

Supplementary information

Upon chimera removal, a total of 811871 sequences and 1035283 sequences were obtained from Illumina Miseq sequencing of the 16S rDNA gene, and the 18S rDNA gene, respectively. All prokaryotic and eukaryotic samples were rarefied at 24379 and 36020 sequences per sample, respectively, to retain as many samples as possible. The RDP classifier and Greengene database were used to assign taxonomy to OTUs from domain to genus levels. OTUs were used to calculate Shannon-Wiener diversity and richness indexes, and these data are shown in supplementary Table S1 (prokaryotic) and Table S2 (eukaryotic).

A total of 6763 prokaryotic OTUs were identified and assigned into 921 genera, 490 families, 260 orders, 134 classes and 54 phyla. And 432 genera, 254 families, 218 orders, 134 classes and 69 phyla were categorized by the identified 2483 eukaryotic OTUs. For whole gene sequences obtained from each sample, rarefaction curves were established at a nucleotide genetic distance of 0.03. About 2.25% and 2.85% of sequences could not be classified at the phylum level, and were defined as bacteria-unclassified and eukaryota-unclassified, respectively. The bacterial community and eukaryotic community composition at the phylum level in different samples is shown in Figure S1 and Figure S2, respectively.

Table S1. Richness (Sobs, Chao and Ace), Diversity (Shannon and Simpson) and Coverage (Coverage) of the bacterial 16S rRNA for each sample site by Operational Taxonomic Units (OTUs) based analyses.

Sample\Estimators	sobs	shannon	simpson	ace	chao	coverage
Jan_1	2742	6.8207	0.0041	3444.10	3486.14	0.9675
Jan_2	2742	6.9005	0.0024	3558.06	3709.80	0.9648
Jan_3	3056	7.1300	0.0018	3845.31	3918.14	0.9633
Jan_4	2859	6.9345	0.0025	3617.88	3638.02	0.9652
Jan_5	2910	7.0044	0.0019	3739.29	3769.89	0.9636
Mar_1	2878	7.1170	0.0015	3641.83	3727.13	0.9656
Mar_2	3323	7.2104	0.0017	4364.66	4360.60	0.9564
Mar_3	2680	6.7492	0.0032	3612.90	3649.43	0.9635
Mar_4	3148	7.1003	0.0021	4039.06	4069.60	0.9602
Mar_5	2670	6.8843	0.0022	3436.92	3453.61	0.9669
May_1	1855	6.2843	0.0046	2376.27	2465.04	0.9776
May_2	3386	7.2716	0.0015	4308.67	4433.21	0.9576
May_3	3356	7.2588	0.0015	4251.67	4306.43	0.9587
May_4	3122	7.1705	0.0016	3954.55	3981.48	0.9622
May_5	2843	6.9996	0.0019	3759.23	3760.15	0.9628
Water_1	381	4.2832	0.0297	474.30	519.10	0.9963
Water_2	202	2.6579	0.1471	261.40	250.36	0.9977
Water_3	317	3.1830	0.1402	369.58	378.42	0.9973

Table S2. Richness (Sobs, Chao and Ace), Diversity (Shannon and Simpson) and Coverage (Coverage) of the bacterial 18S rRNA for each sample site by Operational Taxonomic Units (OTUs) based analyses.

Sample\Estimators	sobs	shannon	simpson	ace	chao	coverage
Jan_1	649	2.8363	0.2180	906.19	884.01	0.9935
Jan_2	1161	4.3962	0.0571	1436.74	1425.20	0.9913
Jan_3	1040	4.4042	0.0484	1259.54	1247.22	0.9927
Jan_4	1165	4.7362	0.0274	1425.49	1441.99	0.9916
Jan_5	976	4.2844	0.0342	1603.64	1425.55	0.9904
Mar_1	666	3.4906	0.1027	892.18	894.80	0.9942
Mar_2	1045	4.2724	0.0456	1340.65	1326.42	0.9914
Mar_3	848	3.9145	0.0662	1126.41	1101.40	0.9927
Mar_4	676	2.8219	0.2031	1094.41	965.20	0.9933
Mar_5	644	3.3795	0.0854	1149.67	985.03	0.9930
May_1	286	2.4626	0.2652	297.70	311.20	0.9992
May_2	517	2.1540	0.3317	915.93	781.47	0.9945
May_3	570	2.1186	0.4072	830.36	875.53	0.9940
May_4	648	3.1920	0.1197	936.30	905.65	0.9936
May_5	424	2.5656	0.2141	598.73	620.98	0.9960
Water_1	160	2.8339	0.1042	189.94	191.06	0.9991
Water_2	162	2.7520	0.1099	194.05	191.75	0.9990
Water_3	126	2.1720	0.1788	155.87	145.38	0.9991

