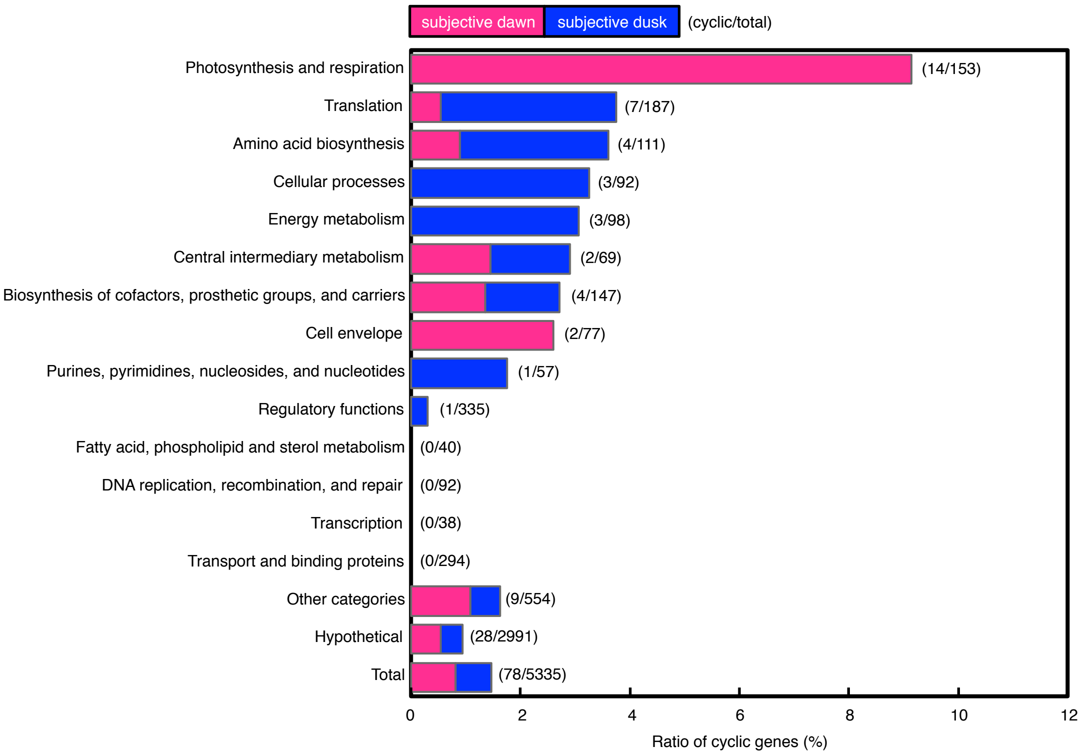

FIGURE S1. Functional categories of clock-controlled genes.
The clock-controlled genes in *Anabaena* were classified according to their functional categories. The proportions of clock-controlled genes in the total genes in each category are shown as a stacked bar graph. Red and blue bars indicate the proportions of dawn- and dusk-induced genes, respectively, out of the total cycling genes in each category. The numbers of cyclic genes and total genes in each category are shown in parentheses.

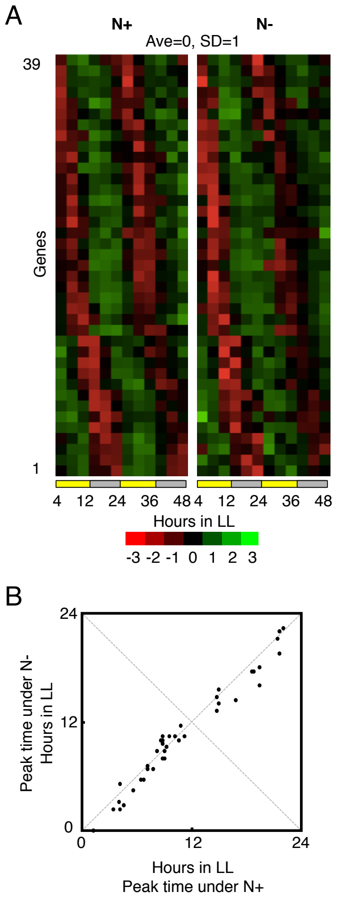

FIGURE S2. Genome-wide circadian expression profiles of common clock-controlled genes in the presence and absence of nitrate.

