



Supplemental Fig. S2. Phylogenetic tree of the family Caprifoliaceae based on nucleotide sequences of the chloroplast *atpB-rbcL* region, depicted by RAxML-NG version 1.2.0. The evolutionary history was inferred by using the maximum likelihood (ML) method based on the TVM + I + Γ model. Accession numbers were listed behind each name. Statistical support values more than 50 % obtained by RAxML-NG for bootstrap probabilities (BP) with 10,000 replicates are shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The root is arbitrarily placed on the branch leading to the clade which includes species of the subfamily Diervillioidae, following Lee et al. (2021) and Wang et al. (2020).