

Supplementary Figures

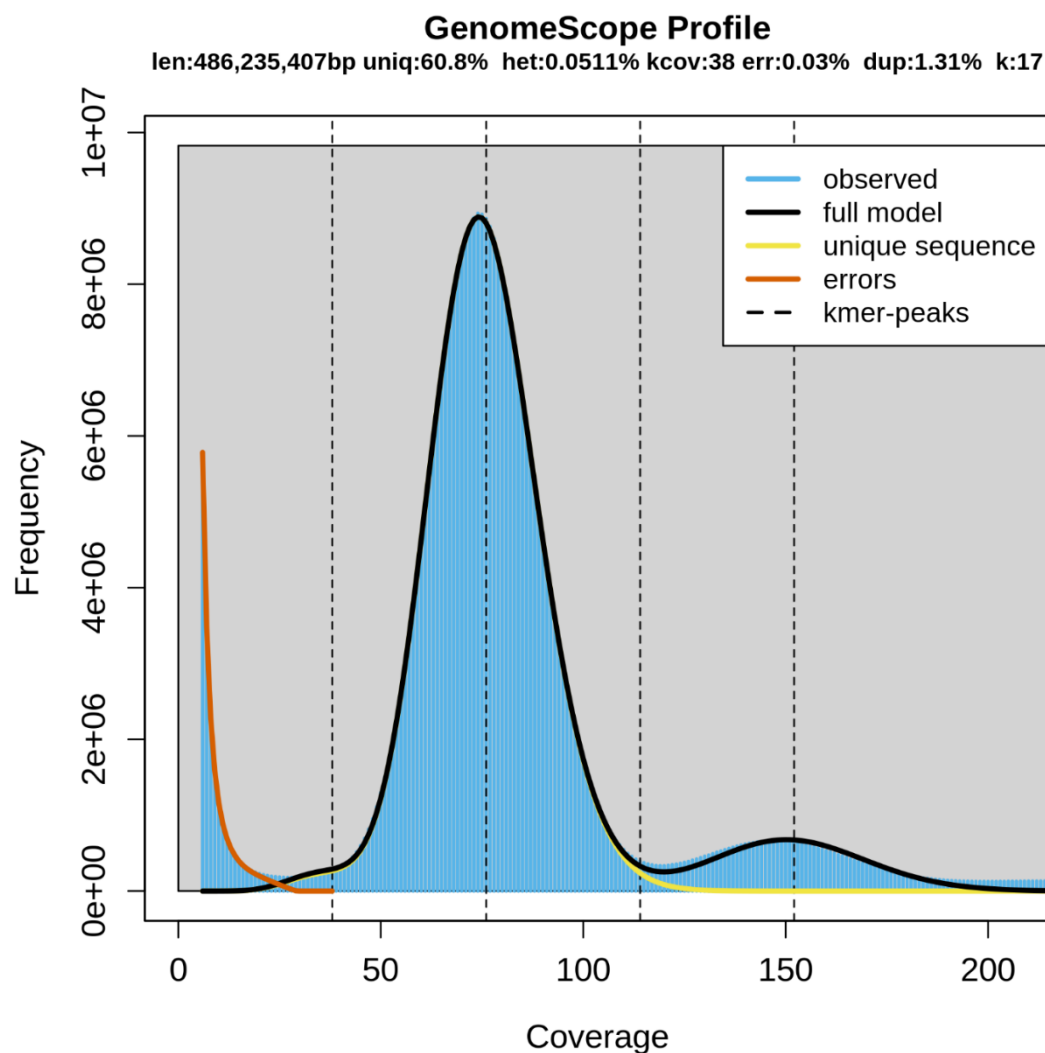


Figure S1. Genome size estimation of *Nypa fruticans* based on *k*-mer distribution analysis. The above *k*-mer plot shows the distribution of the *k*-mer copy number (KCN) at 17-mer for the *N. fruticans* genome. The results show that the heterozygosity of the *N. fruticans* genome is nearly 0.0511%, and the haploid genome size is approximately 486.24 Mb.

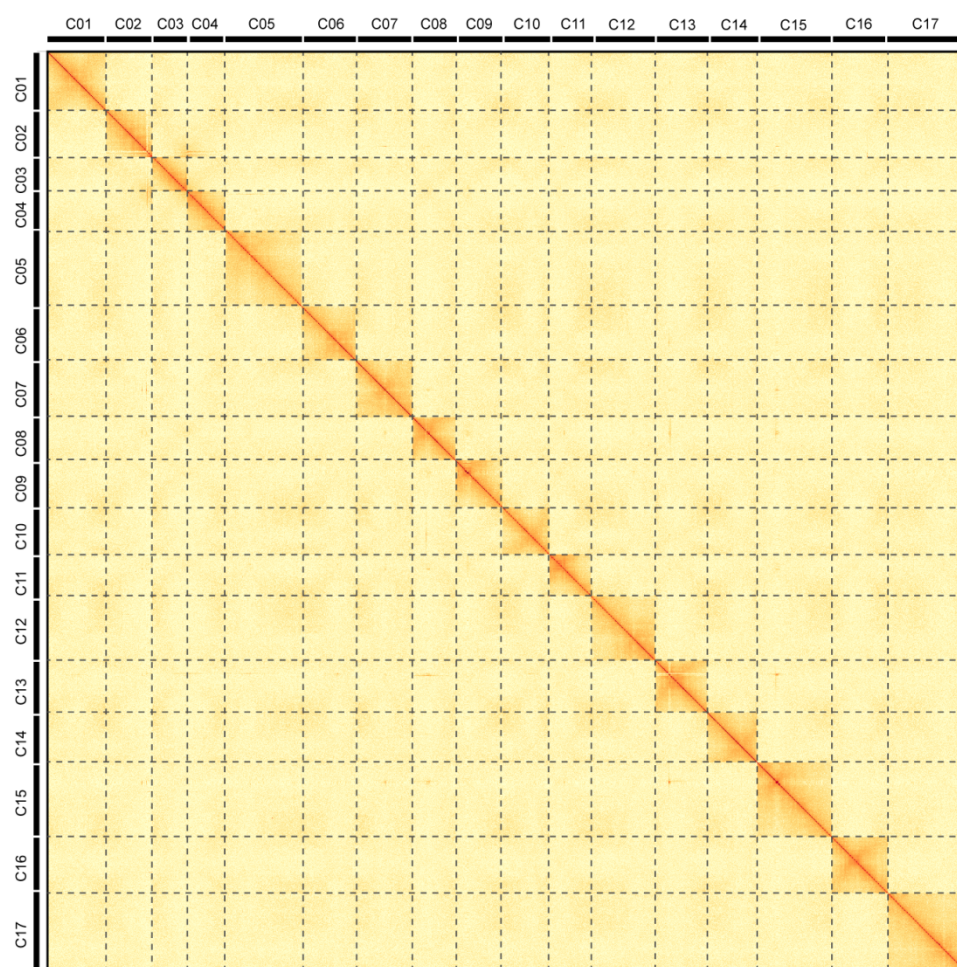


Figure S2. Hi-C contact map of the *N. fruticans* genome assembly.

