





Fig. S2. Comprehensive bipartition network based on 250 maximum likelihood (ML) bootstrap (BS) replicates illustrating compatibility of phylogenetic signal in the concatenated data. Edges correspond to potential branches in phylogenetic trees; their lengths are proportional to the occurrence frequency of the corresponding bipartition (edge/branch) in the bootstrap replicate tree sample. See text-Fig. 2 for a version focussing on backbone topological alternatives providing support values from non-parametric bootstrapping under ML and Bayesian inference; File S1 for a graphically enhanced tabulation of ML-BS support for ML-preferred and alternative bipartitions based on the concatenated data and one- or two-partition data sets.

Fig. S3. Comprehensive bipartition network based on 2000 Bayesian-inferred saved topologies (BIST) illustrating compatibility of phylogenetic signal in the concatenated data. Edges correspond to potential branches in phylogenetic trees; their lengths are proportional to the occurrence frequency of the corresponding bipartition (edge/branch) in the BIST tree sample. The posterior probabilities calculated from this sample are shown in text-Figs. 1 and 2, and included in File S1 for direct comparison with maximum likelihood non-parametric bootstrap support.