A. Expression profiles of 39 cycling genes commonly expressed in the absence (N–) or presence (N+) of sodium nitrate, sorted by peak time under nitrate-replete conditions (N+). The results of two independent experiments (N+) and a single series of experiments (N–) are shown. The data are represented as for Fig. 2B. **B.** Variations in the peak time of each gene in the presence (N+) or absence (N–) of sodium nitrate.

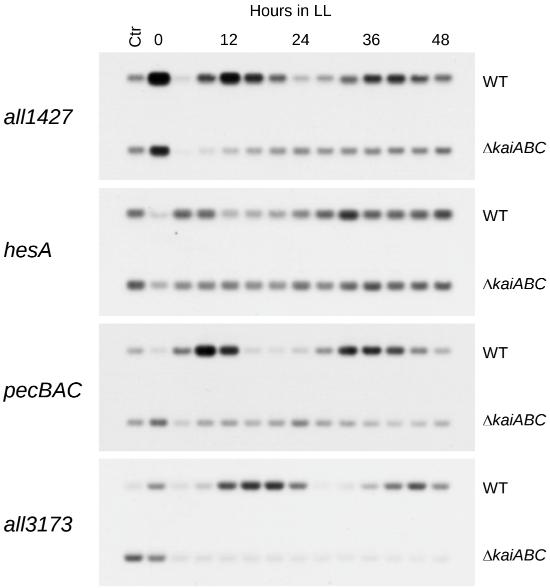

FIGURE S3. Nullification of transcription rhythms of heterocyst-specific genes and representative high-amplitude genes by genetic disruption of the *kaiABC* cluster in the absence of combined nitrogen. Northern blot analysis using the total RNAs extracted from wild-type (WT) and *kaiABC*-null mutant (**Δ***kaiABC*) cells with each genes-specific probe are shown. Circadian expression of *all1427*, *hesA*, *pecBAC* and *all3173* genes was nullified in the *kaiABC*-null mutant strain. We loaded samples collected at hour 48 in LL under different (**Δ***kaiABC* for WT, WT for **Δ***kaiABC*) strains as control samples indicated by "Ctr".

Table S1. *Anabaena* strains used in this study

Strains	Genotype	Reporter cassette	Host Strain	DNA used for transformation	Marker*	References
ILC292	Wild type	*Palr0523::luxAB, Pall0011::luxCDE*	*Anabaena* WT	pIL407	Km, Nm	This study
ILC379	Wild type	*Pall3173::luxAB, Pall0011::luxCDE*	*Anabaena* WT	pIL411	Km, Nm	This study
ILC352	*kaiABC-null*	none	*Anabaena* WT	pIL204	Sp	This study
ILC505	*kaiABC-null*	*Palr0523::luxAB, Pall0011::luxCDE*	ILC352	pIL407	Km, Nm, Sp	This study
ILC507	*kaiABC-null*	*Pall3173::luxAB, Pall0011::luxCDE*	ILC352	pIL411	Km, Nm, Sp	This study

*Km, Nm and Sp represent kanamycin-, neomycin- and spectinomycin/streptomycin-resistant genes, respectively.

Table S2. List of 78 'cycling' genes.

Definition of correlation *p-value* and *amplitude* was described in the text.

*All tested genes are classified into "Arrhythmic" (AR) and "Cycling" genes using the standerd (*b* : p-value of < 0.05 and amplitude of > 10^–0.7),
more stringent (*a* : *p-value* of < 0.01 and *amplitude* of > 10^–0.6) or less strigent (c: *p-value* of < 0.1 and *amplitude* of > 10^–0.8) filtering conditions under nitrogen supplemented conditions (*n* =2).

**Under nitrogen deprivation, genes are classified into AR or Cycling genes using the same filtration methods, while one series of expereiments were performed (*n* =1).

