Supplementary Information:

1. **Supplemental Methods –** Supplementary text describing measurement of biological oxygen via the EIMS method, calculation of net community productivity, assessment of vertical biological oxygen fluxes, and evaluation of internal standard spike quantities, as well as procedures and parameters for statistical analyses of 16S and 18S rRNA amplicon data.

2. **Supplementary Figures –** Document including figures and descriptions for Supplementary Figures 1 and 2.

3. **BIOM format 16S OTU table** – BIOM format OTU table used in downstream analyses for processing of prokaryotic 16S rRNA sequencing data.

4. **BIOM format 18S OTU table –** BIOM format OTU table used in downstream analyses for processing of eukaryotic 18S rRNA sequencing data.

5. **AE15 ship data –** MATLAB structure array containing 2-min averaged ship and EIMS data including time, position, water temperature, sea surface salinity, O_2/Ar supersaturation (%), attenuation coefficient, and O_2 concentration (μM). Arrays appended "_badp" contain data collected during periods of anomalous mass spectrometer pressure.

6. **QIIME log – commands – Bermuda 2015** – Text document describing series of tools, scripts, and commands utilized during processing of raw Illumina sequencing data.

7. **Supplementary Table 1 – Table of regression coefficients** between environmental variables and the first principal component axis generated by Principal Coordinates Analysis (PCoA) of eukaryotic 18S and prokaryotic 16S community taxonomy using Bray-Curtis dissimilarity. Bold coefficients are significant at p≤.05.

8. **Supplementary Table 2 – Station metadata** – Spreadsheet document containing metadata recorded for all sequencing stations, including discrete measurement data from cruise.

9. **Supplementary Table 3 – MiSeq primer sequences** – Spreadsheet document containing adapter, barcode, and primer sequences employed.

10. **Supplementary Table 4a.xlsx; Supplementary Table 4b –** Tables of PLS correlation coefficients for 16S and 18S taxa, respectively, at the fourth taxonomic rank.

11. **Supplementary Table 5 – sample and primer guide – Ion Torrent test run –** Spreadsheet document containing primer sequences used for Ion Torrent pilot sequencing run.

12. **Supplementary Table 6 – read and OTU counts –** Spreadsheet document containing read and OTU counts for all sequenced 18S and 16S rRNA samples.