



Fig. S1 Map of sampling sites in mangrove sediments across Southeastern China.

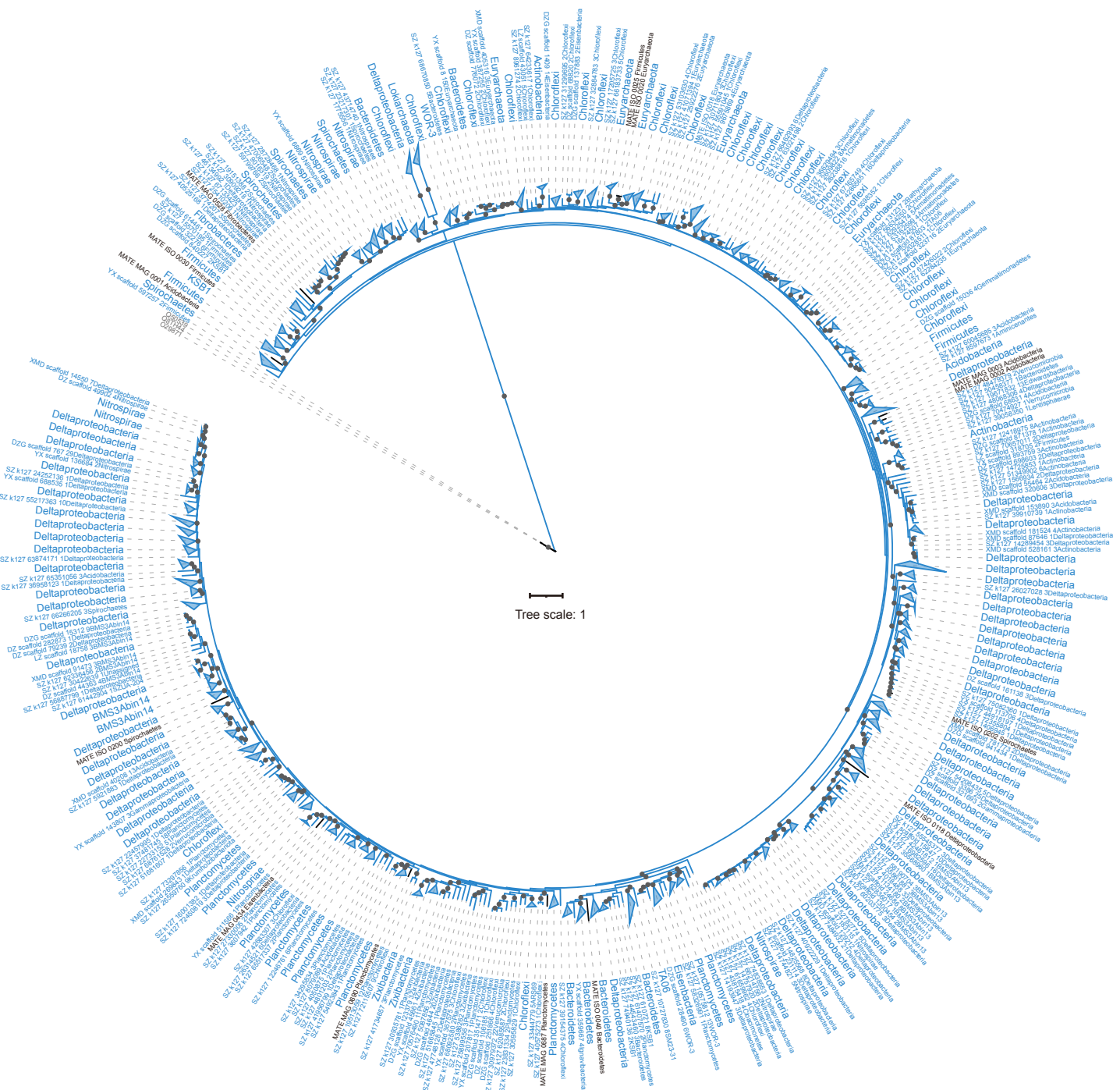


Fig. S2 Maximum-likelihood phylogenetic tree of HgcA amino acid sequences. (1000 bootstraps; values >90% are shown by grey dots at the nodes). The 1087 HgcA sequences in this study are highlighted in blue. HgcA sequences retrieved from public databases are shown in black. HgcA paralogues from non-methylating microorganisms were used as outgroups and are shown in gray.