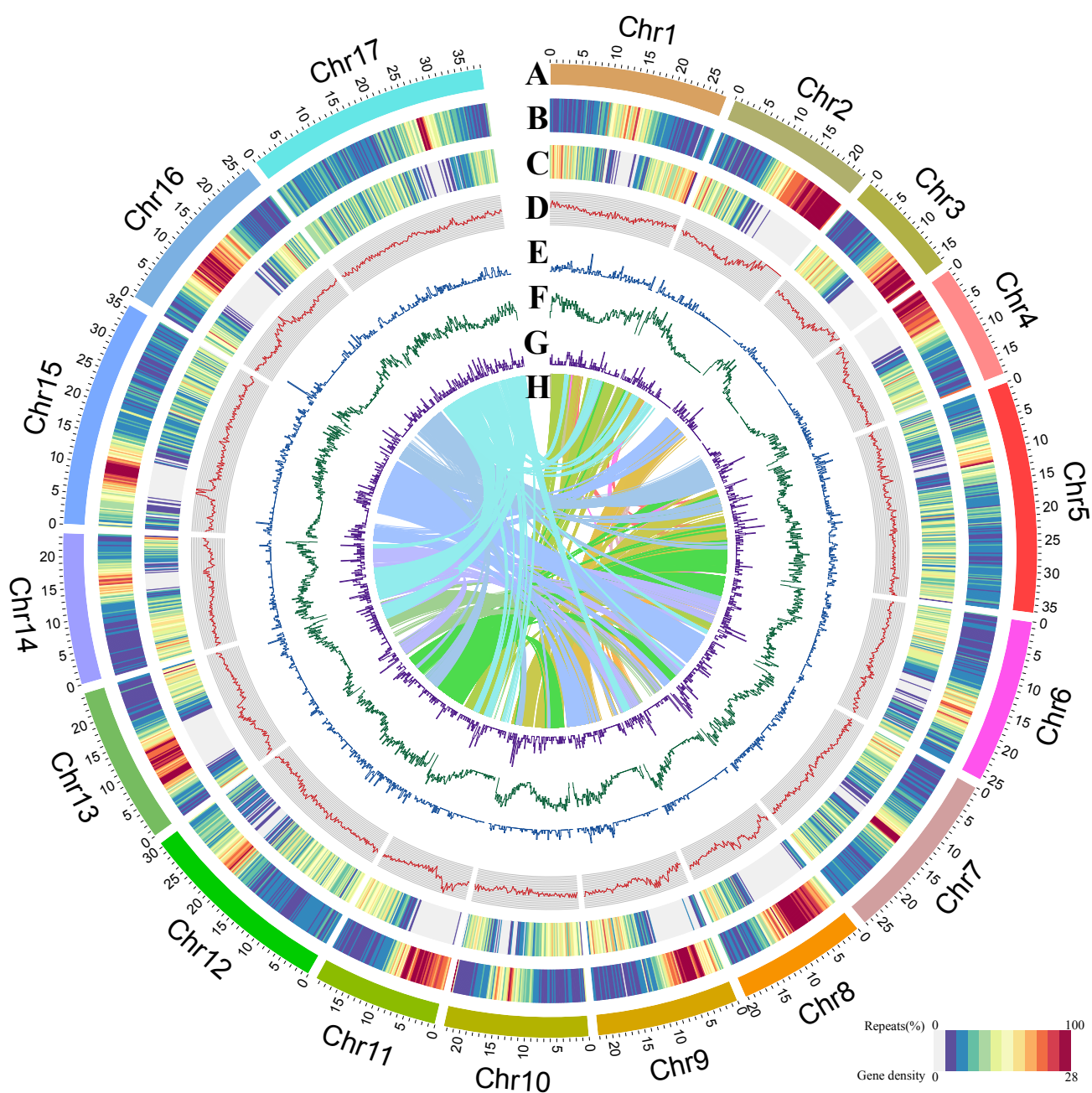


Figure S3. Features of the *N. fruticans* genome. (A) Seventeen *N. fruticans* chromosomes covering 89.92% of the genome assembly, (B) Percentage of repeats (0%-100% per 200 Kb), (C) Gene density (0-28 per 200 Kb), (D) GC content (0.30%-0.45% per 200 Kb), (E) The density of duplicates from tandem duplication (0-21 per 200 Kb), (F) The density of duplicates from segment duplication (0-20 per 200 Kb), (G) The density of duplicates from *N. fruticans*-specific retain after WGD (0-15 per 200 Kb), (H) A cluster of lines indicates collinear regions across the chromosomes.

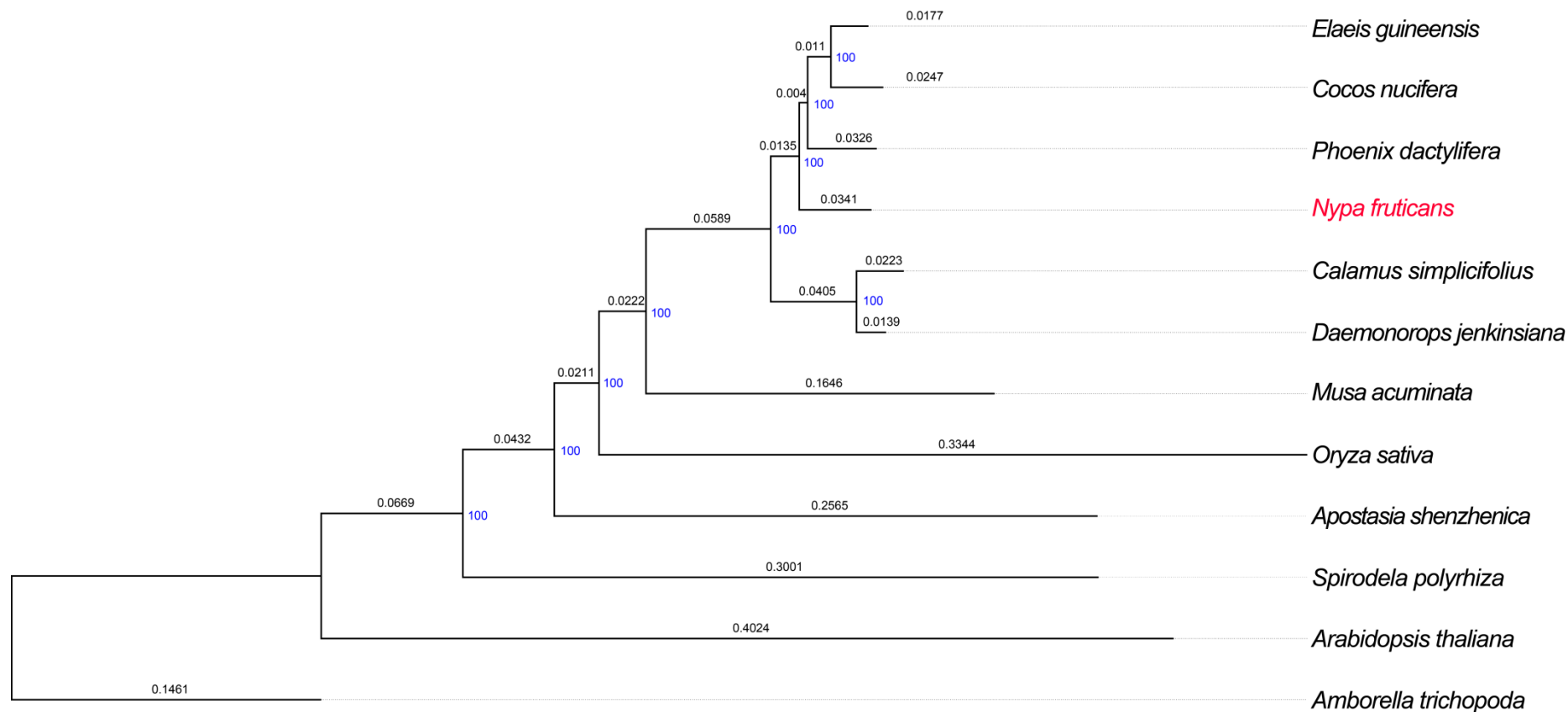
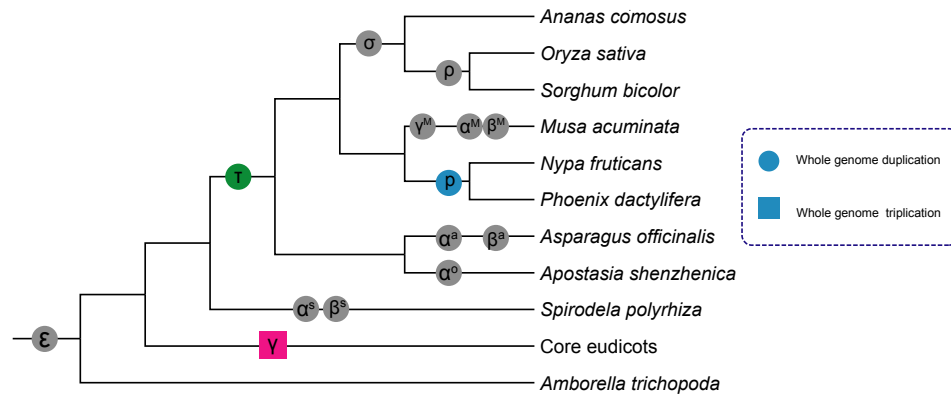


