

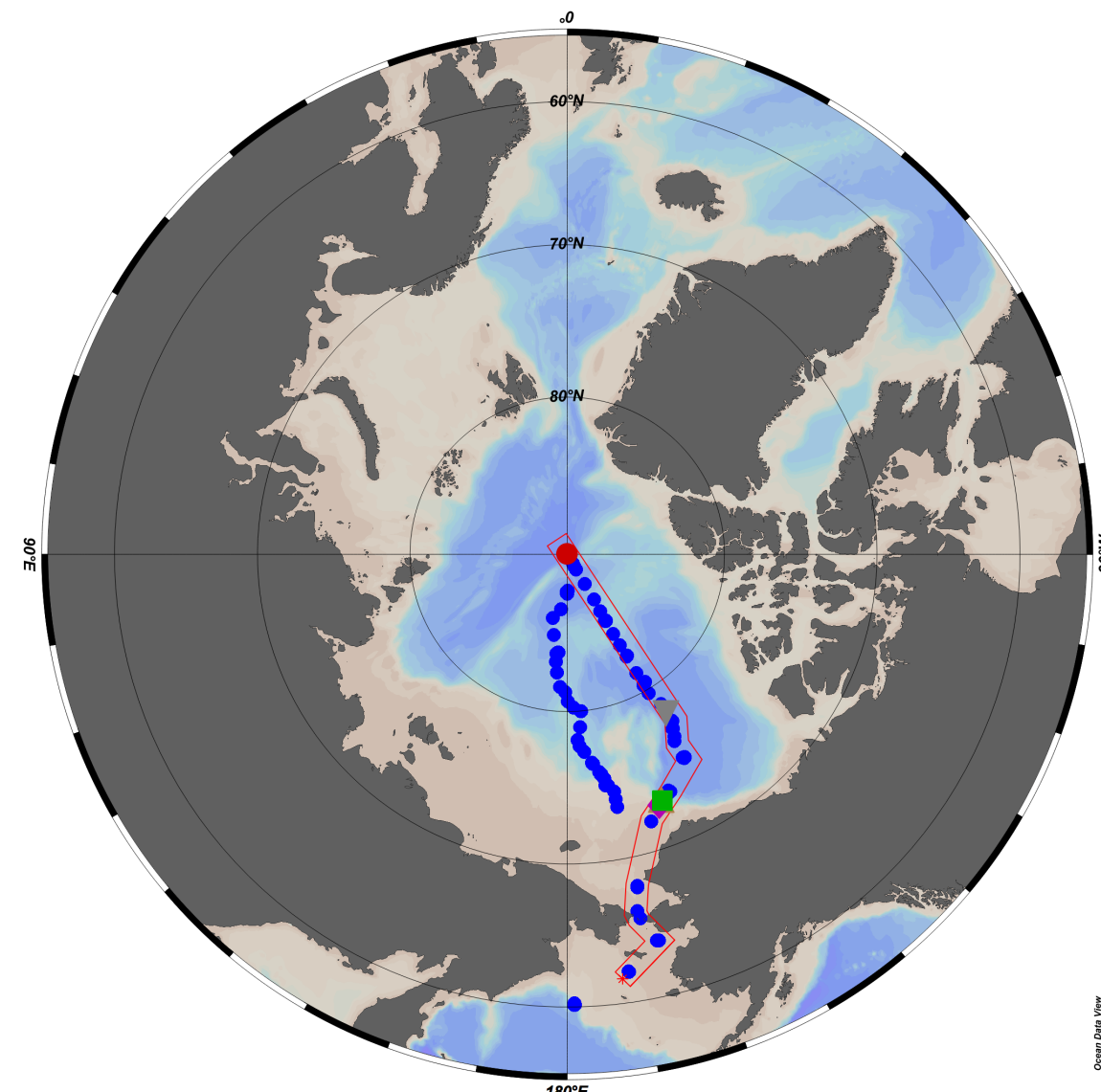
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## Introduction

Metals are essential in biology as substrates in energy-generating redox reactions and as cofactors in metalloproteins, often acting as catalysts in the reactive sites of enzymes. The distribution and concentration of bioactive metals in the Arctic Ocean – and their influence and modification by microbes – has remained unknown until recently.

