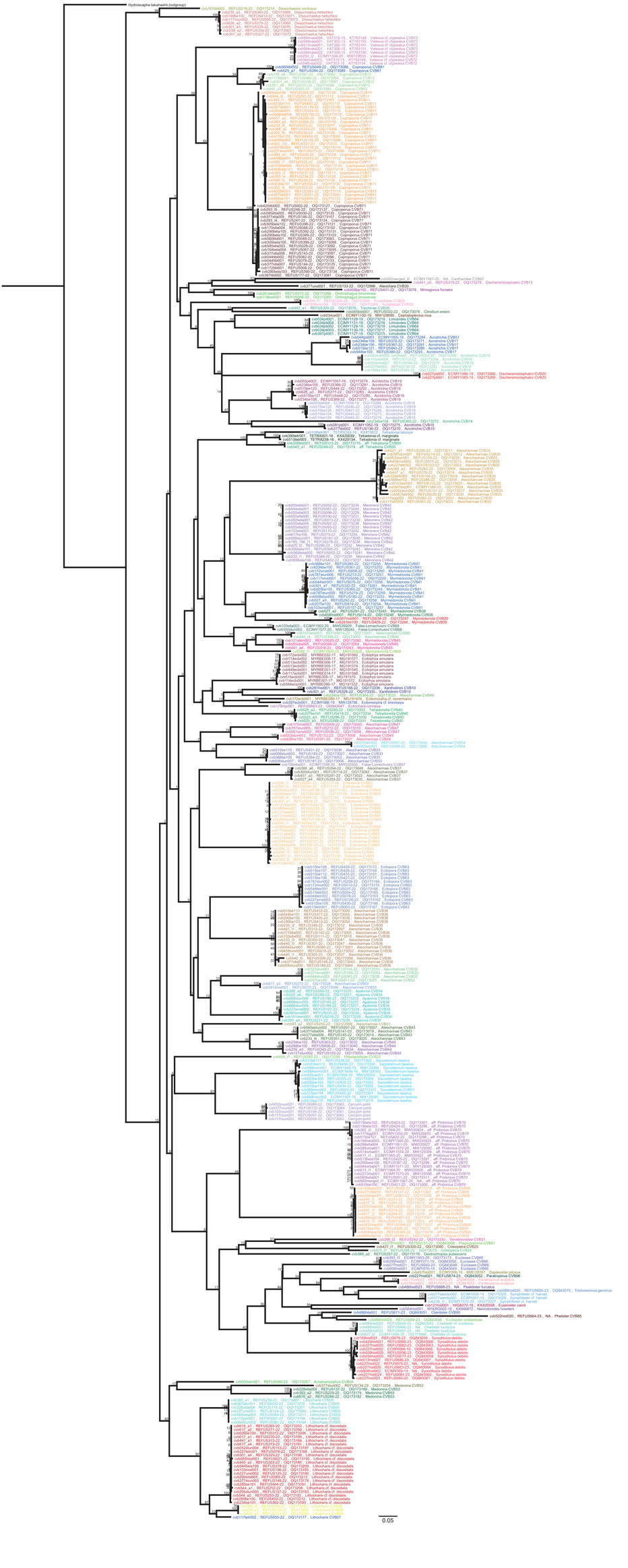
Appendix 3. RAxML tree based on GTR GAMMA as substitution model of 414 *COI* sequences of refuse-visiting beetles. We used the RAxML plugin for GENEIOUS PRIME (version 2020.2.1) to generate the tree. Terminal labels provide the following information: sample ID, BOLD Process ID, GenBank accession number, species name. The RAxML tree was rooted using the following outgroup: *Hydroscapha takahashii* (GenBank accession number: MT132896), a beetle of the suborder Myxophaga. The scale bar indicates expected nucleotide substitutions per site as inferred by the RAxML algorithm. Bootstrap support values are shown at nodes (1,000 repetitions). Colors highlight the different species.



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