Supplementary figures

Figure S1. Tree reconstruction results of the 71 taxa mitogenome data set. Maximum likelihood tree inferred from combined nucleotide sequences of 13 PCGs and two rRNA genes using IQ-TREE. Node numbers show bootstrap support values.

Figure S2. Tree reconstruction results of the 71 taxa mitogenome data set. Maximum likelihood tree inferred from combined amino acid sequences of 13 PCGs and two rRNA genes using IQ-TREE. Node numbers show bootstrap support values.

Figure S3. Tree reconstruction results of the 71 taxa mitogenome data set. Bayesian Inference tree inferred from combined nucleotide sequences of 13 PCGs and two rRNA genes using PhyloBayes. Node numbers show posterior probability values.

Figure S4. Tree reconstruction results of the 71 taxa mitogenome data set. Bayesian Inference tree inferred from combined amino acid sequences of 13 PCGs and two rRNA genes using PhyloBayes. Node numbers show posterior probability values.

Figure S1

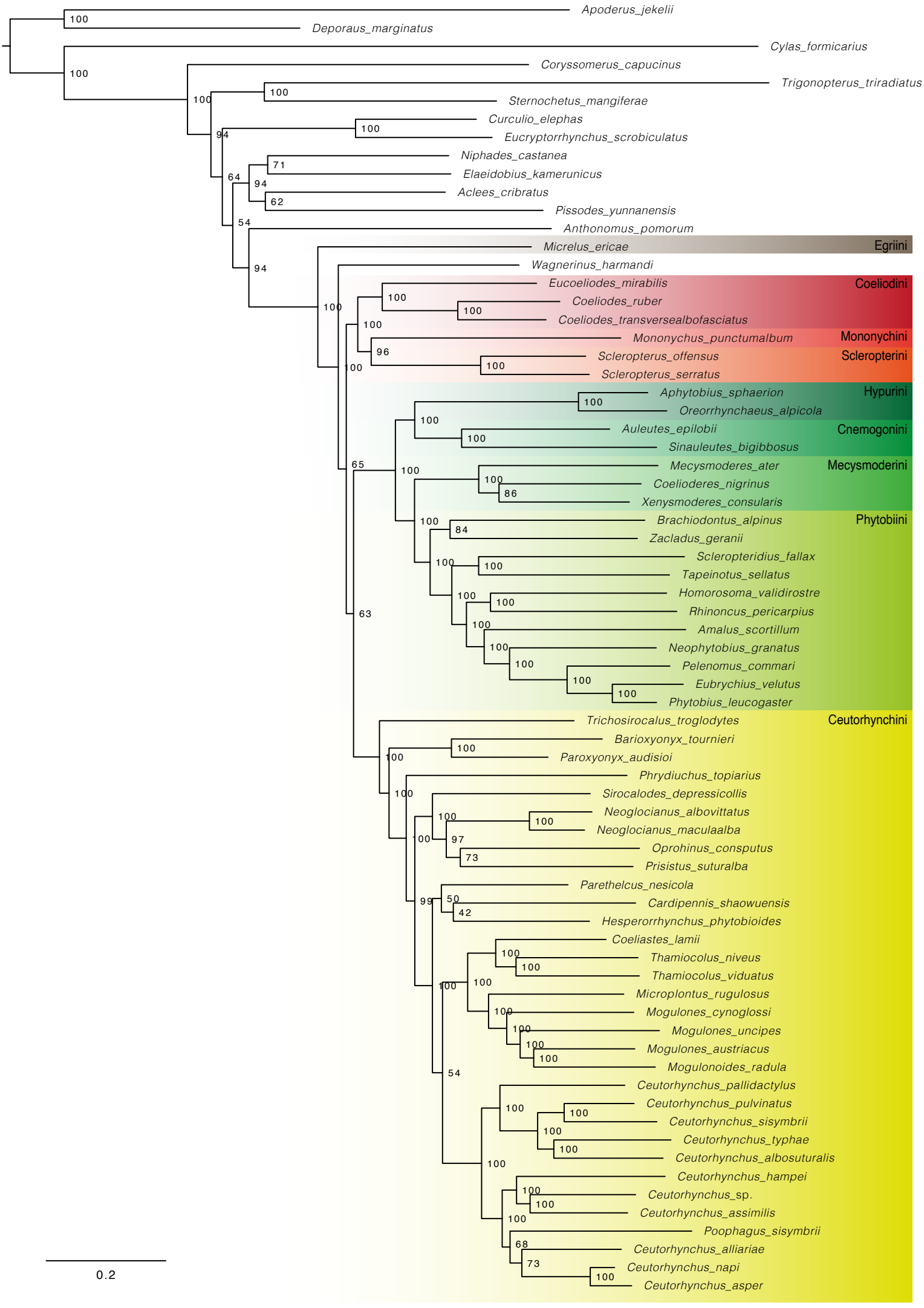
