

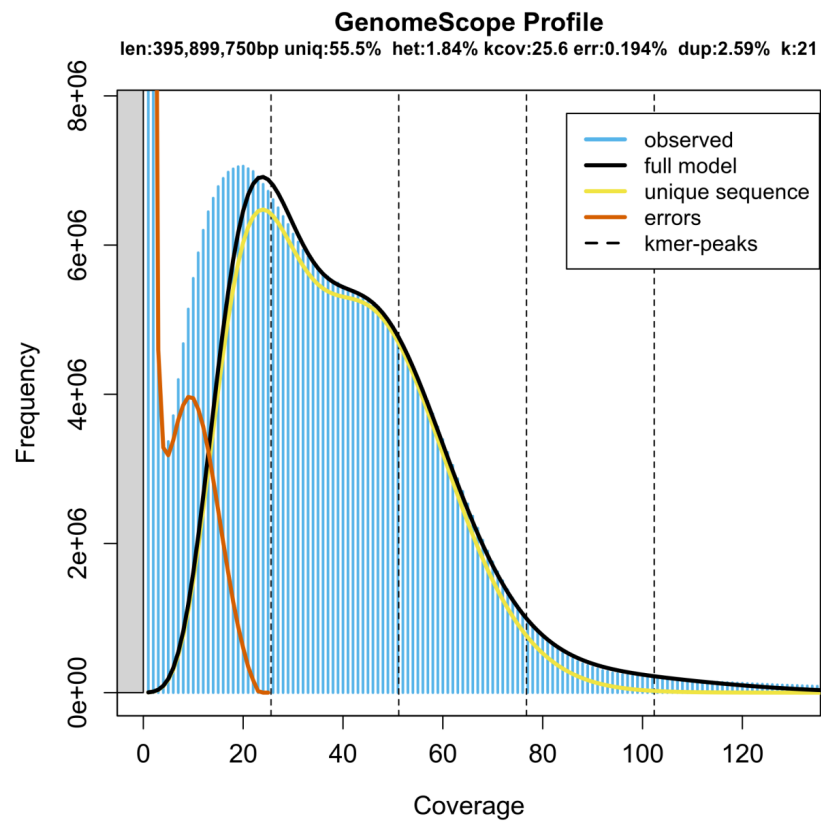


Figure S1. GenomeScope projection of *P. deltooides* genome size and heterogeneity using a 21bp *k*-mer analysis.

