

Maximum likelihood phylogenomic analysis inferred with IQ-TREE v2, using a supermatrix of 318 taxa, 240 proteins and 72,614 amino acids sites. First, a tree was inferred with the ELM GTRpmix empirical exchangeabilities matrix, C60 profile mixture model and Gamma with 4 discrete site-rate classes (ELM+C60+G4). After inference of this first tree, it was then used as a guide tree to fit the data model site heterogeneity under the posterior mean site-frequencies approach (ELM+C60+G4_PMSF). IQ-TREE was ran with -mwopt option that optimized mixture weights for each C-Class in the C60 mixture model. Bootstrapped using 1000 ultrafast bootstrap replicates. Black circles on nodes represent full support. The scale bar indicates the expected number of amino acid substitutions per site. The histograms to the right of the tree indicate data coverage by genes (top, darker) and by sites (bottom, brighter).

