

Metagenomic Insights into Microbial Adaptations to the North American Monsoon in Southwestern Arid Soils

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Introduction

- Dryland ecosystems cover around 41.5% of the terrestrial surface [1].
- Arid soil are harsh environments with high temperatures, high UV exposure and low water and nutrient availability [2,3].
- In Southwestern USA, the North American monsoon, delivers rainfall from July through September driving biological activity by alleviating water limitation for plants and microbes [4].
- Because pulse dynamics result in low plant productivity, soil microbial communities are the principal ecological drivers in arid ecosystem [5].
- The overarching goal of our study is to understand the genomic adaptations that enable arid soil microbial communities to survive in these harsh conditions and capitalize on monsoon rains.

Materials and Methods

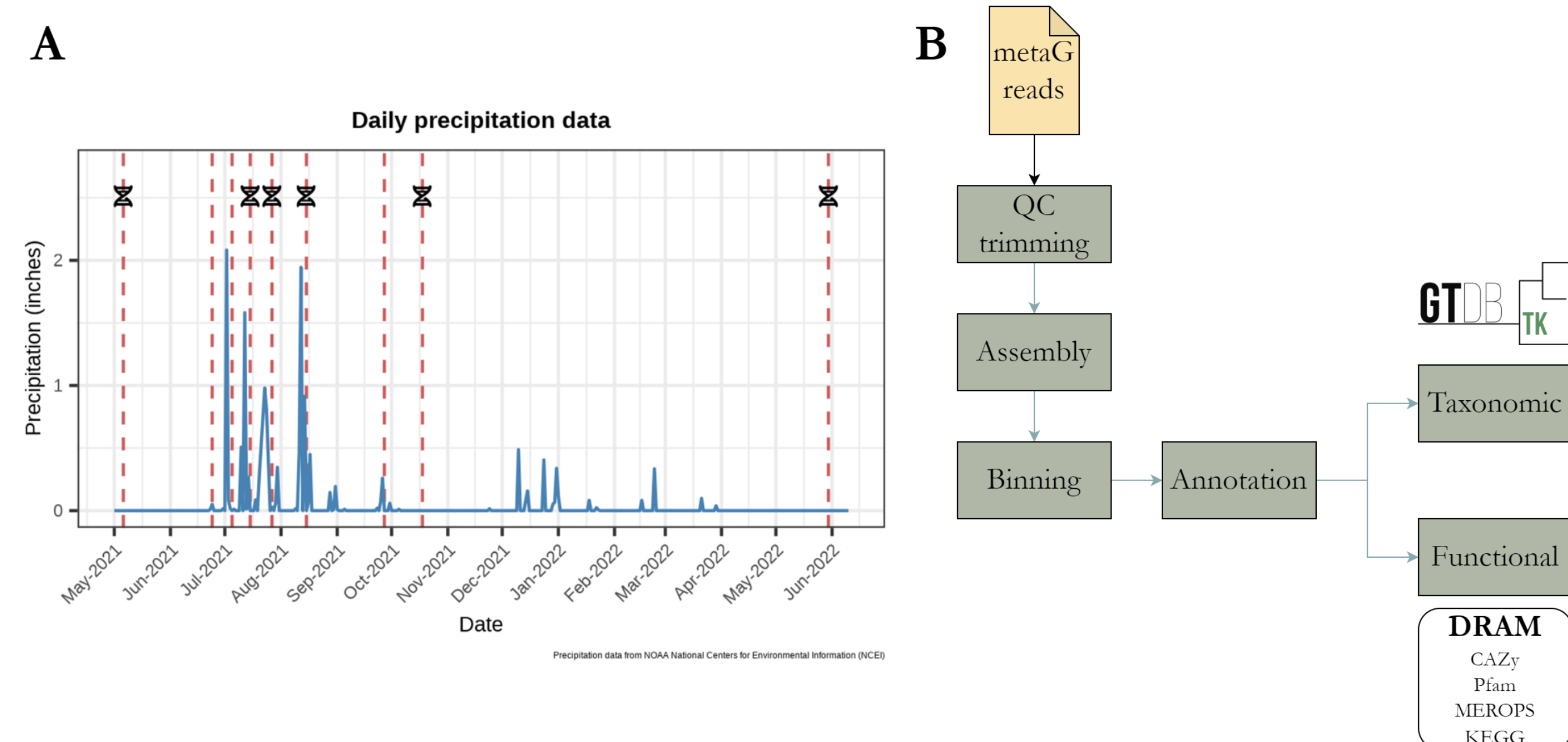


Figure 1. (A) Sampling dates when metagenomics data was collected. **(B)** Quick workflow of the metagenomics pipeline used for data analysis, including the databases used for taxonomical and functional annotation.

Results

- A total of 230 bacterial (Figure 2) and 7 archaeal metagenome-assembled genomes (MAGs) were recovered from the co-assembly of all collected datasets.

