Table S1. The basic sampling information and environment variables of surface seawater at three stations. T: temperature; S: salinity; Chl a: chlorophyll a; DO: dissolved oxygen; TOC: total organic carbon; DOC: dissolved organic carbon; NO_3^-: nitrate nitrogen; NO_2^-: nitrite nitrogen; NH_4^+: ammonia nitrogen; PO_4^{3-}: phosphorus; SiO_3^{2-}: silicate; *P. g* colony: *Phaeocystis globosa* colony abundance; *P. g* cells: *Phaeocystis globosa* colony cell abundance. Standard deviation of replicated measurements is shown in parentheses.

Station	ZN2-2 offshore station			ZN4-2 inshore station			ZN4-5 coastal station		
Longitude	108.62°E			108.62°E			109.60°E		
Latitude	20.50°N			21.17°N			21.17°N		
Depth (m)	48			20			11		
Date	11 Dec 2016	18 Jan 2017	27 Feb 2017	11 Dec 2016	17 Jan 2017	27 Feb 2017	13 Dec 2016	16 Jan 2017	23 Feb 2017
Time	6:36	10:56	17:35	13:00	22:31	13:25	6:13	11:23	0:35
T (°C)	23.29	21.45	20.42	21.42	19.45	18.85	21.00	19.08	21.09
S (‰)	32.50	32.35	32.4	32.34	32.05	31.61	30.29	31.16	31.24
pH	8.19	8.17	8.27	8.11	8.27	8.29	8.22	8.21	8.21
Chl a ($\mu g\ l^{-1}$)	0.50	0.30	0.48	1.15	1.78	2.00	2.27	1.75	1.73
DO ($mg\ l^{-1}$)	6.83	7.81	7.65	6.93	7.99	8.48	7.07	8.18	8.52
TOC ($mg\ l^{-1}$)	1.71	1.00	1.14	1.53	1.41	1.40	2.28	1.39	1.42
DOC ($mg\ l^{-1}$)	1.17	0.84	1.16	1.46	0.92	1.27	1.70	1.07	0.99
NO_3^- ($\mu mol\ l^{-1}$)	2.90	4.91	2.93	4.16	2.50	1.05	0.11	0.48	0.96
NO_2^- ($\mu mol\ l^{-1}$)	0.30	0.89	0.73	1.41	0.46	0.12	0.09	0.10	0.23
NH_4^+ ($\mu mol\ l^{-1}$)	1.49	1.73	2.26	1.53	3.38	2.73	1.81	3.33	1.90
PO_4^{3-} ($\mu mol\ l^{-1}$)	0.58	0.68	0.70	0.59	0.57	0.50	0.51	0.55	0.41
SiO_3^{2-} ($\mu mol\ l^{-1}$)	10.22	11.47	8.73	13.96	8.95	2.92	2.52	6.85	10.61
P. g colony ($\times10^3$ col m^{-3})	0.44	0.55	0	0.11	6.17	10.81	8.12	0	0
Diameter mean (mm)	1.54 (0.35)	1.25 (0.25)	0	3.55 (1.30)	2.60 (1.29)	3.14 (0.24)	1.37 (0.67)	0	0
P. g cells ($\times10^7$ cells m^{-3})	1.89	1.54	0	2.9	81.98	213.64	27.5	0	0

Table S2. Sequencing information and alpha diversity estimates (at 97% similarity) for samples collected from the Beibu Gulf. Prefix: D, December; J, January; F, February. Suffix: A, Particle-attached prokaryotes; F, Free-living prokaryotes.

Sample name	Effective tags	Observed species	Shannon	Chao1	Good's coverage
DZ2.2A1	66,298	244	1.75	357.16	0.997
DZ2.2A2	58,324	321	2.22	391.53	0.997
DZ2.2A3	59,945	164	1.43	206.89	0.998
DZ4.2A1	65,805	537	3.60	663.75	0.996
DZ4.2A2	54,870	620	5.05	725.01	0.996
DZ4.2A3	69,425	570	4.84	714.72	0.996
DZ4.5A1	56,890	638	2.71	755.27	0.995
DZ4.5A2	63,041	736	3.55	833.01	0.995
DZ4.5A3	63,205	613	2.78	726.41	0.995
JZ2.2A1	60,591	1364	6.45	1472.13	0.994
JZ2.2A2	62,291	1111	6.79	1239.59	0.994
JZ2.2A3	48,969	1513	6.15	1678.12	0.992
JZ4.2A1	44,150	1242	5.61	1401.09	0.993
JZ4.2A2	61,426	884	6.06	1007.38	0.995
JZ4.2A3	54,650	1336	6.22	1474.97	0.993
JZ4.5A1	51,620	1130	6.04	1320.93	0.992
JZ4.5A2	54,550	1312	6.33	1498.51	0.992
JZ4.5A3	52,773	1253	6.30	1395.12	0.993
FZ2.2A1	59,172	1112	6.47	1263.81	0.994
FZ2.2A2	67,105	1438	6.20	1720.65	0.990
FZ2.2A3	56,572	1933	6.57	2292.43	0.985
FZ4.2A1	52,071	1655	6.60	1960.28	0.989
FZ4.2A2	43,869	1110	6.18	1272.38	0.993
FZ4.2A3	56,316	811	5.63	886.11	0.996
FZ4.5A1	64,276	882	5.83	1058.54	0.994
FZ4.5A2	53,779	1045	5.92	1209.02	0.993
FZ4.5A3	67,091	1107	6.00	1379.27	0.992
DZ2.2F1	61,809	259	1.87	287.10	0.999
DZ2.2F2	46,703	400	4.46	433.76	0.998
DZ2.2F3	56,208	366	3.88	416.89	0.998
DZ4.2F1	43,709	398	4.38	437.51	0.998
DZ4.2F2	62,597	504	3.91	581.60	0.997
DZ4.2F3	60,647	556	4.62	648.29	0.996
DZ4.5F1	53,257	771	5.78	894.44	0.995
DZ4.5F2	50,505	680	5.94	792.99	0.996
DZ4.5F3	48,991	679	5.89	761.78	0.996
JZ2.2F1	61,556	836	5.41	981.58	0.994

