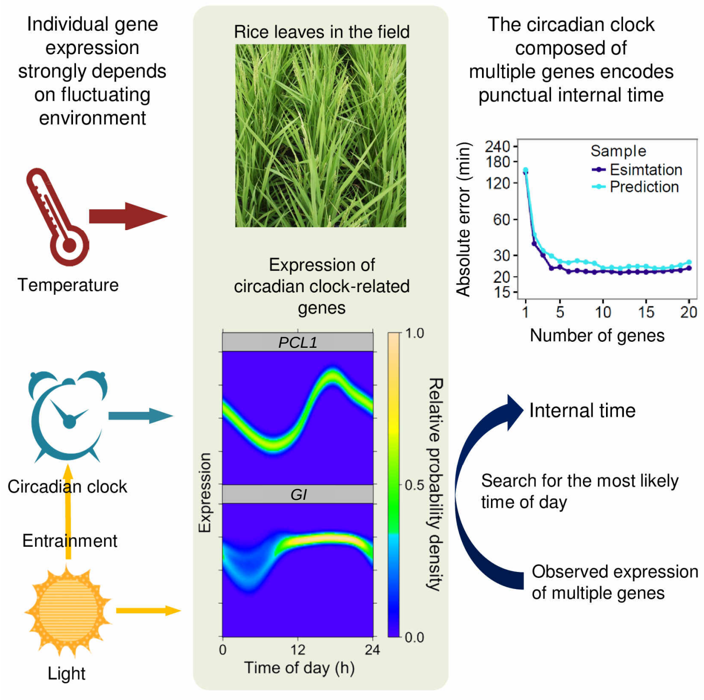
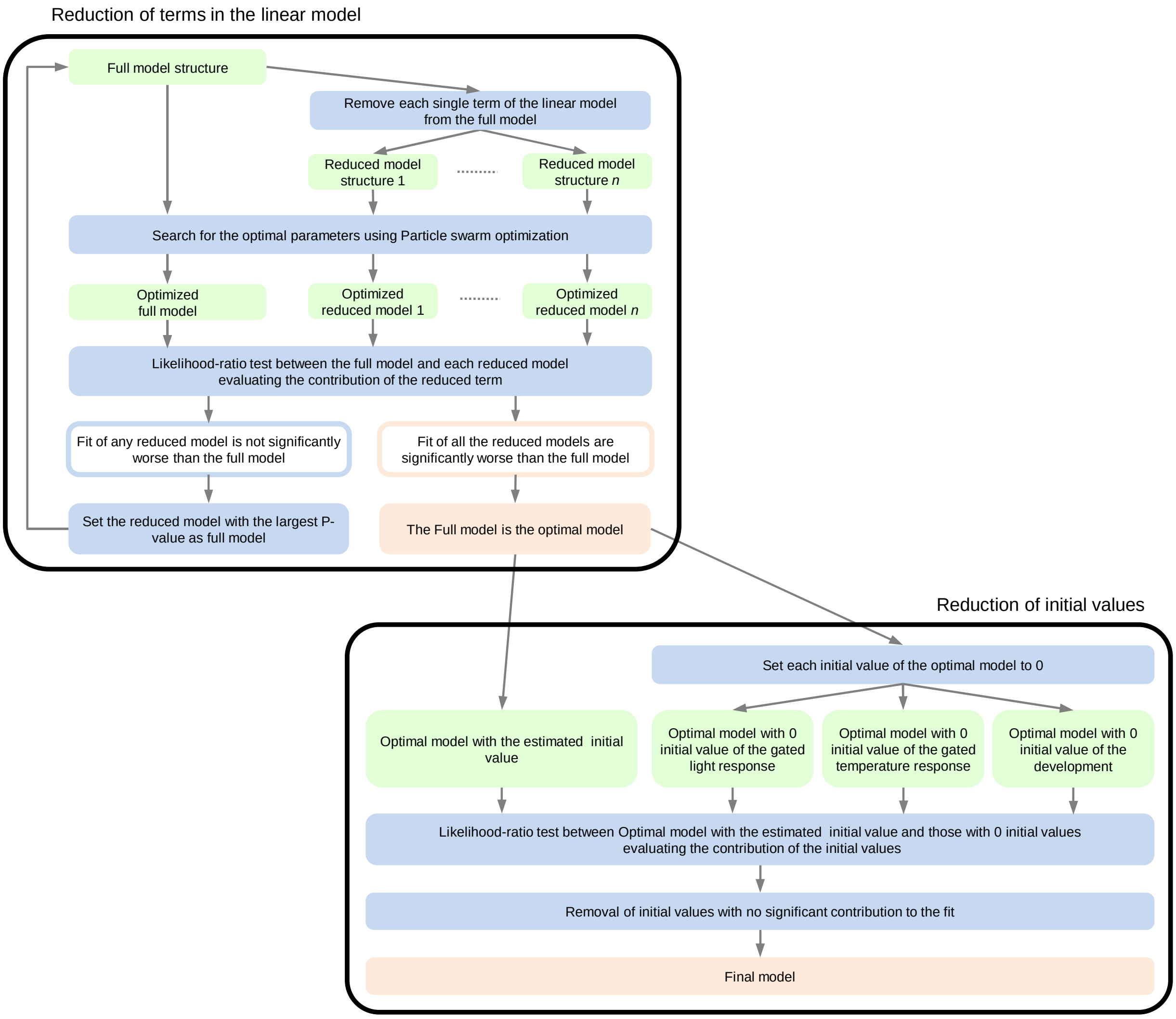
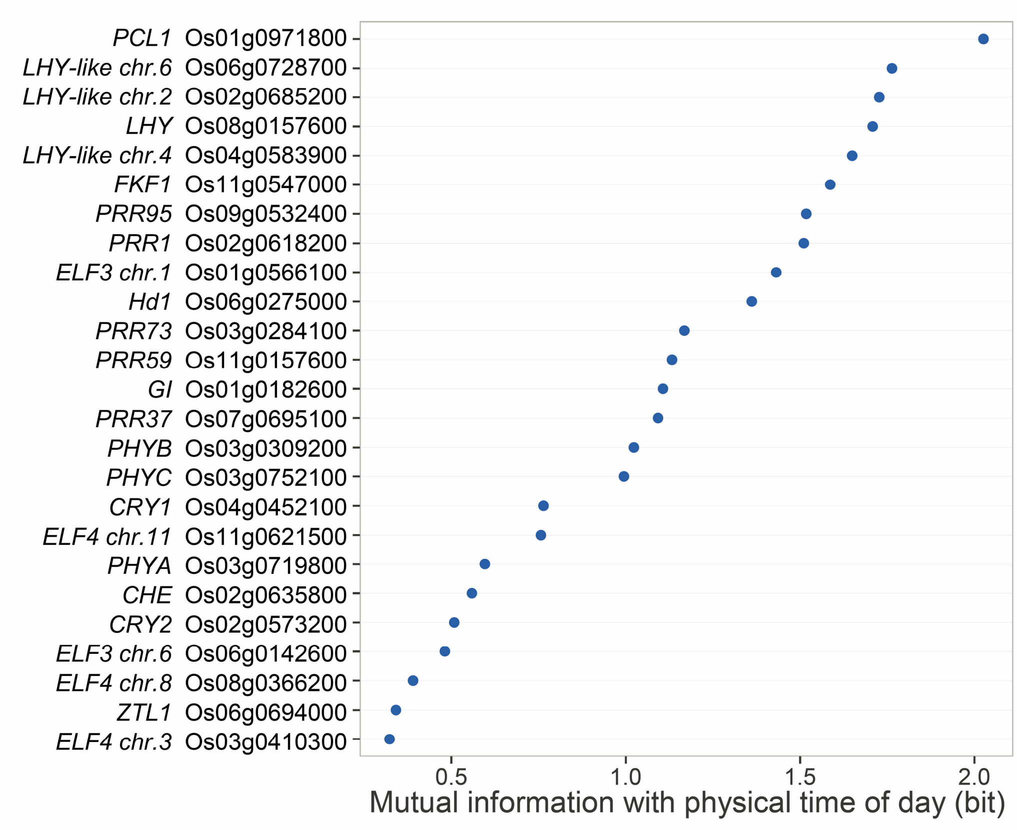
Supplemental Data



Supplemental Figure 1. Major findings and outline of methods in this study.
Left, a model of individual gene expression in WT rice growing in the field responding to solar radiation and ambient temperature was built for circadian clock–related genes and found strong effect of temperature. Middle, prediction by the model was used to obtain relationship between physical time of day and expression. Right, by using the relationship, we can infer internal time from expression of multiple genes and found punctuality to 22 min relative to physical time regardless of weather, day-length, or plant developmental age.

