

Table S2. Genes down-regulated to half or less in the control strain after a 24-h treatment at 40 °C.

ORF	FC*	P value	Function	Gene name (if assigned)	Functional category**
<i>slI0450</i>	-2.386	0.0002	cytochrome b subunit of nitric oxide reductase	<i>norB</i>	A
<i>slI1688</i>	-1.017	0.0029	threonine synthase	<i>thrC</i>	A
<i>slr0426</i>	-1.018	0.0405	GTP cyclohydrolase I	<i>folE</i>	B
<i>slr0749</i>	-1.108	0.0042	light-independent protochlorophyllide reductase iron protein subunit ChlL	<i>chlL</i>	B
<i>slr1434</i>	-1.1	0.0068	pyridine nucleotide transhydrogenase beta subunit	<i>pntB</i>	B
<i>slr0984</i>	-1.371	0.0001	CDP-glucose 4,6-dehydratase	<i>rfbG</i>	C
<i>slr1072</i>	-1.108	0.0001	GDP-D-mannose dehydratase	<i>rfbD, yefA</i>	C
<i>slI1724</i>	-1.094	0.0243	probable glycosyltransferase	<i>icsA</i>	C
<i>slr1064</i>	-1.662	0.0008	probable glycosyltransferase	<i>rfbU, mtfA</i>	C
<i>slr1351</i>	-1.013	0.0415	UDP-N-acetylmuramoylalanyl-D-glutamyl-2 6-diaminopimelate--D-alanyl-D-alanine ligase	<i>murF</i>	C
<i>slr2075</i>	-1.083	0.0106	10kD chaperonin	<i>groES</i>	D
<i>slI0430</i>	-1.732	0.0050	HtpG, heat shock protein 90, molecular chaperone	<i>htpG</i>	D
<i>slr0427</i>	-1.001	0.0023	putative competence-damage protein	<i>psbA2</i>	D
<i>ssl2922</i>	-1.153	0.0251	similar to virulence-associated protein VapB	<i>vapB</i>	D
<i>sml0009</i>	-1.138	0.0227	similar to virulence-associated protein VapC		D
<i>slr1705</i>	-1.256	0.0038	aspartoacylase	<i>aspA</i>	F
<i>slr0293</i>	-1.174	0.0007	glycine dehydrogenase	<i>gcvP</i>	F
<i>slr1350</i>	-1.145	0.0005	acyl-lipid desaturase (delta 12)	<i>desA</i>	G
<i>slI1441</i>	-2.398	0.0019	acyl-lipid desaturase (omega-3)	<i>desB</i>	G
<i>slI0330</i>	-1.192	0.0470	sepiapterine reductase	<i>fabG</i>	G
<i>slr1291</i>	-1.868	0.0002	NADH dehydrogenase subunit 4	<i>ndhD2</i>	H
<i>slr2007</i>	-3.324	0.0016	NADH dehydrogenase subunit 4	<i>ndhD5</i>	H
<i>slr2009</i>	-1.738	0.0023	NADH dehydrogenase subunit 4	<i>ndhD6</i>	H
<i>ssl3044</i>	-1.233	0.0069	probable ferredoxin		H
<i>slr1164</i>	-1.405	0.0000	ribonucleotide reductase subunit alpha	<i>nrdA, dnaF</i>	I
<i>slI1626</i>	-1.328	0.0082	LexA repressor	<i>lexA</i>	J
<i>slI1594</i>	-3.105	0.0003	ndhF3 operon transcriptional regulator, LysR family protein	<i>ccmR, ndhR</i>	J
<i>slr1214</i>	-1.087	0.0143	two-component response regulator	<i>rre15</i>	J
<i>slr1285</i>	-1.056	0.0159	two-component sensor histidine kinase	<i>hik34</i>	J
<i>slI1772</i>	-1.313	0.0236	DNA mismatch repair protein MutS	<i>mutS</i>	K2
<i>slr0790</i>	-1.473	0.0440	similar to ultraviolet light resistance protein B	<i>umuC</i>	K2
<i>slr0653</i>	-1.118	0.0001	principal RNA polymerase sigma factor SigA	<i>sigA</i>	L
<i>slI0555</i>	-1.258	0.0256	methionine aminopeptidase	<i>map-3, mapC</i>	M
<i>slr1592</i>	-2.288	0.0002	probable pseudouridine synthase		M
<i>slI1263</i>	-1.364	0.0028	cation efflux system protein		N
<i>slr0067</i>	-1.233	0.0001	MRP protein homolog		O
<i>slr1410</i>	-1.04	0.0080	periplasmic WD-repeat protein		O
<i>slr1019</i>	-1.491	0.0454	phenazine biosynthetic protein PhzF homolog		O
<i>slr1063</i>	-1.573	0.0016	probable glycosyltransferase		O
<i>slr1065</i>	-1.493	0.0003	probable glycosyltransferase		O
<i>slr1076</i>	-1.291	0.0000	probable glycosyltransferase		O
<i>slr1077</i>	-1.195	0.0000	probable glycosyltransferase	<i>gumH</i>	O
<i>slr1610</i>	-1.118	0.0297	putative C-3 methyl transferase		O
<i>slI0222</i>	-1.04	0.0155	putative purple acid phosphatase	<i>phoA</i>	O
<i>slI0185</i>	-1.601	0.0342	hypothetical protein		P

