

Source Identification of Fecal-associated Bacteria in Coastal Waters via Integration of eDNA, qPCR, and Nutrient Indicator Methods



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Introduction

- Coastal waters can experience elevated levels of fecal inputs
 - This can pose human health risks by contaminating fisheries and recreation areas
- Management of fecal contamination demands advanced approaches that can identify biological sources and public health risk (e.g., antimicrobial resistance (AMR))

Methods

- Water samples were collected monthly from 13 sites that represent potential fecal inputs to Alabama's coast (Fig. 1)
- Our microbial source tracking approach integrates molecular methods (eDNA metagenomics and *Bacteroides* qPCR) with nutrients (TDN, NH₄⁺, NO₃⁻, NO₂)

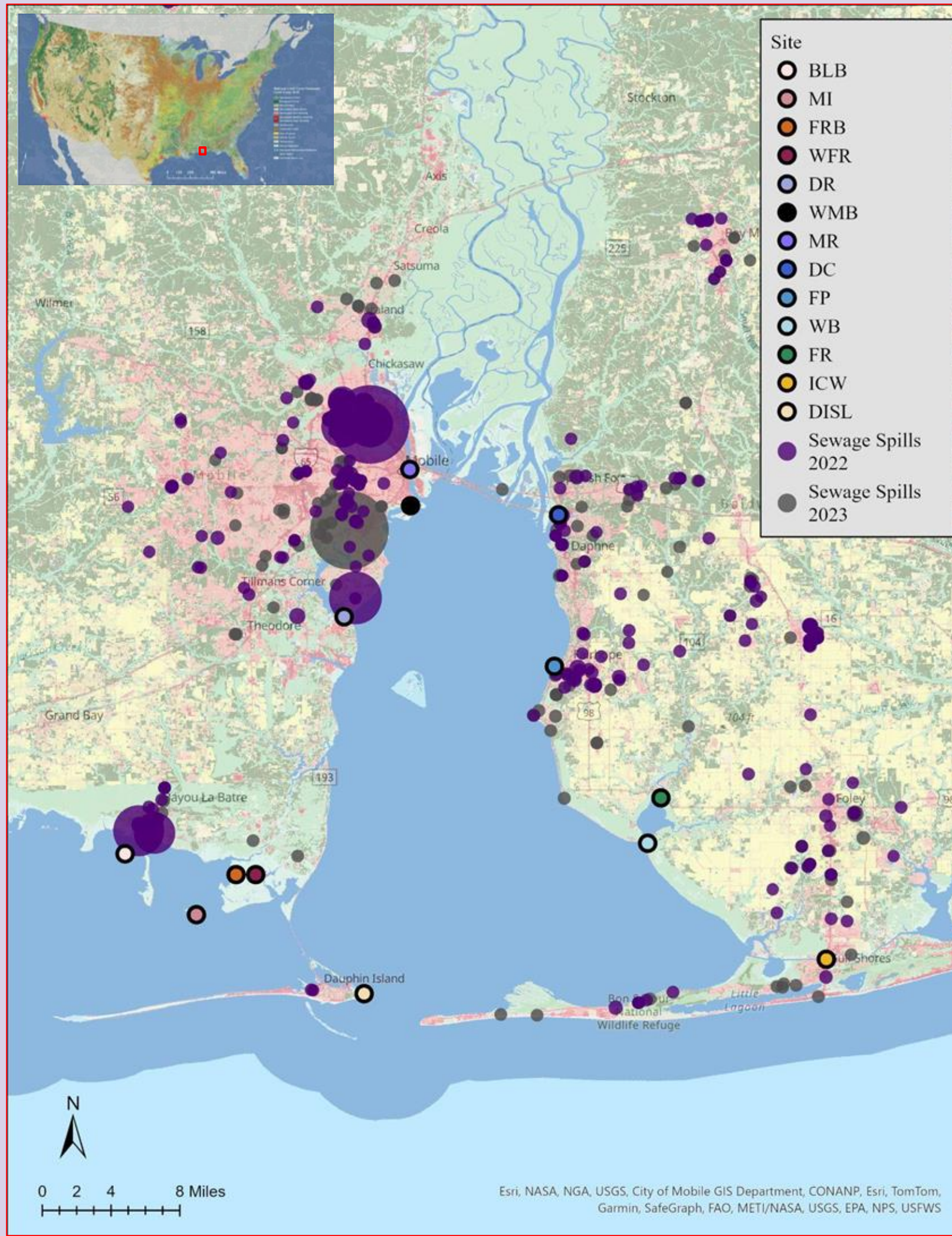


Figure 1. Sampling sites and locations of known sewage spills (Basemap: USGS National Land Cover Database).

