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Supplementary information

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Grapevine pangenome facilitates trait genetics and genomic breeding

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SUPPLEMENTARY INFORMATION

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Supplementary Notes

Supplementary Note 1. Background information on the sequenced accessions

Supplementary Note 1.1 Nine grape accessions for genome assembly

In this work, we newly sequenced nine accessions and performed genome assemblies to the telomere-to-telomere (T2T) level (**Supplementary Table 1**).

The descriptions of the nine accessions sequenced in the current work are listed below, which are mainly based on phenotypic observations and cultivation conditions. These sequenced plants are presented within the institutions in brackets (ZFRI, Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, Zhengzhou, China; XAAS, Xinjiang Academy of Agricultural Sciences, Urumqi, China; AGIS, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China).

Shine Muscat (SM) (*Vitis labrusca* × *Vitis vinifera*) is characterized by large leaves, bisexual flowers, conical bunches. The berries are large, yellow-green or purple with crunchy, candy-like, seedless flesh, carrying a muscat floral aroma. It is a crisp, fragrant seedless green table grape variety (ZFRI).

Muscat Hamburg (MH) (*Vitis vinifera*) is a classical cultivar of black table grapes. It is widely known for its large dark-blue round oval shape berries (1.8-3.5 g), highly developed bunches (200-400 g) and pleasant muscat aroma, highly appreciated in grapes destined for fresh consumption. Muscat Hamburg is an economically very important table grape variety (ZFRI).

Manicure Finger (MF) (*Vitis vinifera*) is characterized by a specific color: most of the berries are light yellow, and the tip of the grape has a bright red color. In shape, the elongated berry resembles a finger. The peel is thin and tough with difficult to crack. The flesh is translucent, juicy, crispy and has high sugar content. The berries are medium in weight and size. The variety is mainly for fresh consumption and cultivation for sale (ZFRI).

Pinot Noir (PN) (*Vitis vinifera*) is one of the world's renowned wine grapes, whose fruit present a unique ruby red hue. It is closely related to many other renowned wine grape varieties, such as Chardonnay, a popular white wine grape. Pinot Noir yields many bud sports varieties, such as Pinot Grigio, Pinot Meunier, and Pinot Blanc (ZFRI).

Baimunage (BMNG) (*Vitis vinifera*) is a seeded grape with chartreuse peel. The

fruit cluster and berries are larger than other table grapes. The fruit has a sweet and crisp taste, and long fruit bunch, making it easy to store and transport (XAAS).

Hongmunage (HMNG) (*Vitis vinifera*) is a close variety of the Baimunage grape. The fruit has a red peel and shares all traits with Baimunage, including a crisp taste, large fruit size and cluster, late maturation, and suitability for storage (XAAS).

Black Monukka (BM) (*Vitis vinifera*) is a hybrid progeny resulting from the cross between 'Ichkimar' and 'Sultanina.' It produces seedless grapes in tight clusters with dark violet peel. The fruit is crisp and firm, exhibiting a subtle fruity aroma. Black Monukka grapes are commonly cultivated for consumption in Xinjiang, China (XAAS).

Thompson Seedless (TS) (*Vitis vinifera*) is a renowned seedless grape believed to have originated in the Mediterranean region. It is known by 160 synonyms worldwide, including 'Sultania'. The fruit of Thompson Seedless is light green to light yellow, with high sugar content and crisp texture. Although the individual berries are small, the clusters can be longer than those of other cultivated grapes (XAAS).

Woolly grape (WG) (*Vitis retordii*), one of the wild grape species in South Asia, is characterized by its abaxially tomentose oval leaf blade, small flowers, and acidic or acidic-sweet fruit. It is one of rare grape species that could grow in costal environment, serving as treasurable rootstock for salt resistance (AGIS).

Additionally, nine of these grape accessions were reanalyzed from previous published works, including five cultivar species: near homozygous Pinot Noir (PN40024, *Vitis vinifera*), Zinfandel (ZI, *Vitis vinifera*), Chardonnay (CH, *Vitis vinifera*), Cabernet Sauvignon (CS, *Vitis vinifera*), Melot (ME,*Vitis vinifera*); and four wild species: *Vitis arizonica* (Var), *Vitis labrusca* (VL), *Vitis vinifera* ssp. *sylvestris* (VsyA, VsyB).

Supplementary Note 1.1 Major classification of grapes

***Vitis vinifera* ssp. *vinifera*.** The common grape is a member of the Vitaceae (grape) family native to the north temperate zone including Europe and Central Asia. Varieties can be split to two main types: those eaten as table fruit, or crushed to make grape juice or wine. We named these two types Table1 and Wine based on genomic information, respectively.

***Vitis labrusca* × *Vitis vinifera*.** Hybrids between *Vitis labrusca* and *Vitis vinifera* are widely cultivated, compared to *Vitis vinifera*, they exhibit characteristics of cold resistance, disease resistance, and vigorous growth, making cultivation easier. They are mainly used as table fruit, and some varieties are also used for winemaking. We found tight clustering and high genetic relatedness of this class

of grapes in this work, hence we named it Table 2.

Vitis labrusca. Cultivated for its edible fruit, *Vitis labrusca* is a vigorous deciduous vine that produces medium-sized grapes of glossy, juicy, blue-black grapes in late mid-season. Native to eastern North America. *Vitis labrusca* is the parent of many grape cultivars.

***Vitis vinifera* ssp. *sylvestris*.** The Eurasian species of common grapevine, *Vitis vinifera* ssp. *sylvestris*, is the ancestor of most cultivated today. Mainly distributed in Europe and Central Asia, we classified these samples based on the geographical information collected in NCBI.

Other types grape. We selected other seven types of wild grapes to enrich the genetic diversity of our research and to use them as outgroup for analysis. We used the first few letters of their scientific name as abbreviations, mustangensis (MUS), cinerea (CIN), californica (CAL), arizonica (ARI), rotundifolia (ROT), rupestris (RUP) and retordii (RET).

Supplementary Note 1.2 Sample selection for GWAS

A total of 324 grape germplasm samples for whole-genome resequencing were collected from the National Grape Germplasm Repository located at the ZFRI (Zhengzhou, Henan Province; coordinates: 113°42E and 34°42N). Annual precipitation data for Zhengzhou in 2016 and 2017 were 648.4 mm and 547.1 mm, respectively, while the corresponding annual average temperatures were 16.2 °C and 16.1 °C, respectively. For cultivated varieties, we focused on the primary purposes of grape usage: table grapes and winemaking. Therefore, we identified three main categories: *Vitis vinifera* Table (namely Table1), *Vitis vinifera* Wine (namely Wine), and *Vitis vinifera* × *Vitis labrusca* Table (namely Table2). To fully represent commercial viticulture in this work, we took into account diverse varieties from different countries including China, Germany, France, Canada, Japan and the USA. Following initial screening, we performed morphological collections and concurrently verified the identity of each variety using the International Variety Catalogue website (https://www.vivc.de/index.php). As a result, we chose 324 cultivars that met our criteria, with more than 100 representatives present across all three previously mentioned main categories (106 Wine grapes, 108 Table1 grapes and 110 Table2 grapes). These samples were used for genome sequencing (15-fold coverage). These newly sequenced data were employed for subsequent analyses, including GWAS analysis, genomic prediction, heritability estimation and genetic correlation calculation.

To study the genetic diversity and adaptive evolution of grape populations, we download an additional 142 published samples from the National Center for Biotechnology Information (NCBI) database (https://www.ncbi.nlm.nih.gov/).

Additionally, we performed a SNP profile analyses to confirm the true-to-type of varieties. We downloaded SNP markers from VIVC database and identified these genotypes in our sequenced grape accessions. The genotypes of the database records are identical with sequenced samples (https://www.vivc.de/index.php). In total, WGS of 466 grape varieties were investigated in this work.

Supplementary Note 2. Sequencing data summary

Supplementary Note 2.1 Previously genome sequencing data

PN40024 (PNT2T, *Vitis vinifera*): PN40024 material collected from INRAE under a Material Transfer Agreement (MTA) and was transplanted to the greenhouse at AGIS (Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China). Two single-molecule real-time cells were sequenced on a PacBio Sequel II platform, and a total of 21 Gb of HiFi reads were generated using CCS mode with the default parameter for the sequenced accessions. The relevant data was collected from this paper (https://academic.oup.com/hr/article/10/5/uhad061/7103438?login=true#406687485).

Zinfandel (ZI, *Vitis vinifera*): Zinfandel reference FPS clone 03 (Zin03) was collected at the University of California Davis. Zin03 SMRTbell libraries were sequenced on a PacBio RS II (DNA Technology Core Facility, University of California, Davis). The relevant data was collected from this paper (https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-019-6211-2#Sec11).

Chardonnay (CH, *Vitis vinifera*): The sample chosen for sequencing was FPS04, a clone commonly grown in California and throughout the world. The reference plant is located at Foundation Plant Services, University of California, Davis. SMRTbell libraries were sequenced on a PacBio RS II system, generating a total of 31.51 Gb (52×). Relevant data was collected from this paper (https://www.nature.com/articles/s41477-019-0507-8#Sec10).

Cabernet Sauvignon (CS, *Vitis vinifera*): The sample was collected from *Vitis vinifera* cv. Cabernet Sauvignon at Foundation Plant Services (UC Davis, Davis, CA). The range of sequenced fragment size ranged from 15 kb to 40 kb. Sequencing was performed on the PacBio RS II platform. Relevant data was collected from this paper (https://www.nature.com/articles/nmeth.4035#Sec9).

Merlot (ME, *Vitis vinifera*): The data was generated on PacBio RS II using the *Vitis vinifera* cv. Merlot (DNA Technology Core Facility, University of California, Davis). Relevant data was collected from this paper

(https://www.nature.com/articles/s41467-020-16700-z#Sec8).

Vitis labrusca (VL): Genomic DNA was shipped to the University of Delaware DNA Sequencing and Genotyping Center. Six PacBio SMRTbell libraries were prepared and sequenced with the PacBio Sequel I platform. A total of 58.46 GB of raw reads were generated with the subread N50 larger than 20.2 kb, totaling approximately 115-fold coverage. Relevant data was collected from this paper (https://www.frontiersin.org/articles/10.3389/fpls.2023.1234130/full).

Vitis vinifera ssp. *sylvestris* (VsyA: VvSylDVIT3603.16 and VsyB: VvSylDVIT3351.27): SMRTbell libraries were prepared and sequenced on a PacBio Sequel system (DNA Technology Core Facility, University of California, Davis). These relevant data were collected from this paper (https://www.nature.com/articles/s41467-020-16700-z#Sec8).

Vitis arizonica (Var): SMRTbell libraries were prepared and sequenced similar to VsyA and VsyB. The relevant data was collected from this paper (https://www.nature.com/articles/s41467-020-16700-z#Sec8).

TS and BM: The resulting libraries were employed for HiFi sequencing on a PacBio Sequel II instrument (CCS mode) with Sequencing Primer V2 and Sequel II Binding Kit 2.0 in Grandomics, yielding 59.78 Gbp and 60.35 Gbp of sequencing data for TS and BM, respectively. The isolated nuclei were then digested with 100 units of restriction enzyme DpnII. The resulting Hi-C sequencing data amounted to 59.39 Gbp (TS) and 57.67 Gbp (BM) via the Illumina Novaseq/MGI-2000 platform. The relevant data was collected from this paper(https://www.biorxiv.org/content/10.1101/2023.12.22.573032v1)

WG: A 15-kb PacBio SMRTbell library was constructed and sequenced with PacBio Sequel II platform. Hi-C libraries were prepared using the standard Hi-C protocol and sequenced on an Illumina NovaSeq instrument with 2×150-bp reads. The relevant data was collected from this paper (https://doi.org/10.1111/jipb.13653).

PN: For PacBio HiFi sequencing, single-molecule real-time cells were sequenced on the PacBio Sequel II platform using CCS with default parameters. For the Hi-C library, samples were digested with the restriction enzyme DpnII and constructed using a standard Hi-C protocol as described previously. These Hi-C libraries were sequenced on the Illumina HiSeq X Ten platform.

HMNG and BMNG: A 15-kb PacBio SMRTbell library was constructed and sequenced with PacBio Sequel II platform. The relevant data was collected from paper: Haplotype-resolved genomes provide insights into the genetic underpinnings of berry color variation (https://doi.org/10.1101/2024.09.11.612401).

Supplementary Note 2.2 New genome assembly sequencing data

For three grape accessions (SM, MH, MF): We performed sequencing using the consensus sequencing (CCS) mode. A 15-kb PacBio SMRTbell library was constructed and sequenced with PacBio Sequel II platform. Hi-C libraries were prepared using the standard Hi-C protocol and sequenced on an Illumina NovaSeq instrument with 2×150-bp reads.

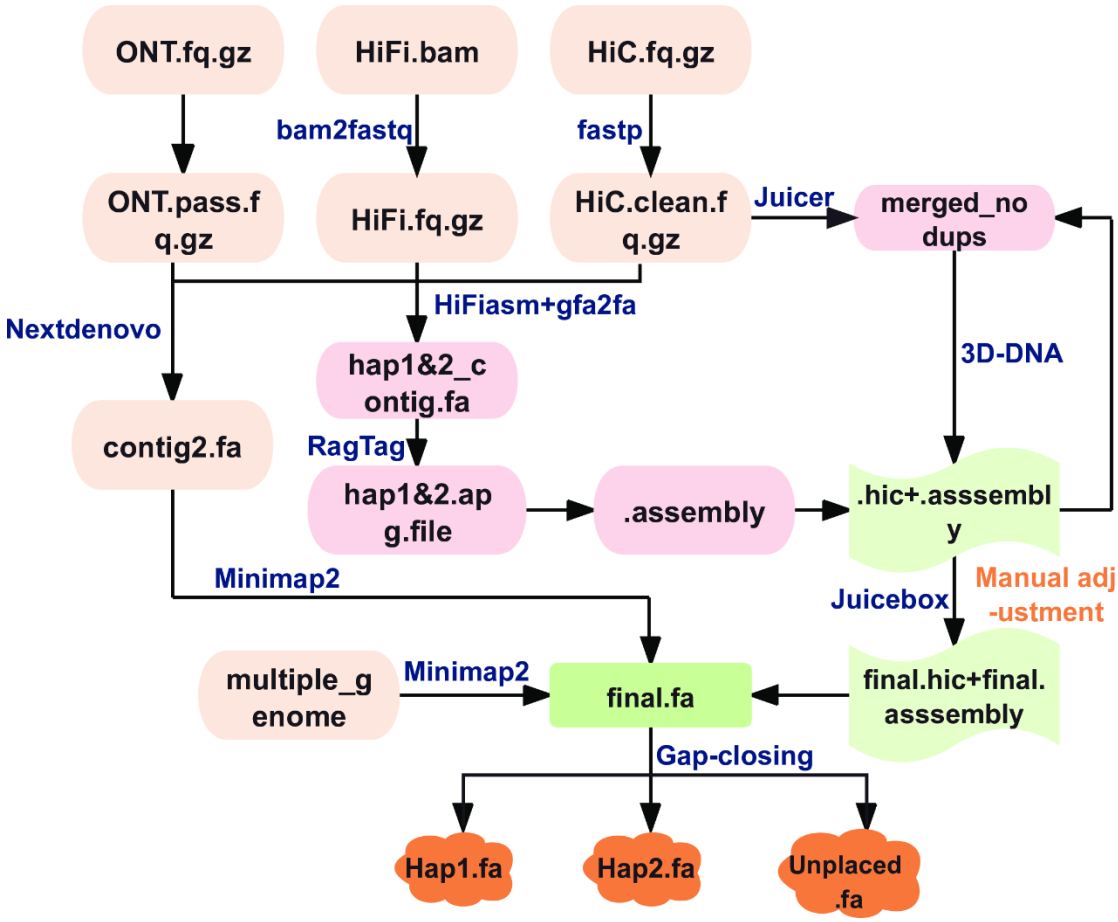
For nine grape accessions (SM, MH, MF, TS, BM, WG, PN, HMNG, BMNG): We newly sequenced based on the Oxford Nanopore Ultra-long sequencing (ONT) mode. Library was constructed by Sage HLS HMW library system and sequenced on the PromethION.

Supplementary Note 2.3 New 324 sequencing data

Our sequencing libraries were prepared with NEBNext® Ultra™ DNA Library Prep Kit (Illumina, USA) according to the manufacturer's directions. Paired-end sequencing was performed on an Illumina NovaSeq 6000 platform. The target sequencing depth was 15-fold for each accession.

Supplementary Note 3. Haplotype-resolved T2T assemblies

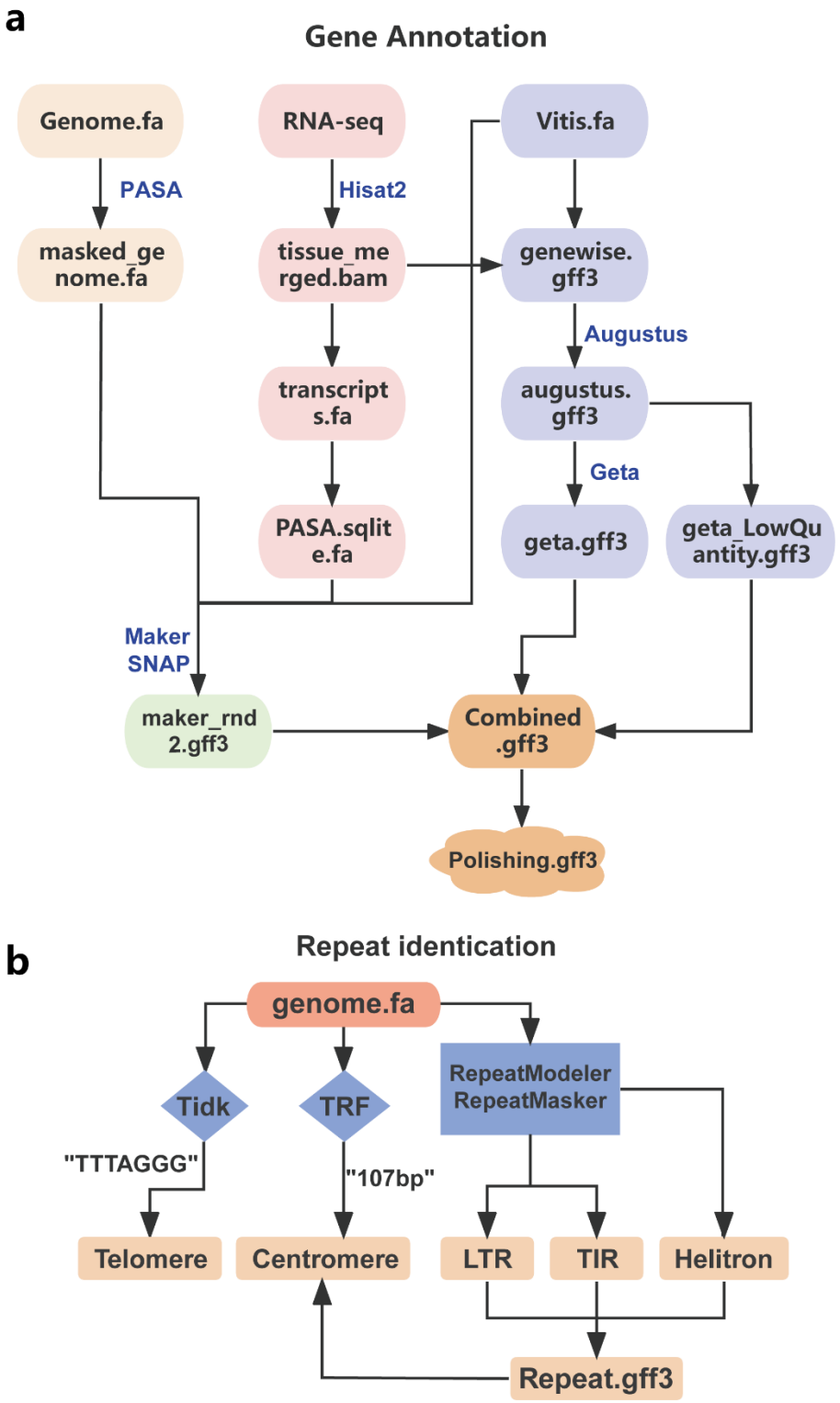
Recent advancements in sequencing technology have significantly enhanced the accuracy and length of sequencing reads, resulting in highly continuous genome assemblies. By integrating HiFi, ONT, and Hi-C data, we employed a pipeline to obtain the phase-resolved T2T assemblies of nine diploid accessions sequenced in this study (**Supplementary Note Figure 1**). Briefly, our methodology involves using HiFi reads for an initial phased assembly, then using Hi-C data to generate chromosome-level assemblies, and finally, using ONT ultra-long data for gap filling (**Supplementary Method 1**).



Supplementary Note Figure 1 | Overview of the genome assembly.

To validate the quality of these phase-resolved T2T assemblies, we assessed the genome integrity using multiple metrics including detecting phased errors and assembly errors. The accuracy of the phasing process was quantified via two statistical measures: switch error rate and hamming error rate[1]. Specifically, switch error refers to the occurrence of incorrect switching between maternal and paternal haplotypes for adjacent phased variants, while hamming error rate represents the total number of mis-phased variants per assembled contig. The completeness of genome assembly was checked according to benchmarking universal single-copy orthologs (BUSCOs) score. To identify assembly errors in these phase-resolved T2T assemblies, we used the calc_switchErr (v1.0) tool (https://github.com/tangerzhang/calc_switchErr), Yak (v0.1) (https://github.com/lh3/yak) and the WhatShap[2] (v2.0) pipeline (https://github.com/whatshap/whatshap). These tools enable weighted haplotype the assembly quality using the next-generation sequencing (NGS) reads.

For the 18 haplotypes from nine diploid accessions, we employed both *ab initio* prediction and evidence-based prediction methods to identify protein-coding genes (**Supplementary Note Figure 2a**), as well as repetitive regions such as centromeres and telomeres (**Supplementary Note Figure 2b**).



Supplementary Note Figure 2 | Overview of the genome and repetitive sequence annotations. a. Overview of the genome annotation pipeline. b. A panorama of repetitive sequence annotation.

Supplementary Note 4. Construction of graph pangenome

To represent the diverse grape genome, we constructed graph pangenome incorporating a total of 29 haplotype assemblies (from 18 grape accessions), including 18 newly sequenced haplotype assemblies and 11 previously published primary assemblies based on CLR data.

To reduce mapping errors commonly associated with raw read data, we constructed the graph pangenome directly from genome assemblies, which helped avoid the inherent errors from PacBio CLR-type reads. To obtain a high quality graph pangenome, we employed two tools to build grape graph pangenome, Minigraph-Cactus[3] (MC) (version 2.6.11) and PanGenome Graph Builder[4] (PGGB) (version 0.5.4), respectively (**Supplementary Note Figure 3**). The MC pipeline encompasses structural variations (SVs) exceeding 50 bp in length, as well as smaller variants, down to the SNP level, while allowing the graph to thoroughly represent the majority of variations and embed the input haplotypes within it as graphic paths. On the other hand, PGGB leverages a symmetrical, all-to-all comparison of genomes to produce and refine a pangenome. The resulting PGGB graph contains all alignment relationships in a singular graph. Therefore, we combined two graph pangenomes to investigate the full representation of grape genomic variations (**Supplementary Method 3**).

To classify gene families into core and variable categories, we employed the longest transcript from each haplotype as input. To reduce the impact of CLR sequencing-based assemblies in the core/variable gene family annotation, we selected one haplotype from each grape diploid accession. The high-quality primary assemblies derived from CLR sequencing were utilized, specifically opting for the H1 haplotype in haplotype-resolved assemblies. The CD-HIT[5] (version 4.8.1) tool was used to reduce redundant sequences. Then, we infer gene families by the OrthoFinder[6] (version 2.5.4) program. The resulting statistical summary was used for identifying the core and non-essential gene family sets. The results were classified according to their presence across different grape accessions: core gene families were designated as present in all 18 accessions; dispensable gene families were designated as present in 2 to 17 accessions; and unique to a single accession were denoted as private gene families.

Supplementary Note 4.1 Validation of graph pangenome

We combined reads mapping and assembly alignments to validate the graph paths, edges and nodes in the grape pangenome. These HiFi read-based assemblies were conducted in two haplotypes. Additionally, we carefully selected the primary haplotype of CLR read-based assemblies for validation. To address the issue of

small fragmented in assemblies, we implemented filtering steps to exclude minor, fragmented, and diverse assemblies that could introduce wrong structures.

Supplementary Note 4.2 Validation of pangenome SV map

We generated the high-quality pangenome SV map combining MC and PGGB algorithms (**Supplementary Methods 4 and 5**). The PGGB pangenome based on all-to-all mapping strategies, produced SV sets that lacked position information. Therefore, we used the PNT2T assembly as the reference to order the position of SVs. Based on each individual, we compared the SV generated by MC and SVIM-asm and obtained three validation metrics (precision, recall ratio and f1 score). The high-quality pangenome SVs were filtered for the downstream analysis.

Supplementary Note 4.3 Genomic landscape of structural variations

To investigate the landscape of SVs emerging in pan-genomes across genomes, we extracted sequences from the graph-based pan-genome that are absent in the reference genome for each individual genome, filtering out sequences shorter than 50 base pairs to constitute the dataset for analysis. We examined the distribution of these sequences within their respective genomes and concurrently assessed whether these sequences are present in other genomes. Furthermore, we also scrutinized whether these non-reference sequences overlap with Transposable Elements (TEs) or gene regions by referring to annotations for each genome (**Supplementary Methods 5**).

Supplementary Note 4.4 Re-genotyping pangenome SVs in a large population

To perform GWAS combined SVs and SNPs, we genotype the pangenome SVs and SNPs in 466 grape accessions with NGS data. The complex regions of PGGB pangenome may introduce additional challenges and uncertainties during SV or SNP genotyping based on Illumina sequencing data. Therefore, we chose to employ MC pangenome to generate the SV set as a reference file for population-scale SV and SNP genotyping. We created a Variant Call Format (VCF) file from a snarl traverse of the MC pangenome. This VCF contains entries representing bubbles within the fundamental pangenome graph and their embedded variations, deduced from the snarl tree. Each variant has been assigned a label corresponding to its position in the tree, with 'LV=0' denoting the uppermost bubbles. Given the limitation of short-read sequence length in identifying novel SVs, we used the re-genotyping tool PanGenie[7] (version 2.1.0) to genotype the variations (**Supplementary Method 6**). Based on this method, we avoided introducing unverified SVs and minimized the risk of false positives. As a result, we obtain a population-scale pangenome-based SNP and SV map.

Supplementary Note 5. Population structure

In this study, we aimed to elucidate the population structure using WGS data from 466 grape accessions (324 newly sequenced and 142 previously published accessions). We analysed the population structure and identified the major categories in grape cultivars (Table1, Table2 and Wine) using phylogenetic tree, principal component analysis (PCA), and ADMIXTURE. Due to the high frequency of heterozygous loci in grape genomes with an average of ~2% genome heterozygosity. Furthermore, we adopted an Potential of Heat-diffusion for Affinity-based Trajectory Embedding (PHATE) (https://github.com/KrishnaswamyLab/PHATE) (version 1.0.11) method to detect subtle genetic differences and captures global relationships transcending breed clusters. PHATE could translate high-dimensional data into two-dimensional representations and preserve global structures.

The resulting two-dimensional embeddings could reveal prominent linear trajectories from the central region of the plot, each linear trajectory indicates 2–5 principal components (PCs). These trajectories show the evolutionary paths traversed in grape populations, with the terminal ends representing the most divergent genetic states within the dataset and the basal sections approximating transitional states between inferred ancestral and terminal genomes.

Supplementary Note 6. Population differentiation

To identify signals of selection in grape populations during domestication, we performed several population statistics analyses using the genome-wide SNP map, including pairwise population fixation indices (F_{ST}) and nucleotide diversity (π). These genetic statistics analyses allowed us to detect selection sweeps in the single population and infer divergence between different populations. Additionally, we employed Selscan[8] (version 2.0.0) program to perform EHH-based (XP-EHH analysis) scans for positive selection in grape populations and candidate selected significant haplotype homozygous blocks.

To further examine the demography of different grape populations, we calculated identity-by-state (IBS) sharing pattern estimators. In addition, the selection of genome-wide SVs was analyzed by the linkage disequilibrium (LD) decay. The fate of SVs might be related to the frequency of genomic SVs in grape populations. Therefore, we used Sorting Intolerant from Tolerant (SIFT)[9] method to identify deleterious variants in grape populations (**Supplementary Method 9**).

Supplementary Note 7. Phenotype measure of 29 grape traits

We have investigated 29 agronomic traits in field experiments. The measurements and criteria of 21 phenotypes were based on the standardized protocols from the International Organization of Vine and Wine (OIV), with minor adaptations made for certain traits as necessary. In this work, our field experiments were conducted over two growing seasons, 2016 and 2017, to evaluate various berry traits.

For six bunch traits (shape; number of wings of the primary bunch; number of subsidiary bunches; density; weight of a single bunch; ease of detachment from the pedicel), three bunches collected from every table and wine accession were used to assess. Among them, the weight of a single bunch was measured using an electronic balance, and the average value of the three bunches was recorded. Individual berries were separated from their pedicels, and approximately 50 ripe berries were collected for further evaluation. Ease of detachment from the pedicel was also assessed at this time.

For eight berry traits (firmness of flesh; juiciness of flesh; particularity of flavor; shape; number of seeds; length of seeds; color of skin; uniformity of time of physiological stage of full maturity of the berry), we evaluated these traits through direct observation. The uniformity of the time of physiological stage of full maturity of the berry was evaluated through annual observation and documents. We collected samples and crushed them in a hand juicer, and the resulting pulp was examined to determine the number and length of seeds present. Firmness of flesh was determined employing a digital fruit hardness tester (STEP™ 41050+).

For four fruit size traits (berry length; berry width; single berry volume; single berry weight), we measured utilizing a vernier caliper or an electronic balance, and the average value of 50 berries was calculated. At the same time, the single berry volume was determined indirectly via the method of water immersion.

For three berry skin traits (astringency of skin; thickness of skin; bloom), the bloom and thickness of skin were determined by direct observation and judgement. And the astringency of skin based on subjective evaluation of human chewing.

We performed additional analyses to precisely measure eight flavor content traits (content of soluble solids; content of titratable acid; content of glucose; content of fructose; content of sucrose; content of tartaric acid; content of malic acid; content of citric acid). The must was then collected in a 50 ml centrifuge tube and subjected to centrifugation at 3000 g for a period of 10 min. The resulting supernatant was rapidly frozen in liquid nitrogen and stored at a temperature of 40℃ for

subsequent analysis of sugars and acids.

To assess the content of soluble solids, we employed a PAL-1 Brix Meter (ATAGO). We performed titration using a 0.1 M NaOH solution to quantify the titratable acid content. For the analysis of sugars and acids, 1 ml of each sample was initially passed through a Supelclean™ ENVI LC-18 SPE cartridge (Sigma-Aldrich, St. Louis, USA), followed by dilution to a final volume of 5 ml with deionized water. The diluted sample was then filtered through a 0.22 μm membrane filter to remove any impurities.

We utilized a Dionex P680 HPLC system for separation and detection of sugars and acids. Specifically, the sugar contents were detected using a Shodex RI-101 refractive index detector, which was maintained at a constant temperature of 40 degrees Celsius. We selected the Sugar-Pak I column (300 mm × 6.5 mm I.D., 10 μm particle size, Waters, USA) coupled with a Sugar-Pak I Guard-Pak Insert (10 μm particle size, Waters, USA) for our analyses. The column was kept at a temperature of 90°C using a Dionex TCC-100 thermostat column compartment. Double-distilled water served as the mobile phase, and the flow rate was set at 0.6 ml/min. Peak area integration was carried out using the Chromeleon chromatography data system, with reference to external standard solutions obtained from Sigma-Aldrich (St. Louis, USA).

For the detection of malic and tartaric acid contents, we employed a Dionex PDA-100 detector. Our analytical approach involved the utilization of the Dikma PLATISIL ODS column (250 mm × 4.6 mm I.D., 5 μm particle size, Dikma, China), paired with a Dikma Spursil C18 Guard Cartridge (3 μm, 10 mm × 2.1 mm, Dikma, China). The column temperature was maintained at 40°C throughout the analysis. Elution occurred with a 0.02 mol/L KH_2PO_4 solution at pH 2.4, and the flow rate was 0.8 ml/min. Ultraviolet absorption at a wavelength of 210 nm allowed for the detection of eluted compounds. Finally, acid concentrations were determined based on external standard solution calibrations.

Supplementary Note 8. Genome-wide association studies (GWAS)

Supplementary Note 8.1 Graph pangenome SNP based GWAS

This study conducted GWAS analyses on 324 newly sequenced grape varieties with two-year phenotype data (two growing seasons, 2016 and 2017), leveraging high-quality population-scale SNP and SV datasets. The GWAS employed a mixed linear model (MLM) and performed 1000 permutations analysis (see **supplementary Method 10**). An important assessment of GWAS is to perform

multiple testing correction thresholds. Given the vast number of tests involved, the Bonferroni correction may be overly conservative, since it assumes independence between markers, which does not hold true for high-density genomic data sets such as ours. To address this issue, we resorted to permutations instead of the Bonferroni test, thereby maintaining result accuracy while maximizing the retention of relevant sites. Following identification of significant loci, we computed the phenotypic variation explained (PVE) for each locus using a specific formula (see **supplementary Method 10**). Additionally, we screened adjacent loci via LD and retained only the most significantly associated site exhibiting the highest PVE value, thus representing the significant genomic loci.

Supplementary Note 8.2 Graph pangenome SNP+SV based GWAS

GWAS employs the identical approach outlined in **Supplementary Note 8.1**. Because of the inherent features of SV, it is impossible to integrate the kinship generated by SV into GWAS to adjust for population substructure; therefore, we utilize the same kinship matrix and PCA as covariates computed using pangenome SNP. Due to the limited linkage between SV and SNP, our analysis revealed genetic loci that were not detected when relying solely on pangenome SNP data.

Supplementary Note 8.3 PNT2T reference SNP based GWAS

To facilitate comparison with the findings derived from the pangenome, we leveraged traditionally obtained SNPs and employed the same statistical model and parameter settings, we performed GWAS using the single reference (PNT2T) SNP datasets. Our results demonstrate a high degree of concordance between the two sets of findings, providing support for the validity of our approach.

Supplementary Note 9. Heritability estimation and genetic correlation

The heritability of a trait is the fraction of PVE by additive contributions from genome-wide SNPs. Accurate estimates of heritability are central to resolving the missing heritability debate. The LDAK program provides us with an improved model for heritability estimation by deriving approximate relationships between the expected heritability of a SNP and MAF.

We incorporated LDAK program to calculate the heritability using the genome-wide variation map. LDAK incorporates a generalized restricted maximum likelihood (REML) solver to estimate the heritability attributed to kinship matrices. To determine the heritability ratio of SNP and SV in traits, we must first obtain separate kinship matrices calculated using SNP and SV, and then estimate

the appropriate alpha value (**Supplementary Method 11**). Our approach involves filtering out genotyping error and nearly linked mutation sites, followed by utilization of the LDAK-Thin model for kinship matrix estimation. Since LDAK cannot directly estimate alpha, we adopt an alternative strategy involving trial of multiple alpha values by comparing the highest log likelihood and the value estimates derived from identifying the Gaussian distribution, ultimately selecting the one that best fits the data.

In addition, we quantify the genetic correlation between two traits as the average correlation between variant effect sizes. A positive correlation signifies that variants with a positive impact on Trait 1 tend to have a positive influence on Trait 2. To estimate the genetic correlation between a pair of traits, we perform calculations using the LDAK-Thin Model and subsequently regress two sets of GWAS summary statistics against the tagging file (**Supplementary Method 11**).

Supplementary Note 10. Compute Polygenic score (PGS)

Complex traits are influenced by a multitude of genetic loci, each having a minor effect on the phenotype. Individual trait evaluation is not feasible with a single variation, and polygenic scores are necessary to capture the collective effects of multiple genetic variants. All traits examined in this study belong to the category of complex traits. To establish a connection between genetic variation and phenotype, we employed a method that combines LD between loci and multiple genetic variations, calculating polygenic scores (PGS) through the application of LDpred2 program (**Supplementary Method 12**).

To mitigate overfitting issues arising from excessive variable numbers and enhance computational efficiency, we initially clustered all genomic variations using BigSNPR[10]. Subsequently, we partitioned the dataset into three subsets: a training dataset comprising 70%, a tuning dataset consisting of 20%, and a test dataset constituting 10%. The training dataset was leveraged to produce SNP summary statistical data as described in **Supplementary Method 8**. The test dataset assumed the role of an independent test set for assessing the performance of the ultimate models.

Supplementary Methods

Supplementary Method 1. Genome sequencing and assembly

Supplementary Method 1.1 DNA extraction

Young and fresh leaves were harvested from each individual grape genotype. Samples were immediately stored in liquid nitrogen and moved to a −80 °C freezer. Genomic DNA was extracted from the young leaves freezing in liquid nitrogen using DNeasy Plant Mini kit (Qiagen). At all steps, DNA quantity and quanlity were checked by NanoDrop One spectrophotometer (NanoDrop Technologies, Wilmington, DE), and Qubit 3.0 Fluorometer (Life Technologies, Carlsbad, CA, USA) with a dsDNA HS Assay kit (Thermo Fisher). The Blue Pippin system (Sage Science, Beverly, MA) was used to retrieve large DNA fragments by gel cutting.

Supplementary Method 1.2 HiFi sequencing

High-molecular-weight DNA using a Femto Pulse gDNA 165kb analysis kit and sheared using a Diagenode Megaruptor III to 5 - 100 kb DNA mode size. SMRTbell libraries were prepared for sequencing according to the protocol 'Procedure & Checklist-Preparing HiFi SMRTbell Libraries using the SMRTbell Express Template Prep Kit 2.0'. After SMRTbell generation, material was size-selected on a AMPure PB system (PacBio), DNA fragments smaller than 5-kb were removed for sequencing. The selected library fractions were bound with Sequencing Primer v.2.0 and Sequel II Polymerase v.2.0 and sequenced on Sequel system (PacBio) on Pacific Bioscience Sequel II platform. Each sample was sequenced to a minimum HiFi data amount of 30 Gb (60-fold estimated genome coverage).

Supplementary Method 1.3 Nanopore ultra-long sequencing

For the ultra-long Nanopore library, approximately 2.5 μg of genomic DNA was selected (> 100-kb) with the Sage HLS HMW library system (Sage Science), and then processed using the Ligation sequencing Kit (Catalog No. SQK-LSK110, Oxford Nanopore Technologies, Oxford, UK) according to the manufacturer's instructions. DNA libraries were constructed and sequenced on the PromethION (Oxford Nanopore Technologies) at the BENAGEN (Wuhan, China).

Supplementary Method 1.4 Hi-C sequencing

Hi-C library was prepared from cross-linked chromatins of plant cells using a standard Hi-C protocol. At last, the Hi-C libraries were amplified by 12-14 cycles PCR, and sequenced in Illumina HiSeq platform. Sequencing interacting pattern was obtained by Illumina NovaSeq instrument with 2×150-bp reads.

Supplementary Method 1.5 Phase-resolved assembly pipeline

For three grape accessions (SM, MH, MF), we integrated HiFi, ultra-long ONT and Hi-C reads for nine genome assemblies using Hifiasm[11] (version v0.19.5-r587) program with default parameters. The remaining contig-level assemblies were then anchored and oriented to 19 chromosomes based on PNT2T genome

similarity using RagTag[12] (version 1.0.1) with default parameters. Two sets of HiFi haplotype contigs were subsequently validated, grouped, sorted, and anchored with the Hi-C reads to generate two pseudochromosomes using Juicer and 3D-DNA programs. Additionally, we utilized Juicebox[13] (version 1.11.08) to visualize and inspect the Hi-C data. Furthermore, NextDenovo[14] (version 2.5.0) was employed to assemble the ONT data with the following parameters: genome_size = 480M, read_cutoff = 1k. We mapped the HiFi and ONT reads to the genome using Minimap2, respectively. Breakpoint locations were inferred using the BAM files and visualized based on Integrative Genomics Viewer[15] (IGV) (version 2.13.1) tool. The gaps filling was performed using the ONT assemblies and mapped reads, resulting in gap-free T2T assemblies of nine diploid grapes. For other grapes (TS, BM, WG, PN, HMNG, BMNG): We mapped ONT readings to the genome and manually filled in the gaps.

Supplementary Method 1.6 Validation of gapless T2T assembly

We validated the quality of T2T assemblies based on the phase variation map, we calculated hamming error and switch error for nine accessions. Firstly, we used the software package WhatsHap[2] (version 1.1) for constructing a precise phase variation map based on the PacBio HiFi reads. The HiFi and Hi-C reads were used to generate individual BAM files using minimap2[16] (version 2.26-r1175) (minimap2 --cs --MD -ax map-hifi --secondary=no) and BWA[17] (version 0.7.17) (bwa mem), respectively. By combining these resulting BAM files, we designated phased SNPs bearing the 'PS' label as putative true positives for further evaluation. The ‘true’ phased SNP was calculated based on two phased SNPs datasets by getTrueData.pl. Secondly, we compared the genome-phased SNPs with the true phased SNP dataset using 'calc_switchErr.pl' and calculated the hamming error values. To facilitate this step, we converted the 'clrT_SNPs' file generated earlier into a VCF format using 'my-mummer-2-vcf.py'. We then added genotypes to each SNP using '01_add_GT.py'. Finally, we detected the consensus SNP in the two VCF files (true_vcf and genome_VCF) using bcftools (bcftools isec) and computed the switch error value using 'whatshap compare'.

We also assessed the completeness of the genome assembly. We used Yak to generate a K-mer database for each haplotype using the HiFi reads with the following command: yak count -t16 -b37 -o line.yak line.fq.gz. Then, we estimated the QV (consensus accuracy) for each haplotype using Yak's qv function (yak qv -t 20 -p line.yak line.fa). In addition, we also employed BUSCOs[18] (version 5.2.2) to assess the completeness and repeat content of the genome assembly. The contig N50 length was calculated by seqkit (version v2.2.0) program and we evaluated genome heterozygosity through a K-mer-based approach implemented using GenomeScope2.0[19] (version 1.0.0). We identify hemizygous genomic regions by analyzing heterozygous SVs, particularly deletions and insertions, between two

homologous haplotypes. Regions where the entire gene structure (100%) is located within an insertion/deletion region were classified as hemizygous.

Supplementary Method 2. Genome annotation

Supplementary Method 2.1 The annotation of repeat sequences

Telomere repeat units were investigated utilizing TIDK (https://github.com/tolkit/telomeric-identifier) (version 0.2.0) with the following command-line arguments: tidk explore -f genome.fa --minimum 5 --maximum 12 -o tidk_explore -t 2 --log --dir telomere_find --extension TSV. Subsequently, the entire genome underwent an in-depth search employing the parameter: tidk search -f genome.fa -s 'TTTAGGG' -o tidk_search --dir telomere_find. Lastly, we rapidly generated statistics pertaining to telomere regions and visualized the telomere peaks.

To investigate tandem repetitive sequences and centromeric areas, we used Tandem Repeats Finder[20] (TRF, version 4.09) to generate the statistics of the number of repeats and position information. These statistics were combined to annotate the centromeric repeats.

Transposable elements (TEs) were identified by the combined multiple programs. We combined all assemblies to generate the non-redundant TE catalogs. The RepeatMasker (https://github.com/rmhubley/RepeatMasker) (version 4.1.2, -e rmblast -lcambig -pa 2 -s) was used to execute homolog annotation. Thus, we created a full TE annotation for each accession by merging the EDTA-constructed library.

Supplementary Method 2.2 The annotation of genes

We implemented a uniform annotation workflow to enhance the prediction of gene structure of all assemblies. We combined transcript evidences from RNA-seq datasets across diverse tissues, including floral, leaf, stem, root and fruit. To improve the annotation process, we employed Hisat2[21] (version 2.10.2) to align RNA sequencing reads against the repeat-masked assemblies. The mapping states were extracted using the StringTie[22] (version 1.3.0) program. We mainly relied on the customs scripts integrating Braker (version 3.0.1), PASA[23] (version 2.5.1) and MAKER[24] (version 3.01.03) programs for our genome annotations. We developed gene models and conducted subsequent searches utilizing AUGUSTUS[25] (version 3.4.0). In addition, we removed genes residing within duplicated regions, had coding sequence lengths below 90, or lacked supporting evidence. We then checked the incomplete genes and alternative splicing events and filter low confidence gene structures based on hidden Markov models and Pfam[26] (version

1.6) database.

Furthermore, we assess the start codon errors, nonsense mutations and frameshifts to improve the quality of annotation. We eliminated transcripts that failed to initiate with ATG start codon and premature termination codons. By iteratively traversing each codon in the coding sequence, we identified nonsense mutations. We looked for gaps in the alignment by iterating over the sequence. If the gap had a non-multiple-of-three length and under 30 base pairs, we classified it as a frameshift and adjusted the affected transcript appropriately.

Supplementary Method 3. Graph pangenome construction

Supplementary Method 3.1 Minigraph-Cactus (MC) pangenome

The Comparative Genomics Toolkit (CGT) provides guidelines for data preparation in this study. We implemented the MC pipeline using the command line "cactus-pangenome js pan.txt --outDir grape-pan --outName grape-pan --reference PNT2T --vcf --giraffe --gfa –gbz" to generate the MC grape pangenome graph. This command will produce multiple graph file types that can be utilized in subsequent analytical pipelines. The latest reference genome of grapes (PNT2T) was used as the guide reference for the underlying graph paths. MC constructs a pangenome graph through five distinct phases.

Phase 1: Highly repetitive sequence masking:

Minigraph is unable to map through highly repetitive sequences such as centromeres and telomeres and, as these regions are also enriched for misassembles, we exclude them from the MC graphs.

Phase 2: Assembly-to-graph mapping

Minigraph_construct generalizes the fast seeding and chaining algorithms of minimap2. The resulting minimizers were then converted into PAF files with cigars representing exact pairwise alignments between the query contigs and node sequences.

Phase 3: Chromosome decomposition

These alignments were divided by reference chromosome. We identified the coverage of each query contig with each chromosome component. This coverage was used to assign each query contig to a single chromosome. Contigs with insufficient coverage were not included in the graph.

Phase 4: Cactus base alignment:

Cactus was used to combine sets of pairwise alignments into a multiple genome alignment. The pairwise alignments were used to induce a sequence graph, and components of unaligned sequence were then processed by the refinement algorithm. Software hal2vg converts the HAL alignment into a sequence graph in VG format.

Phase 5: Post-processing:

Unaligned sequences (>100 kb) were removed that might later be mistaken for insertions. GFAffix was used to normalize the graphs by merging together redundant node prefixes and suffixes. Nodes were flipped as necessary to ensure that reference paths always keep forward orientations. The chromosomes were combined into a whole-genome graph, and we indexed the graph and exported it into the VCF format using vg. The improved graph was produced by removing all nodes traversed by fewer than 2 haplotype paths using vg clip -d 2.

Supplementary Method 3.2 PanGenome Graph Builder (PGGB)

We employed the software package (https://nf-co.re/pangenome/1.0.0) to execute an adapted variant of the PGGB algorithm, which enables the distribution of computationally intensive alignment steps across an entire cluster, thereby accelerating tasks. PGGB constructs a pangenome graph through four distinct phases.

Phase 1: Alignment

Wfmash was specifically designed and developed to address the challenge of building all-to-all alignments for extensive pangenomes. We set the percent identity in the wfmash mashmap step to 90, the segment length for mapping to 5000, and the kmer size for mashmap to 19. Subsequently, we merged successive mappings.

Phase 2: Graph Induction

We transformed the input FASTA sequences and PAF-format alignments generated by wfmash into a graph (in GFA format) using seqwish. This process converts the input alignments and sequences into a graph while ignoring exact matches below 19 bp. We set the parameter for transitive closure batch to 10 M base pairs.

Phase 3: Graph Normalization

To simplify complex motifs occurring in STRs and other repetitive sequences, we applied a normalization algorithm called smoothxg. We specified the score parameters for POA as presets: 'asm5'. The maximum sequence length

to put in POA was set to 700,900 and 1100, and smoothxg was executed once for each integer.

Phase 4: Redundant Furcation Removal

We utilized GFAffix (https://github.com/marschall-lab/GFAffix) to eliminate redundant furcation from the topology of the graph.

Supplementary Method 4. Graph pangenome assessment

This study employs the odgi[27] (version 0.8.4) pangenome analysis toolkit to investigate the growth of the grape pangenome. We focused on estimating the pangenome's size incorporating 28 non-reference haplotypes (excluding PNT2T), followed by calculations of the pangenome's size after sequentially integrating haplotypes with the designated permutation. Our methodology consists with the command line 'odgi heaps -i <graph.gfa> -S -n200' to produce pangenome saturation curves for 200 permutations. These computations yield a collection of saturation curves with a power law function, commonly referred to as Heaps' Law. In addition, we perform two types of base counting: one for cumulative base counts without permuting, and another for common (occurring in ≥5% of all non-reference haplotypes) and core (present in ≥95% of all non-reference haplotypes) bases in the pangenome graphs. Then, we used the panacus tool and supply it with a list of samples organized by their assigned superpopulation “pangenome-growth -m -t bp graph.gfa sample_order”. We repeat the base counting process and consider at least two supported segments in all haplotype sequences.

Supplementary Method 5. Structural variation benchmarking

To identify variant sites in both the MC and PGGB graph pangenomes, we employed the utility vg deconstruct. Large deletions exceeding 10 Mb in length were filtered from the MC and PGGB graphs using vcfbub (https://github.com/pangenome/vcfbub) (version 0.1.0) with the following parameters: -l 0 -r 10000000. Then, we categorized variant sites into two distinct classes: small variants (<50 bp) and structural variants (SVs) (≥50 bp). Utilizing SVIM-asm[28] (version 1.0.2), we performed SV call command based on haplotype-resolved assemblies. These assemblies were aligned to the PNT2T reference genome using Minimap2[16] (version 2.21), with the following flags: -x asm5 -a --eqx --cs. The resulting SAM files were then sorted and indexed employing SAMtools. For the purpose of calling SVs, we leveraged SVIM-asm in both diploid and haploid modes, with the following options: --query_names --

interspersed_duplications_as_insertions --min_sv_size 50. The output VCF files were subsequently sorted and indexed using BCFtools.

Furthermore, we refined the SV dataset by removing variant sites featuring alleles larger than 100 kb in both MC and PGGB graphs via vcfbub (version 0.1.0), with the following options: -l 0 -a 100000. Following this, we applied vcfwave from vcflib, selecting the -I 1000 option, to realign alternate alleles against the reference and decompose complex alleles into their constituent parts. We transformed the multi-sample VCF files into single-sample VCF files and split multiallelic sites into biallelic records through the use of bcftools view and norm. To assess the performance of our SV (≥50 bp) calling procedure, we pursued the following three-step strategy: 1) We created confident regions applying Dipcall. 2) We contrasted the SV sets obtained from the pangenome graph and SVIM-asm for every individual utilizing truvari (version 4.1.0), with the following options: --multimatch -r 1000 -C 1000 -O 0.0 -p 0.0 -P 0.3 -s 50 -S 15 --sizemax 100000. 3) We calculated recall and precision values while considering the GIAB (version 3.0) genomic environment and variant length.

In order to extract non-PNT2T reference node BED files from the pan-genome generated using PGGB, we employed odgi paths with the --non-reference-ranges parameter. Subsequently, different genomic path instances were isolated utilizing grep. The distribution density of SVs along the genomes was visualized through CMplot[29] in R. Next, we utilized odgi pav to calculate the percentage of alignments for these sequences in other genomes; sequences with an alignment similarity threshold of 80% or higher were considered present in those genomes. We then enumerated the occurrences of each sequence in different genomes. Lastly, to assess overlaps, we employed bedtools (version 2.30.0) intersect to statistically quantify intersections between SVs and intervals of various types of Transposable Elements (TEs) as well as gene regions.

Supplementary Method 6. Using PanGenie for SV genotyping

We used PanGenie (version 2.1.0) to perform genotyping based on 466 samples with Illumina reads. We prepared a VCF file representation of a directed and acyclic pangenome graph from four essential attributes: multi-sample, fully phased, non-overlapping variants, and sequence resolution. We used vcfbub with parameters -l 0 and -r 100000 to filter the pangenome variation map. This filtering process eliminated non-top-level bubbles from the VCF unless they were embedded within a top-level bubble with a reference length surpassing 100 kb. The top-level bubbles longer than that were substituted by their child nodes in the snarl tree. 1.VCF preprocessing

The MC pangenome contained various bubble and their nested SVs. We used vcfbub (v.0.1.0) to filter the SV correspond to the top-level bubbles and keep non-top-level bubbles. Next, we used PanGenie to genotype these bubbles across all 466 samples. PanGenie is a re-genotyping tool. These re-genotype variants were provided in the input VCF, meaning the output VCF will contain the same variant records as the input. We run PanGenie-index to process the input variants and determining unique k-mers in the graph. We combine paired reads file and run PanGenie on each accession separately. We performed the genotyping step independently for each sample, culminating in the generation of a unique VCF file for each sample. By employing 'bcftools merge', we produced a solitary VCF file suitable for further examination.

Whereas biallelic bubble can be easily classified, this becomes more difficult for multiallelic bubble. To address this issue, we implemented a adds annotations to the alleles encoding variants nested inside of graph bubbles. The biallelic bubble-based VCF is used for downstream GWAS analysis, utilizing positional information to trace the original multi allele information. The multiallelic bubble-based VCF was used for haplotype graph classification.

Supplementary Method 7. SNPs and InDels genotyping

Short reads were aligned to the MC pangenome utilizing Giraffe command from vg program. The allele-filtered graphs, which served as inputs for short-read mapping, were created by vg clip -d 2 -m 10000, removing all nodes traversed by a single haplotype path. An index file was generated for the pangenome using vg autoindex with the option -w giraffe. Subsequently, three index files with the suffixes "gbz", "d2.dist", and "d2.min" were used to produce BAM files. The resulting BAM files underwent sorting and splitting according to chromosomal coordinates using SAMtools[30] (version 1.3.1) . Variants were identified at an accelerated pace courtesy of GTX (version 2.2.1) to generate high-quality InDel and SNP maps.

Supplementary Method 8. Analysis of gene families

We used the OrthoFinder[6] (version 2.5.4) to analyze gene families based on our gene annotations and identified non-redundant gene clusters. To facilitate further analysis, we categorized these clusters into four distinct groups: (i) core gene clusters, characterized by their conservation across all 29 grape assemblies; (ii) soft-core gene clusters, present in 16–17 grape assemblies; (iii) dispensable gene clusters, detected in 2–15 grape assemblies; and (iv) private gene clusters,

containing genes exclusive to a single grape accession, including unassigned genes. For each gene cluster, we selected the longest encoded protein as its representative.

Supplementary Method 9. Identification of deleterious variants

To examine the deleterious burden of grapevine populations with varied outgroup compositions, we employed the SIFT algorithm to predict potential deleterious single nucleotide polymorphisms (dSNPs). We computed derived deleterious mutations based on ancestral genotypes inferred from three outgroups. Utilizing the make-SIFT-db-all.pl software, we generated the SIFT genomic databases by importing the reference genome, gene annotation file, and SWISS-PROT protein file. Subsequently, we used SIFT 4G Annotator for identifying deleterious mutation assessment (https://github.com/paulineng/SIFT4G_Create_GenomicDB). The amino acid substitutions were classified as deleterious if the score was ≤0.05, and tolerable if the score was >0.05. However, it is important to note that reference bias may still exist in the classification of SIFT prediction functions. Moreover, for each individual, we calculated homozygous loci of the derived deleterious allele as recessive deleterious mutations and added the number of heterozygous deleterious mutation loci plus two times the number of homozygous deleterious mutation sites to calculate additive deleterious mutations.

Supplementary Method 10. GWAS

Supplementary Method 10.1 Model selection

In this study, we utilize permGWAS[31] to perform GWAS employing permutation-based thresholds. For each genomic locus, we specify a linear mixed model (LMM) of the form:

$$y = X\beta + u + \varepsilon$$

where n represents the sample size, m is the number of genetic markers, $y \in R^n$ is a vector of observed phenotypic values, $X \in R^{n \times c}$ is a matrix of fixed effects comprising columns for the mean, covariates, and the genetic marker, and $\beta \in R^c$ denote fixed effects. The random effects, $u \in R^n$, follow a Gaussian distribution with a zero mean and a (genetic) variance of $\sigma^2_g K$, where $K \in R^{n \times n}$ represents the kinship matrix. Finally, $\varepsilon \in R^n$ is a vector of residual effects with $\varepsilon \sim N(0, \sigma^2_e I)$.

To facilitate downstream analysis, we employed bcftools norm to split multiallelic genotypes in the SV file into single alleles. Subsequently, we leveraged bcftools

concat command to merge the resulting SNP and SV files. Furthermore, we converted the genotype matrix to an additively encoded format (012) using PLINK[32] (version v1.90b6.21), which also enabled us to generate an H5 file as input for further analyses using create_h5_file.py, a utility provided by permGWAS. To establish a kinship matrix, we availed ourselves of the capabilities of permGWAS, which computed the kinship matrix as part of its preprocessing steps. As a prerequisite for our association analysis, we selected the first five principal components as covariates and incorporated them into the model by specifying the appropriate parameter, '--cov'. Additionally, we specified '--perm 1000' to instruct permGWAS to perform 1000 iterations of permutation testing. PermGWAS executed a standard GWAS initially, followed by generating 1000 permutations of the phenotype. It then calculated permutation-based p-values and minimal p-values, which allowed us to determine a permutation-based threshold using the maxT/minP approach.

Supplementary Method 10.2 Phenotypic variation explained (PVE)

The phenotypic variation explained (PVE) of the most significantly associated single variant was estimated using the following formula:

$$PVE = [2 \times (beta^2) \times MAF \times (1 - MAF)]/[2 \times (beta^2) \times MAF(1\text{-}MAF) + ((s.e. \times (beta))^2) \times 2 \times N \times MAF \times (1 - MAF)]$$

Where N represents the sample size, s.e. is the standard error of the effect size of genetic variants, *beta* is the effect size of genetic variants, and MAF is the minor allele frequency of the target marker. We obtained the frequency based on the pangenome SV and SNP map using the custom script. The *beta* and s.e. value were calculated by permGWAS. We used N=324 in the calculation of PVE for most significant variant in each GWAS loci for 29 traits.

Supplementary Method 11. Estimation of heritability and genetic correlation

Supplementary Method 11.1 Heritability calculation

To estimate the proportion of phenotypic variance explained by genetic variants, we employed the LDAK-thin model. First, we pruned the genetic variants using LDAK-thin with parameters '--window-prune 0.98 --window-kb 100' to exclude nearby SNPs in perfect LD. We tried 16 values between -1 and 0.5 for the step size, and found that $alpha_{SNP} = 0.2$ and $alpha_{SV} = -0.5$ provided the optimal fit for most scenarios. As covariates for estimating heritability, we used the first five principal components. To assess the contributions to heritability from various types of

genetic variants, we derived the kinship for each variant category and applied a composite model with multiple kinship matrices using the parameters '--mgrm'. Finally, we included the parameter '--constrain YES' to prevent negative estimates of heritability.

Supplementary Method 11.2 Genetic correlation

We did not distinguish between SNP and SV in our genetic correlation analysis of traits. The genetic variants were filtered using LDAK-thin with parameters '--window-prune 0.98 and --window-kb 100' to eliminate nearby SNPs in perfect LD. We employed the LDAK-thin model to generate a tagfile containing the relevant genetic information. We extracted the location, allele frequency, beta coefficient, and significance of each genetic variant from the results of GWAS and compiled them into a summary file. These summaries of the two traits were generated by the parameter '--summary' and the generated tagfile into LDAK with parameter '--tagfile'. Finally, we extracted the relevant information from the output file <trait1_trait2>.cors and used it as input for visualization in Cytoscape.

Supplementary Method 11.3 Polygenic scores (PGS)

To retain a subset of SNPs that are nearly uncorrelated with one another, we used clumping to select one representative SNP per region of LD. Specifically, we set the parameter 'thr_r2 = 0.2' and 'size = 100/thr.r2' , which determines the minimum correlation threshold for clustering SNPs. We utilized snp_cor with the parameter 'size = 200' to calculate the correlations between SNPs, assuming that correlations with other variants outside of a 200 kb window as zero. To infer PGS, we used the software packages LDpred2-auto and lassosum2. The test set was verified using the generated model and we calculated the correlation between the predicted and actual values of the quantitative trait using the 'pcor' function in R.

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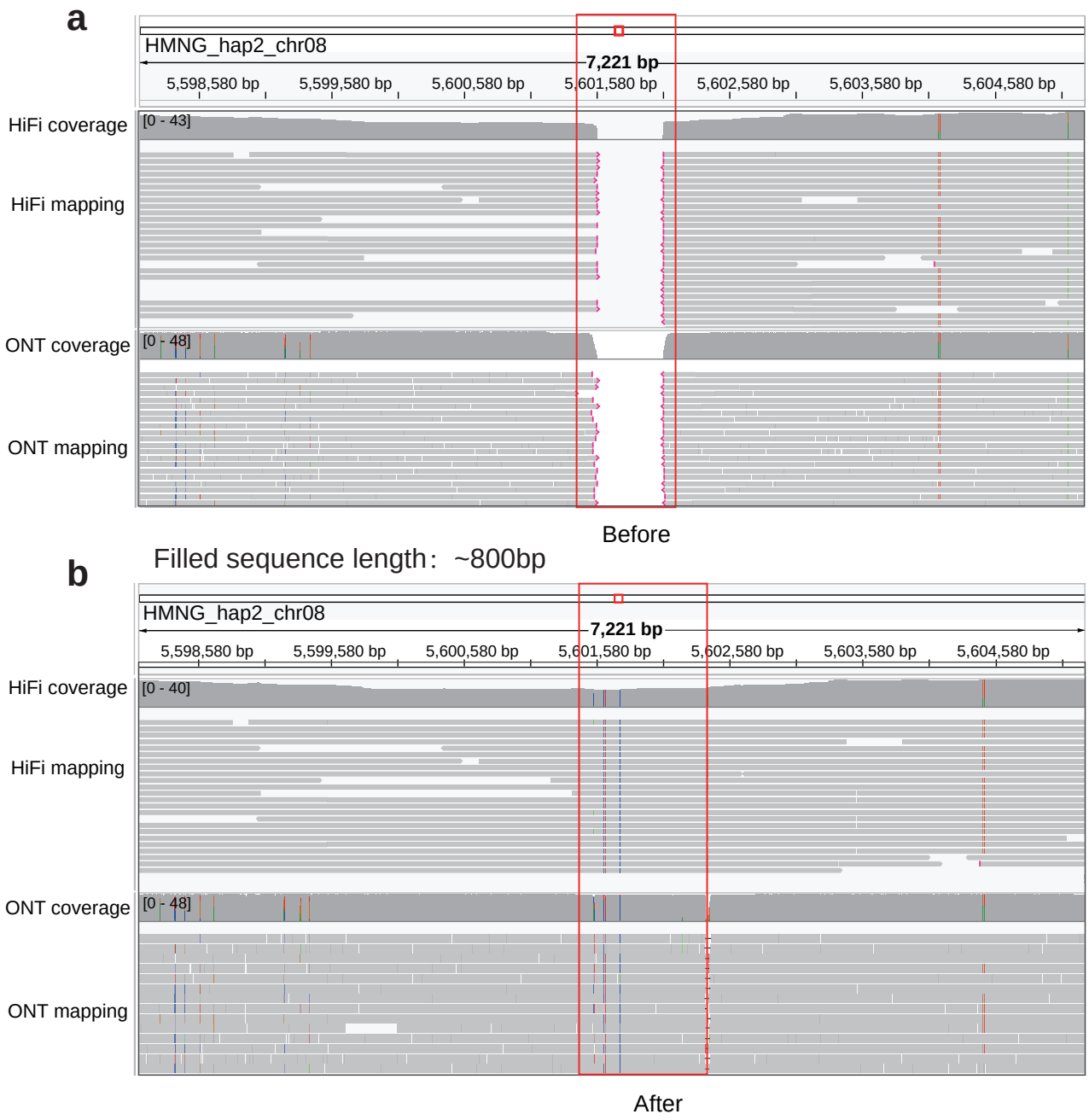
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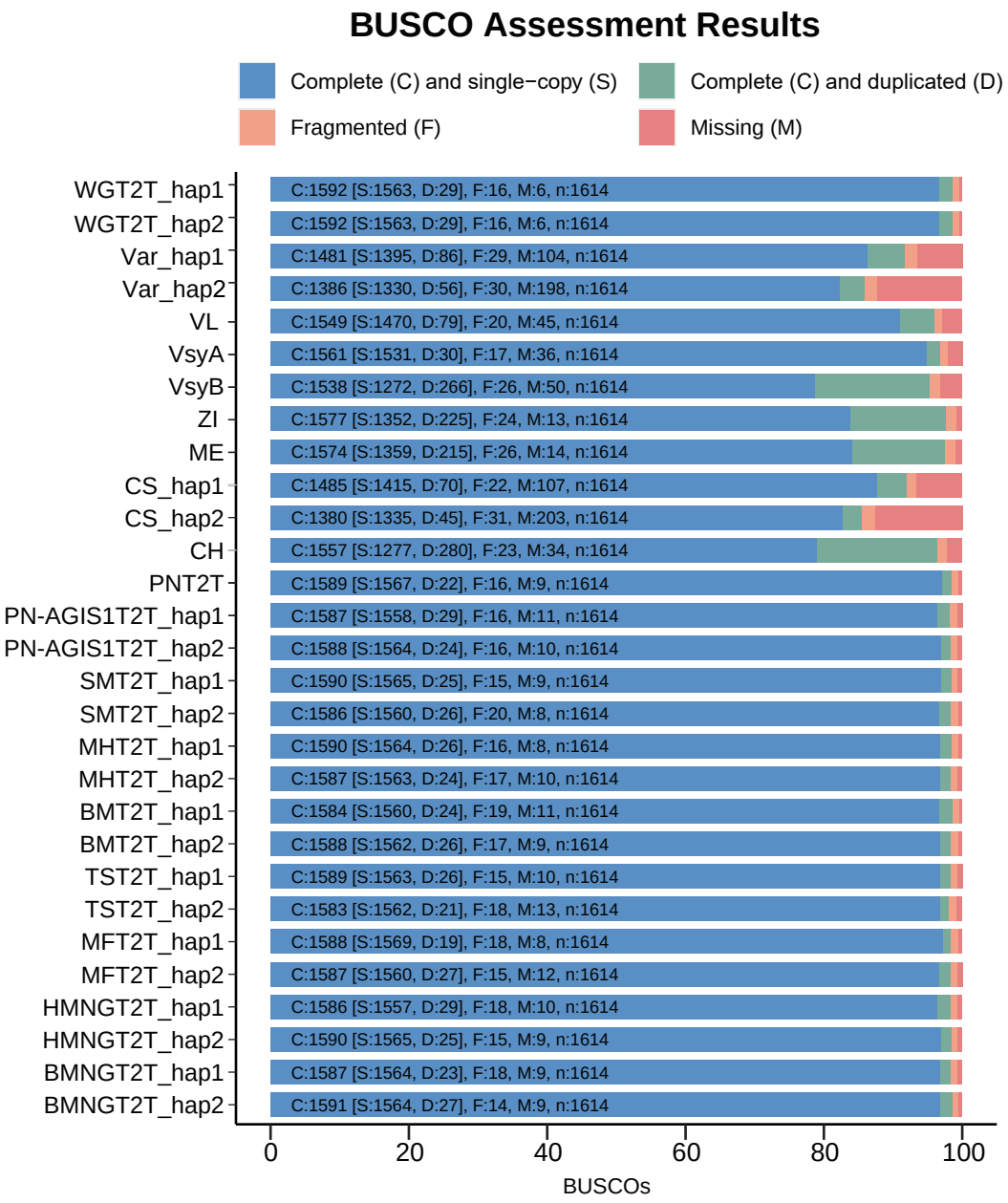
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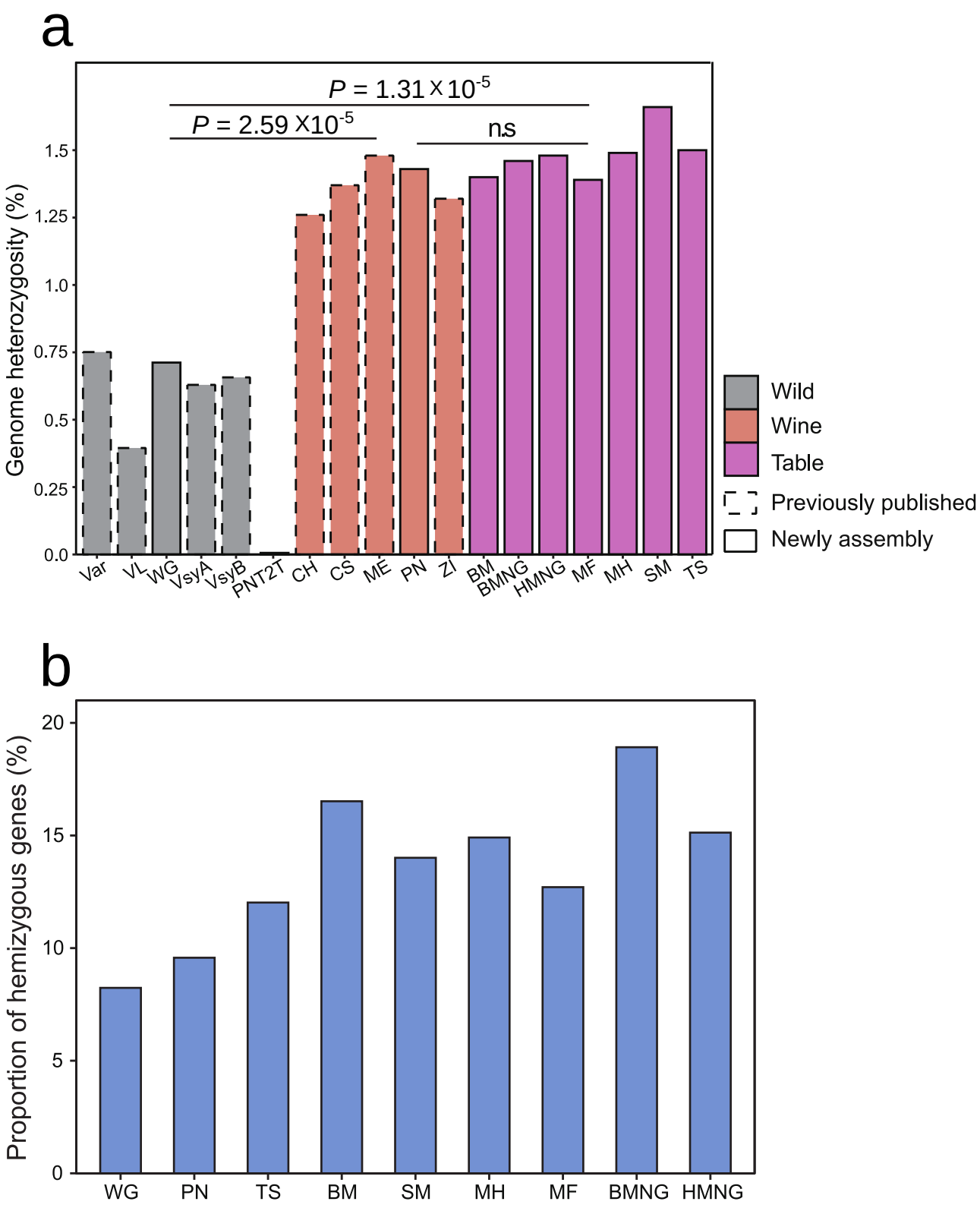
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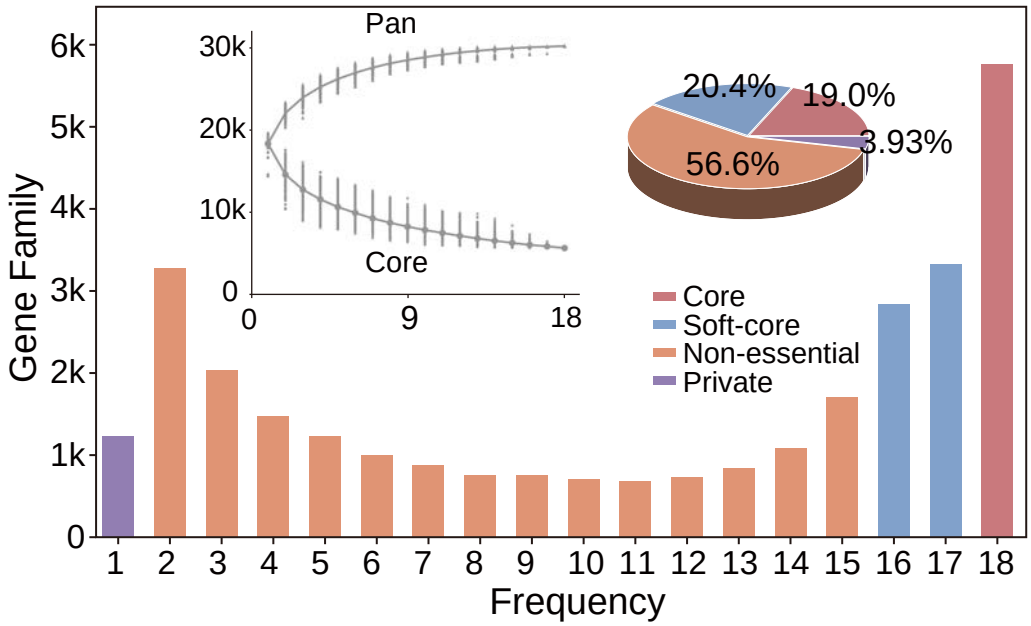
Supplementary Fig. 1. | An example of a filled gap visualized by Integrative Genomics Viewer (IGV). a. A gap (red line area) on chr08 of assembly of HMNG_hap2 before gap filling. **b.** The genome alignment visualization after gap filling.



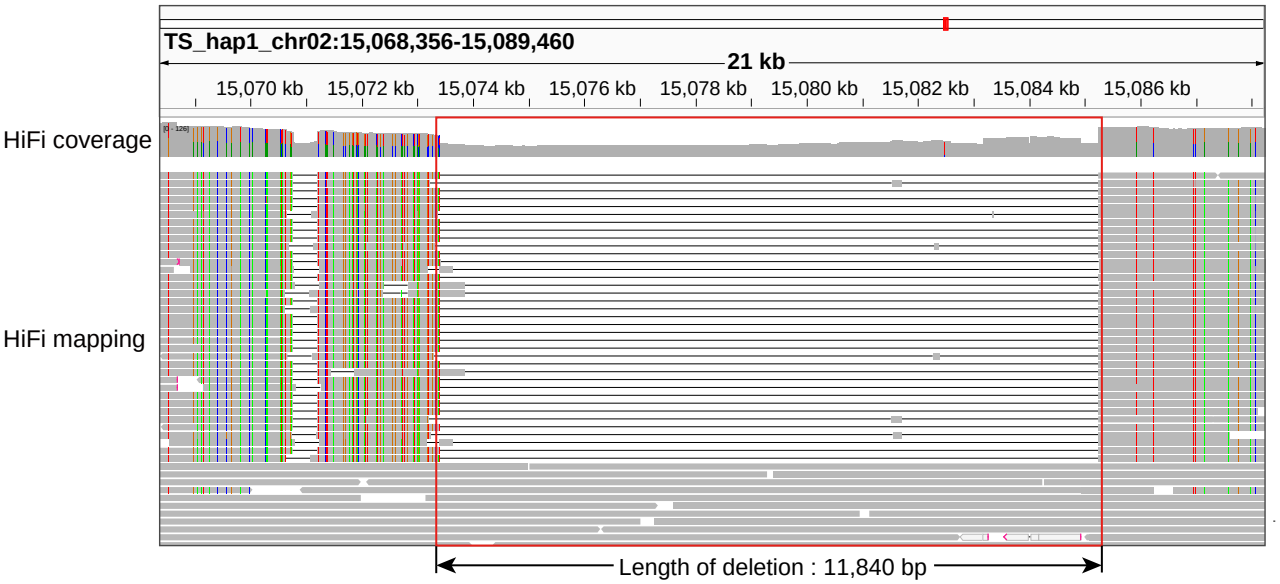
Supplementary Fig. 2. | Genomic completeness estimation of assemblies by benchmarking universal single-copy orthologs (BUSCOs).



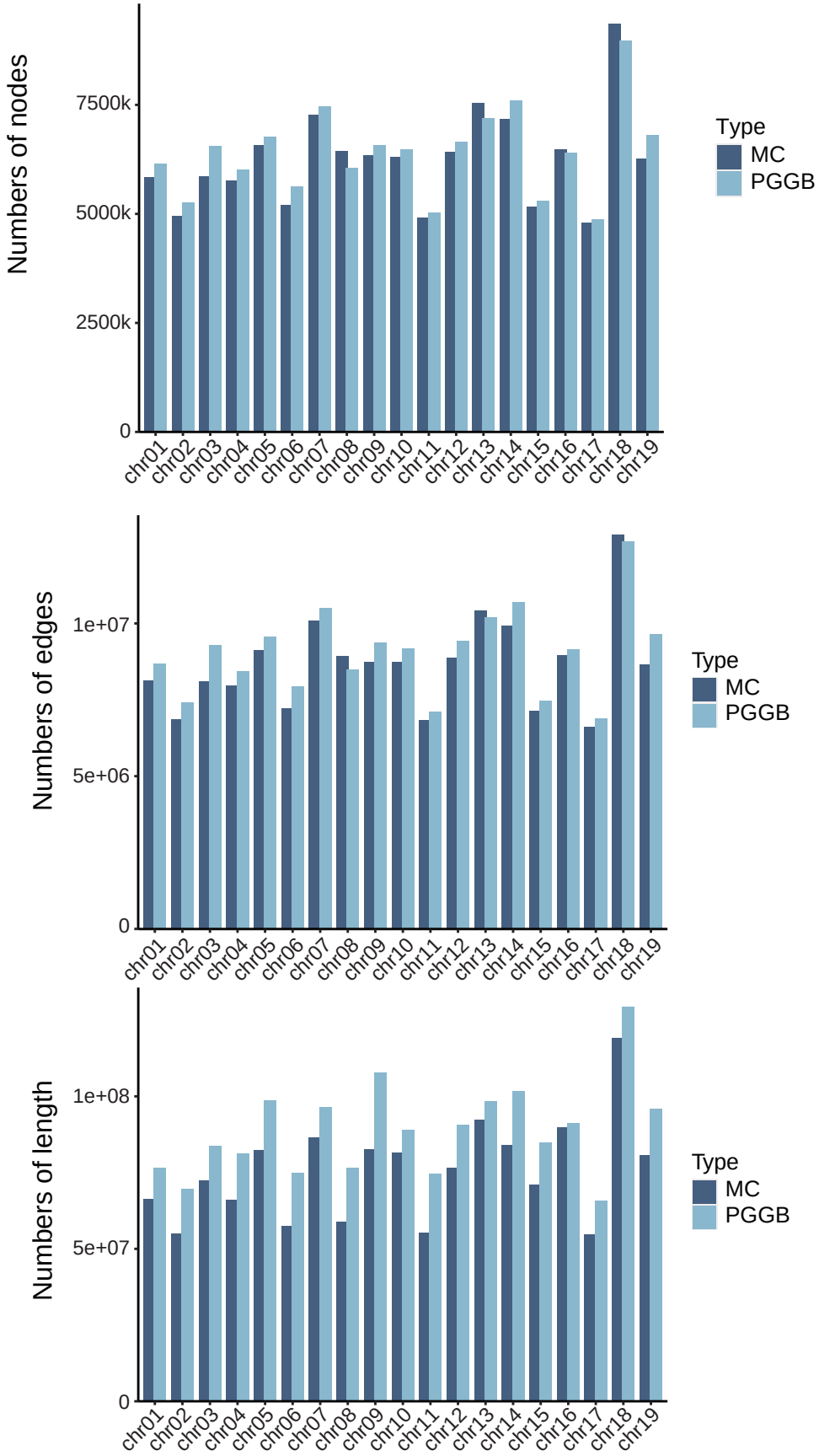
Supplementary Fig. 3 | The heterozygosity and proportion of hemizygous genes of the grape genomes. a. The heterozygosity of the grape genomes. The two-sided student's t-test was used for significance test. The color of the bar graph implies different groups. b. Proportion of hemizygous genes in different accessions.



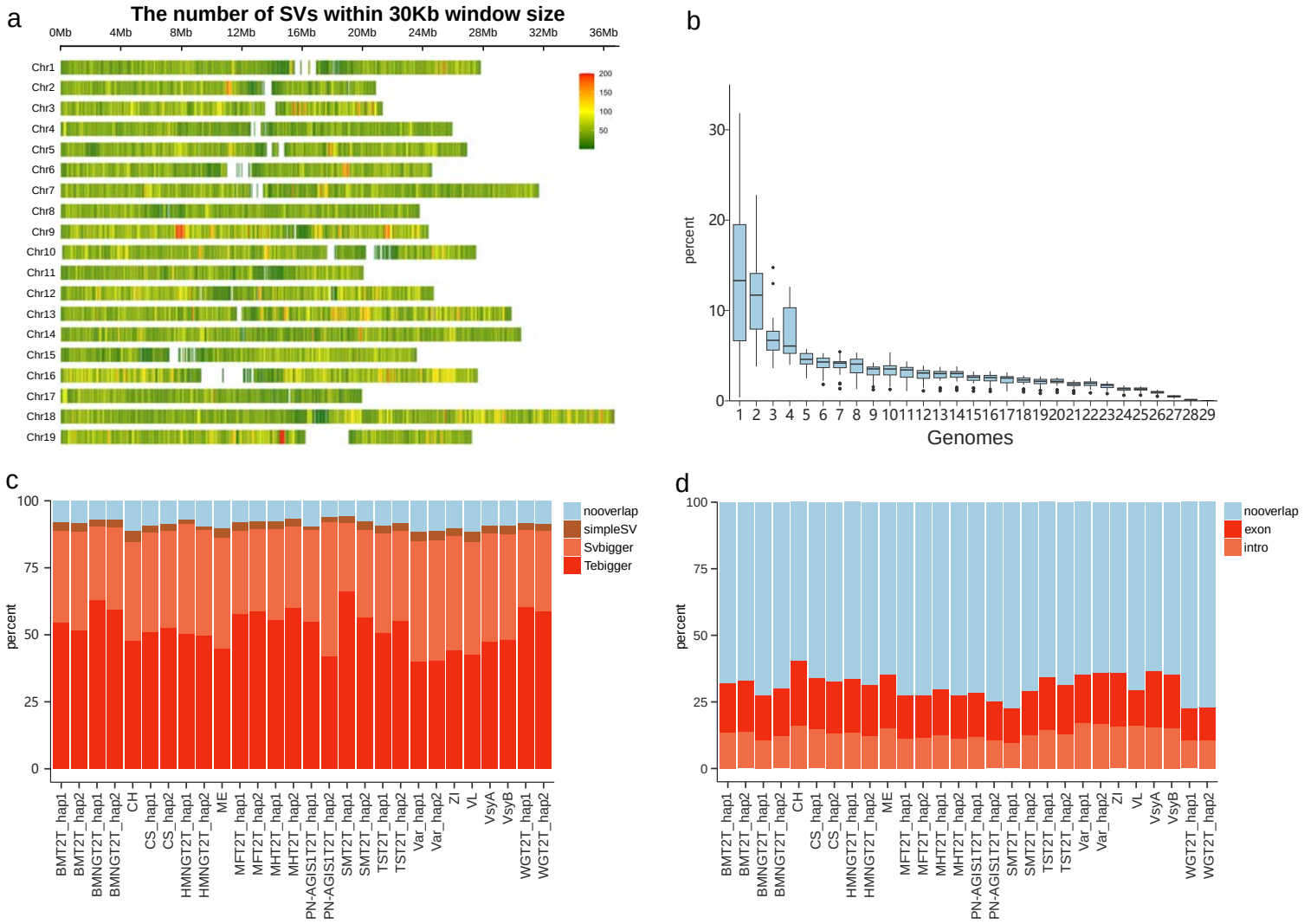
Supplementary Fig. 4. | Gene family clustering analysis of core and variable gene in 18 grape accessions. Histograms display the number of gene families at varying frequencies. Three dimensional pie charts illustrate the proportions of different gene families.



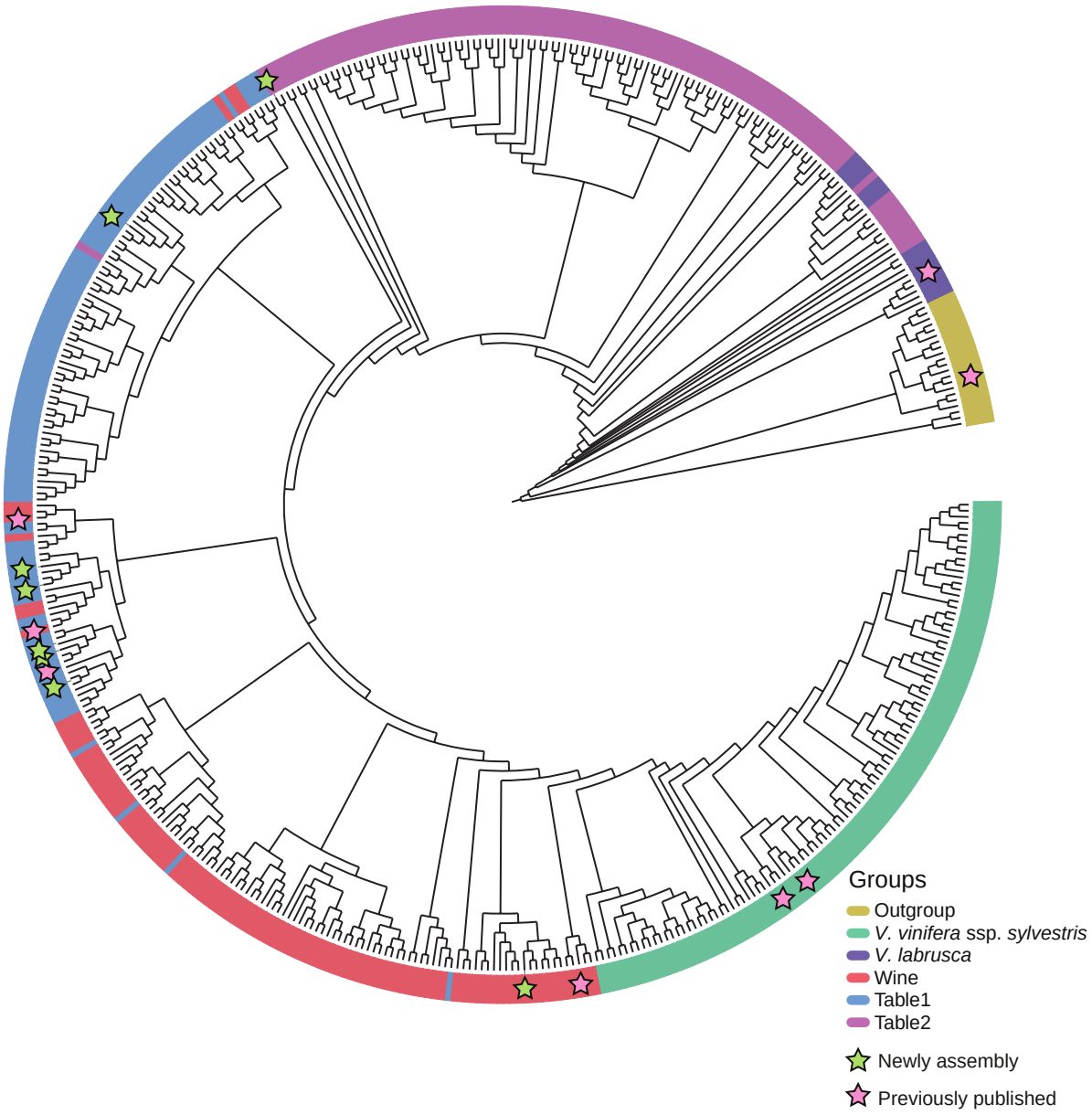
Supplementary Fig. 5. | Integrative Genomics Viewer (IGV) visualization of a large SVs on chr02 of TS_hap1 remapping HiFi reads to genome assembly.



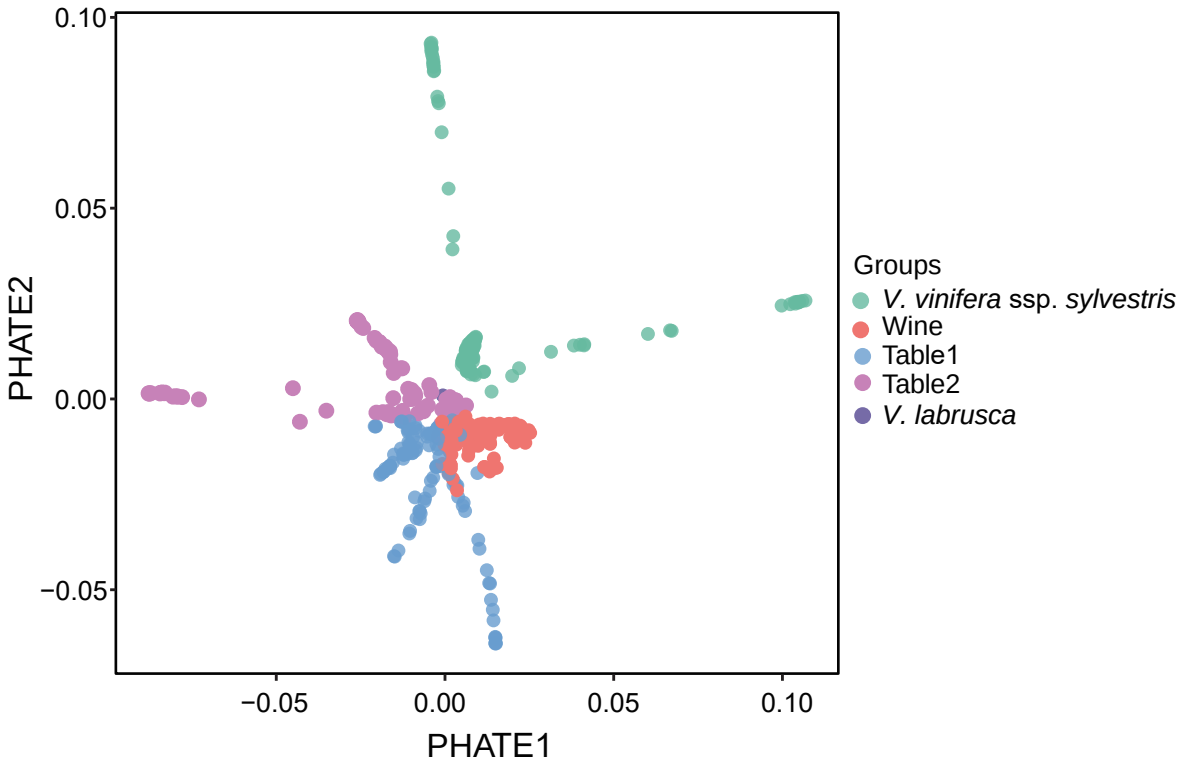
Supplementary Fig. 6. | Comparison between the PGGB grape pangenome and the MC grape pangenome.



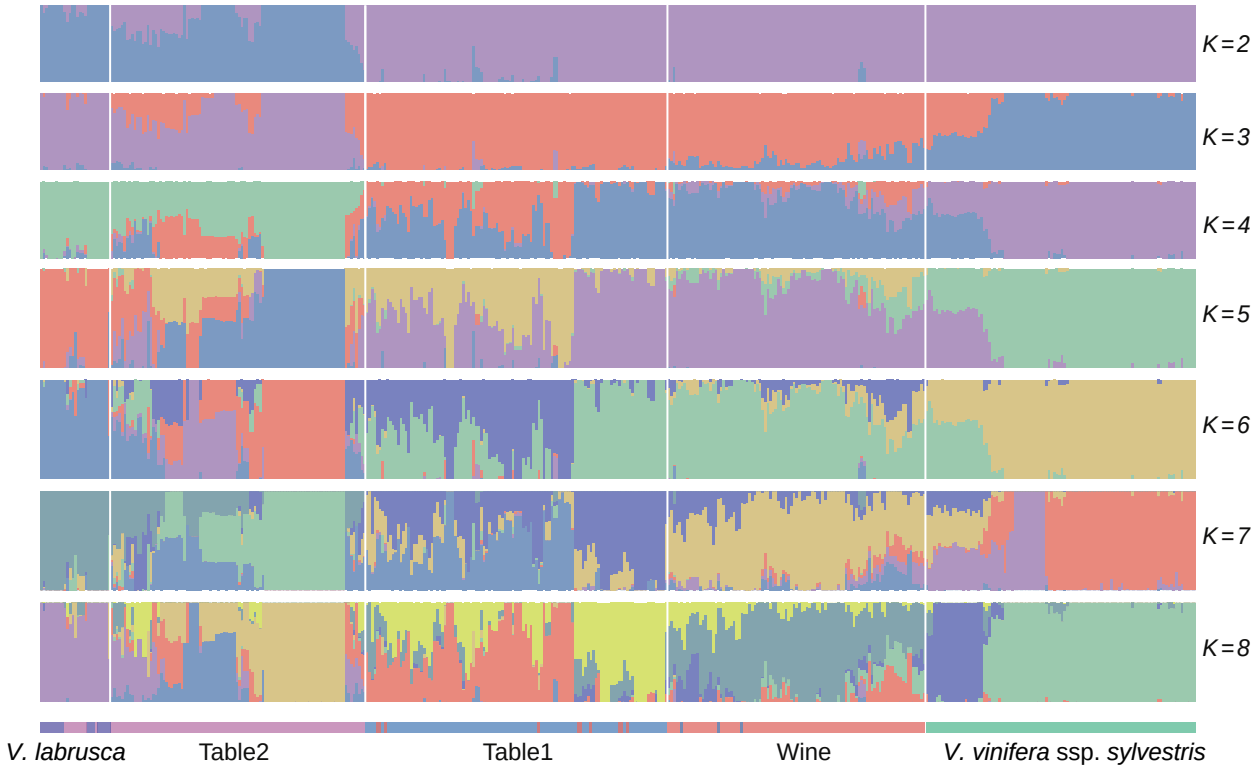
Supplementary Fig. 7 | Genomic landscape of structural variations: distribution, inter-genome sharing, and association with transposable elements and genic regions. a. The distribution of structural variations (SVs) along 19 chromosomes. b. The frequency of shared SVs across multiple genomes, represented as the percentage of SVs identified in a given genome that are also detected in other genomes under consideration. c and d. The percentage of transposable elements and genic regions that spatially coincide with the loci of SVs along the genome



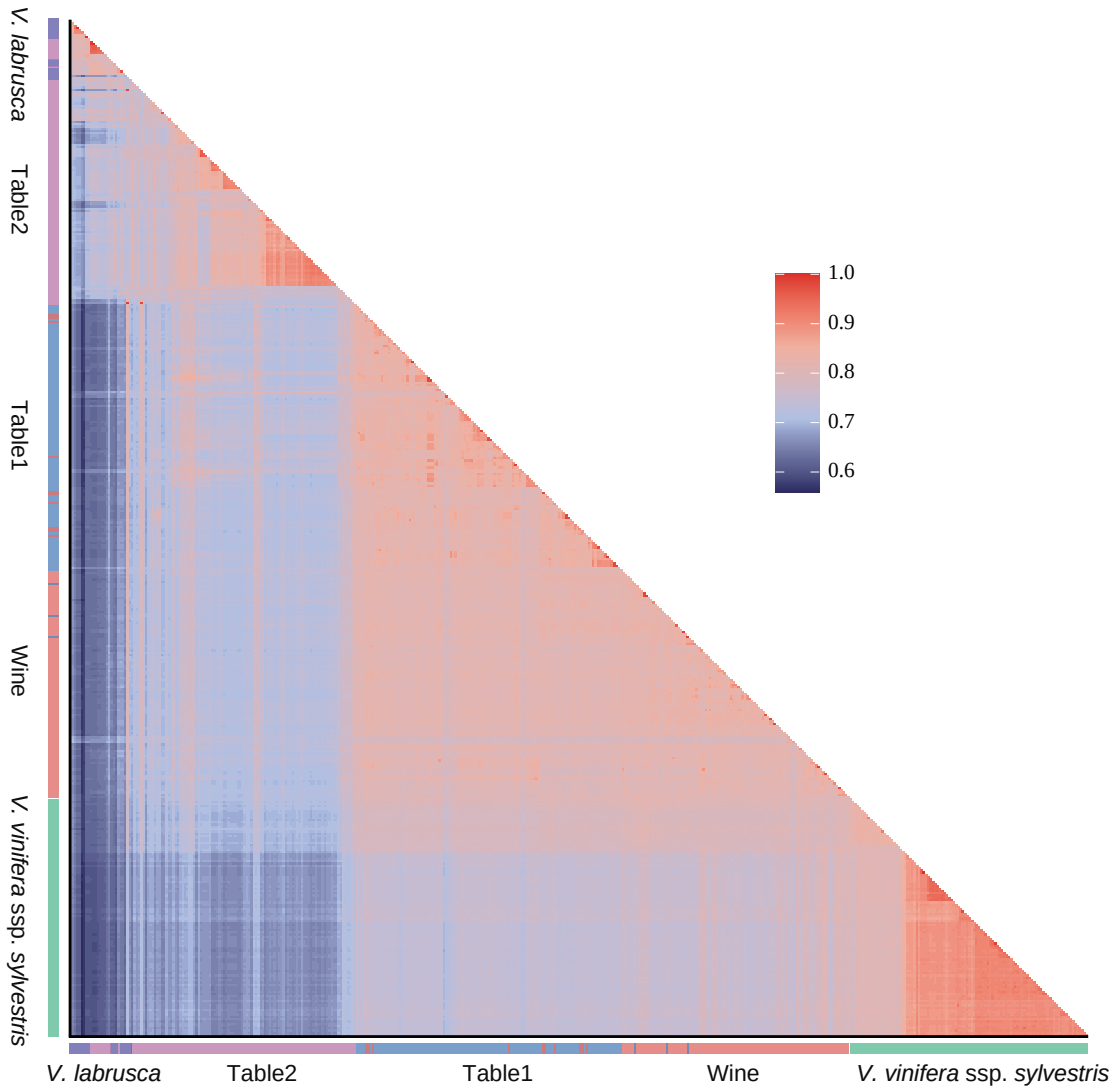
Supplementary Fig. 8. | Phylogenic tree of 466 accessions. The phylogenetic tree is constructed with SNPs. 21 grape accessions are used as the outgroup. The red asterisk indicates the T2T genome sample that we have assembled. IQTREE software is applied with 1000-times bootstrap and VT+F+R5 model parameters.



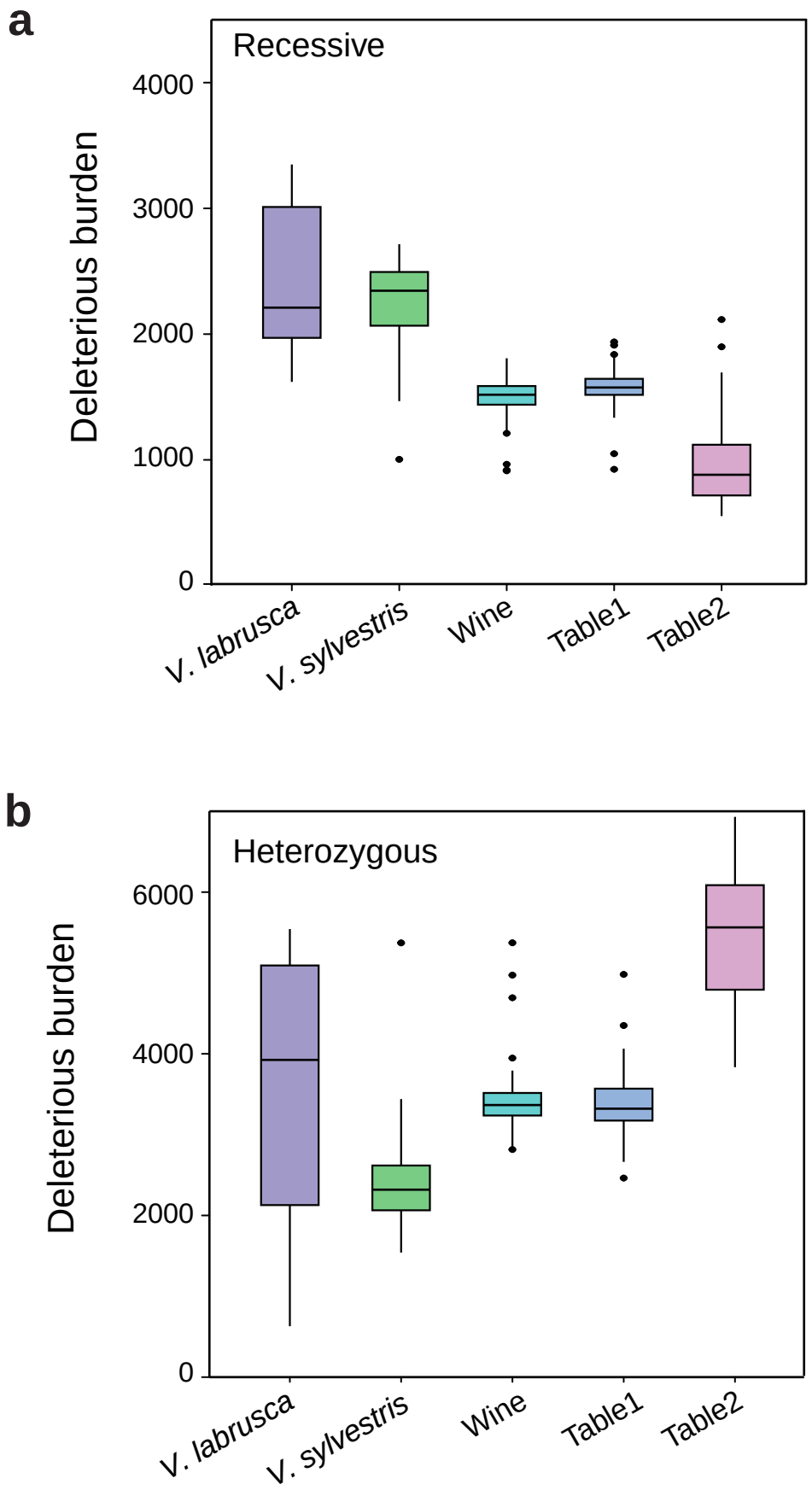
Supplementary Fig. 9. | **PHATE analysis of all accessions.** Different colors indicated different groups.



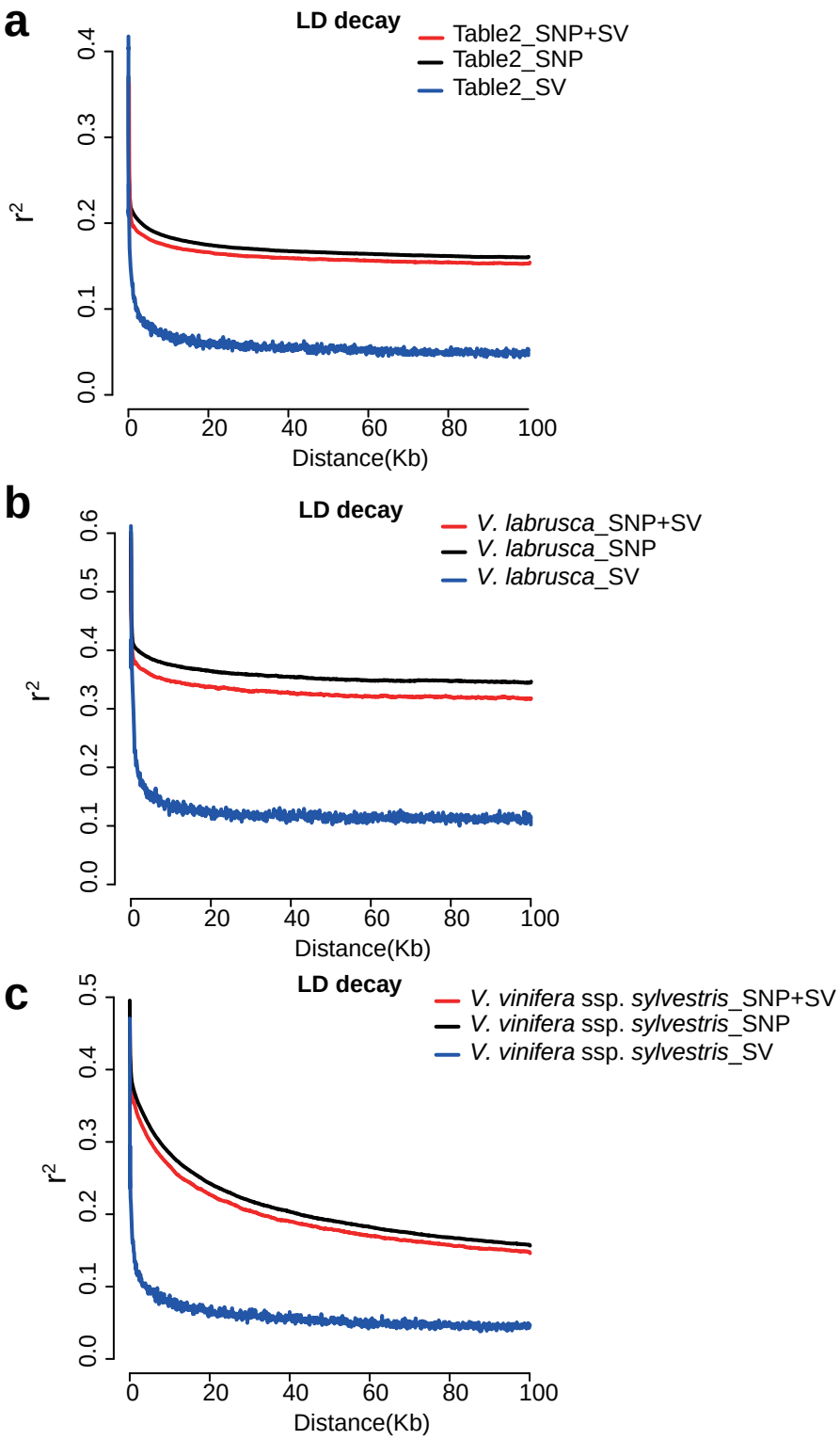
Supplementary Fig. 10. **| Structure of different *K* values.** The phylogenetic tree was shown on above. The lines with different colors indicated different groups.



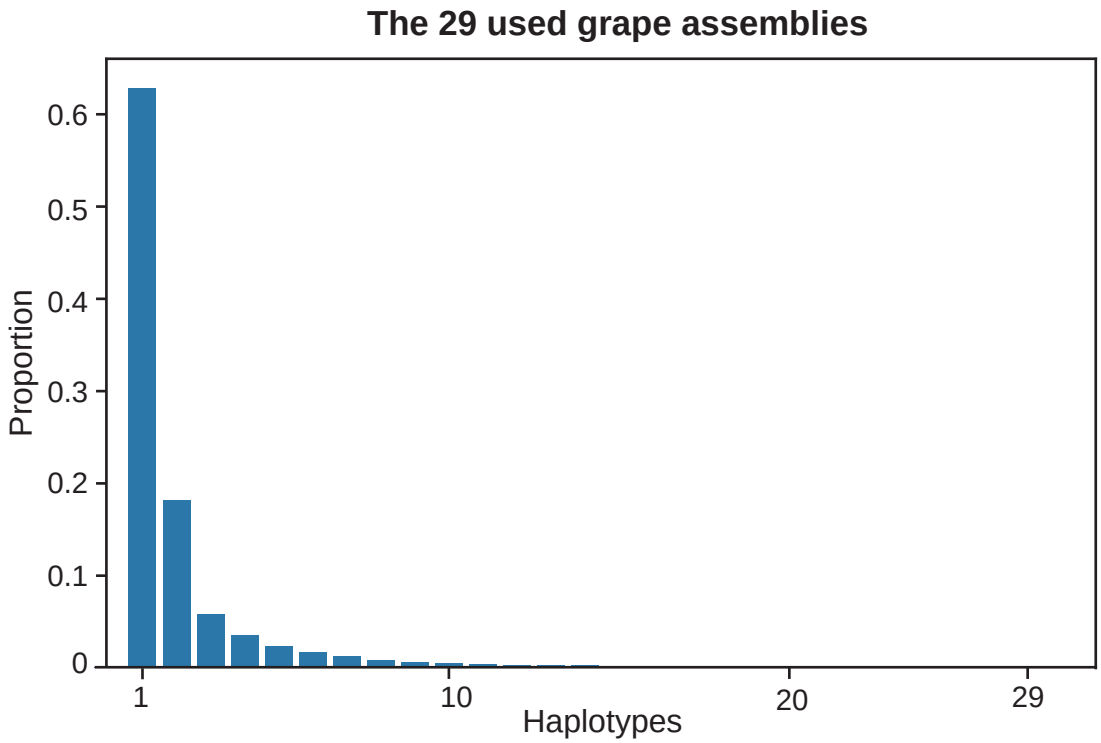
Supplementary Fig. 11. | Identical by state (IBS) values between different individuals. Heatmap colors indicate the distant of IBS blocks for each pairwise comparison.



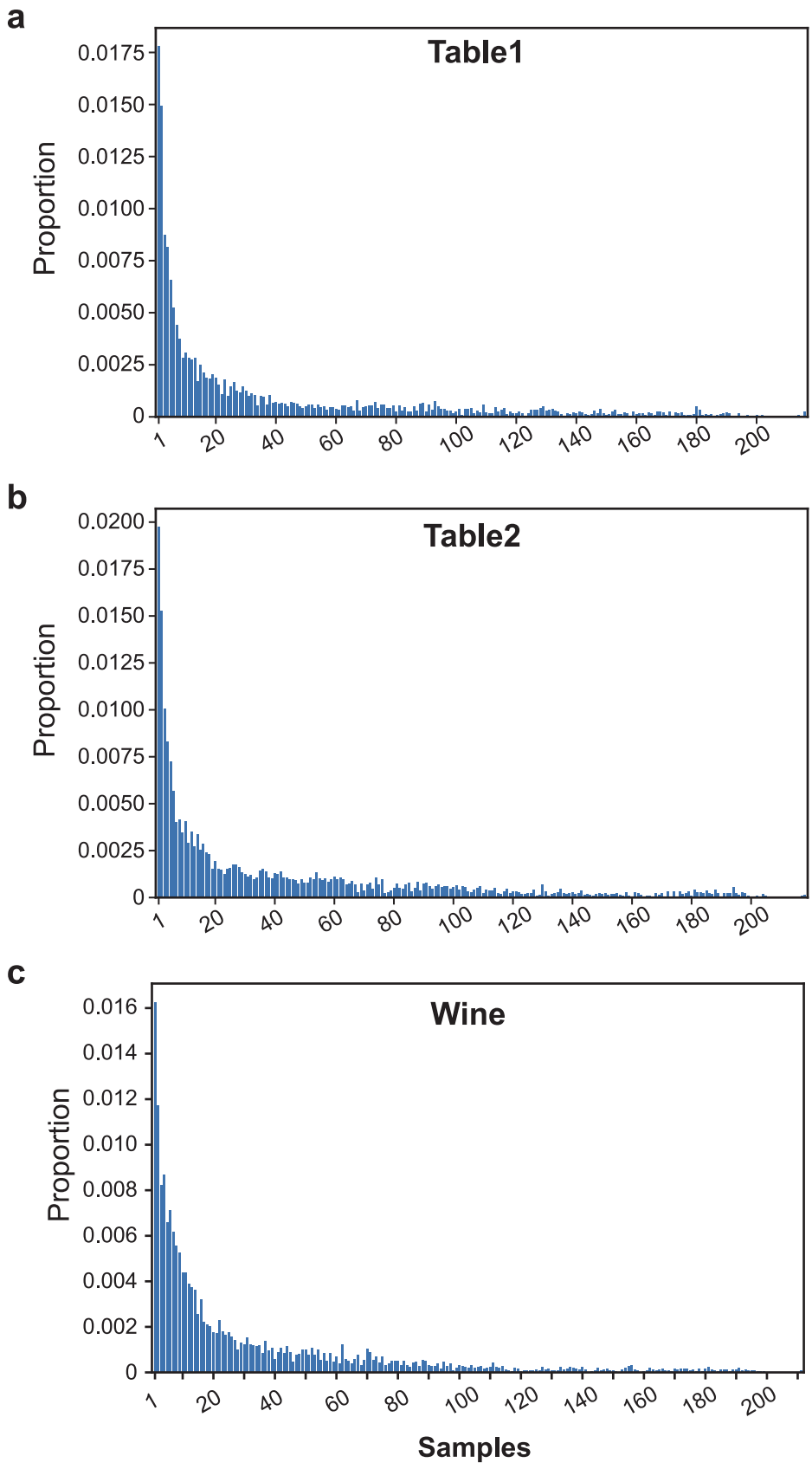
Supplementary Fig. 12 | The deleterious burden (recessive and heterozygous) in each group. *V. sylvestris* is the abbreviation of *V. vinifera* ssp. *sylvestris.* a. The recessive burden in different population. b. The heterozygous burden in different population. *Vitis labrusca*, n = 16 accessions; *Vitis sylvestris*, n = 105 accessions; Wine, n = 106 accessions; Table1, n = 108 accessions; Table2, n = 110 accessions; (centerline, median; box limits, first and third quartiles; whiskers, 1.5× interquartile range).



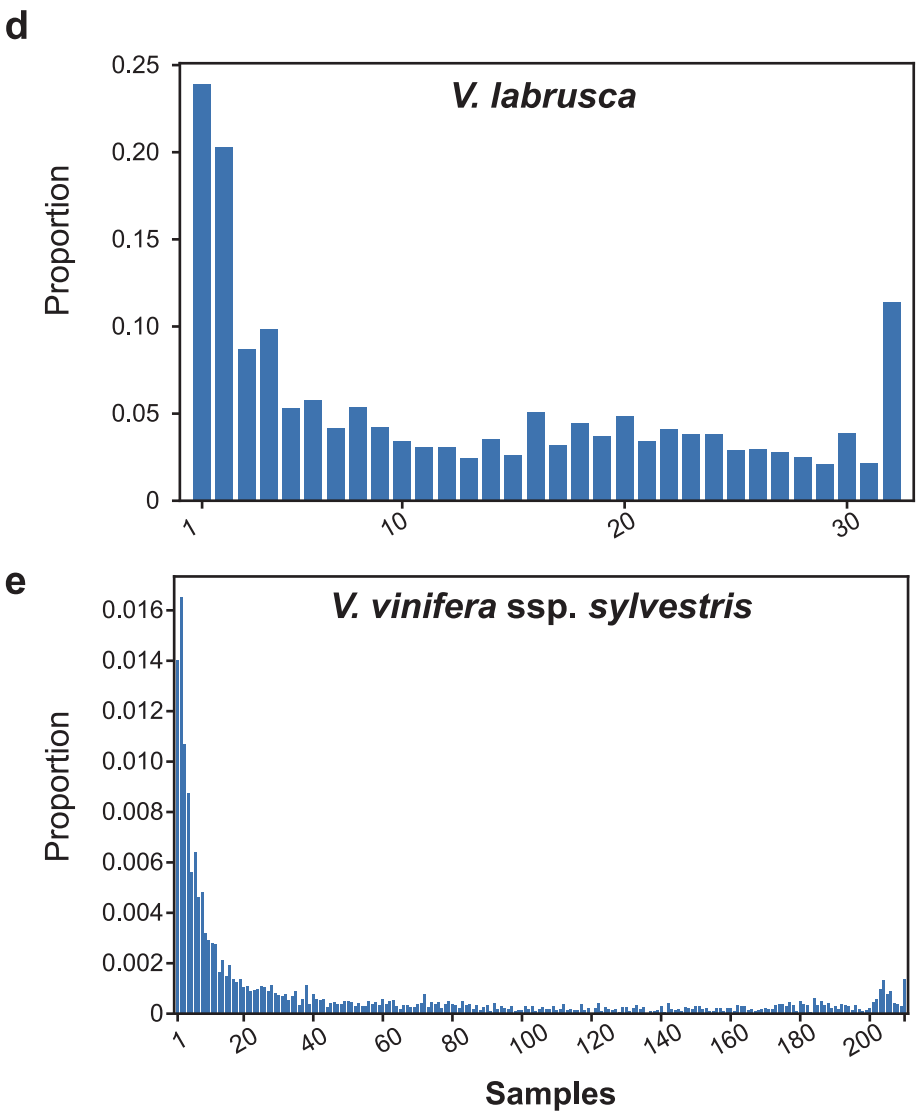
Supplementary Fig. 13. | Linkage disequilibrium (LD) decay patterns of the grape population. LD levels were estimated with PopLDdecay based SNPs, SVs and (SVs +SNPs) in different population: Table2 (**a**), *V. labrusca* (**b**) and *V. vinifera* ssp. *sylvestris* (**c**).



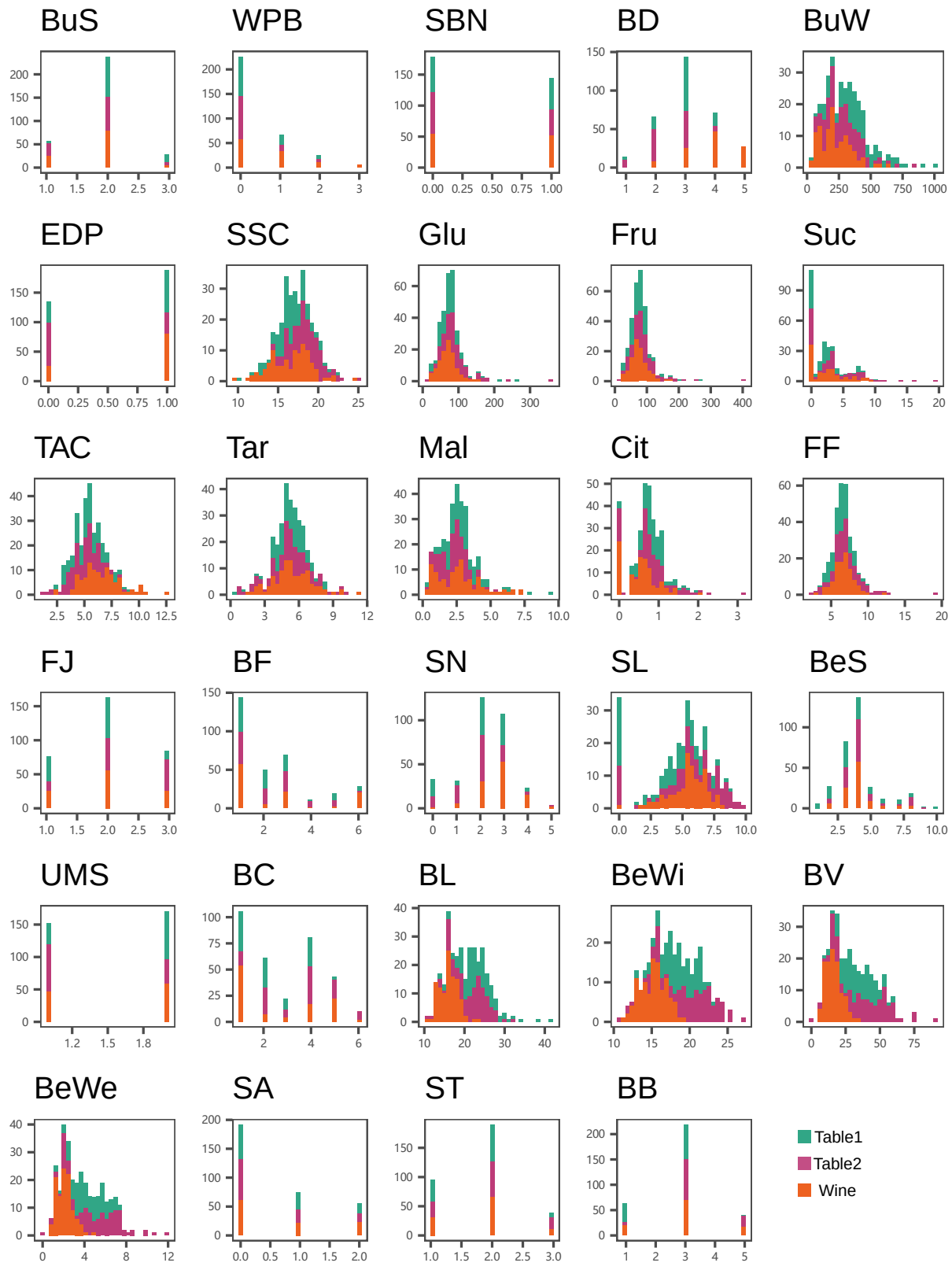
Supplementary Fig. 14. | The frequency for SVs in each grape assembly.



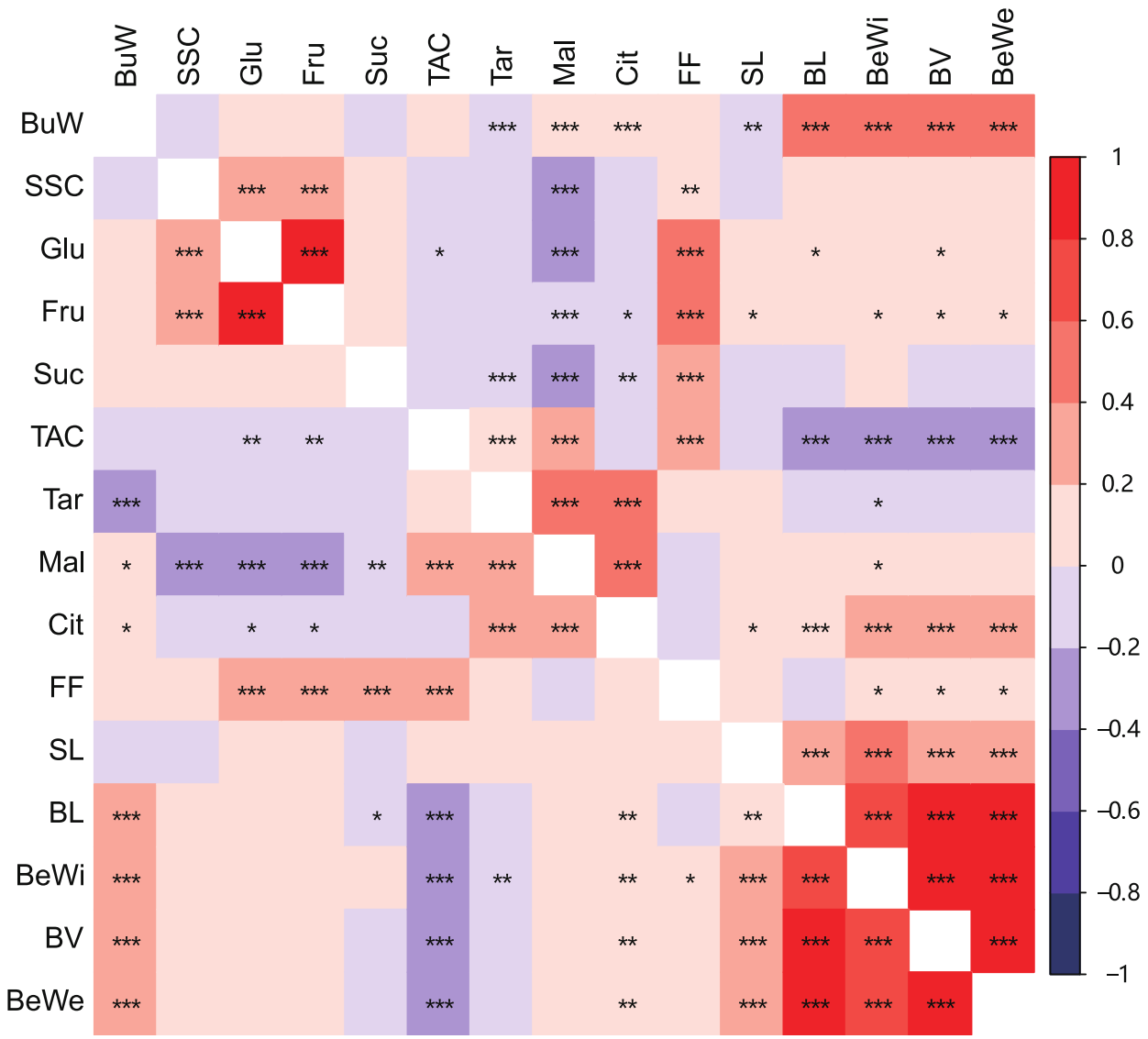
Supplementary Fig. 15. | The frequency for SVs in each group. a-e Table1, Tale2, Wine, *V. labrusca*, *V. vinifera* ssp. *sylvestris*.



Supplementary Fig. 15. (following) | **The frequency for SVs in each group. a-e** Table1, Tale2, Wine, *V. labrusca*, *V. vinifera* ssp. *sylvestris*.



