Supplemental Methods

Measurement of Biological O_2

O_2/Ar was measured continuously during the cruise from the *R/V Atlantic Explorer*'s underway intake using Equilibrator Inlet Mass Spectrometry (Cassar et al 2009). The ship's inlet is located approximately 2.5 meters below the waterline. The O_2/Ar ion current ratio was recorded from the headspace of the membrane contactor, which undergoes gas exchange and equilibration with the sampled seawater, for 2-3 hours at a time, punctuated by 30-minute measurements of the O_2/Ar of ambient room air to correct for instrumental drift. An automated Valco valve (VICI, Houston, TX, USA) governed the regular switching between air and water O_2/Ar gas sample flow.

At each CTD station during the cruise, triplicate Winkler dissolved oxygen samples were collected from both in-situ surface water and from the ship's seawater tap directly upstream of the EIMS to measure the degree of microbial respiration within the ship's lines, a phenomenon that has been documented in the underway seawater systems of multiple research vessels (Juranek et al 2010). All Winkler sample bottles were collected according to the standard BATS protocol and analyzed at Rod Johnson's laboratory at the Bermuda Institute of Ocean Sciences.

As in previous O_2/Ar work conducted aboard the same vessel (Estapa et al 2015), O_2 measurements revealed insignificant differences between the dissolved oxygen concentration of surface seawater and seawater collected from the ship's underway seawater lines, suggesting that any microbial respiration taking place within the ship's underway system was negligible.

Calculation of net community production

Mass spectrometer and ship underway data were time-averaged at two-minute intervals. Seawater O_2/Ar values were calibrated using O_2/Ar measurements of ambient room air, then quality-filtered to remove O_2/Ar data collected during anomalous spikes in mass spectrometer pressure. Data was filtered according to a moving average and a moving standard deviation criterion, removing data collected whenever pressure within a one-hour window exceeded a moving standard deviation of 10^{-7} mbar and/or a moving average greater than 5×10^{-6} mbar. Daily NCP rates were calculated using the following equation (Cassar et al 2011):

1) NCP (mmol O_2/m^3/day) = $\frac{\frac{O_2}{Ar}(\%)}{100} * \frac{[O_2]_{sat}\left(\frac{umol}{kg}\right)}{1000} * \rho(S,T) * k * (\frac{1}{MLD})$

Where $\frac{O_2}{Ar}(\%)$ is the percent supersaturation of the O_2/Ar ratio relative to that of interpolated ambient air O_2/Ar measurements, which reflect the expected O_2/Ar ratio at equilibrium. ρ signifies the density of seawater (kg/m^3) according to the 1983 UNESCO equation of state, and k denotes the piston velocity, estimated according to the quadratic wind-speed dependence of (Wanninkhof 1992). MLD is the mixed layer depth in meters. The oxygen concentration corresponding to saturation was calculated using the oxygen solubility relationship described in (Garcia and Gordon 1992).

As biological oxygen concentrations in the surface ocean are also dependent on past wind speeds, gas transfer velocities were weighted using the 30-day wind speed history prior to measurement (Reuer et al 2007), with previous wind speeds along the cruise track obtained from the corresponding daily NCEP/NCAR 10 m wind speed reanalysis. Mixed layer depths for this calculation were calculated using potential density profiles obtained from fourteen CTD casts according to a density difference criterion of 0.03 kg/m^3 from a reference depth of 10 m (de

Boyer Montegut et al 2004). Calculated mixed layer depths were linearly interpolated across the cruise track between CTD casts.

As NCEP/NCAR wind speed values corresponding to cruise dates and locations appear to underestimate ship-measured wind speeds, the ship-measured values were corrected to a 10 m reference height using Equation (1) of (Thomas et al 2005) and used to adjust the NCEP/NCAR wind speed history based on a linear regression between predicted and measured wind speeds for the cruise period.

Accounting for vertical fluxes of O_2/Ar

The integrated biological oxygen concentrations in the mixed layer can be expressed via the following equation:

$$2) \qquad MLD\frac{dO_{2_{bio}}}{dt} = NCP - F_g + F_v + F_e$$

$O_{2_{bio}}$ represents the concentration of biological oxygen in the surface ocean. F_g denotes the gas exchange term, while F_v and F_e represent vertical fluxes via eddy diffusion and entrainment. Traditionally, the system is assumed at steady-state with limited $F_v + F_e$ (Hamme and Emerson 2006), with F_g equal to NCP , leaving just $F_v + F_e$ to consider. We estimated the vertical eddy diffusive flux F_v, using equation (6) of (Castro-Morales et al 2013), with a vertical eddy diffusivity coefficient of 1 x 10^{-5} m^2 s^{-1} as measured for the Mid-Atlantic Bight (Wallace 1994), calculating oxygen gradients from CTD profile data using a Model-II least-squares fit. Estimated depth-integrated F_v fluxes ranged between just 0.2 and 5.35 mmol O_2 m^{-2} day^{-1} (median: 1.41 mmol O_2 m^{-2} day^{-1}). These flux estimates likely represent an upper bound, as much of the observed increase in O_2 beneath the mixed layer may be thermally rather than biologically-driven. Argon vertical profiles are however likely close to equilibrium within the first few

hundred meters, minimizing errors associated with using O_2 concentration profiles rather than O_2/Ar (Hamme and Severinghaus 2007).

