Supplemental data summary

Biogeography of sediment bacterial community responds to a nitrogen pollution gradient in East China Sea

Table S1 Measurements of environmental parameters of the 5 sampling sites in East China Sea. The data represent the mean ± standard deviation (N = 5). Different small letters indicate significant differences between sites for that parameter. Means compared using one-way ANOVA, $P < 0.05$ level.

Environmental factor	Site				
	A	B	C	D	E
Longitude (°E)	122°1.508'	122°4.433'	122°16.033'	122°30.791'	122°34.801'
Latitude (°N)	29°22.972'	29°22.932'	29°22.716'	29°22.900'	29°22.879'
Water depth (m)	5.3	6.8	11.6	31.6	33.5
Salinity (‰)	23.89	24.22	26.80	27.91	28.57
pH	6.83 ± 0.03 b	6.91 ± 0.02 a	6.90 ± 0.01 a	6.88 ± 0.01 ab	6.87 ± 0.01 ab
Eh	76.8 ± 4.25 a	54.0 ± 4.09 c	64.6 ± 3.59 b	48.0 ± 1.95 c	50.0 ± 2.86 c
Moisture content (%)	40.15 ± 1.37 b	43.79 ± 1.29 a	43.82 ± 1.35 a	43.06 ± 0.63 ab	43.86 ± 1.25 a
TOC (mg/kg)	0.67 ± 0.02 a	0.67 ± 0.06 a	0.51 ± 0.03 ab	0.65 ± 0.02 a	0.58 ± 0.02 ab
NO_2^--N (mg/kg)	0.09 ± 0.01 a	0.09 ± 0.02 a	0.05 ± 0.01 b	0.07 ± 0.02 ab	0.05 ± 0.01b
NH_4^+-N (mg/kg)	0.26 ± 0.03 bc	0.30 ± 0.02 ab	0.41 ± 0.07 a	0.21 ± 0.07 bc	0.15 ± 0.04 c
NO_3^--N (mg/kg)	10.80 ± 0.99 a	9.63 ± 1.75 ab	8.96 ± 1.61 ab	7.53 ± 0.51 ab	7.13 ± 0.79 b
DIN (mg/kg)	11.16 ± 0.98 a	10.02 ± 1.75 ab	9.41 ± 1.64 ab	7.81 ± 0.48 ab	7.32 ± 0.80 b
PO_4^{3+}-P (mg/kg)	1.07 ± 0.36 b	1.86 ± 0.29 a	0.83 ± 0.15 b	1.24 ± 0.16 ab	0.63 ± 0.09 b
SO_4^{2+}-S (mg/kg)	927.9 ± 84.9 c	1324.7 ± 45.4 b	1381.4 ± 67.8 b	1901.6 ± 104.8a	2110.4 ± 68.9 a
TN (mg/kg)	580.2 ± 34.0 a	527.1 ± 6.2 ab	476.8 ± 26.2 b	553.7 ± 22.6 a	515.2 ± 14.8 ab
TP (mg/kg)	323.3 ± 9.9 c	356.9 ± 4.3 b	407.7 ± 11.4 a	407.1 ± 4.50a	414.1 ± 16.9 a

TOC: total organic carbon; TN: total nitrogen; TP: total phosphorus;

The total inorganic N concentration (DIN) was calculated as the sum of NH_4^+, NO_2^--N, and NO_3^--N.

Table S2 Sediment bacterial community data, including operate taxonomic units (OTUs) uniqueness, and their percentage (in bracket values) at each site, and OTUs overlap and their percentages between two sites.

Site	A	B	C	D	E
A	**2993 (34.9%)** [a]	*3817 (28.3%)* [b]	*3822 (26.8%)*	*3537 (24.7%)*	*3361 (23.6%)*
B		**3083 (35.2%)**	*3950 (27.6%)*	*3583 (24.8%)*	*3380 (23.4%)*
C			**3577 (37.7%)**	*3700 (24.6%)*	*3591 (24.0%)*
D				**3379 (36.4%)**	*4036 (28.3%)*
E					**3417 (37.8%)**

[a] Values in boldface type represent unique OTUs and their percentage at each site.

[b] Values in italic type represent overlap OTUs and their percentage between two sites.

Figure S1 Sites of samples used in this study. The area depicted is in the East China Sea. To cover an array of sea water pollution levels, samples are collected along a transect on Oct. 25, 2012.

