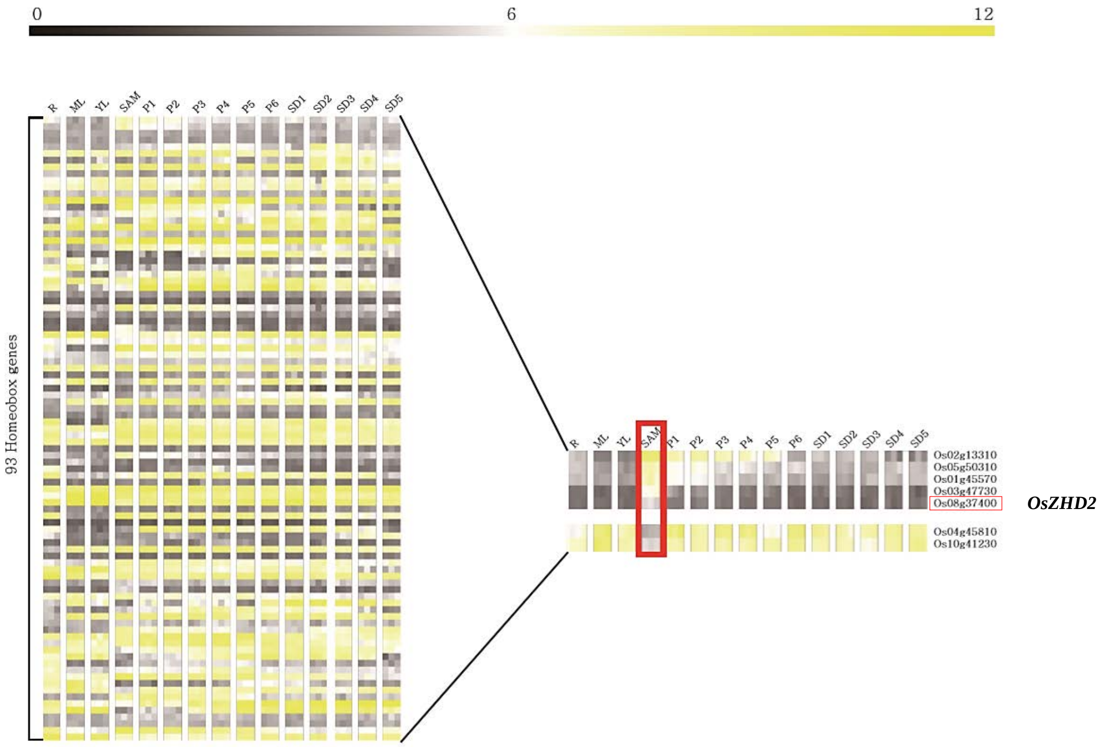
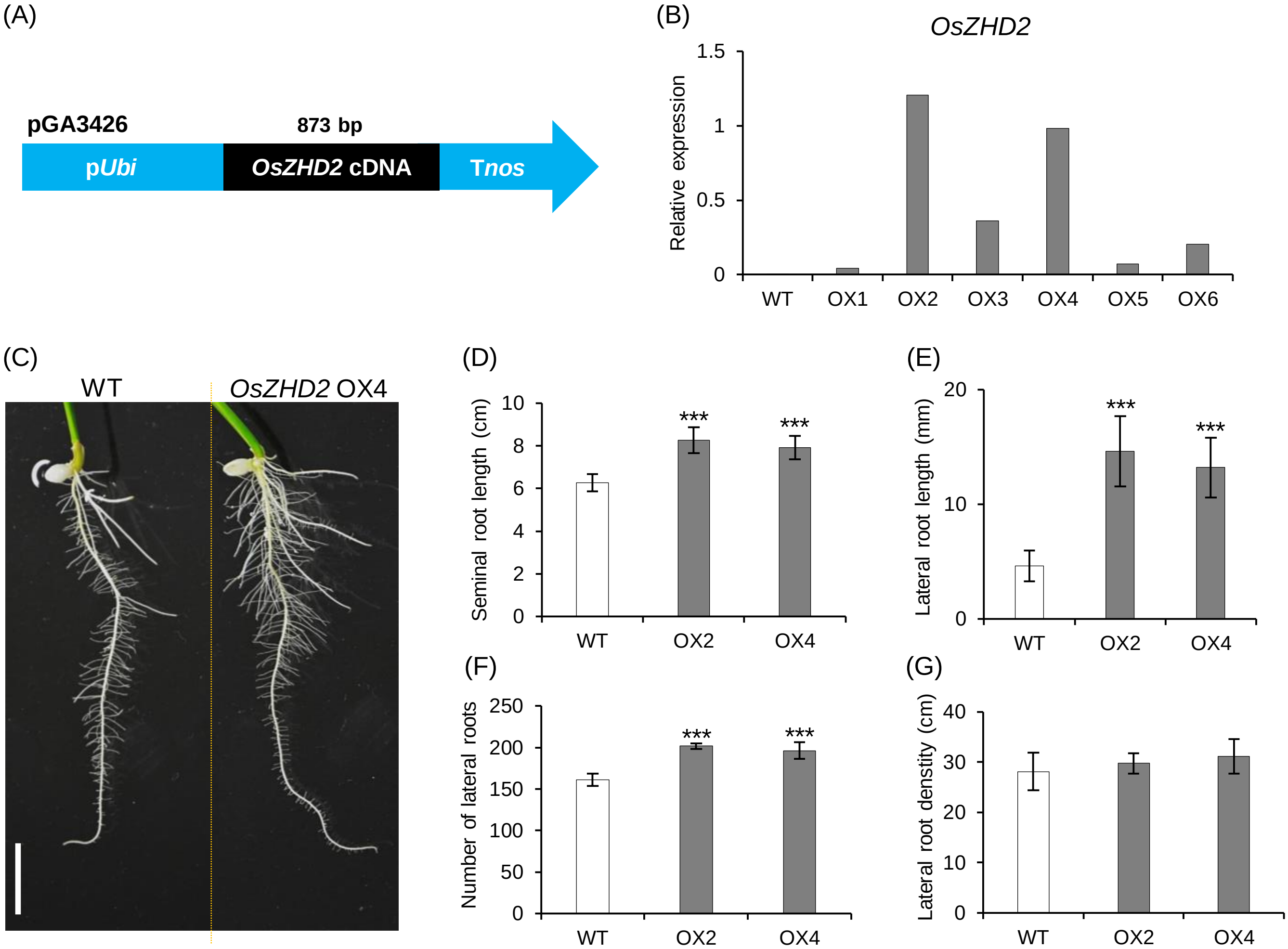
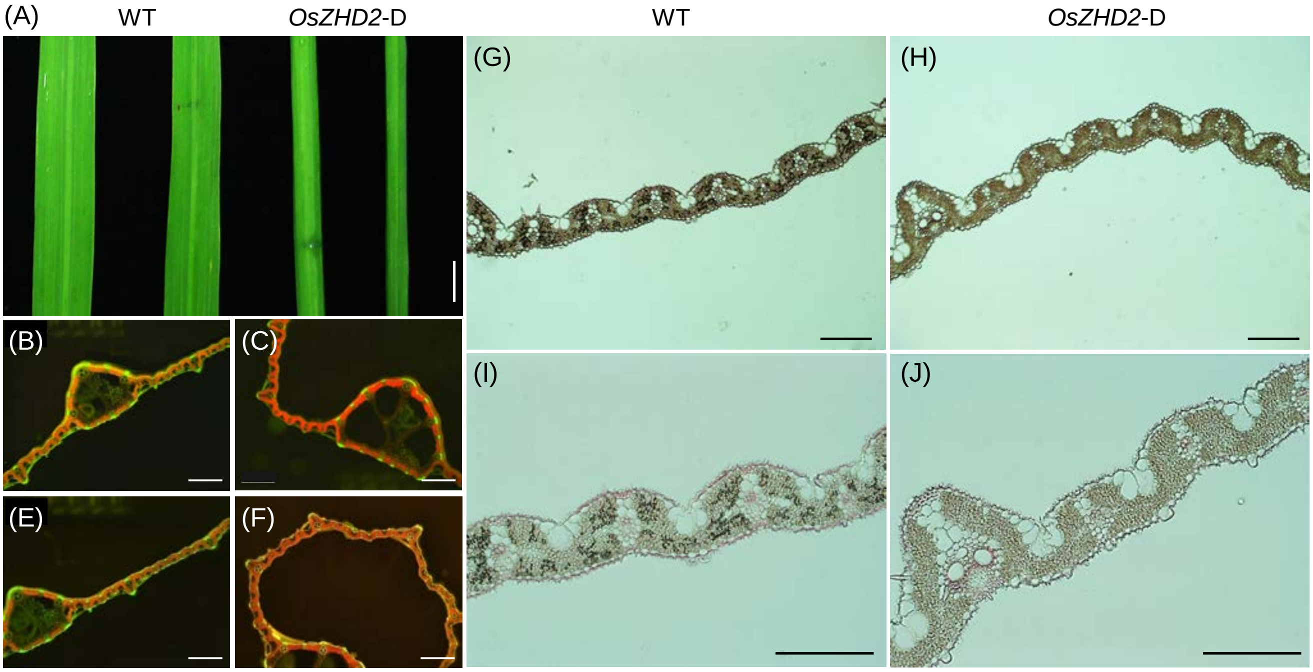


**Supplementary Figure S1.** Expression pattern heatmaps of SAM-preferential homeobox genes. R, root; ML, mature leaf; YL, young leaf; SAM, shoot apical meristem; P1 to P6, developing panicle; SD1 to SD5, developing seeds.



**Supplementary Figure S2.** Characterization of the *OsZHD2* overexpressing plants. (A) Schematic diagram