

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

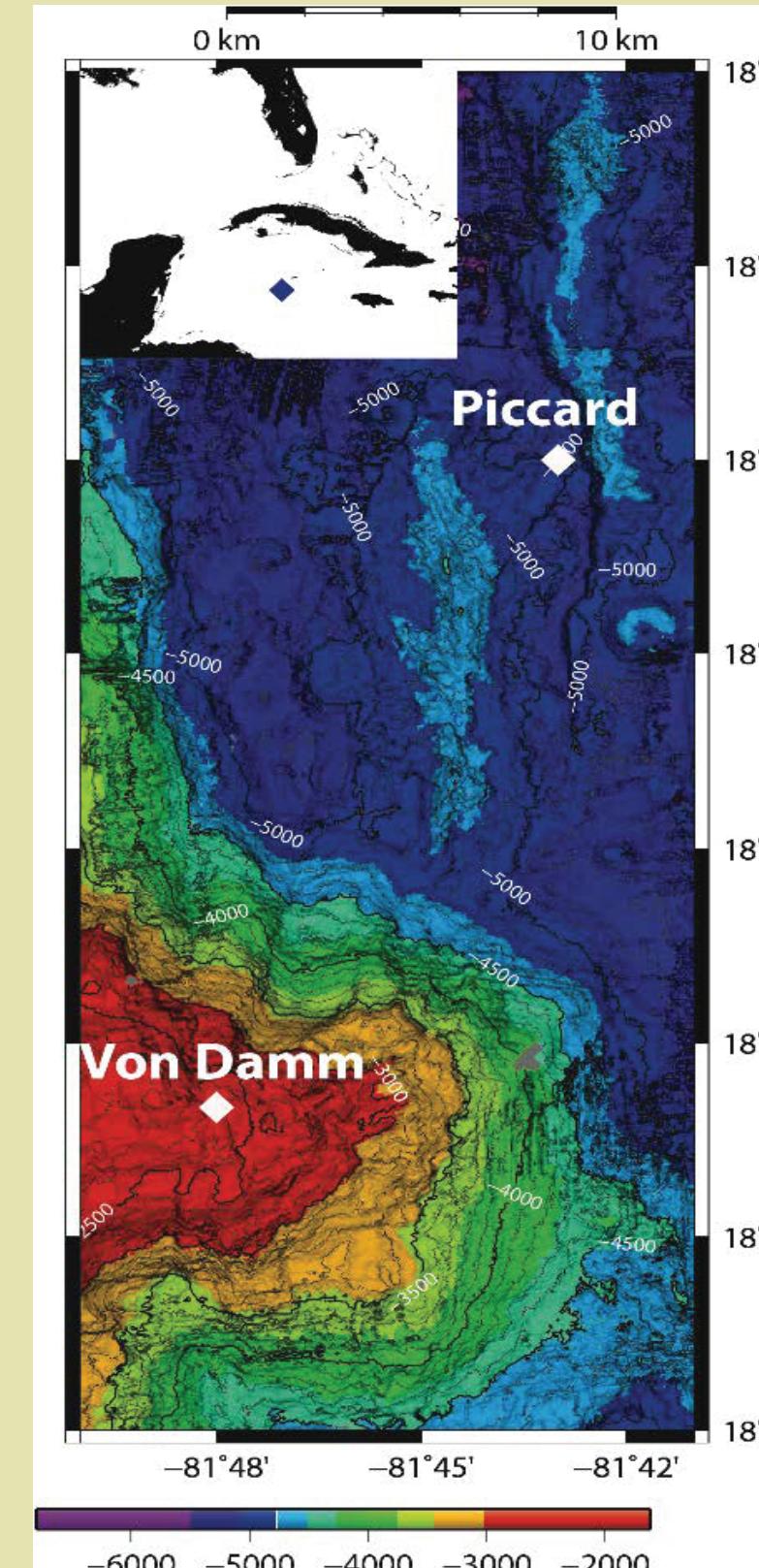
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# Motivating Questions

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?

