent_gene=GRMZM2G028929 seq=translation; coord=4:145240980..145242532:1;	GRMZM2G028929_P01,GRMZM2G028929_P02, GRMZM2G028929_P04	TRUE	TRUE	eAYLIFQDFAEk	95%	n+304 (+304), K+304 (+304)	37.97	26.12
6748	parent_transcript=GRMZM2G111756_T01; parent_gene=GRMZM2G111756 seq=translation; coord=7:138559787..138562909:1;	GRMZM2G111756_P01	TRUE	TRUE	dLFMDPDEAR	95%	n+304 (+304)	42.50	25.00
6749	parent_transcript=GRMZM5G876773_T01; parent_gene=GRMZM5G876773 seq=translation; coord=5:77757345..7777262:-1;	GRMZM5G876773_P01	TRUE	TRUE	iYLQQPAPESQLR	95%	n+304 (+304)	34.52	25.00
6750	parent_transcript=GRMZM2G011456_T02; parent_gene=GRMZM2G011456 seq=translation; coord=8:175400786..175402729:-1;	GRMZM2G011456_P02,GRMZM2G011456_P03, GRMZM2G169927_P01	TRUE	TRUE	IEGWESLTVISSDMR	94%	n+304 (+304)	27.12	25.00
6751	parent_transcript=GRMZM2G002786_T01; parent_gene=GRMZM2G002786 seq=translation; coord=6:141144515..141145787:-1;	GRMZM2G002786_P01	TRUE	TRUE	sPPNIPEVk	95%	n+304 (+304), K+304 (+304)	37.33	25.00
6752	parent_transcript=GRMZM2G030116_T01; parent_gene=GRMZM2G030116 seq=translation; coord=2:45518503..45524129:1;	GRMZM2G030116_P01,GRMZM2G034810_P01, GRMZM2G135332_P01,GRMZM2G359892_P01, GRMZM2G413687_P01	TRUE	TRUE	qAWGSLDALIGR	95%	n+304 (+304)	43.90	26.54
6753	parent_transcript=GRMZM2G131321_T01; parent_gene=GRMZM2G131321	GRMZM2G131321_P01,GRMZM2G131321_P02, GRMZM2G131321_P03	TRUE	TRUE	eGVLVEGLFWk	95%	n+304 (+304), K+304 (+304)	40.14	25.60

6754	seq=translation; coord=9:14820841..14824999:-1; parent_transcript=GRMZM2G167156_T01; parent_gene=GRMZM2G167156 seq=translation; coord=5:19048283..19055775:1;	GRMZM2G167156_P01,GRMZM2G167156_P02	TRUE	TRUE	dVLQSLMAk	92%	n+304 (+304), K+304 (+304)	26.13	25.49
6755	parent_transcript=GRMZM2G375984_T01; parent_gene=GRMZM2G375984 seq=translation; coord=5:202224551..202225926:1;	GRMZM2G375984_P01,GRMZM2G375984_P02	TRUE	TRUE	fVDDGTSSk	89%	n+304 (+304), K+304 (+304)	28.25	26.28
6756	parent_transcript=GRMZM2G475349_T01; parent_gene=GRMZM2G475349 seq=translation; coord=1:255254285..255262311:1;	GRMZM2G475349_P01	TRUE	TRUE	IAGEDIAHLDDLIIVLSk	95%	n+304 (+304), K+304 (+304)	39.48	25.00
6757	parent_transcript=GRMZM2G016875_T01; parent_gene=GRMZM2G016875 seq=translation; coord=1:193317120..193323452:1;	GRMZM2G016875_P01	TRUE	TRUE	tILQDVLEQk	91%	n+304 (+304), K+304 (+304)	26.22	25.68
6758	parent_transcript=GRMZM2G424241_T01; parent_gene=GRMZM2G424241 seq=translation; coord=7:141644109..141654531:-1;	GRMZM2G424241_P01,GRMZM2G424241_P03, GRMZM2G424241_P04	TRUE	TRUE	gRPWFGLLALLR	92%	n+304 (+304)	26.40	25.07
6759	parent_transcript=GRMZM2G073504_T01; parent_gene=GRMZM2G073504 seq=translation; coord=3:23430825..23436929:1;	GRMZM2G073504_P01	TRUE	TRUE	tDkLQFLDFDLIGR	92%	n+304 (+304), K+304 (+304)	26.48	25.00
6760	parent_transcript=GRMZM2G121683_T01; parent_gene=GRMZM2G121683 seq=translation; coord=3:23430825..23436929:1;	GRMZM2G121683_P01,GRMZM2G155709_P01, GRMZM2G155709_P02,GRMZM2G155709_P03	TRUE	TRUE	eAVDVFIVcLTQNAESYk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.24	25.00
6761	parent_transcript=GRMZM2G121683_T01; parent_gene=GRMZM2G121683 seq=translation; coord=4:220605264..220609013:1;	GRMZM2G121683_P01,GRMZM2G155709_P01, GRMZM2G155709_P02,GRMZM2G155709_P03	TRUE	TRUE	IVPPVSFDLFMR	89%	n+304 (+304)	27.04	25.00
6762	parent_transcript=GRMZM2G125239_T01; parent_gene=GRMZM2G125239 seq=translation; coord=4:220605264..220609013:1;	GRMZM2G125239_P01,GRMZM2G125239_P02, GRMZM2G125239_P03	TRUE	TRUE	eSAPSTANQSGDSQk	93%	n+304 (+304), K+304 (+304)	26.31	25.00
6763	parent_transcript=GRMZM2G125239_T01; parent_gene=GRMZM2G125239 seq=translation; coord=9:139614346..139617289:1;	GRMZM2G125239_P01,GRMZM2G125239_P02, GRMZM2G125239_P03	TRUE	TRUE	vFEFIADek	91%	n+304 (+304), K+304 (+304)	26.55	25.50
6764	parent_transcript=GRMZM2G103490_T01; parent_gene=GRMZM2G103490 seq=translation; coord=1:223161919..223165331:1;	GRMZM2G103490_P01,GRMZM2G103490_P02, GRMZM2G160906_P01,GRMZM2G160906_P02, GRMZM2G160906_P03,GRMZM2G160906_P04	TRUE	TRUE	ILETLEEFMR	93%	n+304 (+304)	30.38	25.19
6765	parent_transcript=GRMZM2G450498_T01; parent_gene=GRMZM2G450498 seq=translation; coord=3:201782882..201788032:1;	GRMZM2G450498_P01	TRUE	TRUE	aTFVDADDEAAVR	95%	n+304 (+304)	44.20	25.00
6766	parent_transcript=GRMZM2G171426_T01; parent_gene=GRMZM2G171426 seq=translation; coord=7:153816870..153819108:1;	GRMZM2G171426_P01	TRUE	TRUE	sTGFGLIYDNLEAAk	95%	n+304 (+304), K+304 (+304)	41.07	25.73
6767	parent_transcript=GRMZM2G009412_T02; parent_gene=GRMZM2G009412 seq=translation; coord=1:241508117..241529441:-1;	GRMZM2G009412_P02,GRMZM2G009412_P04, GRMZM2G103059_P01,GRMZM2G125527_P01, GRMZM2G125527_P02,GRMZM2G160351_P01, GRMZM2G160351_P02	TRUE	TRUE	IQcQSck	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304), n+304 (+304),	33.20	25.29
6768	parent_transcript=GRMZM2G520535_T01; parent_gene=GRMZM2G520535 seq=translation; coord=1:227250144..22725278:-1;	GRMZM2G520535_P01	TRUE	TRUE	gFLSDAEcDHIALAk	95%	Carbamidomethyl (+57), K+304 (+304)	26.54	25.29
6769	parent_transcript=GRMZM2G449083_T01; parent_gene=GRMZM2G449083 seq=translation; coord=1:233330196..233331681:-1;	GRMZM2G449083_P01,GRMZM2G449083_P02, GRMZM2G449083_P03,GRMZM2G449083_P04, GRMZM2G449083_P06	TRUE	TRUE	IPFQEMYAILEAMk	90%	n+304 (+304), K+304 (+304)	25.88	25.60
6770	parent_transcript=AC198361.3_FGT004; parent_gene=AC198361.3_FG004	AC198361.3_FGP004	TRUE	TRUE	gFGFVVADPAVVDR	95%	n+304 (+304)	31.76	25.42

6771	seq=translation; coord=9:142806737..142811172:-1; parent_transcript=AC205419.3_FGT001; parent_gene=AC205419.3_FG001 seq=translation; coord=5:210593958..210594236:-1;	AC205419.3_FGP001,GRMZM2G165944_P01	TRUE	TRUE	ILEFEQELIR	95%	n+304 (+304)	32.85	25.01
6772	parent_transcript=AC216353.2_FGT005; parent_gene=AC216353.2_FG005 seq=translation; coord=10:149747387..149749334:-1;	AC216353.2_FGP005	TRUE	TRUE	VIQETNESWEK	95%	n+304 (+304), K+304 (+304)	34.80	25.00
6773	parent_transcript=AC234201.1_FGT003; parent_gene=AC234201.1_FG003 seq=translation; coord=2:12128999..12130348:1;	AC234201.1_FGP003	TRUE	TRUE	IDDGLLDQIFR	95%	n+304 (+304)	31.47	25.04
6774	parent_transcript=GRMZM2G000397_T01; parent_gene=GRMZM2G000397 seq=translation; coord=1:267153118..267154071:-1;	GRMZM2G000397_P01	TRUE	TRUE	ILITLVAAPALAMATk	95%	n+304 (+304), K+304 (+304)	36.81	25.00
6775	parent_transcript=GRMZM2G004106_T01; parent_gene=GRMZM2G004106 seq=translation; coord=9:131576429..131579600:-1;	GRMZM2G004106_P01,GRMZM2G004160_P01	TRUE	TRUE	gGWSFNTANWPK	95%	n+304 (+304), K+304 (+304)	44.59	25.00
6776	parent_transcript=GRMZM2G006080_T01; parent_gene=GRMZM2G006080 seq=translation; coord=8:149039624..149041045:1;	GRMZM2G006080_P01,GRMZM2G100288_P01	TRUE	TRUE	eEVSLAEWALHcQk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.38	25.59
6777	parent_transcript=GRMZM2G007630_T01; parent_gene=GRMZM2G007630 seq=translation; coord=7:148179239..148183212:-1;	GRMZM2G007630_P01	TRUE	TRUE	IALGPTYLVAR	95%	n+304 (+304)	32.09	25.00
6778	parent_transcript=GRMZM2G018950_T01; parent_gene=GRMZM2G018950 seq=translation; coord=1:85054120..85057214:1;	GRMZM2G018950_P01	TRUE	TRUE	hNEATISNDLYDFLQAAFEHPK	95%	n+304 (+304), K+304 (+304)	43.39	25.00
6779	parent_transcript=GRMZM2G026767_T02; parent_gene=GRMZM2G026767 seq=translation; coord=1:81602813..81603918:-1;	GRMZM2G026767_P02,GRMZM2G026767_P03	TRUE	TRUE	aSGEVPALAEFSLAELR	95%	n+304 (+304)	49.59	25.76
6780	parent_transcript=GRMZM2G028821_T01; parent_gene=GRMZM2G028821 seq=translation; coord=5:208090222..208094428:-1;	GRMZM2G028821_P01	TRUE	TRUE	IFPAWYGMVvk	95%	n+304 (+304), K+304 (+304)	31.25	25.65
6781	parent_transcript=GRMZM2G035503_T01; parent_gene=GRMZM2G035503 seq=translation; coord=4:236110495..236114268:-1;	GRMZM2G035503_P01	TRUE	TRUE	aATSFPQVILTAASFNPHLWYR	95%	n+304 (+304)	51.18	25.65
6782	parent_transcript=GRMZM2G051276_T01; parent_gene=GRMZM2G051276 seq=translation; coord=1:189081768..189085843:-1;	GRMZM2G051276_P01	TRUE	TRUE	vAAPTTPGPIPAELLGVIEAAk	95%	n+304 (+304), K+304 (+304)	35.50	25.00
6783	parent_transcript=GRMZM2G055992_T01; parent_gene=GRMZM2G055992 seq=translation; coord=6:22305548..22306995:-1;	GRMZM2G055992_P01	TRUE	TRUE	iLALPEAIGMLSSLak	94%	n+304 (+304), K+304 (+304)	28.09	25.00
6784	parent_transcript=GRMZM2G060373_T02; parent_gene=GRMZM2G060373 seq=translation; coord=6:142484063..142487768:-1;	GRMZM2G060373_P02,GRMZM2G060373_P03, GRMZM2G165208_P01,GRMZM2G165619_P02, GRMZM2G165619_P03,GRMZM2G305154_P01	TRUE	TRUE	vcANPHGLIR	95%	n+304 (+304), Carbamidomethyl (+57)	34.48	25.00
6785	parent_transcript=GRMZM2G062481_T01; parent_gene=GRMZM2G062481 seq=translation; coord=9:134132145..134139171:-1;	GRMZM2G062481_P01	TRUE	TRUE	tAVDFIASHPQAK	95%	n+304 (+304), K+304 (+304)	32.21	25.48
6786	parent_transcript=GRMZM2G064725_T01; parent_gene=GRMZM2G064725 seq=translation; coord=2:230866079..230869236:-1;	GRMZM2G064725_P01	TRUE	TRUE	eIPALIVWTLGGk	95%	n+304 (+304), K+304 (+304)	30.78	25.00
6787	parent_transcript=GRMZM2G066902_T01; parent_gene=GRMZM2G066902	GRMZM2G066902_P01	TRUE	TRUE	eIAEAYLGTTvk	95%	n+304 (+304), K+304 (+304)	38.03	26.04

6788	seq=translation; coord=4:45266261..45269925:-1; parent_transcript=GRMZM2G070693_T01; parent_gene=GRMZM2G070693	GRMZM2G070693_P01,GRMZM2G070693_P02, GRMZM2G070693_P03,GRMZM2G070693_P04, GRMZM2G070693_P05,GRMZM2G083551_P01, GRMZM2G083551_P02,GRMZM2G083551_P03	TRUE	TRUE	IDEALYNIQFEQHWLEAQTDR	95%	n+304 (+304)	80.48	25.00
6789	seq=translation; coord=5:13280268..13284484:-1; parent_transcript=GRMZM2G076676_T01; parent_gene=GRMZM2G076676	GRMZM2G076676_P01,GRMZM2G388911_P01	TRUE	TRUE	skPVVAALIDELER	95%	n+304 (+304), K+304 (+304)	37.53	25.00
6790	seq=translation; coord=6:62544640..62546740:1; parent_transcript=GRMZM2G077837_T01; parent_gene=GRMZM2G077837	GRMZM2G077837_P01,GRMZM2G077837_P02, GRMZM2G077837_P03,GRMZM2G077837_P04, GRMZM2G077837_P05,GRMZM2G077837_P06	TRUE	TRUE	gTPLPLILLGk	95%	n+304 (+304), K+304 (+304)	32.18	25.00
6791	seq=translation; coord=7:98556648..98559891:-1; parent_transcript=GRMZM2G082019_T01; parent_gene=GRMZM2G082019	GRMZM2G082019_P01	TRUE	TRUE	akEEIEAIVEAIHPk	95%	n+304 (+304), K+304 (+304)	27.83	25.00
6792	seq=translation; coord=1:59061226..59087208:1; parent_transcript=GRMZM2G083689_T01; parent_gene=GRMZM2G083689	GRMZM2G083689_P01,GRMZM2G083689_P02	TRUE	TRUE	dAIFEFLLQcTEQLPHk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	36.11	25.34
6793	seq=translation; coord=5:23896374..23903276:-1; parent_transcript=GRMZM2G085747_T01; parent_gene=GRMZM2G085747	GRMZM2G085747_P01,GRMZM2G085747_P02, GRMZM2G085747_P03,GRMZM2G085747_P04, GRMZM2G085747_P05	TRUE	TRUE	iLGLGDLGVQGIGIPIGk	95%	n+304 (+304), K+304 (+304)	52.22	25.00
6794	seq=translation; coord=10:138858423..138859497:-1; parent_transcript=GRMZM2G091534_T01; parent_gene=GRMZM2G091534	GRMZM2G091534_P01,GRMZM2G391272_P01, GRMZM2G391286_P01,GRMZM2G406313_P01, GRMZM2G410338_P01	TRUE	TRUE	IGVcANVLGLik	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	34.23	25.00
6795	seq=translation; coord=8:13336541..13339982:-1; parent_transcript=GRMZM2G094273_T01; parent_gene=GRMZM2G094273	GRMZM2G094273_P01	TRUE	TRUE	aGVEMALIDAVANSIR	95%	n+304 (+304)	37.30	25.85
6796	seq=translation; coord=5:6525725..6529505:1; parent_transcript=GRMZM2G095185_T03; parent_gene=GRMZM2G095185	GRMZM2G095185_P02,GRMZM2G095185_P03	TRUE	TRUE	vMPTGWFLLLR	95%	n+304 (+304)	33.68	25.00
6797	seq=translation; coord=8:135085183..135090834:-1; parent_transcript=GRMZM2G098212_T01; parent_gene=GRMZM2G098212	GRMZM2G098212_P01	TRUE	TRUE	tDVcEFLIGELGPLVDPk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.31	25.31
6798	seq=translation; coord=6:159759627..159763263:1; parent_transcript=GRMZM2G101457_T01; parent_gene=GRMZM2G101457	GRMZM2G101457_P01	TRUE	TRUE	vFVLTLTGDGEHR	95%	n+304 (+304)	49.75	25.59
6799	seq=translation; coord=8:171709672..171712582:-1; parent_transcript=GRMZM2G106344_T01; parent_gene=GRMZM2G106344	GRMZM2G106344_P01,GRMZM2G106344_P02	TRUE	TRUE	gAGFEVVLVScDEDRPSFER	92%	n+304 (+304), Carbamidomethyl (+57)	26.74	25.00
6800	seq=translation; coord=10:148815875..148817265:1; parent_transcript=GRMZM2G106792_T01; parent_gene=GRMZM2G106792	GRMZM2G106792_P01	TRUE	TRUE	gTQLQGDVTAAEFR	95%	n+304 (+304)	56.52	25.00
6801	seq=translation; coord=1:182898704..182903336:-1; parent_transcript=GRMZM2G107163_T01; parent_gene=GRMZM2G107163	GRMZM2G107163_P01,GRMZM2G131957_P01, GRMZM2G131957_P02	TRUE	TRUE	gYcQVDFYDPGAAAack	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	46.93	25.00
6802	seq=translation; coord=1:264209651..264226078:1; parent_transcript=GRMZM2G109056_T01; parent_gene=GRMZM2G109056	GRMZM2G109056_P01	TRUE	TRUE	aIIeAVLPTLGTfVDDTPk	95%	n+304 (+304), K+304 (+304)	52.56	25.00
6803	seq=translation; coord=1:200075221..200076952:-1; parent_transcript=GRMZM2G117378_T01; parent_gene=GRMZM2G117378	GRMZM2G117378_P01,GRMZM2G349749_P01	TRUE	TRUE	gIIpGTILAFLEEK	95%	n+304 (+304), K+304 (+304)	55.63	25.00

6804	seq=translation; coord=7:85262878..85264551:1; parent_transcript=GRMZM2G117878_T01; parent_gene=GRMZM2G117878	GRMZM2G117878_P01	TRUE	TRUE	iGVLLGVLER	95%	n+304 (+304)	40.68	25.00
6805	seq=translation; coord=1:59670870..59675001:-1; parent_transcript=GRMZM2G124576_T02; parent_gene=GRMZM2G124576	GRMZM2G124576_P02	TRUE	TRUE	eSEEAAPAAEGDGEK	95%	n+304 (+304), K+304 (+304)	50.25	25.00
6806	seq=translation; coord=6:82963690..82967765:1; parent_transcript=GRMZM2G126361_T01; parent_gene=GRMZM2G126361	GRMZM2G126361_P01,GRMZM2G126361_P02, GRMZM2G126361_P03	TRUE	TRUE	IELQEVVDfLk	95%	n+304 (+304), K+304 (+304)	48.90	25.45
6807	seq=translation; coord=1:86168160..86176332:-1; parent_transcript=GRMZM2G127168_T01; parent_gene=GRMZM2G127168	GRMZM2G127168_P01,GRMZM2G127168_P02	TRUE	TRUE	gVGAPFHDVGAPFR	95%	n+304 (+304)	31.10	25.00
6808	seq=translation; coord=6:153309231..153314326:1; parent_transcript=GRMZM2G127297_T01; parent_gene=GRMZM2G127297	GRMZM2G127297_P01,GRMZM2G410782_P01	TRUE	TRUE	aLLLLDSWQEAfGGPGGk	95%	n+304 (+304), K+304 (+304)	53.69	25.01
6809	seq=translation; coord=2:144192738..144194495:1; parent_transcript=GRMZM2G127418_T01; parent_gene=GRMZM2G127418	GRMZM2G127418_P01	TRUE	TRUE	iRPVAGLMSVIEVYP	95%	n+304 (+304)	34.52	25.74
6810	seq=translation; coord=2:181110668..181120123:1; parent_transcript=GRMZM2G127717_T01; parent_gene=GRMZM2G127717	GRMZM2G127717_P01,GRMZM2G127717_P02	TRUE	TRUE	gFcVVcVAEGAGDfLLQk	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	34.92	25.21
6811	seq=translation; coord=5:203712290..203717409:1; parent_transcript=GRMZM2G128922_T01; parent_gene=GRMZM2G128922	GRMZM2G128922_P01,GRMZM2G128922_P03, GRMZM2G129146_P01,GRMZM2G129146_P03, GRMZM2G129146_P04,GRMZM2G129146_P05	TRUE	TRUE	vPEVTMAFAGGAALK	95%	n+304 (+304), K+304 (+304)	46.18	26.19
6812	seq=translation; coord=7:156715826..156717458:-1; parent_transcript=GRMZM2G129973_T01; parent_gene=GRMZM2G129973	GRMZM2G129973_P01	TRUE	TRUE	aVTSFAALVAALAk	95%	n+304 (+304), K+304 (+304)	33.91	25.00
6813	seq=translation; coord=10:17930259..17933520:1; parent_transcript=GRMZM2G136563_T01; parent_gene=GRMZM2G136563	GRMZM2G136563_P01	TRUE	TRUE	eLDIPGEIYER	95%	n+304 (+304)	35.74	25.00
6814	seq=translation; coord=8:139450959..139452582:-1; parent_transcript=GRMZM2G142705_T01; parent_gene=GRMZM2G142705	GRMZM2G142705_P01	TRUE	TRUE	sLADALHLR	95%	n+304 (+304)	67.20	27.19
6815	seq=translation; coord=8:16755280..16757481:-1; parent_transcript=GRMZM2G143258_T01; parent_gene=GRMZM2G143258	GRMZM2G143258_P01,GRMZM2G143258_P02	TRUE	TRUE	IVVPTLLFFGASGTR	95%	n+304 (+304)	32.28	25.33
6816	seq=translation; coord=1:219379298..219385327:-1; parent_transcript=GRMZM2G146286_T01; parent_gene=GRMZM2G146286	GRMZM2G146286_P01,GRMZM2G146286_P02, GRMZM2G146286_P03,GRMZM2G146286_P04, GRMZM2G147712_P01	TRUE	TRUE	eYIEEVYAAEYQHk	95%	n+304 (+304), K+304 (+304)	33.77	25.00
6817	seq=translation; coord=8:20971995..20976240:-1; parent_transcript=GRMZM2G147882_T01; parent_gene=GRMZM2G147882	GRMZM2G147882_P01,GRMZM2G147882_P02, GRMZM2G147882_P03,GRMZM2G147882_P04	TRUE	TRUE	gGFIVNLGDMLER	95%	n+304 (+304)	42.30	25.40
6818	seq=translation; coord=1:205531096..205533366:-1; parent_transcript=GRMZM2G149414_T01; parent_gene=GRMZM2G149414	GRMZM2G149414_P01	TRUE	TRUE	eEAEGAPAVAAHH	95%	n+304 (+304)	57.96	25.00
6819	seq=translation; coord=7:164564301..164565776:1; parent_transcript=GRMZM2G152179_T01; parent_gene=GRMZM2G152179	GRMZM2G152179_P01	TRUE	TRUE	dMVVSLWHFLR	95%	n+304 (+304)	43.42	25.09
6820	seq=translation; coord=7:156569292..156577217:1; parent_transcript=GRMZM2G153162_T01; parent_gene=GRMZM2G153162	GRMZM2G153162_P01	TRUE	TRUE	dGIAADILGAVLDSIk	95%	n+304 (+304), K+304 (+304)	33.54	25.00

6821	seq=translation; coord=1:278907896..278910140:1; parent_transcript=GRMZM2G154828_T01; parent_gene=GRMZM2G154828 seq=translation; coord=5:73229280..73231295:1;	GRMZM2G154828_P01	TRUE	TRUE	sMLAVLLALQk	95%	n+304 (+304), K+304 (+304)	30.44	25.00
6822	parent_transcript=GRMZM2G157026_T01; parent_gene=GRMZM2G157026 seq=translation; coord=1:14804662..14809417:1;	GRMZM2G157026_P01,GRMZM5G838961_P01	TRUE	TRUE	dILHEFTQEFR	95%	n+304 (+304)	32.13	25.00
6823	parent_transcript=GRMZM2G162725_T01; parent_gene=GRMZM2G162725 seq=translation; coord=7:147155879..147158705:-1;	GRMZM2G162725_P01	TRUE	TRUE	aLAADDLAAAATAVHEFLAIDAR	95%	n+304 (+304)	69.31	26.19
6824	parent_transcript=GRMZM2G168588_T01; parent_gene=GRMZM2G168588 seq=translation; coord=6:2447171..2452276:-1;	GRMZM2G168588_P01	TRUE	TRUE	sLLAGQVLDVPLR	95%	n+304 (+304)	44.98	25.00
6825	parent_transcript=GRMZM2G178192_T01; parent_gene=GRMZM2G178192 seq=translation; coord=3:175775929..175780870:-1;	GRMZM2G178192_P01,GRMZM2G178192_P02, GRMZM2G178192_P03	TRUE	TRUE	iDELLGSILEk	95%	n+304 (+304), K+304 (+304)	35.20	25.01
6826	parent_transcript=GRMZM2G178244_T01; parent_gene=GRMZM2G178244 seq=translation; coord=2:211946552..211950130:1;	GRMZM2G178244_P01	TRUE	TRUE	sATADGTQQWAFILTDALAR	95%	n+304 (+304)	55.02	25.00
6827	parent_transcript=GRMZM2G314955_T03; parent_gene=GRMZM2G314955 seq=translation; coord=1:205241339..205247763:-1;	GRMZM2G314955_P03	TRUE	TRUE	sVTPASQQNPAER	95%	n+304 (+304)	29.73	25.00
6828	parent_transcript=GRMZM2G319357_T01; parent_gene=GRMZM2G319357 seq=translation; coord=4:239129384..239130094:-1;	GRMZM2G319357_P01	TRUE	TRUE	dFDLILAMDR	95%	n+304 (+304)	31.60	25.00
6829	parent_transcript=GRMZM2G324162_T01; parent_gene=GRMZM2G324162 seq=translation; coord=2:229081805..229082275:1;	GRMZM2G324162_P01	TRUE	TRUE	IIWAHIk	92%	n+304 (+304), K+304 (+304)	26.35	25.00
6830	parent_transcript=GRMZM2G371620_T01; parent_gene=GRMZM2G371620 seq=translation; coord=10:28388505..28394470:-1;	GRMZM2G371620_P01,GRMZM5G816772_P01	TRUE	TRUE	iTLISDFGEISGSR	95%	n+304 (+304)	42.92	25.71
6831	parent_transcript=GRMZM2G383088_T01; parent_gene=GRMZM2G383088 seq=translation; coord=8:133440146..133441157:1;	GRMZM2G383088_P01	TRUE	TRUE	aGGIFLPLVk	95%	n+304 (+304), K+304 (+304)	31.80	25.00
6832	parent_transcript=GRMZM2G386228_T01; parent_gene=GRMZM2G386228 seq=translation; coord=7:143820122..143821948:-1;	GRMZM2G386228_P01	TRUE	TRUE	gTAAAAAGMR	95%	n+304 (+304)	33.77	25.17
6833	parent_transcript=GRMZM2G401664_T01; parent_gene=GRMZM2G401664 seq=translation; coord=4:7260920..7265403:1;	GRMZM2G401664_P01	TRUE	TRUE	IFIAEAFak	95%	n+304 (+304), K+304 (+304)	34.97	25.00
6834	parent_transcript=GRMZM2G403636_T01; parent_gene=GRMZM2G403636 seq=translation; coord=4:233519831..233542576:1;	GRMZM2G403636_P01	TRUE	TRUE	tAAFcFPIISGIMk	91%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	26.36	25.48
6835	parent_transcript=GRMZM2G417658_T01; parent_gene=GRMZM2G417658 seq=translation; coord=3:181276458..181277675:1;	GRMZM2G417658_P01,GRMZM2G417658_P02	TRUE	TRUE	IIFPEGTLAQTLAQlk	95%	n+304 (+304), K+304 (+304)	48.90	25.00
6836	parent_transcript=GRMZM2G429982_T01; parent_gene=GRMZM2G429982 seq=translation; coord=4:191750819..191753856:1;	GRMZM2G429982_P01	TRUE	TRUE	tGcAGAGAQlHcATGDcGGR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), Carbamidomethyl (+57)	70.48	25.00
6837	parent_transcript=GRMZM2G441541_T01; parent_gene=GRMZM2G441541	GRMZM2G441541_P01,GRMZM2G441541_P02, GRMZM2G441541_P03,GRMZM2G441541_P04	TRUE	TRUE	ePEFAGELFDALSR	95%	n+304 (+304)	35.36	25.00