ORF No.	Gene name	Annotation	peak time (N+, *n* =2)	*p-value* (N+, *n* =2)	*amplitude* (N+, *n* =2)	Cycling property (N+, *n* =2)*	peak time (N-, *n* =1)	*p-value* (N-, *n* =1)	*amplitude* (N-, *n* =1)	Cycling property (N-, *n* =1)**
all0232	-	hypothetical protein	10.8	0.007	0.273	a	11.6	0.010	0.364	b
all0333	-	hypothetical protein	10.6	0.008	0.338	a	10	0.003	0.470	a
all0334	-	hypothetical protein	9	0.011	0.335	b	8.8	0.002	0.439	a
all0605	-	NirB-like protein	13.2	0.029	0.268	b	-	-	-	AR
all0713	*glgB*	1,4-alpha-glucan branching enzyme	7.8	0.008	0.301	a	6.8	0.030	0.323	b
all0888	-	ribose 5-phosphate isomerase	21.8	0.019	0.232	b	20.8	0.041	0.166	c
all1272	-	probable glycogen phosphorylase	15	0.028	0.676	b	15.6	0.003	0.538	a
all1353	-	putative hydrolase	7.2	0.031	0.206	b	6.8	0.033	0.381	b
all1743	*por*	light-dependent NADPH-protochlorophyllide oxidoreductase	8.6	0.042	0.340	b	10	0.017	0.365	b
all1797	-	unknown protein	6.4	0.043	0.349	b	5.6	0.003	0.497	a
all1897	-	heme oxygenase	8.2	0.007	0.450	a	8.8	0.046	0.402	b
all2327	*apcF*	allophycocyanin beta-18 subunit	8.8	0.005	0.337	a	8	0.035	0.421	b
all2566	*gap1*	glyceraldehyde-3-phosphate dehydrogenase	16.8	0.020	0.476	b	14.4	0.008	0.517	a
all2567	-	hypothetical protein	14.8	0.043	0.527	b	14.8	0.023	1.032	b
all2906	*moeB*	molybdopterin biosynthesis protein	18.8	0.040	0.250	b	17.6	0.018	0.224	b
all3173	-	hypothetical protein	18.6	0.007	0.708	a	17.6	0.001	0.712	a
all3259	-	hypothetical protein	10.8	0.028	0.203	b	-	-	-	AR
all3319	-	hypothetical protein	12	0.009	0.365	a	-	-	-	AR
all3516	-	unknown protein	19.4	0.021	0.206	b	16	0.020	0.214	b
all3572	*psbAIV*	photosystem II reaction center D1 protein	5.4	0.044	0.415	b	-	-	-	AR
all3941	-	unknown protein	8.8	0.042	0.391	b	-	-	-	AR
all4103	*ribG*	riboflavin-specific deaminase	20.8	0.033	0.268	b	20.8	0.064	0.265	c
all4189	-	tRNA-pseudouridine synthase I	22	0.024	0.379	b	-	-	-	AR
all4197	*secY*	preprotein translocase SecY subunit	21.8	0.025	0.329	b	-	-	-	AR
all4336	*rps10*	30S ribosomal protein S10	22.2	0.039	0.445	b	20.4	0.090	0.307	c
all4349	-	unknown protein	22	0.043	0.341	b	-	-	-	AR
all4563	*fda*	fructose-1,6-bisphosphate aldolase	5.6	0.029	0.472	b	4.4	0.046	0.392	b
all4578	-	unknown protein	22.2	0.034	0.390	b	-	-	-	AR
all4822	-	similar to beta-lactamase	21.6	0.039	0.222	b	22	0.050	0.253	b
all5062	*gap2*	glyceraldehyde-3-phosphate dehydrogenase	4.2	0.030	0.401	b	2.4	0.010	0.249	b
alr0020	*apcE*	phycobilisome core-membrane linker polypeptide Lcm, allophy	8.8	0.011	0.510	b	10	0.035	0.538	b
alr0022	*apcB*	allophycocyanin beta subunit	8.6	0.003	0.304	a	-	-	-	AR
alr0515	-	hypothetical protein	22.6	0.036	0.336	b	19.2	0.088	0.175	c
alr0523	*pecB*	phycoerythrocyanin beta chain	11.2	0.034	0.526	b	10.4	0.001	0.741	a
alr0524	*pecA*	phycoerythrocyanin alpha chain	9.6	0.002	0.656	a	10.4	0.007	0.950	a
alr0525	*pecC*	phycoerythrocyanin-associated rod linker protein	10.2	0.005	0.592	a	10.4	0.002	0.802	a
alr0530	*cpcC*	phycobilisome rod linker polypeptide Lr, phycocyanin-associate	8.8	0.035	0.477	b	10.4	0.024	0.390	b
alr0532	*cpcE*	phycocyanin alpha subunit phycocyanobilin lyase, CpcE subuni	9.4	0.007	0.390	a	-	-	-	AR
alr0533	*cpcF*	phycocyanin alpha subunit phycocyanobilin lyase, CpcF subuni	9.2	0.009	0.370	a	9.2	0.010	0.601	b
alr0535	*cpcG2*	phycobilisome rod-core linker polypeptide Lrc, C-phycocyanin	8.8	0.022	0.462	b	9.6	0.011	0.448	b
alr0545	-	probable pseudouridine synthase	9	0.039	0.342	b	8	0.007	0.325	a
alr0577	-	FKBP-type peptidyl-prolyl cis-trans isomerase	8	0.037	0.310	b	-	-	-	AR
alr0608	*nrtA*	ABC-type nitrate/nitrite transport system substrate-binding prot	12.6	0.045	0.316	b	-	-	-	AR
alr0609	*nrtB*	ABC-type nitrate/nitrite transport system permease protein	12.8	0.049	0.238	b	-	-	-	AR
alr0611	*nrtD*	ABC-type nitrate/nitrite transport system ATP-binding protein	13	0.010	0.285	a	-	-	-	AR
alr0612	*narB*	ferredoxin--nitrate reductase	11.6	0.046	0.231	b	-	-	-	AR
alr0683	-	hypothetical protein	23	0.049	0.319	b	-	-	-	AR
alr1674	-	hypothetical protein	8.2	0.047	0.346	b	5.6	0.057	0.290	c
alr1690	-	cell wall-binding protein	8.6	0.028	0.275	b	-	-	-	AR
alr2311	*rbpF*	RNA-binding protein	18.8	0.042	0.265	b	-	-	-	AR
alr2885	*kaiB*	circadian oscillation regulator	21	0.046	0.246	b	16	0.065	0.213	c
alr3606	-	dihydrolipoamide S-acetyltransferase	21.8	0.050	0.237	b	-	-	-	AR
alr3662	*groEL*	chaperonin GroEL	19.4	0.019	0.626	b	18	0.004	0.539	a
alr3692	-	hypothetical protein	15	0.004	0.535	a	14	0.030	0.956	b
alr3843	*hoxR*	rubredoxin	4.2	0.010	0.266	b	4.8	0.065	0.314	c
alr3844	-	hypothetical protein	6.8	0.048	0.372	b	5.6	0.016	0.354	b
alr4077	-	hypothetical protein	3.4	0.007	0.477	a	2.4	0.007	0.341	a
alr4156	*ndhF3*	NADH dehydrogenase subunit 5	4.2	0.018	0.258	b	5.2	0.012	0.251	b
alr4777	-	hypothetical protein	4.6	0.029	0.271	b	2.8	0.043	0.307	b
alr4784	-	adenylosuccinate synthetase	20.2	0.022	0.340	b	-	-	-	AR
alr4939	-	unknown protein	7.2	0.046	0.449	b	7.2	0.005	0.479	a
alr4957	-	hypothetical protein	9.6	0.021	0.203	b	10.4	0.065	0.298	c
alr5275	-	6-phosphogluconate dehydrogenase	16	0.038	0.491	b	-	-	-	AR
alr5286	-	probable short-chain dehydrogenase	1.2	0.024	0.419	b	0	0.006	0.458	a

