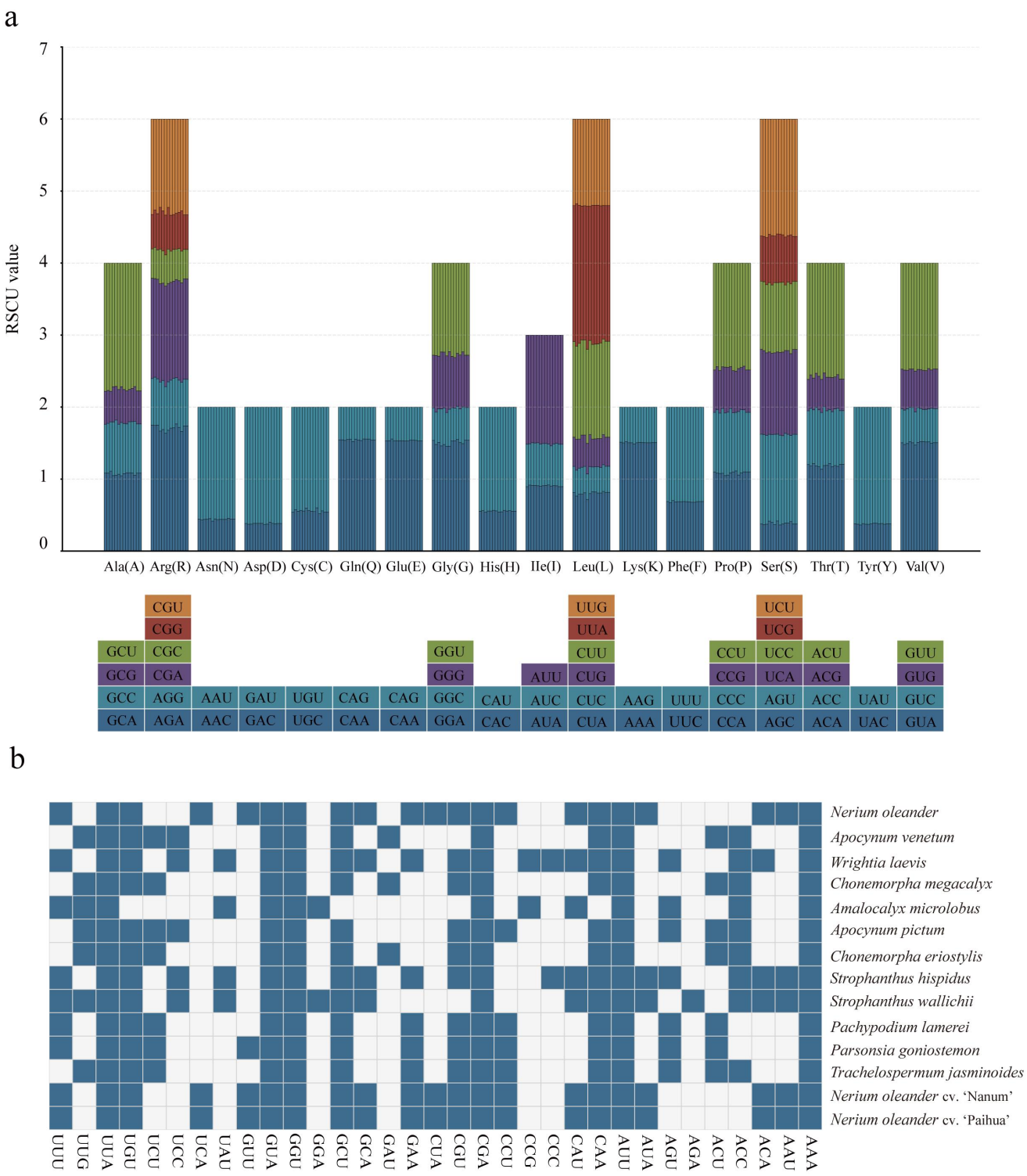

Figure S1. Synonymous and optimal codon usage patterns in chloroplast genomes of Apocynoideae. (a) Synonymous codon analysis of the 14 chloroplast genomes of Apocynoideae. (b) Optimal codon analysis of the 14 chloroplast genomes. Dark blue cells represent codons with both RSCU > 1 and ΔRSCU ≥ 0.08, i.e., optimal codons that are preferentially used in highly expressed genes. The light gray background corresponds to codons that do not meet these criteria, including those with RSCU < 1, which are less frequently used.