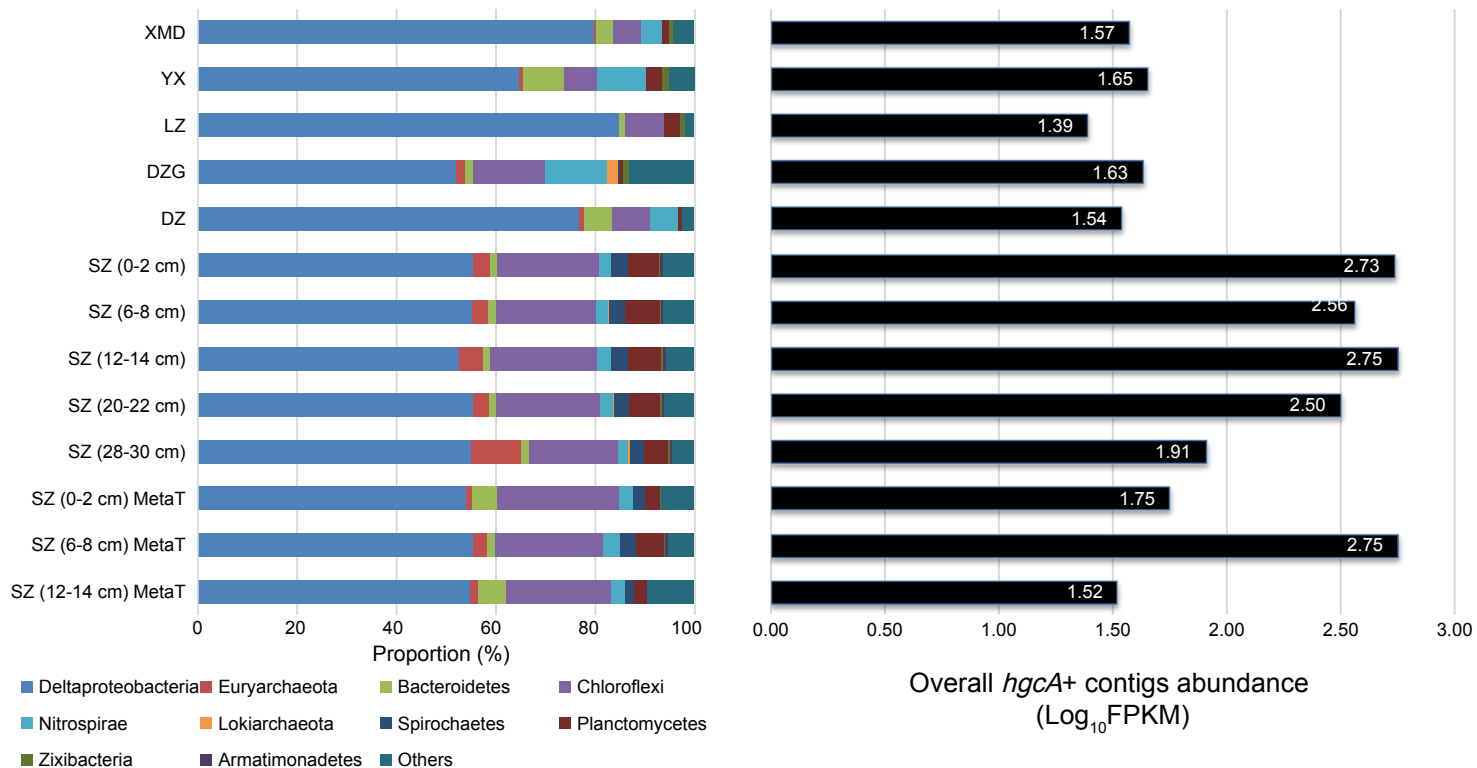


Fig. S3 Relative abundances of *hgcA* genes affiliated to different taxonomic groups and RPKM values of the sum of *hgcA* genes and transcripts in different mangrove sediment samples. Gene abundances and transcript abundances, represented as RPKM values, are normalized by gene length and sequence. MetaT represent metatranscriptomic.

