

Table S1. Genes at least two fold up-regulated in the control strain after a 24-h treatment at 40 °C.

ORF	FC*	P value	Annotation/Function	Gene name	Functional category**
<i>slr0288</i>	2.65	0.042303	glutamate--ammonia ligase	<i>glnN</i>	A
<i>slr1756</i>	2.01	0.012725	glutamate--ammonia ligase	<i>glnA</i>	A
<i>slr1898</i>	1.27	0.031619	N-acetylglutamate kinase	<i>argB</i>	A
<i>ssl0707</i>	1.42	0.030626	nitrogen regulatory protein P-II	<i>glnB</i>	A
<i>sll1514</i>	1.45	0.039969	16.6 kDa small heat shock protein, molecular chaperone	<i>hspA</i> ,	D
<i>sll1694</i>	1.88	0.000174	pilin polypeptide PilA1	<i>pilA1</i>	D
<i>sll1695</i>	2.19	0.000052	pilin polypeptide PilA2	<i>pilA2</i>	D
<i>slr1289</i>	1.81	0.009670	isocitrate dehydrogenase (NADP+)	<i>icdA</i>	F
<i>ssl2559</i>	1.23	0.002315	ferredoxin		H
<i>sll0248</i>	1.07	0.047051	flavodoxin	<i>isiB</i>	H
<i>sll0247</i>	1.86	0.012778	iron-stress chlorophyll-binding protein	<i>isiA</i>	H
<i>ssr0390</i>	1.04	0.044694	photosystem I reaction center subunit X	<i>psaK1</i>	H
<i>slr0851</i>	1.20	0.035004	type 2 NADH dehydrogenase	<i>ndbA</i>	H
<i>sll1161</i>	1.71	0.000343	probable adenylate cyclase	<i>cya3</i>	J
<i>sll0782</i>	1.94	0.020364	transcriptional regulator		J
<i>slr1759</i>	1.07	0.037249	two-component hybrid sensor and regulator	<i>hik14</i>	J
<i>sll1330</i>	1.83	0.019695	two-component system response regulator	<i>rre37</i>	J
<i>slr1543</i>	1.00	0.012326	DNA-damage-inducible protein F		K2
<i>slr1912</i>	1.67	0.002181	putative PP2C-type protein phosphatase		L
<i>sll2008</i>	1.08	0.015432	processing protease	<i>prp1</i>	M
<i>sll1198</i>	1.73	0.004000	tRNA (guanine-N1)-methyltransferase	<i>trmD</i>	M
<i>slr1316</i>	1.15	0.008354	ABC-type iron(III) dicitrate transport system permease protein	<i>fecC</i>	N
<i>sll0108</i>	2.23	0.021606	ammonium/methylammonium permease	<i>amt1</i>	N
<i>sll0537</i>	1.04	0.006726	ammonium/methylammonium permease	<i>amt3</i>	N
<i>sll1017</i>	2.17	0.036233	ammonium/methylammonium permease	<i>amt2</i>	N
<i>slr1735</i>	1.13	0.036765	ATP-binding subunit of the ABC-type Bgt permease for basic amino acids and glutamine	<i>bgtA</i>	N
<i>sll1404</i>	2.10	0.004326	biopolymer transport ExbB protein homolog	<i>exbB3</i>	N
<i>sll1405</i>	1.97	0.004938	biopolymer transport ExbD protein homolog	<i>exbD</i>	N
<i>sll1406</i>	1.69	0.001927	ferrichrome-iron receptor	<i>fhuA</i>	N
<i>slr1295</i>	2.19	0.000083	iron transport system substrate-binding protein	<i>futA1</i>	N
<i>slr0513</i>	1.11	0.000820	iron transport system substrate-binding protein, periplasmic protein	<i>futA2</i>	N
<i>slr1318</i>	1.11	0.001189	iron(III) dicitrate transport system ATP-binding protein	<i>fecE</i>	N
<i>slr0096</i>	1.07	0.018806	low affinity sulfate transporter		N
<i>sll1599</i>	1.63	0.015019	manganese transport system ATP-binding protein MntA	<i>mntA</i>	N
<i>sll1598</i>	1.88	0.011558	Mn transporter MntC	<i>mntC</i>	N
<i>slr1488</i>	1.25	0.000606	multidrug resistance family ABC transporter		N
<i>slr0944</i>	1.03	0.028080	multidrug-efflux transporter	<i>arsB</i>	N
<i>sll1270</i>	1.95	0.015768	periplasmic substrate-binding and integral membrane protein of the ABC-type Bgt permease for basic amino acids and glutamine BgtB	<i>bgtB</i>	N
<i>sll0536</i>	2.09	0.015045	probable potassium channel protein	<i>kchX</i>	N
<i>sll0764</i>	1.34	0.005542	urea transport system ATP-binding protein	<i>urtD</i>	N
<i>slr1200</i>	3.12	0.005600	urea transport system permease protein	<i>urtB</i>	N
<i>slr1201</i>	1.87	0.013713	urea transport system permease protein	<i>urtC</i>	N
<i>slr2002</i>	1.66	0.036906	cyanophycin synthetase	<i>cphA</i>	O
<i>sll1159</i>	2.86	0.000003	probable bacterioferritin comigratory protein		O

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<i>sll1407</i>	1.30	0.003801	probable methyltransferase		O
<i>sll0335</i>	1.62	0.022188	hypothetical protein		P
<i>sll0944</i>	1.25	0.027989	hypothetical protein		P
<i>sll1119</i>	2.65	0.014692	hypothetical protein		P
<i>sll1158</i>	3.42	0.000001	hypothetical protein		P
<i>sll1160</i>	2.07	0.000036	hypothetical protein		P
<i>sll1469</i>	1.02	0.001049	hypothetical protein		P
<i>sll1696</i>	1.41	0.000093	hypothetical protein		P
<i>slr0144</i>	1.14	0.000628	hypothetical protein		P
<i>slr0146</i>	1.03	0.001516	hypothetical protein		P
<i>slr1152</i>	2.08	0.001139	hypothetical protein	rfrK	P
<i>slr1290</i>	1.05	0.023606	hypothetical protein		P
<i>slr1770</i>	1.16	0.037408	hypothetical protein		P
<i>slr1913</i>	1.01	0.002005	hypothetical protein		P
<i>ssl0331</i>	1.12	0.035017	hypothetical protein		P
<i>ssl1762</i>	1.21	0.043332	hypothetical protein		P
<i>sll0327</i>	1.13	0.048209	unknown protein		Z
<i>sll0441</i>	1.35	0.011751	unknown protein		Z
<i>sll0733</i>	2.06	0.011220	unknown protein		Z
<i>sll0783</i>	3.84	0.027555	unknown protein		Z
<i>slr0145</i>	1.14	0.000459	unknown protein		Z
<i>slr0442</i>	1.29	0.005213	unknown protein		Z
<i>slr1484</i>	1.80	0.001646	unknown protein		Z
<i>slr1681</i>	1.17	0.020969	unknown protein		Z
<i>slr1726</i>	1.06	0.001357	unknown protein		Z
<i>slr1920</i>	1.10	0.026555	unknown protein		Z
<i>ssl2384</i>	2.15	0.000229	unknown protein		Z

*FC: log₂ of fold change.

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