



Euryarchaeota

TACK + Asgard

Cluster2

DPANN

Cluster1

364 species
50% top ranked proteins
(n=56)
removal of heterogeneous sites
Pruner, 20% site removal
10,280 amino acid
Iqtree, LG+C60+F+R

UAP2

Supplementary Figure S17 Phylogenetic placement of the UAP2 lineage based on an alignment generated with the 50% top ranked proteins (n=56) and the 364 species set where 20% of heterogeneous sites were removed (alignment length = 10,280 aa). A ML phylogenetic tree was inferred with the LG+C60+F+R model with an ultrafast bootstrap approximation (left) and SH-like approximate likelihood tests (right), each run with 1000 replicates. The tree was artificially rooted with the DPANN archaea and the grey arrow shows the root position inferred with minimal ancestor deviation rooting (Tria et al., 2017). Tree statistics for tree number 13 can be found in Supplementary Table S5.