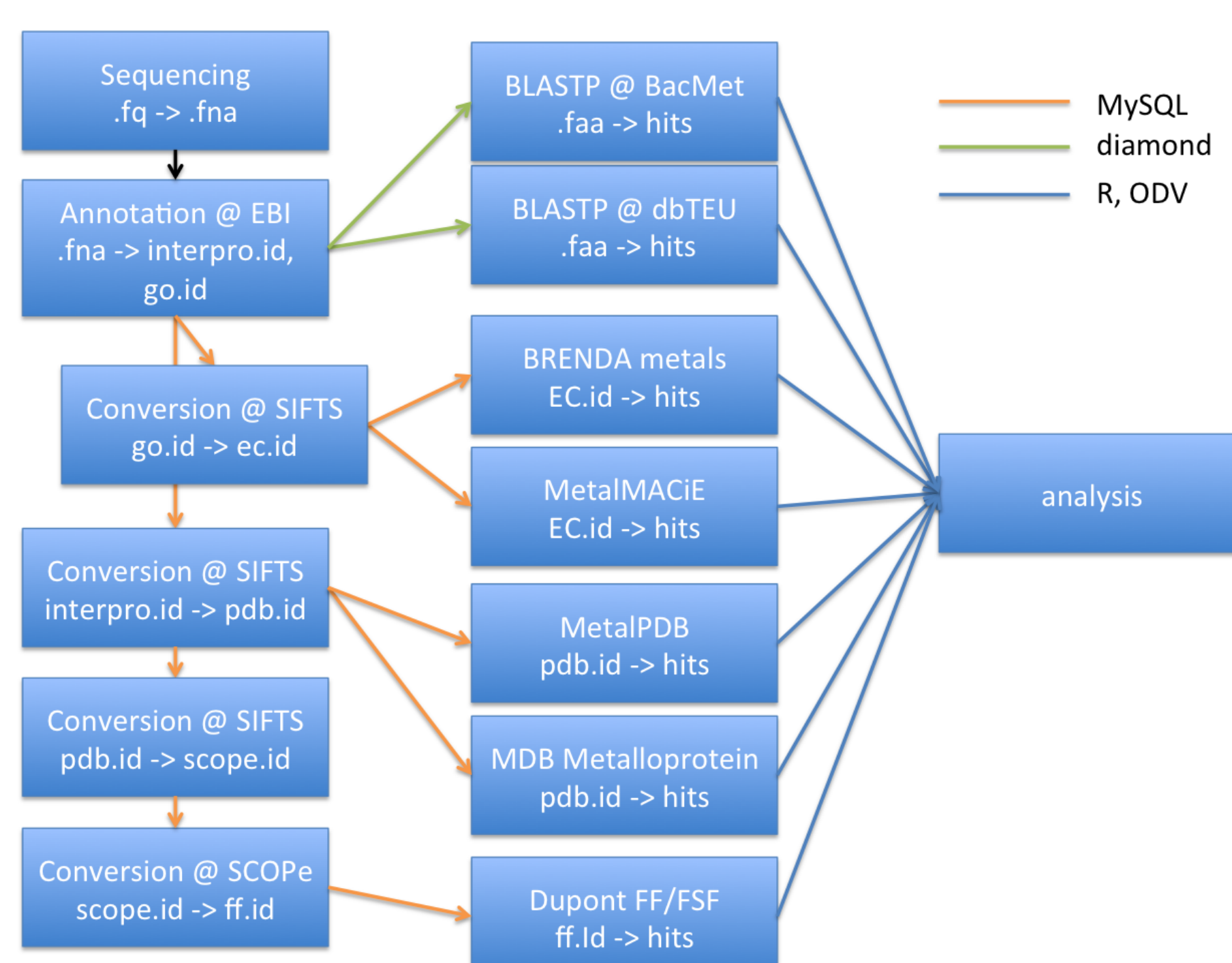
## Background

During the 2015 U.S. GEOTRACES Arctic research cruise to the North Pole aboard the CGC Healy, samples were collected concurrently for quantification of major and trace elements (including Cd, Co, Cu, Fe, Mn, Mo, Ni, P, V, and Zn) and microbial functional diversity, as assessed using metagenomics.



