

Fig. S1. HPLC analysis of polyamines showing the role of *CASDC* in synthesis of spermidine in *Synechocystis* 6803.

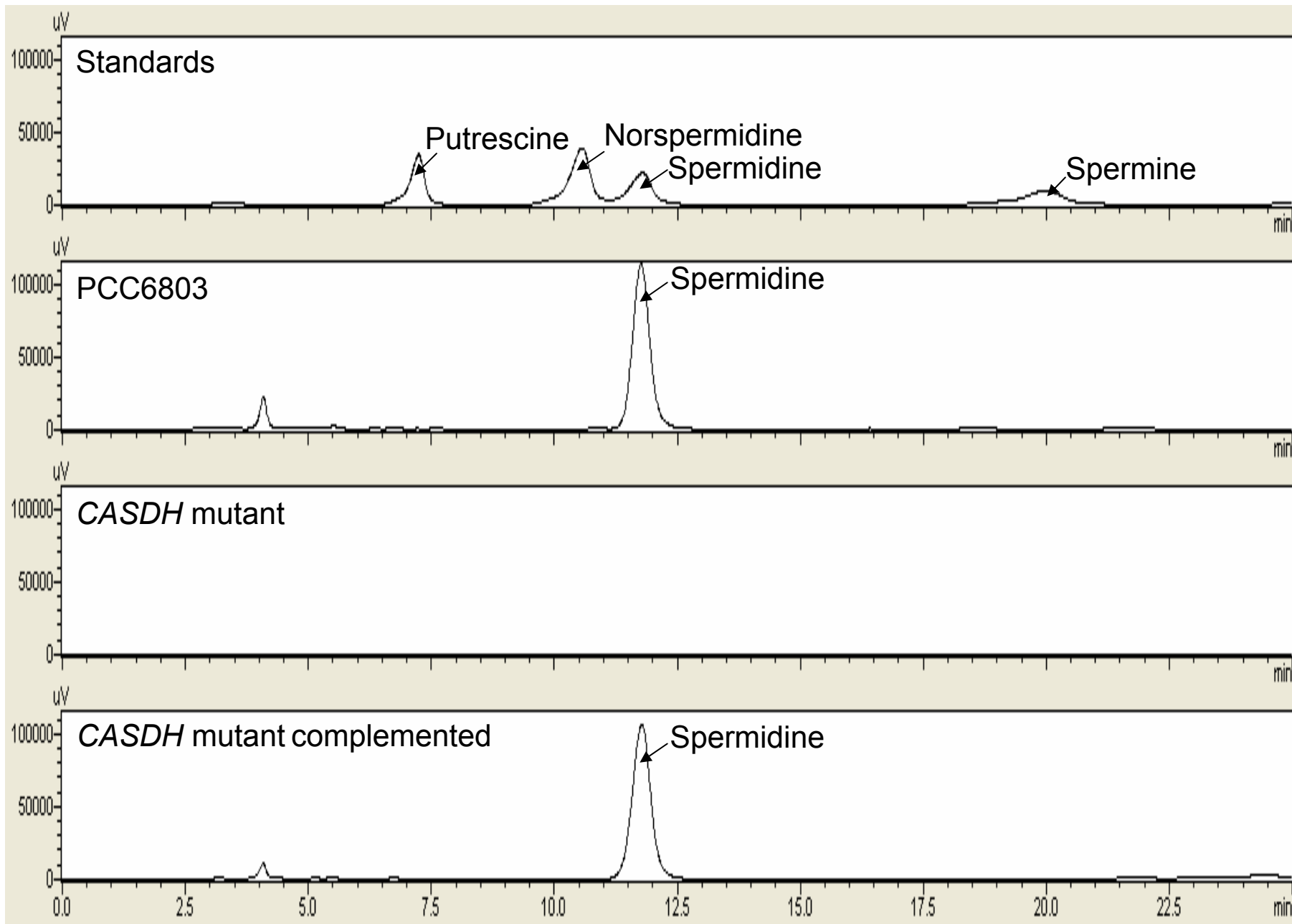


Fig. S2. HPLC analysis of polyamines showing the role of *CASDH* in synthesis of spermidine in *Synechocystis* 6803.

