

Supporting Information

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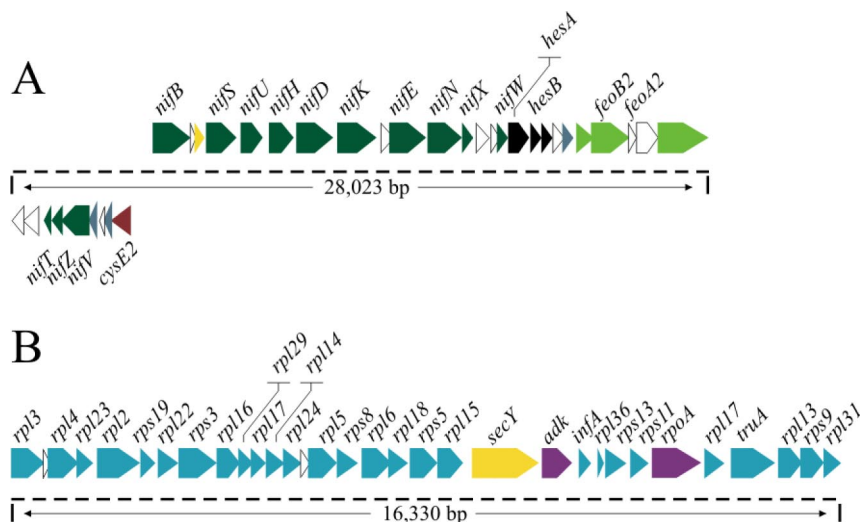


Fig. S1. Chromosomal organization of genes involved in nitrogen fixation (A) and genes encoding ribosomal proteins (B). The arrows indicate the direction of transcription. Genes are colored according to the functional categories in CyanoBase (<http://bacteria.kazusa.or.jp>). Labeled arrows represent genes of known function. The length of each gene cluster is given in bp.

Table S2. Comparison of log₂ ratios and fold changes observed from microarray and real-time PCR

ORF*/Annotation†	Experiment	Log ₂ ratio	Fold change	Time point
<i>cce_0565/nifX</i>	Microarray	-5.489	30.129	L5-1
	Real-time PCR	-7.146	51.067	
<i>cce_0565/nifX</i>	Microarray	0.896	0.802	D5-2
	Real-time PCR	0.000	0.000	
<i>cce_4716/kaiC2</i>	Microarray	-0.207	0.043	L5-1
	Real-time PCR	-0.808	0.653	
<i>cce_3501/psbA1</i>	Microarray	0.200	0.040	L5-1
	Real-time PCR	0.123	0.015	
<i>cce_0435/kaiB3</i>	Microarray	-1.681	2.826	D9-1
	Real-time PCR	-1.903	3.623	
<i>cce_0989/psaA</i>	Microarray	0.325	0.106	L5-1
	Real-time PCR	0.087	0.008	

* ORFs are labeled according to the deposited genome sequence in GenBank (accession nos. CP000806–CP000811).

†Annotations were manually curated, based on sequence homology to other known proteins. The time points are labeled as D5, D9 for 5, 9 hrs in the dark, and L5 for 5 hrs in the light. The extensions (-1) and (-2) indicate the corresponding diurnal cycle. The values for the microarray analyses are given as the average log₂ ratios and corresponding fold changes of the replicates for each time point ($n = 12$). The values for the Real-time PCR are given as the average log₂ ratios and corresponding fold changes for four replicates ($n = 4$).

Other Supporting Information Files

[Table S3 \(XLS\)](#)

[Table S4 \(XLS\)](#)

[Table S5 \(XLS\)](#)

[Table S6 \(XLS\)](#)

[Movie S1\(MOV\)](#)