

Supplementary Data File 2

Supplementary Figures

Figure S1. Phylogeny of archaeal genomes, including isolates and MAGs from arthropod guts analyzed in this study (Table S2). The phylogenomic tree is based on an alignment of 53 archaeal marker genes generated using the GTDB toolkit (GTDB-Tk v2.3.0) with GTDB release 214 as reference and was reconstructed with IQ-TREE 2 under the LG+F+I+G4 model of evolution. Branch support was assessed by ultrafast bootstrap approximation (1,000 replicates). A rank-normalized version of this tree is shown in Fig. 2 of the main manuscript. Selected low-quality MAGs (LQ) were included to provide additional context.

Figure S2. Phylogenomic analysis of the family *Methanocorpusculaceae*, including novel genomes of isolates and MAGs from Volmer et al. (2023). Isolates and MAGs from arthropod guts are in bold. For further information, see legend of Fig. S1.

Figure S3. Expanded version of the phylogenetic tree of *Methanobacteriaceae* (Fig. 3 of the main manuscript). Shorter sequences were added using the parsimony tool implemented in Arb. The maximum-likelihood tree is based on a curated alignment of near-full-length 16S rRNA genes (>1,400 sites) and was generated using IQ-TREE with the model GTR+I+G4. Node support was tested with ultrafast bootstrap analysis (● ≥ 95% and ○ ≥ 70%; 1,000 replicates). The scale bar indicates the number of substitutions per site. Sequences from arthropod guts are color-coded (millipedes, green; cockroaches, orange; lower termites, light blue; higher termites, dark blue; beetles; red).

Figure S4. Expanded version of the phylogenetic tree of *Methanomicrobiales* (Fig. 4 of the main manuscript). Shorter sequences were added using the parsimony tool implemented in Arb. For more details, see the legend of Fig. S3.

Figure S5. Expanded version of the phylogenetic tree of *Methanosarcinaceae* (Fig. 5 of the main manuscript). Shorter sequences were added using the parsimony tool implemented in Arb. For more details, see the legend of Fig. S3.

Figure S6. Expanded version of the phylogenetic tree of *Methanomethylophilaceae* (Fig. 6 of the main manuscript). Shorter sequences were added using the parsimony tool implemented in Arb. For more details, see the legend of Fig. S3.

Figure S7. Expanded version of the phylogenetic tree of *Bathycorpusculaceae* (Fig. 7 of the main manuscript). Shorter sequences were added using the parsimony tool implemented in Arb. For more details, see the legend of Fig. S3.

Figure S8. Phylogenetic tree of *Nitrososphaeraceae*, illustrating the position of the sequences from arthropods obtained in this and previous studies. Other *Nitrososphaerales* were used as an outgroup. Shorter sequences were added using the parsimony tool implemented in Arb. For more details, see the legend of Fig. S3.