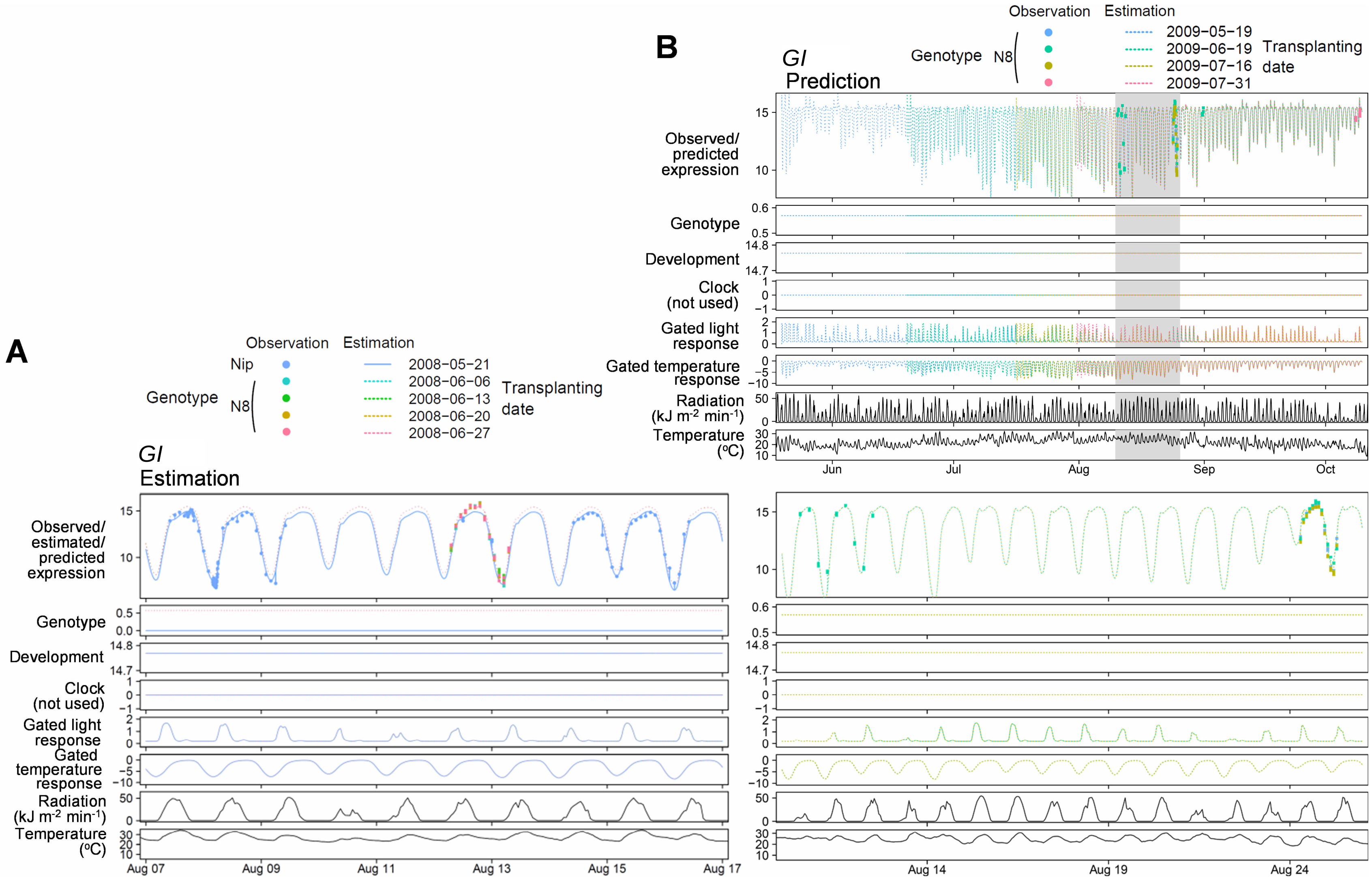


Supplemental Figure 2. Model improvement by reducing the number of parameters. Green, models to be compared; blue, processes and conditions of model improvement; pink, selected models and their conditions. Items shown in outline represent possible outcomes that lead to the next action to take.



Supplemental Figure 3. Rhythmicity of gene expression.

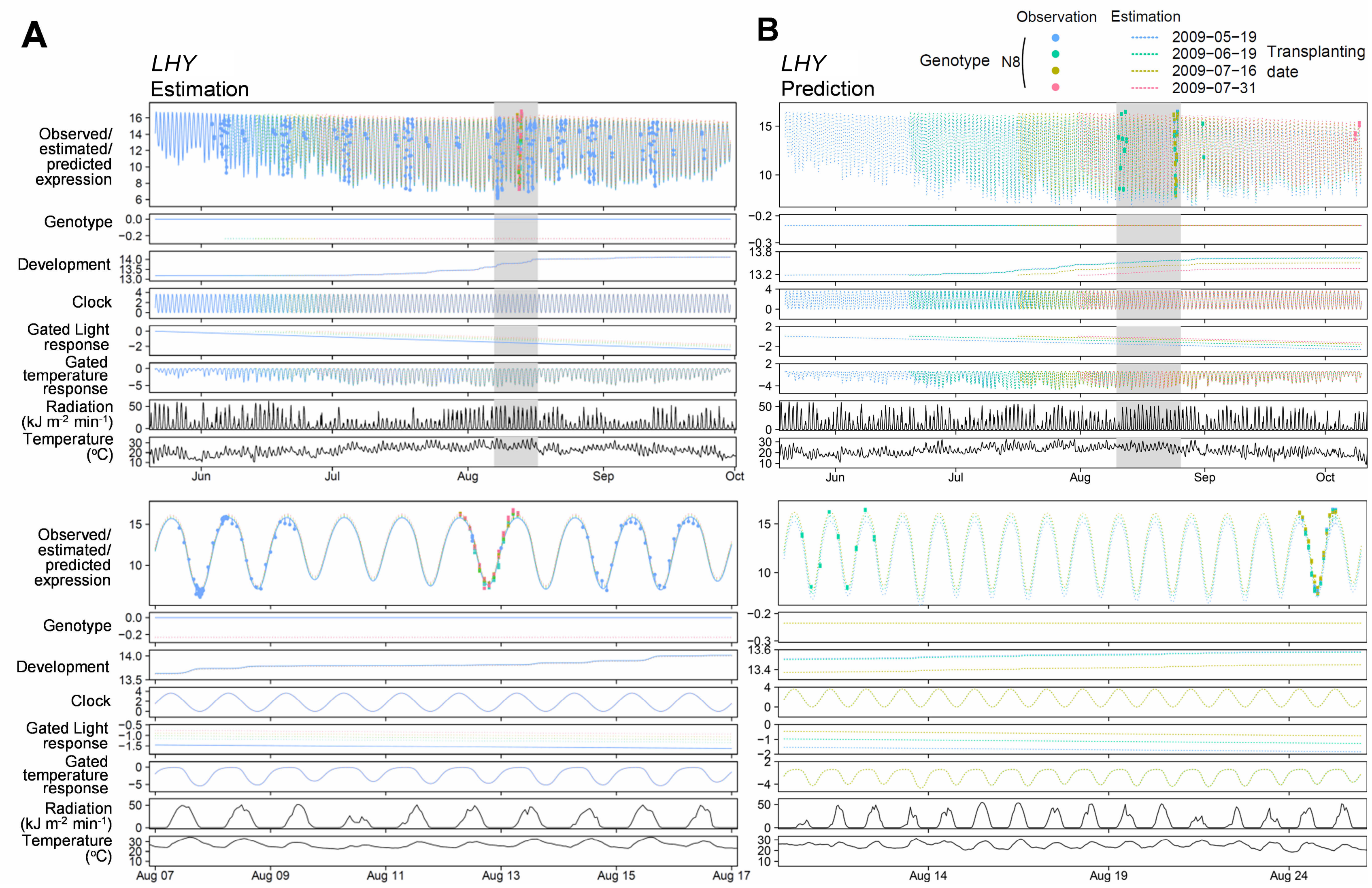
Mutual information between physical (sampling) time of day and estimated expression of the clock-related genes at 10-min intervals during the period when the expression data from training samples was available.



Supplemental Figure 4. A model for *GI*.

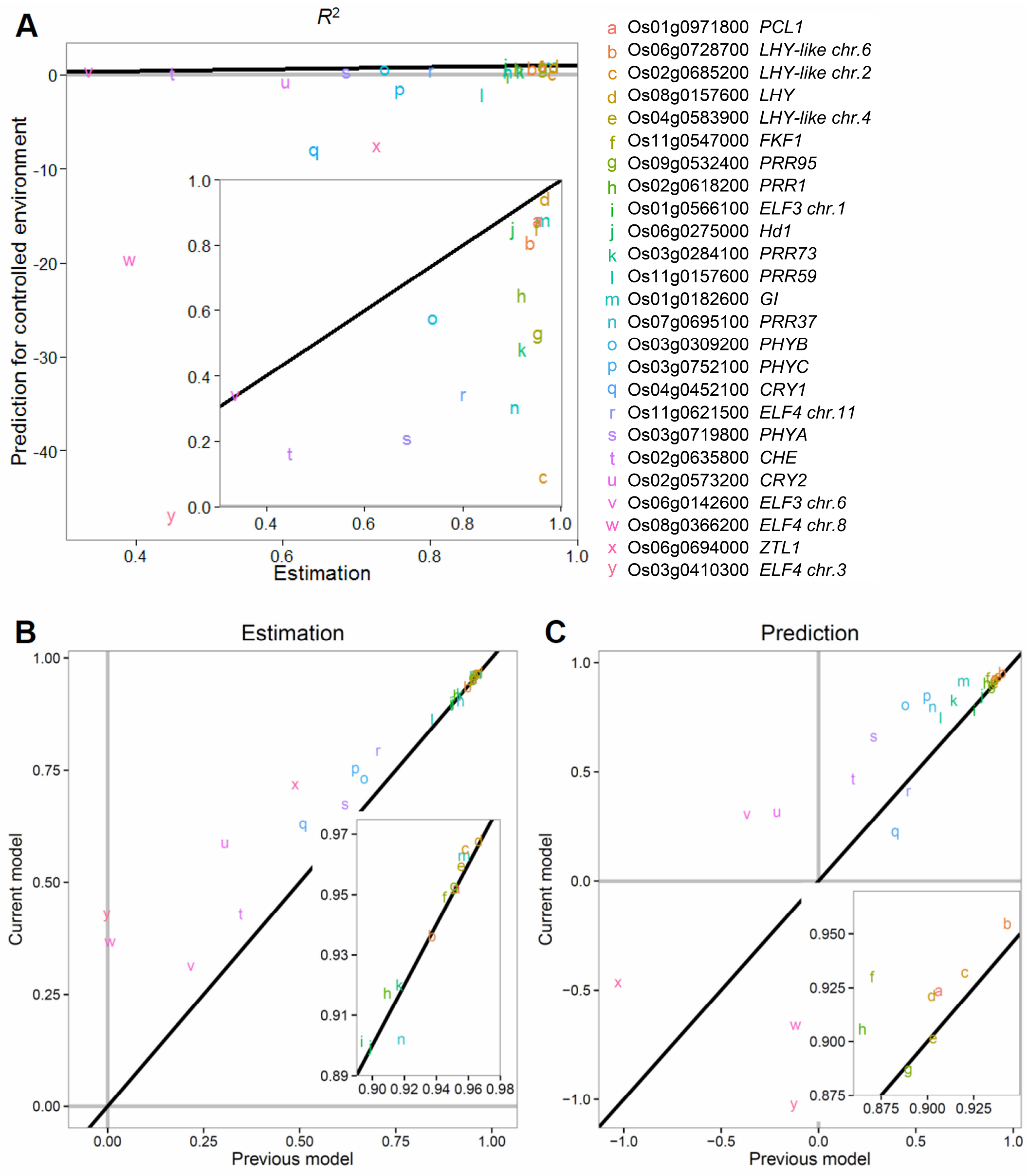
Supplemental Figure 4. A model for *GI*.

