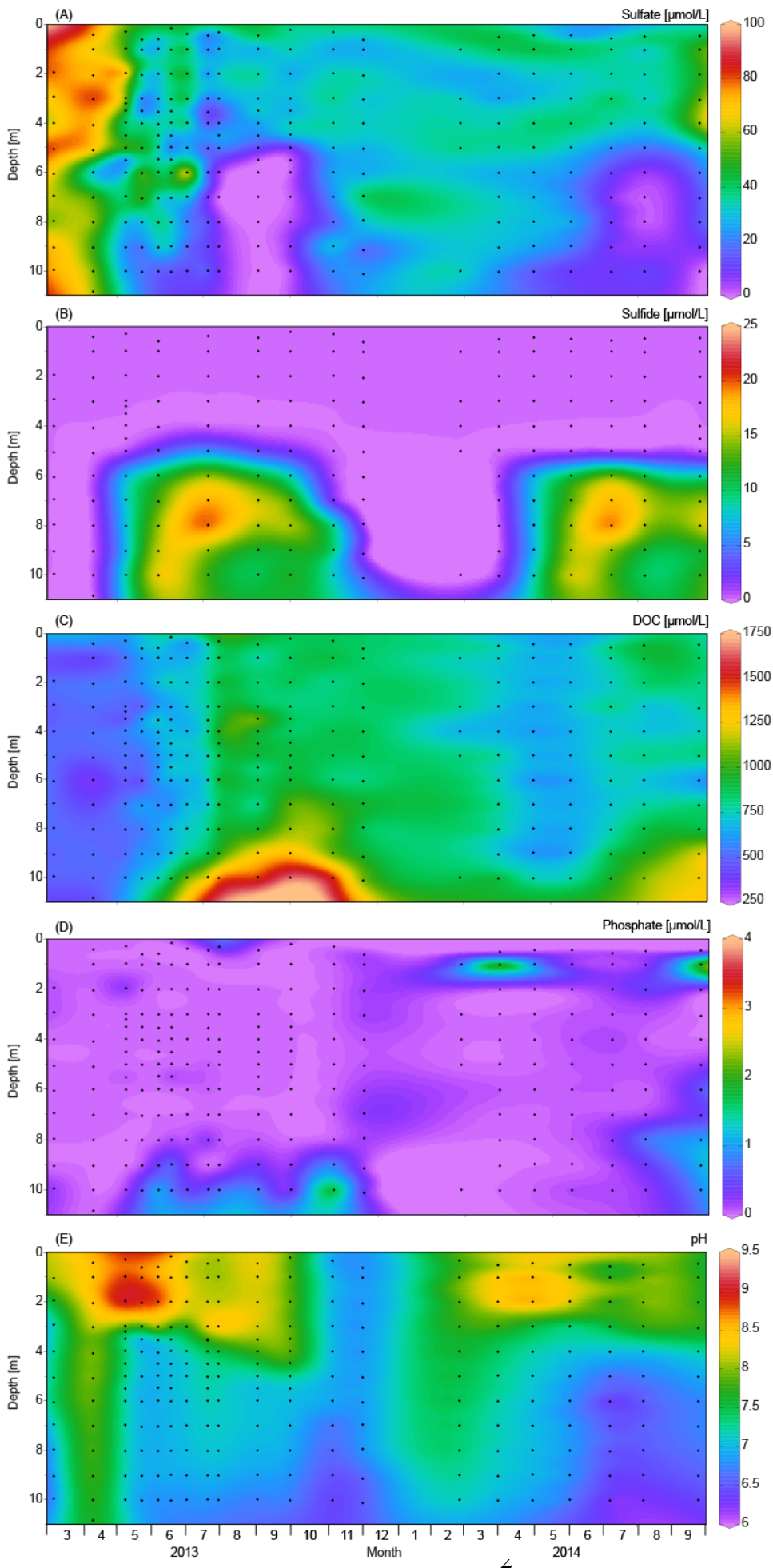


## **Supplementary Information**

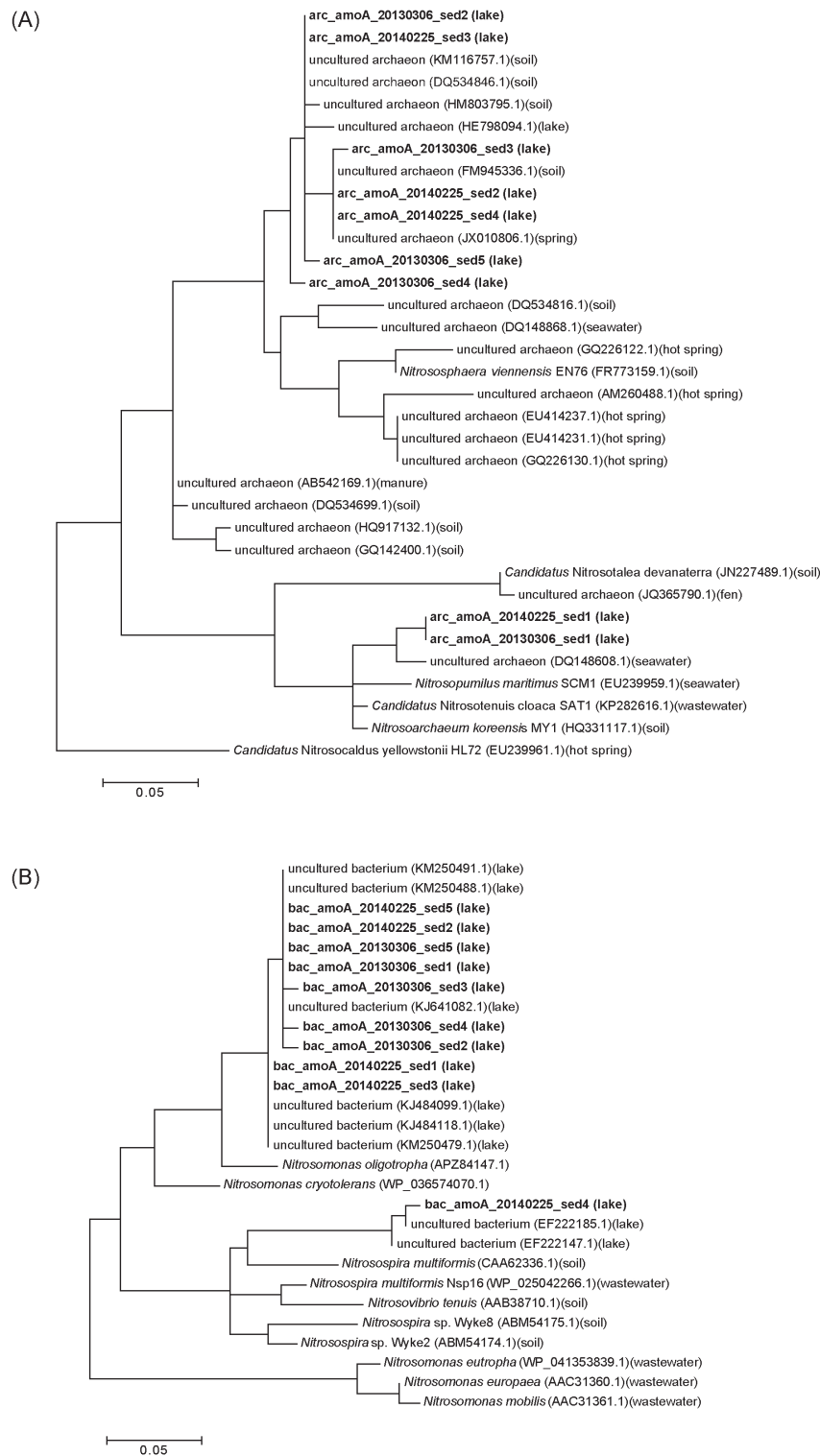
Number of pages: 10

Number of figures: 4

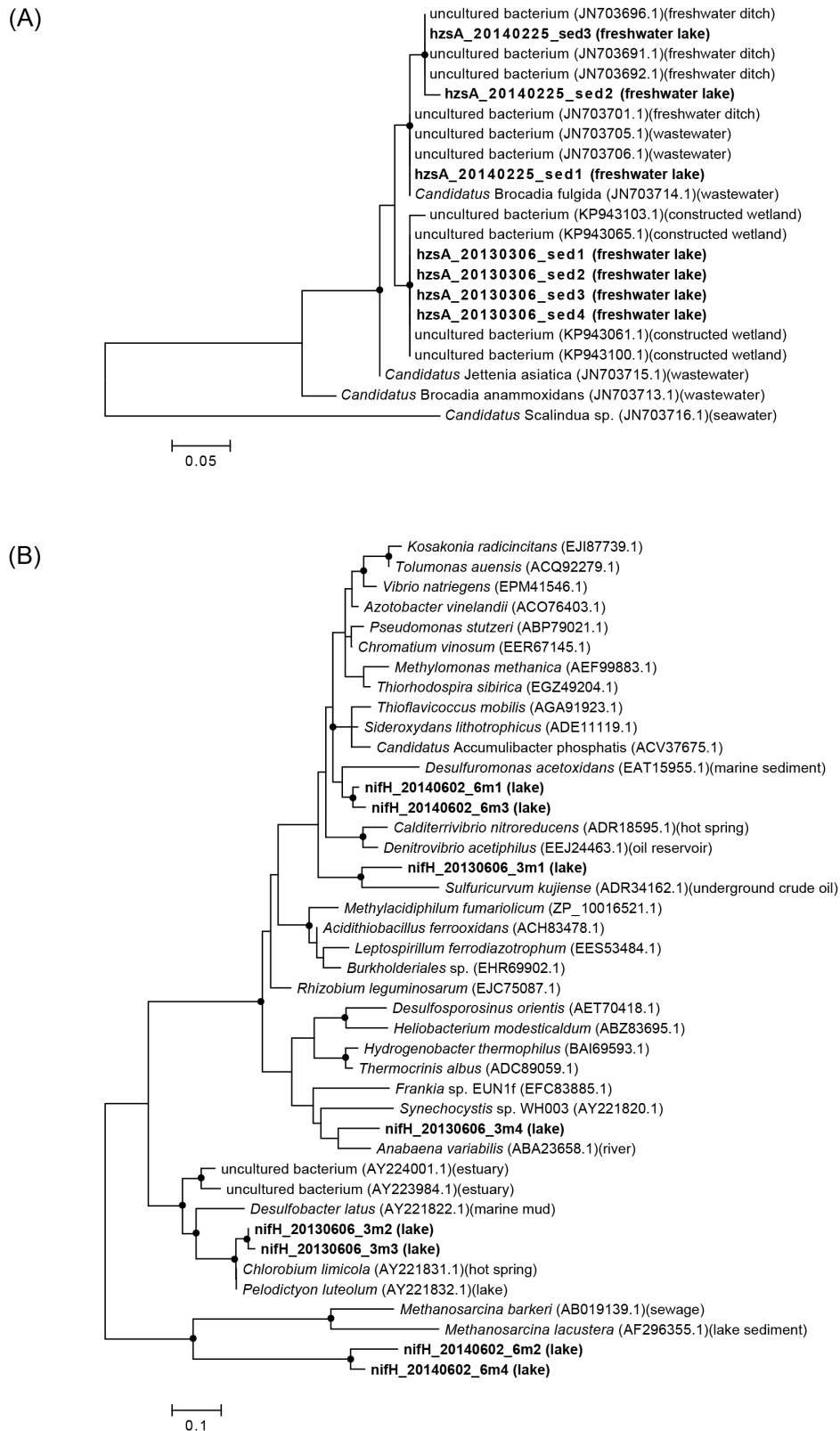
