Additional files 1:

Figure S1. Temporal expressions of AP2 genes and *Ehd1* under SD.

(A,B) RT-PCR analysis of the transcript levels of *SNB* (A) and *OsIDS1* (B) under SD. Middle regions of fully emerged uppermost leaves were harvested at 15, 18, 21, 24, 27 and 30 DAG. (C) RT-PCR analysis of the transcript levels of *Ehd1* under SD. Middle regions of fully emerged uppermost leaves were harvested at 15, 18, 21, 24, 27 and 30 DAG. Expressions of the AP2 genes and *Ehd1* were analyzed at ZT 2 h. Y axis, relative transcript level compared with rice *ubi1*. Error bars indicate standard deviations; n = 4 or more.

Figure S2. Construction of *SNB* and *OsIDS1* over-expression plants.

(A-C) Expression levels of *SNB* (endogenous) and t*SNB* (transgene) in the *SNB* OX plants via RT-PCR (A) and qRT-PCR (B, C). *Ubiquitin1* was used as reference.(D-F) Expression levels of *OsIDS1* (endogenous) and t*OsIDS1* (transgene) in the *OsIDS1* OX plants via RT-PCR (D) and qRT-PCR (E, F). *Ubiquitin1* was used as reference.

Figure S3. Expressions of floral regulators in the *OsIDS1* OX.

(A-H) Expression levels of *OsPhyB* (A), *OsMADS50* (B), *Ghd7* (C), *OsId1* (D), *OsCOL4* (E), *OsMADS56* (F), *Ehd3* (G) and *OsTrx1* (H) in the wild-type (closed boxes) and *OsIDS1* overexpression plants (open boxes) under short day (SD) conditions. For expression analysis, plants were grown in SD (12 h light/ 12 h dark) conditions. Middle regions of fully emerged uppermost leaves were harvested at 30 days after germination. Expressions of these genes were monitored at ZT 2 h. Y axis, relative transcript level of each gene compared with that of rice *ubi1*. Error bars indicate standard deviations; *n* = 4 or more.

Figure S4. Expressions of floral regulators in the *SNB* OX.

(A-H) Expression levels of *SNB* (A), *Hd3a* (B), *RFT1* (C), *Ehd1* (D), *OsGI* (E), *Hd1* (F), *OsMADS51* (G) and *OsCOL4* (H) in the wild-type (closed boxes) and *SNB* over-expression plants (open boxes) under short day (SD) conditions. For expression analysis, plants were grown in SD (12 h light/ 12 h dark) conditions. Middle regions of fully emerged uppermost leaves were harvested at 30 days after germination. Expressions of *OsGI* and *Hd1* were observed at ZT 10 h and ZT 14 h, respectively and other regulators were monitored at ZT 2 h. Y axis, relative transcript level of each gene compared with that of rice *ubi1*. Error bars indicate standard deviations; *n* = 4 or more.

Figure S5. Expression levels of AP2s in the various flowering-time mutants.

(A, B) Expression levels of *SNB* (A) and *OsIDS1* (B) in the Dongjin (black bars), Kitaake (gray bars), *ghd7*, *osgi*, *Ehd1* RNAi, *hd1*, *osmads50*, *osmads51*, *OsId1* RNAi, *ostrx1* and *osvil2* (open bars) plants. For expression analysis, middle regions of fully emerged uppermost leaves were harvested at 40 days after germination. Expressions of AP2 genes were observed at ZT 2 h. Y axis, relative transcript level of each gene compared with that of rice *ubi1*. Expressions of AP2 genes in each mutant were normalized by those of WT. Error bars indicate standard deviations; *n* = 4 or more.

Figure S6. Phenotypes of *miR172*-resistant *OsIDS1*overexpression.

