

Figure S1. Work-flow of transcriptome sequencing and phylogenomic analyses.

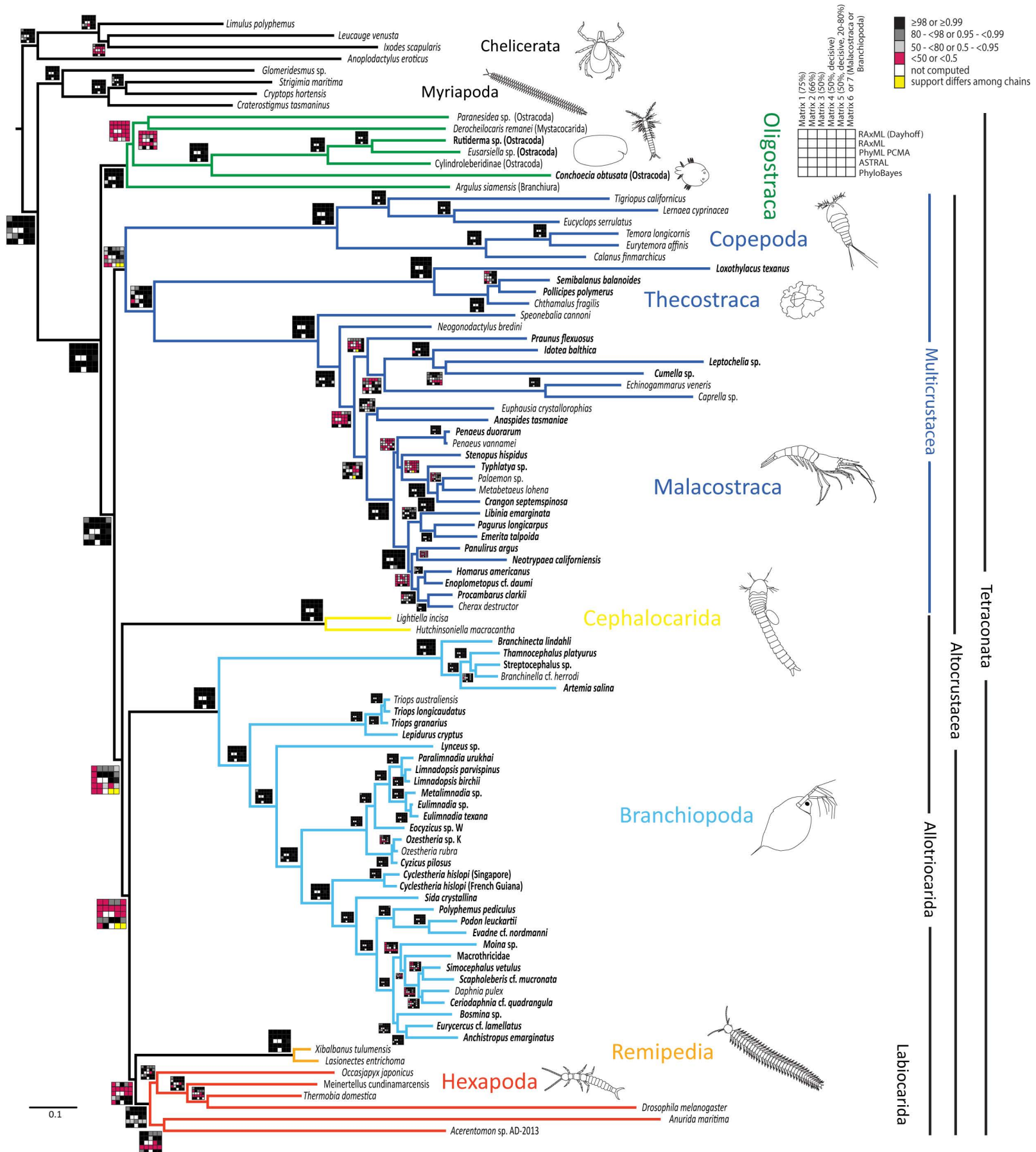


Figure S2. Phylogenetic relationships within Tetraconata inferred by PhyloBayes CAT-GTR with Matrix 4 (455 decisive genes). Support values for all analyses are depicted as rug plots, with each cell representing a specific combination of matrix and analytical method. Nodes supported in only one of two PhyloBayes chains are marked in yellow (the two PhyloBayes chains did not converge for these nodes). Individuals newly sequenced for this study are highlighted in bold. This is the same phylogenetic tree depicted in Fig. 1, but with all nodes within Malacostraca and Branchiopoda shown.