

Stability of denitrification and nitrification genes in activated sludge revealed by quantitative genomics



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Introduction

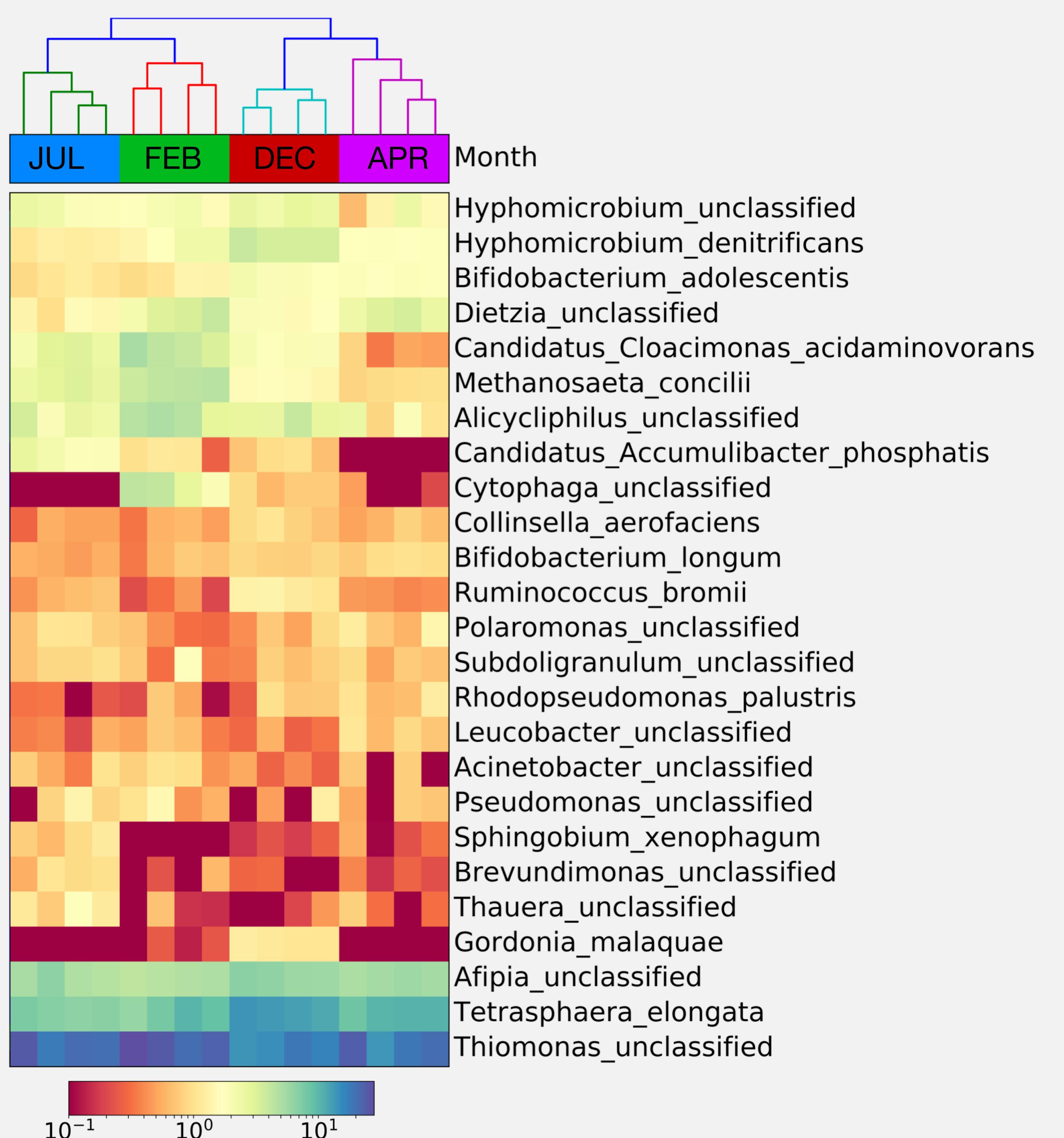
- Wastewater treatment plants (WWTPs) that use biological nutrient removal (BNR) or activated sludge systems rely on the metabolic activity of microorganisms to effectively treat wastewater prior to its release into the environment
- Treatment can become disrupted by various environmental factors that affect the microbial community within the WWTP
- How does the microbial community within an activated sludge environment respond to the seasonal temperature fluctuations of the Canadian prairies?

