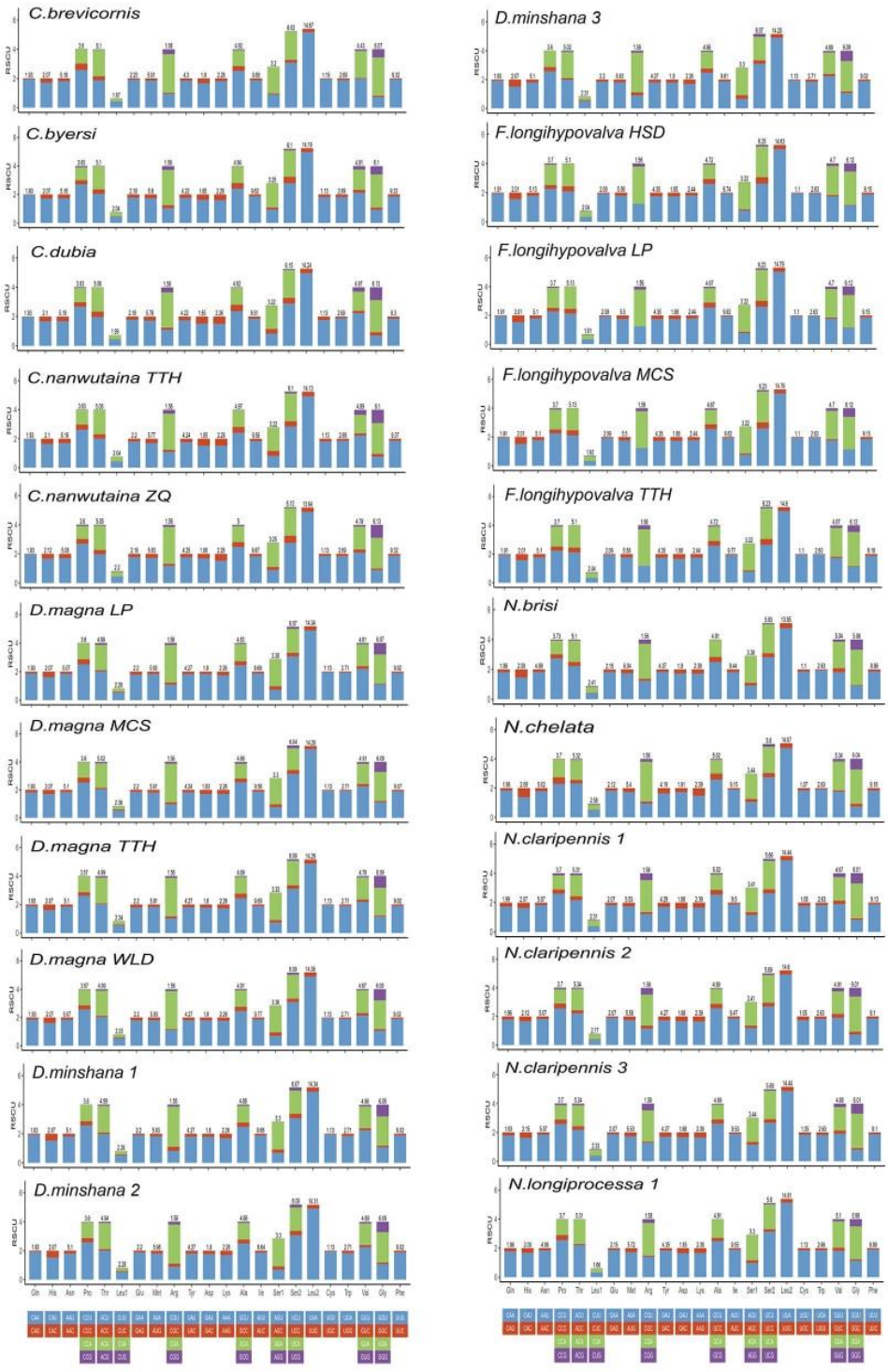

Figure S1. Relative synonymous codon usage (RSCU) of Panorpidae mitogenomes.