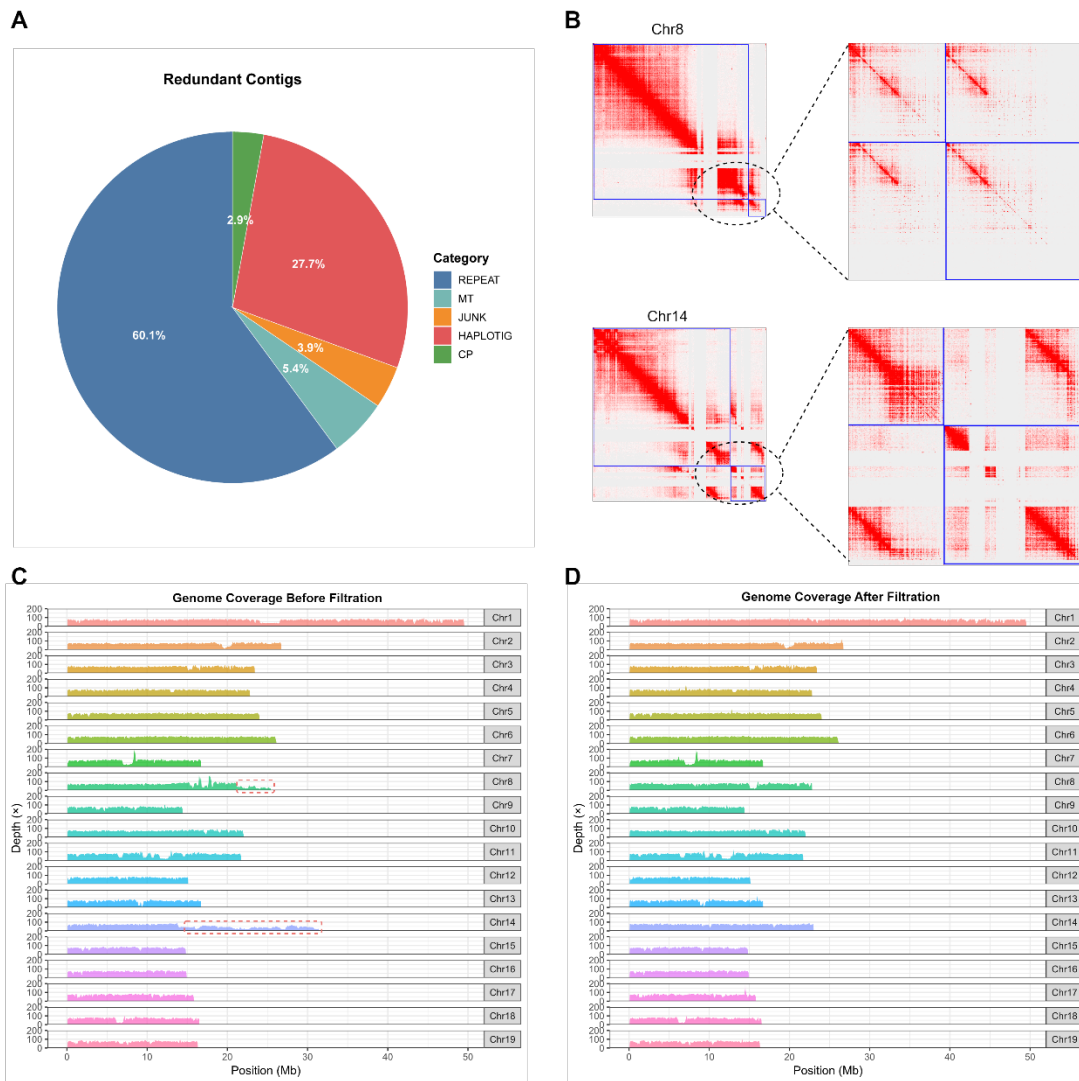


Figure S2. Validated information about the redundant contigs. **A** Category of the redundant contigs. **B** The Hi-C contact map of Chr8 and Chr14. **C** Genome coverage before filtration. The red dashed boxes highlight genomic regions with uneven coverage depth on Chr8 and Chr14. **D** Genome coverage after filtration.

