

Figure S1. Gene maps of the 18 *Taxus* species chloroplast genomes. Genes inside the circle are transcribed in a clockwise direction, and genes outside of the circle are transcribed counter clockwise. Genes belonging to different functional groups are marked in different colors. Dashed area in the inner circle indicates GC content of the chloroplast genome.

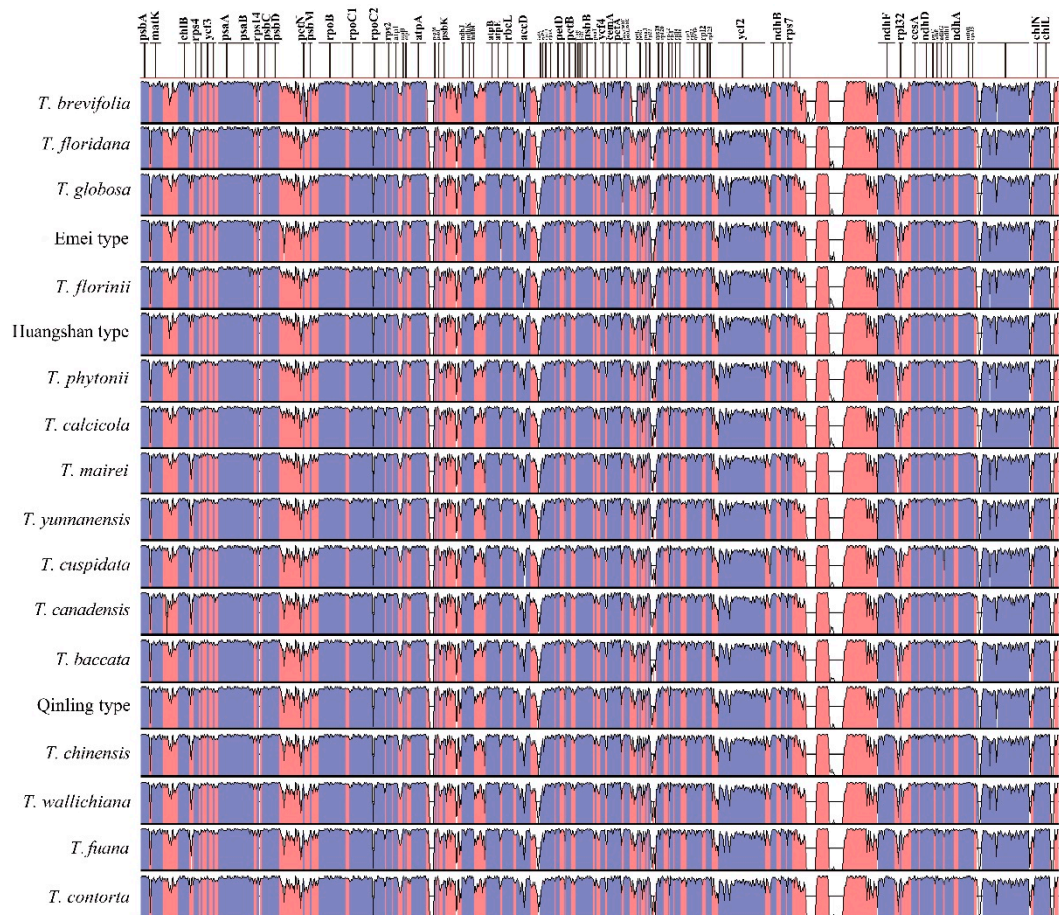


Figure S2. Visualization of sequence alignment of the 18 chloroplast genomes, with *P. chienii* as an outgroup