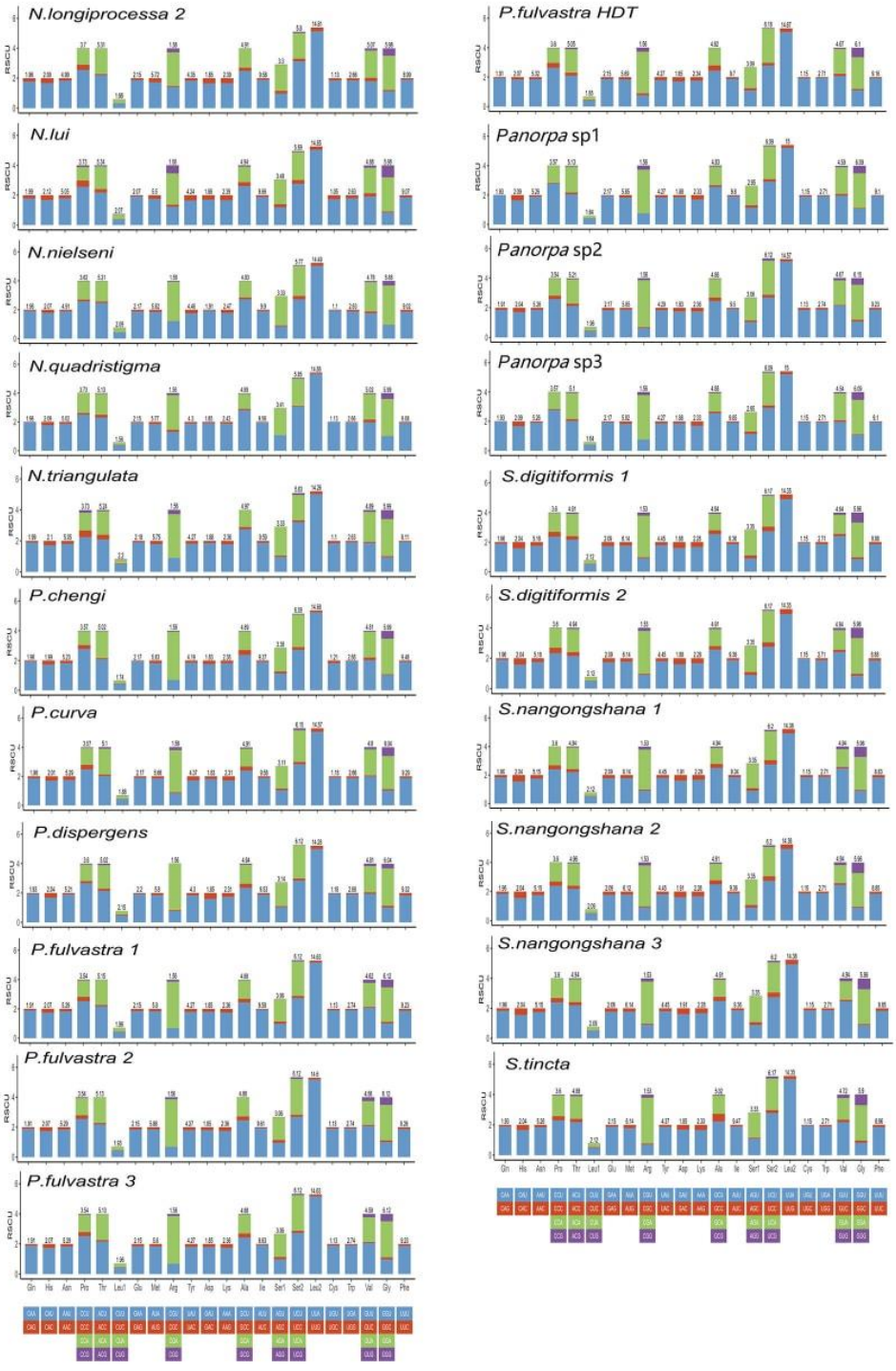

Figure S2. Relative synonymous codon usage (RSCU) of Panorpidae mitogenomes.

