Genetic Diversity and Association Study of Aromatics in Grapevine

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ABSTRACT. Monoterpenoid metabolism and aroma compounds are influenced by genetic characteristics. Linalool, α -terpineol, nerol, and geraniol are primary monoterpenoids that have previously been studied in grape (*Vitis vinifera*) berries. Previous studies were restricted by the lack of relevant studies investigating population structure and the regulatory mechanism underlying monoterpenoid synthesis. In this study, a total of 1133 alleles were amplified, with each locus having on average 6.06 alleles. We also assessed the genetic variability among the genotypes based on 187 microsatellite primer pairs amplified in 96 grape genotypes. The results of the phylogenetic tree analysis showed that the grapevine accessions grouped into five genetic clusters that largely coincided with the recognized species classification and the result of principal coordinates analysis (PCoA). The molecular characterization of these accessions provides insight into genetic diversity, population structure, and linkage disequilibrium (LD) in grapevines. A total of 51 quantitative trait loci (QTLs) were detected that were significantly associated with linalool, α -terpineol, nerol, and geraniol. We found that *Deoxyxylulose phosphate synthase (DXS)* was located in the region UDV060 on linkage group (LG) 5, whereas *Farnesyl diphosphate synthase (FPPS)* and *Hydroxymethylbutenyl diphosphate reductase (HDR)* were located in the VLG19-I-1 and VLG3-A-1 regions, respectively. These novel QTLs will potentially assist in the screening of aroma compounds in grapevines.

Flavor and aroma compounds belong to the large group of secondary metabolites in grapevine berries (Lund and Bohlmann, 2006). Monoterpenoids are also responsible for aroma development in these berries, with the amount of monoterpenoids present substantially affecting aromatic characteristics of grapevines. Linalool, α -terpineol, nerol, and geraniol are major organic aromatic volatile compounds found in different groups (Mateo and Jimenez, 2000). Recently, aroma compounds have been the subject of many peer-reviewed research articles (Chacón et al., 2012; Chang et al., 2014; Ghaste et al., 2015; Maoz et al., 2016). Grape genetics, genomics studies, and simple sequence repeat (SSR) analysis have provided an efficient means of assessing genetic diversity and population structure in *Vitis* species. Huang et al. (2011) used 145 SSR primer pairs to compare the loci of ‘Cabernet Sauvignon’ (*Vitis vinifera*) and ‘Riesling’ (*V. vinifera*) grapevines, with the results showing that 70 loci were heterozygous in at least one cultivar, whereas 72 were homozygous in both cultivars. Marrano et al. (2015) reported the genetic diversity, relationships, and population structure of 80 grapevine cultivars and 21 *Vitis sylvestris* accessions that originated from central Asia. The expanded coverage of the grapevine genetic structure in different areas has facilitated worldwide use of grapevine germplasm for diversification of the cultivated gene pool. However, despite these previous studies on the genetic diversity and structure of grapevine, further research is still needed to understand

grapevine population structures. The methylerythritol phosphate (MEP) and mevalonate (MVA) pathways are the main monoterpene biosynthesis pathways in plants (Bohlmann and Keeling, 2008). The biosynthesis of flavor compounds has been shown to occur via the MEP pathway in berries (Luan and Wust, 2002). Several monoterpene synthases have been functionally catalyzed during monoterpeneol biosynthesis including linalool, α -terpineol, nerol, and geraniol. The early pathway genes are *DXS*, *DXS1*, *Deoxyxylulose phosphate reductoisomerase*, and *HDR*. *FPPS* and *Geranyl diphosphate synthase* are middle pathway genes, and *Linalool/nerolidol synthase*, *α -Terpineneol synthase*, *E-a-Bergomotene synthase*, and *Germacrene D synthase* are late pathway genes (Martin et al., 2012). These genes are involved in catalyzing monoterpeneol biosynthesis at different stages in the MEP and MVA pathways, with the expression of some of them correlating with flavor compound accumulation (Martin et al., 2012).

In recent years, genome-wide association studies (GWAS) have gained preeminence (Atwell et al., 2010). Some crops and fruit have also been studied using LD analysis to infer the evolutionary history of species (Barnaud et al., 2006, 2010; Jannoo et al., 1999). Cultivated grapevine has previously been examined with long-range LD (Barnaud et al., 2006), making a GWAS feasible. GWAS is widely employed in QTL analyses in crops. GWAS has previously been used to examine verticillium wilt (*Verticillium dahliae*) resistance in cotton (*Gossypium hirsutum*) based on 158 cotton germplasm accessions (Zhao et al., 2014). Jun et al. (2008) reported that Satt571, Satt551, and Satt431 were significantly associated with soybean (*Glycine max*) seed protein content by GWAS. The results of a peach GWAS investigating pomological traits indicated three significant marker-trait associations based on 40 SSR markers in 94 peach (*Prunus persica*) cultivars (Forcada et al., 2013). A GWAS is, therefore, an effective means of analyzing

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in depth the relationship between markers and traits. In grapevine, the colocalization of *DXS* and the QTLs on LG 5 for aroma compound levels indicated that *DXS* functions in regulating metabolic flux through the MEP pathway (Battilana et al., 2009). Subsequent research further confirmed that the function of *DXS* was effected through polymorphisms in the gene that potentially regulated and controlled terpenoid metabolism in grapevine (Battilana et al., 2011).

The aim of this investigation was to genotype a population of 96 grapevine germplasm accessions using genome-wide molecular markers and to explore the genetic structure and functional QTLs' association with aroma production in these grapevine accessions.

Materials and Methods

Plant material and phenotypic evaluation

The plant material consisted of 96 grapevine cultivars collected from the Shenyang Agriculture University in Shenyang (lat. 41°49'24"N, long. 126°33'41"E), Liaoning Province, China. This included five species under the genus *Vitis* namely *V. vinifera*, *V. vinifera* × *V. labrusca*, *V. vinifera* × *V. amurensis*, *V. amurensis*, and *V. labrusca* (Supplemental Table 1), with the accessions selected to maximize flavor diversity. Berries were sampled when they were fully ripe mainly in Sept. 2014 and 2015 (sampling timing according to the berry

maturity features among cultivars), and 300 g of each sample was stored at −80 °C for monoterpenoid analysis using gas chromatography–mass spectrometry (GC-MS). Levels of linalool, terpineol, nerol, and geraniol were evaluated using solid-phase microextraction according to the method of Wu et al. (2009). The GC-MS oven program was as follows: step 1: 60 °C for 3 min; step 2: 12 °C·min^{−1} to 100 °C; step 3: 4 °C·min^{−1} to 210 °C; and step 4: 210 °C for 3 min. The GC-MS detector (7890A-5795C; Agilent, Santa Clara, CA) was scanned within a mass range of m·z^{−1} 30–500 amu. It was equipped with a VF-max column (30 m × 0.25 mm × 0.25 μm, Agilent), and helium (flow rate of 1.0 mL·min^{−1}) was used as the carrier gas. Mass spectra were retrieved using the NIST11 spectral library. A calibration curve was obtained using a neutral grape 'Tenzan' (*V. vinifera*); grapes of a similar size were added with linalool (25 μg·kg^{−1}), α-terpineol (25.1 μg·kg^{−1}), nerol (25.2 μg·kg^{−1}), and geraniol (25.1 μg·kg^{−1}) (Tokyo Chemical Industry, Tokyo, Japan) dissolved in MilliQ (Millipore, Billerica, MA) water and ethanol (1:1, v/v) to obtain a final concentration of 350 μg·kg^{−1} (six scores) and to control the linearity of the curve up to 1 μg·kg^{−1}.

DNA extraction and polymerase chain reaction

Genomic DNA was extracted from 300 mg of fresh young leaves from the shoot tips of individual vines in the experimental field using the modified cetyltrimethyl ammonium bromide method described by Hanania et al. (2004). DNA was quantified using electrophoresis on 0.8% agarose gels with lambda DNA as a standard (Guo et al., 2014).

Among the 713 pairs of SSR primers used in this experiment, 375 primer pairs were already published at the National Center for Biotechnology Information (NCBI, Bethesda, MD), and 338 pairs were designed by our group (Supplemental Table 2). All primers were uniformly distributed across the genome. Finally, we selected 187 pairs of SSR primers with clear polymorphic bands for use in this study. Polymerase chain reaction (PCR) reactions were carried out in a total volume of 10 μL comprising 10 ng of genomic DNA, 5 μL Premix Ex Taq Version 2.0 (Takara, Tokyo, Japan), and forward primer: 5 μM, reverse primer: 5 μM then add double distilled water (ddH₂O) to 10 μL. The PCR amplification was carried out according to the Premix Ex Taq Version 2.0 manufacturer's instructions. The amplification products were separated by electrophoresis on silver-stained 5% polyacrylamide gels run in 0.5× TBE buffer.

Statistical analysis

GENETIC DIVERSITY. The genetic diversity, number of alleles, heterozygosity, frequency of major alleles, and polymorphic information content of SSR markers were estimated using PowerMarker version 3.25 (Guo et al., 2007). The genetic variation was calculated using GenAlEx version 6.5 (Peakall and Smouse, 2012).

GENETIC STRUCTURE. STRUCTURE version 2.3.4 (Pritchard et al., 2000a) was used to sort individuals into ΔK clusters based on their genetic similarity. We ran STRUCTURE under the "admixture model" with a burn-in period of 1 × 10⁴ followed by 1 × 10⁵ replications of Markov chain Monte Carlo. The number of presumed clusters (K) was set from 2 to 10, and the analysis was repeated five times. Phylogenetic analysis

Fig. 1. The frequency distribution of linalool, α-terpineol, nerol, and geraniol concentrations ratings in 2014 (gray bars) and 2015 (white bars). Phenotypic variations in aroma compounds were evaluated using GC-MS among the 96 grapevine accessions.

