

The underappreciated role of chemoautotrophy in the *Geodia parva* holobiont

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Aim

The recently found sponge ground in the Central Arctic along Langseth Ridge (1, 2) is dominated by *Geodia parva*. Large, globally distributed sponge grounds are ecosystems that provide benthic structures that support suspension-feeding fauna and can serve as nurseries, shelter and feeding grounds for commercial fish species. This study seeks to explore the following questions:

- who are the main (most abundant and active) symbionts in the microbial community of *G. parva* at this location?
- what are their functions?
- how could they be contributing to the sponge holobiont's success under the specific conditions at this location?

A combination of transmission electron microscopy, metagenomics/ metatranscriptomics, and qPCR sheds light on unprecedented detail on microbial symbiont pathways in the northernmost sponge ground known to date.

References

- Morganti *et al.* (2022) *Nat. Comm.* DOI: 10.1038/s41467-022-28129-7
- Morganti *et al.* (2021). *Curr. Biol.* 31 DOI:10.1016/j.cub.2021.03.014
- Bayer *et al.* (2020). *mSystems* 5.e00473-20. DOI: 10.1128/mSystems.00473-20
- Busch *et al.* (2020). *Front. Mar. Sci.* 7. DOI: 10.3389/fmars.2020.00674.

Sampling Site

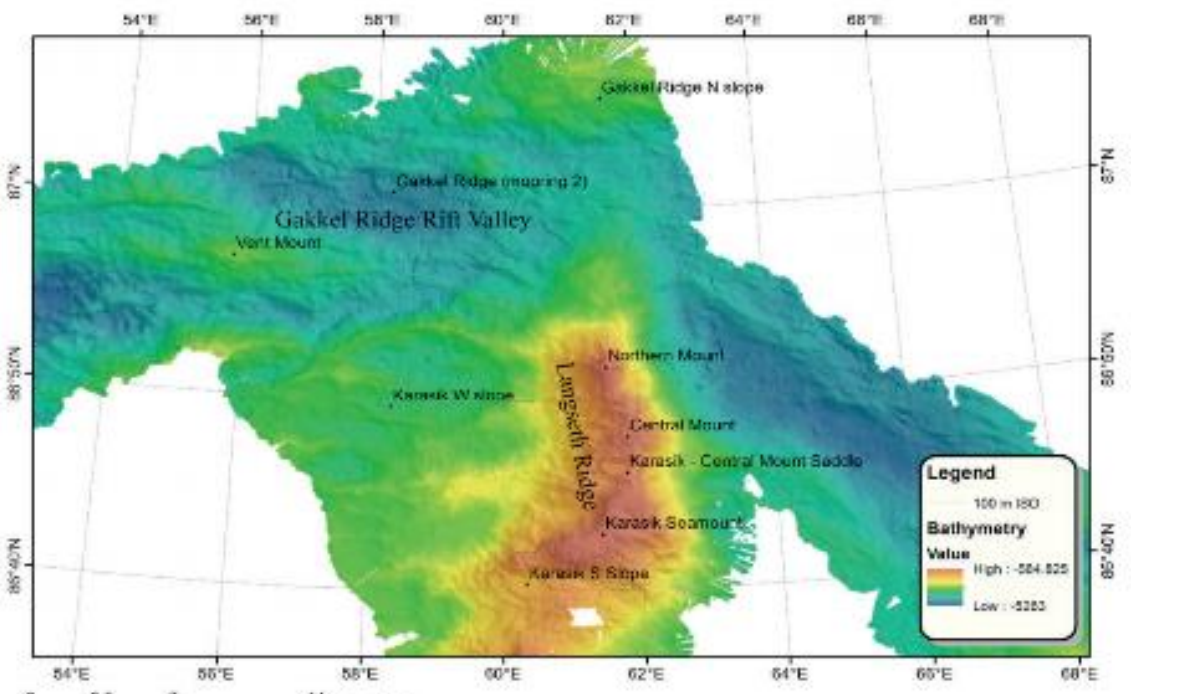


Figure 1: Sampling locations on RV Polarstern cruise PS101 in Sep-Oct 2016. Bathymetry shows the chain of seamounts along Langseth Ridge (87°N 62°E to 85°55'N 57°45'E) in the Central Arctic Ocean.