6838	seq=translation; coord=7:104615801..104620303:1; parent_transcript=GRMZM2G472376_T02; parent_gene=GRMZM2G472376 seq=translation; coord=7:138591141..138594806:1;	GRMZM2G472376_P02	TRUE	TRUE	vSIEIER	95%	n+304 (+304)	32.10	25.00
6839	parent_transcript=GRMZM5G800734_T02; parent_gene=GRMZM5G800734 seq=translation; coord=10:88191606..88197105:1;	GRMZM5G800734_P02	TRUE	TRUE	yGAAVTLQNLGdk	95%	n+304 (+304), K+304 (+304)	32.40	26.54
6840	parent_transcript=GRMZM5G803275_T01; parent_gene=GRMZM5G803275 seq=translation; coord=2:193648937..193649473:-1;	GRMZM5G803275_P01,GRMZM5G817255_P03	TRUE	TRUE	mSVDWAFSSGPak	95%	n+304 (+304), K+304 (+304)	41.79	25.38
6841	parent_transcript=GRMZM5G808017_T01; parent_gene=GRMZM5G808017 seq=translation; coord=2:144982955..144985696:1;	GRMZM5G808017_P01	TRUE	TRUE	ILEDLDALAGTIAVk	95%	n+304 (+304), K+304 (+304)	33.60	25.00
6842	parent_transcript=GRMZM2G145651_T01; parent_gene=GRMZM2G145651 seq=translation; coord=5:2705885..2708336:1;	GRMZM2G145651_P01	TRUE	TRUE	eVWcVak	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	32.27	25.91
6843	parent_transcript=GRMZM2G107076_T02; parent_gene=GRMZM2G107076 seq=translation; coord=8:118889246..118891848:-1;	GRMZM2G107076_P02	TRUE	TRUE	aGVLDPPDRAETDHLALAAGAGR	94%	n+304 (+304)	26.02	25.00
6844	parent_transcript=GRMZM5G827266_T02; parent_gene=GRMZM5G827266 seq=translation; coord=5:64335786..64339361:-1;	GRMZM5G827266_P02	TRUE	TRUE	dVQEAcVYDGYVLPk	94%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	29.16	25.85
6845	parent_transcript=AC190909.3_FGT004; parent_gene=AC190909.3_FG004 seq=translation; coord=8:139014642..139020725:-1;	AC190909.3_FGP004,GRMZM2G430680_P01,G RMZM2G430680_P02	TRUE	TRUE	fVELLELLQk	95%	n+304 (+304), K+304 (+304)	30.71	25.00
6846	parent_transcript=AC196426.3_FGT007; parent_gene=AC196426.3_FG007 seq=translation; coord=7:170099729..170103818:1;	AC196426.3_FGP007,GRMZM5G873287_P01	TRUE	TRUE	fVPTVMNIlk	95%	n+304 (+304), K+304 (+304)	35.33	25.00
6847	parent_transcript=AC198481.3_FGT004; parent_gene=AC198481.3_FG004 seq=translation; coord=2:194391631..194395595:-1;	AC198481.3_FGP004	TRUE	TRUE	ILAVVNALLHR	95%	n+304 (+304)	55.28	25.00
6848	parent_transcript=AC199782.5_FGT001; parent_gene=AC199782.5_FG001 seq=translation; coord=7:140686655..140691401:1;	AC199782.5_FGP001	TRUE	TRUE	sALQEAETELDR	95%	n+304 (+304)	39.00	25.00
6849	parent_transcript=AC200057.4_FGT007; parent_gene=AC200057.4_FG007 seq=translation; coord=10:83447249..83454536:1;	AC200057.4_FGP007,GRMZM2G112483_P01,G RMZM2G112483_P02,GRMZM2G180847_P01	TRUE	TRUE	IAELALVDPk	92%	n+304 (+304), K+304 (+304)	25.98	25.00
6850	parent_transcript=GRMZM2G003897_T01; parent_gene=GRMZM2G003897 seq=translation; coord=2:216610669..216612249:1;	GRMZM2G003897_P01	TRUE	TRUE	eAFAEFGEVLHAR	95%	n+304 (+304)	74.55	25.02
6851	parent_transcript=GRMZM2G010991_T01; parent_gene=GRMZM2G010991 seq=translation; coord=6:151770259..151778529:1;	GRMZM2G010991_P01	TRUE	TRUE	iMEIASLEk	95%	n+304 (+304), K+304 (+304)	33.62	25.00
6852	parent_transcript=GRMZM2G012052_T01; parent_gene=GRMZM2G012052 seq=translation; coord=9:11216956..11220850:1;	GRMZM2G012052_P01,GRMZM2G085600_P01, GRMZM2G085600_P02,GRMZM2G085600_P03	TRUE	TRUE	ftSEMWHPNVYPDGR	95%	n+304 (+304)	35.30	25.00
6853	parent_transcript=GRMZM2G012863_T01; parent_gene=GRMZM2G012863 seq=translation; coord=6:156927300..156931413:-1;	GRMZM2G012863_P01,GRMZM2G012863_P02	TRUE	TRUE	ILAGESGIGPIDR	95%	n+304 (+304)	45.91	26.18
6854	parent_transcript=GRMZM2G015100_T01; parent_gene=GRMZM2G015100	GRMZM2G015100_P01	TRUE	TRUE	mPLGIVDELFGPVk	95%	n+304 (+304), K+304 (+304)	50.90	25.13

6855	seq=translation; coord=6:40207604..40209489:1; parent_transcript=GRMZM2G017966_T01; parent_gene=GRMZM2G017966	GRMZM2G017966_P01,GRMZM2G017966_P02, GRMZM2G073535_P01,GRMZM2G073535_P02, GRMZM2G073535_P03,GRMZM2G073535_P04, GRMZM2G073535_P05,GRMZM2G113414_P01, GRMZM2G113414_P02,GRMZM5G835323_P01, GRMZM5G835323_P02	TRUE	TRUE	sLTTVQGLk	95%	n+304 (+304), K+304 (+304)	33.82	25.00
6856	seq=translation; coord=8:144958450..144963956:-1; parent_transcript=GRMZM2G024738_T04; parent_gene=GRMZM2G024738	GRMZM2G024738_P04,GRMZM2G025031_P01, GRMZM2G025031_P02,GRMZM2G377609_P03	TRUE	TRUE	tPEEAVAHFFDVTR	95%	n+304 (+304)	35.04	25.00
6857	seq=translation; coord=3:228543979..228551345:1; parent_transcript=GRMZM2G027867_T01; parent_gene=GRMZM2G027867	GRMZM2G027867_P01,GRMZM2G027867_P02	TRUE	TRUE	IFLLPDVLCLaK	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	35.11	25.00
6858	seq=translation; coord=8:6394352..6397914:-1; parent_transcript=GRMZM2G029845_T01; parent_gene=GRMZM2G029845	GRMZM2G029845_P01,GRMZM2G029845_P02, GRMZM2G134149_P01,GRMZM2G134149_P02	TRUE	TRUE	sPELEVGLTTTFGNVHTALATR	95%	n+304 (+304)	69.68	25.85
6859	seq=translation; coord=1:97673409..97679050:1; parent_transcript=GRMZM2G033526_T01; parent_gene=GRMZM2G033526	GRMZM2G033526_P01,GRMZM2G033526_P02, GRMZM2G144730_P01,GRMZM2G152686_P01	TRUE	TRUE	aEVSDIAIAVR	95%	n+304 (+304)	36.04	26.33
6860	seq=translation; coord=1:266950013..266955592:-1; parent_transcript=GRMZM2G041770_T01; parent_gene=GRMZM2G041770	GRMZM2G041770_P01	TRUE	TRUE	gFDLLQEILQHRLR	95%	n+304 (+304)	30.35	25.50
6861	seq=translation; coord=7:140706875..140710245:1; parent_transcript=GRMZM2G043600_T01; parent_gene=GRMZM2G043600	GRMZM2G043600_P01	TRUE	TRUE	dASALEELFR	95%	n+304 (+304)	54.79	25.00
6862	seq=translation; coord=3:133067971..133077051:1; parent_transcript=GRMZM2G047362_T01; parent_gene=GRMZM2G047362	GRMZM2G047362_P01	TRUE	TRUE	nILDHLLLLGVESQWAPVALR	95%	n+304 (+304)	33.86	25.00
6863	seq=translation; coord=2:173282474..173286392:-1; parent_transcript=GRMZM2G047404_T01; parent_gene=GRMZM2G047404	GRMZM2G047404_P01,GRMZM2G103047_P01	TRUE	TRUE	vSPAVLQSAGLNlk	95%	n+304 (+304), K+304 (+304)	41.47	25.00
6864	seq=translation; coord=4:53440616..53446854:-1; parent_transcript=GRMZM2G049525_T01; parent_gene=GRMZM2G049525	GRMZM2G049525_P01,GRMZM2G049525_P02, GRMZM2G049525_P03	TRUE	TRUE	ISFVPGAIEWVHR	95%	n+304 (+304)	55.21	25.68
6865	seq=translation; coord=1:296002128..296008705:-1; parent_transcript=GRMZM2G053803_T01; parent_gene=GRMZM2G053803	GRMZM2G053803_P01,GRMZM2G053803_P02, GRMZM2G326195_P01	TRUE	TRUE	IEVDVAELR	92%	n+304 (+304)	30.02	27.04
6866	seq=translation; coord=5:76621430..76624952:-1; parent_transcript=GRMZM2G054706_T01; parent_gene=GRMZM2G054706	GRMZM2G054706_P01	TRUE	TRUE	fLHEVAFk	95%	n+304 (+304), K+304 (+304)	30.66	25.68
6867	seq=translation; coord=1:266913672..266916510:-1; parent_transcript=GRMZM2G057394_T01; parent_gene=GRMZM2G057394	GRMZM2G057394_P01,GRMZM2G057394_P02	TRUE	TRUE	tALDLLQSLPR	95%	n+304 (+304)	44.49	25.54
6868	seq=translation; coord=6:160625203..160629814:1; parent_transcript=GRMZM2G060817_T01; parent_gene=GRMZM2G060817	GRMZM2G060817_P01,GRMZM2G060817_P02	TRUE	TRUE	iLGELEGLDTMLHLAK	95%	n+304 (+304), K+304 (+304)	48.29	25.00
6869	seq=translation; coord=1:147082260..147087160:1; parent_transcript=GRMZM2G065205_T01; parent_gene=GRMZM2G065205	GRMZM2G065205_P01,GRMZM2G112074_P01	TRUE	TRUE	aLLLLLVGAPHR	95%	n+304 (+304)	45.80	25.00
6870	seq=translation; coord=3:169617043..169620923:-1; parent_transcript=GRMZM2G070562_T01; parent_gene=GRMZM2G070562	GRMZM2G070562_P01	TRUE	TRUE	iNIIAALVAAGR	95%	n+304 (+304)	38.26	25.00

6871	seq=translation; coord=9:147166752..147170885:-1; parent_transcript=GRMZM2G073498_T01; parent_gene=GRMZM2G073498	GRMZM2G073498_P01,GRMZM2G073498_P02, GRMZM2G073498_P03,GRMZM2G130987_P01, GRMZM2G130987_P02,GRMZM2G130987_P04, GRMZM2G307252_P01,GRMZM2G307252_P02	TRUE	TRUE	aTELGFFGF	95%	n+304 (+304)	45.55	25.00
6872	seq=translation; coord=10:148605305..148610112:-1; parent_transcript=GRMZM2G074787_T01; parent_gene=GRMZM2G074787	GRMZM2G074787_P01,GRMZM2G074787_P02	TRUE	TRUE	ILAVPLFELYDNIQR	95%	n+304 (+304)	30.95	26.30
6873	seq=translation; coord=3:226476662..226482081:1; parent_transcript=GRMZM2G078826_T01; parent_gene=GRMZM2G078826	GRMZM2G078826_P01	TRUE	TRUE	gRDDDEEGIIDEDGEIGEDDPR	95%	n+304 (+304)	74.83	25.00
6874	seq=translation; coord=6:137142553..137144384:-1; parent_transcript=GRMZM2G079440_T01; parent_gene=GRMZM2G079440	GRMZM2G079440_P01	TRUE	TRUE	tGGILHR	95%	n+304 (+304)	36.82	25.97
6875	seq=translation; coord=9:143329347..143333500:1; parent_transcript=GRMZM2G081175_T01; parent_gene=GRMZM2G081175	GRMZM2G081175_P01	TRUE	TRUE	IMPGEVILASLDGFGK	95%	n+304 (+304), K+304 (+304)	36.73	25.15
6876	seq=translation; coord=8:2110920..2115595:1; parent_transcript=GRMZM2G082214_T01; parent_gene=GRMZM2G082214	GRMZM2G082214_P01	TRUE	TRUE	iREEAGELIQTLLNEDQSR	95%	n+304 (+304)	33.64	25.00
6877	seq=translation; coord=3:135445422..135448935:-1; parent_transcript=GRMZM2G084647_T01; parent_gene=GRMZM2G084647	GRMZM2G084647_P01,GRMZM2G084647_P02, GRMZM2G084647_P03	TRUE	TRUE	rkPEAAEAVAAIMALAAVIR	95%	n+304 (+304), K+304 (+304)	37.45	25.00
6878	seq=translation; coord=1:51291271..51292598:1; parent_transcript=GRMZM2G084783_T02; parent_gene=GRMZM2G084783	GRMZM2G084783_P02	TRUE	TRUE	qVFDGDQPAAETTAEAVNR	95%	n+304 (+304)	36.98	25.00
6879	seq=translation; coord=9:149894129..149896657:-1; parent_transcript=GRMZM2G091362_T01; parent_gene=GRMZM2G091362	GRMZM2G091362_P01	TRUE	TRUE	rIDGSSDDFSFR	95%	n+304 (+304)	63.14	25.00
6880	seq=translation; coord=3:53980991..53987563:1; parent_transcript=GRMZM2G092661_T01; parent_gene=GRMZM2G092661	GRMZM2G092661_P01,GRMZM2G092661_P02, GRMZM2G092661_P03	TRUE	TRUE	wVPLSLEFGVPLFSPk	95%	n+304 (+304), K+304 (+304)	33.00	25.00
6881	seq=translation; coord=3:220129576..220134164:1; parent_transcript=GRMZM2G095534_T01; parent_gene=GRMZM2G095534	GRMZM2G095534_P01,GRMZM2G095534_P02, GRMZM2G095534_P03,GRMZM2G095534_P04, GRMZM2G095534_P05,GRMZM2G095534_P06	TRUE	TRUE	ISVETTVQSAVTEVAAMVGENVk	95%	n+304 (+304), K+304 (+304)	51.13	25.05
6882	seq=translation; coord=5:212233142..212237929:1; parent_transcript=GRMZM2G097977_T01; parent_gene=GRMZM2G097977	GRMZM2G097977_P01	TRUE	TRUE	aLLDFAASLMPGLAAk	95%	n+304 (+304), K+304 (+304)	47.27	25.00
6883	seq=translation; coord=8:135062540..135065340:1; parent_transcript=GRMZM2G098153_T01; parent_gene=GRMZM2G098153	GRMZM2G098153_P01	TRUE	TRUE	vIGTLLGSLLPDGTVHVR	95%	n+304 (+304)	29.32	25.00
6884	seq=translation; coord=7:175302491..175305743:-1; parent_transcript=GRMZM2G102167_T01; parent_gene=GRMZM2G102167	GRMZM2G102167_P01,GRMZM2G102167_P04, GRMZM2G102167_P05	TRUE	TRUE	hVLLPVLDLR	95%	n+304 (+304)	50.62	25.00
6885	seq=translation; coord=2:165262816..165266884:-1; parent_transcript=GRMZM2G103345_T01; parent_gene=GRMZM2G103345	GRMZM2G103345_P01,GRMZM2G103345_P02	TRUE	TRUE	iGQGAEITLER	95%	n+304 (+304)	47.74	26.46
6886	seq=translation; coord=5:28674682..28681161:1; parent_transcript=GRMZM2G104254_T01; parent_gene=GRMZM2G104254	GRMZM2G104254_P01,GRMZM2G104254_P02	TRUE	TRUE	iTMDMASQIFEILR	95%	n+304 (+304)	46.48	25.73
6887	seq=translation; coord=2:172843794..172863857:-1; parent_transcript=GRMZM2G104546_T02; parent_gene=GRMZM2G104546	GRMZM2G104546_P02,GRMZM2G136712_P01, GRMZM2G437977_P01	TRUE	TRUE	dDLSGTDVAR	95%	n+304 (+304)	33.18	25.00

6888	seq=translation; coord=1:73634614..73642065:-1; parent_transcript=GRMZM2G104983_T01; parent_gene=GRMZM2G104983	GRMZM2G104983_P01	TRUE	TRUE	IGVMSLLAVFk	95%	n+304 (+304), K+304 (+304)	33.18	25.00
6889	seq=translation; coord=6:56102468..56105100:-1; parent_transcript=GRMZM2G107073_T01; parent_gene=GRMZM2G107073	GRMZM2G107073_P01,GRMZM2G107073_P02	TRUE	TRUE	IQGIQGAPFR	89%	n+304 (+304)	26.17	25.00
6890	seq=translation; coord=7:7453972..7459323:1; parent_transcript=GRMZM2G107089_T01; parent_gene=GRMZM2G107089	GRMZM2G107089_P01,GRMZM2G107089_P02	TRUE	TRUE	iAPIQVHPIWk	95%	n+304 (+304), K+304 (+304)	30.25	25.00
6891	seq=translation; coord=5:12580030..12585678:-1; parent_transcript=GRMZM2G111475_T01; parent_gene=GRMZM2G111475	GRMZM2G111475_P01	TRUE	TRUE	mELSSLTQTNISLPFITATADGPK	95%	n+304 (+304), K+304 (+304)	27.97	25.00
6892	seq=translation; coord=6:121537212..121538751:1; parent_transcript=GRMZM2G117057_T01; parent_gene=GRMZM2G117057	GRMZM2G117057_P01,GRMZM2G117057_P02	TRUE	TRUE	hDLGLPVAAMFFNAQk	95%	n+304 (+304), K+304 (+304)	33.14	25.48
6893	seq=translation; coord=10:12600584..12608266:-1; parent_transcript=GRMZM2G118714_T01; parent_gene=GRMZM2G118714	GRMZM2G118714_P01	TRUE	TRUE	aNQLLGEIAEIQESLMHVk	95%	n+304 (+304), K+304 (+304)	54.31	25.00
6894	seq=translation; coord=5:213055055..213058997:1; parent_transcript=GRMZM2G122231_T01; parent_gene=GRMZM2G122231	GRMZM2G122231_P01,GRMZM2G312521_P01, GRMZM2G430607_P01	TRUE	TRUE	fLAMEQLLVEHR	95%	n+304 (+304)	77.09	25.88
6895	seq=translation; coord=6:45182651..45183616:1; parent_transcript=GRMZM2G124617_T01; parent_gene=GRMZM2G124617	GRMZM2G124617_P01	TRUE	TRUE	aQQAAGGTGTSTDNk	95%	n+304 (+304), K+304 (+304)	38.94	25.00
6896	seq=translation; coord=1:82508572..82509915:1; parent_transcript=GRMZM2G125266_T01; parent_gene=GRMZM2G125266	GRMZM2G125266_P01	TRUE	TRUE	sVGTAVVDLLAAQLAYETHLAATk	95%	n+304 (+304), K+304 (+304)	42.64	25.00
6897	seq=translation; coord=4:30469845..30474256:1; parent_transcript=GRMZM2G126253_T01; parent_gene=GRMZM2G126253	GRMZM2G126253_P01	TRUE	TRUE	IFDTLLELIHR	95%	n+304 (+304)	40.14	25.00
6898	seq=translation; coord=6:131454814..131463174:-1; parent_transcript=GRMZM2G126435_T01; parent_gene=GRMZM2G126435	GRMZM2G126435_P01,GRMZM2G126435_P02	TRUE	TRUE	fEEAISAGDDER	95%	n+304 (+304)	56.47	25.00
6899	seq=translation; coord=7:5515951..5519578:-1; parent_transcript=GRMZM2G129357_T01; parent_gene=GRMZM2G129357	GRMZM2G129357_P01	TRUE	TRUE	vLEFVQFLQSk	95%	n+304 (+304), K+304 (+304)	47.22	25.00
6900	seq=translation; coord=3:4635480..4641804:1; parent_transcript=GRMZM2G133121_T01; parent_gene=GRMZM2G133121	GRMZM2G133121_P01	TRUE	TRUE	gIPVATVAIGIAENAGLLAAR	95%	n+304 (+304)	52.47	25.00
6901	seq=translation; coord=3:190321122..190324751:-1; parent_transcript=GRMZM2G138800_T01; parent_gene=GRMZM2G138800	GRMZM2G138800_P01	TRUE	TRUE	iWQVPEILSEEVLGk	95%	n+304 (+304), K+304 (+304)	48.56	25.00
6902	seq=translation; coord=1:247626491..247632248:-1; parent_transcript=GRMZM2G140602_T01; parent_gene=GRMZM2G140602	GRMZM2G140602_P01	TRUE	TRUE	vIEASDVILEVLDAR	95%	n+304 (+304)	37.57	25.56
6903	seq=translation; coord=10:59506710..59518288:1; parent_transcript=GRMZM2G141399_T01; parent_gene=GRMZM2G141399	GRMZM2G141399_P01,GRMZM2G141399_P02	TRUE	TRUE	qDLSIVGISNEFQtk	95%	n+304 (+304), K+304 (+304)	46.17	26.82
6904	seq=translation; coord=10:111287744..111290073:1; parent_transcript=GRMZM2G149543_T01; parent_gene=GRMZM2G149543	GRMZM2G149543_P01	TRUE	TRUE	tALADLHDLGR	95%	n+304 (+304)	45.11	25.55
6905	GRMZM2G163711_P01-R	GRMZM2G163711_P01-R	TRUE	TRUE	IGLHSLR	95%	n+304 (+304)	30.42	26.49

6906	seq=translation; coord=3:3308380..3311497:1; parent_transcript=GRMZM2G166597_T01; parent_gene=GRMZM2G166597 seq=translation; coord=1:299754155..299755202:-1;	GRMZM2G166597_P01	TRUE	TRUE	dTRPTGAYLLDAALQGINAIVGAR	95%	n+304 (+304)	50.56	25.00
6907	parent_transcript=GRMZM2G167031_T04; parent_gene=GRMZM2G167031 seq=translation; coord=3:19939526..19944315:1;	GRMZM2G167031_P04	TRUE	TRUE	ffALQLESVIK	95%	n+304 (+304), K+304 (+304)	33.00	25.00
6908	parent_transcript=GRMZM2G169152_T02; parent_gene=GRMZM2G169152	GRMZM2G169152_P02,GRMZM2G169152_P03	TRUE	TRUE	IGVLGALEIIDAAR	95%	n+304 (+304)	39.90	25.00
6909	seq=translation; coord=4:80533096..80538602:-1; parent_transcript=GRMZM2G171921_T01; parent_gene=GRMZM2G171921	GRMZM2G171921_P01,GRMZM2G171921_P02, GRMZM2G171921_P03,GRMZM2G171921_P04, GRMZM2G171921_P05,GRMZM2G171921_P06	TRUE	TRUE	eLFSEVGHLK	95%	n+304 (+304), K+304 (+304)	42.32	26.50
6910	seq=translation; coord=6:145123773..145126701:-1; parent_transcript=GRMZM2G179346_T01; parent_gene=GRMZM2G179346	GRMZM2G179346_P01	TRUE	TRUE	mFFHIVLER	95%	n+304 (+304)	37.99	25.00
6911	seq=translation; coord=4:36122702..36125196:1; parent_transcript=GRMZM2G179976_T01; parent_gene=GRMZM2G179976	GRMZM2G179976_P01	TRUE	TRUE	fAFAAPVAAADSSAAAPK	95%	n+304 (+304), K+304 (+304)	60.29	25.66
6912	seq=translation; coord=8:160763133..160770225:1; parent_transcript=GRMZM2G312365_T01; parent_gene=GRMZM2G312365	GRMZM2G312365_P01	TRUE	TRUE	dSDLSPLGLLWSELEGRPK	95%	n+304 (+304), K+304 (+304)	57.15	25.38
6913	seq=translation; coord=9:45354730..45357776:1; parent_transcript=GRMZM2G314094_T01; parent_gene=GRMZM2G314094	GRMZM2G314094_P01	TRUE	TRUE	iIGFLGGTDGLFAQK	95%	n+304 (+304), K+304 (+304)	32.79	25.12
6914	seq=translation; coord=8:165181600..165183220:-1; parent_transcript=GRMZM2G316362_T01; parent_gene=GRMZM2G316362	GRMZM2G316362_P01	TRUE	TRUE	dYADIVEFLVK	95%	n+304 (+304), K+304 (+304)	39.26	25.50
6915	seq=translation; coord=3:49619034..49624780:-1; parent_transcript=GRMZM2G322186_T01; parent_gene=GRMZM2G322186	GRMZM2G322186_P01,GRMZM2G322186_P02	TRUE	TRUE	IFLAQPDafYFHVlQQGLLR	95%	n+304 (+304)	65.46	25.34
6916	seq=translation; coord=7:172727421..172731206:1; parent_transcript=GRMZM2G322413_T02; parent_gene=GRMZM2G322413	GRMZM2G322413_P02	TRUE	TRUE	aPLGQNTVLLR	89%	n+304 (+304)	26.18	25.00
6917	seq=translation; coord=6:113233723..113238779:1; parent_transcript=GRMZM2G348551_T01; parent_gene=GRMZM2G348551	GRMZM2G348551_P01	TRUE	TRUE	tVEGGWGLHDIIR	95%	n+304 (+304)	86.40	25.66
6918	seq=translation; coord=1:81918413..81920944:-1; parent_transcript=GRMZM2G353553_T01; parent_gene=GRMZM2G353553	GRMZM2G353553_P01	TRUE	TRUE	vQILQTEATTLsAQLTLlQR	95%	n+304 (+304)	80.51	25.00
6919	seq=translation; coord=5:207060907..207063925:-1; parent_transcript=GRMZM2G380184_T01; parent_gene=GRMZM2G380184	GRMZM2G380184_P01	TRUE	TRUE	IVNTLLDLIK	95%	n+304 (+304), K+304 (+304)	29.60	25.00
6920	seq=translation; coord=1:179988453..179990792:-1; parent_transcript=GRMZM2G392791_T01; parent_gene=GRMZM2G392791	GRMZM2G392791_P01	TRUE	TRUE	gAADAPAVllIHGFPElWLSWR	95%	n+304 (+304)	35.77	25.84
6921	seq=translation; coord=3:174367886..174371254:-1; parent_transcript=GRMZM2G400604_T01; parent_gene=GRMZM2G400604	GRMZM2G400604_P01	TRUE	TRUE	tMAITDQAMALR	95%	n+304 (+304)	40.65	25.00
6922	seq=translation; coord=7:20171657..20172327:1; parent_transcript=GRMZM2G404688_T01; parent_gene=GRMZM2G404688	GRMZM2G404688_P01	TRUE	TRUE	fAPALVAAAeCGLlTAHGR	95%	n+304 (+304), Carbamidomethyl (+57)	74.15	26.21

6923	seq=translation; coord=10:70632831..70633760:-1; parent_transcript=GRMZM2G448627_T01; parent_gene=GRMZM2G448627	GRMZM2G448627_P01	TRUE	TRUE	eAAANVGASANAGMQk	95%	n+304 (+304), K+304 (+304)	58.72	25.35
6924	seq=translation; coord=9:33840187..33858081:-1; parent_transcript=GRMZM2G457415_T01; parent_gene=GRMZM2G457415	GRMZM2G457415_P01,GRMZM2G457415_P02, GRMZM2G457415_P03	TRUE	TRUE	vQPDGLVAGSLDLLTMVLk	95%	n+304 (+304), K+304 (+304)	56.82	25.00
6925	seq=translation; coord=5:96354714..96362409:1; parent_transcript=GRMZM2G462613_T01; parent_gene=GRMZM2G462613	GRMZM2G462613_P01	TRUE	TRUE	eHLWPFIQEFVDGALSHIVR	95%	n+304 (+304)	28.26	25.00
6926	seq=translation; coord=5:189804974..189811226:-1; parent_transcript=GRMZM2G463291_T01; parent_gene=GRMZM2G463291	GRMZM2G463291_P01	TRUE	TRUE	gGIKEENIVVFMYYDDIANSALNPR	95%	n+304 (+304), K+304 (+304)	56.39	25.00
6927	seq=translation; coord=2:167977405..167982718:-1; parent_transcript=GRMZM2G504906_T01; parent_gene=GRMZM2G504906	GRMZM2G504906_P01	TRUE	TRUE	qSNQLLDITGDILQQIVR	95%	n+304 (+304)	70.38	25.00
6928	seq=translation; coord=7:81127590..81139739:-1; parent_transcript=GRMZM2G542753_T01; parent_gene=GRMZM2G542753	GRMZM2G542753_P01	TRUE	TRUE	nESTIEENEIR	95%	n+304 (+304)	56.45	25.00
6929	seq=translation; coord=6:86255384..86258220:1; parent_transcript=GRMZM5G832166_T01; parent_gene=GRMZM5G832166	GRMZM5G832166_P01,GRMZM5G832166_P02	TRUE	TRUE	gEPGSGTDFPSEYEENDMDELALVk	95%	n+304 (+304), K+304 (+304)	32.37	25.00
6930	seq=translation; coord=7:10775147..10779088:1; parent_transcript=GRMZM5G841619_T01; parent_gene=GRMZM5G841619	GRMZM5G841619_P01	TRUE	TRUE	eAGVHGLVVPDVPLEETDVLr	95%	n+304 (+304)	46.53	25.15
6931	seq=translation; coord=3:146437030..146439921:1; parent_transcript=GRMZM5G843368_T01; parent_gene=GRMZM5G843368	GRMZM5G843368_P01	TRUE	TRUE	iEALPTFIIFk	95%	n+304 (+304), K+304 (+304)	30.53	25.00
6932	seq=translation; coord=6:33247120..33251009:1; parent_transcript=GRMZM5G886561_T02; parent_gene=GRMZM5G886561	GRMZM5G886561_P02,GRMZM5G886561_P03	TRUE	TRUE	iPHPDAALEESISEVWDQSLQR	95%	n+304 (+304)	63.15	25.00
6933	seq=translation; coord=2:173604553..173607325:-1; parent_transcript=GRMZM5G887303_T01; parent_gene=GRMZM5G887303	GRMZM5G887303_P01	TRUE	TRUE	aGWPVADTPDPTRL	95%	n+304 (+304)	60.42	25.00
6934	seq=translation; coord=5:4253373..4257134:1; parent_transcript=GRMZM2G007063_T01; parent_gene=GRMZM2G007063	GRMZM2G007063_P01,GRMZM2G007063_P04, GRMZM2G016150_P01	TRUE	TRUE	aAHLNELEAQVAQLR	95%	n+304 (+304)	28.87	25.76
6935	seq=translation; coord=2:1717982..1719190:-1; parent_transcript=GRMZM2G436199_T01; parent_gene=GRMZM2G436199	GRMZM2G436199_P01	TRUE	TRUE	vYGLPTLILFk	92%	n+304 (+304), K+304 (+304)	26.64	25.00
6936	seq=translation; coord=10:131593783..131595368:-1; parent_transcript=GRMZM2G034651_T01; parent_gene=GRMZM2G034651	GRMZM2G034651_P01,GRMZM2G034709_P01, GRMZM2G041724_P01,GRMZM2G041724_P02, GRMZM2G046916_P01,GRMZM2G053622_P01, GRMZM2G073041_P01	TRUE	TRUE	rIDELDLPR	94%	n+304 (+304)	28.85	25.84
6937	seq=translation; coord=1:76339507..76340561:1; parent_transcript=GRMZM2G174708_T01; parent_gene=GRMZM2G174708	GRMZM2G174708_P01	TRUE	TRUE	aLPDLTLFLR	94%	n+304 (+304)	30.27	25.00
6938	seq=translation; coord=5:36664128..36680454:1; parent_transcript=GRMZM2G051174_T01; parent_gene=GRMZM2G051174	GRMZM2G051174_P01	TRUE	TRUE	aVGEQLIAANPIELAVGNIVR	93%	n+304 (+304)	27.37	25.00
6939	seq=translation; coord=6:69621822..69626211:1; parent_transcript=GRMZM2G168299_T01; parent_gene=GRMZM2G168299	GRMZM2G168299_P01,GRMZM2G168299_P02	TRUE	TRUE	aVAWDMLk	94%	n+304 (+304), K+304 (+304)	28.77	26.45