of *OsZHD2*-overexpression construct. The 873-bp full-length *OsZHD2* cDNA was placed between a *Ubi* promoter (p*Ubi*) and a *nopaline synthase* terminator (T*nos*). (B) Expression levels of *OsZHD2* in *OsZHD2*-overexpressing (OX) transgenic plants. RNA samples were collected from leaf blades at the seedling stage. (C) Phenotypes of WT and *OsZHD2* OX plants grown under hydroponic culture conditions at 8 DAG. Bar = 1 cm. (D-G) Root phenotypes of WT and *OsZHD2* OX seedlings at 8 DAG. (D) Seminal root lengths. (E) Lateral root lengths at the top 1-cm region of seminal roots. (F) Total number of lateral roots. (G) Density of lateral roots within the top 1-cm region of seminal roots. Error bars show standard deviations. Statistical significance is indicated by *** (*P* <0.001).

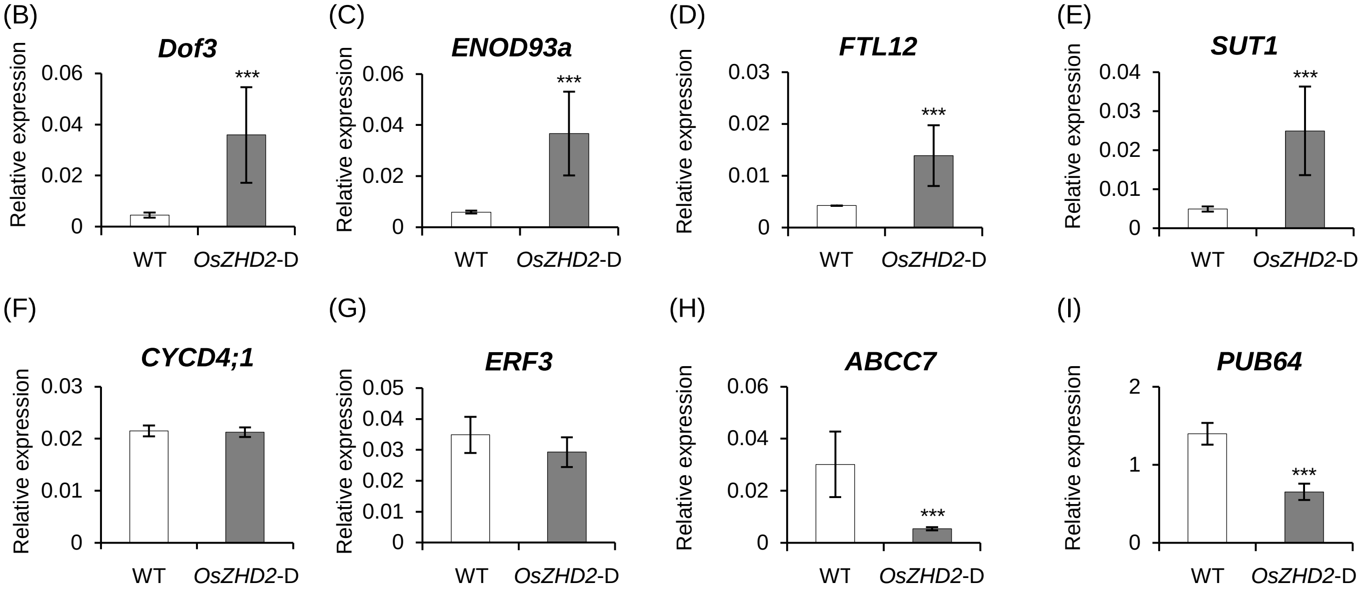


**Supplementary Figure S3.