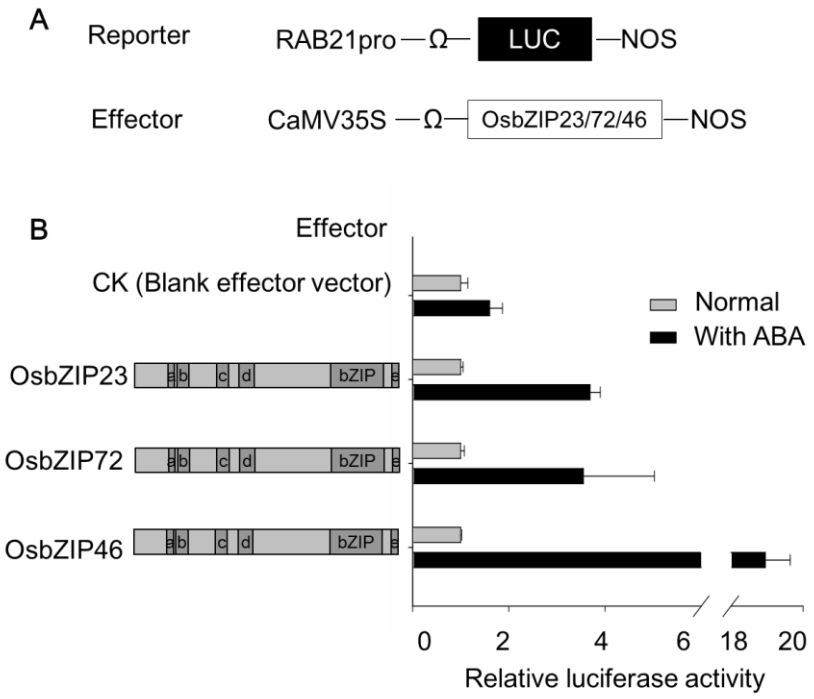
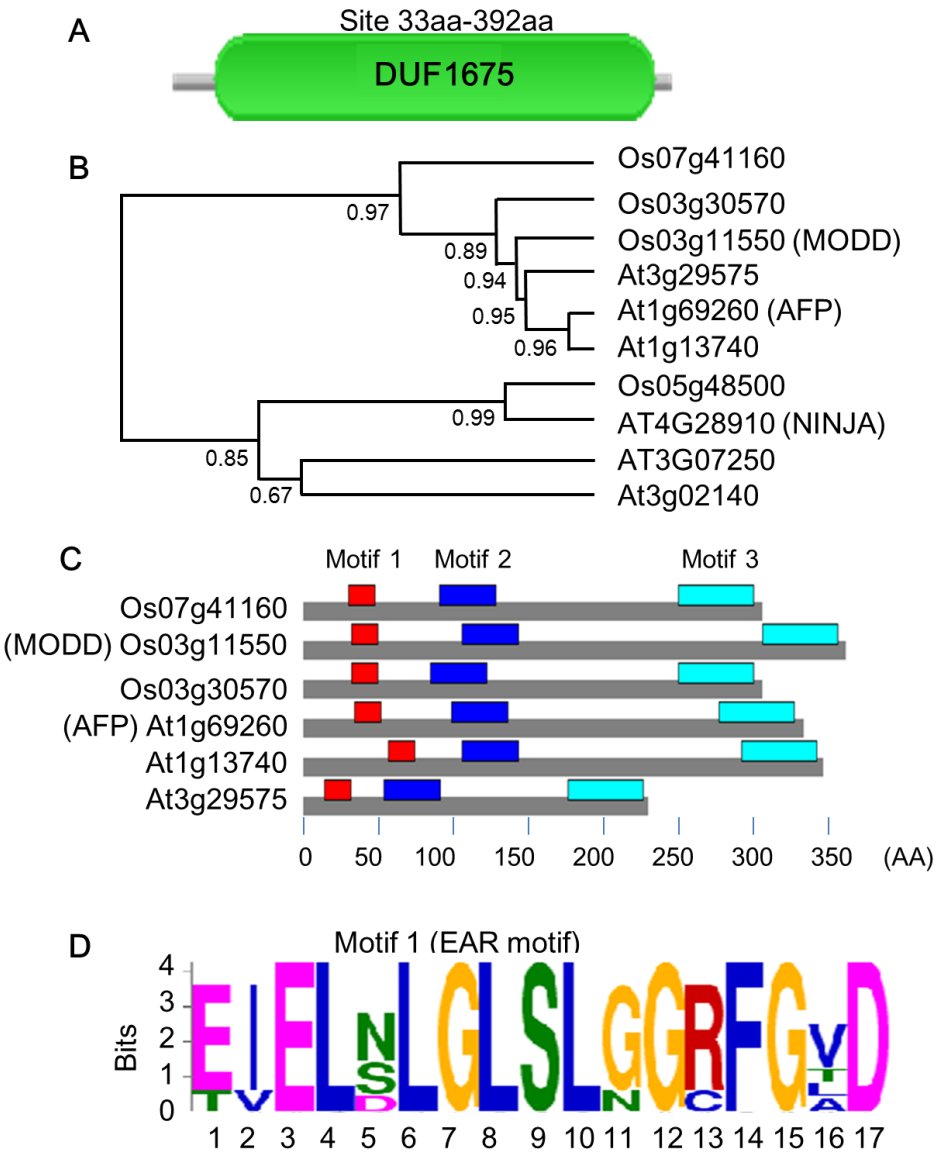