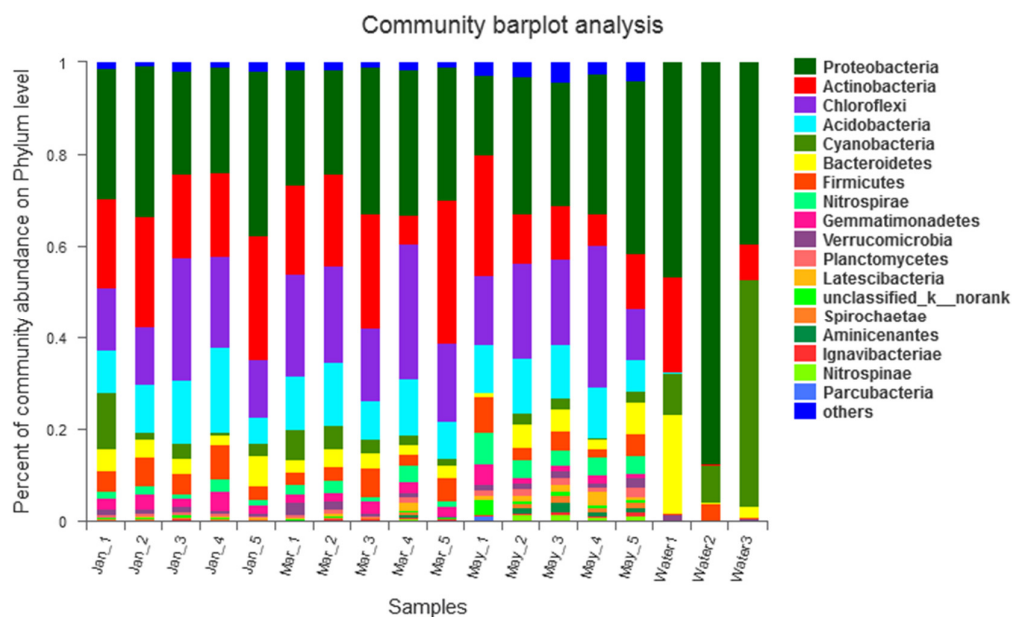


Figure S1. The relative percentage contribution of the bacteria community composition at the phyla level for the different sample sites.

