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Electronic Supplementary Information

A photoautotrophic platform for sustainable production of valuable plant natural products from CO_2

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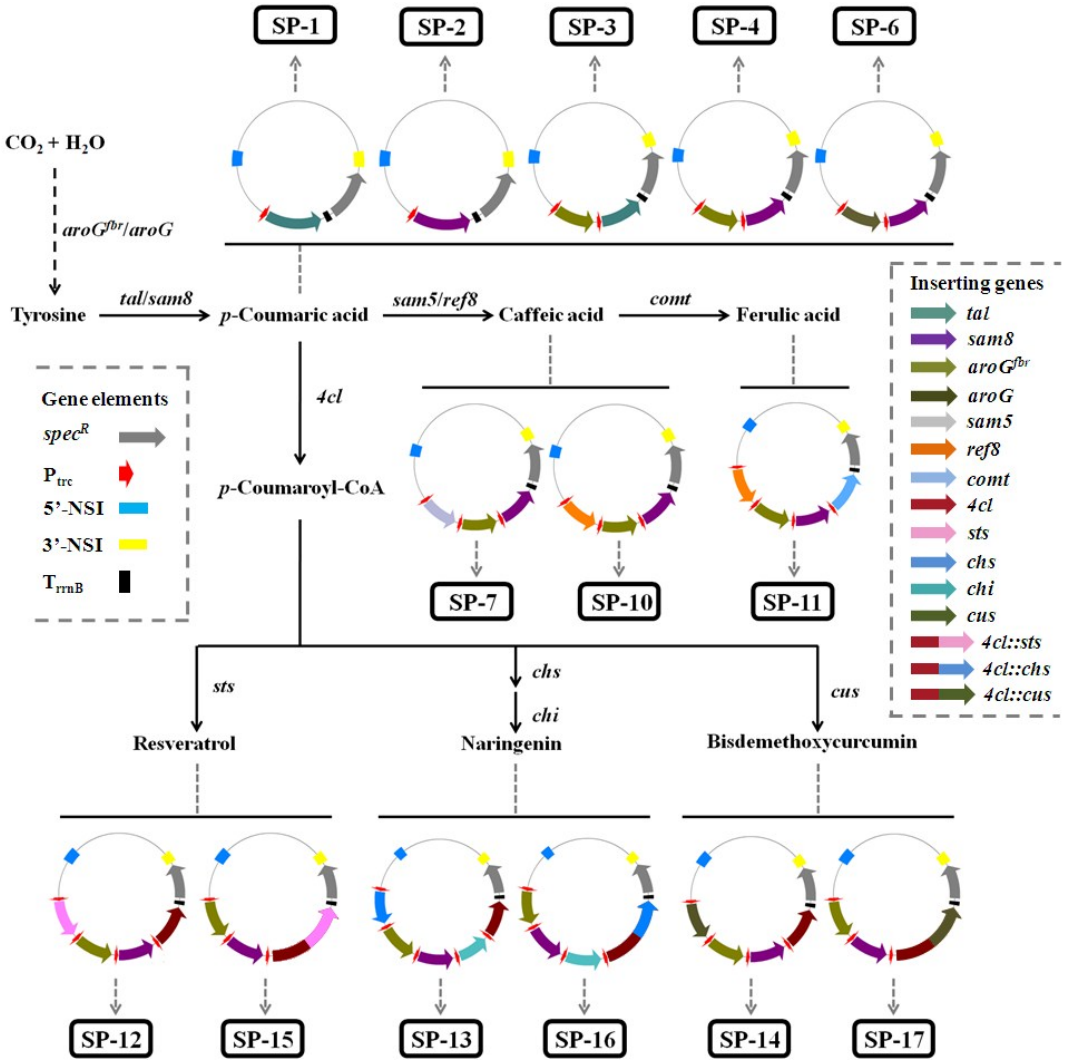

Figure S1. Schematic presentation of plasmids used in this study. All of the genes introduced into these plasmids were placed under the control of promoter trc, and the catalytic reactions of these exogenous genes were presented. *spec*^{R} (spectinomycin resistance gene), Ptrc (promoter trc), 5'-NSI (upstream region of Neutral Site I), 3'-NSI (downstream region of Neutral Site I), TrrnB (terminator).

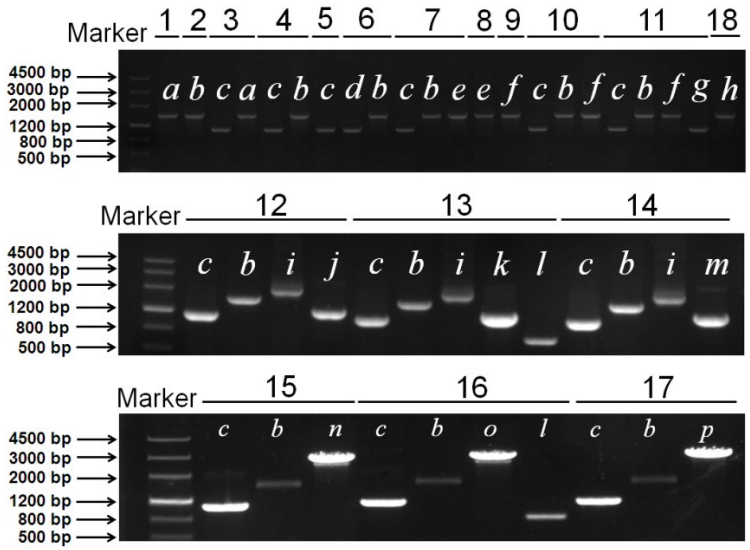

Figure S2. Colony PCR with gene-specific primers. These genes were correct. "a" to "p" respectively mean these target genes: *tal* (1.57 kb), *sam8* (1.53 kb), *aroG*^{fbr} (1.05 kb), *aroG* (1.05 kb), *sam5* (1.54 kb), *ref8* (1.53 kb), *comt* (1.09 kb), *c4h* (1.52 kb), *4cl* (1.63 kb), *sts* (1.17 kb), *chs* (1.17 kb), *chi* (0.74 kb), *cus* (1.21 kb), *4cl::sts* (2.80 kb), *4cl::chs* (2.80 kb), and *4cl::cus* (2.84 kb). The numbers "1-18" mean the recombinant strains SP-1 to SP-18, respectively.

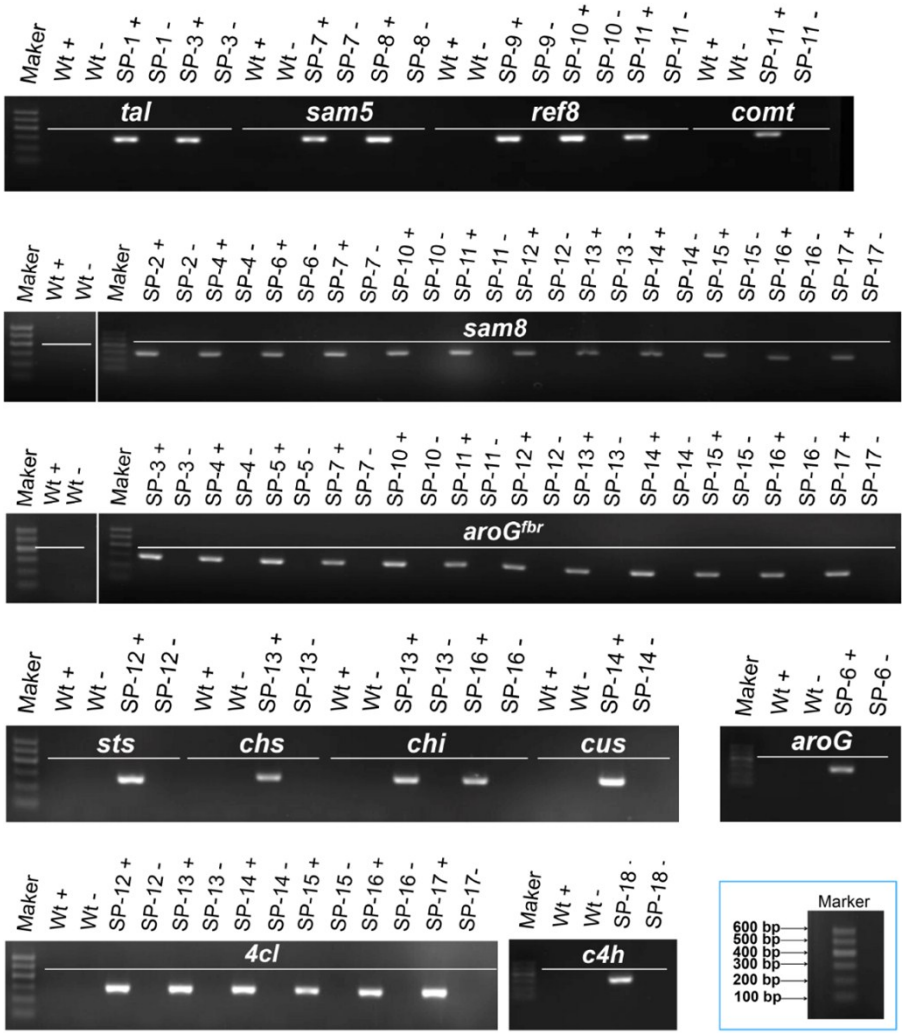

Figure S3. Verification of the heterologus gene expression in engineered *S. elongatus* strains by RT-PCR. Target size of each gene products were approximately 0.3 kb. wt, wild-type *S. elongatus* PCC7942; "+" means RT-PCR using RNA from the strains as template for reverse transcription; "-" means without reverse transcription before the reaction.

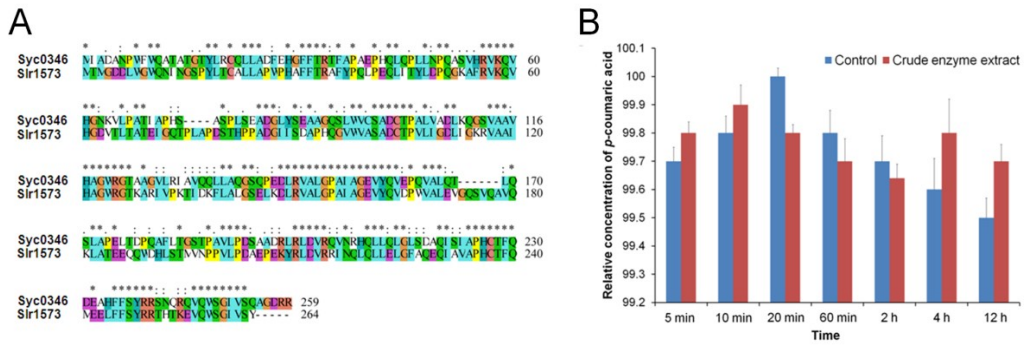

Figure S4. The hypothetical laccase of *S. elongatus* PCC7942. (A) Alignment of the amino acid sequences of Syc0346 (uncharacterized protein in *S. elongatus* PCC7942) and Slr1573 (laccase in *Synechocystis* sp. PCC6803). (B) For determined whether the activity of hypothetical laccase is present, the action of *S. elongatus* PCC7942 cell extracts on *p*-coumaric acid was tested. Data are representative of at least three independent experiments, and error bars indicate the standard deviation.

