ONLINE RESOURCES

Genetic and genomic analysis of RNases in model cyanobacteria

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Online Resource 1 Plasmids used in this study

Plasmid ID	Description/Purpose	Resistance marker	Reference
pJCC248	pUC19-Δ*A0788*:Km^R	Amp/Km	This work
pJCC249	pUC19-Δ*A0061*:Sp^R	Amp/Sp	This work
pJCC250	pUC19-Δ*A2542*:Km^R	Amp/Km	This work
pJCC251	pUC19-Δ*A0384*:Gm^R	Amp/Gm	This work
pJCC252	pUC19-Δ*A1273*:Km^R	Amp/Km	This work
pJCC253	pUC19-Δ*A0574*:Sp^R	Amp/Sp	This work
pJCC254	pUC19-Δ*A1543*:Sp^R	Amp/Sp	This work
pJCC255	pUC19-Δ*A1066*:Gm^R	Amp/Gm	This work
pJCC256	pUC19-Δ*glpK*:Amp^R-*A0061*	Amp	This work
pJCC257	pUC19-Δ*glpK*:Km^R-*A1543*	Km	This work
pUC19	Cloning vector	Amp	Invitrogen
pSRA81	Source of Sp^R	Sp	(Frigaard et al. 2004)
pBBR1MCS5	Source of Gm^R	Gm	(Kovach et al. 1995)
pET28b(+)	Source of Km^R	Km	Novagen

Frigaard NU, Maresca JA, Yunker CE, Jones AD, Bryant DA (2004) Genetic manipulation of carotenoid biosynthesis in the green sulfur bacterium *Chlorobium tepidum*. *J* Bacteriol 186 (16):5210-5220

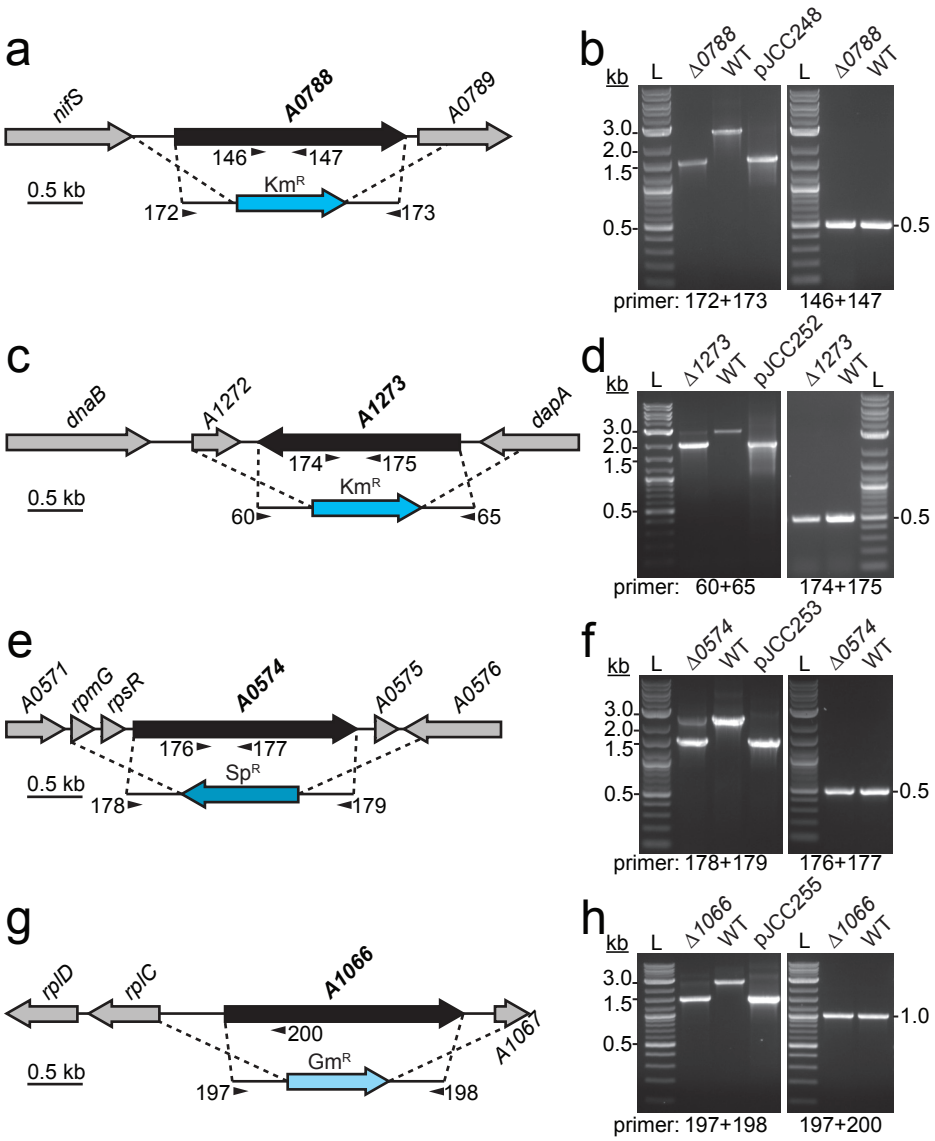
Kovach ME, Elzer PH, Hill DS, Robertson GT, Farris MA, Roop RM, 2nd, Peterson KM (1995) Four new derivatives of the broad-host-range cloning vector pBBR1MCS, carrying different antibiotic-resistance cassettes. Gene 166 (1):175-176

