

SUPPLEMENTARY FIGURES

Combining molecular data sets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of Stoneflies (Insecta: Plecoptera)

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Fig. S1: Results of the super tree reconstruction analyses of the transcriptomic single gene tree data sets using “Matrix representation with Parsimony” (MRP). a) 278 gene trees data set, b) 389 gene trees data set, c) 1764 gene trees data set, d) 2997 gene trees data set.

Fig. S2: Results of the super tree reconstruction analyses of the transcriptomic single gene tree data sets using FastRFS. a) 278 gene trees data set, b) 389 gene trees data set, c) 1764 gene trees data set, d) 2997 gene trees data set.

Fig. S3: Results of the ML tree reconstruction analyses of the concatenated transcriptomic data sets. a) 278 genes data set, b) 389 genes data set, c) 1764 genes data set, d) 2997 genes data set.

Fig. S4: Heat maps showing the results from pairwise comparison of species in the concatenated transcriptomic data sets using Bowker's test of symmetry. White boxes with p-values > 0.05 indicate that the corresponding species pair does not violate the assumption of global stationarity, reversibility, and homogeneity (SRH conditions). a) 278 genes data set, b) 389 genes data set, c) 1764 genes data set, d) 2997 genes data set.

Fig. S5: Results of the unconstrained best ML tree reconstruction analyses in IQ-TREE of the concatenated Sanger sequence data set.

Fig. S6: Results of the BEAST Bayesian Inference analyses, showing the relationships and divergence times of stoneflies.

Fig. S7: Results of net diversification rate over time estimations in Systellognatha and Euholognatha. Rates of the individual (super-)families were extracted by the rate-through-time approach with BAMMtools. Grey polygon denotes the 10% through 90% Bayesian credible regions on the distribution of rates as calculated in BAMM.

