Supplementary figures and tables

Figure S1. Transmission electron microscopy (TEM) images of *Synechococcus* and associated heterotrophic bacteria in the *Synechococcus* sp. XM-24 culture.

Figure S2. The dynamic relationships between *Synechococcus* and heterotrophic bacteria in *Synechococcus* sp. XM-24 culture. The abundances of *Synechococcus* and heterotrophic bacteria were measured by flow cytometer. A, the original abundances of *Synechococcus* and heterotrophic bacteria were 1.54×10^7 and 6.01×10^5 cells mL^{-1}, respectively. B, the original abundances of *Synechococcus* and heterotrophic bacteria were 3.69×10^7 and 1.77×10^7 cells mL^{-1}, respectively. **The red dots mean the size-fractionated samples were collected for subsequent community composition analyses.**

Figure S3. Histogram representation of qPCR analysis of 16S rRNA gene copy-number from the 0.22-3-μm and >3-μm size fractions of *Synechococcus* culture samples.

Figure S4. The relative abundance of *Synechococcus* (OTU0) in the total 16S rRNA sequences and dominant heterotrophic bacterial groups (OTU1-3) in the total heterotrophic bacterial 16S rRNA sequences (after removing *Synechococcus* sequences) from the 0.22-3-μm (red) and >3-μm (green) size-fractions during the *Synechococcus* sp. XM-24 culture growth with different inocula (A- and B-). OTU0, *Synechococcus*; OTU1, *Fluviicola*; OTU2, *Roseivirga*; OTU3, *Marivita*.

Figure S5. Processes of forming associations between *Synechococcus* and heterotrophic bacteria. A, natural seawater is spread on a plate; B, *Synechococcus* cells interacting with heterotrophic bacteria grow and begin to form colonies; C, *Synechococcus* cells release organic matter (such as exopolysaccharides); D, heterotrophic bacteria attach to *Synechococcus* colonies and grow along with them, with interactions and exchange of metabolites that allow the different organisms to continue to grow and survive on the plate.

Table S1. Information for isolated *Synechococcus* strains.

Table S2. General classification for representative OTUs from 10 *Synechococcus* cultures.

Table S3. The distribution patterns of representative OTUs from 10 *Synechococcus* cultures in coastal water around Xiamen Island.

Table S4. Taxonomic affiliations of the dominant OTUs and their abundances in the different size fractions.

Table S5. Environmental variables in the seawaters corresponding to samples from around Xiamen and Xisha Islands respectively.

