



**Supplemental Figure 1.** Taxa sampled with corresponding transposable element (TE) abundance and genome size for 20% sampling effort of genome wide coverage. (A) Phylogeny with whole-genome duplications indicated by black stars. Support values are shown for those branched with less than 0.7 local posterior probability. (B) Proportion of transposable element abundance scaled to 100%, (C) proportion of transposable element abundance converted to base pairs (Mbp), and (D) genome size (Mbp).