Fig. S1a

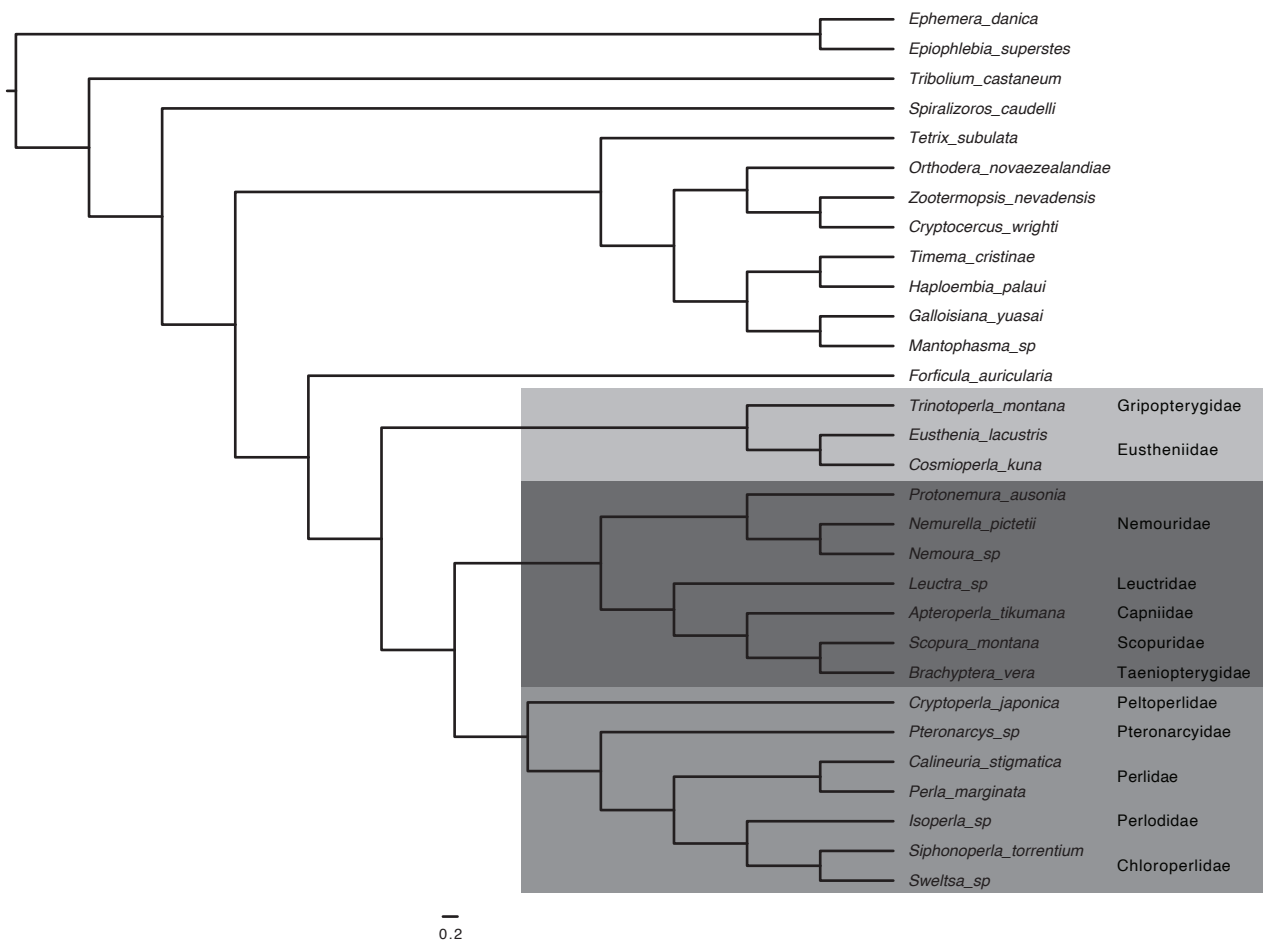


Fig. S1b

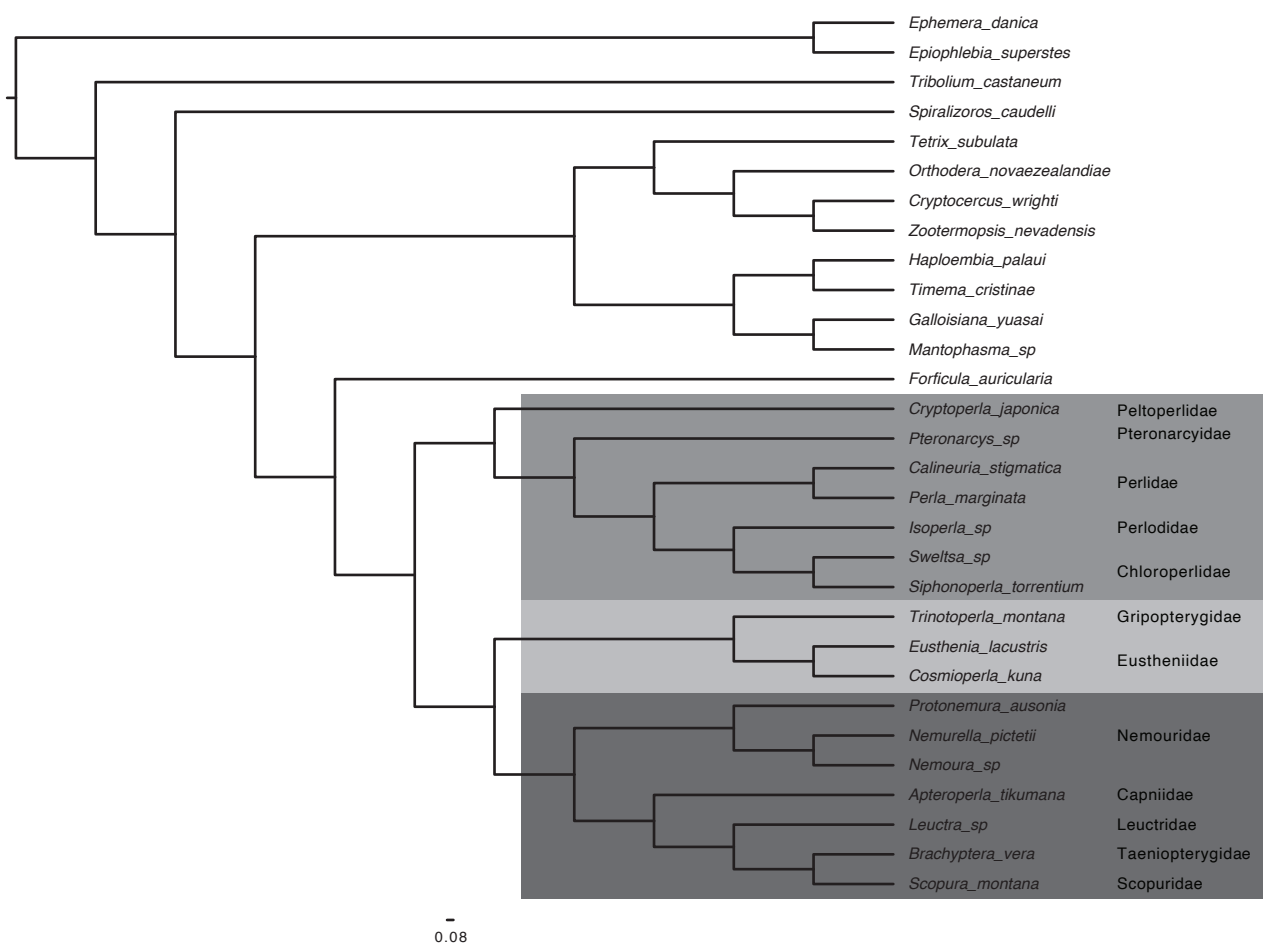


Fig. S1c

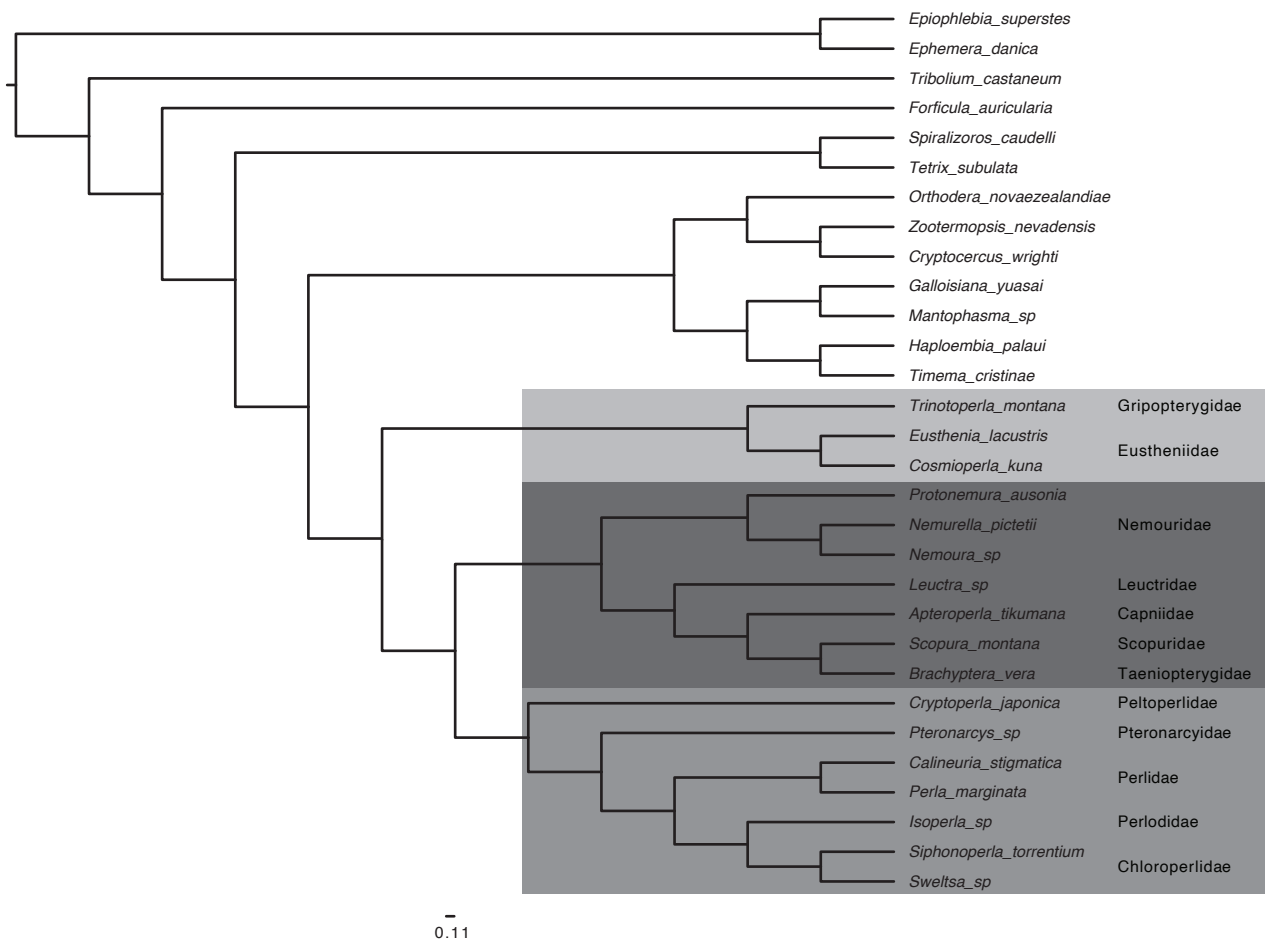