(A) Scheme of *miR172*-resistant *OsIDS1* (r*OsIDS1*) construct. Four silent mutations (red characters) were introduced into *miR172* target sequences on C-terminus of *OsIDS1* full-length cDNA. Primers t*OsIDS1* F and R were used for observing a transgene expression of *OsIDS1* in the r*OsIDS1* over-expression plants. Underlined and italic sequences (*tccgga*) were indicated restriction enzyme site by *Aor13*HI or *ACC*III. A.A, Amino Acid sequences; *nos*T, *nos* terminator; P*act*, *actin* promoter. (B) Expression level of *OsIDS1* (transgene) in the r*OsIDS1* OX plants. (C) Phenotypes of r*OsIDS1* OX plants. Numbers indicated individual primary transgenic number of r*OsIDS1* OX plants. Plants were grown under short day conditions (12 h light/ 12 h dark). Photograph was taken at 132 DAT (days after transfer of regenerates).

Figure S7. Verification of r*SNB* construct

(A) Restriction enzyme site for *Aor13*HI and *ACC*III in the r*SNB* construct.

(B) Digestion of t*SNB* PCR products for the *SNB* and r*SNB* by *ACC*III.

Figure S8. Phenotypes of *Ehd1*overexpression.

(A) Scheme of *Ehd1* OX construct. *Ehd1* full-length cDNA was sub-cloned into pGA3426 vector between maize *ubiquitin* promoter (P*ubi*) and *nopaline synthase* terminator (*nos*T). (B) Phenotypes of *Ehd1* OX plants. Plants were grown under short day conditions (12 h light/ 12 h dark). Photograph was taken at 42 DAT (days after transfer of regenerates). Red arrows indicate emerged panicles.

