

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

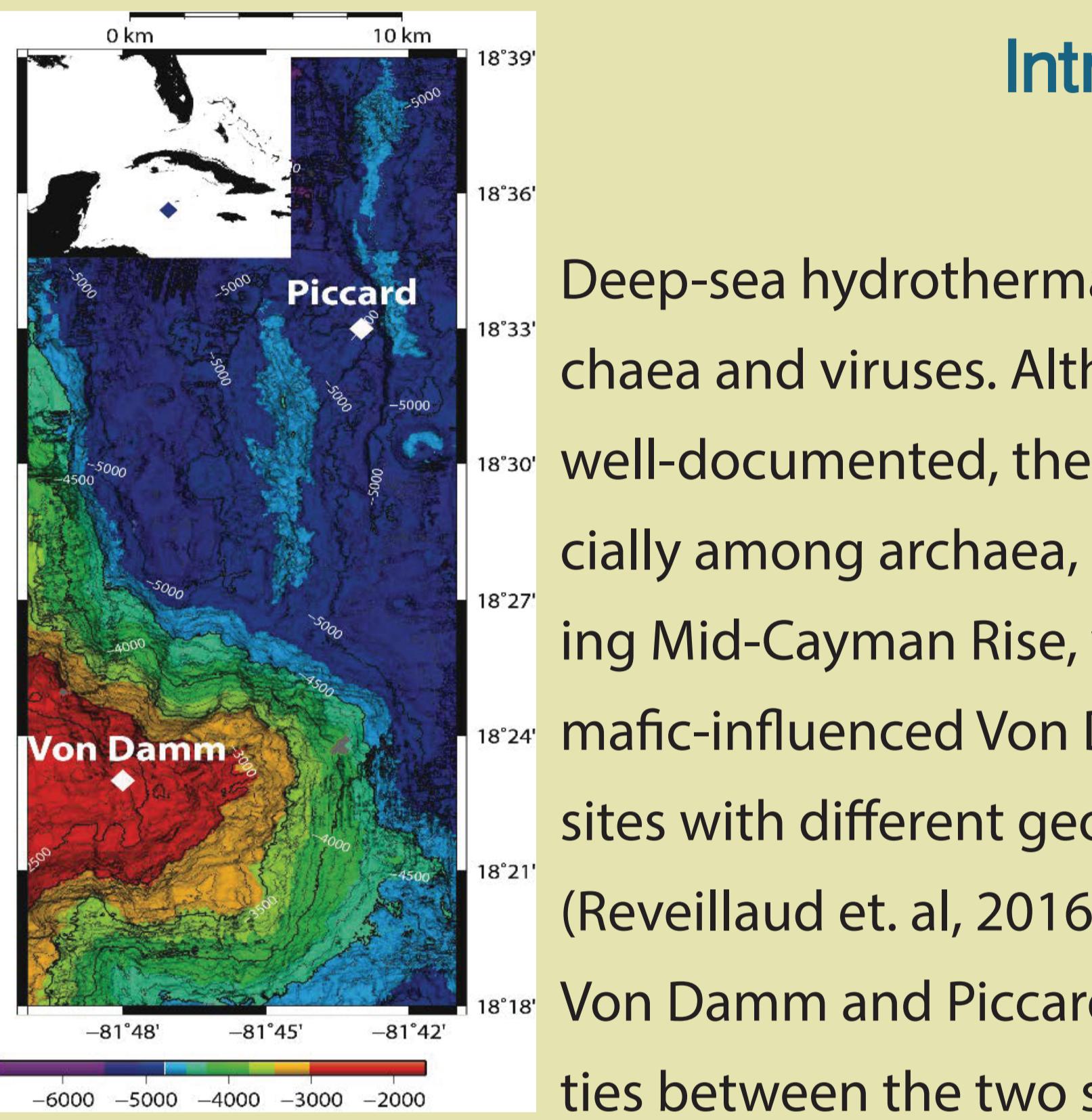
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Motivating Questions

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?



