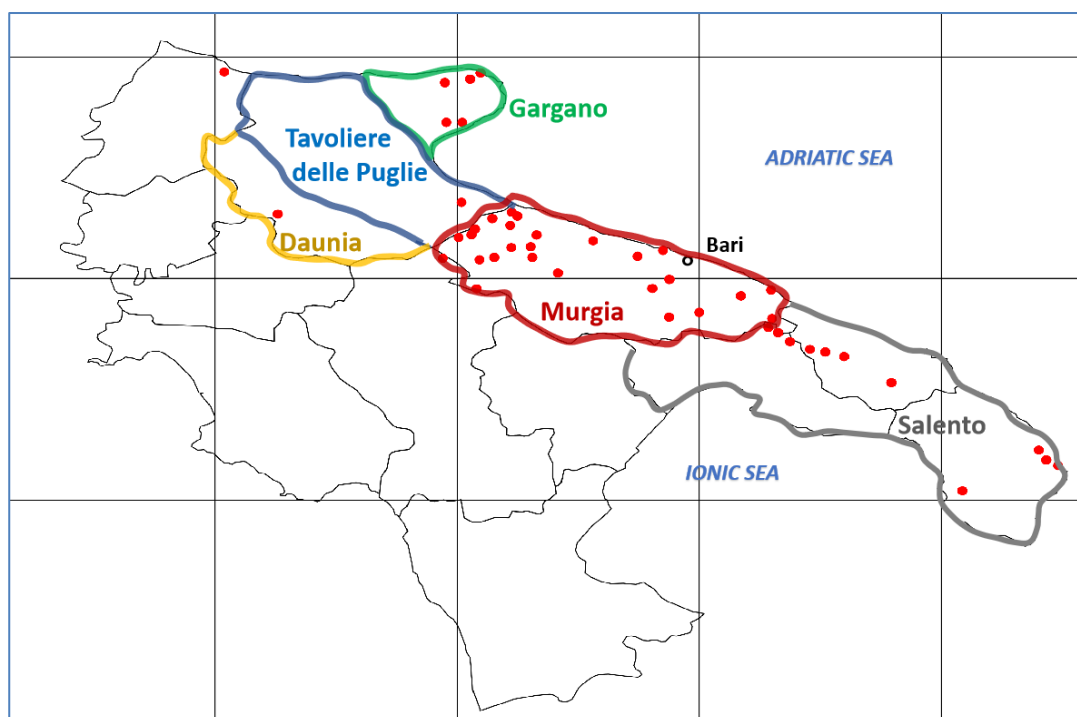
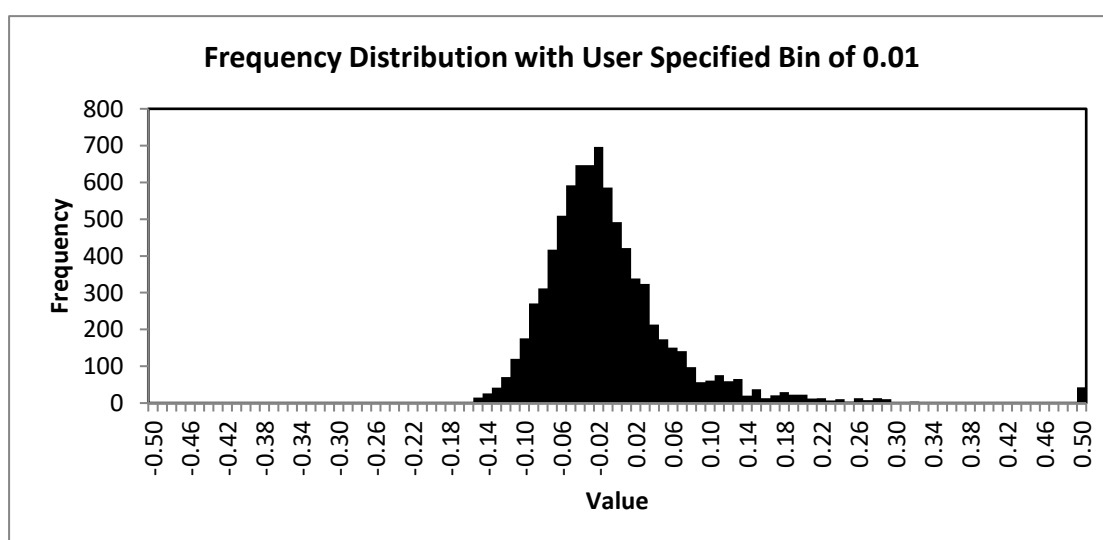
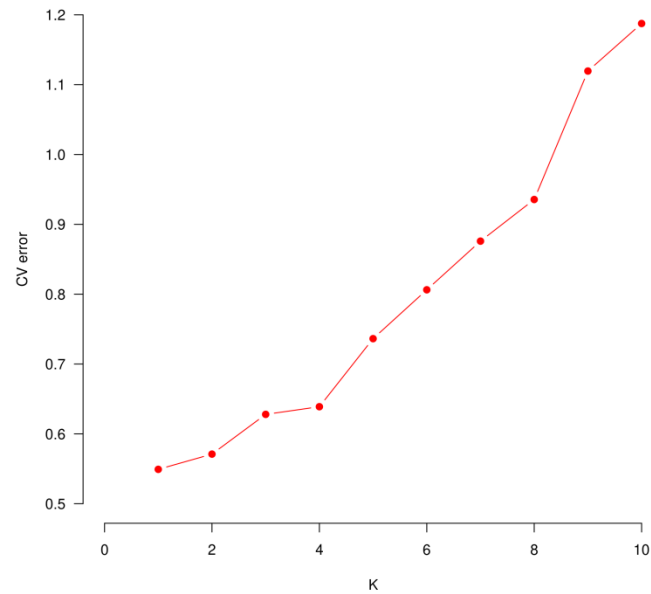




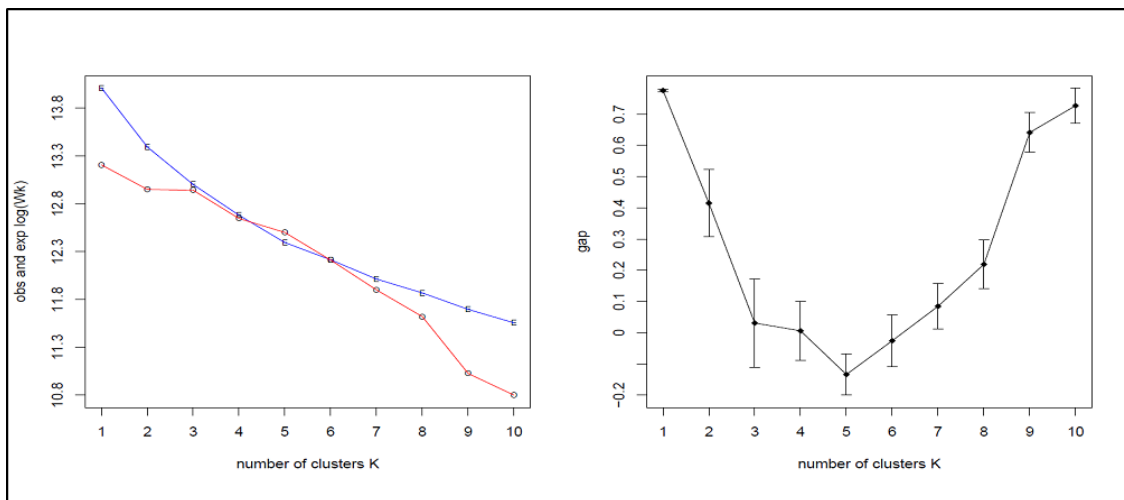
Supplementary Figure S1. Graphical representation of the five physiographic areas of Apulia region. Yellow = Daunia mountainous region; light blue = Tavoliere delle Puglie plain; green = Gargano cape (North); red = Murgia plateau (Central South); grey = Salento peninsula (South). Red dots represent the geographical coordinates of sampling sites.



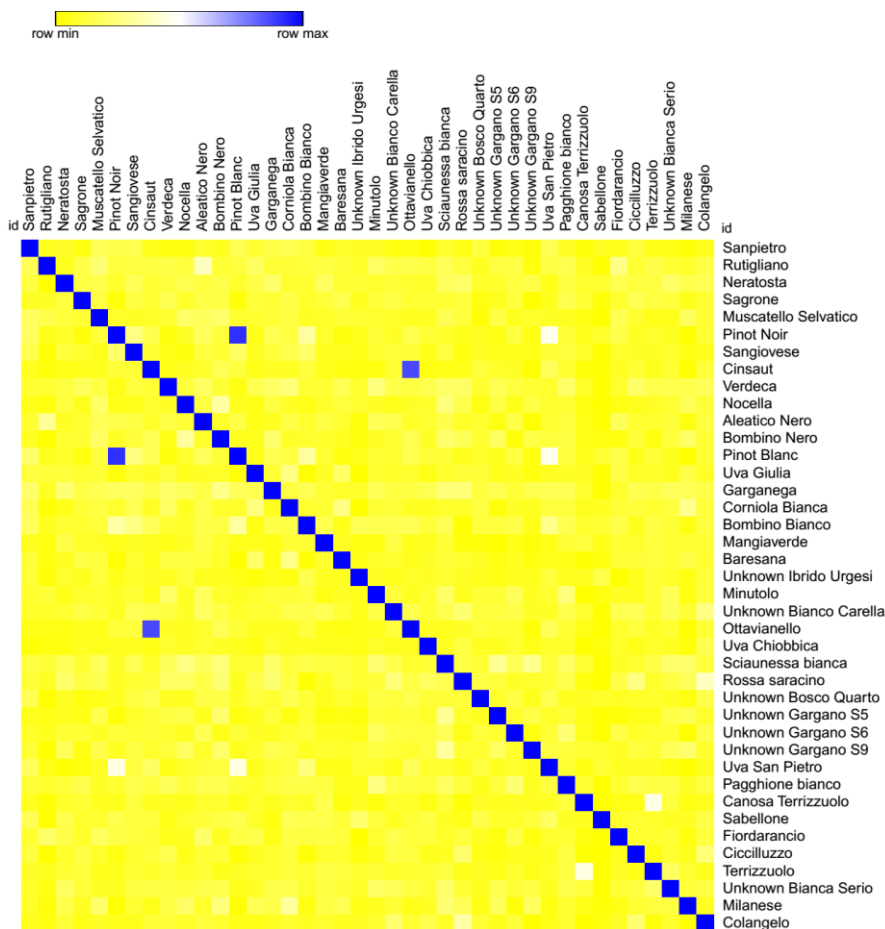
Supplementary Figure S2. Frequency distribution of Lynch and Ritland estimator (LRM) values across the Apulian grapevine germplasm.



