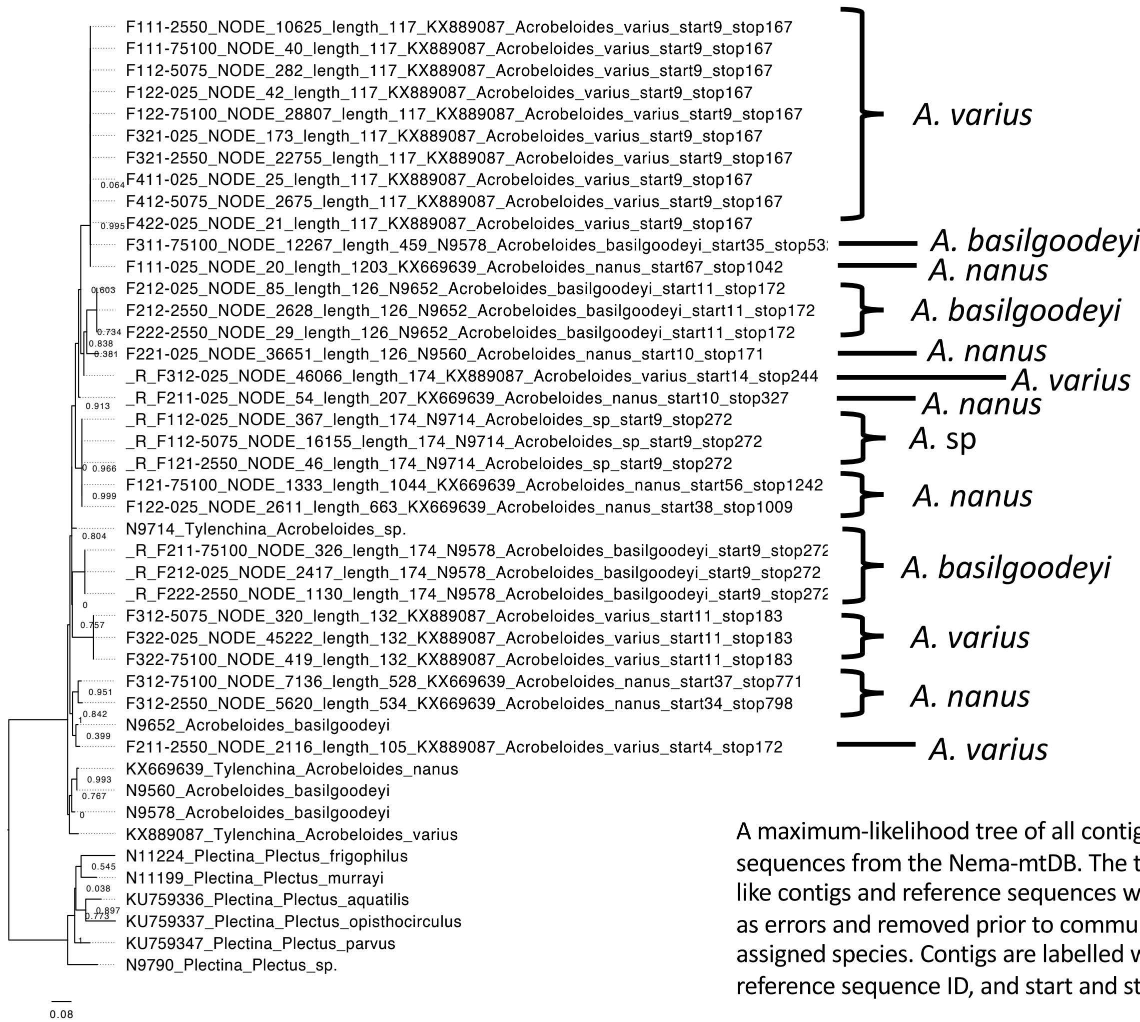
Supplemental Material 10

Supplemental Information Figure 4: *Acrobeloides* COX1 Maximum-Likelihood Tree



A maximum-likelihood tree of all contigs identified as belonging to the genus *Acrobeloides*, along with their reference sequences from the Nema-mtDB. The tree is rooted using *Plectus* COX1 sequences as the outgroup. Clustering with like contigs and reference sequences were used for haplotype detection and poorly aligned contigs were considered as errors and removed prior to community analyses. Clusters are outlined with brackets and labelled with the assigned species. Contigs are labelled with sample ID, assembled contig node ID, reference sequence match length, reference sequence ID, and start and stop positions within the reference sequence.