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Regulation of nitrous oxide production in low-oxygen waters off the coast of Peru

Claudia Frey et al.

Correspondence to: Claudia Frey (claudia.frey@unibas.ch)

Table S1: Average alpha diversities of total and active archaeal *amoA* and *nirS* communities.

	nirS	***amoA***
DNA	3.8 ± 0.4	3.6 ± 0.1
cDNA	3.4 ± 0.5	3.2 ± 0.3

Table S2: Overview of abundant archetypes (> 1%) that are significantly enriched in respective O_2 levels (Lefse analysis). O_2 levels were split in 3 categories: anoxic (<1 µmol L^{-1} O_2, Seabird O_2 and Winkler titration detection limits), hypoxic (1 – 10 µmol L^{-1} O_2), oxic (> 10 µmol L^{-1} O_2).

amoA	**archetype**	**anoxic**	**hypoxic**	**oxic**	*nirS*	**archetype**	**anoxic**	**hypoxic**	**oxic**
DNA	AOA3			x	DNA	nir4			x
	AOA7	x				nir14			x
	AOA78			x		nir23	x		
	AOA83			x		nir46	x		
						nir166	x		
cDNA	AOA3			x	cDNA	nir4			x
	AOA7		x			nir14			x
	AOA83			x		nir23	x		
						nir141			x
						nir166	x		

Table S3: All samples with rates, standard errors, fraction label (f_N), yields, copy numbers mL^{-1} of *nirS* and *amoA* genes and transcripts.

