**Table S1**. Results of annotation adjustment. The number of divided and combined annotations were counted in terms of the number of original annotations that were altered.



**Table S2**. Summary statistics of 1329 multiple sequence alignments containing between 6 and 11 sequences for each alignment treatment. Statistics are the mean alignment length, the mean count and proportion of parsimony informative sites, and the mean proportion of empty cells in the alignments. Empty cells are defined as those containing non-nucleotide characters (gap, “N” or “?”). Alignment length and empty cells are calculated after removing empty alignment columns created by masking.



**Table S3**. Number of fully resolved unrooted gene trees inferred for each alignment set from 473 alignments containing all 11 genomes.

