

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.

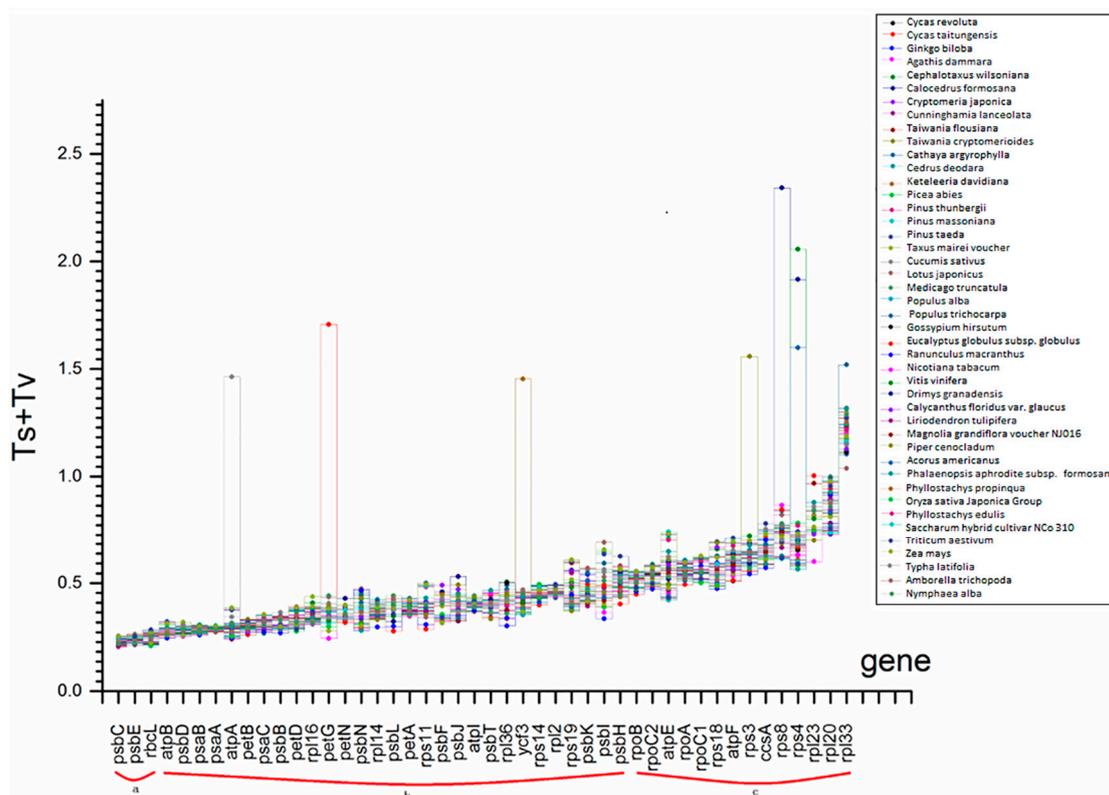


Figure S3. Comparison of the total nucleotide substitution rates (Ts + Tv) of the 46 common protein-coding genes in the 45-species matrix. The matrix consisted of all 45 species listed in Table 2. a, b and c represent Ts + Tv ranges groups according to the description in Section 3.6.