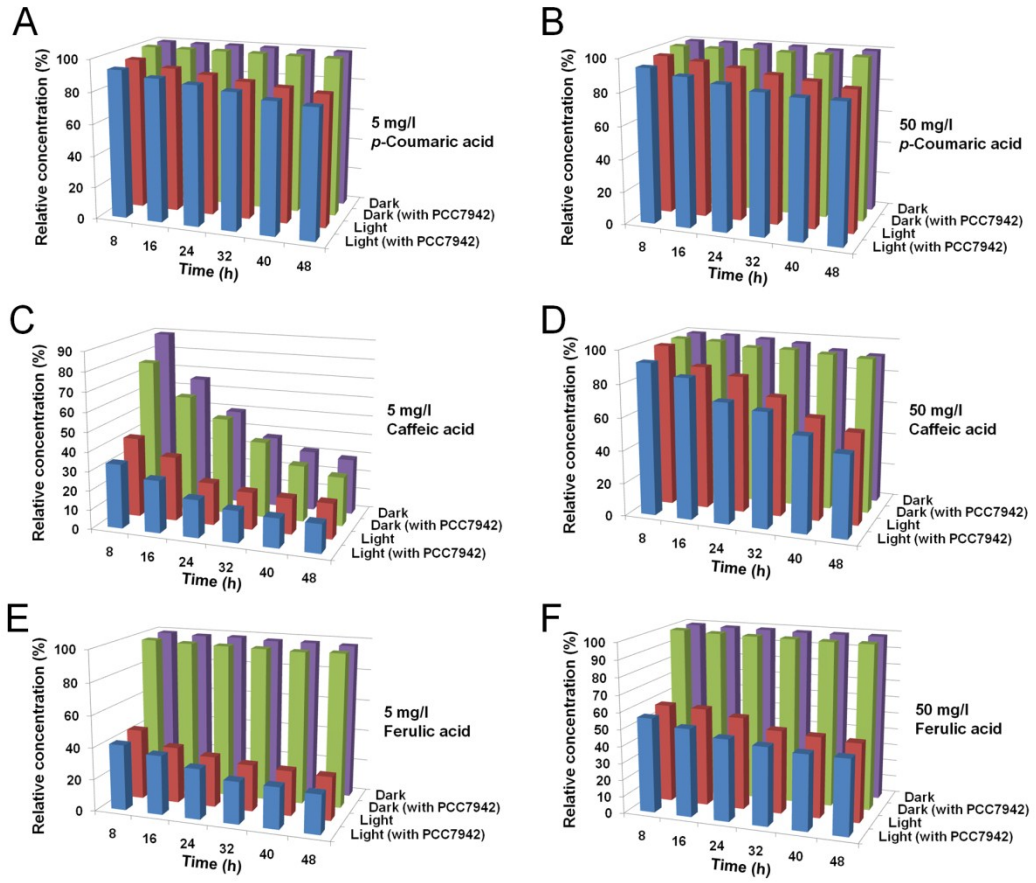

Figure S5. The stability of phenylpropanoic acids. To a final concentration of (A) 5 mg/l *p*-coumaric acid, (B) 50 mg/l *p*-coumaric acid, (C) 5 mg/l caffeic acid, (D) 50 mg/l caffeic acid, (E) 5 mg/l ferulic acid and (F) 50 mg/l ferulic acid, different phenylpropanoic acids were individually added to the BG11 medium. And then, cultivations were carried out under dark or continuous-light at 30°C for 48 h, the remaining amount of corresponding compounds were compared with the additive amounts. "With PCC7942" means that *S. elongatus* PCC7942 was cultured to OD_{730} = 1.5 under continuous-light before the addition of phenylpropanoic acids. Results are representative of at least three independent experiments.

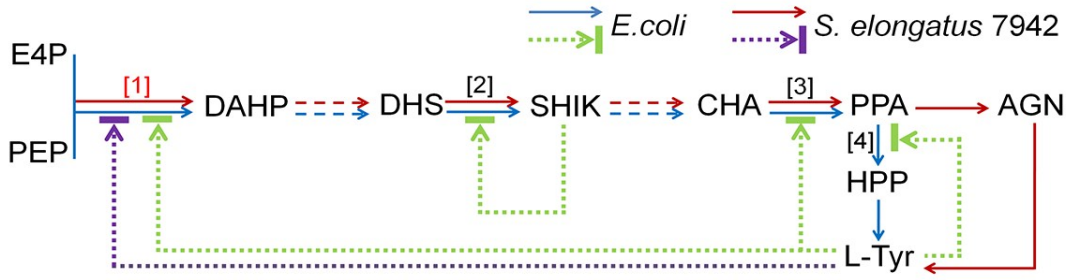

Figure S6. Comparison of biosynthetic pathways in *E. coli* and *S. elongatus* PCC7942 for L-tyrosine production and regulation. Blue and red lines respectively indicate the biosynthetic pathways of L-tyrosine in *E. coli* and *S. elongatus* PCC7942. Green dashed lines indicate the feedback inhibition points of L-tyrosine biosynthetic pathway in *E. coli*. Purple dashed lines indicate the sole feedback inhibition point of L-tyrosine biosynthetic pathway in *S. elongatus* PCC7942. The branchs to L-tryptophan and L-phenylalanine diverge from CHA and PPA, respectively. Enzyme 1 is DAHP synthase; enzyme 2 is skikimate dehydrogenase; enzyme 3 is chorismate mutase; enzyme 4 is prephenate dehydrogenase. Abbreviations: E4P, erythrose 4-phosphate; PEP, phosphoenolpyruvate; DAHP, 3-deoxy-D-arabino-heptulosonate 7-phosphate; SHIK, shikimic acid; CHA, chorismic acid; PPA, prephenic acid; HPP, hydroxyphenylpyruvic acid; L-Tyr, L-tyrosine.

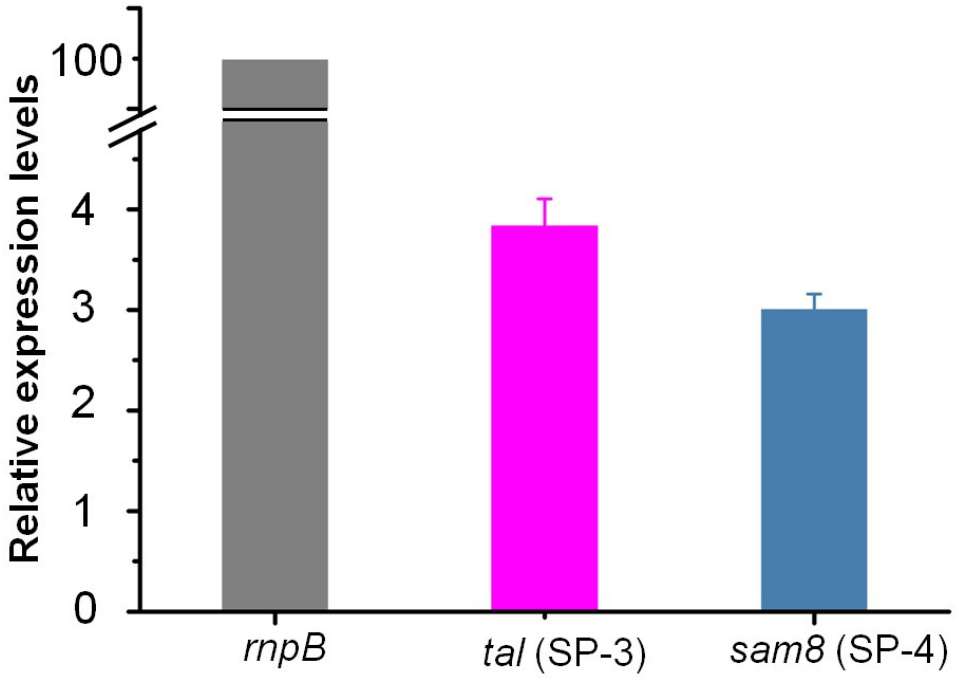

Figure S7. Relative transcription levels of tyrosine ammonia-lyases genes. All values are relative to the expression levels of corresponding *rnpB* gene (the house keeping gene, whose transcription product is the RNA component of RNase P), which were set at 100. Pink and blue columns indicate the expression levels of the *tal* and *sam8* gene, respectively. Results are presented as the average of six repetitions (triplicate reverse transcription reactions from two independent total RNA samples).

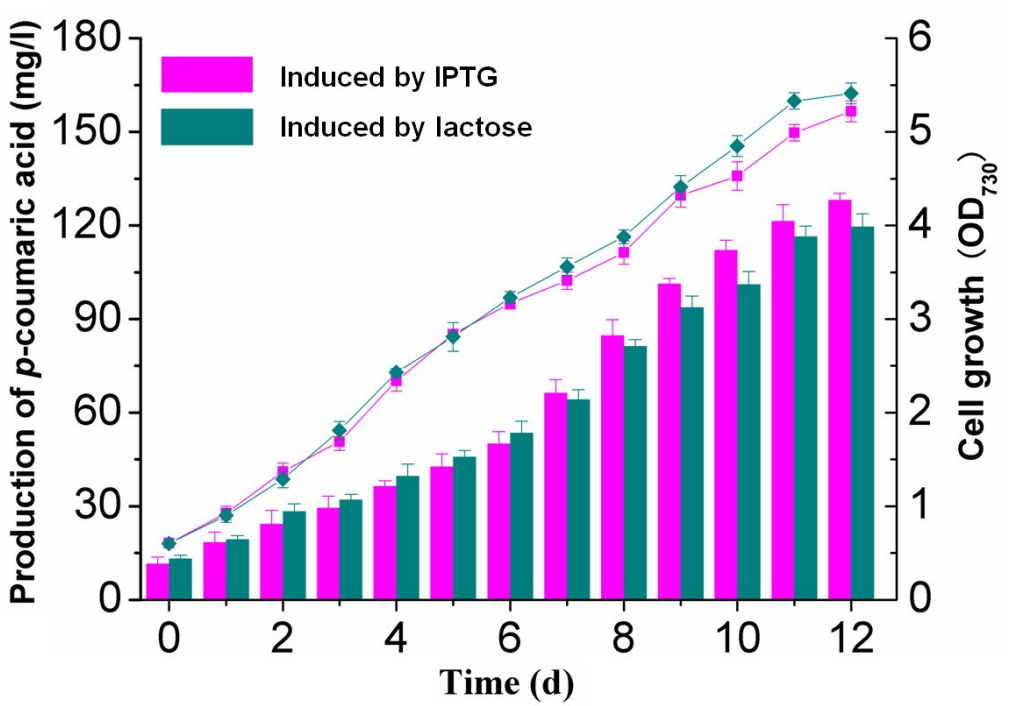

Figure S8. Effect of the different inducers on the production of *p*-coumaric acid. The strains were grown in BG-11 medium at 30°C under constant light exposure (100 $\mu E \cdot s^{-1} \cdot m^{-2}$). After an OD_{730} of 0.5–0.6 was achieved, IPTG or lactose was added into the cultures to produce a final concentration of 0.5 mM. Error bars indicate SD (n = 3).

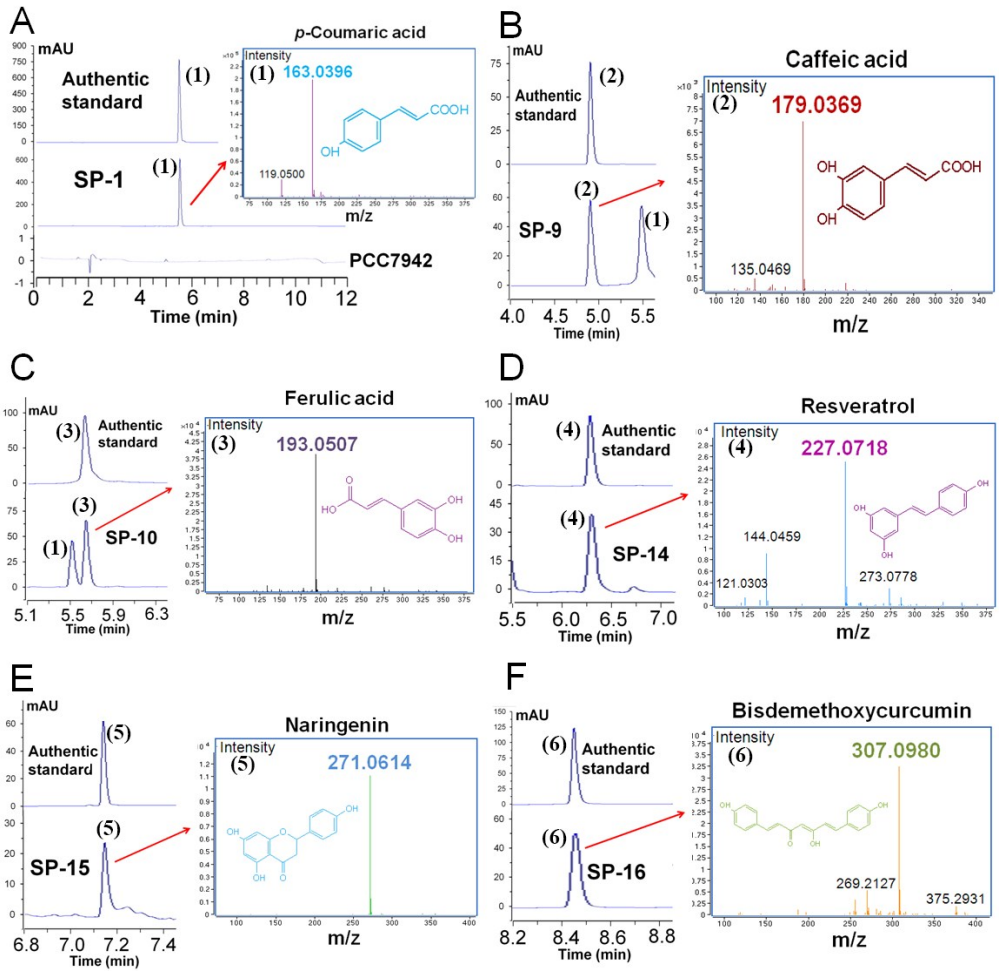

Figure S9. HPLC and LC-MS analysis. (A) *p*-coumaric acid, (B) caffeic acid, (C) ferulic acid, (D) resveratrol, (E) naringenin, and (F) bisdemethoxycurcumin produced by recombinant strains. Peak 1-6 corresponded to *p*-coumaric acid, caffeic acid, ferulic acid, resveratrol, naringenin, and bisdemethoxycurcumin, respectively, and the retention times were 5.49 min, 4.89 min, 5.67 min, 6.34 min, 7.18, and 8.47 min, respectively. ESI-MS spectra were obtained after LC-TOF MS analysis of the recombinant strains and authentic standards; the masses represent MH^- ions.