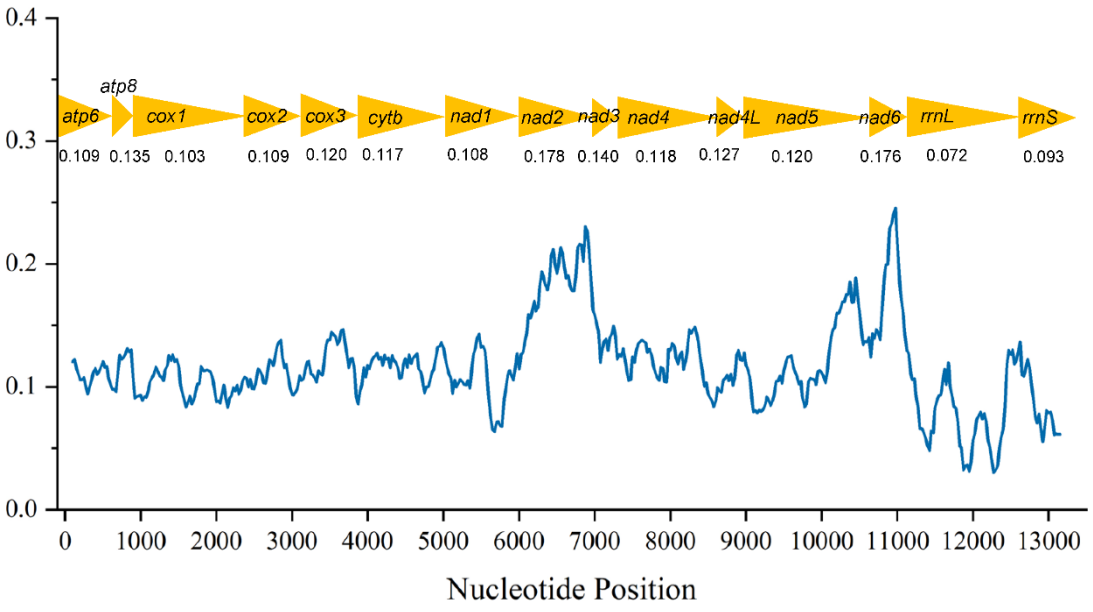

Figure S3. Sliding window analysis of 13 PCGs and two rRNAs. The blue curve shows the value of nucleotide diversity (π). π value of each PCG was shown above the arrows.

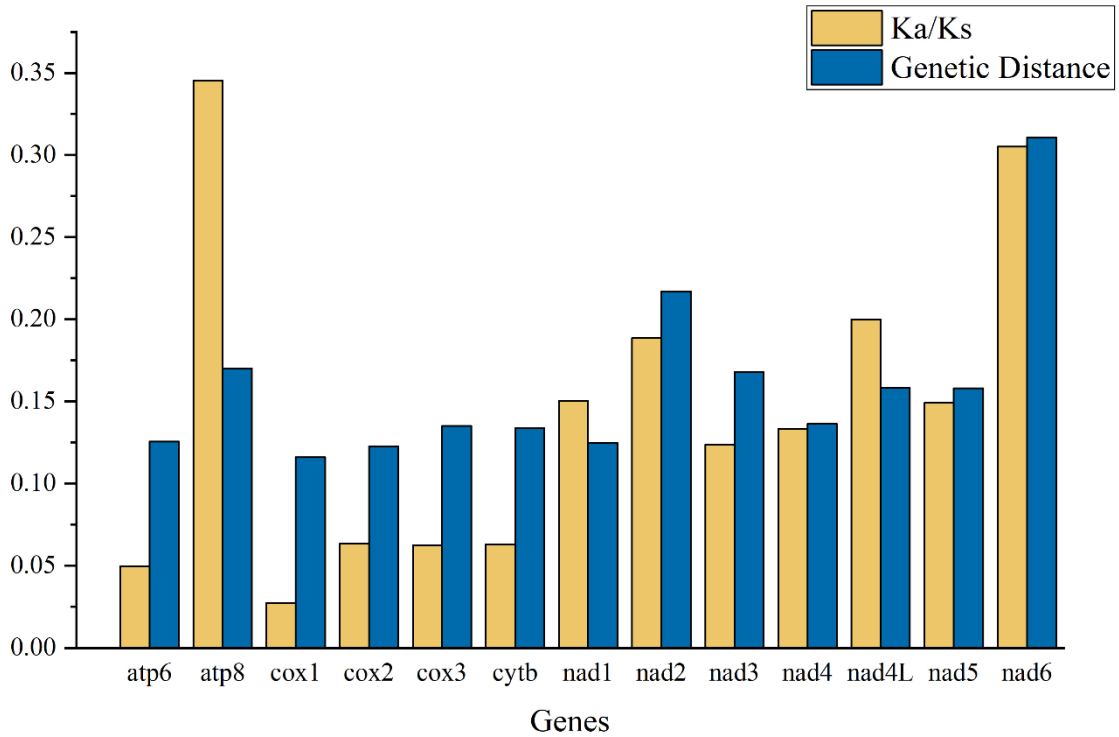

Figure S4. Evolutionary rates and selection pressures among 48 mitogenomes of Panorpidae. Genetic distance and ratio of non-synonymous (Ka) to synonymous (Ks) substitution rates of each protein-coding gene.