JZ2.2F2	61,022	762	5.46	896.22	0.995
JZ2.2F3	57,481	1202	6.16	1381.81	0.992
JZ4.2F1	54,647	1037	6.18	1207.35	0.993
JZ4.2F2	52,904	1085	6.42	1246.09	0.993
JZ4.2F3	52,440	1021	6.54	1131.00	0.995
JZ4.5F1	61,494	926	5.61	1143.87	0.993
JZ4.5F2	60,440	857	5.79	1039.42	0.994
JZ4.5F3	58,600	878	5.79	998.54	0.994
FZ2.2F1	66,956	817	6.47	1018.76	0.994
FZ2.2F2	65,666	815	6.37	1071.89	0.993
FZ2.2F3	54,003	921	6.37	1071.99	0.994
FZ4.2F1	64,236	897	5.26	1103.36	0.993
FZ4.2F2	61,148	993	5.53	1184.31	0.993
FZ4.2F3	66,154	865	5.39	1126.44	0.993
FZ4.5F1	61,028	497	5.17	571.08	0.997
FZ4.5F2	57,130	548	4.76	629.56	0.997
FZ4.5F3	61,923	702	5.11	862.36	0.994

Table S3. The differences in α-diversity between pairs of two groups were tested by the Wilcoxon test. PA, particle-attached; FL, free-living. Prefix: D, December; J, January; F, February. Suffix: A, particle-attached prokaryotes; F, free-living prokaryotes. Significant differences ($p < 0.05$) are denoted in bold

Group-Pair	Observed species		Shannon		Chao1	
	difference	p	difference	p	difference	p
DecPA VS. FebPA	-30.89	**0**	-32.56	**0**	-30.78	**0**
DecPA VS. JanPA	-34.89	**0**	-33.33	**0**	-33.56	**0**
JanPA VS. FebPA	4	0.2946	0.78	0.8741	2.78	0.4934
DZ2.2A VS. JZ2.2A	-45.67	**0**	-44.00	**0**	-43.67	**0**
DZ2.2A VS. FZ2.2A	-47.00	**0**	-45.33	**0**	-46.33	**0**
JZ2.2A VS. FZ2.2A	-1.33	0.7944	-1.33	0.7772	-2.67	0.6369
DZ4.2A VS. JZ4.2A	-29.33	**0**	-21.33	**0.0001**	-26.67	**0**
DZ4.2A VS. FZ4.2A	-26.33	**0**	-26.33	**0**	-25.00	**0.0001**
JZ4.2A VS. FZ4.2A	3.00	0.5584	-5.00	0.2922	1.67	0.7677
DZ4.5A VS. JZ4.5A	-29.67	**0**	-34.67	**0**	-30.33	**0**
DZ4.5A VS. FZ4.5A	-19.33	**0.0005**	-26.00	**0**	-21.00	**0.0006**
JZ4.5A VS. FZ4.5A	10.33	**0.0493**	8.67	0.0721	9.33	0.1043
DecFL VS. FebFL	-12.89	**0.0013**	-11.33	**0.0246**	-14.44	**0.0008**
DecFL VS. JanFL	-21.67	**0**	-16.78	**0.0012**	-21.56	**0**
JanFL VS. FebFL	8.78	**0.0243**	5.44	0.2704	7.11	0.0836
DZ2.2F VS. JZ2.2F	-25.67	**0**	-19.00	**0.0003**	-26.33	**0**
DZ2.2F VS. FZ2.2F	-22.33	**0.0001**	-38.67	**0**	-25.00	**0.0001**
JZ2.2F VS. FZ2.2F	3.33	0.5158	-19.67	**0.0002**	1.33	0.8132
DZ4.2F VS. JZ4.2F	-28.33	**0**	-34.67	**0**	-28.00	**0**
DZ4.2F VS. FZ4.2F	-22.67	**0.0001**	-9.33	0.0536	-24.67	**0.0001**
JZ4.2F VS. FZ4.2F	5.67	0.2719	25.33	**0**	3.33	0.5555
DZ4.5F VS. FZ4.5F	6.33	0.2204	14.00	**0.0050**	6.33	0.2656
DZ4.5F VS. JZ4.5F	-11.00	**0.0370**	3.33	0.4806	-10.33	0.0733
JZ4.5F VS. FZ4.5F	17.33	**0.0016**	10.67	**0.0286**	16.67	**0.0052**
DZ2.2A VS. DZ4.2A	-10.33	**0.0493**	-10.67	**0.0286**	-11.00	0.0573
DZ2.2A VS. DZ4.5A	-14.33	**0.0077**	-3.67	0.4382	-13.33	**0.0227**
DZ4.2A VS. DZ4.5A	-4.00	0.4361	7.00	0.1432	-2.33	0.6794
JZ2.2A VS. JZ4.2A	6.00	0.2452	12.00	**0.0146**	6.00	0.2912
JZ2.2A VS. JZ4.5A	1.67	0.7447	5.67	0.2336	0.00	1.0000
JZ4.2A VS. JZ4.5A	-4.33	0.3991	-6.33	0.1842	-6.00	0.2912
FZ2.2A VS. FZ4.2A	10.33	**0.0493**	8.33	0.0832	10.33	0.0733
FZ2.2A VS. FZ4.5A	13.33	**0.0126**	15.67	**0.0019**	12.00	**0.0390**
FZ4.2A VS. FZ4.5A	3.00	0.5584	7.33	0.1257	1.67	0.7677
DZ2.2F VS. DZ4.2F	-4.00	0.4361	-3.33	0.4806	-4.67	0.4102
DZ2.2F VS. DZ4.5F	-14.00	**0.0091**	-22.33	**0**	-14.67	**0.0128**
DZ4.2F VS. DZ4.5F	-10.00	0.0567	-19.00	**0.0003**	-10.00	0.0826