Entrainment due to deepening of the mixed layer is unlikely to be significant in the highly stratified summer Sargasso Sea. A similar study in the Sargasso Sea in September-October 2011/2012 assessed entrainment flux to comprise less than +/- 6% of calculated O_2/Ar-derived NCP (Estapa et al 2015). We are, however, unable to account for entrainment fluxes in the more dynamic coastal region. O_2 concentrations below the mixed layer consistently increased with depth based on CTD profiles taken throughout our cruise, however, with the result that any entrainment fluxes would bias NCP values upwards. On the other hand, observed negative NCP values in open-ocean regions of the Sargasso Sea likely represent true heterotrophic activity.

Determination of appropriate control DNA spike quantity

We conducted a qPCR using 18S V4 primers to assess the average concentration of 18S rDNA genes in our samples. Serial dilutions (1:10 to 1:1 000 000) of the *S. pombe* control DNA were used to generate the qPCR standard curve. The sample with the lowest 18S DNA abundance was determined to contain approximately 1/4th the number of 18S rDNA sequences ul^{-1} as 1.14 ng of the *S. pombe* standard (9 702 000 copies), suggesting an appropriate addition of 0.00285 ng to maintain the standard sequences added at a relative abundance of no more than 1% of reads following sequencing.

We subsequently conducted an Ion Torrent PGM sequencing run to verify our ability to detect such a dilute spike in our sequencing output data. Two sets of samples from the 2015 cruise were run in technical duplicates: one pair from an oligotrophic location near Bermuda and another from a large phytoplankton bloom south of Long Island. These sites were chosen to span

the range of 16S and 18S rDNA gene concentrations encountered in this study. These samples were extracted with the addition of 152 ng or 15.2 ng of 16S and 0.679 ng or 0.0679 ng of 18S internal standards, both in 50 ul volumes, following the same extraction and PCR protocols described in the main text. Ion Torrent PGM sequencing was performed at the Boston University Microarray Core on a 314 chip. Primer, barcode, and adapter sequences used for this Ion Torrent sequencing run are detailed in Supplementary Table 6.

Statistical Analysis

For comparison to sequenced samples, underway NCP data was time-averaged across 45-minute bins centered on the time of sample collection. If sample collection took place during a gap in NCP measurements, a 22.5-minute average of the closest NCP data to the sample location was used instead. If the time difference between sample collection and the nearest NCP data exceeded three hours, then the station was assigned the median value for NCP across the entire cruise track. The latter approach was only implemented for three sample stations (S06, S24, S25) [Supplementary Table 2]. Prior to reaching stations 24 and 25, technical issues prevented further O_2/Ar data collection. The nearest NCP data to these stations differ from the cruse median (~0.2 mmol O_2 m^{-3} d^{-1}) by less than 0.21 mmol O_2 m^{-3} d^{-1}. The closest NCP data to S06 is virtually identical to the cruise median rate (<.03 mmol O_2 m^{-3} d^{-1} difference). Given the low number of stations at which this approach was used, the location of these stations in the oligotrophic ocean, and the small differences between the estimated station rates and the nearest recorded data—all of which are in near-balance with the atmosphere in terms of biological O_2 saturation—any bias to the dataset from this approximation is likely negligible.

Statistical analyses were performed on 16S rDNA and 18S rDNA taxonomy data using the vegan (Okansen et al 2017) and phyloseq packages in R.

Ordination of samples was performed with Principal Coordinate Analysis (PCoA), using weighted Bray-Curtis dissimilarity to express ecological distance. The first principal component of each projection was further modeled against the dataset of NCP and environmental measurements using linear regression. For these and all subsequent statistical comparisons with our molecular data, which represent volumetric sequence counts, NCP rates were expressed as volumetric values (mmol m^{-3} d^{-1}), though we obtained similar results if mixed-layer integrated NCP values were used.

Partial Least Squares Regression Analysis

Partial least squares (PLS) regression analysis was performed using the 'mixOmics' package in R (Rohart et al 2017) in 'regression' mode with two model components to identify bacterial and eukaryotic taxa with good predictive power in estimating NCP and environmental variables. Analyses were performed at the taxonomic levels corresponding to the order level for both the 18S and 16S datasets, excluding less-abundant taxa that comprised <0.5% of total 18S or 16S reads. Leave-one-out cross-validation was performed to evaluate model performance.

Online data availability

Sequences and metadata are available from the NCBI Sequence Read Archive under accession number SRP126177. Other data available upon request.

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