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Dynamic changes in gene expression of the cyanobacterium *Synechocystis* sp. PCC 6803 in response to nitrogen starvation

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Appendices*

***Note:**

Supporting information for Chapter 5 is available for download from the website of the journal:
<http://www.plantphysiol.org/content/155/3/1445/suppl/DC1>

Supporting information for Chapter 6 is available for download from the website of the journal:
<http://onlinelibrary.wiley.com/doi/10.1111/j.1399-3054.2012.01585.x/supinfo>

Appendix 2A. List of up-regulated ORFs.

Numbers represent the log ratio of gene expression, which is defined as $2\log(I_{\text{treatment}}/I_{\text{control}})$. Up-regulations are highlighted in dark gray, and down-regulations in light gray. The column 'Category' is the functional category number assigned as in Table 3. Columns 'S', 'N', and 'P' represent 'salt stress', 'nitrogen starvation', and 'phosphorus starvation', respectively. The column 'other studies' indicates regulation of the corresponding ORF in other *Synechocystis* microarray studies; reference list is as in Table 2.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
2	<i>sll1685</i>	<i>ycf10</i>	light-induced Na ⁺ -dependent proton extrusion	2.09	-0.06	-0.41		
3	<i>slr1908</i>		probable porin; major outer membrane protein	1.70	0.13	-1.16		13
4	<i>slr0228</i>	<i>ftsH</i>	cell division protein FtsH	1.17	0.61	0.12	8b,10,11b,15	
6	<i>sll1023</i>		succinyl-CoA synthetase beta chain	1.04	0.22	-0.49		
6	<i>slr0370</i>		succinate-semialdehyde dehydrogenase (NADP ⁺)	1.07	0.07	-0.12		
7	<i>slr1051</i>		enoyl-[acyl-carrier-protein] reductase	0.96	0.09	-0.38		
8	<i>sll1031</i>	<i>ccmM</i>	CO ₂ concentrating mech. protein CcmM	1.33	-0.36	-0.21	8a,11a	11b,15
8	<i>sll1584</i>		ferredoxin like protein	1.12	-0.11	-0.14		
8	<i>sll0199</i>	<i>petE</i>	plastocyanin	1.30	0.26	0.15	11b	15
8	<i>slr2007</i>	<i>ndhD5</i>	NADH dehydrogenase subunit 4	0.83	0.02	0.02	11a	
8	<i>slr1655</i>	<i>psaL</i>	photosystem I subunit XI	0.82	-1.17	-0.21		7,10,11ab
8	<i>smr0004</i>	<i>psaI</i>	photosystem I subunit VIII	0.88	-1.32	-0.60		15
10	<i>slr1042</i>		two-component response regulator CheY subfamily	0.99	-0.19	-1.03		
10	<i>slr0724</i>		HtaR suppressor protein hom.	1.30	-0.42	-0.09		
10	<i>slr1037</i>		two-component response regulator CheY subfamily	1.08	0.02	-0.21		
10	<i>sll1771</i>	<i>pphA</i>	protein serin-threonin phosphatase	2.40	0.39	-0.21		
10	<i>sll1353</i>		two-component sensor histidine kinase	1.43	0.28	0.20		
10	<i>slr1871</i>		transcriptional regulator	1.37	-0.16	-1.71		
10	<i>sll0030</i>	<i>cmpR</i>	Cmp operon transcriptional reg., LysR family protein	1.85	0.43	0.66		
11	<i>slr1536</i>	<i>recQ</i>	ATP-dependent DNA helicase RecQ	1.51	0.08	0.01		
11	<i>slr0451</i>		putative helicase	0.97	0.04	-1.17	13	
12	<i>slr1564</i>	<i>sigF</i>	group III RNA polymerase sigma factor SigF	1.09	-0.37	-0.50		
12	<i>slr0653</i>	<i>sigA</i>	principal RNA polymerase sigma factor SigA	1.06	-0.31	-0.24	15	2ab
13	<i>slr0612</i>		prob. pseudouridine synthase	2.00	-0.53	-0.57		
13	<i>slr1204</i>		protease	1.78	0.05	-0.35	1,2ab,4,5a,6,8b,15	
13	<i>sll0195</i>		probable ATP-dependent protease	2.65	0.26	0.40		
13	<i>slr0120</i>		probable tRNA/rRNA methyltransferase	1.00	-0.07	-0.34		
13	<i>slr0535</i>		protease	2.12	-0.21	-1.53		
13	<i>slr1592</i>		probable pseudouridine synthase	0.84	0.16	-2.71		
13	<i>sll1967</i>		probable RNA methyltransferase	1.56	0.17	-1.28		
13	<i>slr0542</i>	<i>clpP</i>	ATP-dependent protease ClpP	0.83	0.06	-0.34		
14	<i>sll1404</i>		biopolymer transport ExbB protein hom.	1.61	0.28	-0.56	15	
14	<i>sll1768</i>		prob. Oligopeptide ABC transporter permease protein	0.89	-0.25	-0.65		
14	<i>sll0273</i>	<i>nhaS2</i>	Na ⁺ /H ⁺ antiporter	0.80	-0.14	0.06		
14	<i>sll0484</i>		ATP-binding protein of ABC transp.	1.35	-0.04	-0.30		
14	<i>sll0993</i>		potassium channel	1.15	0.08	-0.37		
15	<i>slr1302</i>	<i>cupB</i>	protein involved in constitutive low affinity CO ₂ uptake	1.86	0.44	-0.60		
15	<i>slr2135</i>		hydrogenase accessory protein	1.12	0.02	0.02		
15	<i>sll1283</i>		similar to stage II sporulation protein D	1.11	0.15	-0.30		
15	<i>sll1968</i>	<i>pmgA</i>	photomixotrophic growth related protein, PmgA	1.43	0.17	-0.29		
15	<i>sll1308</i>		probable oxidoreductase	1.48	0.31	0.02		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
16	<i>sll1734</i>	<i>cupA</i>	prot. inv. in low CO ₂ -induc., high affinity CO ₂ uptake	1.28	-0.03	-0.19		
16	<i>slr0613</i>		hypothetical protein	1.61	-0.41	-0.33		
16	<i>sll0558</i>	<i>ycf53</i>	hypothetical protein YCF53	1.90	-0.63	-0.22		
16	<i>sll0983</i>		hypothetical protein	1.09	-0.44	0.04		
16	<i>slr1699</i>		hypothetical protein	1.95	-0.24	-0.45		
16	<i>sll1737</i>	<i>ycf60</i>	hypothetical protein YCF60	1.50	-0.05	-0.31		
16	<i>sll0261</i>		hypothetical protein	0.83	0.23	0.00		
16	<i>slr0878</i>		hypothetical protein	1.81	0.37	-0.03		
16	<i>slr1935</i>		hypothetical protein	0.90	-0.27	-0.50		
16	<i>slr0039</i>		hypothetical protein	1.23	0.43	0.11		
16	<i>slr0554</i>		hypothetical protein	0.83	-0.04	0.68		
16	<i>slr1593</i>		hypothetical protein	1.22	-0.02	-2.75		
16	<i>slr1417</i>	<i>ycf57</i>	hypothetical protein YCF57	1.86	0.12	-1.30		
16	<i>slr1917</i>		hypothetical protein	1.41	0.17	-0.28	1,11b	
16	<i>sll0867</i>		hypothetical protein	1.71	0.30	-0.31		
16	<i>ssr2016</i>		hypothetical protein	1.26	-0.05	0.19	2ab,4,6,8ab, 10,11b	
17	<i>sll1061</i>		unknown protein	1.33	-0.10	0.10		
17	<i>slr1396</i>		unknown protein	1.11	0.31	-0.33		13
17	<i>slr1397</i>		unknown protein	0.86	-0.17	-0.20	11b	7
17	<i>slr0226</i>		unknown protein	1.21	-0.54	-0.43		
17	<i>sll1344</i>		unknown protein	1.44	0.46	-0.08		
17	<i>sll0943</i>		unknown protein	1.13	-0.05	-1.33		
17	<i>slr1028</i>		unknown protein	1.00	-0.03	-1.17		
1	<i>slr0644</i>		nitrogen regulation protein NifR3 homolog	-0.58	1.07	-0.43		
1	<i>slr0898</i>	<i>nirA</i>	ferredoxin-nitrite reductase	0.46	1.43	0.50	3b,16	
1	<i>sll1499</i>	<i>glsF</i>	ferredoxin-dependent glutamate synthase	-0.10	1.25	-0.23		
4	<i>sll0057</i>	<i>grpE</i>	heat shock protein GrpE	-0.23	0.88	-0.12		
4	<i>slr0063</i>		general secretion pathway protein E	-0.14	1.03	-0.69		
6	<i>slr0662</i>		arginine decarboxylase	-0.22	0.99	0.51		
8	<i>slr1136</i>	<i>ctaC</i>	cytochrome c oxidase subunit II	-0.26	1.49	0.61	16	
8	<i>slr1137</i>	<i>ctaD</i>	cytochrome c oxidase subunit I	-0.25	1.19	0.42	16	
8	<i>slr1138</i>	<i>ctaE</i>	cytochrome c oxidase subunit III	-1.11	0.80	-0.06	16	
9	<i>sll1631</i>		putative cytidine and deoxycytidylate deaminase	-1.55	0.88	-0.19		
10	<i>slr1225</i>		serine/threonine kinase	-2.64	1.21	-0.26		
10	<i>sll1708</i>		two-component response regulator NarL subfamily	-2.40	1.11	-0.60		
10	<i>slr1805</i>		two-component sensor histidine kinase	-0.16	1.43	-0.03		
10	<i>sll1624</i>		two-component response regulator	-3.41	1.24	-1.02		
10	<i>slr0449</i>		Probable transcriptional regulator	0.62	0.88	-0.62		
14	<i>sll1623</i>		ABC transp. ATP-binding protein	-2.09	1.24	-1.02		
15	<i>slr0067</i>		MRP protein hom.	0.69	1.38	0.10		
16	<i>slr0723</i>		hypothetical protein	0.09	0.83	0.19		
16	<i>slr2070</i>		hypothetical protein	0.07	1.20	0.12		
16	<i>sll0514</i>		hypothetical protein	-0.01	0.96	-0.24		
17	<i>sll1942</i>		unknown protein	0.22	1.08	0.18		
17	<i>sll1939</i>		unknown protein	-0.13	1.22	-0.61		
17	<i>sll0991</i>		unknown protein	0.67	1.54	-0.23		
17	<i>slr0069</i>		unknown protein	0.11	0.82	-0.49		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
17	<i>sll0723</i>		unknown protein	0.31	1.82	-0.92		
1	<i>sll1363</i>	<i>ilvC</i>	ketol-acid reductoisomerase	-1.11	-1.03	0.86		
2	<i>slr0917</i>	<i>bioF</i>	7-keto-8-aminopelargonic acid synthetase	-0.40	-0.13	1.81		
4	<i>sll0170</i>	<i>dnaK</i>	DnaK protein	0.12	0.13	0.89	1,2ab,4,5a, 6,8b,11b,13	
5	<i>slr1622</i>	<i>ppa</i>	soluble inorganic pyrophosphatase	-0.74	-1.56	1.08		
8	<i>sll1525</i>	<i>prk</i>	phosphoribulokinase	0.04	-0.49	1.37		15
10	<i>sll1387</i>	<i>pppA</i>	serine/threonine protein phosphatase PppA	-2.32	0.15	1.29		
10	<i>sll0789</i>		two-component response regulator OmpR subfamily	-0.62	0.25	1.17	2ab,5a,13	11a
10	<i>sll1334</i>		two-component sensor histidine kinase	0.40	-0.02	2.25		
11	<i>slr0915</i>		putative endonuclease	-0.86	-1.07	1.81		
13	<i>slr0164</i>	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit	0.12	-0.32	1.70	13,15	
14	<i>slr1247</i>		phosphate-binding periplasmic protein precursor	-0.40	0.19	1.39	14	
14	<i>slr1248</i>		phosphate transport system permease protein PstC hom.	0.24	0.27	1.18	14	
14	<i>slr1249</i>		phosphate transport system permease protein PstA hom.	0.15	-0.01	0.94	14	
14	<i>slr1250</i>		phosphate transport ATP-binding protein PstB hom.	0.04	0.03	1.05	14	
14	<i>sll1870</i>		ATP-binding protein of ABC transp.	-0.51	0.49	2.21		
14	<i>sll0574</i>		prob. Permease prot. of lipopolysaccharide ABC transp.	0.02	0.08	2.77		
14	<i>sll0540</i>		P _i -binding protein PetS hom.	0.33	-0.75	1.14		
15	<i>sll0378</i>	<i>cobA</i>	uroporphyrin-III C-methyltransferase	-0.11	-1.69	1.22		
15	<i>slr0799</i>		putative transposase [ISY802_c]	-0.28	0.49	1.66		
15	<i>slr0800</i>		putative transposase [ISY802_c]	0.13	0.22	0.94		
15	<i>sll0431</i>		putative transposase [ISY100_h]	-0.42	-0.10	1.17		
15	<i>slr1682</i>		putative transposase [ISY391_b1]	0.50	0.05	1.71		
15	<i>sll1560</i>		putative transposase [ISY203_d]	-0.33	-0.15	1.87		
16	<i>sll1203</i>		hypothetical protein	-1.65	-0.58	1.15		
16	<i>sll1191</i>		hypothetical protein	-0.53	-0.47	1.22		
16	<i>sll0788</i>		hypothetical protein	-0.42	0.28	1.81	2ab,8b,10,13	11a
16	<i>slr0651</i>		hypothetical protein	-0.90	0.00	2.01	12	
16	<i>slr1429</i>		hypothetical protein	0.40	0.19	2.27		
16	<i>slr1557</i>		hypothetical protein	0.10	0.10	1.43	11b	
17	<i>slr1257</i>		unknown protein	-0.94	-1.24	0.99		
17	<i>slr0914</i>		unknown protein	-1.42	-1.03	1.39		
17	<i>sll0479</i>		unknown protein	0.14	0.15	1.05		
17	<i>sll1333</i>		unknown protein	-0.36	0.33	1.53		
1	<i>sll0402</i>	<i>aspC</i>	aspartate aminotransferase	1.07	1.13	-0.32		
1	<i>sll0450</i>		probable nitric oxide reductase	1.04	1.05	-0.53		11a
1	<i>slr0036</i>	<i>aspC</i>	aspartate aminotransferase	1.21	1.79	0.04		
2	<i>slr0526</i>	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.64	2.17	0.26		
3	<i>slr1024</i>		fibrillin	1.95	1.85	-0.11		
3	<i>slr0191</i>		similar to amidase enhancer	1.55	1.15	-0.42	5a	
3	<i>sll1724</i>		probable glycosyltransferase	1.66	0.97	-1.61		
4	<i>sll0416</i>	<i>groEL2</i>	60kD chaperonin 2	1.61	2.53	0.46	2ab,4,5a,6, 8b,10,11ab	13,15
4	<i>sll1463</i>	<i>ftsH</i>	cell division protein FtsH	2.88	1.76	-0.66	11b, 15	
4	<i>sll0041</i>		probable methyl-accepting chemotaxis protein	1.62	1.50	-0.20		
4	<i>sll0533</i>		trigger factor	1.12	1.02	0.24		
5	<i>slr0897</i>		probable endoglucanase	2.28	1.24	-0.03		
5	<i>slr1899</i>	<i>ureF</i>	urease accessory protein F	1.15	1.04	0.07		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
6	<i>slr0091</i>		aldehyde dehydrogenase	1.87	2.12	0.70		
6	<i>slr1448</i>		fructokinase	1.40	1.29	0.11		
6	<i>sll1479</i>		6-phosphogluconolactonase	1.57	2.20	0.19		
8	<i>sll0522</i>	<i>ndhE</i>	NADH dehydrogenase subunit 4L	1.18	1.25	-0.09		
8	<i>sll0521</i>	<i>ndhG</i>	NADH dehydrogenase subunit 6	2.68	1.59	0.01		
8	<i>sll0520</i>	<i>ndhI</i>	NADH dehydrogenase subunit NdhI	2.96	1.86	0.21		
8	<i>sll0519</i>	<i>ndhA</i>	NADH dehydrogenase subunit 1	2.61	1.65	0.36		
8	<i>slr0342</i>	<i>petB</i>	cytochrome b6	1.56	2.12	0.75		
8	<i>slr0343</i>	<i>petD</i>	cytochrome b6-f complex subunit 4	1.23	1.51	0.54	15	
8	<i>slr0927</i>	<i>psbD2</i>	photosystem II reaction center D2 protein	1.22	1.61	0.05	10	
8	<i>sll1317</i>	<i>petA</i>	apocytochrome f, comp. of cyt. b6/f complex	3.10	2.45	0.06		7
8	<i>sll1733</i>	<i>ndhD3</i>	NADH dehydrogenase subunit 4	1.56	1.15	0.14	5a,10,11a	11b
8	<i>sll1732</i>	<i>ndhF3</i>	NADH dehydrogenase subunit 5	1.26	1.19	-0.04	10,11a	
10	<i>sll0094</i>		two-component sensor histidine kinase	1.89	2.12	0.42		
10	<i>slr0527</i>		transcription regulator ExsB homolog	2.32	2.64	-0.18		
10	<i>slr0533</i>		two-component sensor histidine kinase	2.86	2.04	-1.01		10
11	<i>sll0865</i>	<i>uvrC</i>	excinuclease ABC subunit C	1.76	1.47	-0.17	12	
11	<i>sll1772</i>	<i>mutS</i>	DNA mismatch repair protein MutS	1.96	0.91	-1.18		
12	<i>sll1043</i>		polyribonucleotide nucleotidyltransferase	1.48	1.44	0.75		
13	<i>slr0070</i>	<i>fmt</i>	methionyl-tRNA formyltransferase	0.83	1.19	0.22		
13	<i>sll2008</i>		processing protease	1.78	1.40	-0.48		
13	<i>slr1751</i>		carboxyl-terminal protease	1.83	2.50	0.59	2a,11a,13	
14	<i>sll1276</i>		ATP-binding protein of ABC transp.	1.43	1.26	-0.46		
14	<i>sll0507</i>		probable cation transp.	1.74	1.73	0.57		
15	<i>sll1723</i>		probable glycosyltransferase	2.56	1.64	-1.53	2a	
15	<i>sll0506</i>		undecaprenyl pyrophosphate synthetase	1.24	1.51	0.10		
15	<i>sll0034</i>		putative carboxypeptidase	1.79	1.91	0.69		
15	<i>slr0580</i>		aluminum resistance protein homolog	1.68	1.26	0.51		
16	<i>slr0192</i>		hypothetical protein	1.10	1.34	-0.36		
16	<i>slr0304</i>		hypothetical protein	1.69	1.72	0.55		
16	<i>sll0898</i>		hypothetical protein	2.08	1.45	-0.87	11b	
16	<i>sll0051</i>		hypothetical protein	1.15	1.34	0.36		7
16	<i>sll1464</i>		hypothetical protein	2.40	1.72	-0.08		
16	<i>sll1770</i>		hypothetical protein	2.09	1.27	-0.40	11ab	
16	<i>slr1449</i>		hypothetical protein	2.88	1.46	0.14		
16	<i>sll1477</i>		hypothetical protein	1.96	2.30	0.73		
16	<i>slr0031</i>		hypothetical protein	0.81	0.88	0.85		
17	<i>sll1265</i>		unknown protein	1.25	1.47	-0.50		
17	<i>slr1032</i>		unknown protein	2.30	1.12	0.36		
17	<i>sll1761</i>		unknown protein	2.05	1.40	-0.37		
17	<i>slr0581</i>		unknown protein	1.39	0.95	0.73	2ab,6,13	
1	<i>ssl0707</i>	<i>glnB</i>	nitrogen regulatory protein P-II	1.53	0.48	1.55		
2	<i>slr0623</i>	<i>trxA</i>	thioredoxin	1.15	0.21	1.35		11b
3	<i>sll0657</i>		phospho-N-acetylmuramoyl-pentapeptide transferase	1.75	0.55	1.31		
7	<i>sll0262</i>	<i>desD</i>	delta-6 desaturase	1.19	0.42	1.12		2a
10	<i>slr1305</i>		Two-component response regulator	2.43	-0.33	1.99		
10	<i>slr0322</i>		two-component hybrid sensor and regulator	1.07	0.63	1.13		
13	<i>slr0469</i>	<i>rps4</i>	30S ribosomal protein S4	1.22	0.28	1.42		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
16	<i>slr0765</i>		hypothetical protein	1.60	0.11	1.33	3b	
16	<i>sll0499</i>		hypothetical protein	1.78	0.26	2.53		
2	<i>slr0633</i>	<i>thiG</i>	thiamine biosynthesis protein ThiG	0.52	2.44	1.80		
6	<i>sll1070</i>		transketolase	0.19	2.52	1.70		
13	<i>sll1427</i>		protease	-0.36	3.50	2.98	11ab	
13	<i>slr1331</i>		processing protease	-0.42	2.09	2.40		11b
14	<i>sll1920</i>	<i>pacS</i>	copper transporting CPx-type ATPase PacS	-0.57	1.42	1.13		
14	<i>slr0794</i>		Cation efflux system protein	0.52	2.13	1.92		
14	<i>slr1740</i>		oligopeptide binding protein of ABC transp.	-0.67	1.96	2.79		
14	<i>sll1699</i>		oligopeptide-bind. protein of oligopeptide ABC transp.	0.86	2.25	3.03		
15	<i>sll1664</i>		probable glycosyl transferase	-0.37	1.44	2.89		
15	<i>sll0621</i>	<i>ccdA</i>	putative c-type cytochrome biogenesis protein CcdA	-0.11	1.35	1.28		
15	<i>sll0677</i>		putative transposase [ISY523_h]	0.85	1.85	2.35		
16	<i>sll0678</i>		hypothetical protein	0.03	2.21	2.18		
16	<i>sll1618</i>		hypothetical protein	0.14	1.21	2.13		
17	<i>sll1665</i>		unknown protein	0.87	2.30	2.31		11b
17	<i>slr1809</i>		unknown protein	0.56	2.25	3.03		
1	<i>slr1022</i>	<i>argD</i>	N-acetylornithine aminotransferase	1.34	1.77	1.22		
1	<i>slr0710</i>	<i>gdhA</i>	glutamate dehydrogenase (NADP+)	1.44	1.23	1.41		
1	<i>slr1848</i>	<i>hisD</i>	histidinol dehydrogenase	1.47	2.20	1.57		
1	<i>sll0373</i>	<i>proA</i>	gamma-glutamyl phosphate reductase	2.57	2.79	2.63		
1	<i>sll0902</i>	<i>argF</i>	ornithine carbamoyltransferase	1.71	2.30	1.63		
1	<i>slr0549</i>	<i>asd</i>	Aspartate beta-semialdehyde dehydrogenase	1.82	1.59	1.16	5b	
2	<i>sll0635</i>	<i>thiE</i>	probable thiamine-phosphate pyrophosphorylase	2.46	2.49	1.65		
2	<i>sll1127</i>	<i>menB</i>	naphthoate synthase	2.57	2.04	1.38		
2	<i>slr1239</i>	<i>pntA</i>	pyridine nucleotide transhydrogenase alpha subunit	1.77	2.36	1.78		11b
2	<i>sll1890</i>	<i>cobN</i>	similar to cobalamin biosynthetic protein CobN	2.42	1.92	3.23		
2	<i>slr0056</i>	<i>chlG</i>	chlorophyll a synthase	1.68	1.87	1.40		
3	<i>slr1423</i>	<i>murC</i>	UDP-N-acetylmuramate-alanine ligase	0.85	1.01	1.11		
3	<i>sll0380</i>		probable glycosyltransferase	1.35	1.49	1.48		
4	<i>slr0093</i>	<i>dnaJ</i>	DnaJ protein	1.62	1.67	1.88	1,2ab,4,5a, 6,8b,11b,13	
4	<i>slr1366</i>		lipoprotein signal peptidase	2.57	1.63	1.35		
4	<i>slr0488</i>		virulence factor MviN hom..	2.03	2.67	1.65		
4	<i>sll0897</i>	<i>dnaJ</i>	DnaJ protein	2.65	2.58	0.96	11b	
4	<i>sll1933</i>	<i>dnaJ</i>	DnaJ protein	2.61	2.80	2.04		
6	<i>sll1189</i>	<i>glcE</i>	glycolate oxidase subunit GlcE	3.36	1.78	1.57		
6	<i>sll1019</i>		hydroxyacylglutathione hydrolase	2.19	2.77	2.13		
7	<i>sll0541</i>	<i>desC</i>	acyl-CoA desaturase 1	2.06	1.59	0.77		
8	<i>ssl2559</i>		ferredoxin	2.48	2.61	2.67		
8	<i>slr1181</i>	<i>psbA1</i>	photosystem II D1 protein	2.07	2.26	1.44		
8	<i>slr1185</i>		Rieske Fe-S protein with unknown function	3.14	2.48	1.44		
8	<i>sll0634</i>	<i>btpA</i>	photosystem I biogenesis protein BtpA	2.38	1.89	1.62		
8	<i>slr0844</i>	<i>ndhF1</i>	NADH dehydrogenase subunit 5	1.91	2.21	1.99		
8	<i>ssl1386</i>	<i>ndhL</i>	NADH dehydrogenase subunit NdhL	0.88	1.30	1.62		
9	<i>sll1018</i>	<i>pyrC</i>	dihydroorotase	1.19	1.06	1.66		
10	<i>sll1296</i>		two-component hybrid sensor and regulator	2.02	1.83	2.22		11b
10	<i>sll1574</i>		similar to serine/threonine kinase	1.20	1.13	1.08		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
10	<i>slr0081</i>		two-component response regulator OmpR subfamily	2.53	2.78	2.13		
10	<i>sll0474</i>		two-component hybrid sensor and regulator	2.73	2.51	2.53	3a	
10	<i>sll0594</i>		transcriptional regulatory protein	1.83	2.09	1.28		
10	<i>sll1005</i>		MazG protein hom.	1.56	2.48	2.25		
10	<i>sll1286</i>		transcriptional regulator	1.38	1.80	1.06		
10	<i>slr0835</i>		MoxR protein homolog	1.32	2.12	2.35		
11	<i>slr1543</i>		DNA-damage-inducible protein F	2.33	1.51	1.74		
11	<i>slr0417</i>	<i>gyrA</i>	DNA gyrase A subunit	1.98	1.65	1.63		
11	<i>slr1426</i>	<i>recR</i>	recombination protein RecR	1.88	1.41	1.03		
12	<i>sll0184</i>	<i>sigC</i>	group 2 RNA polymerase sigma factor SigC	1.23	1.10	0.86	11ab, 15	
13	<i>sll1746</i>	<i>rpl12</i>	50S ribosomal protein L12	0.95	1.04	0.92		11b
13	<i>sll1745</i>	<i>rpl10</i>	50S ribosomal protein L10	2.25	1.39	2.13		11b
13	<i>sll1744</i>	<i>rpl1</i>	50S ribosomal protein L1	2.23	1.97	2.36	10	11b
13	<i>sll1743</i>	<i>rpl11</i>	50S ribosomal protein L11	1.50	1.77	2.02	5b	11b
13	<i>sll1362</i>	<i>ileS</i>	isoleucyl-tRNA synthetase	1.63	1.03	1.21		
13	<i>sll0555</i>		methionine aminopeptidase	1.27	2.07	2.02		
13	<i>slr1031</i>	<i>tyrS</i>	tyrosyl tRNA synthetase	1.89	2.01	1.87	3b	
13	<i>slr0156</i>	<i>clpB</i>	ClpB protein	1.64	1.16	2.19	8b	15
13	<i>sll1802</i>	<i>rpl2</i>	50S ribosomal protein L2	1.78	1.72	1.91	10	11b,13
13	<i>sll1801</i>	<i>rpl23</i>	50S ribosomal protein L23	1.34	1.29	1.34	5b,7,10	11b,13
13	<i>sll1800</i>	<i>rpl4</i>	50S ribosomal protein L4	2.11	2.16	2.50	5b,7,8ab,10	11b,13
13	<i>sll1799</i>	<i>rpl3</i>	50S ribosomal protein L3	1.93	1.82	1.53	2a,7,8a,10	13
14	<i>slr0982</i>		prob. polysaccharide ABC transp. ATP binding subunit	1.87	2.30	1.45		
14	<i>sll0680</i>	<i>pbp</i>	phosphate-binding periplasmic protein precursor	0.81	1.11	0.87	5a,10,14	
14	<i>sll1076</i>		cation-transporting ATPase Pacl hom.	1.84	2.26	1.92		
14	<i>sll1453</i>	<i>nrtD</i>	nitrate/nitrite transport system ATP-binding protein	1.12	1.05	1.23	13, 16	2a, 11b
14	<i>sll1452</i>	<i>nrtC</i>	nitrate/nitrite transport system ATP-binding protein	1.72	1.14	0.93	13, 16	
14	<i>sll0064</i>		binding protein of ABC transp. component	2.07	3.53	1.39		
14	<i>sll0681</i>		phosphate transport system permease protein PstC hom.	1.92	2.14	1.72	5a, 10, 14	
14	<i>sll0682</i>		phosphate transport system permease protein PstA hom.	1.07	2.17	1.43	14	
14	<i>sll0683</i>		phosphate transport ATP-binding protein PstB hom.	1.73	2.17	1.94	10, 14	
14	<i>sll0684</i>		phosphate transport ATP-binding protein PstB hom.	1.50	1.99	1.65	14	
14	<i>sll0679</i>		periplasmic phosphate-binding protein of ABC transp.	1.16	1.27	1.23	14	
14	<i>slr0415</i>	<i>nhaS5</i>	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter	1.16	1.34	0.89		
14	<i>sll0374</i>		prob. branched chain ABC transp. ATP-binding protein	2.50	2.18	2.20	15	
14	<i>sll0556</i>		Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter	3.26	2.25	2.04	1, 3b, 5a	
15	<i>ssr1789</i>	<i>hliD</i>	CAB/ELIP/HLIP-related protein HliD	4.06	2.54	1.74		
15	<i>sll1255</i>		putative transposase [ISY203_c]	1.12	1.14	1.23		
15	<i>slr1208</i>		probable oxidoreductase	2.02	1.99	1.06		
15	<i>sll1297</i>		probable dioxygenase, Rieske iron-sulfur component	2.64	2.19	2.14		11b
15	<i>slr2053</i>		putative hydrolase	2.27	2.67	1.70		
15	<i>slr0201</i>		heterodisulfide reductase subunit B	1.12	1.31	0.95		
15	<i>slr2113</i>		putative transposase [ISY100_o]	1.46	2.01	2.39		
15	<i>sll0816</i>		probable oxidoreductase	2.91	2.42	1.34		
16	<i>slr1303</i>		hypothetical protein	1.89	2.12	2.41		
16	<i>sll1934</i>		hypothetical protein	2.15	2.20	1.37		
16	<i>slr1911</i>		hypothetical protein	1.99	1.75	1.95		
16	<i>slr1394</i>		hypothetical protein	1.80	1.50	1.46		