JZ2.2F VS. JZ4.2F	-6.67	0.1976	-19.00	**0.0003**	-6.33	0.2656
JZ2.2F VS. JZ4.5F	0.67	0.8963	0.00	1.0000	1.33	0.8132
JZ4.2F VS. JZ4.5F	7.33	0.1574	19.00	**0.0003**	7.67	0.1795
FZ2.2F VS. FZ4.2F	-4.33	0.3991	26.00	**0**	-4.33	0.4442
FZ2.2F VS. FZ4.5F	14.67	**0.0065**	30.33	**0**	16.67	**0.0052**
FZ4.2F VS. FZ4.5F	19.00	**0.0006**	4.33	0.3604	21.00	**0.0006**
DecPA VS. DecFL	-0.44	0.9068	-9.44	0.0590	0	1.0000
JanPA VS. JanFL	12.78	**0.0014**	7.11	0.1518	12	**0.0045**
FebPA VS. FebFL	17.56	**0**	11.78	**0.0197**	16.33	**0.0002**
DZ2.2A VS. DZ2.2F	-2.67	0.6027	-5.67	0.2336	-1.67	0.7677
DZ4.2A VS. DZ4.2F	3.67	0.4750	1.67	0.7237	4.67	0.4102
DZ4.5A VS. DZ4.5F	-2.33	0.6487	-24.33	**0**	-3.00	0.5955
JZ2.2A VS. JZ2.2F	17.33	**0.0016**	19.33	**0.0002**	15.67	**0.0082**
JZ4.2A VS. JZ4.2F	4.67	0.3643	-11.67	**0.0173**	3.33	0.5555
JZ4.5A VS. JZ4.5F	16.33	**0.0027**	13.67	**0.0060**	17.00	**0.0044**
FZ2.2A VS. FZ2.2F	22.00	**0.0001**	1.00	0.8319	19.67	**0.0012**
FZ4.2A VS. FZ4.2F	7.33	0.1574	18.67	**0.0003**	5.00	0.3779
FZ4.5A VS. FZ4.5F	23.33	**0.0001**	15.67	**0.0019**	24.33	**0.0001**

Table S4. The results of ANOSIM analysis based on Bray-Curtis distances of the PA and FL fractions. Significant differences ($p < 0.05$) are denoted in bold

Group	Group Pair	r	p
Months	DecFL VS. FebFL	0.5806	**0.001**
	JanFL VS. DecFL	0.5147	**0.002**
	JanFL VS. FebFL	0.4518	**0.001**
	JanPA VS. DecPA	0.9911	**0.001**
	JanPA VS. FebPA	0.2942	**0.011**
	FebPA VS. DecPA	0.9726	**0.001**
Stations	Z2.2F VS. Z4.5F	0.4232	**0.001**
	Z4.2F VS. Z4.5F	0.2365	**0.006**
	Z4.2F VS. Z2.2F	-0.0532	0.698
	Z2.2A VS. Z4.5A	0.1027	0.126
	Z4.2A VS. Z4.5A	0.0264	0.263
	Z4.2A VS. Z2.2A	0.0580	0.184
Fractions	DecFL VS. DecPA	0.3237	**0.004**
	JanPA VS. JanFL	0.5703	**0.001**
	FebPA VS. FebFL	0.5178	**0.001**
	Z4.5A VS. Z4.5F	0.4647	**0.001**
	Z4.2A VS. Z4.2F	0.1289	0.082
	Z2.2A VS. Z2.2F	0.2870	**0.013**
	FL VS. PA	0.2872	**0.001**

Table S5. The average relative abundance of the 17 identified OTUs serving as indicator taxa for the FL and PA prokaryotic communities, with their contributions to community dissimilarities. The "indicative" OTUs were identified by the SIMPER analysis and only OTUs that contributed ≥ 1% of dissimilarities (Bray-Curtis dissimilarity) between PA and FL communities were displayed. Contrib.: Contributions of taxonmy to the similarity within cluster. Cum.: Cumulate contribution

OUT ID	Classification	Average abundance (PA) %	Average abundance (FL) %	Contrib. %	Cum. %
OTU_1	p__Proteobacteria; g__Phyllobacterium	15.28	9.60	13.24	13.24
OTU_2	p__Proteobacteria; g__Delftia	6.29	1.95	9.55	22.78
OTU_3	p__Thaumarchaeota; f__Nitrosopumilaceae	2.11	3.54	6.23	29.02
OTU_4	p__Cyanobacteria; g__unidentified Cyanobacteria	10.09	1.58	4.79	33.81
OTU_5	p__Proteobacteria; g__Sphingomonas	2.97	0.78	3.18	36.98
OTU_6	p__Proteobacteria; g__unidentified Alphaproteobacteria	4.73	17.20	3.11	40.10
OTU_7	p__Proteobacteria; g__Pseudoalteromonas	2.56	2.01	2.26	42.35
OTU_8	p__Cyanobacteria; o__Synechococcales	2.69	1.35	2.11	44.46
OTU_9	p__Cyanobacteria; g__unidentified Cyanobacteria	2.14	0.28	1.85	46.30
OTU_10	p__Proteobacteria; f__Rhodobacteraceae	0.90	1.80	1.62	47.92
OTU_11	p__Proteobacteria; g__ Candidatus Pelagibacter	0.81	2.53	1.45	49.37
OTU_12	p__Euryarchaeota; c__Thermoplasmata	0.27	1.51	1.39	50.76
OTU_13	p__Actinobacteria; g__Candidatus Actinomarina	1.52	5.77	1.38	52.14
OTU_14	p__Cyanobacteria; g__unidentified Cyanobacteria	1.35	2.24	1.12	53.26
OTU_15	p__Proteobacteria; g__unidentified Rhodospirillales	0.47	1.34	1.12	54.38
OTU_16	p__Euryarchaeota; g__unidentified Thermoplasmata	0.42	1.51	1.11	55.48
OTU_17	p__Proteobacteria; g__SUP05 cluster	0.48	1.20	1.06	56.55

Table S6. The significance analysis of environmental variables based on ENVFIT functions. Highly significant correlation coefficients ($p < 0.01$) are denoted in bold

Environmental variables	PA		FL	
	r^2	p	r^2	p
P.g cells	0.0606	0.4988	0.1528	0.1209
S	0.2149	0.0530	0.5937	**0.0005**
DO	0.8680	**0.0005**	0.6753	**0.0005**
pH	0.2264	0.0535	0.5633	**0.0005**
DOC	0.5064	**0.0010**	0.1181	0.2159
NO_2^-	0.1076	0.2559	0.5913	**0.0005**
NH_4^+	0.4175	**0.0025**	0.5286	**0.0005**
PO_4^{3-}	0.6662	**0.0005**	0.6701	**0.0005**

