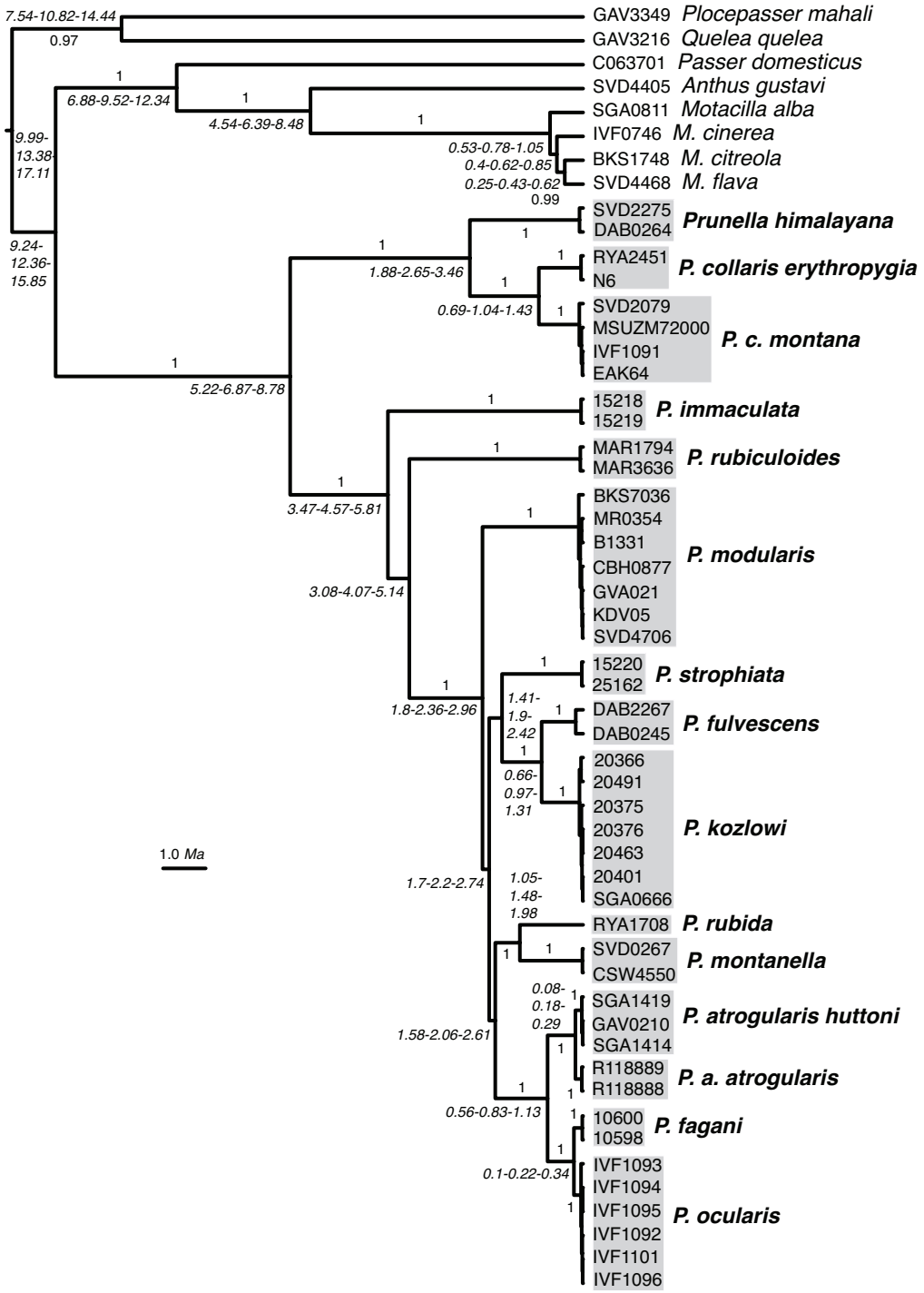

Supplementary Appendix 3. Phylogenetic tree based on complete sequences of mtDNA ND2 gene. Numbers next to the branches show the posterior probability. The tree was reconstructed in BEAST v1.7.4 (Drummond *et al.*, 2012) using GTR+G+I model of substitutions, Yule process speciation and strict molecular clock priors. A single number next to the branch shows its posterior probability, whereas a series of three numbers connected by dashes next to the nodes represent, left to right, the minimum 95% HPD interval, mean, and its maximum 95% HPD interval for the node age in million years.