

Description of Additional Supplementary Files

Supplementary Data 1. Total dissolved metal concentrations (nM), macronutrients (μ M), and particulate metals (pM) for each station and depth.

Supplementary Data 2. Summary of factors influencing concordance between transcripts and proteins in marine microeukaryotes

Supplementary Data 3. Examples of disagreement between proteins and transcripts found in this study and the organisms affected

Supplementary Data 4. Metatranscriptomic assembly statistics, including read mapping percentages and number of annotated open reading frames.

Supplementary Data 5. Total protein extracted from filters (μ g), amount injected onto the mass spectrometer (μ g), and volume filtered (L) by Clio.

Supplementary Data 6. Taxonomic groups and KEGG functional processes associated with each module of the protein network.

Supplementary Data 7. Taxonomic groups and KEGG functional processes associated with each module of the transcript network.

Supplementary Data 8. Summary of Clio dives during AE1913.

Supplementary Data 9. TPM-normalized transcript counts for each eukaryotic open reading frame (ORF). Only ORFs with single KO annotations are included.

Supplementary Data 10. NSAF-normalized protein spectral counts for each eukaryotic open reading frame (ORF). Only ORFs with single KO annotations are included.