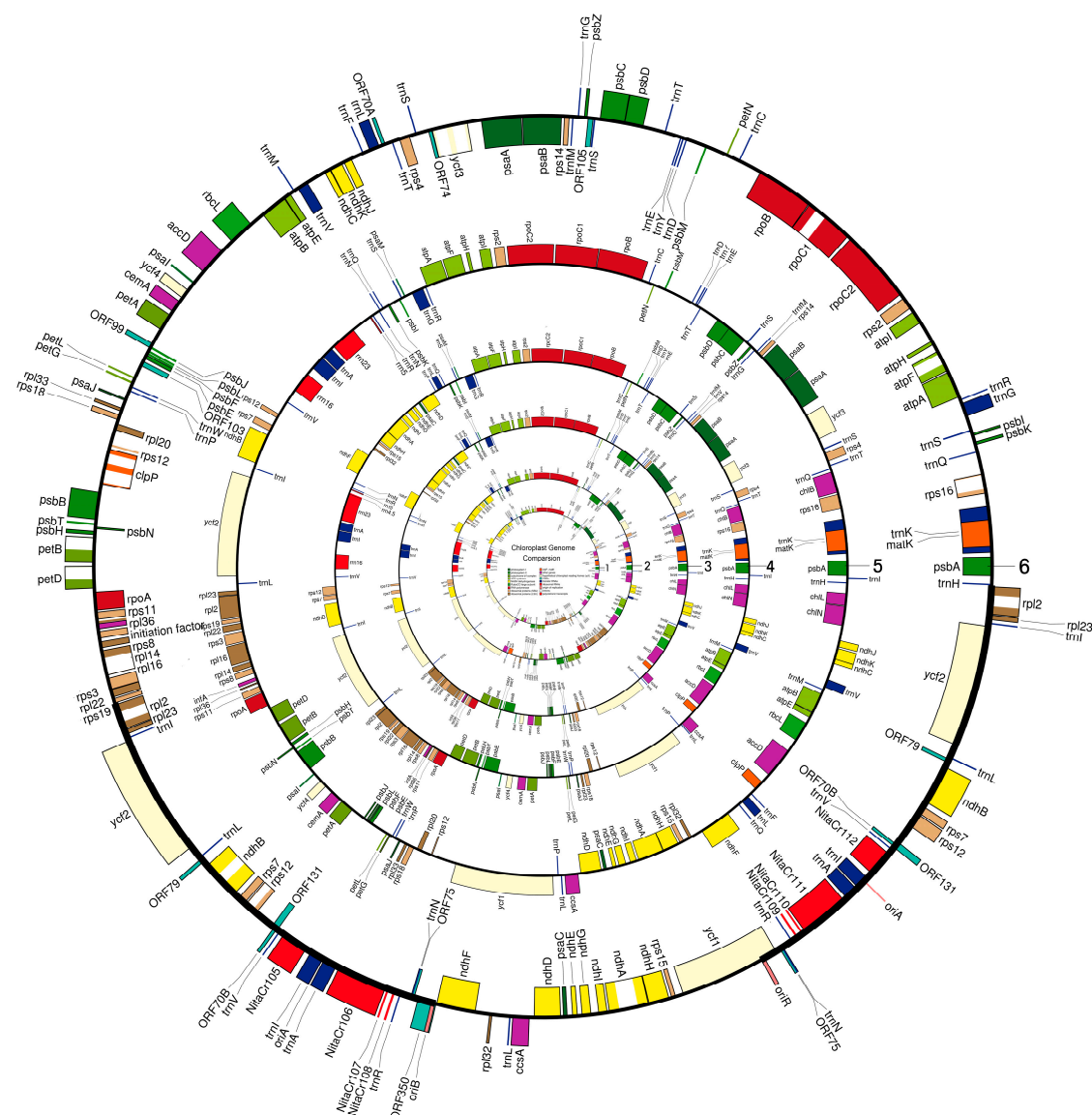
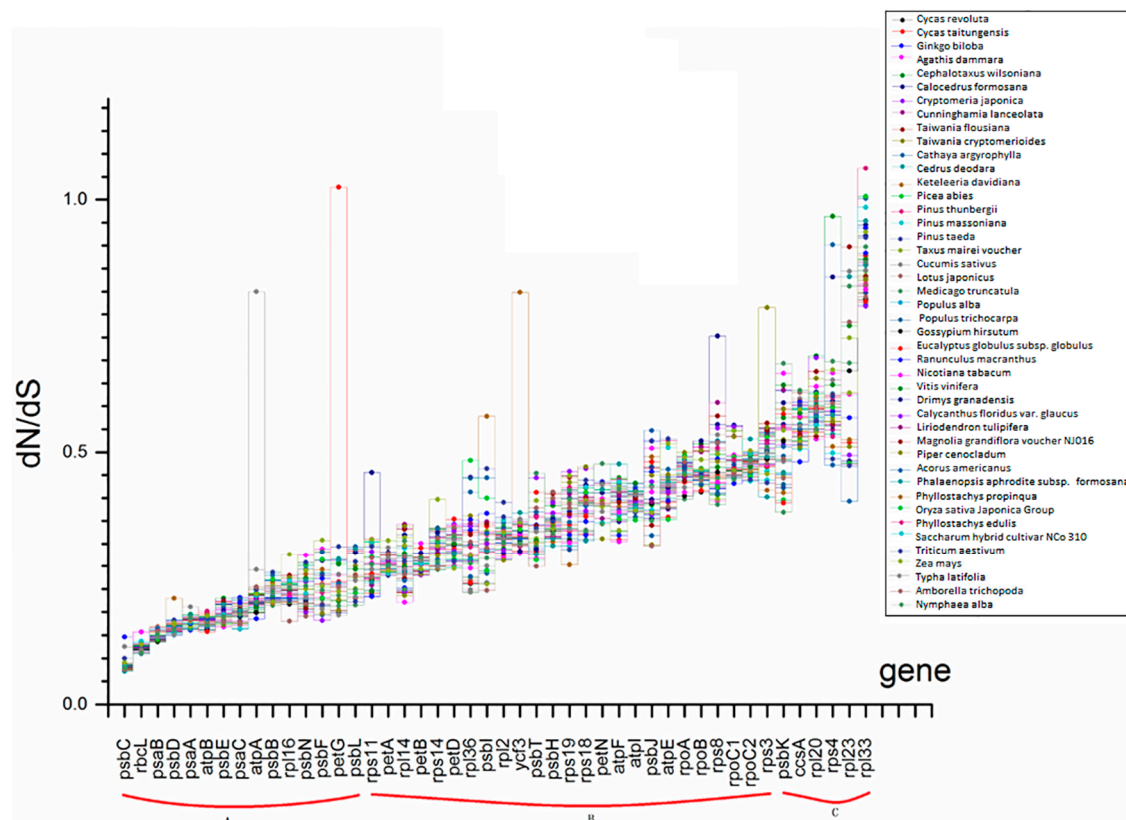


# Supplementary Materials: Comparative Analysis of the Chloroplast Genomic Information of *Cunninghamia lanceolata* (Lamb.) Hook with Sibling Species from the Genera *Cryptomeria* D. Don, *Taiwania* Hayata, and *Calocedrus* Kurz

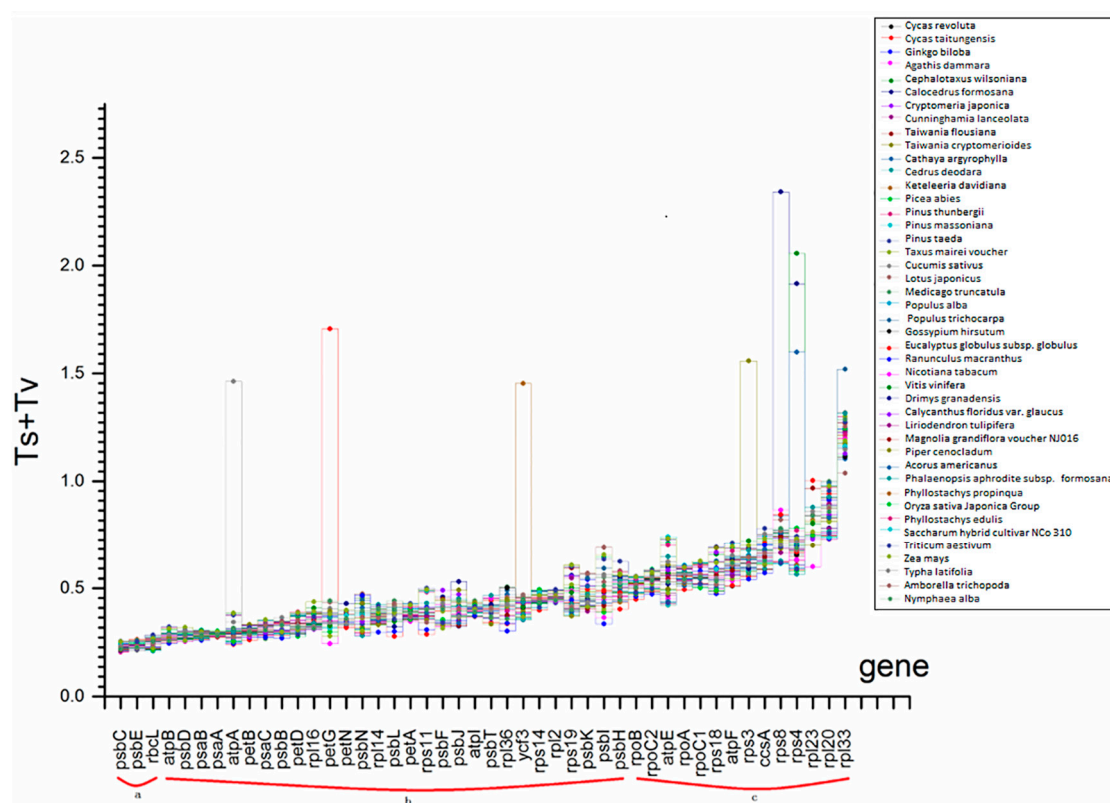
