Table S2. The effect of novobiocin on NaCl-induced gene expression

ORF no.	Gene	Product	IF - NB	IF + NB
Genes whose NaCl inducibility was markedly reduced by novobiocin treatment				
sll1514	*hspA*	16.6 kDa small heat shock protein	70.2 ± 2.1	15.1 ± 0.6
sll0528		Hypothetical protein	69.5 ± 2.5	4.4 ± 0.6
sll0939		Hypothetical protein	51.9 ± 3.0	9.4 ± 0.7
slr1285	*hik34*	Histidine kinase Hik34	44.0 ± 3.4	1.6 ± 0.4
slr0967		Hypothetical protein	42.0 ± 1.5	5.5 ± 0.3
slr1544		Hypothetical protein	25.7 ± 1.1	2.1 ± 0.1
sll0846		Hypothetical protein	25.7 ± 1.0	5.3 ± 0.1
slr1963		Water-soluble carotenoid protein	22.8 ± 0.7	1.0 ± 0.1
slr1641	*clpB1*	ClpB protein	22.5 ± 0.5	2.4 ± 0.1
sll0306	*sigB*	RNA polymerase sigma factor	21.4 ± 1.5	2.2 ± 0.1
slr1603		Hypothetical protein	20.4 ± 1.5	1.0 ± 0.1
slr0959		Hypothetical protein	18.1 ± 0.9	5.9 ± 0.3
sll1722		Hypothetical protein	16.6 ± 0.4	1.6 ± 0.2
sll1167	*pbp*	Penicillin-binding protein 4	15.9 ± 0.3	1.4 ± 0.3
slr1516	*sodB*	Superoxide dismutase	15.5 ± 0.4	2.2 ± 0.3
sll1594	*ndhR*	Transcriptional regulator	15.0 ± 1.2	0.7 ± 0.1
slr1971		Hypothetical protein	13.7 ± 0.7	2.4 ± 0.2
slr1704		Hypothetical protein	13.3 ± 0.5	3.3 ± 0.2
sll1085	*glpD*	Glycerol-3-P dehydrogenase	12.8 ± 0.5	2.0 ± 0.2
ssl2542	*hliA*	High light inducible protein	12.6 ± 0.3	7.1 ± 0.1
slr1915		Hypothetical protein	12.6 ± 0.3	4.1 ± 0.3
sll1483		Periplasmic protein	11.6 ± 1.2	2.9 ± 0.1
sll0170	*dnaK2*	Heat shock protein 70	11.5 ± 0.7	0.9 ± 0.1
sll1884		Hypothetical protein	11.1 ± 0.4	1.3 ± 0.1
slr1686		Hypothetical protein	11.0 ± 0.4	4.9 ± 0.2
ssr2595	*hliB*	High light inducible protein	10.9 ± 0.4	2.1 ± 0.2
slr1485		Phosphatidylinositol phosphate kinase	10.5 ± 0.3	4.3 ± 0.2
sll0938		N-Succinyldiaminopimelate aminotransferase	10.3 ± 0.5	6.0 ± 0.4
sll1797	*ycf21*	Ycf21 gene product	9.8 ± 0.4	1.3 ± 0.1
sll1330	*rre37*	Two-component response regulator	9.5 ± 0.3	1.5 ± 0.1
slr0529	*ggtB*	Glucosylglycerol transport system	9.0 ± 0.2	1.3 ± 0.1
sll1652		Hypothetical protein	8.8 ± 0.2	3.3 ± 0.1
sll1566	*ggpS*	Glucosylglycerol-phosphate synthase	8.8 ± 1.1	1.1 ± 0.1
ssl2971		Hypothetical protein	8.7 ± 0.6	2.0 ± 0.1
slr0581		Hypothetical protein	8.6 ± 0.3	1.8 ± 0.1
slr1738		Hypothetical protein	8.1 ± 0.3	0.9 ± 0.1
sll1773		Hypothetical protein	7.8 ± 0.4	0.6 ± 0.1
sll1086		Hypothetical protein	7.7 ± 0.5	3.1 ± 0.1
sll1621		Membrane protein	7.3 ± 0.3	1.1 ± 0.1
sll1965		Hypothetical protein	7.3 ± 0.7	1.3 ± 0.3