(A) Estimation using the training data. Here, the time interval shaded in **Figure 1C** is expanded. **(B)** Prediction using the validation data of solar radiation and ambient temperature, obtained from samples taken in a year other than that for the training data. Time intervals shaded in the upper panel is expanded in the lower panels. Nip, ‘Nipponbare’; N8, ‘Norin 8’.



Supplemental Figure 5. A model for *LHY*.

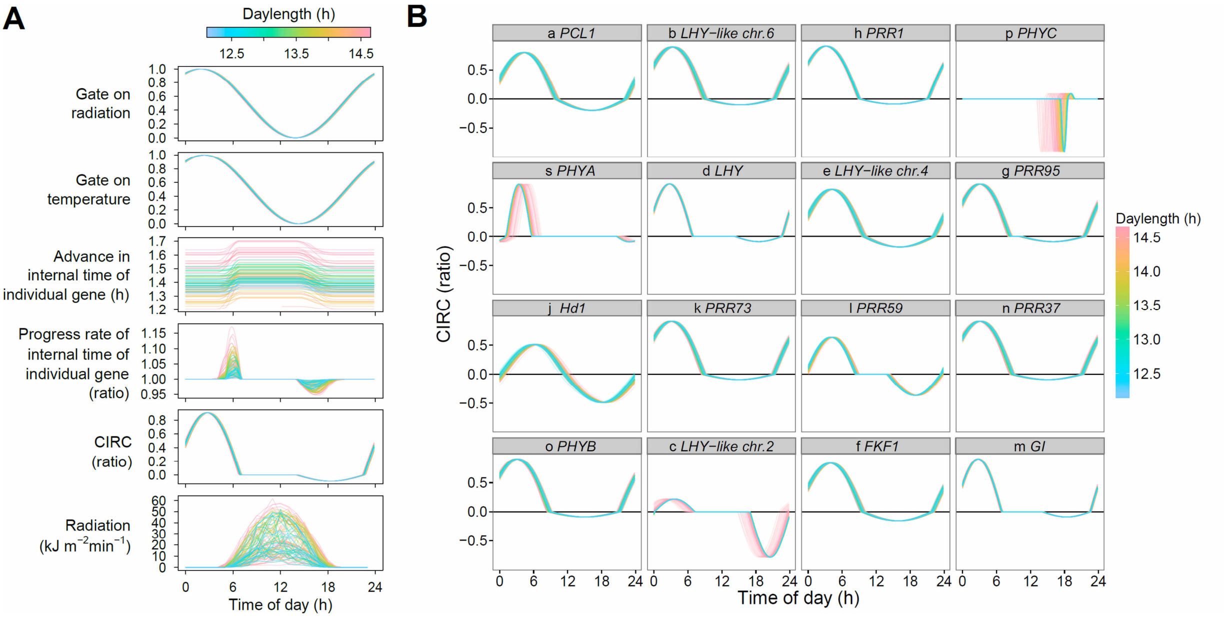
Supplemental Figure 5. A model for *LHY*.
(A) Estimation using the training data. **(B)** Prediction using the validation data of solar radiation and ambient temperature. Corresponding inputs to the linear model are also shown. Time intervals shaded in the upper panels in **A** and **B** are expanded in the lower panels. Nip, ‘Nipponbare’; N8, ‘Norin 8’.



Supplemental Figure 6. Comparison of model performance with datasets under controlled environment and with previous models.

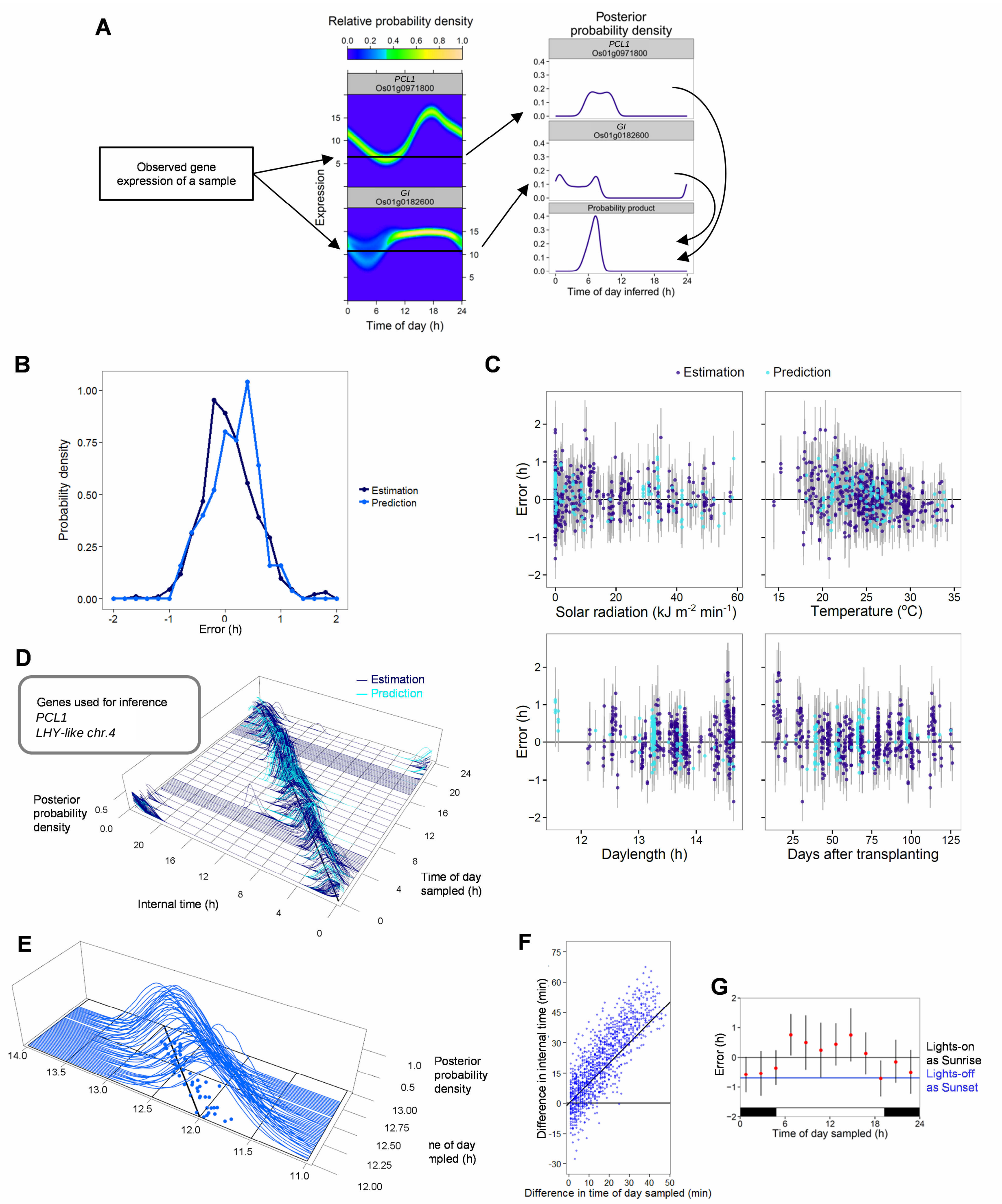
Supplemental Figure 6. Comparison of model performance with datasets under controlled environment and with previous models.

(A) Prediction performance of the models for the clock–related genes for controlled light/dark environment compared with the estimation performance in the field. The estimation performance was for the same training samples (n = 461) as horizontal axis of **Figure 1B**. R^2, the fraction of variance explained by the model relative to variance of the data, was used as an index of fit for each gene model. Genes are listed in the same order as in **Supplemental Figure 3**. **(B)** Comparison of estimation performance (R^2) between the previous model (Nagano et al., 2012) and the current model using the training data. **(C)** Comparison of prediction performance between the previous and the current model using the validation data of solar radiation and ambient temperature.