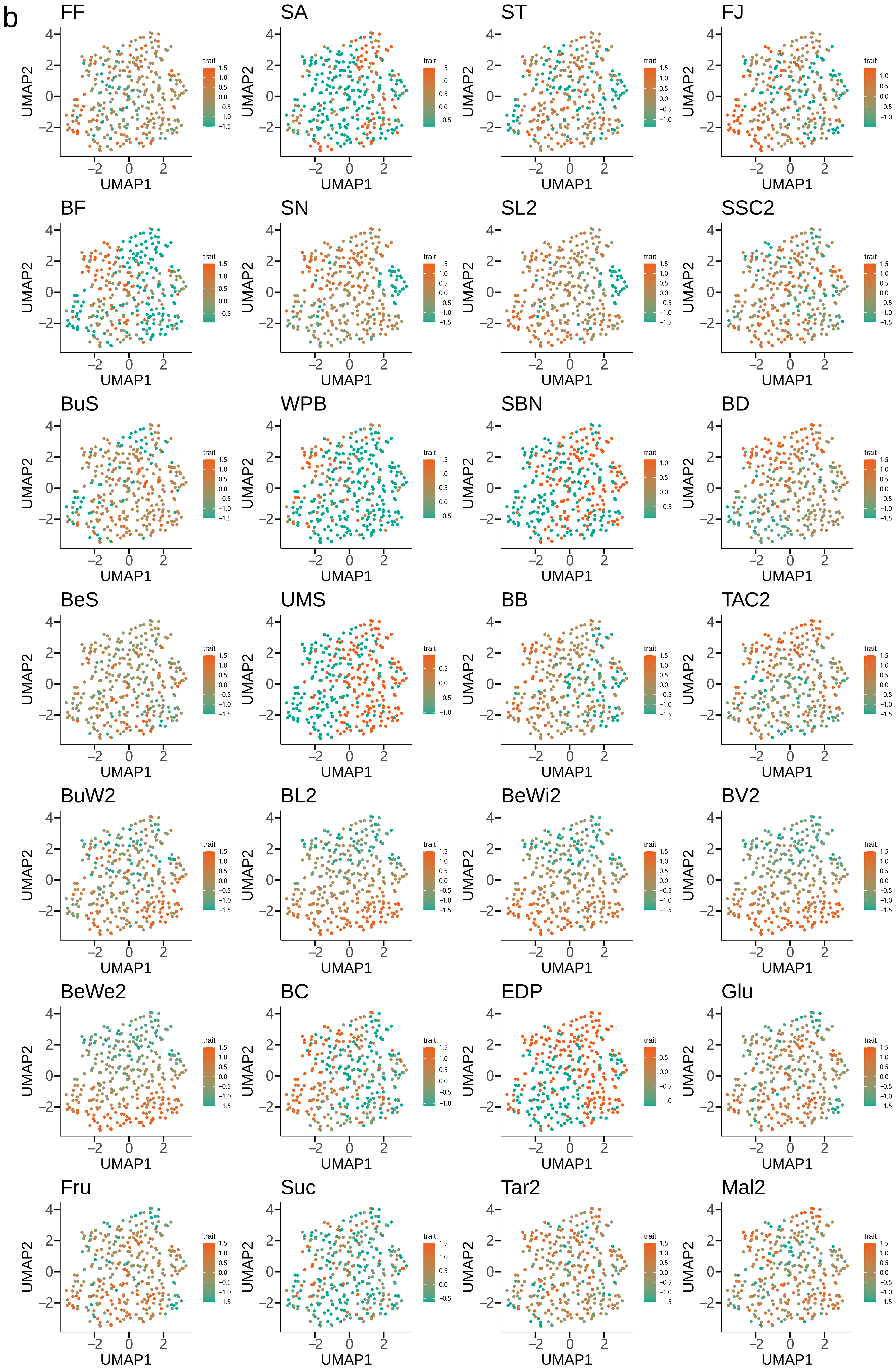
Supplementary Fig. 16 | The distribution characteristic of different traits in three groups.

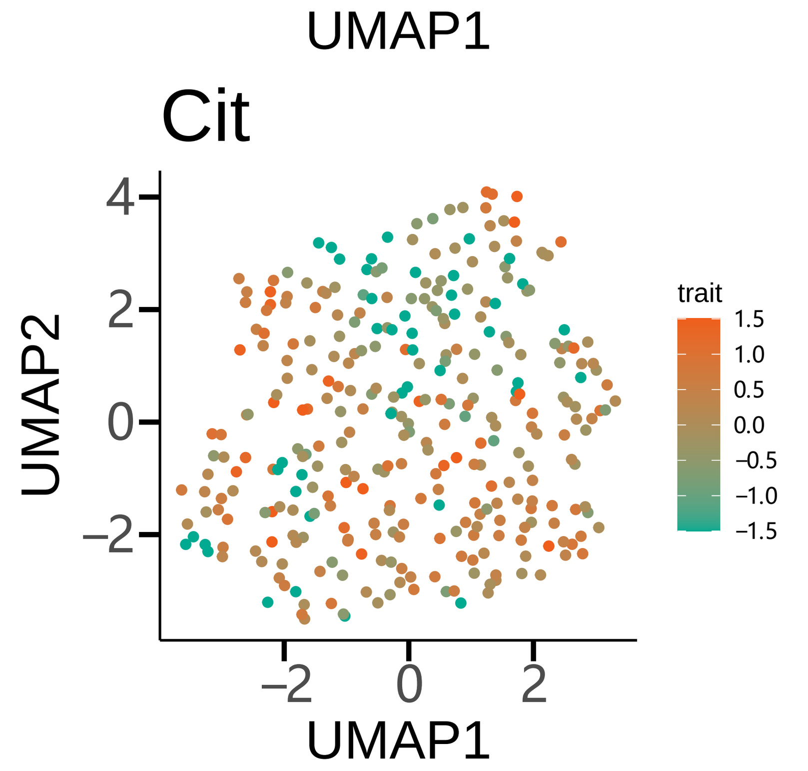


Supplementary Fig. 17 | The correlation among the traits in each year. The right and upper part: year 2017; The left and lower part: year 2016. The significance of the linear relationship between variables was evaluated through Pearson correlation coefficients with no correction. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

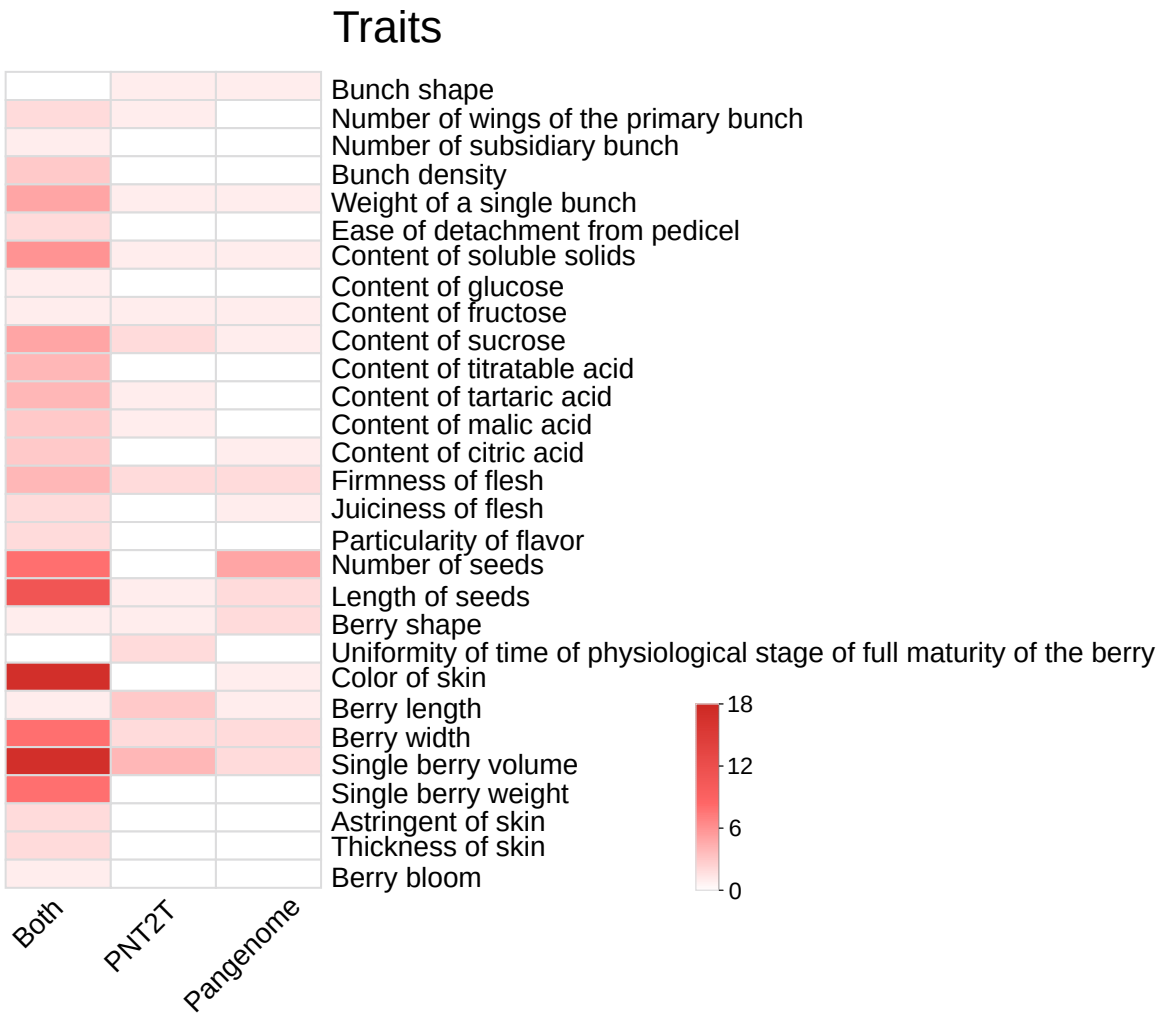
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Supplementary Fig. 18. |UMAP plot generated from 29 trait scores for all grapes. Points indicate individual grape and are colored by trait scores per plot. Scores were scaled and centered (Z score) across all individuals for each trait independently. a. year 2016; b. year 2017

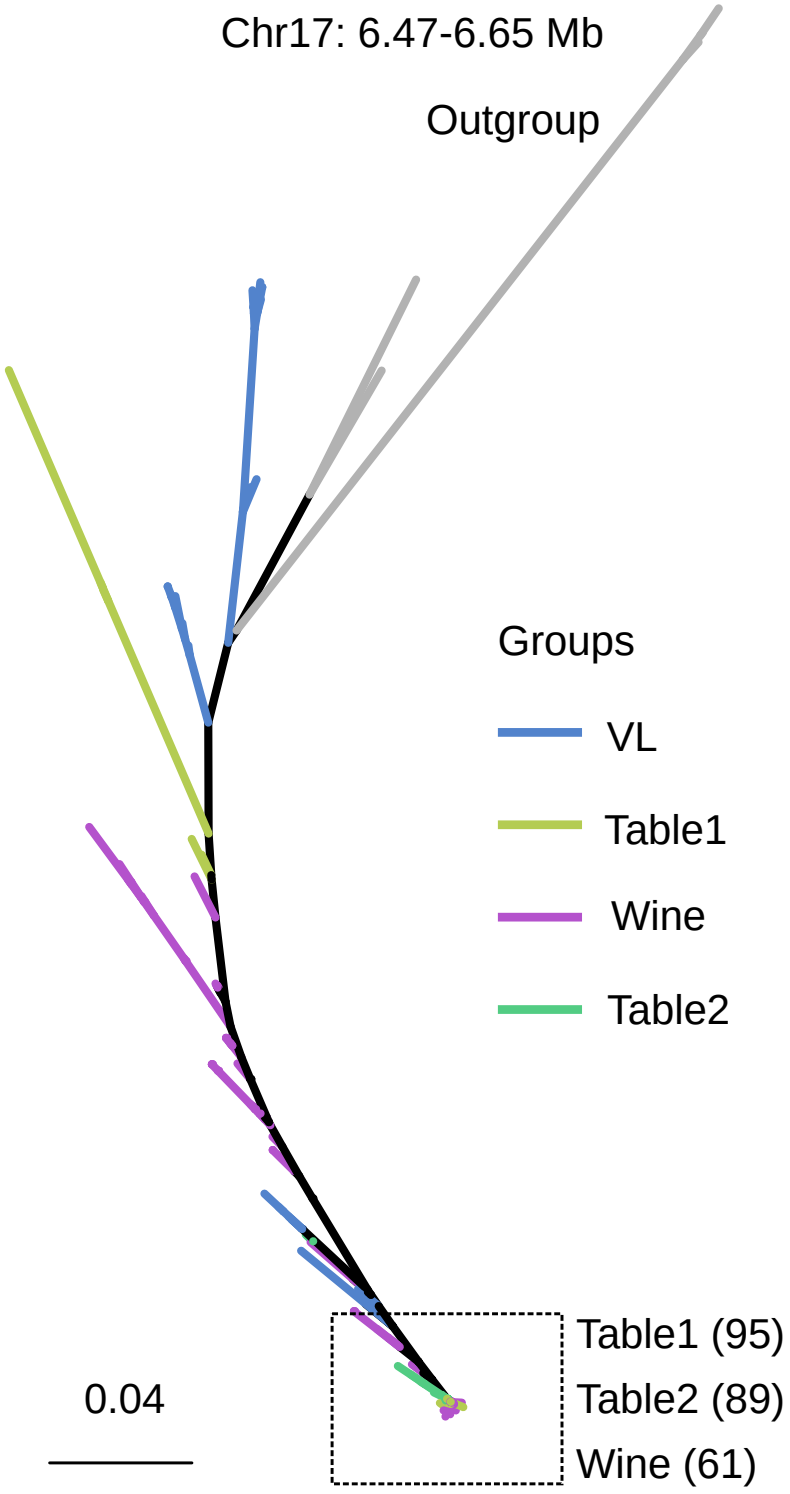




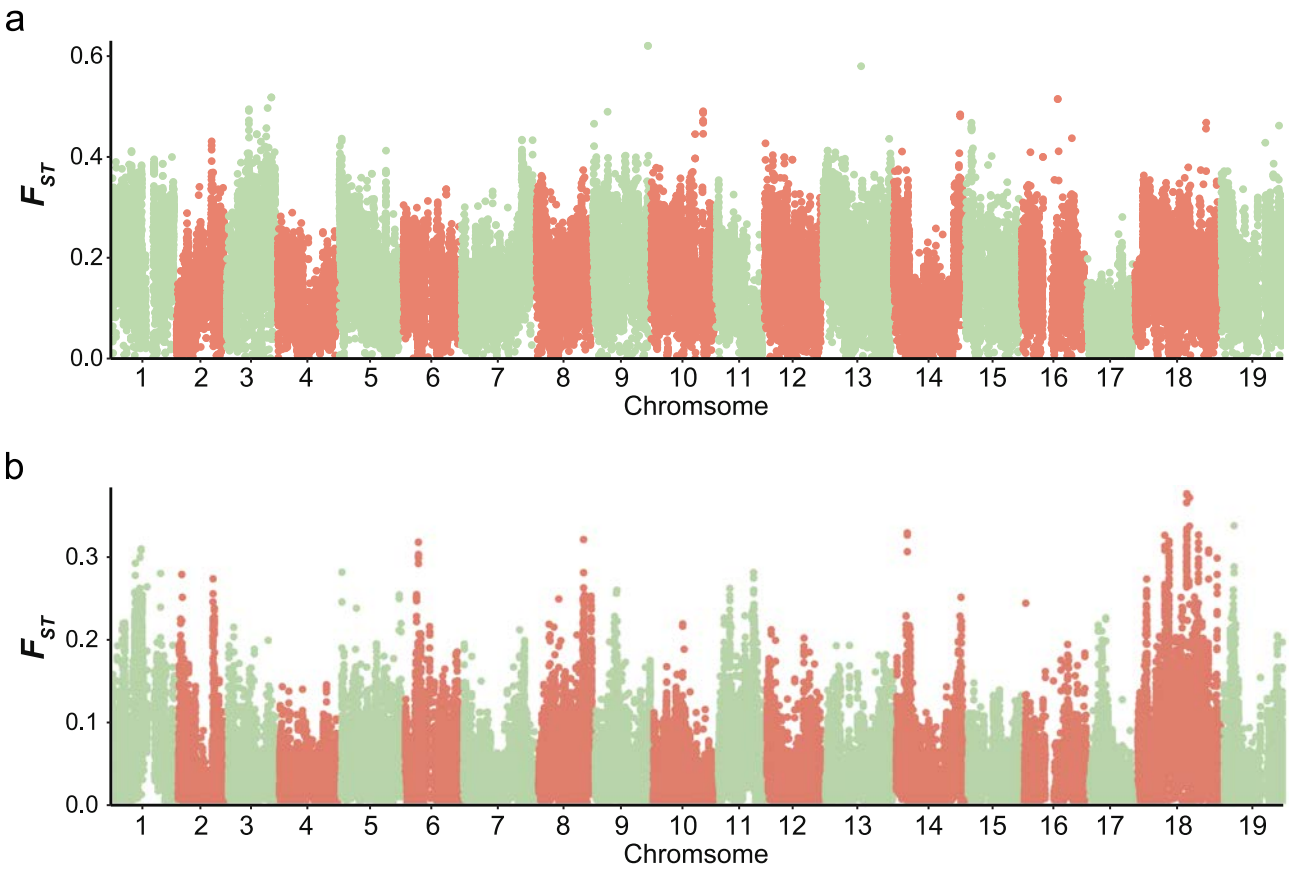
Supplementary Fig. 18. (following) | UMAP plot generated from 29 trait scores for all grapes. Points indicate individual grape and are colored by trait scores per plot. Scores were scaled and centered (Z score) across all individuals for each trait independently. a. year 2016; b. year 2017



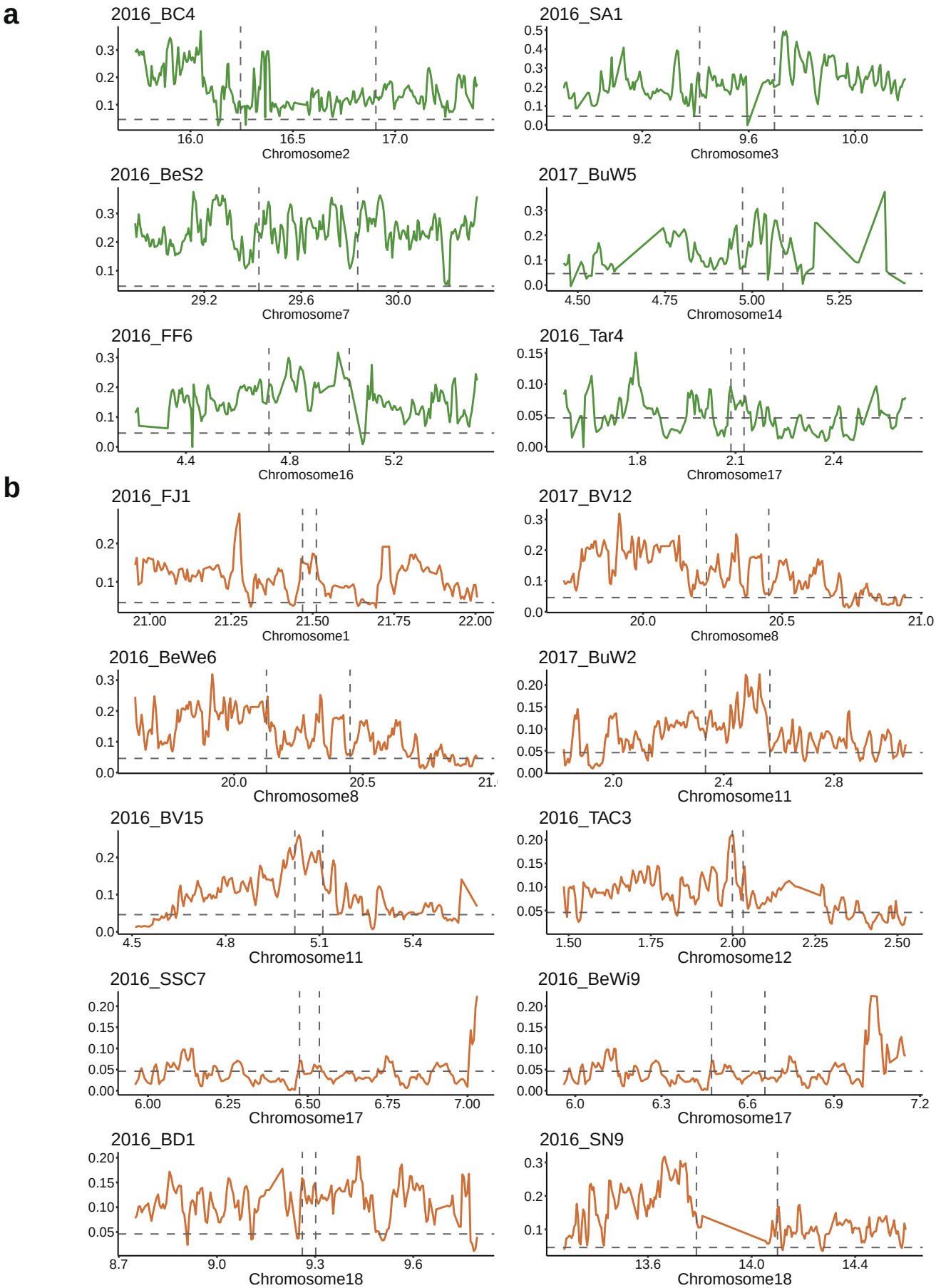
Supplementary Fig. 19. | Comparison GWAS results between PNT2T based SNPs and pangenome based SNPs.



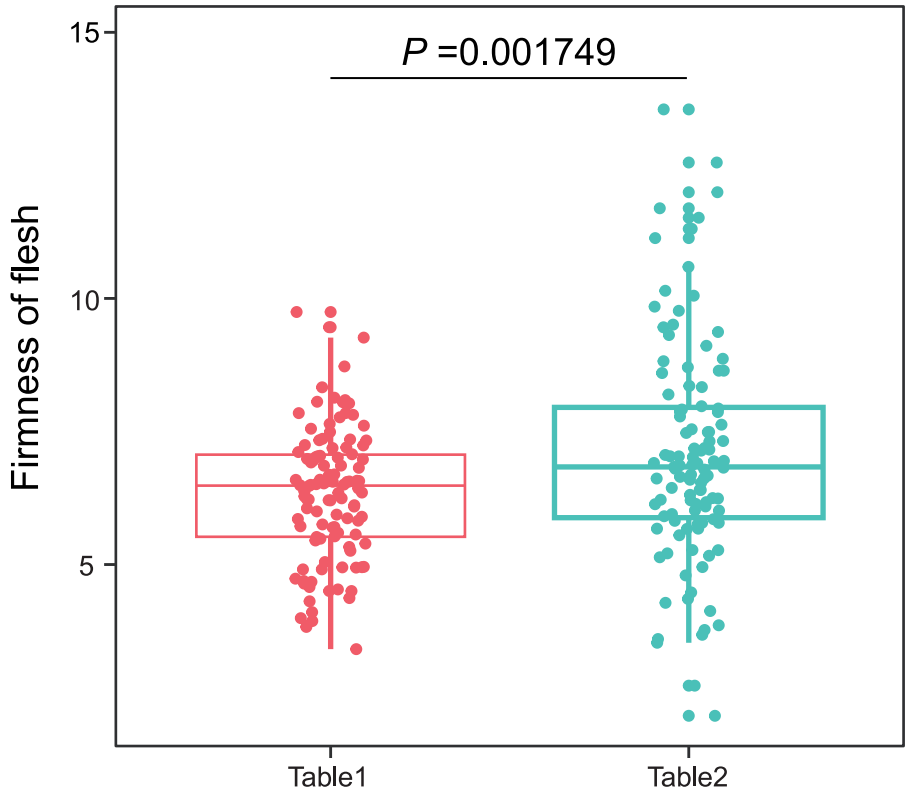
Supplementary Fig. 20. | The phylogenetic tree on 6.47 to 6.65 Mb of chromosome 17. Different colors indicated different populations. The number in bracket indicated the number of samples in box.



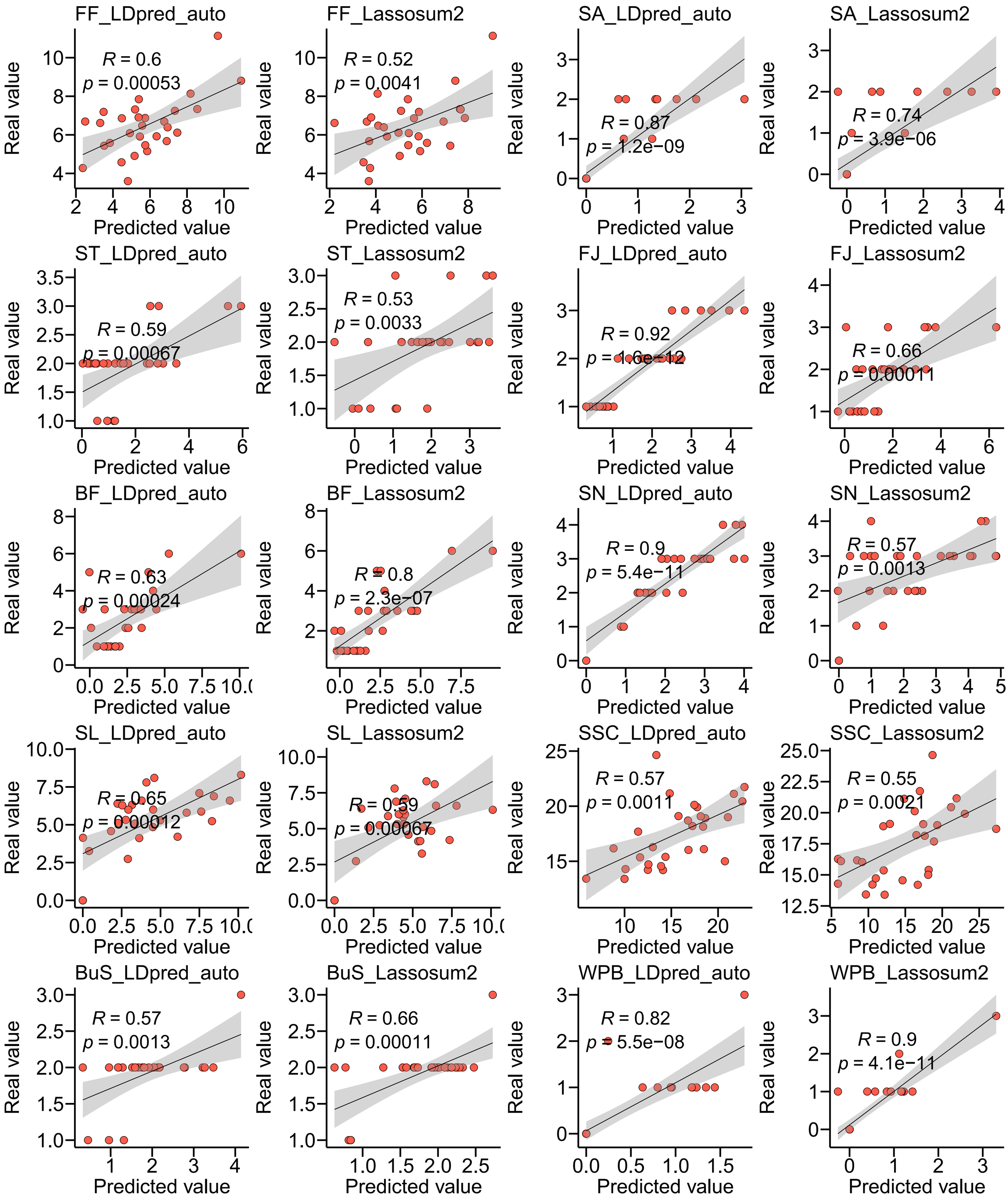
Supplementary Fig. 21 | F_{ST} between Table1 / Table2(a) and Table1 / Wine (b).



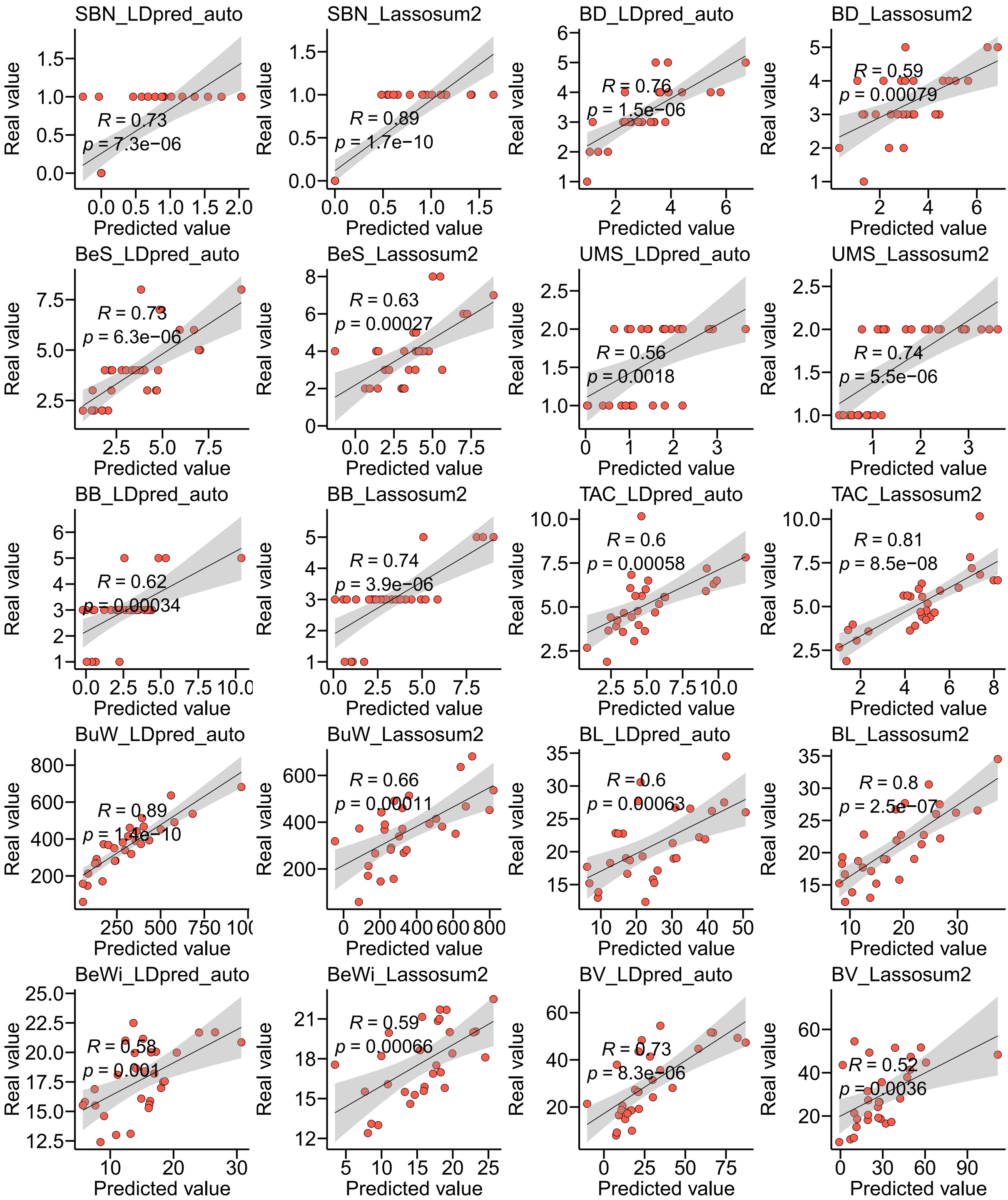
Supplementary Fig. 22. | F_{ST} between different groups. **a**. Table1 and Table2 around GWAS candidate loci for six traits: berry color (BC4), skin astringent (SA1), berry shape (BeS2), bunch weight (BuW5), flesh firmness (FF6) and content of tartaric acid (Tar4). **b**. Table1 and Wine around GWAS candidate loci for ten traits: berry size (BV12, BeWe6, BuW2, BV15, and BeWi9), metabolites (TAC3, SSC7).



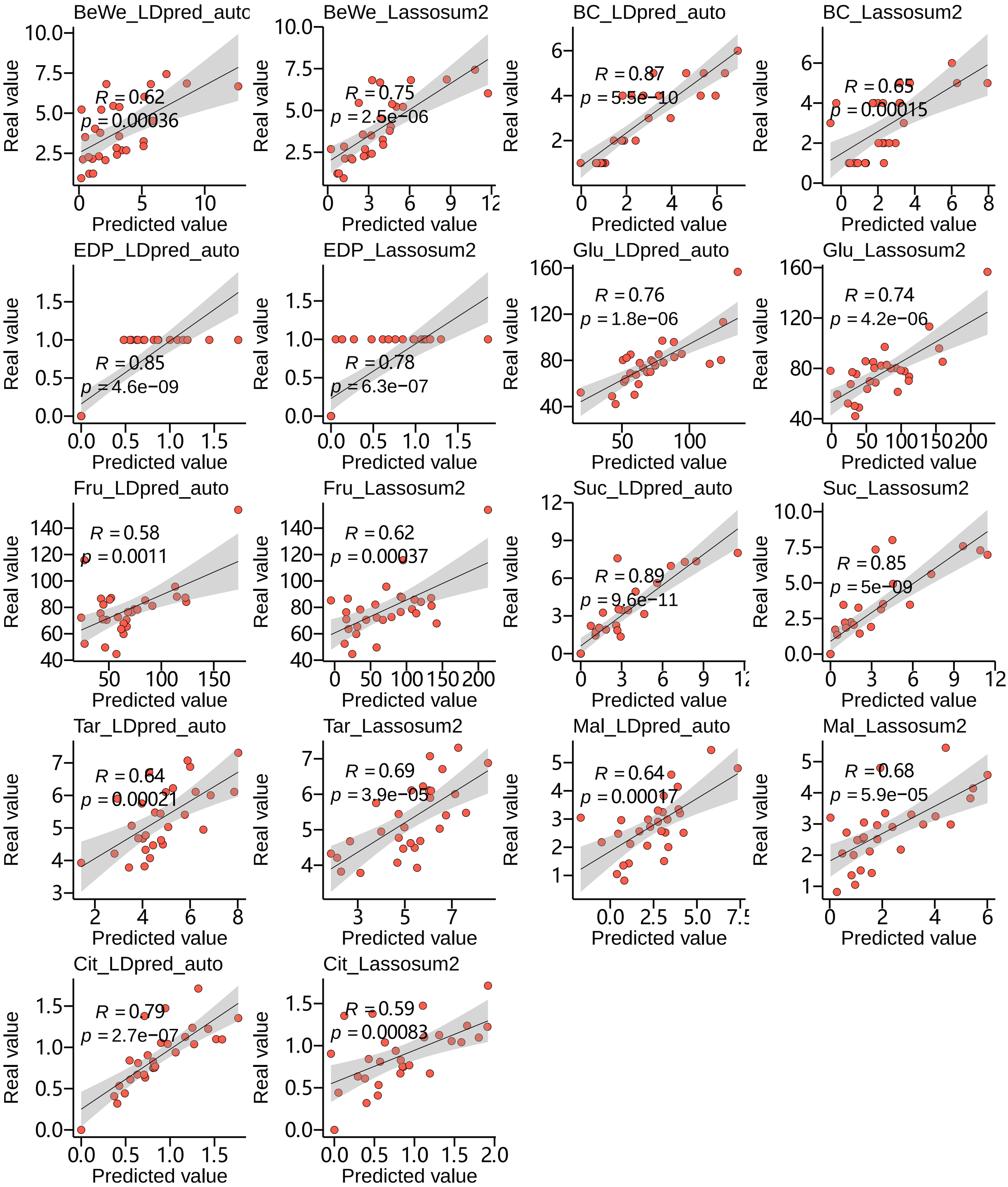
Supplementary Fig. 23 | The comparison of the flesh firmness between the Table1(n=108) and Table2(n=110) group. Statistical significance was determined by two-sided Student's t-tests (centerline, median; box limits, first and third quartiles; whiskers, 1.5× interquartile range).



Supplementary Fig. 24 | The correlation between trait values predicted by LDpred2/lassoum2 and the true values. The significance of the linear relationship between variables was evaluated through Pearson correlation coefficients. The smoothed line represents a linear regression fit of the actual data, and the shading represents the CI. The simple size n = 29.



Supplementary Fig. 24 (following) | The correlation between trait values predicted by LDpred2/lassoum2 and the true values. The significance of the linear relationship between variables was evaluated through Pearson correlation coefficients. The smoothed line represents a linear regression fit of the actual data, and the shading represents the CI. The simple size n = 29.



Supplementary Fig. 24 (following) | The correlation between trait values predicted by LDpred2/lassoum2 and the true values. The significance of the linear relationship between variables was evaluated through Pearson correlation coefficients. The smoothed line represents a linear regression fit of the actual data, and the shading represents the CI. The simple size n = 29.

Supplementary Table 1. Summary of grape genomes used in this study. The red font in the Data Source column indicates data newly generated in this study.

Number	Accession	Haplotype	Species	Source	Collection	Classification	Type	Assemblied Strategy	Data Type	Data Source
1	BM_AGIS_01	BMT2T_hap1 BMT2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Black Monukka	Xinjiang Academy of Agricultural Sciences, Urumqi, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA1021353;ONT:PRJNA1048106
2	MF_AGIS_01	MFT2T_hap1 MFT2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Manicure Finger	Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, Zhengzhou, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC+ONT:PRJNA1048106
3	MH_AGIS_01	MHT2T_hap1 MHT2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Muscat Hamburg	Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, Zhengzhou, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC+ONT:PRJNA1048106
4	TS_AGIS_01	TST2T_hap1 TST2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Thompson Seedless	Xinjiang Academy of Agricultural Sciences, Urumqi, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA1021353;ONT:PRJNA1048106
5	SM_AGIS_01	SMT2T_hap1 SMT2T_hap2	*Vitis labrusca* × *Vitis vinifera*	a clone of Shine Muscat	Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, Zhengzhou, China	Table2	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC+ONT:PRJNA1048106
6	BMNG_AGIS_01	BMNGT2T_hap1 BMNGT2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Baimunage	Xinjiang Academy of Agricultural Sciences, Urumqi, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA1158437;ONT:PRJNA1048106
7	HMNG_AGIS_01	HMNGT2T_hap1 HMNGT2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Hongmunage	Xinjiang Academy of Agricultural Sciences, Urumqi, China	Table1	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA1158437;ONT:PRJNA1048106
8	PN_AGIS_01	PN-AGIS1T2T_hap1 PN-AGIS1T2T_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Pinot Noir (cultivar)	Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, Zhengzhou, China	Wine	Cultivar	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA951461;ONT:PRJNA1048106
9	WG_AGIS_01	WGT2T_hap1 WGT2T_hap2	*Vitis retordii*	Wolley grape	Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China	Wild	Wild	Haplotype-resovled	HiFi+HiC+ONT	HiFi+HiC:PRJNA953920;ONT:PRJNA1048106
10	PNT2T	PNT2T	*Vitis vinifera* ssp. *vinifera*	a clone of Pinot Noir (PN40024)	/	Wine	Near homozygous line	Primary+Alternative	HiFi	HiFi:PRJNA882193
11	Var	Var_hap1 Var_hap2	*Vitis arizonica*	a wild individual of *Vitis arizonica*	/	Wild	Wild	Haplotype-resovled	CLR	CLR:PRJNA593045
12	VL	VL	*Vitis labrusca*	a wild individual of *Vitis labrusca*	/	VL	Wild	Primary+Alternative	CLR	CLR:PRJNA701071
13	VsyA	VsyA	*Vitis vinifera* ssp. *sylvestris*	a wild individual of *Vitis vinifera* ssp. *sylvestris*	/	Vsy	Wild	Primary+Alternative	CLR	CLR:PRJNA593045
14	VsyB	VsyB	*Vitis vinifera* ssp. *sylvestris*	a wild individual of *Vitis vinifera* ssp. *sylvestris*	/	Vsy	Wild	Primary+Alternative	CLR	CLR:PRJNA593045
15	ME	ME	*Vitis vinifera* ssp. *vinifera*	a clone of Merlot	/	Wine	Cultivar	Primary+Alternative	CLR	CLR:PRJNA593045
16	CS	CS_hap1 CS_hap2	*Vitis vinifera* ssp. *vinifera*	a clone of Cabernet Sauvignon	/	Wine	Cultivar	Haplotype-resovled	CLR	CLR:PRJNA316730
17	CH	CH	*Vitis vinifera* ssp. *vinifera*	a clone of Chardonnay	/	Wine	Cultivar	Primary+Alternative	CLR	CLR:PRJNA550461
18	ZI	ZI	*Vitis vinifera* ssp. *vinifera*	a clone of Zinfandel	/	Wine	Cultivar	Primary+Alternative	CLR	CLR:PRJNA527006
19	Outgroup	Outgroup	*Vitis rotundifolia*	a *Muscadinia* grape cultivar of Noble	/	Outgroup	Outgroup	Haplotype-resovled	CLR	CLR:PRJNA738474

Supplementary Table 2. Statistic of 18 newly generated grape genome haplotypes from nine accessions.

Number	Accessions	Haplotypes	Genome length (Mb)	Scaffold N50 (Mb)	Longest scaffold (Mb)	Number of centromeres	Number of telomeres	Protein-coding genes
1	BM_AGIS_01	BMT2T_hap1	489.52	25.76	38.04	19/19	34/38	36,621
		BMT2T_hap2	484.53	25.50	38.09	19/19	35/38	36,664
2	MF_AGIS_01	MFT2T_hap1	489.74	25.78	37.93	19/19	36 /38	36,768
		MFT2T_hap2	487.02	25.63	38.76	19/19	35/38	36,571
3	MH_AGIS_01	MHT2T_hap1	493.25	25.96	38.09	19/19	36/38	37,286
		MHT2T_hap2	491.41	25.86	37.46	19/19	35/38	36,862
4	TS_AGIS_01	TST2T_hap1	479.15	25.22	37.62	19/19	36/38	36,514
		TST2T_hap2	493.48	25.97	39.33	19/19	35/38	36,963
5	SM_AGIS_01	SMT2T_hap1	486.49	25.60	37.32	19/19	35/38	36,286
		SMT2T_hap2	486.34	25.60	37.88	19/19	36/38	36,017
6	BMNG_AGIS_01	BMNGT2T_hap1	488.80	25.73	37.72	19/19	36/38	38,526
		BMNGT2T_hap2	489.44	25.76	37.70	19/19	35/38	37,100
7	HMNG_AGIS_01	HMNGT2T_hap1	489.01	25.74	37.73	19/19	34/38	34,536
		HMNGT2T_hap2	483.88	25.47	37.08	19/19	35/38	37,549
8	PN_AGIS_01	PN-AGIS1T2T_hap1	496.45	26.29	36.89	19/19	35/38	37,358
		PN-AGIS1T2T_hap2	489.78	25.78	37.42	19/19	35/38	36,600
9	WG_AGIS_01	WGT2T_hap1	530.73	28.08	41.00	19/19	37/38	35,233
		WGT2T_hap2	539.30	28.37	41.94	19/19	37/38	35,311

Supplementary Table 3. Validation of quality in nine newly assembled grape accessions.

Number	Accessions	Mapping rate (%)	Switch error (%)	Hamming error (%)	Consensus accuracy
1	BM_AGIS_01	99.93	0.0347	0.94	60.115
2	MF_AGIS_01	99.99	0.0189	0.99	59.689
3	MH_AGIS_01	99.99	0.0353	2.16	58.553
4	TS_AGIS_01	99.98	0.0400	0.30	62.250
5	SM_AGIS_01	99.99	0.0389	2.83	41.609
6	BMNG_AGIS_01	99.99	0.0463	1.43	60.005
7	HMNG_AGIS_01	99.99	0.0326	0.90	59.958
8	PN_AGIS_01	99.98	0.0400	0.83	45.179
9	WG_AGIS_01	99.99	0.0432	1.40	62.893

Supplementary Table 4. Summary of repeated sequence annotations.

Haplotype	Total length	GC level	Proportion	Bases masked	Retroelements										
					SINEs:	LINEs:	L2/CR1/Rex	R1/LOA/Jockey	L1/CIN4	LTR elements:	BEL/Pao	Gypsy/DIRS1	Ty1/Copia	Retroviral	Sum
			number of elements		4,984	49,514	26	700	47,548	294,752	210	145,704	132,267	1,426	349,250
WGT2T_hap1	530,730,429	35.12%	length occupied	303,374,589	898,044	27,441,615	9,614	217,604	25,786,265	183,869,953	38,461	78,415,422	101,402,410	489,331	212,209,612
			percentage of sequence	57.16%	0.17%	5.17%	0%	0.04%	4.86%	34.64%	0.01%	14.78%	19.11%	0.09%	39.98%
			number of elements		5,092	49,458	25	688	47,518	298,590	217	146,319	135,668	1,436	353,140
WGT2T_hap2	539,303,321	35.31%	length occupied	312,100,537	985,963	27,670,436	7,663	239,156	26,067,242	191,694,915	34,244	79,031,475	109,416,417	511,934	220,351,314
			percentage of sequence	57.87%	0.18%	5.13%	0%	0.04%	4.83%	35.54%	0.01%	14.65%	20.29%	0.09%	40.86%
			number of elements		4,479	48,186	19	631	46,409	281,208	204	138,705	125,875	1,263	333,873
PN-AGIS1T2T_hap1	496,447,703	35.02%	length occupied	275,220,135	715,474	25,697,604	3,420	163,777	24,433,240	166,324,589	36,255	72,772,382	87,376,331	458,301	192,737,667
			percentage of sequence	55.44%	0.14%	5.18%	0.00%	0.03%	4.92%	33.50%	0.01%	14.66%	17.60%	0.09%	38.82%
			number of elements		4,424	48,002	19	635	46,201	272,600	201	136,701	119,036	1,279	325,026
PN-AGIS1T2T_hap2	489,779,116	34.92%	number of elements	267,785,632	778,261	25,850,521	3,428	179,242	24,455,524	161,108,922	35,092	71,590,543	81,405,069	491,700	187,737,704
			length occupied	54.68%	0.16%	5.28%	0%	0.04%	4.99%	32.89%	0.01%	14.62%	16.62%	0.10%	38.33%
			number of elements		4,620	47,988	19	619	46,206	273,140	215	136,314	120,311	1,310	325,748
TST2T_hap1	479,153,877	34.75%	length occupied	263,863,222	802,682	25,484,461	3,338	156,672	24,138,962	158,944,266	36,215	70,298,039	82,535,643	536,862	185,231,409
			percentage of sequence	55.06%	0.17%	5.32%	0%	0.03%	5.04%	33.17%	0.01%	14.67%	17.23%	0.11%	38.66%
			number of elements		4,636	48,360	17	634	46,522	282,254	212	141,020	124,055	1,343	335,250
TST2T_hap2	493,479,834	34.74%	length occupied	274948475	873034	25920555	3284	158435	24543320	166485147	36282	74240566	85595341	564592	193278736
			percentage of sequence	55.71%	0.18%	5.25%	0%	0.03%	4.97%	33.74%	0.01%	15.04%	17.35%	0.11%	39.17%
			number of elements		4,702	48,225	16	608	46,443	278,091	217	137,935	123,501	1,320	331,018
BMT2T_hap1	489,516,100	34.86%	length occupied	271,800,367	791,233	25,655,255	3,191	157,053	24,287,440	164,429,188	36,716	72,410,781	86,069,120	546,840	190,875,676
			percentage of sequence	55.53%	0.16%	5.24%	0%	0%	4.96%	33.59%	0.01%	14.79%	17.58%	0.11%	38.99%
			number of elements		4,543	48,083	17	630	46,254	276,767	212	138,545	121,372	1,320	329,393
BMT2T_hap2	484,525,449	34.70%	length occupied	266,741,176	806,065	25,720,123	3,280	164,177	24,287,495	160,794,883	35,026	72,216,557	81,831,570	553,000	187,321,071
			percentage of sequence	55.06%	0.17%	5.31%	5.31%	0.03%	5.01%	33.19%	0.01%	14.90%	16.89%	0.11%	38.66%
			number of elements		4,055	42,407	240	428	41,946	285,478	976	123,297	139,968	1,309	331,940
SMT2T_hap1	486,490,243	35.02%	number of elements	285,488,588	556,320	26,972,514	204,543	136,659	26,679,318	182,583,081	314,616	72,172,112	100,426,260	734,159	210,111,915
			length occupied	58.68%	0.11%	5.54%	0.04%	0.03%	5.48%	37.53%	0.06%	14.84%	20.64%	0.15%	43.19%
			number of elements		3,866	42,605	251	419	42,136	286,679	972	124,404	139,825	1,259	333,150
SMT2T_hap2	486,339,816	34.93%	number of elements	284,395,456	544,012	26,914,464	222,563	131,131	26,604,860	181,572,524	270,199	73,028,559	98,041,643	654,387	209,031,000
			length occupied	58.48%	0.11%	5.53%	0.05%	0.03%	5.47%	37.33%	0.06%	15.02%	20.16%	0.13%	42.98%
			number of elements		4,111	43,111	274	615	42,604	293,514	974	126,872	143,416	1,319	340,736
MHT2T_hap1	493,251,850	34.96%	length occupied	290,866,311	593,472	27,426,633	246,071	150,885	27,087,814	186,860,281	285,131	75,264,032	100,624,739	713,758	214,880,386
			percentage of sequence	0.5897	0.12%	5.56%	0.05%	0.03%	5.49%	37.88%	0.06%	15.26%	20.4%	0.14%	43.56%
			number of elements		3,910	42,631	241	442	42,178	287,354	963	124,358	140,399	1,316	333,895
MHT2T_hap2	491,413,581	35.02%	length occupied	290,104,180	560,327	26,958,260	197,682	140,074	26,675,133	186,123,233	282,421	73,128,149	102,531,168	710,432	213,641,820
			percentage of sequence	59.03%	0.11%	5.49%	0.04%	0.03%	5.43%	37.88%	0.06%	14.88%	20.86%	0.14%	43.47%
			number of elements		4,631	48,088	17	616	46,297	277,617	214	137,691	123,207	1,320	330,336
MFT2T_hap1	489,744,692	34.89%	length occupied	271,661,714	914,235	25,911,348	3,168	170,287	24,550,812	163,967,358	34,828	71,803,754	85,612,408	534,135	190,792,941
			percentage of sequence	55.47%	0.19%	5.29%	0%	0.03%	5.01%	33.48%	0.01%	14.66%	17.48%	0.11%	38.96%
			number of elements		4,609	47,864	22	642	46,076	272,584	214	136,259	119,611	1,296	325,057
MFT2T_hap2	487,016,145	34.96%	length occupied	267,651,631	823,302	25,495,706	3,664	163,850	24,145,677	159,887,614	34,636	70,533,913	82,134,455	503,753	186,206,622
			percentage of sequence	54.96%	0.17%	5.24%	0%	0.03%	4.96%	32.83%	0.01%	14.48%	16.86%	0.10%	35.13%
			number of elements		4,466	48,086	18	623	46,243	275,353	213	137,357	121,515	1,299	327,905
BMNGT2T_hap1	488,798,270	34.93%	length occupied	271,766,147	735,903	25,801,684	3,447	159,901	24,331,531	163,175,175	38,514	72,151,210	84,893,767	529,240	189,712,762
			percentage of sequence	55.60%	0.15%	5.28%	0%	0.03%	4.98%	33.38%	0.01%	14.76%	17.37%	0.11%	38.81%
			number of elements		4,534	48,131	23	634	46,290	274,964	219	137,243	120,997	1,290	327,629
BMNGT2T_hap2	489,441,882	34.92%	length occupied	271,137,002	895,814	25,774,822	3,798	170,267	24,396,877	161,949,438	37,735	71,338,938	83,917,069	492,276	188,620,074
			percentage of sequence	55.40%	0.18%	5.27%	0%	0.03%	4.98%	33.09%	0.01%	14.58%	17.15%	0.10%	38.54%
			number of elements		4,566	48,349	23	643	46,467	275,875	222	137,947	121,260	1,322	328,790
HMNGT2T_hap1	489,014,862	34.86%	length occupied	272,277,829	798,180	25,938,407	3,947	173,297	24,470,118	161,721,912	39,198	71,594,865	84,095,766	511,242	188,458,499
			percentage of sequence	55.68%	0.16%	5.30%	0%	0.04%	5.00%	33.07%	0.01%	14.64%	17.20%	0.10%	38.54%
			number of elements		4,504	48,182	19	623	46,361	275,994	219	137,757	121,566	1,286	328,680
HMNGT2T_hap2	483,876,499	34.78%	length occupied	267,255,248	908,432	25,760,689	3,508	159,228	24,385,298	162,527,335	38,302	72,523,799	83,147,989	516,098	189,196,456
			percentage of sequence	55.23%	0.19%	5.32%	0%	0.03%	5.04%	33.59%	0.01%	14.99%	17.18%	0.11%	39.10%

Haplotype	DNA transposons	hobo-Activator	DNA Tc1-IS630-Pogo	PiggyBac	Tourist/Harbinger	Rolling-circles	Total interspersed repeats:	Small RNA:	Satellites:	Simple repeats:	Low complexity:
	290,645	122,641	45,231	40	48,155	7,410	/	5,692	298	123,464	25,295
WGT2T_hap1	75,427,211	33,793,044	9,194,699	7,132	7,894,279	3,777,770	339,793,415	827,906	68,136	5,265,262	1,304,888
	14.21%	6.37%	1.73%	0%	1.49%	0.71%	64.02%	0.16%	0.01%	0.99%	0.25%
	287,549	119,720	45,461	40	47,801	7,481	/	5,785	305	123,070	25,484
WGT2T_hap2	75,202,831	33,480,208	9,434,053	7,275	7,809,194	3,875,506	347,665,566	799,313	71,960	5,214,166	1,314,255
	13.94%	6.21%	1.75%	0%	1.45%	0.72%	64.47%	0.15%	0.01%	0.97%	0.24%
	273,076	111,841	42,709	42	46,288	6,496	/	5,174	263	118,725	24,594
PN-AGIS1T2T_hap1	69,213,059	30,179,521	8,403,725	7,104	7,582,967	3,237,809	311,512,442	735,024	66,331	5,209,338	1,223,119
	13.94%	6.08%	1.69%	0.00%	1.53%	0.65%	62.75%	0.15%	0.01%	1.05%	0.25%
	275,649	114,622	42,895	43	45,719	6,329	/	5,103	278	117,690	24,632
PN-AGIS1T2T_hap2	67,708,819	28,303,964	8,568,933	7,448	7,528,652	3,177,341	306,582,736	699,494	78,669	5,153,510	1,332,092
	13.82%	5.78%	1.75%	0%	1.54%	0.65%	62.60%	0.14%	0.02%	1.05%	0.27%
	274,021	113,359	42,243	43	46,124	6,430	/	5,349	275	118,505	24,556
TST2T_hap1	65,270,602	26,784,635	8,213,804	6,954	7,505,051	3,217,308	294,944,016	759,213	65,087	5,127,060	1,263,114
	13.62%	5.59%	1.71%	0%	1.57%	0.67%	61.56%	0.16%	0.01%	1.07%	0.26%
	282,006	117,354	43,649	47	47,664	6,414	repeats:	5,372	266	120,297	24,916
TST2T_hap2	68281447	28509945	8513432	7750	7786651	3233267	307875383	739863	61837	5233871	1252864
	13.84%	5.78%	1.73%	0%	1.58%	0.66%	62.39%	0.15%	0.01%	1.06%	0.25%
	276,534	114,659	42,934	45	46,697	6,465	/	5,407	267	119,412	24,661
BMT2T_hap1	66,922,278	27,139,462	8,367,536	7,478	8,200,654	3,212,826	304,162,002	732,008	62,454	5,362,251	1,253,622
	13.67%	5.54%	1.71%	0%	1.68%	0.66%	62.14%	0.15%	0.01%	1.10%	0.26%
	276,536	113,699	42,931	44	46,420	6,476	/	5,357	273	119,238	24,724
BMT2T_hap2	66,097,829	26,762,008	8,354,970	7,182	7,634,442	3,294,252	299,468,111	868,673	60,254	5,306,879	1,242,928
	13.64%	5.52%	1.72%	0%	1.58%	0.68%	61.81%	0.18%	0.01%	1.10%	0.26%
	291,528	168,173	42,808	158	35,518	11,824	/	7,306	998	106,656	21,420
SMT2T_hap1	61,174,593	37,115,991	8,332,855	55,112	5,788,163	6,330,340	314,932,814	1,982,894	229,052	4,613,023	1,381,643
	12.57%	7.63%	1.71%	0.01%	1.19%	1.3%	64.74%	0.41%	0.05%	0.95%	0.28%
	293,638	170,138	42,519	145	35,741	11,849	/	7,493	1,021	107,221	21,241
SMT2T_hap2	61,352,530	37,502,852	8,241,431	46,054	5,674,458	6,316,195	314,264,535	1,801,339	235,018	4,773,992	1,227,782
	12.62%	7.71%	1.69%	0.01%	1.17%	1.3%	64.62%	0.37%	0.05%	0.98%	0.25%
	295,406	169,183	43,725	151	36,227	12,175	/	7,543	1,033	107,556	21,430
MHT2T_hap1	61,789,147	37,158,790	8,696,789	46,891	5,738,604	6,368,343	320,755,462	1,910,778	231,996	4,840,758	1,216,185
	12.53%	7.53%	1.76%	0.01%	1.16%	1.29%	65.03%	0.39%	0.05%	0.98%	0.25%
	294,172	170,907	42,843	150	35,423	11,755		7,987	1,014	106,336	21,158
MHT2T_hap2	62,240,481	38,355,881	8,323,580	47,039	5,616,998	6,227,098	319,562,602	2,058,625	231,312	4,805,006	1,226,880
	12.67%	7.81%	1.69%	0.01%	1.14%	1.27%	65.03%	0.42%	0.05%	0.98%	0.25%
	272,093	112,496	42,264	45	45,899	6,443	/	5,366	251	118,550	24,531
MFT2T_hap1	66,834,148	28,382,293	8,308,290	7,417	7,488,540	3,142,229	304,454,530	804,300	51,192	5,346,003	1,502,552
	13.65%	5.80%	1.70%	0%	1.53%	0.64%	62.17%	0.16%	0.01%	1.09%	0.31%
	271,654	111,293	41,763	42	47,215	6,279	/	5,324	268	118,316	24,487
MFT2T_hap2	68,357,613	29,758,781	8,124,796	7,037	8,117,553	3,032,338	302,773,825	743,060	60,354	5,220,297	1,465,896
	14.04%	6.11%	1.67%	0%	1.67%	0.62%	62.17%	0.15%	0.01%	1.07%	0.30%
	276,284	115,901	42,417	44	er 46182	6,309	repeats:	5,146	300	118,517	24,616
BMNGT2T_hap1	69,062,673	30,537,668	8,302,524	7,334	7,538,891	3,147,886	304,526,388	676,109	68,169	5,199,181	1,236,898
	14.13%	6.25%	1.70%	0%	1.54%	0.64%	62.30%	0.14%	0.01%	1.06%	0.25%
	276,991	115,868	42,513	45	46,485	6,209	/	5,222	278	118,450	24,635
BMNGT2T_hap2	69,567,624	30,976,111	8,310,043	7,347	7,702,787	3,023,354	305,365,172	700,777	65,674	5,238,895	1,268,196
	14.21%	6.33%	1.70%	0%	1.57%	0.62%	62.39%	0.14%	0.01%	1.07%	0.26%
	278,213	116,660	42,723	44	46,375	6,303	/	5,303	294	119,057	24,669
HMNGT2T_hap1	70,288,517	31,427,116	8,353,889	7,226	7,544,560	3,085,846	303,879,053	825,676	66,959	5,255,513	1,332,270
	14.37%	6.43%	1.71%	0%	1.54%	0.63%	62.14%	0.17%	0.01%	1.07%	0.27%
	276,844	116,237	42,379	45	46,294	6,305	/	5,271	285	119,018	24,717
HMNGT2T_hap2	65,505,140	27,096,926	8,203,781	7,455	7,618,287	3,097,620	299,757,649	793,277	67,483	5,016,832	1,250,570
	13.54%	5.60%	1.70%	0%	1.57%	0.64%	61.95%	0.16%	0.01%	1.04%	0.26%

Supplementary Table 5. Summary of centromere and telomere.

Accesions	Haplotypes	Chromosome	Centromere				Telomere	
			Start	End	Length	Unit	Length(CCCTAAA)	Length(TTTAGGG)
BM_AGIS_01	hap1	chr01	15,274,679	17,260,842	1,986,163	107	28,896	13,594
BM_AGIS_01	hap1	chr02	13,114,681	13,471,665	356,984	107	2,485	12,369
BM_AGIS_01	hap1	chr03	14,676,438	15,389,735	713,297	135	11,081	5,173
BM_AGIS_01	hap1	chr04	13,557,088	14,119,436	562,348	107	2,954	19,446
BM_AGIS_01	hap1	chr05	13,296,656	14,692,618	1,395,962	107	20,622	14,994
BM_AGIS_01	hap1	chr06	10,259,964	12,602,817	2,342,853	107	14,651	10,598
BM_AGIS_01	hap1	chr07	12,597,564	13,063,816	466,252	107	17,003	10,689
BM_AGIS_01	hap1	chr08	8,259,569	8,309,248	49,679	107	4,529	4,305
BM_AGIS_01	hap1	chr09	15,532,178	15,647,499	115,321	107	7,189	273
BM_AGIS_01	hap1	chr10	20,562,397	21,209,837	647,440	107	11,354	18,396
BM_AGIS_01	hap1	chr11	14,022,232	14,061,538	39,306	107	13,055	16,744
BM_AGIS_01	hap1	chr12	11,207,153	11,490,935	283,782	107	11,396	26,572
BM_AGIS_01	hap1	chr13	12,420,492	12,795,429	374,937	107	26,733	13,209
BM_AGIS_01	hap1	chr14	14,177,045	14,682,213	505,168	134	13,734	14,441
BM_AGIS_01	hap1	chr15	7,200,960	7,732,156	531,196	107	56	15,540
BM_AGIS_01	hap1	chr16	9,857,738	9,912,177	54,439	107	7,147	1,071
BM_AGIS_01	hap1	chr17	14,003,160	14,951,607	948,447	107	56	63
BM_AGIS_01	hap1	chr18	16,021,834	16,726,493	704,659	40	6,279	21,091
BM_AGIS_01	hap1	chr19	17,336,277	17,650,534	314,257	107	11,963	63
BM_AGIS_01	hap2	chr01	14,372,781	14,956,716	583,935	107	21,693	17,066
BM_AGIS_01	hap2	chr02	13,177,424	15,866,081	2,688,657	107	15,169	7,245
BM_AGIS_01	hap2	chr03	14,453,488	14,959,800	506,312	107	2,863	9,632
BM_AGIS_01	hap2	chr04	12,364,893	13,867,332	1,502,439	107	17,367	9,576
BM_AGIS_01	hap2	chr05	13,712,120	14,022,941	310,821	107	7,091	15,064
BM_AGIS_01	hap2	chr06	10,212,434	11,112,560	900,126	107	16,744	12,250
BM_AGIS_01	hap2	chr07	12,455,851	12,898,057	442,206	107	23,247	10,675
BM_AGIS_01	hap2	chr08	8,308,972	8,566,712	257,740	107	1,043	11,403
BM_AGIS_01	hap2	chr09	17,410,994	17,998,621	587,627	107	13,118	25,284
BM_AGIS_01	hap2	chr10	19,083,912	19,686,058	602,146	107	5,614	2,940
BM_AGIS_01	hap2	chr11	13,380,271	13,681,022	300,751	107	13,055	13,174
BM_AGIS_01	hap2	chr12	11,006,345	11,459,186	452,841	107	1,666	12,250
BM_AGIS_01	hap2	chr13	11,932,148	12,380,970	448,822	107	11,522	14,133
BM_AGIS_01	hap2	chr14	14,566,121	15,071,296	505,175	107	13,664	10,990
BM_AGIS_01	hap2	chr15	8,483,132	8,741,635	258,503	107	56	6,797
BM_AGIS_01	hap2	chr16	9,165,081	10,137,960	972,879	107	15,666	11,627
BM_AGIS_01	hap2	chr17	14,656,840	15,257,912	601,072	107	11,802	42
BM_AGIS_01	hap2	chr18	26,344,137	27,936,348	1,592,211	191	21,098	371
BM_AGIS_01	hap2	chr19	18,466,688	18,814,388	347,700	107	3,283	16,184
BM_AGIS_01	hap1	chr01	14,377,901	15,689,578	1,311,677	107	10,269	6,153
BM_AGIS_01	hap1	chr02	12,734,205	13,439,179	704,974	107	7,294	14,581
BM_AGIS_01	hap1	chr03	14,343,754	14,950,924	607,170	135	17,290	19,243
BM_AGIS_01	hap1	chr04	13,497,728	14,369,322	871,594	107	10,339	7,350
BM_AGIS_01	hap1	chr05	13,839,966	15,731,108	1,891,142	107	11,935	12,159
BM_AGIS_01	hap1	chr06	10,274,929	13,995,265	3,720,336	107	4,137	10,612
BM_AGIS_01	hap1	chr07	13,147,557	13,835,687	688,130	107	8,022	2,744
BM_AGIS_01	hap1	chr08	6,615,999	7,379,061	763,062	107	6,020	15,302
BM_AGIS_01	hap1	chr09	14,063,327	15,397,235	1,333,908	107	15,295	15,736
BM_AGIS_01	hap1	chr10	20,582,990	21,191,206	608,216	107	11,473	10,269
BM_AGIS_01	hap1	chr11	14,228,725	16,624,443	2,395,718	107	13,342	8,799
BM_AGIS_01	hap1	chr12	10,931,735	11,191,991	260,256	107	12,439	13,489
BM_AGIS_01	hap1	chr13	12,509,032	13,052,302	543,270	107	9,723	12,600
BM_AGIS_01	hap1	chr14	14,675,066	15,024,950	349,884	107	2,436	2,667
BM_AGIS_01	hap1	chr15	7,112,772	7,285,604	172,832	107	49	10,668
BM_AGIS_01	hap1	chr16	8,646,630	9,419,284	772,654	107	11,837	10,129
BM_AGIS_01	hap1	chr17	14,858,905	16,093,989	1,235,084	107	12,096	42
BM_AGIS_01	hap1	chr18	/	/	/	/	3,010	12,103
BM_AGIS_01	hap1	chr19	16,511,472	17,741,631	1,230,159	107	3,808	5,411
BM_AGIS_01	hap2	chr01	14,025,065	14,607,739	582,674	107	11,949	6,146
BM_AGIS_01	hap2	chr02	12,698,289	13,066,559	368,270	107	2,786	10,423
BM_AGIS_01	hap2	chr03	15,048,721	15,426,356	377,635	135	6,685	11,991
BM_AGIS_01	hap2	chr04	12,409,517	14,030,145	1,620,628	107	9,905	13,762
BM_AGIS_01	hap2	chr05	13,076,335	14,652,843	1,576,508	107	11,900	938
BM_AGIS_01	hap2	chr06	10,262,722	13,633,356	3,370,634	107	13,034	11,683
BM_AGIS_01	hap2	chr07	12,472,030	13,132,717	660,687	107	10,794	9,828
BM_AGIS_01	hap2	chr08	7,856,069	8,489,494	633,425	107	11,151	15,309
BM_AGIS_01	hap2	chr09	17,165,039	19,026,704	1,861,665	107	11,207	2,058
BM_AGIS_01	hap2	chr10	19,948,560	21,738,335	1,789,775	107	7,770	11,655
BM_AGIS_01	hap2	chr11	13,912,156	14,544,900	632,744	107	9,646	17,185
BM_AGIS_01	hap2	chr12	11,146,522	12,051,308	904,786	107	12,544	63
BM_AGIS_01	hap2	chr13	12,044,138	12,637,165	593,027	107	15,477	4,816
BM_AGIS_01	hap2	chr14	14,282,936	14,300,958	18,022	107	12,873	5,719
BM_AGIS_01	hap2	chr15	7,007,202	7,182,336	175,134	107	49	10,738

Supplementary Table 5. Summary of centromere and telomere.

Accesions	Haplotypes	Chromosome	Centromere				Telomere	
			Start	End	Length	Unit	Length(CCCTAAA)	Length(TTTAGGG)
BM_AGIS_01	hap2	chr16	8,919,340	10,130,840	1,211,500	107	13,664	11,277
BM_AGIS_01	hap2	chr17	14,583,944	16,021,745	1,437,801	107	3,157	56
BM_AGIS_01	hap2	chr18	16,244,954	16,492,591	247,637	187	1,995	8,659
BM_AGIS_01	hap2	chr19	17,823,860	19,246,183	1,422,323	107	15,015	14,301
HMNG_AGIS_(	hap1	chr01	14,027,021	14,609,706	582,685	107	13,538	4,284
HMNG_AGIS_(	hap1	chr02	12,740,153	13,446,944	706,791	107	13,048	11,088
HMNG_AGIS_(	hap1	chr03	15,052,378	15,096,047	43,669	135	12,222	11,641
HMNG_AGIS_(	hap1	chr04	12,410,915	14,021,340	1,610,425	107	11,536	3,087
HMNG_AGIS_(	hap1	chr05	13,268,410	15,133,691	1,865,281	107	9,632	9,961
HMNG_AGIS_(	hap1	chr06	10,261,539	13,655,879	3,394,340	107	11,501	8,260
HMNG_AGIS_(	hap1	chr07	13,028,267	13,716,767	688,500	107	2,086	12,663
HMNG_AGIS_(	hap1	chr08	7,855,254	8,488,679	633,425	107	10,157	10,220
HMNG_AGIS_(	hap1	chr09	17,040,064	17,799,933	759,869	107	10,633	10,913
HMNG_AGIS_(	hap1	chr10	19,972,042	20,284,967	312,925	107	12,278	9,856
HMNG_AGIS_(	hap1	chr11	13,648,682	14,641,727	993,045	107	28	11,746
HMNG_AGIS_(	hap1	chr12	11,138,117	11,660,519	522,402	107	4,305	1,925
HMNG_AGIS_(	hap1	chr13	12,510,984	13,054,255	543,271	107	11,522	11,193
HMNG_AGIS_(	hap1	chr14	14,663,950	15,013,846	349,896	107	2,443	3,829
HMNG_AGIS_(	hap1	chr15	7,152,376	7,223,582	71,206	107	49	12,089
HMNG_AGIS_(	hap1	chr16	8,909,820	9,845,419	935,599	107	3,815	8,617
HMNG_AGIS_(	hap1	chr17	15,081,352	15,714,116	632,764	107	9,961	35
HMNG_AGIS_(	hap1	chr18	/	/	/	/	2,730	10,241
HMNG_AGIS_(	hap1	chr19	17,768,303	19,266,303	1,498,000	107	21	9,044
HMNG_AGIS_(	hap2	chr01	14,340,374	15,652,251	1,311,877	107	11,578	4,277
HMNG_AGIS_(	hap2	chr02	12,691,488	20,005,887	7,314,399	107	10,220	1,554
HMNG_AGIS_(	hap2	chr03	14,358,456	14,434,033	75,577	107	11,655	3,290
HMNG_AGIS_(	hap2	chr04	13,498,659	14,363,351	864,692	107	10,906	2,254
HMNG_AGIS_(	hap2	chr05	13,090,801	14,640,405	1,549,604	107	10,367	11,473
HMNG_AGIS_(	hap2	chr06	10,286,338	13,943,219	3,656,881	107	15,372	11,914
HMNG_AGIS_(	hap2	chr07	12,474,607	13,136,954	662,347	107	13,097	12,313
HMNG_AGIS_(	hap2	chr08	6,611,912	7,377,870	765,958	107	2,429	12,614
HMNG_AGIS_(	hap2	chr09	14,060,145	14,629,228	569,083	107	9,863	10,731
HMNG_AGIS_(	hap2	chr10	20,494,781	20,725,549	230,768	107	5,782	11,039
HMNG_AGIS_(	hap2	chr11	13,902,696	14,532,746	630,050	107	2,723	13,293
HMNG_AGIS_(	hap2	chr12	10,897,577	11,161,302	263,725	107	56	1,113
HMNG_AGIS_(	hap2	chr13	11,946,463	12,538,019	591,556	107	9,653	11,599
HMNG_AGIS_(	hap2	chr14	14,272,430	14,290,452	18,022	107	1,827	1,932
HMNG_AGIS_(	hap2	chr15	7,107,444	7,283,650	176,206	107	56	4,830
HMNG_AGIS_(	hap2	chr16	8,641,802	9,417,326	775,524	107	6,839	9,674
HMNG_AGIS_(	hap2	chr17	14,579,726	14,717,593	137,867	107	301	28
HMNG_AGIS_(	hap2	chr18	23,371,931	23,503,924	131,993	187	10,941	2,793
HMNG_AGIS_(	hap2	chr19	16,273,585	16,277,554	3,969	107	2,982	12,789
MF_AGIS_01	hap1	chr01	14,305,685	14,880,691	575,006	107	8,841	10,640
MF_AGIS_01	hap1	chr02	12,803,539	13,535,219	731,680	107	10,388	2,527
MF_AGIS_01	hap1	chr03	15,055,101	15,237,072	181,971	107	3,430	13,076
MF_AGIS_01	hap1	chr04	13,544,026	13,799,545	255,519	107	3,318	27,559
MF_AGIS_01	hap1	chr05	12,738,405	13,517,688	779,283	107	18,886	13,832
MF_AGIS_01	hap1	chr06	10,564,726	12,054,845	1,490,119	107	12,901	11,767
MF_AGIS_01	hap1	chr07	12,510,177	13,094,126	583,949	107	7,189	13,265
MF_AGIS_01	hap1	chr08	7,824,625	8,578,435	753,810	107	5,397	2,926
MF_AGIS_01	hap1	chr09	8,430,465	9,606,723	1,176,258	107	11,683	15,645
MF_AGIS_01	hap1	chr10	19,776,733	20,451,989	675,256	107	4,683	13,664
MF_AGIS_01	hap1	chr11	13,807,330	14,103,328	295,998	107	14,252	13,111
MF_AGIS_01	hap1	chr12	11,186,529	12,090,415	903,886	107	13,167	12,313
MF_AGIS_01	hap1	chr13	12,295,435	12,888,986	593,551	107	13,713	14,868
MF_AGIS_01	hap1	chr14	13,764,330	14,269,509	505,179	107	10,906	14,301
MF_AGIS_01	hap1	chr15	7,221,200	7,395,212	174,012	107	49	15,379
MF_AGIS_01	hap1	chr16	8,526,224	9,707,855	1,181,631	107	19,012	7,875
MF_AGIS_01	hap1	chr17	14,833,458	16,519,701	1,686,243	107	21,182	49
MF_AGIS_01	hap1	chr18	/	/	/	/	12,684	8,806
MF_AGIS_01	hap1	chr19	18,692,663	20,065,105	1,372,442	107	11,956	13,573
MF_AGIS_01	hap2	chr01	14,646,448	14,724,842	78,394	107	4,004	11,683
MF_AGIS_01	hap2	chr02	12,874,093	13,775,347	901,254	107	2,653	9,562
MF_AGIS_01	hap2	chr03	14,442,377	15,176,177	733,800	107	11,011	10,486
MF_AGIS_01	hap2	chr04	12,024,795	13,710,410	1,685,615	107	4,081	49
MF_AGIS_01	hap2	chr05	12,829,120	14,291,021	1,461,901	107	16,254	9,814
MF_AGIS_01	hap2	chr06	10,340,916	13,401,515	3,060,599	107	12,901	7,140
MF_AGIS_01	hap2	chr07	13,170,419	13,892,552	722,133	107	14,812	12,369
MF_AGIS_01	hap2	chr08	7,767,367	8,522,490	755,123	107	9,877	2,933
MF_AGIS_01	hap2	chr09	8,814,951	9,642,430	827,479	107	11,081	15,645
MF_AGIS_01	hap2	chr10	20,000,703	21,796,748	1,796,045	107	15,750	13,671
MF_AGIS_01	hap2	chr11	13,795,599	14,440,858	645,259	107	13,685	14,896

Supplementary Table 5. Summary of centromere and telomere.

Accesions	Haplotypes	Chromosome	Centromere				Telomere	
			Start	End	Length	Unit	Length(CCCTAAA)	Length(TTTAGGG)
MF_AGIS_01	hap2	chr12	11,014,006	12,176,103	1,162,097	107	28,294	11,949
MF_AGIS_01	hap2	chr13	12,655,003	13,174,743	519,740	107	13,713	7,847
MF_AGIS_01	hap2	chr14	14,126,764	14,301,819	175,055	107	14,406	11,235
MF_AGIS_01	hap2	chr15	7,142,317	7,318,634	176,317	107	49	10,493
MF_AGIS_01	hap2	chr16	9,933,036	10,382,839	449,803	107	13,594	11,718
MF_AGIS_01	hap2	chr17	15,393,965	16,734,278	1,340,313	107	21,182	42
MF_AGIS_01	hap2	chr18	16,117,646	16,627,120	509,474	40	10,010	1,526
MF_AGIS_01	hap2	chr19	17,163,149	17,338,966	175,817	107	13,230	23,765
MH_AGIS_01	hap1	chr01	14,257,801	14,843,028	585,227	107	8,050	12,502
MH_AGIS_01	hap1	chr02	13,041,498	14,161,104	1,119,606	107	12,530	16,933
MH_AGIS_01	hap1	chr03	14,254,229	15,904,414	1,650,185	135	2,821	4,354
MH_AGIS_01	hap1	chr04	13,451,594	14,217,010	765,416	107	11,200	14,679
MH_AGIS_01	hap1	chr05	13,263,197	14,947,954	1,684,757	107	8,820	19,586
MH_AGIS_01	hap1	chr06	10,257,675	13,638,958	3,381,283	107	4,284	10,577
MH_AGIS_01	hap1	chr07	12,692,785	14,040,138	1,347,353	107	13,132	18,396
MH_AGIS_01	hap1	chr08	6,462,057	7,226,132	764,075	107	8,260	4,641
MH_AGIS_01	hap1	chr09	15,264,238	16,487,585	1,223,347	107	9,716	13,965
MH_AGIS_01	hap1	chr10	20,345,841	21,447,996	1,102,155	107	2,800	1,862
MH_AGIS_01	hap1	chr11	13,498,243	13,766,011	267,768	107	16,303	14,805
MH_AGIS_01	hap1	chr12	10,934,536	11,841,266	906,730	107	5,166	3,213
MH_AGIS_01	hap1	chr13	11,632,519	12,887,749	1,255,230	107	3,696	5,439
MH_AGIS_01	hap1	chr14	13,935,470	15,303,545	1,368,075	107	8,617	16,695
MH_AGIS_01	hap1	chr15	7,323,609	9,127,654	1,804,045	107	0	4,004
MH_AGIS_01	hap1	chr16	7,692,157	8,159,357	467,200	107	5,866	5,264
MH_AGIS_01	hap1	chr17	15,238,368	15,832,035	593,667	107	6,825	14
MH_AGIS_01	hap1	chr18	15,946,496	16,657,786	711,290	107	2,450	10,829
MH_AGIS_01	hap1	chr19	16,652,426	18,114,052	1,461,626	107	11,186	4,802
MH_AGIS_01	hap2	chr01	15,055,409	19,096,088	4,040,679	107	5,523	12,012
MH_AGIS_01	hap2	chr02	12,984,885	13,707,420	722,535	107	3,556	2,037
MH_AGIS_01	hap2	chr03	14,350,890	15,894,176	1,543,286	107	13,377	8,309
MH_AGIS_01	hap2	chr04	12,721,332	13,816,370	1,095,038	107	679	1,162
MH_AGIS_01	hap2	chr05	13,272,228	14,868,079	1,595,851	107	10,822	7,861
MH_AGIS_01	hap2	chr06	10,400,438	14,029,062	3,628,624	107	16,429	14,273
MH_AGIS_01	hap2	chr07	13,063,852	13,542,528	478,676	107	22,953	1,932
MH_AGIS_01	hap2	chr08	6,588,767	7,364,584	775,817	107	5,817	3,556
MH_AGIS_01	hap2	chr09	15,322,130	17,184,964	1,862,834	107	9,716	406
MH_AGIS_01	hap2	chr10	19,514,980	20,116,677	601,697	107	15,848	15,757
MH_AGIS_01	hap2	chr11	13,673,060	13,999,896	326,836	107	9,674	13,223
MH_AGIS_01	hap2	chr12	11,251,597	12,773,678	1,522,081	107	8,785	6,524
MH_AGIS_01	hap2	chr13	11,666,309	12,290,505	624,196	107	6,321	14,854
MH_AGIS_01	hap2	chr14	15,046,148	15,471,953	425,805	107	8,442	13,090
MH_AGIS_01	hap2	chr15	6,197,047	6,504,357	307,310	107	0	21,980
MH_AGIS_01	hap2	chr16	8,844,997	11,101,437	2,256,440	107	5,369	11,249
MH_AGIS_01	hap2	chr17	14,522,373	16,897,248	2,374,875	107	5,530	7
MH_AGIS_01	hap2	chr18	15,837,683	16,804,155	966,472	107	28	15,218
MH_AGIS_01	hap2	chr19	16,289,289	19,172,527	2,883,238	107	10,598	13,055
PN_AGIS_01	hap1	chr01	14,051,540	15,413,988	1,362,448	107	8,113	16,233
PN_AGIS_01	hap1	chr02	12,907,478	14,023,611	1,116,133	107	16,611	16,870
PN_AGIS_01	hap1	chr03	14,382,209	14,566,148	183,939	135	5,194	16,135
PN_AGIS_01	hap1	chr04	12,301,439	15,858,579	3,557,140	107	18,025	14,042
PN_AGIS_01	hap1	chr05	13,509,679	15,141,309	1,631,630	107	7,119	11,844
PN_AGIS_01	hap1	chr06	10,447,886	12,630,111	2,182,225	107	5,537	15,505
PN_AGIS_01	hap1	chr07	12,797,871	13,638,882	841,011	107	29,960	14,924
PN_AGIS_01	hap1	chr08	7,830,991	7,972,052	141,061	107	5,971	10,297
PN_AGIS_01	hap1	chr09	17,248,816	19,408,218	2,159,402	107	7,700	3,724
PN_AGIS_01	hap1	chr10	20,181,210	21,999,555	1,818,345	107	3,024	9,513
PN_AGIS_01	hap1	chr11	14,205,178	15,154,424	949,246	107	5,481	11,991
PN_AGIS_01	hap1	chr12	10,920,238	11,857,377	937,139	107	6,510	9,149
PN_AGIS_01	hap1	chr13	12,226,126	12,335,491	109,365	107	14,175	10,661
PN_AGIS_01	hap1	chr14	3,482,337	3,525,337	43,000	100	588	3,556
PN_AGIS_01	hap1	chr15	7,265,635	9,118,414	1,852,779	107	49	6,503
PN_AGIS_01	hap1	chr16	8,388,909	11,178,269	2,789,360	107	1,183	35
PN_AGIS_01	hap1	chr17	15,040,046	15,635,226	595,180	107	6,069	70
PN_AGIS_01	hap1	chr18	16,285,473	16,946,516	661,043	136	11,018	12,089
PN_AGIS_01	hap1	chr19	14,135,350	14,982,247	846,897	107	14,133	9,989
PN_AGIS_01	hap2	chr01	14,898,207	15,928,730	1,030,523	107	4,242	5,145
PN_AGIS_01	hap2	chr02	12,862,872	13,655,881	793,009	107	5,971	12,999
PN_AGIS_01	hap2	chr03	14,206,380	15,842,040	1,635,660	135	16,681	12,754
PN_AGIS_01	hap2	chr04	12,480,094	14,145,698	1,665,604	107	18,025	6,979
PN_AGIS_01	hap2	chr05	13,309,501	14,907,841	1,598,340	107	11,578	12,026
PN_AGIS_01	hap2	chr06	10,236,379	13,908,127	3,671,748	107	10,500	4,032
PN_AGIS_01	hap2	chr07	12,504,275	15,039,695	2,535,420	107	6,587	24,164

Supplementary Table 5. Summary of centromere and telomere.

Accesions	Haplotypes	Chromosome	Centromere				Telomere	
			Start	End	Length	Unit	Length(CCCTAAA)	Length(TTTAGGG)
PN_AGIS_01	hap2	chr08	6,588,169	7,280,436	692,267	107	18,361	11,676
PN_AGIS_01	hap2	chr09	15,089,932	16,538,721	1,448,789	107	7,700	12,033
PN_AGIS_01	hap2	chr10	20,236,420	21,511,746	1,275,326	107	3,640	35
PN_AGIS_01	hap2	chr11	13,764,026	14,067,029	303,003	107	4,200	8,449
PN_AGIS_01	hap2	chr12	11,312,437	11,660,969	348,532	107	742	6,188
PN_AGIS_01	hap2	chr13	11,671,000	12,931,968	1,260,968	107	12,222	8,925
PN_AGIS_01	hap2	chr14	3,461,494	3,504,494	43,000	100	4,627	17,668
PN_AGIS_01	hap2	chr15	8,274,602	8,502,038	227,436	106	63	3,269
PN_AGIS_01	hap2	chr16	10,176,730	10,276,914	100,184	66	2,842	12,201
PN_AGIS_01	hap2	chr17	15,140,282	15,544,535	404,253	107	6,069	56
PN_AGIS_01	hap2	chr18	15,806,124	15,899,586	93,462	192	15,120	9,772
PN_AGIS_01	hap2	chr19	18,703,955	19,384,299	680,344	107	4,305	13,531
SM_AGIS_01	hap1	chr01	14,452,581	15,037,977	585,396	107	8,946	7,308
SM_AGIS_01	hap1	chr02	12,844,398	13,548,833	704,435	107	10,416	2,632
SM_AGIS_01	hap1	chr03	13,945,977	14,382,759	436,782	107	11,214	6,986
SM_AGIS_01	hap1	chr04	13,418,225	14,182,916	764,691	107	8,365	2,310
SM_AGIS_01	hap1	chr05	12,108,909	13,114,638	1,005,729	107	3,892	20,482
SM_AGIS_01	hap1	chr06	10,566,357	14,186,011	3,619,654	107	693	4,214
SM_AGIS_01	hap1	chr07	13,797,123	14,564,392	767,269	107	17,150	11,886
SM_AGIS_01	hap1	chr08	7,433,750	10,398,898	2,965,148	107	924	4,669
SM_AGIS_01	hap1	chr09	14,295,977	15,728,059	1,432,082	107	8,890	3,409
SM_AGIS_01	hap1	chr10	19,266,954	21,273,383	2,006,429	107	7,343	6,748
SM_AGIS_01	hap1	chr11	13,209,753	13,931,755	722,002	107	4,816	658
SM_AGIS_01	hap1	chr12	10,090,647	11,435,976	1,345,329	107	329	12,572
SM_AGIS_01	hap1	chr13	12,123,825	12,605,219	481,394	107	1,687	868
SM_AGIS_01	hap1	chr14	14,076,976	15,430,710	1,353,734	107	7,497	1,029
SM_AGIS_01	hap1	chr15	6,112,152	6,397,955	285,803	107	0	1,393
SM_AGIS_01	hap1	chr16	8,990,482	12,406,890	3,416,408	107	1,946	7,448
SM_AGIS_01	hap1	chr17	14,594,048	16,615,421	2,021,373	107	14	0
SM_AGIS_01	hap1	chr18	15,959,890	16,585,040	625,150	107	2,114	9,835
SM_AGIS_01	hap1	chr19	16,206,783	17,628,464	1,421,681	107	1,050	3,360
SM_AGIS_01	hap2	chr01	13,683,654	14,777,027	1,093,373	107	1,736	11,697
SM_AGIS_01	hap2	chr02	12,849,409	13,962,002	1,112,593	107	7,252	4,487
SM_AGIS_01	hap2	chr03	14,537,057	14,678,266	141,209	107	8,344	5,586
SM_AGIS_01	hap2	chr04	13,273,587	13,961,553	687,966	107	10,927	7,238
SM_AGIS_01	hap2	chr05	13,569,837	15,173,141	1,603,304	107	3,892	11,837
SM_AGIS_01	hap2	chr06	9,950,037	13,268,516	3,318,479	107	3,451	2,590
SM_AGIS_01	hap2	chr07	12,791,403	13,258,590	467,187	107	16,982	5,523
SM_AGIS_01	hap2	chr08	5,669,081	7,211,652	1,542,571	107	6,062	2,667
SM_AGIS_01	hap2	chr09	15,001,065	16,217,009	1,215,944	107	7,266	7,490
SM_AGIS_01	hap2	chr10	19,506,364	20,179,389	673,025	107	2,933	5,397
SM_AGIS_01	hap2	chr11	13,908,863	14,545,472	636,609	107	4,774	10,864
SM_AGIS_01	hap2	chr12	10,644,869	12,160,816	1,515,947	107	5,362	2,751
SM_AGIS_01	hap2	chr13	11,940,004	12,130,195	190,191	107	8,400	3,164
SM_AGIS_01	hap2	chr14	14,434,050	17,428,625	2,994,575	107	7,420	8,379
SM_AGIS_01	hap2	chr15	6,762,444	8,137,331	1,374,887	107	21	1,379
SM_AGIS_01	hap2	chr16	8,610,115	10,305,681	1,695,566	107	1,932	14,588
SM_AGIS_01	hap2	chr17	14,866,516	17,260,768	2,394,252	107	3,654	21
SM_AGIS_01	hap2	chr18	16,102,136	16,704,485	602,349	107	1,799	2,772
SM_AGIS_01	hap2	chr19	16,394,176	19,240,350	2,846,174	107	6,930	3,542
TS_AGIS_01	hap2	chr01	14,379,990	14,962,669	582,679	107	15,680	13,055
TS_AGIS_01	hap2	chr02	13,138,649	13,495,629	356,980	107	27,762	4,634
TS_AGIS_01	hap2	chr03	14,467,738	14,957,616	489,878	135/107	16,121	12,516
TS_AGIS_01	hap2	chr04	13,432,570	14,305,739	873,169	107	4,599	2,016
TS_AGIS_01	hap2	chr05	13,072,927	13,991,580	918,653	107	11,235	13,475
TS_AGIS_01	hap2	chr06	10,028,514	13,317,448	3,288,934	107	1,911	966
TS_AGIS_01	hap2	chr07	12,614,243	13,322,892	708,649	107	2,884	3,612
TS_AGIS_01	hap2	chr08	7,747,503	7,888,566	141,063	107	49	13,692
TS_AGIS_01	hap2	chr09	16,169,655	16,776,523	606,868	187	4,088	11,564
TS_AGIS_01	hap2	chr10	20,262,736	20,620,770	358,034	107	14,217	3,745
TS_AGIS_01	hap2	chr11	13,765,426	14,099,571	334,145	107	1,302	15,918
TS_AGIS_01	hap2	chr12	11,008,523	11,461,925	453,402	107	861	12,467
TS_AGIS_01	hap2	chr13	12,294,049	12,888,887	594,838	107	4,438	18,830
TS_AGIS_01	hap2	chr14	14,523,024	14,940,117	417,093	107	13,510	14,434
TS_AGIS_01	hap2	chr15	8,283,033	8,527,779	244,746	107	49	3,822
TS_AGIS_01	hap2	chr16	9,102,074	9,898,561	796,487	107	5,705	13,083
TS_AGIS_01	hap2	chr17	14,521,282	15,031,872	510,590	107	3,052	70
TS_AGIS_01	hap2	chr18	15,025,101	17,064,808	2,039,707	132	2,359	3,052
TS_AGIS_01	hap2	chr19	18,635,041	19,259,055	624,014	107	6,888	24,773
TS_AGIS_01	hap1	chr01	15,267,983	15,294,875	26,892	107	1,197	8,561
TS_AGIS_01	hap1	chr02	12,670,351	13,376,938	706,587	107	1,890	6,237
TS_AGIS_01	hap1	chr03	14,256,113	14,313,605	57,492	135	6,125	15,631

Supplementary Table 5. Summary of centromere and telomere.

Accesions	Haplotypes	Chromosome	Centromere				Telomere	
			Start	End	Length	Unit	Length(CCCTAAA)	Length(TTTAGGG)
TS_AGIS_01	hap1	chr04	12,073,904	13,765,888	1,691,984	107	10,024	14,665
TS_AGIS_01	hap1	chr05	12,971,459	13,479,227	507,768	107	5,229	4,179
TS_AGIS_01	hap1	chr06	10,259,893	12,613,453	2,353,560	107	11,865	1,001
TS_AGIS_01	hap1	chr07	12,451,180	12,917,641	466,461	107	14,287	13,496
TS_AGIS_01	hap1	chr08	7,703,606	8,333,837	630,231	107	11,984	3,311
TS_AGIS_01	hap1	chr09	16,861,523	17,341,238	479,715	107	9,849	13,972
TS_AGIS_01	hap1	chr10	19,953,461	20,342,036	388,575	107	770	1,701
TS_AGIS_01	hap1	chr11	13,921,713	14,542,461	620,748	107	14,581	9,681
TS_AGIS_01	hap1	chr12	10,911,325	11,169,920	258,595	107	4,977	749
TS_AGIS_01	hap1	chr13	11,933,385	12,380,561	447,176	107	12,684	13,748
TS_AGIS_01	hap1	chr14	14,604,102	15,084,633	480,531	107	5,327	3,563
TS_AGIS_01	hap1	chr15	7,168,210	7,335,683	167,473	107	0	12,117
TS_AGIS_01	hap1	chr16	8,845,737	9,747,938	902,201	107	2,422	14,777
TS_AGIS_01	hap1	chr17	14,676,093	15,594,727	918,634	107	6,440	0
TS_AGIS_01	hap1	chr18	15,022,390	17,704,857	2,682,467	66	5,782	15,078
TS_AGIS_01	hap1	chr19	16,766,976	17,288,709	521,733	107	8,897	18,424
WG_AGIS_01	hap1	chr01	14,649,826	16,371,722	1,721,896	107	12,684	5,593
WG_AGIS_01	hap1	chr02	14,874,425	15,031,396	156,971	107	20,433	1,232
WG_AGIS_01	hap1	chr03	14,537,009	16,009,692	1,472,683	107	9,380	15,519
WG_AGIS_01	hap1	chr04	12,744,376	14,462,747	1,718,371	107	749	17,927
WG_AGIS_01	hap1	chr05	14,079,765	14,834,858	755,093	107	14,378	10,402
WG_AGIS_01	hap1	chr06	12,040,708	14,407,611	2,366,903	107	14,917	10,066
WG_AGIS_01	hap1	chr07	14,871,377	15,655,059	783,682	107	3,710	20,321
WG_AGIS_01	hap1	chr08	8,429,086	8,841,755	412,669	107	8,715	17,045
WG_AGIS_01	hap1	chr09	16,831,555	19,632,593	2,801,038	107	10,353	12,551
WG_AGIS_01	hap1	chr10	18,702,096	19,552,291	850,195	107	15,519	35
WG_AGIS_01	hap1	chr11	14,363,096	17,783,925	3,420,829	107	938	15,337
WG_AGIS_01	hap1	chr12	11,736,741	13,654,326	1,917,585	107	4,116	4,977
WG_AGIS_01	hap1	chr13	12,877,828	13,896,111	1,018,283	107	12,768	1,764
WG_AGIS_01	hap1	chr14	15,522,764	16,465,002	942,238	107	14,609	11,186
WG_AGIS_01	hap1	chr15	6,786,330	7,435,194	648,864	107	12,880	6,020
WG_AGIS_01	hap1	chr16	10,353,276	11,058,979	705,703	66	10,570	2,422
WG_AGIS_01	hap1	chr17	14,865,357	15,190,110	324,753	107	3,570	49
WG_AGIS_01	hap1	chr18	15,532,101	16,243,964	711,863	107	10,752	18,144
WG_AGIS_01	hap1	chr19	9,792,403	11,441,641	1,649,238	107	16,639	6,160
WG_AGIS_01	hap2	chr01	14,858,260	16,188,512	1,330,252	107	12,201	13,146
WG_AGIS_01	hap2	chr02	14,058,139	15,437,909	1,379,770	107	9,632	11,627
WG_AGIS_01	hap2	chr03	14,730,279	15,109,842	379,563	107	9,380	4,830
WG_AGIS_01	hap2	chr04	13,857,181	14,964,454	1,107,273	107	14,448	17,927
WG_AGIS_01	hap2	chr05	14,049,555	14,822,713	773,158	107	14,378	10,402
WG_AGIS_01	hap2	chr06	11,815,073	13,222,586	1,407,513	107	7,273	12,257
WG_AGIS_01	hap2	chr07	16,087,857	16,189,932	102,075	107	4,732	20,412
WG_AGIS_01	hap2	chr08	8,472,463	9,162,745	690,282	107	8,715	6,552
WG_AGIS_01	hap2	chr09	17,187,579	20,390,067	3,202,488	107	13,055	4,032
WG_AGIS_01	hap2	chr10	19,472,693	21,063,542	1,590,849	107	854	63
WG_AGIS_01	hap2	chr11	14,592,664	17,883,414	3,290,750	107	5,579	15,687
WG_AGIS_01	hap2	chr12	12,377,817	13,912,710	1,534,893	107	4,116	609
WG_AGIS_01	hap2	chr13	12,916,804	13,934,513	1,017,709	107	3,766	14,084
WG_AGIS_01	hap2	chr14	15,521,959	16,464,197	942,238	107	14,609	11,186
WG_AGIS_01	hap2	chr15	5,921,923	5,947,928	26,005	187	9,317	35
WG_AGIS_01	hap2	chr16	10,277,263	12,033,701	1,756,438	107	5,222	2,422
WG_AGIS_01	hap2	chr17	14,795,210	15,023,905	228,695	107	4,942	28
WG_AGIS_01	hap2	chr18	15,636,897	18,301,923	2,665,026	107	10,752	3,969
WG_AGIS_01	hap2	chr19	8,997,560	10,635,731	1,638,171	107	20,503	13,258

Supplementary Table 6. A total of 466 accessions for genotyping SV based on pangenome (including 324 newly sequenced).

Accessions	Group	Species	Common name	Note	SRR_ID	Assay Type	AvgSpotLen	Bases	BioProject	BioSample	Bytes	Center Name
ARI_1	Wild	*Vitis arizonica*	wild grape	Previously published	-	WGS	-	-	PRJNA842753	-	-	-
ARI_2	Wild	*Vitis arizonica*	wild grape	Previously published	-	WGS	-	-	PRJNA842753	-	-	-
ARI_3	Wild	*Vitis arizonica*	wild grape	Previously published	-	WGS	-	-	PRJNA842753	-	-	-
CAL_1	Wild	*Vitis californica*	wild grape	Previously published	-	WGS	-	-	PRJNA1048091	-	-	-
CAL_2	Wild	*Vitis californica*	wild grape	Previously published	-	WGS	-	-	PRJNA1048096	-	-	-
CAL_3	Wild	*Vitis californica*	wild grape	Previously published	-	WGS	-	-	PRJNA1048097	-	-	-
CINE_1	Wild	*Vitis cinerea*	wild grape	Previously published	SRR14618016	WGS	300	8441241600	PRJNA731597	SAMN19291117	3854857875	UC IRVINE
CINE_2	Wild	*Vitis cinerea*	wild grape	Previously published	-	WGS	-	-	PRJNA1048092	-	-	-
CINE_3	Wild	*Vitis cinerea*	wild grape	Previously published	-	WGS	-	-	PRJNA1048093	-	-	-
MUS_1	Wild	*Vitis mustangensis*	wild grape	Previously published	SRR14618010	WGS	300	4944901500	PRJNA731597	SAMN19291133	2217038201	UC IRVINE
MUS_2	Wild	*Vitis mustangensis*	wild grape	Previously published	SRR14618008	WGS	300	16311067500	PRJNA731597	SAMN19291132	7731144595	UC IRVINE
MUS_3	Wild	*Vitis mustangensis*	wild grape	Previously published	SRR14617992	WGS	300	10678307400	PRJNA731597	SAMN19291137	5036287252	UC IRVINE
OG_1	Wild	*Vitis rotundifolia*	wild grape	Previously published	SRR094945	WGS	-	-	-	-	-	-
OG_2	Wild	*Vitis rotundifolia*	wild grape	Previously published	SRR6729330	WGS	189	12950767612	PRJNA397021	SAMN07446115	7658897770	INRA_EPGV (US1279)
OG_3	Wild	*Vitis rotundifolia*	wild grape	Previously published	SRR6729331	WGS	202	9319498664	PRJNA397021	SAMN07446122	5335102964	INRA_EPGV (US1279)
OG_4	Wild	*Vitis californica*	wild grape	Previously published	SRR22585228	WGS	294	7144550448	PRJNA910315	SAMN32121966	3141164129	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
OG_5	Wild	*Vitis californica*	wild grape	Previously published	SRR22585227	WGS	293	7507716878	PRJNA910315	SAMN32121965	3356690772	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
OG_6	Wild	*Vitis californica*	wild grape	Previously published	SRR22585216	WGS	294	5458501894	PRJNA910315	SAMN32121967	2406928977	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
RUP_1	Wild	*Vitis rupestris*	wild grape	Previously published	SRR5891645	WGS	300	9021261000	PRJNA393611	SAMN07341474	3374373341	YUNNAN AGRICULTURAL UNIVERSITY
RUP_2	Wild	*Vitis rupestris*	wild grape	Previously published	SRR5891652	WGS	300	9657853200	PRJNA393611	SAMN07341481	3493026806	YUNNAN AGRICULTURAL UNIVERSITY
RUP_3	Wild	*Vitis rupestris*	wild grape	Previously published	SRR5891911	WGS	300	9842214600	PRJNA393611	SAMN07341454	3582762017	YUNNAN AGRICULTURAL UNIVERSITY
VL_1	Wild	*Vitis labrusca*	wild grape	Previously published	-	WGS	-	-	PRJNA1048094	-	-	-
VL_10	Wild	*Vitis labrusca*	wild grape	Previously published	SRR8534315	WGS	152	1062634432	PRJNA505513	SAMN10874111	396683879	DNA4 TECHNOLOGIES LLC
VL_11	Wild	*Vitis labrusca*	wild grape	Previously published	SRR8534314	WGS	152	2534586168	PRJNA505513	SAMN10874112	947749657	DNA4 TECHNOLOGIES LLC
VL_12	Wild	*Vitis labrusca*	wild grape	Previously published	SRR5892051	WGS	300	7362592800	PRJNA393611	SAMN07341672	2674830829	YUNNAN AGRICULTURAL UNIVERSITY
VL_13	Wild	*Vitis labrusca*	wild grape	Previously published	SRR11078309	WGS	502	4460483852	PRJNA606045	SAMN14085376	1857240865	CORNELL UNIVERSITY
VL_14	Wild	*Vitis labrusca*	wild grape	Previously published	SRR11078310	WGS	502	5894850460	PRJNA606045	SAMN14085375	2485285504	CORNELL UNIVERSITY
VL_15	Wild	*Vitis labrusca*	wild grape	Previously published	SRR11078311	WGS	502	6673654264	PRJNA606045	SAMN14085374	2852730483	CORNELL UNIVERSITY
VL_16	Wild	*Vitis labrusca*	wild grape	Previously published	SRR11078312	WGS	502	4915732090	PRJNA606045	SAMN14085373	2075719031	CORNELL UNIVERSITY
VL_18	Wild	*Vitis labrusca*	wild grape	Previously published	SRR8835146	WGS	202	14585057914	PRJNA450929	SAMN09737216	8757068530	INRA_EPGV (US1279)
VL_19	Wild	*Vitis labrusca*	wild grape	Previously published	SRR5891798	WGS	300	7246144500	PRJNA393611	SAMN07341472	2692003537	YUNNAN AGRICULTURAL UNIVERSITY
VL_2	Wild	*Vitis labrusca*	wild grape	Previously published	-	WGS	-	-	PRJNA1048095	-	-	-
VL_4	Wild	*Vitis labrusca*	wild grape	Previously published	SRR5891917	WGS	300	5812805100	PRJNA393611	SAMN07341473	2090914319	YUNNAN AGRICULTURAL UNIVERSITY
VL_6	Wild	*Vitis labrusca*	wild grape	Previously published	SRR7819191	WGS	250	11014038500	PRJNA490319	SAMN10032680	5658648540	HUAZHONG AGRICULTURE UNIVERSITY
VL_7	Wild	*Vitis labrusca*	wild grape	Previously published	SRR8835149	WGS	202	10049146500	PRJNA450929	SAMN09737213	6723354980	INRA_EPGV (US1279)
VL_8	Wild	*Vitis labrusca*	wild grape	Previously published	SRR8835151	WGS	202	11547350200	PRJNA450929	SAMN09737211	7734972953	INRA_EPGV (US1279)
VL_9	Wild	*Vitis labrusca*	wild grape	Previously published	-	WGS	-	-	PRJNA1048091	-	-	-
VSE_1	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011039	WGS	200	9168931200	PRJEB37020	SAMEA6619705	4220270157	INRAE GRAND EST-COLMAR
VSE_10	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011048	WGS	200	10602355400	PRJEB37020	SAMEA6619714	4899102966	INRAE GRAND EST-COLMAR
VSE_11	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011049	WGS	200	12519548400	PRJEB37020	SAMEA6619715	5800072648	INRAE GRAND EST-COLMAR
VSE_12	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011050	WGS	200	11193270600	PRJEB37020	SAMEA6619716	5321334587	INRAE GRAND EST-COLMAR
VSE_15	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4028632	WGS	302	22403125570	PRJEB37020	SAMEA6655959	14555669268	INRAE GRAND EST-COLMAR
VSE_16	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4028633	WGS	302	22255008764	PRJEB37020	SAMEA6655960	14517189047	INRAE GRAND EST-COLMAR
VSE_17	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585226	WGS	296	18771835452	PRJNA910315	SAMN32121975	6546823344	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSE_18	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585225	WGS	296	24273626774	PRJNA910315	SAMN32121976	8429598726	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSE_19	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891605	WGS	300	8082578700	PRJNA393611	SAMN07341232	2944973297	YUNNAN AGRICULTURAL UNIVERSITY
VSE_2	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011040	WGS	200	14087525600	PRJEB37020	SAMEA6619706	6406700952	INRAE GRAND EST-COLMAR
VSE_20	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891606	WGS	300	6952750200	PRJNA393611	SAMN07341233	2523647066	YUNNAN AGRICULTURAL UNIVERSITY
VSE_21	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891608	WGS	300	12624719100	PRJNA393611	SAMN07341231	4689841225	YUNNAN AGRICULTURAL UNIVERSITY
VSE_22	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891609	WGS	300	7314126600	PRJNA393611	SAMN07341228	2698112354	YUNNAN AGRICULTURAL UNIVERSITY
VSE_23	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891676	WGS	300	8420146800	PRJNA393611	SAMN07341266	3160452722	YUNNAN AGRICULTURAL UNIVERSITY
VSE_24	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891678	WGS	300	6663279000	PRJNA393611	SAMN07341264	2680670489	YUNNAN AGRICULTURAL UNIVERSITY
VSE_25	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR9591081	WGS	252	38143195524	PRJNA549602	SAMN12094264	17045923991	INSTITUTO SUPERIOR DE AGRONOMIA
VSE_26	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR9591082	WGS	252	29830495464	PRJNA549602	SAMN12094265	13208913431	INSTITUTO SUPERIOR DE AGRONOMIA
VSE_27	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891613	WGS	300	6705294900	PRJNA393611	SAMN07341224	2473817144	YUNNAN AGRICULTURAL UNIVERSITY
VSE_28	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891717	WGS	300	6853696500	PRJNA393611	SAMN07341216	2465596101	YUNNAN AGRICULTURAL UNIVERSITY
VSE_29	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891614	WGS	300	7020885900	PRJNA393611	SAMN07341225	2802651430	YUNNAN AGRICULTURAL UNIVERSITY
VSE_3	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011041	WGS	200	14954281800	PRJEB37020	SAMEA6619707	6986060925	INRAE GRAND EST-COLMAR
VSE_30	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891760	WGS	300	10056816600	PRJNA393611	SAMN07341262	3923440447	YUNNAN AGRICULTURAL UNIVERSITY
VSE_31	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891718	WGS	300	6454646100	PRJNA393611	SAMN07341215	2493944003	YUNNAN AGRICULTURAL UNIVERSITY
VSE_32	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891705	WGS	300	8567159700	PRJNA393611	SAMN07341210	3291968339	YUNNAN AGRICULTURAL UNIVERSITY
VSE_33	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891716	WGS	300	6950925900	PRJNA393611	SAMN07341217	2520102386	YUNNAN AGRICULTURAL UNIVERSITY
VSE_34	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891715	WGS	300	6934557900	PRJNA393611	SAMN07341218	2507926936	YUNNAN AGRICULTURAL UNIVERSITY
VSE_35	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891720	WGS	300	6339719100	PRJNA393611	SAMN07341223	2463210631	YUNNAN AGRICULTURAL UNIVERSITY
VSE_36	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891612	WGS	300	6785907900	PRJNA393611	SAMN07341227	2659949700	YUNNAN AGRICULTURAL UNIVERSITY
VSE_37	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891702	WGS	300	7870942800	PRJNA393611	SAMN07341209	2845000727	YUNNAN AGRICULTURAL UNIVERSITY
VSE_38	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891719	WGS	300	8561375700	PRJNA393611	SAMN07341214	3358388417	YUNNAN AGRICULTURAL UNIVERSITY
VSE_39	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891721	WGS	300	12999059400	PRJNA393611	SAMN07341222	5142216760	YUNNAN AGRICULTURAL UNIVERSITY
VSE_4	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011042	WGS	200	12859090000	PRJEB37020	SAMEA6619708	5858220414	INRAE GRAND EST-COLMAR
VSE_40	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891882	WGS	300	10277788500	PRJNA393611	SAMN07341252	3817260906	YUNNAN AGRICULTURAL UNIVERSITY
VSE_41	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891706	WGS	300	11939917200	PRJNA393611	SAMN07341205	4547862921	YUNNAN AGRICULTURAL UNIVERSITY
VSE_42	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891768	WGS	300	9651304200	PRJNA393611	SAMN07341258	3746877200	YUNNAN AGRICULTURAL UNIVERSITY
VSE_43	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891876	WGS	300	14741913900	PRJNA393611	SAMN07341250	5824271553	YUNNAN AGRICULTURAL UNIVERSITY
VSE_44	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891877	WGS	300	12463959900	PRJNA393611	SAMN07341251	4665524168	YUNNAN AGRICULTURAL UNIVERSITY
VSE_45	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891711	WGS	300	9196500600	PRJNA393611	SAMN07341212	3324105626	YUNNAN AGRICULTURAL UNIVERSITY
VSE_46	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891939	WGS	300	7141628700	PRJNA393611	SAMN07341240	2586023763	YUNNAN AGRICULTURAL UNIVERSITY
VSE_47	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891875	WGS	300	10053705900	PRJNA393611	SAMN07341249	3829680731	YUNNAN AGRICULTURAL UNIVERSITY
VSE_48	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891710	WGS	300	9299666100	PRJNA393611	SAMN07341213	3410090004	YUNNAN AGRICULTURAL UNIVERSITY
VSE_49	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891883	WGS	300	6456486300	PRJNA393611	SAMN07341253	2536648699	YUNNAN AGRICULTURAL UNIVERSITY
VSE_5	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011043	WGS	200	8597617000	PRJEB37020	SAMEA6619709	3946560222	INRAE GRAND EST-COLMAR
VSE_50	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891611	WGS	300	15821535600	PRJNA393611	SAMN07341226	6248817128	YUNNAN AGRICULTURAL UNIVERSITY
VSE_51	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891766	WGS	300	10912789800	PRJNA393611	SAMN07341260	4231849048	YUNNAN AGRICULTURAL UNIVERSITY
VSE_52	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891704	WGS	300	8277863400	PRJNA393611	SAMN07341211	3002300984	YUNNAN AGRICULTURAL UNIVERSITY
VSE_53	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891759	WGS	300	11122715400	PRJNA393611	SAMN07341263	4242986625	YUNNAN AGRICULTURAL UNIVERSITY
VSE_54	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891878	WGS	300	13000610400	PRJNA393611	SAMN07341244	4975193659	YUNNAN AGRICULTURAL UNIVERSITY
VSE_55	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891703	WGS	300	10746910500	PRJNA393611	SAMN07341208	4352873436	YUNNAN AGRICULTURAL UNIVERSITY
VSE_56	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891708	WGS	300	5892771600	PRJNA393611	SAMN07341207	2393466383	YUNNAN AGRICULTURAL UNIVERSITY
VSE_57	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891879	WGS	300	11941828500	PRJNA393611	SAMN07341245	4565865562	YUNNAN AGRICULTURAL UNIVERSITY
VSE_58	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891610	WGS	300	11163163200	PRJNA393611	SAMN07341229	3997894563	YUNNAN AGRICULTURAL UNIVERSITY
VSE_59	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891765	WGS	300	8199675000	PRJNA393611	SAMN07341261	3180148252	YUNNAN AGRICULTURAL UNIVERSITY
VSE_6	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011044	WGS	200	13007190800	PRJEB37020	SAMEA6619710	5951796140	INRAE GRAND EST-COLMAR
VSE_60	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891764	WGS	300	12726711600	PRJNA393611	SAMN07341254	4715875601	YUNNAN AGRICULTURAL UNIVERSITY
VSE_61	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891940	WGS	300	15682135200	PRJNA393611	SAMN07341235	5633986154	YUNNAN AGRICULTURAL UNIVERSITY
VSE_62	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891874	WGS	300	9581340600	PRJNA393611	SAMN07341248	3662095627	YUNNAN AGRICULTURAL UNIVERSITY
VSE_63	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891942	WGS	300	9808149300	PRJNA393611	SAMN07341237	3881298045	YUNNAN AGRICULTURAL UNIVERSITY
VSE_64	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891943	WGS	300	7831929600	PRJNA393611	SAMN07341236	2784662257	YUNNAN AGRICULTURAL UNIVERSITY
VSE_65	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891713	WGS	300	6521174700	PRJNA393611	SAMN07341220	2565787302	YUNNAN AGRICULTURAL UNIVERSITY
VSE_66	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891937	WGS	300	7130919300	PRJNA393611	SAMN07341238	2688018531	YUNNAN AGRICULTURAL UNIVERSITY
VSE_67	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891938	WGS	300	9492661500	PRJNA393611	SAMN07341241	3716162345	YUNNAN AGRICULTURAL UNIVERSITY
VSE_68	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891709	WGS	300	10076157600	PRJNA393611	SAMN07341206	3866946319	YUNNAN AGRICULTURAL UNIVERSITY
VSE_69	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR8835138	WGS	202	6665120492	PRJNA450929	SAMN09737236	4182577261	INRA_EPGV (US1279)
VSE_7	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011045	WGS	200	12396028400	PRJEB37020	SAMEA6619711	5691150868	INRAE GRAND EST-COLMAR
VSE_70	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891935	WGS	300	10422387900	PRJNA393611	SAMN07341242	4101751901	YUNNAN AGRICULTURAL UNIVERSITY
VSE_71	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891934	WGS	300	9117013200	PRJNA393611	SAMN07341243	3368579122	YUNNAN AGRICULTURAL UNIVERSITY
VSE_72	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891712	WGS	300	6788868300	PRJNA393611	SAMN07341221	2439173249	YUNNAN AGRICULTURAL UNIVERSITY
VSE_73	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891761	WGS	300	8352750300	PRJNA393611	SAMN07341257	3250992029	YUNNAN AGRICULTURAL UNIVERSITY
VSE_74	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891881	WGS	300	8563996800	PRJNA393611	SAMN07341247	3413452490	YUNNAN AGRICULTURAL UNIVERSITY
VSE_75	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891941	WGS	300	9385809300	PRJNA393611	SAMN07341234	3400834148	YUNNAN AGRICULTURAL UNIVERSITY
VSE_76	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891880	WGS	300	12938673000	PRJNA393611	SAMN07341246	5174501179	YUNNAN AGRICULTURAL UNIVERSITY
VSE_77	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891714	WGS	300	7581770100	PRJNA393611	SAMN07341219	2992533772	YUNNAN AGRICULTURAL UNIVERSITY
VSE_78	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891763	WGS	300	11614225200	PRJNA393611	SAMN07341255	4517075953	YUNNAN AGRICULTURAL UNIVERSITY
VSE_79	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891762	WGS	300	7438566600	PRJNA393611	SAMN07341256	2870274240	YUNNAN AGRICULTURAL UNIVERSITY
VSE_8	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011046	WGS	200	10956482400	PRJEB37020	SAMEA6619712	5253417548	INRAE GRAND EST-COLMAR
VSE_80	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891707	WGS	300	7338219600	PRJNA393611	SAMN07341204	2855151227	YUNNAN AGRICULTURAL UNIVERSITY
VSE_81	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5891679	WGS	300	9480828600	PRJNA393611	SAMN07341265	3674965617	YUNNAN AGRICULTURAL UNIVERSITY
VSE_82	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR8835141	WGS	202	6900912466	PRJNA450929	SAMN09737231	4213628864	INRA_EPGV (US1279)
VSE_83	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR8835162	WGS	202	7054146838	PRJNA450929	SAMN09737219	4371229199	INRA_EPGV (US1279)
VSE_84	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR8835164	WGS	202	6026464364	PRJNA450929	SAMN09737217	3778982668	INRA_EPGV (US1279)
VSE_9	Wild	*Vitis sylvestris*	wild grape	Previously published	ERR4011047	WGS	200	13260921200	PRJEB37020	SAMEA6619713	6144447203	INRAE GRAND EST-COLMAR
VSM_1	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585223	WGS	296	20412122822	PRJNA910315	SAMN32121978	7119574615	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_23	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5627786	WGS	300	9746619900	PRJNA388292	SAMN07174800	4565507447	UNIVERSITY OF CALIFORNIA, IRVINE
VSM_25	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR5627789	WGS	300	9752367600	PRJNA388292	SAMN07174797	4577391958	UNIVERSITY OF CALIFORNIA, IRVINE
VSM_27	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585197	WGS	296	14425934524	PRJNA910315	SAMN32122002	4990825614	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_28	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585208	WGS	297	20093972935	PRJNA910315	SAMN32121992	7005802564	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_29	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585211	WGS	296	17040811707	PRJNA910315	SAMN32121989	5982885118	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_30	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585210	WGS	297	17826223579	PRJNA910315	SAMN32121990	6184432202	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_31	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585204	WGS	297	22421654767	PRJNA910315	SAMN32121995	7791497159	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_32	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585207	WGS	296	15697192877	PRJNA910315	SAMN32121993	5482947560	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_33	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585206	WGS	297	18608684977	PRJNA910315	SAMN32121994	6415466161	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_34	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585212	WGS	297	20634368685	PRJNA910315	SAMN32121988	7156006121	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_35	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585199	WGS	297	18128627285	PRJNA910315	SAMN32122000	6453085327	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_36	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585198	WGS	296	20001498831	PRJNA910315	SAMN32122001	6994446361	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_37	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585203	WGS	297	12725495902	PRJNA910315	SAMN32121996	4540326422	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_38	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585202	WGS	297	14680006205	PRJNA910315	SAMN32121997	5136867441	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_39	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585214	WGS	296	12269894709	PRJNA910315	SAMN32121986	4367734287	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_40	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585213	WGS	297	16848885722	PRJNA910315	SAMN32121987	5860227000	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_41	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585201	WGS	297	14362074688	PRJNA910315	SAMN32121998	4997924325	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_42	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585209	WGS	296	13110941276	PRJNA910315	SAMN32121991	4635287333	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_5	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585219	WGS	297	17534443383	PRJNA910315	SAMN32121982	6079059675	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_6	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585218	WGS	296	11301881113	PRJNA910315	SAMN32121983	3936900695	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_7	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585217	WGS	296	18949401108	PRJNA910315	SAMN32121984	6557782175	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VSM_8	Wild	*Vitis sylvestris*	wild grape	Previously published	SRR22585215	WGS	297	23267222930	PRJNA910315	SAMN32121985	8114329820	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_116	Table1	*Vitis vinifera* ssp. *vinifera*	Ada Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_117	Table1	*Vitis vinifera* ssp. *vinifera*	Aishenmeigui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_118	Wine	*Vitis vinifera* ssp. *vinifera*	Aoyuo Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_119	Table1	*Vitis vinifera* ssp. *vinifera*	Dali Midknight Beauty	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_120	Table1	*Vitis vinifera* ssp. *vinifera*	Emerald Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_122	Table1	*Vitis vinifera* ssp. *vinifera*	Black Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_123	Table1	*Vitis vinifera* ssp. *vinifera*	Hongqi Tezaomeigui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_124	Table2	*V. vinifera × V.labrusca*	Golden Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_125	Table1	*Vitis vinifera* ssp. *vinifera*	Jintian Meigui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_126	Table2	*V. vinifera × V.labrusca*	Jumeigui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_128	Table1	*Vitis vinifera* ssp. *vinifera*	Muscat hamburg	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_129	Table2	*V. vinifera × V.labrusca*	Meiguiyi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_130	Table1	*Vitis vinifera* ssp. *vinifera*	Molière Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_131	Table2	*V. vinifera × V.labrusca*	Newyork Midknight Beauty	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_132	Table1	*Vitis vinifera* ssp. *vinifera*	Miskat Plevenski	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_133	Table1	*Vitis vinifera* ssp. *vinifera*	Christmas Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_135	Table2	*V. vinifera × V.labrusca*	Shine Muscat	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_136	Wine	*Vitis vinifera* ssp. *vinifera*	Rose Italia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_137	Table1	*Vitis vinifera* ssp. *vinifera*	Zaomeigui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_257	Table2	*V. vinifera × V.labrusca*	8611	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_258	Table2	*V. vinifera × V.labrusca*	Blauer Poutugieser	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_259	Table2	*V. vinifera × V.labrusca*	Anyun Huanghou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_260	Table2	*V. vinifera × V.labrusca*	Queenora Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_261	Table2	*V. vinifera × V.labrusca*	Bashi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_262	Table2	*V. vinifera × V.labrusca*	Baiaolin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_263	Table2	*V. vinifera × V.labrusca*	Baimeikang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_264	Table2	*V. vinifera × V.labrusca*	Triumph	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_265	Table2	*V. vinifera × V.labrusca*	Baieya	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_266	Table2	*V. vinifera × V.labrusca*	Bilvzhu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_267	Table2	*V. vinifera × V.labrusca*	Bronx Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_268	Table2	*V. vinifera × V.labrusca*	Chunguang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_269	Table2	*V. vinifera × V.labrusca*	Cuifeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_270	Table2	*V. vinifera × V.labrusca*	Tai Ho	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_271	Table1	*Vitis vinifera* ssp. *vinifera*	Fengbao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_272	Table2	*V. vinifera × V.labrusca*	Fenghou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_273	Table2	*V. vinifera × V.labrusca*	Highland	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_274	Table2	*V. vinifera × V.labrusca*	Takasumi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_275	Table2	*V. vinifera × V.labrusca*	Takatsuma	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_276	Table2	*V. vinifera × V.labrusca*	Takasago	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_277	Table2	*V. vinifera × V.labrusca*	Kokuko	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_278	Table2	*V. vinifera × V.labrusca*	Hartford	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_279	Table2	*V. vinifera × V.labrusca*	Hanxiangmi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_280	Table2	*V. vinifera × V.labrusca*	Black Olimpia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_281	Table2	*V. vinifera × V.labrusca*	Blank Balado	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_282	Table2	*V. vinifera × V.labrusca*	Darkridge	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_283	Table2	*V. vinifera × V.labrusca*	Heiguixiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_284	Table2	*V. vinifera × V.labrusca*	Honey Black	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES

Accessions	collected_by	geo_loc_name_country	geo_loc_name_country_continent	geographic_location_(country_and/or_sea)	geographic_location_(region_and_locality)	geo_loc_name	Instrument
ARI_1	-	-	-	-	-	-	-
ARI_2	-	-	-	-	-	-	-
ARI_3	-	-	-	-	-	-	-
CAL_1	-	-	-	-	-	-	-
CAL_2	-	-	-	-	-	-	-
CAL_3	-	-	-	-	-	-	-
CINE_1	-	USA	North America	TX9722	28.7091 N 100.0495 W	USA	Illumina HiSeq 2500
CINE_2	-	-	-	-	-	-	-
CINE_3	-	-	-	-	-	-	-
MUS_1	-	USA	North America	T56	31.0982 N 97.3428 W	USA	Illumina HiSeq 2500
MUS_2	-	USA	North America	T2	33.2576 N 97.5832 W	USA	Illumina HiSeq 2500
MUS_3	-	USA	North America	TX16-006	31.1061 N 97.9181 W	USA	Illumina HiSeq 2500
OG_1	-	-	-	-	-	-	-
OG_2	INRA	France	Europe	Regale 6624Col1	-	France:Colmar	Illumina Genome Analyzer II
OG_3	INRA	France	Europe	Regale 6624Col1	-	France:Colmar	Illumina HiSeq 2000
OG_4	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
OG_5	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
OG_6	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
RUP_1	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
RUP_2	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
RUP_3	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VL_1	-	-	-	-	-	-	-
VL_10	D. E. Atha	USA	North America	NYBG 01087448	41.452 N 73.6156 W	USA	NextSeq 500
VL_11	V. Bustamante	USA	North America	NYBG 03082179	41.043 N 71.9015 W	USA	NextSeq 500
VL_12	-	USA	North America	-	-	USA	Illumina HiSeq 4000
VL_13	-	uncalculated	uncalculated	-	-	-	Illumina HiSeq 2500
VL_14	-	uncalculated	uncalculated	-	-	-	Illumina HiSeq 2500
VL_15	-	uncalculated	uncalculated	-	-	-	Illumina HiSeq 2500
VL_16	-	uncalculated	uncalculated	-	-	-	Illumina HiSeq 2500
VL_18	JKI	Germany	Europe	Labrusca	-	Germany	Illumina HiSeq 2000
VL_19	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VL_2	-	-	-	-	-	-	-
VL_4	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VL_6	-	China	Asia	-	-	China: Henan	Illumina HiSeq 2500
VL_7	JKI	Germany	Europe	Fredonia	-	Germany	Illumina HiSeq 2000
VL_8	JKI	Germany	Europe	Concord	-	Germany	Illumina HiSeq 2000
VL_9	-	-	-	-	-	-	-
VSE_1	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_10	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_11	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_12	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_15	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 2000
VSE_16	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 2000
VSE_17	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSE_18	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSE_19	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_2	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_20	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_21	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_22	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_23	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_24	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_25	Margarida Rocheta\, LEAF (ISA\, ULisboa\, Portugal)	Portugal	Europe	Male1	39.04 N 9.18 W	Portugal: Dois Portos	Illumina HiSeq 4000
VSE_26	Margarida Rocheta\, LEAF (ISA\, ULisboa\, Portugal)	Portugal	Europe	Female1	39.04 N 9.18 W	Portugal: Dois Portos	Illumina HiSeq 4000
VSE_27	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_28	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_29	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_3	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_30	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_31	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_32	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_33	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_34	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_35	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_36	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_37	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_38	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_39	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_4	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_40	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_41	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_42	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_43	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_44	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_45	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_46	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_47	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_48	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_49	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_5	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_50	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_51	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_52	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_53	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_54	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_55	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_56	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_57	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_58	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_59	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_6	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSE_60	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_61	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_62	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_63	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_64	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_65	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_66	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_67	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_68	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_69	INRA	France	Europe	Vitis sylvestris Dirmstein male	-	France:Domaine de Vassal	Illumina Genome Analyzer IIx
VSE_7	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	not applicable	Illumina HiSeq 4000
VSE_70	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_71	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_72	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_73	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_74	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_75	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_76	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_77	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_78	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_79	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_8	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	not applicable	Illumina HiSeq 4000
VSE_80	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_81	-	uncalculated	uncalculated	-	-	not applicable	Illumina HiSeq 4000
VSE_82	INRA	France	Europe	Teulere pied sauvage	-	France:Domaine de Vassal	Illumina Genome Analyzer IIx
VSE_83	INRA	France	Europe	Lambrusque PSL2	-	France:Domaine de Vassal	Illumina Genome Analyzer IIx
VSE_84	INRA	France	Europe	Lambrusque Campmarcel	-	France:Domaine de Vassal	Illumina Genome Analyzer IIx
VSE_9	INRAE Grand Est-Colmar (WIEWS code : FRA038)	France	Europe	France	Grand-Est\, Colmar	-	Illumina HiSeq 4000
VSM_1	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_23	-	uncalculated	uncalculated	-	-	missing	Illumina HiSeq 2500
VSM_25	-	uncalculated	uncalculated	-	-	missing	Illumina HiSeq 2500
VSM_27	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_28	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_29	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_30	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_31	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_32	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_33	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_34	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_35	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_36	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_37	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_38	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_39	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_40	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_41	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_42	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_5	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_6	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_7	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VSM_8	-	uncalculated	uncalculated	-	-	not collected	Illumina HiSeq 3000
VV_116	-	China	Henan Province	Zhengzhou	113°42E 34°42N	Zhengzhou Fruit Research Ins	-
VV_117	-	China	Henan Province	Zhengzhou	113°42E 34°43N	Zhengzhou Fruit Research Ins	-
VV_118	-	China	Henan Province	Zhengzhou	113°42E 34°44N	Zhengzhou Fruit Research Ins	-
VV_119	-	China	Henan Province	Zhengzhou	113°42E 34°45N	Zhengzhou Fruit Research Ins	-
VV_120	-	China	Henan Province	Zhengzhou	113°42E 34°46N	Zhengzhou Fruit Research Ins	-
VV_122	-	China	Henan Province	Zhengzhou	113°42E 34°47N	Zhengzhou Fruit Research Ins	-
VV_123	-	China	Henan Province	Zhengzhou	113°42E 34°48N	Zhengzhou Fruit Research Ins	-
VV_124	-	China	Henan Province	Zhengzhou	113°42E 34°49N	Zhengzhou Fruit Research Ins	-
VV_125	-	China	Henan Province	Zhengzhou	113°42E 34°50N	Zhengzhou Fruit Research Ins	-
VV_126	-	China	Henan Province	Zhengzhou	113°42E 34°51N	Zhengzhou Fruit Research Ins	-
VV_128	-	China	Henan Province	Zhengzhou	113°42E 34°52N	Zhengzhou Fruit Research Ins	-
VV_129	-	China	Henan Province	Zhengzhou	113°42E 34°53N	Zhengzhou Fruit Research Ins	-
VV_130	-	China	Henan Province	Zhengzhou	113°42E 34°54N	Zhengzhou Fruit Research Ins	-
VV_131	-	China	Henan Province	Zhengzhou	113°42E 34°55N	Zhengzhou Fruit Research Ins	-
VV_132	-	China	Henan Province	Zhengzhou	113°42E 34°56N	Zhengzhou Fruit Research Ins	-
VV_133	-	China	Henan Province	Zhengzhou	113°42E 34°57N	Zhengzhou Fruit Research Ins	-
VV_135	-	China	Henan Province	Zhengzhou	113°42E 34°58N	Zhengzhou Fruit Research Ins	-
VV_136	-	China	Henan Province	Zhengzhou	113°42E 34°59N	Zhengzhou Fruit Research Ins	-
VV_137	-	China	Henan Province	Zhengzhou	113°42E 34°60N	Zhengzhou Fruit Research Ins	-
VV_257	-	China	Henan Province	Zhengzhou	113°42E 34°61N	Zhengzhou Fruit Research Ins	-
VV_258	-	China	Henan Province	Zhengzhou	113°42E 34°62N	Zhengzhou Fruit Research Ins	-
VV_259	-	China	Henan Province	Zhengzhou	113°42E 34°63N	Zhengzhou Fruit Research Ins	-
VV_260	-	China	Henan Province	Zhengzhou	113°42E 34°64N	Zhengzhou Fruit Research Ins	-
VV_261	-	China	Henan Province	Zhengzhou	113°42E 34°65N	Zhengzhou Fruit Research Ins	-
VV_262	-	China	Henan Province	Zhengzhou	113°42E 34°66N	Zhengzhou Fruit Research Ins	-
VV_263	-	China	Henan Province	Zhengzhou	113°42E 34°67N	Zhengzhou Fruit Research Ins	-
VV_264	-	China	Henan Province	Zhengzhou	113°42E 34°68N	Zhengzhou Fruit Research Ins	-
VV_265	-	China	Henan Province	Zhengzhou	113°42E 34°69N	Zhengzhou Fruit Research Ins	-
VV_266	-	China	Henan Province	Zhengzhou	113°42E 34°70N	Zhengzhou Fruit Research Ins	-
VV_267	-	China	Henan Province	Zhengzhou	113°42E 34°71N	Zhengzhou Fruit Research Ins	-
VV_268	-	China	Henan Province	Zhengzhou	113°42E 34°72N	Zhengzhou Fruit Research Ins	-
VV_269	-	China	Henan Province	Zhengzhou	113°42E 34°73N	Zhengzhou Fruit Research Ins	-
VV_270	-	China	Henan Province	Zhengzhou	113°42E 34°74N	Zhengzhou Fruit Research Ins	-
VV_271	-	China	Henan Province	Zhengzhou	113°42E 34°75N	Zhengzhou Fruit Research Ins	-
VV_272	-	China	Henan Province	Zhengzhou	113°42E 34°76N	Zhengzhou Fruit Research Ins	-
VV_273	-	China	Henan Province	Zhengzhou	113°42E 34°77N	Zhengzhou Fruit Research Ins	-
VV_274	-	China	Henan Province	Zhengzhou	113°42E 34°78N	Zhengzhou Fruit Research Ins	-
VV_275	-	China	Henan Province	Zhengzhou	113°42E 34°79N	Zhengzhou Fruit Research Ins	-
VV_276	-	China	Henan Province	Zhengzhou	113°42E 34°80N	Zhengzhou Fruit Research Ins	-
VV_277	-	China	Henan Province	Zhengzhou	113°42E 34°81N	Zhengzhou Fruit Research Ins	-
VV_278	-	China	Henan Province	Zhengzhou	113°42E 34°82N	Zhengzhou Fruit Research Ins	-
VV_279	-	China	Henan Province	Zhengzhou	113°42E 34°83N	Zhengzhou Fruit Research Ins	-
VV_280	-	China	Henan Province	Zhengzhou	113°42E 34°84N	Zhengzhou Fruit Research Ins	-
VV_281	-	China	Henan Province	Zhengzhou	113°42E 34°85N	Zhengzhou Fruit Research Ins	-
VV_282	-	China	Henan Province	Zhengzhou	113°42E 34°86N	Zhengzhou Fruit Research Ins	-
VV_283	-	China	Henan Province	Zhengzhou	113°42E 34°87N	Zhengzhou Fruit Research Ins	-
VV_284	-	China	Henan Province	Zhengzhou	113°42E 34°88N	Zhengzhou Fruit Research Ins	-

Accessions	Library Name	LibraryLayout	LibrarySelection	LibrarySource	Platform	Sample Name	Submitter_Id	sex	dev_stage	tissue_type
AR1_1	-	-	-	-	-	-	-	-	-	-
AR1_2	-	-	-	-	-	-	-	-	-	-
AR1_3	-	-	-	-	-	-	-	-	-	-
CAL_1	-	-	-	-	-	-	-	-	-	-
CAL_2	-	-	-	-	-	-	-	-	-	-
CAL_3	-	-	-	-	-	-	-	-	-	-
CINE_1	vber05	PAIRED	RANDOM	GENOMIC	ILLUMINA	vber05	-	-	adult	leaf
CINE_2	-	-	-	-	-	-	-	-	-	-
CINE_3	-	-	-	-	-	-	-	-	-	-
MUS_1	vcan08	PAIRED	RANDOM	GENOMIC	ILLUMINA	vcan08	-	-	adult	leaf
MUS_2	vcan10	PAIRED	RANDOM	GENOMIC	ILLUMINA	vcan10	-	-	adult	leaf
MUS_3	vcan25	PAIRED	RANDOM	GENOMIC	ILLUMINA	vcan25	-	-	adult	leaf
OG_1	-	-	-	-	-	-	-	-	-	-
OG_2	174T_L1	PAIRED	RANDOM	GENOMIC	ILLUMINA	Muscares_Regale_B00174T	-	not applicable	not collected	leaves
OG_3	A0040QD	PAIRED	RANDOM	GENOMIC	ILLUMINA	Muscares_Regale_B00FFX1	-	not applicable	not collected	leaves
OG_4	4R112_L4	PAIRED	unspecified	GENOMIC	ILLUMINA	OG_4	-	-	-	leaf
OG_5	4R112_L5	PAIRED	unspecified	GENOMIC	ILLUMINA	OG_5	-	-	-	leaf
OG_6	4R112_L6	PAIRED	unspecified	GENOMIC	ILLUMINA	OG_6	-	-	-	leaf
RUP_1	TA-351	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-351	-	-	not applicable	leaf
RUP_2	TA-5888	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-5888	-	-	not applicable	leaf
RUP_3	TA-167	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-167	-	-	not applicable	leaf
VL_1	-	-	-	-	-	-	-	-	-	-
VL_10	DNA4_1332	PAIRED	RANDOM	GENOMIC	ILLUMINA	Vitis labrusca L.	-	-	adult	leaf
VL_11	DNA4_1333	PAIRED	RANDOM	GENOMIC	ILLUMINA	Vitis labrusca L	-	-	adult	leaf
VL_12	TA-133	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-133	-	-	not applicable	leaf
VL_13	PI 588164 Worden	PAIRED	RANDOM	GENOMIC	ILLUMINA	PI 588164 Worden	-	-	seedling	Leaf
VL_14	PI 597203 Glenfeld	PAIRED	RANDOM	GENOMIC	ILLUMINA	PI 597203 Glenfeld	-	-	seedling	Leaf
VL_15	PI 597172 Wheeler	PAIRED	RANDOM	GENOMIC	ILLUMINA	PI 597172 Wheeler	-	-	seedling	Leaf
VL_16	PI 483163 REM NE36	PAIRED	RANDOM	GENOMIC	ILLUMINA	PI 483163 REM NE36	-	-	seedling	Leaf
VL_18	A00402A	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Labrusca_B00E7OP	-	not applicable	missing	leaves
VL_19	TA-166	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-166	-	-	not applicable	leaf
VL_2	-	-	-	-	-	-	-	-	-	-
VL_4	TA-3	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-3	-	-	not applicable	leaf
VL_6	ZZ2	PAIRED	RANDOM	GENOMIC	ILLUMINA	ZZ2	-	-	vegetative growth	leaf
VL_7	A00402S	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Fredonia_B00E7ON	-	not applicable	missing	leaves
VL_8	A00402O	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Concord_B00E7OO	-	not applicable	missing	leaves
VL_9	-	-	-	-	-	-	-	-	-	-
VSE_1	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Sylvestris_C1-5	Sylvestris_C1-5	female	-	-
VSE_10	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5050T	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5050T	female	-	-
VSE_11	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5057T	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5057T	female	-	-
VSE_12	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5046T	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5046T	female	-	-
VSE_15	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Sylvestris_C1-2_WGS_Illumina_3	Sylvestris_C1-2_WGS_Illumina_3	female	-	-
VSE_16	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Sylvestris_C1-2_WGS_Illumina_4	Sylvestris_C1-2_WGS_Illumina_4	female	-	-
VSE_17	P50	PAIRED	unspecified	GENOMIC	ILLUMINA	VSE_17	-	-	-	leaf
VSE_18	P51	PAIRED	unspecified	GENOMIC	ILLUMINA	VSE_18	-	-	-	leaf
VSE_19	TA-6228	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6228	-	-	not applicable	leaf
VSE_2	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Martigny_2	Martigny_2	male	-	-
VSE_20	TA-6230	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6230	-	-	not applicable	leaf
VSE_21	TA-6225	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6225	-	-	not applicable	leaf
VSE_22	TA-6223	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6223	-	-	not applicable	leaf
VSE_23	TA-5607	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-5607	-	-	not applicable	leaf
VSE_24	RM02	PAIRED	RANDOM	GENOMIC	ILLUMINA	RM02	-	-	not applicable	leaf
VSE_25	VvsMale1	PAIRED	unspecified	GENOMIC	ILLUMINA	VvsMale1	-	male	not applicable	Leaf
VSE_26	VvsFemale1	PAIRED	unspecified	GENOMIC	ILLUMINA	VvsFemale1	-	female	not applicable	Leaf
VSE_27	TA-6216	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6216	-	-	not applicable	leaf
VSE_28	TA-6204	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6204	-	-	not applicable	leaf
VSE_29	TA-6219	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6219	-	-	not applicable	leaf
VSE_3	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5026T	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5026T	male	-	-
VSE_30	TA-6267	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6267	-	-	not applicable	leaf
VSE_31	TA-6201	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6201	-	-	not applicable	leaf
VSE_32	TA-6194	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6194	-	-	not applicable	leaf
VSE_33	TA-6207	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6207	-	-	not applicable	leaf
VSE_34	TA-6208	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6208	-	-	not applicable	leaf
VSE_35	TA-6213	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6213	-	-	not applicable	leaf
VSE_36	TA-6222	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6222	-	-	not applicable	leaf
VSE_37	TA-6190	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6190	-	-	not applicable	leaf
VSE_38	TA-6199	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6199	-	-	not applicable	leaf
VSE_39	TA-6212	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6212	-	-	not applicable	leaf
VSE_4	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5028T	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5028T	male	-	-
VSE_40	TA-6256	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6256	-	-	not applicable	leaf
VSE_41	K2	PAIRED	RANDOM	GENOMIC	ILLUMINA	K2	-	-	not applicable	leaf
VSE_42	TA-6263	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6263	-	-	not applicable	leaf
VSE_43	TA-6254	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6254	-	-	not applicable	leaf
VSE_44	TA-6255	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6255	-	-	not applicable	leaf
VSE_45	TA-6197	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6197	-	-	not applicable	leaf
VSE_46	TA-6239	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6239	-	-	not applicable	leaf
VSE_47	TA-6253	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6253	-	-	not applicable	leaf
VSE_48	TA-6198	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6198	-	-	not applicable	leaf
VSE_49	TA-6257	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6257	-	-	not applicable	leaf
VSE_5	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5029T	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5029T	male	-	-
VSE_50	TA-6220	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6220	-	-	not applicable	leaf
VSE_51	TA-6265	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6265	-	-	not applicable	leaf
VSE_52	TA-6195	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6195	-	-	not applicable	leaf
VSE_53	KE 23	PAIRED	RANDOM	GENOMIC	ILLUMINA	KE 23	-	-	not applicable	leaf
VSE_54	TA-6245	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6245	-	-	not applicable	leaf
VSE_55	K27	PAIRED	RANDOM	GENOMIC	ILLUMINA	K27	-	-	not applicable	leaf
VSE_56	K26	PAIRED	RANDOM	GENOMIC	ILLUMINA	K26	-	-	not applicable	leaf
VSE_57	TA-6246	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6246	-	-	not applicable	leaf
VSE_58	TA-6224	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6224	-	-	not applicable	leaf
VSE_59	TA-6266	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6266	-	-	not applicable	leaf
VSE_6	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5033T	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5033T	male	-	-
VSE_60	TA-6258	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6258	-	-	not applicable	leaf
VSE_61	TA-6234	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6234	-	-	not applicable	leaf
VSE_62	TA-6250	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6250	-	-	not applicable	leaf
VSE_63	TA-6236	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6236	-	-	not applicable	leaf
VSE_64	TA-6235	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6235	-	-	not applicable	leaf
VSE_65	TA-6210	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6210	-	-	not applicable	leaf
VSE_66	TA-6237	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6237	-	-	not applicable	leaf
VSE_67	TA-6242	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6242	-	-	not applicable	leaf
VSE_68	K22	PAIRED	RANDOM	GENOMIC	ILLUMINA	K22	-	-	not applicable	leaf
VSE_69	A00APYO	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Dirmstein-male_B00CVGM	-	not applicable	missing	leaves
VSE_7	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5053T	Male_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5053T	male	-	-
VSE_70	TA-6243	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6243	-	-	not applicable	leaf
VSE_71	TA-6244	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6244	-	-	not applicable	leaf
VSE_72	TA-6211	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6211	-	-	not applicable	leaf
VSE_73	TA-6262	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6262	-	-	not applicable	leaf
VSE_74	TA-6248	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6248	-	-	not applicable	leaf
VSE_75	TA-6233	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6233	-	-	not applicable	leaf
VSE_76	TA-6247	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6247	-	-	not applicable	leaf
VSE_77	TA-6209	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6209	-	-	not applicable	leaf
VSE_78	TA-6259	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6259	-	-	not applicable	leaf
VSE_79	TA-6260	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6260	-	-	not applicable	leaf
VSE_8	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5035T	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5035T	female	-	-
VSE_80	TA-6187	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-6187	-	-	not applicable	leaf
VSE_81	TA-5905	PAIRED	RANDOM	GENOMIC	ILLUMINA	TA-5905	-	-	not applicable	leaf
VSE_82	A00AQ00	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Teulere-pied-sauvage_B00CVGK	-	not applicable	missing	leaves
VSE_83	A00APYM	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Lambrusque-PSL2_B00CVDE	-	not applicable	missing	leaves
VSE_84	A00APYP	PAIRED	RANDOM	GENOMIC	ILLUMINA	GrapeReSeq_Lambrusque-Campmarcel_B00CVGN	-	not applicable	missing	leaves
VSE_9	unspecified	PAIRED	RANDOM	GENOMIC	ILLUMINA	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5040T	Female_descendant_Sylvestris_C1-5_x_Martigny_2_44613Col5040T	female	-	-
VSM_1	P53	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_1	-	-	-	leaf
VSM_23	Wild grape_Turkmenistan2(Vitis vinifera ssp. sylvestris)_Illumina	PAIRED	RANDOM	GENOMIC	ILLUMINA	Wild grape_Turkmenistan2(Vitis vinifera ssp. sylvestris)	-	-	mature	Leaf
VSM_25	Wild grape_Georgia(Vitis vinifera ssp. sylvestris)_Illumina	PAIRED	RANDOM	GENOMIC	ILLUMINA	Wild grape_Georgia(Vitis vinifera ssp. sylvestris)	-	-	mature	Leaf
VSM_27	P91	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_27	-	-	mature	leaf
VSM_28	P77	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_28	-	-	mature	leaf
VSM_29	P69	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_29	-	-	mature	leaf
VSM_30	P73	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_30	-	-	mature	leaf
VSM_31	P80	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_31	-	-	mature	leaf
VSM_32	P78	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_32	-	-	mature	leaf
VSM_33	P79	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_33	-	-	mature	leaf
VSM_34	P67	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_34	-	-	mature	leaf
VSM_35	P89	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_35	-	-	mature	leaf
VSM_36	P90	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_36	-	-	mature	leaf
VSM_37	P81	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_37	-	-	mature	leaf
VSM_38	P86	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_38	-	-	mature	leaf
VSM_39	P65	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_39	-	-	mature	leaf
VSM_40	P66	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_40	-	-	mature	leaf
VSM_41	P87	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_41	-	-	mature	leaf
VSM_42	P74	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_42	-	-	mature	leaf
VSM_5	P61	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_5	-	-	mature	leaf
VSM_6	P62	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_6	-	-	mature	leaf
VSM_7	P63	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_7	-	-	mature	leaf
VSM_8	P64	PAIRED	unspecified	GENOMIC	ILLUMINA	VSM_8	-	-	mature	leaf
VV_116	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_117	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_118	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_119	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_120	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_122	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_123	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_124	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_125	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_126	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_128	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_129	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_130	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_131	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_132	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_133	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_135	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_136	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_137	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_257	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_258	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_259	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_260	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_261	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_262	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_263	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_264	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_265	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_266	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_267	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_268	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_269	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_270	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_271	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_272	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_273	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_274	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_275	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_276	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_277	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_278	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_279	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_280	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_281	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_282	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_283	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_284	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf

Supplementary Table 6. A total of 466 accessions for genotyping SV based on pangenome (including 324 newly sequenced).

Accessions	Group	Species	Common name	Note	SRR_ID	Assay Type	AvgSpotLen	Bases	BioProject	BioSample	Bytes	Center Name
VV_285	Table2	*V. vinifera* × *V.labrusca*	Black Beet	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_287	Table2	*V. vinifera* × *V.labrusca*	Hurricane	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_288	Table2	*V. vinifera* × *V.labrusca*	Heiyuanshuai	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_289	Table2	*V. vinifera* × *V.labrusca*	Benni Fuji	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_290	Table2	*V. vinifera* × *V.labrusca*	Red Queen	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_291	Table2	*V. vinifera* × *V.labrusca*	Red Ikawa	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_292	Table2	*V. vinifera* × *V.labrusca*	Benizuiho	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_293	Table2	*V. vinifera* × *V.labrusca*	Suffold Red	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_294	Table2	*V. vinifera* × *V.labrusca*	Beniyamabiko	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_296	Table2	*V. vinifera* × *V.labrusca*	Hongxiangjiao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_297	Table2	*V. vinifera* × *V.labrusca*	Hongxing	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_298	Table2	*V. vinifera* × *V.labrusca*	Hongyidou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_299	Table2	*V. vinifera* × *V.labrusca*	Beniizu(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_300	Table2	*V. vinifera* × *V.labrusca*	Hutai No.8(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_301	Table2	*V. vinifera* × *V.labrusca*	Hupei 2(3N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_302	Table2	*V. vinifera* × *V.labrusca*	Huangguan	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_303	Table2	*V. vinifera* × *V.labrusca*	Mars Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_304	Table2	*V. vinifera* × *V.labrusca*	Jifeng(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_305	Table2	*V. vinifera* × *V.labrusca*	Jinfeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_306	Table2	*V. vinifera* × *V.labrusca*	Goldfinger	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_307	Table1	*Vitis vinifera* ssp. *vinifera*	Jintian 0608	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_308	Table1	*Vitis vinifera* ssp. *vinifera*	Jintian Feicui	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_310	Table2	*V. vinifera* × *V.labrusca*	Venus Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_311	Table2	*V. vinifera* × *V.labrusca*	Jingya(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_312	Table2	*V. vinifera* × *V.labrusca*	Jingyou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_313	Table2	*V. vinifera* × *V.labrusca*	Ikawa 1055	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_314	Table2	*V. vinifera* × *V.labrusca*	Kyoho	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_315	Table2	*V. vinifera* × *V.labrusca*	Kyogei(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_316	Table2	*V. vinifera* × *V.labrusca*	Juyou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_318	Table2	*V. vinifera* × *V.labrusca*	Kasite	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_319	Table2	*V. vinifera* × *V.labrusca*	Kangneng seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_321	Table2	*V. vinifera* × *V.labrusca*	Ryuho(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_322	Table2	*V. vinifera* × *V.labrusca*	Rocde Berry	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_323	Table2	*V. vinifera* × *V.labrusca*	Meizhoubai	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_324	Table2	*V. vinifera* × *V.labrusca*	Mills	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_325	Table2	*V. vinifera* × *V.labrusca*	Miguang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_326	Table2	*V. vinifera* × *V.labrusca*	Mihong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_328	Table2	*V. vinifera* × *V.labrusca*	Molixiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_329	Table2	*V. vinifera* × *V.labrusca*	Mofeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_331	Table2	*V. vinifera* × *V.labrusca*	Sagami	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_332	Table2	*V. vinifera* × *V.labrusca*	Shandongdazi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_333	Table2	*V. vinifera* × *V.labrusca*	Shenhua(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_334	Table2	*V. vinifera* × *V.labrusca*	Shenxiu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_335	Table2	*V. vinifera* × *V.labrusca*	Shennongxiangfeng(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_336	Table2	*V. vinifera* × *V.labrusca*	Steuben	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_337	Table2	*V. vinifera* × *V.labrusca*	Fujiminori (4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_338	Table2	*V. vinifera* × *V.labrusca*	Tiangongmoyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_339	Table2	*V. vinifera* × *V.labrusca*	Tano Black	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_340	Table2	*V. vinifera* × *V.labrusca*	Tianyehong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_341	Table2	*V. vinifera* × *V.labrusca*	Sunset	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_342	Table2	*V. vinifera* × *V.labrusca*	Vikinas	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_343	Table2	*V. vinifera* × *V.labrusca*	Xiyanghong(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_344	Table2	*V. vinifera* × *V.labrusca*	Himrod	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_345	Table2	*V. vinifera* × *V.labrusca*	Summer Black(3N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_346	Table2	*V. vinifera* × *V.labrusca*	Xianfeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_347	Table2	*V. vinifera* × *V.labrusca*	Champion	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_349	Table2	*V. vinifera* × *V.labrusca*	Xinnonghong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_350	Table2	*V. vinifera* × *V.labrusca*	Xinnongle	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_351	Table2	*V. vinifera* × *V.labrusca*	Yipinxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_352	Table2	*V. vinifera* × *V.labrusca*	Izunishiki	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_353	Table2	*V. vinifera* × *V.labrusca*	Yongyou No.1	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_354	Table2	*V. vinifera* × *V.labrusca*	Yuxuan No.1	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_355	Table2	*V. vinifera* × *V.labrusca*	Zaojuxuan	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_356	Table2	*V. vinifera* × *V.labrusca*	Zaokangke	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_357	Table2	*V. vinifera* × *V.labrusca*	Zhuosexiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_358	Table2	*V. vinifera* × *V.labrusca*	Zhengguo No.21	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_359	Table2	*V. vinifera* × *V.labrusca*	Zhenghei	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_360	Table2	*V. vinifera* × *V.labrusca*	Zhengkang No.1	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_361	Table2	*V. vinifera* × *V.labrusca*	Zhuangyuanhong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_362	Table2	*V. vinifera* × *V.labrusca*	Zifeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_363	Table2	*V. vinifera* × *V.labrusca*	Shigyoku	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_364	Table2	*V. vinifera* × *V.labrusca*	Ziyunshuijing	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_365	Table2	*V. vinifera* × *V.labrusca*	Zizao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_366	Table2	*V. vinifera* × *V.labrusca*	Zizhenxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_367	Table2	*V. vinifera* × *V.labrusca*	Zuijinxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_368	Table2	*V. vinifera* × *V.labrusca*	Zuirenxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_369	Table2	*V. vinifera* × *V.labrusca*	Sato	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_376	Wine	*Vitis vinifera* ssp. *vinifera*	Alikesi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_377	Wine	*Vitis vinifera* ssp. *vinifera*	Alieajike	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_378	Wine	*Vitis vinifera* ssp. *vinifera*	Iona	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_379	Wine	*Vitis vinifera* ssp. *vinifera*	Errachheni	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_380	Wine	*Vitis vinifera* ssp. *vinifera*	Aibulin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_381	Table1	*Vitis vinifera* ssp. *vinifera*	Otifia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_382	Table1	*Vitis vinifera* ssp. *vinifera*	Augusta	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_383	Wine	*Vitis vinifera* ssp. *vinifera*	Aohuofusiji	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_384	Wine	*Vitis vinifera* ssp. *vinifera*	Blauer Poutugieser	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_385	Wine	*Vitis vinifera* ssp. *vinifera*	Barbera	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_386	Wine	*Vitis vinifera* ssp. *vinifera*	Bakhtiori	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_387	Wine	*Vitis vinifera* ssp. *vinifera*	Bakusi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_388	Wine	*Vitis vinifera* ssp. *vinifera*	Pamid	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_389	Wine	*Vitis vinifera* ssp. *vinifera*	Bamidi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_390	Wine	*Vitis vinifera* ssp. *vinifera*	Vastaldo Grape	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_391	Table1	*Vitis vinifera* ssp. *vinifera*	Thompson	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_392	Wine	*Vitis vinifera* ssp. *vinifera*	Gamay Blanc	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_393	Wine	*Vitis vinifera* ssp. *vinifera*	Begonia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_395	Wine	*Vitis vinifera* ssp. *vinifera*	Bailaqina	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_396	Wine	*Vitis vinifera* ssp. *vinifera*	White Laura	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_397	Table1	*Vitis vinifera* ssp. *vinifera*	Rosario Bianco	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_399	Wine	*Vitis vinifera* ssp. *vinifera*	Slankamenka Biele	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_400	Wine	*Vitis vinifera* ssp. *vinifera*	White Sheehy	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_401	Wine	*Vitis vinifera* ssp. *vinifera*	Bahian Chirei	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_402	Wine	*Vitis vinifera* ssp. *vinifera*	Rkatsiteli	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_403	Wine	*Vitis vinifera* ssp. *vinifera*	Ugni Blanc	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_404	Wine	*Vitis vinifera* ssp. *vinifera*	Bakador	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_405	Wine	*Vitis vinifera* ssp. *vinifera*	Baiqieer	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_406	Wine	*Vitis vinifera* ssp. *vinifera*	Beijinghong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_407	Table1	*Vitis vinifera* ssp. *vinifera*	Beimeijia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_408	Wine	*Vitis vinifera* ssp. *vinifera*	Petit Bouschet	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_409	Wine	*Vitis vinifera* ssp. *vinifera*	Pideluokeximeinie	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_410	Table1	*Vitis vinifera* ssp. *vinifera*	Bixiang Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_411	Wine	*Vitis vinifera* ssp. *vinifera*	Borracal	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_412	Wine	*Vitis vinifera* ssp. *vinifera*	Pollawayi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_413	Wine	*Vitis vinifera* ssp. *vinifera*	Bouaki Tach	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_414	Wine	*Vitis vinifera* ssp. *vinifera*	Bouaki Nor	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_415	Wine	*Vitis vinifera* ssp. *vinifera*	Bougainvillea	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_417	Wine	*Vitis vinifera* ssp. *vinifera*	Bressa	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_418	Wine	*Vitis vinifera* ssp. *vinifera*	Tsyrzira	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_419	Wine	*Vitis vinifera* ssp. *vinifera*	Chalchin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_420	Table1	*Vitis vinifera* ssp. *vinifera*	chaobao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_421	Wine	*Vitis vinifera* ssp. *vinifera*	Cabernet Sauvignon	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_422	Wine	*Vitis vinifera* ssp. *vinifera*	Daheiputao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_423	Table1	*Vitis vinifera* ssp. *vinifera*	Dongfangfeng	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_424	Table1	*Vitis vinifera* ssp. *vinifera*	Dongfangzhi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_425	Table1	*Vitis vinifera* ssp. *vinifera*	Miputao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_426	Wine	*Vitis vinifera* ssp. *vinifera*	Duluth	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_427	Wine	*Vitis vinifera* ssp. *vinifera*	Domina	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_428	Wine	*Vitis vinifera* ssp. *vinifera*	Blur French	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_429	Table1	*Vitis vinifera* ssp. *vinifera*	Aromatic	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_430	Wine	*Vitis vinifera* ssp. *vinifera*	Fetiska Legner	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_433	Table1	*Vitis vinifera* ssp. *vinifera*	Flame Tokay	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_434	Wine	*Vitis vinifera* ssp. *vinifera*	Veltlinske Cerveno-Biele	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_435	Table1	*Vitis vinifera* ssp. *vinifera*	Fengshou	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_436	Wine	*Vitis vinifera* ssp. *vinifera*	Gamay Freo	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_437	Wine	*Vitis vinifera* ssp. *vinifera*	Faude Cabene	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_440	Wine	*Vitis vinifera* ssp. *vinifera*	Gaibeisai	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_441	Wine	*Vitis vinifera* ssp. *vinifera*	Gansang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_442	Wine	*Vitis vinifera* ssp. *vinifera*	Gaoerdan	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_443	Table1	*Vitis vinifera* ssp. *vinifera*	Takachiho	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_444	Wine	*Vitis vinifera* ssp. *vinifera*	Godin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_445	Wine	*Vitis vinifera* ssp. *vinifera*	Gefikonari	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_446	Wine	*Vitis vinifera* ssp. *vinifera*	Ribola Grun	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_447	Table1	*Vitis vinifera* ssp. *vinifera*	Guibao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_448	Wine	*Vitis vinifera* ssp. *vinifera*	Italian Riesling	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_449	Wine	*Vitis vinifera* ssp. *vinifera*	Xamnpak	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_450	Table1	*Vitis vinifera* ssp. *vinifera*	Hetianlv	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_451	Wine	*Vitis vinifera* ssp. *vinifera*	Heiasaier	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_452	Wine	*Vitis vinifera* ssp. *vinifera*	Heibabaisika	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_453	Wine	*Vitis vinifera* ssp. *vinifera*	Batuta Neagra	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_454	Wine	*Vitis vinifera* ssp. *vinifera*	Blackburkeville	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_455	Wine	*Vitis vinifera* ssp. *vinifera*	Pinot Noir	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_456	Wine	*Vitis vinifera* ssp. *vinifera*	Black Berkhof	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_457	Table1	*Vitis vinifera* ssp. *vinifera*	Large Black Grapes	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_458	Wine	*Vitis vinifera* ssp. *vinifera*	Indogny	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_459	Table1	*Vitis vinifera* ssp. *vinifera*	Heijixin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_460	Wine	*Vitis vinifera* ssp. *vinifera*	Gamay	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_461	Wine	*Vitis vinifera* ssp. *vinifera*	Cabasma Neagra	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_462	Wine	*Vitis vinifera* ssp. *vinifera*	Medoc Noir	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_463	Wine	*Vitis vinifera* ssp. *vinifera*	Tzimlansky Noir	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_464	Wine	*Vitis vinifera* ssp. *vinifera*	Heisanduoli	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_465	Table1	*Vitis vinifera* ssp. *vinifera*	Black Swan	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_466	Wine	*Vitis vinifera* ssp. *vinifera*	Shani Black	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_467	Wine	*Vitis vinifera* ssp. *vinifera*	Heixiexi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_468	Table1	*Vitis vinifera* ssp. *vinifera*	Red Balado	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_469	Table1	*Vitis vinifera* ssp. *vinifera*	Ruby Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_470	Table1	*Vitis vinifera* ssp. *vinifera*	Red Globe	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_471	Table1	*Vitis vinifera* ssp. *vinifera*	Benitaka	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_472	Table1	*Vitis vinifera* ssp. *vinifera*	Flame Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_473	Table1	*Vitis vinifera* ssp. *vinifera*	Honglianzi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_474	Table1	*Vitis vinifera* ssp. *vinifera*	Blush Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_475	Table1	*Vitis vinifera* ssp. *vinifera*	Rosario Rosso	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_476	Table1	*Vitis vinifera* ssp. *vinifera*	Red Milk	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_477	Table1	*Vitis vinifera* ssp. *vinifera*	Red Italian	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_478	Table1	*Vitis vinifera* ssp. *vinifera*	Red Cosmic	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_479	Table1	*Vitis vinifera* ssp. *vinifera*	Hongzhenzhu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_480	Wine	*Vitis vinifera* ssp. *vinifera*	Gamy Teinturier	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_482	Table1	*Vitis vinifera* ssp. *vinifera*	Autumn royal	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_483	Wine	*Vitis vinifera* ssp. *vinifera*	Huangmisi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_484	Wine	*Vitis vinifera* ssp. *vinifera*	Carinena	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_485	Table1	*Vitis vinifera* ssp. *vinifera*	Kaiotome	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_488	Table1	*Vitis vinifera* ssp. *vinifera*	Gold Queen	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_489	Table1	*Vitis vinifera* ssp. *vinifera*	Jintian Huangjia Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_490	Table1	*Vitis vinifera* ssp. *vinifera*	Jintianmeizhi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_491	Table1	*Vitis vinifera* ssp. *vinifera*	Jingfeng Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_492	Table1	*Vitis vinifera* ssp. *vinifera*	Jingkejing	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_493	Table1	*Vitis vinifera* ssp. *vinifera*	Jingxiangyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_494	Table1	*Vitis vinifera* ssp. *vinifera*	Jingxiu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_495	Table1	*Vitis vinifera* ssp. *vinifera*	Jingyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_496	Table1	*Vitis vinifera* ssp. *vinifera*	Jingzaojing	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_497	Table1	*Vitis vinifera* ssp. *vinifera*	Jingzijing	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES

Accessions	collected_by	geo_loc_name_country	geo_loc_name_country_continent	geographic_location_(country_and/or_sea)	geographic_location_(region_and_locality)	geo_loc_name	Instrument
VV_285	-	China	Henan Province	Zhengzhou	113°42E 34°89N	Zhengzhou Fruit Research Ins	-
VV_287	-	China	Henan Province	Zhengzhou	113°42E 34°90N	Zhengzhou Fruit Research Ins	-
VV_288	-	China	Henan Province	Zhengzhou	113°42E 34°91N	Zhengzhou Fruit Research Ins	-
VV_289	-	China	Henan Province	Zhengzhou	113°42E 34°92N	Zhengzhou Fruit Research Ins	-
VV_290	-	China	Henan Province	Zhengzhou	113°42E 34°93N	Zhengzhou Fruit Research Ins	-
VV_291	-	China	Henan Province	Zhengzhou	113°42E 34°94N	Zhengzhou Fruit Research Ins	-
VV_292	-	China	Henan Province	Zhengzhou	113°42E 34°95N	Zhengzhou Fruit Research Ins	-
VV_293	-	China	Henan Province	Zhengzhou	113°42E 34°96N	Zhengzhou Fruit Research Ins	-
VV_294	-	China	Henan Province	Zhengzhou	113°42E 34°97N	Zhengzhou Fruit Research Ins	-
VV_296	-	China	Henan Province	Zhengzhou	113°42E 34°98N	Zhengzhou Fruit Research Ins	-
VV_297	-	China	Henan Province	Zhengzhou	113°42E 34°99N	Zhengzhou Fruit Research Ins	-
VV_298	-	China	Henan Province	Zhengzhou	113°42E 34°100N	Zhengzhou Fruit Research Ins	-
VV_299	-	China	Henan Province	Zhengzhou	113°42E 34°101N	Zhengzhou Fruit Research Ins	-
VV_300	-	China	Henan Province	Zhengzhou	113°42E 34°102N	Zhengzhou Fruit Research Ins	-
VV_301	-	China	Henan Province	Zhengzhou	113°42E 34°103N	Zhengzhou Fruit Research Ins	-
VV_302	-	China	Henan Province	Zhengzhou	113°42E 34°104N	Zhengzhou Fruit Research Ins	-
VV_303	-	China	Henan Province	Zhengzhou	113°42E 34°105N	Zhengzhou Fruit Research Ins	-
VV_304	-	China	Henan Province	Zhengzhou	113°42E 34°106N	Zhengzhou Fruit Research Ins	-
VV_305	-	China	Henan Province	Zhengzhou	113°42E 34°107N	Zhengzhou Fruit Research Ins	-
VV_306	-	China	Henan Province	Zhengzhou	113°42E 34°108N	Zhengzhou Fruit Research Ins	-
VV_307	-	China	Henan Province	Zhengzhou	113°42E 34°109N	Zhengzhou Fruit Research Ins	-
VV_308	-	China	Henan Province	Zhengzhou	113°42E 34°110N	Zhengzhou Fruit Research Ins	-
VV_310	-	China	Henan Province	Zhengzhou	113°42E 34°111N	Zhengzhou Fruit Research Ins	-
VV_311	-	China	Henan Province	Zhengzhou	113°42E 34°112N	Zhengzhou Fruit Research Ins	-
VV_312	-	China	Henan Province	Zhengzhou	113°42E 34°113N	Zhengzhou Fruit Research Ins	-
VV_313	-	China	Henan Province	Zhengzhou	113°42E 34°114N	Zhengzhou Fruit Research Ins	-
VV_314	-	China	Henan Province	Zhengzhou	113°42E 34°115N	Zhengzhou Fruit Research Ins	-
VV_315	-	China	Henan Province	Zhengzhou	113°42E 34°116N	Zhengzhou Fruit Research Ins	-
VV_316	-	China	Henan Province	Zhengzhou	113°42E 34°117N	Zhengzhou Fruit Research Ins	-
VV_318	-	China	Henan Province	Zhengzhou	113°42E 34°118N	Zhengzhou Fruit Research Ins	-
VV_319	-	China	Henan Province	Zhengzhou	113°42E 34°119N	Zhengzhou Fruit Research Ins	-
VV_321	-	China	Henan Province	Zhengzhou	113°42E 34°120N	Zhengzhou Fruit Research Ins	-
VV_322	-	China	Henan Province	Zhengzhou	113°42E 34°121N	Zhengzhou Fruit Research Ins	-
VV_323	-	China	Henan Province	Zhengzhou	113°42E 34°122N	Zhengzhou Fruit Research Ins	-
VV_324	-	China	Henan Province	Zhengzhou	113°42E 34°123N	Zhengzhou Fruit Research Ins	-
VV_325	-	China	Henan Province	Zhengzhou	113°42E 34°124N	Zhengzhou Fruit Research Ins	-
VV_326	-	China	Henan Province	Zhengzhou	113°42E 34°125N	Zhengzhou Fruit Research Ins	-
VV_328	-	China	Henan Province	Zhengzhou	113°42E 34°126N	Zhengzhou Fruit Research Ins	-
VV_329	-	China	Henan Province	Zhengzhou	113°42E 34°127N	Zhengzhou Fruit Research Ins	-
VV_331	-	China	Henan Province	Zhengzhou	113°42E 34°128N	Zhengzhou Fruit Research Ins	-
VV_332	-	China	Henan Province	Zhengzhou	113°42E 34°129N	Zhengzhou Fruit Research Ins	-
VV_333	-	China	Henan Province	Zhengzhou	113°42E 34°130N	Zhengzhou Fruit Research Ins	-
VV_334	-	China	Henan Province	Zhengzhou	113°42E 34°131N	Zhengzhou Fruit Research Ins	-
VV_335	-	China	Henan Province	Zhengzhou	113°42E 34°132N	Zhengzhou Fruit Research Ins	-
VV_336	-	China	Henan Province	Zhengzhou	113°42E 34°133N	Zhengzhou Fruit Research Ins	-
VV_337	-	China	Henan Province	Zhengzhou	113°42E 34°134N	Zhengzhou Fruit Research Ins	-
VV_338	-	China	Henan Province	Zhengzhou	113°42E 34°135N	Zhengzhou Fruit Research Ins	-
VV_339	-	China	Henan Province	Zhengzhou	113°42E 34°136N	Zhengzhou Fruit Research Ins	-
VV_340	-	China	Henan Province	Zhengzhou	113°42E 34°137N	Zhengzhou Fruit Research Ins	-
VV_341	-	China	Henan Province	Zhengzhou	113°42E 34°138N	Zhengzhou Fruit Research Ins	-
VV_342	-	China	Henan Province	Zhengzhou	113°42E 34°139N	Zhengzhou Fruit Research Ins	-
VV_343	-	China	Henan Province	Zhengzhou	113°42E 34°140N	Zhengzhou Fruit Research Ins	-
VV_344	-	China	Henan Province	Zhengzhou	113°42E 34°141N	Zhengzhou Fruit Research Ins	-
VV_345	-	China	Henan Province	Zhengzhou	113°42E 34°142N	Zhengzhou Fruit Research Ins	-
VV_346	-	China	Henan Province	Zhengzhou	113°42E 34°143N	Zhengzhou Fruit Research Ins	-
VV_347	-	China	Henan Province	Zhengzhou	113°42E 34°144N	Zhengzhou Fruit Research Ins	-
VV_349	-	China	Henan Province	Zhengzhou	113°42E 34°145N	Zhengzhou Fruit Research Ins	-
VV_350	-	China	Henan Province	Zhengzhou	113°42E 34°146N	Zhengzhou Fruit Research Ins	-
VV_351	-	China	Henan Province	Zhengzhou	113°42E 34°147N	Zhengzhou Fruit Research Ins	-
VV_352	-	China	Henan Province	Zhengzhou	113°42E 34°148N	Zhengzhou Fruit Research Ins	-
VV_353	-	China	Henan Province	Zhengzhou	113°42E 34°149N	Zhengzhou Fruit Research Ins	-
VV_354	-	China	Henan Province	Zhengzhou	113°42E 34°150N	Zhengzhou Fruit Research Ins	-
VV_355	-	China	Henan Province	Zhengzhou	113°42E 34°151N	Zhengzhou Fruit Research Ins	-
VV_356	-	China	Henan Province	Zhengzhou	113°42E 34°152N	Zhengzhou Fruit Research Ins	-
VV_357	-	China	Henan Province	Zhengzhou	113°42E 34°153N	Zhengzhou Fruit Research Ins	-
VV_358	-	China	Henan Province	Zhengzhou	113°42E 34°154N	Zhengzhou Fruit Research Ins	-
VV_359	-	China	Henan Province	Zhengzhou	113°42E 34°155N	Zhengzhou Fruit Research Ins	-
VV_360	-	China	Henan Province	Zhengzhou	113°42E 34°156N	Zhengzhou Fruit Research Ins	-
VV_361	-	China	Henan Province	Zhengzhou	113°42E 34°157N	Zhengzhou Fruit Research Ins	-
VV_362	-	China	Henan Province	Zhengzhou	113°42E 34°158N	Zhengzhou Fruit Research Ins	-
VV_363	-	China	Henan Province	Zhengzhou	113°42E 34°159N	Zhengzhou Fruit Research Ins	-
VV_364	-	China	Henan Province	Zhengzhou	113°42E 34°160N	Zhengzhou Fruit Research Ins	-
VV_365	-	China	Henan Province	Zhengzhou	113°42E 34°161N	Zhengzhou Fruit Research Ins	-
VV_366	-	China	Henan Province	Zhengzhou	113°42E 34°162N	Zhengzhou Fruit Research Ins	-
VV_367	-	China	Henan Province	Zhengzhou	113°42E 34°163N	Zhengzhou Fruit Research Ins	-
VV_368	-	China	Henan Province	Zhengzhou	113°42E 34°164N	Zhengzhou Fruit Research Ins	-
VV_369	-	China	Henan Province	Zhengzhou	113°42E 34°165N	Zhengzhou Fruit Research Ins	-
VV_376	-	China	Henan Province	Zhengzhou	113°42E 34°166N	Zhengzhou Fruit Research Ins	-
VV_377	-	China	Henan Province	Zhengzhou	113°42E 34°167N	Zhengzhou Fruit Research Ins	-
VV_378	-	China	Henan Province	Zhengzhou	113°42E 34°168N	Zhengzhou Fruit Research Ins	-
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VV_380	-	China	Henan Province	Zhengzhou	113°42E 34°170N	Zhengzhou Fruit Research Ins	-
VV_381	-	China	Henan Province	Zhengzhou	113°42E 34°171N	Zhengzhou Fruit Research Ins	-
VV_382	-	China	Henan Province	Zhengzhou	113°42E 34°172N	Zhengzhou Fruit Research Ins	-
VV_383	-	China	Henan Province	Zhengzhou	113°42E 34°173N	Zhengzhou Fruit Research Ins	-
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VV_386	-	China	Henan Province	Zhengzhou	113°42E 34°176N	Zhengzhou Fruit Research Ins	-
VV_387	-	China	Henan Province	Zhengzhou	113°42E 34°177N	Zhengzhou Fruit Research Ins	-
VV_388	-	China	Henan Province	Zhengzhou	113°42E 34°178N	Zhengzhou Fruit Research Ins	-
VV_389	-	China	Henan Province	Zhengzhou	113°42E 34°179N	Zhengzhou Fruit Research Ins	-
VV_390	-	China	Henan Province	Zhengzhou	113°42E 34°180N	Zhengzhou Fruit Research Ins	-
VV_391	-	China	Henan Province	Zhengzhou	113°42E 34°181N	Zhengzhou Fruit Research Ins	-
VV_392	-	China	Henan Province	Zhengzhou	113°42E 34°182N	Zhengzhou Fruit Research Ins	-
VV_393	-	China	Henan Province	Zhengzhou	113°42E 34°183N	Zhengzhou Fruit Research Ins	-
VV_395	-	China	Henan Province	Zhengzhou	113°42E 34°184N	Zhengzhou Fruit Research Ins	-
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VV_397	-	China	Henan Province	Zhengzhou	113°42E 34°186N	Zhengzhou Fruit Research Ins	-
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VV_406	-	China	Henan Province	Zhengzhou	113°42E 34°194N	Zhengzhou Fruit Research Ins	-
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VV_412	-	China	Henan Province	Zhengzhou	113°42E 34°200N	Zhengzhou Fruit Research Ins	-
VV_413	-	China	Henan Province	Zhengzhou	113°42E 34°201N	Zhengzhou Fruit Research Ins	-
VV_414	-	China	Henan Province	Zhengzhou	113°42E 34°202N	Zhengzhou Fruit Research Ins	-
VV_415	-	China	Henan Province	Zhengzhou	113°42E 34°203N	Zhengzhou Fruit Research Ins	-
VV_417	-	China	Henan Province	Zhengzhou	113°42E 34°204N	Zhengzhou Fruit Research Ins	-
VV_418	-	China	Henan Province	Zhengzhou	113°42E 34°205N	Zhengzhou Fruit Research Ins	-
VV_419	-	China	Henan Province	Zhengzhou	113°42E 34°206N	Zhengzhou Fruit Research Ins	-
VV_420	-	China	Henan Province	Zhengzhou	113°42E 34°207N	Zhengzhou Fruit Research Ins	-
VV_421	-	China	Henan Province	Zhengzhou	113°42E 34°208N	Zhengzhou Fruit Research Ins	-
VV_422	-	China	Henan Province	Zhengzhou	113°42E 34°209N	Zhengzhou Fruit Research Ins	-
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VV_424	-	China	Henan Province	Zhengzhou	113°42E 34°211N	Zhengzhou Fruit Research Ins	-
VV_425	-	China	Henan Province	Zhengzhou	113°42E 34°212N	Zhengzhou Fruit Research Ins	-
VV_426	-	China	Henan Province	Zhengzhou	113°42E 34°213N	Zhengzhou Fruit Research Ins	-
VV_427	-	China	Henan Province	Zhengzhou	113°42E 34°214N	Zhengzhou Fruit Research Ins	-
VV_428	-	China	Henan Province	Zhengzhou	113°42E 34°215N	Zhengzhou Fruit Research Ins	-
VV_429	-	China	Henan Province	Zhengzhou	113°42E 34°216N	Zhengzhou Fruit Research Ins	-
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VV_433	-	China	Henan Province	Zhengzhou	113°42E 34°218N	Zhengzhou Fruit Research Ins	-
VV_434	-	China	Henan Province	Zhengzhou	113°42E 34°219N	Zhengzhou Fruit Research Ins	-
VV_435	-	China	Henan Province	Zhengzhou	113°42E 34°220N	Zhengzhou Fruit Research Ins	-
VV_436	-	China	Henan Province	Zhengzhou	113°42E 34°221N	Zhengzhou Fruit Research Ins	-
VV_437	-	China	Henan Province	Zhengzhou	113°42E 34°222N	Zhengzhou Fruit Research Ins	-
VV_440	-	China	Henan Province	Zhengzhou	113°42E 34°223N	Zhengzhou Fruit Research Ins	-
VV_441	-	China	Henan Province	Zhengzhou	113°42E 34°224N	Zhengzhou Fruit Research Ins	-
VV_442	-	China	Henan Province	Zhengzhou	113°42E 34°225N	Zhengzhou Fruit Research Ins	-
VV_443	-	China	Henan Province	Zhengzhou	113°42E 34°226N	Zhengzhou Fruit Research Ins	-
VV_444	-	China	Henan Province	Zhengzhou	113°42E 34°227N	Zhengzhou Fruit Research Ins	-
VV_445	-	China	Henan Province	Zhengzhou	113°42E 34°228N	Zhengzhou Fruit Research Ins	-
VV_446	-	China	Henan Province	Zhengzhou	113°42E 34°229N	Zhengzhou Fruit Research Ins	-
VV_447	-	China	Henan Province	Zhengzhou	113°42E 34°230N	Zhengzhou Fruit Research Ins	-
VV_448	-	China	Henan Province	Zhengzhou	113°42E 34°231N	Zhengzhou Fruit Research Ins	-
VV_449	-	China	Henan Province	Zhengzhou	113°42E 34°232N	Zhengzhou Fruit Research Ins	-
VV_450	-	China	Henan Province	Zhengzhou	113°42E 34°233N	Zhengzhou Fruit Research Ins	-
VV_451	-	China	Henan Province	Zhengzhou	113°42E 34°234N	Zhengzhou Fruit Research Ins	-
VV_452	-	China	Henan Province	Zhengzhou	113°42E 34°235N	Zhengzhou Fruit Research Ins	-
VV_453	-	China	Henan Province	Zhengzhou	113°42E 34°236N	Zhengzhou Fruit Research Ins	-
VV_454	-	China	Henan Province	Zhengzhou	113°42E 34°237N	Zhengzhou Fruit Research Ins	-
VV_455	-	China	Henan Province	Zhengzhou	113°42E 34°238N	Zhengzhou Fruit Research Ins	-
VV_456	-	China	Henan Province	Zhengzhou	113°42E 34°239N	Zhengzhou Fruit Research Ins	-
VV_457	-	China	Henan Province	Zhengzhou	113°42E 34°240N	Zhengzhou Fruit Research Ins	-
VV_458	-	China	Henan Province	Zhengzhou	113°42E 34°241N	Zhengzhou Fruit Research Ins	-
VV_459	-	China	Henan Province	Zhengzhou	113°42E 34°242N	Zhengzhou Fruit Research Ins	-
VV_460	-	China	Henan Province	Zhengzhou	113°42E 34°243N	Zhengzhou Fruit Research Ins	-
VV_461	-	China	Henan Province	Zhengzhou	113°42E 34°244N	Zhengzhou Fruit Research Ins	-
VV_462	-	China	Henan Province	Zhengzhou	113°42E 34°245N	Zhengzhou Fruit Research Ins	-
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VV_464	-	China	Henan Province	Zhengzhou	113°42E 34°247N	Zhengzhou Fruit Research Ins	-
VV_465	-	China	Henan Province	Zhengzhou	113°42E 34°248N	Zhengzhou Fruit Research Ins	-
VV_466	-	China	Henan Province	Zhengzhou	113°42E 34°249N	Zhengzhou Fruit Research Ins	-
VV_467	-	China	Henan Province	Zhengzhou	113°42E 34°250N	Zhengzhou Fruit Research Ins	-
VV_468	-	China	Henan Province	Zhengzhou	113°42E 34°251N	Zhengzhou Fruit Research Ins	-
VV_469	-	China	Henan Province	Zhengzhou	113°42E 34°252N	Zhengzhou Fruit Research Ins	-
VV_470	-	China	Henan Province	Zhengzhou	113°42E 34°253N	Zhengzhou Fruit Research Ins	-
VV_471	-	China	Henan Province	Zhengzhou	113°42E 34°254N	Zhengzhou Fruit Research Ins	-
VV_472	-	China	Henan Province	Zhengzhou	113°42E 34°255N	Zhengzhou Fruit Research Ins	-
VV_473	-	China	Henan Province	Zhengzhou	113°42E 34°256N	Zhengzhou Fruit Research Ins	-
VV_474	-	China	Henan Province	Zhengzhou	113°42E 34°257N	Zhengzhou Fruit Research Ins	-
VV_475	-	China	Henan Province	Zhengzhou	113°42E 34°258N	Zhengzhou Fruit Research Ins	-
VV_476	-	China	Henan Province	Zhengzhou	113°42E 34°259N	Zhengzhou Fruit Research Ins	-
VV_477	-	China	Henan Province	Zhengzhou	113°42E 34°260N	Zhengzhou Fruit Research Ins	-
VV_478	-	China	Henan Province	Zhengzhou	113°42E 34°261N	Zhengzhou Fruit Research Ins	-
VV_479	-	China	Henan Province	Zhengzhou	113°42E 34°262N	Zhengzhou Fruit Research Ins	-
VV_480	-	China	Henan Province	Zhengzhou	113°42E 34°263N	Zhengzhou Fruit Research Ins	-
VV_482	-	China	Henan Province	Zhengzhou	113°42E 34°264N	Zhengzhou Fruit Research Ins	-
VV_483	-	China	Henan Province	Zhengzhou	113°42E 34°265N	Zhengzhou Fruit Research Ins	-
VV_484	-	China	Henan Province	Zhengzhou	113°42E 34°266N	Zhengzhou Fruit Research Ins	-
VV_485	-	China	Henan Province	Zhengzhou	113°42E 34°267N	Zhengzhou Fruit Research Ins	-
VV_488	-	China	Henan Province	Zhengzhou	113°42E 34°268N	Zhengzhou Fruit Research Ins	-
VV_489	-	China	Henan Province	Zhengzhou	113°42E 34°269N	Zhengzhou Fruit Research Ins	-
VV_490	-	China	Henan Province	Zhengzhou	113°42E 34°270N	Zhengzhou Fruit Research Ins	-
VV_491	-	China	Henan Province	Zhengzhou	113°42E 34°271N	Zhengzhou Fruit Research Ins	-
VV_492	-	China	Henan Province	Zhengzhou	113°42E 34°272N	Zhengzhou Fruit Research Ins	-
VV_493	-	China	Henan Province	Zhengzhou	113°42E 34°273N	Zhengzhou Fruit Research Ins	-
VV_494	-	China	Henan Province	Zhengzhou	113°42E 34°274N	Zhengzhou Fruit Research Ins	-
VV_495	-	China	Henan Province	Zhengzhou	113°42E 34°275N	Zhengzhou Fruit Research Ins	-
VV_496	-	China	Henan Province	Zhengzhou	113°42E 34°276N	Zhengzhou Fruit Research Ins	-
VV_497	-	China	Henan Province	Zhengzhou	113°42E 34°277N	Zhengzhou Fruit Research Ins	-

Accessions	Library Name	LibraryLayout	LibrarySelection	LibrarySource	Platform	Sample Name	Submitter_Id	sex	dev_stage	tissue_type
VV_285	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_287	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_288	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_289	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_290	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_291	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_292	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_293	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_294	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_296	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_297	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_298	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_299	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_300	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_301	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_302	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_303	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_304	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_305	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_306	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_307	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_308	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_310	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_311	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_312	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_313	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_314	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_315	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_316	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_318	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_319	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_321	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_322	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_323	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_324	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_325	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_326	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_328	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_329	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_331	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_332	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_333	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_334	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_335	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_336	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_337	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_338	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_339	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_340	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_341	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_342	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_343	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_344	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_345	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_346	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_347	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_349	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_350	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_351	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_352	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_353	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_354	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_355	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_356	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_357	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_358	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_359	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_360	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_361	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_362	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_363	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_364	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_365	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_366	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_367	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_368	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_369	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_376	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_377	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_378	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_379	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_380	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_381	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_382	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_383	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_384	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_385	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_386	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_387	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_388	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_389	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_390	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_391	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_392	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_393	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_395	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_396	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_397	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_399	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_400	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_401	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_402	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_403	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_404	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_405	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_406	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_407	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_408	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_409	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_410	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_411	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_412	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_413	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_414	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_415	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_417	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_418	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_419	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_420	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_421	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_422	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_423	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_424	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_425	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_426	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_427	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_428	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_429	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_430	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_433	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_434	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_435	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_436	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_437	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_440	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_441	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_442	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_443	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_444	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_445	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_446	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_447	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_448	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_449	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_450	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_451	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_452	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_453	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_454	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_455	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_456	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_457	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_458	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_459	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_460	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_461	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_462	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_463	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_464	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_465	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_466	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_467	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_468	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_469	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_470	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_471	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_472	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_473	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_474	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_475	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_476	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_477	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_478	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_479	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_480	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_482	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_483	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_484	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_485	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_488	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_489	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_490	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_491	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_492	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_493	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_494	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_495	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_496	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_497	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf

Supplementary Table 6. A total of 466 accessions for genotyping SV based on pangenome (including 324 newly sequenced).

Accessions	Group	Species	Common name	Note	SRR ID	Assay Type	AvgSpotLen	Bases	BioProject	BioSample	Bytes	Center Name
VV_498	Wine	*Vitis vinifera* ssp. *vinifera*	Carilliere	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_499	Wine	*Vitis vinifera* ssp. *vinifera*	Camarte	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_500	Wine	*Vitis vinifera* ssp. *vinifera*	Kamulaxia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_501	Table1	*Vitis vinifera* ssp. *vinifera*	Carthage Rose	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_503	Wine	*Vitis vinifera* ssp. *vinifera*	Kondavas	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_504	Wine	*Vitis vinifera* ssp. *vinifera*	Caucachaba	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_505	Table1	*Vitis vinifera* ssp. *vinifera*	Khoussaine Khelime Harmak	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_506	Table1	*Vitis vinifera* ssp. *vinifera*	Crimson Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_507	Table1	*Vitis vinifera* ssp. *vinifera*	Dawn Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_508	Table1	*Vitis vinifera* ssp. *vinifera*	Plum Aromatic	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_509	Table1	*Vitis vinifera* ssp. *vinifera*	Rizamat	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_510	Table1	*Vitis vinifera* ssp. *vinifera*	Lihongbao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_512	Table1	*Vitis vinifera* ssp. *vinifera*	Lumanage	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_513	Wine	*Vitis vinifera* ssp. *vinifera*	Mavrud	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_514	Wine	*Vitis vinifera* ssp. *vinifera*	Malivassia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_515	Table1	*Vitis vinifera* ssp. *vinifera*	Horse Milk	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_516	Table1	*Vitis vinifera* ssp. *vinifera*	Camelia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_517	Wine	*Vitis vinifera* ssp. *vinifera*	Manimishka	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_518	Wine	*Vitis vinifera* ssp. *vinifera*	Merlot	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_519	Table1	*Vitis vinifera* ssp. *vinifera*	Manicure Finger	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_520	Table1	*Vitis vinifera* ssp. *vinifera*	Melissa Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_521	Wine	*Vitis vinifera* ssp. *vinifera*	Müller Thurgau	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_523	Wine	*Vitis vinifera* ssp. *vinifera*	Nayeli	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_524	Wine	*Vitis vinifera* ssp. *vinifera*	Geoskib	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_525	Table1	*Vitis vinifera* ssp. *vinifera*	Nimulange	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_526	Table1	*Vitis vinifera* ssp. *vinifera*	Ningxiawuhebai	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_527	Table1	*Vitis vinifera* ssp. *vinifera*	Milk	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_528	Wine	*Vitis vinifera* ssp. *vinifera*	Cabernet Franc	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_529	Table1	*Vitis vinifera* ssp. *vinifera*	Pinger	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_530	Table1	*Vitis vinifera* ssp. *vinifera*	Queen Of Vineyard	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_531	Table1	*Vitis vinifera* ssp. *vinifera*	Qiuhei	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_532	Table1	*Vitis vinifera* ssp. *vinifera*	Qiuheibao(4N)	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_533	Table1	*Vitis vinifera* ssp. *vinifera*	Qiuhongbao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_534	Table1	*Vitis vinifera* ssp. *vinifera*	Ribier	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_535	Table1	*Vitis vinifera* ssp. *vinifera*	Ruiducuixia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_536	Table1	*Vitis vinifera* ssp. *vinifera*	Ruizhongyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_537	Table1	*Vitis vinifera* ssp. *vinifera*	Ruiduwuheyi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_538	Table1	*Vitis vinifera* ssp. *vinifera*	Ruiduxiangyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_539	Wine	*Vitis vinifera* ssp. *vinifera*	Sangiovese	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_541	Wine	*Vitis vinifera* ssp. *vinifera*	Samoveanca	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_542	Wine	*Vitis vinifera* ssp. *vinifera*	Cabernet Gernischt	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_543	Wine	*Vitis vinifera* ssp. *vinifera*	Neo Muscat	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_544	Wine	*Vitis vinifera* ssp. *vinifera*	Chaselas Muscat	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_545	Table1	*Vitis vinifera* ssp. *vinifera*	Yatomi Rosa	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_546	Wine	*Vitis vinifera* ssp. *vinifera*	zander	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_547	Wine	*Vitis vinifera* ssp. *vinifera*	Taphav	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_548	Wine	*Vitis vinifera* ssp. *vinifera*	Tainter	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_549	Wine	*Vitis vinifera* ssp. *vinifera*	Tuscany Malavasia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_550	Wine	*Vitis vinifera* ssp. *vinifera*	Vama Bevaci	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_551	Wine	*Vitis vinifera* ssp. *vinifera*	Vagisbeyli	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_553	Wine	*Vitis vinifera* ssp. *vinifera*	Petit Verdot	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_554	Table1	*Vitis vinifera* ssp. *vinifera*	Thompson Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_555	Table1	*Vitis vinifera* ssp. *vinifera*	Wuhebai No.1	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_556	Table1	*Vitis vinifera* ssp. *vinifera*	Centennial Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_557	Table2	*V. vinifera* × *V.labrusca*	Wuhemi	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_558	Table1	*Vitis vinifera* ssp. *vinifera*	Black Monukka	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_559	Wine	*Vitis vinifera* ssp. *vinifera*	Syrah	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_560	Table1	*Vitis vinifera* ssp. *vinifera*	Xinong No.2	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_561	Wine	*Vitis vinifera* ssp. *vinifera*	Chardonnay	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_562	Table1	*Vitis vinifera* ssp. *vinifera*	Xiabai putao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_563	Table1	*Vitis vinifera* ssp. *vinifera*	Xiangfei	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_564	Wine	*Vitis vinifera* ssp. *vinifera*	Xiaobaiputao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_566	Table1	*Vitis vinifera* ssp. *vinifera*	Xinyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_567	Table1	*Vitis vinifera* ssp. *vinifera*	Yanhong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_568	Wine	*Vitis vinifera* ssp. *vinifera*	Yekeshenlaer	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_569	Table1	*Vitis vinifera* ssp. *vinifera*	Night Beauty	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_570	Wine	*Vitis vinifera* ssp. *vinifera*	Ida	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_571	Table1	*Vitis vinifera* ssp. *vinifera*	Ispissar	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_572	Wine	*Vitis vinifera* ssp. *vinifera*	Ergodan	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_573	Wine	*Vitis vinifera* ssp. *vinifera*	Ezra Grape	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_574	Table1	*Vitis vinifera* ssp. *vinifera*	Italia	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_575	Table1	*Vitis vinifera* ssp. *vinifera*	Zaoheibao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_576	Table1	*Vitis vinifera* ssp. *vinifera*	Zaojinxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_577	Table1	*Vitis vinifera* ssp. *vinifera*	Zaokangbao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_578	Table1	*Vitis vinifera* ssp. *vinifera*	Zaomanao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_579	Table1	*Vitis vinifera* ssp. *vinifera*	Zaoshuhong Seedless	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_580	Table1	*Vitis vinifera* ssp. *vinifera*	Zaotian	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_581	Table1	*Vitis vinifera* ssp. *vinifera*	Zeyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_582	Table1	*Vitis vinifera* ssp. *vinifera*	Zhengguo No.3	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_583	Table1	*Vitis vinifera* ssp. *vinifera*	Zhengzhou zaohong	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_584	Table1	*Vitis vinifera* ssp. *vinifera*	Zhengzhou zaoyu	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_585	Table1	*Vitis vinifera* ssp. *vinifera*	Zijinxin	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_586	Wine	*Vitis vinifera* ssp. *vinifera*	Zitao	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_587	Table1	*Vitis vinifera* ssp. *vinifera*	Purple Pearl	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_588	Wine	*Vitis vinifera* ssp. *vinifera*	Zizhongmei	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_589	Wine	*Vitis vinifera* ssp. *vinifera*	Zuishixian	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_590	Table2	*V. vinifera* × *V.labrusca*	Heihuxiang	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES
VV_591	Table2	*V. vinifera* × *V.labrusca*	Concord	In this study	-	WGS	-	-	PRJNA994294	-	-	AGRICULTURAL GENOMICS INSTITUTE AT SHENZHEN, CHINESE ACADEMY OF AGRICULTURAL SCIENCES

Accessions	collected_by	geo_loc_name_country	geo_loc_name_country_continent	geographic_location_(country_and/or_sea)	geographic_location_(region_and_locality)	geo_loc_name	Instrument
VV_498	-	China	Henan Province	Zhengzhou	113°42E 34°278N	Zhengzhou Fruit Research Ins	-
VV_499	-	China	Henan Province	Zhengzhou	113°42E 34°279N	Zhengzhou Fruit Research Ins	-
VV_500	-	China	Henan Province	Zhengzhou	113°42E 34°280N	Zhengzhou Fruit Research Ins	-
VV_501	-	China	Henan Province	Zhengzhou	113°42E 34°281N	Zhengzhou Fruit Research Ins	-
VV_503	-	China	Henan Province	Zhengzhou	113°42E 34°282N	Zhengzhou Fruit Research Ins	-
VV_504	-	China	Henan Province	Zhengzhou	113°42E 34°283N	Zhengzhou Fruit Research Ins	-
VV_505	-	China	Henan Province	Zhengzhou	113°42E 34°284N	Zhengzhou Fruit Research Ins	-
VV_506	-	China	Henan Province	Zhengzhou	113°42E 34°285N	Zhengzhou Fruit Research Ins	-
VV_507	-	China	Henan Province	Zhengzhou	113°42E 34°286N	Zhengzhou Fruit Research Ins	-
VV_508	-	China	Henan Province	Zhengzhou	113°42E 34°287N	Zhengzhou Fruit Research Ins	-
VV_509	-	China	Henan Province	Zhengzhou	113°42E 34°288N	Zhengzhou Fruit Research Ins	-
VV_510	-	China	Henan Province	Zhengzhou	113°42E 34°289N	Zhengzhou Fruit Research Ins	-
VV_512	-	China	Henan Province	Zhengzhou	113°42E 34°290N	Zhengzhou Fruit Research Ins	-
VV_513	-	China	Henan Province	Zhengzhou	113°42E 34°291N	Zhengzhou Fruit Research Ins	-
VV_514	-	China	Henan Province	Zhengzhou	113°42E 34°292N	Zhengzhou Fruit Research Ins	-
VV_515	-	China	Henan Province	Zhengzhou	113°42E 34°293N	Zhengzhou Fruit Research Ins	-
VV_516	-	China	Henan Province	Zhengzhou	113°42E 34°294N	Zhengzhou Fruit Research Ins	-
VV_517	-	China	Henan Province	Zhengzhou	113°42E 34°295N	Zhengzhou Fruit Research Ins	-
VV_518	-	China	Henan Province	Zhengzhou	113°42E 34°296N	Zhengzhou Fruit Research Ins	-
VV_519	-	China	Henan Province	Zhengzhou	113°42E 34°297N	Zhengzhou Fruit Research Ins	-
VV_520	-	China	Henan Province	Zhengzhou	113°42E 34°298N	Zhengzhou Fruit Research Ins	-
VV_521	-	China	Henan Province	Zhengzhou	113°42E 34°299N	Zhengzhou Fruit Research Ins	-
VV_523	-	China	Henan Province	Zhengzhou	113°42E 34°300N	Zhengzhou Fruit Research Ins	-
VV_524	-	China	Henan Province	Zhengzhou	113°42E 34°301N	Zhengzhou Fruit Research Ins	-
VV_525	-	China	Henan Province	Zhengzhou	113°42E 34°302N	Zhengzhou Fruit Research Ins	-
VV_526	-	China	Henan Province	Zhengzhou	113°42E 34°303N	Zhengzhou Fruit Research Ins	-
VV_527	-	China	Henan Province	Zhengzhou	113°42E 34°304N	Zhengzhou Fruit Research Ins	-
VV_528	-	China	Henan Province	Zhengzhou	113°42E 34°305N	Zhengzhou Fruit Research Ins	-
VV_529	-	China	Henan Province	Zhengzhou	113°42E 34°306N	Zhengzhou Fruit Research Ins	-
VV_530	-	China	Henan Province	Zhengzhou	113°42E 34°307N	Zhengzhou Fruit Research Ins	-
VV_531	-	China	Henan Province	Zhengzhou	113°42E 34°308N	Zhengzhou Fruit Research Ins	-
VV_532	-	China	Henan Province	Zhengzhou	113°42E 34°309N	Zhengzhou Fruit Research Ins	-
VV_533	-	China	Henan Province	Zhengzhou	113°42E 34°310N	Zhengzhou Fruit Research Ins	-
VV_534	-	China	Henan Province	Zhengzhou	113°42E 34°311N	Zhengzhou Fruit Research Ins	-
VV_535	-	China	Henan Province	Zhengzhou	113°42E 34°312N	Zhengzhou Fruit Research Ins	-
VV_536	-	China	Henan Province	Zhengzhou	113°42E 34°313N	Zhengzhou Fruit Research Ins	-
VV_537	-	China	Henan Province	Zhengzhou	113°42E 34°314N	Zhengzhou Fruit Research Ins	-
VV_538	-	China	Henan Province	Zhengzhou	113°42E 34°315N	Zhengzhou Fruit Research Ins	-
VV_539	-	China	Henan Province	Zhengzhou	113°42E 34°316N	Zhengzhou Fruit Research Ins	-
VV_541	-	China	Henan Province	Zhengzhou	113°42E 34°317N	Zhengzhou Fruit Research Ins	-
VV_542	-	China	Henan Province	Zhengzhou	113°42E 34°318N	Zhengzhou Fruit Research Ins	-
VV_543	-	China	Henan Province	Zhengzhou	113°42E 34°319N	Zhengzhou Fruit Research Ins	-
VV_544	-	China	Henan Province	Zhengzhou	113°42E 34°320N	Zhengzhou Fruit Research Ins	-
VV_545	-	China	Henan Province	Zhengzhou	113°42E 34°321N	Zhengzhou Fruit Research Ins	-
VV_546	-	China	Henan Province	Zhengzhou	113°42E 34°322N	Zhengzhou Fruit Research Ins	-
VV_547	-	China	Henan Province	Zhengzhou	113°42E 34°323N	Zhengzhou Fruit Research Ins	-
VV_548	-	China	Henan Province	Zhengzhou	113°42E 34°324N	Zhengzhou Fruit Research Ins	-
VV_549	-	China	Henan Province	Zhengzhou	113°42E 34°325N	Zhengzhou Fruit Research Ins	-
VV_550	-	China	Henan Province	Zhengzhou	113°42E 34°326N	Zhengzhou Fruit Research Ins	-
VV_551	-	China	Henan Province	Zhengzhou	113°42E 34°327N	Zhengzhou Fruit Research Ins	-
VV_553	-	China	Henan Province	Zhengzhou	113°42E 34°328N	Zhengzhou Fruit Research Ins	-
VV_554	-	China	Henan Province	Zhengzhou	113°42E 34°329N	Zhengzhou Fruit Research Ins	-
VV_555	-	China	Henan Province	Zhengzhou	113°42E 34°330N	Zhengzhou Fruit Research Ins	-
VV_556	-	China	Henan Province	Zhengzhou	113°42E 34°331N	Zhengzhou Fruit Research Ins	-
VV_557	-	China	Henan Province	Zhengzhou	113°42E 34°332N	Zhengzhou Fruit Research Ins	-
VV_558	-	China	Henan Province	Zhengzhou	113°42E 34°333N	Zhengzhou Fruit Research Ins	-
VV_559	-	China	Henan Province	Zhengzhou	113°42E 34°334N	Zhengzhou Fruit Research Ins	-
VV_560	-	China	Henan Province	Zhengzhou	113°42E 34°335N	Zhengzhou Fruit Research Ins	-
VV_561	-	China	Henan Province	Zhengzhou	113°42E 34°336N	Zhengzhou Fruit Research Ins	-
VV_562	-	China	Henan Province	Zhengzhou	113°42E 34°337N	Zhengzhou Fruit Research Ins	-
VV_563	-	China	Henan Province	Zhengzhou	113°42E 34°338N	Zhengzhou Fruit Research Ins	-
VV_564	-	China	Henan Province	Zhengzhou	113°42E 34°339N	Zhengzhou Fruit Research Ins	-
VV_566	-	China	Henan Province	Zhengzhou	113°42E 34°340N	Zhengzhou Fruit Research Ins	-
VV_567	-	China	Henan Province	Zhengzhou	113°42E 34°341N	Zhengzhou Fruit Research Ins	-
VV_568	-	China	Henan Province	Zhengzhou	113°42E 34°342N	Zhengzhou Fruit Research Ins	-
VV_569	-	China	Henan Province	Zhengzhou	113°42E 34°343N	Zhengzhou Fruit Research Ins	-
VV_570	-	China	Henan Province	Zhengzhou	113°42E 34°344N	Zhengzhou Fruit Research Ins	-
VV_571	-	China	Henan Province	Zhengzhou	113°42E 34°345N	Zhengzhou Fruit Research Ins	-
VV_572	-	China	Henan Province	Zhengzhou	113°42E 34°346N	Zhengzhou Fruit Research Ins	-
VV_573	-	China	Henan Province	Zhengzhou	113°42E 34°347N	Zhengzhou Fruit Research Ins	-
VV_574	-	China	Henan Province	Zhengzhou	113°42E 34°348N	Zhengzhou Fruit Research Ins	-
VV_575	-	China	Henan Province	Zhengzhou	113°42E 34°349N	Zhengzhou Fruit Research Ins	-
VV_576	-	China	Henan Province	Zhengzhou	113°42E 34°350N	Zhengzhou Fruit Research Ins	-
VV_577	-	China	Henan Province	Zhengzhou	113°42E 34°351N	Zhengzhou Fruit Research Ins	-
VV_578	-	China	Henan Province	Zhengzhou	113°42E 34°352N	Zhengzhou Fruit Research Ins	-
VV_579	-	China	Henan Province	Zhengzhou	113°42E 34°353N	Zhengzhou Fruit Research Ins	-
VV_580	-	China	Henan Province	Zhengzhou	113°42E 34°354N	Zhengzhou Fruit Research Ins	-
VV_581	-	China	Henan Province	Zhengzhou	113°42E 34°355N	Zhengzhou Fruit Research Ins	-
VV_582	-	China	Henan Province	Zhengzhou	113°42E 34°356N	Zhengzhou Fruit Research Ins	-
VV_583	-	China	Henan Province	Zhengzhou	113°42E 34°357N	Zhengzhou Fruit Research Ins	-
VV_584	-	China	Henan Province	Zhengzhou	113°42E 34°358N	Zhengzhou Fruit Research Ins	-
VV_585	-	China	Henan Province	Zhengzhou	113°42E 34°359N	Zhengzhou Fruit Research Ins	-
VV_586	-	China	Henan Province	Zhengzhou	113°42E 34°360N	Zhengzhou Fruit Research Ins	-
VV_587	-	China	Henan Province	Zhengzhou	113°42E 34°361N	Zhengzhou Fruit Research Ins	-
VV_588	-	China	Henan Province	Zhengzhou	113°42E 34°362N	Zhengzhou Fruit Research Ins	-
VV_589	-	China	Henan Province	Zhengzhou	113°42E 34°363N	Zhengzhou Fruit Research Ins	-
VV_590	-	China	Henan Province	Zhengzhou	113°42E 34°364N	Zhengzhou Fruit Research Ins	-
VV_591	-	China	Henan Province	Zhengzhou	113°42E 34°365N	Zhengzhou Fruit Research Ins	-

Accessions	Library Name	LibraryLayout	LibrarySelection	LibrarySource	Platform	Sample Name	Submitter_Id	sex	dev_stage	tissue_type
VV_498	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_499	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_500	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_501	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_503	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_504	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_505	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_506	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_507	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_508	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_509	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_510	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_512	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_513	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_514	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_515	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_516	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_517	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_518	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_519	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_520	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_521	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_523	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_524	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_525	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_526	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_527	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_528	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_529	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_530	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_531	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_532	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_533	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_534	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_535	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_536	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_537	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_538	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_539	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_541	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_542	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_543	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_544	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_545	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_546	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_547	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_548	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_549	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_550	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_551	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_553	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_554	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_555	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_556	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_557	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_558	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_559	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_560	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_561	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_562	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_563	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_564	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_566	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_567	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_568	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_569	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_570	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_571	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_572	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_573	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_574	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_575	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_576	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_577	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_578	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_579	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_580	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_581	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_582	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_583	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_584	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_585	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_586	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_587	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_588	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_589	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_590	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf
VV_591	-	PAIRED	unspecified	GENOMIC	ILLUMINA	-	-	-	mature	leaf

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
ARI 1	GG	AA	0	GG	CC	CC	TT	CT	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	0	TT	GG	TT	CC	GG	GA	TT	CC	CC
ARI 2	GG	AA	0	GG	CC	CC	TT	CT	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	0	TT	GG	TT	CC	GG	GA	TT	CC	CC
ARI 3	GG	AA	0	GG	CC	CC	CT	CT	AA	GG	GG	CC	AA	TT	TT	GG	CC	CG	GG	AA	TT	CC	CC	0	TT	GG	TT	CC	GG	GG	TT	CC	CC
CAL 1	GG	AA	CC	GG	TC	CC	TT	CT	AA	GA	AG	CC	AA	TT	CT	GG	TC	CC	0	GA	TT	CC	CC	TT	TT	GG	TT	CT	GG	GA	TT	CC	CT
CAL 2	GA	AA	CT	AG	CC	TC	TT	CT	AA	GA	GG	TC	GA	TT	TT	GG	TC	CG	GG	GA	CT	CA	CC	CT	TT	GG	TT	CC	GG	GG	TT	AC	CT
CAL_3	GG	AA	CC	GG	CC	CC	TT	TT	AA	GG	GG	CC	AA	TT	TT	GG	CC	CC	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CC
CINE 1	GG	AA	CC	GG	CC	CC	CC	CC	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	GA	TT	CC	CC
CINE 2	GG	AA	CC	GG	CC	CC	CC	CC	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	GG	TT	CC	CC
CINE 3	GG	AA	CC	GG	CC	CC	CC	CC	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	GG	TT	CC	CC
MUS_1	GG	GG	CC	GG	CC	CC	CC	CC	AA	GG	GG	TT	AA	TT	TT	GG	CC	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CC
MUS 2	GG	GG	CC	GG	CC	CC	CC	CC	AA	GG	GG	TT	AA	TT	TT	GG	CC	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CC
MUS 3	GG	GG	CC	GG	CC	CC	CC	CC	AA	GG	GG	TT	AA	TT	TT	GG	CC	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CC
OG 1	GG	AA	CC	GG	CC	CC	0	TT	0	GG	0	TT	AA	TT	TT	GG	CC	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GA	AA	TT	CC	TT
OG 2	GG	AA	CC	GG	CC	CC	0	TT	0	GG	0	TT	AA	TT	TT	0	0	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GA	AA	TT	CC	TT
OG 3	GG	AA	CC	GG	CC	CC	0	TT	0	GG	0	TT	AA	TT	TT	GG	CC	GG	0	AA	TT	CC	CC	TT	TT	GG	TT	CC	GA	AA	TT	CC	TT
OG 4	GG	AA	CC	GG	CC	CC	CT	TT	AA	GG	GG	CC	AA	TT	TT	GG	CC	CC	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	GA	TT	CC	CC
OG 5	GG	AA	CC	GG	CC	CC	TT	TT	AA	GG	GG	CC	AA	TT	TT	GG	CC	CC	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	GA	TT	CC	CC
OG 6	GG	AA	CC	GG	CC	CC	CT	TT	AA	GG	AG	TC	GA	TT	TT	CC	TC	CC	0	AA	TT	CC	CC	TT	TT	AG	TT	CT	GG	GA	CT	AC	CC
RUP 1	GG	AA	0	GG	CC	CC	CT	CC	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	CC
RUP 2	GG	AA	0	GG	CC	CC	CT	CC	AA	GG	GG	CC	AA	TT	TT	GG	TC	GG	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CC
RUP 3	GG	AA	0	GG	CC	CC	CC	CC	TA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GA	AA	TT	CC	CC
VL 1	GG	AA	CC	GG	CC	CC	CC	CC	AA	GG	GG	TT	AA	TT	TT	GG	CC	CG	GG	GG	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	CT
VL 10	GG	0	0	GG	CC	0	0	0	0	GG	0	0	0	TT	0	GG	0	CC	0	GG	0	CC	CC	0	TT	0	TT	0	0	AA	TT	CC	0
VL 11	GG	AA	CC	GG	CC	CC	0	CC	AA	GG	0	TT	AA	TT	0	GG	CC	CG	0	GA	TT	CC	CC	0	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 12	GG	AA	CC	GG	TC	CC	CC	0	TA	GG	GG	TC	AA	TT	CT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 13	GG	AA	CC	GG	TC	CC	CC	CT	TA	GG	GG	TC	AA	TT	CC	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	0	AA	TT	CC	TT
VL_14	GG	AA	CC	GG	TT	CC	CC	CT	TA	GG	GG	CC	AA	TT	CT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL_15	GG	AA	CC	GG	CC	CC	CC	CT	TA	GG	GG	TC	AA	TT	CT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 16	GG	AA	CC	GG	TT	CC	CC	CT	TA	GG	GG	TC	AA	TT	TT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 18	GG	AA	CC	GG	TC	CC	CC	CT	TA	GG	GG	TC	AA	TT	CT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 19	GG	AA	CC	GG	CC	CC	CC	CT	AA	GA	GG	TC	AA	TT	TT	GG	CC	CG	GG	GA	CT	CA	CC	CT	TT	GG	TT	CC	GG	AA	CT	AC	TT
VL 2	GG	AA	CC	GG	CC	CC	TT	CC	AA	GG	GG	TT	AA	TT	TT	GG	CC	CC	GG	AA	TT	CC	CC	TT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 4	GG	AA	0	GG	CC	CC	CC	0	AA	GG	GG	CC	AA	TT	TT	GG	CC	GG	GG	GA	TT	CC	CC	0	TT	GG	0	CT	GG	AA	0	AC	CT
VL 6	GG	AA	CC	GG	TC	CC	CC	CT	TA	GG	GG	TC	AA	TT	CT	GC	CC	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 7	GG	AA	CC	GG	CC	CC	CC	CT	AA	GA	GG	TC	AA	TT	TT	GG	CC	CG	GG	GA	CT	CA	CC	CT	TT	GG	TT	CC	GG	AA	CT	AC	TT
VL 8	GG	AA	CC	GG	TC	CC	CC	CT	TA	GG	GG	TC	AA	TT	CT	GC	0	GG	GG	GG	TT	CC	CC	CT	TT	GG	TT	CC	GG	AA	TT	CC	TT
VL 9	GG	AA	CC	GG	CC	CC	0	CC	AA	GG	0	TT	AA	TT	0	GG	CC	CG	0	GA	TT	CC	CC	0	TT	GG	TT	CC	GG	AA	TT	CC	TT
VSE 1	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	CA	TT	TT	TT	GG	CC	TT	GG	AA	TT	AA	CT
VSE 10	AA	GG	TT	GG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CT	CA	TC	TT	TT	GG	CC	TT	GG	AA	CT	AA	CT
VSE 11	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TC	TT	TT	GG	CC	TT	GG	AA	CT	AA	CT
VSE 12	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	CT	AA	TC	TT	TT	GG	CC	TT	GG	AA	CT	AA	CT
VSE 15	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GC	TC	GG	GG	AA	TT	CC	CC	CT	CC	GG	CT	TT	GG	AA	TT	AA	TT
VSE 16	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GC	TC	GG	GG	AA	TT	CC	CC	CT	CC	GG	CT	TT	GG	AA	TT	AA	TT
VSE_17	AA	GG	CT	GG	TT	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	GG	CC	CA	CC	TT	CT	GG	CC	TT	GG	AA	TT	AA	TT
VSE 18	AA	AG	CT	AG	CC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	GG	CC	CC	TC	TT	TT	GG	TT	TT	GG	AA	TT	AA	TT
VSE 19	AA	GG	CC	AA	CC	TC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	AG	AA	CT	AA	TC	TT	CC	GG	CT	TT	GG	GG	TT	AA	TT
VSE 2	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	CC	TT	TT	GG	CC	TT	GG	GA	CT	AA	CT
VSE_20	AA	GG	CT	AA	CC	TC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TC	GG	AG	AA	TT	AA	TC	TT	CT	GG	TT	TT	GG	GA	TT	AA	TT
VSE 21	AA	GG	CT	AG	CC	TC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GC	TC	GG	AG	AA	CT	AA	CC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 22	AA	GG	TT	AA	TC	CC	TT	TT	AA	AA	AG	CC	GG	TT	TT	GC	CC	GG	GG	AA	TT	AA	TC	TT	TT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 23	AA	GG	TT	AA	CC	CC	TT	TT	AA	AA	AA	0	GG	TT	TT	GG	TC	GG	GG	AA	TT	CC	TT	TT	CT	GG	CC	TT	GG	GA	TT	AA	CT
VSE 24	AA	GG	TT	AG	CC	CC	TT	TT	AA	GA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	CC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 25	AA	AG	CT	AG	TC	CC	TT	TT	TA	GA	AG	TC	GG	TT	TT	GG	CC	GG	GG	GA	TT	CA	CC	TT	TT	GG	CC	CT	GA	GA	CT	AC	CT
VSE 26	AA	AG	CT	AG	CC	CC	TT	TT	AA	AA	AA	TT	GG	TT	CT	GG	TC	GG	AG	GA	TT	CA	TT	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 27	AA	GG	CT	AA	CC	CC	TT	TT	TA	GA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	0	GG	CT	TT	GG	GG	TT	AA	TT
VSE 28	AA	GG	CC	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	0	TT	GG	CC	GG	GG	AA	CT	AA	TC	TT	CC	GG	CT	TT	GG	AA	TT	AA	TT
VSE 29	AA	GG	TT	AG	TC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 3	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CT	CA	TC	TT	TT	GG	CC	TT	GG	GA	CT	AA	CC
VSE 30	AA	GG	CT	AG	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	GA	TT	CA	CC	CT	CT	GG	CT	TT	GG	GA	CT	AA	TT
VSE 31	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	CC	TT	TT	GG	CT	CT	GA	AA	TT	AA	TT
VSE_32	AA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 33	AA	GG	CT	AG	CC	TC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	CC	AA	CC	CT	CT	GG	CC	TT	GG	AA	TT	AA	TT
VSE 34	AA	GG	CT	AG	CC	CC	TT	TT	TA	GA	AA	0	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	TC	0	CT	GG	TT	TT	GG	GA	CT	AA	TT
VSE 35	AA	GG	TT	GG	TC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	CC	GG	AG	AA	CT	AA	TT	TT	CC	0	CT	TT	GG	GA	CT	AA	TT
VSE_36	AA	GG	TT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	AG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	GA	TT	AA	CT
VSE 37	AA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	CA	CC	TT	CT	GG	CC	TT	GG	GG	TT	AA	CT
VSE 38	AA	GG	TT	AA	CC	TC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	AG	GA	CC	AA	CC	TT	CT	GG	CC	TT	GG	GG	CT	AC	TT
VSE 39	AA	GG	CT	GG	TC	CC	TT	TT	TT	AA	AA	0	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	TC	TT	CT	GG	CC	TT	GG	AA	TT	AA	TT
VSE 4	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	CA	TC	TT	TT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 40	AA	GG	CT	AA	CC	TT	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	TC	TT	CC	GG	CT	TT	GG	AA	TT	AA	TT
VSE 41	AA	GG	CC	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	CC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 42	AA	GG	CC	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	CT	AA	CC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 43	AA	GG	CT	AG	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	AA	TT	AA	CT
VSE 44	AA	GG	CT	AA	CC	TC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TT	TT	TT	GG	TT	TT	GG	GA	TT	AA	TT
VSE 45	AA	GG	CC	AA	CC	TC	TT	TT	TT	GA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TC	CT	CT	GG	CT	TT	GA	AA	TT	AA	TT
VSE 46	AA	GG	CT	AG	TC	TT	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	AG	AA	CT	AA	CC	CT	CT	GG	TT	TT	GG	GA	TT	AA	TT
VSE 47	AA	GG	TT	AG	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GC	CC	GG	AG	AA	CT	AA	CC	TT	CC	GG	CC	TT	GG	GA	TT	AC	TT
VSE_48	AA	GG	CC	AG	CC	CC	TT	TT	TT	AA	AA	TC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	TT	GG	CT	TT	GG	GA	TT	AA	TT
VSE 49	AA	GG	CT	AG	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TC	TT	TT	GG	TT	TT	GG	GG	TT	AA	TT
VSE 5	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	TT	CA	TC	TT	TT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 50	AA	GG	TT	AA	CC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	TT	AA	TC	CT	TT	GG	CT	TT	GG	GA	TT	AA	TT
VSE_51	AA	GG	TT	AA	CC	CC	TT	TT	TA	AA	AA	0	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TC	CT	CT	GG	TT	TT	GG	GA	TT	AA	TT
VSE 52	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	CC	TT	CT	GG	CT	TT	GG	GA	TT	AA	TT
VSE 53	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	CT	GC	CC	GG	AG	AA	TT	AA	CC	TT	CC	GG	CC	TT	GG	GA	TT	AA	CT
VSE 54	AA	GG	CT	GG	TT	CC	TT	TT	TA	AA	AA	CC	GG	TT	CT	GG	CC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 55	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	CT	GC	CC	GG	GG	AA	CT	AA	TC	CT	CC	GG	CC	TT	GG	GG	TT	AA	TT
VSE 56	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	CT	CC	CC	GG	GG	AA	CT	AA	TC	CT	CC	0	CC	TT	GG	GG	TT	AA	TT
VSE 57	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	GA	CT	AA	TC	TT	CT	GG	CC	TT	GG	AA	TT	AA	CT
VSE 58	AA	GG	CT	GG	TC	CC	TT	TT	TT	AA	AA	0	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 59	AA	GG	TT	AG	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TC	TT	CC	GG	CT	TT	GG	AA	TT	AA	CT

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
GG	AA	TT	CC	AA	GG	CC	GG	CC	CC	TT	GG	AA	CA	TT	GG	TT	CC	AG	AG	GG	TT	CC	GG	GG	TT	AA	GG	CC	AA	AA	GG	CC	CC	TT
GG	AA	TT	CC	AA	GG	CC	GG	CC	CC	TT	GG	AA	CA	TT	GG	TT	CC	AG	AG	GG	TT	CC	GG	GG	TT	AA	GG	CC	AA	AA	GG	CC	CC	TT
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GG	TA	TT	TC	AA	AG	CC	GG	CC	CT	CT	TG	CA	CA	TT	AA	AT	CC	AA	AG	GG	TT	TC	TG	TT	TT	AA	GG	CT	AA	AA	GG	CC	CC	TT
GG	AA	TT	CC	AA	GG	CC	0	CC	CC	TT	GG	AA	AA	TT	AG	TT	CC	AA	GG	GG	TT	CC	TG	TT	TT	AA	GG	CC	AA	AA	GG	CC	CC	TT
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GG	AA	TT	CC	AA	GG	CC	GG	CC	CC	TT	GG	AA	AA	TT	GG	TT	CC	AG	AG	AG	TT	TC	TG	TG	CC	AA	GG	CC	AA	AA	TG	CC	TC	TT
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GG	AA	TT	CC	AA	GG	CC	GG	CC	CC	TT	GG	AA	AA	TT	GG	TT	CC	AG	GG	GG	TT	CC	GG	GG	TT	AA	GG	TT	AA	0	GG	0	CC	TT
GG	AA	0	CC	AA	GG	0	0	CC	0	TT	GG	0	0	0	GG	0	0	0	GG	0	0	CC	0	GG	0	AA	0	0	0	0	GG	AA	0	TT
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GG	TT	TT	CC	AA	GG	CC	GG	CC	CC	CT	TG	AA	CC	TT	GG	TT	CC	AG	GG	GG	TT	CC	GG	TG	TT	AA	GG	TT	AA	AA	GG	AA	CC	TT
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GG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	TG	AA	CA	TT	AG	TT	CC	GG	GG	AA	TT	CC	0	TT	TT	AA	GG	TT	AA	AA	TT	AA	TT	TT
AA	AA	CC	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TG	CA	TT	TT
AG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	GG	AA	AA	TT	AG	TT	TC	GG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	GA	GA	TT	CA	TT	TT
GG	AA	CC	TC	AA	GG	TT	AG	TT	TT	TT	TG	AA	AA	TT	AA	TT	CC	GG	GG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GA	GG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TC	TT	TT	GG	AA	AA	TT	AG	TT	CC	AG	GG	AA	TT	TC	GG	TT	TT	AA	AG	TT	AA	AA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	TC	GG	TT	TT	AA	AG	TT	AA	AA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TC	TT	TT	GG	AA	CA	TT	AA	TT	CC	GG	GG	AA	TT	TC	GG	TT	TT	AA	GG	TT	AA	AA	GG	AA	TT	TT
AG	AA	CC	CC	AA	GG	TT	GG	0	TT	TT	TG	AA	AA	TT	AG	TT	CC	GG	GG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TC	AG	TT	TT	TT	TG	AA	AA	TT	AA	TT	CC	GG	AG	AA	TT	CC	GG	TT	TT	AA	GG	TT	GA	GA	TG	CC	TC	TT
AG	AA	CC	CC	AA	GG	CC	AG	TT	TT	TT	GG	AA	CA	TT	AA	TT	CC	GG	AA	AG	TT	CC	GG	TT	TT	AA	GG	TT	GA	GA	TT	CA	TT	TT
GG	AA	CC	CC	CA	GG	TT	AG	TT	TT	TT	TG	AA	AA	TT	AA	TT	CC	GG	GG	AG	TT	CC	GG	TT	TT	AA	GG	CT	GA	GA	TT	CA	TT	TT
AG	AA	CC	CC	AA	GG	TT	AG	TT	TT	TT	GG	AA	CA	TT	AA	TT	CC	AG	GG	AA	CC	CC	GG	TT	TT	AA	GG	TT	AA	GG	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TC	TT	TT	GG	AA	CA	TT	AG	TT	CC	AG	GG	AG	CT	CC	GG	TT	TT	AA	GG	TT	AA	GG	TT	CC	TT	TT
AG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	GG	AA	AA	TT	AG	TT	TC	AG	GG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GG	TG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	GG	TT	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TT	AA	TT	TT
GG	AA	CC	TC	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	CC	TC	TG	TT	TT	AA	AG	CT	GG	AA	TG	CC	TT	TT
GG	AA	CC	CC	AA	GG	TC	AG	TC	TT	CT	GG	CA	CA	TT	AG	TT	CC	AG	GG	AG	CT	TC	TT	TT	TT	AA	GG	CT	GG	GA	TG	CC	TT	TT
GG	AA	CC	CC	AA	GG	TT	AA	TT	TT	CT	GG	CA	CA	TT	AG	TT	CC	AG	GG	AG	CC	TC	TG	TT	TT	AA	GG	CT	GA	GA	TG	CA	TT	TT
AG	AA	CC	CC	AA	GG	TC	AG	TC	TT	TT	GG	AA	AA	TT	AG	TT	CC	AG	GG	AA	CT	CC	GG	TT	CT	AA	GG	CT	GA	GA	TG	CA	TC	TT
GG	AA	CC	TC	AA	GG	TT	AG	TC	TT	TT	GG	AA	AA	TT	AG	TT	CC	AG	GG	AA	CT	CC	0	TT	CT	AA	GG	CT	0	AA	TT	CA	TC	TT
GG	AA	CC	CC	AA	GG	0	GG	TC	TT	CT	GG	CA	CA	TT	AG	TT	CC	AG	GG	AA	CT	CC	GG	TG	TT	AA	GG	TT	GA	GA	GG	CA	TC	TT
AG	AA	CC	TC	AA	GG	TT	AG	TC	CT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	AA	GG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TT	TT	TT	TG	AA	CA	TT	AG	TT	CC	AG	GG	AA	CT	CC	0	TT	TT	AA	GG	TT	AA	AA	TT	CC	TT	TT

chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	AA	GG	GT	TT	GG	GG	GG	GG	GG	AA	GT	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	AA	GG	GT	TT	GG	GG	GG	GG	GG	AA	GT	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	AA	GG	GT	TT	GG	GG	GG	GG	GG	AA	GT	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AG	CA	GT	GT	GG	GG	AG	AA	GG	GA	AA	GG	AA	TT	CC	TT	CT	CC	CC	CT	TG	TC	AT	AA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	TT	TT	GG	GG	GG	GA	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	TT	TG	TC	AA	GA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	TT	TT	GG	GG	GG	GG	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	AT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AG	AA	GG	TT	TT	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	CC	GG	TT	AA	AA	GG
TT	AG	AA	AA	GG	AA	TT	CC	TT	AG	AA	GG	TT	TT	AG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	CT	GG	TT	AT	AA	GG
TT	AG	AA	AA	GG	AA	TT	CC	TT	AG	AA	GG	TT	TT	AG	GG	GG	AA	GG	AA	GG	AA	TT	TC	TT	CC	CC	CC	CT	GG	TT	AA	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	0	GG	GG	TT	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	0	GG	GG	TT	GG	GG	GG	AA	GG	AA	GT	AA	TT	CC	TT	CC	CC	CC	TT	GG	0	TT	AA	GG
TT	AG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GG	TT	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
0	GG	AA	AA	GG	TT	TT	CC	TT	AA	AA	GG	GG	0	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	TT	TT	CC	TT	GG	TT	TT	AA	GG
0	GG	AA	AA	GG	TT	TT	CC	TT	AA	0	GG	GG	TT	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CT	TT	CC	TT	GG	TT	TT	AA	GG
0	GG	AA	AA	GG	TT	TT	CC	TT	AA	AA	GG	GG	TT	GG	GG	GG	AA	GG	AA	GG	AA	TT	CC	TT	CT	TT	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GG	AA	GG	AA	TT	CC	TT	CT	CC	CC	TT	GG	TT	AT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	AG	GG	GG	GA	AA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GG	TT	GG	GG	GG	0	GG	AA	GG	AA	TT	CC	TT	CC	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	0	GG	AA	TT	0	TT	0	AA	GG	GT	TT	GG	GG	GG	0	GG	AA	GT	AA	TT	TC	TT	CC	CC	CC	0	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	AG	GG	GG	GA	GA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
0	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	AA	GA	AA	GT	AA	TT	CC	GT	TT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GG	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	TT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	AG	GG	GG	GA	AA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GG	TT	GG	GG	GG	0	GG	AA	GG	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	0	GG	AA	TT	0	TT	0	AA	GG	GT	TT	GG	GG	GG	0	GG	AA	GT	AA	TT	TC	TT	CC	CC	CC	0	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	AA	AA	GG	GT	TT	AG	GG	GG	GA	AA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	GG	TT	TT	AA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AA	AA	GG	GT	TT	GG	GG	GG	GA	GA	AA	GT	AA	TT	CC	GT	CT	CC	TC	TT	GG	TT	TT	AA	GG
0	GG	AA	AA	0	0	TT	CC	TT	AA	0	GG	GG	0	GG	GG	GG	GA	GG	AA	GG	AA	TT	CC	TT	TT	0	0	TT	0	0	0	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	GA	AA	AA	AA	GT	AA	TT	CC	TT	CC	CC	CC	TT	TG	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CA	TT	TT	TT	AG	AG	AA	AA	GA	AA	TT	AA	TT	CC	GT	CT	CC	CC	TT	TG	CC	TT	GA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	AG	AG	AA	AA	AA	AA	GT	AA	TT	CC	GT	CT	CC	CC	TT	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	GT	GT	AG	AG	GA	AA	GA	AA	TT	AA	TT	CC	GT	CT	CC	CC	TT	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	GG	GT	TT	AG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	GA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	GG	GT	TT	AG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	GA	GG
TT	GG	AA	AA	TG	AA	TA	CC	TT	GG	CC	TT	TT	TT	AG	GG	GA	GA	GA	AA	GT	AA	TT	CC	TT	TT	CC	CC	CT	GG	TT	AT	GA	GG
TT	GG	AA	AA	TG	TA	TT	CC	TT	GG	CC	GG	GT	GG	AG	GG	GA	GA	GA	AA	GT	AA	TT	CC	TT	CT	CC	CC	CC	GG	TC	AT	GA	GG
CT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	GT	AA	GG	AA	AA	GA	AA	TT	AA	TT	CC	TT	CT	CC	CC	CC	TT	TG	CC	TT	GA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	GG	CC	TT	GT	GT	AA	AA	AA	AA	GA	AA	GT	AA	TT	CC	GG	TT	CC	CC	TT	TG	CC	TT	GA	GG
TT	GG	AA	AA	TG	AA	TA	TC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	GT	GT	AG	GG	AA	GA	GA	AA	GG	AA	TT	CC	TT	CT	CC	CC	CC	TG	CC	AT	AA	AA
TT	AG	AA	GA	GG	AA	TT	CC	TT	GG	CC	TT	TT	GG	GG	GG	AA	AA	AA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	TT	CC	TT	AA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	AA	AA	GT	AA	TT	TC	TT	TT	CC	CC	CT	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	TT	TT	CC	TT	GA	AG
TT	AA	TA	GA	TG	AA	AA	CC	TT	GG	CC	TT	TT	GG	GG	AG	GA	GA	AA	GA	GT	AA	TT	CC	TT	CC	CC	TC	CC	TG	TC	TT	GG	AA
TT	GG	AA	AA	TT	AA	AA	CC	TT	AG	AA	GT	GG	GG	AG	GG	AA	GA	GA	AA	GT	AA	TT	CC	TT	CC	CC	CC	CT	TG	TT	AT	GG	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	0	TT	TT	TT	GG	GG	AA	GG	GG	AA	0	AA	TT	CC	TT	CT	CC	CC	TT	TT	CC	0	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	GA	GG
TT	GG	AA	AA	TG	AA	TT	CC	CT	GG	CC	TT	TT	GT	GG	GG	AA	AA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CC	TG	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	GT	GT	AG	AG	GA	AA	GA	AA	GT	AA	TT	CC	GT	CT	CC	CC	TT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	TT	AG	GG	AA	GA	AA	AA	GT	AA	CT	TC	TT	TT	CC	CC	CT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	AG	AA	AA	GG	AA	GG	AA	TT	CC	GT	CT	CC	CC	TT	TG	CC	AT	AA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	AA	TT	TT	TT	GG	GG	AA	AA	GG	AA	GG	AA	TT	CC	GT	CT	CC	CC	CT	TG	CC	AT	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	GG	GA	AA	GT	AA	CT	CC	TT	TT	CC	CC	0	TG	CC	TT	AA	GG
CT	GG	AA	AA	GG	AA	TT	CC	CT	AG	CA	GT	TT	TT	GG	GG	AA	AA	AA	AA	TT	AA	TT	CC	TT	TT	CC	CC	0	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	CT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GA	AA	GT	AA	TT	CC	TT	CT	CC	CC	TT	TG	CC	TT	AA	GG
CT	GG	AA	AA	TG	AA	TT	CC	TT	GG	AA	TT	TT	TT	AG	GG	AA	AA	AA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TT	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	AA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	GA	GA	AA	GT	AA	TT	CC	TT	TT	CC	CC	CC	TT	CC	TT	GA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GG	AA	GT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	AA	AG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	AG	AG	GA	AA	GA	AA	GG	AA	TT	CC	GT	CT	CC	CC	TT	TT	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CC	TT	TT	GT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	TT	TT	CC	TT	GA	AG
TT	GG	AA	AA	TT	AA	TT	CC	TT	GG	CC	TT	TT	GG	AG	GG	AA	AA	GA	AA	GG	AA	TT	CC	TT	TT	CC	CC	TT	TG	CC	TT	AA	GG
TT	GG	AA	GA	TG	AA	TT	TC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GA	GA	GG	AA	TT	CC	GT	TT	CC	CC	CC	TG	CC	TT	GA	AG
TT	GG	AA	GA	GG	AA	TT	CC	TT	GG	CA	TT	TT	GT	GG	GG	AA	GA	GA	GA	GT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	GA	AA
TT	GG	AA	GA	TT	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GA	GA	GG	AA	TT	CC	TT	TT	CC	CC	CC	TG	CC	TT	AA	AG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	GT	GG	GG	AA	GA	GA	AA	GG	AA	TT	CC	TT	CT	CC	CC	TT	TT	CC	TT	AA	AG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GG	AA	GG	AA	TT	CC	TT	CT	0	CC	TT	TT	CC	TT	GA	AG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	AA	AA	GA	GA	GG	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	GA	AG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CA	TT	TT	TT	GG	GG	GG	GG	GA	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TT	CC	TT	GG	CA	TT	TT	TT	AG	GG	AA	AA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	GA	GG

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
VSE 6	AA	GG	TT	AG	TC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	TC	TT	TT	GG	CC	TT	GG	AA	TT	AA	TT
VSE 60	AA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GC	TC	GG	GG	GA	TT	CA	CC	CT	CC	GG	CC	TT	GG	GG	CT	AA	CT
VSE 61	GA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GC	TC	GG	GG	GA	CT	CA	CC	CT	CC	GG	TT	TT	GG	GA	CT	AA	CT
VSE 62	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	CC	CT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE 63	AA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	CC	TT	CT	GG	CC	TT	GG	GA	TT	AA	TT
VSE_64	AA	GG	CC	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	CC	TT	TT	GG	CC	TT	GG	GG	TT	AA	CT
VSE 65	AA	GG	TT	AG	CC	CC	TT	TT	TA	AA	AA	0	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	TC	TT	TT	GG	CC	TT	GG	GG	TT	AA	TT
VSE 66	AA	GG	CT	AA	CC	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	CC	TT	CT	GG	CC	TT	GG	GG	TT	AA	CT
VSE 67	AA	GG	CT	AA	CC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	TC	CT	CT	GG	CC	TT	GG	GG	TT	AA	TT
VSE_68	AA	GG	CT	AG	TC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	TT	GG	CC	TT	GG	AA	TT	AA	CT
VSE 69	AA	GG	CT	AA	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	0	0	GG	GG	AA	TT	AA	TT	TT	TT	0	CC	TT	GG	GG	TT	AA	TT
VSE 7	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	TT	AA	TC	TT	TT	GG	CC	TT	GG	AA	TT	AA	CT
VSE 70	AA	GG	CC	AA	CC	TC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CC	TT	GG	AA	TT	AA	TT
VSE 71	AA	GG	CC	AG	TC	CC	TT	TT	TA	AA	AG	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TC	TT	CT	GG	CT	TT	GG	AA	TT	AA	CT
VSE 72	AA	GG	CT	AA	CC	CC	CT	TT	TT	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	CC	GG	CT	TT	GG	0	TT	AA	TT
VSE 73	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	AT	TT	GG	CC	GG	GG	AA	CT	AA	TT	TT	CC	GG	CC	TT	GG	GA	TT	AA	TT
VSE 74	AA	GG	TT	AG	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CC	AA	TT	CT	TT	GG	CT	TT	GG	GA	TT	AA	CT
VSE 75	AA	GG	TT	GG	TC	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	AA	TT	TT	CC	GG	CC	TT	GG	AA	TT	AA	TT
VSE 76	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	TT	TT	CC	GG	CC	TT	GG	GA	TT	AA	TT
VSE 77	AA	GG	CT	AG	TC	TC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	AA	TT	TT	TT	GG	CT	TT	GG	AA	TT	AA	TT
VSE 78	AA	GG	TT	AA	CC	TC	TT	TT	AA	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	TT	AA	TT	TT	TT	GG	TT	TT	GG	AA	TT	AA	TT
VSE 79	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	0	GG	TT	TT	GG	TT	GG	GG	AA	CT	AA	TC	TT	TT	GG	CT	TT	GG	GA	TT	AA	TT
VSE 8	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TT	GG	GG	AA	CT	CA	TC	TT	TT	GG	CC	TT	GG	AA	CT	AA	TT
VSE 80	AA	GG	TT	GG	TT	CC	TT	TT	TA	AA	AG	0	GG	TT	TT	GG	CC	GG	GG	AA	CT	AA	TT	TT	CT	GG	TT	TT	GG	GA	TT	AA	TT
VSE 81	AA	GG	TT	AA	TC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	CC	GG	GG	AA	TT	CA	CC	CT	CC	GG	CT	TT	GG	AA	TT	AA	TT
VSE 82	AA	GG	TT	AG	CC	CC	TT	TT	TA	AA	AA	CC	GG	TT	TT	GG	0	GG	AG	AA	CT	CC	TT	TT	TT	GG	CT	TT	GG	GA	TT	AA	CT
VSE_83	AA	GG	CT	AA	CC	CC	TT	TT	TA	AA	AA	TC	GG	TT	TT	0	0	GG	GG	AA	CT	CC	TT	TT	CT	0	CT	TT	GG	GA	TT	AA	TT
VSE 84	AA	GG	CT	AA	0	CC	TT	TT	AA	AA	AA	CC	GG	TT	TT	0	TT	GG	GG	GA	CC	AA	CC	CT	TT	0	TT	TT	GG	AA	TT	AA	TT
VSE 9	AA	GG	TT	GG	TT	CC	TT	TT	TT	AA	AA	CC	GG	TT	TT	GG	TC	GG	GG	AA	CT	CA	TC	TT	TT	GG	CC	TT	GG	GA	CT	AA	CT
VSM 1	GA	AG	CT	AG	TT	TT	CC	TT	TA	AA	AG	CC	GG	TT	TT	CC	TT	GG	GG	AA	CT	CA	CC	CT	TT	GG	CT	TT	GG	AA	TT	AA	TT
VSM 23	GG	AA	CT	AA	TC	TC	CC	CC	AA	GA	AG	CC	GG	TT	TT	GC	CC	GG	GG	GG	CT	CA	CC	CC	CT	GG	TT	TT	GA	AA	CT	CC	CC
VSM 25	AA	AG	CT	AG	TC	CC	TT	TT	AA	GA	AG	TC	GG	TT	TT	GC	TC	GG	AG	0	CT	CA	TC	CC	TT	GG	CC	TT	AA	AA	CC	AA	CC
VSM 27	AA	AG	TT	AA	TC	TC	TT	CT	AA	GG	AA	TC	GG	TT	TT	GG	TC	GG	AG	GG	CC	CA	CC	TT	TT	GG	CC	TT	GA	AA	CC	AA	CC
VSM 28	AA	AG	CT	AA	TT	TT	TT	TT	AA	GG	AG	TT	GG	TT	TT	GC	CC	GG	AG	GA	CC	CA	TC	TT	TT	GG	CT	CT	GG	AA	CC	AA	CT
VSM 29	GA	GG	TT	AG	TT	TC	CT	CT	TA	GG	AA	TC	GG	TT	CT	GC	TC	GG	AG	GA	CC	CC	CC	CT	TT	AG	CC	TT	GA	AA	CT	AC	CT
VSM 30	AA	AG	TT	AG	TC	TC	CT	CT	AA	GA	AG	TT	GG	TT	CT	GC	CC	GG	GG	GA	CC	AA	CC	CT	TT	GG	TT	TT	AA	AA	CC	AA	CC
VSM 31	GA	GG	CT	AG	TC	TC	CT	CT	TA	AA	AA	TT	GG	TT	TT	GG	CC	GG	AA	AA	CC	AA	TC	CC	TT	GG	CC	TT	GA	AA	CC	AC	CT
VSM 32	GG	GG	CT	AA	TC	TC	TT	TT	TA	GA	AG	TT	GG	TT	CT	GG	CC	GG	AG	AA	CT	CA	TC	CT	CT	AG	CT	TT	GA	AA	CC	AC	CT
VSM 33	GG	AG	CT	AA	TC	TC	TT	TT	TA	AA	AA	TT	GG	TT	CT	GC	CC	GG	AG	AA	CT	CA	CC	CC	CT	GG	CC	TT	GA	AA	CC	AC	CT
VSM 34	GA	GG	CT	GG	TT	TC	TT	TT	AA	GA	AG	CC	GG	TT	TT	GG	CC	GG	AG	AA	GG	CC	CA	CC	TT	TT	GG	CC	CT	GG	AA	CT	AC	CT
VSM 35	GA	GG	CT	AA	TC	CC	TT	TT	AA	AA	AG	TC	GG	TT	TT	GG	CC	GG	GG	GG	CC	CC	CC	CC	CT	GG	CT	TT	GG	AA	CC	AC	CT
VSM 36	GA	GG	CT	AG	TC	CC	CT	TT	TA	GA	AA	TT	GG	TT	TT	GG	CC	GG	AG	AA	CC	CA	CC	TT	TT	GG	CC	TT	GA	GA	TT	AC	CC
VSM 37	GG	AA	CT	AG	TC	TC	CC	CT	AA	AA	AA	TT	GG	TT	TT	GG	CC	GG	AG	GA	TT	CA	CC	CT	TT	GG	CT	CT	GA	GA	TT	CC	CT
VSM_38	GA	AG	TT	AG	TC	CC	TT	TT	TA	GA	AG	TT	GG	TT	TT	GC	CC	GG	GG	GG	CT	CA	TC	CC	TT	AG	CT	CC	GG	AA	TT	AA	CT
VSM 39	AA	GG	CC	GG	TT	CC	CT	TT	AA	AA	AG	TT	GG	TT	TT	GG	TC	GG	AG	AA	CT	CC	CC	CT	CT	GG	CT	TT	GA	AA	CT	AA	CC
VSM 40	GA	GG	CC	GG	TT	CC	CC	CT	AA	GA	AG	TC	GG	TT	TT	GG	TC	GG	AG	AA	CT	CA	CC	CC	TT	GG	CT	TT	GA	AA	TT	AC	CT
VSM 41	GA	GG	CT	AA	TT	TC	CC	TT	AA	GA	AA	TT	GG	TT	TT	GC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AG	TT	TT	GA	AA	CT	AC	TT
VSM_42	GG	AG	CT	AG	TC	CC	TT	TT	TA	GA	AA	TC	GG	TT	TT	GG	CC	GG	GG	GG	CC	AA	CC	CT	TT	AG	CC	TT	GG	AA	CC	AC	CT
VSM 5	GA	GG	CT	AG	TC	TT	TT	CT	AA	AA	AG	TT	GG	TT	TT	GC	TC	GG	AG	AA	AA	CT	CC	CC	CC	TT	GG	CT	TT	GA	AA	CT	AC	CT
VSM 6	GG	AG	CT	AA	TC	TC	TT	CT	AA	GA	GG	TC	GG	TT	CT	GG	TC	GG	GG	GG	CT	CC	CC	CT	TT	AG	CC	TT	GG	AA	CT	AA	CC
VSM 7	GG	AA	CC	AG	CC	CC	CC	TT	TA	AA	GG	CC	GG	TT	CT	GG	CC	GG	AG	GA	CT	CC	CC	CT	TT	AG	CT	TT	GG	AA	CT	AA	TT
VSM 8	GA	AG	TT	AG	CC	CC	CT	TT	AA	GA	AG	TT	GG	TT	TT	GG	CC	GG	AG	AA	CC	CA	CC	CT	CT	GG	CT	CT	GA	AA	TT	AA	TT
VV 116	GA	GG	TT	GG	TC	TC	CT	TT	AA	AA	AG	TC	GA	AT	CC	CC	CC	GG	GG	GA	CC	AA	TC	CT	TT	AG	CT	CT	AA	AA	TT	AC	CT
VV 117	GA	GG	CT	GG	CC	TT	TT	CC	TA	GA	AA	CC	AA	AT	CC	CC	CC	GG	GG	AA	TT	CC	CC	CT	TT	AG	CT	TT	AA	GA	TT	AC	CT
VV 118	GA	AG	CT	AG	CC	TT	CT	TT	TA	AA	GG	TC	GA	TT	CT	CC	TC	GG	AG	GA	CT	AA	TC	CT	CT	AG	CC	CT	AA	GG	CT	AC	TT
VV 119	GA	GG	TT	AG	CC	TT	TT	CT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AA	CT	CT	AA	GA	TT	AC	CT
VV 120	GA	GG	CT	AG	CC	TT	TT	TT	AA	GA	GG	CC	AA	TT	CT	CC	CC	GG	AG	GA	CT	CA	CC	CC	TT	AA	CT	CC	AA	AA	CT	CC	TT
VV 122	GA	GG	CT	GG	TC	TC	CT	CC	AA	AA	AG	TC	GA	TT	TT	GG	TC	GG	AG	AA	CT	CC	CC	CC	TT	AA	TT	TT	AA	GA	CT	AC	CC
VV 123	GA	GG	CT	GG	CC	TT	TT	CC	TA	GA	AG	CC	AA	AT	CC	CC	CC	GG	AG	GA	CC	0	CC	CC	TT	AA	CT	CT	AA	AA	TT	CC	CC
VV 124	GA	AG	CC	GG	CC	TC	CT	CC	AA	GA	GG	TC	AA	TT	CT	CC	CC	GG	AG	GA	TT	CC	CC	CT	TT	AG	TT	CC	GA	AA	TT	CC	CT
VV_125	GG	GG	TT	AG	CC	TT	TT	TT	AA	AA	GG	CC	AA	TT	CT	CC	CC	GG	AA	AA	CT	CA	CC	CC	TT	AG	CT	TT	AA	GG	CT	CC	CC
VV 126	GG	GG	TT	GG	CC	TT	TT	CT	AA	GA	AG	TC	AA	AT	CT	GC	CC	CG	AG	AA	CT	CC	CC	CT	TT	AG	CT	TT	GA	GA	CT	AC	CT
VV 128	GA	GG	TT	AG	CC	TT	TT	CT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AA	CT	CT	AA	GA	TT	AC	CT
VV 129	GA	AG	CT	AG	TC	TC	TT	CT	AA	GA	AG	CC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CC	CC	CT	TT	AG	TT	TT	GA	AA	TT	AC	CT
VV_130	GA	GG	CT	AG	CC	TT	CT	CC	TA	GG	AG	TC	GA	TT	CT	CC	CC	GG	GG	AA	CT	AA	TC	CC	TT	AG	TT	CT	AA	GA	CC	AC	CT
VV 131	GG	AA	CT	AA	CC	TC	CT	CC	AA	GA	AG	TC	AA	TT	CC	CC	CC	GG	GG	GA	CT	0	CC	CT	TT	AG	CT	CT	GA	AA	TT	CC	CT
VV 132	AA	AG	CT	GG	CC	TT	TT	CT	TA	GA	GG	TC	GA	TT	CT	CC	CC	GG	GG	GA	CT	CA	CC	CC	TT	AA	CT	CC	AA	GA	TT	AC	TT
VV 133	GA	AG	TT	GG	CC	TC	TT	CT	TA	GG	AG	TC	GA	TT	CT	CC	TC	GG	AG	AA	CT	CA	CC	CC	TT	AG	CT	TT	AA	GG	TT	AA	CT
VV 135	GA	GG	TT	GG	CC	TC	CC	CC	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	AA	CC	AA	CC	CT	TT	AG	CT	CC	GA	GG	TT	CC	CT
VV 136	GA	AA	CC	GG	TC	TC	CC	TT	AA	GG	GG	TT	GG	TT	TT	GC	CC	GG	AG	GG	CT	CA	CC	CC	CT	GG	CT	TT	AA	AA	CC	CC	CC
VV 137	AA	GG	CT	GG	TC	TC	CT	CC	AA	GG	GG	TC	GA	TT	CT	CC	CC	GG	AG	AA	CT	CC	CC	CC	TT	AG	CC	TT	AA	AA	CT	CC	CT
VV 257	GA	GG	CT	GG	TC	TC	CT	CT	TA	GA	AG	CC	AA	AT	CT	CC	CC	GG	AG	GA	CT	CA	CC	CC	TT	AG	TT	CT	GA	GA	TT	AC	CT
VV 258	GA	AG	CT	GG	CC	CC	CC	CC	AA	GA	GG	TC	AA	TT	TT	GC	CC	GG	GG	GG	CT	CA	CC	TT	TT	AG	TT	CT	GG	AA	CT	AC	TT
VV 259	GG	AG	CC	GG	TT	CC	CT	CC	TA	GA	AA	TC	GA	TT	CT	CC	CC	GG	AA	GA	TT	CC	CC	CT	TT	AG	TT	TT	GA	GA	CT	AC	CT
VV 260	GA	AG	CT	GG	CC	TC	CC	CC	AA	GA	AG	TC	GA	TT	CT	GC	CC	CG	AA	GG	CT	CA	CC	TT	TT	AG	TT	CT	GG	GG	CT	CC	CT
VV 261	GG	AG	CT	GG	CC	TC	CT	CT	AA	AA	GG	CC	AA	TT	CT	GC	TC	CG	GG	GG	CT	CA	CC	CT	TT	GG	CT	CT	GA	AA	TT	AC	TT
VV 262	GA	AG	CT	GG	CC	TC	CT	CT	AA	GA	AG	TC	GA	AT	CC	GC	TC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GA	GA	CT	AC	CT
VV 263	GA	AG	CT	GG	CC	TC	CT	CC	AA	GA	GG	TC	AA	TT	CT	CC	CC	GG	AG	GA	TT	CC	CC	CT	TT	AG	TT	CC	GA	AA	TT	CC	CT
VV 264	GA	AG	CT	GG	CC	TC	CT	CC	AA	GA	GG	TC	AA	TT	CT	CC	CC	GG	AG	AA	TT	CC	CC	CT	TT	AG	TT	CC	GA	AA	TT	CC	CT
VV 265	GG	AG	CT	GG	TC	TC	TT	CC	TA	GA	AA	CC	AA	TT	CT	GC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AG	TT	CT	GA	AA	CT	AC	CT
VV 266	GG	AG	CT	GG	CC	CC	CC	CC	AA	GA	GG	TC	AA	TT	TT	CC	CC	GG	AG	GG	CT	CA	CC	CT	TT	AG	TT	CT	GG	AA	CT	AC	TT
VV_267	GA	GG	CT	GG	TC	TC	CT	CT	AA	0	GG	TC	AA	AT	CT	GG	CC	GG	AG	GA	CT	CA	CC	CC	TT	AA	CT	TT	GA	AA	CT	CC	CT
VV 268	GA	AG	CC	GG	TC	TC	CT	CT	TA	GA	GG	TC	GA	TT	TT	GC	CC	GG	AG	GG	CC	AA	CC	CT	TT	AG	CT	CT	GA	GA	CT	CC	CT
VV 269	GG	AG	CT	GG	CC	TT	CT	CT	AA	GG	GG	CC	AA	AA	CC	CC	CC	CG	AA	GA	CT	AA	CC	CC	TT	AG	CT	CT	GA	AA	TT	AC	CT
VV 270	GA	AG	CT	AG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	GG	TT	CC	CC	CT	TT	GG	TT	CT	GG	AA	CT	AC	CT
VV 271	GG	GG	CT	AG	CC	TT	TT	CT	TA	GA	GG	CC	AA	AT	CC	CC	CC	GG	AG	GG	CT	CC	CC	CC	TT	AG	TT	CT	AA	AA	CT	CC	CC
VV 272	GA	GG	CT	GG	CC	TT	TT	CT	TA	GG	GG	CC	AA	AT	CC	GC	CC	GG	AG	GA	CT	CC	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	TT
VV 273	GG	AA	CC	GG	CC	CC	CT	CT	AA	GA	GG	TC	AA	TT	TT	GC	CC	GG	GG	GG	TT	CA	TC	CC	TT	GG	CT	CC	GA	GA	CT	CC	TT
VV 274	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	GA	TT	AC	CT
VV 275	GG	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	CC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CC	CC	CT	TT	AG	TT	CT	GA	AA	TT	AC	TT

