

Archaeal Metabolic Profiles at Deep-Sea Hydrothermal Vents in the Mid-Cayman Rise

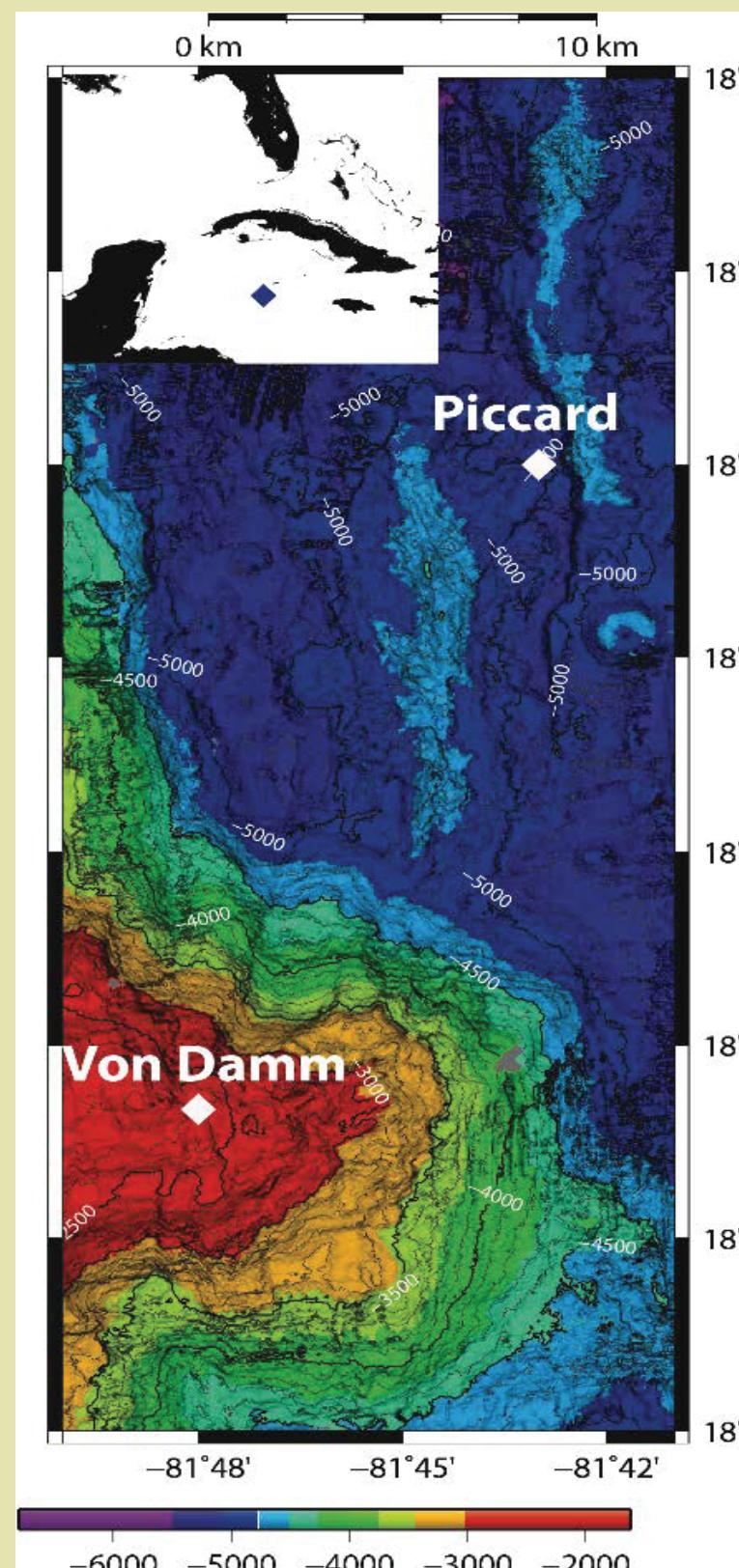
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Motivating Questions

1. What kinds of metabolic genes are found in the Mid-Cayman Rise vent fields?
 2. Which genes are most highly expressed at the community level?
 3. Which taxonomic groups have the highest rates of overall gene expression?
 4. What is the metabolic potential of each taxonomic group?



Introduction

Deep-sea hydrothermal vent systems host a wide diversity of bacteria, archaea and viruses. Although the geochemical conditions at these vents are well-documented, the relative metabolic activity of microbial lineages, especially among archaea, remains poorly characterized. The deep, slow-spreading Mid-Cayman Rise, which hosts the mafic-influenced Piccard and ultramafic-influenced Von Damm vent fields, allows for the comparison of vent sites with different geochemical characteristics. Previous metagenomic work (Revillaud et. al, 2016) indicates that despite the distinct geochemistry at Von Damm and Piccard, the overall functional profile of microbial communities between the two sites is similar.