Objective

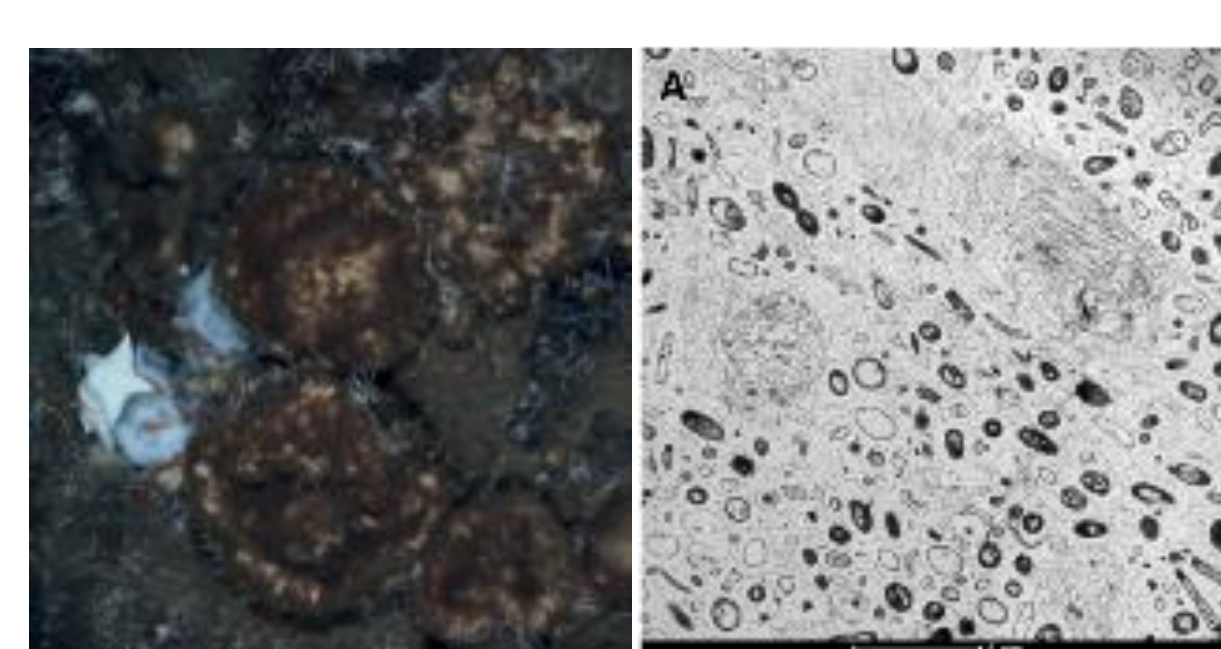


Figure 2: *Geodia parva* specimens at Langseth Ridge and a TEM picture of the sponge mesohyl showing microbial symbionts.

Conclusions

- Metagenomic and metatranscriptomic analysis showed that *Thermoproteota*, *Chloroflexota* and *Poribacteria* are the most active symbionts in *G. parva* sponges. qPCR confirmed relative symbiont abundances found earlier (1).
- Analysis of metabolic pathways provided strong evidence for chemoautotrophy (CO₂-fixation by rTCA cycle) a pathway that may contribute significantly to carbon assimilation (1) by the symbionts described above.
- Symbiont metabolism enables sponge life in this Arctic deep-sea habitat by adding autotrophic pathways (e.g., rTCA cycle, sulfate reduction) to the holobiont metabolism and thus making use of the available (anorganic) nutrients (1, 3, 4).

(i) 125 High Quality Metagenome-Assembled Genomes (MAGs)