Weiwei Zheng, Jinhui Chen, Zhaodong Hao and Jisen Shi



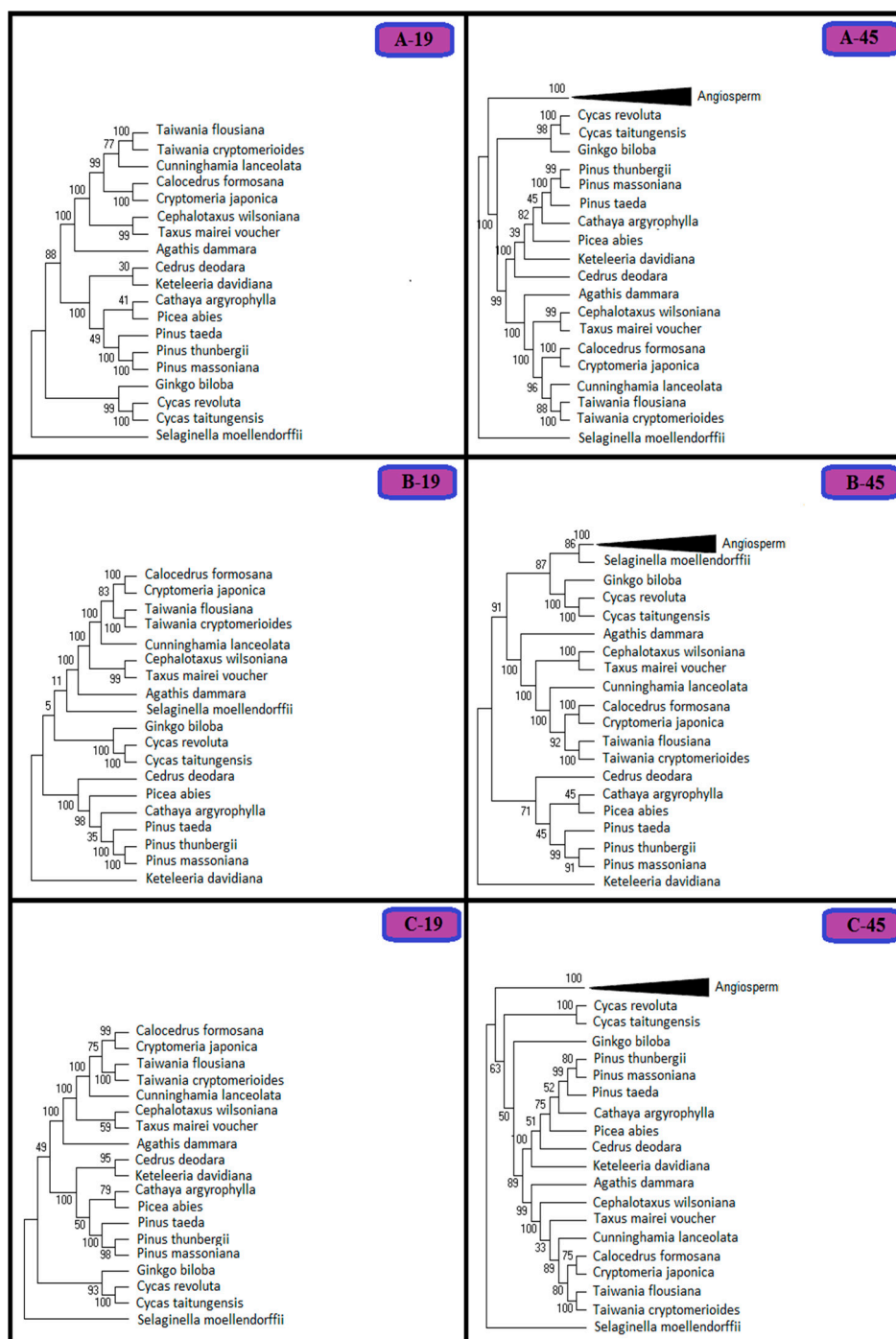
**Figure S1.** From Outer to inner circles correspond to the cp genome maps: 6-*Nicotiana tabacum*, 5-*Cunninghamia lanceolata*, 4-*Taiwania cryptomerioides*, 3-*Taiwania flousiana*, 2-*Calocedrus formosana* and 1-*Cryptomeria