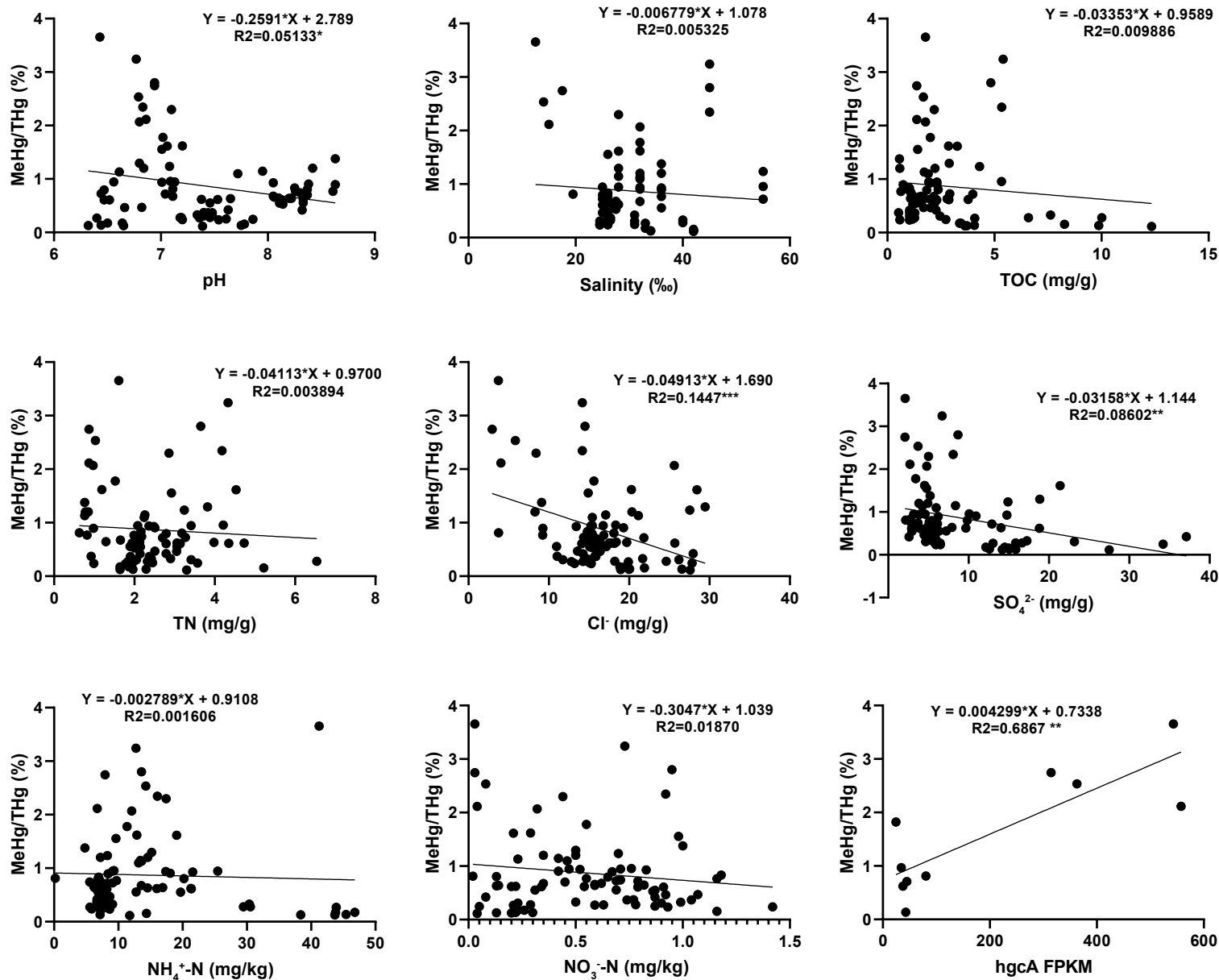


Fig. S4 Correlations between environmental factors, *hgcA* RPKM and MeHg/THg ratios.