Results

- The *Bacteroides* community was dominated by human-associated species ($p < 2.2 \times 10^{-16}$, $r^2 = 0.696$)
- There was a distinct treated wastewater community, driven by N (Fig. 2) and further supported by complete or near complete N cycle pathways (Fig. 3)
- A diverse suite of AMR genes were observed (Fig. 4), with some classes (rifamycin, quinolone, colistin, trimethoprim) restricted to effluent outfall areas
- Quaternary ammonium resistance (linked to disinfectant use) was seen at sites that received consistent human inputs

The metabolic pathways present in the treated effluent samples may serve as a guide for identifying human sewage signatures

Acknowledgments

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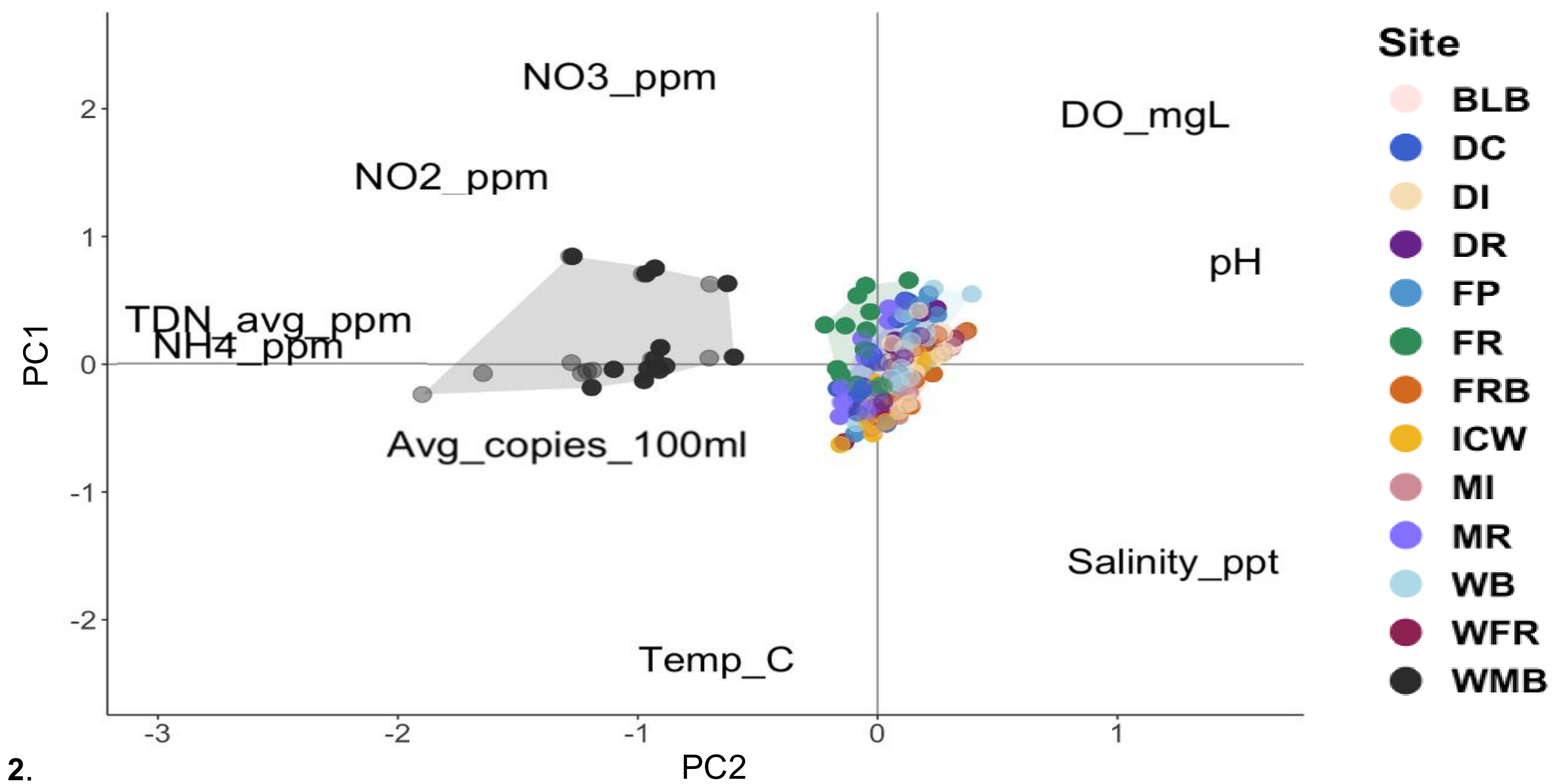