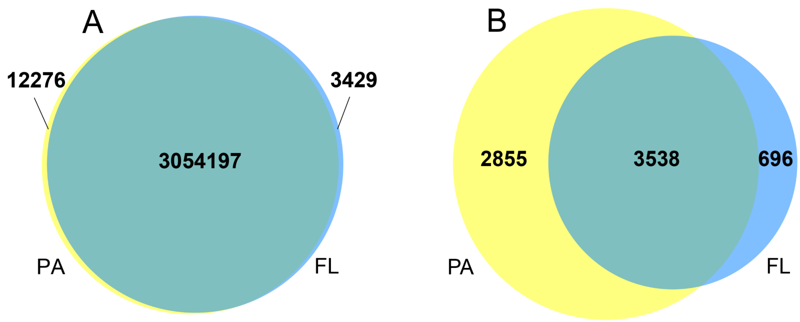


Fig. S1. (A) The Venn diagram of effective tags distribution between PA and FL fractions. (B) The Venn diagram of all operational taxonomic unit (OTU) distribution between particle-attached (PA) and free-living (FL) prokaryotic communities. The size of the circles is proportional to the number of tags in (A) and the number of OTUs in (B).

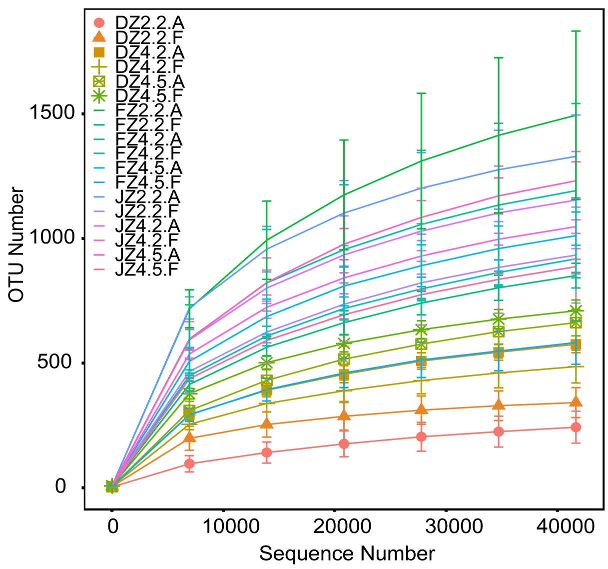
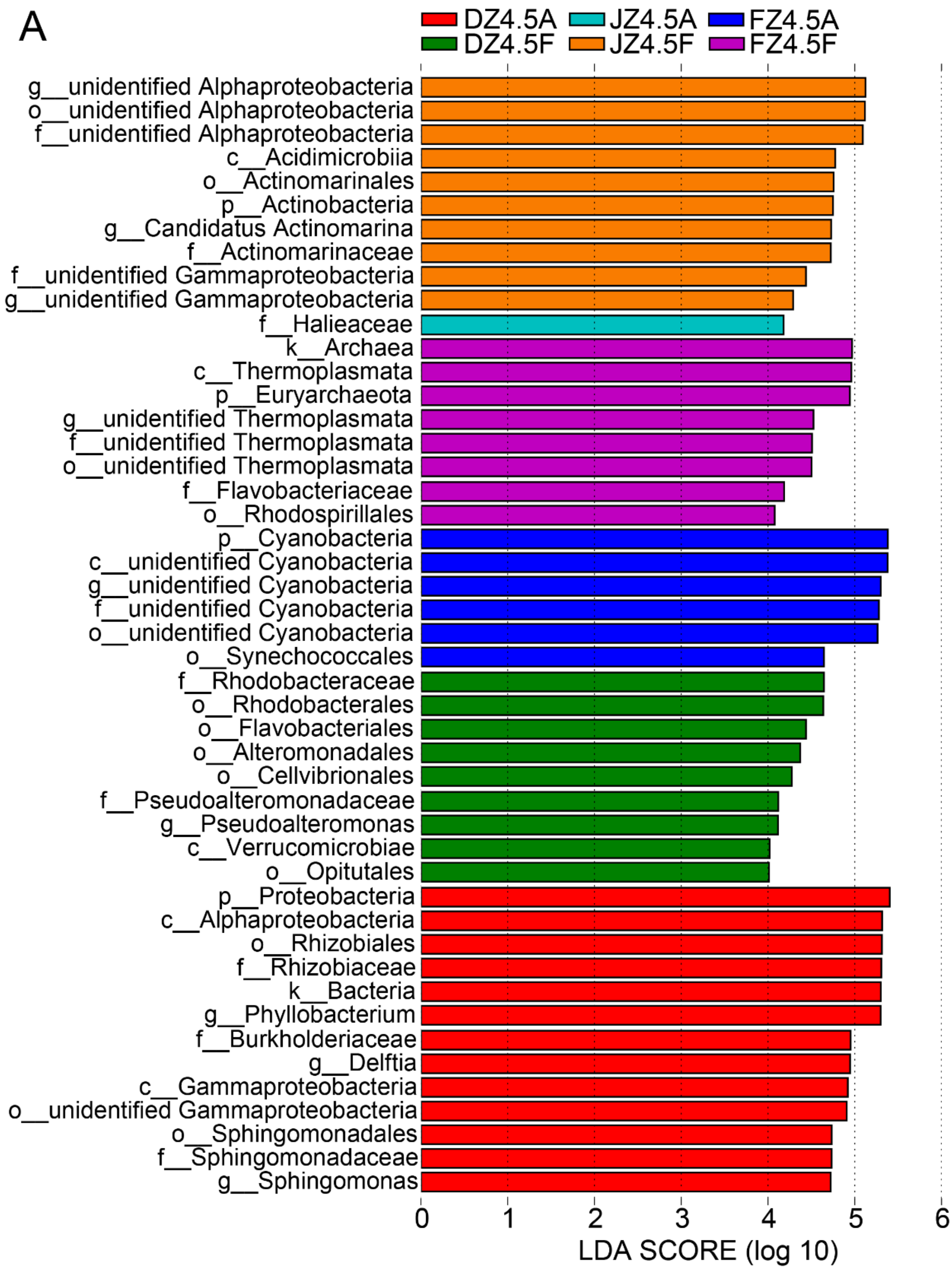
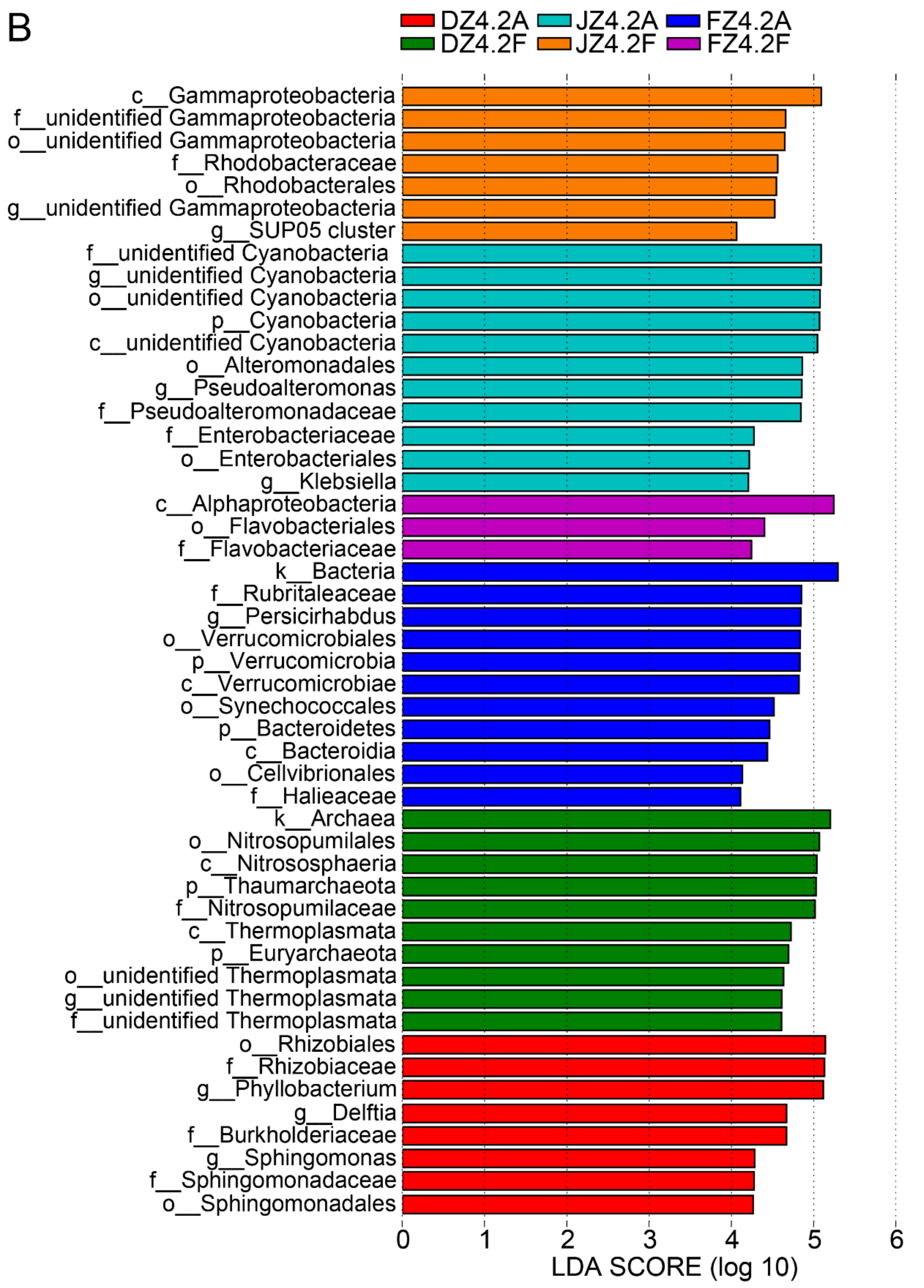