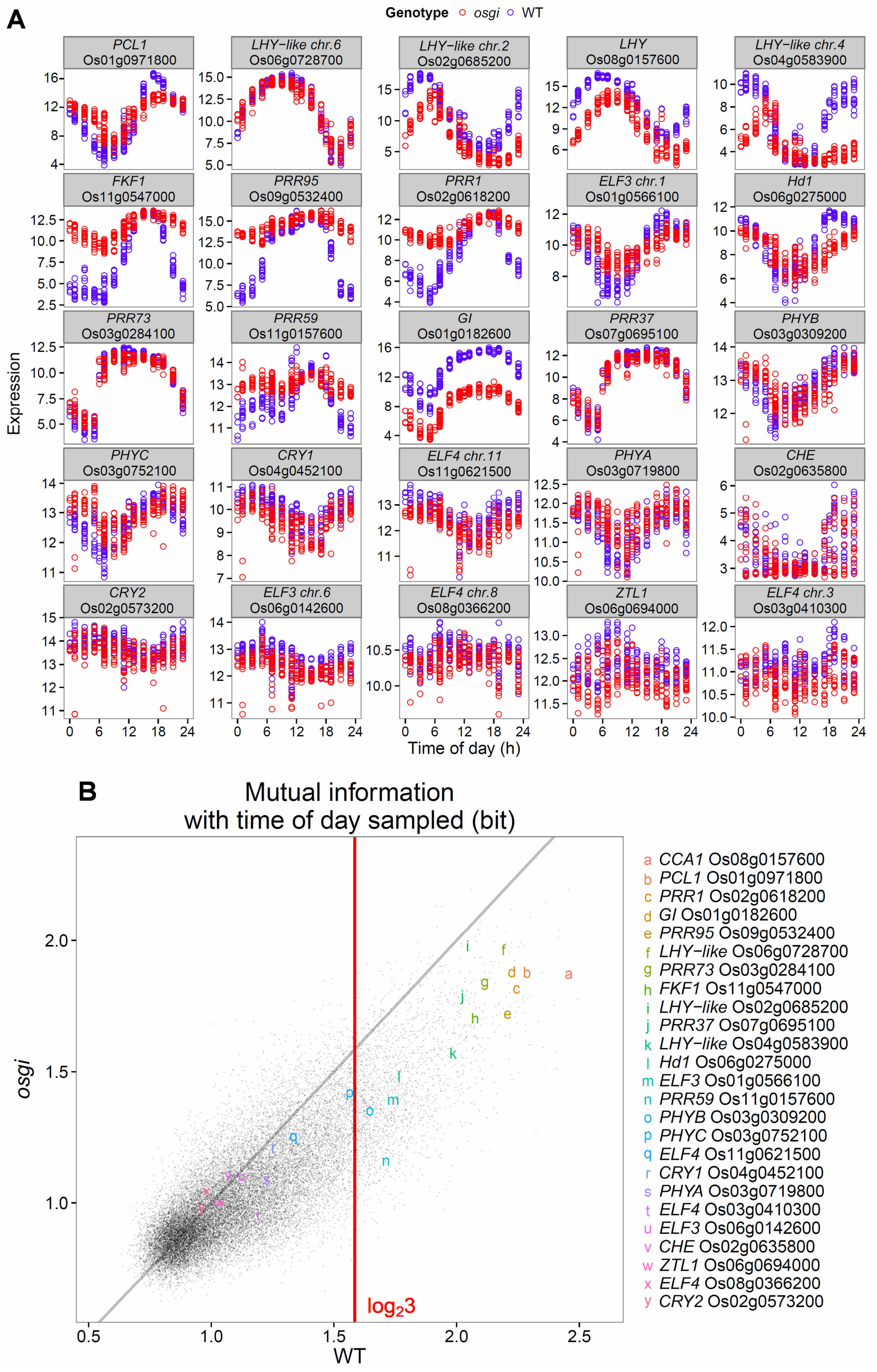
Supplemental Figure 7. Entrainment of the circadian clock to solar radiation in the field.

(A) Features of entrainment for *GI*. Each curve corresponds to the time course for each day during sampling period, June to September 2008. Day-length in this figure was the astronomical estimate at the longitude, latitude and altitude where the samples were taken (National Astronomical Observatory of Japan). Gate on radiation and gate on temperature indicate diurnal sensitivity to solar radiation and ambient temperature regulated by the circadian clock in the model, respectively. These corresponds to $\{1 + g_L\ C_L(t)\} / 2$ and $\{1 + g_T\ C_T(t)\} / 2$ of **Eq. 5** and **6** in Methods, respectively. Advance in internal time of individual gene indicates the difference between internal time of individual gene and physical time of day. Progress rate of internal time of individual gene indicates the change of internal time of individual gene per unit physical time. CIRC, circadian integrated response characteristic (Ronneberg et al., 2010). This is change in progress rate of internal time of individual gene per unit response to solar radiation dependent on the internal time of individual gene, which corresponds to $S(\varphi)$ of **Eq. 3** and **4** in Methods. **(B)** Estimated CIRC for clock–related genes. Each curve corresponds to the time course showing advances or delays of the internal time of individual gene for each day. Letters preceding gene names correspond to those in **Figure 1B**.



Supplemental Figure 8. Processes and results of Bayesian inference of internal time.

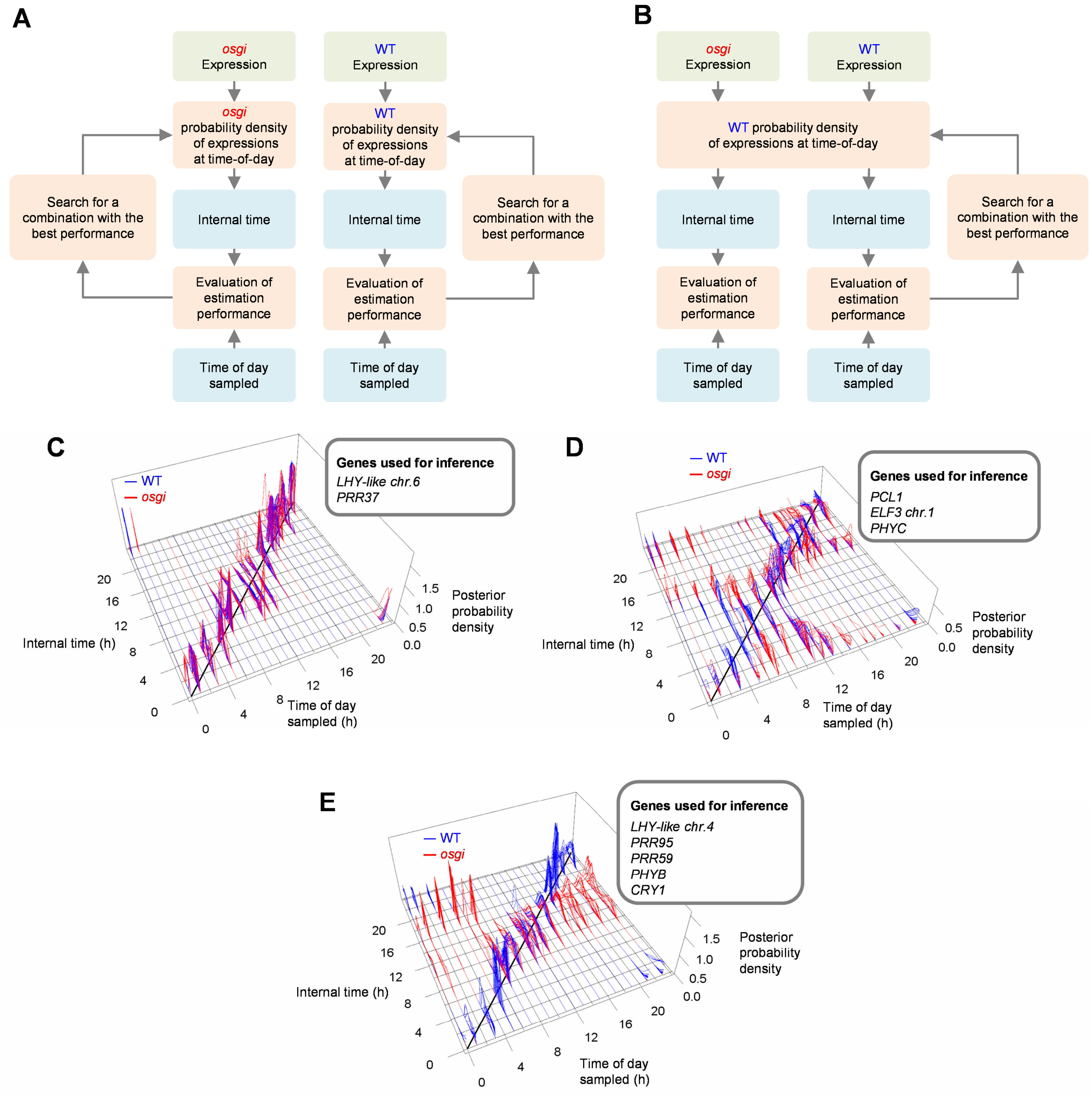
Supplemental Figure 8. Processes and results of Bayesian inference of internal time.
(A) Scheme for obtaining posterior distribution of time of day from the observed gene expression levels by using probability density distributions of gene expression as a function of physical (sampling) time of day for each gene. **(B)** Distribution of error for the combination of genes with the best estimation performance (**Figure 3C**). The error here is a difference between the expectation of internal time (mean of time of day weighted with posterior probabilities) and time of day sampled. The estimation is for training samples (*n* = 461) and the prediction is for validation samples (*n* = 125). **(C)** Relationships between estimation and prediction error for the combination of genes with the best estimation performance (**Figure 3C**) and solar radiation, ambient temperature, astronomical daylength (National Astronomical Observatory of Japan, http://eco.mtk.nao.ac.jp/cgi-bin/koyomi/koyomix_en.cgi) and days after transplanting when sampled. Points denote expectations and vertical bars denote 90 % credible intervals of posterior distributions for each sample. **(D)** Inference of internal time with the best estimation performance among combinations of two core genes. **(E)** Inference of internal time from 48 validation samples collected at 1-min (or 2-min) intervals. Points indicate expectation, which is the mean of internal time weighted with the posterior probability (indicated by blue curved lines) for each sample. Thick black line indicates coincidence between internal time and time of day sampled. **(F)** Relationship between the difference in time of day sampled and the difference in internal time for all possible pairs of the 48 validation samples. Correct prediction of the sampling order corresponds to the points with positive values for the difference in internal time. **(G)** Prediction error of internal time for samples under a controlled environment. Expectations (red points) and 90% credible intervals (vertical bars) of averaged posterior distributions for respective time of day sampled are shown. Time of day sampled was defined so that lights-on time under the controlled environment corresponded to the average time of sunrise in the field and zero error was shown as the black horizontal line. We also tried to define time of day so that the lights-off time under the controlled environment corresponded to the average time of sunset in the field, and zero error in this case is indicated by the blue horizontal line. White and black bars indicate light and dark periods, respectively. See **Figure 4** for posterior distribution of each sample.



Supplemental Figure 9. Comparison of diurnal gene expression and rhythmicity between the *osgi* mutant and WT.

Supplemental Figure 9. Comparison of diurnal gene expression and rhythmicity between the *osgi* mutant and WT.