Figure S1

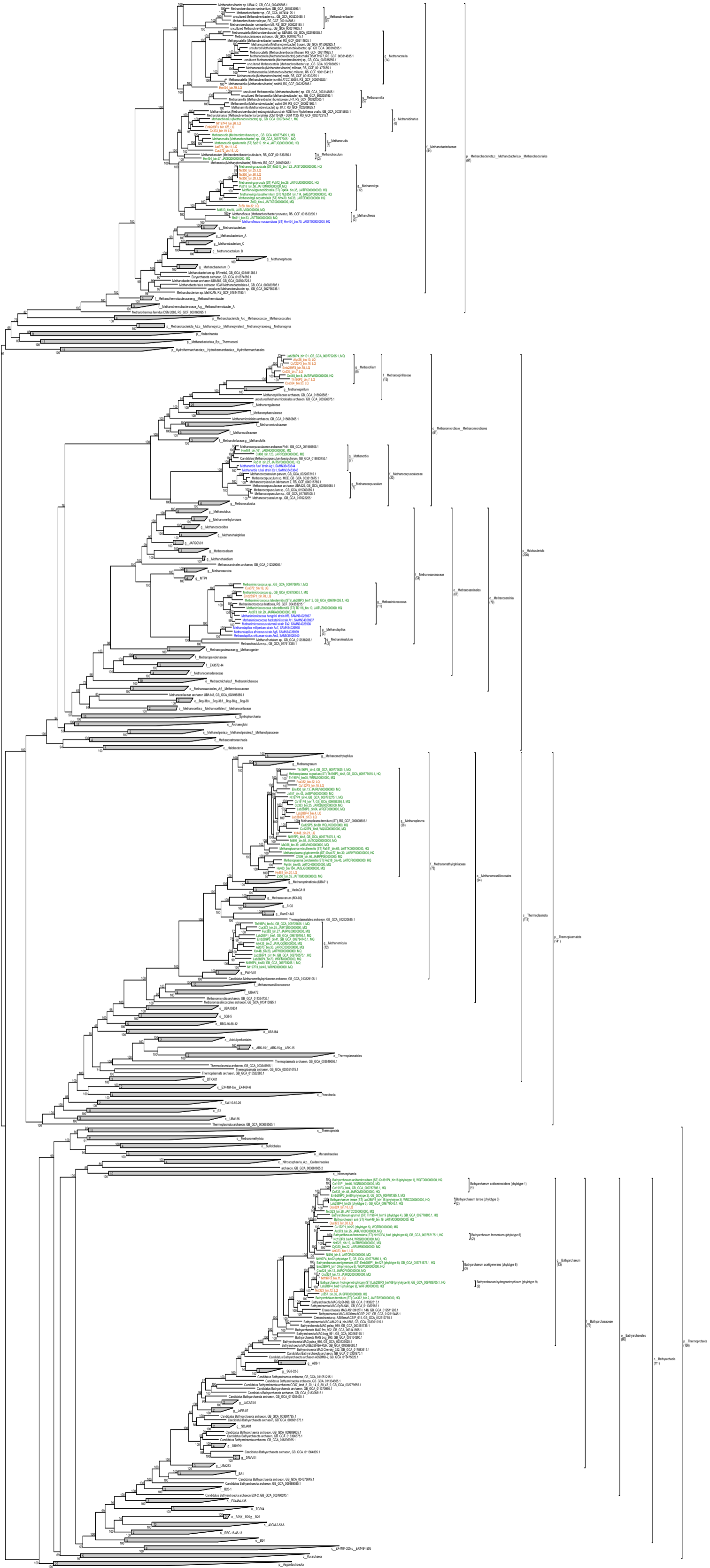