Fig. 2. Diagrams for (A) lnP(D) and (B) ΔK of the grapevine lines subdivided into five groups based on 1133 alleles from 187 SSR primer pairs amplified in 96 individuals. K = number of genetic clusters, lnP(D) and ΔK = to determine the best K.

LINKAGE DISEQUILIBRIUM AND ASSOCIATION ANALYSIS. Kinship coefficients and ancestry coefficients (Q-matrix) were used as covariates for the association studies general linear model constructed using STRUCTURE version 2.3.4 (Evanno et al., 2005; Pritchard et al., 2000b). LD analysis was estimated using Tassel 5.0 software (Bradbury et al., 2007). The LD plot was constructed using SPSS software (version 18.0.4; IBM Corp., Armonk, NY). The general linear model was combined with the Q-matrix to obtain association results using Tassel 5.0 software.

accessions from P1, P2, and P3 could not be completely separated indicating that these genetic clusters have a similar genetic background (Aradhya et al., 2003). The results were consistent with both the phylogenetic analysis and population structure analysis. Many *V. vinifera* species were found in P1 and P2, whereas P3 mainly consisted of the ‘Concord’ and some *V. vinifera* × *V. labrusca* hybrids. P4 mainly consisted of *V. vinifera* × *V. amurensis*, whereas P5 encompassed the *Vitis amurensis* pedigree including *V. vinifera* × *V. amurensis* cultivars such as Beijinghong and Zuoyouhong that were bred by the Chinese Academy of Agricultural Sciences (Fig. 3). Human selection and complex pedigrees are the major factors influencing the genetic structure of accessions (Aradhya et al., 2003; Myles et al., 2011). The genetic distance among different clusters in this study ranged from 0.0720 (between P1 and P2) to 0.6554 (between P3 and P5), and the genetic identity ranged from 0.5192 (between P3 and P5) to 0.9305 (between P1 and P2). There were greater genetic distance and lower genetic identity between P5 and the other genetic clusters (Table 1). These results indicate that *V. amurensis* was most distantly related to the other species, consistent with the study by Wen et al. (2011).

LINKAGE DISEQUILIBRIUM AND ASSOCIATION STUDY. LD decay was estimated by analyzing the kinship coefficients (r^2) between each pair of markers. The relationships between r^2 and genetic distance (centimorgans) for the 96 grapevine accessions are shown in Supplemental Fig. 3. As expected, the r^2 declined as the genetic distance increased. However, the plot also indicated a rapid decay of LD in grapevine, with the r^2 values declining to around 0.1 within 40–50 cM. Conversely, Barnaud et al. (2006) found that the r^2 values declined to around 0.1 within 5–10 cM in some cultivate grapevines. This rate of decay is even more rapid than that observed in this study and is primarily due to the use of different accessions.

A total of 51 QTLs detected were significantly associated with aroma (Table 2). This study identified 6 QTLs related to linalool that were

Table 2. A total of 51 quantitative trait loci (QTLs) detected were significantly associated with linalool, α -terpineol, nerol, and geraniol in 96 grapevines in 2014 and 2015. The general linear model was combined with the ancestry coefficients (Q-matrix) to obtain association results using Tassel [version 5.0 (Bradbury et al., 2007)]. The value of p-Marker and Rsq-Marker may assist in identifying the relationship between QTLs and aroma.

Aromatic substance and QTLs	Yr	Linkage group	Position (M) ^z	p-Marker ^y	Rsq-Marker ^x
Linalool					
UDV060	2014	5	4.4	5.89E-05**	0.5364
UDV060	2015	5	4.4	9.08E-06**	0.5722
UDV011	2014	7	3.1	0.0035**	0.3207
UDV011	2015	7	3.1	0.0063**	0.3082
VLG107	2014	1	5.8	0.0137*	0.3099
VLG107	2015	1	5.8	0.0094**	0.3238
VLG19-I-1	2014	19	8.5	0.0013**	0.5849
VLG19-I-1	2015	19	8.5	0.0414*	0.6782
VLG5-F-1	2014	5	4.8	0.0331*	0.1195
VVIP17A	2015	19	0.2	0.0107*	0.4458
α-Terpineol					
VLG107	2014	1	5.8	5.37E-05**	0.4099
VLG107	2015	1	5.8	0.0024**	0.3646
VLG17-D-1	2014	17	3.5	0.0029**	0.3829
VLG17-D-1	2015	17	3.5	0.0267*	0.3504
VLG5-H-1	2014	5	7.5	0.0118*	0.3262
VLG5-F-1	2014	5	5.5	0.0167*	0.1299
VVS29	2014	1	1	0.0319*	0.1427
UDV011	2014	7	3.1	0.0322*	0.2522
UDV005	2014	18	14.5	0.0495*	0.182
VMC3G9	2015	1	7.6	0.0016**	0.2622
VMC2B3	2015	1	18.2	0.0189*	0.2529
VLG16-I-1	2015	16	8.5	0.0417*	0.2618
Nerol					
VVIC72	2014	1	1.8	1.97E-09**	0.4872
VVIC72	2015	1	1.8	2.16E-08**	0.5741
VMC16D4	2014	5	16.5	0.0003**	0.5498
VMC16D4	2015	5	16.5	8.36E-06**	0.5719
VVIP17A	2014	19	0.2	0.0004**	0.5794
VVIP17A	2015	19	0.2	1.76E-06**	0.6694
VLG5-U-1	2014	5	20.5	0.0004**	0.4857
VLG5-U-1	2015	5	20.5	5.1E-06**	0.6152
VLG3-K-1	2014	3	10.5	0.0008**	0.5129
VLG3-K-1	2015	3	10.5	5.01E-06**	0.6711
VVIN52	2014	16	0.8	0.0016**	0.6129
VVIN52	2015	16	0.8	0.0002**	0.585
VLG2-E-1	2014	2	4.5	0.0018**	0.2506
VLG2-E-1	2015	2	4.5	0.0005**	0.3883
VLG5-F-1	2014	5	5.5	0.0048**	0.1814
VLG5-F-1	2015	5	5.5	0.0034**	0.3208
VMC6C10	2014	14	22	0.0331*	0.5361
VMC6C10	2015	14	22	0.0054**	0.1909
VMC8C2	2014	2	17.5	0.0037**	0.2791
VMCNG2E1	2014	4	5.3	0.0056**	0.3245
VMCNG4B9	2014	6	18.5	0.0102*	0.2688
VMC8E6	2014	13	22.5	0.0221*	0.2688
UDV123	2014	14	8.5	0.0433*	0.0872
VLG6-E-1	2014	6	4.5	0.0498*	0.2607
VMCNG2H2-2	2015	8	7.2	0.0005**	0.6602
VLG2-S-1	2015	2	18.5	0.0014**	0.2808
VLG6-D-1	2015	6	3.5	0.0015**	0.3056
VLG6-P-1	2015	6	15.5	0.0116*	0.5675
VMC6B11	2015	2	8.1	0.0218*	0.2902

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intensively distributed on chromosomes LG1, LG5, LG7, and LG19. On LG1, LG 5, LG7, LG13, LG16, LG17, and LG18, we identified 9 QTLs associated with α -terpineol. We also found 22 and 14 QTLs associated with nerol and geraniol, respectively. In this study, many QTLs were identified in both years, whereas others were detected only in the first year. Martin et al. (2012) has previously summarized the correlations between the transcript levels of genes associated with the MEP and MVA pathways and reported the relationships between monoterpene accumulation and the transcript levels of early terpenoid pathway genes. We can conclude here that the three markers UDV060, VLG19-I-1, and VLG3-A-1 were found in close proximity to the genes that correlated with aroma on LG5, LG19, and LG3, respectively (Fig. 4). All position information for QTLs and genes discussed in this study was obtained from NCBI and the Grape Genome Browser. Doligez et al. (2006) detected a major QTL for linalool, nerol, and geraniol contents on LG 5 in the interval between VrZAG79 and VVC6. Monoterpene content was previously found to be significantly associated with *DXS* (LOC100249323) in *V. riparia* and with VrZAG47 in ‘Moscato Bianco’ (Battilana et al., 2009). We found that *DXS* was nearest to UDV060 on LG 5 and that the QTLs were also located in the interval between VrZAG79 and VVC6 (Fig. 4A). *DXS* was 0.6 M distant from UDV060, 3.5 M from VVC6, 2.1 M from VrZAG79, and 0.7 M from VrZAG47. Emanuelli et al. (2010) found an association between *DXS* and monoterpene levels in grapevine, whereas Sun et al. (2014) reported that terpene accumulation was related to *DXS* transcript profiles in developing ‘Alexandria’ grapes (*V. vinifera*). In this study, UDV060 was shown to be related to monoterpene content and significantly associated with linalool (explained by 53.64% and 57.22% of the total variation in 2014 and 2015, respectively). Our results regarding the correlation between *DXS* and monoterpene content are, therefore, consistent with those previously reported. We also found the specific monoterpenoids that were potentially associated with *DXS* in grapevine. Other studies did not detect a significant increase in *DXS* transcript abundance associated with increasing monoterpene levels during berry development in grapevine and, therefore, suggested that increases in monoterpenoids were caused by additional isopentenyl diphosphate precursors from the MVA pathway (Martin et al., 2012). *FPPS* (LOC100232975) was located close to VLG19-I-1 (0.4 M distant from *FPPS*) (Fig. 4B), but its transcript level remained unchanged during berry development (Martin et al., 2012). VLG19-I-1 related to monoterpene content and significantly associated with linalool (explained by 58.49% and 67.82% of the total variation in 2014 and 2015, respectively). To date, *FPPS* has not been reported to function in monoterpene

Table 2. Continued.