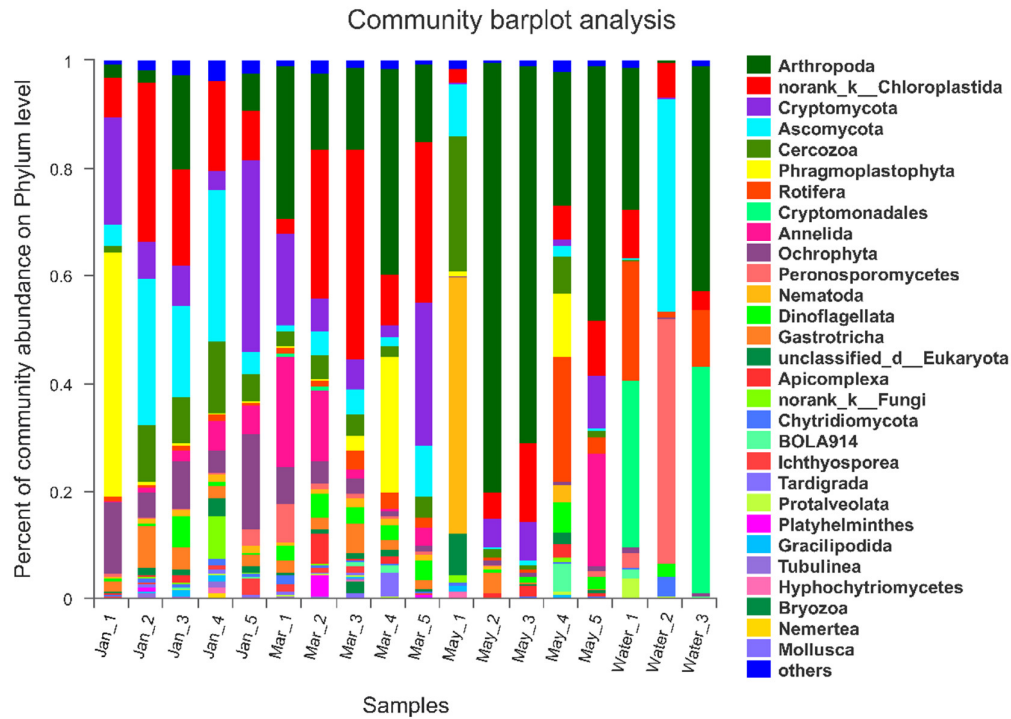


Figure S2. The relative percentage contribution of the eukaryote community composition at the phyla level for the different sample sites.

Table S3. The Detrended Correspondence Analysis (DCA) results of cyanobacteria community and the Principal Component Analysis (PCA) result of eukaryotic phytoplankton community

cyanobacteria				
Statistic	Axis 1	Axis 2	Axis 3	Axis 4
Eigenvalues	0.3917	0.2484	0.0904	0.0527
Explained variation (cumulative)	24.00	39.22	44.76	47.99
eukaryotic phytoplankton				
Statistic	Axis 1	Axis 2	Axis 3	Axis 4
Eigenvalues	0.3040	0.1748	0.1178	0.0746
Explained variation (cumulative)	30.40	47.88	59.67	67.13

Table S4. The redundancy analysis (RDA) results of the influence of each significant parameter on the cyanobacteria or eukaryotic phytoplankton community composition.

Parameters (cyanobacteria)	Variation explained solely (%)	Pseudo-F value	P value
T	32.1	6.1	0.002

TP	29.5	5.4	0.004
TC	28.9	5.3	0.002
Vel-max	25.0	4.3	0.002
TN	17.2	2.7	0.032
Parameters (eukaryotic phytoplankton)	Variation explained (%)	Pseudo-F solely value	P value
TP	23.6	4.0	0.002
T	23.1	3.9	0.006
TC	22.8	3.8	0.002
Vel-max	18.9	3.0	0.004
TN	17.0	2.7	0.012

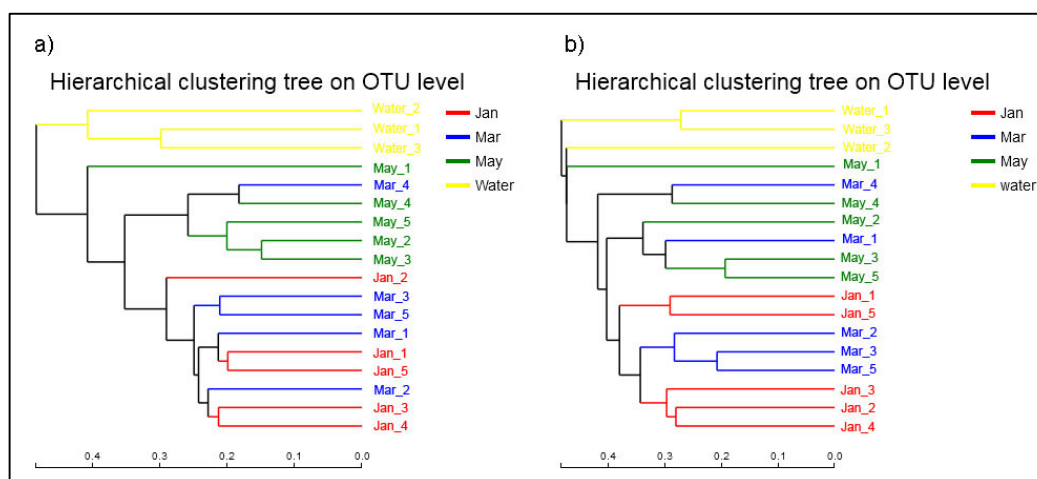


Figure S3. The Hierarchical clustering tree of **a)** cyanobacteria and **b)** the eukaryotic phytoplankton on OTU level.