Methods

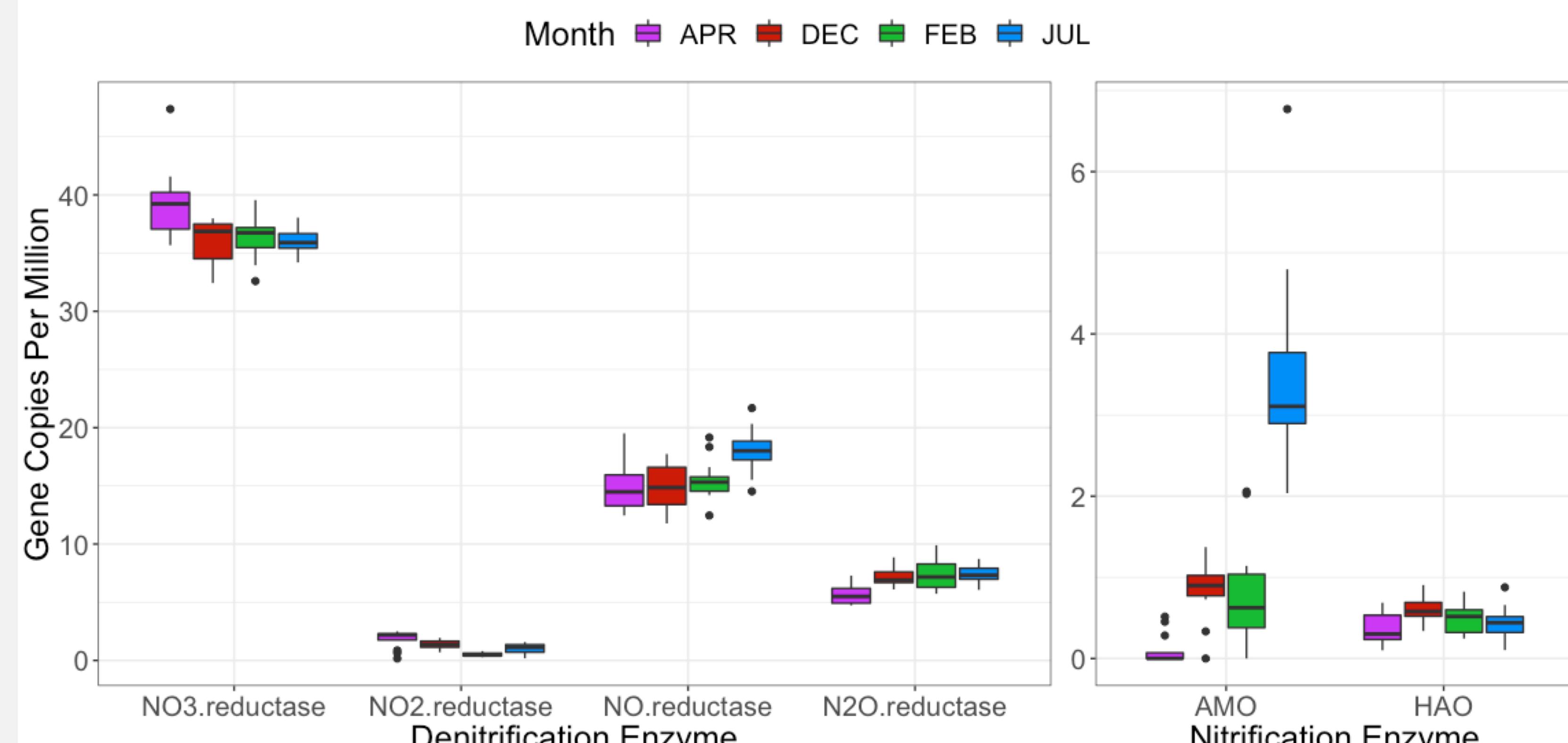
- Activated sludge was collected from the Regina WWTP on four occasions from December of 2017 until July of 2018 to encompass the highest and lowest temperatures throughout the year
- Microbial community DNA was extracted and sequenced on a HiSeq 2500 using paired-end 150 bp reads.
- Quantitative genetic and taxonomic data was generated using **Humann2** and **Metaphlan2**
- Binning, quality assessment, and visualization was done with **Metabat2**, **CheckM**, and **anvi'o**, respectively.

Results: Taxonomy

- Regardless of month, the dominant members of the microbial community were *Thiomonas*, *Afipia*, and *Tetrasphaera* spp.
- The abundance of certain organisms varied with month, including *Accumulibacter phosphatis*, *Gordonia malaquae*, and *Cytophaga* sp.



