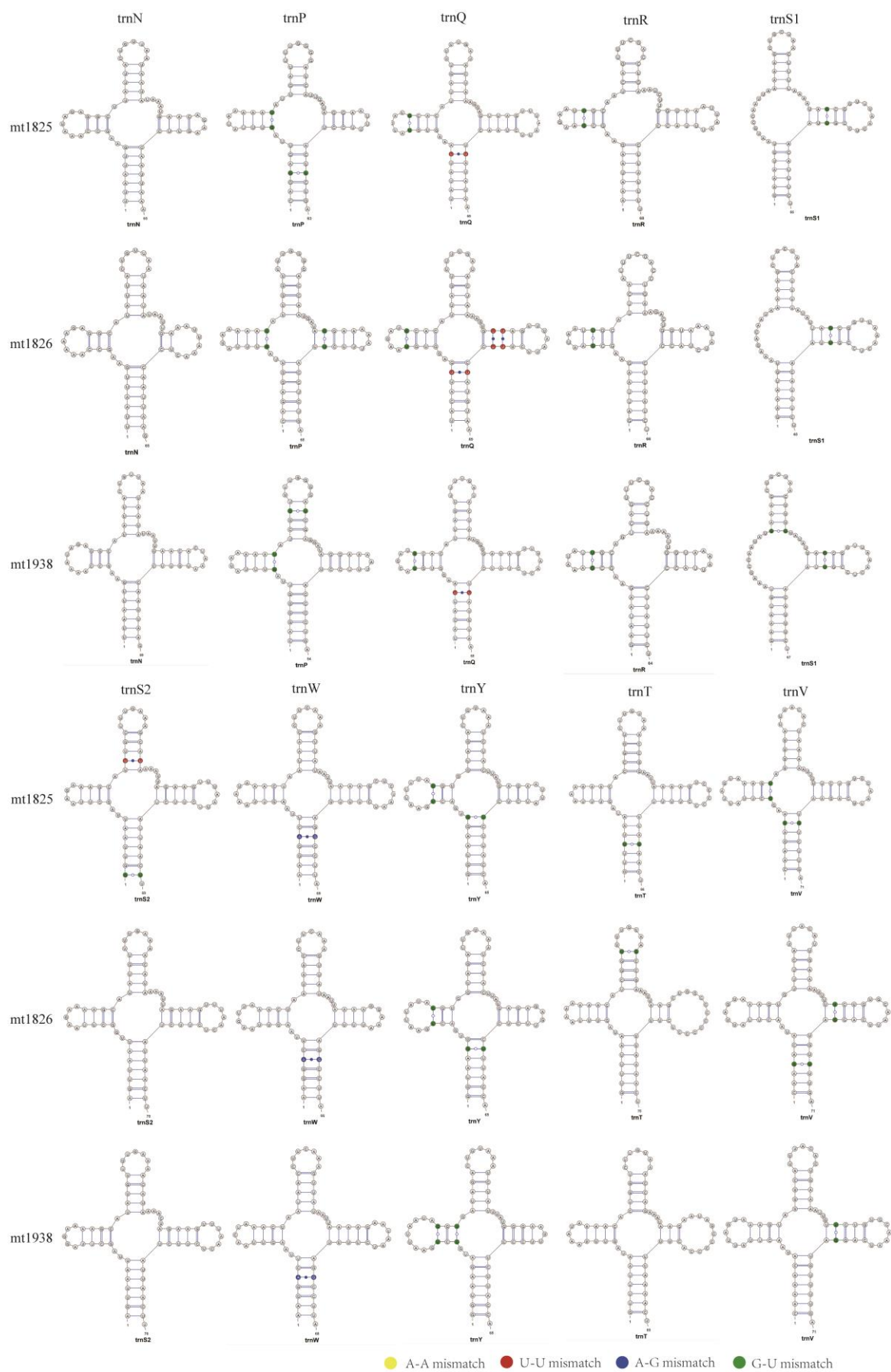
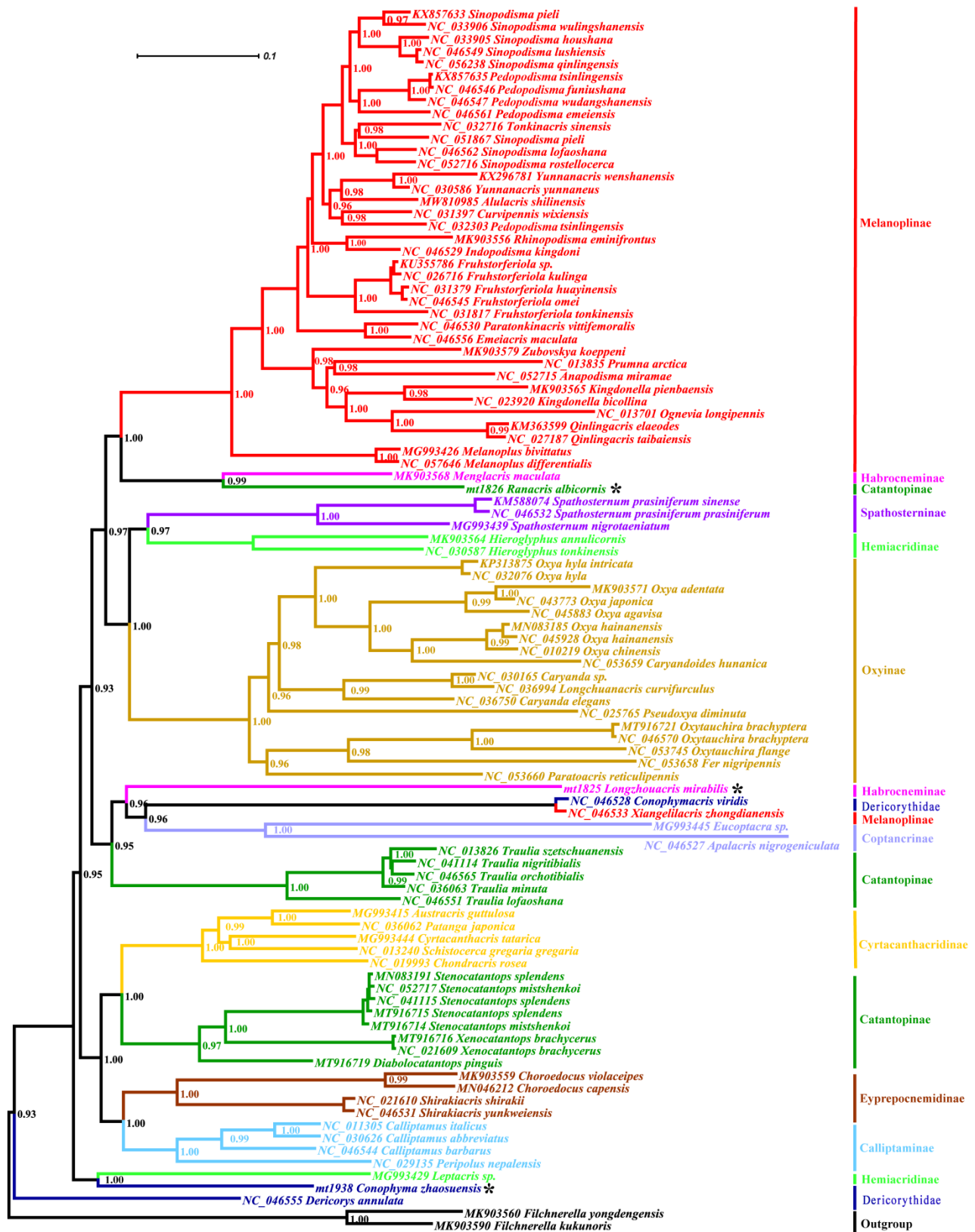


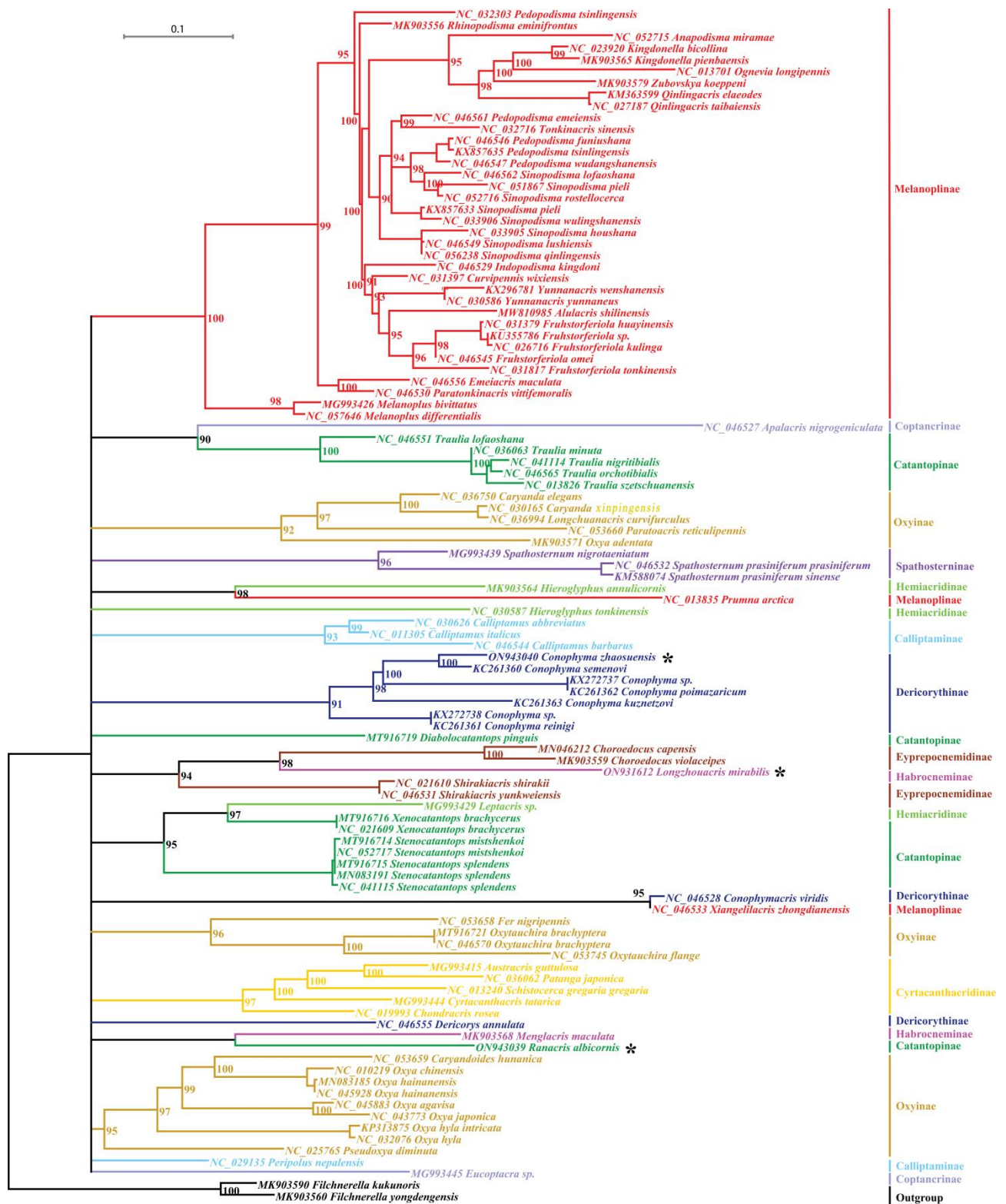
**Figure S1.** Secondary structures of 22 tRNAs of the three newly sequenced mitogenomes. mt1825: *Longzhouacris mirabilis*, mt1826: *Ranacris albicornis*, mt1938: *Conophyma zhaosuensis*.