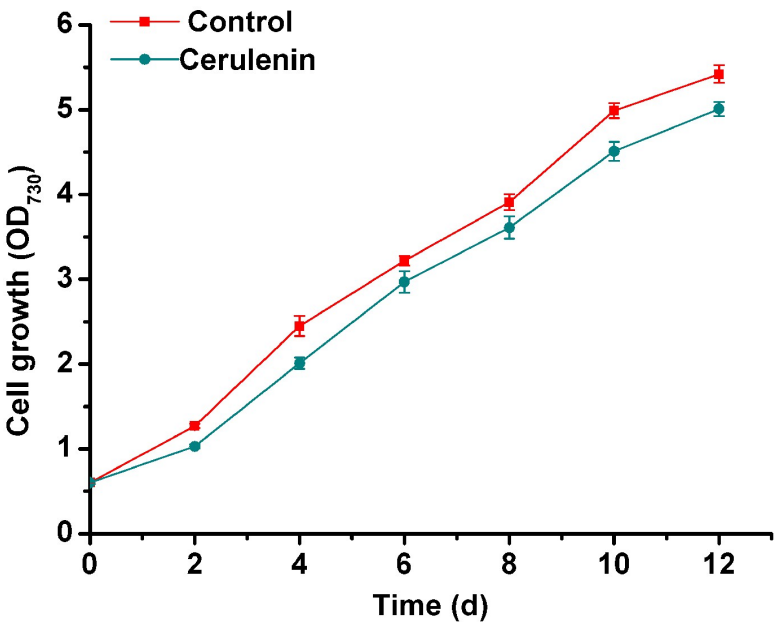

Figure S10. Effect of cerulenin on the growth of *Synechococcus* strain. Wild type *Synechococcus* sp. strains was cultured in BG-11 medium at 30°C, under continuous lighting with an illumination intensity of 100 $\mu E \cdot s^{-1} \cdot m^{-2}$. Cerulenin was added at a concentration of 20 mg/l after the OD_{730} reached 0.5–0.6. The data were generated from at least triplicate independent experiments, and the standard deviations were shown.

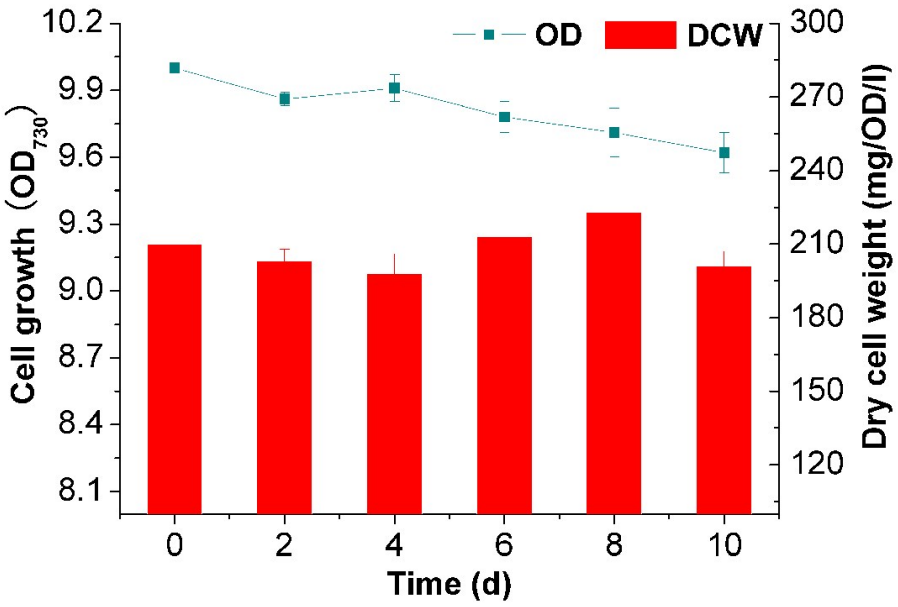

Figure S11. The optical density and corresponding dry cell weight (DCW) of *S. elongatus* PCC7942. Cells were grown in 100 ml BG-11 medium at 30°C under constant light exposure (100 $\mu E \cdot s^{-1} \cdot m^{-2}$) until the OD_{730} reached 1.0. Subsequently, cells were collected by centrifugation and resuspended in a tenth of the original volume in fresh BG-11 medium. After wrapping the tubes with aluminum foil, cells were cultured at 30°C and harvested at 1-day intervals. All samples were collected in triplicate at each time point, and the standard deviations were shown.

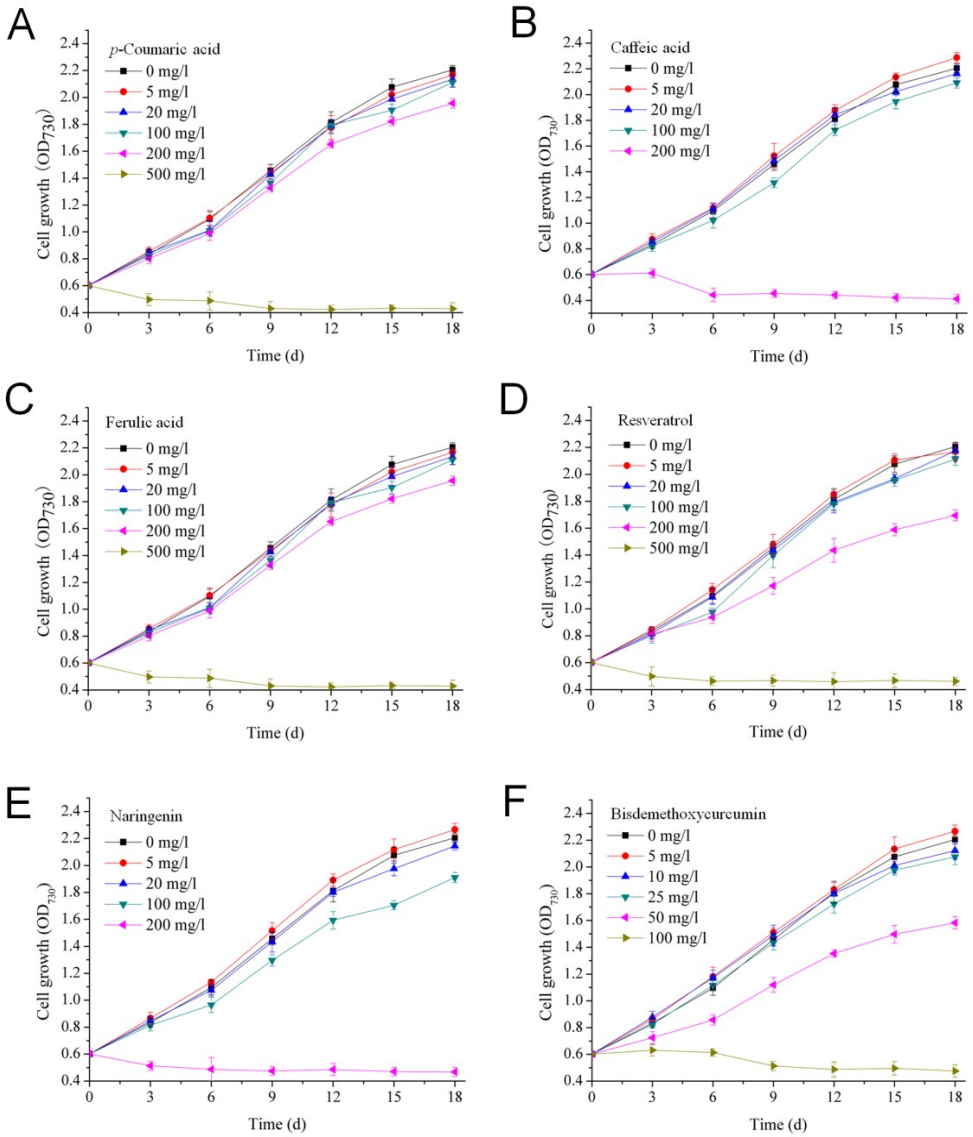

Figure S12. Effect of phenylpropanoids on growth of *S. elongatus* PCC7942. Time course for the growth of *S. elongatus* in the different concentrations of (A) *p*-coumaric acid, (B) caffeic acid, (C) ferulic acid, (D) resveratrol, (E) naringenin, and (F) bisdemethoxycurcumin. Results were generated from at least triplicate independent experiments, and the standard deviations were shown.

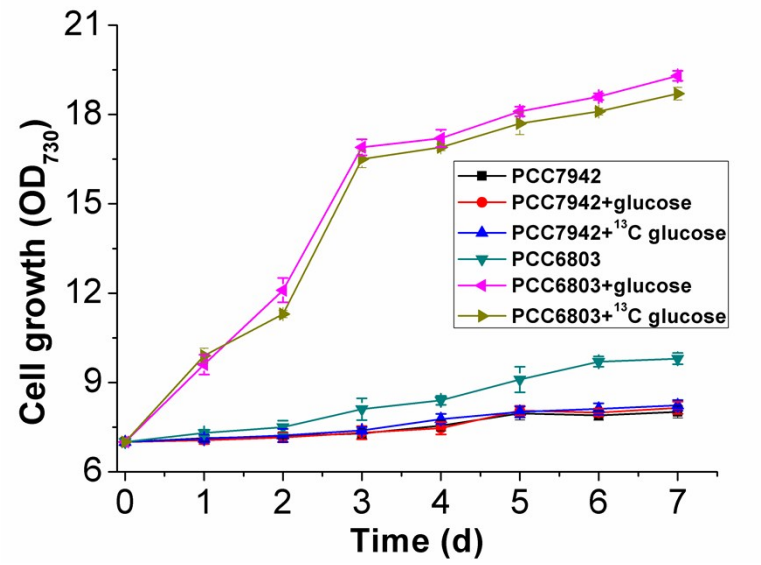

Figure S13. Effect of glucose on the growth of *Synechococcus* PCC7962 and *Synechocystis* sp. PCC6803. Strains were grown in BG-11 medium at 30°C under normal light (50 $\mu E \cdot s^{-1} \cdot m^{-2}$) until an OD_{730} of ~0.7. Cells were concentrated by centrifugation at 3,500 × g for 10 min and resuspended in BG-11 medium at 1/10 of the original volume. Then, 5 mM glucose or ^{13}C labeled glucose was added to the culture, and samples were collected for about 7 d. The data were generated from at least triplicate independent experiments, and the standard deviations were shown.