Online Resource 2 Oligonucleotides used in this study for generation of plasmids and segregation analysis

Oligo ID	Sequence (5'-3')	Description	Purpose	Reference
Δ*A0788* strain				
JC128	gctcggtacccggggatcctCGATATCGATCACGTCGC	*A0788*_upstream_F	KO/Segregation	This work
JC129	tgagcgtcagTCAAATTCCTCGATTTTTTTC	*A0788*_upstream_R	KO	This work
JC130	aggaatttgaCTGACGCTCAGTGGAACG	KmR_F	KO	This work
JC131	taattgggttTTCAGGTGGCACTTTTCG	KmR_R	KO	This work
JC132	gccacctgaaAACCCAATTACCGTTAACCTAAGG	*A0788*_downstream_F	KO	This work
JC133	tgcatgcctgcaggtcgactCGGACTTCAGCGACGGTG	*A0788*_downstream_R	KO/Segregation	This work
JC146	ACATGGATTCTCGCCATGAT	*A0788*_gene_specific_F	Segregation	This work
JC147	CGGCTTACTCGAAACCTCTG	*A0788*_gene_specific_R	Segregation	This work
JC172	TCATCTCACCCAGCCATACA	*A0788*_flanking_F	Segregation	This work
JC173	GGGCTTGTAAAACGACTTGC	*A0788*_flanking_R	Segregation	This work
Δ*A0061* strain				
JC42	gctcggtacccggggatcctTCTTTGCCCCATAAGCAG	*A0061*_upstream_F	KO/Segregation	This work
JC43	aattcactggAAAAGCGCCCGGAGATCT	*A0061*_upstream_R	KO	This work
JC44	gggcgcttttCCAGTGAATTCGAGCTCGG	SpR_F	KO	This work
JC45	tagtatttccCAAGCTTGCATGCCTGCA	SpR_R	KO	This work
JC46	tgcaagcttgGGAAATACTAAGATAGCAAAAGTAGGGAACTTTGC	*A0061*_downstream_F	KO	This work
JC47	tgcatgcctgcaggtcgactGCAGCGGCGATCCACGTC	*A0061*_downstream_R	KO/Segregation	This work
JC140	TCCCCCGACAAAAATTATGA	*A0061*_gene_specific_F	Segregation	This work
JC141	AGCAAAGTATCCCCCAGCTT	*A0061*_gene_specific_R	Segregation	This work
Δ*A2542* strain				
JC48	gctcggtacccggggatcctATGATCACGCGGATATATTG	*A2542*_upstream_F	KO/Segregation	This work
JC49	agaccccgtaGGTTAAGCGAAACTTTATAATG	*A2542*_upstream_R	KO	This work
JC50	tcgcttaaccTACGGGGTCTGACGCTCA	KmR_F	KO	This work
JC51	tctcgcccaaGATTTTGCCGATTTCGGC	KmR_R	KO	This work
JC52	cggcaaaatcTTGGGCGAGAAAATGGCT	*A2542*_downstream_F	KO	This work
JC53	tgcatgcctgcaggtcgactAAAGGCAATCTCGTTATCAAAAG	*A2542*_downstream_R	KO/Segregation	This work
JC142	GCGATCGCCTCTTCTGTTAC	*A2542*_gene_specific_F	Segregation	This work
JC143	GAATTTCACCGTGGTTTGCT	*A2542*_gene_specific_R	Segregation	This work
Δ*A0384* strain				
JC134	gctcggtacccggggatcctCAGCAAAAAATCTGTAGTTTG	*A0384*_upstream_F	KO/Segregation	This work
JC135	tatgcatgcgTGGTTTTCTCGTCCCTAT	*A0384*_upstream_R	KO	This work
JC136	gagaaaaccaCGCATGCATAAAAACTGTTG	GmR_F	KO	This work
JC137	gtcgatcataTTAGGTGGCGGTACTTGG	GmR_R	KO	This work
JC138	cgccacctaaTATGATCGACTCTCTTTTGTGTTTC	*A0384*_downstream_F	KO	This work
JC139	tgcatgcctgcaggtcgactTGGGGCGTCTTTTATTCG	*A0384*_downstream_R	KO/Segregation	This work
JC144	GTCCCTGACATTACCGCTGA	*A0384*_gene_specific_F	Segregation	This work
JC145	CAGACCGTTCTTGGGGTAAA	*A0384*_gene_specific_R	Segregation	This work
Δ*A1273* strain				
JC60	gctcggtacccggggatcctGCGCTGGCCCATTAACAG	*A1273*_upstream_F	KO/Segregation	This work
JC61	tgagcgtcagTGTAGGAAAAGGATTTGGGATC	*A1273*_upstream_R	KO	This work
JC62	ttttcctacaCTGACGCTCAGTGGAACG	KmR_F	KO	This work
JC63	aaggagttttTTCAGGTGGCACTTTTCG	KmR_R	KO	This work
JC64	gccacctgaaAAAACTCCTTAGATTTGCTTG	*A1273*_downstream_F	KO	This work
JC65	tgcatgcctgcaggtcgactGATGATAGTCTAACTCTACCTTTGATG	*A1273*_downstream_R	KO/Segregation	This work
JC174	CGCATCATCAGACGATCAAT	*A1273*_gene_specific_F	Segregation	This work
JC175	GGCGAAAAAGGTGTTCTCTG	*A1273*_gene_specific_R	Segregation	This work
Δ*A0574* strain				
JC148	gctcggtacccggggatcctCCGAATGTCGCACCAATA	*A0574*_upstream_F	KO	This work
JC149	aattcactggCAGCTTTGTTGCCTAACG	*A0574*_upstream_R	KO	This work
JC150	aacaaagctgCCAGTGAATTCGAGCTCGG	SpR_F	KO	This work
JC151	gcttttgatcCAAGCTTGCATGCCTGCA	SpR_F	KO	This work
JC152	tgcaagcttgGATCAAAAGCCGACAAAAC	*A0574*_downstream_F	KO	This work
JC153	tgcatgcctgcaggtcgactCGGAGCTAACCACCGATG	*A0574*_downstream_R	KO	This work
JC176	TCAAACGCAAAGGGGATTAC	*A0574*_gene_specific_F	Segregation	This work
JC177	ACTGAGGCCATCGTCAATTT	*A0574*_gene_specific_R	Segregation	This work
JC178	TGTTGCCCTTCATCAACAAA	*A0574*_flanking_F	Segregation	This work
JC179	TCCAAGTGGAGTTGGGATTC	*A0574*_flanking_R	Segregation	This work
Δ*A1543* strain				
JC188	gctcggtacccggggatcctCCATTGATCCAGGCGAAT	*A1543*_upstream_F	KO	This work
JC189	aattcactggTCACCCGTCTATGACTCAG	*A1543*_upstream_R	KO	This work
JC190	agacgggtgaCCAGTGAATTCGAGCTCGG	SpR_F	KO	This work
JC191	atagttttgcCAAGCTTGCATGCCTGCA	SpR_R	KO	This work
JC192	tgcaagcttgGCAAAACTATCCTTTTCGTTAGAAAGTAAAGTGAAACGACAAC	*A1543*_downstream_F	KO	This work
JC193	tgcatgcctgcaggtcgactGTGGGGCGATCGCCGGGG	*A1543*_downstream_R	KO	This work
JC180	CGCGATATTCGTACCAGTCA	*A1543*_gene_specific_F	Segregation	This work
JC181	TCAGGAAACCCTCGATGTTC	*A1543*_gene_specific_R	Segregation	This work
JC182	AAAAAGAGGGAAGCATGCAA	*A1543*_flanking_F	Segregation	This work
JC183	TATGCTGGGTTTGCTTAGCC	*A1543*_flanking_R	Segregation	This work
Δ*A1066* strain				
JC160	gctcggtacccggggatcctGAAAGAGTTGTGGTTCTTGTC	*A1066*_upstream_F	KO	This work