The black lines are the slopes. Significance level is as follows: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

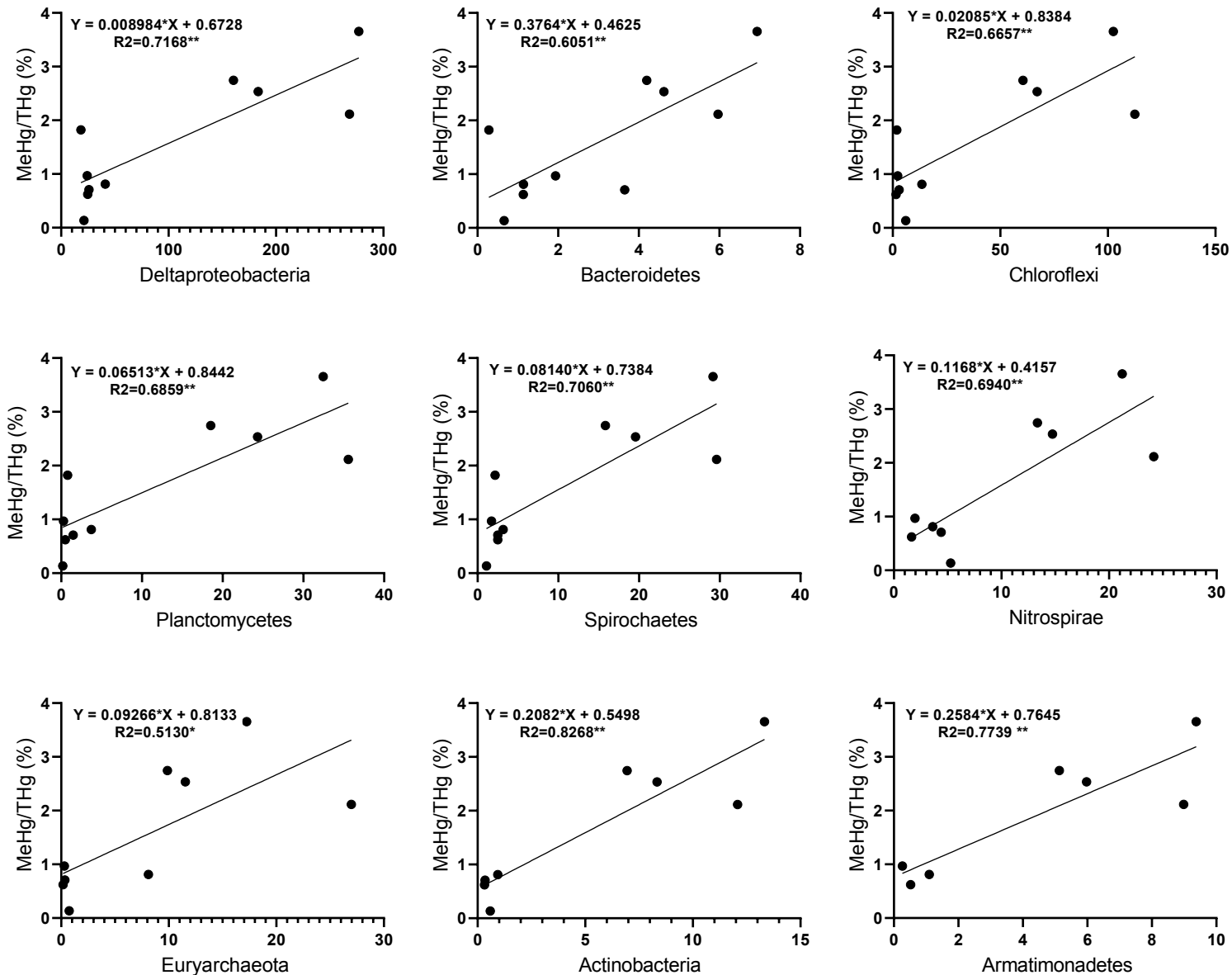


Fig. S5 Correlations between *hgcA* RPKM of different taxa and MeHg/THg ratios. The black lines are the slopes. Significance level is as follows: * $p < 0.05$; ** $p < 0.01$.