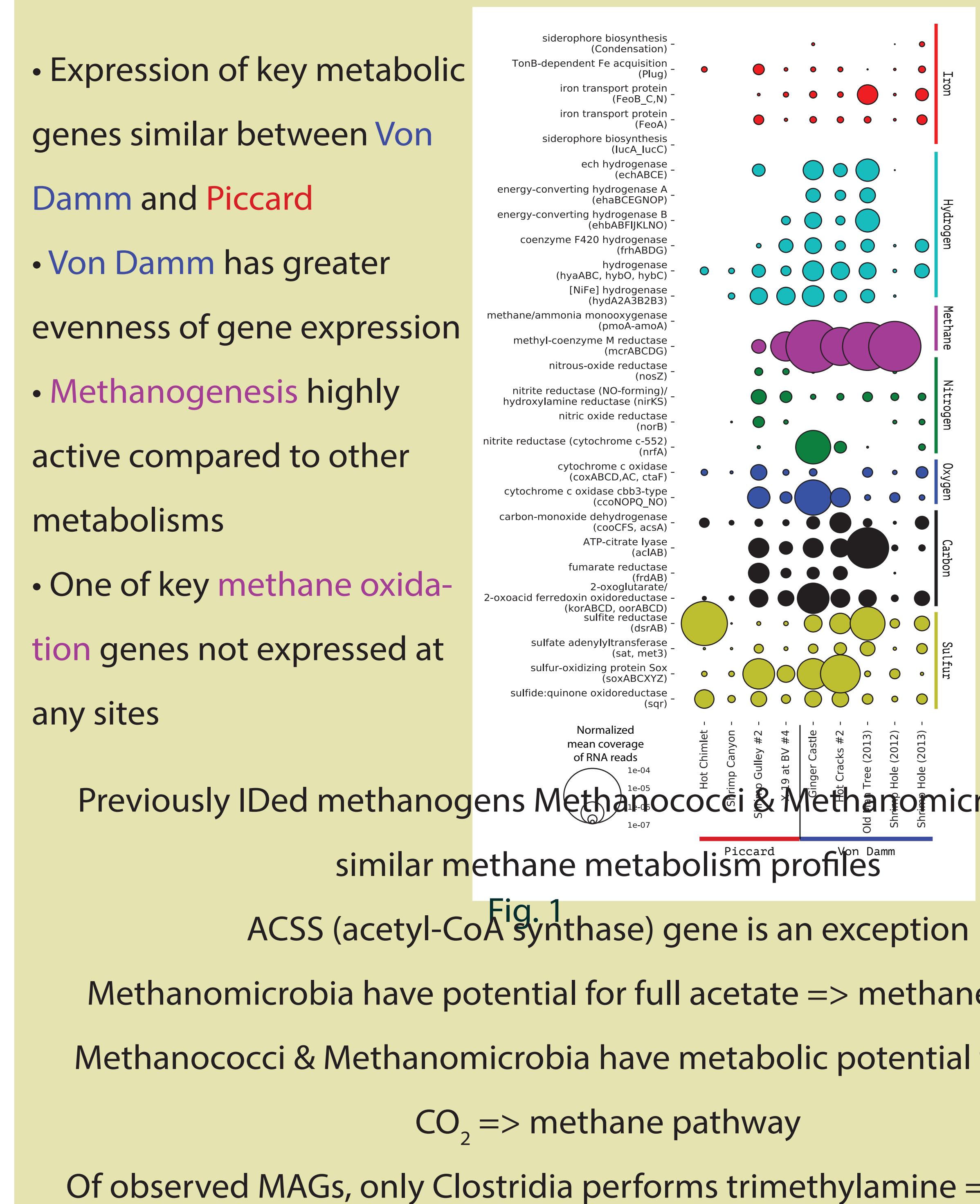


# Introduction

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

- Expression of key metabolic genes similar between Von Damm and Piccard
  - Von Damm has greater evenness of gene expression
  - Methanogenesis highly active compared to other metabolisms
  - One of key methane oxidation genes not expressed at any sites