Supplemental Figure 1. The transcriptional regulation activity of OsbZIP23, OsbZIP72, and OsbZIP46 is activated by ABA.
(A) Scheme of the constructs used in the co-transfection experiments.
(B) Relative luciferase activities in rice protoplasts that had been co-transfected with the effector and reporter plasmids. Schemes of the native full length OsbZIP23, OsbZIP72, and OsbZIP46 are shown at the left. “Normal”, in normal conditions; “With ABA”, treated with ABA; All luciferase activities are expressed relative to the values obtained under normal conditions. Error bars indicate the standard errors based on three replicates.



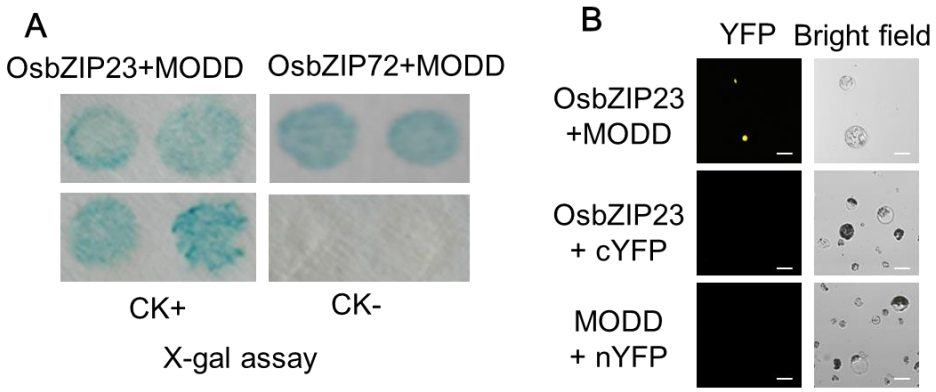
Supplemental Figure 2. Protein sequence analysis of the MODD family members.

(A) The unknown function domain DUF6175 of MODD predicted by the annotation database. The corresponding region of DUF6175 is from 33 aa to 392 aa of the MODD protein sequence.

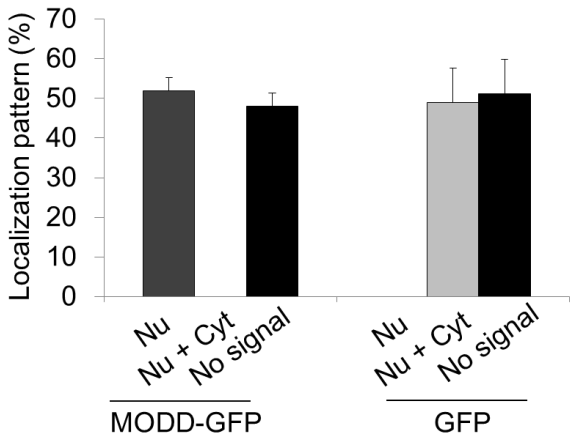
(B) Phylogenetic tree of the MODD and its homologous members from Arabidopsis and rice.

(C) Alignment of conserved motifs based on the sequences of the MODD sub-group members. The length of the amino acid sequence is indicated at the bottom.