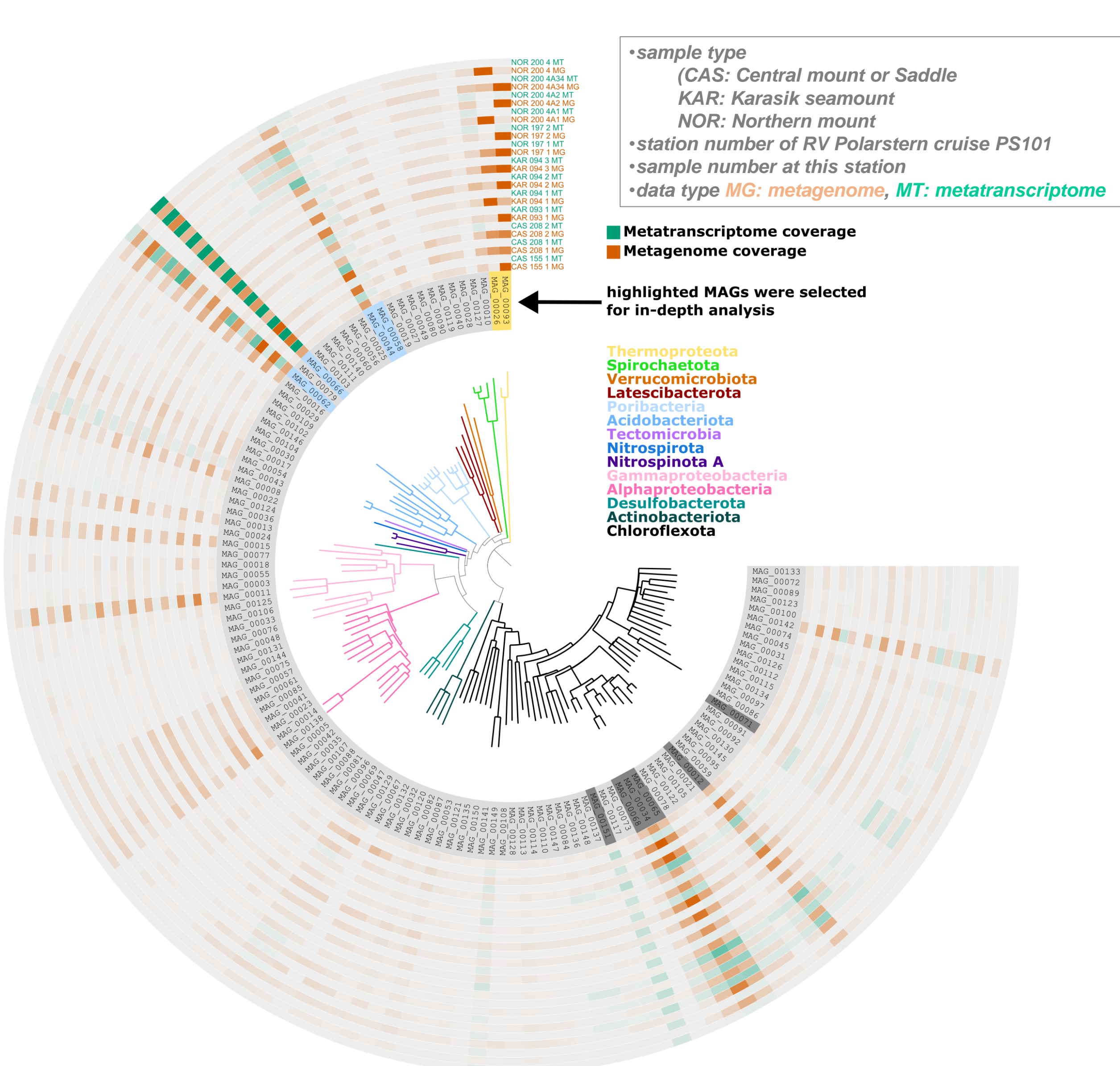


Figure 3: High-quality metagenome-assembled genomes (MAGs) with >70% completeness and <10% redundancy. Coverage information from metagenomic and metatranscriptomic reads was used to distinguish between MAGs concentrated in *G. parva* ($n=125$) as opposed to in sea water. From inside to outside: GTDB-Tk phylogenetic tree (colors indicate microbial phyla), MAG name (MAGs selected for in-depth analysis highlighted in the color of their respective phylum), 26 rings with mean coverage Q2Q3 data (green: metatranscriptome coverage; orange: metagenome coverage).