Figure S1

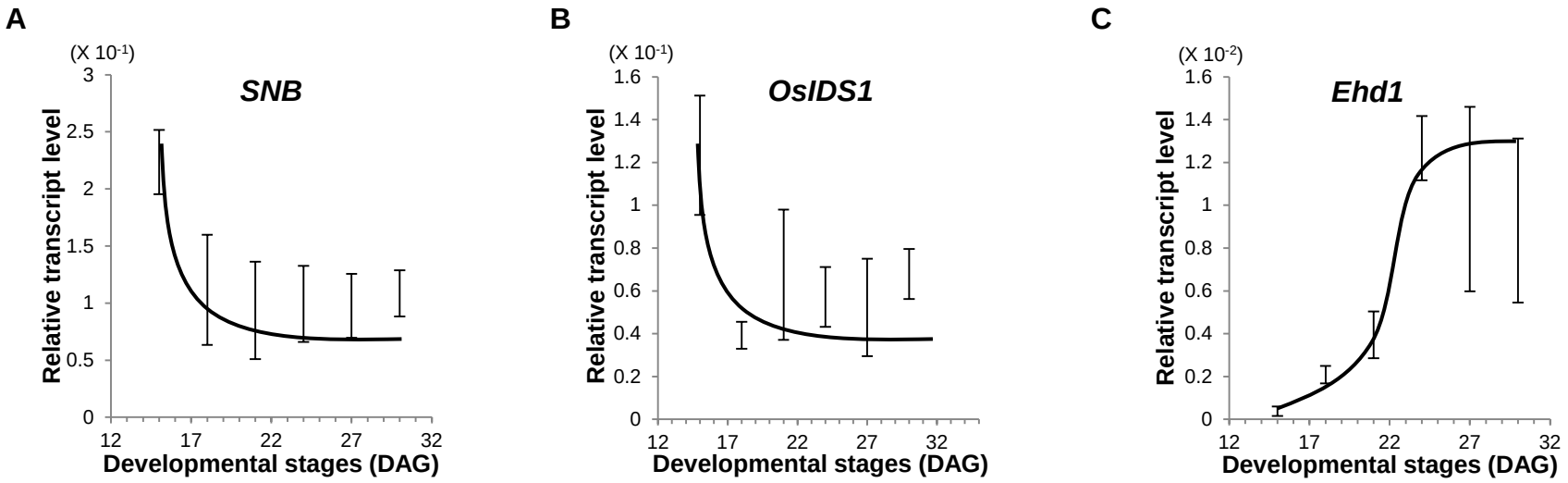

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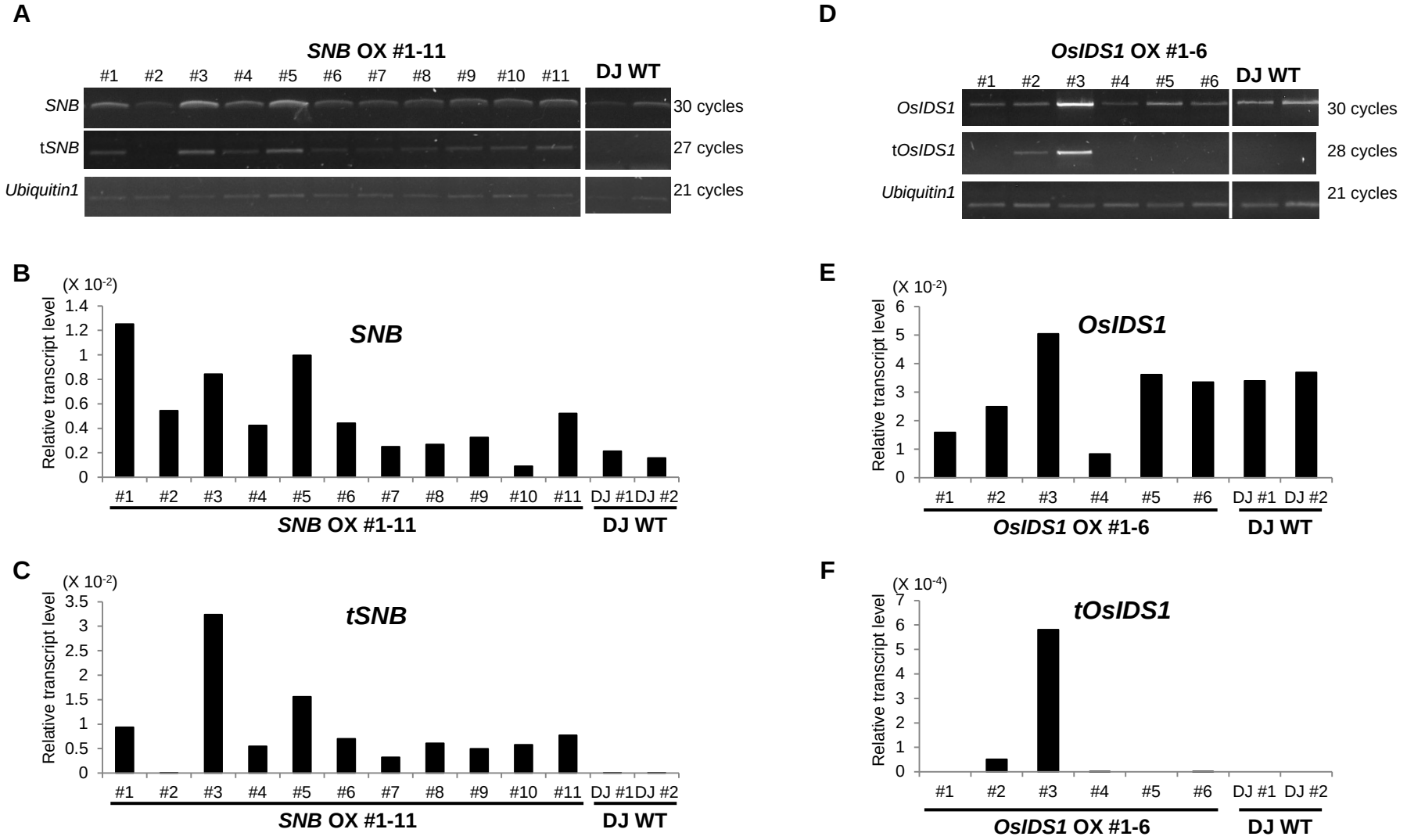
Figure S2



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(D-F) Expression levels of *OsIDS1* (endogenous) and t*OsIDS1* (transgene) in the *OsIDS1* OX plants via RT-PCR (D) and qRT-PCR (E, F). *Ubiquitin1* was used as reference.

