

Table S4. The effect of novobiocin on heat-induced gene expression

ORF	gene	Product	IF -NB	IF +NB
Genes whose heat inducibility was markedly reduced by novobiocin treatment				
sll0430	<i>htpG</i>	HtpG, heat shock protein 90	43.2 ± 2.1	10.2 ± 1.4
slr2075	<i>groES</i>	10 kD chaperonin, GroES protein	30.2 ± 1.1	5.4 ± 0.4
slr2076	<i>groEL1</i>	60 kDa chaperonin 1, GroEL1	23.4 ± 3.0	4.4 ± 0.4
<u>sll0416</u>	<u><i>groEL2</i></u>	60 kDa chaperonin 2, GroEL2	16.7 ± 2.5	3.6 ± 0.2
sll0170	<i>dnaK2</i>	DnaK protein 2, heat shock protein 70	15.5 ± 1.5	9.6 ± 0.2
slr1963		Water-soluble carotenoid protein	12.9 ± 1.5	5.7 ± 0.2
slr1516	<i>sodB</i>	Superoxide dismutase	10.6 ± 2.0	4.5 ± 0.2
sll0441		Hypothetical protein	9.4 ± 0.7	1.2 ± 0.1
ssl2971		Hypothetical protein	9.2 ± 0.5	4.2 ± 0.3
sll1041		ABC transporter ATP-binding protein	8.3 ± 0.8	0.9 ± 0.1
sll1106		Hypothetical protein	6.6 ± 0.3	1.0 ± 0.1
slr1603		Hypothetical protein	6.1 ± 0.4	3.9 ± 0.4
sll1621		Membrane protein	6.0 ± 0.2	1.6 ± 0.2
slr0156	<i>clpB2</i>	ClpB protein	4.8 ± 0.3	0.8 ± 0.1
slr1634		Hypothetical protein	4.3 ± 0.2	0.2 ± 0.1
sll0575	<i>rfbB</i>	Export system ATP-binding protein	4.3 ± 0.2	0.8 ± 0.1
Genes whose heat inducibility was enhanced by novobiocin treatment				
slr0093	<i>dnaJ</i>	DnaJ protein, molecular chaperone	10.3 ± 0.7	88.4 ± 3.0
slr1674		Hypothetical protein	22.6 ± 2.1	40.9 ± 2.6
slr0095		O-methyltransferase	3.7 ± 0.2	40.6 ± 3.5
sll1652		Hypothetical protein	1.9 ± 0.1	41.0 ± 2.5
sll0939		Hypothetical protein	3.0 ± 0.1	36.2 ± 2.8
sll0843		Hypothetical protein	1.9 ± 0.1	33.3 ± 3.1
slr1675	<i>hypA1</i>	Putative hydrogenase	15.9 ± 1.0	32.1 ± 3.0
slr0798	<i>ziaA</i>	Zinc-transporting P-type ATPase	0.9 ± 0.2	31.2 ± 2.0
<u>sll0306</u>	<u><i>sigB</i></u>	RNA polymerase group 2 sigma factor	11.5 ± 1.0	26.8 ± 2.2
sll0938		N-succinyldiaminopimelate aminotransferase	1.3 ± 0.3	26.0 ± 1.4
slr0272		Hypothetical protein	1.2 ± 0.1	25.5 ± 2.3
slr2037		Hypothetical protein	1.0 ± 0.1	20.8 ± 1.4
slr1185	<i>petC2</i>	Rieske iron sulfur protein	1.0 ± 0.1	19.2 ± 0.8
slr1398		Hypothetical protein	1.2 ± 0.2	19.2 ± 1.6
slr1851		Hypothetical protein	1.7 ± 0.1	18.9 ± 1.1
sll1549		Salt-enhanced periplasmic protein	1.5 ± 0.2	18.5 ± 1.0
slr1204	<i>htrA</i>	Serine protease HtrA	5.6 ± 0.4	18.2 ± 1.2
sll1863		Hypothetical protein	1.2 ± 0.1	18.2 ± 1.2
slr0967		Hypothetical protein	5.1 ± 0.4	16.8 ± 2.1
slr1915		Hypothetical protein	6.8 ± 0.8	15.7 ± 1.4
slr1413		Hypothetical protein	4.4 ± 0.2	18.0 ± 2.4
slr0271		Hypothetical protein	1.6 ± 0.3	17.2 ± 1.3
sll0790	<i>hik31</i>	Sensor histidine kinase Hik31	0.7 ± 0.1	16.0 ± 1.1
sll1862		Hypothetical protein	1.4 ± 0.2	15.2 ± 0.5
sll0528		Hypothetical protein	6.3 ± 0.5	14.1 ± 1.1
sll0877		Hypothetical protein	1.1 ± 0.1	13.9 ± 1.0
sll0038	<i>rre36</i>	Two-component response regulator	0.9 ± 0.1	13.3 ± 2.1
slr1916		Esterase	1.5 ± 0.1	13.2 ± 0.5
sll1849		Hypothetical protein	1.2 ± 0.3	13.1 ± 1.0
ssl3769		Hypothetical protein	0.8 ± 0.1	12.6 ± 2.0
slr0518	<i>abfB</i>	Arabinofuranosidase	1.6 ± 0.2	12.2 ± 0.9