sample ID	station	depth (m)	oxygen (µM)	f NH4+	f NO2-	f NO3-	N2O pro (nM /d) NH4-	SE	%hybrid from total N2O	NH4 oxi (nM /d)	SE	N2O Yield (%) NH4+	SE yield	N2O pro (nM /d) NO2-	SE	%hybrid from total N2O	N2O pro (nM /d) NO3-	SE	NO3- reduction (nM /d)	SE	N2O Yield (%) NO3	STD yield	nirS gene copy numbers*mL-1	STD	nirS transcript copy numbers*mL-1	STD	amoA gene copy numbers*mL-1	STD	amoA transcript copy numbers *mL-1	STD
S1	882	298	0.2	0.98	0.45	0.058	0.0	0.002	-	0.89	0.22	nd	0.00	0.04	0.00	0.000	2.67	0.39	7.20	1.7	42.53	0.28	412319.0	1879.7	2707.3	135.7	2548.1	17.3	30.6	12.2
S2	882	352.6	bd	0.97	0.39	0.055	0.0	0.001	-	0.00	0.24	nd	0.00	0.09	0.03	18.98	2.20	0.35	19.42	8.3	18.49	0.45	530804.0	36269.9	4880.8	362.9	4082.7	259.3	143.4	10.4
S3	882	258.7	1.5	0.99	0.22	0.059	0.0253	0.000	77.8	3.62	1.21	1.40	0.49	0.11	0.02	21.9	1.36	0.61	14.8	1.5	15.45	0.46	116275.5	3138.8	424.9	17.4	974.8	97.2	20.6	0.8
S4	882	218.9	6.06	0.97	0.77	0.056	0.0310	0.000	78.1	8.00	1.69	0.78	0.18	0.06	0.01	63.6	1.05	0.47	7.53	2.1	21.76	0.53	81055.2	10685.0	829.8	45.9	2018.8	187.6	240.9	41.4
S5	882	73.9	8.4	0.98	0.95	0.059	0.1411	0.003	79.4	35.71	9.07	0.79	0.43	0.02	0.00	79.2	0.00	0.78	5.90	2.4	0.00	0.00	19971.7	1455.5	54.8	22.1	14462.8	656.3	628.4	10.0
S6	883	304.1	bd	0.99	0.21	0.064	0.0	0.001	-	0.33	0.99	nd	0.00	0.29	0.29	37.16	1.57	0.32	34.67	5.59	8.30	0.26	618285.8	19727.5	2716.5	247.3	4000.4	99.9	44.0	10.8
S7	883	268.1	0.2	0.99	0.18	0.065	0.0	0.001	-	0.98	0.30	nd	0.00	0.71	0.38	0.00	5.65	2.82	46.65	6.97	19.49	0.52	293503.7	45312.4	1749.2	198.9	1920.1	21.8	47.3	0.2
S8	883	249.4	2.25	0.99	0.21	0.062	0.0017	0.000	83.3	0.95	0.40	0.35	0.35	0.20	0.07	0.00	2.62	0.90	17.44	4.61	23.11	0.43	372479.5	1698.1	4006.6	690.7	2601.8	124.0	104.8	3.1
S9	883	189	1.6	0.99	0.99	0.058	0.0647	0.001	83.8	10.94	1.27	1.18	0.31	0.14	0.02	88.04	1.05	0.77	15.08	1.61	12.20	0.75	16892.7	539.0	48.9	0.7	18113.5	452.2	626.2	29.8
S10	883	28	30.1	0.99	0.91	0.065	0.1596	0.003	86.6	34.07	0.11	0.94	0.42	0.07	0.03	52.79	0.00	2.53	13.49	4.44	0.00	0.00	6331.1	86.6	42.1	5.0	24513.8	389.5	521.7	8.3
S11	894	118.9	bd	0.98	0.96	0.060	0.0879	0.001	78.9	2.71	1.01	0.27	0.14	0.09	0.01	76.3	5.86	0.48	6.4	2.1	64.86	0.34	185531.9	845.8	2421.5	154.4	6800.4	15.4	284.8	7.4
S12	904	179.4	bd	nd	0.26	0.070	nd	nd	nd	nd	nd	nd	nd	0.19	0.06	0.00	4.39	0.77	8.47	4.05	50.90	0.51	426523.5	1944.5	4347.9	632.0	6000.2	108.9	233.5	8.5
S13	904	124.0	0.25	nd	0.82	0.060	nd	nd	nd	nd	nd	nd	nd	0.16	0.00	90.52	7.20	1.64	9.06	2.62	61.40	0.37	153881.6	2806.0	562.2	74.1	6435.6	14.6	198.2	10.3
S14	906	147.1	bd	nd	0.33	0.070	nd	nd	nd	nd	nd	nd	nd	0.32	0.07	13.67	3.63	0.28	38.0	11.7	16.05	0.32	318507.1	1452.0	2104.1	67.1	6031.7	150.6	88.7	14.2
S15	907	130	0.44	0.97	0.25	0.110	0.0180	0.000	82.0	11.38	1.80	0.32	0.13	0.30	0.10	39.3	1.23	0.23	17.51	4.66	12.36	0.32	729635.6	3326.3	4276.9	0.0	4212.9	143.4	140.6	8.6
S16	907	9.2	209.3	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	6250.4	795.7	14.8	4.4	994.1	6.8	45.9	5.9
S17	912	89.8	1.44	0.97	0.38	0.090	0.1227	0.002	80.2	11.86	1.90	2.07	0.34	3.06	1.17	83.55	118.00	27.80	32.50	12.38	87.8	39.3	789262.1	21586.2	9472.8	647.3	3077.8	7.0	246.6	5.0
S18	912	4.7	204.5	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	15921.1	508.0	44.3	10.8	2589.8	152.7	110.7	2.8
S19	892	143.7	bd	0.76	0.11	0.090	0.0337	0.000	71.0	1.79	0.356	0.16	0.05	0.72	0.19	0.0	1.63	0.30	12.69	1.12	20.47	0.20	1010946.4	4608.8	291021.5	31778.2	2936.5	119.9	49.8	5.8
S20	906	92.2	0.46	nd	0.11	0.080	nd	nd	nd	nd	nd	nd	nd	2.37	0.54	0.00	4.88	0.41	53.8	4.2	15.34	0.11	351334.8	9609.0	1556.3	835.7	6529.0	59.3	204.0	18.5
S21	917	139.2	bd	nd	0.1	0.100	nd	nd	nd	nd	nd	nd	nd	0.76	0.25	0.0	0.36	0.13	27.5	4.8	2.63	0.20	969128.0	8836.2	759.6	80.2	2725.7	0.0	32.7	0.7
Average							0.049		80.1	8.8		0.8		0.5		35.0	8.7		20.4		26.0									
STD							0.057		4.2	11.9		0.6		0.8		35.4	2.2		14.4		24.2									