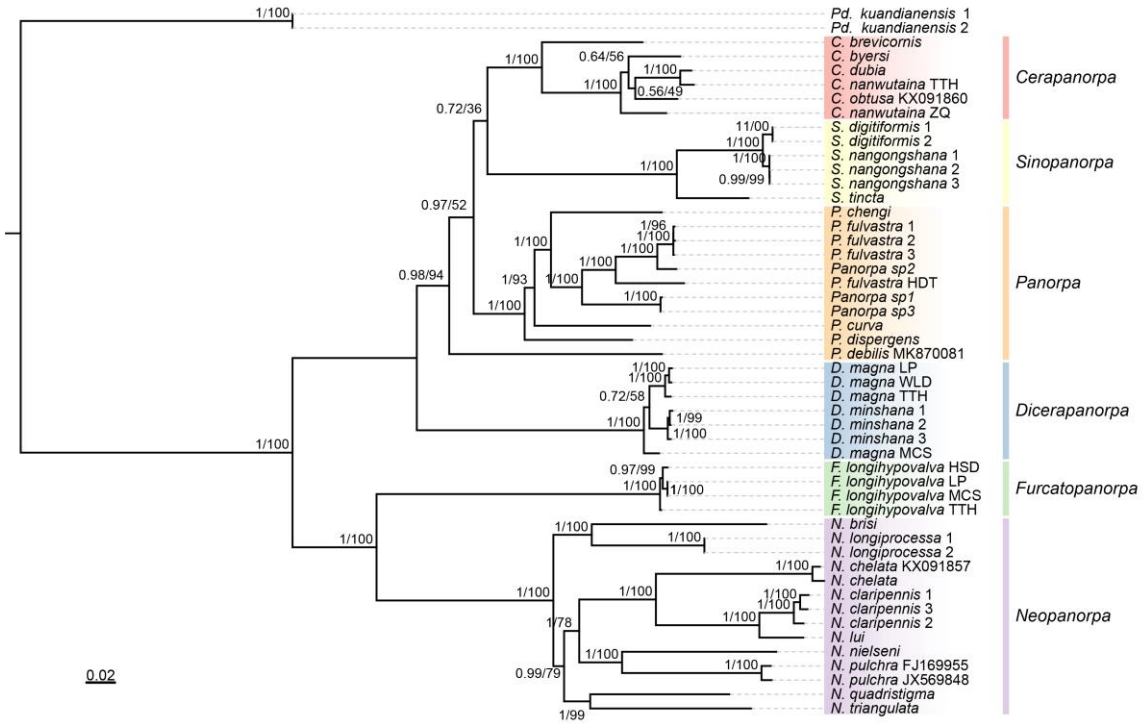

Figure S5. Phylogenetic tree generated by Bayesian inference and maximum likelihood based on the dataset of PCG. Numerals at nodes are Bayesian posterior probabilities (PP) and bootstrap support values (BS).