Figure S4. Maximum likelihood tree of 12 angiosperm species. The 545 single-copy orthologous genes were concatenated and used for inferring an ML phylogenetic tree by RAxML-NG. Black numbers at the branches and blue numbers at the nodes indicate values of branch length and bootstrap support, respectively.

A



B

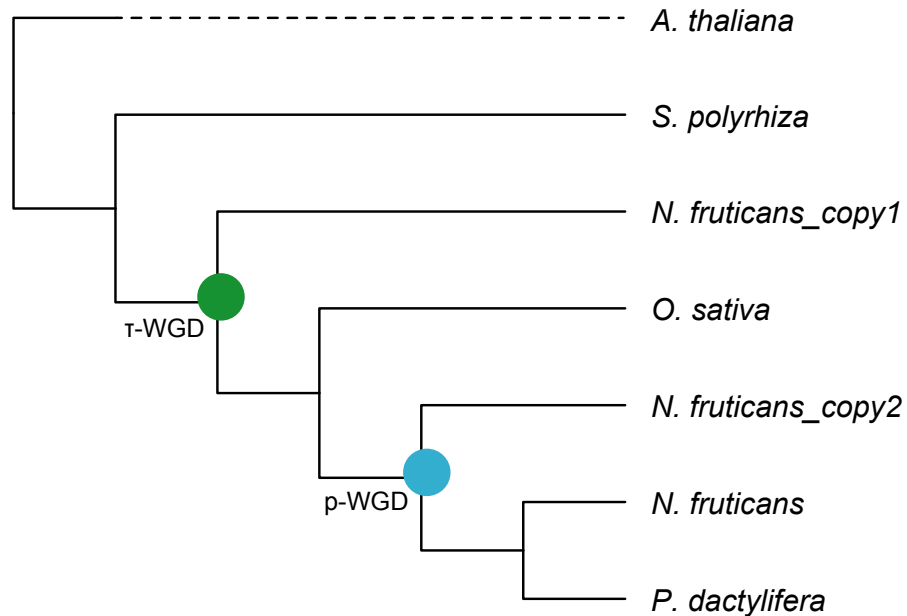


Figure S5. The positions of two WGDs (τ -WGD and p-WGD). (A) Summary of polyploid events among monocot species since monocot-eudicot divergence. (B) The pattern of the two WGD events is reflected in the gene trees. The first event is the τ -WGD shared by most monocots excluding Alismatales and the second event is the p-WGD shared by all palms.