HgcA

HgcB

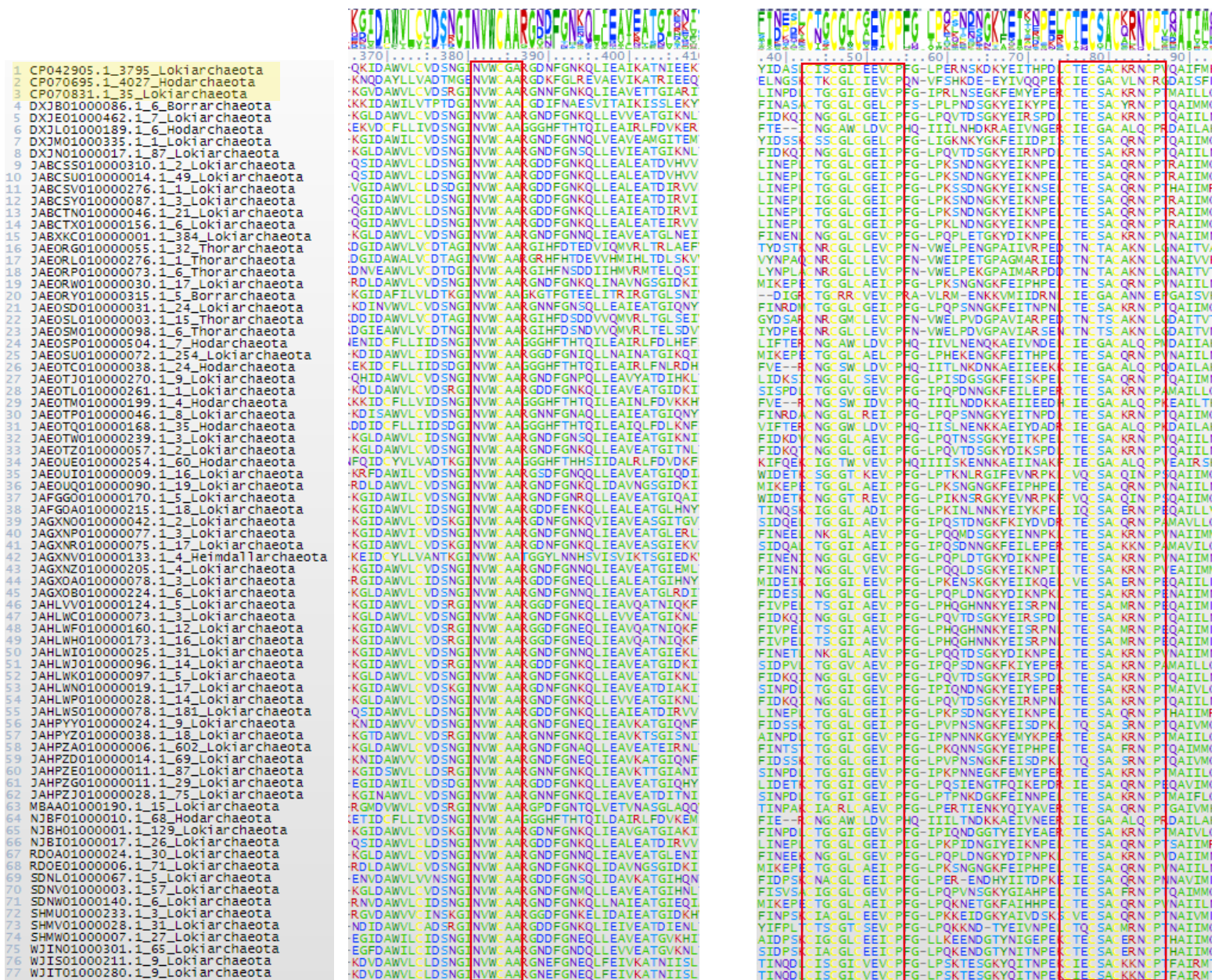


Fig. S6 Multiple Asgard HgcA and HgcB sequence alignment. The sequence alignment shows conserved regions of 77 HgcA and HgcB sequences in Asgard. Sequence logo above the alignment shows the occurrence of each amino acid in each position.