Methods

Sequencing of metagenomes and metatranscriptomes was conducted on an Illumina Hi Seq 1000. Reads were assembled with IDBA (Peng et. al, 2010). Mapping was done with Bowtie2 (Langmead and Salzberg, 2012). We used anvi'o v2.3.2 (Eren et. al, 2015) for supervised binning of the metagenome-assembled genomes (MAGs) based on coverage and tetranucleotide frequency. We also used anvi'o v2.3.2 for the pangenomic analysis. Figures were generated using matplotlib (Hunter, 2007) and seaborn.

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- Key metabolic gene expression similar between Von Damm and Piccard
 - Von Damm: Higher evenness of gene expression
 - Methanogenesis gene (mcr) highly active compared to other metabolic groups
 - Key methane oxidation gene (pmoA) not expressed at any sites

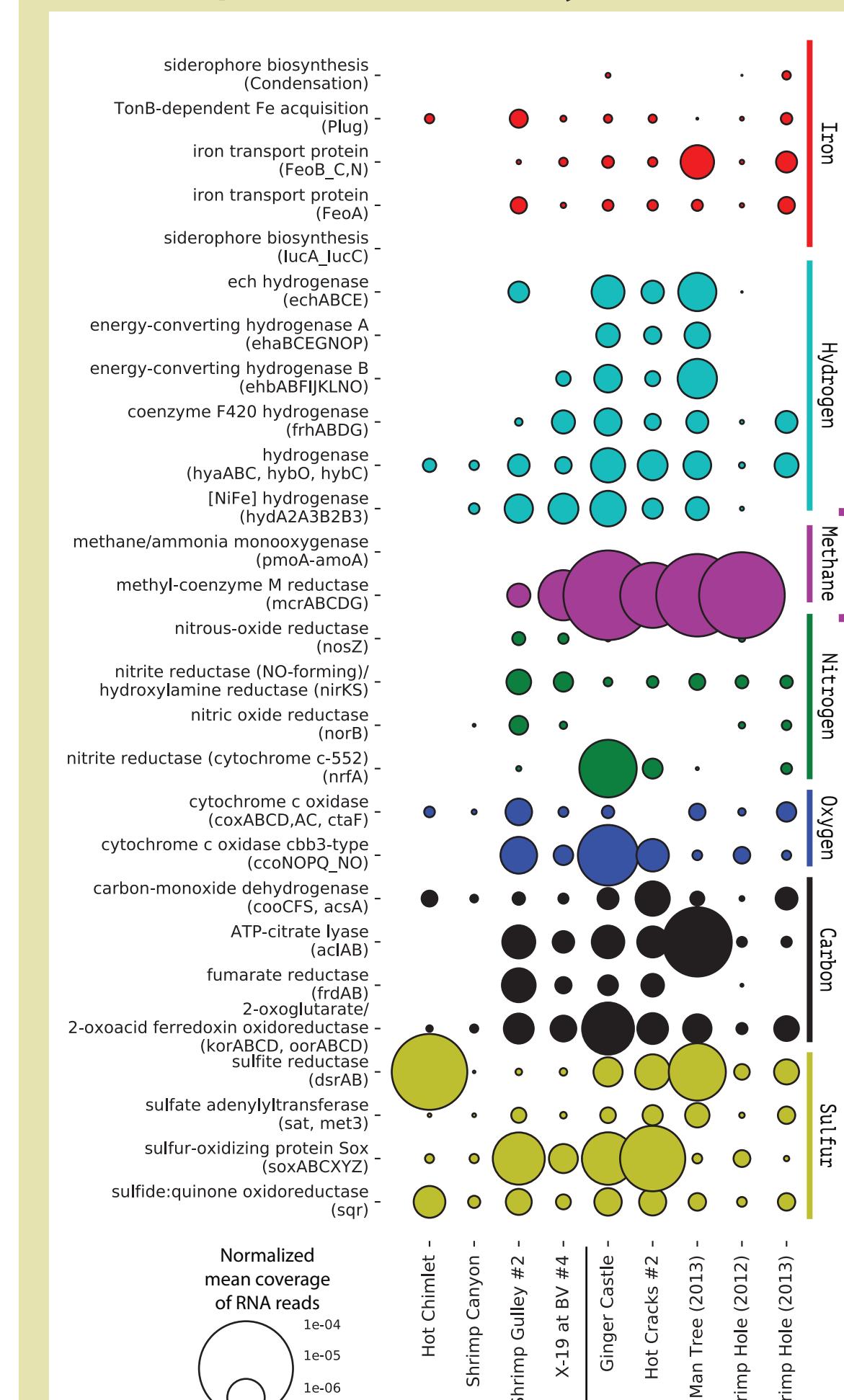


Fig. 1. RNA expression of key metabolic genes

- Results



Fig. 2. RNA expression of archaeal MAGs

- Methanomicrobia: Only active at Shrimp Hole site
 - Methanococci: active at all other sites