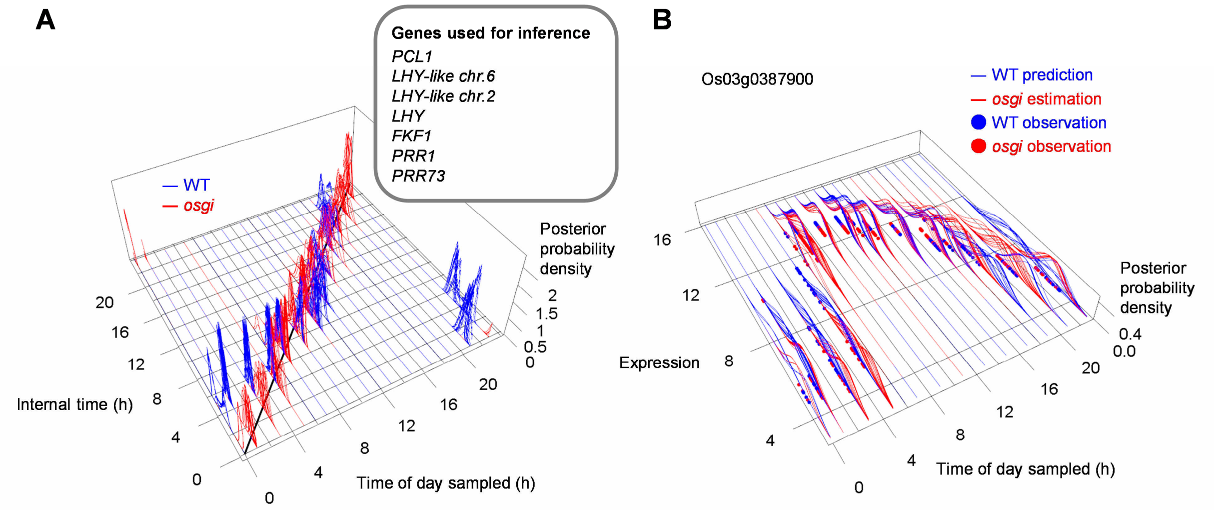
(A) Diurnal expression patterns of 25 clock–related genes in *osgi* and WT (212 pairs of samples with the same timing: 13 time-points in a day, 4 developmental stages, sampling on 12–13/08/2008 and 24–25/08/2009). The genes are listed in order of rhythmicity evaluated as mutual information between the estimated gene expression and time of day (**Supplemental Figure 3**). **(B)** Mutual information between the observed expression of all 23,446 genes on the microarray and physical time of day sampled for *osgi* and WT. The grey line indicates no difference between *osgi* and WT. The genes are listed in order of rhythmicity for WT evaluated as mutual information between the observed gene expression and time of day. By definition of mutual information, we can distinguish a day into three time interval from gene expression with mutual information above $\log_2 3$. Therefore we chose genes with $\geq \log_2 3$ mutual information as the most rhythmic ones (2006 genes; **Figure 6A**).



Supplemental Figure 10. Evaluations of time inference based on gene expression in *osgi* and WT.

Supplemental Figure 10. Evaluations of time inference based on gene expression in *osgi* and WT.

(A) A scheme of time inference for **Figure 5A**. Note that calculation of probability densities of gene expression as a function of time of day sampled and optimization of the set of core genes were performed separately for *osgi* and WT. **(B)** A scheme of time inference for **Figure 5B.** Note that calculations of probability density of gene expression as a function of time of day sampled and optimization of the set of core genes were performed only for WT. **(C–E)** Variation of progression of internal time for *osgi* and WT. Progressions of internal time are shown for the gene combination with **(C)** the least mean absolute error for *osgi*, **(D)** the maximum difference in mean absolute error between *osgi* and WT, and **(E)** the maximum difference in standard deviation between *osgi* and WT.



Supplemental Figure 11. Prediction of WT gene expression of a downstream gene from a combination of core genes that gives the most accurate internal time in *osgi*.

(A) Progression of internal time in WT inferred from the combination of core genes which gives the most accurate internal time relative to physical time in *osgi*. The combination was selected according to the procedure described in *osgi* part of **Supplemental Figure 10A** and its performance was shown in **Figure 5A**. Os-*GI* was excluded from the combination of eight genes shown in **Figure 5A** and the other seven genes indicated were used for the inference. The internal time was inferred based on probability density of expression at time-of-day for *osgi*, in contrast to that for WT in **Figure 6A-C**. **(B)** WT Expression of a downstream gene (Os03g0387900) predicted from internal time inferred in **(A),** based on probability density of Os03g0387900 expression at time-of-day for *osgi*, in contrast to that for WT in **Figure 6A-C**.

Supplemental Table 1. Circadian clock-related genes analysed in this study and corresponding Figures.

Gene	OsID	"Clock-related genes"	"Core genes"	Figure											
				1		2	3				4	5	6		7
				B	C	A,B	A	B,D	C,E	F		A,B	A	B, C	A-I
PCL1	Os01g0971800	X	X		X	X	X	X	X	X	X	X	X	X	X
LHY chr.6	Os06g0728700	X	X		X	X	X	X	X	X	X	X	X	X	X
LHY chr.2	Os02g0685200	X	X		X	X	X	X	X	X	X	X	X		X
LHY	Os08g0157600	X	X		X	X	X	X	X	X	X	X	X	X	X
LHY chr.4	Os04g0583900	X	X		X	X	X	X	X	X		X	X		X
FKF1	Os11g0547000	X			X	X	X	X	X	X	X	X			
PRR95	Os09g0532400	X	X		X	X	X	X	X	X	X	X	X		X
PRR1	Os02g0618200	X	X		X	X	X	X	X	X	X	X	X		X
ELF3 chr.1	Os01g0566100	X	X		X		X	X		X		X	X	X	X
Hd1	Os06g0275000	X			X	X	X	X	X	X	X	X			
PRR73	Os03g0284100	X	X		X	X	X	X	X	X	X	X	X	X	X
PRR59	Os11g0157600	X	X		X	X	X	X		X		X	X	X	X
GI	Os01g0182600	X	X	X	X	X	X	X	X	X	X	X	X		X
PRR37	Os07g0695100	X	X		X	X	X	X	X	X	X	X	X		X
PHYB	Os03g0309200	X	X		X	X	X	X	X	X	X	X	X	X	X
PHYC	Os03g0752100	X	X		X	X	X	X	X	X	X	X	X		X
CRY1	Os04g0452100	X	X		X		X	X		X		X	X	X	X
ELF4 chr.11	Os11g0621500	X			X		X	X	X	X	X	X			
PHYA	Os03g0719800	X			X	X	X	X	X	X	X	X			
CHE	Os02g0635800	X			X		X	X		X		X			
CRY2	Os02g0573200	X			X		X			X		X			
ELF3 chr.6	Os06g0142600	X			X		X			X		X			
ELF4 chr.8	Os08g0366200	X			X		X			X		X			
ZTL1	Os06g0694000	X			X		X			X		X			
ELF4 chr.3	Os03g0410300	X			X		X			X		X			

X, denoted by the term or used in the analysis presented in the indicated figure. The genes are listed in order of rhythmicity evaluated as mutual information between the estimated gene expression and time of day (**Supplemental Fig. 3**).

Supplemental Table 2. Circadian clock-related genes analysed in this study and corresponding Supplemental Figures.

Gene	OsID	“Clock-related genes”	“Core genes”	Supplemental Figure															
				3	4	5	6		7		8				9	10			11
					A, B	A, B	A	B, C	A	B	A	B, C, E-F	D	G	A, B	C	D	E	A, B
PCL1	Os01g0971800	X	X	X			X	X		X	X	X	X	X	X		X		X
LHY chr.6	Os06g0728700	X	X	X			X	X		X		X		X	X	X			X
LHY chr.2	Os02g0685200	X	X	X			X	X		X		X		X	X				X
LHY	Os08g0157600	X	X	X		X	X	X		X		X		X	X				X
LHY chr.4	Os04g0583900	X	X	X				X		X		X	X		X			X	
FKF1	Os11g0547000	X		X			X	X		X		X		X	X				X
PRR95	Os09g0532400	X	X	X			X	X		X		X		X	X			X	
PRR1	Os02g0618200	X	X	X			X	X		X		X		X	X				X
ELF3 chr.1	Os01g0566100	X	X	X			X	X							X		X		
Hd1	Os06g0275000	X		X			X	X		X		X		X	X				
PRR73	Os03g0284100	X	X	X			X	X		X		X		X	X				X
PRR59	Os11g0157600	X	X	X			X	X		X					X			X	
GI	Os01g0182600	X	X	X	X		X	X	X	X	X	X		X	X				
PRR37	Os07g0695100	X	X	X			X	X		X		X		X	X	X			
PHYB	Os03g0309200	X	X	X			X	X		X		X		X	X			X	
PHYC	Os03g0752100	X	X	X			X	X		X		X		X	X		X		
CRY1	Os04g0452100	X	X	X			X	X							X			X	
ELF4 chr.11	Os11g0621500	X		X			X	X				X		X	X				
PHYA	Os03g0719800	X		X			X	X		X		X		X	X				
CHE	Os02g0635800	X		X			X	X							X				
CRY2	Os02g0573200	X		X			X	X							X				
ELF3 chr.6	Os06g0142600	X		X			X	X							X				
ELF4 chr.8	Os08g0366200	X		X			X	X							X				
ZTL1	Os06g0694000	X		X			X	X							X				
ELF4 chr.3	Os03g0410300	X		X			X	X							X				

X, denoted by the term or used in the analysis presented in the indicated figure. The genes are listed in order of rhythmicity evaluated as mutual information between the estimated gene expression and time of day (**Supplemental Fig. 3**).

Supplemental Table 3. Circadian clock-related genes analysed in this study and corresponding Supplemental Tables and Data Set.