Figure S1

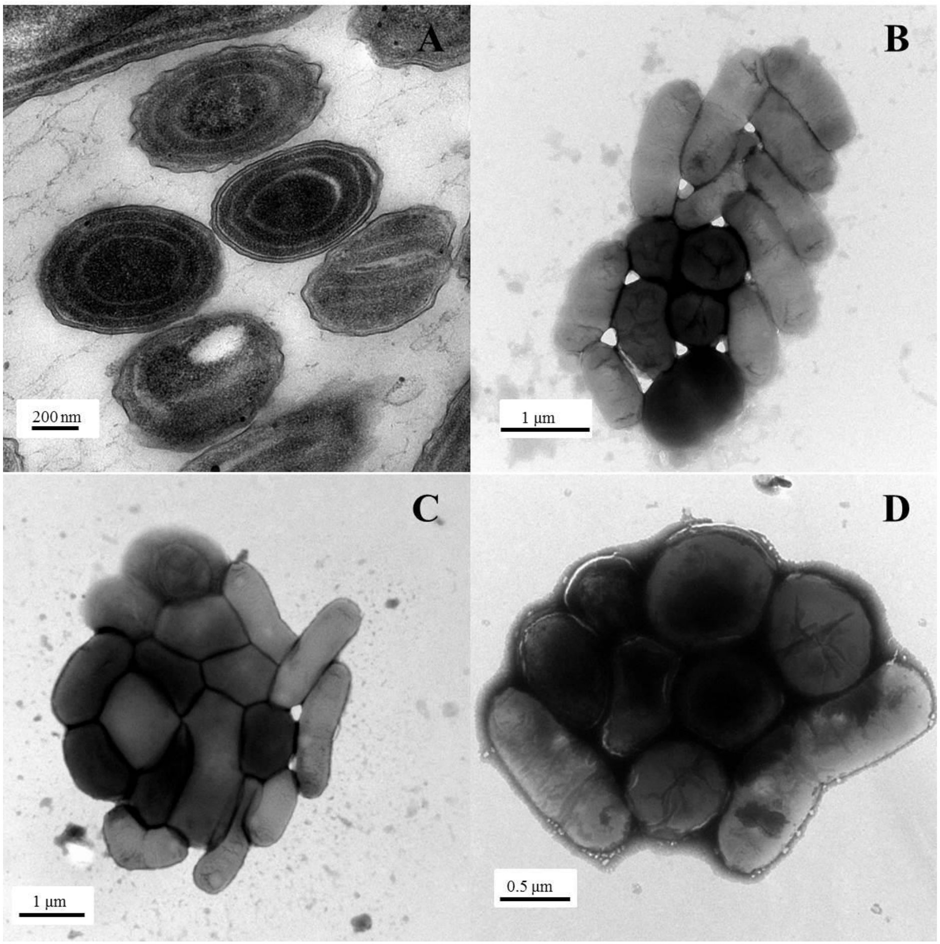


Figure S2

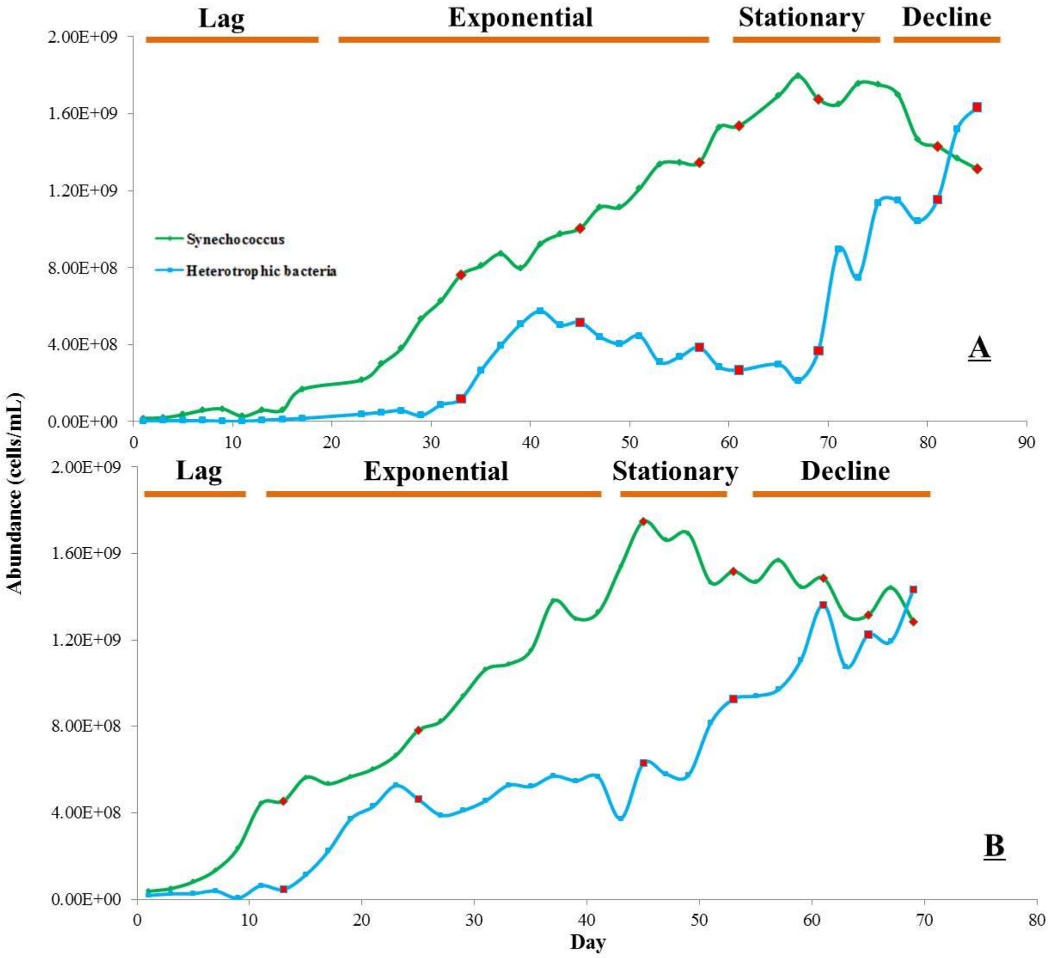

Lag
Exponential
Stationary
Decline
2.00E+09
1.60E+09
1.20E+09
8.00E+08
4.00E+08
0.00E+00
Synechococcus
Heterotrophic bacteria
A
0
10
20
30
40
50
60
70
80
90
Abundance (cells/mL)
Lag
Exponential
Stationary
Decline
2.00E+09
1.60E+09
1.20E+09
8.00E+08
4.00E+08
0.00E+00
B
0
10
20
30
40
50
60
70
80
Day

