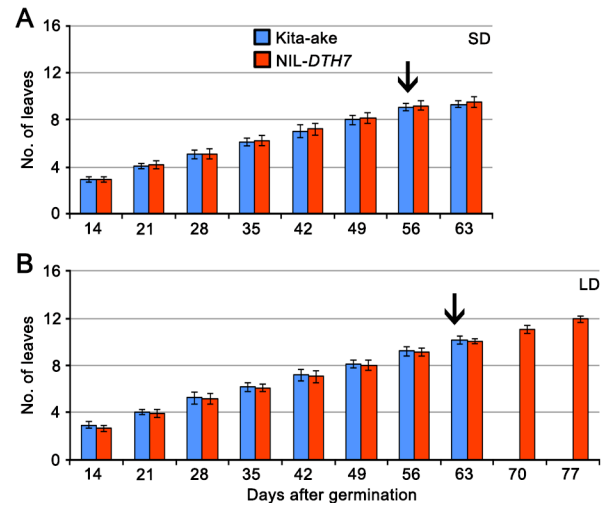
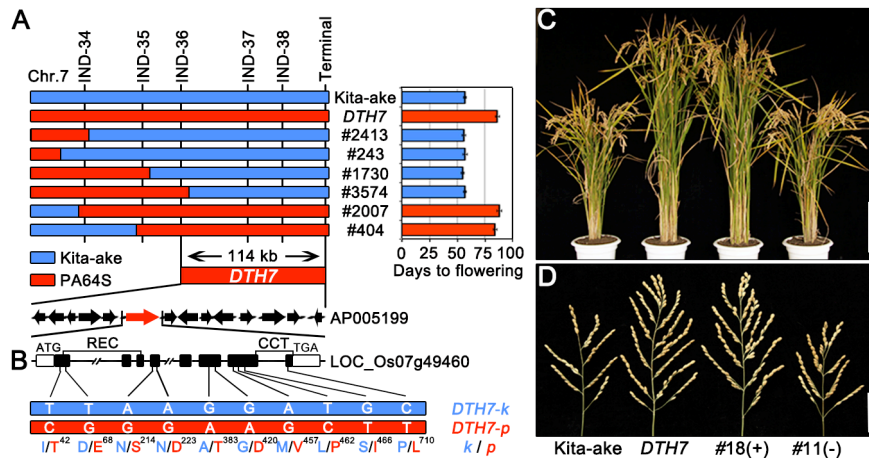


# Supporting Information

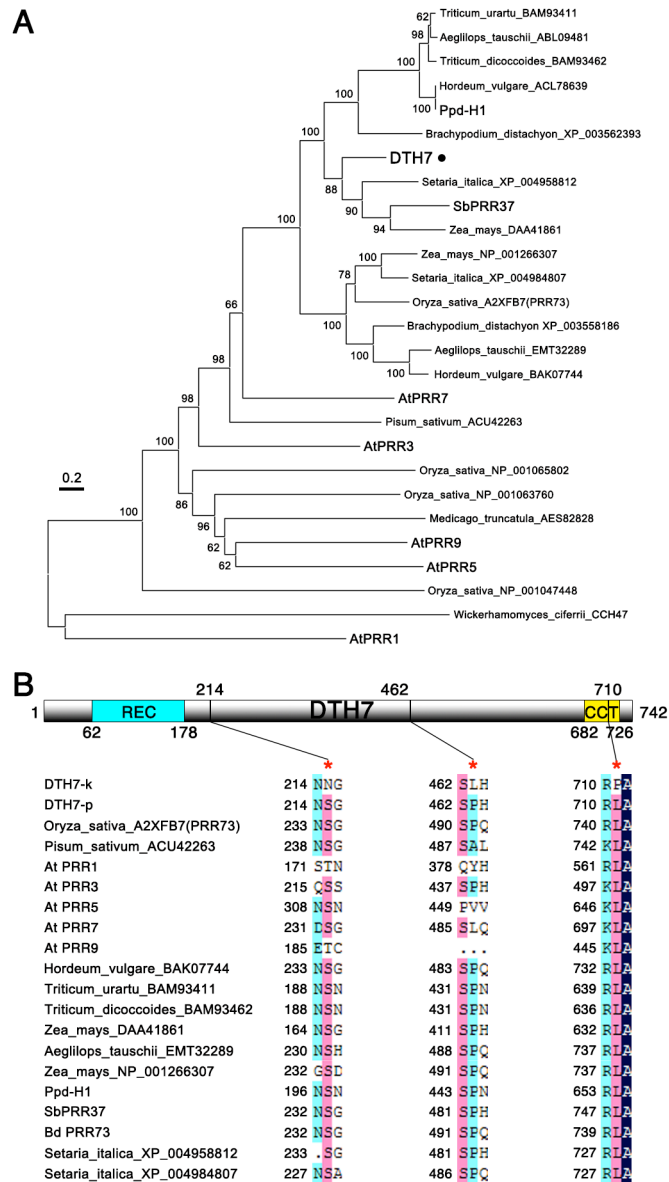
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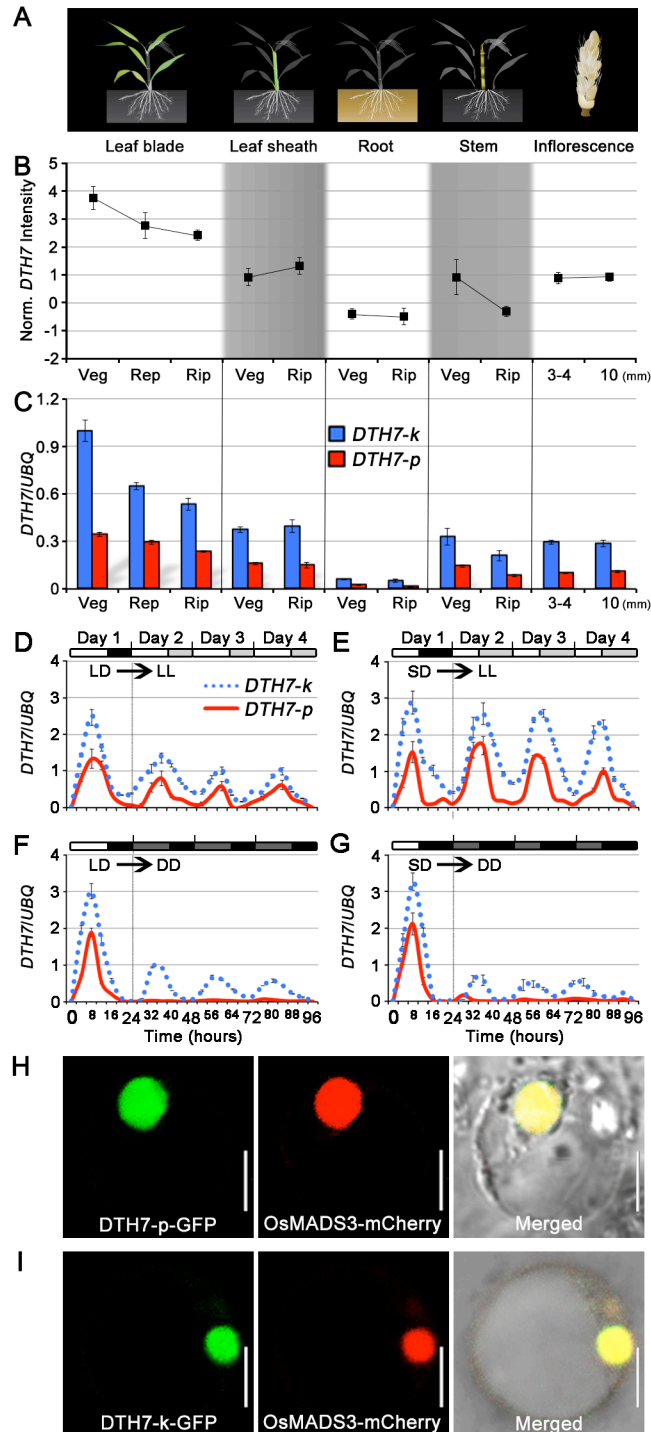
**Fig. S1.** NIL (*DTH7*) plants have the same leaf emergence rate as Kita-ake under controlled short day (A) and long day (B) conditions. Arrows indicate the flowering time of Kita-ake plants. Values are shown as mean  $\pm$  s.d. ( $n=8$ ).