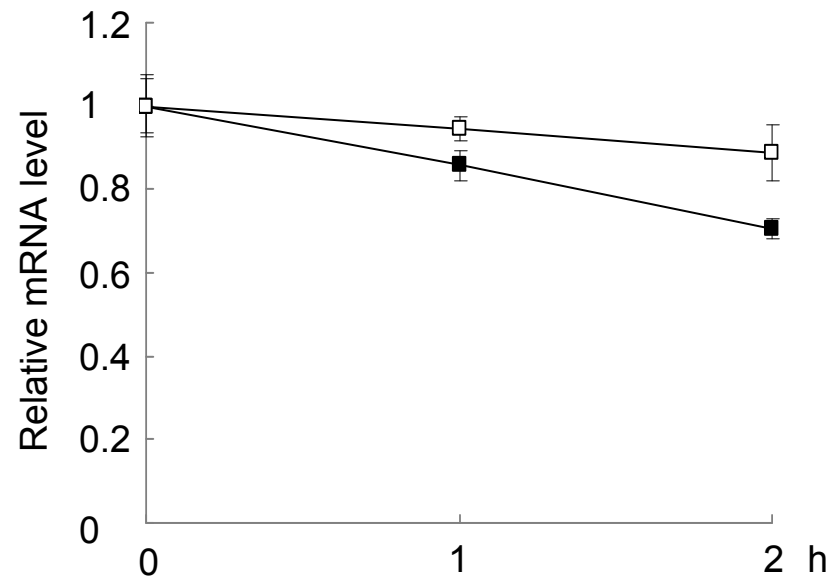


Fig. S3. qRT-PCR analysis of *rbp1* mRNA decay in the wild type (solid square) and the *CASDC* mutant (empty square) of *Synechocystis* 6803 under chill-light stress.

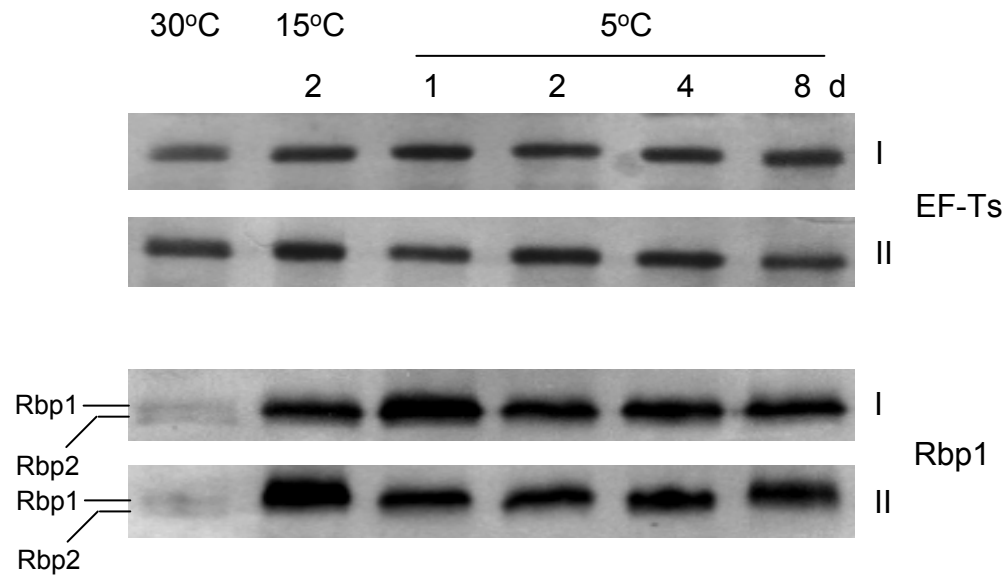


Fig. S4. Western blot detection of EF-Ts and Rbp1 in *Synechocystis* 6803::P_{CASDC}-lacZ (I) and *Synechocystis* 6803 DRHB2193::P_{CASDC}-lacZ (II). DRHB2193, the CASDC mutant.