Figure S3

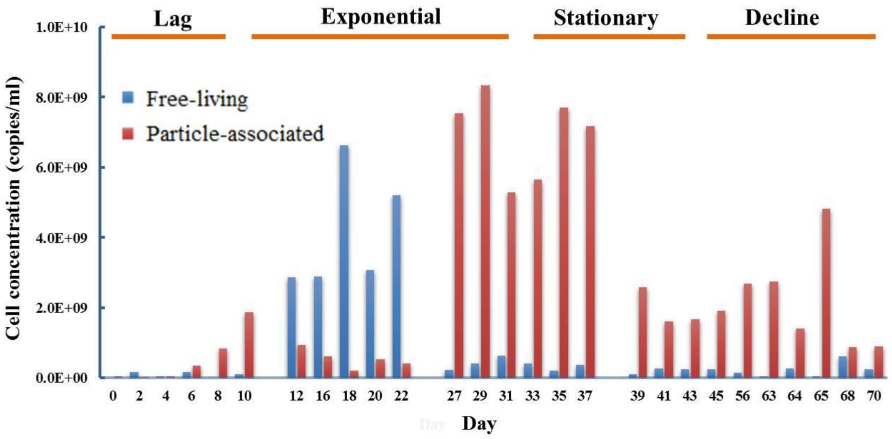
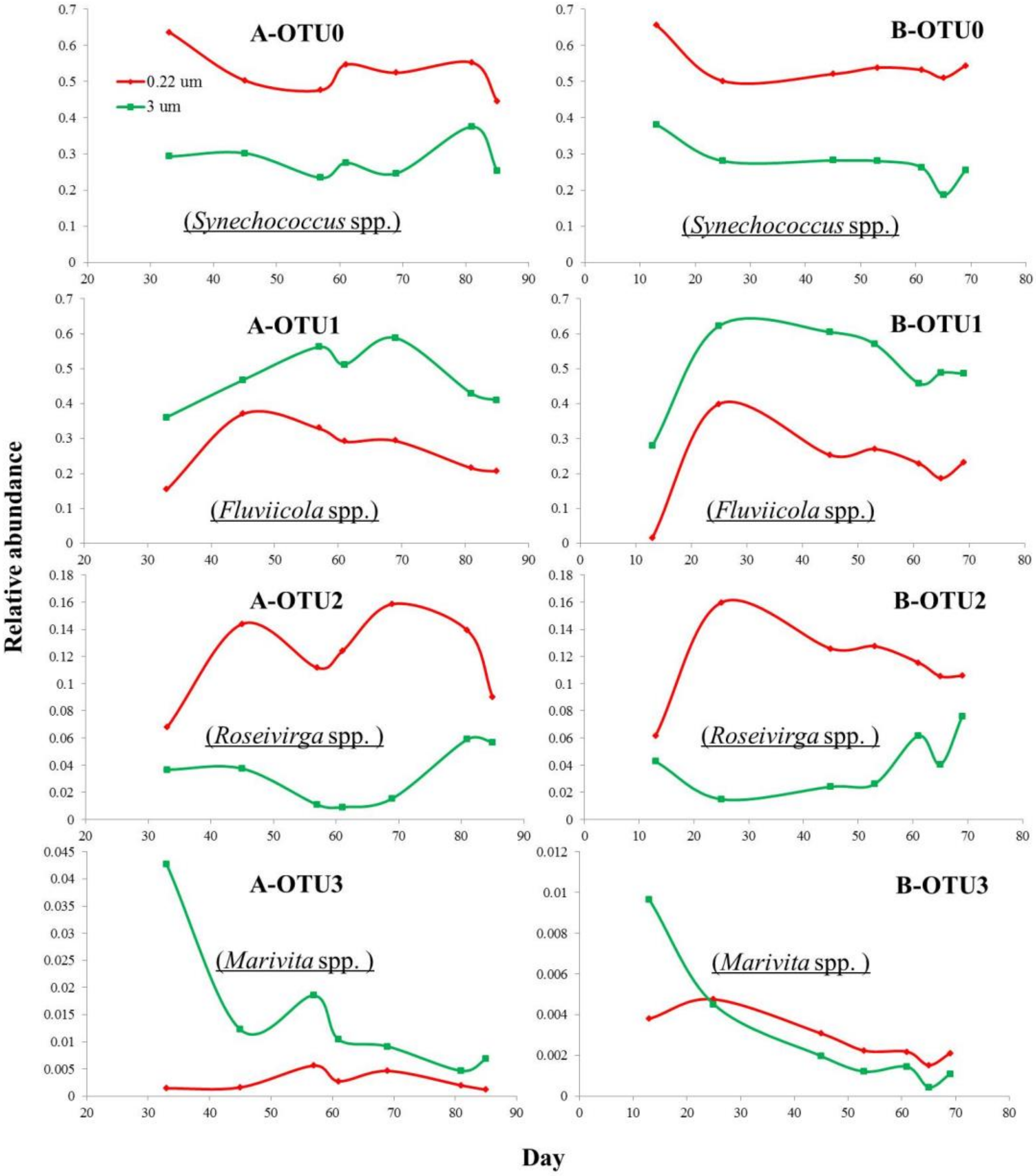
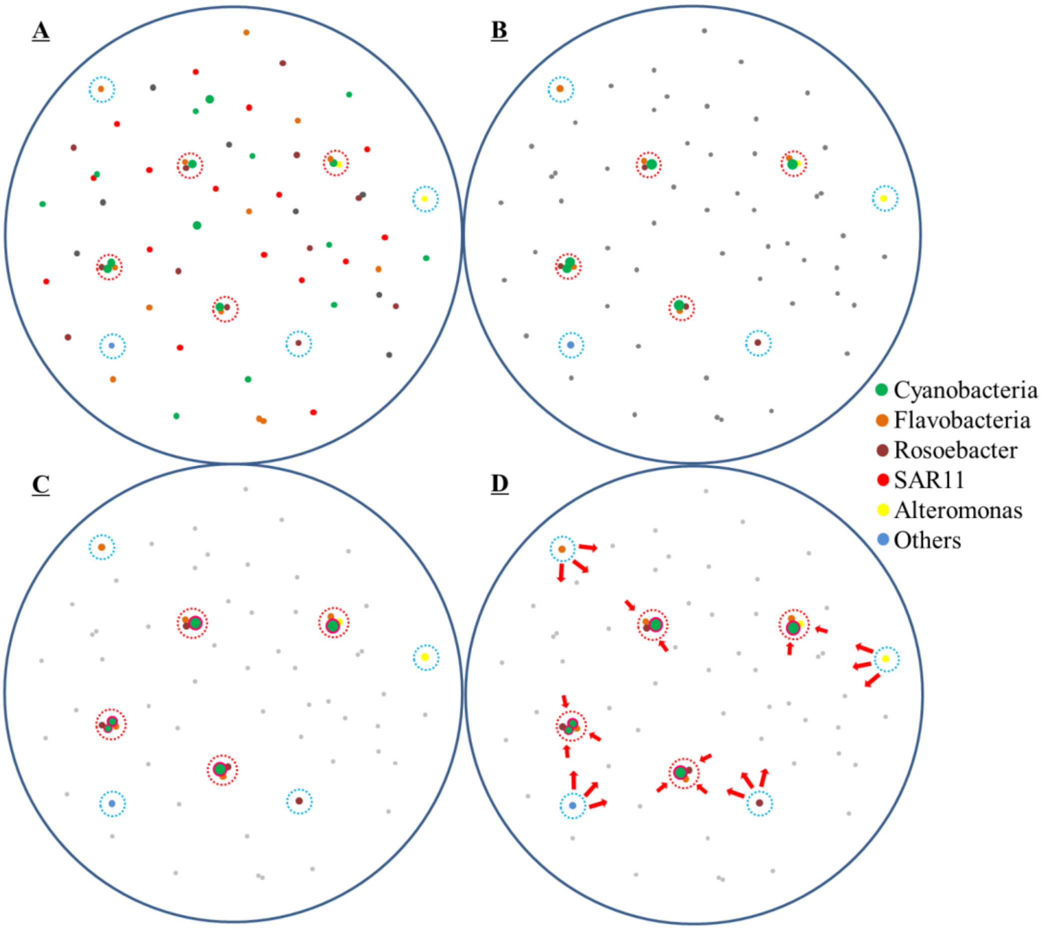

Lag
Exponential
Stationary
Decline
Free-living
Particle-associated
Cell concentration (copies/ml)
1.0E+10
8.0E+09
6.0E+09
4.0E+09
2.0E+09
0.0E+00
0
2
4
6
8
10
12
16
18
20
22
27
29
31
33
35
37
39
41
43
45
56
63
64
65
68
70
Day

Figure S4


A-OTU0
B-OTU0
0.22 um
3 um
(Synechococcus spp.)
A-OTU1
B-OTU1
(Fluviicola spp.)
A-OTU2
B-OTU2
(Roseivirga spp.)
A-OTU3
B-OTU3
(Marivita spp.)
Relative abundance
Day

66

67 Figure S5



68

69

70

Table S1. Information for isolated *Synechococcus* strains.

