

Supplementary Materials for

**Aerobic anoxygenic phototrophs play important roles in nutrient cycling
within cyanobacterial *Microcystis* bloom microbiomes**

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SUPPLEMENTARY TABLES

Table S1. Collection date, location, sample type, and accession information for Lake Taihu samples.

Sample ID	Sample type	Location	Date	SRR accession
F-04-M	Free-living	Meiliang bay, Lake Taihu	Apr, 2018	SRR24980017
F-04-Z	Free-living	Zhushan Bay, Lake Taihu	Apr, 2018	SRR24980026
A-04-M	aggregates	Meiliang bay, Lake Taihu	Apr, 2018	SRR24980030
A-04-Z	aggregates	Zhushan Bay, Lake Taihu	Apr, 2018	SRR24980031
F-05-M	Free-living	Meiliang bay, Lake Taihu	May, 2018	SRR24980029
F-05-Z	Free-living	Zhushan Bay, Lake Taihu	May, 2018	SRR24980016
A-05-M	aggregates	Meiliang bay, Lake Taihu	May, 2018	SRR24980027
A-05-Z	aggregates	Zhushan Bay, Lake Taihu	May, 2018	SRR24980028
F-06-M	Free-living	Meiliang bay, Lake Taihu	Jun, 2018	SRR24980032
F-06-Z	Free-living	Zhushan Bay, Lake Taihu	Jun, 2018	SRR24980033
A-06-M	aggregates	Meiliang bay, Lake Taihu	Jun, 2018	SRR24980015
A-06-Z	aggregates	Zhushan Bay, Lake Taihu	Jun, 2018	SRR24980039
F-07-M	Free-living	Meiliang bay, Lake Taihu	Jul, 2018	SRR24980036
F-07-Z	Free-living	Zhushan Bay, Lake Taihu	Jul, 2018	SRR24980037
A-07-M	aggregates	Meiliang bay, Lake Taihu	Jul, 2018	SRR24980034
A-07-Z	aggregates	Zhushan Bay, Lake Taihu	Jul, 2018	SRR24980035
F-08-M	Free-living	Meiliang bay, Lake Taihu	Aug, 2018	SRR24980041
F-08-Z	Free-living	Zhushan Bay, Lake Taihu	Aug, 2018	SRR24980042
A-08-M	aggregates	Meiliang bay, Lake Taihu	Aug, 2018	SRR24980038
A-08-Z	aggregates	Zhushan Bay, Lake Taihu	Aug, 2018	SRR24980040
F-09-M	Free-living	Meiliang bay, Lake Taihu	Sep, 2018	SRR24980021
F-09-Z	Free-living	Zhushan Bay, Lake Taihu	Sep, 2018	SRR24980020
A-09-M	aggregates	Meiliang bay, Lake Taihu	Sep, 2018	SRR24980018
A-09-Z	aggregates	Zhushan Bay, Lake Taihu	Sep, 2018	SRR24980019
F-10-M	Free-living	Meiliang bay, Lake Taihu	Oct, 2018	SRR24980025
F-10-Z	Free-living	Zhushan Bay, Lake Taihu	Oct, 2018	SRR24980024
A-10-M	aggregates	Meiliang bay, Lake Taihu	Oct, 2018	SRR24980022
A-10-Z	aggregates	Zhushan Bay, Lake Taihu	Oct, 2018	SRR24980023

Table S2. Source, location, date of collection and accession information for Lake Erie and Taihu transcriptome samples.

Bioproject	Sample ID	Lake	Date	SRR accession	Submission by	reference
PRJNA262053	Station LET1 replicate 1	Lake Erie	Oct, 2013	SRR1596057	Stony University	Brook
PRJNA262053	Station LET1 replicate 2	Lake Erie	Oct, 2013	SRR1596599	Stony University	Brook
PRJNA262053	Station LET2 replicate 1	Lake Erie	Oct, 2013	SRR1596606	Stony University	Brook
PRJNA262053	Station LET2 replicate 2	Lake Erie	Oct, 2013	SRR1596607	Stony University	Brook
PRJNA262053	Station LET3 replicate 1	Lake Erie	Oct, 2013	SRR1601407	Stony University	Brook
PRJNA262053	Station LET3 replicate 2	Lake Erie	Oct, 2013	SRR1601408	Stony University	Brook
PRJNA262053	Station LET4 replicate 1	Lake Erie	Oct, 2013	SRR1601409	Stony University	Brook
PRJNA262053	Station LET4 replicate 2	Lake Erie	Oct, 2013	SRR1601410	Stony University	Brook
PRJNA262053	Station LET5 replicate 1	Lake Erie	Oct, 2013	SRR1601412	Stony University	Brook
PRJNA262053	Station LET5 replicate 2	Lake Erie	Oct, 2013	SRR1601413	Stony University	Brook
PRJNA262053	Station LET6 replicate 1	Lake Erie	Oct, 2013	SRR1601414	Stony University	Brook
PRJNA262053	Station LET6 replicate 2	Lake Erie	Oct, 2013	SRR1601415	Stony University	Brook
PRJNA262053	Station LET7 replicate 1	Lake Erie	Oct, 2013	SRR1601416	Stony University	Brook
PRJNA262053	Station LET7 replicate 2	Lake Erie	Oct, 2013	SRR1601417	Stony University	Brook
PRJNA354726	W4b	Lake Erie	Aug, 2014	SRR5079666	University of Tennessee Knoxville	

