INVESTIGATING SOURCES OF CONFLICT IN DEEP PHYLOGENOMICS OF VETIGASTROPOD SNAILS

SUPPLEMENTARY FIGURES

Tauana Junqueira Cunha\textsuperscript{1,2,*}, James Davis Reimer\textsuperscript{3} and Gonzalo Giribet\textsuperscript{1}

\textsuperscript{1}Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology
Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA

\textsuperscript{2}Smithsonian Tropical Research Institute, Panama City, Panama

\textsuperscript{3}University of the Ryukyus, 1 Senbaru, Nishihara, Okinawa 903-0213, Japan

*Corresponding author: CunhaT@si.edu | orcid.org/0000-0002-8493-2117
Figure S1: Number of quartets per gene for all genes in the likelihood mapping analyses of nodes regarding the position of Haliotidae (596 genes) and Fissurellidae (835 genes), colored by whether the gene was selected for Matrix 5 for being most informative. See Material and Methods in the main text for details.
Figure S2: Vetigastropod phylogeny based on Astral-II. a) Matrix 1. b) Matrix 2. c) Matrix 3. d) Matrix 4. Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.
| Matrix 1 | Matrix 2 | Matrix 3 | Matrix 4 |
|----------|----------|----------|----------|
|           |           |           |           |

**Figure S3:** Vetigastropod phylogeny based on IQTREE, unpartitioned dataset with profile mixture models. a) Matrix 1. b) Matrix 2. c) Matrix 3. d) Matrix 4. Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.
Figure S4: Vetigastropod phylogeny based on IQTREE, partitioned dataset. a) Matrix 1. b) Matrix 2. c) Matrix 3. d) Matrix 4. Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.
Figure S5: Vetigastropod phylogeny based on PhyloBayes. a) Matrix 1. b) Matrix 2. c) Dayhoff-recoded matrix 1. d) Dayhoff-recoded matrix 2. Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.
Figure S6: No adverse effect of species with high missing data on the vetigastropod phylogeny. a) IQTREE unpartitioned analysis of matrix 1 after removing 13 terminals with the most missing data (marked with ** in (b)). Squares mark branches with full support. b) Neighbor-joining tree of the presence/absence matrix of the 1027 genes in matrix 1. New transcriptomes in bold. See Material and Methods in the main text for details.
Figure S7: Vetigastropod phylogeny based on StarBEAST2. a) Matrix 5. b) Matrix 6. Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.
Figure S8: Distribution of genes according to the topology with highest quartet support for all genes in the likelihood mapping test of each recalcitrant node (a,b,c), and for the set of most informative genes used for StarBEAST analyses (d,e,f). The category Other includes genes where the highest quartet support went to either one of the edges or central area of likelihood maps. In each row of graphs, the same genes are colored according to different properties. See Material and Methods in the main text for details.
Figure S9: a) Partitioned coalescence support for all 1027 genes in matrix 1. Calculated from the Astral tree from matrix 1 (Topology 2), with the unpartitioned IQTREE tree as alternative tree (Topology 1). Orthogroups with especially high scores are labeled. b) Distribution of bootstrap, gene and site concordance factors (gCF, sCF) along branches. Calculated from the unpartitioned (Topology 1) and the partitioned (Topology 2) IQTREE trees from matrix 1. Solid and dashed vertical lines mark the two recalcitrant nodes, regarding the position of Fissurellidae and Haliotidae respectively. c) Astral analysis of matrix 1 after removing the 4 genes labeled in (a). Squares mark branches with full support. New transcriptomes in bold. See Material and Methods in the main text for details.