

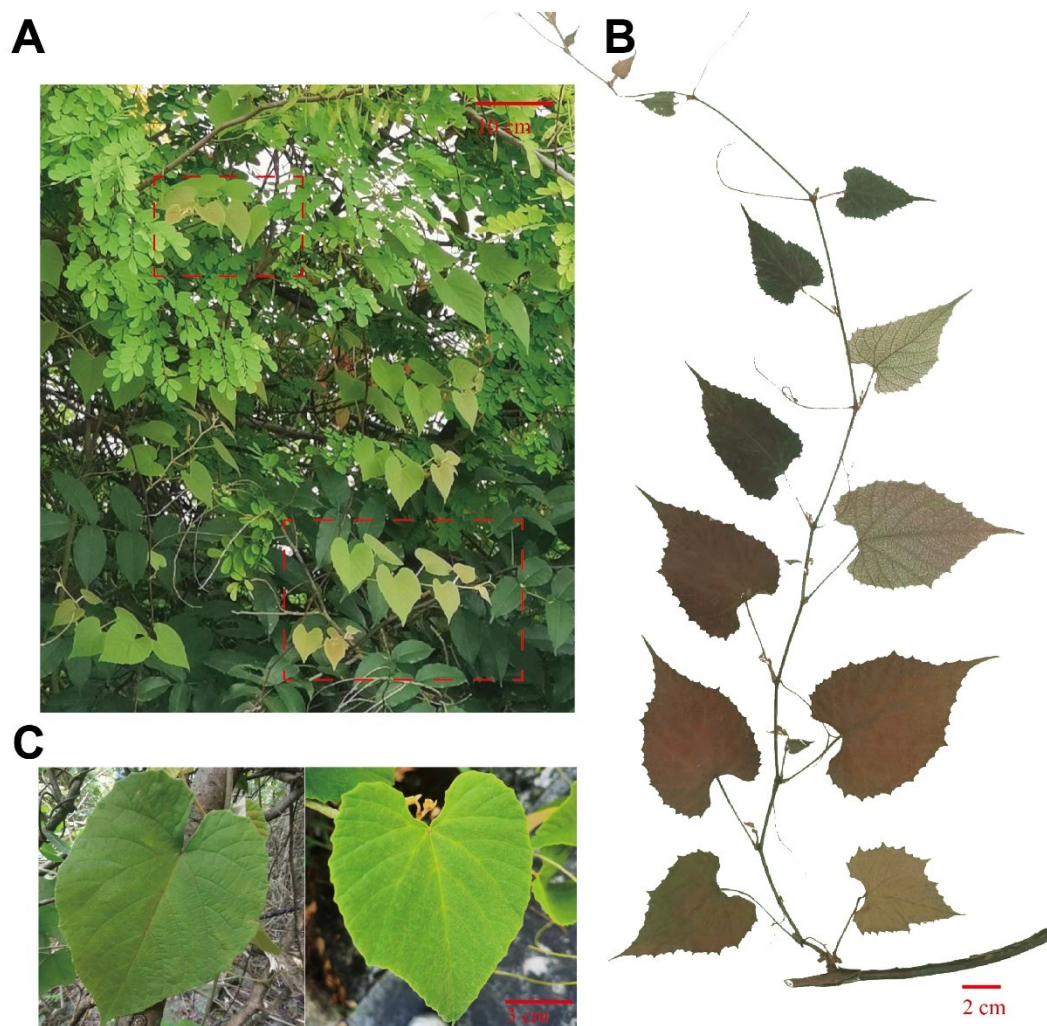


Figure S1. The *V. retordii* (*Vitis retordii*) brief introduction of habitat and morphology.

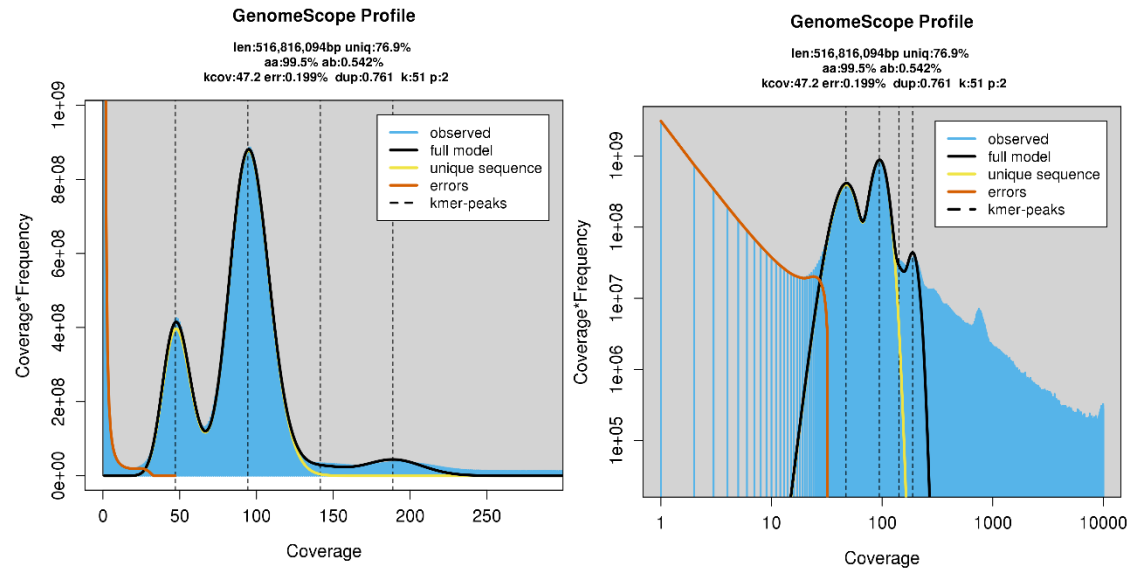
(A) Picture of habitat location of the *V. retordii*, which was taken in Shenzhen City, Guangdong Province (Geographic Latitude 22°32' 49.66" N, Geographic Longitude 114°28' 45.07" E, Altitude 21.05 m). (B) Plant specimen of the *V. retordii*, collected by Tianhao Zhang in May 2022. (C) The *V. retordii* leaf morphological detail, the left leaf is inland ecotype which collected in Luocheng City, and the right leaf is coastal ecotype which collected in Shenzhen City. The shape of leaf blade base has a bit difference.

Note: Descriptions of the phenotypic and economic characteristics

Phenotypic characteristics: Plants polygamo-dioecious. Branchlets terete, with longitudinal ridges, densely brownish villous when young, eventually glabrescent; tendrils bifurcate. Leaves simple; stipules brown, ovate-lanceolate, 3-5 × 2-3 mm, membranous, subglabrate, apex acuminate, caducous; petiole 1.5-9 cm, densely pubescent with brown and arachnoid hairs; leaf blade oval or

14 ovate-elliptic, 6-15 × 4-11 cm, abaxially tomentose with brown and villous hairs, adaxially densely
15 pubescent, basal veins 5, lateral veins 4 or 5 pairs, veinlets tomentose and raised abaxially, raised
16 and pubescent adaxially, base deeply cordate, notch with an acute angle, rarely overlapping, margin
17 19-43-toothed on each side, teeth sharp. Panicle leaf-opposed, loose, 6-10 cm, basal branches well
18 developed; peduncle 1.2-2.5 cm, usually brown tomentose. Pedicel 1-1.5 mm, glabrous. Buds
19 obelliptic, 1.2-1.5 mm, apex rounded. Calyx cupular, ca. 1.5 mm, glabrous, subentire. Filaments
20 filiform, 1-1.2 mm; anthers yellow, oblong, ca. 0.5 mm. Ovary oval; style short. Berry globose, ca.
21 8 mm in diam. Seeds obelliptic, apex rounded, chalazal knot ovate-elliptic, ventral holes furrowed
22 upward ca. 1/3 from base. Fl. May, fr. Jun-Jul. [Chen Zhiduan (陈之端), Ren Hui (任辉); Jun Wen
23 (文君). Flora of China, Vitaceae, Vol.12, 2007.]

24 **Economic characteristics:** Woolly grapes serve as a treasure trove of genetic material,
25 offering dual utility in grape cultivation. They are prized as rootstocks and for hybrid breeding,
26 while also being versatile in their direct applications, which range from fresh consumption to
27 medicinal purposes, wine production, and the extraction of natural pigments. [Kong Qingshan(孔
28 庆山). Grape Chronicles of China (中国葡萄志), 60-62.]



29

30 **Figure S2. Estimate of the genome size and complexity of woolly grape by K-mers method.**

31 The plot is generated using GenomeScope2.0 (K = 51). Estimated genome size is 516,816,094 bp,

32 heterozygosity is 0.542%.