**Fig. S2.** Map-based cloning of *DTH7*. (A) Delimitation of *DTH7*. Blue and red bars indicate the Kita-ake chromosomes and PA64S genomic fragment, respectively. 14 genes were annotated in the region. (B) Structure and allelic variation of *DTH7*. Lines, black and white boxes represent introns, exons and untranslated regions, respectively. (C) and (D) Complementation test of *DTH7*. Mature plants (C) and panicles (D) of WT (Kita-ake), *DTH7* and two T1 transgenic lines, #18 (transgene-positive) and #11(transgene-negative) are shown. All plants were grown under E3. Scale bars in (C) and (D) are 20 cm and 4 cm, respectively.

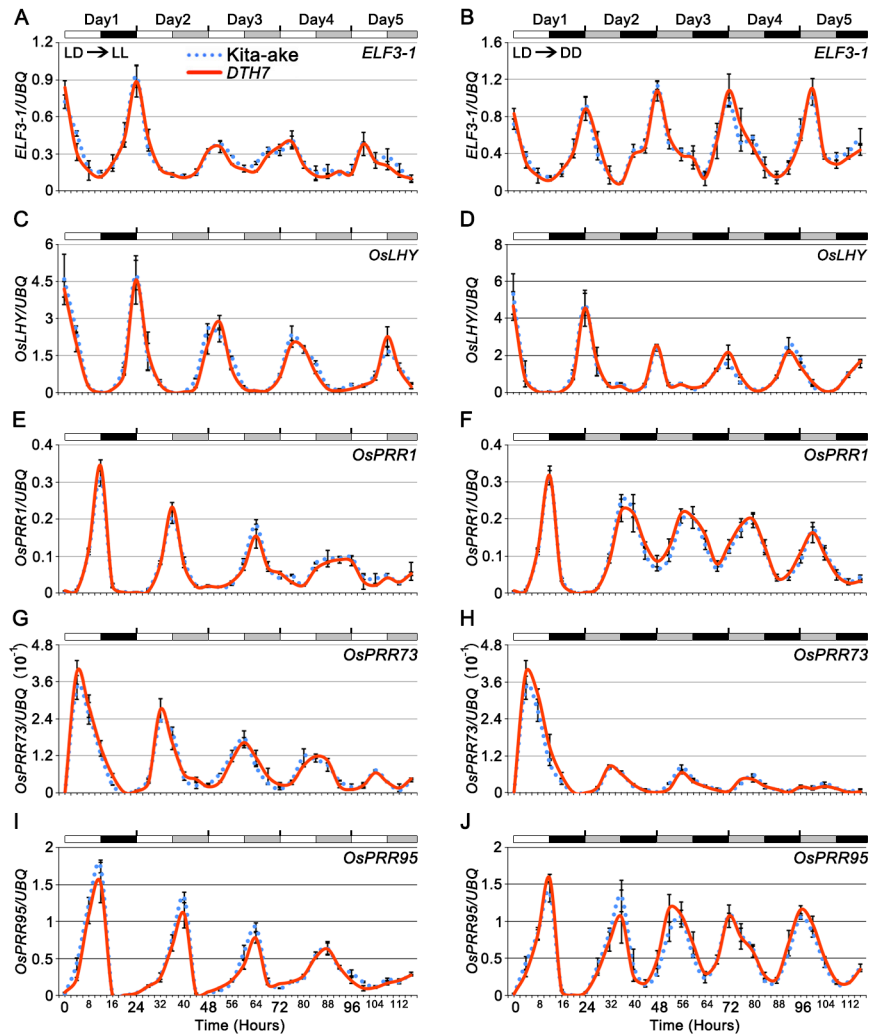


**Fig. S3.** (A) A phylogenetic tree of the DTH7-like proteins in higher plants. Amino acid sequences of 28 DTH7 homologs were obtained from NCBI (<http://www.ncbi.nlm.nih.gov/>) and used to construct a bootstrap N-J phylogenetic tree. 1,000 replicates were conducted to determine the statistical support for each node. DTH7 was denoted with a black dot. (B) A diagram showing that DTH7-k has three amino acid substitutions at the conserve positions across the DTH7-like proteins.