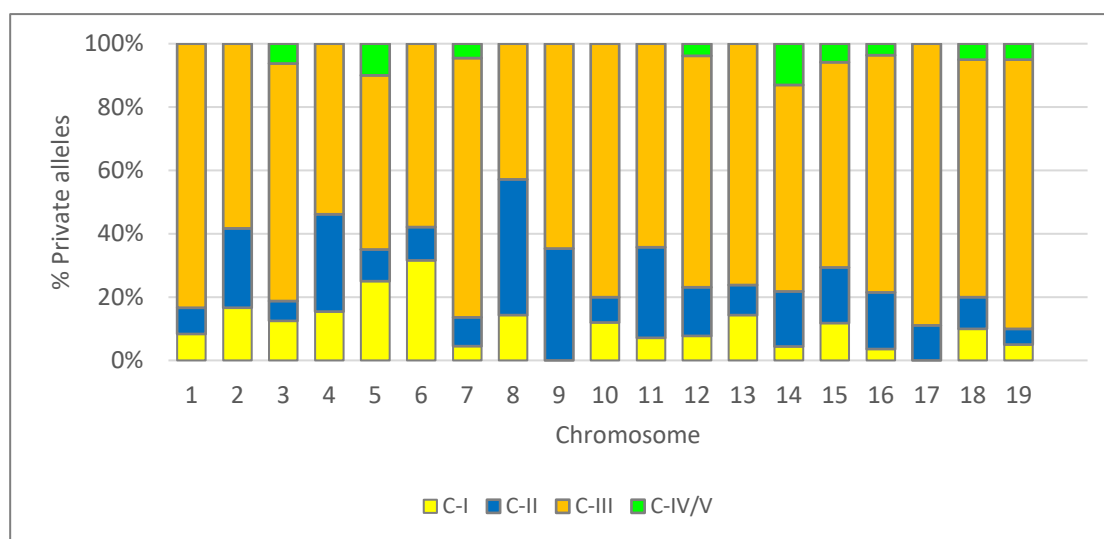
Supplementary Figure 3. Cross-validation (CV) plot of ADMIXTURE analysis for K values from 1 to 10.



Supplementary Figure 4. Gap statistic plot indicates K=5 as the best value of K in which to divide the population (Figure 3). The number of inferred cluster (K) ranging from 1 to 10 are shown in the graph. **A)** The blue and red curves are the estimated expectation of log (Wk) and the observed log (Wk), respectively. **B)** The x-axis indicates different possible K (K = 5 is the best value) and gap value is on the y-axis.



Supplementary Figure 5. Heatmap illustrating the pair-wise allele sharing distances (i.e. identity-by-state values) for the 40 grapevine accessions subjected to genotyping-by-sequencing.



Supplementary Figure S6. Stacked bar chart describing the distribution of private alleles on the 19 grape chromosomes. % of private alleles for each of the four clusters identified by AWclust (Figure 2) is reported. C-IV and C-V were merged in a unique cluster renamed C-IV/V.

Table S1. List of grapevine genotypes analyzed in this study. * samples subjected also to genotyping by sequencing. W = wine, T = table; VIV = Vitis International Variety catalogue; n.a. = not available.

Sample Genotype		Berry colour	Use Geographical origin		Type	Coordinates (latitude - longitude)
1	ACCHITEDDA	white	W	Brindisi	Minor	40,6683333333 - 17,5211111111
2	BARBAROSSA (SACRONE ROSSO) *	red	T	Barletta-Andria-Trani	Minor	41,3438472222 - 16,0182583333
3	CALDARESE ROSSO	red	W	Lecce	Minor	40,2256611111 - 18,4033611111
4	CANNELLINO BIANCO	white	W	Foggia	Minor	41,7050722222 - 16,0215472222
5	CANOSA TERRIZZUOLO*	n.a.	n.a.	Barletta-Andria-Trani	Minor	41,2233388889 - 16,0741472222
6	CHIAPPARONE VISCIO	white	W	Foggia	Minor	41,8850000000 - 15,9500000000
7	CICCILLUZZO*	black	n.a.	Barletta-Andria-Trani	Minor	41,2819277778 - 16,2491916667
8	COLANGELO*	black	T	Bari	Minor	40,8474944444 - 17,0000333333
9	CORNALETTA NERA	black	T	Bari	Minor	40,8474944444 - 17,0000333333
10	CORNIOLA BIANCA*	white	T	Barletta-Andria-Trani	Minor	40,9963888889 - 16,8772222222
11	CORNIOLA ROSA	rose	T	Bari	Minor	40,8253305559 - 16,8758944437
12	DOLCIOLO PENDOLINO	n.a.	n.a.	Foggia	Minor	41,8844444444 - 15,9505555556
13	DON MICHELE	black	W	Foggia	Minor	41,9283333333 - 16,0963888889
14	DUNDURIN	black	W	Foggia	Minor	41,9283333333 - 16,0963888889
15	FIORDARANCIO*	yellow	W-	Barletta-Andria-Trani	Minor	40,9535694444 - 16,0805083333
16	FRANCESINA ROSA	red	n.a.	Barletta-Andria-Trani	Minor	41,2403638889 - 16,2198500000
17	FRASCAROSA	white	W	Taranto	Minor	40,7150000000 - 17,3747222222
18	GIORGIONE	black	n.a.	Barletta-Andria-Trani	Minor	41,0952730000 - 16,1536650000
19	MALAGA	black	W	Lecce	Minor	40,2256 000000 - 18,4033416667
20	MALVASIA ANTICA	white	W	Foggia	Minor	41,9283333333 - 16,0963888889
21	MALVASIA NERA	black	W	Bari	Minor	41,0952472222 - 16,3117472222
22	MALVASIA SARACINO	white	W	Bari	Minor	41,1001666667 - 16,7454083333
23	MANGIAVERDE*	n.a.	n.a.	Bari	Minor	40,9550000000 - 16,8066666667
24	MENNAVERDE	n.a.	n.a.	Bari	Minor	41,0252777778 - 16,4165416667
25	MILANESE*	n.a.	W	Lecce	Minor	41,9283333333 - 16,0963888889
26	MOSCARDINELLA	white	n.a.	Foggia	Minor	41,0852370000 - 16,0921450000
27	MOSCATELLO SELVATICO*	white	W	n.a.	Minor	41,1400111111 - 16,2244083333
28	MOSCATIDDONE	black	W	Foggia	Minor	40,5302777778 - 17,7941666667
29	NARDOBELLO 1	white	W	Foggia	Minor	41,8852777778 - 15,9502777778
30	NARDOBELLO 2	black	n.a.	Foggia	Minor	41,8852777778 - 15,9505555556
31	NERA OVALE	black	n.a.	Bari	Minor	40,5297222222 - 17,7938888889
32	NERATOSTA (1)*	black	W	Foggia	Minor	41,8852777778 - 15,9500000000
33	NOCELLA *	black	W	Foggia	Minor	41,8844444444 - 15,9502777778
34	OTTAVIANELLO*	black	W	Lecce	Minor	40,9211555556 - 17,1725361111
35	PAGGHIONE BIANCO*	white	n.a.	Foggia	Minor	41,7054083333 - 15,9561750000

36	PAGLIONE BIANCO	white	n.a.	Foggia	Minor	41,7054083333 - 15,9561750000
37	PICCOLA NERA LONGO	black	W	Bari	Minor	40,9475000000 - 17,2969444444
38	80-PLAUS BIANCA	white	W	Foggia	Minor	41,9286111111 - 16,0972222222
39	PORCINARO	black	n.a.	n.a.	Minor	41,2999333333 - 16,2262583333
40	PRIMITIVO PAZZO	n.a.	n.a.	n.a.	Minor	40,9550000000 - 16,8066666667
41	PRUNESTA BIANCA (FALSE)	white	T	Bari	Minor	41,1703416667 - 16,5619888889
42	PRUNESTA NERA	black	T	Bari	Minor	41,0954194444 - 16,3107111111
43	ROSSA SARACINO*	red	W	Bari	Minor	41,1001666667 - 16,7454083333
44	ROSSA SCORRESE	red	n.a.	Lecce	Minor	40,1805722222 - 18,4337722222
45	ROSSO DI LECCE	red	W	Lecce	Minor	40,1805722222 - 18,4337722222
46	RUTIGLIANO*	black	W	Taranto	Minor	40,7150000000 - 17,3747222222
47	SABELLONE*	black	W	Barletta-Andria-Trani	Minor	41,1855250000 - 16,0060611111
48	SACRA ROSSA GUIDACCI	red	T	Foggia	Minor	41,2909361111 - 15,2593500000
49	SAGRA	white	T	n.a.	Minor	41,1440777778 - 16,3044694444
50	SAGRA ROSSA	red	n.a.	Barletta-Andria-Trani	Minor	41,0917194444 - 15,9412527778
51	SAGRONE	red	T	Barletta-Andria-Trani	Minor	41,1962722222 - 16,3287361111
52	SAN LEONARDO	n.a.	n.a.	Taranto	Minor	40,7794444444 - 17,2855555556
53	SAN MARTINO	black	T	Brindisi	Minor	40,6470555556 - 17,5991500000
54	SANPIETRO*	white	W	Lecce	Minor	40,1806222222 - 18,4337500000
55	SCIALI	white	W	Foggia	Minor	41,9283333333 - 16,0963888889
56	SCIAUNESSA BIANCA*	white	n.a.	Foggia	Minor	41,9280555556 - 16,0975000000
57	SOMARELLO NERO	black	n.a.	BR	Minor	41,9283333333 - 16,0963888889
58	STRAZZACAMBIALI	white	n.a.	Barletta-Andria-Trani	Minor	41,2711194444 - 16,1454500000
59	TARANTINA NERA	black red	T	Lecce	Minor	40,1553527778 - 18,4825722222
60	TERRIZZUOLO*	white	W	Barletta-Andria-Trani	Minor	41,1975222222 - 16,0594027778
61	TINTIGLIO	n.a.	n.a.	Foggia	Minor	41,9329777778 - 15,0387388884
62	TINTURINO	black	W	Foggia	Minor	41,8852777778 - 15,9500000000
63	UNKNOWN BIANCO CARELLA*	white	n.a.	Taranto	Minor	41,8850000000 - 15,9500000000
64	UNKNOWN 1 NERA	black	W	Foggia	Minor	40,0416694445 - 18,0872249994
65	UNKNOWN 2 BOSCO QUARTO	n.a.	W	Foggia	Minor	41,8800000005 - 15,9500000000
66	UNKNOWN 3	n.a.	n.a.	n.a.	Minor	41,1268777778 - 16,8506666667
67	UNKNOWN BOSCO QUARTO*	black	W	Foggia	Minor	41,8850000000 - 15,9500000000
68	UNKNOWN GARGANO S14	n.a.	W	Foggia	Minor	41,9000000000 - 16,0540000000
69	UNKNOWN GARGANO S5*	n.a.	W	Foggia	Minor	41,9000000000 - 16,0540000000
70	UNKNOWN GARGANO S6*	white	W	Foggia	Minor	41,9000000000 - 16,0540000000
71	UNKNOWN GARGANO S8*	n.a.	W	Foggia	Minor	41,9000000000 - 16,0540000000
72	UNKNOWN GARGANO S9	n.a.	W	Foggia	Minor	41,9000000000 - 16,0540000000
73	UNKNOWN VITE LONGO	n.a.	W	n.a.	Minor	40,9475000000 - 17,2969444444
74	UNKNOWN BIANCA ACINO OVOIDE	white	n.a.	n.a.	Minor	40,4794444445 - 17,8936111110
75	UNKNOWN BIANCA SERIO	white	n.a.	n.a.	Minor	40,7150000000 - 17,3750000000
76	UNKNOWN PINTO MURO*	n.a.	W	n.a.	Minor	40,7794444444 - 17,2855555556
77	UNKNOWN IBRIDO URGESI*	white	n.a.	Brindisi	Minor	40,6802777778 - 17,4572222222