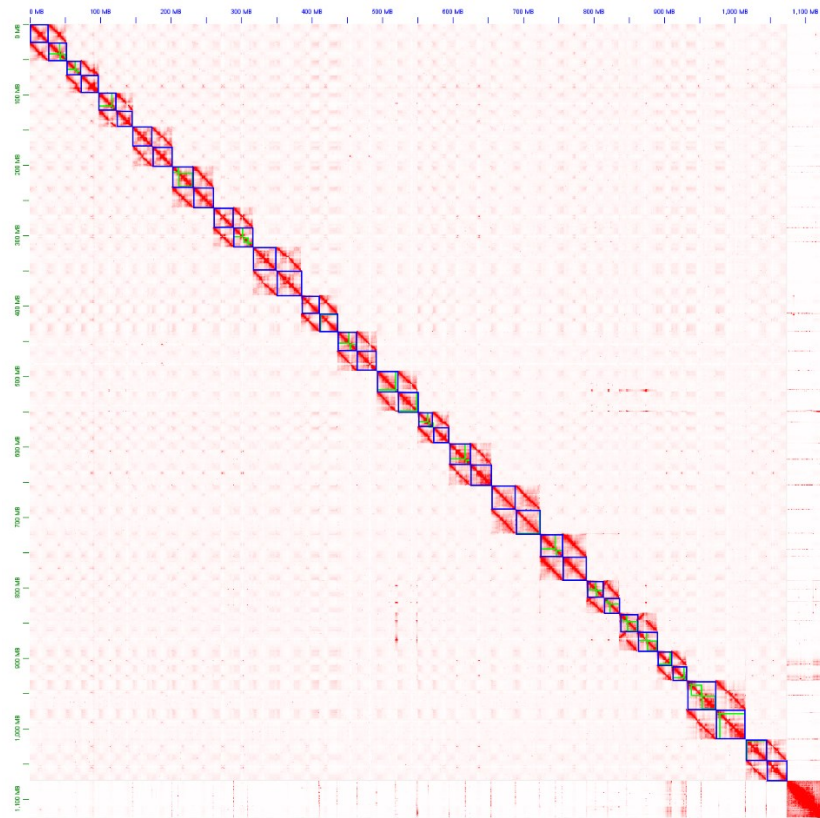


Figure S3. Hi-C map in Juicebox of woolly grape two haplotypes.

The figure depicts the situation before checked. A blue square is a pseudo-chromosome, green squares represent different contigs. It shows that the assembly is relatively complete, only a few gaps. From top left to bottom right are chromosome 1 to 19, and every two blue squares are the same chromosome of haplotypes 1 (top left) and haplotypes 2 (bottom right), respectively. Lower right corner are unanchored contigs.

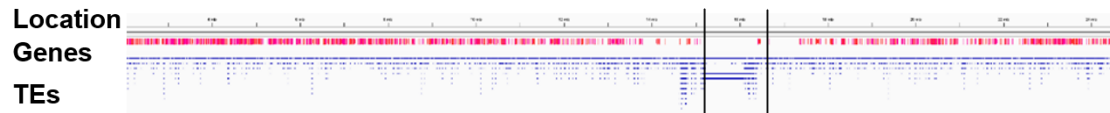


Figure S4. Display of chromosome centromere region.

The figure depicts *V. retordii*_hap1_chr1 as an example. And was visualized in IGV with protein-coding genes annotation (red) and transposable elements annotation (blue). Generally, the centromere region with less protein-coding genes and more transposable elements as shown in the figure.

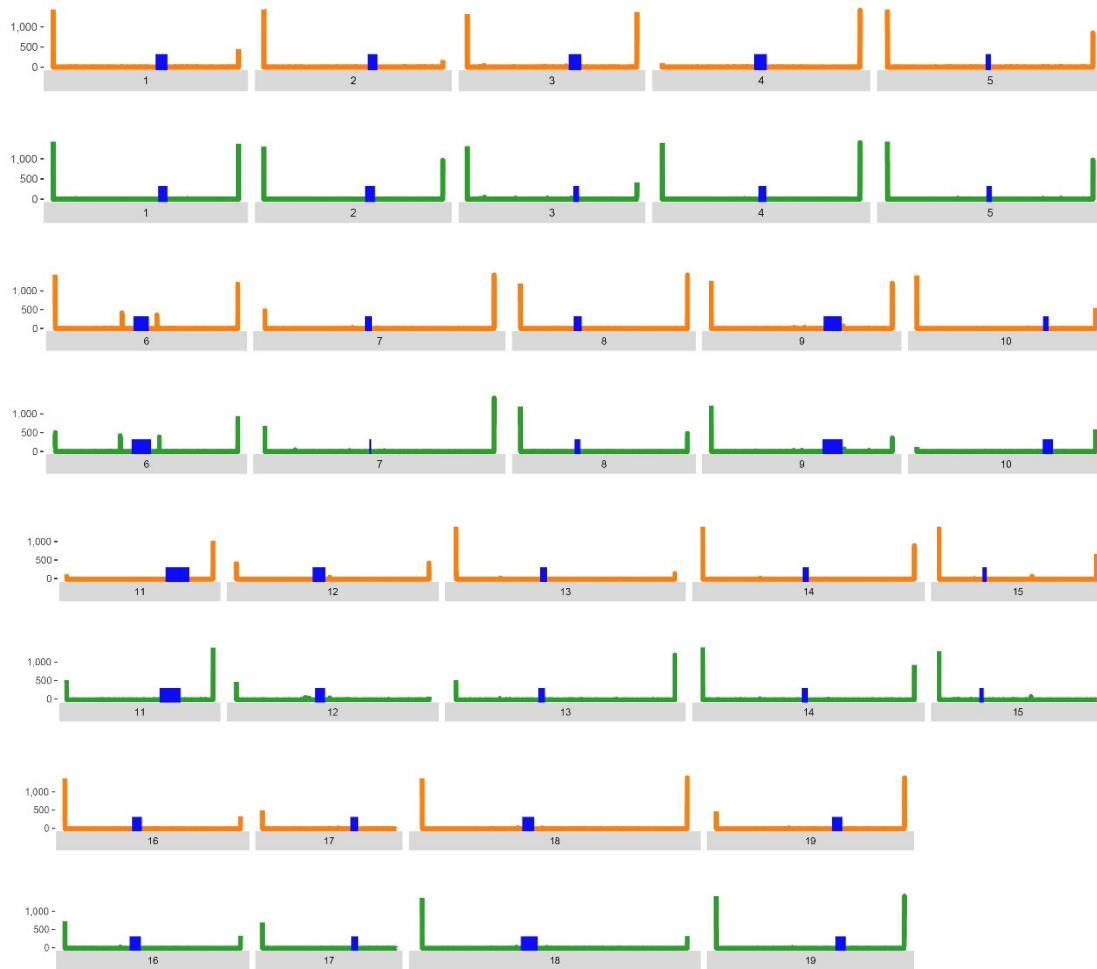
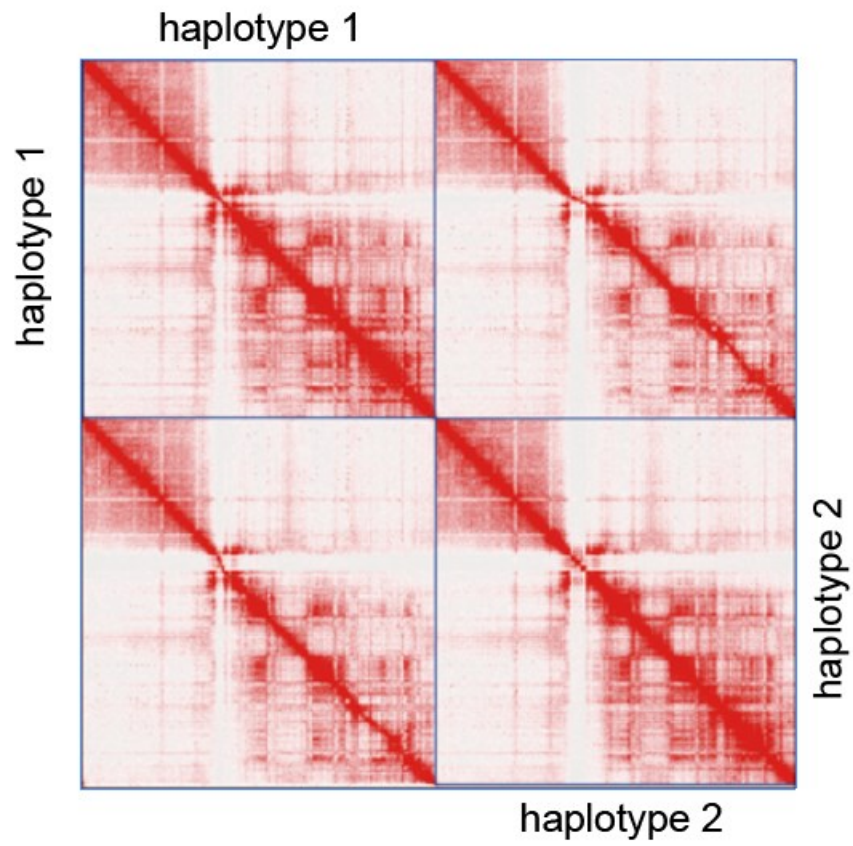


Figure S5. Telomere region (TTTAGGG) n repeats count and centromeric regions of woolly grape.