Appendix 2A (continued). List of up-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
16	<i>ssr1425</i>	<i>ycf34</i>	hypothetical protein YCF34	1.67	2.07	1.58	11b	
16	<i>slr1566</i>		hypothetical protein	1.87	0.81	1.43		
16	<i>sll1500</i>		hypothetical protein	2.01	1.49	1.59		
16	<i>sll1925</i>		hypothetical protein	1.82	0.80	1.39		
16	<i>slr0882</i>	<i>ycf84</i>	hypothetical protein YCF84	3.34	1.30	0.85		
16	<i>sll0871</i>		hypothetical protein	2.16	1.81	1.89	3a	
16	<i>slr0643</i>		hypothetical protein	2.20	2.61	2.03		
16	<i>sll0606</i>		hypothetical protein	2.04	2.80	2.21		
16	<i>sll0372</i>		hypothetical protein	1.38	1.73	1.70		
16	<i>sll0185</i>		hypothetical protein	1.13	1.60	1.48	2b,8b,10,11ab	
16	<i>slr0199</i>		hypothetical protein	1.18	0.76	1.86		
16	<i>sll0544</i>		hypothetical protein	1.71	1.64	1.36		
16	<i>slr0082</i>		hypothetical protein	2.36	2.82	1.88	1,7,8a	8b,10
16	<i>slr0092</i>		hypothetical protein	2.24	2.39	2.06		
16	<i>sll0103</i>		hypothetical protein	2.04	2.28	2.18		
16	<i>sll0095</i>		hypothetical protein	2.42	2.44	2.77		
16	<i>sll1254</i>		hypothetical protein	2.15	1.43	1.48		
16	<i>slr0303</i>		hypothetical protein	2.30	1.94	1.24		
16	<i>sll0047</i>	<i>ycf12</i>	hypothetical protein YCF12	1.52	2.17	1.62		
16	<i>slr1998</i>		hypothetical protein	2.38	1.42	0.90		
16	<i>slr1184</i>		hypothetical protein	1.99	3.13	1.70		
16	<i>slr0104</i>		hypothetical protein	1.24	1.34	1.37		
17	<i>slr2037</i>		unknown protein	1.76	1.88	2.03		
17	<i>slr0416</i>		unknown protein	1.70	1.70	0.91		
17	<i>sll1891</i>		unknown protein	2.72	2.37	1.54	11b	
17	<i>sll0473</i>		unknown protein	2.29	2.31	2.16		
17	<i>sll0595</i>		unknown protein	2.41	2.04	1.37		
17	<i>sll0048</i>		unknown protein	2.34	2.95	2.28		
17	<i>sll1338</i>		unknown protein	2.74	1.82	1.89		
17	<i>sll1784</i>		unknown protein	2.39	2.00	2.02		2ab,7,10,11ab
17	<i>sll1837</i>		unknown protein	1.89	1.82	2.07		
17	<i>slr1023</i>		unknown protein	1.71	2.00	1.23		
17	<i>sll1785</i>		unknown protein	3.25	2.46	1.68		2ab,7

Appendix 2B. List of down-regulated ORFs.