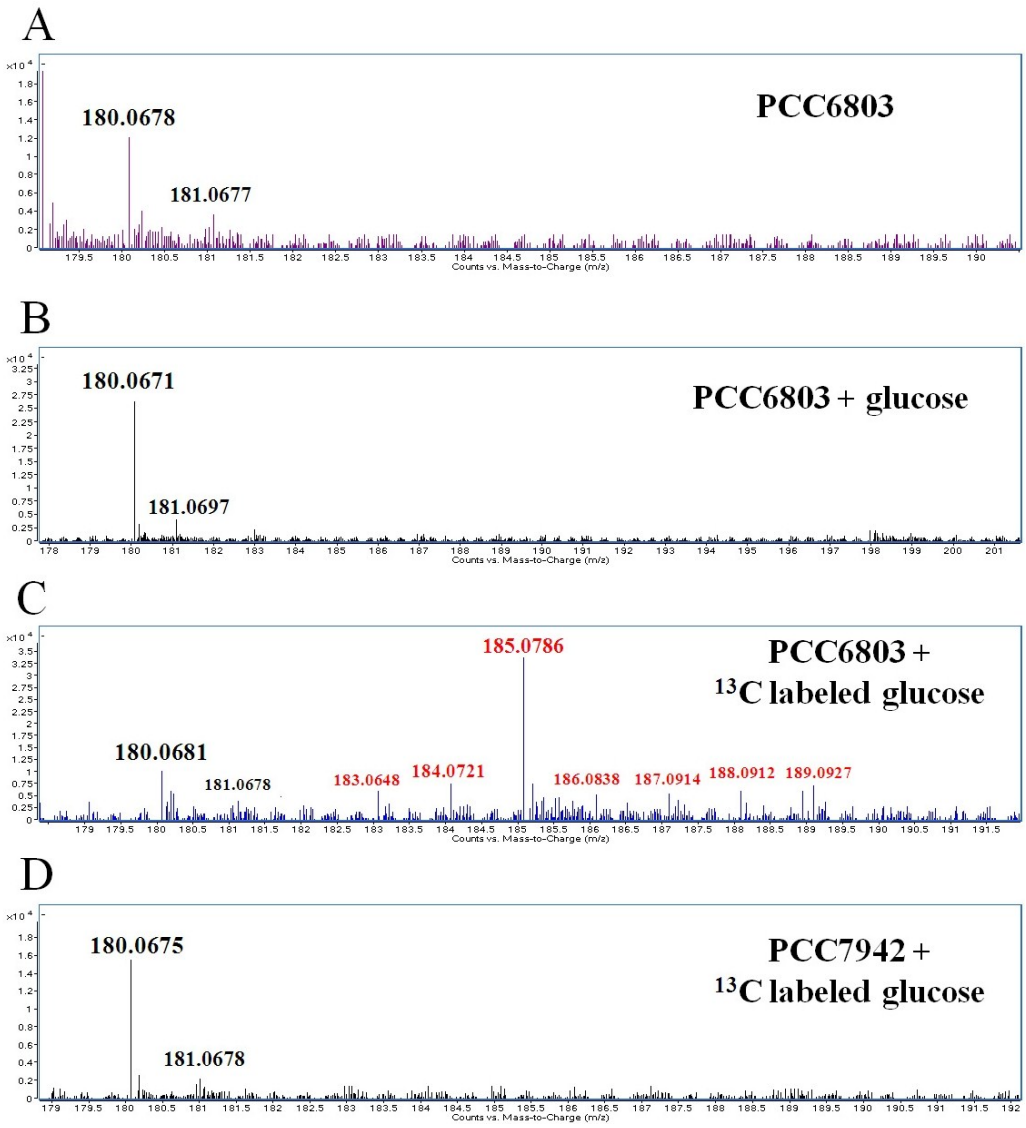

Figure S14. LC-MS analysis of tyrosine. Strains were grown in BG-11 medium at 30°C under normal light (50 $\mu E \cdot s^{-1} \cdot m^{-2}$) until an OD_{730} of ~0.7. *Synechocystis* sp. PCC6803 (A, B, C) and *Synechococcus* PCC7962 (D) were concentrated by centrifugation at 3,500 × g for 10 min and resuspended in BG-11 medium at 1/10 of the original volume. Then, 5 mM glucose (B) or ^{13}C labeled glucose (C, D) was added to the culture, and samples were collected for about 7 d. ESI-MS spectra were obtained after LC-TOF MS analysis of free tyrosine in the culture; the masses represent MH^- ions.

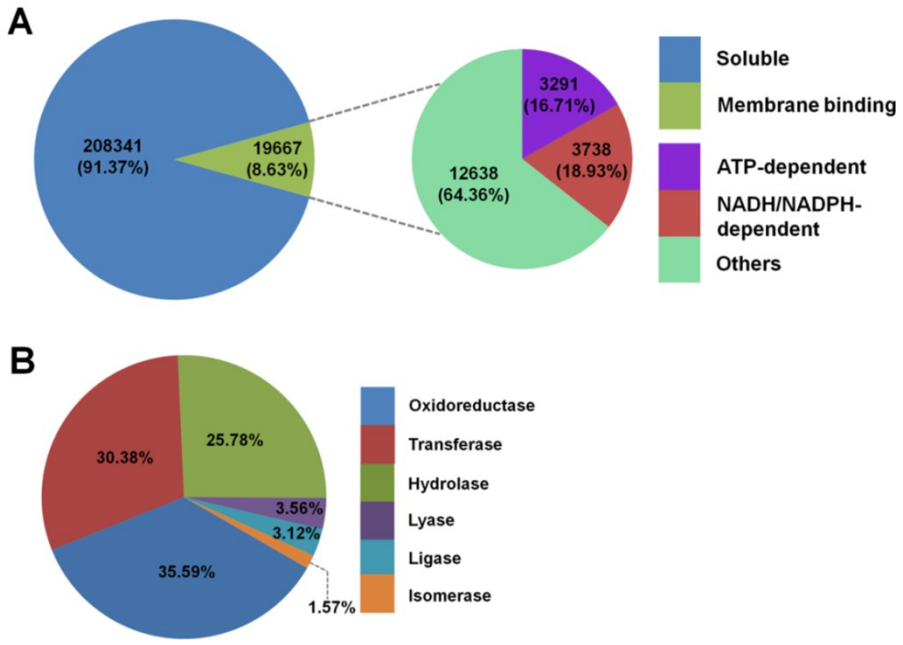

Figure S15. Analysis of the proteins based on the UniProt database (http://www.uniprot.org). (A) Analysis of the transmembrane domains. Total 228,008 proteins were firstly selected based on the information integrity of annotation from Swiss-Prot (release of Nov. 20, 2014) of the UniProt database, which had been manually annotated and reviewed. Then, all the selected proteins were analyzed for finding transmembrane helix by using the stand-alone software package TMHMM 2.0, which was developed by Danmarks Tekniske University (Sonnhammer et al., 1998). The proteins with transmembrane helix(s) were classified as membrane proteins. The information of the requirements for ATP and/or NADH/NADPH was also extracted directly from the annotation of database records. (B) Enzyme classification of the proposed membrane proteins. The information of enzyme classification was also extracted directly from the uniprot database.

Reference

Sonnhammer EL, von Heijne G, Krogh A. (1998) A hidden Markov model for predicting transmembrane helices in protein sequences. *Proc Int Conf Intell Syst Mol Biol* 6:175-82.

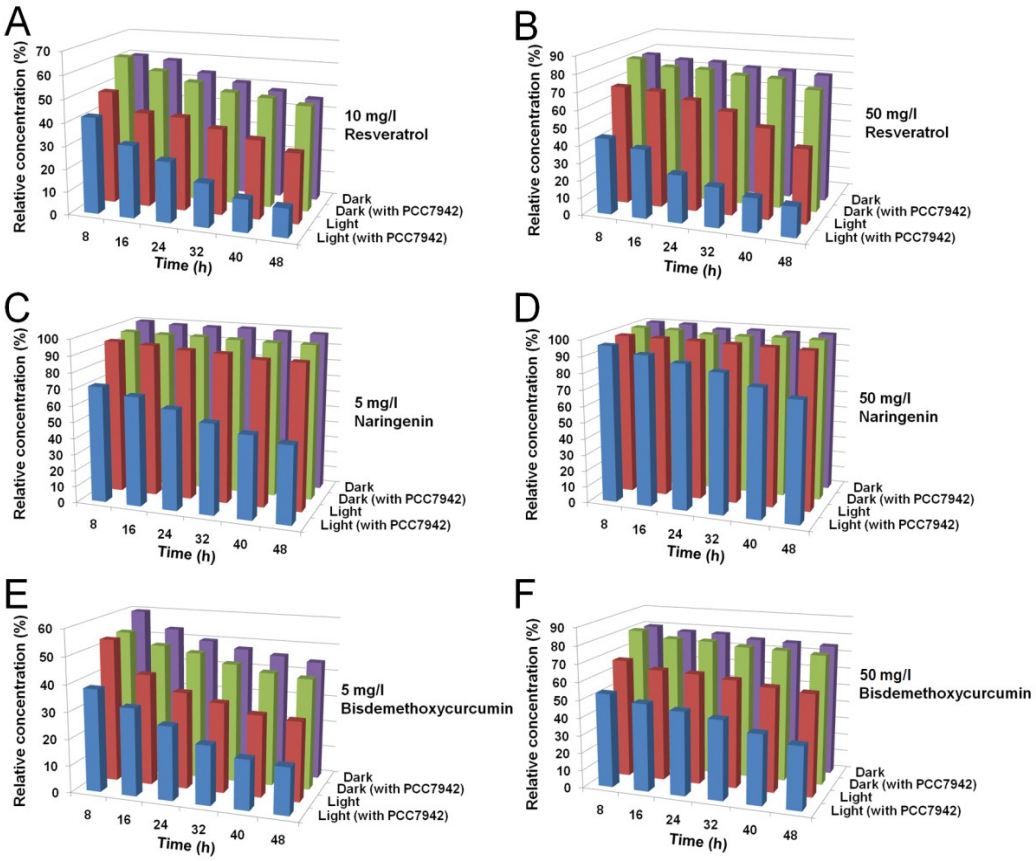

Figure S16. The stability of polyketides. To a final concentration of (A) 5 mg/l resveratrol, (B) 50 mg/l resveratrol, (C) 5 mg/l naringenin, (D) 50 mg/l naringenin, (E) 5 mg/l bisdemethoxycurcumin and (F) 50 mg/l bisdemethoxycurcumin, different polyketides were individually added to the BG11 medium. And then, cultivations were carried out under dark or continuous-light at 30°C for 48 h, the remaining amount of corresponding compounds were compared with the additive amounts. "With PCC7942" means that *S. elongatus* PCC7942 was cultured to OD_{730} = 1.5 under continuous-light before the addition of polyketides. Results are representative of at least three independent experiments.

Table S1. Cost and value comparison of photosynthetic products

Molecule	Relative molecular mass	Photons required	Present cost (USD/kg)	Relative economic value (USD/photon)
Octane (C_8H_{18})	114	100	0.94	1
Sugar ($C_6H_{12}O_6$)	180	48	0.50	1.75
Lactic acid ($C_3H_6O_3$)	90	24	1.00	3.5
***p*-Coumaric acid**($C_9H_8O_3$)	164	76	80.00	**161**
Caffeic acid ($C_9H_8O_4$)	180	72	90.00	**210**
Ferulic acid ($C_{10}H_{10}O_4$)	194	84	150.00	**323**
Naringenin ($C_{15}H_{12}O_5$)	272	124	134.00	**274**
Resveratrol ($C_{14}H_{12}O_3$)	228	124	230.00	**395**
Bisdemethoxycurcumin ($C_{19}H_{16}O_4$)	308	168	160.00	**274**

In each case, the number of photons required to produce a given compound is calculated as twice the number of electrons required to reduce carbon in the compound from CO_2. The "relative economic value" calculates the economic value of producing compounds relative to producing octane:

$$\frac{MW compound \times Present\ cost}{Photons\ required} \Big/ \frac{MW octane \times Cost\ of\ octane}{Photons\ required\ for\ octane}$$

Table S2. List of genes, enzyme, source organism, and reactions.

Gene	Enzyme	Source organism	Reaction catalyzed
sam8	*Se*TAL	*Saccharothrix espanaensis*	*L*-tyrosine → *p*-Coumaric acid
tal	*Rs*TAL	*Rhodobacter sphaeroides*	
aroG^{fbr}	fbr-DAHPS	*Escherichia coli*	Phosphoenolpyruvate + *D*-erythrose 4-phosphate→3-Deoxy-*D*-arabino-hept-2-ulosonate 7-phosphate
aroG	DAHPS		
sam5	*Se*C3H	*Saccharothrix espanaensis*	*p*-Coumaric acid → Caffeic acid
ref8	*At*C3H	*Arabidopsis thaliana*	
comt	COMT		Caffeic acid → Ferulic acid
c4h	C4H		trans-Cinnamic acid → *p*-Coumaric acid
chi	CHI		Naringenin-chalcone → Naringenin
4cl	4CL	*Petroselinum crispum*	*p*-Coumaric acid → 4-Coumaroyl -CoA
sts	STS	*Arachis hypogaea*	4-Coumaroyl -CoA → Resveratrol
chs	CHS	*Petunia hybrida*	4-Coumaroyl -CoA → Naringenin-chalcone
cus	CUS	*Oryza sativa*	4-Coumaroyl -CoA → bisdemethoxycurcumin

Table S3. *In vitro* activity of thylakoid membranes (C3H and C4H)

Thylakoid membrane	Activity toward substrate (U/mg DCW)	
	(*p*-coumaric acid)	(trans-cinnamic acid)
SP-9	0.062	—
SP-18	—	0.114
PCC7942	ND	ND

The sign 'ND' indicated that the thylakoid membrane of wild-type *Synechococcus* sp. PCC7942 did not exhibit any activity. One U (unit) is defined as the amount (1 uM) of product formed per minute.