All chromosomes are depicted in the figure. The orange is haplotype 1 and the green is haplotype 2 respectively, and the blue square represents the centromere region. The telomere repeat unit (TTTAGGG) n repeats was detected by TRF, it showed that all the telomeres were found except for the end of chromosome 17.



55

56 **Figure S6. The Chromosome 18 Hi-C heat map between woolly grape haplotype 1 and 2.**

57 The centromere region could be clearly seen in the figure.

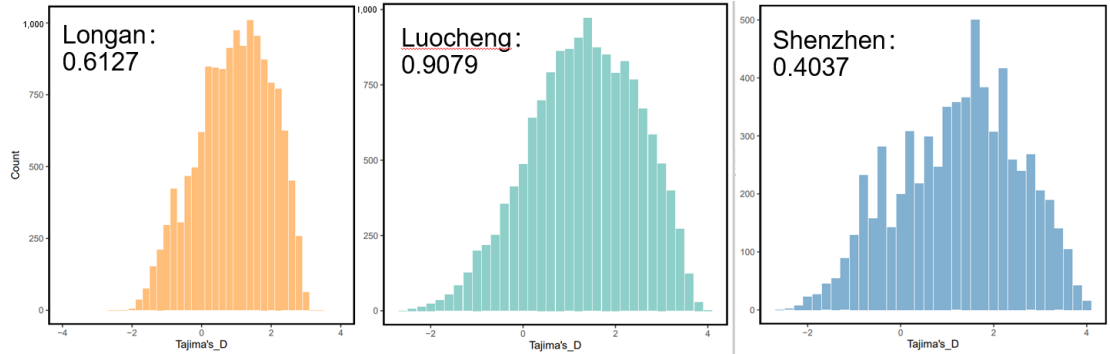
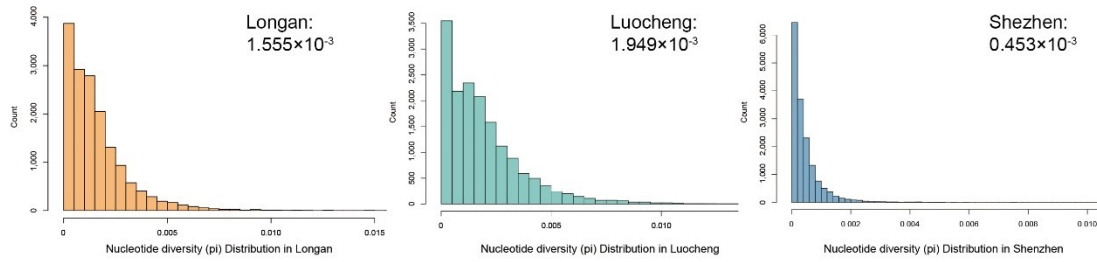


Figure S7. Whole-genome distributions of nucleotide diversity (π) and Tajima's D.

All values were calculated by VCFTools with 50-kb sliding windows in 10-kb steps. The estimated mean is marked on the graph. Coastal population (Shenzhen) had lower synonymous nucleotide diversities (π) than inland population (Luocheng and Longan), while coastal population had lower Tajima's D values than inland population as well and all three populations had positive Tajima's D values. From left to right are population Longan (inland), Luocheng (inland) and Shenzhen (coastal) respectively.

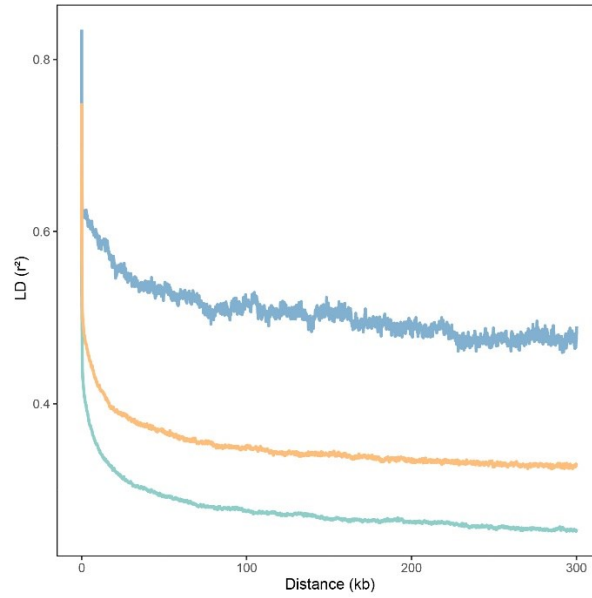
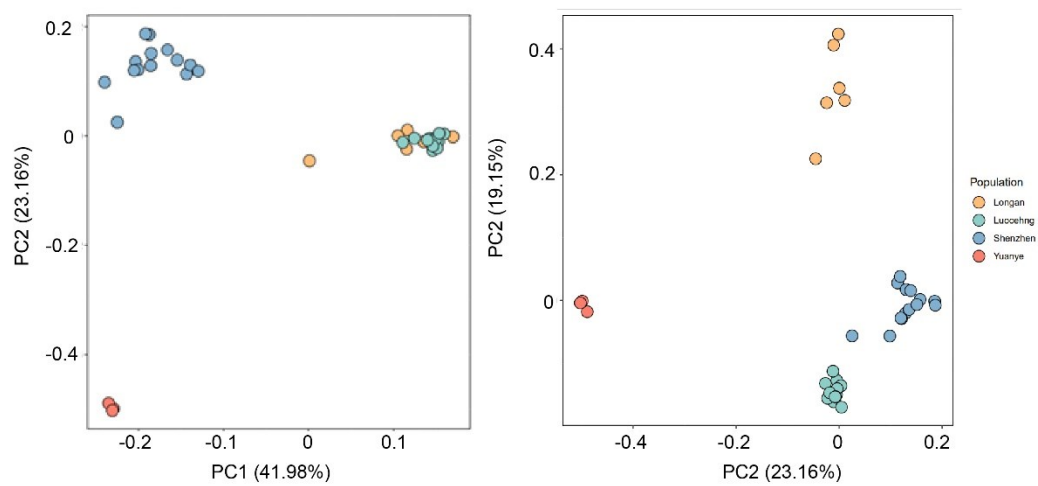


Figure S8. Decay of linkage disequilibrium (LD) of three populations measured by the genome-wide average r^2 .

Blue, yellow, and green are stand for population Shenzhen (coastal), Longan (inland) and Luocheng (inland) respectively.



72

73 **Figure S9. PCA analysis with outgroup *Muscadinia* (Yuanye) population.**

74 The first two principal components did not separate the inland populations (Luocheng and Longan),

75 while separation happens at PC2 and PC3.

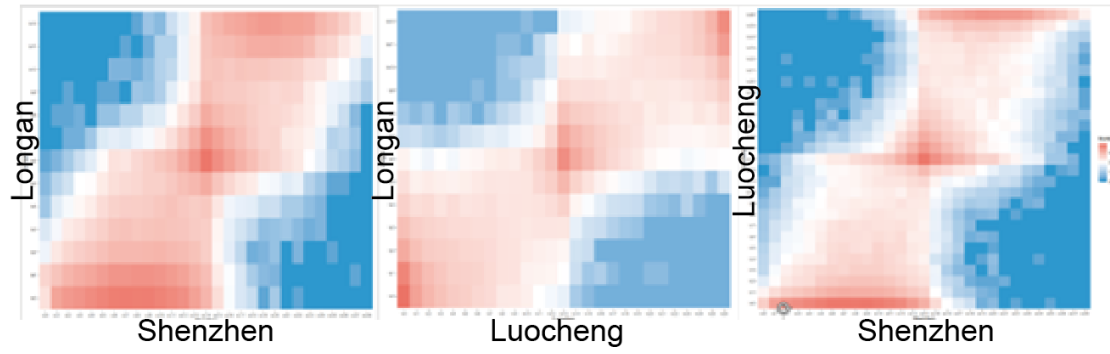


Figure S10. Observed joint 2D-SFS for each pair of three populations.

The number of loci in this heatmap was plotted after the logarithmic operation.