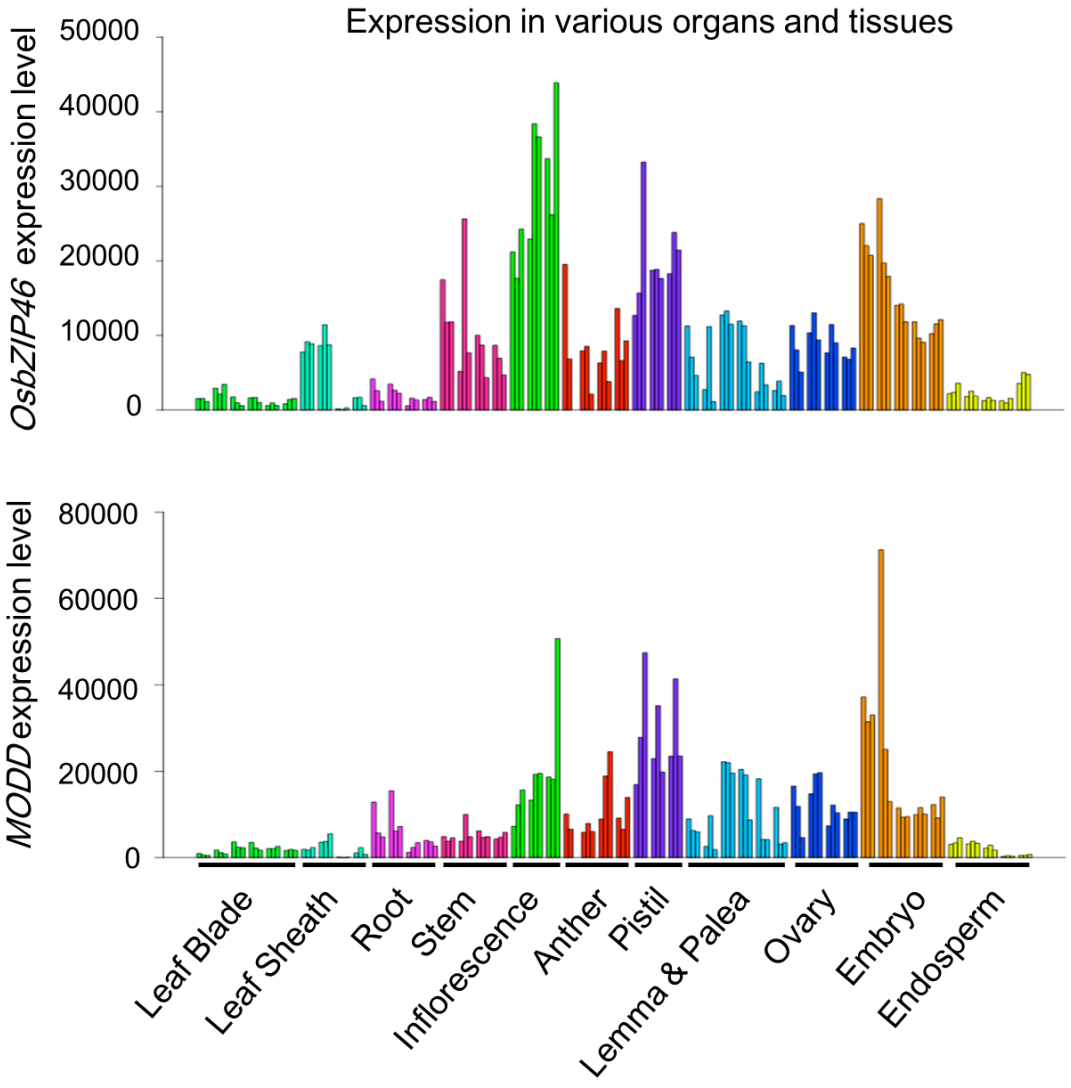
(D) Sequence LOGO view of the consensus EAR motif, which is equivalent to motif 1 presented in panel C. The height of the letter (amino acid) at each position represents the degree of conservation.