(i2) Symbiont Abundance

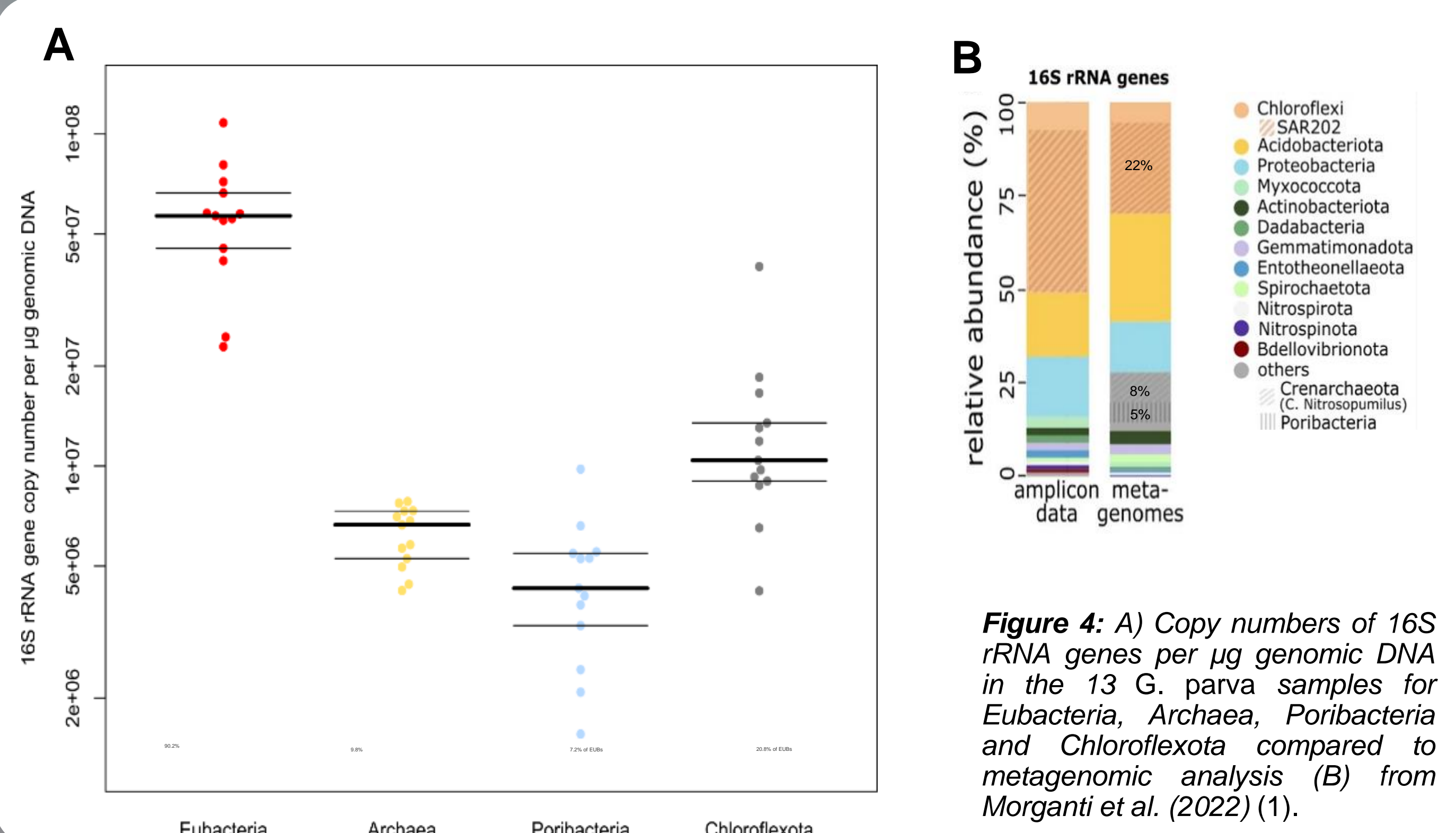


Figure 4: A) Copy numbers of 16S rRNA genes per μg genomic DNA in the 13 *G. parva* samples for Eubacteria, Archaea, Poribacteria and Chloroflexota compared to Morganti *et al.* (2022) (1). B) Relative abundance (%) of 16S rRNA genes in the 13 *G. parva* samples for Eubacteria, Archaea, Poribacteria and Chloroflexota compared to Morganti *et al.* (2022) (1).