Fig. S1d

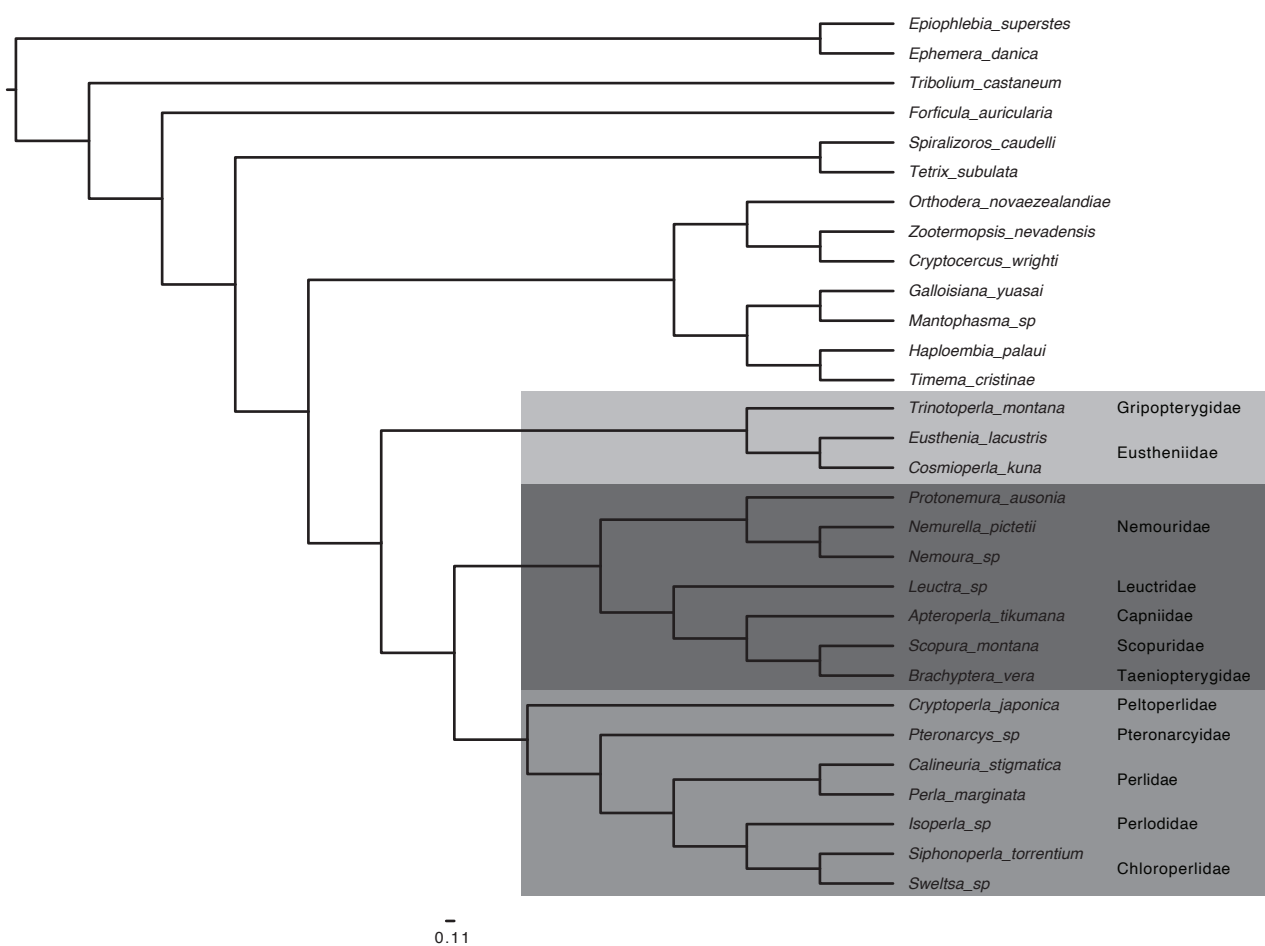


Fig. S2a

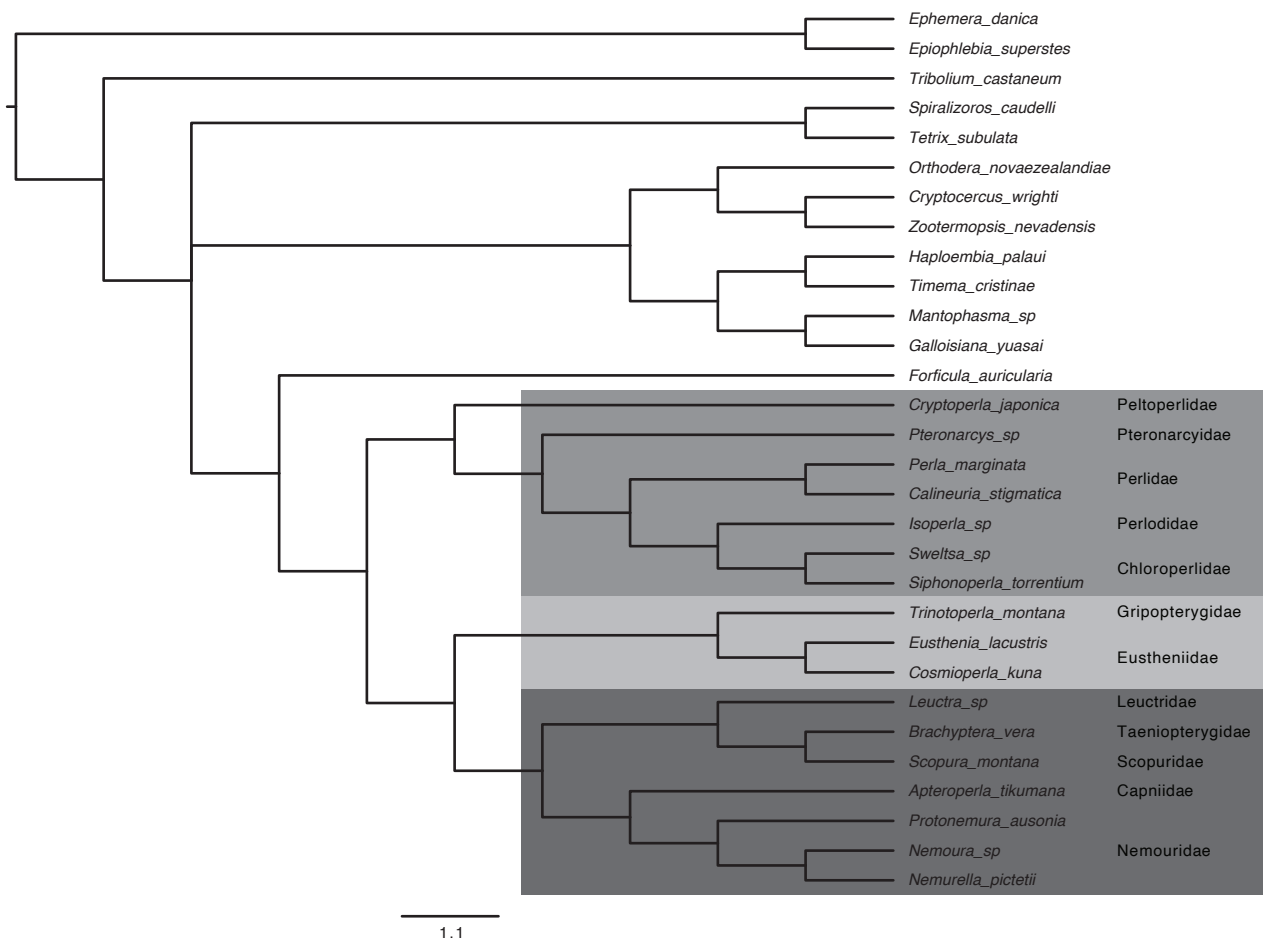


Fig. S2b