Fig. S2. Rarefaction curves of OTUs clustered at the 97% sequence similarity level from 18 groups of samples.


A
DZ4.5A
JZ4.5A
FZ4.5A
DZ4.5F
JZ4.5F
FZ4.5F
g__unidentified Alphaproteobacteria
o__unidentified Alphaproteobacteria
f__unidentified Alphaproteobacteria
c__Acidimicrobiia
o__Actinomarinales
p__Actinobacteria
g__Candidatus Actinomarina
f__Actinomarinaceae
f__unidentified Gammaproteobacteria
g__unidentified Gammaproteobacteria
f__Halieaceae
k__Archaea
c__Thermoplasmata
p__Euryarchaeota
g__unidentified Thermoplasmata
f__unidentified Thermoplasmata
o__unidentified Thermoplasmata
f__Flavobacteriaceae
o__Rhodospirillales
p__Cyanobacteria
c__unidentified Cyanobacteria
g__unidentified Cyanobacteria
f__unidentified Cyanobacteria
o__unidentified Cyanobacteria
o__Synechococcales
f__Rhodobacteraceae
o__Rhodobacterales
o__Flavobacteriales
o__Alteromonadales
o__Cellvibrionales
f__Pseudoalteromonadaceae
g__Pseudoalteromonas
c__Verrucomicrobiae
o__Opitutales
p__Proteobacteria
c__Alphaproteobacteria
o__Rhizobiales
f__Rhizobiaceae
k__Bacteria
g__Phyllobacterium
f__Burkholderiaceae
g__Delftia
c__Gammaproteobacteria
o__unidentified Gammaproteobacteria
o__Sphingomonadales
f__Sphingomonadaceae
g__Sphingomonas
0
1
2
3
4
5
6
LDA SCORE (log 10)