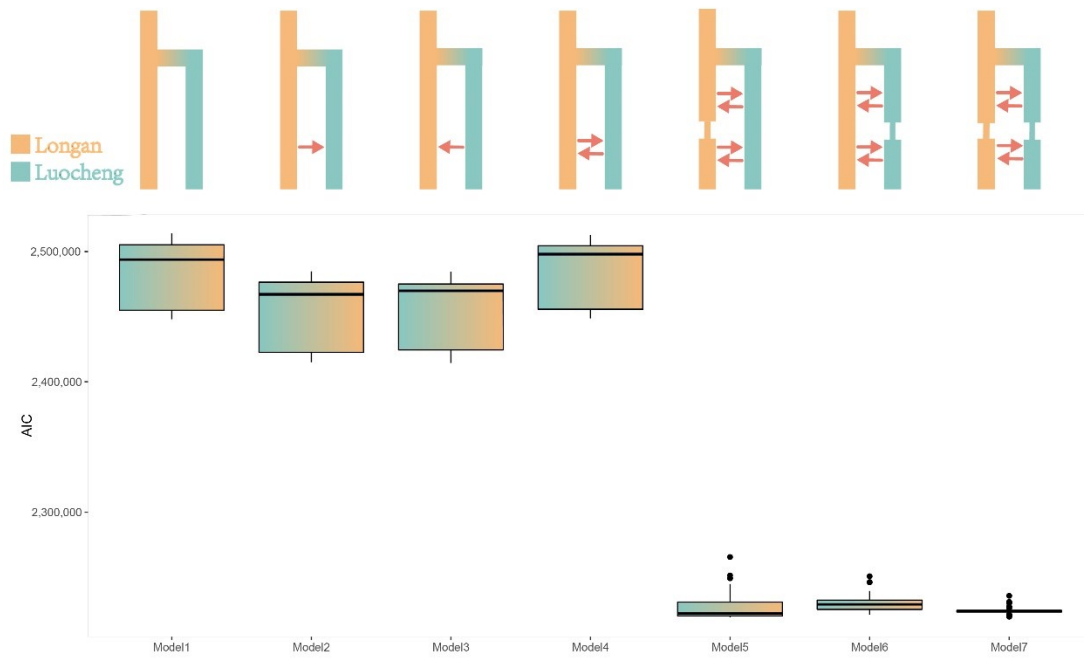


Figure S11. 2 population models simulated by fastsimcoal27 in population LA and LC.

The thin rectangle stands for bottleneck happened and red arrow represents gene flow. Akaike's information criterion (AIC) were calculated in each model's 100 independent runs. (The same below).

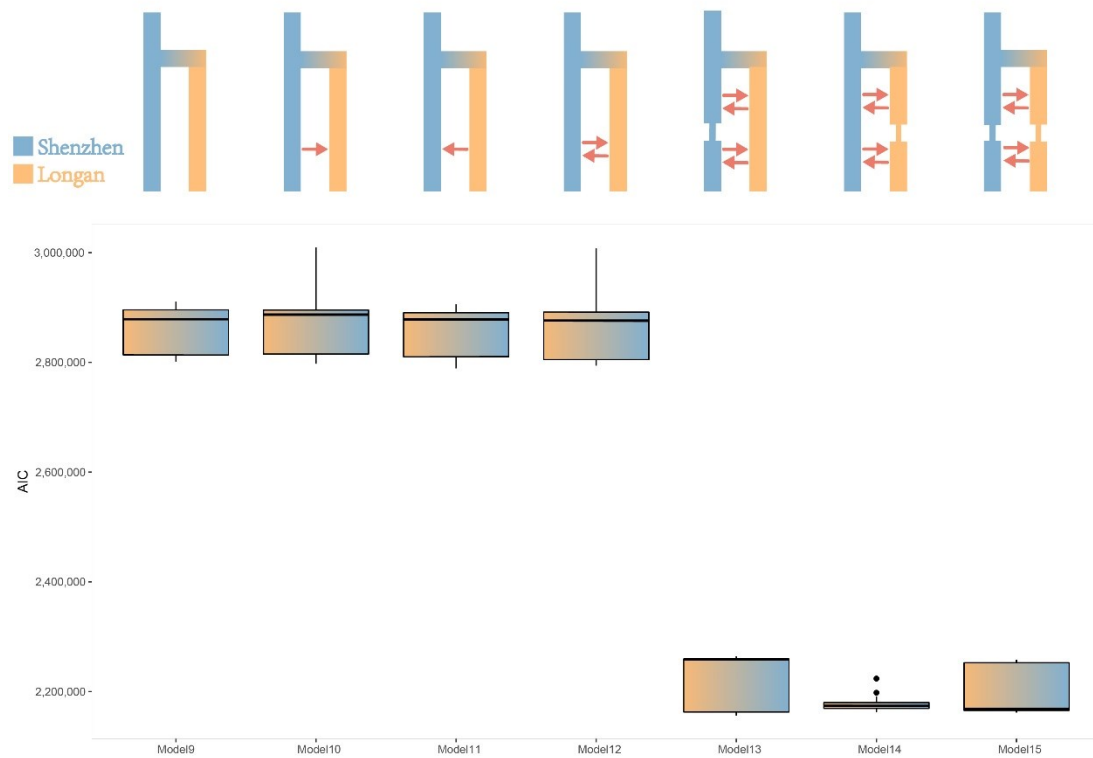


Figure S12. 2 population models simulated by fastsimcoal27 in population LA and SZ.

The thin rectangle stands for bottleneck happened and red arrow represents gene flow. Akaike's information criterion (AIC) were calculated in each model's 100 independent runs. (The same below).

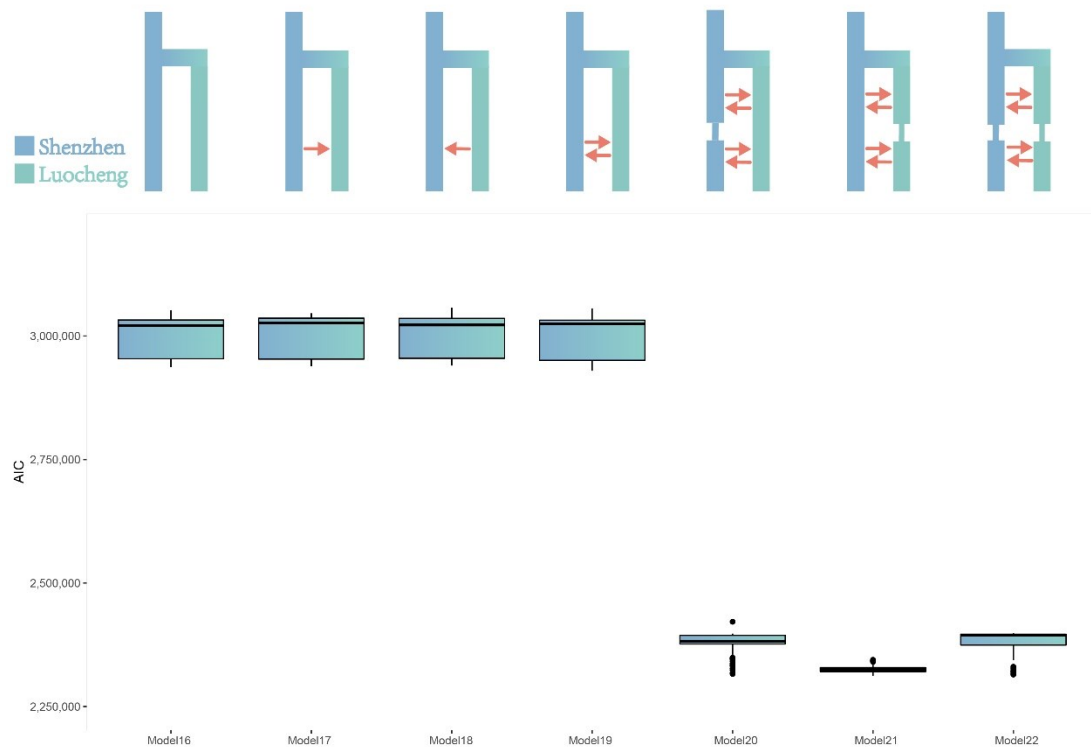


Figure S13. 2 population models simulated by fastsimcoal27 in population LC and SZ.

The thin rectangle stands for bottleneck happened and red arrow represents gene flow. Akaike's information criterion (AIC) were calculated in each model's 100 independent runs. (The same below).

