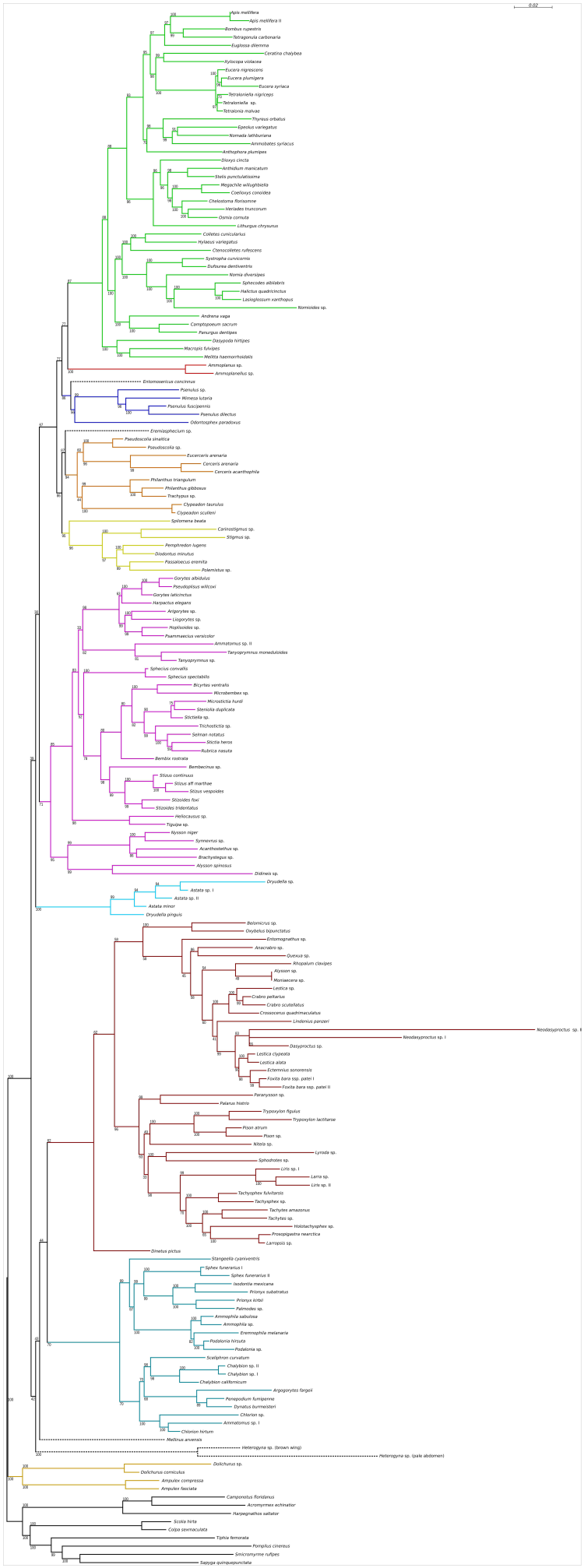

Figure S5: Best ML phylogenetic tree inferred from re-analysing the concatenated nucleotide dataset with 1st and 2nd codon positions included (sm-nt12). The phylogenetic tree was inferred from analysing 192,220 nucleotide sites comprising 194 single-copy genes with IQTree. The data matrix was analysed with partition-specific substitution models selected by IQTree. Bootstrap convergence was achieved after 200 bootstrap replicates. Taxa are colour-coded according to their potential taxonomic grouping.