Aromatic substance and QTLs	Yr	Linkage group	Position (M) ^z	p-Marker ^y	RsQ-Marker ^x
VLG102	2015	1	2.8	0.0297*	0.1016
VLG19-D-1	2015	19	3.5	0.0445*	0.229
Geraniol					
UDV041	2014	5	6.5	0.0290*	0.3062
UDV041	2015	5	6.5	0.0003**	0.4264
VLG4-L-1	2014	4	11.5	0.0452*	0.1819
VLG4-L-1	2015	4	11.5	0.0387*	0.1921
VMC6D12	2014	9	4	0.0474*	0.2748
VMC6D12	2015	9	4	0.0006**	0.3959
VLG3-A-1	2014	3	5	0.0056**	0.3321
VLG3-A-1	2015	3	5	0.0026**	0.5026
VLG5-F-1	2014	5	5.5	0.0010**	0.1922
VLG5-C-1	2014	5	2.5	0.0023**	0.4235
VMCNG2E1	2014	4	5.3	0.0102*	0.2606
VLG5-G-1	2014	5	6.5	0.0278*	0.2414
UDV011	2014	7	3.1	0.0474*	0.2482
UDV127	2015	9	17.8	0.0007**	0.2894
VLG5-F-1	2015	5	5.5	0.0065**	0.1576
VVIV04	2015	7	17.5	0.0069**	0.3038
VMC6B11	2015	2	8.1	0.0182*	0.3037
VLG107	2015	1	5.8	0.0390*	0.2776

*, **Significant at $P < 0.05$ or 0.01 , respectively.

^zChromosome location of QTLs.

^ySignificance level of markers.

^xTotal explained phenotypic variation.

metabolism. However, it has been shown that the MEP pathway is the dominant route for the biosynthesis of monoterpene substrates in the grape berry (Luan and Wust, 2002). As *FPPS* is involved in the subordinate MVA pathway, it could be assumed that monoterpene biosynthesis would be less affected by changes in the expression of *FPPS*. However, as *FPPS* is the only middle terpenoid pathway enzyme in the MVA pathway, its function in monoterpene biosynthesis should not be ignored. We also need to consider the possibility of complex gene interactions in both pathways. The *HDR* (LOC100267479) synthase was identified close to VLG3-A-1 (0.3 M distant from *HDR*) and was significantly associated with geraniol (explained by 33.21% and 50.26% of the total variation in 2014 and 2015, respectively) (Fig. 4C). In addition, *HDR* transcript levels increased significantly during berry development suggesting that it may also be associated with monoterpene biosynthesis in grapevine (Wen et al., 2015). Sun et al. (2014) also confirmed a positive correlation between the transcript profile of *HDR* and monoterpene accumulation. Research has shown that the expression profiles of *HDR* and *FPPS* could serve as biomarkers for monoterpene-glycoside accumulation during berry development (Martin et al., 2010). Taken together, these results suggest that *HDR* may play an important role in monoterpene metabolism. Whereas few articles have, to date, been devoted to understanding the roles of *FPPS* and *HDR*, their functions in monoterpene biosynthesis should be further investigated.

In summary, this study identified five genetic clusters that were consistent with species classification and mating system. We also used a GWAS to identify three QTLs that lie close to the functional genes associated with aroma compounds. These novel QTLs may contribute to further association studies and

Fig. 4. Position of SSR markers and genes on the grapevine chromosome: (A) chromosome 5, (B) chromosome 19, and (C) chromosome 3. VVC6, VAZAG47, and VrZAG79 were previously found to be significantly associated with monoterpene content in close proximity to the genes in this study. *Deoxyxylulose phosphate synthase (DXS)*, *Farnesyl diphosphate synthase (FPPS)*, and *Hydroxymethylbutenyl diphosphate reductase (HDR)* have been functionally catalyzed during monoterpenol biosynthesis.

supply marker candidates for marker-assisted selection of aroma compounds in grapevine.

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Supplemental Fig. 1. Main weather parameters of 2014 and 2015 of Shenyang county, Liaoning province, China. The weather parameters include average temperature, rainfall, and sunshine hours (data provided by China Meteorological Data Sharing Service System).

Supplemental Fig. 2. Principal coordinate analysis (PCoA) of 96 grapevine accessions. The different shapes represent the five populations based on the 187 SSR loci. The first and second principal coordinates account for 7.07% and 5.34% of the total variation, respectively.

Supplemental Fig. 3. The pattern of linkage disequilibrium (LD) for 187 SSR loci indicating correlations of allele frequencies (r^2) value against genetic distance (in cM) between all loci pairs in all 96 grapevine accessions. The horizontal line in the plot indicates $r^2 = 0.1$.

Supplemental Table 1. Sources and cultivar type of 96 grapevines. This included five species/hybrids under the genus *Vitis* namely *V. vinifera*, *V. vinifera* *V. labrusca*, *V. vinifera* *V. amurensis*, *V. amurensis*, and *V. labrusca*.

Code	Cultivar or line	Source ²	Cultivar type	Species
1	Venus seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
2	Suffolk Red	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
3	Centennial Seedless	USA	Introduced	<i>V. vinifera</i>
4	Christmas Rose	USA	Introduced	<i>V. vinifera</i>
5	Autumn Black	USA	Introduced	<i>V. vinifera</i>
6	Red Globe	USA	Introduced	<i>V. vinifera</i>
7	LN333	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
8	Yatomi Rosa	JPN	Introduced	<i>V. vinifera</i>
9	Emerald Seedless	USA	Introduced	<i>V. vinifera</i>
10	Crimson Seedless	USA	Introduced	<i>V. vinifera</i>
11	Cayuga white	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
12	Canadice Seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
13	Tamina	ROU	Introduced	<i>V. vinifera</i> .
14	Lakemont Seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
15	Exotic	USA	Introduced	<i>V. vinifera</i>
16	Thompson Seedless	USA	Introduced	<i>V. vinifera</i>
17	Horizon	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
18	Autumn Seedless	USA	Introduced	<i>V. vinifera</i>
19	Queenora	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
20	Jingzaojin	CHN	Synthetic	<i>V. vinifera</i>
21	Muscat Hamburg	UK	Introduced	<i>V. vinifera</i>
22	Ruby seedless	USA	Introduced	<i>V. vinifera</i>
23	Bixiang wuhe	CHN	Synthetic	<i>V. vinifera</i>
24	87-1	CHN	Line	<i>V. vinifera</i>
25	Zaoheibao	CHN	Synthetic	<i>V. vinifera</i>
26	Victoria	ROU	Introduced	<i>V. vinifera</i>
27	Zhuosexiang	CHN	Synthetic	<i>V. vinifera</i> <i>V. labrusca</i>
28	Italia	ITA	Introduced	<i>V. vinifera</i>
29	Rizamat	RUS	Introduced	<i>V. vinifera</i>
30	Red Balad	CHN	Synthetic	<i>V. vinifera</i>
31	Flame seedless	USA	Introduced	<i>V. vinifera</i>
32	Brown Seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
33	Remaily Seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
34	Jingyu	CHN	Synthetic	<i>V. vinifera</i>
35	Mars seedless	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
36	Skyler	USA	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
37	01-36	CHN	Line	<i>V. vinifera</i>
38	Shine Muscat	JPN	Introduced	<i>V. vinifera</i> <i>V. labrusca</i>
39	4-355	CHN	Line	<i>V. vinifera</i> <i>V. labrusca</i>
40	D-419	CHN	Line	<i>V. vinifera</i>
41	D-15	CHN	Line	<i>V. vinifera</i>
42	4-162	CHN	Line	<i>V. vinifera</i> <i>V. labrusca</i>
43	Black Balad	JPN	Introduced	<i>V. vinifera</i>
44	Shennongjinhuanhou	CHN	Synthetic	<i>V. vinifera</i>
45	4-342	CHN	Line	<i>V. vinifera</i> <i>V. labrusca</i>
46	14-10A	CHN	Line	<i>V. vinifera</i>
47	1-344	CHN	Line	<i>V. vinifera</i> <i>V. amurensis</i>
48	1-243	CHN	Line	<i>V. vinifera</i> <i>V. amurensis</i>
49	1-260	CHN	Line	<i>V. vinifera</i> <i>V. amurensis</i>
50	1-357	CHN	Line	<i>V. vinifera</i> <i>V. amurensis</i>
51	Zaoxiameigui	CHN	Synthetic	<i>V. vinifera</i>
52	12-16	CHN	Line	<i>V. vinifera</i>
53	Beibinghong	CHN	Synthetic	<i>V. vinifera</i> <i>V. amurensis</i>
54	Shennongcuifeng	CHN	Synthetic	<i>V. vinifera</i>
55	14-52	CHN	Line	<i>V. vinifera</i>
56	Jingxiu	CHN	Synthetic	<i>V. vinifera</i>
57	D-341	CHN	Line	<i>V. vinifera</i>

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Supplemental Table 1. Continued.

