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], and are harsh environments with high temperatures, high UV exposure and low water and nutrient availability [2,3].
- In Southwestern USA, the North American monsoon drives biological activity by alleviating water limitation for plants and microbes [4].
- Pulse dynamics make microbial communities 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.
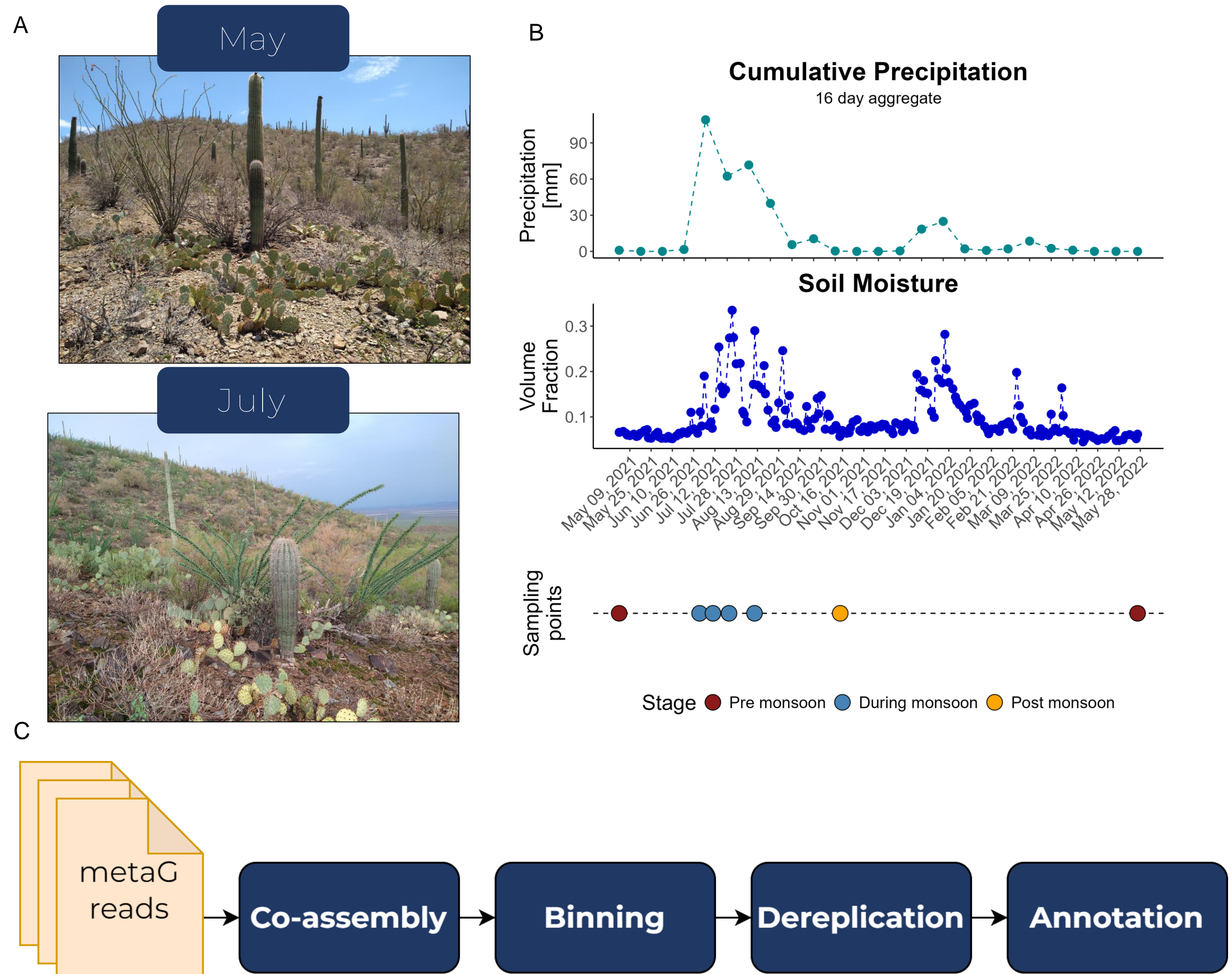
Materials and Methods

Figure 1. Soil samples were collected from the Saguaro National Park at multiple times during the 2021 North American monsoon season. (A) Pictures contrasting the changes in vegetation produced by the monsoon rains. (B) Precipitation and soil moisture at the sampling site. Data from the USCRN [6,7] and NASA SMAP [8]. During the monsoon, samples were collected within 72 hours of a precipitation event. (C) Simplified metagenomics workflow.