JC161	atgcatgcgcTATTGCGTGTTGTCCTTTTG	*A1066*_upstream_F	KO	This work
JC162	acacgcaataGCGCATGCATAAAAACTGTTGTAATTC	GmR_F	KO	This work
JC163	atgttttatatttAAACAGGCCCAGCGCCAG	GmR_R	KO	This work
JC164	gggcctgtttAAATATAAAACATCACTATTTTTCGGTG	*A1066*_downstream_F	KO	This work
JC165	tgcatgcctgcaggtcgactGTCAATGATGGCCGCTGA	*A1066*_downstream_R	KO	This work
JC200	TTCGGCTCTTCTGTGGTTTT	*A1066*_gene_specific_R	Segregation	This work
JC197	TTGGGAGTTCAAGGAACCAG	*A1066*_flanking_F	Segregation	This work
JC198	CGTTGAAAAGGGGTTTGAGA	*A1066*_flanking_R	Segregation	This work
Complementation Analysis				
JCC207	agctcggtacccgggTGAAGCGATTGGCTATGATC	*glpK*_upstream_F	for pUC19-Δ*glpK*_NS	This work
JCC208	ggggatccTTTTTTAAATGGGTTAAATTAGGTC	*glpK*_upstream_BamHI_R	for pUC19-Δ*glpK*_NS	This work
JCC209	ccatttaaaaaaggatccCCCCCTCTTGCCTACAGC	*glpK*_downstream_BamHI_F	for pUC19-Δ*glpK*_NS	This work
JCC210	caggtcgactctagagGAAACGAGATTATCTAAAACAGAAGC	*glpK*_upstream_R	for pUC19-Δ*glpK*_NS	This work
JCC263	atttaacccatttaaaaaagctcgagTACGGGGTCTGACGCTCA	KmR_F	for pUC19-Δ*glpK*:KmR_NS	This work
JCC264	taggcaagagggggggatccGATTTTGCCGATTTCGGC	KmR_F	for pUC19-Δ*glpK*:KmR_NS	This work
JCC368	atttaacccatttaaaaaaggatatcGGAAATGTGCGCGGAACC	AmpR_F	for pUC19-Δ*glpK*:AmpR_NS	This work
JCC369	taggcaagagggggggatccACGCTCAGTGGAACGAAAAC	AmpR_R	for pUC19-Δ*glpK*:AmpR_NS	This work
JCC374	aacccatttaaaaaaggatatcATGGAACCCTAAATCTGG	*A0061*_terminator_region_F	Complementation	This work
JCC375	cgcgcacatttccgatatcTTATAGAGAGTAGACGAAAATCAC	*A0061*_Promoter_region_R	Complementation	This work
JCC282	ttaacccatttaaaaaagctcgaGAACGCAATAGGAAAAGTTTAACTCAATTTATTAGTTGAG	*A1543*_promoter_region_F	Complementation	This work
JCC283	cgtcagaccccgtacCCTAGGCCACCGGGGGCC	*A1543*_terminator_region_R	Complementation	This work
JCC397	TCTCGATCCTGCAAGGGG	*glpK*_flanking_F	Segregation of Δ*glpK*	This work
JCC398	AGGCTTCATGATCAAGGGAA	*glpK*_flanking_R	Segregation of Δ*glpK*	This work
JCC399	CACCGCTGGGGCTTGTACC	*glpK*_gene_specific_R	Segregation of Δ*glpK*	This work

