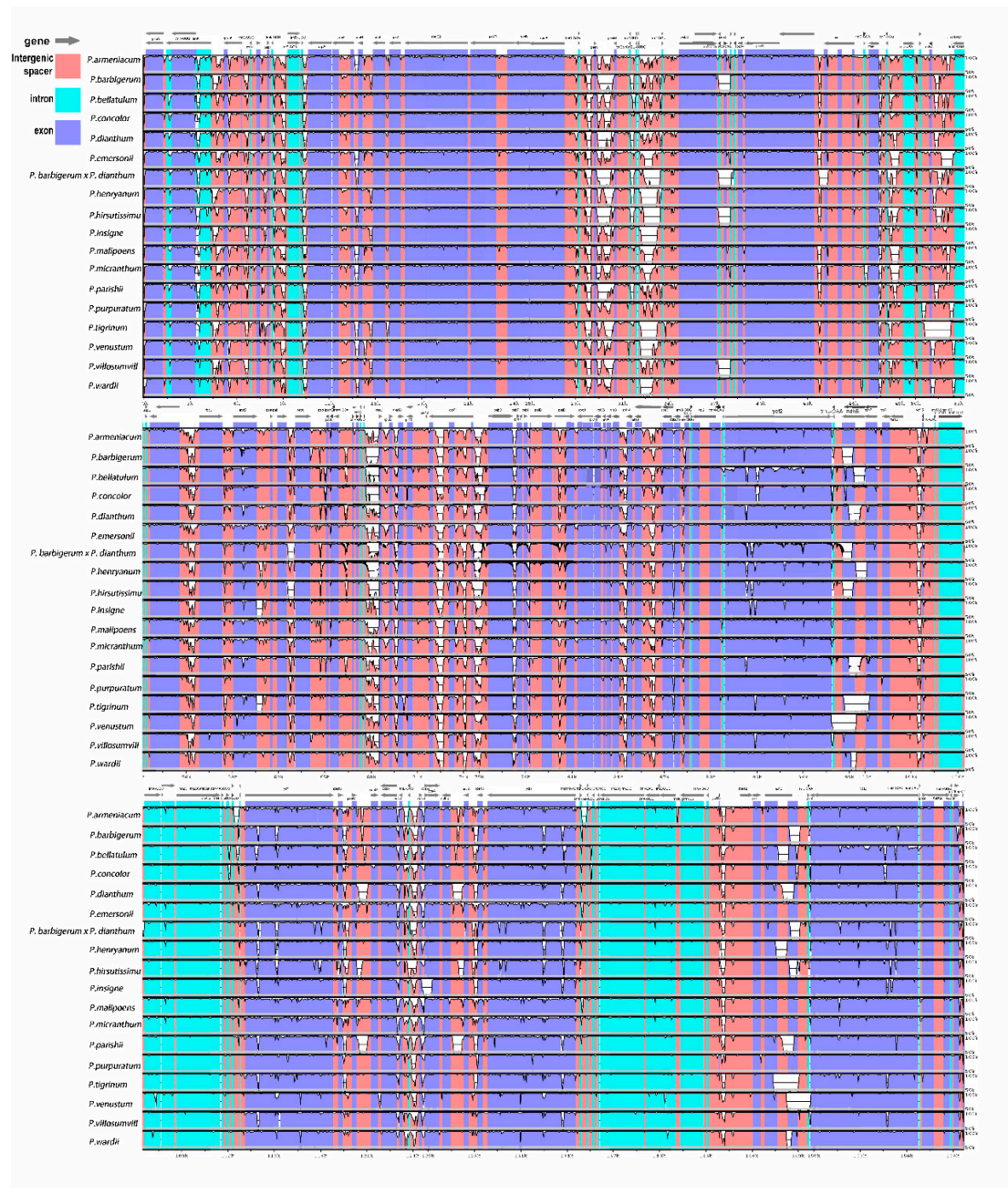
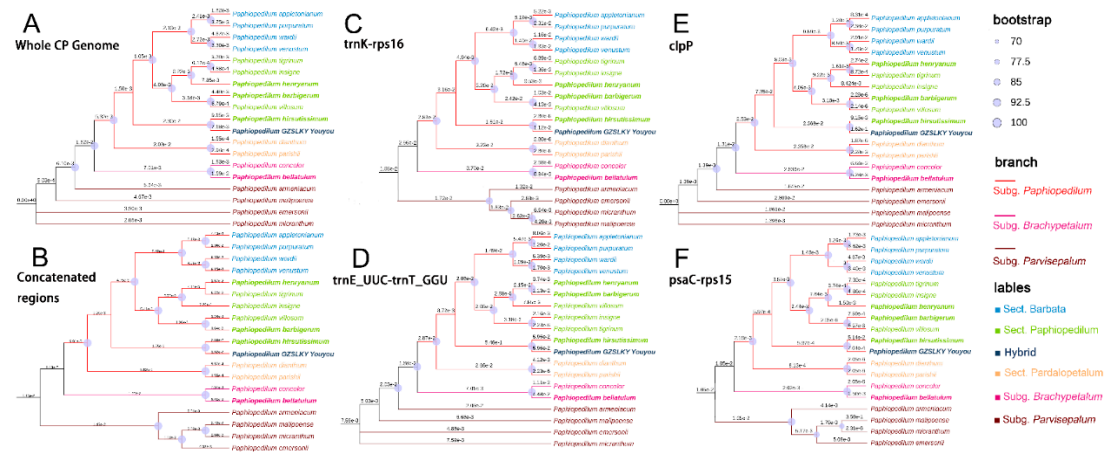