(iii) Chemoautotrophy

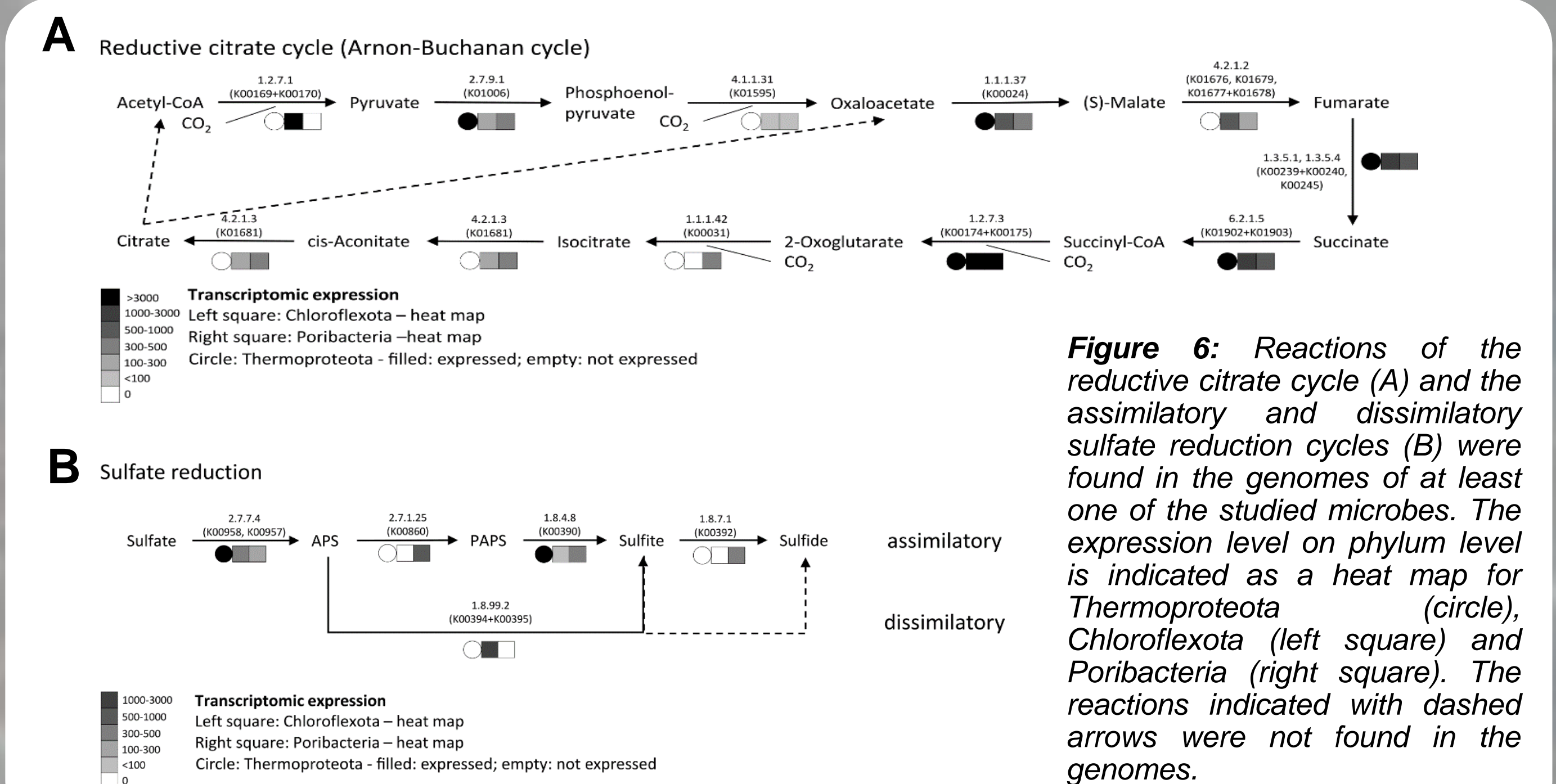


Figure 6: Reactions of the reductive citrate cycle (A) and the assimilatory and dissimilatory sulfate reduction cycles (B) as found in the genomes of at least one of the studied microbes. The expression level on phylum level is indicated as a heat map for Thermoproteota (circle), Chloroflexota (left square) and Poribacteria (right square). The reactions indicated with dashed arrows were not found in the genomes.

