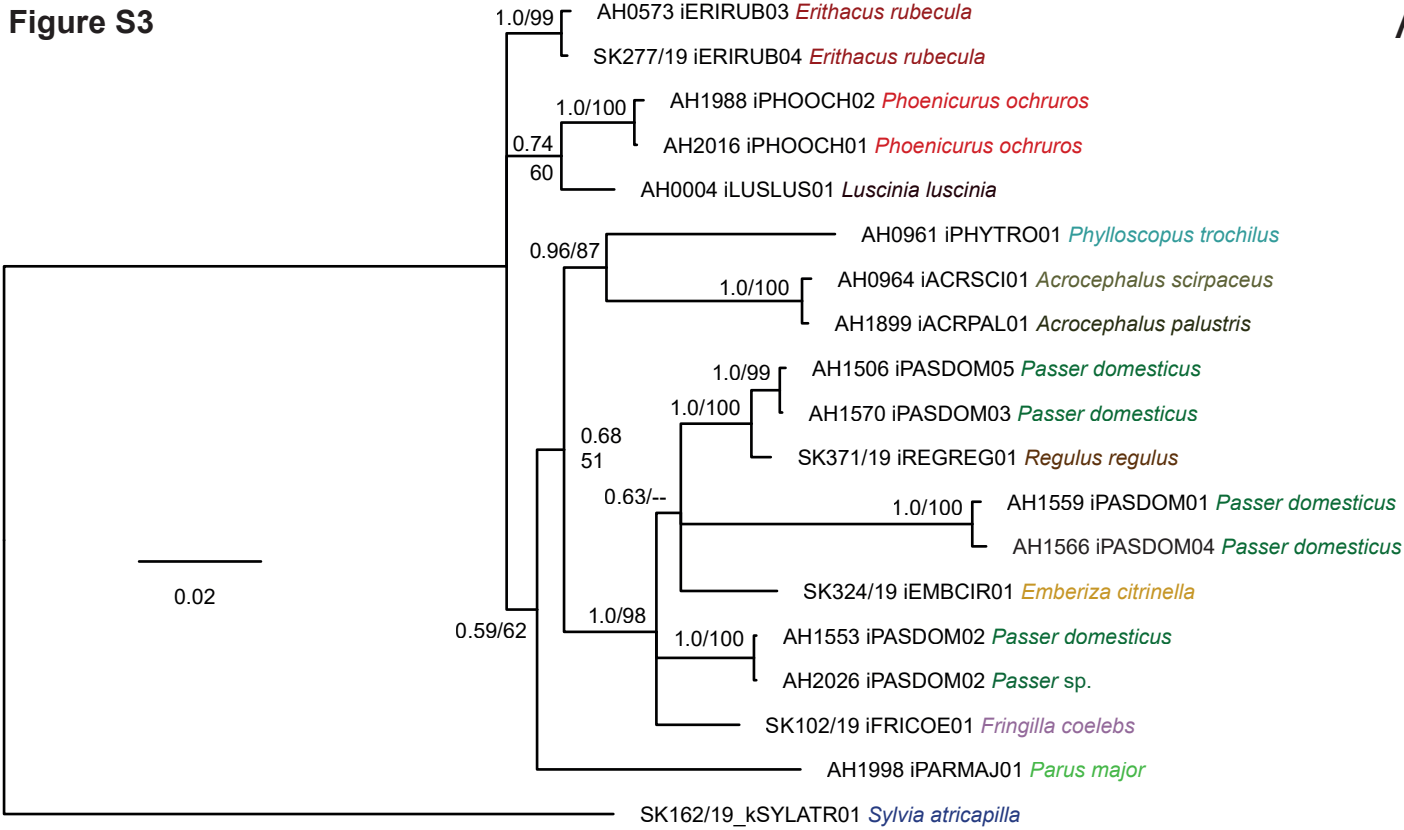
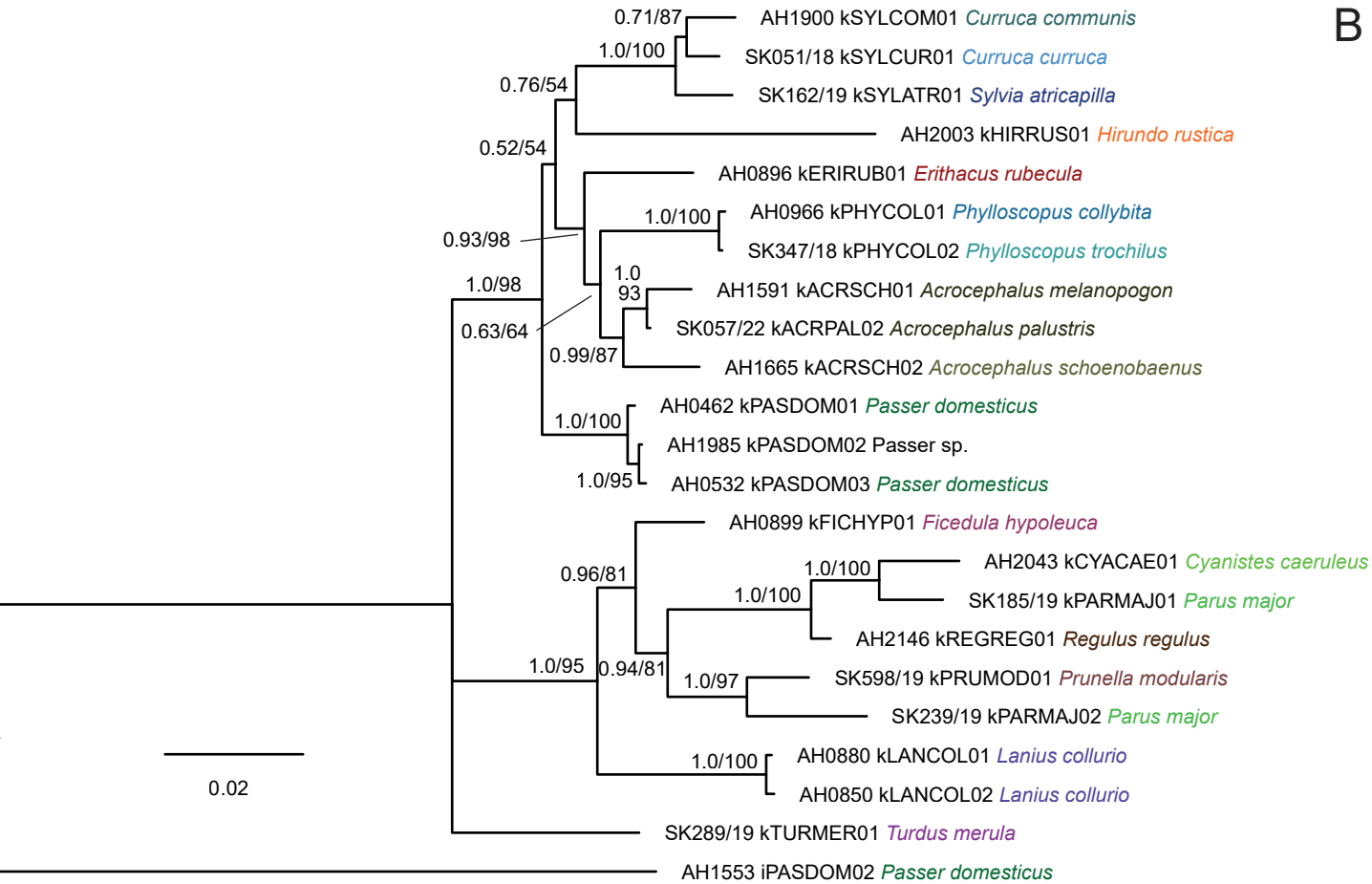


Figure S3



Bayesian Inference tree of partial concatenated *Isospora* COI (860 bp) and *CytB* (827 bp) sequences. Posterior probabilities and maximum likelihood bootstrap values are indicated at all nodes. The scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied. A sequence of *Lankesterella* sp. kSYLATR01 was included as outgroup.



Bayesian Inference tree of partial concatenated *Lankesterella* COI (860 bp) and *CytB* (827 bp) sequences. Posterior probabilities and maximum likelihood bootstrap values are indicated at all nodes. The scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied. A sequence of *Isospora* sp. iPASDOM02 was included as outgroup.