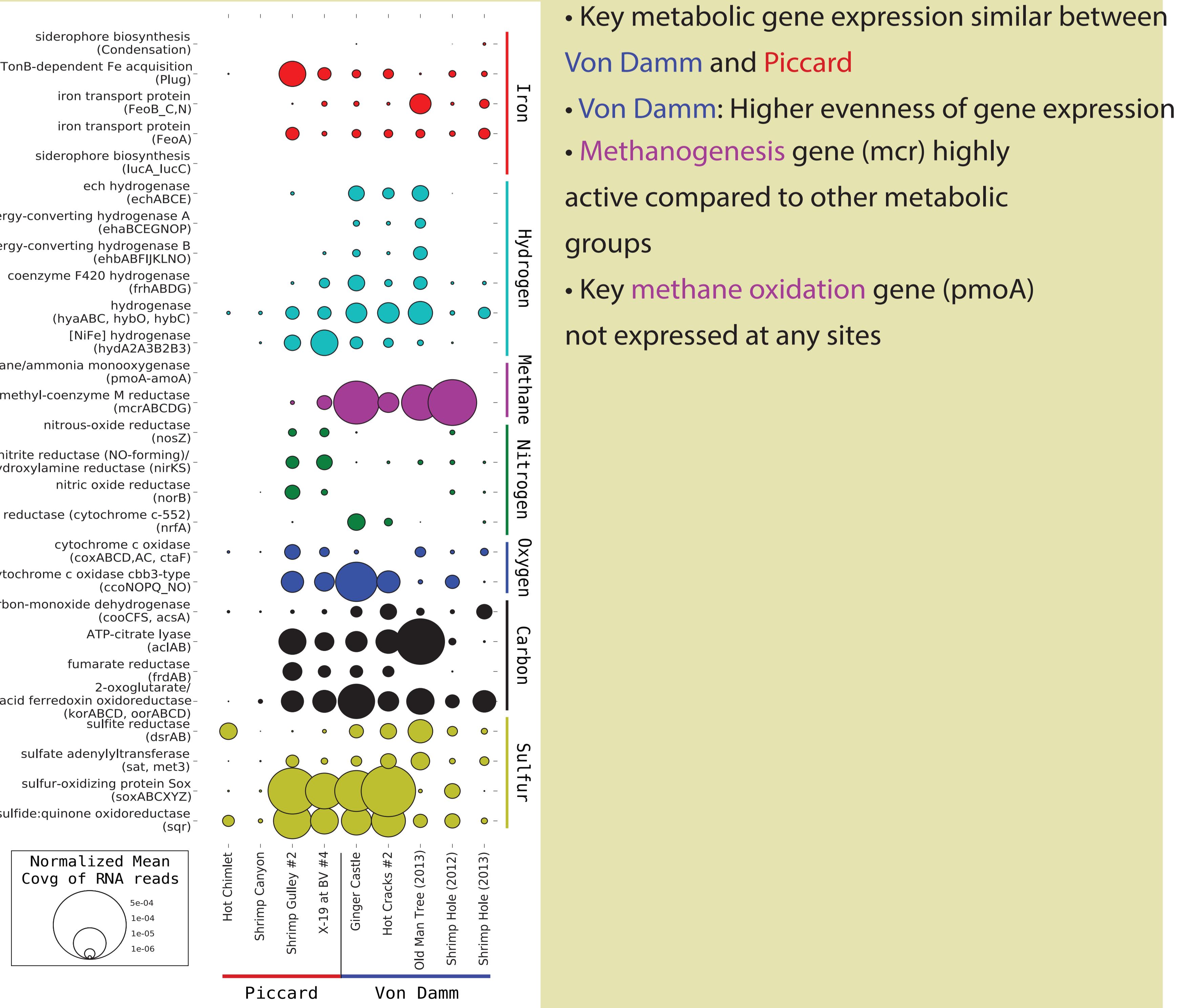
Introduction

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 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.