Table S4. Plasmids and strains used in this study

Plasmid or Strain	Relevant characteristics	Source
Plasmid		
pEASY-Blunt	f1 ori, T7 promoter, Kan^R and Amp^R	Transgen
PAM2991	ColE1, trc promoter, NSI targeting, $Spec^R$	Stored in lab
pAM2	ColE1, double trc promoter, NSI targeting, $Spec^R$	This study
tyrA^{fbr}-aroG^{fbr}-tktA-ppsA/pCOLA	pCOLADuet-1 contained the *tyrA^{fbr}*, *aroG^{fbr}*, *tktA*, and *ppsA* genes	Nakagawa A, et al. 2011
tal/pAM	pAM2991 contained the *tal* gene	This study
sam8/pAM	pAM2991 contained the *sam8* gene	This study
aroG^{fbr}/pAM	pAM2991 contained the *aroG^{fbr}* gene	This study
aroG^{fbr}-tal/pAM	pAM2991 contained the *tal* and *aroG^{fbr}* genes	This study
aroG^{fbr}-sam8/pAM	pAM2991 contained the *sam8* and *aroG^{fbr}* genes	This study
aroG-sam8/pAM	pAM2991 contained the *sam8* and *aroG* genes	This study
sam5/pAM	pAM2991 contained the *sam5* gene	This study
ref8/pAM	pAM2991 contained the *ref8* gene	This study
aroG^{fbr}-sam8-sam5/pAM	pAM2 contained the *sam8, aroG^{fbr}* and *sam5* genes	This study
aroG^{fbr}-sam8-ref8/pAM	pAM2 contained the *sam8*, *aroG^{fbr}* and *sam5* genes	This study
aroG^{fbr}-sam8-ref8-comt/pAM	pAM2 contained the *sam8, aroG^{fbr}, ref8* and *comt* genes	This study
sam8-aroG^{fbr}-4cl-sts/pAM	pAM2 contained the *sam8, aroG^{fbr}, 4cl* and *sts* genes	This study
sam8-aroG^{fbr}-4cl-chs-chi/pAM	pAM2 contained the *sam8, aroG^{fbr}, 4cl, chs* and *chi* genes	This study
sam8-aroG^{fbr}-4cl-cus/pAM	pAM2 contained the sam8, *aroG^{fbr}, 4cl* and *cus* genes	This study
sam8-aroG^{fbr}-4cl::sts/pAM	pAM2 contained the *sam8, aroG^{fbr}*and fusion gene of *4cl* and *sts*	This study
sam8-aroG^{fbr}-4cl::chs-chi/pAM	pAM2 contained the *sam8, aroG^{fbr}*, *chi* and fusion gene of *4cl* and *chs*	This study
sam8-aroG^{fbr}-4cl::cus/pAM	pAM2 contained the *sam8, aroG^{fbr}*and fusion gene of *4cl* and *cus*	This study
Strain		
E. coli DH5α	Cloning host	Invitrogen
E. coli BL21(DE3)	Expression host	Novagen
E. coli K12	Used for cloning the *aroG* gene	Invitrogen
Saccharothrix espanaensis	Used for cloning the *sam8* and *sam5* genes	ATCC 51144
Rhodobacter sphaeroides	Used for cloning the *tal* gene	ATCC 17023
Synechococcus elongatus PCC7942	Wild type	ATCC 33912

Synechocystis sp. PCC6803	Wild type	ATCC 27184
SP-1	PCC7942 with *tal* integrated at NSI	This study
SP-2	PCC7942 with *sam8* integrated at NSI	This study
SP-3	PCC7942 with *tal* and $aroG^{fbr}$ integrated at NSI	This study
SP-4	PCC7942 with *sam8* and $aroG^{fbr}$ integrated at NSI	This study
SP-5	PCC7942 with $aroG^{fbr}$ integrated at NSI	This study
SP-6	PCC7942 with *sam8* and *aroG* integrated at NSI	This study
SP-7	PCC7942 with *sam8,* $aroG^{fbr}$ and *sam5* integrated at NSI	This study
SP-8	PCC7942 with *sam5* integrated at NSI	This study
SP-9	PCC7942 with *ref8* integrated at NSI	This study
SP-10	PCC7942 with *sam8*, $aroG^{fbr}$ and *ref8* integrated at NSI	This study
SP-11	PCC7942 with *sam8,* $aroG^{fbr}$*, ref8* and *comt* integrated at NSI	This study
SP-12	PCC7942 with *sam8,* $aroG^{fbr}$*, 4cl* and *sts* integrated at NSI	This study
SP-13	PCC7942 with *sam8,* $aroG^{fbr}$*, 4cl, chs* and *chi* integrated at NSI	This study
SP-14	PCC7942 with *sam8,* $aroG^{fbr}$*, 4cl* and *cus* integrated at NSI	This study
SP-15	PCC7942 with *sam8,* $aroG^{fbr}$ and fusion gene of *4cl* and *sts* integrated at NSI	This study
SP-16	PCC7942 with *sam8,* $aroG^{fbr}$ and fusion gene of *4cl* and *chs* integrated at NSI	This study
SP-17	PCC7942 with *sam8,* $aroG^{fbr}$ and fusion gene of *4cl* and *cus* integrated at NSI	This study
SP-18	PCC7942 with *c4h* gene integrated at NSI	This study

Table S5. DNA sequences of the primers used in this study

Primer	Sequence (5' to 3')
*Xho*I-*tal*-F	CATGCTCGAGATGGGCGACACGAAGGAGC
*Bam*HI-*tal*-R	CATGGGATCCTTACGGGCCGGCTTCGCT
*Xho*I-*sam8*-F	CATGCTCGAGATGACGCAGGTCGTGGAACG
*Bam*HI-*sam8*-R	CATGGGATCCTTATCCGAAATCCTTCCCGT
*Eco*RI-*sam5*-F	CATGGAATTCATGACCATCACGTCACCTGC
*Afl*II-*sam5*-R	CATGCTTAAGTTAGGTGCCGGGGTTGATCA
*Bgl*II-Ptrc-F	CATGAGATCTCAGCTTATCATCGACTGCACG
*Xho*I-Ptrc-R	CATGCTCGAGGTCTGTTTCCTGTGTGAAATTGTT
*Afl*II-*aroG*-F	CATGCTTAAGATGAATTATCAGAACGACGATTTACG
*Bgl*II-*aroG*-R	CATGAGATCTTTACCCGCGACGCGCT
*Xho*I-*4cl*-F	CATGCTCGAGATGGGTGACTGCGTTGCCC
*Bam*HI-*4cl*-R	CATGGGATCCTTACTTCGGCAGGTCGCCG
*Sal*I-*aroG*^{fbr}-F	CATGGTCGACATGAATTATCAGAACGACGATTTACG
*Hind*III-*aroG*^{fbr}-R	CATGAAGCTTACCCGCGACGCGCT
*Bgl*II-*sam8*-R	CATGAGATCTTTATCCGAAATCCTTCCCGT
*Afl*II-Ptrc-F	CATGCTTAAGCAGCTTATCATCGACTGCACG
*Sal*I-Ptrc-R	CATGGTCGACGTCTGTTTCCTGTGTGAAATTGTT
*Sal*I-*chi*-F	CATGGTCGACATGTCTAGCTCCAACGCCTGC
*Bgl*II-*chi*-R	CATGAGATCTTTAGTTCTCTTTGGCCAGTTTTTCC
*Hind*III-Ptrc-F	CATGAAGCTTCAGCTTATCATCGACTGCACG
4cl::chs-R	CGGTCACCATGCCGCTGCCCTTCGGCAGGTCGCCG
4cl::chs-F	CCTGCCGAAGGGCAGCGGCATGGTGACCGTTGAGGAGTATCG
*Bam*HI-*chs*-R	CATGGGATCCTTAAGTAGCAACAGAGTGCAGAACA
4cl::sts-R	CAGACACCATGCCGCTGCCCTTCGGCAGGTCGCCG
4cl::sts-F	CCTGCCGAAGGGCAGCGGCATGGTGTCTGTGTCTGGCATTC
*Bam*HI-*sts*-R	CATGGGATCCTTAGATGGCCATGCTGCGC
4cl::cus-R	TCGGTGCCATGCCGCTGCCCTTCGGCAGGTCGCCG
4cl::cus-F	CCTGCCGAAGGGCAGCGGCATGGCACCGACCACCACC
*Bam*HI-*cus*-R	CATGGGATCCTTAGTTCACATGAGAGGTGGCG

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S6. DNA sequences of primers used for the synthesis of *ref8* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Eco*RI-*ref8*-F)	CATGGAATTCATGTCTTGGTTCC
2	AGCGATGGTAGCAACAGCGATCAGGAACCAAGACATGAATTCCAT
3	GCTGTTGCTACCATCGCTGCTGTTGTTTCTTACAAACTGATCCAG
4	CGGGAATTTGTAACGCAGACGCTGGATCAGTTTGTAAGAAACAAC
5	GTCTGCGTTACAAATTCCCGCCGGGTCCGTCTCCGAAACCGATCG
6	CCGGTTTGATGTCGTACAGGTTACCAACGATCGGTTTCGGAGACG
7	CCTGTACGACATCAAACCGGTTCGTTTCCGTTGCTACTACGAATG
8	TGATCGGACCGTAAGACTGAGCCCATTCGTAGTAGCAACGGAAAC
9	TCAGTCTTACGGTCCGATCATCTCTGTTTGGATCGGTTCTATCCT
10	CAGCAGAAGAAACAACAACGTTCAGGATAGAACCGATCCAAACAG
11	ACGTTGTTGTTTCTTCTGCTGAACTGGCTAAAGAAGTTCTGAAAG
12	CAGCCAGTTTCTGGTCGTGTTCTTTCAGAACTTCTTTAGCCAGTT
13	CACGACCAGAAACTGGCTGACCGTCACCGTAACCGTTCTACCGAA
14	GGTCCTGACCGTTACGAGAGAAAGCTTCGGTAGAACGGTTACGGT
15	TCTCGTAACGGTCAGGACCTGATCTGGGCTGACTACGGTCCGCAC
16	GGTGCAAACTTTACGAACTTTAACGTAGTGCGGACCGTAGTCAGC
17	GTTAAAGTTCGTAAAGTTTGCACCCTGGAACTGTTCACCCCGAAA
18	CGGATCGGACGCAGAGATTCCAGACGTTTCGGGGTGAACAGTTCC
19	TCTCTGCGTCCGATCCGTGAAGACGAAGTTACCGCTATGGTTGAA
20	AGGTTGCAGTCACGGAAAACAGATTCAACCATAGCGGTAACTTCG
21	TTTTCCGTGACTGCAACCTGCCGGAAAACCGTGCTAAAGGTCTGC
22	AACAGCACCCAGGTATTTACGCAGCTGCAGACCTTTAGCACGGTT
23	CGTAAATACCTGGGTGCTGTTGCTTTCAACAACATCACCCGTCTG
24	CGTTCATGAAACGTTTACCGAAAGCCAGACGGGTGATGTTGTTGA
25	TCGGTAAACGTTTCATGAACGCTGAAGGTGTTGTTGACGAACAGG
26	GAAACGATAGCTTTAAATTCCAGACCCTGTTCGTCAACAACACCT
27	GTCTGGAATTTAAAGCTATCGTTTCTAACGGTCTGAAACTGGGTG
28	ATGTGTTCAGCGATAGACAGAGAAGCACCCAGTTTCAGACCGTTA
29	TCTGTCTATCGCTGAACACATCCCGTGGCTGCGTTGGATGTTCCC
30	TGTTCAGCGAAAGCTTTTTCGTCAGCCGGGAACATCCAACGCAGC
31	CGAAAAAGCTTTCGCTGAACACGGTGCTCGTCGTGACCGTCTGAC
32	AGGGTGTGTTCTTCCATGATAGCACGGGTCAGACGGTCACGACGA
33	CTATCATGGAAGAACACACCCTGGCTCGTCAGAAATCTTCTGGTG
34	AGCGTCAACGAAGTGCTGTTTAGCACCAGAAGATTTCTGACGAGC
35	CAGCACTTCGTTGACGCTCTGCTGACCCTGAAAGACCAGTACGAC
36	GACCGATGATGGTGTCTTCAGACAGGTCGTACTGGTCTTTCAGGG
37	CTGAAGACACCATCATCGGTCTGCTGTGGGACATGATCACCGCTG
38	CAGCGGTGATAGCGGTGGTGTCCATACCAGCGGTGATCATGTCCC