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
AG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	TG	AA	AA	TT	AG	TT	TC	GG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	AG	AG	TT	TC	GG	TT	TT	AA	AG	TT	AA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	TG	AA	AA	TT	AA	TT	CC	GG	AG	AA	TT	TT	0	TT	TT	AA	AG	TT	AA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	AG	AA	TT	CC	GG	TT	TT	AA	GG	TT	GA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	GG	AA	CT	TC	GG	TT	TT	AA	GG	TT	AA	AA	TT	CC	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	TC	GG	TT	TT	AA	AG	TT	AA	AA	TT	CA	TT	TT
AG	AA	CC	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	CA	TT	AG	TT	CC	AA	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	AA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	GG	AA	CA	TT	GG	TT	CC	AG	GG	AA	TT	CC	0	TT	TT	AA	GG	TT	AA	AA	TG	CC	TT	TT
AG	AA	CT	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	AG	AG	TT	CC	GG	TT	TT	AA	GG	TT	AA	AA	TG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	GG	AA	CT	CC	GG	TT	TT	AA	AG	TT	AA	GG	TG	CA	TT	TT
AG	AA	CC	0	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	GG	AA	CT	0	0	TT	TT	AA	GG	TT	AA	0	TT	CC	TT	TT
AG	AA	CC	CC	AA	GG	TT	GG	TT	TT	TT	GG	AA	AA	TT	AG	TT	TC	GG	GG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TT	AA	TT	TT
GG	AA	CC	CC	AA	GG	CC	GG	CC	TT	TT	GG	AA	CA	TT	AA	TT	CC	GG	GG	AA	TT	CC	0	TT	TT	AA	AG	TT	AA	AA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TT	GG	CC	TT	TT	TG	AA	CA	TT	GG	TT	CC	GG	AG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TT	AA	TT	TT
GG	AA	0	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	CA	TT	AG	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	0	TT	AA	AA	TG	CC	TT	TT
GG	AA	CC	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TG	CA	TT	TT
AG	TA	CC	CC	AA	GG	TT	GG	TC	TT	TT	GG	AA	CC	TT	AA	TT	CC	GG	GG	AA	CT	CC	GG	TT	CT	AA	GG	TT	AA	GA	GG	AA	TT	TT
AG	AA	CC	CC	AA	GG	TT	AG	TC	TT	TT	GG	AA	CA	TT	AA	TT	CC	AG	GG	AA	TT	CC	GG	TT	TT	AA	AG	TT	AA	AA	GG	AA	TT	TT
GG	AA	CC	CC	AA	GG	TT	AA	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	GG	AA	CT	CC	GG	TT	TT	AA	GG	TT	AA	GA	TT	AA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	AG	AG	AA	TT	CC	TT	TT	TT	AA	GG	TT	GA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TT	TT	TT	GG	AA	AA	TT	AA	TT	CC	GG	GG	AA	CT	CC	TG	TT	TT	AA	GG	TT	AA	AA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	CC	GG	TT	TT	TT	TG	AA	AA	TT	AA	TT	CC	AG	GG	AA	CT	CC	0	TT	TT	AA	AG	TT	GA	GG	TG	CC	TT	TT
AG	AA	CC	CC	AA	AA	TT	GG	TC	TT	CC	TG	AA	AA	CT	AA	TT	CC	GG	AG	AA	CT	CC	GG	TT	TT	AA	GG	TT	GA	GA	TG	CC	TC	TT
GG	AA	CC	TC	AA	AG	TT	GG	CC	CT	TT	GG	CA	CA	CT	AG	AA	TT	AG	GG	AG	CC	TT	TG	TG	TT	CA	GG	TT	GG	AA	GG	CA	TC	TT
GG	AA	CC	TT	AA	AA	CC	GG	CC	TT	CT	TG	AA	CA	CT	AG	TT	TC	AA	GG	AA	CT	TT	TG	TT	CC	CA	GG	CT	GA	GA	GG	CC	TT	TT
0	AA	CC	TC	AA	AG	TC	AG	TC	CT	CT	GG	CA	AA	CT	AG	TT	TC	GG	GG	AG	CT	TC	GG	TG	TT	CA	GG	TT	GA	AA	GG	CC	CC	TT
GG	AA	CC	CC	AA	AG	TT	AG	CC	CT	CT	GG	CA	AA	TT	AA	TT	CC	GG	GG	AA	CT	TT	GG	TT	TT	AA	GG	TT	AA	AA	GG	CC	CC	TT
GG	AA	CC	CC	AA	AA	CC	AG	TC	TT	CT	GG	CA	AA	TT	AG	TT	CC	GG	GG	AG	CT	CC	GG	TG	CT	CA	GG	CT	GA	AA	GG	CC	TC	CT
GG	AA	CT	CC	AA	GG	TC	GG	TC	TT	TT	TG	AA	AA	TT	GG	TT	CC	AG	GG	AG	CT	TC	GG	TG	CT	CA	GG	CT	GA	GA	TG	CC	TT	TT
GG	AA	CC	CC	AA	AG	CC	GG	CC	TT	CT	TT	AA	AA	CT	AG	AT	TC	GG	GG	AA	TT	TC	GG	GG	CT	AA	GG	CT	GA	AA	GG	CA	TT	TT
GG	AA	CC	CC	AA	GG	CC	GG	TC	TT	TT	GG	CA	CA	TT	GG	AT	CC	GG	GG	GG	CC	TT	TG	TT	TT	CA	GG	CT	GA	AA	GG	CC	TT	TT
AG	AA	CC	CC	AA	GG	TC	GG	CC	TT	CT	GG	CA	AA	CT	AG	TT	TC	GG	GG	AG	CC	TT	TT	TT	CT	AA	GG	TT	GA	AA	GG	CA	TC	TT
GG	AA	CC	CC	AA	GG	TC	GG	CC	TT	CC	TT	CC	CA	CC	AG	AT	CC	AG	AG	AA	CT	CC	TT	TT	CC	CC	GG	CT	AA	GA	TG	CA	TT	TT
GG	AA	CC	CC	AA	GG	TC	GG	TC	TT	CT	GG	CA	AA	CT	GG	AA	TC	AG	AG	AA	CT	CC	GG	TG	CC	CA	GG	CT	GA	AA	TG	CA	TC	TT
GG	TA	CT	CC	AA	GG	TC	GG	TC	TT	CT	TT	AA	CA	TT	GG	TT	CC	GG	GG	AA	CC	TT	GG	TT	TT	AA	GG	CT	GA	AA	GG	CC	CC	TT
GG	AA	CC	CC	AA	GG	TT	GG	CC	CT	TT	GG	AA	AA	CT	AA	TT	TC	GG	GG	AA	CC	TT	GG	TG	CT	AA	GG	CT	GA	AA	GG	CA	CC	TT
AA	AA	CC	TC	AA	AG	TC	GG	CC	TT	CC	TT	AA	CA	CC	AG	TT	TC	GG	GG	AG	CC	TC	TG	TG	CT	CA	GG	TT	GA	GA	TG	CC	TC	TT
GG	TA	CC	CC	AA	AG	TC	GG	CC	CT	TT	GG	CC	AA	CT	AA	AT	CC	GG	GG	AG	CT	TT	TG	TG	CT	CA	GG	CT	GG	AA	GG	CC	CC	TT
GG	AA	CC	CC	AA	GG	CC	GG	CC	CT	CC	TG	AA	CA	TT	AG	AT	TC	GG	GG	AG	AA	CT	TG	GG	CT	CA	GG	TT	GA	GA	GG	CC	TT	TT
GG	TA	CC	CC	AA	AG	CC	GG	TC	TT	CC	TG	CA	AA	TT	GG	AT	CC	AG	GG	AA	CT	TT	TT	TG	CT	CC	AG	CT	GA	AA	GG	CC	TT	TT
AG	TA	CC	TC	AA	AG	CC	GG	TC	TT	CC	TT	0	AA	TT	GG	AA	TC	AA	AG	AA	CC	TT	GG	GG	CC	CA	AA	TT	GA	AA	TG	CA	TC	TT
AG	TT	CT	TC	AA	AA	CC	AA	TC	CT	TT	TT	0	AA	TT	GG	AA	TC	AA	AG	AA	CC	TT	GG	GG	CC	CA	AA	TT	GA	AA	TG	CA	TC	TT
AG	TA	CC	TC	AA	GG	TT	AG	CC	CT	CT	TG	AA	CA	CC	GG	AT	TC	AA	AA	AG	CT	CC	GG	TG	CC	CA	AG	CT	GA	AA	GG	AA	TT	TT
GG	TT	TT	CC	AA	AA	CC	AG	TC	CT	CT	TT	CA	AA	CT	AG	AT	CC	AA	GG	AG	CC	TT	TT	TG	CC	CA	AG	TT	GG	AA	TG	AA	TC	TT
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GG	TA	CT	CC	AA	AG	TC	AA	TC	TT	CT	TG	AA	AA	CT	AG	AT	TC	AG	AG	GG	CT	TT	GG	GG	CC	CA	AG	CT	GA	AA	GG	CA	TC	TT
GG	TA	TT	TC	AA	AG	CC	AG	TC	CT	CT	TG	CA	CA	CC	AA	AT	TC	AG	GG	AG	CC	TC	TG	TG	CT	CA	AG	TT	GA	AA	TG	AA	CC	TT
GG	TT	TT	CC	AA	AA	CC	AG	TC	CT	CT	TT	CA	AA	CT	AG	AT	CC	AA	GG	AG	CC	TT	TT	TG	CC	CA	AG	TT	GG	AA	TG	AA	TC	TT
GG	TA	TT	CC	AA	AA	CC	AG	TC	CT	TT	TG	CA	CA	CT	AG	AT	TC	AA	GG	GG	CC	TC	TG	TG	CT	CA	GG	TT	GA	AA	TG	AA	TC	TT
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GG	TT	TT	CC	AA	AG	CC	AG	TC	CT	CT	TG	AA	CA	CT	AG	AT	CC	AG	GG	GG	CT	TT	TT	TT	CT	AA	GG	CT	GA	AA	GG	AA	CC	TT
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GG	TA	TT	TC	AA	AG	CC	AA	TC	CC	TT	GG	CC	AA	CC	AA	AT	TC	AG	AG	AG	CT	TC	TT	TT	TG	CT	CA	AG	TT	GA	AA	TG	CC	TT
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GG	TT	TT	CC	AA	AG	CC	GG	CC	CT	CT	TG	AA	CA	CT	AG	AT	CC	AA	GG	AG	CT	TC	TG	TG	CT	CA	AG	CT	AA	GA	GG	AA	CC	TT
GG	TA	CT	CC	AA	AG	CC	GG	CC	CC	TT	GG	CA	CA	CC	AG	AT	TC	AA	GG	AG	CC	TC	TG	TG	CT	CA	AG	TT	GA	AA	TG	AA	CC	TT
GG	TA	CT	TC	AA	AG	CC	GG	CC	CT	TT	GG	CA	CA	CT	AG	AT	TC	AG	GG	AG	CT	TC	TT	TG	CT	CA	AG	TT	GA	AA	TG	AA	TC	TT
GG	TT	TT	CC	AA	AG	CC	AG	TT	CC	TT	TG	AA	CA	TT	GG	TT	CC	AA	GG	AG	CT	TC	TG	TG	CT	AA	AG	TT	GA	AA	TG	AA	TC	TT
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GG	TT	TT	TT	AA	GG	CC	AG	TC	CT	TT	GG	CA	CA	CC	AG	AA	CC	AA	AG	GG	CT	TC	TT	TG	CC	CC	AG	TT	GA	0	TT	CA	CC	TT
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GG	TA	TT	TC	AA	GG	CC	GG	CC	CT	TT	GG	CA	CA	CT	AG	AT	TC	AG	GG	AG	CT	TC	TG	TG	CT	CC	AG	TT	GA	GA	TG	CA	CC	TT

chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
TT	GG	AA	AA	GG	AA	TA	CC	TT	GG	CC	TT	TT	TT	AG	AG	GA	AA	AA	AA	GG	AA	TT	CC	GT	CT	CC	CC	TT	TG	CC	TT	GA	GG
TT	GG	AA	AA	TT	AA	TA	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	AA	AG
TT	GG	AA	AA	TT	AA	TA	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GG	AA	GT	AA	TT	CC	TT	TT	CC	CC	TT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TA	TC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TT	CC	TT	AA	GG
TT	GG	AA	AA	TT	AA	TA	TC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	AA	AA	TT	AA	CT	TC	TT	TT	CC	CC	CT	TG	CC	TT	AA	AG
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TT	GG	AA	AA	0	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	AA	GG	AA	TT	AA	TT	CC	TT	TT	CC	CC	TT	TT	CC	TT	AA	GG
TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	0	TT	TT	TT	GG	GG	AA	GA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	AA	GG
TT	GG	AA	AA	TG	AA	TA	TC	TT	GG	CA	TT	TT	TT	AG	GG	AA	AA	GA	AA	TT	AA	CT	TC	TT	TT	CC	CC	TT	TG	CC	TT	AA	GG
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TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	AA	TT	TT	TT	GG	AG	AA	AA	AA	AA	GT	AA	TT	CC	TT	TT	CC	CC	CC	TT	CC	TT	AA	AG
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TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	AA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CT	TG	CC	TT	AA	GG
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TT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	AA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CC	TG	CC	TT	GA	GG
CT	GG	AA	AA	GG	AA	TT	CC	TT	GG	CC	TT	TT	TT	GG	GG	AA	GA	GA	AA	TT	AA	TT	CC	TT	TT	CC	CC	CC	TG	CC	TT	AA	GG
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CT	AA	AA	AA	TT	AA	TA	CC	CT	AG	CA	GT	GG	GT	GG	AG	GA	GA	GG	AA	GG	AA	TT	CC	GT	TT	CC	CC	CT	TT	TC	AT	GG	GG
CT	AA	TA	GA	TG	AA	AA	TC	CT	AG	CA	TT	GT	TT	AG	GG	GA	GA	GG	GA	TT	AA	CT	CC	GT	CT	TC	CC	TT	TT	CC	AT	GA	GG
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CT	AG	TT	AA	TT	AA	AA	CC	CT	AG	CA	GT	TT	GT	AG	GG	AA	GA	AA	AA	TT	AA	TT	TT	TT	TT	CC	CC	CT	TT	CC	AT	GA	AG
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CT	GG	AA	AA	TT	AA	AA	CC	TT	AG	AA	TT	TT	GG	AG	GG	GA	AA	GA	GG	GT	AA	TT	TT	TT	TT	CC	TC	CC	TT	TC	TT	GG	GG
CT	AA	AA	GA	GG	AA	AA	TC	CC	AG	AA	GT	GT	GG	GG	GG	GA	GA	AA	GA	GG	AA	TT	TT	TT	CC	CC	CC	CT	TT	TT	TT	GA	GG
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CT	AG	TA	GA	TG	AA	AA	TC	CC	AG	AA	GT	TT	GG	AG	AA	GG	AA	AA	GA	GT	AA	TT	TT	TT	TT	TC	TC	TC	CT	GG	TC	AT	GA	AG
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TT	AG	AA	AA	TG	AA	TA	CC	CT	AA	AA	GG	GG	GT	AA	AG	GG	0	AA	GA	GT	AA	TT	TC	TT	CT	TC	TC	TT	GG	TC	AT	AA	AG
TT	AG	TA	GG	TG	AA	AA	TT	CT	GG	AA	GT	GT	GT	AG	AG	GA	AA	AA	AA	GT	AA	TT	TT	TT	TT	TT	TT	CT	TG	CC	AT	GA	AA
CT	AG	TA	GA	TG	AA	TA	TT	CC	AA	AA	GT	TT	GT	AA	AA	GG	GG	GG	GA	GA	AA	CT	TT	GG	CC	CC	TC	CT	GG	TC	AT	GA	AG
TT	AG	TA	GA	TG	AA	AA	TT	CT	GG	AA	GG	TT	GG	AA	AG	GG	GA	AA	GA	GG	GA	CT	TC	GG	CC	CC	TC	CT	GG	TC	AT	GA	AG
CT	AG	TT	GG	GG	TT	TA	CC	TT	AA	AA	GT	GT	GG	AG	AG	GA	AA	GA	GA	GG	GA	CT	TC	GG	CT	TT	TT	TC	TT	TG	TT	AT	AA	GG
CC	GG	TA	AA	TG	AA	AA	TC	CT	AA	AA	GG	TT	GG	AG	AG	GA	AA	AA	AA	GT	AA	CT	TT	TT	TT	TC	TT	TT	TG	CC	AA	GA	AG
CT	AG	TA	AA	GG	AA	TA	TT	CT	AG	CA	TT	GT	GT	AG	AG	GA	AA	GA	AA	GG	AA	TT	TC	TT	TT	TC	TT	TT	TG	TC	AT	AA	AG
TT	AA	TA	GA	GG	AA	TA	CC	TT	AG	AA	GT	TT	GT	AG	AG	GG	0	GA	GA	GT	AA	TT	TC	GT	CC	CC	CC	TT	GG	TC	TT	AA	GG
TT	AG	AA	GA	GG	AA	TT	TC	CT	AG	CA	GT	GT	TT	GG	GG	GA	0	GA	AA	TT	AA	CT	TC	TT	CT	CC	TC	CT	TG	TC	TT	AA	AG
TT	GG	AA	GA	GG	TA	TA	TC	CT	AG	AA	GG	GT	TT	AG	GG	GA	0	GA	AA	GT	AA	TT	CC	TT	TT	TC	TC	TT	TG	TT	AT	AA	AG
CT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	GT	GT	GT	AG	GG	GA	0	GA	GA	GG	AA	TT	TC	TT	CT	TC	TC	CT	GG	TC	AT	GA	AG
CT	GG	AA	AA	TG	AA	TA	TC	CT	AG	AA	GG	GT	GT	GG	AA	GA	AA	AA	GA	GT	AA	TT	TT	TT	CT	CC	CC	CT	GG	TC	AT	GA	AG
CT	AG	AA	AA	TG	AA	TA	TT	CT	AG	AA	GT	GT	GT	GG	AG	GG	0	GA	AA	TT	AA	TT	TC	TT	CT	CC	CC	CT	GG	CC	TT	GA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AG	AA	GG	GT	TT	AG	GG	GG	0	GA	AA	GT	AA	TT	TC	GT	CC	CC	TC	TT	GG	TT	TT	AA	AG
CT	GG	TA	GA	TG	AA	AA	TT	TT	AG	AA	GT	GT	TT	AG	GG	GA	GG	AA	GA	GT	AA	TT	TC	GT	CC	CC	TC	CT	GG	TT	AT	AA	AG
TT	AG	TA	GA	GG	TA	TA	0	CT	AA	AA	TT	TT	GT	AG	AG	GA	GA	AA	AA	GT	AA	CT	TC	TT	CT	TC	TC	CT	TG	TT	TT	GA	GG
TT	AG	TA	GG	GG	TA	AA	TT	TT	AA	AA	TT	GT	GT	AA	AG	GA	GA	GA	GA	GT	AA	CT	TC	TT	CT	TT	TC	CT	TG	TT	AT	AA	GG
TT	AG	TA	GA	TG	TA	TA	TC	TT	AA	AA	GT	GT	GT	AG	GG	GA	0	GA	AA	GG	AA	TT	TC	GT	CT	TC	CC	CT	GG	TT	AT	AA	AG
CT	AG	TA	AA	TT	AA	TT	CC	CT	AA	AA	TT	GT	TT	GG	AG	GA	GG	GA	AA	TT	AA	TT	TT	TT	TT	TC	TT	TT	GG	TT	AT	GA	AG
TT	AG	TT	GA	GG	AA	AA	TT	CT	AG	AA	GT	GG	GT	AG	AG	GA	GG	GA	AA	GT	AA	TT	TC	TT	CT	TC	CC	CT	TG	TT	AT	GA	GG
CT	GG	AA	AA	TG	AA	TT	TC	TT	AG	AA	GT	GT	TT	GG	AG	GG	AA	GA	AA	GG	AA	CT	CC	GT	TT	TC	CC	TT	TG	TT	TT	AA	AG
TT	AG	TA	GA	TG	TA	AA	TT	CT	AG	AA	GT	GT	GT	AA	AG	GA	GG	GA	AA	GT	AA	CT	TC	TT	CT	TC	TC	TT	TG	TT	AT	GA	GG
TT	AG	TA	GA	TG	TA	AA	TT	CT	AG	AA	GT	GT	GT	AA	AG	GA	GA	GA	AA	GT	AA	CT	TC	TT	CT	TC	TC	CT	TT	TT	AT	GA	GG

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
VV_276	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	AG	TC	AA	AT	CC	GC	CC	CC	GG	GA	CT	CA	CC	CT	TT	AA	CT	TT	GA	AA	TT	AC	CT
VV_277	AA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CC	GG	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	TT	TT	AA	AA	CT	AC	CT
VV_278	GG	AA	CC	GG	CC	CC	CC	CC	AA	GG	AG	TC	AA	TT	TT	GC	CC	CG	GG	GG	TT	CC	CC	CT	TT	AG	TT	CT	GG	AA	TT	CC	TT
VV_279	GA	AG	CT	GG	CC	TC	CC	CC	AA	GA	GG	TC	AA	TT	CT	GC	CC	CG	GG	GA	TT	CA	CC	CT	TT	GG	TT	CC	GG	GG	CT	AC	TT
VV_280	GA	AG	CT	GG	TC	TC	CT	CT	TA	GG	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CC	CA	CC	CT	TT	GG	CT	TT	GA	AA	TT	CC	CT
VV_281	GG	AA	CC	GG	TC	CC	CC	CT	TA	GA	GG	TC	AA	TT	CT	GG	CC	GG	GG	GG	CT	CA	CC	CT	TT	AG	TT	CT	GG	AA	TT	AC	TT
VV_282	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AA	CC	GC	CC	CG	AG	GA	CT	CC	CC	CT	TT	AG	TT	CT	GA	AA	TT	AC	CT
VV_283	GA	GG	CT	AG	CC	TT	CT	CT	AA	GA	AG	TC	AA	AT	CT	CC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AG	CT	TT	AA	GA	CT	AC	CT
VV_284	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CC	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_285	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	CC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_287	GA	AG	CT	GG	TC	TC	CT	CT	TA	GG	GG	TC	AA	AA	CC	GC	CC	CG	AA	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_288	GG	AG	CT	AG	CC	TC	CT	CT	TA	GA	AG	TC	AA	TT	CT	GC	CC	GG	GG	GA	CC	CA	CC	CT	TT	GG	CT	CT	GA	AA	TT	AC	CT
VV_289	GG	AG	CT	GG	CC	TC	CC	CC	AA	GA	GG	CC	AA	TT	CC	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CC
VV_290	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_291	GA	GG	CT	GG	CC	TC	CT	CC	TA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_292	GG	AG	CT	GG	TC	TC	CC	CC	AA	GA	GG	CC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CC
VV_293	GA	AG	CT	GG	CC	TC	CC	CC	AA	GA	GG	CC	AA	TT	TT	GG	CC	GG	GG	GG	TT	CC	CC	CT	TT	AG	CT	CT	GA	GA	CC	AC	CT
VV_294	GA	AG	CC	GG	CC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	TT	GA	AA	TT	AC	CT
VV_296	GA	AG	CT	AG	CC	TC	CT	CT	AA	AA	GG	CC	AA	TT	CC	CC	CC	GG	AG	GA	TT	CC	CC	CT	TT	AA	TT	CT	AA	AA	TT	CC	CT
VV_297	GG	AA	CC	GG	TC	CC	CT	TT	TT	GA	GG	CC	AA	TT	CT	GC	CC	CG	GG	GA	TT	CC	CC	CC	TT	AA	TT	CT	GG	AA	CT	AC	TT
VV_298	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	CC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_299	GA	AG	CT	GG	CC	TT	CT	CT	TA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	AA	AA	CT	AC	CT
VV_300	GA	AG	CT	GG	TC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GA	AA	CT	AC	CT
VV_301	GA	AG	CT	AG	CC	TC	CT	CC	AA	GA	GG	TC	GA	TT	CT	GC	TC	GG	AG	GA	CC	AA	CC	TT	TT	AG	TT	CT	GA	GA	CT	CC	CT
VV_302	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CC	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	TT	AC	CT
VV_303	GG	AA	CC	GG	CC	CC	CC	CT	AA	GA	AG	CC	AA	TT	CT	GC	CC	CG	GG	GA	TT	CA	CC	CT	TT	GG	TT	CC	GG	AA	CC	AC	CT
VV_304	GA	AG	CT	GG	TC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	AA	CT	CC	CC	TT	TT	AA	TT	CT	AA	AA	CT	CC	TT
VV_305	GG	AG	CT	GG	CC	TC	CT	CC	TA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	AA	CC	CT	TT	AG	TT	CT	GA	AA	TT	AC	TT
VV_306	GA	AG	TT	GG	TT	CC	CT	CT	AA	AA	GG	CC	AA	TT	CT	CC	TC	GG	GG	AA	TT	CC	CC	CT	TT	AG	TT	TT	GA	GG	CT	CC	CT
VV_307	GA	GG	CT	GG	CC	TC	CT	TT	AA	GG	GG	CC	AA	TT	CT	GC	CC	GG	AG	GA	CT	CC	CC	CC	TT	AA	TT	CT	GA	GA	TT	AC	CC
VV_308	AA	GG	CT	GG	CC	TC	CT	TT	AA	GG	GG	CC	AA	TT	CT	GG	CC	GG	AG	GA	CC	CC	CC	CC	TT	AA	TT	CT	GA	GA	TT	AC	CC
VV_310	GG	AG	CC	GG	TC	CC	CT	CC	AA	GA	AG	TC	AA	TT	CT	GC	CC	CG	GG	GA	CT	CC	CC	CT	TT	GG	TT	CC	GG	AA	CT	CC	CC
VV_311	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	CC	CC	CG	GG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GA	AA	CT	CC	CT
VV_312	GG	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TT	AA	AT	CT	GC	CC	CG	AG	GA	CT	CC	CC	CC	TT	GG	CT	CT	AA	AA	TT	AC	CT
VV_313	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	CC	AA	AT	CT	GC	CC	GG	AG	GA	CT	AA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_314	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	TT	CC	CT
VV_315	GA	AG	CT	GG	CC	TC	CT	CC	AA	GG	GG	TC	AA	TT	CT	CC	CC	GG	AA	GA	TT	CC	CC	CT	TT	AG	TT	CC	GA	AA	TT	CC	TT
VV_316	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	0	TT	GG	CT	CT	GA	AA	CT	AC	CT
VV_318	GA	AA	0	AG	CC	CC	CT	TT	TA	GA	AG	TC	GA	AA	CC	GG	TT	GG	GG	AA	TT	CA	CC	CT	TT	GG	TT	CT	GA	GA	TT	AC	CT
VV_319	GA	AA	CC	GG	CC	TC	CT	CT	AA	AA	AG	CC	AA	TT	CC	GC	CC	CG	GG	AA	TT	AA	CC	CC	TT	AG	TT	CT	GA	GA	TT	AC	TT
VV_321	GA	GG	CT	GG	CC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_322	GG	AG	CT	GG	CC	TC	CT	CC	AA	GA	AG	CC	AA	TT	CC	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GA	AA	TT	CC	CT
VV_323	GG	GG	CT	GG	CC	CC	CC	CC	AA	GA	GG	TC	AA	TT	TT	CC	CC	GG	GG	GG	CT	CC	CC	CT	TT	AG	TT	CT	GG	AA	TT	AC	TT
VV_324	GG	GG	TT	GG	CC	TC	CT	CC	AA	GA	AG	TC	AA	TT	CT	GC	CC	GG	GG	GA	CC	AA	TC	CC	TT	AG	CT	CC	GA	GA	TT	AC	TT
VV_325	GA	AG	CC	GG	CC	TC	CC	TT	TA	GA	GG	TC	GA	AT	CC	CC	CC	GG	AG	GG	CT	CA	CC	CT	TT	AG	CT	CT	AA	AA	TT	CC	CC
VV_326	GA	AG	CT	GG	CC	TC	CT	CT	TA	GG	GG	CC	AA	TT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_328	GA	AG	CT	AG	CC	TT	CT	CT	AA	GA	AG	TC	AA	AT	CT	GC	CC	GG	AA	AA	CT	AA	CC	CC	TT	AG	TT	CT	GA	GA	CT	AC	CT
VV_329	GG	AG	0	AG	CC	TC	CT	CT	TA	GA	GG	TC	AA	TT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	GG	CT	CT	GA	AA	TT	AC	CT
VV_331	GA	AG	CC	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_332	GG	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	AA	AA	CT	AC	CT
VV_333	GG	AG	CT	GG	CC	TC	CC	CT	AA	GA	GG	TC	AA	TT	CT	GC	CC	CG	GG	GG	CC	CA	CC	CT	TT	AG	CT	CT	GA	AA	TT	CC	TT
VV_334	GG	AG	CT	GG	TC	CC	CT	CT	TA	GA	GG	TC	AA	TT	CT	GG	CC	GG	AG	GA	CT	CA	CC	CC	TT	AG	TT	TT	GA	AA	CT	AC	CT
VV_335	GG	AA	CC	GG	CC	TC	CT	CT	AA	GA	AG	TC	AA	TT	CC	GC	CC	CG	GG	GA	CT	CA	CC	CT	TT	AA	CT	CT	GA	GA	TT	AC	CT
VV_336	GG	AG	CT	GG	CC	CC	CC	CC	AA	GA	AG	CC	GA	AT	CC	CC	CC	GG	GG	GA	TT	CA	CC	CT	TT	AG	TT	CC	GG	GA	CT	CC	TT
VV_337	GG	AG	CC	GG	CC	TC	CT	CC	AA	GG	GG	CC	AA	AT	CC	GC	CC	GG	AG	GA	TT	CC	CC	TT	TT	AG	TT	CT	GA	AA	TT	AC	CT
VV_338	GA	AG	CC	GG	TC	CC	CC	CT	TA	GG	GG	TC	AA	AT	CT	GC	CC	GG	AG	GG	CT	CA	CC	CT	TT	AG	CT	CT	AA	GA	CT	AC	CT
VV_339	GG	AG	CT	GG	TC	TC	CT	CT	AA	GA	AG	TC	AA	AT	CC	GC	CC	CG	GG	GA	CT	CA	CC	TT	TT	AA	TT	TT	GA	AA	TT	AC	TT
VV_340	GG	AG	CT	GG	CC	TC	CC	CC	AA	GG	GG	CC	AA	TT	CT	CC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CC
VV_341	GG	GG	CT	GG	CC	TT	TT	CT	AA	GA	GG	CC	AA	TT	CC	CC	CC	GG	AG	GA	CT	CA	CC	CC	TT	AG	CT	TT	AA	GA	TT	AC	CT
VV_342	GG	AG	CT	GG	CC	CC	CC	CT	TA	GA	GG	TC	AA	TT	TT	GC	CC	CG	GG	AA	CC	CA	CC	CC	TT	GG	TT	CT	GG	GA	CC	AA	TT
VV_343	GA	AG	CT	AG	CC	TC	CT	CT	TA	GA	AG	TC	AA	AT	CT	CC	CC	CG	AA	AA	CT	CA	CC	CC	TT	AG	CT	CT	AA	GA	TT	AC	CT
VV_344	GA	AG	CT	GG	TC	CC	CC	CC	AA	GA	AA	TC	GA	TT	CT	GC	TT	CG	AG	GA	CT	CA	CC	TT	TT	AG	TT	CT	GG	GA	CT	AA	CT
VV_345	GA	AG	CT	GG	TC	TC	CT	CT	AA	GG	GG	TC	AA	AT	CC	GC	CC	CG	AA	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	GA	CT	AC	CT
VV_346	GG	AG	CT	GG	CC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GG	AA	TT	AC	TT
VV_347	GG	AG	CT	AG	TC	TC	CT	CT	TA	GA	GG	TC	AA	TT	TT	GC	CC	CG	GG	AA	CT	CA	CC	CT	TT	AG	TT	CC	GG	AA	CT	AC	TT
VV_349	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	TT	GA	AA	CT	AC	CT
VV_350	GA	AG	CT	GG	TC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CC	GC	CC	GG	GG	GA	CT	CC	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_351	GA	AG	CT	AG	CC	TC	CT	CT	AA	GA	GG	TC	GA	AT	CT	GC	CC	CG	GG	GA	TT	CC	CC	CT	TT	AA	TT	CC	GA	GA	CT	AC	TT
VV_352	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	GA	AT	CC	CC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_353	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	TT	AC	CT
VV_354	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	AC	CT
VV_355	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AG	TT	TT	AA	AA	CT	AC	CT
VV_356	GG	AA	CT	AG	TC	TC	CC	CC	AA	GG	GG	TC	AA	TT	CT	CC	CC	GG	GG	GA	CT	CC	CC	CT	TT	GG	TT	CC	GG	AA	CT	AC	TT
VV_357	GA	AA	CT	GG	CC	CC	CT	CT	AA	GA	GG	TT	GA	TT	TT	GC	CC	GG	0	GA	TT	CA	CC	CT	TT	GG	CT	CT	GG	GA	TT	AA	CT
VV_358	GA	AG	CT	GG	CC	TC	CT	CT	TA	GG	GG	CC	AA	AT	CT	GC	CC	GG	GG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_359	GG	AG	CC	GG	CC	TC	TT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CT
VV_360	GG	AG	CT	AG	CC	TC	CT	CT	AA	GA	AG	TC	AA	TT	CT	GC	CC	GG	GG	AA	TT	CC	CC	CT	TT	AG	TT	CC	GA	GA	TT	AC	TT
VV_361	GG	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CT	GC	CC	CG	GG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GG	AA	CT	AC	CT
VV_362	GG	AG	TT	AG	TC	TC	CT	CT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	GG	GA	CC	CA	CC	CT	TT	AA	TT	CT	GA	GA	CT	AC	TT
VV_363	GA	AG	CT	GG	TC	TC	CT	CT	TA	GA	GG	TC	AA	AT	CC	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	TT	CT	GA	AA	CT	AC	CT
VV_364	GG	AG	CT	GG	TC	TC	CC	CC	AA	GA	GG	CC	AA	AT	CT	GC	CC	CG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CC
VV_365	GG	AG	0	GG	CC	CC	CC	CC	AA	GG	GG	TC	GA	TT	TT	GC	CC	CG	GG	GG	CT	AA	TC	CT	TT	AG	TT	TT	GA	GA	TT	AC	TT
VV_366	GA	AG	CT	GG	CC	TC	CT	CT	AA	GA	AG	TC	AA	TT	CT	GC	CC	CG	GG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	GA	TT	AC	CT
VV_367	GA	AG	CT	AG	CC	TC	CT	CT	TA	GA	AG	TC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CC	TT	AG	TT	CC	GA	GA	CT	AC	CT
VV_368	GG	AG	CT	GG	TC	TC	CC	CC	AA	GA	GG	CC	AA	AT	CC	GC	CC	CG	GG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CT	CC	CC
VV_369	GA	AG	CT	GG	CC	TC	CT	CT	TA	GA	GG	CC	AA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	TT	CC	CT
VV_376	GA	GG	TT	AG	CC	TC	CT	CT	AA	AA	GG	TC	GA	AT	CT	GC	TT	GG	AG	GG	TT	CA	CC	CC	TT	AG	CT	TT	GA	AA	CT	AC	CC
VV_377	AA	GG	CT	GG	TC	TC	CT	CC	TT	AA	AG	CC	GA	TT	TT	GC	CC	GG	GG	AA	CT	AA	CC	CC	TT	AG	CT	CT	AA	GG	CT	CC	CT
VV_378	GA	AA	CT	GG	TC	TC	CC	TT	AA	GA	GG	TC	GA	TT	CT	GC	CC	GG	AA	GA	CT	AA	CC	CC	TT	GG	TT	TT	GA	GA	CT	AC	CT
VV_379	GA	AG	CT	AG	TC	TC	CT	CT	AA	GA	AG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	CA	CC	CT	TT	AG	CT	TT	GA	GA	CC	CC	CT

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
AG	AA	CT	CC	AA	AG	CC	AG	TC	CC	TT	TG	AA	CA	TT	GG	TT	CC	AG	AG	AG	CT	CC	TG	TG	CT	CA	GG	TT	AA	AA	TG	CA	CC	CT
GG	TA	TT	TT	AA	GG	CC	GG	CC	TT	TT	GG	CA	CA	TT	GG	AT	TC	AG	GG	AG	TT	CC	TG	TG	CT	CA	GG	TT	GA	GA	TG	AA	CC	TT
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GG	AA	TT	CC	AA	GG	CC	GG	CC	CC	TT	GG	AA	CA	TT	GG	TT	CC	AG	GG	AG	TT	CC	0	GG	TT	AA	AG	TT	AA	AA	GG	AA	CC	TT
GG	AA	CT	TC	AA	GG	CC	GG	CC	TT	TT	GG	CA	CA	CT	AG	AT	CC	AG	0	AG	CT	TC	TG	TG	CT	CA	AG	TT	GA	GA	TG	CA	CC	TT
GG	TA	TT	CC	AA	AG	CC	AG	TC	CT	CT	TG	CA	CA	CT	AG	AT	TC	AG	GG	AG	CT	TC	TG	TG	CC	CA	AG	TT	GA	GA	TG	CA	TC	TT
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GG	TA	TT	TC	AA	AG	CC	GG	TC	CT	TT	TG	CA	CA	CT	AG	AT	CC	AA	GG	AG	CT	TC	TT	GG	CT	CA	AG	TT	GA	GA	TG	AA	CC	TT
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GG	TT	TT	CC	AA	AG	CC	AG	TC	CC	TT	TG	CA	CA	CT	AG	AT	TC	AG	GG	AG	CT	TC	TG	TG	CT	CA	GG	TT	GA	AA	TG	AA	TC	TT
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chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
TT	GG	AA	AA	TG	AA	AA	TT	CT	GG	AA	GT	GT	GT	AA	GG	GG	0	GG	GA	GT	AA	CT	CC	GT	CC	TC	TC	TT	GG	TT	AT	GA	AG
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CT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	TT	GT	TT	AG	AG	GA	GA	GA	AA	GT	AA	CT	TT	TT	CT	TT	TC	CT	TG	TT	AT	GA	GG
CT	GG	AA	AA	TG	AA	TA	TT	CT	AG	AA	GG	GT	GT	AA	AG	GG	GA	GA	AA	GT	AA	TT	AA	TT	GT	CT	TC	TC	TT	GG	TC	AA	GA	AG
CT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	TC	GT	CC	CC	TC	TT	GG	TC	AT	AA	AG
TT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	GG	GT	GT	GG	AA	GA	AA	AA	GA	GT	AA	TT	TT	TT	CT	CC	CC	CT	GG	TC	AT	AA	AG
CT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	TT	GT	TT	AG	AG	GA	GA	GA	AA	GT	AA	CT	TT	TT	CT	TT	TC	CT	TG	TT	AT	GA	GG
CT	GG	AA	AA	TG	AA	TA	TT	CT	AG	AA	GG	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	AA	TT	GT	CT	TC	TT	GG	TC	AA	GA	AG
CT	AG	TA	GA	TG	TA	TA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	TC	TC	CT	GG	TC	AT	GA	GG
CT	AG	TA	GA	GG	TA	AA	TT	TT	AA	0	TT	GT	GT	AG	AG	GG	GG	GA	AA	GT	AA	CT	CC	TT	CC	TC	CC	TT	GG	TT	AT	AA	AG
CT	AG	TA	GA	TG	TA	AA	TT	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	CT	TC	TT	CC	TC	TC	TT	GG	TT	AT	GA	GG
CT	AG	TA	GA	TT	TA	AA	TC	CT	AG	AA	GT	GT	GT	AA	AG	GA	GA	AA	AA	GT	AA	TT	TC	TT	CC	TC	TC	TT	GG	TT	TT	GA	GG
CT	GG	AA	GA	GG	AA	TA	TC	TT	AA	AA	GT	GG	TT	AG	AG	GA	AA	GA	AA	GG	AA	TT	CC	TT	CC	TC	TC	TT	GG	TC	AA	GA	AG
CT	AG	TA	GA	TG	AA	AA	TC	CT	AG	AA	GT	TT	GT	AG	AG	GG	GA	AA	AA	GT	AA	TT	TT	TT	CT	TC	TC	CT	GG	TT	TT	GA	GG
CT	AG	TA	GA	GG	AA	TT	TT	CT	AA	AA	GT	GG	TT	GG	GG	GA	0	GA	AA	GT	AA	TT	CC	TT	CC	CC	TC	CT	GG	TC	TT	AA	GG
CT	AG	TA	GA	TG	TA	TA	TT	CT	AG	CA	TT	GG	GT	AA	AG	GA	GA	GA	GA	GT	AA	CT	TT	TT	CT	TT	TC	CT	TG	TC	AT	0	AG
TT	AG	TA	GA	GG	TA	AA	TT	CT	AG	AA	TT	GT	GT	AG	AG	GG	GA	GA	AA	GT	AA	TT	TC	TT	CT	TC	TC	CT	TG	TT	AT	GA	GG
TT	GG	AA	AA	TG	AA	TA	TC	TT	AG	AA	GG	GG	TT	AA	AG	GA	GA	GA	AA	GG	AA	TT	CC	TT	CT	CC	CC	TT	GG	TT	TT	AA	GG
TT	AG	TA	GA	TG	TA	AA	TT	CT	AG	AA	GT	GT	GT	AG	AG	GA	GG	AA	AA	GT	AA	CT	TC	TT	CT	TC	TC	CT	TG	TT	AT	GA	GG
TT	AG	TA	GA	GG	AA	TA	CC	CT	AA	AA	GT	GT	GT	AA	AG	GA	GG	AA	AA	GT	AA	CT	TC	TT	CT	TC	TC	CT	TG	TT	AT	GA	GG
TT	AG	TA	GA	TG	TA	TA	TT	CT	AG	AA	GT	GT	GT	AG	GG	GA	GG	AA	AA	GT	AA	CT	TC	TT	CT	TC	TC	CT	TG	TT	AT	GA	GG
CT	AG	TT	GA	GG	TA	AA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CT	TC	TC	CT	TG	TT	AT	GA	GG
TT	AG	TA	GA	GG	AA	TA	TC	CT	AG	CA	GT	GG	GT	AG	AG	GG	GA	GA	AA	GT	AA	CT	TC	TT	CT	CC	TC	CT	GG	TC	AT	GA	GG
TT	GG	AA	AA	TG	AA	AA	TC	TT	AA	AA	GT	GT	GT	AG	GG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	CC	TT	CT	GG	TC	AT	AA	AA
TT	AG	TA	AA	TG	AA	AA	TT	CT	AG	AA	TT	GT	GT	AG	GG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	TC	TC	CT	GG	TC	AT	GA	GG
CT	AG	TA	GA	TG	TA	AA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	TC	TC	CT	GG	TT	AT	GA	GG
TT	GG	AA	AA	GG	AA	TA	CC	TT	AG	AA	GG	GT	TT	GG	GG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	TC	TC	TT	GG	TT	TT	AA	AG
CT	AG	TA	GA	TG	AA	AA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	TT	TC	TT	CC	CC	TC	CT	GG	TC	AT	GA	AG
CT	AG	TA	GA	TG	AA	AA	TC	CC	AG	AA	GT	GT	GT	AA	AG	GG	GA	GA	AA	GT	AA	CT	TT	TT	CT	TT	TC	CT	TG	TC	AT	GA	AG
CT	AG	TA	GA	TG	TA	TA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GA	GT	AA	TC	TT	CC	TC	TC	CT	GG	TC	AT	GA	GG
CT	GG	AA	AA	TG	AA	TA	TC	CT	AG	AA	GT	GT	GT	AG	AG	GA	GA	GA	AA	GT	AA	CT	TC	TT	CC	TC	TC	CT	GG	TC	AA	AA	AG
CT	AA	TA	GG	GG	AA	AA	TC	CT	AA	AA	TT	GG	TT	AG	AA	GA	GA	AA	GG	TT	AA	TT	TC	GT	CT	TC	TT	CC	TG	CC	AT	GA	GG
TT	AG	TA	GA	TG	AA	TT	TT	CT	GG	AA	GT	TT	GT	AG	AA	AA	AA	AA	AA	GT	AA	CT	TC	GT	CT	TC	CC	CT	TG	TC	TT	GA	AG
CC	AG	TA	GA	TG	AA	AA	TT	TT	GG	CA	GT	GT	GG	AG	AG	AA	GG	GA	GA	TT	AA	CT	TC	GT	CC	CC	CC	CT	GG	TC	TT	AA	AG
TT	AG	TT	GA	TG	AA	TA	CC	CC	AG	AA	GT	GT	GT	AA	AG	GA	AA	GA	GA	GT	AA	CT	TC	GT	CC	TT	TT	CC	TG	TC	AA	GA	AA

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
VV_380	AA	AG	TT	AA	CC	TT	CT	TT	AA	AA	AG	CC	GA	TT	CT	CC	TC	GG	AG	AA	CT	AA	CC	CT	CT	AG	CT	TT	GA	AA	CT	AC	TT
VV_381	GG	GG	CT	GG	CC	TT	TT	CC	TA	GA	AG	TC	GA	TT	TT	GC	CC	GG	GG	GA	CT	AA	CC	CC	TT	AA	CT	CT	AA	GA	TT	CC	CC
VV_382	GA	AG	CC	GG	CC	TT	TT	CT	TA	GA	AG	TC	GA	AT	CC	CC	CC	GG	AG	GA	CC	AA	CC	CC	TT	AG	TT	TT	AA	AA	TT	CC	CT
VV_383	AA	AA	TT	AG	TT	TC	CT	TT	TA	GG	AG	TC	GA	TT	CT	CC	TT	GG	AG	GA	CC	CC	CC	CT	CT	AA	CC	CT	AA	AA	CC	CC	CT
VV_384	GA	AG	CT	AA	TC	TT	TT	TT	TA	AA	AG	TC	GA	TT	CT	CC	TC	GG	AG	AA	CT	AA	CC	CT	TT	AG	TT	TT	AA	GA	TT	AC	CC
VV_385	AA	AA	CT	AG	CC	TC	CC	0	AA	AA	GG	TC	GA	TT	CC	CC	CC	GG	GG	GA	CT	CA	CC	CC	TT	GG	TT	TT	AA	GG	CT	AA	CT
VV_386	AA	AG	CT	AG	TC	TT	CT	TT	AA	AA	GG	TC	GA	TT	CT	GC	CC	GG	AG	GA	CT	AA	TC	CC	TT	AG	CT	TT	AA	GA	CC	CC	CT
VV_387	AA	AA	TT	AA	TC	TT	TT	TT	TA	AA	AG	CC	GA	TT	TT	GC	CC	GG	GG	GA	CT	CA	CC	CC	TT	GG	CT	TT	AA	GG	CT	AC	TT
VV_388	AA	AG	TT	AG	TC	TC	CT	CT	AA	GA	AG	TC	GA	TT	CT	CC	TC	GG	AG	AA	CT	CA	CC	CC	TT	AG	CC	TT	GG	GA	CT	CC	CT
VV_389	GA	AA	CC	AG	TT	TC	CT	CT	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	GG	CC	CA	CC	CT	TT	GG	CT	TT	AA	GA	CT	AC	TT
VV_390	GA	AG	CC	AG	TT	TC	CT	CT	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	GG	CT	CA	CC	CT	TT	GG	CT	TT	AA	GA	CT	AC	TT
VV_391	GA	GG	CC	AA	TC	TT	TT	CC	AA	GA	AG	TC	GA	TT	TT	CC	CC	GG	AG	AA	CC	CA	CC	CC	CT	GG	CT	TT	GG	GA	CC	AC	CT
VV_392	AA	AA	TT	AG	TC	TC	CT	CT	AA	GA	GG	TC	GA	AT	CC	CC	TC	GG	AG	AA	CC	AA	CC	CT	TT	GG	CT	TT	AA	GA	CT	CC	CT
VV_393	GG	AG	CC	GG	TT	CC	TT	TT	AA	GA	GG	TC	GA	AT	CC	CC	TC	GG	AA	AA	CT	CC	CC	CC	TT	AA	CT	CT	AA	GA	CC	CC	CC
VV_395	AA	AG	TT	GG	TC	TC	CT	CT	AA	AA	AG	TC	GA	TT	TT	GC	TC	GG	AA	GA	CC	CA	CC	CT	TT	GG	TT	TT	GA	GA	CT	CC	CT
VV_396	GA	AA	CT	GG	TC	TC	CC	CT	AA	GG	AG	TC	GG	TT	CT	CC	CC	GG	GG	GG	CT	AA	CC	CT	TT	GG	CC	TT	AA	GA	CT	AC	CT
VV_397	AA	GG	CT	GG	CC	TT	TT	CT	AA	GG	AG	TC	GA	AT	CC	CC	CC	GG	AA	AA	CT	CA	CC	CC	TT	AG	TT	TT	AA	AA	CT	CC	CC
VV_399	AA	AG	TT	GG	TC	TC	CC	CT	AA	GG	AG	TC	GA	TT	CT	CC	TC	GG	AG	GA	CC	CC	CC	CC	TT	AG	TT	TT	AA	GA	CT	AA	CC
VV_400	AA	AA	TT	AG	TC	TC	CT	CT	AA	GA	GG	TC	GA	AA	CC	CC	TC	GG	AG	AA	CC	AA	CC	CT	TT	GG	CT	TT	AA	GA	CT	CC	CT
VV_401	GA	AG	TT	AG	CC	TT	TT	CT	AA	GA	AG	CC	AA	TT	TT	CC	TC	GG	AG	AA	CC	CC	CC	CC	TT	AA	CT	TT	GA	GA	CC	AC	CC
VV_402	GA	AG	CT	AG	TC	TT	CT	TT	AA	AA	GG	TC	GA	TT	CT	GC	CC	GG	AG	GA	CT	AA	TC	CC	TT	AG	CT	TT	AA	GA	CC	CC	CT
VV_403	AA	AG	CT	AG	CC	TT	CT	CT	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AA	GA	CC	CC	CC	CT	TT	AG	TT	TT	AA	GA	CT	AC	CT
VV_404	GA	AG	TT	AG	TT	TC	CT	TT	AA	GA	GG	TT	GG	TT	CT	GC	TC	GG	AA	AA	CT	CC	CC	CT	TT	AA	CT	TT	GA	GG	CT	CC	CT
VV_405	AA	AG	TT	GG	TC	TC	CT	TT	AA	AA	GG	TC	GA	TT	CC	CC	CC	GG	AA	AA	CC	CA	CC	TT	TT	GG	CC	TT	GG	GG	CC	CC	CT
VV_406	AA	AA	CC	AG	CC	CC	CT	TT	AA	GA	AG	TT	GG	AT	CT	CC	TT	GG	AA	AA	CT	CA	CC	CT	TT	AG	CT	TT	AA	GG	CC	AC	CT
VV_407	GA	GG	TT	AG	CC	TT	TT	CT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AA	CT	CT	AA	GA	TT	AC	TT
VV_408	AA	AG	TT	AA	TC	TT	CT	CT	TA	GA	GG	TC	GA	TT	TT	GG	CC	GG	GG	AA	CC	AA	CC	CT	TT	GG	CC	TT	AA	AA	CT	AC	TT
VV_409	AA	GG	CT	AG	CC	TC	CT	TT	AA	GG	GG	TC	GA	AA	CC	CC	TC	GG	AA	GA	TT	CA	CC	CC	TT	AA	CC	TT	AA	GG	CC	AC	CT
VV_410	GA	GG	CT	GG	CC	TT	TT	CC	TA	GA	AG	CC	AA	TT	TT	GC	TC	GG	GG	AA	TT	CA	CC	CC	TT	AG	CT	CT	AA	GA	TT	CC	CC
VV_411	GA	GG	CC	AG	TC	TC	CT	CT	AA	GG	AG	TC	GA	AT	CT	CC	CC	GG	AA	GG	CC	CA	CC	TT	TT	AA	CC	TT	GG	AA	CC	AA	TT
VV_412	AA	AG	CT	AA	CC	TT	CT	TT	AA	AA	AG	TC	GA	TT	CT	GC	CC	GG	AA	AA	CC	CA	CC	CT	TT	AA	TT	TT	GA	AA	CT	CC	CT
VV_413	GA	AG	CT	AG	TC	TC	CT	TT	AA	GA	AA	TC	GA	TT	CC	CC	TC	GG	AG	GA	CT	CA	CC	CT	TT	AA	TT	CT	AA	GG	CT	AA	TT
VV_414	AA	GG	CT	AA	TC	CC	CT	CT	TA	GA	AG	TC	GG	TT	TT	GG	CC	GG	GG	GG	CC	AA	0	CT	TT	GG	CC	TT	AA	GA	CC	CC	CT
VV_415	GG	AG	CT	AG	CC	TT	TT	CT	AA	GA	GG	TC	GA	AT	CT	CC	CC	GG	AA	AA	CC	CA	CC	CT	TT	AA	TT	TT	GG	AA	CC	CC	CC
VV_417	AA	AG	TT	GG	CC	TC	CT	CT	AA	AA	GG	TC	GG	TT	CT	CC	CC	GG	AA	AA	CT	AA	CC	CT	TT	GG	CC	TT	GG	GG	CC	CC	CC
VV_418	AA	AA	TT	AG	TC	TT	CT	TT	AA	AA	GG	TC	GA	TT	TT	GC	CC	GG	AG	GA	CC	CA	CC	CC	TT	AG	TT	TT	GA	AA	CT	CC	CT
VV_419	GA	AA	CT	AG	CC	TT	CT	CT	AA	AA	GG	TC	GA	TT	CT	GC	CC	GG	AA	GA	CT	CC	CC	CC	TT	AG	TT	TT	GA	AA	CT	AA	CT
VV_420	GG	GG	CT	GG	CC	TT	TT	TT	AA	GA	AG	TC	GA	AT	CT	CC	CC	GG	GG	AA	TT	CC	CC	CT	TT	AG	CT	TT	AA	AA	TT	AC	CC
VV_421	AA	AA	CC	AA	CC	TC	TT	TT	TA	GA	AA	TC	GA	AT	CT	CC	CC	GG	GG	GA	CC	AA	TC	TT	CT	AG	CC	CT	GA	GA	CT	AC	TT
VV_422	AA	GG	CT	AA	TC	CC	CT	CT	TT	GA	AG	TC	GG	TT	TT	GG	CC	GG	GG	GG	CC	AA	TC	CT	TT	GG	CC	TT	AA	GA	CC	AC	CT
VV_423	AA	AG	TT	GG	CC	TT	CC	CT	AA	GA	AG	CC	AA	TT	TT	GC	CC	GG	AA	GG	TT	CA	CC	CT	TT	AA	CT	TT	AA	AA	CT	AC	CC
VV_424	AA	AG	TT	GG	CC	TT	CC	CT	AA	GA	GG	TC	GA	TT	CT	CC	TC	GG	GG	GA	TT	CC	CC	CC	TT	AG	TT	TT	AA	AA	CC	AC	CC
VV_425	GG	AG	TT	AG	CC	TT	CC	CT	TA	GG	AG	TC	GA	TT	TT	CC	TC	GG	AG	GA	CT	CC	CC	TT	TT	AA	CT	TT	AA	AA	CC	AA	CC
VV_426	AA	GG	TT	AA	CC	TT	CT	CT	TA	GG	AG	TC	GG	AT	CT	CC	CC	GG	AG	GA	TT	CA	CC	CT	CT	AG	CC	TT	AA	AA	CT	AA	CC
VV_427	AA	AG	TT	AA	TT	TC	TT	TT	AA	GA	AA	TC	GG	TT	CT	GC	TC	GG	GG	GG	TT	AA	CC	TT	TT	AG	CT	TT	AA	GG	TT	AA	CC
VV_428	AA	AG	TT	AA	TC	TT	CT	CT	AA	AA	AA	TC	GA	TT	TT	GC	CC	GG	GG	GA	CT	AA	CC	CT	TT	AA	TT	TT	GA	AA	TT	AA	CT
VV_429	AA	GG	TT	AG	CC	TT	CT	CT	AA	AA	GG	TC	GA	TT	CT	CC	TC	GG	GG	AA	CT	CA	CC	CT	TT	AA	CT	TT	AA	AA	CT	CC	TT
VV_430	AA	GG	TT	AG	TT	TT	TT	TT	AA	GA	AG	TC	GA	TT	TT	GG	CC	GG	AG	AA	CT	CA	CC	CT	TT	AG	TT	TT	AA	GA	TT	CC	CT
VV_433	GG	AG	CT	GG	TC	TC	CT	CT	TA	GG	AG	TC	GA	TT	CC	GC	CC	GG	AG	AA	TT	CA	CC	CT	TT	AA	TT	CT	AA	GG	CT	AC	CT
VV_434	AA	AA	TT	AG	CC	TT	CC	CT	AA	GA	AG	TC	GA	TT	CC	CC	TT	GG	GG	AA	CT	AA	CC	CC	TT	AG	CT	TT	GG	GG	TT	CC	TT
VV_435	AA	GG	TT	GG	CC	TT	TT	CT	AA	GG	AG	TC	GA	TT	CT	CC	CC	GG	AG	GA	CT	CA	CC	CT	TT	AA	CT	CT	AA	AA	TT	AC	CT
VV_436	GA	AG	0	AG	CC	TC	CT	TT	AA	GA	AG	TC	GA	TT	CT	GG	CC	GG	GG	GA	CC	CA	CC	CC	TT	AA	CC	TT	AA	AA	CC	AC	CC
VV_437	AA	AG	TT	AA	TC	TC	CT	CT	AA	GA	AG	TC	GA	TT	CT	GC	CC	GG	AA	AA	CC	CA	CC	CC	TT	GG	CT	TT	AA	GA	CC	CC	CT
VV_440	AA	AG	TT	AA	TC	TT	CC	CT	TA	GA	0	TC	GA	TT	TT	GC	CC	GG	GG	GA	CT	AA	CC	CT	TT	AG	CC	TT	AA	AA	TT	AC	TT
VV_441	AA	AG	TT	AG	TT	CC	CT	CT	AA	GA	AG	TC	GG	TT	TT	GC	CC	GG	GG	AA	CT	CA	CC	CT	TT	AG	TT	TT	GA	GG	TT	AA	CC
VV_442	GA	AA	CT	AA	CC	TC	CT	CT	AA	AA	GG	TC	GA	TT	CT	GC	CC	GG	AG	AA	TT	CA	CC	CC	TT	AG	TT	TT	GG	GA	CT	CC	CT
VV_443	GA	GG	TT	AG	CC	TT	TT	CT	AA	GA	AG	CC	AA	AT	CC	CC	CC	GG	AG	AA	CC	AA	CC	CT	TT	AA	CC	TT	AA	AA	CT	AC	CT
VV_444	GA	AA	CT	AG	CC	TT	CT	TT	AA	AA	GG	TC	GA	TT	CT	CC	CC	GG	AA	AA	CT	CA	CC	CT	TT	AG	TT	TT	AA	GA	CT	CC	TT
VV_445	GA	AG	TT	AA	TC	TT	CT	CC	AA	AA	AG	TC	GA	TT	CT	GC	CC	GG	AG	GA	CC	CA	CC	CT	TT	AA	TT	TT	GA	AA	CT	CC	TT
VV_446	AA	AA	CT	AG	TC	TT	CT	TT	AA	GA	GG	CC	GA	TT	CT	CC	TC	GG	AG	GA	CC	CA	CC	TT	TT	AG	TT	TT	GA	GA	CT	CC	CT
VV_447	AA	GG	CT	GG	TC	TC	CT	TT	TT	AA	GG	CC	GA	TT	CT	CC	TC	GG	GG	GA	CT	CC	CC	CC	TT	AA	CT	CT	AA	AA	CC	CC	CT
VV_448	AA	AG	TT	AG	TT	TC	CT	CT	AA	AA	AA	TC	AA	TT	CT	GC	CC	GG	GG	GA	CT	AA	TC	CT	TT	AG	CT	TT	GA	GA	TT	AC	TT
VV_449	GA	AG	CC	GG	TC	CC	CC	CT	AA	GA	AG	TC	GA	TT	TT	CC	TC	GG	AG	AA	TT	CA	CC	CC	TT	AA	CT	TT	AA	AA	CC	CC	TT
VV_450	GG	GG	CT	AG	TT	TT	CT	CT	AA	GA	AA	TC	GA	AT	TT	GC	TC	GG	AA	GG	CC	AA	CC	CC	TT	AA	CC	CT	GA	GA	CT	AA	CC
VV_451	GA	GG	CT	GG	TC	TC	TT	CT	AA	GA	GG	TC	GA	TT	CT	GC	TC	GG	AG	AA	CC	CC	CC	CT	TT	AG	CT	TT	GA	GA	CT	AC	TT
VV_452	AA	GG	CT	GG	TT	CC	TT	TT	AA	GA	GG	TC	GA	TT	TT	GC	CC	GG	AA	GA	CT	CC	CC	CC	TT	AG	CT	CT	GA	GA	CT	AC	CT
VV_453	AA	AA	CT	GG	TC	TT	CC	CT	AA	GG	GG	TC	GA	TT	CT	GC	TC	GG	AG	GA	CC	CA	CC	TT	TT	GG	TT	TT	AA	GG	CT	CC	CT
VV_454	AA	AG	TT	AG	TC	TC	CT	CT	AA	GA	AG	TC	GA	TT	CT	CC	TC	GG	AG	AA	CT	CA	CC	CT	TT	AG	CC	TT	GG	GA	CT	CC	CT
VV_455	AA	GG	TT	AA	TT	TC	CC	TT	TA	GA	AG	TC	GG	TT	CT	GC	TC	GG	GG	GG	CT	AA	TC	CT	CT	AG	CT	CT	AA	GG	TT	AA	CT
VV_456	AA	GG	CT	AG	TC	TC	CT	TT	AA	AA	AG	TC	GG	TT	CT	GC	TC	GG	AG	GA	CT	CA	TC	CT	CT	AG	CT	CT	AA	GA	TT	CC	CC
VV_457	GG	GG	TT	GG	CC	TT	CT	TT	AA	GA	AG	CC	AA	TT	CT	GG	CC	GG	GG	AA	TT	CA	CC	CC	TT	AA	TT	TT	AA	GG	CT	CC	CC
VV_458	AA	AG	CT	AA	TC	TT	TT	CT	AA	GA	GG	TC	GA	AT	CT	GG	CC	GG	AA	GA	CT	CC	CC	CC	CT	AA	CT	TT	AA	GA	CC	AC	CT
VV_459	GG	AG	CT	GG	TT	CC	CT	CC	TT	GG	AG	TT	GG	AT	TT	GC	CC	GG	AA	GG	CT	AA	CC	CT	TT	AG	CT	TT	GA	GA	CC	AA	CT
VV_460	GA	AA	0	AA	TC	TT	CC	CT	AA	GA	AG	TC	GA	TT	TT	GC	CC	GG	AG	GA	TT	CC	CC	TT	TT	AG	TT	CT	GG	GG	CT	CC	CT
VV_461	AA	AA	CT	AG	TT	TT	CC	CT	AA	GA	GG	CC	GA	TT	CC	GC	TC	GG	AG	GA	CC	CA	CC	TT	TT	GG	TT	TT	AA	GG	CT	CC	CT
VV_462	AA	AG	CT	GG	TC	CC	CT	CT	AA	GA	AG	CC	GA	TT	TT	GC	CC	GG	AG	GG	CT	CC	CC	CT	TT	AG	TT	CT	GG	GA	CT	AC	CT
VV_463	GA	AA	CT	GG	TT	TC	CC	TT	AA	GA	AG	TC	GA	TT	CT	GC	TC	GG	AG	AA	CT	CA	CC	TT	TT	AG	CT	CT	AA	GG	CT	CC	CT
VV_464	GA	AG	CT	AG	TC	TC	CT	CT	TA	AA	AG	TC	GA	AT	CT	GC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AG	CT	TT	GA	AA	CT	AC	TT
VV_465	AA	GG	TT	GG	TC	TC	CT	CC	AA	GA	GG	TC	GA	TT	TT	CC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AG	CT	CT	GA	AA	CC	AC	CC
VV_466	GA	AA	TT	GG	TT	CC	CT	TT	AA	GA	GG	TC	GA	AT	CT	GC	CC	GG	AA	AA	CT	CC	CC	CC	TT	AA	CT	CT	AA	GA	CC	CC	CT
VV_467	AA	AA	CT	GG	TC	TC	TT	TT	AA	GA	GG	TC	GA	TT	CT	GC	CC	GG	AG	AA	CT	AA	CC	CT	TT	AA	TT	TT	GA	GA	TT	AC	CT
VV_468	AA	GG	CT	AG	CC	TT	CT	CT	AA	GG	AG	TC	GA	TT	TT	CC	CC	GG	AG	GA	TT	AA	CC	CC	TT	AG	TT	TT	AA	AA	CT	AC	CT
VV_469	AA	AG	TT	GG	TC	CC	CT	CT	AA	GA	GG	TC	AA	TT	CT	CC	TC	GG	AG	AA	CT	CA	CC	CC	TT	AA	CT	TT	GG	GA	CT	AC	CT
VV_470	GA	AG	CT	GG	CC	TT	CT	TT	AA	GA	GG	TC	AA	TT	CT	CC	CC	GG	AA	AA	TT	CC	CC	CT	TT	AG	CT	TT	AA	GG	CT	AC	CC
VV_471	GA	AG	TT	GG	CC	TT	CT	TT	AA	AA	AA	TC	GA	TT	TT	CC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AA	CT	TT	AA	AA	TT	AC	CC
VV_472	AA	GG	CT	GG	TC	TC	CC	CC	AA	GA	AA	TC	GA	TT	CT	CC	CC	GG	AG	GA	CC	AA	CC	CC	TT	AA	CT	TT	AA	GA	TT	AC	CC
VV_473	GG	GG	CT	AG	CC	TT	TT	TT	AA	GA	GG	CC	AA	AT	CC	CC	CC	GG	AA	AA	CT	CA	CC	CC	TT	AG	TT	TT	AA	GA	TT	CC	CC
VV_474	AA	AG	CC	GG	CC	TC	TT	TT	AA	GA	AG	TC	AA	AT	CT	CC	TC	GG	AA	AA	TT	CC	CC	CT	TT	AG	CT	TT	AA	GA	TT	AC	CC
VV_475	GA	GG	TT	GG	CC	TT	TT	CT	AA	GA	AG	TC	GA	AT	CT	CC	CC	GG	AG	AA	TT	CC	CC	CC	TT	GG	TT	TT	AA	AA	TT	AC	CC
VV_476	AA	AG	TT	GG	TC	TT	CT	CT	AA	GA	GG	CC	AA	TT	TT	CC	CC	GG	GG	AA	CT	CC	CC	CT	TT	AG	TT	TT	GA	AA	CC	AC	CT

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
GG	TA	CT	CC	AA	GG	TT	AG	TT	TT	CT	GG	CA	AA	TT	GG	TT	TC	GG	AG	GG	CT	TT	TG	TT	CC	CC	GG	CT	GG	AA	TT	CA	TC	TT
GG	TA	CT	CC	AA	AG	TC	GG	CC	TT	TT	TT	CC	AA	CC	AA	AT	TC	AG	AG	GG	CC	TT	TG	GG	CC	CA	GG	CT	GG	AA	GG	CA	TC	TT
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GG	AA	CT	TC	AA	GG	CC	AG	TC	CT	CT	TG	CA	CA	CC	AA	AT	CC	GG	GG	AG	CC	TT	TG	TG	CC	CA	GG	CC	GG	AA	TG	CC	CC	TT
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GG	AA	CC	CC	AA	GG	CC	GG	TC	CT	TT	GG	CA	CA	CT	GG	TT	CC	GG	GG	AG	CT	TC	TT	TG	TT	CA	GG	CC	AA	AA	TG	CA	TC	TT
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GG	AA	CT	CC	AA	GG	TC	AA	TC	TT	CT	TG	CA	AA	CC	AG	TT	TC	GG	GG	AG	CT	TC	TT	GG	CC	AA	AG	CT	GA	AA	TT	CC	TC	TT
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chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
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CT	AA	TA	GG	TG	TA	AA	TC	TT	GG	CA	TT	GG	GT	AA	AG	AA	AA	GA	AA	GT	AA	CT	TC	TT	TT	TC	CC	CT	TT	TC	TT	GA	AG
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TT	AG	TT	AA	TT	AA	TA	TC	TT	AA	AA	GG	GG	TT	AG	AG	GA	GA	AA	GA	GG	AA	CC	CC	TT	CT	TC	TT	CC	TG	TC	AA	GG	GG
TT	AG	TA	GA	TG	AA	AA	TC	TT	AG	AA	GG	GG	GT	AG	AA	GA	GG	GA	GG	GG	AA	CC	CC	GT	CC	TC	TT	CT	GG	TT	TT	AA	GG
CC	AG	AA	GG	TG	AA	AA	CC	CT	AG	AA	GT	GG	TT	AG	GG	GG	GA	GA	GG	AA	CT	TC	GT	TT	CC	TC	CT	TG	TC	AT	GA	AG	
CT	GG	TA	GA	TT	AA	AA	TC	CT	AG	AA	TT	GT	GT	AG	AA	GA	GG	GA	GG	GG	AA	CT	TC	GG	TT	TC	CC	CT	TT	TC	TT	GA	AG
CT	GG	AA	AA	TT	AA	AA	TT	CC	GG	AA	GG	TT	GT	AA	GG	GG	AA	AA	GG	TT	AA	TT	TT	TT	CT	TT	TC	TT	GG	CC	AA	AA	AG
CT	GG	TA	GA	TT	AA	TT	TT	CT	AA	CA	GT	TT	GG	AG	AA	AA	GA	AA	GT	AA	CC	CC	GT	TT	TT	TC	CT	TG	TC	AA	AA	AG	
CC	AG	TA	GA	TG	TA	AA	TT	TT	AG	AA	GT	GT	GG	AA	AG	GA	GA	GG	GA	GT	AA	TT	TC	GT	CT	TT	TC	CT	TG	TC	AT	GA	AG
CC	AG	AA	GG	GG	AA	TA	TC	CT	AG	AA	TT	GG	GG	AA	AG	AA	GG	GA	GA	TT	AA	CT	TT	GG	CT	TC	CC	CT	TG	TC	AT	GG	AA
CC	AG	AA	GA	TG	AA	TA	CC	TT	AG	AA	GT	GG	GG	AG	AG	GA	GG	GA	GG	GT	AA	CT	TC	GG	TT	CC	TT	CC	TG	TC	AA	GG	AA
CT	AG	TA	GG	GG	TT	AA	TT	TT	AG	CA	GT	TT	GT	GG	GG	GA	GG	GA	AA	TT	AA	TT	TC	GT	CC	CC	CC	CT	TG	TC	AT	GA	AG
TT	AA	TT	GG	GG	TA	AA	TT	CT	AG	AA	GT	GT	GG	AA	AG	GA	AA	AA	AA	GT	AA	CT	TT	TT	CT	TT	TT	TT	GG	TT	AT	GA	GG
CC	AA	TA	GG	GG	TA	AA	TT	CT	GG	AA	GT	GT	GG	AA	AG	AA	GG	GG	GG	GT	AA	TT	TT	GG	TT	TC	CC	CT	GG	TC	AA	AA	AG
TT	AG	AA	GA	TG	TA	AA	TT	TT	GG	CC	TT	GT	GT	AA	GG	AA	GG	AA	GG	GG	AA	CT	TC	GG	CT	CC	CC	CT	TT	CC	TT	GA	AA
CT	AG	AA	GA	TG	TA	AA	TC	CT	AG	CA	TT	GG	GG	AA	AG	AA	GA	GA	GG	GA	TT	AA	CT	TC	GT	CT	TC	CC	TT	TT	AT	GG	AG
TT	AA	TA	GG	GG	AA	TA	CC	CC	AG	AA	TT	TT	GT	GG	GG	GA	AA	GA	AA	GT	AA	TT	TT	TT	CT	TT	CC	CT	GG	TT	TT	GA	GG
TT	AG	TT	AA	TG	AA	TA	CC	CT	GG	CA	TT	TT	TT	AG	GG	GA	AA	AA	GA	GG	AA	CT	TC	GT	CT	CC	CC	CT	TT	TC	AT	GA	AA
TT	AA	TA	AA	GG	AA	AA	TC	TT	AG	AA	TT	TT	GT	AG	AA	GG	GA	GG	GG	GG	AA	CC	TC	GT	CT	TT	TC	CT	TG	CC	AA	AA	GG
CC	AG	AA	GA	TG	AA	TA	TC	TT	AG	AA	GT	GG	TT	AG	GG	GA	AA	GG	GG	GG	AA	TT	CC	GG	CC	TT	TC	CT	TG	TC	AT	AA	GG
CT	AA	TA	GA	GG	TA	AA	TC	TT	AG	CA	GT	TT	GT	AA	AG	GA	GG	GA	GG	GT	AA	CT	TT	GG	CT	TC	TC	TC	CT	TG	TC	AT	GA	AG
CC	AA	TT	GA	GG	TA	AA	TC	TT	GG	CA	GT	TT	GG	AA	AG	GA	GG	GA	GG	TT	AA	CC	TT	GG	CT	TC	TC	TC	CT	TG	TT	AT	GG	GG
TT	AG	TA	AA	GG	AA	AA	TT	TT	AG	AA	TT	GG	TT	AG	AG	GA	GA	AA	GA	TT	AA	CT	TC	GG	CT	TC	TC	TC	CC	TG	CC	AT	AA	AA
CC	AA	TA	GA	TG	TA	TA	CC	CT	AG	CA	TT	GT	TT	GG	GG	GG	GG	GA	GG	GG	AA	TT	TC	GG	TT	TC	TC	TC	CC	TT	TC	AT	AA	AA
CC	AG	TA	GG	TG	TA	TA	CC	CT	AG	CA	GT	TT	GT	GG	AG	GG	GA	GG	GA	GG	AA	TT	TC	GT	TT	TC	TC	TC	CC	TT	GG	CC	AA	GG	AA
CT	AG	TA	GG	TG	TA	TA	TC	TT	AG	CA	GT	GT	GT	AA	AG	GA	GA	GA	AA	AA	GT	AA	CT	TT	GT	TT	TT	TC	TT	GG	CC	TT	AA	AG
TT	AA	AA	GA	TG	AA	TA	TC	TT	AA	AA	GT	TT	GT	AG	AA	GA	GA	GA	AA	AA	GA	GT	GA	CT	TC	GT	TT	TC	TT	TT	CC	TT	GA	AG
TT	AG	TA	GG	TT	AA	AA	TT	CT	AG	AA	TT	GT	GT	AG	AG	GA	GA	GG	GA	TT	AA	CT	TC	GG	CT	TC	TT	TC	TT	TT	TC	TT	GA	GG
CT	AA	AA	GA	GG	AA	AA	CC	CC	GG	AA	GT	GT	GG	AG	GG	AA	GA	AA	GA	GT	GA	TT	CC	GT	CT	TC	CC	CT	GG	CC	AT	GA	AA
TT	AG	TA	AA	GG	AA	AA	TT	TT	AG	AA	TT	GT	GT	TT	AG	GG	AA	GA	GA	GT	GA	TT	CC	GT	CT	CC	CC	CT	TT	TT	TC	AT	GA	AA
CT	AA	TA	GA	TG	AA	TA	TC	CC	GG	AA	GT	GT	GT	TT	GG	GG	GA	GA	GA	GT	GA	TT	CC	GT	CT	TC	CC	CT	TT	TT	TC	AT	GG	AG
CC	AA	TA	GG	GG	TT	AA	TT	TT	AG	AA	TT	GT	GT	TT	AG	GG	AA	GA	GA	GT	AA	CC	TT	GG	CT	TC	TC	CT	TG	TC	AT	GA	AG
CT	AG	TA	GA	TG	AA	TA	TC	CT	AG	AA	GT	GT	GT	AG	AA	GA	GA	GG	GG	GG	GA	CT	TC	GT	CT	CC	TT	CT	GG	TC	TT	GG	AG
TT	AA	TT	AA	TT	AA	TT	TT	CT	GG	AA	TT	TT	TT	AA	GG	GA	GG	GG	GG	GG	AA	TT	TT	GT	TT	CC	CC	CC	GG	TT	TT	GG	AG
CC	GG	TA	AA	TT	AA	AA	TT	CC	AG	AA	TT	GT	GT	GG	AG	GA	GA	AA	AA	GT	AA	TT	TC	TT	TT	CC	TC	CC	GG	CC	AT	GA	AG
CC	AA	AA	AA	TG	AA	AA	TT	CT	AA	AA	TT	GT	TT	AG	AA	AA	GA	AA	GA	TT	AA	TT	TC	TT	CT	CC	TT	CC	TG	CC	TT	AA	AG
CT	AA	TA	GG	GG	AA	TA	CC	CC	AG	AA	TT	GT	GG	AG	AG	GA	GA	GA	AA	TT	AA	TT	TC	TT	TT	TC	TT	CT	GG	CC	AA	AA	AA
TT	AA	TT	GA	TG	AA	AA	TT	CT	AG	AA	GT	GT	TT	AA	AA	GG	AA	GA	AA	GT	GA	CT	TC	GT	CT	CC	TT	CC	GG	TC	TT	GG	AG
CT	AG	TA	GA	TG	TA	AA	TT	CC	AG	AA	GT	GG	TT	AG	AG	GA	GG	AA	GA	TT	AA	CT	TC	TT	CT	TC	TT	CT	GG	TC	TT	GG	AG
CT	AA	TT	AA	TT	AA	AA	TT	TT	AA	AA	GG	GT	GG	AG	AA	GA	GA	AA	AA	GT	AA	CC	CC	TT	CT	TT	TC	CT	GG	TC	TT	AA	GG

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
VV_477	GG	GG	CT	AG	TC	CC	TT	CT	TA	GA	AG	TC	GA	AA	CT	CC	0	GG	AG	GG	CT	CC	CC	TT	AA	CT	CT	GA	AA	CT	CC	CC
VV_478	GA	GG	CT	GG	CC	TT	CT	TT	AA	GA	GG	TC	AA	TT	CT	CC	CC	GG	AA	AA	TT	CC	CC	CT	TT	AG	CT	TT	AA	GA	CT	AC	CC
VV_479	GG	AA	0	AG	TC	TC	CT	CT	AA	GA	AG	TC	GG	AT	CT	GC	CC	GG	AG	AA	TT	CC	CC	TT	TT	AA	CT	TT	GA	GA	CT	CC	CT
VV_480	AA	AA	TT	AG	TC	TC	CT	CT	AA	GA	AG	CC	GG	AT	CT	GC	CC	GG	GG	AA	TT	CA	CC	CT	TT	AA	CC	TT	GA	GA	TT	AC	CT
VV_482	GA	GG	TT	GG	CC	TT	CT	CC	AA	AA	AA	CC	AA	TT	TT	GG	TC	GG	AG	GA	CT	CA	CC	CC	TT	AA	CT	TT	AA	AA	TT	AC	CC
VV_483	AA	AG	TT	AG	TC	CC	CC	TT	AA	GA	GG	TT	GG	TT	TT	CC	TC	GG	GG	GG	CC	AA	TC	CT	TT	GG	TT	TT	AA	GA	CC	AC	CT
VV_484	GA	AA	CC	AG	TT	TC	CT	TT	AA	GA	GG	TC	GA	AT	CT	CC	CC	GG	AA	AA	TT	CC	CC	TT	TT	AG	TT	TT	GA	GG	CT	AC	TT
VV_485	GA	GG	CT	GG	CC	TC	CT	TT	AA	GA	AG	TC	AA	TT	CC	GC	CC	GG	GG	AA	CC	AA	CC	CC	TT	AA	CT	TT	AA	GA	CT	AC	CC
VV_488	GA	GG	CT	AA	CC	TT	CT	TT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	AG	AA	CT	AA	CC	CT	TT	AA	CT	TT	AA	AA	TT	AC	CT
VV_489	AA	GG	CT	GG	CC	TT	CC	CT	AA	GA	AG	CC	AA	TT	TT	GG	TC	GG	AG	AA	CC	CC	CC	CT	TT	AG	TT	TT	AA	AA	CT	CC	CC
VV_490	AA	AA	TT	GG	CC	TT	CC	CT	AA	GG	GG	CC	AA	TT	CT	CC	TC	GG	AG	GA	CT	CC	CC	CT	TT	AG	TT	TT	AA	AA	CC	AC	CC
VV_491	AA	GG	TT	GG	TC	TT	CC	CT	AA	GG	AG	TC	GA	TT	TT	GC	CC	GG	AG	GA	CT	AA	CC	CT	TT	AA	CT	TT	GA	GA	CT	AC	CT
VV_492	AA	GG	CT	GG	TC	TC	CT	CC	TA	GG	GG	TC	GA	AT	CT	CC	TC	GG	GG	AA	TT	CA	CC	CC	TT	AA	CC	TT	AA	AA	TT	CC	CT
VV_493	AA	GG	CT	GG	CC	TT	CT	CC	AA	AA	AA	CC	AA	TT	CT	CC	CC	GG	AG	AA	CT	AA	CC	CC	TT	GG	CT	TT	AA	AA	TT	CC	CT
VV_494	AA	GG	TT	AG	CC	TT	CC	CT	AA	GA	AA	CC	AA	TT	CT	CC	CC	GG	AA	AA	TT	AA	CC	CT	TT	AG	TT	TT	AA	AA	CT	AC	CT
VV_495	AA	GG	CT	GG	CC	TT	TT	TT	AA	GA	AG	TC	GA	AT	CT	CC	CC	GG	GG	GA	CC	AA	CC	CT	TT	AG	TT	TT	AA	GA	CT	CC	CT
VV_496	GA	AG	CT	GG	CC	TT	CT	CC	TT	GG	AG	CC	AA	AT	CT	GC	TC	GG	AG	AA	TT	CA	CC	CC	TT	AG	TT	TT	AA	GA	TT	CC	CT
VV_497	GA	GG	CT	GG	CC	TT	CT	CT	AA	GA	AG	CC	AA	AT	TT	CC	TC	GG	AG	GA	CC	AA	CC	CC	TT	AA	CT	TT	AA	AA	CT	CC	CC
VV_498	AA	AG	TT	AG	TC	TT	CC	CT	AA	GA	AG	TC	GG	TT	CT	CC	CC	GG	AG	GA	TT	CA	CC	CT	TT	GG	CT	TT	GA	AA	TT	AA	CT
VV_499	GG	AG	CC	GG	TT	CC	TT	TT	AA	GG	GG	TC	AA	TT	TT	GG	TC	GG	GG	AA	CT	CA	CC	CT	TT	AA	CT	TT	AA	GA	CC	CC	TT
VV_500	AA	GG	TT	AG	TC	TC	CT	CC	AA	GA	GG	TC	GA	AT	CT	GC	CC	GG	GG	GA	CT	AA	CC	CT	CT	AA	CC	CT	AA	GA	CT	AA	TT
VV_501	GG	AG	TT	AG	CC	TC	TT	CT	AA	GA	AG	TC	GA	TT	CT	CC	TC	GG	AG	AA	CC	AA	CC	CT	TT	AA	CC	TT	AA	AA	CT	CC	CC
VV_503	GG	AG	CC	GG	TT	CC	CT	CC	AA	GA	GG	TC	GA	TT	CT	CC	CC	GG	AA	AA	CT	CA	CC	CT	TT	GG	TT	TT	GA	GA	CC	AC	CT
VV_504	GA	AA	CT	AG	TC	TC	CT	TT	AA	GA	GG	TC	GA	TT	TT	CC	CC	GG	AG	AA	CC	CA	CC	CT	TT	AG	CC	TT	AA	GA	CC	CC	CT
VV_505	GA	AG	CT	GG	CC	TT	CT	TT	AA	AA	AA	TC	GA	TT	TT	CC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AA	CT	TT	AA	AA	TT	AC	CC
VV_506	GA	GG	TT	GG	TC	TT	CC	CC	TA	GA	AG	TC	GA	TT	TT	CC	CC	GG	AA	AA	CT	CA	CC	CC	TT	AA	CT	TT	GA	GA	CT	AC	CC
VV_507	GA	GG	CT	GG	TC	TC	CT	CC	TA	GG	GG	TC	GA	AT	CT	CC	TC	GG	AA	AA	CT	CA	CC	CC	TT	GG	CT	TT	AA	AA	CT	CC	CC
VV_508	GA	AG	TT	AG	TC	TC	CT	CC	TA	GA	AG	TT	GG	AT	CT	CC	TC	GG	AG	GA	CT	CC	CC	CC	TT	AA	CT	TT	AA	AA	CC	AC	CC
VV_509	GA	GG	TT	GG	CC	TT	CC	CT	AA	GA	GG	TC	GA	AT	CT	GG	TC	GG	AG	GA	TT	CA	CC	CC	TT	AA	CT	TT	AA	GA	TT	AC	CC
VV_510	GA	AG	CT	GG	TC	TC	CT	CC	TA	GG	GG	TC	AA	TT	CC	CC	TT	GG	GG	GA	0	CA	CC	CC	TT	AA	CT	CC	AA	AA	CT	CC	CT
VV_512	GA	GG	TT	AG	CC	TC	TT	TT	AA	AA	GG	TC	GA	AT	CT	GC	CC	GG	AG	GA	CT	CA	CC	CC	TT	AA	CT	TT	AA	AA	CT	CC	CC
VV_513	AA	GG	TT	GG	TC	TT	CT	CC	AA	GA	GG	TC	GA	TT	TT	GG	CC	GG	AA	GA	CC	CA	CC	CC	TT	AG	TT	TT	GG	AA	CT	CC	CC
VV_514	AA	AA	CT	GG	TC	TT	CT	CT	AA	GG	AG	TC	GG	TT	TT	CC	CC	GG	AG	AA	CT	AA	CC	TT	TT	GG	CC	TT	AA	GG	CC	CC	CC
VV_515	AA	AG	CT	GG	TC	TC	CT	TT	AA	GA	GG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	CC	CC	CT	TT	GG	TT	TT	GA	GA	CC	CC	CC
VV_516	AA	AG	CT	GG	TC	TC	CT	TT	AA	GA	GG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	CC	CC	CT	TT	AG	TT	TT	GA	GA	CC	CC	CC
VV_517	AA	AA	TT	GG	CC	TC	TT	TT	AA	GG	GG	TC	GA	TT	CT	GC	CC	GG	AG	GA	CT	AA	CC	CC	TT	GG	CC	TT	GA	GG	CT	CC	CC
VV_518	AA	GG	TT	AG	CC	CC	TT	TT	AA	GA	AG	TC	GA	AT	CC	GC	TC	GG	AG	GG	TT	CC	CC	CC	TT	AG	TT	TT	AA	AA	CT	CC	CC
VV_519	AA	AG	TT	GG	CC	TT	CT	CT	AA	GG	GG	CC	AA	TT	CT	CC	TC	GG	GG	AA	CT	AA	CC	CC	TT	AG	TT	TT	AA	AA	CC	AA	CC
VV_520	GA	GG	TT	GG	CC	TT	CC	CC	AA	GA	AG	CC	GA	TT	TT	CC	TC	GG	AG	AA	TT	CC	CC	CC	TT	AA	CT	TT	AA	GA	TT	AA	CC
VV_521	AA	AG	TT	AA	TT	TC	CT	TT	AA	AA	AG	TC	GA	TT	TT	CC	CC	GG	GG	GG	CT	CA	CC	CT	TT	GG	CT	TT	AA	GA	CT	AC	TT
VV_523	GG	GG	TT	AG	TC	TC	CT	CC	TA	GA	GG	TC	GA	TT	TT	GC	CC	GG	GG	AA	CC	CA	CC	CT	TT	AA	CT	CT	AA	GA	CT	CC	CT
VV_524	GA	GG	CT	AG	CC	TT	CT	CC	TA	AA	AA	TC	GA	TT	TT	CC	CC	GG	GG	GA	CT	AA	TC	CC	TT	AG	CT	CT	GA	GA	CT	CC	TT
VV_525	GA	GG	CT	AG	CC	TT	CT	TT	AA	GG	AA	TT	GG	TT	TT	GC	TC	GG	AG	GG	TT	CA	CC	CT	TT	AG	TT	TT	AA	GA	CC	CC	CC
VV_526	AA	GG	TT	GG	TC	TC	CC	CT	AA	GG	AG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	AA	CC	CT	TT	AA	CT	TT	GA	GA	CT	AC	CT
VV_527	AA	GG	TT	AG	CC	TT	TT	TT	AA	GG	AG	TC	GA	TT	TT	GC	TC	GG	AG	AA	CT	CA	CC	CC	TT	AG	TT	TT	GA	AA	CC	AC	CC
VV_528	GA	AG	CT	AA	CC	TC	CT	CT	AA	AA	AG	TC	GA	TT	CC	CC	CC	GG	GG	GG	CC	AA	CC	TT	TT	GG	CT	TT	AA	GG	CT	AA	CC
VV_529	AA	AA	TT	AG	TT	TC	CT	TT	AA	GG	AG	TC	GA	TT	CT	CC	TC	GG	AG	GA	CC	CC	CC	CT	CT	AA	CC	CT	AA	AA	CC	CC	CT
VV_530	AA	GG	CC	GG	CC	TC	CT	TT	TA	GA	GG	TC	GA	TT	TT	CC	CC	GG	GG	GG	CC	AA	TC	CC	TT	AG	CT	CT	AA	GG	CT	CC	CT
VV_531	GA	GG	TT	GG	CC	TC	CT	CT	AA	GA	AG	CC	AA	TT	TT	GC	TC	GG	AG	GA	CT	CA	CC	CC	TT	AA	TT	TT	GA	GA	TT	AA	CC
VV_532	AA	AG	TT	GG	CC	TC	TT	TT	AA	GA	GG	TC	GA	TT	TT	CC	TC	GG	AG	GA	CC	CC	CC	CC	TT	AG	CT	CT	AA	GA	CT	AC	CT
VV_533	GA	GG	CT	GG	CC	TT	TT	CC	TT	GA	AG	TC	GA	TT	CT	CC	TT	GG	GG	GA	TT	CC	CC	CC	TT	AG	CT	CT	AA	GA	CT	AC	CT
VV_534	GA	GG	CT	GG	TC	TC	TT	CT	AA	AA	AG	CC	AA	TT	CT	GC	CC	GG	AG	AA	CT	CA	CC	CT	TT	AA	TT	CT	AA	GA	TT	CC	CC
VV_535	AA	AA	TT	GG	CC	TT	CC	CT	AA	GG	GG	CC	AA	TT	CT	CC	TC	GG	AG	GA	CT	CA	CC	CT	TT	AG	TT	TT	AA	AA	CC	AC	CC
VV_536	GA	GG	TT	GG	CC	TT	CT	CC	AA	AA	AA	CC	AA	TT	TT	CC	CC	GG	AG	GA	CT	AA	CC	CT	TT	AA	CT	TT	AA	AA	CT	CC	CT
VV_537	AA	GG	CT	GG	CC	TT	CC	CT	AA	GA	AG	CC	AA	TT	TT	GG	TC	GG	AG	AA	CC	CC	CC	CT	TT	AG	TT	TT	AA	AA	CT	CC	CC
VV_538	GA	GG	CC	AG	CC	TT	CT	CT	AA	AA	AG	CC	AA	TT	CC	CC	CC	GG	AG	AA	CT	AA	CC	CC	TT	AA	CT	TT	AA	AA	TT	AC	CC
VV_539	GA	AG	CT	GG	TC	CC	CT	CT	AA	GA	AG	CC	AA	TT	CT	GC	CC	GG	AG	AA	TT	CC	CC	CT	TT	AA	CC	TT	AA	GA	CC	AC	CC
VV_541	GA	AA	TT	AG	TC	TC	CT	CT	AA	GA	GG	TC	GA	TT	TT	CC	CC	GG	GG	GG	CC	CA	CC	TT	TT	AG	CT	TT	AA	AA	CT	AC	CT
VV_542	GA	AA	CT	AA	CC	TC	CT	TT	AA	GG	AG	CC	AA	AT	CC	CC	CC	GG	AG	GA	CT	CA	CC	TT	TT	AG	CC	CT	GA	GA	TT	AA	TT
VV_543	GA	AG	CT	AG	CC	TT	CT	TT	TA	AA	GG	TC	GA	TT	CT	CC	TC	GG	AG	GA	CT	AA	TC	CT	CT	AG	CC	CT	AA	GG	CT	AC	TT
VV_544	AA	AG	TT	AG	CC	TT	CC	TT	AA	AA	AG	TC	GA	TT	CC	CC	TC	GG	GG	GG	CC	AA	TC	TT	TT	AG	CT	TT	AA	GG	CT	AC	TT
VV_545	GA	GG	TT	AG	CC	TT	CT	CT	TA	GG	GG	TC	GA	AT	CT	GC	TC	GG	AA	GA	TT	AA	CC	CT	TT	AA	TT	TT	AA	AA	CC	CC	CT
VV_546	GG	GG	CT	AG	CC	TC	TT	CT	AA	GA	AG	TC	GA	TT	TT	CC	TC	GG	AG	GG	CC	AA	CC	TT	TT	AG	CT	TT	AA	AA	CC	AC	CC
VV_547	GA	GG	CT	AG	CC	TT	TT	TT	AA	GG	AA	TC	GA	TT	TT	GC	TC	GG	GG	GG	TT	CA	CC	CT	TT	GG	CT	TT	AA	GG	CC	CC	CT
VV_548	GG	AG	TT	GG	TC	CC	CT	CT	TA	GG	GG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CC	CA	CC	TT	TT	AG	TT	TT	AA	GG	CC	CC	CC
VV_549	GA	AA	CT	GG	TC	TT	CT	CT	TA	GG	AG	TC	GA	TT	TT	CC	CC	GG	AG	AA	CT	AA	CC	CT	TT	AG	CT	TT	AA	GG	CT	CC	CC
VV_550	AA	GG	TT	AG	CC	TT	CC	TT	AA	AA	GG	TC	GG	TT	CC	CC	CC	GG	AA	AA	CT	CA	CC	CT	TT	GG	TT	TT	GA	GG	CT	CC	CT
VV_551	GA	AG	CT	AA	TC	TT	TT	TT	AA	AA	GG	TC	GA	TT	CT	GC	CC	GG	AG	GA	CT	AA	TC	CC	TT	AG	CT	TT	AA	GA	CC	CC	CT
VV_553	GA	AG	CT	AA	CC	TC	CT	CT	AA	AA	AG	TC	GA	TT	CC	CC	CC	GG	AG	GG	CC	AA	CC	TT	TT	GG	CT	TT	AA	GG	CT	AA	CC
VV_554	AA	GG	TT	GG	TC	TC	CC	CT	AA	GG	AG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	AA	CC	CT	TT	AA	CT	TT	GA	GA	CT	AC	CT
VV_555	AA	AG	CT	GG	TC	TC	CT	TT	AA	GA	GG	TC	GA	TT	TT	GC	TC	GG	AG	GA	CT	CC	CC	CT	TT	AG	TT	TT	GA	GA	CC	CC	CC
VV_556	GG	AG	CT	GG	TC	TC	CT	CC	TT	GA	AG	TC	AA	AT	CC	CC	TC	GG	AG	AA	CT	CA	CC	CC	TT	AA	CT	TT	AA	AA	TT	CC	CT
VV_557	GA	AG	CT	GG	CC	TC	CC	CC	AA	GA	GG	TC	AA	TT	CT	GC	CC	GG	GG	GA	TT	CA	CC	CT	TT	GG	TT	CC	GG	GG	CT	CC	TT
VV_558	GA	GG	CT	GG	TC	TC	CC	CC	AA	GG	GG	TC	GA	TT	TT	GG	CC	GG	AG	GG	CT	CA	CC	CT	TT	AA	CT	TT	AA	GA	CC	AC	CC
VV_559	AA	AG	CT	AG	TC	TT	CT	CT	TA	GG	AG	TC	GA	TT	CT	GG	CC	GG	AG	GA	CC	CC	CC	TT	CT	AG	CC	TT	GG	GA	CT	AA	CC
VV_560	AA	GG	CT	GG	CC	TT	TT	TT	AA	GA	AG	TC	GA	AT	CT	CC	CC	GG	AG	GA	CC	AA	CC	CT	TT	AG	TT	TT	AA	GA	CT	CC	CT
VV_561	GA	AG	CC	GG	TC	CC	CC	CT	AA	GA	AG	TC	GA	TT	TT	CC	TC	GG	AG	AA	TT	CA	CC	CC	TT	AA	CC	TT	AA	AA	CC	CC	TT
VV_562	GA	GG	CC	GG	TC	CC	CC	CT	TA	GG	AG	TC	GA	AT	TT	CC	TC	GG	AA	GA	CC	AA	CC	CT	TT	AA	TT	TT	AA	GA	CC	AC	TT
VV_563	GA	GG	CT	AG	CC	TT	TT	CC	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	GG	GA	CC	AA	CC	CC	TT	AA	CT	TT	AA	AA	TT	CC	CC
VV_564	AA	GG	TT	AG	TC	TC	CT	CT	AA	AA	AG	TC	GA	TT	CT	GC	CC	GG	GG	GA	TT	AA	CC	CT	TT	AG	TT	TT	AA	AA	CT	CC	TT
VV_566	GA	GG	TT	GG	CC	TT	CC	TT	AA	GA	GG	TC	AA	AT	CT	CC	CC	GG	GG	AA	GA	TT	CA	CC	0	TT	AG	TT	TT	AA	AA	TT	CC	CC
VV_567	GA	GG	CT	GG	CC	TT	TT	CT	TA	GA	GG	CC	AA	AT	CC	CC	CC	GG	AA	AA	CT	CA	CC	CC	TT	AG	TT	TT	AA	GA	TT	CC	CC
VV_568	GA	AG	CT	AG	TC	TC	TT	TT	AA	AA	GG	TT	GG	TT	CC	CC	CC	GG	AA	AA	CT	CC	CC	CC	TT	AG	TT	CT	AA	AA	CT	CC	CT
VV_569	GA	GG	TT	AG	TC	TC	CT	CT	AA	GA	GG	TC	AA	AT	CT	CC	CC	GG	AG	AA	CT	CA	CC	CC	TT	AA	TT	TT	GA	GA	CT	AC	CT
VV_570	GA	AG	TT	AA	CC	TC	CT	CT	AA	AA	GG	TC	GA	TT	CT	GC	TC	GG	AG	GG	CT	CA	CC	TT	TT	GG	CT	TT	GA	GG	TT	AC	CC
VV_571	GA	GG	CT	GG	TC	TC	CC	CT	TA	AA	GG	TC	GA	TT	TT	CC	TC	GG	AG	GG	TT	CC	CC	CT	TT	AG	TT	TT	GA	GA	CC	CC	CC
VV_572	AA	AA	TT	AG	TC	TT	CC	CT	AA	AA	GG	TC	GA	TT	CT	GC	TC	GG	AG	AA	CC	AA	CC	CC	TT	AG	TT	TT	AA	AA	CC	CC	CT
VV_573	GA	AA	TT	GG	TC	TC	CT	CT	AA	GA	GG	TC	GA	TT	TT	GC	CC	GG	AA	GA	CC	CC	CC	CC	TT	GG	TT	CT	AA	GA	CT	CC	CT
VV_574	GA	GG	CT	GG	CC	TT	CT	TT	AA	AA	AA	TC	GA	TT	TT	CC	CC	GG	AG	AA	CT	CC	CC	CT	TT	AA	CT	TT	AA	AA	TT	AA	CC
VV_575	GA	GG	CC	GG	CC	TC	CT	CT	TA	GA	GG	TC	GA	TT	CT	CC	CC	GG	GG	GG	CT	CA	CC	CT	TT	AA	CT	CC	AA	GA	CT	CC	CC

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
AA	TA	CT	CC	AA	AG	TC	AA	TC	CT	CC	TT	CC	CA	CC	AA	AT	CC	GG	AA	AG	CT	TT	TT	TT	CC	CC	0	CC	GG	GA	TT	CC	CC	TT
GG	AA	CT	TC	AA	AG	GG	TC	AA	TC	TT	TT	GG	CA	AA	CT	AG	AA	TC	AG	AG	GG	TT	TC	GG	GG	CC	CC	AG	CT	AA	AA	GG	CA	TT	TT
GG	AA	CT	TC	AA	AG	CC	GG	CC	CT	CT	TG	CA	CC	TT	GG	AT	TC	AG	GG	GG	TT	CC	GG	TG	CT	CA	GG	CT	AA	AA	GG	CA	TC	CT
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GG	TT	TT	CC	AA	AG	CC	AA	TT	CT	TT	GG	CC	CA	CT	AG	AA	CC	AG	AG	GG	TT	TC	TT	TG	CT	CA	GG	TT	GG	AA	GG	AA	TT	TT
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GG	TT	TT	CC	AA	AG	CC	AG	TC	CC	CT	TG	CA	AA	CT	AG	AA	CC	AG	AG	GG	CT	TT	TC	TT	TG	CC	CC	AG	CT	GA	AA	TG	CA	TT	TT
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chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
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CT	AA	TA	AA	TT	AA	AA	TT	CT	AG	AA	GG	GG	TT	AG	AG	GA	GA	AA	AA	GG	AA	CC	CC	TT	CC	TC	TT	CC	TG	CC	TT	AA	GG
CT	AA	TT	GA	GG	AA	TA	TC	CT	AG	CA	TT	GT	TT	AG	AG	AA	AA	GA	GG	GG	AA	TT	TC	GT	CC	CC	TT	CC	TG	CC	TT	AA	GG
CT	AA	TT	GA	TG	AA	TA	CC	TT	AG	AA	GT	GG	GT	AG	GG	AA	AA	GA	GG	GT	AA	TT	CC	GT	CT	CC	TC	CC	GG	CC	AT	AA	AG
TT	AA	TA	AA	TT	AA	AA	CC	CT	AA	AA	GT	GT	GT	AG	AG	GA	GA	AA	AA	TT	AA	CC	CC	TT	TT	TC	TT	CC	GG	CC	TT	AA	AA
CT	AG	TT	GA	TG	AA	AA	TC	CT	GG	AA	TT	GG	TT	GG	GG	AA	GA	AA	GA	GT	AA	CT	CC	TT	TT	CC	TT	CC	TG	CC	TT	GG	AA
CT	AA	TT	GA	TG	AA	TA	TC	CT	AG	AA	TT	GT	GG	AG	GG	AA	GA	AA	GA	TT	AA	TT	TC	TT	TT	CC	TC	CC	GG	TC	AT	AA	AG
CT	AA	AA	GA	GG	AA	AA	TC	TT	AA	AA	TT	GG	TT	GG	GG	AA	AA	GA	GG	GT	AA	CT	TC	GT	CT	CC	TT	CC	GG	TC	AT	AA	GG
CT	AG	AA	GA	TG	AA	TA	CC	CC	AG	AA	TT	GG	TT	GG	AG	GA	AA	GA	GG	GT	AA	CT	TC	GT	CT	CC	TT	CC	GG	TC	AT	AA	GG
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TT	GG	AA	GG	GG	TA	AA	TC	TT	AG	AA	GT	TT	GT	AG	AG	GA	GA	AA	GA	GT	AA	CT	TC	GT	TT	TC	TC	CC	TT	TC	AT	GA	AA
CT	AA	TA	GG	TG	TA	TA	TT	TT	GG	AA	TT	TT	GT	AA	AG	GG	GG	AA	GG	GG	AA	CT	TT	GT	CC	TT	TC	CT	TG	TC	AT	AA	GG
CT	GG	TA	AA	TT	AA	AA	TT	CC	AG	AA	TT	GT	GT	GG	AG	GA	GA	AA	AA	GT	AA	TT	TC	TT	TT	CC	TC	CC	GG	CC	AA	GA	AA
TT	GG	TA	GA	TG	AA	AA	TT	CC	AG	AA	TT	GT	GG	AA	AA	GA	GA	GA	GG	GG	GA	CT	TT	GT	CT	CC	TC	CC	GG	TC	TT	GG	AG
TT	AG	TT	AA	TT	AA	TA	TC	CC	AG	AA	TT	GG	GT	AG	AG	GA	GA	GA	GA	GT	AA	CT	TC	GT	CT	TC	TC	CC	GG	TC	AT	AA	GG
TT	AG	TA	GG	TT	AA	AA	TC	CC	AG	AA	GG	GT	GT	GG	AA	AA	GA	GA	GG	GT	AA	CC	TC	GT	CT	TT	TT	CC	TG	TT	TT	AA	GG
TT	AA	TA	AA	TT	AA	AA	TC	CC	AA	AA	TT	GT	TT	GG	AA	GA	GA	GG	GG	GT	AA	CC	TC	TT	CC	TC	TC	CT	GG	CC	TT	GA	AG
TT	AG	TT	GA	TG	AA	TA	CC	TT	AA	AA	TT	TT	TT	AG	AG	GG	AA	GG	AA	TT	AA	TT	TT	TT	TT	CC	TC	CT	GG	TT	TT	GA	GG
CT	AA	TA	GA	TG	TA	AA	CC	CC	AA	AA	GT	GG	TT	AG	AA	GA	GA	GA	GG	TT	AA	TT	TC	GT	CT	TC	TC	CC	TG	TC	TT	AA	GG
CC	AA	TA	GG	GG	TA	TA	TT	CT	GG	CA	GT	TT	GT	AG	GG	GA	GA	GA	GA	GT	AA	CT	TT	GT	CT	CC	CC	CC	TT	TC	TT	GA	AG
TT	AA	TA	GG	GG	0	AA	TC	TT	0	CA	TT	TT	TT	GG	GG	AA	GG	GG	GG	GT	GA	CC	CC	GG	CT	TT	CC	CC	TT	TC	AT	AA	AA
TT	AA	TA	GA	TT	AA	TA	TC	CT	AG	AA	GG	GT	GT	GG	GG	GA	AA	AA	GA	GT	AA	CC	CC	TT	CT	TC	TT	CC	TG	TT	AT	GA	GG
TT	AG	TA	GA	TT	AA	TA	TC	CT	AG	AA	GG	GT	GT	GG	GG	GA	AA	AA	GA	GT	AA	CC	CC	TT	CT	TC	TT	CC	TG	TT	AT	GA	GG
CC	AA	TA	GA	GG	AA	AA	TT	CT	AG	AA	TT	GG	GT	AA	AG	GA	GA	AA	GG	GT	AA	TT	CC	GT	CT	TC	CC	CT	TG	TC	TT	AA	AG
CT	AA	TA	GA	GG	TT	AA	TC	CT	AG	AA	GT	GT	TT	AA	AG	GA	GA	AA	GG	GT	AA	CT	TT	GT	TT	TT	TC	CC	TG	TT	TT	AA	GG
TT	AA	TA	GA	TT	AA	AA	TT	TT	AG	AA	GG	GG	TT	AA	AA	GA	GG	AA	AA	GG	AA	CC	CC	GT	CC	TC	TC	CC	TG	TC	AT	GA	GG
TT	GG	TA	GA	TG	AA	AA	TT	CC	AA	CA	GG	TT	GG	AA	AA	GA	GA	GA	AA	GG	GA	TT	TC	GT	TT	TC	TT	CC	GG	TC	TT	GA	AG
0	AA	TA	GA	TT	AA	AA	CC	CT	AA	AA	GT	GG	GT	AG	GG	AA	GA	AA	AA	GT	AA	TT	TC	GT	CC	TC	TC	CT	TG	TC	TT	GG	AA
TT	GG	TA	AA	TG	AA	TT	TT	CT	AG	AA	GT	TT	GG	AA	AG	AA	AA	GA	AA	GG	AA	CT	CC	TT	CC	CC	TC	CT	GG	CC	TT	GA	AA
CC	GG	AA	GG	GG	AA	TA	TC	TT	GG	AA	GT	TT	TT	AG	AG	GA	AA	AA	GA	GT	AA	CT	CC	GG	CT	TC	TC	CT	TG	TT	TT	GA	AA
CT	AA	TA	GA	TG	AA	TA	TC	CT	AG	AA	GG	GG	TT	AA	AA	GA	GA	GA	GG	GT	AA	CT	CC	GT	CC	TC	TC	CC	TG	TC	AT	GA	AG
CT	AG	TT	GA	GG	AA	TA	CC	CT	AG	CA	TT	GT	TT	AG	AG	AA	GA	GA	GG	GG	AA	TT	TC	GT	CC	TC	TT	CC	TG	CC	TT	AA	GG
TT	AG	AA	GA	TG	AA	TA	TC	CT	AA	AA	GG	GT	GT	GG	AG	AA	GA	GA	GG	GG	AA	CC	TC	GT	CT	TT	TT	CC	TG	TT	TT	AA	GG
TT	AG	AA	AA	TG	AA	TT	TC	TT	AA	CA	GT	GG	GG	AA	AA	AA	GA	GA	AA	GT	AA	CC	TC	GT	CT	TT	TC	CT	TG	TT	TC	AA	AG
CT	AG	TA	GA	TG	AA	TA	TC	TT	AG	AA	GT	GG	TT	AA	AG	GA	GG	GA	GA	GT	AA	CT	CC	GG	CT	TT	TC	CT	TG	TT	AA	AA	AG
CC	AG	AA	GG	GG	AA	TA	TC	CT	AG	AA	GT	GT	TT	AG	AG	AA	AA	AA	AA	GT	AA	TT	TC	TT	TT	TC	TT	CC	TG	CC	AT	GA	AA
TT	GG	TT	AA	TG	AA	TA	TT	CT	AG	CC	GT	TT	GT	AG	AG	GG	AA	GG	GA	GG	GA	TT	TT	TT	CT	TC	TT	TC	CC	GG	CC	TT	AA	GG
TT	AA	TT	GG	GG	AA	TA	TC	CC	AG	AA	TT	TT	TT	AG	AG	GA	GA	GA	GA	GG	AA	CT	TT	GT	CT	TC	TC	CT	GG	TC	TT	GG	GG
CT	AG	AA	GA	TG	AA	TT	TC	CC	AA	AA	TT	TT	GT	AG	AG	GA	GA	GA	GA	GG	GA	GT	AA	CC	TT	GT	CT	TC	CC	CT	GG	TT	TT	GA	AG
CC	GG	TA	GA	TG	TA	AA	TT	CT	AG	CA	GG	TT	GG	AA	AA	GA	GA	GA	AA	GA	GA	GT	AA	CC	TT	GT	CT	TC	CC	CT	TG	TT	TT	GA	AG
TT	AA	TA	AA	TT	AA	AA	TT	CT	AG	AA	GG	GG	AA	AG	GG	GA	GG	GA	AA	GA	GA	GT	AA	CC	TT	GT	CT	TC	CC	CT	TG	TT	TT	GA	AG
CT	AG	TA	GA	TG	TA	AA	TT	CT	GG	AA	TT	GG	TT	AG	AA	GA	GA	GA	AA	GA	GA	GT	AA	CC	TT	GT	CT	TC	CC	CT	TG	TT	TT	GA	AG
CT	AA	AA	GA	GG	AA	TA	TC	CT	GG	AA	GG	GG	TT	AA	AA	GA	GA	GA	GG	GG	GA	GT	AA	CC	TT	GT	CT	TC	CC	CT	TG	TT	TT	AA	AG
TT	AG	AA	AA	TG	AA	TT	TC	TT	AG	CA	GT	GG	GG	AA	AA	AA	GA	GA	AA	GT	AA	TT	TC	GG	TT	TC	CC	CT	TT	TC	AT	AA	GG
CT	AG	TT	GA	GG	AA	TA	TC	CT	AG	CA	TT	GT	TT	AG	AG	AA	GA	GA	GG	GG	AA	TT	TC	GT	CC	CC	TT	CC	TG	CC	TT	AA	GG
0	AG	TA	GA	TT	AA	TA	TC	CT	AG	AA	GG	GT	GT	GG	GG	GA	AA	AA	GA	GT	AA	CC	CC	TT	CT	TC	TT	CC	TG	TT	AT	0	GG
CT	GG	TA	GA	TG	AA	AA	TC	CT	AA	CA	GT	GT	TT	AG	AG	GA	AA	GG	AA	GT	GA	TT	TT	GT	CT	TC	TT	CC	GG	TC	TT	AA	AG
CT	AG	AA	AA	GG	AA	TA	CC	TT	AA	CA	GT	GT	TT	GG	GG	GA	0	AA	AA	TT	AA	TT	CC	TT	TT	TC	TC	CC	TG	TT	AT	AA	GG
TT	AG	TA	GA	GG	AA	TA	TC	CT	GG	AA	GT	GT	GT	AG	GG	AA	AA	GA	GA	GT	AA	CT	TT	TT	CT	TC	TT	TC	TG	TC	AT	GA	AG
TT	AA	AA	GA	TT	AA	AA	TC	CT	GG	AA	GT	GG	GT	AA	AA	GA	AA	GA	GG	GT	AA	TT	TC	GG	CT	TC	TC	CC	CT	TG	TC	AA	AG
TT	AG	TT	GA	TG	AA	TA	TC	CT	AG	AA	TT	GT	GG	AG	AG	GA	GA	GA	GG	GT	AA	TT	TC	GT	CC	CC	TT	CT	TC	TT	CC	TG	TT	AT	GA
TT	AA	TA	AA	GG	AA	AA	TC	TT	AG	AA	TT	TT	GT	AG	AA	GG	GA	GA	GG	GG	AA	CC	TC	GT	CT	TC	TC	CT	TG	CC	AA	AA	GG
TT	AA	TT	GG	TT	AA	AA	TT	TT	AG	AA	GT	GG	TT	GG	AG	GG	GA	GG	GG	GT	AA	CC	CC	GG	CT	TC	TC	CC	TG	TC	TT	AA	GG
CT	AA	TA	GA	TG	TA	AA	TC	CT	AA	CA	GG	TT	GT	GT	AG	GG	GA	GG	GG	GT	AA	CT	TC	TT	TT	TC	TC	CT	GG	CC	AT	AA	AA
CT	GG	AA	GG	GG	TT	AA	TT	TT	AG	CA	TT	GT	GT	AG	GG	GG	GA	GG	GG	GT	AA	TT	TT	GT	CC	TC	TC	CT	TG	TC	TT	GA	AA
TT	AA	TA	AA	TT	AA	TA	TC	CC	AG	AA	TT	GT	TT	AG	AG	GG	GA	GG	GG	GG	AA	CT	TC	TC	CT	CC	TC	CC	GG	TC	TT	GG	GG
CT	AG	AA	GA	GG	AA	AA	CC	CT	AA	AA	TT	GT	GT	GG	AG	GG	GA	GA	GG	TT	AA	CT	TC	TT	CT	CC	TC	CT	GG	CC	AT	AA	AG
CC	AG	TA	GG	GG	TA	AA	TT	CT	GG	CA	GT	GG	GG	AG	GG	GA	GA	GA	GA	TT	AA	CC	TT	GT	TT	TC	TC	CC	GG	TC	AT	AA	GG
CT	AG	TA	GA	GG	AA	TA	TC	CC	AA	CA	GG	TT	GT	AA	AG	GA	GG	GA	GG	GG	AA	CC	TC	TT	CT	TC	TC	CT	GG	CC	AT	AA	AA
TT	GG	TA	GA	GG	AA	TT	TC	TT	GG	CA	TT	GT	GG	AA	AG	GA	GG	GA	GG	GT	AA	TT	TC	GG	CT	TT	TC	CC	GG	TC	AT	GA	GG
TT	AG	TA	GG	TG	AA	TA	TC	CT	AA	AA	GT	TT	GG	AG	GG	GG	AA	GA	GG	GG	AA	CC	TC	TT	CT	TC	TC	CC	GG	TT	TT	AA	GG
CT	GG	TA	GG	TG	TA	AA	TT	TT	AG	CA	GT	TT	GT	AA	AG	GA	GG	GA	GG	GT	AA	CT	CC	GT	CC	TC	TC	TT	TG	CC	AT	GA	AG
TT	AA	TA	GA	TG	TA	TA	TC	CT	AG	AA	TT	GG	TT	AG	AG	AA	AA	GA	AA	TT	AA	TT	TT	GG	TT	CC	TC	CT	TT	TC	TT	0	AG
CT	GG	TT	AA	TT	AA	AA	TT	CC	AG	AA	TT	GT	GT	GG	AG	GA	GA	AA	AA	GT	AA	TT	TC	TT	TT	CC	TC	CC	GG	CC	AT	GA	AG
CT	AA	TT	GA	TG	AA	TA	TC	CC	AG	AA	TT	GT	TT	AG	AG	GA	AA	GA	AA	GT	AA	CT	TT	TT	CT	TT	TC	CT	GG	TT	TT	GG	AG

Supplementary Table 7. The information of 102 SNPs of 466 accessions for variety identification.