B
DZ4.2A
JZ4.2A
FZ4.2A
DZ4.2F
JZ4.2F
FZ4.2F
c__Gammaproteobacteria
f__unidentified Gammaproteobacteria
o__unidentified Gammaproteobacteria
f__Rhodobacteraceae
o__Rhodobacterales
g__unidentified Gammaproteobacteria
g__SUP05 cluster
f__unidentified Cyanobacteria
g__unidentified Cyanobacteria
o__unidentified Cyanobacteria
p__Cyanobacteria
c__unidentified Cyanobacteria
o__Alteromonadales
g__Pseudoalteromonas
f__Pseudoalteromonadaceae
f__Enterobacteriaceae
o__Enterobacteriales
g__Klebsiella
c__Alphaproteobacteria
o__Flavobacteriales
f__Flavobacteriaceae
k__Bacteria
f__Rubritaleaceae
g__Persicirhabdus
o__Verrucomicrobiales
p__Verrucomicrobia
c__Verrucomicrobiae
o__Synechococcales
p__Bacteroidetes
c__Bacteroidia
o__Cellvibrionales
f__Halieaceae
k__Archaea
o__Nitrosopumilales
c__Nitrososphaeria
p__Thaumarchaeota
f__Nitrosopumilaceae
c__Thermoplasmata
p__Euryarchaeota
o__unidentified Thermoplasmata
g__unidentified Thermoplasmata
f__unidentified Thermoplasmata
o__Rhizobiales
f__Rhizobiaceae
g__Phyllobacterium
g__Delftia
f__Burkholderiaceae
g__Sphingomonas
f__Sphingomonadaceae
o__Sphingomonadales
0
1
2
3
4
5
6
LDA SCORE (log 10)

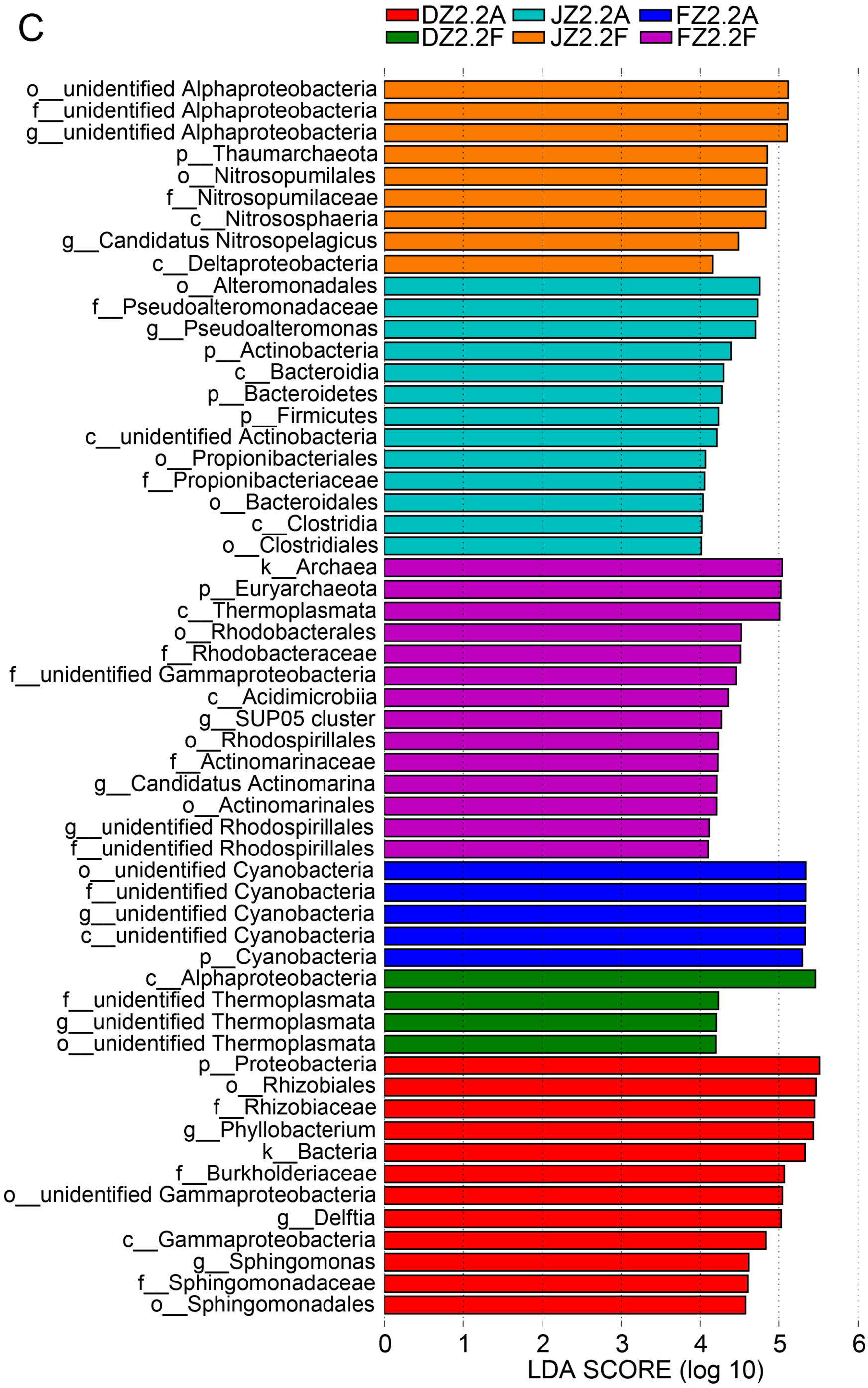


Fig. S3. The distribution histogram in LDA value showed the differentially abundant prokaryotes of different fractions and different months at Stns ZN4-5 (A), ZN4-2 (B), and ZN2-2 (C), respectively. Taxa in this graph were both statistically significant ($P < 0.05$) and had an LDA Score > 4, considered a significant effect size.