Numbers represent the log ratio of gene expression, which is defined as $2\log(I_{\text{treatment}}/I_{\text{control}})$. Up-regulations are highlighted in dark gray, and down-regulations in light gray. The column ‘Category’ is the functional category number assigned as in Table 3. Columns ‘S’, ‘N’, and ‘P’ represent ‘salt stress’, ‘nitrogen starvation’, and ‘phosphorus starvation’, respectively. The column ‘other studies’ indicates regulation of the corresponding ORF in other *Synechocystis* microarray studies; reference list is as in Table 2.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
1	<i>slr0963</i>	<i>sir</i>	ferredoxin-sulfite reductase	-2.48	-0.27	-0.79		
1	<i>slr0288</i>	<i>glnN</i>	glutamate-ammonia ligase	-1.28	0.16	-0.74		
1	<i>slr1979</i>	<i>trpE</i>	anthranilate synthase component I	-1.92	-0.65	0.00		
2	<i>sll1185</i>	<i>hemF</i>	coproporphyrinogen III oxidase	-1.48	-0.14	0.02		7,11ab,13
3	<i>slr1227</i>		chloroplastic outer envelope membr protein homolog	-2.42	0.29	-0.91		
3	<i>slr1744</i>		N-acetylmuramoyl-L-alanine amidase	-2.52	0.00	-0.18		
4	<i>sll1814</i>	<i>secY</i>	preprotein translocase SecY subunit	-1.85	-0.15	-0.16		11a
4	<i>slr1747</i>		cell death suppressor protein Lls1 homolog	-1.25	0.28	-0.08	11ab	
4	<i>slr1267</i>	<i>ftsW</i>	cell division protein FtsW	-2.15	-0.39	0.07		
5	<i>sll0158</i>	<i>glgB</i>	1,4-alpha-glucan branching enzyme	-1.97	-0.51	-0.71		
6	<i>sr11289</i>		isocitrate dehydrogenase (NADP+)	-2.32	0.37	-0.30		
6	<i>sll1077</i>		agmatinase	-2.36	-0.43	-0.54		11ab,13
6	<i>sll1709</i>		3-ketoacyl-acyl carrier protein reductase	-1.16	0.11	-0.32		
6	<i>slr1734</i>	<i>opcA</i>	putative OxPPCycle protein OpcA	-2.29	0.04	0.04		
6	<i>sll0807</i>	<i>rpe</i>	pentose-5-phosphate-3-epimerase	-2.40	-0.57	-0.59	3b	
8	<i>slr0261</i>	<i>ndhH</i>	NADH dehydrogenase subunit 7	-1.18	-0.43	-0.72		
8	<i>slr1329</i>	<i>atpB</i>	ATP synthase beta subunit	-1.30	0.19	0.40		11a,13
8	<i>slr1280</i>	<i>ndhK</i>	NADH dehydrogenase subunit NdhK	-2.28	0.03	-0.22		
8	<i>sll0427</i>	<i>psbO</i>	photosystem II manganese-stabilizing polypeptide	-0.96	-0.06	0.07		2ab,11ab,15
8	<i>slr0171</i>	<i>ycf37</i>	photosystem I assembly related protein Ycf37	-1.91	-0.10	0.12		
8	<i>sll1471</i>	<i>cpcG2</i>	phycobilisome rod-core linker polypeptide	-1.06	0.12	-0.11		13,15
8	<i>slr0335</i>	<i>apcE</i>	phycobilisome core-membrane linker polypeptide	-1.43	-0.09	-0.44		2ab,7,10,11ab,15
8	<i>slr1138</i>	<i>ctaE</i>	cytochrome c oxidase subunit III	-1.11	0.80	-0.06		
9	<i>slr1226</i>	<i>purC</i>	phosphoribosyl aminodazole succinocarboxamide	-1.85	0.18	-0.85		
9	<i>sll1815</i>		adenylate kinase	-1.88	0.01	-0.05		
9	<i>sll1631</i>		putative cytidine and deoxycytidylate deaminase	-1.55	0.88	-0.19		
9	<i>sll0838</i>	<i>pyrF</i>	orotidine 5' monophosphate decarboxylase	-1.10	0.25	0.01		
9	<i>slr0213</i>	<i>guaA</i>	GMP synthetase	-1.04	-0.24	-0.02		2a
10	<i>sll1708</i>		two-component response regulator NarL subfamily	-2.40	1.11	-0.60		
10	<i>slr1325</i>		GTP pyrophosphokinase	-1.99	0.09	-0.30		
10	<i>sll1228</i>		two-component hybrid sensor and regulator	-3.20	-0.43	-0.19		
10	<i>slr1225</i>		serine/threonine kinase	-2.64	1.21	-0.26		
10	<i>slr1969</i>		two-component sensor histidine kinase	-2.33	-0.52	0.40		
10	<i>sll1888</i>		two-component sensor histidine kinase	-3.01	-0.65	-0.66		
10	<i>sll1387</i>	<i>pppA</i>	serine/threonine protein phosphatase PppA	-2.32	0.15	1.29		
11	<i>slr1803</i>		adenine-specific DNA methylase	-1.43	0.44	0.56		
11	<i>slr1822</i>		endonuclease III	-1.59	0.37	0.63		
11	<i>sll1165</i>		DNA mismatch repair protein	-1.59	-0.92	-0.26	12	
12	<i>slr1265</i>	<i>rpoC1</i>	RNA polymerase gamma-subunit	-1.58	-0.59	-0.66		
12	<i>sll1818</i>	<i>rpoA</i>	RNA polymerase alpha subunit	-1.55	-0.21	-0.21	5b,7	11a,15
12	<i>sll1789</i>	<i>rpoC2</i>	RNA polymerase beta prime subunit	-1.75	0.21	-1.00		

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
13	<i>ssl3445</i>	<i>rpl31</i>	50S ribosomal protein L31	-1.73	-0.17	-0.16		11a
13	<i>sll1822</i>	<i>rps9</i>	30S ribosomal protein S9	-1.51	-0.25	-0.05		11a
13	<i>sll1821</i>	<i>rpl13</i>	50S ribosomal protein L13	-1.52	-0.26	-0.26		11a
13	<i>sll1820</i>		tRNA pseudouridine synthase 1	-1.30	-0.37	-0.23		
13	<i>sll1819</i>	<i>rpl17</i>	50S ribosomal protein L17	-1.23	-0.13	-0.24		11a
13	<i>sll1817</i>	<i>rps11</i>	30S ribosomal protein S11	-1.78	0.01	-0.16		
13	<i>sll1816</i>	<i>rps13</i>	30S ribosomal protein S13	-1.70	0.17	0.22		
13	<i>sml0006</i>	<i>rpl36</i>	50S ribosomal protein L36	-1.38	-0.01	0.01		
13	<i>ssl3441</i>	<i>infA</i>	initiation factor IF-1	-2.02	0.10	0.10		
13	<i>sll1813</i>	<i>rpl15</i>	50S ribosomal protein L15	-2.19	-0.33	-0.28		11a
13	<i>sll1812</i>	<i>rps5</i>	30S ribosomal protein S5	-2.23	-0.34	-0.27		11a
13	<i>sll1811</i>	<i>rpl18</i>	50S ribosomal protein L18	-1.83	-0.34	-0.26		11a
13	<i>slr1228</i>		peptide-chain-release factor 3	-3.01	-0.12	-0.58		
13	<i>sll1703</i>		protease IV	-1.79	-0.08	-0.27		
13	<i>slr1463</i>	<i>fus</i>	elongation factor EF-G	-1.79	-0.20	-0.50		
14	<i>slr1735</i>	<i>bgtA</i>	ATP-binding subunit of the ABC-type Bgt permease	-2.40	0.41	-0.01		
14	<i>slr0864</i>		ATP-binding protein of ABC transporter	-3.01	-0.64	0.07		
14	<i>slr2057</i>		water channel protein	-2.94	0.04	-0.39		
14	<i>sll0240</i>		ABC transporter ATP-binding protein	-2.80	0.53	0.24		
14	<i>slr0817</i>		salicylate biosynthesis isochorismate synthase	-1.38	-0.27	-0.22		
14	<i>sll1374</i>		probable sugar transporter	-3.22	-0.27	-0.03		
14	<i>sll0912</i>		ABC transporter ATP binding protein	-1.32	0.42	0.22		
14	<i>sll1864</i>		probable chloride channel protein	-1.73	-0.28	-0.08	2a,12,13	
14	<i>slr0074</i>	<i>ycf24</i>	ABC transporter subunit	-1.48	-0.22	-0.20	11b,12,13	15
14	<i>slr0075</i>	<i>ycf16</i>	ABC transporter ATP-binding protein	-1.49	0.06	0.13	10,12,13	
14	<i>sll0672</i>		cation-transporting ATPase PaL homolog	-1.65	0.08	-0.39		
14	<i>slr1575</i>		probable potassium efflux system	-1.74	-0.03	-0.06		
14	<i>slr2107</i>		probable polysaccharide ABC transp permease protein	-1.49	-0.35	-0.85	12	
14	<i>slr2108</i>		prob polysaccharide ABC transp ATP bind subunit	-2.33	-0.57	-0.39		
15	<i>sll1653</i>		similar to menaquinone biosynth methyltransferase	-1.86	0.22	-0.83	1,3ab,4	
15	<i>sll1079</i>	<i>hypB</i>	hydrogenase expression/formation protein HypB	-2.22	-0.78	0.02		
15	<i>sll1078</i>	<i>hypA</i>	hydrogenase expression/formation protein HypA	-2.45	-0.46	-0.06		
15	<i>sll1710</i>		putative transposase [ISY523_b]	-2.18	0.22	0.15		
15	<i>sll1704</i>		probable short chain dehydrogenase	-2.00	0.41	-0.45		
15	<i>sll1369</i>		putative peptidase	-2.55	0.20	-0.17		
15	<i>sll0322</i>	<i>hypF</i>	hydrogenase maturation protein HypF	-1.54	-0.13	-0.09		
15	<i>slr0230</i>		putative transposase [ISY100_f]	-1.31	-0.35	0.14		
15	<i>sll0626</i>		putative neutral invertase	-1.55	-0.20	-0.11		
15	<i>slr1501</i>		probable acetyltransferase	-1.49	0.09	0.25	4,6,8b	
16	<i>slr1736</i>		homogenisate phytlyltransferase	-3.66	0.21	-0.09		
16	<i>sll1399</i>		hypothetical protein	-1.17	-0.11	0.32		
16	<i>sll1203</i>		hypothetical protein	-1.65	-0.58	1.15		
16	<i>sll1659</i>		hypothetical protein	-2.79	-0.07	0.34		
16	<i>sll1658</i>		hypothetical protein	-2.73	-0.17	0.00		
16	<i>sll1652</i>		hypothetical protein	-2.31	0.46	0.15	1,3a,4	
16	<i>sll1186</i>		hypothetical protein	-1.38	-0.21	0.09		
16	<i>slr1220</i>		hypothetical protein	-2.07	0.20	-0.52		
16	<i>sll1138</i>		hypothetical protein	-1.84	0.13	0.54		

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
16	<i>sll1702</i>	<i>ycf51</i>	hypothetical protein YCF51	-1.96	-0.48	-0.19		
16	<i>slr1732</i>		hypothetical protein	-1.46	0.21	-0.09		
16	<i>slr1737</i>		hypothetical protein	-2.32	-0.35	0.22	1	
16	<i>slr0865</i>		hypothetical protein	-3.36	-0.46	0.24		
16	<i>sll0839</i>		hypothetical protein	-1.23	-0.18	0.35		
16	<i>sll1897</i>		hypothetical protein	-2.18	-0.66	0.35		
16	<i>slr1978</i>		hypothetical protein	-1.84	0.11	-0.28		
16	<i>slr1278</i>	<i>ycf62</i>	hypothetical protein YCF62	-2.79	-0.16	-0.12		
16	<i>slr1687</i>		hypothetical protein	-1.68	-0.07	0.17	1,2ab,3ab,4,8ab,11a,13	
16	<i>slr0337</i>		hypothetical protein	-2.44	-0.09	-0.62		
16	<i>slr0169</i>		hypothetical protein	-1.22	0.01	0.40		
16	<i>sll0412</i>		hypothetical protein	-1.47	-0.45	0.13		
16	<i>slr0049</i>		hypothetical protein	-0.94	0.36	0.63		
16	<i>sll0549</i>		hypothetical protein	-1.96	-0.24	-0.37	8b,11a,13	
16	<i>ssr2047</i>		hypothetical protein	-1.65	0.10	-0.25		
16	<i>slr1471</i>		hypothetical protein	-3.24	0.44	-1.05		
16	<i>sll1697</i>		hypothetical protein	-2.98	-0.17	0.25		
16	<i>slr1807</i>		hypothetical protein	-1.84	-0.01	-0.24		
16	<i>sll0157</i>		hypothetical protein	-1.21	0.15	-0.27	11b	
16	<i>slr0362</i>		hypothetical protein	-1.21	0.28	-0.14		
16	<i>slr0380</i>		hypothetical protein	-1.02	0.07	-0.17		
16	<i>sll0740</i>		hypothetical protein	-2.48	-0.24	-0.48		
16	<i>slr1807</i>		hypothetical protein	-1.84	-0.01	-0.24		
16	<i>slr1114</i>		hypothetical protein	-2.51	-0.66	-0.19	13	
17	<i>slr1222</i>		unknown protein	-2.42	0.27	-0.55		
17	<i>sll1267</i>		unknown protein	-0.96	-0.32	0.04		
17	<i>slr0867</i>		unknown protein	-2.90	0.33	-0.56		
17	<i>slr0262</i>		unknown protein	-1.21	-0.84	-0.58		
17	<i>sll0241</i>		unknown protein	-2.28	0.11	-0.43		
17	<i>sll1528</i>		unknown protein	-1.10	-0.13	0.11		
17	<i>slr1865</i>		unknown protein	-2.01	-0.86	-0.66		
17	<i>slr1243</i>		unknown protein	-2.70	-0.55	0.07		
17	<i>slr0377</i>		unknown protein	-1.12	0.13	-0.10		
17	<i>sll1135</i>		unknown protein	-2.92	-0.64	-1.10		
4	<i>sll1212</i>		GDP-D-mannose dehydratase	-0.74	-1.07	-0.25		13,15
4	<i>sll1325</i>	<i>atpD</i>	ATP synthase d subunit	0.56	-1.40	-0.27		11b,13,15
4	<i>sll1028</i>	<i>ccmK</i>	carbon dioxide concentr. mechanism protein CcmK	-0.37	-1.43	0.39	11a	11b,15
4	<i>sll1298</i>		putative carboxymethylenebutenolidase	-0.46	-1.42	0.34		11b
4	<i>sll1688</i>		threonine synthase	-0.83	-1.35	-0.21		11b
4	<i>sll1982</i>		putative transposase [ISY352_c2]	0.04	-1.30	0.54		
5	<i>slr1622</i>	<i>ppa</i>	soluble inorganic pyrophosphatase	-0.84	-1.56	1.08		
6	<i>sll1983</i>		putative transposase [ISY100_n]	-0.62	-1.01	0.40		
8	<i>sll1056</i>	<i>purL</i>	phosphoribosylformyl glycinamide synthetase II	0.57	-1.26	-0.43		
8	<i>sll0698</i>	<i>dfr</i>	drug sensory protein A	0.09	-1.06	-0.40		
8	<i>sll1327</i>	<i>atpC</i>	ATP synthase g subunit	0.12	-1.43	0.12		11b
8	<i>ssl2615</i>	<i>atpH</i>	ATP synthase subunit c	0.01	-1.50	-0.52		15
8	<i>sll1322</i>	<i>atpI</i>	ATP synthase subunit a	-1.03	-1.36	-0.83		11b,15

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
8	<i>slr1075</i>		putative transposase [ISY100_b]	-0.22	-1.03	0.71		15
8	<i>slr1604</i>		cell division protein FtsH	0.40	-1.34	-0.30	2a,10,11,13	
8	<i>smr0004</i>	<i>psaI</i>	photosystem I subunit VIII	0.88	-1.32	-0.60		
8	<i>slr1254</i>	<i>pds</i>	phytoene dehydrogenase (phytoene desaturase)	-0.24	-0.98	-0.07	11ab	
8	<i>slr0500</i>	<i>hisB</i>	imidazoleglycerol-phosphate dehydratase	-0.03	-1.38	-0.40		
8	<i>slr0118</i>	<i>thiC</i>	thiamine biosynthesis protein ThiC	-0.07	-1.39	0.04		
8	<i>slr1380</i>	<i>cydB</i>	cytochrome oxidase d subunit II	0.10	-1.69	-0.76		
8	<i>slr2083</i>	<i>ctaEII</i>	cytochrome c oxidase subunit III	-0.81	-1.92	0.04		
11	<i>sll1985</i>		putative transposase [ISY352_c1]	-0.74	-2.26	0.62		
11	<i>sll1033</i>		probable protein phosphatase	0.20	-1.70	-0.53		
11	<i>slr0915</i>		putative endonuclease	-0.76	-1.07	1.81		
12	<i>sll1323</i>	<i>atpG</i>	ATP synthase subunit b'	0.23	-1.34	-0.22		11b,13,15
12	<i>slr1655</i>	<i>psaL</i>	photosystem I subunit XI	0.82	-1.17	-0.21		
13	<i>sll1326</i>	<i>atpA</i>	ATP synthase a subunit	0.00	-1.24	-0.83		11b,13,15
14	<i>sll1030</i>	<i>ccmL</i>	carbon dioxide concentr. mechanism protein CcmL	-0.50	-1.13	0.01	11a	
14	<i>sll1984</i>		putative transposase [ISY100_n]	-0.64	-1.61	0.24		
14	<i>sll0759</i>		ABC transporter ATP-binding protein	-0.28	-1.57	-0.19	11ab	
15	<i>sll1407</i>		probable methyltransferase	-0.49	-1.18	-0.43		
15	<i>sll1676</i>		4-alpha-glucanotransferase	-0.55	-1.49	-0.24		
15	<i>sll0378</i>	<i>cobA</i>	uroporphyrin-III C-methyltransferase	-0.11	-1.69	1.22		
15	<i>sll0377</i>		transcription-repair coupling factor	-0.26	-1.05	-0.45		
15	<i>slr1787</i>		thiamine-monophosphate kinase	-0.56	-1.75	-0.84		
16	<i>slr0272</i>		unknown protein	-0.81	-1.18	-0.02	13	
16	<i>sll0072</i>		hypothetical protein	0.04	-1.35	-0.19		
16	<i>sll0590</i>		unknown protein	0.04	-1.66	-0.34		
16	<i>slr0316</i>		hypothetical protein	-0.75	-1.43	-0.46		
16	<i>sll0031</i>		hypothetical protein	0.25	-1.25	0.00		
16	<i>sll0659</i>		hypothetical protein	-0.27	-1.83	-0.09		
16	<i>slr0625</i>		hypothetical protein	-0.77	-1.17	-0.13		
16	<i>slr0729</i>		hypothetical protein	-0.33	-1.10	-0.65		
16	<i>slr0729</i>		hypothetical protein	-0.72	-1.35	-0.32		
17	<i>slr0635</i>		hypothetical protein	-0.11	-1.22	0.42		
17	<i>sll0436</i>		hypothetical protein	-0.05	-1.04	0.10		
17	<i>sll1151</i>		unknown protein	0.15	-1.20	-0.20		
17	<i>slr1484</i>		unknown protein	0.82	-1.46	-0.75		
1	<i>sll0100</i>		N-acyl-L-amino acid amidohydrolase	0.35	0.33	-2.20	8b	
2	<i>slr1093</i>		2-amino-4-OH-6-hydroxymethyl dihydropteridine pk	0.36	-0.38	-1.23	5b	
3	<i>slr1908</i>		probable porin; major outer membrane protein	1.70	0.13	-1.16	10	
3	<i>sll1724</i>		probable glycosyltransferase	1.66	0.97	-1.61		
4	<i>sll0716</i>		signal peptidase I	0.82	-0.43	-1.40		
6	<i>sll0244</i>		UDP-glucose 4-epimerase	-0.76	-0.88	-1.34		
8	<i>sll0226</i>	<i>ycf4</i>	photosystem I assembly related protein	-0.84	-0.84	-1.24		
8	<i>slr1838</i>	<i>ccmK</i>	carbon dioxide concentr. mechanism protein CcmK	0.05	-0.20	-1.34		
8	<i>slr1839</i>	<i>ccmK</i>	carbon dioxide concentr. mechanism protein CcmK	-0.42	-0.35	-1.51		
10	<i>slr1871</i>		transcriptional regulator	1.37	-0.16	-1.71		
11	<i>slr0451</i>		putative helicase	0.97	0.04	-1.17		
11	<i>sll1772</i>	<i>mutS</i>	DNA mismatch repair protein MutS	1.96	0.91	-1.18		
13	<i>slr1592</i>		probable pseudouridine synthase	0.84	0.16	-2.71		