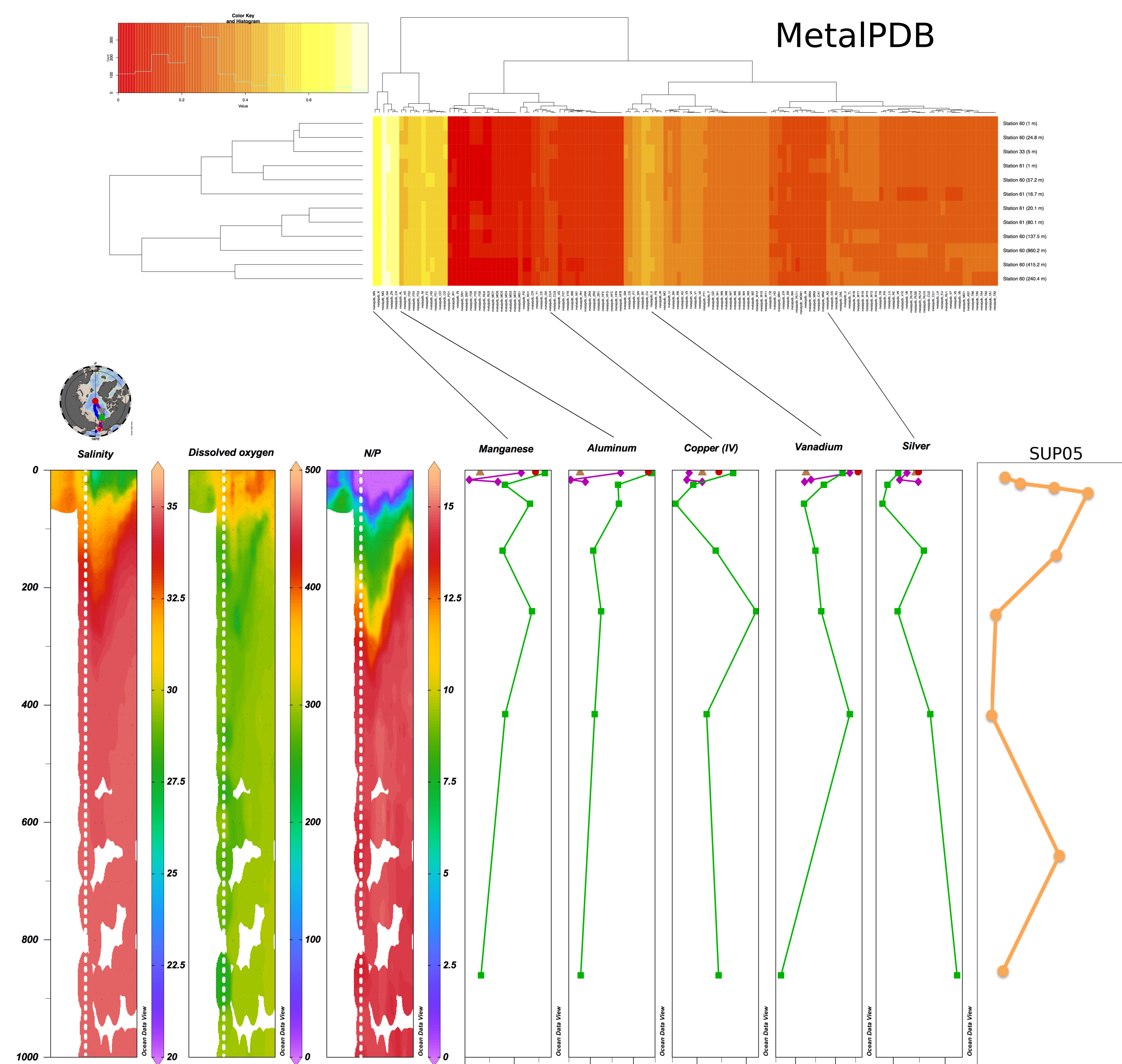
## Bioinformatics Pipeline

Microbial samples, collected from surface seawater down to a depth of 885 m, were shotgun sequenced on an Illumina MiSeq and assembled using SPAdes. Phylogenetic diversity was assessed using Phylosift. To assess changes in metal usage by microorganisms across the central Arctic Ocean, we designed an automated pipeline to compare assembled sequences against databases of known metal-containing proteins (including BRENDA, MetalMACIE, MetalPDB, MDB Metalloproteins, dbTEU, and BacMet). Metalloproteins were measured as BLAST hits per million reads.