alr5299	*nusG*	transcription antitermination protein	21.2	0.027	0.307	b	-	-	-	AR
alr5302	*rpl10*	50S ribosomal protein L10	21.4	0.013	0.362	b	21.2	0.024	0.235	b
alr5303	*rpl12*	50S ribosomal protein L12	22	0.003	0.387	a	22.4	0.012	0.245	b
asl0597	-	hypothetical protein	8.4	0.039	0.631	b	-	-	-	AR
asl3322	-	unknown protein	14.8	0.024	0.404	b	13.2	0.012	0.447	b
asl3518	-	unknown protein	21	0.022	0.309	b	-	-	-	AR
asl4207	*rpl29*	50S ribosomal protein L29	20.4	0.034	0.513	b	-	-	-	AR
asr0023	*apcC*	phycobilisome small core linker polypeptide Lc, allophycocyani	8.8	0.004	0.401	a	-	-	-	AR
asr0461	-	unknown protein	8.8	0.039	0.356	b	-	-	-	AR
asr0531	*cpcD*	phycobilisome small rod linker polypeptide Lr, phycocyanin-ass	10	0.017	0.260	b	-	-	-	AR
asr1667	-	unknown protein	4	0.038	0.752	b	3.2	0.015	0.739	b
asr2665	-	unknown protein	10.4	0.018	0.330	b	-	-	-	AR
asr3168	-	hypothetical protein	21.6	0.002	0.293	a	19.6	0.012	0.215	b
asr5298	*secE*	secretory protein	21.2	0.034	0.342	b	-	-	-	AR