20

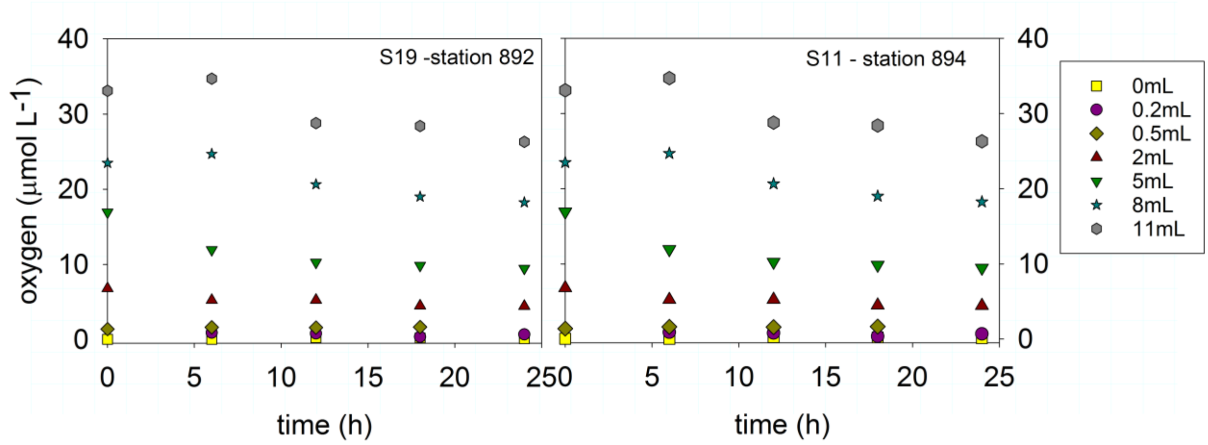

Figure S1: Dissolved oxygen concentrations inside the serum bottles during the 24h incubations of the oxygen manipulation experiments at station 892 and 894. No tracer was added to these bottles. Only the $^{15}NO_3^-$ incubations received 8mL and 11mL additions of saturated site water.

