



# Ecological Niches of Uncultivated Freshwater Phyla Revealed Through Comparative Genomics

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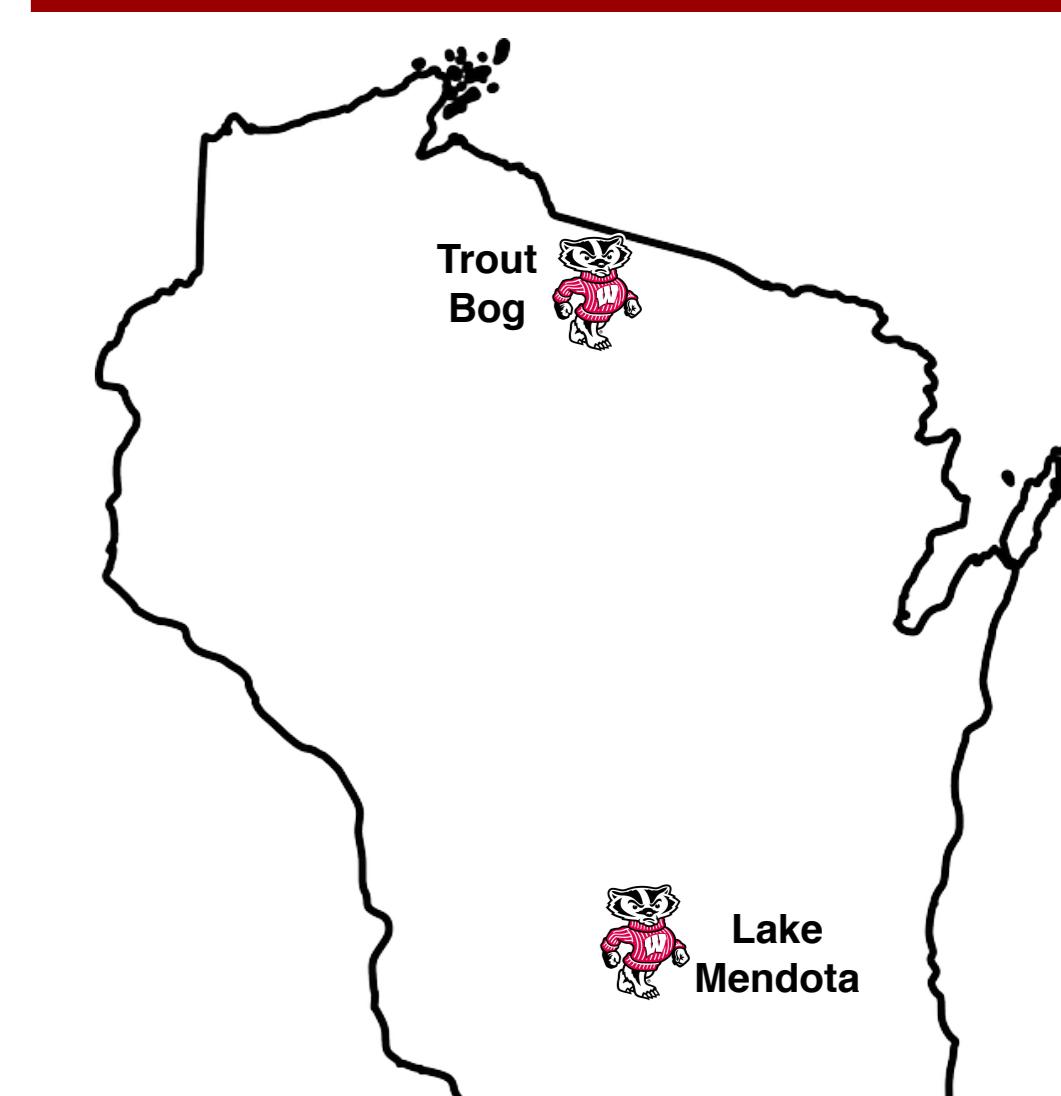
## Abstract

Microbes are critical players in all freshwater ecosystems, where they support essential ecosystem functions such as nutrient cycling. Because many of these microbes cannot be cultured, metagenomic approaches are increasingly being utilized to study their genetics and physiology. We have extensively sampled two freshwater lakes in Wisconsin, from which we have sequenced and assembled:

- 97 shotgun metagenomes from Lake Mendota
- 90 shotgun metagenomes from Trout Bog
- 202 genomes from these metagenomes (GFM)
- 46 single-cell genomes (SAGs) from Lake Mendota and Trout Bog

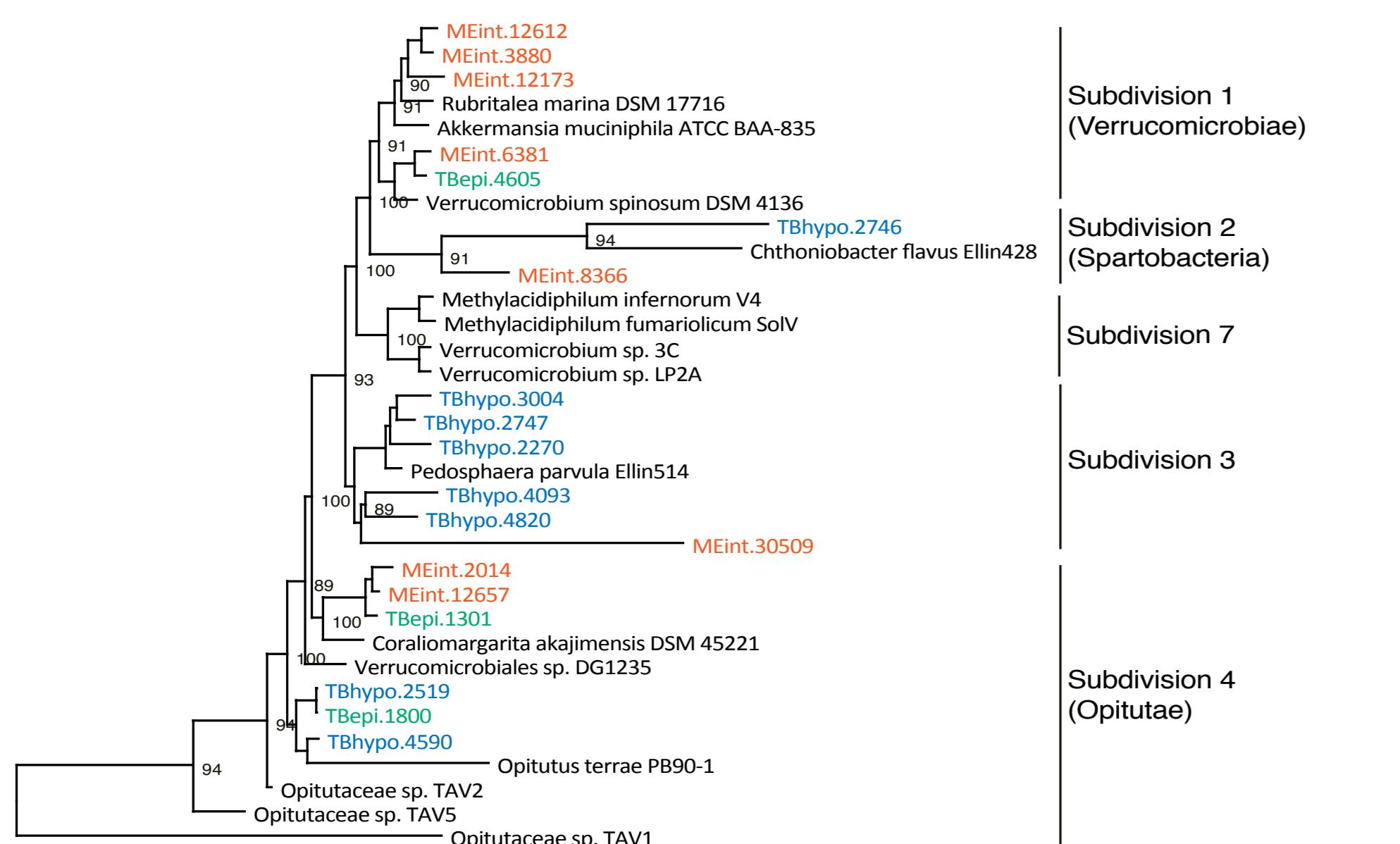
which we have used to identify metabolic features and potential niches for members of two freshwater phyla, the Verrucomicrobia and Actinobacteria.