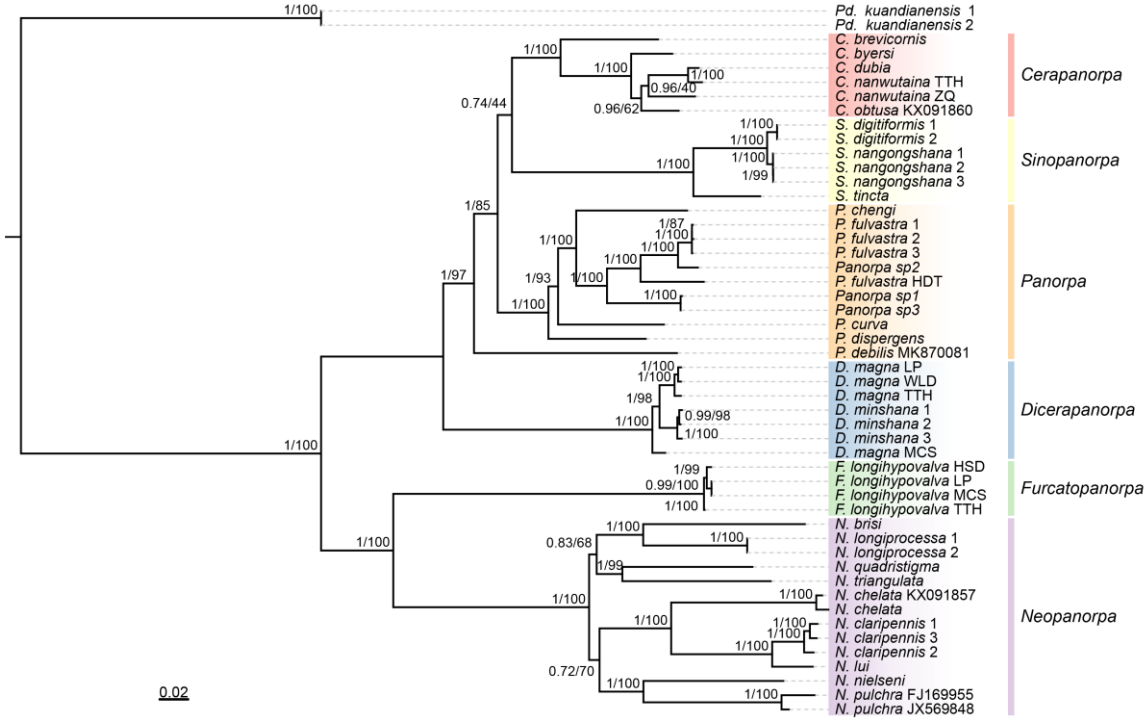

Figure S6. Phylogenetic tree generated by Bayesian inference and maximum likelihood based on the dataset of PCG + R + T. Numerals at nodes are Bayesian posterior probabilities (PP) and bootstrap support values (BS).

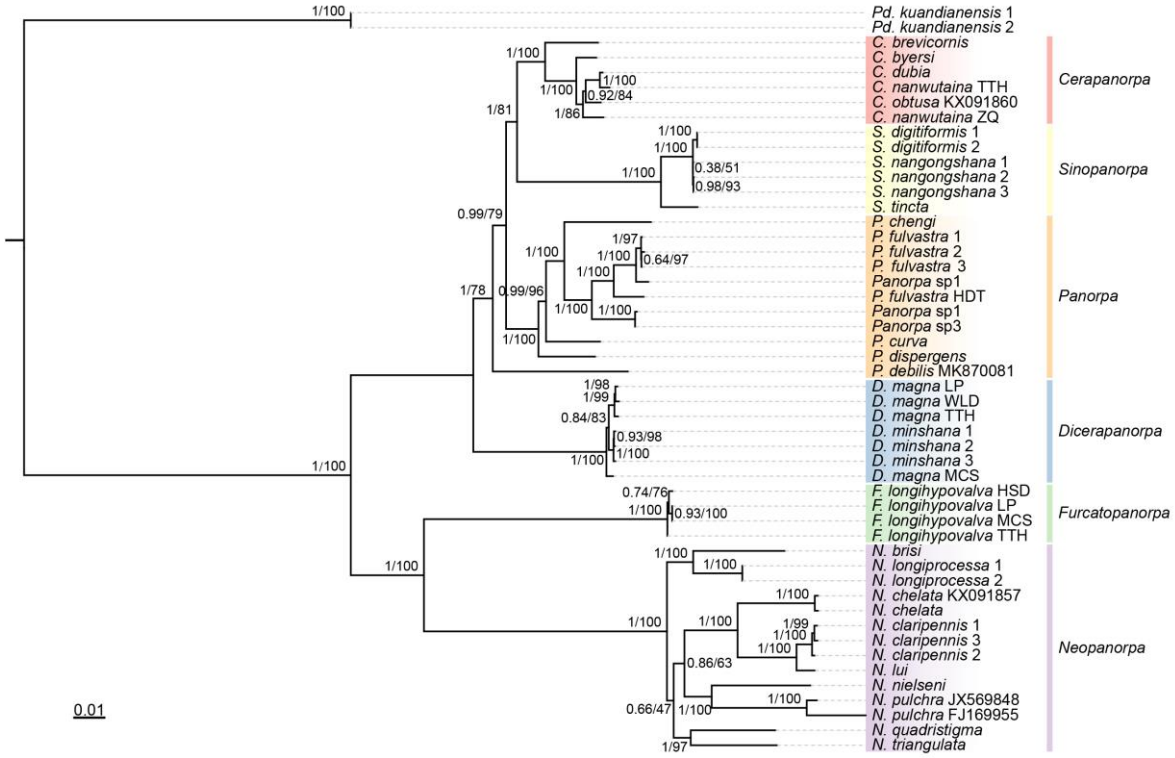

Figure S7. Phylogenetic tree generated by Bayesian inference and maximum likelihood based on the dataset of PCG12 + R. Numerals at nodes are Bayesian posterior probabilities (PP) and bootstrap support values (BS).

