

Supplementary figure legends

Figure S1: Tree reconstruction results of the 113 taxa mitogenome data set. Maximum likelihood tree inferred from nucleotide data set using IQ-TREE. Node numbers show bootstrap support values.

Figure S2: Tree reconstruction results of the 113 taxa mitogenome data set. Maximum likelihood tree inferred from amino acid and rRNA data set using IQ-TREE. Node numbers show bootstrap support values.

Figure S3: Bayesian tree inferred from the nucleotide data set using PhyloBayes under the site-heterogeneous CAT-GTR model. Node numbers show the posterior probability values.

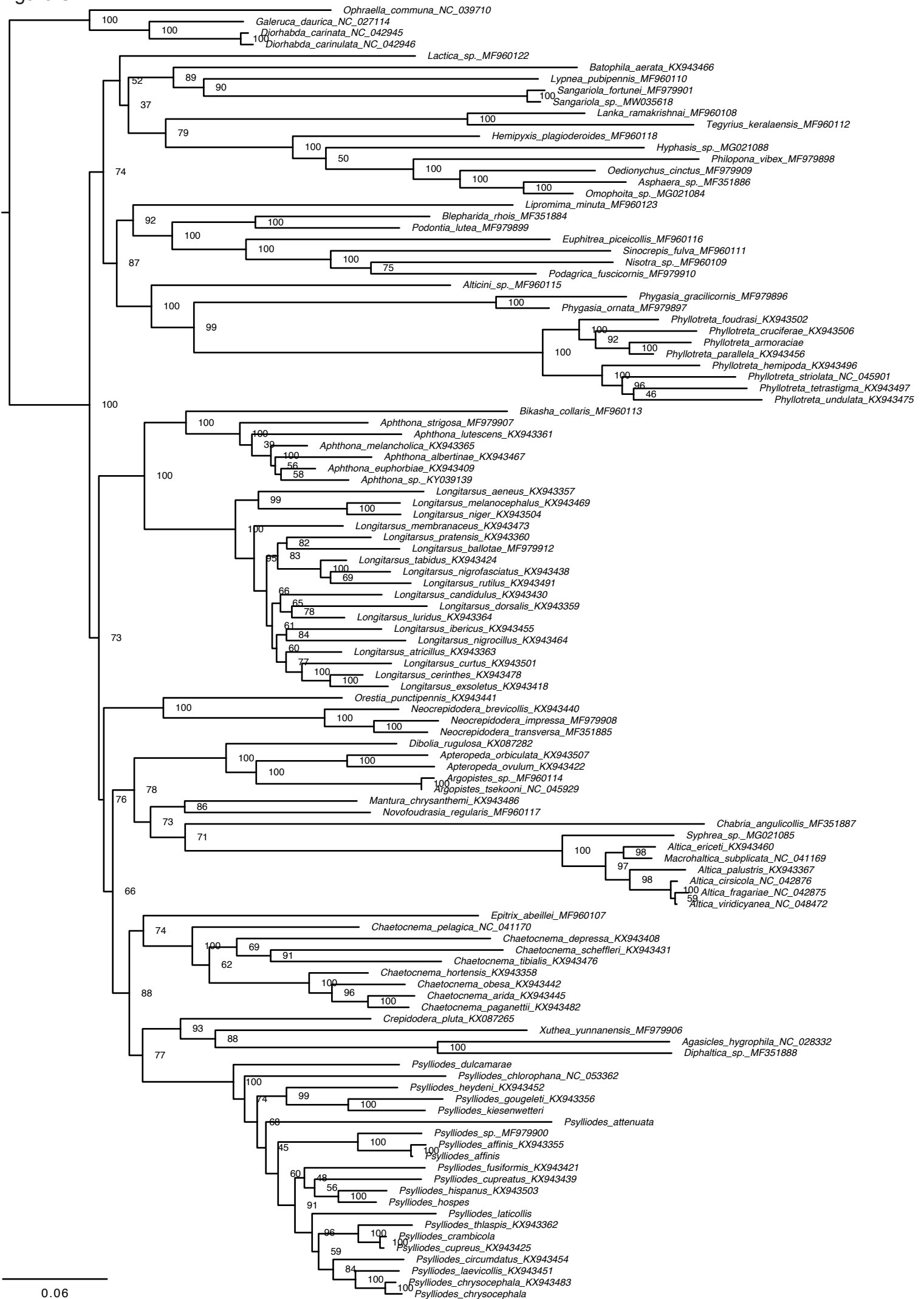
Figure S4: Bayesian tree inferred from the amino acid data set using PhyloBayes under the site-heterogeneous CAT-GTR model. Node numbers show the posterior probability values.