** Characterization of the rolled leaf phenotypes in *OsZHD2*-D. (A) Rolled leaf phenotypes in *OsZHD2*-D. Bar = 5 mm. (B-F) Hand section of WT (B and E) and *OsZHD2*-D (C and F). Bars = 500 μm. (G-J) Cross sectioned samples after paraffin embedding in WT (G and I) and *OsZHD2*-D (H and J). Bars = 200 μm.

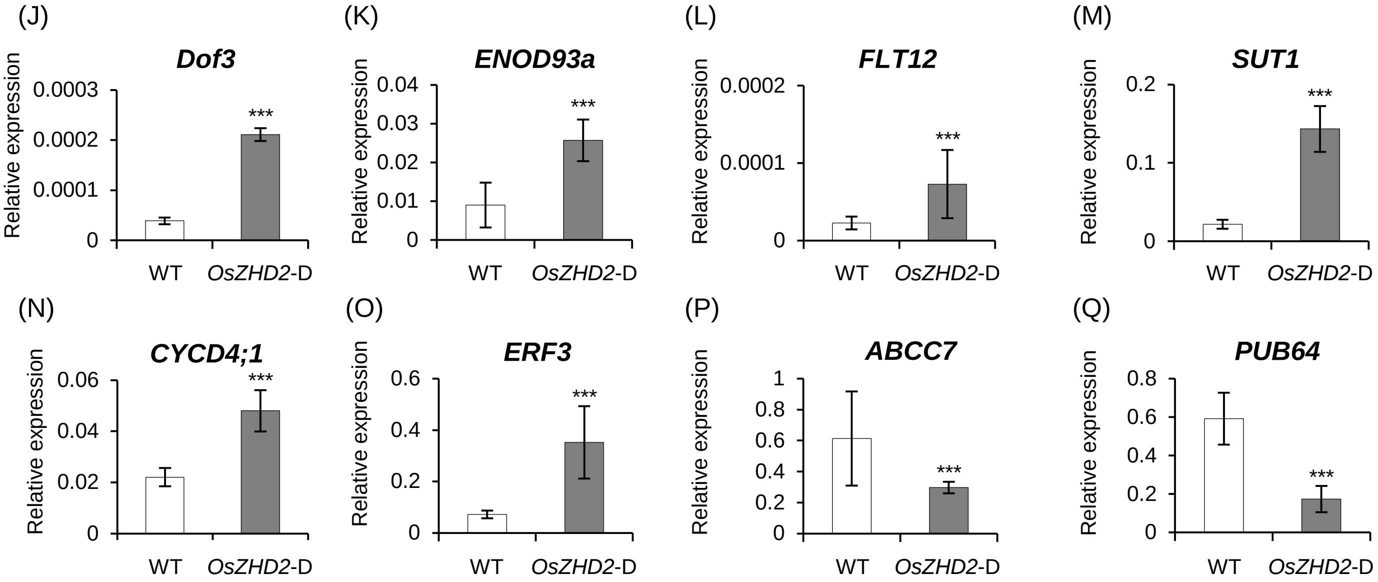
(A)

| | | LOC_ID | Function | 4 days | 6 days |
|---|---|---|---|---|---|
| Up | 4, 6 DAG | OS02G0252400 | OsDof3, dof zinc finger domain containing protein | 2.9 | 7.9 |