	Strain	Genotype	Isolation environment	Station
Eutrophic strains	XM-5	5.2 Clade CB5	Xiamen estuary/coastal	S12
	XM-11	5.2 Clade CB5	Xiamen estuary/coastal	S07
	XM-24	5.2 Clade CB5	Xiamen estuary/coastal	S07
	XM-13	5.1 Clade IX	Xiamen estuary/coastal	S07
	Cy04	5.1 Clade VIII	Dalian coastal	-
Oligotrophic strains	YX-A3-2	5.1 Clade II	South China Sea	YX-A3
	ZS02-2	5.1 Clade II	South China Sea	ZS02
	YX04-3	5.1 Clade III	South China Sea	YX04
	YX02-3	5.1 Clade III	South China Sea	YX02
	ZS01-1	5.1 Clade V	South China Sea	ZS01

Table S2. General classification for representative OTUs from 10 *Synechococcus* cultures.

	OTU ID	taxonomy
1	denovo 12385	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola; s__
2	denovo 16098	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Cyclobacteriaceae; g__Algoriphagus; s__ornithinivorans
3	denovo 17405	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__; g__; s__
4	denovo 3086	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__; s__Polaribacter sp.MED152
5	denovo 521	k__Bacteria; p__Bacteroidetes; c__[Rhodothermi]; o__[Rhodothermales]; f__[Balneolaceae]; g__Balneola; s__
6	denovo 4543	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__; s__
7	denovo 4545	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o__[Saprospirales]; f__Saprospiraceae; g__; s__
8	denovo 15190	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae; g__; s__
9	denovo 15071	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae; g__; s__
10	denovo 8101	k__Bacteria; p__Bacteroidetes; c__[Rhodothermi]; o__[Rhodothermales]; f__[Balneolaceae]; g__Balneola; s__
11	denovo 6175	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o__[Saprospirales]; f__Saprospiraceae; g__; s__
12	denovo 18503	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales; f__Flammeovirgaceae; g__Roseivirga; s__
13	denovo 16987	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Thalassobius; s__gelatinovorus
14	denovo 19760	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Thalassobius; s__mediterraneus
15	denovo 5251	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Hyphomonadaceae; g__Maricaulis; s__
16	denovo 3482	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Marivita; s__
17	denovo 10098	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Roseicyclus; s__mahoneyensis
18	denovo19086	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__; s__
19	denovo 4738	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Kiloniellales; f__; g__; s__
20	denovo 8422	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__; s__
21	denovo 13832	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola; s__
22	denovo 18145	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
23	denovo 10628	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Microbacteriaceae; g__Candidatus Aquiluna; s__rubra

Table S3. The distribution patterns of representative OTUs from 10 *Synechococcus* cultures in coastal waters around Xiamen Island.

Season	Winter					Spring					Summer					Autumn					Total
#OTU ID	1.3	1.5	1.7	1.12	1.18	4.3	4.5	4.7	4.12	4.18	7.3	7.5	7.7	7.12	7.18	10.3	10.5	10.7	10.12	10.18	
denovo 12385	0.000	0.001	0.001	0.006	0.000	0.000	0.004	0.005	0.001	0.002	0.000	0.000	0.000	0.000	0.001	0.001	0.002	0.004	0.008	0.003	2322
denovo 16098	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	7
denovo 17405	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	85
denovo 3086	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.002	0.001	333
denovo 521	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 4543	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 4545	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 15190	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	42
denovo 15071	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 8101	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 6175	0.000	0.002	0.001	0.004	0.000	0.000	0.004	0.006	0.001	0.002	0.001	0.000	0.003	0.001	0.006	0.000	0.000	0.001	0.001	0.000	2036
denovo 18503	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	22
denovo 16987	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	17
denovo 19760	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.001	0.000	0.001	0.000	0.000	0.000	435
denovo 5251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	14
denovo 3482	0.004	0.003	0.003	0.000	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.002	0.000	0.000	0.000	0.000	1146
denovo 10098	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	20
denovo 19086	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	19
denovo 4738	0.000	0.003	0.001	0.021	0.000	0.002	0.002	0.002	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.009	0.013	0.002	3804
denovo 8422	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	5
denovo 13832	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.024	0.000	0.002	0.002	0.011	0.000	0.001	0.000	0.000	0.000	2459
denovo 18145	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
denovo 10628	0.042	0.006	0.003	0.003	0.037	0.011	0.006	0.002	0.011	0.012	0.004	0.003	0.005	0.003	0.007	0.008	0.002	0.003	0.012	0.006	10528