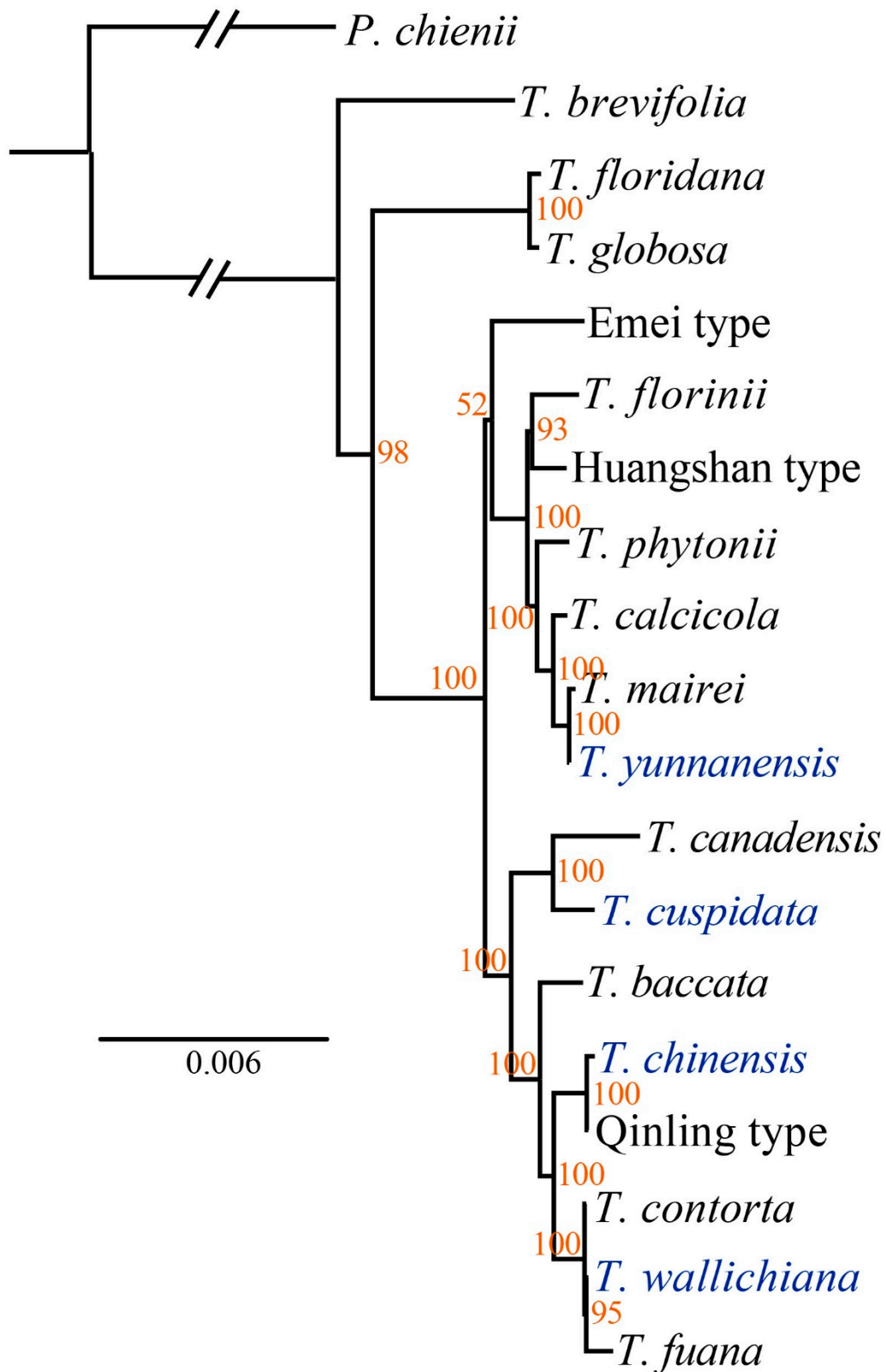


Figure S3. ML phylogeny of *Taxus* inferred from the concatenated sequences of 82 genes of chloroplasts using *P. chienii* as an outgroup.