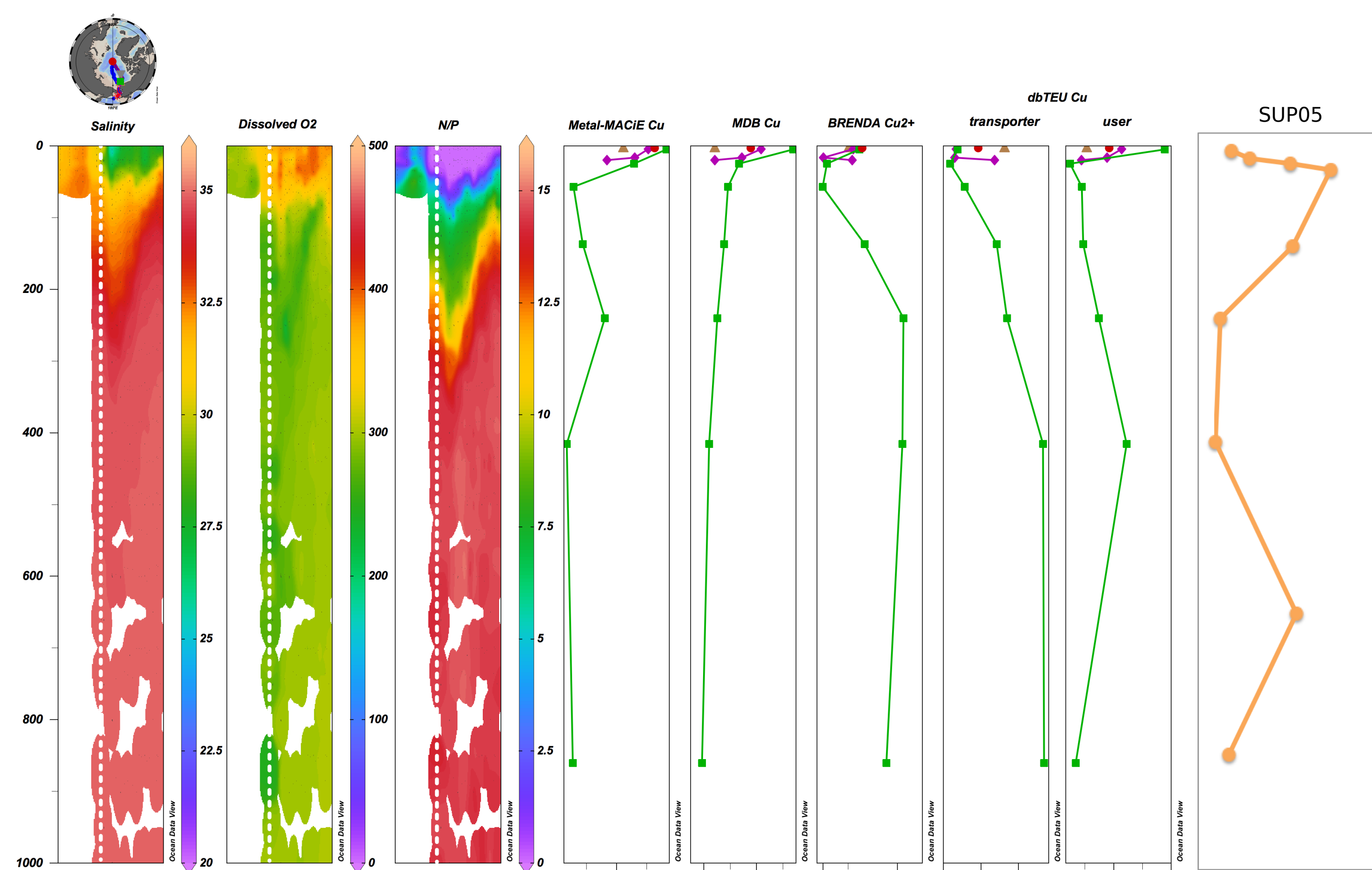


## Results / Metalloproteins

In the water column, most metalloproteins exhibited vertical structure, often including a peak in the surface with a general decline in relative abundance to depth.