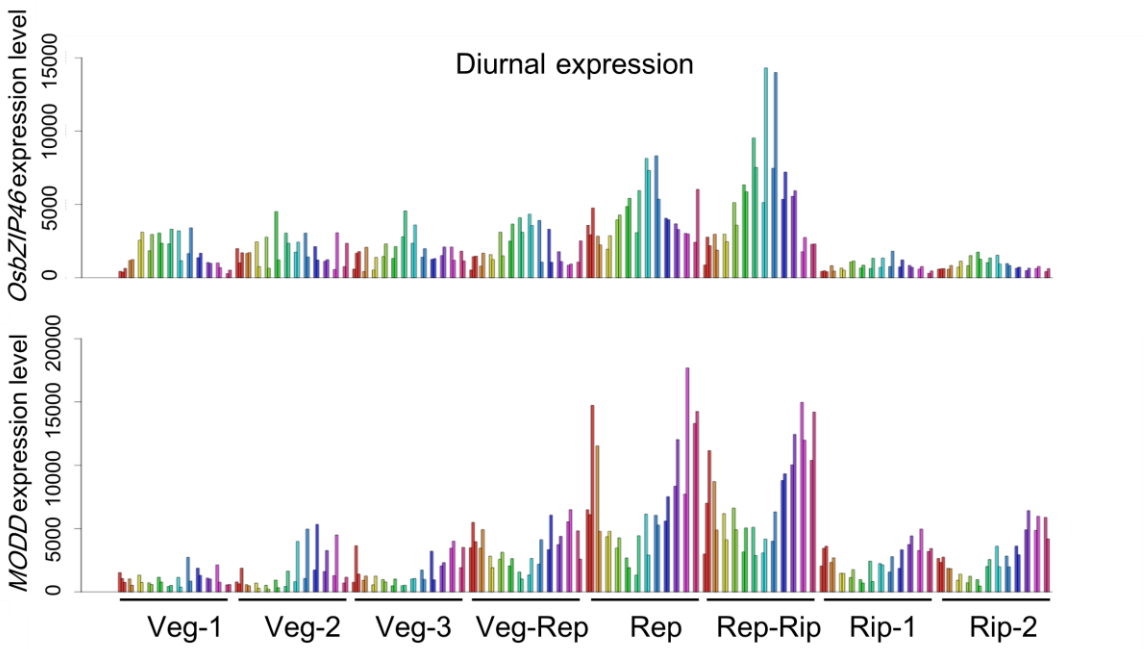
Supplemental Figure 3. OsbZIP23 and OsbZIP72 interact with MODD.
(A) Yeast two-hybrid assay of MODD with OsbZIP23 (OsbZIP23 + MODD) or OsbZIP72 (OsbZIP72 + MODD). CK+ and CK- indicate the positive and negative control, respectively.
(B) Confirmation of the interaction of OsbZIP23 and MODD by BiFC (Bimolecular fluorescence complementation) in rice protoplasts. Scale bars indicate 20 μm.



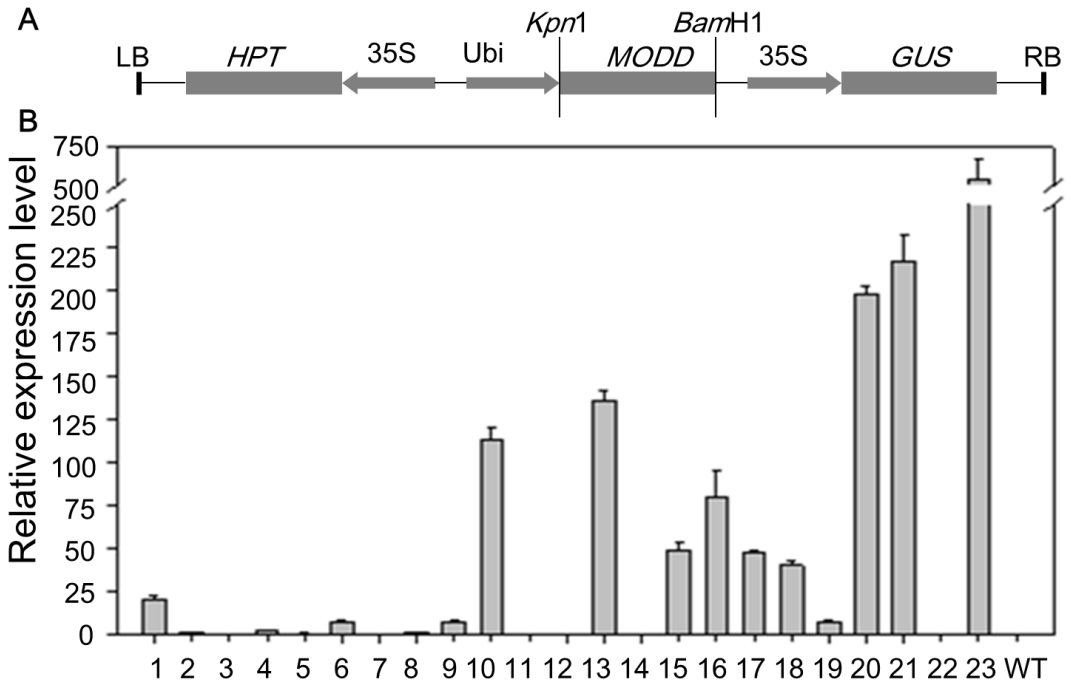
Supplemental Figure 4. Statistical information on the subcellular localization of MODD-GFP and the control (GFP). Nu, nucleus; Nu+Cyt: Nucleus and cytoplasm. Error bars indicate the standard deviation based on 3 replicates, and more than 20 protoplasts were counted for each replicate.