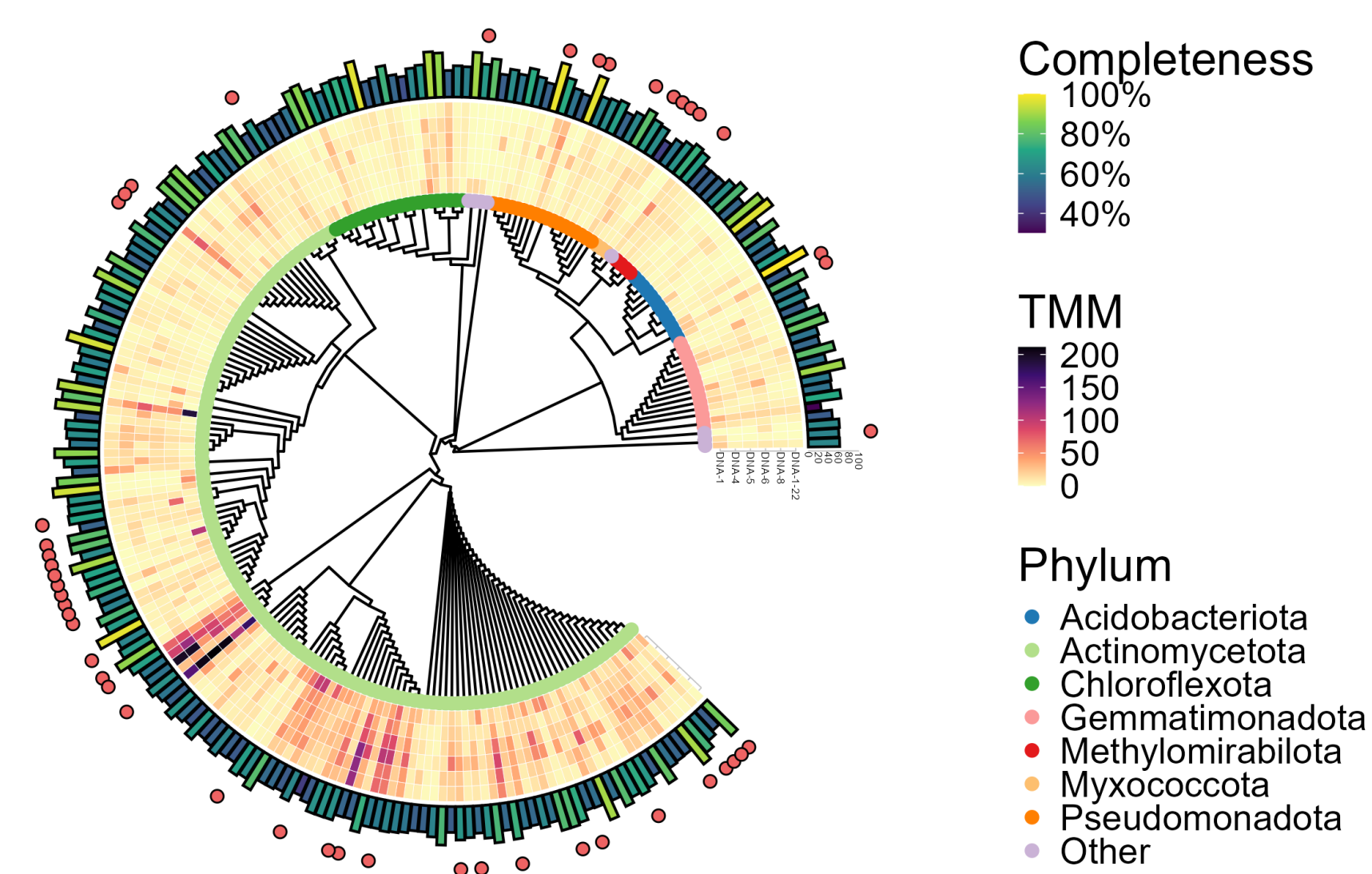


Figure 2. Phylogenetic tree of the recovered bacterial MAGs, showing their completeness. Red points indicate potential new species (< 95% ANI similarity to species in the database).

- MAGs annotation revealed that different phyla uses different strategies for survival in the desert (Figure 3 and Figure 4).