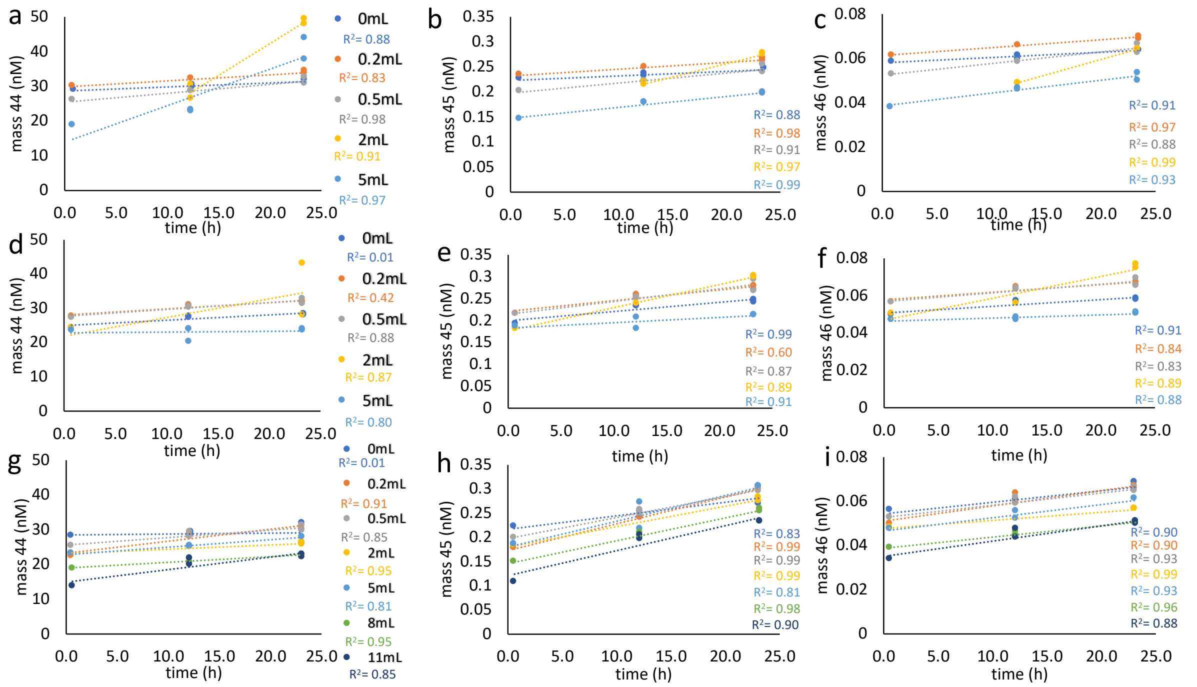

Figure S2: Examples of the production of mass 44 (a,b,c), 45 (d,e,f),and 46 (g,h,i) over 24hfrom the oxygen manipulation experiment performed at station 892, sample S11. R^2 of the linear regression is given for each treatment and mass. Treatments in center and right panels are same as labeled in the left panel.

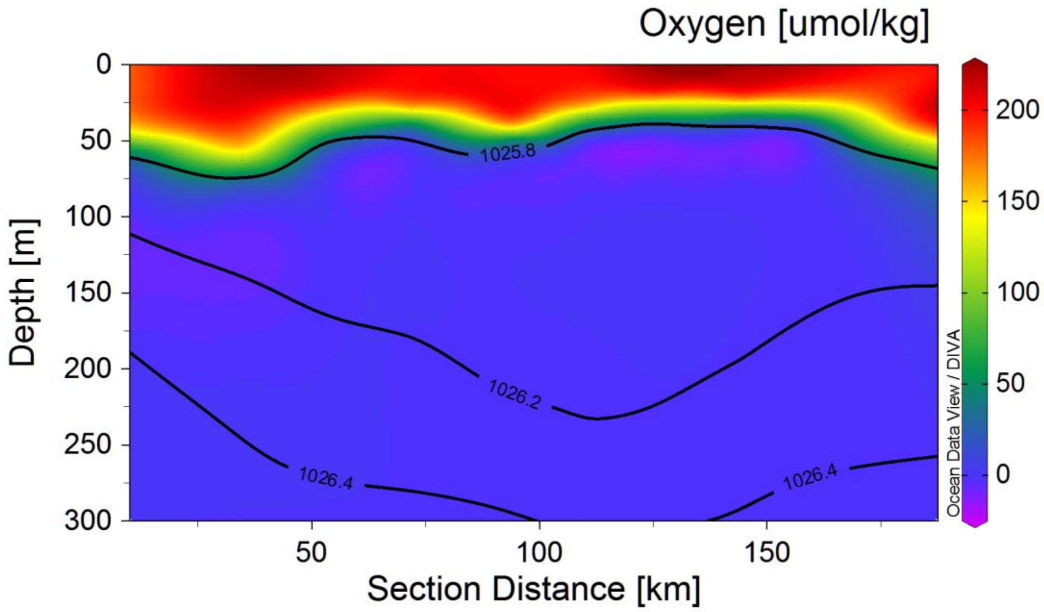

Figure S3: Oxygen and density contours plot from CTD data across the eddy transect 4.