Figure S5: Divergence time estimations of the 612 taxa COI data set in BEAST, using the random local clock (RLC) and a Yule pure birth tree model. Node values represent the 95% height posterior density of the age estimations.

Figure S1



Figure S2



0.06

Figure S3

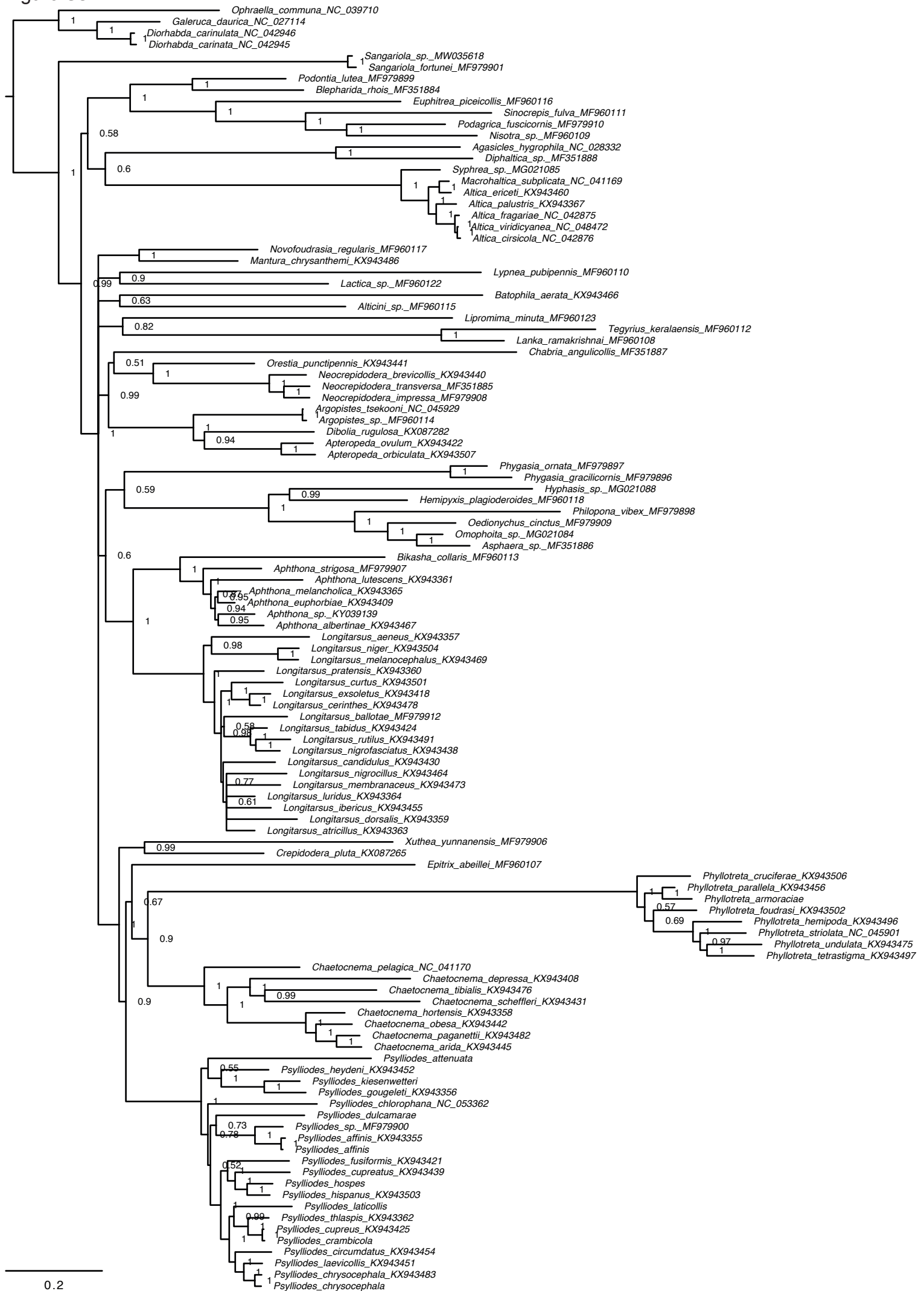
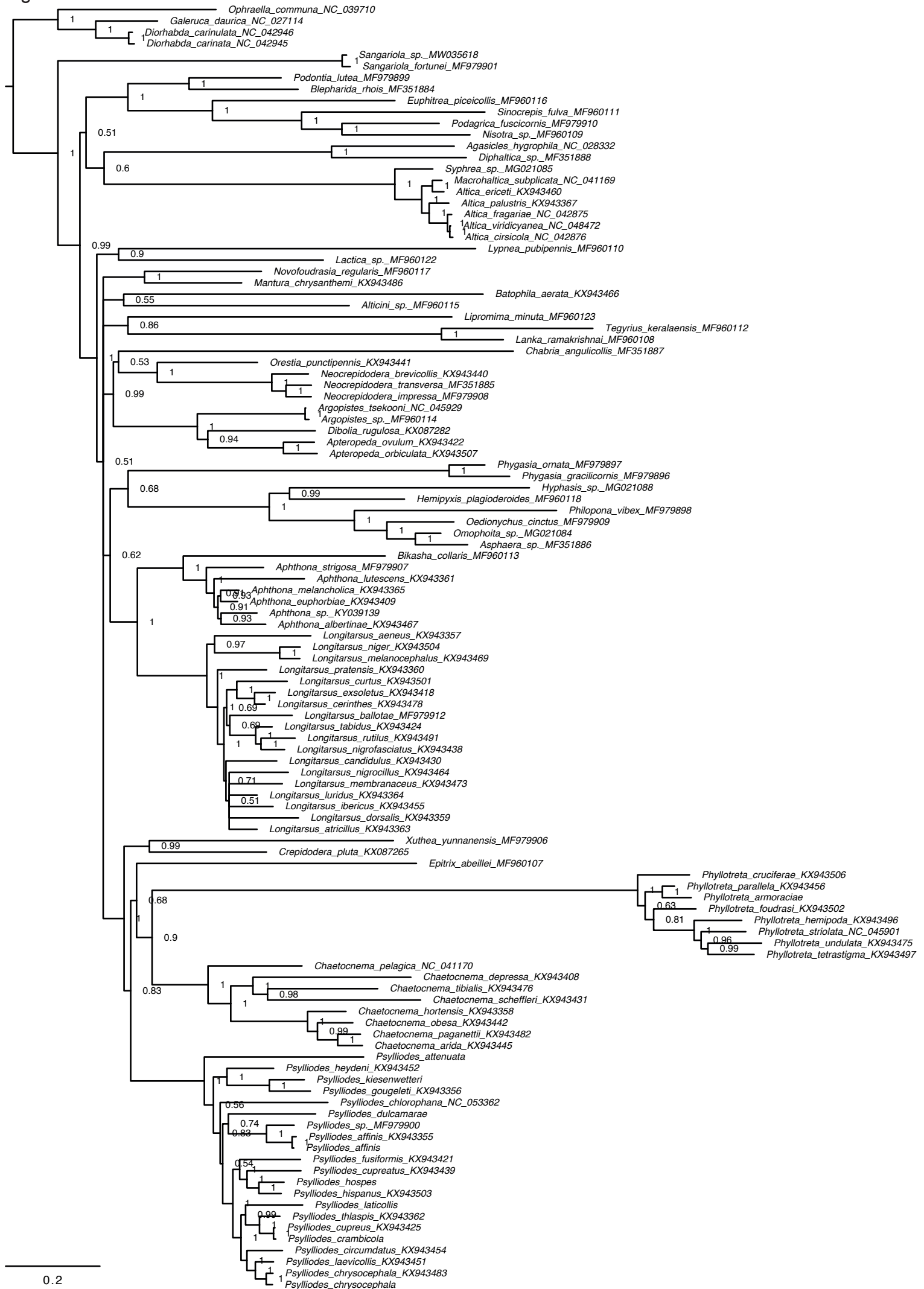


Figure S4



0.2

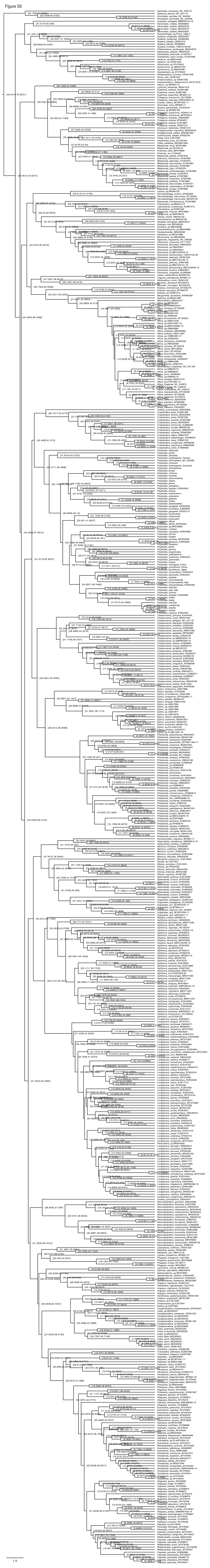


Figure S5