

Table S2: Single Nucleotide Polymorphisms (SNPs) in three 3 common introgressed regions (CIRs)

Chromosome	pos	ref	DRD	DRD_depth	DRD45NC	DRDSBA	DRD45NC_depth	45NC
Cla97Chr10	29385009	A	A	22 22	A	A	22 22	T
Cla97Chr10	29419696	A	A	17 18	A	A	18 18	T
Cla97Chr10	29425958	T	T	15 15	T	T	29 29	C
Cla97Chr10	29427454	A	A	19 19	A	A	19 19	G
Cla97Chr10	29428130	A	A	26 26	A	A	23 23	G
Cla97Chr10	29428358	G	G	16 16	G	G	29 29	A
Cla97Chr10	29431146	G	G	14 14	G	G	19 19	A
Cla97Chr10	29440068	G	G	17 17	G	G	25 25	T
Cla97Chr10	29442713	A	A	24 24	A	A	19 19	G
Cla97Chr10	29442794	G	G	33 33	G	G	21 21	A
Cla97Chr10	29443115	G	G	23 23	G	G	17 17	C
Cla97Chr10	29443243	A	A	14 14	A	A	17 17	G
Cla97Chr10	29444589	T	T	12 12	T	T	25 25	C
Cla97Chr10	29445010	A	A	26 26	A	A	15 16	T
Cla97Chr10	29447001	T	T	12 12	T	T	31 31	C
Cla97Chr10	29447460	C	C	14 14	C	C	28 29	T
Cla97Chr10	29452466	A	A	17 17	A	A	21 21	T
Cla97Chr10	29453166	C	C	20 20	C	C	27 27	T
Cla97Chr10	29453946	G	G	17 17	G	G	27 27	A
Cla97Chr10	29454665	T	T	19 19	T	T	22 22	A
Cla97Chr10	29455194	C	C	18 18	C	C	33 33	A
Cla97Chr10	29455285	C	C	19 19	C	C	26 26	A
Cla97Chr10	29456074	G	G	18 18	G	G	26 26	A
Cla97Chr10	29456093	A	A	19 19	A	A	23 23	G
Cla97Chr10	29456508	A	A	16 16	A	A	28 28	G
Cla97Chr10	29457583	G	G	18 18	G	G	15 15	T
Cla97Chr10	29457926	C	C	15 15	C	C	27 27	T
Cla97Chr10	29457999	T	T	13 13	T	T	28 28	A
Cla97Chr10	29458292	G	G	17 17	G	G	32 32	A
Cla97Chr10	29459085	T	T	22 22	T	T	27 27	C
Cla97Chr10	29459565	G	G	19 19	G	G	34 34	A
Cla97Chr10	29459744	T	T	16 16	T	T	25 25	C
Cla97Chr10	29460107	G	G	13 13	G	G	17 17	T
Cla97Chr10	29460801	A	A	7 7	A	A	16 16	G
Cla97Chr10	29460810	A	A	7 7	A	A	17 17	G
Cla97Chr10	29460826	A	A	8 8	A	A	14 14	G
Cla97Chr10	29461089	C	C	7 7	C	C	21 21	A
Cla97Chr10	29461181	C	C	17 17	C	C	25 25	T
Cla97Chr10	29461369	T	T	20 20	T	T	26 26	C
Cla97Chr10	29461632	T	T	20 20	T	T	28 31	C
Cla97Chr10	29461878	C	C	21 21	C	C	29 29	A
Cla97Chr10	29461945	C	C	21 21	C	C	25 25	T
Cla97Chr10	29462031	C	C	14 14	C	C	32 32	T
Cla97Chr10	29462275	T	T	13 13	T	T	24 24	A
Cla97Chr10	29462519	C	C	19 19	C	C	29 29	T
Cla97Chr10	29462748	C	C	20 20	C	C	31 31	T
Cla97Chr10	29463298	C	C	18 18	C	C	32 32	T

Cla97Chr10	29463963	A	A	27 27	A	A	32 32	G
Cla97Chr10	29464899	C	C	18 18	C	C	22 22	A
Cla97Chr10	29465058	C	C	28 28	C	C	32 32	T