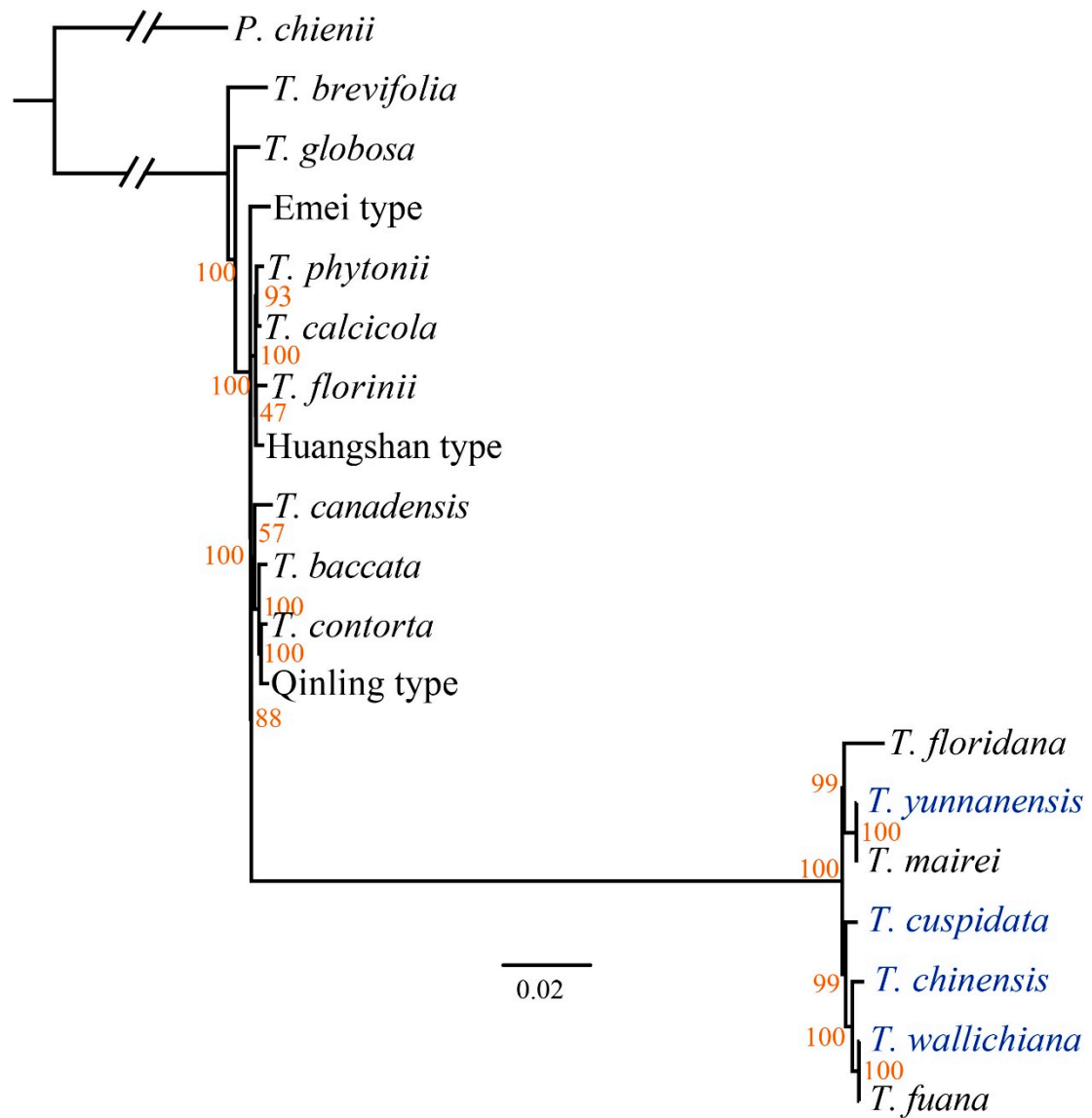


Figure S4. ML phylogeny of *Taxus* inferred from the concatenated sequences of noncoding sequences of the chloroplast genome using *P. chienii* as an outgroup.