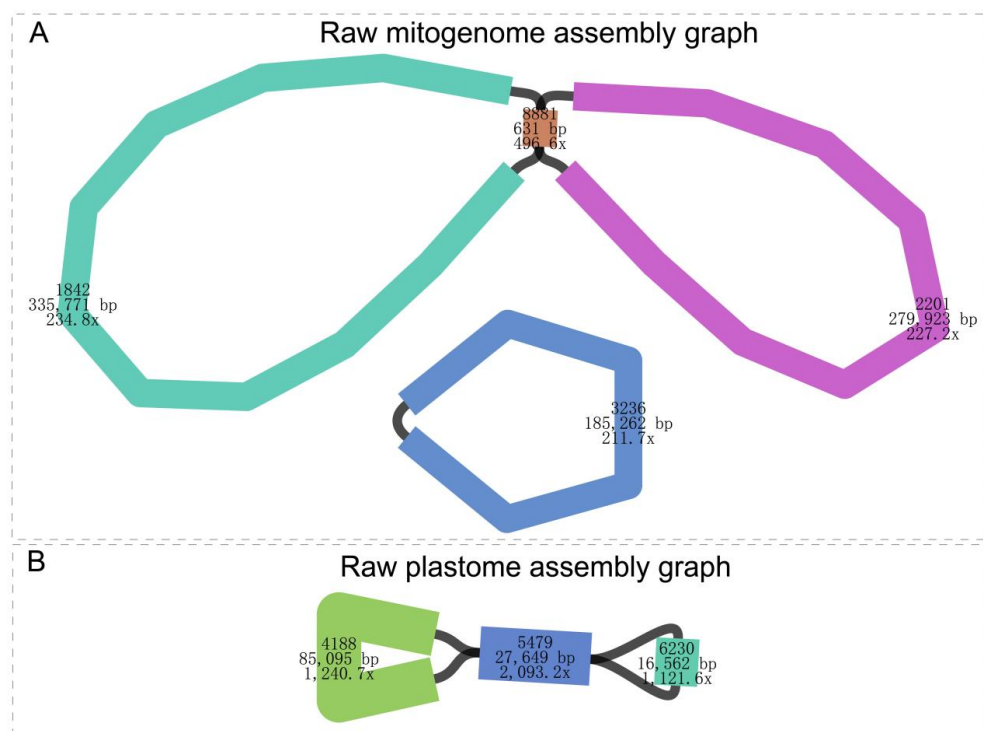


Figure S3. The raw assembly graphs of *P. deltoides* mitochondrial genome and plastid genome.

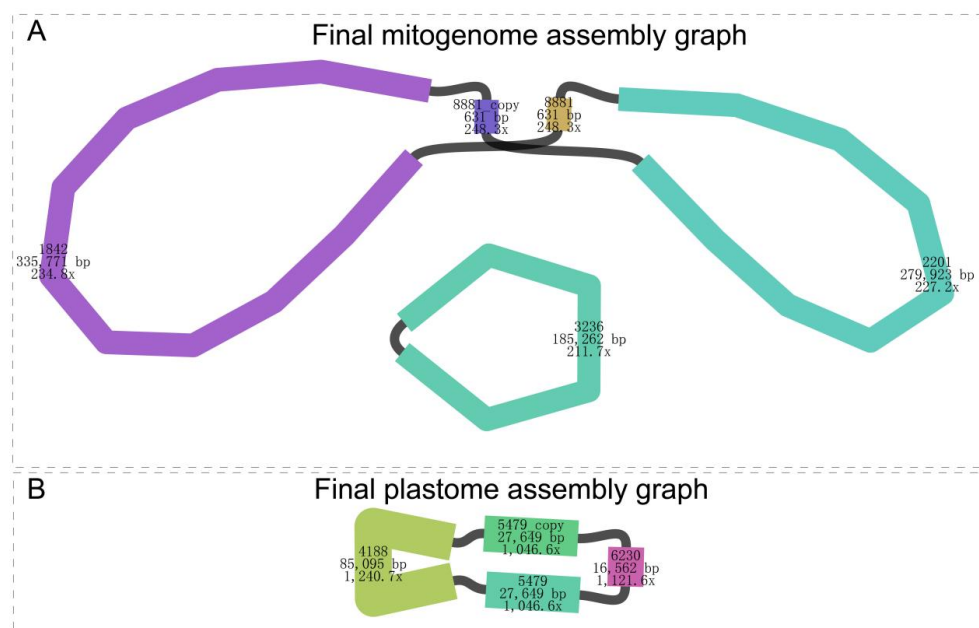


Figure S4. The final assembly graph after disentangling of *P. deltoides* mitochondrial genome and plastid genome.