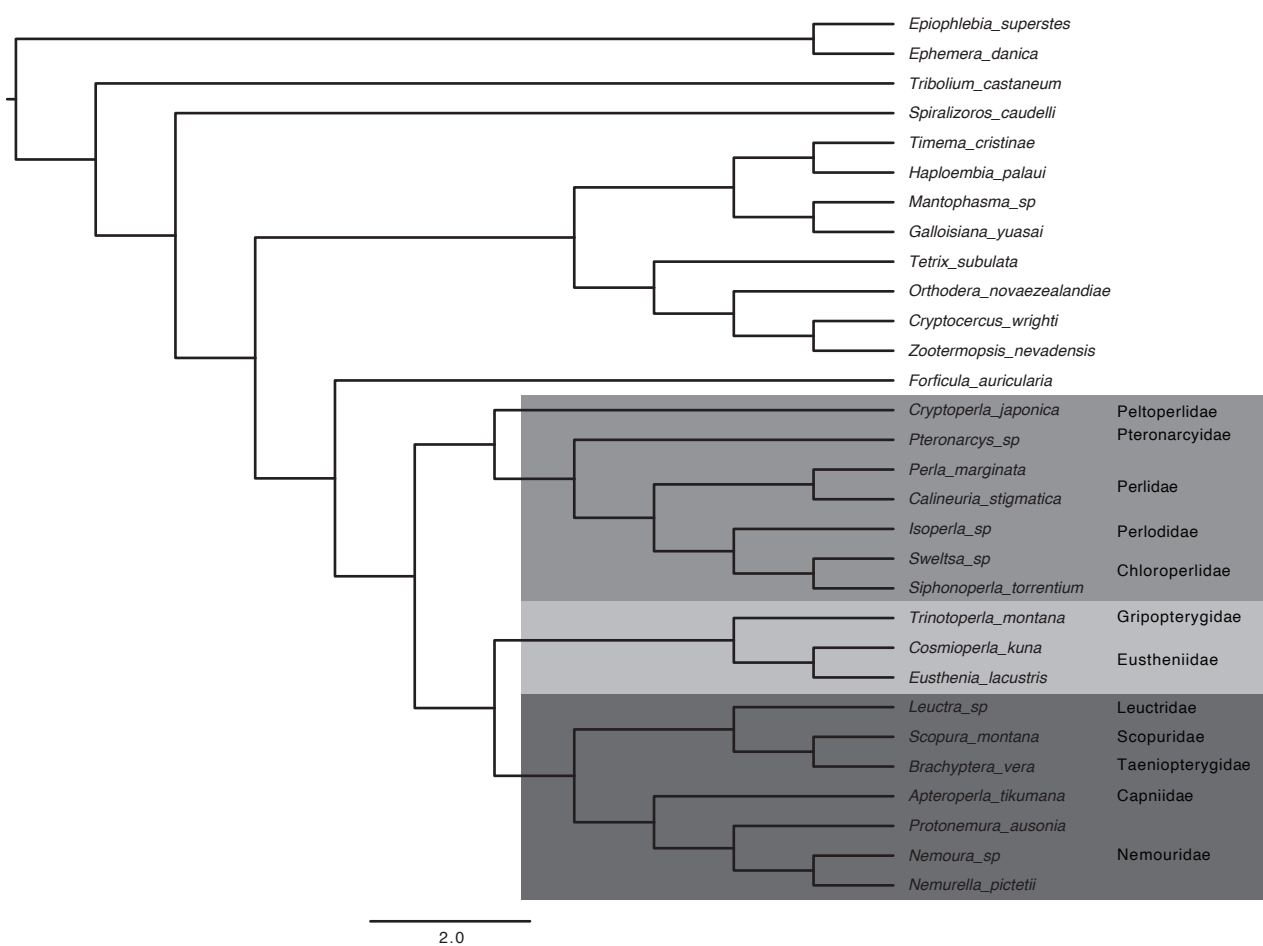


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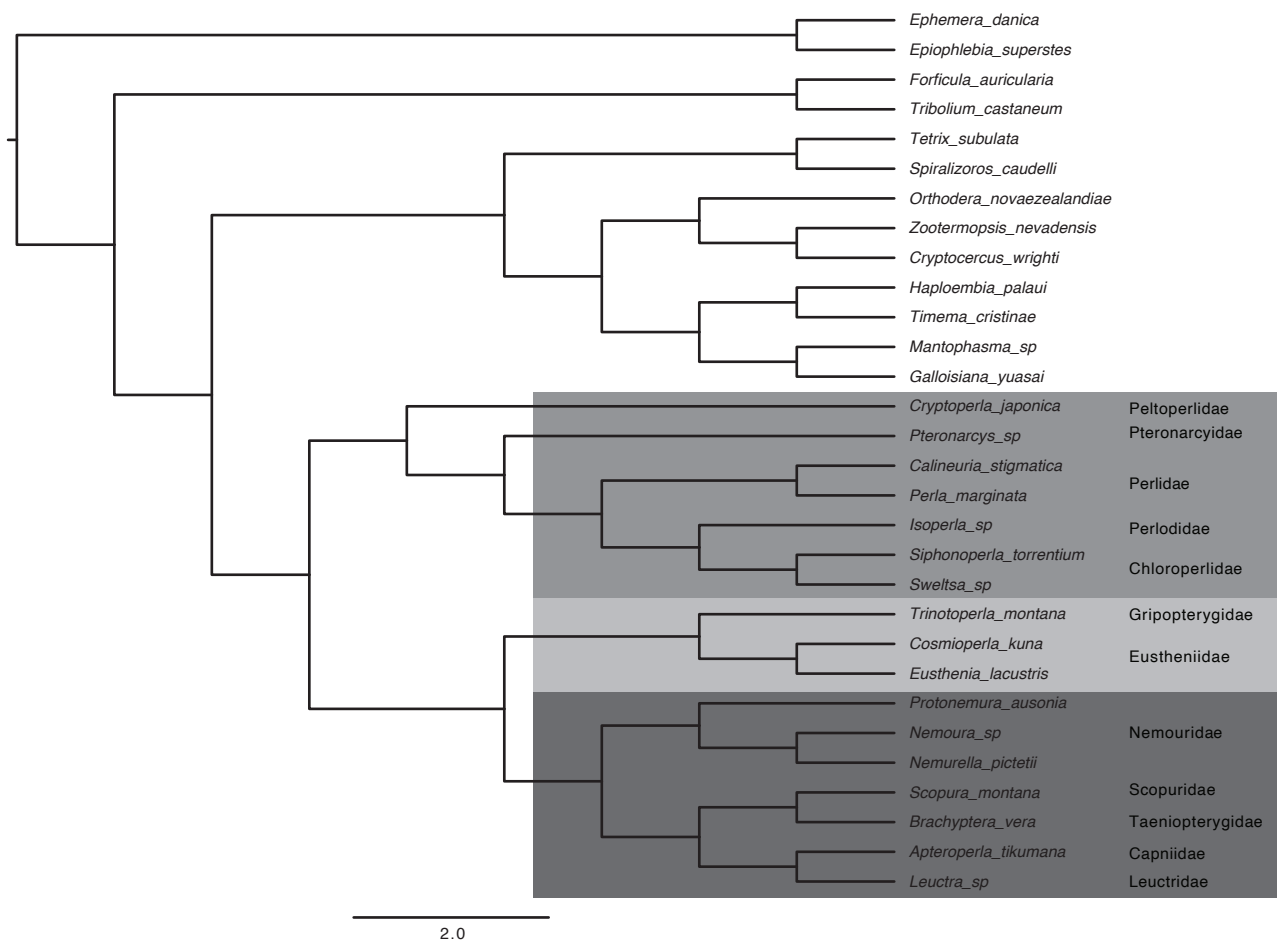