**Figure S1.** (continued)

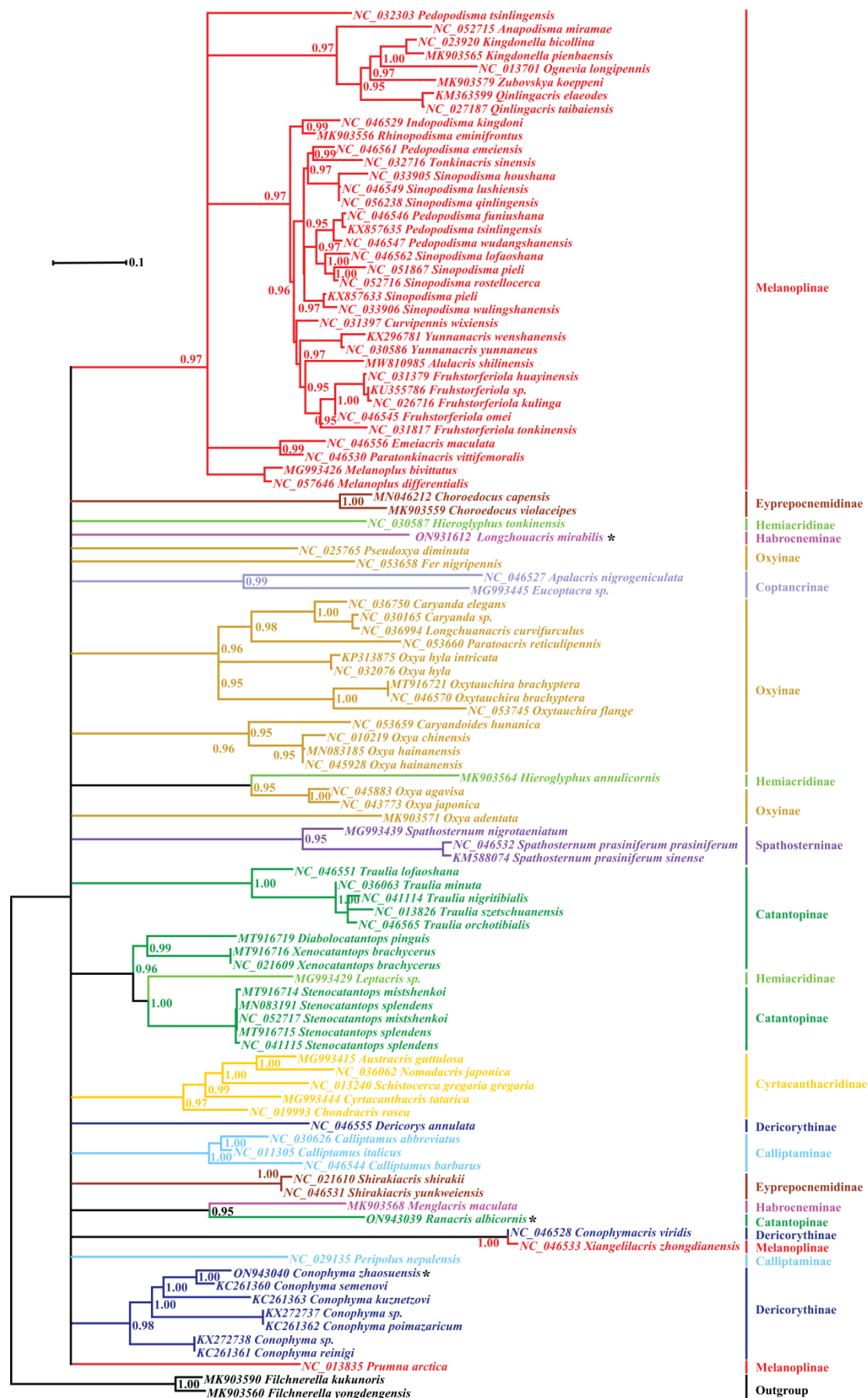


**Figure S2.** Phylogenetic tree reconstructed from sequences of the 13 mitochondrial PCGs using Bayesian inference. The asterisk indicates the three newly sequenced species.