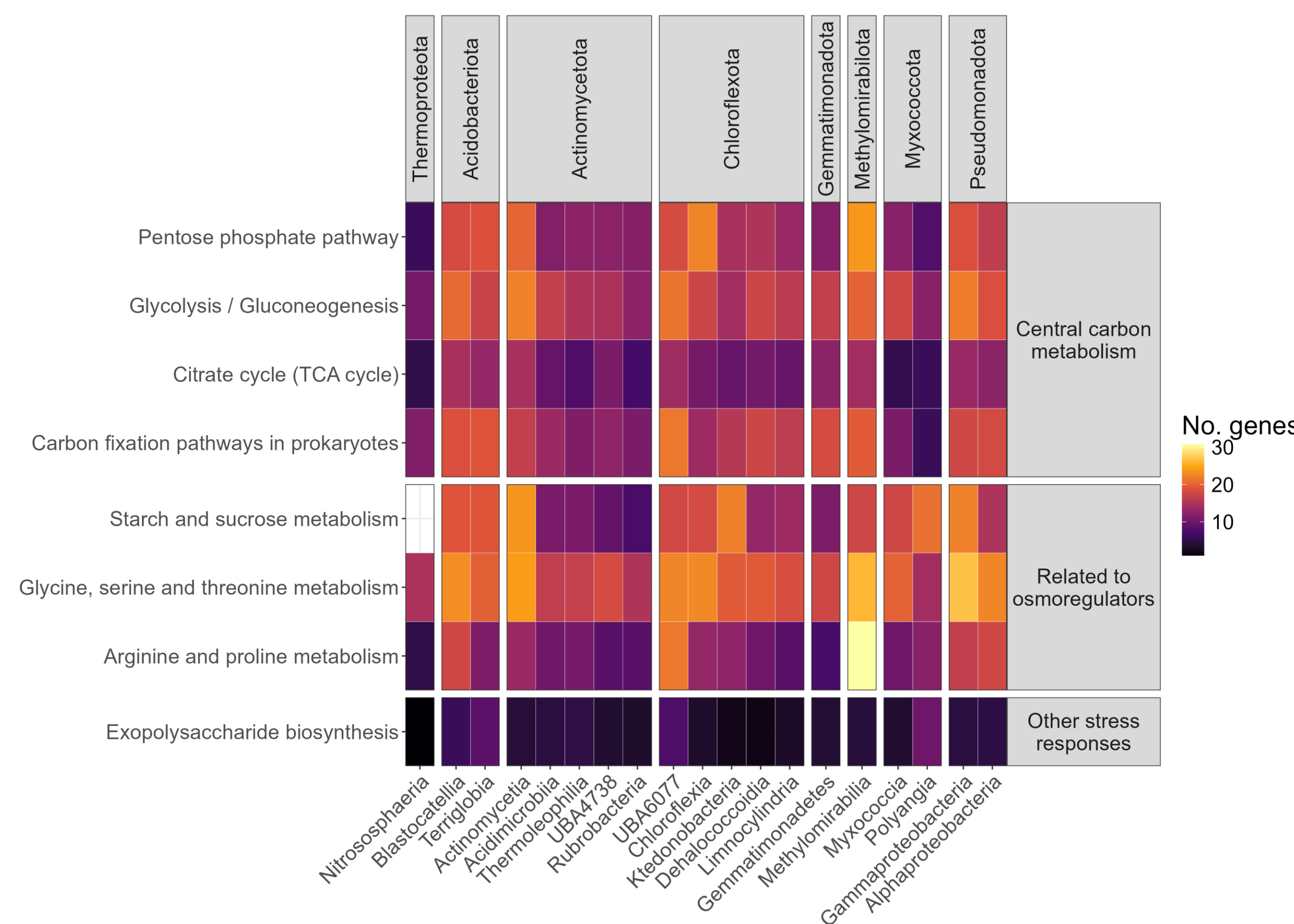


Figure 3. Average number of annotated genes per pathway for different bacterial and archaeal classes.

Results (Cont.)