Uppercase nucleotides are gene-specific; lowercase indicate homologous flanking regions for Gibson assembly reaction. KO, generation of knock out mutant. NS, neutral site.



Online Resource 3 Segregation analysis of ribonucleases in PCC7002

Targeted gene deletion via homologous recombination was used to replace the entire ORF of *A0788*, *A1273*, *A0574*, and *A1066* with an antibiotic resistance cassette (**a**, **c**, **e**, and **g**). Insertion of the cassette into each of these genes was confirmed by PCR using primer pairs flanking the insert (Left gel panel in **b**, **d**, **f**, and **h**). WT genomic DNA was used as the negative control and the plasmid (pJCC#) used to generate the strain was used as a positive size control. PCR using primers that amplify the WT gene (Right gel panel in **b**, **d**, **f**, and **h**) indicates that these strains are heterozygous at the locus of interest. Arrows and numbers below antibiotic resistance cassette and gene in **a**, **c**, **e**, and **g** indicate approximate regions of flanking and gene specific primers respectively. For the gene specific reaction shown in **g** and **h**, a flanking primer and gene specific primer combination was used to amplify a 1 kb band that should not be present in a fully segregated mutant. Plasmids used as the positive control are listed in Online Resource 1. All primers used in segregation analysis are listed in Online Resource 2.

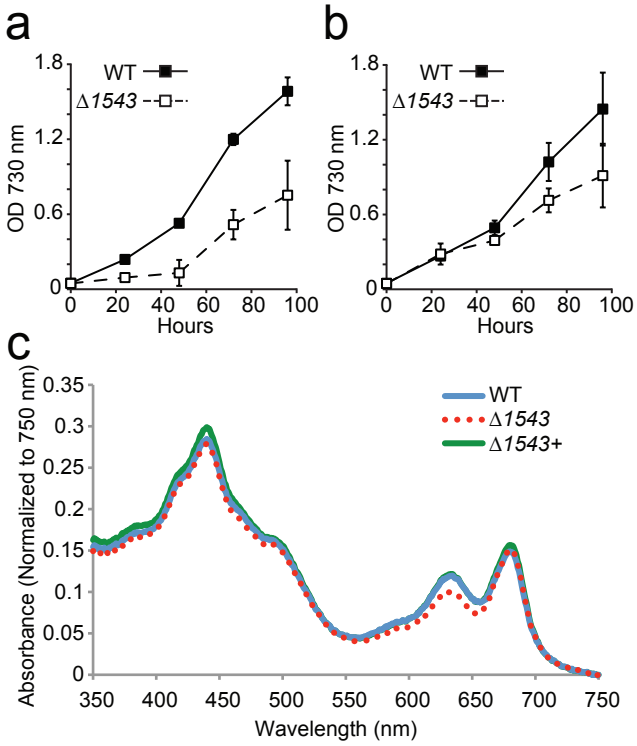
Online Resource 4 Analysis of RNase III-like proteins in diverse cyanobacterial genomes