japonica*, respectively. Using the graphical annotation tool DOGMA [33].



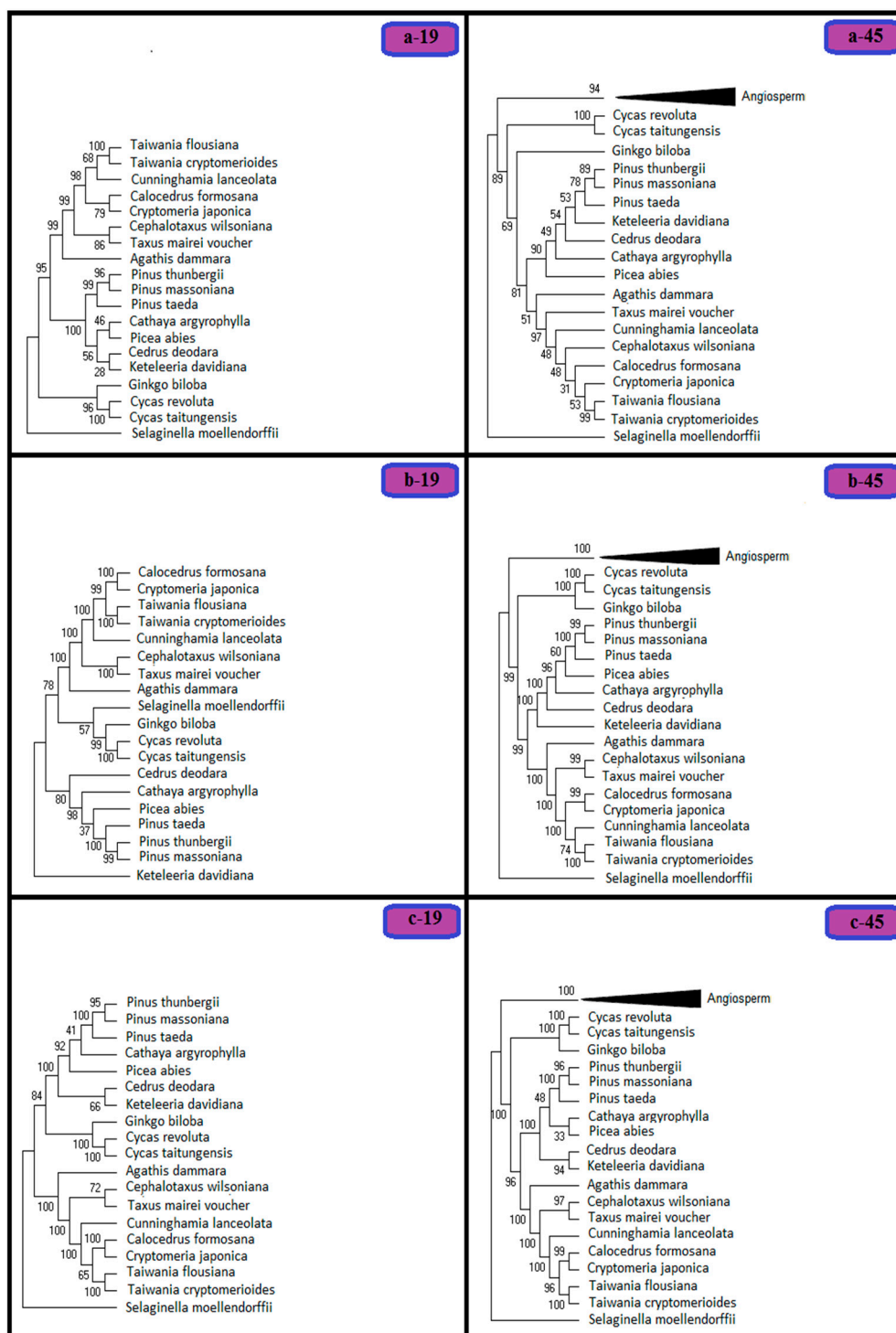
**Figure S2.** Comparison of the selection forces ( $dN/dS$ ) of the 46 common protein-coding genes in the 45-species matrix. The matrix consisted of all 45 species listed in Table 2. A, B and C represent different  $dN/dS$  