## Study Sites

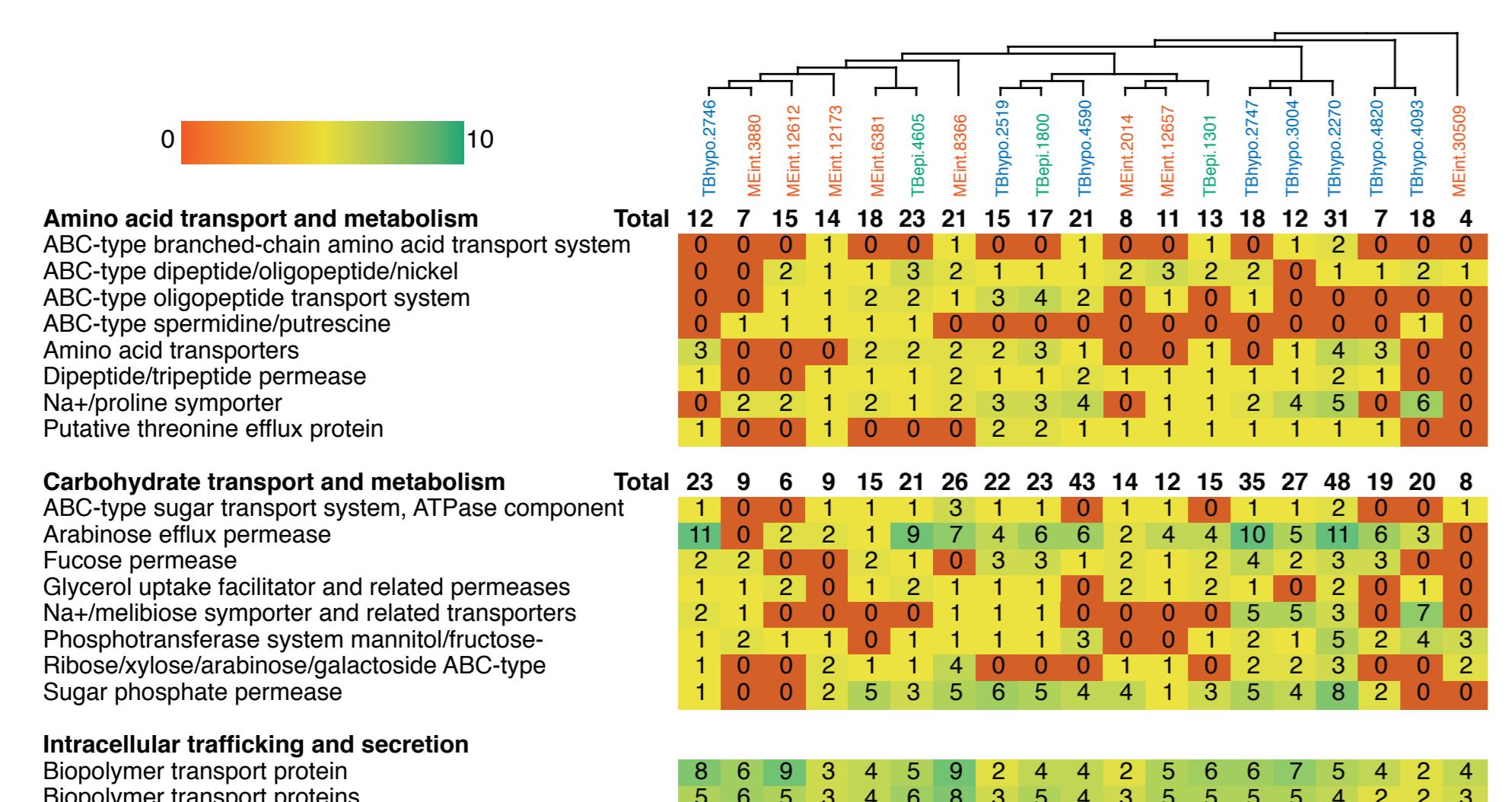


## Verrucomicrobia

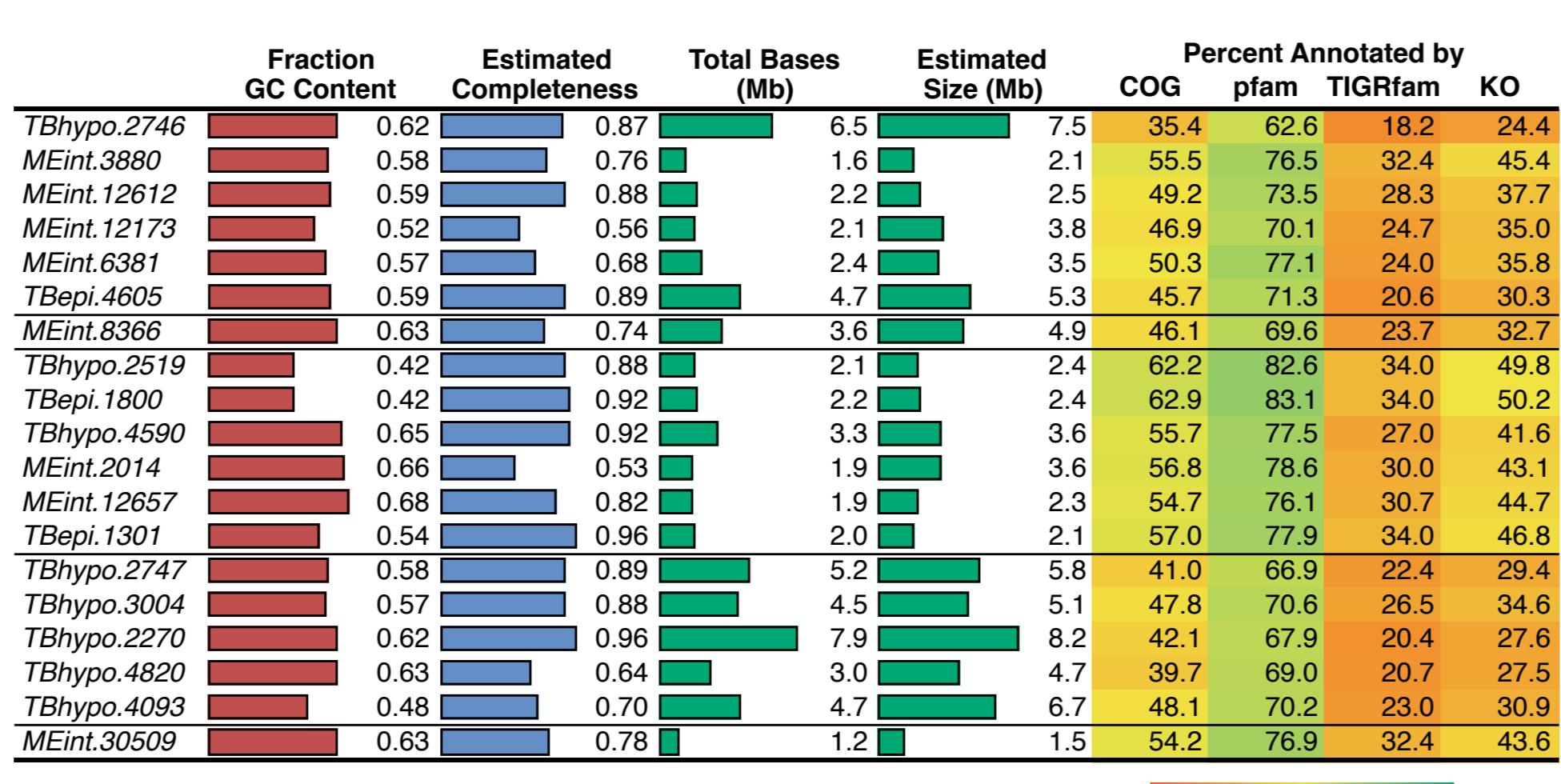
Verrucomicrobia species are cosmopolitan across lakes, yet found in low abundance. Relatively little is known about them.



