

# Supporting Information

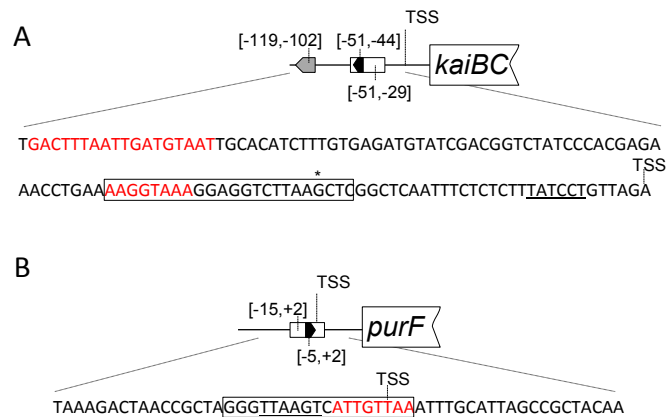
Espinosa et al. 10.1073/pnas.1424632112

## Extended Phos-Tag Methods

To analyze RpaB and RpaA phosphorylation, protein samples were resolved using 25  $\mu$ M Phos-tag acrylamide gels in combination with immunoblotting detection with polyclonal antibodies raised against RpaB and RpaA. IPTG (1 mM) was added to exponentially growing cells and at indicated times a cell aliquot was harvested by centrifugation (4  $^{\circ}$ C, 10,000  $\times$  g), frozen in liquid nitrogen, and stored at  $-20$   $^{\circ}$ C. Cell extracts were prepared by mechanic cell lysis using glass beads (three rounds of 1 min using a Minibeatbeater with cooling between cycles). Unbroken cells,

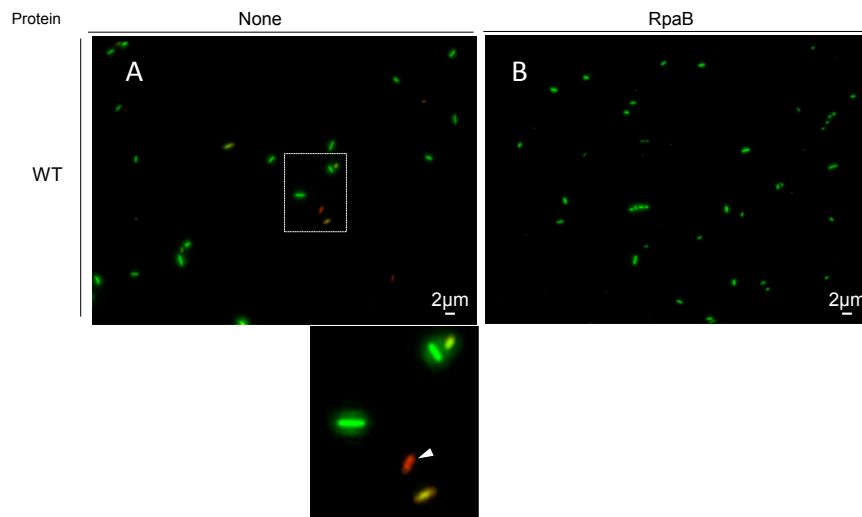
debris, and glass beads were pelleted down (5 min 5,500  $\times$  g) and the supernatant collected. Protein content was determined using the modified Lowry method (Bio-Rad). We used proteins extracts with no more than two freeze-thaw cycles as we notice that repeated cycles promote phospho-hydrolysis of RpaB~P and RpaA~P.

When necessary, cells were entrained to at least two 12:12 LD cycles: exponentially growing cells were diluted with fresh media to  $DO_{750}$  0.3 and incubated in LD. Cells were released in LL or kept in LD and aliquots harvested at indicated timepoints and processed as described above.