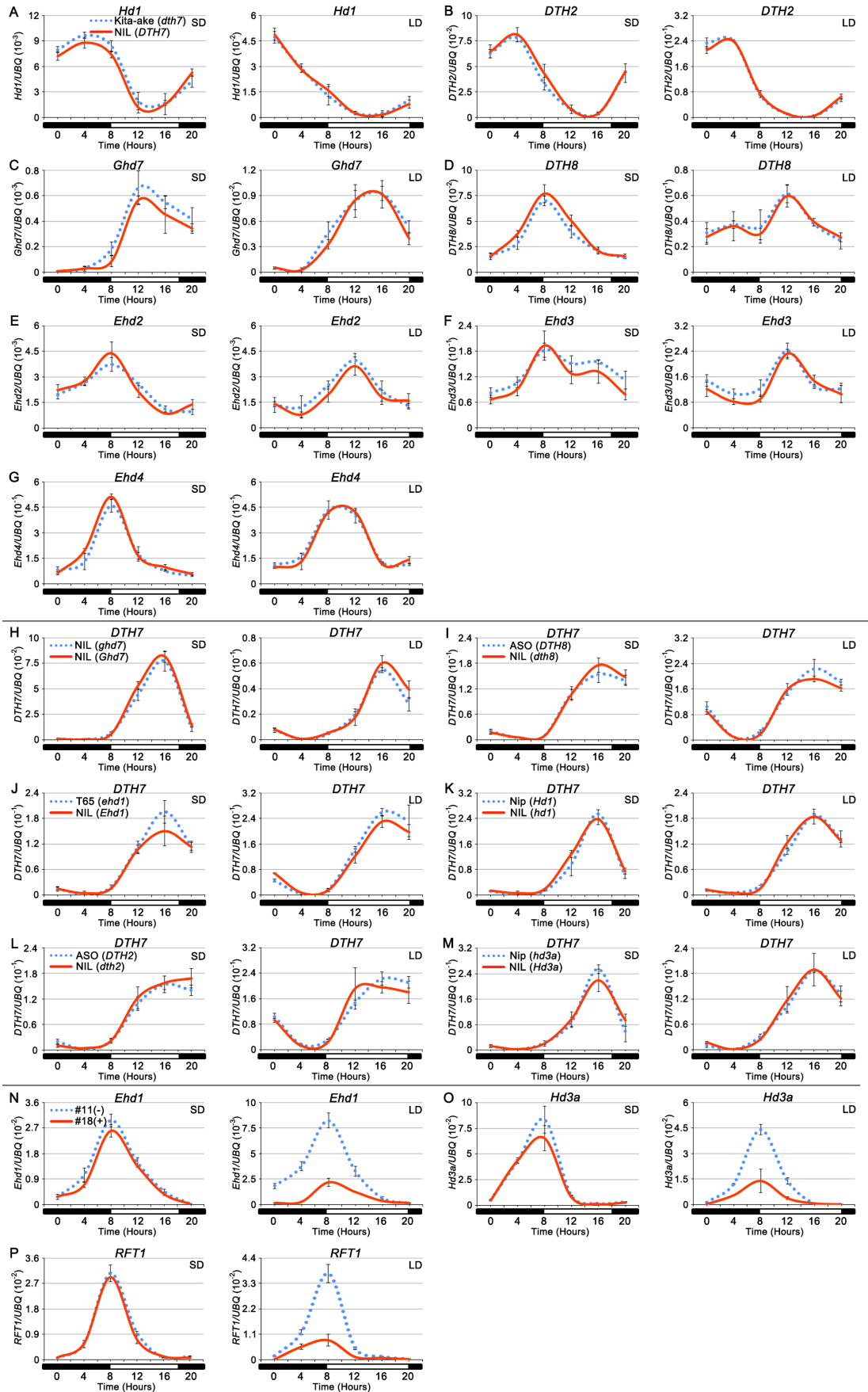


**Fig. S4.** Spatial and temporal expression of *DTH7*, and its protein sub-cellular localization. Measurement of *DTH7* transcript levels by microarray and qRT-PCR in various organs. (A) Pictures of the various organs. (B) Microarray data; (C) qRT-PCR data. (A) and (B) were cited from RiceXPro(31)(<http://ricexpro.dna.affrc.go.jp>). (D) and (E) qRT-PCR analysis of diurnal expression patterns of *DTH7*-k and *DTH7*-p alleles from LD (D) or SD (E) to LL (D) and DD (F) conditions. (F) and (G)

qRT-PCR analysis of diurnal expression patterns of *DTH7-k* and *DTH7-p* alleles from LD (F) or SD (G) to DD conditions. The white and black bars represent light and dark periods, respectively. The dark gray bars indicate subjective light during DD conditions; the light gray bars indicate subjective dark during LL conditions. The rice *Ubiquitin-1* (UBQ) gene was used as the internal control. The data are mean  $\pm$  standard deviations of three independent amplifications and two biological replicates. Fluorescence microscopic images showing that DTH7-p-GFP(H) and DTH7-k-GFP(I) fusion proteins were co-localized with the nuclear marker MADS3-mCherry fusion protein in rice protoplasts. Scale bars, 7.5  $\mu$ m.