78	UNKNOWN MACCHIA 2	black	n.a.	Foggia	Minor	41,9286111111 - 16,0977777778
79	UNKNOWN MACCHIA 3	black	n.a.	Foggia	Minor	41,8850000000 - 15,9500000000
80	UVA CHIOBBICA*	white	W	Taranto	Minor	40,8191666667 - 17,3011111111
81	UVA GIULIA*	n.a.	n.a.	Taranto	Minor	40,9211555556 - 17,1725361111
82	UVA ROMANA	red	T	Bari	Minor	40,9963888889 - 16,8772222222
83	UVA SAN PIETRO*	white	W	Barletta-Andria-Trani	Minor	41,1436777778 - 16,3039833333
84	VESPRO	white	W	Foggia	Minor	41,9283333333 - 16,0963888889
85	MALVASIA BIANCA	white	W	CRSFA-Locorotondo	Apulian	40.7559000000 - 17.3263000000
86	ALEATICO NERO*	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
87	AGLIANICO NERO	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
88	BARESANA BIANCA*	white	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
89	BOMBINO BIANCO*	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
90	BOMBINO NERO*	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
91	FRANCAVIDDA BIANCO	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
92	IMPIGNO BIANCA	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
93	MALVASIA BIANCA LUNGA	white	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
94	MARCHIONE	white	w	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
95	NEGROAMARO	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
96	OTTAVIANO NERO	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
97	PALUMBO UVA CARRIERI	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
98	AGRESTA	black	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
99	PLAUS BIANCA	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
100	PRIMITIVO	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
101	ROSSA BITONTO	red	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
102	SANT'ANNA DI LIPSIA	white	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
103	SGARRAPARETE	red	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
104	SOMARELLO ROSSO	red	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
105	TRIFERA	black	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
106	UVA ATTINA	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
107	UVA DI TROIA	black	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
108	UVA RUGGIA	red	T	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
109	MINUTOLO*	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
110	VERDECA*	white	W	CRSFA _Locorotondo	Apulian	40.7559000000 - 17.3263000000
111	MOSCATO DI ALESSANDRIA	white	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
112	GARGANEGA BIANCO*	black	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
113	ITALIA	white	T	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
114	SANGIOVESE*	black	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
115	TREBBIANO	white	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
116	SANTA SOFIA	white	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
117	MOSTOSA BIANCA	white	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
118	CILIEGIOLO	black	W	CRSFA _Locorotondo	Italian	40.7559000000 - 17.3263000000
119	JABIXHAR	white	W	CRSFA _Locorotondo	International	40.7559000000 - 17.3263000000

120	VLOSH	black	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
121	SHESH I BARDHE	white	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
122	BALBUT	black	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
123	PERLA DI CSABA	white	T	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
124	CHASSELAS BLANC	white	T	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
125	CINSAUT NERO*	black	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
126	PINOT BLANC*	white	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
127	PINOT NOIR*	black	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000
128	CABERNET_ SAUVIGNON	black	W	CRSFA_Locorotondo	International	40.7559000000 - 17.3263000000

Table S2: List of the 10 microsatellite markers (SSR) used for genotyping. For each SSR, the identification code, oligo sequences, the expected fragment size range, annealing temperature and bibliographic reference are indicated.

Marker	Primer Forward	Primer Reverse	Fragment size range	T ^a (°C)	Reference
VvS2	CAGCCCGTAAATGTATCCATC	AAATTCAAAATTCTAATTCAACTGG	121-151	50	THOMAS <i>et al.</i> 1994
VvMD7	AGAGTTGCGGAGAACAGGAT	CGAACCTTCACACGCTTGAT	233-255	52	BOWERS <i>et al.</i> 1996
VvMD25	TTCCGTTAAAGCAAAAGAAAAAGG	TTGGATTTGAAATTTATTGAGGGG	222-259	52	BOWERS <i>et al.</i> 1999
VvMD27	GTACCAGATCTGAATACATCCGTAAGT	ACGGGTATAGAGCAAACGGTGT	170-192	55	BOWERS <i>et al.</i> 1999
VvMD28	AACAATTCAATGAAAAGAGAGAGAGAGA	TCATCAATTTTCGTATCTCTATTGCTG	213-255	52	BOWERS <i>et al.</i> 1999
VvMD32	TATGATTTTTTAGGGGGGTGAGG	GGAAAGATGGGATGACTCGC	221-272	55	BOWERS <i>et al.</i> 1999
VrvZAG21	TCATTCACTCACTGCATTCATCGGC	GGGGCTACTCCAAAGTCAGTTCTTG	229-262	50	SEFC <i>et al.</i> 1999
VrZAG62	GGTGAAATGGGCACCGAACACACGC	CCATGTCTCTCCTCAGCTTCTCAGC	180-204	60	SEFC <i>et al.</i> 1999
VrZAG64	TATGAAAGAAACCCAACGCGGCACG	TGCAATGTGGTCAGCCTTTGATGGG	132-158	55	SEFC <i>et al.</i> 1999
VrZAG79	AGATTGTGGAGGAGGGAACAAACCG	TGCCCCATTTTCAAACCTCCCTTCC	232-261	60	SEFC <i>et al.</i> 1999

Table S3. Genetic diversity indices evaluated on the 84 minor/neglected Apulian grapevine genotypes.

Locus	<i>Na</i>	<i>Ne</i>	<i>I</i>	<i>Ho</i>	<i>He</i>	F
VvS2	12.0	5.405	1.937	0.869	0.815	-0.066
VvMD7	10.0	4.876	1.813	0.845	0.795	-0.063
VvMD25	7.0	3.989	1.535	0.714	0.749	0.047
VvMD27	9.0	5.135	1.845	0.845	0.805	-0.050
VvMD28	14.0	6.751	2.141	0.817	0.852	0.041
VvMD32	11.0	6.641	2.054	0.810	0.849	0.047
VrZAG21	11.0	4.979	1.809	0.878	0.799	-0.099
VrZAG62	11.0	7.612	2.134	0.905	0.869	-0.042
VrZAG79	13.0	7.056	2.177	0.881	0.858	-0.026
VrZAG64	7.0	4.836	1.674	0.917	0.793	-0.156
Mean	10.5	5.728	1.912	0.848	0.819	-0.037
Total	105.0					

Na = Number of different alleles; *Ne* = effective alleles; *I* = Shannon's information index; *Ho* = observed heterozygosity; *He* = expected heterozygosity; F = inbreeding coefficient = (He - Ho) / He = 1 - (Ho / He)

Table S4. Gene ontology (GO) analysis. Chromosome, position (start/stop), annotation and Gene ontology terms for the 10 SSRs used in the analysis of grapevine germplasm. n.a. = not available.

SSR ID	Chr	Start (bp)	Stop (bp)	Annotation	Gene ontology	
VvS2	11	3909894	3910030	intergenic		
VvMD7	7	1178552	1178797	Vv7s0151g00970	GO:0005515 GO:0005634 GO:0019941	glycoprotein binding cell nucleus modification-dependent protein catabolic process
VvMD25	11	2971693	2971933	intergenic		
VvMD27	5	4472022	4472201	Vv5s0020g02760	GO:0005787 GO:0006465 GO:0008233 GO:0016021	signal peptidase complex signal peptide processing peptidase activity integral component of membrane
VvMD28	3	11617504	11617740	Vv3s0132g00200	GO:0004491 GO:0005739 GO:0006573 GO:0006979 GO:0008152 GO:0016491 GO:0055114	methymalonate-semialdehyde dehydrogenase (acylating) activity valine metabolic process response to oxidative stress metabolic process oxidoreductase activity oxidation-reduction process
VvMD32	4	18035578	18035848	Vv4s0023g01490	n.a.	
VrZAG21	4	13648595	13648800	Vv4s0043g00340	GO:0003677 GO:0005634 GO:0009887 GO:0009943 GO:0009944 GO:0009956 GO:0010051 GO:0010158 GO:0045449 GO:0048440 GO:0048481	DNA binding nucleus organ morphogenesis adaxial/abaxial axis specification polarity specification adaxial/abaxial radial pattern formation xylem and phloem pattern formation abaxial cell fate specification regulation of transcription, DNA-templated carpel development plant ovule development
VrZAG62	7	1766878	1767112	Vv7s0104g00540	GO:0016301	kinase activity
VrZAG64	10	1339872	1340120	intergenic		
VrZAG79	n.a.					

Table S5 Matrix of the pairwise F_{ST} genetic distances among the four groups detected by AWclust (C-IV and C-V were merged in a unique cluster renamed C-IV/V).

Cluster	C-I	C-II	C-III	C-IV/V
C-I	0.000	0.068	0.041	0.135
C-II	0.068	0.000	0.029	0.127
C-III	0.041	0.029	0.000	0.066
C-IV/V	0.135	0.127	0.066	0.000

F_{ST} indices interpretation (Wright, 1949):

$F_{ST} < 0.05$ low genetic differentiation

$0.05 < F_{ST} < 0.15$ moderate genetic differentiation

$F_{ST} > 0.15$ high genetic differentiation

Table S6. List of pairs of genotypes with allele sharing distance (IBS; identity-by-state) ≥ 0.80

Genotype 1	Genotype 2	IBS value
PINOT NOIR	PINOT BLANC	0.97
CINSAUT	OTTAVIANELLO	0.96
PINOT NOIR	UVA SAN PIETRO	0.85
PINOT BLANC	UVA SAN PIETRO	0.85
CANOSA TERRIZZUOLO	TERRIZZUOLO	0.85
ROSSA SARACINO	COLANGELO	0.82
NOCELLA	BOMBINO NERO	0.81
RUTIGLIANO	ALEATICO	0.81
PINOT NOIR	BOMBINO BIANCO	0.81
PINOT BLANC	BOMBINO BIANCO	0.80
CORNIOLA BIANCA	MILANESE	0.80
SCIAUNESSA BIANCA	UNKNOWN GARGANO S6	0.80
SCIAUNESSA BIANCA	UNKNOWN GARGANO S8	0.80
CORNIOLA BIANCA	BARESANA	0.80
UVA GIULIA	CORNIOLA BIANCA	0.80

Table S7. List of divergent SNP loci derived from pairwise comparisons between clusters identified by AWclust. (C-IV and C-V were merged in a unique cluster renamed C-IV/V). Chromosome, position (bp), F_{ST} value, gene ID and annotation were reported.

