

## S1 Supplementary Methods

**Modelling of oxygen consumption rates.** Density was calculated using the data processing program SeaSoft (Sea-Bird Electronics). The stability of the water column was expressed using the Brunt-Väisälä frequency  $N$ , defined as:

$$N^2 = \frac{g}{\rho} \frac{\partial \rho}{\partial z}$$

where  $\rho$  is the water density,  $g$  is the gravitational acceleration and  $z$  is the water depth. The density gradient was calculated over 3-6 m bins. The turbulent diffusivity  $Ez$  was calculated according to Gregg et al. [1] from the Brunt-Väisälä-Frequency and the dissipation rate of turbulent kinetic energy  $\varepsilon$ :

$$Ez = \frac{\gamma \varepsilon}{N^2}$$

A mixing coefficient  $\gamma$  of 0.2 was applied. We used a mean  $\varepsilon$  of  $1.85 \times 10^{-9} \text{ W kg}^{-1}$ . This value was measured by Gregg et al. [1] for the open ocean thermocline and was applied in several rate diffusion models [2] [3]. Concentration gradients for  $\text{O}_2$  were calculated over 2-6 m bins. Oxygen fluxes at respective depths were calculated according to Fick's law:

$$J = -Ez \frac{\partial C}{\partial z}$$

$\text{O}_2$  consumption was determined from  $\text{O}_2$  flux gradients, calculated over 1-4 m bins:

$$R = \frac{\partial J}{\partial z}$$

**Processing of Peruvian OMZ metagenome data.** A total of 1,204,437 raw reads were obtained for the metagenome samples from the Peruvian OMZ. Raw reads were clustered using Cd-hit [4] with a sequence identity threshold of 98% and a word length of 8. The ribosomal-gene cluster representative sequences were identified by BLASTn searches [5] against the SILVA database [6] (bit score cut off: 86). Of all sequences, 0.24% were of ribosomal gene origin and subsequently separated from non-ribosomal-gene cluster representative sequences using MEGAN [7]. The latter were compared against the non-redundant NCBI database using BLASTx (bit score cut off: 35) and scanned with profile hidden Markov models of the ModEnzA Enzyme Commission groups [8]. Of all non-ribosomal-gene sequences, 69.6% were identified as protein-coding; the remainder could not be assigned. Sequences, cluster sizes and cluster identification numbers as well as results from the BLAST searches and EC scans were added to a MySQL database for analysis [9,10]. For the functional (cytochrome oxidase type) and taxonomic assignment of the cluster representatives the top hit of each BLAST search was used.

**Aggregate-size-dependent respiration rates.** Diffusion-limited aerobic respiration ( $R$ ) below a threshold  $O_2$  concentration was estimated by rearranging the analytical solution for solute transport and reaction in a sphere [11]:

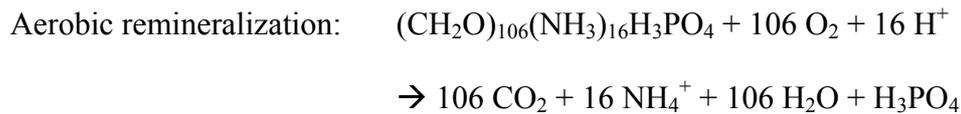
$$R = R_0 - R_0 \left( 1 - \frac{6 * C * D_{agg}}{R_0 * r_0^2} \right)^{\frac{3}{2}}$$

Here,  $R_0$  is the non-limited  $O_2$  consumption rate,  $C$  is the ambient  $O_2$  concentration,  $D_{agg}$  is the diffusion coefficient inside the aggregate ( $1.3 \times 10^{-9} \text{ m}^2 \text{ s}^{-1}$ ), and  $r_0$  is the aggregate diameter. For simplicity, the diffusive boundary layer around the aggregate was neglected and zero-order  $O_2$  consumption was assumed. An empirically