Results

- The analysis of the taxonomic profile (inferred with SingleM[9]) of the samples revealed that microbial communities remain mostly stable throughout the monsoon season.
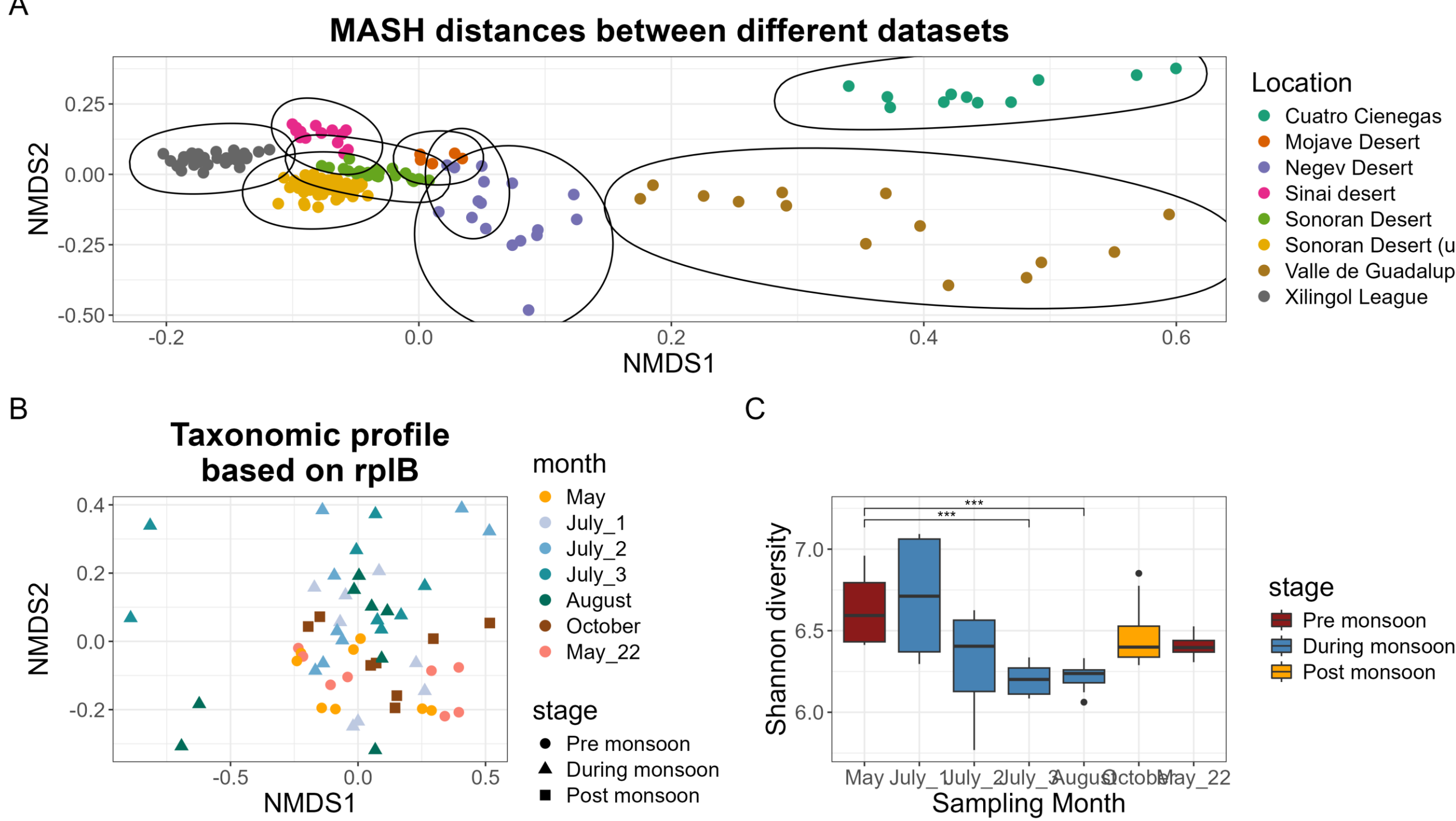