Paiwise comparison	Marker	Chr	Pos	$F_{ST}>0.25$	Gene ID	Annotation
C-III vs C-IV/V	S1_2795404	1	2795404	0.558	VIT_201s0011g03130	N-glycosylation site
	S1_12410054	1	12410054	0.300	VIT_201s0026g02680	oxygen evolving enhancer protein 3
	S1_4360266	1	4360266	0.259	VIT_201s0011g04780	uncharacterized protein at1g66480-like
	S2_17516802	2	17516802	0.541	VIT_202s0087g00270	serine threonine-protein kinase at5g01020-like
	S2_14008183	2	14008183	0.499	intergenic	
	S2_8634120	2	8634120	0.426	VIT_202s0012g01990	4-hydroxyphenylpyruvate dioxygenase
	S2_3816758	2	3816758	0.376	intergenic	
	S2_4289898	2	4289898	0.301	VIT_202s0025g04730	oxidoreductase activity
	S2_11176307	2	11176307	0.260	intergenic	
	S3_1692692	3	1692692	0.504	VIT_203s0038g02440	farnesylated protein
	S3_2108561	3	2108561	0.456	intergenic	
	S3_8149934	3	8149934	0.434	intergenic	
	S3_18633065	3	18633065	0.361	intergenic	
	S3_11401731	3	11401731	0.299	VIT_203s0132g00050	uncharacterized protein loc100245618
	S3_12748836	3	12748836	0.298	intergenic	
	S3_2254108	3	2254108	0.285	VIT_203s0038g03140	probable flavin-containing monooxygenase 1-like
	S3_1426686	3	1426686	0.267	VIT_203s0038g02070	translocase of chloroplast chloroplastic-like
	S4_714852	4	714852	0.442	VIT_204s0008g00830	nadh dehydrogenase
	S5_20801876	5	20801876	0.434	intergenic	
	S5_24554829	5	24554829	0.422	VIT_205s0094g01300	polygalacturonase
	S5_8734989	5	8734989	0.342	VIT_205s0049g01430	uncharacterized protein
	S5_23402393	5	23402393	0.262	VIT_205s0094g00020	rwp-rk domain-containing protein
	S5_24567707	5	24567707	0.262	VIT_205s0094g01310	polygalacturonase
	S6_2124790	6	2124790	0.324	VIT_206s0004g01730	protein
	S6_745382	6	745382	0.318	VIT_206s0004g00570	Myb-like DNA-binding domain
	S7_843696	7	843696	0.532	VIT_207s0151g00280	glutamate binding protein
	S7_4867146	7	4867146	0.516	VIT_207s0005g02510	phytochrome-interacting factor

S7_3345690	7	3345690	0.426	VIT_207s0005g00700	epoxide hydrolase 2-like
S7_252469	7	252469	0.402	intergenic	
S7_15344663	7	15344663	0.397	VIT_207s0129g00050	uncharacterized protein
S7_6022869	7	6022869	0.380	intergenic	
S7_18225497	7	18225497	0.342	intergenic	
S7_3454258	7	3454258	0.285	VIT_207s0005g00830	subtilisin-like protease-like
S8_16542339	8	16542339	0.465	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_16542324	8	16542324	0.285	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_16542284	8	16542284	0.262	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S9_21838021	9	21838021	0.549	VIT_209s0054g00970	mediator subunit 8
S9_18940862	9	18940862	0.389	VIT_209s0018g01650	ap2-like ethylene-responsive transcription factor at1g16060-like
S10_13324332	10	13324332	0.470	VIT_210s0042g00440	pentatricopeptide repeat-containing protein chloroplastic
S10_14607576	10	14607576	0.391	intergenic	
S10_939454	10	939454	0.314	VIT_210s0116g01680	ankyrin repeat family protein
S10_509756	10	509756	0.289	VIT_210s0116g01030	protein
S10_15551368	10	15551368	0.280	VIT_210s0042g01390	pentatricopeptide repeat-containing protein
S11_2440845	11	2440845	0.434	VIT_211s0016g03030	iq domain-containing protein
S11_1379525	11	1379525	0.376	VIT_211s0016g01720	threonine synthase
S12_8095101	12	8095101	0.568	VIT_212s0134g00470	uncharacterized protein loc100853582
S12_12328673	12	12328673	0.516	VIT_212s0121g00296	uncharacterized protein
S12_8182780	12	8182780	0.478	VIT_212s0134g00560	uncharacterized gpi-anchored protein at4g28100-like
S12_20634528	12	20634528	0.336	VIT_212s0035g00990	receptor protein kinase clavata1
S12_20698464	12	20698464	0.298	intergenic	
S12_9321952	12	9321952	0.262	VIT_212s0057g00690	histidine kinase cytokinin receptor
S13_21831983	13	21831983	0.402	VIT_213s0064g00300	uncharacterized protein loc100260134
S13_667744	13	667744	0.336	VIT_213s0067g01190	glycosyl hydrolase family 9 protein
S13_23055941	13	23055941	0.272	VIT_213s0064g01150	transducin wd-40 repeat-containing protein
S14_1176140	14	1176140	0.575	VIT_214s0060g01490	heat shock protein binding
S14_16084682	14	16084682	0.409	intergenic	
S14_2815220	14	2815220	0.356	VIT_214s0128g00120	e3 ubiquitin-protein ligase at16-like
S14_20693796	14	20693796	0.277	intergenic	

	S14_2814722	14	2814722	0.276	VIT_214s0128g00120	e3 ubiquitin-protein ligase at16-like
	S14_6071819	14	6071819	0.272	VIT_214s0030g01470	late embryogenesis abundant protein d-34-like
	S15_7625566	15	7625566	0.646	intergenic	
	S15_11266929	15	11266929	0.380	intergenic	
	S15_18433525	15	18433525	0.299	VIT_215s0046g01450	gds1 esterase lipase
	S15_13144458	15	13144458	0.276	VIT_215s0021g02200	structural constituent of nuclear
	S16_7784310	16	7784310	0.277	intergenic	
	S16_12555471	16	12555471	0.252	intergenic	
	S17_14576374	17	14576374	0.538	VIT_217s0053g00110	pentatricopeptide repeat-containing protein at5g66520-like
	S17_14838883	17	14838883	0.324	intergenic	
	S17_4602023	17	4602023	0.316	VIT_217s0000g04393	protein
	S17_14576438	17	14576438	0.296	VIT_217s0053g00110	pentatricopeptide repeat-containing protein at5g66520-like
	S18_16151588	18	16151588	0.446	VIT_218s0076g00310	eukaryotic translation initiation factor 5b
	S18_8407320	18	8407320	0.385	VIT_218s0001g10040	uncharacterized protein at4g06744-like
	S18_10725515	18	10725515	0.323	VIT_218s0001g12540	maf-like protein
	S18_24246031	18	24246031	0.314	intergenic	
	S18_23509538	18	23509538	0.295	VIT_218s0117g00270	protein
	S19_3208699	19	3208699	0.652	intergenic	
	S19_2109644	19	2109644	0.563	VIT_219s0014g01910	uncharacterized protein
	S19_1360860	19	1360860	0.464	VIT_219s0014g01250	tubby-like f-box protein 7-like
	S19_350268	19	350268	0.360	VIT_219s0014g00330	nadh kinase
	S19_7443843	19	7443843	0.353	intergenic	
	S19_3856412	19	3856412	0.335	intergenic	
	S19_7474602	19	7474602	0.304	VIT_219s0090g01410	probable long-chain-alcohol o-fatty-acyltransferase 1-like
					intergenic	
C-III vs C-I	S1_10836	1	10836	0.329	VIT_201s0011g00010	general transcription factor iie subunit 1-like
	S1_6068995	1	6068995	0.302	VIT_201s0011g06270	hydroxyproline-rich glyco protein
	S2_4289898	2	4289898	0.267	VIT_202s0025g04730	oxidoreductase activity
	S3_2823098	3	2823098	0.402	VIT_203s0038g03860	protein exordium like 5
	S3_10172186	3	10172186	0.380	intergenic	
	S3_12748793	3	12748793	0.298	intergenic	
	S3_2117004	3	2117004	0.260	VIT_203s0038g02980	mechanosensitive channel of small conductance-like 5

S4_1063770	4	1063770	0.546	VIT_204s0008g01290	gata transcription factor 22
S4_11466696	4	11466696	0.366	intergenic	
S4_4192762	4	4192762	0.314	VIT_204s0008g04750	3-hydroxybenzoate 6-hydroxylase
S5_23891717	5	23891717	0.380	VIT_205s0094g00530	protein iq-domain 14
S5_610996	5	610996	0.353	VIT_205s0077g00800	gins complex subunit 4
S6_5918485	6	5918485	0.750	VIT_206s0004g04950	gras family transcription factor
S6_16617284	6	16617284	0.549	VIT_206s0009g03385	protein
S6_19781052	6	19781052	0.424	VIT_206s0080g00085	xylem serine proteinase
S6_19781085	6	19781085	0.261	VIT_206s0080g00085	xylem serine proteinase
S7_15344663	7	15344663	0.397	VIT_207s0129g00050	uncharacterized protein
S7_1847650	7	1847650	0.316	VIT_207s0104g00660	2og-fe oxygenase family protein
S7_16910501	7	16910501	0.288	intergenic	
S8_8221364	8	8221364	0.424	VIT_208s0217g00100	pyruvate decarboxylase
S8_13385726	8	13385726	0.411	VIT_208s0040g02280	protein
S8_17361527	8	17361527	0.387	VIT_208s0007g03400	iron-sulfur cluster assembly
S8_12775962	8	12775962	0.354	VIT_208s0040g01640	protein trf-like 8
S9_2660726	9	2660726	0.271	VIT_209s0002g02930	rna polymerase transcriptional regulation mediator-like protein
S10_592238	10	592238	0.297	VIT_210s0116g01150	protein
S10_15502797	10	15502797	0.288	intergenic	
S10_1443658	10	1443658	0.285	VIT_210s0003g00140	ethylene response factor 3
S12_4004619	12	4004619	0.428	VIT_212s0028g03270	ethylene response factor 3
S13_20295609	13	20295609	0.446	VIT_213s0139g00070	disease resistance rpp13-like protein 1-like
S13_23887943	13	23887943	0.427	VIT_213s0156g00140	e3 ubiquitin-protein ligase ring1-like
S14_27846259	14	27846259	0.643	VIT_214s0066g01440	homeodomain leucine zipper protein
S14_30257640	14	30257640	0.380	intergenic	
S14_23352220	14	23352220	0.303	intergenic	
S15_16029189	15	16029189	0.542	VIT_215s0048g01895	protein seuss-like 2
S15_19094920	15	19094920	0.444	VIT_215s0046g02290	atp-dependent helicase brm
S15_12454802	15	12454802	0.336	VIT_215s0021g01800	hypothetical protein VITISV_037538 [Vitis vinifera]
S15_14994561	15	14994561	0.278	VIT_215s0048g00840	protein
S16_7784308	16	7784308	0.296	intergenic	
S17_14838896	17	14838896	0.428	intergenic	

C-III vs C-II	S17_70902	17	70902	0.327	intergenic	
	S17_2264413	17	2264413	0.258	VIT_217s0000g02480	polcalcin jun
	S18_4674058	18	4674058	0.396	intergenic	
	S18_1431955	18	1431955	0.380	VIT_218s0001g00570	pentatricopeptide repeat-containing protein
	S19_10807056	19	10807056	0.449	VIT_219s0015g01940	peroxisome biogenesis protein 5-like
	S19_2231401	19	2231401	0.434	VIT_219s0014g02070	udp-glycosyltransferase 79b9-like
	S19_6782112	19	6782112	0.395	VIT_219s0090g00710	rna binding
	S19_8876945	19	8876945	0.364	VIT_219s0015g00740	protein plastid movement impaired 2-like
	S19_8246853	19	8246853	0.312	VIT_219s0015g00260	mitochondrial import inner membrane translocase subunit tim50
	S19_1684608	19	1684608	0.304	VIT_219s0014g01600	uncharacterized protein
					intergenic	
	S1_1505501	1	1505501	0.307	VIT_201s0011g01660	vesicle-associated membrane protein
	S2_3231574	2	3231574	0.322	VIT_202s0025g03710	kdel motif-containing protein 1
	S2_872026	2	872026	0.250	VIT_202s0025g00900	6-phosphogluconate dehydrogenase
	S2_7363868	2	7363868	0.250	VIT_202s0012g01250	mitochondrial carnitine acylcarnitine carrier-like protein
	S3_3555389	3	3555389	0.313	VIT_203s0063g00010	uncharacterized protein at4g06744-like
	S4_22226569	4	22226569	0.325	VIT_204s0044g00940	set domain protein
	S4_14140584	4	14140584	0.279	intergenic	
	S4_7025032	4	7025032	0.251	VIT_204s0008g07000	zinc finger ccch domain-containing protein 18-like
	S5_23557316	5	23557316	0.470	VIT_205s0094g00240	endochitinase pr4
	S5_23557227	5	23557227	0.377	VIT_205s0094g00240	endochitinase pr4
	S5_5708044	5	5708044	0.311	VIT_205s0020g04020	uncharacterized protein
	S5_23402393	5	23402393	0.275	VIT_205s0094g00020	rwp-rk domain-containing protein
	S6_687601	6	687601	0.417	VIT_206s0004g00500	ran-binding protein
	S6_5918485	6	5918485	0.336	VIT_206s0004g04950	gras family transcription factor
	S7_2917545	7	2917545	0.415	VIT_207s0005g00110	uncharacterized protein loc100264106
	S7_3454290	7	3454290	0.413	VIT_207s0005g00830	subtilisin-like protease-like
	S7_4867146	7	4867146	0.404	VIT_207s0005g02510	phytochrome-interacting factor
	S7_20107065	7	20107065	0.341	VIT_207s0031g03220	protein
	S7_1847650	7	1847650	0.281	VIT_207s0104g00660	2og-fe oxygenase family protein
	S7_20454713	7	20454713	0.260	VIT_207s0130g00170	transmembrane clptm1 family protein
	S9_887276	9	887276	0.369	intergenic	