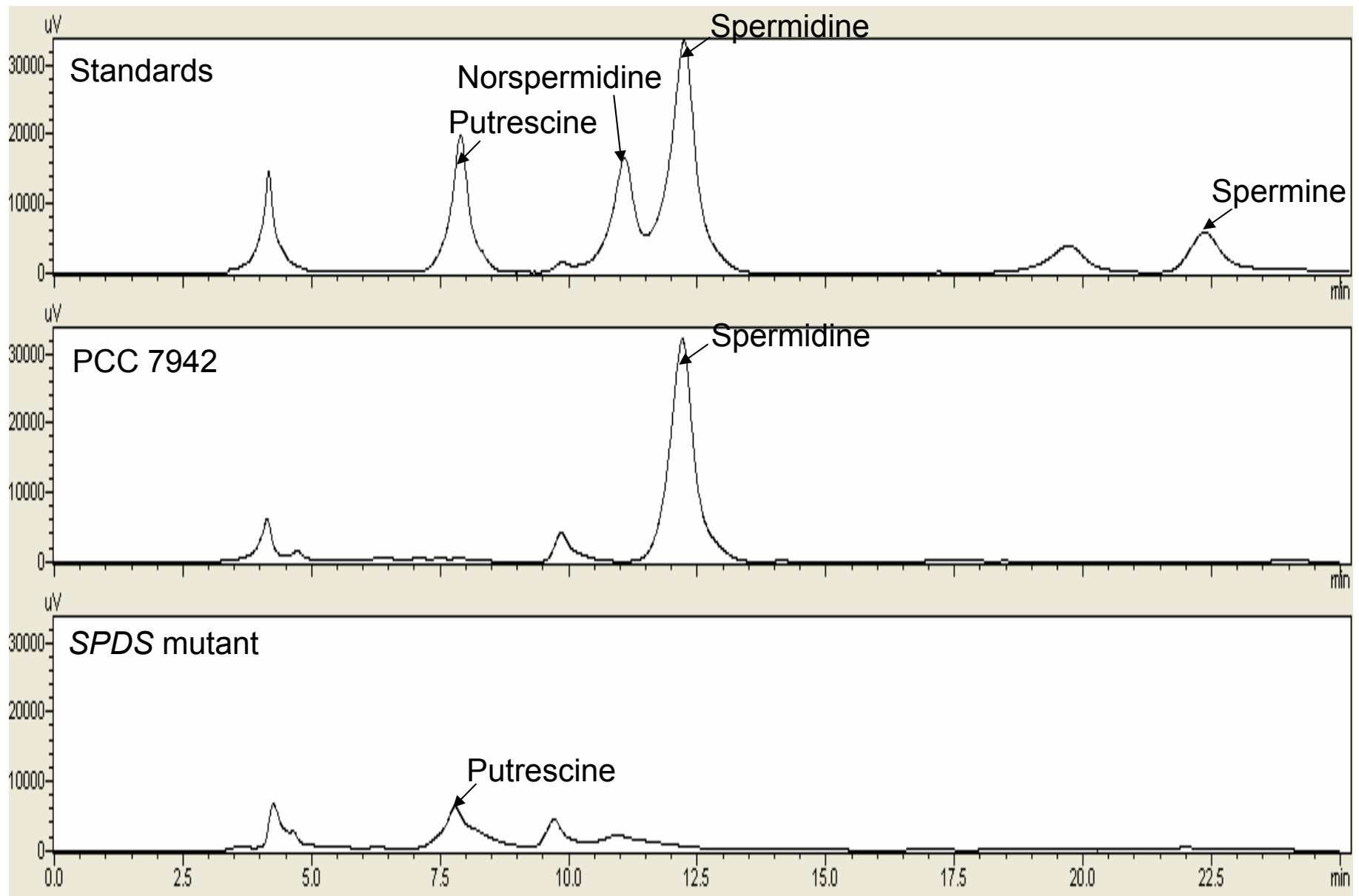


Fig. S5. HPLC analysis of polyamines showing the role of *SPDS* in synthesis of spermidine in *Synechococcus* 7942.

