



**Additional data file 5.** Testing the effect of rate bias caused by the fast-evolving genes of the F-genome. Left: Histogram of relative evolutionary rates of the F-genome for 142 genes, which is represented by the ratio of the mean distance between the F-genome and each of the A-, B-, and C-genomes to the average of the distances among the A-, B-, and C-genomes for each gene. Right: Bootstrap support for placing the G-genome at the basal position when sequentially and cumulatively discarding the fast-evolving genes of the F-genome in decreasing order three at a time and reconstructed the phylogeny for each pruned data set. The blue triangles represent the results of ML method and the red squares the results of MP method.