TABLE S3. Genes highly upregulated in heterocysts under nitrogen deprivation.

R*i* , I*i* , *Sum(N-)/Sum(N+)* values are defined as described in the text.

*All tested genes are classified into "Arrhythmic" (AR) and "Cycling" genes using the standerd (*b* : p-value of < 0.05 and amplitude of > 10^–0.7), more stringent (*a* : *p-value* of < 0.01 and *amplitude* of > 10^–0.6) or less strigent (c: *p-value* of < 0.1 and *amplitude* of > 10^–0.8) filtering conditions under nitrogen deprivation (*n* =1).

ORF No.	Gene name	Annotation	R*i* value	I*i* value	*Sum(N-)/Sum(N+)*	Cycling property*	Peak time
all1440	*nifK*	nitrogenase MoFe protein subunit beta	8.981	310.929	13.087	AR	-
alr5358	*hetN*	ketoacyl reductase	8.904	244.936	4.506	AR	-
asl1434	-	hypothetical protein	8.427	102.039	5.452	AR	-
all1457	*nifS*	nitrogenase cofactor synthesis protein	7.450	41.877	4.350	AR	-
all1439	-	hypothetical protein	7.200	35.578	4.099	AR	-
alr2731	*ctaC*	ARTO, homolog of cytochrome c oxidase subunit II	7.091	33.283	3.275	AR	-
all1517	*nifB*	nitrogen fixation protein	7.035	32.189	4.698	AR	-
all1455	*nifH*	nitrogenase iron protein, Fe-protein, dinitrogenase reductase, nitrogenase component II	6.942	30.476	49.624	AR	-
all1427	-	hypothetical protein	6.744	27.277	8.066	b	13.2
alr5360	-	hypothetical protein	6.299	21.616	3.499	AR	-
all1516	*fdxN*	ferrodoxin-like protein (fdxN)	5.790	16.923	3.285	AR	-
asl1516	*fdxN*	ferrodoxin-like protein (fdxN)	5.700	16.227	3.186	AR	-
all1432	*hesA*	HesA protein	5.659	15.922	3.894	c	3.6
alr2525	-	unknown protein	5.595	15.465	4.004	AR	-
alr2517	-	hypothetical protein	4.892	11.291	3.402	c	14.8
asr2513	*fdxB*	ferredoxin	4.582	9.846	3.529	b	3.6
all1431	*hesB*	HesB protein	4.514	9.555	5.535	AR	-
all1430	*fdxH*	heterocyst-specific [2Fe-2S] ferredoxin	4.481	9.415	3.950	AR	-
all1424	-	unknown protein	4.286	8.632	3.001	AR	-
all1454	*nifD*	nitrogenase MoFe protein subunit alpha	4.198	8.300	12.159	AR	-
asl2052	-	unknown protein	4.193	8.282	7.796	AR	-
all1425	-	unknown protein	3.247	5.320	3.979	AR	-
asr0905	-	hypothetical protein	3.103	4.949	6.555	b	18