	S9_21898925	9	21898925	0.315	VIT_209s0054g01040	uncharacterized protein
	S9_2660764	9	2660764	0.260	VIT_209s0002g02930	rna polymerase transcriptional regulation mediator-like protein
	S10_12942945	10	12942945	0.467	VIT_210s0042g00170	transcription factor tcp7-like
	S10_134839	10	134839	0.279	intergenic	
	S13_9034682	13	9034682	0.546	VIT_213s0074g00730	protein kinase g11a-like
	S13_9263384	13	9263384	0.353	intergenic	
	S14_16084681	14	16084681	0.305	intergenic	
	S15_15690859	15	15690859	0.418	VIT_215s0048g01530	cytochrome p450 76c4
	S15_17988354	15	17988354	0.357	VIT_215s0046g00930	ring-h2 finger protein atl21a-like
	S15_15241869	15	15241869	0.296	VIT_215s0048g01120	subtilisin-like protease-like
	S15_16029252	15	16029252	0.292	VIT_215s0048g01895	protein seuss-like 2
	S15_18433585	15	18433585	0.285	VIT_215s0046g01450	gdsl esterase lipase
	S16_17830632	16	17830632	0.349	intergenic	
	S16_6539729	16	6539729	0.268	VIT_216s0013g00870	zing finger transcription factor pei1
	S19_17003493	19	17003493	0.452	intergenic	
C-IV/V vs C-I	S1_2795404	1	2795404	0.781	VIT_201s0011g03130	N-glycosylation site
	S1_4360266	1	4360266	0.781	VIT_201s0011g04780	uncharacterized protein at1g66480-like
	S1_12410054	1	12410054	0.756	VIT_201s0026g02680	oxygen evolving enhancer protein 3
	S1_21769359	1	21769359	0.508	VIT_201s0146g00020	metal ion transport
	S1_10836	1	10836	0.500	VIT_201s0011g00010	general transcription factor iie subunit 1-like
	S1_1888193	1	1888193	0.375	VIT_201s0011g02170	Glycosyl hydrolase family 9
	S1_6243157	1	6243157	0.300	VIT_201s0011g06430	probable nad h-dependent oxidoreductase 1
	S1_10985517	1	10985517	0.300	VIT_201s0026g01740	snf1-related protein kinase regulatory subunit gamma-1-like
	S1_11697553	1	11697553	0.250	intergenic	
	S2_4289898	2	4289898	0.889	VIT_202s0025g04730	oxidoreductase activity
	S2_345650	2	345650	0.375	VIT_202s0025g00210	uncharacterized protein
	S2_14008243	2	14008243	0.375	intergenic	
	S2_6286075	2	6286075	0.355	VIT_202s0012g00470	Putative methyltransferase
	S2_14008183	2	14008183	0.300	intergenic	
	S2_16988113	2	16988113	0.250	intergenic	
	S3_4068529	3	4068529	0.583	VIT_203s0063g00560	cell number regulator 1

S3_10172186	3	10172186	0.583	intergenic	
S3_1692692	3	1692692	0.542	VIT_203s0038g02440	farnesylated protein
S3_2108561	3	2108561	0.542	intergenic	
S3_2876578	3	2876578	0.485	VIT_203s0038g03940	monosaccharide-sensing protein 2-like
S3_8149938	3	8149938	0.450	intergenic	
S3_18633065	3	18633065	0.450	intergenic	
S3_2254108	3	2254108	0.400	VIT_203s0038g03140	probable flavin-containing monooxygenase 1-like
S3_2031946	3	2031946	0.375	intergenic	
S3_7674574	3	7674574	0.375	VIT_203s0091g01060	d1-type cyclin
S3_12748793	3	12748793	0.375	intergenic	
S3_12748836	3	12748836	0.375	intergenic	
S3_6406887	3	6406887	0.353	VIT_203s0091g00160	p27-like protein
S3_1528001	3	1528001	0.310	VIT_203s0038g02220	actin depolymerizing factor 5
S3_41370	3	41370	0.300	VIT_203s0038g00050	bel1 homeotic
S3_8149934	3	8149934	0.300	intergenic	
S3_1426686	3	1426686	0.250	VIT_203s0038g02070	translocase of chloroplast chloroplastic-like
S3_2823098	3	2823098	0.250	VIT_203s0038g03860	protein exordium like 5
S3_2873915	3	2873915	0.250	VIT_203s0038g03930	ring-h2 finger protein atl80
S3_11401731	3	11401731	0.250	VIT_203s0132g00050	uncharacterized protein loc100245618
S4_714852	4	714852	0.643	VIT_204s0008g00830	nadh dehydrogenase
S4_1063770	4	1063770	0.583	VIT_204s0008g01290	gata transcription factor 22
S4_4192762	4	4192762	0.450	VIT_204s0008g04750	3-hydroxybenzoate 6-hydroxylase
S4_11466696	4	11466696	0.375	intergenic	
S4_18007386	4	18007386	0.375	VIT_204s0023g01450	splicing factor u2af large subunit a
S4_19986397	4	19986397	0.375	intergenic	
S4_19359339	4	19359339	0.313	VIT_204s0023g02780	short internodes 2
S4_540507	4	540507	0.250	intergenic	
S4_14140470	4	14140470	0.250	intergenic	
S4_14140549	4	14140549	0.250	intergenic	
S4_21757532	4	21757532	0.250	intergenic	
S5_24567707	5	24567707	0.643	VIT_205s0094g01310	polygalacturonase
S5_4305132	5	4305132	0.583	VIT_205s0020g02610	duf21 domain-containing protein at4g14240-like

S5_20801876	5	20801876	0.500	intergenic	
S5_23891717	5	23891717	0.500	VIT_205s0094g00530	protein iq-domain 14
S5_8734989	5	8734989	0.400	VIT_205s0049g01430	uncharacterized protein
S5_20801857	5	20801857	0.375	intergenic	
S5_24554829	5	24554829	0.315	VIT_205s0094g01300	polygalacturonase
S5_1129085	5	1129085	0.313	VIT_205s0077g01390	protein
S5_1223389	5	1223389	0.250	VIT_205s0077g01510	uncharacterized protein
S5_20801824	5	20801824	0.250	intergenic	
S6_745382	6	745382	0.679	VIT_206s0004g00570	Myb-like DNA-binding domain
S6_5918485	6	5918485	0.679	VIT_206s0004g04950	gras family transcription factor
S6_16617284	6	16617284	0.679	VIT_206s0009g03385	protein
S6_2124790	6	2124790	0.643	VIT_206s0004g01730	protein
S6_19254810	6	19254810	0.450	VIT_206s0061g01400	cbf-like transcription factor
S6_19781052	6	19781052	0.450	VIT_206s0080g00085	xylem serine proteinase
S6_745427	6	745427	0.313	VIT_206s0004g00570	Myb-like DNA-binding domain
S6_8314179	6	8314179	0.300	VIT_206s0004g07550	wound-induced protein
S6_10481785	6	10481785	0.300	VIT_206s0009g00310	uncharacterized protein
S6_16617325	6	16617325	0.300	VIT_206s0009g03385	protein
S6_21090110	6	21090110	0.250	VIT_206s0080g01000	momilactone a synthase-like
S7_199350	7	199350	0.508	VIT_207s0141g00330	f-box lrr-repeat protein 17-like
S7_2104933	7	2104933	0.485	VIT_207s0104g01020	oxidoreductase aldo keto reductase family
S7_843696	7	843696	0.355	VIT_207s0151g00280	glutamate binding protein
S7_1847650	7	1847650	0.355	VIT_207s0104g00660	2og-fe oxygenase family protein
S7_3345690	7	3345690	0.353	VIT_207s0005g00700	epoxide hydrolase 2-like
S7_3454258	7	3454258	0.313	VIT_207s0005g00830	subtilisin-like protease-like
S7_277400	7	277400	0.250	intergenic	
S7_1025289	7	1025289	0.250	VIT_207s0151g00630	vicilin-like antimicrobial peptides 2-1-like
S7_9064608	7	9064608	0.250	intergenic	
S7_9064636	7	9064636	0.250	intergenic	
S7_19905664	7	19905664	0.250	VIT_207s0031g03110	f-box protein fbw2
S8_13385726	8	13385726	0.781	VIT_208s0040g02280	protein
S8_14233948	8	14233948	0.679	VIT_208s0040g03280	pentatricopeptide repeat-containing protein chloroplastic-like

S8_16542339	8	16542339	0.508	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_12775962	8	12775962	0.500	VIT_208s0040g01640	protein trf-like 8
S8_16542284	8	16542284	0.500	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_8221364	8	8221364	0.450	VIT_208s0217g00100	pyruvate decarboxylase
S8_10462511	8	10462511	0.313	VIT_208s0058g01100	arm repeat protein
S8_21375645	8	21375645	0.250	intergenic	
S9_19578598	9	19578598	0.632	VIT_209s0018g01960	uncharacterized protein
S9_21838021	9	21838021	0.628	VIT_209s0054g00970	mediator subunit 8
S9_18940862	9	18940862	0.315	VIT_209s0018g01650	ap2-like ethylene-responsive transcription factor at1g16060-like
S9_22903290	9	22903290	0.313	intergenic	
S9_11587262	9	11587262	0.250	intergenic	
S9_13696740	9	13696740	0.250	VIT_209s0070g00480	extensin-like protein
S9_18410499	9	18410499	0.250	VIT_209s0018g01370	serine threonine protein
S9_20922049	9	20922049	0.250	intergenic	
S10_5218775	10	5218775	0.583	VIT_210s0003g03070	beta-ketoacyl-acyl synthase i
S10_592238	10	592238	0.581	VIT_210s0116g01150	protein
S10_740795	10	740795	0.529	VIT_210s0116g01440	probable f-box protein at4g22030-like
S10_17285129	10	17285129	0.508	VIT_210s0071g00770	aspartic proteinase nepenthesin-1-like
S10_939454	10	939454	0.500	VIT_210s0116g01680	ankyrin repeat family protein
S10_9317900	10	9317900	0.500	intergenic	
S10_509756	10	509756	0.450	VIT_210s0116g01030	protein
S10_10455105	10	10455105	0.450	intergenic	
S10_1443637	10	1443637	0.375	VIT_210s0003g00140	ethylene response factor 3
S10_15551359	10	15551359	0.375	VIT_210s0042g01390	pentatricopeptide repeat-containing protein
S10_1676905	10	1676905	0.355	intergenic	
S10_10577248	10	10577248	0.355	VIT_210s0003g05690	protein
S10_1443658	10	1443658	0.313	VIT_210s0003g00140	ethylene response factor 3
S10_1036332	10	1036332	0.250	VIT_210s0116g01770	trna wybutosine-synthesizing protein 2 3 4-like
S10_1036341	10	1036341	0.250	VIT_210s0116g01770	trna wybutosine-synthesizing protein 2 3 4-like
S11_4902361	11	4902361	0.679	VIT_211s0016g05500	transducin wd40 domain-containing protein
S11_1379525	11	1379525	0.500	VIT_211s0016g01720	threonine synthase
S11_13790255	11	13790255	0.313	intergenic	