Genome	Subsection[a]	#RNase III, #MiniIII	RNase III Locus Tag	Mini-III Locus Tag	AA Seq Length	RNase III Signature Motif	Mini-III Signature Motif	# RNase III domains	dsRBD Present	Other Domains
Acaryochloris marina MBIC11017	1	1,1	*AM1_1717*		247	EQLEFVGDS		1	Y	
				AM1_5197	143		AALAYIGDA	1	N	
Anabaena cylindrica PCC 7122	4	3,1	*Anacy_4655*		228	ERLEFLGDA		1	Y	
			Anacy_0811		240	EQLEFVGDA		1	Y	
			Anacy_3962		395	EQLEFLGDC		1	Y	
				Anacy_3641	160		SALAYLGDS	1	N	
Anabaena sp. PCC 7108	4	2,1	*Ana7108_1646*		230	ERLEFLGDA		1	Y	
			Ana7108_0695		245	EQLEFVGDA		1	Y	
				Ana7108_2529	193		SALAYLGDA	1	N	
Anabaena sp. PCC 7120	4	2,1	*all4107*		202	EQLEFVGDA		1	Y	
			alr0280		228	ERLEFLGDA		1	Y	
				alr1158	161		AALAYVGDA	1	N	
Anabaena variabilis ATCC 29413	4	2,1	*Ava_3081*		228	ERLEFLGDA		1	Y	
			Ava_0797		242	EQLEFVGDA		1	Y	
				Ava_4412	161		AALAYVGDA	1	N	
Arthrospira platensis NIES-39	3	2,0	*NIES39_Q02990*		246	EQLEFVGDS		1	Y	
			NIES39_N00330		395	ELLEFLGDS		1	Y	
Calothrix sp. PCC 6303	4	2,1	*Cal6303_1320*		228	ERLEFLGDA		1	Y	
			Cal6303_1680		239	EQLEFVGDA		1	Y	
				Cal6303_1532	160		KSLAYLGDA	1	N	
Calothrix sp. PCC 7103	4	2,1	*Cal7103DRAFT_00026520*		240	EQLEFVGDA		1	Y	
			Cal7103DRAFT_00079520		248	ERLEFLGDA		1	Y	
				Cal7103DRAFT_00060540	164		TALAYLGDA	1	N	
Calothrix sp. PCC 7507	4	2,1	*Cal7507_4153*		227	ERLEFLGDA		1	Y	
			Cal7507_3430		237	EQLEFVGDA		1	Y	
				Cal7507_1114	159		TALAYMGDA	1	N	
Chroococcidiopsis sp. PCC 6712	2	2,1	*Chr6712_2695*		238	ERLEFLGDA		1	Y	
			Chr6712_3177		244	EQLEFVGDA		1	Y	
				Chr6712_4648	152		VALAYIGDA	1	N	
Chroococcidiopsis thermalis PCC 7203	2	2,1	*Chro_4112*		237	EQLEFVGDA		1	Y	
			Chro_5889		493	EWLALLGDT		2	N	Gun4-like
				Chro_4036	169		MALAYLGDA	1	N	
Crocosphaera watsonii WH 8501	1	2,1	*CWat_WH8501_draft2_00045690*		238	QQLEFVGDS		1	Y	
			CWat_WH8501_draft2_00017180		328	QRLESLGEN		1	N	
				CWat_WH8501_draft2_00007740	137		AFLAYIGDA	1	N	
Cyanobacterium PCC 7702	5	2,1	*Chl7702DRAFT_0536*		225	ERLEFLGDA		1	Y	
			Chl7702DRAFT_2265		244	EHLEFVGDA		1	Y	
				Chl7702DRAFT_2383	160		TTLAYLGDA	1	N	
Cyanobacterium sp. UCYN-A	1	1,1	*UCYN_03680*		243	QQLEFVGDS		1	Y	
				UCYN_00750	137		AFLAYIGDA	1	N	
Cyanothece sp. BH68, ATCC 51142	1	1,1	*cce_3135*		242	QQLEFVGDS		1	Y	
				cce_1800	137		AFLAYIGDA	1	N	
Cyanothece sp. PCC 7424	1	2,1	*PCC7424_3959*		228	ERLEFLGDA		1	Y	
			PCC7424_2664		235	QQLEFVGDA		1	Y	
				PCC7424_3194	154		ASLAYIGDA	1	N	
Cyanothece sp. PCC 7425	1	1,1	*Cyan7425_0389*		238	EQLEFFGDA		1	Y	