Cla97Chr10	29466918	G	G	23 23	G	G	22 22	A
Cla97Chr10	29466965	T	T	22 22	T	T	27 27	A
Cla97Chr10	29467685	A	A	21 21	A	A	34 34	G
Cla97Chr10	29468398	T	T	15 15	T	T	23 23	A
Cla97Chr10	29468454	C	C	24 24	C	C	23 23	T
Cla97Chr10	29468469	T	T	25 25	T	T	24 24	C
Cla97Chr10	29470884	C	C	22 22	C	C	18 18	A
Cla97Chr10	29470890	T	T	21 21	T	T	18 18	C
Cla97Chr10	29473197	C	C	19 19	C	C	23 23	T
Cla97Chr10	29476334	T	T	18 18	T	T	23 23	C
Cla97Chr10	29476855	G	G	21 21	G	G	37 37	A
Cla97Chr10	29479816	A	A	18 18	A	A	30 30	G
Cla97Chr10	29481002	A	A	27 27	A	A	33 33	T
Cla97Chr10	29481030	C	C	24 24	C	C	26 26	T
Cla97Chr10	29530475	T	T	18 18	T	T	36 36	C
Cla97Chr10	29533171	G	G	16 16	G	G	11 11	A
Cla97Chr10	29537693	G	G	21 21	G	G	18 18	A
Cla97Chr10	29538043	G	G	33 33	G	G	26 26	C
Cla97Chr10	29548144	A	A	18 18	A	A	27 27	T
Cla97Chr10	29556663	G	G	27 27	G	G	44 44	A
Cla97Chr10	29557773	A	A	13 13	A	A	21 21	T
Cla97Chr10	29569235	A	A	24 24	A	A	24 24	G
Cla97Chr10	29570254	C	C	21 21	C	C	17 17	T
Cla97Chr10	29570514	G	G	31 31	G	G	21 21	A
Cla97Chr10	29580134	A	A	14 15	A	A	21 21	T
Cla97Chr10	29580772	A	A	15 15	A	A	20 20	T
Cla97Chr10	29582180	T	T	14 14	T	T	23 23	C
Cla97Chr10	29586177	C	C	17 17	C	C	25 25	T
Cla97Chr10	29586628	T	T	22 22	T	T	23 23	C
Cla97Chr10	29587047	T	T	22 22	T	T	12 12	C
Cla97Chr10	29592118	T	T	16 16	T	T	28 28	A
Cla97Chr10	29592764	A	A	27 27	A	A	25 25	T
Cla97Chr10	29596687	T	T	10 10	T	T	14 14	C
Cla97Chr10	29602266	C	C	24 24	C	C	26 26	A
Cla97Chr10	29612076	C	C	29 29	C	C	31 31	A
Cla97Chr10	29612999	G	G	19 19	G	G	19 19	T
Cla97Chr10	29616384	A	A	31 31	A	A	29 29	T
Cla97Chr10	29634487	A	A	22 22	A	A	19 19	G
Cla97Chr10	29634777	G	G	22 22	G	G	20 20	A
Cla97Chr10	29642692	A	A	21 21	A	A	27 27	G
Cla97Chr10	29663135	G	G	9 9	G	G	27 27	A
Cla97Chr10	29663323	C	C	18 18	C	C	24 24	A
Cla97Chr10	29667313	T	T	12 12	T	T	27 27	C
Cla97Chr10	29667399	G	G	13 13	G	G	25 25	A
Cla97Chr10	29667829	T	T	14 14	T	T	15 15	C
Cla97Chr10	29667931	A	A	18 18	A	A	15 15	G
Cla97Chr10	29668814	A	A	22 22	A	A	36 36	C

Cla97Chr10	29668826	A	A	22 22	A	A	30 30	G
Cla97Chr10	29668996	A	A	18 18	A	A	31 31	G
Cla97Chr10	29670535	T	T	31 31	T	T	38 38	G
Cla97Chr10	29670723	C	C	22 22	C	C	17 17	T
Cla97Chr10	29670872	T	T	22 22	T	T	33 33	A
Cla97Chr10	29670962	A	A	28 28	A	A	41 41	T
Cla97Chr10	29671708	T	T	20 20	T	T	20 20	A