39	CACCGCTATCACCGCTGAATGGGCTATGGCTGAAATGATCAAAAA
40	AACTTTCTGCTGAACACGCGGGTTTTTGATCATTTCAGCCATAGC
41	GCGTGTTCAGCAGAAAGTTCAGGAAGAATTTGACCGTGTTGTTGG
42	GCTTCGGTCAGGATACGGTCCAGACCAACAACACGGTCAAATTCT
43	CCGTATCCTGACCGAAGCTGACTTCTCTCGTCTGCCGTACCTGCA
44	CAGACGGAAAGATTCTTTAACAACGCACTGCAGGTACGGCAGACG
45	GTTGTTAAAGAATCTTTCCGTCTGCACCCGCCGACCCCGCTGATG
46	TTAACGTCAGCGTTAGAACGGTGCGGCAGCATCAGCGGGGTCGGC
47	CCGTTCTAACGCTGACGTTAAAATCGGTGGTTACGACATCCCGAA
48	ACACGTTAACGTGCACGTTAGAACCTTTCGGGATGTCGTAACCAC
49	AACGTGCACGTTAACGTGTGGGCAGTTGCTCGTGACCCGGCTGTT
50	CGGGACGAAATTCGAACGGGTTTTTCCAAACAGCCGGGTCACGAG
51	CCGTTCGAATTTCGTCCCGAACGCTTCCTGGAAGAAGACGTTGAC
52	CAGACGGAAGTCGTGACCTTTCATGTCAACGTCTTCTTCCAGGAA
53	AGGTCACGACTTCCGTCTGCTGCCGTTCGGTGCTGGTCGTCGTGT
54	GTTGATACCCAGCTGAGCACCCGGGCAAACACGACGACCAGCACC
55	GTGCTCAGCTGGGTATCAACCTGGTTACCTCTATGATGTCTCACC
56	GTCCAAACGAAGTGGTGCAGCAGGTGAGACATCATAGAGGTAACC
57	TGCACCACTTCGTTTGGACCCCGCCGCAGGGTACCAAACCGGAAG
58	ACCCGGGTTTTCAGACATGTCGATTTCTTCCGGTTTGGTACCCTG
59	CATGTCTGAAAACCCGGGTCTGGTTACCTACATGCGTACCCCGGT
60	CGGCAGACGCGGGGTAGCAACAGCCTGAACCGGGGTACGCATGTA
61	CCCCGCGTCTGCCGTCTGACCTGTACAAACGTGTTCCGTACGACA
62 (*Afl*II-*ref8*-R)	CATG<u>CTTAAG</u>TTACATGTCGTACGGAACACGTTTG

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S7. DNA sequences of primers used for the synthesis of *4cl* gene (fused with promoter trc and codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Eco*RI-Ptrc-F)	CATGGAATTCCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGG
2	CACAGCCATACCACAGCTTCCGATGGCTGCCTGACGCCAGAAGCA
3	AAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG
4	CGGGAGTGCGCCTTGAGCGACACGAATTATGCAGTGATTTACGAC
5	TCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATC
6	TTCAGAATATTTGCCAGAACCGTTATGATGTCGGCGCAAAAAACA
7	CGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATC
8	TTCCACACATTATACGAGCCGGATGATTAATTGTCAACAGCTCAT
9	CGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTCACA
10	TCTCGAGCATGGTCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC
11	GAAACAGACCATGCTCGAGATGGGTGACTGCGTTGCCCCGAAAGA
12	CGGCAGCTTGCTGCGGAAGATCAGATCCTCTTTCGGGGCAACGCA
13	CGCAGCAAGCTGCCGGACATCTACATCCCGAAGCATCTGCCGCTG
14	TGCTGATGTTCTCAAAACAATAGGTATGCAGCGGCAGATGCTTCG
15	CCTATTGTTTTGAGAACATCAGCAAGGTTGGCGACAAGAGCTGTC
16	AGGTTTCGCCGGTTGCGCCGTTGATCAGACAGCTCTTGTCGCCAA
17	GCAACCGGCGAAACCTTTACCTACAGCCAGGTTGAGCTGCTGTCC
18	CTTGTTCAGGCCGCTGGCAACTTTACGGGACAGCAGCTCAACCTG
19	CCAGCGGCCTGAACAAGCTGGGCATTCAACAAGGTGATACCATTA
20	GAGAGTTCGGCAGCAGCAGCATAATGGTATCACCTTGTTGAATGC
21	GCTGCTGCCGAACTCTCCCGAGTACTTCTTCGCGTTCCTGGGTGC
22	CCATAGTGCTGATTGCACCGCGATAGCTCGCACCCAGGAACGCGA
23	CGGTGCAATCAGCACTATGGCGAACCCGTTCTTTACCAGCGCAGA
24	GGCTCGCTTTCAGTTGCTTGATCACTTCTGCGCTGGTAAAGAACG
25	AGCAACTGAAAGCGAGCCAAGCGAAGCTGATTATCACCCAGGCAT
26	TAGTCCTTAACCTTGTCAACATAGCATGCCTGGGTGATAATCAGC
27	CTATGTTGACAAGGTTAAGGACTACGCAGCGGAGAAAAACATCCA
28	CGGTGCATCGTCAATACAAATGATCTGGATGTTTTTCTCCGCTGC
29	ATTTGTATTGACGATGCACCGCAAGATTGTCTGCACTTCAGCAAG
30	TTCGCTCTCATCCGCTTCCATCAGCTTGCTGAAGTGCAGACAATC
31	GAAGCGGATGAGAGCGAAATGCCGGAAGTGGTTATTAACAGCGAT
32	CTGTACGGCAGTGCCACCACATCATCGCTGTTAATAACCACTTCC
33	GTGGCACTGCCGTACAGCTCTGGCACCACCGGCCTGCCGAAAGGC
34	GGTAACCAGACCCTTGTGGGTCAGCATAACGCCTTTCGGCAGGCC
35	CCACAAGGGTCTGGTTACCAGCGTTGCACAACAGGTGGATGGTGA
36	CGGAGTGCATATACAGGTTCGGGTTATCACCATCCACCTGTTGTG
37	CGAACCTGTATATGCACTCCGAGGATGTTATGATCTGCATCCTGC
38	CAGGCTATAGATATGGAACAGCGGCAGGATGCAGATCATAACATC

39	GCTGTTCCATATCTATAGCCTGAACGCTGTTCTGTGTTGTGGTCT
40	GATCAGAATGGTAACGCCCGCACGCAGACCACAACACAGAACAGC
41	CGGGCGTTACCATTCTGATCATGCAAAAGTTCGATATCGTGCCGT
42	TATACTTCTGGATCAGCTCCAGGAACGGCACGATATCGAACTTTT
43	CTGGAGCTGATCCAGAAGTATAAGGTTACCATTGGTCCGTTTGTT
44	CGCGATGGCCAGCACGATCGGCGGAACAAACGGACCAATGGTAAC
45	GTGCTGGCCATCGCGAAAAGCCCGGTTGTTGACAAGTACGACCTG
46	GCTCATAACGGTGCGCACGCTAGACAGGTCGTACTTGTCAACAAC
47	TGCGCACCGTTATGAGCGGTGCAGCGCCGCTGGGTAAAGAGCTGG
48	TCGGGAATTTCGCACGAACAGCGTCCTCCAGCTCTTTACCCAGCG
49	GTTCGTGCGAAATTCCCGAACGCGAAGCTGGGTCAAGGCTATGGC
50	CGCCAGAACCGGACCGGCTTCGGTCATGCCATAGCCTTGACCCAG
51	CGGTCCGGTTCTGGCGATGTGTCTGGCGTTCGCCAAAGAGCCGTA
52	GTACCGCATGCGCCAGACTTAATCTCATACGGCTCTTTGGCGAAC
53	CTGGCGCATGCGGTACCGTTGTGCGTAACGCCGAGATGAAAATCG
54	GAGACGCGTTGGTTTCCGGGTCAACGATTTTCATCTCGGCGTTAC
55	CGGAAACCAACGCGTCTCTGCCGCGTAACCAGCGTGGTGAGATTT
56	TCATAATCTGATCACCACGGATGCAAATCTCACCACGCTGGTTAC
57	ATCCGTGGTGATCAGATTATGAAAGGTTACCTGAACGACCCGGAA
58	CCTCTTCGTCGATGGTGGTGCGGGTGCTTTCCGGGTCGTTCAGGT
59	ACCACCATCGACGAAGAGGGTTGGCTGCACACCGGTGACATTGGT
60	GAACAGTTCATCGTCATCGTCGATGAAACCAATGTCACCGGTGTG
61	GACGATGACGATGAACTGTTCATTGTTGATCGTCTGAAAGAAATCA
62	GCAACTTGAAAACCTTTGTACTTAATGATTTCTTTCAGACGATCAACAAT
63	TTAAGTACAAAGGTTTTCAAGTTGCTCCGGCGGAGCTGGAAGCAC
64	ATCGCTGATGGTCGGGTGGGTCAGCAGCAGTGCTTCCAGCTCCGC
65	ACCCGACCATCAGCGATGCCGCGGTGGTTCCGATGATTGACGAGA
66	AACGCCACCGGCACTTCACCCGCTTTCTCGTCAATCATCGGAACC
67	AAGTGCCGGTGGCGTTTGTTGTGCGTACCAACGGTTTTACCACCA
68	ACAAATTGTTTGATTTCTTCTTCGGTGGTGGTAAAACCGTTGGTAC
69	CCGAAGAAGAAATCAAACAATTTGTGAGCAAACAGGTTGTGTTCTAC
70	AAGAAAACGCGGAAGATACGTTTGTAGAACACAACCTGTTTGCTC
71	ACGTATCTTCCGCGTTTTCTTCGTTGACGCTATTCCGAAATCCCC
72	GATCCTTACGCAGAATCTTGCCGCTCGGGGATTTCGGAATAGCGT
73	GCAAGATTCTGCGTAAGGATCTGCGCGCTCGTATTGCGAGCGGCG
74 (*Bam*HI-*4cl*-R)	CATGGGATCCTTACTTCGGCAGGTCGCCGCTCGCAATACG

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S8. DNA sequences of primers used for the synthesis of *chs* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Eco*RI-*chs*-F)	CATGGAATTCATGGTGACCGTTGAGGA
2	CCTCACAGCGTTGTGCCTTACGATACTCCTCAACGGTCACCATGA
3	GGCACAACGCTGTGAGGGTCCGGCCACTGTTATGGCCATTGGCAC
4	GATCAACACAGTTGGTCGGGGTGGCGGTGCCAATGGCCATAACAG
5	CCCGACCAACTGTGTTGATCAAAGCACTTACCCGGATTATTATTT
6	GTGCTCAGAGTTAGTGATACGAAAATAATAATCCGGGTAAGTGCTTT
7	TCGTATCACTAACTCTGAGCACAAGACTGATCTGAAGGAGAAATTTA
8	GCTTTTTTCACACATGCGCTTAAATTTCTCCTTCAGATCAGTCTT
9	AGCGCATGTGTGAAAAAAGCATGATTAAGAAACGCTACATGCACC
10	TCTCTTTCAGGATTTCCTCGGTCAGGTGCATGTAGCGTTTCTTAA
11	CCGAGGAAATCCTGAAAGAGAACCCGTCTATGTGTGAATACATGG
12	TTGGCGAGCATCCAGAGACGGTGCCATGTATTCACACATAGACGG
13	TCTCTGGATGCTCGCCAAGACATCGTGGTGGTTGAAGTGCCGAAA
14	GCTTTTTGGGCTGCCTCTTTGCCCAGTTTCGGCACTTCAACCACC
15	AGAGGCAGCCCAAAAAGCTATCAAGGAATGGGGCCAGCCGAAGTC
16	TGGTGCAAAAAACCAGATGGGTAATTTTGGACTTCGGCTGGCCCC
17	CCATCTGGTTTTTTGCACCACTTCTGGTGTGGACATGCCGGGCTG
18	GGCCCAGCAGCTTAGTCAGTTGATAGTCACAGCCCGGCATGTCCA
19	TGACTAAGCTGCTGGGCCTGCGTCCGTCTGTTAAGCGCCTGATGA
20	CCCGCGAAGCAGCCCTGTTGGTACATCATCAGGCGCTTAACAGAC
21	GGGCTGCTTCGCGGGTGGCACCGTTCTGCGTCTGCGCAAGGACCT
22	CACACGAGCGCCCTTGTTGTTTTCAGCCAGGTCCTTGCGCAGACG
23	CAAGGGCGCTCGTGTGCTGGTTGTTTGCAGCGAGATCACCGCGGT
24	GATGAGTATCGTTCGGGCCACGGAAGGTAACCGCGGTGATCTCGC
25	GGCCCGAACGATACTCATCTGGATTCTCTGGTTGGCCAAGCACTG
26	TAATGATCGCGCCTGCGCCATCACCAAACAGTGCTTGGCCAACCA
27	CGCAGGCGCGATCATTATCGGTTCTGATCCGATTCCGGGTGTTGA
28	GCGCTAACCAGCTCGAACAGCGGGCGCTCAACACCCGGAATCGGA
29	GTTCGAGCTGGTTAGCGCAGCCCAAACTCTGCTGCCGGATAGCCA
30	TTCACGCAGATGGCCATCAATAGCACCATGGCTATCCGGCAGCAG
31	GATGGCCATCTGCGTGAAGTTGGCCTGACCTTCCACCTGCTGAAA
32	TTTTTGCTGATCAGGCCCGGAACATCTTTCAGCAGGTGGAAGGTC
33	CGGGCCTGATCAGCAAAAACATTGAGAAGAGCCTGGAGGAAGCAT
34	CCAATCAGAAATGCCCAGCGGTTTAAATGCTTCCTCCAGGCTCTT
35	GCTGGGCATTTCTGATTGGAACTCTCTGTTCTGGATTGCTCATCC
36	TGGTCCAGAATTGCCGGGCCACCCGGATGAGCAATCCAGAACAGA
37	CCCGGCAATTCTGGACCAAGTTGAAATCAAGCTGGGCCTGAAGCC
38	GCACGTTGCGGGTAGCCTTCAGTTTCTCCGGCTTCAGGCCCAGCT

