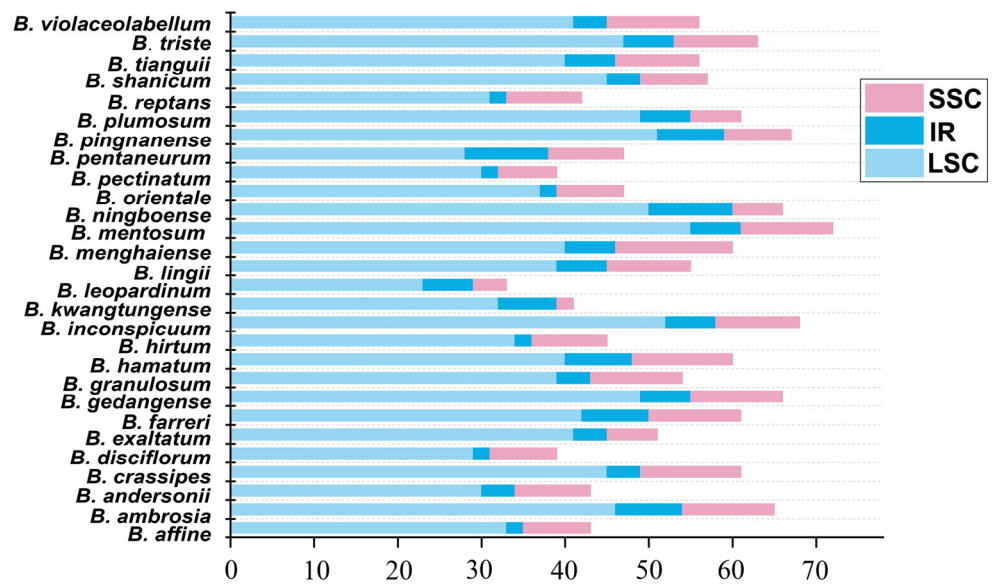
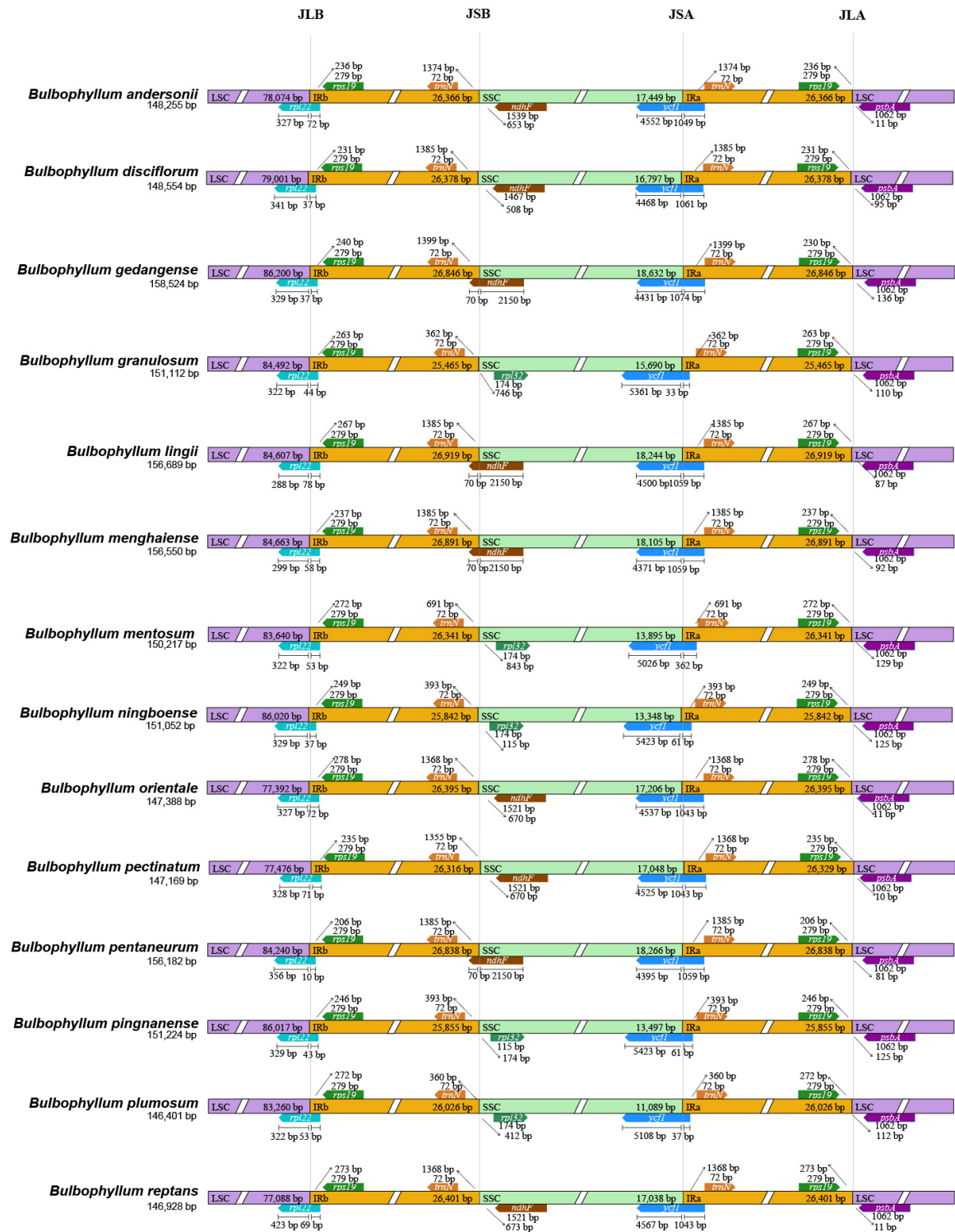