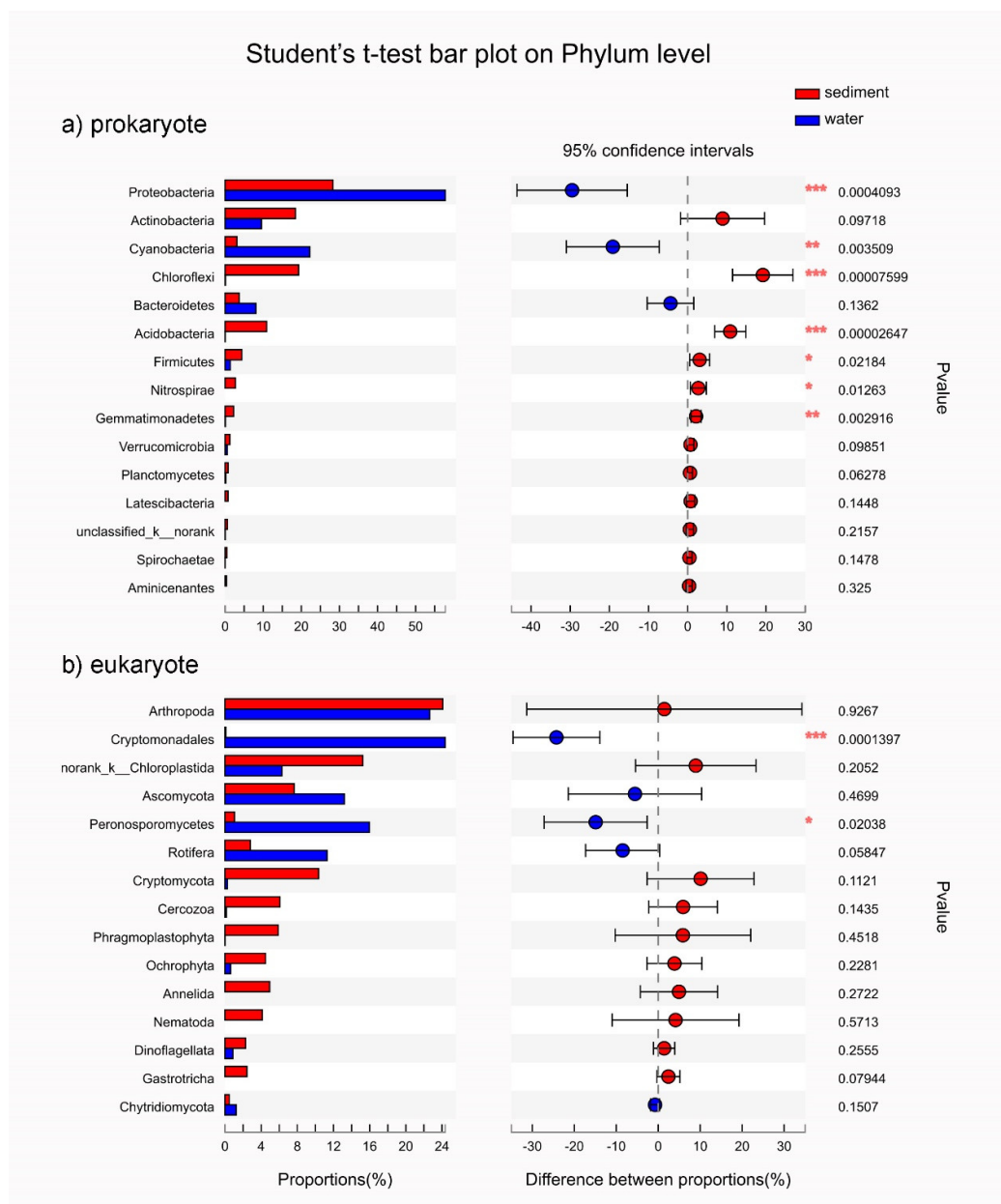


Figure S4. Student's t-test of communities between sediment and surface water on phylum level. **a)** Prokaryote using the result of 16S rRNA; **b)** Eukaryote phytoplankton using the result of 18S rRNA. The note * indicate $P \leq 0.01$, ** indicate $0.001 \leq P \leq 0.01$, *** indicate $P \leq 0.001$.