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<i>slI0360</i>	-1.004	0.0148	hypothetical protein		P
<i>slI0451</i>	-1.148	0.0142	hypothetical protein		P
<i>slI0529</i>	-1.174	0.0295	hypothetical protein		P
<i>slI0822</i>	-1.056	0.0122	hypothetical protein		P
<i>slI1504</i>	-1.574	0.0014	hypothetical protein		P
<i>slI1505</i>	-1.938	0.0145	hypothetical protein		P
<i>slI1516</i>	-1.18	0.0049	hypothetical protein		P
<i>slI1911</i>	-1.144	0.0218	hypothetical protein		P
<i>slr0870</i>	-1.072	0.0008	hypothetical protein		P
<i>slr0959</i>	-1.676	0.0009	hypothetical protein		P
<i>slr1069</i>	-1.628	0.0003	hypothetical protein		P
<i>slr1472</i>	-1.06	0.0075	hypothetical protein		P
<i>slr1677</i>	-1.073	0.0371	hypothetical protein		P
<i>slr1692</i>	-1.06	0.0294	hypothetical protein		P
<i>slr2006</i>	-3.627	0.0012	hypothetical protein	<i>mrpC</i>	P
<i>slr2008</i>	-1.898	0.0004	hypothetical protein	<i>mrpC</i>	P
<i>slr2010</i>	-1.963	0.0016	hypothetical protein	<i>mrpE</i>	P
<i>slr2011</i>	-1.734	0.0020	hypothetical protein	<i>mrpA</i>	P
<i>slr2012</i>	-1.581	0.0010	hypothetical protein	<i>mrpB</i>	P
<i>slr2013</i>	-1.248	0.0007	hypothetical protein		P
<i>ssl2874</i>	-1.233	0.0011	hypothetical protein		P
<i>ssl2920</i>	-1.532	0.0232	hypothetical protein		P
<i>ssl2921</i>	-1.398	0.0310	hypothetical protein		P
<i>ssr1251</i>	-1.428	0.0173	hypothetical protein		P
<i>ssr2062</i>	-1.269	0.0038	hypothetical protein		P
<i>ssr2998</i>	-1.016	0.0077	hypothetical protein		P
<i>ssr3409</i>	-1.583	0.0008	hypothetical protein	<i>mrpF</i>	P
<i>ssr3410</i>	-1.637	0.0021	hypothetical protein	<i>mrpG</i>	P
<i>slI1483</i>	-1.04	0.0031	periplasmic protein, similar to transforming growth factor induced protein		P
<i>slr0708</i>	-1.098	0.0102	periplasmic protein		Z
<i>slI0263</i>	-1.543	0.0052	unknown protein		Z
<i>slI0710</i>	-1.299	0.0004	unknown protein		Z
<i>slI1239</i>	-1.395	0.0371	unknown protein		Z
<i>slI1241</i>	-1.677	0.0099	unknown protein		Z
<i>slI1611</i>	-1.11	0.0099	unknown protein		Z
<i>slr0262</i>	-1.033	0.0208	unknown protein		Z
<i>slr0871</i>	-1.467	0.0091	unknown protein		Z
<i>slr1066</i>	-1.328	0.0038	unknown protein		Z
<i>slr1071</i>	-1.59	0.0001	unknown protein		Z
<i>slr1073</i>	-1.404	0.0000	unknown protein		Z
<i>slr1074</i>	-1.575	0.0004	unknown protein		Z
<i>slr1383</i>	-1.178	0.0251	unknown protein		Z
<i>slr1618</i>	-1.058	0.0027	unknown protein		Z
<i>ssr2153</i>	-1.416	0.0040	unknown protein		Z
<i>ssr2194</i>	-1.923	0.0011	unknown protein		Z

*FC: log₂ of fold change.

**The categories are listed according to Cyanobase (see Fig. 2).