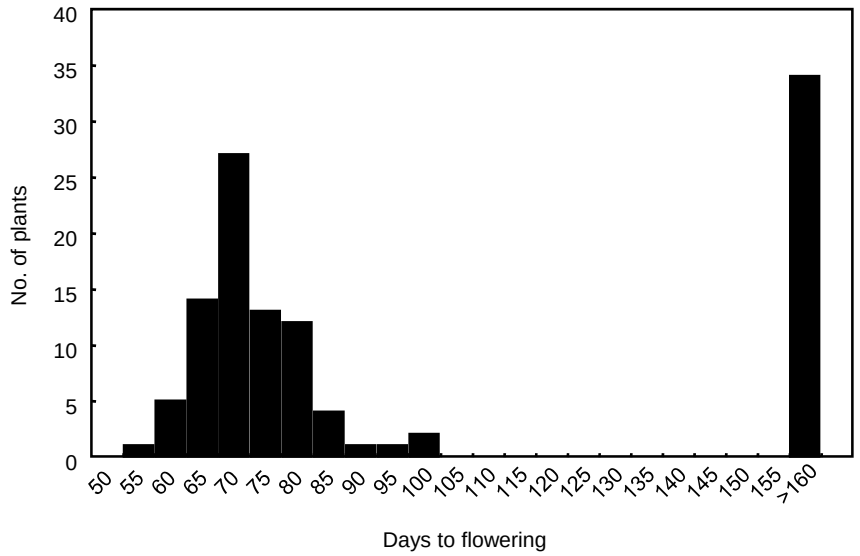
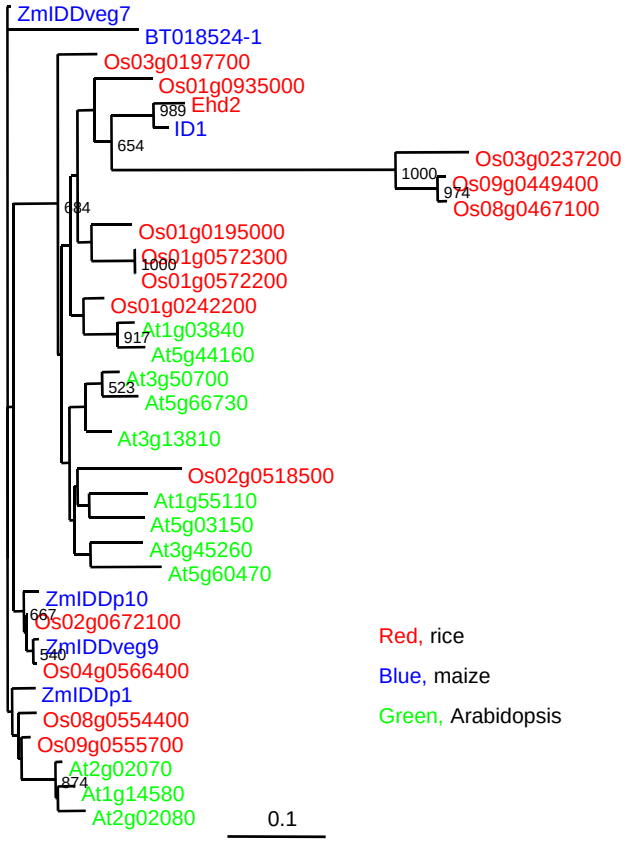
**Supplemental Figure S1.** Distribution of days to flowering under natural-day conditions in $BC_1F_2$ population (*n* = 109) from the cross between the *ehd2* mutant and 'Guang Lu Ai 4'. The segregation ratio of normal to late-flowering phenotype was 81 : 28 (the expected ratio 3 : 1, $\chi^2 = 0.03^{ns}$). Days to flowering of the wild-type plants ('Tohoku IL9'), 'Guang Lu Ai 4' and the *ehd2* mutants were 80.7 ± 2.5, 78.3 ± 2.9 and 169.7 ± 0.6, respectively (*n* = 10). The seeds were sown in the middle of June and the plants were grown in a paddy field in Tsukuba, Japan.