				Cyan7425_1940	153		AALAYLGDA	1	N	
Cyanothece sp. PCC 7822	1	2,1	*Cyan7822_0327*		228	ERLEFLGDA		1	Y	
			Cyan7822_1001		235	QQLEFVGDA		1	Y	
				Cyan7822_0774	131		ASLAYIGDA	1	N	
Cyanothece sp. PCC 8801	1	3,1	*PCC8801_3303*		225	ERLEFLGDA		1	Y	
			PCC8801_2820		236	QQLEFLGDS		1	Y	
			PCC8801_0645		323	ERLEYLGET		1	N	
				PCC8801_2425	158		AFLAYLGDA	1	N	
Dactylococcopsis salina PCC 8305	1	2,1	*Dacsa_1083*		237	ERLEFLGDA		1	Y	
			Dacsa_3634		264	QQLEFVGDA		1	Y	
				Dacsa_2494	150		AALAYIGDA	1	N	
Fischerella sp. PCC 9339	5	2,1	*PCC9339DRAFT_01064*		224	ERLEFLGDA		1	Y	
			PCC9339DRAFT_03154		239	EHLEFVGDA		1	Y	
				PCC9339DRAFT_04090	160		VALAYLGDA	1	N	
Fischerella sp. PCC 9431	5	2,1	*Fis9431DRAFT_3759*		239	EHLEFVGDA		1	Y	
			Fis9431DRAFT_1534		242	ERLEFLGDA		1	Y	
				Fis9431DRAFT_4808	160		VALAYLGDA	1	N	
Fischerella sp. PCC 9605	5	2,1	*FIS9605DRAFT_02642*		232	ERLEFLGDA		1	Y	
			FIS9605DRAFT_04201		243	EHLEFVGDA		1	Y	
				FIS9605DRAFT_03180	159		TALAYLGDA	1	N	
Geitlerinema sp. PCC 7105	3	2,0	*Gei7105DRAFT_1223*		247	EQLEFIGDA		1	Y	
			Gei7105DRAFT_5151		366	ERLEFLGDS		1	Y	NYN
Geitlerinema sp. PCC 7407	3	2,1	*GEI7407_1007*		231	ERLEFLGDA		1	Y	
			GEI7407_0526		246	EQLEFMGDA		1	Y	
				GEI7407_3792	167		VALAYLGDA	1	N	
Gloeobacter violaceus PCC 7421	1	1,1	*gvip371*		242	DRLEFLGDE		1	Y	
				glr4180	106			1	N	
Leptolyngbya boryana PCC 6306	3	1,1	*LepboDRAFT_1185*		238	EQLEFVGDA		1	Y	
				LepboDRAFT_4252	139		AAFAYLGDA	1	N	
Leptolyngbya sp. PCC 6406	3	3,1	*LEP6406DRAFT_2207*		133	ERLEFIGDG		1	N	
			LEP6406DRAFT_1871		224	ERLEFLGDA		1	Y	
			LEP6406DRAFT_1169		254	EQLEFLGDA		1	Y	
				LEP6406DRAFT_3537	166		QALAYIGDA	1	N	
Leptolyngbya sp. PCC 7375	3	3,1	*Lepto7375DRAFT_7811*		153	EIFRTLGDA		1	N	
			Lepto7375DRAFT_5336		223	ERLEFLGDA		1	Y	
			Lepto7375DRAFT_3393		256	EVLEFLGDA		1	Y	
				Lepto7375DRAFT_2718	154		IALAYIGDA	1	N	
Leptolyngbya sp. PCC 7376	3	2,1	*Lepto7376_1012*		241	EVLEFLGDA		1	Y	
			Lepto7376_0760		258	ERLEFLGDA		1	Y	
				Lepto7376_3431	129		TALAYVGDA	1	N	
Mastigocladopsis repens PCC 10914	5	2,1	*Mas10914DRAFT_2231*		239	EHLEFVGDA		1	Y	
			Mas10914DRAFT_2728		388	ERLEFLGDA		1	Y	
				Mas10914DRAFT_3118	160		TALAYLGDA	1	N	
Microcoleus vaginatus FGP-2	3	3,1	*MicvaDRAFT_0740*		235	EQLEFVGDA		1	Y	
			MicvaDRAFT_1301		237	RLEFLGDA		1	Y	
			MicvaDRAFT_0189		588	KRLSLLGGA		1	N	
				MicvaDRAFT_1151	148		AAWAYLGDA	1	N	
Microcystis aeruginosa NIES-843	1	2,1	*MAE_31570*		226	ERLEFLGDA		1	Y	