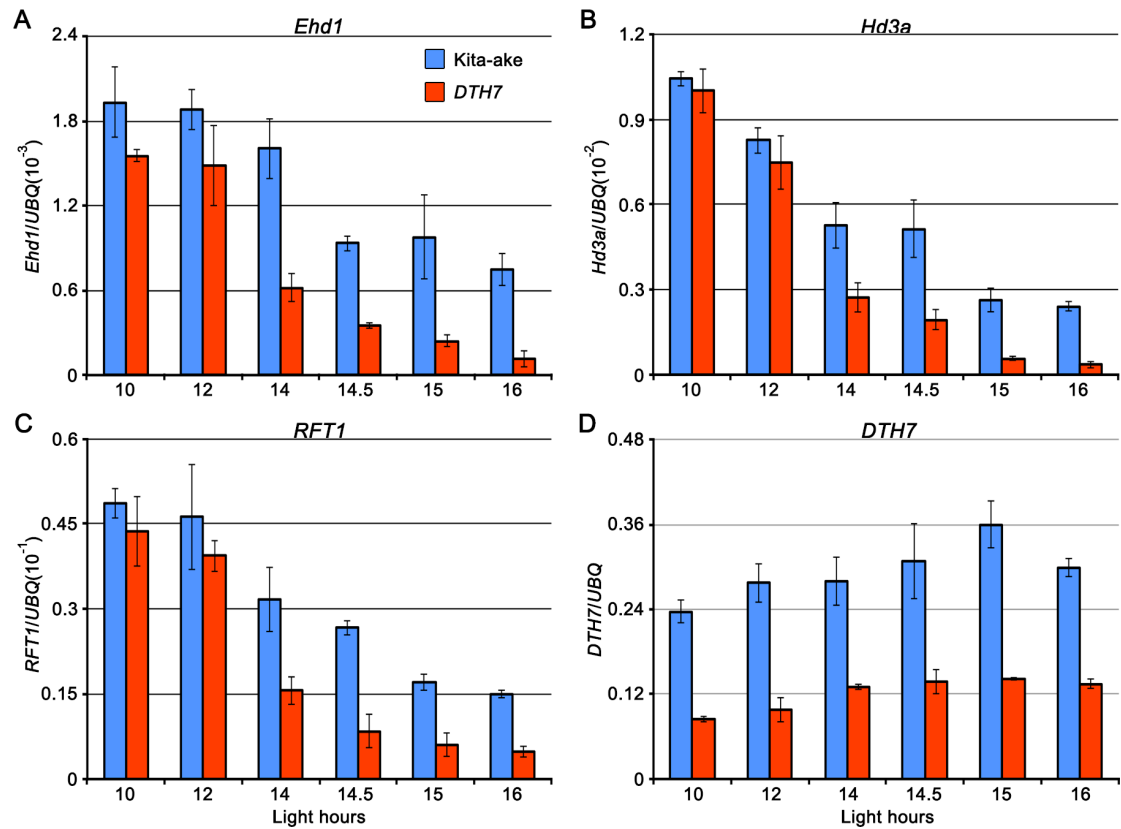


**Fig. S5.** Circadian expression of clock-associated genes in Kita-ake and *DTH7* plants. Transcript levels of *ELF3-1* (A and B), *OsLHY* (C and D), *OsPRR1* (E and F), *OsPRR73* (G and H), and *OsPRR95* (I and J) were examined under LL and DD conditions. The plants were first grown to cycles of 12-hour light/12-hour darkness for 28 days at 28°C and then transferred to the continuous light (LL) or continuous darkness (DD) at dawn. The white and black bars represent light and dark periods, respectively. The dark gray bars indicate subjective light during DD conditions; the light gray bars indicate subjective dark during LL conditions. The rice *Ubiquitin-1* (*UBQ*) gene was used as the internal control. The data are mean  $\pm$  standard deviations of three independent amplifications and two biological replicates.