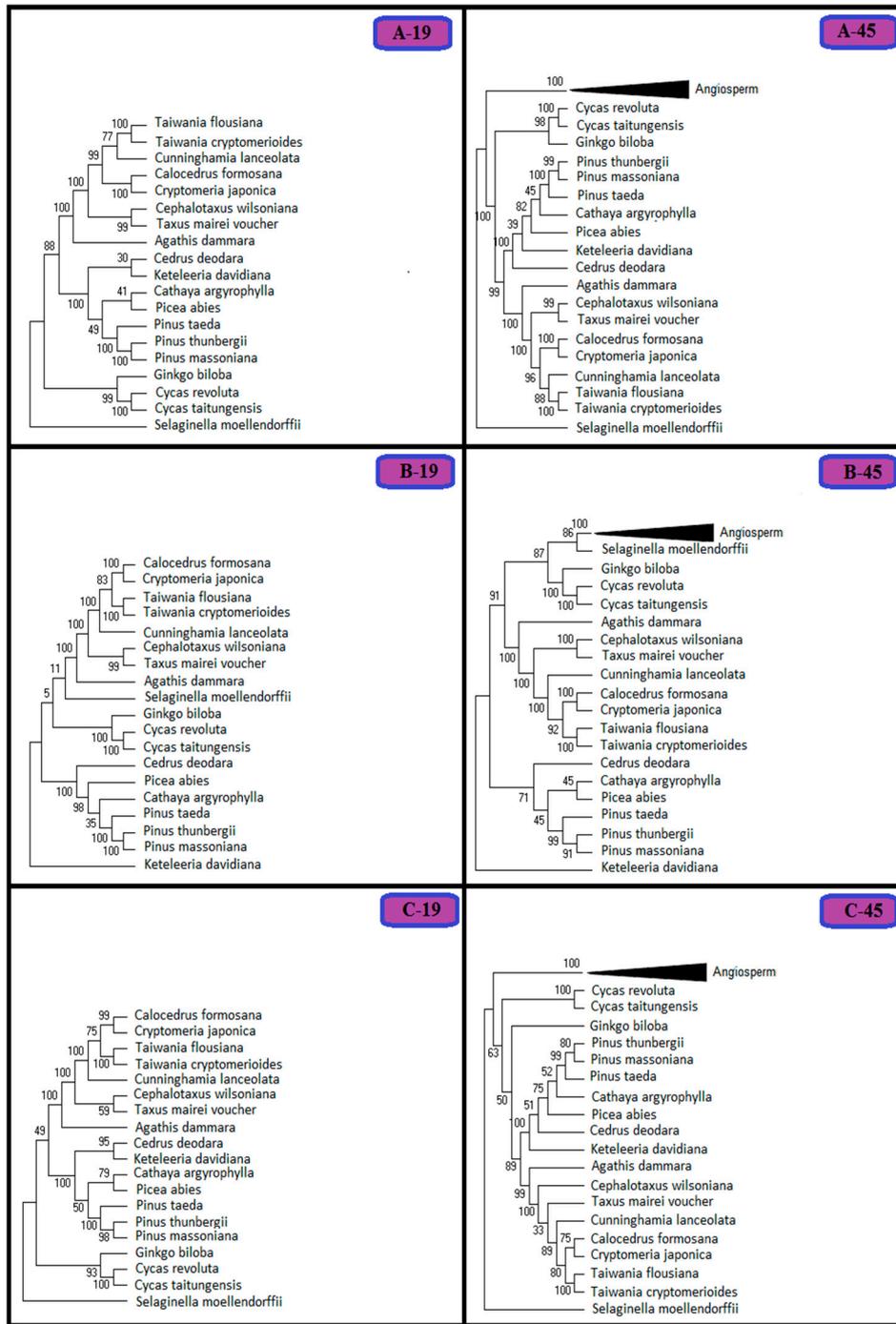


Figure S4. Phylogenetic trees based on the selection force groups in the 19-species matrix and the 45-species matrix respectively. The three selection force groups were defined as group A ($dN/dS \leq 0.25$), group B ($0.25 < dN/dS \leq 0.5$) and group C ($0.5 < dN/dS$).