ranges groups according to the description in Section 3.6.



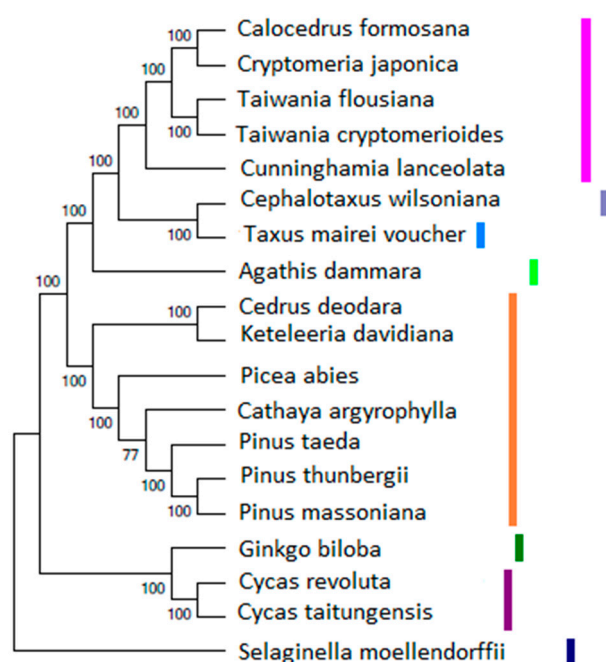
**Figure S3.** Comparison of the total nucleotide substitution rates (Ts + Tv) of the 46 common protein-coding genes in the 45-species matrix. The matrix consisted of all 45 species listed in Table 2. a, b and c represent Ts + Tv ranges groups according to the description in Section 3.6.



**Figure S4.** Phylogenetic trees based on the selection force groups in the 19-species matrix and the 45-species matrix respectively. The three selection force groups were defined as group A ( $dN/dS \leq 0.25$ ), group B ( $0.25 < dN/dS \leq 0.5$ ) and group C ( $0.5 < dN/dS$ ).