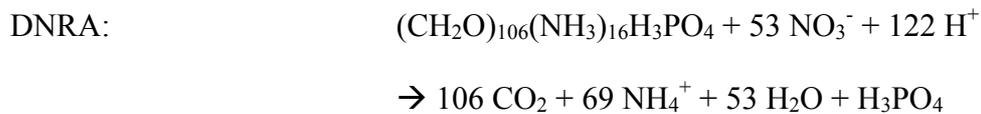
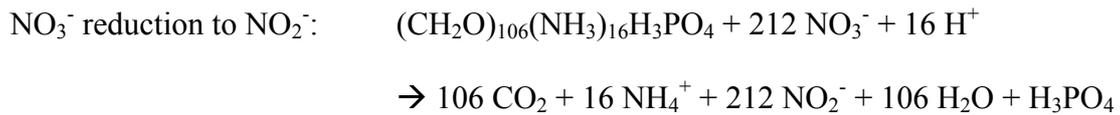
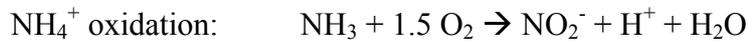
determined relationship between aggregate diameter (in mm) and respiration rate (in  $\text{nmol h}^{-1}$ ) in the Mauritanian upwelling region [12], with  $R_0 = 1.8 \text{ d}^{1.8}$ , was used to calculate  $\text{O}_2$  consumption as a function of  $\text{O}_2$  concentration for particles of 0.01 - 10 mm in diameter. To account for the somewhat lower incubation temperatures in our study ( $\Delta\text{O}_2 \approx 5 \text{ }^\circ\text{C}$ , Supplementary Table 1 and 2),  $\text{O}_2$  consumption rates were corrected using a temperature coefficient ( $Q_{10}$ ) of 2 [13].

### **Stoichiometries used to calculate $\text{NH}_4^+$ budgets for the upper Namibian and**

#### **Peruvian OMZs:**



#### Nitrification:



## References

1. Gregg MC, D'Asaro EA, Shay TJ, Larson N. Observations of Persistent Mixing and Near-Inertial Internal Waves. *J Phys Ocean*. 1986;16: 856–885.
2. Fennel W. A model of the yearly cycle of nutrients and plankton in the Baltic Sea. *J Mar Sci*. 1995;6: 313–329.
3. Lam P, Jensen MM, Lavik G, McGinnis DF, Muller B, Schubert CJ, et al. Linking crenarchaeal and bacterial nitrification to anammox in the Black Sea. *PNAS*. 2007;104: 7104–7109.
4. Li W, Godzik A. Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. *Bioinformatics*. 2006;22: 1658–1659.
5. Altschul S, Gish W, Miller W, Myers E, Lipman D. Basic Local Alignment Search Tool. *J Mol Biol*. 1990;215: 403–410.
6. Prsse E, Quast C, Knittel K, Fuchs B, W L, Peplies J, et al. SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. *Nucleic Acids Res*. 2007;35: 7188–7196.
7. Huson D, Auch A, Qi J, Schuster S. MEGAN analysis of metagenomic data. *Genome Res*. 2007;17: 377–386.
8. Desai D, Nandi S, Srivastata P, Lynn A. ModEnza: Accurate Identification of Metabolic Enzymes Using Function Specific Profile HMMs with Optimized Discrimination Threshold and Modified Emission Probabilities. *Adv Bioinformatics*. 2011; 743782.
9. Desai DK, Schunck H, Lser JW, LaRoche J. Fragment Recruitment on Metabolic Pathways: comparative metabolic profiling of metagenomes and metatranscriptomes. *Bioinformatics*. 2013;29: 790–791.
10. Schunck H, Lavik G, Desai DK, Grokopf T, Kalvelage T, Lscher CR, et al. Giant Hydrogen Sulfide Plume in the Oxygen Minimum Zone off Peru Supports Chemolithoautotrophy. *PLoS One*. 2013;8: e68661.
11. Ploug H, Khl M, Buchholz-Cleven B, Jrgensen BB. Anoxic aggregates - an ephemeral phenomenon in the pelagic environment? *Aquat Microb Ecol*. 1997;13: 285–294.
12. Iversen MH, Nowald N, Ploug H, Jackson GA, Fischer G. High resolution profiles of vertical particulate organic matter export off Cape Blanc, Mauritania: Degradation processes and ballasting effects. *Deep Res I*. 2010;57: 771–784.
13. Thamdrup B, Hansen JW, Jrgensen BB. Temperature dependence of aerobic respiration in a coastal sediment. *FEMS Microbiol Ecol*. 1998;25: 189–200.