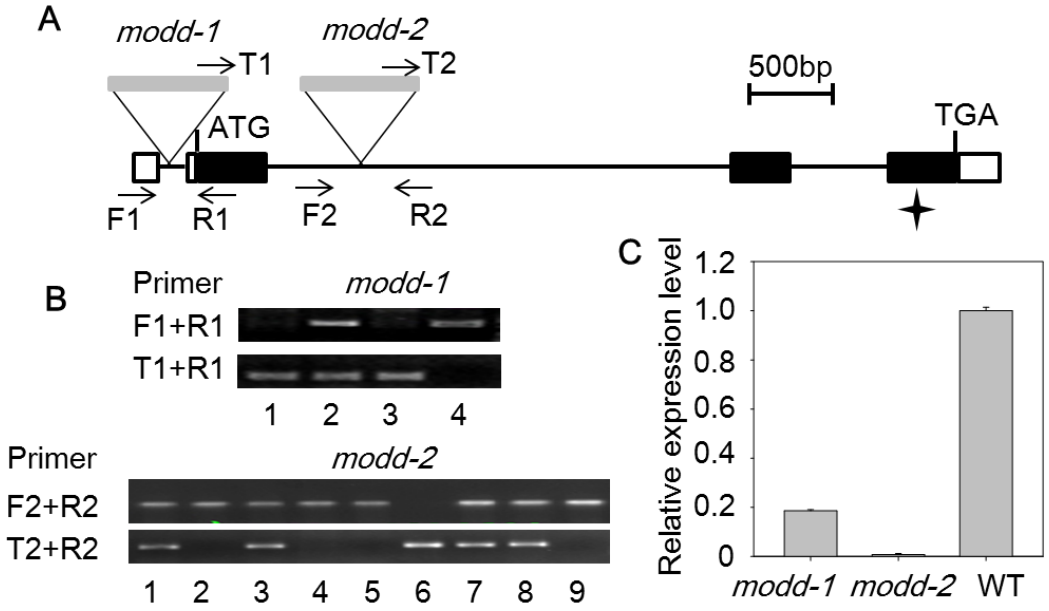
Supplemental Figure 5. Similar expression patterns of *MODD* and *OsbZIP46* across various tissues and organs.



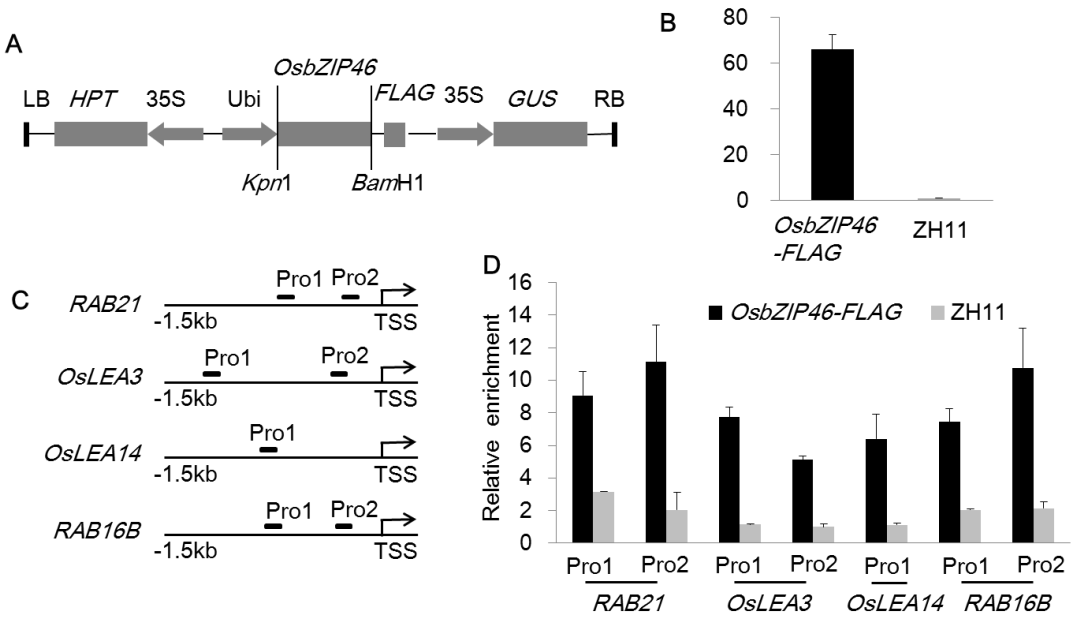
Supplemental Figure 6. Circadian rhythmic expression profiles of *MODD* and *OsbZIP46*. The *x*-axis indicates different growth stages for the experiment in leaf. Veg, vegetative stage; Rep, reproductive stage; Rip, ripening stage. Each experiment includes 12 time points in 24 hours, with a start point at 10 AM.