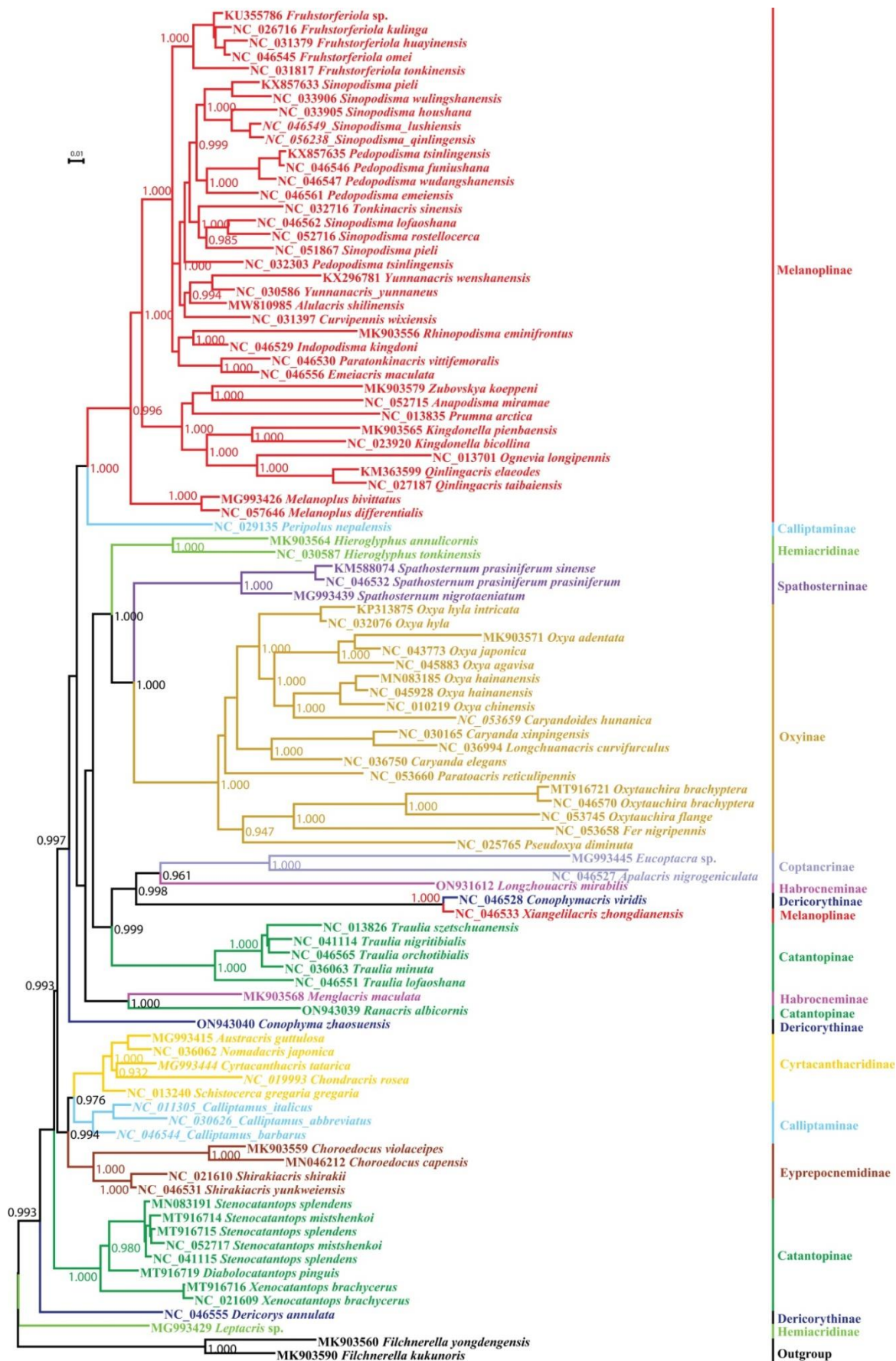


**Figure S3.** Phylogenetic tree reconstructed from partial sequences of the *COX1* gene using maximum likelihood. The asterisk indicates the three newly sequenced species.





**Figure S4.** Phylogenetic tree reconstructed from partial sequences of the *COX1* gene using Bayesian inference. The asterisk indicates the three newly sequenced species.



**Figure S5.** Phylogenetic tree reconstructed from amino acid sequences of the 13 mitochondrial PCGs gene using Bayesian inference with MtRev model. The asterisk indicates the three newly sequenced species.