Gene	OsID	"Clock-related genes"	"Core genes"	Supplemental Table						Supplemental Data Set
				7	8	9	10	11	12	1
PCL1	Os01g0971800	X	X	X	X	X	X	X	X	X
LHY chr.6	Os06g0728700	X	X	X	X	X	X	X	X	X
LHY chr.2	Os02g0685200	X	X	X	X	X	X	X	X	X
LHY	Os08g0157600	X	X	X	X	X	X	X	X	X
LHY chr.4	Os04g0583900	X	X	X	X	X	X	X	X	X
FKF1	Os11g0547000	X		X		X	X	X	X	X
PRR95	Os09g0532400	X	X	X	X	X	X	X	X	X
PRR1	Os02g0618200	X	X	X	X	X	X	X	X	X
ELF3 chr.1	Os01g0566100	X	X	X	X	X	X	X	X	X
Hd1	Os06g0275000	X		X		X	X	X	X	X
PRR73	Os03g0284100	X	X	X	X	X	X	X	X	X
PRR59	Os11g0157600	X	X	X	X	X	X	X	X	X
GI	Os01g0182600	X	X	X	X	X	X	X	X	X
PRR37	Os07g0695100	X	X	X	X	X	X	X	X	X
PHYB	Os03g0309200	X	X	X	X	X	X	X	X	X
PHYC	Os03g0752100	X	X	X	X	X	X	X	X	X
CRY1	Os04g0452100	X	X	X	X	X	X	X	X	X
ELF4 chr.11	Os11g0621500	X		X	X	X	X	X	X	X
PHYA	Os03g0719800	X		X	X	X	X	X	X	X
CHE	Os02g0635800	X		X		X	X	X	X	X
CRY2	Os02g0573200	X		X		X	X	X	X	
ELF3 chr.6	Os06g0142600	X		X		X	X	X	X	
ELF4 chr.8	Os08g0366200	X		X		X	X	X	X	
ZTL1	Os06g0694000	X		X		X	X	X	X	
ELF4 chr.3	Os03g0410300	X		X		X	X	X	X	

X, denoted by the term or used in the analysis presented in the indicated table. The genes are listed in order of rhythmicity evaluated as mutual information between the estimated gene expression and time of day (**Supplemental Figure 3**).

Supplemental Table 4. Transcriptome dataset analysed in this study and corresponding Figures.

GEO ID	Reference	Year	Vari-ety	Geno-type	*n*	Figure									
						1	2	3			4	5		6	7
						B, C	A,B	A,B,F	C,D	E		A	B	A-C	A-I
GSE21397	Sato et al. (2011), Nagano et al. (2012)	2008	Nip	WT	51	T	T	T	T	T	T				
GSE36040	Nagano et al. (2012)	2008	Nip	WT	225	T	T	T	T	T	T				
GSE36042	Nagano et al. (2012)	2008	Nip	WT	34	T	T	T	T	T	T				
GSE36043	Nagano et al. (2012)	2008	Nip	WT	28	T	T	T	T	T	T				
GSE36044	Nagano et al. (2012)	2008	Nip	WT	19	T	T	T	T	T	T				
GSE18685 (WT)	Izawa et al. (2011)	2008	N8	WT	104	T	T	T	T	T	T	T	T	T	T
GSE36777 (WT)	Nagano et al. (2012)	2009	N8	WT	108	V			V			T	T	T	T
GSE39520	Nagano et al. (2012)	2010	Nip	WT	17				V						
GSE52120	This study	2008	Nip	WT	48					V					
GSE54525	This study	2013	Kos	WT	26						V				
GSE18685 (*osgi*)	Izawa et al. (2011)	2008	N8	*osgi*	104							T	V	V	V
GSE36777 (*osgi*)	This study	2009	N8	*osgi*	108							T	V	V	V

T, used as training data for model fitting and estimation. V, used as validation data for prediction using the model fitted to the training data. Nip, Nipponbare; N8, Norin 8; Kos, Koshihikari.

Supplemental Table 5. Transcriptome dataset analysed in this study and corresponding Supplemental Figures.

GEO ID	Reference	Year	Variety	Genotype	*n*	Supplemental Figure												
						3	4, 5	6			7	8				9	10	11
							A, B	A	B	C	A, B	A	B-D	E, F	G	A, B	C-E	A, B
GSE21397	Sato et al. (2011), Nagano et al. (2012)	2008	Nip	WT	51	T	T	T	T	T	T	T	T	T	T			
GSE36040	Nagano et al. (2012)	2008	Nip	WT	225	T	T	T	T	T	T	T	T	T	T			
GSE36042	Nagano et al. (2012)	2008	Nip	WT	34	T	T	T	T	T	T	T	T	T	T			
GSE36043	Nagano et al. (2012)	2008	Nip	WT	28	T	T	T	T	T	T	T	T	T	T			
GSE36044	Nagano et al. (2012)	2008	Nip	WT	19	T	T	T	T	T	T	T	T	T	T			
GSE18685 (WT)	Izawa et al. (2011)	2008	N8	WT	104	T	T	T	T	T	T	T	T	T	T	R	T	V
GSE36777 (WT)	Nagano et al. (2012)	2009	N8	WT	108		V			V			V			R	T	V
GSE39520	Nagano et al. (2012)	2010	Nip	WT	17					V			V					
GSE52120	This study	2008	Nip	WT	48									V				
GSE54525	This study	2013	Kos	WT	26			V							V			
GSE18685 (*osgi*)	Izawa et al. (2011)	2008	N8	*osgi*	104											R	V	T
GSE36777 (*osgi*)	This study	2009	N8	*osgi*	108											R	V	T

T, used as training data for model fitting and estimation. V, used as validation data for prediction using the model fitted to the training data. R, raw data are plotted without modeling. Nip, Nipponbare; N8, Norin 8; Kos, Koshihikari.

Supplemental Table 6. Transcriptome dataset analysed in this study and corresponding Supplemental Tables and Data Set.

GEO ID	Reference	Year	Vari-ety	Geno-type	*n*	Supplemental Table						Supplemental Data Set
						7	8	9	10	11	12	1
GSE21397	Sato et al. (2011), Nagano et al. (2012)	2008	Nip	WT	51	T		T	T	T	T	T
GSE36040	Nagano et al. (2012)	2008	Nip	WT	225	T		T	T	T	T	T
GSE36042	Nagano et al. (2012)	2008	Nip	WT	34	T		T	T	T	T	T
GSE36043	Nagano et al. (2012)	2008	Nip	WT	28	T		T	T	T	T	T
GSE36044	Nagano et al. (2012)	2008	Nip	WT	19	T		T	T	T	T	T
GSE18685 (WT)	Izawa et al. (2011)	2008	N8	WT	104	T	T	T	T	T	T	T
GSE36777 (WT)	Nagano et al. (2012)	2009	N8	WT	108		T					V
GSE39520	Nagano et al. (2012)	2010	Nip	WT	17							V
GSE52120	This study	2008	Nip	WT	48							
GSE54525	This study	2013	Kos	WT	26							
GSE18685 (*osgi*)	Izawa et al. (2011)	2008	N8	*osgi*	104		V					
GSE36777 (*osgi*)	This study	2009	N8	*osgi*	108		V					

T, used as training data for model fitting and estimation. V, used as validation data for prediction using the model fitted to the training data. Nip, Nipponbare; N8, Norin 8; Kos, Koshihikari.

Supplemental Table 7. Contributions of the genes to the time inference.

Gene	OsID	Median difference in L-criterion (h)	W-statistic of Wilcoxon signed-rank test	P-value (random permutation test with Bonferroni-correction, log $_{10}$ scale)	Mean of W-statistic for null distribution	Standard deviation of W-statistic for null distribution	P-value of Kolmogorov-Smirnov test for normality
PRR73	Os03g0284100	-0.056	-1.437E+11	-2121.6	-1.419E+11	1.814E+07	0.813
PRR37	Os07g0695100	-0.065	-1.437E+11	-2036.8	-1.420E+11	1.751E+07	0.841
LHY chr.2	Os02g0685200	-0.214	-1.437E+11	-1973.2	-1.422E+11	1.640E+07	0.311
GI	Os01g0182600	-0.106	-1.437E+11	-1958.4	-1.422E+11	1.636E+07	0.702
PHYB	Os03g0309200	-0.062	-1.437E+11	-1920.7	-1.421E+11	1.722E+07	0.866
Hd1	Os06g0275000	-0.106	-1.437E+11	-1879.5	-1.422E+11	1.640E+07	0.810
PRR95	Os09g0532400	-0.097	-1.437E+11	-1871.0	-1.421E+11	1.732E+07	0.893
FKF1	Os11g0547000	-0.155	-1.437E+11	-1686.1	-1.424E+11	1.441E+07	0.863
LHY chr.4	Os04g0583900	-0.174	-1.437E+11	-1655.3	-1.423E+11	1.588E+07	0.750
PCL1	Os01g0971800	-0.256	-1.437E+11	-1528.0	-1.426E+11	1.327E+07	0.106
LHY chr.6	Os06g0728700	-0.202	-1.437E+11	-1507.8	-1.426E+11	1.335E+07	0.748
LHY	Os08g0157600	-0.257	-1.437E+11	-1480.0	-1.426E+11	1.315E+07	0.884
PHYC	Os03g0752100	-0.046	-1.435E+11	-1388.7	-1.421E+11	1.699E+07	0.825
ELF3 chr.1	Os01g0566100	-0.104	-1.435E+11	-1326.1	-1.422E+11	1.649E+07	0.972
PRR1	Os02g0618200	-0.084	-1.435E+11	-1294.9	-1.422E+11	1.651E+07	0.783
PRR59	Os11g0157600	-0.058	-1.427E+11	-278.5	-1.421E+11	1.712E+07	0.941
ELF4 chr.11	Os11g0621500	-0.025	-1.409E+11	1.4	-1.422E+11	1.631E+07	0.060
CRY1	Os04g0452100	-0.021	-1.416E+11	1.4	-1.420E+11	1.763E+07	0.832
CHE	Os02g0635800	-0.010	-1.314E+11	1.4	-1.419E+11	1.856E+07	0.817
PHYA	Os03g0719800	-0.009	-1.331E+11	1.4	-1.419E+11	1.835E+07	0.974
CRY2	Os02g0573200	-0.008	-1.299E+11	1.4	-1.420E+11	1.831E+07	0.294
ELF4 chr.8	Os08g0366200	-0.008	-1.382E+11	1.4	-1.420E+11	1.799E+07	0.667
ELF3 chr.6	Os06g0142600	-0.005	-1.144E+11	1.4	-1.418E+11	1.871E+07	0.596
ELF4 chr.3	Os03g0410300	-0.003	-1.417E+11	1.4	-1.419E+11	1.802E+07	0.764
ZTL1	Os06g0694000	-0.003	-1.249E+11	1.4	-1.418E+11	1.888E+07	0.383

Supplemental Table 8. Downstream genes found, their prediction performance and principal component scores.

