

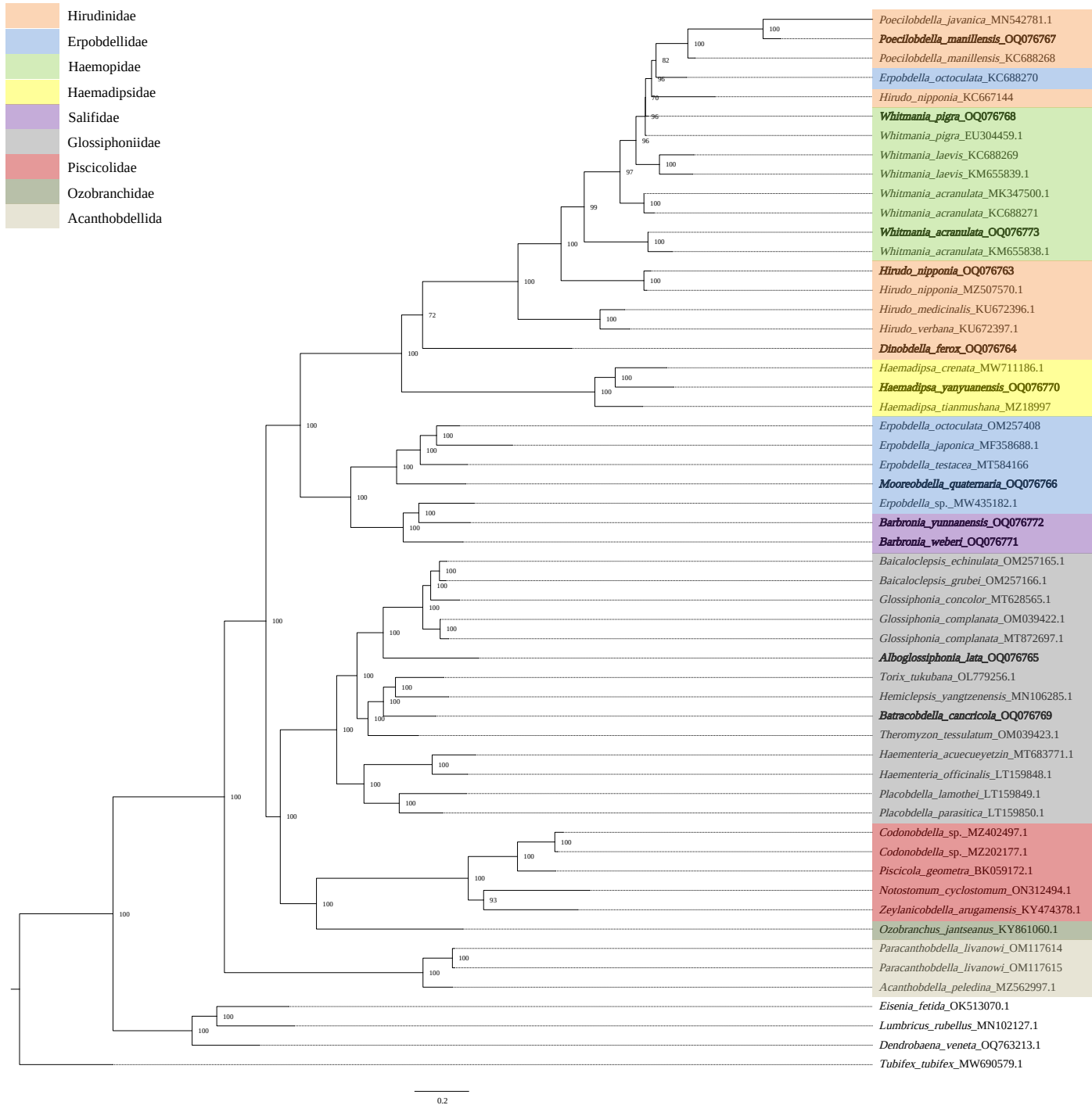


Fig. S9 Phylogenetic relationships inferred from all codon positions of PCGs and 2 rRNAs (PCGrRNA). Numbers are posterior probabilities calculated according to Bayesian inference method (BI tree).