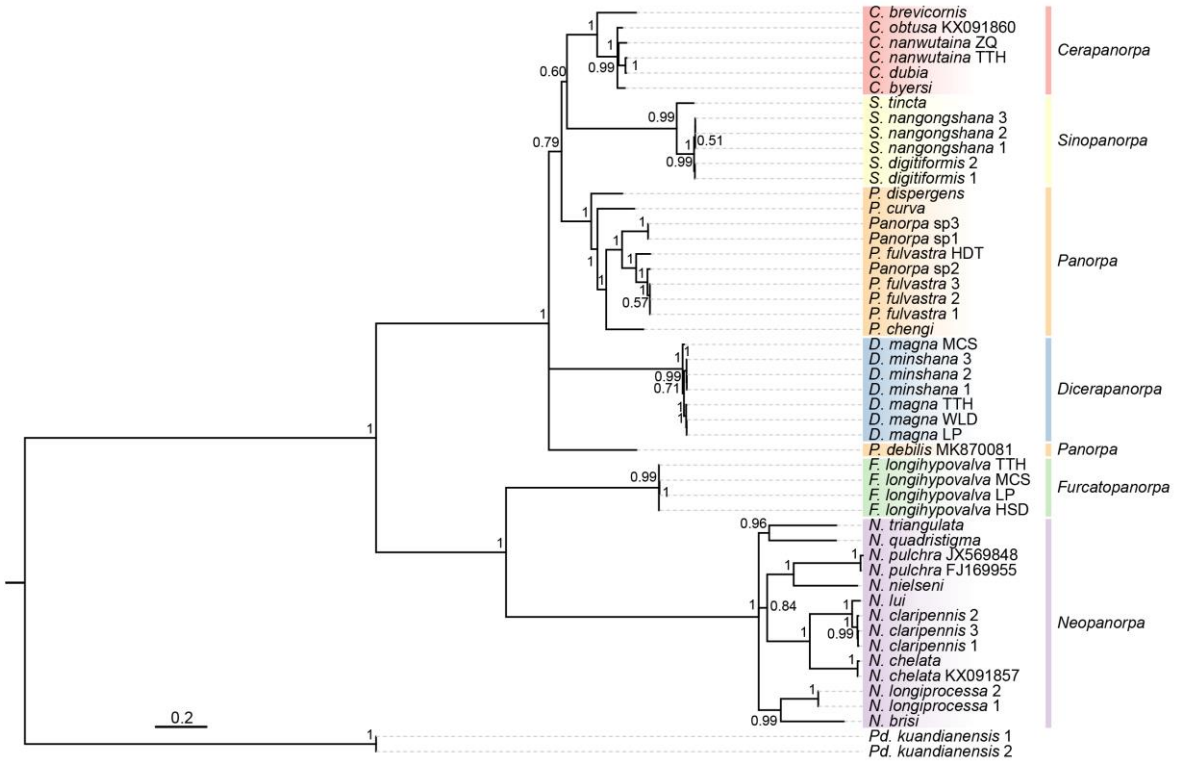

Figure S8. Bayesian inference tree generated by Phylobayes with CAT-GTR model based on the dataset of PCG. Numerals at nodes are Bayesian posterior probabilities (PP).