35

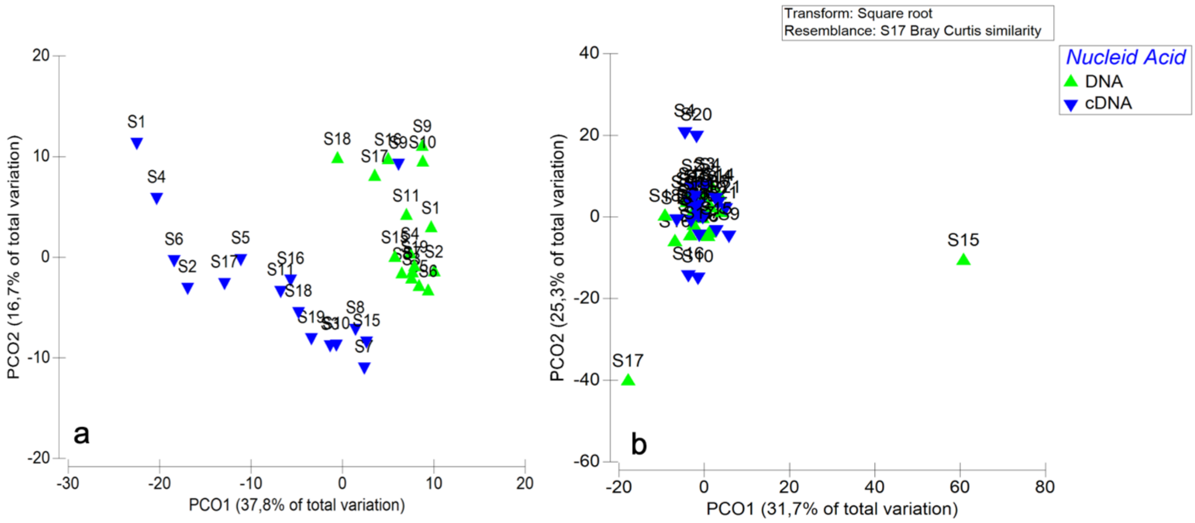

Figure S4: Principle component analysis of amoA DNA and cDNA (a) and *nirS* DNA and cDNA (b).

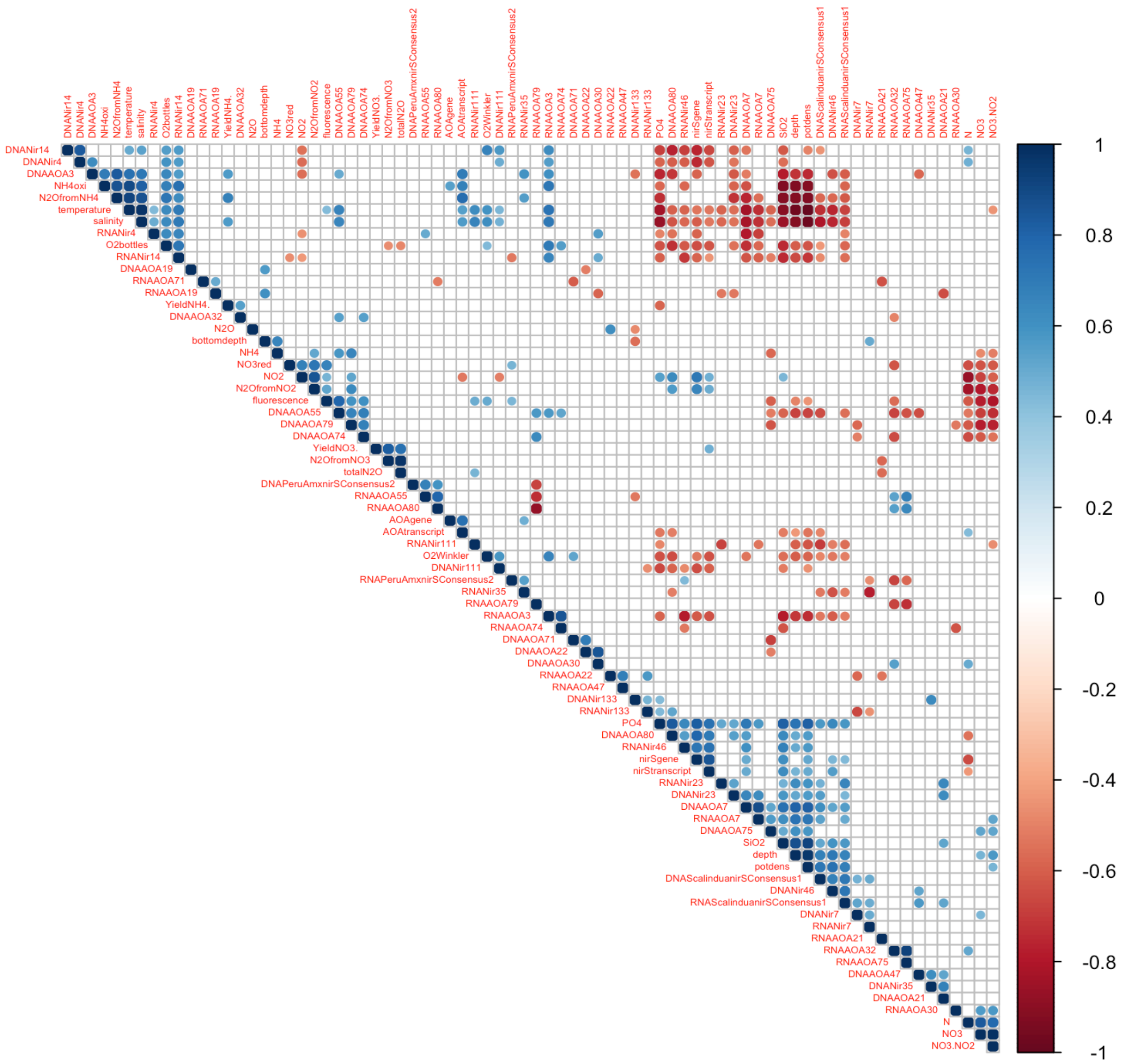

Figure S5: Heat map of significant positive (blue) or negative (red) correlations ($p<0.05$) based on a Spearman Rank correlation analysis.