Code	Cultivar or line	Source ^z	Cultivar type	Species
58	13-18	CHN	Line	<i>V. vinifera</i>
59	Wink	JPN	Introduced	<i>V. vinifera</i>
60	Moldova	MDA	Introduced	<i>V. vinifera</i>
61	D-480	CHN	Line	<i>V. vinifera</i>
62	Colin Ba Mark	UZB	Introduced	<i>V. vinifera</i>
63	Concord	USA	Introduced	<i>V. labrusca</i>
64	Muscat of Alexandria	USA	Introduced	<i>V. vinifera</i>
65	Cabernet Sauvignon	FRA	Introduced	<i>V. vinifera</i>
66	Zaoxiawuhe	CHN	Synthetic	<i>V. vinifera</i> <i>V. labrusca</i>
67	Zidiqui	CHN	Synthetic	<i>V. vinifera</i>
68	Jinnan zaohong	JPN	Synthetic	<i>V. vinifera</i>
69	Black Muscat	CHN	Synthetic	<i>V. vinifera</i> <i>V. labrusca</i>
70	4-345	CHN	Synthetic	<i>V. vinifera</i> <i>V. labrusca</i>
71	Aishenmeigui	CHN	Synthetic	<i>V. vinifera</i>
72	14-66	CHN	Line	<i>V. vinifera</i>
73	Tenzan	JPN	Introduced	<i>V. vinifera</i>
74	01-40	CHN	Line	<i>V. vinifera</i>
75	Hongru	JPN	Introduced	<i>V. vinifera</i>
76	D-517	CHN	Line	<i>V. vinifera</i>
77	Shenxiangwuhe	CHN	Synthetic	<i>V. vinifera</i>
78	2-13	CHN	Line	<i>V. vinifera</i>
79	Shuangyou	CHN	Synthetic	<i>V. amurensis</i>
80	12-17	CHN	Line	<i>V. vinifera</i>
81	Riesling	GER	Introduced	<i>V. vinifera</i>
82	Chardonnay	FRA	Introduced	<i>V. vinifera</i>
83	Zuoyouhong	CHN	Synthetic	<i>V. vinifera</i> <i>V. amurensis</i>
84	4-248	CHN	Line	<i>V. vinifera</i> <i>V. labrusca</i>
85	D-95	CHN	Line	<i>V. vinifera</i>
86	13-53	CHN	Line	<i>V. vinifera</i>
87	4-297	CHN	Line	<i>V. vinifera</i> <i>V. labrusca</i>
88	13-29	CHN	Line	<i>V. vinifera</i>
89	D-248	CHN	Line	<i>V. vinifera</i>
90	D-278	CHN	Line	<i>V. vinifera</i>
91	D-99	CHN	Line	<i>V. vinifera</i>
92	14-15	CHN	Line	<i>V. vinifera</i>
93	14-10	CHN	Line	<i>V. vinifera</i>
94	Shuanghong	CHN	Synthetic	<i>V. amurensis</i>
95	13-87	CHN	Line	<i>V. vinifera</i>
96	9-22	CHN	Line	<i>V. vinifera</i>

^zCHN = China; FRA = France; GER = Germany; ITA = Italy; JPN = Japan; MDA = Moldova; ROU = Romania; RUS = Russian; UK = United Kingdom; USA = United States of America; UZB = Uzbekistan.

Supplemental Table 2. We selected 187 pairs of SSR primers with clear polymorphic bands for use in this study. These primers may contribute to genetic diversity and association study of aromatics in grapevine. The information of linkage group, position, and sequence for the 187 SSR primers is listed in the table.

Code	Primer name	Linkage group	Position (M) ^z	Forward primer	Reverse primer
1	VLG1-A-1	LG1	0.5	TCACATATGCCTTTTGTAC	CACACCAATATCATGAGCAA
2	VMC4F8	LG1	0.6	CATTTTCATAGGGTTTTACAGC	CTGCCAGTATACTGATTCTCTC
3	VVS29	LG1	1.0	CCCCAAGGCTCTGAAAACAAT	TGCAAAGCAAATAAAGCTTCCA
4	VVIC72	LG1	1.8	GTATTGTGTAAGCATTGTGTGG	GGACAAGGAGTTAGATATGAAC
5	VLG102	LG1	2.8	TATCAGGGCTTTGCGTAACC	TGTGCAACACTGCAAACAAA
6	VLG104	LG1	3.5	TGCTTCTCGAGTTCCCTTTT	CCTGTTAGAACCAAAGAAGACCA
7	UDV055	LG1	4.5	AAGGCGAAAAGAGTACACACG	AACAGGAAAACATGAATCAACAA
8	VLG1-E-1	LG1	4.5	GCCACAGTTGTGTTATTTTC	AATATGGTGAAATGCTGTCC
9	VLG107	LG1	5.8	CCAGAGTGCCATCAGAATCC	CATTGAAGTTTGGGGAGGAA
10	VVIQ35	LG1	6.6	AGAGTTTACTAGGAGAACAGTG	CCTTCTCTATACGTCACAACTT
11	VMC3G9	LG1	7.6	GATCCTTTTTTGGGGAATCTCA	CAAGCCACTAGTAGTCATCCCTT
12	VLG106	LG1	8.1	TGGAATACGAGGGGAGTCTG	CTGATGGTGGGAAGAAAAGC
13	VMC7G5	LG1	9.8	CCCACCTTCATCTCACAGATTCA	TTTCAGGGTTGTTGTCCCATTG
14	VLG1-M-1	LG1	12.5	GTGGGTGAATATGGAATATG	AGAGATCAGCTTGCGTTTAG
15	VLG112	LG1	15.8	ATTGCTTTTGTGTGGAGGAA	CAGGGAGCCCTTTGCATTAT
16	VMC4D2	LG1	16.9	TGCAGATACCATACCCACCT	AACAGCAAACATCCCAACTCAG
17	VLG113	LG1	17.6	TCTGACTGACATTACCCGATTC	TCTGTTACATCACACCCAAT
18	VMC2B3	LG1	18.2	TCTGTGAATTTGCAGAGACGC	GGCTCAGACACAAACATGACCT
19	VLG115	LG1	21.3	CAAGTTGCAGAAGTGGCTGA	CCTCTTCTTCCCCATCAACA
20	VLG116	LG1	21.5	TCAAGAACAGACGGAAACCA	AGGGCCTTCAATGCTCTACA
21	VMC9D3	LG1	22.8	GATTTGAAAGTCGAAAGCCAGG	TGCAAAGACTGTGAGATGAGGG
22	VLG2-A-1	LG2	0.5	TAATTTTCGCTGTTCCCTCAAG	TAAGCGCATATCACAAGAAG
23	VLG2-B-1	LG2	1.5	GCTTAGACGATAGTGACAACAA	TGTTGAAGAAAGACACTTGC
24	VLG2-E-1	LG2	4.5	CCTTTGGCTCTAAATGTGAA	GTAAGGTTGCCATGTCTGTT
25	VMC6F1	LG2	5.1	AAGGAGGAGTTGAGATGTAGTA	GAGTAAGAGAGAAGCAAGAAAA
26	VMC6B11	LG2	8.1	TGATTATGGCAATAATCACACC	TTGCTTACCCATCAAAAAGAAA
27	VMC8C2	LG2	17.5	AAGGAATTTGGATACTGAAGGT	TGAAGACATCTACGTAGGTGAA
28	VLG2-R-1	LG2	17.5	CTCGCCAAAAAGAAAAGTG	CATGGCCACCTTTCTGAG
29	VLG2-S-1	LG2	18.5	CCAATAGACAGGAAAATCCA	GGCCGCAATACAATAGATAA
30	VLG3-A-1	LG3	5.0	TTTGGTCTCAGTGGTAAAGT	GACAAGCCTAAGTCAACAG
31	VLG3-K-1	LG3	10.5	CCGGTAATACAGAAAATGATGC	ACTTCCTTTGCAGCCAAAAA
32	VLG3-Q-1	LG3	16.5	GGGTAGGAGATACCAAACATGAA	TCGATATCGTAACTTTTCCCTCTC
33	VLG3-R-1	LG3	17.5	GGAAGGAAGGCATTGGAATA	TCAAGACTATCCCCAAAACCA
34	VLG4-D-1	LG4	3.5	TCCTCTGGTGGGAGAGAGAA	GAGACCCCCAAATGCAGTAA
35	VMC4D4	LG4	3.8	GTCTTGTAATGGAACCAACTGC	AGATTGACCTGGACCTGAAACT
36	VLG4-E-1	LG4	4.5	GGGAAGGCAAATCCCTCTAC	GAGGTCCAGTCGAGAAGTGC
37	VMC7H3	LG4	4.7	TCAGATATTGAAGAACCACACA	ACTAGAAAATGCACAATCTCCC
38	VMCNG2E1	LG4	5.3	TTTGTGCTTCACTGTTCTGTCG	TATGGAGGGAGACCGTTGTTTC
39	VLG4-H-1	LG4	7.5	TTCCCCCATCATCGAAATAA	TCAAAAGAAGTGTCTCCATGCT
40	VLG4-J-1	LG4	9.5	CTCTTTGGATCGGAGGAGTT	CTCTACTGCTCCCCGTTTCAG
41	UDV074	LG4	11.5	GCCAGGGAAGTTGGTTCTCT	TGCATGTGTGTTTGACAAAG
42	VLG4-L-1	LG4	11.5	TGCTGGTGAATCAAGCAAAC	TCTTAGCCATCCCCAAGGAA
43	VVIN75	LG4	14.8	TGTTAAGTGAGATGCAAGAGAA	AGACAGACACAGTAAATATTGC
44	VVIP37	LG4	18.3	AGGACCAAGTGAAAAGCTTATA	GTATGTTTCATATGCTCCTAAGC
45	VLG4-S-1	LG4	18.5	TGGTTCCTCCAACAAACACA	TTGAATACCTTGGCTGTTGC
46	VLG4-U-1	LG4	20.5	ACTTGGGAGGAGGAGGAAAA	ATCAACCCCGCTACAATCAC
47	VLG5-B-1	LG5	1.5	TGGATCATCTCACCATCATTG	TTGTCTTTGGCCCTGCTAAT
48	VLG5-C-1	LG5	2.5	GGTCCGTATCACCAAAATGC	TCATGGCTGTAGGCTTTGAA
49	UDV060	LG5	4.4	CCTGCCACACCACAATACAA	TGGGGTAAAAGTGGGTGTTT
50	UDV106	LG5	5.0	CCCAGAAAAAGGGGTATGC	CCATGATGGGGAAGAAGAAA
51	UDV111	LG5	5.5	AATTAACAAGAGCTAGGTACATC	TTCTTATTGGAATCTCCTCTCT
52	VLG5-F-1	LG5	4.8	GTTGAAAAGGGCCTACCACAA	TGATTGAAAAGCCAGGTGA
53	UDV041	LG5	6.5	AAGATCCCTCCACCCAAAAA	TGGGATCTCTTTTCCACATCA
54	VLG5-G-1	LG5	6.5	CTGAAGGATGGAGGGAATTG	TCCCCCAGATTAAATGCCTA
55	VLG5-H-1	LG5	7.5	CCAGAGCAGAACATAACCAGAA	TGAATGCTGAGCTACGAGGA