Supplemental Figure 7. Generation of transgenic rice overexpressing *MODD*.
(A) Overexpression construct of *MODD* for rice transformation.
(B) Expression level analysis of *MODD* in transgenic plants with real-time quantitative RT PCR. Among 23 transgenic lines produced, 9 lines showed an expression level more than 25 times higher than the wild-type (WT) Zhonghua 11. Error bars indicate standard errors based on 3 replicates.



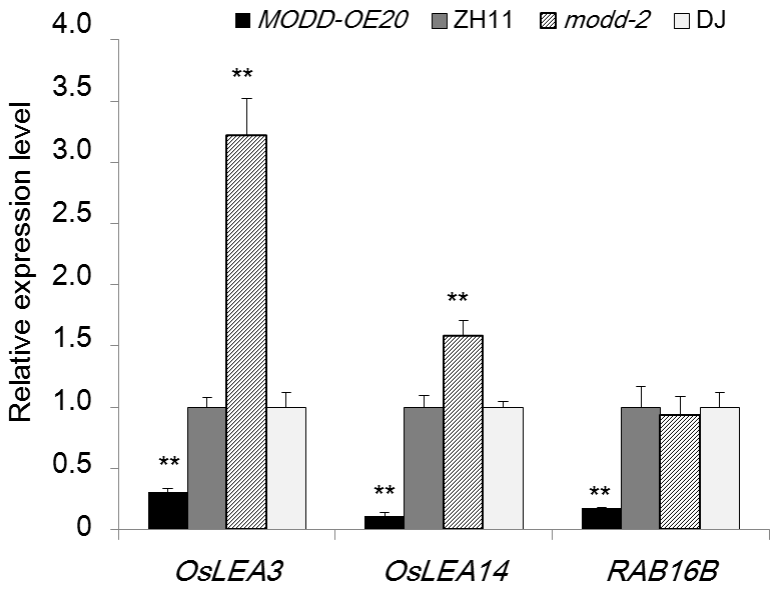
Supplemental Figure 8. Characterization of *modd* T-DNA insertion mutants
(A) Schematic representation of *MODD* and insertion positions of the T-DNA in two allelic mutants. The rectangular blocks indicate exons.
(B) Genotyping for *modd-1* and *modd-2* plants. Gene-specific and T-DNA-specific primers, with locations indicated in A, were used for genomic PCR.
(C) Real-time PCR analysis of *modd* in the WT, *modd-1*, and *modd-2*. The amplification region is indicated with an asterisk in figure A. *Actin* was used as an internal control. Error bars indicate standard errors based on 3 replicates.