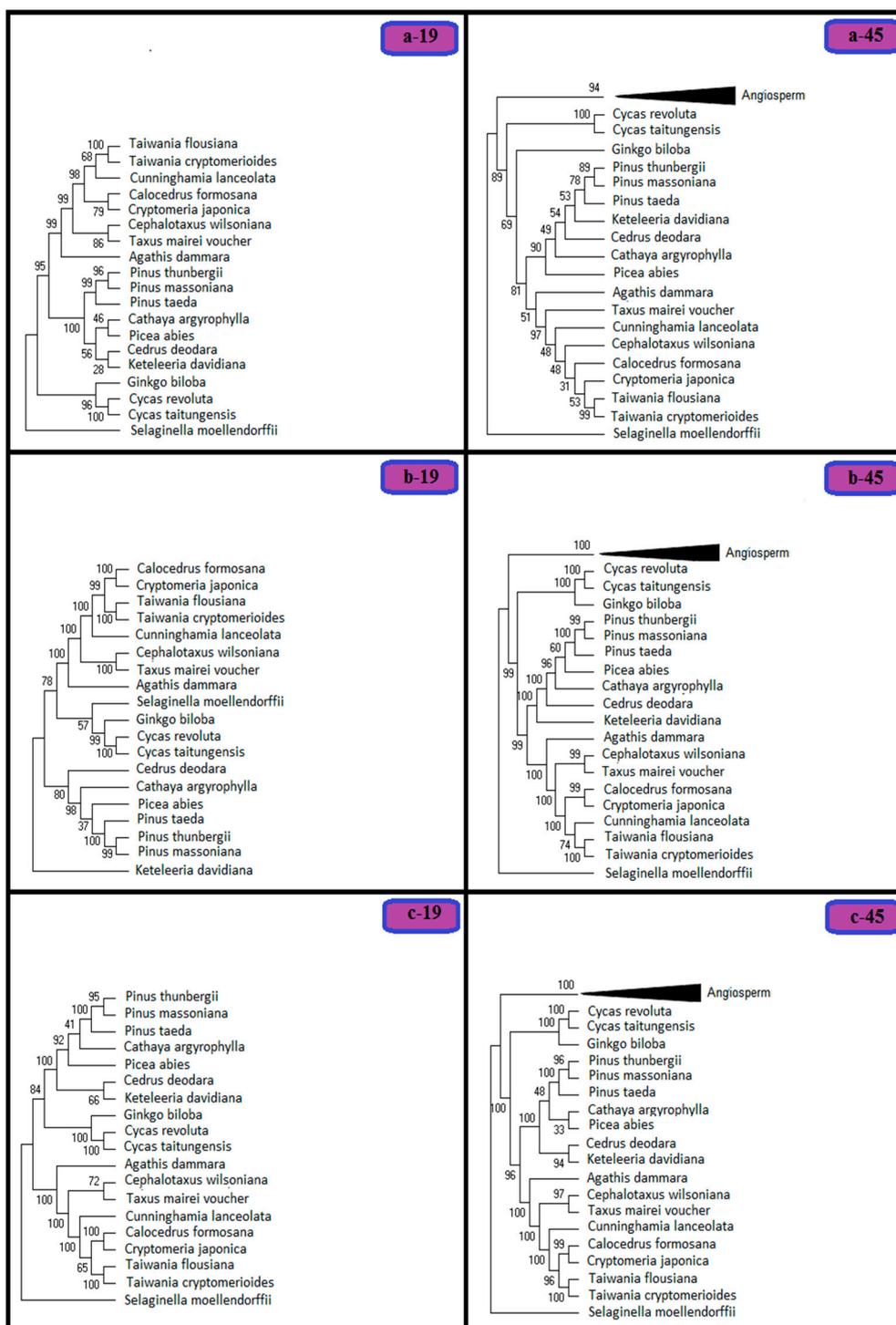


Figure S5. Phylogenetic trees based on the total nucleotide substitution rates in the 19-species matrix and the 45-species matrix respectively. The three nucleotide substitution groups were defined as group a ($T_s + T_v \leq 0.25$), group b ($0.25 < T_s + T_v \leq 0.5$) and group c ($0.5 < T_s + T_v$).

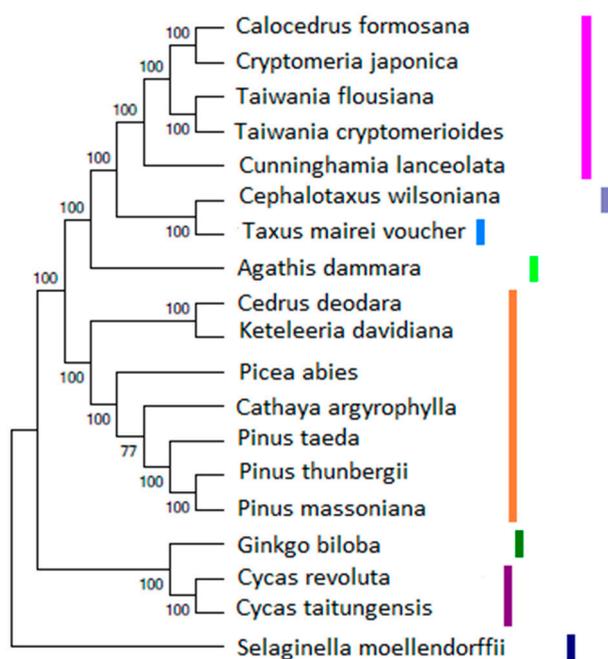


Figure S6. Phylogenetic analyses were performed based on the 46 common protein-coding sequences in the 19-species matrix using the maximum likelihood (ML) methods implemented in MEGA5 [46] with the best models [47] calculated using the MEGA5 [46] embedded software “Find DNA/Protein Models” and rapid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