6940	seq=translation; coord=1:264497788..264511128:1; parent_transcript=GRMZM2G033619_T01; parent_gene=GRMZM2G033619	GRMZM2G033619_P01,GRMZM2G033619_P02	TRUE	TRUE	nLEQVVGMLNSFQDPHPR	93%	n+304 (+304)	27.29	25.00
6941	seq=translation; coord=8:155393198..155396041:-1; parent_transcript=GRMZM2G042034_T01; parent_gene=GRMZM2G042034	GRMZM2G042034_P01,GRMZM2G042034_P03, GRMZM2G069061_P01,GRMZM5G878308_P01, GRMZM5G878308_P03	TRUE	TRUE	vDDLNMWAR	92%	n+304 (+304)	28.64	25.00
6942	seq=translation; coord=8:167085302..167087579:1; parent_transcript=GRMZM2G162329_T01; parent_gene=GRMZM2G162329	GRMZM2G162329_P01	TRUE	TRUE	nVEEIR	93%	n+304 (+304)	30.84	26.51
6943	seq=translation; coord=5:68395460..68398901:-1; parent_transcript=GRMZM2G074957_T01; parent_gene=GRMZM2G074957	GRMZM2G074957_P01	TRUE	TRUE	vEDAIEILEHVLK	93%	n+304 (+304), K+304 (+304)	27.03	25.00
6944	seq=translation; coord=5:209670201..209672210:1; parent_transcript=GRMZM2G072861_T01; parent_gene=GRMZM2G072861	GRMZM2G072861_P01	TRUE	TRUE	gVYSQPDNIMGR	92%	n+304 (+304)	29.22	25.00
6945	seq=translation; coord=4:48543090..48545401:-1; parent_transcript=GRMZM2G078283_T01; parent_gene=GRMZM2G078283	GRMZM2G078283_P01,GRMZM2G078283_P02	TRUE	TRUE	gLEVLAEFEK	90%	n+304 (+304), K+304 (+304)	25.74	25.42
6946	seq=translation; coord=6:140907550..140916545:1; parent_transcript=GRMZM2G141760_T01; parent_gene=GRMZM2G141760	GRMZM2G141760_P01,GRMZM2G141760_P02	TRUE	TRUE	IAEHPIGSPDELK	92%	n+304 (+304)	27.08	25.74
6947	seq=translation; coord=2:156327934..156329194:-1; parent_transcript=GRMZM2G164440_T01; parent_gene=GRMZM2G164440	GRMZM2G164440_P01,GRMZM2G164440_P02	TRUE	TRUE	tDPPAAPSQAccDALAGADLK	91%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57), K+304 (+304)	26.30	25.00
6948	seq=translation; coord=3:4344526..4345251:-1; parent_transcript=GRMZM2G346457_T01; parent_gene=GRMZM2G346457	GRMZM2G346457_P01	TRUE	TRUE	aLLADLLALR	91%	n+304 (+304)	29.57	26.35
6949	seq=translation; coord=8:110686795..110688334:1; parent_transcript=GRMZM2G150134_T01; parent_gene=GRMZM2G150134	GRMZM2G150134_P01	TRUE	TRUE	sLAPIFAVDITSPAALLR	91%	n+304 (+304)	26.05	25.00
6950	seq=translation; coord=7:138459627..138464600:1; parent_transcript=GRMZM2G166897_T01; parent_gene=GRMZM2G166897	GRMZM2G166897_P01,GRMZM2G166897_P02	TRUE	TRUE	ISADELLER	91%	n+304 (+304)	28.94	26.22
6951	seq=translation; coord=2:206365031..206369304:1; parent_transcript=GRMZM2G030713_T01; parent_gene=GRMZM2G030713	GRMZM2G030713_P01	TRUE	TRUE	eAELHALYLLR	91%	n+304 (+304)	26.63	25.74
6952	seq=translation; coord=4:1487016..1490811:1; parent_transcript=GRMZM2G107239_T01; parent_gene=GRMZM2G107239	GRMZM2G107239_P01,GRMZM2G107239_P02	TRUE	TRUE	iVSLAFDVISR	92%	n+304 (+304)	29.01	26.28
6953	seq=translation; coord=10:99471562..99472802:1; parent_transcript=GRMZM2G074585_T02; parent_gene=GRMZM2G074585	GRMZM2G074585_P02	TRUE	TRUE	iScDYQADPR	91%	n+304 (+304), Carbamidomethyl (+57)	27.78	25.00
6954	seq=translation; coord=1:157064978..157068691:1; parent_transcript=GRMZM2G315848_T01; parent_gene=GRMZM2G315848	GRMZM2G315848_P01,GRMZM2G315848_P02, GRMZM2G315848_P03	TRUE	TRUE	aSPLVLGLK	90%	n+304 (+304), K+304 (+304)	25.69	25.00
6955	seq=translation; coord=4:86282879..86284714:-1; parent_transcript=GRMZM2G089698_T01; parent_gene=GRMZM2G089698	GRMZM2G089698_P01	TRUE	TRUE	aALGAALVPFYPLAGR	90%	n+304 (+304)	25.67	25.00
6956	seq=translation; coord=8:89528703..89529666:1; parent_transcript=GRMZM2G000777_T01; parent_gene=GRMZM2G000777	GRMZM2G000777_P01	TRUE	TRUE	dAANEALAAFDALLAR	90%	n+304 (+304)	25.99	25.55
6957	GRMZM2G159013_P01-R	GRMZM2G159013_P01-R	TRUE	TRUE	IEILGLK	91%	n+304 (+304), K+304 (+304)	25.42	25.00

6958	seq=translation; coord=8:147431766..147436951:1; parent_transcript=GRMZM2G000177_T01; parent_gene=GRMZM2G000177	GRMZM2G000177_P01	TRUE	TRUE	vFLDLVTMR	89%	n+304 (+304)	28.79	27.16
6959	seq=translation; coord=1:204683833..204695252:-1; parent_transcript=GRMZM2G058402_T01; parent_gene=GRMZM2G058402	GRMZM2G058402_P01	TRUE	TRUE	vLSEER	88%	n+304 (+304)	26.84	25.56
6960	GRMZM2G180082_P01-R seq=translation; coord=5:203313494..203315969:-1;	GRMZM2G180082_P01-R	TRUE	TRUE	IQIDHAK	87%	n+304 (+304), K+304 (+304)	25.79	25.00
6961	parent_transcript=GRMZM2G158568_T01; parent_gene=GRMZM2G158568 seq=translation; coord=8:69589821..69590301:1;	GRMZM2G158568_P01	TRUE	TRUE	aMGTTDVR	86%	n+304 (+304)	25.26	25.00
6962	parent_transcript=GRMZM2G025240_T01; parent_gene=GRMZM2G025240 seq=translation; coord=4:204339354..204343743:1;	GRMZM2G025240_P01	TRUE	TRUE	gQYTTFMR	86%	n+304 (+304)	25.12	25.00
6963	parent_transcript=GRMZM2G117064_T01; parent_gene=GRMZM2G117064 seq=translation; coord=5:6671638..6674577:-1;	GRMZM2G117064_P01	TRUE	TRUE	ILWDMLVFR	87%	n+304 (+304)	27.09	26.86
6964	parent_transcript=GRMZM5G808610_T01; parent_gene=GRMZM5G808610 seq=translation; coord=9:152556214..152556891:-1;	GRMZM5G808610_P01	TRUE	TRUE	gAALLIR	87%	n+304 (+304)	25.10	25.00
6965	parent_transcript=AC149475.2_FGT007; parent_gene=AC149475.2_FG007 seq=translation; coord=5:4582792..4584392:1;	AC149475.2_FGP007	TRUE	TRUE	rLDLSASPLADPEAAAFASPR	95%	n+304 (+304)	44.18	25.00
6966	parent_transcript=AC159612.1_FGT007; parent_gene=AC159612.1_FG007 seq=translation; coord=5:128454834..128463337:1;	AC159612.1_FGP007	TRUE	TRUE	vTFPALQNIQNALNEAGLGDTVK	95%	n+304 (+304), K+304 (+304)	32.21	25.00
6967	parent_transcript=AC198206.5_FGT001; parent_gene=AC198206.5_FG001 seq=translation; coord=3:126509251..126510797:-1;	AC198206.5_FGP001	TRUE	TRUE	gLFDSPWSDEVVGGVELAK	95%	n+304 (+304), K+304 (+304)	34.08	25.17
6968	parent_transcript=AC210168.4_FGT003; parent_gene=AC210168.4_FG003 seq=translation; coord=1:224037328..224040990:1;	AC210168.4_FGP003	TRUE	TRUE	tTPTDVEVPQR	95%	n+304 (+304)	35.38	25.00
6969	parent_transcript=AC210173.4_FGT005; parent_gene=AC210173.4_FG005 seq=translation; coord=9:149274596..149278053:1;	AC210173.4_FGP005	TRUE	TRUE	IQQELADVGLDR	95%	n+304 (+304)	41.81	26.38
6970	parent_transcript=GRMZM2G004172_T01; parent_gene=GRMZM2G004172 seq=translation; coord=8:1523477..1527610:-1;	GRMZM2G004172_P01,GRMZM2G070716_P01, GRMZM2G070716_P02	TRUE	TRUE	sAILPMLQAEEDER	95%	n+304 (+304)	37.74	25.00
6971	parent_transcript=GRMZM2G005980_T01; parent_gene=GRMZM2G005980 seq=translation; coord=8:25119900..25122631:1;	GRMZM2G005980_P01,GRMZM2G130366_P01	TRUE	TRUE	gELYVLLNLR	95%	n+304 (+304)	33.22	26.04
6972	parent_transcript=GRMZM2G007021_T01; parent_gene=GRMZM2G007021 seq=translation; coord=8:80681448..80685002:-1;	GRMZM2G007021_P01,GRMZM2G007021_P02, GRMZM2G102795_P01,GRMZM2G127850_P01, GRMZM5G871980_P01	TRUE	TRUE	dVAWAPNLGLPK	95%	n+304 (+304), K+304 (+304)	43.85	25.88
6973	parent_transcript=GRMZM2G008464_T02; parent_gene=GRMZM2G008464 seq=translation; coord=5:14814824..14815810:1;	GRMZM2G008464_P02,GRMZM5G886688_P01	TRUE	TRUE	ecSGVQQLWAR	95%	n+304 (+304), Carbamidomethyl (+57)	32.50	25.00
6974	parent_transcript=GRMZM2G010048_T01; parent_gene=GRMZM2G010048	GRMZM2G010048_P01	TRUE	TRUE	vGFEPITLAEYSLGGTGADR	95%	n+304 (+304)	43.10	25.00
6975	seq=translation; coord=7:15074371..15076305:-1; parent_transcript=GRMZM2G013065_T01; parent_gene=GRMZM2G013065	GRMZM2G013065_P01,GRMZM2G014400_P01, GRMZM2G022313_P01,GRMZM2G022313_P02, GRMZM2G144890_P01,GRMZM2G162954_P01	TRUE	TRUE	gFGFITYDSEDAVDK	95%	n+304 (+304), K+304 (+304)	70.28	25.00

6976	seq=translation; coord=9:16717314..16722369:1; parent_transcript=GRMZM2G014076_T01; parent_gene=GRMZM2G014076 seq=translation; coord=5:35276306..35278954:-1;	GRMZM2G014076_P01,GRMZM2G014076_P02	TRUE	TRUE	IQIPDVETVAAPDNVnKDEL	95%	n+304 (+304), K+304 (+304)	37.62	26.49
6977	parent_transcript=GRMZM2G018082_T01; parent_gene=GRMZM2G018082 seq=translation; coord=2:43117505..43119018:-1;	GRMZM2G018082_P01	TRUE	TRUE	sILWAVDYELPETVIAHR	95%	n+304 (+304)	36.62	25.51
6978	parent_transcript=GRMZM2G018275_T01; parent_gene=GRMZM2G018275 seq=translation; coord=1:235360116..235365801:1;	GRMZM2G018275_P01	TRUE	TRUE	dLAGWGGLMGAGHDYyER	95%	n+304 (+304), iTRAQ8plex (+304)	28.35	25.00
6979	parent_transcript=GRMZM2G020295_T01; parent_gene=GRMZM2G020295 seq=translation; coord=1:267867135..267870655:-1;	GRMZM2G020295_P01,GRMZM2G020295_P02, GRMZM2G020295_P03	TRUE	TRUE	aILGSSVPFQSLk	95%	n+304 (+304), K+304 (+304)	45.40	25.00
6980	parent_transcript=GRMZM2G023110_T01; parent_gene=GRMZM2G023110 seq=translation; coord=5:84248220..84252180:1;	GRMZM2G023110_P01	TRUE	TRUE	iSEIGELQHEFIVPLR	95%	n+304 (+304)	45.66	25.82
6981	parent_transcript=GRMZM2G026117_T01; parent_gene=GRMZM2G026117 seq=translation; coord=9:1443455..1448097:1;	GRMZM2G026117_P01,GRMZM2G026117_P02, GRMZM2G026117_P03,GRMZM2G041159_P01, GRMZM2G041159_P02	TRUE	TRUE	eGDVSATLLALAGLR	95%	n+304 (+304)	57.97	25.84
6982	parent_transcript=GRMZM2G027627_T01; parent_gene=GRMZM2G027627 seq=translation; coord=5:4684019..4687923:-1;	GRMZM2G027627_P01	TRUE	TRUE	gGDPVAAFAELMGR	95%	n+304 (+304)	38.32	25.00
6983	parent_transcript=GRMZM2G028218_T01; parent_gene=GRMZM2G028218 seq=translation; coord=3:225301514..225308308:1;	GRMZM2G028218_P01,GRMZM2G028218_P02, GRMZM2G134917_P01,GRMZM2G337845_P01	TRUE	TRUE	yYEILGVSk	95%	n+304 (+304), K+304 (+304)	36.27	25.00
6984	parent_transcript=GRMZM2G040401_T01; parent_gene=GRMZM2G040401 seq=translation; coord=1:63645310..63646802:1;	GRMZM2G040401_P01,GRMZM2G040401_P02	TRUE	TRUE	hAFIGLGR	95%	n+304 (+304)	39.60	25.00
6985	parent_transcript=GRMZM2G040638_T01; parent_gene=GRMZM2G040638 seq=translation; coord=1:195400126..195416505:1;	GRMZM2G040638_P01	TRUE	TRUE	gMSLEDLVLSGAHTVGR	95%	n+304 (+304)	64.72	25.62
6986	parent_transcript=GRMZM2G043198_T01; parent_gene=GRMZM2G043198 seq=translation; coord=7:163371037..163375463:1;	GRMZM2G043198_P01,GRMZM2G043198_P03	TRUE	TRUE	mVGyALQAADILak	95%	n+304 (+304), K+304 (+304)	31.92	25.00
6987	parent_transcript=GRMZM2G044023_T01; parent_gene=GRMZM2G044023 seq=translation; coord=9:43114595..43121822:1;	GRMZM2G044023_P01,GRMZM2G044023_P03, GRMZM5G873123_P01,GRMZM5G873123_P02	TRUE	TRUE	aALAIIDEMVDAGFTPSk	95%	n+304 (+304), K+304 (+304)	51.34	26.28
6988	parent_transcript=GRMZM2G047178_T01; parent_gene=GRMZM2G047178 seq=translation; coord=4:219992405..219994767:-1;	GRMZM2G047178_P01,GRMZM2G105598_P02, GRMZM2G105598_P03,GRMZM2G105598_P04	TRUE	TRUE	fAVGALAFDDVSVAVDHLK	95%	n+304 (+304), K+304 (+304)	45.14	25.42
6989	parent_transcript=GRMZM2G051185_T01; parent_gene=GRMZM2G051185 seq=translation; coord=4:187289565..187295583:1;	GRMZM2G051185_P01	TRUE	TRUE	aAGTLNALADQDQIQLLYHVLPR	95%	n+304 (+304)	71.32	25.00
6990	parent_transcript=GRMZM2G055507_T01; parent_gene=GRMZM2G055507 seq=translation; coord=5:65203097..65206027:1;	GRMZM2G055507_P01	TRUE	TRUE	aVDQIIQIPTVLR	95%	n+304 (+304)	43.02	25.00
6991	parent_transcript=GRMZM2G055682_T01; parent_gene=GRMZM2G055682 seq=translation; coord=1:276989217..276990796:1;	GRMZM2G055682_P01	TRUE	TRUE	aLAIEALEQQR	95%	n+304 (+304)	38.59	26.30
6992	parent_transcript=GRMZM2G058032_T01; parent_gene=GRMZM2G058032 seq=translation; coord=8:16690779..16693942:-1;	GRMZM2G058032_P01,GRMZM2G058032_P02	TRUE	TRUE	gEFcIDDIDFDEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	37.00	25.00
6993	parent_transcript=GRMZM2G061187_T01; parent_gene=GRMZM2G061187	GRMZM2G061187_P01,GRMZM2G459861_P01	TRUE	TRUE	ILAVDIPMASGPDQR	95%	n+304 (+304)	44.13	25.93

6994	seq=translation; coord=1:290103711..290108581:1; parent_transcript=GRMZM2G062394_T01; parent_gene=GRMZM2G062394	GRMZM2G062394_P01,GRMZM2G108355_P01, GRMZM2G108355_P02,GRMZM2G108355_P03	TRUE	TRUE	sPVTicGDIHGQFHDLAELFR	95%	n+304 (+304), Carbamidomethyl (+57)	35.07	25.07
6995	GRMZM2G066274_P01-R seq=translation; coord=9:8459603..8468658:-1;	GRMZM2G066274_P01-R	TRUE	TRUE	yNQILR	95%	n+304 (+304)	31.26	25.11
6996	parent_transcript=GRMZM2G066373_T01; parent_gene=GRMZM2G066373 seq=translation; coord=2:203713965..203723595:1;	GRMZM2G066373_P01	TRUE	TRUE	IWSEADEIALLTGAAAFk	95%	n+304 (+304), K+304 (+304)	37.57	25.00
6997	parent_transcript=GRMZM2G067063_T01; parent_gene=GRMZM2G067063 seq=translation; coord=7:163915244..163920524:-1;	GRMZM2G067063_P01,GRMZM2G067063_P02, GRMZM2G067063_P03	TRUE	TRUE	vDcTEEVeLcR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	39.44	25.00
6998	parent_transcript=GRMZM2G069405_T01; parent_gene=GRMZM2G069405 seq=translation; coord=7:127252507..127255099:-1;	GRMZM2G069405_P01,GRMZM2G069405_P02	TRUE	TRUE	nLPFEATVEMVEQEFSk	95%	n+304 (+304), K+304 (+304)	51.46	25.00
6999	parent_transcript=GRMZM2G072240_T01; parent_gene=GRMZM2G072240 seq=translation; coord=3:222996465..222998811:-1;	GRMZM2G072240_P01,GRMZM2G072240_P02	TRUE	TRUE	gIFLGNPLLDLYLYek	95%	n+304 (+304), K+304 (+304)	38.00	25.00
7000	parent_transcript=GRMZM2G074599_T01; parent_gene=GRMZM2G074599 seq=translation; coord=9:1848054..1851533:1;	GRMZM2G074599_P01	TRUE	TRUE	sDTSdVSGEQNEGDEHK	95%	n+304 (+304), K+304 (+304)	42.25	25.00
7001	parent_transcript=GRMZM2G075470_T01; parent_gene=GRMZM2G075470 seq=translation; coord=4:170814386..170816284:1;	GRMZM2G075470_P01,GRMZM2G075470_P02	TRUE	TRUE	aIEVLLGDFHdR	95%	n+304 (+304)	38.69	25.00
7002	parent_transcript=GRMZM2G075513_T01; parent_gene=GRMZM2G075513 seq=translation; coord=1:300464398..300469096:1;	GRMZM2G075513_P01	TRUE	TRUE	gVVADPEGLAGR	95%	n+304 (+304)	32.72	25.26
7003	parent_transcript=GRMZM2G077222_T01; parent_gene=GRMZM2G077222 seq=translation; coord=1:251088454..251096714:-1;	GRMZM2G077222_P01	TRUE	TRUE	aAVESEMEVLLk	95%	n+304 (+304), K+304 (+304)	45.25	25.16
7004	parent_transcript=GRMZM2G080828_T01; parent_gene=GRMZM2G080828 seq=translation; coord=4:116701848..116708846:-1;	GRMZM2G080828_P01,GRMZM2G080828_P02	TRUE	TRUE	IAPPLTISPEELAEAsk	95%	n+304 (+304), K+304 (+304)	44.72	25.24
7005	parent_transcript=GRMZM2G082642_T01; parent_gene=GRMZM2G082642 seq=translation; coord=1:202765503..202766778:1;	GRMZM2G082642_P01,GRMZM2G082642_P02, GRMZM2G082642_P03,GRMZM2G082642_P05, GRMZM2G082642_P06,GRMZM2G082642_P07	TRUE	TRUE	INLETISHWIVR	95%	n+304 (+304)	53.81	26.67
7006	parent_transcript=GRMZM2G090177_T01; parent_gene=GRMZM2G090177 seq=translation; coord=5:24436192..24442540:-1;	GRMZM2G090177_P01	TRUE	TRUE	IPLRDVLDDAGGVGGAR	95%	n+304 (+304)	31.76	25.09
7007	parent_transcript=GRMZM2G090736_T01; parent_gene=GRMZM2G090736 seq=translation; coord=7:988166..993667:1;	GRMZM2G090736_P01	TRUE	TRUE	nEEAGQPESATEk	95%	n+304 (+304), K+304 (+304)	41.44	25.00
7008	parent_transcript=GRMZM2G090824_T01; parent_gene=GRMZM2G090824 seq=translation; coord=7:34171226..34185881:1;	GRMZM2G090824_P01,GRMZM2G090824_P02	TRUE	TRUE	qSFITNLQALNcASFLGak	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	53.32	25.00
7009	parent_transcript=GRMZM2G092129_T01; parent_gene=GRMZM2G092129 seq=translation; coord=9:154438057..154439339:1;	GRMZM2G092129_P01,GRMZM2G092129_P02	TRUE	TRUE	IaVNTLESEITQDATLk	95%	n+304 (+304), K+304 (+304)	38.75	26.06
7010	parent_transcript=GRMZM2G092718_T01; parent_gene=GRMZM2G092718 seq=translation; coord=9:154404210..154409319:-1;	GRMZM2G092718_P01	TRUE	TRUE	aMEAVADIYGIDSIAADVk	95%	n+304 (+304), K+304 (+304)	56.24	25.44
7011	parent_transcript=GRMZM2G092741_T01; parent_gene=GRMZM2G092741	GRMZM2G092741_P01,GRMZM2G092741_P02, GRMZM2G137236_P01	TRUE	TRUE	IVLFLGNk	95%	n+304 (+304), K+304 (+304)	29.67	25.00

7012	seq=translation; coord=2:64929955..64930706:1; parent_transcript=GRMZM2G097747_T01; parent_gene=GRMZM2G097747	GRMZM2G097747_P01	TRUE	TRUE	aARPDVDEAAVAEAAAR	95%	n+304 (+304)	48.36	25.00
7013	seq=translation; coord=8:23887719..23890042:1; parent_transcript=GRMZM2G099483_T01; parent_gene=GRMZM2G099483	GRMZM2G099483_P01	TRUE	TRUE	sADGVDGEYAATASR	95%	n+304 (+304)	52.95	25.00
7014	seq=translation; coord=2:37049378..37052466:1; parent_transcript=GRMZM2G100315_T01; parent_gene=GRMZM2G100315	GRMZM2G100315_P01	TRUE	TRUE	aVGIEHVPEIVASSVENVQR	95%	n+304 (+304)	31.43	25.25
7015	seq=translation; coord=5:200934680..200937975:1; parent_transcript=GRMZM2G101287_T01; parent_gene=GRMZM2G101287	GRMZM2G101287_P01	TRUE	TRUE	hAFDWALGHIAR	95%	n+304 (+304)	44.69	25.00
7016	seq=translation; coord=8:1091537..1092833:-1; parent_transcript=GRMZM2G103512_T01; parent_gene=GRMZM2G103512	GRMZM2G103512_P01	TRUE	TRUE	tVATGDVVFVPR	95%	n+304 (+304)	65.84	26.03
7017	seq=translation; coord=8:153794205..153796938:-1; parent_transcript=GRMZM2G112535_T01; parent_gene=GRMZM2G112535	GRMZM2G112535_P01,GRMZM2G112535_P02	TRUE	TRUE	nVEATVLEILR	95%	n+304 (+304)	37.15	25.17
7018	seq=translation; coord=2:196406920..196412546:-1; parent_transcript=GRMZM2G114107_T01; parent_gene=GRMZM2G114107	GRMZM2G114107_P01,GRMZM2G114107_P02	TRUE	TRUE	hMNDQGWVPINLILGFNR	95%	n+304 (+304)	32.21	25.35
7019	seq=translation; coord=5:60777721..60779927:-1; parent_transcript=GRMZM2G115621_T01; parent_gene=GRMZM2G115621	GRMZM2G115621_P01,GRMZM2G115621_P02, GRMZM2G115621_P03	TRUE	TRUE	hLFYQDASDLR	95%	n+304 (+304)	49.69	25.00
7020	seq=translation; coord=1:70247200..70252204:1; parent_transcript=GRMZM2G117222_T02; parent_gene=GRMZM2G117222	GRMZM2G117222_P02,GRMZM2G117222_P03, GRMZM2G117222_P04	TRUE	TRUE	mGWSESAMVAGAR	95%	n+304 (+304)	34.53	25.00
7021	seq=translation; coord=1:68133178..68136953:-1; parent_transcript=GRMZM2G120587_T01; parent_gene=GRMZM2G120587	GRMZM2G120587_P01	TRUE	TRUE	sWGSLLDFIDTk	95%	n+304 (+304), K+304 (+304)	41.84	25.84
7022	seq=translation; coord=4:12974975..12984124:-1; parent_transcript=GRMZM2G124593_T01; parent_gene=GRMZM2G124593	GRMZM2G124593_P01,GRMZM2G124593_P02	TRUE	TRUE	yRPTMPILAVIFPR	95%	n+304 (+304)	40.25	25.15
7023	seq=translation; coord=5:44404760..44408781:1; parent_transcript=GRMZM2G128737_T01; parent_gene=GRMZM2G128737	GRMZM2G128737_P01	TRUE	TRUE	iDELSALLAEAMTk	95%	n+304 (+304), K+304 (+304)	33.00	25.05
7024	seq=translation; coord=10:141365369..141372247:-1; parent_transcript=GRMZM2G128914_T01; parent_gene=GRMZM2G128914	GRMZM2G128914_P01,GRMZM2G128914_P02, GRMZM2G128914_P03,GRMZM2G130889_P01, GRMZM2G130889_P03	TRUE	TRUE	qMWETSMEGLLSLTk	95%	n+304 (+304), K+304 (+304)	40.61	25.55
7025	seq=translation; coord=3:220638696..220641589:1; parent_transcript=GRMZM2G130305_T01; parent_gene=GRMZM2G130305	GRMZM2G130305_P01,GRMZM2G130305_P02	TRUE	TRUE	dYSLITDLAAALTk	95%	n+304 (+304), K+304 (+304)	51.13	25.00
7026	seq=translation; coord=4:240155787..240160770:1; parent_transcript=GRMZM2G133660_T01; parent_gene=GRMZM2G133660	GRMZM2G133660_P01,GRMZM2G133660_P02, GRMZM2G133660_P03,GRMZM2G133660_P04	TRUE	TRUE	rVEVNLEQTGSEP	95%	n+304 (+304)	34.18	25.00
7027	seq=translation; coord=6:109879472..109881654:1; parent_transcript=GRMZM2G135970_T01; parent_gene=GRMZM2G135970	GRMZM2G135970_P01	TRUE	TRUE	tPILLHDHNEFLEDR	95%	n+304 (+304)	31.10	25.00
7028	seq=translation; coord=2:55687675..55688855:-1; parent_transcript=GRMZM2G136364_T01; parent_gene=GRMZM2G136364	GRMZM2G136364_P01,GRMZM2G136364_P02	TRUE	TRUE	aEVAITIPk	95%	n+304 (+304), K+304 (+304)	32.50	25.00
7029	seq=translation; coord=7:109056610..109058446:-1; parent_transcript=GRMZM2G146225_T01; parent_gene=GRMZM2G146225	GRMZM2G146225_P01	TRUE	TRUE	IkDPINVATDQATSGMLSPR	95%	n+304 (+304), K+304 (+304)	54.81	25.73