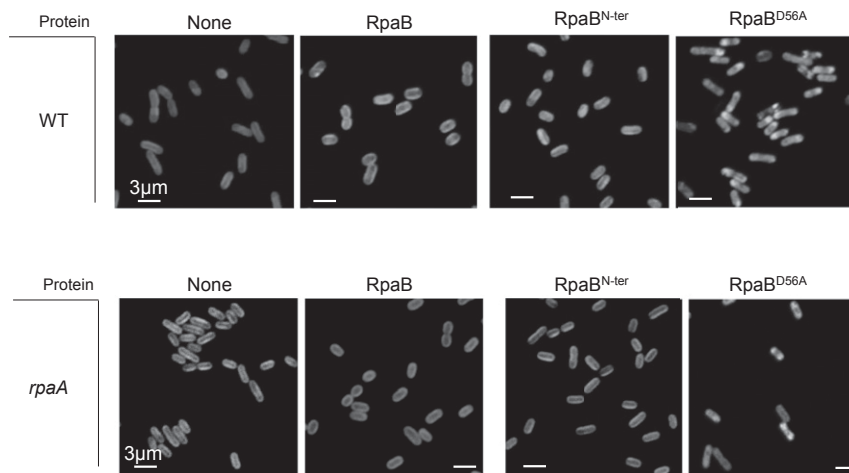


**Fig. S1.** Schematic representation and regulatory sequences of the *kaiBC* and *purF* promoter regions. In both A and B empty, gray and black boxes represent RpaA, RpaB and half RpaB sites, respectively, with numbers indicating their positions relative to the transcription start sites (TSS). Nucleotides, RpaA (boxed) and RpaB (in red) recognition sites are shown. The putative  $-10$  elements are underlined. (A) *kaiBC* and (B) *purF*. In A and B, the TSS were reported by Kutsuna et al. (1) and Vijayan et al. (2), respectively. Alternative start points were described for *kaiBC* (2) (indicated with an asterisk) and in *purF* (3) (90 nt upstream of the indicated TSS). The half RpaB motif in *kaiBC* was described by Hanaoka et al. (4). RpaB sites were predicted in silico, whereas RpaA sites correspond to nucleotides protected in footprinting assays (5).

1. Kutsuna S, Nakahira Y, Katayama M, Ishiura M, Kondo T (2005) Transcriptional regulation of the circadian clock operon *kaiBC* by upstream regions in cyanobacteria. *Mol Microbiol* 57(5):1474–1484.
2. Vijayan V, Jain IH, O’Shea EK (2011) A high resolution map of a cyanobacterial transcriptome. *Genome Biol* 12(5):R47.
3. Liu Y, Tsinoremas NF, Golden SS, Kondo T, Johnson CH (1996) Circadian expression of genes involved in the purine biosynthetic pathway of the cyanobacterium *Synechococcus* sp. strain PCC 7942. *Mol Microbiol* 20(5):1071–1081.
4. Hanaoka M, et al. (2012) RpaB, another response regulator operating circadian clock-dependent transcriptional regulation in *Synechococcus elongatus* PCC 7942. *J Biol Chem* 287(31): 26321–26327.
5. Markson JS, Piechura JR, Puzyszynska AM, O’Shea EK (2013) Circadian control of global gene expression by the cyanobacterial master regulator RpaA. *Cell* 155(6):1396–1408.



**Fig. S2.** Cell viability test on the basis of membrane integrity after 96 h of overexpression of RpaB and staining with “LIVE/DEAD BacLight kit” following the manufacturer’s instructions. After staining with a mixture of the SYTO 9 and propidium iodide stains, cells with intact membranes fluoresce in green, whereas those with damaged membranes fluoresce in red (because of cyanobacterial pigments, autofluorescence, and propidium iodide emission spectrum overlap). Fluorescence was recorded with a Leica fluorescence microscope at a magnification of 1,000 $\times$ . The dashed box was magnified 3 $\times$  to show an example of a cell with nucleic acids stained in red by propidium iodide (white arrowhead) that would be classified as dead. WT background without and with RpaB-overexpression are shown in *A* and *B*, respectively.



**Fig. S3.** Cell appearance under confocal microscope of the indicated strains after 72 h of IPTG induction. Note that 1P<sub>trc</sub>-rpaB<sup>D56A</sup> shows atypical auto-fluorescence distribution.