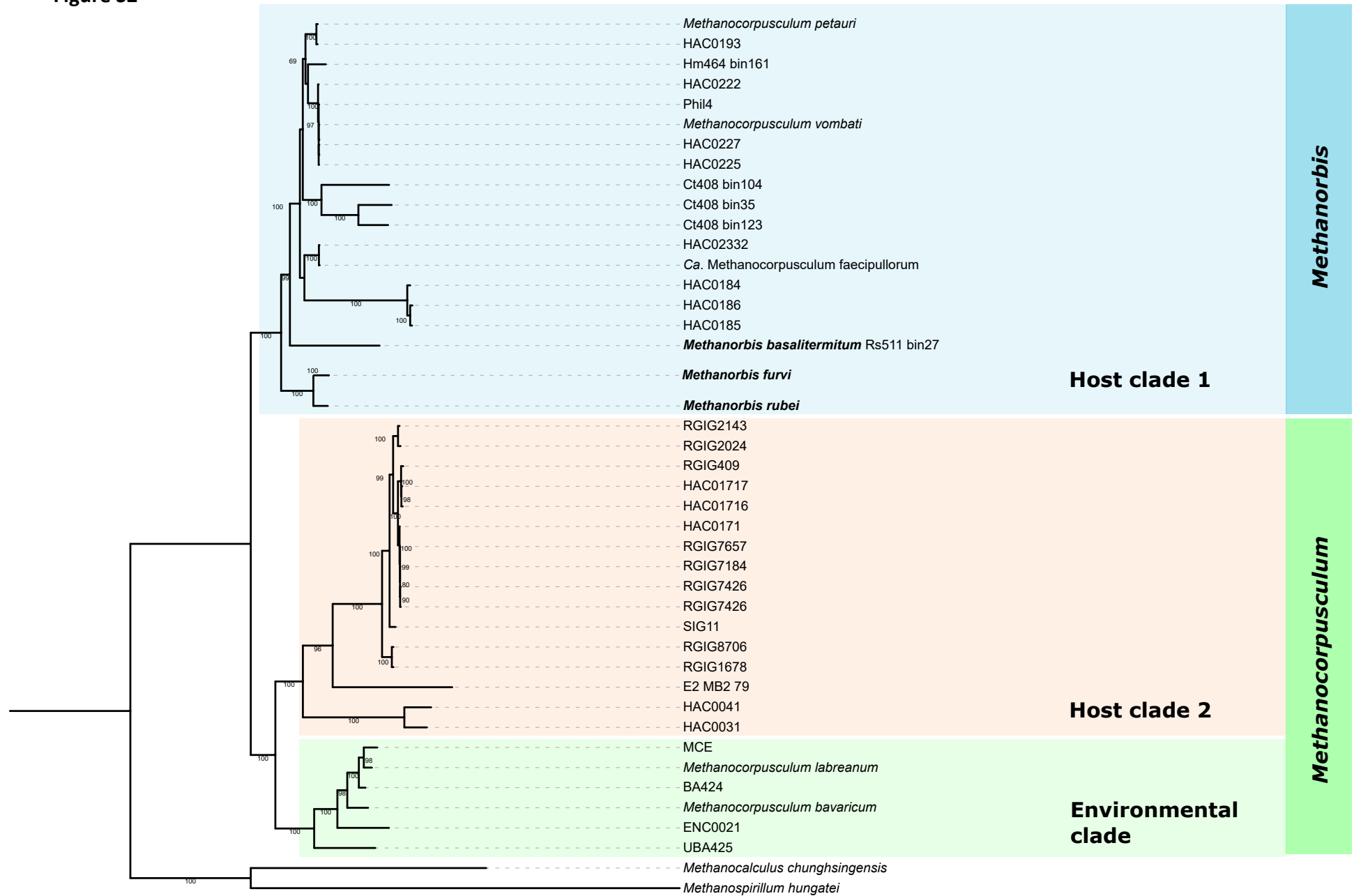