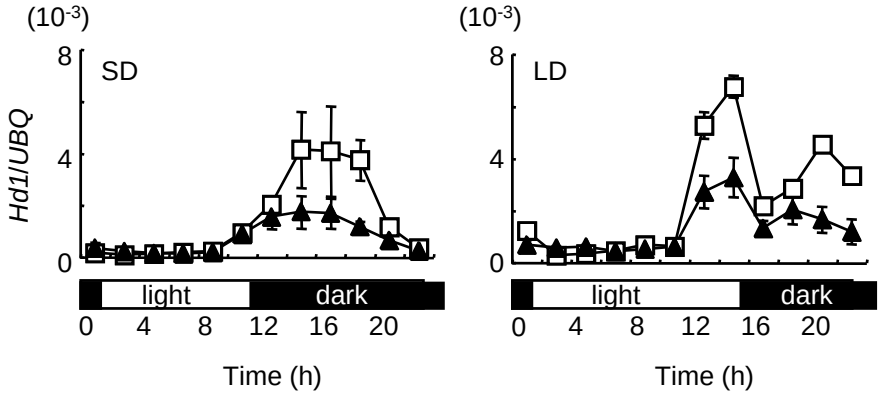
**Supplemental Figure S2.** Alignment of deduced amino acid sequences of rice Ehd2 and maize ID1. This alignment was performed using CLUSTALW version 1.83 (http://clustalw.ddbj.nig.ac.jp/top-j.html). Underlines show the position of a putative zinc finger domain (ID domain). The C2H2-type and two C2HC-type zinc finger motifs were shown by red and green letters, respectively. The putative NLS sequences were shown by blue letters. The nearly identical C-terminal peptide regions were shown by grey letters.

```
Ehd2   ---MLLSDLSSD-QEATGSNSHGGGGGDRMVVGSHGAAHVVLSNLFLPPAAAAAATMLLP 56
ID1    MQMMMLSDLSSDDHEATGSSSYGG----------DMASYALSPLFLAPAASATAPLPPP 49

Ehd2   AAPVMVRPAAMAAAQEPRAKKKRSLPGNPDPEAEVIALSPRALVATNRFVCEVCNKGFQR 116
ID1    PQPPAEELTNKQAAG--GGKRKRSQPGNPDPGAEVIALSPRTLVATNRFVCEICNKGFQR 107

Ehd2   DQNLQLHRRGHNLPWKLRHRAAAVSAVTTAAP---------------APRKRVYVCPEP 160
ID1    DQNLQLHRRGHNLPWKLRQRSSLVVPSSSAAAGSGGRQQQQQGEAAPTPPRKRVYVCPEP 167

Ehd2   TCVHHDPARALGDLTGIKKHFSRKHGEKRWRCERCGKRYAVHSDWKAHVKNCGTREYRCD 220
ID1    TCVHHDPARALGDLTGIKKHFSRKHGEKRWCCERCGKRYAVQSDWKAHVKGCGTREYRCD 227

Ehd2   CGILFSRKDSLLTHRAFCDALAEESARLLAAANNSSSITTTTCNNSNISSNNNNNNINSI 280
ID1    CGILFSRKDSLLTHRAFCDALAEESARLLAAAANNGSTITTTS------SSNNNDLLNAS 281

Ehd2   SNSNNLLITSSSSSPPLFLPFSTTPAENPNPNQLLFLQQHQAAHHQLLLPQFQQPPSSPP 340
ID1    NNITPLFLPFASSPP----PVVVAAAQNPN-NTLFFLHQELSPFLQPRVTMQQQP--SP- 333

Ehd2   AYFDHLAFGGGGGVITGSSCNDDNSSIAGDVMVAAGGDSVSFGLTSEGSVTMHAGDVGRR 400
ID1    -YLD-LHMHVDASIVTTTGG------------LADGTPVSFGLALDGSVAT----VGHR 374

Ehd2   RLTRDFLGVDHDAGEVDELELDELPADLSTTAAACQGCNFAAATTAACCATDFTTGSRQY 460
ID1    RLTRDFLGVDGGGRQVEELQLP-----LCATAAAAG------ASRTASCATDLT---RQC 420

Ehd2   LG-RLPPVNETWSHNF 475
ID1    LGGRLPPVNETWSHNF 436
```

