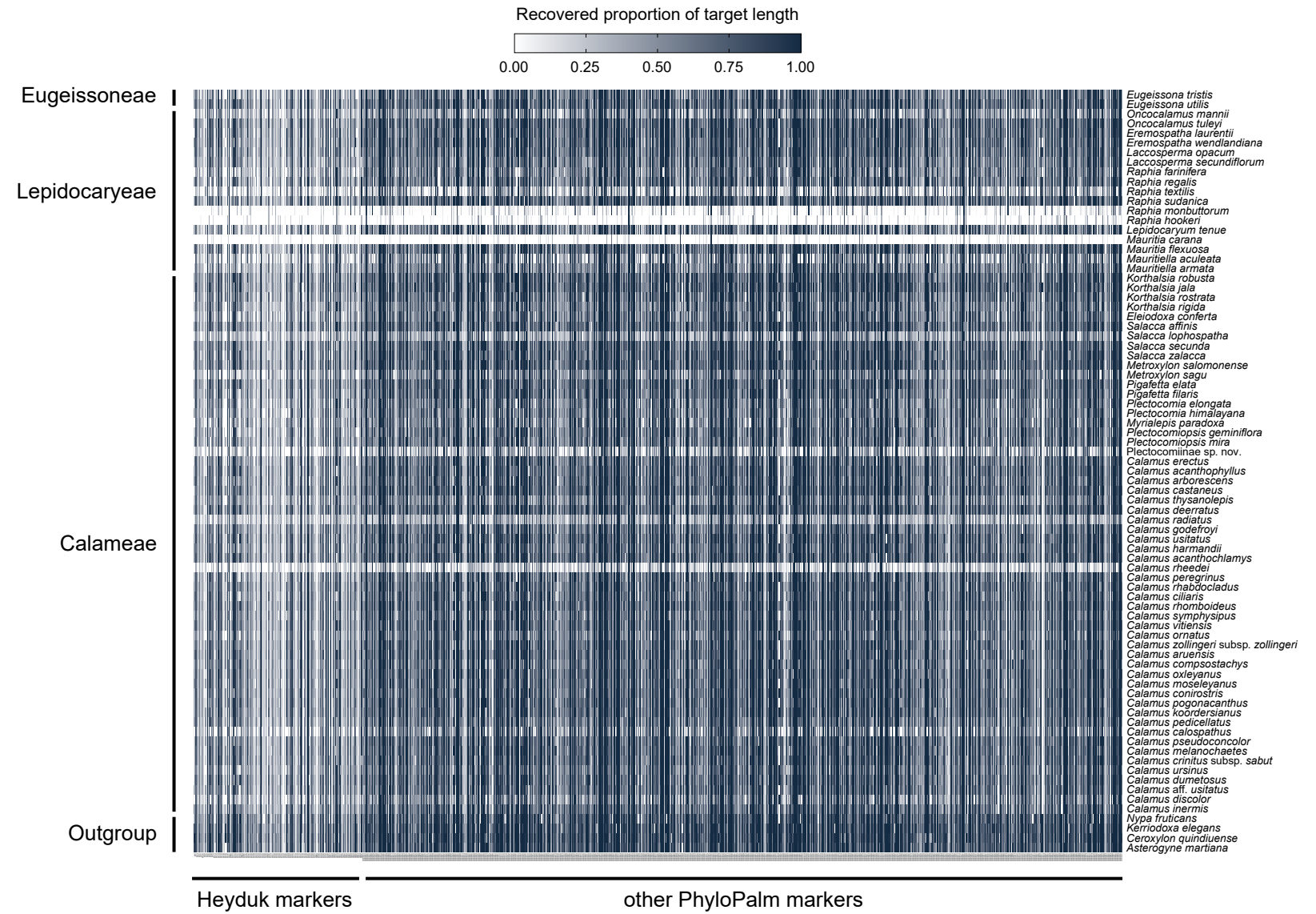
Supplementary Fig. 1. Retrieval of PhyloPalm markers in the Calamoideae and outgroups. Data matrix showing recovery of the 971 PhyloPalm markers (Loiseau et al., 2019), which include all 176 markers by Heyduk et al. (2015), relative to the length of the target reference. Retrieved markers that were longer than the target reference are represented as maximal recovery. Darker colors indicate higher recovery.



Supplementary Fig. 2. Comparison of phylogenomic inferences of the Calamoideae in this study. a, Strict consensus of four coalescent-based and four concatenation-based species trees of 75 calamoid species and four outgroup species, with conflicting topologies collapsed to polytomies. Un-collapsed branches without support values were maximally supported by all analyses. Branches without maximal support values in all analyses are indicated by roman numerals. For these, the support values are given in the inset, with the upper row giving local posterior probabilities of coalescent analyses (in the order exons / exons with substitution model testing / supercontigs / supercontigs with substitution model testing), and the lower row giving bootstrap percentages of concatenation analyses (in the order exons / exons with partitioning / supercontigs / supercontigs with partitioning). Squares indicate tribes: C=Calameae, E=Eugeissoneae, L=Lepidocaryeae, and circles indicate subtribes: A=Ancistrophyllinae, C=Calaminae, F=Pigafettinae, K=Korthalsiinae, M=Mauritiinae, P=Plectocomiinae, R=Raphiinae, S=Salaccinae, X=Metroxylinae. **b**, Matrix of normalized Robinson-Foulds distances between the eight species trees inferred in this study. EX = exons, SC = supercontigs, m = with substitution model testing, p = with partitioning. Smaller distances and lighter colors indicate more similar tree topologies.