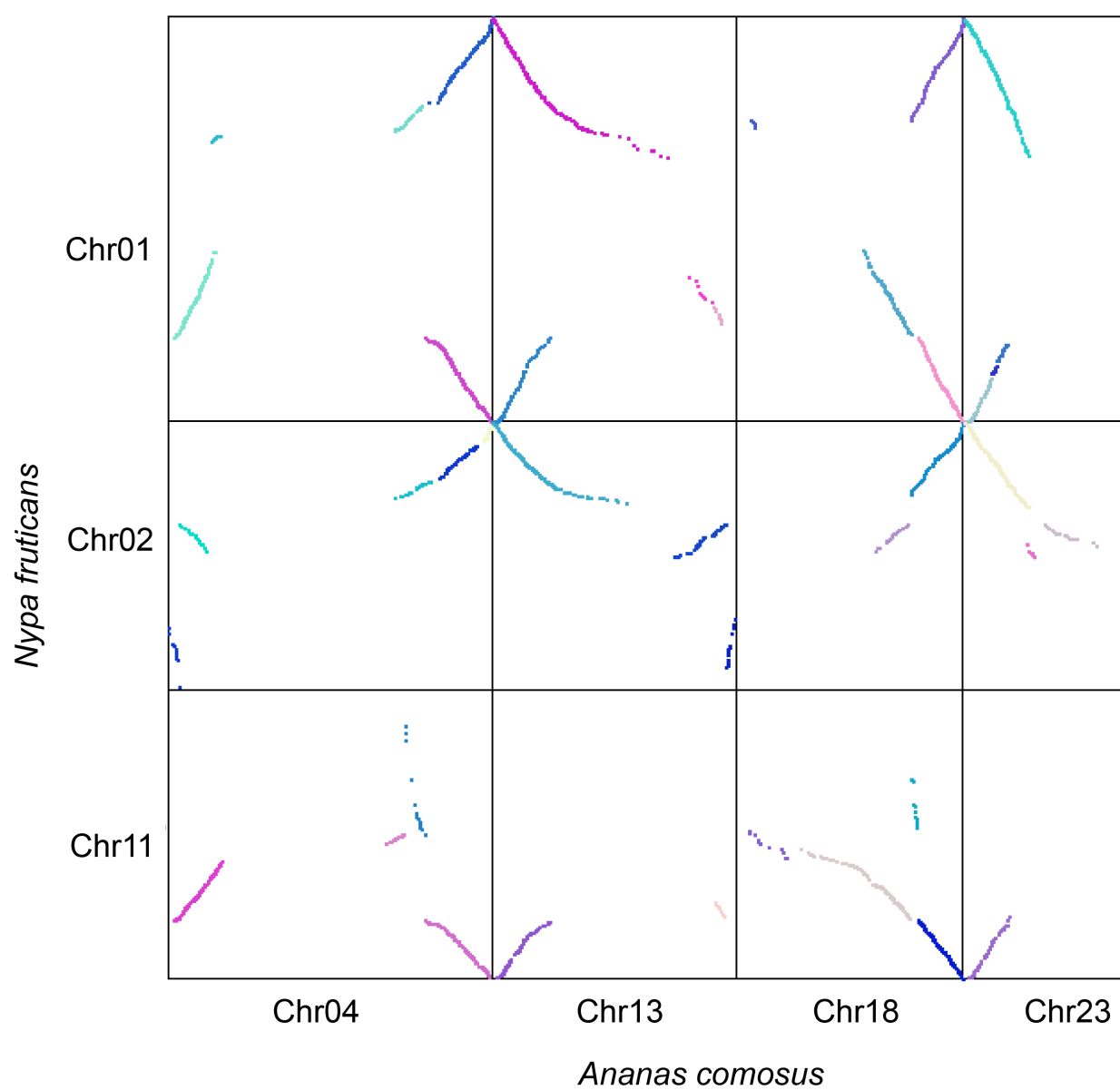


Figure S6. Syntenic blocks between genomic regions in *Nypa fruticans* and *Ananas comosus*.

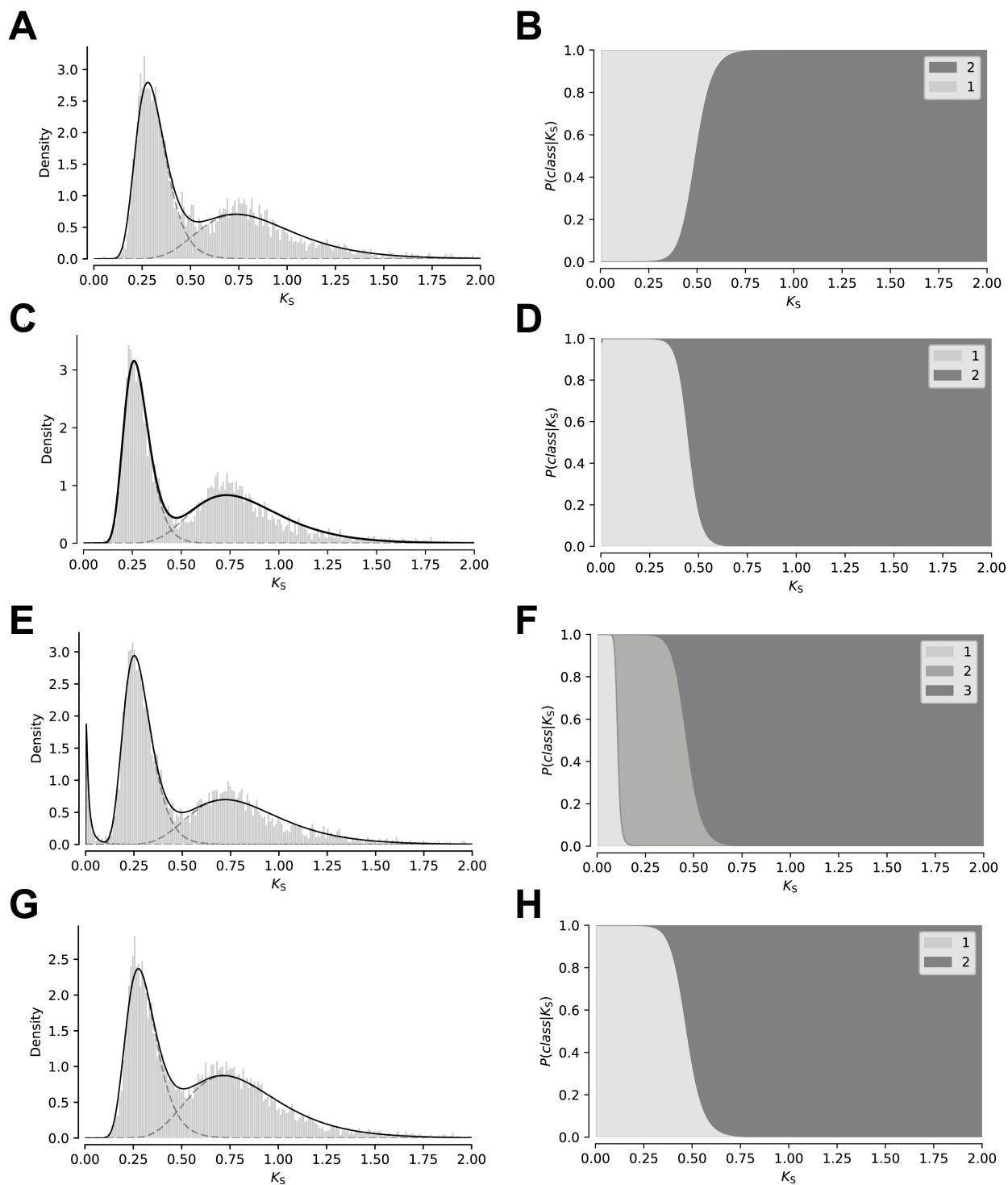


Figure S7. The K_S distributions for paralogs in four palm species, including *C. nucifera* (A), *E. guineensis* (C), *P. dactylifera* (E), and *N. fruticans* (G). Each distribution was split into two peaks by a fitted mixture model (GMM). Figures B, D, F, and H indicate the proportion of paralogous pairs from hypothesized WGDs at different K_S values.