Figure 2. (A) Comparison with other metagenomic datasets based on MASH distances. (B) NMDS ordination based on OTU abundances inferred by SingleM using the single copy gene rplB. (C) Boxplot of the Shannon diversity index calculated based on OTU abundances.
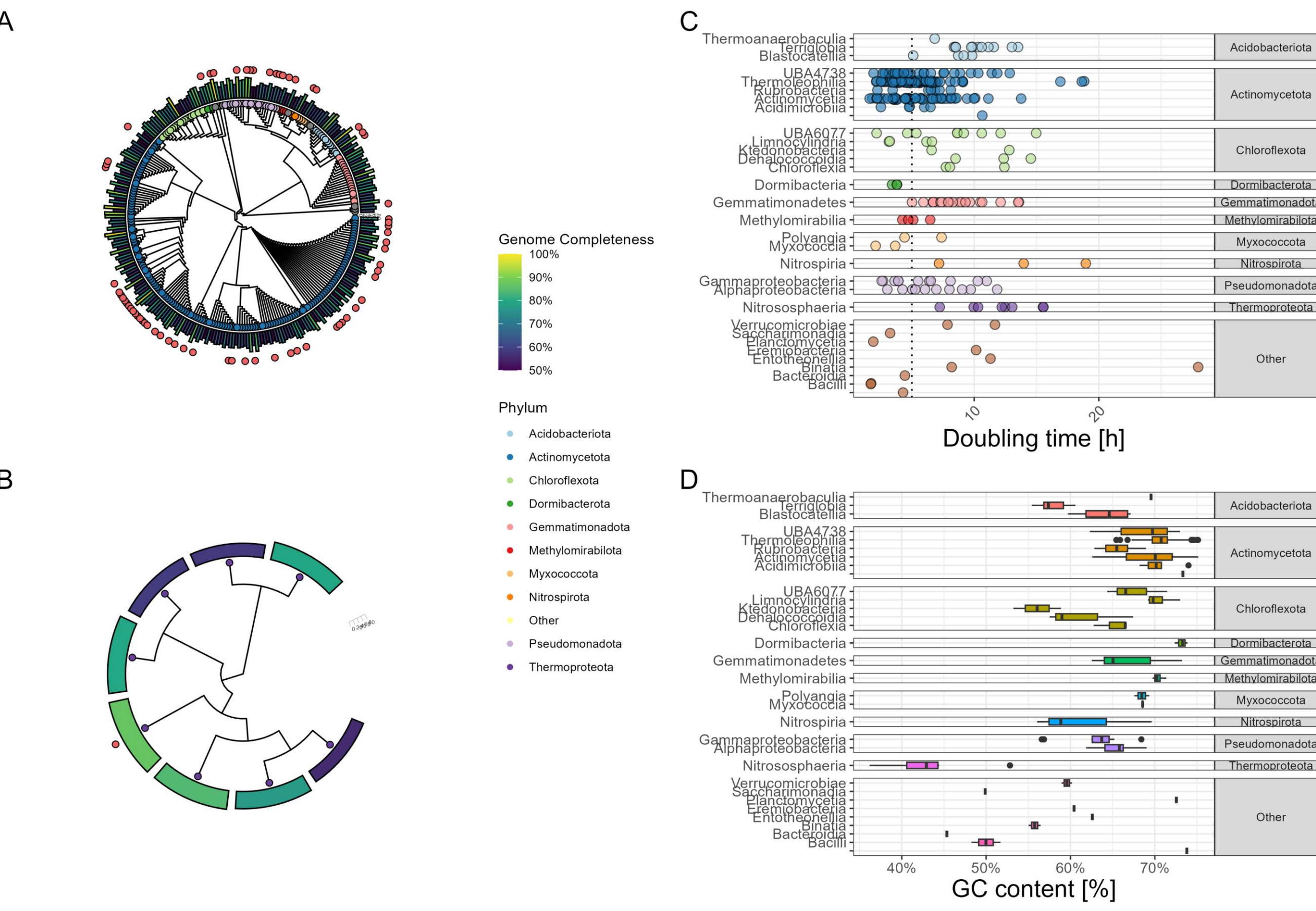