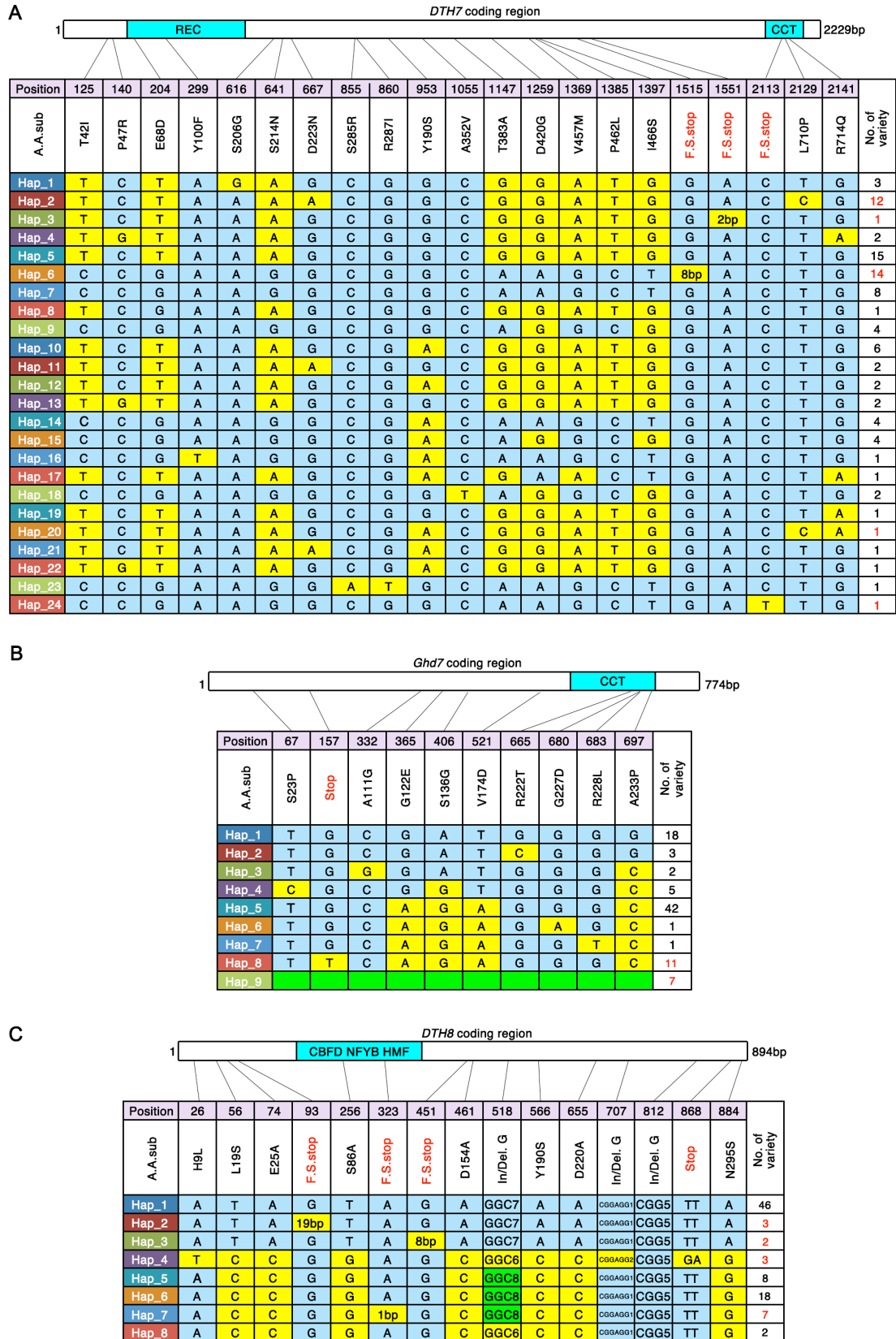


**Fig. S6.** qRT-PCR analysis of representative flowering-related genes in Kita-ake and *DTH7* plants, and *DTH7* in various flowering-time mutants or their NILs and corresponding WTs under SDs and LDs. Transcript levels of *Hd1* (A), *DTH2* (B), *Ghd7* (C), *DTH8* (D), *Ehd2* (E), *Ehd3* (F) and *Ehd4* (G), were examined in Kita-ake and *DTH7* plants, and the transcript level of *DTH7* was examined in *Ghd7* (H), *DTH8* (I), *Ehd1* (J), *Hd1* (K), *DTH2* (L) and *Hd3a* (M) NILs, and corresponding WTs. For comparison, the following accessions and their NILs were used: Nipponbare carrying a partially functional *Hd3a* allele and a NIL carrying a functional *Hd3a* allele; Taichun 65 carrying a non-functional *Ehd1* allele and a NIL carrying a functional *Ehd1* allele; Nipponbare carrying a functional *Hd1* allele and a NIL carrying a non-functional *Hd1* allele; Asominori carrying a functional *DTH2* allele and a NIL carrying a non-functional *DTH2* allele; A NIL carrying a functional *Ghd7* allele and a NIL carrying a non-functional *Ghd7* allele in the Shanyou 63 background; Asominori carrying a functional *DTH8* allele and a NIL carrying a non-functional *DTH8* allele. Transcript levels of *Ehd1* (N), *Hd3a* (O) and *RFT1* (P) were also examined in *DTH7* transgenic positive (#18 (+)) and negative (#11 (-)) lines. The rice *Ubiquitin-1* (*UBQ*) gene was used as the internal control. The data are mean  $\pm$  standard deviations of three independent amplifications and two biological replicates.





**Fig. S7.** qRT-PCR analysis of *Ehd1* (A), *Hd3a* (B), *RFT1*(C) and *DTH7* (d) under various photoperiod conditions. Penultimate leaves were harvested around the reported peak expression time points for each gene during the 24 hrs photoperiod – at dawn for *Ehd1*, *Hd3a* and *RFT1*, 8 h after dawn for *DTH7* from 28 d-old (SDs) and 35 d-old (LDs) plants. The rice *Ubiquitin-1* (*UBQ*) gene was used as the internal control. The data are mean  $\pm$  standard deviations of three independent amplifications and two biological replicates.



**Fig. S8.** Haplotype analysis of *DTH7*, *Ghd7* and *DTH8* coding sequences. (A) The *DTH7* nucleotide sequences of the accessions in the core collection were compared

with that of cv. PA64s (Hap\_7). Polymorphic nucleotides are indicated by different colors. Deletion and insertion sites are indicated by open and closed arrowheads, respectively. The number of accessions with each haplotype (Hap\_1-24) is shown in the column at the right, with the numbers for loss-of-function types in red. F.S., frame shift. PA64S type (Hap\_7, functional), Nipponbare type (Hap\_13), Chimaio type (Hap\_5), Yajiaoshu 1 type (Hap\_8) and Haolai type (Hap\_9) and loss-of-function allelic of Kita-ake type (Hap\_2), Baimaodao type (Hap\_3), Lucaihao type (Hap\_6), SHADA BORO type (Hap\_20) and Kasalash type (Hap\_24) were used for the ANOVA analysis (SI Appendix: Table S1). (B) The *Ghd7* nucleotide sequences of the accessions in the core collection were compared with that of cv. MH63 (Hap\_1). Polymorphic nucleotides are indicated by different colors. The number of accessions with each haplotype (Hap\_1-9) is shown in the column at the right, with the numbers for loss-of-function types in red. Hap\_9 is *Ghd7* deletion type. F.S., frame shift. Functional haplotypes of MH63 type (Hap\_1) and Nipponbare type (Hap\_5) and loss-of-function haplotypes of Kita-ake type (Hap\_8) and ZS97 type (Hap\_9)<sup>5</sup> were used for the ANOVA analysis (SI Appendix: Table S1). (C) The *DTH8* nucleotide sequences of the accessions in the core collection were compared with that of cv. Asominori (Hap\_1). Polymorphic nucleotides are indicated by different colors. The number of accessions with each haplotype (Hap\_1-9) is shown in the column at the right, with the numbers for loss-of-function types in red. Asominori type (Hap\_1, functional), IR24 type (Hap\_7, non-functional), ZS97 type (Hap\_4), Yangeng 15 type (Hap\_2) and Longtepu B type (Hap\_3)<sup>6</sup> were used for the ANOVA analysis (Table S1).