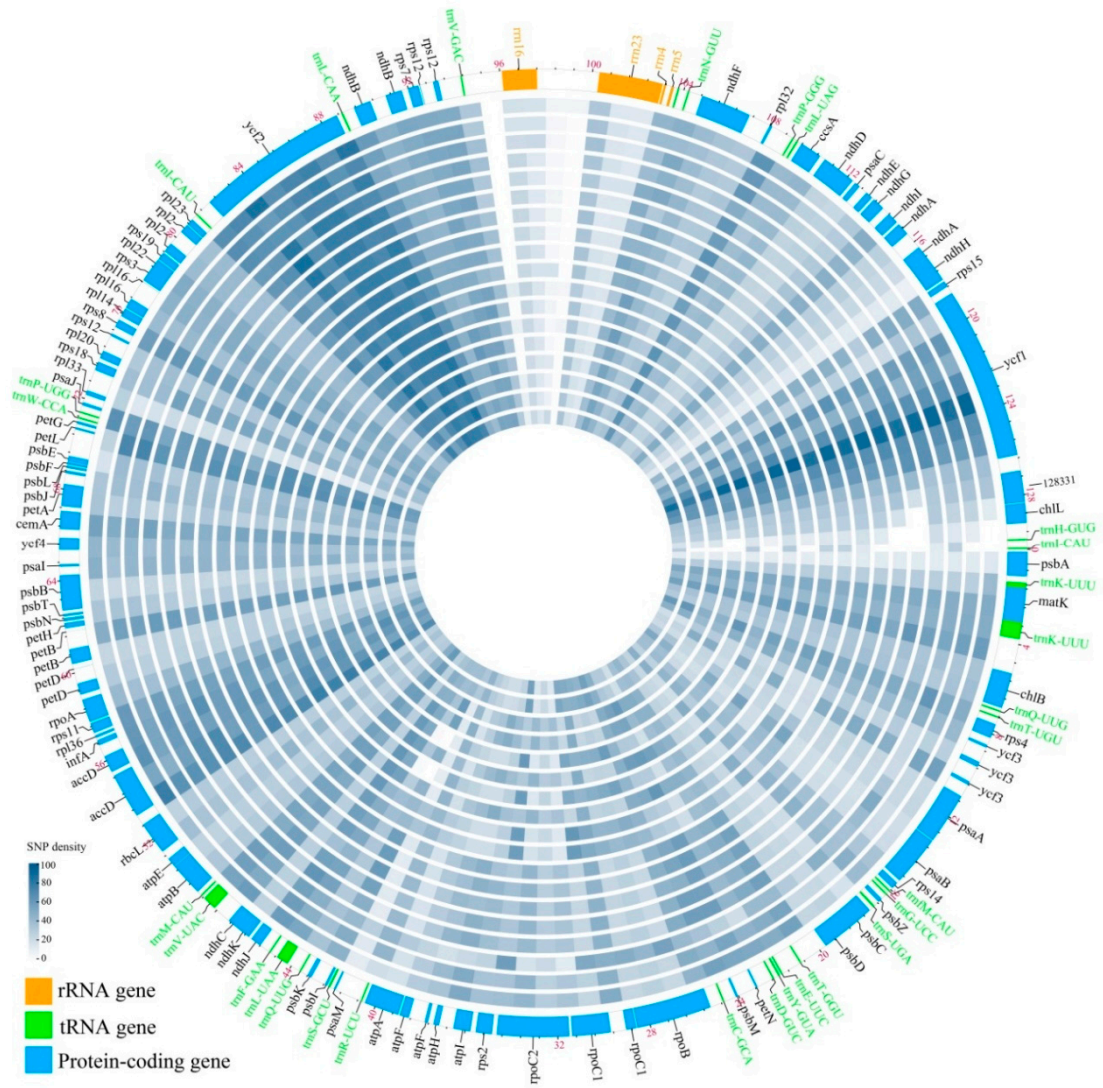


Figure S5. A map of chloroplast nucleotide variation across the *Taxus* plastomes.