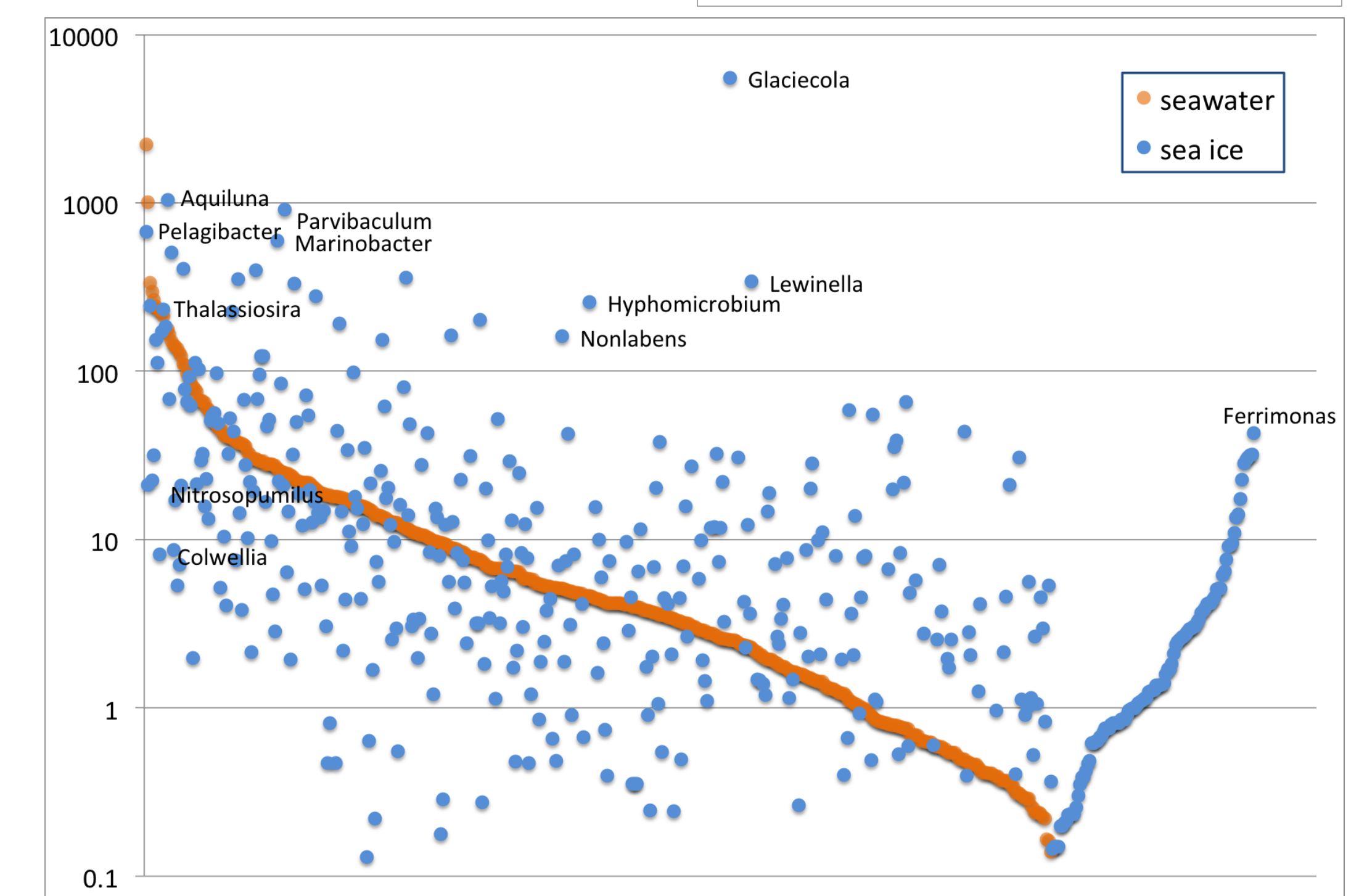
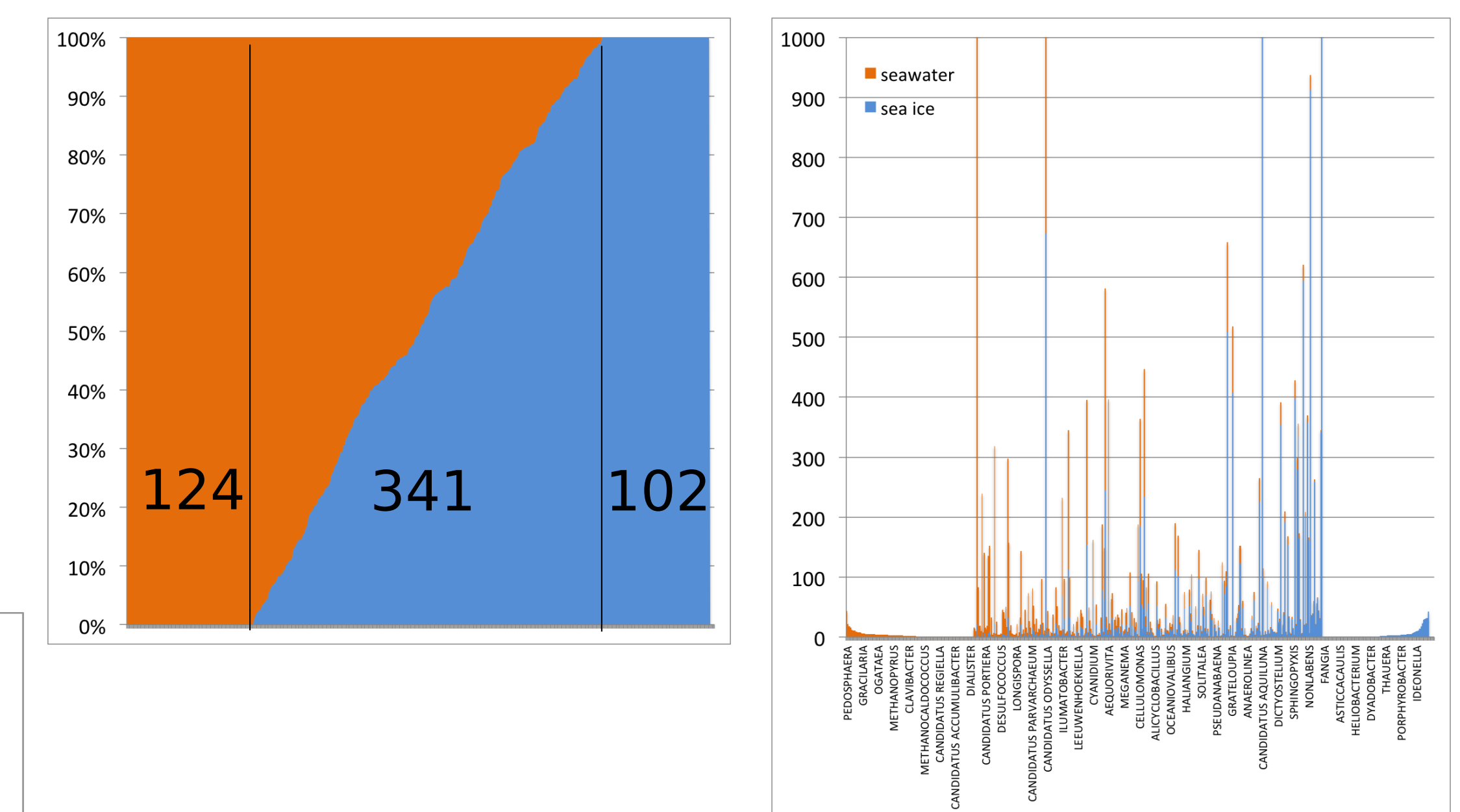


Many metalloprotein profiles also showed an additional peak in the subsurface, generally between 250 and 500m (e.g. proteins using or transporting As, Ca, Co, Cu, Fe, Mo, Ni, Se). This depth range, which is near the boundary between the upper halocline waters and the Atlantic layer, was often dominated by sequences with best hits to *Candidatus Thioglobus*, a genus of strictly aerobic sulfur-oxidizing autotrophic Gammaproteobacteria from the SUP05-A clade (Arctic96BD-19).



## Results / Phylogenetic Diversity

Sea ice and seawater exhibited a large overlap in diversity as measured by Phylosift, which uses HMMs to find conserved core genes. Each biome had OTUs that were not present in the other, but overall the diversity was higher in seawater than sea ice.



We obtained complete metagenomic assemblies from several important clades, including *Candidatus Thioglobus* and *Pelagibacter* from seawater, and *Polaribacter* in sea ice.