7030	seq=translation; coord=3:161846976..161856015:1; parent_transcript=GRMZM2G146697_T02; parent_gene=GRMZM2G146697 seq=translation; coord=7:143409271..143414278:-1;	GRMZM2G146697_P02,GRMZM2G146697_P03	TRUE	TRUE	aYELQALLGLDk	95%	n+304 (+304), K+304 (+304)	38.03	25.00
7031	parent_transcript=GRMZM2G147422_T01; parent_gene=GRMZM2G147422 seq=translation; coord=8:173244055..173251921:-1;	GRMZM2G147422_P01	TRUE	TRUE	tPGSDVAAEAAAAMAAASVMFk	95%	n+304 (+304), K+304 (+304)	44.09	26.03
7032	parent_transcript=GRMZM2G153274_T01; parent_gene=GRMZM2G153274	GRMZM2G153274_P01,GRMZM2G153274_P02	TRUE	TRUE	vFLIDDISVR	95%	n+304 (+304)	35.55	25.00
7033	seq=translation; coord=1:210841573..210847241:1; parent_transcript=GRMZM2G155753_T01; parent_gene=GRMZM2G155753	GRMZM2G155753_P01,GRMZM2G155753_P02, GRMZM2G155753_P03,GRMZM2G155753_P04, GRMZM2G155753_P05,GRMZM2G155753_P06, GRMZM2G155753_P07	TRUE	TRUE	tLLFDIELLk	95%	n+304 (+304), K+304 (+304)	37.98	25.00
7034	seq=translation; coord=4:161049394..161067009:-1; parent_transcript=GRMZM2G156320_T01; parent_gene=GRMZM2G156320	GRMZM2G156320_P01,GRMZM2G156320_P02	TRUE	TRUE	dHPLSVEEWTSFLDR	95%	n+304 (+304)	59.90	25.00
7035	seq=translation; coord=8:118401123..118402532:-1; parent_transcript=GRMZM2G162109_T01; parent_gene=GRMZM2G162109	GRMZM2G162109_P01	TRUE	TRUE	vAAGSAGDGSSASGSAAAK	95%	n+304 (+304), K+304 (+304)	88.40	25.00
7036	seq=translation; coord=2:19199595..19200656:-1; parent_transcript=GRMZM2G162276_T01; parent_gene=GRMZM2G162276	GRMZM2G162276_P01	TRUE	TRUE	gNVLGVVFDVPIk	95%	n+304 (+304), K+304 (+304)	41.34	25.00
7037	seq=translation; coord=2:37117338..37120603:-1; parent_transcript=GRMZM2G165633_T01; parent_gene=GRMZM2G165633	GRMZM2G165633_P01	TRUE	TRUE	gWPVILSEFGVDNR	95%	n+304 (+304)	35.97	25.29
7038	seq=translation; coord=1:259212747..259218080:-1; parent_transcript=GRMZM2G165747_T01; parent_gene=GRMZM2G165747	GRMZM2G165747_P01,GRMZM2G165747_P02, GRMZM2G165747_P03	TRUE	TRUE	aAGASWIQFDEPTLVk	95%	n+304 (+304), K+304 (+304)	45.14	25.59
7039	seq=translation; coord=8:162849948..162860082:-1; parent_transcript=GRMZM2G166855_T01; parent_gene=GRMZM2G166855	GRMZM2G166855_P01	TRUE	TRUE	aEILHIFR	95%	n+304 (+304)	33.27	26.28
7040	seq=translation; coord=1:245027693..245031977:1; parent_transcript=GRMZM2G174574_T02; parent_gene=GRMZM2G174574	GRMZM2G174574_P02	TRUE	TRUE	fDVEDAVLAAIER	95%	n+304 (+304)	33.63	25.69
7041	seq=translation; coord=4:62334569..62340150:1; parent_transcript=GRMZM2G175499_T01; parent_gene=GRMZM2G175499	GRMZM2G175499_P01	TRUE	TRUE	sDLQSWLSGALGNQDTck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	41.29	25.00
7042	seq=translation; coord=7:161443263..161445533:1; parent_transcript=GRMZM2G178839_T01; parent_gene=GRMZM2G178839	GRMZM2G178839_P01,GRMZM2G178839_P02	TRUE	TRUE	sSPAAATTDASTGADSIIVk	95%	n+304 (+304), K+304 (+304)	65.19	25.67
7043	seq=translation; coord=5:198573774..198578071:1; parent_transcript=GRMZM2G181273_T01; parent_gene=GRMZM2G181273	GRMZM2G181273_P01,GRMZM2G181273_P02	TRUE	TRUE	gTTDcLGHVALVAQLMR	95%	n+304 (+304), Carbamidomethyl (+57)	37.58	25.97
7044	seq=translation; coord=4:37020795..37024171:1; parent_transcript=GRMZM2G302259_T02; parent_gene=GRMZM2G302259	GRMZM2G302259_P02,GRMZM2G302259_P03	TRUE	TRUE	dLVVDMTNFYSQYk	95%	n+304 (+304), K+304 (+304)	39.65	25.00
7045	seq=translation; coord=7:8467553..8472428:-1; parent_transcript=GRMZM2G312839_T01; parent_gene=GRMZM2G312839	GRMZM2G312839_P01	TRUE	TRUE	aVPGFGFHDVVIETPR	95%	n+304 (+304)	49.91	25.59
7046	seq=translation; coord=2:14534118..14542446:-1; parent_transcript=GRMZM2G314396_T01; parent_gene=GRMZM2G314396	GRMZM2G314396_P01,GRMZM2G321239_P01, GRMZM2G441511_P01	TRUE	TRUE	ITAHEVLcHPWIR	95%	n+304 (+304), Carbamidomethyl (+57)	28.75	25.68

7047	seq=translation; coord=1:55070838..55075644:-1; parent_transcript=GRMZM2G320325_T01; parent_gene=GRMZM2G320325	GRMZM2G320325_P01,GRMZM2G320325_P02, GRMZM2G320325_P03	TRUE	TRUE	sGLPALGPLFYSVVSPk	95%	n+304 (+304), K+304 (+304)	43.73	25.00
7048	seq=translation; coord=8:33309931..33317187:-1; parent_transcript=GRMZM2G367001_T02; parent_gene=GRMZM2G367001	GRMZM2G367001_P02	TRUE	TRUE	IADLLcLSLQEAEk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	30.69	25.13
7049	seq=translation; coord=3:138776830..138783206:-1; parent_transcript=GRMZM2G401934_T01; parent_gene=GRMZM2G401934	GRMZM2G401934_P01,GRMZM2G401934_P02, GRMZM2G401934_P03	TRUE	TRUE	fNPDDLFLYAVTDSGMNk	95%	n+304 (+304), K+304 (+304)	38.62	25.00
7050	seq=translation; coord=1:21082681..21083661:-1; parent_transcript=GRMZM2G411084_T01; parent_gene=GRMZM2G411084	GRMZM2G411084_P01,GRMZM2G479245_P01	TRUE	TRUE	IVETLAGDTILck	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	40.60	25.83
7051	seq=translation; coord=9:146890292..146891477:1; parent_transcript=GRMZM2G423331_T01; parent_gene=GRMZM2G423331	GRMZM2G423331_P01	TRUE	TRUE	aVIELGLIDDLAADGR	95%	n+304 (+304)	43.88	25.63
7052	seq=translation; coord=1:81105265..81107853:-1; parent_transcript=GRMZM2G430039_T01; parent_gene=GRMZM2G430039	GRMZM2G430039_P01	TRUE	TRUE	aDDYIPYLcGLGLGDDGVTEIAHRPVAcGGLR	95%	n+304 (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)	28.52	25.00
7053	seq=translation; coord=6:117823274..117843150:-1; parent_transcript=GRMZM2G431708_T01; parent_gene=GRMZM2G431708	GRMZM2G431708_P01,GRMZM2G431708_P02	TRUE	TRUE	dMAVFASGMIQAEKk	95%	n+304 (+304), K+304 (+304)	40.90	25.88
7054	seq=translation; coord=1:16822675..16826498:1; parent_transcript=GRMZM2G445602_T01; parent_gene=GRMZM2G445602	GRMZM2G445602_P01	TRUE	TRUE	aEASTAMFAALDELFDk	95%	n+304 (+304), K+304 (+304)	30.13	25.19
7055	seq=translation; coord=7:151193308..151195193:1; parent_transcript=GRMZM2G455075_T01; parent_gene=GRMZM2G455075	GRMZM2G455075_P01	TRUE	TRUE	gGSAYAALQAVVQDMLESHVPGTAPk	95%	n+304 (+304), K+304 (+304)	33.25	25.00
7056	seq=translation; coord=7:9368739..9372491:-1; parent_transcript=GRMZM2G456086_T01; parent_gene=GRMZM2G456086	GRMZM2G456086_P01	TRUE	TRUE	fIVIVDEtk	95%	n+304 (+304), K+304 (+304)	39.70	25.00
7057	seq=translation; coord=9:42834971..42841058:-1; parent_transcript=GRMZM2G465169_T01; parent_gene=GRMZM2G465169	GRMZM2G465169_P01,GRMZM2G465169_P02	TRUE	TRUE	iPALVETLVak	95%	n+304 (+304), K+304 (+304)	37.42	25.00
7058	seq=translation; coord=9:154307169..154311241:-1; parent_transcript=GRMZM2G467007_T01; parent_gene=GRMZM2G467007	GRMZM2G467007_P01,GRMZM2G467007_P02, GRMZM2G467007_P04	TRUE	TRUE	sAALDVEELADALGLGpk	95%	n+304 (+304), K+304 (+304)	39.08	25.53
7059	seq=translation; coord=7:92078951..92089092:-1; parent_transcript=GRMZM2G479906_T01; parent_gene=GRMZM2G479906	GRMZM2G319138_P01,GRMZM2G391815_P01, GRMZM2G479906_P01,GRMZM5G892675_P01	TRUE	TRUE	gVADFLQEVTsk	95%	n+304 (+304), K+304 (+304)	33.86	25.74
7060	seq=translation; coord=3:210695505..210702109:1; parent_transcript=GRMZM5G816356_T02; parent_gene=GRMZM5G816356	GRMZM5G816356_P02,GRMZM5G816356_P03	TRUE	TRUE	iHFGNLFLEVR	95%	n+304 (+304)	30.45	25.13
7061	seq=translation; coord=6:121308710..121312198:-1; parent_transcript=GRMZM5G841142_T02; parent_gene=GRMZM5G841142	GRMZM5G841142_P02	TRUE	TRUE	qAITAAGSGcMAALDAEHYLQEVGAQEGk	95%	n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	41.82	25.00
7062	seq=translation; coord=2:139066950..139068044:1; parent_transcript=GRMZM5G854138_T02; parent_gene=GRMZM5G854138	GRMZM5G854138_P02	TRUE	TRUE	iTEEVAAAAAVGAGGYVFHEHHEk	95%	n+304 (+304), K+304 (+304)	26.78	25.47
7063	seq=translation; coord=6:130130465..130134088:1; parent_transcript=GRMZM5G886257_T01; parent_gene=GRMZM5G886257	GRMZM5G886257_P01	TRUE	TRUE	vRDDMLLAASEALAEQVTEEHFAk	95%	n+304 (+304), K+304 (+304)	42.63	25.00
7064	seq=translation; coord=8:161423128..161428079:-1; parent_transcript=GRMZM2G133621_T02; parent_gene=GRMZM2G133621	GRMZM2G133621_P02,GRMZM2G171622_P01	TRUE	TRUE	nPVFVLADTLAVEALQk	95%	n+304 (+304), K+304 (+304)	29.04	25.00

7065	seq=translation; coord=1:9491186..9500155:1; parent_transcript=GRMZM2G103599_T01; parent_gene=GRMZM2G103599	GRMZM2G103599_P01	TRUE	TRUE	ILDVLLQLDHLk	95%	n+304 (+304), K+304 (+304)	28.79	25.00
7066	GRMZM2G087165_P01-R seq=translation; coord=10:9379084..9402965:1;	GRMZM2G087165_P01-R	TRUE	TRUE	gFVASDSk	94%	n+304 (+304), K+304 (+304)	32.75	26.76
7067	parent_transcript=GRMZM2G118286_T01; parent_gene=GRMZM2G118286 seq=translation; coord=6:78610403..78619923:1;	GRMZM2G118286_P01	TRUE	TRUE	ILWDTLVFGk	94%	n+304 (+304), K+304 (+304)	28.41	25.00
7068	parent_transcript=AC195587.4_FGT004; parent_gene=AC195587.4_FG004 seq=translation; coord=9:150418899..150423446:1;	AC195587.4_FGP004	TRUE	TRUE	ySVVVPIIGVQGFR	94%	n+304 (+304)	29.30	25.95
7069	parent_transcript=AC149828.2_FGT002; parent_gene=AC149828.2_FG002 seq=translation; coord=7:27669317..27671990:1;	AC149828.2_FGP002	TRUE	TRUE	vLTTEEIDQHlTAISERD	95%	n+304 (+304)	44.52	25.00
7070	parent_transcript=AC191534.3_FGT003; parent_gene=AC191534.3_FG003 seq=translation; coord=4:32243054..32246208:1;	AC191534.3_FGP003	TRUE	TRUE	dIMDVIESLQR	95%	n+304 (+304)	53.14	25.00
7071	parent_transcript=AC196475.3_FGT005; parent_gene=AC196475.3_FG005	AC196475.3_FGP005	TRUE	TRUE	dVASDGDEAESTGIVIR	95%	n+304 (+304)	69.06	25.00
7072	AC200754.4_FGP004-R seq=translation; coord=6:151130639..151134853:-1;	AC200754.4_FGP004-R	TRUE	TRUE	vLTGSIPR	95%	n+304 (+304)	33.63	27.78
7073	parent_transcript=AC203754.4_FGT008; parent_gene=AC203754.4_FG008 seq=translation; coord=3:44316015..44340734:-1;	AC203754.4_FGP008	TRUE	TRUE	iLLDVADALEk	95%	n+304 (+304), K+304 (+304)	37.30	25.02
7074	parent_transcript=AC213600.3_FGT002; parent_gene=AC213600.3_FG002 seq=translation; coord=1:296991644..296996802:-1;	AC213600.3_FGP002	TRUE	TRUE	vQQTQVQNVFQk	95%	n+304 (+304), K+304 (+304)	37.98	25.00
7075	parent_transcript=AC217358.3_FGT011; parent_gene=AC217358.3_FG011 seq=translation; coord=4:32433..63643:-1;	AC217358.3_FGP011	TRUE	TRUE	vSNIIDDVLEWSPk	95%	n+304 (+304), K+304 (+304)	33.43	25.63
7076	parent_transcript=GRMZM2G000510_T02; parent_gene=GRMZM2G000510 seq=translation; coord=6:74598823..74604163:-1;	GRMZM2G000510_P02,GRMZM2G000510_P03, GRMZM2G000510_P04	TRUE	TRUE	gLLGTAATiAR	95%	n+304 (+304)	41.31	25.00
7077	parent_transcript=GRMZM2G002100_T01; parent_gene=GRMZM2G002100 seq=translation; coord=2:221313310..221325791:1;	GRMZM2G002100_P01,GRMZM2G002100_P02, GRMZM2G020216_P01	TRUE	TRUE	tTSETDFMTEYVVTR	95%	n+304 (+304)	60.73	25.00
7078	parent_transcript=GRMZM2G005990_T01; parent_gene=GRMZM2G005990 seq=translation; coord=7:158460078..158467848:-1;	GRMZM2G005990_P01,GRMZM2G072608_P01, GRMZM2G139880_P01,GRMZM2G421493_P01	TRUE	TRUE	gVVEELLWFISGSTNAk	95%	n+304 (+304), K+304 (+304)	50.28	25.28
7079	parent_transcript=GRMZM2G006942_T01; parent_gene=GRMZM2G006942 seq=translation; coord=8:2990866..3047187:1;	GRMZM2G006942_P01	TRUE	TRUE	lQQLASVAGDVLLGk	95%	n+304 (+304), K+304 (+304)	31.36	25.00
7080	parent_transcript=GRMZM2G007915_T01; parent_gene=GRMZM2G007915 seq=translation; coord=4:93254018..93267787:1;	GRMZM2G007915_P01,GRMZM2G007915_P02	TRUE	TRUE	aELFGISGVTYSLTQGVVk	95%	n+304 (+304), K+304 (+304)	30.12	25.00
7081	parent_transcript=GRMZM2G008497_T01; parent_gene=GRMZM2G008497 seq=translation; coord=8:36505635..36507206:-1;	GRMZM2G008497_P01,GRMZM2G008497_P02	TRUE	TRUE	fQNLmHTLDFSYQALASGIAQHAEQR	95%	n+304 (+304)	38.86	25.00
7082	parent_transcript=GRMZM2G009719_T01; parent_gene=GRMZM2G009719 seq=translation; coord=6:39077271..39084693:1;	GRMZM2G009719_P01	TRUE	TRUE	mAADLLVMGSHGYGFIQR	95%	n+304 (+304)	45.71	25.00
7083	parent_transcript=GRMZM2G012964_T01; parent_gene=GRMZM2G012964	GRMZM2G012964_P01,GRMZM2G042623_P01, GRMZM2G042623_P02,GRMZM2G112769_P01	TRUE	TRUE	lPPPLLSk	95%	n+304 (+304), K+304 (+304)	29.14	25.20

7084	seq=translation; coord=1:171230397..171235966:1; parent_transcript=GRMZM2G015097_T01; parent_gene=GRMZM2G015097	GRMZM2G015097_P01	TRUE	TRUE	mATVLPkPVQTfEAGQDIVEQVIR	95%	n+304 (+304), K+304 (+304)	44.67	25.00
7085	seq=translation; coord=1:2876246..2896381:-1; parent_transcript=GRMZM2G015384_T01; parent_gene=GRMZM2G015384	GRMZM2G015384_P01,GRMZM2G015384_P02, GRMZM2G015384_P03	TRUE	TRUE	dGTVTDWDIVDNIWNHAFR	95%	n+304 (+304)	83.61	25.00
7086	seq=translation; coord=1:196696007..196703390:-1; parent_transcript=GRMZM2G019050_T01; parent_gene=GRMZM2G019050	GRMZM2G019050_P01,GRMZM2G019050_P02, GRMZM2G019050_P05	TRUE	TRUE	IDDFVASHPELFVIEGDFIHLR	95%	n+304 (+304)	43.47	25.05
7087	seq=translation; coord=4:34921125..34931317:1; parent_transcript=GRMZM2G020302_T01; parent_gene=GRMZM2G020302	GRMZM2G020302_P01	TRUE	TRUE	sLAGEEAQDWR	95%	n+304 (+304)	42.36	25.00
7088	seq=translation; coord=2:6033112..6040532:-1; parent_transcript=GRMZM2G022563_T01; parent_gene=GRMZM2G022563	GRMZM2G022563_P01	TRUE	TRUE	aLQEAGLPASSIDWLLLHQANQR	95%	n+304 (+304)	98.72	25.31
7089	seq=translation; coord=6:146462466..146475721:1; parent_transcript=GRMZM2G025074_T01; parent_gene=GRMZM2G025074	GRMZM2G025074_P01	TRUE	TRUE	yLVIIIEIR	95%	n+304 (+304)	30.91	25.00
7090	seq=translation; coord=5:155030183..155038462:-1; parent_transcript=GRMZM2G028366_T01; parent_gene=GRMZM2G028366	GRMZM2G028366_P01	TRUE	TRUE	mLFLDEADELLTGGSk	95%	n+304 (+304), K+304 (+304)	60.84	25.67
7091	seq=translation; coord=1:174669610..174673449:-1; parent_transcript=GRMZM2G028900_T01; parent_gene=GRMZM2G028900	GRMZM2G028900_P01,GRMZM2G028900_P02	TRUE	TRUE	aMPLESVIDVSDIDAVLQR	95%	n+304 (+304)	41.28	25.77
7092	seq=translation; coord=7:165245766..165253354:1; parent_transcript=GRMZM2G030578_T01; parent_gene=GRMZM2G030578	GRMZM2G030578_P01,GRMZM2G030578_P02	TRUE	TRUE	aISLQIIIVAlNMVSk	95%	n+304 (+304), K+304 (+304)	55.33	25.00
7093	seq=translation; coord=10:130301051..130304967:-1; parent_transcript=GRMZM2G031660_T01; parent_gene=GRMZM2G031660	GRMZM2G031660_P01	TRUE	TRUE	fGEVNPAGIAFYNR	95%	n+304 (+304)	40.25	25.00
7094	seq=translation; coord=2:51097812..51100252:1; parent_transcript=GRMZM2G035948_T01; parent_gene=GRMZM2G035948	GRMZM2G035948_P01	TRUE	TRUE	vEVVQSLPLVDSFEK	95%	n+304 (+304), K+304 (+304)	32.85	25.00
7095	seq=translation; coord=5:183615085..183618814:-1; parent_transcript=GRMZM2G036590_T01; parent_gene=GRMZM2G036590	GRMZM2G036590_P01	TRUE	TRUE	eESSEYEEGIIHQEFR	95%	n+304 (+304)	79.13	25.00
7096	seq=translation; coord=2:233746497..233750655:1; parent_transcript=GRMZM2G037614_T01; parent_gene=GRMZM2G037614	GRMZM2G037614_P01,GRMZM2G037614_P02	TRUE	TRUE	aVNLFTAVNQALHIALDTPR	95%	n+304 (+304)	53.44	25.34
7097	seq=translation; coord=5:70023297..70028827:1; parent_transcript=GRMZM2G044348_T02; parent_gene=GRMZM2G044348	GRMZM2G044348_P02,GRMZM2G044348_P03	TRUE	TRUE	tESEEGSTEEQDDSSk	95%	n+304 (+304), K+304 (+304)	32.55	25.00
7098	seq=translation; coord=5:217005369..217007365:1; parent_transcript=GRMZM2G048497_T01; parent_gene=GRMZM2G048497	GRMZM2G048497_P01	TRUE	TRUE	aPLIPGMAAvk	95%	n+304 (+304), K+304 (+304)	36.85	25.00
7099	seq=translation; coord=2:30305181..30329537:-1; parent_transcript=GRMZM2G052078_T01; parent_gene=GRMZM2G052078	GRMZM2G052078_P01,GRMZM2G052078_P02	TRUE	TRUE	vSAIESLLk	95%	n+304 (+304), K+304 (+304)	32.01	25.00
7100	seq=translation; coord=3:229384643..229387013:-1; parent_transcript=GRMZM2G053726_T01; parent_gene=GRMZM2G053726	GRMZM2G053726_P01	TRUE	TRUE	hVQLTVPLEQLIDR	95%	n+304 (+304)	49.09	25.51
7101	seq=translation; coord=2:936008..941357:1; parent_transcript=GRMZM2G058948_T01; parent_gene=GRMZM2G058948	GRMZM2G058948_P01	TRUE	TRUE	vISSVDTVVELTSLAEQk	95%	n+304 (+304), K+304 (+304)	32.31	25.01

7102	seq=translation; coord=6:135509765..135513009:1; parent_transcript=GRMZM2G061912_T01; parent_gene=GRMZM2G061912 seq=translation; coord=3:219370471..219375471:1;	GRMZM2G061912_P01,GRMZM2G061912_P02, GRMZM2G093186_P01	TRUE	TRUE	aQIWDTAGQER	95%	n+304 (+304)	31.42	25.00
7103	parent_transcript=GRMZM2G061990_T01; parent_gene=GRMZM2G061990 seq=translation; coord=10:5523751..5529199:-1;	GRMZM2G061990_P01	TRUE	TRUE	eLVDVEQFLLSR	95%	n+304 (+304)	43.72	26.21
7104	parent_transcript=GRMZM2G066496_T01; parent_gene=GRMZM2G066496 seq=translation; coord=9:24335015..24362059:1;	GRMZM2G066496_P01,GRMZM2G109785_P01, GRMZM5G825902_P02	TRUE	TRUE	IGALLDTMK	95%	n+304 (+304), K+304 (+304)	31.84	25.62
7105	parent_transcript=GRMZM2G069008_T01; parent_gene=GRMZM2G069008 seq=translation; coord=4:175130526..175133952:-1;	GRMZM2G069008_P01,GRMZM2G069008_P02, GRMZM2G069008_P03	TRUE	TRUE	aLSAIALYEMAK	95%	n+304 (+304), K+304 (+304)	30.14	25.72
7106	parent_transcript=GRMZM2G070138_T01; parent_gene=GRMZM2G070138	GRMZM2G070138_P01	TRUE	TRUE	vSAPVDSALQLK	95%	n+304 (+304), K+304 (+304)	39.35	26.30
7107	GRMZM2G073861_P01-R	GRMZM2G073861_P01- R,GRMZM2G073861_P02- R,GRMZM2G073861_P03- R,GRMZM2G173868_P04-R	TRUE	TRUE	gLSQIIR	95%	n+304 (+304)	33.01	25.00
7108	seq=translation; coord=2:209010511..209011342:1; parent_transcript=GRMZM2G077845_T01; parent_gene=GRMZM2G077845	GRMZM2G077845_P01	TRUE	TRUE	cQGcVSPSPYASK	95%	Carbamidomethyl (+57), n+304 (+304), Carbamidomethyl (+57), K+304 (+304)	31.59	25.00
7109	seq=translation; coord=5:23891310..23896229:1; parent_transcript=GRMZM2G086116_T01; parent_gene=GRMZM2G086116 seq=translation; coord=1:157223914..157238707:1;	GRMZM2G086116_P01,GRMZM2G129007_P01, GRMZM2G129007_P02	TRUE	TRUE	ILAPEFQPSVEALIHFLPPSR	95%	n+304 (+304)	46.08	25.00
7110	parent_transcript=GRMZM2G086887_T01; parent_gene=GRMZM2G086887 seq=translation; coord=6:156253579..156255646:1;	GRMZM2G086887_P01,GRMZM2G086887_P02	TRUE	TRUE	eWTL EEFEELHK	95%	n+304 (+304), K+304 (+304)	69.97	25.09
7111	parent_transcript=GRMZM2G088961_T01; parent_gene=GRMZM2G088961 seq=translation; coord=6:157023426..157028246:-1;	GRMZM2G088961_P01	TRUE	TRUE	dDIGSLLPTAIDSTDFEASLR	95%	n+304 (+304)	59.12	25.00
7112	parent_transcript=GRMZM2G090338_T01; parent_gene=GRMZM2G090338 seq=translation; coord=3:231597894..231608769:-1;	GRMZM2G090338_P01	TRUE	TRUE	vPNQLyLAMDTLADEFGIGTLR	95%	n+304 (+304), iTRAQ8plex (+304)	39.51	25.24
7113	parent_transcript=GRMZM2G090722_T01; parent_gene=GRMZM2G090722 seq=translation; coord=4:74266074..74269595:-1;	GRMZM2G090722_P01	TRUE	TRUE	IQWFLNSIK	95%	n+304 (+304), K+304 (+304)	40.01	25.00
7114	parent_transcript=GRMZM2G091503_T01; parent_gene=GRMZM2G091503 seq=translation; coord=1:290553103..290555088:1;	GRMZM2G091503_P01,GRMZM2G091503_P04, GRMZM2G091503_P05	TRUE	TRUE	vAVAEGAGLTGDVSAVEQFIR	95%	n+304 (+304)	72.32	25.25
7115	parent_transcript=GRMZM2G092663_T01; parent_gene=GRMZM2G092663 seq=translation; coord=1:98542421..98547539:1;	GRMZM2G092663_P01,GRMZM2G092663_P02	TRUE	TRUE	fSMTPFQYTDLLAKPTK	95%	n+304 (+304), K+304 (+304), K+304 (+304)	27.67	25.00
7116	parent_transcript=GRMZM2G094390_T01; parent_gene=GRMZM2G094390 seq=translation; coord=9:16108443..16118632:1;	GRMZM2G094390_P01,GRMZM2G134045_P01	TRUE	TRUE	iSFQATQDLSSLK	95%	n+304 (+304), K+304 (+304)	33.09	26.39
7117	parent_transcript=GRMZM2G099355_T01; parent_gene=GRMZM2G099355 seq=translation; coord=10:5869546..5875906:1;	GRMZM2G099355_P01,GRMZM2G433801_P01	TRUE	TRUE	gMLDPLEVHLLDFPNIVIK	95%	n+304 (+304), K+304 (+304)	28.29	25.00
7118	parent_transcript=GRMZM2G104310_T01; parent_gene=GRMZM2G104310	GRMZM2G104310_P01,GRMZM2G104310_P03	TRUE	TRUE	fDAGFTESQMLDHMR	95%	n+304 (+304)	65.48	25.00