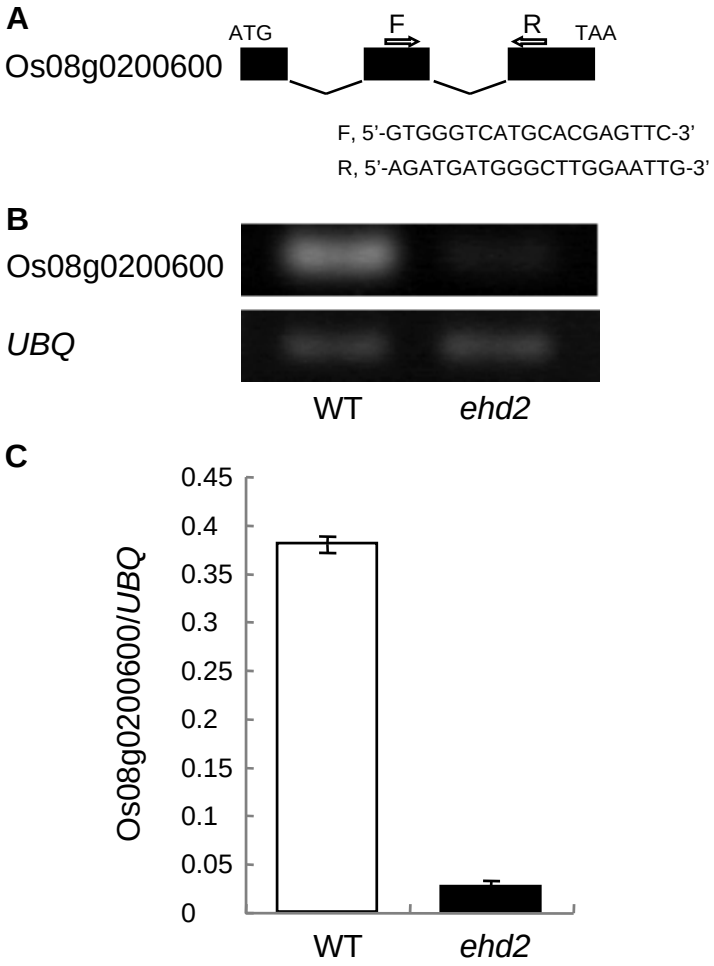
**Supplemental Figure S3.** Phylogenetic comparison of ID-domain amino acid sequences from rice, maize and *Arabidopsis thaliana*. Multiple sequence alignments were produced with CLUSTALW versiopn 1.83 (http://clustalw.ddbj.nig.ac.jp/top-j.html) using default settings. The phylogenetic tree was calculated using the neighbor-joining method and bootstrap analysis (1000 replicates) using PHYLIP via the same website and visualized with Treeview version 1.6.6 (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html). Bootstrap values for nodes supported in > 50% were shown.



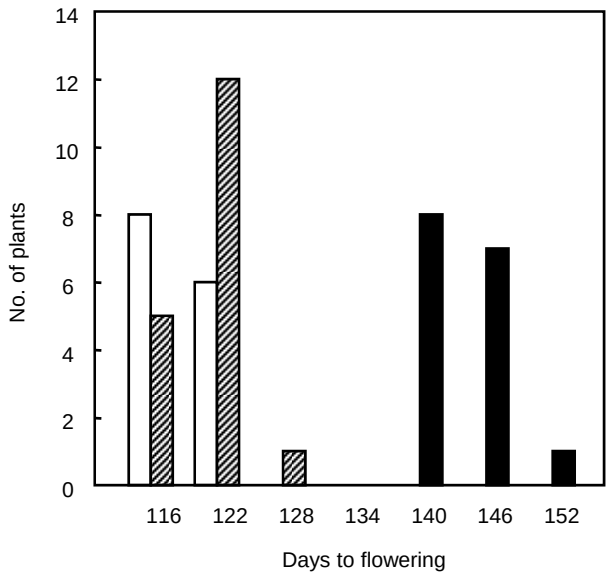
**Supplemental Figure S4**. Diurnal changes in levels of *Hd1* transcripts under SD (10 h light / 14 h dark) and LD (14.5 h light / 9.5 h dark) conditions. UBQ, ubiquitin. Open squares represent wild-type plants; filled triangles represent the *ehd2* mutants. Developing leaves were harvested every 2 h. Values are shown as mean ± s.d. of three independent experiments. Data are representative of two independent biological replicates.



**Supplemental Figure S5**. Expression analyses of Os08g0200600 (NAM protein domain containing protein). (A) Putative gene structure of Os08g0200600. F and R are primers used for RT-PCR and real-time RT-PCR analyses. Expression of Os08g0200600 shown by RT-PCR (B) and real-time RT-PCR (C). Values are shown as means ± s.d. of three independent experiments in (C). UBQ, ubiquitin. Young leaves of the *ehd2* mutants and its wild-type plants (Tohoku IL9) were collected at two hours after dawn from one-month-old plants grown under LD (14.5h light / 9.5 h dark) condition.