39	GCTACCCGCAACGTGCTGTCTGACTATGGTAACATGAGCTCTGCT
40	TTCATCCAGGATAAACAGAACGCAAGCAGAGCTCATGTTACCATA
41	CGTTCTGTTTATCCTGGATGAAATGCGCAAGGCCAGCGCCAAAGA
42	CCAGGCCTTCACCAGTAGTGCCCAGACCTTCTTTGGCGCTGGCCT
43	ACTACTGGTGAAGGCCTGGAGTGGGGTGTTCTGTTTGGCTTTGGC
44	CAACAGTCTCAACGGTCAGGCCCGGGCCAAAGCCAAACAGAACAC
45	CCTGACCGTTGAGACTGTTGTTCTGCACTCTGTTGCTACTTAACT
46 (*Afl*II-*chs*-R)	CATGCTTAAGTTAAGTAGCAACAGAGTGCA

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S9. DNA sequences of primers used for the synthesis of *chi* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Xho*I-*chi*-F)	CATGCTCGAGATGTCTAGCTCCAACG
2	GGGAACGGGCTCGGAGAGGCGCAGGCGTTGGAGCTAGACATCTCG
3	CTCCGAGCCCGTTCCCGGCCGTTACCAAGCTGCATGTGGACTCCG
4	GGGCTCTTAACGGACGGCACAAAGGTAACGGAGTCCACATGCAGC
5	GCCGTCCGTTAAGAGCCCGGCCTCCTCCAACCCGCTGTTCCTGGG
6	GATATCCAGGCCGCGAACACCGGCGCCGCCCAGGAACAGCGGGTT
7	GTTCGCGGCCTGGATATCCAAGGTAAATTCGTGATCTTCACCGTT
8	TACCCTCCAGGTACACGCCAATAACGGTGAAGATCACGAATTTAC
9	GCGTGTACCTGGAGGGTAACGCCGTTCCGTCTCTGTCTGTTAAGT
10	CTCCTCGGTAGTTTTGCCCTTCCACTTAACAGACAGAGACGGAAC
11	GGGCAAAACTACCGAGGAGCTGACCGAATCTATCCCGTTCTTCCG
12	TCAAACGCACCGGTAACGATTTCACGGAAGAACGGGATAGATTCG
13	CGTTACCGGTGCGTTTGAGAAGTTTATCAAGGTGACCATGAAACT
14	TATTGTTGGCCGGTCAGCGGCAGTTTCATGGTCACCTTGATAAAC
15	GCTGACCGGCCAACAATATTCTGAGAAAGTGACCGAGAACTGTGT
16	AGGCCCAGTTGTTTCCAGATAGCCACACAGTTCTCGGTCACTTTC
17	TCTGGAAACAACTGGGCCTGTATACCGACTGTGAAGCTAAAGCTG
18	TTGAAGATCTCCAGGAACTTCTCCACAGCTTTAGCTTCACAGTCG
19	GAGAAGTTCCTGGAGATCTTCAAGGAAGAAACCTTCCCGCCGGGT
20	GGTCGGGGACAGAGCGAACAGGATAGAGCTACCCGGCGGGAAGGT
21	CGCTCTGTCCCCGACCGGCTCTCTGACTGTTGCGTTCAGCAAAGA
22	GATGCCGGTTTCCGGGATAGAATCATCTTTGCTGAACGCAACAGT
23	TCCCGGAAACCGGCATCGCTGTGATCGAGAACAAACTGCTGGCGG
24	TGCCGATGATAGATTCCAGAACCGCCTCCGCCAGCAGTTTGTTCT
25	TTCTGGAATCTATCATCGGCAAGAACGGTGTGAGCCCGGGCACTC
26	CTGAGACAGGCGTTCTGCAACAGACAGGCGAGTGCCCGGGCTCAC
27	GCAGAACGCCTGTCTCAGCTGATGATGAAGAACAAGGACGAAAAG
28	CTCAACAGAGTGATCAGAAACTTCCTTTTCGTCCTTGTTCTTCATCA
29	GAAGTTTCTGATCACTCTGTTGAGGAAAAACTGGCCAAAGAGAACTA
30 (*Eco*RI-*chi*-R)	CATGGAATTCTTAGTTCTCTTTGGCCAGTTTTTC

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S10. DNA sequences of primers used for the synthesis of *sts* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Eco*RI-*sts*-F)	CATGGAATTCATGGTGTCTGTGTCTGGCATTCGC
2	TGCCGGACCTTCTGCGCGTTGAACCTTGCGAATGCCAGACACAGA
3	CGCAGAAGGTCCGGCAACCGTGCTGGCGATTGGCACCGCAAACCC
4	GTAGGTGCTCTGATCAACACAGTTCGGCGGGTTTGCGGTGCCAAT
5	TGTGTTGATCAGAGCACCTACGCAGATTACTATTTTCGCGTGACC
6	GGTCGGTCATGTGCTCGCTGTTGGTCACGCGAAAATAGTAATCTG
7	GCGAGCACATGACCGACCTGAAGAAGAAATTTCAGCGCATTTGTG
8	GCGGTTCTTGATCTGGGTGCGCTCACAAATGCGCTGAAATTTCTT
9	CACCCAGATCAAGAACCGCCATATGTATCTGACCGAAGAAATCCT
10	ACATGTTCGGGTTCTCCTTCAGGATTTCTTCGGTCAGATACATAT
11	GAAGGAGAACCCGAACATGTGCGCATACAAAGCACCGTCCCTGGA
12	CTCGCGGATCATCATGTCTTCGCGTGCATCCAGGGACGGTGCTTT
13	AAGACATGATGATCCGCGAGGTGCCGCGCGTTGGCAAAGAGGCTG
14	GACCCCATTCCTTGATTGCCTTAGTTGCAGCCTCTTTGCCAACGC
15	GGCAATCAAGGAATGGGGTCAGCCGATGTCTAAGATCACCCATCT
16	CACCGCTGGTGGTGCAGAAGATCAGATGGGTGATCTTAGACATCG
17	TGCACCACCAGCGGTGTTGCGCTGCCGGGCGTTGATTACGAACTG
18	CTCGGGTCCAGGCCCAGCAGCACGATCAGTTCGTAATCAACGCCC
19	GGGCCTGGACCCGAGCGTTAAGCGCTACATGATGTACCACCAAGG
20	GAACAGTGCCGCCAGCGAAGCAGCCTTGGTGGTACATCATGTAGC
21	GCTGGCGGCACTGTTCTGCGTCTGGCTAAGGACCTGGCTGAAAAC
22	CAATCAGCACACGAGCATCCTTGTTGTTTTCAGCCAGGTCCTTAG
23	GATGCTCGTGTGCTGATTGTTTGTTCTGAAAACACTAGCGTTACT
24	CGGTCTCAGACGGACCACGAAAAGTAACGCTAGTGTTTTCAGAAC
25	TGGTCCGTCTGAGACCGACATGGATTCTCTGGTGGGCCAGGCACT
26	ATGATAATTGCAGCAGCGCCGTCGGCGAACAGTGCCTGGCCCACC
27	GCGCTGCTGCAATTATCATTGGTTCTGATCCGGTTCCGGAGGTTG
28	GTGCTAACGATCTCGAACAGCGGGTTTTCAACCTCCGGAACCGGA
29	CTGTTCGAGATCGTTAGCACTGATCAACAACTGGTTCCGAACAGC
30	CGCAGCAGACCACCGATGGCGCCATGGCTGTTCGGAACCAGTTGT
31	TCGGTGGTCTGCTGCGTGAAGTTGGCCTGACCTTCTATCTGAACA
32	GGCTAATAATATCCGGAACAGACTTGTTCAGATAGAAGGTCAGGC
33	GTCTGTTCCGGATATTATTAGCCAAAACATCAACGATGCACTGTC
34	ATACCCAGCGGATCAAAAGCTTTAGACAGTGCATCGTTGATGTTT
35	GCTTTTGATCCGCTGGGTATCTCTGATTATAACAGCATCTTTTGG
36	CGACCACCCGGATGTGCAATCCAAAAGATGCTGTTATAATCAGAG
37	CACATCCGGGTGGTCGTGCAATCCTGGACCAAGTTGAAGAGAAGG
38	TCATCTTCTCCGGCTTCAGGTTCACCTTCTCTTCAACTTGGTCCA

39	CCTGAAGCCGGAGAAGATGAAAGCCACCCGCGATGTGCTGAGCAA
40	CACACACGCAGAGCTCATGTTACCATAGTTGCTCAGCACATCGCG
41	ATGAGCTCTGCGTGTGTGTTCTTCATTATGGATCTGATGCGCAAG
42	TTTCAGGCCTGCTTCCAGGCTCTTCTTGCGCATCAGATCCATAAT
43	CTGGAAGCAGGCCTGAAAACCACCGGCGAAGGCCTGGATTGGGGT
44	TCAGACCCGGACCAAAACCAAACAGCACACCCCAATCCAGGCCTT
45	GGTTTTGGTCCGGGTCTGACTATTGAAACTGTTGTTCTGCGCAGC
46 (*Afl*II-*sts*-R)	CATGCTTAAGTTAGATGGCCATGCTGCGCAGAACAACAGT