7119	seq=translation; coord=10:148856004..148866385:-1; parent_transcript=GRMZM2G106647_T01; parent_gene=GRMZM2G106647 seq=translation; coord=4:47718704..47724118:-1;	GRMZM2G106647_P01,GRMZM2G106647_P02	TRUE	TRUE	vAGIEGGLQWPLHVFGk	95%	n+304 (+304), K+304 (+304)	40.99	25.00
7120	parent_transcript=GRMZM2G107289_T02; parent_gene=GRMZM2G107289 seq=translation; coord=4:145562864..145569248:1;	GRMZM2G107289_P02,GRMZM2G107289_P06	TRUE	TRUE	tRDPQVSDYVVMMFFR	95%	n+304 (+304)	37.75	25.08
7121	parent_transcript=GRMZM2G111225_T01; parent_gene=GRMZM2G111225 seq=translation; coord=9:94575435..94578265:-1;	GRMZM2G111225_P01,GRMZM2G111225_P02	TRUE	TRUE	IIAEAAGYGSQVLVVFPEAFIGyPR	95%	n+304 (+304), iTRAQ8plex (+304)	27.57	25.00
7122	parent_transcript=GRMZM2G117935_T01; parent_gene=GRMZM2G117935 seq=translation; coord=9:151488003..151502416:-1;	GRMZM2G117935_P01,GRMZM2G117935_P02	TRUE	TRUE	IMNQIFDLk	95%	n+304 (+304), K+304 (+304)	35.25	25.97
7123	parent_transcript=GRMZM2G120975_T01; parent_gene=GRMZM2G120975 seq=translation; coord=10:127972866..127975632:-1;	GRMZM2G120975_P01	TRUE	TRUE	iSGQEAVAFFQGANLPQQVLAQVWMHADR	95%	n+304 (+304)	52.27	25.00
7124	parent_transcript=GRMZM2G125452_T01; parent_gene=GRMZM2G125452 seq=translation; coord=3:205260905..205264890:-1;	GRMZM2G125452_P01	TRUE	TRUE	aSVFGFGVYGSik	95%	n+304 (+304), K+304 (+304)	46.23	25.08
7125	parent_transcript=GRMZM2G126853_T02; parent_gene=GRMZM2G126853 seq=translation; coord=1:248612984..248616352:-1;	GRMZM2G126853_P02,GRMZM2G126853_P03	TRUE	TRUE	aAASEPDEEETk	95%	n+304 (+304), K+304 (+304)	57.63	25.00
7126	parent_transcript=GRMZM2G129540_T01; parent_gene=GRMZM2G129540 seq=translation; coord=1:34969590..34970683:-1;	GRMZM2G129540_P01	TRUE	TRUE	gWALALHGGAGDVPR	95%	n+304 (+304)	29.04	25.29
7127	parent_transcript=GRMZM2G138103_T01; parent_gene=GRMZM2G138103 seq=translation; coord=1:294999855..295003926:-1;	GRMZM2G138103_P01	TRUE	TRUE	hkDDEAAPAEASASAAPPs	95%	n+304 (+304), K+304 (+304)	41.09	25.00
7128	parent_transcript=GRMZM2G138382_T01; parent_gene=GRMZM2G138382 seq=translation; coord=5:215232823..215235104:1;	GRMZM2G138382_P01	TRUE	TRUE	eHILAGDIFQVVLsQR	95%	n+304 (+304)	33.62	25.69
7129	parent_transcript=GRMZM2G144146_T01; parent_gene=GRMZM2G144146 seq=translation; coord=9:12022646..12025248:1;	GRMZM2G144146_P01	TRUE	TRUE	eSVFAQSSSPPPPPQAK	95%	n+304 (+304), K+304 (+304)	31.14	25.94
7130	parent_transcript=GRMZM2G146358_T01; parent_gene=GRMZM2G146358 seq=translation; coord=1:246710302..246723688:1;	GRMZM2G146358_P01	TRUE	TRUE	ePAAAPVSATAPFAAAPk	95%	n+304 (+304), K+304 (+304)	34.31	25.00
7131	parent_transcript=GRMZM2G146486_T03; parent_gene=GRMZM2G146486 seq=translation; coord=7:97615127..97619263:1;	GRMZM2G146486_P03	TRUE	TRUE	ILPQVLDSALDAQVLr	95%	n+304 (+304)	33.49	25.00
7132	parent_transcript=GRMZM2G146670_T01; parent_gene=GRMZM2G146670 seq=translation; coord=2:51808541..51813988:-1;	GRMZM2G146670_P01	TRUE	TRUE	aLAVGAEISFDSATGNFTk	95%	n+304 (+304), K+304 (+304)	40.98	25.05
7133	parent_transcript=GRMZM2G147685_T01; parent_gene=GRMZM2G147685 seq=translation; coord=7:170565928..170569005:1;	GRMZM2G147685_P01	TRUE	TRUE	gNAAAVEDVDHDLHIFTER	95%	n+304 (+304)	48.84	25.00
7134	parent_transcript=GRMZM2G148176_T01; parent_gene=GRMZM2G148176 seq=translation; coord=8:174276790..174282847:1;	GRMZM2G148176_P01	TRUE	TRUE	dFHLGWFLDPiVHGR	95%	n+304 (+304)	47.26	26.18
7135	parent_transcript=GRMZM2G148985_T01; parent_gene=GRMZM2G148985 seq=translation; coord=7:13208679..13209853:1;	GRMZM2G148985_P01,GRMZM2G148985_P02	TRUE	TRUE	gTEGIiQIENPNLVk	95%	n+304 (+304), K+304 (+304)	50.18	25.00
7136	parent_transcript=GRMZM2G150091_T01; parent_gene=GRMZM2G150091	GRMZM2G150091_P01	TRUE	TRUE	yPSAVFLEVDVDELLEVAK	95%	n+304 (+304), iTRAQ8plex (+304), K+304 (+304)	55.24	25.00

7137	seq=translation; coord=6:96678651..96684463:-1; parent_transcript=GRMZM2G158627_T02; parent_gene=GRMZM2G158627 seq=translation; coord=6:166882444..166885328:1;	GRMZM2G158627_P02,GRMZM2G158627_P03	TRUE	TRUE	aDQSLFEAGVAR	95%	n+304 (+304)	31.10	25.00
7138	parent_transcript=GRMZM2G159028_T01; parent_gene=GRMZM2G159028 seq=translation; coord=1:213097242..213099953:-1;	GRMZM2G159028_P01,GRMZM2G159028_P02	TRUE	TRUE	yVELFPSTPEEASR	95%	n+304 (+304)	35.01	25.00
7139	parent_transcript=GRMZM2G161245_T01; parent_gene=GRMZM2G161245 seq=translation; coord=4:240610886..240613481:1;	GRMZM2G161245_P01,GRMZM2G161245_P02	TRUE	TRUE	vALLGAAGGIGQPLGLLIK	95%	n+304 (+304), K+304 (+304)	70.75	25.00
7140	parent_transcript=GRMZM2G167103_T02; parent_gene=GRMZM2G167103 seq=translation; coord=4:5666220..5677820:-1;	GRMZM2G167103_P02	TRUE	TRUE	vkDELVLLEGNDVELVSR	95%	n+304 (+304), K+304 (+304)	40.38	25.31
7141	parent_transcript=GRMZM2G169160_T01; parent_gene=GRMZM2G169160 seq=translation; coord=2:148054055..148060611:1;	GRMZM2G169160_P01,GRMZM2G169160_P02, GRMZM2G169160_P03	TRUE	TRUE	eGLIALEEDLVQLTDK	95%	n+304 (+304), K+304 (+304)	51.12	25.81
7142	parent_transcript=GRMZM2G173035_T01; parent_gene=GRMZM2G173035 seq=translation; coord=10:148514958..148517583:-1;	GRMZM2G173035_P01	TRUE	TRUE	sLEEALALK	95%	n+304 (+304), K+304 (+304)	31.81	26.67
7143	parent_transcript=GRMZM2G173636_T02; parent_gene=GRMZM2G173636 seq=translation; coord=5:38978060..38995105:1;	GRMZM2G173636_P02	TRUE	TRUE	tPLHWAVDR	95%	n+304 (+304)	32.52	25.00
7144	parent_transcript=GRMZM2G303631_T01; parent_gene=GRMZM2G303631 seq=translation; coord=4:182736035..182740799:1;	GRMZM2G303631_P01,GRMZM2G303631_P02, GRMZM2G303631_P03,GRMZM2G303631_P04	TRUE	TRUE	kPWVWWDYVTFHIR	95%	K+304 (+304), n+304 (+304)	27.95	25.09
7145	parent_transcript=GRMZM2G361693_T01; parent_gene=GRMZM2G361693 seq=translation; coord=6:119676436..119695343:-1;	GRMZM2G361693_P01	TRUE	TRUE	gFGVESFGPDR	95%	n+304 (+304)	33.68	25.00
7146	parent_transcript=GRMZM2G368678_T01; parent_gene=GRMZM2G368678 seq=translation; coord=2:229995293..230001701:-1;	GRMZM2G368678_P01	TRUE	TRUE	aLEQILLQk	95%	n+304 (+304), K+304 (+304)	32.65	25.00
7147	parent_transcript=GRMZM2G379252_T01; parent_gene=GRMZM2G379252 seq=translation; coord=1:37202583..37215962:-1;	GRMZM2G379252_P01,GRMZM2G379252_P02, GRMZM2G379252_P04	TRUE	TRUE	rIPQNWAATQFAEALGR	95%	n+304 (+304)	42.64	25.25
7148	parent_transcript=GRMZM2G408305_T02; parent_gene=GRMZM2G408305 seq=translation; coord=3:20425735..20426696:-1;	GRMZM2G408305_P02,GRMZM2G408305_P03	TRUE	TRUE	tMVVATLAEVAQEMGAPISAYVDK	95%	n+304 (+304), K+304 (+304)	43.67	25.24
7149	parent_transcript=GRMZM2G437100_T01; parent_gene=GRMZM2G437100 seq=translation; coord=8:135348667..135351325:1;	GRMZM2G437100_P01	TRUE	TRUE	rGSVDFPFSDVLDPFDSVFR	95%	n+304 (+304)	40.64	25.00
7150	parent_transcript=GRMZM2G477847_T01; parent_gene=GRMZM2G477847 seq=translation; coord=1:285074425..285077363:-1;	GRMZM2G477847_P01	TRUE	TRUE	aDPTFDIVDLILSk	95%	n+304 (+304), K+304 (+304)	45.35	25.00
7151	parent_transcript=GRMZM2G519210_T01; parent_gene=GRMZM2G519210 seq=translation; coord=2:176442835..176451880:1;	GRMZM2G519210_P01	TRUE	TRUE	eGTVDNEGLGR	95%	n+304 (+304)	34.95	25.00
7152	parent_transcript=GRMZM2G579432_T01; parent_gene=GRMZM2G579432 seq=translation; coord=2:24363170..24366723:-1;	GRMZM2G579432_P01,GRMZM2G579432_P02	TRUE	TRUE	gADLIHFQDFNAEVLRL	95%	n+304 (+304)	40.52	25.48
7153	parent_transcript=GRMZM5G803490_T01; parent_gene=GRMZM5G803490 seq=translation; coord=5:80387639..80389787:1;	GRMZM5G803490_P01	TRUE	TRUE	dVLSLAGALEGVELR	95%	n+304 (+304)	37.91	25.90
7154	parent_transcript=GRMZM5G829894_T01; parent_gene=GRMZM5G829894	GRMZM5G829894_P01	TRUE	TRUE	aAIAETYNLTDSFLK	95%	n+304 (+304), K+304 (+304)	69.44	25.30

7155	seq=translation; coord=9:26592926..26595121:-1; parent_transcript=GRMZM5G847530_T01; parent_gene=GRMZM5G847530 seq=translation; coord=10:131899758..131901846:1;	GRMZM5G847530_P01	TRUE	TRUE	ILIQSLGk	95%	n+304 (+304), K+304 (+304)	28.48	25.00
7156	parent_transcript=GRMZM5G854655_T01; parent_gene=GRMZM5G854655 seq=translation; coord=3:133174831..133177335:1;	GRMZM5G854655_P01	TRUE	TRUE	gADTLDDVNEWLQR	95%	n+304 (+304)	49.59	25.00
7157	parent_transcript=GRMZM5G891834_T02; parent_gene=GRMZM5G891834 seq=translation; coord=3:167686905..167690778:1;	GRMZM2G054250_P01,GRMZM5G891834_P02	TRUE	TRUE	fPGSEMMGIik	95%	n+304 (+304), K+304 (+304)	37.12	25.72
7158	parent_transcript=GRMZM2G064914_T03; parent_gene=GRMZM2G064914 seq=translation; coord=4:187449297..187450591:-1;	GRMZM2G064914_P03	TRUE	TRUE	eYALSDVIDTIk	94%	n+304 (+304), K+304 (+304)	29.92	26.65
7159	parent_transcript=GRMZM5G891282_T01; parent_gene=GRMZM5G891282 seq=translation; coord=8:134902882..134904730:1;	GRMZM5G891282_P01	TRUE	TRUE	IGcTGAIPVEVIPFGALHTLGLIR	94%	n+304 (+304), Carbamidomethyl (+57)	28.26	25.00
7160	parent_transcript=AC199001.3_FGT005; parent_gene=AC199001.3_FG005 seq=translation; coord=6:154319672..154322588:-1;	AC199001.3_FGP005,AC209206.3_FGP011,GRMZM2G039455_P01,GRMZM2G441583_P01	TRUE	TRUE	aDLHHLAMFLAGR	95%	n+304 (+304)	29.10	25.98
7161	parent_transcript=AC214817.3_FGT004; parent_gene=AC214817.3_FG004 seq=translation; coord=4:180370604..180372480:-1;	AC214817.3_FGP004,AC218972.3_FGP004,GRMZM2G465771_P01	TRUE	TRUE	IDALEVLSLR	94%	n+304 (+304)	30.69	25.00
7162	parent_transcript=GRMZM2G041699_T01; parent_gene=GRMZM2G041699 seq=translation; coord=8:95420793..95435911:-1;	GRMZM2G041699_P01,GRMZM2G041699_P02	TRUE	TRUE	dAVASLIAELMEGEQGk	94%	n+304 (+304), K+304 (+304)	28.77	25.60
7163	parent_transcript=GRMZM2G337616_T01; parent_gene=GRMZM2G337616 seq=translation; coord=1:39732003..39737097:1;	GRMZM2G337616_P01	TRUE	TRUE	iLVAEDIATFTR	94%	n+304 (+304)	30.63	25.02
7164	parent_transcript=GRMZM2G001918_T01; parent_gene=GRMZM2G001918 seq=translation; coord=5:5772725..5776442:1;	GRMZM2G001918_P01,GRMZM2G001918_P02	TRUE	TRUE	nILELATELR	95%	n+304 (+304)	30.20	25.33
7165	parent_transcript=GRMZM2G137847_T01; parent_gene=GRMZM2G137847 seq=translation; coord=8:171762195..171768664:1;	GRMZM2G137847_P01,GRMZM2G137847_P02,GRMZM2G137847_P03	TRUE	TRUE	rDPLGVLEALLWR	95%	n+304 (+304)	27.84	25.00
7166	parent_transcript=GRMZM2G139296_T01; parent_gene=GRMZM2G139296 seq=translation; coord=1:264550351..264553480:-1;	GRMZM2G139296_P01,GRMZM2G139296_P02,GRMZM5G801031_P02	TRUE	TRUE	vLSEEEK	93%	n+304 (+304), K+304 (+304)	31.87	26.72
7167	parent_transcript=GRMZM2G031022_T01; parent_gene=GRMZM2G031022 seq=translation; coord=7:167333820..167340329:1;	GRMZM2G031022_P01,GRMZM2G031022_P02,GRMZM2G031022_P03,GRMZM2G031022_P04,GRMZM2G031022_P05	TRUE	TRUE	iPLEVAHTLVEIAEVAR	94%	n+304 (+304)	27.56	25.00
7168	parent_transcript=GRMZM2G158021_T01; parent_gene=GRMZM2G158021 seq=translation; coord=3:187336087..187340155:-1;	GRMZM2G158021_P01	TRUE	TRUE	vGLVGFPVSVGk	94%	n+304 (+304), K+304 (+304)	27.55	25.00
7169	parent_transcript=GRMZM2G020002_T01; parent_gene=GRMZM2G020002 seq=translation; coord=4:6624888..6626733:1;	GRMZM2G020002_P01,GRMZM2G020002_P02,GRMZM2G020002_P03	TRUE	TRUE	fINTPLYVVHVMSIDAMDEIAk	94%	n+304 (+304), K+304 (+304)	25.77	25.20
7170	parent_transcript=GRMZM2G133781_T01; parent_gene=GRMZM2G133781 seq=translation; coord=6:89402866..89408903:1;	GRMZM2G133781_P01	TRUE	TRUE	dLYYNVLQFAQk	93%	n+304 (+304), K+304 (+304)	28.15	25.80
7171	parent_transcript=GRMZM2G322328_T01; parent_gene=GRMZM2G322328 seq=translation; coord=7:118310662..118312830:1;	GRMZM2G322328_P01,GRMZM2G322328_P02	TRUE	TRUE	iTIQSAEHILTMFDER	92%	n+304 (+304)	27.29	25.33
7172	parent_transcript=GRMZM2G041175_T01; parent_gene=GRMZM2G041175	GRMZM2G041175_P01,GRMZM2G041175_P02	TRUE	TRUE	IGDYSNWLQk	92%	n+304 (+304), K+304 (+304)	27.64	25.80

7173	seq=translation; coord=1:164506466..164507692:1; parent_transcript=GRMZM5G878058_T01; parent_gene=GRMZM5G878058 seq=translation; coord=5:136314239..136314853:1;	GRMZM5G878058_P01,GRMZM5G878058_P02	TRUE	TRUE	sLAELLELPk	92%	n+304 (+304), K+304 (+304)	26.73	25.00
7174	parent_transcript=AC226221.2_FGT011; parent_gene=AC226221.2_FG011 seq=translation; coord=2:44187637..44189354:-1;	AC226221.2_FGP011,GRMZM2G013695_P01,GRMZM2G022248_P01	TRUE	TRUE	sLDVPFETLDVLANEALR	93%	n+304 (+304)	26.87	25.12
7175	parent_transcript=GRMZM2G470882_T01; parent_gene=GRMZM2G470882 seq=translation; coord=10:63613518..63620810:1;	GRMZM2G470882_P01,GRMZM2G470882_P04	TRUE	TRUE	dVDSIVDPIIGk	92%	n+304 (+304), K+304 (+304)	26.81	25.16
7176	parent_transcript=GRMZM2G368902_T01; parent_gene=GRMZM2G368902 seq=translation; coord=1:43133344..43136676:1;	GRMZM2G368902_P01	TRUE	TRUE	dYPALLEYLEGk	93%	n+304 (+304), K+304 (+304)	27.02	25.43
7177	parent_transcript=GRMZM2G042032_T01; parent_gene=GRMZM2G042032 seq=translation; coord=1:61613000..61620826:1;	GRMZM2G042032_P01,GRMZM2G042032_P02,GRMZM2G042032_P03	TRUE	TRUE	fGMPVLMSEEEK	93%	n+304 (+304), K+304 (+304)	26.54	25.00
7178	parent_transcript=AC204530.4_FGT002; parent_gene=AC204530.4_FG002 seq=translation; coord=1:271969731..271986783:-1;	AC204530.4_FGP002	TRUE	TRUE	ILEDLPVQAMLETLtk	91%	n+304 (+304), K+304 (+304)	26.26	25.00
7179	parent_transcript=GRMZM2G101460_T02; parent_gene=GRMZM2G101460 seq=translation; coord=3:27429838..27434586:-1;	GRMZM2G101460_P02,GRMZM2G101460_P03,GRMZM2G101460_P04	TRUE	TRUE	tSAVTGTGLQELLALIER	93%	n+304 (+304)	26.60	25.35
7180	parent_transcript=GRMZM2G018664_T01; parent_gene=GRMZM2G018664 seq=translation; coord=5:11394624..11404854:1;	GRMZM2G018664_P01,GRMZM2G112030_P01,GRMZM2G314427_P01,GRMZM5G884707_P01	TRUE	TRUE	dVEGGWLLR	91%	n+304 (+304)	28.78	25.60
7181	parent_transcript=GRMZM2G011219_T01; parent_gene=GRMZM2G011219 seq=translation; coord=1:76234318..76235779:-1;	GRMZM2G011219_P01,GRMZM2G011219_P02	TRUE	TRUE	ISLLNSLLk	92%	n+304 (+304), K+304 (+304)	25.96	25.00
7182	parent_transcript=GRMZM2G075892_T01; parent_gene=GRMZM2G075892 seq=translation; coord=4:234328342..234339725:1;	GRMZM2G075892_P01,GRMZM2G138710_P01,GRMZM2G479340_P01	TRUE	TRUE	eHGFLGFR	91%	n+304 (+304)	25.76	25.00
7183	parent_transcript=GRMZM2G040320_T01; parent_gene=GRMZM2G040320 seq=translation; coord=5:178320733..178325109:-1;	GRMZM2G040320_P01,GRMZM2G040320_P02	TRUE	TRUE	vELQQAHAEAQSLVAMR	90%	n+304 (+304)	26.17	25.75
7184	parent_transcript=GRMZM2G106412_T01; parent_gene=GRMZM2G106412 seq=translation; coord=7:172200913..172206224:1;	GRMZM2G106412_P01	TRUE	TRUE	dAAGYGAALADALRPPPLTR	91%	n+304 (+304)	25.96	25.45
7185	parent_transcript=GRMZM2G008232_T01; parent_gene=GRMZM2G008232 seq=translation; coord=7:170961145..170979959:-1;	GRMZM2G008232_P01,GRMZM2G158766_P01,GRMZM2G158766_P02,GRMZM2G158766_P03	TRUE	TRUE	eDIAIVLISQyIANMIR	91%	n+304 (+304), iTRAQ8plex (+304)	25.43	25.00
7186	parent_transcript=GRMZM2G036609_T01; parent_gene=GRMZM2G036609 seq=translation; coord=9:107311479..107314462:1;	GRMZM2G036609_P01,GRMZM2G036609_P02	TRUE	TRUE	gQMEAWDGPALLLFSDDR	90%	n+304 (+304)	25.29	25.00
7187	parent_transcript=GRMZM2G027835_T01; parent_gene=GRMZM2G027835 seq=translation; coord=3:5571644..5577275:1;	GRMZM2G027835_P01,GRMZM2G027835_P02,GRMZM2G556131_P01,GRMZM2G556131_P02	TRUE	TRUE	IPYVPLPLEk	91%	n+304 (+304), K+304 (+304)	25.48	25.16
7188	parent_transcript=GRMZM2G143246_T01; parent_gene=GRMZM2G143246 seq=translation; coord=2:153399473..153402030:1;	GRMZM2G143246_P01	TRUE	TRUE	iLIFMDTk	91%	n+304 (+304), K+304 (+304)	25.32	25.00
7189	parent_transcript=GRMZM2G117300_T01; parent_gene=GRMZM2G117300 seq=translation; coord=1:248422905..248450276:-1;	GRMZM2G117300_P01	TRUE	TRUE	vAVSDEETPDR	91%	n+304 (+304)	27.04	25.00
7190	parent_transcript=GRMZM2G153928_T01; parent_gene=GRMZM2G153928	GRMZM2G153928_P01,GRMZM2G153928_P03	TRUE	TRUE	mLVILEk	89%	n+304 (+304), K+304 (+304)	25.16	25.00

7191	seq=translation; coord=5:204006064..204008467:1; parent_transcript=GRMZM2G018126_T01; parent_gene=GRMZM2G018126	GRMZM2G018126_P01,GRMZM2G113899_P01, GRMZM2G126865_P01	TRUE	TRUE	IVVGDVFR	89%	n+304 (+304)	26.97	25.00
7192	seq=translation; coord=1:183908459..183912375:-1; parent_transcript=GRMZM2G080652_T01; parent_gene=GRMZM2G080652	GRMZM2G080652_P01	TRUE	TRUE	sLMDINESPVYLLNPTINLSQk	91%	n+304 (+304), K+304 (+304)	25.14	25.00
7193	GRMZM2G081644_P01-R seq=translation; coord=2:162962062..162982456:1;	GRMZM2G081644_P01-R	TRUE	TRUE	eLALVR	88%	n+304 (+304)	26.42	25.00
7194	parent_transcript=GRMZM2G065276_T02; parent_gene=GRMZM2G065276	GRMZM2G065276_P02,GRMZM2G065276_P03	TRUE	TRUE	gcEQPLIIR	88%	n+304 (+304), Carbamidomethyl (+57)	27.38	26.01
7195	seq=translation; coord=10:148237983..148239542:-1; parent_transcript=GRMZM2G008583_T01; parent_gene=GRMZM2G008583	GRMZM2G008583_P01	TRUE	TRUE	ISGLER	88%	n+304 (+304)	27.43	26.06
7196	seq=translation; coord=4:66615286..66619252:1; parent_transcript=GRMZM2G115775_T01; parent_gene=GRMZM2G115775	GRMZM2G115775_P01,GRMZM2G115775_P02, GRMZM2G115775_P03,GRMZM2G115775_P04, GRMZM2G115775_P05,GRMZM2G115775_P06	TRUE	TRUE	IADISSMIADR	87%	n+304 (+304)	25.60	25.00
7197	seq=translation; coord=9:143050607..143053350:1; parent_transcript=GRMZM2G149798_T01; parent_gene=GRMZM2G149798	GRMZM2G149798_P01,GRMZM2G346861_P01, GRMZM2G346861_P02	TRUE	TRUE	aVPAPSGWWSGR	86%	n+304 (+304)	25.86	25.53
7198	seq=translation; coord=7:155614507..155619264:1; parent_transcript=GRMZM2G158062_T01; parent_gene=GRMZM2G158062	GRMZM2G158062_P01,GRMZM2G158062_P02	TRUE	TRUE	gVDVLASDLER	88%	n+304 (+304)	26.10	25.63

Table S3. Specific proteins expressed in endosperm and pericarp

Identified Proteins	Component	Functional Categories	Function Description	Molecular Weight	N1	D1	D2	D3	D4	D5	D6	D7	D8
GRMZM2G051219_P01	pericarp	Amino acid transport and metabolism	Anthranilate phosphoribosyltransferase	41 kDa	Ref	-2.3	-1.7	-1.3	-2.1	No Values	No Values	No Values	No Values
GRMZM2G126541_P01	pericarp	Amino acid transport and metabolism	Carboxypeptidase C (cathepsin A)	54 kDa	Ref	-0.3	0	1.1	2.1	No Values	No Values	No Values	No Values
GRMZM2G104542_P01	pericarp	Amino acid transport and metabolism	Dipeptide/tripeptide permease	64 kDa	Ref	Reference Missing	Reference Missing	0.2	Reference	No Values	No Values	No Values	No Values
GRMZM2G140432_P01	pericarp	Amino acid transport and metabolism	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	95 kDa	Ref	0.6	-0.1	0.9	-0.3	No Values	No Values	No Values	No Values
GRMZM2G065073_P02	pericarp	Amino acid transport and metabolism	Gamma-glutamyltransferase	61 kDa	Ref	0.4	0.7	0.9	1.3	No Values	No Values	No Values	No Values
GRMZM5G826838_P01	pericarp	Amino acid transport and metabolism	Glutamate decarboxylase and related PLP-dependent proteins	55 kDa	Ref	0.1	0.2	0.3	0.3	No Values	No Values	No Values	No Values
GRMZM2G178415_P01	pericarp	Amino acid transport and metabolism	Glutamate dehydrogenase/leucine dehydrogenase	44 kDa	Ref	-0.6	-0.1	-0.3	-0.4	No Values	No Values	No Values	No Values
GRMZM2G074604_P01	pericarp	Amino acid transport and metabolism	Histidine ammonia-lyase	75 kDa	Ref	-0.1	0.3	0.6	1.4	No Values	No Values	No Values	No Values
GRMZM2G441347_P01	pericarp	Amino acid transport and metabolism	Histidine ammonia-lyase	76 kDa	Ref	0.2	0.4	0.1	0	No Values	No Values	No Values	No Values
GRMZM2G064159_P01	pericarp	Amino acid transport and metabolism	Peptidylarginine deiminase and related enzymes	42 kDa	Ref	0.1	-0.2	0.2	0.1	No Values	No Values	No Values	No Values
GRMZM2G084942_P01	pericarp	Amino acid transport and metabolism	Prephenate dehydrogenase	40 kDa	Ref	0.8	0.8	0.7	0.9	No Values	No Values	No Values	No Values
GRMZM2G175171_P01	pericarp	Amino acid transport and metabolism ; Coenzyme transport and metabolism	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]	60 kDa	Ref	0.3	-0.1	0.4	1	No Values	No Values	No Values	No Values
GRMZM2G004932_P01	pericarp	Carbohydrate transport and metabolism	6-phosphofructokinase	63 kDa	Ref	0.6	0.1	0.1	1.1	No Values	No Values	No Values	No Values
GRMZM2G009282_P01	pericarp	Carbohydrate transport and metabolism	Alpha-glucosidases, family 31 of glycosyl hydrolases	102 kDa	Ref	1.1	0.1	-0.7	0.7	No Values	No Values	No Values	No Values
GRMZM2G172369_P03	pericarp	Carbohydrate transport and metabolism	Alpha-mannosidase	114 kDa	Ref	0.3	0.1	-0.2	0.7	No Values	No Values	No Values	No Values
GRMZM2G004699_P01	pericarp	Carbohydrate transport and metabolism	Beta-glucanase/Beta-glucan synthetase	34 kDa	Ref	-0.7	0.3	0.6	0.2	No Values	No Values	No Values	No Values
GRMZM2G030173_P01	pericarp	Carbohydrate transport and metabolism	Beta-glucanase/Beta-glucan synthetase	27 kDa	Ref	-0.2	-0.2	-0.4	-1	No Values	No Values	No Values	No Values
AC217401.3_FGP002	pericarp	Carbohydrate transport and metabolism	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	63 kDa	Ref	-0.1	-0.4	-0.6	0.5	No Values	No Values	No Values	No Values
GRMZM2G016890_P01	pericarp	Carbohydrate transport and metabolism	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	64 kDa	Ref	-0.8	-1.5	-0.6	-1	No Values	No Values	No Values	No Values
GRMZM2G136895_P01	pericarp	Carbohydrate transport and metabolism	Beta-glucosidase-related glycosidases	81 kDa	Ref	0	-0.1	0.3	0.4	No Values	No Values	No Values	No Values
GRMZM2G177923_P01	pericarp	Carbohydrate transport and metabolism	Beta-glucosidase-related glycosidases	83 kDa	Ref	-0.7	-0.5	-0.4	0.3	No Values	No Values	No Values	No Values