Cla97Chr10	29675580	G	G	5 5	G	G	8 8	A
Cla97Chr10	29676339	T	T	21 21	T	T	24 24	C
Cla97Chr10	29677836	A	A	9 9	A	A	8 8	T
Cla97Chr10	29678169	C	C	25 25	C	C	15 16	T
Cla97Chr10	29682757	C	C	13 13	C	C	18 18	T
Cla97Chr10	29686212	T	T	19 19	T	T	22 22	C
Cla97Chr10	29689363	G	G	20 20	G	G	32 32	A
Cla97Chr10	29691236	A	A	25 25	A	A	13 13	T
Cla97Chr10	29693902	C	C	32 32	C	C	33 33	T
Cla97Chr10	29696337	T	T	21 21	T	T	37 37	G
Cla97Chr10	29696965	A	A	26 26	A	A	25 25	C
Cla97Chr10	29701102	T	T	28 28	T	T	34 34	C
Cla97Chr10	29701427	G	G	35 35	G	G	25 25	T
Cla97Chr10	29702684	C	C	23 23	C	C	25 25	T
Cla97Chr10	29705538	C	C	33 33	C	C	25 25	T
Cla97Chr10	29706274	C	C	22 22	C	C	29 29	A
Cla97Chr10	29710794	T	T	21 21	T	T	24 24	C
Cla97Chr10	29712390	G	G	10 10	G	G	22 22	C
Cla97Chr10	29712772	T	T	11 11	T	T	19 19	C
Cla97Chr10	29713911	G	G	25 25	G	G	27 27	A
Cla97Chr10	29714236	G	G	23 23	G	G	25 25	C
Cla97Chr10	29715035	G	G	25 25	G	G	24 24	A
Cla97Chr10	29715935	G	G	18 18	G	G	19 19	A
Cla97Chr10	29720960	A	A	30 30	A	A	32 32	G
Cla97Chr10	29721039	T	T	24 24	T	T	25 25	C
Cla97Chr10	29724360	G	G	18 18	G	G	26 26	A
Cla97Chr10	29725056	T	T	20 20	T	T	28 28	C
Cla97Chr10	29725293	C	C	24 24	C	C	25 25	A
Cla97Chr10	29759694	C	C	18 18	C	C	21 21	T
Cla97Chr10	29762765	G	G	23 23	G	G	21 21	A
Cla97Chr10	29782306	A	A	20 20	A	A	28 28	G
Cla97Chr10	29790057	T	T	18 18	T	T	25 25	C
Cla97Chr10	29792075	A	A	27 27	A	A	28 28	G
Cla97Chr10	29819233	G	G	11 12	G	G	16 19	A

45NC_depth	DRDSBA	DRDSBA_depth	SBA	SBA_depth	Genic/Interg. Transcript.	Feature	Description
16 16	A	11 11	T	9 9	Intergenic		
12 12	A	14 14	T	8 8	Intergenic		
25 25	T	33 33	C	30 30	Cla97C10G199460	promoter	
15 15	A	10 10	G	7 7	Intergenic		
14 14	A	29 29	G	19 19	Intergenic		
34 34	G	33 33	A	27 27	Intergenic		
15 15	G	17 17	A	18 18	Cla97C10G19	Cla97C10G19 Intron	ARM repeat s
24 24	G	29 29	T	26 26	Cla97C10G19	Cla97C10G19 CDS,exon	ARM repeat s
24 24	A	26 26	G	16 16	Intergenic		
22 22	G	28 28	A	22 22	Intergenic		
18 18	G	21 21	C	15 15	Intergenic		
24 24	A	21 21	G	8 8	Intergenic		
22 22	T	30 30	C	24 24	Intergenic		
17 19	A	28 28	T	20 20	Intergenic		
24 24	T	35 35	C	41 41	Cla97C10G19	Cla97C10G19 CDS,exon	Protein of un
26 26	C	28 28	T	38 38	Cla97C10G19	Cla97C10G19 Intron	Protein of un
29 29	A	17 17	T	15 15	Intergenic		