Figure S2



Tree scale: 0.1

Figure S3

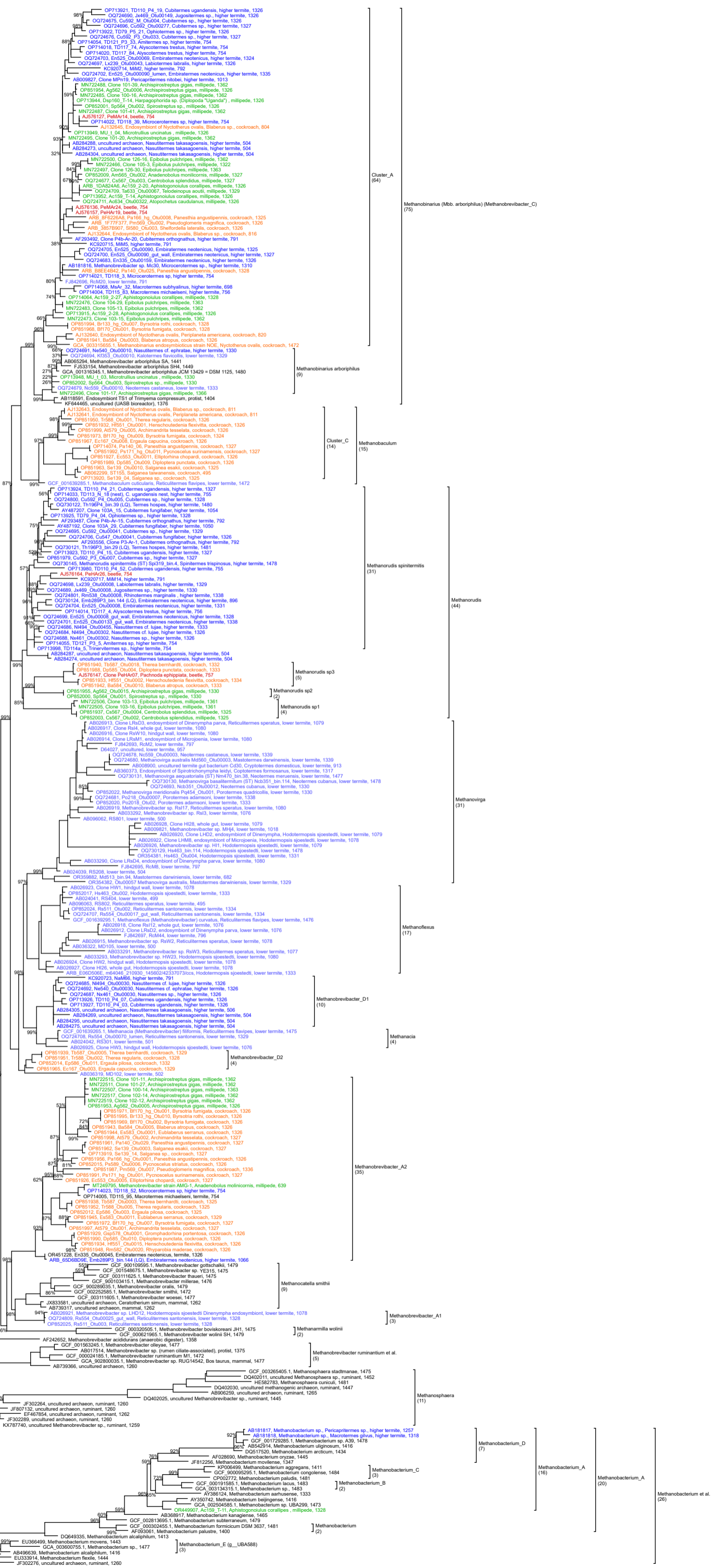


Figure S4