Chromosome	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr01	chr02	chr02	chr02	chr02	chr02	chr02	chr02	chr03	chr03	chr03	chr04	chr04	chr04	chr04	chr04	chr04	chr05	chr05	chr05	chr05	chr05	chr06	chr06	chr06
Position	725679	5332210	5901144	12406250	12492521	12540047	24497651	27484462	27597412	238470	2311431	4819248	5171354	7938134	8280257	19276556	1338747	5755134	18710777	688977	1561129	2976830	6397345	19945587	23924939	4199526	4753271	5959627	6917573	26158932	386681	2582442	4301271
VV 576	GA	GG	CT	GG	CC	TC	CT	CT	AA	AA	GG	TC	GA	TT	TT	CC	CC	CC	GG	GG	GA	CT	CA	CC	CC	TT	AA	CT	CC	AA	GG	TT	AC	CT
VV 577	GA	AG	CT	GG	CC	TC	CC	CT	AA	GA	GG	TC	AA	TT	CC	CC	CC	CC	GG	GG	GA	TT	CC	CC	CT	TT	AA	CC	CT	AA	AA	CT	CC	CT
VV 578	GA	AG	TT	GG	CC	TT	TT	CC	TA	GA	AA	CC	AA	TT	CC	CC	CC	GG	AG	AA	TT	CC	CC	CC	TT	AG	TT	CT	AA	GG	TT	AC	CT
VV 579	AA	GG	TT	GG	CC	TC	TT	CC	AA	GG	GG	CC	AA	AT	CC	CC	TT	GG	AA	GA	CC	AA	CC	CT	TT	AA	CC	CT	GA	GA	CT	CC	CC
VV 580	GA	GG	CT	GG	CC	TC	CT	TT	AA	GG	AG	TC	GA	TT	CT	CC	CC	GG	GG	GG	CC	AA	TC	CC	TT	AA	CC	CC	AA	GG	TT	CC	CT
VV_581	GA	GG	CT	AG	CC	TC	CT	TT	AA	GA	AA	CC	AA	TT	TT	CC	TC	GG	AG	AA	CC	AA	CC	CT	TT	AA	CT	TT	AA	AA	CT	AC	TT
VV 582	GA	GG	CT	GG	CC	TT	TT	CC	TA	GA	AG	CC	AA	AT	CC	CC	CC	GG	AG	GA	CC	CA	CC	CT	TT	AA	CT	CT	AA	AA	TT	CC	CC
VV 583	GA	GG	CT	GG	CC	TT	TT	TT	AA	AA	AG	CC	AA	TT	CT	CC	CC	GG	AA	GA	CT	CA	CC	CC	TT	AG	TT	CT	AA	GG	CT	CC	CT
VV 584	AA	AG	CC	GG	CC	TT	TT	CT	TA	GA	AG	CC	GA	AT	CT	CC	CC	GG	GG	AA	CT	CA	CC	CC	TT	AG	TT	TT	AA	AA	TT	AC	CT
VV_585	GA	AG	CT	GG	CC	TC	CT	CC	AA	AA	AG	TC	GA	TT	CC	CC	CC	GG	AA	AA	CT	AA	CC	CC	TT	AG	CC	TT	GA	AA	CT	AC	CT
VV 586	AA	AG	CT	AG	CC	TC	TT	TT	AA	GA	AG	TC	GA	AT	CT	CC	TC	GG	AG	AA	CT	CA	CC	TT	TT	AA	CT	CT	AA	GG	CC	AC	TT
VV 587	GA	GG	TT	GG	CC	TT	TT	CC	TA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	GA	CT	AA	TC	CC	TT	AG	CT	TT	AA	GA	CT	AC	CT
VV 588	AA	AG	CT	GG	TT	CC	CT	TT	AA	AA	AA	TC	GA	TT	CC	GC	CC	GG	AA	GA	CT	CC	CC	CT	TT	AG	CT	TT	AA	GA	TT	AA	CT
VV 589	GA	AA	CT	AG	CC	CC	TT	TT	AA	GA	AA	CC	GA	TT	CC	CC	CC	GG	GG	GA	CT	CA	CC	TT	TT	GG	TT	TT	GA	GG	CT	AA	CT
VV 590	GA	GG	TT	GG	CC	TC	CC	CC	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	AA	CC	AA	CC	CT	TT	AG	CT	CC	GA	GG	TT	CC	CT
VV 591	GA	GG	TT	GG	CC	TC	CC	CC	AA	GA	AG	TC	GA	TT	CT	CC	CC	GG	AG	AA	CC	AA	CC	CT	TT	AG	CT	CC	GA	GG	TT	CC	CT
RED GLOBE	AG	AG	AG	GG	CC	TT	CT	AA	TT	AG	GG	CT	AA	TT	CT	CC	CC	AA	AA	TT	AA	CC	CC	CT	AA	CT	CT	TT	AA	AG	AG	AC	CC
FLAME SEEDL	AA	GG	AG	GG	CT	CT	CC	GG	TT	AG	AA	CT	AG	TT	CT	CC	CC	AA	AG	CT	GG	AA	CC	CT	AA	TT	CT	TT	AA	AG	AA	AC	CC
CRIMSON SEE	AG	GG	AA	GG	CT	TT	CC	GG	AT	AG	AG	CT	AG	TT	TT	CC	CC	AA	AA	TT	AG	AC	CC	CC	AA	TT	CT	TT	AG	AG	AG	AC	CC
CENTENNIAL :	0	AG	0	GG	CT	CT	CT	GG	0	0	AG	CT	AA	0	CC	0	CT	0	AG	TT	AG	AC	CC	CC	AA	TT	CT	TT	0	AA	AA	CC	CT
MUSCAT HAM	AG	GG	AA	AG	CC	TT	TT	AG	TT	AA	AG	CC	AA	TT	CT	CC	CC	AA	AG	TT	AG	AC	CC	CC	AA	TT	CT	CT	AA	AG	AA	AC	CT
BLACK MONU	0	AG	0	GG	CT	CT	CC	GG	0	0	AG	CT	AG	0	TT	0	CT	0	AG	TT	AG	AA	CC	CC	AA	TT	CT	TT	0	AA	AG	CC	CT
BAKHTIORI	0	GG	0	GG	CT	CT	CC	AA	0	0	GG	CT	AG	0	TT	0	CT	0	AA	TT	GG	AC	CC	CT	AA	TT	CC	TT	0	AG	GG	CC	CC
ITALIA	AG	AG	0	GG	CC	TT	CT	AA	TT	AA	AA	CT	AG	TT	TT	CC	CC	AA	AG	TT	AG	AC	CC	CT	AA	TT	CT	TT	AA	AA	AA	AC	CC
PAMID	AA	AG	AA	AG	0	CT	0	AG	TT	AG	AG	0	AG	TT	0	CC	CT	AA	0	TT	AG	0	CC	0	AA	CT	0	TT	GG	0	AG	0	CT
BORRACAL	AG	AG	AG	AA	CT	CC	TT	AA	AT	AA	AG	CC	GG	TT	CT	CG	CC	AA	AG	CT	GG	AC	CC	TT	AA	CT	CT	TT	AG	AG	AA	AA	CT
CABERNET_SA	AA	AA	GG	AA	CC	CT	TT	AA	AT	AG	AG	CT	AG	AT	CT	CC	CC	AC	GG	CT	GG	AA	CT	TT	AG	CT	CC	CT	AG	AG	AG	AC	TT
RKATSITELI	AG	AG	AG	AG	CT	TT	CT	AA	TT	AA	GG	CT	AG	TT	CT	CG	CC	AC	AG	CT	AG	AA	CT	CC	AA	CT	CT	TT	AA	AG	GG	CC	CT
CABERNET FR	AG	AA	AG	AG	CC	CC	TT	AA	TT	AG	AA	CC	AG	TT	CT	CC	CC	CC	GG	CT	GG	AC	CC	TT	AA	CC	CT	TT	AG	GG	AG	AA	CT
DOMINA	0	AG	0	AA	TT	CT	CT	AA	0	0	AA	CT	GG	0	CT	0	CT	0	GG	CT	AA	AA	CC	TT	AG	CT	CT	TT	0	GG	AA	AA	CC
PINOT NOIR	AA	GG	0	AA	TT	CT	CC	AA	0	AG	AG	CT	GG	0	CT	0	CT	0	GG	CC	AG	AA	CT	CT	AG	CT	CT	CT	0	GG	AA	AA	CT
SANGIOVESE	AG	AG	0	GG	CT	CC	CT	AG	0	AG	AG	CC	AA	0	CT	0	CC	0	AG	CT	AA	CC	CC	CT	AA	TT	CC	TT	0	AG	GG	AC	CC
SYRAH	AA	GG	0	AA	CT	CT	CT	AG	0	AA	AG	CT	AG	0	CT	0	CC	0	AG	CC	GG	AC	CT	TT	AA	CC	CT	TT	0	AG	AG	CC	CT
RUBY SEEDLE	AA	AG	0	GG	0	CC	0	AG	TT	AG	GG	0	AA	TT	0	CC	CT	AA	0	TT	AG	0	CC	0	AA	TT	0	TT	0	0	AG	0	CT

chr06	chr06	chr06	chr07	chr07	chr07	chr07	chr07	chr07	chr08	chr08	chr08	chr08	chr08	chr08	chr08	chr09	chr09	chr09	chr09	chr10	chr10	chr10	chr10	chr11	chr11	chr11	chr11	chr12	chr12	chr12	chr12	chr12	chr13	chr13
19450499	20643542	20891585	1772191	4887023	8504809	11364396	27931721	28693769	3346486	14068390	14558827	17455732	19943405	22884616	23470081	3120625	5730661	10775153	21348939	2197172	10174796	10564516	14067209	313254	3437175	5380410	19617365	763236	6737303	7809515	23264086	24228235	284575	5694277
AG	TA	TT	CC	AA	AG	TC	AG	CC	CC	TT	TG	CA	AA	CT	AG	AT	TC	AG	AG	GG	CC	TC	TG	GG	CT	CA	AG	CT	GG	AA	TT	CA	TT	TT
GG	TA	CT	TT	AA	AG	TC	AG	CC	CC	TT	TG	CA	AA	CT	AG	AA	TC	AG	GG	GG	CC	TC	TG	TG	CC	CC	AA	TT	GA	AA	TG	CA	TC	TT
AG	TT	CT	CC	AA	AG	CC	AA	TC	CT	TT	TG	CA	AA	CT	AG	AT	TC	AA	AG	AG	CC	TT	TG	TG	CC	CA	AA	TT	GA	AA	TT	CC	CC	TT
GG	TA	CT	TC	AA	GG	TT	AG	TC	CT	TT	TG	CC	AA	CT	AG	AA	TT	AG	AA	AG	TT	TT	GG	GG	CC	CC	GG	CC	GA	AA	GG	CA	TC	TT
AG	TA	CT	CC	AA	AA	TC	AG	TC	CC	CT	TT	AA	CA	CT	GG	TT	TC	AA	GG	AA	CC	TC	TT	TT	CT	CC	GG	CT	GG	AA	TG	AA	TC	TT
AG	TA	CT	CC	AA	AG	CC	AA	TC	TT	TT	TG	CA	AA	CT	AG	AT	CC	AG	GG	AG	CT	TC	TG	TG	CC	CC	AA	CT	GG	GA	TG	CA	TC	TT
AG	TA	CC	TC	AA	AA	CC	GG	CC	CT	CT	GG	CA	AA	CT	AG	AT	CC	AA	AG	AG	CC	TT	GG	GG	CC	CC	GG	CT	GG	AA	TT	CC	CC	TT
AG	TT	CT	CC	AA	AA	CC	AA	TC	CT	CT	TG	CA	AA	TT	AG	TT	TC	AA	GG	AA	CC	TT	0	GG	CT	AA	AG	CT	GG	AA	TT	CA	TT	TT
AG	AA	CC	CC	AA	AG	CC	AG	TC	CC	TT	GG	CA	AA	CT	GG	AA	TC	AG	AG	GG	CC	TT	TG	GG	TT	CC	GG	CT	GG	AA	TG	CA	TT	TT
AG	TT	CT	TC	AA	AA	CC	GG	CC	CT	CT	TT	CA	CA	CT	GG	TT	CC	AA	AG	GG	CC	TC	TT	TG	CC	CC	AG	CT	GG	GA	GG	CA	TC	TT
AG	TA	TT	TC	AA	GG	TC	AG	TT	TT	CT	TG	AA	AA	TT	GG	TT	TC	AA	AG	AG	TT	CC	TT	TT	CT	CA	GG	TT	GA	GA	TT	CA	TT	TT
AG	TT	CT	CC	AA	AG	TT	AG	CC	CC	TT	TG	CA	AA	TT	GG	TT	TC	AG	AG	GG	CC	TT	GG	TG	CT	CA	GG	CT	GG	AA	TG	CA	TT	TT
AG	TT	CT	TC	AA	GG	TT	GG	TT	CT	CT	TG	AA	CA	CT	AA	AT	TC	AA	AG	AA	CT	CC	TG	TG	CT	CA	GG	TT	GA	AA	TG	CC	TC	TT
AA	AA	CC	CC	AA	GG	TC	GG	TT	TT	CC	TG	CA	CA	CT	AA	AT	TC	GG	GG	GG	CT	TC	TT	GG	TT	CC	AG	CT	AA	AA	TG	AA	TC	TT
GG	TT	TT	TC	AA	GG	TT	AG	TC	CT	CT	TG	CA	CA	TT	AG	AT	TT	AG	AG	AG	CT	TT	TT	GG	CC	CA	AG	CT	GA	AA	TG	CA	TC	TT
GG	TT	TT	TC	AA	GG	TC	AG	TC	CT	CT	TG	CA	CA	TT	AG	AT	TT	AG	AG	AG	CT	TT	TT	GG	CC	CA	AG	CT	GA	AA	TG	CA	TC	TT
GG	AT	CT	AG	TT	CC	CT	AA	AG	TT	TT	CC	GT	TT	CT	AG	TT	CT	AG	AG	GG	TT	CT	GG	CC	CC	CC	AG	CT	AA	TT	GG	0	TT	AA
AG	AT	CC	AG	TT	CC	TT	AG	GG	TT	TT	AA	GT	TT	CT	GG	TT	CT	AG	AG	GG	CC	TT	TT	CC	CT	AC	GG	CC	GG	TT	GT	CC	TT	AA
GG	AT	CT	AG	TT	CC	TT	AG	AG	CT	CT	AA	GT	TT	TT	GG	AT	CT	GG	AA	GG	TT	CT	GG	AC	CC	CC	GG	CC	AG	TT	GG	AA	CT	AA
GG	0	CT	AA	GT	TT	CC	AG	GG	CC	TT	CC	GG	TT	CT	AG	0	CC	AG	AG	0	TT	CT	GG	0	CT	CC	AG	CT	AG	TT	GG	AC	TT	AA
GG	AA	TT	GG	GT	TT	CC	AG	AG	CT	CT	AA	GT	TT	CT	AG	AT	CC	AA	GG	AG	CC	TT	GT	AC	CC	AC	AG	TT	GG	TT	GT	AA	CT	AA
AG	0	CT	GG	TT	CC	CT	AA	AG	TT	TT	AC	GT	TT	CT	GG	0	CT	AG	AG	0	CT	CT	GT	0	CC	CC	AA	TT	AG	TT	GT	CC	CT	AA
AA	0	CT	GG	TT	CC	TT	AA	AG	TT	CC	AA	GT	TT	CT	AA	0	TT	GG	GG	0	TT	CT	GG	0	CC	AC	AA	CC	AG	TT	GG	AC	CT	AA
GG	AT	CT	GG	TT	CT	CC	GG	AA	CT	CT	AC	GT	TT	CT	GG	AT	CT	AG	AG	GG	CC	CT	TT	CC	CT	CC	AG	TT	GG	TT	GG	AA	CT	AA
AG	AT	0	AA	GT	CT	0	0	GG	CC	0	CC	GT	GG	CT	0	AA	0	0	GG	GG	0	TT	0	CC	0	0	GG	TT	0	CT	0	AC	0	AA
AG	TT	CT	GG	GT	CC	TT	AG	AG	CT	CC	AA	TT	TT	CT	AG	AA	CT	AG	AG	GG	TT	CT	GT	CC	TT	AC	AA	CT	GG	TT	GT	AA	TT	AA
AG	TT	CC	AG	GT	CT	CC	GG	AA	CT	CT	CC	GT	TT	TT	AG	AT	CT	GG	GG	AG	CC	CT	GG	AC	TT	AC	AG	CC	AA	CT	GT	AC	CC	AA
GG	TT	CC	GG	0	CC	0	0	AG	CT	TT	CC	GT	GT	0	GG	AA	CC	0	GG	AG	CT	CT	TT	AC	TT	AC	GG	CC	AA	TT	GT	AC	CT	AA
AG	TT	CC	GG	TT	CC	TT	GG	AA	TT	CC	AC	GT	GT	CT	AA	AT	CT	GG	GG	GG	CT	CT	GT	CC	TT	CC	AG	CT	AA	TT	GT	AA	CT	AA
AG	0	CC	GG	GT	CC	TT	AG	AG	TT	CT	AC	TT	TT	TT	GG	0	CT	GG	GG	0	CT	CC	GG	0	CT	AC	AG	CT	AG	TT	GG	AC	CC	AG
AA	0	CC	AG	GT	CC	TT	AG	AG	CT	CT	AC	TT	TT	TT	AG	0	CT	GG	AG	GG	CC	CC	GG	AA	CT	AC	AG	CT	AG	CT	GT	AA	CT	AA
GG	0	CT	GG	GT	CC	TT	GG	GG	CT	CT	AC	GT	TT	CT	AG	0	CT	AG	AG	AG	CT	CT	TT	CC	TT	AA	GG	CT	GG	CT	GT	AA	CT	AA
GG	0	CC	AG	GT	CC	TT	AG	AG	CT	TT	CC	TT	GT	CT	GG	0	CT	AG	AA	AG	CT	CT	GG	AC	TT	AC	GG	TT	AG	CT	GT	AC	CT	AA
GG	AA	0	AG	TT	CC	0	0	AG	CC	0	AC	GG	TT	0	0	AT	0	0	AG	GG	0	CT	0	AC	0	0	GG	CC	0	TT	0	AC	0	AA

chr13	chr13	chr13	chr14	chr14	chr14	chr14	chr14	chr14	chr15	chr15	chr15	chr15	chr15	chr15	chr16	chr16	chr16	chr16	chr17	chr17	chr17	chr17	chr17	chr18	chr18	chr18	chr18	chr18	chr18	chr19	chr19	chr19	chr19
16648069	21577747	27055823	4383127	4965016	5708394	23052201	24330364	29799217	13863223	18163034	21285011	21381247	21816458	22578285	18252856	20981646	22887819	26743754	595010	1547719	6396882	12603453	18942983	3829167	6533289	11087581	11492868	24557139	36254417	2038608	7224837	9132773	26962583
CT	AA	AA	GA	TG	AA	AA	TT	CC	AA	AA	TT	GT	GT	GG	AG	GA	AA	AA	GA	GG	AA	TT	TC	TT	TT	TC	TC	CC	TG	CC	AT	GA	AA
CT	AG	TA	GG	GG	AA	TA	CC	CT	AA	AA	GT	TT	GT	AG	GG	GA	AA	GG	GA	GG	GA	CT	TT	GT	CT	CC	TC	CT	GG	TT	TT	AA	GG
TT	AA	TA	AA	TG	AA	AA	TT	CT	AG	AA	GT	GT	GT	GG	AG	GA	AA	AA	GA	TT	AA	CT	CC	TT	TT	CC	CC	CC	GG	CC	AT	AA	AG
TT	GG	TT	GA	TG	TA	TA	TT	CT	AA	AA	TT	GG	TT	GG	AG	GA	GG	GA	GG	GG	AA	CC	TC	GT	CT	TC	TT	CC	GG	CC	AT	AA	AG
CC	AG	AA	GG	GG	AA	AA	TT	CT	AG	AA	TT	GT	GT	GG	GG	GA	AA	AA	AA	TT	AA	TT	TC	TT	TT	TC	TT	CC	GG	CC	AA	GA	AG
CT	AG	TA	AA	TG	AA	AA	TT	CC	AG	AA	GT	GT	GT	GG	AG	GG	GA	GA	GA	GG	AA	CT	TT	GT	TT	TT	TT	CT	GG	TT	TT	AA	AG
CT	AG	AA	GA	TG	TA	AA	TT	TT	AA	CA	GT	GT	GT	AG	AG	AA	GA	AA	GG	GT	AA	CT	CC	TT	TT	TC	TT	CT	GG	TC	AT	AA	AA
CT	AG	AA	GA	TG	AA	AA	TT	CT	AA	AA	TT	GT	GT	AA	AA	GA	AA	AA	AA	GT	AA	TT	TC	TT	TT	CC	TC	CC	GG	CC	AT	GA	AA
CC	AG	TA	GA	TG	AA	TA	TT	CT	AA	AA	TT	GG	GT	AG	GG	AA	AA	AA	AA	TT	AA	TT	TC	TT	TT	CC	TC	CC	GG	TC	AA	AA	AG
TT	AA	AA	GA	TG	AA	AA	TC	CT	AG	AA	GT	GT	GG	AG	AA	GG	GA	AA	AA	GT	AA	CT	TC	TT	TT	TC	TT	TT	TG	CC	AT	AA	AA
TT	AG	AA	GA	TG	AA	AA	TC	TT	AG	AA	TT	GT	TT	GG	AG	GA	GA	AA	GG	GT	AA	CT	TC	TT	CC	CC	TC	CT	GG	TC	AT	GA	AG
CC	AA	TA	GG	GG	AA	AA	TC	CT	AG	AA	GT	TT	GT	GG	AG	GA	AA	AA	GA	GG	AA	TT	TT	TT	TT	CC	TC	CC	GG	CC	AT	GG	AG
CT	AG	TT	GA	TG	TA	TT	CC	TT	AG	CA	GT	GT	GT	AG	GG	GA	AA	GG	GA	GT	AA	CC	CC	TT	CT	TC	CC	CT	TG	TT	TT	AA	AA
TT	AA	TA	GA	GG	TA	AA	TT	TT	AG	CC	GT	GG	GT	AA	AA	AA	AA	GG	GA	GG	AA	TT	TT	GT	TT	TC	CC	CT	TT	TC	TT	GA	GG
TT	AG	AA	GA	TG	AA	AA	TT	CT	GG	AA	GG	TT	GG	AA	AG	GA	GA	GA	GA	GT	AA	TT	TC	TT	CC	CC	TT	CT	TT	TT	AA	AA	AG
TT	AG	TA	GA	TG	AA	AA	TT	CT	GG	AA	GG	TT	GG	AA	AG	GA	GA	GA	GA	GT	AA	TT	TC	TT	CC	CC	TT	CT	TT	TT	AA	AA	AG
TT	AA	AA	AA	TT	AA	0	TT	CT	CC	AC	AA	TT	TT	TT	GG	AG	GG	GG	GG	GG	TT	AA	TT	AC	TT	GG	CC	GG	GG	TT	TT	GG	AG
CC	AA	TT	AA	GT	AA	0	TT	CT	TT	AA	AA	GT	TT	CT	AA	AA	AG	AA	AG	TT	TT	AA	CT	AA	CT	GG	TT	GG	GT	CC	TT	AA	AG
TT	GG	AT	AG	GT	AA	0	TT	CC	CT	AA	AC	GT	GG	TT	AA	AG	AG	AG	GG	GG	CT	AG	TT	AC	CT	GG	CT	GG	GG	CT	TT	GG	AG
CT	GG	0	AG	GT	0	0	CT	CT	TT	0	0	GT	TT	CT	AG	AG	AA	GG	AA	GT	CT	AG	TT	AC	CT	0	TT	GG	GG	CT	0	AA	AG
CT	AG	AT	AG	GT	AA	0	CT	CC	CT	AA	AC	TT	GG	CT	AA	GG	AA	AA	AG	GT	TT	AA	TT	AA	TT	AG	CT	AG	GG	CT	AT	AG	AG
CT	AG	0	AA	GT	0	0	CT	CT	TT	0	0	GG	TT	CC	AG	AG	AA	GG	GG	GG	TT	AG	CC	AC	CC	0	TT	GG	GG	CT	0	AA	AG
TT	AA	0	GG	GG	0	0	CC	CT	CT	0	0	TT	TT	TT	AG	GG	AA	GG	GG	GT	TT	GG	CT	CC	CC	0	CT	GG	GG	CT	0	AG	GG
CT	GG	0	AA	TT	AA	0	TT	CC	CT	AA	AA	GT	GT	CC	AG	AG	AG	AA	AA	GT	TT	AA	CT	AA	TT	GG	CT	GG	GG	CT	AT	AG	AG
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TT	GG	AT	AA	TT	AA	0	CT	CT	CC	AC	CC	GT	GT	TT	AG	GG	GG	GG	GG	GG	TT	AG	TT	AC	CT	GG	CT	AA	GG	CT	TT	AG	AG
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TT	AA	AT	AG	GG	AT	0	TT	TT	CT	0	AC	GG	GT	TT	AA	AA	AA	GG	AG	GG	TT	AA	TT	AC	TT	AG	CC	AG	TT	CT	TT	AG	GG
CC	AG	0	GG	GG	0	0	CT	TT	CT	0	0	GG	TT	CT	GG	AG	AA	AA	AG	TT	TT	AA	TT	AA	TT	0	CC	AA	GT	CC	0	GG	AA
CC	AG	0	GG	GG	0	0	CC	TT	CT	AA	0	GG	GT	CT	GG	AG	AG	AA	AA	GT	TT	AA	CT	AC	TT	0	CT	AA	GT	CC	0	GG	AA
TT	AG	0	AG	GT	0	0	CT	TT	TT	AA	0	TT	GG	CC	AG	AG	GG	AG	GG	GG	TT	AG	CT	CC	TT	0	CC	AG	TT	TT	0	GG	AA
CT	AA	0	AG	GT	0	0	CT	CT	CC	AC	0	GT	0	CT	GG	AG	AA	GG	AG	GT	TT	AA	CT	AC	CT	0	CC	AG	GT	CT	0	AG	AG
0	AG	0	0	0	AA	0	0	CT	CT	AA	AC	0	0	CT	AA	0	0	AG	0	GG	CT	AG	0	AC	CT	GG	0	AG	0	0	TT	0	0

Supplementary Table 8. Candidate regions of 29 traits in GWAS results.

Chromesome	Start	End	Main	Additional	Significant Marker	Marker nu	PVE(main)	PVE(addition)
1	5,400,292	5,718,595	2016 Cit1		SNP 1 5522692	1	6.64E-02	
1	9,590,642	9,610,742	2016 BeWe1		SNP 1 9600725	5	8.20E-02	
1	19,360,413	19,560,413	2017 SL1		SV 1 19460413	1	6.57E-02	
1	20,494,969	20,526,984	2016 Mal1		SNP 1 20526293	1	6.46E-02	
1	20,532,857	20,631,163	2017 Tar1		SNP 1 20584576	3	6.46E-02	
1	21,474,035	21,506,463	2016 FJ1		SNP 1 21484252	2	6.06E-02	
1	24,196,597	24,220,512	2016 SN1		SNP 1 24209061	1	6.57E-02	
2	2,210,519	2,233,670	2017 BuW1		SNP 2 2220519	1	6.60E-02	
2	8,925,187	9,234,222	2017 FF1	2016 FF	SNP 2 9089792	2	0.068185911	0.068184963
2	9,661,928	9,682,014	2016 FF2	2017 FF	SNP 2 9672014	24	0.106936776	0.106932251
2	12,045,733	12,110,254	2016 BC1	2016 BB	SNP 2 12062192	23	0.076654326	0.062790733
2	15,973,704	16,005,939	2016 BC2	2016 FF,2017 FF	SNP 2 15978257	54	0.092189443	0.080742794,0.080739503
2	16,099,578	16,110,342	2016 BC3	2016 BB	SNP 2 16099578	37	0.14943516	0.07364597
2	16,249,584	16,900,682	2016 BC4		SNP 2 16291213	167	1.44E-01	
2	16,255,355	16,556,578	2016 BC5		SNP 2 16421597	60	1.20E-01	
2	16,344,788	16,795,984	2016 BC6	2016 BB	SNP 2 16585556	152	0.162205147	0.08066265
2	16,583,037	16,899,182	2016 BC7		SNP 2 16665777	108	1.17E-01	
2	16,943,304	17,791,342	2016 BC8	2016 BB	SNP 2 16949926	440	0.122993638	0.06497016
2	16,944,506	17,310,587	2016 BC9	2016 BB	SNP 2 17119651	66	0.128330235	0.068760187
2	17,012,776	17,236,498	2016 BC10	2016 BB	SNP 2 17331577	87	0.1618869	0.072423692
2	17,323,054	17,655,291	2016 BC11	2016 BB	SNP 2 17438803	191	0.147109421	0.063509161
2	17,655,291	18,213,101	2016 BC12	2016 BB,2017 FF,2016 FF	SNP 2 17854977	73	0.132438221	0.071487562,0.071064022,0.07106654
2	17,855,131	18,214,145	2016 BC13	2016 BB	SNP 2 18209804	71	0.112341446	0.062725802
2	18,158,668	18,434,632	2016 BC14		SNP 2 18328469	75	1.18E-01	
2	18,343,476	18,548,535	2016_BC15	2016 BB	SNP_2__18413980	76	0.107721724	0.065383387
2	18,343,521	18,548,535	2016 BC16		SV 2 18438953	1	8.01E-02	
2	18,348,187	18,548,535	2016 BC17	2016 BB,2016 Suc,2016 BC	SNP 2 18547758	225	0.132520307	0.070416432,0.068795335,0.06110745
2	19,605,103	20,048,686	2016 BC18	2017 FF,2016 FF	SNP 2 19609135	26	0.086079006	0.07491998,0.074917442
3	265,631	309,038	2016 BeS1		SNP 3 276475	2	7.10E-02	
3	9,420,596	9,691,716	2016 SA1		SNP 3 9568352	5	6.46E-02	
3	17,576,275	17,596,334	2017 Cit2		SNP 3 17586309	2	6.49E-02	
3	20,374,473	20,448,042	2016 SA2		SNP 3 20374473	3	6.91E-02	
4	8,850,392	9,050,392	2016 Suc1		SV 4 8950392	1	6.60E-02	
4	19,353,541	19,447,621	2016 TAC1		SNP 4 19370888	6	6.80E-02	
5	896,732	1,287,533	2017 SL2		SNP 5 1094012	2	7.21E-02	
5	6,004,244	6,359,786	2016 SN2		SNP 5 6161083	1	6.07E-02	
5	12,064,332	12,076,966	2016 SSC1		SNP 5 12076966	2	6.47E-02	
6	4,625,975	4,885,016	2017 Mal2		SNP 6 4625975	2	6.97E-02	
6	5,541,615	5,859,464	2016 Suc2		SNP 6 5859417	2	6.74E-02	
6	8,786,474	9,131,003	2016 BeWi1	2016 BV,2016 BeWe	SNP 6 8931429	2	0.071845607	0.060782445,0.064728071
6	8,910,507	9,467,488	2016 BV1	2016 BeWe	SNP 6 8982458	3	0.072522543	0.070956538
6	8,927,607	9,462,812	2016 BV2	2016 BeWi,2016 BeWe	SNP 6 9069762	3	0.071139444	0.070054612,0.066880872
6	8,981,444	9,237,410	2016 BV3	2016 BeWe	SNP 6 9141498	2	0.068753074	0.064443809
6	9,233,018	9,628,241	2016 BV4	2016 BeWe	SNP 6 9430063	2	0.071512973	0.068255245
6	9,350,764	9,630,260	2016 BV5	2016 BeWe	SNP 6 9460942	3	0.079559368	0.079196303
6	13,235,330	13,781,835	2016 BV6	2016 BeWe	SNP 6 13300392	4	0.068929306	0.066558398
6	14,028,832	14,048,950	2016 BV7	2016 BeWe	SNP 6 14038909	2	0.067047217	0.065664265
6	14,064,063	14,084,117	2016 SL3		SNP 6 14074076	3	7.18E-02	
6	14,226,836	14,259,786	2017 Suc3		SNP 6 14231893	2	7.03E-02	

Supplementary Table 8. Candidate regions of 29 traits in GWAS results.

Chromesome	Start	End	Main	Additional	Significant Marker	Marker nu	PVE(main)	PVE(addition)
6	14,860,910	15,021,199	2016 SL4		SNP 6 15021129	3	7.37E-02	
6	15,221,443	15,612,711	2016 BV8	2016 SL	SNP 6 15420613	2	0.080959473	0.06114943
6	15,537,148	15,886,564	2016 BeWe2	2016 BV,2016 BeWi	SNP 6 15688167	1	0.077352263	0.070308188,0.069043025
6	16,682,116	16,902,425	2016 SN3		SV 6 16792116	1	6.52E-02	
6	16,733,548	17,070,625	2016 BeWe3	2016 BeWi,2016 BV	SNP 6 16882290	1	0.071022607	0.066818668,0.070723158
6	18,835,886	18,855,939	2016 SL5		SNP 6 18845926	6	7.38E-02	
6	20,466,281	20,777,873	2017 FF3	2016 FF	SNP 6 20659423	3	0.070178108	0.070172887
6	20,649,707	20,669,743	2017 Suc4		SNP 6 20659708	2	7.50E-02	
7	1,163,959	1,184,518	2016 Mal3		SNP 7 1174518	1	7.16E-02	
7	1,791,344	2,051,838	2016 SSC2		SV 7 2029369	1	6.23E-02	
7	2,382,032	2,576,589	2016 SSC3		SNP 7 2463733	5	7.22E-02	
7	2,448,301	2,622,282	2016 BL1	2017 BV	SV 7 2484748	2	0.06309347	0.060790825
7	2,382,032	2,576,589	2016 SSC4		SNP 7 2512956	2	6.61E-02	
7	4,190,068	4,218,168	2017 Cit3		SNP 7 4203597	3	7.37E-02	
7	7,022,992	7,054,769	2016 Tar2		SNP 7 7053390	1	6.07E-02	
7	10,308,637	10,328,667	2016 BuS1		SNP 7 10318667	1	6.39E-02	
7	22,168,117	22,379,451	2016 FJ2		SV 7 22278117	1	6.76E-02	
7	27,399,653	27,798,233	2016 EDP1		SNP 7 27598254	8	6.09E-02	
7	29,430,341	29,827,773	2016 BeS2		SNP 7 29628725	2	6.69E-02	
8	9,261,256	9,289,851	2016 BV9	2016 BeWi	SNP 8 9273391	1	0.066780575	0.061254839
8	14,131,831	14,186,484	2016 WPB1		SNP 8 14173576	7	7.81E-02	
8	18,757,025	19,100,992	2016 BeWe4	2016 BV,2017 BV,2016 BeWi,2017	SNP 8 18902348	2	0.084484304	0.080420886,0.063845809,0.07633162
8	19,086,409	19,106,473	2016 BV10	2016 BeWe,2017 SL	SNP 8 19096473	4	0.078565191	0.073863979,0.072087744
8	19,126,399	19,204,307	2016 SN4	2016 BV	SNP 8 19154960	8	0.071659172	0.061958281
8	19,270,174	19,346,445	2016_SN5	2016 BeWe	SNP_8__19316944	16	0.073540198	0.066225958
8	19,491,018	19,711,111	2016 BeWe5		SV 8 19601018	1	6.49E-02	
8	20,233,066	20,263,103	2016 BV11	2016 BeWe	SNP 8 20243103	5	0.073728106	0.066000533
8	20,130,743	20,445,931	2016 BeWe6	2016 BV	SNP 8 20308558	3	0.067588072	0.066283002
8	20,233,066	20,447,381	2017 BV12	2016 BV,2016 BeWi,2016 BeWe,20	SNP 8 20462554	15	0.103915263	0.071210768,0.095163392,0.05983386
8	20,492,080	20,516,569	2016 SBN1		SNP 8 20506569	1	6.03E-02	
8	22,830,264	22,859,463	2016 SL6		SNP 8 22846386	4	6.81E-02	
8	23,232,134	23,245,478	2016 BeWi2		SNP 8 23232561	4	6.78E-02	
9	1,480,750	1,727,865	2016 BeWi3		SNP 9 1680389	3	7.17E-02	
9	10,481,806	10,508,658	2017 SSC5	2016 SSC	SNP 9 10497137	2	0.062189351	0.060367705
9	13,539,720	13,739,084	2016 Fru1		SNP 9 13629031	1	7.32E-02	
9	13,756,020	13,944,415	2016 BeWi4	2016 BeWe,2017 BeWi,2017 SL,201	SNP 9 13936378	2	0.068545582	0.062101166,0.065160471,0.06313645
9	14,457,991	14,830,812	2017 SL7		SNP 9 14643750	2	6.26E-02	
9	17,531,212	17,688,708	2016 FJ3		SNP 9 17653982	1	6.19E-02	
9	19,544,112	19,929,784	2017 SL8		SNP 9 19743471	2	7.00E-02	
9	19,929,732	20,280,376	2016 BeWe7	2016 BeWi,2016 BV	SNP 9 20129459	1	0.073813324	0.064594686,0.066892915
9	21,175,586	21,395,586	2017 BeWi5		SV 9 21285586	2	6.18E-02	
9	23,837,084	24,321,165	2016 BV13	2016 BeWe,2016 BeWi	SNP 9 23925059	1	0.074209183	0.066425393,0.073009876
10	2,266,313	2,287,932	2016 TAC2		SNP 10 2277922	5	7.65E-02	
10	9,035,749	9,056,678	2017 BL2	2017 BV,2017 BEWE	SNP 10 9052243	3	6.64E-02	0.0659345750406860 7,0.06592052101
10	15,910,448	15,931,300	2017 BV14	2017 BeWe,2017 BL	SNP 10 15920837	2	0.080059916	0.07662683,0.072361198
10	17,162,893	17,315,372	2017 SL9		SNP 10 17278095	2	6.60E-02	
11	2,339,018	2,562,545	2017 BuW2		SNP 11 2514359	1	6.41E-02	
11	5,026,302	5,105,932	2016 BV15	2016 BeWi,2017 BeWe,2016 BeWe,	SNP 11 5041122	2	0.087899332	0.069514729,0.064113697,0.08340041
11	6,424,693	6,444,769	2017 Suc5		SNP 11 6434740	5	7.35E-02	

Supplementary Table 8. Candidate regions of 29 traits in GWAS results.

Chromesome	Start	End	Main	Additional	Significant Marker	Marker nu	PVE(main)	PVE(addition)
11	6,407,247	6,607,247	2016 Suc6		SV 11 6507247	1	6.69E-02	
11	8,371,200	8,393,278	2016 SSC6		SNP 11 8383257	3	6.83E-02	
11	10,484,481	10,514,226	2016 BeWi6	2016 BV	SNP 11 10502440	2	0.079690752	0.060827234
11	19,894,527	20,019,885	2016 EDP2		SNP 11 19943930	1	6.23E-02	
12	2,002,745	2,025,551	2016 TAC3		SNP 12 2012745	1	6.65E-02	
12	2,967,876	2,979,491	2016 BeS3		SNP 12 2979491	2	6.60E-02	
12	13,469,287	13,489,323	2016 FF4	2017 FF	SNP 12 13479317	3	0.087048926	0.087048714
12	13,929,820	13,949,923	2017 FF5	2016 FF	SNP 12 13939923	3	0.073550148	0.073546118
12	20,027,781	20,041,468	2017 TAC4		SNP 12 20037574	1	6.21E-02	
12	20,500,470	20,988,490	2016 Fru2	2016 Glu	SNP 12 20515975	5	0.092872494	0.079659032
12	20,976,532	20,998,490	2016 Cit4		SNP 12 20986562	1	6.98E-02	
12	23,226,036	23,253,225	2016 ST1		SNP 12 23240542	1	6.26E-02	
13	8,148,781	8,168,801	2016 BeWe8	2016 BV	SNP 13 8158785	3	0.070268046	0.064851916
14	4,301,783	4,793,591	2017 BuW3		SNP 14 4304405	5	7.37E-02	
14	4,580,278	5,081,186	2017 BuW4		SNP 14 4974359	3	7.64E-02	
14	4,977,356	5,083,225	2017 BuW5		SNP 14 5063890	6	7.06E-02	
14	19,613,376	19,635,864	2017 BV16	2017 BL,2016 BL	SNP 14 19616283	10	0.076052281	0.074574924,0.073601278
15	1,222,292	1,422,292	2016 BeWi7	2017 BeWi,2016 BV	SV 15 1322292	1	0.065714625	0.063431702,0.062864813,
15	2,371,843	2,391,903	2016 BeWi8	2016 BV	SNP 15 2381856	5	0.075539681	0.075001553
15	3,046,250	3,066,250	2016 BV17	2016 BeWe	SNP 15 3056250	2	0.064875501	0.063538801
15	9,919,308	10,014,879	2016 BV18	2017 BeWi,2016 BeWe,2016 BeWi	SNP 15 10014879	1	0.066393332	0.061127202,0.063392624,0.06440592
15	21,381,506	21,450,435	2016 BuW6		SNP 15 21418603	2	7.71E-02	
16	4,724,557	5,023,318	2016 FF6	2017 FF	SNP 16 4727136	4	0.095071553	0.09507023
16	18,021,918	18,221,918	2016 SN6		SV 16 18121918	1	6.08E-02	
17	14,539	500,746	2016_Tar3		SNP_17__34397	3	6.50E-02	
17	866,755	889,195	2016 ST2		SNP 17 877751	4	7.18E-02	
17	935,661	1,172,728	2016 SN7		SNP 17 1035661	48	7.91E-02	
17	1,139,962	1,187,715	2016 SN8		SNP 17 1165221	63	9.18E-02	
17	2,090,943	2,120,877	2016 Tar4		SNP 17 2103024	3	6.09E-02	
17	6,479,262	6,654,967	2016 BeWi9		SNP 17 6484258	4	5.91E-02	
17	6,479,375	6,531,384	2016 SSC7		SNP 17 6489512	1	6.06E-02	
17	18,639,529	18,921,912	2016 BeWi10	2016 BeWe,2016 BV	SNP 17 18744822	2	0.067834382	0.066695739,0.060391836
18	956,799	1,150,135	2016 WPB2		SNP 18 1147676	1	6.98E-02	
18	2,392,074	2,415,371	2016 BF1		SNP 18 2403865	3	7.15E-02	
18	2,887,108	2,912,681	2016 BF2		SNP 18 2902681	2	6.93E-02	
18	3,396,467	3,616,485	2016 BV19	2016 BeWi	SNP 18 3512021	1	0.069784268	0.068368083
18	3,850,418	3,871,247	2016 BB1		SNP 18 3870882	1	6.49E-02	
18	9,265,805	9,296,748	2016 BD1		SNP 18 9265930	3	6.39E-02	
18	12,047,530	12,429,387	2016 BD2		SNP 18 12245678	1	6.19E-02	
18	13,791,972	14,095,030	2016 SN9		SNP 18 14089086	2	6.68E-02	
18	14,281,884	14,609,066	2016 BD3		SNP 18 14470580	1	6.39E-02	
18	14,507,026	14,983,675	2017 SL10	2016 SL,2016 SN	SNP 18 14871348	13	0.074843233	0.063670333,0.062729394
18	18,637,431	18,716,693	2017 SL11		SNP 18 18679351	5	6.94E-02	
18	31,271,355	31,682,643	2016 SN10	2016 SL,2017 SL	SNP 18 31298156	12	0.083471652	0.074325948,0.08237723
18	31,412,453	31,456,515	2016 SN11	2017 SL,2016 SN,2016 SL,2016 SL	SNP 18 31450317	106	0.119333896	0.099266924,0.067065304,0.08279311
18	31,996,377	32,025,997	2016 Glu1	2016 Fru	SNP 18 32015346	2	0.092048851	0.09112301
18	32,049,870	32,272,634	2016 SN12	2017 SL	SNP 18 32261097	17	0.086394235	0.071603127
18	32,305,310	32,380,375	2016 SN13		SNP 18 32378686	11	8.42E-02	
18	34,929,397	34,958,661	2017 SL12		SNP 18 34942216	4	6.82E-02	

Supplementary Table 8. Candidate regions of 29 traits in GWAS results.

Chromesome	Start	End	Main	Additional	Significant Marker	Marker nu	PVE(main）	PVE(addition）
19	19,950,733	19,978,604	2016_SL13	2017_SL	SNP_19_19970852	14	0.075587472	0.071174749

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
1	Vitvi000581	2016_Cit1	GO:0000160; GO:0003677; GO:0003700; GO:0005634;	cytokinin-activated signaling pathway [GO:0009736]; phosphorelay signal transduction system [GO:0000160]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity	A2XE31	RR21	Two-component response regulator ORR21		
1	Vitvi000586	2016_Cit1	GO:0030749; GO:0032259; GO:0035834; GO:0046872	indole alkaloid metabolic process [GO:0035834]; methylation [GO:0032259]		loganate O-methyltransferase activity [GO:0030749]; metal ion binding [GO:0046872]	B2KPR3	LAMT	Loganic acid O-methyltransferase (CrLAMT) (EC 2.1.1.50)		
1	Vitvi000602	2016_Cit1	GO:0005085; GO:0016192; GO:0035658	vesicle-mediated transport [GO:0016192]	Mon1-Ccz1 complex [GO:0035658]	guanyl-nucleotide exchange factor activity [GO:0005085]	C0Z274	CCZ1B	Vacuolar fusion protein CCZ1 homolog B		
1	Vitvi000597	2016_Cit1	GO:0003677; GO:0005634; GO:0005737; GO:0010589; GO:0005643; GO:0005730;	leaf proximal/distal pattern formation [GO:0010589]; positive regulation of DNA-templated transcription [GO:0045893]	cytoplasm [GO:0005737]; nucleus [GO:0056341 nuclear pore [GO:0005643]; nucleolus	DNA binding [GO:0003677]	F4HXU3	KNATM	Protein KNATM (KNOX Arabidopsis thaliana MEINOX protein)		
1	Vitvi000570	2016_Cit1	GO:0005886; GO:0006913; GO:0009506; GO:0015031; GO:0017056; GO:0051028	mRNA transport [GO:0051028]; nucleocytoplasmic transport [GO:0006913]; protein transport [GO:0015031]	[GO:0005730]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	structural constituent of nuclear pore [GO:0017056]	F4HXV6	NUP155	Nuclear pore complex protein NUP155 (Nucleoporin 155)		
1	Vitvi000548	2016_Cit1	GO:0016592		mediator complex [GO:0016592]		F4I4P3	MED23	Mediator of RNA polymerase II transcription subunit 23		
1	Vitvi000572	2016_Cit1	GO:0005739; GO:0008759; GO:0009245; GO:0046872; GO:0103117; GO:2001289	lipid A biosynthetic process [GO:0009245]; lipid X metabolic process [GO:2001289]	mitochondrion [GO:0005739]	metal ion binding [GO:0046872]; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity [GO:0008759]; UDP-3-O-acyl-N-acetylglucosamine deacetylase activity [GO:0103117]	F4IAT8	LPXC1	Probable UDP-3-O-acyl-N-acetylglucosamine deacetylase 1, mitochondrial (UDP-3-O-acyl-GlcNAc deacetylase 1) (EC 3.5.1.108) (Protein LIPID X C1) (AtLpxC1) (UDP-3-O-[R-3-hydroxymyristoyl]-N-acetylglucosamine deacetylase 1)		
1	Vitvi000599	2016_Cit1	GO:0005384; GO:0005774; GO:0006880; GO:0030026; GO:0034755; GO:0042803; GO:0046872	intracellular manganese ion homeostasis [GO:0030026]; intracellular sequestering of iron ion [GO:0006880]; iron ion transmembrane transport [GO:0034755]	vacuolar membrane [GO:0005774]	manganese ion transmembrane transporter activity [GO:0005384]; metal ion binding [GO:0046872]; protein homodimerization activity	P0DO17	VIT1	Vacuolar iron transporter 1 (EgVIT1)		
1	Vitvi000561	2016_Cit1	GO:0005576; GO:0016491; GO:0046872		extracellular region [GO:0005576]	metal ion binding [GO:0046872]; oxidoreductase activity [GO:0016491]	P93824		1-aminocyclopropane-1-carboxylate oxidase homolog 6 (EC 1.14.-.-)		
1	Vitvi000603	2016_Cit1	GO:0000724; GO:0051026; GO:0051301	cell division [GO:0051301]; chiasma assembly [GO:0051026]; double-strand break repair via homologous recombination [GO:0000724]			Q1PFW3	SDS	Cyclin-SDS (Protein SOLO DANCERS)		
1	Vitvi000583	2016_Cit1	GO:0004073; GO:0009088; GO:0009089; GO:0009097; GO:0019877; GO:0046983; GO:0050661; GO:0051287; GO:0071266	'de novo' L-methionine biosynthetic process [GO:0071266]; diaminopimelate biosynthetic process [GO:0019877]; isoleucine biosynthetic process [GO:0009097]; lysine biosynthetic process via diaminopimelate [GO:0009089]; threonine biosynthetic process [GO:0009088]		aspartate-semialdehyde dehydrogenase activity [GO:0004073]; NAD binding [GO:0051287]; NADP binding [GO:0050661]; protein dimerization activity [GO:0046983]	Q55512	asd	Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)		
1	Vitvi000543	2016_Cit1	GO:0005737; GO:0005868; GO:0005874; GO:0007017; GO:0045505	microtubule-based process [GO:0007017]	cytoplasm [GO:0005737]; cytoplasmic dynein complex [GO:0005868]; microtubule [GO:0005874]	dynein intermediate chain binding [GO:0045505]	Q86A88	dlcB	Dynein light chain, cytoplasmic (Dynein light chain LC8-type 2)		
1	Vitvi000573	2016_Cit1	GO:0009793; GO:0016020; GO:0016567; GO:0016740; GO:0046872	embryo development ending in seed dormancy [GO:0009793]; protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q8GUU2	RIE1	E3 ubiquitin protein ligase RIE1 (EC 2.3.2.27) (Protein RING-FINGER FOR EMBRYOGENESIS 1) (RING-type E3 ubiquitin transferase RIE1)		
1	Vitvi000574	2016_Cit1	GO:0004518; GO:0005634; GO:0006397; GO:0010197	mRNA processing [GO:0006397]; polar nucleus fusion [GO:0010197]	nucleus [GO:0005634]	nuclease activity [GO:0004518]	Q8GUU3	CPSF73-II	Cleavage and polyadenylation specificity factor subunit 3-II (EC 3.1.27.-) (Cleavage and polyadenylation specificity factor 73 kDa subunit II) (AtCPSF73-II) (CPSF 73 kDa subunit II) (Protein EMBRYO SAC DEVELOPMENT ARREST 26)		
1	Vitvi000595	2016_Cit1	GO:0009626; GO:2000031	plant-type hypersensitive response [GO:0009626]; regulation of salicylic acid mediated signaling pathway [GO:2000031]			Q8L612		MACPF domain-containing protein At1g14780		
1	Vitvi000577	2016_Cit1	GO:0005737; GO:0005874; GO:0007010; GO:0008017	cytoskeleton organization [GO:0007010]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	microtubule binding [GO:0008017]	Q8L7S4	MAP70.2	Microtubule-associated protein 70-2 (AtMAP70-2) (70 kDa microtubule-associated		
1	Vitvi000579	2016_Cit1	GO:0000266; GO:0003924; GO:0005525; GO:0005576; GO:0005737; GO:0005874; GO:0005886; GO:0005938; GO:0007005; GO:0007049; GO:0009504; GO:0009506; GO:0009524; GO:0010152; GO:0030136; GO:0051301	cell cycle [GO:0007049]; cell division [GO:0051301]; mitochondrial fission [GO:0000266]; mitochondrion organization [GO:0007005]; pollen maturation [GO:0010152]	cell cortex [GO:0005938]; cell plate [GO:0009504]; clathrin-coated vesicle [GO:0030136]; cytoplasm [GO:0005737]; extracellular region [GO:0005576]; microtubule [GO:0005874]; phragmoplast [GO:0009524]; plasma membrane [GO:0005886]; plasmodesma	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	Q8LF21	DRP1C	Phragmoplastin DRP1C (EC 3.6.5.-) (Dynamin-like protein 1C) (Dynamin-like protein 5) (Dynamin-like protein DLP1) (Dynamin-related protein 1C) (AtDRP1C)		
1	Vitvi000560	2016_Cit1	GO:0006301; GO:0031372; GO:1902916	positive regulation of protein polyubiquitination [GO:1902916]; postreplication repair [GO:0006301]	UBC13-MMS2 complex [GO:0031372]		Q93YP0	UEV1A	Ubiquitin-conjugating enzyme E2 variant 1A (Ubc enzyme variant 1A) (Protein MMS ZWEI HOMOLOG 1)		
1	Vitvi000596	2016_Cit1	GO:0003825; GO:0004805; GO:0005992	trehalose biosynthetic process [GO:0005992]		alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity [GO:0003825]; trehalose-phosphatase activity [GO:0004805]	Q94AH8	TPS6	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 6 (EC 2.4.1.15) (Trehalose-6-phosphate synthase 6) (AtTPS6)		
1	Vitvi000580	2016_Cit1	GO:0005634; GO:0005737; GO:0006355; GO:0007623; GO:0009637; GO:0009881; GO:0009908; GO:0009911; GO:0010468; GO:0016567; GO:2001007	circadian rhythm [GO:0007623]; flower development [GO:0009908]; negative regulation of cellulose biosynthetic process [GO:2001007]; positive regulation of flower development [GO:0009911]; protein ubiquitination [GO:0016567]; regulation of DNA-templated transcription [GO:0006355]; regulation of gene expression [GO:0010468]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	photoreceptor activity [GO:0009881]	Q9C9W9	ADO3	Adagio protein 3 (F-box only protein 2a) (FBX2a) (Flavin-binding kelch repeat F-box protein 1)		
1	Vitvi000559	2016_Cit1	GO:0005811; GO:0009737; GO:0009819; GO:0046872; GO:0102070; GO:1990137	drought recovery [GO:0009819]; response to abscisic acid [GO:0009737]	lipid droplet [GO:0005811]	18-hydroxyoleate peroxygenase activity [GO:0102070]; metal ion binding [GO:0046872]; plant seed peroxidase activity [GO:1990137]	Q9CAB7	PXG4	Probable peroxygenase 4 (AtPXG4) (EC 1.11.2.3) (Caleosin-4)		
1	Vitvi000604	2016_Cit1	GO:0003723; GO:0005886; GO:0009536; GO:0034051; GO:0000325; GO:0004672;	defense response to fungus [GO:0050832]; negative regulation of plant-type hypersensitive response [GO:0034051]	plasma membrane [GO:0005886]; plastid [GO:0009536]	RNA binding [GO:0003723]	Q9LFD5	BPA1	Binding partner of ACD11 1		
1	Vitvi000556	2016_Cit1	GO:0005524; GO:0005634; GO:0005886; GO:0009506; GO:0042802		nucleus [GO:0005634]; plant-type vacuole [GO:0000325]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	ATP binding [GO:0005524]; identical protein binding [GO:0042802]; protein kinase activity [GO:0004672]	Q9LP77	RKL1	Probable inactive receptor kinase At1g48480		
1	Vitvi000563	2016_Cit1	GO:0005739; GO:0016462; GO:0046872		mitochondrion [GO:0005739]	metal ion binding [GO:0046872]; pyrophosphatase activity [GO:0016462]	Q9LQU5	NUDT18	Nudix hydrolase 18, mitochondrial (AtNUDT18) (EC 3.6.1.-)		
1	Vitvi000584	2016_Cit1	GO:0003723; GO:0003968; GO:0006952; GO:0009615; GO:0009751; GO:0010025; GO:0030422; GO:0060148	defense response [GO:0006952]; positive regulation of post-transcriptional gene silencing [GO:0060148]; response to salicylic acid [GO:0009751]; response to virus [GO:0009615]; siRNA processing [GO:0030422]; wax biosynthetic process [GO:0010025]		RNA binding [GO:0003723]; RNA-dependent RNA polymerase activity [GO:0003968]	Q9LQV2	RDR1	RNA-dependent RNA polymerase 1 (AtRDRP1) (EC 2.7.7.48) (RNA-directed RNA polymerase 1)		
1	Vitvi000593	2016_Cit1	GO:0008757; GO:0032259; GO:0046872	methylation [GO:0032259]		metal ion binding [GO:0046872]; S-adenosylmethionine-dependent methyltransferase activity [GO:0008757]	Q9LS10		Probable S-adenosylmethionine-dependent methyltransferase At5g38100 (EC 2.1.1.-)		
1	Vitvi000554	2016_Cit1	GO:0005634; GO:0006952; GO:0009867; GO:0031347; GO:0042802	defense response [GO:0006952]; jasmonic acid mediated signaling pathway [GO:0009867]; regulation of defense response [GO:0031347]	nucleus [GO:0005634]	identical protein binding [GO:0042802]	Q9LVI4	TIFY6B	Protein TIFY 6B (Jasmonate ZIM domain-containing protein 3) (Protein JASMONATE INSENSITIVE 3)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
1	Vitvi000598	2016_Cit1	GO:0000976; GO:0003700; GO:0005634; GO:0005737		cytoplasm [GO:0005737]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9S7U5	HSFA8	Heat stress transcription factor A-8 (AtHsfA8) (AtHsf-03) (Heat shock factor protein 5) (HSF 5) (Heat shock transcription factor 5) (HSTF 5)		
1	Vitvi000601	2016_Cit1	GO:0000278; GO:0000387; GO:0000398; GO:0003723; GO:0005681; GO:0005682; GO:0005685; GO:0005686; GO:0005829; GO:0030532; GO:0034715; GO:0046540; GO:0071011; GO:0071013	mitotic cell cycle [GO:0000278]; mRNA splicing, via spliceosome [GO:0000398]; spliceosomal snRNP assembly [GO:0000387]	catalytic step 2 spliceosome [GO:0071013]; cytosol [GO:0005829]; pICln-Sm protein complex [GO:0034715]; precatalytic spliceosome [GO:0071011]; small nuclear ribonucleoprotein complex [GO:0030532]; spliceosomal complex [GO:0005681]; U1 snRNP [GO:0005685]; U2 snRNP [GO:0005686]; U4/U6 x U5 tri-snRNP	RNA binding [GO:0003723]	Q9VI10	SmD2	Probable small nuclear ribonucleoprotein Sm D2 (Sm-D2) (snRNP core protein D2)		
1	Vitvi000544	2016_Cit1	GO:0009793; GO:0016567	embryo development ending in seed dormancy [GO:0009793]; protein ubiquitination [GO:0016567]			Q9ZU90	SKIP28	F-box protein SKIP28 (Protein MATERNAL EFFECT EMBRYO ARREST 11) (SKP1-interacting partner 28)		
1	Vitvi000545	2016_Cit1	GO:0005739; GO:0005886; GO:0005975; GO:0006952; GO:0042973; GO:0098552	carbohydrate metabolic process [GO:0005975]; defense response [GO:0006952]	mitochondrion [GO:0005739]; plasma membrane [GO:0005886]; side of membrane [GO:0098552]	glucan endo-1,3-beta-D-glucosidase activity [GO:0042973]	Q9ZU91		Glucan endo-1,3-beta-glucosidase 3 (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase 3) ((1->3)-beta-glucanase 3) (Beta-1,3-endoglucanase 3) (Beta-1,3-glucanase 3)		
1	Vitvi000555	2016_Cit1	GO:0005739; GO:0009620; GO:0016020; GO:0046872; GO:0050832	defense response to fungus [GO:0050832]; response to fungus [GO:0009620]	membrane [GO:0016020]; mitochondrion [GO:0005739]	metal ion binding [GO:0046872]	Q9ZU93	PUX2	Plant UBX domain-containing protein 2 (PUX2) (AtPUB3) (CDC48-interacting UBX-domain protein 2)		
1	Vitvi000558	2016_Cit1	GO:0005886; GO:0009506		plasma membrane [GO:0005886]; plasmodesma [GO:0009506]		Q9ZU94	PDLP6	Plasmodesmata-located protein 6 (PD-located protein 6) (Cysteine-rich repeat secretory protein 12)		
1	Vitvi000567	2016_Cit1	GO:0016020		membrane [GO:0016020]		Q9ZU96		Ankyrin repeat-containing protein At2g01680		
1	Vitvi000569	2016_Cit1	GO:0006661; GO:0010008; GO:0070772	phosphatidylinositol biosynthetic process [GO:0006661]	endosome membrane [GO:0010008]; PAS complex [GO:0070772]		Q9ZU97	VAC14	Protein VAC14 homolog		
1	Vitvi000947	2016_BeWe1	GO:0016020; GO:0022857		membrane [GO:0016020]	transmembrane transporter activity [GO:0022857]	Q94JU2		WAT1-related protein At3g28050		
1	Vitvi001403	2016_Mal1	GO:0009507; GO:0009536		chloroplast [GO:0009507]; plastid [GO:0009536]		P0C304	ycf68-1; ycf68-2	Uncharacterized protein ycf68		
1	Vitvi001401	2016_Mal1	GO:0005576; GO:0016042; GO:0016788	lipid catabolic process [GO:0016042]	extracellular region [GO:0005576]	hydrolase activity, acting on ester bonds [GO:0016788]	Q8L5Z1		GDSL esterase/lipase At1g33811 (EC 3.1.1.-) (Extracellular lipase At1g33811)		
1	Vitvi001408	2017_Tar1	GO:0003677; GO:0003899; GO:0006390; GO:0034245	mitochondrial transcription [GO:0006390]	mitochondrial DNA-directed RNA polymerase complex [GO:0034245]	DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]	Q8L6J5	RPOT1-TOM	DNA-directed RNA polymerase 1B, mitochondrial (EC 2.7.7.6) (NictaRpoT1-tom) (T7 bacteriophage-type single subunit RNA polymerase 1B)		
1	Vitvi001406	2017_Tar1	GO:0000325; GO:0005524; GO:0005739; GO:0009408; GO:0009414; GO:0009507; GO:0009536; GO:0009570; GO:0009651; GO:0009704; GO:0009941; GO:0010157	de-etiolation [GO:0009704]; protein import into chloroplast stroma [GO:0045037]; response to chlorate [GO:0010157]; response to heat [GO:0009408]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; mitochondrion [GO:0005739]; plant-type vacuole [GO:0000325]; plastid [GO:0009536]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATP-dependent protein folding chaperone [GO:0140662]; protein homodimerization activity [GO:0042803]; unfolded protein binding	Q9SIF2	HSP90-5	Heat shock protein 90-5, chloroplastic (AtHSP90.5) (AtHsp90-5) (Heat shock protein 88-1) (Hsp88-1) (Hsp90C) (Protein EMBRYO DEFECTIVE 1956) (Protein chlorate-resistance 88)		
1	Vitvi001454	2016_FJ1	GO:0005783; GO:0005789; GO:0006665; GO:0010256; GO:0042761; GO:0046513; GO:0050291; GO:2000012	ceramide biosynthetic process [GO:0046513]; endomembrane system organization [GO:0010256]; regulation of auxin polar transport [GO:2000012]; sphingolipid metabolic process [GO:0006665]; very long-chain fatty acid biosynthetic process [GO:0042761]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]	sphingosine N-acyltransferase activity [GO:0050291]	Q6NQI8	LOH3	Ceramide synthase 1 LOH3 (CS1) (CSII) (EC 2.3.1.-) (Protein LONGEVITY ASSURANCE GENE ONE HOMOLOG 3) (LAG One Homolog 3) (LAG1 homolog 3) (LAG1 longevity assurance homolog 3)		
1	Vitvi001636	2016_SN1	GO:0005047; GO:0005783; GO:0005786; GO:0005829; GO:0006614; GO:0008312; GO:0030911; GO:0043022	SRP-dependent cotranslational protein targeting to membrane [GO:0006614]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; signal recognition particle, endoplasmic reticulum targeting [GO:0005786]	7S RNA binding [GO:0008312]; ribosome binding [GO:0043022]; signal recognition particle binding [GO:0005047]; TPR domain binding	P33731	SRP72	Signal recognition particle subunit SRP72 (SRP72) (Signal recognition particle 72 kDa protein)		
2	Vitvi002262	2017_BuW1	GO:0004843; GO:0006508	proteolysis [GO:0006508]		cysteine-type deubiquitinase activity [GO:0004843]	Q93Y01	UBP9	Ubiquitin carboxyl-terminal hydrolase 9 (EC 3.4.19.12) (Deubiquitinating enzyme 9) (AtUBP9) (Ubiquitin thioesterase 9) (Ubiquitin-specific-processing protease 9)		10.1093/g3journal/jkac103
2	Vitvi002907	2017_FF1	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0006952; GO:0043565; GO:0045893; GO:0046983	defense response [GO:0006952]; positive regulation of DNA-templated transcription [GO:0045893]; regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]; sequence-specific DNA binding [GO:0043565]; transcription cis-regulatory region	A0A3Q7HRZ6	MYC2	Transcription factor MYC2 (LeMYC2) (SlMYC2) (Basic helix-loop-helix protein 147) (Transcription factor bHLH147) (bHLH transcription factor bHLH147)		
2	Vitvi002940	2017_FF1	GO:0000287; GO:0005524; GO:0016310; GO:0032957; GO:0047325; GO:0052725; GO:0052726	inositol trisphosphate metabolic process [GO:0032957]; phosphorylation [GO:0016310]		ATP binding [GO:0005524]; inositol tetrakisphosphate 1-kinase activity [GO:0047325]; inositol-1,3,4-trisphosphate 5-kinase activity [GO:0052726]; inositol-1,3,4-trisphosphate 6-kinase activity [GO:0052725]; magnesium ion binding	A0JJZ6	ITPK5	Inositol-tetrakisphosphate 1-kinase 5 (EC 2.7.1.134) (Inositol 1,3,4-trisphosphate 5/6-kinase 5) (Inositol-triphosphate 5/6-kinase 5) (Ins(1,3,4)P(3) 5/6-kinase 5) (OsITP5/6K-5) (OsITPK5) (EC 2.7.1.159)		
2	Vitvi002924	2017_FF1	GO:0008374; GO:0016020		membrane [GO:0016020]	O-acyltransferase activity [GO:0008374]	B3H6K1		Uncharacterized protein At4g17910		
2	Vitvi002932	2017_FF1	GO:0016020; GO:0016567; GO:0016740; GO:0046872	protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; transferase activity [GO:0016740]	O49691	ATL29	RING-H2 finger protein ATL29 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase ATL29)		
2	Vitvi002898	2017_FF1	GO:0003700; GO:0005634; GO:0006355; GO:0046872	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]	O80942	ZFP10	Zinc finger protein 10 (AtZFP10)		
2	Vitvi002906	2017_FF1	GO:0009960; GO:0043078; GO:0080113	endosperm development [GO:0009960]; regulation of seed growth [GO:0080113]	polar nucleus [GO:0043078]		O82170	IKU1	Protein HAIKU1 (MPK3/6-targeted VQ-motif-containing protein 9) (VQ motif-containing protein 14) (AtVQ14)		
2	Vitvi002937	2017_FF1	GO:0005975; GO:0006952; GO:0042973	carbohydrate metabolic process [GO:0005975]; defense response [GO:0006952]		glucan endo-1,3-beta-D-glucosidase activity [GO:0042973]	Q02439		Putative glucan endo-1,3-beta-glucosidase GVI (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase GVI) ((1->3)-beta-glucanase isoenzyme GVI) (Beta-1,3-endoglucanase		
2	Vitvi002918	2017_FF1	GO:0003723; GO:0003729; GO:0005829; GO:0006396; GO:0006397; GO:0008266; GO:0009409; GO:0009451; GO:0009507; GO:0009535; GO:0009570; GO:0009579; GO:0009611; GO:0009941	base conversion or substitution editing [GO:0016553]; cold acclimation [GO:0009631]; innate immune response [GO:0045087]; mRNA processing [GO:0006397]; response to cold [GO:0009409]; RNA modification [GO:0009451]; RNA processing [GO:0006396]; RNA stabilization [GO:0043489]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; chloroplast thylakoid membrane [GO:0009535]; cytosol [GO:0005829]; ribonucleoprotein complex [GO:1990904]; thylakoid [GO:0009579]	mRNA binding [GO:0003729]; poly(U) RNA binding [GO:0008266]; RNA binding [GO:0003723]	Q04836	CP31A	31 kDa ribonucleoprotein, chloroplastic (RNA-binding protein 1/2/3) (AtRBP33) (RNA-binding protein CP31A) (RNA-binding protein RNP-T) (RNA-binding protein cp31)		
2	Vitvi002934	2017_FF1	GO:0003854; GO:0006694; GO:0009809; GO:0016616; GO:0042742	defense response to bacterium [GO:0042742]; lignin biosynthetic process [GO:0009809]; steroid biosynthetic process [GO:0006694]		3-beta-hydroxy-delta5-steroid dehydrogenase activity [GO:0003854]; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616]	Q0JKZ0	SNL6	Cinnamoyl-CoA reductase-like SNL6 (EC 1.2.-.-) (Protein SUPPRESSOR OF NH1-MEDIATED LESION 6)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
2	Vitvi002896	2017_FF1	GO:0000287; GO:0004743; GO:0005524; GO:0005737; GO:0006096; GO:0009570; GO:0016301; GO:0016310; GO:0030955	glycolytic process [GO:0006096]; phosphorylation [GO:0016310]	chloroplast stroma [GO:0009570]; cytoplasm [GO:0005737]	ATP binding [GO:0005524]; kinase activity [GO:0016301]; magnesium ion binding [GO:0000287]; potassium ion binding [GO:0030955]; pyruvate kinase activity [GO:0004743]	Q40546		Pyruvate kinase isozyme G, chloroplastic (EC 2.7.1.40)		
2	Vitvi002930	2017_FF1	GO:0003677; GO:0003689; GO:0005524; GO:0005663; GO:0006260; GO:0016887	DNA replication [GO:0006260]	DNA replication factor C complex [GO:0005663]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; DNA clamp loader activity [GO:0003689]	Q4JAB0	rfcS	Replication factor C small subunit (RFC small subunit) (Clamp loader small subunit)		
2	Vitvi002923	2017_FF1	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0046983	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]	Q56XR0	BHLH71	Transcription factor bHLH71 (Basic helix-loop-helix protein 71) (AtbHLH71) (bHLH 71) (Transcription factor EN 17) (bHLH transcription factor bHLH071)		
2	Vitvi002922	2017_FF1	GO:0004842; GO:0016020; GO:0016567; GO:0046872	protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin-protein transferase activity [GO:0004842]	Q7XLY8		E3 ubiquitin-protein ligase Os04g0590900 (EC 2.3.2.27) (RING-H2 finger protein Os04g0590900) (RING-type E3 ubiquitin transferase Os04g0590900)		
2	Vitvi002938	2017_FF1	GO:0000463; GO:0005654; GO:0005694; GO:0005730;	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) [GO:0000463]	chromosome [GO:0005694]; nucleolus [GO:0005730]; nucleoplasm	rRNA binding [GO:0019843]	Q8C5L7	Rbm34	RNA-binding protein 34 (RNA-binding motif protein 34)		
2	Vitvi002910	2017_FF1	GO:0005096; GO:0046872			GTPase activator activity [GO:0005096]; metal ion binding [GO:0046872]	Q8H100	AGD8	Probable ADP-ribosylation factor GTPase-activating protein AGD8 (ARF GAP AGD8) (Protein ARF-GAP DOMAIN 8) (AtAGD8)		
2	Vitvi002939	2017_FF1	GO:0005783; GO:0016020		endoplasmic reticulum [GO:0005783]; membrane [GO:0016020]		Q8L586		Uncharacterized membrane protein At4g09580		
2	Vitvi002942	2017_FF1	GO:0005524; GO:0005829; GO:0016020; GO:0016887; GO:0140359		cytosol [GO:0005829]; membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q8LPK2	ABCB2	ABC transporter B family member 2 (ABC transporter ABCB.2) (AtABCB2) (Multidrug resistance protein 2) (P-glycoprotein 2)		
2	Vitvi002928	2017_FF1	GO:0003677; GO:0005524; GO:0005634; GO:0006260; GO:0016887	DNA replication [GO:0006260]	nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]	Q8VXX4	RFC3	Replication factor C subunit 3 (AtRFC3) (Activator 1 subunit 3) (Protein EMBRYO DEFECTIVE 161) (Protein EMBRYO DEFECTIVE 251) (Protein EMBRYO DEFECTIVE 2775)		
2	Vitvi002905	2017_FF1	GO:0004864; GO:0005634; GO:0005737; GO:0005886; GO:0006952; GO:0009536; GO:0009738; GO:0010427; GO:0038023; GO:0042802; GO:0047803; GO:0062049	abscisic acid-activated signaling pathway [GO:0009738]; defense response [GO:0006952]; regulation of protein serine/threonine phosphatase activity [GO:0080163]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; plastid [GO:0009536]; protein phosphatase inhibitor complex [GO:0062049]	abscisic acid binding [GO:0010427]; identical protein binding [GO:0042802]; protein homodimerization activity [GO:0042803]; protein phosphatase inhibitor activity [GO:0004864]; signaling receptor activity [GO:0038023]	Q8VZS8	PYL1	Abscisic acid receptor PYL1 (ABI1-binding protein 6) (PYR1-like protein 1) (Regulatory components of ABA receptor 9)		
2	Vitvi002903	2017_FF1	GO:0005739; GO:0005743; GO:0006839; GO:0009507; GO:0009536	mitochondrial transport [GO:0006839]	chloroplast [GO:0009507]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]		Q93XM7	BOU	Mitochondrial carnitine/acylcarnitine carrier-like protein (Carnitine/acylcarnitine translocase-like protein) (CAC-like protein) (Protein A BOUT DE SOUFFLE)		
2	Vitvi002900	2017_FF1	GO:0006526; GO:0008777; GO:0046872	arginine biosynthetic process [GO:0006526]		acetylornithine deacetylase activity [GO:0008777]; metal ion binding [GO:0046872]	Q9C5C4		Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)		
2	Vitvi002917	2017_FF1	GO:0009506; GO:0009554; GO:0009734; GO:0009933; GO:0009934; GO:0009956; GO:0010015; GO:0010305; GO:0016020	auxin-activated signaling pathway [GO:0009734]; leaf vascular tissue pattern formation [GO:0010305]; megasporogenesis [GO:0009554]; meristem structural organization [GO:0009933]; radial pattern formation [GO:0009956]; regulation of meristem structural organization [GO:0009934]; root morphogenesis [GO:0010015]	membrane [GO:0016020]; plasmodesma [GO:0009506]		Q9FIQ5	TRN2	Protein TORNADO 2 (Protein EKEKO) (TETRASPANIN-1)		
2	Vitvi002911	2017_FF1	GO:0004843; GO:0006508	proteolysis [GO:0006508]		cysteine-type deubiquitinase activity [GO:0004843]	Q9FPS7	UBP20	Ubiquitin carboxyl-terminal hydrolase 20 (EC 3.4.19.12) (Deubiquitinating enzyme 20) (AtUBP20) (Ubiquitin thioesterase 20) (Ubiquitin-specific-processing protease 20)		
2	Vitvi002927	2017_FF1	GO:0005524; GO:0009408; GO:0009507; GO:0009532; GO:0009536; GO:0009570; GO:0009658; GO:0016887;	chloroplast organization [GO:0009658]; protein refolding [GO:0042026]; response to heat [GO:0009408]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; plastid [GO:0009536]; plastid stroma [GO:0009532]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LF37	CLPB3	Chaperone protein ClpB3, chloroplastic (ATP-dependent Clp protease ATP-binding subunit ClpB homolog 3) (Casein lytic proteinase B3) (Protein ALBINO OR PALE GREEN 6)		
2	Vitvi002895	2017_FF1	GO:0005886; GO:0010150; GO:0010167; GO:0015112; GO:0015293; GO:0015386; GO:0015706; GO:0055075;	leaf senescence [GO:0010150]; nitrate transmembrane transport [GO:0015706]; potassium ion homeostasis [GO:0055075]; proton transmembrane transport [GO:1902600]; response to nitrate [GO:0010167]	plasma membrane [GO:0005886]	nitrate transmembrane transporter activity [GO:0015112]; potassium:proton antiporter activity [GO:0015386]; symporter activity [GO:0015293]	Q9LQL2	NPF7.3	Protein NRT1/ PTR FAMILY 7.3 (AtNPF7.3) (Nitrate transporter 1.5)		
2	Vitvi002933	2017_FF1	GO:0000976; GO:0003700; GO:0003729; GO:0006355; GO:0046872	regulation of DNA-templated transcription [GO:0006355]		DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; mRNA binding [GO:0003729]; transcription cis-regulatory region binding [GO:0000976]	Q9LQM3		Zinc finger CCCH domain-containing protein 12 (AtC3H12)		
2	Vitvi002941	2017_FF1	GO:0000976; GO:0003700; GO:0005634; GO:0005737; GO:0071365; GO:1901332	cellular response to auxin stimulus [GO:0071365]; negative regulation of lateral root development [GO:1901332]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9S9Z2	MYB93	Transcription factor MYB93 (Myb-related protein 93) (AtMYB93)		
2	Vitvi003077	2016_BC1	GO:0005634; GO:0005739; GO:0005794; GO:0005886; GO:0015031; GO:0030658	protein transport [GO:0015031]	Golgi apparatus [GO:0005794]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; transport vesicle membrane [GO:0030658]		Q9C6X2	SCAMP4	Secretory carrier-associated membrane protein 4 (Secretory carrier membrane protein 4)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003235	2016_BC3	GO:0001822; GO:0005525; GO:0005634; GO:0005737; GO:0016787; GO:0046872	kidney development [GO:0001822]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	GTP binding [GO:0005525]; hydrolase activity [GO:0016787]; metal ion binding [GO:0046872]	Q9BRT8	ZNG1A	Zinc-regulated GTPase metalloprotein activator 1A (EC 3.6.5.-) (Cobalamin synthase W domain-containing protein 1) (COBW domain-containing protein 1) (NPC-A-6 COBW domain-containing protein 1) (NPC-A-6)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003254	2016_BC4	GO:0003774; GO:0003779; GO:0005516; GO:0005524; GO:0007015; GO:0016459; GO:0030048	actin filament organization [GO:0007015]; actin filament-based movement [GO:0030048]	myosin complex [GO:0016459]	actin binding [GO:0003779]; ATP binding [GO:0005524]; calmodulin binding [GO:0005516]; cytoskeletal motor activity [GO:0003774]	F4I5Q6	XI-A	Myosin-7 (Myosin XI A) (AtXIA)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003247	2016_BC4	GO:0000028; GO:0003735; GO:0006412; GO:0022627;	maturation of SSU-rRNA [GO:0030490]; ribosomal small subunit assembly [GO:0000028]; translation [GO:0006412]	cytosolic small ribosomal subunit [GO:0022627]	structural constituent of ribosome [GO:0003735]	P46302	RPS28	Small ribosomal subunit protein eS28 (40S ribosomal protein S28)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003255	2016_BC4	GO:0003676; GO:0003887; GO:0008270; GO:0015074; GO:0019899; GO:0042575	DNA integration [GO:0015074]	DNA polymerase complex [GO:0042575]	DNA-directed DNA polymerase activity [GO:0003887]; enzyme binding [GO:0019899]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q09575		Uncharacterized protein K02A2.6	12.5Mb-17.5Mb	10.1073/pnas.1009363108

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
2	Vitvi003269	2016_BC4	GO:0005634; GO:0005886; GO:0009734; GO:0009736; GO:0009737; GO:0010078; GO:0010088; GO:0010315; GO:0030154; GO:0042802; GO:0048364; GO:0048527; GO:0048756; GO:2000280	auxin export across the plasma membrane [GO:0010315]; auxin-activated signaling pathway [GO:0009734]; cell differentiation [GO:0030154]; cytokinin-activated signaling pathway [GO:0009736]; lateral root development [GO:0048527]; maintenance of root meristem identity [GO:0010078]; phloem development [GO:0010088]; regulation of root development [GO:2000280]; response to abscisic acid [GO:0009737]; root development [GO:0048364]; stem cell differentiation [GO:0048756]	nucleus [GO:0005634]; plasma membrane [GO:0005886]	identical protein binding [GO:0042802]	Q17TI5	BRX	Protein BREVIS RADIX (AtBRX)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003263	2016_BC4	GO:0005737; GO:0009506; GO:0016926; GO:0016929	protein desumoylation [GO:0016926]	cytoplasm [GO:0005737]; plasmodesma [GO:0009506]	deSUMOylase activity [GO:0016929]	Q8GYL3	ULP1A	Ubiquitin-like-specific protease 1A (EC 3.4.22.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003259	2016_BC4	GO:0005524; GO:0006952; GO:0043531	defense response [GO:0006952]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9LMP6		Probable disease resistance protein At1g15890	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003267	2016_BC4	GO:0005739		mitochondrion [GO:0005739]		Q9M8M3		Pentatricopeptide repeat-containing protein At1g80550, mitochondrial	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003254	2016_BC5	GO:0003774; GO:0003779; GO:0005516; GO:0005524; GO:0007015; GO:0016459; GO:0030048	actin filament organization [GO:0007015]; actin filament-based movement [GO:0030048]	myosin complex [GO:0016459]	actin binding [GO:0003779]; ATP binding [GO:0005524]; calmodulin binding [GO:0005516]; cytoskeletal motor activity [GO:0003774]	F4I5Q6	XI-A	Myosin-7 (Myosin XI A) (AtXIA)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003247	2016_BC5	GO:0000028; GO:0003735; GO:0006412; GO:0022627; GO:0030048	maturation of SSU-rRNA [GO:0030490]; ribosomal small subunit assembly [GO:0000028]; translation [GO:0006412]	cytosolic small ribosomal subunit [GO:0022627]	structural constituent of ribosome [GO:0003735]	P46302	RPS28	Small ribosomal subunit protein eS28 (40S ribosomal protein S28)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003255	2016_BC5	GO:0003676; GO:0003887; GO:0008270; GO:0015074; GO:0019899; GO:0042575	DNA integration [GO:0015074]	DNA polymerase complex [GO:0042575]	DNA-directed DNA polymerase activity [GO:0003887]; enzyme binding [GO:0019899]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q09575		Uncharacterized protein K02A2.6	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003263	2016_BC5	GO:0005737; GO:0009506; GO:0016926; GO:0016929	protein desumoylation [GO:0016926]	cytoplasm [GO:0005737]; plasmodesma [GO:0009506]	deSUMOylase activity [GO:0016929]	Q8GYL3	ULP1A	Ubiquitin-like-specific protease 1A (EC 3.4.22.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003259	2016_BC5	GO:0005524; GO:0006952; GO:0043531	defense response [GO:0006952]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9LMP6		Probable disease resistance protein At1g15890	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003254	2016_BC6	GO:0003774; GO:0003779; GO:0005516; GO:0005524; GO:0007015; GO:0016459; GO:0030048	actin filament organization [GO:0007015]; actin filament-based movement [GO:0030048]	myosin complex [GO:0016459]	actin binding [GO:0003779]; ATP binding [GO:0005524]; calmodulin binding [GO:0005516]; cytoskeletal motor activity [GO:0003774]	F4I5Q6	XI-A	Myosin-7 (Myosin XI A) (AtXIA)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003255	2016_BC6	GO:0003676; GO:0003887; GO:0008270; GO:0015074; GO:0019899; GO:0042575	DNA integration [GO:0015074]	DNA polymerase complex [GO:0042575]	DNA-directed DNA polymerase activity [GO:0003887]; enzyme binding [GO:0019899]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q09575		Uncharacterized protein K02A2.6	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003263	2016_BC6	GO:0005737; GO:0009506; GO:0016926; GO:0016929	protein desumoylation [GO:0016926]	cytoplasm [GO:0005737]; plasmodesma [GO:0009506]	deSUMOylase activity [GO:0016929]	Q8GYL3	ULP1A	Ubiquitin-like-specific protease 1A (EC 3.4.22.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003259	2016_BC6	GO:0005524; GO:0006952; GO:0043531	defense response [GO:0006952]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9LMP6		Probable disease resistance protein At1g15890	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003267	2016_BC6	GO:0005739		mitochondrion [GO:0005739]		Q9M8M3		Pentatricopeptide repeat-containing protein At1g80550, mitochondrial	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003269	2016_BC7	GO:0005634; GO:0005886; GO:0009734; GO:0009736; GO:0009737; GO:0010078; GO:0010088; GO:0010315; GO:0030154; GO:0042802; GO:0048364; GO:0048527; GO:0048756; GO:2000280	auxin export across the plasma membrane [GO:0010315]; auxin-activated signaling pathway [GO:0009734]; cell differentiation [GO:0030154]; cytokinin-activated signaling pathway [GO:0009736]; lateral root development [GO:0048527]; maintenance of root meristem identity [GO:0010078]; phloem development [GO:0010088]; regulation of root development [GO:2000280]; response to abscisic acid [GO:0009737]; root development [GO:0048364]; stem cell differentiation [GO:0048756]	nucleus [GO:0005634]; plasma membrane [GO:0005886]	identical protein binding [GO:0042802]	Q17TI5	BRX	Protein BREVIS RADIX (AtBRX)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003263	2016_BC7	GO:0005737; GO:0009506; GO:0016926; GO:0016929	protein desumoylation [GO:0016926]	cytoplasm [GO:0005737]; plasmodesma [GO:0009506]	deSUMOylase activity [GO:0016929]	Q8GYL3	ULP1A	Ubiquitin-like-specific protease 1A (EC 3.4.22.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003259	2016_BC7	GO:0005524; GO:0006952; GO:0043531	defense response [GO:0006952]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9LMP6		Probable disease resistance protein At1g15890	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003267	2016_BC7	GO:0005739		mitochondrion [GO:0005739]		Q9M8M3		Pentatricopeptide repeat-containing protein At1g80550, mitochondrial	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003323	2016_BC8	GO:0003677; GO:0003723; GO:0003887; GO:0003964; GO:0004190; GO:0004523; GO:0006310; GO:0006508; GO:0008270; GO:0015074; GO:0016020; GO:0019013; GO:0019068; GO:0020002; GO:0039660; GO:0044185; GO:0044826; GO:0046718; GO:0072494; GO:0075713	DNA integration [GO:0015074]; DNA recombination [GO:0006310]; establishment of integrated proviral latency [GO:0075713]; proteolysis [GO:0006508]; viral entry into host cell [GO:0046718]; viral genome integration into host DNA [GO:0044826]; virion assembly [GO:0019068]	host cell late endosome membrane [GO:0044185]; host cell plasma membrane [GO:0020002]; host multivesicular body [GO:0072494]; membrane [GO:0016020]; viral nucleocapsid [GO:0019013]	aspartic-type endopeptidase activity [GO:0004190]; DNA binding [GO:0003677]; DNA-directed DNA polymerase activity [GO:0003887]; RNA binding [GO:0003723]; RNA-directed DNA polymerase activity [GO:0003964]; RNA-DNA hybrid ribonuclease activity [GO:0004523]; structural constituent of virion [GO:0039660]; zinc ion binding	P10272	pol	Gag-Pol polyprotein [Cleaved into: Matrix protein p15 (MA); RNA-binding phosphoprotein p12 (pp12); Capsid protein p30 (CA); Nucleocapsid protein p10-Pol (NC-pol); Protease (EC 3.4.23.-); Reverse transcriptase/ribonuclease H (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase (IN) (EC 2.7.7.-) (EC 3.1.-.-)]	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003295	2016_BC8	GO:0000323; GO:0004197; GO:0005634; GO:0005773; GO:0005886; GO:0006508; GO:0009506; GO:0009611	defense response to bacterium [GO:0042742]; proteolysis [GO:0006508]; response to osmotic stress [GO:0006970]; response to salt stress [GO:0009611]	lytic vacuole [GO:0000323]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; vacuole [GO:0005773]	cysteine-type endopeptidase activity [GO:0004197]	P43296	RD19A	Cysteine protease RD19A (EC 3.4.22.-) (Protein RESPONSIVE TO DEHYDRATION 19) (RD19)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003324	2016_BC8	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0009733; GO:0009734; GO:0009793; GO:0009908; GO:0009942; GO:0010051; GO:0010305; GO:0042802; GO:0048364; GO:0048507	auxin-activated signaling pathway [GO:0009734]; embryo development ending in seed dormancy [GO:0009793]; flower development [GO:0009908]; leaf vascular tissue pattern formation [GO:0010305]; longitudinal axis specification [GO:0009942]; meristem development [GO:0048507]; regulation of DNA-templated transcription [GO:0006355]; response to auxin [GO:0009733]; root development [GO:0048364]; xylem and phloem pattern formation [GO:0010051]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; identical protein binding [GO:0042802]; transcription cis-regulatory region binding [GO:0000976]	P93024	ARF5	Auxin response factor 5 (Auxin-responsive protein IAA24) (Transcription factor MONOPTEROS)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003304	2016_BC8	GO:0003777; GO:0005524; GO:0005874; GO:0007017; GO:0007018; GO:0008017	microtubule-based movement [GO:0007018]; microtubule-based process [GO:0007017]	microtubule [GO:0005874]; microtubule cytoskeleton [GO:0015630]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	Q10MN5	KIN14F	Kinesin-like protein KIN-14F	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003283	2016_BC8	GO:0019500; GO:0047427; GO:0047558; GO:0051410	cyanide catabolic process [GO:0019500]; detoxification of nitrogen compound [GO:0051410]		3-cyanoalanine hydratase activity [GO:0047558]; cyanoalanine nitrilase activity [GO:0047427]	Q3LRV4	NIT4B	Bifunctional nitrilase/nitrile hydratase NIT4B (LaNIT4B) (EC 3.5.5.4) (EC 4.2.1.65) (3-cyanoalanine hydratase) (Cyanoalanine nitrilase B)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003314	2016_BC8	GO:0003924; GO:0005525; GO:0005768; GO:0005794; GO:0005886		endosome [GO:0005768]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	Q40522	RAB11D	Ras-related protein Rab11D	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003302	2016_BC8	GO:0005774; GO:0006813; GO:0015079; GO:0016020	potassium ion transport [GO:0006813]	membrane [GO:0016020]; vacuolar membrane [GO:0005774]	potassium ion transmembrane transporter activity [GO:0015079]	Q67VS5	HAK10	Potassium transporter 10 (OsHAK10)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003277	2016_BC8	GO:0003677; GO:0003682; GO:0003886; GO:0005634; GO:0006325; GO:0010426; GO:0032183; GO:0034605	cellular response to heat [GO:0034605]; chromatin organization [GO:0006325]; DNA methylation on cytosine within a CHH sequence [GO:0010426]	nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA (cytosine-5-)-methyltransferase activity [GO:0003886]; DNA binding [GO:0003677]; SUMO binding [GO:0032183]	Q94F87	CMT2	DNA (cytosine-5)-methyltransferase CMT2 (EC 2.1.1.37) (Chromomethylase 2) (Protein CHROMOMETHYLASE 2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
2	Vitvi003315	2016_BC8	GO:0000149; GO:0005773; GO:0005789; GO:0006624; GO:0006890; GO:0015031; GO:0051604; GO:0070939	protein maturation [GO:0051604]; protein transport [GO:0015031]; retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum [GO:0006890]; vacuolar protein processing [GO:0006624]	Dsl1/NZR complex [GO:0070939]; endoplasmic reticulum membrane [GO:0005789]; vacuole [GO:0005773]	SNARE binding [GO:0000149]	Q9FIN7	MIP2	MAG2-interacting protein 2	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003281	2016_BC8	GO:0004364; GO:0005737; GO:0005829; GO:0009407	toxin catabolic process [GO:0009407]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	glutathione transferase activity [GO:0004364]	Q9LZI9	GSTF13	Glutathione S-transferase F13 (AtGSTF13) (EC 2.5.1.18) (GST class-phi member 13)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003292	2016_BC8	GO:0004674; GO:0005524; GO:0005739; GO:0016310; GO:0017018; GO:0046872	phosphorylation [GO:0016310]	mitochondrion [GO:0005739]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; myosin phosphatase activity [GO:0017018]; protein serine/threonine kinase activity [GO:0004674]	Q9SL76		Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein [Includes: Probable protein phosphatase 2C 19 (AtPP2C19) (EC 3.1.3.16); Probable inactive cyclic nucleotide-dependent protein kinase At2g20050]	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003283	2016_BC9	GO:0019500; GO:0047427; GO:0047558; GO:0051410	cyanide catabolic process [GO:0019500]; detoxification of nitrogen compound [GO:0051410]		3-cyanoalanine hydratase activity [GO:0047558]; cyanoalanine nitrilase activity [GO:0047427]	Q3LRV4	NIT4B	Bifunctional nitrilase/nitrile hydratase NIT4B (LaNIT4B) (EC 3.5.5.4) (EC 4.2.1.65) (3-cyanoalanine hydratase) (Cyanoalanine nitrilase B)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003277	2016_BC9	GO:0003677; GO:0003682; GO:0003886; GO:0005634; GO:0006325; GO:0010426; GO:0032183; GO:0034605	cellular response to heat [GO:0034605]; chromatin organization [GO:0006325]; DNA methylation on cytosine within a CHH sequence [GO:0010426]	nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA (cytosine-5-)-methyltransferase activity [GO:0003886]; DNA binding [GO:0003677]; SUMO binding [GO:0032183]	Q94F87	CMT2	DNA (cytosine-5)-methyltransferase CMT2 (EC 2.1.1.37) (Chromomethylase 2) (Protein CHROMOMETHYLASE 2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003281	2016_BC9	GO:0004364; GO:0005737; GO:0005829; GO:0009407	toxin catabolic process [GO:0009407]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	glutathione transferase activity [GO:0004364]	Q9LZI9	GSTF13	Glutathione S-transferase F13 (AtGSTF13) (EC 2.5.1.18) (GST class-phi member 13)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003295	2016_BC11	GO:0000323; GO:0004197; GO:0005634; GO:0005773; GO:0005886; GO:0006508;	defense response to bacterium [GO:0042742]; proteolysis [GO:0006508]; response to osmotic stress [GO:0006970]; response to salt stress [GO:0009651]	lytic vacuole [GO:0000323]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; vacuole [GO:0005773]	cysteine-type endopeptidase activity [GO:0004197]	P43296	RD19A	Cysteine protease RD19A (EC 3.4.22.-) (Protein RESPONSIVE TO DEHYDRATION 19) (RD19)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003304	2016_BC11	GO:0003777; GO:0005524; GO:0005874; GO:0007017; GO:0007018; GO:0008017;	microtubule-based movement [GO:0007018]; microtubule-based process [GO:0007017]	microtubule [GO:0005874]; microtubule cytoskeleton [GO:0015630]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	Q10MN5	KIN14F	Kinesin-like protein KIN-14F	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003314	2016_BC11	GO:0003924; GO:0005525; GO:0005768; GO:0005794; GO:0005886		endosome [GO:0005768]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	Q40522	RAB11D	Ras-related protein Rab11D	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003302	2016_BC11	GO:0005774; GO:0006813; GO:0015079; GO:0016020	potassium ion transport [GO:0006813]	membrane [GO:0016020]; vacuolar membrane [GO:0005774]	potassium ion transmembrane transporter activity [GO:0015079]	Q67VS5	HAK10	Potassium transporter 10 (OsHAK10)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003315	2016_BC11	GO:0000149; GO:0005773; GO:0005789; GO:0006624; GO:0006890; GO:0015031; GO:0051604; GO:0070939	protein maturation [GO:0051604]; protein transport [GO:0015031]; retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum [GO:0006890]; vacuolar protein processing [GO:0006624]	Dsl1/NZR complex [GO:0070939]; endoplasmic reticulum membrane [GO:0005789]; vacuole [GO:0005773]	SNARE binding [GO:0000149]	Q9FIN7	MIP2	MAG2-interacting protein 2	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003292	2016_BC11	GO:0004674; GO:0005524; GO:0005739; GO:0016310; GO:0017018; GO:0046872	phosphorylation [GO:0016310]	mitochondrion [GO:0005739]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; myosin phosphatase activity [GO:0017018]; protein serine/threonine kinase activity [GO:0004674]	Q9SL76		Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein [Includes: Probable protein phosphatase 2C 19 (AtPP2C19) (EC 3.1.3.16); Probable inactive cyclic nucleotide-dependent protein kinase At2g20050]	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003323	2016_BC12	GO:0003677; GO:0003723; GO:0003887; GO:0003964; GO:0004190; GO:0004523; GO:0006310; GO:0006508; GO:0008270; GO:0015074; GO:0016020; GO:0019013; GO:0019068; GO:0020002; GO:0039660; GO:0044185; GO:0044826; GO:0046718; GO:0072494; GO:0075713	DNA integration [GO:0015074]; DNA recombination [GO:0006310]; establishment of integrated proviral latency [GO:0075713]; proteolysis [GO:0006508]; viral entry into host cell [GO:0046718]; viral genome integration into host DNA [GO:0044826]; virion assembly [GO:0019068]	host cell late endosome membrane [GO:0044185]; host cell plasma membrane [GO:0020002]; host multivesicular body [GO:0072494]; membrane [GO:0016020]; viral nucleocapsid [GO:0019013]	aspartic-type endopeptidase activity [GO:0004190]; DNA binding [GO:0003677]; DNA-directed DNA polymerase activity [GO:0003887]; RNA binding [GO:0003723]; RNA-directed DNA polymerase activity [GO:0003964]; RNA-DNA hybrid ribonuclease activity [GO:0004523]; structural constituent of virion [GO:0039660]; zinc ion binding [GO:0008270]	P10272	pol	Gag-Pol polyprotein [Cleaved into: Matrix protein p15 (MA); RNA-binding phosphoprotein p12 (pp12); Capsid protein p30 (CA); Nucleocapsid protein p10-Pol (NC-pol); Protease (EC 3.4.23.-); Reverse transcriptase/ribonuclease H (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase (IN) (EC 2.7.7.-) (EC 3.1.-.-)]	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003324	2016_BC12	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0009733; GO:0009734; GO:0009793; GO:0009908; GO:0009942; GO:0010051; GO:0010305; GO:0042802; GO:0048364; GO:0048507	auxin-activated signaling pathway [GO:0009734]; embryo development ending in seed dormancy [GO:0009793]; flower development [GO:0009908]; leaf vascular tissue pattern formation [GO:0010305]; longitudinal axis specification [GO:0009942]; meristem development [GO:0048507]; regulation of DNA-templated transcription [GO:0006355]; response to auxin [GO:0009733]; root development [GO:0048364]; xylem and phloem pattern formation	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; identical protein binding [GO:0042802]; transcription cis-regulatory region binding [GO:0000976]	P93024	ARF5	Auxin response factor 5 (Auxin-responsive protein IAA24) (Transcription factor MONOPTEROS)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003333	2016_BC12	GO:0016746			acyltransferase activity [GO:0016746]	Q3ZPN4	AMAT	Methanol O-anthraniloyltransferase (EC 2.3.1.232) (Anthraniloyl-CoA:methanol acyltransferase) (Benzyl alcohol O-benzoyltransferase) (EC 2.3.1.196)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003334	2016_BC12	GO:0003735; GO:0006412; GO:0009507; GO:0015935;	translation [GO:0006412]	chloroplast [GO:0009507]; small ribosomal subunit [GO:0015935]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	Q6EM62	rps7	Small ribosomal subunit protein uS7c (30S ribosomal protein S7, chloroplastic)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003330	2016_BC12	GO:0003697; GO:0003729; GO:0005739; GO:0006260	DNA replication [GO:0006260]	mitochondrion [GO:0005739]	mRNA binding [GO:0003729]; single-stranded DNA binding [GO:0003697]	Q84J78		Single-stranded DNA-binding protein, mitochondrial	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003333	2016_BC13	GO:0016746			acyltransferase activity [GO:0016746]	Q3ZPN4	AMAT	Methanol O-anthraniloyltransferase (EC 2.3.1.232) (Anthraniloyl-CoA:methanol acyltransferase) (Benzyl alcohol O-benzoyltransferase) (EC 2.3.1.196)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003334	2016_BC13	GO:0003735; GO:0006412; GO:0009507; GO:0015935;	translation [GO:0006412]	chloroplast [GO:0009507]; small ribosomal subunit [GO:0015935]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	Q6EM62	rps7	Small ribosomal subunit protein uS7c (30S ribosomal protein S7, chloroplastic)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003330	2016_BC13	GO:0003697; GO:0003729; GO:0005739; GO:0006260	DNA replication [GO:0006260]	mitochondrion [GO:0005739]	mRNA binding [GO:0003729]; single-stranded DNA binding [GO:0003697]	Q84J78		Single-stranded DNA-binding protein, mitochondrial	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003356	2016_BC14	GO:0004674; GO:0005524; GO:0006952; GO:0016020; GO:0016310; GO:0030246; GO:0051707; GO:0106310	defense response [GO:0006952]; phosphorylation [GO:0016310]; response to other organism [GO:0051707]	membrane [GO:0016020]	ATP binding [GO:0005524]; carbohydrate binding [GO:0030246]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	A0A075F7E9	LECRK1	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK1 (OsLecRK1) (EC 2.7.11.1) (OsRLCK134)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003355	2016_BC14	GO:0000502; GO:0005634; GO:0005829; GO:0006511; GO:0009506; GO:0019773	ubiquitin-dependent protein catabolic process [GO:0006511]	cytosol [GO:0005829]; nucleus [GO:0005634]; plasmodesma [GO:0009506]; proteasome complex [GO:0000502]; proteasome core complex, alpha-subunit complex		O23712	PAF2	Proteasome subunit alpha type-1-B (20S proteasome alpha subunit F-2) (Proteasome component 2B) (Proteasome subunit alpha type-6)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003357	2016_BC14	GO:0006869; GO:0006914; GO:0034045; GO:0050832;	autophagy [GO:0006914]; defense response to fungus [GO:0050832]; lipid transport [GO:0006869]	phagophore assembly site membrane [GO:0034045]		Q8RUS5	ATG9	Autophagy-related protein 9 (AtAPG9)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003350	2016_BC14	GO:0001650; GO:0005634; GO:0005654; GO:0005730; GO:0005829; GO:0006355; GO:0008284	positive regulation of cell population proliferation [GO:0008284]; regulation of DNA-templated transcription [GO:0006355]	cytosol [GO:0005829]; fibrillar center [GO:0001650]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]		Q96GN5	CDCA7L	Cell division cycle-associated 7-like protein (Protein JPO2) (Transcription factor RAM2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003363	2016_BC15	GO:0003924; GO:0005525; GO:0005783; GO:0005794;	intracellular protein transport [GO:0006886]; vesicle-mediated transport [GO:0016192]	endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	O04267	SAR1B	GTP-binding protein SAR1B	12.5Mb-17.5Mb	10.1073/pnas.1009363108

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
2	Vitvi003359	2016_BC15	GO:0004674; GO:0004693; GO:0005524; GO:0005634; GO:0005737; GO:0008353; GO:0016310; GO:0035556; GO:0106310	intracellular signal transduction [GO:0035556]; phosphorylation [GO:0016310]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; cyclin-dependent protein serine/threonine kinase activity [GO:0004693]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; RNA polymerase II CTD heptapeptide repeat kinase activity [GO:0008353]	Q6Z8C8	CDKF-4	Cyclin-dependent kinase F-4 (CDKF;4) (EC 2.7.11.22) (EC 2.7.11.23) (Serine/threonine-protein kinase MHK-like protein 2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003365	2016_BC15	GO:0005737; GO:0009694; GO:0009753; GO:0080131; GO:0102055; GO:0102056	jasmonic acid metabolic process [GO:0009694]; response to jasmonic acid [GO:0009753]	cytoplasm [GO:0005737]	11-hydroxyjasmonate sulfotransferase activity [GO:0102056]; 12-hydroxyjasmonate sulfotransferase activity [GO:0102055]; hydroxyjasmonate sulfotransferase	Q8L5A7	SOT15	Cytosolic sulfotransferase 15 (AtSOT15) (EC 2.8.2.39) (Sulfotransferase 2a) (AtST2a)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003361	2016_BC15	GO:0000139; GO:0005768; GO:0005794; GO:0005797; GO:0005802; GO:0008757; GO:0032259	methylation [GO:0032259]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; Golgi medial cisterna [GO:0005797]; Golgi membrane [GO:0000139]; trans-Golgi network [GO:0005802]	S-adenosylmethionine-dependent methyltransferase activity [GO:0008757]	Q9C6S7		Probable methyltransferase PMT20 (EC 2.1.1.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003366	2016_BC15	GO:0005783; GO:0061630; GO:0071784; GO:0071786	endoplasmic reticulum cisternal network assembly [GO:0071784]; endoplasmic reticulum tubular network organization [GO:0071786]	endoplasmic reticulum [GO:0005783]	ubiquitin protein ligase activity [GO:0061630]	Q9ZQ34		Uncharacterized protein At2g24330	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003363	2016_BC16	GO:0003924; GO:0005525; GO:0005783; GO:0005794;	intracellular protein transport [GO:0006886]; vesicle-mediated transport [GO:0016192]	endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	O04267	SAR1B	GTP-binding protein SAR1B	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003359	2016_BC16	GO:0004674; GO:0004693; GO:0005524; GO:0005634; GO:0005737; GO:0008353; GO:0016310; GO:0035556; GO:0106310	intracellular signal transduction [GO:0035556]; phosphorylation [GO:0016310]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; cyclin-dependent protein serine/threonine kinase activity [GO:0004693]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; RNA polymerase II CTD heptapeptide repeat kinase activity [GO:0008353]	Q6Z8C8	CDKF-4	Cyclin-dependent kinase F-4 (CDKF;4) (EC 2.7.11.22) (EC 2.7.11.23) (Serine/threonine-protein kinase MHK-like protein 2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003365	2016_BC16	GO:0005737; GO:0009694; GO:0009753; GO:0080131; GO:0102055; GO:0102056	jasmonic acid metabolic process [GO:0009694]; response to jasmonic acid [GO:0009753]	cytoplasm [GO:0005737]	11-hydroxyjasmonate sulfotransferase activity [GO:0102056]; 12-hydroxyjasmonate sulfotransferase activity [GO:0102055]; hydroxyjasmonate sulfotransferase	Q8L5A7	SOT15	Cytosolic sulfotransferase 15 (AtSOT15) (EC 2.8.2.39) (Sulfotransferase 2a) (AtST2a)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003361	2016_BC16	GO:0000139; GO:0005768; GO:0005794; GO:0005797; GO:0005802; GO:0008757; GO:0032259	methylation [GO:0032259]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; Golgi medial cisterna [GO:0005797]; Golgi membrane [GO:0000139]; trans-Golgi network [GO:0005802]	S-adenosylmethionine-dependent methyltransferase activity [GO:0008757]	Q9C6S7		Probable methyltransferase PMT20 (EC 2.1.1.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003366	2016_BC16	GO:0005783; GO:0061630; GO:0071784; GO:0071786	endoplasmic reticulum cisternal network assembly [GO:0071784]; endoplasmic reticulum tubular network organization [GO:0071786]	endoplasmic reticulum [GO:0005783]	ubiquitin protein ligase activity [GO:0061630]	Q9ZQ34		Uncharacterized protein At2g24330	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003440	2016_BC18	GO:0007623; GO:0009699; GO:0009723; GO:0010597; GO:0034318; GO:0102387; GO:0102720	circadian rhythm [GO:0007623]; green leaf volatile biosynthetic process [GO:0010597]; phenylpropanoid biosynthetic process [GO:0009699]; response to ethylene [GO:0009723]		2-phenylethanol acetyltransferase activity [GO:0102387]; acetyl-coenzyme A:acetyl alcohol acetyltransferase activity [GO:0102720]; alcohol O-acyltransferase activity [GO:0034318]	A1XWY7	CFAT	Coniferyl alcohol acyltransferase (PhCFAT) (EC 2.3.1.-) ((E)-cinnamyl alcohol acyltransferase) (EC 2.3.1.224) ((E)-sinapoyl alcohol acyltransferase) (EC 2.3.1.-) (Geraniol acyltransferase) (EC 2.3.1.-) (Octan-1-ol acyltransferase) (EC 2.3.1.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003441	2016_BC18	GO:0000289; GO:0003723; GO:0004532; GO:0004535; GO:0005634; GO:0005737; GO:0009507; GO:0042752; GO:0043621; GO:0046872; GO:0048511	nuclear-transcribed mRNA poly(A) tail shortening [GO:0000289]; regulation of circadian rhythm [GO:0042752]; rhythmic process [GO:0048511]	chloroplast [GO:0009507]; cytoplasm [GO:0005737]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; poly(A)-specific ribonuclease activity [GO:0004535]; protein self-association [GO:0043621]; RNA binding [GO:0003723]; RNA exonuclease activity [GO:0004532]	A8MS41	CCR4-4	Carbon catabolite repressor protein 4 homolog 4 (CCR4 homolog 4) (EC 3.1.13.4) (Protein HESPERIN) (AtHESP) (AtHesperin)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003437	2016_BC18	GO:0000741; GO:0005739; GO:0009651; GO:0010197;	karyogamy [GO:0000741]; polar nucleus fusion [GO:0010197]; response to salt stress [GO:0009651]	membrane [GO:0016020]; mitochondrion [GO:0005739]		F4I9E1	NFD4	Protein NUCLEAR FUSION DEFECTIVE 4	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003448	2016_BC18	GO:0005085; GO:0005886; GO:0080092	regulation of pollen tube growth [GO:0080092]	plasma membrane [GO:0005886]	guanyl-nucleotide exchange factor activity [GO:0005085]	Q56WM6	ROPGEF14	Rop guanine nucleotide exchange factor 14 (AtRopGEF14) (Rho of plants guanine nucleotide exchange factor 14)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003455	2016_BC18	GO:0000139; GO:0005794; GO:0009834; GO:0016491; GO:0016740; GO:0045491;	plant-type secondary cell wall biogenesis [GO:0009834]; xylan acetylation [GO:1990937]; xylan biosynthetic process [GO:0045492]; xylan metabolic process [GO:0045491]	Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]	oxidoreductase activity [GO:0016491]; transferase activity [GO:0016740]	Q66GQ5	RWA3	Protein REDUCED WALL ACETYLATION 3 (EC 2.3.1.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003445	2016_BC18	GO:0005737; GO:0006511; GO:0012505; GO:0015031; GO:0032586; GO:0046872;	protein transport [GO:0015031]; ubiquitin-dependent protein catabolic process [GO:0006511]	cytoplasm [GO:0005737]; endomembrane system [GO:0012505]; protein storage vacuole membrane	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q69U49	RMR1	Receptor homology region, transmembrane domain- and RING domain-containing protein 2 (OsRMR2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003444	2016_BC18	GO:0005576; GO:0016787;	cell wall organization [GO:0071555]	extracellular region [GO:0005576]	hydrolase activity [GO:0016787]	Q6DBP4	PAE8	Pectin acetylesterase 8 (EC 3.1.1.-)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003438	2016_BC18	GO:0009507		chloroplast [GO:0009507]		Q940A6		Pentatricopeptide repeat-containing protein At4g19440, chloroplastic	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003446	2016_BC18	GO:0000272; GO:0003700; GO:0005634; GO:0005737; GO:0048831; GO:0102229	polysaccharide catabolic process [GO:0000272]; regulation of shoot system development [GO:0048831]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	amylopectin maltohydrolase activity [GO:0102229]; DNA-binding transcription factor activity	Q9FH80	BAM8	Beta-amylase 8 (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) (Beta-amylase 2)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003459	2016_BC18	GO:0005829; GO:0015293; GO:0016020; GO:0042128	nitrate assimilation [GO:0042128]	cytosol [GO:0005829]; membrane [GO:0016020]	symporter activity [GO:0015293]	Q9LVE0	NPF6.4	Protein NRT1/ PTR FAMILY 6.4 (AtNPF6.4) (Nitrate transporter 1.3)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
2	Vitvi003453	2016_BC18	GO:0001727; GO:0004430; GO:0005546; GO:0005634; GO:0005886; GO:0006468; GO:0009506; GO:0009555; GO:0031234; GO:0046854; GO:0048015; GO:0048364; GO:0048471; GO:0048831; GO:0051015; GO:0070273;	phosphatidylinositol phosphate biosynthetic process [GO:0046854]; phosphatidylinositol-mediated signaling [GO:0048015]; pollen development [GO:0009555]; protein phosphorylation [GO:0006468]; regulation of shoot system development [GO:0048831]; root development [GO:0048364]	extrinsic component of cytoplasmic side of plasma membrane [GO:0031234]; membrane microdomain [GO:0098857]; nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]; plasma membrane [GO:0005886]; plasma membrane protein complex [GO:0098797]; plasmodesma	1-phosphatidylinositol 4-kinase activity [GO:0004430]; actin filament binding [GO:0051015]; lipid kinase activity [GO:0001727]; phosphatidic acid binding [GO:0070300]; phosphatidylinositol-4,5-bisphosphate binding [GO:0005546]; phosphatidylinositol-4-phosphate binding	Q9SXA1	PI4KA1	Phosphatidylinositol 4-kinase alpha 1 (PI4-kinase alpha 1ao) (PtdIns-4-kinase alpha 1) (EC 2.7.1.67) (Phosphatidylinositol 4-OH kinase alpha1) (AtPI4Kalpha1) (PI-4Kalpha1)	12.5Mb-17.5Mb	10.1073/pnas.1009363108
3	Vitvi003545	2016_BeS1	GO:0000347; GO:0000727; GO:0000785; GO:0003678; GO:0003697; GO:0005524; GO:0005634; GO:0006268; GO:0006271; GO:0009555; GO:0030337;	DNA strand elongation involved in DNA replication [GO:0006271]; DNA unwinding involved in DNA replication [GO:0006268]; double-strand break repair via break-induced replication [GO:0000727]; mitotic DNA replication initiation [GO:1902975]; pollen development [GO:0009555]	chromatin [GO:0000785]; MCM complex [GO:0042555]; nucleus [GO:0005634]; THO complex [GO:0000347]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA helicase activity [GO:0003678]; metal ion binding [GO:0046872]; single-stranded DNA binding [GO:0003697]	Q5JKB0	MCM4	DNA replication licensing factor MCM4 (EC 3.6.4.12) (Minichromosome maintenance protein 4) (OsMCM4)		
3	Vitvi003544	2016_BeS1	GO:0000220; GO:0000325; GO:0005739; GO:0005773; GO:0005774; GO:0005794; GO:0009678; GO:0009705; GO:0015986; GO:0032119; GO:0043181; GO:0046961; GO:0070072;	proton motive force-driven ATP synthesis [GO:0015986]; sequestering of zinc ion [GO:0032119]; vacuolar proton-transporting V-type ATPase complex assembly [GO:0070072]; vacuolar sequestering [GO:0043181]	Golgi apparatus [GO:0005794]; mitochondrion [GO:0005739]; plant-type vacuole [GO:0000325]; plant-type vacuole membrane [GO:0009705]; vacuolar membrane [GO:0005774]; vacuolar proton-transporting V-type ATPase, V0 domain [GO:0000220];	diphosphate hydrolysis-driven proton transmembrane transporter activity [GO:0009678]; proton-transporting ATPase activity, rotational mechanism [GO:0046961]	Q9SJT7	VHA-a2	V-type proton ATPase subunit a2 (V-ATPase subunit a2) (V-type proton ATPase 95 kDa subunit a isoform 2) (V-ATPase 95 kDa isoform a2) (Vacuolar H(+)-ATPase subunit a isoform 2) (Vacuolar proton pump subunit a2) (Vacuolar proton translocating ATPase 95 kDa subunit a isoform 2)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
3	Vitvi003546	2016_BeS1	GO:0000976; GO:0003700; GO:0005634; GO:0009555; GO:0009734; GO:0009739; GO:0009740; GO:0009851; GO:0009938; GO:0046872; GO:0046982; GO:0048653	anther development [GO:0048653]; auxin biosynthetic process [GO:0009851]; auxin-activated signaling pathway [GO:0009734]; gibberellic acid mediated signaling pathway [GO:0009740]; negative regulation of gibberellic acid mediated signaling pathway [GO:0009938]; pollen development [GO:0009555]; response to gibberellin	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; protein heterodimerization activity [GO:0046982]; transcription cis-regulatory region binding [GO:0000976]	Q9XGX0	SHI	Protein SHORT INTERNODES		
3	Vitvi004582	2016_SA1	GO:0001653; GO:0004672; GO:0004674; GO:0005524; GO:0006979; GO:0009845; GO:0016020; GO:0042277; GO:0042802; GO:0045087; GO:0046777; GO:0106310	innate immune response [GO:0045087]; protein autophosphorylation [GO:0046777]; response to oxidative stress [GO:0006979]; seed germination [GO:0009845]	membrane [GO:0016020]	ATP binding [GO:0005524]; identical protein binding [GO:0042802]; peptide binding [GO:0042277]; peptide receptor activity [GO:0001653]; protein kinase activity [GO:0004672]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	F4I2N7	RLK7	Receptor-like protein kinase 7 (EC 2.7.11.1)		
3	Vitvi004577	2016_SA1	GO:0002238; GO:0004506; GO:0005789; GO:0009723; GO:0009751; GO:0009753; GO:0010038; GO:0016126; GO:0042542; GO:0046246; GO:0050660; GO:0071731; GO:1902438	response to ethylene [GO:0009723]; response to hydrogen peroxide [GO:0042542]; response to jasmonic acid [GO:0009753]; response to metal ion [GO:0010038]; response to molecule of fungal origin [GO:0002238]; response to nitric oxide [GO:0071731]; response to salicylic acid [GO:0009751]; response to vanadate(3-) [GO:1902438]; sterol biosynthetic process [GO:0016126]; terpene biosynthetic	endoplasmic reticulum membrane [GO:0005789]	flavin adenine dinucleotide binding [GO:0050660]; squalene monooxygenase activity [GO:0004506]	O48651	SQE1	Squalene monooxygenase SE1 (EC 1.14.14.17) (Squalene epoxidase 1) (PgSQE1) (SE) (SE1) (gse)		
3	Vitvi004586	2016_SA1	GO:0005829; GO:0006012; GO:0010349; GO:0019853	galactose metabolic process [GO:0006012]; L-ascorbic acid biosynthetic process [GO:0019853]	cytosol [GO:0005829]	L-galactose dehydrogenase activity [GO:0010349]	O81884	LGALDH	L-galactose dehydrogenase (At-GalDH) (L-GalDH) (EC 1.1.1.316)		
3	Vitvi004583	2016_SA1	GO:0006097; GO:0006099; GO:0006108; GO:0009514	glyoxylate cycle [GO:0006097]; malate metabolic process [GO:0006108]; tricarboxylic acid cycle [GO:0006099]	glyoxysome [GO:0009514]	L-malate dehydrogenase activity [GO:0030060]	P19446		Malate dehydrogenase, glyoxysomal (EC 1.1.1.37)		10.1073/pnas.87.15.5773
3	Vitvi004581	2016_SA1	GO:0004177; GO:0005739; GO:0005829; GO:0006508; GO:0009414; GO:0009507; GO:0010038; GO:0099503	proteolysis [GO:0006508]; response to metal ion [GO:0010038]; response to salt [GO:1902074]; response to water deprivation [GO:0009414]	chloroplast [GO:0009507]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; secretory vesicle [GO:0099503]	aminopeptidase activity [GO:0004177]	P93732	PIP	Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase) (PAP)		
3	Vitvi004587	2016_SA1	GO:0000139; GO:0005794; GO:0019706		Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]	protein-cysteine S-palmitoyltransferase activity [GO:0019706]	Q3EC11	PAT23	Probable protein S-acyltransferase 23 (EC 2.3.1.225) (Probable palmitoyltransferase At2g14255) (Zinc finger DHHC domain-containing protein At2g14255)		
3	Vitvi004591	2016_SA1	GO:0000287; GO:0004427; GO:0005886; GO:0006796; GO:0009507; GO:0009536; GO:0009570; GO:0009579; GO:0009941	phosphate-containing compound metabolic process [GO:0006796]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; plasma membrane [GO:0005886]; plastid [GO:0009536]; thylakoid [GO:0009579]	inorganic diphosphate phosphatase activity [GO:0004427]; magnesium ion binding [GO:0000287]	Q9LXC9	PPA6	Soluble inorganic pyrophosphatase 6, chloroplastic (EC 3.6.1.1) (Inorganic pyrophosphatase 6) (Pyrophosphate phospho-hydrolase 6) (PPase 6)		
3	Vitvi004585	2016_SA1	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0046983	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]; transcription cis-regulatory region binding [GO:0000976]	Q9T072	BHLH25	Transcription factor bHLH25 (Basic helix-loop-helix protein 25) (AtbHLH25) (bHLH 25) (Transcription factor EN 29) (bHLH transcription factor bHLH025)		
3	Vitvi004592	2016_SA1	GO:0005739		mitochondrion [GO:0005739]		Q9ZUY1		Pentatricopeptide repeat-containing protein At2g27800, mitochondrial		
3	Vitvi005119	2016_SA2	GO:0005576; GO:0030599; GO:0042545; GO:0045330; GO:0045490	cell wall modification [GO:0042545]; pectin catabolic process [GO:0045490]	extracellular region [GO:0005576]	aspartyl esterase activity [GO:0045330]; pectinesterase activity [GO:0030599]	O23038	PME8	Probable pectinesterase 8 (PE 8) (EC 3.1.1.11) (Pectin methylesterase 2) (AtPME2) (Pectin methylesterase 8) (AtPME8)		10.1007/s00425-006-0261-9
3	Vitvi005120	2016_SA2	GO:0000049; GO:0003743; GO:0003924; GO:0005525; GO:0005737; GO:0006413; GO:0006446; GO:0042255; GO:0045702; GO:0046872	regulation of translational initiation [GO:0006446]; ribosome assembly [GO:0042255]; translational initiation [GO:0006413]	cytoplasm [GO:0005737]; synapse [GO:0045202]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; metal ion binding [GO:0046872]; translation initiation factor activity [GO:0003743]; tRNA binding [GO:0000049]	Q05D44	Eif5b	Eukaryotic translation initiation factor 5B (eIF-5B) (EC 3.6.5.3) (Translation initiation factor IF-2)		
3	Vitvi005122	2016_SA2	GO:0008194			UDP-glycosyltransferase activity [GO:0008194]	Q66PF3	GT3	Putative UDP-glucose flavonoid 3-O-glucosyltransferase 3 (FaGT3) (EC 2.4.1.-) (Flavonol 3-O-glucosyltransferase 3)		10.1104/pp.105.074955
4	Vitvi006020	2016_Suc1	GO:0005739; GO:0005829; GO:0008460; GO:0009506; GO:0010253; GO:0010280; GO:0010315; GO:0016491; GO:0016853; GO:0030154; GO:0042127; GO:0050377; GO:0051555; GO:0071555	auxin export across the plasma membrane [GO:0010315]; cell differentiation [GO:0030154]; cell wall organization [GO:0071555]; flavonol biosynthetic process [GO:0051555]; regulation of cell population proliferation [GO:0042127]; UDP-rhamnose biosynthetic process [GO:0010253]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasmodesma [GO:0009506]	dTDP-glucose 4,6-dehydratase activity [GO:0008460]; isomerase activity [GO:0016853]; oxidoreductase activity [GO:0016491]; UDP-glucose 4,6-dehydratase activity [GO:0050377]; UDP-L-rhamnose synthase activity [GO:0010280]	Q9SYM5	RHM1	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 (Protein REPRESSOR OF LRX1 1) (Rhamnose biosynthetic enzyme 1) (AtRHM1) [Includes: UDP-glucose 4,6-dehydratase (EC 4.2.1.76); UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-4-keto-reductase (EC 1.1.1.-) (EC		10.1105/tpc.107.053249
4	Vitvi006589	2016_TAC1	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0009740; GO:0009937; GO:0010029; GO:0010431; GO:0046872	gibberellic acid mediated signaling pathway [GO:0009740]; regulation of DNA-templated transcription [GO:0006355]; regulation of gibberellic acid mediated signaling pathway [GO:0009937]; regulation of seed germination [GO:0010029]; seed maturation [GO:0010431]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; transcription cis-regulatory region binding [GO:0000976]	Q9LVQ7	ENY	Zinc finger protein ENHYDROUS (Protein indeterminate-domain 1)		
4	Vitvi006592	2016_TAC1	GO:0005524; GO:0005829; GO:0016020; GO:0016887; GO:0140359		cytosol [GO:0005829]; membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9M3B9	ABCB20	ABC transporter B family member 20 (ABC transporter ABCB.20) (AtABCB20) (Multidrug resistance protein 14) (P-glycoprotein 20)		
4	Vitvi006587	2016_TAC1	GO:0017018; GO:0046872			metal ion binding [GO:0046872]; myosin phosphatase activity	Q9SUK9		Probable protein phosphatase 2C 55 (AtPP2C55) (EC 3.1.3.16)		
5	Vitvi007314	2017_SL2	GO:0016627; GO:0043693	monoterpene biosynthetic process [GO:0043693]		oxidoreductase activity, acting on the CH-CH group of donors [GO:0016627]	A0A1C9CX66	CYC2	(S)-8-oxocitronellyl enol synthase CYC2 (EC 1.3.1.122) (Cyclase 2) (Iridoid synthase) (ISY)		
5	Vitvi007325	2017_SL2	GO:0004148; GO:0005829; GO:0009507; GO:0009570; GO:0009941; GO:0046685; GO:0050660	response to arsenic-containing substance [GO:0046685]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]	dihydrolipoyl dehydrogenase activity [GO:0004148]; flavin adenine dinucleotide binding [GO:0050660]	F4JLP5	LPD2	Dihydrolipoyl dehydrogenase 2, chloroplastic (ptLPD2) (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase 2) (Protein LIPOAMIDE DEHYDROGENASE 2) (Pyruvate dehydrogenase complex E3 subunit 2) (E3-2) (PDC-E3 2)		
5	Vitvi007347	2017_SL2	GO:0003723; GO:0005634; GO:0006397; GO:0042802	mRNA processing [GO:0006397]	nucleus [GO:0005634]	identical protein binding [GO:0042802]; RNA binding [GO:0003723]	F4KDH9	FIPS5	FIP1[V]-like protein (AtFIP1(V)) (Factor interacting with poly(A) polymerase 1-like 5) (AtFIPS5) (Protein HOMOLOG OF YEAST FIP1 [V])		
5	Vitvi007318	2017_SL2	GO:0003987; GO:0005524; GO:0005829; GO:0016405; GO:0043759; GO:0047760; GO:0050218		cytosol [GO:0005829]	acetate-CoA ligase activity [GO:0003987]; ATP binding [GO:0005524]; butyrate-CoA ligase activity [GO:0047760]; CoA-ligase activity [GO:0016405]; methylbutanoate-CoA ligase activity [GO:0043759]; propionate-CoA ligase activity [GO:0050218]	M4IS88	CCL3	Acetate--CoA ligase CCL3 (HICCL3) (EC 6.2.1.1) (2-methylbutanoate--CoA ligase CCL4) (EC 6.2.1.-) (2-methylpropanoate--CoA ligase CCL4) (EC 6.2.1.-) (Butanoate--CoA ligase CCL3) (EC 6.2.1.-) (Hexanoate--CoA ligase CCL3) (EC 6.2.1.-) (Isovalerate--CoA ligase CCL3) (EC 6.2.1.-) (Pentanoate--CoA ligase CCL3) (EC 6.2.1.-) (Propionate--CoA ligase CCL3) (EC 6.2.1.17)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
5	Vitvi007322	2017_SL2	GO:0003924; GO:0005525; GO:0005783; GO:0005794; GO:0005886; GO:0006886; GO:0016192	intracellular protein transport [GO:0006886]; pollen development [GO:0009555]; vesicle-mediated transport [GO:0016192]	endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	O04834	SAR1A	GTP-binding protein SAR1A		
5	Vitvi007304	2017_SL2	GO:0005634; GO:0005737; GO:0006607; GO:0008139; GO:0061608	NLS-bearing protein import into nucleus [GO:0006607]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	nuclear import signal receptor activity [GO:0061608]; nuclear localization sequence binding [GO:0008139]	O22478		Importin subunit alpha (Karyopherin subunit alpha) (KAP alpha)		
5	Vitvi007321	2017_SL2	GO:0003700; GO:0005516; GO:0005634; GO:0006355; GO:0009409; GO:0043565; GO:0070417	cellular response to cold [GO:0070417]; regulation of DNA-templated transcription [GO:0006355]; response to cold [GO:0009409]	nucleus [GO:0005634]	calmodulin binding [GO:0005516]; DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	O23463	CAMTA5	Calmodulin-binding transcription activator 5 (AtCAMTA5) (Ethylene-induced calmodulin-binding protein f) (EICBP.f) (Signal-responsive protein 6) (AtSR6)		
5	Vitvi007345	2017_SL2	GO:0016747			acyltransferase activity, transferring groups other than amino-acyl groups [GO:0016747]	O64815		Probable N-acetyltransferase HLS1-like (EC 2.3.1.-)		
5	Vitvi007354	2017_SL2	GO:0000155; GO:0005634; GO:0005783; GO:0006355; GO:0009584; GO:0009585; GO:0009881; GO:0010105; GO:0042803; GO:0051740	detection of visible light [GO:0009584]; negative regulation of ethylene-activated signaling pathway [GO:0010105]; red, far-red light phototransduction [GO:0009585]; regulation of DNA-templated transcription [GO:0006355]	endoplasmic reticulum [GO:0005783]; nucleus [GO:0005634]	ethylene binding [GO:0051740]; phosphorelay sensor kinase activity [GO:0000155]; photoreceptor activity [GO:0009881]; protein homodimerization activity	P29130	PHYB	Phytochrome B		
5	Vitvi007332	2017_SL2	GO:0005773; GO:0005975; GO:0006952; GO:0042973	carbohydrate metabolic process [GO:0005975]; defense response [GO:0006952]	vacuole [GO:0005773]	glucan endo-1,3-beta-D-glucosidase activity [GO:0042973]	P52407	HGN1	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) (allergen Hev b 2) [Cleaved into: Glucan endo-1,3-beta-glucosidase minor form 3; Glucan endo-1,3-beta-glucosidase minor form 2; Glucan endo-1,3-beta-glucosidase minor form 1; Glucan endo-1,3-beta-glucosidase major form]		
5	Vitvi007363	2017_SL2	GO:0017018; GO:0046872			metal ion binding [GO:0046872]; myosin phosphatase activity	Q0V7V2	PP2C42	Probable protein phosphatase 2C 42 (AtPP2C42) (EC 3.1.3.16)		
5	Vitvi007327	2017_SL2	GO:0006811; GO:0009527; GO:0009707; GO:0015171; GO:0015288; GO:0042803; GO:0046930	monoatomic ion transport [GO:0006811]	chloroplast outer membrane [GO:0009707]; plastid outer membrane [GO:0009527]; pore complex [GO:0046930]	amino acid transmembrane transporter activity [GO:0015171]; porin activity [GO:0015288]; protein homodimerization activity [GO:0042803]	Q0WMZ5	OEP162	Outer envelope pore protein 16-2, chloroplastic (Chloroplastic outer envelope pore protein of 16 kDa 2) (AtOEP16-2) (OEP16-2) (Outer plastid envelope protein 16-S) (AtOEP16-S) (Seeds outer plastid envelope protein 16)		
5	Vitvi007342	2017_SL2	GO:0004029; GO:0005576; GO:0005783; GO:0043878		endoplasmic reticulum [GO:0005783]; extracellular region [GO:0005576]	aldehyde dehydrogenase (NAD+) activity [GO:0004029]; glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non-phosphorylating) activity	Q0WSF1	ALDH22A1	Aldehyde dehydrogenase 22A1 (EC 1.2.1.3) (Novel aldehyde dehydrogenase family 22 member A1)		
5	Vitvi007307	2017_SL2	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0009736; GO:0009738; GO:0009740; GO:0009788; GO:0010026; GO:0010090; GO:0022626; GO:0046872	abscisic acid-activated signaling pathway [GO:0009738]; cytokinin-activated signaling pathway [GO:0009736]; gibberellic acid mediated signaling pathway [GO:0009740]; negative regulation of abscisic acid-activated signaling pathway [GO:0009788]; regulation of DNA-templated transcription [GO:0006355]; trichome differentiation [GO:0010026]; trichome morphogenesis [GO:0010090]	cytosolic ribosome [GO:0022626]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; transcription cis-regulatory region binding [GO:0000976]	Q39265	ZFP6	Zinc finger protein 6		
5	Vitvi007311	2017_SL2	GO:0005737; GO:0005770; GO:0005774; GO:0006897; GO:0007033; GO:0015031; GO:0044090; GO:0046872; GO:0046907; GO:0061578; GO:0070536; GO:0071108	endocytosis [GO:0006897]; intracellular transport [GO:0046907]; positive regulation of intracellular protein transport [GO:0090316]; positive regulation of vacuole organization [GO:0044090]; protein K48-linked deubiquitination [GO:0071108]; protein K63-linked deubiquitination [GO:0070536]; protein transport	cytoplasm [GO:0005737]; late endosome [GO:0005770]; vacuolar membrane [GO:0005774]	K63-linked deubiquitinase activity [GO:0061578]; metal ion binding [GO:0046872]; metal-dependent deubiquitinase activity [GO:0140492]	Q5PNU3	AMSH3	AMSH-like ubiquitin thioesterase 3 (EC 3.4.19.-) (Deubiquitinating enzyme AMSH3)		
5	Vitvi007326	2017_SL2					Q6INN7	smek1	Serine/threonine-protein phosphatase 4 regulatory subunit 3 (SMEK homolog 1)		
5	Vitvi007360	2017_SL2	GO:0004300; GO:0005777; GO:0006635	fatty acid beta-oxidation [GO:0006635]	peroxisome [GO:0005777]	enoyl-CoA hydratase activity [GO:0004300]	Q6NL24	ECHIA	Probable enoyl-CoA hydratase 1, peroxisomal (EC 4.2.1.17) (Enoyl-CoA hydratase isoform		
5	Vitvi007329	2017_SL2	GO:0000419; GO:0003676; GO:0003899; GO:0005665; GO:0005730; GO:0006351; GO:0008270	DNA-templated transcription [GO:0006351]	nucleolus [GO:0005730]; RNA polymerase II, core complex [GO:0005665]; RNA polymerase V complex [GO:0000419]	DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q6NLH0	NRPB9A	DNA-directed RNA polymerases II, IV and V subunit 9A		
5	Vitvi007300	2017_SL2	GO:0005768; GO:0005794; GO:0005802; GO:0005886; GO:0009506; GO:0010215; GO:0098552	cellulose microfibril organization [GO:0010215]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]; side of membrane [GO:0098552]; trans-Golgi network [GO:0005802]		Q8GZ17	COBL7	COBRA-like protein 7		
5	Vitvi007302	2017_SL2	GO:0000976; GO:0003700; GO:0005634; GO:0008270		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]; zinc ion binding	Q8LG10	GATA15	GATA transcription factor 15		
5	Vitvi007346	2017_SL2	GO:0000325; GO:0003727; GO:0003729; GO:0006396; GO:0006397; GO:0006417; GO:0009507; GO:0009570; GO:0009657; GO:0009941; GO:0042793	mRNA processing [GO:0006397]; negative regulation of exoribonuclease activity [GO:1901918]; plastid organization [GO:0009657]; regulation of translation [GO:0006417]; response to red light [GO:0010114]; RNA processing [GO:0006396]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast membrane [GO:0031969]; chloroplast stroma [GO:0009570]; plant-type vacuole [GO:0000325]	mRNA binding [GO:0003729]; protein self-association [GO:0043621]; single-stranded RNA binding [GO:0003727]	Q8RWG2	HCF107	Protein high chlorophyll fluorescent 107		
5	Vitvi007330	2017_SL2	GO:0001932; GO:0005158; GO:0005634; GO:0006357; GO:0007010; GO:0008284; GO:0008286; GO:0008360; GO:0022604; GO:0043066; GO:0043568; GO:0045840; GO:0045893; GO:0045944; GO:0070577; GO:2001237	cytoskeleton organization [GO:0007010]; insulin receptor signaling pathway [GO:0008286]; negative regulation of apoptotic process [GO:0043066]; negative regulation of extrinsic apoptotic signaling pathway [GO:2001237]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of DNA-templated transcription [GO:0045893]; positive regulation of insulin-like growth factor receptor signaling pathway [GO:0043568]; positive regulation of mitotic nuclear division [GO:0045840]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of cell morphogenesis [GO:0022604]; regulation of cell shape [GO:0008360]; regulation of protein phosphorylation [GO:0001932]	nucleus [GO:0005634]	insulin receptor binding [GO:0005158]; lysine-acetylated histone binding [GO:0070577]	Q8WWQ0	PHIP	PH-interacting protein (PHIP) (DDB1- and CUL4-associated factor 14) (IRS-1 PH domain-binding protein) (WD repeat-containing protein 11)		
5	Vitvi007362	2017_SL2	GO:0005737; GO:0009312; GO:0033532; GO:0047268	oligosaccharide biosynthetic process [GO:0009312]; stachyose biosynthetic process [GO:0033532]	cytoplasm [GO:0005737]	galactinol-raffinose galactosyltransferase activity [GO:0047268]	Q93XK2	STS1	Stachyose synthase (EC 2.4.1.67) (Galactinol--raffinose galactosyltransferase)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
5	Vitvi007299	2017_SL2	GO:0000156; GO:0000976; GO:0003700; GO:0005634; GO:0005829; GO:0009414; GO:0009735; GO:0009736; GO:0010082; GO:0010380; GO:0010492; GO:0031537; GO:0048364; GO:0048367; GO:0071368; GO:0080022; GO:0080036; GO:0080113; GO:0090506; GO:1990110	axillary shoot meristem initiation [GO:0090506]; callus formation [GO:1990110]; cellular response to cytokinin stimulus [GO:0071368]; cytokinin-activated signaling pathway [GO:0009736]; maintenance of shoot apical meristem identity [GO:0010492]; primary root development [GO:0080022]; regulation of anthocyanin metabolic process [GO:0031537]; regulation of chlorophyll biosynthetic process [GO:0010380]; regulation of cytokinin-activated signaling pathway [GO:0080036]; regulation of root meristem growth [GO:0010082]; regulation of seed growth [GO:0080113]; response to cytokinin [GO:0009735]; response to water deprivation [GO:0009414]; root development [GO:0048364]; shoot system development [GO:0048367]	cytosol [GO:0005829]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; phosphorelay response regulator activity [GO:0000156]; transcription cis-regulatory region binding [GO:0000976]	Q940D0	ARR1	Two-component response regulator ARR1		
5	Vitvi007344	2017_SL2	GO:0003755; GO:0005768; GO:0005794; GO:0005797; GO:0005802; GO:0016020		endosome [GO:0005768]; Golgi apparatus [GO:0005794]; Golgi medial cisterna [GO:0005797]; membrane [GO:0016020]; trans-Golgi network	peptidyl-prolyl cis-trans isomerase activity [GO:0003755]	Q9C835	CYP21-4	Peptidyl-prolyl cis-trans isomerase CYP21-4 (PPIase CYP21-4) (EC 5.2.1.8) (Cyclophilin of 21 kDa 4) (Cyclophilin-21-4)		
5	Vitvi007353	2017_SL2	GO:0003878; GO:0005524; GO:0005829; GO:0006085; GO:0006099; GO:0006629; GO:0009044; GO:0009536;	acetyl-CoA biosynthetic process [GO:0006085]; lipid metabolic process [GO:0006629]; tricarboxylic acid cycle [GO:0006099]	ATP-dependent citrate lyase complex [GO:0140615]; cytosol [GO:0005829]	ATP binding [GO:0005524]; ATP citrate synthase activity [GO:0003878]; metal ion binding [GO:0046872]	Q9FGX1	ACLB-2	ATP-citrate synthase beta chain protein 2 (ATP-citrate synthase B-2) (EC 2.3.3.8) (ATP-citrate lyase B-2) (Citrate cleavage enzyme B-		
5	Vitvi007317	2017_SL2	GO:0010214; GO:0045493; GO:0046556; GO:0048046	seed coat development [GO:0010214]; xylan catabolic process [GO:0045493]	apoplast [GO:0048046]; plastid [GO:0009536]	alpha-L-arabinofuranosidase activity [GO:0046556]; xylan 1,4-beta-xylosidase activity [GO:0009044]	Q9FGY1	BXL1	Beta-D-xylosidase 1 (AtBXL1) (EC 3.2.1.-) (Alpha-L-arabinofuranosidase) (EC 3.2.1.55)		
5	Vitvi007312	2017_SL2	GO:0016020; GO:0016413		membrane [GO:0016020]	O-acetyltransferase activity	Q9FJ06	TBL4	Protein trichome birefringence-like 4		
5	Vitvi007310	2017_SL2	GO:0003677; GO:0003700; GO:0005634; GO:0009416; GO:0010224; GO:0051555; GO:1900386	flavonol biosynthetic process [GO:0051555]; positive regulation of flavonol biosynthetic process [GO:1900386]; response to light stimulus [GO:0009416]; response to UV-B [GO:0010224]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	Q9FJ07	MYB111	Transcription factor MYB111 (Myb-related protein 111) (AtMYB111) (Protein PRODUCTION OF FLAVONOL GLYCOSIDES 3)		
5	Vitvi007358	2017_SL2	GO:0005576; GO:0006979; GO:0020037; GO:0042744; GO:0046872; GO:0140825	hydrogen peroxide catabolic process [GO:0042744]; response to oxidative stress [GO:0006979]	extracellular region [GO:0005576]	heme binding [GO:0020037]; lactoperoxidase activity [GO:0140825]; metal ion binding [GO:0046872]	Q9LSP0	PER29	Peroxidase 29 (Atperox P29) (EC 1.11.1.7) (ATP40)		
5	Vitvi007357	2017_SL2	GO:0005576; GO:0030599; GO:0042545; GO:0045330; GO:0045490	cell wall modification [GO:0042545]; pectin catabolic process [GO:0045490]	extracellular region [GO:0005576]	aspartyl esterase activity [GO:0045330]; pectinesterase activity [GO:0030599]	Q9LSP1	PME67	Probable pectinesterase 67 (PE 67) (EC 3.1.1.11) (Pectin methylesterase 67)		
5	Vitvi007336	2017_SL2	GO:0004842; GO:0005524; GO:0005783; GO:0006511; GO:0016020; GO:0016567; GO:0042631; GO:0048471; GO:0060321	cellular response to water deprivation [GO:0042631]; negative regulation of stomatal opening [GO:1902457]; protein ubiquitination [GO:0016567]; ubiquitin-dependent protein catabolic process [GO:0006511]	endoplasmic reticulum [GO:0005783]; membrane [GO:0016020]; perinuclear region of cytoplasm [GO:0048471]	ATP binding [GO:0005524]; ubiquitin conjugating enzyme activity [GO:0061631]; ubiquitin-protein transferase activity [GO:0004842]	Q9LSP7	UBC32	Ubiquitin-conjugating enzyme E2 32 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 32) (Ubiquitin carrier protein 32)		
5	Vitvi007320	2017_SL2	GO:0005576; GO:0005975; GO:0006032; GO:0016998	carbohydrate metabolic process [GO:0005975]; cell wall macromolecule catabolic process [GO:0016998]; chitin catabolic process [GO:0006032]	extracellular region [GO:0005576]		Q9LSP9	CTL2	Chitinase-like protein 2 (AtCTL2)		
5	Vitvi007313	2017_SL2	GO:0005739; GO:0006979; GO:0009651; GO:0009737; GO:0042775	mitochondrial ATP synthesis coupled electron transport [GO:0042775]; response to abscisic acid [GO:0009737]; response to oxidative stress [GO:0006979]; response to salt stress [GO:0009651]	mitochondrion [GO:0005739]		Q9LSQ2	PPR40	Putative pentatricopeptide repeat-containing protein At3g16890, mitochondrial (Protein PENTATRICOPEPTIDE REPEAT 40)		
5	Vitvi007333	2017_SL2	GO:0003700; GO:0005634; GO:0006971; GO:0009267; GO:0043565; GO:0045735; GO:0045893; GO:0046982; GO:2000693	cellular response to starvation [GO:0009267]; hypotonic response [GO:0006971]; positive regulation of DNA-templated transcription [GO:0045893]; positive regulation of seed maturation [GO:2000693]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; nutrient reservoir activity [GO:0045735]; protein heterodimerization activity [GO:0046982]; sequence-specific DNA	Q9LZP8	BZIP53	bZIP transcription factor 53 (AtbZIP53)		
5	Vitvi007323	2017_SL2	GO:0003735; GO:0005730; GO:0006412; GO:0022625	translation [GO:0006412]	cytosolic large ribosomal subunit [GO:0022625]; nucleolus [GO:0005730]	structural constituent of ribosome [GO:0003735]	Q9M7X7	RPL29A	Large ribosomal subunit protein eL29z (60S ribosomal protein L29-1)		
5	Vitvi007351	2017_SL2	GO:0004674; GO:0004714; GO:0005524; GO:0016310; GO:0016324; GO:0090404; GO:0106310	phosphorylation [GO:0016310]	apical plasma membrane [GO:0016324]; pollen tube tip [GO:0090404]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; transmembrane receptor protein tyrosine kinase activity [GO:0004714]	Q9SR05	ANX1	Receptor-like protein kinase ANXUR1 (EC 2.7.11.1)		
5	Vitvi007315	2017_SL2	GO:0005829; GO:0008202; GO:0009611; GO:0010051; GO:0033671; GO:0046983; GO:0047787	response to wounding [GO:0009611]; steroid metabolic process [GO:0008202]; xylem and phloem pattern formation [GO:0010051]	cytosol [GO:0005829]	delta4-3-oxosteroid 5beta-reductase activity [GO:0047787]; enone reductase activity [GO:0033671]; protein dimerization activity [GO:0046983]	Q9STX2	VEP1	3-oxo-Delta(4,5)-steroid 5-beta-reductase (EC 1.3.1.3) (Delta(4)-3-oxosteroid 5-beta-reductase) (Delta-4,5-steroid 5-beta-reductase) (At5beta-StR) (Progesterone 5-beta-reductase) (5beta-POR) (Protein VEIN PATTERNING 1)		
5	Vitvi007334	2017_SL2	GO:0005829; GO:0009228; GO:0009229; GO:0050334	thiamine biosynthetic process [GO:0009228]; thiamine diphosphate biosynthetic process [GO:0009229]	cytosol [GO:0005829]	thiaminase activity [GO:0050334]	Q9SWB6	TENA_E	Probable bifunctional TENA-E protein (EC 3.5.1.-) (EC 3.5.99.2) (Aminopyrimidine aminohydrolase) (Formylaminopyrimidine amidohydrolase) (Formylaminopyrimidine deformylase) (Seed maturation protein PM36)		
5	Vitvi007306	2017_SL2	GO:0005634; GO:0006355;	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	zinc ion binding [GO:0008270]	Q9SY66	FRS11	Protein FAR1-RELATED SEQUENCE 11		
5	Vitvi007861	2016_SN2	GO:0005516; GO:0005737; GO:0005856; GO:0005886; GO:0010091	trichome branching [GO:0010091]	cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; plasma membrane [GO:0005886]	calmodulin binding [GO:0005516]	A0A1P8B590	IQD19	Protein IQ-DOMAIN 19 (AtIQD19) (Protein FURCA 3)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007926	2016_SN2	GO:0019853; GO:0047918; GO:0051287	L-ascorbic acid biosynthetic process [GO:0019853]		GDP-mannose 3,5-epimerase activity [GO:0047918]; NAD binding [GO:0051287]	A3C4S4	GME-1	GDP-mannose 3,5-epimerase 1 (GDP-Man 3,5-epimerase 1) (EC 5.1.3.18) (OsGME-1)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007856	2016_SN2	GO:0003735; GO:0006412; GO:0022627	translation [GO:0006412]	cytosolic small ribosomal subunit [GO:0022627]	structural constituent of ribosome [GO:0003735]	A5B4K1		Small ribosomal subunit protein eS1z (40S ribosomal protein S3a-1)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007921	2016_SN2	GO:0005886; GO:0007186; GO:0098552	G protein-coupled receptor signaling pathway [GO:0007186]	plasma membrane [GO:0005886]; side of membrane [GO:0098552]		B8AN27	RGG1	Guanine nucleotide-binding protein subunit gamma 1 (Ggamma-subunit 1) (Heterotrimeric G protein gamma-subunit 1)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007870	2016_SN2	GO:0005506; GO:0005634; GO:0005737; GO:0006555; GO:0010308; GO:0010309; GO:0016151; GO:0019509	L-methionine salvage from methylthioadenosine [GO:0019509]; methionine metabolic process [GO:0006555]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	acireductone dioxygenase (Ni2+-requiring) activity [GO:0010308]; acireductone dioxygenase [iron(II)-requiring] activity [GO:0010309]; iron ion binding [GO:0005506]; nickel cation binding [GO:0016151]	D7T737		Acireductone dioxygenase 1 (Acireductone dioxygenase (Fe(2+)-requiring) 1) (ARD' 1) (Fe-ARD 1) (EC 1.13.11.54) (Acireductone dioxygenase (Ni(2+)-requiring) 1) (ARD 1) (Ni-ARD 1) (EC 1.13.11.53)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007871	2016_SN2	GO:0005506; GO:0005634; GO:0005737; GO:0006555; GO:0010308; GO:0010309; GO:0016151; GO:0019509	L-methionine salvage from methylthioadenosine [GO:0019509]; methionine metabolic process [GO:0006555]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	acireductone dioxygenase (Ni2+-requiring) activity [GO:0010308]; acireductone dioxygenase [iron(II)-requiring] activity [GO:0010309]; iron ion binding [GO:0005506]; nickel cation binding [GO:0016151]	F6HDT7		Acireductone dioxygenase 2 (Acireductone dioxygenase (Fe(2+)-requiring) 2) (ARD' 2) (Fe-ARD 2) (EC 1.13.11.54) (Acireductone dioxygenase (Ni(2+)-requiring) 2) (ARD 2) (Ni-ARD 2) (EC 1.13.11.53)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007903	2016_SN2	GO:0000325; GO:0005509; GO:0005634; GO:0005739; GO:0005783; GO:0005788; GO:0006457; GO:0009506; GO:0030246; GO:0034976; GO:0051082; GO:0099503	protein folding [GO:0006457]; response to endoplasmic reticulum stress [GO:0034976]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; mitochondrion [GO:0005739]; nucleus [GO:0005634]; plant-type vacuole [GO:0000325]; plasmodesma [GO:0009506]; secretory vesicle [GO:0099503]	calcium ion binding [GO:0005509]; carbohydrate binding [GO:0030246]; unfolded protein binding [GO:0051082]	O04151	CRT1	Calreticulin-1	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
5	Vitvi007936	2016_SN2	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0006970; GO:0009567; GO:0009737; GO:0010468; GO:0031347; GO:0046983; GO:1902074; GO:2000031	double fertilization forming a zygote and endosperm [GO:0009567]; regulation of defense response [GO:0031347]; regulation of DNA-templated transcription [GO:0006355]; regulation of gene expression [GO:0010468]; regulation of salicylic acid mediated signaling pathway [GO:2000031]; response to abscisic acid [GO:0009737]; response to osmotic stress [GO:0006970]; response to salt [GO:1902074]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]	O22768	UNE12	Transcription factor UNE12 (Basic helix-loop-helix protein 59) (AtbHLH59) (bHLH 59) (Protein UNFERTILIZED EMBRYO SAC 12) (Transcription factor EN 93) (bHLH transcription factor bHLH059)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007917	2016_SN2	GO:0005509; GO:0005737; GO:0005886; GO:0030234		cytoplasm [GO:0005737]; plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; enzyme regulator activity [GO:0030234]	P0DH95	CAM1	Calmodulin-1 (CaM-1)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007874	2016_SN2	GO:0031969		chloroplast membrane [GO:0031969]		P11432		Early light-induced protein, chloroplastic	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007918	2016_SN2	GO:0009706; GO:0010189; GO:0032259; GO:0051741; GO:0051742; GO:0102550	methylation [GO:0032259]; vitamin E biosynthetic process [GO:0010189]	chloroplast inner membrane [GO:0009706]	2-methyl-6-geranylgeranyl-1,4-benzoquinol methyltransferase activity [GO:0102550]; 2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity [GO:0051741]; 2-methyl-6-solanyl-1,4-benzoquinone methyltransferase activity	P23525		2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic (EC 2.1.1.295) (37 kDa inner envelope membrane protein) (E37) (MPBQ/MSBQ methyltransferase)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007913	2016_SN2	GO:0005737; GO:0047366		cytoplasm [GO:0005737]	quercetin-3-sulfate 4'-sulfotransferase activity [GO:0047366]	P52837		Flavonol 4'-sulfotransferase (F4-ST) (EC 2.8.2.27)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007868	2016_SN2	GO:0005576; GO:0010052; GO:0010374	guard cell differentiation [GO:0010052]; stomatal complex development [GO:0010374]	extracellular region [GO:0005576]		Q2V3I3	EPFL4	EPIDERMAL PATTERNING FACTOR-like protein 4 (EPF-like protein 4) [Cleaved into: CHALLAH-LIKE2]	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007877	2016_SN2	GO:0009820; GO:0016491	alkaloid metabolic process [GO:0009820]		oxidoreductase activity [GO:0016491]	Q3L181	PR	Perakine reductase (EC 1.1.1.317)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007922	2016_SN2	GO:0003924; GO:0005525; GO:0005802; GO:0006886; GO:0016192; GO:1903292	intracellular protein transport [GO:0006886]; protein localization to Golgi membrane [GO:1903292]; vesicle-mediated transport [GO:0016192]	trans-Golgi network [GO:0005802]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	Q55AD9	arl5	ADP-ribosylation factor-like protein 5	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007873	2016_SN2	GO:0005737; GO:0005794; GO:0007030; GO:0016020	bone development [GO:0060348]; Golgi organization [GO:0007030]	cytoplasm [GO:0005737]; Golgi apparatus [GO:0005794]; membrane	enzyme binding [GO:0019899]	Q7RTS9	DYM	Dymeclin (Dyggve-Melchior-Clausen syndrome protein)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007858	2016_SN2	GO:0005634; GO:0120293		dynein axonemal particle [GO:0120293]; nucleus [GO:0005634]		Q7ZWU1	stip1	Stress-induced-phosphoprotein 1 (STI1)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007933	2016_SN2	GO:0004252; GO:0005634; GO:0005737; GO:0005773; GO:0005829; GO:0006508; GO:0009507; GO:0051289	protein homotetramerization [GO:0051289]; proteolysis [GO:0006508]	chloroplast [GO:0009507]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]; vacuole [GO:0005773]	serine-type aminopeptidase activity [GO:0070009]; serine-type endopeptidase activity [GO:0004252]	Q84LM4	AARE	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Oxidized protein hydrolase) (OPH)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007869	2016_SN2	GO:0005634; GO:0048366; GO:1901371	leaf development [GO:0048366]; regulation of leaf morphogenesis [GO:1901371]	nucleus [GO:0005634]		Q8GY55	TIFY4B	Protein TIFY 4B (Protein PEAPOD 2)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007850	2016_SN2	GO:0008270; GO:0009086; GO:0032259; GO:0061627	methionine biosynthetic process [GO:0009086]; methylation [GO:0032259]		S-methylmethionine-homocysteine S-methyltransferase activity [GO:0061627]; zinc ion binding [GO:0008270]	Q8LAX0	HMT3	Homocysteine S-methyltransferase 3 (EC 2.1.1.10) (S-methylmethionine:homocysteine methyltransferase 3) (AtHMT-3) (SMM:Hcy S-methyltransferase 3)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007875	2016_SN2	GO:0005524; GO:0005737; GO:0005829; GO:0009408; GO:0010596; GO:0010628; GO:0016020; GO:0030544; GO:0042026; GO:0046872	negative regulation of endothelial cell migration [GO:0010596]; negative regulation of inclusion body assembly [GO:0090084]; positive regulation of gene expression [GO:0010628]; protein refolding [GO:0042026]; response to heat [GO:0009408]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; membrane [GO:0016020]	ATP binding [GO:0005524]; Hsp70 protein binding [GO:0030544]; metal ion binding [GO:0046872]; protein-folding chaperone binding [GO:0051087]; unfolded protein binding [GO:0051082]	Q8WW22	DNAJA4	DnaJ homolog subfamily A member 4	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007937	2016_SN2	GO:0006811; GO:0009507; GO:0009536; GO:0009941; GO:0042170	monoatomic ion transport [GO:0006811]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; plastid [GO:0009536]; plastid membrane [GO:0042170]		Q940Y9		Putative ion channel POLLUX-like 2	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007884	2016_SN2	GO:0000150; GO:0000730; GO:0000794; GO:0003690; GO:0003697; GO:0005524; GO:0006312; GO:0007131; GO:0008094; GO:0016887; GO:0042148; GO:0070192; GO:0140664	chromosome organization involved in meiotic cell cycle [GO:0070192]; DNA recombinase assembly [GO:0000730]; mitotic recombination [GO:0006312]; reciprocal meiotic recombination [GO:0007131]; strand invasion [GO:0042148]	condensed nuclear chromosome [GO:0000794]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATP-dependent activity, acting on DNA [GO:0008094]; ATP-dependent DNA damage sensor activity [GO:0140664]; DNA strand exchange activity [GO:0000150]; double-stranded DNA binding [GO:0003690]; single-stranded DNA binding [GO:0003697]	Q96449		Meiotic recombination protein DMC1 homolog	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007893	2016_SN2	GO:0000398; GO:0005634; GO:0005737; GO:0046540	mRNA splicing, via spliceosome [GO:0000398]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; U4/U6 x U5 tri-snRNP complex [GO:0046540]		Q9FE62	YLS8	Thioredoxin-like protein YLS8 (Protein YELLOW-LEAF-SPECIFIC GENE 8)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007889	2016_SN2	GO:0003723; GO:0009451	RNA modification [GO:0009451]		RNA binding [GO:0003723]	Q9FG85	PCMP-E30	Pentatricopeptide repeat-containing protein At5g43790	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007934	2016_SN2	GO:0006979; GO:0009507; GO:0009535; GO:0009536; GO:0031969	response to oxidative stress [GO:0006979]	chloroplast [GO:0009507]; chloroplast membrane [GO:0031969]; chloroplast thylakoid membrane [GO:0009535]; plastid [GO:0009536]		Q9FG89	PNSB5	Photosynthetic NDH subunit of subcomplex B 5, chloroplastic (Protein PnsB5) (NAD(P)H dehydrogenase 18)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007891	2016_SN2	GO:0005388; GO:0005516; GO:0005524; GO:0016020; GO:0016887; GO:0046872		membrane [GO:0016020]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; calmodulin binding [GO:0005516]; metal ion binding [GO:0046872]; P-type calcium transporter activity	Q9LIK7	ACA13	Putative calcium-transporting ATPase 13, plasma membrane-type (EC 7.2.2.10) (Ca(2+)-ATPase isoform 13)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007890	2016_SN2	GO:0000103; GO:0001887; GO:0004781; GO:0005524; GO:0009507; GO:0009570	hydrogen sulfide biosynthetic process [GO:0070814]; response to cadmium ion [GO:0046686]; selenium compound metabolic process [GO:0001887]; sulfate assimilation	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]	ATP binding [GO:0005524]; sulfate adenylyltransferase (ATP) activity [GO:0004781]	Q9LIK9	APS1	ATP sulfurylase 1, chloroplastic (AtPS1) (EC 2.7.7.4)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007879	2016_SN2	GO:0000325; GO:0005783; GO:0005794; GO:0015031; GO:0016192; GO:0032580	protein transport [GO:0015031]; vesicle-mediated transport [GO:0016192]	endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]; Golgi cisterna membrane [GO:0032580]; plant-type vacuole [GO:0000325]		Q9LIL4		Transmembrane emp24 domain-containing protein p24beta3 (p24 family protein beta2) (p24beta2) (p24 family protein beta3) (p24beta3)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007932	2016_SN2	GO:0006355; GO:0009507; GO:0010343; GO:1904821	chloroplast disassembly [GO:1904821]; regulation of DNA-templated transcription [GO:0006355]; singlet oxygen-mediated programmed cell death [GO:0010343]	chloroplast [GO:0009507]		Q9LS88		Pentatricopeptide repeat-containing protein At3g23020	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007927	2016_SN2	GO:0005634; GO:0006338; GO:0009793; GO:0009908; GO:0016514; GO:0035060; GO:0048366; GO:0048653; GO:0051783; GO:2000014	anther development [GO:0048653]; chromatin remodeling [GO:0006338]; embryo development ending in seed dormancy [GO:0009793]; flower development [GO:0009908]; leaf development [GO:0048366]; regulation of endosperm development [GO:2000014]; regulation of nuclear division [GO:0051783]	brahma complex [GO:0035060]; nucleus [GO:0005634]; SWI/SNF complex [GO:0016514]		Q9LS90	LFR	Armadillo repeat-containing protein LFR (Protein LEAF AND FLOWER RELATED)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007872	2016_SN2	GO:0000976; GO:0003700; GO:0005634; GO:0005737		cytoplasm [GO:0005737]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9LUH8	HSFA6b	Heat stress transcription factor A-6b (AtHsfA6b) (AtHsf-07)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007857	2016_SN2	GO:0005199; GO:0005576; GO:0071555	cell wall organization [GO:0071555]	extracellular region [GO:0005576]	structural constituent of cell wall [GO:0005199]	Q9LUI1	LRX6	Leucine-rich repeat extensin-like protein 6 (AtLRX6) (LRR/EXTENSIN6) (Cell wall hydroxyproline-rich glycoprotein)	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007855	2016_SN2	GO:0005737; GO:0005856; GO:0005886; GO:0009506; GO:0051015		cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	actin filament binding [GO:0051015]	Q9LUI2	NET1A	Protein NETWORKED 1A	chr5：127,259；127,278：127,301	10.1007/s10681-017-1919-z