Total Sequences	62,097	80,187	67,146	89,791	55,296	64,719	63,805	60,894	54,855	59,615	63,539	45,394	49,985	49,566	65,379	71,859	51,599	47,242	53,790	52,238

*The relative abundance of each OTU that is more than 0.1% is highlighted.

1.3, 1.5, 1.7. 1.12 and 1.18 mean samples collected in January (winter); 4.3, 4.5, 4.7. 4.12 and 4.18 indicate samples collected in April (spring); 7.3, 7.5, 7.7. 7.12 and 7.18 mean samples collected in July (summer); 10.3, 10.5, 10.7. 10.12 and 10.18 indicate samples collected in October (autumn).

1.3, 4.3, 7.3 and 10.3 mean samples collected from station S03; 1.5, 4.5, 7.5 and 10.5 mean samples collected from station S05; 1.7, 4.7, 7.7 and 10.7 mean samples collected from station S07; 1.12, 4.12, 7.12 and 10.12 mean samples collected from station S12; 1.18, 4.18, 7.18 and 10.18 mean samples collected from station S18.

Total sequences indicate the total number of 16S rRNA gene sequences in each library.

Table S4. Taxonomic affiliations of the dominant OTUs and their abundances in the different size fractions.

OTU ID	Corresponding previous OTUs	Order	Genus	0.22-3 μm	>3 μm	Total	Ratio*
OTU0	-	Synechococcales	*Synechococcus*	336,821	201,890	538,711	0.57
OTU1	denovo12385	Flavobacteriales	*Fluviicola*	20,884	190,125	211,009	4.93
OTU2	denovo3482	Rhodobacterales	*Marivita*	49,431	66,677	116,108	0.73
OTU3	denovo17405	Cytophagales	*Roseivirga*	55,439	14,143	69,582	0.14
OTU4	-	Flavobacteriales		4,105	21,413	25,518	2.82
OTU5	-	Sphingomonadales		2,152	12,799	14,951	3.22
OTU6	denovo10628	Actinomycetales	*Aquiluna*	9,815	1,347	11,162	0.07
OTU7	-	Rhizobiales		3,264	7,092	10,356	1.18
OTU8	-	Rhodobacterales	*Pseudoruegeria*	2,889	6,722	9,611	1.26
OTU9	denovo19760	Rhodobacterales		4,720	2,058	6,778	0.24
OTU10	denovo13832	Alteromonadales		2,944	3,582	6,526	0.66
Total sequences				530,451	553,534	1,083,985	-
Total *Synechococcus*				341,228	204,042	545,270	-
Total heterotrophic bacteria				189,223	349,492	538,715	1.00

* (sequences from the >3-μm fraction out of the total *Synechococcus* or heterotrophic bacteria) to (sequences from the 0.22-3-μm fraction out of the total *Synechococcus* or heterotrophic bacteria)

OTUs 4 and 5 were only abundant in the late of decline phase, and the relative abundance of OTUs 7 and 8 were relatively low and had no obvious changes after lag phase. These four OTUs were not detected with high relative abundance in one time sampling (stationary phase).

Table S5. Environmental variables in the seawaters corresponding to samples from around Xiamen and Xisha Islands respectively.

Variables	Xisha	Xiamen
Temperature (℃)	27.6-28.8	23.1-23.6
Salinity (‰)	33.7 -34.2	22.4-27.1
NO_3^- (µmol/L)	<0.1	18.3-29.2
PO_4^{3-} (µmol/L)	<0.1	0.47-1.33
Bacteria (cells/mL)	2.0-5.0E+05	1.4-3.1E+06
Prochlorococcus (cells/mL)	0.8-3.3E+05	-
Synechococcus (cells/mL)	0.6-2.0E+04	1.3-1.7E+04
Pico-eukaryotes (cells/mL)	1.0-4.0E+02	5.7-6.4E+03