GRMZM2G458549_P01	pericarp	Carbohydrate transport and metabolism	Galactokinase	64 kDa	Ref	-0.3	-0.4	-0.4	0.1	No Values	No Values	No Values	No Values
GRMZM2G130230_P01	pericarp	Carbohydrate transport and metabolism	Glucose-6-phosphate 1-dehydrogenase	58 kDa	Ref	-0.7	-1.3	-0.7	-0.5	No Values	No Values	No Values	No Values
GRMZM2G412611_P01	pericarp	Carbohydrate transport and metabolism	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	164 kDa	Ref	-0.8	-0.8	-0.4	-0.9	No Values	No Values	No Values	No Values
GRMZM2G031496_P01	pericarp	Cell cycle control, cell division, chromosome partitioning	ATPases involved in chromosome partitioning	37 kDa	Ref	0.3	-0.4	0.9	0	No Values	No Values	No Values	No Values
GRMZM2G166767_P01	pericarp	Cell wall/membrane/envelope biogenesis	dTDP-D-glucose 4,6-dehydratase	76 kDa	Ref	0	-0.6	-0.8	-0.5	No Values	No Values	No Values	No Values
AC231180.2_FGP006	pericarp	Cell wall/membrane/envelope biogenesis	Endopolygalacturonase	48 kDa	Ref	0.6	-0.2	-1.4	-1.6	No Values	No Values	No Values	No Values
GRMZM2G479112_P01	pericarp	Cell wall/membrane/envelope biogenesis	Phospholipase C	57 kDa	Ref	-0.1	0.1	0.1	0.8	No Values	No Values	No Values	No Values
GRMZM2G032160_P01	pericarp	Cell wall/membrane/envelope biogenesis	Predicted glycosyl hydrolase	82 kDa	Ref	0.1	0	0.6	1.3	No Values	No Values	No Values	No Values
GRMZM2G081017_P01	pericarp	Cell wall/membrane/envelope biogenesis	Secreted and surface protein containing fasciclin-like repeats	33 kDa	Ref	0.1	0.6	0.4	0.7	No Values	No Values	No Values	No Values
GRMZM2G007404_P01	pericarp	Cell wall/membrane/envelope biogenesis ; Carbohydrate transport and metabolism ;	Nucleoside-diphosphate-sugar epimerases	48 kDa	Ref	0.1	0.3	0.3	0.3	No Values	No Values	No Values	No Values
GRMZM2G044027_P01	pericarp	Cell wall/membrane/envelope biogenesis ; Carbohydrate transport and metabolism ;	Nucleoside-diphosphate-sugar epimerases	39 kDa	Ref	0.6	1.3	0.7	-0.2	No Values	No Values	No Values	No Values
AC226235.2_FGP001	pericarp	Cell wall/membrane/envelope biogenesis ; Carbohydrate transport and metabolism ;	Predicted nucleoside-diphosphate-sugar epimerases	33 kDa	Ref	-1.8	-1.9	-1.1	-1.9	No Values	No Values	No Values	No Values
GRMZM2G326116_P01	pericarp	Cell wall/membrane/envelope biogenesis ; Carbohydrate transport and metabolism ;	Predicted nucleoside-diphosphate-sugar epimerases	35 kDa	Ref	-1.7	-1.6	-0.9	-1.1	No Values	No Values	No Values	No Values
GRMZM2G171588_P01	pericarp	Chromatin structure and dynamics	SWIB-domain-containing proteins implicated in chromatin remodeling	36 kDa	Ref	1.1	0.4	0.2	0	No Values	No Values	No Values	No Values
GRMZM2G073045_P01	pericarp	Coenzyme transport and metabolism	2-polyprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol methylase	38 kDa	Ref	-0.3	-0.3	-0.3	-0.5	No Values	No Values	No Values	No Values
GRMZM2G397247_P04	pericarp	Coenzyme transport and metabolism	Delta-aminolevulinic acid dehydratase	46 kDa	Ref	0.3	0	0.4	0.2	No Values	No Values	No Values	No Values
GRMZM2G098569_P01	pericarp	Coenzyme transport and metabolism	Geranylgeranyl pyrophosphate synthase	41 kDa	Ref	0.7	0.5	0.6	1.1	No Values	No Values	No Values	No Values
GRMZM2G073814_P02	pericarp	Coenzyme transport and metabolism ; Amino acid transport and metabolism	Phosphoglycerate dehydrogenase and related dehydrogenases	65 kDa	Ref	-0.4	-1.7	-1	-0.4	No Values	No Values	No Values	No Values
GRMZM2G126190_P01	pericarp	Cytoskeleton	Actin and related proteins	42 kDa	Ref	0.4	-0.3	-0.3	-0.2	No Values	No Values	No Values	No Values
GRMZM2G032367_P01	pericarp	Energy production and conversion	Cytochrome c1	34 kDa	Ref	1.3	1.2	1.8	1.8	No Values	No Values	No Values	No Values
GRMZM2G080839_P01	pericarp	Energy production and conversion	FAD/FMN-containing dehydrogenases	58 kDa	Ref	0.6	0.6	1.7	3.3	No Values	No Values	No Values	No Values
GRMZM2G403076_P01	pericarp	Energy production and conversion	FAD/FMN-containing dehydrogenases	62 kDa	Ref	0.8	-0.1	0.3	2.2	No Values	No Values	No Values	No Values
GRMZM2G033515_P01	pericarp	Energy production and conversion	Isocitrate dehydrogenases	46 kDa	Ref	Value Missing	Value Missing	Value Missing	-3.7	Value Missing	Value Missing	Value Missing	Value Missing

GRMZM2G077415_P01	pericarp	Energy production and conversion	Malate/lactate dehydrogenases	24 kDa	Ref	-0.4	0.1	-0.2	0	No Values	No Values	No Values	No Values
GRMZM2G108076_P01	pericarp	Energy production and conversion	NAD-dependent aldehyde dehydrogenases	12 kDa	Ref	0.2	0.4	0.4	0.9	No Values	No Values	No Values	No Values
GRMZM2G118800_P01	pericarp	Energy production and conversion	NAD-dependent aldehyde dehydrogenases	52 kDa	Ref	1.4	0.5	0.9	1.9	No Values	No Values	No Values	No Values
GRMZM2G145972_P02	pericarp	Energy production and conversion	NADH dehydrogenase, FAD-containing subunit	65 kDa	Ref	0.9	0.8	1.4	2.5	No Values	No Values	No Values	No Values
GRMZM2G473001_P01	pericarp	Energy production and conversion	Phosphoenolpyruvate carboxylase	110 kDa	Ref	0.1	-0.9	-0.9	-0.9	Value Missing	2.9	Value Missing	2.3
GRMZM2G574782_P01	pericarp	Energy production and conversion	Predicted enolase-phosphatase	57 kDa	Ref	0.3	0.2	0.4	0.3	No Values	No Values	No Values	No Values
GRMZM2G024315_P01	pericarp	Energy production and conversion	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	38 kDa	Ref	0.1	0.1	0.9	1.2	No Values	No Values	No Values	No Values
GRMZM2G052812_P02	pericarp	Energy production and conversion	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	37 kDa	Ref	-0.4	0.2	0.2	0.5	No Values	No Values	No Values	No Values
GRMZM2G033226_P01	pericarp	Energy production and conversion	Succinyl-CoA synthetase, alpha subunit	20 kDa	Ref	-0.2	-0.3	-0.8	-0.4	No Values	No Values	No Values	No Values
GRMZM2G034083_P01	pericarp	Energy production and conversion	Succinyl-CoA synthetase, beta subunit	47 kDa	Ref	-1.1	-0.8	-0.7	-0.6	No Values	No Values	No Values	No Values
GRMZM2G107082_P01	pericarp	Energy production and conversion	Succinyl-CoA synthetase, beta subunit	47 kDa	Ref	0.1	0.1	-0.1	0.1	No Values	No Values	No Values	No Values
GRMZM2G024303_P01	pericarp	Energy production and conversion	Zn-dependent alcohol dehydrogenases, class III	44 kDa	Ref	0.4	0.5	0.3	1.2	No Values	No Values	No Values	No Values
GRMZM2G170602_P01	pericarp	Energy production and conversion ; Coenzyme transport and metabolism ; General function prediction only ;	Lactate dehydrogenase and related dehydrogenases	42 kDa	Ref	0.2	0	0.7	2.4	No Values	No Values	No Values	No Values
GRMZM2G008728_P02	pericarp	Energy production and conversion ; General function prediction only ;	NADPH:quinone reductase and related Zn-dependent oxidoreductases	34 kDa	Ref	0	0.1	0.5	0.2	No Values	No Values	No Values	No Values
AC209206.3_FGP014	pericarp	Function unknown		60 kDa	Ref	0.3	0.3	0.8	1.5	No Values	No Values	No Values	No Values
AC231745.1_FGP003	pericarp	Function unknown		41 kDa	Ref	0	2	1.5	2.3	No Values	No Values	No Values	No Values
GRMZM2G004878_P01	pericarp	Function unknown		19 kDa	Ref	2.7	0.9	0.1	-0.1	No Values	No Values	No Values	No Values
GRMZM2G007151_P01	pericarp	Function unknown		21 kDa	Ref	1.8	1.7	2.7	1	No Values	No Values	No Values	No Values
GRMZM2G012160_P01	pericarp	Function unknown		15 kDa	Ref	0.8	0.5	3.5	2.7	No Values	No Values	No Values	No Values
GRMZM2G012566_P02	pericarp	Function unknown		18 kDa	Ref	1.4	1.8	1	0	No Values	No Values	No Values	No Values
GRMZM2G013002_P01	pericarp	Function unknown		32 kDa	Ref	1.1	0.8	0.6	1.1	No Values	No Values	No Values	No Values
GRMZM2G014994_P01	pericarp	Function unknown		18 kDa	Ref	0.5	-0.4	-1.2	-2	No Values	No Values	No Values	No Values
GRMZM2G017249_P01	pericarp	Function unknown		64 kDa	Ref	0.9	0.5	0.4	0.9	No Values	No Values	No Values	No Values
GRMZM2G018108_P01	pericarp	Function unknown		50 kDa	Ref	0.5	1.5	2.2	2.9	No Values	No Values	No Values	No Values

GRMZM2G024310_P01	pericarp	Function unknown	28 kDa	Ref	1.4	0.8	1.5	0.6	No Values	No Values	No Values	No Values
GRMZM2G028104_P01	pericarp	Function unknown	47 kDa	Ref	0.5	1.5	1.4	2.7	No Values	No Values	No Values	No Values
GRMZM2G031028_P02	pericarp	Function unknown	34 kDa	Ref	-0.8	-0.7	-0.4	-0.5	No Values	No Values	No Values	No Values
GRMZM2G039639_P01	pericarp	Function unknown	24 kDa	Ref	-0.1	-0.5	Reference Missing	Reference	No Values	No Values	No Values	No Values
GRMZM2G042865_P01	pericarp	Function unknown	51 kDa	Ref	-0.2	-0.4	-0.4	-0.4	No Values	No Values	No Values	No Values
GRMZM2G044132_P01	pericarp	Function unknown	28 kDa	Ref	0.9	1.8	2.7	3.7	No Values	No Values	No Values	No Values
GRMZM2G047298_P01	pericarp	Function unknown	42 kDa	Ref	0	-0.2	-1.8	-1.5	No Values	No Values	No Values	No Values
GRMZM2G050412_P01	pericarp	Function unknown	34 kDa	Ref	2.4	1	0.6	0.7	No Values	No Values	No Values	No Values
GRMZM2G051338_P01	pericarp	Function unknown	20 kDa	Ref	-0.3	0	1.9	0.7	No Values	No Values	No Values	No Values
GRMZM2G051898_P01	pericarp	Function unknown	40 kDa	Ref	0.8	0.8	Reference Missing	2.8	No Values	No Values	No Values	No Values
GRMZM2G058568_P03	pericarp	Function unknown	57 kDa	Ref	0.4	0.1	0.4	0.4	No Values	No Values	No Values	No Values
GRMZM2G059693_P01	pericarp	Function unknown	58 kDa	Ref	1.6	1.1	-0.4	-0.3	No Values	No Values	No Values	No Values
GRMZM2G060567_P01	pericarp	Function unknown	26 kDa	Ref	2.6	2.5	2.5	1.4	No Values	No Values	No Values	No Values
GRMZM2G061950_P01	pericarp	Function unknown	35 kDa	Ref	0.1	-0.4	0.1	-0.4	No Values	No Values	No Values	No Values
GRMZM2G064753_P01	pericarp	Function unknown	18 kDa	Ref	1.2	0.4	0.5	0.1	No Values	No Values	No Values	No Values
GRMZM2G064993_P01	pericarp	Function unknown	38 kDa	Ref	0.5	-0.3	0.1	-0.2	No Values	No Values	No Values	No Values
GRMZM2G066202_P01	pericarp	Function unknown	27 kDa	Ref	1.3	0.6	1.1	0.2	No Values	No Values	No Values	No Values
GRMZM2G067225_P01	pericarp	Function unknown	53 kDa	Ref	1	0.6	1	1.7	No Values	No Values	No Values	No Values
GRMZM2G071089_P01	pericarp	Function unknown	25 kDa	Ref	3.6	2.6	1.8	0.5	No Values	No Values	No Values	No Values
GRMZM2G073934_P01	pericarp	Function unknown	53 kDa	Ref	0.8	0.5	0.1	0.4	No Values	No Values	No Values	No Values
GRMZM2G074028_P01	pericarp	Function unknown	16 kDa	Ref	1.4	1.2	1.2	1.3	No Values	No Values	No Values	No Values
GRMZM2G075283_P01	pericarp	Function unknown	17 kDa	Ref	0.3	0.2	2.2	2.9	No Values	No Values	No Values	No Values
GRMZM2G075796_P01	pericarp	Function unknown	21 kDa	Ref	0.4	0.1	0.5	-0.1	No Values	No Values	No Values	No Values
GRMZM2G077034_P01	pericarp	Function unknown	10 kDa	Ref	0.4	0.7	0.8	0.9	No Values	No Values	No Values	No Values

GRMZM2G077233_P01	pericarp	Function unknown	55 kDa	Ref	0.5	0	0.9	3	No Values	No Values	No Values	No Values
GRMZM2G080466_P01	pericarp	Function unknown	14 kDa	Ref	2.9	2	2.7	3.3	No Values	No Values	No Values	No Values
GRMZM2G081652_P01	pericarp	Function unknown	62 kDa	Ref	0.8	0.2	0.5	0.6	No Values	No Values	No Values	No Values
GRMZM2G090245_P01	pericarp	Function unknown	23 kDa	Ref	Reference Missing	0.4	0.5	Reference	No Values	No Values	No Values	No Values
GRMZM2G094928_P01	pericarp	Function unknown	12 kDa	Ref	1.3	0.8	1.4	0.3	No Values	No Values	No Values	No Values
GRMZM2G095164_P01	pericarp	Function unknown	13 kDa	Ref	5	4.1	4.5	3.4	No Values	No Values	No Values	No Values
GRMZM2G098397_P01	pericarp	Function unknown	63 kDa	Ref	0.2	0.2	0.1	0.7	No Values	No Values	No Values	No Values
GRMZM2G103342_P01	pericarp	Function unknown	38 kDa	Ref	0.2	0	1.7	3.6	No Values	No Values	No Values	No Values
GRMZM2G107228_P01	pericarp	Function unknown	38 kDa	Ref	0.3	0.1	Reference Missing	1.7	No Values	No Values	No Values	No Values
GRMZM2G107757_P01	pericarp	Function unknown	25 kDa	Ref	Reference Missing	2.3	1.9	1.3	No Values	No Values	No Values	No Values
GRMZM2G108153_P01	pericarp	Function unknown	35 kDa	Ref	1.6	0.7	Reference Missing	2.4	No Values	No Values	No Values	No Values
GRMZM2G108849_P02	pericarp	Function unknown	23 kDa	Ref	0.4	0.1	0.3	1.3	No Values	No Values	No Values	No Values
GRMZM2G109130_P01	pericarp	Function unknown	96 kDa	Ref	0	0.9	1.5	2.2	No Values	No Values	No Values	No Values
GRMZM2G112805_P01	pericarp	Function unknown	30 kDa	Ref	Reference Missing	2	Reference Missing	Reference	No Values	No Values	No Values	No Values
GRMZM2G115491_P01	pericarp	Function unknown	25 kDa	Ref	0.2	0.8	0.7	1.1	No Values	No Values	No Values	No Values
GRMZM2G117989_P01	pericarp	Function unknown	18 kDa	Ref	0.1	0	4.1	4.2	No Values	No Values	No Values	No Values
GRMZM2G122302_P01	pericarp	Function unknown	20 kDa	Ref	0.1	1.6	0.6	-0.5	No Values	No Values	No Values	No Values
GRMZM2G122937_P01	pericarp	Function unknown	22 kDa	Ref	2.3	1.6	2	0.3	No Values	No Values	No Values	No Values
GRMZM2G123029_P01	pericarp	Function unknown	32 kDa	Ref	0.3	0.6	1.3	2	No Values	No Values	No Values	No Values
GRMZM2G123499_P01	pericarp	Function unknown	74 kDa	Ref	0.1	0.1	-0.2	0.2	No Values	No Values	No Values	No Values
GRMZM2G123558_P01	pericarp	Function unknown	23 kDa	Ref	Reference Missing	2.3	Reference Missing	Reference	No Values	No Values	No Values	No Values
GRMZM2G126397_P01	pericarp	Function unknown	13 kDa	Ref	3.1	0.4	0.3	0.1	No Values	No Values	No Values	No Values
GRMZM2G127087_P01	pericarp	Function unknown	66 kDa	Ref	0.4	0.1	2.1	3.7	No Values	No Values	No Values	No Values

GRMZM2G128268_P01	pericarp	Function unknown	45 kDa	Ref	1.3	-0.7	-0.2	-0.1	No Values	No Values	No Values	No Values
GRMZM2G132077_P01	pericarp	Function unknown	18 kDa	Ref	0.6	-0.3	-0.3	0.1	No Values	No Values	No Values	No Values
GRMZM2G137535_P01	pericarp	Function unknown	35 kDa	Ref	0.2	-0.1	1.5	3	No Values	No Values	No Values	No Values
GRMZM2G138782_P01	pericarp	Function unknown	67 kDa	Ref	1.6	1.3	1.2	1.3	No Values	No Values	No Values	No Values
GRMZM2G143568_P01	pericarp	Function unknown	69 kDa	Ref	0	-0.4	-0.6	-0.2	No Values	No Values	No Values	No Values
GRMZM2G143627_P01	pericarp	Function unknown	13 kDa	Ref	1.4	0.5	1.2	-0.4	No Values	No Values	No Values	No Values
GRMZM2G145133_P01	pericarp	Function unknown	48 kDa	Ref	-1	-0.6	-0.9	-0.8	No Values	No Values	No Values	No Values
GRMZM2G147014_P01	pericarp	Function unknown	31 kDa	Ref	0.4	1.2	1.8	1.3	No Values	No Values	No Values	No Values
GRMZM2G149809_P01	pericarp	Function unknown	32 kDa	Ref	0.4	0.8	2.6	3.3	No Values	No Values	No Values	No Values
GRMZM2G150172_P01	pericarp	Function unknown	18 kDa	Ref	1.3	1.8	1.6	1.4	No Values	No Values	No Values	No Values
GRMZM2G150772_P02	pericarp	Function unknown	179 kDa	Ref	-0.4	-0.3	-1.1	-1.1	No Values	No Values	No Values	No Values
GRMZM2G152925_P01	pericarp	Function unknown	19 kDa	Ref	2.5	2.2	2.6	2	No Values	No Values	No Values	No Values
GRMZM2G153181_P01	pericarp	Function unknown	61 kDa	Ref	1.5	0.5	0.1	0.6	No Values	No Values	No Values	No Values
GRMZM2G153208_P01	pericarp	Function unknown	24 kDa	Ref	-0.5	1.5	1.3	1.8	No Values	No Values	No Values	No Values
GRMZM2G154578_P01	pericarp	Function unknown	25 kDa	Ref	-0.2	0	-0.9	-1	No Values	No Values	No Values	No Values
GRMZM2G155329_P01	pericarp	Function unknown	24 kDa	Ref	-0.1	-0.3	1.2	2.1	No Values	No Values	No Values	No Values
GRMZM2G155911_P01	pericarp	Function unknown	52 kDa	Ref	-0.8	0	0.1	0.3	No Values	No Values	No Values	No Values
GRMZM2G156365_P02	pericarp	Function unknown	33 kDa	Ref	0.7	0.1	-1.1	-1.5	No Values	No Values	No Values	No Values
GRMZM2G156861_P02	pericarp	Function unknown	98 kDa	Ref	1.6	2.2	0.5	0.9	No Values	No Values	No Values	No Values
GRMZM2G156861_P03	pericarp	Function unknown	98 kDa	Ref	0.7	Reference Missing	Reference Missing	-0.1	No Values	No Values	No Values	No Values
GRMZM2G157018_P01	pericarp	Function unknown	20 kDa	Ref	1.7	0.9	1.9	0.6	No Values	No Values	No Values	No Values
GRMZM2G168552_P01	pericarp	Function unknown	20 kDa	Ref	0.4	0	2.3	-0.2	No Values	No Values	No Values	No Values
GRMZM2G168833_P01	pericarp	Function unknown	21 kDa	Ref	-0.1	0.7	1.3	2.5	No Values	No Values	No Values	No Values
GRMZM2G170969_P01	pericarp	Function unknown	10 kDa	Ref	2.7	2.4	3.7	2.6	No Values	No Values	No Values	No Values
GRMZM2G173341_P01	pericarp	Function unknown	39 kDa	Ref	-1.3	-1.1	-1.4	-0.9	No Values	No Values	No Values	No Values

GRMZM2G175076_P01	pericarp	Function unknown	24 kDa	Ref	0.1	-0.2	1.6	2.4	No Values	No Values	No Values	No Values
GRMZM2G175273_P01	pericarp	Function unknown	8 kDa	Ref	2.3	2.1	1.9	0.9	No Values	No Values	No Values	No Values
GRMZM2G176595_P01	pericarp	Function unknown	30 kDa	Ref	0.8	1.1	1.9	1.7	No Values	No Values	No Values	No Values
GRMZM2G177828_P01	pericarp	Function unknown	14 kDa	Ref	4.9	4.5	3.2	1.8	No Values	No Values	No Values	No Values
GRMZM2G178398_P01	pericarp	Function unknown	99 kDa	Ref	0.8	0.5	0.2	0.1	No Values	No Values	No Values	No Values
GRMZM2G181135_P01	pericarp	Function unknown	54 kDa	Ref	-0.1	0.5	1.5	2.3	No Values	No Values	No Values	No Values
GRMZM2G305851_P01	pericarp	Function unknown	41 kDa	Ref	1.7	1.6	1	1.7	No Values	No Values	No Values	No Values
GRMZM2G337229_P01	pericarp	Function unknown	16 kDa	Ref	-0.5	2.1	0.7	0.4	No Values	No Values	No Values	No Values
GRMZM2G348125_P01	pericarp	Function unknown	23 kDa	Ref	-0.1	0.3	2	0.3	No Values	No Values	No Values	No Values
GRMZM2G352855_P01	pericarp	Function unknown	49 kDa	Ref	0.4	0.8	1.7	2.6	No Values	No Values	No Values	No Values
GRMZM2G354053_P01	pericarp	Function unknown	84 kDa	Ref	1	0.1	-0.5	-1.6	No Values	No Values	No Values	No Values
GRMZM2G357595_P01	pericarp	Function unknown	31 kDa	Ref	0.5	0.4	0	0.7	No Values	No Values	No Values	No Values
GRMZM2G361064_P01	pericarp	Function unknown	26 kDa	Ref	0	0.4	0.3	0.6	No Values	No Values	No Values	No Values
GRMZM2G378106_P01	pericarp	Function unknown	67 kDa	Ref	-0.9	-0.6	-0.2	0.1	No Values	No Values	No Values	No Values
GRMZM2G383404_P01	pericarp	Function unknown	52 kDa	Ref	0.4	1.4	0.6	0.4	No Values	No Values	No Values	No Values
GRMZM2G394500_P01	pericarp	Function unknown	38 kDa	Ref	0	1.7	1.7	1.7	No Values	No Values	No Values	No Values
GRMZM2G410991_P01	pericarp	Function unknown	37 kDa	Ref	-1.1	0	0.2	0.5	No Values	No Values	No Values	No Values
GRMZM2G420733_P01	pericarp	Function unknown	25 kDa	Ref	-0.2	0.3	0.2	-0.4	No Values	No Values	No Values	No Values
GRMZM2G420743_P01	pericarp	Function unknown	26 kDa	Ref	-0.3	0.8	0	0.6	No Values	No Values	No Values	No Values
GRMZM2G424205_P01	pericarp	Function unknown	26 kDa	Ref	-0.7	-1.2	-0.4	0.2	No Values	No Values	No Values	No Values
GRMZM2G448883_P01	pericarp	Function unknown	33 kDa	Ref	2	2.2	2.3	3	No Values	No Values	No Values	No Values
GRMZM2G450233_P01	pericarp	Function unknown	38 kDa	Ref	0	0.6	1	2.4	No Values	No Values	No Values	No Values
GRMZM2G538535_P01	pericarp	Function unknown	49 kDa	Ref	0.5	0.2	1.2	1.8	No Values	No Values	No Values	No Values
GRMZM5G843748_P02	pericarp	Function unknown	38 kDa	Ref	-0.1	-0.2	0.4	0.8	No Values	No Values	No Values	No Values
GRMZM5G858249_P01	pericarp	Function unknown	33 kDa	Ref	0.4	0.7	1.3	2	No Values	No Values	No Values	No Values

GRMZM5G861077_P01	pericarp	Function unknown		66 kDa	Ref	-0.3	-0.1	-0.4	0.2	No Values	No Values	No Values	No Values
GRMZM5G868679_P01	pericarp	Function unknown		69 kDa	Ref	0.2	0.2	0.4	1	No Values	No Values	No Values	No Values
GRMZM5G896560_P01	pericarp	Function unknown		24 kDa	Ref	2.9	3.1	Reference Missing	Reference	No Values	No Values	No Values	No Values
AC155352.2_FGP010	pericarp	Function unknown		14 kDa	Ref	1.1	1.3	1	0.5	No Values	No Values	No Values	No Values
GRMZM2G145088_P01	pericarp	Function unknown	Uncharacterized archaeal coiled-coil protein	131 kDa	Ref	-0.2	-0.4	-0.6	-0.6	No Values	No Values	No Values	No Values
GRMZM2G465226_P01	pericarp	Function unknown	Uncharacterized protein with SCP/PR1 domains	17 kDa	Ref	0.3	0	-0.2	-0.1	No Values	No Values	No Values	No Values
AC202185.4_FGP004	pericarp	Function unknown		23 kDa	Ref	-0.2	0	1.6	0.3	No Values	No Values	No Values	No Values
GRMZM2G050193_P01	pericarp	General function prediction only	Ca2+-dependent lipid-binding protein, contains C2 domain	61 kDa	Ref	1	1	0.7	0.9	No Values	No Values	No Values	No Values
GRMZM5G821637_P05	pericarp	General function prediction only	FOG: Ankyrin repeat	38 kDa	Ref	1.8	1.6	0.7	-0.2	No Values	No Values	No Values	No Values
GRMZM2G022275_P01	pericarp	General function prediction only	FOG: WD40 repeat	53 kDa	Ref	-0.2	-0.4	-0.8	-0.5	No Values	No Values	No Values	No Values
GRMZM2G106960_P01	pericarp	General function prediction only	GTPase SAR1 and related small G proteins	23 kDa	Ref	-1.6	-1.7	-1.4	-1.4	No Values	No Values	No Values	No Values
GRMZM2G126732_P01	pericarp	General function prediction only	Isopenicillin N synthase and related dioxxygenases	41 kDa	Ref	0.6	1.5	2	1.8	No Values	No Values	No Values	No Values
GRMZM2G154523_P01	pericarp	General function prediction only	Patatin	44 kDa	Ref	1.2	2.8	2.1	2.4	No Values	No Values	No Values	No Values
GRMZM2G077673_P01	pericarp	General function prediction only	Predicted amidohydrolase	38 kDa	Ref	-0.5	0	-0.2	0.2	No Values	No Values	No Values	No Values
GRMZM2G701801_P02	pericarp	General function prediction only	Predicted flavoprotein	22 kDa	Ref	0.4	0.4	0.8	1.1	No Values	No Values	No Values	No Values
AC211394.4_FGP004	pericarp	General function prediction only	Predicted phosphohydrolases	55 kDa	Ref	0	0.8	0.9	0.4	No Values	No Values	No Values	No Values
GRMZM2G109405_P01	pericarp	General function prediction only	Predicted phosphohydrolases	43 kDa	Ref	0.2	0.3	0.3	0.6	No Values	No Values	No Values	No Values
GRMZM2G138572_P01	pericarp	General function prediction only	RNA-binding proteins (RRM domain)	19 kDa	Ref	0.8	-0.2	1	-0.8	No Values	No Values	No Values	No Values
GRMZM5G828229_P02	pericarp	General function prediction only	Uncharacterized NAD(FAD)-dependent dehydrogenases	54 kDa	Ref	-1.1	-1.5	-1.7	-1.5	No Values	No Values	No Values	No Values
GRMZM5G844562_P01	pericarp	General function prediction only	Zn-dependent alcohol dehydrogenases	39 kDa	Ref	-0.2	0.6	0.7	1.5	No Values	No Values	No Values	No Values
GRMZM2G076943_P01	pericarp	General function prediction only ; Signal transduction mechanisms ; Transcription ; Replication, recombination and repair	Serine/threonine protein kinase	76 kDa	Ref	1.4	2.2	1	1.4	No Values	No Values	No Values	No Values
GRMZM2G339540_P04	pericarp	General function prediction only ; Signal transduction mechanisms ; Transcription ; Replication, recombination and repair	Serine/threonine protein kinase	70 kDa	Ref	0.3	0.8	0.4	0.9	No Values	No Values	No Values	No Values
GRMZM2G079348_P01	pericarp	Inorganic ion transport and metabolism	Catalase	79 kDa	Ref	-1.5	-2.6	-2.2	-1.3	-1.8	-2.1	-2.3	-2.7
GRMZM2G014397_P02	pericarp	Inorganic ion transport and metabolism	Catalase (peroxidase I)	34 kDa	Ref	1.2	1.5	1.7	1.7	No Values	No Values	No Values	No Values