slI0360		Hypothetical protein	1.1 ± 0.2	10.8 ± 0.5
slr1676		Hypothetical protein	1.5 ± 0.3	11.4 ± 0.7
slr1927		Hypothetical protein	0.5 ± 0.1	10.6 ± 0.5
slr0549	<i>asd</i>	Aspartate beta-semialdehyde dehydrogenase	0.7 ± 0.1	10.2 ± 0.8
slr1906		Hypothetical protein	0.9 ± 0.2	10.0 ± 0.5
slr0210	<i>hik9</i>	Sensor histidine kinase Hik9	1.1 ± 0.1	9.9 ± 0.8
slr1245		Transcriptional regulator	1.1 ± 0.2	9.6 ± 0.8
slr0550	<i>dapA</i>	Dihydrodipicolinate synthase	0.6 ± 0.2	8.5 ± 0.5
slI0462		Hypothetical protein	0.6 ± 0.1	8.2 ± 0.3
slr1042	<i>rre7</i>	Two-component response regulator	1.0 ± 0.1	6.8 ± 0.2
slr1285	<i>hik34</i>	Sensor histidine kinase Hik34	3.1 ± 0.2	6.5 ± 0.2
slI0039	<i>rre35</i>	Two-component response regulator	0.7 ± 0.1	5.7 ± 0.2
slI1786	<i>tatD</i>	Putative deoxyribonuclease, TatD	0.3 ± 0.1	4.3 ± 0.1
slr1305	<i>rre41</i>	Two-component response regulator	1.1 ± 0.2	3.8 ± 0.3

Genes whose heat inducibility was not affected by novobiocin treatment

<u>slI1514</u>	<u><i>hspA</i></u>	16.6 kDa small heat shock protein	66.2 ± 3.2	52.8 ± 2.5
slr1641	<i>clpB1</i>	ClpB protein	58.9 ± 3.0	40.2 ± 4.1
slI0846		Hypothetical protein	17.0 ± 2.0	15.9 ± 0.9
slr0008	<i>ctpA</i>	Carboxyl-terminal processing protease	4.8 ± 0.4	4.4 ± 0.2

Cells, which had been grown under normal conditions and then incubated in the presence (50 µg ml⁻¹) or absence of novobiocin at 34°C for 30 min, were incubated at 44°C for 30 min. Each value indicates the ratio of the level of the transcript in heat-stressed cells in the presence of novobiocin to that in heat-stressed cells in the absence of novobiocin. The numbering of open reading frames (ORFs) corresponds to that in the database on the Cyanobase website (<http://bacteria.kazusa.or.jp/cyano/Synechocystis/>). This table lists the heat stress-inducible genes with induction factors higher than 4.0 in control cells (average of values from 2-3 independent experiments). The entire list can be accessed at http://www.genome.jp/kegg-bin/get_htext?htext=Exp_DB&hier=1. Genes that had been used as probes in Northern blotting are underlined. IF – induction factor; NB – novobiocin. The table represents the results of two independent experiments.