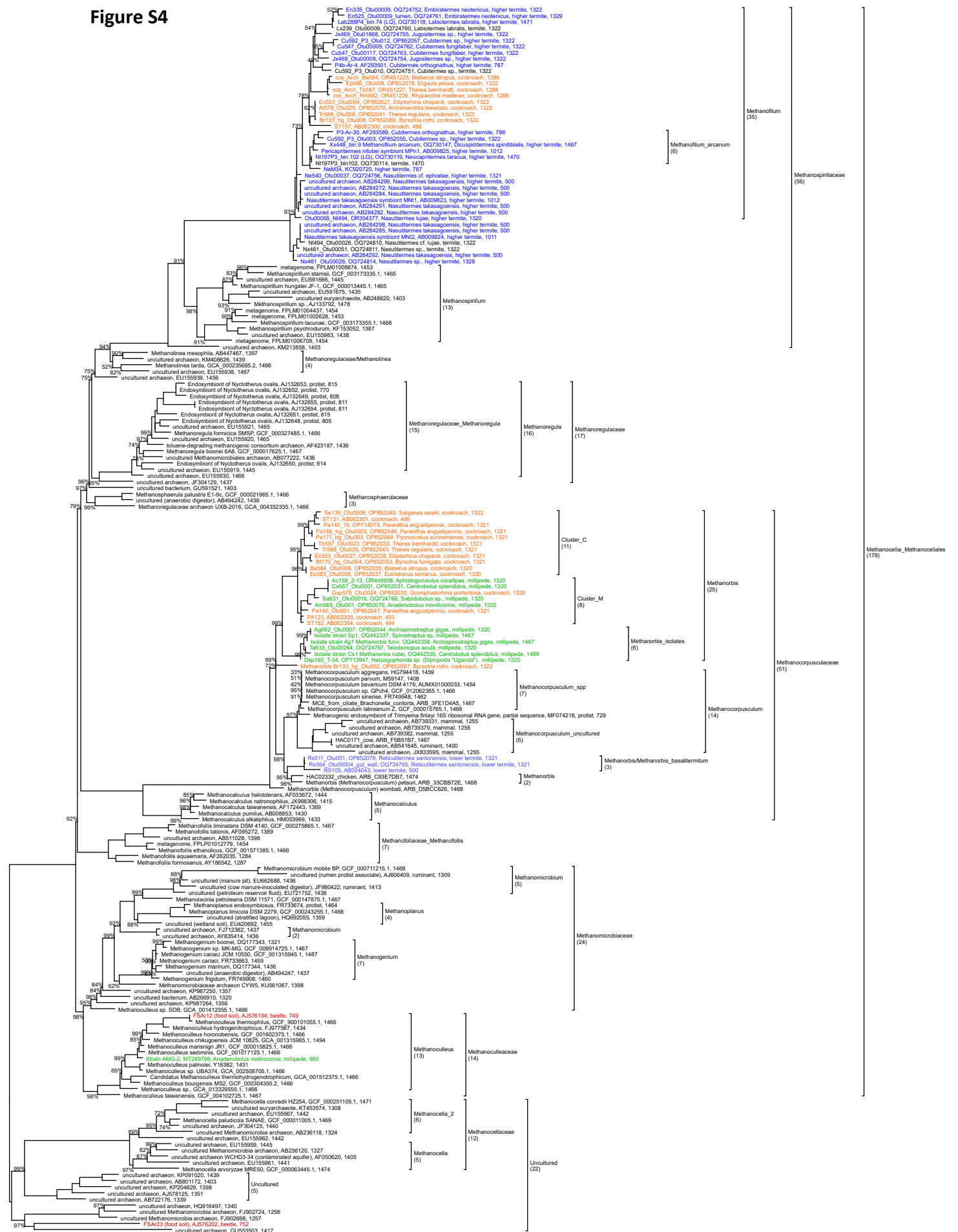


Figure S6

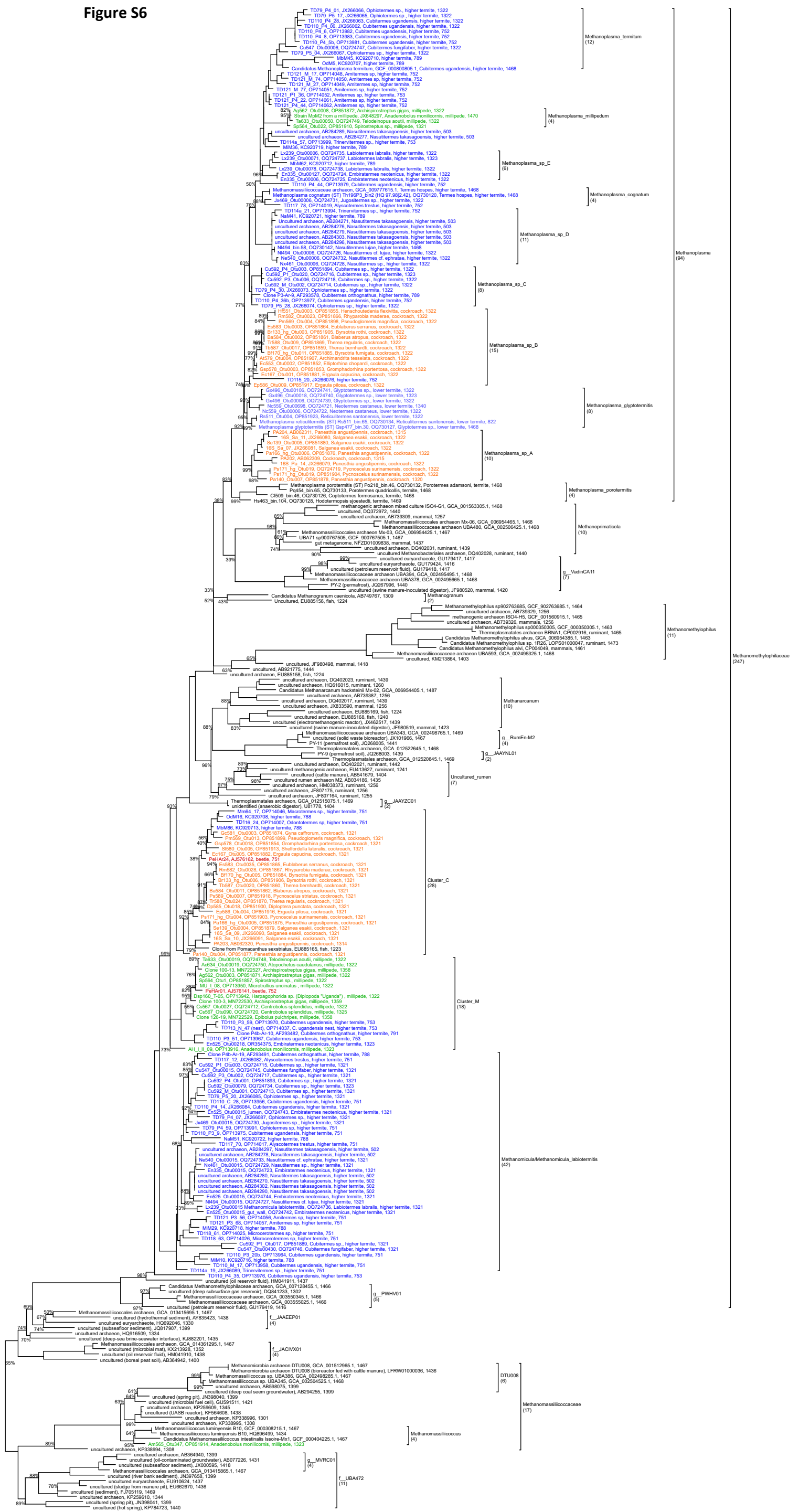


Figure S8