GRMZM2G104325_P01	pericarp	Inorganic ion transport and metabolism	Cation transport ATPase	105 kDa	Ref	1.6	1.2	Reference Missing	0.6	No Values	No Values	No Values	No Values
GRMZM2G162426_P01	pericarp	Inorganic ion transport and metabolism	Cation transport ATPase	116 kDa	Ref	0.5	0	-0.4	0.2	No Values	No Values	No Values	No Values
AC213884.3_FGP001	pericarp	Intracellular trafficking, secretion, and vesicular transport	Ran GTPase-activating protein (Ran-binding protein)	24 kDa	Ref	0.2	0.2	0.5	-0.2	No Values	No Values	No Values	No Values
GRMZM2G153984_P01	pericarp	Lipid transport and metabolism	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	31 kDa	Ref	-0.3	-0.3	-0.3	-0.3	No Values	No Values	No Values	No Values
GRMZM2G019926_P02	pericarp	Lipid transport and metabolism	Acetyl/propionyl-CoA carboxylase, alpha subunit	35 kDa	Ref	0	0.2	-0.1	0.7	No Values	No Values	No Values	No Values
GRMZM2G110201_P01	pericarp	Lipid transport and metabolism	Acetyl-CoA acetyltransferase	48 kDa	Ref	-0.3	-0.5	-0.5	-0.8	No Values	No Values	No Values	No Values
GRMZM2G042818_P01	pericarp	Lipid transport and metabolism	Enoyl-CoA hydratase/carnithine racemase	43 kDa	Ref	-0.3	0.2	-0.1	0.2	No Values	No Values	No Values	No Values
GRMZM2G181227_P01	pericarp	Lipid transport and metabolism	Enoyl-CoA hydratase/carnithine racemase	43 kDa	Ref	-0.9	-0.5	1.1	1.7	No Values	No Values	No Values	No Values
GRMZM2G137409_P01	pericarp	Lipid transport and metabolism	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis	82 kDa	Ref	0.1	0.2	1.4	2.2	No Values	No Values	No Values	No Values
GRMZM2G079949_P01	pericarp	Lipid transport and metabolism	Esterase/lipase	35 kDa	Ref	-0.3	-0.2	-0.1	0.3	No Values	No Values	No Values	No Values
GRMZM2G156310_P01	pericarp	Lipid transport and metabolism	Esterase/lipase	35 kDa	Ref	0.4	0.3	0.1	0.1	No Values	No Values	No Values	No Values
GRMZM5G826321_P01	pericarp	Lipid transport and metabolism	Esterase/lipase	34 kDa	Ref	-0.8	-1	-0.9	-1.2	No Values	No Values	No Values	No Values
GRMZM5G840955_P01	pericarp	Lipid transport and metabolism	Long-chain acyl-CoA synthetases (AMP-forming)	33 kDa	Ref	1.4	1	1.2	1.6	No Values	No Values	No Values	No Values
GRMZM2G061969_P01	pericarp	Lipid transport and metabolism	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	92 kDa	Ref	-0.1	-0.3	-0.7	-0.4	No Values	No Values	No Values	No Values
GRMZM2G442551_P01	pericarp	Lipid transport and metabolism	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	91 kDa	Ref	0.4	0.3	-0.1	0.3	No Values	No Values	No Values	No Values
GRMZM2G369815_P01	pericarp	Lipid transport and metabolism ; General function prediction only	Phospholipase/lecithinase/hemolysin	42 kDa	Ref	2	-1	-2.5	-2.3	No Values	No Values	No Values	No Values
GRMZM2G469898_P01	pericarp	Lipid transport and metabolism ; General function prediction only	Phospholipase/lecithinase/hemolysin	43 kDa	Ref	1.2	0.3	-0.6	-0.6	No Values	No Values	No Values	No Values
GRMZM2G055320_P01	pericarp	Lipid transport and metabolism ; Secondary metabolites biosynthesis, transport and catabolism	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	68 kDa	Ref	-0.9	-0.8	-1.2	-1.6	No Values	No Values	No Values	No Values
GRMZM2G069523_P01	pericarp	Lipid transport and metabolism ; Secondary metabolites biosynthesis, transport and catabolism ; General function prediction only	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	28 kDa	Ref	0	-0.2	0.2	0.2	0.9	0.6	1.1	0.7
GRMZM2G170017_P01	pericarp	Lipid transport and metabolism ; Secondary metabolites biosynthesis, transport and catabolism ; General function prediction only	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	34 kDa	Ref	Reference Missing	0.1	3.7	5.5	No Values	No Values	No Values	No Values

GRMZM2G141473_P01	pericarp	Nucleotide transport and metabolism	Xanthine dehydrogenase, molybdopterin-binding subunit B	146 kDa	Ref	0	0	0.9	2.3	No Values	No Values	No Values	No Values
GRMZM5G872934_P01	pericarp	Nucleotide transport and metabolism	Xanthine dehydrogenase, molybdopterin-binding subunit B	31 kDa	Ref	0.3	1.3	1.5	1.6	No Values	No Values	No Values	No Values
GRMZM2G021816_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Activator of HSP90 ATPase	39 kDa	Ref	-0.6	-0.7	-0.3	-0.9	No Values	No Values	No Values	No Values
GRMZM2G006377_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Cysteine protease	49 kDa	Ref	0.3	0.6	1.3	1.7	No Values	No Values	No Values	No Values
GRMZM2G150256_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Cysteine protease	52 kDa	Ref	0.1	-0.2	-0.1	0.1	No Values	No Values	No Values	No Values
GRMZM5G820822_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Cysteine protease	27 kDa	Ref	No Values	No Values	No Values	No Values	No Values	No Values	No Values	No Values
GRMZM2G335618_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Glutathione S-transferase	26 kDa	Ref	-0.7	-0.7	-0.3	0.7	No Values	No Values	No Values	No Values
GRMZM2G020040_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Molecular chaperone	104 kDa	Ref	-0.2	0	0	-0.5	No Values	No Values	No Values	No Values
GRMZM2G361605_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Molecular chaperone	94 kDa	Ref	-0.4	-0.6	-0.8	-0.8	No Values	No Values	No Values	No Values
GRMZM2G145449_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Peroxiredoxin	21 kDa	Ref	-2.5	-3.1	-2.7	-2.2	No Values	No Values	No Values	No Values
GRMZM2G414915_P01	pericarp	Posttranslational modification, protein turnover, chaperones	Subtilisin-like serine proteases	82 kDa	Ref	-0.7	-0.7	-1.2	-1.2	No Values	No Values	No Values	No Values
GRMZM5G883741_P02	pericarp	Posttranslational modification, protein turnover, chaperones	Subtilisin-like serine proteases	66 kDa	Ref	-0.3	-0.7	-0.6	-0.3	No Values	No Values	No Values	No Values
GRMZM2G118809_P01	pericarp	Secondary metabolites biosynthesis, transport and catabolism	Cytochrome P450	57 kDa	Ref	0.3	0.1	Reference Missing	Reference	No Values	No Values	No Values	No Values
GRMZM2G045192_P01	pericarp	Secondary metabolites biosynthesis, transport and catabolism	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis	27 kDa	Ref	-0.7	-0.7	-0.1	-0.6	No Values	No Values	No Values	No Values
GRMZM2G094375_P01	pericarp	Secondary metabolites biosynthesis, transport and catabolism	Putative multicopper oxidases	47 kDa	Ref	0.5	0.3	1	2	No Values	No Values	No Values	No Values
GRMZM2G408768_P01	pericarp	Signal transduction mechanisms	14-3-3 family protein	29 kDa	Ref	1.4	0.9	1.1	0.9	No Values	No Values	No Values	No Values
GRMZM2G069631_P01	pericarp	Signal transduction mechanisms	Serine/threonine protein phosphatase 2A, regulatory subunit	58 kDa	Ref	0.1	-0.1	-0.1	-0.1	0.1	-0.4	-0.5	-0.5
GRMZM2G036427_P01	pericarp	Signal transduction mechanisms	Universal stress protein UspA and related nucleotide-binding proteins	18 kDa	Ref	0.7	1.8	2	1.9	No Values	No Values	No Values	No Values
GRMZM2G021149_P01	pericarp	Transcription	Small nuclear ribonucleoprotein (snRNP) homolog	28 kDa	Ref	0.3	0.1	0.2	0.1	No Values	No Values	No Values	No Values
GRMZM2G038606_P01	pericarp	Transcription	Small nuclear ribonucleoprotein (snRNP) homolog	19 kDa	Ref	1.6	1.1	0.9	0	No Values	No Values	No Values	No Values
GRMZM2G144387_P01	pericarp	Translation, ribosomal structure and biogenesis	Ribosomal protein L1	25 kDa	Ref	0.9	1.1	1.3	0.3	No Values	No Values	No Values	No Values
GRMZM2G446960_P01	pericarp	Translation, ribosomal structure and biogenesis	Ribosomal protein S10E	20 kDa	Ref	1.2	0.9	0.4	0.4	No Values	No Values	No Values	No Values
GRMZM2G099454_P02	pericarp		Glycoside hydrolase, family 19, catalytic	28 kDa	Ref	1.3	2.1	1.2	2.5	No Values	No Values	No Values	No Values
GRMZM2G573867_P01	endosperm	Amino acid transport and metabolism	3-dehydroquinate synthetase	48 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	-0.3	-0.3	-0.4

GRMZM2G007647_P01	endosperm	Amino acid transport and metabolism	Acetolactate synthase, small (regulatory) subunit	52 kDa	Ref	No Values	No Values	No Values	No Values	1.9	1.5	0.7	0.3
GRMZM2G067265_P01	endosperm	Amino acid transport and metabolism	Aspartate/tyrosine/aromatic aminotransferase	54 kDa	Ref	No Values	No Values	No Values	No Values	0.2	Reference Missing	0.6	1
GRMZM5G836910_P01	endosperm	Amino acid transport and metabolism	Aspartate/tyrosine/aromatic aminotransferase	50 kDa	Ref	No Values	No Values	No Values	No Values	0.4	1.4	Reference Missing	Reference Missing
GRMZM2G076885_P01	endosperm	Amino acid transport and metabolism	Aspartate-semialdehyde dehydrogenase	41 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	0.1	-0.7
GRMZM2G068862_P01	endosperm	Amino acid transport and metabolism	ATP phosphoribosyltransferase	44 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.4	0.1	0.5
GRMZM2G386155_P01	endosperm	Amino acid transport and metabolism	Carboxypeptidase C (cathepsin A)	54 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.6	1.8	1.8
GRMZM2G124365_P01	endosperm	Amino acid transport and metabolism	Chorismate mutase	35 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.4	-0.7	1.7
AC182617.3_FGP001	endosperm	Amino acid transport and metabolism	Diaminopimelate epimerase	38 kDa	Ref	No Values	No Values	No Values	No Values	0.4	0.3	0.1	-0.1
GRMZM2G058584_P01	endosperm	Amino acid transport and metabolism	Histidinol dehydrogenase	51 kDa	Ref	No Values	No Values	No Values	No Values	1.4	1.2	2.2	2.1
GRMZM2G050371_P01	endosperm	Amino acid transport and metabolism	Ornithine carbamoyltransferase	40 kDa	Ref	No Values	No Values	No Values	No Values	-1	-1.3	-1.3	-1
GRMZM2G068665_P01	endosperm	Amino acid transport and metabolism	Pyrroline-5-carboxylate reductase	30 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.8	0.7	0
GRMZM2G143008_P01	endosperm	Amino acid transport and metabolism ; Coenzyme transport and metabolism	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]	69 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.5	1.2	0.9
GRMZM2G440208_P01	endosperm	Carbohydrate transport and metabolism	6-phosphogluconate dehydrogenase	54 kDa	Ref	No Values	No Values	No Values	No Values	1	0.7	0.4	0.4
GRMZM2G163437_P01	endosperm	Carbohydrate transport and metabolism	ADP-glucose pyrophosphorylase	56 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	2.5	2.9	2.9
GRMZM2G065083_P01	endosperm	Carbohydrate transport and metabolism	Glucose-6-phosphate isomerase	15 kDa	Ref	No Values	No Values	No Values	No Values	0	0	0.5	0.7
GRMZM2G104081_P01	endosperm	Carbohydrate transport and metabolism	Hexokinase	54 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	0.9	0.5	-0.5
GRMZM2G066290_P01	endosperm	Carbohydrate transport and metabolism	Pyruvate kinase	63 kDa	Ref	No Values	No Values	No Values	No Values	0.5	-0.3	-0.8	-0.9
GRMZM2G118462_P01	endosperm	Carbohydrate transport and metabolism	Trehalose-6-phosphate synthase	102 kDa	Ref	No Values	No Values	No Values	No Values	1	0.6	0.6	0.2
GRMZM2G138060_P01	endosperm	Carbohydrate transport and metabolism	Type II secretory pathway, pullulanase PuIA and related glycosidases	88 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.5	-0.1
AC197705.4_FGP001	endosperm	Carbohydrate transport and metabolism ; Coenzyme transport and metabolism ; General function prediction only	Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes	65 kDa	Ref	No Values	No Values	No Values	No Values	2.1	1.2	1.6	1.3
GRMZM2G085711_P02	endosperm	Carbohydrate transport and metabolism ; Posttranslational modification, protein turnover, chaperones	Golgi nucleoside diphosphatase	50 kDa	Ref	No Values	No Values	No Values	No Values	0.6	1.5	1.9	2.5
AC197705.4_FGP007	endosperm	Cell wall/membrane/envelope biogenesis	Outer membrane protein/protective antigen OMA87	57 kDa	Ref	No Values	No Values	No Values	No Values	1.2	-1	-0.8	-2

GRMZM2G034069_P01	endosperm	Cell wall/membrane/envelope biogenesis ; Carbohydrate transport and metabolism	Nucleoside-diphosphate-sugar epimerases	35 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.4	0	0
GRMZM2G013821_P01	endosperm	Chromatin structure and dynamics	Chromatin-associated proteins containing the HMG domain	15 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	-1.9	-1.8	-2
AC233922.1_FGP005	endosperm	Coenzyme transport and metabolism	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	40 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.6	1.6	0.7
GRMZM2G168681_P01	endosperm	Coenzyme transport and metabolism	Geranylgeranyl pyrophosphate synthase	40 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.1	1.2	3
GRMZM2G051782_P01	endosperm	Cytoskeleton	Tubulin	50 kDa	Ref	No Values	No Values	No Values	No Values	0.3	1.6	1.3	0.8
GRMZM2G082581_P01	endosperm	Energy production and conversion	Isocitrate dehydrogenases	36 kDa	Ref	No Values	No Values	No Values	No Values	0	-0.2	-0.1	0.3
GRMZM2G076239_P02	endosperm	Energy production and conversion	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	40 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.6	1.4	0.9
GRMZM2G154595_P01	endosperm	Energy production and conversion	Malate/lactate dehydrogenases	35 kDa	Ref	-0.1	Value Missing	-0.2	Value Miss	-3.5	-3.9	-3.5	-3.3
GRMZM2G466833_P01	endosperm	Energy production and conversion	Malate/lactate dehydrogenases	44 kDa	Ref	No Values	No Values	No Values	No Values	0.1	-0.1	-0.2	0.3
GRMZM2G424857_P01	endosperm	Energy production and conversion	Predicted acetamidase/formamidase	50 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0	Reference Missing	Reference Missing
AC233850.1_FGP002	endosperm	Function unknown		19 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
GRMZM2G012928_P01	endosperm	Function unknown		8 kDa	Ref	No Values	No Values	No Values	No Values	0	Reference Missing	Reference Missing	Reference Missing
GRMZM2G023242_P01	endosperm	Function unknown		17 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.2	-0.2	0.3
GRMZM2G024131_P01	endosperm	Function unknown		50 kDa	Ref	No Values	No Values	No Values	No Values	2.3	3.2	3	2.1
GRMZM2G025646_P01	endosperm	Function unknown		15 kDa	Ref	No Values	No Values	No Values	No Values	3.2	2.9	2.3	1.6
GRMZM2G031033_P01	endosperm	Function unknown		16 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.2	0.6	-0.1
GRMZM2G033130_P01	endosperm	Function unknown		104 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
GRMZM2G034326_P01	endosperm	Function unknown		17 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.5	0.4	0
GRMZM2G048194_P01	endosperm	Function unknown		41 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	-1.4	-1.6	-2.2
GRMZM2G050607_P01	endosperm	Function unknown		16 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	0.4	2.1
GRMZM2G053019_P01	endosperm	Function unknown		47 kDa	Ref	No Values	No Values	No Values	No Values	1.3	1.2	1.3	1.5
GRMZM2G053652_P01	endosperm	Function unknown		22 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
GRMZM2G055434_P01	endosperm	Function unknown		23 kDa	Ref	No Values	No Values	No Values	No Values	2.6	0.1	1.3	0.7
GRMZM2G056661_P01	endosperm	Function unknown		222 kDa	Ref	No Values	No Values	No Values	No Values	1.5	0.3	0.8	-1.9

GRMZM2G066815_P01	endosperm	Function unknown	57 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.5	0.5
GRMZM2G085260_P01	endosperm	Function unknown	34 kDa	Ref	No Values	No Values	No Values	No Values	0	1	1.6	3.3
GRMZM2G092627_P01	endosperm	Function unknown	155 kDa	Ref	No Values	No Values	No Values	No Values	1.2	1.5	0.6	-0.2
GRMZM2G096806_P01	endosperm	Function unknown	115 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.3	0.7	0.2
GRMZM2G097207_P01	endosperm	Function unknown	53 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.5	0.3	0.7
GRMZM2G100146_P01	endosperm	Function unknown	33 kDa	Ref	No Values	No Values	No Values	No Values	0.5	-0.9	-1.5	-1.5
GRMZM2G101515_P01	endosperm	Function unknown	91 kDa	Ref	No Values	No Values	No Values	No Values	1	-0.1	-0.8	-1.3
GRMZM2G102483_P02	endosperm	Function unknown	42 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	-0.1	Reference Missing	Reference Missing
GRMZM2G118363_P01	endosperm	Function unknown	67 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
GRMZM2G119627_P01	endosperm	Function unknown	54 kDa	Ref	No Values	No Values	No Values	No Values	-1.6	-1.3	-1.7	-1.7
GRMZM2G122357_P01	endosperm	Function unknown	14 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0	Reference Missing	0.6
GRMZM2G127160_P01	endosperm	Function unknown	47 kDa	Ref	No Values	No Values	No Values	No Values	2.1	0.6	0.6	0.2
GRMZM2G132130_P01	endosperm	Function unknown	29 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.4	-0.2	0.4
GRMZM2G139341_P01	endosperm	Function unknown	73 kDa	Ref	No Values	No Values	No Values	No Values	2.2	1.4	1.3	0.2
GRMZM2G144081_P01	endosperm	Function unknown	47 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	2.9	0.8	0
GRMZM2G145226_P01	endosperm	Function unknown	25 kDa	Ref	No Values	No Values	No Values	No Values	-1.6	-0.8	-0.5	-0.6
GRMZM2G149321_P01	endosperm	Function unknown	53 kDa	Ref	No Values	No Values	No Values	No Values	0.7	-0.6	0.6	-1.6
GRMZM2G151387_P01	endosperm	Function unknown	80 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0	-0.2	-0.2
GRMZM2G153162_P02	endosperm	Function unknown	101 kDa	Ref	No Values	No Values	No Values	No Values	0.1	-0.9	-0.5	-1
GRMZM2G161222_P03	endosperm	Function unknown	58 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	Reference Missing
GRMZM2G161534_P01	endosperm	Function unknown	39 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	0.9	1.1
GRMZM2G164868_P01	endosperm	Function unknown	58 kDa	Ref	No Values	No Values	No Values	No Values	0.8	-1.5	-0.4	-0.7
GRMZM2G167932_P01	endosperm	Function unknown	49 kDa	Ref	No Values	No Values	No Values	No Values	-0.9	-1.7	-1.6	-1.6
GRMZM2G169182_P01	endosperm	Function unknown	70 kDa	Ref	No Values	No Values	No Values	No Values	-0.7	0.2	0.1	-0.2
GRMZM2G172523_P01	endosperm	Function unknown	60 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.5	0.7	0.9

GRMZM2G304548_P01	endosperm	Function unknown	20 kDa	Ref	No Values	No Values	No Values	No Values	1.2	Reference Missing	0.1	-0.1
GRMZM2G347541_P01	endosperm	Function unknown	69 kDa	Ref	No Values	No Values	No Values	No Values	0.3	-0.2	-0.1	0.1
GRMZM2G353213_P01	endosperm	Function unknown	35 kDa	Ref	No Values	No Values	No Values	No Values	-0.5	-0.9	-0.5	0
GRMZM2G353266_P01	endosperm	Function unknown	14 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	-0.2	-0.1	0
GRMZM2G359397_P01	endosperm	Function unknown	51 kDa	Ref	No Values	No Values	No Values	No Values	0.8	1.7	2	2
GRMZM2G375593_P01	endosperm	Function unknown	104 kDa	Ref	No Values	No Values	No Values	No Values	1	1.1	0.5	0.5
GRMZM2G376743_P01	endosperm	Function unknown	59 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	-0.1	0.3	0.9
GRMZM2G402564_P01	endosperm	Function unknown	8 kDa	Ref	No Values	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing
GRMZM2G410134_P01	endosperm	Function unknown	22 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0.3	Reference Missing	-0.7
GRMZM2G412436_P01	endosperm	Function unknown	62 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	2.1
GRMZM2G412470_P02	endosperm	Function unknown	79 kDa	Ref	No Values	No Values	No Values	No Values	0.9	0.9	0.4	0.8
GRMZM2G425629_P02	endosperm	Function unknown	24 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	Reference Missing	3.5
GRMZM2G428040_P01	endosperm	Function unknown	13 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.9	1.3	Reference Missing
GRMZM2G439339_P04	endosperm	Function unknown	226 kDa	Ref	No Values	No Values	No Values	No Values	0.7	0.6	0.1	-0.2
GRMZM2G442057_P01	endosperm	Function unknown	47 kDa	Ref	No Values	No Values	No Values	No Values	1.3	0.6	Reference Missing	0.8
GRMZM2G453424_P03	endosperm	Function unknown	23 kDa	Ref	No Values	No Values	No Values	No Values	0.2	-0.2	-0.8	-0.7
GRMZM2G467169_P01	endosperm	Function unknown	107 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	Reference Missing	1.4	0.8
GRMZM2G474575_P01	endosperm	Function unknown	23 kDa	Ref	No Values	No Values	No Values	No Values	-1.1	-0.2	1.1	2.4
GRMZM2G480002_P01	endosperm	Function unknown	187 kDa	Ref	No Values	No Values	No Values	No Values	1.6	1.2	0.7	0.7
GRMZM2G704475_P02	endosperm	Function unknown	38 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	-1.1	-0.4	0.8
GRMZM5G823017_P01	endosperm	Function unknown	46 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	-1.4	-0.3	-0.1
GRMZM5G888696_P02	endosperm	Function unknown	68 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.7	0.3	-0.2
GRMZM2G065292_P01	endosperm	Function unknown	82 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.6	0.6	0.5
GRMZM2G172574_P01	endosperm	Function unknown	15 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	Reference Missing	2.1	3.5
GRMZM2G169943_P01	endosperm	General function prediction only	36 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	1.2	1.8	3.2

GRMZM2G070863_P01	endosperm	General function prediction only	FOG: TPR repeat	65 kDa	Ref	No Values	No Values	No Values	No Values	1	0.4	0.4	2.3
GRMZM2G143330_P01	endosperm	General function prediction only	FOG: WD40 repeat	36 kDa	Ref	No Values	No Values	No Values	No Values	0.9	1	0.8	0.3
GRMZM2G060940_P01	endosperm	General function prediction only	Isopenicillin N synthase and related dioxygenases	40 kDa	Ref	No Values	No Values	No Values	No Values	1	2.1	Reference Missing	1.1
GRMZM2G003789_P01	endosperm	General function prediction only	Metal-dependent amidase/aminoacylase/carboxypeptidase	47 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	0.1	0.7	0.5
AC197705.4_FGP003	endosperm	General function prediction only	Phospholipid-binding protein	19 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.1	1.1	3.9
GRMZM2G021614_P01	endosperm	General function prediction only	Phospholipid-binding protein	19 kDa	Ref	No Values	No Values	No Values	No Values	-0.4	1.1	1.6	2.1
GRMZM2G006178_P01	endosperm	General function prediction only	Predicted ATPase, RNase L inhibitor (RLI) homolog	68 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.4	0.4	-0.2
GRMZM2G016827_P02	endosperm	General function prediction only	Predicted dioxygenase	33 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	Reference Missing	0.1	0.4
GRMZM2G062425_P01	endosperm	General function prediction only	Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	28 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.4	-1.1	-1.2
GRMZM2G475293_P01	endosperm	General function prediction only	Predicted phosphatase/phosphohexomutase	27 kDa	Ref	No Values	No Values	No Values	No Values	-1.2	-0.5	-0.3	1.4
GRMZM2G049866_P01	endosperm	General function prediction only	RNA-binding proteins (RRM domain)	45 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	0.1	-1.2	-1.2
GRMZM2G073700_P01	endosperm	General function prediction only	RNA-binding proteins (RRM domain)	35 kDa	Ref	No Values	No Values	No Values	No Values	1.2	0.8	0.8	0.9
GRMZM2G082198_P01	endosperm	General function prediction only	RNA-binding proteins (RRM domain)	23 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	-0.3	-1.1	-0.3
GRMZM2G123234_P01	endosperm	General function prediction only	RNA-binding proteins (RRM domain)	31 kDa	Ref	No Values	No Values	No Values	No Values	-1	-1.7	-1	-2
GRMZM2G352129_P01	endosperm	General function prediction only	RNA-binding proteins (RRM domain)	72 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	0.7	0.4
GRMZM2G091819_P01	endosperm	Inorganic ion transport and metabolism	Predicted flavoprotein involved in K ⁺ transport	44 kDa	Ref	No Values	No Values	No Values	No Values	2.7	0.3	0	-1.5
AC204711.3_FGP003	endosperm	Inorganic ion transport and metabolism	Rhodanese-related sulfurtransferase	16 kDa	Ref	No Values	No Values	No Values	No Values	0.6	0.5	Reference Missing	0.7
GRMZM2G376731_P01	endosperm	Intracellular trafficking, secretion, and vesicular transport	Karyopherin (importin) beta	99 kDa	Ref	No Values	No Values	No Values	No Values	0.9	-0.7	-0.9	-0.9
AC197672.3_FGP002	endosperm	Lipid transport and metabolism	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	257 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	-0.5	Reference Missing	-0.3
GRMZM2G004528_P03	endosperm	Lipid transport and metabolism	Myo-inositol-1-phosphate synthase	56 kDa	Ref	No Values	No Values	No Values	No Values	2	0.4	0.2	0.2
GRMZM2G071846_P01	endosperm	Nucleotide transport and metabolism	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	24 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0.6	0.5	-0.3
GRMZM2G044762_P01	endosperm	Nucleotide transport and metabolism	dUTPase	23 kDa	Ref	No Values	No Values	No Values	No Values	0.3	-0.2	0	-0.4
GRMZM2G100084_P01	endosperm	Nucleotide transport and metabolism	IMP dehydrogenase/GMP reductase	53 kDa	Ref	No Values	No Values	No Values	No Values	0.3	0.8	0.9	1

GRMZM2G013478_P01	endosperm	Nucleotide transport and metabolism	Nucleoside diphosphate kinase	24 kDa	Ref	No Values	No Values	No Values	No Values	-0.8	-0.3	0.3	0.9
GRMZM2G000622_P01	endosperm	Nucleotide transport and metabolism	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	155 kDa	Ref	No Values	No Values	No Values	No Values	0.8	-0.1	-0.2	-0.4
GRMZM2G060163_P01	endosperm	Nucleotide transport and metabolism	Ribonucleotide reductase, beta subunit	39 kDa	Ref	No Values	No Values	No Values	No Values	3.2	-0.6	0.1	-1
GRMZM2G028346_P01	endosperm	Posttranslational modification, protein turnover, chaperones	20S proteasome, alpha and beta subunits	25 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0	-0.2	-0.5
GRMZM2G587327_P01	endosperm	Posttranslational modification, protein turnover, chaperones	ATPases of the AAA+ class	81 kDa	Ref	No Values	No Values	No Values	No Values	0.9	-0.8	-1.2	-1.6
AC215201.3_FGP005	endosperm	Posttranslational modification, protein turnover, chaperones	Chaperonin GroEL (HSP60 family)	63 kDa	Ref	No Values	No Values	No Values	No Values	-0.5	0.8	1.2	1.3
GRMZM2G091189_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Co-chaperonin GroES (HSP10)	26 kDa	Ref	No Values	No Values	No Values	No Values	1	0	-0.8	-0.7
GRMZM2G039886_P01	endosperm	Posttranslational modification, protein turnover, chaperones	DnaJ-class molecular chaperone with C-terminal Zn finger domain	39 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.8	0.9	1.2
GRMZM2G330635_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Glutathione S-transferase	25 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	1.5	1.8	1.9
GRMZM5G802801_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone	71 kDa	Ref	No Values	No Values	No Values	No Values	-0.7	0.6	0.2	0.4
GRMZM2G080724_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone (small heat shock protein)	27 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.2	-0.8	-0.3
GRMZM2G083810_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone (small heat shock protein)	18 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	0.2	0.7	2.6
GRMZM2G404249_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone (small heat shock protein)	17 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	1.4	2.5	3.4
GRMZM2G044684_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone GrpE (heat shock protein)	36 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	0	-0.4	2
GRMZM2G002220_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone, HSP90 family	89 kDa	Ref	No Values	No Values	No Values	No Values	1	0.6	0.1	0.1
GRMZM2G047434_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone, HSP90 family	38 kDa	Ref	No Values	No Values	No Values	No Values	1	-1.9	-1.3	-1.3
GRMZM2G069651_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone, HSP90 family	80 kDa	Ref	No Values	No Values	No Values	No Values	-1.3	-0.5	-1	-1.1
GRMZM5G833699_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Molecular chaperone, HSP90 family	82 kDa	Ref	No Values	No Values	No Values	No Values	-0.3	2	2.4	2.5
GRMZM2G329306_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	43 kDa	Ref	No Values	No Values	No Values	No Values	-0.1	-0.6	0.5	-0.9
GRMZM2G139680_P01	endosperm	Posttranslational modification, protein turnover, chaperones	Peroxioredoxin	28 kDa	Ref	No Values	No Values	No Values	No Values	-0.6	-0.4	-0.4	-0.1
GRMZM2G413652_P01	endosperm	Posttranslational modification, protein turnover, chaperones ; Transcription	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase	30 kDa	Ref	No Values	No Values	No Values	No Values	-1.4	-1.3	-1.6	-1.5
GRMZM2G014750_P01	endosperm	Posttranslational modification, protein turnover, chaperones ; Translation, ribosomal structure and biogenesis	La protein, small RNA-binding pol III transcript stabilizing protein and related La-motif-containing proteins involved in translation	52 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.5	-0.7	-0.9
AC207890.3_FGP002	endosperm	Replication, recombination and repair	Micrococcal nuclease (thermonuclease) homologs	108 kDa	Ref	No Values	No Values	No Values	No Values	0.5	0.6	0.7	0.9