(ii) Metabolic Activity

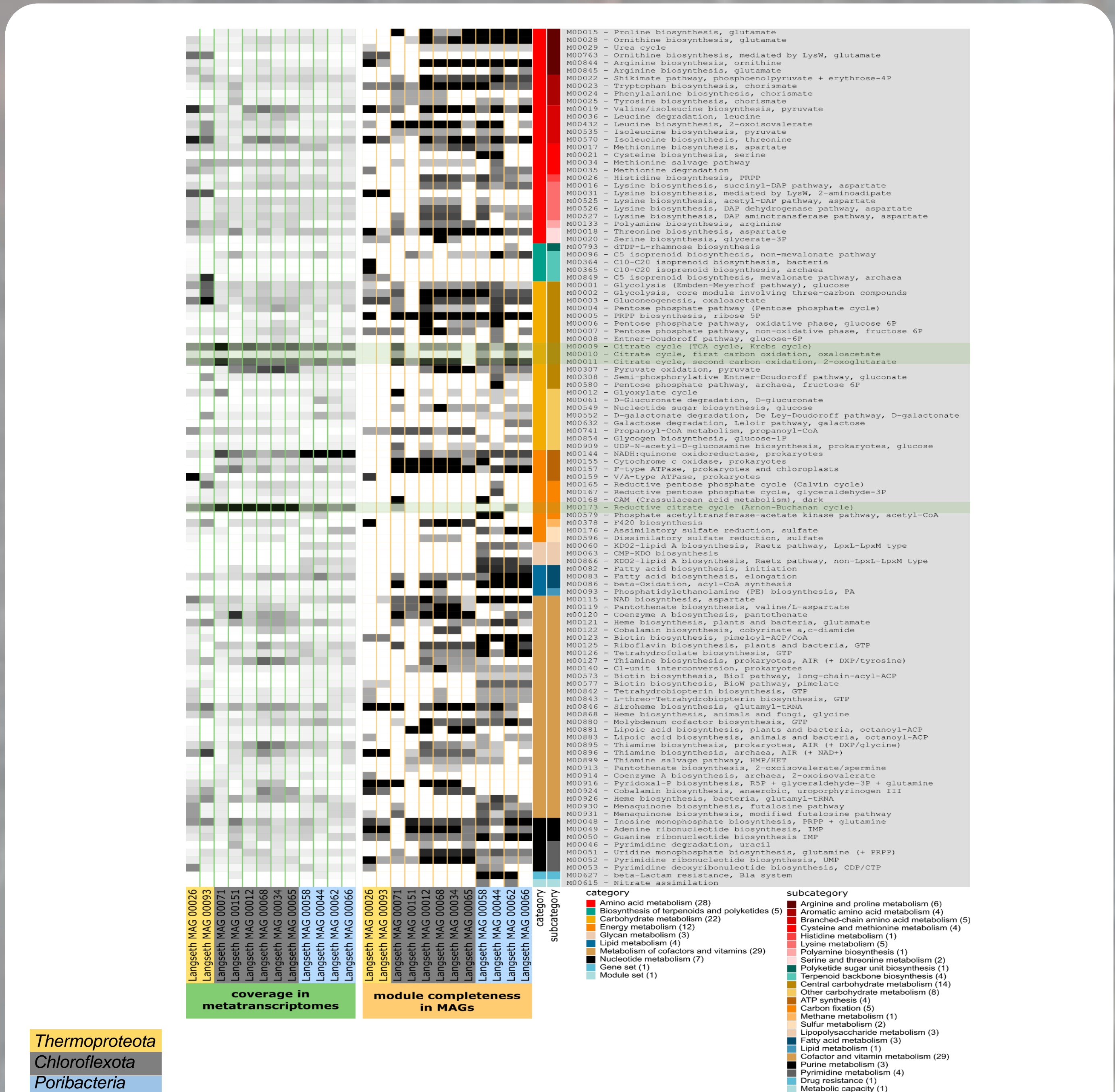


Figure 5: KEGG pathway modules with $\geq 60\%$ completeness in min. one of the MAGs, clustered by KEGG module classes, categories and subcategories (indicated by the colored bars next to the heat maps). Module names are listed on the right side. The heat map with the orange background shows the completeness of the respective module in each MAG from <60% completeness (white) to 100% (black). The heat map with the green background shows the coverage in the respective metatranscriptome.