31 31	C	24 24	T	25 25	Intergenic		
22 22	G	40 40	A	22 22	Intergenic		
25 25	T	28 28	A	30 31	Intergenic		
24 24	C	28 28	A	21 21	Intergenic		
33 33	C	26 26	A	31 31	Intergenic		
30 30	G	33 33	A	24 24	Cla97C10G19	Cla97C10G19 Intron	40S ribosoma
27 28	A	35 35	G	26 26	Cla97C10G19	Cla97C10G19 Intron	40S ribosoma
22 22	A	34 34	G	22 23	Cla97C10G19	Cla97C10G19 Intron	40S ribosoma
22 22	G	18 18	T	22 22	Cla97C10G199490	promoter	
12 12	C	12 12	T	7 7	Cla97C10G199490	promoter	
14 14	T	13 13	A	8 8	Cla97C10G199490	promoter	
26 26	G	25 25	A	17 17	Cla97C10G199490	promoter	
17 17	T	29 29	C	29 29	Intergenic		
29 29	G	26 26	A	25 25	Intergenic		
25 25	T	20 20	C	15 15	Intergenic		
19 19	G	24 24	T	10 10	Intergenic		
8 8	A	11 11	G	4 4	Intergenic		
7 7	A	10 10	N	0 2	Intergenic		
6 6	A	7 7	N	0 2	Intergenic		
7 7	C	14 14	A	8 8	Intergenic		
14 14	C	26 26	T	21 21	Intergenic		
10 10	T	38 38	C	15 15	Intergenic		
9 9	T	37 37	C	13 13	Intergenic		
15 15	C	31 31	A	15 15	Intergenic		
9 9	C	33 33	Y	1,8 9	Intergenic		
16 16	C	25 25	T	14 14	Intergenic		
17 17	T	43 43	A	8 8	Intergenic		
21 21	C	34 34	T	18 18	Intergenic		
25 25	C	25 25	T	33 33	Intergenic		
21 22	C	40 40	T	33 33	Intergenic		

17 17	A	47 47	G	24 25	Intergenic	
20 20	C	46 46	A	24 24	Intergenic	
22 23	C	26 27	T	30 30	Intergenic	
17 17	G	17 17	A	17 17	Intergenic	
21 21	T	28 28	A	18 20	Intergenic	
29 29	A	21 21	G	33 33	Intergenic	
19 19	T	30 30	A	28 28	Intergenic	
20 20	C	28 28	T	31 31	Intergenic	
22 22	T	28 28	C	31 31	Intergenic	
15 15	C	21 21	A	20 20	Cla97C10G199500	promoter
19 19	T	25 25	C	19 19	Cla97C10G199500	promoter
18 18	C	29 29	T	28 28	Cla97C10G19 Cla97C10G19	Intron kinesin-4-like
28 28	T	45 45	C	38 38	Cla97C10G19 Cla97C10G19	Intron kinesin-4-like
23 23	G	29 29	A	33 33	Cla97C10G19 Cla97C10G19	CDS,exon kinesin-4-like
23 23	A	20 20	G	33 33	Intergenic	
24 24	A	41 41	T	25 25	Intergenic	
21 21	C	35 35	T	25 25	Intergenic	
22 22	T	14 14	C	16 16	Intergenic	
26 26	G	14 14	A	13 13	Cla97C10G199550	promoter
30 30	G	25 25	A	16 16	Intergenic	
33 33	G	26 26	C	29 29	Intergenic	
20 20	A	36 36	T	30 30	Cla97C10G19 Cla97C10G19	CDS,exon Arf GTPase ac
32 32	G	25 25	A	22 22	Cla97C10G19 Cla97C10G19	Intron Carboxypepti
21 21	A	20 20	T	16 16	Cla97C10G19 Cla97C10G19	Intron Carboxypepti
31 31	A	38 38	G	17 17	Cla97C10G19 Cla97C10G19	Intron regulation of