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
13	<i>slr1967</i>		probable RNA methyltransferase	1.56	0.17	-1.28		
13	<i>slr0535</i>		Protease	1.75	-0.21	-1.53		
14	<i>slr1595</i>		Na ⁺ /H ⁺ antiporter	-0.32	-0.85	-1.42		
14	<i>slr1776</i>		high affinity sulfate transp.	0.55	-0.64	-1.05		
15	<i>slr0210</i>		bacitracin resistance protein	0.28	-0.62	-1.43		
15	<i>slr1723</i>		probable glycosyltransferase	2.56	1.64	-1.53		
16	<i>slr1593</i>		hypothetical protein	1.22	-0.02	-2.75		
16	<i>ssr2708</i>		hypothetical protein	-0.51	-0.52	-1.29		
16	<i>ssr2711</i>		hypothetical protein	-0.37	-0.77	-1.65		
16	<i>slr1900</i>		hypothetical protein	-0.26	-0.28	-1.28		
16	<i>slr1123</i>		hypothetical protein	0.41	-0.10	-1.05		
16	<i>slr0016</i>		hypothetical protein	-0.15	-0.38	-1.97		
16	<i>slr0195</i>		hypothetical protein	0.30	-0.11	-1.68		
16	<i>slr0374</i>		hypothetical protein	0.05	0.21	-1.17	13	10
16	<i>slr0524</i>		hypothetical protein	-0.11	0.28	-2.08		
16	<i>slr1417</i>	<i>ycf57</i>	hypothetical protein YCF57	1.86	0.12	-1.30		
16	<i>slr0692</i>	<i>ycf45</i>	hypothetical protein YCF45	-0.25	-0.69	-1.48		
16	<i>slr1039</i>		hypothetical protein	-0.58	-0.82	-1.52		
17	<i>slr0943</i>		unknown protein	1.13	-0.05	-1.33		
17	<i>slr0656</i>		unknown protein	-0.61	-0.38	-0.94	14	
17	<i>slr1028</i>		unknown protein	1.00	-0.03	-1.17		
17	<i>slr0907</i>		unknown protein	0.56	-0.47	-1.63		
17	<i>slr0286</i>		unknown protein	-0.39	0.09	-1.44		
1	<i>slr1363</i>	<i>ilvC</i>	ketol-acid reductoisomerase	-1.11	-1.03	0.86	10	
2	<i>slr1777</i>	<i>chlD</i>	magnesium-chelatase subunit ChID	-1.18	-1.12	-0.29		
2	<i>slr1055</i>	<i>chlH</i>	magnesium-protoporphyrin methyltransferase	-1.66	-1.11	-0.20		11b
2	<i>slr1875</i>		heme oxygenase	-1.72	-0.97	-0.79		
2	<i>slr0600</i>		NADP-thioredoxin reductase	-2.32	-1.33	-0.23	13	
3	<i>slr1271</i>		prob. UDP-N-acetyl-D-mannosaminuronic acid transf.	-2.94	-1.20	-0.16		
3	<i>slr1272</i>		probable porin; major outer membrane protein	-3.09	-2.53	-0.80		2b
4	<i>slr1274</i>		probable fimbrial assembly protein PilM	-2.45	-1.50	-0.25		11b
4	<i>slr0774</i>		protein-export membrane protein SecD	-2.41	-1.60	-0.36		
5	<i>slr1639</i>	<i>ureD</i>	urease accessory protein D	-2.78	-1.35	0.26		
6	<i>slr0920</i>		phosphoenolpyruvate carboxylase	-1.40	-1.82	0.13		
8	<i>slr2082</i>	<i>ctaDII</i>	cytochrome c oxidase subunit I	-0.87	-0.92	0.38		
8	<i>slr1281</i>	<i>ndhJ</i>	NADH dehydrogenase subunit I	-2.32	-0.85	-0.04		
8	<i>slr0813</i>	<i>ctaC</i>	cytochrome c oxidase subunit II	-1.54	-1.20	-0.57		
8	<i>slr1300</i>		putative methyltransferase	-1.41	-1.91	-0.84		
11	<i>slr1209</i>	<i>lig</i>	DNA ligase	-1.53	-1.64	-0.01		
11	<i>slr1868</i>	<i>dnaG</i>	DNA primase	-2.18	-2.05	0.56		
11	<i>slr0920</i>		mutator MutT protein	-1.28	-1.02	-0.20		
11	<i>slr1134</i>		mutator MutT homolog	-1.58	-0.89	-0.82		
13	<i>slr1984</i>	<i>rps1b</i>	nucl. acid-bind. protein, 30S ribosomal protein S1 hom.	-1.46	-0.99	0.71		
13	<i>slr0786</i>		methionine aminopeptidase	-1.81	-1.55	0.18	3b	
13	<i>slr1299</i>		acetate kinase	-0.89	-1.64	-0.53		
14	<i>slr1316</i>		iron(III) dicitrate transport system permease protein	-1.08	-1.11	-0.27		
14	<i>slr1317</i>		iron(III) dicitrate transport system permease protein	-1.42	-1.00	0.38		
14	<i>slr1319</i>		iron-uptake system ATP-binding protein	-1.72	-1.28	-0.07		

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
14	<i>slr1200</i>		permease prot of branched-chain a.a. ABC transp	-1.20	-1.62	-0.25	15	11a
15	<i>sll1437</i>		putative transposase [ISY100_q]	-1.16	-1.58	0.20		
15	<i>sll1436</i>		putative transposase [ISY100_q]	-2.56	-1.19	0.27		
15	<i>sll1408</i>		transcriptional regulator	-0.70	-1.44	0.77	15	
15	<i>slr1019</i>		phenazine biosynthetic protein PhzF homolog	-2.29	-2.35	0.47		
15	<i>slr0298</i>		FraH protein homolog	-1.14	-1.08	0.10		
16	<i>sll1252</i>		hypothetical protein	-2.53	-1.70	-0.83		
16	<i>slr1270</i>		hypothetical protein	-3.15	-1.40	0.23		
16	<i>slr1273</i>		hypothetical protein	-2.23	-1.49	-0.34		
16	<i>slr1152</i>		hypothetical protein	-1.62	-1.38	-0.07		
16	<i>slr1677</i>		hypothetical protein	-1.26	-1.05	-0.06	11ab	
16	<i>slr0771</i>		hypothetical protein	-0.98	-1.01	-0.10		
16	<i>sll1433</i>		hypothetical protein	-1.78	-1.07	0.06		
16	<i>sll1532</i>		hypothetical protein	-1.45	-1.96	0.17		
16	<i>slr1464</i>		hypothetical protein	-1.73	-1.28	0.05		
17	<i>slr1670</i>		unknown protein	-1.99	-1.90	0.40	3ab	
17	<i>slr0914</i>		unknown protein	-1.42	-1.03	1.39		11b
17	<i>slr1257</i>		unknown protein	-0.94	-1.24	0.99		
17	<i>slr2017</i>		unknown protein	-3.15	-1.70	0.11		
17	<i>slr2018</i>		unknown protein	-2.67	-1.64	-0.26		
17	<i>sll1167</i>		hypothetical protein	-2.51	-1.31	-0.16	1,2a,4,13	
17	<i>slr1163</i>		unknown protein	-1.88	-1.21	0.15		
1	<i>slr0966</i>		tryptophan synthase alpha chain	-2.78	-0.42	-1.14		
1	<i>slr1665</i>	<i>dapF</i>	diaminopimelate epimerase	-1.27	-0.89	-2.05		
3	<i>sll1271</i>		probable porin; major outer membrane protein	-1.69	-0.39	-0.85		
6	<i>sll1625</i>	<i>sdhB</i>	succinate dehydrogenase iron- sulphur protein subunit	-2.79	0.87	-1.55		
6	<i>sll0329</i>		6-phosphogluconate dehydrogenase	-1.51	-0.02	-1.38		
7	<i>sll1068</i>	<i>acp</i>	acyl carrier protein	-2.79	0.07	-2.59		
10	<i>sll1624</i>		two-component response regulator	-3.41	1.24	-1.02		
10	<i>slr1285</i>		two-component sensor histidine kinase	-0.81	0.21	-0.93	1,5a,6,11b,13	
11	<i>slr2058</i>	<i>topA</i>	DNA topoisomerase I	-1.77	0.58	-0.98		
14	<i>sll1623</i>		ABC transporter ATP-binding protein	-2.09	1.24	-1.02		
14	<i>sll1623</i>		ABC transporter ATP-binding protein	-2.09	1.24	-1.02		
15	<i>sll1647</i>		probable phosphinothricin N-acetyltransferase	-2.28	-0.47	-1.35	13	
16	<i>slr1451</i>		hypothetical protein	-1.23	-0.81	-1.28		
16	<i>slr1864</i>		hypothetical protein	-2.75	0.01	-1.24		
16	<i>slr1927</i>		hypothetical protein	-1.33	-0.14	-1.65		
17	<i>sll1755</i>		unknown protein	-3.21	-0.68	-1.23		
8	<i>slr1834</i>	<i>psaA</i>	P700 apoprotein subunit la	-0.32	-1.53	-1.90		10,11ab,15
8	<i>slr1835</i>	<i>psaB</i>	P700 apoprotein subunit lb	-0.39	-0.98	-1.35		10,11ab,15
8	<i>slr1379</i>	<i>cydA</i>	cytochrome oxidase d subunit I	-0.81	-2.63	-1.65		
8	<i>sll1578</i>	<i>cpcA</i>	phycocyanin alpha subunit	-0.64	-2.19	-1.31		7,10,11ab,15
8	<i>sll1051</i>	<i>cpcF</i>	phycocyanin alpha-subunit phycocyanobilin lyase	-0.72	-1.56	-1.43		
12	<i>slr0743</i>		similar to N utilization substance protein	-0.89	-1.39	-1.25		
13	<i>slr0992</i>		probable tRNA/rRNA methyltransferase	-0.25	-1.02	-1.25	5a	
15	<i>sll1253</i>		similar to polyA polymerase	-0.61	-1.78	-1.27		
16	<i>ssl2069</i>		hypothetical protein	-0.82	-1.06	-1.50		
16	<i>ssl2009</i>		hypothetical protein	0.46	-0.93	-1.62		

Appendix 2B (continued). List of down-regulated ORFs.

Category	ORF	Gene	Product	S	N	P	Other studies	
							Up	Down
16	<i>slr0207</i>		hypothetical protein	-0.52	-1.41	-1.28		
17	<i>slr0358</i>		unknown protein	-0.79	-1.33	-1.40		13
2	<i>sll1184</i>	<i>ho1</i>	heme oxygenase	-1.46	-1.60	-1.12		7,10,11ab
4	<i>sll0430</i>	<i>htpG</i>	heat shock protein HtpG	-2.76	-2.37	-2.24	2b,3b,5a,6,8b, 10,11b,13,15	
7	<i>slr1755</i>		NAD+ dependent glycerol-3-phosphate dehydrogenase	-1.80	-1.20	-2.14		
8	<i>ssl3093</i>	<i>cpcD</i>	phycobilisome small rod linker polypeptide	-1.38	-2.79	-1.33		10,15
8	<i>sll1580</i>	<i>cpcC1</i>	phycobilisome rod linker polypeptide	-2.52	-3.44	-2.05		2ab,7,10, 13,15
8	<i>sll1579</i>	<i>cpcC2</i>	phycobilisome rod linker polypeptide	-2.00	-3.12	-2.49		7,10,13,15
8	<i>sll1577</i>	<i>cpcB</i>	phycocyanin beta subunit	-1.95	-2.60	-2.08		2ab,10,11ab, 13,15
10	<i>slr0640</i>		two-component sensor histidine kinase	-1.31	-1.58	-1.87		
12	<i>slr0346</i>	<i>mc</i>	ribonuclease III	-0.97	-1.29	-1.17		
13	<i>slr1703</i>	<i>serS</i>	seryl-tRNA synthetase	-0.91	-2.14	-1.61		11b
13	<i>sll1098</i>	<i>fus</i>	elongation factor EF-G	-1.44	-1.57	-1.28		
14	<i>slr2019</i>		ATP-binding protein of ABC transporter	-4.29	-1.85	-1.54		
14	<i>slr1318</i>		iron-uptake system ATP-binding protein	-2.65	-1.47	-1.02		
15	<i>slr0788</i>		similar to pre-B cell enhancing factor	-2.45	-1.31	-1.94		
16	<i>slr0348</i>		hypothetical protein	-1.15	-1.11	-0.94		
16	<i>slr2030</i>		hypothetical protein	-2.11	-0.97	-1.35		
16	<i>slr1493</i>		hypothetical protein	-1.53	-1.29	-1.20		

Appendix 3.

R-script used to assess differential expression patterns ### in the nitrogen starvation experiments

>"Command in R"

+ denotes commands longer than one string

Output of the command in R-shell is in italic

Comments

```
>library(limma)          # Main library
>library(vsn)           # Library for vsn-normalization
>library(gplots)
  # Library with advanced heatmap function used for data
  # visualisation and clustering.
```

Data import:

```
>loadPath <- "D:/R/Data/DataNnt"
  # Path for the folder containing raw hybridization data
>savePath <- "D:/R/Data/Out"
  # Path to the output folder
>targetsFile <- "ExpDescr.txt"
  # Text file describing experiment; contains file names for all
  # hybridizations and targets applied in red and green
  # channels.
>targets <- readTargets(file=targetsFile, path=loadPath, sep="\t")
  # targets – variable collecting information about two nitrogen
  # starvation experiments: 12 hours starvation and time seria
  # starvation-recovery experiment.
>targets.Nt <- targets[9:26,]
  # variable selecting data related only to the time seria experiment
>show(targets.Nt)
```

	<i>fileName</i>	<i>sampleID</i>	<i>Cy3</i>	<i>Cy5</i>
9	<i>Nt_006_0003_A02.txt</i>	<i>N1.X</i>	<i>Nt.6</i>	<i>Nt.0</i>
10	<i>Nt_006_0005_A01.txt</i>	<i>N2.X</i>	<i>Nt.6</i>	<i>Nt.0</i>
11	<i>Nt_006_0002_A01.txt</i>	<i>N3.X</i>	<i>Nt.6</i>	<i>Nt.0</i>
12	<i>Nt_012_0002_A02.txt</i>	<i>N2.X</i>	<i>Nt.12</i>	<i>Nt.0</i>
13	<i>Nt_012_0003_A01.txt</i>	<i>N3.X</i>	<i>Nt.12</i>	<i>Nt.0</i>
14	<i>Nt_012_0007_A01.txt</i>	<i>N4.X</i>	<i>Nt.12</i>	<i>Nt.0</i>
15	<i>Nt_024_0001_A02.txt</i>	<i>N2.X</i>	<i>Nt.24</i>	<i>Nt.0</i>
16	<i>Nt_024_0004_A02.txt</i>	<i>N3.X</i>	<i>Nt.24</i>	<i>Nt.0</i>
17	<i>Nt_024_0007_A02.txt</i>	<i>N4.X</i>	<i>Nt.24</i>	<i>Nt.0</i>
18	<i>Nt_096_0004_A01.txt</i>	<i>N3.X</i>	<i>Nt.96</i>	<i>Nt.0</i>
19	<i>Nt_096_0008_A01.txt</i>	<i>N4.X</i>	<i>Nt.96</i>	<i>Nt.0</i>
20	<i>Nt_096_0009_A01.txt</i>	<i>N6.X</i>	<i>Nt.96</i>	<i>Nt.0</i>
21	<i>Nt_102_0008_A02.txt</i>	<i>N4.X</i>	<i>Nt.102</i>	<i>Nt.0</i>

```

22 Nt_102_0005_A02.txt      N5.X Nt.102 Nt.0
23 Nt_102_0009_A02.txt      N6.X Nt.102 Nt.0
24 Nt_108_0001_A01.txt      N3.X Nt.108 Nt.0
25 Nt_108_0006_A02.txt      N4.X Nt.108 Nt.0
26 Nt_108_0006_A01.txt      N5.X Nt.108 Nt.0

```

```

>data.columns <- list(R="rMeanSignal", G="gMeanSignal",
+ Rb="rBGMedianSignal", Gb="gBGMedianSignal")
  # Variable specifying column names in raw data file;
  # this columns contains raw probe intensities and
  # background intensities in red and green channels
>anno.columns <- c("ControlType", "ProbeName")
  # Variable specifying column names with annotation data
>RG.Nt <- read.maimages(targets.Nt$fileName, path=loadPath,
+ source="generic", quote="", columns = data.columns,
+ annotation=anno.columns)
  # read.maimages - Generic function for data import
>dim(RG.Nt)
[1] 8635  18
  # Dimensions of the imported data matrix; denotes number of
  # probes in each hybridization and number of loaded hybridizations

```

SpotTypes attachment:

```

>spottypes <- readSpotTypes(file = "SpotTypeFile.txt", path = "D:/R/DataV")
  # Import of the text file describing types of probes spotted on
  # the microarray (e.g. positive and negative controls and probes)
>show(spottypes)
  SpotType ControlType color cex
1 Gene * black 0.2
2 PosContr 1 red 0.2
3 NegContr -1 blue 0.2
>RG.Nt$genes$Status <- controlStatus(spottypes, RG.Nt)
  Matching patterns for: ControlType
  Found 8635 Gene
  Found 465 PosContr
  Found 79 NegContr
  Setting attributes: values color cex
  # function attaching to each probe on the array its status:
  # whether it belongs to the control type or not

```

Removal from the data-set probes related to the control:

```

>isGene.Nt <- RG.Nt$genes$Status == "Gene"
  # isGene.Nt – list of indexes of probes,
  # which are not of the control type
>RG.Nt <- RG.Nt[isGene.Nt,]
>dim(RG.Nt)
[1] 8091  18