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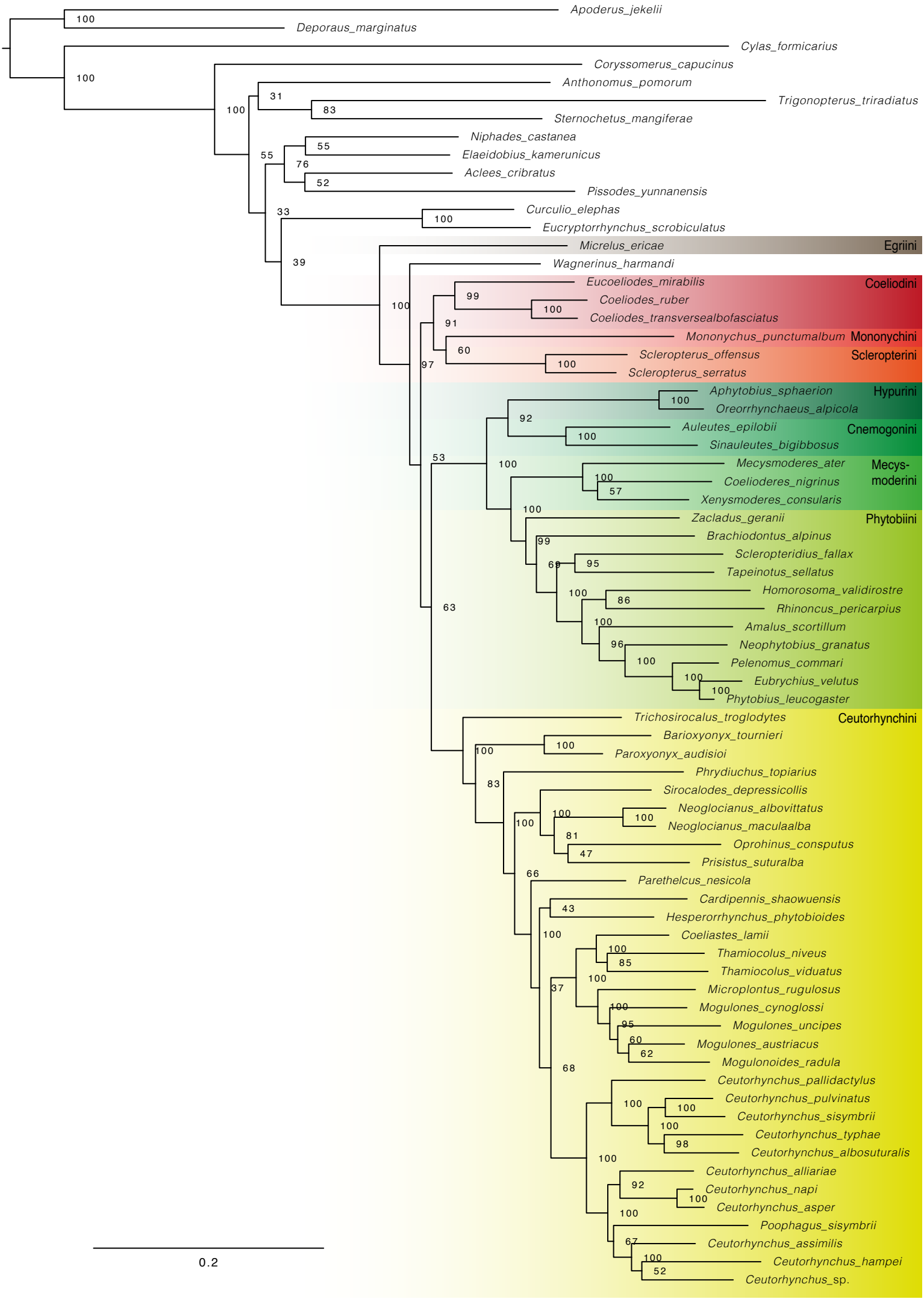
Figure S2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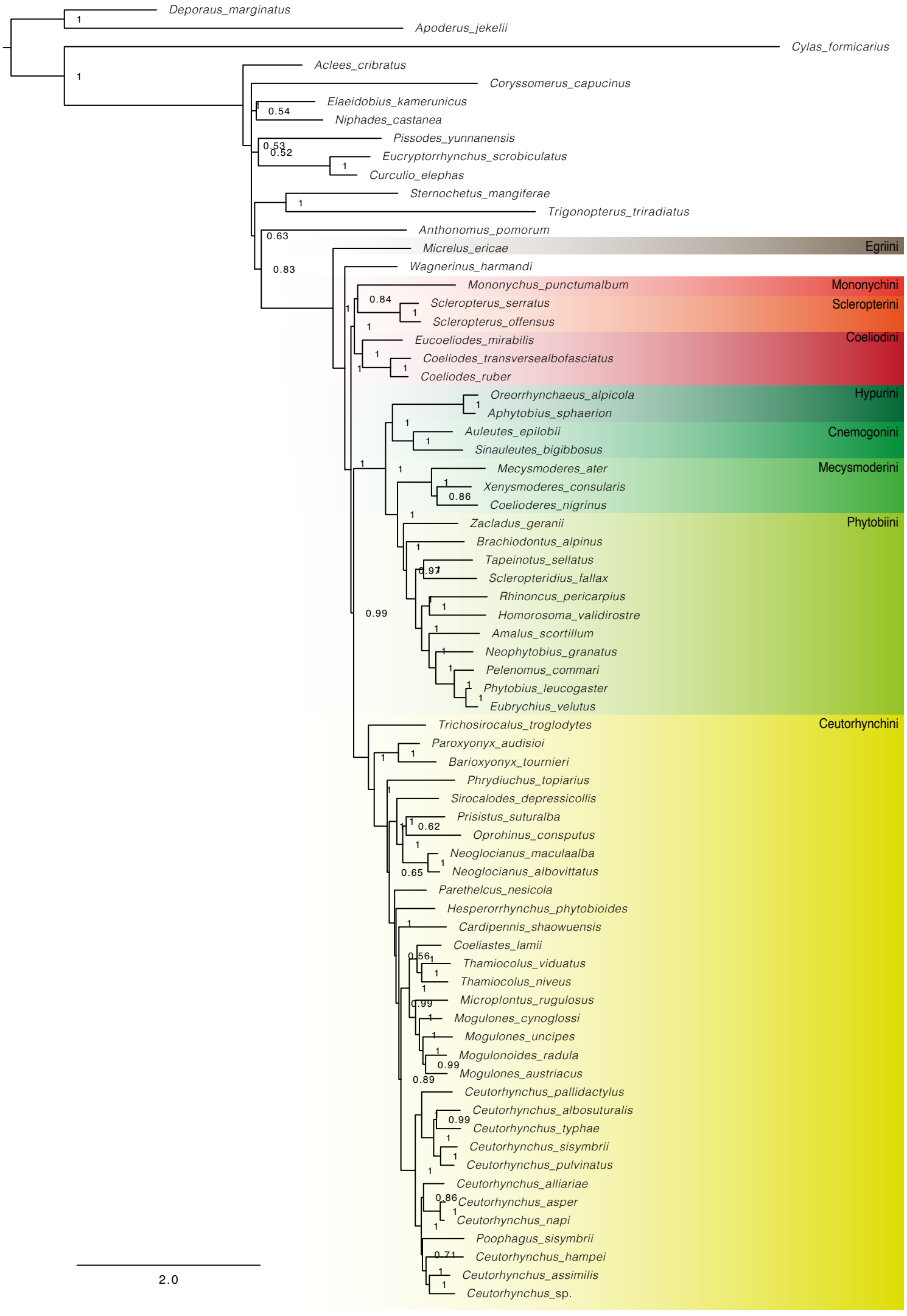
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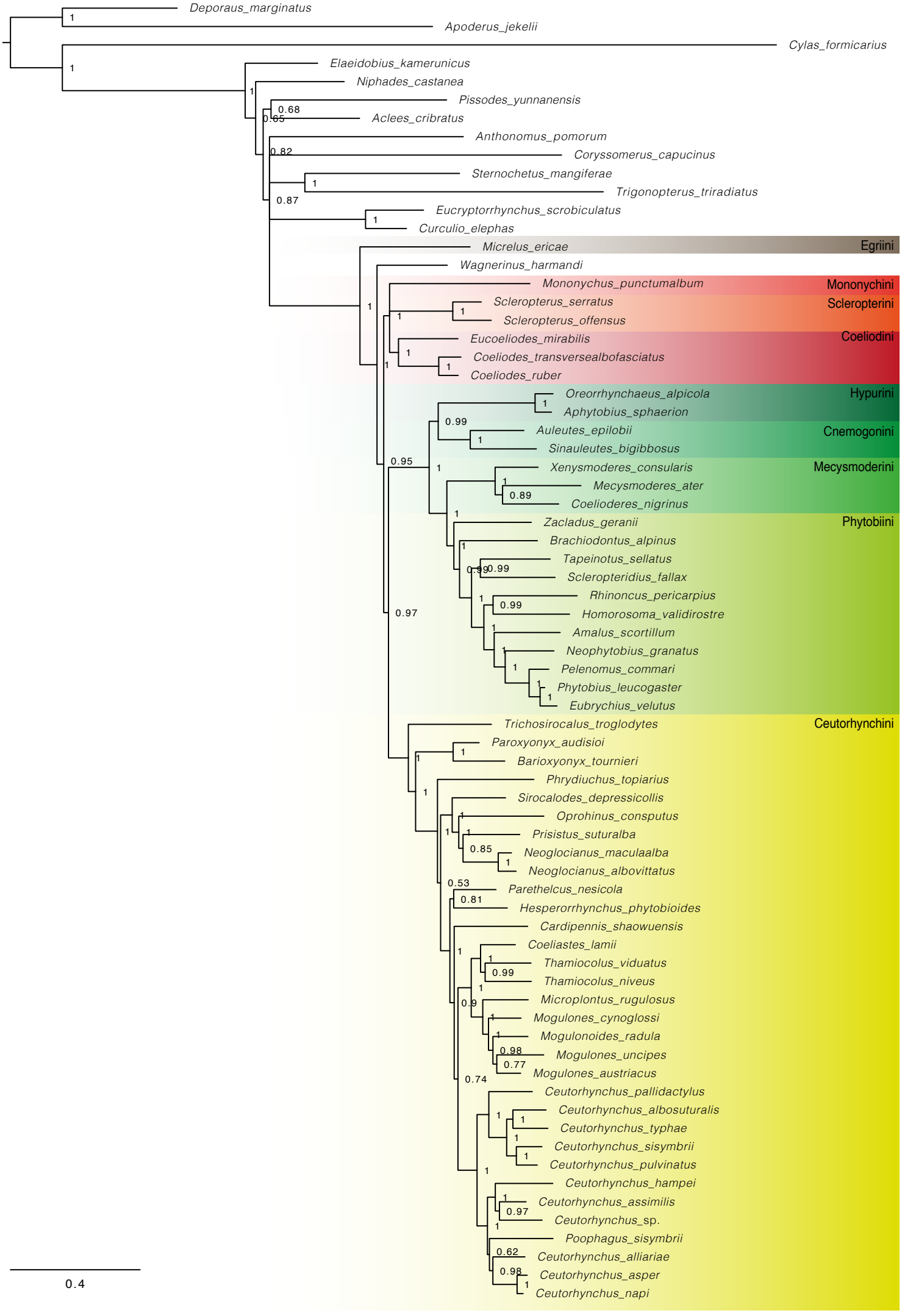
2.0

Figure S4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