18 18	C	30 30	T	24 25	Cla97C10G19 Cla97C10G19	Intron regulation of
18 18	G	34 34	A	29 29	Cla97C10G19 Cla97C10G19	Intron regulation of
27 28	A	23 24	T	16 16	Cla97C10G19 Cla97C10G19	Intron regulation of
19 19	A	25 26	T	26 26	Cla97C10G19 Cla97C10G19	Intron regulation of
27 27	T	29 29	C	29 29	Cla97C10G19 Cla97C10G19	Intron regulation of
34 34	C	39 39	T	26 26	Cla97C10G19 Cla97C10G19	Intron regulation of
12 12	T	28 28	C	12 12	Cla97C10G19 Cla97C10G19	Intron regulation of
25 25	T	20 20	C	26 26	Cla97C10G19 Cla97C10G19	Intron regulation of
25 25	T	37 37	A	32 32	Cla97C10G19 Cla97C10G19	Intron regulation of
18 18	A	47 47	T	34 34	Cla97C10G19 Cla97C10G19	Intron regulation of
14 14	T	32 32	C	14 14	Intergenic	
24 24	C	43 43	A	24 24	Cla97C10G19 Cla97C10G19	CDS,exon membrane st
31 31	C	38 38	A	39 39	Cla97C10G199630	promoter
19 19	G	37 37	T	28 28	Cla97C10G19 Cla97C10G19	Intron protein PLAN
15 15	A	20 20	T	12 12	Intergenic	
35 35	A	19 19	G	23 23	Intergenic	
26 26	G	21 21	A	20 20	Intergenic	
22 22	A	40 40	G	37 37	Intergenic	
21 21	G	20 20	A	20 20	Intergenic	
33 33	C	27 27	A	26 27	Intergenic	
19 19	T	11 11	C	7 7	Intergenic	
19 19	G	20 20	A	7 7	Intergenic	
22 22	T	19 19	C	18 18	Intergenic	
22 22	A	28 28	G	38 38	Intergenic	
16 16	A	20 20	C	20 20	Intergenic	

14 14	A	19 19	G	18 18	Intergenic	
29 29	A	19 19	G	25 25	Intergenic	
38 38	T	36 36	G	35 35	Intergenic	
20 20	C	32 32	T	19 19	Intergenic	
28 28	T	35 36	A	34 34	Intergenic	
27 27	A	29 29	T	21 21	Intergenic	
17 17	T	22 22	A	20 20	Intergenic	
7 7	G	12 12	A	7 7	Cla97C10G19 Cla97C10G19 Intron	14 kDa zinc-b
16 16	T	42 42	C	21 21	Cla97C10G199740	promoter
11 11	A	7 7	T	4 4	Intergenic	
25 25	C	38 38	T	26 26	Intergenic	
3 3	C	9 9	T	3 3	Cla97C10G19 Cla97C10G19 Intron	MYB transcrip
18 18	T	20 20	C	16 16	Intergenic	
36 36	G	39 39	A	29 29	Intergenic	
15 15	A	19 19	T	16 16	Cla97C10G199760	promoter
27 27	C	43 43	T	28 28	Cla97C10G19 Cla97C10G19 Intron	Ribosome prc
27 27	T	35 35	G	26 26	Intergenic	
30 30	A	21 21	C	7 7	Cla97C10G199770	promoter
22 23	T	41 41	C	33 33	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
23 23	G	45 45	T	29 29	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
16 16	C	33 33	T	23 23	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