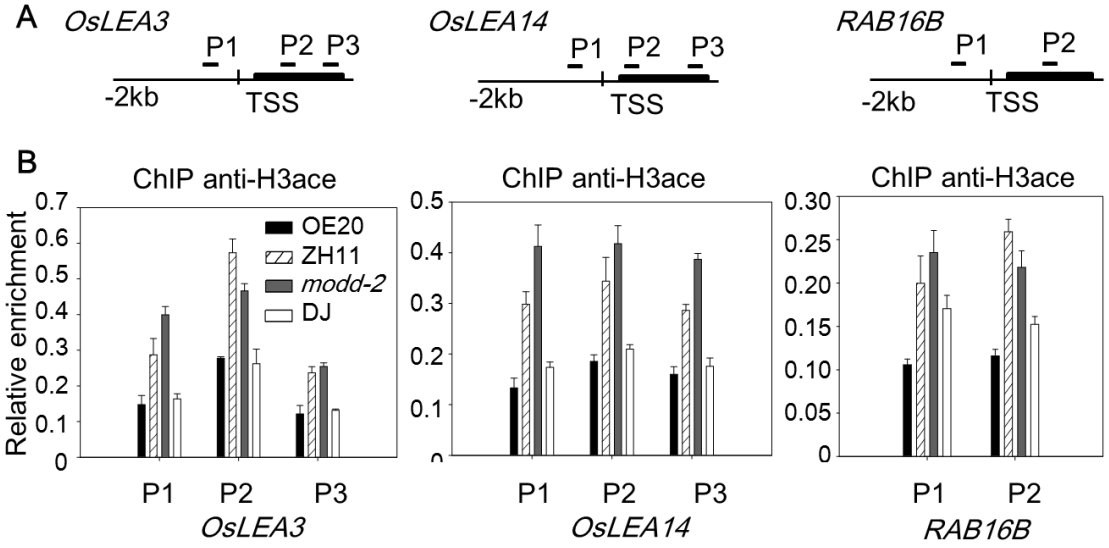
Supplemental Figure 9. Validation of the direct binding of OsbZIP46 to the promoters of target genes.

(**A** and **B**) Plant materials used for the ChIP-qPCR. **A**, *OsbZIP46-FLAG* fusion construct for rice transformation. **B**, Expression level analysis of *OsbZIP46* in transgenic plants with real-time quantitative RT-PCR. Error bars indicate standard errors based on 3 replicates.

(**C** and **D**) Validation of the direct binding of OsbZIP46 to the promoter of *RAB21*, *OsLEA3*, *OsLEA14*, and *RAB16B* by ChIP-qPCR with antibody against FLAG. Schemes show the promoter regions of the tested genes. Short lines indicate the regions detected by ChIP-qPCR in (**D**). The enrichment values were normalized to *ACTIN*. Error bars indicate standard errors based on 3 replicates.



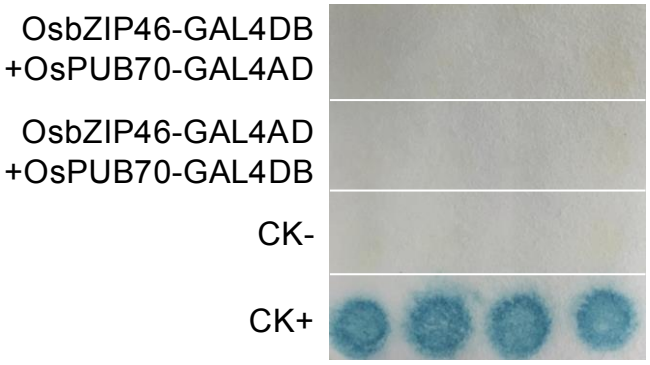
Supplemental Figure 10. The expression of OsbZIP46-targeted genes in the *MODD*-overexpression (OE-20) and *modd* loss-of-function mutant (*modd-2*) lines. ZH11 and DJ are the wild-type controls of the *MODD* overexpressor and *modd-2*, respectively. Error bars indicate standard errors based on 3 replicates (**, $P < 0.01$, Student's t-test).



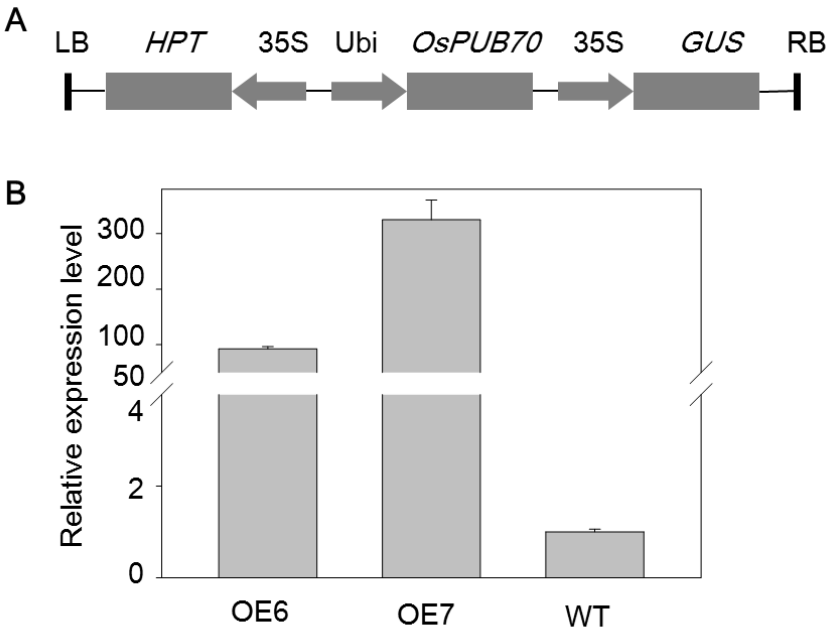
Supplemental Figure 11. Histone acetylation levels at the OsbZIP46 target genes in *MODD* overexpressor (OE20), *modd-2* mutant and wild-type (ZH11 and DJ) using ChIP-qPCR.