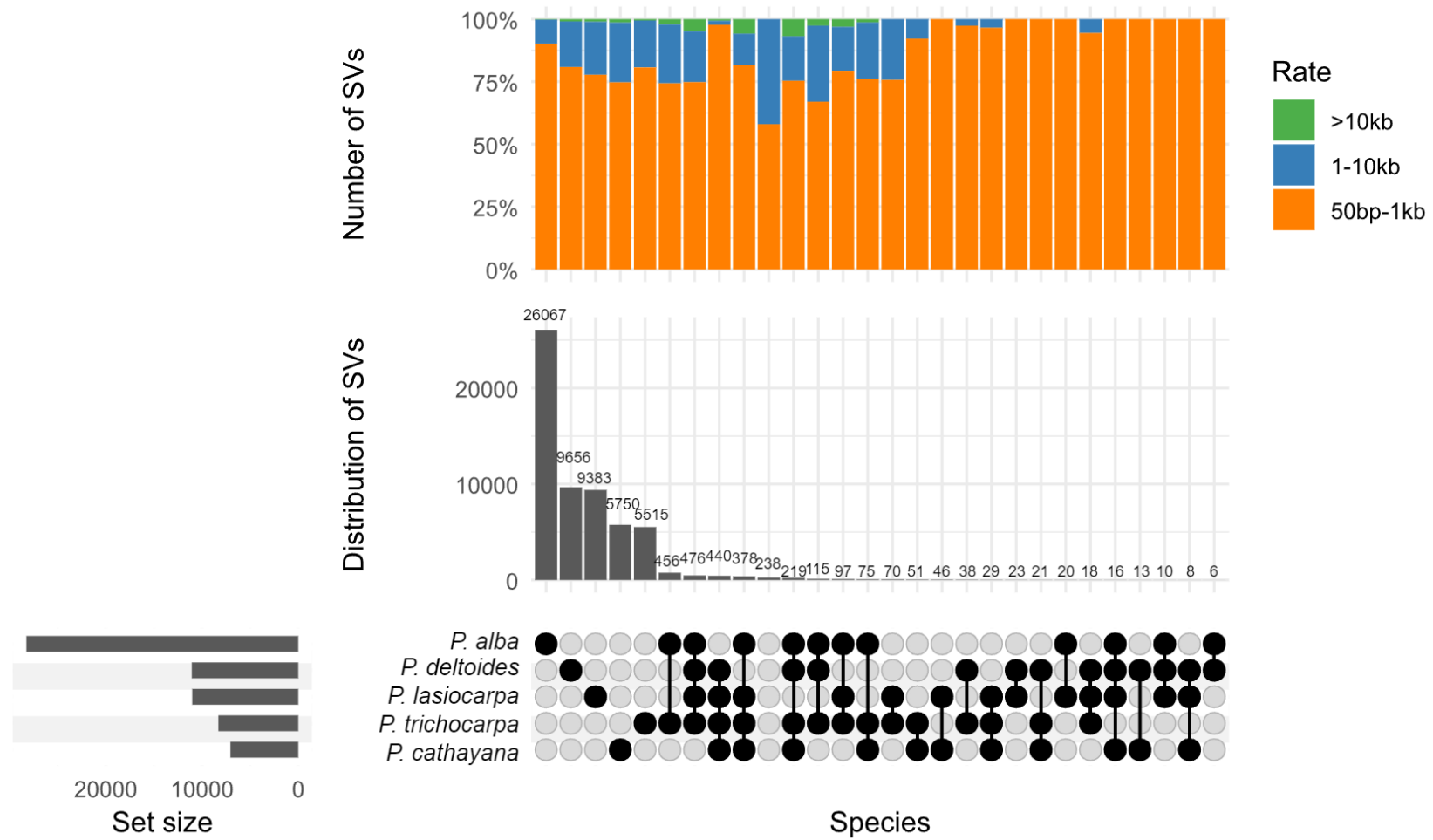


Figure S5. The number and distribution of structural variations across *P. alba*, *P. deltoides*, *P. lasiocarpa*, *P. cathayana*, and *P. trichocarpa*.