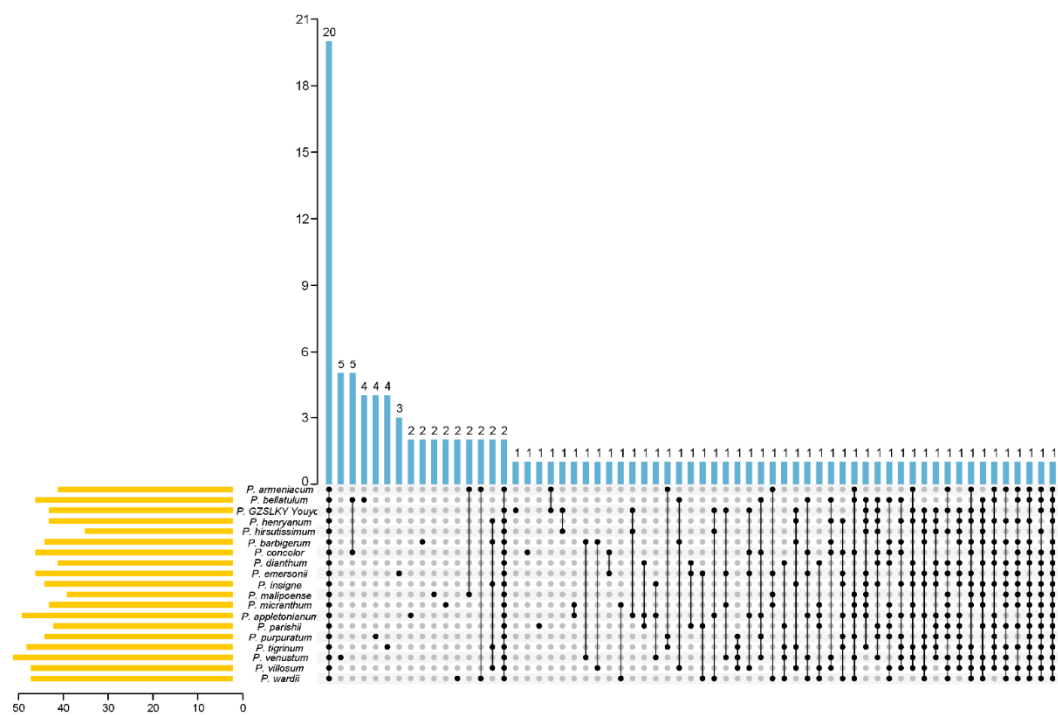
## Supplementary Figures



**Figure S1.** Comparative analysis (using the MVISTA program) of the whole-chloroplast genomes of the 19 *Paphiopedilum* species. The identity percentage shown in the vertical axis ranged from 50 % to 100 %, while the horizontal axis exhibited the position within the chloroplast genome. Each arrow displays the transcription direction of the annotated genes in the reference genome (*P. appletonianum*). Genome regions are colored as exons, introns, and intergenic spacer, respectively.



**Figure S2.** The ML tree of the nineteen studied *Paphiopedilum* species constructed by whole cp genome and divergent hotspots regions. The circle size on each node represented the bootstrap value. A: the whole cp genome. B: The concatenated regions. C: The trnK-rps16. D: trnE\_UUC-trnT\_GGU. E: The clpP. F: The psaC-rps15.