**Table S1.** Summary of the *DTH7*, *Ghd7* and *DTH8* allele types in modern cultivar of a rice germplasm core collection.

Variety Name	Subpop.	Accession No.	Hainan (E1)	Nanjing (E2)	Beijing (E3)	Haerbin (E4)	<i>DTH7</i>	<i>Ghd7</i>	<i>DTH8</i>	Hainan (E1)	Nanjing (E2)	Beijing (E3)	Haerbin (E4)	Origin	PS index
<b>I</b>															
Guangtoughulu	TEJ	07-00004	45.39	47.83	48.53	77.80	Hap2	Hap8	Hap2	n.d.	n.d.	92.00	104.11	China	0.065
Zaoyouzhuan	IND	15-02740	59.58	68.65	78.87	102.00	Hap6	Hap9	Hap4	89.29	137.40	133.80	117.56	China	0.245
Zhuqing	IND	N/A	53.70	56.60	59.56	92.50	Hap6	Hap9	Hap7	n.d.	n.d.	186.43	n.d.	China	0.098
Longtepu B	IND	N/A	67.60	79.10	89.88	96.70	Hap6	Hap9	Hap3	n.d.	n.d.	217.86	n.d.	China	0.248
Zhenshan 97B	IND	N/A	62.50	68.70	73.38	102.40	Hap6	Hap9	Hap7	n.d.	n.d.	183.71	n.d.	China	0.148
Zaoxian 14	IND	N/A	59.60	62.10	63.44	93.40	Hap6	Hap9	Hap7	n.d.	n.d.	197.14	n.d.	China	0.061
Yangeng 15	TEJ	ZD-02337	47.80	49.00	49.19	83.50	Hap2	Hap8	Hap2	n.d.	n.d.	81.64	n.d.	China	0.028
Fangzhu	TEJ	WD-11028	46.34	48.10	49.19	79.20	Hap2	Hap8	Hap2	n.d.	n.d.	101.36	n.d.	Japan	0.058
Yuenanzaodao	IND	WD-11661	62.69	66.03	69.10	99.30	Hap6	Hap9	Hap7	n.d.	n.d.	131.09	n.d.	Vietnam	0.093
<b>II</b>															
Kita-ake	TEJ	N/A	53.65	55.13	59.27	73.31	Hap2	Hap8	Hap1	33.35	43.87	66.73	78.59	Japan	0.095
Hejiang 19	TEJ	N/A	55.50	56.10	58.20	88.30	Hap2	Hap8	Hap1	n.d.	n.d.	77.64	n.d.	China	0.048
Kongyu1 31	TEJ	ZD-05454	56.10	57.30	58.70	89.10	Hap2	Hap8	Hap1	n.d.	n.d.	73.73	n.d.	China	0.044
Hejiang 21	TEJ	ZD-02375	52.59	55.67	57.76	85.50	Hap2	Hap8	Hap1	n.d.	n.d.	86.18	n.d.	China	0.09
Fushiguang	TEJ	ZD-05468	58.34	62.30	66.95	92.60	Hap2	Hap8	Hap1	n.d.	n.d.	83.27	n.d.	Japan	0.129
Shangyu 397	TEJ	WD-16547	56.36	60.58	63.86	85.30	Hap2	Hap8	Hap1	n.d.	n.d.	94.18	n.d.	Japan	0.112
Xiongji 12	TEJ	WD-104562	58.38	64.79	69.29	105.50	Hap2	Hap8	Hap1	n.d.	n.d.	112.09	n.d.	North Korean	0.157
Hongguo	TEJ	07-00002	53.97	61.09	63.93	85.87	Hap2	Hap8	Hap1	n.d.	108.60	119.40	164.56	China	0.156
Quqianbai	IND	11-00389	69.97	72.39	85.13	108.53	Hap6	Hap1	Hap7	n.d.	177.60	212.00	186.33	China	0.178
<b>III</b>															
Xingguo	TEJ	06-00035	55.09	81.52	83.33	95.93	Hap2	Hap5	Hap1	n.d.	165.60	174.60	132.33	China	0.339
Kasalath	IND	N/A	68.53	76.50	85.30	99.53	Hap24	Hap1	Hap5	n.d.	n.d.	246.43	n.d.	India	0.197
SHADA BORO	TRJ	8839	81.70	87.83	96.07	113.53	Hap20	Hap5	Hap5	52.80	211.60	126.40	70.67	Bangladesh	0.15
Baimaodao	TEJ	07-00109	72.42	76.26	87.67	114.60	Hap3	Hap5	Hap5	n.d.	165.00	188.00	155.22	China	0.174
PA64S	IND	N/A	85.63	90.53	108.76	n.d.	Hap7	Hap5	Hap7	n.d.	n.d.	241.00	n.d.	China	0.213
<b>IV</b>															
Yelicanghua	TEJ	02-00295	57.48	71.39	94.67	140.80	Hap5	Hap5	Hap1	n.d.	176.40	188.80	134.41	China	0.393
Zhonglou 1 hao	TEJ	04-00115	49.42	60.65	82.47	99.53	Hap5	Hap5	Hap1	n.d.	146.40	203.40	118.49	China	0.401
Weiguo	TEJ	05-00024	67.58	75.13	93.53	113.67	Hap5	Hap5	Hap1	n.d.	163.80	224.00	134.03	China	0.278
Chimao	TEJ	06-00010	43.91	47.96	50.73	92.00	Hap5	Hap5	Hap1	n.d.	n.d.	119.60	162.00	China	0.135
Nipponbare	TEJ	WD-10576	62.48	76.91	110.53	160.00	Hap13	Hap5	Hap1	n.d.	129.40	169.60	n.d.	Japan	0.435
T65	TEJ	30-00205	86.06	90.26	97.13	119.47	Hap5	Hap5	Hap1	n.d.	136.60	161.80	129.00	taiwan	0.114
Zhouandao	TEJ	WD-18718	61.27	74.70	89.73	104.93	Hap5	Hap5	Hap1	n.d.	168.60	182.20	127.00	Korea	0.317
Huadongdao	TEJ	WD-19115	69.82	79.78	93.53	108.27	Hap5	Hap5	Hap1	n.d.	217.20	193.40	139.67	Korea	0.254
Jingyue 1 hao	TEJ	ZD-00881	64.42	74.09	101.93	134.87	Hap13	Hap5	Hap1	n.d.	192.20	286.00	188.00	China	0.368
Zhendao 88	TEJ	ZD-05531	67.58	85.61	118.47	160.00	Hap5	Hap5	Hap1	88.20	197.20	159.00	n.d.	China	0.43
Xishen 15	TRJ	15-04286	71.33	86.96	117.13	160.00	Hap7	Hap5	Hap1	117.45	89.80	107.80	n.d.	China	0.391
Lengshuinnuo	TRJ	21-01989	137.27	153.20	160.00	160.00	Hap5	Hap5	Hap1	236.88	n.d.	n.d.	n.d.	China	n.d.
Yuyannuo	TRJ	21-02235	112.94	131.50	160.00	160.00	Hap5	Hap5	Hap1	172.37	n.d.	n.d.	n.d.	China	n.d.