Number of tables: 5



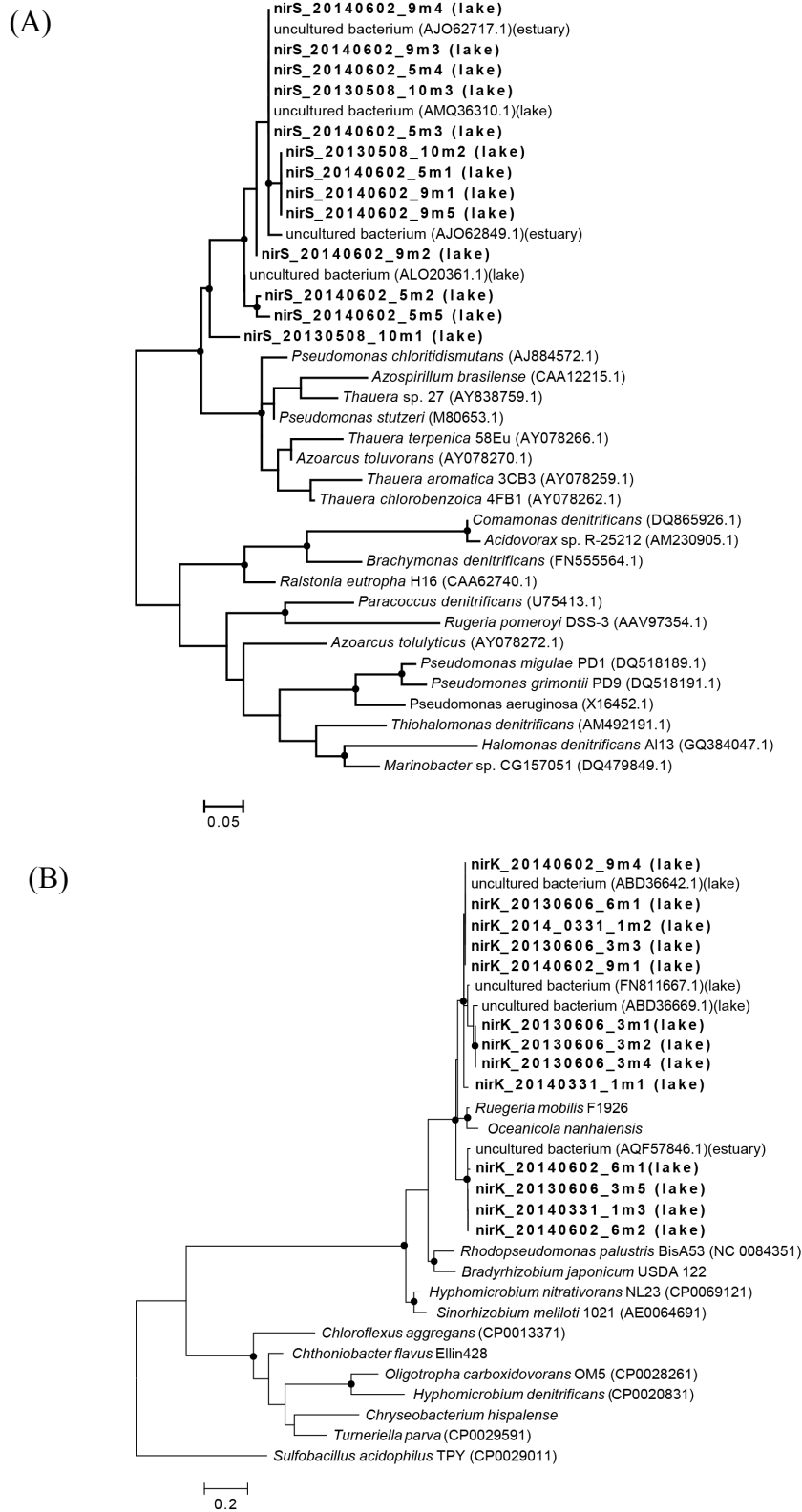
**Figure S1.** Spatio-temporal dynamics of environmental parameters in Lake Vechten over a period of 19 months. (A) Sulfate, (B) Sulfide, (C) DOC, (D) Phosphate, and (E) pH.



**Figure S2.** Maximum likelihood trees based on protein sequences of (A) archaeal *amoA* genes (ammonia-oxidizing archaea), and (B) bacterial *amoA* genes (ammonia-oxidizing bacteria) of Lake Vechten. Names in boldface are sequences determined in our study. The scale bars indicate the number of amino acid substitutions per site. Black dots on the branches indicate bootstrap values between 90 and 100%.