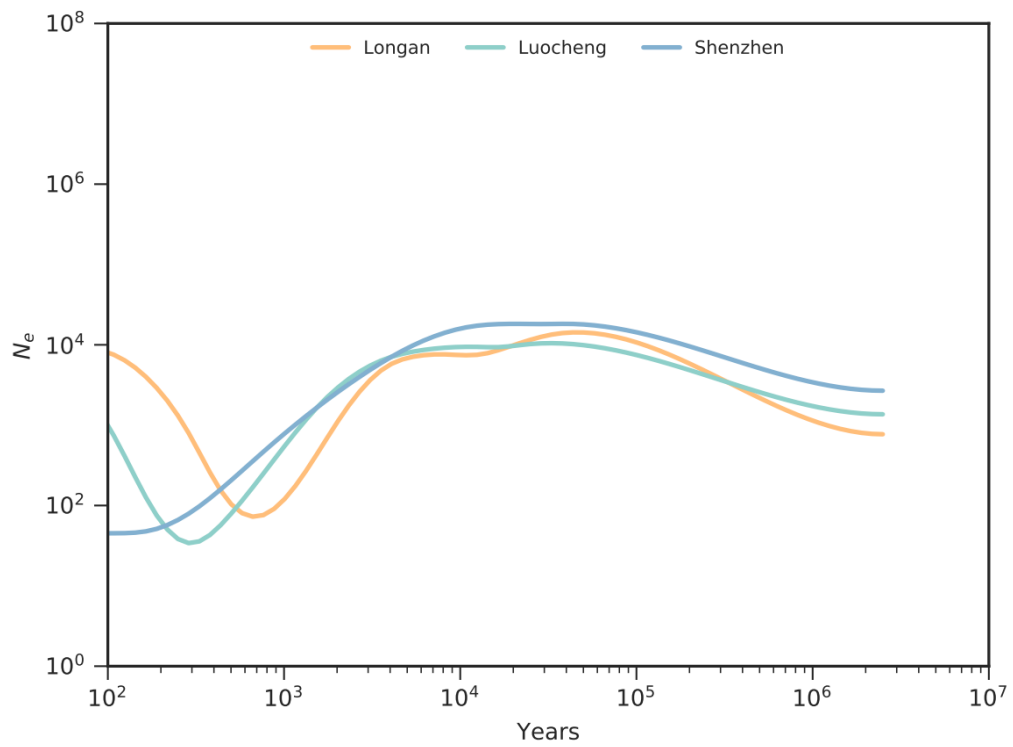


Figure S14. Population fluctuations during the demographic history by SMC++ estimated.

Three population represented by three colors are shown in the figure legend. This figure estimated the single population history.

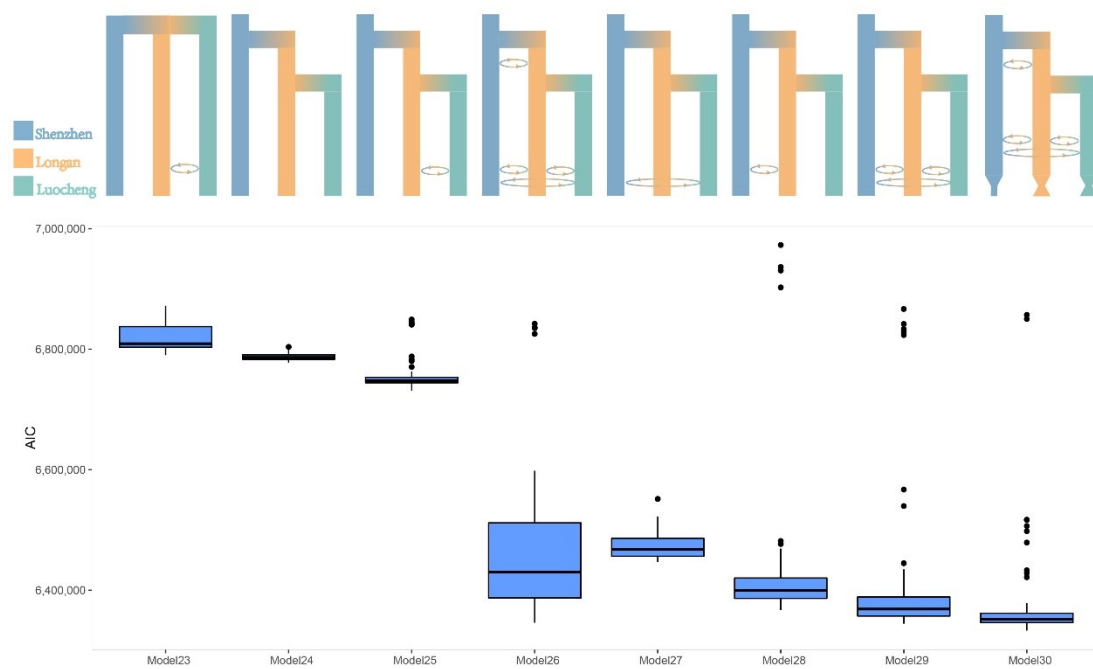


Figure S15.3 population models simulated by fastsimcoal2.

The thin rectangle stands for bottleneck happened and the circles represent bidirectional gene flows. Akaike's information criterion (AIC) were calculated in each model's 100 independent runs.

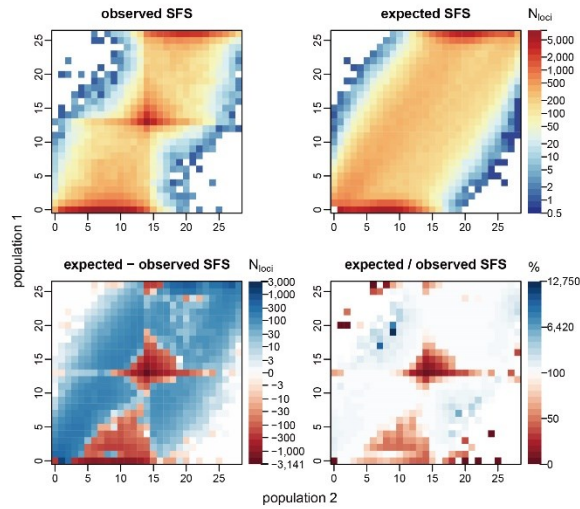
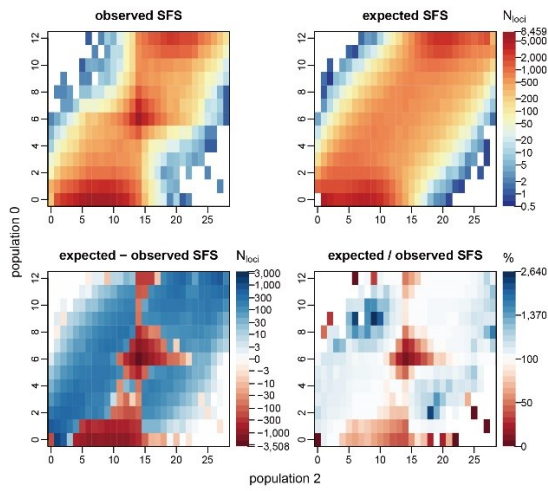
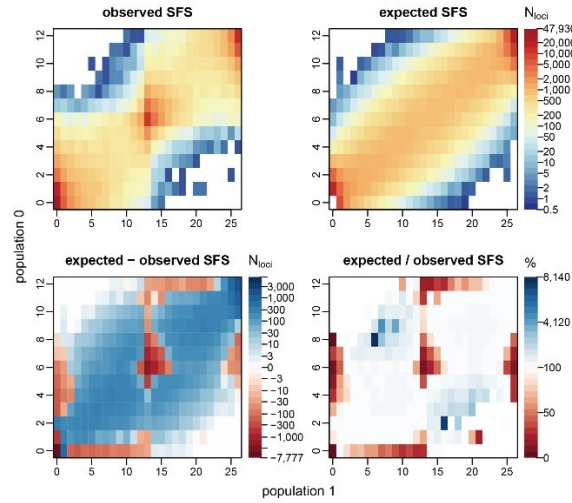
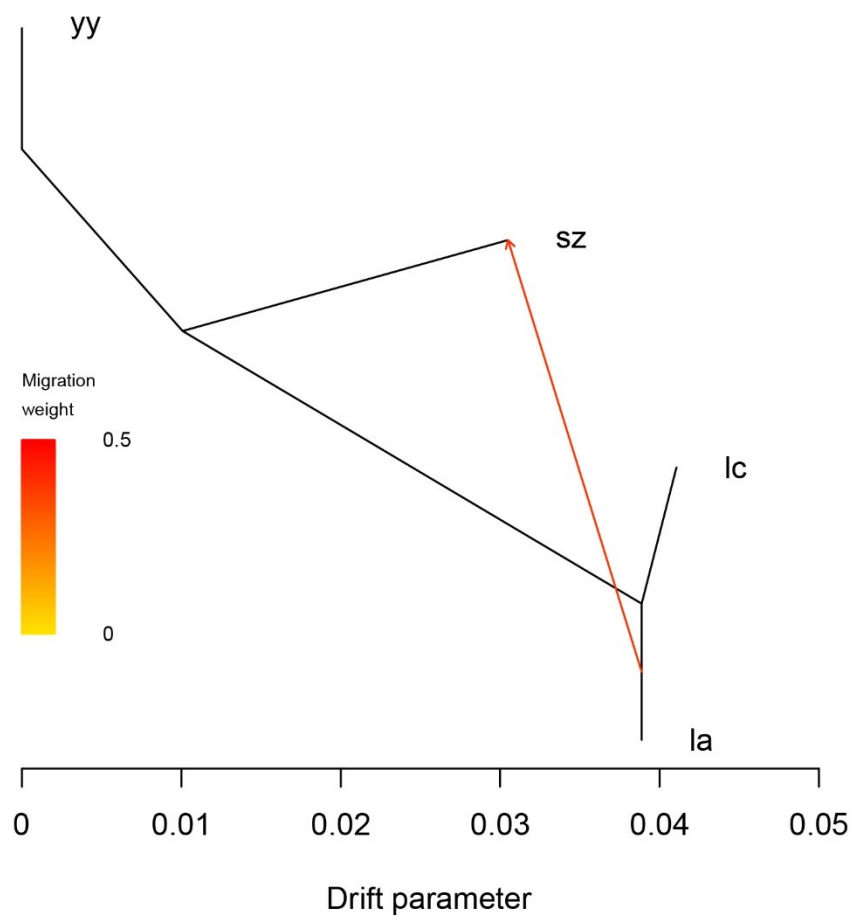


