



**Figure S6:** Best ML phylogenetic tree inferred from re-analysing the concatenated nucleotide dataset with all codon positions included (sm-nt123). The phylogenetic tree was inferred from analysing 288,330 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 100 bootstrap replicates. Taxa are colour-coded according to their potential taxonomic grouping.