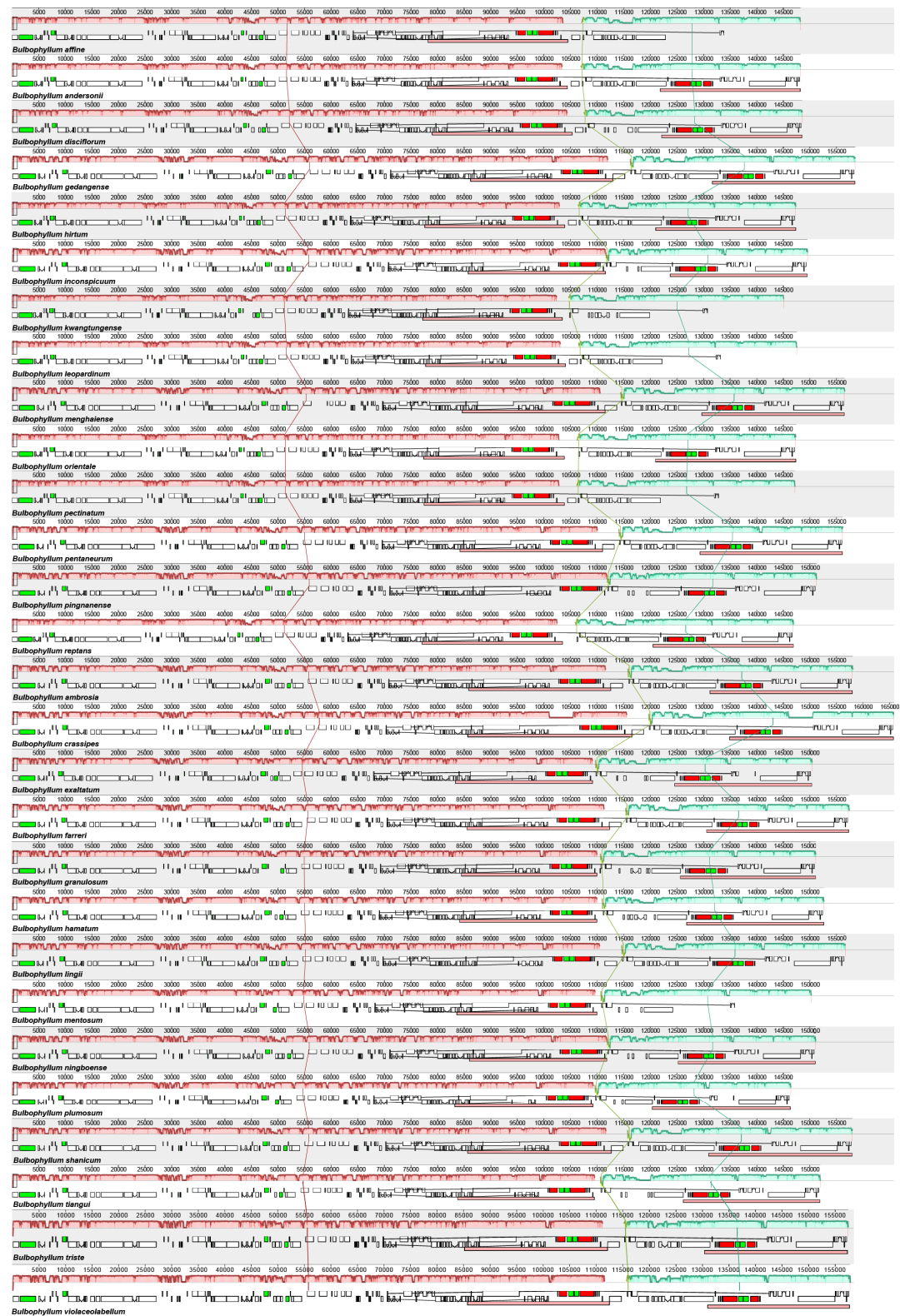
Supplementary Figures



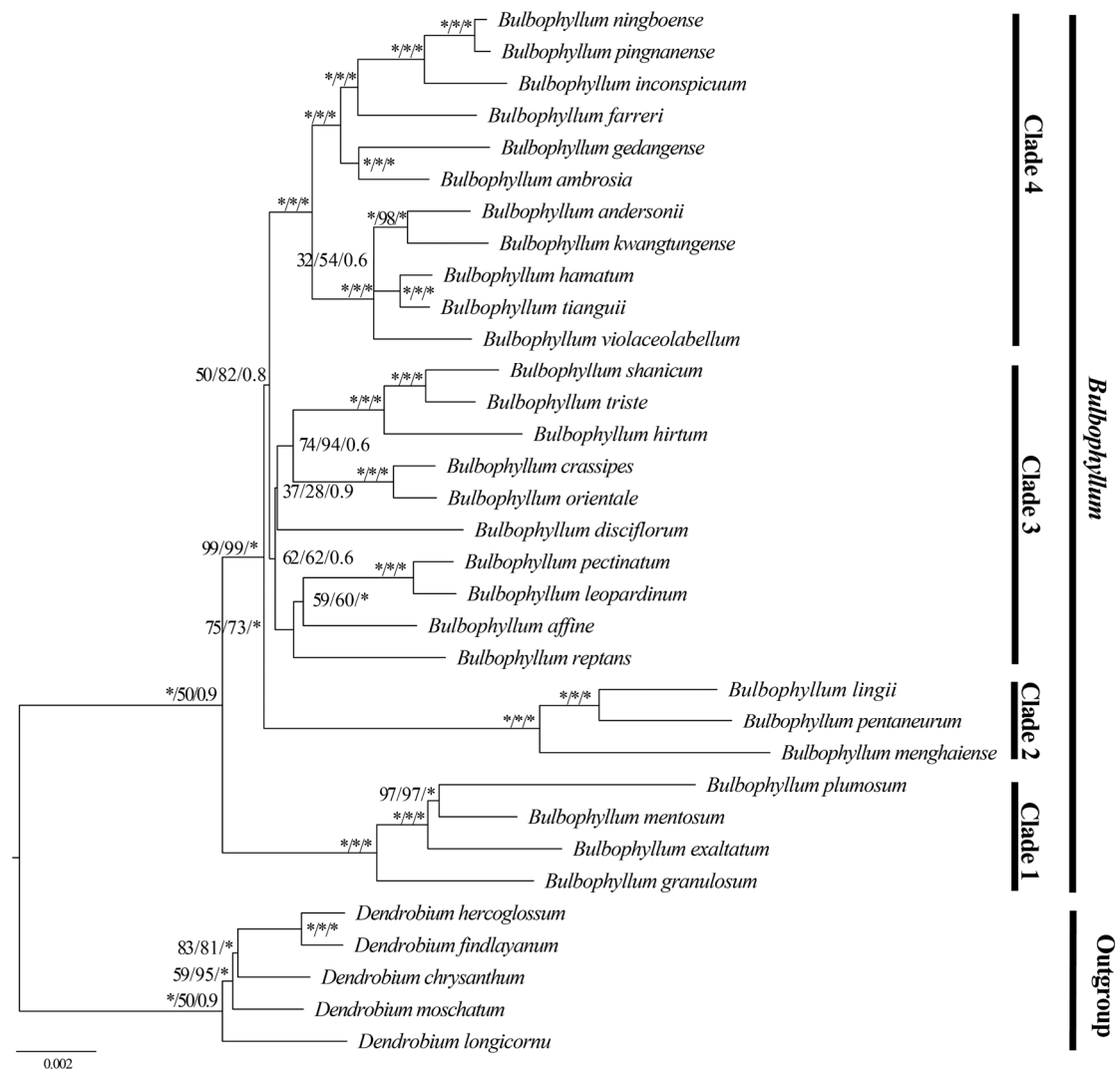
Supplementary Figure S1 Number of SSRs for each *Bulbophyllum* species by location in IR, LSC, and SSC.



Supplementary Figure S2 Comparison of junctions between the LSC, SSC, and IR regions among the other 14 *Bulbophyllum* cp genomes.



Supplementary Figure S4 Alignment of the 28 *Bulbophyllum* cp genomes (mauve graphs). Local collinear blocks within each alignment are represented by blocks of the same color connected with lines.



Supplementary Figure S5 The phylogenetic tree of 28 *Bulbophyllum* species and five outgroups based on concatenated 68 protein-coding genes. The numbers near the nodes are bootstrap percentages and Bayesian posterior probabilities (BP_{ML}, BP_{MP}, PP), *node is 100 bootstrap percentage or 1.00 posterior probability.