Fig. S1 Phylogenetic analysis of the 26G dataset using PhyloBayes 3.2. The topology of the tree (a single optimal tree shown with branch length) is identical with the tree topology estimated by BEAST v1.61, which was used as a starting tree in the downstream molecular clock analyses. Support values for nodes 4, 10, 12, 23, and 28 are indicated in the inset box for all four datasets (26G, 26GA, 71G, 71GA) inferred using RAxML 7.0.4 and PhyloBayes. All other nodes received maximal support in all analyses.