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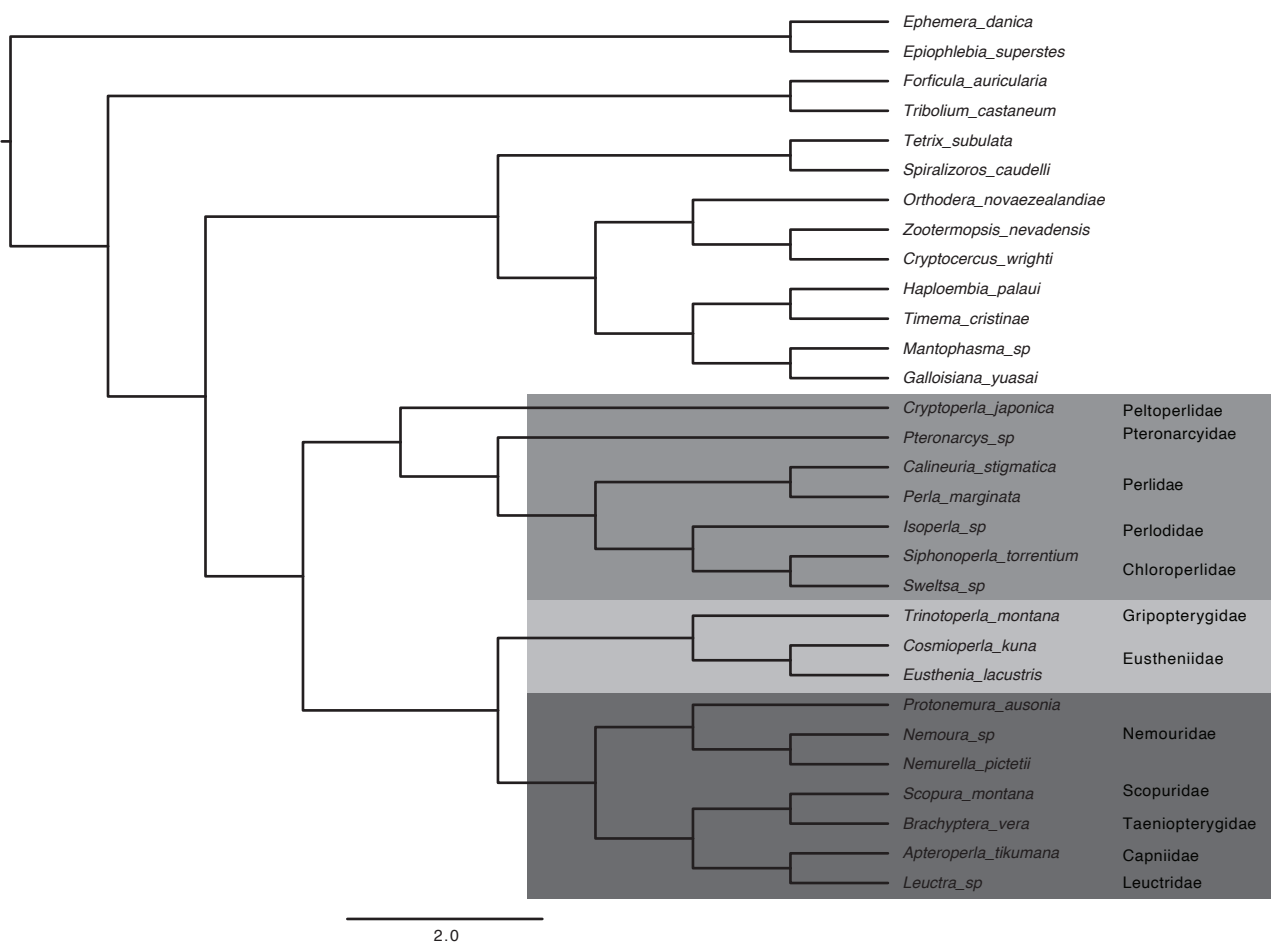


