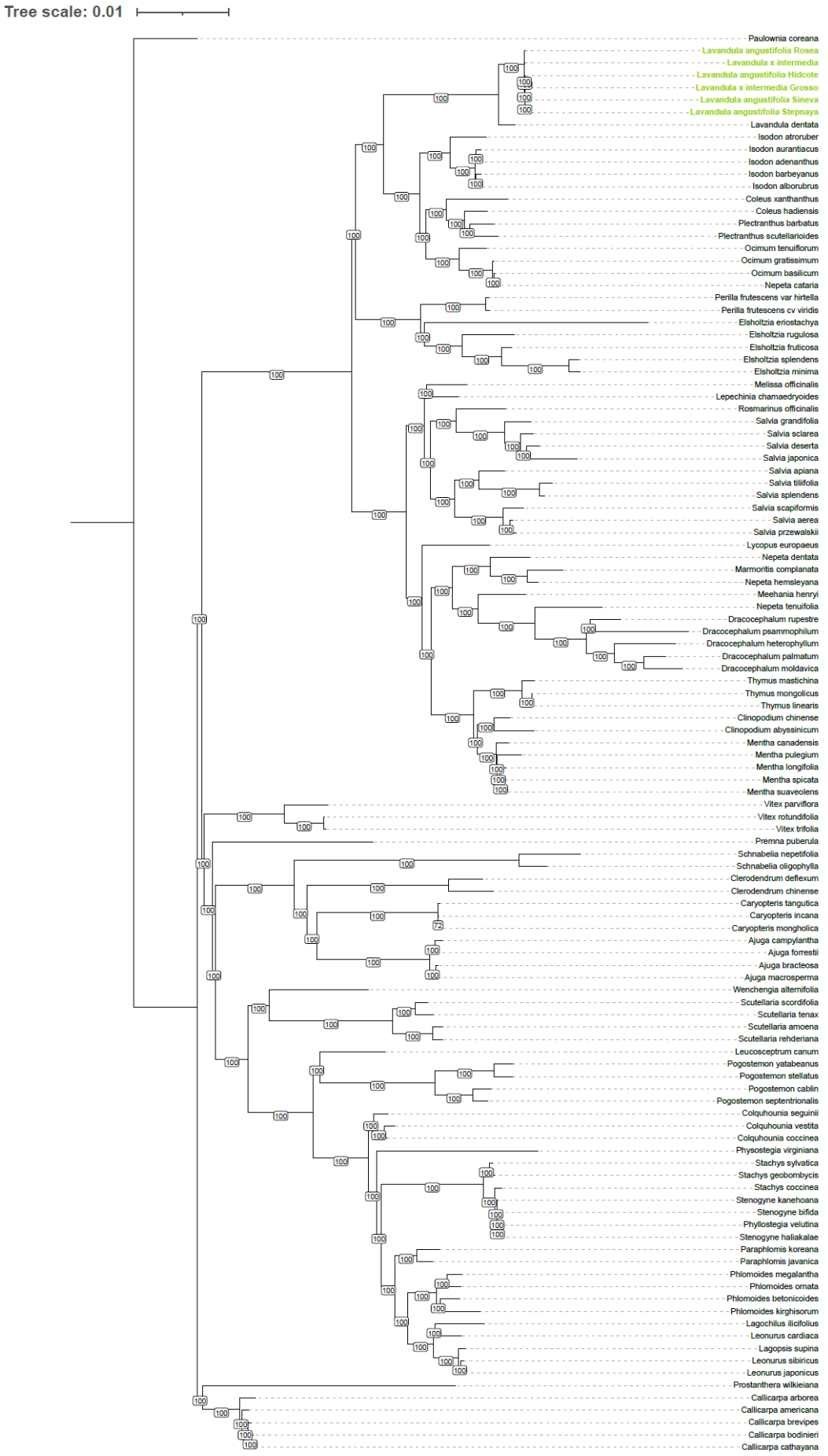


Figure S14. Bayesian Inference (BI) phylogenetic tree of the family Lamiaceae based on whole chloroplast genome sequence alignments. The tree was reconstructed using ExaBayes with *Paulownia coreana* designated as the outgroup. Bayesian posterior probability (BPP) values are displayed at the nodes.