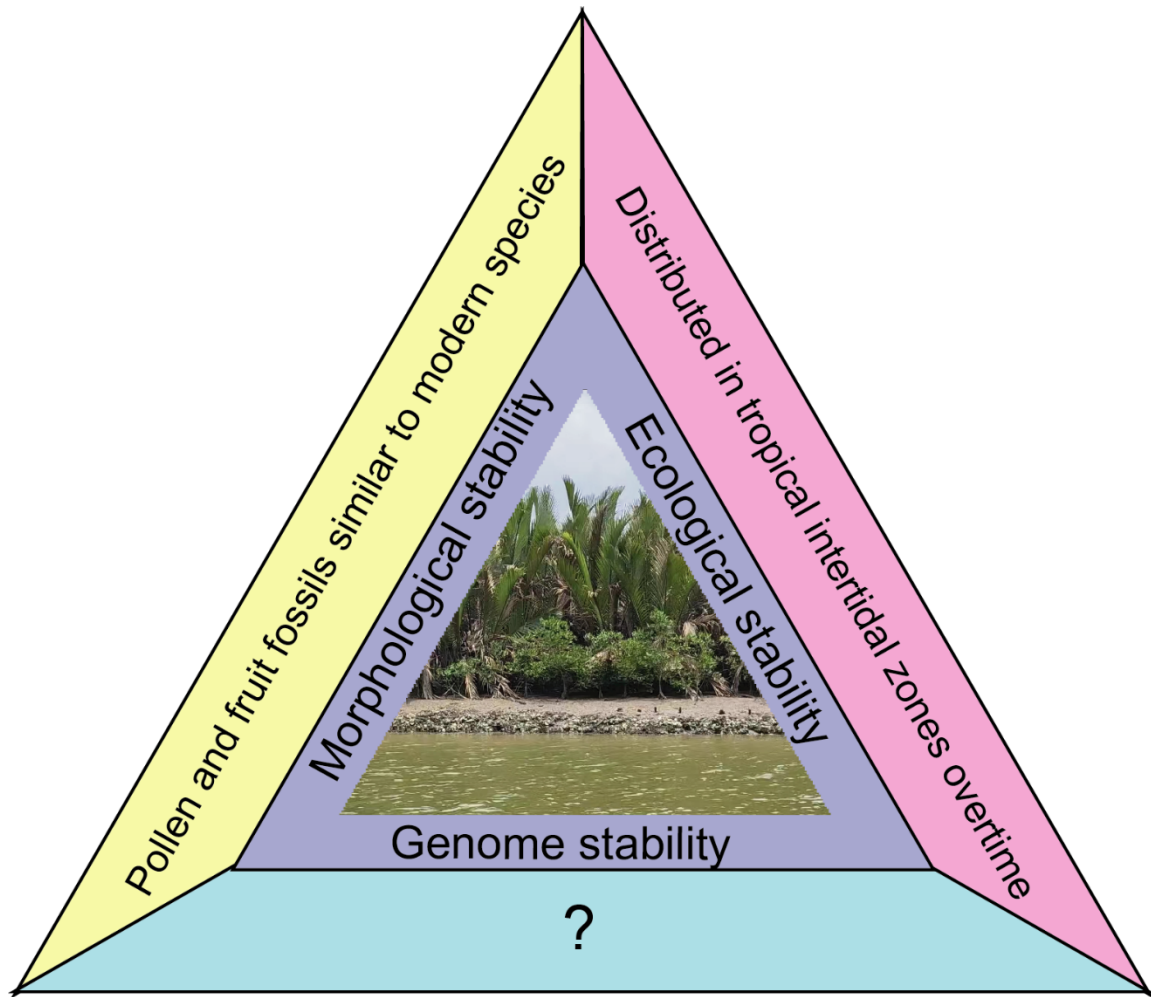


Figure S8. The stability of *N. fruticans* over long-term evolution. The morphological structure and ecological preferences of *N. fruticans* have remained largely unchanged. Therefore, we wondered whether the genome of *N. fruticans* reflects its slow evolution.

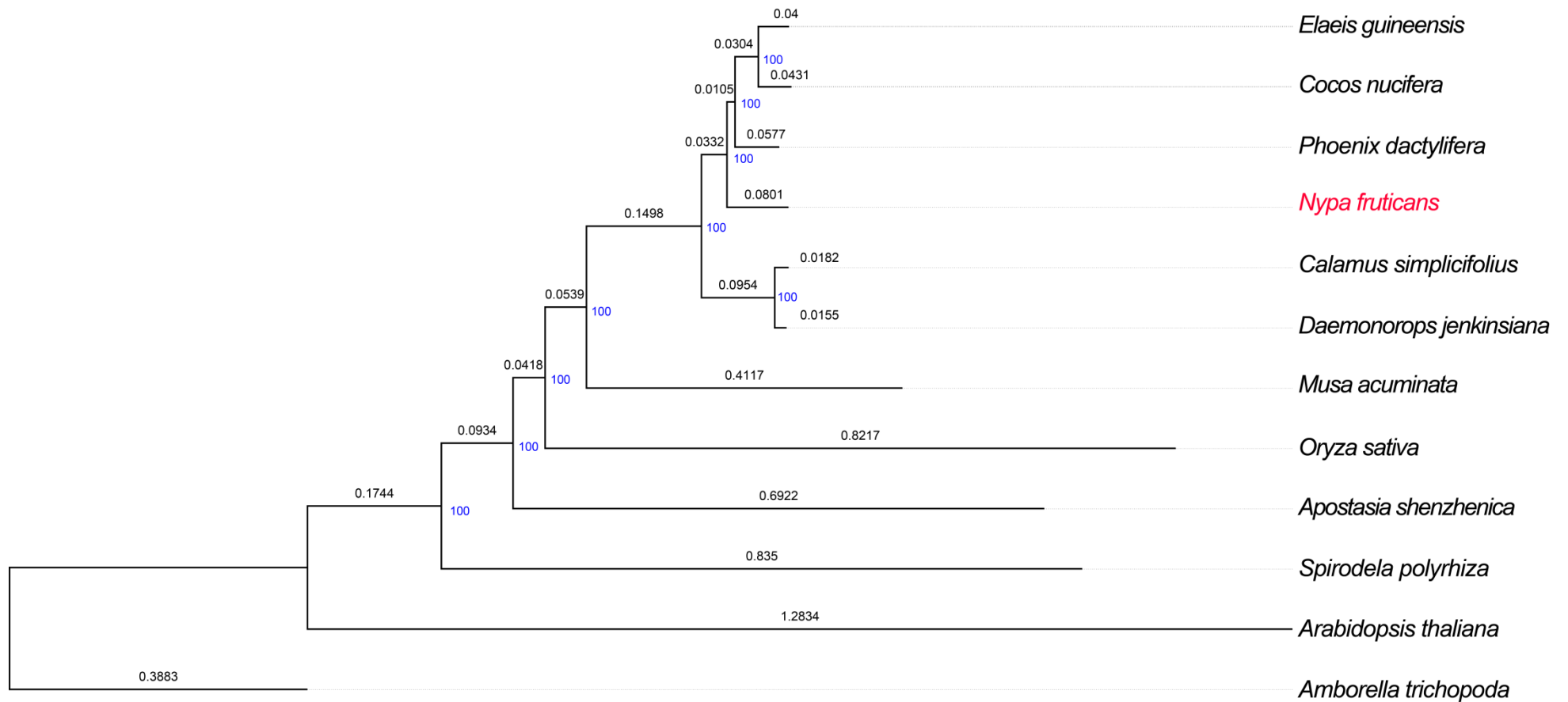


Figure S9. ML phylogenetic tree inferred using four-fold degenerate (4d) sites. The 4d sites of 545 single-copy orthologous genes were extracted and used for inferring an ML phylogenetic tree by RAXML-NG. Black numbers at the branches and blue numbers at the nodes indicate values of branch length and bootstrap support, respectively.