PRJNA354726	W13b		Lake Erie	Aug, 2014	SRR5079667	University of Tennessee Knoxville
PRJNA354726	W2b		Lake Erie	Aug, 2014	SRR5079668	University of Tennessee Knoxville
PRJNA354726	73 July A		Lake Erie	July, 2014	SRR5079670	University of Tennessee Knoxville
PRJNA354726	73 July B		Lake Erie	July, 2014	SRR5079671	University of Tennessee Knoxville
PRJNA354726	LE Aug1		Lake Erie	Aug, 2014	SRR5079672	University of Tennessee Knoxville
PRJNA354726	LE W13a		Lake Erie	Aug, 2014	SRR5079673	University of Tennessee Knoxville
PRJNA354726	Aug2b		Lake Erie	Aug, 2014	SRR5079674	University of Tennessee Knoxville
PRJNA354726	LE W4a		Lake Erie	Aug, 2014	SRR5079675	University of Tennessee Knoxville
PRJNA354726	LE W2a		Lake Erie	Aug, 2014	SRR5079676	University of Tennessee Knoxville
PRJNA354726	LE W6		Lake Erie	Aug, 2014	SRR5079677	University of Tennessee Knoxville
PRJNA354726	LE W8		Lake Erie	Aug, 2014	SRR5079678	University of Tennessee Knoxville
PRJNA354726	LE site Aug1		Lake Erie	Aug, 2014	SRR5079679	University of Tennessee Knoxville
PRJNA354726	LE Aug2a		Lake Erie	Aug, 2014	SRR5079681	University of Tennessee Knoxville
PRJNA823389	Time 48h replicate A	Ammonium,	Lake Erie	Jul, 2019	SRR18613350	University of Tennessee
PRJNA823389	Time 48h replicate B	Ammonium,	Lake Erie	Jul, 2019	SRR18613349	University of Tennessee
PRJNA823389	Time 48h replicate C	Ammonium,	Lake Erie	Jul, 2019	SRR18613348	University of Tennessee
PRJNA823389	Time 48h Phosphate, replicate		Lake Erie	Jul, 2019	SRR18613357	University of Tennessee

PRJNA823389	A Time 48h Phosphate, replicate B	Lake Erie	Jul, 2019	SRR18613356	Tennessee University	of	
PRJNA823389	C Time 48h Phosphate, replicate C	Lake Erie	Jul, 2019	SRR18613354	Tennessee University	of	
PRJNA823389	Time 48h Urea, replicate A	Lake Erie	Jul, 2019	SRR18613361	Tennessee University	of	
PRJNA823389	Time 48h Urea, replicate B	Lake Erie	Jul, 2019	SRR18613360	Tennessee University	of	
PRJNA823389	Time 48h Urea, replicate C	Lake Erie	Jul, 2019	SRR18613359	Tennessee University	of	
PRJNA823389	Time 48h Nitrate, replicate A	Lake Erie	Jul, 2019	SRR18613365	Tennessee University	of	
PRJNA823389	Time 48h Nitrate, replicate B	Lake Erie	Jul, 2019	SRR18613364	Tennessee University	of	
PRJNA823389	Time 48h Nitrate, replicate C	Lake Erie	Jul, 2019	SRR18613363	Tennessee University	of	
PRJNA823389	Time 48h Control, replicate A	Lake Erie	Jul, 2019	SRR18613353	Tennessee University	of	
PRJNA823389	Time 48h Control, replicate B	Lake Erie	Jul, 2019	SRR18613352	Tennessee University	of	
PRJNA823389	Time 48h Control, replicate C	Lake Erie	Jul, 2019	SRR18613351	Tennessee University	of	
PRJNA823389	Time 0h Control, replicate A	Lake Erie	Jul, 2019	SRR18613367	Tennessee University	of	
PRJNA823389	Time 0h Control, replicate B	Lake Erie	Jul, 2019	SRR18613366	Tennessee University	of	
PRJNA823389	Time 0h Control, replicate C	Lake Erie	Jul, 2019	SRR18613355	Tennessee University	of	
PRJNA359157	Cyanobacterial aggregates_Metatranscriptome	Lake Taihu	May, 2015	SRR5134202	Southeast University, China		[1]
PRJNA664620	CA151123	Lake Taihu	Nov, 2015	SRR12686996	Southeast University, China		[2]

PRJNA664620	CA151028	Lake Taihu	Oct, 2015	SRR12686983	Tsinghua University, China	[2]
PRJNA664620	CA150902	Lake Taihu	Sep, 2015	SRR12686984	Tsinghua University ,China	[2]
PRJNA664620	CA150806	Lake Taihu	Aug, 2015	SRR12686985	Tsinghua University, China	[2]
PRJNA664620	CA150804	Lake Taihu	Aug, 2015	SRR12686986	Tsinghua University, China	[2]
PRJNA664620	CA150701	Lake Taihu	Jul, 2015	SRR12686987	Tsinghua University, China	[2]
PRJNA664620	CA150615	Lake Taihu	Jun, 2015	SRR12686988	Tsinghua University, China	[2]
PRJNA664620	CA150608	Lake Taihu	Jun, 2015	SRR12686989	Tsinghua University, China	[2]
mgp103977*	Jul2016	Lake Taihu	July, 2016	4773250.3	Chinese Academy of Sciences, China	[3]
mgp103977*	Aug2016	Lake Taihu	Aug, 2016	4729510.3	Chinese Academy of Sciences, China	[3]
mgp103977*	Sep2016	Lake Taihu	Sep, 2016	4775083.3	Chinese Academy of Sciences, China	[3]
mgp103977*	Oct2016	Lake Taihu	Oct, 2016	4747924.3	Chinese Academy of Sciences, China	[3]

*Metatranscriptomes are publicly available from the MG-RAST server.

Table S3. Taxonomic, completeness and contamination data for non-redundant microbiome MAGs

accession	lineage	AAP bacteria YES or NO	Completeness (%)	Contamination (%)
JAJTDF01	<i>Planctomycetaceae</i> bacterium	NO	95.45	0
JAJTHL01	Alphaproteobacteria bacterium	NO	95.7	0
JAJTHN01	<i>Phycisphaeraceae</i> bacterium	NO	96.59	0
JADBXD01	<i>Chitinophagaceae</i> bacterium	NO	96.88	0
DA04	<i>Methylophilus</i> sp.	NO	96.89	0
JADDKF01	<i>Cutibacterium</i> sp.	NO	97.7	0
JADCBM01	<i>Methylobacterium</i> sp.	YES	97.75	0
JADBXC01	<i>Chitinophagaceae</i> bacterium	NO	97.78	0
JADBXP01	<i>Chitinophagaceae</i> bacterium	NO	97.78	0
JADCCD01	<i>Methylobacterium</i> sp.	YES	98.07	0
JADCGS01	<i>Burkholderiales</i> bacterium	YES	98.15	0
JADCGV01	<i>Burkholderiales</i> bacterium	YES	98.15	0
JADCCF01	<i>Methylobacterium</i> sp.	YES	98.36	0
TW01	<i>Flavobacterium</i> sp.	NO	98.44	0
JADCFT01	<i>Roseomonas</i> sp.	YES	98.51	0
SGWC01	<i>Exiguobacterium</i> sp.	NO	98.68	0
SGWE01	<i>Deinococcus</i> sp.	NO	99.15	0
DW08	<i>Flavobacterium</i> sp.	NO	99.28	0
DF15	<i>Brevundimonas</i> sp.	NO	99.35	0
JADBXR01	<i>Chitinophagaceae</i> bacterium	NO	99.51	0
TW09	<i>Flaviumibacter</i> sp.	NO	99.75	0
JADCGE01	<i>Roseomonas</i> sp.	YES	99.75	0
JAJTHB01	<i>Rickettsiales</i> bacterium	NO	100	0
JADCGF01	<i>Roseomonas</i> sp.	YES	100	0
JADCDU01	<i>Rhodobacter</i> sp.	YES	99.64	0.02
JADCHI01	<i>Burkholderiales</i> bacterium	NO	99.57	0.03
JAJTDL01	<i>Burkholderiaceae</i> bacterium	YES	99.03	0.08
JAJTIA01	Candidatus <i>Jidaibacter</i> sp.	NO	98.9	0.1
JADCDs01	<i>Rhodobacter</i> sp.	YES	99.33	0.1
JADCHW01	<i>Rhodocyclaceae</i> bacterium	YES	99.53	0.12
JADCEC01	<i>Rhodobacter</i> sp.	YES	99.94	0.12
JADCER01	<i>Roseomonas</i> sp.	YES	99.5	0.17
SGWF01	<i>Paenibacillus</i> sp.	NO	98.39	0.2
JADCDI01	<i>Rhodobacter</i> sp.	YES	99.64	0.2

JAJTEW01	<i>Comamonadaceae</i> bacterium	NO	99.6	0.22
JAJTDM01	<i>Rubrivivax</i> sp.	YES	95.35	0.23
JADCGR01	<i>Curvibacter</i> sp.	YES	97.51	0.23
JADCIV01	<i>Rhodocyclaceae</i> bacterium	YES	97.06	0.24
JADCEO01	<i>Rhodobacter</i> sp.	YES	98.83	0.25
TF07	<i>Sphingopyxis</i> sp.	YES	98.65	0.26
JADCIX01	<i>Rhodocyclaceae</i> bacterium	YES	98.58	0.29
JADCCN01	<i>Methylobacterium</i> sp.	YES	96.66	0.31
JADCCC01	<i>Methylobacterium</i> sp.	YES	98.22	0.31
JADCAS01	<i>Phenylobacterium</i> sp.	NO	97.62	0.32
JADCCL01	<i>Methylobacterium</i> sp.	YES	98.1	0.32
SGWD01	<i>Enterobacter</i> sp.	NO	99.89	0.35
DW05	<i>Sphingomonadaceae</i> bacterium	YES	98.12	0.39
JADBZX01	<i>Bacteroidetes</i> bacterium	NO	99.05	0.41
JAJTEM01	<i>Burkholderiales</i> bacterium	NO	97.55	0.43
JADCDB01	<i>Aestuariivirga</i> sp.	YES	98.26	0.43
JADCGL01	<i>Telmatospirillum</i> sp.	YES	100	0.43
JAJTEG01	<i>Rhodobacter</i> sp.	YES	97.24	0.45
DF16	<i>Limnobacter</i> sp.	NO	98.36	0.45
JADCEN01	<i>Rhodobacter</i> sp.	YES	98.99	0.45
JADCHP01	<i>Burkholderiales</i> bacterium	NO	99.57	0.45
TF06	<i>Rhizobium/Agrobacterium</i> sp.	YES	98.91	0.46
DF14	<i>Silanimonas</i> sp.	NO	99.22	0.46
JAJTEN01	<i>Sphingobacteriales</i> bacterium	NO	98.14	0.48
DF05	<i>Hyphomonadaceae</i> bacterium	YES	96.37	0.49
JADCFX01	<i>Roseomonas</i> sp.	YES	98.73	0.5
JADCEV01	<i>Roseomonas</i> sp.	YES	99	0.5
JADCFA01	<i>Roseomonas</i> sp.	YES	99	0.5
JADCGA01	<i>Roseomonas</i> sp.	YES	99.25	0.5
TA06	<i>Rhizobium/Agrobacterium</i> sp.	YES	99.48	0.52
JADBZH01	<i>Phenylobacterium</i> sp.	NO	97.21	0.54
JADDJO01	<i>Burkholderia</i> sp.	NO	97.18	0.55
JAJTIE01	<i>Bacteroidetes</i> bacterium	NO	97.96	0.55
JADBYM01	<i>Cytophagales</i> bacterium	NO	97.45	0.6
JAJTDW01	Proteobacteria bacterium	NO	95.02	0.61
JADCCU01	<i>Methylocystis</i> sp.	YES	97.49	0.63

JADBYT01	<i>Bacteroidetes</i> bacterium	NO	99.52	0.63
JADBZC01	<i>Phenylobacterium</i> sp.	NO	97.13	0.65
TF08	<i>Brevundimonas</i> sp.	NO	99.59	0.65
JADCIZ01	<i>Rhodocyclaceae</i> bacterium	YES	95.73	0.66
DA12	<i>Pseudomonas</i> sp.	NO	98.15	0.76
JADCEM01	<i>Rhodobacter</i> sp.	YES	99.03	0.83
JADBZP01	<i>Phenylobacterium</i> sp.	NO	96.3	0.87
JAJTIC01	Proteobacteria bacterium	NO	95.98	0.89
JADBYQ01	<i>Cytophagales</i> bacterium	NO	97.45	0.89
JADCBK01	<i>Aquidulcibacter</i> sp.	YES	97.19	0.92
JADCGP01	<i>Rubrivivax</i> sp.	YES	98.83	0.93
JADCHQ01	<i>Rhodocyclaceae</i> bacterium	YES	97.79	0.95
JADBXW01	<i>Chitinophagaceae</i> bacterium	NO	96.31	0.99
JAJTHQ01	<i>Sediminibacterium</i> sp.	NO	96.8	0.99
JAJTHM01	<i>Sphingobacteriales</i> bacterium	NO	97.29	0.99
JADCHA01	<i>Cupriavidus</i> sp.	NO	99.03	0.99
JADCFN01	<i>Roseomonas</i> sp.	YES	99.5	1
JADCGC01	<i>Roseomonas</i> sp.	YES	99.75	1
JADCFQ01	<i>Roseomonas</i> sp.	YES	100	1
JADCAZ01	<i>Phenylobacterium</i> sp.	NO	97.94	1.01
JAJTER01	<i>Saprospiraceae</i> bacterium	NO	98.48	1.01
JADCHE01	<i>Burkholderiales</i> bacterium	YES	96.3	1.03
JAJTHY01	Candidatus <i>Jidaibacter</i> sp.	NO	96.7	1.1
TW08	<i>Pseudomonas</i> sp.	NO	99.25	1.1
JAJTDE01	<i>Rubrivivax</i> sp.	YES	95.99	1.11
JADCJE01	<i>Phycisphaerales</i> bacterium	NO	97.73	1.14
JAJTHT01	Betaproteobacteria bacterium	YES	96.68	1.16
JADCFP01	<i>Roseomonas</i> sp.	YES	98.42	1.16
CP035951	<i>Acidovorax</i> sp.	NO	98.97	1.16
JAJTFC01	<i>Planctomycetaceae</i> bacterium	NO	95.22	1.18
JADCJC01	<i>Rhodocyclaceae</i> bacterium	YES	96.45	1.18
JADCAL01	<i>Phenylobacterium</i> sp.	NO	97.94	1.2
JADCCY01	<i>Bradyrhizobium</i> sp.	NO	97.07	1.23
JADCBF01	<i>Phenylobacterium</i> sp.	NO	97.46	1.23
JAJTGP01	<i>Hyphomonadaceae</i> bacterium	YES	95.08	1.28
JAJTGY01	<i>Flammeovirgaceae</i> bacterium	NO	97.17	1.29
JADCAH01	<i>Phenylobacterium</i> sp.	NO	96.54	1.32

JAJTEA01	Betaproteobacteria bacterium	YES	95.73	1.37
JADCAP01	<i>Phenylobacterium sp.</i> <i>Xanthomonadaceae</i>	NO	97.94	1.43
JAJTHZ01	bacterium	YES	96.84	1.47
JADCFK01	<i>Roseomonas sp.</i> <i>Flammeovirgaceae</i>	YES	95.6	1.64
JAJTHH01	bacterium <i>Xanthomonadaceae</i>	NO	96.26	1.79
DF12	bacterium	NO	97.8	1.8
JAJTHS01	<i>Burkholderiales</i> bacterium	NO	95.11	2.03
JAINDL01	<i>Bryobacteraceae</i> bacterium <i>Gemmatimonadetes</i>	NO	98.26	2.17
JAJTHG01	bacterium	YES	96.15	2.2
JADCGQ01	<i>Rubrivivax sp.</i> <i>Hyphomonadaceae</i>	YES	97.2	2.34
DA05	bacterium	YES	97.19	2.38
JADCFW01	<i>Roseomonas sp.</i>	YES	99.75	2.49
JADCGK01	<i>Azospirillum sp.</i> <i>Rhizobium/Agrobacterium</i>	YES	98.91	2.55
TW06	<i>sp.</i>	YES	99.1	2.71
JAJTEJ01	<i>Rickettsiaceae</i> bacterium	NO	95.34	2.84

Table S4. Diel Bloom transcriptomes from Lake Erie.

Sample ID	Lake	Sampling time	SRR accession	reference
Diel_1S_2200h	western Lake Erie	26 Aug, 2014. 22:00h	SRR6048562	[4]
Diel_2S_0400h	western Lake Erie	27 Aug, 2014. 04:00h	SRR6466459	[4]
Diel_3S_1000h	western Lake Erie	27 Aug, 2014. 10:00h	SRR6466487	[4]
Diel_4S_1600h	western Lake Erie	27 Aug, 2014. 16:00h	SRR6048585	[4]
Diel_5S_2200h	western Lake Erie	27 Aug, 2014. 22:00h	SRR6048582	[4]
Diel_6S_1000h	western Lake Erie	28 Aug, 2014. 10:00h	SRR6048648	[4]
Diel_7S_1600h	western Lake Erie	28 Aug, 2014. 16:00h	SRR6466476	[4]

Table S5. Environmental variables of Meiliang Bay (M) and Zushan Bay (Z) in Lake Taihu. Chl *a* concentrations indicated that the *Microcystis* bloom grew rapidly peaking between August and September, and the bloom began to decline in October. The pH in bloom samples (from August to October) ranged from 8.0 to 10.0. The mass ratios of total nitrogen (TN) to total phosphorus (TP) ranged from 6.7 to >31.8, but were lowest in the months of summer and fall, suggesting the *Microcystis* bloom was potentially N-limited.

	Temp (°C)	pH	TN (mg/L)	NO ₃ (mg/L)	NH ₄ (mg/L)	TP (mg/L)	PO ₄ (mg/L)	N/P	Chl <i>a</i> (µg/L)
Apr-M	13.2	7.3	3.82	1.03	0.27	0.12	0.01	30.2	6.0
May-M	20.2	7.5	2.84	1.26	0.18	0.10	0.01	27.9	6.4
Jun-M	24.6	7.8	2.59	0.65	0.25	0.10	0.02	24.5	14.9
Jul-M	27.2	8.2	2.73	0.44	0.50	0.20	0.02	13.5	23.4
Aug-M	29.0	9.5	2.20	0.10	0.31	0.35	0.05	6.1	79.8
Sep-M	27.6	9.2	2.54	0.11	0.18	0.30	0.08	8.3	63.6
Oct-M	19.6	8.7	4.08	2.55	0.50	0.20	0.08	19.8	43.1
Apr-Z	13.3	7.1	5.07	1.36	0.45	0.14	0.05	34.8	12.9
May-Z	21.3	7.2	4.42	1.33	0.42	0.15	0.07	29.1	23.4
Jun-Z	24.9	7.6	4.08	1.72	1.28	0.16	0.10	24.3	34.6
Jul-Z	27.4	8.4	3.69	0.52	0.27	0.23	0.14	16.0	37.7
Aug-Z	29.3	9.1	2.23	0.27	0.87	0.40	0.22	5.5	92.1
Sep-Z	27.5	8.6	3.03	0.70	1.02	0.25	0.09	12.4	69.8
Oct-Z	19.6	7.2	3.20	0.38	0.51	0.15	0.09	21.5	43.6

SUPPLEMENTARY FIGURES

Figure Legends

Fig. S1. Map of Lake Taihu and the sampling sites at Meiliang Bay and Zushan Bay, and Taihu Laboratory for Lake Ecosystem Research (TLLER).

Fig. S2. Linear relationship between concentrations of DOC and Chl *a* of water samples in Lake Taihu. Data are based on 8 samples from site 1 at Meiliang Bay in September 2018.

Fig. S3. Diel variation of DO and pH during a *Microcystis* bloom. Samples were collected from site 1 in Meiliang Bay, Taihu, over a 24-hour period from 10 AM to 10 AM on 10-11 August and 10-11 October 2018. Data are mean $\pm$ standard deviation (SD) ($n = 3$).

Fig. S4. Alpha- and beta-diversity of samples from Lake Taihu. Free-living communities are displayed in blue and aggregate communities in orange. PD faith is used as an index for alpha-diversity (A). Significant differences between the groups are indicated with asterisks ($***p < 0.001$). For beta-diversity (B), PCoA plot of the weighted UniFrac measures is shown. The x- and y-axes represent the first and second principal coordinates with the proportion of variance. Both diversity measures show significant differences between free-living and aggregate communities.

Fig. S5. Relative abundances of AAP bacterial genera in non-cyanobacterial communities in bloom samples from Lake Taihu (A) and ten global lakes (B). The sample IDs in Lake Taihu are shown in Table S1.

Fig. S6. Relationships between gene abundance of anoxygenic photosystem pathways and important C, N, S, and P cycling pathways. Instead of using genes from MAGs, genes were derived from contigs co-assembled by metaSPAdes v3.15.4 using the metagenome data from each lake with *Microcystis* reads removed. Two biological replicates were obtained for each sample. Gene identification, annotation, and KO (KEGG Orthology) analysis were described in the text. Then reads of the ten lake metagenomes were mapped to genes derived from the contigs, and calculated GPMs. The GPMs were the input to calculate the relative abundance of pathways of each metagenome using formulae suggested by DiTing v0.9 [5].

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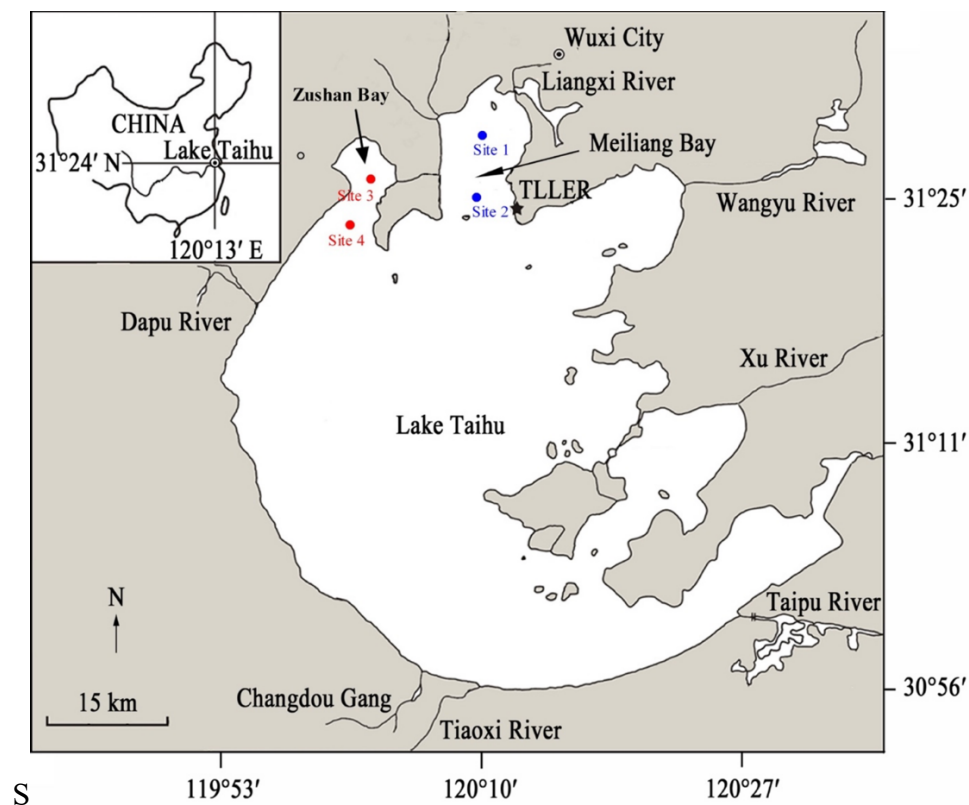


Figure S1

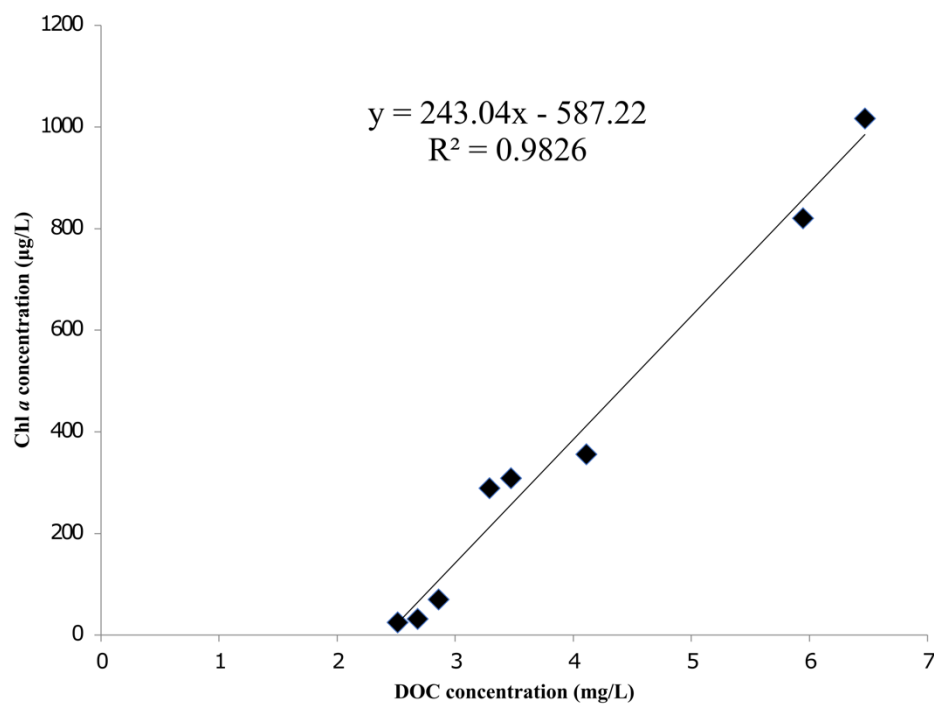


Figure S2

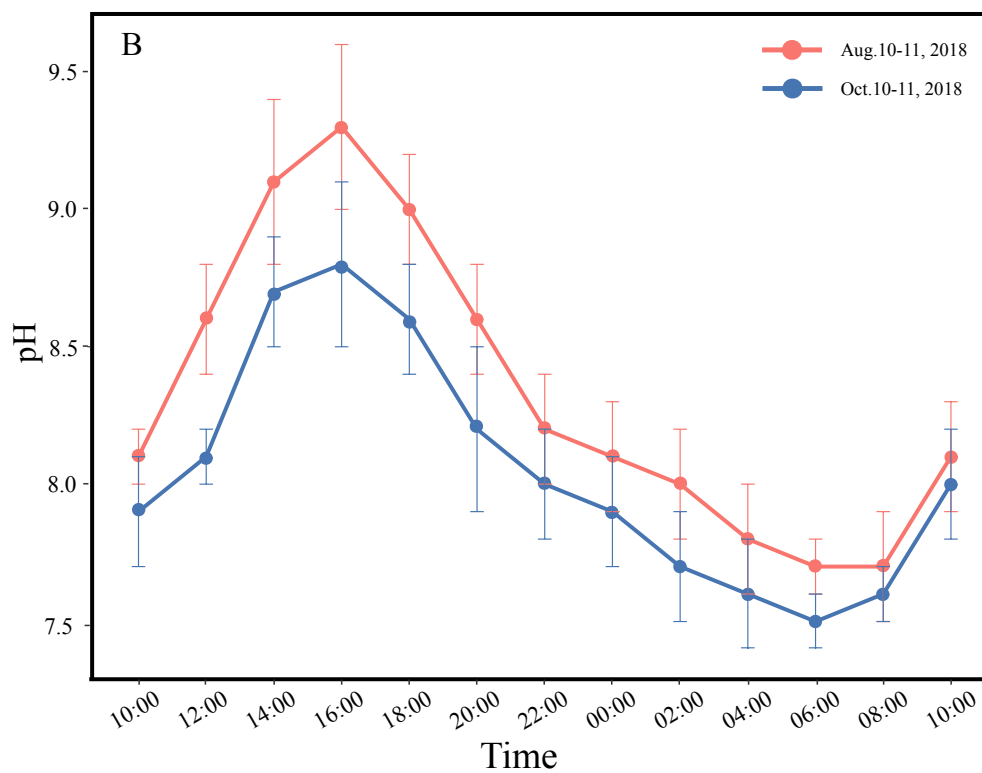
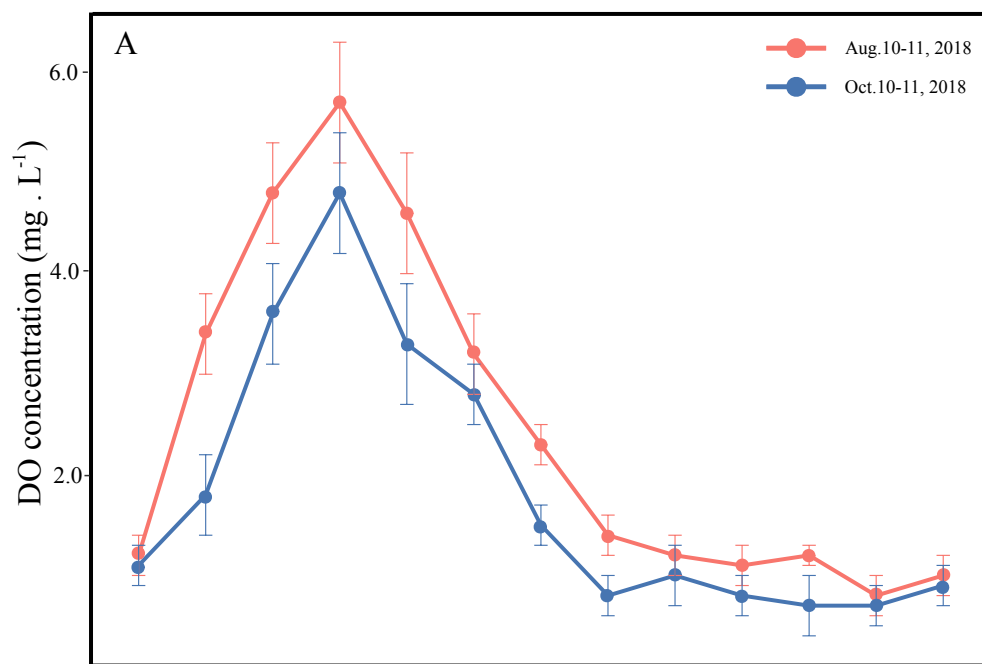


Figure S3

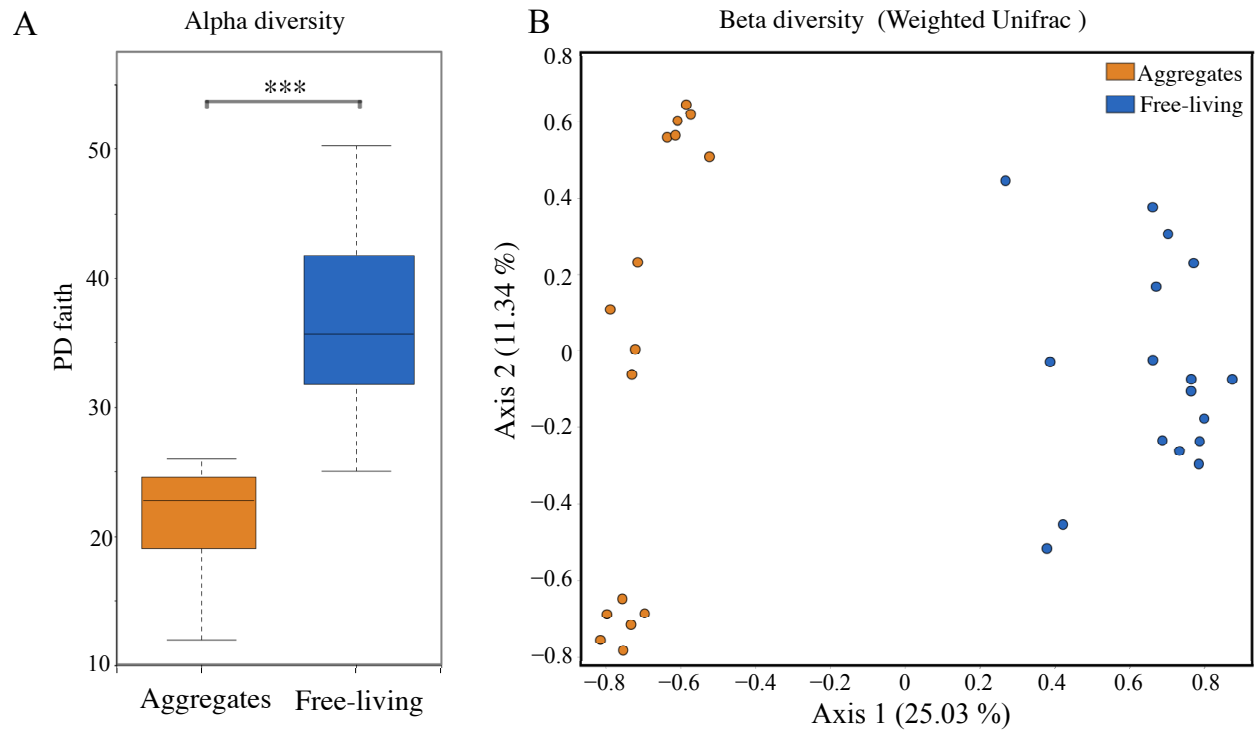


Figure S4

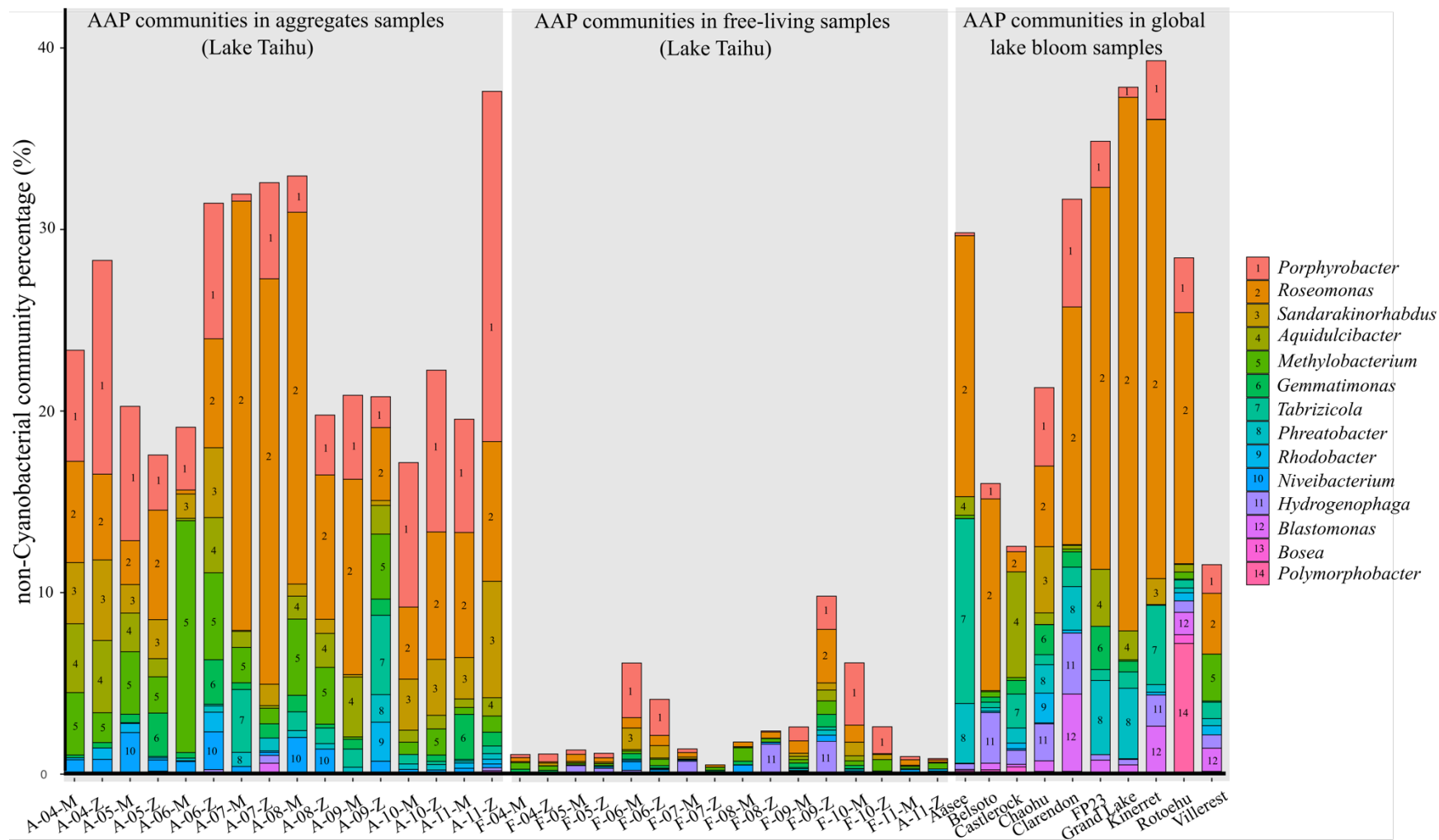
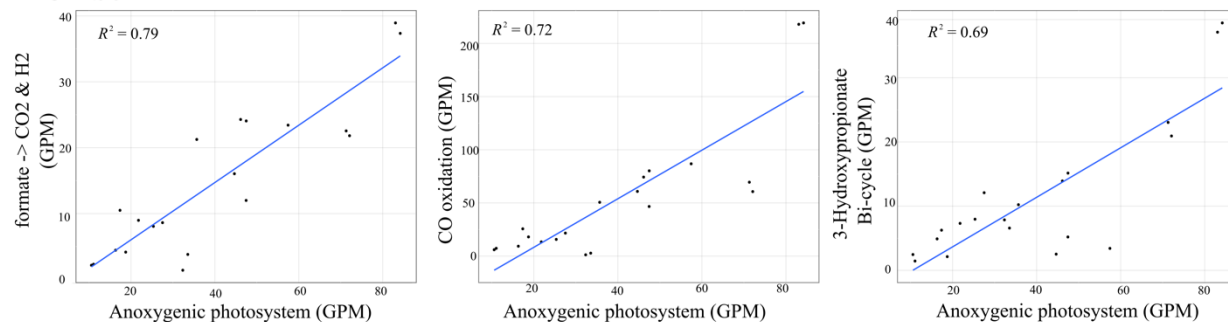
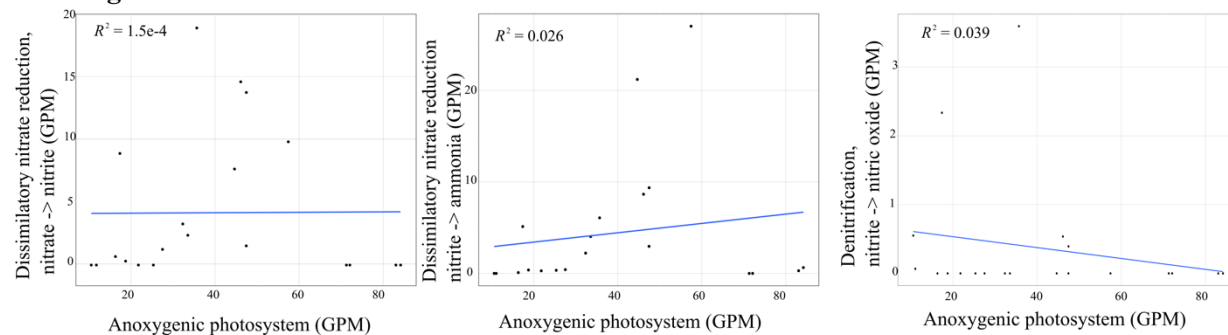


