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Figure 1. Relative RNA expression of select metabolic genes. Selected genes are representative of major steps in metabolic pathways. We calculated the coverage of each gene at each sample by summing the mean per-base coverages of each contig in the sample with the corresponding annotation. Coverage values were normalized by dividing by the total number of RNA reads present in the sample.

Figure 2. Relative RNA expression levels of select bins. We calculated the mean per-base coverage of each MAG and then normalized by dividing by the total number of RNA reads in the sample. These values were then standardized to a 0-1 scale. A) Relative RNA expression of 56 MAGs at 9 samples. Red and blue legends indicate samples from Piccard and Von Damm vent fields, respectively. B) Relative RNA expression of all archaeal MAGs at 9 samples. Methanococcus MAGs are highlighted with a purple bracket; Methanomicrobia MAGs are highlighted with a red bracket.

Figure 3. Presence-absence table of key methanogenesis genes in 43 MAGs. Genes were selected to represent all steps of the CO2 🡪 methane, acetate 🡪 methane, and trimethylamine🡪methane pathways. Genes from all 73 MAGs were clustered using MCL; these clusters were matched to a functional annotation. Some protein clusters have annotations to >1 functionally similar genes. MAGs included in the table 1. had >1 methanogenesis gene or 2. shared a taxonomic classification with a MAG that had >1 methanogenesis gene. The tree along the horizontal axis shows the clustering of samples. The samples are divided into four metabolic groups based on methanogenic potential. Taxonomic groups highlighted in the text are indicated with brackets of the corresponding color.