Haolai	IND	21-02824	108.24	147.20	156.00	160.00	Hap9	Hap1	Hap1	53.46	n.d.	n.d.	n.d.	China	0.306
Jiuyuehuang	TRJ	24-00173	75.61	85.61	116.53	160.00	Hap5	Hap5	Hap1	n.d.	144.60	132.20	n.d.	China	0.351
Gaojiaozhengdao	TRJ	09-00972	75.39	106.74	110.93	160.00	Hap5	Hap5	Hap1	136.23	205.60	221.80	n.d.	China	0.32
Tiegangwu	TRJ	10-00463	93.82	116.13	160.00	160.00	Hap5	Hap5	Hap1	101.87	n.d.	n.d.	n.d.	China	n.d.
Feidongtangdao	TEJ	11-00529	51.21	87.26	126.73	160.00	Hap5	Hap5	Hap1	n.d.	153.40	233.60	n.d.	China	0.56
Yajiaoshu 1	TRJ	13-00940	116.94	160.00	160.00	160.00	Hap8	Hap5	Hap1	n.d.	n.d.	n.d.	n.d.	China	n.d.
<b>Unclassified</b>															
JC92	IND	67171	90.42	101.04	110.47	160.00	Hap14	Hap1	Hap8	n.d.	224.60	201.00	n.d.	India	0.182
TD25	IND	68407	139.52	160.00	160.00	160.00	Hap7	Hap1	Hap6	86.60	n.d.	n.d.	n.d.	Thailand	n.d.
RTS13	IND	8234	142.42	160.00	160.00	160.00	Hap15	Hap1	Hap6	164.00	n.d.	n.d.	n.d.	Vietnam	n.d.
Tam Cau-10A	IND	8228	86.18	160.00	160.00	160.00	Hap16	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	Vietnam	n.d.
DV85	AUS	5207	85.03	96.70	99.67	116.00	Hap17	Hap5	Hap5	n.d.	143.00	141.80	94.67	Bangladesh	0.147
Dhala Shaita	AUS	8388	76.82	82.26	91.53	120.33	Hap14	Hap5	Hap5	n.d.	275.40	269.40	243.00	Bangladesh	0.161
T1	AUS	9479	82.70	86.04	96.07	115.40	Hap18	Hap5	Hap6	n.d.	225.40	213.40	180.67	India	0.14
BJ1	AUS	12333	82.15	96.61	96.53	121.40	Hap19	Hap5	Hap5	n.d.	152.40	320.60	120.33	India	0.149
DV1	AUS	8803	82.85	85.13	96.13	110.93	Hap7	Hap5	Hap5	48.60	217.60	259.20	180.33	Bangladesh	0.138
SAMPONG P9	AUS	23218	160.00	160.00	160.00	160.00	Hap15	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	Cambodia	n.d.
Firooz	ARO	10315	93.24	130.20	133.53	160.00	Hap14	Hap1	Hap6	60.80	n.d.	193.40	n.d.	Iran	0.302
Dom Sofid	ARO	17616	80.76	91.17	102.27	121.53	Hap18	Hap5	Hap5	77.40	192.80	358.80	276.67	Iran	0.21
JC1	ARO	68399	160.00	160.00	160.00	160.00	Hap7	Hap1	Hap6	327.20	n.d.	n.d.	n.d.	India	n.d.
Mansaku	TEJ	13338	75.36	76.39	90.13	106.80	Hap21	Hap5	Hap1	n.d.	247.60	295.80	164.67	Japan	0.164
Geumobyeko	TEJ	15020	69.48	73.43	92.53	108.27	Hap10	Hap5	Hap1	n.d.	156.20	178.00	145.67	Korea	0.249
Koshihikari	TEJ	20526	68.67	83.48	101.73	136.13	Hap22	Hap5	Hap1	n.d.	n.d.	180.40	117.33	Japan	0.325
Tainan Iku 487	TEJ	9110	88.94	91.30	99.67	122.07	Hap10	Hap4	Hap1	n.d.	159.80	202.40	136.67	taiwan	0.108
Dholi Boro	TRJ	13736	82.12	86.91	94.13	111.00	Hap4	Hap5	Hap5	n.d.	192.40	211.20	134.33	Bangladesh	0.128
N 22	TRJ	25750	73.64	84.52	96.73	114.67	Hap23	Hap5	Hap6	n.d.	167.20	197.00	166.33	India	0.239
Taidonggludao	TEJ	30-00195	72.24	79.48	94.73	111.67	Hap10	Hap5	Hap1	n.d.	181.20	205.20	129.56	taiwan	0.2379
Fengjing	TEJ	WD-10954	63.48	72.83	93.53	116.27	Hap11	Hap5	Hap1	n.d.	161.20	192.40	168.33	Japan	0.3219
Qiuguang	TEJ	WD-10974	61.73	76.61	89.07	105.67	Hap10	Hap5	Hap1	n.d.	136.00	181.40	110.44	Japan	0.307
Yiwetdao	TEJ	WD-19087	64.33	76.70	102.73	133.13	Hap10	Hap5	Hap1	n.d.	170.20	211.20	165.78	Korea	0.374
Fenshouguang	TEJ	WD-19876	66.36	70.35	87.53	111.00	Hap12	Hap5	Hap1	n.d.	199.00	225.60	168.00	Japan	0.242
zhonghua 11	TEJ	ZD-03874	58.79	73.96	103.07	135.60	Hap12	Hap5	Hap1	111.40	257.00	311.60	197.67	China	0.43
Taduan	IND	5215	77.48	92.17	107.33	160.00	Hap10	Hap1	Hap6	n.d.	255.00	n.d.	n.d.	Philippines	0.279
Khao Dawk Mali 105	AUS	31899	106.76	160.00	160.00	160.00	Hap7	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	Thailand	n.d.
Patnai 23	IND	61690	160.00	160.00	160.00	160.00	Hap14	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	India	n.d.
CO 18	IND	67068	110.00	149.30	160.00	160.00	Hap7	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	India	n.d.
Gie 57	IND	67148	108.70	160.00	160.00	160.00	Hap15	Hap1	Hap8	n.d.	n.d.	n.d.	n.d.	Vietnam	n.d.
Qiyuexian	IND	16-06887	57.03	136.70	160.00	160.00	Hap9	Hap4	Hap6	n.d.	n.d.	n.d.	n.d.	China	n.d.
Wenxiangnuo	IND	21-00272	69.58	135.80	160.00	160.00	Hap9	Hap1	Hap6	n.d.	n.d.	n.d.	n.d.	China	n.d.</