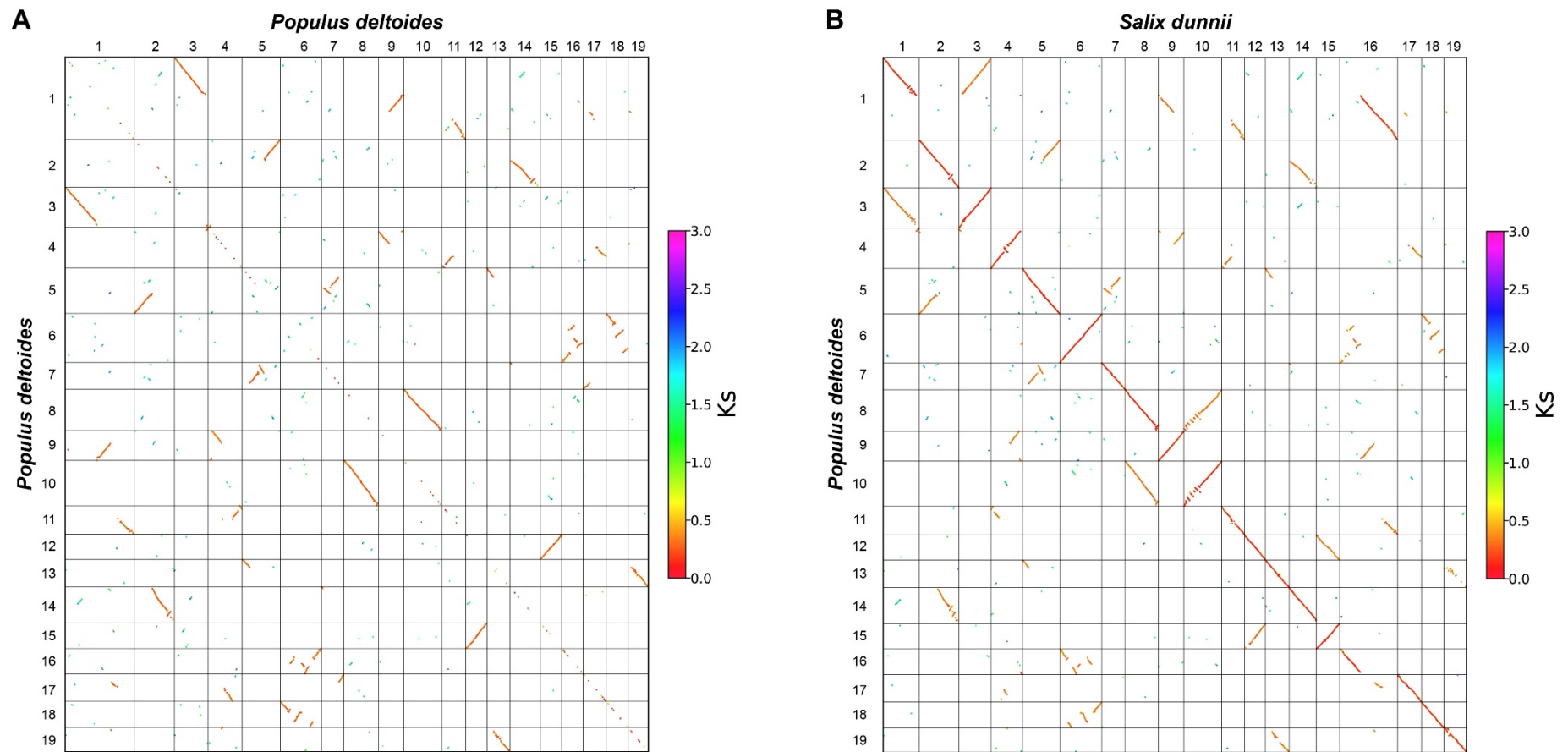