| | | OS06G0142200 | OsENOD93a, early nodulin 93 ENOD93 protein | 2.2 | 7.1 |
| | | OS06G0552900 | FT-Like12 | 109.9 | 206.9 |
| | | OS03G0170900 | OsSUT1, SUCROSE TRANSPORTER 1 | 5.7 | 5.1 |
| | 6 DAG | OS09G0466100 | CYCD4;1 | 1.4 | 2.3 |
| | | OS01G0797600 | ERF2 | 0.9 | 3.2 |
| Down | 4, 6 DAG | OS04G0588700 | OsABCC7, ABC transporter superfamily ABCC subgroup member 7 | 0.3 | 0.3 |
| | | OS06G0159600 | OsPUB64, U-box protein 64 | 0.3 | 0.3 |

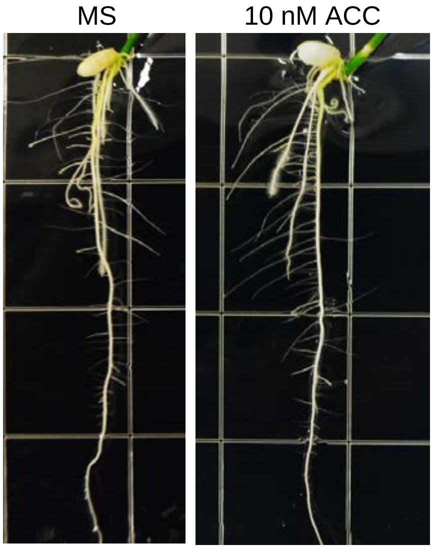
**4 DAG**



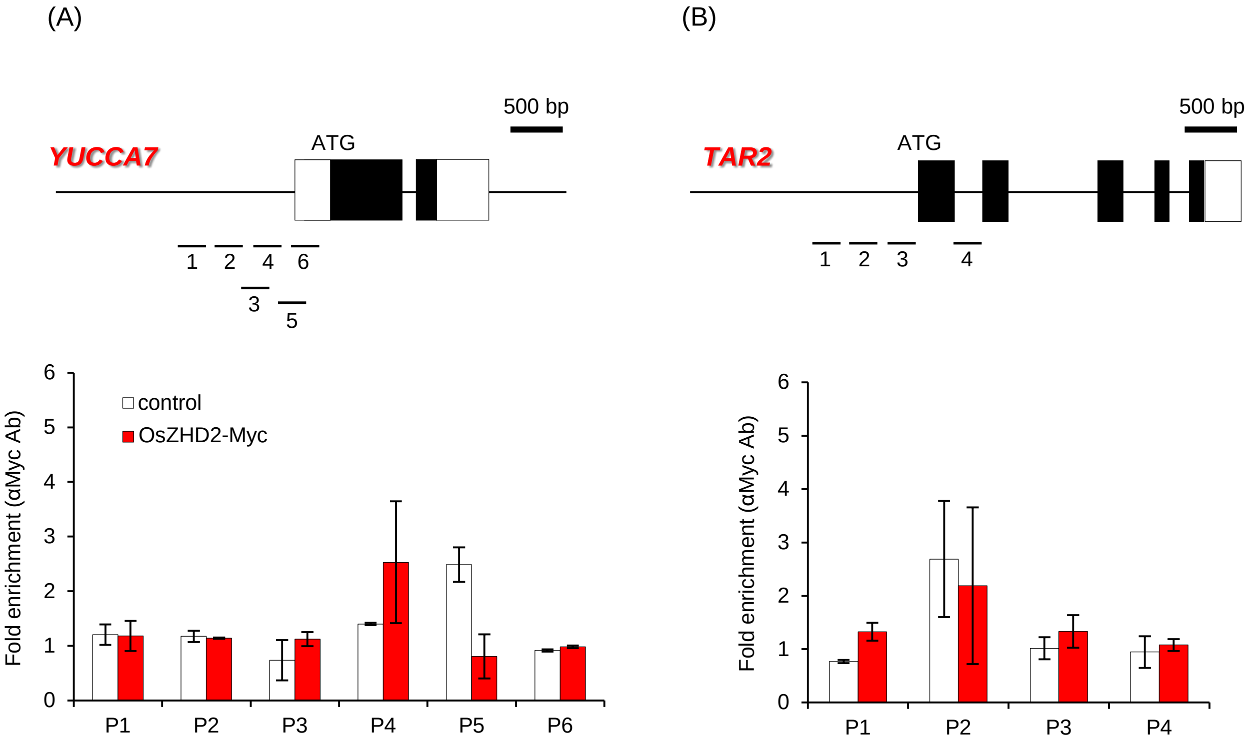
**6 DAG**



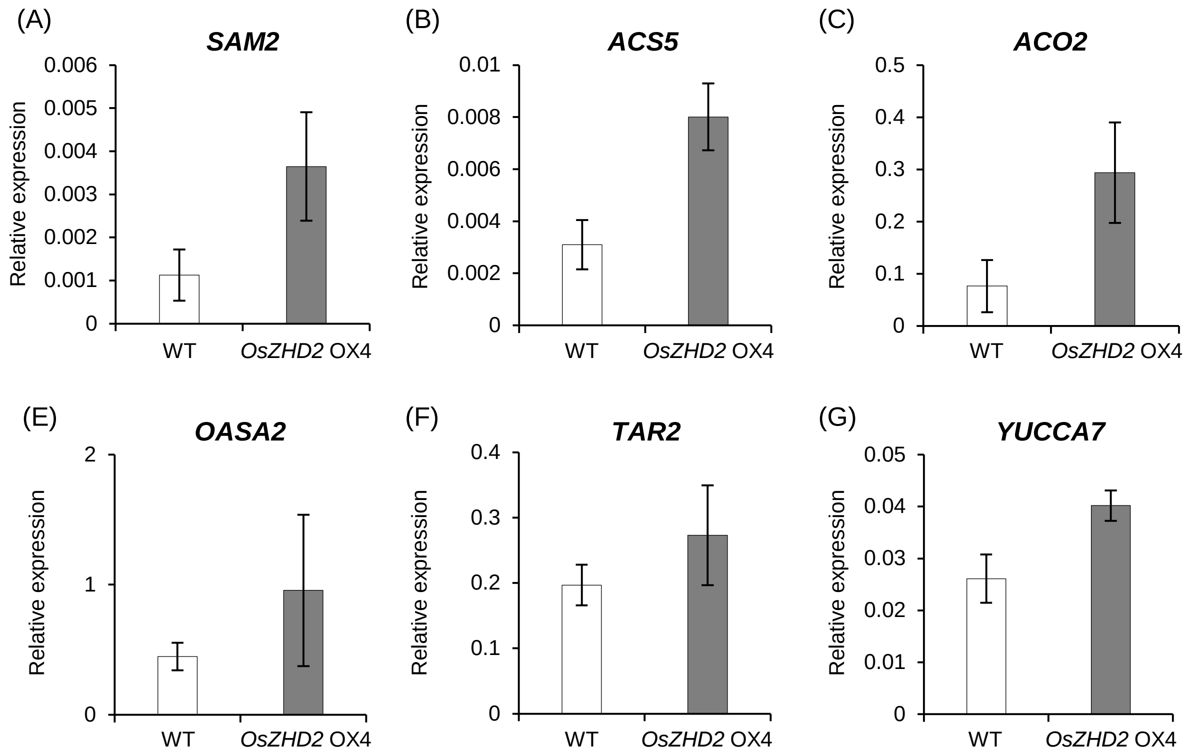
**Supplementary Figure S4.** Validation of RNA-sequencing by qRT-PCR. (A) Genes differentially expressed in *OsZHD2*-D. (B-I) Transcript levels of selected genes at 4 DAG. (J-H) Transcript levels of selected genes at 6 DAG, compared with *Ubi*. Error bars indicate standard deviations. *n* = 4.