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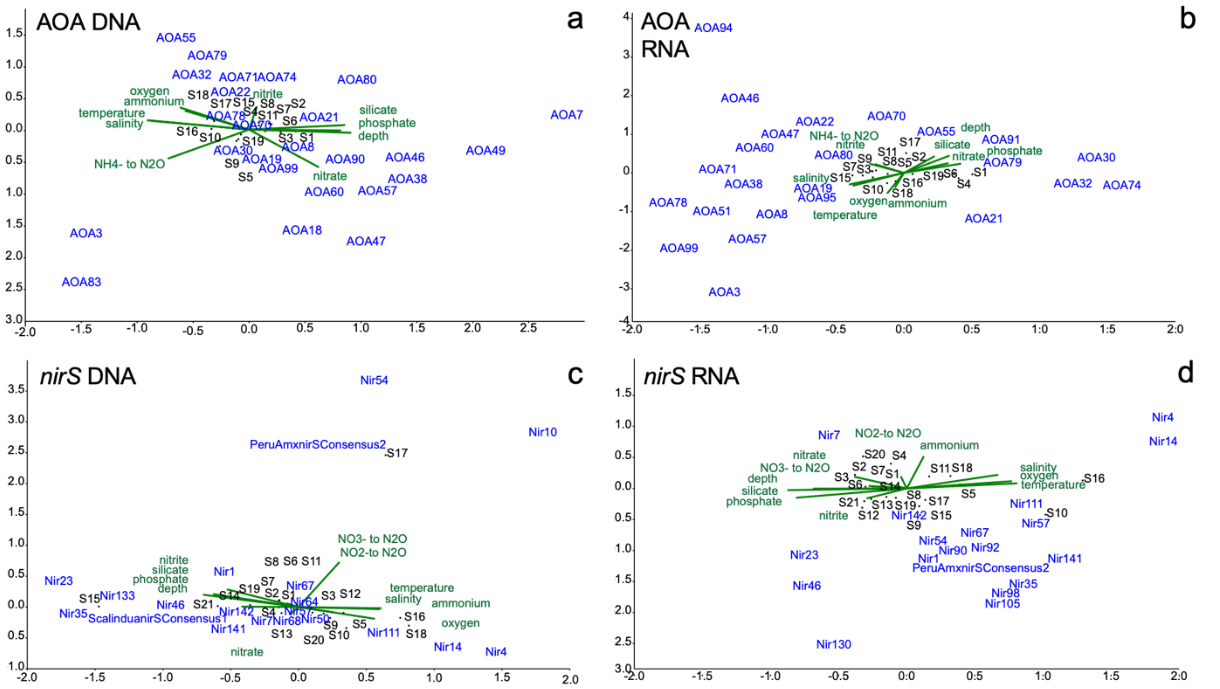
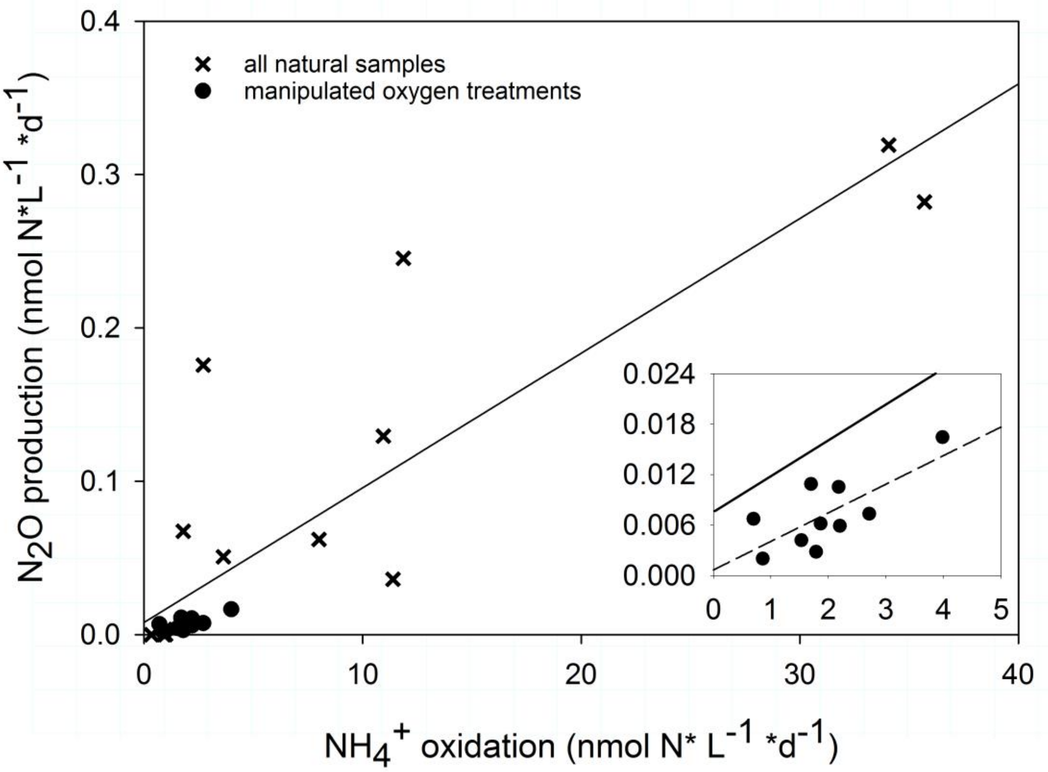


