Supplemental tables legends

Supplemental Table 1. Summary of water column (10 m) geochemical data collected across the OUTPACE cruise transect. *Measurement obtained at 30 m.

Supplemental Table 2. qPCR counts of *Trichodesmium* Clade I and Clade III obtained across the transect.

Supplemental Table 3. Table of gene expression counts (tags per million, TPM) summed across orthologous groups (OGs) and partitioned between the *Trichodesmium* and microbiome fractions.

Supplemental Table 4. The sequence of the assembled scaffold containing the *ppm* cassette from the *Trichodesmium* metagenome assembly.

Supplemental figures legends

Supplemental Figure 1. Diagram detailing approach used to assemble and partition the metagenome between *Trichodesmium* and the microbiome, annotate and cluster protein coding sequences into orthologous groups (OGs), and obtain gene expression values from metatranscriptomes. Eukaryote identified sequences as well as phototrophs other than *Trichodesmium* were excluded from downstream analysis after the genome binning and analysis step. TPM, transcripts per million.

Supplemental Figure 2. 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 3. Metagenome reads aligned to the scaffold containing the *ppm* cassette. Thick black rectangles depict ~100 bp reads, connected by thin black lines to their mate paired read.

Supplemental Figure 4. 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 5. 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.