sll1723		Hypothetical protein	6.8 ± 0.5	1.2 ± 0.2
sll1620		Hypothetical protein	6.7 ± 0.5	0.8 ± 0.2
slr0251	*ycf85*	ABC transporter ATP-binding protein	6.3 ± 0.2	1.0 ± 0.2
sll0416	*groEL2*	60 kDa chaperonin 2, GroEL2	6.2 ± 0.2	0.6 ± 0.1
sll1549		Salt-enhanced periplasmic protein	6.2 ± 0.3	1.6 ± 0.2
slr1192		Alcohol dehydrogenase family	5.9 ± 0.2	1.2 ± 0.1
slr0530	*ggtC*	Glucosylglycerol transport system	5.9 ± 0.4	1.5 ± 0.2
slr2006		Hypothetical protein	5.9 ± 0.2	1.4 ± 0.1
slr0083	*crhR*	ATP-dependent RNA helicase	5.8 ± 0.2	2.9 ± 0.1
sll1724	*icsA*	LPS glycosyltransferase IcsA	5.7 ± 0.2	1.7 ± 0.1
sll0005		Hypothetical protein	5.7 ± 0.6	0.8 ± 0.1
slr0853	*rimI*	Ribosomal alanine acetyltransferase	5.6 ± 0.9	1.5 ± 0.1
slr0974	*infC*	Translation initiation factor IF-3	5.5 ± 0.3	1.2 ± 0.2
ssl1633	*hliC*	CAB/ELIP/HLIP superfamily	5.4 ± 0.3	1.9 ± 0.2
sll0169		Hypothetical protein	5.4 ± 0.4	0.5 ± 0.2
slr0589		Hypothetical protein	5.4 ± 0.2	0.9 ± 0.2
slr1894		Hypothetical protein	5.4 ± 0.2	1.6 ± 0.1
slr0746	*stpA*	Glucosylglycerolphosphate phosphatase	5.1 ± 0.2	1.6 ± 0.1
sll1491		Periplasmic WD-repeat protein	5.0 ± 0.5	0.6 ± 0.1

Genes whose NaCl inducibility was markedly enhanced by novobiocin treatment

sll1862		Hypothetical protein	172.1 ± 5.5	372.3 ± 5.0
sll1863		Hypothetical protein	166.5 ± 4.0	267.6 ± 4.2
sll0462		Hypothetical protein	1.8 ± 0.2	23.0 ± 1.1
slr1927		Hypothetical protein	2.4 ± 0.2	16.2 ± 0.4
slr0798	*ziaA*	Zinc-transporting P-type ATPase	4.3 ± 0.4	13.2 ± 0.8
slr1851		Hypothetical protein	2.5 ± 0.2	11.8 ± 0.4
sll1558		Mannose-1-phosphate guanyltransferase	4.3 ± 0.4	11.3 ± 0.9
slr1392	*feoB*	Ferrous iron transport protein B	4.6 ± 0.3	11.2 ± 1.1
sll1544	*rre40*	two-component response regulator	1.1 ± 0.1	9.1 ± 0.9
slr0550	*dapA*	Dihydrodipicolinate synthase	1.4 ± 0.2	7.0 ± 1.1

Genes whose NaCl inducibility was not affected by novobiocin treatment

slr1687		Hypothetical protein	15.7 ± 2.1	13.8 ± 2.0
slr1204	*htrA*	Serine protease HtrA	11.4 ± 1.5	7.5 ± 0.5
slr0093	*dnaJ*	DnaJ protein. heat shock protein	9.9 ± 0.5	12.8 ± 2.6
slr1916		Esterase	7.7 ± 0.4	5.5 ± 0.5
sll1653	*menG*	Phylloquinone methlytransferase	6.5 ± 0.3	4.4 ± 0.6
slr0095		O-Methyltransferase	6.0 ± 0.9	7.8 ± 0.6

Cells, which had been grown under normal conditions and then incubated in the presence (50 µg ml^{-1}) or absence of novobiocin for 30 min, were incubated with 0.5 M NaCl for 30 min. Each value indicates the ratio of the level of the transcript in salt-stressed cells in the presence of novobiocin to that in salt 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 salt 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.