Figure S3

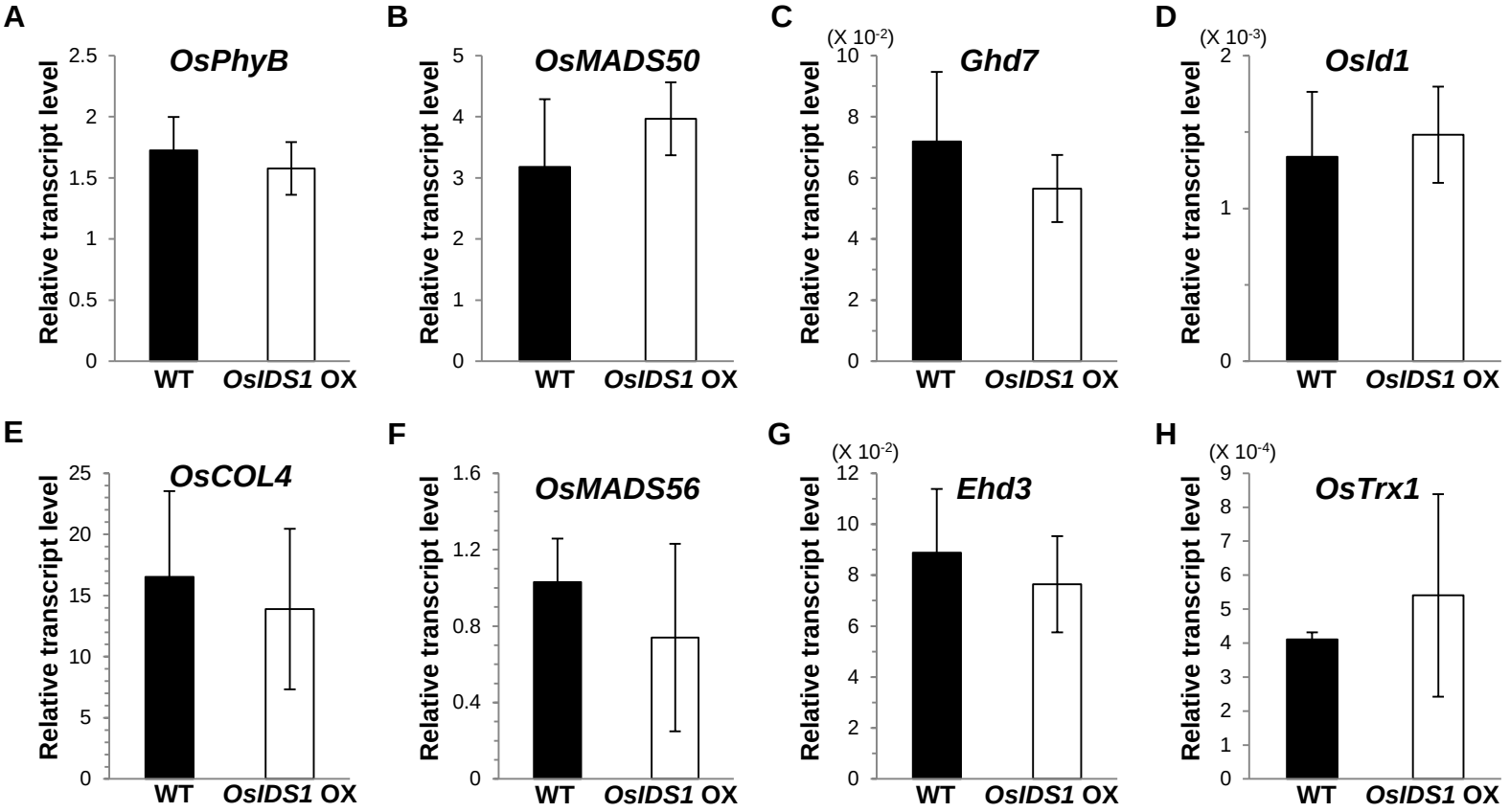

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Figure S4

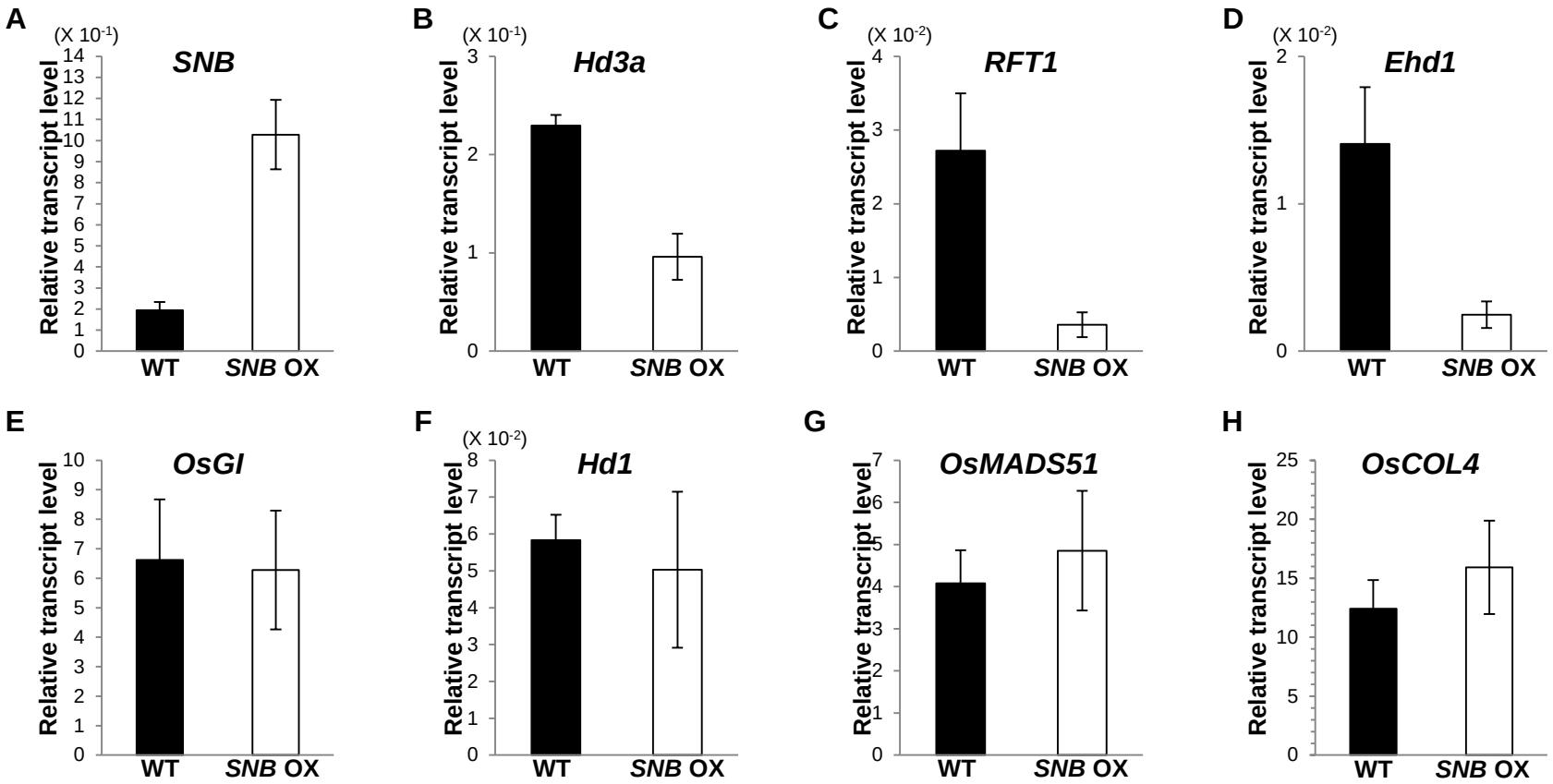

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Figure S5