29 29	C	33 33	T	30 30	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
21 21	C	39 39	A	27 27	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
20 20	T	42 42	C	24 24	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
21 21	G	33 33	C	27 27	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
11 11	T	17 17	C	25 25	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
21 21	G	23 23	A	25 25	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
31 31	G	36 36	C	32 32	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
35 35	G	29 29	A	38 38	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
27 27	G	35 35	A	29 29	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
35 35	A	21 21	G	39 40	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
22 22	T	38 38	C	28 28	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
20 20	G	30 31	A	32 32	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
25 25	T	23 23	C	22 22	Cla97C10G19 Cla97C10G19 Intron	Unknown pro
25 25	C	34 34	A	26 26	Cla97C10G19 Cla97C10G19 Intron,promc	Unknown pro
15 15	C	12 12	T	9 9	Cla97C10G19 Cla97C10G19 Intron	Pleiotropic dr
18 18	G	25 25	A	16 16	Cla97C10G19 Cla97C10G19 Intron	Pleiotropic dr
30 30	A	22 22	G	22 22	Cla97C10G19 Cla97C10G19 Intron	Pleiotropic dr
24 24	T	34 34	C	16 16	Cla97C10G199810	promoter
35 35	A	25 25	G	21 21	Intergenic	
21 21	G	13 13	A	10 10	Intergenic	

Interpro	GO	GO.desc	EC.number	Flanking_seq.(600bp)	Allele
IPR016024 (Armadillo-type uncharacteriz NA IPR016024 (Armadillo-type uncharacteriz NA				AAAAATGAAAAATTTTCGGAAT	A/T
				AATATAAAGGGTCAAATTGGA	A/T
				TGGGTATGGTTTTGATTGGAC	T/C
				AATTGAGGGTTATAAGAATAT	A/G
				TTAATTTATATAAATTGAAGA	A/G
				TTTATATAATGCATCACACAT	A/G
				TTTGGGATTGACAATCTTACT	A/G
				TAGCCAGGTTTCTATAATGCT	G/T
				CAAGTTTGAAATTTATGTGAC	A/G
				GATTCAAATTGATAAGTTTGA	A/G
IPR005049 (Protein of unkn probable glyc NA IPR005049 (Protein of unkn probable glyc NA				TTAAGAATTATTTGAAAAAT	C/G
				TACTATTGAAATGGGGAGAG	A/G
				CATTCTCATCTTTCATTTGGT	T/C
				TAAATAGCTCATTGTAGCTAC	A/T
				TATCAAACCTCTCTTTCCTTT	T/C
				CAATCTGAGCTTCAACGGAG	C/T
				ACACAAATACAAAATTTAGTT	A/T
				AATAATTATACTACTTTAAATT	C/T
				CTAAGCACAACTACAAAGGC	G/A
				AAGGAAATGTTTAGTCGGAT	A/T
IPR000851 (R GO:0003723, 40s ribosoma NA IPR000851 (R GO:0003723, 40s ribosoma NA IPR000851 (R GO:0003723, 40s ribosoma NA				AAGCACAGCTAAATTGACATA	C/A