			MAE_60800	234	EQLEFVGDS		1	Y
				MAE_28410	138	ASLAYLGDA	1	N
Nostoc azollae 0708	4	2,1	*Aazo_4580*	227	ERLEFLGDA		1	Y
			Aazo_3201	237	EQLEFVGDA		1	Y
				Aazo_2284	159	SALAYLGDA	1	N
Nostoc punctiforme PCC 73102	4	2,1	*Npun_R1331*	228	ERLEFLGDA		1	Y
			Npun_F1233	239	EQLEFVGDA		1	Y
				Npun_R1191	159	TALAYLGDA	1	N
Nostoc sp. PCC 7107	4	3,1	*Nos7107_4879*	227	ERLEFLGDA		1	Y
			Nos7107_2456	234	EVLEFFGDS		1	Y
			Nos7107_0948	239	EQLEFVGDA		1	Y
				Nos7107_3662	160	AALAYIGDA	1	N
Nostoc sp. PCC 7524	4	3,1	*Nos7524_1070*	228	ERLEFLGDA		1	Y
			Nos7524_4545	234	EVLEFFGDS		1	Y
			Nos7524_1546	238	EQLEFVGDA		1	Y
				Nos7524_3113	159	AALAYVGDA	1	N
Oscillatoria nigro-viridis PCC 7112	3	3,1	*Osc7112_2758*	230	ERLEFLGDA		1	Y
			Osc7112_3480	234	EQLEFVGDA		1	Y
			Osc7112_2759	400	QLLEFLGDA		1	Y
				Osc7112_2944	148	AAWAYLGDA	1	N
Pleurocapsa sp. PCC 7319	2	3,1	*Pleur7313DRAFT_05633*	240	ERLEFLGDA		1	Y
			Pleur7313DRAFT_00733	246	EQLEFVGDS		1	Y
			Pleur7313DRAFT_05876	319	QRLEFLGKA		1	N
				Pleur7313DRAFT_05600	158	IALAYIGDA	1	N
Pleurocapsa sp. PCC 7327	2	2,1	*Ple7327_4215*	228	ERLEFLGDS		1	Y
			Ple7327_0296	244	QQLEFVGDA		1	Y
				Ple7327_2958	152	IALAYIGDA	1	N
Prochlorococcus marinus AS9601	1	1,1	*A9601_18131*	249	EKLEFFGDA		1	Y
				A9601_09111	132	IQLAWLGDS	1	N
Prochlorococcus marinus marinus CCMP 1375	1	1,1	*Pro1762*	249	ERLEFQGDA		1	Y
				Pro0747	137	LQLAWLGDA	1	N
Prochlorococcus marinus MIT 9211	1	1,1	*P9211_17271*	249	ERLEFLGDA		1	Y
				P9211_06951	144	LQLAWLGDA	1	N
Prochlorococcus marinus MIT 9215	1	1,1	*P9215_18771*	249	EKLEFFGDA		1	Y
				P9215_09411	132	IQLAWLGDS	1	N
Prochlorococcus marinus MIT 9301	1	1,1	*P9301_17961*	249	EKLEFFGDA		1	Y
				P9301_09091	132	IQLAWLGDS	1	N
Prochlorococcus marinus MIT 9303	1	1,1	*P9303_26001*	262	ERLEFLGDA		1	Y
				P9303_15791	135	LQLAWLGDA	1	N
Prochlorococcus marinus MIT 9312	1	1,1	*PMT9312_1696*	249	EKLEFFGDA		1	Y
				PMT9312_0850	132	IQLAWLGDS	1	N
Prochlorococcus marinus MIT 9313	1	1,1	*PMT1949*	281	ERLEFLGDA		1	Y
				PMT0651	132	LQLAWLGDA	1	N
Prochlorococcus marinus MIT 9515	1	1,1	*P9515_1791*	249	EKLEFFGDA		1	Y
				P9515_10321	130	IQLAWLGDS	1	N
Prochlorococcus marinus NATL1A	1	1,1	*NATL1_20541*	247	ENLEFLGDA		1	Y
				NATL1_09301	132	LQLAWLGDA	1	N
Prochlorococcus marinus NATL2A	1	1,1	*PMN2A_1179*	247	ENLEFLGDA		1	Y
				PMN2A_0261	132	LQLAWLGDA	1	N
Prochlorococcus marinus pastoris CCMP 1986	1	1,1	*PMM1603*	249	EKLEFFGDA		1	Y
				PMM0949	130	IQLAWLGDS	1	N
Prochlorococcus sp. CC931	1	1,1	*sync_0200*	254	EQLEFLGDA		1	Y
				sync_1634	135	LQLAWLGDA	1	N
Prochlorococcus sp. CC9605	1	1,1	*Syncc9605_0149*	241	ERLEFLGDA		1	Y
				Syncc9605_1154	136	LQLAWIGDA	1	N
Prochlorococcus sp. CC9902	1	1,1	*Syncc9902_0179*	249	ERLEFLGDA		1	Y
				Syncc9902_1305	143	LQLAWIGDA	1	N
Prochlorococcus sp. WH 7803	1	1,1	*SynWH7803_0204*	240	EQLEFLGDA		1	Y
				SynWH7803_1063	136	LQLAWLGDA	1	N
Prochlorothrix hollandica PCC 9006	3	2,1	*Pro9006DRAFT_0098*	242	EQLEFVGDA		1	Y
			Pro9006DRAFT_0103	256	ERLEFLGDA		1	Y
				Pro9006DRAFT_2926	132	VLLAYVGDA	1	N
Pseudanabaena sp. PCC 6802	3	2,1	*Pse6802_5090*	220	QRLEFLGDC		1	Y
			Pse6802_2378	245	DVLEFVGDS		1	Y
				Pse6802_4789	120	ASLAYLGDA	1	N
Pseudanabaena sp. PCC 7367	3	2,1	*Pse7367_2482*	221	QRLEFLGDA		1	Y
			Pse7367_1487	269	EKLEFFGDS		1	Y
				Pse7367_2852	132	AALAYIGDA	1	N
Spirulina major PCC 6313	3	2,1	*Spi6313_3729*	235	ERLEFLGDA		1	Y
			Spi6313_2493	239	EQLEFVGDA		1	Y
				Spi6313_1300	150	TALAYIGDG	1	N
Spirulina subsalsa PCC 9445	3	4,1	*Spi9445_2508*	227	ERLEFLGDA		1	Y
			Spi9445_1629	246	EQLEFVGDA		1	Y
			Spi9445_4283	311	ERLVVLGGM		1	N
			Spi9445_1201	377	ERLEFLGDT		1	Y
				Spi9445_3328	151	LALAYLGDA	1	N
Synechococcus elongatus PCC 7942	1	1,1	*Synpcc7942_1645*	247	DRLEFLGDA		1	Y
				Synpcc7942_2120	138	QALAYLGDA	1	N
Synechococcus sp. PCC 7002	1	2,1	*SYNPCC7002_A0061*	239	EQLEFIGDA		1	Y
			SYNPCC7002_A2542	258	ERLEFLGDA		1	Y
				SYNPCC7002_A0384	131	ASLAYVGDA	1	N
Synechocystis sp. PCC 6803	1	2,1	*slr1646*	231	DRLEFLGDA		1	Y
			slr0346	244	QQLEFVGDA		1	Y
				slr0954	143	VALAYLGDA	1	N
Thermosynechococcus elongatus BP-1	1	0,1		*tlr0428*	151	AALAYFGDA	1	N
Trichodesmium erythraeum IMS101	3	3,1	*Tery_2839*	209	QGLANLGYV		1	N
			Tery_2144	233	ESLEFIGDA		1	Y
			Tery_1105	250	EKLEFFGDA		1	Y
				Tery_2312	130	SAWAYLGDA	1	N
Arabidopsis thaliana	N/A	N/A		*AT1G55140*	237	ASLAYIGDS	1	N
Bacillus subtilis	N/A	N/A		*gnl*	143	LALAY IGDA	1	N
Escherichia coli MG1655	N/A	N/A	*rnc*		226	ERLEFLGDS	1	Y