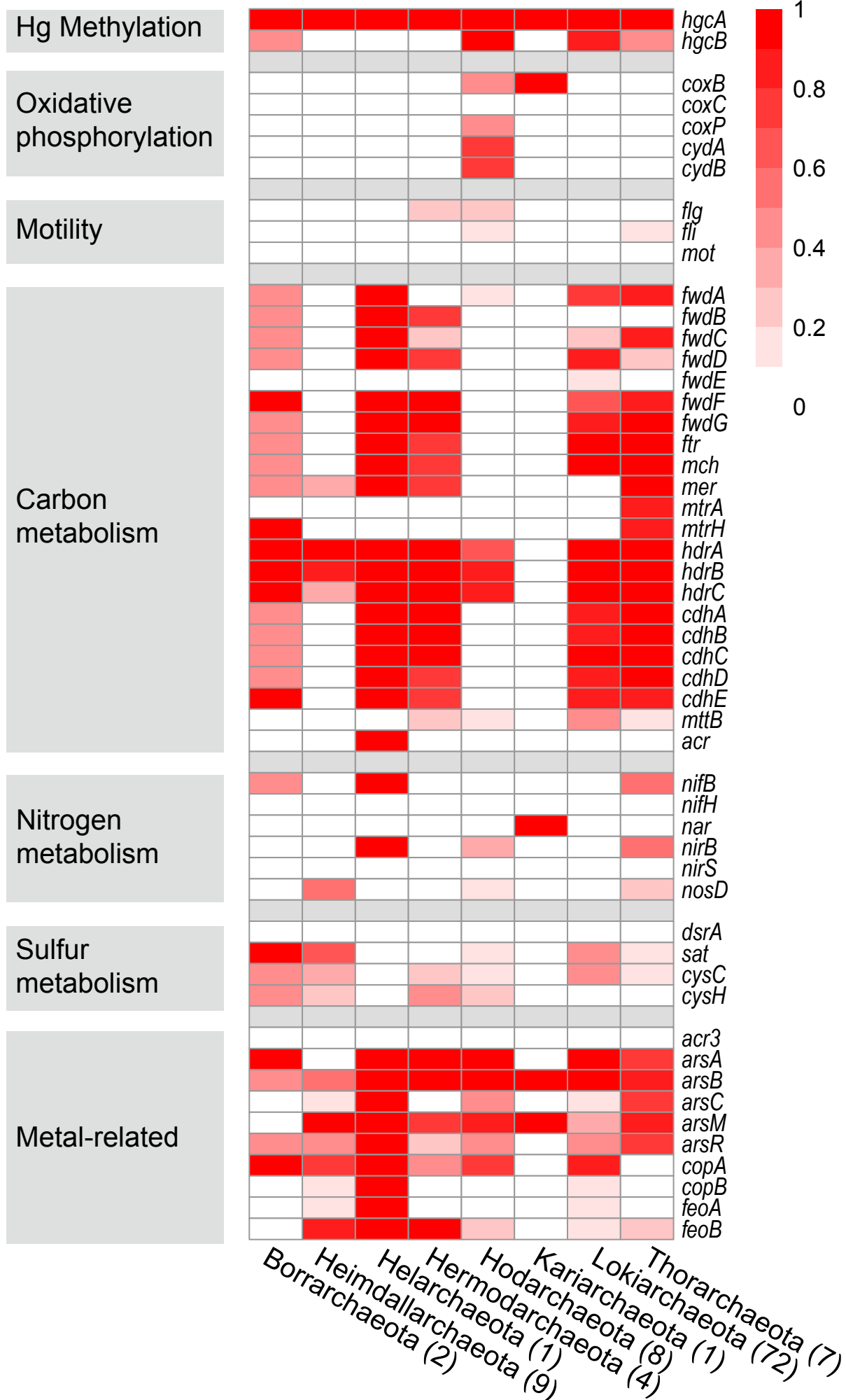


Fig. S7 Metabolic potentials of the *hgcA*-carrying Asgard MAGs. Taxonomic classifications of MAGs are represented at the bottom of heatmap. Corresponding numbers of MAGs are shown in parentheses. Genes are shown at the right of heatmap. Color of each cell refers to ratios of numbers of MAGs containing the corresponding gene to the total number of MAGs.

