A

Synechococcus PCC7002	TTAACT**GTA**AGACCCGC**TCA**…N$_{23}$…**TA**CCGATCC N$_{326}$ ATG
Prochlorococcus marinus MIT 9301	AATTTG**GTG**ATATCGGT**TAC**…N$_{20}$…**CA**GAGAATGTTCTAAGTTTTTTTAATTTTCATG
Synechococcus elongatus PCC7942	TATTTA**GTA**GTCACCGT**TAC**…N$_{20}$…**TA**GTTAATTG…N46….ATG
S*ynechococcus* WH8102	TGTGTT**GTA**GCCAAGGC**CAC**…N$_{23}$…**TC**ATCCAGTTT…N71…ATG
Acaryochloris marina MBIL11017	GGCTGC**GTA**CCCCTTAA**TAC**…N$_{24}$…**TA**AGAAGCCTCA…N$_{273}$…ATG

B

				-35	-10	+1
sll0783	A**GAT** AATCTTCA	**TAC**A....N$_{59}$...TGATACA N$_{21}$ TA N$_3$ T GATACAT<u>GA</u>
glnA	T**GTA** TCAGCTGT	**TAC**A...N22..............TA N3 T GGATAGT<u>CG</u>
	GTA N8	**TAC** N22 TA N3 T N4-5 <u>tsp</u>

Supplement 3: (A) Putative NtcA binding sites in the upstream region of *sll0783* homologues in cyanobacteria containing this gene cluster. Startcodon is marked in red. Nucleotides matching those of the GTA and TAC triplets of the NtcA recognition motiv are boldface. (B) Sequence of 5' end of *sll0783* transcript**.** Total RNA from nitrogen-starved *Synechocystis* wild-type cells was isolated and analysed by using the 5'RACE method. Sequencing the cDNA revealed the 5'end of the *sll0783*-transcript (+1), indicating a potential transcription start site (tsp). The potential NtcA recognition site upstream of the tsp is aligned to the NtcA binding site in the promoter of the *glnA* gene *(slr1765)*. Below, the consensus canonical NtcA binding sequence is shown. The putative NtcA-binding motif is highlighted in bold and the possible tsp is underlined.