Table S1 Plasmids and primers

Plasmids or primer	Derivation, relevant characteristics, or sequences (5'→3')	Source or reference(s)
Plasmids		
pHB1117	Ap ^r , a plasmid containing <i>lacZ</i> from <i>E. coli</i> GM48, cloned into pMD18-T	Gao et al, 2007
pHB1957	Ap ^r , the PCR fragment containing <i>sll0873</i> , amplified with primers sll0873-1/-2, cloned into pMD18-T	This study
pHB2193	Ap ^r Km ^r , the Km ^r cassette excised with PvuII from pRL446, cloned into NheI-cut and T4 DNA polymerase-blunted pHB1957, interrupting <i>sll0873</i>	This study
pHB2739	Ap ^r , the PCR fragment containing P _{<i>rbcL</i>} , amplified with primers prbcL-1/-6, cloned into pMD18-T	This study
pHB2759	Ap ^r Sp ^r , Ω cassette excised with DraI from pRL57, cloned into Sall-cut and T4 DNA polymerase-blunted pHB2739, with Ω positioned upstream of P _{<i>rbcL</i>}	This study
pHB2926	Ap ^r , the PCR fragment containing <i>sll0873</i> , amplified with primers sll0873c-1/-2, cloned into pMD18-T	This study
pHB2926a	Ap ^r Sp ^r , Ω-P _{<i>rbcL</i>} excised with PstI and XbaI from pHB2759, blunted with T4 DNA polymerase, cloned into Sall-cut and T4 DNA polymerase-blunted pHB2926, forming Ω-P _{<i>rbcL-sll0873</i>}	This study
pHB2972	Ap ^r Sp ^r , Ω-P _{<i>rbcL-sll0873</i>} excised with HindIII and BamHI from pHB2926a, blunted with T4 DNA polymerase, cloned into EcoRI-cut and T4 DNA polymerase-blunted pKW1188	This study
pHB4233	Ap ^r , the PCR fragment containing <i>slr0049</i> , amplified with primers slr0049-1/-2, cloned into pMD18-T	This study
pHB4239	Ap ^r Km ^r , the Km ^r cassette excised with PvuII from pRL446, cloned into NcoI-cut and T4 DNA polymerase-blunted pHB4233, interrupting <i>slr0049</i>	This study
pHB4289	Ap ^r , the PCR fragment containing P _{<i>sll0873</i>} , amplified with primers sll0873p-1/-2, cloned into pMD18-T	This study
pHB4311	Ap ^r Sp ^r , the Ω cassette excised with DraI from pRL57, cloned into XbaI-cut and T4 DNA polymerase-blunted pHB4289, with Ω positioned upstream of P _{<i>sll0873</i>}	This study
pHB4321	Ap ^r Sp ^r , Ω-P _{<i>sll0873</i>} excised with Sall and BamHI from pHB4311, cloned into the BglI-cut and T4 DNA polymerase-blunted pHB1117, forming Ω-P _{<i>sll0873-lacZ</i>}	This study
pHB4324	Ap ^r Sp ^r , Ω-P _{<i>sll0873-lacZ</i>} excised with BamHI and	This study

	HindIII from pHB4321, blunted with T4 DNA polymerase, cloned into EcoRI-cut and T4 DNA polymerase-blunted pKW1188	
pHB4740	Ap ^r , the PCR fragment containing P _{slr0049-slr0049} , amplified with primers slr0049c-1/-2, cloned into pMD18-T	This study
pHB4744	Ap ^r Sp ^r , the Ω cassette excised with DraI from pRL57, cloned into SalI-cut and T4 DNA polymerase-blunted pHB4740, with Ω positioned upstream of P _{slr0049-slr0049}	This study
pHB4768	Ap ^r Sp ^r , the Ω-P _{slr0049-slr0049} fragment excised with PstI and SacI from pHB4744, blunted with T4 DNA polymerase, cloned into EcoRI-cut and T4 DNA polymerase-blunted pKW1188	This study
pHB5449	Ap ^r , the PCR fragment containing <i>Synpcc7942_0628</i> , amplified with primers <i>Synpcc7942_0628-1/-2</i> , cloned into pMD18-T	This study
pHB5450	Ap ^r Km ^r , the Km ^r cassette excised with PvuII from pRL446, cloned into BssHII-cut and T4 DNA polymerase-blunted pHB5449, interrupting <i>Synpcc7942_0628</i>	This study
pKW1188	Ap ^r Km ^r , a plasmid bearing a neutral integrative platform of <i>Synechocystis</i> 6803	Williams 1988; Gao and Xu, 2009
pMD18-T	Ap ^r , a cloning vector	Takara, Japan
pRL57	Km ^r Sm ^r Sp ^r , a pDU1-based plasmid containing the spectinomycin/streptomycin resistance cassette Ω	Elhai and Wolk, 1988
pRL446	Ap ^r Km ^r , a plasmid containing a Km ^r cassette	NCBI GenBank accession no. EU346690

