

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



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Motivating Questions

- Which metabolic genes are most highly expressed at the community level?
- Which taxonomic groups (esp. archaea) have the highest rates of overall gene expression?
- What is the metabolic potential (esp. methanogenesis) of each taxonomic group?
- What nutrient cycling relationships define community-level methane metabolism?

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 ultra-mafic-influenced Von Damm vent fields, allows for the comparison of vent sites with different geochemical characteristics. Previous metagenomic work (Reveillaud 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). Genes were called using Prodigal (Hyatt et al., 2010) and annotated using the IMG-JGI pipeline and the KO (Kanehisa and Goto, 2000) and Pfam (Finn et al., 2016) databases. 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.

Community-Level Metabolism

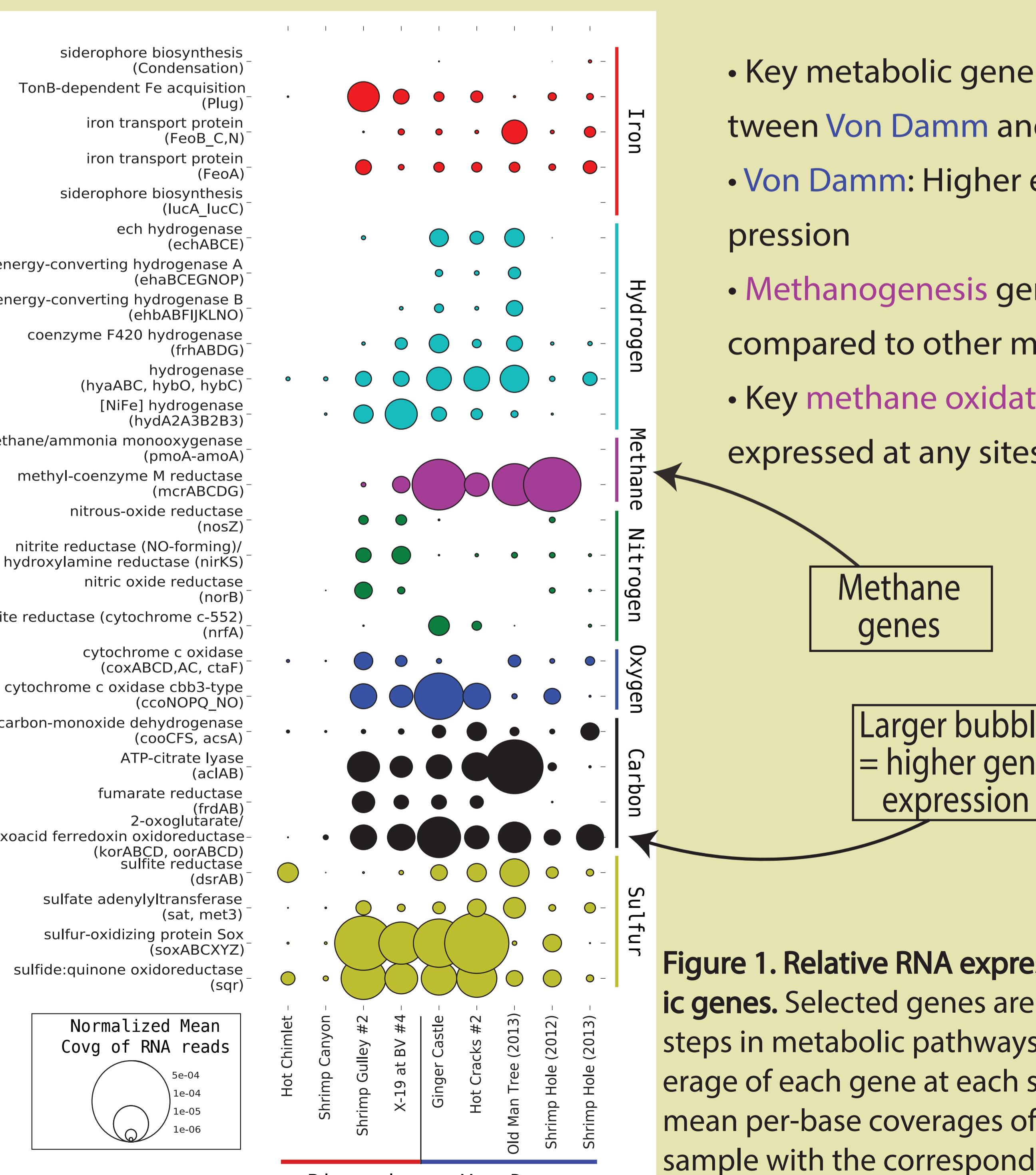


Figure 1. Relative RNA expression of select metabolic genes. Selected genes are representative of major steps in metabolic pathways. We calculated the coverage of each gene at each sample by summing the mean per-base coverages of each contig in the sample with the corresponding annotation. Coverage values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