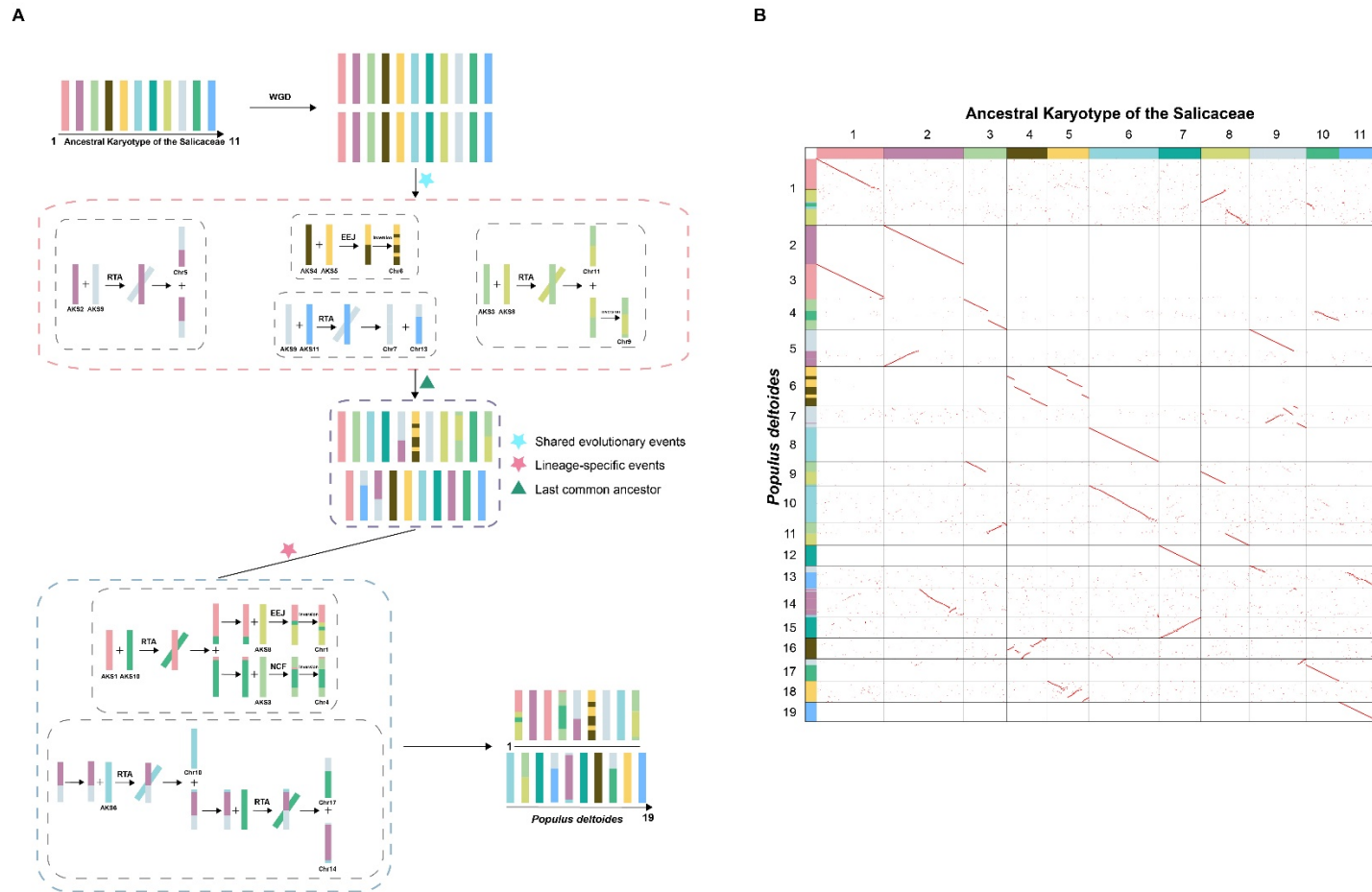