Primers (5'→3')

lacZqRT-3	ACGGATTCACTGGCCGTC
lacZqRT-4	CAAAGCGCCATTCGCCAT
prbcL-1	CCGATGAAGTGGTGGAGCA
prbcL-6	GGTCAGTCCTCCATAAACATTG
rnpBn-1	GTTAGGGAGGGAGTTGCGG
rnpBn-2	AAGAGAGTTAGTCGTAAGCCG
rnpB-qRT-1	CGGTTGGAAGCAAGGTCG
rnpB-qRT-2	AAGAGAGTTAGTCGTAAGCCG
sll0517qRT-1	ATAGCTTTTACGACCGCC
sll0517qRT-2	CGGGAAACTGGTCGCATG
sll0873-1	GACTTGATTGGGCTACTGTTTT
sll0873-2	ACCGAGTATGACCTGTGGTTC
sll0873c-1	GACTTGATTGGGCTACTGTTTT

sll0873c-2	ACCGAGTATGACCTGTGGTTC
sll0873n-1	GCATCGTTATCGGGAATC
sll0873n-2	ACCAAAGGTACGCCACAG
sll0873p-1	AAGACGACGGCCTCTGCTCC
sll0873p-2	AAGATCGGTCTGCACGGG
sll0873qRT-5	AACCCCAGGTTATCCAGC
sll0873qRT-6	CCCTGCTAACCCTGACCGCAA
sll0873up-2	CCCTGCTAACCCTGACCGCA
sll0873up-7	AAATTCCCTCCGCCGCCAG
sll1261qRT-3	ACCAAGGTTAAAGCGGAT
sll1261qRT-4	AAAAGATTGTCCAAGGGC
sll1818qRT-3	CTCAATCACCTCCTCTGC
sll1818qRT-4	AGGACGAGGTCAATCCGG
slr0049-1	GCATGATTGTGGGAGCTGGGGGC
slr0049-2	GCCGTTGACTACTTCGTGCCA
slr0049c-1	CCGTGACGAATAAGGTAAA
slr0049c-2	CGGCAATGTA ACTGGACTA
slr0338qRT-3	TGGGGTGGGCAATAATGGG
slr0338qRT-4	CCGCCACACAAACCGCAT
Synpcc7942_0628-1	AGGCAAGTGGAGTTTGAGCA
Synpcc7942_0628-2	CATTGGAAGAGCCTCCGG

REFERENCES

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- Gao H, Tang Q, Xu X. 2007. Construction of copper-induced gene expression platform in *Synechocystis* 6803. *Acta Hydrobiol Sin.* **31**: 240-243.
- Gao H, Xu X. 2009. Depletion of Vipp1 in *Synechocystis* sp. PCC 6803 affects photosynthetic activity prior to the loss of thylakoid membranes. *FEMS Microbiol Lett.* **292**: 63-70.
- Williams JGK. 1988. Construction of specific mutations in photosystem II photosynthetic reaction center by genetic engineering methods in *Synechocystis* 6803. *Methods Enzymol.* **167**: 766-778.