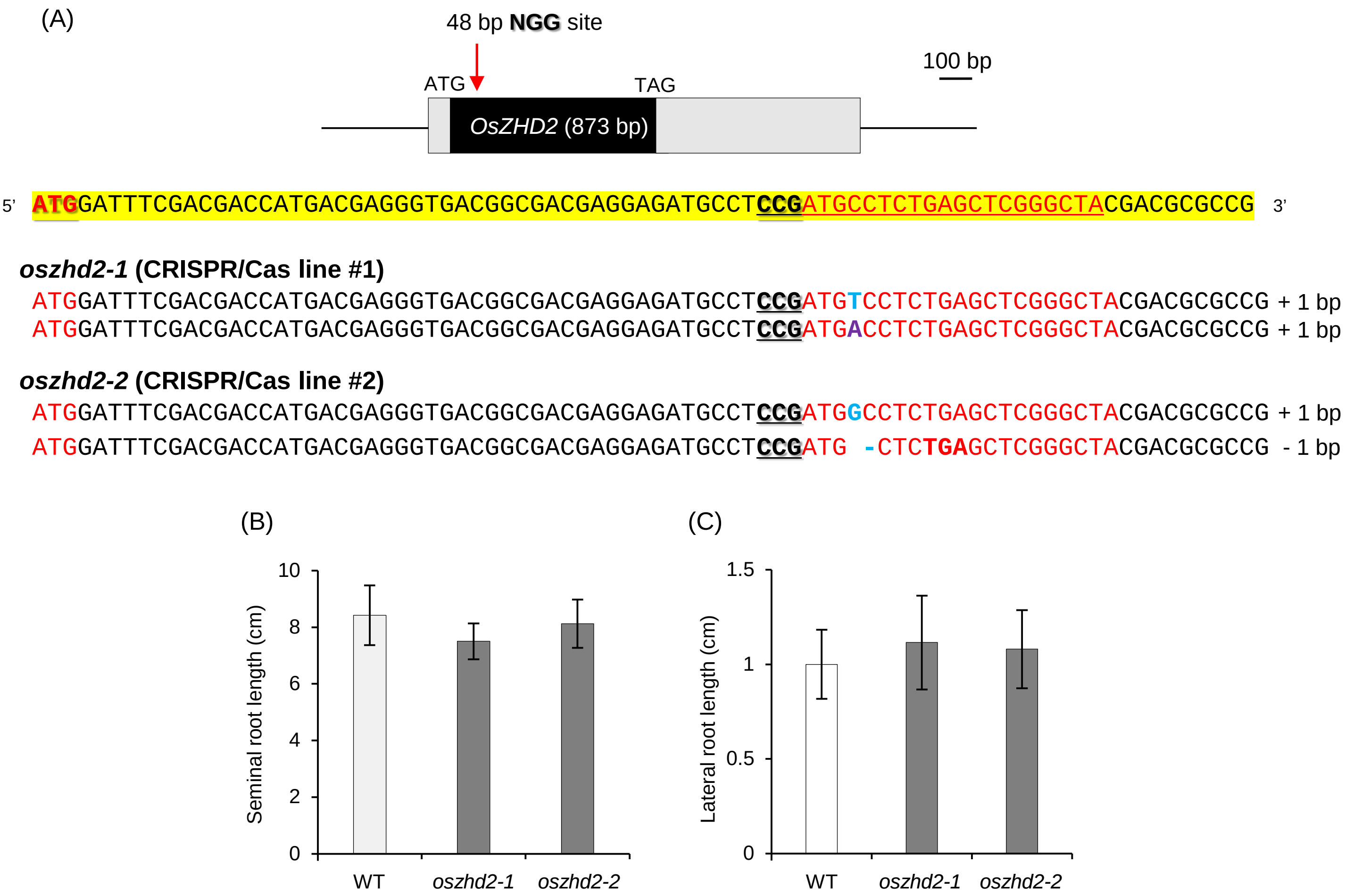
**Supplementary Figure S5.** Phenotype of WT plants after mock (left) and 10 nM ACC (right) treatment.



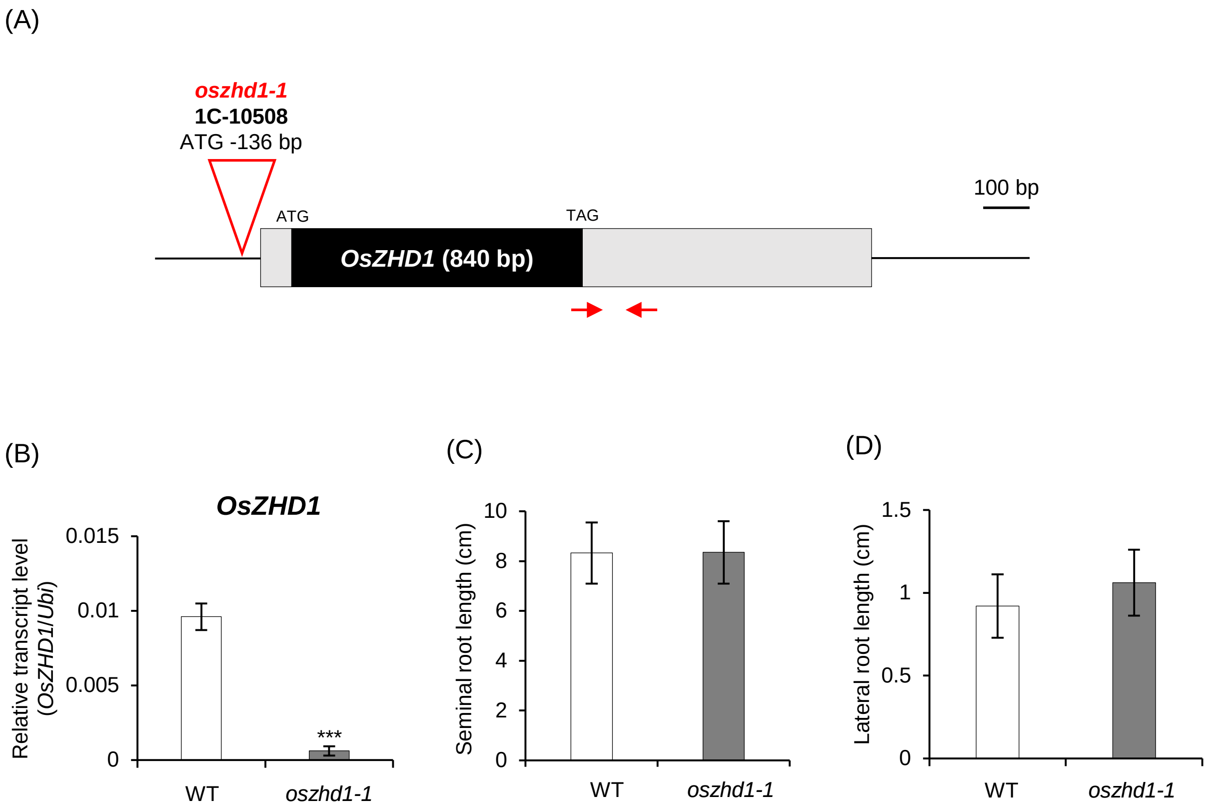
**Supplementary Figure S6.** ChIP assay with OsZHD2-Myc protein. OsZHD2-Myc enrichment in chromatin regions of *YUCCA7* (A) and *TAR2* (B).



**Supplementary Figure S7.** Expression levels of ethylene biosynthesis genes and auxin biosynthesis genes in roots at 6 DAG. Error bars show standard deviations. n = 4.



**Supplementary Figure S8.** Generation of *oszhd2* mutants. (A) Schematic diagram of *OsZHD2* and mutation sites generated using the CRISPR/Cas9 system. (B) Seminal root lengths of WT and *oszhd2* mutants at 8 DAG. $n = 5$. (C) Lateral root lengths of WT and *oszhd2* mutants at 8 DAG. $n > 60$.



**Supplementary Figure S9.** Analysis of *oszhd1* mutant. (A) Schematic diagram of *OsZHD1* genome and T-DNA insertion site in Line 1C-10508. T-DNA was inserted 136 bp upstream from the ATG start codon. (B) Transcript levels of *OsZHD1* in WT and *oszhd1* plants. RNA samples were collected from leaf blades at the seedling stage. (C) Seminal root lengths of WT and *oszhd1* plants at 8 DAG. $n = 5$. (D) Lateral root lengths of WT and *oszhd1-1* plants at 8 DAG. $n > 60$.