OsID	Minimum scaled L-criterion	Bonferroni-corrected P-value of the L-criterion (random permutation test, log$_{10}$ scale)	Mean of L-criterion for null distribution	Standard deviation of L-criterion for null distribution	P-value of Kolmogorov-Smirnov test for normality	PC1 score based on P-value of Wilcoxon's signed-rank test (Figure 7B)	PC2 score based on P-value of Wilcoxon's signed-rank test (Figure 7B)
Os08g0468100	0.424	-34.5	3.048	0.122	0.931	-2.488	-0.198
Os06g0701600	0.491	-44.0	3.443	0.134	0.950	-2.366	-0.282
Os01g0226600	0.452	-45.6	2.529	0.103	0.382	-2.283	-0.788
Os02g0704300	0.438	-38.3	2.633	0.107	0.887	-2.133	-1.731
Os07g0659300	0.445	-41.6	2.723	0.098	0.766	-2.077	-1.052
Os03g0228200	0.331	-34.9	4.932	0.204	0.755	-2.035	-0.181
Os01g0949500	0.436	-39.9	1.771	0.070	0.784	-1.998	-0.838
Os06g0662200	0.488	-41.8	2.090	0.078	0.870	-1.922	0.052
Os02g0116500	0.472	-44.9	0.885	0.033	0.893	-1.796	1.110
Os07g0425000	0.492	-40.6	2.894	0.112	0.938	-1.777	1.028
Os02g0594700	0.399	-40.5	2.186	0.082	0.650	-1.698	-1.076
Os07g0637300	0.424	-48.4	2.725	0.108	0.776	-1.682	-0.342
Os02g0137700	0.355	-31.8	4.305	0.188	0.808	-1.681	-0.806
Os01g0346700	0.429	-38.7	1.421	0.058	0.807	-1.656	-0.860
Os07g0630800	0.407	-40.8	2.561	0.104	0.919	-1.626	-0.451
Os01g0826900	0.477	-50.0	1.923	0.072	0.345	-1.582	-0.962
Os01g0823600	0.441	-41.3	3.760	0.140	0.326	-1.529	-0.891
Os03g0387900	0.249	-44.4	3.166	0.108	0.859	-1.464	-1.988
Os03g0197000	0.427	-49.8	2.027	0.077	0.855	-1.398	1.587
Os02g0816600	0.481	-47.2	2.352	0.088	0.741	-1.388	-0.444
Os03g0625300	0.390	-36.5	2.496	0.102	0.494	-1.384	-2.170
Os08g0557200	0.406	-37.9	3.005	0.124	0.969	-1.279	-0.947
Os08g0157600	0.465	-50.4	3.449	0.120	0.975	-1.189	1.902
Os01g0825500	0.412	-40.9	1.886	0.075	0.921	-1.149	-1.504
Os09g0511600	0.492	-42.8	1.560	0.059	0.847	-1.136	1.939
Os03g0290300	0.473	-45.8	2.499	0.093	0.795	-1.109	0.068
Os04g0578400	0.386	-37.5	3.296	0.130	0.520	-1.056	0.450
Os05g0582300	0.438	-40.5	2.168	0.083	0.934	-0.997	-0.543
Os01g0281100	0.353	-40.4	3.715	0.145	0.912	-0.941	-0.357
Os08g0178800	0.499	-45.7	2.507	0.095	0.364	-0.891	-1.195
Os05g0170950	0.384	-44.5	2.944	0.114	0.443	-0.814	0.138
Os02g0498300	0.451	-41.8	1.868	0.073	0.554	-0.793	1.428
Os07g0448800	0.495	-51.1	1.540	0.057	0.790	-0.785	0.102
Os01g0954000	0.479	-46.8	2.928	0.099	0.755	-0.685	2.369

Supplemental Table 8. (Continued).

OsID	Minimum scaled L-criterion	Bonferroni-corrected P-value of the L-criterion (random permutation test, $\log_{10}$ scale)	Mean of L-criterion for null distribution	Standard deviation of L-criterion for null distribution	P-value of Kolmogorov-Smirnov test for normality	PC1 score based on P-value of Wilcoxon's signed-rank test (Figure 7B)	PC2 score based on P-value of Wilcoxon's signed-rank test (Figure 7B)
Os05g0510100	0.482	-47.2	1.102	0.040	0.955	-0.675	1.485
Os03g0230500	0.499	-45.8	1.348	0.050	0.669	-0.641	1.288
Os05g0534400	0.485	-46.7	2.032	0.075	0.962	-0.591	1.211
Os01g0846800	0.351	-34.1	4.273	0.173	0.959	-0.541	0.171
Os10g0510500	0.490	-40.1	2.699	0.112	0.835	-0.535	-2.696
Os12g0577600	0.407	-46.2	2.335	0.083	0.455	-0.458	2.614
Os01g0804400	0.484	-44.1	2.458	0.092	0.952	-0.384	-0.278
Os05g0586600	0.390	-40.8	3.186	0.129	0.669	-0.338	-0.154
Os03g0176700	0.490	-50.6	2.198	0.078	0.720	-0.191	0.860
Os12g0132800	0.468	-49.8	2.294	0.085	0.579	-0.021	1.715
Os01g0266800	0.436	-44.5	2.914	0.109	0.832	0.024	1.525
Os04g0578200	0.409	-40.9	2.194	0.082	0.997	0.398	2.085
Os06g0133100	0.478	-42.1	3.044	0.126	0.675	0.453	-2.807
Os05g0561600	0.424	-45.8	1.897	0.073	0.924	0.510	1.146
Os01g0767600	0.407	-33.8	2.099	0.092	0.654	0.611	-2.509
Os06g0712300	0.489	-56.7	1.172	0.041	0.880	0.673	1.856
Os03g0807900	0.467	-56.5	1.394	0.047	0.431	0.724	0.950
Os01g0700100	0.409	-41.1	4.129	0.159	0.791	0.927	1.327
Os06g0554200	0.400	-33.1	4.055	0.169	0.834	1.119	-3.147
Os07g0617700	0.483	-52.8	2.888	0.101	0.510	1.243	1.814
Os03g0592500	0.432	-39.9	3.407	0.143	0.847	1.248	-2.875
Os09g0553800	0.461	-50.7	1.268	0.048	0.194	1.926	2.617
Os01g0817000	0.474	-52.2	1.263	0.044	0.961	2.293	2.499
Os05g0365600	0.495	-55.0	1.776	0.062	0.561	2.544	2.347
Os09g0346500	0.431	-33.0	3.863	0.171	0.593	2.575	-3.330
Os08g0249000	0.492	-44.2	3.303	0.132	0.872	2.978	-6.563
Os02g0643000	0.470	-49.9	1.340	0.049	0.993	3.036	1.456
Os01g0228400	0.419	-41.0	2.082	0.075	0.931	3.167	2.292
Os02g0827400	0.488	-51.0	3.641	0.129	0.976	3.597	2.047
Os12g0512100	0.496	-44.5	3.135	0.113	0.660	3.715	2.300
Os04g0679900	0.492	-44.3	1.413	0.052	0.930	4.067	2.514
Os03g0703300	0.478	-44.1	1.586	0.059	0.722	4.885	0.347
Os04g0448900	0.437	-40.5	2.363	0.094	0.897	5.326	-4.395
Os10g0330400	0.496	-46.5	2.806	0.104	0.959	7.125	-2.278

PC, principal component. NA, not available.

Supplemental Table 9. Coefficients for the terms in the linear model.

Gene	OsID	Clock (β_C)	Gated light response (β_L)	Gated temperature response (β_T)	Development (β_D)	Genotype (β_G)
PCL1	Os01g0971800	-7.30E+00	1.75E-04	-7.61E-02	NA	-3.16E-01
LHY chr.6	Os06g0728700	5.26E+00	6.04E-03	8.38E-02	-8.28E-08	-3.91E-01
LHY chr.2	Os02g0685200	NA	2.46E-02	-5.49E-03	1.95E-05	-4.39E-01
LHY	Os08g0157600	3.64E+00	-4.39E-07	-9.22E-04	2.88E-05	-2.35E-01
LHY chr.4	Os04g0583900	-2.06E+00	NA	-5.85E-02	1.98E-04	-2.17E-01
FKF1	Os11g0547000	NA	8.61E-03	-4.83E-03	NA	2.50E-01
PRR95	Os09g0532400	1.52E+00	1.72E-02	8.93E-02	4.51E-06	-2.73E-01
PRR1	Os02g0618200	7.85E+00	2.29E-03	-1.97E-03	8.76E-08	-6.26E-01
ELF3 chr.1	Os01g0566100	-7.98E+00	2.57E-05	-9.31E-04	-2.34E-05	5.95E-01
Hd1	Os06g0275000	-2.32E+00	NA	-3.34E-03	1.03E-05	NA
PRR73	Os03g0284100	3.42E+00	2.01E-01	-1.31E-03	-8.99E-07	4.00E-01
PRR59	Os11g0157600	2.18E+00	1.29E+06	-2.55E-03	1.33E-05	NA
GI	Os01g0182600	NA	5.29E-03	-1.42E-03	1.44E-05	5.69E-01
PRR37	Os07g0695100	1.74E+00	2.50E-01	-9.47E-03	-1.43E-06	3.42E-01
PHYB	Os03g0309200	-1.17E+00	7.05E-05	-1.33E-02	NA	NA
PHYC	Os03g0752100	-1.21E+00	-1.95E-02	2.47E-04	1.35E-05	NA
CRY1	Os04g0452100	-5.94E-01	-5.70E-04	-3.12E+00	1.12E-05	NA
ELF4 chr.11	Os11g0621500	-4.69E-01	-1.26E+06	4.59E-04	5.14E-08	3.82E-01
PHYA	Os03g0719800	-5.62E-01	-2.98E-02	1.77E-03	1.27E-07	-2.08E-01
CHE	Os02g0635800	NA	-1.30E-03	1.01E-01	-1.42E-07	NA
CRY2	Os02g0573200	7.23E-01	4.32E-05	-9.45E-03	1.25E-07	2.82E-01
ELF3 chr.6	Os06g0142600	6.73E-01	1.26E-05	8.84E-04	NA	NA
ELF4 chr.8	Os08g0366200	-2.56E-01	5.46E-03	-2.55E-04	2.40E-05	NA
ZTL1	Os06g0694000	2.64E-01	1.08E-02	-1.19E-03	1.47E-07	NA
ELF4 chr.3	Os03g0410300	7.09E-01	-1.25E-03	-3.22E-02	1.01E-04	NA

In parenthesis is symbols in the model description. NA, not available. The term is excluded in the final model.