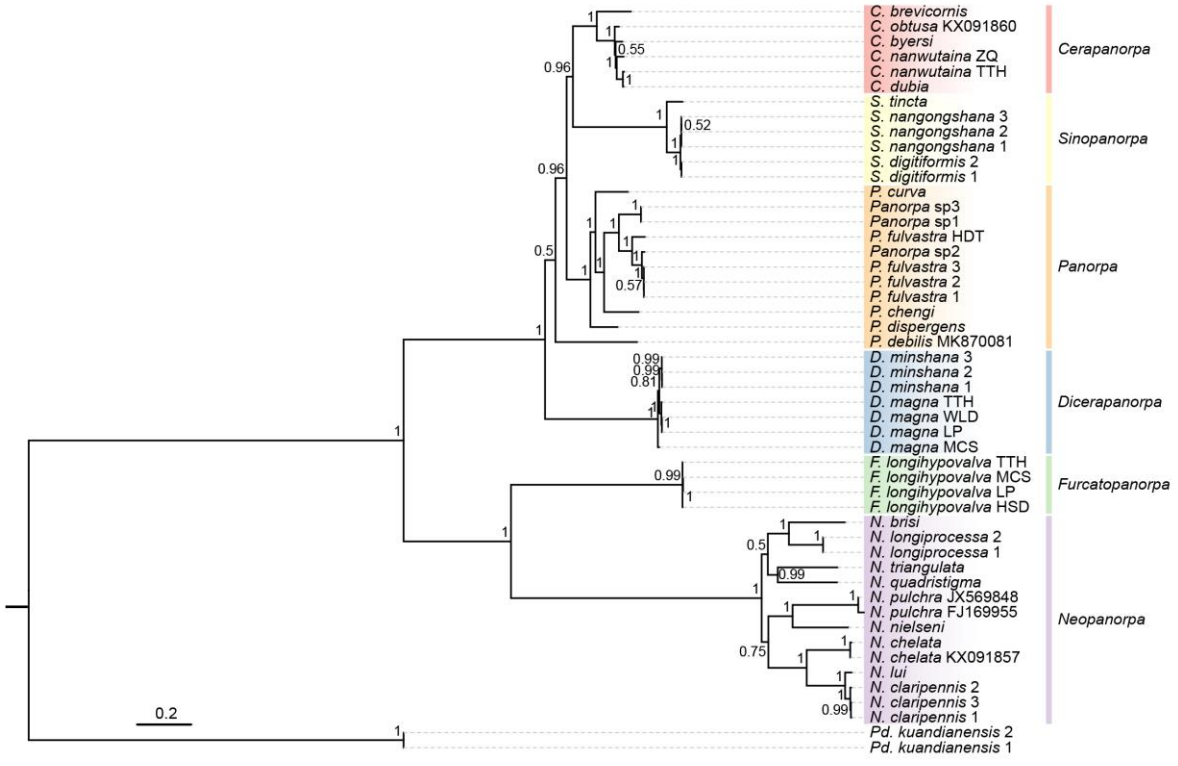

Figure S9. Bayesian inference tree generated by Phylobayes with CAT-GTR model based on the dataset of PCG + R. Numerals at nodes are Bayesian posterior probabilities (PP).