				TACATATAGATCATTAAAGCA	A/C
				GTGGGTTTGGCCAATAAATCC	G/A
				CCGTGTGCTCTTGAATGGAG	A/G
				TAAATTTCTTATGATTAAGATT	A/G
				CTGGCATAATCTTCATAACCT	C/G
				GACGGAGAGAGGAATTTATA	A/C
				AGTGGCCCGGAGTTCCTATA	A/T
				TAATAACTTACATTAACACTA	A/G
				TTTAAAAAGTGTAATTGTTG	T/C
				CAAAATAAACCAATACGAGCA	G/A
				GGGTAGTCACTAGAAACCTTG	T/C
				GAGAATATGAAGTGTAAAAA	G/T
				TTGGGTAAATCGGTCAAAGTG	A/G
				TCGGTCAAAGTGTGGAGTCT	A/G
				AGTCTAAAGTTGGAATTCCAT	A/G
				GAGCAAATGACAGAAAAAC	C/A
				AACTAAATTAATAAACTTAA	A/C
				ATGTCTCGTTAAACCTTACCA	A/T
				GATCATGAGTGTAGAAAAGTT	T/C
				GCCAATATATAGCAGTTCCTC	C/A
				AGATAAATATCCAGAATCTGC	T/C
				AATAATGGAGTATATGCTTAA	C/T
				CCATATAAAATCTTTTAAAT	T/A
				TTGAATTATTTGATATCCTTC	C/T
				TCCAAATTTTCATACACAGTCA	C/T
				TTTTTCGAGGATTTTATCTTT	C/T

	ACGTTTAATAAATGATTCTGCTA/G
	TGCTAGACATAGATCTTCATT C/A
	TCTCAAATAAAAAAAAAACAT C/T
	TTAATGAATATTTTATTCTTTC G/A
	TTAAGTTTGATCAAAATAAGT T/A
	GTCCGAATGGAAAATAAAAA/ A/G
	TTCAACAATAAATTATCCTCAT T/A
	TTTTTTCTTTCCAGCAATTGG C/T
	CAATTGGAATTGAAATATCAA T/C
	TTCTCTCTCTTTGATGTCATT C/A
	CTCTTTTGATGTCATTCTCCTT T/C
IPR001715 (C GO:0000166, kinesin-like p NA	AAAGCAAGGTCGTTATGCTGA C/T
IPR001715 (C GO:0000166, kinesin-like p NA	TGGTCCGAATGGTGCTACTAA T/C
IPR001715 (C GO:0000166, kinesin-like p NA	ACTCTCAAATGTTTATCTCAGT G/A
	TGGGATCCAAGGCTCTAATAT A/G
	AGGAAACATGGAAGTAGCAT A/T
	ACCAAGTCTAGCACAATGAGC C/T
	AACATTGACATGACATCACCG T/C
	TTGTATGATTAAGTGTGATG G/A
	GGAGATCATAGGATACTTCCA G/A
	ATAATTGAGTAGAGTGAGTTT G/C
IPR001164 (A GO:0005096, probable adp NA	ACCTAGTACATCAGGAGTTTT A/T
IPR001563 (P GO:0004180, serine carbox EC:3.4.16.0	AAAATGATGACATAGAATATT G/A
IPR001563 (P GO:0004180, serine carbox EC:3.4.16.0	TAGAATTTTTTAGCTATATTTA A/T
IPR006569 (CID domain), If NA NA	ATTTCAGTATGCTTATAAAAC A/G
IPR006569 (CID domain), If NA NA	CTCAAGCATCACAGCCATTGA C/T
IPR006569 (CID domain), If NA NA	TTGTTTAGAACTAATAAAGC G/A
IPR006569 (CID domain), If NA NA	CTAGAAGGGTATGGACATAAC A/T
IPR006569 (CID domain), If NA NA	TCCAAACCAAAAAGATGCAAC A/T
IPR006569 (CID domain), If NA NA	AACTTGTAACAGAACGCAT T/C
IPR006569 (CID domain), If NA NA	CGAGCCAATTCAAACACTTA C/T
IPR006569 (CID domain), If NA NA	CCGCGGATATTTCTTTTCTG T/C
IPR006569 (CID domain), If NA NA	TCCCAAACAAAATTAACAAAC T/C