Figure 2.

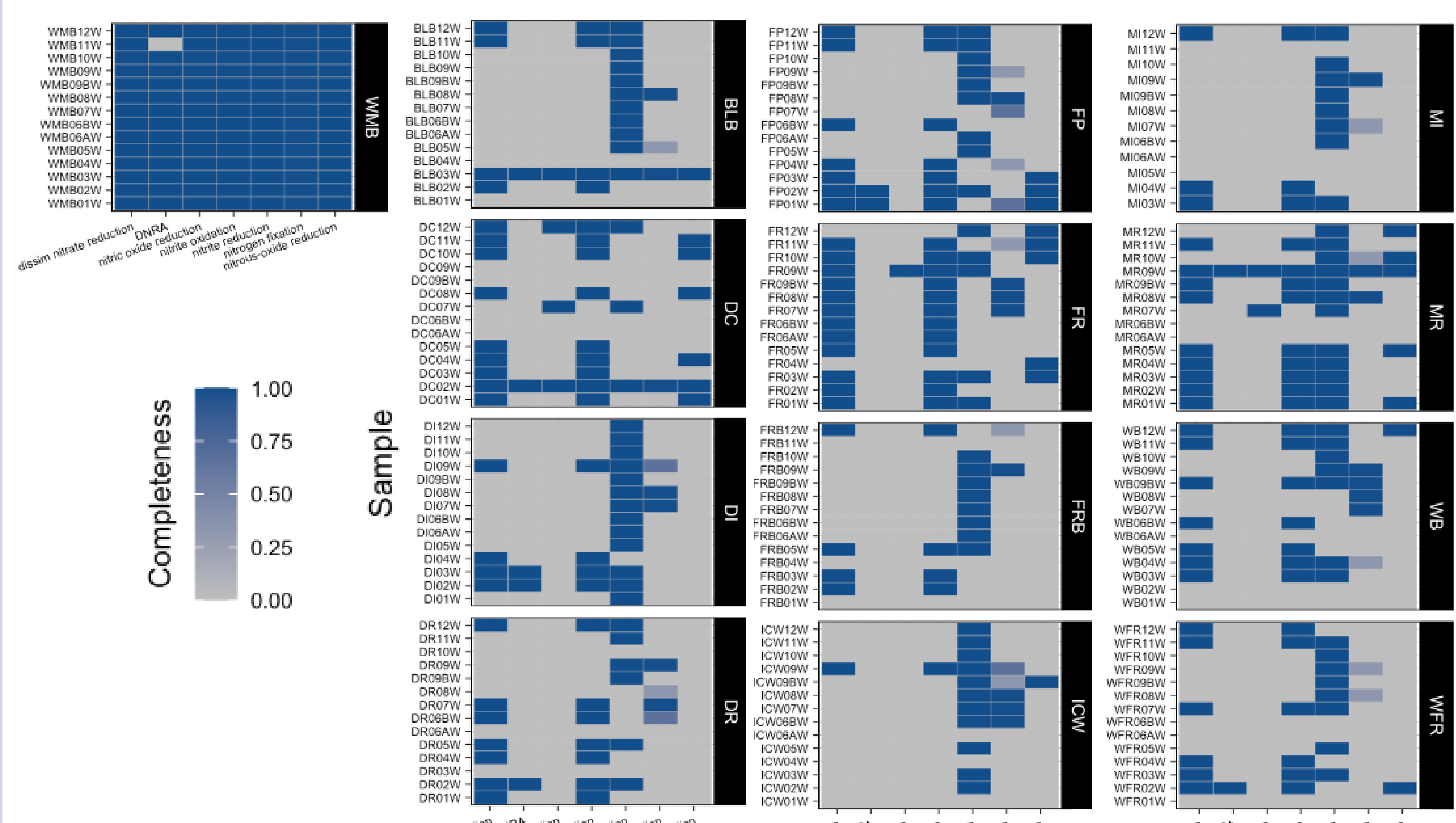


Figure 3.