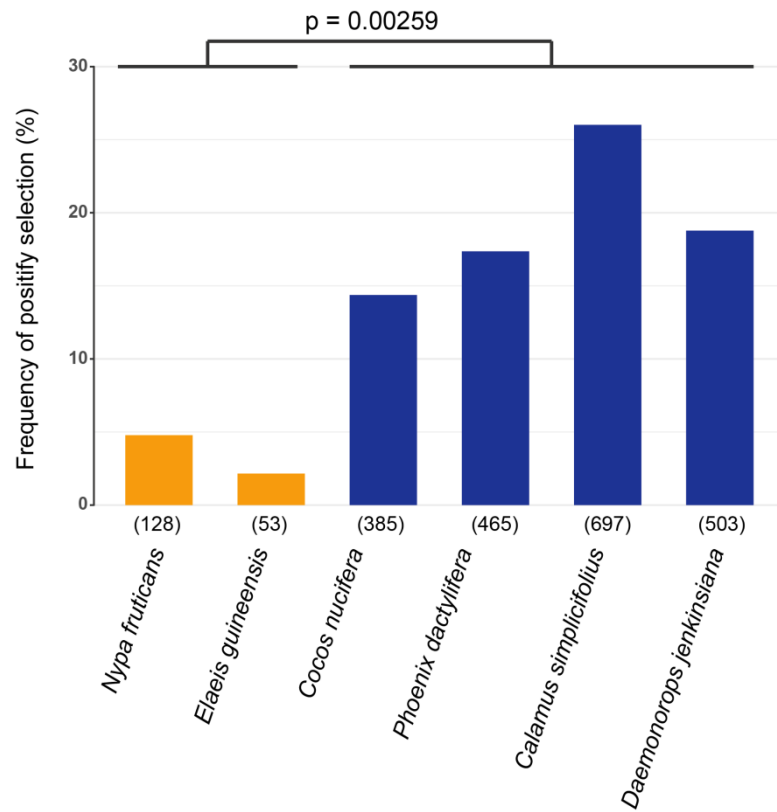


Figure S10. The bar plot shows the frequency of genes evolved under positive selection. Poor species diversity palms lineages vs. other palms lineages, Welch's two-sample t-test, P -value = 0.00259.

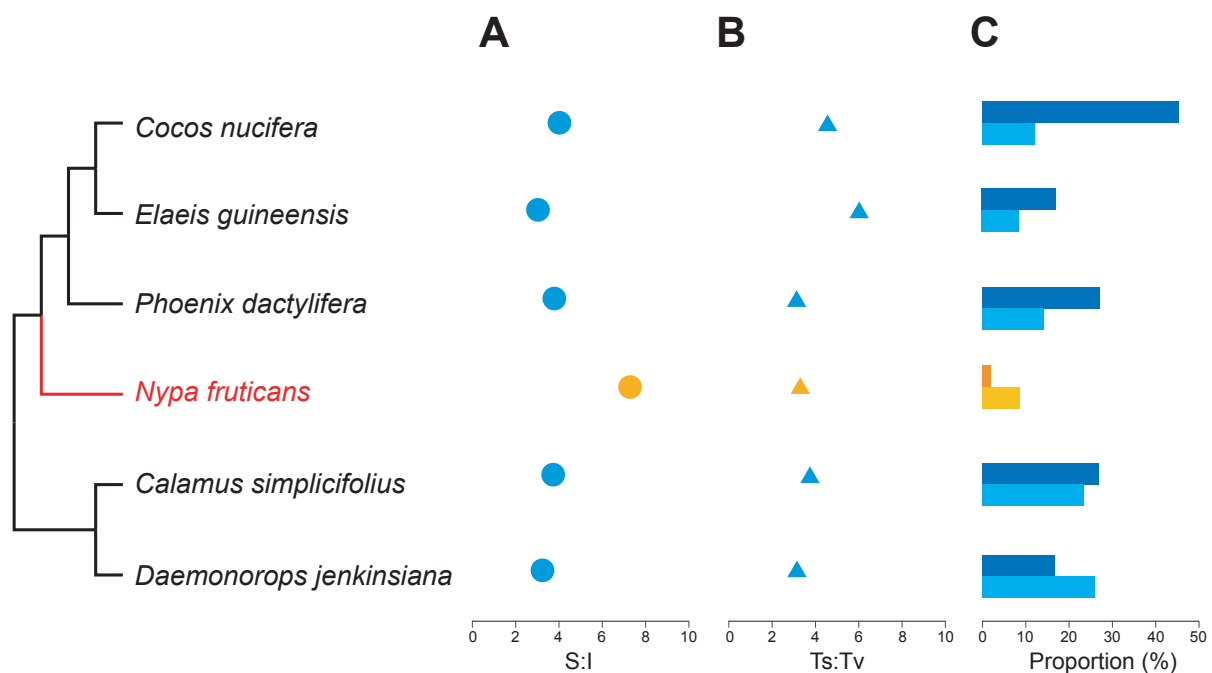


Figure S11. The statistical information of LTR-RTs. (A) The scatter plot represents the relative abundances of solo and intact LTRs (S:I). (B) The scatter plot for the ratio of transition: transversion (Ts:Tv). (C) The bar plot represents the percentage of *Copia* (upward side and dark color) and *Gypsy* (downward side and light color).

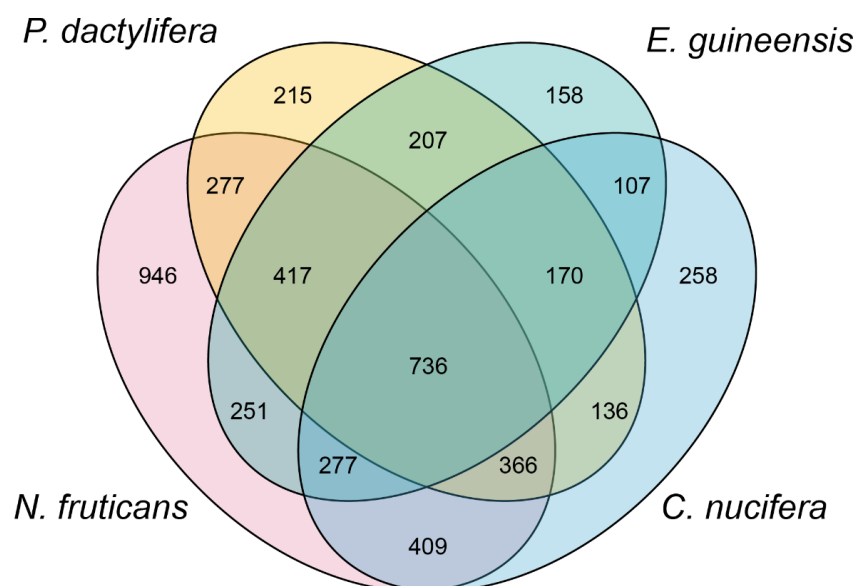


Figure S12. A Venn diagram of the shared and unique gene families among the p-WGD retained genes in four palm species.