Figure S16. Observed and expected joint 2D-SFS of the best fit model. Three population corresponds to **Figure 9**, Population 0, 1 and 2 corresponds to population Longan, Luocheng and Shenzhen. High similarity between the observed and expected joint 2D-SFS indicated that the model fits well.



110

111 **Figure S17. TreeMix trees with 1 migration events from population LA (inland) to SZ (coastal).**

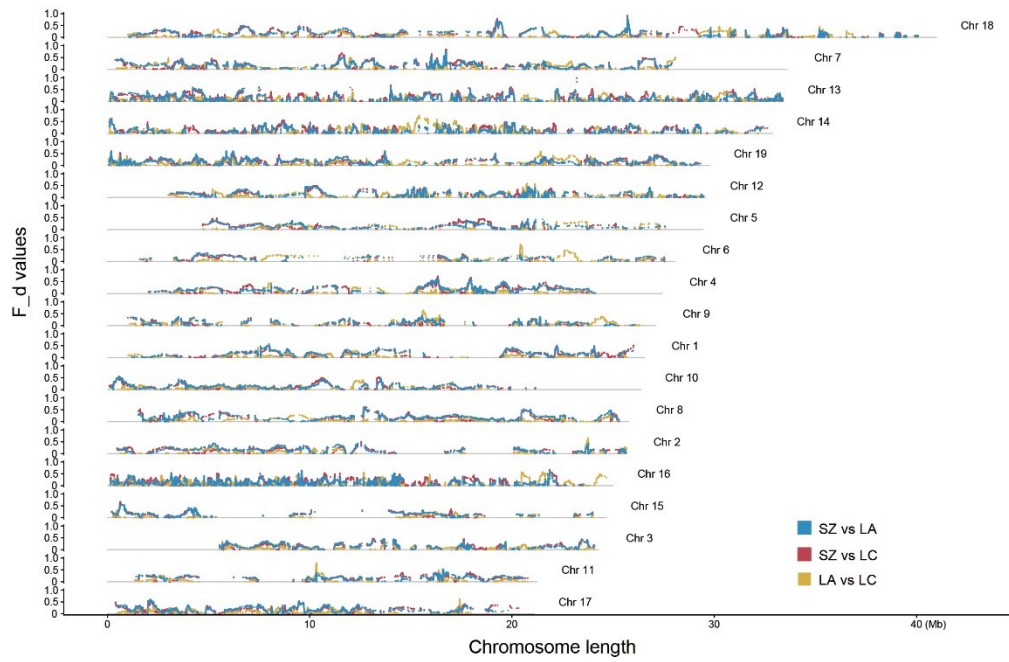


Figure S18. Whole-genome scatter plot of f_{dM} values performed by Dsuite D-statistics.

The f_{dM} values Valued from 0 to 1, and population SZ versus LA was highest, followed by SZ versus LC, LA versus LC was lowest.

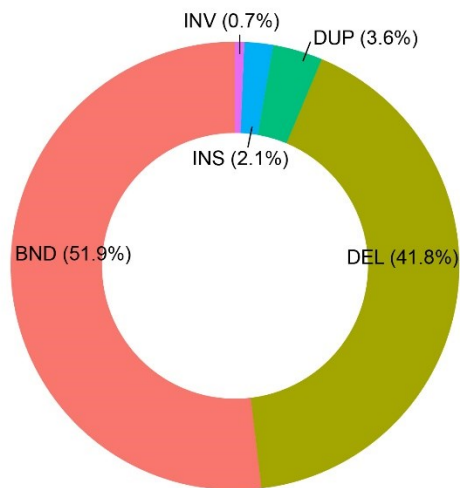
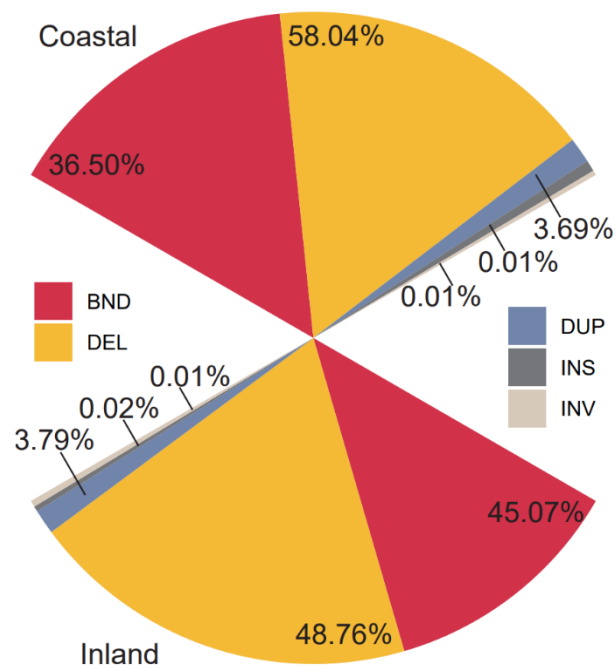


Figure S19. Distribution of the five SVs types of proportion between the coastal and inland populations.



119

120 **Figure S20. The five types of SVs proportion between the coastal and inland populations.**

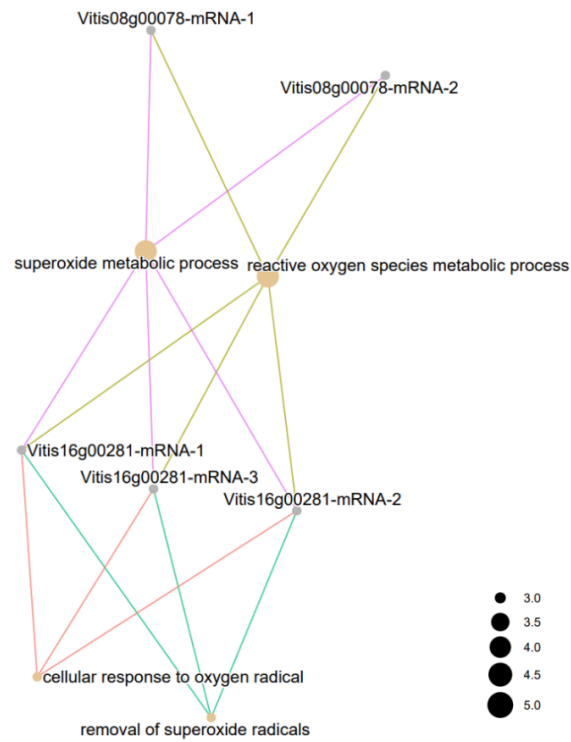


Figure S21. GO enrichment analysis with outlier genes in coastal population by SVs.