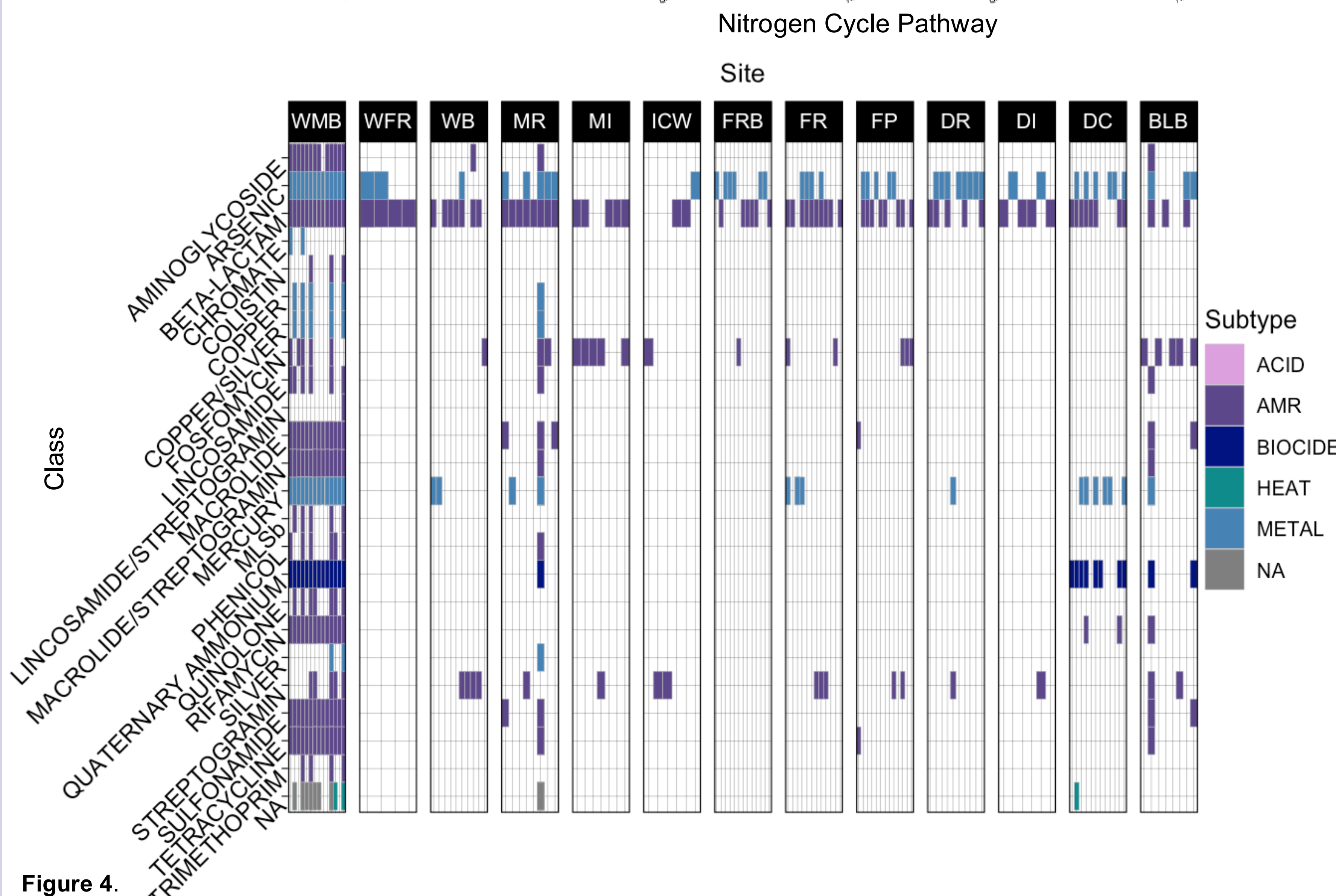


Figure 4.