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Supplemental Table 2. Continued.

Code	Primer name	Linkage group	Position (M) ^z	Forward primer	Reverse primer
56	UDV053	LG5	8.5	GTTGGTGGCTTTCTTTTTCG	GGGAGAAAAAGGCATGGATA
57	VLG5-J-1	LG5	9.5	TTGGGATTGGCATCTTCAAT	GGAGAAATTTGGCTAAGAAAGG
58	VVIV21	LG5	11.0	TACCATCATACTTCATGCAGAG	AGTTCTTGTTTAGGCTTCGTAC
59	VVIN33	LG5	11.3	TGCCAAAGCAAGTATCAACATG	ATTTTGATCCCACCTAACTCTG
60	VMC3C7	LG5	12.3	AATTTGGCTAAGAAAGGA	AATATTCAGAAAATTTGTGTC
61	VLG5-M-1	LG5	12.5	TTTGTGTGTGAAAGACAGCAAC	CGCAATGGTGGATTTAAAGG
62	VLG5-N-1	LG5	13.5	GTCACCAACCGGTCCCTAAA	GTGCGTTCTCCGATCTTCTC
63	VLG5-O-1	LG5	14.5	GAGTGCTTCGGGTTTAATGG	AAAGGGACAAGTCAATGCAGA
64	VMC16D4	LG5	16.5	TAGAATACACAGGCCATATACAA	GGTTAGGATGCATATAGAAGAAG
65	VLG5-T-1	LG5	19.5	CACCTCTGCCCATTTACCAC	CGCTTCGGAATCGATCTTAG
66	VLG5-U-1	LG5	20.5	CCCCAACACACAAACAAAAC	TTGTCGGATGGTTCTTGACA
67	UDV064	LG5	22.3	TCTGCGAGTATTTGCAACC	CAACCGTGGCTAGCAATTTT
68	VMC2E9	LG5	23.1	GTTGTTTCTCTCCCATTCCTAA	GACATTTTTGTGTAGGGGTTG
69	VMC5F2	LG5	24.8	TAATCCCTTAATTATGAGACCAA	TCTTCGTATACGACATGTATACTTT
70	UDV090	LG6	1.0	TCAATGAGGATTGCATGGAC	GTCCAACACCAAATCCAGGT
71	VVIP72	LG6	2.2	ACTTTGAAGGGATCAGATGAAT	GCATACGGCTTAATATATGTT
72	VLG6-D-1	LG6	3.5	GGAAGCACTCGATCGACAAT	TTCACCTCGCTGTAATCC
73	VLG6-E-1	LG6	4.5	GGATGCATAAATAATGGGGTCA	TTGTTGCAAAACCATGCCTA
74	VMC2H9	LG6	5.9	AAGCAAAGCAGACCACAACG	CCCAGCTCCTTAGCTCCTCA
75	VLG6-G-1	LG6	6.5	CCCACAAGCTCTATCCCTCA	CCGCCCTTTTATTTTCATTT
76	VLG6-O-1	LG6	14.5	TTTACCCTACTACAAGGCTTTC	TCTGGGCTTCCCTATCTTT
77	VLG6-P-1	LG6	15.5	CATGGTCCAACAGCCATTTA	TGTGCTATCACACCCCTCA
78	VMC3A8	LG6	16.5	ACCATGAGATCAAATTGGAACA	TGAAGCTGGAAAAGAATAGAAA
79	VLG6-R-1	LG6	17.5	TGGGGAGGACTTCTCATGTT	TCTGGTGTGTGTTACCTGGA
80	VMCNG4B9	LG6	18.5	CTGGGGAGCATATACACATACCAG	CTCTCTCTCCCGATAGCCACC
81	VLG7-C-1	LG7	2.5	GGTAGCATCTTTTTCATTCCCTA	ATGCTTCTTTTCCACGGTTG
82	VVIB22	LG7	3.1	CCCTCCAATCTACATCCATGAA	CAGTGTGTTTCTTGATGGTCCA
83	UDV011	LG7	3.1	TTTATGGCAACCCTCCAATC	TTGATGGTCCACTGGAAGT
84	VMC5H5	LG7	4.5	TACTTGCCCAATGGGTAATGAC	ATGGCCTCCCTACAAAAGAAAC
85	VLG7-H-1	LG7	7.5	ACCTGTGGCCAGTCATGATA	TCCTCTCCAATGGAATCAG
86	VVIV36	LG7	8.4	AGCAAGAGCTCAATCCATAAAA	TAGTTAGTTGGCATAGTAGGTT
87	VLG7-O-1	LG7	14.5	GGCTGCCTACAAAGATTGTCA	TTGAGATTTACCCCCAGGTT
88	VVIQ17	LG7	16.5	TGCTTTCAAATCTCTCTGGTT	CAAATACCAGCAGTTGACAATG
89	VVIV04	LG7	17.5	TTTCTCCGAGAGCACAAAAAAC	CGGATTTTCTCCCTCTTCATTT
90	VLG7-T-1	LG7	19.5	GCAGCGAGGATATGATCAGG	GCAAATCGGACTGGTAGCTT
91	VLG7-V-1	LG7	21.5	GCTTGAGGCTTGAAAAACAG	GGCAGGATATTCATGGTTGG
92	VLG7-Z-1	LG7	25.5	AACCCAAAGCCTCAAAAGC	GAGCAATGAGTGCTTCTTCTTG
93	VMC2F12	LG8	0.5	GGATTGGGCTCAGAAATAGGCT	TTCCAGAACACAGGCCACATAC
94	UDV075	LG8	2.5	TCACCTGTAGACCCAAACAACC	GCCTCAGACCAAAGGAATGA
95	VVS4	LG8	5.6	CCATCAGTGATAAAACCTAATGCC	CCCACCTTGCCCTTAGATGTTA
96	VMCNG-2H2-2	LG8	7.2	CCAAGTCCACGTTTTTGT	CTACTACACTTCACCTCAATTATG
97	VVIM07	LG8	10.7	TGGTGTCAACATTCCTTACAAG	TTATTACATGGATAGGCACCTCA
98	VMC1E8	LG8	11.2	CAGCGAGCTCTTGATTTATTGT	GATCATAGCTTCAACGGCTTTT
99	VMC3F8	LG8	15.3	GCAATATGGACACTAGGATCAAA	AGAAATCAGCATATCCAACAACA
100	VMC3C9	LG8	17.5	ATAAAATGGAATTAAGGGGGGA	CAAACGCTAGATACCATGGAGA
101	VMCNG2B6	LG8	21.5	GCCACAATTGGTGGATTTTGTCTTA	ATTTGGAAGGTATGAAGCACGAGGT
102	VMC6D12	LG9	4.0	CTCTCTTTTCCGAAATTGGGGT	ATTTTCCCTGGAAACAAAGTGG
103	VVIQ66	LG9	10.8	CTTGCACTGCTTTCAACAATGA	ACCAATATGATGACTTTAGCCA
104	VMC2D9	LG9	19.0	TGAATTCGAATTGGGTCT	TCAACCTCGTCTTTAGTC
105	VMC3H5	LG9	20.0	CATGTAGGTGTAGCTTACATTTT	GACACAAGACTCTATTCCTTCAA
106	VVIQ52	LG9	21.5	TAAAGGATGGTAGATGACAGA	ACAGGAAAGTGTCAATGGTTA
107	UDV073	LG10	1.2	ACCATCTGCAAAAAAGAAAA	CCCTCTTCCCCCTCTTTCTA
108	VVIR21	LG10	3.6	TTTCCCTTCTCACTCAATGATG	GAAAAAGAAAAAGTGTATCCCC
109	VMC8D3	LG10	6.0	TGGCAAGACACAATAAAACAG	ATAGAGTCTGCAAATCCAAGA
110	VVIN78	LG10	8.5	TAAAGGACCCATCTCAATGTTT	ACTGAGTATGGTGAATGATTGAT
111	UDV063	LG10	11.9	CAAACCTGCCCTTCCTTTTTG	TTGCATATGCCACAAGTGATT

Continued next page

Supplemental Table 2. Continued.

