**Figure S2. Strict consensus of four maximum parsimony trees for *21AA* data set plus bootstrap values (above branches) from *20AA* (left) and *21AA* (right) analyses.**

MP topology based on 250 search replicates. Bootstrap results based on 1000 bootstrap replicates (5 search reps / bootstrap rep).

: bootstrap percentage *(20AA 21AA)*

[ ] : node not present in *20AA* MP strict consensus

● : Identifies 6 taxa with large differences in BP between *degen1* and *20AA* analyses.
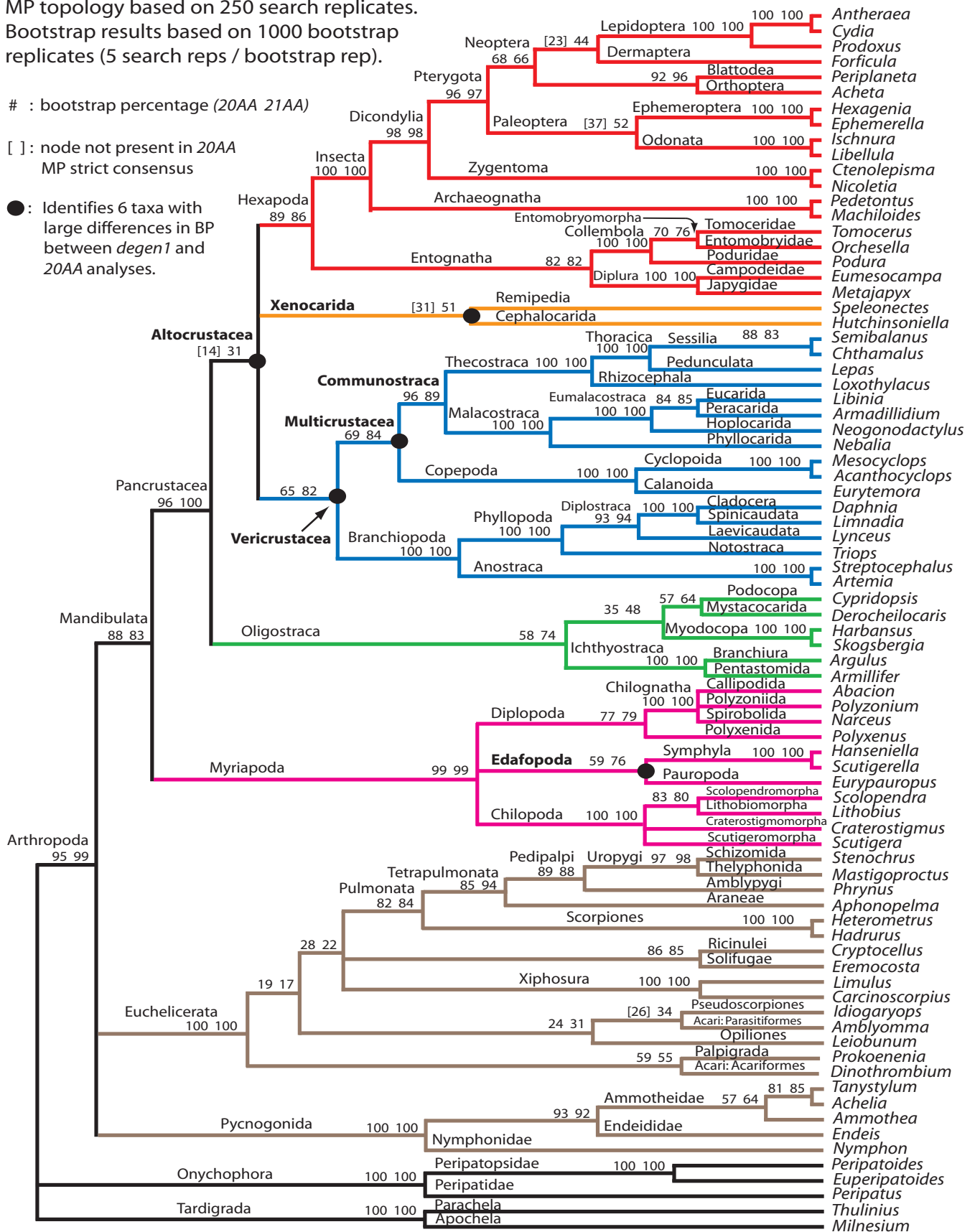
Commentary on Figure S2: Miracrustacea (BP, 24%), Progoneata (BP, 33%), and Chelicerata (BP, 57%) are all present in subsets of the four MP trees for the *21AA* analysis. Miracrustacea (BP, 12%) and Xenocarida (BP, 31%) are both present in subsets of the five MP trees for the *20AA* analysis, but not Altocrustacea (BP, 14%) and Chelicerata (40%). Progoneata (BP, 35%) is present in the strict consensus of the *20AA* analysis.