**Table S2.** Primers used in this study.

Primer name	Primer sequence (5'-3')	Description
Primers used for map-based cloning and marker-assisted selection		
IND-34-F	GGACAGAATGTGAAGACAGTCG	Indel
IND-34-R	ACTAATCCACCAACGCATCC	
IND-35-F	TGCAGCTGCGCCACAGCCATAG	Indel
IND-35-R	CAACCACGACACCGCCGTGTTG	
IND-36-F	AGTTTGCGCCACACATATCA	Indel
IND-36-R	TCACGACAATTGGACTGAGC	
IND-37-F	TGGAGAATTCAGGGAAAGGA	Indel
IND-37-R	CAGGCAGGTCAGAATCACATT	
IND-38-F	TGGAGGCTTTCTCGCTTTC	Indel
IND-38-R	GAGGAAGTCGAGGATGAGGA	
Primers used for transgenic construction		
<i>pDTH7::DTH7-F</i>	CCATGATTACGAATTCCACAAGGTTAGCACATGATGTCG	<i>pDTH7::DTH7</i> complementati on
pDTH7-DTH7-R	CCAAGCTTGCATGCCTGCAGTCCTTTCGCTTCCAGAACA TACATT	
Primers used for subcellular localization		
DTH7-GFP-F	GCCCAGATCAACTAGTATGATGGGAACCGCTCATCAC	DTH7-GFP fusion
DTH7-GFP-R	TCGAGACGTCTCTAGATCTGTCCGCTGCCGCTTCG	
Primers used for quantitative RT-PCR		
Ehd4-F	CAGCCAGCGGAATCATCAC	Reference 3
Ehd4-R	CCAAATCCATCAGACCTACTCCT	
Ehd2-F	CGACGACAATAGCTCGATCGC	Reference 3
Ehd2-R	GTGCATGGTCACGGAGCCTT	
Ehd3-F	GACCACCTCGTCACCTACAAG	Reference 3
Ehd3-R	GAGTGTCCCTCCAGCTAATCC	
Hd1-F	TCAGCAACAGCATATCTTTCTCATCA	Reference 3
Hd1-R	TCTGGAATTTGGCATATCTATCACC	

Ehd1-F	CCTACAGTGATTATGGCTTCA	Reference 3
Ehd1-R	GTGCTGCCAAATGTTGCTC	
Hd3a-F	GCTCACTATCATCATCCAGCATG	Reference 3
Hd3a-R	CCTTGCTCAGCTATTTAATTGCATAA	
RFT1-F	TGACCTAGATTCAAAGTCTAATCCTT	Reference 3
RFT1-R	TGCCGGCCATGTCAAATTAATAAC	
DTH8-F	CAGGAGTGCCTGTCGGAGTT	Reference 6
DTH8-R	GGTCGTCGCCGTTGATGGT	
Ghd7-F	GCTTGAACCCAAACACGG	Reference 6
Ghd7-R	CTCATCTCGGCATAGGCTT	
UBQ-F	ACCCTGGCTGACTACAACATC	Reference 3
UBQ-R	AGTTGACAGCCCTAGGGTG	
PhyB-F	CTCATCTTCAAGGAATCTGAGG	This study
PhyB-R	CCTGCTAGAACAAGCATTAC	
DTH7-F	GAACCTATGGCAGCATGTGT	This study
DTH7-R	CGTCATTGCTGCCATTGTT	
DTH2-F	CCAGTTTCAACGACGCCTAA	Reference 4
DTH2-R	GTCTCCATATACGCTCCCATCA	
OsPRR1-F	CAAACGTTGCTCCCTCAGTA	This study
OsPRR1-R	GAATGCTCATACCAGCAGGA	
OsPRR73-F	AGGAGCGGAAAGAAACATAA	Reference 32
OsPRR73-R	AACCTTGGAGGAGCAATCAG	
OsPRR95-F	CGCTCAGTGGCAGTGTCTGT	Reference 32
OsPRR95-R	GGTATCGCACCTTCTTCTCA	
OsLHY-F	CAGATAAGGCCGACACCAAAC	Reference 32
OsLHY-R	GGTGTGTTGGAACCACATG	
OsELF3-1F	TGTCGCCCTTCGTCAA	Reference 32
OsELF3-1R	GGTCTTTTCCCAGCTCATT	