Code	Primer name	Linkage group	Position (M) ^z	Forward primer	Reverse primer
112	VMC6G1	LG11	9.0	TGCATAGTGCTGTAGGCCATTG	TCTGTCAATTGCTGTCCCTTTCA
113	VVIV35	LG11	15.5	AATTAATGAAGTCTGCCTAGGC	ACGAGTGAAACTTCCTAGCAAT
114	UDV048	LG11	17.0	GCACCTGTGTGTGCAGTCCT	CCTTTCCTCACCAGAACTC
115	VVIP36B	LG11	18.5	AATATATACTTAGCCACCTCTG	GCCAGTTGTGAACTTGTAATTG
116	VVIP36A	LG11	19.0	TCCGATGAAAAACAGATTGACT	GGTGCAACATATGTGATGAAAT
117	VNCNG2H7-DG-C	LG12	3.5	ACGTTAAATAGAACATGGTCCC	CAACCTCTTTTTTTGAGGTAGC
118	VVIQ06	LG12	5.7	CCATTAATGGAGAATAAACCCA	TAATTTTCCACCATTTCTTGGC
119	VLG12-I-1	LG12	8.5	CGTGGACGCAAAACATTTC	TCAATGGCCCTGATTTTATCGT
120	UDV006	LG12	12.6	ATGGTGATGATCCTCCGTTG	TTTTCTTGTTTGTGTTGAAGATGG
121	UDV120	LG12	19.5	GACATGCACAAGGGAGACAA	GATGTTGGTGGAGTCACAGC
122	VMC8G9	LG12	20.5	AACATTATCAACAACATGGTTTA	ATATTCATCCTTCCCATCACTA
123	VMC3G11-DG-B	LG13	2.0	TTTCCAGAATTTTCAGAGAGTC	TAGAGGCAAGAAAAAGCTACAA
124	VVIH54	LG13	3.5	CCGCACTTGTGTTGAATTTGAG	CAAACCGTTTTTACACCAGCAG
125	UDV012	LG13	7.6	TGAGGTTCCGGTCAAGAGGAG	ACCGTTTCCCTAGCCGAAAGT
126	UDV028	LG13	12.6	AACAACCTGGCCCGACATTC	TTGAACATGAAAGATCGAAGAA
127	UDV044	LG13	17.9	GGAACCTATCAACCCGACCAA	CATTTCCAACACATGGGTCA
128	VMC8E6	LG13	22.5	AAGGGGTTTCAATTTGATTGAGAG	CTTCATCCATCCTTACAGCTTAGA
129	UDV050	LG14	2.3	TAATGGCCCCCTTACAACACC	AGCTTCACTGCCAAAGGATG
130	VLG14-J-1	LG14	5.5	GTGAACGGAAACCAAACCAGG	TTAGTGTGGAGTCGAACCGA
131	UDV123	LG14	8.5	GGTCGCTCATGTGAAAGAGTC	CATATGTCATAGATCATTATTGATTGG
132	VLG14-L-1	LG14	11.5	TGCAACGAATTTTCAGAAGGGA	TAGGGGTTTTCTCAGGCCAG
133	VLG14-M-1	LG14	15.5	ACCCAGAGAGATTGTAGCA	ACACACAACGCACGAATACC
134	VMC2C3	LG14	17.2	TGCAATCCCATTATTATCTCTT	AATATTTGTAGAATGGTGCTTTT
135	VLG14-AD-1	LG14	18.7	GGACATGGATTGGGGTTTCAC	AAACATATCCCAACCCCGGC
136	VMC6C10	LG14	22.0	TTCTGCGAATTCTAACCCCTT	CCACTTCCATTCCCTCTCCTGT
137	CHR7V004	LG15	3.1	TACCAAACTTTTGGCCTTG	GCTGCTCACCGTTAATGAAA
138	VLG15-G-1	LG15	6.5	TGTGTCTCATGGATGTTGCT	ACCACATGCGTCTAGATTGC
139	VLG15-M-1	LG15	12.5	GAACAACCTACAACGCCAC	TCACCACCTCATTACCACA
140	VVIM42B	LG15	15.9	CCCTCAAGACCTTGAAAATTGT	ACACAAATATGCATACACACGC
141	VLG15-S-1	LG15	18.5	GCATTTTCCCTCATCTTCCCT	CGAATGGTTCTTTTGCCCCA
142	VVIN52	LG16	0.8	TTTTTGTCGACAACCAAGAAGG	CCATACACCTCACTAAATTCAG
143	VLG16-D-1	LG16	3.5	CGTGTTACCACAGTATTGATGC	GGTCTGAGTGGTACTTTCAGGA
144	VLG16-F-1	LG16	5.5	CCAATTTCTCACCTAATGC	CCCTTCAAGCTTTACAACCA
145	VLG16-I-1	LG16	8.5	GTGGAATTAGAGGAATTAGGG	TCATCAGCACTTATCAAGAC
146	VLG16-J-1	LG16	9.5	CTTGTTGGAGGAGTAAATCCAA	CAGTCGGACAAATGGTTTTT
147	VLG16-K-1	LG16	10.5	CAATCCTGAGGAAAATGGTG	GGTGATCAACATTGGAGCAT
148	VLG16-O-1	LG16	14.5	TTGATGCTGGAAGCACATAA	AAACCCGGGATAGGTTATATT
149	VLG16-S-1	LG16	18.5	CGAGTTTGAATCCCCATTAT	CCGGTTTTGGCTCTTTAGT
150	VVIP47B	LG17	3.3	TTGAAGATGTTGGTTGTATACG	GAAGTTTCTTAGTTGCATACAC
151	VLG17-D-1	LG17	3.5	GAAGTGGTTTTTACGGATAG	CAGCACTGATGAGCTGTGTC
152	VLG17-F-1	LG17	5.5	CCCAGGGTTTCCATTCTAT	TTCTCTCCCCATTCTCTCT
153	VLG17-H-1	LG17	7.5	GCTCTTTCCTCCATTCTTCC	CTCACGATCTTGCCAATTTT
154	VMC9G4	LG17	9.0	AAATGTGCAAGTTGAAGAGGGA	AGACCGTTCAAACAAGCAAATG
155	VLG17-J-1	LG17	9.5	AGGAAGAGGATTGATCACCA	AATCTTGTAAGGTGCCAAC
156	VLG17-P-1	LG17	15.5	CACCTCCTTGCTCTCAAAAA	AGGAGAAGAGAATGGGTG
157	VLG17-Q-1	LG17	16.5	AGAATTAGTGTGGGGAACAA	CTTGCAAATTAGACACATGG
158	VLG18-A-1	LG18	0.5	ATATTGCATGGGGATTGATG	CGAATGCACACCAAATCTTA
159	VMC3E5	LG18	1.0	GATTTGTCTTTACAAGGCGTTC	CCAGGAGACTTGCTTTGTATTT
160	VLG18-C-1	LG18	2.5	AGCAAGCAAGCAAGAAACAT	TCCATCATTCCTCATCTCC
161	VMC8B5	LG18	4.0	AAAGAGACATCTGCATCAT	GCCTTGATCTTCTTCTAAT
162	VVIM93	LG18	7.0	CAACGTTTATTGTAAGAGCCTC	GCTTAGCTGTAGAAAACCTGA
163	VLG18-I-1	LG18	8.5	GCTGTCTAAGAAGTGGGATT	AAAACCGAAGACTGTTGTGC
164	VMC8F4-2	LG18	10.1	GCGTAAAGCATATTCAAGCATT	GAAGTTAGCGCAGATGAAAGAT
165	VVIM79B	LG18	12.0	AAACTTCTCTAGAGATCTCACC	AGTGTGTTTGACTCCAGAAAAG
166	VMC2A7	LG18	13.5	TGGGGATATGCAACTTCAACTG	AATATCCCTTCAAAAATTGCCGT
167	UDV005	LG18	14.5	TGCCTATCTGCCAAAAATGA	CCCATTGAATGTGGATGACA

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Supplemental Table 2. Continued.