S11_2440845	11	2440845	0.300	VIT_211s0016g03030	iq domain-containing protein
S11_542859	11	542859	0.250	VIT_211s0016g00540	respiratory burst
S11_18816893	11	18816893	0.250	VIT_211s0052g01090	4-coumarate: ligase
S12_8182780	12	8182780	0.781	VIT_212s0134g00560	uncharacterized gpi-anchored protein at4g28100-like
S12_3110015	12	3110015	0.679	VIT_212s0028g02370	cmv 1a interacting protein 1
S12_4004619	12	4004619	0.628	VIT_212s0028g03270	ethylene response factor 3
S12_19854777	12	19854777	0.500	intergenic	
S12_8095101	12	8095101	0.485	VIT_212s0134g00470	uncharacterized protein loc100853582
S12_20537836	12	20537836	0.375	VIT_212s0035g00920	protein
S12_20698464	12	20698464	0.375	intergenic	
S12_3110087	12	3110087	0.313	VIT_212s0028g02370	cmv 1a interacting protein 1
S12_11779538	12	11779538	0.250	intergenic	
S12_19854849	12	19854849	0.250	intergenic	
S12_21233395	12	21233395	0.250	VIT_212s0035g01400	cytochrome c oxidase biogenesis protein cmc1-like protein
S13_20295609	13	20295609	0.375	VIT_213s0139g00070	disease resistance rpp13-like protein 1-like
S13_23055941	13	23055941	0.375	VIT_213s0064g01150	transducin wd-40 repeat-containing protein
S13_7432619	13	7432619	0.250	intergenic	
S13_11471429	13	11471429	0.250	intergenic	
S13_20061385	13	20061385	0.250	VIT_213s0084g00820	aspartic proteinase nepenthesin-1
S13_21831983	13	21831983	0.250	VIT_213s0064g00300	uncharacterized protein loc100260134
S14_28538026	14	28538026	0.542	VIT_214s0066g02320	abc transporter b family member
S14_23352220	14	23352220	0.508	intergenic	
S14_30257640	14	30257640	0.485	intergenic	
S14_24101486	14	24101486	0.453	VIT_214s0068g00390	alpha beta fold family protein
S14_27846259	14	27846259	0.450	VIT_214s0066g01440	homeodomain leucine zipper protein
S14_26954509	14	26954509	0.355	VIT_214s0066g00440	armadillo beta-catenin-like repeat-containing protein
S14_1176140	14	1176140	0.250	VIT_214s0060g01490	heat shock protein binding
S14_15691893	14	15691893	0.250	VIT_214s0006g00830	uncharacterized protein
S14_20080117	14	20080117	0.250	intergenic	
S14_20693777	14	20693777	0.250	intergenic	
S14_26184787	14	26184787	0.250	VIT_214s0171g00360	uncharacterized protein
S15_14994561	15	14994561	0.583	VIT_215s0048g00840	protein

S15_6678704	15	6678704	0.508	VIT_215s0045g01190	3-hydroxyisobutyryl-coenzyme a expressed
S15_12454802	15	12454802	0.500	VIT_215s0021g01800	hypothetical protein VITISV_037538 [Vitis vinifera]
S15_18433525	15	18433525	0.500	VIT_215s0046g01450	gdsI esterase lipase
S15_19157629	15	19157629	0.400	intergenic	
S15_11266929	15	11266929	0.397	intergenic	
S15_19094920	15	19094920	0.355	VIT_215s0046g02290	atp-dependent helicase brm
S15_15520624	15	15520624	0.250	VIT_215s0048g01390	probable carboxylesterase 8-like
S16_12555471	16	12555471	0.485	intergenic	
S16_20676529	16	20676529	0.450	VIT_216s0098g00290	glutamate synthase 1
S16_11480496	16	11480496	0.400	VIT_216s0022g00440	protein
S16_21375504	16	21375504	0.400	VIT_216s0098g01130	uncharacterized protein
S16_10612281	16	10612281	0.375	intergenic	
S16_746925	16	746925	0.300	intergenic	
S16_7784310	16	7784310	0.300	intergenic	
S16_747013	16	747013	0.250	intergenic	
S16_3436773	16	3436773	0.250	intergenic	
S16_3436816	16	3436816	0.250	intergenic	
S16_10612323	16	10612323	0.250	intergenic	
S16_15282381	16	15282381	0.250	intergenic	
S16_19519997	16	19519997	0.250	VIT_216s0050g02560	cyclic nucleotide-gated ion channel 1-like
S16_21978973	16	21978973	0.250	VIT_216s0098g01900	pectinesterase family protein
S17_14576374	17	14576374	0.583	VIT_217s0053g00110	pentatricopeptide repeat-containing protein at5g66520-like
S17_4602023	17	4602023	0.485	VIT_217s0000g04393	protein
S17_14838883	17	14838883	0.474	intergenic	
S17_2264413	17	2264413	0.400	VIT_217s0000g02480	polcalcine jun
S17_14838896	17	14838896	0.369	intergenic	
S17_1245621	17	1245621	0.313	VIT_217s0000g01680	adenylate kinase 1
S17_9608083	17	9608083	0.264	VIT_217s0000g08410	peroxisomal membrane protein pex14
S17_634159	17	634159	0.250	VIT_217s0000g00910	zinc finger
S17_3249147	17	3249147	0.250	VIT_217s0000g03370	calmodulin binding protein
S17_3748489	17	3748489	0.250	VIT_217s0000g03790	uncharacterized protein
S17_6124870	17	6124870	0.250	VIT_217s0000g05600	short-chain alcohol dehydrogenase

	S18_23509538	18	23509538	0.583	VIT_218s0117g00270	protein
	S18_5652482	18	5652482	0.542	VIT_218s0001g07380	dna-binding protein escarola-like
	S18_4674058	18	4674058	0.450	intergenic	
	S18_1272064	18	1272064	0.400	VIT_218s0001g00320	lysine histidine transporter
	S18_8407320	18	8407320	0.400	VIT_218s0001g10040	uncharacterized protein at4g06744-like
	S18_16151588	18	16151588	0.375	VIT_218s0076g00310	eukaryotic translation initiation factor 5b
	S18_4673988	18	4673988	0.313	intergenic	
	S18_10725515	18	10725515	0.313	VIT_218s0001g12540	maf-like protein
	S18_977553	18	977553	0.250	intergenic	
	S18_5652470	18	5652470	0.250	VIT_218s0001g07380	dna-binding protein escarola-like
	S18_5669859	18	5669859	0.250	intergenic	
	S18_11387001	18	11387001	0.250	VIT_218s0001g13360	auxin-induced protein 5ng4-like
	S19_350268	19	350268	0.679	VIT_219s0014g00330	nadh kinase
	S19_7471796	19	7471796	0.679	VIT_219s0090g01400	acyl- --sterol o-acyltransferase 1-like
	S19_1684608	19	1684608	0.583	VIT_219s0014g01600	uncharacterized protein
	S19_7471892	19	7471892	0.583	VIT_219s0090g01400	acyl- --sterol o-acyltransferase 1-like
	S19_3208699	19	3208699	0.500	intergenic	
	S19_1360860	19	1360860	0.450	VIT_219s0014g01250	tubby-like f-box protein 7-like
	S19_3218568	19	3218568	0.413	intergenic	
	S19_6782112	19	6782112	0.397	VIT_219s0090g00710	rna binding
	S19_8056653	19	8056653	0.375	intergenic	
	S19_17003450	19	17003450	0.369	intergenic	
	S19_3856412	19	3856412	0.355	intergenic	
	S19_10807056	19	10807056	0.355	VIT_219s0015g01940	peroxisome biogenesis protein 5-like
	S19_7059539	19	7059539	0.313	intergenic	
	S19_8876974	19	8876974	0.300	VIT_219s0015g00740	protein plastid movement impaired 2-like
	S19_7443843	19	7443843	0.270	intergenic	
	S19_8924891	19	8924891	0.250	VIT_219s0015g00800	ran-binding protein
	S19_17009000	19	17009000	0.250	intergenic	
C-IV/V vs C-II	S1_2795404	1	2795404	0.664	VIT_201s0011g03130	N-glycosylation site
	S1_12410054	1	12410054	0.464	VIT_201s0026g02680	oxygen evolving enhancer protein 3

S1_12601790	1	12601790	0.440	VIT_201s0026g02740	uncharacterized protein loc100241338
S1_10985517	1	10985517	0.341	VIT_201s0026g01740	snf1-related protein kinase regulatory subunit gamma-1-like
S1_1505501	1	1505501	0.317	VIT_201s0011g01660	vesicle-associated membrane protein
S1_19836023	1	19836023	0.257	VIT_201s0010g02800	ankyrin repeat-containing
S2_4289898	2	4289898	0.627	VIT_202s0025g04730	oxidoreductase activity
S2_3816758	2	3816758	0.524	intergenic	
S2_5277254	2	5277254	0.402	VIT_202s0154g00520	aspartic proteinase nepenthesin-2
S2_17516802	2	17516802	0.402	VIT_202s0087g00270	serine threonine-protein kinase at5g01020-like
S2_7526057	2	7526057	0.401	intergenic	
S2_7363868	2	7363868	0.330	VIT_202s0012g01250	mitochondrial carnitine acylcarnitine carrier-like protein
S2_11176307	2	11176307	0.293	intergenic	
S2_3642174	2	3642174	0.277	intergenic	
S2_15903238	2	15903238	0.276	intergenic	
S2_8634120	2	8634120	0.261	VIT_202s0012g01990	4-hydroxyphenylpyruvate dioxygenase
S2_3268667	2	3268667	0.250	intergenic	
S3_2108561	3	2108561	0.714	intergenic	
S3_1692692	3	1692692	0.687	VIT_203s0038g02440	farnesylated protein
S3_3555389	3	3555389	0.627	VIT_203s0063g00010	uncharacterized protein at4g06744-like
S3_2152144	3	2152144	0.550	VIT_203s0038g03040	protein kinase like protein
S3_8149879	3	8149879	0.500	intergenic	
S3_11401731	3	11401731	0.439	VIT_203s0132g00050	uncharacterized protein loc100245618
S3_8149994	3	8149994	0.402	intergenic	
S3_8149934	3	8149934	0.341	intergenic	
S3_8149942	3	8149942	0.341	intergenic	
S3_1426686	3	1426686	0.339	VIT_203s0038g02070	translocase of chloroplast chloroplastic-like
S3_2031946	3	2031946	0.330	intergenic	
S3_2876578	3	2876578	0.284	VIT_203s0038g03940	monosaccharide-sensing protein 2-like
S3_4068529	3	4068529	0.276	VIT_203s0063g00560	cell number regulator 1
S3_18633065	3	18633065	0.276	intergenic	
S3_3554121	3	3554121	0.257	intergenic	
S4_7025032	4	7025032	0.664	VIT_204s0008g07000	zinc finger ccch domain-containing protein 18-like
S4_22226569	4	22226569	0.548	VIT_204s0044g00940	set domain protein