```

Dimensions of the resulting data-set

Normalisation:

```
>RG.non <- RG.Nt
  # not normalized intensity data set
>MA.non <- MA.RG(RG.non)
  # conversion of the intensities into the not normalized MA data set,
  # where M is the ratio of the intensities in red and green channels
  # in log-scale and A is the average intensity in both channels
>RG.b <- backgroundCorrect(RG.non, method="minimum")
  # Correction for the background;
  # option "method" selects method for background correction
>MA.lo <- normalizeWithinArrays(RG.b, method="loess")
  # Data normalized within each array with LOESS normalization
>MA.aq <- normalizeBetweenArrays(MA.lo, method="Aq")
  # MA normalized by "Aquantile" method between all arrays
>RG.aq <- RG.MA(MA.aq)
  # conversion of the normalized MA data into the normalized
  # intensity data set
```

Diagnostic plots:

```
>arrayNo <- 3
  # array Number to plot
>plot(0:12, 0:12, xlab = "Green", ylab = "Red", type = "n")
>abline(0,1)
>points(log(RG.non[,arrayNo]$R), log(RG.non[,arrayNo]$G), cex = 0.3)
  # plot(...) function sets scale; abline(0,1) sets diagonal;
  # Intensity RG-plot of not normalized data of the array 3;
  # intensities are log-trasformed
>plot(0:12, 0:12, xlab = "Green", ylab = "Red", type = "n")
>abline(0,1)
>points(log(RG.aq[,arrayNo]$R), log(RG.aq[,arrayNo]$G), cex = 0.3)
  # plot(...) sets scale; abline(0,1) sets diagonal;
  # Intensity RG-plot of normalized data of the array 3;
  # intensities are log-trasformed
>plotMA(MA.non[,arrayNo])
>abline(0,0)
  # MA-plot of not normalized data of the array 3
>plotMA(MA.aq[,arrayNo])
>abline(0,0)
  # MA-plot of normalized data of the array 3
>plotDensities(MA.non)
  # Density-plot of not normalized complete data set
```

```

>plotDensities(MA.aq)
  # Density-plot of normalized complete data set
>boxplot(MA.non$M~col(MA.non$M),names=colnames(MA.non$M))
  # Box-plot of not normalized complete data set
>boxplot(MA.aq$M~col(MA.aq$M),names=colnames(MA.aq$M))
  # Box-plot of normalized complete data set

### Cluster analysis and Intensity Heatmap of the complete data set:
>RG.R <- RG.aq$R
>RG.G <- RG.aq$G
  # Extraction of the separate R (Red) and G (Green) channel intensities
>colnames(RG.R) <- paste(colnames(RG.R),"R", sep=".")
>colnames(RG.G) <- paste(colnames(RG.G),"G", sep=".")
  # Assignment of the column names to separate channels
>RG.only <- cbind(RG.R, RG.G)
  # Combining Separate Red and Green channels into one data matrix
>DataCol = colorpanel(256, 'green', , 'red')
  # Sets up colour-range represented on the image varying from green to red
>heatdata <- log10(RG.only)
  # Converts data to the log-scale
>heatmap.2(heatdata, col=DataCol, Rowv=NA, scale="non", dendrogram="col",
+ cexCol=0.7, mar=c(7,5), symkey=FALSE, trace="none", density.info="none")
  # heatmap.2() function performs visualisation and cluster analysis
  # in search for similarities and dissimilarities in the data;
  # Rowv=NA defines that there would be no clustering on rows
  # of the data matrix (representing 8091 probes);
  # Clustering is performed on columns which represent separate
  # normalized intensities in red and green channels of all
  # hybridizations; # heatmap.2() function utilises functions
  # dist() for calculation of distances between data columns with
  # "Euclidian" distance measure and hclust() to perform
  # "hierarchical" cluster analysis.

### Ratio Heatmap:
>MA.M <- MA.aq$M
  # Extraction of M-values (Ratio) only from the data
>DataCol = colorpanel(256, 'green', 'black', 'red')
  # Sets up colour-range represented on the image varying from
  # green (down-regulation) to black (no-regulation) and to red (up-regulation)
>heatdata <- MA.M
>heatmap.2(heatdata, col=DataCol, Rowv=NA, scale="non", dendrogram="col",
+ cexCol=0.8, mar=c(7,5), symkey=FALSE, trace="none", density.info="none")
  # Here columns represents ratios of individual arrays,

```

```

# so the cluster analysis highlights similarities between biological
# replicates and dissimilarities between time-points.

### Fit linear model for each probe on the array, application of empirical
### Bayes statistics, band adjustment for multiple testing in search
### for differentially expressed genes.
>design.Nt <- modelMatrix(targets.Nt, ref="Nt.0")
  Found unique target names:
  Nt.0 Nt.102 Nt.108 Nt.12 Nt.24 Nt.6 Nt.96
> show(design.Nt)
  Nt.102 Nt.108 Nt.12 Nt.24 Nt.6 Nt.96
  9      0      0      0      0     -1      0
 10      0      0      0      0     -1      0
 11      0      0      0      0     -1      0
 12      0      0     -1      0      0      0
 13      0      0     -1      0      0      0
 14      0      0     -1      0      0      0
 15      0      0      0     -1      0      0
 16      0      0      0     -1      0      0
 17      0      0      0     -1      0      0
 18      0      0      0      0      0     -1
 19      0      0      0      0      0     -1
 20      0      0      0      0      0     -1
 21     -1      0      0      0      0      0
 22     -1      0      0      0      0      0
 23     -1      0      0      0      0      0
 24      0     -1      0      0      0      0
 25      0     -1      0      0      0      0
 26      0     -1      0      0      0      0

# Sets design matrix with zero time point as a reference
>fit.Nt <- lmFit(MA.aq, design.Nt)
# This function fits multiple linear models. It accepts data from
# a experiment involving a series of microarrays with the same set
# of probes. A linear model is fitted to the expression data
# for each probe. The coefficients of the fitted models describe
# the differences between the RNA sources hybridized to the arrays.
>cont.matrix.Nt <- makeContrasts(Nt.6, Nt.12, Nt.24, Nt.96, Nt.102, Nt.108,
+ Nt.6.rec=Nt.102-Nt.96, Nt.12.rec=Nt.108-Nt.96, levels=design.Nt)
# Construct the contrasts matrix; as contrasts we define here
# comparisons of interests, e.g. Nt.6 is the comparison of expression
# of Nt.6 (which is 6 hours time point) against reference (which is 0
# hours time point), Nt.6.rec is the 6 hours recovery time point
>fit.Nt <- contrasts.fit(fit.Nt, cont.matrix.Nt)
# Given a linear model fit to microarray data, compute estimated
# coefficients and standard errors for a given set of contrasts.
>fit.Nt <- eBayes(fit.Nt)

```

```

# These functions is used to rank genes in order of evidence for
# differential expression. It uses an empirical Bayes method to
# shrink the gene-wise sample variances towards a common values and,
# in so doing, augmenting the degrees of freedom for the individual
# variances. It computes moderated t-statistics and log-odds of
# differential expression.
>d.Nt <- decideTests(fit.Nt, method="separate", adjust.method="fdr", p.value=0.01)
# Classify a series of related t-statistics as up, down or not
# significant. A number of different multiple testing schemes are
# offered which adjust for multiple testing down the genes as well
# as across contrasts for each gene.
# It produce essentially a numeric matrix with elements '-1', '0'
# or '1' depending on whether each t-statistic is classified
# as significantly negative, not significant or significantly
# positive respectively.
>summary(d.Nt)
      Nt.6 Nt.12 Nt.24 Nt.96 Nt.102 Nt.108 Nt.6.rec Nt.12.rec
-1  1473  1902  1859  2186   1825   1855     2262     2048
 0   5131  4279  4421  3683   4476   4480     3951     4146
 1   1487  1910  1811  2222   1790   1756     1878     1897
# This function counts number of regulated genes
# in each specified contrast
>vennCounts(d.Nt[,1:3], include="up")
      Nt.6 Nt.12 Nt.24 Counts
[1,]    0    0    0   5490
[2,]    0    0    1   322
[3,]    0    1    0   281
[4,]    0    1    1   511
[5,]    1    0    0   308
[6,]    1    0    1    61
[7,]    1    1    0   201
[8,]    1    1    1   917
# This function produce classification counts for any number
# of contrasts specified; in this particular case it highlights
# up-regulated genes in 6, 12 and 24 hours of time-seria experiment,
# and calculates number of specifically or commonly regulated probes
>plotMA(fit.Nt, status=d.Nt[,1], cex=0.2, legend=TRUE)
>abline(0,0)
# plotMA() function graphically represents here up- and
# down-regulated probes for one of the contrasts;
# Here we used as example 6 hours time point
>vennDiagram(d.Nt[,1:3], include="up")

```

```
# This function is analogous to the previous one, but it creates
# Venn diagram; number of contrasts is limited to three
# parameter include="down" will plot commonly down-regulated probes.
```

Export of the resulting matrix:

```
>write.fit(fit.Nt, results=d.Nt, file="D:/R/Data/Out/fit.Nt.txt", digits=3, adjust="fdr", sep="\t")
# Data exported as text tab-delimited file with Ratios for each
# contrast specified by cont.matrix and with the decision whether
# probe is differentially expressed or not in particular contrast.
```

Analysis of the expression behaviour of selected genes of interest

```
>fit.Nt.File <- "D:/R/Data/Out/fit.Nt.txt"
# filename and the path to the file storing the results of the
# the specified contrasts and decisions about differential probe
# expression
>geneList.File <- "D:/R/Data/GeneList.PSI.txt"
# filename and the path to the file storing the list of probes
# corresponding to genes of interest; here we used as an example
# list of structural genes encoding subunits of Photosystem I (PSI)
>Nt.complete <- read.table(file=fit.Nt.File, header=TRUE, sep="\t", quote="")
# Import of the complete linear fit in text format
>g.list <- read.table(file = geneList.File, header = TRUE, sep = "\t", quote="")
# Import of the list of genes of interest
>g.Probe <- g.list$Probe.ID
# Extraction from the list of genes probe identifiers only
>g.Name <- g.list$GeneName
# Extraction from the list of genes gene names only
>i.names.Nt <- match(g.Probe, Nt.complete$Genes.ProbeName)
# Extracting indexes from complete fit table matching
# the identifiers from the list of genes of interest
>write.table(Nt.complete[i.names.Nt,], file="D:/R/Data/Out/fit.Nt.PSI.txt",
+ row.names = TRUE, sep="\t")
# Save of the fit information for the PSI genes only in text file
>M.list.fit <- as.matrix(Nt.complete[i.names.Nt,2:7])
# Extracting from the complete fit-object only ratios related to
# PSI genes and converting it into the matrix format
>min(M.list.fit)
>max(M.list.fit)
# Check for the min and max of the matrix
>rownames(M.list.fit) <- paste(g.Name, "-", g.Probe)
# Assignment of the row names for the PSI genes in form: # "gene name – probe ID"
>heatdata.fit <- M.list.fit
```

```
>heatmap.2(heatdata.fit, col=DataCol, Colv=FALSE, scale="non",  
+ dendrogram="row", cexCol=0.7, cexRow=0.7, mar=c(8,9),  
+ symkey=FALSE, trace="none", density.info="none", breaks=seq(-2,2,0.015625))  
  # This function performs hierarchical clustering and visualisation of  
  # the expression profile of the photosystem I related genes
```

Appendix 4A. List of functional categories of *Synechocystis* genes.

Category and subcategory annotation are as in Cyanobase (genome.kazusa.or.jp/cyanobase)..
Category numbers are assigned in alphabetical order.

Category	SubCategory
1 - Amino acid biosynthesis	1a - Aromatic amino acid family 1b - Aspartate family 1c - Branched chain family 1d - Glutamate family / Nitrogen assimilation 1e - Serine family / Sulfur assimilation
2 - Biosynthesis of cofactors, prosthetic groups, and carriers	2a - Carotenoid 2b - Cobalamin, heme, phycobilin and porphyrin 2c - Folic acid 2d - Menaquinone and ubiquinone 2e - Molybdopterin 2f - Thiamin 2g- Thioredoxin, glutaredoxin, and glutathione
3 - Cell envelope	3a - Membranes, lipoproteins, and porins 3b - Murein sacculus and peptidoglycan 3c - Surface polysaccharides, lipopolysaccharides
4 - Cellular processes	4a - Chaperones 4b - Chemotaxis 4c - Detoxification 4d - Protein and peptide secretion 4e - Transformation
5 - Central intermediary metabolism	5a - Other 5b - Polysaccharides and glycoproteins
6 - Energy metabolism	6a - Amino acids and amines 6b - Glycolysis 6c - Pentose phosphate pathway 6d - Pyruvate and acetyl-CoA metabolism 6e - Pyruvate dehydrogenase 6f - Sugars 6g - TCA cycle
7 - Fatty acid, phospholipid and sterol metabolism	
8 - Photosynthesis and respiration	8a - ATP synthase 8b - CO ₂ fixation 8c - Cytochrome b ₆ /f complex 8d - NADH dehydrogenase 8e - Photosystem I 8f - Photosystem II 8g - Phycobilisome 8h - Respiratory terminal oxidases 8i - Soluble electron carriers
9 - Purines, pyrimidines, nucleosides, and nucleotides	9a - Purine ribonucleotide biosynthesis 9b - Pyrimidine ribonucleotide biosynthesis
10 - Regulatory functions	
11 - DNA replication, restriction, modification, recombination, and repair	
12 - Transcription	12a - RNA synthesis, modification, and DNA transcription
13 - Translation	13a - Aminoacyl tRNA synthetases and tRNA modification 13b - Degradation of proteins, peptides, and glycopeptides

Appendix 4A (continued). List of functional categories of *Synechocystis* genes.

Category	SubCategory
	13c - Nucleoproteins
	13d - Protein modification and translation factors
	13e - Ribosomal proteins: synthesis and modification
14 - Transport and binding proteins	
15 - Other categories	15a - Adaptations and atypical conditions
	15b - Drug and analog sensitivity
	15c - Hydrogenase
	15d - Other
	15e - Transposon-related functions
	15f - WD repeat proteins
16 - Hypothetical	
17 - Unknown	

Appendix 4B. List of significantly down-regulated genes.

ORF, gene, gene product, category and subcategory and functional annotation are as in Cyanobase (genome.kazusa.or.jp/cyanobase). Category numbers are assigned in alphabetical order. Categories description is listed in Appendix 4A. p-value - significance of differential expression, adjusted for multiple hypothesis testing using the false discovery rate; FC - fold change; only genes with $p < 0.01$ and $FC > 1.5$ are listed. Top 50 of most strongly down-regulated genes are highlighted in bold.

ORF	Gene	p-value	FC	Gene Product	Category
slr0608	hisI	6,10E-04	-1,78	histidine biosynthesis bifunctional protein HisI	1a
slr0966	trpA	4,22E-03	-1,65	tryptophan synthase alpha chain	1a
slr1867	trpD	1,32E-03	-1,96	anthranilate phosphoribosyltransferase	1a
slI1662		1,92E-04	-2,01	probable prephenate dehydratase	1a
slI1058	dapB	1,70E-04	-2,13	dihydrodipicolinate reductase	1b
slI1172	thrC	3,75E-03	-1,74	threonine synthase	1b
slI0006		2,01E-04	-2,26	putative aminotransferase	1b
slr2072	ilvA	5,29E-04	-2,61	L-threonine deaminase	1c
slr0452	ilvD	1,14E-03	-3,55	dihydroxyacid dehydratase	1c
slI0065	ilvN	2,17E-03	-2,02	acetolactate synthase small subunit	1c
slr1517	leuB	1,95E-03	-1,81	3-isopropylmalate dehydrogenase	1c
slI0504	lysA	6,06E-05	-2,20	diaminopimelate decarboxylase	1c
slr0710	gdhA	9,07E-05	-2,91	glutamate dehydrogenase (NADP+)	1d
slI0450	norB	8,43E-04	-1,65	cytochrome b subunit of nitric oxide reductase	1d
slI0461	proA	1,19E-03	-1,53	gamma-glutamyl phosphate reductase	1d
slI0601		9,15E-04	-1,99	nitrilase homolog	1d
slr0644		7,07E-03	-1,64	nitrogen regulation protein NifR3 homolog	1d
slI1931	glyA	4,13E-04	-2,11	serine hydroxymethyltransferase	1e
slr0739	crtE	5,99E-03	-1,52	geranylgeranyl pyrophosphate synthase	2a
slr0772	chlB	1,81E-04	-2,07	light-independent protochlorophyllide reductase subunit ChlB	2b
slr1777	chlD	5,09E-03	-1,66	magnesium protoporphyrin IX chelatase subunit D	2b
slr0749	chlL	5,52E-04	-4,56	light-independent protochlorophyllide reductase iron protein subunit ChlL	2b
slr0750	chlN	3,00E-05	-3,93	light-independent protochlorophyllide reductase subunit ChlN	2b
slI1091	chlP	1,28E-04	-1,65	geranylgeranyl hydrogenase	2b
slI1184	ho1	3,41E-03	-2,02	heme oxygenase	2b
slr0506	por	9,73E-04	-2,73	light-dependent NADPH-protochlorophyllide oxidoreductase	2b
slr1467		2,09E-04	-1,59	precorrin isomerase	2b
slr0426	folE	1,11E-03	-1,89	GTP cyclohydrolase I	2c
slr1093	folK	2,39E-04	-1,50	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	2c
slI0409		3,09E-03	-1,57	similar to O-succinylbenzoate-CoA synthase	2d
slI0635	thiE	2,77E-03	-1,70	probable thiamine-phosphate pyrophosphorylase	2f
slr1787		2,32E-04	-1,91	thiamine-monophosphate kinase	2f
slr0623	trxA	2,75E-05	-3,12	thioredoxin	2g
slI1057	trxM2	2,98E-04	-1,79	thioredoxin M	2g
slr0236		1,64E-03	-1,52	similar to glutathione S-transferase	2g
slr1423	murC	4,03E-03	-1,77	UDP-N-acetylmuramate-alanine ligase	3b
slI2010	murD	4,33E-03	-1,50	UDP-N-acetylmuramoylalanine--D-glutamate ligase	3b
slI0379		1,42E-03	-2,21	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine o-acyltransferase	3b
slr0015		1,65E-03	-1,67	lipid A disaccharide synthase	3c
slr1118		8,13E-03	-1,54	probable UDP-N-acetyl-D-mannosaminuronic acid transferase	3c
slI1213		2,17E-03	-1,50	GDP-fucose synthetase	3c
slI0170	dnaK2	8,85E-04	-1,56	DnaK protein 2, heat shock protein 70, molecular chaperone	4a