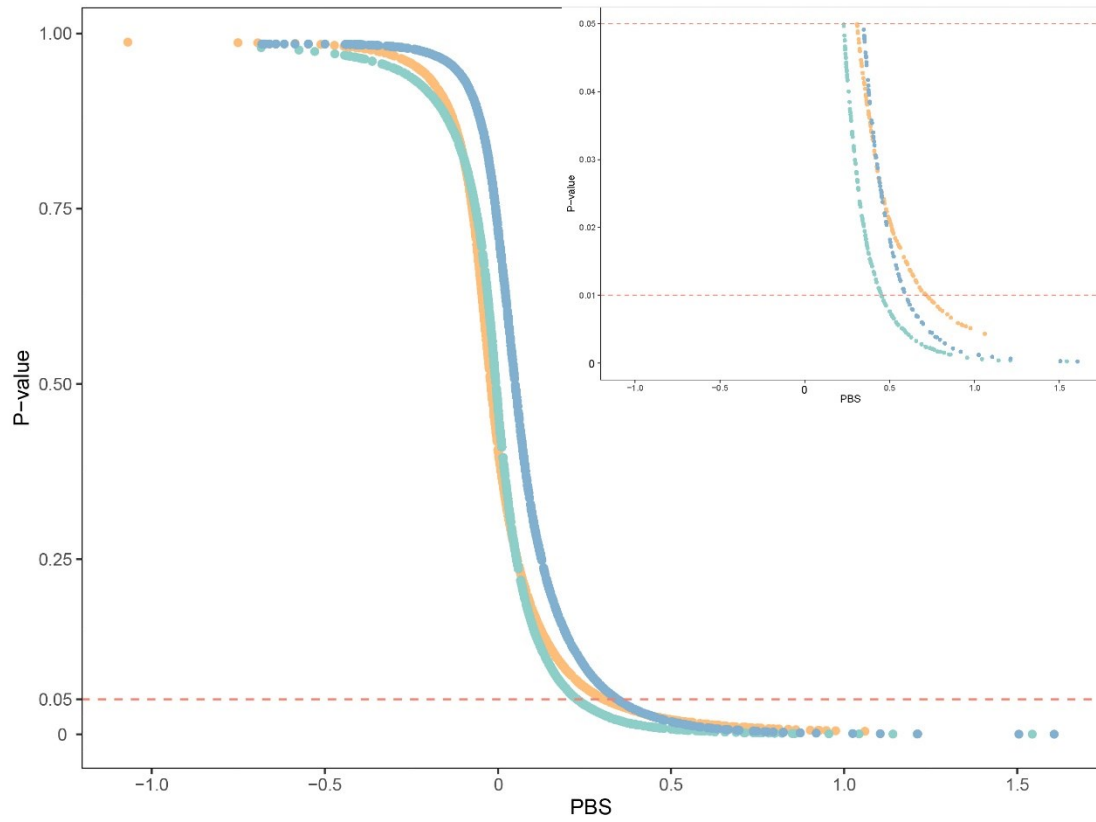


Figure S22. Observed population branch statistic (PBS) and P value distributions.

Blue, yellow, and green are stand for population Shenzhen (coastal), Longan (inland) and Luocheng (inland) respectively.

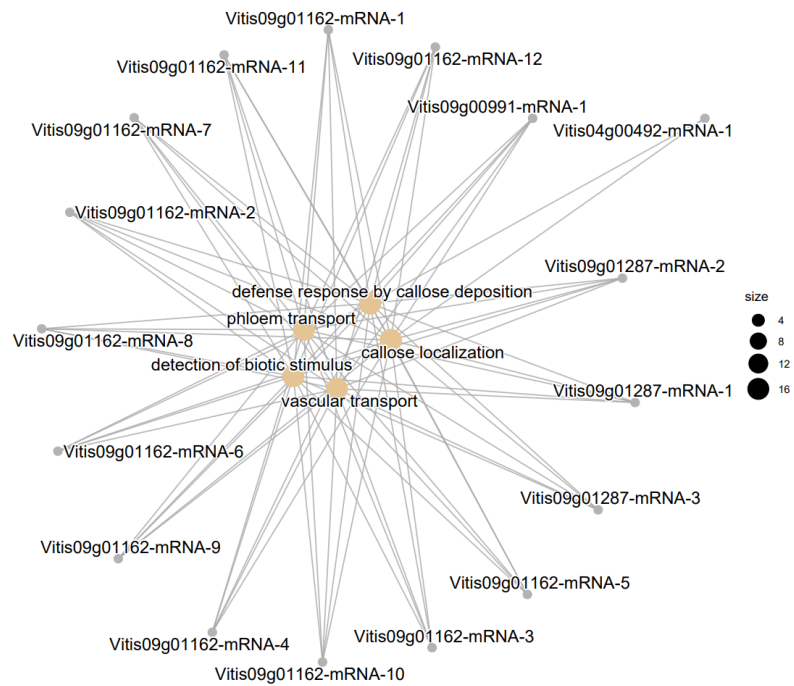


Figure S23. GO enrichment analysis with same outlier genes of three populations.

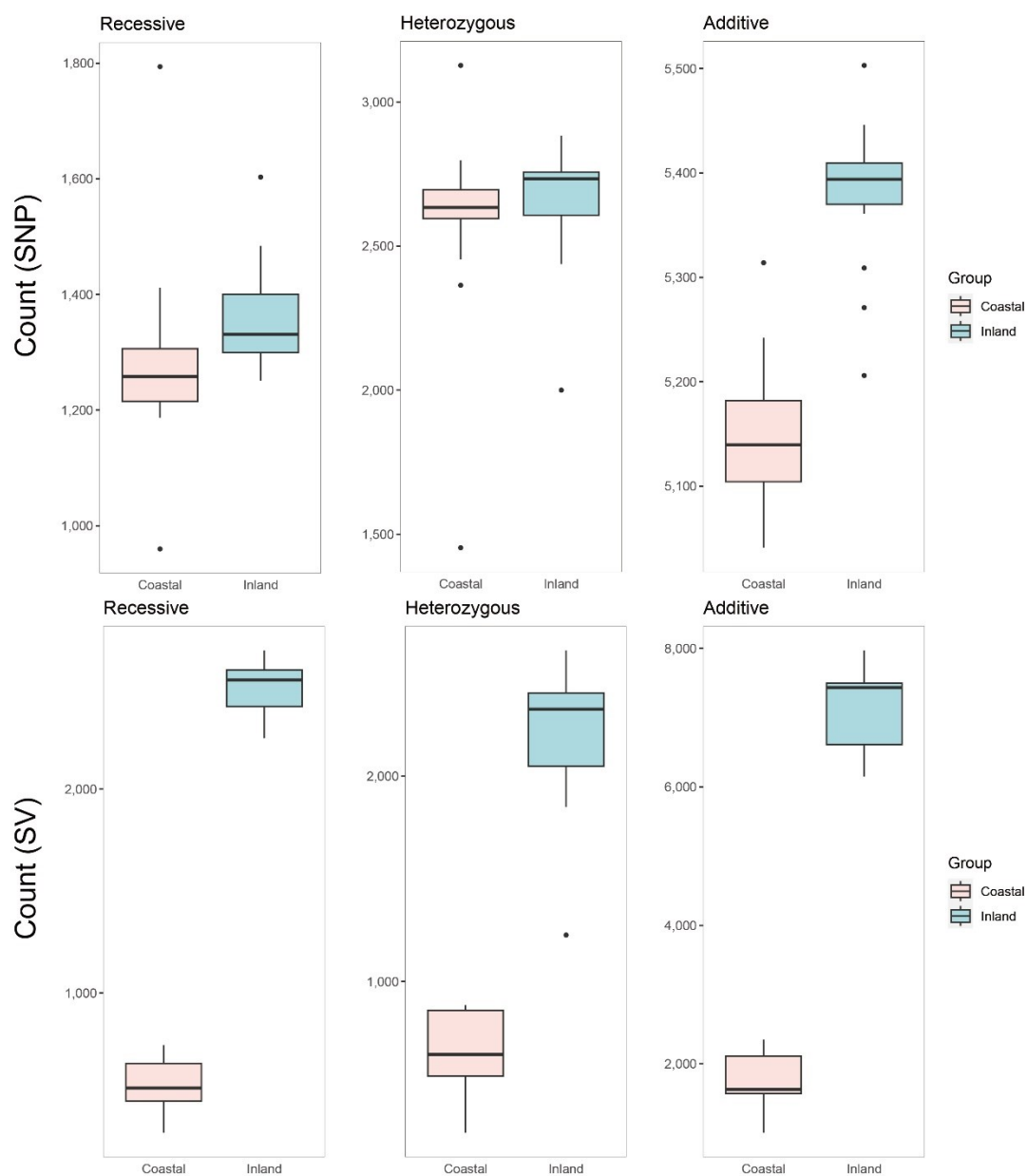


Figure S24. SVs and SNPs burdens between coastal and inland populations.