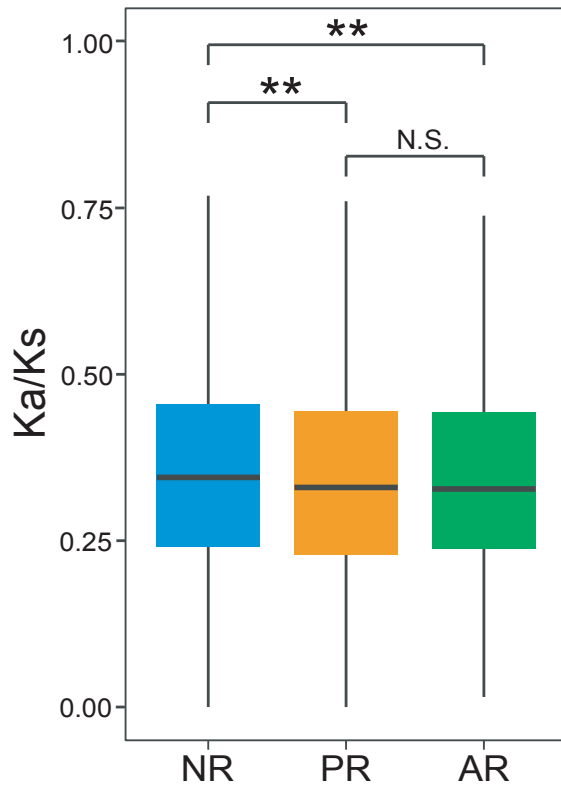
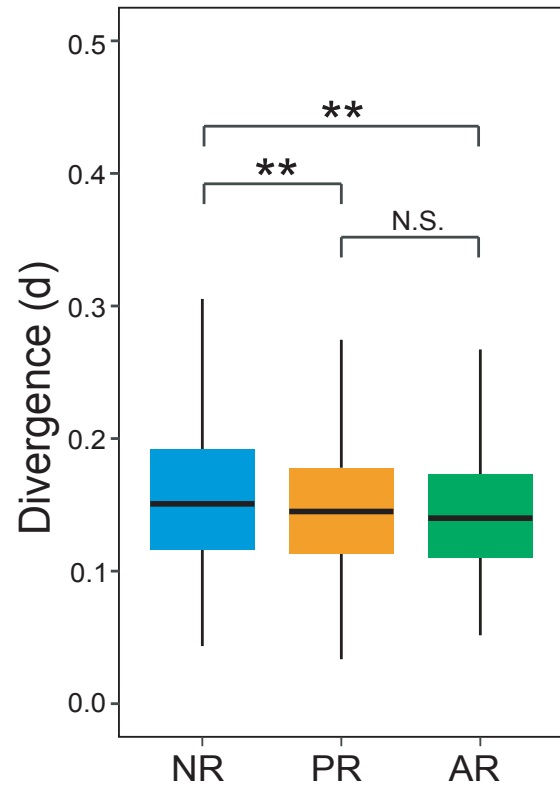
A**B**

Figure S13. The selective pressure (Ka/Ks) and the sequence divergence (d) between the pairs of p-WGD-derived duplicates. (A) The whisker plot shows the selective pressure on the pairs of p-WGD duplicates from *N. fruticans* into three clusters: NR (*N. fruticans* specific gene retentions, representing only *N. fruticans* retained their p-WGD-derived duplicates in these gene families), PR (at least one of the other palm species but not all palm species retained their p-WGD-derived duplicates in these gene families), and AR (all palm species retained their p-WGD-derived duplicates in these gene families). The Ka/Ks values of retained gene pairs were compared to other groups using Wilcoxon's rank sum test. The double asterisks mean P -value < 0.001 , while N.S. means non-significant. (B) The whisker plot shows the sequence divergence between the pairs of p-WGD duplicates from *N. fruticans* into three clusters.

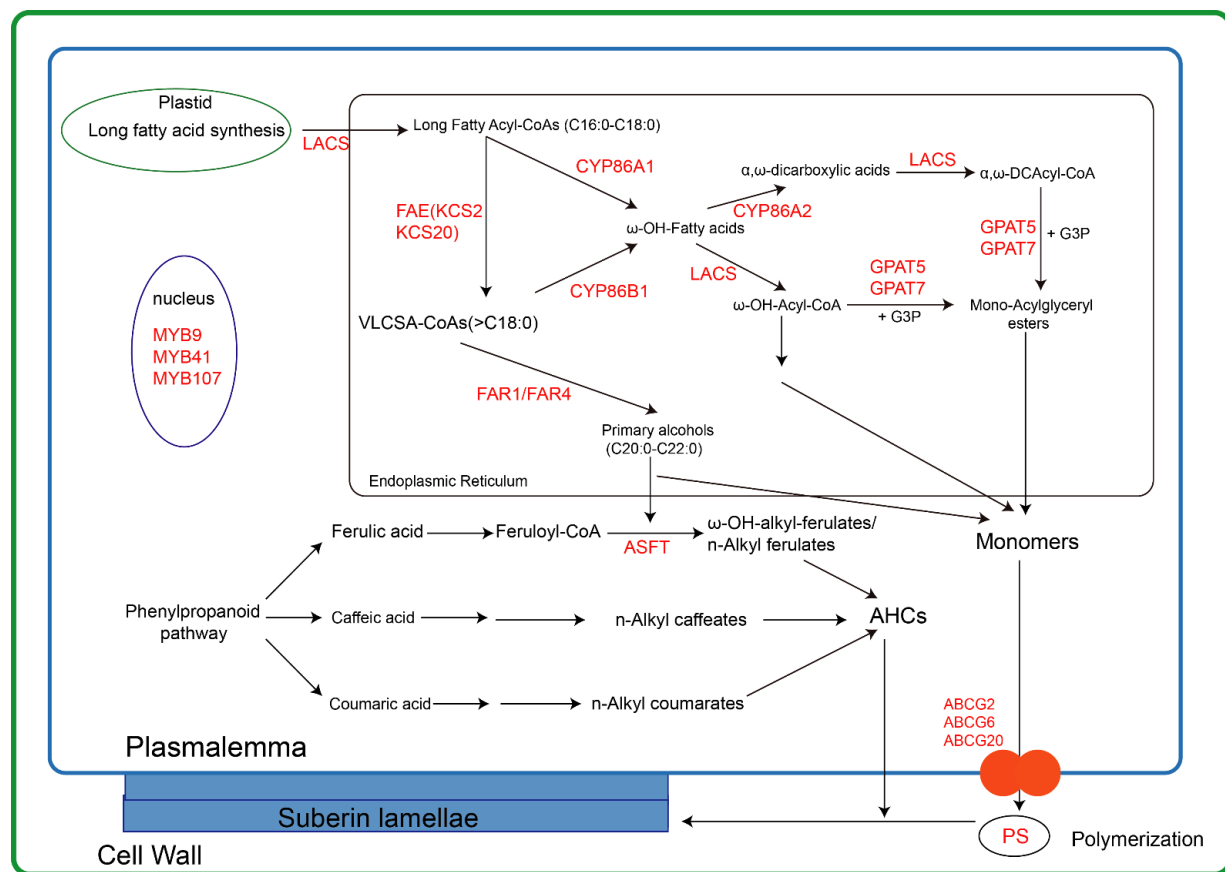


Figure S15. Overview of the suberin biosynthetic pathway. The red typeface represents the key genes involved in the suberin biosynthetic pathway. Two key suberin biosynthetic genes were involved in the NR group, *CYP86A* and *KCS*. A crucial regulator *MYB9* was also involved in the NR group. Additionally, we detected that the suberin transport protein *ABCG1* had undergone positive selection.