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1533	pilT2	1,73E-03	-1,77	twitching mobility protein	4b
slI1987	cpx, katG	2,59E-04	-1,99	catalase peroxidase	4c
ssl3335	secE	1,58E-04	-1,71	preprotein translocase SecE subunit	4d
slI1639	ureD	4,97E-05	-2,04	urease accessory protein D	5a
slr1176		1,21E-04	-4,03	glucose-1-phosphate adenylyltransferase	5b
slI0573		9,45E-03	-2,85	carbamate kinase	6a
slr0879		3,24E-03	-1,64	glycine decarboxylase complex H-protein	6a
slr0394	pgk	1,47E-04	-3,04	phosphoglycerate kinase	6b
slr1945		6,76E-04	-1,81	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	6b
slI1070		7,35E-04	-1,85	transketolase	6c
slr0301		5,18E-05	-2,55	phosphoenolpyruvate synthase	6d
slI1841		3,77E-04	-2,00	pyruvate dehydrogenase dihydrolipoamide acetyltransferase comp. (E2)	6e
slI1721		2,30E-04	-1,98	pyruvate dehydrogenase E1 component, beta subunit	6e
slI1212		2,29E-05	-2,26	GDP-mannose 4,6-dehydratase	6f
slI0053	accC	4,25E-04	-2,94	biotin carboxylase	7
ssl2084	acpP	1,03E-03	-2,30	acyl carrier protein	7
slr1369	cdsA	9,86E-03	-1,54	phosphatidate cytidyltransferase	7
slr1510	plsX	3,15E-04	-2,04	fatty acid/phospholipid synthesis protein PlsX	7
slr1020	sqdB	6,81E-03	-2,58	sulfolipid biosynthesis protein SqdB	7
slI1655		8,93E-04	-3,38	similar to biotin [acetyl-CoA-carboxylase] ligase	7
slI1069		6,52E-03	-3,08	3-oxoacyl-[acyl-carrier-protein] synthase II	7
slr0776		2,70E-05	-2,46	UDP-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase	7
slr1051		5,08E-03	-1,98	enoyl-[acyl-carrier-protein] reductase	7
slI1605		2,30E-03	-1,76	(3R)-hydroxymyristol acyl carrier protein dehydrase	7
slI1326	atpA	5,11E-04	-5,26	ATP synthase alpha chain	8a
slr1329	atpB	2,43E-03	-3,31	ATP synthase beta subunit	8a
slI1327	atpC	3,48E-05	-5,46	ATP synthase gamma chain	8a
slr1330	atpE	2,80E-03	-2,42	ATP synthase epsilon chain of CF(1)	8a
slI1323	atpG	1,11E-05	-4,39	ATP synthase subunit b' of CF(0)	8a
ssl2615	atpH	2,10E-04	-3,87	ATP synthase C chain of CF(0)	8a
slI1322	atpI	9,64E-06	-5,46	ATP synthase A chain of CF(0)	8a
slI1321		9,37E-05	-3,60	hypothetical protein	8a
slI1029	ccmK1	5,28E-05	-4,54	carbon dioxide concentrating mechanism protein CcmK	8b
slI1028	ccmK2	1,09E-04	-6,20	carbon dioxide concentrating mechanism protein CcmK	8b
slr1838	ccmK3	7,94E-05	-2,45	carbon dioxide concentrating mechanism protein CcmK homolog 3	8b
slr1839	ccmK4	1,67E-05	-3,75	carbon dioxide concentrating mechanism protein CcmK homolog 4	8b
slI1031	ccmM	1,58E-04	-4,15	carbon dioxide concentrating mechanism protein CcmM	8b
slI1342	gap2	1,18E-03	-1,90	NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase	8b
slI1525	prk	1,23E-03	-2,66	phosphoribulokinase	8b
slr0009	rbcL	2,21E-05	-8,73	ribulose biphosphate carboxylase large subunit	8b
slr0012	rbcS	1,67E-04	-4,38	ribulose biphosphate carboxylase small subunit	8b
slr1347		9,43E-04	-1,56	beta-type carbonic anhydrase localized in the carboxysome	8b
slI1317	petA	1,47E-04	-2,62	apocytochrome f, component of cytochrome b6/f complex	8c
slI1316	petC1	1,90E-04	-2,76	cytochrome b6-f complex iron-sulfur subunit (Rieske iron sulfur protein)	8c
smr0010	petG	3,80E-04	-1,50	cytochrome b6-f complex subunit 5	8c
smr0003	petM	6,12E-06	-5,58	cytochrome b6-f complex subunit PetM	8c
smI0004	petN	5,29E-05	-2,84	cytochrome b6-f complex subunit VIII	8c
slr2007	ndhD5	1,34E-03	-2,15	NADH dehydrogenase subunit 4	8d
slr2009	ndhD6	4,92E-03	-1,57	NADH dehydrogenase subunit 4	8d

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
ssl0563	psaC	8,14E-05	-3,50	photosystem I subunit VII	8e
slr0737	psaD	2,10E-04	-2,34	photosystem I subunit II	8e
ssr2831	psaE	1,03E-05	-4,91	photosystem I subunit IV	8e
sl0819	psaF	2,35E-03	-1,89	photosystem I reaction center subunit III precursor (PSI-F)	8e
smr0004	psaI	1,15E-04	-3,18	photosystem I subunit VIII	8e
smI0008	psaJ	1,46E-05	-2,91	photosystem I subunit IX	8e
ssr0390	psaK1	6,50E-05	-2,74	photosystem I reaction center subunit X	8e
slI0629	psaK2	6,29E-04	-2,96	alternative photosystem I reaction center subunit X	8e
slr1655	psaL	1,21E-04	-2,85	photosystem I subunit XI	8e
smr0005	psaM	7,13E-05	-3,30	photosystem I subunit XII	8e
slr0171	ycf37	6,89E-03	-2,42	photosystem I assembly related protein Ycf37	8e
slr1645	psb27, psbZ	5,27E-03	-1,96	photosystem II 11 kD protein	8f
slr0906	psbB	3,77E-05	-2,70	photosystem II core light harvesting protein	8f
slI0851	psbC	4,23E-03	-2,17	photosystem II CP43 protein	8f
slI0849	psbD	4,04E-03	-1,90	photosystem II reaction center D2 protein	8f
slr0927	psbD2	1,51E-03	-1,67	photosystem II reaction center D2 protein	8f
ssr3451	psbE	3,58E-05	-2,58	cytochrome b559 alpha subunit	8f
smr0006	psbF	3,87E-05	-3,19	cytochrome b559 b subunit	8f
ssl2598	psbH	1,02E-04	-2,52	photosystem II PsbH protein	8f
smr0008	psbJ	3,33E-04	-3,31	photosystem II PsbJ protein	8f
smI0005	psbK	5,21E-04	-2,43	photosystem II PsbK protein	8f
smr0007	psbL	6,01E-05	-2,96	photosystem II PsbL protein	8f
smI0003	psbM	2,84E-05	-6,34	photosystem II reaction center M protein	8f
slI0427	psbO	6,42E-06	-10,71	photosystem II manganese-stabilizing polypeptide	8f
smr0001	psbT, ycf8	1,87E-04	-1,72	photosystem II PsbT protein	8f
slI1194	psbU	5,90E-05	-2,17	photosystem II 12 kDa extrinsic protein	8f
slI0258	psbV	3,13E-05	-3,37	cytochrome c550	8f
smI0002	psbX	3,02E-04	-1,72	photosystem II PsbX protein	8f
smI0007	psbY	2,93E-04	-1,69	photosystem II protein Y	8f
slr2067	apcA	1,56E-03	-2,04	allophycocyanin alpha subunit	8g
slr1986	apcB	5,13E-04	-2,97	allophycocyanin beta subunit	8g
ssr3383	apcC	2,81E-05	-5,76	phycobilisome small core linker polypeptide	8g
slI0928	apcD	1,24E-04	-2,03	allophycocyanin-B	8g
slr0335	apcE	1,26E-05	-6,66	phycobilisome core-membrane linker polypeptide	8g
slI1578	cpcA	6,72E-04	-2,96	phycocyanin alpha subunit	8g
slI1577	cpcB	2,87E-05	-3,81	phycocyanin beta subunit	8g
slI1580	cpcC1	2,62E-05	-6,81	phycobilisome rod linker polypeptide	8g
slI1579	cpcC2	1,17E-04	-7,27	phycobilisome rod linker polypeptide	8g
ssl3093	cpcD	2,42E-05	-8,07	phycobilisome small rod linker polypeptide	8g
slr2051	cpcG1	1,74E-03	-2,46	phycobilisome rod-core linker polypeptide	8g
slI1471	cpcG2	3,14E-03	-3,96	phycobilisome rod-core linker polypeptide	8g
slI1663		2,92E-05	-2,47	phycocyanin alpha phycocyanobilin lyase related protein	8g
slI1815	adk	3,47E-04	-1,80	adenylate kinase	9a
slI0421	purB	1,04E-03	-1,75	adenylosuccinate lyase	9a
slI1056	purL	9,73E-03	-1,79	phosphoribosylformyl glycnamidine synthetase II	9a
slr0861	purT	6,47E-04	-2,02	glycinamide ribonucleotide transformylase	9a
slr1722		2,63E-05	-2,83	inosine-5'-monophosphate dehydrogenase	9a
slI1059		2,64E-04	-1,72	adenylate kinase	9a
slI1443	pyrG	1,65E-03	-1,90	CTP synthetase	9b

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI0750	hik8, sasA	2,08E-03	-1,53	two-component sensor histidine kinase, KaiC-interacting protein	10
slI1423	ntcA, ycf28	5,74E-03	-1,56	global nitrogen regulator	10
slI0038	pixG, pisG	2,53E-04	-1,68	positive phototaxis protein, two-comp. response regulator PatA subfamily	10
slr1584		2,74E-04	-3,00	two-component transcription regulator OmpR subfamily	10
slI1286		4,42E-04	-1,72	transcriptional regulator	10
slr0418		1,26E-03	-1,51	putative transcription factor DevT homolog	10
slr0965	dnaN	4,79E-03	-1,64	DNA polymerase III beta subunit	11
slr1689	fpg	3,02E-03	-1,55	formamidopyrimidine-DNA glycosylase	11
slr0417	gyrA	6,24E-05	-2,16	DNA gyrase subunit A	11
slI2005	gyrB	1,23E-03	-1,81	DNA gyrase B subunit [Contains: Ssp gyrB intein]	11
slI1854		1,33E-03	-1,81	exodeoxyribonuclease III	11
slr1469	mpA	6,60E-05	-1,96	protein subunit of ribonuclease P (RNase P)	12a
slI1818	rpoA	6,34E-05	-2,21	RNA polymerase alpha subunit	12a
slI1789	rpoC2	6,14E-05	-2,18	RNA polymerase beta prime subunit	12a
ssr1600		6,88E-04	-1,58	similar to anti-sigma f factor antagonist	12a
slr0220	glyS	1,50E-03	-1,72	glycyl-tRNA synthetase beta chain	13a
slr1560	hisS	4,15E-03	-1,69	histidyl tRNA synthetase	13a
slI1074	leuS	8,60E-04	-1,90	leucyl-tRNA synthetase	13a
slr1550	lysS	5,56E-05	-2,25	lysyl-tRNA synthetase	13a
slI1820		3,77E-04	-1,72	tRNA pseudouridine synthase 1	13a
slr0008	ctpA	1,59E-03	-1,61	carboxyl-terminal processing protease	13b
slr0193	rbp3	1,77E-04	-1,57	RNA-binding protein	13c
slr0434	efp	4,94E-05	-2,70	elongation factor P	13d
slI0145	frr, rrf	3,20E-03	-2,90	ribosome releasing factor	13d
slI0830	fus	1,98E-03	-2,11	elongation factor EF-G	13d
slr1463	fus	3,56E-04	-1,63	elongation factor EF-G	13d
slr0744	infB	4,36E-04	-1,72	translation initiation factor IF-2	13d
slI0227	ppiB	5,52E-03	-2,03	peptidyl-prolyl cis-trans isomerase B, periplasmic protein	13d
slI1110	prfA	4,09E-04	-1,50	peptide chain release factor 1	13d
slI1261	tsf	2,25E-05	-2,63	elongation factor TS	13d
slr1251		9,54E-03	-2,17	peptidyl-prolyl cis-trans isomerase	13d
slI0408		4,97E-04	-1,85	peptidyl-prolyl cis-trans isomerase	13d
slI1744	rpl1	1,87E-04	-4,32	50S ribosomal protein L1	13e
slI1745	rpl10	2,96E-05	-6,37	50S ribosomal protein L10	13e
slI1743	rpl11	2,73E-04	-3,14	50S ribosomal protein L11	13e
slI1746	rpl12	1,15E-05	-6,59	50S ribosomal protein L12	13e
slI1806	rpl14	1,70E-04	-5,63	50S ribosomal protein L14	13e
slI1813	rpl15	2,20E-05	-2,81	50S ribosomal protein L15	13e
slI1805	rpl16	9,33E-05	-7,46	50S ribosomal protein L16	13e
slI1819	rpl17	9,05E-05	-1,97	50S ribosomal protein L17	13e
slI1811	rpl18	4,85E-05	-3,77	50S ribosomal protein L18	13e
slI1740	rpl19	3,33E-04	-1,55	50S ribosomal protein L19	13e
slI1802	rpl2	5,14E-05	-7,50	50S ribosomal protein L2	13e
slI1803	rpl22	1,46E-05	-6,87	50S ribosomal protein L22	13e
slI1801	rpl23	9,05E-05	-8,06	50S ribosomal protein L23	13e
slI1807	rpl24	3,87E-05	-5,78	50S ribosomal protein L24	13e
ssI3436	rpl29	1,71E-04	-5,06	50S ribosomal protein L29	13e
slI1799	rpl3	4,85E-05	-8,92	50S ribosomal protein L3	13e
ssr1398	rpl33	1,78E-04	-2,05	50S ribosomal protein L33	13e

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
smr0011	rpl34	4,63E-05	-1,86	50S ribosomal protein L34	13e
slI1808	rpl5	1,27E-05	-7,56	50S ribosomal protein L5	13e
slI1810	rpl6	9,20E-05	-4,81	50S ribosomal protein L6	13e
slI1101	rps10	4,22E-05	-2,59	30S ribosomal protein S10	13e
slI1817	rps11	7,55E-05	-1,92	30S ribosomal protein S11	13e
ssl3437	rps17	7,40E-06	-7,78	30S ribosomal protein S17	13e
ssr1399	rps18	2,69E-03	-1,91	30S ribosomal protein S18	13e
ssl3432	rps19	6,78E-06	-10,67	30S ribosomal protein S19	13e
slI1260	rps2	3,40E-04	-3,06	30S ribosomal protein S2	13e
slI1804	rps3	1,63E-05	-8,60	30S ribosomal protein S3	13e
slI1812	rps5	1,37E-04	-3,21	30S ribosomal protein S5	13e
slI1767	rps6	1,84E-04	-3,47	30S ribosomal protein S6	13e
slI1809	rps8	6,85E-06	-6,21	30S ribosomal protein S8	13e
slr1295	futA1	5,95E-04	-3,11	iron transport system substrate-binding protein	14
slI0771	glcP, gtr	9,57E-04	-2,47	glucose transport protein	14
slI1599	mntA	4,18E-04	-1,65	manganese transport system ATP-binding protein MntA	14
slI0146	natC	2,50E-04	-2,25	Integral membrane protein of the ABC-type, Nat permease for neutral a.a.	14
slr0415	nhaS5	5,79E-03	-1,92	Na ⁺ /H ⁺ antiporter	14
slI1920	pacS	1,02E-03	-2,56	copper-transporting P-type ATPase PacS	14
slr0681		1,86E-05	-2,98	probable sodium/calcium exchanger protein	14
slr1890		1,53E-04	-1,93	bacterioferritin	14
slr2057		2,10E-04	-1,92	water channel protein	14
slI0574		8,14E-03	-1,73	probable permease protein of lipopolysaccharide ABC transporter	14
slI0477		6,67E-04	-1,67	putative biopolymer transport ExbB-like protein	14
slr2043		1,13E-03	-1,54	zinc transport system substrate-binding protein	14
slI0947	lrtA	4,38E-05	-2,60	light repressed protein A homolog	15a
ssl2250		1,27E-04	-2,28	bacterioferritin-associated ferredoxin	15b
slI0648		5,86E-04	-1,66	probable glycosyltransferase	15b
slr2094	fbpl	4,13E-03	-2,73	fructose-1,6-/sedoheptulose-1,7-bisphosphatase	15d
slI1595	kaiC2	8,58E-04	-1,51	circadian clock protein KaiC homolog	15d
slr1942	kaiC3	3,86E-03	-1,80	circadian clock protein KaiC homolog	15d
slr1761		4,70E-05	-2,70	FKBP-type peptidyl-prolyl cis-trans isomerase, periplasmic protein	15d
slI1308		8,20E-04	-2,29	probable oxidoreductase	15d
slr1106		8,53E-05	-2,12	prohibitin	15d
slI1945		2,66E-03	-1,73	1-deoxyxylulose-5-phosphate synthase	15d
slr1916		4,10E-04	-1,68	probable esterase	15d
slI1521		1,79E-03	-1,59	flavoprotein	15d
slI0550		3,40E-04	-1,54	flavoprotein	15d
slI1284		1,30E-03	-1,52	esterase	15d
sml0010		5,51E-05	-3,24	putative transposase	15e
ssr2227		6,61E-04	-2,60	putative transposase	15e
slr0800		2,99E-04	-1,77	putative transposase [ISY802_c]	15e
slI1792		6,49E-03	-1,58	putative transposase [ISY802_a]	15e
ssl1911	gifA	1,96E-03	-4,71	glutamine synthetase inactivating factor IF7	16
slI1281	psbZ, ycf9	1,31E-04	-5,04	photosystem II PsbZ protein	16
slr0011	rbcX	5,08E-05	-3,95	possible Rubisco chaperonin	16
slr1780	ycf54	4,26E-05	-2,88	hypothetical protein YCF54	16
slI1214	ycf59	5,61E-04	-1,52	hypothetical protein YCF59	16
slI0253		6,12E-06	-21,21	hypothetical protein	16