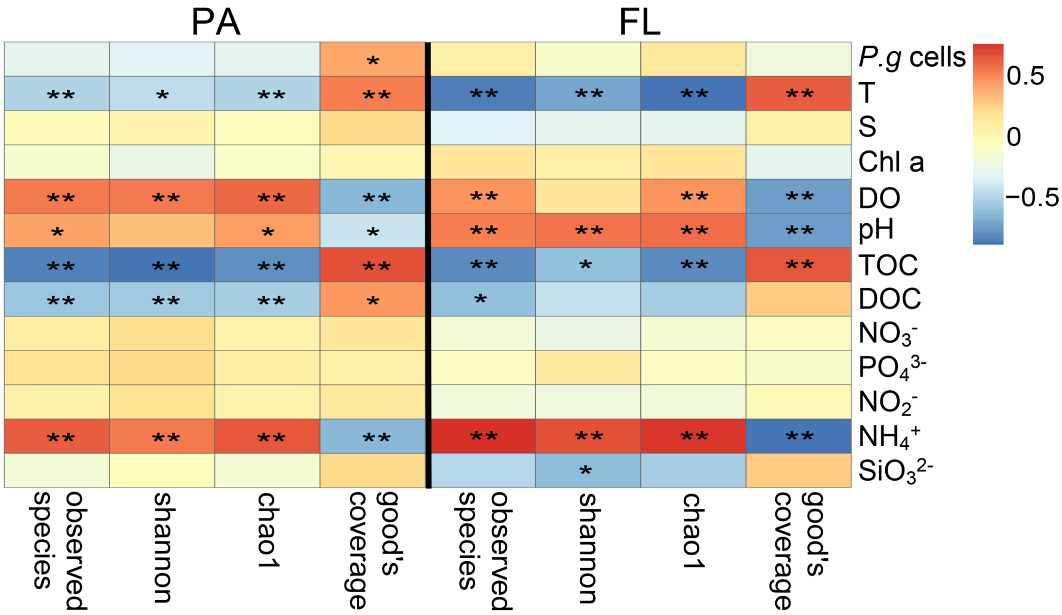
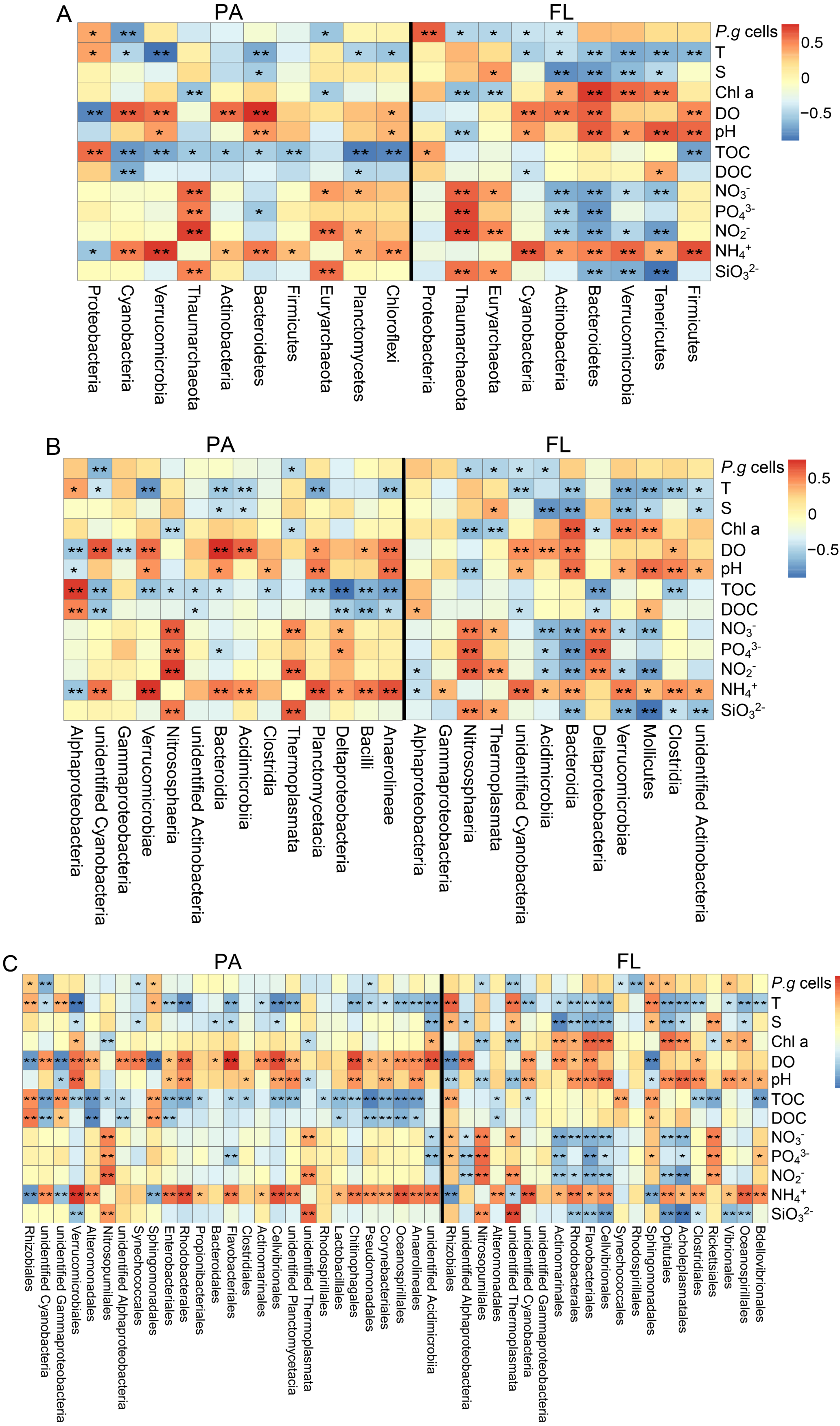


Fig. S4. Spearman correlation coefficients between the environmental variables and the alpha diversity of the prokaryotic communities. The left and right panel represented the particle-attached (PA) and free-living (FL) prokaryotic communities, respectively. The values of Spearman correlation coefficients were indicated according to the scale bar. Significance codes for p-values are as follows: ** $p < 0.01$, * $p < 0.05$.