Table S2 Genes regulated in *Synechocystis* 6803 preconditioned at 15°C and exposed to chill (4°C) and light

ORF*	Gene	Product	4°C/15°C
Up-regulated			
<i>slr1254</i>	<i>crtD</i>	phytoene dehydrogenase	5.900±3.470
<i>ssl0452</i>	<i>nblA1</i>	phycobilisome degradation protein NblA	5.721±2.813
<i>slr0150</i>	<i>petF, fdx</i>	ferredoxin, petF-like protein	10.457±6.808
<i>ssl3044</i>		probable ferredoxin	8.823±2.579
<i>sll0741</i>		pyruvate flavodoxin oxidoreductase	3.604±1.726
<i>ssr2061</i>		glutaredoxin	3.218±0.492
<i>slr1300</i>		similar to 2-octaprenyl-6-methoxyphenol hydroxylase	3.344±1.797
<i>slr1609</i>		long-chain-fatty-acid CoA ligase	3.250 ±0.734
<i>slr1516</i> ^b	<i>sodB</i>	superoxide dismutase	3.812±1.742
<i>slr0798</i>	<i>ziaA</i>	zinc-transporting P-type ATPase (zinc efflux pump) involved in zinc tolerance	3.833±0.695
<i>slr0324</i> ^a		probable oligopeptides ABC transporter permease protein	2.623±0.621
<i>sll1154</i> ^a		putative antibiotic efflux protein	2.813±0.585
<i>sll0086</i>		putative arsenical pump-driving ATPase	3.508±0.495
<i>slr1545</i> ^b	<i>sigG</i>	RNA polymerase ECF-type (group 3) sigma factor	2.327±0.466
<i>slr1105</i> ^b		GTP-binding protein TypA/BipA homolog	2.841±0.068
<i>slr1974</i>		GTP binding protein	3.200±0.913
<i>sll1967</i> ^a		probable RNA methyltransferase	3.405±1.192
<i>slr0083</i> ^a	<i>crhR</i>	RNA helicase Light	3.962±1.070
<i>slr1604</i> ^b	<i>ftsH</i>	cell division protein FtsH	2.621±0.794
<i>sll1695</i>	<i>pilA2</i>	pilin polypeptide PilA2	4.462±1.773
<i>slr0804</i> ^a		probable D-alanyl-D-alanine carboxypeptidase	3.949±2.227
<i>sll0873</i> ^a		carboxynorspermidine decarboxylase	10.795±6.352
<i>slr0550</i>	<i>dapA</i>	dihydrodipicolinate synthase	2.471±0.265
<i>slr0611</i>	<i>sds</i>	solaneyl diphosphate synthase	3.975±0.707
<i>slr0406</i>	<i>pyrC</i>	dihydroorotase	3.054±1.688
<i>slr1675</i>	<i>hypA1</i>	putative hydrogenase expression/formation protein HypA1	3.395±0.787
<i>slr0756</i>	<i>kaiA</i>	circadian clock protein KaiA homolog	2.701 ±1.045
<i>sll0296</i>		hypothetical protein	3.080±1.172
<i>sll0414</i>		hypothetical protein	2.878 ±1.299
<i>sll0549</i>		hypothetical protein	4.537±1.632
<i>sll1022</i>		hypothetical protein	4.187 ±3.057
<i>sll1130</i>		unknown protein	2.286±0.161