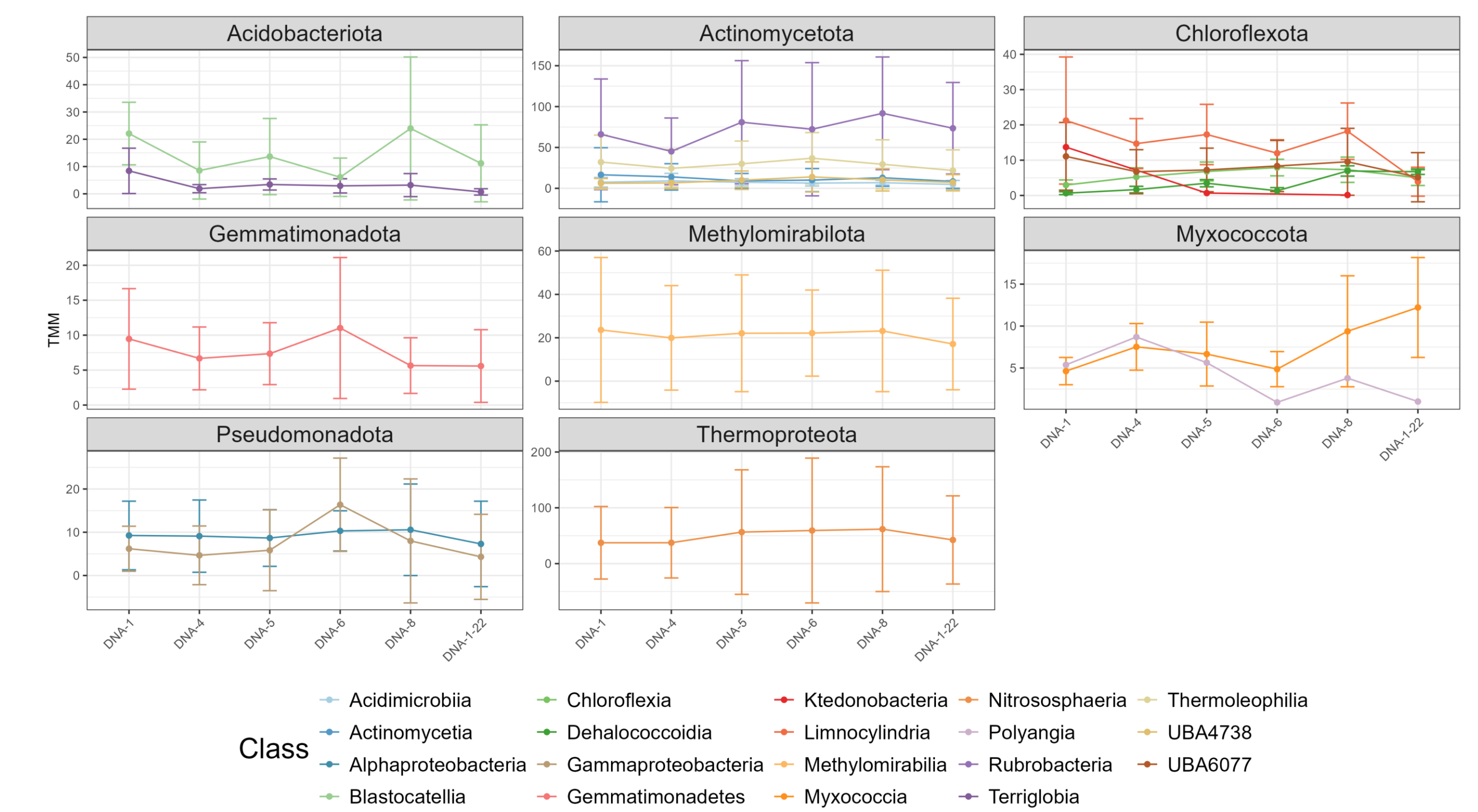
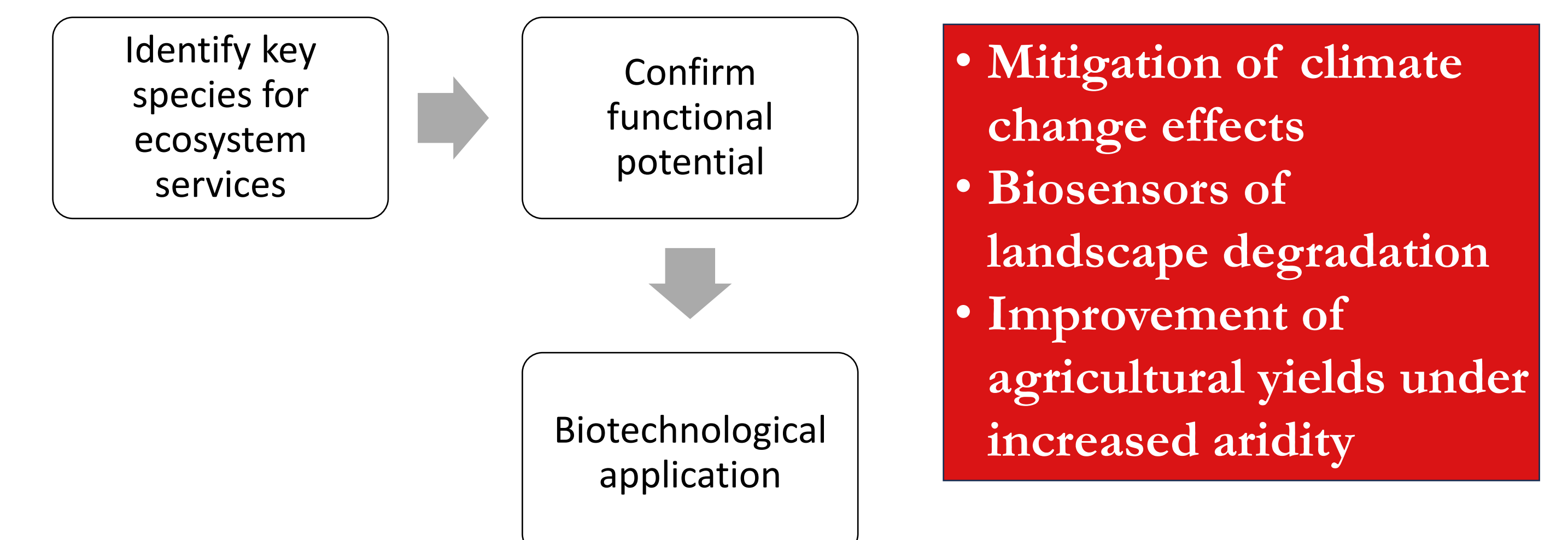


Figure 4. Changes in coverage (TMM) of the annotated sporulation genes among different classes of bacteria and archaea

Conclusions and Future Work

- Microbial communities present in the Sonoran Desert soil, seem to be stable throughout the different resource pulses.
- Prevalence of microbial groups characterized by high GC content (e.g., Actinobacteria) as well as groups known for their adaptability to arid conditions (e.g., Thermoproteota).
- Different taxa has evolved different survival mechanisms, which seem to persist over time.



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