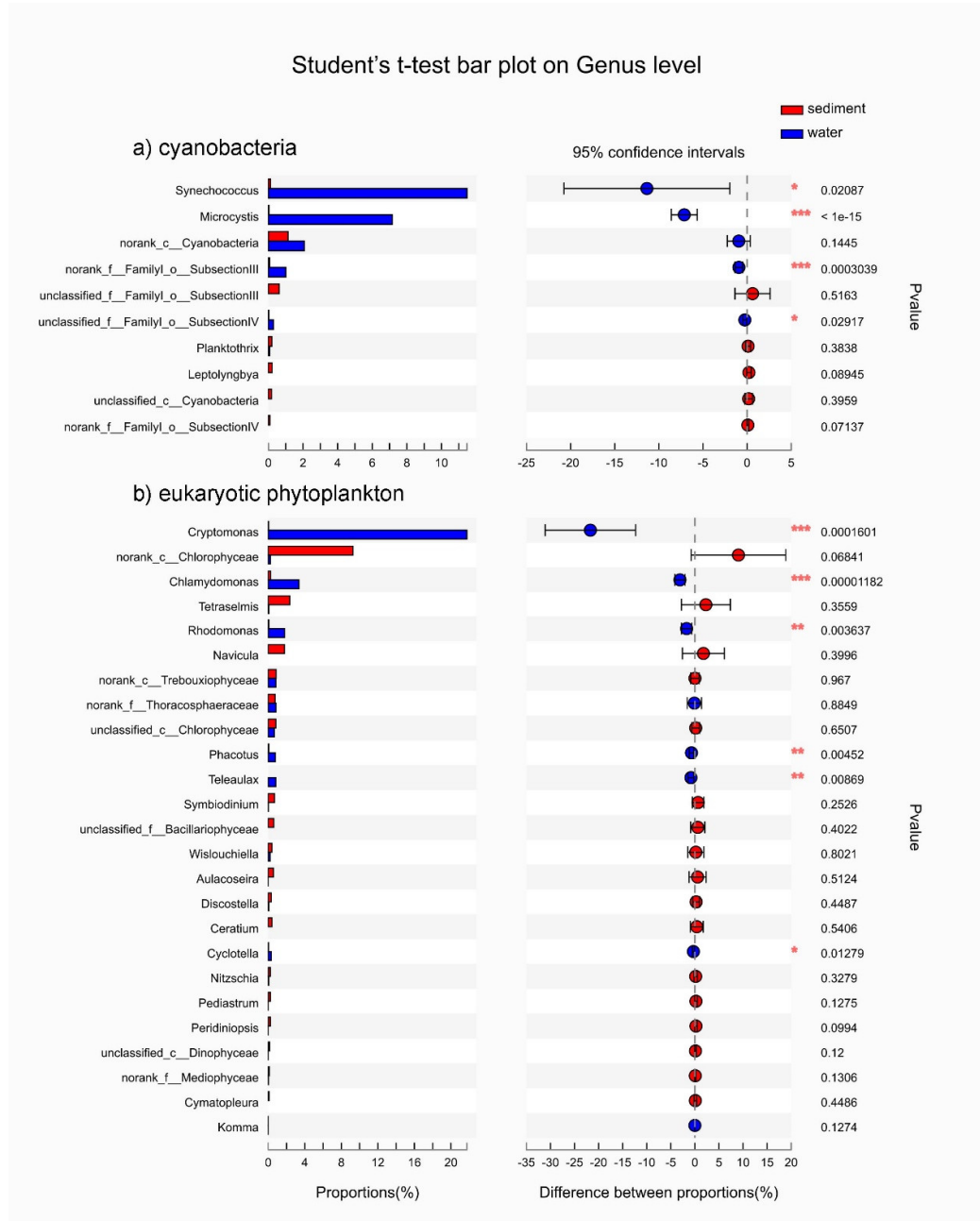


Figure S5. Student's t test of phytoplankton communities between sediment and surface water on genus level. The figure shows all the genus detected in this study. **a)** Cyanobacteria using the result of 16S rRNA sequencing; **b)** Eukaryotic phytoplankton using the result of 18S rRNA sequencing. The note * indicate $P \leq 0.01$, ** indicate $0.001 \leq P \leq 0.01$, *** indicate $P \leq 0.001$.