Supplemental Table 10. Parameters for the development and clock terms.

		Development			Clock			
Gene	OsID	Initial value (D_1, [0, 2^{20}])	Gain (a_D, [0, 30])	Intercept (b_D, range of the relative temperature)	Response window (w, [0.1, 1])	Asymmetry in response (q, [0.1, 10])	Gain (a_C, [0, 8])	Phase (p_C, [0, 2π])
PCL1	Os01g0971800	NA	NA	NA	1.00	4.01	4.91	1.03
LHY chr.6	Os06g0728700	NA	29.46	0.02	1.00	8.54	8.00	1.44
LHY chr.2	Os02g0685200	1.02E+06	29.83	1.00	0.59	0.28	2.46	NA
LHY	Os08g0157600	4.58E+05	30.00	0.74	0.69	9.99	8.00	0.50
LHY chr.4	Os04g0583900	4.96E+04	29.99	0.84	1.00	4.44	4.97	2.83
FKF1	Os11g0547000	NA	NA	NA	1.00	5.36	5.03	NA
PRR95	Os09g0532400	1.05E+06	6.61	1.00	0.92	9.91	8.00	3.14
PRR1	Os02g0618200	NA	18.53	0.00	1.00	10.00	3.35	2.61
ELF3 chr.1	Os01g0566100	NA	0.08	0.25	1.00	5.75	5.10	0.62
Hd1	Os06g0275000	1.05E+06	9.80	1.00	1.00	1.05	7.33	0.40
PRR73	Os03g0284100	NA	30.00	0.58	1.00	10.00	7.53	2.99
PRR59	Os11g0157600	1.05E+06	16.34	1.00	0.77	1.75	8.00	0.00
GI	Os01g0182600	1.03E+06	29.95	1.00	0.70	10.00	8.00	NA
PRR37	Os07g0695100	NA	29.99	0.63	1.00	10.00	8.00	3.14
PHYB	Os03g0309200	NA	NA	NA	1.00	9.99	8.00	0.53
PHYC	Os03g0752100	1.05E+06	12.44	1.00	0.10	0.10	1.42	1.71
CRY1	Os04g0452100	1.01E+06	30.00	1.00	0.47	0.72	2.96	3.06
ELF4 chr.11	Os11g0621500	9.45E+05	29.40	0.15	0.99	9.55	4.53	2.40
PHYA	Os03g0719800	NA	30.00	0.42	0.37	9.39	3.75	0.09
CHE	Os02g0635800	NA	0.00	0.78	1.00	8.13	8.00	NA
CRY2	Os02g0573200	NA	29.96	0.37	0.46	1.31	6.93	0.30
ELF3 chr.6	Os06g0142600	NA	NA	NA	1.00	9.95	7.99	0.35
ELF4 chr.8	Os08g0366200	1.05E+06	24.39	0.84	0.22	10.00	2.09	0.49
ZTL1	Os06g0694000	NA	29.89	0.32	1.00	2.11	8.00	1.70
ELF4 chr.3	Os03g0410300	1.05E+06	30.00	0.80	0.61	2.11	7.97	2.25

In parenthesis are symbols in the model description with search range. NA, not available. For the initial values, fixed to 0 in the final model. For the other parameters, the term is excluded in the final model.

Supplemental Table 11. Parameters for the gated light response term.

Gene	OsID	Initial value (L_0, [0, 2^{20}])	Phase of the gate (p_L, [0, 2π])	Ampulitude of the gate (g_L, [0, 1])	Gain (a_L, [0, 30])	Intercept (b_L, range of the relative radiation)	Decay (k_L, [0, n(2)/60])
PCL1	Os01g0971800	1.05E+06	0.08	0.178	0.0	0.07	4.43E-06
LHY chr.6	Os06g0728700	NA	4.38	1.000	3.7	0.00	9.89E-04
LHY chr.2	Os02g0685200	NA	3.16	1.000	30.0	0.00	1.12E-02
LHY	Os08g0157600	NA	6.11	0.858	0.1	0.60	0.00E+00
LHY chr.4	Os04g0583900	NA	NA	NA	NA	NA	NA
FKF1	Os11g0547000	NA	5.06	1.000	2.1	0.99	6.98E-05
PRR95	Os09g0532400	3.96E+03	2.07	0.999	30.0	0.76	2.78E-06
PRR1	Os02g0618200	NA	5.47	1.000	7.9	0.00	1.65E-04
ELF3 chr.1	Os01g0566100	1.05E+06	0.03	1.000	0.3	0.49	0.00E+00
Hd1	Os06g0275000	NA	NA	NA	NA	NA	NA
PRR73	Os03g0284100	NA	5.98	1.000	6.5	0.00	1.16E-02
PRR59	Os11g0157600	NA	4.62	1.000	30.0	0.86	4.28E-05
GI	Os01g0182600	NA	5.60	1.000	30.0	0.07	2.84E-03
PRR37	Os07g0695100	NA	5.95	1.000	4.4	0.00	1.16E-02
PHYB	Os03g0309200	2.41E+05	3.35	0.993	0.7	0.99	1.73E-06
PHYC	Os03g0752100	NA	1.81	1.000	30.0	0.00	1.15E-02
CRY1	Os04g0452100	NA	4.25	0.893	30.0	0.00	3.07E-04
ELF4 chr.11	Os11g0621500	4.22E+04	5.43	0.494	23.4	1.00	3.39E-03
PHYA	Os03g0719800	NA	4.47	0.991	10.7	0.00	1.15E-02
CHE	Os02g0635800	NA	4.63	1.000	18.5	0.00	5.83E-04
CRY2	Os02g0573200	3.44E+05	0.07	0.826	0.0	0.91	1.63E-06
ELF3 chr.6	Os06g0142600	9.83E+05	1.84	1.000	23.7	0.60	3.81E-09
ELF4 chr.8	Os08g0366200	NA	6.28	1.000	16.5	0.02	1.15E-02
ZTL1	Os06g0694000	NA	5.42	1.000	0.5	0.01	4.07E-04
ELF4 chr.3	Os03g0410300	NA	3.43	1.000	30.0	0.00	1.42E-03

In parenthesis are symbols in the model description with search range. NA, not available. For the initial values, fixed to 0 in the final model. For the other parameters, the term is excluded in the final model.

Supplemental Table 12. Parameters for the gated temperature response term.

Gene	OsID	Initial value (T_0, [0, 2^{20}])	Phase of the gate (p_T, [0, 2π])	Ampulitude of the gate (g_T, [0, 1])	Gain (a_T, [0, 30])	Intercept (b_T, range of the relative temperature)	Decay (k_T, [0, ln(2)/60])
PCL1	Os01g0971800	NA	0.00	0.951	23.3	0.045	1.15E-02
LHY chr.6	Os06g0728700	NA	1.24	1.000	25.5	0.000	1.15E-02
LHY chr.2	Os02g0685200	NA	2.27	0.871	6.7	0.188	3.14E-04
LHY	Os08g0157600	NA	3.37	0.939	12.2	0.417	1.49E-04
LHY chr.4	Os04g0583900	NA	1.68	1.000	16.8	0.318	1.16E-02
FKF1	Os11g0547000	NA	6.06	0.956	15.9	0.178	4.63E-04
PRR95	Os09g0532400	NA	2.21	1.000	24.4	0.163	1.15E-02
PRR1	Os02g0618200	NA	1.35	1.000	5.8	0.460	2.22E-04
ELF3 chr.1	Os01g0566100	NA	2.38	1.000	10.6	0.000	5.41E-05
Hd1	Os06g0275000	NA	1.02	1.000	24.1	0.356	1.06E-03
PRR73	Os03g0284100	NA	5.93	1.000	30.0	0.411	2.68E-04
PRR59	Os11g0157600	NA	5.60	0.695	18.5	0.157	5.68E-04
GI	Os01g0182600	NA	5.71	1.000	14.6	0.416	1.25E-04
PRR37	Os07g0695100	NA	0.00	1.000	10.0	0.530	6.65E-04
PHYB	Os03g0309200	NA	2.29	1.000	17.5	0.154	1.15E-02
PHYC	Os03g0752100	NA	2.63	1.000	13.2	0.458	1.70E-04
CRY1	Os04g0452100	1.05E+06	3.51	1.000	30.0	1.000	1.41E-05
ELF4 chr.11	Os11g0621500	4.46E+05	4.77	1.000	0.7	0.559	1.68E-05
PHYA	Os03g0719800	NA	3.89	0.513	30.0	0.008	1.37E-04
CHE	Os02g0635800	NA	4.44	0.690	1.8	0.000	1.16E-02
CRY2	Os02g0573200	NA	1.29	0.677	30.0	0.104	1.13E-02
ELF3 chr.6	Os06g0142600	NA	2.18	0.976	30.0	0.762	5.31E-06
ELF4 chr.8	Os08g0366200	NA	1.95	0.619	30.0	0.000	1.69E-05
ZTL1	Os06g0694000	NA	1.63	0.061	30.0	0.154	5.56E-04
ELF4 chr.3	Os03g0410300	NA	0.80	0.056	30.0	0.000	3.39E-04

In parenthesis are symbols in the model description with search range. NA, not available. For the initial values, fixed to 0 in the final model. For the other parameters, the term is excluded in the final model.