**Table S1. Strains and plasmids used in this work**

Strain/plasmid	Genotype or relevant characteristics	Source
WT	Wild-type <i>Synechococcus elongatus</i> PCC 7942	Pasteur culture collection
AMC541	WT <i>PkaiBC::luc</i> NS2, Cm <sup>r</sup>	(1)
AMC601	WT <i>PpurF::luc</i> NS2, Km <sup>r</sup>	(2)
1 <i>Ptrc</i> * <sup>†</sup>	<i>Ptrc</i> NS1, Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> * <sup>†</sup>	Φ( <i>Ptrc::rpaB</i> ) NS1, Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>N-ter</sup> * <sup>†</sup>	Φ( <i>Ptrc::rpaB</i> <sup>1-131</sup> ) NS1, Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>D56A</sup> * <sup>†</sup>	Φ( <i>Ptrc::rpaB</i> <sup>D56A</sup> ) NS1, Sm <sup>r</sup>	Present work
<i>rpaA</i> <sup>†</sup>	<i>rpaA::Gm</i> , Gm <sup>r</sup>	(3)
1 <i>rpaA::Gm</i> , Φ( <i>Ptrc::rpaB</i> ) <i>rpaA</i> <sup>†</sup>	<i>rpaA::Gm</i> , Φ( <i>Ptrc::rpaB</i> ) NS1, Sm <sup>r</sup> Gm <sup>r</sup>	Present work
<i>cikA</i> * <sup>†</sup>	<i>cikA::Gm</i> , Gm <sup>r</sup>	(4)
1 <i>Ptrc cikA</i> * <sup>†</sup>	<i>cikA::Gm</i> , <i>Ptrc</i> NS1, Sm <sup>r</sup> Gm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB cikA</i> * <sup>†</sup>	<i>cikA::Gm</i> , Φ( <i>Ptrc::rpaB</i> ) NS1, Sm <sup>r</sup> Gm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>N-ter</sup> <i>cikA</i> * <sup>†</sup>	<i>cikA::Gm</i> , Φ( <i>Ptrc::rpaB</i> <sup>1-131</sup> ) NS1, Sm <sup>r</sup> Gm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>D56A</sup> <i>cikA</i> * <sup>†</sup>	<i>cikA::Gm</i> , Φ( <i>Ptrc::rpaB</i> <sup>D56A</sup> ) NS1, Sm <sup>r</sup> Gm <sup>r</sup>	Present work
<i>sasA</i>	Gm cassette cloned into <i>sasA</i> , Gm <sup>r</sup>	(5)
<i>kaiC</i>	Ω-cassette inserted into <i>kaiC</i> , Km <sup>r</sup>	(3)
<i>rpaA</i>	Gm cassette cloned into <i>rpaA</i> , Gm <sup>r</sup>	(3)
1 <i>Ptrc</i>	<i>Ptrc</i> NS1, Sm <sup>r</sup>	(6)
1 <i>Ptrc</i> - <i>rpaB</i>	Φ( <i>Ptrc::rpaB</i> ) NS1, Sm <sup>r</sup>	(6)
1 <i>Ptrc</i> - <i>rpaB</i> <sup>N-ter</sup>	Φ( <i>Ptrc::rpaB</i> <sup>1-131</sup> ) NS1, Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>D56A</sup>	Φ( <i>Ptrc::rpaB</i> <sup>D56A</sup> ) NS1, Sm <sup>r</sup>	Present work
1 <i>Ptrc rpaA</i>	<i>Ptrc</i> NS1, <i>rpaA::Gm</i> , Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB rpaA</i>	Φ( <i>Ptrc::rpaB</i> ) NS1, <i>rpaA::Gm</i> (heteroallelic), Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>N-ter</sup> <i>rpaA</i>	Φ( <i>Ptrc::rpaB</i> <sup>1-131</sup> ) NS1, <i>rpaA::Gm</i> , Sm <sup>r</sup>	Present work
1 <i>Ptrc</i> - <i>rpaB</i> <sup>D56A</sup> <i>rpaA</i>	Φ( <i>Ptrc::rpaB</i> <sup>D56A</sup> ) NS1, <i>rpaA::Gm</i> , Sm <sup>r</sup> Gm <sup>r</sup>	Present work
pAM2152	<i>cikA::Gm</i> , Gm <sup>r</sup>	(4)
pAM2176	<i>sasA::Gm</i> , Gm <sup>r</sup>	(5)
pAM4523	<i>rpaA::Gm</i> , Gm <sup>r</sup> Ap <sup>r</sup>	(3)
pUAGC758	Φ(C.K1(+)- <i>rpaB</i> ), Ap <sup>r</sup> Sm <sup>r</sup>	(6)
pUAGC763	Φ(C.S3(+)- <i>rpaB</i> ), Ap <sup>r</sup> Sm <sup>r</sup>	(6)
pUAGC280	C.S3 <i>lacI</i> <sup>r</sup> and <i>Ptrc</i> , into NS1, Ap <sup>r</sup> Sm <sup>r</sup>	(6)
pUAGC282	pUAGC280 with <i>Ptrc</i> - <i>rpaB</i> , Ap <sup>r</sup> Sm <sup>r</sup>	(6)
pUAGC283	pUAGC280 with <i>Ptrc::rpaB</i> <sup>N-ter</sup> , Ap <sup>r</sup> Sm <sup>r</sup>	Present work
pUAGC284	pUAGC280 with <i>Ptrc::rpaB</i> <sup>D56A</sup> , Ap <sup>r</sup> Sm <sup>r</sup>	Present work

\*In reporter strain AMC541.

†In reporter strain AMC601.

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- Ditty JL, Canales SR, Anderson BE, Williams SB, Golden SS (2005) Stability of the *Synechococcus elongatus* PCC 7942 circadian clock under directed anti-phase expression of the *kai* genes. *Microbiology* 151(Pt 8):2605–2613.
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**Table S2. Oligonucleotides used in this work**

Oligo name	Sequence
RpaB-ptcr-1F	5′-AGAGGGAATTCCTTGGAAAATCGCAAG-3′
RpaB-HCN-1R	5′-GATCGGATCCGGCGCTGGCTGCTCTAAC-3′
RpaB-HCN-2R	5′-GTCGGGATCCTAGCTGTGTGATCTGGATG-3′