**Figure S3.** Maximum likelihood trees based on protein sequences of (A) *hzsA* genes (anammox bacteria), and (B) *nifH* genes (nitrogen-fixing bacteria) of Lake Vechten. Names in boldface are sequences determined in our study. The scale bars indicate the number of amino acid substitutions per site. Black dots on the branches indicate bootstrap values between 90 and 100%.



**Figure S4.** Maximum likelihood trees based on protein sequences of (A) *nirS* genes (denitrifying bacteria), and (B) *nirK* genes (denitrifying bacteria) of Lake Vechten. Names in boldface are sequences determined in our study. The scale bars indicate the number of amino acid substitutions per site. Black dots on the branches indicate bootstrap values between 90 and 100%.

**Table S1.** Fragment length and thermal programs of PCR primers used in this study

Primers	Target gene	Fragment (bp)	PCR program
Arch-amoAF Arch-amoAR	<i>Arc amoA</i>	635	3 min at 95.0°C; 35 cycles of: 45 s at 95.0°C, 45 s at 53.0°C, 45 s at 72.0°C; 5 min at 72.0°C.
amoA-1F amoA-2R	<i>Bac amoA</i>	491	3 min at 95.0°C; 35 cycles of: 40 s at 95.0°C, 40 s at 48.0°C, 40 s at 72.0°C; 5 min at 72.0°C.
hzsA_1597F hzsA_1857R	<i>hzsA</i>	260	3 min at 95.0°C; 35 cycles of: 30 s at 95.0°C, 30 s at 50.0°C, 30 s at 72.0°C; 5 min at 72.0°C.
nirS1F nirS-q-R	<i>nirS</i>	265	3 min at 95.0°C; 35 cycles of: 30 s at 95.0°C, 30 s at 56.0°C, 30 s at 72.0°C; 5 min at 72.0°C.
nirK-q-F nirK1040	<i>nirK</i>	472	3 min at 95.0°C; 35 cycles of: 30 s at 95.0°C, 30 s at 56.0°C, 30 s at 72.0°C; 5 min at 72.0°C.
IGK3 DVVR	<i>nifH</i>	395	3 min at 95.0°C; 35 cycles of: 30 s at 95.0°C, 30 s at 50.0°C, 30 s at 72.0°C; 5 min at 72.0°C.

**Table S2.** List of samples for cloning

Functional gene	Date	Depth (m)	Fragment (bp)	Cloning ID
<i>Arc amoA</i>	2013-03-06	Sediment	635	arc_amoA_20130306_sed1
				-
<i>Arc amoA</i>	2014-02-25	Sediment	635	arc_amoA_20130306_sed5 arc_amoA_20140225_sed1
				-
<i>Bac amoA</i>	2013-03-06	Sediment	491	arc_amoA_20140225_sed4 bac_amoA_20130306_sed1
				-
<i>Bac amoA</i>	2014-02-25	Sediment	491	bac_amoA_20130306_sed5 bac_amoA_20140225_sed1
				-
<i>hzsA</i>	2013-03-06	Sediment	260	bac_amoA_20140225_sed5 hzsA_20130306_sed1
				-
<i>hzsA</i>	2014-02-25	Sediment	260	hzsA_20130306_sed4 hzsA_20140225_sed1
				-
<i>nifH</i>	2013-06-06	3	395	hzsA_20140225_sed3 nifH_20130606_3m1
				-
<i>nifH</i>	2014-06-02	6	395	nifH_20130606_3m4 nifH_20140602_6m1
				-
<i>nirS</i>	2013-05-08	10	265	nifH_20140602_6m4 nirS_20130508_10m1
				-
<i>nirS</i>	2014-06-02	5	265	nirS_20130508_10m3 nirS_20140602_5m1
				-
<i>nirS</i>	2014-06-02	9	265	nirS_20140602_5m5 nirS_20140602_9m1
				-
<i>nirK</i>	2013-06-06	3	472	nirS_20140602_9m5 nirK_20130606_3m1
				-
<i>nirK</i>	2014-03-31	1	472	nirK_20130606_3m5 nirK_20140331_1m1
				-
<i>nirK</i>	2014-06-02	6	472	nirK_20140331_1m3 nirK_20140602_6m1
				-
<i>nirK</i>	2014-06-02	9	472	nirK_20140602_6m2 nirK_20140602_9m1
				-
				nirK_20140602_9m2