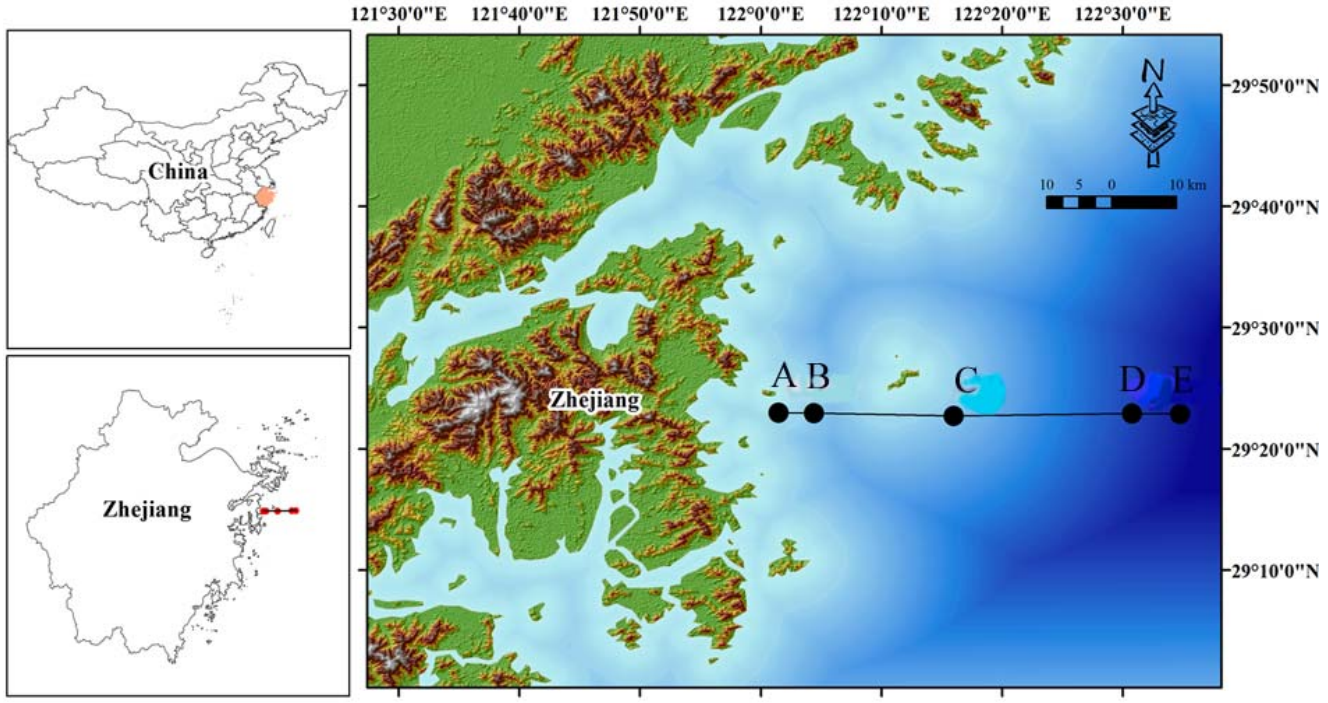

Figure S2 Relative abundances of the dominant bacterial phyla (relative abundance > 1%) in sediment samples within each site (N = 5). Relative abundances are based on the proportional frequencies of those DNA sequences that could be classified at the phylum level with the exception of the predominant Proteobacteria, which were grouped at the class level. Unclassified means that the taxa are not assigned to any known phylum in the current Greengenes database.