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
5	Vitvi007909	2016_SN2	GO:0005388; GO:0005516; GO:0005524; GO:0016020; GO:0016887; GO:0046872		membrane [GO:0016020]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; calmodulin binding [GO:0005516]; metal ion binding [GO:0046872]; P-type calcium transporter activity	Q9LY77	ACA12	Calcium-transporting ATPase 12, plasma membrane-type (EC 7.2.2.10) (Ca(2+)-ATPase isoform 12)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007867	2016_SN2	GO:0005829; GO:0009507; GO:0015996; GO:0047746; GO:0102293	chlorophyll catabolic process [GO:0015996]	chloroplast [GO:0009507]; cytosol [GO:0005829]	chlorophyllase activity [GO:0047746]; pheophytinase b activity [GO:0102293]	Q9M7I7	CLH2	Chlorophyllase-2 (AtCLH2) (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 2) (Chlase 2)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007866	2016_SN2	GO:0016020		membrane [GO:0016020]		Q9SA63	LFG4	Protein LIFEGUARD 4 (AtLFG4)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007859	2016_SN2	GO:0008271; GO:0008272; GO:0009507; GO:0015116; GO:0015293; GO:0016020	sulfate transport [GO:0008272]	chloroplast [GO:0009507]; membrane [GO:0016020]	secondary active sulfate transmembrane transporter activity [GO:0008271]; sulfate transmembrane transporter activity [GO:0015116]; symporter activity [GO:0015293]	Q9SV13	SULTR3;1	Sulfate transporter 3.1 (AST12) (AtST1)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007886	2016_SN2	GO:0005737; GO:0006417; GO:0009536; GO:0009934; GO:0010072; GO:0010586; GO:0031047; GO:0035019; GO:0035198; GO:0051607; GO:1902183; GO:1990904	defense response to virus [GO:0051607]; miRNA metabolic process [GO:0010586]; primary shoot apical meristem specification [GO:0010072]; regulation of meristem structural organization [GO:0009934]; regulation of shoot apical meristem development [GO:1902183]; regulation of translation [GO:0006417]; regulatory ncRNA-mediated gene silencing [GO:0031047]; somatic stem cell population maintenance [GO:0035019]	cytoplasm [GO:0005737]; plastid [GO:0009536]; ribonucleoprotein complex [GO:1990904]	miRNA binding [GO:0035198]	Q9XGW1	AGO10	Protein argonaute 10 (Protein PINHEAD) (Protein ZWILLE)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi007931	2016_SN2	GO:0004674; GO:0005524; GO:0007165; GO:0009409; GO:0016310; GO:0106310	phosphorylation [GO:0016310]; response to cold [GO:0009409]; signal transduction [GO:0007165]		ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9XIW0	CIPK7	CBL-interacting serine/threonine-protein kinase 7 (EC 2.7.11.1) (SNF1-related kinase 3.10) (SOS2-like protein kinase PKS7) (Serine/threonine-protein kinase SR2) (AtSR2)	chr5：127,259，127,278：127,301	10.1007/s10681-017-1919-z
5	Vitvi008320	2016_SSC1	GO:0005244; GO:0005576; GO:0005886; GO:0006813; GO:0009506; GO:0034765	potassium ion transport [GO:0006813]; regulation of monoatomic ion transmembrane transport [GO:0034765]	extracellular region [GO:0005576]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	voltage-gated monoatomic ion channel activity [GO:0005244]	O23016	KAB1	Probable voltage-gated potassium channel subunit beta (K(+) channel subunit beta) (Potassium voltage beta 1) (KV-beta1)		
6	Vitvi009781	2017_Mal2	GO:0000160; GO:0005634; GO:0009736; GO:0048511	cytokinin-activated signaling pathway [GO:0009736]; phosphorelay signal transduction system [GO:0000160]; rhythmic process [GO:0048511]	nucleus [GO:0005634]		A2YQ93	PRR37	Two-component response regulator-like PRR37 (Pseudo-response regulator 37) (OsPRR37)		
6	Vitvi009800	2017_Mal2	GO:0003723; GO:0005634; GO:0005655; GO:0005739; GO:0006364; GO:0008033;	rRNA processing [GO:0006364]; tRNA processing [GO:0008033]	mitochondrion [GO:0005739]; nucleolar ribonuclease P complex [GO:0005655]; nucleus [GO:0005634]	hydrolase activity [GO:0016787]; RNA binding [GO:0003723]	F4JXF1	GAF1	Protein GAMETOPHYTE DEFECTIVE 1 (Probable ribonuclease P protein subunit p30) (AtRPP30) (RNaseP protein p30) (EC 3.1.26.-)		
6	Vitvi009787	2017_Mal2	GO:0000428; GO:0003677; GO:0003899; GO:0005634; GO:0006351; GO:0046872	DNA-templated transcription [GO:0006351]	DNA-directed RNA polymerase complex [GO:0000428]; nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; metal ion binding [GO:0046872]	F4JXF9	NRPC1	DNA-directed RNA polymerase III subunit 1 (DNA-directed RNA polymerase III subunit RPC1) (DNA polymerase I subunit C1) (EC 2.7.7.6) (Nuclear RNA polymerase C1)		
6	Vitvi009785	2017_Mal2	GO:0000325; GO:0003729; GO:0004672; GO:0004674; GO:0005524; GO:0005737; GO:0007623; GO:0009637; GO:0009638; GO:0009882; GO:0009898; GO:0009903; GO:0009904; GO:0009986; GO:0010119; GO:0010155; GO:0010181; GO:0010362; GO:0016301; GO:0042802;	chloroplast accumulation movement [GO:0009904]; chloroplast avoidance movement [GO:0009903]; circadian rhythm [GO:0007623]; negative regulation of anion channel activity by blue light [GO:0010362]; phototropism [GO:0009638]; protein autophosphorylation [GO:0046777]; regulation of proton transport [GO:0010155]; regulation of stomatal movement [GO:0010119]; response to blue light [GO:0009637]	cell surface [GO:0009986]; cytoplasm [GO:0005737]; cytoplasmic side of plasma membrane [GO:0009898]; plant-type vacuole [GO:0000325]	ATP binding [GO:0005524]; blue light photoreceptor activity [GO:0009882]; FMN binding [GO:0010181]; identical protein binding [GO:0042802]; kinase activity [GO:0016301]; mRNA binding [GO:0003729]; protein kinase activity [GO:0004672]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	O48963	PHOT1	Phototropin-1 (EC 2.7.11.1) (Non-phototropic hypocotyl protein 1) (Root phototropism protein 1)		
6	Vitvi009801	2017_Mal2	GO:0000786; GO:0003677; GO:0005634; GO:0006334; GO:0030527; GO:0046982	nucleosome assembly [GO:0006334]	nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:0030527]	P0CG89		Histone H4		
6	Vitvi009779	2017_Mal2	GO:0005739; GO:0016787;	glycerophospholipid biosynthetic process [GO:0046474]	mitochondrion [GO:0005739]	hydrolase activity [GO:0016787]	P36151		Mitochondrial hydrolase YKR070W (EC 3.-.-		
6	Vitvi009793	2017_Mal2	GO:0000723; GO:0002020; GO:0003677; GO:0005634; GO:0005654; GO:0006275; GO:0006281; GO:0006282; GO:0006310; GO:0006338; GO:0031011; GO:0033044; GO:0045739; GO:0045893; GO:0045995; GO:0051726; GO:0060382; GO:1904507	chromatin remodeling [GO:0006338]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; positive regulation of DNA repair [GO:0045739]; positive regulation of DNA-templated transcription [GO:0045893]; positive regulation of telomere maintenance in response to DNA damage [GO:1904507]; regulation of cell cycle [GO:0051726]; regulation of chromosome organization [GO:0033044]; regulation of DNA repair [GO:0006282]; regulation of DNA replication [GO:0006275]; regulation of DNA strand elongation [GO:0060382]; regulation of embryonic development [GO:0045995]; telomere maintenance	Ino80 complex [GO:0031011]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protease binding [GO:0002020]	Q6P4R8	NFRKB	Nuclear factor related to kappa-B-binding protein (DNA-binding protein R kappa-B) (INO80 complex subunit G)		
6	Vitvi009798	2017_Mal2	GO:0000272; GO:0004568; GO:0006032; GO:0008061	chitin catabolic process [GO:0006032]; polysaccharide catabolic process [GO:0000272]		chitin binding [GO:0008061]; chitinase activity [GO:0004568]	Q7M443		Chitinase 2 (EC 3.2.1.14) (Tulip bulb chitinase-2) (TBC-2)		
6	Vitvi009780	2017_Mal2	GO:0005507; GO:0005524; GO:0005634; GO:0005739; GO:0005829; GO:0006633;	fatty acid biosynthetic process [GO:0006633]	chloroplast [GO:0009507]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	ATP binding [GO:0005524]; copper ion binding [GO:0005507]; enoyl-[acyl-carrier-protein] reductase activity	Q8LCU7		Enoyl-[acyl-carrier-protein] reductase, mitochondrial (EC 1.3.1.104) (2-enoyl thioester reductase)		
6	Vitvi009789	2017_Mal2	GO:0005507; GO:0009505; GO:0009698; GO:0009809; GO:0016491; GO:0046274; GO:0048046; GO:0052716	lignin biosynthetic process [GO:0009809]; lignin catabolic process [GO:0046274]; phenylpropanoid metabolic process [GO:0009698]	apoplast [GO:0048046]; plant-type cell wall [GO:0009505]	copper ion binding [GO:0005507]; hydroquinone:oxygen oxidoreductase activity [GO:0052716]; oxidoreductase activity [GO:0016491]	Q9FJD5	LAC17	Laccase-17 (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase 17) (Diphenol oxidase 17) (Urishiol oxidase 17)		
6	Vitvi009792	2017_Mal2	GO:0004601; GO:0005509; GO:0016020; GO:0050664		membrane [GO:0016020]	calcium ion binding [GO:0005509]; oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor [GO:0050664]; peroxidase activity [GO:0004601]	Q9FJD6	RBOHH	Putative respiratory burst oxidase homolog protein H (EC 1.11.1.-) (EC 1.6.3.-) (NADPH oxidase RBOHH) (AtRBOHH)		
6	Vitvi009782	2017_Mal2	GO:0004674; GO:0005524; GO:0005886; GO:0006952; GO:0016310; GO:0106310	defense response [GO:0006952]; phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9LQQ8	PBL5	Probable serine/threonine-protein kinase PBL5 (EC 2.7.11.1) (PBS1-like protein 5) (Serine/threonine-protein kinase RLCKVII)		
6	Vitvi009786	2017_Mal2	GO:0016567	protein ubiquitination [GO:0016567]			Q9LVG9		BTB/POZ domain-containing protein		
6	Vitvi009803	2017_Mal2	GO:0004672; GO:0004674; GO:0004714; GO:0005524; GO:0005886; GO:0009506; GO:0009741; GO:0009826; GO:0016310	phosphorylation [GO:0016310]; response to brassinosteroid [GO:0009741]; unidimensional cell growth [GO:0009826]	plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]; protein serine/threonine kinase activity [GO:0004674]; transmembrane receptor protein tyrosine kinase activity [GO:0004714]	Q9LX66	HERK1	Receptor-like protein kinase HERK 1 (EC 2.7.11.-) (Protein HERCULES RECEPTOR KINASE 1)		
6	Vitvi009790	2017_Mal2	GO:0005576; GO:0009793	embryo development ending in seed dormancy [GO:0009793]	extracellular region [GO:0005576]		Q9LYP6	ATS3	Embryo-specific protein ATS3 (Protein ARABIDOPSIS THALIANA SEED 3)		
6	Vitvi009784	2017_Mal2	GO:0004364; GO:0005829; GO:0005886; GO:0009636;	protein glutathionylation [GO:0010731]; response to toxic substance [GO:0009636]	cytosol [GO:0005829]; plasma membrane [GO:0005886]	glutathione transferase activity [GO:0004364]	Q9LZ06	GSTL3	Glutathione S-transferase L3 (AtGSTL3) (EC 2.5.1.18) (GST class-lambda member 3)		
6	Vitvi009794	2017_Mal2	GO:0003777; GO:0005524; GO:0005737; GO:0005819; GO:0005874; GO:0007018;	microtubule-based movement [GO:0007018]	cytoplasm [GO:0005737]; microtubule [GO:0005874]; spindle [GO:0005819]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	Q9LZU5	KIN5D	Kinesin-like protein KIN-5D		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi009791	2017_Mal2	GO:0003677; GO:0003700; GO:0005634; GO:0009908; GO:0009943; GO:0009947; GO:0010482; GO:0010865; GO:0030154; GO:0099402	adaxial/abaxial axis specification [GO:0009943]; cell differentiation [GO:0030154]; centrolateral axis specification [GO:0009947]; flower development [GO:0009908]; plant organ development [GO:0099402]; regulation of epidermal cell division [GO:0010482]; stipule development	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	Q9SIB4	WOX3	WUSCHEL-related homeobox 3 (Protein PRESSED FLOWER)		
6	Vitvi009802	2017_Mal2	GO:0005388; GO:0005524; GO:0005576; GO:0005783; GO:0016020; GO:0016887; GO:0046872		endoplasmic reticulum [GO:0005783]; extracellular region [GO:0005576]; membrane [GO:0016020]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; metal ion binding [GO:0046872]; P-type calcium transporter activity	Q9XES1	ECA4	Calcium-transporting ATPase 4, endoplasmic reticulum-type (EC 7.2.2.10)		
6	Vitvi009889	2016_Suc2	GO:0000287; GO:0003924; GO:0005525; GO:0005739		mitochondrion [GO:0005739]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; magnesium ion binding [GO:0000287]	F4HSD4	ATOBGM	Probable GTP-binding protein OBGM, mitochondrial		
6	Vitvi009888	2016_Suc2					F4HSD5	TRM32	Protein TRM32 (TON1-RECRUITING MOTIF protein 32)		
6	Vitvi009919	2016_Suc2	GO:0005576; GO:0006949; GO:0009505; GO:0009506; GO:0009664; GO:0016020	plant-type cell wall organization [GO:0009664]; syncytium formation [GO:0006949]	extracellular region [GO:0005576]; membrane [GO:0016020]; plant-type cell wall [GO:0009505]; plasmodesma [GO:0009506]		O48818	EXPA4	Expansin-A4 (AtEXPA4) (Alpha-expansin-4) (At-EXP4) (AtEx4) (Ath-ExpAlpha-1.6)		
6	Vitvi009883	2016_Suc2	GO:0005524; GO:0005737; GO:0005856; GO:0016787		cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]	ATP binding [GO:0005524]; hydrolase activity [GO:0016787]	O81221		Actin (EC 3.6.4.-)		
6	Vitvi009906	2016_Suc2	GO:0004807; GO:0005737; GO:0006094; GO:0006096	gluconeogenesis [GO:0006094]; glycolytic process [GO:0006096]	cytoplasm [GO:0005737]	triose-phosphate isomerase activity [GO:0004807]	P21820		Triosephosphate isomerase, cytosolic (TIM) (Triose-phosphate isomerase) (EC 5.3.1.1)		
6	Vitvi009902	2016_Suc2	GO:0005975; GO:0006952; GO:0042973	carbohydrate metabolic process [GO:0005975]; defense response [GO:0006952]		glucan endo-1,3-beta-D-glucosidase activity [GO:0042973]	P52409	GLC1	Glucan endo-1,3-beta-glucosidase (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-		
6	Vitvi009907	2016_Suc2	GO:0004674; GO:0004713; GO:0005524; GO:0005886; GO:0006952; GO:0016310; GO:0106310	defense response [GO:0006952]; phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; protein tyrosine kinase activity [GO:0004713]	Q06548	PBL9	Probable serine/threonine-protein kinase PBL9 (EC 2.7.11.1) (PBS1-like protein 9) (Protein kinase 1A)		
6	Vitvi009896	2016_Suc2	GO:0006811; GO:0009707; GO:0015288; GO:0034426; GO:0042803; GO:0045037; GO:0046930	monoatomic ion transport [GO:0006811]; protein import into chloroplast stroma [GO:0045037]	chloroplast outer membrane [GO:0009707]; etioplast membrane [GO:0034426]; pore complex [GO:0046930]	porin activity [GO:0015288]; protein homodimerization activity [GO:0042803]	Q41050	OEP16	Outer envelope pore protein 16, chloroplastic (Chloroplastic outer envelope pore protein of 16 kDa)		
6	Vitvi009909	2016_Suc2	GO:0009909	regulation of flower development [GO:0009909]			Q5Q0B3	FLP1	Flowering-promoting factor 1-like protein 1 (FPF1-like protein 1)		
6	Vitvi009898	2016_Suc2	GO:0003676; GO:0005634; GO:0005737; GO:0008270		cytoplasm [GO:0005737]; nucleus [GO:0005634]	nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q84Y18	CXIP4	CAX-interacting protein 4		
6	Vitvi009884	2016_Suc2	GO:0004674; GO:0004842; GO:0005524; GO:0005829; GO:0016310; GO:0016567; GO:0106310	phosphorylation [GO:0016310]; protein ubiquitination [GO:0016567]	cytosol [GO:0005829]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; ubiquitin-protein transferase activity [GO:0004842]	Q8GUH1	PUB33	U-box domain-containing protein 33 (Plant U-box protein 33) [Includes: E3 ubiquitin ligase (EC 2.3.2.27) (RING-type E3 ubiquitin transferase); Serine/threonine-protein kinase (EC 2.7.11.-)]		
6	Vitvi009893	2016_Suc2	GO:0004029; GO:0005634; GO:0005759; GO:0043878		mitochondrial matrix [GO:0005759]; nucleus [GO:0005634]	aldehyde dehydrogenase (NAD+) activity [GO:0004029]; glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non-phosphorylating) activity	Q8S528	ALDH2B7	Aldehyde dehydrogenase family 2 member B7, mitochondrial (ALDH2b) (EC 1.2.1.3)		
6	Vitvi009914	2016_Suc2	GO:0003723; GO:0006306; GO:0010569; GO:0046686; GO:0080188	DNA methylation [GO:0006306]; gene silencing by RNA-directed DNA methylation [GO:0080188]; regulation of double-strand break repair via homologous recombination [GO:0010569]; response to cadmium ion [GO:0046686]		RNA binding [GO:0003723]	Q8VZ79	IDN2	Protein INVOLVED IN DE NOVO 2 (Protein RNA-DIRECTED DNA METHYLATION 12)		
6	Vitvi009895	2016_Suc2	GO:0005739		mitochondrion [GO:0005739]		Q940Q2		Pentatricopeptide repeat-containing protein At1g07590, mitochondrial		
6	Vitvi009880	2016_Suc2	GO:0009408; GO:0016567; GO:0016740; GO:0046872	protein ubiquitination [GO:0016567]; response to heat [GO:0009408]		metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q94B55	XBAT31	Putative E3 ubiquitin-protein ligase XBAT31 (EC 2.3.2.27) (Ankyrin repeat domain and RING finger-containing protein XBAT31) (Protein XB3 homolog 1) (RING-type E3 ubiquitin transferase XB31)		
6	Vitvi009879	2016_Suc2	GO:0000139; GO:0005783; GO:0005789; GO:0005794; GO:0006612; GO:0016409; GO:0018230; GO:0018345; GO:0019706; GO:0032230; GO:0097116; GO:1900226	gephyrin clustering involved in postsynaptic density assembly [GO:0097116]; negative regulation of NLRP3 inflammasome complex assembly [GO:1900226]; peptidyl-L-cysteine S-palmitoylation [GO:0018230]; positive regulation of synaptic transmission, GABAergic [GO:0032230]; protein palmitoylation [GO:0018345]; protein targeting to membrane	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]	palmitoyltransferase activity [GO:0016409]; protein-cysteine S-palmitoyltransferase activity [GO:0019706]	Q96GR4	ZDHHC12	Palmitoyltransferase ZDHHC12 (EC 2.3.1.225) (DHHC domain-containing cysteine-rich protein 12) (DHHC-12) (Zinc finger DHHC domain-containing protein 12) (Zinc finger protein 400)		
6	Vitvi009901	2016_Suc2	GO:0031929; GO:0031931; GO:0031932; GO:0032956	regulation of actin cytoskeleton organization [GO:0032956]; TOR signaling [GO:0031929]	TORC1 complex [GO:0031931]; TORC2 complex [GO:0031932]		Q9AYE4	LST8	Target of rapamycin complex subunit LST8 (TORC subunit LST8) (Lethal with SEC13 protein 8 homolog) (WD40 repeat-containing protein 81) (OsWD40-81)		
6	Vitvi009910	2016_Suc2	GO:0004252; GO:0005576; GO:0006508	proteolysis [GO:0006508]	extracellular region [GO:0005576]	serine-type endopeptidase activity [GO:0004252]	Q9FGU3	SBT4.4	Subtilisin-like protease SBT4.4 (EC 3.4.21.-) (Subtilase subfamily 4 member 4) (AtSBT4.4)		
6	Vitvi009886	2016_Suc2	GO:0005634; GO:0017018; GO:0046872; GO:0048366	leaf development [GO:0048366]	nucleus [GO:0005634]	metal ion binding [GO:0046872]; myosin phosphatase activity [GO:0017018]	Q9LQN6	PLL5	Probable protein phosphatase 2C 4 (AtPP2C04) (EC 3.1.3.16) (Protein POLTERGEIST-LIKE 5) (Protein phosphatase		
6	Vitvi009904	2016_Suc2	GO:0000792; GO:0005634; GO:0005731; GO:0008327; GO:0009536; GO:0010370; GO:0019899; GO:0031047; GO:0004860; GO:0005634; GO:0007049; GO:0032875	regulatory ncRNA-mediated gene silencing [GO:0031047]	heterochromatin [GO:0000792]; nucleolus organizer region [GO:0005731]; nucleus [GO:0005634]; perinucleolar chromocenter	enzyme binding [GO:0019899]; methyl-CpG binding [GO:0008327]; protein self-association [GO:0043621]	Q9LTJ1	MBD6	Methyl-CpG-binding domain-containing protein 6 (AtMBD6) (MBD06) (Methyl-CpG-binding protein MBD6)		
6	Vitvi009882	2016_Suc2		cell cycle [GO:0007049]; regulation of DNA endoreduplication [GO:0032875]	nucleus [GO:0005634]	protein kinase inhibitor activity [GO:0004860]	Q9LZ60	SMR3	Cyclin-dependent protein kinase inhibitor SMR3 (Protein SIAMESE-RELATED 3)		
6	Vitvi009900	2016_Suc2	GO:0016020; GO:0016567; GO:0016740; GO:0046872	cellular response to hypoxia [GO:0071456]; protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q9M0C3	ATL14	RING-H2 finger protein ATL14 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase ATL14)		
6	Vitvi009917	2016_Suc2	GO:0003677; GO:0003723; GO:0003725; GO:0009506; GO:0010569; GO:0043621; GO:0080188	gene silencing by RNA-directed DNA methylation [GO:0080188]; regulation of double-strand break repair via homologous recombination [GO:0010569]	plasmodesma [GO:0009506]	DNA binding [GO:0003677]; double-stranded RNA binding [GO:0003725]; protein self-association [GO:0043621]; RNA binding [GO:0003723]	Q9S9P3	FDM1	Factor of DNA methylation 1 (Protein IDN2 PARALOG 1) (Protein IDN2-LIKE 1)		
6	Vitvi009908	2016_Suc2	GO:0002221; GO:0004674; GO:0005524; GO:0005829; GO:0005886; GO:0009617; GO:0016310; GO:0042742; GO:0005886; GO:0007155; GO:0009651; GO:0009738;	defense response to bacterium [GO:0042742]; pattern recognition receptor signaling pathway [GO:0002221]; phosphorylation [GO:0016310]; regulation of salicylic acid biosynthetic process [GO:0080142]; response to bacterium	cytosol [GO:0005829]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9SF86	PCRK1	Serine/threonine-protein kinase PCRK1 (EC 2.7.11.1) (Protein PTI-COMPROMISED RECEPTOR-LIKE CYTOPLASMIC KINASE 1)		
6	Vitvi009887	2016_Suc2	GO:0009825; GO:0009897; GO:0010192; GO:0030247; GO:0048354	abscisic acid-activated signaling pathway [GO:0009738]; cell adhesion [GO:0007155]; mucilage biosynthetic process [GO:0010192]; mucilage biosynthetic process involved in seed coat development [GO:0048354]; multidimensional cell growth [GO:0009825]; response to salt stress [GO:0009651]	external side of plasma membrane [GO:0009897]; plasma membrane [GO:0005886]	polysaccharide binding [GO:0030247]	Q9SNC3	FLA4	Fasciclin-like arabinogalactan protein 4 (Protein SALT OVERLY SENSITIVE 5)		
6	Vitvi009903	2016_Suc2	GO:0005739; GO:0009737; GO:0080156	mitochondrial mRNA modification [GO:0080156]; response to abscisic acid [GO:0009737]	mitochondrion [GO:0005739]		Q9T0D6		Pentatricopeptide repeat-containing protein At4g11690		
6	Vitvi009897	2016_Suc2	GO:0005743; GO:0007005; GO:0015031; GO:0046872	mitochondrion organization [GO:0007005]; protein transport [GO:0015031]	mitochondrial inner membrane [GO:0005743]	metal ion binding [GO:0046872]	Q9XGX7	TIM9	Mitochondrial import inner membrane translocase subunit Tim9		

Supplementary Table 9. Candidate genes of 29 traits in_GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi009899	2016_Suc2	GO:0016020; GO:0016567; GO:0016740; GO:0046872;	cellular response to hypoxia [GO:0071456]; protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q9ZV51	ATL56	RING-H2 finger protein ATL56 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase ATL56)		
6	Vitvi010275	2016_BeWil	GO:0004222; GO:0005829; GO:0006508; GO:0046872	proteolysis [GO:0006508]	cytosol [GO:0005829]	metal ion binding [GO:0046872]; metalloendopeptidase activity [GO:0004222]	F4HNU6		Nardilysin-like (EC 3.4.24.61) (N-arginine dibasic convertase-like) (NRD convertase-like) (NRD-C)		
6	Vitvi010326	2016_BeWil	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		
6	Vitvi010324	2016_BeWil	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010295	2016_BeWil	GO:0003779; GO:0005774		vacuolar membrane [GO:0005774]	actin binding [GO:0003779]	F4KEW8	NET4A	Protein NETWORKED 4A		
6	Vitvi010297	2016_BeWil	GO:0004843; GO:0005634; GO:0006511	ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	O22207	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (AtUBP5) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)		
6	Vitvi010329	2016_BeWil	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		
6	Vitvi010325	2016_BeWil	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010293	2016_BeWil	GO:0005506; GO:0016020; GO:0016710; GO:0020037		membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; trans-cinnamate 4-monooxygenase activity [GO:0016710]	P48522	CYP73A4	Trans-cinnamate 4-monooxygenase (EC 1.14.14.91) (Cinnamic acid 4-hydroxylase) (C4H) (CA4H) (Cytochrome P450 73) (Cytochrome P450 C4H)		
6	Vitvi010321	2016_BeWil	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010296	2016_BeWil	GO:0003743; GO:0046872			metal ion binding [GO:0046872]; translation initiation factor activity	P55871		Eukaryotic translation initiation factor 2 subunit beta (eIF-2-beta)		
6	Vitvi010301	2016_BeWil	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010281	2016_BeWil	GO:0004564; GO:0005975	carbohydrate metabolic process [GO:0005975]		beta-fructofuranosidase activity [GO:0004564]	Q43089	BFRUCT1	Beta-fructofuranosidase, cell wall isozyme (EC 3.2.1.26) (Acid invertase) (Sucrose hydrolase)		
6	Vitvi010305	2016_BeWil	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904;	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010294	2016_BeWil	GO:0000184; GO:0003723; GO:0003724; GO:0005524; GO:0005634; GO:0005737; GO:0006364; GO:0016887	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]	Q6BY27	DBP2	ATP-dependent RNA helicase DBP2 (EC 3.6.4.13)		
6	Vitvi010327	2016_BeWil	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010288	2016_BeWil	GO:0003677; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity	Q6S4P4	RF2b	Transcription factor RF2b		10.1073/pnas.0307687100
6	Vitvi010312	2016_BeWil	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010290	2016_BeWil	GO:0003677; GO:0003700; GO:0005634; GO:0005739; GO:0008270; GO:0009737; GO:0009744; GO:0045892	negative regulation of DNA-templated transcription [GO:0045892]; response to abscisic acid [GO:0009737]; response to sucrose [GO:0009744]	mitochondrion [GO:0005739]; nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; zinc ion binding [GO:0008270]	Q8W4L5	VAL1	B3 domain-containing transcription repressor VAL1 (Protein HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE 2) (Protein VP1/ABI3-LIKE 1)		
6	Vitvi010314	2016_BeWil	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010287	2016_BeWil	GO:0006869; GO:0008289; GO:0043245; GO:0045735; GO:0048316	lipid transport [GO:0006869]; seed development [GO:0048316]	extraorganismal space [GO:0043245]	lipid binding [GO:0008289]; nutrient reservoir activity [GO:0045735]	Q9ATH2		Non-specific lipid-transfer protein Cor a 8.0101 (nsLTP Cor a 8) (Allergen Cor a 8) (Lipid transfer protein Cor a 8) (LTP Cor a 8) (allergen Cor a 8.0101)		
6	Vitvi010320	2016_BeWil	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		
6	Vitvi010311	2016_BeWil	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BeWil	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BeWil	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BeWil	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BeWil	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BeWil	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010286	2016_BeWil	GO:0000785; GO:0000786; GO:0003691; GO:0003700; GO:0005634; GO:0005730; GO:0006334; GO:0042803; GO:0043047	nucleosome assembly [GO:0006334]	chromatin [GO:0000785]; nucleolus [GO:0005730]; nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; double-stranded telomeric DNA binding [GO:0003691]; protein homodimerization activity [GO:0042803]; single-stranded telomeric DNA binding [GO:0043047]	Q9M2X3	TRB3	Telomere repeat-binding factor 3 (AtTRB3) (MYB transcription factor) (Telomere-binding protein 2) (AtTBP2)		
6	Vitvi010289	2016_BeWil	GO:0016020; GO:0016567; GO:0016740; GO:0046872	protein ubiquitination [GO:0016567]	membrane [GO:0016020]	metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q9SG96	ATL72	RING-H2 finger protein ATL72 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase ATL72)		
6	Vitvi010326	2016_BV1	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		
6	Vitvi010324	2016_BV1	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010295	2016_BV1	GO:0003779; GO:0005774		vacuolar membrane [GO:0005774]	actin binding [GO:0003779]	F4KEW8	NET4A	Protein NETWORKED 4A		
6	Vitvi010297	2016_BV1	GO:0004843; GO:0005634; GO:0006511	ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	O22207	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (AtUBP5) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)		
6	Vitvi010329	2016_BV1	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		
6	Vitvi010325	2016_BV1	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010321	2016_BV1	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010296	2016_BV1	GO:0003743; GO:0046872			metal ion binding [GO:0046872]; translation initiation factor activity	P55871		Eukaryotic translation initiation factor 2 subunit beta (eIF-2-beta)		
6	Vitvi010301	2016_BV1	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010305	2016_BV1	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904; GO:0016567	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010294	2016_BV1	GO:0000184; GO:0003723; GO:0003724; GO:0005524; GO:0005634; GO:0005737; GO:0006364; GO:0016887	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]	Q6BY27	DBP2	ATP-dependent RNA helicase DBP2 (EC 3.6.4.13)		
6	Vitvi010327	2016_BV1	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010312	2016_BV1	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010314	2016_BV1	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010320	2016_BV1	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		
6	Vitvi010311	2016_BV1	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BV1	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BV1	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BV1	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BV1	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BV1	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		
6	Vitvi010326	2016_BV2	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		
6	Vitvi010324	2016_BV2	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010295	2016_BV2	GO:0003779; GO:0005774		vacuolar membrane [GO:0005774]	actin binding [GO:0003779]	F4KEW8	NET4A	Protein NETWORKED 4A		
6	Vitvi010297	2016_BV2	GO:0004843; GO:0005634; GO:0006511	ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	O22207	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (AtUBP5) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)		
6	Vitvi010329	2016_BV2	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010325	2016_BV2	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010321	2016_BV2	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010296	2016_BV2	GO:0003743; GO:0046872			metal ion binding [GO:0046872]; translation initiation factor activity	P55871		Eukaryotic translation initiation factor 2 subunit beta (eIF-2-beta)		
6	Vitvi010301	2016_BV2	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010305	2016_BV2	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904; GO:0016567	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010294	2016_BV2	GO:0000184; GO:0003723; GO:0003724; GO:0005524; GO:0005634; GO:0005737; GO:0006364; GO:0016887	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]	Q6BY27	DBP2	ATP-dependent RNA helicase DBP2 (EC 3.6.4.13)		
6	Vitvi010327	2016_BV2	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010312	2016_BV2	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010314	2016_BV2	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010320	2016_BV2	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		
6	Vitvi010311	2016_BV2	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BV2	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BV2	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BV2	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BV2	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BV2	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		
6	Vitvi010326	2016_BV4	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		
6	Vitvi010324	2016_BV4	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010295	2016_BV4	GO:0003779; GO:0005774		vacuolar membrane [GO:0005774]	actin binding [GO:0003779]	F4KEW8	NET4A	Protein NETWORKED 4A		
6	Vitvi010297	2016_BV4	GO:0004843; GO:0005634; GO:0006511	ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	O22207	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (AtUBP5) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)		
6	Vitvi010329	2016_BV4	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		
6	Vitvi010325	2016_BV4	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010321	2016_BV4	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010296	2016_BV4	GO:0003743; GO:0046872			metal ion binding [GO:0046872]; translation initiation factor activity	P55871		Eukaryotic translation initiation factor 2 subunit beta (eIF-2-beta)		
6	Vitvi010301	2016_BV4	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010305	2016_BV4	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904; GO:0016567	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010327	2016_BV4	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010312	2016_BV4	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010314	2016_BV4	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010320	2016_BV4	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010311	2016_BV4	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BV4	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BV4	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BV4	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BV4	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BV4	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		
6	Vitvi010326	2016_BV3	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		
6	Vitvi010324	2016_BV3	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010295	2016_BV3	GO:0003779; GO:0005774		vacuolar membrane [GO:0005774]	actin binding [GO:0003779]	F4KEW8	NET4A	Protein NETWORKED 4A		
6	Vitvi010297	2016_BV3	GO:0004843; GO:0005634; GO:0006511	ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	O22207	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (AtUBP5) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)		
6	Vitvi010329	2016_BV3	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		
6	Vitvi010325	2016_BV3	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010321	2016_BV3	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010296	2016_BV3	GO:0003743; GO:0046872			metal ion binding [GO:0046872]; translation initiation factor activity	P55871		Eukaryotic translation initiation factor 2 subunit beta (eIF-2-beta)		
6	Vitvi010301	2016_BV3	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010305	2016_BV3	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010327	2016_BV3	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010312	2016_BV3	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010314	2016_BV3	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010320	2016_BV3	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		
6	Vitvi010311	2016_BV3	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BV3	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BV3	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BV3	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BV3	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BV3	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		
6	Vitvi010326	2016_BV5	GO:0005262; GO:0005739; GO:0005743; GO:0051560	mitochondrial calcium ion homeostasis [GO:0051560]	mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]	calcium channel activity [GO:0005262]	F4I111		Calcium uniporter protein 6, mitochondrial		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010324	2016_BV5	GO:0000166; GO:0043530; GO:0047352; GO:0047627; GO:0047710			adenosine 5'-monophosphoramidase activity [GO:0043530]; adenylylsulfatase activity [GO:0047627]; adenylylsulfate-ammonia adenylyltransferase activity [GO:0047352]; bis(5'-adenosyl)-triphosphatase activity [GO:0047710]; nucleotide binding [GO:0000166]	F4KEV7	FHIT	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT (EC 3.6.1.29) (Adenosine 5'-monophosphoramidase FHIT) (EC 3.9.1.-) (Adenylylsulfatase) (EC 3.6.2.1) (Adenylylsulfate-ammonia adenylyltransferase) (EC 2.7.7.51) (Fragile histidine triad protein)		
6	Vitvi010329	2016_BV5	GO:0000976; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	O65685	BLH6	BEL1-like homeodomain protein 6 (BEL1-like protein 6)		
6	Vitvi010325	2016_BV5	GO:0000287; GO:0003677; GO:0005524; GO:0005654; GO:0005730; GO:0006259; GO:0006260; GO:0006281; GO:0006310; GO:0008408; GO:0016887; GO:0030145; GO:0043138	DNA metabolic process [GO:0006259]; DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]	3'-5' DNA helicase activity [GO:0043138]; 3'-5' exonuclease activity [GO:0008408]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; DNA binding [GO:0003677]; magnesium ion binding [GO:0000287]; manganese ion binding	O93530	wrn	Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN (Focus-forming activity 1) (FFA-1) (Werner syndrome protein homolog) [Includes: 3'-5' exonuclease (EC 3.1.-.-); ATP-dependent helicase (EC 3.6.4.12)]		
6	Vitvi010321	2016_BV5	GO:0009507		chloroplast [GO:0009507]		P51204	ycf54	Uncharacterized protein ycf54 (ORF108)		
6	Vitvi010301	2016_BV5	GO:0000502; GO:0005524; GO:0005634; GO:0005737; GO:0016887		cytoplasm [GO:0005737]; nucleus [GO:0005634]; proteasome complex [GO:0000502]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	P85200		26S proteasome regulatory subunit 6B homolog		
6	Vitvi010305	2016_BV5	GO:0005634; GO:0005737; GO:0005777; GO:0007165; GO:0009638; GO:0009904;	chloroplast accumulation movement [GO:0009904]; phototropism [GO:0009638]; protein ubiquitination [GO:0016567]; signal transduction [GO:0007165]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; peroxisome [GO:0005777]		Q682S0	RPT2	Root phototropism protein 2 (BTB/POZ domain-containing protein RPT2)		
6	Vitvi010327	2016_BV5	GO:0016020		membrane [GO:0016020]		Q6PGS5	tlcd4-b	TLC domain-containing protein 4-B (Transmembrane protein 56-B)		
6	Vitvi010312	2016_BV5	GO:0003723; GO:0005634		nucleus [GO:0005634]	RNA binding [GO:0003723]	Q8GYR4		KH domain-containing protein At3g08620 (Quaking-like protein 4)		
6	Vitvi010314	2016_BV5	GO:0016020; GO:0046872; GO:0061630; GO:1904294	positive regulation of ERAD pathway [GO:1904294]	membrane [GO:0016020]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q96EX2	RNFT2	E3 ubiquitin-protein ligase RNFT2 (RING finger and transmembrane domain-containing protein 2) (Transmembrane protein 118)		
6	Vitvi010320	2016_BV5	GO:0005634; GO:0005737; GO:0007059; GO:0007064; GO:0009793; GO:0051301	cell division [GO:0051301]; chromosome segregation [GO:0007059]; embryo development ending in seed dormancy [GO:0009793]; mitotic sister chromatid cohesion	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9FGN7	SCC4	Sister chromatid cohesion protein SCC4 (Protein SISTER-CHROMATID COHESION 4) (AtSCC4)		
6	Vitvi010311	2016_BV5	GO:0003677; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9FHB2		Putative B3 domain-containing protein		
6	Vitvi010307	2016_BV5	GO:0003677; GO:0005634; GO:0006260; GO:0006281; GO:0006310; GO:0046872	DNA recombination [GO:0006310]; DNA repair [GO:0006281]; DNA replication [GO:0006260]	nucleus [GO:0005634]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FHJ6	RPA1C	Replication protein A 70 kDa DNA-binding subunit C (AtRPA70c) (AtRPA1-2) (Replication factor A protein 1C) (Replication protein A 1C) (AtRPA1C)		
6	Vitvi010328	2016_BV5	GO:0005739; GO:0005829; GO:0005886; GO:0045454; GO:0050897	cell redox homeostasis [GO:0045454]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cobalt ion binding [GO:0050897]	Q9LEV3	CBSX3	CBS domain-containing protein CBSX3, mitochondrial		
6	Vitvi010300	2016_BV5	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q9LVM0		Probable inactive receptor kinase At5g58300		
6	Vitvi010316	2016_BV5	GO:0005524; GO:0005739; GO:0005743; GO:0006777; GO:0006879; GO:0009507; GO:0009536; GO:0009555; GO:0009658; GO:0009941; GO:0010288; GO:0010380; GO:0016887; GO:0034755; GO:0046686; GO:0048364;	chloroplast organization [GO:0009658]; chromosome organization [GO:0051276]; intracellular iron ion homeostasis [GO:0006879]; iron ion transmembrane transport [GO:0034755]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; pollen development [GO:0009555]; regulation of catalytic activity [GO:0050790]; regulation of chlorophyll biosynthetic process [GO:0010380]; response to cadmium ion [GO:0046686]; response to lead ion	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastid [GO:0009536]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9LVM1	ABCB25	ABC transporter B family member 25, mitochondrial (ABC transporter ABCB.25) (AtABCB25) (ABC transporter of the mitochondrion 3) (AtATM3) (Iron-sulfur clusters transporter ATM3) (Protein STARIK 1)		
6	Vitvi010319	2016_BV5	GO:0009507; GO:0009535; GO:0009536; GO:0009941; GO:0010258; GO:0010598; GO:0016655; GO:0048038; GO:0050832	defense response to fungus [GO:0050832]; NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid membrane [GO:0009535]; NAD(P)H dehydrogenase complex (plastoquinone) [GO:0010598]; plastid [GO:0009536]	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor [GO:0016655]; quinone binding [GO:0048038]	Q9LVM2	ndhN	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic (EC 7.1.1.-) (NAD(P)H dehydrogenase subunit N) (NDH subunit N) (NDH-N) (NADH-plastoquinone oxidoreductase subunit N)		
6	Vitvi010415	2016_BV6	GO:0005516; GO:0005635; GO:0005876; GO:0005886; GO:0007017; GO:0009524; GO:0009574; GO:0016020; GO:0035556; GO:0051211; GO:0055028; GO:0070507; GO:0071699; GO:0090436;	anisotropic cell growth [GO:0051211]; intracellular signal transduction [GO:0035556]; leaf pavement cell development [GO:0090436]; microtubule-based process [GO:0007017]; protein localization to cortical microtubule cytoskeleton [GO:0072699]; regulation of cellulose biosynthetic process [GO:2001006]; regulation of microtubule cytoskeleton organization [GO:0070507]	cortical microtubule [GO:0055028]; membrane [GO:0016020]; nuclear envelope [GO:0005635]; phragmoplast [GO:0009524]; plasma membrane [GO:0005886]; preprophase band [GO:0009574]; spindle microtubule [GO:0005876]	calmodulin binding [GO:0005516]	F4J061	IQD5	Protein IQ-DOMAIN 5 (AtIQD5)		
6	Vitvi010427	2016_BV6	GO:0005634; GO:0005737; GO:0005783; GO:0009507; GO:0009788; GO:0010922; GO:0019902; GO:0042326	negative regulation of abscisic acid-activated signaling pathway [GO:0009788]; negative regulation of phosphorylation [GO:0042326]; positive regulation of phosphatase activity [GO:0010922]	chloroplast [GO:0009507]; cytoplasm [GO:0005737]; endoplasmic reticulum [GO:0005783]; nucleus [GO:0005634]	phosphatase binding [GO:0019902]	Q0V865		Protein FAF-like, chloroplastic		
6	Vitvi010421	2016_BV6	GO:0009507; GO:0009707; GO:0015267		chloroplast [GO:0009507]; chloroplast outer membrane [GO:0009707]	channel activity [GO:0015267]	Q5PP51	P39	Outer envelope protein 39, chloroplastic		
6	Vitvi010424	2016_BV6	GO:0005634; GO:0030544		nucleus [GO:0005634]	Hsp70 protein binding [GO:0030544]	Q642C0	Dnajc8	DnaJ homolog subfamily C member 8		
6	Vitvi010429	2016_BV6	GO:0002679; GO:0004842; GO:0005829; GO:0006952; GO:0009414; GO:0016567; GO:0051865; GO:0061630	defense response [GO:0006952]; protein autoubiquitination [GO:0051865]; protein ubiquitination [GO:0016567]; respiratory burst involved in defense response [GO:0002679]; response to water deprivation [GO:0009414]	cytosol [GO:0005829]	ubiquitin protein ligase activity [GO:0061630]; ubiquitin-protein transferase activity [GO:0004842]	Q84TG3	PUB23	E3 ubiquitin-protein ligase PUB23 (EC 2.3.2.27) (Plant U-box protein 23) (RING-type E3 ubiquitin transferase PUB23) (U-box domain-containing protein 23)		
6	Vitvi010422	2016_BV6	GO:0003924; GO:0005525; GO:0005634; GO:0005730; GO:0005829; GO:0006364; GO:0042254; GO:0043022; GO:0048366; GO:0048825;	cotyledon development [GO:0048825]; leaf development [GO:0048366]; positive regulation of ribosome biogenesis [GO:0090070]; regulation of auxin polar transport [GO:2000012]; ribosome biogenesis [GO:0042254]; rRNA processing [GO:0006364]	cytosol [GO:0005829]; nucleolus [GO:0005730]; nucleus [GO:0005634]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; ribosome binding [GO:0043022]	Q9SJF1	LSG1-2	GTPase LSG1-2 (AtLSG1-2) (DAR GTPase 7) (Protein YEAST LSG1 ORTHOLOG 2)		
6	Vitvi010448	2017_Suc3	GO:0000287; GO:0005524; GO:0005886; GO:0016887; GO:0045332; GO:0140326	phospholipid translocation [GO:0045332]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled intramembrane lipid transporter activity [GO:0140326]; magnesium ion binding [GO:0000287]	P57792	ALA12	Probable phospholipid-transporting ATPase 12 (AtALA12) (EC 7.6.2.1) (Aminophospholipid flippase 12)		
6	Vitvi010467	2016_SL4	GO:0003777; GO:0005524; GO:0005641; GO:0005819; GO:0005874; GO:0007018; GO:0008017; GO:0009574	microtubule-based movement [GO:0007018]; spindle assembly [GO:0051225]	microtubule [GO:0005874]; nuclear envelope lumen [GO:0005641]; phragmoplast [GO:0009524]; spindle [GO:0005819]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity [GO:0003777]	F4J1U4	KIN12E	Kinesin-like protein KIN-12E		
6	Vitvi010468	2016_SL4	GO:0000325; GO:0005783; GO:0009058	biosynthetic process [GO:0009058]	endoplasmic reticulum [GO:0005783]; plant-type vacuole [GO:0000325]		Q8VWF6	SSL3	Protein STRICTOSIDINE SYNTHASE-LIKE 3 (AtSSL3) (Strictosidine synthase 9) (AtSS9)		
6	Vitvi010470	2016_SL4	GO:0005524; GO:0005829; GO:0005886; GO:0006897; GO:0007164; GO:0009827; GO:0009846; GO:0009860; GO:0010118; GO:0016308; GO:0016310; GO:0016324;	endocytosis [GO:0006897]; establishment of tissue polarity [GO:0007164]; phosphatidylinositol metabolic process [GO:0046488]; phosphorylation [GO:0016310]; plant-type cell wall modification [GO:0009827]; pollen germination [GO:0009846]; pollen tube growth [GO:0009860]; stomatal movement [GO:0010118]	apical plasma membrane [GO:0016324]; cytosol [GO:0005829]; plasma membrane [GO:0005886]; pollen tube [GO:0090406]	1-phosphatidylinositol-4-phosphate 5-kinase activity [GO:0016308]; ATP binding [GO:0005524]	Q9M1K2	PIP5K4	Phosphatidylinositol 4-phosphate 5-kinase 4 (AtPIP5K4) (EC 2.7.1.68) (1-phosphatidylinositol 4-phosphate kinase 4) (Diphosphoinositide kinase 4) (PtdIns(4)P-5-kinase 4)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010471	2016_SL4	GO:0000976; GO:0003700; GO:0005634; GO:0010158; GO:0046872	abaxial cell fate specification [GO:0010158]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; transcription cis-regulatory region binding [GO:00009761	Q9XFB0	YAB2	Putative axial regulator YABBY 2		
6	Vitvi010496	2016_BV8	GO:0005789; GO:0009536; GO:0009707; GO:0015031; GO:0046967	cytosol to endoplasmic reticulum transport [GO:0046967]; protein transport [GO:0015031]	chloroplast outer membrane [GO:0009707]; endoplasmic reticulum membrane [GO:0005789]; plastid [GO:00095361		B7ZWR6	OEP61	Outer envelope protein 61 (Tetratricopeptide repeat domain-containing protein 7)		
6	Vitvi010506	2016_BV8	GO:0009536; GO:0009570; GO:0010258	NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast stroma [GO:0009570]; plastid [GO:0009536]		F4K6X0	CRR42	Protein CHLORORESPIRATORY REDUCTION 42, chloroplastic		
6	Vitvi010490	2016_BV8	GO:0004364; GO:0005737; GO:0006749; GO:0042221; GO:0043295	glutathione metabolic process [GO:0006749]; response to chemical [GO:0042221]	cytoplasm [GO:0005737]	glutathione binding [GO:0043295]; glutathione transferase activity [GO:0004364]	O65857	GSTF1	Probable glutathione S-transferase GSTF1 (EC 2.5.1.18) (GST-I)		
6	Vitvi010522	2016_BV8	GO:0003729; GO:0005634; GO:0006952; GO:0008219; GO:0009693; GO:0010150	cell death [GO:0008219]; defense response [GO:0006952]; ethylene biosynthetic process [GO:0009693]; leaf senescence [GO:0010150]	nucleus [GO:0005634]	mRNA binding [GO:0003729]	O80678	UBA2B	UBP1-associated protein 2B		
6	Vitvi010507	2016_BV8	GO:0003871; GO:0005829; GO:0008270; GO:0009086; GO:0032259	methionine biosynthetic process [GO:0009086]; methylation [GO:0032259]	cytosol [GO:0005829]	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871]; zinc ion binding [GO:00082701	Q2QLY4		5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 (EC 2.1.1.14) (Cobalamin-independent methionine synthase 2)		
6	Vitvi010515	2016_BV8	GO:0005524; GO:0006777; GO:0008940; GO:0009734; GO:0010038; GO:0030151; GO:0061598; GO:0061599	auxin-activated signaling pathway [GO:0009734]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; response to metal ion [GO:0010038]		ATP binding [GO:0005524]; molybdenum ion binding [GO:0030151]; molybdopterin adenylyltransferase activity [GO:0061598]; molybdopterin molybdotransferase activity [GO:0061599]; nitrate reductase activity [GO:0008940]	Q39054	CNX1	Molybdopterin biosynthesis protein CNX1 (Molybdenum cofactor biosynthesis enzyme CNX1) [Includes: Molybdopterin molybdenumtransferase (MPT Mo-transferase) (EC 2.10.1.1) (Domain E); Molybdopterin adenylyltransferase (MPT adenylyltransferase) (EC 2.7.7.75) (Domain G)]		
6	Vitvi010499	2016_BV8	GO:0004674; GO:0005524; GO:0005634; GO:0005737; GO:0016310; GO:0042802; GO:0106310; GO:1900368	phosphorylation [GO:0016310]; regulation of post-transcriptional gene silencing by regulatory ncRNA [GO:1900368]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; identical protein binding [GO:0042802]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q39238	TOUSLED	Serine/threonine-protein kinase TOUSLED (EC 2.7.11.1)		
6	Vitvi010508	2016_BV8	GO:0003725			double-stranded RNA binding [GO:0003725]	Q5N8Z0	DRB1	Double-stranded RNA-binding protein 1 (dsRNA-binding protein 1)		
6	Vitvi010518	2016_BV8	GO:0000339; GO:0000932; GO:0003723; GO:0005829; GO:0005844; GO:0006402;	heat acclimation [GO:0010286]; mRNA catabolic process [GO:0006402]; mRNA stabilization [GO:0048255]	cytosol [GO:0005829]; P-body [GO:0000932]; polysome [GO:0005844]	RNA binding [GO:0003723]; RNA cap binding [GO:0000339]	Q940X9	LARP1A	La-related protein 1A (AtLARP1a)		
6	Vitvi010472	2016_BV8	GO:0004843; GO:0006508	proteolysis [GO:0006508]		cysteine-type deubiquitinase activity [GO:0004843]	Q9C585	UBP8	Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.4.19.12) (Deubiquitinating enzyme 8) (AtUBP8) (Ubiquitin thioesterase 8) (Ubiquitin-specific-processing protease 8)		
6	Vitvi010512	2016_BV8	GO:0003723; GO:0005739; GO:0009451	RNA modification [GO:0009451]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]	Q9C8L6	PCMP-E63	Pentatricopeptide repeat-containing protein At1g53600, mitochondrial		
6	Vitvi010492	2016_BV8	GO:0005634; GO:0005829; GO:0106435; GO:1901600;	regulation of secondary shoot formation [GO:2000032]; strigolactone metabolic process [GO:19016001	cytosol [GO:0005829]; nucleus [GO:0005634]	carboxylesterase activity [GO:0106435]	Q9FG13	CXE15	Carboxylesterase 15 (AtCXE15) (EC 3.1.1.-) (Strigolactones hydrolase CXE15)		
6	Vitvi010511	2016_BV8	GO:0005774; GO:0006813; GO:0006814; GO:0015297	potassium ion transport [GO:0006813]; sodium ion transport [GO:00068141	vacuolar membrane [GO:0005774]	antiporter activity [GO:0015297]	Q9FKP1	CCX1	Cation/calcium exchanger 1 (AtCCX1) (Protein CATION EXCHANGER 7)		
6	Vitvi010521	2016_BV8	GO:0003729; GO:0005634; GO:0006952; GO:0008219; GO:0009693; GO:0009738; GO:0010150; GO:0035925;	abscisic acid-activated signaling pathway [GO:0009738]; cell death [GO:0008219]; defense response [GO:0006952]; ethylene biosynthetic process [GO:0009693]; leaf senescence [GO:00101501; mRNA stabilization [GO:0048255]	nucleus [GO:0005634]	mRNA 3'-UTR AU-rich region binding [GO:0035925]; mRNA binding [GO:0003729]	Q9LES2	UBA2A	UBP1-associated protein 2A (UBP1-interacting protein 2a)		
6	Vitvi010493	2016_BV8	GO:0006813; GO:0015297; GO:0016020; GO:1902600	potassium ion transport [GO:0006813]; proton transmembrane transport [GO:19026001	membrane [GO:0016020]	antiporter activity [GO:0015297]	Q9SA37	CHX1	Cation/H(+) antiporter 1 (Protein CATION/H+ EXCHANGER 1) (AtCHX1)		
6	Vitvi010497	2016_BV8	GO:0005829; GO:0006970; GO:0016567; GO:0042631; GO:0071472	cellular response to salt stress [GO:0071472]; cellular response to water deprivation [GO:0042631]; protein ubiquitination [GO:0016567]; response to osmotic stress	cytosol [GO:0005829]		Q9SRV1	BPM4	BTB/POZ and MATH domain-containing protein 4 (Protein BTB-POZ AND MATH DOMAIN 4) (AtBPM4)		
6	Vitvi010471	2016_BV8	GO:0000976; GO:0003700; GO:0005634; GO:0010158; GO:0046872	abaxial cell fate specification [GO:0010158]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; transcription cis-regulatory region binding [GO:00009761	Q9XFB0	YAB2	Putative axial regulator YABBY 2		
6	Vitvi010494	2016_BV8	GO:0009561; GO:0016567; GO:0016740; GO:0046872; GO:0051603; GO:0051726; GO:0055046	megagametogenesis [GO:0009561]; microgametogenesis [GO:0055046]; protein ubiquitination [GO:0016567]; proteolysis involved in protein catabolic process [GO:0051603]; regulation of cell cycle [GO:0051726]		metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q9ZT42	RHF2A	E3 ubiquitin-protein ligase RHF2A (EC 2.3.2.27) (RING-H2 finger F2a) (RING-H2 zinc finger protein RHF2a) (RING-type E3 ubiquitin transferase RHF2A)		
6	Vitvi010523	2016_BV8	GO:0000791; GO:0003682; GO:0004521; GO:0005654; GO:0005730; GO:0006306; GO:0006417; GO:0015030; GO:0019048; GO:0030422; GO:0031048; GO:0031507; GO:0035197; GO:0035198; GO:0042742; GO:0051567;	defense response to bacterium [GO:0042742]; defense response to virus [GO:0051607]; DNA methylation [GO:0006306]; gene silencing by RNA-directed DNA methylation [GO:0080188]; heterochromatin formation [GO:0031507]; histone H3-K9 methylation [GO:0051567]; modulation by virus of host process [GO:0019048]; regulation of translation [GO:0006417]; regulatory ncRNA-mediated heterochromatin formation [GO:0031048]; siRNA processing	Cajal body [GO:0015030]; euchromatin [GO:0000791]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; ribonucleoprotein complex [GO:1990904]	chromatin binding [GO:0003682]; miRNA binding [GO:0035198]; RNA endonuclease activity [GO:0004521]; siRNA binding [GO:0035197]	Q9ZVD5	AGO4	Protein argonaute 4 (AtAGO4) (Protein OVEREXPRESSOR OF CATIONIC PEROXIDASE 11)		
6	Vitvi010496	2016_BeWe2	GO:0005789; GO:0009536; GO:0009707; GO:0015031; GO:0046967	cytosol to endoplasmic reticulum transport [GO:0046967]; protein transport [GO:0015031]	chloroplast outer membrane [GO:0009707]; endoplasmic reticulum membrane [GO:0005789]; plastid [GO:00095361		B7ZWR6	OEP61	Outer envelope protein 61 (Tetratricopeptide repeat domain-containing protein 7)		
6	Vitvi010506	2016_BeWe2	GO:0009536; GO:0009570; GO:0010258	NADH dehydrogenase complex (plastoquinone) assembly [GO:0010258]	chloroplast stroma [GO:0009570]; plastid [GO:0009536]		F4K6X0	CRR42	Protein CHLORORESPIRATORY REDUCTION 42, chloroplastic		
6	Vitvi010490	2016_BeWe2	GO:0004364; GO:0005737; GO:0006749; GO:0042221; GO:0043295	glutathione metabolic process [GO:0006749]; response to chemical [GO:0042221]	cytoplasm [GO:0005737]	glutathione binding [GO:0043295]; glutathione transferase activity [GO:0004364]	O65857	GSTF1	Probable glutathione S-transferase GSTF1 (EC 2.5.1.18) (GST-I)		
6	Vitvi010522	2016_BeWe2	GO:0003729; GO:0005634; GO:0006952; GO:0008219; GO:0009693; GO:0010150	cell death [GO:0008219]; defense response [GO:0006952]; ethylene biosynthetic process [GO:0009693]; leaf senescence [GO:0010150]	nucleus [GO:0005634]	mRNA binding [GO:0003729]	O80678	UBA2B	UBP1-associated protein 2B		
6	Vitvi010507	2016_BeWe2	GO:0003871; GO:0005829; GO:0008270; GO:0009086; GO:0032259	methionine biosynthetic process [GO:0009086]; methylation [GO:0032259]	cytosol [GO:0005829]	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871]; zinc ion binding [GO:00082701	Q2QLY4		5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 (EC 2.1.1.14) (Cobalamin-independent methionine synthase 2)		
6	Vitvi010515	2016_BeWe2	GO:0005524; GO:0006777; GO:0008940; GO:0009734; GO:0010038; GO:0030151; GO:0061598; GO:0061599	auxin-activated signaling pathway [GO:0009734]; Mo-molybdopterin cofactor biosynthetic process [GO:0006777]; response to metal ion [GO:0010038]		ATP binding [GO:0005524]; molybdenum ion binding [GO:0030151]; molybdopterin adenylyltransferase activity [GO:0061598]; molybdopterin molybdotransferase activity [GO:0061599]; nitrate reductase activity [GO:0008940]	Q39054	CNX1	Molybdopterin biosynthesis protein CNX1 (Molybdenum cofactor biosynthesis enzyme CNX1) [Includes: Molybdopterin molybdenumtransferase (MPT Mo-transferase) (EC 2.10.1.1) (Domain E); Molybdopterin adenylyltransferase (MPT adenylyltransferase) (EC 2.7.7.75) (Domain G)]		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010499	2016_BeWe2	GO:0004674; GO:0005524; GO:0005634; GO:0005737; GO:0016310; GO:0042802; GO:0106310; GO:1900368	phosphorylation [GO:0016310]; regulation of post-transcriptional gene silencing by regulatory ncRNA [GO:1900368]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; identical protein binding [GO:0042802]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q39238	TOUSLED	Serine/threonine-protein kinase TOUSLED (EC 2.7.11.1)		
6	Vitvi010529	2016_BeWe2	GO:0005507; GO:0005576; GO:0008447; GO:0016491		extracellular region [GO:0005576]	copper ion binding [GO:0005507]; L-ascorbate oxidase activity [GO:0008447]; oxidoreductase activity	Q40588	AAO	L-ascorbate oxidase (ASO) (Ascorbase) (EC 1.10.3.3)		
6	Vitvi010508	2016_BeWe2	GO:0003725			double-stranded RNA binding [GO:0003725]	Q5N8Z0	DRB1	Double-stranded RNA-binding protein 1 (dsRNA-binding protein 1)		
6	Vitvi010518	2016_BeWe2	GO:0000339; GO:0000932; GO:0003723; GO:0005829; GO:0005844; GO:0006402;	heat acclimation [GO:0010286]; mRNA catabolic process [GO:0006402]; mRNA stabilization [GO:0048255]	cytosol [GO:0005829]; P-body [GO:0000932]; polysome [GO:0005844]	RNA binding [GO:0003723]; RNA cap binding [GO:0000339]	Q940X9	LARP1A	La-related protein 1A (AtLARP1a)		
6	Vitvi010512	2016_BeWe2	GO:0003723; GO:0005739; GO:0009451	RNA modification [GO:0009451]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]	Q9C8L6	PCMP-E63	Pentatricopeptide repeat-containing protein At1g53600, mitochondrial		
6	Vitvi010492	2016_BeWe2	GO:0005634; GO:0005829; GO:0106435; GO:1901600;	regulation of secondary shoot formation [GO:2000032]; strigolactone metabolic process [GO:1901600]	cytosol [GO:0005829]; nucleus [GO:0005634]	carboxylesterase activity [GO:0106435]	Q9FG13	CXE15	Carboxylesterase 15 (AtCXE15) (EC 3.1.1.-) (Strigolactones hydrolase CXE15)		
6	Vitvi010511	2016_BeWe2	GO:0005774; GO:0006813; GO:0006814; GO:0015297	potassium ion transport [GO:0006813]; sodium ion transport [GO:0006814]	vacuolar membrane [GO:0005774]	antiporter activity [GO:0015297]	Q9FKP1	CCX1	Cation/calcium exchanger 1 (AtCCX1) (Protein CATION EXCHANGER 7)		
6	Vitvi010521	2016_BeWe2	GO:0003729; GO:0005634; GO:0006952; GO:0008219; GO:0009693; GO:0009738; GO:0010150; GO:0035925;	abscisic acid-activated signaling pathway [GO:0009738]; cell death [GO:0008219]; defense response [GO:0006952]; ethylene biosynthetic process [GO:0009693]; leaf senescence [GO:0010150]; mRNA stabilization [GO:0048255]	nucleus [GO:0005634]	mRNA 3'-UTR AU-rich region binding [GO:0035925]; mRNA binding [GO:0003729]	Q9LES2	UBA2A	UBP1-associated protein 2A (UBP1-interacting protein 2a)		
6	Vitvi010493	2016_BeWe2	GO:0006813; GO:0015297; GO:0016020; GO:1902600	potassium ion transport [GO:0006813]; proton transmembrane transport [GO:1902600]	membrane [GO:0016020]	antiporter activity [GO:0015297]	Q9SA37	CHX1	Cation/H(+) antiporter 1 (Protein CATION/H+ EXCHANGER 1) (AtCHX1)		
6	Vitvi010497	2016_BeWe2	GO:0005829; GO:0006970; GO:0016567; GO:0042631; GO:0071472	cellular response to salt stress [GO:0071472]; cellular response to water deprivation [GO:0042631]; protein ubiquitination [GO:0016567]; response to osmotic stress	cytosol [GO:0005829]		Q9SRV1	BPM4	BTB/POZ and MATH domain-containing protein 4 (Protein BTB-POZ AND MATH DOMAIN 4) (AtBPM4)		
6	Vitvi010494	2016_BeWe2	GO:0009561; GO:0016567; GO:0016740; GO:0046872; GO:0051603; GO:0051726; GO:0055046	megagametogenesis [GO:0009561]; microgametogenesis [GO:0055046]; protein ubiquitination [GO:0016567]; proteolysis involved in protein catabolic process [GO:0051603]; regulation of cell cycle [GO:0051726]		metal ion binding [GO:0046872]; transferase activity [GO:0016740]	Q9ZT42	RHF2A	E3 ubiquitin-protein ligase RHF2A (EC 2.3.2.27) (RING-H2 finger F2a) (RING-H2 zinc finger protein RHF2a) (RING-type E3 ubiquitin transferase RHF2A)		
6	Vitvi010523	2016_BeWe2	GO:0000791; GO:0003682; GO:0004521; GO:0005654; GO:0005730; GO:0006306; GO:0006417; GO:0015030; GO:0019048; GO:0030422; GO:0031048; GO:0031507; GO:0035197; GO:0035198; GO:0042742; GO:0051567;	defense response to bacterium [GO:0042742]; defense response to virus [GO:0051607]; DNA methylation [GO:0006306]; gene silencing by RNA-directed DNA methylation [GO:0080188]; heterochromatin formation [GO:0031507]; histone H3-K9 methylation [GO:0051567]; modulation by virus of host process [GO:0019048]; regulation of translation [GO:0006417]; regulatory ncRNA-mediated heterochromatin formation [GO:0031048]; siRNA processing	Cajal body [GO:0015030]; euchromatin [GO:0000791]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; ribonucleoprotein complex [GO:1990904]	chromatin binding [GO:0003682]; miRNA binding [GO:0035198]; RNA endonuclease activity [GO:0004521]; siRNA binding [GO:0035197]	Q9ZVD5	AGO4	Protein argonaute 4 (AtAGO4) (Protein OVEREXPRESSOR OF CATIONIC PEROXIDASE 11)		
6	Vitvi010611	2016_SN3	GO:0009718; GO:0047893; GO:0102360; GO:0102425; GO:0102454	anthocyanin-containing compound biosynthetic process [GO:0009718]		cyanidin 3-O-galactosyltransferase activity [GO:0102454]; daphnetin 3-O-glucosyltransferase activity [GO:0102360]; flavonol 3-O-glucosyltransferase activity [GO:0047893]; myricetin 3-O-	A0A2R6P624	F3GT2	Flavonol 3-O-glucosyltransferase F3GT2 (EC 2.4.1.91) (Flavonoid 3-O-glycosyltransferase 2)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010616	2016_SN3	GO:0003779; GO:0005737; GO:0005856; GO:0007015;	actin filament organization [GO:0007015]; regulation of stomatal movement [GO:0010119]	cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]	actin binding [GO:0003779]	O48791	SCAB1	Stomatal closure-related actin-binding protein 1	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010606	2016_SN3	GO:0005509			calcium ion binding [GO:0005509]	P27164	CAM53	Calmodulin-related protein	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010615	2016_SN3	GO:0000226; GO:0000278; GO:0003924; GO:0005200; GO:0005525; GO:0005737; GO:0005874; GO:0046872	microtubule cytoskeleton organization [GO:0000226]; mitotic cell cycle [GO:0000278]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; metal ion binding [GO:0046872]; structural constituent of cytoskeleton	P45960	TUBB4	Tubulin beta-4 chain (Beta-4-tubulin)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010609	2016_SN3	GO:0009718; GO:0033303; GO:0033485; GO:0047213; GO:0047893; GO:0102360; GO:0102425	anthocyanin-containing compound biosynthetic process [GO:0009718]; cyanidin 3-O-glucoside biosynthetic process [GO:0033485]; quercetin O-glucoside biosynthetic process [GO:0033303]		anthocyanidin 3-O-glucosyltransferase activity [GO:0047213]; daphnetin 3-O-glucosyltransferase activity [GO:0102360]; flavonol 3-O-glucosyltransferase activity [GO:0047893]; myricetin 3-O-	P51094	UFGT	Anthocyanidin 3-O-glucosyltransferase UFGT (EC 2.4.1.115) (Flavonol 3-O-glucosyltransferase) (EC 2.4.1.91) (UDP-glucose flavonoid 3-O-glucosyltransferase)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010571	2016_SN3	GO:0004672; GO:0005524; GO:0005886		plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q0WR59		Probable inactive receptor kinase At5g10020	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010597	2016_SN3	GO:0004674; GO:0005524; GO:0016310; GO:0035556; GO:0106310	intracellular signal transduction [GO:0035556]; phosphorylation [GO:0016310]		ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q2QY53	CIPK32	CBL-interacting protein kinase 32 (EC 2.7.11.1) (OsCIPK32)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010589	2016_SN3	GO:0000307; GO:0004693; GO:0005524; GO:0005634; GO:0008353; GO:0016310; GO:0032968; GO:0106310	phosphorylation [GO:0016310]; positive regulation of transcription elongation by RNA polymerase II [GO:0032968]	cyclin-dependent protein kinase holoenzyme complex [GO:0000307]; nucleus [GO:0005634]	ATP binding [GO:0005524]; cyclin-dependent protein serine/threonine kinase activity [GO:0004693]; protein serine kinase activity [GO:0106310]; RNA polymerase II CTD heptapeptide repeat kinase activity [GO:0008353]	Q5JK68	CDKC-2	Cyclin-dependent kinase C-2 (CDKC;2) (EC 2.7.11.22) (EC 2.7.11.23)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010593	2016_SN3	GO:0004564; GO:0005829; GO:0005987; GO:0033926; GO:0048364	root development [GO:0048364]; sucrose catabolic process [GO:0005987]	cytosol [GO:0005829]	beta-fructofuranosidase activity [GO:0004564]; glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926]	Q67XD9	CINV2	Alkaline/neutral invertase CINV2 (EC 3.2.1.26) (Alkaline/neutral invertase I) (A/N-INVI) (Cytosolic invertase 2)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010607	2016_SN3	GO:0005524; GO:0005886; GO:0005975; GO:0006633; GO:0009507; GO:0042128	carbohydrate metabolic process [GO:0005975]; fatty acid biosynthetic process [GO:0006633]; nitrate assimilation [GO:0042128]	chloroplast [GO:0009507]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]	Q84VQ1	KINB1	SNF1-related protein kinase regulatory subunit beta-1 (AKIN subunit beta-1) (AKINB1) (AKINbeta1)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010598	2016_SN3	GO:0005634; GO:0005737; GO:0007623; GO:0009585; GO:0010017; GO:0042752	circadian rhythm [GO:0007623]; red or far-red light signaling pathway [GO:0010017]; red, far-red light phototransduction [GO:0009585]; regulation of circadian rhythm [GO:0042752]	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q8GWZ6	SRR1	Protein SENSITIVITY TO RED LIGHT REDUCED 1	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010584	2016_SN3	GO:0005634; GO:0005737; GO:0016036	cellular response to phosphate starvation [GO:0016036]	cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q94AD8		F-box/WD-40 repeat-containing protein At5g21040	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010594	2016_SN3	GO:0004564; GO:0005975; GO:0033926	carbohydrate metabolic process [GO:0005975]		beta-fructofuranosidase activity [GO:0004564]; glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926]	Q9C560	INVF	Probable alkaline/neutral invertase F (A/N-INVF) (EC 3.2.1.26)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010587	2016_SN3	GO:0005506; GO:0005789; GO:0016020; GO:0016709; GO:0020037; GO:0102684		endoplasmic reticulum membrane [GO:0005789]; membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; L-phenylalanine N-monooxygenase activity [GO:0102684]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	Q9FLC8	CYP79A2	Phenylalanine N-monooxygenase (EC 1.14.14.40) (Cytochrome P450 79A2) (Phenylalanine N-hydroxylase)	chr6: 16862053	10.1038/hortres.2017.35
6	Vitvi010585	2016_SN3	GO:0005576; GO:0016042; GO:0016298	lipid catabolic process [GO:0016042]	extracellular region [GO:0005576]	lipase activity [GO:0016298]	Q9FVV1		GDSL esterase/lipase At1g71250 (EC 3.1.1.-) (Extracellular lipase At1g71250)	chr6: 16862053	10.1038/hortres.2017.35