**Table S3.** List of DNA samples for amplicon sequencing

<b>Sample ID</b>	<b>Date</b>	<b>Depth (m)</b>	<b>Sample ID</b>	<b>Date</b>	<b>Depth (m)</b>
A0301	2013-03-06	1	G0901	2013-09-02	1
A0305		5	G0903		3
A0310		10	G0904		4
A03S		Sediment	G0905		5
B0401	2013-04-10	1	G0906		6
B0405		5	G0910		10
B0410		10	H0901	2013-09-30	1
C0501	2013-05-08	1	H0903		3
C0503		3	H0904		4
C0504		4	H0905		5
C0505		5	H0906		6
C0510		10	H0910		10
D0601	2013-06-06	1	I1101	2013-11-07	1
D0603		3	I1107		7
D0604		4	I1108		8
D0605		5	I1110		10
D0610		10	I11S		Sediment
E0701	2013-07-01	1	J1201	2013-12-03	1
E0703		3	J1205		5
E0704		4	J1210		10
E0705		5	K0201	2014-02-25	1
E0710		10	K0205		5
E07S		Sediment	K0210		10
F0701	2013-07-29	1	K02S		Sediment
F0703		3	L0301	2014-03-31	1
F0704		4	L0305		5
F0705		5	L0310		10
F0710		10			

**Table S4.** qPCR programs, efficiency and R<sup>2</sup> of functional marker genes

Primers	Target gene	Fragment (bp)	qPCR program	qPCR efficiency	R <sup>2</sup>
Arch-amoAF Arch-amoAR	<i>Arc amoA</i>	635	3 min at 95.0°C; 40 cycles of: 45 s at 95.0°C, 45 s at 59.0°C, 45 s at 72.0°C; 5 min at 72.0°C.	95.1-99.2%	0.991-0.994
amoA-1F amoA-2R	<i>Bac amoA</i>	491	3 min at 95.0°C; 40 cycles of: 30 s at 95.0°C, 30 s at 59.0°C, 30 s at 72.0°C; 5 min at 72.0°C.	90.1-92.7%	0.997-0.999
hzsA_1597F hzsA_1857R	<i>hzsA</i>	260	3 min at 95.0°C; 40 cycles of: 30 s at 95.0°C, 30 s at 50.0°C, 30 s at 72.0°C; 5 min at 72.0°C.	83.8-86.4%	0.998-0.999
nirS1F nirS-q-R	<i>nirS</i>	265	3 min at 95.0°C; 40 cycles of: 30 s at 95.0°C, 30 s at 60.0°C, 30 s at 72.0°C; 5 min at 72.0°C.	92.6- 95.5%	0.996-0.998
nirK-q-F nirK1040	<i>nirK</i>	472	3 min at 95.0°C; 40 cycles of: 30 s at 95.0°C, 30 s at 62.5°C, 30 s at 72.0°C; 5 min at 72.0°C.	95.4-99.8%	0.995-0.997
IGK3 DVVR	<i>nifH</i>	395	3 min at 95.0°C; 40 cycles of: 30 s at 95.0°C, 30 s at 55.0°C, 30 s at 72.0°C; 5 min at 72.0°C.	81.9- 83.4%	0.998-0.999

**Table S5.** Significance of the selected explanatory variables in the RDA correlation triplots (see **Figure 5**).

<b>Explanatory Variable</b>	<b>AIC</b>	<b>Pseudo-F</b>	<b>P</b>
DO	124.52	10.58	0.005
PO <sub>4</sub> <sup>3-</sup>	128.26	6.63	0.005
NH <sub>4</sub> <sup>+</sup>	129.70	5.15	0.005
pH	130.52	4.32	0.005
SO <sub>4</sub> <sup>2-</sup>	133.26	1.55	0.005

*The explanatory variables were selected by forward selection based on the pseudo-F statistic, using 9999 permutations to assess their significance. AIC = Akaike information criterion. Total variation explained by the RDA model was 29.4%.*