

Supplemental Tables

Supplemental Table 1. Summary of geochemical data collected across the OUTPACE cruise transect.

Supplemental Table 2. Table of gene expression counts (tags per million, TPM) summed across orthologous groups (OGs) and partitioned between the *Trichodesmium* and microbiome fractions.

Supplemental Figure Legends

Supplemental Figure 1. Distribution and annotations of KEGG functional annotations of OGs found uniquely in the *Trichodesmium* (T) or microbiome (M) or those composed of both *Trichodesmium* and microbiome proteins (B). (a) Total number of OGs in each category. (b) A functional breakdown of these annotations at the KEGG module level and detailed annotations from within two KEGG module categories.

Supplemental Figure 2. Amino acid alignment of the Ppm protein recovered from a *Trichodesmium* metagenome bin against experimentally verified Ppm sequences in other organisms. Genes highlighted in green denote regions with 100% amino acid identity across all sequences. Shades of yellow denote conservation across the majority of amino acids in the column. Un-highlighted amino acids indicate divergent residues or regions with little conservation. Purple and grey highlighted columns denote residues that were previously determined to be important to the structure or activity of this enzyme (Chen et al., 2006).

Supplemental Figure 3. Phylogenetic tree showing the placement of the *Trichodesmium* Ppm protein (red), a microbiome proteins from this study's metagenome assembly that is similar to Ppm but lacking conservation at key residues (green), as well as homologous proteins from a previously assembled North Atlantic *Trichodesmium* metagenome assembly (blue) (Frischkorn et al., 2017), along with homologous sequences obtained from the NCBI nr database (black). The tree was generated with FastTree using the default settings (Price et al., 2010). Numbers at the branch labels indicate FastTree support percentages for the sequences in that branch.