**Figure S3.** The upset plot of the identified SSRs in 19 *Paphiopedilum* chloroplast genomes. Here, to identify the unique SSRs in corresponding species, the main focus was on the types of SSRs units without considering the repeat times.

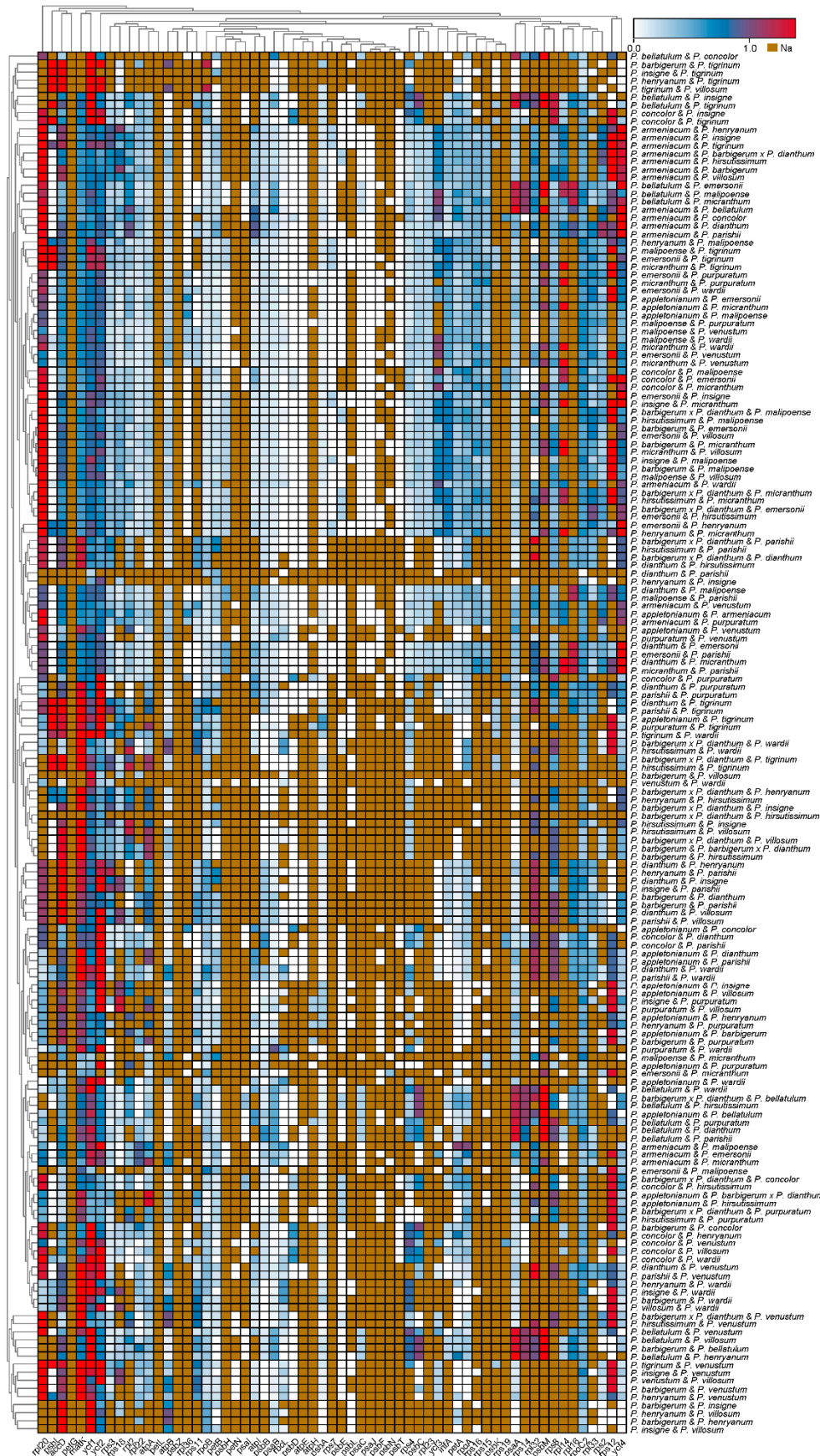


Figure S4. Heat map of the Ka/Ks value of each gene in each pair of species.