

Supplementary materials

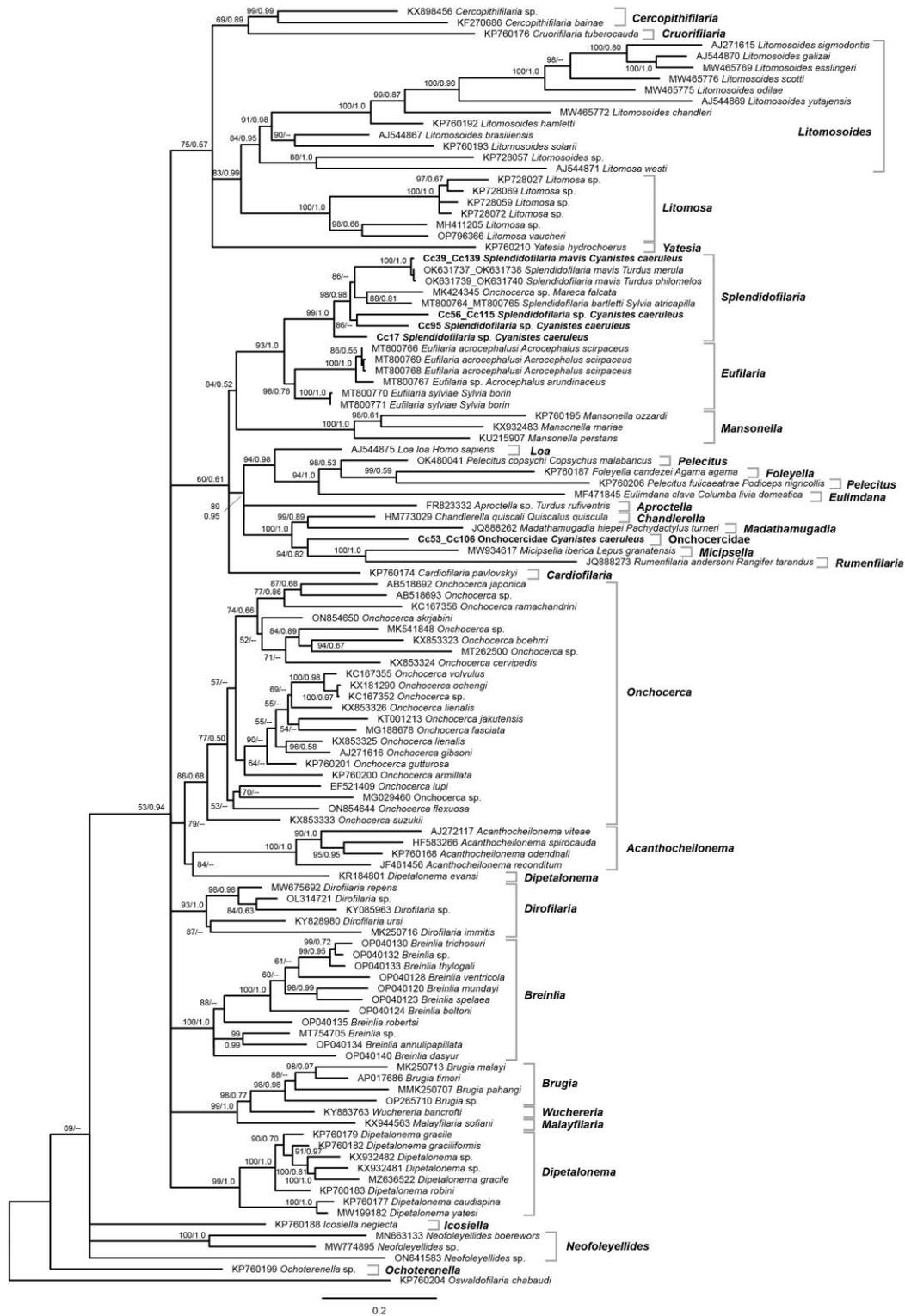


Figure S1: Clades of maximum likelihood tree based on a 600 pb section of the COI gene, including representatives of all Onchocercidae species. Maximum likelihood bootstrap values and Bayesian posterior probabilities are indicated at all nodes. The scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied.