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Genome-wide expression analysis of environmental stress in the cyanobacterium *Synechocystis* PCC 6803

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Appendices

Note: Appendix numbers correspond to the chapters where the data are discussed

Appendix 2A. Genes significantly up-regulated after an 8 h salt stress treatment. Log ratios are expressed as $^2\log(I_{\text{salt}}/I_{\text{control}})$, where I_{salt} and I_{control} are the signal intensities of the salt-stressed sample and control sample, respectively.

Gene	Description	p-value	log ratio
slr1728	potassium-transporting P-type ATPase A chain	1.53E-12	1.761
slI1862	unknown protein	3.44E-09	3.145
slI1863	unknown protein	5.22E-09	3.139
sml0013	hypothetical protein	4.79E-07	0.812
slr1730	potassium-transporting P-type ATPase C chain	1.69E-06	0.892
slr0250	hypothetical protein	2.69E-06	0.838
slI1525	phosphoribulokinase	3.29E-06	0.831
slI0553	hypothetical protein	3.45E-06	0.833
ssr2857	mercuric transport protein periplasmic component precursor	4.46E-06	0.660
slI1483	periplasmic protein, similar to transforming growth factor induced protein	7.02E-06	1.292
slr0923	hypothetical protein YCF65	1.21E-05	0.446
slr0974	initiation factor IF-3	1.38E-05	0.443
slI0470	hypothetical protein	1.67E-05	0.618
slr1550	lysyl-tRNA synthetase	1.86E-05	1.372
slI0169	cell division protein Ftn2 homolog	2.40E-05	1.118
slI0517	putative RNA binding protein	2.80E-05	1.032
ssl2615	ATP synthase C chain of CF(0)	3.05E-05	0.446
ssl3076	unknown protein	3.52E-05	0.679
ssl3335	preprotein translocase SecE subunit	4.50E-05	0.540
slI1803	50S ribosomal protein L22	5.56E-05	0.601
ssr2912	unknown protein	5.97E-05	0.736
slI1329	inositol monophosphate family protein	6.22E-05	0.763
slr1599	hypothetical protein	7.12E-05	0.206
ssl1426	50S ribosomal protein L35	7.63E-05	0.510
slI0319	periplasmic protein, function unknown	7.77E-05	0.820
slI1799	50S ribosomal protein L3	0.00011	0.512
slI0554	ferredoxin-thioredoxin reductase, catalytic chain	0.00011	0.856
slr1729	potassium-transporting P-type ATPase B chain	0.00013	0.867
slr0287	hypothetical protein	0.00013	0.434
slI1426	unknown protein	0.00014	0.601
slr0083	RNA helicase Light	0.00017	0.667
slI1450	nitrate/nitrite transport system substrate-binding protein	0.00021	0.679
slr1608	putative glucose dehydrogenase-B, periplasmic protein	0.00022	0.798
ssr2142	hypothetical protein YCF19	0.00023	0.893
slI1443	CTP synthetase	0.00023	0.925
slr0322	two-component hybrid sensor and regulator	0.00028	0.947
slr1277	pilus assembly protein homologous to general secretion pathway protein D	0.00032	0.844
slI1121	hypothetical protein	0.00036	0.846
slr1971	hypothetical protein	0.00048	0.595
ssr1251	hypothetical protein	0.00052	0.239
slI1752	hypothetical protein	0.00057	0.600
slI0450	cytochrome b subunit of nitric oxide reductase	0.00057	0.545
slr1672	glycerol kinase	0.00058	0.376
slI1980	thiol:disulfide interchange protein TrxA	0.00058	0.545
slr1301	hypothetical protein	0.00060	0.522
slr0542	ATP-dependent protease ClpP	0.00064	0.297
slI1590	two-component sensor histidine kinase	0.00070	0.684
slr0967	hypothetical protein	0.00075	1.130
slr1991	adenylate cyclase	0.00081	0.734
slr1895	hypothetical protein	0.00082	0.384
slI1414	hypothetical protein	0.00085	0.319
slI1070	transketolase	0.00086	0.901

slr0581	unknown protein	0.00088	1.317
slI1679	periplasmic protease HhoA	0.00089	0.403
slr0082	hypothetical protein	0.00093	0.409
slr0689	hypothetical protein	0.00095	0.355
slI0108	ammonium/methylammonium permease	0.00106	0.607
ssl1762	hypothetical protein	0.00108	1.270
slI0549	hypothetical protein	0.00121	0.439
slI1217	unknown protein	0.00129	0.370
ssl2245	unknown protein	0.00147	0.780
ssr2194	unknown protein	0.00148	1.535
slr1877	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	0.00157	0.367
slr1923	hypothetical protein	0.00163	0.597
slI1933	DnaJ protein, heat shock protein 40, molecular chaperone	0.00168	0.608
slI0767	50S ribosomal protein L20	0.00170	0.452
slr0038	hypothetical protein	0.00171	0.358
slI1633	cell division protein FtsZ	0.00174	0.453
slI1702	hypothetical protein YCF51	0.00178	0.481
slI1824	50S ribosomal protein L25	0.00183	0.644
slr1113	ATP-binding protein of ABC transporter	0.00191	0.637
slr0364	hypothetical protein	0.00208	1.062
slI1491	periplasmic WD-repeat protein	0.00214	0.466
slr1756	glutamate--ammonia ligase	0.00222	0.552
slr1459	phycobilisome core component	0.00228	1.108
slr2067	allophycocyanin alpha subunit	0.00246	0.660
slI1665	unknown protein	0.00253	0.173
slI1095	hypothetical protein	0.00256	0.994
ssr2153	unknown protein	0.00282	1.084
slr0073	two-component sensor histidine kinase	0.00287	0.225
ssr0482	30S ribosomal protein S16	0.00287	0.615
slr0971	hypothetical protein	0.00296	0.703
smr0011	50S ribosomal protein L34	0.00296	0.378
slr2046	unknown protein	0.00301	0.769
slr1694	expression activator appA homolog	0.00306	0.732

Appendix 2B. Genes significantly down-regulated after an 8 h salt stress treatment. Log ratios are expressed as ${}^2\log(I_{\text{salt}}/I_{\text{control}})$, where I_{salt} and I_{control} are the signal intensities of the salt-stressed sample and control sample, respectively.

Gene	Description	p-value	log ratio
slI0856	RNA polymerase ECF-type (group 3) sigma-E factor	1.20E-09	-1.746
slr0473	cyanobacterial phytochrome 1, two-component sensor histidine kinase	1.91E-08	-1.378
slr1667	hypothetical protein (target gene of sycrp1)	2.35E-08	-2.259
slr1668	periplasmic protein, function unknown (target gene of sycrp1)	3.31E-08	-1.837
slI0858	hypothetical protein	3.66E-08	-1.794
slI0573	carbamate kinase	3.05E-07	-1.532
slr0378	similar to 7-beta-(4-carboxybutanamido)cephalosporanic acid acylase	8.49E-07	-1.015
slr0474	two-component response regulator for phytochrome 1 (Cph1)	1.07E-06	-0.753
slI1514	16.6 kDa small heat shock protein, molecular chaperone	3.36E-06	-1.657
slr0146	hypothetical protein	3.36E-06	-1.492
slr0587	unknown protein	5.68E-06	-1.363
slI0857	unknown protein	6.40E-06	-1.237
slI1543	hypothetical protein	7.05E-06	-0.432
slr0376	hypothetical protein	7.21E-06	-1.135
slI0170	DnaK protein 2, heat shock protein 70, molecular chaperone	8.72E-06	-1.271
slI1515	glutamine synthetase inactivating factor IF17	9.20E-06	-1.678
slr2075	10kD chaperonin	1.14E-05	-1.049
slI0254	probable phytoene dehydrogenase Rieske iron-sulfur component	1.30E-05	-0.256
slr0226	unknown protein	2.01E-05	-0.779
ssl2999	hypothetical protein	2.85E-05	-0.223
slr1928	type 4 pilin-like protein	3.67E-05	-1.041
slr0147	hypothetical protein	5.01E-05	-1.197
slI1712	DNA binding protein HU	5.88E-05	-0.744
slr1299	UDP-glucose dehydrogenase	5.93E-05	-0.547
slI1694	pilin polypeptide PilA1	7.54E-05	-0.662
slr1159	glycinamide ribonucleotide synthetase	9.15E-05	-0.415

slr1291	NADH dehydrogenase subunit 4	9.69E-05	-0.295
ssr0692	hypothetical protein	0.0001239	-1.883
slr2051	phycobilisome rod-core linker polypeptide	0.0001321	-0.997
slr1597	chromosome partitioning ATPase, ParA family	0.0001546	-0.525
slr1232	unknown protein	0.0002230	-0.994
slr1152	hypothetical protein	0.0002610	-0.674
slI1577	phycocyanin beta subunit	0.0003019	-0.867
slr0233	thioredoxin M	0.0003157	-0.498
slr0891	N-acetylmuramoyl-L-alanine amidase	0.0003188	-0.432
slr0151	unknown protein	0.0003234	-0.930
slr0888	hypothetical protein	0.0003240	-0.830
slr1545	RNA polymerase ECF-type (group 3) sigma-E factor	0.0003501	-0.803
slr0518	similar to alpha-L-arabinofuranosidase B	0.0003664	-0.798
slI0891	malate dehydrogenase	0.0003779	-0.628
ssl1911	glutamine synthetase inactivating factor IF7	0.0003844	-1.308
slI0788	hypothetical protein	0.0004979	-0.808
slr0476	unknown protein	0.0007974	-0.585
slr0149	hypothetical protein	0.0008240	-1.138
slr1634	hypothetical protein	0.0008508	-0.862
slr0374	hypothetical protein	0.0009220	-0.923
slr0144	hypothetical protein	0.0010287	-1.176
slr1072	GDP-D-mannose dehydratase	0.0011946	-0.408
slr1077	probable glycosyltransferase	0.0012576	-0.497
slr1076	probable glycosyltransferase	0.0013852	-0.285
slI1905	two-component hybrid sensor and regulator	0.0014837	-0.467
slr0191	amidase enhancer, periplasmic protein	0.0014983	-0.481
slr1070	unknown protein	0.0015003	-0.324
slr0599	serine/threonine kinase	0.0015663	-0.619
slr1119	hypothetical protein	0.0016232	-0.282
slr1584	two-component transcription regulator OmpR subfamily	0.0016382	-0.493
ssr3129	unknown protein	0.0016978	-0.766
slr1929	type 4 pilin-like protein	0.0018153	-0.789
slI1580	phycobilisome rod linker polypeptide	0.0018156	-0.980
slI0423	hypothetical protein	0.0020306	-0.278
slr1546	hypothetical protein	0.0024599	-0.347
slI0242	unknown protein	0.0026109	-0.445
slr1074	unknown protein	0.0027282	-0.291
slI0737	hypothetical protein	0.0029695	-0.171

Appendix 3. Matlab code for normalization of microarray data using the Generalized Extreme Value distribution

```

%% load values
load data.txt
a=log(data); b1=sort(a);
notSaturated=(a<=(log(2^16)*0.99));
saturated=~notSaturated;
numNotSat=sum(notSaturated);
%% fit extreme value distribution
for i=1:n
    parm(i,:)=gevfit(a(:,i));
    [parm(i,:) cis]=mle(a(:,i),'censoring',saturated(:,i),'pdf',@pdfun, ...
        'cdf',@cdfun,'start',parm(i,),'lower',[-Inf,0,-Inf]);
    ciu(i,:)=cis(1,:);
    cil(i,:)=cis(2,:);
    k(i)=parm(i,1);
    s(i)=parm(i,2);
    m(i)=parm(i,3);
end
%% Calculate underlying uniform distribution
for i=1:n
    r=(a(:,i)-m(i))/s(i);
    u(:,i)=exp(-(r*(k(i))+1).^(-1/k(i)));
    u(logical(u==0))=1e-16;
end
%% Return to a common gev distribution
k1=-0.1;
aNew=(-log(u)).^(-k1) - 1) ./ k1;
%% Rescale
mt=-2.5961.*k1+6.2262;
st=-1.6832.*k1+0.8047;
for i=1:n
    aNew(:,i)=(aNew(:,i).*st)+mt;
end
aNew2=aNew;
%% Deal with saturated values
maxT=log(2.^16);
aNew(aNew>log(2.^16))=log(2.^16); aNew2=aNew;
b3=sort(aNew);
maxu=max(u,[ ],1);
numSaturated=(8091-(maxu.*8091));
numSaturated=floor(numSaturated);
% numSaturated=floor(numSaturated./(0.7869.*k(i)+0.7669));
maxSaturated=max(aNew,[ ],1);
for i=1:n
    mins=b3(8091-numSaturated(i)+1,i);
    maxs=maxSaturated(i);
    if mins<maxs
        slope=(maxT-mins)/(maxs-mins);
    elseif mins==maxs
        slope=0;
    end
    in=mins-slope.*mins;
    datos=aNew(:,i);
    %size(find(datos>=mins))
    datos(datos>=mins)=datos(datos>=mins).*slope+in;
    aNew(:,i)=datos;
end

```

Appendix 4A. Significantly up-regulated genes of *Synechocystis* PCC 6803 after 12 hours nitrogen starvation. This hardcopy presents only a short excerpt with genes showing a greater than two-fold expression change. The complete Appendix is available in electronic format upon request from the corresponding author (J.C.P.Matthijs@uva.nl).

ORF	Fold Change	p-value	Description
slr0376	27.42397	8.1X10 ⁻¹³	hypothetical protein
ssl0453	23.16692	0.001148	phycobilisome degradation protein NblA
ssl0452	15.16974	1.19X10 ⁻¹⁴	phycobilisome degradation protein NblA
slI0783	14.65579	3.42X10 ⁻⁰⁹	unknown protein
ssl2501	8.795469	8.21X10 ⁻¹¹	unknown protein
slr0373	7.147664	1.53X10 ⁻⁷	hypothetical protein
slI1450	6.442441	9.07X10 ⁻¹⁴	nitrate/nitrite transport system substrate-binding protein
slr1594	5.111636	2.22X10 ⁻¹⁶	two-component response regulator PatA subfamily
ssl1633	4.887583	< 1X10 ⁻¹⁶	high light-inducible polypeptide HliC,
slI0108	3.614831	4.18X10 ⁻⁶	ammonium/methylammonium permease
slI0733	3.504509	1.94X10 ⁻¹¹	unknown protein
slr1770	3.498066	1.27X10 ⁻⁹	hypothetical protein
ssl1762	3.382045	1.05X10 ⁻⁵	hypothetical protein
slI1951	3.322943	0.000192	unknown protein
ssl2507	3.303521	2.09X10 ⁻¹³	unknown protein
slI0785	3.247742	3.98X10 ⁻⁹	unknown protein
slI0784	3.091371	1.98X10 ⁻¹²	nitrilase
slr1593	3.040396	1.25X10 ⁻⁸	hypothetical protein
slI1081	3.029845	< 1X10 ⁻¹⁶	ABC transport system permease protein
slr1829	2.946513	1.25X10 ⁻¹⁴	putative poly(3-hydroxyalkanoate) synthase component
ssl1464	2.92076	5.42X10 ⁻¹²	unknown protein
slr1681	2.91162	3.57X10 ⁻⁵	unknown protein
slr1612	2.907198	8.44X10 ⁻¹⁴	hypothetical protein
ssl2502	2.903453	1.09X10 ⁻⁶	unknown protein
slr1136	2.846265	< 1X10 ⁻¹⁶	cytochrome c oxidase subunit II
slr0447	2.768354	9.4X10 ⁻¹²	periplasmic protein, ABC-type urea transport system
slI1225	2.754024	7.06X10 ⁻¹³	unknown protein
slr2073	2.746935	3.79X10 ⁻⁸	hypothetical protein YCF50
slr1618	2.66344	2.96X10 ⁻¹²	unknown protein
slI0172	2.605065	3.5X10 ⁻⁹	periplasmic protein, function unknown
slI0764	2.603335	< 1X10 ⁻¹⁶	urea transport system ATP-binding protein
ssr1768	2.580212	4.88X10 ⁻¹⁵	unknown protein
slr0374	2.573481	6.38X10 ⁻¹⁴	hypothetical protein
slI0173	2.572301	2.3X10 ⁻¹²	virginiamycin B hydrolase, periplasmic protein
slI0786	2.552056	6.49 X10 ⁻⁹	unknown protein
slI1009	2.54134	2.32 X10 ⁻⁷	unknown protein
slr1616	2.505452	3.23 X10 ⁻¹²	unknown protein
slI1222	2.501552	9.99 X10 ⁻¹⁶	hypothetical protein
slI1486	2.48235	3.46 X10 ⁻⁵	hypothetical protein
slI1223	2.479596	< 1X10 ⁻¹⁶	diaphorase subunit of the bidirectional hydrogenase
slI0330	2.453818	1.24X10 ⁻¹⁴	sepiapterine reductase
ssl0707	2.446056	< 1X10 ⁻¹⁶	nitrogen regulatory protein P-II
slr1611	2.432113	5.54 X10 ⁻¹³	hypothetical protein
slr0898	2.430799	9.66 X10 ⁻¹⁵	ferredoxin--nitrite reductase
slr1614	2.421516	2.36 X10 ⁻⁸	hypothetical protein
ssr1766	2.39424	2.41 X10 ⁻¹³	hypothetical protein
slr1119	2.392343	1.15 X10 ⁻⁶	hypothetical protein
slr1841	2.343007	0.000241	probable porin; major outer membrane protein
slr1063	2.320785	3.33 X10 ⁻¹⁵	probable glycosyltransferase
slr0645	2.315768	1.17 X10 ⁻⁶	hypothetical protein
slr1912	2.290248	2.02 X10 ⁻⁷	putative PP2C-type protein phosphatase
slI1714	2.284477	7 X10 ⁻¹⁰	unknown protein

slr1138	2.273957	0.000153	cytochrome c oxidase subunit III
slr0337	2.263797	0.000151	hypothetical protein
slr2030	2.257654	0.000499	hypothetical protein
slI1271	2.251258	1.89X10 ⁻¹²	probable porin; major outer membrane protein
slr1065	2.24818	< 1X10 ⁻¹⁶	probable glycosyltransferase
slr0981	2.240534	2.84 X10 ⁻¹²	hypothetical protein
slI0888	2.233621	1.78 X10 ⁻¹⁵	hypothetical protein
slr0288	2.206711	2.2 X10 ⁻¹⁰	glutamate--ammonia ligase
slr0899	2.18024	3.59 X10 ⁻¹³	cyanate lyase
slr1185	2.163183	0.000256	cytochrome b6-f complex alternative iron-sulfur subunit
slI0982	2.162904	1.63 X10 ⁻¹³	unknown protein
slI1895	2.160202	3.78 X10 ⁻¹⁰	hypothetical protein
slr0740	2.151307	1.37 X10 ⁻⁹	hypothetical protein
slI1102	2.132171	9.92 X10 ⁻⁹	iprotein (small) of TRAP-type permease, glutamate transport GtrA
slr1062	2.129276	1.17 X10 ⁻⁶	unknown protein
slr1074	2.125426	2.62 X10 ⁻⁵	unknown protein
slI1201	2.122075	1.86 X10 ⁻⁵	hypothetical protein
slr1814	2.11976	4.06 X10 ⁻⁹	hypothetical protein
sml0013	2.110632	2.12 X10 ⁻¹¹	hypothetical protein
slI1330	2.097191	2.65 X10 ⁻¹²	two-component system response regulator OmpR subfamily
slr1619	2.094438	6.16 X10 ⁻⁸	hypothetical protein
slr1069	2.088911	1.09 X10 ⁻¹²	hypothetical protein
slr1367	2.087603	7.42 X10 ⁻¹¹	glycogen phosphorylase
slr1137	2.084174	2 X10 ⁻¹⁵	cytochrome c oxidase subunit I
slr1830	2.082989	8.04 X10 ⁻¹²	poly(3-hydroxyalkanoate) synthase
slI0536	2.073383	4.28 X10 ⁻¹¹	probable potassium channel protein
slI1396	2.064936	3.31X10 ⁻¹²	unknown protein
slI0185	2.055931	6.79 X10 ⁻⁹	hypothetical protein
slr1081	2.055825	2.1 X10 ⁻¹²	hypothetical protein
slr1712	2.049725	1.38 X10 ⁻¹⁰	hypothetical protein
slr0851	2.048345	9.45 X10 ⁻⁶	type 2 NADH dehydrogenase
slI1272	2.034291	1.47 X10 ⁻¹⁰	unknown protein
slr0980	2.031233	4.64 X10 ⁻⁹	hypothetical protein
slI1634	2.011683	5.35 X10 ⁻⁹	hypothetical protein
slI0266	2.011562	4.19 X10 ⁻¹⁰	unknown protein
slI1774	2.005579	1.59 X10 ⁻⁸	hypothetical protein
slI2008	2.0045	8.88 X10 ⁻¹⁶	processing peptase
ssr1966	2.002705	1.97 X10 ⁻⁶	hypothetical protein
slI1451	2.000408	1.32 X10 ⁻⁹	nitrate/nitrite transport system permease protein

Appendix 4B. Significantly down-regulated genes of *Synechocystis* PCC 6803 after 12 hours nitrogen starvation. This hardcopy presents only a short excerpt with genes showing a greater than two-fold expression change. The complete Appendix is available in electronic format upon request from the corresponding author (J.C.P.Matthijs@uva.nl).

ORF	Fold Change	p-value	Description
slI1579	-17.7103	< 1X10 ⁻¹⁶	phycobilisome rod linker polypeptide
slI1577	-17.2	< 1X10 ⁻¹⁶	phycocyanin beta subunit
slI1578	-12.9971	1.11 X10 ⁻¹²	phycocyanin alpha subunit
slI1580	-10.3192	< 1X10 ⁻¹⁶	phycobilisome rod linker polypeptide
ssl3093	-8.51079	3.33 X10 ⁻¹⁶	phycobilisome small rod linker polypeptide
slr2067	-8.41963	2.33 X10 ⁻¹⁵	allophycocyanin alpha subunit
ssr1038	-8.27502	2.47 X10 ⁻¹²	unknown protein
slr0737	-7.72113	5 X10 ⁻¹⁵	photosystem I subunit II
slI0427	-7.45961	< 1X10 ⁻¹⁶	photosystem II manganese-stabilizing polypeptide
slI0253	-7.38566	7.11X10 ⁻¹⁵	hypothetical protein
slr1986	-6.55384	1.79X10 ⁻¹⁴	allophycocyanin beta subunit
ssl0563	-6.33784	7.61X10 ⁻¹¹	photosystem I subunit VII

slr0009	-5.84948	7.77X10 ⁻¹⁶	ribulose biphosphate carboxylase large subunit
slr1655	-5.45801	< 1X10 ⁻¹⁶	photosystem I subunit XI
slr0012	-5.36463	1.5X10 ⁻¹²	ribulose biphosphate carboxylase small subunit
ssr3383	-5.35113	< 1X10 ⁻¹⁶	phycobilisome small core linker polypeptide
smr0004	-5.13944	3.46X10 ⁻⁸	photosystem I subunit VIII
ssl3432	-4.8292	< 1X10 ⁻¹⁶	30S ribosomal protein S19
ssr1251	-4.80555	< 1X10 ⁻¹⁶	hypothetical protein
ssr0692	-4.79701	1.01X10 ⁻¹¹	hypothetical protein
slr1835	-4.70261	6.1X10 ⁻¹⁰	P700 apoprotein subunit Ib
ssl3437	-4.67323	< 1X10 ⁻¹⁶	30S ribosomal protein S17
slil1745	-4.6315	< 1X10 ⁻¹⁶	50S ribosomal protein L10
slil1808	-4.61624	< 1X10 ⁻¹⁶	50S ribosomal protein L5
slil1799	-4.43872	1.5X10 ⁻¹⁴	50S ribosomal protein L3
slil1804	-4.3876	< 1X10 ⁻¹⁶	30S ribosomal protein S3
slil1801	-4.38211	< 1X10 ⁻¹⁶	50S ribosomal protein L23
slr1834	-4.35306	1.6X10 ⁻⁹	P700 apoprotein subunit Ia
ssr2831	-4.28783	1.56X10 ⁻¹²	photosystem I subunit IV
slr0335	-4.26981	< 1X10 ⁻¹⁶	phycobilisome core-membrane linker polypeptide
slil1805	-4.13067	< 1X10 ⁻¹⁶	50S ribosomal protein L16
slil1746	-4.1193	1.11X10 ⁻¹⁶	50S ribosomal protein L12
slil1803	-4.00174	< 1X10 ⁻¹⁶	50S ribosomal protein L22
slil1809	-3.82243	< 1X10 ⁻¹⁶	30S ribosomal protein S8
slr0011	-3.75236	6.66X10 ⁻¹⁶	possible Rubisco chaperonin
slr1802	-3.7518	1.11X10 ⁻¹⁶	50S ribosomal protein L2
slr1634	-3.69095	0.000679	hypothetical protein
slr2051	-3.65484	1.96X10 ⁻⁹	phycobilisome rod-core linker polypeptide
ssl2615	-3.64508	7.12X10 ⁻¹¹	ATP synthase C chain of CF(0)
slil1327	-3.62445	< 1X10 ⁻¹⁶	ATP synthase gamma chain
slil1028	-3.58772	< 1X10 ⁻¹⁶	carbon dioxide concentrating mechanism protein CcmK
slil1807	-3.5427	1.11X10 ⁻¹⁶	50S ribosomal protein L24
slil0819	-3.51782	1.49X10 ⁻¹¹	photosystem I reaction center subunit III precursor (PSI-F)
slil1322	-3.51414	4.44X10 ⁻¹⁶	ATP synthase A chain of CF(0)
ssl0483	-3.44977	7.11X10 ⁻¹¹	hypothetical protein
slil1326	-3.43441	6.64X10 ⁻¹⁴	ATP synthase alpha chain
ssl3436	-3.32517	< 1X10 ⁻¹⁶	50S ribosomal protein L29
slil1321	-3.30583	< 1X10 ⁻¹⁶	hypothetical protein
slil1806	-3.26252	< 1X10 ⁻¹⁶	50S ribosomal protein L14
slr0749	-3.25921	< 1X10 ⁻¹⁶	light-independent protochlorophyllide reductase subunit ChL
slil1029	-3.23913	< 1X10 ⁻¹⁶	carbon dioxide concentrating mechanism protein CcmK
slil1281	-3.18589	< 1X10 ⁻¹⁶	photosystem II PsbZ protein
slil1810	-3.18555	< 1X10 ⁻¹⁶	50S ribosomal protein L6
smr0006	-3.02193	0.000337	cytochrome b559 b subunit
slil1744	-3.00111	< 1X10 ⁻¹⁶	50S ribosomal protein L1
slil0863	-2.9722	1.46X10 ⁻⁶	hypothetical protein
slil1515	-2.96641	1.37X10 ⁻⁸	glutamine synthetase inactivating factor IF17
slr0906	-2.95869	2.3X10 ⁻⁸	photosystem II core light harvesting protein
slr0927	-2.94957	8.6X10 ⁻⁷	photosystem II reaction center D2 protein
slil0849	-2.94877	2.06X10 ⁻⁸	photosystem II reaction center D2 protein
slr0006	-2.94221	7.88X10 ⁻¹¹	unknown protein
smr0003	-2.8866	0.000194	cytochrome b6-f complex subunit PetM
slil0851	-2.86193	1.89X10 ⁻⁵	photosystem II CP43 protein
smr0005	-2.81448	2.41X10 ⁻⁵	photosystem I subunit XII
slil1323	-2.80588	1.55X10 ⁻¹⁵	ATP synthase subunit b' of CF(0)
smil0003	-2.80128	0.000209	photosystem II reaction center M protein
slil1811	-2.79108	< 1X10 ⁻¹⁶	50S ribosomal protein L18
ssr3451	-2.78585	2.78X10 ⁻¹⁵	cytochrome b559 alpha subunit
ssl1911	-2.71341	6.66X10 ⁻⁸	glutamine synthetase inactivating factor IF7
smr0007	-2.68998	0.000196	photosystem II PsbL protein
slr1176	-2.68343	1.82X10 ⁻¹⁴	glucose-1-phosphate adenylyltransferase
slr1963	-2.66265	1.39X10 ⁻¹⁴	water-soluble carotenoid protein

slr0476	-2.6207	6.45X10 ⁻¹³	unknown protein
slI1920	-2.57098	8.45X10 ⁻⁵	copper-transporting P-type ATPase PacS
slr1839	-2.55852	< 1X10 ⁻¹⁶	carbon dioxide concentrating mechanism protein CcmK,
smI0008	-2.51678	0.000719	photosystem I subunit IX
slr0750	-2.51235	4.29X10 ⁻¹⁴	light-independent protochlorophyllide reductase subunit ChlN
slr0623	-2.48262	< 1X10 ⁻¹⁶	thioredoxin
smr0008	-2.47017	1.33X10 ⁻¹⁰	photosystem II PsbJ protein
slI1767	-2.46743	1.25X10 ⁻¹³	30S ribosomal protein S6
slr0244	-2.4151	9.04X10 ⁻¹¹	hypothetical protein
slI1031	-2.4129	1.65X10 ⁻¹³	carbon dioxide concentrating mechanism protein CcmM,
slI1525	-2.41091	0.000119	phosphoribulokinase
slr0452	-2.40949	6.88X10 ⁻¹⁵	dihydroxyacid dehydratase
slI0258	-2.39763	< 1X10 ⁻¹⁶	cytochrome c550
slI1812	-2.36049	4.44X10 ⁻¹⁶	30S ribosomal protein S5
slI1471	-2.36041	5.91X10 ⁻⁸	phycobilisome rod-core linker polypeptide
ssr2062	-2.35154	8.96X10 ⁻¹⁴	hypothetical protein
slI1743	-2.34031	5.55X10 ⁻¹⁶	50S ribosomal protein L11
ssl2384	-2.33266	0.000113	unknown protein
slI1500	-2.32252	1.08X10 ⁻¹⁰	hypothetical protein
slr0144	-2.31476	4.57X10 ⁻⁸	hypothetical protein
slI1260	-2.30928	3.33X10 ⁻¹⁶	30S ribosomal protein S2
smI0010	-2.27951	3.19X10 ⁻⁹	putative transposase
slr1098	-2.2731	8.12X10 ⁻⁹	hypothetical protein
slI1638	-2.25646	4.33X10 ⁻¹⁵	hypothetical protein
slI0629	-2.25294	< 1X10 ⁻¹⁶	alternative photosystem I reaction center subunit X
ssr1528	-2.2469	5.04X10 ⁻⁹	hypothetical protein
slI0947	-2.22169	2.83X10 ⁻¹⁴	light repressed protein A homolog
smI0004	-2.21545	0.000127	cytochrome b6-f complex subunit VIII
slI1655	-2.21486	1.22X10 ⁻¹⁵	similar to biotin [acetyl-CoA-carboxylase] ligase
slr2094	-2.20979	4.22X10 ⁻¹¹	fructose-1,6-/sedoheptulose-1,7-bisphosphatase
slI2013	-2.20774	2.69X10 ⁻¹⁰	hypothetical protein
slI1184	-2.20358	3.5X10 ⁻⁹	heme oxygenase
slI1142	-2.20075	6.28X10 ⁻⁵	hypothetical protein
slr1329	-2.19096	8.33X10 ⁻⁷	ATP synthase beta subunit
slr0394	-2.16666	3.67X10 ⁻¹³	phosphoglycerate kinase
slI1472	-2.13268	3.81X10 ⁻⁸	unknown protein
slr0710	-2.12995	< 1X10 ⁻¹⁶	glutamate dehydrogenase (NADP+)
ssl2598	-2.12627	< 1X10 ⁻¹⁶	photosystem II PsbH protein
slI1069	-2.12625	2.55X10 ⁻¹⁰	3-oxoacyl-[acyl-carrier-protein] synthase II
slI1316	-2.12585	3.23X10 ⁻¹⁴	cytochrome b6-f complex iron-sulfur subunit
slr1394	-2.1258	9.07X10 ⁻⁶	hypothetical protein
ssr0390	-2.11961	3.95X10 ⁻¹³	photosystem I reaction center subunit X
slI1813	-2.1123	6.88X10 ⁻¹⁵	50S ribosomal protein L15
slI0145	-2.11111	1.08X10 ⁻¹⁰	ribosome releasing factor
slr0681	-2.09744	< 1X10 ⁻¹⁶	probable sodium/calcium exchanger protein
slI1325	-2.0875	0.000587	ATP synthase delta chain of CF(1)
slr2070	-2.08157	1.88X10 ⁻¹¹	hypothetical protein
slI1101	-2.07925	< 1X10 ⁻¹⁶	30S ribosomal protein S10
slr0434	-2.07154	2.62X10 ⁻¹³	elongation factor P
slr1584	-2.05976	3.33X10 ⁻¹⁵	two-component transcription regulator OmpR subfamily
slr1513	-2.04891	0.008521	periplasmic protein, function unknown
slI1261	-2.04515	6.66X10 ⁻¹⁶	elongation factor TS
ssr1375	-2.04411	3.17X10 ⁻¹³	hypothetical protein
slr1780	-2.03467	1.55X10 ⁻¹⁵	hypothetical protein YCF54
slr1295	-2.02787	8.55X10 ⁻¹³	iron transport system substrate-binding protein
slr1177	-2.02637	8.99X10 ⁻⁷	hypothetical protein
slr0506	-2.02107	5.87X10 ⁻¹³	light-dependent NADPH-protochlorophyllide oxidoreductase
slr1722	-2.02084	2.66X10 ⁻¹⁵	inosine-5'-monophosphate dehydrogenase
slr1020	-2.01872	4.8X10 ⁻¹¹	sulfolipid biosynthesis protein SqdB
ssl3803	-2.01303	0.000315	hypothetical protein

Appendix 5. Overview of changes in gene expression of all 3264 ORF of *Synechocystis* PCC 6803 during the continuous-culture experiment.

The ORF are grouped into functional categories according to Cyanobase (see <http://bacteria.kazusa.or.jp/cyanobase/>). The entries in the Table present the normalized log-intensities, on a ²log-scale, at different time points during the experiment. A grey background indicates ORF that were significantly regulated (ANOVA; $p < 0.01$); their cluster assignment is indicated.

We compared our results with the batch-culture experiments of Osanai et al. (2006). Blue and orange colors (dark gray and white in excerpt) indicate ORF with more than twofold downregulation and upregulation, respectively, in their batch-culture experiment. Pale blue and pale orange (light gray and white in excerpt) indicate ORF with less than twofold downregulation and upregulation, respectively.

For ease of reference, we also provide the EC codes used by the Kyoto Encyclopedia of Genes and Genomes (KEGG). Furthermore, the KEGG map numbers in which a certain gene product appears functionally are listed. When gene products are used in more than one metabolic pathway, more KEGG map numbers are shown. At the KEGG website one has to specify the organism as Syn for the *Synechocystis* enzymes to appear in metabolic maps and diagrams.

This hardcopy presents only a short excerpt with two pages of the Appendix. The complete Appendix would cover more than 160 pages and is available in electronic format (3 MB) upon request from the corresponding author (J.C.P.Matthijs@uva.nl).

