

Additional file 1:

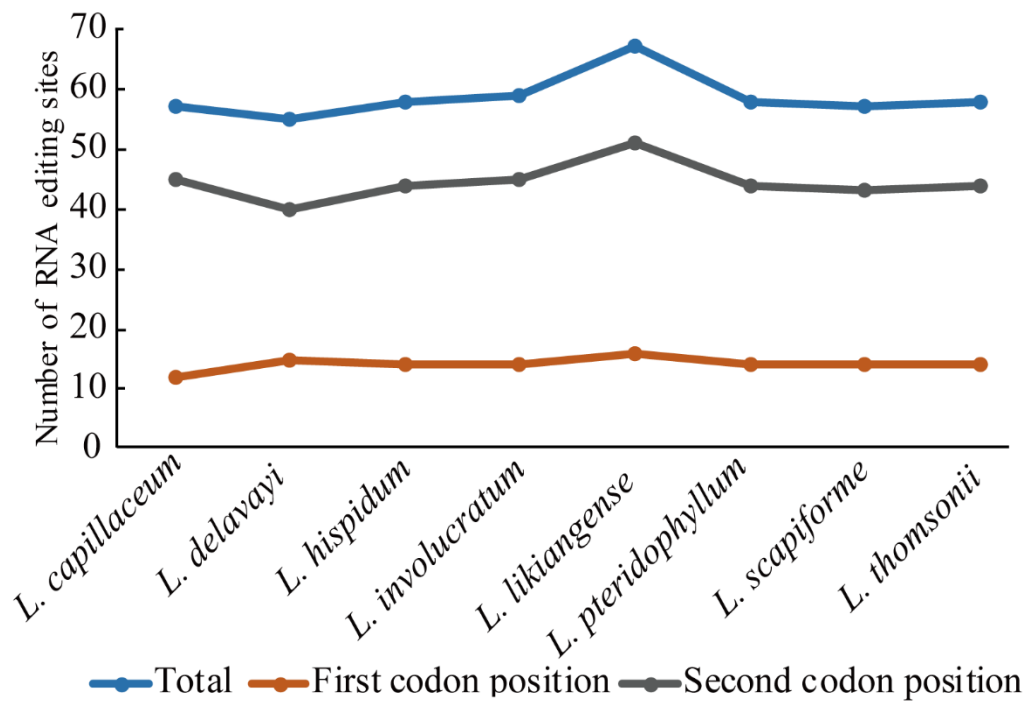


Figure S1. Number of RNA editing sites in the eight *Ligusticum* plastomes.

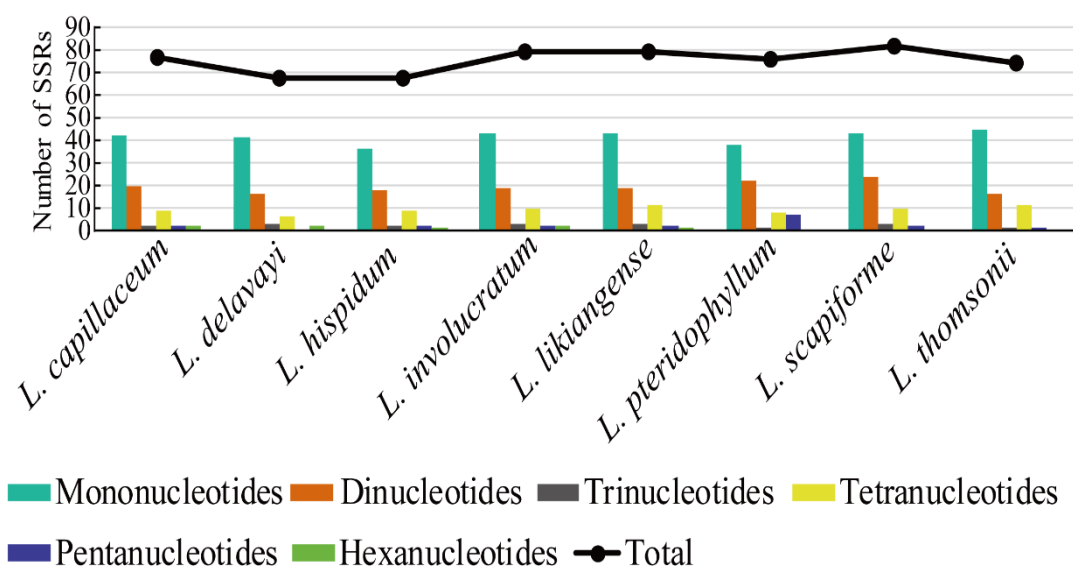


Figure S2. Analysis of simple sequence repeats (SSRs) in the eight *Ligusticum* plastomes.

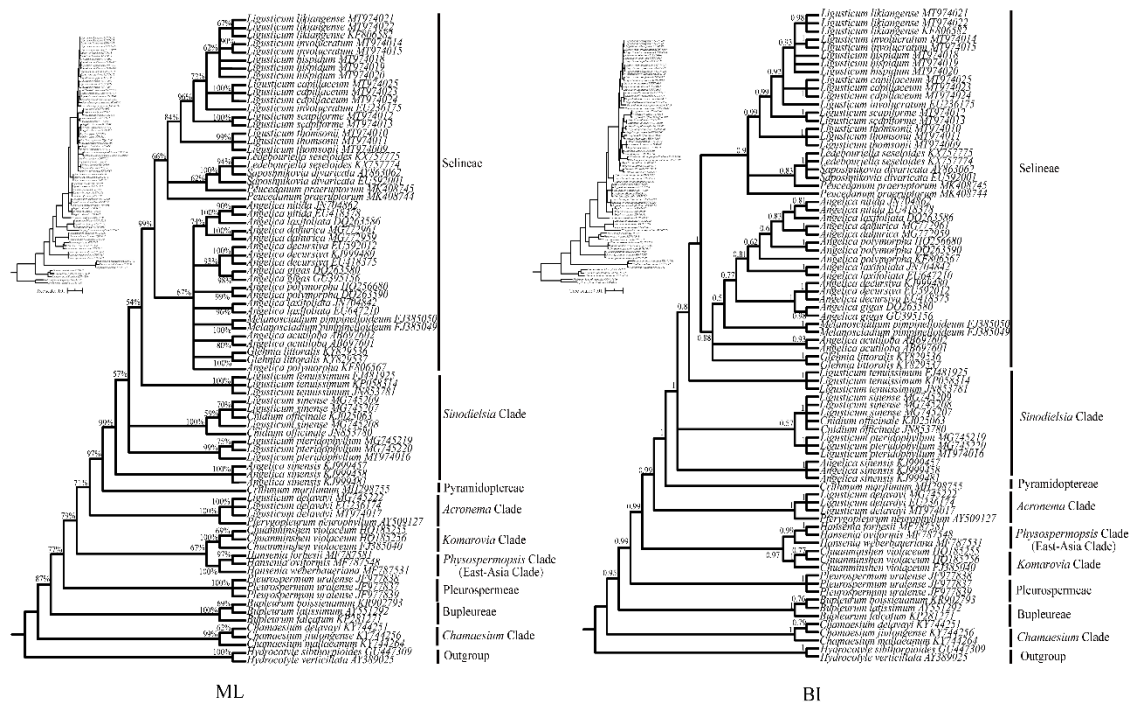


Figure S3. Phylogenetic tree reconstruction of the 39 species inferred from Maximum likelihood (ML) and Bayesian inference (BI) analyses based on nuclear internal transcribed spacer (ITS) sequences. The bootstrap support values and posterior probability values are listed at each node.