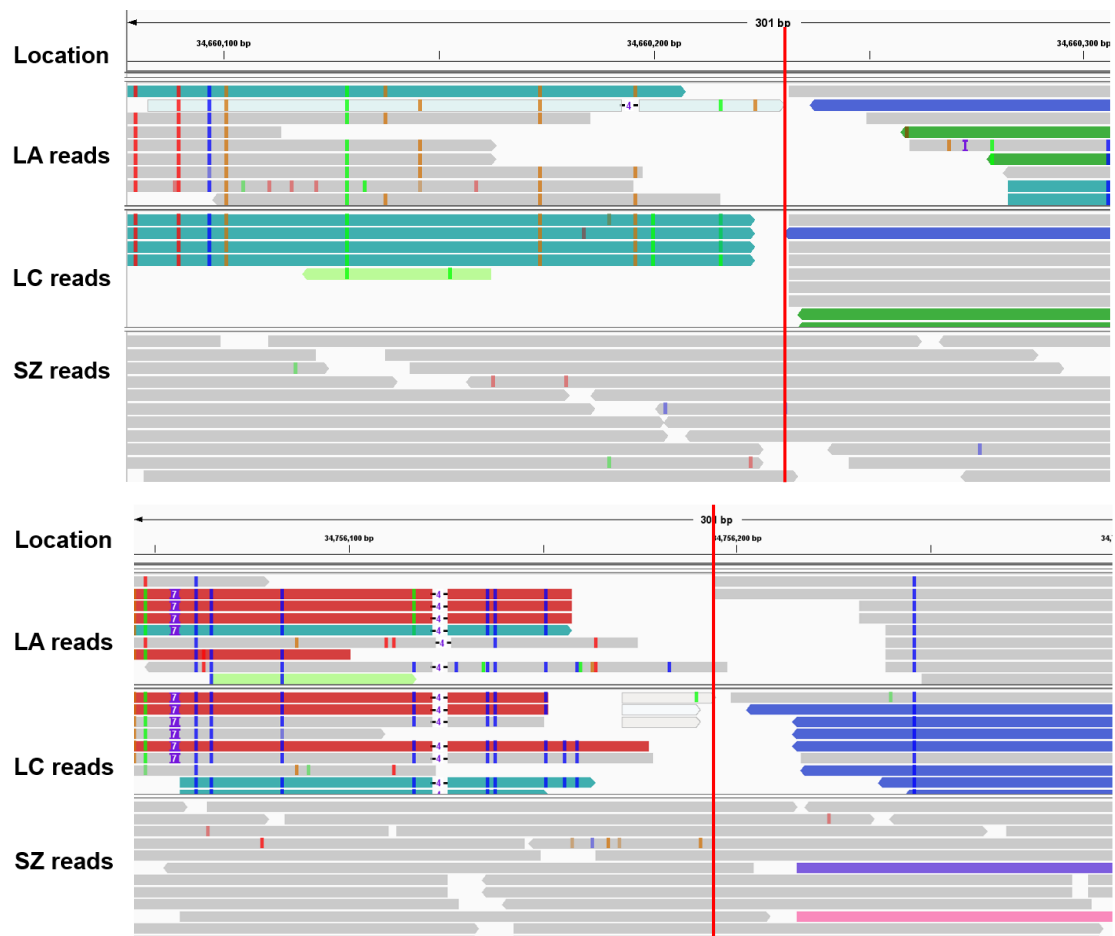


Figure S25. Breakpoint locations of the outlier inversion in Chromosome 18.

With length 95,967bp from 34,660,228 bp to 34,756,195 bp, the above two are individuals of inland populations while the below one is from coastal population. Breakpoint locations coincides with that identified by Delly.

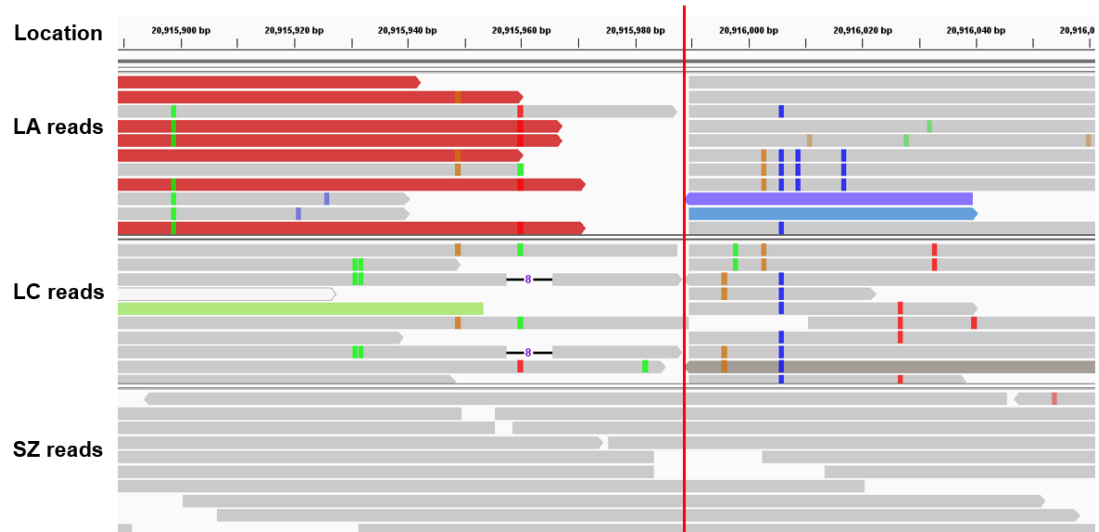


Figure S26. The inland populations occurred deletion events on chromosome 7 downstream of *RGAI* gene.

The above two are individuals of inland populations while the below one is from coastal population.
The breakpoint locations of that deletion events identified by Delly and verified by IGV.

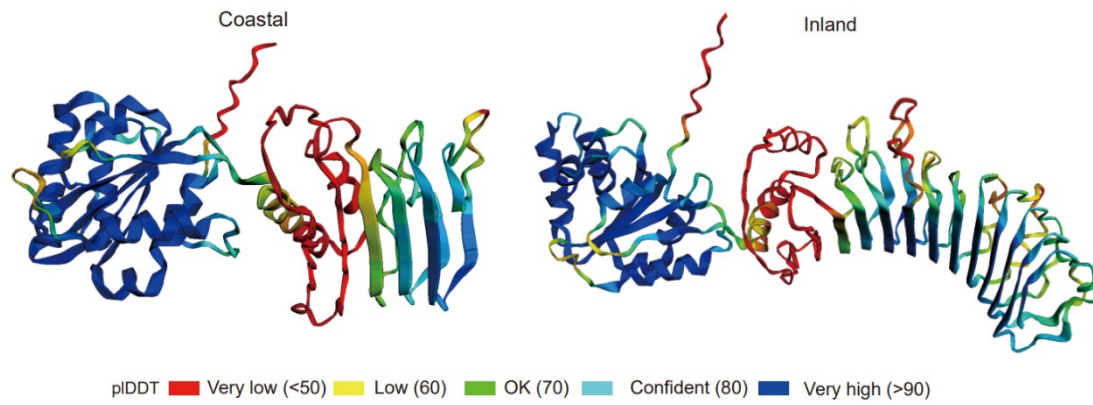


Figure S27. The coastal and inland populations possible protein three-dimensional structural prediction of *RGA* genes.

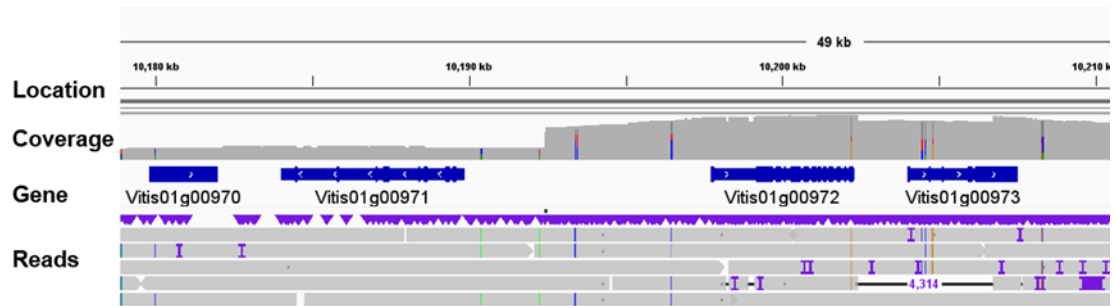


Figure S28. Identification of Hemizygous Genes.

We have verified the exact number of hemizygous genes through image verification within the IGV. As shown in the figure below, we randomly displayed partial alignment results of chromosome 1 in the woolly grape, and we could find that *Vitis01g00970* and *Vitis01g00971* are clearly hemizygous genes, while *Vitis01g00972* and *Vitis01g00973* are common homozygous genes.