Figure S5

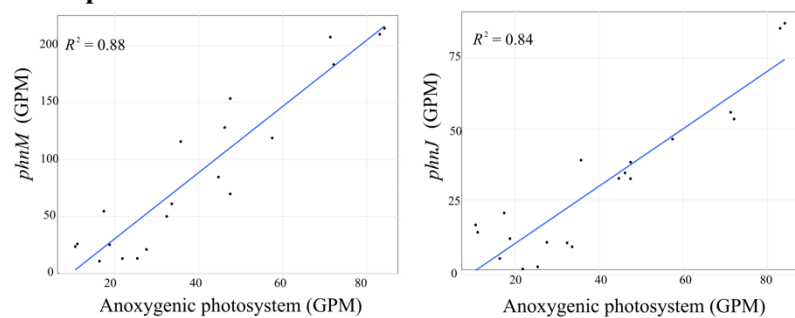
A Carbon



B Nitrogen



C Phosphorus



D Sulfur

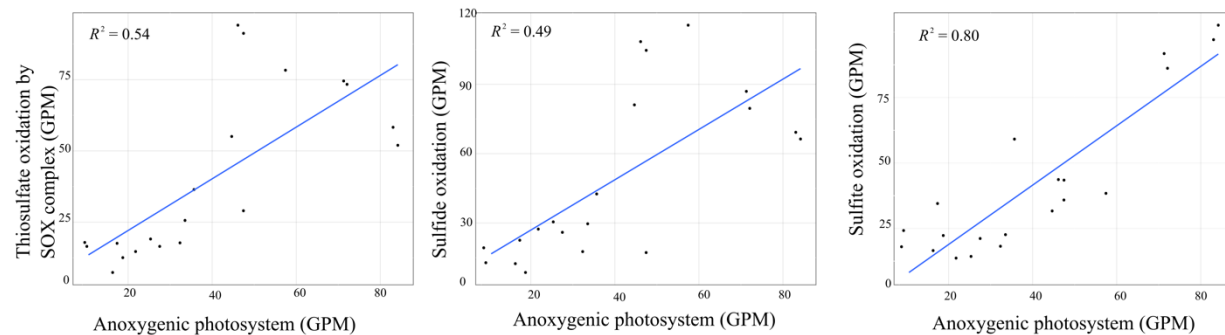


Figure S6