# Fig. 1 ACSS (acetyl-CoA synthase) gene is an exception

Methanomicrobia have potential for full acetate => methane pathway

Methanococci & Methanomicrobia have metabolic potential for most of

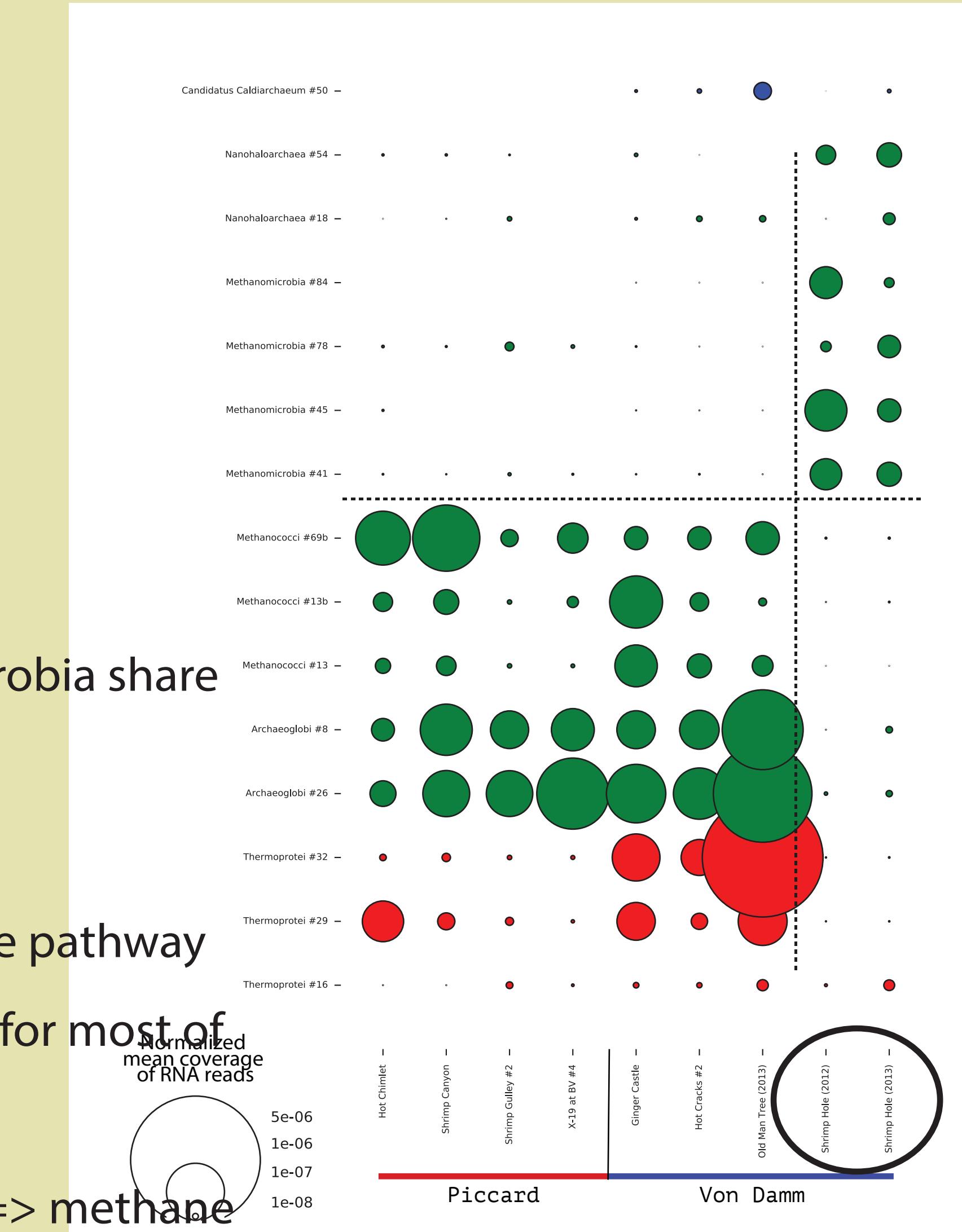
# $\text{CO}_2 \Rightarrow$ methane pathway

Of observed MAGs, only Clostridia performs trimethylamine => methane

g. 2

# Results

- Methanomicrobia only active at Shrimp Hole site; Methanococci active at all other sites



**Fig. 3**

# Conclusions + Future Directions

# Acknowledgements

# References