(**A**) The diagram of the target genes is shown in the upper panel. The primer sets (P1 to P3) used in the ChIP experiments are indicated.

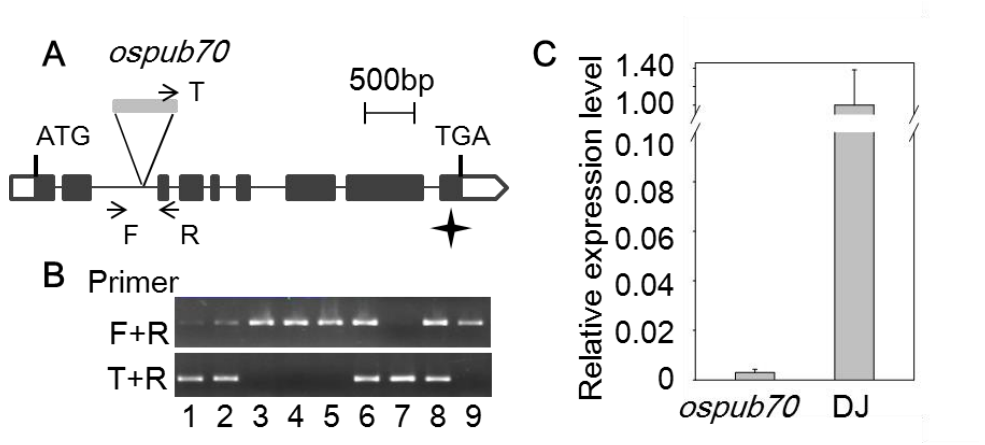
(**B**) ChIP was performed with anti-acetyl-histone H3 antibody. Enrichment values were normalized to *ACTIN*. The data indicate mean values with standard errors of three biological replicates.



Supplemental Figure 12. Yeast two-hybrid assay of OsbZIP46 and OsPUB70. CK+ and CK- indicate the positive and negative control, respectively.



Supplemental Figure 13. Generation of *OsPUB70*-overexpression transgenic rice.
(A) Construct of *OsPUB70*-overexpression for rice transformation.
(B) Expression level analysis of *OsPUB70* in transgenic plants with real-time quantitative RT PCR. OE6 and OE7, two overexpression lines. WT, wild type. Error bars indicate standard errors based on 3 replicates.



Supplemental Figure 14. Characterization of *ospub70* T-DNA insertion mutants.

(A), Schematic representation of *ospub70* and insertion position of T-DNA. The rectangular blocks indicate exons.

(B), Genotyping for *ospub70* plants. Gene-specific and T-DNA-specific primers, with locations indicated in A, were used for genomic PCR.

(C), Real-time PCR analysis of *OsPUB70* in the WT (DJ) and *ospub70*. The amplification region is indicated with a star in **(A)**. *Actin* was used as internal control. Error bars indicate standard errors based on 3 replicates.

Supplemental Table 1. Interaction proteins of AFP obtained from the Plant Interactome Database.

ID	Gene Name
AT2G36270	*ABI5, GIA1*
AT2G41070	*ATBZIP12, DPBF4, EEL*
AT3G02140	*AFP4, TMAC2*
AT3G19290	*ABF4, AREB2*
AT3G29575	*AFP3*
AT3G44460	*AtbZIP67, DPBF2*
AT3G56850	*AREB3, DPBF3*
AT4G34000	*ABF3, DPBF5*
AT1G13740	*AFP2*
AT1G49720	*ABF1*