Code	Primer name	Linkage group	Position (M) ^z	Forward primer	Reverse primer
168	VLG18-O-1	LG18	14.5	TCCCACATCGGTAAAGAAAA	TTGGTTCCTCCTGTGTAAA
169	VLG18-P-1	LG18	15.5	GGCGCTTTGGTAATGTATGA	CAACAATTGGCTGAGAGCTT
170	VLG18-R-1	LG18	17.5	GATGCAACCACATCCTCTTC	AAAAAGCCACCCAAGGTAAC
171	VLG18-S-1	LG18	18.5	TTGTGTTGCCATTTCACTGT	TATCCCGGAAAAAGAAACC
172	VLG18-W-1	LG18	22.5	AAAAATGCGTCGTTGTGG	TCCCCAACAATTCTCCATTA
173	VVIP17A	LG19	0.2	TTGGATCCATCACTCTTGTTTC	TTGGTTGAGGGAAAAAGGAAAG
174	VLG19-B-1	LG19	1.5	TTTTACCATTCACCTCCTCAG	CCTAGAATTCATCCTCATAGGTCT
175	VLG19-C-1	LG19	2.5	GGACATAGCTAGGGCATTCA	GGTAATGAATCTGCCCAGTG
176	VLG19-D-1	LG19	3.5	TCTGGAACCTAAACCCCAAT	TCCTAACACAAGGGTGCATT
177	VMC5D11	LG19	5.0	CTTCCACAATCACCAAATCACA	GAAATGAATGGGAAGAGACACTG
178	VLG19-H-1	LG19	5.5	CAACCTGTTTGTTCCTTTGG	GAACCTCCCTCACTCCACT
179	VMC6C7	LG19	8.5	CCTTATCTTATCCCTGTCCTGA	AGCTTCTGGGTTGGCTATG
180	VLG19-I-1	LG19	8.5	ACATATATCCGAAAGTGTGGGGC	CTTAAAGCTTGAAGCTTTTGGTGC
181	VLG19-L-1	LG19	11.5	GACTTGTGTTAAAGTGTCTACCC	ATTCACACCCATCCATGTTT
182	VLG19-N-1	LG19	13.5	TTGAAAGAGGGCATTCAAAG	CCTCATTGTCATCCCTATGC
183	UDV127	LG19	17.8	CGTCAATCGCTTGTAATCTGC	TGAGCATTTTGCTCCTTCATT
184	VLG19-S-1	LG19	18.5	CAGAGTCCATCCCATCATGT	CACACCAATCTTGCTTTTCC
185	VMC5A10	LG19	21.0	GTAAAGAATAAATGGAGAGGGG	CAGTTGAGGAAAGGAAGGATAG
186	VLG19-W-1	LG19	22.5	TGAGATCAACATGGGCAAAC	GCCAAATTGTGTTTGATGGT
187	VMC7B1	LG19	23.0	GTAAAGAATAAATGGAGAGGGG	CAGTTGAGGAAAGGAAGGATAG

^zChromosome location of primers.

Supplemental Table 3. Variability parameters of the 187 SSR loci and population-genetic statistics for 96 grapevine cultivars. The statistics of SSR markers were estimated using PowerMarker [version 3.25 (Guo et al., 2007)].

Marker	SS ^z	NO	MA	NG	NA	AV	GD	HE	PIC
VMC4F8	96	96	0.93	4	3	1.00	0.14	0.10	0.13
VVIQ35	96	89	0.56	6	3	0.93	0.57	0.25	0.50
VMC3G9	96	89	0.89	6	4	0.93	0.21	0.08	0.20
VMC7G5	96	96	0.46	7	5	1.00	0.57	0.60	0.48
VMC4D2	96	96	0.34	20	8	1.00	0.78	0.75	0.75
VMC2B3	96	96	0.98	3	3	1.00	0.03	0.03	0.03
VMC9D3	96	96	0.91	8	7	1.00	0.18	0.17	0.17
VMC8C2	96	94	0.31	24	7	0.98	0.80	0.78	0.77
VMC6B11	96	91	0.71	15	10	0.95	0.48	0.37	0.46
VMC6F1	96	92	0.27	32	12	0.96	0.83	0.60	0.81
VMC2E9	96	96	0.64	15	7	1.00	0.56	0.44	0.53
VMC4D4	96	94	0.48	11	8	0.98	0.61	0.62	0.53
VMC7H3	96	94	0.70	16	7	0.98	0.49	0.38	0.46
VMCNG2E1	96	96	0.44	12	5	1.00	0.68	0.56	0.63
VVIN75	96	96	0.30	20	8	1.00	0.77	0.60	0.74
VVIP37	96	93	0.39	17	7	0.97	0.75	0.37	0.72
VMC3C7	96	91	0.46	13	7	0.95	0.68	0.57	0.63
VMC2H9	96	82	0.72	5	3	0.85	0.41	0.32	0.34
VVIP72	96	76	0.42	23	9	0.79	0.77	0.34	0.75
VVIB22	96	95	0.51	11	6	0.99	0.64	0.62	0.58
VVIV04	96	94	0.49	16	7	0.98	0.69	0.60	0.65
VMC2F12	96	96	0.31	18	9	1.00	0.75	0.55	0.71
VMCNG2H2-2	96	96	0.67	6	5	1.00	0.50	0.57	0.46
VVS4	96	83	0.31	15	10	0.86	0.78	0.67	0.75
VVIM07	96	92	0.84	7	6	0.96	0.28	0.18	0.26
VMCNG2B6	96	96	0.53	12	6	1.00	0.64	0.27	0.59
VMC6D12	96	93	0.44	13	8	0.97	0.65	0.39	0.59
VVIQ66	96	74	0.57	11	5	0.77	0.61	0.39	0.57
VMC2D9	96	85	0.49	8	4	0.89	0.65	0.22	0.59
VVIQ52	96	96	0.29	25	9	1.00	0.82	0.58	0.80
VMC8D3	96	96	0.63	18	10	1.00	0.58	0.43	0.56
VVIN78	96	96	0.67	11	6	1.00	0.51	0.27	0.47
VMC6G1	96	88	0.62	10	7	0.92	0.52	0.53	0.45
VVIV35	96	96	0.47	16	6	1.00	0.67	0.54	0.63
VMC8G9	96	96	0.45	10	5	1.00	0.64	0.44	0.57
VVIH54	96	95	0.71	11	7	0.99	0.46	0.37	0.42
VMC6C10	96	96	0.64	21	10	1.00	0.55	0.46	0.51
VVIN52	96	95	0.69	8	6	0.99	0.47	0.06	0.42
VMC9G4	96	90	0.42	13	7	0.94	0.71	0.31	0.67
VMC3E5	96	94	0.45	13	8	0.98	0.65	0.61	0.59
VMC8B5	96	95	0.51	11	6	0.99	0.64	0.62	0.58
VVIM93	96	94	0.49	16	7	0.98	0.69	0.60	0.65
VMC5A10	96	96	0.31	18	9	1.00	0.75	0.55	0.71
VMC7B1	96	90	0.41	6	3	0.94	0.65	0.61	0.57
VVS29	96	85	0.72	3	2	0.89	0.40	0.22	0.32
UDV055	96	96	0.67	6	5	1.00	0.50	0.57	0.46
VVIV21	96	83	0.31	15	10	0.86	0.78	0.67	0.75
UDV106	96	92	0.86	5	4	0.96	0.25	0.15	0.23
VMCNG4B9	96	94	0.68	14	8	0.98	0.52	0.26	0.49
UDV090	96	95	0.47	16	8	0.99	0.66	0.38	0.61
VMC5H5	96	84	0.63	10	7	0.88	0.56	0.26	0.52
UDV075	96	93	0.56	9	6	0.97	0.60	0.49	0.54
VMC1E8	96	95	0.69	6	6	0.99	0.49	0.62	0.45
VMC3F8	96	87	0.45	20	10	0.91	0.72	0.21	0.69
VMC3H5	96	96	0.35	25	11	1.00	0.77	0.67	0.73
UDV073	96	96	0.51	7	4	1.00	0.61	0.67	0.54
VVIR21	96	83	0.33	16	6	0.86	0.78	0.55	0.74

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Supplemental Table 3. Continued.

Marker	SS ^z	NO	MA	NG	NA	AV	GD	HE	PIC
UDV063	96	86	0.37	16	9	0.90	0.78	0.58	0.75
VNCNG2H7-DG-C	96	94	0.44	13	6	0.98	0.71	0.27	0.67
VMC3G11-DG-B	96	86	0.59	13	6	0.90	0.59	0.57	0.54
VMC8E6	96	90	0.88	6	4	0.94	0.21	0.17	0.20
UDV050	96	87	0.79	7	4	0.91	0.35	0.31	0.33
VMC8F4-2	96	90	0.62	11	5	0.94	0.58	0.47	0.55
VMC2A7	96	96	0.53	8	5	1.00	0.57	0.66	0.49
VMC5D11	96	87	0.93	5	3	0.91	0.13	0.03	0.12
VMC6C7	96	88	0.46	12	5	0.92	0.68	0.84	0.63
UDV127	96	86	0.44	17	6	0.90	0.72	0.67	0.68
VVIC72	96	91	0.43	17	7	0.95	0.73	0.70	0.69
VMC5F2	96	54	0.79	3	2	0.56	0.34	0.02	0.28
UDV064	96	93	0.43	15	7	0.97	0.72	0.66	0.68
VMC16D4	96	86	0.49	13	6	0.90	0.67	0.38	0.63
VVIN33	96	91	0.47	16	6	0.95	0.70	0.49	0.66
UDV053	96	92	0.38	14	5	0.96	0.70	0.62	0.65
UDVO41	96	82	0.52	14	5	0.85	0.65	0.50	0.61
UDV060	96	95	0.69	3	2	0.99	0.42	0.23	0.33
VMC3A8	96	61	0.43	8	5	0.64	0.67	0.15	0.61
UDV011	96	74	0.53	13	6	0.77	0.64	0.65	0.60
VVIV36	96	87	0.44	13	5	0.91	0.68	0.59	0.63
VMC3C9	96	93	0.58	12	6	0.97	0.62	0.57	0.58
UDV048	96	57	0.38	10	6	0.59	0.69	0.32	0.63
VMC2C3	96	96	0.69	10	5	1.00	0.49	0.39	0.45
VVIM42B	96	95	0.34	26	9	0.99	0.81	0.78	0.79
VVIM79B	96	91	0.39	6	4	0.95	0.66	0.19	0.58
VVIP17A	96	95	0.56	5	3	0.99	0.54	0.49	0.45
VVIP36A	96	96	0.46	9	6	1.00	0.66	0.63	0.60
VVIP36B	96	95	0.34	26	8	0.99	0.80	0.83	0.77
VVIP47B	96	91	0.53	14	6	0.95	0.65	0.43	0.61
VVIQ06	96	94	0.33	23	10	0.98	0.78	0.43	0.76
VVIQ17	96	72	0.40	10	5	0.75	0.69	0.44	0.63
UDV005	96	96	0.49	19	8	1.00	0.69	0.52	0.65
UDV006	96	96	0.94	3	2	1.00	0.12	0.06	0.11
UDV012	96	95	0.57	16	8	0.99	0.64	0.71	0.61
UDV028	96	88	0.78	6	4	0.92	0.37	0.28	0.34
UDV044	96	88	0.65	5	4	0.92	0.48	0.01	0.41
UDV074	96	94	0.48	10	4	0.98	0.59	0.52	0.51
UDV111	96	81	0.52	11	6	0.84	0.65	0.47	0.61
UDV120	96	90	0.33	16	10	0.94	0.79	0.11	0.77
UDV123	96	94	0.70	6	4	0.98	0.44	0.04	0.38
CHR7V004	96	95	0.47	12	6	0.99	0.61	0.57	0.53
VLG102	96	89	0.29	18	7	0.93	0.79	0.52	0.76
VLG104	96	93	0.35	10	6	0.97	0.72	0.19	0.67
VLG106	96	96	0.55	7	4	1.00	0.59	0.61	0.52
VLG107	96	96	0.57	2	2	1.00	0.49	0.86	0.37
VLG112	96	91	0.66	10	6	0.95	0.49	0.16	0.42
VLG113	96	87	0.48	6	4	0.91	0.64	0.26	0.57
VLG115	96	86	0.69	9	6	0.90	0.49	0.13	0.47
VLG116	96	93	0.54	13	7	0.97	0.64	0.39	0.59
VLG1-A-1	96	94	0.51	7	4	0.98	0.62	0.53	0.55
VLG1-E-1	96	90	0.30	19	7	0.94	0.79	0.78	0.76
VLG1-M-1	96	84	0.48	10	5	0.88	0.61	0.44	0.53
VLG2-A-1	96	96	0.64	13	5	1.00	0.56	0.56	0.53
VLG2-B-1	96	87	0.63	3	2	0.91	0.47	0.25	0.36
VLG2-E-1	96	92	0.57	7	4	0.96	0.55	0.54	0.46
VLG2-R-1	96	94	0.22	27	10	0.98	0.84	0.84	0.82