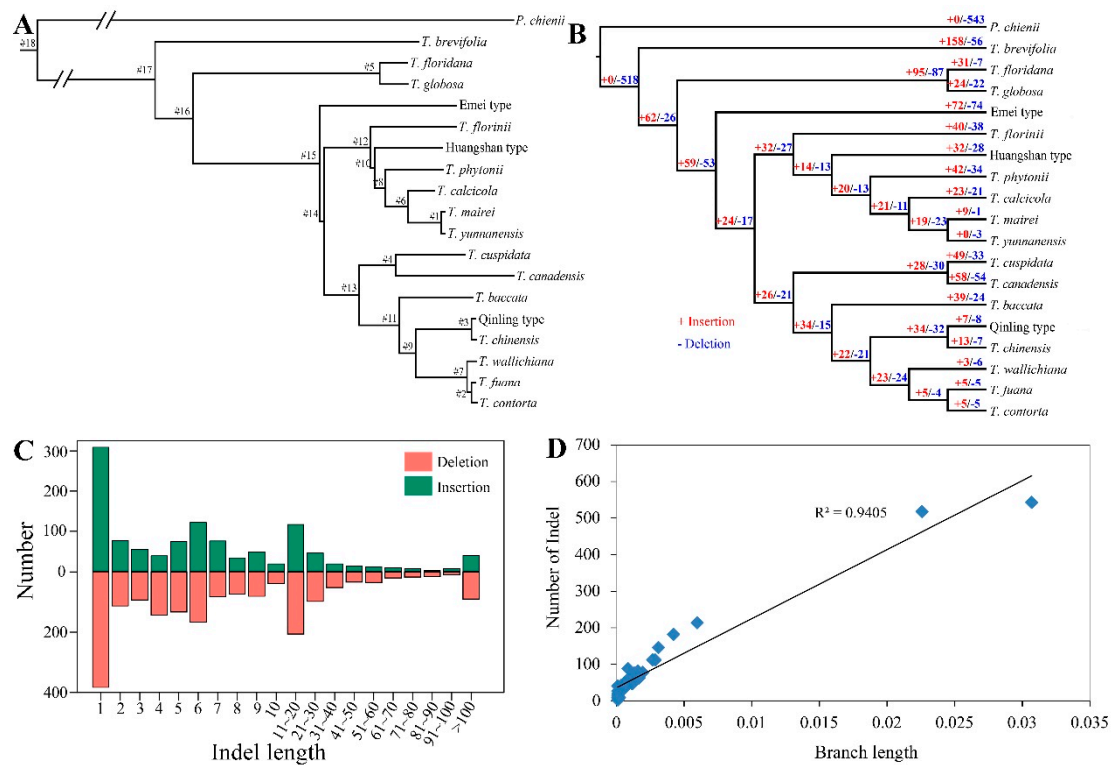


Figure S6. The rate of chloroplast genomic variation in the genus *Taxus*. (A) Numbers of all *Taxus* branches to characterize the occurrence of chloroplast genomic variation. (B) The detection of insertion and deletion events occurred in different *Taxus* plastomes. (C) Overall length distribution of insertions and deletions across the chloroplast genomes. (D) Correlation between branch lengths and indel numbers for the 18 *Taxus* species and *P. chienii* chloroplast genomes.

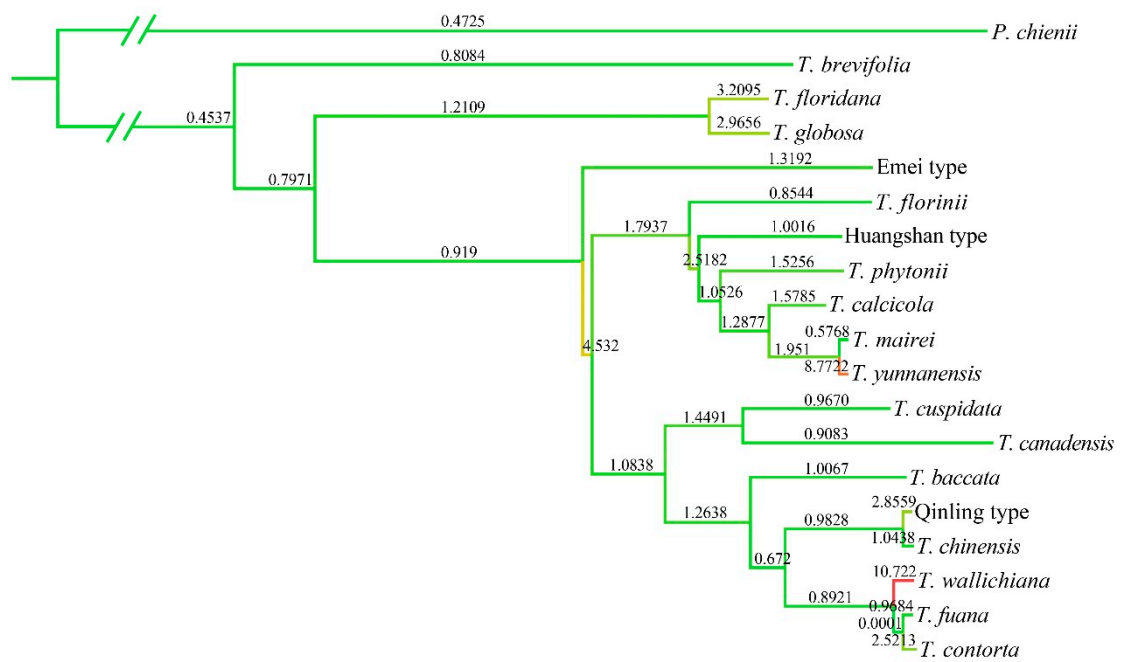


Figure S7. The  $\omega$  ( $dN/dS$ ) of chloroplast protein-coding genes in *Taxus* species using *P. chienii* as an outgroup.