Fig. S3a

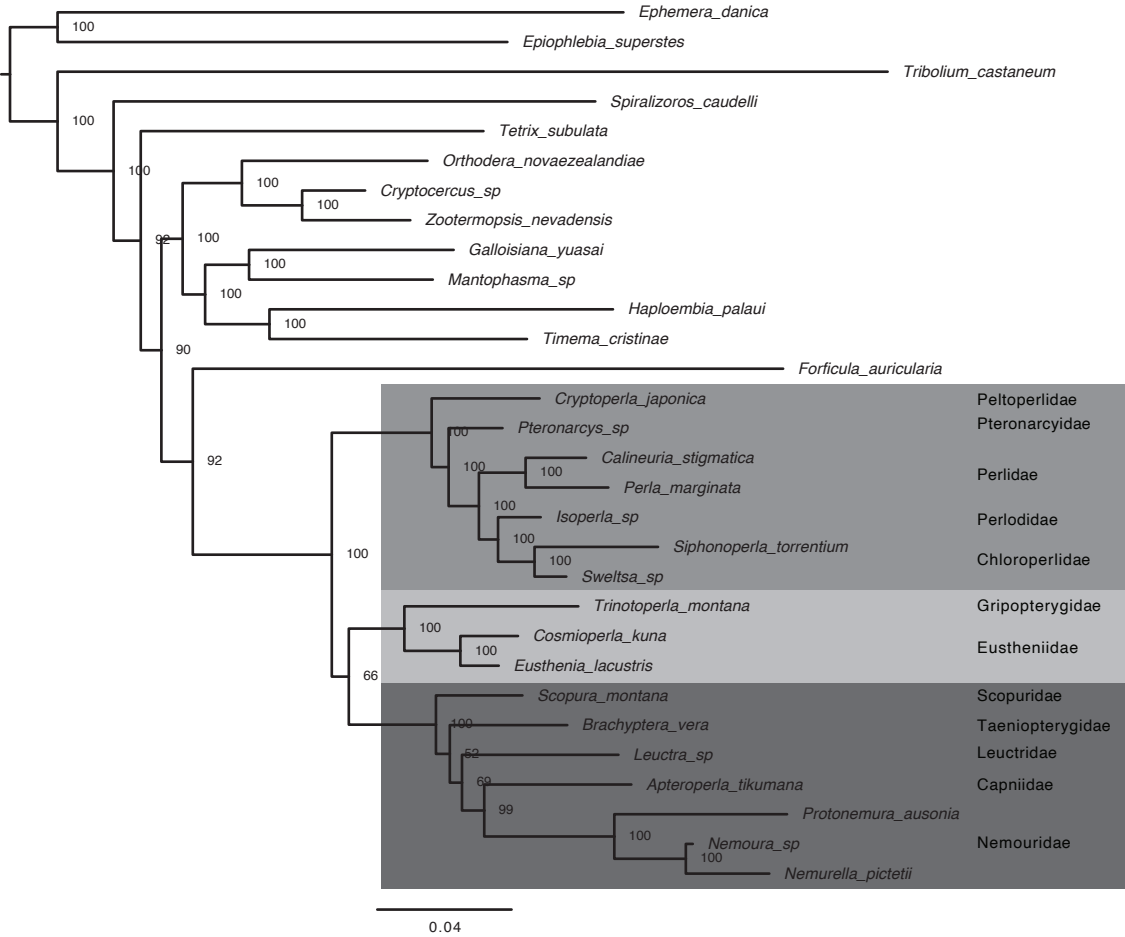


Fig. S3b

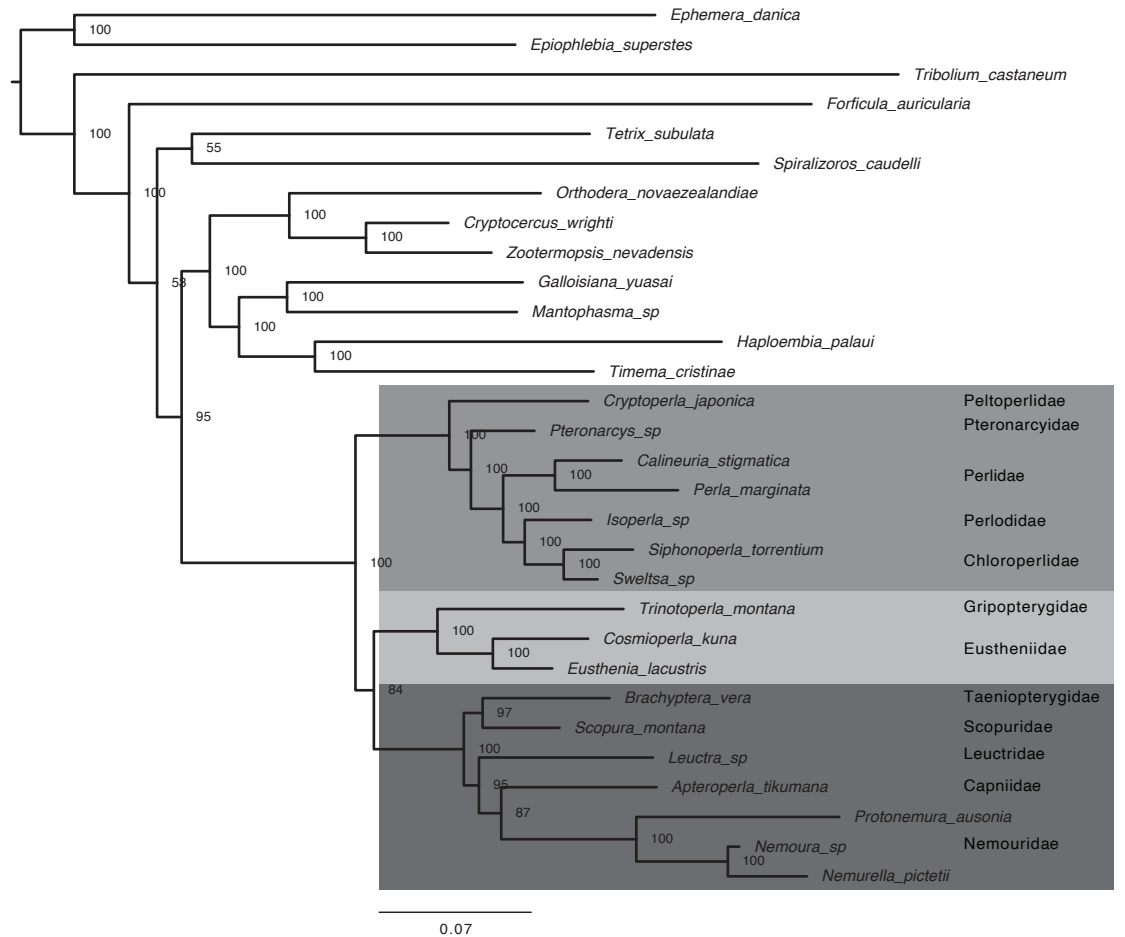


Fig. S3c

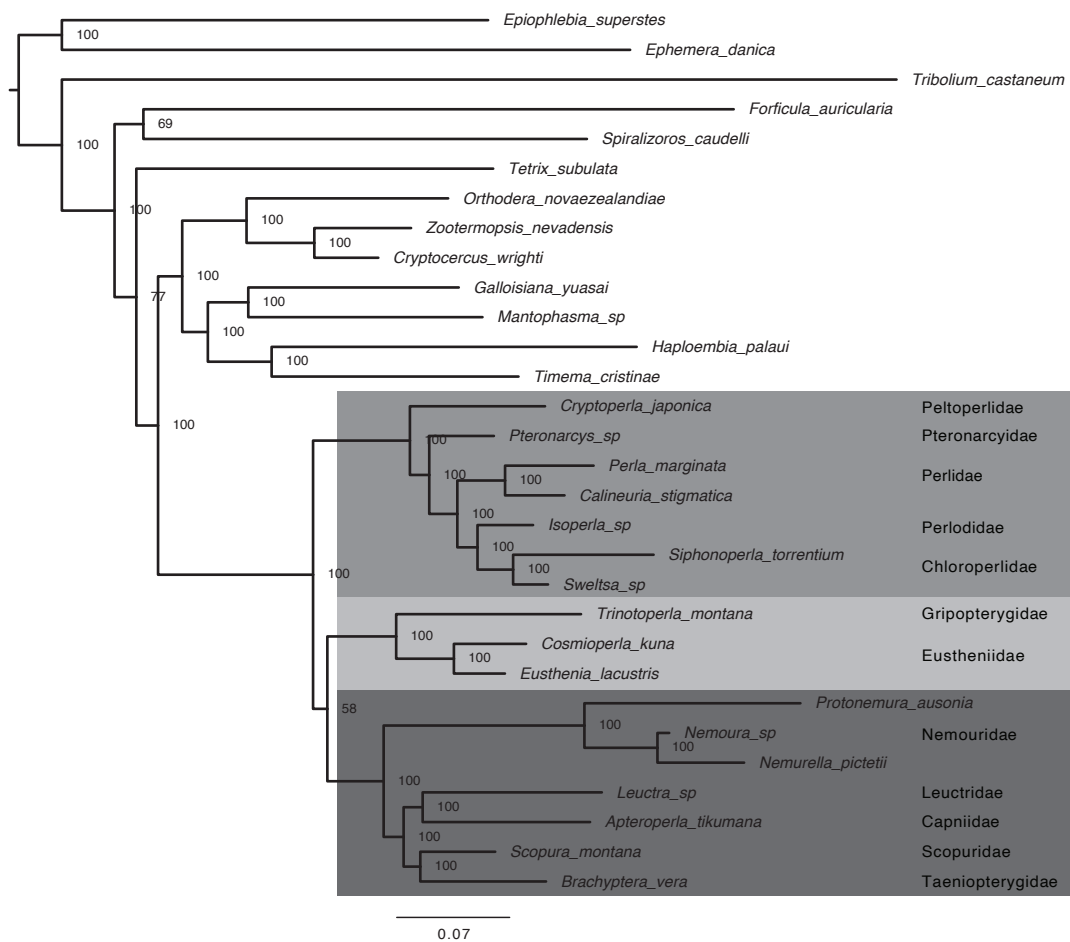


Fig. S3d

