Supplemental Materials 6

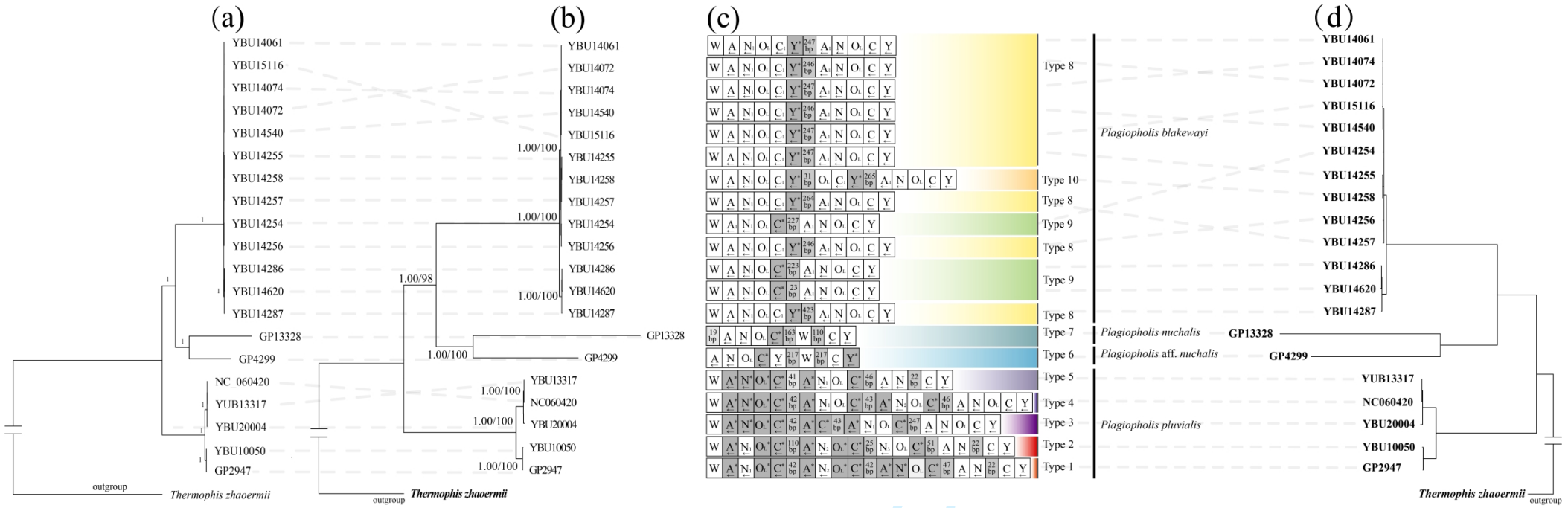


Figure S6. (a)MAP tree inferred from static alignments of PCGs and rRNAs, with the highest values shown on each major node. (b) ML and BI phylogenetic tree inferred from static alignments of PCGs and rRNAs, with PP and BS values shown on each major node. (c) WANCY regions arrangement types of each individual. Dark gray represents pseudo tRNA genes and pseudo OL, while light gray represents the number of intervening bases. (d) Parsimonious tree under dynamic homology from the PCGs and rRNA datasets.