Figure 3. Phylogenetic tree of the recovered bacterial MAGs from the (A) Bacteria and (B) Archaea domains. Colored bars show their completeness. Red points indicate potential new species (< 95% ANI similarity to species in the database). (C) Predicted doubling time based on codon usage bias. (D) GC content of each recovered MAG.
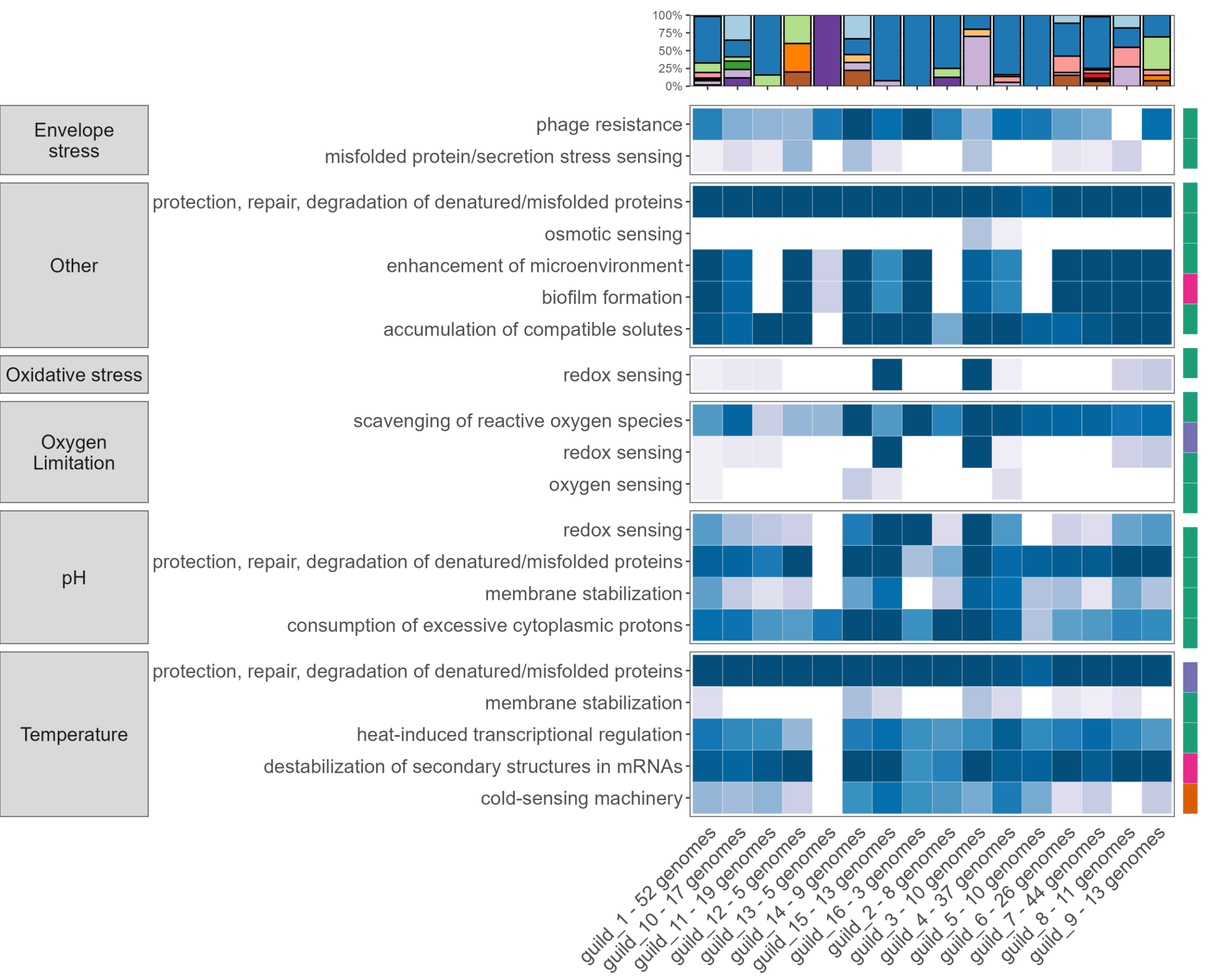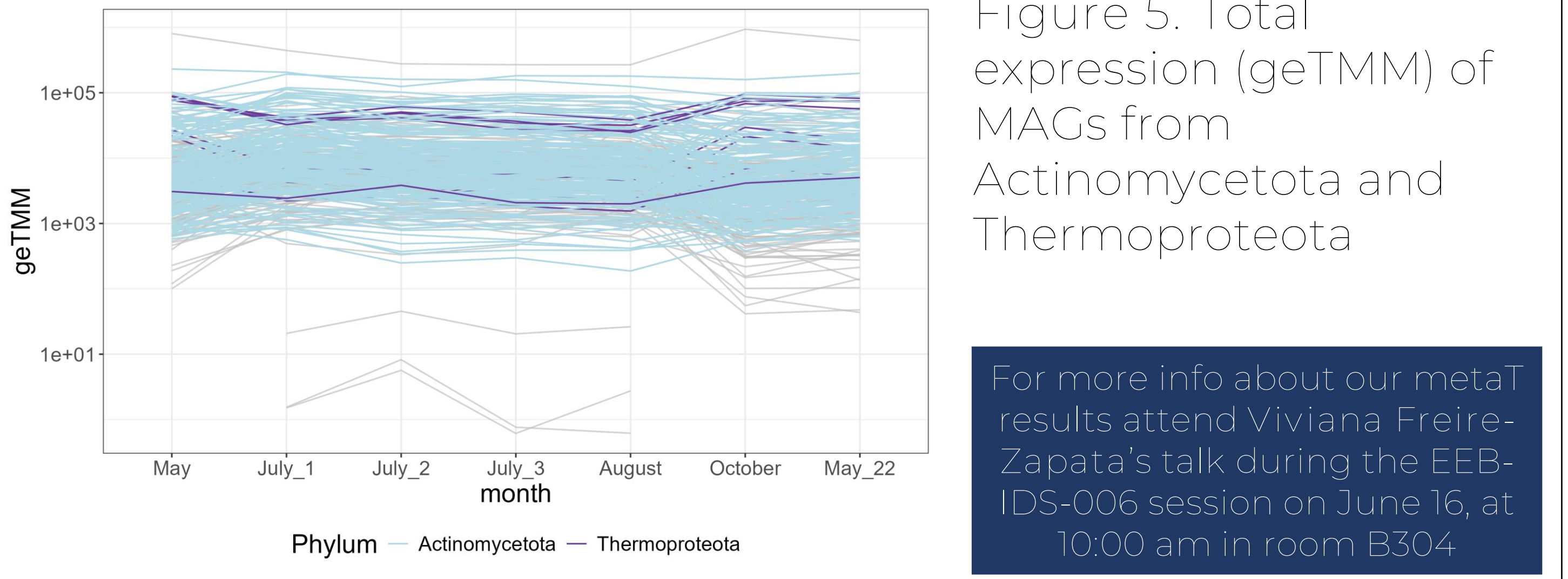
Results (Cont.)

Figure 4. MAG classification into stress tolerance guilds based on trait presence. Guilds explain 50% of the genome variation among MAGs

Figure 5. Total expression (geTMM) of MAGs from Actinomycetota and Thermoproteota

For more info about our metaT results attend Viviana Freire-Zapata's talk during the EEB-IDS-006 session on June 16, at 10:00 am in room B304

Conclusions and Future Work

- Microbial communities present in the Sonoran Desert soil, seem to be stable throughout the different resource pulses.
- Some stress response strategies such as systems to avoid protein denaturation caused by heat, or the accumulation of osmolytes seem to be common among all taxa.

Identify key species for ecosystem services ➡ Confirm functional potential ➡ Biotechnological application

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