**Supplemental Figure S6.** Distribution of days to flowering under natural-day condition in the selfed-progeny (*n* = 48) of the *Tos17*-induced mutants heterozygous for *Ehd2*. The segregation ratio of homozygotes for 'Nipponbare' allele (open boxes), heterozygotes (slashed boxes) and homozygotes for *Tos17*-inserted allele (filled boxes) was 14 : 18 : 16 (the expected ratio 1 : 2 : 1, $\chi^2$ = 3.17$^{ns}$). Days to flowering of 'Nipponbare' was 116.9 ± 1.2 (*n* = 10). The seeds were sown in the middle of April and the plants were grown in a paddy field in Tsukuba, Japan.



**Supplemental Table S1.** *Genetic markers used in the delimitation of candidate genomic region of Ehd2*

| Primer name | Sequence (5' - 3') | | Remarks |
|---|---|---|---|
| | Forward | Reverse | |
| Indel-1 | CTAGTTTGTTGCAACTAAGCAAGTGG | GTTTCTTAATGTTGCCATGCATGC | - |
| CAPS-1 | AAGCAGTGGGATTGGTTGAC | CCATGACAGCAGGAGAGACA | *Hin*dIII |
| SNP-1 | TGAGTGGCAGAGGTTACAACA | GGTGGTGGTCCAAGAAAAGA | Direct sequencing |
| SSR-1 | AGGATTTGCAGGTTTTCAA | TCTAATGCATACATGGTGCT | - |
| SNP-2 | GGCCAGGAGACTCTTATTGG | GTCCCCATGACCATCTTCC | Direct sequencing |
| CAPS-2 | ATTTCCAAGAACTCTACCACCC | CTTGTCTCTGCCACTCACG | *Bam*HI |

**Supplemental Table S2.** *Summary of microarray data*

Top three genes that showed the greatest fold-change and *Ehd2* were represented. Young leaves of the *ehd2* mutants and its wild-type plants (Tohoku IL9) were collected at two hours after dawn from one-month-old plants grown under LD (14.5h light / 9.5 h dark) condition. Total RNA was isolated using a Plant RNA Isolation plant Mini Kit (Agilent Technologies). The RNAs (400-ng aliquots) were labeled with a Low RNA Input Linear Amplification/Labeling Kit (Agilent Technologies) according to the manufacturer's instructions. Aliquots of Cy3- and Cy5-labeled cRNAs (1 mg each) of samples from the *ehd2* mutants or its wild-type plants were used for hybridization in an Agilent Rice Oligo Microarray (44K, custom-made; Agilent Technologies). After hybridization, microarray slides were scanned (scanner model G2505B and software G2565BA; Agilent), and data were analyzed using Feature Extraction software (version 9.1; Agilent Technologies) at the default settings. All microarray procedures and data analyses were performed according to the manufacturer's manual. Two independent biological repricates were performed with color-swap experiments. Down, down-regulation by the *ehd2* mutation.

| Locus ID | Annotation | Fold-change (*Ehd2*/*ehd2*) | | *P* value | Fold-change (*Ehd2*/*ehd2*) | | *P* value |
|---|---|---|---|---|---|---|---|
| 1st experiment | | | | | | | |
| Os10g0463400 | Early heading date 1 (Ehd1) | 12.0 | Down | 3.48E-13 | 8.2 | Down | 2.20E-16 |
| Os08g0200600 | NO APICAL MERISTEM (NAM) protein domain containing protein | 4.8 | Down | 6.94E-22 | 3.6 | Down | 4.99E-18 |
| Os04g0640700 | Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme (ARA-I) | 4.4 | Down | 1.13E-09 | 2.9 | Down | 1.87E-08 |
| Os10g0419200 | Early heading date 2 (Ehd2) | 3.4 | - | 5.41E-05 | 2.2 | - | 3.13E-03 |
| 2nd experiment | | | | | | | |
| Os10g0463400 | Early heading date 1 (Ehd1) | 12.8 | Down | 2.10E-04 | 50.2 | Down | 1.52E-21 |
| Os08g0200600 | NO APICAL MERISTEM (NAM) protein domain containing protein | 4.8 | Down | 5.51E-14 | 5.7 | Down | 4.92E-16 |
| Os04g0640700 | Alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme (ARA-I) | 5.9 | Down | 1.19E-02 | 3.4 | Down | 9.93E-11 |
| Os10g0419200 | Early heading date 2 (Ehd2) | 5.6 | - | 0.12 | 25.4 | - | 3.76E-18 |