Fig. 1

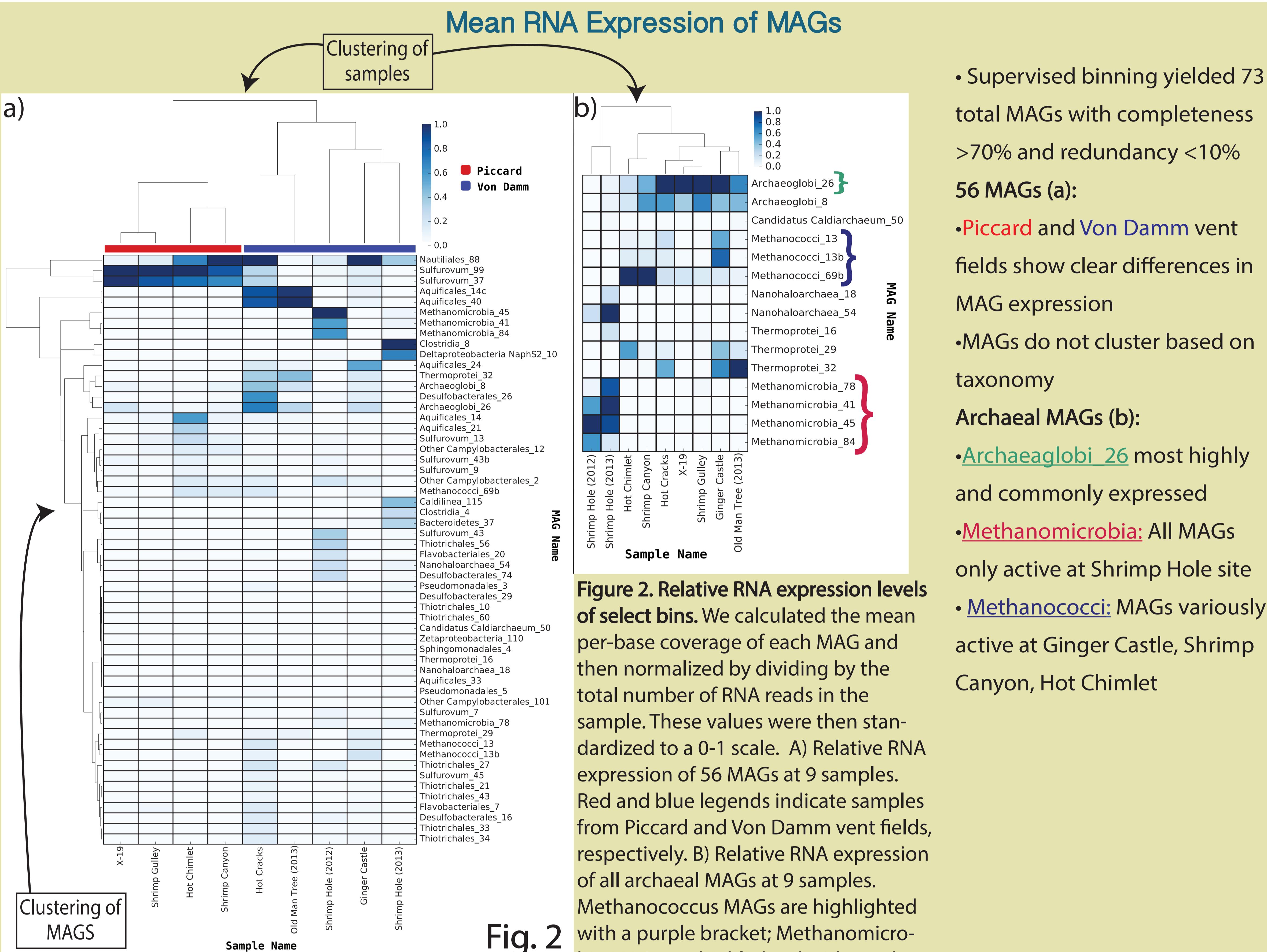


Fig. 2

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.

- Supervised binning yielded 73 total MAGs with completeness >70% and redundancy <10%
- 56 MAGs (a):
 - Piccard** and **Von Damm** vent fields show clear differences in MAG expression
 - MAGs do not cluster based on taxonomy
- Archaeal MAGs (b):**
 - Archaeoglobi_26 most highly and commonly expressed
 - Methanococcus: All MAGs only active at Shrimp Hole site
 - Methanomicrobia: MAGs variously active at Ginger Castle, Shrimp Canyon, Hot Chimlet

Conclusions

- No obvious correlations between vent geochemistry/vent field and community-level expression of metabolic genes in the Mid-Cayman Rise
- At the community level, genes for methane oxidation and sulfur redox most highly expressed
- Nautiliales and Sulfurovum are most active taxa overall
- Archaeoglobi are most active archaea
- Despite having similar methane metabolism profiles, Methanococci & Methanomicrobia show different expression levels across sample sites
- Previously identified methanogens Methanococci and Methanomicrobia (Evans et. al, 2015) control last step of methanogenesis (mcr gene)
- In terms of metabolic potential for methanogenesis, Archaeoglobi, Methanomicrobia and Methanococci are generalists rather than specialists
- Output of Archaeoglobi methane metabolism likely feeds into $\text{CO}_2 \rightarrow$ methane pathway of Methanococci and Methanomicrobia
- Methanococci and Methanomicrobia likely require Clostridia for trimethylamine \rightarrow methane metabolism
- Bacteria of metabolic Groups II and III (see Fig. 3) may contribute to acetate \rightarrow methane metabolism in Archaeoglobi, Methanococci, and Methanomicrobia

