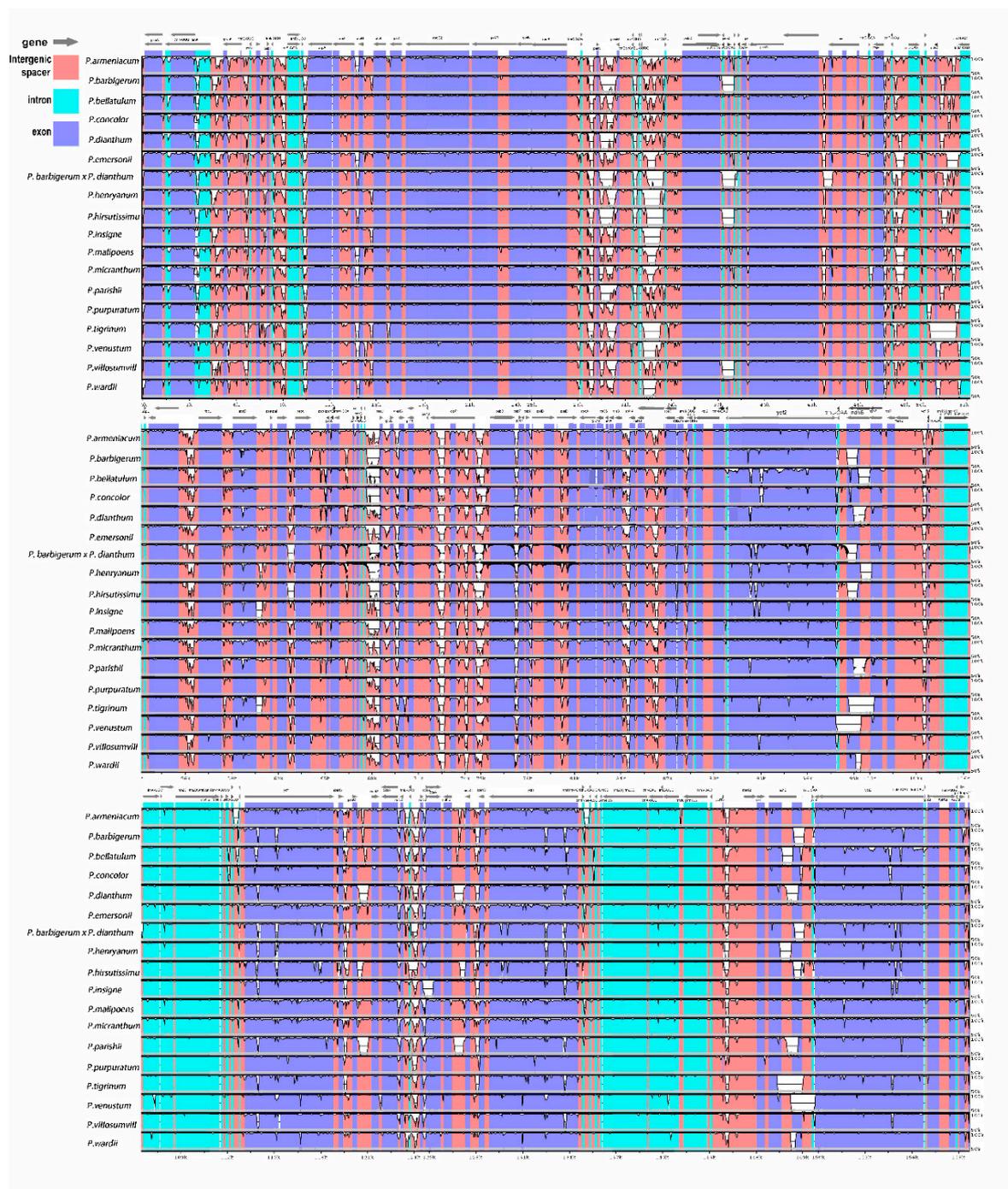
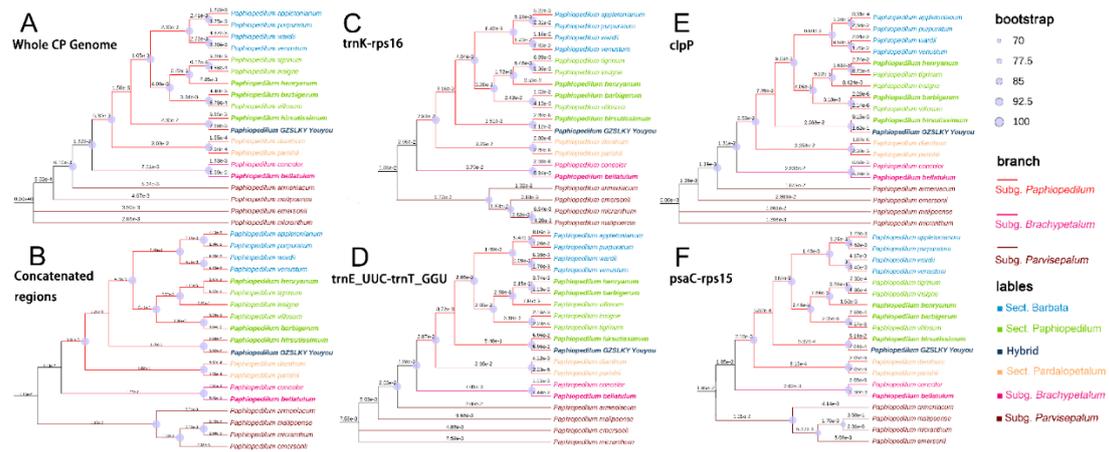


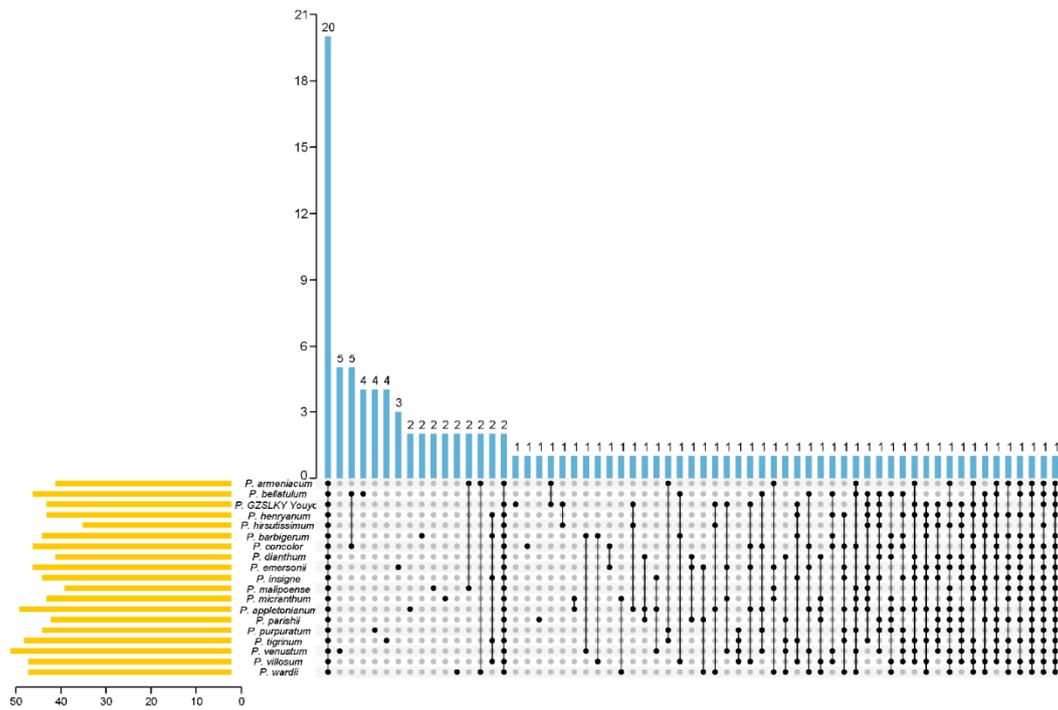
## Supplementary Figures



**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.