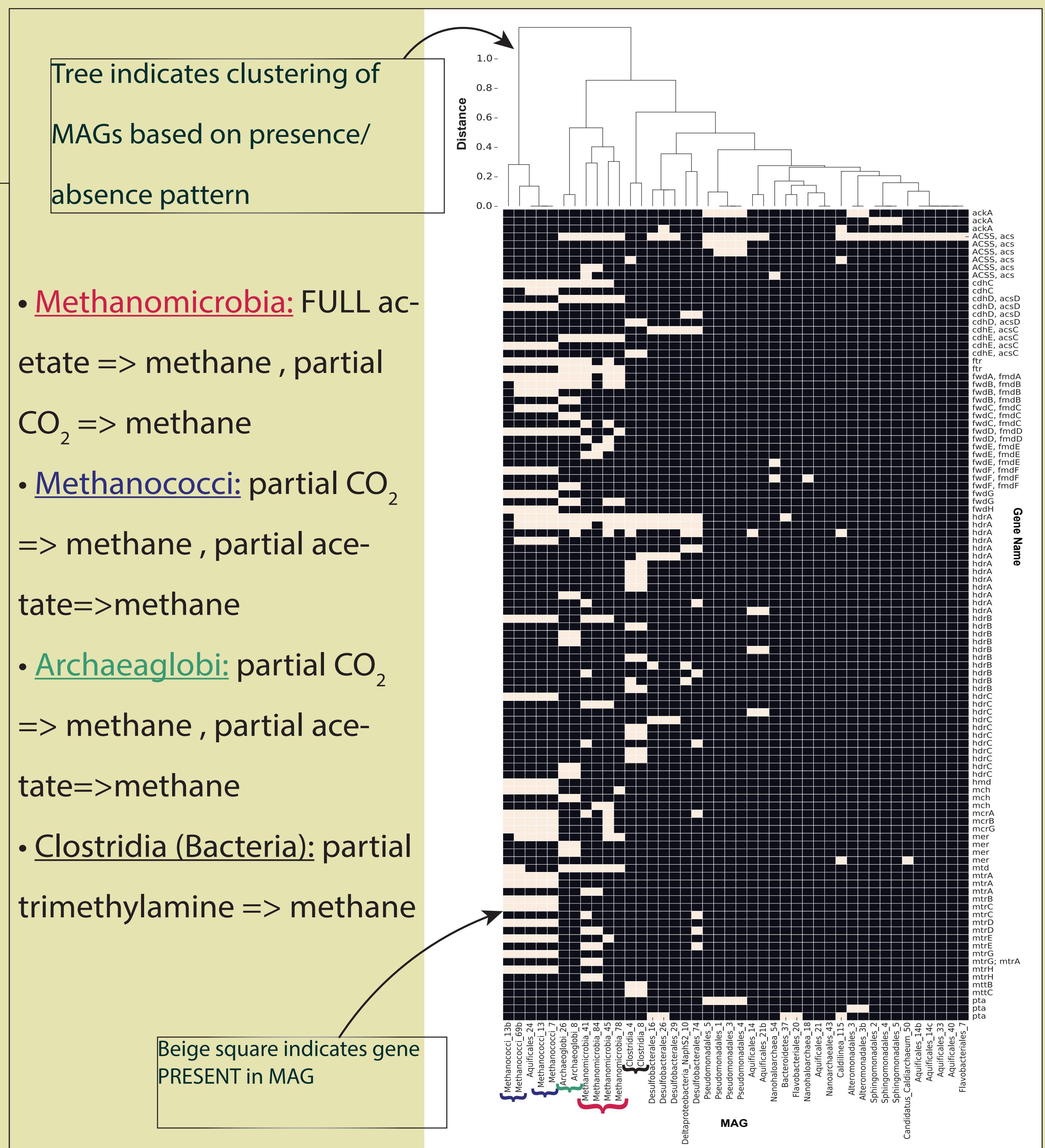


Fig. 3. Presence/absence of key methane genes in selected MAGs

Conclusions

- No obvious correlations between vent geochemistry and community-level expression of metabolic genes in the Mid-Cayman Rise
 - Genes for methane oxidation and sulfur redox most highly expressed
 - Previously identified methanogens *Methanococci* and *Methanomicrobia* (Evans et. al, 2015) control last step of methanogenesis (mcr gene)
 - Despite having similar methane metabolism profiles, *Methanococci* & *Methanomicrobia* show different expression levels at Shrimp Hole
 - In terms of metabolic potential, *Archaeoglobi*, *Methanomicrobia* and *Methanococci* are methane generalists rather than specialists

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