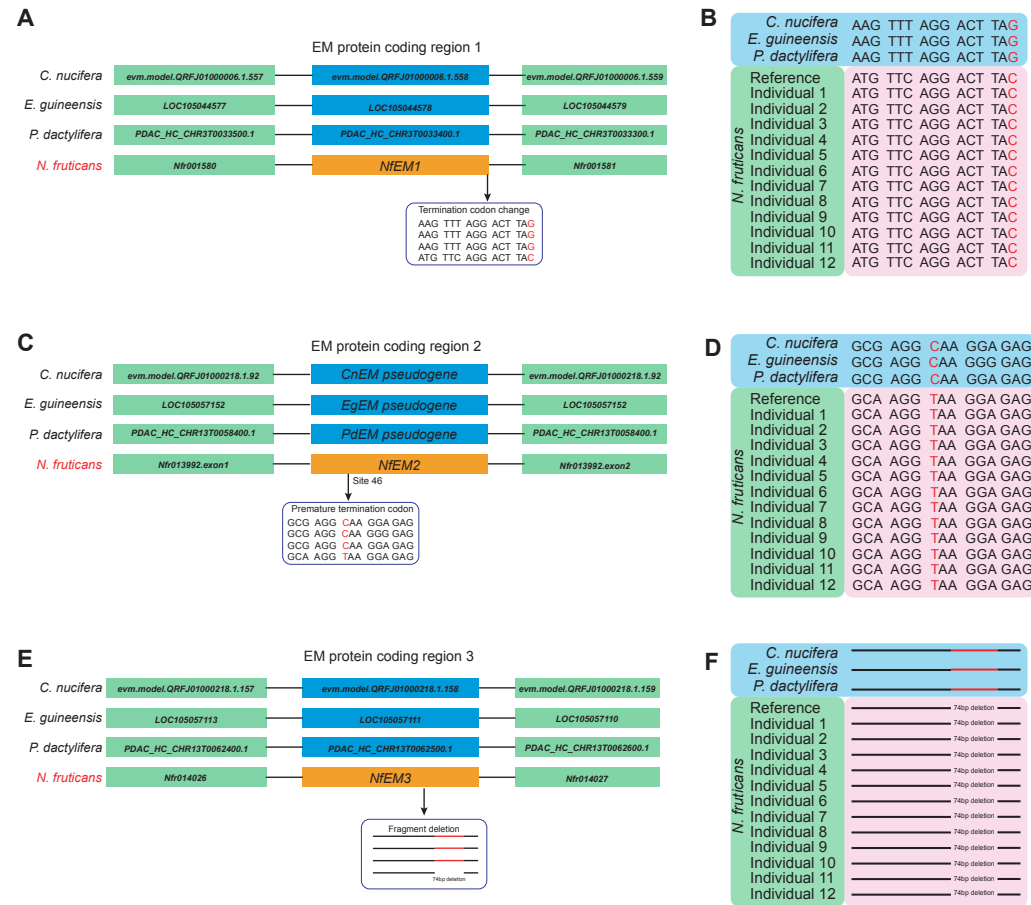


Figure S16. Loss of function mutations in three *EM* putative pseudogene regions in *N. fruticans* genome. (A) The *EM* putative pseudogene region 1. The termination codon of *EM* protein coding region 1 (*NfEM1*) has been turned into TAC from TAG. (B) The re-sequencing data of 12 individuals mapped to the reference genome of *EM* protein coding region 1. (C) The *EM* putative pseudogene region 2. The *EM* protein coding region 2 has a premature termination codon mutation. This region is located in the intron of *Nfr013992* and its orthologs also have been pseudogenization. (D) The re-sequencing data of 12 individuals mapped to the reference genome of *EM* protein coding region 2. (E) The *EM* putative pseudogene region 3. The *EM* protein coding region 2 has 74 bp deletion at the *EM* gene body. (F) The re-sequencing data of 12 individuals mapped to the reference genome of *EM* protein coding region 3.

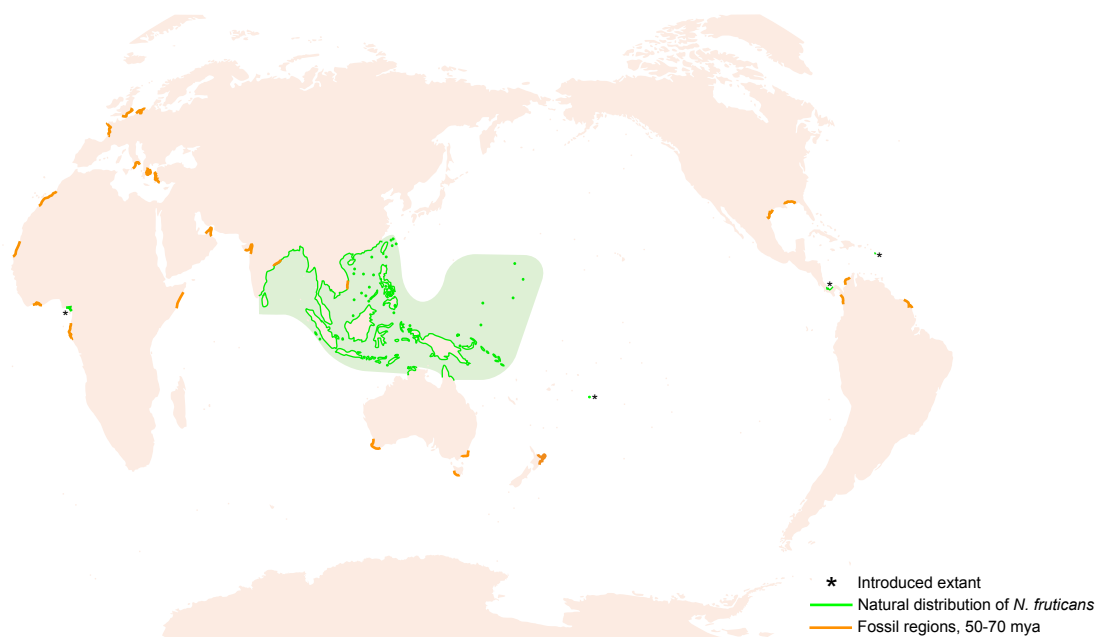


Figure S17. The natural distribution of *N. fruticans*. The asterisks in the image indicate the introduced extant, the green lines represent the natural distribution of the *N. fruticans* along the coast, and the orange lines indicate the distribution of *N. fruticans* fossil records from 50-70 million years ago (mya). (Data from World Mangrove ID e-book)



Figure S18. The morphological structure of *N. fruticans*. (A) Male and female flower heads, petals absent; (B) Fruit, carpel aggregate; many crypto-viviparous propagules; (C) Palm trunkless, Marovo Lagoon, western Solomon Islands; (D) Stem base, with buried growth progression leftward; (E) Leaves pinnate, alternate, up to 10 m tall; (F) Striking carpel propagules, on release. (Image credit: Dr. Norman C. Duke)