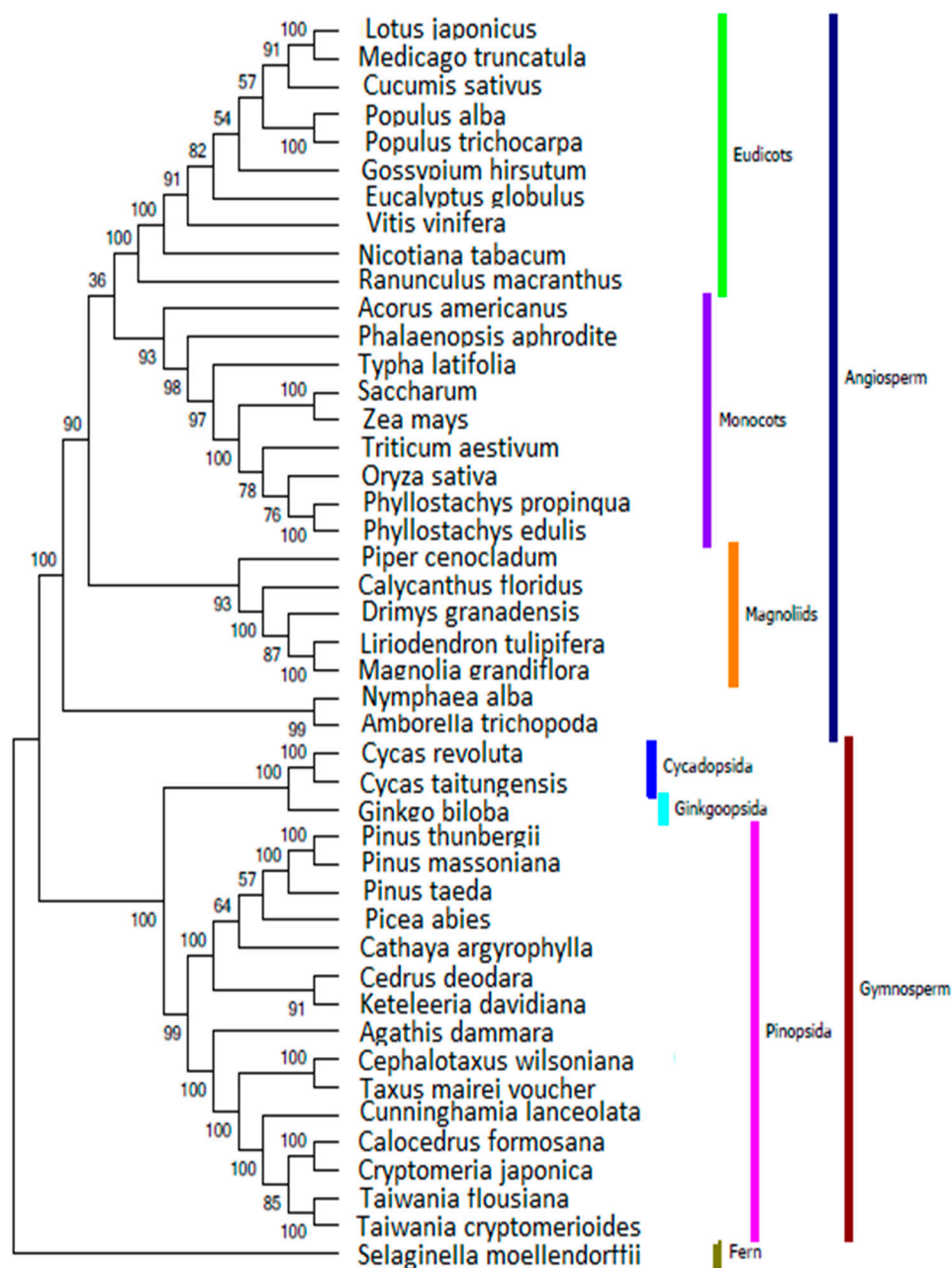


**Figure S5.** Phylogenetic trees based on the total nucleotide substitution rates in the 19-species matrix and the 45-species matrix respectively. The three nucleotide substitution groups were defined as group a ( $Ts + Tv \leq 0.25$ ), group b ( $0.25 < Ts + Tv \leq 0.5$ ) and group c ( $0.5 < Ts + Tv$ ).



**Figure S6.** Phylogenetic analyses were performed based on the 46 common protein-coding sequences in the 19-species matrix using the maximum likelihood (ML) methods implemented in MEGA5 [46] with the best models [47] calculated using the MEGA5 [46] embedded software “Find DNA/Protein Models” and rapid bootstrapping of 1000 replicates.





**Figure S7.** Phylogenetic analyses were performed based on the 46 common protein-coding sequences in the 45-species matrix using the maximum likelihood (ML) methods implemented in MEGA5 [46] with the best models [47] calculated using the MEGA5 [46] embedded software “Find DNA/Protein Models” and rapid bootstrapping of 1000 replicates.