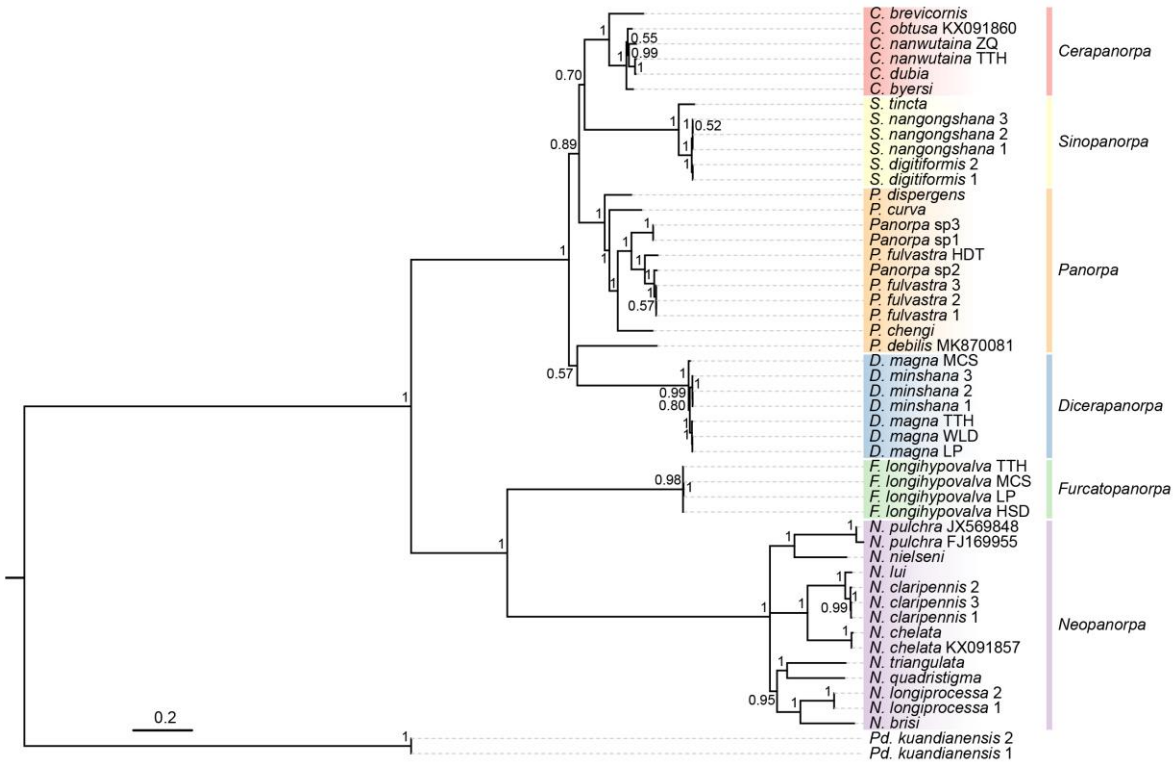

Figure S10. Bayesian inference tree generated by Phylobayes with CAT-GTR model based on the dataset of PCG + R + T. Numerals at nodes are Bayesian posterior probabilities (PP).

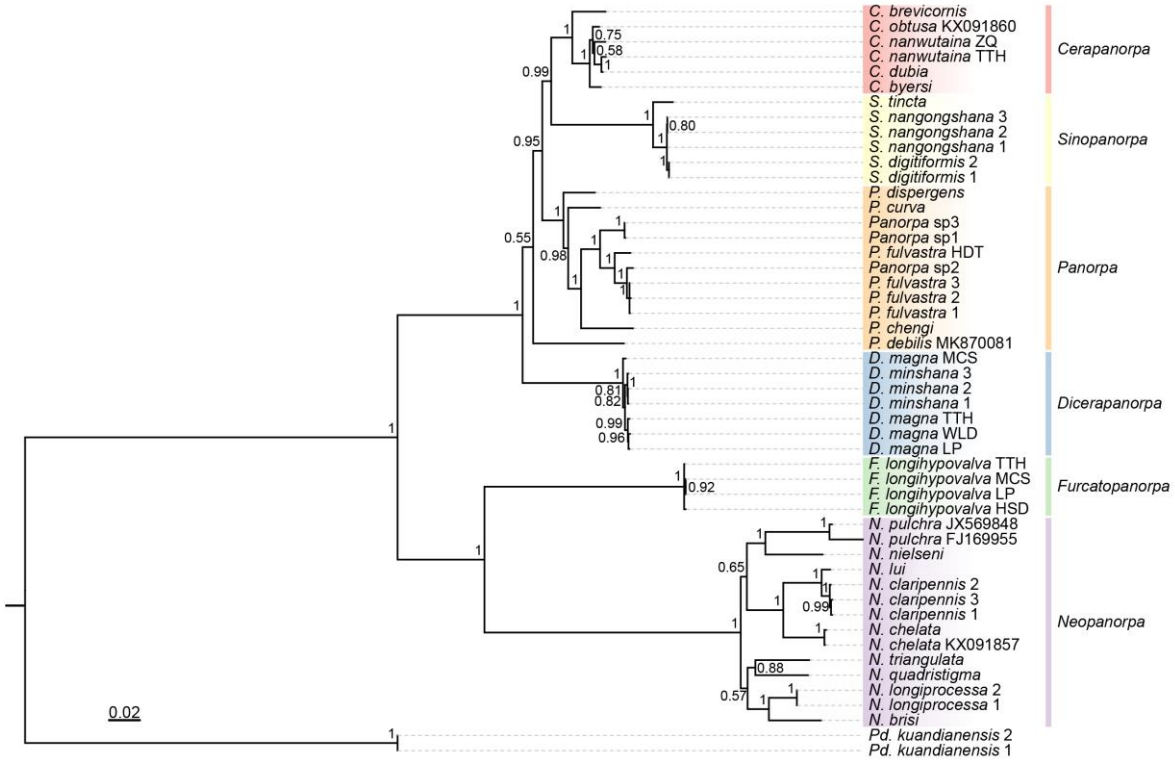

Figure S11. Bayesian inference tree generated by Phylobayes with CAT-GTR model based on the dataset of PCG12 + R. Numerals at nodes are Bayesian posterior probabilities (PP).