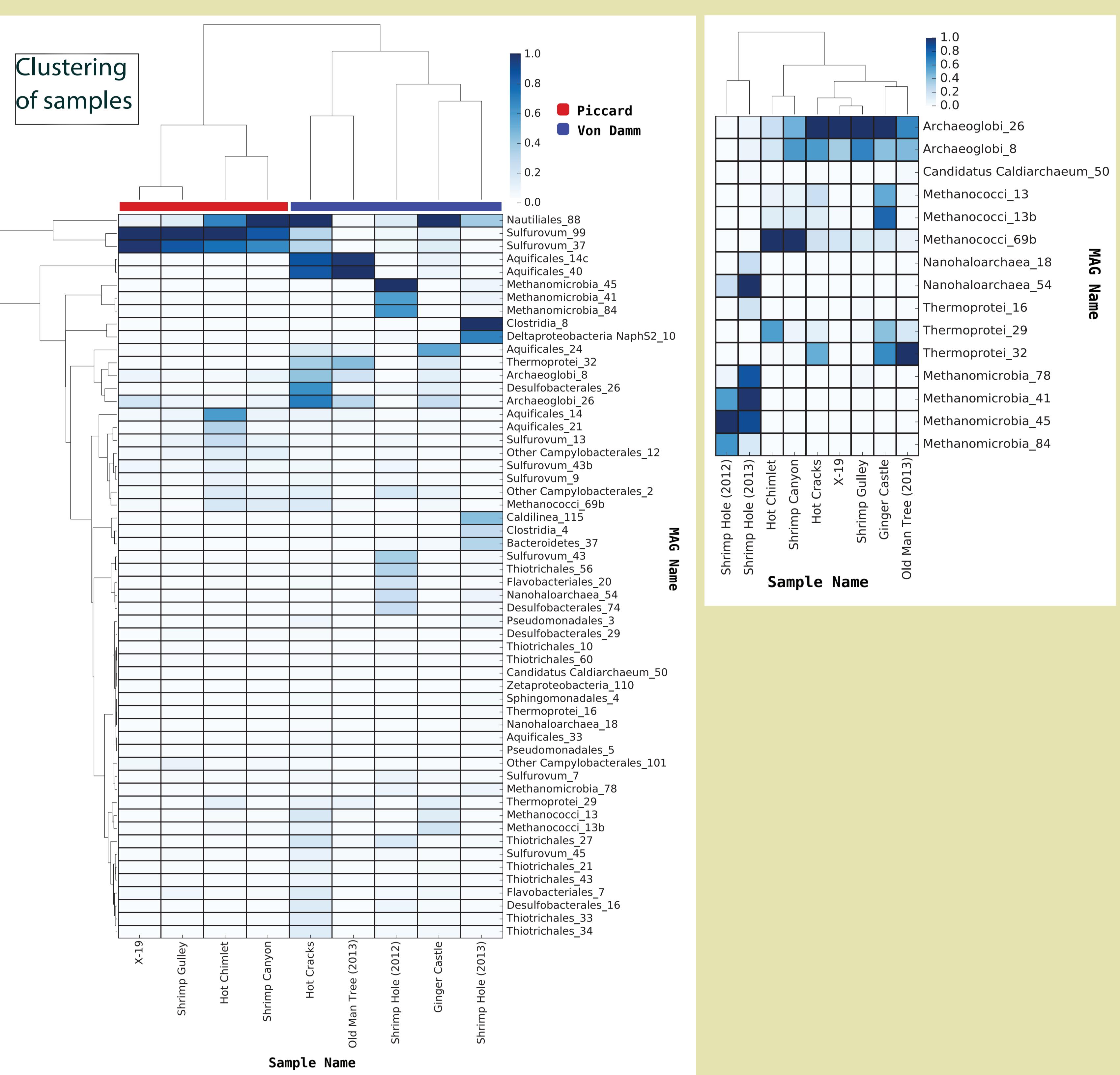
Methods

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 and annotated using the IMG-JGI pipeline. 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



MAG RNA Expression



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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