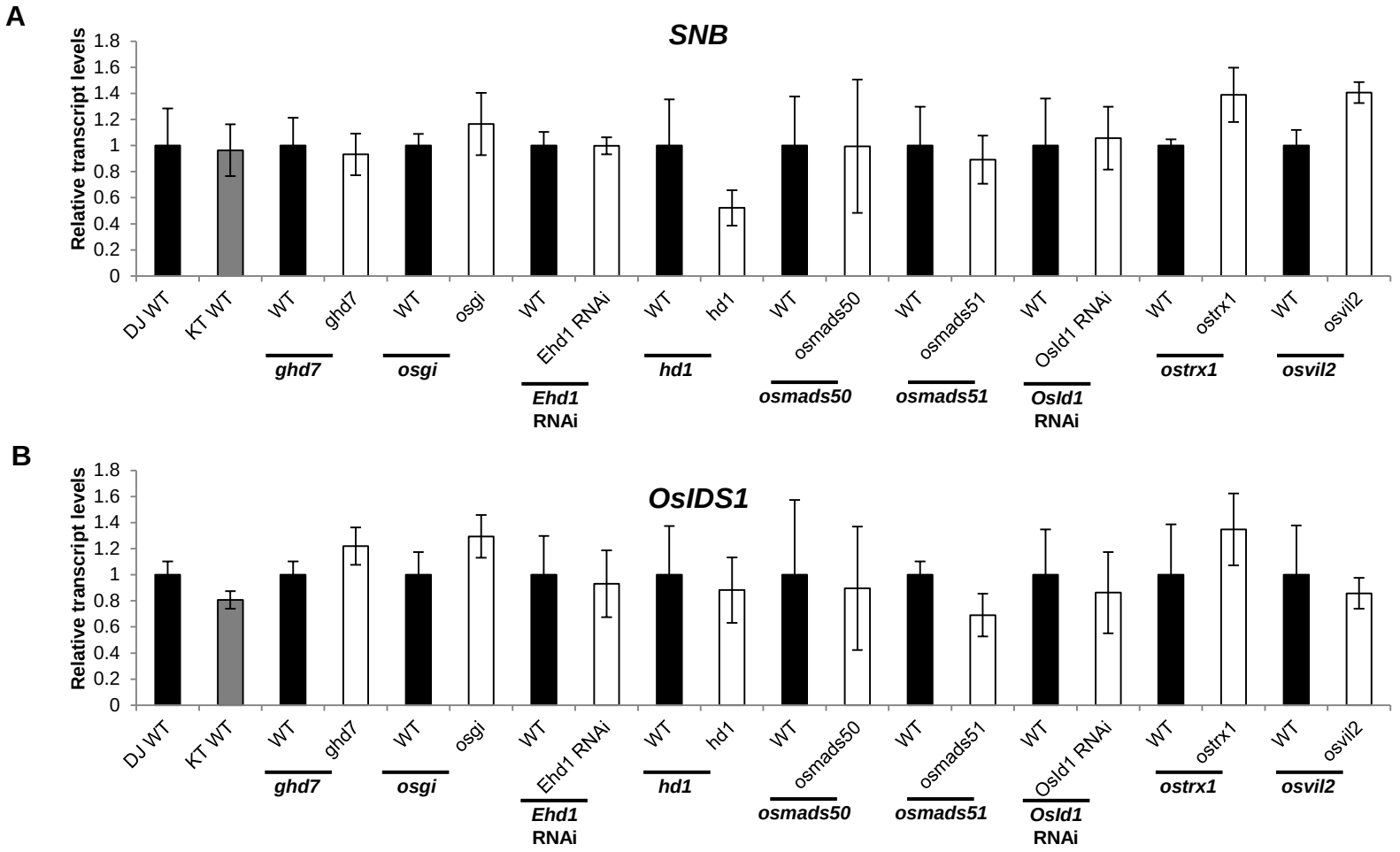

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Figure S6

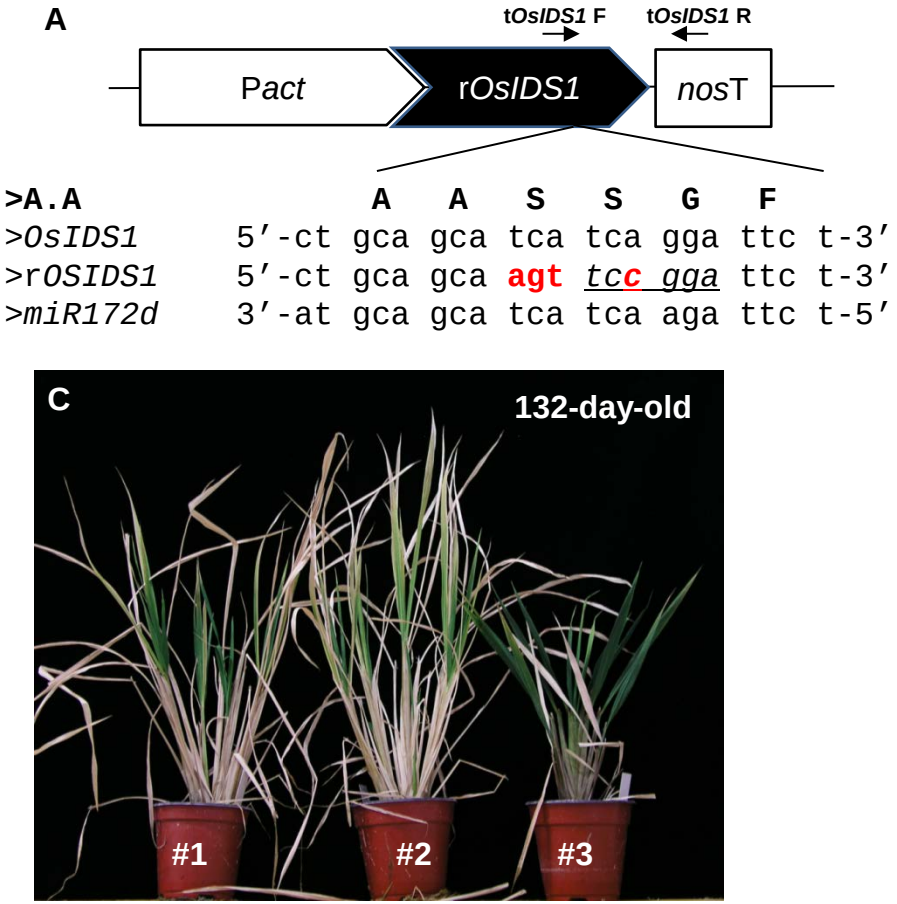

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Figure S7