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Supplemental Table 3. Continued.

Marker	SS ^z	NO	MA	NG	NA	AV	GD	HE	PIC
VLG2-S-1	96	93	0.56	6	4	0.97	0.55	0.44	0.47
VLG3-A-1	96	72	0.37	14	5	0.75	0.76	0.53	0.72
VLG3-K-1	96	86	0.61	17	8	0.90	0.59	0.23	0.57
VLG3-Q-1	96	72	0.73	6	3	0.75	0.42	0.14	0.37
VLG3-R-1	96	95	0.51	15	7	0.99	0.65	0.48	0.60
VLG4-D-1	96	92	0.43	6	4	0.96	0.64	0.08	0.56
VLG4-E-1	96	96	0.63	7	5	1.00	0.53	0.31	0.47
VLG4-H-1	96	96	0.32	10	4	1.00	0.74	0.70	0.69
VLG4-J-1	96	86	0.46	14	5	0.90	0.71	0.43	0.67
VLG4-L-1	96	92	0.69	11	8	0.96	0.48	0.14	0.43
VLG4-S-1	96	80	0.86	8	5	0.83	0.26	0.13	0.24
VLG4-U-1	96	67	0.38	11	8	0.70	0.71	0.33	0.66
VLG5-B-1	96	94	0.41	24	11	0.98	0.77	0.38	0.75
VLG5-C-1	96	96	0.78	8	5	1.00	0.37	0.23	0.34
VLG5-F-1	96	96	0.45	20	8	1.00	0.70	0.63	0.66
VLG5-G-1	96	95	0.23	31	11	0.99	0.84	0.84	0.82
VLG5-H-1	96	89	0.60	11	6	0.93	0.58	0.47	0.53
VLG5-J-1	96	95	0.45	11	6	0.99	0.65	0.67	0.58
VLG5-M-1	96	88	0.53	11	6	0.92	0.63	0.40	0.57
VLG5-N-1	96	94	0.32	16	6	0.98	0.76	0.76	0.72
VLG5-O-1	96	93	0.81	7	5	0.97	0.32	0.29	0.30
VLG5-T-1	96	88	0.49	14	7	0.92	0.67	0.33	0.62
VLG5-U-1	96	89	0.47	15	7	0.93	0.70	0.58	0.66
VLG6-D-1	96	72	0.58	3	2	0.75	0.49	0.14	0.37
VLG6-E-1	96	92	0.71	10	5	0.96	0.47	0.38	0.44
VLG6-G-1	96	96	0.79	10	6	1.00	0.36	0.26	0.35
VLG6-O-1	96	94	0.60	16	9	0.98	0.60	0.57	0.57
VLG6-P-1	96	89	0.67	9	5	0.93	0.49	0.35	0.44
VLG6-R-1	96	89	0.36	14	6	0.93	0.75	0.67	0.71
VLG7-C-1	96	94	0.66	8	5	0.98	0.50	0.32	0.44
CLG7-H-1	96	89	0.42	14	7	0.93	0.68	0.55	0.63
VLG7-O-1	96	95	0.94	3	2	0.99	0.12	0.02	0.11
VLG7-T-1	96	93	0.49	16	7	0.97	0.69	0.38	0.65
VLG7-V-1	96	77	0.39	8	4	0.80	0.68	0.47	0.61
VLG7-Z-1	96	92	0.45	21	8	0.96	0.73	0.68	0.70
VLG18-A-1	96	90	0.41	19	6	0.94	0.75	0.38	0.72
VLG18-C-1	96	96	0.67	8	4	1.00	0.48	0.33	0.41
VLG18-I-1	96	87	0.37	19	7	0.91	0.77	0.51	0.74
VLG18-O-1	96	90	0.48	14	6	0.94	0.64	0.24	0.58
VLG18-P-1	96	78	0.49	12	6	0.81	0.69	0.12	0.65
VLG18-R-1	96	85	0.53	9	5	0.89	0.58	0.49	0.50
VLG18-S-1	96	96	0.61	14	7	1.00	0.59	0.63	0.57
VLG18-W-1	96	79	0.52	9	5	0.82	0.64	0.29	0.59
VLG19-B-1	96	87	0.47	13	6	0.91	0.65	0.48	0.59
VLG19-C-1	96	96	0.40	23	9	1.00	0.78	0.94	0.75
VLG19-D-1	96	89	0.49	8	4	0.93	0.59	0.33	0.51
VLG19-H-1	96	89	0.70	8	5	0.93	0.48	0.53	0.44
VLG19-I-1	96	87	0.62	3	2	0.91	0.47	0.18	0.36
VLG19-L-1	96	96	0.46	20	7	1.00	0.72	0.68	0.68
VLG19-N-1	96	82	0.74	5	3	0.85	0.40	0.16	0.34
VLG19-S-1	96	95	0.41	13	5	0.99	0.74	0.52	0.71
VLG19-W-1	96	93	0.56	6	3	0.97	0.59	0.51	0.52
VLG12-I-1	96	94	0.66	13	7	0.98	0.53	0.23	0.49
VLG15-G-1	96	91	0.22	37	12	0.95	0.87	0.77	0.85
VLG15-M-1	96	88	0.54	3	2	0.92	0.50	0.51	0.37
VLG15-S-1	96	96	0.35	12	5	1.00	0.73	0.64	0.68
VLG14-J-1	96	96	0.61	7	4	1.00	0.56	0.43	0.50

Continued next page

Supplemental Table 3. Continued.

Marker	SS ^z	NO	MA	NG	NA	AV	GD	HE	PIC
VLG14-L-1	96	93	0.65	11	5	0.97	0.55	0.57	0.51
VLG14-M-1	96	94	0.40	11	5	0.98	0.70	0.61	0.65
VLG14-AD-1	96	94	0.39	19	8	0.98	0.77	0.69	0.75
VLG16-D-1	96	96	0.38	19	8	1.00	0.75	0.70	0.72
VLG16-F-1	96	96	0.51	11	6	1.00	0.64	0.58	0.58
VLG16-I-1	96	96	0.32	19	9	1.00	0.76	0.86	0.72
VLG16-J-1	96	93	0.40	15	6	0.97	0.68	0.48	0.63
VLG16-K-1	96	93	0.40	23	8	0.97	0.77	0.59	0.74
VLG16-O-1	96	91	0.35	19	9	0.95	0.77	0.62	0.73
VLG16-S-1	96	86	0.76	5	4	0.90	0.40	0.01	0.37
VLG17-D-1	96	93	0.67	10	6	0.97	0.50	0.26	0.45
VLG17-F-1	96	96	0.41	9	5	1.00	0.67	0.56	0.60
VLG17-H-1	96	80	0.34	18	11	0.83	0.81	0.15	0.78
VLG17-J-1	96	95	0.29	20	8	0.99	0.79	0.77	0.76
VLG17-P-1	96	91	0.81	10	5	0.95	0.33	0.20	0.32
VLG17-Q-1	96	94	0.52	10	6	0.98	0.65	0.67	0.60
Mean	96	90	0.53	12	6	0.94	0.60	0.44	0.56
Total	96	/	/	/	2315	1133	/	/	/

^zSS = sample size; NO = number of observer alleles; MA = major allele frequency; NG = number of genotypes; AV = availability; GD = gene diversity; HE = heterozygosity; PIC = polymorphism information content.