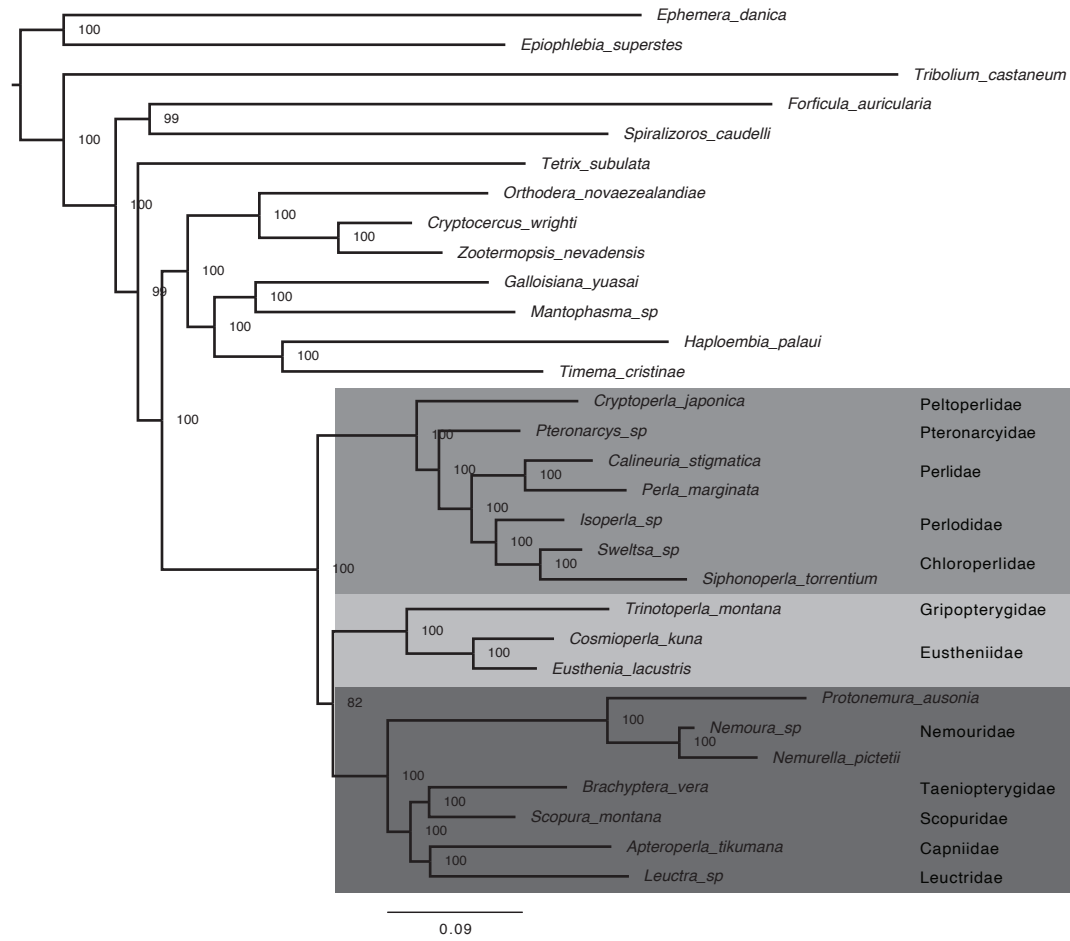


Fig. S4a

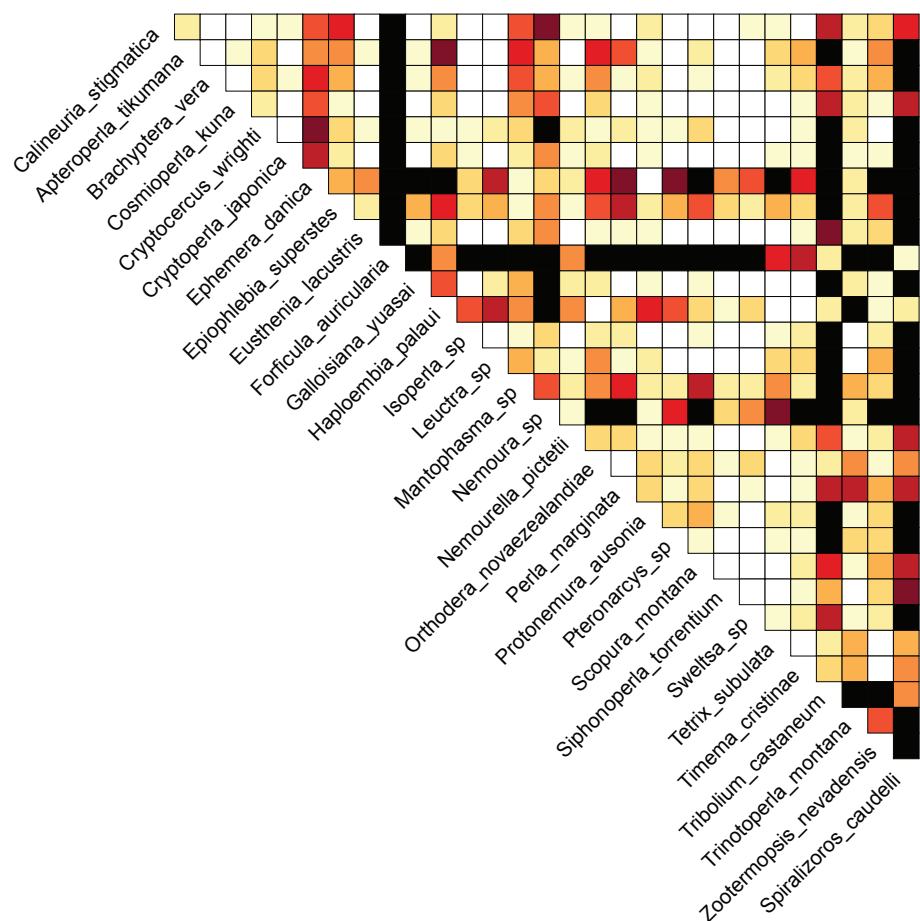


Fig. S4b

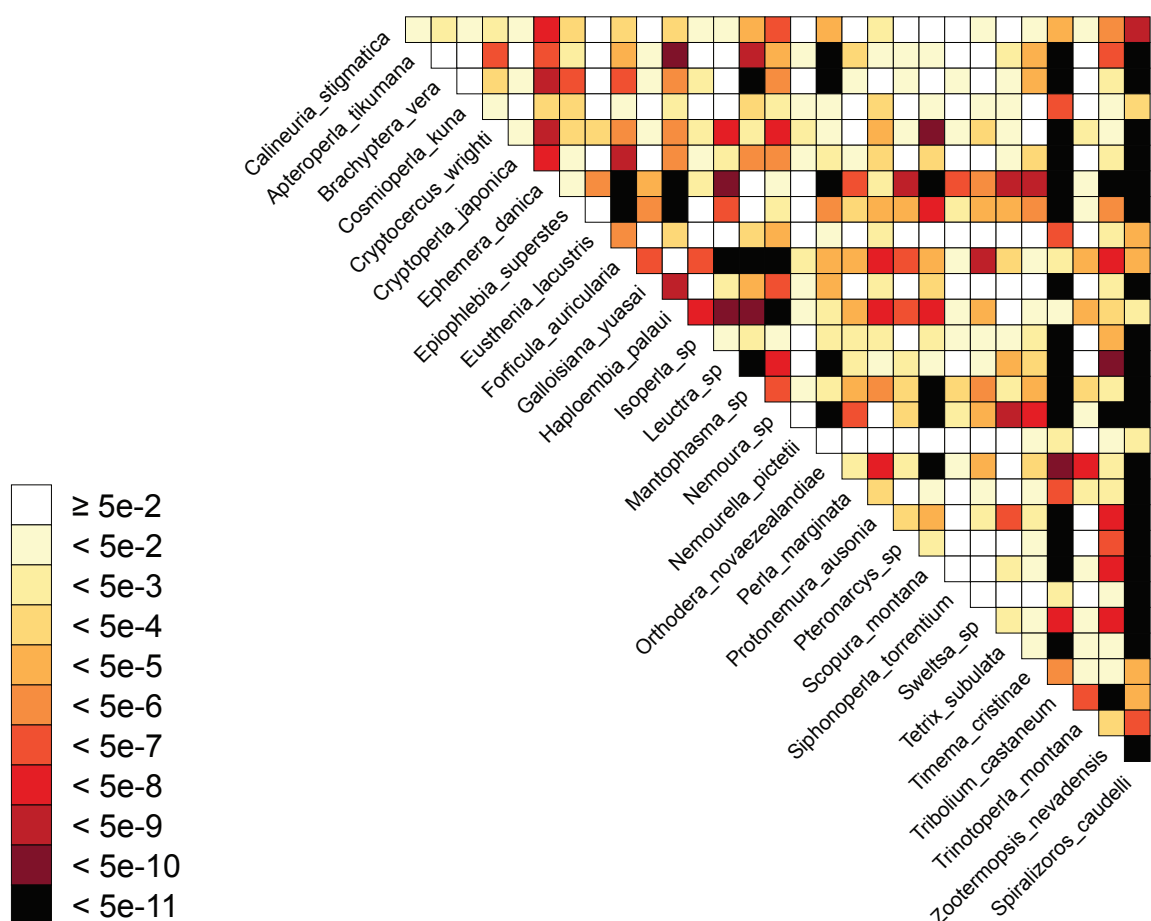


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