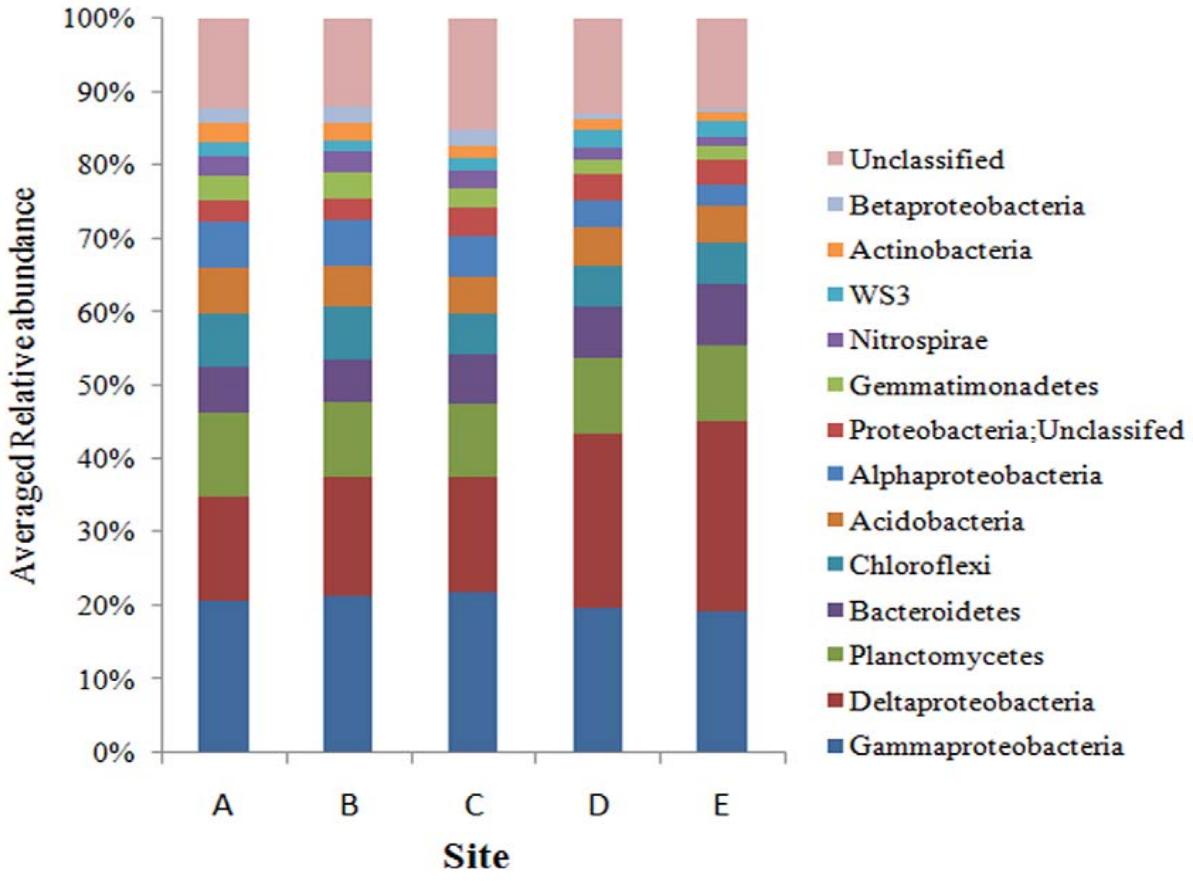

Figure S3 The average of bacterial diversities: phylogenetic diversity (a), phylotypes (b) and Shannon diversity (c) within sites (N =5). The diversities are not significantly changed among the sites.

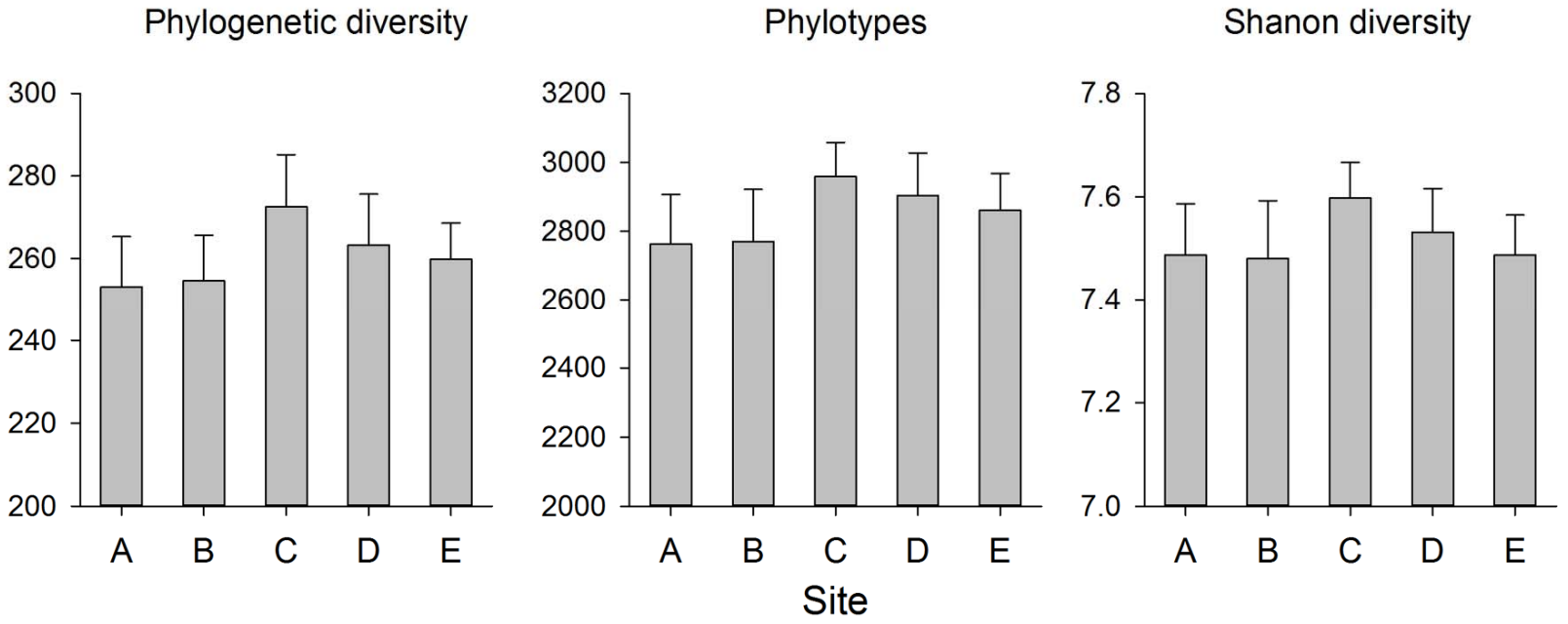

Figure S4 The first component from NMDS of the Bray-Curtis distances (as a proxy for the bacterial community dissimilarity) regressed against pollution parameter using a linear function for the bacterial community.