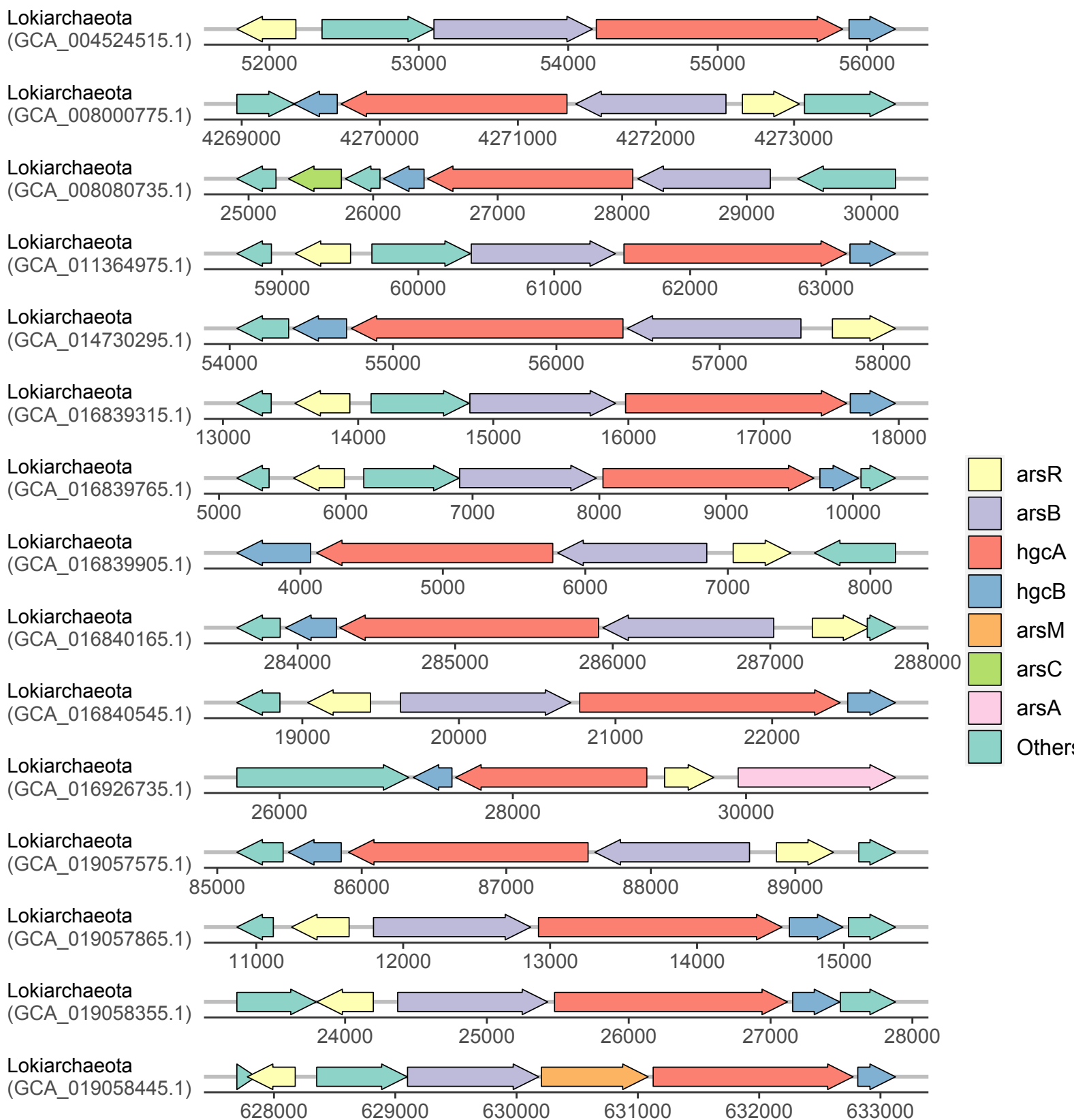


Fig. S8 Gene clusters of Asgard methylators containing *hgcA* and *ars* regions. Colors correspond to predicted functions of each gene. HgcAB sequences were identified based on HMMs, while all other genes were based on prodigal predictions.

