

**Figure S5.** Results of Phyparts analysis along RAxML phylogeny, including discordance visualizations for every node in phylogeny. Colors in pie chart correspond to the proportion of gene trees that fall into different categories of concordance (blue: concordant genes; green: most common conflicting bipartition; red: other conflicting bipartitions; grey: gene trees with no information). Tip names corresponding to Sample\_ID from Appendix S1.