IPR006569 (CID domain), If NA NA	GAAGGGATGATGATAGAAGT T/A
IPR006569 (CID domain), If NA NA	TGGTGTAAATTGTCACCTCCTT A/T
	CATAATTCATATTAAGTTGAA1T/C
IPR001199 (C GO:0016020, membrane st NA	AATATGTAGACCTTATTATTA C/A
	ATTCAGAAGCGGAGATCATTT C/A
IPR006461 (Uncharacterise protein plant NA	AAATGGGTAGCTCATTGCAAC G/T
	ATTTTTTAAAATAAATTTTAAA A/T
	CTGGCCAGCTTGATTTTTTTAT A/G
	GTTTTTAAGAAATCAAATAG G/A
	ATAAAGGTGGGATGACGAAA A/G
	TTTTAAGTAACAAACCATCA G/A
	AGTATTGTTTGAAATTATTGT C/A
	AAACATCAATTTATGATTAAT T/C
	TTGACTTTTTTTTTCTTTTTTG G/A
	AAGAATCACTAAATTTGAAAT T/C
	CATTTTTTATGACATTAGTATT A/G
	CATCTCTATTCTATTTTATAAT A/C

			ATTTTATAATAAAAGGAACAT A/G
			TACATTCTTCATTACATTCTGT A/G
			GATATGTGTAATTTGATATGT T/G
			TAGGAACTCAAACATGATAAG C/T
			TAATAGAACCAAGAACTATTC T/A
			TTGGTTCTATAAGCAACCAAA A/T
			GGAAAATAATCGTCATTTGGA T/A
IPR001310 (F GO:0003824 14 kda zinc-b EC:3.6.2.1			TGTTTTTTATGAAGTCTTTGTG G/A
			GCTTAAACTGAGAGCCGAGT T/C
			TATAAAATGCAAGAGTTATAT A/T
			TATCAGTCTTTCTCCAATGTAA C/T
IPR009057 (F GO:0003677, myb family tr NA			GTAATTAATTATCTGTCTCTAA C/T
			TTATAGGGTAAGACTCTACTT T/C
			TTTACCTTGTTACCAAACGTAT G/A
			GTAATAATTGTCGAAAGCTT A/T
IPR004154 (Anticodon-bin ribosome prc NA			CATCATCGGTGAGATACTATA C/T
			GTTGCTATCGTCACAATTTCA T/G
			TCGTGACACAAGTGTTATCCA A/C
rotein	NA	NA	AGTTATTTTCAATGGACATGG T/C
rotein	NA	NA	CATTTGAGGACCTAATCGAAA G/T
rotein	NA	NA	ATGTACGGAGGAAGGAAGAT C/T
rotein	NA	NA	TACAAGGCGGAAGGGCAAGA C/T
rotein	NA	NA	GGACTACTGCATAGGATACAC C/A
rotein	NA	NA	TGGATATAAGATTTTAGTCAA T/C
rotein	NA	NA	GCTGTATAAAGACAGCCAAC G/C
rotein	NA	NA	CTTTTGTTAAGTCGAGTCGC T/C
rotein	NA	NA	AGGTTTATTGCTACGTATGTA G/A
rotein	NA	NA	CATATTTATATTTTACCCGAAA G/C
rotein	NA	NA	CTATCTTTAACATGGAGGTTT G/A
rotein	NA	NA	GAAGTCATTTCCATTGACAT G/A
rotein	NA	NA	AGTAAGATAGGTTACAAGAA A/G
rotein	NA	NA	TTTGGATAAAGGATTAGCAAA T/C
rotein	NA	NA	GAAGCTCCTTATTGTTGTATA G/A
rotein	NA	NA	CCATCAGTTTGACCCATTGAC T/C
rotein	NA	NA	AACTACTGTGGGGGTGGGGT C/A
IPR003439 (A GO:0000166, pleiotropic dr EC:3.6.1.3			TTATATTATTATACATATTTTA C/T
IPR003439 (A GO:0000166, pleiotropic dr EC:3.6.1.3			AACTGTCCAATCCATTTGTTAT G/A
IPR003439 (A GO:0000166, pleiotropic dr EC:3.6.1.3			CTAATTTATTTATAAATATAGC A/G
			ATATTGTAGATTTGTGGAAAT T/C
			CTACTATTTATGGGTGTTTTAC A/G
			GACCAAGGTCGTTTAGTCAAT G/A