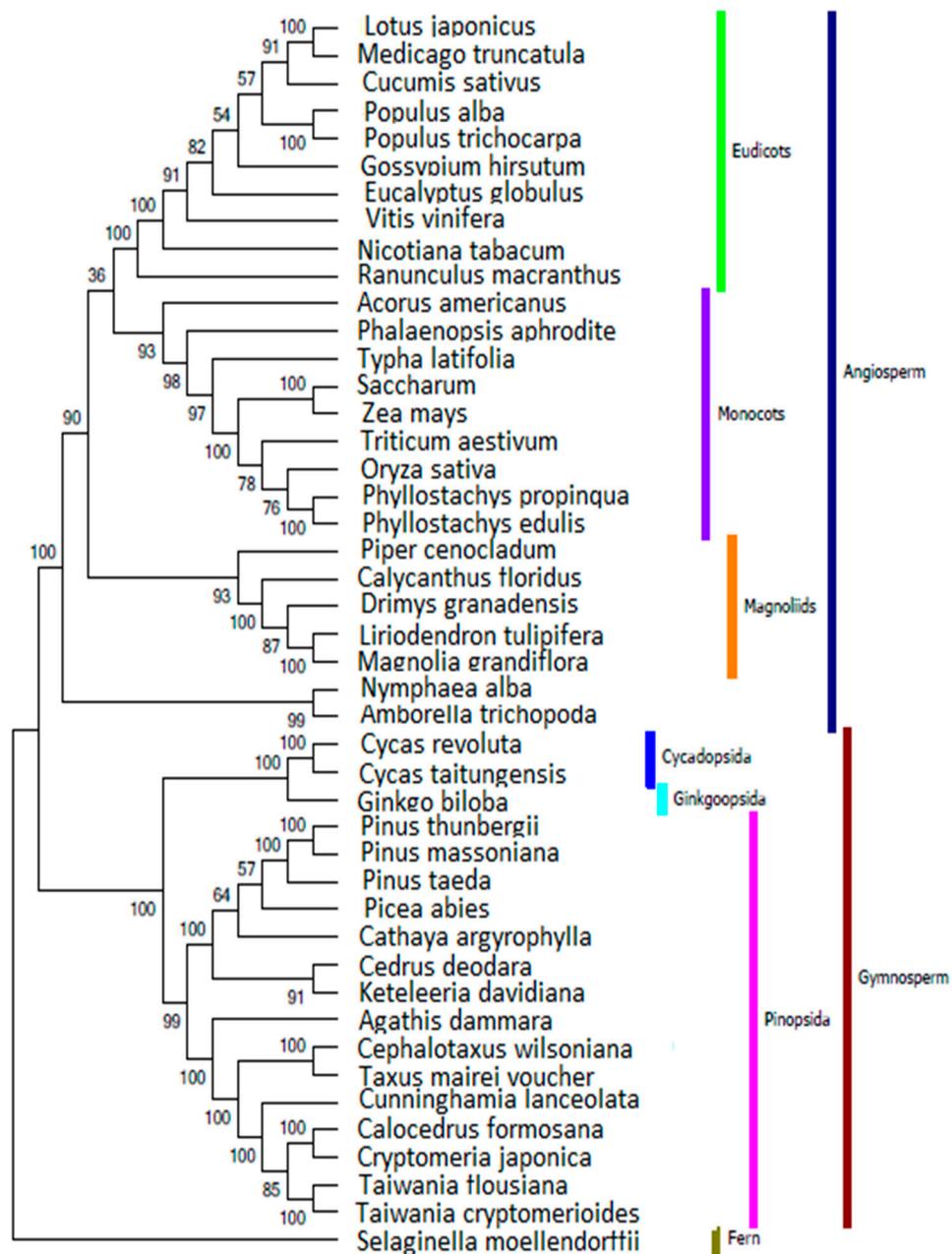


Figure S7. Phylogenetic analyses were performed based on the 46 common protein-coding sequences in the 45-species matrix using the maximum likelihood (ML) methods implemented in MEGA5 [46] with the best models [47] calculated using the MEGA5 [46] embedded software “Find DNA/Protein Models” and rapid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