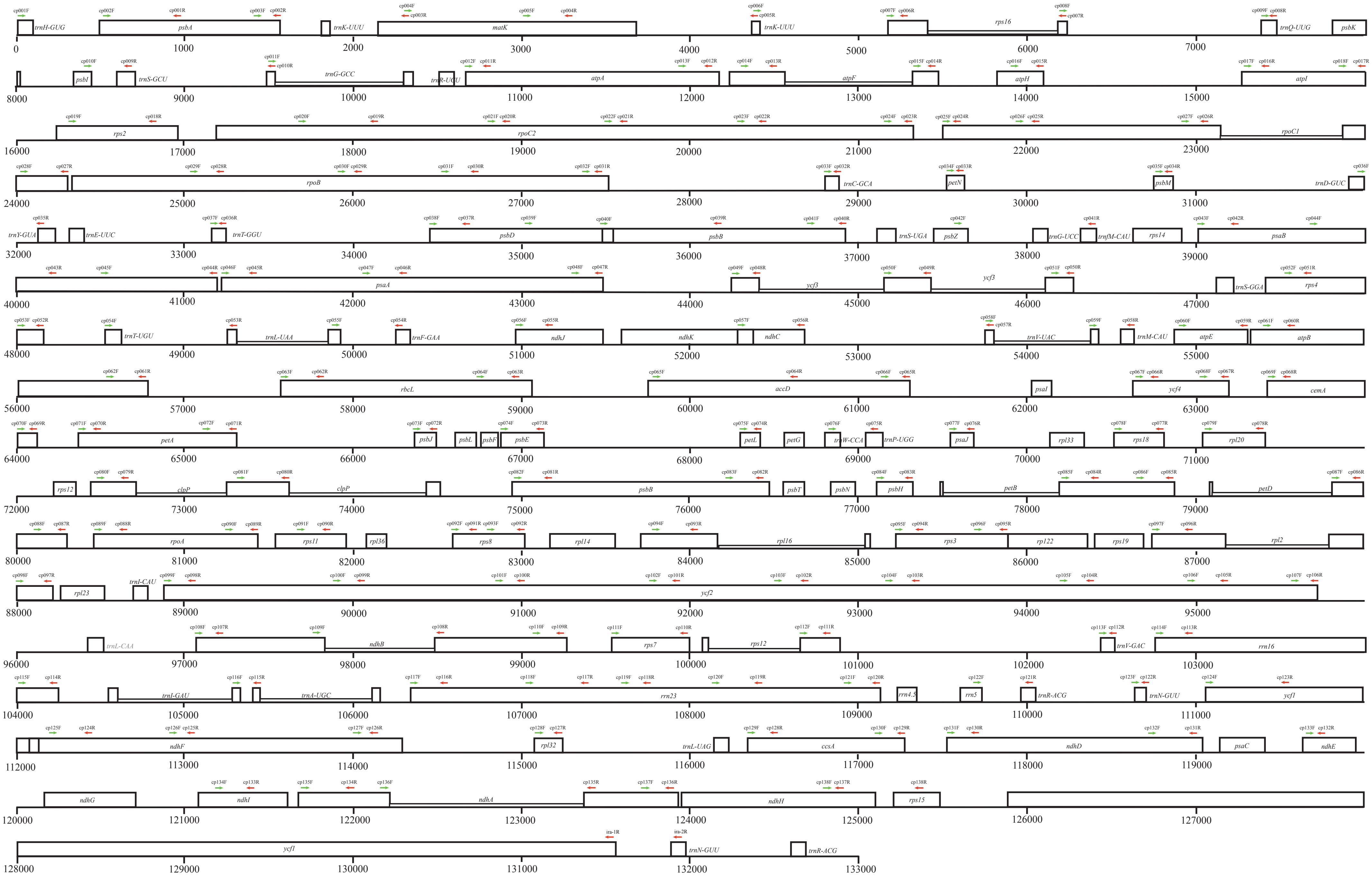
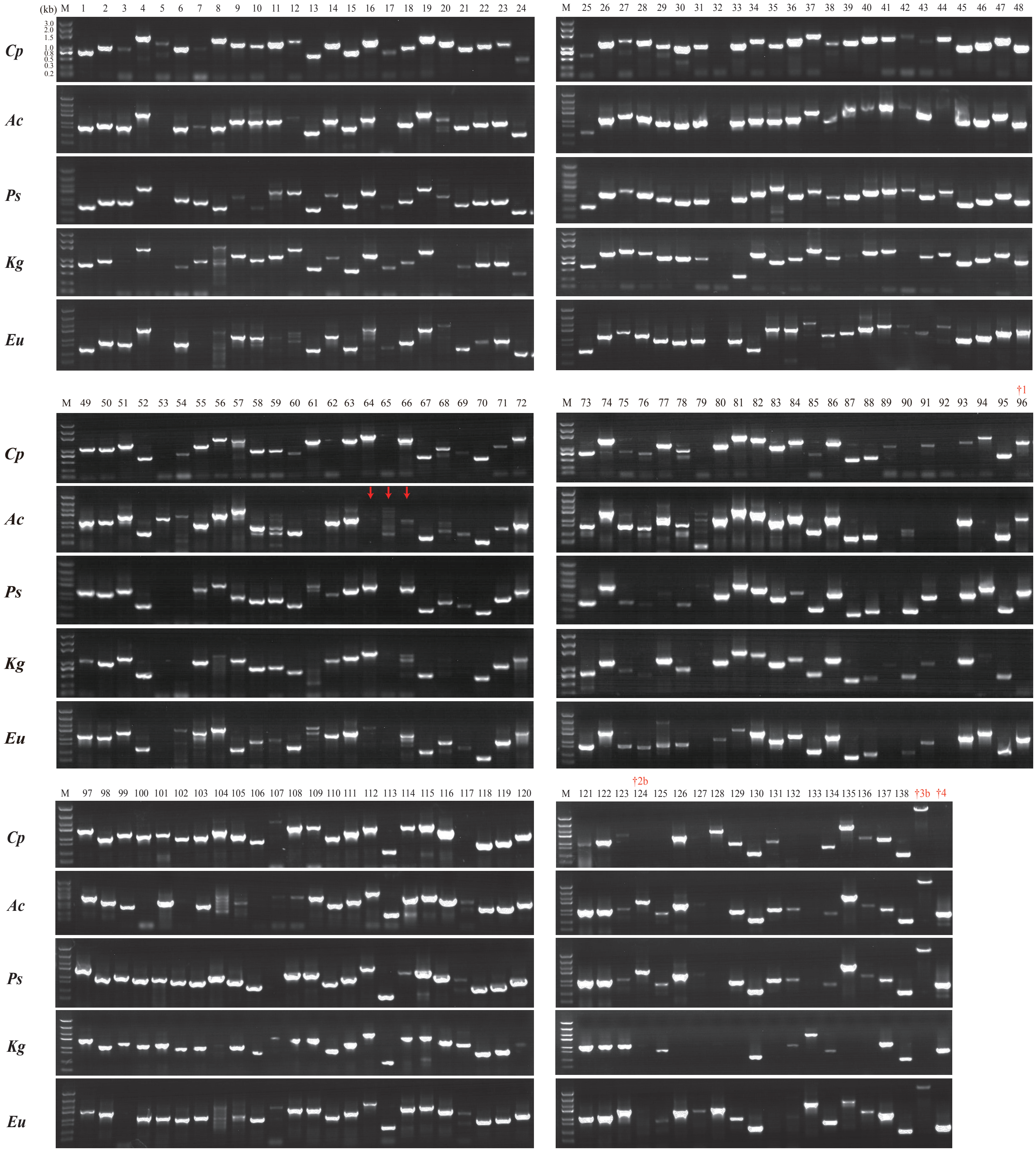
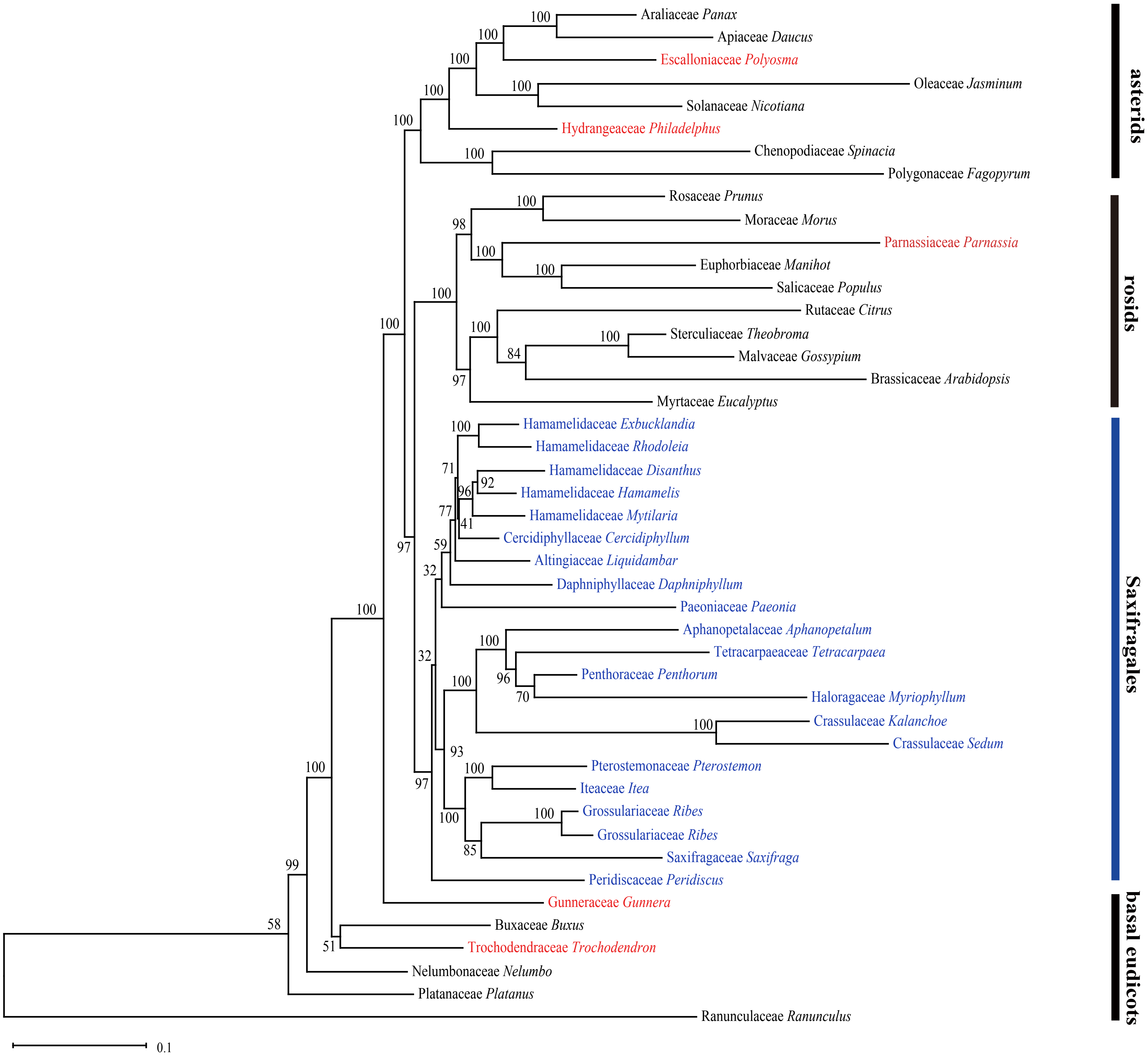


Supplementary fig. S1. Priming sites of 138 universal primer pairs in a plastid genome.



Supplementary fig. S2. PCR gel profiles of five plant species unsequenced. *Cp*: *Chimonanthus praecox*, *Ac*: *Acorus calamus*, *Ps*: *Prunus serrulata*, *Kg*: *Keiskea glandulosa*, and *Eu*: *Eucommia ulmoides*. ↓ indicates gene loss. † indicates a single-copy inverted repeat boundary region.



Supplementary fig. S3. Phylogram of the bootstrap consensus ML tree based on the amino acid sequences of 18 chloroplast regions with 1,804 parsimony- informative sites from a total length of 9,562 amino acids. Numbers associated with branches are bootstrap supports.