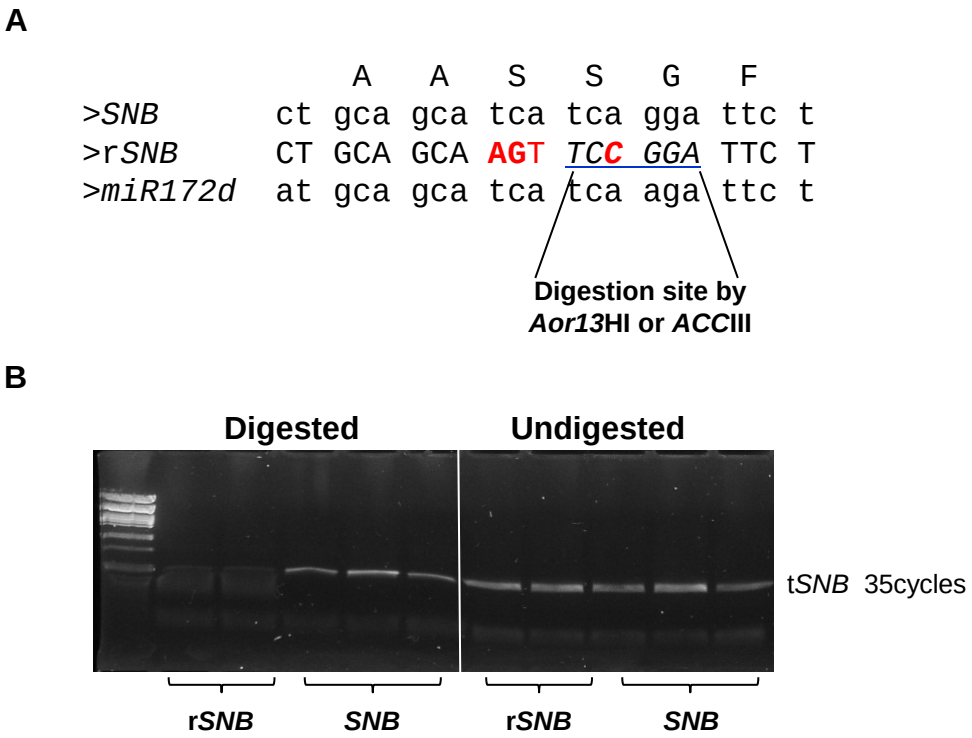

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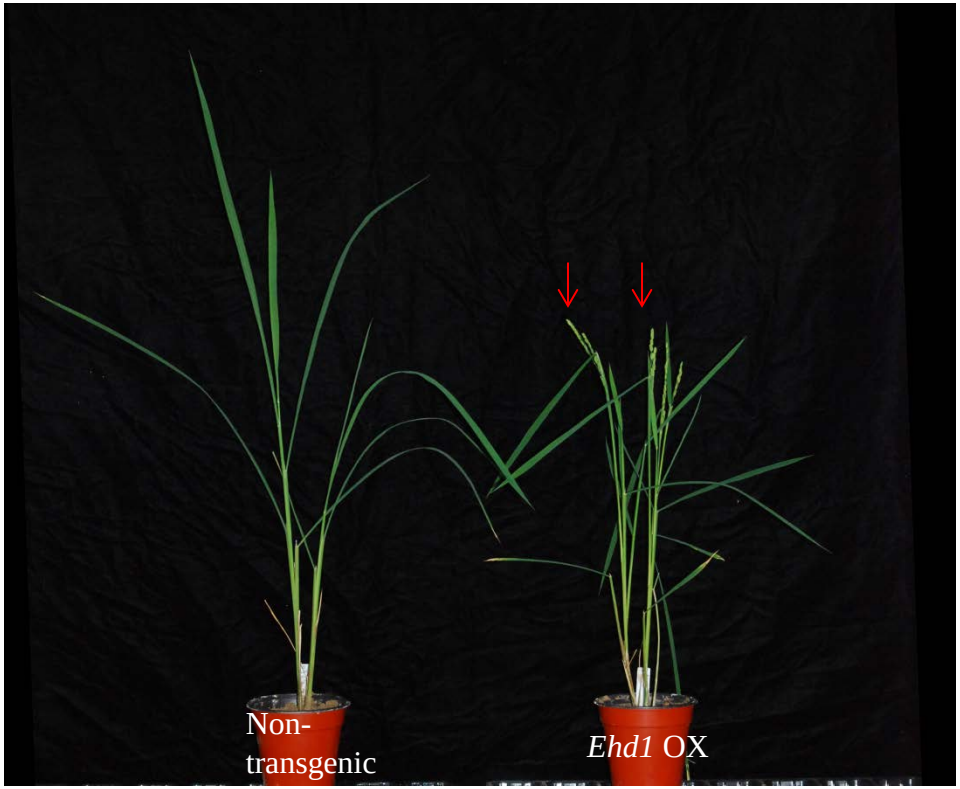
Figure S8

A

B



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(A) Scheme of *Ehd1* OX construct. *Ehd1* full-length cDNA was sub-cloned into pGA3426 vector between maize *ubiquitin* promoter (P*ubi*) and *nopaline synthase* terminator (*nos*T). (B) Phenotypes of *Ehd1* OX plants. Plants were grown under short day conditions (12 h light/ 12 h dark). Photograph was taken at 42 DAT (days after transfer of regenerates). Red arrows indicate emerged panicles.