S4_18007386	4	18007386	0.402	VIT_204s0023g01450	splicing factor u2af large subunit a
S4_714852	4	714852	0.401	VIT_204s0008g00830	nadh dehydrogenase
S4_14140470	4	14140470	0.277	intergenic	
S4_14140549	4	14140549	0.277	intergenic	
S4_1955043	4	1955043	0.276	VIT_204s0008g02380	f-box protein afr
S5_4305132	5	4305132	0.609	VIT_205s0020g02610	duf21 domain-containing protein at4g14240-like
S5_24554829	5	24554829	0.538	VIT_205s0094g01300	polygalacturonase
S5_4385684	5	4385684	0.524	VIT_205s0020g02670	uncharacterized protein
S5_20801876	5	20801876	0.524	intergenic	
S5_23560554	5	23560554	0.439	VIT_205s0094g00250	endochitinase pr4
S5_24567707	5	24567707	0.439	VIT_205s0094g01310	polygalacturonase
S5_11296359	5	11296359	0.413	intergenic	
S5_23557316	5	23557316	0.401	VIT_205s0094g00240	endochitinase pr4
S5_23557227	5	23557227	0.317	VIT_205s0094g00240	endochitinase pr4
S5_8734989	5	8734989	0.257	VIT_205s0049g01430	uncharacterized protein
S6_16617325	6	16617325	0.524	VIT_206s0009g03385	protein
S6_745382	6	745382	0.515	VIT_206s0004g00570	Myb-like DNA-binding domain
S6_7234230	6	7234230	0.464	VIT_206s0004g06510	phosphoesterase family protein
S6_17353686	6	17353686	0.450	VIT_206s0061g00120	beta- -glucanase
S6_687601	6	687601	0.439	VIT_206s0004g00500	ran-binding protein
S6_20920857	6	20920857	0.402	VIT_206s0080g00870	rna recognition motif-containing protein
S6_19254810	6	19254810	0.401	VIT_206s0061g01400	cbf-like transcription factor
S6_12802872	6	12802872	0.376	VIT_206s0009g01190	ubp1-associated protein 2a
S6_8314179	6	8314179	0.341	VIT_206s0004g07550	wound-induced protein
S6_18383816	6	18383816	0.341	intergenic	
S6_14485809	6	14485809	0.298	VIT_206s0009g02160	cellulose synthase
S6_5918485	6	5918485	0.276	VIT_206s0004g04950	gras family transcription factor
S7_3454258	7	3454258	0.714	VIT_207s0005g00830	subtilisin-like protease-like
S7_3454290	7	3454290	0.714	VIT_207s0005g00830	subtilisin-like protease-like
S7_18225497	7	18225497	0.672	intergenic	
S7_843696	7	843696	0.664	VIT_207s0151g00280	glutamate binding protein
S7_20107065	7	20107065	0.627	VIT_207s0031g03220	protein

S7_3345690	7	3345690	0.405	VIT_207s0005g00700	epoxide hydrolase 2-like
S7_9064581	7	9064581	0.402	intergenic	
S7_16327824	7	16327824	0.390	VIT_207s0031g00090	trna-dihydrouridine synthase 1-like
S7_1847650	7	1847650	0.317	VIT_207s0104g00660	2og-fe oxygenase family protein
S7_4391566	7	4391566	0.293	VIT_207s0005g01950	myb-like transcription factor partial
S7_6022869	7	6022869	0.284	intergenic	
S7_2104933	7	2104933	0.284	VIT_207s0104g01020	oxidoreductase aldo keto reductase family
S7_10301672	7	10301672	0.277	intergenic	
S7_252469	7	252469	0.250	intergenic	
S8_14233948	8	14233948	0.598	VIT_208s0040g03280	pentatricopeptide repeat-containing protein chloroplastic-like
S8_11720076	8	11720076	0.369	VIT_208s0040g00760	protein kinase and pp2c-like domain-containing protein
S8_16542324	8	16542324	0.315	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_16542284	8	16542284	0.313	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S8_5893814	8	5893814	0.277	intergenic	
S8_9008840	8	9008840	0.277	intergenic	
S8_10462511	8	10462511	0.276	VIT_208s0058g01100	arm repeat protein
S8_16542339	8	16542339	0.259	VIT_208s0007g02440	aspartic proteinase nepenthesin-2-like
S9_21838021	9	21838021	0.899	VIT_209s0054g00970	mediator subunit 8
S9_18940862	9	18940862	0.679	VIT_209s0018g01650	ap2-like ethylene-responsive transcription factor at1g16060-like
S9_22903290	9	22903290	0.439	intergenic	
S9_19578598	9	19578598	0.401	VIT_209s0018g01960	uncharacterized protein
S9_3107430	9	3107430	0.339	VIT_209s0002g03440	type receptor kinase
S9_2383793	9	2383793	0.330	VIT_209s0002g02610	agglutinin alpha chain
S9_2383800	9	2383800	0.284	VIT_209s0002g02610	agglutinin alpha chain
S9_21881544	9	21881544	0.284	VIT_209s0054g01010	subtilisin-like protease
S9_3565122	9	3565122	0.276	VIT_209s0002g03860	probable disease resistance protein at5g63020-like
S9_2660726	9	2660726	0.256	VIT_209s0002g02930	rna polymerase transcriptional regulation mediator-like protein
S10_939454	10	939454	0.500	VIT_210s0116g01680	ankyrin repeat family protein
S10_1036341	10	1036341	0.401	VIT_210s0116g01770	trna wybutosine-synthesizing protein 2 3 4-like
S10_740795	10	740795	0.350	VIT_210s0116g01440	probable f-box protein at4g22030-like
S10_10577248	10	10577248	0.317	VIT_210s0003g05690	protein
S10_1107440	10	1107440	0.298	intergenic	

S10_15502797	10	15502797	0.277	intergenic	
S11_10541957	11	10541957	0.583	VIT_211s0037g01240	uncharacterized protein
S11_4902361	11	4902361	0.375	VIT_211s0016g05500	transducin wd40 domain-containing protein
S11_18816893	11	18816893	0.277	VIT_211s0052g01090	4-coumarate: ligase
S11_16426263	11	16426263	0.250	intergenic	
S12_20634528	12	20634528	0.781	VIT_212s0035g00990	receptor protein kinase clavata1
S12_20537836	12	20537836	0.714	VIT_212s0035g00920	protein
S12_3110015	12	3110015	0.598	VIT_212s0028g02370	cmv 1a interacting protein 1
S12_8182780	12	8182780	0.515	VIT_212s0134g00560	uncharacterized gpi-anchored protein at4g28100-like
S12_8095101	12	8095101	0.449	VIT_212s0134g00470	uncharacterized protein loc100853582
S12_20698464	12	20698464	0.402	intergenic	
S12_21233395	12	21233395	0.330	VIT_212s0035g01400	cytochrome c oxidase biogenesis protein cmc1-like protein
S12_16586125	12	16586125	0.298	intergenic	
S12_5321359	12	5321359	0.284	VIT_212s0059g00470	uncharacterized protein loc100267070
S12_19854849	12	19854849	0.277	intergenic	
S12_8183444	12	8183444	0.250	VIT_212s0134g00560	uncharacterized gpi-anchored protein at4g28100-like
S13_22875400	13	22875400	0.538	VIT_213s0064g01000	telomerase reverse transcriptase
S13_18603976	13	18603976	0.464	VIT_213s0084g00070	cytochrome p450
S13_23055941	13	23055941	0.402	VIT_213s0064g01150	transducin wd-40 repeat-containing protein
S13_5429593	13	5429593	0.390	VIT_213s0019g04140	chlorophyll a b-binding protein
S13_20061385	13	20061385	0.330	VIT_213s0084g00820	aspartic proteinase nepenthesin-1
S13_9263384	13	9263384	0.313	intergenic	
S13_13521126	13	13521126	0.276	VIT_213s0073g00180	rieske domain containing expressed
S13_667744	13	667744	0.261	VIT_213s0067g01190	glycosyl hydrolase family 9 protein
S13_7432621	13	7432621	0.250	intergenic	
S14_1176140	14	1176140	0.687	VIT_214s0060g01490	heat shock protein binding
S14_2815220	14	2815220	0.439	VIT_214s0128g00120	e3 ubiquitin-protein ligase at16-like
S14_23412945	14	23412945	0.439	VIT_214s0083g01082	gras family transcription factor
S14_20953570	14	20953570	0.401	intergenic	
S14_16084684	14	16084684	0.399	intergenic	
S14_16033454	14	16033454	0.330	VIT_214s0006g00990	xeroderma pigmentosum group c-complementing protein
S14_28538026	14	28538026	0.330	VIT_214s0066g02320	abc transporter b family member

S14_16084682	14	16084682	0.321	intergenic	
S14_23352220	14	23352220	0.315	intergenic	
S14_355324	14	355324	0.313	VIT_214s0060g00360	isopenicillin n epimerase-like isoform 1
S14_16084681	14	16084681	0.295	intergenic	
S14_11601747	14	11601747	0.277	VIT_214s0036g01040	hydrolyzing o-glycosyl
S14_22696881	14	22696881	0.277	intergenic	
S14_26184787	14	26184787	0.277	VIT_214s0171g00360	uncharacterized protein
S14_16031847	14	16031847	0.250	VIT_214s0006g00980	dna mismatch repair protein mlh1
S14_20080117	14	20080117	0.250	intergenic	
S14_20693811	14	20693811	0.250	intergenic	
S14_29303784	14	29303784	0.250	intergenic	
S15_17988354	15	17988354	0.550	VIT_215s0046g00930	ring-h2 finger protein atl21a-like
S15_11266929	15	11266929	0.440	intergenic	
S15_1644882	15	1644882	0.375	VIT_215s0024g00820	protein
S15_18433525	15	18433525	0.300	VIT_215s0046g01450	gdsI esterase lipase
S15_13144458	15	13144458	0.276	VIT_215s0021g02200	structural constituent of nuclear
S15_19157629	15	19157629	0.276	intergenic	
S15_20179402	15	20179402	0.276	VIT_215s0046g03670	malic enzyme
S16_746925	16	746925	0.524	intergenic	
S16_7784310	16	7784310	0.524	intergenic	
S16_11480496	16	11480496	0.439	VIT_216s0022g00440	protein
S16_13468410	16	13468410	0.422	VIT_216s0022g01450	udp-d-glucuronate 4-epimerase 2
S16_10959544	16	10959544	0.375	intergenic	
S16_746979	16	746979	0.277	intergenic	
S16_21375504	16	21375504	0.257	VIT_216s0098g01130	uncharacterized protein
S16_10612323	16	10612323	0.250	intergenic	
S17_4602023	17	4602023	0.422	VIT_217s0000g04393	protein
S17_14576374	17	14576374	0.298	VIT_217s0053g00110	pentatricopeptide repeat-containing protein at5g66520-like
S17_3249138	17	3249138	0.284	VIT_217s0000g03370	calmodulin binding protein
S17_2264413	17	2264413	0.257	VIT_217s0000g02480	polcalcin jun
S17_6124870	17	6124870	0.250	VIT_217s0000g05600	short-chain alcohol dehydrogenase
S18_8407320	18	8407320	0.805	VIT_218s0001g10040	uncharacterized protein at4g06744-like