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
ssr0692		2,79E-04	-9,35	hypothetical protein	16
ssr1251		7,55E-06	-8,02	hypothetical protein	16
slI0863		1,36E-04	-4,97	hypothetical protein	16
slr1634		9,05E-03	-4,63	hypothetical protein	16
ssl0483		3,87E-05	-4,33	hypothetical protein	16
slr1963		4,97E-05	-3,58	water-soluble carotenoid protein	16
slI1500		5,28E-05	-3,41	hypothetical protein	16
slr0244		1,52E-05	-3,19	hypothetical protein	16
slI1654		2,03E-04	-3,19	hypothetical protein	16
slr1098		2,98E-04	-3,17	hypothetical protein	16
slI2013		2,27E-03	-3,16	hypothetical protein	16
slr0144		3,97E-05	-3,13	hypothetical protein	16
ssr1528		2,99E-05	-3,06	hypothetical protein	16
ssr2062		4,18E-05	-2,96	hypothetical protein	16
slr2070		1,46E-05	-2,92	hypothetical protein	16
slr1394		3,32E-05	-2,91	hypothetical protein	16
slr1177		3,62E-05	-2,86	hypothetical protein	16
slr1209		1,80E-05	-2,83	hypothetical protein	16
slI1638		1,20E-05	-2,77	hypothetical protein	16
slr0680		7,56E-05	-2,73	hypothetical protein	16
slr0013		1,74E-04	-2,68	hypothetical protein	16
slI1386		1,95E-04	-2,52	hypothetical protein	16
slr1513		3,99E-05	-2,49	periplasmic protein, function unknown	16
slI0735		1,85E-05	-2,46	hypothetical protein	16
ssl3803		2,24E-05	-2,46	hypothetical protein	16
slI1835		1,69E-04	-2,42	periplasmic protein, function unknown	16
slr0695		5,28E-05	-2,42	hypothetical protein	16
ssr1375		4,64E-05	-2,32	hypothetical protein	16
slI1390		2,81E-05	-2,28	hypothetical protein	16
slr0172		9,42E-05	-2,20	hypothetical protein	16
ssl0105		1,75E-03	-2,20	hypothetical protein	16
slI1109		6,68E-05	-2,19	hypothetical protein	16
slI1973		1,28E-03	-2,18	hypothetical protein	16
slr0709		1,11E-04	-2,17	hypothetical protein	16
slI1469		9,70E-04	-2,17	hypothetical protein	16
slr0110		8,12E-05	-2,17	hypothetical protein	16
slr1431		3,39E-05	-2,14	hypothetical protein	16
slI0615		3,62E-05	-2,07	hypothetical protein	16
slI1606		9,49E-05	-2,07	hypothetical protein	16
slI1656		2,45E-04	-1,96	hypothetical protein	16
slr0351		7,62E-04	-1,96	hypothetical protein	16
slr0990		4,53E-03	-1,94	hypothetical protein	16
ssr1562		1,27E-03	-1,93	hypothetical protein	16
slI2002		9,07E-05	-1,91	hypothetical protein	16
slr0887		2,41E-03	-1,91	hypothetical protein	16
ssr0550		4,55E-05	-1,90	hypothetical protein	16
slI0283		5,47E-05	-1,89	hypothetical protein	16
slr0598		1,65E-04	-1,89	hypothetical protein	16
slr0146		4,51E-03	-1,88	hypothetical protein	16

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
sl11911		4,39E-03	-1,88	hypothetical protein	16
sl11543		1,39E-03	-1,88	hypothetical protein	16
ssl1498		7,33E-05	-1,88	hypothetical protein	16
slr0519		1,76E-04	-1,85	hypothetical protein	16
slr1600		6,64E-05	-1,82	hypothetical protein	16
slr1935		1,47E-04	-1,81	hypothetical protein	16
slr1704		1,52E-03	-1,79	hypothetical protein	16
slr2005		6,71E-04	-1,78	periplasmic protein, function unknown	16
slr1451		1,70E-04	-1,77	hypothetical protein	16
slr0148		1,33E-04	-1,77	hypothetical protein	16
sl11188		2,48E-03	-1,76	hypothetical protein	16
slr0147		3,58E-04	-1,74	hypothetical protein	16
sl11348		1,65E-04	-1,72	hypothetical protein	16
slr1506		3,37E-03	-1,69	hypothetical protein	16
sl10545		8,68E-05	-1,69	hypothetical protein	16
ssr2340		2,43E-04	-1,69	hypothetical protein	16
ssr3304		2,92E-03	-1,65	hypothetical protein	16
slr1471		3,53E-04	-1,64	hypothetical protein	16
sl10932		1,42E-03	-1,63	hypothetical protein	16
slr2010		2,70E-03	-1,63	hypothetical protein	16
slr1468		6,32E-04	-1,62	hypothetical protein	16
slr0748		2,58E-04	-1,62	hypothetical protein	16
ssl3291		1,11E-04	-1,62	hypothetical protein	16
slr0806		1,81E-04	-1,61	hypothetical protein	16
slr0280		2,13E-04	-1,60	hypothetical protein	16
slr1470		1,41E-03	-1,59	hypothetical protein	16
slr2105		5,21E-03	-1,59	hypothetical protein	16
sl11022		6,93E-03	-1,59	hypothetical protein	16
slr1557		6,80E-04	-1,58	hypothetical protein	16
slr0400		1,21E-04	-1,57	hypothetical protein	16
slr2025		1,27E-04	-1,56	hypothetical protein	16
ssr0336		2,53E-04	-1,56	hypothetical protein	16
sl11414		1,60E-03	-1,55	hypothetical protein	16
sl11979		4,40E-04	-1,54	hypothetical protein	16
slr0954		4,00E-04	-1,54	hypothetical protein	16
ssl3379		2,27E-04	-1,53	hypothetical protein	16
slr1160		2,63E-04	-1,52	periplasmic protein, function unknown	16
slr0241		1,25E-03	-1,52	hypothetical protein	16
sl11515	gifB	1,06E-04	-6,01	glutamine synthetase inactivating factor IF17	17
ssr1038		1,39E-05	-32,74	unknown protein	17
slr0006		1,73E-05	-4,99	unknown protein	17
ssl2384		1,83E-05	-3,38	unknown protein	17
sl11472		4,45E-05	-3,35	unknown protein	17
slr0476		6,67E-05	-3,25	unknown protein	17
slr1210		3,08E-05	-2,17	unknown protein	17
sl11583		7,16E-03	-2,14	unknown protein	17
sl10630		1,41E-04	-2,10	unknown protein	17
sl10518		4,41E-05	-2,07	unknown protein	17
sl11456		3,58E-03	-1,98	unknown protein	17

Appendix 4B (continued). List of significantly down-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1873		6,90E-03	-1,97	unknown protein	17
ssl1326		1,59E-03	-1,97	unknown protein	17
slI0022		9,15E-05	-1,92	unknown protein	17
slI0624		4,71E-04	-1,89	unknown protein	17
slI0068		9,07E-05	-1,87	unknown protein	17
slr0145		1,36E-04	-1,87	unknown protein	17
ssr2333		1,37E-04	-1,83	unknown protein	17
slr1396		1,28E-03	-1,82	unknown protein	17
ssr2553		3,17E-03	-1,81	unknown protein	17
ssr1853		1,27E-03	-1,80	unknown protein	17
slr1788		1,43E-04	-1,73	unknown protein	17
slI0376		1,25E-03	-1,72	unknown protein	17
slI0140		5,08E-03	-1,66	unknown protein	17
ssr0680		3,89E-03	-1,61	unknown protein	17
slr0962		3,30E-04	-1,58	unknown protein	17
ssl3142		1,56E-04	-1,57	unknown protein	17
slr0318		3,44E-03	-1,56	unknown protein	17
slI0066		2,00E-04	-1,56	unknown protein	17
slr1437		3,62E-04	-1,52	unknown protein	17
slr0209		2,45E-03	-1,50	unknown protein	17

Appendix 4C. List of significantly up-regulated genes.

ORF, gene, gene product, category and subcategory and functional annotation are as in Cyanobase (genome.kazusa.or.jp/cyanobase). Category numbers are assigned in alphabetical order. Categories description is listed in Appendix 4A. p-value - significance of differential expression, adjusted for multiple hypothesis testing using the false discovery rate; FC - fold change; only genes with $p < 0.01$ and $FC > 1.5$ are listed. Top 50 of most strongly down-regulated genes are highlighted in bold.

ORF	Gene	p-value	FC	Gene Product	Category
slI0402	aspC	4,52E-03	1,55	aspartate aminotransferase	1b
slr1898	argB	4,02E-04	1,54	N-acetylglutamate kinase	1d
slr1133	argH	8,46E-04	1,51	L-argininosuccinate lyase	1d
slr0899	cynS	1,67E-05	3,56	cyanate lyase	1d
ssl0707	glnB	4,35E-05	3,17	nitrogen regulatory protein P-II	1d
slr0288	glnN	8,45E-03	3,23	glutamate--ammonia ligase	1d
slI0784	merR	1,11E-04	4,04	nitrilase	1d
slr0898	nirA	1,33E-05	3,83	ferredoxin--nitrite reductase	1d
slr1254	pds, crtD	3,17E-04	1,59	phytoene dehydrogenase (phytoene desaturase)	2a
slI0378	cobA	2,31E-03	1,79	uroporphyrin-III C-methyltransferase	2b
slr0969	cobJ	1,88E-03	1,55	precorrin methylase	2b
slr1368	cobL	5,09E-04	1,58	precorrin decarboxylase	2b
slI0794	corR, coaR	7,73E-03	1,53	cobalt-dependent transcriptional regulator	2b
slr0900	moeA	2,02E-04	2,04	molybdopterin biosynthesis MoeA protein	2e
slI1271		1,78E-04	2,85	probable porin; major outer membrane protein	3a
slr0827		1,30E-03	1,51	alanine racemase	3b
slr0983	rfbF	2,50E-05	2,41	glucose-1-phosphate cytidyltransferase	3c
slr0984	rfbG	1,58E-04	2,04	CDP-glucose 4,6-dehydratase	3c
slr1064		2,37E-04	2,06	probable glycosyltransferase	3c
slr1072		1,82E-04	1,95	GDP-D-mannose dehydratase	3c
slI1294		2,43E-04	1,92	methyl-accepting chemotaxis protein	4b
ssr2784		4,47E-04	1,64	antitoxin ChpI homolog	4c
slr1377		1,58E-04	1,70	leader peptidase I (signal peptidase I)	4d
ssl2922	vapB	2,81E-04	1,64	similar to virulence-associated protein VapB	4e
ssl2923	vapC	1,12E-04	1,93	similar to virulence-associated protein VapC	4e
smI0009		3,70E-04	1,51	similar to virulence-associated protein VapC	4e
slI0158	glgB	6,52E-04	1,59	1,4-alpha-glucan branching enzyme	5b
slr1830	phaC	1,52E-04	2,60	poly(3-hydroxyalkanoate) synthase	5b
slr1367		7,75E-05	2,76	glycogen phosphorylase	5b
slr0237		1,20E-03	1,83	glycogen operon protein GlgX homolog	5b
slr0884	gap1	5,75E-03	2,48	glyceraldehyde 3-phosphate dehydrogenase 1 (NAD+)	6b
slI0587		6,16E-04	2,10	pyruvate kinase	6b
slr1843	zwf	5,23E-04	1,60	glucose 6-phosphate dehydrogenase	6c
slI0329		7,92E-03	2,00	6-phosphogluconate dehydrogenase	6c
slI0920	ppc	7,28E-04	1,56	phosphoenolpyruvate carboxylase	6d
slr1067		4,11E-05	2,31	UDP-glucose 4-epimerase	6f
slr1617		2,50E-05	2,31	similar to UDP-glucose 4-epimerase	6f
slr0493		7,75E-05	1,84	similar to mannose-1-phosphate guanylyltransferase	6f
slr1078		1,41E-03	1,73	similar to UDP-glucose 4-epimerase	6f
slr1289	icd	6,96E-05	2,38	isocitrate dehydrogenase (NADP+)	6g
slr1993	phaA	1,53E-03	2,04	PHA-specific beta-ketothiolase	7
slI0330		8,82E-05	3,74	sepiapterine reductase	7

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slr0054		1,40E-03	2,17	diacylglycerol kinase	7
slr0574		1,00E-03	1,71	cytochrome P450	7
slr0851	ndbA	5,17E-04	2,05	type 2 NADH dehydrogenase	8d
ssl0452	nblA1	1,21E-05	19,40	phycobilisome degradation protein NblA	8g
ssl0453	nblA2	2,12E-05	9,30	phycobilisome degradation protein NblA	8g
sl1899	ctaB	3,42E-03	1,75	cytochrome c oxidase folding protein	8h
slr1136	ctaCl	1,27E-05	3,90	cytochrome c oxidase subunit II	8h
slr1137	ctaDI	6,48E-05	2,47	cytochrome c oxidase subunit I	8h
slr1379	cydA	3,67E-04	2,30	quinol oxidase subunit I	8h
slr1380	cydB	3,68E-05	2,15	quinol oxidase subunit II	8h
sl1382	petF, fdx	2,18E-03	1,50	ferredoxin, petF-like protein	8i
ssl2559		7,11E-04	1,76	ferredoxin	8i
slr0222	hik25	1,50E-03	1,54	two-component hybrid sensor and regulator	10
sl11871	hik6	2,00E-04	1,84	two-component system sensory histidine kinase	10
slr1860	icfG	4,76E-04	1,66	carbon metabolisms regulatory protein IcfG	10
slr1594		5,12E-05	9,98	two-component response regulator PatA subfamily	10
sl11330		2,53E-04	2,82	two-component system response regulator OmpR subfamily	10
sl11291		1,04E-03	2,61	two-component response regulator PatA subfamily	10
sl10690		9,02E-03	2,21	probable transcription regulator	10
sl10782		2,09E-03	2,06	transcriptional regulator	10
slr1694		1,06E-03	1,87	expression activator appA homolog	10
slr0741		9,64E-05	1,80	transcriptional regulator	10
slr1693		6,73E-05	1,80	two-component response regulator PatA subfamily	10
sl11383		7,01E-04	1,58	probable myo-inositol-1(or 4)-monophosphatase	10
slr0653	sigA, rpoDI	9,51E-04	1,84	principal RNA polymerase sigma factor SigA	12a
slr1912		5,39E-04	2,25	putative PP2C-type protein phosphatase	12a
slr1861		1,09E-04	2,12	probable sigma regulatory factor	12a
sl12008		1,70E-04	2,41	processing protease	13b
sl12009		1,71E-04	2,12	processing protease	13b
sl11270	bgtB	3,08E-05	2,55	periplasmic substrate-binding and integral membrane protein of the ABC-type Bgt permease for basic a. a. and glutamine BgtB	14
sl11450	nrtA	5,16E-05	6,76	nitrate/nitrite transport system substrate-binding protein	14
sl11451	nrtB	3,21E-05	2,74	nitrate/nitrite transport system permease protein	14
sl11452	nrtC	9,00E-05	2,11	nitrate/nitrite transport system ATP-binding protein	14
sl11453	nrtD	9,88E-03	1,61	nitrate/nitrite transport system ATP-binding protein	14
slr0447	urtA	2,13E-03	1,64	periplasmic protein, ABC-type urea transport system substrate-binding protein	14
sl10764	urtD	1,23E-05	4,00	urea transport system ATP-binding protein	14
sl11081		4,50E-05	5,53	ABC transport system permease protein	14
sl10536		9,22E-03	2,97	probable potassium channel protein	14
slr1200		5,16E-05	2,06	urea transport system permease protein	14
slr0977		3,54E-04	1,92	ABC transporter, permease component	14
sl11001		5,39E-04	1,91	ATP-binding protein of ABC transporter	14
slr0096		8,18E-04	1,79	low affinity sulfate transporter	14
slr0982		3,92E-03	1,77	probable polysaccharide ABC transporter ATP binding subunit	14
sl11374		3,39E-04	1,73	probable sugar transporter	14
slr2002	cphA	5,48E-04	1,53	cyanophycin synthetase	15a
ssr2595	hliB, scpD	9,82E-04	1,83	high light-inducible polypeptide HliB, CAB/ELIP/HLIP superfamily	15a
sl10086		1,38E-03	1,78	putative arsenical pump-driving ATPase	15b
sl1159		3,72E-04	1,55	probable bacterioferritin comigratory protein	15b