Figure S6: Triplot of Canonical Correspondence Analysis showing the archetype composition as a response to the environmental parameters. Upper panel *amoA* archetypes (a,b) and lower panel *nirS* archetypes (c,d). On the right is the DNA (a,c) and on the left is the cDNA (b,d).



55 **Figure S7:** Scatter plot of AO versus N_2O production from $NH_4^+$with linear fit through all data (y = 0.0088 x + 0.0080 R^2= 0.75, p<0.0001). Zoom in shows manipulated treatments with small AO rates and linear fit through treatments (y = 0.0034x + 0.0007, R^2= 0.73, p<0.0001).

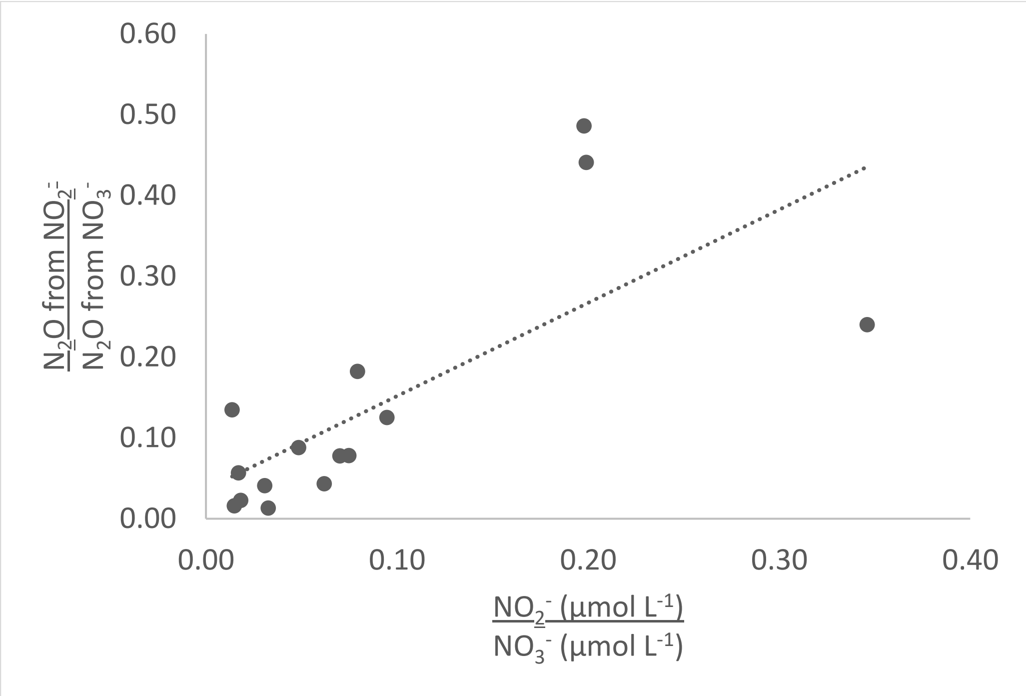


Figure S8: Scatter plot of the ratio of N_2O production rates from NO_2^- and that from NO_3^- plotted against ratio of NO_2^- and NO_3^- concentrations. Linear fit ($y = 1.153\ x + 0.0365$ $R^2 = 0.62$, $p<0.0001$).

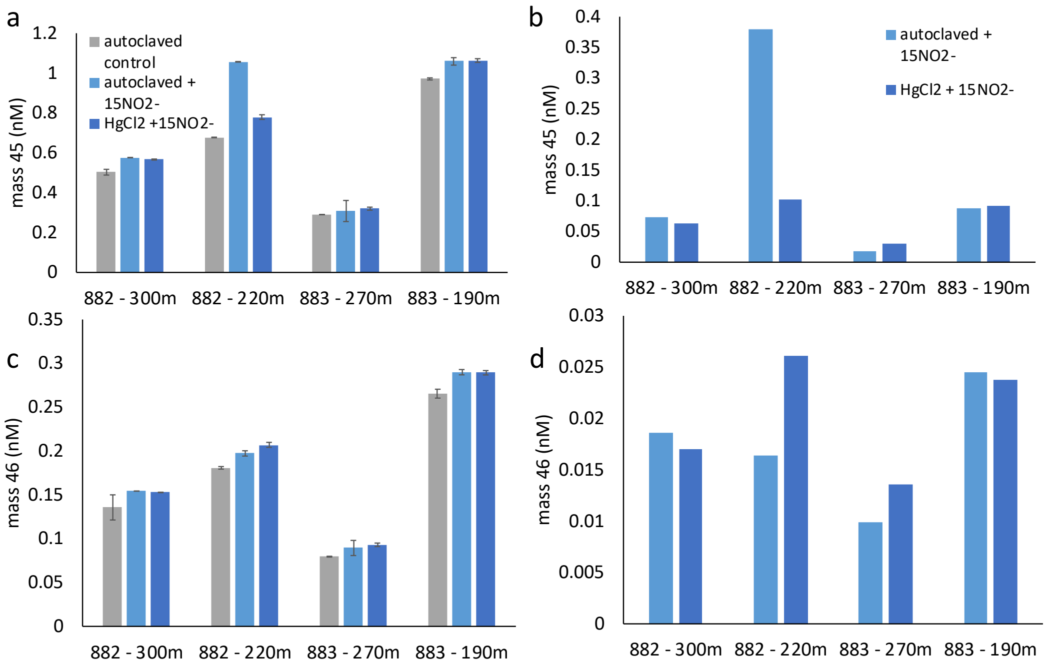


Figure S9: Abiotic N_2O Production of mass 45 (a) and mass 46 (c) from $^{15}NO_2^-$ for 4 depths. The control did not receive tracer addition. The bottles incubated for 65 - 80 days from simultaneous tracer and $HgCl_2$ addition or autoclaving until the measurement in the lab. Figure b) and d) show offset between control and the treatments. Error bars are from duplicates. There is little abiotic production from both masses, between 0.018 – 0.37 for mass 45 and 0.009 – 0.026 for mass 46. There was no significant difference between addition of $HgCl_2$ and autoclaving to stop biological activity. Only at station 882, depth 220m mass 45 and 46 responded very differently.