	S18_10725515	18	10725515	0.515	VIT_218s0001g12540	maf-like protein
	S18_24467798	18	24467798	0.515	intergenic	
	S18_6946494	18	6946494	0.500	intergenic	
	S18_9548907	18	9548907	0.439	VIT_218s0001g11240	protein kinase domain containing expressed
	S18_12911165	18	12911165	0.402	VIT_218s0001g14870	subtilisin-like serine endopeptidase-like protein
	S18_23509538	18	23509538	0.401	VIT_218s0117g00270	protein
	S18_12780814	18	12780814	0.341	VIT_218s0001g14730	prostaglandin e synthase
	S18_24246031	18	24246031	0.341	intergenic	
	S18_10708992	18	10708992	0.294	VIT_218s0001g12520	probable lrr receptor-like serine threonine-protein kinase at2g16250-like
	S18_28168228	18	28168228	0.276	VIT_218s0089g00380	probable carboxylesterase 18-like
	S18_8235190	18	8235190	0.257	intergenic	
	S19_1360860	19	1360860	0.901	VIT_219s0014g01250	tubby-like f-box protein 7-like
	S19_6963413	19	6963413	0.515	VIT_219s0090g00910	pyridoxal phosphate-dependent ybl036c type
	S19_2368764	19	2368764	0.440	VIT_219s0014g02240	ethylene-responsive transcription
	S19_3856412	19	3856412	0.422	intergenic	
	S19_7471796	19	7471796	0.413	VIT_219s0090g01400	acyl- --sterol o-acyltransferase 1-like
	S19_17003493	19	17003493	0.376	intergenic	
	S19_6778200	19	6778200	0.298	intergenic	
	S19_5340008	19	5340008	0.293	VIT_219s0014g05010	uncharacterized protein
	S19_2109644	19	2109644	0.284	VIT_219s0014g01910	uncharacterized protein
	S19_8924891	19	8924891	0.277	VIT_219s0015g00800	ran-binding protein
	S19_17009000	19	17009000	0.277	intergenic	
	S19_1684608	19	1684608	0.276	VIT_219s0014g01600	uncharacterized protein
C-I vs C-II	S1_4360266	1	4360266	0.643	VIT_201s0011g04780	uncharacterized protein at1g66480-like
	S1_1888193	1	1888193	0.515	VIT_201s0011g02170	Glycosyl hydrolase family 9
	S1_336420	1	336420	0.450	VIT_201s0011g00280	feronia receptor-like kinase
	S1_11697553	1	11697553	0.375	intergenic	
	S1_1505501	1	1505501	0.317	VIT_201s0011g01660	vesicle-associated membrane protein
	S2_14008243	2	14008243	0.402	intergenic	
	S2_3268667	2	3268667	0.400	intergenic	
	S2_7363868	2	7363868	0.330	VIT_202s0012g01250	mitochondrial carnitine acylcarnitine carrier-like protein

S2_14008197	2	14008197	0.277	intergenic	
S2_15903238	2	15903238	0.276	intergenic	
S3_8149938	3	8149938	0.481	intergenic	
S3_3555389	3	3555389	0.464	VIT_203s0063g00010	uncharacterized protein at4g06744-like
S3_1895945	3	1895945	0.440	VIT_203s0038g02670	protein
S3_6406887	3	6406887	0.397	VIT_203s0091g00160	p27-like protein
S4_7025032	4	7025032	0.550	VIT_204s0008g07000	zinc finger ccch domain-containing protein 18-like
S4_22226569	4	22226569	0.548	VIT_204s0044g00940	set domain protein
S4_11466696	4	11466696	0.402	intergenic	
S4_1063770	4	1063770	0.298	VIT_204s0008g01290	gata transcription factor 22
S4_4192762	4	4192762	0.250	VIT_204s0008g04750	3-hydroxybenzoate 6-hydroxylase
S5_23557227	5	23557227	0.601	VIT_205s0094g00240	endochitinase pr4
S5_23557316	5	23557316	0.361	VIT_205s0094g00240	endochitinase pr4
S5_5708044	5	5708044	0.339	VIT_205s0020g04020	uncharacterized protein
S5_23891717	5	23891717	0.310	VIT_205s0094g00530	protein iq-domain 14
S5_23560554	5	23560554	0.256	VIT_205s0094g00250	endochitinase pr4
S6_7234230	6	7234230	0.464	VIT_206s0004g06510	phosphoesterase family protein
S6_687601	6	687601	0.439	VIT_206s0004g00500	ran-binding protein
S6_2124790	6	2124790	0.380	VIT_206s0004g01730	protein
S6_16617284	6	16617284	0.293	VIT_206s0009g03385	protein
S6_7072643	6	7072643	0.276	VIT_206s0004g06290	tetratricopeptide repeat-containing protein
S6_14485809	6	14485809	0.261	VIT_206s0009g02160	cellulose synthase
S6_10481785	6	10481785	0.256	VIT_206s0009g00310	uncharacterized protein
S6_14351267	6	14351267	0.250	VIT_206s0009g02040	pectin-related protein
S6_19781052	6	19781052	0.250	VIT_206s0080g00085	xylem serine proteinase
S6_19781085	6	19781085	0.250	VIT_206s0080g00085	xylem serine proteinase
S7_3454290	7	3454290	0.422	VIT_207s0005g00830	subtilisin-like protease-like
S7_16910501	7	16910501	0.353	intergenic	
S7_20107065	7	20107065	0.284	VIT_207s0031g03220	protein
S7_9064636	7	9064636	0.277	intergenic	
S7_20454713	7	20454713	0.276	VIT_207s0130g00170	transmembrane clptm1 family protein
S7_19617272	7	19617272	0.256	VIT_207s0031g02930	ammonium transporter amt2

S8_12775962	8	12775962	0.627	VIT_208s0040g01640	protein trf-like 8
S8_13385726	8	13385726	0.598	VIT_208s0040g02280	protein
S8_9008840	8	9008840	0.277	intergenic	
S9_2660726	9	2660726	0.439	VIT_209s0002g02930	rna polymerase transcriptional regulation mediator-like protein
S9_3107430	9	3107430	0.339	VIT_209s0002g03440	type receptor kinase
S9_20922046	9	20922046	0.330	intergenic	
S9_2383800	9	2383800	0.284	VIT_209s0002g02610	agglutinin alpha chain
S9_2660764	9	2660764	0.276	VIT_209s0002g02930	rna polymerase transcriptional regulation mediator-like protein
S9_3565122	9	3565122	0.276	VIT_209s0002g03860	probable disease resistance protein at5g63020-like
S9_18410499	9	18410499	0.276	VIT_209s0018g01370	serine threonine protein
S9_887273	9	887273	0.261	intergenic	
S10_15502797	10	15502797	0.574	intergenic	
S10_15551359	10	15551359	0.402	VIT_210s0042g01390	pentatricopeptide repeat-containing protein
S10_134839	10	134839	0.400	intergenic	
S10_4844940	10	4844940	0.380	VIT_210s0003g02750	magnesium transporter -like family protein
S10_5489212	10	5489212	0.339	VIT_210s0003g03300	uncharacterized protein loc100265752
S10_592238	10	592238	0.322	VIT_210s0116g01150	protein
S10_1676905	10	1676905	0.293	intergenic	
S10_10455105	10	10455105	0.250	intergenic	
S11_542859	11	542859	0.375	VIT_211s0016g00540	respiratory burst
S11_1379525	11	1379525	0.313	VIT_211s0016g01720	threonine synthase
S12_20634528	12	20634528	0.485	VIT_212s0035g00990	receptor protein kinase clavata1
S12_20698434	12	20698434	0.256	intergenic	
S13_9034682	13	9034682	0.439	VIT_213s0074g00730	protein kinase g11a-like
S13_23887943	13	23887943	0.397	VIT_213s0156g00140	e3 ubiquitin-protein ligase ring1-like
S13_23055962	13	23055962	0.330	VIT_213s0064g01150	transducin wd-40 repeat-containing protein
S13_7432619	13	7432619	0.250	intergenic	
S13_20271011	13	20271011	0.250	intergenic	
S13_22417971	13	22417971	0.250	VIT_213s0064g00670	photosystem ii 5 kda protein
S14_20953570	14	20953570	0.401	intergenic	
S14_16084683	14	16084683	0.299	intergenic	
S14_27846259	14	27846259	0.299	VIT_214s0066g01440	homeodomain leucine zipper protein

S14_1176140	14	1176140	0.259	VIT_214s0060g01490	heat shock protein binding
S14_20693811	14	20693811	0.250	intergenic	
S15_17988354	15	17988354	0.577	VIT_215s0046g00930	ring-h2 finger protein atl21a-like
S15_12454802	15	12454802	0.548	VIT_215s0021g01800	hypothetical protein VITISV_037538 [Vitis vinifera]
S15_16029252	15	16029252	0.515	VIT_215s0048g01895	protein seuss-like 2
S15_19094920	15	19094920	0.422	VIT_215s0046g02290	atp-dependent helicase brm
S15_14994561	15	14994561	0.376	VIT_215s0048g00840	protein
S15_1644882	15	1644882	0.375	VIT_215s0024g00820	protein
S15_20179402	15	20179402	0.276	VIT_215s0046g03670	malic enzyme
S15_15241869	15	15241869	0.257	VIT_215s0048g01120	subtilisin-like protease-like
S16_3077361	16	3077361	0.439	VIT_216s0039g02700	protein
S16_3436773	16	3436773	0.376	intergenic	
S16_10612278	16	10612278	0.375	intergenic	
S16_3436816	16	3436816	0.277	intergenic	
S16_16848612	16	16848612	0.277	intergenic	
S16_11218133	16	11218133	0.276	VIT_216s0022g00320	nitric oxide synthase 1
S16_1190932	16	1190932	0.261	VIT_216s0039g01570	zinc finger ccch domain-containing protein 56-like
S16_16066770	16	16066770	0.261	intergenic	
S16_6539729	16	6539729	0.256	VIT_216s0013g00870	zing finger transcription factor pei1
S16_17830632	16	17830632	0.256	intergenic	
S17_14838896	17	14838896	0.399	intergenic	
S17_503935	17	503935	0.376	VIT_217s0000g00750	uncharacterized protein loc100854620
S17_15582719	17	15582719	0.313	VIT_217s0053g00600	tetratricopeptide repeat-containing protein
S17_70902	17	70902	0.295	intergenic	
S17_3249138	17	3249138	0.284	VIT_217s0000g03370	calmodulin binding protein
S17_5369306	17	5369306	0.277	intergenic	
S18_6946494	18	6946494	0.500	intergenic	
S18_1431955	18	1431955	0.405	VIT_218s0001g00570	pentatricopeptide repeat-containing protein
S18_24467798	18	24467798	0.339	intergenic	
S18_12263043	18	12263043	0.315	VIT_218s0001g14250	uncharacterized protein
S18_9548907	18	9548907	0.277	VIT_218s0001g11240	protein kinase domain containing expressed
S18_28197184	18	28197184	0.259	intergenic	

S19_6963413	19	6963413	0.515	VIT_219s0090g00910	pyridoxal phosphate-dependent ybl036c type
S19_10807056	19	10807056	0.422	VIT_219s0015g01940	peroxisome biogenesis protein 5-like
S19_2231401	19	2231401	0.405	VIT_219s0014g02070	udp-glycosyltransferase 79b9-like
S19_8056653	19	8056653	0.402	intergenic	
S19_1360860	19	1360860	0.299	VIT_219s0014g01250	tubby-like f-box protein 7-like
S19_7444224	19	7444224	0.284	intergenic	
S19_13250162	19	13250162	0.276	intergenic	
S19_8246853	19	8246853	0.261	VIT_219s0015g00260	mitochondrial import inner membrane translocase subunit tim50
S19_8876945	19	8876945	0.261	VIT_219s0015g00740	protein plastid movement impaired 2-like