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1220	hoxE	1,82E-04	1,81	putative diaphorase subunit of the bidirectional hydrogenase	15c
slI1221	hoxF	2,40E-04	1,56	diaphorase subunit of the bidirectional hydrogenase	15c
slI1226	hoxH	3,30E-04	2,55	hydrogenase subunit of the bidirectional hydrogenase	15c
slI1223	hoxU	2,65E-05	3,22	diaphorase subunit of the bidirectional hydrogenase	15c
slI1432	hypB	1,06E-04	1,89	putative hydrogenase expression/formation protein HypB	15c
slI1079	hypB	3,45E-03	1,68	putative hydrogenase expression/formation protein HypB	15c
ssl3580	hypC	2,60E-03	1,58	putative hydrogenase expression/formation protein HypC	15c
slr0756	kaiA	2,70E-04	1,59	circadian clock protein KaiA homolog	15d
slr1063		1,34E-05	3,46	plobable glycosyltransferase	15d
slr1065		1,20E-05	3,08	plobable glycosyltransferase	15d
slr1077		2,92E-05	2,29	plobable glycosyltransferase	15d
slr1076		3,46E-04	2,27	plobable glycosyltransferase	15d
slI1305		4,48E-05	2,10	probable hydrolase	15d
slr0309		5,37E-04	2,08	probable methyltransferase	15d
slr0541		1,84E-03	1,94	probable amidotransferase	15d
slr0665		9,49E-05	1,84	aconitate hydratase	15d
slr1610		8,04E-04	1,78	putative C-3 methyl transferase	15d
slI0777		4,94E-04	1,73	putative carboxypeptidase	15d
ssr0871		3,53E-05	2,21	putative transposase [ISY352_e1]	15e
slr0460		4,91E-05	2,07	putative transposase [ISY352_g1]	15e
ssr0817		5,81E-05	1,91	putative transposase [ISY352_g2]	15e
ssr3452		3,53E-04	1,91	putative transposase [ISY352_a]	15e
slr1960		1,81E-04	1,83	putative transposase	15e
slI1982		2,48E-04	1,78	putative transposase [ISY352_c2]	15e
slI0667		1,55E-04	1,75	putative transposase [ISY352_e2]	15e
slI0092		4,44E-04	1,70	putative transposase [ISY391_c]	15e
slr1522		2,43E-03	1,64	putative transposase [ISY352_d]	15e
ssr1176		3,90E-04	1,58	putative transposase [ISY100_v3]	15e
slI1156		2,44E-04	1,56	putative transposase [ISY120_b]	15e
slr1409		4,40E-04	1,59	periplasmic WD-repeat protein	15f
ssl1633	hliC, scpB	1,95E-05	9,12	high light-inducible polypeptide HliC, CAB/ELIP/HLIP superfamily	16
slI0173	vgb	1,06E-05	3,18	virginiamycin B hydrolase, periplasmic protein	16
ssr1425	ycf34	2,77E-05	2,23	hypothetical protein YCF34	16
slr1218	ycf39	8,21E-03	1,74	hypothetical protein YCF39	16
slr2073	ycf50	1,88E-03	2,26	hypothetical protein YCF50	16
slr0376		1,15E-05	6,32	hypothetical protein	16
slr1770		3,21E-05	5,35	hypothetical protein	16
slr1593		7,52E-05	3,95	hypothetical protein	16
slr1612		2,30E-05	3,85	hypothetical protein	16
slI0888		7,40E-06	3,73	hypothetical protein	16
slI1634		7,18E-05	3,40	hypothetical protein	16
slr0645		1,67E-05	3,40	hypothetical protein	16
slr1119		3,89E-05	3,36	hypothetical protein	16
ssl1762		5,15E-05	3,35	hypothetical protein	16
slr1611		5,78E-05	3,29	hypothetical protein	16
slr1069		1,61E-04	3,29	hypothetical protein	16
slI1222		2,51E-05	3,23	hypothetical protein	16
slI0787		2,49E-05	3,21	hypothetical protein	16
slr1614		6,79E-04	3,16	hypothetical protein	16

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1895		1,80E-05	3,14	hypothetical protein	16
ssr1766		1,07E-05	3,00	hypothetical protein	16
ssr2377		1,10E-04	2,99	hypothetical protein	16
ssl3297		2,94E-04	2,98	hypothetical protein	16
ssr1966		1,64E-03	2,86	hypothetical protein	16
slr0981		4,22E-05	2,83	hypothetical protein	16
slr0374		7,18E-05	2,71	hypothetical protein	16
slI1504		2,94E-05	2,64	hypothetical protein	16
slI0743		2,15E-05	2,64	hypothetical protein	16
slr1814		1,64E-05	2,64	hypothetical protein	16
slr1619		1,99E-04	2,62	hypothetical protein	16
slr1081		1,73E-05	2,59	hypothetical protein	16
sml0013		1,73E-05	2,59	hypothetical protein	16
ssl2921		5,86E-05	2,58	hypothetical protein	16
ssr1765		1,64E-05	2,55	hypothetical protein	16
ssl1918		3,05E-04	2,53	hypothetical protein	16
slI1080		4,50E-05	2,52	ABC transport system substrate-binding protein	16
slI0983		3,36E-05	2,51	hypothetical protein	16
slI0185		4,18E-04	2,50	hypothetical protein	16
slr1712		1,83E-05	2,50	hypothetical protein	16
slI1774		1,92E-05	2,49	hypothetical protein	16
slI1715		3,36E-04	2,47	hypothetical protein	16
slr0980		3,26E-05	2,47	hypothetical protein	16
slr0299		6,50E-05	2,41	hypothetical protein	16
ssl0312		5,28E-05	2,39	hypothetical protein	16
slI1505		2,05E-03	2,37	hypothetical protein	16
slr0300		5,11E-04	2,37	hypothetical protein	16
slr0740		2,82E-04	2,35	hypothetical protein	16
slr1813		2,64E-05	2,34	hypothetical protein	16
slr1083		7,30E-05	2,33	hypothetical protein	16
slI1832		7,52E-04	2,28	hypothetical protein	16
slr0810		4,82E-04	2,28	hypothetical protein	16
slr0957		3,10E-04	2,26	hypothetical protein	16
slI0364		2,70E-05	2,25	hypothetical protein	16
ssl2920		1,27E-04	2,24	hypothetical protein	16
slI1969		2,61E-04	2,22	hypothetical protein	16
slI1201		1,38E-04	2,22	hypothetical protein	16
slI0208		8,24E-05	2,21	hypothetical protein	16
slI0205		3,38E-05	2,18	hypothetical protein	16
slr1657		4,91E-04	2,17	hypothetical protein	16
slr0771		6,50E-05	2,16	hypothetical protein	16
ssl1300		1,56E-04	2,15	hypothetical protein	16
slr1664		2,61E-04	2,15	hypothetical protein	16
slr2128		8,50E-05	2,15	hypothetical protein	16
slr1290		3,53E-05	2,14	hypothetical protein	16
slr0082		2,48E-04	2,13	hypothetical protein	16
slI1609		8,53E-04	2,11	hypothetical protein	16
ssr0756		2,22E-05	2,11	hypothetical protein	16
ssr0761		8,07E-05	2,09	hypothetical protein	16

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI0549		7,95E-03	2,08	hypothetical protein	16
ssr0757		3,39E-05	2,07	hypothetical protein	16
slI1314		4,50E-05	2,07	putative C4-dicarboxylase binding protein, periplasmic protein	16
ssr0663		1,35E-04	2,06	hypothetical protein	16
slI1039		1,75E-04	2,04	hypothetical protein	16
slI0742		1,04E-04	2,03	hypothetical protein	16
slr1812		9,09E-05	2,02	hypothetical protein	16
slr0207		9,43E-04	2,00	hypothetical protein	16
slr0292		1,99E-04	2,00	hypothetical protein	16
slI1541		4,42E-04	1,98	hypothetical protein	16
slr1440		8,00E-03	1,98	hypothetical protein	16
slI1355		1,08E-04	1,97	hypothetical protein	16
slr0978		5,17E-05	1,97	hypothetical protein	16
slr0976		6,83E-05	1,96	hypothetical protein	16
slr1117		4,92E-05	1,95	hypothetical protein	16
slI1783		6,67E-05	1,93	hypothetical protein	16
slI1166		2,65E-04	1,92	hypothetical protein	16
slr0885		1,41E-04	1,91	hypothetical protein	16
slr1913		4,33E-05	1,90	hypothetical protein	16
slr1677		1,48E-04	1,90	hypothetical protein	16
slr1752		3,69E-04	1,87	hypothetical protein	16
slr0373		9,74E-03	1,87	hypothetical protein	16
slI0926		5,56E-05	1,86	hypothetical protein	16
slI1898		1,55E-04	1,86	hypothetical protein	16
slr1275		3,22E-04	1,86	hypothetical protein	16
ssr2754		5,76E-05	1,86	hypothetical protein	16
ssl1004		7,46E-05	1,85	hypothetical protein	16
slI0995		1,25E-04	1,85	hypothetical protein	16
slI0744		3,47E-03	1,85	hypothetical protein	16
slr1184		5,65E-04	1,84	hypothetical protein	16
slr1276		1,16E-04	1,84	hypothetical protein	16
slr0238		1,73E-04	1,81	hypothetical protein	16
slr1767		6,11E-05	1,81	hypothetical protein	16
slr2122		1,95E-04	1,80	hypothetical protein	16
slr1203		2,19E-04	1,80	hypothetical protein	16
slI1119		1,51E-03	1,80	hypothetical protein	16
slr1116		8,49E-05	1,80	hypothetical protein	16
slI1072		6,87E-05	1,79	hypothetical protein	16
slr0869		1,33E-03	1,79	hypothetical protein	16
slr1811		1,56E-04	1,79	hypothetical protein	16
ssr2615		1,61E-04	1,77	hypothetical protein	16
slI1825		6,61E-05	1,77	hypothetical protein	16
slI0192		5,10E-03	1,77	hypothetical protein	16
ssr2066		8,22E-05	1,73	hypothetical protein	16
slI1766		8,31E-04	1,73	hypothetical protein	16
slr1327		6,95E-05	1,72	hypothetical protein	16
slI1652		9,12E-05	1,72	hypothetical protein	16
slI1692		8,31E-04	1,72	hypothetical protein	16
ssr2803		4,70E-04	1,72	hypothetical protein	16

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1581		1,08E-04	1,71	hypothetical protein	16
slr1087		1,12E-03	1,70	hypothetical protein	16
slI1158		7,66E-03	1,70	hypothetical protein	16
slr0517		4,56E-04	1,69	hypothetical protein	16
slI1547		9,52E-04	1,69	hypothetical protein	16
slr1583		1,13E-03	1,68	hypothetical protein	16
slr1676		8,81E-04	1,68	hypothetical protein	16
ssl0832		3,36E-03	1,68	hypothetical protein	16
slr0948		6,25E-03	1,67	hypothetical protein	16
slr0755		1,84E-03	1,67	hypothetical protein	16
ssr1114		9,76E-05	1,67	hypothetical protein	16
slr1940		4,07E-04	1,66	periplasmic protein, function unknown	16
slI1455		1,39E-04	1,65	hypothetical protein	16
slI0525		1,72E-03	1,65	hypothetical protein	16
slr1464		5,13E-04	1,64	hypothetical protein	16
slr0326		2,39E-03	1,64	hypothetical protein	16
slI0781		2,61E-04	1,64	hypothetical protein	16
slr1183		1,08E-03	1,64	hypothetical protein	16
slr1886		1,34E-03	1,64	hypothetical protein	16
slr0770		4,42E-04	1,63	hypothetical protein	16
ssr1880		1,04E-04	1,63	hypothetical protein	16
slI0496		5,65E-03	1,62	hypothetical protein	16
slr1259		1,54E-04	1,62	hypothetical protein	16
ssl1046		1,12E-03	1,62	hypothetical protein	16
slI1884		1,66E-04	1,62	hypothetical protein	16
slI1769		8,25E-04	1,62	hypothetical protein	16
slr1241		6,88E-04	1,61	hypothetical protein	16
slr0551		1,58E-04	1,61	hypothetical protein	16
slr1220		1,29E-04	1,60	hypothetical protein	16
slI0925		1,69E-04	1,59	hypothetical protein	16
ssr2755		4,72E-03	1,59	hypothetical protein	16
slr1338		4,46E-04	1,59	hypothetical protein	16
slr1376		1,35E-04	1,59	hypothetical protein	16
slI1961		6,27E-04	1,58	hypothetical protein	16
slI1738		2,68E-03	1,57	hypothetical protein	16
slr0870		1,88E-03	1,57	hypothetical protein	16
slr0784		3,62E-04	1,56	hypothetical protein	16
slI1675		1,23E-03	1,56	hypothetical protein	16
slr1025		8,65E-03	1,56	hypothetical protein	16
slr1260		6,07E-04	1,55	hypothetical protein	16
slI1773		3,23E-04	1,55	hypothetical protein	16
slI1651		1,69E-04	1,55	hypothetical protein	16
slr1363		6,72E-03	1,54	hypothetical protein	16
smI0012		6,24E-04	1,54	hypothetical protein	16
slI0924		1,85E-04	1,54	hypothetical protein	16
slr2084		2,01E-04	1,53	hypothetical protein	16
slI2015		2,01E-04	1,53	hypothetical protein	16
slr1659		8,11E-04	1,53	hypothetical protein	16
ssl0385		2,43E-03	1,53	hypothetical protein	16

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slr1816		3,27E-04	1,53	hypothetical protein	16
slr0883		1,65E-03	1,51	hypothetical protein	16
slr1732		3,55E-04	1,51	hypothetical protein	16
slr2120		2,31E-03	1,51	hypothetical protein	16
sll0585		6,67E-04	1,51	hypothetical protein	16
sll1687	hik17	2,20E-03	1,61	unknown protein	17
slr1829	phaE	1,32E-05	4,01	putative poly(3-hydroxyalkanoate) synthase component	17
slr2016	pilA10	2,51E-05	2,11	type 4 pilin-like protein, essential for motility	17
slr2017	pilA11	1,03E-03	1,77	type 4 pilin-like protein, essential for motility	17
slr1930	pilA7	2,80E-04	1,53	type 4 pilin-like protein	17
sll0783		6,85E-06	23,24	unknown protein	17
ssl1464		2,27E-05	5,76	unknown protein	17
sll0733		6,19E-06	5,75	unknown protein	17
ssl2507		6,12E-06	5,36	unknown protein	17
ssl2501		4,70E-05	5,31	unknown protein	17
sll0785		4,30E-05	5,14	unknown protein	17
sll0786		4,40E-05	4,78	unknown protein	17
sll1225		1,99E-05	4,19	unknown protein	17
sll0172		6,13E-05	3,60	periplasmic protein, function unknown	17
ssl2502		6,25E-04	3,51	unknown protein	17
slr1618		1,32E-05	3,51	unknown protein	17
slr1616		1,81E-05	3,34	unknown protein	17
ssr1768		1,15E-05	3,33	unknown protein	17
sll1714		4,98E-05	3,17	unknown protein	17
slr1074		1,05E-04	3,12	unknown protein	17
sll1272		1,21E-04	2,95	unknown protein	17
sll0266		1,75E-05	2,78	unknown protein	17
slr1062		2,92E-05	2,77	unknown protein	17
slr1066		1,20E-05	2,75	unknown protein	17
slr1421		1,29E-04	2,69	unknown protein	17
sll0982		1,65E-05	2,69	unknown protein	17
sll1396		5,16E-05	2,59	unknown protein	17
ssl2420		2,02E-04	2,40	unknown protein	17
sll0843		5,53E-03	2,39	unknown protein	17
ssl2162		5,59E-03	2,32	unknown protein	17
ssr3467		3,87E-05	2,31	unknown protein	17
slr0912		2,45E-04	2,30	unknown protein	17
slr0334		3,28E-04	2,17	unknown protein	17
slr1079		7,10E-05	2,17	unknown protein	17
ssl0323		1,01E-04	2,14	unknown protein	17
sll1304		3,71E-05	2,13	unknown protein	17
slr1084		4,97E-05	2,10	unknown protein	17
slr1071		6,74E-04	2,09	unknown protein	17
slr1658		4,79E-03	2,08	unknown protein	17
sll0426		7,56E-05	2,07	unknown protein	17
sll1293		8,03E-05	2,07	unknown protein	17
sll1315		3,59E-04	2,06	unknown protein	17
sll0403		1,12E-04	2,04	unknown protein	17
sll1086		1,80E-04	2,03	unknown protein	17

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slI1241		9,14E-04	2,00	unknown protein	17
slI1273		8,77E-05	2,00	unknown protein	17
ssl1520		8,04E-05	1,94	unknown protein	17
slr0302		1,66E-04	1,92	unknown protein	17
ssr0536		6,48E-05	1,90	unknown protein	17
slI1784		8,57E-05	1,90	periplasmic protein, function unknown	17
slI0406		5,29E-05	1,89	unknown protein	17
slr1135		5,62E-05	1,89	unknown protein	17
slr1865		1,15E-04	1,86	unknown protein	17
slr0708		5,67E-04	1,84	periplasmic protein, function unknown	17
slI1503		1,36E-03	1,84	unknown protein	17
slr2046		7,18E-05	1,83	unknown protein	17
slr0398		1,41E-04	1,83	unknown protein	17
slr0914		7,89E-04	1,82	unknown protein	17
slr0668		1,27E-04	1,80	unknown protein	17
slr1056		2,82E-04	1,80	unknown protein	17
slr0023		3,52E-03	1,80	unknown protein	17
slr1932		1,05E-04	1,79	unknown protein	17
slr1854		1,36E-04	1,78	unknown protein	17
ssr3532		5,51E-05	1,77	unknown protein	17
slI1268		5,67E-04	1,77	unknown protein	17
slr1340		5,05E-04	1,76	unknown protein	17
slr0184		1,39E-04	1,76	unknown protein	17
slr1768		2,38E-03	1,75	unknown protein	17
slr1023		7,21E-04	1,74	unknown protein	17
slr0658		3,32E-04	1,72	unknown protein	17
slr1855		1,74E-04	1,71	unknown protein	17
slI1785		2,28E-03	1,70	periplasmic protein, function unknown	17
slI0614		1,94E-03	1,69	unknown protein	17
slr1862		9,35E-04	1,69	unknown protein	17
slr0960		2,26E-04	1,69	unknown protein	17
slr2018		1,70E-04	1,68	unknown protein	17
slr1544		5,97E-04	1,68	unknown protein	17
slr1082		3,71E-04	1,66	unknown protein	17
slr1407		6,74E-04	1,66	unknown protein	17
slr1240		6,51E-04	1,61	unknown protein	17
slI0923		1,11E-04	1,61	unknown protein	17
ssl3222		4,28E-04	1,61	unknown protein	17
slr0666		2,54E-03	1,60	unknown protein	17
slI0447		2,93E-04	1,60	unknown protein	17
slr1187		2,60E-03	1,58	unknown protein	17
ssr2201		1,24E-04	1,56	unknown protein	17
ssl0410		4,03E-03	1,56	unknown protein	17
slI1373		1,28E-03	1,56	unknown protein	17
slr1073		4,49E-04	1,55	unknown protein	17
slI0588		2,68E-04	1,54	unknown protein	17
slI0327		2,28E-03	1,53	unknown protein	17
ssl1533		1,18E-03	1,52	unknown protein	17
slI1739		2,08E-04	1,52	unknown protein	17

Appendix 4C (continued). List of significantly up-regulated genes.

ORF	Gene	p-value	FC	Gene Product	Category
slr1450		3,53E-04	1,52	unknown protein	17
slI1630		3,26E-04	1,51	unknown protein	17
slr1397		1,78E-04	1,51	unknown protein	17
slr0909		2,00E-03	1,51	unknown protein	17
slI0267		9,68E-04	1,50	unknown protein	17
slr2119		4,23E-04	1,50	unknown protein	17