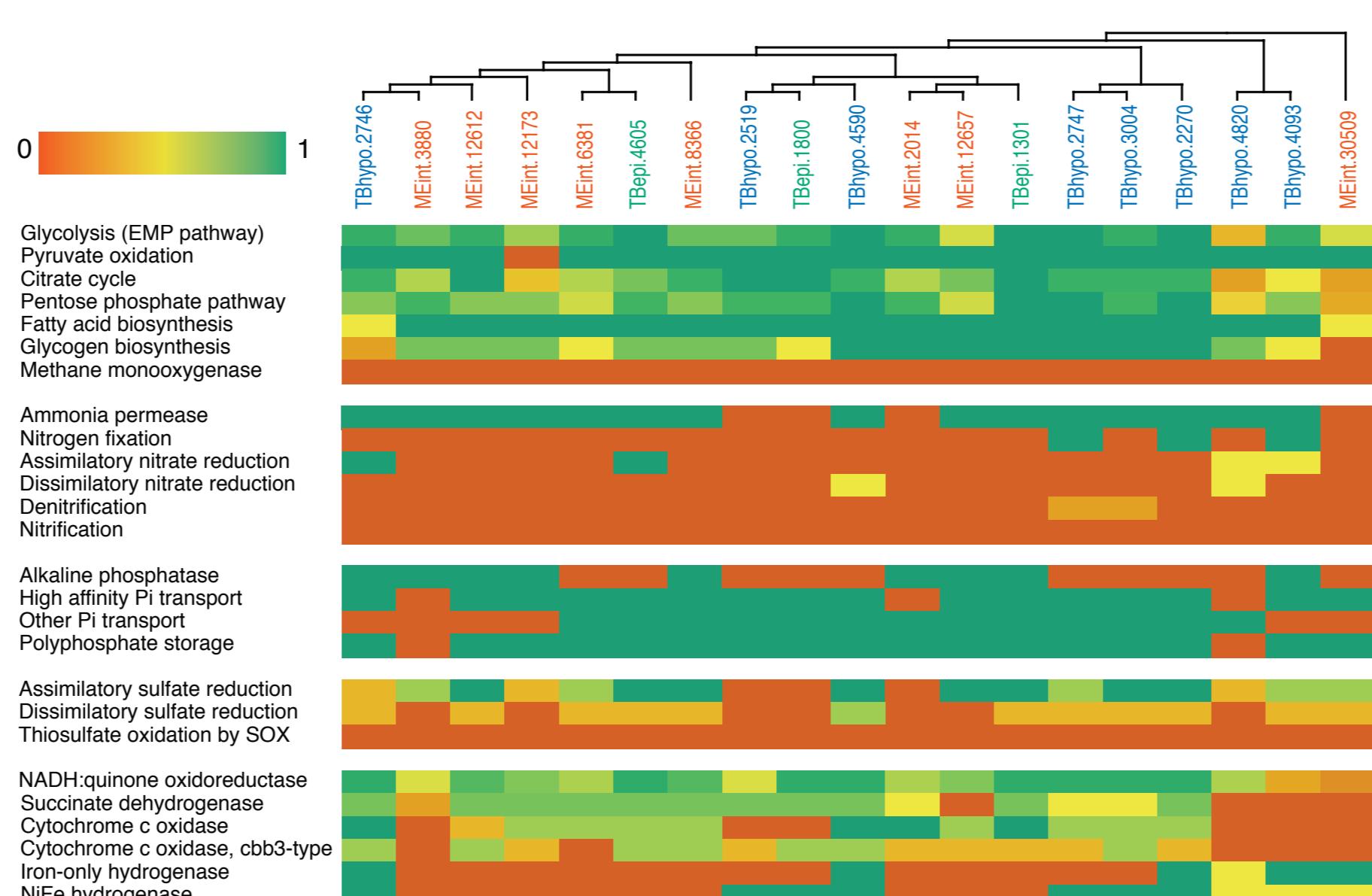
GFM were classified by placement into a tree containing concatenated phylogenetic markers from completed Verrucomicrobial genomes.



Inspection of transporters reveals an abundance of biopolymer transport proteins.



GFM were annotated using IMG. Completeness was estimated based on presence/absence of 139 conserved single-copy genes.



Inspection of metabolic pathways reveals freshwater Verrucomicrobia are most likely heterotrophs which rely on ammonia or amino acids for nitrogen.

## Conclusions

- Freshwater Verrucomicrobia are heterotrophs specialized for biopolymer utilization
- Actinobacterial lineages acl and acV have relatively streamlined genomes
- Freshwater Actinobacteria may niche partition based on substrate preferences

## Actinobacteria

Actinobacteria are often the numerically dominant phylum in freshwater lakes, with phylotypes exhibiting contrasting dynamics through time and space.