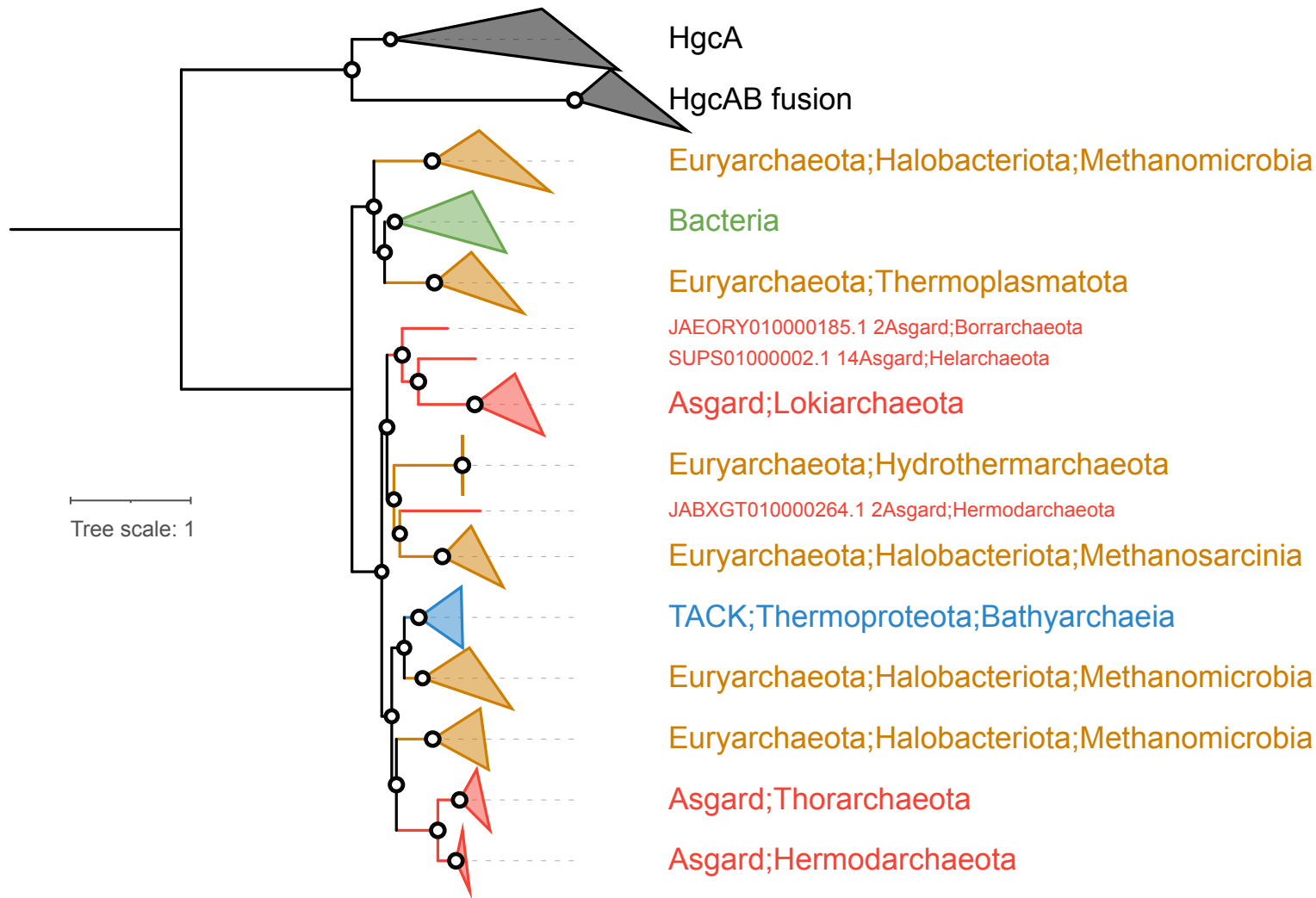


Fig. S9 Maximum likelihood phylogeny of HgcA and the WL pathway carbon monoxide dehydrogenase/ acetyl-CoA synthase gamma subunit (CdHε). HgcA and HgcAB clades were collapsed. Bootstrap support at nodes is indicated by white circles (>50). Some archaeal and bacterial taxa were collapsed and color-coded. CdHε sequences belonging to Euryarchaeota, TACK and Asgard are represented by orange, blue and red, respectively.