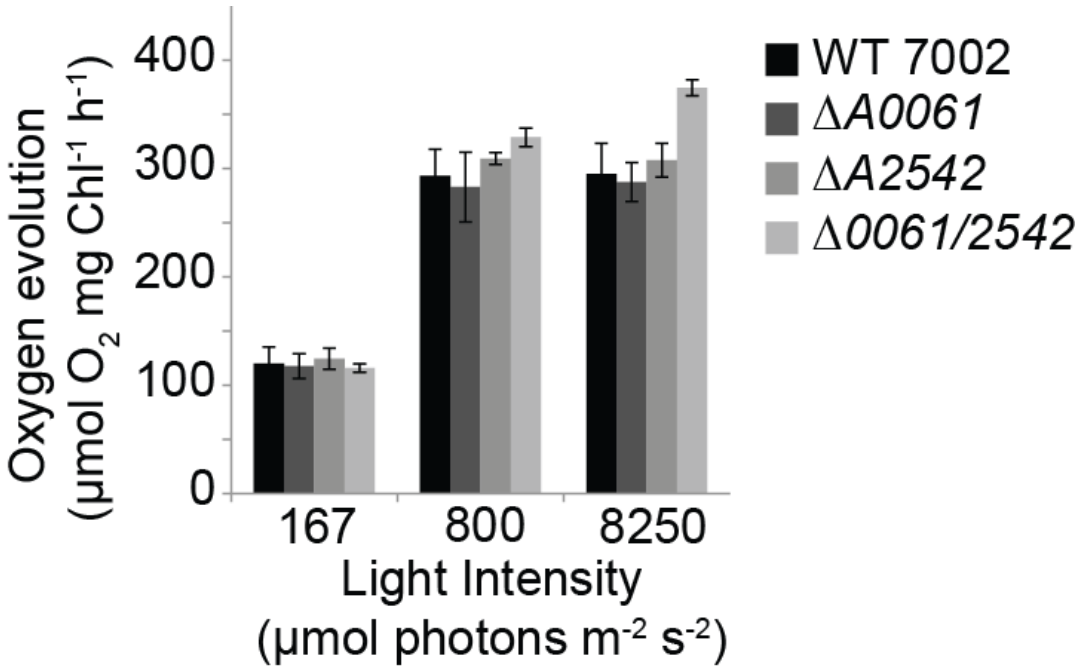
Model organisms used in Table I are highlighted in bold.

[a]Shih PM et al. (2013) Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. Proc Natl Acad Sci U S A. 110 (3): 1053-1058



Online Resource 5 Growth and physiology of Δ*1543* strains

Growth of WT and Δ*1543* strains in liquid medium (12-well tissue culture plates) with shaking (150 rpm) in the absence (a) and presence (b) of 10 mM $NaHCO_3^-$. Error bars are s.d. of three cultures. Cells were grown in standard conditions as described in "Materials and Methods". (c) Absorption spectra of WT, Δ*1543*, and genetically complemented Δ*1543*+ strains following 24 h growth in liquid medium in culture tubes bubbled with air.



Online Resource 6 Light-dependent oxygen evolution activity of RNase III mutants

Oxygen evolution was measured as a function of light intensity on a Clark-type electrode in cell solutions suspended at a chlorophyll concentration of 5 µg/ml in A+ media containing 10 mM $NaHCO_3^-$ as described in "Materials and Methods".