

## Supporting Information

### **Seasonal gene expression and the ecophysiological implications of toxic *Microcystis aeruginosa* blooms in Lake Taihu**

Xiangming Tang<sup>1</sup>, Lauren E. Krausfeldt<sup>2</sup>, Keqiang Shao<sup>1</sup>, Gary R. LeCleir<sup>2</sup>, Joshua M. A. Stough<sup>2</sup>, Guang Gao<sup>1</sup>, Gregory L. Boyer<sup>3</sup>, Yunlin Zhang<sup>1</sup>, Hans W. Paerl<sup>4</sup>, Boqiang Qin<sup>1\*</sup>, Steven W. Wilhelm<sup>2\*</sup>

<sup>1</sup>Taihu Laboratory for Lake Ecosystem Research, State Key Laboratory of Lake Science and Environment, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, Nanjing 210008, China

<sup>2</sup>Department of Microbiology, University of Tennessee, Knoxville, TN 37996, United States

<sup>3</sup>Department of Chemistry, SUNY College of Environmental Science & Forestry, Syracuse, NY 13210, United States

<sup>4</sup>Institute of Marine Sciences, The University of North Carolina at Chapel Hill, Morehead City, North Carolina 28557, United States *and* College of Environment, Hohai University, Nanjing 210098, China

\* Corresponding authors:

Boqiang Qin - Email: qinbq@niglas.ac.cn; Tel.: 86-25-86882192.

Steven W. Wilhelm - Email: wilhelm@utk.edu; Tel.: 1-865-974-0665.

Number of pages: 27

Number of tables: 9

Number of figures: 8

## MATERIALS AND METHODS

### Sample collection and survey of environmental conditions

TN, TDN, TP and TDP were analyzed using a combined peroxodisulfate oxidation followed by spectrophotometric analyses<sup>1</sup>. NH<sub>4</sub><sup>+</sup> and PO<sub>4</sub><sup>3-</sup> were measured using a continuous flow analyzer (Skalar SA 1000, Breda, The Netherlands). Chl-a concentrations were determined by spectrophotometric methods after extraction in 90% hot ethanol<sup>2</sup>.

For quantification of cellular (particulate) toxin, a 50 – 500 ml volume (depending on sample density) of surface water from each station was filtered onto GF/F (Whatman, Buckinghamshire, UK) filters and then dried using a vacuum freeze dryer (Christ Alpha 1-2 LD, Germany). Intracellular microcystin concentrations were determined without preconcentration using HPLC coupled with single quadrupole mass spectroscopy and photodiode array spectroscopy. Standards (MC-RR, LR and LF) were run at the start and end of each run to ensure that the retention times for the microcystins did not drift, and individual toxin congeners ((RR, dRR, mRR, hYR, YR, LR, mLRL, zLR, dLR, mLRL, AR, FR, WR, LA, LY, LW, LF, WR) and R-NOD) were identified on the basis of their retention time, their characteristic absorbance spectrum in the photodiode array detector and their characteristic molecular ions. For many of these congeners, validated reference standards do not exist, so the individual congeners were quantitated using their extracted molecular ions and a standard curve based on microcystin LR after tuning the mass spectrometer to give an equivalent detector response for microcystins LR, RR and LF. Total MC concentrations are reported as the sum of all congeners.

### RNA-seq data processing and phylogenetic analysis

After preprocessing of quality control (QC), removing artificial duplicate reads and clustering of proteins at the 90% identity level, protein-coding sequences (mRNA and their genes) were annotated with the M5nr protein database, which is an integration of many sequence databases into a single and searchable database. Taxonomic hits distribution was carried out and taxonomic categories at different levels of resolution was annotated using protein similarities to entries in the REFseq protein database with an e-value of 1e<sup>-5</sup> (see details in MG-RAST Manual for version 3.6, revision 3).

## REFERENCE

- (1) Ebina, J.; Tsutsui, T.; Shirai, T., Simultaneous determination of total nitrogen and total phosphorus in water using peroxodisulfate oxidation. *Water Res.* **1983**, *17* (12), 1721-1726.
- (2) Pápista, É.; Ács, É.; Böddi, B., Chlorophyll-a determination with ethanol – a critical test. *Hydrobiologia* **2002**, *485* (1), 191-198.

**Table S1** Sampling information as well as concentrations of nutrients, chlorophyll-a and microcystin in Lake Taihu (June - October, 2014).

Sample <sup>①</sup>	Date	Time	Longitude	Latitude	WT (°C)	EC (μS cm <sup>-1</sup> )	TDS (g l <sup>-1</sup> )	pH	NTU	PC (cells ml <sup>-1</sup> )	DO (mg l <sup>-1</sup> )	SD (cm)	Visible bloom level	Filtered for RNA extraction (ml) <sup>②</sup>	Filtered for toxin analysis (ml) <sup>②</sup>	Chl-a (μg l <sup>-1</sup> ) <sup>③</sup>	MC (μg l <sup>-1</sup> ) <sup>③</sup>	TN (mg l <sup>-1</sup> )	TDN (mg l <sup>-1</sup> )	NH <sub>4</sub> <sup>+</sup> (mg l <sup>-1</sup> )	TP (mg l <sup>-1</sup> )	TDP (mg l <sup>-1</sup> )	PO <sub>4</sub> <sup>3-</sup> (mg l <sup>-1</sup> )
T06_1	6/7/2014	9:12	120.19067	31.51317	24.8	670	0.437	8.19	13.3	2831	9.43	40	light	120×2	250×2	40	0.28	2.97	2.50	0.08	0.092	0.028	0.005
T06_2	6/7/2014	17:26	120.22055	31.41747	27.9	712	0.439	8.77	26.4	11107	10.08	15	heavy	60×2	260×2	960	69.39	17.23	1.83	0.08	1.176	0.029	0.006
T06_3	6/7/2014	16:47	120.22945	31.39438	26.9	689	0.433	9.08	10.0	5050	11.56	40	heavy	60×2	310×2	370	7.18	9.39	1.99	0.07	0.515	0.027	0.005
T06_4	6/7/2014	8:34	120.18796	31.43609	23.7	637	0.424	8.35	19.5	7456	9.01	45	light	120×2	250×2	54	1.18	3.55	2.09	0.07	0.136	0.027	0.009
T06_5	6/7/2014	9:49	120.11638	31.44719	25.3	632	0.408	7.94	18.1	1374	4.46	30	heavy	60×2	250×2	368	2.64	10.77	3.89	0.83	0.728	0.093	0.069
T06_6	6/7/2014	10:18	120.02817	31.45001	24.6	577	0.377	7.90	14.9	1315	7.37	40	light	120×2	250×2	36	<0.10	4.46	3.97	1.64	0.168	0.075	0.044
T06_7	6/7/2014	12:11	120.18017	31.33833	25.3	608	0.392	8.31	21.8	2125	9.31	30	light	120×2	250×2	27	<0.10	2.38	1.79	0.08	0.077	0.010	0.012
T06_8	6/7/2014	10:40	120.03182	31.39761	25.0	637	0.414	8.56	22.0	15662	13.00	40	medium	120×2	250×2	116	1.18	4.33	2.62	0.07	0.222	0.069	0.040
T06_9	6/7/2014	11:07	119.94500	31.31450	26.5	699	0.442	8.18	23.2	2516	7.26	20	medium	120×2	250×2	48	3.63	4.02	3.18	0.93	0.215	0.093	0.061
T07_1	7/3/2014	13:17	120.19067	31.51317	26.0	620	0.359	8.75	20.8	2482	8.64	30	light	120×2	500×2	19	0.24	1.78	1.40	0.08	0.060	0.020	0.006
T07_2	7/3/2014	12:31	120.22055	31.41747	27.3	665	0.415	8.90	143.8	62121	7.79	0	heavy	60×2	250×2	119	2.24	4.21	1.17	0.12	0.233	0.017	0.003
T07_3	7/3/2014	16:53	120.22945	31.39438	28.0	691	0.425	9.73	24.6	10098	11.34	30	medium	120×2	500×2	47	5.55	1.94	1.04	0.05	0.094	0.019	0.013
T07_4	7/3/2014	8:42	120.18796	31.43609	24.6	647	0.423	9.03	39.4	9534	8.29	30	heavy	60×2	500×2	320	9.76	4.94	1.06	0.14	0.229	0.018	0.004
T07_5	7/3/2014	13:46	120.11638	31.44719	25.2	590	0.382	8.99	25.3	2304	6.24	30	light	120×2	500×2	38	2.96	3.30	2.78	0.34	0.122	0.036	0.021
T07_6	7/3/2014	14:38	120.02817	31.45001	26.7	558	0.351	9.01	21.0	7035	10.91	40	medium	120×2	500×2	41	0.39	4.86	4.07	1.31	0.174	0.074	0.054
T07_7	7/3/2014	16:10	120.18017	31.33833	27.1	608	0.380	9.14	12.9	2139	10.68	30	light	120×2	500×2	49	0.85	2.51	1.60	0.03	0.076	0.013	0.003
T07_8	7/3/2014	14:54	120.03182	31.39761	27.9	570	0.352	9.11	18.5	6043	8.93	60	medium	120×2	500×2	42	5.78	5.24	4.62	1.30	0.174	0.078	0.058
T07_9	7/3/2014	15:22	119.94500	31.31450	26.1	602	0.383	8.93	33.4	1425	3.84	30	no bloom	120×2	500×2	15	0.21	4.66	4.20	1.67	0.227	0.128	0.101
T08_1	8/4/2014	8:00	120.19067	31.51317	26.7	543	0.342	9.57	57.9	22185	6.60	35	light	120×2	500×2	75	2.71	1.38	0.71	0.09	0.162	0.080	0.050
T08_2	8/4/2014	6:50	120.22055	31.41747	26.5	557	0.352	8.98	51.5	18561	2.33	40	light	120×2	500×2	72	2.53	2.40	1.35	0.65	0.203	0.037	0.019
T08_3	8/4/2014	12:55	120.22945	31.39438	26.8	564	0.349	9.41	32.1	1023	6.88	40	no bloom	120×2	500×2	25	NA	2.23	1.25	0.46	0.138	0.034	0.012
T08_4	8/4/2014	7:30	120.18796	31.43609	26.7	557	0.351	9.38	37.7	21232	7.38	50	medium	120×2	500×2	89	2.76	1.55	0.53	0.06	0.152	0.037	0.015
T08_5	8/4/2014	8:30	120.11638	31.44719	26.7	552	0.348	9.38	71.3	36136	4.64	25	super heavy	50×2	150×2	3258	111.57	21.52	1.29	0.28	2.132	0.061	0.036
T08_6	8/4/2014	9:00	120.02817	31.45001	27.0	532	0.333	9.38	23.8	1821	2.16	35	no bloom	120×2	500×2	28	<0.20	3.67	3.23	1.16	0.236	0.130	0.112
T08_7	8/4/2014	11:25	120.18017	31.33833	26.4	598	0.378	9.38	28.8	4534	7.88	40	no bloom	120×2	500×2	21	0.40	1.10	0.76	0.05	0.067	0.017	0.001
T08_8	8/4/2014	9:30	120.03182	31.39761	26.6	467	0.294	9.32	41.3	21316	6.79	40	heavy	120×2	500×2	101	6.58	2.72	1.63	0.61	0.324	0.188	0.162
T08_9	8/4/2014	10:00	119.94500	31.31450	26.7	517	0.326	9.20	45.0	2159	2.95	32	no bloom	120×2	500×2	21	0.28	3.73	2.97	1.16	0.343	0.138	0.112
T09_1	9/9/2014	14:15	120.19067	31.51317	27.4	542	0.337	10.03	28.2	10618	9.98	40	no bloom	120×2	500×2	57	0.45	1.33	0.52	0.07	0.170	0.075	0.060
T09_2	9/9/2014	13:27	120.22055	31.41747	27.7	544	0.336	8.51	24.1	4022	5.84	30	light	120×2	500×2	62	0.47	1.26	0.66	0.24	0.148	0.069	0.057
T09_3	9/9/2014	17:14	120.22945	31.39438	27.6	524	0.324	9.96	31.4	8714	9.57	30	medium	120×2	270×2	250	2.80	4.52	0.58	0.11	0.451	0.067	0.053
T09_4	9/9/2014	13:52	120.18796	31.43609	27.4	532	0.331	9.60	33.2	9345	9.32	40	light	120×2	500×2	51	<0.30	1.39	0.53	0.09	0.204	0.069	0.058
T09_5	9/9/2014	14:43	120.12684	31.44614	28.3	515	0.315	9.76	881.9	239256	5.27	0	super heavy	20×2	50×2	16182	592.69	48.17	1.31	0.36	11.686	0.034	0.059
T09_6	9/9/2014	15:12	120.02817	31.45001	27.4	470	0.292	9.88	27.3	32381	11.03	20	heavy	120×2	145×2	3415	30.89	17.79	1.22	0.42	1.708	0.049	0.029
T09_7	9/9/2014	16:57	120.18017	31.33833	27.1	482	0.301	9.94	25.0	15009	12.63	30	heavy	90×2	60×2	1205	75.04	39.33	0.67	0.16	4.245	0.045	0.027
T09_8	9/9/2014	15:33	120.03182	31.39761	27.6	486	0.301	9.98	57.6	29456	11.94	20	heavy	120×2	250×2	307	2.54	7.01	1.17	0.12	0.625	0.080	0.058
T09_9	9/9/2014	16:04	119.94500	31.31450	27.3	424	0.264	9.93	27.4	4357	5.64	35	no bloom	120×2	500×2	28	<0.30	2.99	2.70	0.86	0.169	0.089	0.071
T10_1	10/8/2014	8:15	120.19067	31.51317	21.3	492	0.344	9.38	34.2	4989	6.07	30	light	120×2	500×2	33	0.19	1.37	0.77	0.10	0.141	0.064	0.054
T10_2	10/8/2014	13:30	120.22055	31.41747	21.9	473	0.327	10.05	48.5	4267	2.81	25	medium	60×2	150×2	1038	0.62	12.66	0.64	0.12	1.199	0.056	0.044
T10_3	10/8/2014	13:15	120.22945	31.39438	22.7	469	0.319	9.94	79.1	43149	6.60	20	heavy	60×2	100×2	1622	348.51	20.86	0.58	0.09	1.925	0.032	0.021
T10_4	10/8/2014	7:45	120.18796	31.43609	20.7	475	0.337	9.52	43.1	8814	9.25	30	light	120×2	500×2	30	<0.10	1.24	0.66	0.14	0.137	0.055	0.044
T10_5	10/8/2014	8:50	120.12684	31.44614	21.9	544	0.376	9.41	177.3	79328	2.20	0	super heavy	20×2	50×2	46872	6378.76	98.47	1.55	0.65	42.835	0.062	0.020
T10_6	10/8/2014	9:30	120.02817	31.45001	21.5	512	0.357	9.17	23.1	3006	8.61	40	light	120×2	500×2	37	0.93	2.92	2.56	0.55	0.182	0.098	0.082
T10_7	10/8/2014	11:45	120.18017	31.33833	22.2	467	0.321	9.77	47.0	13945	2.85	25	heavy	60×2	150×2	1508	298.08	20.34	0.62	0.13	1.905	0.037	0.026
T10_8	10/8/2014	9:50	120.03182	31.39761	21.9	498	0.345	9.28	14.8	5266	5.01	70	light	120×2	500×2	42	1.14	2.79	2.25	0.65	0.146	0.067	0.051
T10_9	10/8/2014	10:3																					

**Table S2** Summary of sequence information for Lake Taihu metatranscriptomic libraries during June - October 2014. The first letter of each sample name represents Taihu, the following two numbers represent months and the last numbers represent sampling stations (see Figure 1 for details). Length of each raw read was 125 base pairs. QC: quality control.

Sample	No. of total raw reads	No. of reads post-QC	% Reads analyzed post-QC	Avg. length post-QC	No. of reads after rRNA removal	% non-rRNA clean reads	No. of reads mapped to <i>M. aeruginosa</i> NIES 843	% <i>M. aeruginosa</i> NIES 843 to total clean reads	MG-RAST ID
T06_1	23 765 226	20 791 603	87.5	116	16 861 404	81.1	3 893 979	23.1	mgm4663025.3
T06_2	25 916 472	22 789 598	87.9	117	20 352 436	89.3	9 420 403	46.3	mgm4663263.3
T06_3	24 642 268	21 838 389	88.6	117	19 603 956	89.8	9 311 823	47.5	mgm4663272.3
T06_4	25 361 148	22 531 633	88.8	117	19 908 400	88.4	8 361 256	42.0	mgm4663273.3
T06_5	29 455 482	25 721 564	87.3	117	22 701 425	88.3	10 421 164	45.9	mgm4663274.3
T06_7	14 132 414	12 464 137	88.2	117	11 093 239	89.0	5 005 853	45.1	mgm4663278.3
T06_9	18 754 882	16 470 480	87.8	117	14 479 253	87.9	6 322 948	43.7	mgm4663280.3
T07_1	15 217 108	11 485 659	75.5	109	8 075 041	70.3	3 035 310	37.6	mgm4664215.3
T07_2	22 913 270	20 226 976	88.3	117	18 199 464	90.0	8 784 341	48.3	mgm4664214.3
T07_3	24 230 822	20 474 191	84.5	116	17 067 830	83.4	5 842 581	34.2	mgm4664209.3
T07_4	27 860 460	23 680 003	85.0	116	19 872 105	83.9	8 116 792	40.9	mgm4664210.3
T07_5	24 019 620	21 131 768	88.0	117	18 897 192	89.4	9 236 448	48.9	mgm4664213.3
T07_6	27 331 358	22 897 985	83.8	115	18 889 878	82.5	7 063 168	37.4	mgm4664212.3
T07_8	29 839 878	25 632 576	85.9	116	22 270 904	86.9	9 359 519	42.0	mgm4664211.3
T07_9	36 080 570	28 006 722	77.6	109	18 217 150	65.0	33 717	0.2	mgm4664208.3
T08_1	26 393 394	23 440 204	88.8	117	20 818 796	88.8	7 262 888	34.9	mgm4664613.3
T08_2	25 006 404	22 145 662	88.6	117	19 725 077	89.1	7 123 795	36.1	mgm4664610.3
T08_4	23 556 748	19 789 525	84.0	115	16 117 209	81.4	4 755 439	29.5	mgm4664609.3
T08_5	21 064 130	18 691 580	88.7	117	16 800 225	89.9	6 779 446	40.4	mgm4664612.3
T08_8	22 781 612	19 215 669	84.4	116	16 074 771	83.7	5 492 282	34.2	mgm4664608.3

T08_9	25 866 280	21 494 334	83.1	113	15 938 625	74.2	142 750	0.9	mgm4664611.3
T09_1	26 900 236	22 568 143	83.9	116	17 898 383	79.3	2 292 191	12.8	mgm4664691.3
T09_3I	24 182 112	19 792 928	81.9	113	15 734 440	79.5	4 971 514	31.6	mgm4664695.3
T09_3II	25 790 182	21 397 600	83.0	114	17 269 578	80.7	5 475 828	31.7	mgm4664693.3
T09_4	26 357 046	22 420 480	85.1	115	18 682 048	83.3	5 460 332	29.2	mgm4664697.3
T09_5I	25 226 958	22 200 697	88.0	117	19 798 145	89.2	7 536 782	38.1	mgm4664692.3
T09_5II	21 633 042	18 738 404	86.6	117	16 272 418	86.8	5 963 344	36.7	mgm4664689.3
T09_6	25 766 550	21 976 971	85.3	116	18 790 853	85.5	6 732 969	35.8	mgm4664696.3
T09_7	24 550 814	21 136 779	86.1	116	18 437 455	87.2	6 836 040	37.1	mgm4664694.3
T09_8	27 341 606	23 486 818	85.9	116	20 258 614	86.3	7 831 086	38.7	mgm4664690.3
T10_1	36 054 800	30 118 886	83.5	114	23 439 911	77.8	5 076 396	21.7	mgm4663615.3
T10_2	25 758 458	22 661 971	88.0	117	20 154 872	88.9	8 394 878	41.7	mgm4663618.3
T10_3I	24 526 958	20 377 028	83.1	115	16 969 775	83.3	5 069 097	29.9	mgm4663619.3
T10_3II	29 254 962	24 597 017	84.1	116	20 735 044	84.3	6 197 921	29.9	mgm4663616.3
T10_4	32 543 446	27 479 632	84.4	115	22 246 608	81.0	6 796 541	30.6	mgm4663617.3
T10_6	27 735 526	23 377 013	84.3	115	18 670 411	79.9	5 606 761	30.0	mgm4663620.3
T10_7I	43 244 796	36 840 670	85.2	116	30 578 750	83.0	13 458 081	44.0	mgm4663630.3
T10_7II	20 617 104	17 188 922	83.4	115	14 341 258	83.4	6 267 463	43.7	mgm4663633.3
T10_9	16 735 292	13 534 962	80.9	112	10 209 021	75.4	3 746 777	36.7	mgm4663634.3

**Table S3** Amount of RNA (μg) yielded from Lake Taihu samples. A total of 39 metatranscriptomic libraries including 35 samples (grey shaded cells) and 4 technical replicates (bold samples) were successfully constructed from the 45 samples.

Station	June	July	August	September	October
1	2.08	1.10	2.65	0.96	0.99
2	17.20	9.13	3.35	0.45	1.32
3	8.84	1.69	0.22	<b>1.26</b>	<b>43.85</b>
4	1.00	2.21	2.65	1.03	1.19
5	<b>14.67</b>	10.25	<b>14.52</b>	<b>14.83</b>	0.36
6	0.46	<b>2.02</b>	0.61	16.48	1.46
7	<b>6.96</b>	0.63	0.48	8.36	<b>40.23</b>
8	2.53	<b>2.47</b>	3.93	3.27	0.96
9	3.97	0.88	0.93	5.05	1.75

**Table S4** Analysis of similarity (ANOSIM) comparisons of gene expression profiles between months (June to October 2014) for *Microcystis* in Lake Taihu. The statistic  $R$  (ranges between 0 and 1) generated by ANOSIM is indicative of the degree of separation between groups, with a score of 1 indicating complete separation, and 0 indicating no separation.

Groups	Statistic $R$	Significance Level (%)
Jun. vs. Jul.	0.203	5.50
Jun. vs. Aug.	0.801	<b>0.08</b>
Jun. vs. Sep.	0.754	<b>0.03</b>
Jun. vs. Oct.	0.654	<b>0.03</b>
Jul. vs. Aug.	0.904	<b>0.20</b>
Jul. vs. Sep.	0.639	<b>0.10</b>
Jul. vs. Oct.	0.557	<b>0.30</b>
Aug. vs. Sep.	0.405	<b>1.30</b>
Aug. vs. Oct.	0.218	<b>4.90</b>
Sep. vs. Oct.	0.404	<b>0.40</b>

**Table S5** Genes putatively encoding transposase and their differential expression in Cluster II (samples from August to October) compared to Cluster I (samples from June and July). Red and blue characters represent those genes significantly ( $|fold\ change| \geq 1.5 \text{ & } P < 0.05$ ) up-regulated and down-regulated, respectively.

MAE Number	Fold change	FDR p-value correction	Transposase Family
00740	5.08	3.1E-10	IS605
00790	37.45	4.8E-05	
01100	3.34	4.6E-08	
01120	2.00	4.8E-02	
01400	5.48	1.7E-12	
01410	25.49	1.0E-21	
01430	11.06	1.1E-03	IS605
01440	1.82	3.9E-03	ISL3
01620	2.35	4.1E-05	
01660	6.47	2.3E-02	
02260	3.47	5.3E-04	
02300	4.78	3.3E-07	
02940	3.26	5.6E-10	
02950	4.76	2.1E-08	
03050	1.95	1.9E-02	
03060	2.47	2.6E-03	
03270	2.20	2.7E-03	
03690	5.67	1.7E-05	
04150	3.28	1.6E-03	
04160	5.03	1.5E-05	
04420	3.97	2.0E-05	
04810	10.45	4.8E-03	
04830	5.97	2.2E-02	
04950	7.25	1.8E-02	
04980	3.18	6.2E-04	
05120	1.61	2.4E-03	
05300	2.41	1.8E-08	IS605
05720	3.63	3.6E-05	
05730	27.26	7.6E-25	
05920	6.30	3.2E-02	
06030	9.78	1.2E-11	
07480	23.95	5.7E-05	
08290	6.77	1.4E-04	ISL3
08710	4.57	9.7E-04	
10160	1.56	2.1E-02	
10180	2.23	7.3E-04	IS605

10310	-2.63	2.5E-02	
10440	11.23	3.3E-03	
10580	2.19	1.0E-02	ISL3
10630	17.76	3.6E-12	
10690	8.00	3.9E-11	
10750	17.46	6.8E-04	
11420	3.37	2.3E-05	
11630	3.55	8.3E-05	ISL3
11670	3.80	4.2E-06	
11680	3.83	5.4E-07	
11690	4.69	1.5E-16	
11740	2.67	1.8E-06	IS605
13740	20.25	4.0E-12	
13800	16.60	6.0E-04	
13810	5.55	2.2E-02	
13890	5.49	3.7E-02	
14820	1.70	2.1E-02	
15290	4.48	1.9E-16	
15350	2.75	4.0E-11	
16010	2.58	5.7E-04	
16460	3.41	5.2E-04	
16510	5.28	8.9E-11	
16530	2.55	2.2E-05	
16540	2.35	4.0E-06	IS605
16830	4.79	2.5E-07	
16840	4.35	3.2E-06	
16950	9.52	9.4E-04	
17140	2.26	1.9E-04	
17710	2.25	6.2E-08	
17930	5.77	5.8E-05	
17940	5.60	2.2E-04	
18000	3.04	1.2E-04	
19340	2.34	8.0E-06	IS605
19800	4.90	5.0E-02	
20330	2.75	4.1E-05	IS605
20910	29.93	6.7E-05	
20940	1.86	2.0E-03	
21890	2.55	1.7E-03	
21970	-1.84	3.6E-04	
22180	6.76	1.1E-22	
22200	3.53	8.2E-05	

22240	7.35	6.9E-03	
22270	-3.09	1.9E-11	
22350	3.75	2.5E-05	
22400	3.06	5.2E-12	IS605
22840	1.50	4.4E-03	IS605
23110	4.42	1.3E-15	IS605
23170	2.02	2.7E-04	IS605
23260	5.06	3.1E-07	
23420	9.54	8.1E-04	
24700	3.04	1.6E-05	
24780	6.22	1.9E-02	
24800	33.33	4.4E-18	
24970	4.38	7.8E-07	
24980	2.03	1.1E-02	
25530	5.44	1.2E-06	
26000	4.75	7.4E-06	
26950	1.72	6.1E-04	
26970	3.51	1.0E-05	ISL3/204/100/1096/1165
27070	-2.17	8.1E-07	
27330	4.43	1.7E-05	
27490	-1.74	1.0E-05	
27650	2.09	3.0E-06	
27710	5.68	2.6E-07	
28800	7.66	1.0E-02	
29160	6.31	2.1E-09	
29210	3.61	2.5E-05	
29230	1.82	3.5E-05	IS605
29350	23.93	3.2E-07	
29570	3.12	1.2E-04	
29610	2.01	2.4E-04	IS605
29640	2.57	3.5E-04	
29650	5.04	5.4E-08	
29680	-1.66	4.1E-02	
29690	4.22	2.3E-03	
30310	4.89	6.2E-10	
30320	-1.63	1.5E-04	
30340	1.98	1.1E-04	
31200	5.09	8.5E-06	
32760	7.66	2.0E-02	
33100	3.08	9.6E-06	
33340	2.95	2.8E-05	

33490	2.29	1.3E-03	
33580	3.30	7.3E-04	
33620	1.55	7.3E-03	
33840	2.35	4.9E-05	
34130	-1.79	4.2E-05	
34140	2.39	3.0E-05	
34180	25.81	1.3E-06	
34310	6.59	2.1E-05	
34390	1.53	2.0E-02	
34400	2.66	7.3E-07	
34640	2.62	1.3E-02	
34730	-1.77	8.9E-04	
36260	1.67	4.6E-02	IS605
36440	2.19	3.8E-02	
36520	2.61	6.7E-05	IS605
37900	3.57	1.2E-09	IS605
38010	2.50	9.5E-07	
38070	3.13	4.5E-08	IS605
38460	2.32	1.3E-05	IS605
39350	24.11	1.1E-11	
39570	8.70	1.2E-04	
40360	1.79	1.4E-04	
42010	2.01	9.7E-08	
42410	2.57	1.3E-06	IS605
42420	1.98	1.6E-04	IS605
42450	2.38	7.1E-07	IS605
42460	1.79	1.7E-03	
42700	10.32	7.0E-03	
43110	5.20	8.7E-10	
43160	14.17	3.7E-15	
43380	4.18	2.3E-04	
43620	5.13	3.2E-08	
43630	3.93	2.8E-06	IS605
43830	3.12	5.2E-06	
44190	5.33	7.3E-06	
44200	3.14	2.3E-02	
44500	1.97	1.8E-02	IS605
44590	1.53	3.3E-02	IS605
44600	2.00	8.5E-06	
44880	2.80	9.3E-12	IS605
45270	1.95	1.2E-04	

45350	5.10	1.8E-07	
45440	5.28	5.0E-10	
47480	5.42	3.4E-03	
47650	3.11	8.2E-06	
47780	28.65	4.4E-09	
48000	2.20	2.6E-04	
48650	1.93	8.2E-04	
48670	-2.91	3.2E-06	
48700	9.51	1.5E-02	
48780	3.90	2.0E-05	
50010	1.79	3.1E-05	IS605
50750	1.99	8.6E-06	
50890	2.70	3.3E-07	
51110	2.73	7.5E-10	
51600	27.13	1.2E-05	
51800	3.48	7.8E-04	
51830	1.56	5.8E-04	IS605
52020	15.56	2.9E-09	
53420	2.48	8.9E-05	IS605
53530	1.50	1.8E-03	IS605
53540	2.16	8.9E-05	IS605
54250	-1.97	1.4E-04	
54270	2.53	1.5E-04	
54610	2.15	3.2E-04	
54810	1.68	2.5E-02	
54820	1.75	2.8E-04	IS605
54880	-2.30	2.0E-05	
55310	2.37	1.0E-04	
55320	2.60	4.7E-04	
57040	2.70	1.7E-10	
58430	3.58	7.3E-03	
59240	3.62	1.1E-09	
59790	2.61	1.5E-09	
60050	2.51	2.9E-10	IS605
60160	3.08	8.6E-05	
60350	-1.77	7.3E-04	ISL3
60850	2.58	5.0E-06	
60950	1.57	1.2E-02	
61550	8.77	9.7E-03	
62860	2.89	2.2E-03	
62930	2.09	1.6E-03	IS605

63080	3.10	5.7E-08	IS200
63090	5.12	1.9E-17	IS605

**Table S6** Genes involved in nitrogen metabolism and their differential expression in Cluster II (samples from August to October) compared to Cluster I (samples from June and July). Red and blue characters represent those genes significantly ( $|fold\ change| \geq 1.5 \text{ & } P < 0.05$ ) up-regulated and down-regulated, respectively.

MAE Number	Gene Symbol	Product	Fold change	FDR p-value correction
12590	<i>amt</i>	ammonium transport protein	1.09	5.0E-01
40020	<i>amt</i>	ammonium transport protein	-1.61	7.0E-02
17690	<i>amt1</i>	ammonium/methylammonium permease	2.80	1.7E-03
40010	<i>amt1</i>	ammonium/methylammonium permease	-1.47	1.7E-01
08260	<i>gdhA</i>	glutamate dehydrogenase (NADP <sup>+</sup> )	1.27	3.0E-01
19270	<i>glnA</i>	glutamate-ammonia ligase	-1.85	2.0E-02
09050	<i>glnA</i>	glutamate-ammonia ligase	1.29	3.1E-01
59130	<i>glnB</i>	nitrogen regulatory protein P-II	1.09	6.5E-01
57460	<i>glnB</i>	nitrogen regulatory protein P-II	1.01	1.0E+00
29150	<i>cphB</i>	cyanophycinase	5.66	6.0E-06
27450	<i>cphB</i>	cyanophycinase	1.04	8.2E-01
27460	<i>cphA</i>	cyanophycin synthetase	-1.08	6.1E-01
10370	<i>cynS</i>	cyanante hydratase	-1.01	1.0E+00
37080	<i>fur</i>	ferric uptake regulation protein	-1.20	1.7E-01
57540	<i>fur</i>	ferric uptake regulation protein	-1.09	4.0E-01
29110	<i>glsF</i>	ferredoxin-dependent glutamate synthase	-1.08	6.1E-01
07560	<i>sltB</i>	NADH-dependent glutamate synthase large subunit	-2.13	1.6E-02
14900	<i>sltD</i>	NADH-dependent glutamate synthase small subunit	-2.48	1.2E-02
13630	<i>sltS</i>	monocomponent sodium-dependent glutamate permease	-1.64	3.3E-03
52690	<i>sltX</i>	glutamyl-tRNA synthetase	-1.50	2.5E-04
36480	<i>nadB</i>	L-aspartate oxidase	1.01	1.0E+00
53960	<i>narB</i>	ferredoxin-nitrate reductase	-1.13	4.5E-01
00310	<i>natA</i>	amino acid transport ATP-binding protein	1.02	8.7E-01
01200	<i>natA</i>	amino acid transport ATP-binding protein	1.01	9.9E-01
00300	<i>natC</i>	amino acid transport system permease protein	-1.00	1.0E+00
02170	<i>natC</i>	amino acid transport system permease protein	1.02	9.3E-01
18410	<i>nirA</i>	ferredoxin-nitrite reductase	-1.65	4.4E-02
14800	<i>nrtA</i>	ABC transporter nitrate-binding protein	-2.00	2.4E-03
14790	<i>nrtB</i>	nitrate/nitrite transport system permease protein	-1.56	5.9E-02
14780	<i>nrtC</i>	nitrate/nitrite transport system ATP-binding protein	-1.68	9.6E-03

14770	<i>nrtD</i>	nitrate/nitrite transport system ATP-binding protein	-1.59	4.7E-04
18880	<i>nrtB</i>	ABC-transporter substrate-binding protein	-1.02	9.9E-01
18890	<i>nrtC</i>	ABC-transporter permease protein	-1.24	3.6E-01
18900	<i>nrtD</i>	ABC-transporter ATP-binding protein	-1.19	4.0E-01
01830	<i>ntcA</i>	global nitrogen regulatory protein Ycf28	-1.09	5.4E-01
46810	<i>speA</i>	arginine decarboxylase	-1.06	7.2E-01
18840	<i>speB</i>	agmatinase	-1.04	8.7E-01
45220	<i>ureA</i>	urease gamma subunit	-1.14	3.3E-01
45230	<i>ureB</i>	urease beta subunit	-1.28	2.7E-02
61330	<i>ureC</i>	urease subunit alpha	1.27	7.8E-02
04510	<i>ureD</i>	urease accessory protein D	-1.21	5.3E-02
41100	<i>ureE</i>	urease accessory protein E	-1.05	7.5E-01
41820	<i>ureF</i>	urease accessory protein F	1.08	4.6E-01
24230	<i>ureG</i>	urease accessory protein G	-1.34	4.6E-03
06220	<i>urtA</i>	ABC-type urea transport system substrate-binding protein	-1.57	4.2E-02
06210	<i>urtB</i>	urea transport system permease protein	-1.11	5.5E-01
06200	<i>urtC</i>	urea transport system permease protein	-1.14	4.6E-01
06190	<i>urtD</i>	urea transport system ATP-binding protein	1.06	8.2E-01
06180	<i>urtE</i>	urea transport system ATP-binding protein	1.01	1.0E+00
25850		amino acid ABC-transporter permease protein	-1.03	8.6E-01
26850		amino-acid ABC-transporter permease protein	1.12	6.8E-01
26840		amino-acid ABC-transporter ATP-binding protein	1.47	7.9E-02
27820		amino acid adenylation	2.86	2.6E-02
32020		amino-acid ABC-transporter permease protein	-1.02	9.4E-01
55930	<i>pipX</i>	PII interaction protein X	-1.33	1.7E-02

**Table S7** Genes involved in phosphorus metabolism and their differential expression in Cluster II (samples from August to October) compared to Cluster I (samples from June and July). Red and blue characters represent those genes significantly ( $|fold\ change| \geq 1.5 \text{ & } P < 0.05$ ) up-regulated and down-regulated, respectively.

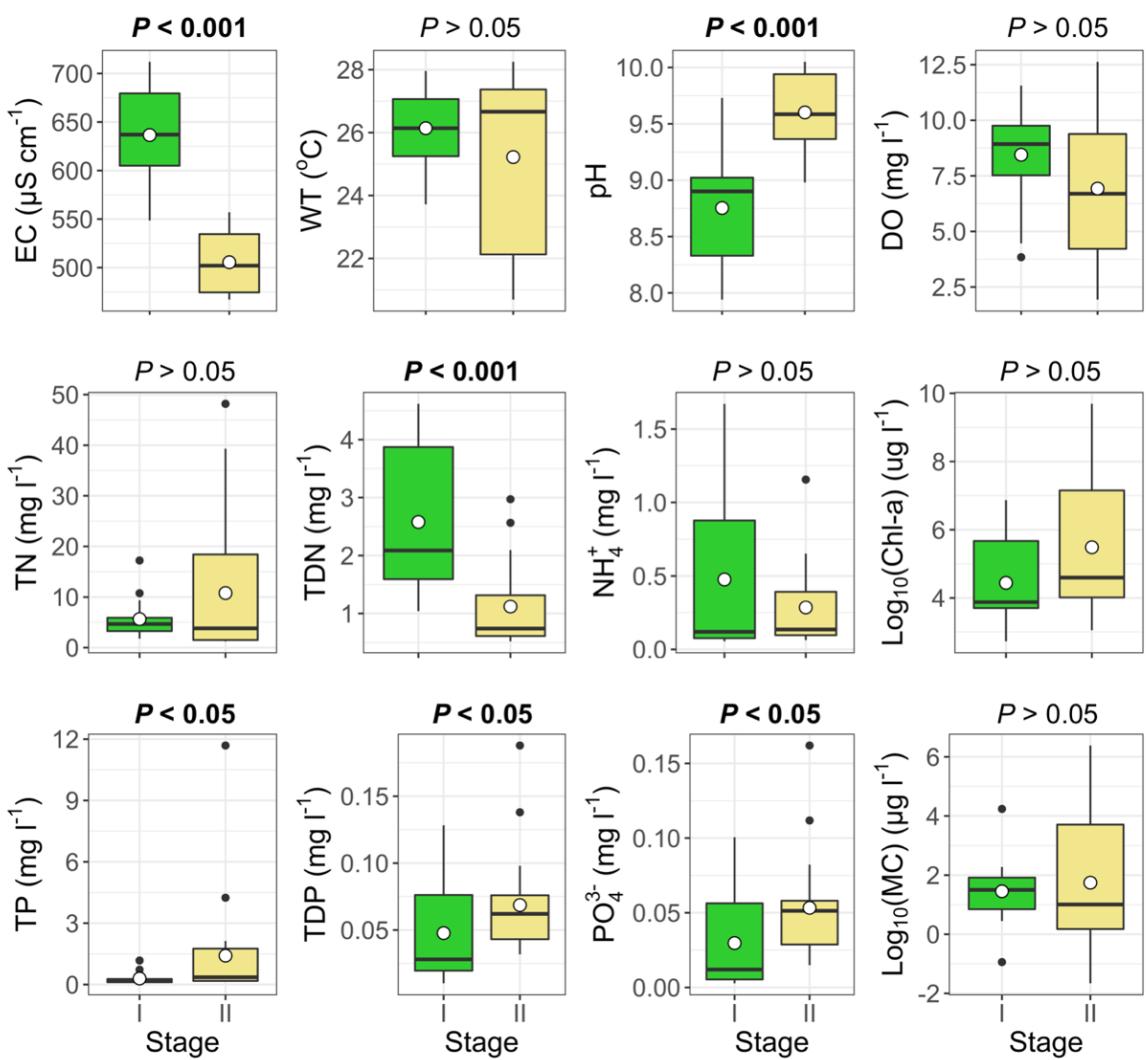
MAE Number	Gene Symbol	Product	Fold change	FDR p-value correction
01300	<i>ppk</i>	polyphosphate kinase	-1.42	1.2E-03
09250	<i>pstB</i>	phosphate ABC transporter ATP-binding protein	1.19	3.2E-01
09260	<i>pstA</i>	phosphate transport system permease protein	-1.14	3.2E-01
09270	<i>pstC</i>	phosphate transport system permease protein	-1.19	3.1E-01
09280	<i>pstS</i>	ABC-transporter periplasmic phosphate-binding protein	-1.14	5.3E-01
09320	<i>phnD</i>	ABC-transporter substrate-binding protein	1.45	4.0E-02
16640		alkaline phosphatase	4.19	2.8E-04
18280	<i>pstA</i>	phosphate transport system permease protein	-1.13	5.8E-01
18290	<i>pstA</i>	phosphate transport system permease protein	-1.10	7.1E-01
18300	<i>pstA</i>	phosphate transport system permease protein	-1.26	2.2E-01
18310	<i>pstS</i>	phosphate-binding periplasmic protein	-5.35	1.0E-08
18340	<i>pstB2</i>	phosphate transport ATP-binding protein	-1.90	8.3E-07
18350	<i>pstB</i>	phosphate transport ATP-binding protein	-1.75	2.0E-05
18360	<i>pstA</i>	phosphate transport system permease protein	-2.05	1.1E-08
18370	<i>pstC</i>	phosphate ABC transporter permease	-1.87	2.8E-06
18380	<i>pstS</i>	phosphate-binding periplasmic protein	-5.16	1.0E-11
18390	<i>sphX</i>	phosphate transport system substrate-binding protein	-2.91	3.2E-09
30190	<i>phoX</i>	alkaline phosphatase	-2.03	1.1E-05
32260	<i>proA</i>	gamma-glutamyl phosphate reductase	-1.01	1.0E+00
32380	<i>pstS</i>	phosphate binding protein PstS homolog	-1.36	2.2E-03
38290		phosphate ABC-transporter periplasmic phosphate-binding protein	5.29	9.2E-07
43330	<i>phoH</i>	<i>phoH</i> -like protein	-1.11	4.9E-01
47020		soluble inorganic pyrophosphatase	-1.30	1.1E-01
50240		alkaline phosphatase-like protein	1.23	2.1E-01
52210	<i>phnZ</i>	metal dependent phosphohydrolase HD region	-1.08	5.5E-01
52630	<i>sphU</i>	creatininase	-1.14	2.5E-01
52640	<i>sphR</i>	response regulator in two-component regulatory system of Pi uptake	1.17	1.9E-01
52650	<i>sphS</i>	two-component sensor histidine kinase	1.04	7.7E-01
52660	<i>phoU</i>	phosphate transport system regulatory protein	-1.02	9.6E-01
53740	<i>ppx</i>	exopolyphosphatase	-1.15	1.7E-01

**Table S8** Genes involved in toxin metabolism and their differential expression in Cluster II (samples from August to October) compared to Cluster I (samples from June and July). Red and blue characters represent those genes significant ( $|fold\ change| \geq 1.5$  &  $P < 0.05$ ) up-regulated and down-regulated, respectively.

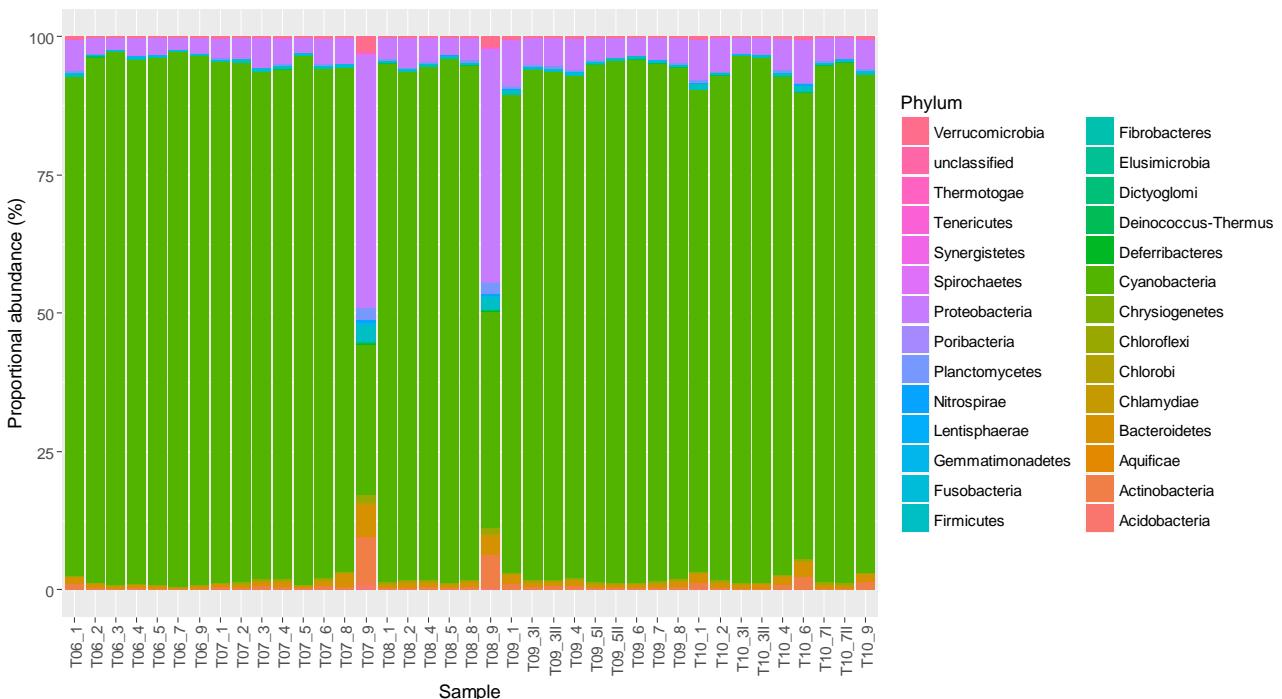
MAE Number	Gene Symbol	Product	Fold change	FDR p-value correction
<i>Microcystin toxin synthesis genes</i>				
38550	<i>mcyC</i>	McyC protein	2.30	9.5E-03
38560	<i>mcyB</i>	McyB protein	2.25	1.2E-02
38570	<i>mcyA</i>	McyA protein	2.24	1.4E-02
38600	<i>mcyD</i>	short-chain dehydrogenase	1.94	4.3E-02
38610	<i>mcyE</i>	thioester reductase	1.86	6.1E-02
38620	<i>mcyF</i>	aspartate racemase	1.94	6.7E-02
38630	<i>mcyG</i>	beta-ketoacyl synthase	1.80	6.7E-02
38640	<i>mcyH</i>	ABC transporter	1.83	8.2E-02
38650	<i>mcyI</i>	dehydrogenase	1.61	2.1E-01
38660	<i>mcyJ</i>	methyltransferase	1.44	3.5E-01
<i>Aeruginosin synthesis genes</i>				
56590	<i>aerA</i>	non-ribosomal peptide synthetase/polyketide synthase hybrid enzyme	-2.34	1.3E-09
56580	<i>aerB</i>	peptide synthetase	-2.09	5.3E-08
56560	<i>aerD</i>	putative aeruginosin synthesis gene	-1.77	7.6E-04
56570	<i>aerK</i>	isopentenyl-dephosphate delta-isomerase	-2.05	1.3E-07
56550	<i>aerE</i>	hypothetical protein	-1.99	1.1E-06
56540	<i>aerF</i>	3-oxoacyl-[acyl-carrier-protein] reductase like	-2.03	5.6E-07
56520	<i>aerG1</i>	non-ribosomal peptide synthetase	-2.00	7.2E-07
56530	<i>aerL</i>	hypothetical protein	-1.39	8.5E-02
56500	<i>aerM</i>	amino acid adenylation participated protein like	-1.48	3.1E-02
56480	<i>aerN</i>	ABC-transporter ATP-binding protein	-1.97	5.2E-08
<i>Microviridin synthesis genes</i>				
59980	<i>mdnA</i>	unknown protein	-2.29	1.1E-08
24100	<i>mdnB</i>	hypothetical protein	-2.46	5.1E-08
24090	<i>mdnC</i>	hypothetical protein	-2.22	8.1E-07
24080	<i>mdnD</i>	acetyltransferase	-1.73	7.4E-05
24070	<i>mdnE</i>	ABC-transporter ATP-binding protein	-1.73	1.5E-06
<i>Cyanopeptolin synthesis genes</i>				
60030	<i>mcnA</i>	synthesis of cyanopeptolin	1.42	1.6E-01
60020	<i>mcnB</i>	McnB protein	1.32	2.5E-01
60010	<i>mcnC</i>	McnC protein	1.30	2.5E-01
60000	<i>mcnE</i>	McnE protein	-1.13	5.8E-01
60060	<i>mcnF</i>	ABC transporter ATP-binding protein	1.10	7.4E-01
60070	<i>mcnG</i>	McnG protein	1.02	1.0E+00

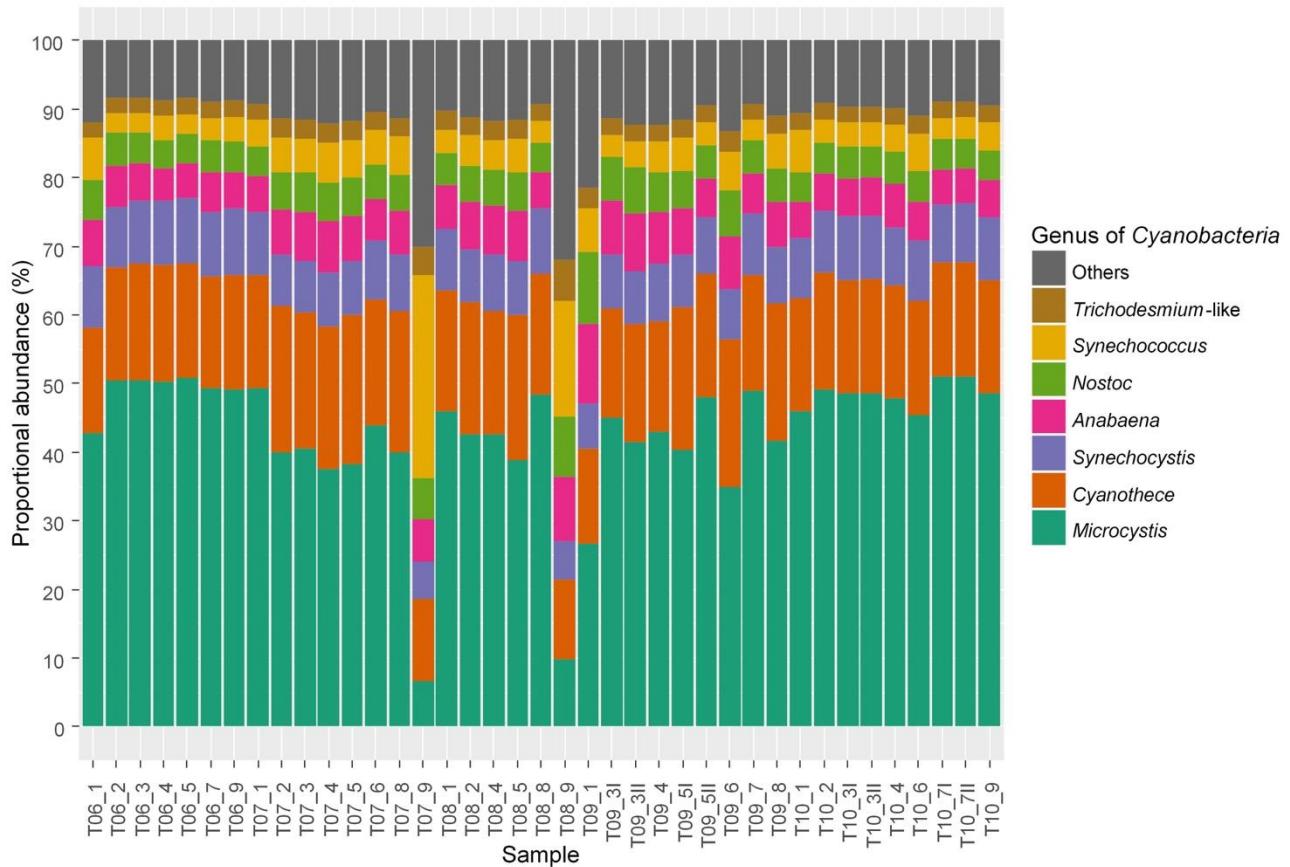
**Table S9** Significantly expressed genes involved in extracellular polysaccharide (EPS) production and export between Cluster II (samples from August to October) and Cluster I (samples from June and July). Red and blue characters represent those genes significant ( $|fold\ change| \geq 1.5$  &  $P < 0.05$ ) up-regulated and down-regulated, respectively.

MAE Number	Gene Symbol	Product	Fold change	FDR p-value correction
02160		glycosyl transferase	1.92	2.1E-04
03140		glycosyl transferase family 1	2.44	1.9E-08
08430		capsular polysaccharide biosynthesis protein	2.73	3.4E-03
10910		lipopolysaccharide (LPS) biosynthesis protein	5.29	2.5E-08
10920	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	3.15	3.9E-05
11050		polysaccharide biosynthesis protein GtrA	5.38	4.7E-06
13210		glycosyl transferase	-2.49	2.5E-11
13220		glycosyl transferase	-1.79	1.3E-06
18140	<i>rfbB</i>	dTDP-glucose 4,6 dehydratase	1.67	1.4E-03
21000		glycosyltransferase	1.71	1.2E-06
24180		glycosyl transferase family 1	13.37	8.9E-06
27990		Porin type major outer membrane protein	-2.29	2.9E-05
29550		glycosyltransferase family 2	3.48	5.5E-06
32710		glycosyl transferase	2.34	3.3E-03
32720		glycosyl transferase family 1	2.80	5.4E-04
32750		glycosyl transferase	1.83	7.6E-04
32850		glycosyl transferase	-2.64	3.2E-05
32860	<i>rfbB</i>	dTDP-glucose 4,6 dehydratase	-2.30	4.5E-04
32920		polysaccharide biosynthesis protein	4.98	5.0E-07
32930		Capsular polysaccharide synthesis enzyme CpsE	6.37	2.0E-07
37750		glycosyl transferase	5.38	1.9E-08
40030		glycosyltransferase	5.56	7.2E-09
41480	<i>cpsF</i>	glucosyl transferase	12.18	1.9E-04
41490		glucosyl transferase	9.67	1.3E-05
41510		glycosyl transferase family 1	6.13	1.4E-03
41520		lipopolysaccharide (LPS) biosynthesis protein	8.00	8.0E-05
41530		glycosyl transferase	6.40	3.4E-04
41540		Polysaccharide biosynthesis protein	6.75	4.4E-06
41550		glucosyl transferase	6.60	7.8E-05
41560		O-antigen polymerase	6.12	7.2E-04
41570		glycosyl transferase family 1	6.35	7.1E-05
41580		hexapeptide transferase	7.21	1.0E-05
41930		glycosyltransferase	5.63	8.2E-10
42550		glycosyltransferase	7.64	2.6E-04
45850		glycosyltransferase	3.59	1.2E-05
46400		Glycosyl transferase family 2	1.70	2.7E-07
46420		Glycosyl transferase family 39	-2.00	6.0E-05
53140		glycosyltransferase family 4 protein	1.94	5.8E-06
55650		glycosyl transferase family A	-2.16	3.6E-08
55700		glycosyl transferase family 1	-1.71	1.2E-04
59490		glycosyl transferase	7.44	4.5E-05
59510		glycosyl transferase	15.14	3.7E-05

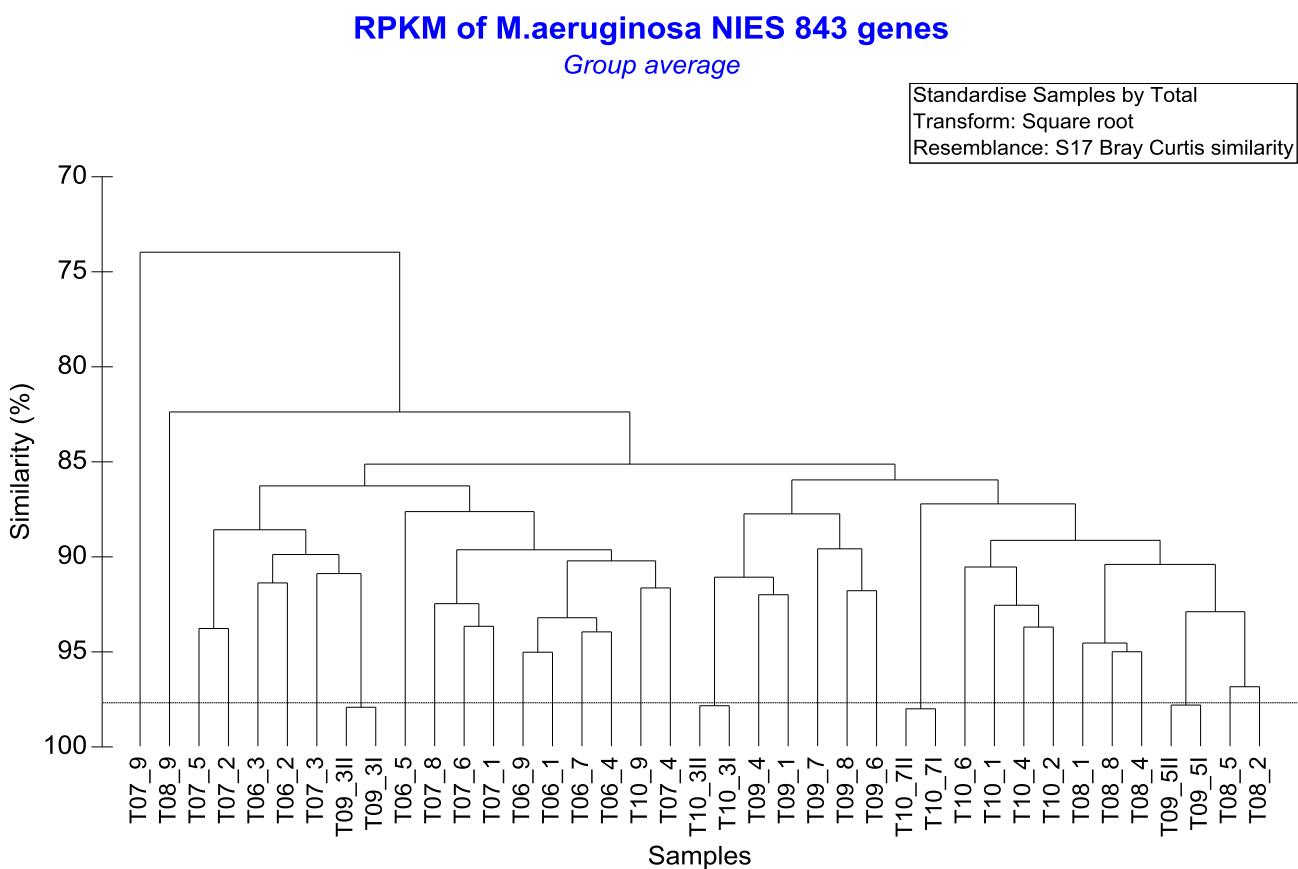


**Figure S1** Boxplot comparing the main environmental parameters between early bloom season (Stage I: June to July) and late bloom season (Stage II: August to October) in Lake Taihu. Non-parametric Kruskal-Wallis rank sum test was used to detect the significance level between the two stages.  $P$  values were listed at the top of each boxplot. EC, electrical conductivity; WT, water temperature; TN, total nitrogen; TDN, total dissolved nitrogen;  $\text{NH}_4^+$ , ammonium; TP, total phosphorus; TDP, total dissolved phosphorus;  $\text{PO}_4^{3-}$ , orthophosphate; Chl-*a*, chlorophyll *a*; MC, microcystin; DO, dissolved oxygen. Horizontal bars and white points in the box plots indicate median and mean values, respectively. Lower and upper edges of the boxes represent the approximate 1<sup>st</sup> and 3<sup>rd</sup> quartiles, respectively. Lower and upper error bar edges indicate the minimum and maximum values, respectively. The points outside the boxes represent outliers. Note: data from samples collected in this study excluding sequencing failed samples.

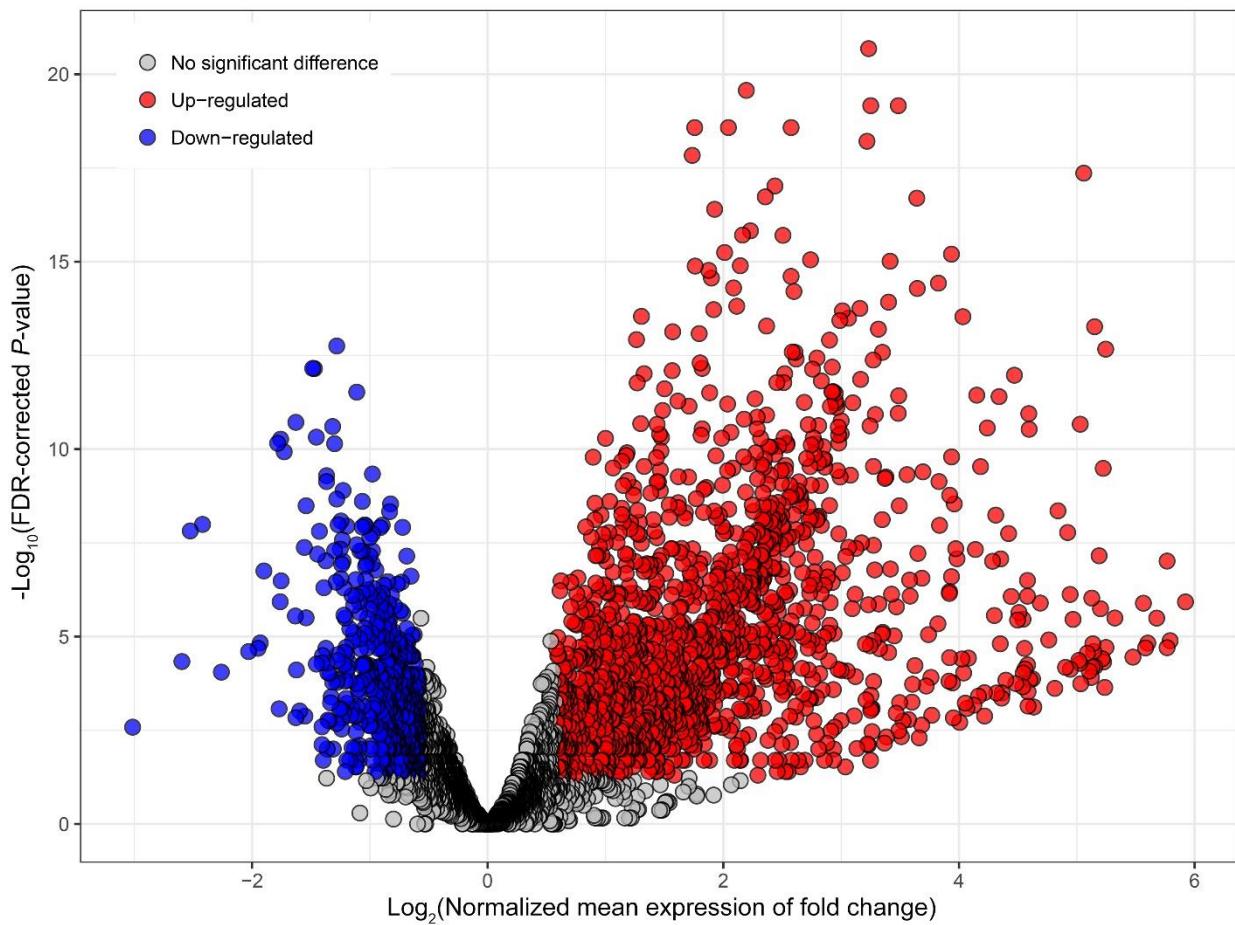
**a****b**

**c**

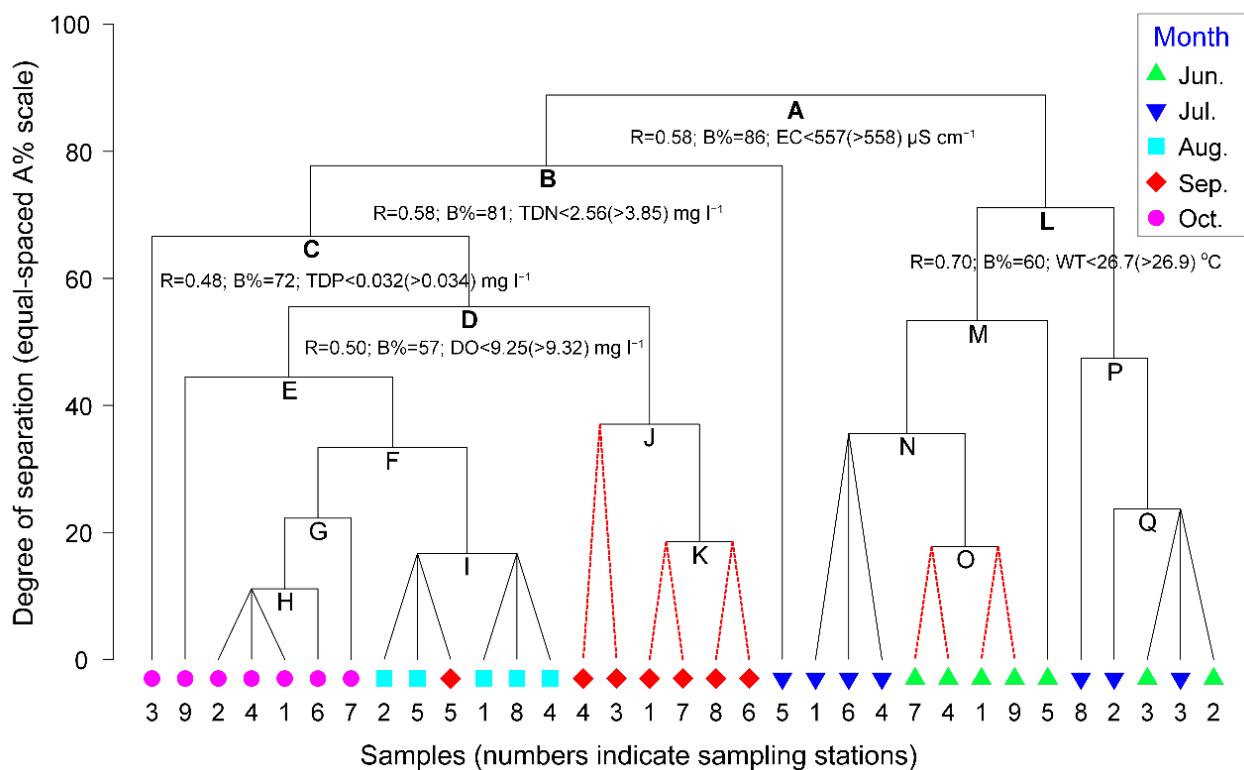
**Figure S2** Overview of community makeup based on transcript abundance at domain (**a**), bacterial phylum level (**b**), and cyanobacterial genus level (**c**, technical replicates were combined). The first letter of each sample name indicates Taihu, the following two numbers indicate months and the last numbers indicate sampling stations.



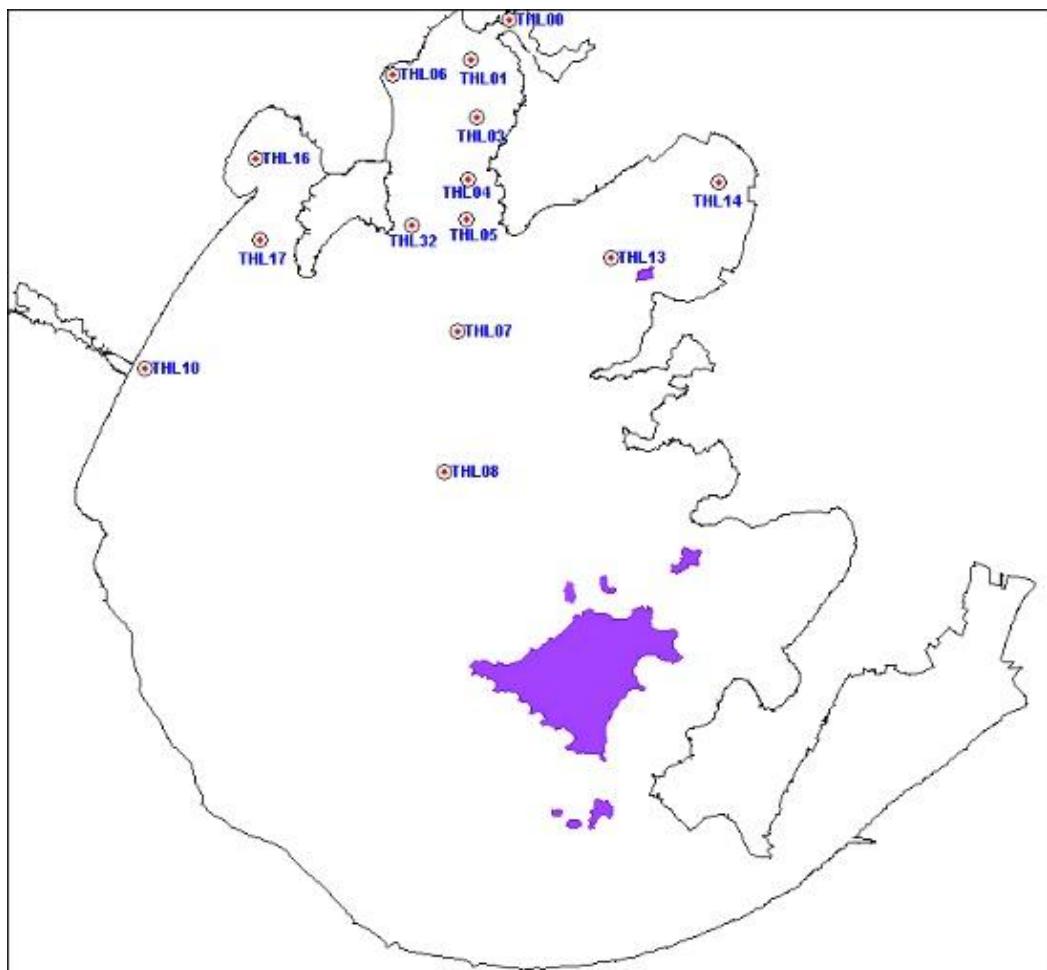
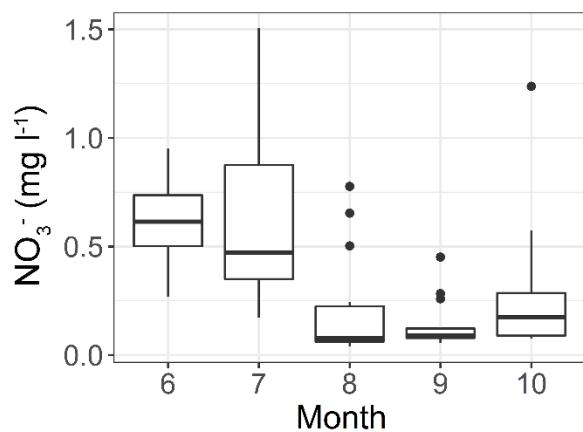
**Figure S3** Cluster analysis of Lake Taihu metatranscriptomics mapped to the genome of *M. aeruginosa* NIES 843. RPKM (Reads Per Kilobase of exon model per Million mapped reads) of each gene were used to generate the plot. Technical replicates showed > 97.7% similarities. Samples T07\_9 and T08\_9 had the most heterogeneity with other samples and were excluded from further analysis.



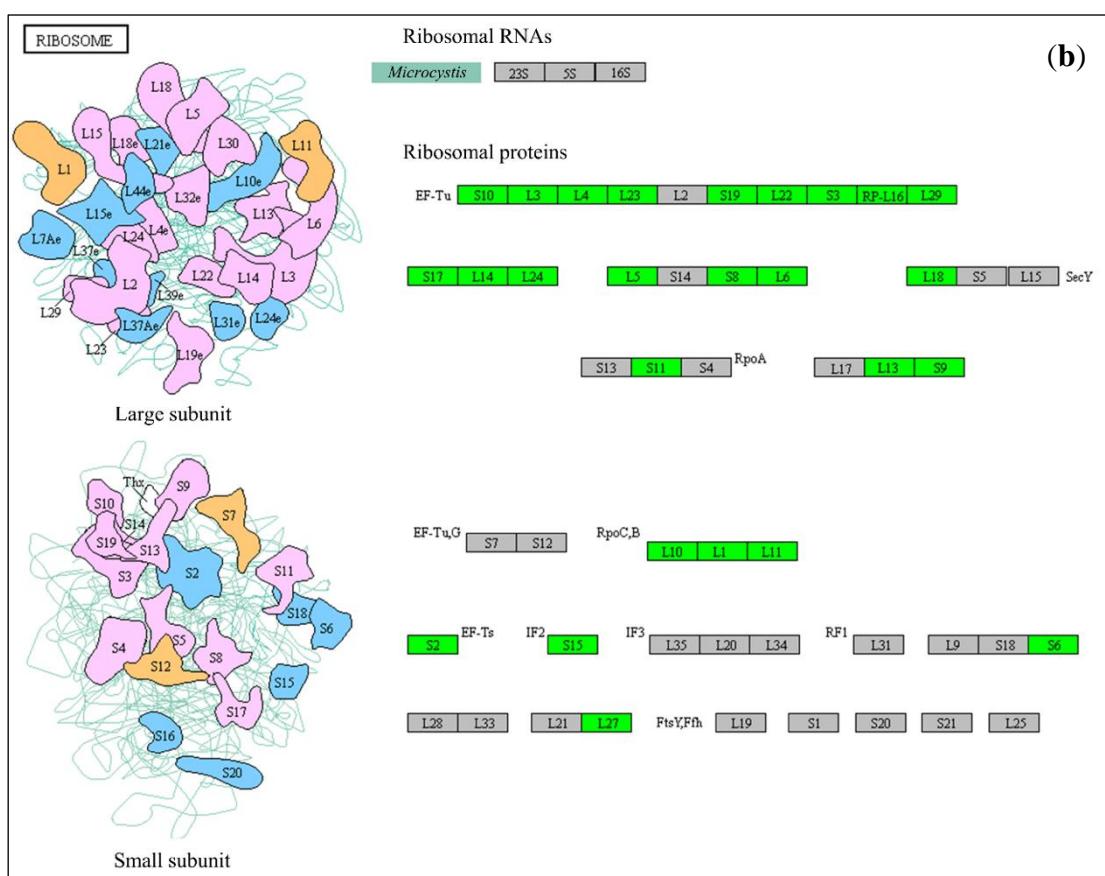
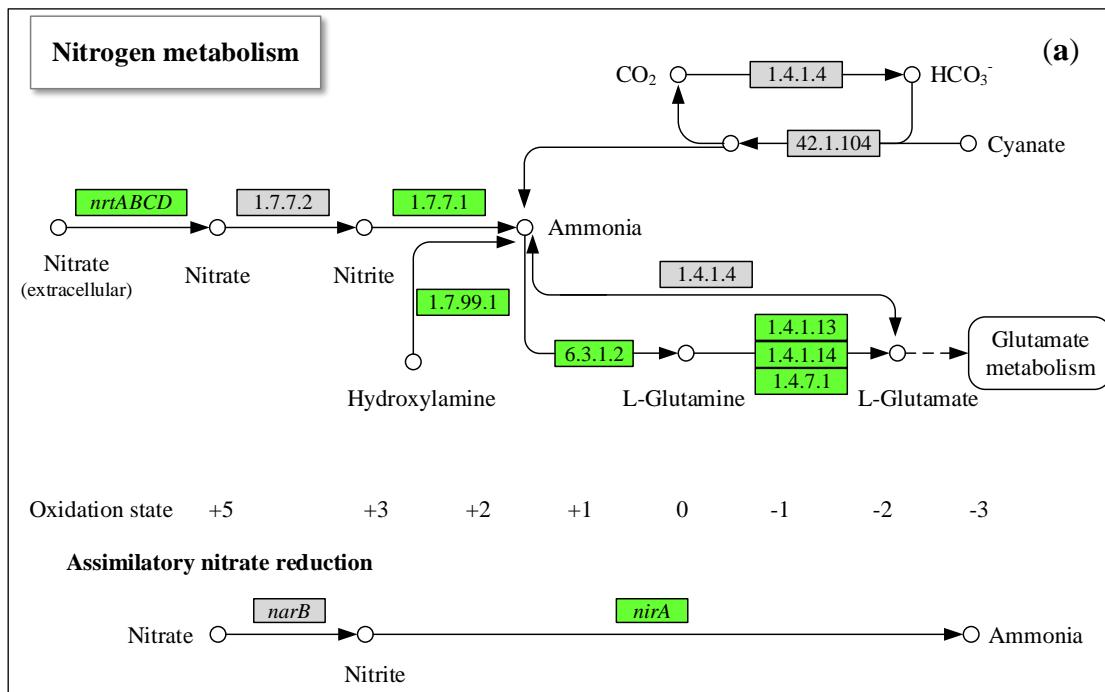
**Figure S4** Volcano plot shows fold changes and corrected  $P$ -value of false discovery rate (FDR) for statistical comparisons between samples in Cluster I (Jun. & Jul. 2014) and in Cluster II (Aug. to Oct. 2014) for *M. aeruginosa* NIES 843 genes. The standards of significantly expressed differential genes are absolute values of fold change  $\geq 1.5$  and FDR-corrected  $P$ -value  $< 0.01$ . In total, there are 1970 genes significantly differentially expressed in which 1425 genes (red points) up-regulated and 545 genes (blue points) down-regulated.



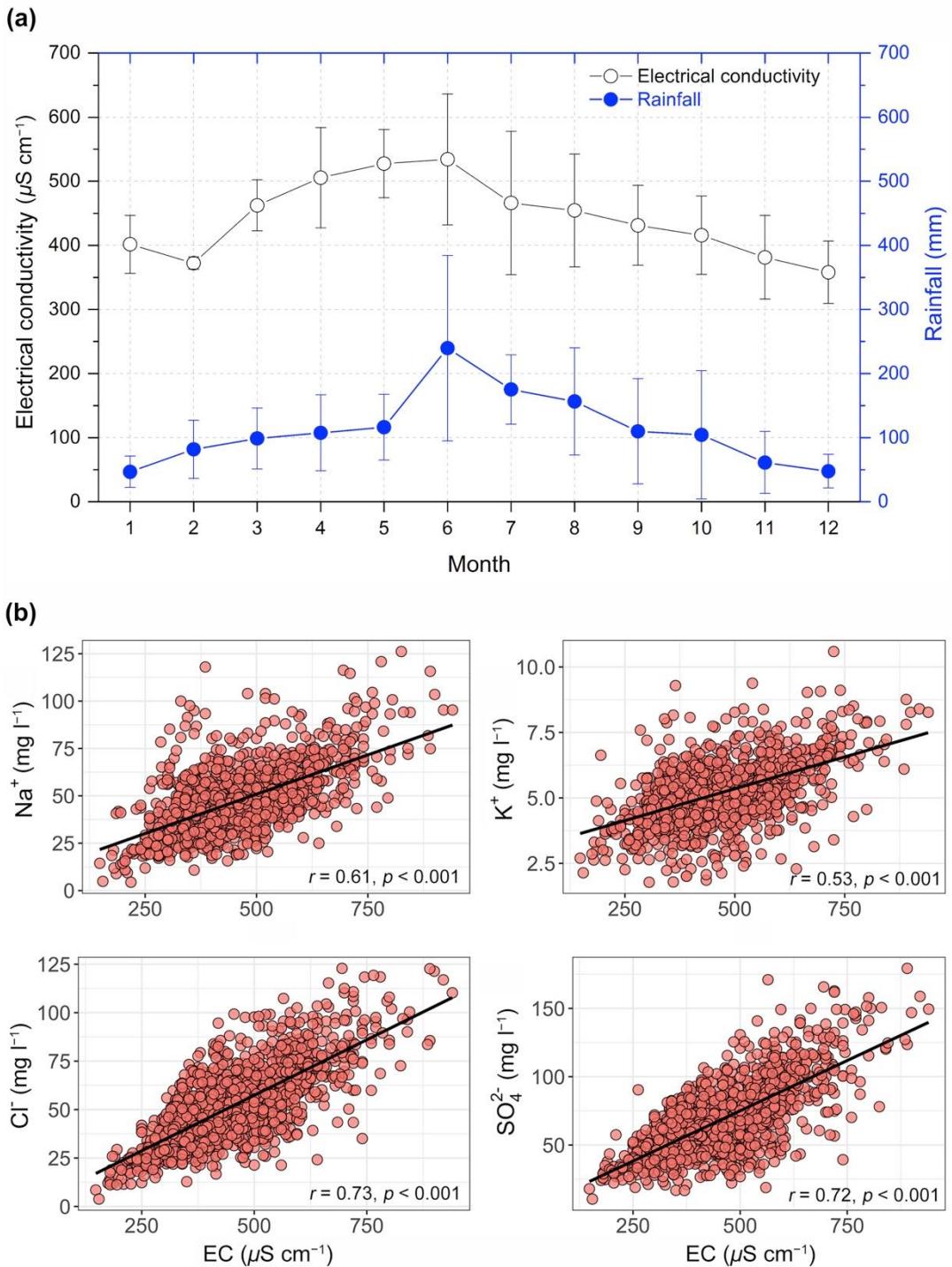
**Figure S5** Linkage tree analysis (LINKTREE) showing clustering of samples based on gene makeup and the environmental parameters. For the binary separation of A-D and L, environmental factor accounting for the clustering to the left are listed first, followed by the factor for the clustering to the right (in parenthesis). R-values were calculated using the analysis of similarity (ANOSIM). The B% indicates the similarity/dissimilarity between grouping: The higher the B%, the greater the dissimilarity between cluster. Red dashed branches indicate insignificant separations (SIMPOF test:  $P > 0.05$ ).



**Figure S6** Boxplot for the concentrations of nitrate ( $\text{NO}_3^-$ ) along months (June to October 2014) in northwest Lake Taihu (upper panel). Data come from monthly monitoring at 14 stations located in northwest Taihu (see the lower panel) conducted by Taihu Laboratory for Lake Ecosystem Research (TLLER).



**Figure S7** KEGG (Kyoto Encyclopedia of Genes and Genomes) map shows gene express patterns of the nitrogen metabolism pathway (**a**) and ribosome pathway (**b**). Green boxes represent significant down-regulation and grey boxes represent insignificant expression of related genes.



**Figure S8 (a)** Dynamics of electrical conductivity (EC) and rainfall in each month in Lake Taihu. Spearman correlation analysis demonstrated a significant positive relationship between the two parameters ( $\rho = 0.81, P = 0.002$ ). **(b)** Relationship between EC and the dissolved anions ( $\text{Na}^+$ ,  $\text{K}^+$ ,  $\text{Cl}^-$ ,  $\text{SO}_4^{2-}$ ). EC and dissolved data (from Jan. 2007 to Jan. 2016) were obtained from Taihu Laboratory for Lake Ecosystem Research (TLLER) and the monthly average rainfall data in surrounding 5 meteorological stations (Wuxi, Yixing, Suzhou, Wujiang and Dongshan) were downloaded from the China Meteorological Data Sharing Service System (<http://cdc.nmic.cn>).