A
PA
FL
P.g cells
T
S
Chl a
DO
pH
TOC
DOC
NO3-
PO43-
NO2-
NH4+
SiO32-
0.5
0
−0.5
Proteobacteria
Cyanobacteria
Verrucomicrobia
Thaumarchaeota
Actinobacteria
Bacteroidetes
Firmicutes
Euryarchaeota
Planctomycetes
Chloroflexi
Proteobacteria
Thaumarchaeota
Euryarchaeota
Cyanobacteria
Actinobacteria
Bacteroidetes
Verrucomicrobia
Tenericutes
Firmicutes
B
PA
FL
Alphaproteobacteria
unidentified Cyanobacteria
Gammaproteobacteria
Verrucomicrobiae
Nitrososphaeria
unidentified Actinobacteria
Bacteroidia
Acidimicrobiia
Clostridia
Thermoplasmata
Planctomycetacia
Deltaproteobacteria
Bacilli
Anaerolineae
Alphaproteobacteria
Gammaproteobacteria
Nitrososphaeria
Thermoplasmata
unidentified Cyanobacteria
Acidimicrobiia
Bacteroidia
Deltaproteobacteria
Verrucomicrobiae
Mollicutes
Clostridia
unidentified Actinobacteria
C
PA
FL
Rhizobiales
unidentified Cyanobacteria
unidentified Gammaproteobacteria
Verrucomicrobiales
Alteromonadales
Nitrosopumilales
unidentified Alphaproteobacteria
Synechococcales
Sphingomonadales
Enterobacteriales
Rhodobacterales
Propionibacteriales
Bacteroidales
Flavobacteriales
Clostridiales
Actinomarinales
Cellvibrionales
unidentified Planctomycetacia
unidentified Thermoplasmata
Rhodospirillales
Lactobacillales
Chitinophagales
Pseudomonadales
Corynebacteriales
Oceanospirillales
Anaerolineales
unidentified Acidimicrobiia
Rhizobiales
unidentified Alphaproteobacteria
Nitrosopumilales
Alteromonadales
unidentified Thermoplasmata
unidentified Cyanobacteria
unidentified Gammaproteobacteria
Actinomarinales
Rhodobacterales
Flavobacteriales
Cellvibrionales
Synechococcales
Rhodospirillales
Sphingomonadales
Opitutales
Acholeplasmatales
Clostridiales
Rickettsiales
Vibrionales
Oceanospirillales
Bdellovibrionales

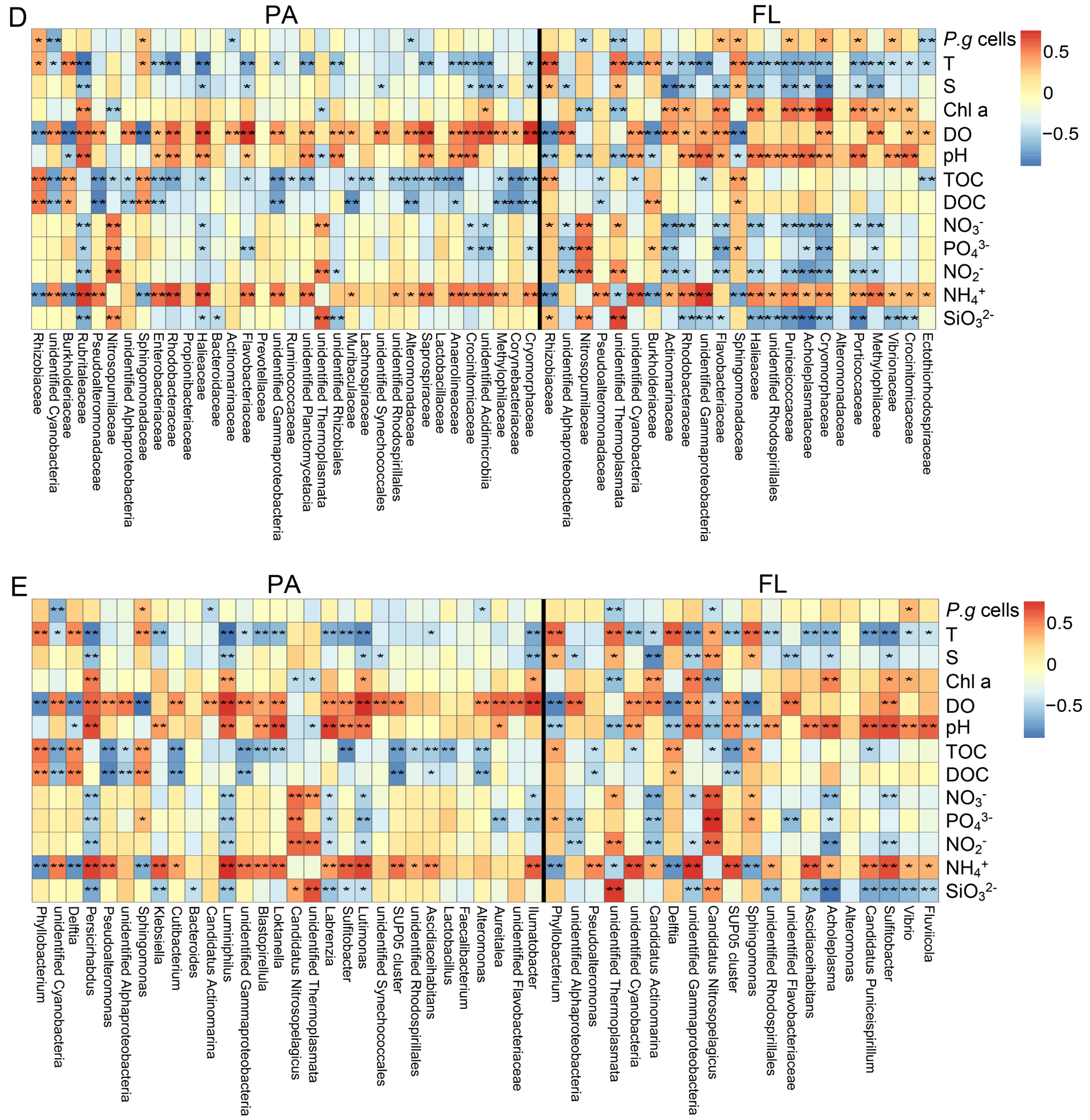


Fig. S5. Spearman correlation coefficients between the environmental variables and major phyla (A), classes (B), orders (C), families (D), and genera (E) (relative abundance > 1.0% in at least one sample) of the prokaryotic communities, respectively. The left and right panel represented the particle-attached (PA) and free-living (FL) prokaryotic communities, respectively. The values of Spearman correlation coefficients were indicated according to the scale bar. Significance codes for p-values are as follows: ** $p < 0.01$, * $p < 0.05$.