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S11. DNA sequences of primers used for the synthesis of *cus* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (EcoRI-*cus*-F)	CATGGAATTCATGGCACCGACCACCACCATGG
2	GCATTTCGCCCAGCGGGTACAGGGCGCTGCCCATGGTGGTGGTCGG
3	CCGCTGGGCGAAATGCGTCGTTCTCAGCGCGCCGACGGCCTGGCCG
4	CGGCGGGTTGGCGGTGCCGATGGCGAGCACGGCGGCCAGGCCGTCG
5	CCGCCAACCCGCCGAACTGCGTTACCCAGGAGGAGATCCCGGACTT
6	GTGGTCGCTGTTGGTAACGCGGAAGTAGAAGTCCGGGATCTCCTCC
7	CGTTACCAACAGCGACCACCTGACTGCCCTGAAGGACAAGTTCAAG
8	TGCACGCCCATTTCCTGACAGATACGCTTGAACTTGTCCTTCAGGG
9	CAGGAAATGGGCGTGCAGCGCCGTTACCTGCACCACACCGAGGAGA
10	GTCCACGAACTCCGGGTGTGCGGACAGCATCTCCTCGGTGTGGTGC
11	ACCCGGAGTTCGTGGACCGCGACGCGCCGTCTCTGGACGCGCGTCT
12	AGCTCCGGCACGGCGTCCGCGGCGATGTCCAGACGCGCGTCCAGAG
13	GCCGTGCCGGAGCTGGCGGCGGAGGCCGCCAAGAAAGCGATCGCCG
14	GTGATGTCGGCGGCCGGGCGGCCCCACTCGGCGATCGCTTTCTTGG
15	GGCCGCCGACATCACCCACCTGGTTGTTACCACCAACTCCGGCGCC
16	GAACCAGGCGGAAGTCAACACCCGGAACGTGGGCGCCGGAGTTGGT
17	GTTGACTTCCGCCTGGTTCCGCTGCTGGGCCTGCGCCCGTCCGTGC
18	GAAGCAGCCGTTCAGGTGCAGCATGGTGCGGCGCACGGACGGGCGC
19	CACCTGAACGGCTGCTTCGCCGGCTGCGCCGCGCTGCGCCTGGCCA
20	GCGCGCGCCGCGGCTGTTCTCGGCCAGGTCCTTGGCCAGGCGCAGC
21	CGCGGCGCGCGCGTTCTGGTTGTTGCCGCCGAGCTGACCCTGATGT
22	AAGCAGCCCTCGTCCGGGCCGGTGAAGTACATCAGGGTCAGCTCGG
23	CGGACGAGGGCTGCTTCCGCACCCTGCTGGTTCAGGGCCTGTTCGG
24	GCCAACAATAACGGCGGCCGCGCCGTCACCGAACAGGCCCTGAACC
25	GCCGCCGTTATTGTTGGCGCCGACGCCGACGACGTTGAGCGCCCGC
26	ATGGTCTGCGCCGCAGACACGATCTCGAACAGCGGGCGCTCAACGT
27	TGCGGCGCAGACCATCATCCCGGAGTCTGACCACGCCCTGAACATG
28	CACCGTCCAGGCGGCGCTCGGTGAAACGCATGTTCAGGGCGTGGTC
29	GCCGCCTGGACGGTGTTCTGGGCCGTCAGGTTCCGGGCCTGATCGG
30	ATGTCCAGCAGGCAACGCTCAACGTTGTCACCGATCAGGCCCGGAA
31	GCGTTGCCTGCTGGACATGTTCGGCCCGCTGCTGGGCGGCGACGGC
32	CACCGCCCAGAACAGGTCGTTCCAGCCGCCGCCGCCGTCGCCGCCC
33	ACCTGTTCTGGGCGGTGCACCCGGGCTCTTCTACCATCATGGACCA
34	CTCCAGGCCCAGCGCCGCGTCAACCTGGTCCATGATGGTAGAAGAG
35	GCGCTGGGCCTGGAGCCGGGCAAGCTGGCGGCGAGCCGCCGTGTGC
36	GTAGCGCCAGACATGTTGCCGTAGTCGCTCAGCACACGGCGGCTCG
37	GCAACATGTCTGGCGCTACCGTGATCTTCGCGCTGGACGAGCTGCG
38	CCCGCCGCCGCCGCCTCCTTGCGCTGACGGCGCAGCTCGTCCAGCG

39	GGCGGCGGCGGGTGAATGGCCGGAGCTGGGCGTGATGATGGCGTTC
40	GCATCGCATCAACGGTCATGCCCGGGCCGAACGCCATCATCACGCC
41	TGACCGTTGATGCGATGCTGCTGCACGCCACCTCTCATGTGAACTA
42 (AflII-*cus*-R)	CATGCTTAAGTTAGTTCACATGAGAGGTGGC

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S12. DNA sequences of primers used for the synthesis of *c4h* gene (codon-optimized based on synonymous codon bias of cyanobacteria)

Primer	Sequence (5' to 3')
1 (*Eco*RI-*c4h*-F)	CATGGAATTCATGGACCTGCTGCTGC
2	ACGAAAACAGCGATCAGAGATTTTTCCAGCAGCAGCAGGTCCATG
3	ATCTCTGATCGCTGTTTTCGTTGCTGTTATCCTGGCTACCGTTAT
4	GTTTTTTACCACGCAGTTTAGAGATAACGGTAGCCAGGATAACAG
5	CTCTAAACTGCGTGGTAAAAAACTGAAACTGCCGCCGGGTCCGAT
6	CTGCAGCCAGTTACCGAAGATCGGGATCGGGATCGGACCCGGCGG
7	CTTCGGTAACTGGCTGCAGGTTGGTGACGACCTGAACCACCGTAA
8	CGAATTTTTTAGCGTAGTCAACCAGGTTACGGTGGTTCAGGTCGT
9	GGTTGACTACGCTAAAAAATTCGGTGACCTGTTCCTGCTGCGTAT
10	AAACAACAACCAGGTTACGCTGACCCATACGCAGCAGGAACAGGT
11	GCGTAACCTGGTTGTTGTTTCTTCTCCGGACCTGACCAAAGAAGT
12	CAAATTCAACACCCTGGGTGTGCAGAACTTCTTTGGTCAGGTCCG
13	CACCCAGGGTGTTGAATTTGGTTCTCGTACCCGTAACGTTGTTTT
14	TGACCTTTACCGGTGAAGATGTCGAAAACAACGTTACGGGTACGA
15	CATCTTCACCGGTAAAGGTCAGGATATGGTTTTTACCGTCTACGG
16	ACGCATTTTACGCCAGTGTTCGCCGTAGACGGTAAAAACCATATC
17	ACACTGGCGTAAAATGCGTCGTATCATGACCGTTCCGTTCTTCAC
18	ACGGTTCTGCTGAACAACTTTGTTGGTGAAGAACGGAACGGTCAT
19	AAAGTTGTTCAGCAGAACCGTGAAGGTTGGGAATTTGAAGCTGCT
20	TTTTTTTAACGTCTTCAACAACAGAAGCAGCTTCAAATTCCCAAC
21	TCTGTTGTTGAAGACGTTAAAAAAAACCCGGACTCTGCTACCAAA
22	TGCAGACGTTTACGCAGAACGATACCTTTGGTAGCAGAGTCCGGG
23	TTCTGCGTAAACGTCTGCAGCTGATGATGTACAACAACATGTTCC
24	AACGACGGTCGAACATGATACGGAACATGTTGTTGTACATCATCA
25	GTATCATGTTCGACCGTCGTTTCGAATCTGAAGACTCTCCGCTGT
26	CCGTTCAGAGCTTTCAGACGCAGGAACAGCGGAGAGTCTTCAGAT
27	CGTCTGAAAGCTCTGAACGGTGAACGTTCTCGTCTGGCGCAGAGC
28	GGGATGAAGTCACCGTAGTTGTATTCGAAGCTCTGCGCCAGACGA
29	CAACTACGGTGACTTCATCCCGATCCTGCGTCCGTTCCTGCGTGG
30	CTTTAACGTCCTGGCAGATTTTCAGGTAACCACGCAGGAACGGAC
31	AAAATCTGCCAGGACGTTAAAGACCGTCGTATCGCTCTGTTCAAA
32	TTTACGTTCGTCAACGAAGTATTTTTTGAACAGAGCGATACGACG
33	AAATACTTCGTTGACGAACGTAAACAGATCGCTTCTTCTAAACCG
34	GCATTTCAGACCTTCAGAACCGGTCGGTTTAGAAGAAGCGATCTG
35	GGTTCTGAAGGTCTGAAATGCGCTATCGACCACATCCTGGAAGCT
36	TCTTCGTTGATTTCACCTTTCTGTTCAGCTTCCAGGATGTGGTCG
37	CAGAAAGGTGAAATCAACGAAGACAACGTTCTGTACATCGTTGAA

38	TCGATAGCAGCAACGTTGATGTTTTCAACGATGTACAGAACGTTG
39	ATCAACGTTGCTGCTATCGAAACCACCCTGTGGTCTATCGAATGG
40	GGTGGTTAACCAGTTCAGCGATACCCCATTCGATAGACCACAGGG
41	CGCTGAACTGGTTAACCACCCGGAAATCCAGTCTAAACTGCGTAA
42	ACCCAGAACGGTGTCCAGTTCGTTACGCAGTTTAGACTGGATTTC
43	CTGGACACCGTTCTGGGTCCGGGTGTTCAGGTTACCGAACCGGAC
44	GCCTGCAGGTACGGCAGTTTGTGCAGGTCCGGTTCGGTAACCTGA
45	TGCCGTACCTGCAGGCTGTTGTTAAAGAAACCCTGCGTCTGCGTA
46	ATGTGCGGAACCAGCAGCGGGATAGCCATACGCAGACGCAGGGTT
47	GCTGCTGGTTCCGCACATGAACCTGCACGACGCTAAACTGGCTGG
48	ATTTTAGATTCAGCCGGGATGTCGTAACCAGCCAGTTTAGCGTCG
49	ACATCCCGGCTGAATCTAAAATCCTGGTTAACGCTTGGTGGCTGG
50	GTTTTTTCCAAGAGTTCGGGTTGTTAGCCAGCCACCAAGCGTTAA
51	ACCCGAACTCTTGGAAAAAACCGGAAGAATTTCGTCCGGAACGCT
52	TTCAACGTGAGACTCTTCTTCGAAGAAGCGTTCCGGACGAAATTC
53	CGAAGAAGAGTCTCACGTTGAAGCTAACGGTAACGACTTCCGTTA
54	CGACGACCAACACCGAACGGAACGTAACGGAAGTCGTTACCGTTA
55	GTTCGGTGTTGGTCGTCGTTCTTGCCCGGGTATCATCCTGGCTCT
56	GACCGATGGTGATACCCAGGATCGGCAGAGCCAGGATGATACCCG
57	CTGGGTATCACCATCGGTCGTATGGTTCAGAACTTCGAACTGCTG
58	AACTTTAGACTGACCCGGCGGCGGCAGCAGTTCGAAGTTCTGAAC
59	AACTTTAGACTGACCCGGCGGCGGCAGCAGTTCGAAGTTCTGAAC
60	AGTGGTTCAGGATGTGCAGAGAGAACTGACCACCTTTTTCAGAGG
61	CTGCACATCCTGAACCACTCTATCATCGTTATGAAACCGCGTAAC
62 (*Bgl*II-*c4h*-R)	CATGAGATCTTTAGCAGTTACGCGGTTTCATAACGAT

Underlining indicates restriction enzyme cleavage sites corresponding to the primer description.

Table S13. DNA sequences of primers used for RT-PCR analysis

Primer	Sequence (5' to 3')
aroG^{fbr}-F	ACTGGCATCAGGGCTTTCTTGT
aroG^{fbr}-R	GGACGAGTTAGCATGGCTGAAAT
tal-F	GATTGCACGTCTGACAGATGAAAG
tal-R	GCAGCTTGTGCAAGACAGAGAG
sam8-F	AAGTCCGACAAGCCCATCTACG
sam8-R	GCTCGCGCTGACCGTGC
q-*tal*-F[a]	GTCTACGGACTGACAACC
q-*tal*-R[a]	CAGATGATGGACAAGATTGG
q-*sam8*-F[a]	GAGTACCTGAAGTCCGACAAG
q-*sam8*-R[a]	CTGCTCCAGCTCCGAGTC
q-*rnpB*-F[a]	AGCAAGGTGGAGGGACAAC
q-*rnpB*-R[a]	CGAAGACAGAGGGCAGTTATC
sam5-F	AGAGGTCTACATCTACGGCGAGC
sam5-R	ACGCCGCCTTGTAGTCCG
ref8-F	GCTGACCGTCACCGTAACCG
ref8-R	GAAAGCCAGACGGGTGATGTTG
comt-F	CTAAAAACGGTTCTCCGATGTCTC
comt-R	CGTCCAGGATAGCGTCTTTCAG
sts-F	ATCAGAGCACCTACGCAGATTACTA
sts-R	GGTGATCTTAGACATCGGCTGAC
4cl-F	CCGCTGCATACCTATTGTTTTGAGA
4cl-R	CGCTTGGCTCGCTTTCAGTTGCTTG
chs-F	TCAGCAAAAACATTGAGAAGAGCCT
chs-R	AAGCCAAACAGAACACCCCAC
cus-F	CCGAGCTGACCCTGATGTACTT
cus-R	CAGCGGGCCGAACATGTC
chi-F	GGAAGGGCAAAACTACCGAGG
chi-R	CAACAGTCAGAGAGCCGGTCG
c4h-F	GCGAACACTGGCGTAAAATG
c4h-R	GTCACCGTAGTTGTATTCGAAGC

[a] The DNAs are used for quantitative RT-PCR.