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010574	2016_SN3	GO:0005524; GO:0006952; GO:0043531	defense response [GO:0006952]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9T048		Disease resistance protein At4g27190	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010599	2016_SN3	GO:0005794; GO:0006886; GO:0010008	intracellular protein transport [GO:0006886]	endosome membrane [GO:0010008]; Golgi apparatus [GO:0005794]		Q9T091	VPS26B	Vacuolar protein sorting-associated protein 26B (Vesicle protein sorting 26B)	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010581	2016_SN3	GO:0003724; GO:0005524; GO:0005634; GO:0005654; GO:0005730; GO:0006364; GO:0006401; GO:0016887;	RNA catabolic process [GO:0006401]; rRNA 3'-end processing [GO:0031125]; rRNA processing [GO:0006364]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA helicase activity [GO:0003724]; rRNA binding [GO:0019843]	Q9XIF2	MTR4	DExH-box ATP-dependent RNA helicase DExH9 (EC 3.6.4.13) (Protein MTR4 homolog) (AtMTR4)		
6	Vitvi010578	2016_SN3	GO:0004128; GO:0005741; GO:0005783; GO:0009505; GO:0009536; GO:0022900	electron transport chain [GO:0022900]	endoplasmic reticulum [GO:0005783]; mitochondrial outer membrane [GO:0005741]; plant-type cell wall [GO:0009505]; plastid [GO:0009536]	cytochrome-b5 reductase activity, acting on NAD(P)H [GO:0004128]	Q9ZNT1	CBR1	NADH--cytochrome b5 reductase 1 (EC 1.6.2.2)	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010580	2016_SN3	GO:0009507; GO:0010189; GO:0015979; GO:0015995; GO:0033385; GO:0033521; GO:0045550; GO:0071949;	chlorophyll biosynthetic process [GO:0015995]; geranylgeranyl diphosphate metabolic process [GO:0033385]; photosynthesis [GO:0015979]; phytyl diphosphate biosynthetic process [GO:0033521]; vitamin E biosynthetic process	chloroplast [GO:0009507]	FAD binding [GO:0071949]; geranylgeranyl diphosphate reductase activity [GO:0102067]; geranylgeranyl reductase activity [GO:0045550]	Q9ZS34	CHLP	Geranylgeranyl diphosphate reductase, chloroplastic (EC 1.3.1.83) (Geranylgeranyl reductase)	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010557	2016_SN3	GO:0000381; GO:0003677; GO:0003700; GO:0003723; GO:0005634; GO:0005730; GO:0005846; GO:0006355; GO:0006397; GO:0008380; GO:0010267; GO:0010445; GO:0016607; GO:0031053;	mRNA processing [GO:0006397]; primary miRNA processing [GO:0031053]; regulation of adaxial/abaxial pattern formation [GO:2000011]; regulation of alternative mRNA splicing, via spliceosome [GO:0000381]; regulation of DNA-templated transcription [GO:0006355]; regulation of meristem development [GO:0048509]; RNA splicing [GO:0008380]; shoot system development [GO:0048367]; ta-	nuclear cap binding complex [GO:0005846]; nuclear dicing body [GO:0010445]; nuclear speck [GO:0016607]; nucleolus [GO:0005730]; nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]; RNA binding [GO:0003723]	Q9ZVD0	SE	Serrate RNA effector molecule	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010569	2016_SN3	GO:0005886; GO:0009506; GO:0042742	defense response to bacterium [GO:0042742]	plasma membrane [GO:0005886]; plasmodesma [GO:0009506]		Q9ZVD2	NHL13	NDR1/HIN1-like protein 13	chr6：16862053	10.1038/hortres.2017.35
6	Vitvi010581	2016_BeWe3	GO:0003724; GO:0005524; GO:0005634; GO:0005654; GO:0005730; GO:0006364; GO:0006401; GO:0016887;	RNA catabolic process [GO:0006401]; rRNA 3'-end processing [GO:0031125]; rRNA processing [GO:0006364]	nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA helicase activity [GO:0003724]; rRNA binding [GO:0019843]	Q9XIF2	MTR4	DExH-box ATP-dependent RNA helicase DExH9 (EC 3.6.4.13) (Protein MTR4 homolog) (AtMTR4)		
6	Vitvi010724	2016_SL5	GO:0005506; GO:0009718; GO:0020037; GO:0033772	anthocyanin-containing compound biosynthetic process [GO:0009718]		flavonoid 3',5'-hydroxylase activity [GO:0033772]; heme binding [GO:0020037]; iron ion binding [GO:0005506]	Q96418	CYP75A5	Flavonoid 3',5'-hydroxylase (F3'5'H) (EC 1.14.14.81) (Cytochrome P450 75A5)		
6	Vitvi010874	2017_FF3	GO:0004478; GO:0005524; GO:0005829; GO:0006556; GO:0006730; GO:0046872	one-carbon metabolic process [GO:0006730]; S-adenosylmethionine biosynthetic process [GO:0006556]	cytosol [GO:0005829]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; methionine adenosyltransferase activity	A7PQS0	METK1	S-adenosylmethionine synthase 1 (AdoMet synthase 1) (EC 2.5.1.6) (Methionine adenosyltransferase 1) (MAT 1)		
6	Vitvi010860	2017_FF3	GO:0004168; GO:0005783; GO:0005789; GO:0006486; GO:0009555; GO:0010483;	phosphorylation [GO:0016310]; pollen development [GO:0009555]; pollen tube reception [GO:0010483]; protein glycosylation [GO:0006486]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]	dolichol kinase activity [GO:0004168]	F4J4C8	EVN	Dolichol kinase EVAN (EC 2.7.1.108)		
6	Vitvi010813	2017_FF3	GO:0005634; GO:0009707; GO:0009941; GO:0010019; GO:0031010; GO:0035064; GO:0045893; GO:0046872	chloroplast-nucleus signaling pathway [GO:0010019]; positive regulation of DNA-templated transcription [GO:0045893]	chloroplast envelope [GO:0009941]; chloroplast outer membrane [GO:0009707]; ISWI-type complex [GO:0031010]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; methylated histone binding [GO:0035064]	F4JYC8	PTM	DDT domain-containing protein PTM (DDT domain-containing protein 1) (Membrane-bound transcription factor PTM) (PHD type transcription factor with transmembrane		
6	Vitvi010867	2017_FF3	GO:0005524; GO:0005829; GO:0016405		cytosol [GO:0005829]	ATP binding [GO:0005524]; CoA-ligase activity [GO:0016405]	M4IRL6	CCL7	Probable CoA ligase CCL7 (HlCCL7) (EC 6.2.1.-)		
6	Vitvi010817	2017_FF3	GO:0005524; GO:0009507; GO:0015979; GO:0015995; GO:0016851; GO:0016887	chlorophyll biosynthetic process [GO:0015995]; photosynthesis [GO:0015979]	chloroplast [GO:0009507]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; magnesium chelatase activity [GO:0016851]	O24133	CHLD	Magnesium-chelatase subunit ChlD, chloroplastic (Mg-chelatase subunit D) (EC 6.6.1.1) (Mg-protoporphyrin IX chelatase subunit ChlD)		
6	Vitvi010849	2017_FF3	GO:0005524; GO:0009507; GO:0042026; GO:0140662	protein refolding [GO:0042026]	chloroplast [GO:0009507]	ATP binding [GO:0005524]; ATP-dependent protein folding chaperone [GO:0140662]	P08926		RuBisCO large subunit-binding protein subunit alpha, chloroplastic (60 kDa chaperonin subunit alpha) (CPN-60 alpha)		
6	Vitvi010857	2017_FF3	GO:0005524; GO:0005634; GO:0005829; GO:0005886; GO:0016887; GO:0030433; GO:0030970; GO:0031593; GO:0034098; GO:0051228;	autophagosome maturation [GO:0097352]; ER-associated misfolded protein catabolic process [GO:0071712]; mitotic spindle disassembly [GO:0051228]; retrograde protein transport, ER to cytosol [GO:0030970]; ubiquitin-dependent ERAD pathway [GO:0030433]	cytosol [GO:0005829]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; VCP-NPL4-UFD1 AAA ATPase complex [GO:0034098]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; polyubiquitin modification-dependent protein binding [GO:0031593]	P54774	CDC48	Cell division cycle protein 48 homolog (Valosin-containing protein homolog) (VCP)		
6	Vitvi010831	2017_FF3	GO:0003677; GO:0003723; GO:0046872			DNA binding [GO:0003677]; metal ion binding [GO:0046872]; RNA binding [GO:0003723]	Q0D3J9		Zinc finger CCCH domain-containing protein 53 (OsC3H53)		
6	Vitvi010821	2017_FF3	GO:0003723; GO:0006400	tRNA modification [GO:0006400]		RNA binding [GO:0003723]	Q24K03	THUMPD1	THUMP domain-containing protein 1		
6	Vitvi010876	2017_FF3	GO:0004185; GO:0005576; GO:0006508	proteolysis [GO:0006508]	extracellular region [GO:0005576]	serine-type carboxypeptidase activity [GO:0004185]	Q56WF8	SCPL48	Serine carboxypeptidase-like 48 (EC 3.4.16.-)		
6	Vitvi010824	2017_FF3	GO:0005634; GO:0005737; GO:0005856		cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]; nucleus [GO:0005634]		Q5R8D8	DNAJC7	DnaJ homolog subfamily C member 7		
6	Vitvi010871	2017_FF3	GO:0000325; GO:0004560; GO:0005975; GO:0006516; GO:0048046; GO:0099503	carbohydrate metabolic process [GO:0005975]; glycoprotein catabolic process [GO:0006516]	apoplast [GO:0048046]; plant-type vacuole [GO:0000325]; secretory vesicle [GO:0099503]	alpha-L-fucosidase activity [GO:0004560]	Q8GW72	FUC1	Alpha-L-fucosidase 1 (EC 3.2.1.51) (Alpha-1,3/4-fucosidase) (AtFUC1) (Alpha-L-fucoside fucohydrolase)		
6	Vitvi010822	2017_FF3	GO:0004842; GO:0005524; GO:0016567; GO:0061631	protein ubiquitination [GO:0016567]		ATP binding [GO:0005524]; ubiquitin conjugating enzyme activity [GO:0061631]; ubiquitin-protein transferase activity [GO:0004842]	Q8L7T3	UBC20	Ubiquitin-conjugating enzyme E2 20 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 20) (Ubiquitin carrier protein 20)		
6	Vitvi010843	2017_FF3	GO:0005524; GO:0016020; GO:0016887; GO:0140359		membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q8RWI9	ABCG15	ABC transporter G family member 15 (ABC transporter ABCG.15) (AtABCG15) (White-brown complex homolog protein 15) (AtWBC15) (White-brown complex homolog protein 22) (AtWBC22)		
6	Vitvi010839	2017_FF3	GO:0005634; GO:0006352; GO:0017025; GO:0046872;	DNA-templated transcription initiation [GO:0006352]; transcription preinitiation complex assembly [GO:0070897]	nucleus [GO:0005634]; transcription preinitiation complex [GO:0097550]	metal ion binding [GO:0046872]; TBP-class protein binding [GO:0017025]	Q8W0W3	TFIIB	Transcription initiation factor IIB (General transcription factor TFIIB)		
6	Vitvi010878	2017_FF3	GO:0000815; GO:0005770; GO:0005829; GO:0007034; GO:0015031; GO:0070676	intralumenal vesicle formation [GO:0070676]; protein transport [GO:0015031]; vacuolar transport [GO:0007034]	cytosol [GO:0005829]; ESCRT III complex [GO:0000815]; late endosome [GO:0005770]		Q9FFB3	VPS24-1	Vacuolar protein sorting-associated protein 24 homolog 1 (AtVPS24-1) (Charged multivesicular body protein 3 homolog 1) (ESCRT-III complex subunit VPS24 homolog		
6	Vitvi010865	2017_FF3	GO:0005634; GO:0005730; GO:0005737; GO:0008270;	negative regulation of flower development [GO:0009910]	cytoplasm [GO:0005737]; nucleolus [GO:0005730]; nucleus [GO:0005634]	zinc ion binding [GO:0008270]	Q9FJH5	HIPP03	Heavy metal-associated isoprenylated plant protein 3 (AtHIP03) (AtHIPP3)		
6	Vitvi010855	2017_FF3	GO:0005886; GO:0015112; GO:0015706; GO:0042128;	cellular response to nitrate [GO:0071249]; nitrate assimilation [GO:0042128]; nitrate transmembrane transport	plasma membrane [GO:0005886]	nitrate transmembrane transporter activity [GO:0015112]	Q9FJH8	NRT2.4	High affinity nitrate transporter 2.4 (AtNRT2.4)		
6	Vitvi010851	2017_FF3	GO:0010264	myo-inositol hexakisphosphate biosynthetic process [GO:0010264]			Q9FJH9		P-loop NTPase domain-containing protein LPA1 homolog 1 (Protein LOW PHYTIC ACID 1 homolog 1)		
6	Vitvi010869	2017_FF3	GO:0000976; GO:0003700; GO:0005634; GO:0008285; GO:0030154; GO:0035987; GO:0045597; GO:0045892; GO:0045893; GO:0048226; GO:0050801; GO:2000067	cell differentiation [GO:0030154]; endodermal cell differentiation [GO:0035987]; monoatomic ion homeostasis [GO:0050801]; negative regulation of cell population proliferation [GO:0008285]; negative regulation of DNA-templated transcription [GO:0045892]; positive regulation of cell differentiation [GO:0045597]; positive regulation of DNA-templated transcription [GO:0045893]; regulation of pot morphogenesis [GO:2000067]	Casparian strip [GO:0048226]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9FKL2	MYB36	Transcription factor MYB36 (Myb-related protein 36) (AtMYB36)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
6	Vitvi010861	2017_FF3	GO:0005886; GO:0009733; GO:0009737	response to abscisic acid [GO:0009737]; response to auxin [GO:0009733]	plasma membrane [GO:0005886]		Q9FXI0	SAUR54	Protein SMALL AUXIN UP-REGULATED RNA 54		
6	Vitvi010819	2017_FF3	GO:0001678; GO:0004396; GO:0005524; GO:0005536; GO:0005739; GO:0005741; GO:0006096; GO:0006970; GO:0009409; GO:0009651	glycolytic process [GO:0006096]; hexose metabolic process [GO:0019318]; intracellular glucose homeostasis [GO:0001678]; response to cold [GO:0009409]; response to osmotic stress [GO:0006970]; response to salt stress [GO:0009651]; root hair cell development [GO:0080147]	mitochondrial outer membrane [GO:0005741]; mitochondrion [GO:0005739]	ATP binding [GO:0005524]; glucose binding [GO:0005536]; hexokinase activity [GO:0004396]	Q9LPS1	HXK3	Hexokinase-3 (EC 2.7.1.1) (Hexokinase-like 1)		
6	Vitvi010834	2017_FF3	GO:0005524; GO:0006952; GO:0043531; GO:0051707	defense response [GO:0006952]; response to other organism [GO:0051707]		ADP binding [GO:0043531]; ATP binding [GO:0005524]	Q9LRR4	RPPL1	Putative disease resistance RPP13-like protein 1		
6	Vitvi010870	2017_FF3	GO:0005576; GO:0060320	rejection of self pollen [GO:0060320]	extracellular region [GO:0005576]		Q9LW22	SPH21	S-protein homolog 21		
6	Vitvi010814	2017_FF3	GO:0000339; GO:0000380; GO:0000394; GO:0000398; GO:0000956; GO:0005634; GO:0005739; GO:0005845; GO:0005846; GO:0006370; GO:0006406; GO:0009737; GO:0031053; GO:0035195; GO:0042789; GO:0048574; GO:0051607; GO:1901527	7-methylguanosine mRNA capping [GO:0006370]; abscisic acid-activated signaling pathway involved in stomatal movement [GO:1901527]; alternative mRNA splicing, via spliceosome [GO:0000380]; defense response to virus [GO:0051607]; long-day photoperiodism, flowering [GO:0048574]; miRNA-mediated post-transcriptional gene silencing [GO:0035195]; mRNA export from nucleus [GO:0006406]; mRNA splicing, via spliceosome [GO:0000398]; mRNA transcription by RNA polymerase II [GO:0042789]; nuclear-transcribed mRNA catabolic process [GO:0000956]; primary miRNA processing [GO:0031053]; response to abscisic acid [GO:0009737]; RNA splicing, via	mitochondrion [GO:0005739]; mRNA cap binding complex [GO:0005845]; nuclear cap binding complex [GO:0005846]; nucleus [GO:0005634]	RNA cap binding [GO:0000339]	Q9SIU2	ABH1	Nuclear cap-binding protein subunit 1 (80 kDa nuclear cap-binding protein) (AtCBP80) (NCBP 80 kDa subunit) (Abscisic acid-hypersensitive protein 1) (ABA-hypersensitive protein 1) (Protein ENSALADA)		
6	Vitvi010859	2017_FF3	GO:0008194			UDP-glycosyltransferase activity [GO:0008194]	Q9SJL0	UGT86A1	UDP-glycosyltransferase 86A1 (EC 2.4.1.-)		
6	Vitvi010879	2017_FF3	GO:0004553; GO:0010411; GO:0016762; GO:0016998; GO:0030247; GO:0042546; GO:0048046; GO:0071555	cell wall biogenesis [GO:0042546]; cell wall macromolecule catabolic process [GO:0016998]; cell wall organization [GO:0071555]; xyloglucan metabolic process [GO:0010411]	apoplast [GO:0048046]	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]; polysaccharide binding [GO:0030247]; xyloglucan:xyloglucosyl transferase activity [GO:0016762]	Q9SJL9	XTH32	Probable xyloglucan endotransglucosylase/hydrolase protein 32 (At-XTH32) (XTH-32) (EC 2.4.1.207)		
6	Vitvi010868	2017_FF3	GO:0004462; GO:0046872			lactoylglutathione lyase activity [GO:0004462]; metal ion binding [GO:0046872]	Q9ZS21	GLXI	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (GmGlyoxI) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)		
6	Vitvi010854	2017_FF3	GO:0005737; GO:0005975; GO:0009507; GO:0009569; GO:0019887; GO:0031588; GO:1901982	carbohydrate metabolic process [GO:0005975]	chloroplast [GO:0009507]; chloroplast starch grain [GO:0009569]; cytoplasm [GO:0005737]; nucleotide-activated protein kinase complex [GO:0031588]	maltose binding [GO:1901982]; protein kinase regulator activity [GO:0019887]	Q9ZUU8	KINB3	SNF1-related protein kinase regulatory subunit beta-3 (AKIN subunit beta-3) (AKINB3) (AKINbeta3)		
6	Vitvi010858	2017_FF3	GO:0005524; GO:0005886; GO:0016887; GO:0140359		plasma membrane [GO:0005886]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9ZUU9	ABCG3	ABC transporter G family member 3 (ABC transporter ABCG.3) (AtABCG3) (White-brown complex homolog protein 3) (AtWBC3)		
6	Vitvi010880	2017_FF3	GO:0000139; GO:0005794; GO:0009834; GO:0010417; GO:0015020; GO:0071555	cell wall organization [GO:0071555]; glucuronoxylan biosynthetic process [GO:0010417]; plant-type secondary cell wall biogenesis [GO:0009834]	Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]	glucuronosyltransferase activity [GO:0015020]	Q9ZUV3	IRX7	Probable glucuronoxylan glucuronosyltransferase IRX7 (EC 2.4.1.-) (Protein FRAGILE FIBER 8) (Protein		
7	Vitvi011354	2016_SSC2	GO:0005634; GO:0009742; GO:0032784	brassinosteroid mediated signaling pathway [GO:0009742]; regulation of DNA-templated transcription elongation [GO:0032784]	nucleus [GO:0005634]		F4ICK8	IWS1	Protein IWS1 homolog 1 (AtIWS1) (Interacts with SPT6 protein 1) (Protein HIGH NITROGEN INSENSITIVE 9) (Protein SUPPRESSOR OF BES-1-D 1)		
7	Vitvi011364	2016_SSC2	GO:0005634; GO:0006397; GO:0009908; GO:0063971	flower development [GO:0009908]; mRNA processing [GO:0006397]	nucleus [GO:0005634]		F4IN78	HULK2	Protein HUA2-LIKE 2 (HUA2-like protein 2)		
7	Vitvi011369	2016_SSC2	GO:0003723; GO:0009501; GO:0009507; GO:0009509; GO:0009513; GO:0009537; GO:0009570; GO:0009658; GO:0009965; GO:0010239; GO:0016070; GO:0019843	cellular response to light stimulus [GO:0071482]; chloroplast mRNA processing [GO:0010239]; chloroplast organization [GO:0009658]; leaf morphogenesis [GO:0009965]; ribosome biogenesis [GO:0042254]; RNA metabolic process [GO:0016070]	amyloplast [GO:0009501]; chloroplast [GO:0009507]; chloroplast nucleoid [GO:0042644]; chloroplast stroma [GO:0009570]; chromoplast [GO:0009509]; etioplast [GO:0009513]; proplastid [GO:0009537]	protein self-association [GO:0043621]; RNA binding [GO:0003723]; rRNA binding [GO:0019843]	Q39089	PAC	Protein PALE CRESS, chloroplastic		
7	Vitvi011373	2016_SSC2	GO:0003676; GO:0005634; GO:0006364; GO:0008408	rRNA processing [GO:0006364]	nucleus [GO:0005634]	3'-5' exonuclease activity [GO:0008408]; nucleic acid binding [GO:0003676]	Q4IEV5	REX4	RNA exonuclease 4 (EC 3.1.-.-)		
7	Vitvi011345	2016_SSC2	GO:0016020; GO:0016413		membrane [GO:0016020]	O-acetyltransferase activity	Q5BPJ0	TBL11	Protein trichome birefringence-like 11		
7	Vitvi011368	2016_SSC2	GO:0005983; GO:0009507; GO:0010021; GO:0019156; GO:0019252; GO:0043033	amylopectin biosynthetic process [GO:0010021]; starch biosynthetic process [GO:0019252]; starch catabolic process [GO:0005983]	chloroplast [GO:0009507]; isoamylase complex [GO:0043033]	isoamylase activity [GO:0019156]	Q8L735	ISA2	Isoamylase 2, chloroplastic (AtISA2) (Protein DEBRANCHING ENZYME 1)		10.1016/j.scienta.2013.11.026
7	Vitvi011356	2016_SSC2	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0046983; GO:0048235; GO:0048765; GO:0048767; GO:0055046; GO:0080147	microgametogenesis [GO:0055046]; pollen sperm cell differentiation [GO:0048235]; regulation of DNA-templated transcription [GO:0006355]; root hair cell development [GO:0080147]; root hair cell differentiation [GO:0048765]; root hair elongation [GO:0048767]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]	Q8S3D5	LRL2	Transcription factor LRL2 (Basic helix-loop-helix protein 69) (AtbHLH69) (bHLH 69) (Protein DEFECTIVE REGION OF POLLEN 2) (Protein LJRHL1- LIKE 2) (AtLRL2) (Transcription factor EN 94) (Transcription factor bHLH69) (bHLH transcription factor bHLH069)		
7	Vitvi011358	2016_SSC2	GO:0005524; GO:0005634; GO:0009507; GO:0009536; GO:0009691; GO:0009824; GO:0031965; GO:0052622; GO:0052623	cytokinin biosynthetic process [GO:0009691]	chloroplast [GO:0009507]; nuclear membrane [GO:0031965]; nucleus [GO:0005634]; plastid [GO:0009536]	ADP dimethylallyltransferase activity [GO:0052623]; AMP dimethylallyltransferase activity [GO:0009824]; ATP binding [GO:0005524]; ATP dimethylallyltransferase activity [GO:0052622]	Q93WC9	IPT3	Adenylate isopentenyltransferase 3, chloroplastic (AtIPT3) (EC 2.5.1.112) (Adenylate dimethylallyltransferase 3) (Cytokinin synthase 3)		
7	Vitvi011366	2016_SSC2	GO:0005634; GO:0006970; GO:0009414; GO:0009651; GO:0009737; GO:0009738; GO:0010029; GO:0010228	abscisic acid-activated signaling pathway [GO:0009738]; regulation of seed germination [GO:0010029]; response to abscisic acid [GO:0009737]; response to osmotic stress [GO:0006970]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]; vegetative to reproductive phase transition of meristem [GO:0010228]	nucleus [GO:0005634]		Q93ZT5	EDL3	EID1-like F-box protein 3		
7	Vitvi011349	2016_SSC2	GO:0009058; GO:0016853	biosynthetic process [GO:0009058]		isomerase activity [GO:0016853]	Q9KG32		Uncharacterized isomerase BH0283 (EC 5.1.-.-)		
7	Vitvi011363	2016_SSC2	GO:0004602; GO:0005783; GO:0005829; GO:0005886; GO:0006979; GO:0009793; GO:0012505	embryo development ending in seed dormancy [GO:0009793]; response to oxidative stress [GO:0006979]	cytosol [GO:0005829]; endomembrane system [GO:0012505]; endoplasmic reticulum [GO:0005783]; plasma membrane [GO:0005886]	glutathione peroxidase activity [GO:0004602]	Q9LYB4	GPX5	Probable glutathione peroxidase 5 (EC 1.11.1.9)		
7	Vitvi011346	2016_SSC2	GO:0000325; GO:0000387; GO:0003729; GO:0005730; GO:0008380; GO:0016607; GO:0035194; GO:0043484	regulation of RNA splicing [GO:0043484]; regulatory ncRNA-mediated post-transcriptional gene silencing [GO:0035194]; RNA splicing [GO:0008380]; spliceosomal snRNP assembly [GO:0000387]	nuclear speck [GO:0016607]; nucleolus [GO:0005730]; plant-type vacuole [GO:0000325]; ribonucleoprotein complex [GO:1990904]	mRNA binding [GO:0003729]	Q9SY09	SMD1B	Small nuclear ribonucleoprotein SmD1b (AtSmD1-b)		
7	Vitvi011367	2016_SSC2	GO:0005227; GO:0016020		membrane [GO:0016020]	calcium activated cation channel activity [GO:0005227]	Q9SY14		CSC1-like protein At4g02900		
7	Vitvi011422	2016_SSC3	GO:0005634; GO:0005737; GO:0005886		cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]		D3J163	VPYL	Protein VAPYRIN-LIKE (MtVpyl)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
7	Vitvi011430	2016_SSC3	GO:0003697; GO:0003700; GO:0005634; GO:0005730; GO:0009845; GO:0009908; GO:0043565; GO:0048364;	flower development [GO:0009908]; negative regulation of antisense RNA transcription [GO:0060195]; root development [GO:0048364]; seed germination [GO:0009845]	nucleolus [GO:0005730]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]; single-stranded DNA binding [GO:0036971	F4JI44	NDX	Nodulin homeobox (NDX1 homeobox protein homolog) (AtNDX1)		
7	Vitvi011425	2016_SSC3	GO:0000786; GO:0003677; GO:0005576; GO:0005634; GO:0030527; GO:0046982		extracellular region [GO:0005576]; nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:00305271	O04848		Probable histone H2AXa (HTA5)		
7	Vitvi011435	2016_SSC3	GO:0004601; GO:0005576; GO:0005783; GO:0006979; GO:0009269; GO:0009409; GO:0020037; GO:0042538;	hydrogen peroxide catabolic process [GO:0042744]; hyperosmotic salinity response [GO:0042538]; response to cold [GO:0009409]; response to desiccation [GO:0009269]; response to oxidative stress [GO:0006979]	endoplasmic reticulum [GO:0005783]; extracellular region [GO:0005576]	heme binding [GO:0020037]; lactoperoxidase activity [GO:0140825]; metal ion binding [GO:0046872]; peroxidase activity [GO:0004601]	O23044	PER3	Peroxidase 3 (Atperox P3) (EC 1.11.1.7) (ATPRC) (RCI3A) (Rare cold-inducible protein)		
7	Vitvi011420	2016_SSC3	GO:0003729			mRNA binding [GO:0003729]	O49343		Pentatricopeptide repeat-containing protein At2g30780		
7	Vitvi011423	2016_SSC3	GO:0000786; GO:0003677; GO:0005634; GO:0030527; GO:0046982		nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:00305271	O65759	HIS2A	Histone H2AX		
7	Vitvi011433	2016_SSC3	GO:0005829; GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]	cytosol [GO:0005829]		O82264		NPL4-like protein 2		
7	Vitvi011432	2016_SSC3	GO:0000278; GO:0005634; GO:0005694; GO:0051301; GO:0051455; GO:0051754	cell division [GO:0051301]; meiotic sister chromatid cohesion, centromeric [GO:0051754]; mitotic cell cycle [GO:0000278]; spindle attachment to meiosis I kinetochore [GO:0051455]	chromosome [GO:0005694]; nucleus [GO:0005634]		O82265	SCC3	Sister-chromatid cohesion protein 3 (AtSCC3) (Stromalin protein)		
7	Vitvi011431	2016_SSC3	GO:0003729; GO:0005730; GO:0006364; GO:0007049; GO:0009553; GO:0009561; GO:0051301; GO:0080008	cell cycle [GO:0007049]; cell division [GO:0051301]; embryo sac development [GO:0009553]; megagametogenesis [GO:0009561]; rRNA processing [GO:0006364]	Cul4-RING E3 ubiquitin ligase complex [GO:0080008]; nucleolus [GO:0005730]	mRNA binding [GO:0003729]	O82266	SWA1	Protein SLOW WALKER 1 (Protein EMBRYO SAC DEVELOPMENT ARREST 13) (Protein EMBRYO SAC DEVELOPMENT ARREST 19)		
7	Vitvi011419	2016_SSC3					Q40153		LEC14B protein		
7	Vitvi011416	2016_SSC3	GO:0005774; GO:0006914; GO:0015031; GO:0034045; GO:0042594	autophagy [GO:0006914]; protein transport [GO:0015031]; response to starvation [GO:0042594]	phagophore assembly site membrane [GO:0034045]; vacuolar membrane [GO:0005774]		Q8GUL1	ATG18G	Autophagy-related protein 18g (AtATG18g)		
7	Vitvi011428	2016_SSC3	GO:0005634; GO:0005829; GO:0009742; GO:0017018;	brassinosteroid mediated signaling pathway [GO:0009742]	cytosol [GO:0005829]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; myosin phosphatase activity	Q8L7U5	BSL1	Serine/threonine-protein phosphatase BSL1 (EC 3.1.3.16) (BSU1-like protein 1)		
7	Vitvi011421	2016_SSC3	GO:0005634; GO:0009739; GO:0009939; GO:0010476; GO:0010629; GO:0016787; GO:0048444; GO:0048530; GO:1905516	floral organ morphogenesis [GO:0048444]; fruit morphogenesis [GO:0048530]; gibberellin mediated signaling pathway [GO:0010476]; negative regulation of gene expression [GO:0010629]; positive regulation of fertilization [GO:1905516]; positive regulation of gibberellic acid mediated signaling pathway [GO:0009939]; response to	nucleus [GO:0005634]	hydrolase activity [GO:0016787]	Q9LYC1	GID1B	Gibberellin receptor GID1B (EC 3.-.-.-) (AtCXE14) (Carboxylesterase 14) (GID1-like protein 2) (Protein GA INSENSITIVE DWARF 1B) (AtGID1B)		
7	Vitvi011440	2016_BL1	GO:0005743; GO:0006839; GO:0022857	mitochondrial transport [GO:0006839]	mitochondrial inner membrane [GO:0005743]	transmembrane transporter activity [GO:0022857]	B0G143	ucpB	Mitochondrial substrate carrier family protein ucpB (Solute carrier family 25 member 30 homolog) (Uncoupler protein B)		
7	Vitvi011422	2016_BL1	GO:0005634; GO:0005737; GO:0005886		cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]		D3J163	VPYL	Protein VAPYRIN-LIKE (MtVpyl)		
7	Vitvi011430	2016_BL1	GO:0003697; GO:0003700; GO:0005634; GO:0005730; GO:0009845; GO:0009908; GO:0043565; GO:0048364;	flower development [GO:0009908]; negative regulation of antisense RNA transcription [GO:0060195]; root development [GO:0048364]; seed germination [GO:0009845]	nucleolus [GO:0005730]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]; single-stranded DNA binding [GO:0036971	F4JI44	NDX	Nodulin homeobox (NDX1 homeobox protein homolog) (AtNDX1)		
7	Vitvi011436	2016_BL1	GO:0005096; GO:0007165	signal transduction [GO:0007165]		GTPase activator activity [GO:0005096]	F4JI46	ROPGAP2	Rho GTPase-activating protein 2 (Rho-type GTPase-activating protein 2)		
7	Vitvi011441	2016_BL1	GO:0000243; GO:0000387; GO:0000395; GO:0003729; GO:0005685; GO:0008270; GO:0030619; GO:0030627;	mRNA 5'-splice site recognition [GO:0000395]; spliceosomal snRNP assembly [GO:0000387]	commitment complex [GO:0000243]; U1 snRNP [GO:0005685]; U2-type prespliceosome [GO:0071004]	mRNA binding [GO:0003729]; pre-mRNA 5'-splice site binding [GO:0030627]; U1 snRNA binding [GO:0030619]; zinc ion binding	F6HQ26		U1 small nuclear ribonucleoprotein C (U1 snRNP C) (U1-C) (U1C)		
7	Vitvi011425	2016_BL1	GO:0000786; GO:0003677; GO:0005576; GO:0005634; GO:0030527; GO:0046982		extracellular region [GO:0005576]; nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:00305271	O04848		Probable histone H2AXa (HTA5)		
7	Vitvi011435	2016_BL1	GO:0004601; GO:0005576; GO:0005783; GO:0006979; GO:0009269; GO:0009409; GO:0020037; GO:0042538;	hydrogen peroxide catabolic process [GO:0042744]; hyperosmotic salinity response [GO:0042538]; response to cold [GO:0009409]; response to desiccation [GO:0009269]; response to oxidative stress [GO:0006979]	endoplasmic reticulum [GO:0005783]; extracellular region [GO:0005576]	heme binding [GO:0020037]; lactoperoxidase activity [GO:0140825]; metal ion binding [GO:0046872]; peroxidase activity [GO:00046011	O23044	PER3	Peroxidase 3 (Atperox P3) (EC 1.11.1.7) (ATPRC) (RCI3A) (Rare cold-inducible protein)		
7	Vitvi011423	2016_BL1	GO:0000786; GO:0003677; GO:0005634; GO:0030527; GO:0046982		nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:00305271	O65759	HIS2A	Histone H2AX		
7	Vitvi011433	2016_BL1	GO:0005829; GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]	cytosol [GO:0005829]		O82264		NPL4-like protein 2		
7	Vitvi011432	2016_BL1	GO:0000278; GO:0005634; GO:0005694; GO:0051301; GO:0051455; GO:0051754	cell division [GO:0051301]; meiotic sister chromatid cohesion, centromeric [GO:0051754]; mitotic cell cycle [GO:0000278]; spindle attachment to meiosis I kinetochore [GO:0051455]	chromosome [GO:0005694]; nucleus [GO:0005634]		O82265	SCC3	Sister-chromatid cohesion protein 3 (AtSCC3) (Stromalin protein)		
7	Vitvi011431	2016_BL1	GO:0003729; GO:0005730; GO:0006364; GO:0007049; GO:0009553; GO:0009561; GO:0051301; GO:0080008	cell cycle [GO:0007049]; cell division [GO:0051301]; embryo sac development [GO:0009553]; megagametogenesis [GO:0009561]; rRNA processing [GO:0006364]	Cul4-RING E3 ubiquitin ligase complex [GO:0080008]; nucleolus [GO:0005730]	mRNA binding [GO:0003729]	O82266	SWA1	Protein SLOW WALKER 1 (Protein EMBRYO SAC DEVELOPMENT ARREST 13) (Protein EMBRYO SAC DEVELOPMENT ARREST 19)		
7	Vitvi011428	2016_BL1	GO:0005634; GO:0005829; GO:0009742; GO:0017018;	brassinosteroid mediated signaling pathway [GO:0009742]	cytosol [GO:0005829]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; myosin phosphatase activity	Q8L7U5	BSL1	Serine/threonine-protein phosphatase BSL1 (EC 3.1.3.16) (BSU1-like protein 1)		
7	Vitvi011439	2016_BL1	GO:0003729; GO:0005737; GO:0005829; GO:0006402; GO:0009626; GO:0009908; GO:0080151; GO:1990904; GO:2000028	flower development [GO:0009908]; mRNA catabolic process [GO:0006402]; plant-type hypersensitive response [GO:0009626]; positive regulation of salicylic acid mediated signaling pathway [GO:0080151]; regulation of photoperiodism, flowering [GO:2000028]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; ribonucleoprotein complex [GO:1990904]	mRNA binding [GO:0003729]	Q8LFS6	BRN1	RNA-binding protein BRN1 (Protein BRUNO-LIKE 1) (AtBRN1) (Protein RNA-BINDING PROTEIN-DEFENSE RELATED 1) (AtRBP-DR1)		
7	Vitvi011638	2017_Cit3					O04251		BRCT domain-containing protein At4g02110		
7	Vitvi011916	2016_Tar2	GO:0005509			calcium ion binding [GO:0005509]	Q5QIT3	B"BETA	Serine/threonine protein phosphatase 2A regulatory subunit B"beta (AtB"beta) (Serine/threonine protein phosphatase 2A regulatory subunit B" beta 1 isoform) (PP2A, B" subunit, beta 1 isoform)		
7	Vitvi013366	2016_EDP1	GO:0004806; GO:0005811; GO:0016020; GO:0016042	lipid catabolic process [GO:0016042]	lipid droplet [GO:0005811]; membrane [GO:0016020]	triglyceride lipase activity [GO:0004806]	A0A1S3ZP85	OBL1	Triacylglycerol lipase OBL1 (EC 3.1.1.-) (Oil body lipase 1) (NtOBL1)		
7	Vitvi013381	2016_EDP1	GO:0005506; GO:0009414; GO:0009733; GO:0009737; GO:0009856; GO:0010295; GO:0016020; GO:0016125;	abscisic acid catabolic process [GO:0046345]; pollination [GO:0009856]; response to abscisic acid [GO:0009737]; response to auxin [GO:0009733]; response to water deprivation [GO:0009414]; sterol metabolic process	membrane [GO:0016020]	(+)-abscisic acid 8'-hydroxylase activity [GO:0010295]; heme binding [GO:0020037]; iron ion binding [GO:0005506]	A9QNE7	CYP707A1	Abscisic acid 8'-hydroxylase CYP707A1 (ABA 8'-hydroxylase CYP707A1) (SlCYP707A1) (EC 1.14.14.137) (Cytochrome P450 707A1)		10.1007/s00425-009-0913-7
7	Vitvi013426	2016_EDP1	GO:0005743		mitochondrial inner membrane [GO:0005743]		C5M3V6	MIC60	MICOS complex subunit MIC60 (Mitofilin)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
7	Vitvi013408	2016_EDP1	GO:0004069; GO:0009094; GO:0009095; GO:0009507; GO:0030170; GO:0033853; GO:0033854; GO:0042802	aromatic amino acid family biosynthetic process, prephenate pathway [GO:0009095]; L-phenylalanine biosynthetic process [GO:0009094]	chloroplast [GO:0009507]	aspartate-prephenate aminotransferase activity [GO:0033853]; glutamate-prephenate aminotransferase activity [GO:0033854]; identical protein binding [GO:0042802]; L-aspartate:2-oxoglutarate aminotransferase activity [GO:0004069]; pyridoxal phosphate	E9L7A5	PPA-AT	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase (PhPPA-AT) (EC 2.6.1.1) (EC 2.6.1.78) (EC 2.6.1.79)		
7	Vitvi013425	2016_EDP1	GO:0005737; GO:0005794; GO:0005829; GO:0005886; GO:0008017; GO:0008360; GO:0009414; GO:0009506; GO:0009833; GO:0009898; GO:0009901; GO:0010208; GO:0010215; GO:0010330; GO:0030244; GO:0036449; GO:0043622; GO:0048467; GO:0048868; GO:0051211; GO:0051592; GO:0055028; GO:0070507; GO:0072699; GO:2000067; GO:2001006	anisotropic cell growth [GO:0051211]; anther dehiscence [GO:0009901]; cellulose biosynthetic process [GO:0030244]; cellulose microfibril organization [GO:0010215]; cortical microtubule organization [GO:0043622]; gynoecium development [GO:0048467]; plant-type primary cell wall biogenesis [GO:0009833]; pollen tube development [GO:0048868]; pollen wall assembly [GO:0010208]; protein localization to cortical microtubule cytoskeleton [GO:0072699]; regulation of cell shape [GO:0008360]; regulation of cellulose biosynthetic process [GO:2001006]; regulation of microtubule cytoskeleton organization [GO:0070507]; regulation of root morphogenesis [GO:2000067]; response to calcium ion [GO:0051592]	cellulose synthase complex [GO:0010330]; cortical microtubule [GO:0055028]; cytoplasm [GO:0005737]; cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; Golgi apparatus [GO:0005794]; microtubule minus-end [GO:0036449]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	microtubule binding [GO:0008017]	F4IIM1	CSI1	Protein CELLULOSE SYNTHASE INTERACTIVE 1 (Protein POM-POM 2)		
7	Vitvi013370	2016_EDP1	GO:0004806; GO:0005811; GO:0016020; GO:0016042; GO:0033878; GO:0047372; GO:0090406	lipid catabolic process [GO:0016042]	lipid droplet [GO:0005811]; membrane [GO:0016020]; pollen tube [GO:0090406]	acylglycerol lipase activity [GO:0047372]; hormone-sensitive lipase activity [GO:0033878]; triglyceride lipase activity [GO:0004806]	F4JFU8	OBL1	Triacylglycerol lipase OBL1 (EC 3.1.1.-) (Oil body lipase 1) (AtOBL1)		
7	Vitvi013407	2016_EDP1	GO:0003676; GO:0004527; GO:0005634; GO:0046872		nucleus [GO:0005634]	exonuclease activity [GO:0004527]; metal ion binding [GO:0046872]; nucleic acid binding [GO:0003676]	F4IJ23	NEN4	Protein NEN4 (NAC45/NAC86-dependent exonuclease-domain protein 4) (EC 3.1.11.-)		
7	Vitvi013325	2016_EDP1	GO:0004843; GO:0005634; GO:0006508	proteolysis [GO:0006508]	nucleus [GO:0005634]	cysteine-type deubiquitinase activity [GO:0004843]	F4K3M6	OTU7	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 7 (OTU domain-containing protein 7) (EC 3.4.19.12) (Deubiquitinating enzyme OTU7)		
7	Vitvi013431	2016_EDP1	GO:0016491; GO:0044249	cellular biosynthetic process [GO:0044249]		oxidoreductase activity [GO:0016491]	G4N286	RED1	Short-chain dehydrogenase RED1 (EC 1.1.1.-) (Pyriculol/pyriculariol biosynthesis cluster protein RED1)		
7	Vitvi013418	2016_EDP1	GO:0005507; GO:0005576; GO:0006952; GO:0008447; GO:0009615; GO:0009753; GO:0016491; GO:0019854; GO:0042542; GO:0050687; GO:0090533; GO:0090615	defense response [GO:0006952]; L-ascorbic acid catabolic process [GO:0019854]; negative regulation of defense response to virus [GO:0050687]; response to hydrogen peroxide [GO:0042542]; response to jasmonic acid [GO:0009753]; response to virus [GO:0009615]	extracellular region [GO:0005576]	copper ion binding [GO:0005507]; L-ascorbate oxidase activity [GO:0008447]; oxidoreductase activity [GO:0016491]	M4DUF2	AO	L-ascorbate oxidase (AAO) (AO) (ASO) (Ascorbase) (EC 1.10.3.3)		10.1038/ng.919
7	Vitvi013395	2016_EDP1	GO:0004620; GO:0005737; GO:0006952; GO:0010311; GO:0016042; GO:0047372	defense response [GO:0006952]; lateral root formation [GO:0010311]; lipid catabolic process [GO:0016042]	cytoplasm [GO:0005737]	acylglycerol lipase activity [GO:0047372]; phospholipase activity [GO:0004620]	O23179	PLP1	Patatin-like protein 1 (AtPLP1) (EC 3.1.1.-) (Patatin-related phospholipase A IIgamma) (pPLAIIg) (Phospholipase A IVA)		
7	Vitvi013357	2016_EDP1	GO:0000166; GO:0003682; GO:0003688; GO:0003697; GO:0003887; GO:0003896; GO:0005634; GO:0005658; GO:0006270; GO:0006272; GO:0006273; GO:0009965; GO:0046872; GO:1902975	DNA replication initiation [GO:0006270]; lagging strand elongation [GO:0006273]; leading strand elongation [GO:0006272]; leaf morphogenesis [GO:0009965]; mitotic DNA replication initiation [GO:1902975]	alpha DNA polymerase:primase complex [GO:0005658]; nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA primase activity [GO:0003896]; DNA replication origin binding [GO:0003688]; DNA-directed DNA polymerase activity [GO:0003887]; metal ion binding [GO:0046872]; nucleotide binding [GO:0000166]; single-stranded DNA binding [GO:0003697]	O48653		DNA polymerase alpha catalytic subunit (EC 2.7.7.7)		
7	Vitvi013429	2016_EDP1	GO:0003723; GO:0003735; GO:0022625		cytosolic large ribosomal subunit [GO:0022625]	RNA binding [GO:0003723]; structural constituent of ribosome [GO:0003735]	O49884	RPL30	Large ribosomal subunit protein eL30 (60S ribosomal protein L30)		
7	Vitvi013374	2016_EDP1	GO:0009507; GO:0009688; GO:0016020; GO:0052662;	abscisic acid biosynthetic process [GO:0009688]	chloroplast [GO:0009507]; membrane [GO:0016020]	FAD binding [GO:0071949]; zeaxanthin epoxidase activity [GO:0052662]	O81360		Zeaxanthin epoxidase, chloroplastic (EC 1.14.15.21) (PA-ZE)		
7	Vitvi013371	2016_EDP1	GO:0003730; GO:0005634; GO:0005737; GO:0005848; GO:0180010	co-transcriptional mRNA 3'-end processing, cleavage and polyadenylation pathway [GO:0180010]	cytoplasm [GO:0005737]; mRNA cleavage stimulating factor complex [GO:0005848]; nucleus [GO:0005634]	mRNA 3'-UTR binding [GO:0003730]	O94432		Uncharacterized RNA-binding protein C660.15		
7	Vitvi013379	2016_EDP1	GO:0003700; GO:0005634; GO:0043565		nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	P22335	HSF24	Heat shock factor protein HSF24 (Heat shock transcription factor 24) (HSTF 24) (Heat stress transcription factor)		
7	Vitvi013414	2016_EDP1	GO:0005507; GO:0005576; GO:0008447		extracellular region [GO:0005576]	copper ion binding [GO:0005507]; L-ascorbate oxidase activity [GO:0008447]	P24792	AAO	L-ascorbate oxidase (ASO) (Ascorbase) (EC 1.10.3.3)		
7	Vitvi013406	2016_EDP1	GO:0008271; GO:0016020		membrane [GO:0016020]	secondary active sulfate transmembrane transporter activity [GO:0008271]	P53393	ST3	Low affinity sulfate transporter 3		
7	Vitvi013341	2016_EDP1	GO:0003727; GO:0005634; GO:0006349; GO:0006355; GO:0009294; GO:0009737; GO:0009738; GO:0009908; GO:0009909; GO:0009965; GO:0010048; GO:0010228; GO:0016571; GO:0030154; GO:0031519; GO:0045814; GO:0140951; GO:1900055; GO:1990110	abscisic acid-activated signaling pathway [GO:0009738]; callus formation [GO:1990110]; cell differentiation [GO:0030154]; DNA-mediated transformation [GO:0009294]; flower development [GO:0009908]; histone methylation [GO:0016571]; leaf morphogenesis [GO:0009965]; negative regulation of gene expression, epigenetic [GO:0045814]; regulation of DNA-templated transcription [GO:0006355]; regulation of flower development [GO:0009909]; regulation of gene expression by genomic imprinting [GO:0006349]; regulation of leaf senescence [GO:1900055]; response to abscisic acid [GO:0009737]; vegetative to reproductive phase transition of meristem [GO:0010228]; vernalization response	nucleus [GO:0005634]; PcG protein complex [GO:0031519]	histone H3K27 trimethyltransferase activity [GO:0140951]; single-stranded RNA binding [GO:0003727]	P93831	CLF	Histone-lysine N-methyltransferase CLF (EC 2.1.1.-) (Polycomb group protein CURLY LEAF) (Protein INCURVATA 1) (Protein SET DOMAIN GROUP 1) (Protein photoperiod insensitive flowering)		
7	Vitvi013377	2016_EDP1	GO:0009507; GO:0009658; GO:1901259	chloroplast organization [GO:0009658]; chloroplast rRNA processing [GO:1901259]	chloroplast [GO:0009507]		Q42463	DCL	Protein DCL, chloroplastic (Defective chloroplasts and leaves protein)		
7	Vitvi013345	2016_EDP1	GO:0003700; GO:0005634; GO:0009640; GO:0009738; GO:0009788; GO:0046872	abscisic acid-activated signaling pathway [GO:0009738]; negative regulation of abscisic acid-activated signaling pathway [GO:0009788]; photomorphogenesis [GO:0009640]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]	Q42485	ZFP1	Zinc finger protein 1 (AtZFP1)		
7	Vitvi013344	2016_EDP1	GO:0009809; GO:0032259; GO:0042409; GO:0046872	lignin biosynthetic process [GO:0009809]; methylation [GO:0032259]		caffeoyl-CoA O-methyltransferase activity [GO:0042409]; metal ion binding [GO:0046872]	Q43095		Caffeoyl-CoA O-methyltransferase (EC 2.1.1.104) (Trans-caffeoyl-CoA 3-O-methyltransferase) (CCoAMT) (CCoAOMT)		
7	Vitvi013388	2016_EDP1	GO:0002183; GO:0003723; GO:0003724; GO:0003743; GO:0005524; GO:0010494; GO:0016887	cytoplasmic translational initiation [GO:0002183]	cytoplasmic stress granule [GO:0010494]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]; translation initiation factor activity [GO:0003743]	Q4P331	TIF1	ATP-dependent RNA helicase eIF4A (EC 3.6.4.13) (Eukaryotic initiation factor 4A) (eIF-4A) (Translation initiation factor 1)		
7	Vitvi013405	2016_EDP1	GO:0005634; GO:0030544; GO:0048471; GO:0051082	chaperone-mediated protein folding [GO:0061077]	nucleus [GO:0005634]; perinuclear region of cytoplasm [GO:0048471]	Hsp70 protein binding [GO:0030544]; unfolded protein binding [GO:0051082]	Q5FWN8	dnajb6-a	DnaJ homolog subfamily B member 6-A		
7	Vitvi013427	2016_EDP1	GO:0000455; GO:0005737; GO:0016740; GO:0030490; GO:0106388; GO:1904047	enzyme-directed rRNA pseudouridine synthesis [GO:0000455]; maturation of SSU-rRNA [GO:0030490]	cytoplasm [GO:0005737]	18S rRNA aminocarboxypropyltransferase activity [GO:0106388]; S-adenosyl-L-methionine binding [GO:1904047]; transferase	Q5HZH2	Tsr3	18S rRNA aminocarboxypropyltransferase (EC 2.5.1.-) (20S S rRNA accumulation protein 3 homolog)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
7	Vitvi013385	2016_EDP1	GO:0003677; GO:0003700; GO:0005634; GO:0009873; GO:0045893; GO:0048510	ethylene-activated signaling pathway [GO:0009873]; positive regulation of DNA-templated transcription [GO:0045893]; regulation of timing of transition from vegetative to reproductive phase [GO:0048510]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	Q70II3	ERF110	Ethylene-responsive transcription factor ERF110		10.1111/tpj.13415
7	Vitvi013384	2016_EDP1	GO:0003677; GO:0003700; GO:0005634; GO:0006952; GO:0006970; GO:0009409; GO:0009414; GO:0009611; GO:0009651; GO:0009658; GO:0009737; GO:0009751; GO:0009753; GO:0009873; GO:0034605; GO:0045893	cellular response to heat [GO:0034605]; chloroplast organization [GO:0009658]; defense response [GO:0006952]; ethylene-activated signaling pathway [GO:0009873]; positive regulation of DNA-templated transcription [GO:0045893]; response to abscisic acid [GO:0009737]; response to cold [GO:0009409]; response to jasmonic acid [GO:0009753]; response to osmotic stress [GO:0006970]; response to salicylic acid [GO:0009751]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]; response to	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	Q7G1L2	RAP2-6	Ethylene-responsive transcription factor RAP2-6 (Protein RELATED TO APETALA2 6)		10.1016/j.gene.2010.02.011
7	Vitvi013356	2016_EDP1	GO:0004516; GO:0009435; GO:0016757; GO:0046872	NAD biosynthetic process [GO:0009435]		glycosyltransferase activity [GO:0016757]; metal ion binding [GO:0046872]; nicotinate phosphoribosyltransferase activity	Q84WV8	NAPRT2	Nicotinate phosphoribosyltransferase 2 (EC 6.3.4.21)		
7	Vitvi013380	2016_EDP1	GO:0005737; GO:0005739; GO:0005829; GO:0005886; GO:0009507; GO:0009535; GO:0009570; GO:0009941; GO:0010363; GO:0015996; GO:0043067; GO:0051743; GO:0098542	chlorophyll catabolic process [GO:0015996]; defense response to other organism [GO:0098542]; regulation of plant-type hypersensitive response [GO:0010363]; regulation of programmed cell death [GO:0043067]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; chloroplast thylakoid membrane [GO:0009535]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	red chlorophyll catabolite reductase activity [GO:0051743]	Q8LDU4	RCCR	Red chlorophyll catabolite reductase, chloroplastic (AtRCCR) (RCC reductase) (EC 1.3.7.12) (Accelerated cell death protein 2)		
7	Vitvi013409	2016_EDP1	GO:0000776; GO:0005634; GO:0005654; GO:0005737; GO:0005793; GO:0005794; GO:0005829; GO:0006888; GO:0007030; GO:0030008; GO:0048208; GO:0051310; GO:0090234; GO:0099022; GO:1905342; GO:1990072	COPII vesicle coating [GO:0048208]; endoplasmic reticulum to Golgi vesicle-mediated transport [GO:0006888]; Golgi organization [GO:0007030]; metaphase chromosome alignment [GO:0051310]; positive regulation of protein localization to kinetochore [GO:1905342]; regulation of kinetochore assembly [GO:0090234]; vesicle tethering [GO:0099022]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; endoplasmic reticulum-Golgi intermediate compartment [GO:0005793]; Golgi apparatus [GO:0005794]; kinetochore [GO:0000776]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; TRAPP complex [GO:0030008]; TRAPPII protein complex		Q8WVT3	TRAPPC12	Trafficking protein particle complex subunit 12 (Tetratricopeptide repeat protein 15) (TPR repeat protein 15) (TTC-15) (Trafficking of membranes and mitosis)		
7	Vitvi013430	2016_EDP1	GO:0000993; GO:0001111; GO:0005634; GO:0005654; GO:0008284; GO:0010564; GO:0031124; GO:0042802; GO:0045944; GO:0097550	mRNA 3'-end processing [GO:0031124]; positive regulation of cell population proliferation [GO:0008284]; positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of cell cycle process [GO:0010564]; RNA polymerase II promoter clearance	nucleoplasm [GO:0005654]; nucleus [GO:0005634]; transcription preinitiation complex [GO:0097550]	identical protein binding [GO:0042802]; RNA polymerase II C-terminal domain binding [GO:0099122]; RNA polymerase II complex binding [GO:0000993]	Q9CSU0	Rprd1b	Regulation of nuclear pre-mRNA domain-containing protein 1B (Cell cycle-related and expression-elevated protein in tumor)		
7	Vitvi013332	2016_EDP1	GO:0006952; GO:0009617; GO:0009697; GO:0009753; GO:0016746; GO:1900150; GO:1900424	defense response [GO:0006952]; regulation of defense response to bacterium [GO:1900424]; regulation of defense response to fungus [GO:1900150]; response to bacterium [GO:0009617]; response to jasmonic acid [GO:0009753]; salicylic acid biosynthetic process [GO:0009697]		acyltransferase activity [GO:0016746]	Q9FH97	EPS1	Protein ENHANCED PSEUDOMONAS SUSCEPTIBILITY 1 (EC 2.3.1.-)		
7	Vitvi013343	2016_EDP1					Q9FH99		F-box protein At5g67140		
7	Vitvi013364	2016_EDP1	GO:0005179; GO:0007267; GO:0019722; GO:0048046	calcium-mediated signaling [GO:0019722]; cell-cell signaling [GO:0007267]	apoplast [GO:0048046]	hormone activity [GO:0005179]	Q9FHA6	RALFL34	Protein RALF-like 34		
7	Vitvi013365	2016_EDP1	GO:0003700; GO:0005634; GO:0006355; GO:0009266; GO:0010468; GO:0010500; GO:0043565; GO:0045893; GO:0046983; GO:0048462; GO:0048467; GO:2000012	carpel formation [GO:0048462]; gynoecium development [GO:0048467]; positive regulation of DNA-templated transcription [GO:0045893]; regulation of auxin polar transport [GO:2000012]; regulation of DNA-templated transcription [GO:0006355]; regulation of gene expression [GO:0010468]; response to temperature stimulus [GO:0009266]; transmitting tissue development	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]; sequence-specific DNA binding [GO:0043565]	Q9FHA7	HEC1	Transcription factor HEC1 (Basic helix-loop-helix protein 88) (AtbHLH88) (bHLH 88) (Protein HECATE 1) (Transcription factor EN 118) (bHLH transcription factor bHLH088)		
7	Vitvi013396	2016_EDP1	GO:0003723; GO:0009451	RNA modification [GO:0009451]		RNA binding [GO:0003723]	Q9FLZ9	PCMP-E16	Pentatricopeptide repeat-containing protein At5g39350		
7	Vitvi013354	2016_EDP1	GO:0016567; GO:0046872; GO:0061630	protein ubiquitination [GO:0016567]		metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]	Q9FMM4	RHG1A	Probable E3 ubiquitin-protein ligase RHG1A (EC 2.3.2.27) (RING-H2 finger G1a) (RING-H2 zinc finger protein RHG1a) (RING-type E3 ubiquitin transferase RHG1A)		
7	Vitvi013355	2016_EDP1	GO:0000976; GO:0003700; GO:0005634; GO:0007623; GO:0009409; GO:0010114; GO:0010154; GO:0010187; GO:0042807; GO:0046983; GO:0004239; GO:0005739;	carpel development [GO:0048440]; circadian rhythm [GO:0007623]; fruit development [GO:0010154]; negative regulation of seed germination [GO:0010187]; response to cold [GO:0009409]; response to red light [GO:0010114]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; identical protein binding [GO:0042802]; protein dimerization activity [GO:0046983]; transcription cis-regulatory region binding [GO:0000976];	Q9FUA4	SPT	Transcription factor SPATULA (Basic helix-loop-helix protein 24) (AtbHLH24) (bHLH 24) (Transcription factor EN 99) (bHLH transcription factor bHLH024)		
7	Vitvi013394	2016_EDP1	GO:0006508; GO:0009507; GO:0031365; GO:0046872; GO:0070006	N-terminal protein amino acid modification [GO:0031365]; proteolysis [GO:0006508]	chloroplast [GO:0009507]; mitochondrion [GO:0005739]	initiator methionyl aminopeptidase activity [GO:0004239]; metal ion binding [GO:0046872]; metalloaminopeptidase activity	Q9FV50	MAP1D	Methionine aminopeptidase 1D, chloroplastic/mitochondrial (MAP 1D) (MetAP 1D) (EC 3.4.11.18) (Peptidase M 1D)		
7	Vitvi013428	2016_EDP1	GO:0003676; GO:0005634; GO:0005654; GO:0005730; GO:0005829; GO:0005886; GO:0006397; GO:0006915; GO:0008380; GO:0016607; GO:0030218; GO:0030263;	apoptotic chromosome condensation [GO:0030263]; apoptotic process [GO:0006915]; erythrocyte differentiation [GO:0030218]; mRNA processing [GO:0006397]; negative regulation of mRNA splicing, via spliceosome [GO:0048025]; positive regulation of apoptotic process [GO:0043065]; positive regulation of monocyte differentiation [GO:0045657];	ASAP complex [GO:0061574]; cytosol [GO:0005829]; nuclear speck [GO:0016607]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886];	nucleic acid binding [GO:0003676]	Q9JIX8	Acin1	Apoptotic chromatin condensation inducer in the nucleus (Acinus)		10.1038/43678; 10.1371/journal.pbio.1000112
7	Vitvi013424	2016_EDP1	GO:0004190; GO:0005886; GO:0006508; GO:0098552	proteolysis [GO:0006508]	plasma membrane [GO:0005886]; side of membrane [GO:0098552]	aspartic-type endopeptidase activity [GO:0004190]	Q9LX20		Aspartic proteinase-like protein 1 (EC 3.4.23.-)		
7	Vitvi013422	2016_EDP1	GO:0003755; GO:0005886; GO:0009507; GO:0009535; GO:0009543; GO:0009579		chloroplast [GO:0009507]; chloroplast thylakoid lumen [GO:0009543]; chloroplast thylakoid membrane [GO:0009535]; plasma membrane [GO:0005886]; thylakoid [GO:0009579]	peptidyl-prolyl cis-trans isomerase activity [GO:0003755]	Q9SCY3	PNSL4	Photosynthetic NDH subunit of lumenal location 4, chloroplastic (FK506-binding protein 16-2) (AtFKBP16-2) (Immunophilin FKBP16-2) (Peptidyl-prolyl cis-trans isomerase FKBP16-2) (PPIase FKBP16-2)		
7	Vitvi013328	2016_EDP1	GO:0016746			acyltransferase activity [GO:0016746]	Q9SND9		Uncharacterized acetyltransferase At3g50280 (EC 2.3.1.-)		
7	Vitvi013404	2016_EDP1	GO:0004512; GO:0005634; GO:0005829; GO:0006021; GO:0008654	inositol biosynthetic process [GO:0006021]; phospholipid biosynthetic process [GO:0008654]	cytosol [GO:0005829]; nucleus [GO:0005634]	inositol-3-phosphate synthase activity [GO:0004512]	Q9SSV4	INPS1	Inositol-3-phosphate synthase (MIP synthase) (EC 5.5.1.4) (Myo-inositol 1-phosphate synthase) (IPS) (MI-1-P synthase)		
7	Vitvi013607	2016_BeS2	GO:0015095; GO:0016020		membrane [GO:0016020]	magnesium ion transmembrane transporter activity [GO:0015095]	A2WY50	MRS2-F	Magnesium transporter MRS2-F		
7	Vitvi013553	2016_BeS2	GO:0005313; GO:0015180; GO:0015185; GO:0015189; GO:0015812; GO:0016020	gamma-aminobutyric acid transport [GO:0015812]	membrane [GO:0016020]	gamma-aminobutyric acid transmembrane transporter activity [GO:0015185]; L-alanine transmembrane transporter activity [GO:0015180]; L-glutamate transmembrane transporter activity [GO:0005313]; L-lysine transmembrane transporter activity	B9EXZ6	BAT1	Amino-acid permease BAT1 homolog		
7	Vitvi013564	2016_BeS2	GO:0003677; GO:0003713; GO:0005634; GO:0060261	positive regulation of transcription initiation by RNA polymerase II [GO:0060261]	nucleus [GO:0005634]	DNA binding [GO:0003677]; transcription coactivator activity	O65154	KIWI	RNA polymerase II transcriptional coactivator KIWI		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
7	Vitvi013563	2016_BeS2	GO:0000325; GO:0001735; GO:0005764; GO:0009738; GO:0030327; GO:0030328; GO:0045338; GO:0102149	abscisic acid-activated signaling pathway [GO:0009738]; farnesyl diphosphate metabolic process [GO:0045338]; prenylated protein catabolic process [GO:0030327]; prenylcysteine catabolic process [GO:0030328]	lysosome [GO:0005764]; plant-type vacuole [GO:0000325]	farnesylcysteine lyase activity [GO:0102149]; prenylcysteine oxidase activity [GO:0001735]	P57681	FCLY	Farnesylcysteine lyase (EC 1.8.3.6)		
7	Vitvi013580	2016_BeS2	GO:0004190; GO:0006508	proteolysis [GO:0006508]		aspartic-type endopeptidase activity [GO:0004190]	Q0IU52	ASP1	Aspartic proteinase Asp1 (OSAP1) (OsAsp1) (EC 3.4.23.-) (Nucellin-like protein)		
7	Vitvi013591	2016_BeS2	GO:0004674; GO:0004693; GO:0005524; GO:0005634; GO:0008353; GO:0016310; GO:0016592; GO:0106310	phosphorylation [GO:0016310]	mediator complex [GO:0016592]; nucleus [GO:0005634]	ATP binding [GO:0005524]; cyclin-dependent protein serine/threonine kinase activity [GO:0004693]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; RNA polymerase II CTD heptapeptide repeat kinase activity [GO:0008353]	Q336M2	CDKE-1	Cyclin-dependent kinase E-1 (CDKE;1) (EC 2.7.11.22) (EC 2.7.11.23)		
7	Vitvi013562	2016_BeS2	GO:0004565; GO:0005773; GO:0005975; GO:0030246;	carbohydrate metabolic process [GO:0005975]	apoplast [GO:0048046]; vacuole [GO:0005773]	beta-galactosidase activity [GO:0004565]; carbohydrate binding	Q5N8X6		Beta-galactosidase 3 (Lactase 3) (EC 3.2.1.23)		
7	Vitvi013579	2016_BeS2	GO:0005634; GO:0009409; GO:0043565; GO:0045893; GO:0048364; GO:1900150; GO:1901002; GO:1902584	positive regulation of DNA-templated transcription [GO:0045893]; positive regulation of response to salt stress [GO:1901002]; positive regulation of response to water deprivation [GO:1902584]; regulation of defense response to fungus [GO:1900150]; response to cold [GO:0009409]; root development [GO:0048364]	nucleus [GO:0005634]	sequence-specific DNA binding [GO:0043565]	Q7F2L3	NAC048	NAC domain-containing protein 48 (ONAC048) (OsNAC6) (Protein STRESS-RESPONSIVE NAC 2)		
7	Vitvi013590	2016_BeS2	GO:0006351; GO:0043565	DNA-templated transcription [GO:0006351]		sequence-specific DNA binding [GO:0043565]	Q84JC2	DOGL4	Protein DOG1-like 4		
7	Vitvi013593	2016_BeS2	GO:0003955; GO:0005739; GO:0005743; GO:0009507; GO:0010287; GO:0016491; GO:0019646; GO:0042372; GO:0050136; GO:0071482	aerobic electron transport chain [GO:0019646]; cellular response to light stimulus [GO:0071482]; phylloquinone biosynthetic process [GO:0042372]	chloroplast [GO:0009507]; mitochondrial inner membrane [GO:0005743]; mitochondrion [GO:0005739]; plastoglobule [GO:0010287]	NAD(P)H dehydrogenase (quinone) activity [GO:0003955]; NADH dehydrogenase (quinone) activity [GO:0050136]; oxidoreductase activity [GO:0016491]	Q8GXR9	NDC1	Alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic/mitochondrial (EC 1.6.5.9) (Alternative NADH dehydrogenase NDC1) (Demethylphylloquinone reductase NDC1) (EC 1.6.5.12) (NADH-ubiquinone reductase		
7	Vitvi013595	2016_BeS2					Q8LLE5	FPP	Filament-like plant protein (LeFPP)		
7	Vitvi013555	2016_BeS2					Q8RWD6		F-box protein At5g39450		
7	Vitvi013554	2016_BeS2	GO:0005509; GO:0009507; GO:0009543; GO:0009579; GO:0009654; GO:0015979; GO:0019898	photosynthesis [GO:0015979]	chloroplast [GO:0009507]; chloroplast thylakoid lumen [GO:0009543]; extrinsic component of membrane [GO:0019898]; photosystem II oxygen evolving complex [GO:0009654]	calcium ion binding [GO:0005509]	Q8VY52	PPD2	PsbP domain-containing protein 2, chloroplastic (PsbP-related thylakoid lumenal protein 3)		
7	Vitvi013583	2016_BeS2	GO:0004028; GO:0004029; GO:0005886; GO:0006081; GO:0009414; GO:0009507; GO:0009536; GO:0009737; GO:0009941; GO:0033721; GO:0043878	cellular aldehyde metabolic process [GO:0006081]; response to abscisic acid [GO:0009737]; response to water deprivation [GO:0009414]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; plasma membrane [GO:0005886]; plastid [GO:0009536]	3-chloroallyl aldehyde dehydrogenase activity [GO:0004028]; aldehyde dehydrogenase (NAD+) activity [GO:0004029]; aldehyde dehydrogenase (NADP+) activity [GO:0033721]; glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non-phosphorylating) activity [GO:0043878]	Q8W033	ALDH3I1	Aldehyde dehydrogenase family 3 member I1, chloroplastic (AtALDH3) (Ath-ALDH3) (EC 1.2.1.3)		
7	Vitvi013565	2016_BeS2	GO:0005634; GO:0005759; GO:0008270; GO:0009873; GO:0016740; GO:0019213; GO:0031348; GO:0034979; GO:0042742; GO:0043970	defense response to bacterium [GO:0042742]; ethylene-activated signaling pathway [GO:0009873]; histone H3-K9 acetylation [GO:0043970]; negative regulation of defense response [GO:0031348]	mitochondrial matrix [GO:0005759]; nucleus [GO:0005634]	deacetylase activity [GO:0019213]; NAD+ binding [GO:0070403]; NAD-dependent protein deacetylase activity [GO:0034979]; transferase activity [GO:0016740]; zinc ion binding	Q94AQ6	SRT2	NAD-dependent protein deacylase SRT2 (EC 2.3.1.286) (Regulatory protein SIR2 homolog 2)		
7	Vitvi013578	2016_BeS2	GO:0004565; GO:0005975; GO:0009536; GO:0009827; GO:0048046; GO:0048354	carbohydrate metabolic process [GO:0005975]; mucilage biosynthetic process involved in seed coat development [GO:0048354]; plant-type cell wall modification	apoplast [GO:0048046]; plastid [GO:0009536]	beta-galactosidase activity [GO:0004565]	Q9FFN4	BGAL6	Beta-galactosidase 6 (Lactase 6) (EC 3.2.1.23)		
7	Vitvi013610	2016_BeS2	GO:0004143; GO:0005524; GO:0005783; GO:0006952; GO:0007205; GO:0009409; GO:0009611; GO:0016310; GO:0046872; GO:0048364	defense response [GO:0006952]; leaf development [GO:0048366]; phosphorylation [GO:0016310]; protein kinase C-activating G protein-coupled receptor signaling pathway [GO:0007205]; response to cold [GO:0009409]; response to wounding [GO:0009611]; root development [GO:0048364]	endoplasmic reticulum [GO:0005783]	ATP binding [GO:0005524]; ATP-dependent diacylglycerol kinase activity [GO:0004143]; metal ion binding [GO:0046872]	Q9FFN7	DGK2	Diacylglycerol kinase 2 (AtDGK2) (DAG kinase 2) (EC 2.7.1.107) (Diglyceride kinase 2) (DGK 2)		
7	Vitvi013599	2016_BeS2	GO:0009555; GO:0009567	double fertilization forming a zygote and endosperm [GO:0009567]; pollen development [GO:0009555]			Q9FFP2	KPL	Protein KOKOPELLI		
7	Vitvi013552	2016_BeS2	GO:0001666; GO:0002213; GO:0005634; GO:0005737; GO:0005829; GO:0009617; GO:0009625; GO:0009626; GO:0009627; GO:0009751; GO:0009862; GO:0009873; GO:0010105; GO:0010150; GO:0010225; GO:0010310; GO:0010618; GO:0016042; GO:0016298; GO:0016740; GO:0031348; GO:0042742; GO:0050829; GO:0051707; GO:0060866; GO:0071327; GO:0080142; GO:0080151; GO:0106093; GO:1900367; GO:1900426; GO:1901183; GO:2000022; GO:2000031	aerenchyma formation [GO:0001618]; cellular response to trehalose stimulus [GO:0071327]; defense response to bacterium [GO:0042742]; defense response to Gram-negative bacterium [GO:0050829]; defense response to insect [GO:0002213]; ethylene-activated signaling pathway [GO:0009873]; leaf abscission [GO:0060866]; leaf senescence [GO:0010150]; lipid catabolic process [GO:0016042]; negative regulation of defense response [GO:0031348]; negative regulation of ethylene-activated signaling pathway [GO:0010105]; plant-type hypersensitive response [GO:0009626]; positive regulation of camalexin biosynthetic process [GO:1901183]; positive regulation of defense response to bacterium [GO:1900426]; positive regulation of defense response to insect [GO:1900367]; positive regulation of salicylic acid mediated signaling pathway [GO:0080151]; regulation of hydrogen peroxide metabolic process [GO:0010310]; regulation of jasmonic acid mediated signaling pathway [GO:2000022]; regulation of salicylic acid biosynthetic process [GO:0080142]; regulation of salicylic acid mediated signaling pathway [GO:2000031]; response to bacterium [GO:0009617]; response to hypoxia [GO:0001666]; response to insect [GO:0009625]; response to other organism [GO:0051707]; response to salicylic acid [GO:0009751]; response to UV-C [GO:0010225]; systemic acquired	cytoplasm [GO:0005737]; cytosol [GO:0005829]; EDS1 disease-resistance complex [GO:0106093]; nucleus [GO:0005634]	lipase activity [GO:0016298]; transferase activity [GO:0016740]	Q9S745	PAD4	Lipase-like PAD4 (EC 2.3.1.-) (Protein ENHANCED DISEASE SUSCEPTIBILITY 9) (Protein PHYTOALEXIN DEFICIENT 4) (AtPAD4)		
7	Vitvi013571	2016_BeS2	GO:0005524; GO:0016020; GO:0016887; GO:0140359		membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9SIT6	ABCG5	ABC transporter G family member 5 (ABC transporter ABCG.5) (AtABCG5) (White-brown complex homolog protein 5) (AtWBC5)		
7	Vitvi013601	2016_BeS2	GO:0009507		chloroplast [GO:0009507]		Q9STN5		Uncharacterized protein At4g08330.		
7	Vitvi013545	2016_BeS2	GO:0005783; GO:0005794; GO:0005829; GO:0005886; GO:0009504; GO:0031410; GO:0045806; GO:0045926; GO:0072583; GO:1900186	clathrin-dependent endocytosis [GO:0072583]; negative regulation of clathrin-dependent endocytosis [GO:1900186]; negative regulation of endocytosis [GO:0045806]; negative regulation of growth [GO:0045926]	cell plate [GO:0009504]; cytoplasmic vesicle [GO:0031410]; cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]		Q9SU08	AUXI1	Auxilin-related protein 1 (Auxilin-like protein 1)		10.1111/jam.15019

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
7	Vitvi013596	2016_BeS2	GO:0000325; GO:0005783; GO:0005789; GO:0005886; GO:0009617; GO:0071782; GO:0071786; GO:0098554	endoplasmic reticulum tubular network organization [GO:0071786]; response to bacterium [GO:0009617]	cytoplasmic side of endoplasmic reticulum membrane [GO:0098554]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; endoplasmic reticulum tubular network [GO:0071782]; plant-type vacuole [GO:0000325]; plasma membrane [GO:0005886]		Q9SUR3	RTNLB1	Reticulon-like protein B1 (AtRTNLB1) (VirB2-interacting protein 1)		
7	Vitvi013589	2016_BeS2	GO:0003756; GO:0005788		endoplasmic reticulum lumen [GO:0005788]	protein disulfide isomerase activity [GO:0003756]	Q9XF61	PDI	Protein disulfide-isomerase (PDI) (EC 5.3.4.1)		
8	Vitvi014620	2016_WPB1	GO:0005886; GO:0015250; GO:0016020; GO:0032991; GO:0051289; GO:0051290	protein heterotetramerization [GO:0051290]; protein homotetramerization [GO:0051289]	membrane [GO:0016020]; plasma membrane [GO:0005886]; protein-containing complex [GO:0032991]	water channel activity [GO:0015250]	Q84RL7	PIP2-1	Aquaporin PIP2-1 (Plasma membrane intrinsic protein 2-1) (ZmPIP2-1) (ZmPIP2;1)		
8	Vitvi014623	2016_WPB1	GO:0004672; GO:0004674; GO:0005524; GO:0016020; GO:0016310; GO:0042803; GO:0106310	phosphorylation [GO:0016310]	membrane [GO:0016020]	ATP binding [GO:0005524]; protein homodimerization activity [GO:0042803]; protein kinase activity [GO:0004672]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity	Q9S7D9	CCR1	Serine/threonine-protein kinase-like protein CCR1 (EC 2.7.11.1) (Protein CRINKLY 4 RELATED 1) (AtCRR1)		
8	Vitvi014621	2016_WPB1	GO:0016471; GO:0046961		vacuolar proton-transporting V-type ATPase complex [GO:0016471]	proton-transporting ATPase activity, rotational mechanism [GO:0046961]	Q9SP55	VATG	V-type proton ATPase subunit G (V-ATPase subunit G) (Vacuolar proton pump subunit G)		
8	Vitvi015163	2016_BeWe4	GO:0003677; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	A2WZI4	DREB1F	Dehydration-responsive element-binding protein 1F (Protein DREB1F) (Protein C-repeat-binding factor 2) (rCBF2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015209	2016_BeWe4	GO:0000287; GO:0004743; GO:0005524; GO:0005829; GO:0016301; GO:0016310; GO:0030955	phosphorylation [GO:0016310]	cytosol [GO:0005829]	ATP binding [GO:0005524]; kinase activity [GO:0016301]; magnesium ion binding [GO:0000287]; potassium ion binding [GO:0030955]; pyruvate kinase activity [GO:0004743]	B8BJ39		Pyruvate kinase 1, cytosolic (OsPK1) (EC 2.7.1.40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015103	2016_BeWe4	GO:0004089; GO:0005783; GO:0008270; GO:0009570		chloroplast stroma [GO:0009570]; endoplasmic reticulum [GO:0005783]	carbonate dehydratase activity [GO:0004089]; zinc ion binding [GO:0008270]	O04846	ACA1	Alpha carbonic anhydrase 1, chloroplastic (AtaCA1) (AtalphaCA1) (EC 4.2.1.1) (Alpha carbonate dehydratase 1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015206	2016_BeWe4	GO:0005737; GO:0009734	auxin-activated signaling pathway [GO:0009734]	cytoplasm [GO:0005737]		O64538	SAUR40	Auxin-responsive protein SAUR40 (Protein SMALL AUXIN UP RNA 40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015116	2016_BeWe4	GO:0005634; GO:0005737; GO:0016226; GO:0097361	iron-sulfur cluster assembly [GO:0016226]	CIA complex [GO:0097361]; cytoplasm [GO:0005737]; nucleus [GO:0005634]		O80990	CIA1	Protein CIA1 (Cytosolic iron-sulfur protein assembly 1) (Protein EMBRYO DEFECTIVE 1345)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015119	2016_BeWe4	GO:0003924; GO:0005525; GO:0005783; GO:0009507; GO:0009534; GO:0009535; GO:0009570; GO:0009739; GO:0010020; GO:0043621; GO:0070938	chloroplast fission [GO:0010020]; response to gibberellin [GO:0009739]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; chloroplast thylakoid [GO:0009534]; chloroplast thylakoid membrane [GO:0009535]; contractile ring [GO:0070938]; endoplasmic reticulum [GO:0005783]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; protein self-association [GO:0043621]	O82533	FTSZ2-1	Cell division protein FtsZ homolog 2-1, chloroplastic (AtFtsZ2-1) (Plastid division protein FTSZ2-1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015108	2016_BeWe4	GO:0000105; GO:0003949; GO:0009507	histidine biosynthetic process [GO:0000105]	chloroplast [GO:0009507]	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase activity [GO:0003949]	O82782	HISN3	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic (EC 5.3.1.16) (5-proFAR isomerase) (BBM II isomerase) (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase) (Protein ALBINO AND PALE GREEN 10) (Protein	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015167	2016_BeWe4	GO:0004332; GO:0005737; GO:0005829; GO:0006094; GO:0006096; GO:0030388;	fructose 1,6-bisphosphate metabolic process [GO:0030388]; gluconeogenesis [GO:0006094]; glycolytic process [GO:0006096]; root development [GO:0048364]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	fructose-bisphosphate aldolase activity [GO:0004332]	P17784	FBA1	Fructose-bisphosphate aldolase 1, cytoplasmic (EC 4.1.2.13) (Cytoplasmic aldolase) (cALD) (Gravity-specific protein GSC 233)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015195	2016_BeWe4	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	P37122	CYP76A2	Cytochrome P450 76A2 (EC 1.14.-.-) (CYPLXXVIA2) (Cytochrome P-450EG7)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015115	2016_BeWe4	GO:0005750; GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c [GO:0006122]	mitochondrial respiratory chain complex III [GO:0005750]		P46270		Cytochrome b-c1 complex subunit 9 (Complex III subunit 9) (Complex III subunit X) (Ubiquinol-cytochrome c reductase complex 8.0 kDa protein)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015125	2016_BeWe4	GO:0003712; GO:0005634; GO:0005737; GO:0005773; GO:0005886; GO:0006623; GO:0009744; GO:0009908;	cell differentiation [GO:0030154]; flower development [GO:0009908]; meristem determinacy [GO:0010022]; negative regulation of flower development [GO:0009910]; protein targeting to vacuole [GO:0006623]; response to	cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; vacuole [GO:0005773]; vesicle [GO:0031982]	transcription coregulator activity [GO:0003712]	P93003	TFL1	Protein TERMINAL FLOWER 1	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015176	2016_BeWe4	GO:0001666; GO:0004674; GO:0004712; GO:0005524; GO:0005789; GO:0009686; GO:0009723; GO:0009744; GO:0009750; GO:0009873; GO:0010105; GO:0010182; GO:0046777; GO:0048510; GO:0106310; GO:2000035; GO:2000069	ethylene-activated signaling pathway [GO:0009873]; gibberellin biosynthetic process [GO:0009686]; negative regulation of ethylene-activated signaling pathway [GO:0010105]; protein autophosphorylation [GO:0046777]; regulation of post-embryonic root development [GO:2000069]; regulation of stem cell division [GO:2000035]; regulation of timing of transition from vegetative to reproductive phase [GO:0048510]; response to ethylene [GO:0009723]; response to fructose [GO:0009750]; response to hypoxia [GO:0001666]; response to sucrose	endoplasmic reticulum membrane [GO:0005789]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; protein serine/threonine/tyrosine kinase activity [GO:0004712]	Q05609	CTR1	Serine/threonine-protein kinase CTR1 (EC 2.7.11.1) (Protein CONSTITUTIVE TRIPLE RESPONSE1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015173	2016_BeWe4	GO:0000993; GO:0003729; GO:0005634; GO:0005737; GO:0006369; GO:0006378; GO:0006397; GO:0009908;	flower development [GO:0009908]; mRNA polyadenylation [GO:0006378]; mRNA processing [GO:0006397]; positive regulation of flower development [GO:0009911]; termination of RNA polymerase II transcription [GO:0063691]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; mRNA binding [GO:0003729]; RNA polymerase II complex binding [GO:0000993]	Q0WPF2	PCFS4	Polyadenylation and cleavage factor homolog 4	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015158	2016_BeWe4	GO:0003844; GO:0004553; GO:0009501; GO:0009507; GO:0009793; GO:0019252; GO:0043169; GO:0102752	embryo development ending in seed dormancy [GO:0009793]; starch biosynthetic process [GO:0019252]	amyloplast [GO:0009501]; chloroplast [GO:0009507]	1,4-alpha-glucan branching enzyme activity [GO:0003844]; 1,4-alpha-glucan branching enzyme activity (using a glucosylated glycogenin as primer for glycogen synthesis) [GO:0102752]; cation binding [GO:0043169]; hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]	Q41058	SBEI	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic (EC 2.4.1.18) (Starch branching enzyme I)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015141	2016_BeWe4	GO:0005737; GO:0016651; GO:0016656; GO:0050660; GO:0098869	cellular oxidant detoxification [GO:0098869]	cytoplasm [GO:0005737]	flavin adenine dinucleotide binding [GO:0050660]; monodehydroascorbate reductase (NADH) activity [GO:0016656]; oxidoreductase activity, acting on NAD(P)H [GO:0016651]	Q43497	AFRR	Monodehydroascorbate reductase (MDAR) (EC 1.6.5.4) (Ascorbate free radical reductase) (AFR reductase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015128	2016_BeWe4					Q56WL5	ZPR4	Protein LITTLE ZIPPER 4	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015127	2016_BeWe4	GO:0004175; GO:0004222; GO:0005783; GO:0005789; GO:0016485; GO:0071586; GO:0080120	CAAX-box protein maturation [GO:0080120]; CAAX-box protein processing [GO:0071586]; protein processing [GO:0016485]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]	endopeptidase activity [GO:0004175]; metalloendopeptidase activity [GO:0004222]	Q8GW19	FACE2	CAAX prenyl protease 2 (EC 3.4.-.-) (Farnesylated proteins-converting enzyme 2) (AtFACE-2) (Prenyl protein-specific endoprotease 2) (Protein RAS-CONVERTING ENZYME 1) (AtRCE1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015110	2016_BeWe4	GO:0009536; GO:0009941; GO:0031969		chloroplast envelope [GO:0009941]; chloroplast membrane [GO:0031969]; plastid [GO:0009536]		Q8GW20		Uncharacterized protein At5g03900, chloroplastic	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015175	2016_BeWe4	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0009408; GO:0043565	regulation of DNA-templated transcription [GO:0006355]; response to heat [GO:0009408]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	Q8GYY1	HSFA3	Heat stress transcription factor A-3 (AtHsfA3) (AtHsf-17)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015136	2016_BeWe4	GO:0016020; GO:0022857		membrane [GO:0016020]	transmembrane transporter activity [GO:0022857]	Q8IXU6	SLC35F2	Solute carrier family 35 member F2	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015120	2016_BeWe4	GO:0005737; GO:0005739; GO:0016226; GO:0046872; GO:0051537; GO:0097428	iron-sulfur cluster assembly [GO:0016226]; protein maturation by iron-sulfur cluster transfer [GO:0097428]	cytoplasm [GO:0005737]; mitochondrion [GO:0005739]	2 iron, 2 sulfur cluster binding [GO:0051537]; metal ion binding [GO:0046872]	Q8LBM4		Iron-sulfur assembly protein IscA-like 1, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015113	2016_BeWe4	GO:0005739; GO:0016226; GO:0046872; GO:0051536	iron-sulfur cluster assembly [GO:0016226]	mitochondrion [GO:0005739]	iron-sulfur cluster binding [GO:0051536]; metal ion binding [GO:0051539]; 4 iron, 4 sulfur cluster binding [GO:0051539]; DNA binding [GO:0003677]; DNA demethylase activity [GO:0035514]; DNA N-glycosylase activity [GO:0019104]; DNA-(apurinic or apyrimidinic site) endonuclease activity [GO:0003906]; metal ion binding [GO:0046872]; SUMO binding [GO:0032183]	Q8LCY2		Iron-sulfur assembly protein IscA-like 2, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015178	2016_BeWe4	GO:0003677; GO:0003906; GO:0005634; GO:0006284; GO:0006306; GO:0006349; GO:0009793; GO:0019104; GO:0032183; GO:0035514; GO:0043078; GO:0046872; GO:0051539; GO:0080111	base-excision repair [GO:0006284]; DNA demethylation [GO:0080111]; DNA methylation [GO:0006306]; embryo development ending in seed dormancy [GO:0009793]; regulation of gene expression by genomic imprinting [GO:0006349]	nucleus [GO:0005634]; polar nucleus [GO:0043078]		Q8LK56	DME	Transcriptional activator DEMETER (EC 3.2.2.-) (DNA glycosylase-related protein DME)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015132	2016_BeWe4	GO:0003993; GO:0005576; GO:0046872		extracellular region [GO:0005576]	acid phosphatase activity [GO:0003993]; metal ion binding [GO:0046872]	Q8S340	PAP22	Purple acid phosphatase 22 (EC 3.1.3.2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015139	2016_BeWe4	GO:0016567; GO:0019005; GO:0031146	protein ubiquitination [GO:0016567]; SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	SCF ubiquitin ligase complex [GO:0019005]		Q8S8F2	FBL11	BTB/POZ domain-containing protein FBL11	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015205	2016_BeWe4	GO:0005739; GO:0009245; GO:0036104; GO:0043842	Kdo2-lipid A biosynthetic process [GO:0036104]; lipid A biosynthetic process [GO:0009245]	mitochondrion [GO:0005739]	Kdo transferase activity [GO:0043842]	Q8VZA5	KDTA	Probable 3-deoxy-D-manno-octulosonic acid transferase, mitochondrial (AtKdtA) (Kdo transferase A) (EC 2.4.99.12) (EC 2.4.99.13) (Bifunctional Kdo transferase) (Kdo-lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase) (Lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015114	2016_BeWe4	GO:0003723; GO:0003735; GO:0005576; GO:0006412; GO:0009506; GO:0022625; GO:0022626; GO:0042788	translation [GO:0006412]	cytosolic large ribosomal subunit [GO:0022625]; cytosolic ribosome [GO:0022626]; extracellular region [GO:0005576]; plasmodesma [GO:0009506]; polysomal ribosome [GO:0042788]	RNA binding [GO:0003723]; structural constituent of ribosome [GO:0003735]	Q8VZB9	RPL10AA	Large ribosomal subunit protein uL1z (60S ribosomal protein L10a-1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015185	2016_BeWe4	GO:0005829; GO:0008379; GO:0009507; GO:0009536; GO:0009570; GO:0009579; GO:0009941; GO:0034599	cellular response to oxidative stress [GO:0034599]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; plastid [GO:0009536]; thylakoid [GO:0009579]	thioredoxin peroxidase activity [GO:0008379]	Q949U7	PRXIIE	Peroxiredoxin-2E, chloroplastic (EC 1.11.1.25) (Glutaredoxin-dependent peroxiredoxin) (Peroxiredoxin IIE) (Thioredoxin peroxidase 2E)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015186	2016_BeWe4	GO:0005739; GO:0008270		mitochondrion [GO:0005739]	zinc ion binding [GO:0008270]	Q9FMQ1		Pentatricopeptide repeat-containing protein At5g12100, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015183	2016_BeWe4	GO:0000398; GO:0003677; GO:0003723; GO:0005634; GO:0005681; GO:0016607; GO:0046872; GO:0048573; GO:0089701	mRNA splicing, via spliceosome [GO:0000398]; photoperiodism, flowering [GO:0048573]	nuclear speck [GO:0016607]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; U2AF complex [GO:0089701]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]; RNA binding [GO:0003723]	Q9FMY5	U2AF35B	Splicing factor U2af small subunit B (U2 auxiliary factor 35 kDa subunit B) (U2 small nuclear ribonucleoprotein auxiliary factor small subunit B) (U2 snRNP auxiliary factor small subunit B) (Zinc finger CCCH domain-containing protein 60) (AtC3H60)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015179	2016_BeWe4	GO:0016020; GO:0016126; GO:0050613; GO:0050661	sterol biosynthetic process [GO:0016126]	membrane [GO:0016020]	delta14-sterol reductase activity [GO:0050613]; NADP binding [GO:0050661]	Q9LDR4	FK	Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase) (Protein FACKEL) (Sterol C14-reductase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015184	2016_BeWe4	GO:0000015; GO:0000287; GO:0004634; GO:0006096	glycolytic process [GO:0006096]	phosphopyruvate hydratase complex [GO:0000015]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0004634]	Q9LEI9	ENO2	Enolase 2 (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase 2) (2-phosphoglycerate dehydratase 2) (allerxen Hev b 9)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015211	2016_BeWe4	GO:0030246			carbohydrate binding [GO:0030246]	Q9LF92	PP2A15	F-box protein PP2-A15 (Protein PHLOEM PROTEIN 2-LIKE A15) (AtPP2-A15)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015143	2016_BeWe4	GO:0005634; GO:0005737		cytoplasm [GO:0005737]; nucleus [GO:0005634]		Q9LFA4	IQM3	IQ domain-containing protein IQM3 (IQ motif-containing protein 3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015112	2016_BeWe4	GO:0004343; GO:0005783; GO:0005789; GO:0006044; GO:0006048	N-acetylglucosamine metabolic process [GO:0006044]; UDP-N-acetylglucosamine biosynthetic process [GO:0006048]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]	glucosamine 6-phosphate N-acetyltransferase activity [GO:0004343]	Q9LFU9	GNA1	Glucosamine 6-phosphate N-acetyltransferase (EC 2.3.1.4) (Glucose-6-phosphate acetyltransferase 1) (AtGNA1) (Phosphoglucosamine acetylase) (Phosphoglucosamine transacetylase) (Protein LGNFSCENS)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015174	2016_BeWe4	GO:0000027; GO:0000470; GO:0005730; GO:0019843; GO:0032774	maturation of LSU-rRNA [GO:0000470]; ribosomal large subunit assembly [GO:0000027]; RNA biosynthetic process [GO:0032774]	nucleolus [GO:0005730]	rRNA binding [GO:0019843]	Q9LUG5		Ribosome production factor 2 homolog (Brix domain-containing protein 1 homolog) (Ribosome biogenesis protein RPF2 homolog)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015130	2016_BeWe4	GO:0003993; GO:0005576; GO:0046872		extracellular region [GO:0005576]	acid phosphatase activity [GO:0003993]; metal ion binding [GO:0046872]	Q9LXI7	PAP20	Probable purple acid phosphatase 20 (EC 3.1.3.2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015187	2016_BeWe4	GO:0000139; GO:0009294; GO:0009617; GO:0047259; GO:0051753; GO:0071555	cell wall organization [GO:0071555]; DNA-mediated transformation [GO:0009294]; response to bacterium [GO:0009617]	Golgi membrane [GO:0000139]	glucomannan 4-beta-mannosyltransferase activity [GO:0047259]; mannan synthase activity [GO:0051753]	Q9LZR3	CSLA9	Glucomannan 4-beta-mannosyltransferase 9 (EC 2.4.1.32) (Cellulose synthase-like protein A9) (AtCslA9) (Glucomannan synthase) (Mannan synthase 9) (Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015171	2016_BeWe4	GO:0005768; GO:0005794; GO:0005802; GO:0016020; GO:0048544	recognition of pollen [GO:0048544]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; membrane [GO:0016020]; trans-Golgi network		Q9LZR8		PAN domain-containing protein At5g03700	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015166	2016_BeWe4	GO:0000976; GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0009909; GO:0019900; GO:0042803; GO:0046621; GO:0048441; GO:0048442; GO:0048498	establishment of petal orientation [GO:0048498]; negative regulation of organ growth [GO:0046621]; perianth development [GO:0090428]; petal development [GO:0048441]; regulation of DNA-templated transcription [GO:0006355]; regulation of flower development [GO:0009911]; sepal development [GO:0048442]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; kinase binding [GO:0019900]; protein homodimerization activity [GO:0042803]; transcription cis-regulatory region binding [GO:0044212]	Q9LZS0	PTL	Trihelix transcription factor PTL (Trihelix DNA-binding protein PETAL LOSS)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015145	2016_BeWe4	GO:0004252; GO:0005576; GO:0006508	proteolysis [GO:0006508]	extracellular region [GO:0005576]	serine-type endopeptidase activity [GO:0004252]	Q9LZS6	SBT4.15	Subtilisin-like protease SBT4.15 (EC 3.4.21.-) (Subtilase subfamily 4 member 15)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015147	2016_BeWe4	GO:0005576; GO:0016042; GO:0016788	lipid catabolic process [GO:0016042]	extracellular region [GO:0005576]	hydrolase activity, acting on ester bonds [GO:0016788]	Q9LZS7		GDSL esterase/lipase At5g03610 (EC 3.1.1.-) (Extracellular lipase At5g03610)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015118	2016_BeWe4	GO:0003723; GO:0008270; GO:0009451	RNA modification [GO:0009451]		RNA binding [GO:0003723]; zinc ion binding [GO:0008270]	Q9S7F4	PCMP-H36	Putative pentatricopeptide repeat-containing protein At2g01510	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015133	2016_BeWe4	GO:0003677; GO:0008270			DNA binding [GO:0003677]; zinc ion binding [GO:0008270]	Q9SJM6	SAP4	Zinc finger A20 and AN1 domain-containing stress-associated protein 4 (AtSAP4)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015149	2016_BeWe4	GO:0005829; GO:0006152; GO:0006218; GO:0042802; GO:0042803; GO:0045437; GO:0046982; GO:0047622; GO:0047724; GO:0072585	purine nucleoside catabolic process [GO:0006152]; uridine catabolic process [GO:0006218]	cytosol [GO:0005829]	adenosine nucleosidase activity [GO:0047622]; identical protein binding [GO:0042802]; inosine nucleosidase activity [GO:0047724]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; uridine nucleosidase activity [GO:0045437]; xanthosine	Q9SJM7	URH1	Uridine nucleosidase 1 (EC 3.2.2.3) (Adenosine nucleosidase) (EC 3.2.2.7) (Inosine nucleosidase) (EC 3.2.2.2) (Nucleoside hydrolase 1) (Uridine ribohydrolase 1) (Xanthosine nucleosidase) (EC 3.2.2.-)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015122	2016_BeWe4	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0009414; GO:0009651; GO:0009737; GO:0009738; GO:0009739; GO:0009845; GO:0010182; GO:0010187; GO:0045893; GO:0048316	abscisic acid-activated signaling pathway [GO:0009738]; negative regulation of seed germination [GO:0010187]; positive regulation of DNA-templated transcription [GO:0045893]; regulation of DNA-templated transcription [GO:0006355]; response to abscisic acid [GO:0009737]; response to gibberellin [GO:0009739]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]; seed development [GO:0048316]; seed germination [GO:0009845]; sugar mediated signaling pathway	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9SJN0	ABI5	Protein ABSCISIC ACID-INSENSITIVE 5 (Dc3 promoter-binding factor 1) (AtDPBF1) (Protein GROWTH-INSENSITIVITY TO ABA 1) (bZIP transcription factor 39) (AtbZIP39)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015165	2016_BeWe4	GO:0003677; GO:0003700; GO:0005634; GO:0009873; GO:0000976; GO:0005524;	defense response to fungus [GO:0050832]; ethylene-activated signaling pathway [GO:0009873]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity	Q9SJR0	ERF024	Ethylene-responsive transcription factor ERF024	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015160	2016_BeWe4	GO:0005634; GO:0006351; GO:0006355; GO:0008285; GO:0009409; GO:0009624; GO:0009739; GO:0048364; GO:0061062	DNA-templated transcription [GO:0006351]; negative regulation of cell population proliferation [GO:0008285]; regulation of DNA-templated transcription [GO:0006355]; regulation of nematode larval development [GO:0061062]; response to cold [GO:0009409]; response to gibberellin [GO:0009739]; response to nematode [GO:0009624]; root	nucleus [GO:0005634]	ATP binding [GO:0005524]; transcription cis-regulatory region binding [GO:0000976]	Q9SJR5	GRF3	Growth-regulating factor 3 (AtGRF3) (Transcription activator GRF3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015155	2016_BeWe4	GO:0004725; GO:0005829; GO:0035335; GO:0046872	peptidyl-tyrosine dephosphorylation [GO:0035335]	cytosol [GO:0005829]	metal ion binding [GO:0046872]; protein tyrosine phosphatase activity [GO:0004725]	Q9SR62	RLPH2	Tyrosine-protein phosphatase RLPH2 (EC 3.1.3.48) (Protein RHIZOBIALE-LIKE PHOSPHATASE 2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015150	2016_BeWe4	GO:0000124; GO:0005669; GO:0006352; GO:0046695; GO:0046982	DNA-templated transcription initiation [GO:0006352]	SAGA complex [GO:0000124]; SLIK (SAGA-like) complex [GO:0046695]; transcription factor TFIID complex [GO:0005669]	protein heterodimerization activity [GO:0046982]	Q9SR71	TAF12	Transcription initiation factor TFIID subunit 12 (TBP-associated factor 12) (AtTAF12)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015123	2016_BeWe4	GO:0030145; GO:0048046		apoplast [GO:0048046]	manganese ion binding [GO:0030145]	Q9SR72		Germin-like protein subfamily 3 member 2	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015163	2016_BV10	GO:0003677; GO:0003700; GO:0005634		nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]	A2WZI4	DREB1F	Dehydration-responsive element-binding protein 1F (Protein DREB1F) (Protein C-repeat-binding factor 2) (rCBF2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015209	2016_BV10	GO:0000287; GO:0004743; GO:0005524; GO:0005829; GO:0016301; GO:0016310; GO:0030955	phosphorylation [GO:0016310]	cytosol [GO:0005829]	ATP binding [GO:0005524]; kinase activity [GO:0016301]; magnesium ion binding [GO:0000287]; potassium ion binding [GO:0030955]; pyruvate kinase activity [GO:0004743]	B8BJ39		Pyruvate kinase 1, cytosolic (OsPK1) (EC 2.7.1.40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015206	2016_BV10	GO:0005737; GO:0009734	auxin-activated signaling pathway [GO:0009734]	cytoplasm [GO:0005737]		O64538	SAUR40	Auxin-responsive protein SAUR40 (Protein SMALL AUXIN UP RNA 40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015167	2016_BV10	GO:0004332; GO:0005737; GO:0005829; GO:0006094; GO:0006096; GO:0030388;	fructose 1,6-bisphosphate metabolic process [GO:0030388]; gluconeogenesis [GO:0006094]; glycolytic process [GO:0006096]; root development [GO:0048364]	cytoplasm [GO:0005737]; cytosol [GO:0005829]	fructose-bisphosphate aldolase activity [GO:0004332]	P17784	FBA1	Fructose-bisphosphate aldolase 1, cytoplasmic (EC 4.1.2.13) (Cytoplasmic aldolase) (cALD) (Gravity-sensitive protein GSC 233)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015195	2016_BV10	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	P37122	CYP76A2	Cytochrome P450 76A2 (EC 1.14.-.-) (CYPLXXVIA2) (Cytochrome P-450EG7)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015176	2016_BV10	GO:0001666; GO:0004674; GO:0004712; GO:0005524; GO:0005789; GO:0009686; GO:0009723; GO:0009744; GO:0009750; GO:0009873; GO:0010105; GO:0010182; GO:0046777; GO:0048510; GO:0106310; GO:2000035; GO:2000069	ethylene-activated signaling pathway [GO:0009873]; gibberellin biosynthetic process [GO:0009686]; negative regulation of ethylene-activated signaling pathway [GO:0010105]; protein autophosphorylation [GO:0046777]; regulation of post-embryonic root development [GO:2000069]; regulation of stem cell division [GO:2000035]; regulation of timing of transition from vegetative to reproductive phase [GO:0048510]; response to ethylene [GO:0009723]; response to fructose [GO:0009750]; response to hypoxia [GO:0001666]; response to oxygen	endoplasmic reticulum membrane [GO:0005789]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; protein serine/threonine/tyrosine kinase activity [GO:0004712]	Q05609	CTR1	Serine/threonine-protein kinase CTR1 (EC 2.7.11.1) (Protein CONSTITUTIVE TRIPLE RESPONSE1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015173	2016_BV10	GO:0000993; GO:0003729; GO:0005634; GO:0005737; GO:0006369; GO:0006378; GO:0006397; GO:0009908;	flower development [GO:0009908]; mRNA polyadenylation [GO:0006378]; mRNA processing [GO:0006397]; positive regulation of flower development [GO:0009911]; termination of RNA polymerase II transcription [GO:0006369]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; mRNA binding [GO:0003729]; RNA polymerase II complex binding [GO:0000993]	Q0WPF2	PCFS4	Polyadenylation and cleavage factor homolog 4	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015158	2016_BV10	GO:0003844; GO:0004553; GO:0009501; GO:0009507; GO:0009793; GO:0019252; GO:0043169; GO:0102752	embryo development ending in seed dormancy [GO:0009793]; starch biosynthetic process [GO:0019252]	amyloplast [GO:0009501]; chloroplast [GO:0009507]	1,4-alpha-glucan branching enzyme activity [GO:0003844]; 1,4-alpha-glucan branching enzyme activity (using a glucosylated glycogenin as primer for glycogen synthesis) [GO:0102752]; cation binding [GO:0043169]; hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]	Q41058	SBEI	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic (EC 2.4.1.18) (Starch branching enzyme I)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015175	2016_BV10	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0009408; GO:0043565	regulation of DNA-templated transcription [GO:0006355]; response to heat [GO:0009408]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	Q8GYY1	HSFA3	Heat stress transcription factor A-3 (AtHsfA3) (AtHsf-17)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015178	2016_BV10	GO:0003677; GO:0003906; GO:0005634; GO:0006284; GO:0006306; GO:0006349; GO:0009793; GO:0019104; GO:0032183; GO:0035514; GO:0043078; GO:0046872; GO:0051539; GO:0080111	base-excision repair [GO:0006284]; DNA demethylation [GO:0080111]; DNA methylation [GO:0006306]; embryo development ending in seed dormancy [GO:0009793]; regulation of gene expression by genomic imprinting [GO:0006349]	nucleus [GO:0005634]; polar nucleus [GO:0043078]	4 iron, 4 sulfur cluster binding [GO:0051539]; DNA binding [GO:0003677]; DNA demethylase activity [GO:0035514]; DNA N-glycosylase activity [GO:0019104]; DNA-(apurinic or apyrimidinic site) endonuclease activity [GO:0003906]; metal ion binding [GO:0046872]; SUMO binding [GO:0032183]	Q8LK56	DME	Transcriptional activator DEMETER (EC 3.2.2.-) (DNA glycosylase-related protein DME)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015205	2016_BV10	GO:0005739; GO:0009245; GO:0036104; GO:0043842	Kdo2-lipid A biosynthetic process [GO:0036104]; lipid A biosynthetic process [GO:0009245]	mitochondrion [GO:0005739]	Kdo transferase activity [GO:0043842]	Q8VZA5	KDTA	Probable 3-deoxy-D-manno-octulosonic acid transferase, mitochondrial (AtKdtA) (Kdo transferase A) (EC 2.4.99.12) (EC 2.4.99.13) (Bifunctional Kdo transferase) (Kdo-lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase) (Lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015185	2016_BV10	GO:0005829; GO:0008379; GO:0009507; GO:0009536; GO:0009570; GO:0009579; GO:0009941; GO:0034599	cellular response to oxidative stress [GO:0034599]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; plastid [GO:0009536]; thylakoid [GO:0009579]	thioredoxin peroxidase activity [GO:0008379]	Q949U7	PRXIIE	Peroxiredoxin-2E, chloroplastic (EC 1.11.1.25) (Glutaredoxin-dependent peroxiredoxin) (Peroxiredoxin IIE) (Thioredoxin peroxidase 2E)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015186	2016_BV10	GO:0005739; GO:0008270		mitochondrion [GO:0005739]	zinc ion binding [GO:0008270]	Q9FMQ1		Pentatricopeptide repeat-containing protein At5g12100, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015183	2016_BV10	GO:0000398; GO:0003677; GO:0003723; GO:0005634; GO:0005681; GO:0016607; GO:0046872; GO:0048573; GO:0089701	mRNA splicing, via spliceosome [GO:0000398]; photoperiodism, flowering [GO:0048573]	nuclear speck [GO:0016607]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; U2AF complex [GO:0089701]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]; RNA binding [GO:0003723]	Q9FMY5	U2AF35B	Splicing factor U2af small subunit B (U2 auxiliary factor 35 kDa subunit B) (U2 small nuclear ribonucleoprotein auxiliary factor small subunit B) (U2 snRNP auxiliary factor small subunit B) (Zinc finger CCCH domain-containing protein 60) (AtC3H60)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015179	2016_BV10	GO:0016020; GO:0016126; GO:0050613; GO:0050661	sterol biosynthetic process [GO:0016126]	membrane [GO:0016020]	delta14-sterol reductase activity [GO:0050613]; NADP binding [GO:0050661]	Q9LDR4	FK	Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase) (Protein FACKEL) (Sterol C14-reductase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015184	2016_BV10	GO:0000015; GO:0000287; GO:0004634; GO:0006096	glycolytic process [GO:0006096]	phosphopyruvate hydratase complex [GO:0000015]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0046341	Q9LEI9	ENO2	Enolase 2 (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase 2) (2-phosphoglycerate dehydratase 2) (allergen Hev b 9)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015174	2016_BV10	GO:0000027; GO:0000470; GO:0005730; GO:0019843; GO:0032774	maturation of LSU-rRNA [GO:0000470]; ribosomal large subunit assembly [GO:0000027]; RNA biosynthetic process [GO:0032774]	nucleolus [GO:0005730]	rRNA binding [GO:0019843]	Q9LUG5		Ribosome production factor 2 homolog (Brix domain-containing protein 1 homolog) (Ribosome biogenesis protein RPF2 homolog)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015187	2016_BV10	GO:0000139; GO:0009294; GO:0009617; GO:0047259; GO:0051753; GO:0071555	cell wall organization [GO:0071555]; DNA-mediated transformation [GO:0009294]; response to bacterium [GO:0009617]	Golgi membrane [GO:0000139]	glucomannan 4-beta-mannosyltransferase activity [GO:0047259]; mannan synthase activity [GO:0051753]	Q9LZR3	CSLA9	Glucomannan 4-beta-mannosyltransferase 9 (EC 2.4.1.32) (Cellulose synthase-like protein A9) (AtCslA9) (Glucomannan synthase) (Mannan synthase 9) (Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015171	2016_BV10	GO:0005768; GO:0005794; GO:0005802; GO:0016020; GO:0048544	recognition of pollen [GO:0048544]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; membrane [GO:0016020]; trans-Golgi network		Q9LZR8		PAN domain-containing protein At5g03700	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015166	2016_BV10	GO:0000976; GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0009909; GO:0019900; GO:0042803; GO:0046621; GO:0048441; GO:0048442; GO:0048498	establishment of petal orientation [GO:0048498]; negative regulation of organ growth [GO:0046621]; perianth development [GO:0090428]; petal development [GO:0048441]; regulation of DNA-templated transcription [GO:0006355]; regulation of flower development [GO:0009909]; sepal development [GO:0048442]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; kinase binding [GO:0019900]; protein homodimerization activity [GO:0042803]; transcription cis-regulatory region binding [GO:0000976]	Q9LZS0	PTL	Trihelix transcription factor PTL (Trihelix DNA-binding protein PETAL LOSS)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015145	2016_BV10	GO:0004252; GO:0005576; GO:0006508	proteolysis [GO:0006508]	extracellular region [GO:0005576]	serine-type endopeptidase activity [GO:0004252]	Q9LZS6	SBT4.15	Subtilisin-like protease SBT4.15 (EC 3.4.21.-) (Subtilase subfamily 4 member 15)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015147	2016_BV10	GO:0005576; GO:0016042; GO:0016788	lipid catabolic process [GO:0016042]	extracellular region [GO:0005576]	hydrolase activity, acting on ester bonds [GO:0016788]	Q9LZS7		GDSL esterase/lipase At5g03610 (EC 3.1.1.-) (Extracellular lipase At5g03610)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015149	2016_BV10	GO:0005829; GO:0006152; GO:0006218; GO:0042802; GO:0042803; GO:0045437; GO:0046982; GO:0047622; GO:0047724; GO:0072585	purine nucleoside catabolic process [GO:0006152]; uridine catabolic process [GO:0006218]	cytosol [GO:0005829]	adenosine nucleosidase activity [GO:0047622]; identical protein binding [GO:0042802]; inosine nucleosidase activity [GO:0047724]; protein heterodimerization activity [GO:0046982]; protein homodimerization activity [GO:0042803]; uridine nucleosidase activity [GO:0045437]; xanthosine	Q9SJM7	URH1	Uridine nucleosidase 1 (EC 3.2.2.3) (Adenosine nucleosidase) (EC 3.2.2.7) (Inosine nucleosidase) (EC 3.2.2.2) (Nucleoside hydrolase 1) (Uridine ribohydrolase 1) (Xanthosine nucleosidase) (EC 3.2.2.-)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015165	2016_BV10	GO:0003677; GO:0003700; GO:0005634; GO:0009873;	defense response to fungus [GO:0050832]; ethylene-activated signaling pathway [GO:0009873]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity	Q9SJR0	ERF024	Ethylene-responsive transcription factor ERF024	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015160	2016_BV10	GO:0000976; GO:0005524; GO:0005634; GO:0006351; GO:0006355; GO:0008285; GO:0009409; GO:0009624; GO:0009739; GO:0048364; GO:0061062	DNA-templated transcription [GO:0006351]; negative regulation of cell population proliferation [GO:0008285]; regulation of DNA-templated transcription [GO:0006355]; regulation of nematode larval development [GO:0061062]; response to cold [GO:0009409]; response to gibberellin [GO:0009739]; response to nematode [GO:0009624]; root	nucleus [GO:0005634]	ATP binding [GO:0005524]; transcription cis-regulatory region binding [GO:0000976]	Q9SJR5	GRF3	Growth-regulating factor 3 (AtGRF3) (Transcription activator GRF3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015155	2016_BV10	GO:0004725; GO:0005829; GO:0035335; GO:0046872	peptidyl-tyrosine dephosphorylation [GO:0035335]	cytosol [GO:0005829]	metal ion binding [GO:0046872]; protein tyrosine phosphatase activity [GO:0004725]	Q9SR62	RLPH2	Tyrosine-protein phosphatase RLPH2 (EC 3.1.3.48) (Protein RHIZOBIALE-LIKE PHOSPHATASE 2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015150	2016_BV10	GO:0000124; GO:0005669; GO:0006352; GO:0046695; GO:0046982	DNA-templated transcription initiation [GO:0006352]	SAGA complex [GO:0000124]; SLIK (SAGA-like) complex [GO:0046695]; transcription factor TFIID complex [GO:0005669]	protein heterodimerization activity [GO:0046982]	Q9SR71	TAF12	Transcription initiation factor TFIID subunit 12 (TBP-associated factor 12) (AtTAF12)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015185	2016_SN4	GO:0005829; GO:0008379; GO:0009507; GO:0009536; GO:0009570; GO:0009579; GO:0009941; GO:0034599	cellular response to oxidative stress [GO:0034599]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; plastid [GO:0009536]; thylakoid [GO:0009579]	thioredoxin peroxidase activity [GO:0008379]	Q949U7	PRXIIE	Peroxiredoxin-2E, chloroplastic (EC 1.11.1.25) (Glutaredoxin-dependent peroxiredoxin) (Peroxiredoxin IIE) (Thioredoxin peroxidase 2E)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015186	2016_SN4	GO:0005739; GO:0008270		mitochondrion [GO:0005739]	zinc ion binding [GO:0008270]	Q9FMQ1		Pentatricopeptide repeat-containing protein At5g12100, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015183	2016_SN4	GO:0000398; GO:0003677; GO:0003723; GO:0005634; GO:0005681; GO:0016607; GO:0046872; GO:0048573; GO:0089701	mRNA splicing, via spliceosome [GO:0000398]; photoperiodism, flowering [GO:0048573]	nuclear speck [GO:0016607]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; U2AF complex [GO:0089701]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]; RNA binding [GO:0003723]	Q9FMY5	U2AF35B	Splicing factor U2af small subunit B (U2 auxiliary factor 35 kDa subunit B) (U2 small nuclear ribonucleoprotein auxiliary factor small subunit B) (U2 snRNP auxiliary factor small subunit B) (Zinc finger CCCH domain-containing protein 60) (AtC3H60)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015179	2016_SN4	GO:0016020; GO:0016126; GO:0050613; GO:0050661	sterol biosynthetic process [GO:0016126]	membrane [GO:0016020]	delta14-sterol reductase activity [GO:0050613]; NADP binding [GO:00506611	Q9LDR4	FK	Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase) (Protein FACKEL) (Sterol C14-reductase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015184	2016_SN4	GO:0000015; GO:0000287; GO:0004634; GO:0006096	glycolytic process [GO:0006096]	phosphopyruvate hydratase complex [GO:0000015]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0046341	Q9LEI9	ENO2	Enolase 2 (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase 2) (2-phosphoglycerate dehydratase 2) (allergen Hev b 9)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015187	2016_SN4	GO:0000139; GO:0009294; GO:0009617; GO:0047259; GO:0051753; GO:0071555	cell wall organization [GO:0071555]; DNA-mediated transformation [GO:0009294]; response to bacterium [GO:0009617]	Golgi membrane [GO:0000139]	glucomannan 4-beta-mannosyltransferase activity [GO:0047259]; mannan synthase activity [GO:0051753]	Q9LZR3	CSLA9	Glucomannan 4-beta-mannosyltransferase 9 (EC 2.4.1.32) (Cellulose synthase-like protein A9) (AtCslA9) (Glucomannan synthase) (Mannan synthase 9) (Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015209	2016_SN5	GO:0000287; GO:0004743; GO:0005524; GO:0005829; GO:0016301; GO:0016310; GO:0030955	phosphorylation [GO:0016310]	cytosol [GO:0005829]	ATP binding [GO:0005524]; kinase activity [GO:0016301]; magnesium ion binding [GO:0000287]; potassium ion binding [GO:0030955]; pyruvate kinase activity [GO:0004743]	B8BJ39		Pyruvate kinase 1, cytosolic (OsPK1) (EC 2.7.1.40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015206	2016_SN5	GO:0005737; GO:0009734	auxin-activated signaling pathway [GO:0009734]	cytoplasm [GO:0005737]		O64538	SAUR40	Auxin-responsive protein SAUR40 (Protein SMALL AUXIN UP RNA 40)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015195	2016_SN5	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	P37122	CYP76A2	Cytochrome P450 76A2 (EC 1.14.-.-) (CYPLXXVIA2) (Cytochrome P-450EG7)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015205	2016_SN5	GO:0005739; GO:0009245; GO:0036104; GO:0043842	Kdo2-lipid A biosynthetic process [GO:0036104]; lipid A biosynthetic process [GO:0009245]	mitochondrion [GO:0005739]	Kdo transferase activity [GO:0043842]	Q8VZA5	KDTA	Probable 3-deoxy-D-manno-octulosonic acid transferase, mitochondrial (AtKdtA) (Kdo transferase A) (EC 2.4.99.12) (EC 2.4.99.13) (Bifunctional Kdo transferase) (Kdo-lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase) (Lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015185	2016_SN5	GO:0005829; GO:0008379; GO:0009507; GO:0009536; GO:0009570; GO:0009579; GO:0009941; GO:0034599	cellular response to oxidative stress [GO:0034599]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; plastid [GO:0009536]; thylakoid [GO:0009579]	thioredoxin peroxidase activity [GO:0008379]	Q949U7	PRXIIE	Peroxiredoxin-2E, chloroplastic (EC 1.11.1.25) (Glutaredoxin-dependent peroxiredoxin) (Peroxiredoxin IIE) (Thioredoxin peroxidase 2E)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015186	2016_SN5	GO:0005739; GO:0008270		mitochondrion [GO:0005739]	zinc ion binding [GO:0008270]	Q9FMQ1		Pentatricopeptide repeat-containing protein At5g12100, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015184	2016_SN5	GO:0000015; GO:0000287; GO:0004634; GO:0006096	glycolytic process [GO:0006096]	phosphopyruvate hydratase complex [GO:0000015]	magnesium ion binding [GO:0000287]; phosphopyruvate hydratase activity [GO:0004634]	Q9LEI9	ENO2	Enolase 2 (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase 2) (2-phosphoglycerate dehydratase 2) (allergen Hev b 9)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015187	2016_SN5	GO:0000139; GO:0009294; GO:0009617; GO:0047259; GO:0051753; GO:0071555	cell wall organization [GO:0071555]; DNA-mediated transformation [GO:0009294]; response to bacterium [GO:0009617]	Golgi membrane [GO:0000139]	glucomannan 4-beta-mannosyltransferase activity [GO:0047259]; mannan synthase activity [GO:0051753]	Q9LZR3	CSLA9	Glucomannan 4-beta-mannosyltransferase 9 (EC 2.4.1.32) (Cellulose synthase-like protein A9) (AtCslA9) (Glucomannan synthase) (Mannan synthase 9) (Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015309	2016_BV11	GO:0004478; GO:0005524; GO:0005737; GO:0006556; GO:0006730; GO:0046872	one-carbon metabolic process [GO:0006730]; S-adenosylmethionine biosynthetic process [GO:0006556]	cytoplasm [GO:0005737]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; methionine adenosyltransferase activity	A7QJG1	METK3	S-adenosylmethionine synthase 3 (AdoMet synthase 3) (EC 2.5.1.6) (Methionine adenosyltransferase 3) (MAT 3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015303	2016_BV11	GO:0000724; GO:0002039; GO:0005634; GO:0005737; GO:0006974; GO:0010212; GO:0016567; GO:0016605; GO:0031297; GO:0031571; GO:0035861; GO:0036297; GO:0046872; GO:0061630	DNA damage response [GO:0006974]; double-strand break repair via homologous recombination [GO:0000724]; interstrand cross-link repair [GO:0036297]; mitotic G1 DNA damage checkpoint signaling [GO:0031571]; protein ubiquitination [GO:0016567]; regulation of DNA damage checkpoint [GO:2000001]; replication fork processing [GO:0031297]; response to ionizing radiation [GO:0010212]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; PML body [GO:0016605]; site of DNA damage [GO:0090734]; site of double-strand break [GO:0035861]	MDM2/MDM4 family protein binding [GO:0097371]; metal ion binding [GO:0046872]; p53 binding [GO:0002039]; ubiquitin protein ligase activity [GO:0061630]	D2HWM5	RFWD3	E3 ubiquitin-protein ligase RFWD3 (EC 2.3.2.27) (RING finger and WD repeat domain-containing protein 3) (RING finger protein 201)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015344	2016_BV11	GO:0003777; GO:0005524; GO:0005874; GO:0007018; GO:0008017	microtubule-based movement [GO:0007018]	microtubule [GO:0005874]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	F4J2K4	KIN7O	Kinesin-like protein KIN-7O	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015311	2016_BV11	GO:0009507; GO:0010581; GO:0019252	regulation of starch biosynthetic process [GO:0010581]; starch biosynthetic process [GO:0019252]	chloroplast [GO:0009507]		F4KFB3	PTST	Protein PTST homolog 3, chloroplastic (PROTEIN TARGETING TO STARCH homolog 3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015374	2016_BV11	GO:0004735; GO:0005737; GO:0009408; GO:0009651; GO:0003676; GO:0003677;	L-proline biosynthetic process [GO:0055129]; response to heat [GO:0009408]; response to salt stress [GO:0009651]	cytoplasm [GO:0005737]	pyrroline-5-carboxylate reductase activity [GO:0004735]	O04016		Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2)		
8	Vitvi015296	2016_BV11	GO:0003729; GO:0005634; GO:0008270; GO:0009409; GO:0009414; GO:0016607;	negative regulation of DNA-templated transcription [GO:0045892]; positive regulation of mRNA splicing, via spliceosome [GO:0048026]; response to cold [GO:0009409]; response to water deprivation [GO:0009414]	nuclear speck [GO:0016607]; nucleus [GO:0005634]	DNA binding [GO:0003677]; mRNA binding [GO:0003729]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	O22703	RZ1B	Glycine-rich RNA-binding protein RZ1B (AtRZ-1a)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015359	2016_BV11	GO:0003723; GO:0005739; GO:0006397; GO:0008270; GO:0016554	cytidine to uridine editing [GO:0016554]; mRNA processing [GO:0006397]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]; zinc ion binding [GO:0008270]	O23266	PCMP-H13	Pentatricopeptide repeat-containing protein At4g14050, mitochondrial (Mitochondrial editing factor 35)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015330	2016_BV11	GO:0003700; GO:0005634; GO:0006351; GO:0043565	DNA-templated transcription [GO:0006351]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	O24160	TGA21	TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015285	2016_BV11	GO:0003924; GO:0005525; GO:0005777; GO:0005886; GO:0015031; GO:0030742; GO:0080115	protein transport [GO:0015031]	peroxisome [GO:0005777]; plasma membrane [GO:0005886]	GTP binding [GO:0005525]; GTP-dependent protein binding [GO:0030742]; GTPase activity [GO:0003924]; myosin XI tail binding	O49841	RABC2A	Ras-related protein RABC2a (AtRABC2a) (Ras-related protein Rab18B) (AtRab18B)		
8	Vitvi015365	2016_BV11	GO:0003723; GO:0005739; GO:0009451	RNA modification [GO:0009451]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]	O64766	PCMP-E15	Pentatricopeptide repeat-containing protein At2g35030, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015350	2016_BV11	GO:0000156; GO:0000160; GO:0005634; GO:0006355; GO:0007623; GO:0009735; GO:0009736	circadian rhythm [GO:0007623]; cytokinin-activated signaling pathway [GO:0009736]; phosphorelay signal transduction system [GO:0000160]; regulation of DNA-templated transcription [GO:0006355]; response to cytokinin	nucleus [GO:0005634]	phosphorelay response regulator activity [GO:0000156]	O80366	ARR9	Two-component response regulator ARR9 (Response reactor 4)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015333	2016_BV11	GO:0000325; GO:0006865; GO:0016020	amino acid transport [GO:0006865]	membrane [GO:0016020]; plant-type vacuole [GO:0003251]		O80668	AVT1A	Amino acid transporter AVT1A (AtAvt1A)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015352	2016_BV11	GO:0004121; GO:0009507; GO:0009570; GO:0019279; GO:0019346; GO:0030170; GO:0047804; GO:0060090	L-methionine biosynthetic process from L-homoserine via cystathionine [GO:0019279]; transsulfuration [GO:0019346]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]	cystathionine beta-lyase activity [GO:0004121]; cysteine-S-conjugate beta-lyase activity [GO:0047804]; molecular adaptor activity [GO:0060090]; pyridoxal phosphate	P53780		Cystathionine beta-lyase, chloroplastic (CBL) (EC 4.4.1.13) (Beta-cystathionase) (Cysteine lyase) (Cysteine-S-conjugate beta-lyase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015337	2016_BV11	GO:0006541; GO:0009570; GO:0016041; GO:0019899; GO:0046872; GO:0051538; GO:0097054	glutamine metabolic process [GO:0006541]; L-glutamate biosynthetic process [GO:0097054]	chloroplast stroma [GO:0009570]	3 iron, 4 sulfur cluster binding [GO:0051538]; enzyme binding [GO:0019899]; glutamate synthase (ferredoxin) activity [GO:0016041]; metal ion binding [GO:0046872]	Q43155	FdGOGAT	Ferredoxin-dependent glutamate synthase, chloroplastic (EC 1.4.7.1) (Fd-GOGAT) (SoFdGOGAT)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015347	2016_BV11	GO:0005773; GO:0005783; GO:0005829; GO:0005886; GO:0009058; GO:0009505; GO:0009506	biosynthetic process [GO:0009058]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; plant-type cell wall [GO:0009505]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]; vacuole [GO:0005773]		Q4V3D9	SSL10	Protein STRICTOSIDINE SYNTHASE-LIKE 10 (AtSSL10) (Strictosidine synthase 8) (AtSS8)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015322	2016_BV11	GO:0003677; GO:0003918; GO:0005524; GO:0005694; GO:0005739; GO:0006265; GO:0009507; GO:0046872	DNA topological change [GO:0006265]	chloroplast [GO:0009507]; chromosome [GO:0005694]; mitochondrion [GO:0005739]	ATP binding [GO:0005524]; DNA binding [GO:0003677]; DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity [GO:0003918]; metal ion binding	Q5YLB4	GYRB	DNA gyrase subunit B, chloroplastic/mitochondrial (EC 5.6.2.2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015353	2016_BV11	GO:0005634; GO:0005737; GO:0005829; GO:0007021; GO:0007023; GO:0009524;	cell division [GO:0051301]; embryo development ending in seed dormancy [GO:0009793]; post-chaperonin tubulin folding pathway [GO:0007023]; tubulin complex assembly	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]; phragmoplast [GO:0009524]	alpha-tubulin binding [GO:0043014]	Q67Z52	TFCB	Tubulin-folding cofactor B (AtTFCB) (Protein EMBRYO DEFECTIVE 2804)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015276	2016_BV11	GO:0000245; GO:0000398; GO:0003676; GO:0005634; GO:0005681; GO:0005684; GO:0005686; GO:0006397; GO:0008270; GO:0010976; GO:0016607; GO:0071004; GO:0071005; GO:0071013; GO:1903241	mRNA processing [GO:0006397]; mRNA splicing, via spliceosome [GO:0000398]; positive regulation of neuron projection development [GO:0010976]; spliceosomal complex assembly [GO:0000245]; U2-type prespliceosome assembly [GO:1903241]	catalytic step 2 spliceosome [GO:0071013]; nuclear speck [GO:0016607]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]; U2 snRNP [GO:0005686]; U2-type precatalytic spliceosome [GO:0071005]; U2-type prespliceosome [GO:0071004]; U2-type spliceosomal complex [GO:0005684]	nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	Q6AXT8	Sf3a2	Splicing factor 3A subunit 2		
8	Vitvi015300	2016_BV11	GO:0000724; GO:0002039; GO:0005634; GO:0005654; GO:0005737; GO:0006974; GO:0010212; GO:0016567; GO:0016605; GO:0031297; GO:0031571; GO:0036297; GO:0046872; GO:0061630	DNA damage response [GO:0006974]; double-strand break repair via homologous recombination [GO:0000724]; interstrand cross-link repair [GO:0036297]; mitotic G1 DNA damage checkpoint signaling [GO:0031571]; protein ubiquitination [GO:0016567]; regulation of DNA damage checkpoint [GO:2000001]; replication fork processing [GO:0031297]; response to ionizing radiation [GO:0010212]	cytoplasm [GO:0005737]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; PML body [GO:0016605]; site of DNA damage [GO:0090734]	MDM2/MDM4 family protein binding [GO:0097371]; metal ion binding [GO:0046872]; p53 binding [GO:0002039]; ubiquitin protein ligase activity [GO:0061630]	Q6PCD5	RFWD3	E3 ubiquitin-protein ligase RFWD3 (EC 2.3.2.27) (RING finger and WD repeat domain-containing protein 3) (RING finger protein 201)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015328	2016_BV11	GO:0005737; GO:0005874; GO:0007010; GO:0008017	cytoskeleton organization [GO:0007010]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	microtubule binding [GO:0008017]	Q6Z746	MAP70.2	Microtubule-associated protein 70-2 (AtMAP70-2) (70 kDa microtubule-associated	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015343	2016_BV11	GO:0005730		nucleolus [GO:0005730]		Q7T0Q5	nol10	Nucleolar protein 10	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015308	2016_BV11					Q7XSQ7		Thioredoxin-like 3-3 (Thioredoxin-like 1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015299	2016_BV11	GO:0004725; GO:0005634; GO:0005739; GO:0006468; GO:0007049; GO:0008794; GO:0009507; GO:0043167; GO:0046685; GO:0046872	cell cycle [GO:0007049]; cell division [GO:0051301]; protein phosphorylation [GO:0006468]; response to arsenic-containing substance [GO:0046685]; sequestering of metal ion [GO:0051238]	chloroplast [GO:0009507]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	arsenate reductase (glutaredoxin) activity [GO:0008794]; ion binding [GO:0043167]; metal ion binding [GO:0046872]; protein tyrosine phosphatase activity [GO:0004725]	Q8GY31	CDC25	Dual specificity phosphatase Cdc25 (EC 3.1.3.48) (Arath;CDC25) (Arsenate reductase) (AtASR) (Arsenate reductase 2) (EC 1.20.4.1) (Sulfurtransferase 5) (AtStr5)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015273	2016_BV11	GO:0005524; GO:0005634; GO:0005829; GO:0005975; GO:0006520; GO:0016020; GO:0016308; GO:0016310	amino acid metabolic process [GO:0006520]; carbohydrate metabolic process [GO:0005975]; phosphatidylinositol metabolic process [GO:0046488]; phosphorylation [GO:0016310]	cytosol [GO:0005829]; membrane [GO:0016020]; nucleus [GO:0005634]	1-phosphatidylinositol-4-phosphate 5-kinase activity [GO:0016308]; ATP binding [GO:0005524]	Q8L850	PIP5K9	Phosphatidylinositol 4-phosphate 5-kinase 9 (AtPIP5K9) (EC 2.7.1.68) (1-phosphatidylinositol 4-phosphate kinase 9) (Diphosphoinositide kinase 9) (PtdIns(4)P-5-		
8	Vitvi015332	2016_BV11	GO:0005739; GO:0016462; GO:0046872		mitochondrion [GO:0005739]	metal ion binding [GO:0046872]; pyrophosphatase activity [GO:0016462]	Q9LHK1	NUDT16	Nudix hydrolase 16, mitochondrial (AtNUDT16) (EC 3.6.1.-)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015315	2016_BV11	GO:0004321; GO:0005524; GO:0005777; GO:0009695; GO:0016874; GO:0031408	jasmonic acid biosynthetic process [GO:0009695]; oxylipin biosynthetic process [GO:0031408]	peroxisome [GO:0005777]	ATP binding [GO:0005524]; fatty-acyl-CoA synthase activity [GO:0004321]; ligase activity [GO:0016874]	Q9M0X9	4CLL7	4-coumarate--CoA ligase-like 7 (EC 6.2.1.-) (4-coumarate--CoA ligase isoform 6) (At4CL6)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015367	2016_BV11	GO:0000419; GO:0003677; GO:0003899; GO:0006351	DNA-templated transcription [GO:0006351]	RNA polymerase V complex [GO:0000419]	DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]	Q9M1J2	NRPE5A	DNA-directed RNA polymerase V subunit 5A		
8	Vitvi015341	2016_BV11	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0010106; GO:0046983	cellular response to iron ion starvation [GO:0010106]; regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]	Q9M1K1	ORG2	Transcription factor ORG2 (Basic helix-loop-helix protein 38) (AtbHLH38) (bHLH 38) (OBP3-responsive gene 2) (Transcription factor EN 8) (bHLH transcription factor bHLH038)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015293	2016_BV11	GO:0003700; GO:0005634; GO:0009646; GO:0043565	response to absence of light [GO:0009646]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	Q9SCP1	MYB27	Transcription factor MYB27 (Myb-related protein 27) (AtMYB27)		
8	Vitvi015292	2016_BV11	GO:0030570; GO:0045490; GO:0046872	pectin catabolic process [GO:0045490]		metal ion binding [GO:0046872]; pectate lyase activity [GO:0030570]	Q9SCP2		Probable pectate lyase 12 (EC 4.2.2.2)		
8	Vitvi015298	2016_BV11					Q9SJM1	ACR10	ACT domain-containing protein ACR10 (Protein ACT DOMAIN REPEATS 10)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015346	2016_BV11	GO:0005773; GO:0009058	biosynthetic process [GO:0009058]	vacuole [GO:0005773]		Q9SLG8	SSL2	Protein STRICTOSIDINE SYNTHASE-LIKE 2 (AtSSL2) (Strictosidine synthase) (Strictosidine synthase 10) (AtSS10)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015320	2016_BV11	GO:0003729; GO:0005739; GO:0080156	mitochondrial mRNA modification [GO:0080156]	mitochondrion [GO:0005739]	mRNA binding [GO:0003729]	Q9XI21		Pentatricopeptide repeat-containing protein At1g15480, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015342	2016_BV11	GO:0005730; GO:0019843; GO:0032040; GO:0070037; GO:0070475	rRNA base methylation [GO:0070475]	nucleolus [GO:0005730]; small-subunit processome [GO:0032040]	rRNA (pseudouridine) methyltransferase activity [GO:0070037]; rRNA binding [GO:0019843]	Q9XX15		Ribosomal RNA small subunit methyltransferase nep-1 (EC 2.1.1.-) (18S rRNA (pseudouridine-N1)-methyltransferase) (Ribosome biogenesis protein nep-1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015318	2016_BV11	GO:0005524; GO:0005783; GO:0005886; GO:0008361; GO:0009506; GO:0009624; GO:0009637; GO:0009639; GO:0009640; GO:0009733; GO:0009734; GO:0009926; GO:0009958; GO:0010315; GO:0010328; GO:0010329; GO:0010817; GO:0042676	anthocyanin accumulation in tissues in response to UV light [GO:0043481]; auxin export across the plasma membrane [GO:0010315]; auxin polar transport [GO:0009926]; auxin-activated signaling pathway [GO:0009734]; photomorphogenesis [GO:0009640]; positive gravitropism [GO:0009958]; regulation of cell size [GO:0008361]; response to auxin [GO:0009733]; response to blue light [GO:0009637]; response to nematode [GO:0009624]; response to red or far-red light [GO:0009639]; stamen	endoplasmic reticulum [GO:0005783]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled transmembrane transporter activity [GO:0042626]; auxin efflux transmembrane transporter activity [GO:0010329]; auxin influx transmembrane transporter activity	Q9ZR72	ABCB1	ABC transporter B family member 1 (ABC transporter ABCB.1) (AtABCB1) (Multidrug resistance protein 1) (P-glycoprotein 1) (AtPgp1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015309	2016_BeWe6	GO:0004478; GO:0005524; GO:0005737; GO:0006556; GO:0006730; GO:0046872	one-carbon metabolic process [GO:0006730]; S-adenosylmethionine biosynthetic process [GO:0006556]	cytoplasm [GO:0005737]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]; methionine adenosyltransferase activity	A7QJG1	METK3	S-adenosylmethionine synthase 3 (AdoMet synthase 3) (EC 2.5.1.6) (Methionine adenosyltransferase 3) (MAT 3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015303	2016_BeWe6	GO:0000724; GO:0002039; GO:0005634; GO:0005737; GO:0006974; GO:0010212; GO:0016567; GO:0016605; GO:0031297; GO:0031571; GO:0035861; GO:0036297; GO:0046872; GO:0061630	DNA damage response [GO:0006974]; double-strand break repair via homologous recombination [GO:0000724]; interstrand cross-link repair [GO:0036297]; mitotic G1 DNA damage checkpoint signaling [GO:0031571]; protein ubiquitination [GO:0016567]; regulation of DNA damage checkpoint [GO:2000001]; replication fork processing [GO:0031297]; response to ionizing radiation [GO:0010212]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; PML body [GO:0016605]; site of DNA damage [GO:0090734]; site of double-strand break [GO:0035861]	MDM2/MDM4 family protein binding [GO:0097371]; metal ion binding [GO:0046872]; p53 binding [GO:0002039]; ubiquitin protein ligase activity [GO:0061630]	D2HWM5	RFWD3	E3 ubiquitin-protein ligase RFWD3 (EC 2.3.2.27) (RING finger and WD repeat domain-containing protein 3) (RING finger protein 201)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015344	2016_BeWe6	GO:0003777; GO:0005524; GO:0005874; GO:0007018; GO:0008017	microtubule-based movement [GO:0007018]	microtubule [GO:0005874]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	F4J2K4	KIN7O	Kinesin-like protein KIN-7O	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015311	2016_BeWe6	GO:0009507; GO:0010581; GO:0019252	regulation of starch biosynthetic process [GO:0010581]; starch biosynthetic process [GO:0019252]	chloroplast [GO:0009507]		F4KFB3	PTST	Protein PTST homolog 3, chloroplastic (PROTEIN TARGETING TO STARCH homolog 3)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015296	2016_BeWe6	GO:0003676; GO:0003677; GO:0003729; GO:0005634; GO:0008270; GO:0009409; GO:0009414; GO:0016607	negative regulation of DNA-templated transcription [GO:0045892]; positive regulation of mRNA splicing, via spliceosome [GO:0048026]; response to cold [GO:0009409]; response to water deprivation [GO:0009414]	nuclear speck [GO:0016607]; nucleus [GO:0005634]	DNA binding [GO:0003677]; mRNA binding [GO:0003729]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	O22703	RZ1B	Glycine-rich RNA-binding protein RZ1B (AtRZ-1a)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015359	2016_BeWe6	GO:0003723; GO:0005739; GO:0006397; GO:0008270; GO:0016554	cytidine to uridine editing [GO:0016554]; mRNA processing [GO:0006397]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]; zinc ion binding [GO:0008270]	O23266	PCMP-H13	Pentatricopeptide repeat-containing protein At4g14050, mitochondrial (Mitochondrial editing factor 35)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015330	2016_BeWe6	GO:0003700; GO:0005634; GO:0006351; GO:0043565	DNA-templated transcription [GO:0006351]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	O24160	TGA21	TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015365	2016_BeWe6	GO:0003723; GO:0005739; GO:0009451	RNA modification [GO:0009451]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]	O64766	PCMP-E15	Pentatricopeptide repeat-containing protein At2g35030, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015350	2016_BeWe6	GO:0000156; GO:0000160; GO:0005634; GO:0006355; GO:0007623; GO:0009735; GO:0009736	circadian rhythm [GO:0007623]; cytokinin-activated signaling pathway [GO:0009736]; phosphorelay signal transduction system [GO:0000160]; regulation of DNA-templated transcription [GO:0006355]; response to cytokinin	nucleus [GO:0005634]	phosphorelay response regulator activity [GO:0000156]	O80366	ARR9	Two-component response regulator ARR9 (Response reactor 4)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
8	Vitvi015333	2016_BeWe6	GO:0000325; GO:0006865; GO:0016020	amino acid transport [GO:0006865]	membrane [GO:0016020]; plant-type vacuole [GO:0000325]		O80668	AVT1A	Amino acid transporter AVT1A (AtAvt1A)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015352	2016_BeWe6	GO:0004121; GO:0009507; GO:0009570; GO:0019279; GO:0019346; GO:0030170; GO:0047804; GO:0060090	L-methionine biosynthetic process from L-homoserine via cystathionine [GO:0019279]; transsulfuration [GO:0019346]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]	cystathionine beta-lyase activity [GO:0004121]; cysteine-S-conjugate beta-lyase activity [GO:0047804]; molecular adaptor activity [GO:0060090]; pyridoxal phosphate	P53780		Cystathionine beta-lyase, chloroplastic (CBL) (EC 4.4.1.13) (Beta-cystathionase) (Cysteine lyase) (Cysteine-S-conjugate beta-lyase)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015337	2016_BeWe6	GO:0006541; GO:0009570; GO:0016041; GO:0019899; GO:0046872; GO:0051538; GO:0097054	glutamine metabolic process [GO:0006541]; L-glutamate biosynthetic process [GO:0097054]	chloroplast stroma [GO:0009570]	3 iron, 4 sulfur cluster binding [GO:0051538]; enzyme binding [GO:0019899]; glutamate synthase (ferredoxin) activity [GO:0016041]; metal ion binding [GO:0046872]	Q43155	FdGOGAT	Ferredoxin-dependent glutamate synthase, chloroplastic (EC 1.4.7.1) (Fd-GOGAT) (SoFdGOGAT)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015347	2016_BeWe6	GO:0005773; GO:0005783; GO:0005829; GO:0005886; GO:0009058; GO:0009505; GO:0009506	biosynthetic process [GO:0009058]	cytosol [GO:0005829]; endoplasmic reticulum [GO:0005783]; plant-type cell wall [GO:0009505]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]; vacuole [GO:0005773]		Q4V3D9	SSL10	Protein STRICTOSIDINE SYNTHASE-LIKE 10 (AtSSL10) (Strictosidine synthase 8) (AtSS8)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015322	2016_BeWe6	GO:0003677; GO:0003918; GO:0005524; GO:0005694; GO:0005739; GO:0006265; GO:0009507; GO:0046872	DNA topological change [GO:0006265]	chloroplast [GO:0009507]; chromosome [GO:0005694]; mitochondrion [GO:0005739]	ATP binding [GO:0005524]; DNA binding [GO:0003677]; DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity [GO:0003918]; metal ion binding	Q5YLB4	GYRB	DNA gyrase subunit B, chloroplastic/mitochondrial (EC 5.6.2.2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015353	2016_BeWe6	GO:0005634; GO:0005737; GO:0005829; GO:0007021; GO:0007023; GO:0009524;	cell division [GO:0051301]; embryo development ending in seed dormancy [GO:0009793]; post-chaperonin tubulin folding pathway [GO:0007023]; tubulin complex assembly	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]; phragmoplast [GO:0009524]	alpha-tubulin binding [GO:0043014]	Q67Z52	TFCB	Tubulin-folding cofactor B (AtTFCB) (Protein EMBRYO DEFECTIVE 2804)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015300	2016_BeWe6	GO:0000724; GO:0002039; GO:0005634; GO:0005654; GO:0005737; GO:0006974; GO:0010212; GO:0016567; GO:0016605; GO:0031297; GO:0031571; GO:0036297; GO:0046872; GO:0061630	DNA damage response [GO:0006974]; double-strand break repair via homologous recombination [GO:0000724]; interstrand cross-link repair [GO:0036297]; mitotic G1 DNA damage checkpoint signaling [GO:0031571]; protein ubiquitination [GO:0016567]; regulation of DNA damage checkpoint [GO:2000001]; replication fork processing [GO:0031297]; response to ionizing radiation [GO:0010212]	cytoplasm [GO:0005737]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; PML body [GO:0016605]; site of DNA damage [GO:0090734]	MDM2/MDM4 family protein binding [GO:0097371]; metal ion binding [GO:0046872]; p53 binding [GO:0002039]; ubiquitin protein ligase activity [GO:0061630]	Q6PCD5	RFWD3	E3 ubiquitin-protein ligase RFWD3 (EC 2.3.2.27) (RING finger and WD repeat domain-containing protein 3) (RING finger protein 201)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015328	2016_BeWe6	GO:0005737; GO:0005874; GO:0007010; GO:0008017	cytoskeleton organization [GO:0007010]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	microtubule binding [GO:0008017]	Q6Z746	MAP70.2	Microtubule-associated protein 70-2 (AtMAP70-2) (70 kDa microtubule-associated	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015343	2016_BeWe6	GO:0005730		nucleolus [GO:0005730]		Q7T0Q5	nol10	Nucleolar protein 10	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015308	2016_BeWe6					Q7XSQ7		Thioredoxin-like 3-3 (Thioredoxin-like 1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015299	2016_BeWe6	GO:0004725; GO:0005634; GO:0005739; GO:0006468; GO:0007049; GO:0008794; GO:0009507; GO:0043167; GO:0046685; GO:0046872	cell cycle [GO:0007049]; cell division [GO:0051301]; protein phosphorylation [GO:0006468]; response to arsenic-containing substance [GO:0046685]; sequestering of metal ion [GO:0051238]	chloroplast [GO:0009507]; mitochondrion [GO:0005739]; nucleus [GO:0005634]	arsenate reductase (glutaredoxin) activity [GO:0008794]; ion binding [GO:0043167]; metal ion binding [GO:0046872]; protein tyrosine phosphatase activity [GO:0004725]	Q8GY31	CDC25	Dual specificity phosphatase Cdc25 (EC 3.1.3.48) (Arath;CDC25) (Arsenate reductase) (AtASR) (Arsenate reductase 2) (EC 1.20.4.1) (Sulfurtransferase 5) (AtStr5)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015332	2016_BeWe6	GO:0005739; GO:0016462; GO:0046872		mitochondrion [GO:0005739]	metal ion binding [GO:0046872]; pyrophosphatase activity [GO:0016462]	Q9LHK1	NUDT16	Nudix hydrolase 16, mitochondrial (AtNUDT16) (EC 3.6.1.-)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015315	2016_BeWe6	GO:0004321; GO:0005524; GO:0005777; GO:0009695; GO:0016874; GO:0031408	jasmonic acid biosynthetic process [GO:0009695]; oxylipin biosynthetic process [GO:0031408]	peroxisome [GO:0005777]	ATP binding [GO:0005524]; fatty-acyl-CoA synthase activity [GO:0004321]; ligase activity [GO:0016874]	Q9M0X9	4CLL7	4-coumarate--CoA ligase-like 7 (EC 6.2.1.-) (4-coumarate--CoA ligase isoform 6) (At4CL6)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015341	2016_BeWe6	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0010106; GO:0046983	cellular response to iron ion starvation [GO:0010106]; regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein dimerization activity [GO:0046983]	Q9M1K1	ORG2	Transcription factor ORG2 (Basic helix-loop-helix protein 38) (AtbHLH38) (bHLH 38) (OBP3-responsive gene 2) (Transcription factor EN 8) (bHLH transcription factor bHLH038)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015298	2016_BeWe6					Q9SJM1	ACR10	ACT domain-containing protein ACR10 (Protein ACT DOMAIN REPEATS 10)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015346	2016_BeWe6	GO:0005773; GO:0009058	biosynthetic process [GO:0009058]	vacuole [GO:0005773]		Q9SLG8	SSL2	Protein STRICTOSIDINE SYNTHASE-LIKE 2 (AtSSL2) (Strictosidine synthase) (Strictosidine synthase 10) (AtSS10)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015320	2016_BeWe6	GO:0003729; GO:0005739; GO:0080156	mitochondrial mRNA modification [GO:0080156]	mitochondrion [GO:0005739]	mRNA binding [GO:0003729]	Q9XI21		Pentatricopeptide repeat-containing protein At1g15480, mitochondrial	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015342	2016_BeWe6	GO:0005730; GO:0019843; GO:0032040; GO:0070037; GO:0070475	rRNA base methylation [GO:0070475]	nucleolus [GO:0005730]; small-subunit processome [GO:0032040]	rRNA (pseudouridine) methyltransferase activity [GO:0070037]; rRNA binding [GO:0019843]	Q9XX15		Ribosomal RNA small subunit methyltransferase nep-1 (EC 2.1.1.-) (18S rRNA (pseudouridine-N1)-methyltransferase) (Ribosome biogenesis protein nep-1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015318	2016_BeWe6	GO:0005524; GO:0005783; GO:0005886; GO:0008361; GO:0009506; GO:0009624; GO:0009637; GO:0009639; GO:0009640; GO:0009733; GO:0009734; GO:0009926; GO:0009958; GO:0010315; GO:0010328; GO:0010329;	anthocyanin accumulation in tissues in response to UV light [GO:0043481]; auxin export across the plasma membrane [GO:0010315]; auxin polar transport [GO:0009926]; auxin-activated signaling pathway [GO:0009734]; photomorphogenesis [GO:0009640]; positive gravitropism [GO:0009958]; regulation of cell size [GO:0008361]; response to auxin [GO:0009733]; response to blue light [GO:0009637]; response to nematode [GO:0009624];	endoplasmic reticulum [GO:0005783]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled transmembrane transporter activity [GO:0042626]; auxin efflux transmembrane transporter activity [GO:0010329]; auxin influx	Q9ZR72	ABCB1	ABC transporter B family member 1 (ABC transporter ABCB.1) (AtABCB1) (Multidrug resistance protein 1) (P-glycoprotein 1) (AtPgp1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015330	2017_BV12	GO:0003700; GO:0005634; GO:0006351; GO:0043565	DNA-templated transcription [GO:0006351]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	O24160	TGA21	TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015333	2017_BV12	GO:0000325; GO:0006865; GO:0016020	amino acid transport [GO:0006865]	membrane [GO:0016020]; plant-type vacuole [GO:0000325]		O80668	AVT1A	Amino acid transporter AVT1A (AtAvt1A)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015337	2017_BV12	GO:0006541; GO:0009570; GO:0016041; GO:0019899; GO:0046872; GO:0051538; GO:0097054	glutamine metabolic process [GO:0006541]; L-glutamate biosynthetic process [GO:0097054]	chloroplast stroma [GO:0009570]	3 iron, 4 sulfur cluster binding [GO:0051538]; enzyme binding [GO:0019899]; glutamate synthase (ferredoxin) activity [GO:0016041]; metal ion binding [GO:0046872]	Q43155	FdGOGAT	Ferredoxin-dependent glutamate synthase, chloroplastic (EC 1.4.7.1) (Fd-GOGAT) (SoFdGOGAT)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015322	2017_BV12	GO:0003677; GO:0003918; GO:0005524; GO:0005694; GO:0005739; GO:0006265; GO:0009507; GO:0046872	DNA topological change [GO:0006265]	chloroplast [GO:0009507]; chromosome [GO:0005694]; mitochondrion [GO:0005739]	ATP binding [GO:0005524]; DNA binding [GO:0003677]; DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity [GO:0003918]; metal ion binding	Q5YLB4	GYRB	DNA gyrase subunit B, chloroplastic/mitochondrial (EC 5.6.2.2)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015328	2017_BV12	GO:0005737; GO:0005874; GO:0007010; GO:0008017	cytoskeleton organization [GO:0007010]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	microtubule binding [GO:0008017]	Q6Z746	MAP70.2	Microtubule-associated protein 70-2 (AtMAP70-2) (70 kDa microtubule-associated	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015332	2017_BV12	GO:0005739; GO:0016462; GO:0046872		mitochondrion [GO:0005739]	metal ion binding [GO:0046872]; pyrophosphatase activity [GO:0016462]	Q9LHK1	NUDT16	Nudix hydrolase 16, mitochondrial (AtNUDT16) (EC 3.6.1.-)	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015344	2016_SBN1	GO:0003777; GO:0005524; GO:0005874; GO:0007018; GO:0008017	microtubule-based movement [GO:0007018]	microtubule [GO:0005874]	ATP binding [GO:0005524]; microtubule binding [GO:0008017]; microtubule motor activity	F4J2K4	KIN7O	Kinesin-like protein KIN-7O	chr8：20186545-20286545；chr8：22101071-22201071	10.1093/g3journal/jkac103
8	Vitvi015638	2016_SL6	GO:0003746; GO:0003924; GO:0005525; GO:0005829; GO:0006364; GO:0009409; GO:0009507; GO:0050821;	protein stabilization [GO:0050821]; response to cold [GO:0009409]; rRNA processing [GO:0006364]	chloroplast [GO:0009507]; cytosol [GO:0005829]; ribonucleoprotein complex [GO:1990904]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; translation elongation factor activity [GO:0003746]	F4K410	SVR3	Putative elongation factor TypA-like SVR3, chloroplastic (Protein HAPPY ON NORFLURAZON 23) (Protein SUPPRESSOR OF VARIEGATION 3)		
8	Vitvi015680	2016_BeWi2	GO:0003723; GO:0005730; GO:0006364; GO:0031965	rRNA processing [GO:0006364]	nuclear membrane [GO:0031965]; nucleolus [GO:0005730]	RNA binding [GO:0003723]	Q5ZKD5	RRP12	RRP12-like protein		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
9	Vitvi015903	2016_BeWi3	GO:0003735; GO:0005840; GO:0006412; GO:1990904	translation [GO:0006412]	ribonucleoprotein complex [GO:1990904]; ribosome [GO:0005840]	structural constituent of ribosome [GO:0003735]	A1WWE1	rpmH	Large ribosomal subunit protein bL34 (50S ribosomal protein L34)		
9	Vitvi015938	2016_BeWi3	GO:0003723; GO:0008270; GO:0009451	RNA modification [GO:0009451]		RNA binding [GO:0003723]; zinc ion binding [GO:0008270]	A8MQA3	PCMP-H28	Pentatricopeptide repeat-containing protein At4g21065		
9	Vitvi015878	2016_BeWi3	GO:0000124; GO:0005669; GO:0006352; GO:0046695; GO:0046982	DNA-templated transcription initiation [GO:0006352]	SAGA complex [GO:0000124]; SLIK (SAGA-like) complex [GO:0046695]; transcription factor TFIID complex [GO:0005669]	protein heterodimerization activity [GO:0046982]	B2C6R6	TAF12B	Transcription initiation factor TFIID subunit 12b (Protein CYTOKININ-HYPERSENSITIVE 1) (Protein ENHANCED ETHYLENE RESPONSE 4) (TBP-associated factor 12b) (AtTAF12b)		
9	Vitvi015902	2016_BeWi3	GO:0000166; GO:0005737; GO:0046872; GO:0106411		cytoplasm [GO:0005737]	metal ion binding [GO:0046872]; nucleotide binding [GO:0000166]; XMP 5'-nucleosidase activity [GO:0106411]	B8FYS8	surE	5'-nucleotidase SurE (EC 3.1.3.5) (Nucleoside 5'-monophosphate phosphohydrolase)		
9	Vitvi015907	2016_BeWi3	GO:0005576; GO:0010052; GO:0010374	guard cell differentiation [GO:0010052]; stomatal complex development [GO:0010374]	extracellular region [GO:0005576]		C4B8C4	EPFL3	EPIDERMAL PATTERNING FACTOR-like protein 3 (EPF-like protein 3) [Cleaved into: MEPFL3]		
9	Vitvi015972	2016_BeWi3	GO:0009507; GO:0009570; GO:0030267; GO:0050661; GO:0051287		chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]	glyoxylate reductase (NADP+) activity [GO:0030267]; NAD binding [GO:0051287]; NADP binding [GO:0050661]	F4I907	GLYR2	Glyoxylate/succinic semialdehyde reductase 2, chloroplastic (AtGLYR2) (AtGR2) (SSA reductase 2) (EC 1.1.1.79) (EC 1.1.1.n11)		
9	Vitvi015969	2016_BeWi3	GO:0005634; GO:0005829; GO:0016787		cytosol [GO:0005829]; nucleus [GO:0005634]	hydrolase activity [GO:0016787]	O74545		Putative hydrolase C777.06c		
9	Vitvi015899	2016_BeWi3	GO:0003735; GO:0005840; GO:0006412; GO:0019843; GO:1990904	translation [GO:0006412]	ribonucleoprotein complex [GO:1990904]; ribosome [GO:0005840]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	P30707	RPL9	Large ribosomal subunit protein uL6 (60S ribosomal protein L9) (Gibberellin-regulated protein GA)		
9	Vitvi015883	2016_BeWi3	GO:0000287; GO:0006633; GO:0008897; GO:0017000	antibiotic biosynthetic process [GO:0017000]; fatty acid biosynthetic process [GO:0006633]		holo-[acyl-carrier-protein] synthase activity [GO:0008897]; magnesium ion binding [GO:0000287]	P40683	gsp	4'-phosphopantetheinyl transferase gsp (EC 2.7.8.-) (Gramicidin synthase-activating enzyme)		
9	Vitvi015952	2016_BeWi3	GO:0004525; GO:0005737; GO:0006364; GO:0019843	rRNA processing [GO:0006364]	cytoplasm [GO:0005737]	ribonuclease III activity [GO:0004525]; rRNA binding [GO:0019843]	P74327	mrnC	Mini-ribonuclease 3 (Mini-3) (Mini-RNase 3) (EC 3.1.26.-) (Mini-RNase III) (Mini-III)		
9	Vitvi015875	2016_BeWi3	GO:0000045; GO:0005737; GO:0015031	autophagosome assembly [GO:0000045]; protein transport [GO:0015031]	cytoplasm [GO:0005737]		Q1SF86	ATG12	Ubiquitin-like protein ATG12 (Autophagy-related protein 12) (APG12-like)		
9	Vitvi015900	2016_BeWi3	GO:0001772; GO:0005739; GO:0005743; GO:0005758; GO:0005886; GO:0006874; GO:0007005; GO:0010876; GO:0015629; GO:0032743; GO:0034982; GO:0035710; GO:0042608; GO:0042776; GO:0045121; GO:0050852; GO:0061760; GO:1900026; GO:2001240; mediator complex [GO:0016592];	CD4-positive, alpha-beta T cell activation [GO:0035710]; intracellular calcium ion homeostasis [GO:0006874]; lipid localization [GO:0010876]; mitochondrial protein processing [GO:0034982]; mitochondrion organization [GO:0007005]; positive regulation of interleukin-2 production [GO:0032743]; protein complex oligomerization [GO:0051259]; proton motive force-driven mitochondrial ATP synthesis [GO:0042776]; stress-induced mitochondrial fusion [GO:1900026]; T cell receptor signaling pathway [GO:0061760];	actin cytoskeleton [GO:0015629]; immunological synapse [GO:0001772]; membrane raft [GO:0045121]; mitochondrial inner membrane [GO:0005743]; mitochondrial intermembrane space [GO:0005758]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cardiolipin binding [GO:1901612]; GTPase binding [GO:0051020]; T cell receptor binding [GO:0042608]	Q4FZT0	Stoml2	Stomatin-like protein 2, mitochondrial (SLP-2)		
9	Vitvi015924	2016_BeWi3	GO:0001188; GO:0003677; GO:0003899; GO:0005736; GO:0006360; GO:0006362	RNA polymerase I preinitiation complex assembly [GO:0001188]; transcription by RNA polymerase I [GO:0006360]; transcription elongation by RNA polymerase I [GO:0006362]	RNA polymerase I complex [GO:0005736]	DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]	Q54FE8	polr1e	DNA-directed RNA polymerase I subunit rpa49 (RNA polymerase I subunit A49) (DNA-directed RNA polymerase I subunit E)		
9	Vitvi015880	2016_BeWi3	GO:0005634; GO:0009648; GO:0042753; GO:0042803; GO:0090594;	photoperiodism [GO:0009648]; positive regulation of circadian rhythm [GO:0042753]; rhythmic process	nucleus [GO:0005634]	protein homodimerization activity [GO:0042803]	Q570U6	EFL4	Protein ELF4-LIKE 4		
9	Vitvi015894	2016_BeWi3	GO:0000375; GO:0000398; GO:0001666; GO:0005634; GO:0005681; GO:0005737; GO:0009611; GO:0032496; GO:0043122; GO:0071013; GO:0090594;	inflammatory response to wounding [GO:0090594]; mRNA splicing, via spliceosome [GO:0000398]; regulation of canonical NF-kappaB signal transduction [GO:0043122]; response to hypoxia [GO:0001666]; response to lipopolysaccharide [GO:0032496]; response to wounding [GO:0009611]; RNA splicing, via transesterification reactions	catalytic step 2 spliceosome [GO:0071013]; cytoplasm [GO:0005737]; nucleus [GO:0005634]; spliceosomal complex [GO:0005681]		Q5BLX8	Wdr83	WD repeat domain-containing protein 83 (Mitogen-activated protein kinase organizer 1) (MAPK organizer 1)		
9	Vitvi015976	2016_BeWi3	GO:0009507; GO:0045454	cell redox homeostasis [GO:0045454]	chloroplast [GO:0009507]		Q5TKD8		Thioredoxin-like 2, chloroplastic (Lilium-type thioredoxin 2) (OsTrx19)		
9	Vitvi015971	2016_BeWi3	GO:0000724; GO:0000785; GO:0003682; GO:0005634; GO:0005737; GO:0006334;	double-strand break repair via homologous recombination [GO:0000724]; nucleosome assembly [GO:0006334]	chromatin [GO:0000785]; cytoplasm [GO:0005737]; nucleus [GO:0005634]	chromatin binding [GO:0003682]; histone binding [GO:0042393]	Q5VND6	NAP1;1	Nucleosome assembly protein 1;1 (OsNAP1;1) (Nucleosome assembly protein 1-like 1) (OsNAP1 L1)		
9	Vitvi015908	2016_BeWi3	GO:0000139; GO:0006886; GO:0006890; GO:0006891; GO:0030126	intra-Golgi vesicle-mediated transport [GO:0006891]; intracellular protein transport [GO:0006886]; retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	COPI vesicle coat [GO:0030126]; Golgi membrane [GO:0000139]		Q6Z844	COPZ2	Coatomer subunit zeta-2 (Non-clathrin coat protein zeta2-COP) (Zeta-2-coat protein) (Zeta-COP 2)		
9	Vitvi015890	2016_BeWi3	GO:0005634		nucleus [GO:0005634]		Q8GYL9	BRXL2	Protein Brevis radix-like 2 (AtBRXL2)		
9	Vitvi015966	2016_BeWi3	GO:0016592		mediator complex [GO:0016592]		Q8RWA2	MED9	Mediator of RNA polymerase II transcription subunit 9		
9	Vitvi015919	2016_BeWi3	GO:0004742; GO:0005507; GO:0005739; GO:0005759; GO:0005829; GO:0006086; GO:0006096; GO:0009941; GO:0045254	acetyl-CoA biosynthetic process from pyruvate [GO:0006086]; glycolytic process [GO:0006096]	chloroplast envelope [GO:0009941]; cytosol [GO:0005829]; mitochondrial matrix [GO:0005759]; mitochondrion [GO:0005739]; pyruvate dehydrogenase complex [GO:0045254]	copper ion binding [GO:0005507]; dihydrolipoyllysine-residue acetyltransferase activity [GO:0004742]	Q8RWN9		Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial (EC 2.3.1.12) (Dihydrolipoamide S-acetyltransferase component 2 of pyruvate dehydrogenase complex) (Pyruvate dehydrogenase complex component E2 2) (PDC-E2 2) (PDCE2 2)		
9	Vitvi015921	2016_BeWi3	GO:0005634; GO:0005737; GO:0006400; GO:0019899; GO:0030488; GO:0052735	tRNA methylation [GO:0030488]; tRNA modification [GO:0006400]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	enzyme binding [GO:0019899]; tRNA (cytosine-3-)-methyltransferase activity [GO:0052735]	Q8TCB7	METTL6	tRNA N(3)-methylcytidine methyltransferase METTL6 (EC 2.1.1.-) (Methyltransferase-like protein 6) (hMETTL6)		
9	Vitvi015889	2016_BeWi3	GO:0005634; GO:0042802; GO:0043388; GO:0051082	positive regulation of DNA binding [GO:0043388]	nucleus [GO:0005634]	identical protein binding [GO:0042802]; unfolded protein binding [GO:0051082]	Q8VZS6	GIP1	GBF-interacting protein 1		10.1038/sj.cr.7290326
9	Vitvi015895	2016_BeWi3	GO:0000981; GO:0003677; GO:0006357; GO:0016602	regulation of transcription by RNA polymerase II [GO:0006357]	CCAAT-binding factor complex [GO:0016602]	DNA binding [GO:0003677]; DNA-binding transcription factor activity, RNA polymerase II-specific	Q93ZH2	NFYA3	Nuclear transcription factor Y subunit A-3 (AtNF-YA-3) (Transcriptional activator HAP2C)		
9	Vitvi015962	2016_BeWi3	GO:0000325; GO:0005524; GO:0005739; GO:0005829; GO:0042026; GO:0140662	protein refolding [GO:0042026]	cytosol [GO:0005829]; mitochondrion [GO:0005739]; plant-type vacuole [GO:0000325]	ATP binding [GO:0005524]; ATP-dependent protein folding chaperone [GO:0140662]	Q93ZM7		Chaperonin CPN60-like 2, mitochondrial (HSP60-like 2)		
9	Vitvi015892	2016_BeWi3	GO:0003729			mRNA binding [GO:0003729]	Q94AM9	CID4	Polyadenylate-binding protein-interacting protein 4 (PABP-interacting protein 4) (Poly(A)-binding protein-interacting protein 4) (PAM2-containing protein CID4) (Protein CTC-INTERACTING DOMAIN 4)		
9	Vitvi015949	2016_BeWi3	GO:0005506; GO:0010268; GO:0016020; GO:0016125; GO:0016132; GO:0016709; GO:0020037	brassinosteroid biosynthetic process [GO:0016132]; brassinosteroid homeostasis [GO:0010268]; sterol metabolic process [GO:0016125]	membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen [GO:0016709]	Q94IW5	CYP90D2	Cytochrome P450 90D2 (OsCYP90D2) (3-dehydro-6-deoxoteasterone synthase) (EC 1.14.19.-) (3-dehydroteasterone synthase) (EC 1.14.19.-) (C6-oxidase)		10.1105/tpc.014712
9	Vitvi015950	2016_BeWi3	GO:0000184; GO:0003723; GO:0003724; GO:0005524; GO:0005634; GO:0006364; GO:0016887	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184]; rRNA processing [GO:0006364]	nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]	Q9C718	RH20	DEAD-box ATP-dependent RNA helicase 20 (EC 3.6.4.13)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
9	Vitvi015901	2016_BeWi3	GO:0000398; GO:0002758; GO:0003723; GO:0005634; GO:0042742	defense response to bacterium [GO:0042742]; innate immune response-activating signaling pathway [GO:0002758]; mRNA splicing, via spliceosome [GO:0000398]	nucleus [GO:0005634]	RNA binding [GO:0003723]	Q9C801	MOS2	Protein MOS2		
9	Vitvi015977	2016_BeWi3	GO:0004630; GO:0005509; GO:0005886; GO:0006970; GO:0006995; GO:0009395; GO:0009791; GO:0009825; GO:0016036; GO:0045848; GO:0046470; GO:0048364; GO:0051301; GO:0051365; GO:0070290	cell division [GO:0051301]; cellular response to nitrogen starvation [GO:0006995]; cellular response to phosphate starvation [GO:0016036]; cellular response to potassium ion starvation [GO:0051365]; multidimensional cell growth [GO:0009825]; phosphatidylcholine metabolic process [GO:0046470]; phospholipid catabolic process [GO:0009395]; positive regulation of nitrogen utilization [GO:0045848]; post-embryonic development [GO:0009791]; response to osmotic stress [GO:0006970]; root development [GO:0048364]	plasma membrane [GO:0005886]	calcium ion binding [GO:0005509]; N-acylphosphatidylethanolamine-specific phospholipase D activity [GO:0070290]; phospholipase D activity [GO:0004630]	Q9C888	PLDALPHA4	Phospholipase D alpha 4 (AtPLDalpha4) (PLD alpha 4) (EC 3.1.4.4) (PLDalpha3) (Phospholipase D epsilon) (AtPLDepsilon) (PLD epsilon)		
9	Vitvi015886	2016_BeWi3	GO:0003729; GO:0003924; GO:0005525; GO:0005739; GO:0019003		mitochondrion [GO:0005739]	GDP binding [GO:0019003]; GTP binding [GO:0005525]; GTPase activity [GO:0003924]; mRNA binding [GO:0003729]	Q9CAI1	DRG2	Developmentally-regulated G-protein 2 (AtDRG2) (Developmentally-regulated G-protein 2B) (AtDRG2b)		
9	Vitvi015910	2016_BeWi3	GO:0004674; GO:0005524; GO:0005634; GO:0005737; GO:0016310; GO:0106310	phosphorylation [GO:0016310]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9CAI5	CKL2	Casein kinase 1-like protein 2 (EC 2.7.11.1) (Protein CASEIN KINASE I-LIKE 2)		
9	Vitvi015943	2016_BeWi3					Q9FJ30		Putative F-box/LRR-repeat protein At5g41840		
9	Vitvi015931	2016_BeWi3					Q9FM94		FBD-associated F-box protein At5g56370		
9	Vitvi015891	2016_BeWi3	GO:0000325; GO:0005783; GO:0006071; GO:0008374; GO:0009536; GO:0016020; GO:0019432; GO:0046027	glycerol metabolic process [GO:0006071]; triglyceride biosynthetic process [GO:0019432]	endoplasmic reticulum [GO:0005783]; membrane [GO:0016020]; plant-type vacuole [GO:0000325]; plastid [GO:0009536]	O-acyltransferase activity [GO:0008374]; phospholipid:diacylglycerol acyltransferase activity [GO:0046027]	Q9FNA9	PDAT1	Phospholipid:diacylglycerol acyltransferase 1 (AtPDAT) (EC 2.3.1.158)		
9	Vitvi015955	2016_BeWi3	GO:0000138; GO:0000139; GO:0000325; GO:0005634; GO:0005737; GO:0005768; GO:0005794; GO:0005802; GO:0006811; GO:0006878; GO:0006882; GO:0010008	intracellular copper ion homeostasis [GO:0006878]; intracellular zinc ion homeostasis [GO:0006882]; monoatomic ion transport [GO:0006811]	cytoplasm [GO:0005737]; endosome [GO:0005768]; endosome membrane [GO:0010008]; Golgi apparatus [GO:0005794]; Golgi membrane [GO:0000139]; Golgi trans cisterna [GO:0000138]; nucleus [GO:0005634]; plant-type vacuole [GO:0000325]; trans-Golgi network [GO:0005802]		Q9LIC2	TMN7	Transmembrane 9 superfamily member 7 (Endomembrane protein 5) (Transmembrane nine protein 7) (AtTMN7)		
9	Vitvi015963	2016_BeWi3	GO:0003723; GO:0009451; GO:0031930	mitochondria-nucleus signaling pathway [GO:0031930]; RNA modification [GO:0009451]		RNA binding [GO:0003723]	Q9LNP2	PCMP-E72	Putative pentatricopeptide repeat-containing protein At1g17630		
9	Vitvi015920	2016_BeWi3	GO:0005743; GO:0005744; GO:0006626; GO:0015450	protein targeting to mitochondrion [GO:0006626]	mitochondrial inner membrane [GO:0005743]; TIM23 mitochondrial import inner membrane translocase complex [GO:0005744]	protein-transporting ATPase activity [GO:0015450]	Q9LNQ1	TIM23-1	Mitochondrial import inner membrane translocase subunit TIM23-1		
9	Vitvi015968	2016_BeWi3	GO:0003677; GO:0003700; GO:0005634; GO:0006355; GO:0046872	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; metal ion binding [GO:0046872]	Q9LRW7	IDD11	Protein indeterminate-domain 11		
9	Vitvi015913	2016_BeWi3	GO:0004379; GO:0005829; GO:0005840; GO:0006499; GO:0009536; GO:0010064; GO:0019107	embryonic shoot morphogenesis [GO:0010064]; N-terminal protein myristoylation [GO:0006499]	cytosol [GO:0005829]; plastid [GO:0009536]; ribosome [GO:0005840]	glycylpeptide N-tetradecanoyltransferase activity [GO:0004379]; myristoyltransferase activity [GO:0019107]	Q9LTR9	NMT1	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase 1) (Peptide N-myristoyltransferase 1)		
9	Vitvi015888	2016_BeWi3	GO:0005886; GO:0009734; GO:0010929; GO:0060918	auxin transport [GO:0060918]; auxin-activated signaling pathway [GO:0009734]; positive regulation of auxin mediated signaling pathway [GO:0010929]	plasma membrane [GO:0005886]		Q9LVK2		Protein BIG GRAIN 1-like A		
9	Vitvi015909	2016_BeWi3	GO:0000287; GO:0005524; GO:0005886; GO:0009860; GO:0012505; GO:0015914; GO:0016887; GO:0140326; GO:1905038	phospholipid transport [GO:0015914]; pollen tube growth [GO:0009860]; regulation of membrane lipid metabolic process [GO:1905038]	endomembrane system [GO:0012505]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled intramembrane lipid transporter activity [GO:0140326]; magnesium ion binding [GO:0000287]	Q9LVK9	ALA7	Probable phospholipid-transporting ATPase 7 (AtALA7) (EC 7.6.2.1) (Aminophospholipid flippase 7)		
9	Vitvi015948	2016_BeWi3					Q9LXQ6		Putative F-box protein At3g44060		
9	Vitvi015953	2016_BeWi3	GO:0004565; GO:0005829; GO:0005975; GO:0009505; GO:0009506; GO:0030246; GO:0048046	carbohydrate metabolic process [GO:0005975]	apoplast [GO:0048046]; cytosol [GO:0005829]; plant-type cell wall [GO:0009505]; plasmodesma [GO:0009506]	beta-galactosidase activity [GO:0004565]; carbohydrate binding [GO:0030246]	Q9SCW1	BGAL1	Beta-galactosidase 1 (Lactase 1) (EC 3.2.1.23)		
9	Vitvi015957	2016_BeWi3	GO:0003924; GO:0005525; GO:0005789		endoplasmic reticulum membrane [GO:0005789]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	Q9SSN0		Protein ROOT HAIR DEFECTIVE 3 homolog 1 (EC 3.6.5.-) (Protein SEY1 homolog 2)		
9	Vitvi016854	2016_Fru1	GO:0003735; GO:0005840; GO:0006412; GO:0019843; GO:0042254	translation [GO:0006412]	ribonucleoprotein complex [GO:1990904]; ribosome [GO:0005840]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	A7HM43	rpsQ	Small ribosomal subunit protein uS17 (30S ribosomal protein S17)		
9	Vitvi016859	2016_Fru1	GO:0004674; GO:0005524; GO:0005783; GO:0007165; GO:0009414; GO:0009651; GO:0010540; GO:0016310; GO:0042538; GO:0051592; GO:0071695	basipetal auxin transport [GO:0010540]; hyperosmotic salinity response [GO:0042538]; phosphorylation [GO:0016310]; response to calcium ion [GO:0051592]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]; signal transduction [GO:0007165]	endoplasmic reticulum [GO:0005783]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	O65554	CIPK6	CBL-interacting serine/threonine-protein kinase 6 (EC 2.7.11.1) (SNF1-related kinase 3.14) (SOS2-like protein kinase PKS4) (SOS3-interacting protein 3)		
9	Vitvi016855	2016_Fru1	GO:0005789; GO:0006506; GO:0016780; GO:0051377	GPI anchor biosynthetic process [GO:0006506]	endoplasmic reticulum membrane [GO:0005789]	mannose-ethanolamine phosphotransferase activity [GO:0051377]; phosphotransferase activity, for other substituted phosphate groups [GO:0016780]	Q9JJI6	Pigo	GPI ethanolamine phosphate transferase 3 (EC 2.-.-.-) (Phosphatidylinositol-glycan biosynthesis class O protein) (PIG-O)		
9	Vitvi016857	2016_Fru1	GO:0000463; GO:0003735; GO:0005730; GO:0022625	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) [GO:0000463]	cytosolic large ribosomal subunit [GO:0022625]; nucleolus [GO:0005730]	structural constituent of ribosome [GO:0003735]	Q9SAI5	RPL7A	Large ribosomal subunit protein uL30z (60S ribosomal protein L7-1)		
9	Vitvi016869	2016_BeWi4	GO:0003735; GO:0005840; GO:0006412; GO:0019843; GO:0042254	translation [GO:0006412]	ribonucleoprotein complex [GO:1990904]; ribosome [GO:0005840]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	B1I1J7	rpsQ	Small ribosomal subunit protein uS17 (30S ribosomal protein S17)		
9	Vitvi016871	2016_BeWi4	GO:0046872; GO:0050896	response to stimulus [GO:0050896]		metal ion binding [GO:0046872]	F4IC29	HIPP28	Heavy metal-associated isoprenylated plant protein 28 (AtHIP28)		
9	Vitvi016870	2016_BeWi4	GO:0003723; GO:0005739; GO:0009451; GO:0043231	RNA modification [GO:0009451]	intracellular membrane-bounded organelle [GO:0043231]; mitochondrion [GO:0005739]	RNA binding [GO:0003723]	O65543	PCMP-E7	Pentatricopeptide repeat-containing protein At4g31070, mitochondrial		
9	Vitvi016873	2016_BeWi4	GO:0005886; GO:0005975; GO:0006952; GO:0009506; GO:0009536; GO:0042973; GO:0098552	carbohydrate metabolic process [GO:0005975]; defense response [GO:0006952]	plasma membrane [GO:0005886]; plasmodesma [GO:0009506]; plastid [GO:0009536]; side of membrane [GO:0098552]	glucan endo-1,3-beta-D-glucosidase activity [GO:0042973]	Q93Z08		Glucan endo-1,3-beta-glucosidase 6 (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase 6) ((1->3)-beta-glucanase 6) (Beta-1,3-endoglucanase 6) (Beta-1,3-glucanase 6)		
9	Vitvi016863	2016_BeWi4	GO:0005381; GO:0005384; GO:0005886; GO:0015086; GO:0034755; GO:0055071; GO:0070574; GO:0071421	cadmium ion transmembrane transport [GO:0070574]; iron ion transmembrane transport [GO:0034755]; manganese ion homeostasis [GO:0055071]; manganese ion transmembrane transport [GO:0071421]	plasma membrane [GO:0005886]	cadmium ion transmembrane transporter activity [GO:0015086]; iron ion transmembrane transporter activity [GO:0005381]; manganese ion transmembrane transporter activity [GO:0005384]	Q9SAH8	NRAMP1	Metal transporter Nramp1 (AtNramp1)		
9	Vitvi016896	2017_SL7	GO:0005886		plasma membrane [GO:0005886]		F4J9A8	RLP45	Receptor-like protein 45 (AtRLP45)		
9	Vitvi016890	2017_SL7	GO:0005576; GO:0071555	cell wall organization [GO:0071555]	extracellular region [GO:0005576]		O48809	LRX2	Leucine-rich repeat extensin-like protein 2 (AtLRX2) (LRR/EXTENSIN2) (Cell wall hydroxyproline-rich glycoprotein)		