Figure S6. Dot plots of collinearity of *P. deltoides* and *S. dunnii*. **A** Collinear dot plot of *P. deltoides* and *P. deltoides*. **B** Collinear dot plot of *P. deltoides* and *S. dunnii*.



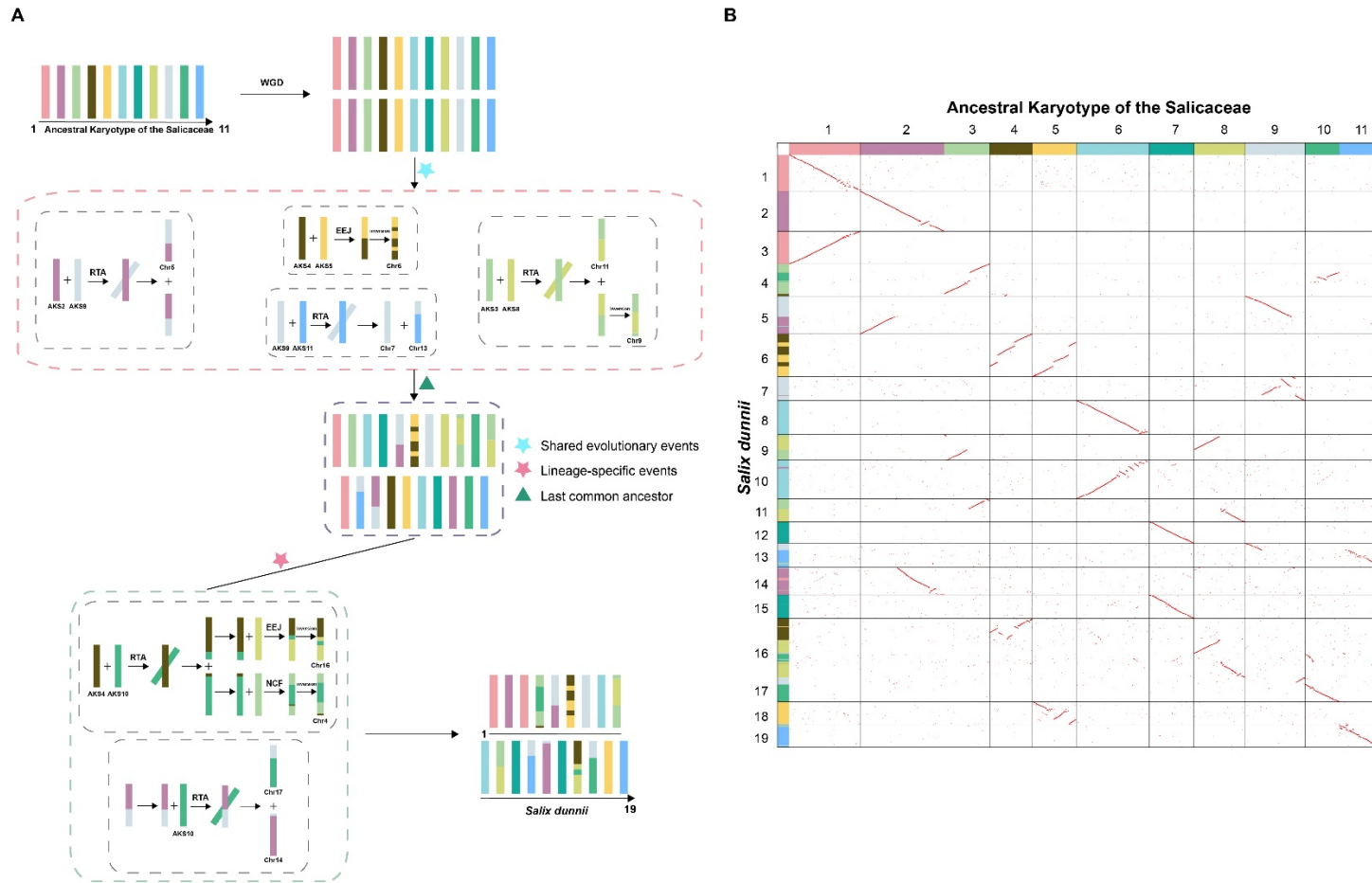


Figure S8. The detailed chromosomal evolution from Ancestral Karyotype of the Salicaceae (AKS) to *S. dunnii*. **A** The detailed chromosomal evolution from AKS to *S. dunnii*. Different colors represent different ancestral chromosomes. Enclosed by dashed lines are chromosomal structural variations. Blue and pink stars stand for the shared evolutionary events and lineage-specific events, respectively. **B** The inter-genomic collinear dot plot of AKS and *S. dunnii*.