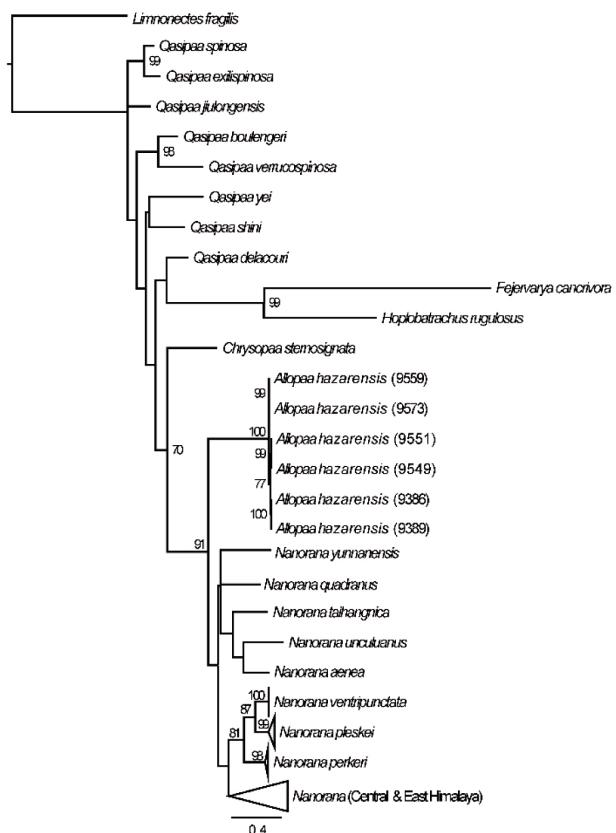
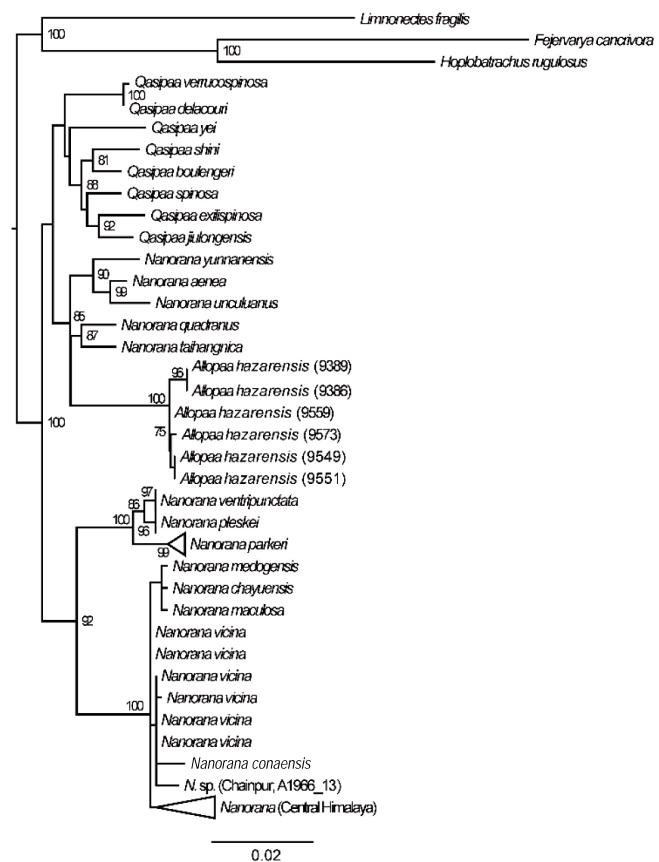


Supplemental Information Fig. S3

a)



b)



ML tree topology. Trees were inferred with RAxML v.8.2.12 (Stamatakis 2014) based on **a)** mitochondrial 16s+COI, and **b)** nuclear Rag1 sequence data. RAxML was performed with the GTRGAMMA model and 1000 bootstrap replicates; the dataset was partitioned by gene and codon fragments. Numbers at nodes reflect bootstrap values ≥ 70 .

Reference

Stamatakis A (2014) RAxML Version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30: 1312–1313.