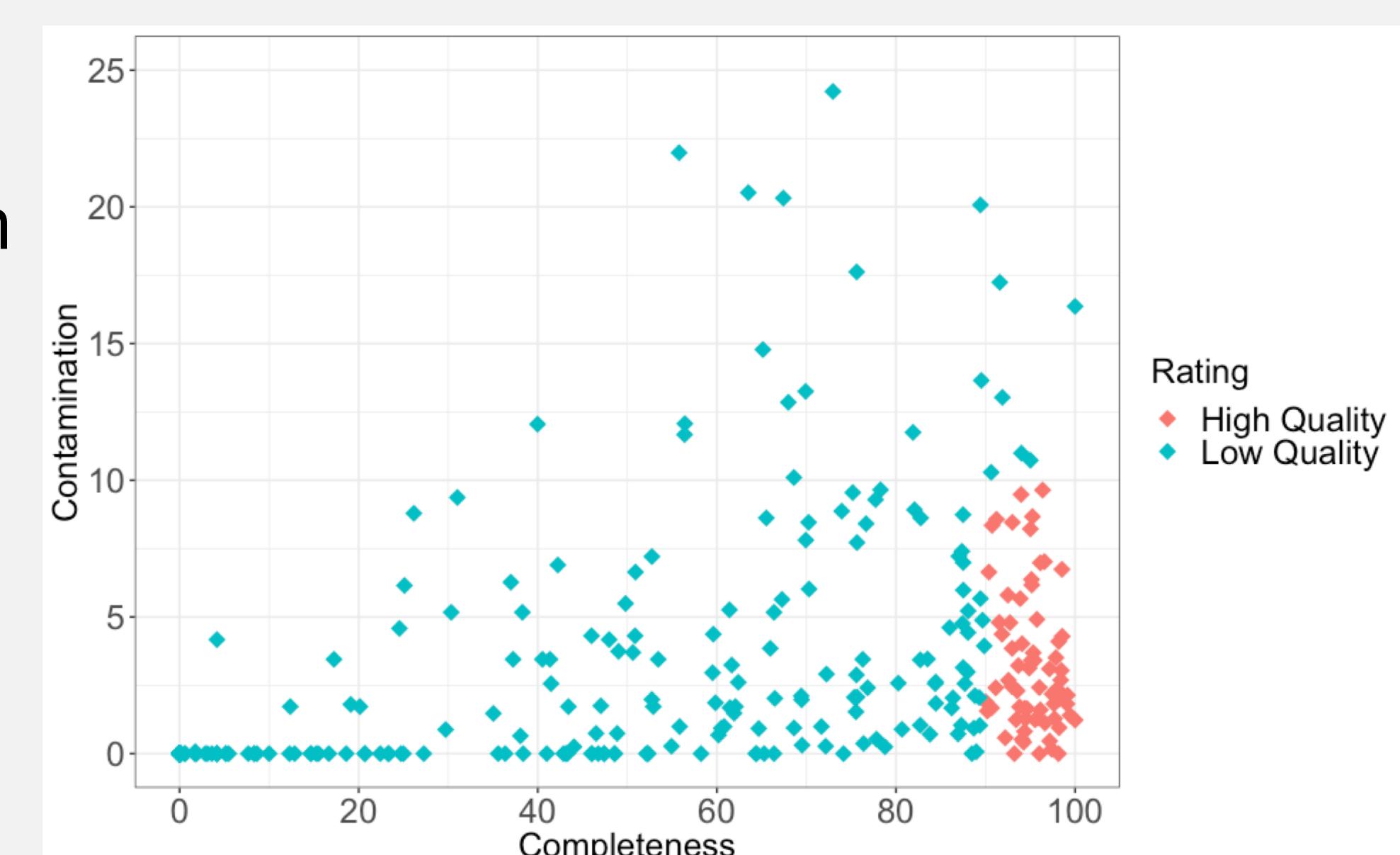
Results: Gene Content



- Nitrification and denitrification genes were present in the same abundances regardless of sampling month
- NO_3 reductase was the most abundant enzyme involved in nitrogen cycling

Results: Binning

- Binning generated 334 metagenome assembled genomes (MAGs), of which 69 passed the >90% completion and <10% contamination threshold
- 29 MAGs above 95% completion and under 5% contamination are displayed below



Binning results revealed that the denitrifying organisms in activated sludge fluctuate in abundance throughout the year

Legend

- NO_3 reductase
- NO_2 reductase
- NO reductase
- N_2O reductase

