

Figure S1. Gene family numbers of pan-transcriptome and functional enrichment analysis. (a) Numbers of gene families in the pan and core transcriptome with increasing species numbers. (b) The top six enriched KEGG pathways of the core, shell, and cloud gene families. (c, d) The top six enriched molecular function (c) and cellular component (d) terms of the core, shell, and cloud gene families from GO enrichment analysis.

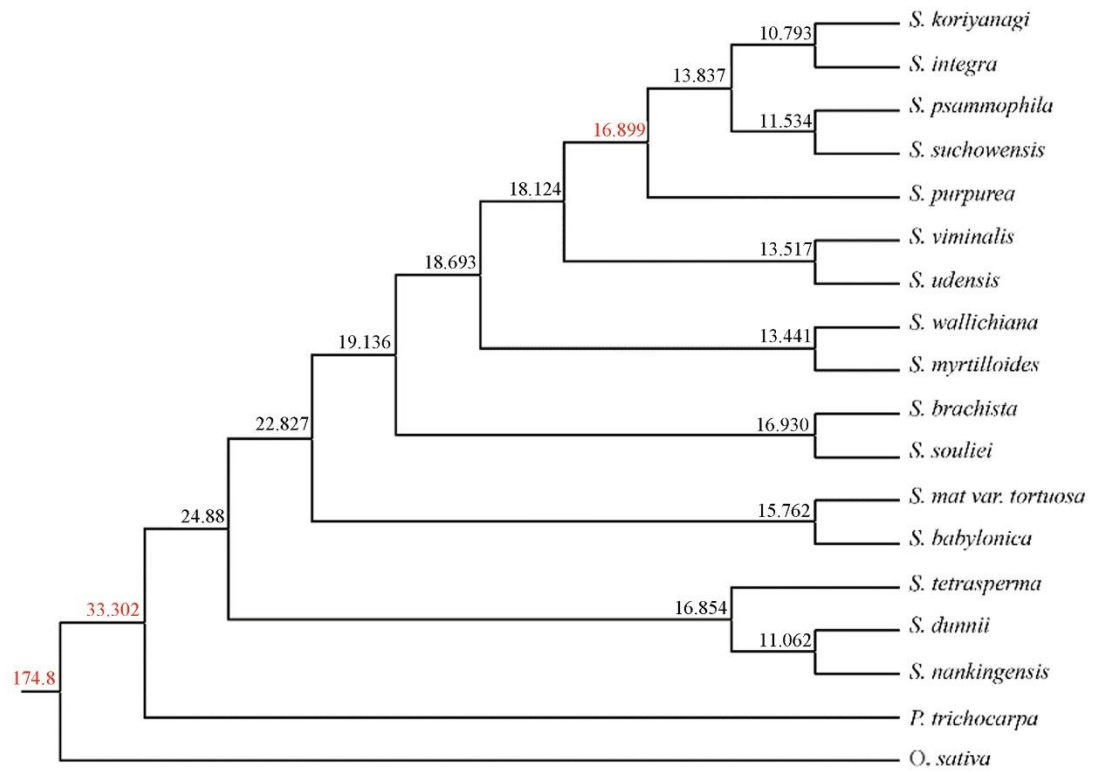


Figure S2: Phylogenetic tree with estimated divergence times (million years ago). Three node calibrations (red number) were defined by the TimeTree database (<http://www.timetree.org/>, accessed on 2 October 2022).

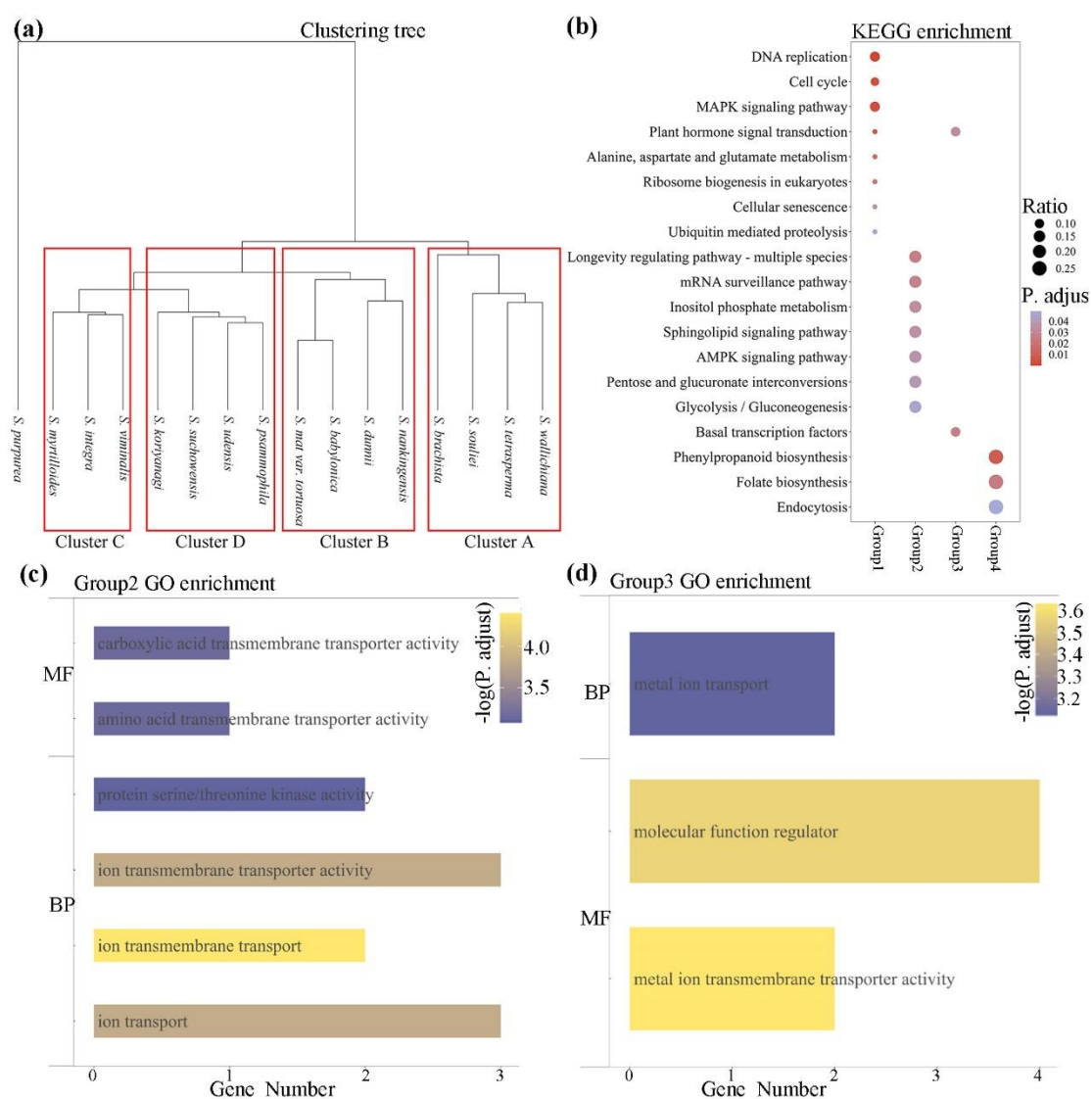


Figure S3: Clustering analysis of willow species. (a) Hierarchical clustering of 16 *Salix* species using 2966 high-variability gene families. (b) KEGG pathways significantly enriched in different groups of gene families. (c, d) GO terms significantly enriched in gene family group 2 (c) and group 3 (d).