



Figure S10: Analysis of the revised Schierwater et al. dataset.

Numerous discrepancies were corrected in the alignments (Table S1) and a few genes were discarded due to dubious orthology assignment; 14,112 unambiguously aligned positions were retained. The tree was inferred as in the original study, i.e., using RAXML with a GTR+ Γ model for nucleotide sequences and a LG+F+ Γ model for protein sequences.