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Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
9	Vitvi016891	2017_SL7	GO:0017018; GO:0046872			metal ion binding [GO:0046872]; myosin phosphatase activity	Q0JAA0		Probable protein phosphatase 2C 44 (OsPP2C44) (EC 3.1.3.16)		
9	Vitvi016899	2017_SL7	GO:0005886; GO:0008836; GO:0009089; GO:0009507; GO:0009570	lysine biosynthetic process via diaminopimelate [GO:0009089]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; plasma membrane [GO:0005886]	diaminopimelate decarboxylase activity [GO:0008836]	Q94A94	LYSA2	Diaminopimelate decarboxylase 2, chloroplastic (DAP decarboxylase 2) (DAPDC 2) (EC 4.1.1.20)		
9	Vitvi016889	2017_SL7	GO:0003677; GO:0005635; GO:0005643; GO:0015031;	mRNA transport [GO:0051028]; protein transport [GO:0015031]	nuclear envelope [GO:0005635]; nuclear pore [GO:0005643]	DNA binding [GO:0003677]; metal ion binding [GO:0046872]	Q9FWS3	CG1	Zinc finger CCCH domain-containing protein 16 (AtC3H16)		
9	Vitvi016901	2017_SL7	GO:0005886		plasma membrane [GO:0005886]		Q9SLI6	RLP8	Putative receptor-like protein 8 (AtRLP8)		
9	Vitvi017013	2016_FJ3	GO:0005524; GO:0008559; GO:0016020; GO:0016887; GO:0042626; GO:0055085	transmembrane transport [GO:0055085]	membrane [GO:0016020]	ABC-type xenobiotic transporter activity [GO:0008559]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled transmembrane transporter activity [GO:0042626]	Q9SKX0	ABCC13	ABC transporter C family member 13 (ABC transporter ABCC.13) (AtABCC13) (EC 7.6.2.2) (ATP-energized glutathione S-conjugate pump 11) (Glutathione S-conjugate-transporting ATPase 11) (Multidrug resistance-associated protein 11)		
9	Vitvi017115	2017_SL8	GO:0004842; GO:0008270; GO:0016020; GO:0016567	protein ubiquitination [GO:0016567]	membrane [GO:0016020]	ubiquitin-protein transferase activity [GO:0004842]; zinc ion binding [GO:0008270]	A4IIY1	rnf144a	Probable E3 ubiquitin-protein ligase RNF144A (EC 2.3.2.31) (RING finger protein 144A)		
9	Vitvi017123	2017_SL8	GO:0005524; GO:0009570; GO:0016887		chloroplast stroma [GO:0009570]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	O49074		Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic (RA) (RuBisCO		
9	Vitvi017147	2017_SL8	GO:0003777; GO:0003779; GO:0005524; GO:0005737; GO:0005874; GO:0007017; GO:0007018; GO:0007097; GO:0008017; GO:0008569; GO:0015629; GO:0015630; GO:0016887; GO:0031534	microtubule-based movement [GO:0007018]; microtubule-based process [GO:0007017]; minus-end directed microtubule sliding [GO:0031534]; nuclear migration [GO:0007097]; nucleus localization [GO:0051647]	actin cytoskeleton [GO:0015629]; cytoplasm [GO:0005737]; microtubule [GO:0005874]; microtubule cytoskeleton [GO:0015630]	actin binding [GO:0003779]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; microtubule binding [GO:0008017]; microtubule motor activity [GO:0003777]; minus-end-directed microtubule motor activity [GO:0008569]; protein self-association	Q0IMS9	KIN14Q	Kinesin-like protein KIN-14Q (Kinesin O12) (OsKCH1)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017154	2017_SL8	GO:0000139; GO:0000938; GO:0005739; GO:0005829; GO:0006890; GO:0006970; GO:0007009; GO:0009408; GO:0010008; GO:0010286; GO:0015031; GO:0042147	heat acclimation [GO:0010286]; plasma membrane organization [GO:0007009]; protein transport [GO:0015031]; response to heat [GO:0009408]; response to osmotic stress [GO:0006970]; retrograde transport, endosome to Golgi [GO:0042147]; retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum [GO:0006890]	cytosol [GO:0005829]; endosome membrane [GO:0010008]; GARP complex [GO:0000938]; Golgi membrane [GO:0000139]; mitochondrion [GO:0005739]		Q0WQF4	VPS53	Vacuolar protein sorting-associated protein 53 A (AtVPS53) (Protein HEAT-INTOLERANT 1)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017116	2017_SL8	GO:0000151; GO:0005737; GO:0005794; GO:0006511; GO:0008270; GO:0016020; GO:0016567; GO:0031624; GO:0005506; GO:0005789;	positive regulation of proteasomal ubiquitin-dependent protein catabolic process [GO:0032436]; protein ubiquitination [GO:0016567]; ubiquitin-dependent protein catabolic process [GO:0006511]	cytoplasm [GO:0005737]; Golgi apparatus [GO:0005794]; membrane [GO:0016020]; ubiquitin ligase complex [GO:0000151]	ubiquitin conjugating enzyme binding [GO:0031624]; ubiquitin protein ligase activity [GO:0061630]; zinc ion binding [GO:0008270]	Q6DH94	rnf144ab	Probable E3 ubiquitin-protein ligase RNF144A-B (EC 2.3.2.31) (RING finger protein 144A-B)		
9	Vitvi017132	2017_SL8	GO:0009414; GO:0009737; GO:0009924; GO:0010025; GO:0016491; GO:0043447; GO:0046184; GO:1990465	aldehyde biosynthetic process [GO:0046184]; alkane biosynthetic process [GO:0043447]; response to abscisic acid [GO:0009737]; response to water deprivation [GO:0009414]; wax biosynthetic process [GO:0010025]	endoplasmic reticulum membrane [GO:0005789]	aldehyde oxygenase (deformylating) activity [GO:1990465]; iron ion binding [GO:0005506]; octadecanal decarbonylase activity [GO:0009924]; oxidoreductase activity [GO:0016491]	Q6ETL8	GL1-2	Very-long-chain aldehyde decarbonylase GL1-2 (EC 4.1.99.5) (Protein GLOSSY 1-2)		
9	Vitvi017135	2017_SL8	GO:0003684; GO:0005634; GO:0005654; GO:0005737; GO:0005829; GO:0006289; GO:0009411; GO:0009650; GO:0031593; GO:0043130	nucleotide-excision repair [GO:0006289]; proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]; response to UV [GO:0009411]; UV protection [GO:0009650]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	damaged DNA binding [GO:0003684]; polyubiquitin modification-dependent protein binding [GO:0031593]; proteasome binding [GO:0070628]; ubiquitin binding [GO:0043130]	Q84L33	RAD23B	Ubiquitin receptor RAD23b (AtRAD23b) (Putative DNA repair protein RAD23-1) (RAD23-like protein 1) (AtRAD23-1)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017112	2017_SL8	GO:0008152; GO:0016747; GO:0047172	metabolic process [GO:0008152]		acyltransferase activity, transferring groups other than amino-acyl groups [GO:0016747]; shikimate O-hydroxycinnamoyltransferase activity [GO:0047172]	Q8GSM7	HST	Shikimate O-hydroxycinnamoyltransferase (EC 2.3.1.133) (Hydroxycinnamoyl transferase) (Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase)		10.1111/eva.13566
9	Vitvi017131	2017_SL8	GO:0005506; GO:0005789; GO:0005886; GO:0006723; GO:0009924; GO:0010025; GO:0016020; GO:0016491; GO:0043447; GO:0048235; GO:0005634; GO:0005730;	alkane biosynthetic process [GO:0043447]; cuticle hydrocarbon biosynthetic process [GO:0006723]; pollen sperm cell differentiation [GO:0048235]; wax biosynthetic process [GO:0010025]	endoplasmic reticulum membrane [GO:0005789]; membrane [GO:0016020]; plasma membrane [GO:0005886]	aldehyde oxygenase (deformylating) activity [GO:1990465]; iron ion binding [GO:0005506]; octadecanal decarbonylase activity [GO:0009924]; oxidoreductase activity [GO:0016491]	Q8H1Z0	CER3	Very-long-chain aldehyde decarbonylase CER3 (EC 4.1.99.5) (Protein ECERIFERUM 3) (Protein FACELESS POLLEN 1) (Protein WAX2) (Protein YORE-YORE)		
9	Vitvi017119	2017_SL8	GO:0004315; GO:0005739; GO:0006633; GO:0010027	fatty acid biosynthetic process [GO:0006633]; thylakoid membrane organization [GO:0010027]	mitochondrion [GO:0005739]	3-oxoacyl-[acyl-carrier-protein] synthase activity [GO:0004315]	Q8L3X9	KAS	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase) (mtKAS)		
9	Vitvi017149	2017_SL8	GO:0000325; GO:0005739; GO:0005829; GO:0008239; GO:0016791; GO:0046872		cytosol [GO:0005829]; mitochondrion [GO:0005739]; plant-type vacuole [GO:0000325]	dipeptidyl-peptidase activity [GO:0008239]; metal ion binding [GO:0046872]; phosphatase activity	Q8L831	NUDT3	Nudix hydrolase 3 (AtNUDT3) (EC 3.6.1.-)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017146	2017_SL8	GO:0005634; GO:0005730; GO:0005737; GO:0005829; GO:0008757; GO:0009452; GO:0015030; GO:0036261;	7-methylguanosine cap hypermethylation [GO:0036261]; 7-methylguanosine RNA capping [GO:0009452]	Cajal body [GO:0015030]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleolus [GO:0005730]; nucleus [GO:0005634]	RNA trimethylguanosine synthase activity [GO:0071164]; S-adenosylmethionine-dependent methyltransferase activity [GO:0008757]	Q923W1	Tgs1	Trimethylguanosine synthase (EC 2.1.1.-) (Nuclear receptor coactivator 6-interacting protein) (PRIP-interacting protein with methyltransferase motif) (PIMT) (PIPMT)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017109	2017_SL8	GO:0001560; GO:0005777; GO:0005829; GO:0006144; GO:0009631; GO:0009741; GO:0009742; GO:0009898; GO:0019428; GO:0019628; GO:0031234; GO:0033971; GO:0042802; GO:0051262; GO:0051997; GO:1900140; GO:1900457	allantoin biosynthetic process [GO:0019428]; brassinosteroid mediated signaling pathway [GO:0009742]; cold acclimation [GO:0009631]; protein tetramerization [GO:0051262]; purine nucleobase metabolic process [GO:0006144]; regulation of brassinosteroid mediated signaling pathway [GO:1900457]; regulation of cell growth by extracellular stimulus [GO:0001560]; regulation of seedling development [GO:1900140]; response to brassinosteroid [GO:0009741]; urate catabolic process [GO:0019628]	cytoplasmic side of plasma membrane [GO:0009898]; cytosol [GO:0005829]; extrinsic component of cytoplasmic side of plasma membrane [GO:0031234]; peroxisome [GO:0005777]	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase activity [GO:0051997]; hydroxyisourate hydrolase activity [GO:0033971]; identical protein binding [GO:0042802]	Q9LVM5	TTL	Uric acid degradation bifunctional protein TTL (Transthyretin-like protein) [Includes: 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase (OHCU decarboxylase) (EC 4.1.1.97); 5-hydroxyisourate hydrolase (HIU hydrolase) (HIUHase) (EC 3.5.2.17)]		
9	Vitvi017156	2017_SL8					Q9S9M8	TULP8	Tubby-like protein 8 (AtTLP8)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017113	2017_SL8	GO:0004674; GO:0005524; GO:0005886; GO:0016310; GO:0106310	phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9ZUI0		Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130 (EC 2.7.11.1)		
9	Vitvi017162	2016_BeWe7	GO:0005634; GO:0009909	regulation of flower development [GO:0009909]	nucleus [GO:0005634]		B8AE37	HDR1	Protein HEADING DATE REPRESSOR 1	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017171	2016_BeWe7	GO:0004307; GO:0005789; GO:0006506; GO:0051377	GPI anchor biosynthetic process [GO:0006506]	endoplasmic reticulum membrane [GO:0005789]	ethanolaminephosphotransferase activity [GO:0004307]; mannose-ethanolamine phosphotransferase activity	Q07326	PIGF	Phosphatidylinositol-glycan biosynthesis class F protein (PIG-F) (GPI11 homolog)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017147	2016_BeWe7	GO:0003777; GO:0003779; GO:0005524; GO:0005737; GO:0005874; GO:0007017; GO:0007018; GO:0007097; GO:0008017; GO:0008569; GO:0015629; GO:0015630; GO:0016887; GO:0031534	microtubule-based movement [GO:0007018]; microtubule-based process [GO:0007017]; minus-end directed microtubule sliding [GO:0031534]; nuclear migration [GO:0007097]; nucleus localization [GO:0051647]	actin cytoskeleton [GO:0015629]; cytoplasm [GO:0005737]; microtubule [GO:0005874]; microtubule cytoskeleton [GO:0015630]	actin binding [GO:0003779]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; microtubule binding [GO:0008017]; microtubule motor activity [GO:0003777]; minus-end-directed microtubule motor activity [GO:0008569]; protein self-association	Q0IMS9	KIN14Q	Kinesin-like protein KIN-14Q (Kinesin O12) (OsKCH1)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017154	2016_BeWe7	GO:0000139; GO:0000938; GO:0005739; GO:0005829; GO:0006890; GO:0006970; GO:0007009; GO:0009408; GO:0010008; GO:0010286; GO:0015031; GO:0042147	heat acclimation [GO:0010286]; plasma membrane organization [GO:0007009]; protein transport [GO:0015031]; response to heat [GO:0009408]; response to osmotic stress [GO:0006970]; retrograde transport, endosome to Golgi [GO:0042147]; retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum [GO:0006890]	cytosol [GO:0005829]; endosome membrane [GO:0010008]; GARP complex [GO:0000938]; Golgi membrane [GO:0000139]; mitochondrion [GO:0005739]		Q0WQF4	VPS53	Vacuolar protein sorting-associated protein 53 A (AtVPS53) (Protein HEAT-INTOLERANT 1)	chr9：16267491	10.1093/hr/uhab011

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
9	Vitvi017135	2016_BeWe7	GO:0003684; GO:0005634; GO:0005654; GO:0005737; GO:0005829; GO:0006289; GO:0009411; GO:0009650; GO:0031593; GO:0043130;	nucleotide-excision repair [GO:0006289]; proteasome-mediated ubiquitin-dependent protein catabolic process [GO:0043161]; response to UV [GO:0009411]; UV protection [GO:0009650]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]	damaged DNA binding [GO:0003684]; polyubiquitin modification-dependent protein binding [GO:0031593]; proteasome binding [GO:0070628]; ubiquitin binding [GO:0043130]	Q84L33	RAD23B	Ubiquitin receptor RAD23b (AtRAD23b) (Putative DNA repair protein RAD23-1) (RAD23-like protein 1) (AtRAD23-1)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017149	2016_BeWe7	GO:0000325; GO:0005739; GO:0005829; GO:0008239; GO:0016791; GO:0046872		cytosol [GO:0005829]; mitochondrion [GO:0005739]; plant-type vacuole [GO:0000325]	dipeptidyl-peptidase activity [GO:0008239]; metal ion binding [GO:0046872]; phosphatase activity	Q8L831	NUDT3	Nudix hydrolase 3 (AtNUDT3) (EC 3.6.1.-)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017163	2016_BeWe7	GO:0003729; GO:0005737; GO:0046540; GO:0048025	negative regulation of mRNA splicing, via spliceosome [GO:00480251	cytoplasm [GO:0005737]; U4/U6 x U5 tri-snRNP complex [GO:0046540]	mRNA binding [GO:0003729]	Q91V81	Rbm42	RNA-binding protein 42 (RNA-binding motif protein 42)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017146	2016_BeWe7	GO:0005634; GO:0005730; GO:0005737; GO:0005829; GO:0008757; GO:0009452; GO:0015030; GO:0036261;	7-methylguanosine cap hypermethylation [GO:0036261]; 7-methylguanosine RNA capping [GO:0009452]	Cajal body [GO:0015030]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleolus [GO:0005730]; nucleus [GO:0005634]	RNA trimethylguanosine synthase activity [GO:0071164]; S-adenosylmethionine-dependent methyltransferase activity [GO:0008757]	Q923W1	Tgs1	Trimethylguanosine synthase (EC 2.1.1.-) (Nuclear receptor coactivator 6-interacting protein) (PRIP-interacting protein with methyltransferase motif) (PIMT) (PIPMT)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017176	2016_BeWe7	GO:0005768; GO:0005794; GO:0005802; GO:0005886; GO:0006888; GO:0009826; GO:0015031; GO:0015774; GO:0032588; GO:0042803; GO:0045489; GO:0048364; GO:0048766; GO:0051223; GO:0052324; GO:0099402	endoplasmic reticulum to Golgi vesicle-mediated transport [GO:0006888]; pectin biosynthetic process [GO:0045489]; plant organ development [GO:0099402]; plant-type cell wall cellulose biosynthetic process [GO:0052324]; polysaccharide transport [GO:0015774]; protein transport [GO:0015031]; regulation of protein transport [GO:0051223]; root development [GO:0048364]; root hair initiation [GO:0048766]; unidimensional cell growth [GO:0009826]	endosome [GO:0005768]; Golgi apparatus [GO:0005794]; plasma membrane [GO:0005886]; trans-Golgi network [GO:0005802]; trans-Golgi network membrane [GO:0032588]	protein homodimerization activity [GO:0042803]	Q93VH1	YIP4B	Protein YIP4b (YPT/RAB GTPase-interacting protein 4b) (YIP4b)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017158	2016_BeWe7	GO:0000981; GO:0003677; GO:0003700; GO:0005634; GO:0009414; GO:0009651; GO:0009737; GO:0009873; GO:0010187; GO:0040008; GO:0045723; GO:1901959	ethylene-activated signaling pathway [GO:0009873]; negative regulation of seed germination [GO:0010187]; positive regulation of cutin biosynthetic process [GO:1901959]; positive regulation of fatty acid biosynthetic process [GO:0045723]; regulation of growth [GO:0040008]; response to abscisic acid [GO:0009737]; response to salt stress [GO:0009651]; response to water deprivation [GO:0009414]	nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]	Q94AN4		AP2-like ethylene-responsive transcription factor At1g16060	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017175	2016_BeWe7	GO:0005634; GO:0009409; GO:0009416; GO:0009507; GO:0009535; GO:0009570; GO:0009744; GO:0009941; GO:0010319	response to cold [GO:0009409]; response to light stimulus [GO:0009416]; response to sucrose [GO:0009744]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast stroma [GO:0009570]; chloroplast thylakoid membrane [GO:0009535]; nucleus [GO:0005634]; stromule [GO:0010319]		Q9FZ47	ACR11	ACT domain-containing protein ACR11 (Protein ACT DOMAIN REPEATS 11)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017156	2016_BeWe7					Q9S9M8	TULP8	Tubby-like protein 8 (AtTLP8)	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017159	2016_BeWe7	GO:0016020		membrane [GO:0016020]		Q9SQN2		Probable folate-biopterin transporter 3	chr9：16267491	10.1093/hr/uhab011
9	Vitvi017413	2016_BV13	GO:0005634; GO:0006355;	regulation of DNA-templated transcription [GO:0006355]	nucleus [GO:0005634]	zinc ion binding [GO:0008270]	Q6NQJ7	FRS4	Protein FAR1-RELATED SEQUENCE 4	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017389	2016_BV13	GO:0004672; GO:0005524; GO:0016020		membrane [GO:0016020]	ATP binding [GO:0005524]; protein kinase activity [GO:0004672]	Q6R2K1	SRF5	Protein STRUBBELIG-RECEPTOR FAMILY 5 (Leucine-rich repeat receptor kinase-like protein SRF5)	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017406	2016_BV13	GO:0003723; GO:0003729; GO:0006413; GO:0009507; GO:0009523; GO:0009535; GO:0009570; GO:0009941; GO:0010207; GO:0031969; GO:0042651	photosystem II assembly [GO:0010207]; translational initiation [GO:0006413]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast membrane [GO:0031969]; chloroplast stroma [GO:0009570]; chloroplast thylakoid membrane [GO:0009535]; photosystem II [GO:0009523]; thylakoid membrane [GO:0042651]	mRNA binding [GO:0003729]; RNA binding [GO:0003723]	Q8W4D6	HCF173	Protein HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173, chloroplastic	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017392	2016_BV13	GO:0005524; GO:0005886; GO:0006811; GO:0090416; GO:0090417; GO:2001142; GO:2001143	monoatomic ion transport [GO:0006811]; N-methylnicotinate transport [GO:2001143]; nicotinate transport [GO:2001142]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; N-methylnicotinate transmembrane transporter activity [GO:0090417]; nicotinate transmembrane transporter activity [GO:0090416]	Q940M4	OCT7	Organic cation/carnitine transporter 7 (AtOCT7)	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017388	2016_BV13	GO:0005811; GO:0016104; GO:0031559	triterpenoid biosynthetic process [GO:0016104]	lipid droplet [GO:0005811]	oxidosqualene cyclase activity [GO:0031559]	Q948R6	IMS1	Isomultiflorenol synthase (LcIMS1) (EC 5.4.99.36)	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017407	2016_BV13	GO:0000123; GO:0003713; GO:0004402; GO:0005634; GO:0005667; GO:0008270; GO:0031490; GO:0045944	positive regulation of transcription by RNA polymerase II [GO:0045944]	histone acetyltransferase complex [GO:0000123]; nucleus [GO:0005634]; transcription regulator complex [GO:0005667]	chromatin DNA binding [GO:0031490]; histone acetyltransferase activity [GO:0004402]; transcription coactivator activity [GO:0003713]; zinc ion binding [GO:0008270]	Q9C5X9	HAC1	Histone acetyltransferase HAC1 (EC 2.3.1.48)	chr9：~23Mb	10.1186/s12870-020-02564-4
9	Vitvi017408	2016_BV13	GO:0000976; GO:0003700; GO:0005634; GO:0009873	ethylene-activated signaling pathway [GO:0009873]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9FZ90	ERF087	Ethylene-responsive transcription factor ERF087	chr9：~23Mb	10.1186/s12870-020-02564-4
10	Vitvi018963	2017_SL9	GO:0004674; GO:0005524; GO:0005886; GO:0016310; GO:0106310	phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	C0LGH2		Probable LRR receptor-like serine/threonine-protein kinase At1g56130 (EC 2.7.11.1)		
10	Vitvi018982	2017_SL9	GO:0009698; GO:0016020; GO:0016592; GO:2000762	phenylpropanoid metabolic process [GO:0009698]; regulation of phenylpropanoid metabolic process [GO:2000762]	mediator complex [GO:0016592]; membrane [GO:0016020]		F4IN69	MED33B	Mediator of RNA polymerase II transcription subunit 33B (Protein REDUCED EPIDERMAL FLUORESCENCE 4)		10.1139/g06-122
10	Vitvi018952	2017_SL9	GO:0000139; GO:0000938; GO:0005829; GO:0009507; GO:0015031; GO:0042147	protein transport [GO:0015031]; retrograde transport, endosome to Golgi [GO:0042147]	chloroplast [GO:0009507]; cytosol [GO:0005829]; GARP complex [GO:0000938]; Golgi membrane [GO:0000139]		F4JT76	VPS54	Vacuolar protein sorting-associated protein 54, chloroplastic (AtVPS54)		10.1139/g06-122
10	Vitvi018967	2017_SL9	GO:0004497; GO:0005506; GO:0016020; GO:0016705; GO:0020037		membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	H2DH20		Cytochrome P450 CYP71D313 (EC 1.14.-.-)		10.1139/g06-122
10	Vitvi018962	2017_SL9	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	O48923	CYP71D10	Cytochrome P450 71D10 (EC 1.14.-.-)		10.1139/g06-122
10	Vitvi018966	2017_SL9	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	P93530	CYP71D6	Cytochrome P450 71D6 (EC 1.14.-.-)		10.1139/g06-122
10	Vitvi018956	2017_SL9	GO:0000815; GO:0007034; GO:0015031	protein transport [GO:0015031]; vacuolar transport [GO:0007034]	ESCRT III complex [GO:0000815]		Q0WTY4	VPS2.2	Vacuolar protein sorting-associated protein 2 homolog 2 (AtVPS2-2) (Charged multivesicular body protein 2 homolog 2) (ESCRT-III complex subunit VPS2 homolog		10.1139/g06-122

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
10	Vitvi018957	2017_SL9	GO:0004497; GO:0005506; GO:0016705; GO:0020037			heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	W8JCE8	CYP71BT1	Cytochrome P450 71BT1 (CrCYP71BT1) (EC 1.14.-.-)		10.1139/g06-122
11	Vitvi019837	2017_BuW2	GO:0003779; GO:0005737; GO:0005856		cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]	actin binding [GO:0003779]	A4K9Z8		Profilin-2 (Allergen Bet v II) (Pollen allergen Bet v 2) (allergen Bet v 2)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019861	2017_BuW2	GO:0016706; GO:0044249; GO:0044283; GO:0044550; GO:0046872; GO:1901362	cellular biosynthetic process [GO:0044249]; organic cyclic compound biosynthetic process [GO:1901362]; secondary metabolite biosynthetic process [GO:0044550]; small molecule biosynthetic process [GO:0044283]		2-oxoglutarate-dependent dioxygenase activity [GO:0016706]; metal ion binding [GO:0046872]	C8VK14	hxnY	2-oxoglutarate-Fe(II) type oxidoreductase hxnY (EC 1.14.11.-) (Nicotinate catabolism cluster protein hxnY)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019855	2017_BuW2	GO:0002239; GO:0009409; GO:0009507; GO:0009651	response to cold [GO:0009409]; response to oomycetes [GO:0002239]; response to salt stress [GO:0009651]	chloroplast [GO:0009507]		F4JNX2	P85	Senescence/dehydration-associated protein At4g35985, chloroplastic	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019842	2017_BuW2	GO:0004814; GO:0005524; GO:0005739; GO:0005829; GO:0006420; GO:0009507; GO:0009570; GO:0009793	arginyl-tRNA aminoacylation [GO:0006420]; embryo development ending in seed dormancy [GO:0009793]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; mitochondrion [GO:0005739]	arginine-tRNA ligase activity [GO:0004814]; ATP binding [GO:0005524]	O23247	EMB1027	Arginine--tRNA ligase, chloroplastic/mitochondrial (EC 6.1.1.19) (Arginyl-tRNA synthetase) (ArgRS) (Protein EMBRYO DEFECTIVE 1027)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019838	2017_BuW2	GO:0003779; GO:0005737; GO:0005856		cytoplasm [GO:0005737]; cytoskeleton [GO:0005856]	actin binding [GO:0003779]	O82572	PRO1	Profilin-1	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019858	2017_BuW2	GO:0000160; GO:0005634; GO:0005737; GO:0009736; GO:0009927; GO:0016310; GO:0035634; GO:0005829;	cytokinin-activated signaling pathway [GO:0009736]; phosphorelay signal transduction system [GO:0000160]; phosphorylation [GO:0016310]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	histidine phosphotransfer kinase activity [GO:0009927]; protein histidine kinase binding [GO:0043424]	Q0DK78	PHP2	Pseudo histidine-containing phosphotransfer protein 2 (OsHpt4)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019856	2017_BuW2	GO:0016763; GO:0019988; GO:0043399	charged-tRNA amino acid modification [GO:0019988]	cytosol [GO:0005829]; nucleus [GO:0005634]	pentosyltransferase activity [GO:0016763]; tRNA A64-2'-O-ribosylphosphate transferase activity	Q10181		Uncharacterized protein C3F10.06c	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019853	2017_BuW2	GO:0000154; GO:0003723; GO:0005739; GO:0016435	rRNA modification [GO:0000154]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]; rRNA (guanine) methyltransferase activity [GO:0016435]	Q76NT0	mrm1	rRNA methyltransferase 1, mitochondrial (EC 2.1.1.-) (rRNA (guanosine-2'-O)-methyltransferase)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019844	2017_BuW2	GO:0004181; GO:0005773; GO:0005783; GO:0005789; GO:0006508; GO:0010073;	meristem maintenance [GO:0010073]; proteolysis [GO:0006508]; regulation of meristem growth [GO:0010075]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]; vacuole [GO:0005773]	metal ion binding [GO:0046872]; metallocarboxypeptidase activity [GO:0004181]	Q7Y228	LAMP1	Probable glutamate carboxypeptidase LAMP1 (EC 3.4.17.21) (Protein LIKE AMP1)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019857	2017_BuW2	GO:0005524; GO:0016020; GO:0016887; GO:0042626; GO:0055085; GO:0140359	transmembrane transport [GO:0055085]	membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled transmembrane transporter activity [GO:0042626]	Q9LHK4	ABCB8	Putative ABC transporter B family member 8 (ABC transporter ABCB.8) (AtABCB8) (P-glycoprotein 8) (Putative multidrug resistance protein 22)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019843	2017_BuW2	GO:0004674; GO:0005524; GO:0005737; GO:0005794; GO:0005942; GO:0009555; GO:0009846; GO:0010008; GO:0015031; GO:0016236; GO:0016310; GO:0045324;	late endosome to vacuole transport [GO:0045324]; macroautophagy [GO:0016236]; phosphorylation [GO:0016310]; pollen development [GO:0009555]; pollen germination [GO:0009846]; protein transport [GO:0015031]	Cul4-RING E3 ubiquitin ligase complex [GO:0080008]; cytoplasm [GO:0005737]; endosome membrane [GO:0010008]; Golgi apparatus [GO:0005794]; phosphatidylinositol 3-kinase complex [GO:0005942]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9M0E5	VPS15	Serine/threonine-protein kinase VPS15 (EC 2.7.11.1) (Vacuolar protein sorting-associated protein 15) (AtVPS15)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019849	2017_BuW2	GO:0001678; GO:0004340; GO:0005524; GO:0005536; GO:0006096; GO:0008865; GO:0009707; GO:0019318;	glycolytic process [GO:0006096]; hexose metabolic process [GO:0019318]; intracellular glucose homeostasis [GO:0001678]	chloroplast outer membrane [GO:0009707]	ATP binding [GO:0005524]; fructokinase activity [GO:0008865]; glucokinase activity [GO:0004340]; glucose binding [GO:0005536]	Q9SEK3	HXK1	Hexokinase-1 (EC 2.7.1.1) (SoHxK1)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019860	2017_BuW2	GO:0004842; GO:0005634; GO:0005737; GO:0005829; GO:0009414; GO:0009737; GO:0009738; GO:0046872;	abscisic acid-activated signaling pathway [GO:0009738]; protein autoubiquitination [GO:0051865]; response to abscisic acid [GO:0009737]; response to water deprivation [GO:0009414]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]	metal ion binding [GO:0046872]; ubiquitin protein ligase activity [GO:0061630]; ubiquitin-protein transferase activity [GO:0004842]	Q9SNB6	RDUF1	E3 ubiquitin-protein ligase RDUF1 (EC 2.3.2.27) (RING and DUF1117 domain-containing protein 1) (AtRDUF1) (RING-type E3 ubiquitin transferase RDUF1)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019852	2017_BuW2	GO:0005739; GO:0005741; GO:0005743; GO:0005744; GO:0005783; GO:0045039	protein insertion into mitochondrial inner membrane [GO:0045039]	endoplasmic reticulum [GO:0005783]; mitochondrial inner membrane [GO:0005743]; mitochondrial outer membrane [GO:0005741]; mitochondrion [GO:0005739]; TIM23 mitochondrial import inner membrane translocase complex [GO:0005744]		Q9SP35	TIM17-2	Mitochondrial import inner membrane translocase subunit TIM17-2	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019851	2017_BuW2	GO:0005739; GO:0006574; GO:0008442; GO:0050661; GO:0051287	valine catabolic process [GO:0006574]	mitochondrion [GO:0005739]	3-hydroxyisobutyrate dehydrogenase activity [GO:0008442]; NAD binding [GO:0051287]; NADP binding [GO:0050661]	Q9SZE1		Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial (HIBADH-like) (EC 1.1.1.31)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi019848	2017_BuW2	GO:0005770; GO:0006952; GO:0010008; GO:0010015; GO:0010600; GO:0015297; GO:0031348; GO:0031902; GO:0042910; GO:0046620; GO:1990961	defense response [GO:0006952]; negative regulation of defense response [GO:0031348]; regulation of auxin biosynthetic process [GO:0010600]; regulation of organ growth [GO:0046620]; root morphogenesis [GO:0010015]; xenobiotic detoxification by transmembrane export across the plasma membrane [GO:1990961]	endosome membrane [GO:0010008]; late endosome [GO:0005770]; late endosome membrane [GO:0031902]	antiporter activity [GO:0015297]; xenobiotic transmembrane transporter activity [GO:0042910]	Q9SZE2	DTX51	Protein DETOXIFICATION 51 (AtDTX51) (Multidrug and toxic compound extrusion protein 51) (MATE protein 51) (Protein ABNORMAL SHOOT 3) (Protein ACTIVATED DISEASE SUSCEPTIBILITY 1) (Protein ADS1) (Protein ALTERED DEVELOPMENT PROGRAM 1) (Protein ADP1) (Protein NOVEL ION CARRIER 4)	chr11: 2348595-2448595	10.1093/g3journal/jkac103
11	Vitvi020118	2016_BV15	GO:0003746; GO:0005759; GO:0070125	mitochondrial translational elongation [GO:0070125]	mitochondrial matrix [GO:0005759]	translation elongation factor activity [GO:0003746]	B9SEZ6	EFTS	Elongation factor Ts, mitochondrial (EF-Ts) (EF-TsMt)		
11	Vitvi020124	2016_BV15	GO:0005096; GO:0005576; GO:0005737; GO:0005739; GO:0043087	regulation of GTPase activity [GO:0043087]	cytoplasm [GO:0005737]; extracellular region [GO:0005576]; mitochondrion [GO:0005739]	GTPase activator activity [GO:0005096]	Q9CXF4	Tbc1d15	TBC1 domain family member 15 (GTPase-activating protein RAB7) (GAP for RAB7) (Rab7-GAP)		
11	Vitvi020122	2016_BV15	GO:0003677; GO:0005634; GO:0010026; GO:0045893; GO:0000993; GO:0001113;	positive regulation of DNA-templated transcription [GO:0045893]; trichome differentiation [GO:0010026]; transcription by RNA polymerase II [GO:0006366];	nucleus [GO:0005634]	DNA binding [GO:0003677]	Q9LTF7	MYB82	Transcription factor MYB82 (Myb-related protein 82) (AtMYB82)		
11	Vitvi021075	2016_EDP2	GO:0005634; GO:0005673; GO:0005739; GO:0006366; GO:0006367; GO:0046872;	transcription initiation at RNA polymerase II promoter [GO:0006367]; transcription open complex formation at RNA polymerase II promoter [GO:0001113]	mitochondrion [GO:0005739]; nucleus [GO:0005634]; transcription factor TFIIE complex [GO:0005673]; transcription preinitiation complex	metal ion binding [GO:0046872]; RNA polymerase II complex binding [GO:0000993]	P36100	TFA1	Transcription initiation factor IIE subunit alpha (TFIIE-alpha) (Factor A 66 kDa subunit) (Transcription factor A large subunit)		
11	Vitvi021071	2016_EDP2	GO:0003723; GO:0030488; GO:0089715	tRNA methylation [GO:0030488]		RNA binding [GO:0003723]; tRNA m6t6A37 methyltransferase activity [GO:0089715]	Q562D6	Trmo	tRNA (adenine(37)-N6)-methyltransferase (EC 2.1.1.-) (tRNA methyltransferase O)		
11	Vitvi021072	2016_EDP2	GO:0004143; GO:0005524; GO:0006952; GO:0007205; GO:0009506; GO:0016310	defense response [GO:0006952]; phosphorylation [GO:0016310]; protein kinase C-activating G protein-coupled receptor signaling pathway [GO:0007205]	plasmodesma [GO:0009506]	ATP binding [GO:0005524]; ATP-dependent diacylglycerol kinase activity [GO:0004143]	Q8VZG1	DGK3	Diacylglycerol kinase 3 (AtDGK3) (DAG kinase 3) (EC 2.7.1.107) (Diglyceride kinase 3) (DGK 3)		
12	Vitvi021314	2016_BeS3	GO:0009534; GO:0009535; GO:0033614	chloroplast proton-transporting ATP synthase complex assembly [GO:0033614]	chloroplast thylakoid [GO:0009534]; chloroplast thylakoid membrane [GO:0009535]		O82279	CGL160	Protein CONSERVED ONLY IN THE GREEN LINEAGE 160, chloroplastic (AtCGL160)		
12	Vitvi022614	2017_TAC4	GO:0003729; GO:0009507; GO:0009658; GO:1900865	chloroplast organization [GO:0009658]; chloroplast RNA modification [GO:1900865]	chloroplast [GO:0009507]	mRNA binding [GO:0003729]	Q0WVV0		Pentatricopeptide repeat-containing protein At1g10910, chloroplastic		
12	Vitvi022616	2017_TAC4	GO:0006633; GO:0009922; GO:0016020	fatty acid biosynthetic process [GO:0006633]	membrane [GO:0016020]	fatty acid elongase activity [GO:0009922]	Q9C992	KCS7	3-ketoacyl-CoA synthase 7 (KCS-7) (EC 2.3.1.199) (Very long-chain fatty acid condensing enzyme 7) (VLCFA condensing		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
12	Vitvi022654	2016_Fru2	GO:0004674; GO:0005524; GO:0016020; GO:0016310; GO:0106310	phosphorylation [GO:0016310]	membrane [GO:0016020]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	O04086		Probable receptor-like protein kinase At1g11050 (EC 2.7.11.1)		
12	Vitvi022657	2016_Fru2	GO:0003980; GO:0005739; GO:0005783; GO:0005788; GO:0009626; GO:0009751; GO:0046283	anthocyanin-containing compound metabolic process [GO:0046283]; plant-type hypersensitive response [GO:0009626]; response to salicylic acid [GO:0009751]	endoplasmic reticulum [GO:0005783]; endoplasmic reticulum lumen [GO:0005788]; mitochondrion [GO:0005739]	UDP-glucose:glycoprotein glucosyltransferase activity [GO:0003980]	Q0WL80	UGGT	UDP-glucose:glycoprotein glucosyltransferase (EC 2.4.1.-) (EMS-mutagenized BRI1 suppressor 1) (Protein PRIORITY IN SWEET LIFE 2)		
12	Vitvi022662	2016_Fru2	GO:0005249; GO:0005789; GO:0009506; GO:0009737; GO:0034765; GO:0042391;	regulation of membrane potential [GO:0042391]; regulation of monoatomic ion transmembrane transport [GO:0034765]; response to abscisic acid [GO:0009737]	endoplasmic reticulum membrane [GO:0005789]; plasmodesma [GO:0009506]	identical protein binding [GO:0042802]; voltage-gated potassium channel activity [GO:0005249]	Q38898	AKT2	Potassium channel AKT2/3		
12	Vitvi022651	2016_Fru2	GO:0009507; GO:0016740		chloroplast [GO:0009507]	transferase activity [GO:0016740]	Q681Y3		Putative transferase At1g60990, chloroplastic (EC 2.1.-.-) (Iron-sulfur cluster assembly factor homolog COG0354)		
12	Vitvi022653	2016_Fru2	GO:0005737; GO:0005829; GO:0005930; GO:0031514; GO:0036126; GO:0051082; GO:0051085; GO:0051087; GO:0097224; GO:1904158	axonemal central apparatus assembly [GO:1904158]; chaperone cofactor-dependent protein refolding [GO:0051085]	axoneme [GO:0005930]; cytoplasm [GO:0005737]; cytosol [GO:0005829]; motile cilium [GO:0031514]; sperm connecting piece [GO:0097224]; sperm flagellum [GO:0036126]	protein-folding chaperone binding [GO:0051087]; unfolded protein binding [GO:0051082]	Q80Y75	Dnajb13	DnaJ homolog subfamily B member 13 (Testis and spermatogenesis cell-related protein 6) (Testis spermatocyte apoptosis-related gene 6 protein) (Testis spermatogenesis apoptosis-related gene 3 protein) (Testis spermatogenesis apoptosis-related gene 6 protein)		
12	Vitvi022674	2016_Fru2	GO:0004372; GO:0005634; GO:0005737; GO:0019264; GO:0030170; GO:0035999; GO:0044030; GO:0046500; GO:0046686; GO:0055063	glycine biosynthetic process from serine [GO:0019264]; regulation of DNA methylation [GO:0044030]; response to cadmium ion [GO:0046686]; S-adenosylmethionine metabolic process [GO:0046500]; sulfate ion homeostasis [GO:0055063]; tetrahydrofolate interconversion	cytoplasm [GO:0005737]; nucleus [GO:0005634]	glycine hydroxymethyltransferase activity [GO:0004372]; pyridoxal phosphate binding [GO:0030170]	Q84WV0	SHM7	Serine hydroxymethyltransferase 7 (AtSHMT7) (EC 2.1.2.1) (Glycine hydroxymethyltransferase 7) (Serine methylase 7)		
12	Vitvi022654	2016_Cit4	GO:0004674; GO:0005524; GO:0016020; GO:0016310; GO:0106310	phosphorylation [GO:0016310]	membrane [GO:0016020]	ATP binding [GO:0005524]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	O04086		Probable receptor-like protein kinase At1g11050 (EC 2.7.11.1)		
14	Vitvi025778	2017_BuW3	GO:0005789; GO:0030544; GO:0051085; GO:0065003; GO:0071218	cellular response to misfolded protein [GO:0071218]; chaperone cofactor-dependent protein refolding [GO:0051085]; protein-containing complex assembly	endoplasmic reticulum membrane [GO:0005789]	Hsp70 protein binding [GO:0030544]	Q17438	dnj-1	DnaJ homolog subfamily B member 1		
14	Vitvi025749	2017_BuW3	GO:0000398; GO:0003723; GO:0005681; GO:0016607	mRNA splicing, via spliceosome [GO:0000398]	nuclear speck [GO:0016607]; spliceosomal complex [GO:0005681]	RNA binding [GO:0003723]	Q1PDV2	SCL28	Serine/arginine-rich SC35-like splicing factor SCL28 (At-SCL28) (AtSCL28) (28 kDa SC35-like splicing factor) (SC35-like splicing factor 28) (Serine/arginine-rich splicing factor		
14	Vitvi025751	2017_BuW3	GO:0005789; GO:0019706; GO:0030659		cytoplasmic vesicle membrane [GO:0030659]; endoplasmic reticulum membrane [GO:0005789]	protein-cysteine S-palmitoyltransferase activity [GO:0019706]	Q3EBC2	PAT17	Probable protein S-acyltransferase 17 (EC 2.3.1.225) (Probable palmitoyltransferase At3g04970) (Zinc finger DHHC domain-containing protein At3g04970)		
14	Vitvi025744	2017_BuW3	GO:0005634; GO:0005737; GO:0009739; GO:0009939; GO:0010331; GO:0010476; GO:0016787; GO:0048444; GO:0048530; GO:0071456; GO:1905516	cellular response to hypoxia [GO:0071456]; floral organ morphogenesis [GO:0048444]; fruit morphogenesis [GO:0048530]; gibberellin mediated signaling pathway [GO:0010476]; positive regulation of fertilization [GO:1905516]; positive regulation of gibberellic acid mediated signaling pathway [GO:0009939]; response to	cytoplasm [GO:0005737]; nucleus [GO:0005634]	gibberellin binding [GO:0010331]; hydrolase activity [GO:0016787]	Q9MAA7	GID1A	Gibberellin receptor GID1A (EC 3.-.-.-) (AtCXE10) (Carboxylesterase 10) (GID1-like protein 1) (Protein GA INSENSITIVE DWARF 1A) (AtGID1A)		
14	Vitvi025791	2017_BuW4	GO:0009908; GO:0030154	cell differentiation [GO:0030154]; flower development [GO:0009908]			A0SWL0	FRL2	FRIGIDA-like protein 2 (AtFRL2)		
14	Vitvi025792	2017_BuW4	GO:0005576; GO:0005789; GO:0005886; GO:0046907	intracellular transport [GO:0046907]	endoplasmic reticulum membrane [GO:0005789]; extracellular region [GO:0005576]; plasma membrane [GO:0005886]		B9DHD7	PVA22	Vesicle-associated protein 2-2 (Plant VAP homolog 22) (AtPVA22) (VAMP-associated protein 2-2) (Vesicle-associated protein 27-2)		
14	Vitvi025778	2017_BuW4	GO:0005789; GO:0030544; GO:0051085; GO:0065003; GO:0071218	cellular response to misfolded protein [GO:0071218]; chaperone cofactor-dependent protein refolding [GO:0051085]; protein-containing complex assembly	endoplasmic reticulum membrane [GO:0005789]	Hsp70 protein binding [GO:0030544]	Q17438	dnj-1	DnaJ homolog subfamily B member 1		
14	Vitvi025786	2017_BuW4	GO:0005783; GO:0005801; GO:0005802; GO:0006888; GO:0007399; GO:0030008	endoplasmic reticulum to Golgi vesicle-mediated transport [GO:0006888]; nervous system development [GO:0007399]	cis-Golgi network [GO:0005801]; endoplasmic reticulum [GO:0005783]; trans-Golgi network [GO:0005802]; TRAPP complex [GO:0030008]		Q32L78	TRAPPC6B	Trafficking protein particle complex subunit 6B (TRAPP complex subunit 6B)		
14	Vitvi025787	2017_BuW4	GO:0005774; GO:0005829; GO:0006885; GO:0015385; GO:0015386; GO:0055075;	potassium ion homeostasis [GO:0055075]; potassium ion import across plasma membrane [GO:1990573]; regulation of pH [GO:0006885]; regulation of stomatal closure	cytosol [GO:0005829]; vacuolar membrane [GO:0005774]	potassium:proton antiporter activity [GO:0015386]; sodium:proton antiporter activity [GO:0015385]	Q56XP4	NHX2	Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2)		
14	Vitvi025795	2017_BuW4	GO:0002237; GO:0005886; GO:0006970; GO:0007186; GO:0008502; GO:0010015; GO:0010555; GO:0019236; GO:0090333; GO:1904408	G protein-coupled receptor signaling pathway [GO:0007186]; regulation of stomatal closure [GO:0090333]; response to mannitol [GO:0010555]; response to molecule of bacterial origin [GO:0002237]; response to osmotic stress [GO:0006970]; response to pheromone [GO:0019236]; root morphogenesis [GO:0010015]	plasma membrane [GO:0005886]	melatonin binding [GO:1904408]; melatonin receptor activity [GO:0008502]	Q94AH1	CAND2	Protein CANDIDATE G-PROTEIN COUPLED RECEPTOR 2 (AtCand2) (Protein PHYTOMELATONIN RECEPTOR 1)		
14	Vitvi025795	2017_BuW5	GO:0002237; GO:0005886; GO:0006970; GO:0007186; GO:0008502; GO:0010015; GO:0010555; GO:0019236; GO:0090333; GO:1904408	G protein-coupled receptor signaling pathway [GO:0007186]; regulation of stomatal closure [GO:0090333]; response to mannitol [GO:0010555]; response to molecule of bacterial origin [GO:0002237]; response to osmotic stress [GO:0006970]; response to pheromone [GO:0019236]; root morphogenesis [GO:0010015]	plasma membrane [GO:0005886]	melatonin binding [GO:1904408]; melatonin receptor activity [GO:0008502]	Q94AH1	CAND2	Protein CANDIDATE G-PROTEIN COUPLED RECEPTOR 2 (AtCand2) (Protein PHYTOMELATONIN RECEPTOR 1)		
15	Vitvi029003	2016_BuW6	GO:0005576; GO:0005764; GO:0005975; GO:0008061	carbohydrate metabolic process [GO:0005975]	extracellular region [GO:0005576]; lysosome [GO:0005764]	chitin binding [GO:0008061]	Q68EX9	chid1	Chitinase domain-containing protein 1	chr15: 20107619-20215797	10.1093/g3journal/jkac103
15	Vitvi029000	2016_BuW6	GO:0004864; GO:0005634; GO:0005737; GO:0005886; GO:0009738; GO:0010427; GO:0038023; GO:0042803	abscisic acid-activated signaling pathway [GO:0009738]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	abscisic acid binding [GO:0010427]; protein homodimerization activity [GO:0042803]; protein phosphatase inhibitor activity [GO:0004864]; signaling receptor activity [GO:0038023]	Q84MC7	PYL9	Abscisic acid receptor PYL9 (ABI1-binding protein 4) (PYR1-like protein 9) (Regulatory components of ABA receptor 1)	chr15: 20107619-20215797	10.1093/g3journal/jkac103
15	Vitvi029007	2016_BuW6	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0010091; GO:0010154; GO:0000775; GO:0000776;	fruit development [GO:0010154]; regulation of DNA-templated transcription [GO:0006355]; regulation of trichome patterning [GO:1900032]; trichome branching [GO:0010091]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q8GV05	TRY	Transcription factor TRY (Protein TRIPTYCHON)	chr15: 20107619-20215797	10.1093/g3journal/jkac103
15	Vitvi029005	2016_BuW6	GO:0000785; GO:0000786; GO:0003677; GO:0005634; GO:0009567; GO:0030527; GO:0034508; GO:0046982	cell division [GO:0051301]; centromere complex assembly [GO:0034508]; double fertilization forming a zygote and endosperm [GO:0009567]; meiotic cell cycle [GO:0051321]; meiotic chromosome separation [GO:0051307]	chromatin [GO:0000785]; chromosome, centromeric region [GO:0000775]; kinetochore [GO:0000776]; nucleosome [GO:0000786]; nucleus [GO:0005634]	DNA binding [GO:0003677]; protein heterodimerization activity [GO:0046982]; structural constituent of chromatin [GO:0030527]	Q8RVQ9	CENH3	Histone H3-like centromeric protein CENH3 (Centromeric histone CENH3) (Centromeric histone H3) (Histone H3-like centromeric protein HTR12)	chr15: 20107619-20215797	10.1093/g3journal/jkac103
15	Vitvi029004	2016_BuW6	GO:0005829; GO:0009507; GO:0009534; GO:0009535; GO:0009772; GO:0009941; GO:0098807	photosynthetic electron transport in photosystem II [GO:0009772]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast thylakoid [GO:0009534]; chloroplast thylakoid membrane [GO:0009535]; chloroplast thylakoid membrane protein complex [GO:0098807]; cytosol [GO:0005829]		Q9M158	STR4	Rhodanese-like domain-containing protein 4, chloroplastic (Protein THYLAKOID RHODANESE-LIKE) (Sulfurtransferase 4) (AtStr4)	chr15: 20107619-20215797	10.1093/g3journal/jkac103
15	Vitvi029001	2016_BuW6	GO:0003723; GO:0005739; GO:0008270; GO:0009451	RNA modification [GO:0009451]	mitochondrion [GO:0005739]	RNA binding [GO:0003723]; zinc ion binding [GO:0008270]	Q9SV26	PCMP-H65	Pentatricopeptide repeat-containing protein At4g01030, mitochondrial	chr15: 20107619-20215797	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
16	Vitvi029627	2016_FF6	GO:0005262; GO:0005388; GO:0005516; GO:0005524; GO:0005634; GO:0005783; GO:0009706; GO:0016887; GO:0046872		chloroplast inner membrane [GO:0009706]; endoplasmic reticulum [GO:0005783]; nucleus [GO:0005634]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; calcium channel activity [GO:0005262]; calmodulin binding [GO:0005516]; metal ion binding [GO:0046872]; P-type calcium transporter activity	Q37145	ACA1	Calcium-transporting ATPase 1 (EC 7.2.2.10) (Ca(2+)-ATPase isoform 1) (Plastid envelope ATPase 1)		
16	Vitvi029619	2016_FF6	GO:0005524; GO:0008559; GO:0016020; GO:0016887; GO:0042626		membrane [GO:0016020]	ABC-type xenobiotic transporter activity [GO:0008559]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATPase-coupled transmembrane transporter activity [GO:0042626]	Q7FB56	ABCC15	Putative ABC transporter C family member 15 (ABC transporter ABCC.15) (AtABCC15) (EC 7.6.2.2) (ATP-energized glutathione S-conjugate pump 15) (Glutathione S-conjugate-transporting ATPase 15) (Putative multidrug resistance-associated protein 15)		
16	Vitvi029624	2016_FF6	GO:0009813; GO:0031418; GO:0045486; GO:0046872	flavonoid biosynthetic process [GO:0009813]		L-ascorbic acid binding [GO:0031418]; metal ion binding [GO:0046872]; naringenin 3-dioxygenase activity [GO:0045486]	Q7XR84	F3H-3	Flavanone 3-dioxygenase 3 (EC 1.14.11.9) (Flavanone 3-beta-hydroxylase 3) (Flavanone 3-hydroxylase 3) (OsF3H-3) (Flavonoid 3-hydroxylase) (OsF3H)		
17	Vitvi031115	2016_Tar3	GO:0005524; GO:0006412; GO:0030956; GO:0050567	translation [GO:0006412]	glutamyl-tRNA(Gln) amidotransferase complex [GO:0030956]	ATP binding [GO:0005524]; glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity [GO:0050567]	A9KBI0	gatA	Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)		
17	Vitvi031120	2016_Tar3	GO:0005739; GO:0006099; GO:0006121; GO:0034553	mitochondrial electron transport, succinate to ubiquinone [GO:0006121]; mitochondrial respiratory chain complex II assembly [GO:0034553]; tricarboxylic acid cycle	mitochondrion [GO:0005739]		Q9FI44	SDHAF2	Succinate dehydrogenase assembly factor 2, mitochondrial (SDH assembly factor 2)		10.1111/tpj.12041
17	Vitvi031187	2016_SN7	GO:0000455; GO:0003723; GO:0009982	enzyme-directed rRNA pseudouridine synthesis [GO:0000455]		pseudouridine synthase activity [GO:0009982]; RNA binding [GO:0003723]	Q0E0Y3		RNA pseudouridine synthase 7 (EC 5.4.99.-) (RNA pseudouridylate synthase 7) (RNA-uridine isomerase 7)	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031190	2016_SN7	GO:0001709; GO:0048653	anther development [GO:0048653]; cell fate determination [GO:0001709]			Q6TLJ2	TPD1	Protein TAPETUM DETERMINANT 1	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031189	2016_SN7	GO:0006782; GO:0008483; GO:0009507; GO:0015995; GO:0030170; GO:0042286	chlorophyll biosynthetic process [GO:0015995]; protoporphyrinogen IX biosynthetic process [GO:0006782]	chloroplast [GO:0009507]	glutamate-1-semialdehyde 2,1-aminomutase activity [GO:0042286]; pyridoxal phosphate binding [GO:0030170]; transaminase activity	Q85WB7	GSA	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (GSA) (EC 5.4.3.8) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT)	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031188	2016_SN7	GO:0005886		plasma membrane [GO:0005886]		Q9SW27	MUB3	Membrane-anchored ubiquitin-fold protein 3 (AtMUB3) (Membrane-anchored ub-fold protein 3) (ATGP4)	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031196	2016_SN8	GO:0003677; GO:0003682; GO:0005634; GO:0005730; GO:0006338; GO:0006355; GO:0003677; GO:0006338; GO:0016514	chromatin remodeling [GO:0006338]; negative regulation of DNA-templated transcription [GO:0045892]; regulation of DNA-templated transcription [GO:0006355]	nucleolus [GO:0005730]; nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA binding [GO:0003677]; histone binding [GO:0042393]	Q84JB7	DEK2	DEK domain-containing chromatin-associated protein 2 (At-DEK2) (AtDEK-2) (Protein DEK 2)	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031198	2016_SN8	chromatin remodeling [GO:0006338]	SWI/SNF complex [GO:0016514]	DNA binding [GO:0003677]	Q8W475	SWI3A	SWI/SNF complex subunit SWI3A (AtSWI3A) (Transcription regulatory protein	chr17：7309793	10.1093/hr/uhab011
17	Vitvi031758	2016_BeWi9	GO:0006720; GO:0016491; GO:0016853	isoprenoid metabolic process [GO:0006720]		isomerase activity [GO:0016853]; oxidoreductase activity [GO:0016491]	A0A3Q8GL18	NEPS1	(+)-cis,trans-nepetalactol synthase NEPS1 (EC 5.5.1.34) (Nepetalactol-related short-chain dehydrogenase) (Nepetalactol dehydrogenase) (EC 1.1.1.419) (Nepetalactol-related short-chain reductase 1) (Nepetalactol-related SDR1) (NmNEPS1)		10.1186/1471-2229-13-217
17	Vitvi031757	2016_BeWi9	GO:0000166; GO:0005739; GO:0018458; GO:0018459; GO:0031525	menthol biosynthetic process [GO:0031525]	mitochondrion [GO:0005739]	carveol dehydrogenase activity [GO:0018459]; isopiperitenol dehydrogenase activity [GO:0018458]; nucleotide binding [GO:0000166]	Q5C9I9		(-)-isopiperitenol/(-)-carveol dehydrogenase, mitochondrial (EC 1.1.1.223) (EC 1.1.1.243)		10.1186/1471-2229-13-217
17	Vitvi032568	2016_BeWi10	GO:0009507		chloroplast [GO:0009507]		F4I933	STR8	Rhodanese-like domain-containing protein 8, chloroplastic (Sulfurtransferase 8) (AtStr8)		
17	Vitvi032580	2016_BeWi10	GO:0000502; GO:0005634; GO:0005829; GO:0006511; GO:0009536; GO:0019773; GO:0030163; GO:0046685	protein catabolic process [GO:0030163]; response to arsenic-containing substance [GO:0046685]; ubiquitin-dependent protein catabolic process [GO:0006511]	cytosol [GO:0005829]; nucleus [GO:0005634]; plastid [GO:0009536]; proteasome complex [GO:0000502]; proteasome core complex, alpha-subunit complex [GO:0019773]		P34066	PAF1	Proteasome subunit alpha type-1-A (20S proteasome alpha subunit F-1) (Proteasome 30 kDa subunit) (Proteasome component 2A) (AtPSM30) (Proteasome subunit alpha type-6) (Protein ARSENIC TOLERANCE 5)		
17	Vitvi032579	2016_BeWi10	GO:0003723; GO:0004521; GO:0005737; GO:0035194	regulatory ncRNA-mediated post-transcriptional gene silencing [GO:0035194]	cytoplasm [GO:0005737]	RNA binding [GO:0003723]; RNA endonuclease activity [GO:0004521]	Q7XSA2	AGO1B	Protein argonaute 1B (OsAGO1b)		
17	Vitvi032565	2016_BeWi10	GO:0003729; GO:0005739		mitochondrion [GO:0005739]	mRNA binding [GO:0003729]	Q9CAT7		Nascent polypeptide-associated complex subunit beta		
17	Vitvi032581	2016_BeWi10	GO:0005576; GO:0005985; GO:0016157; GO:0080165	callose deposition in phloem sieve plate [GO:0080165]; sucrose metabolic process [GO:0005985]	extracellular region [GO:0005576]	sucrose synthase activity [GO:0016157]	Q9FX32	SUS6	Sucrose synthase 6 (AtSUS6) (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 6)		
17	Vitvi032578	2016_BeWi10	GO:0003723; GO:0009451	RNA modification [GO:0009451]		RNA binding [GO:0003723]	Q9LUS3	PCMP-E91	Pentatricopeptide repeat-containing protein At3g16610		
17	Vitvi032560	2016_BeWi10	GO:0003779; GO:0005737		cytoplasm [GO:0005737]	actin binding [GO:0003779]	Q9SX73		Kinase-interacting family protein (KIP1-like family protein)		
18	Vitvi032759	2016_WPB2	GO:0003844; GO:0004553; GO:0005978; GO:0009501; GO:0009507; GO:0019252; GO:0043169; GO:0102752	glycogen biosynthetic process [GO:0005978]; starch biosynthetic process [GO:0019252]	amyloplast [GO:0009501]; chloroplast [GO:0009507]	1,4-alpha-glucan branching enzyme activity [GO:0003844]; 1,4-alpha-glucan branching enzyme activity (using a glucosylated glycogenin as primer for glycogen synthesis) [GO:0102752]; cation binding [GO:0043169]; hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]	Q41059	SBEII	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic (EC 2.4.1.18) (Starch branching enzyme I)		
18	Vitvi032743	2016_WPB2	GO:0005730; GO:0042254	ribosome biogenesis [GO:0042254]	nucleolus [GO:0005730]		Q5XGY1	tsr1	Pre-rRNA-processing protein TSR1 homolog		
18	Vitvi032744	2016_WPB2	GO:0003727; GO:0003729; GO:0006417; GO:0009507; GO:0009534; GO:0009570; GO:0009658; GO:0010239; GO:0042644; GO:0042651	chloroplast mRNA processing [GO:0010239]; chloroplast organization [GO:0009658]; regulation of translation [GO:0006417]	chloroplast [GO:0009507]; chloroplast nucleoid [GO:0042644]; chloroplast stroma [GO:0009570]; chloroplast thylakoid [GO:0009534]; thylakoid membrane [GO:0042651]	mRNA binding [GO:0003729]; single-stranded RNA binding [GO:0003727]	Q8L844	CRP1	Pentatricopeptide repeat-containing protein At5g42310, chloroplastic (Protein CRP1 homolog) (AtCRP1)		
18	Vitvi032747	2016_WPB2	GO:0000139; GO:0016757		Golgi membrane [GO:0000139]	glycosyltransferase activity [GO:0016757]	Q9CA34	GT17	Probable xyloglucan galactosyltransferase GT17 (EC 2.4.1.-) (Glycosyltransferase 17)		
18	Vitvi032758	2016_WPB2	GO:0004582; GO:0005783; GO:0005789; GO:0006488; GO:0019348; GO:0033185; GO:0035269; GO:0046872	dolichol metabolic process [GO:0019348]; dolichol-linked oligosaccharide biosynthetic process [GO:0006488]; protein O-linked mannosylation [GO:0035269]; response to ammonium ion [GO:0060359]	dolichol-phosphate-mannose synthase complex [GO:0033185]; endoplasmic reticulum [GO:0005783]; endoplasmic reticulum membrane [GO:0005789]	dolichyl-phosphate beta-D-mannosyltransferase activity [GO:0004582]; metal ion binding [GO:0046872]	Q9LM93	DPMS1	Dolichol-phosphate mannosyltransferase subunit 1 (EC 2.4.1.83) (Dol-P-Man synthase1) (Dolichol-phosphate mannose synthase subunit 1) (DPM synthase subunit 1)		
18	Vitvi032760	2016_WPB2					Q9SGQ6		Pentatricopeptide repeat-containing protein At1g76280		
18	Vitvi032887	2016_BF1	GO:0005524; GO:0006605; GO:0016464; GO:0017038; GO:0031969	protein import [GO:0017038]; protein targeting [GO:0006605]	chloroplast membrane [GO:0031969]	ATP binding [GO:0005524]; chloroplast protein-transporting ATPase activity [GO:0016464]	D8WUA4	SECA2	Protein translocase subunit SECA2, chloroplastic (EC 7.4.2.4)	chr18: 3Mb-4Mb	10.1093/g3journal/jkac103
18	Vitvi032937	2016_BF2	GO:0016567	protein ubiquitination [GO:0016567]			Q9XHZ8		BTB/POZ domain-containing protein	chr18: 3Mb-4Mb	10.1093/g3journal/jkac103

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
18	Vitvi033013	2016_BV19	GO:0006809; GO:0009703; GO:0020037; GO:0030151; GO:0042128; GO:0043546; GO:0050464; GO:0071949	nitrate assimilation [GO:0042128]; nitric oxide biosynthetic process [GO:0006809]		FAD binding [GO:0071949]; heme binding [GO:0020037]; molybdenum ion binding [GO:0030151]; molybdopterin cofactor binding [GO:0043546]; nitrate reductase (NADH) activity [GO:0009703]; nitrate reductase (NADPH) activity [GO:0050464]	P17569		Nitrate reductase [NADH] (NR) (EC 1.7.1.1)		
18	Vitvi033010	2016_BV19	GO:0003735; GO:0005739; GO:0006412; GO:0009507; GO:0015935; GO:0019843	translation [GO:0006412]	chloroplast [GO:0009507]; mitochondrion [GO:0005739]; small ribosomal subunit [GO:0015935]	rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]	P82163	RPS13	Small ribosomal subunit protein uS13c (30S ribosomal protein S13, chloroplastic)		
18	Vitvi033008	2016_BV19	GO:0003785; GO:0005524; GO:0005886; GO:0016308; GO:0016310; GO:0046488; GO:0051015	phosphatidylinositol metabolic process [GO:0046488]; phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	1-phosphatidylinositol-4-phosphate 5-kinase activity [GO:0016308]; actin filament binding [GO:0051015]; actin monomer binding [GO:0003785]; ATP binding [GO:0005524]	Q56YP2	PIP5K1	Phosphatidylinositol 4-phosphate 5-kinase 1 (AtPIP5K1) (EC 2.7.1.68) (1-phosphatidylinositol 4-phosphate kinase 1) (Diphosphoinositide kinase 1) (PtdIns(4)P-5-kinase 1)		
18	Vitvi033011	2016_BV19	GO:0005509			calcium ion binding [GO:0005509]	Q5Z676	CML29	Probable calcium-binding protein CML29 (Calmodulin-like protein 29)		
18	Vitvi032998	2016_BV19	GO:0005634; GO:0005694; GO:0032259; GO:0042054; GO:0046872	methylation [GO:0032259]	chromosome [GO:0005694]; nucleus [GO:0005634]	histone methyltransferase activity [GO:0042054]; metal ion binding [GO:0046872]	Q7XJS0	ASHR1	Histone-lysine N-methyltransferase ASHR1 (EC 2.1.1.-) (ASH1-related protein 1) (Protein SET DOMAIN GROUP 37)		
18	Vitvi032997	2016_BV19	GO:0004674; GO:0004708; GO:0004713; GO:0005524; GO:0006996; GO:0046777; GO:0106310	organelle organization [GO:0006996]; protein autophosphorylation [GO:0046777]		ATP binding [GO:0005524]; MAP kinase kinase activity [GO:0004708]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; protein tyrosine kinase activity [GO:0004713]	Q84VX4	MPS1	Serine/threonine-protein kinase MPS1 (EC 2.7.12.2) (Monopolar spindle protein 1 homolog)		
18	Vitvi032994	2016_BV19	GO:0006004; GO:0016020; GO:0016757	fucose metabolic process [GO:0006004]	membrane [GO:0016020]	glycosyltransferase activity [GO:0016757]	Q8GUM0	OFUT11	O-fucosyltransferase 11 (O-FucT-11) (EC 2.4.1.-) (O-fucosyltransferase family protein)		
18	Vitvi032993	2016_BV19	GO:0005829; GO:0071569	protein ufmylation [GO:0071569]	cytosol [GO:0005829]		Q9CA23		Ubiquitin-fold modifier 1		
18	Vitvi032991	2016_BV19	GO:0005886; GO:0006865; GO:0009734; GO:0015293	amino acid transport [GO:0006865]; auxin-activated signaling pathway [GO:0009734]	plasma membrane [GO:0005886]	symporter activity [GO:0015293]	Q9FEL6	LAX3	Auxin transporter-like protein 3 (AUX1-like protein 3) (MtLAX3)		
18	Vitvi033005	2016_BV19	GO:0004077; GO:0004078; GO:0005524; GO:0005829; GO:0009507; GO:0009536; GO:0036211; GO:0042966	biotin carboxyl carrier protein biosynthetic process [GO:0042966]; protein modification process [GO:0036211]	chloroplast [GO:0009507]; cytosol [GO:0005829]; plastid [GO:0009536]	ATP binding [GO:0005524]; biotin-[acetyl-CoA-carboxylase] ligase activity [GO:0004077]; biotin-[methylcrotonoyl-CoA-carboxylase] ligase activity [GO:0004078]	Q9SL92	HCS1	Biotin--protein ligase 1, chloroplastic (EC 6.3.4.-) (Holocarboxylase synthetase 1) [Includes: Biotin--[methylcrotonoyl-CoA-carboxylase] ligase (EC 6.3.4.11); Biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15)]		
18	Vitvi033033	2016_BB1	GO:0000976; GO:0003700; GO:0005634; GO:0006351	DNA-templated transcription [GO:0006351]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q39162	TGA4	Transcription factor TGA4 (Ocs element-binding factor 4) (OBF4) (bZIP transcription factor 57) (AtbZIP57)		
18	Vitvi033032	2016_BB1	GO:0004632; GO:0005634; GO:0005737; GO:0015937	coenzyme A biosynthetic process [GO:0015937]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	phosphopantothenate--cysteine ligase activity [GO:0004632]	Q9LZM3	PPCS2	Phosphopantothenate--cysteine ligase 2 (EC 6.3.2.5) (Phosphopantothenoylcysteine synthetase 2) (PPC synthetase 2)		
18	Vitvi033872	2016_BD2	GO:0004497; GO:0005506; GO:0005783; GO:0009611; GO:0009805; GO:0016020; GO:0016705; GO:0020037	coumarin biosynthetic process [GO:0009805]; response to wounding [GO:0009611]	endoplasmic reticulum [GO:0005783]; membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]	A0A2Z5D852	CYP71AZ6	5-OH-xanthotoxin synthase (EC 1.14.14.-) (Cytochrome P450 CYP71AZ6)		
18	Vitvi033940	2016_BD2	GO:0003735; GO:0005840; GO:0006412; GO:1990904	translation [GO:0006412]	ribonucleoprotein complex [GO:1990904]; ribosome [GO:0005840]	structural constituent of ribosome [GO:0003735]	A0L5U1	rpmB	Large ribosomal subunit protein bL28 (50S ribosomal protein L28)		
18	Vitvi033929	2016_BD2	GO:0005634; GO:0005737; GO:0006302; GO:0006325; GO:0006915; GO:0007095; GO:0010212; GO:0031593; GO:0045739; GO:0051301	apoptotic process [GO:0006915]; cell division [GO:0051301]; chromatin organization [GO:0006325]; double-strand break repair [GO:0006302]; mitotic G2 DNA damage checkpoint signaling [GO:0007095]; positive regulation of DNA repair [GO:0045739]; response to ionizing radiation [GO:0010212]	BRCA1-A complex [GO:0070531]; BRISC complex [GO:0070552]; cytoplasm [GO:0005737]; nucleus [GO:0005634]	polyubiquitin modification-dependent protein binding [GO:0031593]	B6NXD5	BABAM2	BRISC and BRCA1-A complex member 2 (BRCA1-A complex subunit BRE) (BRCA1/BRCA2-containing complex subunit 45) (Brain and reproductive organ-expressed protein)		
18	Vitvi033887	2016_BD2	GO:0005737; GO:0009734; GO:0046621; GO:2000012	auxin-activated signaling pathway [GO:0009734]; negative regulation of organ growth [GO:0046621]; regulation of auxin polar transport [GO:2000012]	cytoplasm [GO:0005737]		B7F8P5	SAUR39	Auxin-responsive protein SAUR36 (Protein SMALL AUXIN UP RNA 36)		
18	Vitvi033904	2016_BD2	GO:0003756; GO:0009507; GO:0009535; GO:0010206	photosystem II repair [GO:0010206]	chloroplast [GO:0009507]; chloroplast thylakoid membrane [GO:0009535]	protein disulfide isomerase activity [GO:0003756]	K4BVL1	SPA	Protein SPA, chloroplastic (Sugar partition-affecting protein)		
18	Vitvi033955	2016_BD2	GO:0003924; GO:0005525; GO:0005737; GO:0007264;	small GTPase mediated signal transduction [GO:0007264]	cytoplasm [GO:0005737]; membrane [GO:0016020]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]	O04369	RAC1	Rac-like GTP-binding protein RAC1		
18	Vitvi033903	2016_BD2	GO:0004164; GO:0017183; GO:0032259	methylation [GO:0032259]; protein histidyl modification to diphthamide [GO:0017183]		diphthine synthase activity [GO:0004164]	O81769		Probable diphthine methyl ester synthase (EC 2.1.1.314) (Diphthamide biosynthesis methyltransferase)		
18	Vitvi033953	2016_BD2	GO:0003676; GO:0003899; GO:0005634; GO:0005730; GO:0005736; GO:0005829; GO:0006362; GO:0006363;	termination of RNA polymerase I transcription [GO:0006363]; transcription elongation by RNA polymerase I [GO:0006362]	cytosol [GO:0005829]; nucleolus [GO:0005730]; nucleus [GO:0005634]; RNA polymerase I complex [GO:0005736]	DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; nucleic acid binding [GO:0003676]; zinc ion binding [GO:0008270]	O94703	rpa12	DNA-directed RNA polymerase I subunit RPA12 (DNA-directed RNA polymerase I 13.1 kDa polypeptide)		
18	Vitvi033939	2016_BD2	GO:0005524; GO:0005788; GO:0016887; GO:0051082; GO:0140662		endoplasmic reticulum lumen [GO:0005788]	ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; ATP-dependent protein folding chaperone [GO:0140662]; unfolded protein binding [GO:0051082]	P35016	HSP90	Endoplasmin homolog (Glucose-regulated protein 94 homolog) (GRP-94 homolog)		
18	Vitvi033892	2016_BD2	GO:0000103; GO:0004781; GO:0005524; GO:0005634; GO:0009507; GO:0009570;	cellular response to sulfate starvation [GO:0009970]; hydrogen sulfide biosynthetic process [GO:0070814]; sulfate assimilation [GO:0000103]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; nucleus [GO:0005634]	ATP binding [GO:0005524]; sulfate adenylyltransferase (ATP) activity [GO:0004781]	Q43870	APS2	ATP sulfurylase 2 (EC 2.7.7.4)		
18	Vitvi033907	2016_BD2	GO:0005634; GO:0016429; GO:0031515		nucleus [GO:0005634]; tRNA (m1A) methyltransferase complex [GO:0031515]	tRNA (adenine-N1-)-methyltransferase activity [GO:0016429]	Q54UB1	trmt6	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit trm6 (tRNA(m1A58)-methyltransferase subunit trm6) (tRNA(m1A58)MTase subunit trm6)		
18	Vitvi033915	2016_BD2	GO:0001678; GO:0004340; GO:0005524; GO:0005536; GO:0005739; GO:0005829; GO:0006006; GO:0006096;	carbohydrate phosphorylation [GO:0046835]; glucose 6-phosphate metabolic process [GO:0051156]; glucose metabolic process [GO:0006006]; glycolytic process [GO:0006096]; intracellular glucose homeostasis	chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; mitochondrion [GO:0005739]	ATP binding [GO:0005524]; fructokinase activity [GO:0008865]; glucokinase activity [GO:0004340]; glucose binding [GO:0005536]	Q6Q8A5	HXK2	Hexokinase-2, chloroplastic (EC 2.7.1.1) (NtHxK2)		
18	Vitvi033928	2016_BD2	GO:0000226; GO:0000278; GO:0003924; GO:0005200; GO:0005525; GO:0005737; GO:0005874; GO:0046872	microtubule cytoskeleton organization [GO:0000226]; mitotic cell cycle [GO:0000278]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; metal ion binding [GO:0046872]; structural constituent of cytoskeleton [GO:0005200]	Q6VAF6		Tubulin beta-6 chain (Beta-6-tubulin)		
18	Vitvi033874	2016_BD2	GO:0000226; GO:0000278; GO:0005200; GO:0005525; GO:0005737; GO:0005874; GO:0016787; GO:0046872	microtubule cytoskeleton organization [GO:0000226]; mitotic cell cycle [GO:0000278]	cytoplasm [GO:0005737]; microtubule [GO:0005874]	GTP binding [GO:0005525]; hydrolase activity [GO:0016787]; metal ion binding [GO:0046872]; structural constituent of cytoskeleton [GO:0005200]	Q6VAG1		Tubulin alpha-1 chain (EC 3.6.5.-) (Alpha-1-tubulin)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
18	Vitvi033963	2016_BD2	GO:0000139; GO:0001516; GO:0005739; GO:0016829; GO:0020037; GO:0036134; GO:0043295; GO:0050220	prostaglandin biosynthetic process [GO:0001516]	Golgi membrane [GO:0000139]; mitochondrion [GO:0005739]	12-hydroxyheptadecatrienoic acid synthase activity [GO:0036134]; glutathione binding [GO:0043295]; heme binding [GO:0020037]; lyase activity [GO:0016829]; prostaglandin-E synthase activity [GO:0050220]	Q7ZUC7	ptges2	Prostaglandin E synthase 2 (EC 5.3.99.3) (Microsomal prostaglandin E synthase 2) (mPGES-2)		
18	Vitvi033899	2016_BD2	GO:0005576; GO:0005739; GO:0005886; GO:0008810; GO:0030245; GO:0071555	cell wall organization [GO:0071555]; cellulose catabolic process [GO:0030245]	extracellular region [GO:0005576]; mitochondrion [GO:0005739]; plasma membrane [GO:0005886]	cellulase activity [GO:0008810]	Q8LCP6		Endoglucanase 10 (EC 3.2.1.4) (Endo-1,4-beta glucanase 10)		
18	Vitvi033905	2016_BD2					Q8LE10	HVA22I	HVA22-like protein i (AtHVA22i)		
18	Vitvi033954	2016_BD2	GO:0005524; GO:0016020; GO:0016887; GO:0140359		membrane [GO:0016020]	ABC-type transporter activity [GO:0140359]; ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]	Q9C7F8	ABCB13	ABC transporter B family member 13 (ABC transporter ABCB.13) (AtABCB13) (P-glycoprotein 13) (Putative multidrug resistance protein 15)		
18	Vitvi033906	2016_BD2	GO:0000902; GO:0000976; GO:0000978; GO:0003677; GO:0003700; GO:0005634; GO:0005730; GO:0005737; GO:0006357; GO:0019760; GO:0042023; GO:0043068; GO:0046982; GO:0051301	cell division [GO:0051301]; cell morphogenesis [GO:0000902]; DNA endoreduplication [GO:0042023]; glucosinolate metabolic process [GO:0019760]; negative regulation of cell division [GO:0051782]; positive regulation of programmed cell death [GO:0043068]; regulation of transcription by RNA polymerase II [GO:0006357]	cytoplasm [GO:0005737]; DRM complex [GO:0070176]; nucleolus [GO:0005730]; nucleus [GO:0005634]	DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; protein heterodimerization activity [GO:0046982]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]	Q9FV70	E2FC	Transcription factor E2FC (E2F transcription factor-2) (AtE2F2)		
18	Vitvi033879	2016_BD2	GO:0005516; GO:0005634; GO:0005875; GO:0005886; GO:0009941		chloroplast envelope [GO:0009941]; microtubule associated complex [GO:0005875]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	calmodulin binding [GO:0005516]	Q9FXI5	IQD32	Protein IQ-DOMAIN 32 (AtIQD32)		
18	Vitvi033932	2016_BD2	GO:0003746; GO:0005634; GO:0043434; GO:0045927	positive regulation of growth [GO:0045927]; response to peptide hormone [GO:0043434]	nucleus [GO:0005634]	translation elongation factor activity [GO:0003746]	Q9SA91	PSI2	Protein PSK SIMULATOR 2 (AtPSI2)		
18	Vitvi033949	2016_BD2	GO:0000325; GO:0004674; GO:0005524; GO:0005886; GO:0009506; GO:0009934; GO:0016020; GO:0030154; GO:0033612; GO:0036289; GO:0043621; GO:0106310	cell differentiation [GO:0030154]; peptidyl-serine autophosphorylation [GO:0036289]; regulation of meristem structural organization [GO:0009934]	membrane [GO:0016020]; plant-type vacuole [GO:0000325]; plasma membrane [GO:0005886]; plasmodesma [GO:0009506]	ATP binding [GO:0005524]; protein self-association [GO:0043621]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]; receptor serine/threonine kinase binding [GO:0033612]	Q9SYQ8	CLV1	Receptor protein kinase CLAVATA1 (EC 2.7.11.1)		
18	Vitvi033942	2016_BD2	GO:0003723; GO:0003724; GO:0005524; GO:0016887			ATP binding [GO:0005524]; ATP hydrolysis activity [GO:0016887]; RNA binding [GO:0003723]; RNA helicase activity [GO:0003724]	Q9ZRZ8	RH28	DEAD-box ATP-dependent RNA helicase 28 (EC 3.6.4.13)		
18	Vitvi034078	2016_SN9	GO:0000976; GO:0003700; GO:0005634; GO:0006355; GO:0010167	regulation of DNA-templated transcription [GO:0006355]; response to nitrate [GO:0010167]	nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; transcription cis-regulatory region binding [GO:0000976]	Q9SFW8	NLP5	Protein NLP5 (AtNLP5) (NIN-like protein 5) (Nodule inception protein-like protein 5)	chr18：13888894	10.1038/hortres.2017.35
18	Vitvi034136	2016_BD3	GO:0003743; GO:0003924; GO:0005525; GO:0005737; GO:0046872		cytoplasm [GO:0005737]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; metal ion binding [GO:0046872]; translation initiation factor activity [GO:0003743]	G0S8G9		Eukaryotic translation initiation factor 5B (eIF-5B) (EC 3.6.5.3) (Translation initiation factor IF-2)		
18	Vitvi034127	2016_BD3	GO:0005634; GO:0006511; GO:0016567	protein ubiquitination [GO:0016567]; ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]		O49279	SKIP15	SKP1-interacting partner 15 (F-box only protein 3)		
18	Vitvi034138	2016_BD3	GO:0004725; GO:0005634; GO:0005737; GO:0005886; GO:0006952; GO:0016311; GO:0019900; GO:0033348	defense response [GO:0006952]; dephosphorylation [GO:0016311]; intracellular signal transduction [GO:0035556]; negative regulation of defense response [GO:0031348]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	kinase binding [GO:0019900]; MAP kinase tyrosine phosphatase activity [GO:0033550]; protein tyrosine phosphatase activity [GO:0004725]	O82656	PTP1	Protein-tyrosine-phosphatase PTP1 (EC 3.1.3.48) (Protein tyrosine phosphatase 1) (AtPTP1)		
18	Vitvi034141	2016_BD3	GO:0005634; GO:0005886; GO:0005985; GO:0008506	sucrose metabolic process [GO:0005985]	nucleus [GO:0005634]; plasma membrane [GO:0005886]	sucrose:proton symporter activity [GO:0008506]	Q39231	SUC2	Sucrose transport protein SUC2 (AtSUC2) (Sucrose permease 2) (Sucrose transporter 1) (Sucrose-proton symporter 2)		
18	Vitvi034118	2016_BD3	GO:0000105; GO:0004399; GO:0005829; GO:0009411; GO:0009507; GO:0009536; GO:0009555; GO:0009570	histidine biosynthetic process [GO:0000105]; pollen development [GO:0009555]; response to UV [GO:0009411]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; cytosol [GO:0005829]; plastid [GO:0009536]	histidinol dehydrogenase activity [GO:0004399]; metal ion binding [GO:0046872]; NAD binding [GO:0051287]	Q9C5U8	HISN8	Histidinol dehydrogenase, chloroplastic (HDH) (EC 1.1.1.23) (Protein HISTIDINE BIOSYNTHESIS 8)		
18	Vitvi034133	2016_BD3	GO:0005506; GO:0009414; GO:0009639; GO:0010295; GO:0016020; GO:0020037; GO:0046345; GO:0071456	abscisic acid catabolic process [GO:0046345]; cellular response to hypoxia [GO:0071456]; response to red or far red light [GO:0009639]; response to water deprivation [GO:0009414]	membrane [GO:0016020]	(+)-abscisic acid 8'-hydroxylase activity [GO:0010295]; heme binding [GO:0020037]; iron ion binding [GO:0005506]	Q9FH76	CYP707A3	Abscisic acid 8'-hydroxylase 3 (ABA 8'-hydroxylase 3) (EC 1.14.14.137) (Cytochrome P450 707A3)		
18	Vitvi034093	2016_BD3	GO:0006826; GO:0009507; GO:0009536; GO:0009706; GO:0009941; GO:0010039	iron ion transport [GO:0006826]; response to iron ion [GO:0010039]	chloroplast [GO:0009507]; chloroplast envelope [GO:0009941]; chloroplast inner membrane [GO:0009706]; plastid [GO:0009536]		Q9FHX2	MFL1	Protein MITOFERRINLIKE 1, chloroplastic (AtMFL1)		
18	Vitvi034092	2016_BD3	GO:0002229; GO:0004674; GO:0005524; GO:0005886; GO:0016310; GO:0030246; GO:0042742; GO:0106310	defense response to bacterium [GO:0042742]; defense response to oomycetes [GO:0002229]; phosphorylation [GO:0016310]	plasma membrane [GO:0005886]	ATP binding [GO:0005524]; carbohydrate binding [GO:0030246]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity [GO:0004674]	Q9FHX3	LECRKS6	L-type lectin-domain containing receptor kinase S.6 (LecRK-S.6) (EC 2.7.11.1)		
18	Vitvi034098	2016_BD3	GO:0000166; GO:0003677; GO:0003729; GO:0005634; GO:0005737; GO:0005829; GO:0008270; GO:0009409	response to cold [GO:0009409]	cytoplasm [GO:0005737]; cytosol [GO:0005829]; nucleus [GO:0005634]	DNA binding [GO:0003677]; mRNA binding [GO:0003729]; nucleotide binding [GO:0000166]; zinc ion binding [GO:0008270]	Q9LIN3	RZ1A	Glycine-rich RNA-binding protein RZ1A (AtRZ-1a)		
18	Vitvi034135	2016_BD3	GO:0005384; GO:0005774; GO:0010039; GO:0030026; GO:0034755	intracellular manganese ion homeostasis [GO:0030026]; iron ion transmembrane transport [GO:0034755]; response to iron ion [GO:0010039]	vacuolar membrane [GO:0005774]	manganese ion transmembrane transporter activity [GO:0005384]	Q9M2C3		Vacuolar iron transporter homolog 3 (Protein NODULIN-LIKE 3)		
18	Vitvi034124	2016_BD3	GO:0005829; GO:0005886; GO:0006580; GO:0019752; GO:0030170; GO:0102705	carboxylic acid metabolic process [GO:0019752]; ethanolamine metabolic process [GO:0006580]	cytosol [GO:0005829]; plasma membrane [GO:0005886]	pyridoxal phosphate binding [GO:0030170]; serine decarboxylase activity [GO:0102705]	Q9MA74	SDC	Serine decarboxylase (AtSDC) (EC 4.1.1.-) (Protein EMBRYO DEFECTIVE 1075) (Serine decarboxylase 1) (AtSDC1)		
18	Vitvi034134	2016_BD3	GO:0000976; GO:0003676; GO:0003682; GO:0003700; GO:0005634; GO:0005829; GO:0006952; GO:0006970; GO:0007231; GO:0008272; GO:0009294; GO:0009652; GO:0009970; GO:0043565; GO:0043621; GO:0045596; GO:0051170	cellular response to sulfate starvation [GO:0009970]; defense response [GO:0006952]; DNA-mediated transformation [GO:0009294]; import into nucleus [GO:0051170]; negative regulation of cell differentiation [GO:0045596]; osmosensory signaling pathway [GO:0007231]; response to osmotic stress [GO:0006970]; sulfate transport [GO:0008272]; thigmotropism [GO:0009652]	cytosol [GO:0005829]; nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA-binding transcription factor activity [GO:0003700]; mitogen-activated protein kinase binding [GO:0051019]; nucleic acid binding [GO:0003676]; protein self-association [GO:0043621]; sequence-specific DNA binding [GO:0043565]; transcription cis-regulatory region binding [GO:0000976]	Q9MA75	VIP1	Transcription factor VIP1 (Protein SULPHATE UTILIZATION EFFICIENCY 3) (VirE2-interacting protein 1) (AtVIP1) (bZIP transcription factor 51) (AtbZIP51) (bZIP protein 51)		
18	Vitvi034136	2017_SL10	GO:0003743; GO:0003924; GO:0005525; GO:0005737; GO:0046872		cytoplasm [GO:0005737]	GTP binding [GO:0005525]; GTPase activity [GO:0003924]; metal ion binding [GO:0046872]; translation initiation factor activity [GO:0003743]	G0S8G9		Eukaryotic translation initiation factor 5B (eIF-5B) (EC 3.6.5.3) (Translation initiation factor IF-2)		
18	Vitvi034150	2017_SL10	GO:0003700; GO:0005634; GO:0005737; GO:0006355; GO:0006357; GO:0007584; GO:0009610; GO:0010247; GO:0036377; GO:0043565	arbuscular mycorrhizal association [GO:0036377]; detection of phosphate ion [GO:0010247]; regulation of DNA-templated transcription [GO:0006355]; regulation of transcription by RNA polymerase II [GO:0006357]; response to nutrient [GO:0007584]; response to symbiotic fungus [GO:0009610]	cytoplasm [GO:0005737]; nucleus [GO:0005634]	DNA-binding transcription factor activity [GO:0003700]; sequence-specific DNA binding [GO:0043565]	G7L166	RAM1	GRAS family protein RAM1 (Protein REQUIRED FOR ARBUSCULAR MYCORRHIZATION 1) (MtRAM1)		

Supplementary Table 9. Candidate genes of 29 traits in GWAS results.

Chromosome	GeneID	Trait	GO	Gene Ontology (biological process)	Gene Ontology (cellular component)	Gene Ontology (molecular function)	Swissport	gene_name	Protein name	QTL overlapping	QTL overlapping_Ref
18	Vitvi034127	2017_SL10	GO:0005634; GO:0006511; GO:0016567	protein ubiquitination [GO:0016567]; ubiquitin-dependent protein catabolic process [GO:0006511]	nucleus [GO:0005634]		O49279	SKIP15	SKP1-interacting partner 15 (F-box only protein 3)		
18	Vitvi034138	2017_SL10	GO:0004725; GO:0005634; GO:0005737; GO:0005886; GO:0006952; GO:0016311; GO:0019900; GO:0031348;	defense response [GO:0006952]; dephosphorylation [GO:0016311]; intracellular signal transduction [GO:0035556]; negative regulation of defense response [GO:0031348]	cytoplasm [GO:0005737]; nucleus [GO:0005634]; plasma membrane [GO:0005886]	kinase binding [GO:0019900]; MAP kinase tyrosine phosphatase activity [GO:0033550]; protein tyrosine phosphatase activity [GO:0004725]	O82656	PTP1	Protein-tyrosine-phosphatase PTP1 (EC 3.1.3.48) (Protein tyrosine phosphatase 1) (AtPTP1)		
18	Vitvi034141	2017_SL10	GO:0005634; GO:0005886; GO:0005985; GO:0008506	sucrose metabolic process [GO:0005985]	nucleus [GO:0005634]; plasma membrane [GO:0005886]	sucrose:proton symporter activity [GO:0008506]	Q39231	SUC2	Sucrose transport protein SUC2 (AtSUC2) (Sucrose permease 2) (Sucrose transporter 1) (Sucrose-proton symporter 2)		
18	Vitvi034133	2017_SL10	GO:0005506; GO:0009414; GO:0009639; GO:0010295; GO:0016020; GO:0020037; GO:0046345; GO:0071456	abscisic acid catabolic process [GO:0046345]; cellular response to hypoxia [GO:0071456]; response to red or far red light [GO:0009639]; response to water deprivation [GO:0009414]	membrane [GO:0016020]	(+)-abscisic acid 8'-hydroxylase activity [GO:0010295]; heme binding [GO:0020037]; iron ion binding [GO:0005506]	Q9FH76	CYP707A3	Abscisic acid 8'-hydroxylase 3 (ABA 8'-hydroxylase 3) (EC 1.14.14.137) (Cytochrome P450 707A3)		
18	Vitvi034135	2017_SL10	GO:0005384; GO:0005774; GO:0010039; GO:0030026; GO:0034755	intracellular manganese ion homeostasis [GO:0030026]; iron ion transmembrane transport [GO:0034755]; response to iron ion [GO:0010039]	vacuolar membrane [GO:0005774]	manganese ion transmembrane transporter activity [GO:0005384]	Q9M2C3		Vacuolar iron transporter homolog 3 (Protein NODULIN-LIKE 3)		
18	Vitvi034134	2017_SL10	GO:0000976; GO:0003676; GO:0003682; GO:0003700; GO:0005634; GO:0005829; GO:0006952; GO:0006970; GO:0007231; GO:0008272; GO:0009294; GO:0009652; GO:0009970; GO:0043565; GO:0043621; GO:0045596; GO:0051019; GO:0051170	cellular response to sulfate starvation [GO:0009970]; defense response [GO:0006952]; DNA-mediated transformation [GO:0009294]; import into nucleus [GO:0051170]; negative regulation of cell differentiation [GO:0045596]; osmosensory signaling pathway [GO:0007231]; response to osmotic stress [GO:0006970]; sulfate transport [GO:0008272]; thigmotropism [GO:0009652]	cytosol [GO:0005829]; nucleus [GO:0005634]	chromatin binding [GO:0003682]; DNA-binding transcription factor activity [GO:0003700]; mitogen-activated protein kinase binding [GO:0051019]; nucleic acid binding [GO:0003676]; protein self-association [GO:0043621]; sequence-specific DNA binding [GO:0043565]; transcription cis-regulatory region binding [GO:0000976]	Q9MA75	VIP1	Transcription factor VIP1 (Protein SULPHATE UTILIZATION EFFICIENCY 3) (VirE2-interacting protein 1) (AtVIP1) (bZIP transcription factor 51) (AtbZIP51) (bZIP protein 51)		
18	Vitvi034319	2017_SL11	GO:0005576; GO:0010052; GO:0010374; GO:0019901; GO:0090626; GO:2000122	guard cell differentiation [GO:0010052]; negative regulation of stomatal complex development [GO:2000122]; plant epidermis morphogenesis [GO:0090626]; stomatal complex development [GO:0010374]	extracellular region [GO:0005576]	protein kinase binding [GO:0019901]	Q8LC53	EPF2	Protein EPIDERMAL PATTERNING FACTOR 2 [Cleaved into: MEPF2]		
18	Vitvi035178	2016_SN10	GO:0009706; GO:0015031	protein transport [GO:0015031]	chloroplast inner membrane [GO:0009706]		Q8GT66	TIC40	Protein TIC 40, chloroplastic (Translocon at the inner envelope membrane of chloroplasts 40) (PsTIC40)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035172	2016_SN10	GO:0004672; GO:0004674; GO:0005524; GO:0016020; GO:0016310; GO:0042803; GO:0106310	phosphorylation [GO:0016310]	membrane [GO:0016020]	ATP binding [GO:0005524]; protein homodimerization activity [GO:0042803]; protein kinase activity [GO:0004672]; protein serine kinase activity [GO:0106310]; protein serine/threonine kinase activity	Q9FIJ6	CCR4	Serine/threonine-protein kinase-like protein CCR4 (EC 2.7.11.1) (CRINKLY 4-related kinase 1) (AtCRK1) (Protein CRINKLY 4 RELATED 4) (AtCCR4)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035170	2016_SN10	GO:0004017; GO:0005524; GO:0009507; GO:0009536; GO:0009570; GO:0016310; GO:0097009	energy homeostasis [GO:0097009]; phosphorylation [GO:0016310]	chloroplast [GO:0009507]; chloroplast stroma [GO:0009570]; plastid [GO:0009536]	adenylate kinase activity [GO:0004017]; ATP binding [GO:0005524]	Q9FIJ7		Adenylate kinase 2, chloroplastic (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase 2) (AMK2)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035178	2016_SN11	GO:0009706; GO:0015031	protein transport [GO:0015031]	chloroplast inner membrane [GO:0009706]		Q8GT66	TIC40	Protein TIC 40, chloroplastic (Translocon at the inner envelope membrane of chloroplasts 40) (PsTIC40)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035239	2016_SN12	GO:0004497; GO:0005506; GO:0016020; GO:0016125; GO:0016712; GO:0020037; GO:0102373; GO:0102374	sterol metabolic process [GO:0016125]	membrane [GO:0016020]	heme binding [GO:0020037]; iron ion binding [GO:0005506]; monooxygenase activity [GO:0004497]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen [GO:0016712]; ursolic aldehyde 28-monooxygenase activity [GO:0102374]; uvaol dehydrogenase activity [GO:0102373]	A0A3Q7HBJ5	CYP716A44	Beta-amyrin 28-monooxygenase (EC 1.14.14.126) (Beta-amyrin 28-oxidase) (Cytochrome P450 716A44)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035249	2016_SN12	GO:0005525; GO:1900425	negative regulation of defense response to bacterium [GO:1900425]		GTP binding [GO:0005525]	F4HT21	IAN9	Immune-associated nucleotide-binding protein 9 (AtIAN9) (AIG1-like protein)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035253	2016_SN12	GO:0000978; GO:0000981; GO:0005634; GO:0006357; GO:0045944; GO:0046983; GO:0048316	positive regulation of transcription by RNA polymerase II [GO:0045944]; regulation of transcription by RNA polymerase II [GO:0006357]; seed development [GO:0048316]	nucleus [GO:0005634]	DNA-binding transcription factor activity, RNA polymerase II-specific [GO:0000981]; protein dimerization activity [GO:0046983]; RNA polymerase II cis-regulatory region sequence-specific DNA binding	F6I457	AGL11	Agamous-like MADS-box protein AGL11 (Agamous like-protein 11) (VvAGL11) (MADS-box protein 5) (VvMADS5) (Protein SEED DEVELOPMENT INHIBITOR) (VvAG3) (VviAG3)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035241	2016_SN12	GO:0004617; GO:0006564; GO:0051287	L-serine biosynthetic process [GO:0006564]		NAD binding [GO:0051287]; phosphoglycerate dehydrogenase activity [GO:0004617]	O29445	serA	D-3-phosphoglycerate dehydrogenase (PGDH) (EC 1.1.1.95)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035248	2016_SN12	GO:0005886; GO:0009507; GO:0016787		chloroplast [GO:0009507]; plasma membrane [GO:0005886]	hydrolase activity [GO:0016787]	Q9FVW3	MES14	Putative methylesterase 14, chloroplastic (AtMES14) (EC 3.1.1.-)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035256	2016_SN13	GO:0005249; GO:0016020; GO:0034765	regulation of monoatomic ion transmembrane transport [GO:0034765]	membrane [GO:0016020]	voltage-gated potassium channel activity [GO:0005249]	Q7XUW4		Potassium channel KOR2 (K(+) outward-rectifying channel 2)		10.1186/1471-2229-13-217；10.1186/1471-2229-8-38
18	Vitvi035506	2017_SL12	GO:0004821; GO:0005524; GO:0005829; GO:0006427	histidyl-tRNA aminoacylation [GO:0006427]	cytosol [GO:0005829]	ATP binding [GO:0005524]; histidine-tRNA ligase activity [GO:0004821]	F4IYF8		Histidine--tRNA ligase, cytoplasmic (EC 6.1.1.21) (Histidyl-tRNA synthetase) (HisRS)		
19	Vitvi036975	2016_SL13					Q1PED9		F-box/LRR-repeat protein At3g59190		

Supplementary Table 10. Divergent genomic regions contain GWAS candidate loci between Table1 and Table2 groups.

Chromosome	Genomic regions		*P* value	Trait
	Start	End		
2	16,450,001	16,500,001	1.677317951	2016_BC4
3	9,450,001	9,500,001	2.443603992	2016_SA1
7	29,550,001	29,600,001	2.52803803	2016_BeS2
14	5,100,001	5,150,001	1.640102722	2017_BuW5
16	4,800,001	4,850,001	2.112663663	2016_FF6
17	2,150,001	2,200,001	1.626917925	2016_Tar4

Notes: Statistical significance was determined by generalized least squares (GLS) F est.

Supplementary Table 11. Divergent genomic regions contain GWAS candidate loci between Table1 and wine groups.

Chromosome	Genomic regions		*P* value	Trait
	Start	End		
1	21,500,001	21,550,001	1.525054139	2016_FJ1
8	20,200,001	20,250,001	1.999198293	2017_BV12
8	20,100,001	20,150,001	2.256553445	2016_BeWe6
11	2,450,001	2,500,001	2.95183644	2017_BuW2
11	4,950,001	5,000,001	1.916818903	2016_BV15
12	2,000,001	2,050,001	1.867663154	2016_TAC3
17	6,550,001	6,600,001	1.447512045	2016_SSC7
17	6,550,001	6,600,001	1.447512045	2016_BeWi9
18	9,250,001	9,300,001	2.372089737	2016_BD1
18	13,750,001	13,800,001	1.93188065	2016_SN9

Notes: Statistical significance was determined by generalized least squares (GLS) F est.

Supplementary Table 12. The summary of LDpred2-auto and lassoum2.

NO.	Trait	LDpred2-auto				lassoum2	
		Marker numbers	P-value thı	alpha	Index of Correlation(R)	Marker numbers	Index of Correlation(R)
1	FF	77,523	0.036493	-1.5	0.603683468	532	0.517309222
2	SA	191,049	0.005504	-0.475276	0.867174688	92,576	0.743096257
3	ST	176,997	0.007325	-1.373944	0.594484276	91,584	0.526752048
4	FJ	174,894	0.003681	-0.241014	0.920334474	2,170	0.657099559
5	BF	189,098	0.011719	-0.099296	0.632039084	5,001	0.797301937
6	SN	95,322	0.003696	-1.402489	0.895555035	29,291	0.567708084
7	SL	10,274	0.004282	-0.565286	0.654484919	2,544	0.594585517
8	SSC	9,273	0.017741	-1.013416	0.574646913	17,358	0.548762896
9	BuS	96,890	0.00531	-0.608673	0.567280489	71,029	0.656172659
10	WPB	150,183	0.012612	0.189631	0.819258391	3,572	0.897683174
11	SBN	13,521	0.02519	-0.576216	0.728955989	27,432	0.885696457
12	BD	6,500	0.01888	-0.250004	0.763175119	3,780	0.588442444
13	BeS	12,308	0.020404	-0.998118	0.732322805	7,035	0.62740438
14	UMS	11,516	0.013337	-1.5	0.555283464	16,503	0.735554852
15	BB	10,753	0.025298	-1.5	0.619330798	5,287	0.743294711
16	TAC	13,520	0.027258	-1.079779	0.600195363	3,503	0.812850299
17	BuW	156,473	0.006667	0.206925	0.887772607	5,201	0.655837063
18	BL	151,082	0.014105	-0.734192	0.596817885	88,036	0.795327433
19	BeWi	12,089	0.00928	-1.5	0.577829647	3,710	0.594950319
20	BV	80,655	0.02728	-1.5	0.726104194	14,355	0.522693449
21	BeWe	76,073	0.028691	-1.5	0.617785978	10,851	0.752494816
22	BC	94,499	0.003143	-1.17777	0.874739714	482	0.64667251
23	EDP	181,228	0.0042	-0.457624	0.851971468	15,441	0.779322179
24	Glu	12,583	0.003094	-0.795839	0.75879641	2,327	0.741538414
25	Fru	6,908	0.001776	-1.5	0.57578987	1,894	0.616814365
26	Suc	100,363	0.004748	-0.914075	0.89078106	2,732	0.850895925
27	Tar	32,613	0.039192	-1.5	0.635832955	3,173	0.686882987
28	Mal	14,385	0.032804	-0.499526	0.642205717	4,294	0.675182902
29	Cit	11,380	0.002751	-0.479809	0.794199667	6,415	0.586107882

Notes: Statistical significance was determined by generalized least squares (GLS) F est.