

# Supplementary Material Legends

**Appendix 1.** Total-evidence Matrix for the 420 terminals, including ingroup and outgroup.

**Appendix 2.** Genbank accesses for each sequence included in this study. Second sheet contain the nucleotide substitution model optimized after Maximum Likelihood analysis.

**Appendix 3.** Topologies from Parsimony analysis. Numbers in the nodes indicate bootstrapping support.

**Appendix 4.** Topologies from Maximum Likelihood analysis. Numbers in the nodes indicate bootstrapping support.