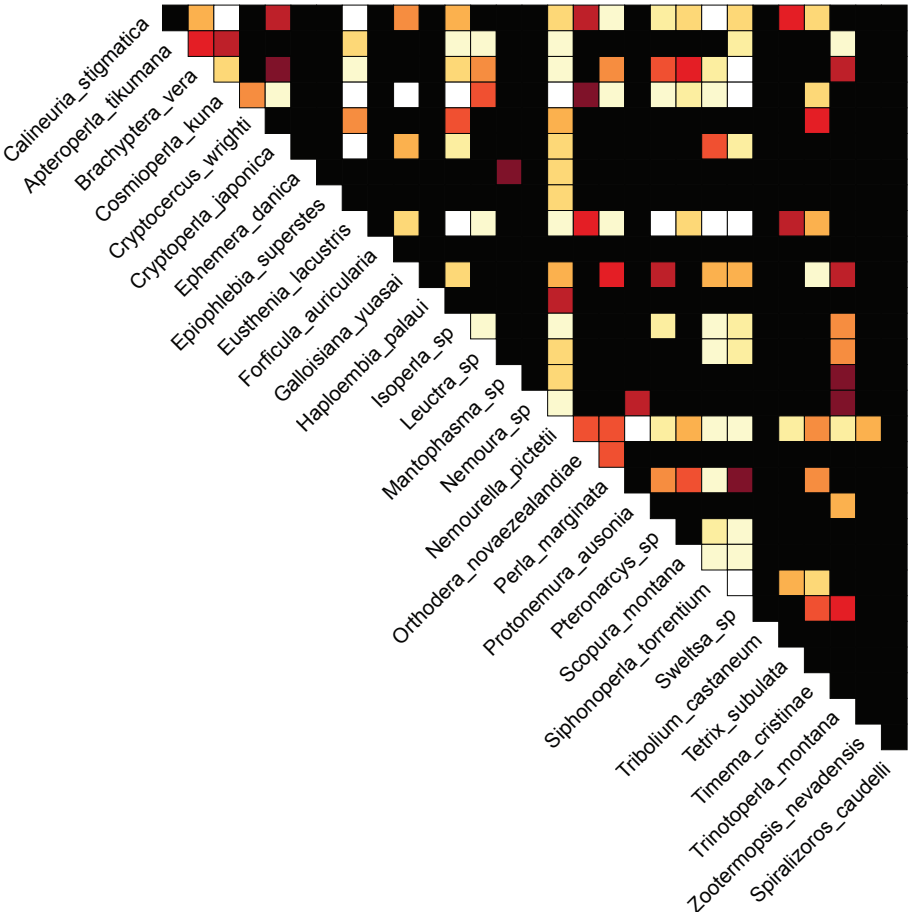


Fig. S4d

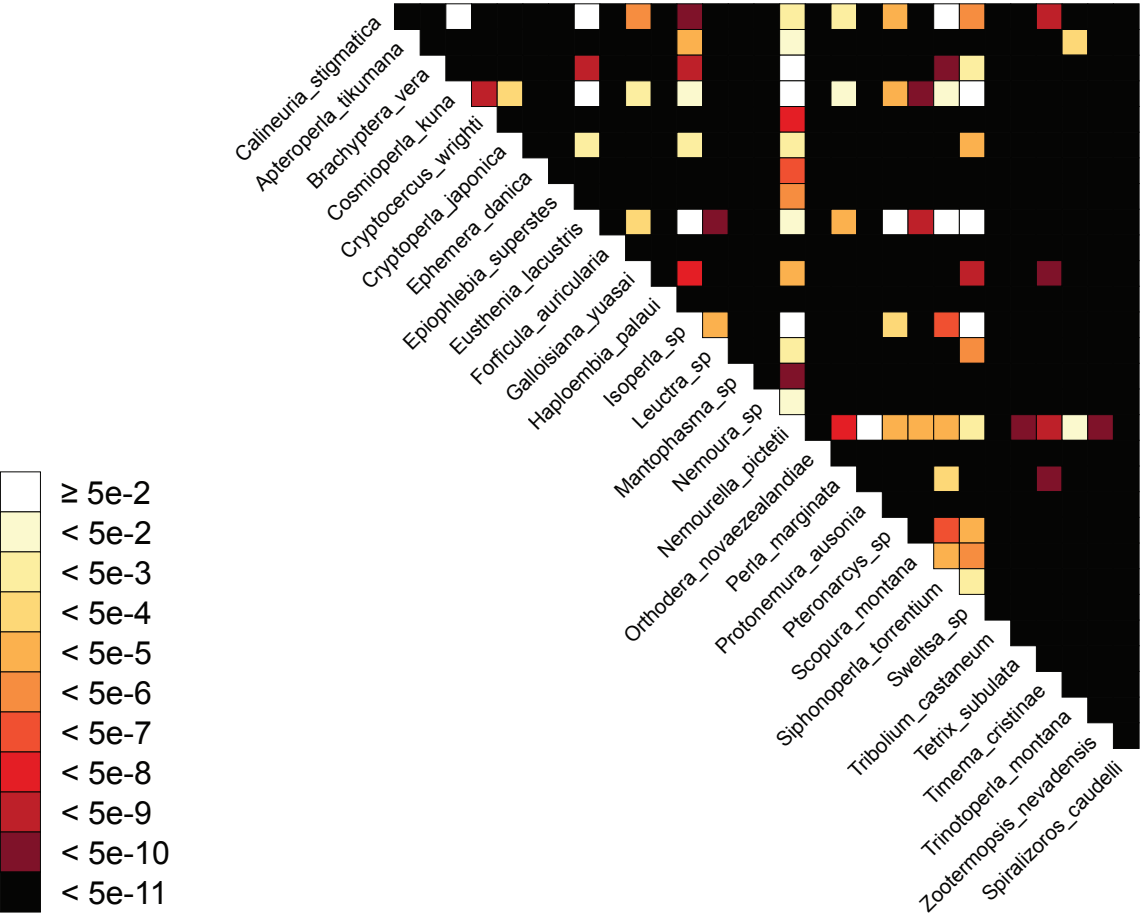


Fig. S6

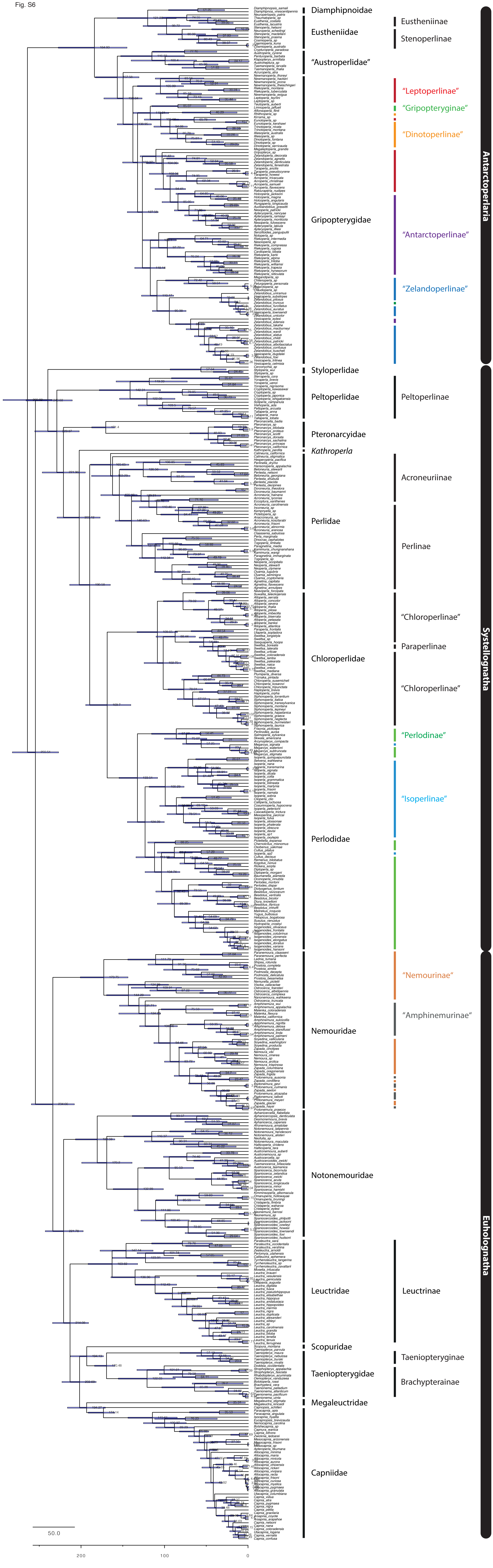


Fig. S7