GRMZM2G017532_P01	endosperm	Replication, recombination and repair ; General function prediction only	NTP pyrophosphohydrolases including oxidative damage repair enzymes	21 kDa	Ref	No Values	No Values	No Values	No Values	-0.2	1.1	0.9	2.7
GRMZM2G000980_P01	endosperm	RNA processing and modification	Splicing factor (branch point binding protein)	80 kDa	Ref	No Values	No Values	No Values	No Values	Reference Missing	1	Reference Missing	1.1
AC194970.5_FGP009	endosperm	Transcription	DNA helicase TIP49, TBP-interacting protein	52 kDa	Ref	1.7	0.9	1.4	0.1	-1.6	-1.8	-2.1	-2.5
GRMZM2G083836_P01	endosperm	Translation, ribosomal structure and biogenesis	Aspartyl/asparaginyl-tRNA synthetases	63 kDa	Ref	No Values	No Values	No Values	No Values	0.4	-0.1	0.1	-0.6
GRMZM2G101463_P01	endosperm	Translation, ribosomal structure and biogenesis	Phenylalanyl-tRNA synthetase alpha subunit	56 kDa	Ref	No Values	No Values	No Values	No Values	0.2	0.9	0.6	0.3
GRMZM2G144995_P01	endosperm	Translation, ribosomal structure and biogenesis	Protein implicated in ribosomal biogenesis, Nop56p homolog	61 kDa	Ref	No Values	No Values	No Values	No Values	1.1	0.5	0.7	-1.1
GRMZM2G125271_P01	endosperm	Translation, ribosomal structure and biogenesis	Ribosomal protein S4E	30 kDa	Ref	No Values	No Values	No Values	No Values	1	1.4	0.9	0.2
GRMZM2G316232_P01	endosperm	Translation, ribosomal structure and biogenesis	Translation elongation factors (GTPases)	57 kDa	Ref	No Values	No Values	No Values	No Values	1.6	0.9	0.2	0.3
GRMZM2G018943_P01	endosperm	Translation, ribosomal structure and biogenesis	Translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	80 kDa	Ref	No Values	No Values	No Values	No Values	0.1	0.1	0.2	-0.3
GRMZM2G069208_P01	endosperm		PUR-alpha/beta/gamma, DNA/RNA- binding	33 kDa	Ref	No Values	No Values	No Values	No Values	1.3	1.6	1	0.8

[illegible]

ko00071_entry_60	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; ECHS1; HADHA; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; ysiB, fadB; MFP2; fadB; enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; fadJ; enoyl-CoA hydratase [EC:4.2.1.17]; paaF, echA; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8] ko:K01692 ko:K10527 ko:K01825 ko:K01782 ko:K07511 ko:K13767 ko:K07514 ko:K07515	Fatty acid metabolism
ko00071_entry_62	enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; HADHA; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2 ko:K07515 ko:K10527	Fatty acid metabolism
ko00071_entry_66	HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]; enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; fadN; fadB; fadJ; MFP2; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8] ko:K00022 ko:K07516 ko:K10527 ko:K07514 ko:K01825 ko:K01782	Fatty acid metabolism
ko00071_entry_67	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; ECHS1; HADHA; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; ysiB, fadB; MFP2; fadB; enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; fadJ; enoyl-CoA hydratase [EC:4.2.1.17]; paaF, echA; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8] ko:K01692 ko:K10527 ko:K01825 ko:K01782 ko:K07511 ko:K13767 ko:K07514 ko:K07515	Fatty acid metabolism
ko00071_entry_70	enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; HADHA; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2 ko:K07515 ko:K10527	Fatty acid metabolism
ko00071_entry_76	HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]; enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; fadN; fadB; fadJ; MFP2; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8] ko:K00022 ko:K07516 ko:K10527 ko:K07514 ko:K01825 ko:K01782	Fatty acid metabolism

					enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; ECHS1; HADHA; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; ysiB, fadB; MFP2; fadB; enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; fadJ; enoyl-CoA hydratase [EC:4.2.1.17]; paaF, echA; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8]	ko:K01692 ko:K10527 ko:K01825 ko:K01782 ko:K07511 ko:K13767 ko:K07514 ko:K07515	Fatty acid metabolism
					enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; HADHA; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2	ko:K07515 ko:K10527	Fatty acid metabolism
					enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; ECHS1; HADHA; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; ysiB, fadB; MFP2; fadB; enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; fadJ; enoyl-CoA hydratase [EC:4.2.1.17]; paaF, echA; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8]	ko:K01692 ko:K10527 ko:K01825 ko:K01782 ko:K07511 ko:K13767 ko:K07514 ko:K07515	Fatty acid metabolism
					HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]; enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]; fadN; fadB; fadJ; MFP2; EHHADH; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase [EC:1.1.1.35 4.2.1.17 5.1.2.3 5.3.3.8]	ko:K00022 ko:K07516 ko:K10527 ko:K07514 ko:K01825 ko:K01782	Fatty acid metabolism
					enoyl-CoA hydratase / long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]; HADHA; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2	ko:K07515 ko:K10527	Fatty acid metabolism
					enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2	ko:K10527	alpha-Linolenic acid metabolism
					enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2	ko:K10527	alpha-Linolenic acid metabolism
					enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35 1.1.1.211]; MFP2	ko:K10527	alpha-Linolenic acid metabolism
5	Endosperm	GRMZM2G090087_P02	D7; D8	ko00250_entry_115	putA; E1.5.1.12; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	ko:K00294 ko:K13821	
				ko00330_entry_199	putA; E1.5.1.12; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	ko:K00294 ko:K13821	

				ko00330_entry_200	putA; E1.5.1.12; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	ko:K00294 ko:K13821	
				ko00330_entry_238	putA; E1.5.1.12; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	ko:K00294 ko:K13821	
				ko00330_entry_308	putA; E1.5.1.12; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	ko:K00294 ko:K13821	
6	Endosperm	GRMZM2G097030_P01	D5; D6; D7; D8	ko00402_entry_21	UDP-glucosyltransferase BX8 [EC:2.4.1.202]; BX8; UDP-glucosyltransferase BX9 [EC:2.4.1.202]; BX9	ko:K13227 ko:K13228	Benzoxazinoid biosynthesis
7	Endosperm	GRMZM2G456217_P01	D6	ko04612_entry_8	CTSL; CTSB; cathepsin L [EC:3.4.22.15]; cathepsin S [EC:3.4.22.27]; CTSS; cathepsin B [EC:3.4.22.1]	ko:K01363 ko:K01365 ko:K01368	Antigen processing and presentation
8	Endosperm	GRMZM2G143862_P01	D7; D8	ko00051_entry_96	E2.7.1.90, pfk; pyrophosphate-fructose-6-phosphate 1-phosphotransferase [EC:2.7.1.90]	ko:K00895	Fructose and mannose metabolism
9	Endosperm	GRMZM2G019404_P01	D5; D6; D7	ko00190_entry_107	E3.6.3.6; H+-transporting ATPase [EC:3.6.3.6] F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]; A1P+UL, atpE; ATPVB, ntpB; ATPeF1D, ATP5D; V-type H+-transporting ATPase 16kDa proteolipid subunit [EC:3.6.3.14]; ATPVI, ntpI; ATPeF0F, ATP5J2; ATPVC, ntpC; F-type H+-transporting ATPase subunit f [EC:3.6.3.14]; F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]; ATPF1D, atpH; ATPeF1G, ATP5C1; ATPeFH, ATP14; ATPF1G, atpG; F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]; ATPeF0E, ATP5I; ATPeVE, ATP6E; F-type H+-transporting ATPase subunit a [EC:3.6.3.14]; V-type H+-transporting ATPase 54 kD subunit [EC:3.6.3.14]; ATPeF0B, ATP5F1; ATPF0B, atpF; ATPeF0A, MTATP6; ATPeFF, ATP17; ATPeF0F6, ATP5J; ATPF0A, atpB; V-type H+-transporting ATPase subunit E [EC:3.6.3.14]; F-type H+-transporting ATPase subunit g [EC:3.6.3.14]; V-type H+-transporting ATPase subunit A [EC:3.6.3.14]; ATPeV54kD; ATPeVPL, ATP6L; F-type H+-transporting ATPase subunit delta [EC:3.6.3.14]; F-type H+-transporting ATPase subunit 6 [EC:3.6.3.14]; V-type H+-transporting ATPase subunit B [EC:3.6.3.14]; F-type H+-transporting ATPase subunit d [EC:3.6.3.14]; ATPeVA, ATP6A1; ATPeVB, ATP6B1; ATPeFK, ATP19; F-type H+-transporting ATPase oligomycin sensitivity conferral protein [EC:3.6.3.14]; ATPVA, ntpA; V-type H+-transporting ATPase subunit H [EC:3.6.3.14]; ATPF1B, atpD; ATPeF1A, ATP5A1; V-type H+-transporting ATPase subunit I [EC:3.6.3.14]; V-type H+-transporting ATPase subunit D [EC:3.6.3.14]; F-type H+-transporting ATPase subunit k [EC:3.6.3.14]; V-type H+-transporting ATPase subunit AC39 [EC:3.6.3.14]; ATPeF1A, ATP5A1; ATPeF1B, ATP5B1; ATPeF1C, ATP5C1; ATPeF1D, ATP5D1; ATPeF1E, ATP5E1; ATPeF1F, ATP5F1; ATPeF1G, ATP5G1; ATPeF1H, ATP5H1; ATPeF1I, ATP5I1; ATPeF1J, ATP5J1; ATPeF1K, ATP5K1; ATPeF1L, ATP5L1; ATPeF1M, ATP5M1; ATPeF1N, ATP5N1; ATPeF1O, ATP5O1; ATPeF1P, ATP5P1; ATPeF1Q, ATP5Q1; ATPeF1R, ATP5R1; ATPeF1S, ATP5S1; ATPeF1T, ATP5T1; ATPeF1U, ATP5U1; ATPeF1V, ATP5V1; ATPeF1W, ATP5W1; ATPeF1X, ATP5X1; ATPeF1Y, ATP5Y1; ATPeF1Z, ATP5Z1	ko:K01535	Oxidative phosphorylation
10	Endosperm	GRMZM2G041275_P01	D7	ko00190_entry_105	E3.6.3.6; H+-transporting ATPase [EC:3.6.3.6] F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]; A1P+UL, atpE; ATPVB, ntpB; ATPeF1D, ATP5D; V-type H+-transporting ATPase 16kDa proteolipid subunit [EC:3.6.3.14]; ATPVI, ntpI; ATPeF0F, ATP5J2; ATPVC, ntpC; F-type H+-transporting ATPase subunit f [EC:3.6.3.14]; F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]; ATPF1D, atpH; ATPeF1G, ATP5C1; ATPeFH, ATP14; ATPF1G, atpG; F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]; ATPeF0E, ATP5I; ATPeVE, ATP6E; F-type H+-transporting ATPase subunit a [EC:3.6.3.14]; V-type H+-transporting ATPase 54 kD subunit [EC:3.6.3.14]; ATPeF0B, ATP5F1; ATPF0B, atpF; ATPeF0A, MTATP6; ATPeFF, ATP17; ATPeF0F6, ATP5J; ATPF0A, atpB; V-type H+-transporting ATPase subunit E [EC:3.6.3.14]; F-type H+-transporting ATPase subunit g [EC:3.6.3.14]; V-type H+-transporting ATPase subunit A [EC:3.6.3.14]; ATPeV54kD; ATPeVPL, ATP6L; F-type H+-transporting ATPase subunit delta [EC:3.6.3.14]; F-type H+-transporting ATPase subunit 6 [EC:3.6.3.14]; V-type H+-transporting ATPase subunit B [EC:3.6.3.14]; F-type H+-transporting ATPase subunit d [EC:3.6.3.14]; ATPeVA, ATP6A1; ATPeVB, ATP6B1; ATPeFK, ATP19; F-type H+-transporting ATPase oligomycin sensitivity conferral protein [EC:3.6.3.14]; ATPVA, ntpA; V-type H+-transporting ATPase subunit H [EC:3.6.3.14]; ATPF1B, atpD; ATPeF1A, ATP5A1; V-type H+-transporting ATPase subunit I [EC:3.6.3.14]; V-type H+-transporting ATPase subunit D [EC:3.6.3.14]; F-type H+-transporting ATPase subunit k [EC:3.6.3.14]; V-type H+-transporting ATPase subunit AC39 [EC:3.6.3.14]; ATPeF1A, ATP5A1; ATPeF1B, ATP5B1; ATPeF1C, ATP5C1; ATPeF1D, ATP5D1; ATPeF1E, ATP5E1; ATPeF1F, ATP5F1; ATPeF1G, ATP5G1; ATPeF1H, ATP5H1; ATPeF1I, ATP5I1; ATPeF1J, ATP5J1; ATPeF1K, ATP5K1; ATPeF1L, ATP5L1; ATPeF1M, ATP5M1; ATPeF1N, ATP5N1; ATPeF1O, ATP5O1; ATPeF1P, ATP5P1; ATPeF1Q, ATP5Q1; ATPeF1R, ATP5R1; ATPeF1S, ATP5S1; ATPeF1T, ATP5T1; ATPeF1U, ATP5U1; ATPeF1V, ATP5V1; ATPeF1W, ATP5W1; ATPeF1X, ATP5X1; ATPeF1Y, ATP5Y1; ATPeF1Z, ATP5Z1	ko:K02108 ko:K02109 ko:K02110 ko:K02111 ko:K02112 ko:K02113 ko:K02114 ko:K02115 ko:K02117 ko:K02118 ko:K02119 ko:K02120 ko:K02121 ko:K02122 ko:K02123 ko:K02124 ko:K02125 ko:K02126 ko:K02127 ko:K02128 ko:K02129 ko:K02130 ko:K02131 ko:K02132 ko:K02133 ko:K02134 ko:K02135 ko:K02136 ko:K02137 ko:K02138 ko:K02139 ko:K02140 ko:K02141 ko:K02142 ko:K02143 ko:K02144 ko:K02145 ko:K02146 ko:K02147 ko:K02148 ko:K02149 ko:K02150 ko:K02151 ko:K02152 ko:K02153 ko:K02154 ko:K02155 ko:K03661 ko:K03662	Oxidative phosphorylation
11	Endosperm	GRMZM2G328893_P01	D6	ko00270_entry_119	cysM; cysO; cysK; MET17; cysteine synthase / O-phosphoserine sulfhydrylase / spermine synthase [EC:2.5.1.47 2.5.1.65 4.2.1.22]; ATCYSC1; cysteine synthase A [EC:2.5.1.47]; L-3-cyanoalanine synthase/ cysteine synthase [EC:2.5.1.47 4.4.1.9]; cysteine synthase B [EC:2.5.1.47]; O-acetylhomoserine/O-acetylserine sulfhydrylase [EC:2.5.1.49 2.5.1.47]	ko:K01738 ko:K12339 ko:K13034 ko:K10150 ko:K17069	Cysteine and methionine metabolism
				ko00270_entry_126	cysM; cysO; cysK; MET17; cysteine synthase / O-phosphoserine sulfhydrylase / spermine synthase [EC:2.5.1.47 2.5.1.65 4.2.1.22]; ATCYSC1; cysteine synthase A [EC:2.5.1.47]; L-3-cyanoalanine synthase/ cysteine synthase [EC:2.5.1.47 4.4.1.9]; cysteine synthase B [EC:2.5.1.47]; O-acetylhomoserine/O-acetylserine sulfhydrylase [EC:2.5.1.49 2.5.1.47]	ko:K01738 ko:K12339 ko:K13034 ko:K10150 ko:K17069	Cysteine

				ko00920_entry_49	cysM; cysO; cysK; cysteine synthase / O-phosphoserine sulfhydrylase / spermine synthase [EC:2.5.1.47 2.5.1.65 4.2.1.22]; ATCYSC1; cysteine synthase A [EC:2.5.1.47]; L-3-cyanoalanine synthase/ cysteine synthase [EC:2.5.1.47 4.4.1.9]; cysteine synthase B [EC:2.5.1.47]	ko:K01738 ko:K12339 ko:K13034 ko:K10150	Sulfur metabolism
12	Endosperm	GRMZM2G117198_P01	D5	ko00270_entry_88	metK; S-adenosylmethionine synthetase [EC:2.5.1.6] ARO1; pentafunctional AROM polypeptide [EC:4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]; 3-dehydroquinase dehydratase / shikimate dehydrogenase [EC:4.2.1.10 1.1.1.25]; shikimate dehydrogenase [EC:1.1.1.25]; aroDE, DHQ-SDH; aroE ARO1; pentafunctional AROM polypeptide [EC:4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]; 3-dehydroquinase dehydratase I [EC:4.2.1.10]; aroQ, qutE; 3-dehydroquinase dehydratase / shikimate dehydrogenase [EC:4.2.1.10 1.1.1.25]; aroD; aroDE, DHQ-SDH; 3-dehydroquinase dehydratase II [EC:4.2.1.10]	ko:K00789	Cysteine and methionine metabolism
13	Endosperm	GRMZM2G014376_P01	D7	ko00400_entry_74		ko:K00014 ko:K13832 ko:K13830	Phenylalanine, tyrosine and tryptophan biosynthesis
				ko00400_entry_75		ko:K03785 ko:K03786 ko:K13832 ko:K13830	Phenylalanine, tyrosine and tryptophan biosynthesis
14	Endosperm	GRMZM2G134708_P01	D5; D6	ko00053_entry_101	monodehydroascorbate reductase (NADH) [EC:1.6.5.4]; E1.6.5.4	ko:K08232	Ascorbate and aldarate metabolism
15	Endosperm	GRMZM2G135283_P03	D5; D6; D7	ko00260_entry_85 ko00460_entry_47 ko00630_entry_216 ko00670_entry_61 ko00680_entry_311 ko00680_entry_74	glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]	ko:K00600 ko:K00600 ko:K00600 ko:K00600 ko:K00600 ko:K00600	Glycine, serine and threonine metabolism Cyanoamino acid metabolism Glyoxylate and dicarboxylate metabolism One carbon pool by folate Methane metabolism Methane metabolism
16	Endosperm	GRMZM2G010321_P01	D6; D7; D8	ko00630_entry_217	gcvH, GCSH; glycine cleavage system H protein	ko:K02437	Glyoxylate and dicarboxylate metabolism
17	Endosperm	GRMZM2G056569_P01	D7	ko05203_entry_23	26S proteasome regulatory subunit T2; PSMC1, RPT2	ko:K03062	Viral carcinogenesis
18	Endosperm	GRMZM2G328171_P01	D7; D8	ko00520_entry_164	bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]; chiA; E3.2.1.14; chitinase [EC:3.2.1.14]	ko:K01183 ko:K13381	Amino sugar and nucleotide sugar metabolism
				ko00520_entry_206	bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]; chiA; E3.2.1.14; chitinase [EC:3.2.1.14]	ko:K01183 ko:K13381	Amino sugar and nucleotide sugar metabolism
19	Endosperm	GRMZM2G149281_P01	D8	ko00240_entry_115	cmk; CMPK2; UMP-CMP kinase [EC:2.7.4.- 2.7.4.14]; UMP-CMP kinase 2, mitochondrial [EC:2.7.4.14]; panC-cmk; CMPK1, UMPK; pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]; cytidylate kinase [EC:2.7.4.14]	ko:K13800 ko:K13809 ko:K00945 ko:K13799	Pyrimidine metabolism
				ko00240_entry_136	cmk; CMPK2; UMP-CMP kinase [EC:2.7.4.- 2.7.4.14]; UMP-CMP kinase 2, mitochondrial [EC:2.7.4.14]; panC-cmk; CMPK1, UMPK; pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]; cytidylate kinase [EC:2.7.4.14]	ko:K13800 ko:K13809 ko:K00945 ko:K13799	Pyrimidine metabolism
				ko00240_entry_155	cmk; CMPK2; UMP-CMP kinase [EC:2.7.4.- 2.7.4.14]; UMP-CMP kinase 2, mitochondrial [EC:2.7.4.14]; panC-cmk; CMPK1, UMPK; pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]; cytidylate kinase [EC:2.7.4.14]	ko:K13800 ko:K13809 ko:K00945 ko:K13799	Pyrimidine metabolism
20	Endosperm	GRMZM2G018947_P01	D7; D8	ko03013_entry_25	ATP-dependent RNA helicase [EC:3.6.4.13]; EIF4A3, FAL1	ko:K13025	RNA transport
21	Endosperm	GRMZM2G149717_P01	D5; D6; D7; D8	ko03015_entry_4 ko05100_entry_33	ATP-dependent RNA helicase [EC:3.6.4.13]; EIF4A3, FAL1 DNM; dynamin GTPase [EC:3.6.5.5]	ko:K13025 ko:K01528	mRNA surveillance pathway Bacterial invasion of epithelial cells
22	Endosperm	GRMZM2G097226_P01	D5; D6; D7; D8	ko00010_entry_47	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Glycolysis / Gluconeogenesis
				ko00010_entry_48	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Glycolysis / Gluconeogenesis
				ko00020_entry_79	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Citrate cycle (TCA cycle)

				ko00020_entry_81	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Citrate cycle (TCA cycle)
				ko00620_entry_131	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Pyruvate metabolism
				ko00620_entry_58	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHA, pdhA; PDHB, pdhB; aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	ko:K00163 ko:K00161 ko:K00162	Pyruvate metabolism
				ko04066_entry_37	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]; PDHB, pdhB; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]; PDHA, pdhA	ko:K00161 ko:K00162	HIF-1 signaling pathway
23	Endosperm	GRMZM2G038821_P01	D5; D6; D7; D8	ko00010_entry_43	E4.1.1.1, pdc; pyruvate decarboxylase [EC:4.1.1.1]	ko:K01568	Glycolysis / Gluconeogenesis
				ko00010_entry_46	E4.1.1.1, pdc; pyruvate decarboxylase [EC:4.1.1.1]	ko:K01568	Glycolysis / Gluconeogenesis
24	Endosperm	GRMZM2G022269_P01	D5; D6; D7; D8	ko04626_entry_4	elongation factor Tu; tuf, TUFM	ko:K02358	Plant-pathogen interaction
25	Endosperm	GRMZM2G008714_P01	D5	ko00010_entry_52	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Glycolysis / Gluconeogenesis
				ko00230_entry_298	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Purine metabolism
				ko00230_entry_299	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Purine metabolism
				ko00230_entry_310	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Purine metabolism
				ko00230_entry_311	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Purine metabolism
				ko00620_entry_68	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Pyruvate metabolism
				ko04930_entry_1	PKLR; pyruvate kinase [EC:2.7.1.40]; pyruvate kinase isozymes R/L [EC:2.7.1.40]; PK, pyk	ko:K00873 ko:K12406	Type II diabetes mellitus
26	Endosperm	GRMZM2G130062_P01	D5; D6	ko00290_entry_38	2-isopropylmalate synthase [EC:2.3.3.13]; leuA	ko:K01649	Valine, leucine and isoleucine biosynthesis
				ko00620_entry_117	2-isopropylmalate synthase [EC:2.3.3.13]; leuA	ko:K01649	Pyruvate metabolism
27	Endosperm	GRMZM2G001898_P01	D5; D6; D7; D8	ko00280_entry_102	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Valine, leucine and isoleucine degradation
				ko00410_entry_45	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	beta-Alanine metabolism
				ko00562_entry_127	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Inositol phosphate metabolism
				ko00640_entry_106	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Propanoate metabolism
				ko00640_entry_54	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Propanoate metabolism
				ko00640_entry_55	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Propanoate metabolism
				ko00640_entry_86	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]; mmsA, iolA, ALDH6A1	ko:K00140	Propanoate metabolism
28	Endosperm	GRMZM2G328500_P01	D8	ko00040_entry_102	UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	ko:K00012	Pentose and glucuronate interconversions

				ko00053_entry_62	UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	ko:K00012	Ascorbate and aldarate metabolism
				ko00500_entry_117	UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	ko:K00012	Starch and sucrose metabolism
				ko00520_entry_43	UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	ko:K00012	Amino sugar and nucleotide sugar metabolism
29	Endosperm	GRMZM2G167669_P01	D6; D7	ko00500_entry_98	endoglucanase [EC:3.2.1.4]; E3.2.1.4	ko:K01179	Starch and sucrose metabolism
					treY, glgY; treX, glgX; maltooligosyltrehalose trehalohydrolase [EC:3.2.1.141]; treZ, glgZ; (1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase [EC:5.4.99.15]; glycogen operon protein [EC:3.2.1.-]	ko:K02438 ko:K06044 ko:K01236	Starch and sucrose metabolism
30	Endosperm	GRMZM2G158043_P02	D6; D7; D8	ko00500_entry_250			
31	Endosperm	GRMZM2G074158_P01	D5; D6; D7; D8	ko00500_entry_150	K16153; phosphorylase / glycogen(starch) synthase [EC:2.4.1.1 2.4.1.11]; starch phosphorylase [EC:2.4.1.1]; E2.4.1.1, glgP, PYG	ko:K00688 ko:K16153	Starch and sucrose metabolism
				ko04910_entry_27	starch phosphorylase [EC:2.4.1.1]; E2.4.1.1, glgP, PYG	ko:K00688	Insulin signaling pathway
32	Endosperm	GRMZM2G147221_P01	D5	ko00500_entry_158	E3.2.1.58; glucan 1,3-beta-glucosidase [EC:3.2.1.58]	ko:K01210	Starch and sucrose metabolism
33	Endosperm	GRMZM2G458164_P01	D8	ko00500_entry_97	glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39]; E3.2.1.39	ko:K01199	Starch and sucrose metabolism
34	Endosperm	GRMZM2G139300_P01	D6; D7	ko00052_entry_61	beta-fructofuranosidase [EC:3.2.1.26]; E3.2.1.26, sacA	ko:K01193	Galactose metabolism
				ko00052_entry_65	beta-fructofuranosidase [EC:3.2.1.26]; E3.2.1.26, sacA	ko:K01193	Galactose metabolism
				ko00500_entry_90	beta-fructofuranosidase [EC:3.2.1.26]; E3.2.1.26, sacA	ko:K01193	Starch and sucrose metabolism
				ko00500_entry_94	beta-fructofuranosidase [EC:3.2.1.26]; E3.2.1.26, sacA	ko:K01193	Starch and sucrose metabolism
35	Endosperm	GRMZM2G047292_P01	D5; D6; D7; D8	ko00052_entry_62	E2.4.1.67; stachyose synthetase [EC:2.4.1.67]	ko:K06611	Galactose metabolism
36	Endosperm	GRMZM2G063536_P01	D5	Not			
37	Endosperm	GRMZM2G342515_P01	D6	Not			
38	Endosperm	GRMZM2G701082_P04	D6; D7; D8	Not			
39	Endosperm	GRMZM2G022931_P01	D5; D6	Not			
40	Endosperm	GRMZM2G027825_P01	D6	Not			
41	Endosperm	GRMZM2G701221_P01	D5; D6; D7; D8	Not			
42	Endosperm	GRMZM2G115757_P01	D6; D7; D8	Not			
43	Endosperm	GRMZM2G078876_P01	D8	Not			
44	Endosperm	GRMZM2G073465_P03	D6; D7; D8	Not			
45	Endosperm	GRMZM2G059299_P01	D5	Not			
46	Endosperm	GRMZM2G134176_P01	D5	Not			
47	Endosperm	GRMZM2G075290_P01	D6; D7	Not			
48	Endosperm	GRMZM2G052266_P01	D7; D8	Not			
49	Endosperm	GRMZM2G148387_P01	D5	Not			
50	Endosperm	GRMZM2G019500_P01	D5; D6; D7; D8	Not			
51	Endosperm	GRMZM2G039757_P01	D5; D6; D7; D8	Not			
52	Endosperm	GRMZM2G460860_P01	D8	Not			
53	Endosperm	GRMZM2G042008_P01	D5	Not			
54	Endosperm	GRMZM2G038126_P01	D5; D6; D7; D8	Not			
55	Endosperm	GRMZM2G139617_P01	D7	Not			
56	Endosperm	GRMZM5G881950_P01	D5; D6; D7; D8	Not			
57	Endosperm	GRMZM2G168119_P01	D8	Not			
58	Endosperm	GRMZM2G358153_P01	D6; D7; D8	Not			
59	Endosperm	GRMZM5G898755_P01	D5; D6; D7; D8	Not			
60	Endosperm	GRMZM2G351125_P01	D6; D7; D8	Not			
61	Endosperm	GRMZM2G373928_P01	D5; D6; D7	Not			
62	Endosperm	GRMZM2G025977_P01	D5; D6; D8	Not			
63	Endosperm	GRMZM2G164020_P01	D8	Not			
64	Endosperm	GRMZM2G021219_P01	D5; D8	Not			
65	Endosperm	GRMZM2G051879_P01	D6; D7	Not			
66	Endosperm	AC211737.3_FGP012	D5; D6; D7	Not			
67	Endosperm	GRMZM2G084406_P02	D5; D6; D7; D8	Not			
68	Endosperm	GRMZM2G030902_P01	D8	Not			
69	Endosperm	GRMZM2G098167_P01	D5; D6; D7; D8	Not			
70	Endosperm	GRMZM2G119361_P01	D5; D6; D7; D8	Not			
71	Endosperm	GRMZM2G009448_P01	D5	Not			
72	Endosperm	GRMZM2G084149_P01	D5; D6; D7; D8	Not			

73	Endosperm	GRMZM2G039263_P01	D5; D6; D8	Not
74	Endosperm	GRMZM5G882228_P02	D6; D7; D8	Not
75	Endosperm	AC204893.3_FGP001	D6; D7; D8	Not
76	Endosperm	GRMZM2G005036_P01	D5	Not
77	Endosperm	GRMZM2G009593_P01	D6; D7; D8	Not
78	Endosperm	GRMZM2G140179_P01	D8	Not
79	Endosperm	GRMZM2G048277_P01	D6; D7; D8	Not

Table S5. Top 10 pathways involving the most proteins.

Pathway ID	Description	Proteins
path:ko00071	Fatty acid degradation	20
path:ko00500	Starch and sucrose metabolism	15
path:ko00230	Purine metabolism	10
path:ko00010	Glycolysis / Gluconeogenesis	9
path:ko00061	Fatty acid biosynthesis	8
path:ko00240	Pyrimidine metabolism	8
path:ko00460	Cyanoamino acid metabolism	7
path:ko00620	Pyruvate metabolism	6
path:ko00020	Citrate cycle (TCA cycle)	4
path:ko00052	Galactose metabolism	4

Table S6. Primers were used in this study

Primer Name	Primers
qADF-F	CCCCGAGAATGACTGCCGATAC
qADF-R	TTCACCTTGGCGGAGGATGG
qEXP-F	GCCGGCCGTCGACACATGTT
qEXP-R	TGGGCTCCGGTAGTGTCGCCT
qGEBGP-F	AGCGGAACTTCGGCATCTT
qGEBGP-R	CACGCACCACTTGCCTCC
qGRF-F	TGCTGTCTTGATTTCGGGTCG
qGRF-R	AGCGTCGCACCCAAGAAAC