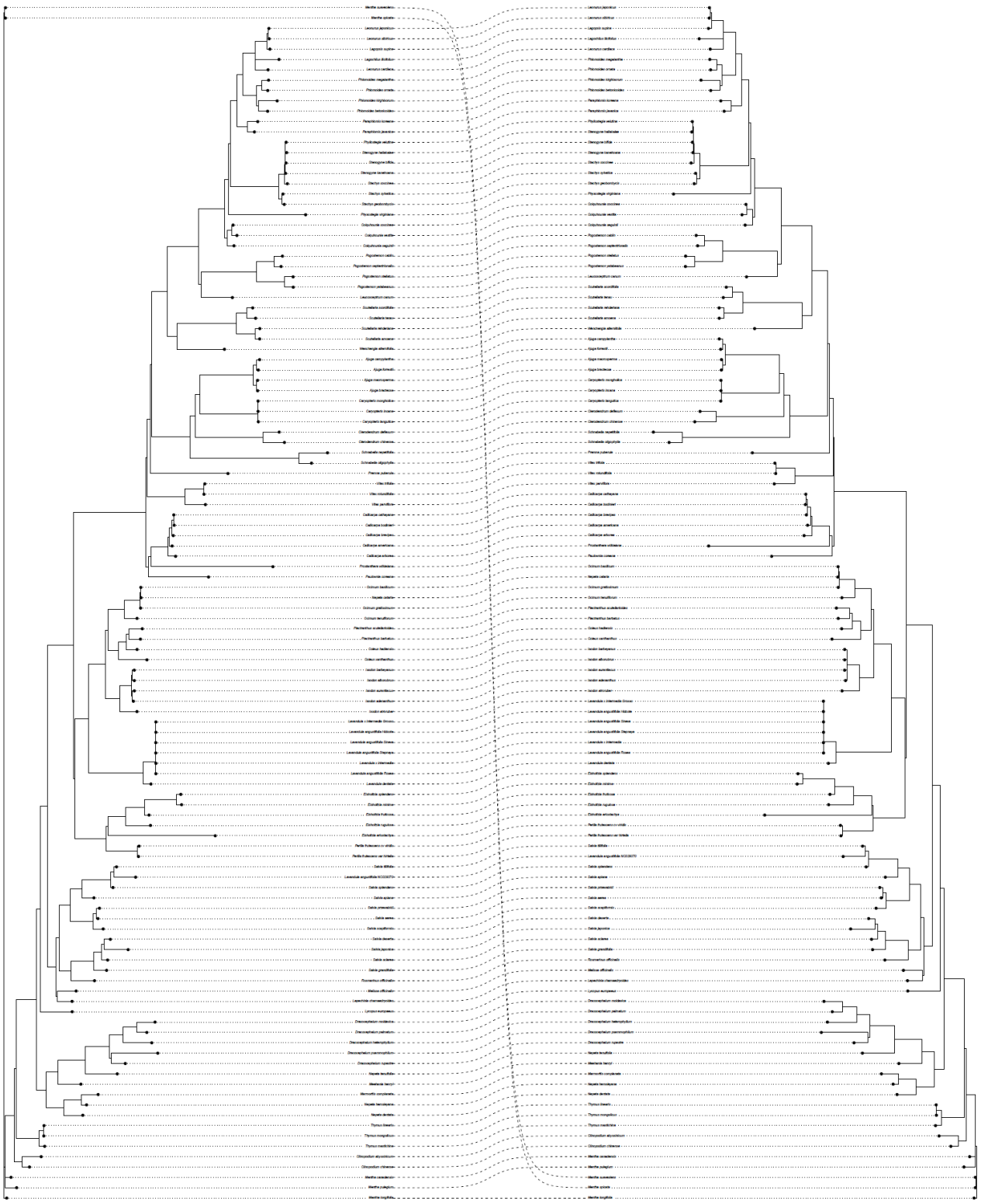


Figure S15. Tanglegram comparison evaluating topological concordance between the Maximum Likelihood (ML; left) and Bayesian Inference (BI; right) phylogenetic trees of Lamiaceae. Both trees were reconstructed from the shared 115-taxon whole chloroplast genome alignment, rooted with *Paulownia coreana*s. Auxiliary connecting lines link corresponding taxa across the two phylogenies. The comparison reveals absolute topological congruence (normalized Robinson–Foulds distance, RF = 0) with no conflicting clade tangles between the two optimality criteria