<i>sll1541</i>		hypothetical protein	8.003±4.248
<i>sll1863</i>		unknown protein	14.799±5.957
<i>sll1884</i>		hypothetical protein	3.630±0.580
<i>sll1911</i>		hypothetical protein	4.055±1.046
<i>sll1951</i>		unknown protein	2.949±0.210
<i>slr0148</i>		hypothetical protein	4.535±0.744
<i>slr0151</i>		unknown protein	5.091±2.139
<i>slr0642</i>		hypothetical protein	4.422±0.960
<i>slr0959</i>		hypothetical protein	4.562 ±1.944
<i>slr1413</i>		hypothetical protein	3.144±0.798
<i>slr1436</i>		unknown protein	3.232±0.843
<i>slr1674</i>		hypothetical protein	5.393±1.215
<i>slr1687</i>		hypothetical protein	9.695±1.950
<i>slr1946</i>		hypothetical protein	2.080±0.014
<i>ssl2162</i>		unknown protein	5.139±0.485
<i>ssl3177</i>		hypothetical protein	4.143±0.716
<i>ssl3769</i>		unknown protein	3.530±1.041
<i>ssr2016</i>		hypothetical protein	23.357 ±17.434
Down-regulated			
<i>sll0520</i>	<i>ndhI</i>	NADH dehydrogenase subunit NdhI	0.316 ±0.068
<i>sll1796</i>	<i>petJ</i>	cytochrome c553	0.282 ±0.127
<i>sll0662</i>		4Fe-4S type iron-sulfur protein	0.208 ±0.092
<i>sll0248</i>	<i>isiB</i>	flavodoxin	0.032 ±0.020
<i>slr1735</i>	<i>bgtA</i>	ATP-binding subunit of the ABC-type Bgt permease for basic amino acids and glutamine	0.435 ±0.073
<i>sll1450</i>	<i>nrtA</i>	nitrate/nitrite transport system substrate-binding protein	0.133 ±0.043
<i>sll1451</i>	<i>nrtB</i>	nitrate/nitrite transport system permease protein	0.273 ±0.049
<i>slr0898</i>	<i>nirA</i>	ferredoxin-nitrite reductase	0.135 ±0.029
<i>sll0771</i>	<i>glcP, gtr</i>	glucose transport protein	0.208 ±0.164
<i>slr1200</i>		urea transport system permease protein	0.296 ±0.027
<i>slr0042</i>		probable porin; major outer membrane protein	0.282 ±0.070
<i>slr0043</i>	<i>cmpC</i>	bicarbonate transport system ATP-binding protein	0.211 ±0.124
<i>sll1271</i>		probable porin; major outer membrane protein	0.303 ±0.119
<i>sll1550</i>		probable porin; major outer membrane protein	0.342 ±0.087
<i>sll1291</i>		two-component response regulator PatA subfamily	0.321 ±0.030
<i>sll1292</i>		two-component response regulator CheY subfamily	0.284 ±0.024
<i>sll1546</i>	<i>ppx</i>	exopolyphosphatase	0.318 ±0.016
<i>sll0220</i>	<i>glmS</i>	L-glutamine:D-fructose-6-P amidotransferase	0.399 ±0.081

<i>slr1830</i>	<i>phaC</i>	poly (3-hydroxyalkanoate) synthase	0.290 ±0.117
<i>slr0899</i>	<i>cynS</i>	cyanate lyase	0.225 ±0.176
<i>slr1853</i>		carboxymuconolactone decarboxylase	0.293 ±0.172
<i>sll1869</i>		probable dioxygenase, Rieske iron-sulfur component	0.319 ±0.203
<i>slr2017</i>	<i>pilA11</i>	type IV pilin-like protein, essential for motility	0.396 ±0.077
<i>sll1533</i>	<i>pilT2</i>	twitching mobility protein	0.290 ±0.137
<i>sll1242</i>		hypothetical protein	0.443 ±0.222
<i>sll0023</i>		hypothetical protein	0.271 ±0.063
<i>sll0149</i>		hypothetical protein	0.430 ±0.050
<i>sll0249</i>		hypothetical protein	0.103 ±0.102
<i>sll0327</i>		unknown protein	0.307 ±0.241
<i>sll1049</i>		hypothetical protein	0.430 ±0.050
<i>sll1119</i>		hypothetical protein	0.202 ±0.129
<i>slr0060</i>		unknown protein	0.293 ±0.051
<i>slr0453</i>		hypothetical protein	0.252 ±0.163
<i>slr0869</i>		hypothetical protein	0.285 ±0.098
<i>slr1391</i>		unknown protein	0.318 ±0.182
<i>slr1484</i>		unknown protein	0.237 ±0.214
<i>slr1854</i>		unknown protein	0.202 ±0.095
<i>slr1957</i>		hypothetical protein	0.261 ±0.032
<i>slr2003</i>		hypothetical protein	0.353 ±0.146

* *Synechocystis* 6803 mutants were constructed by inserting a kanamycin-resistance cassette into ORFs denoted with a or b. a, completely segregated; b, not segregated.