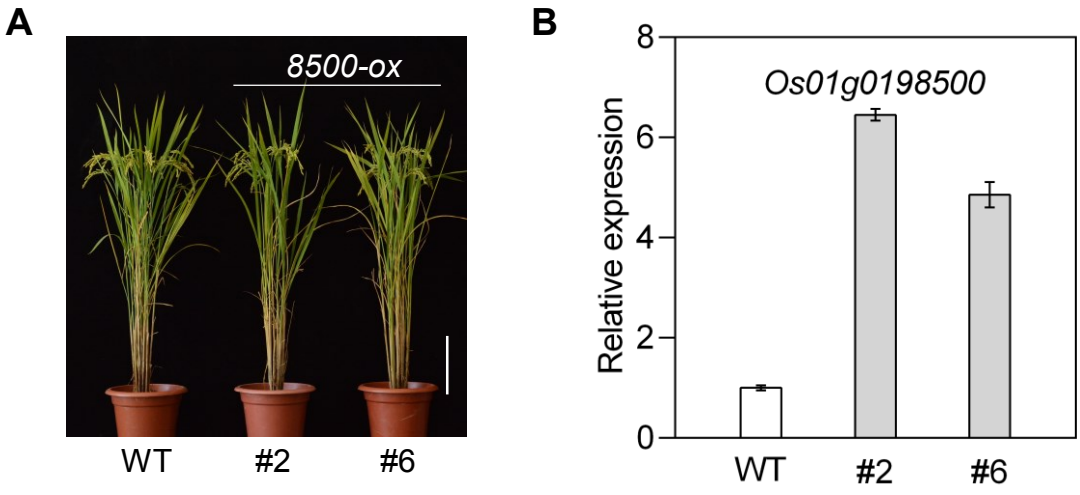
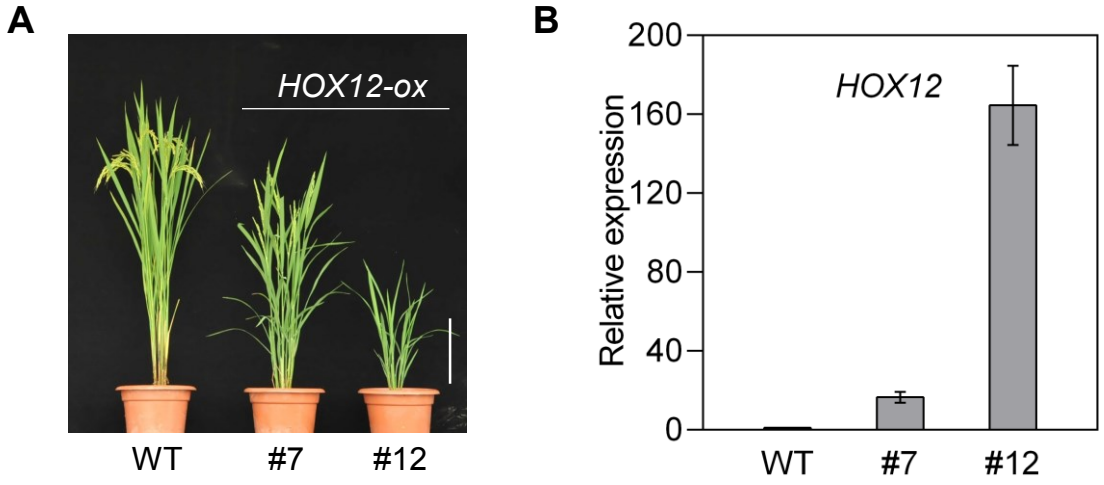


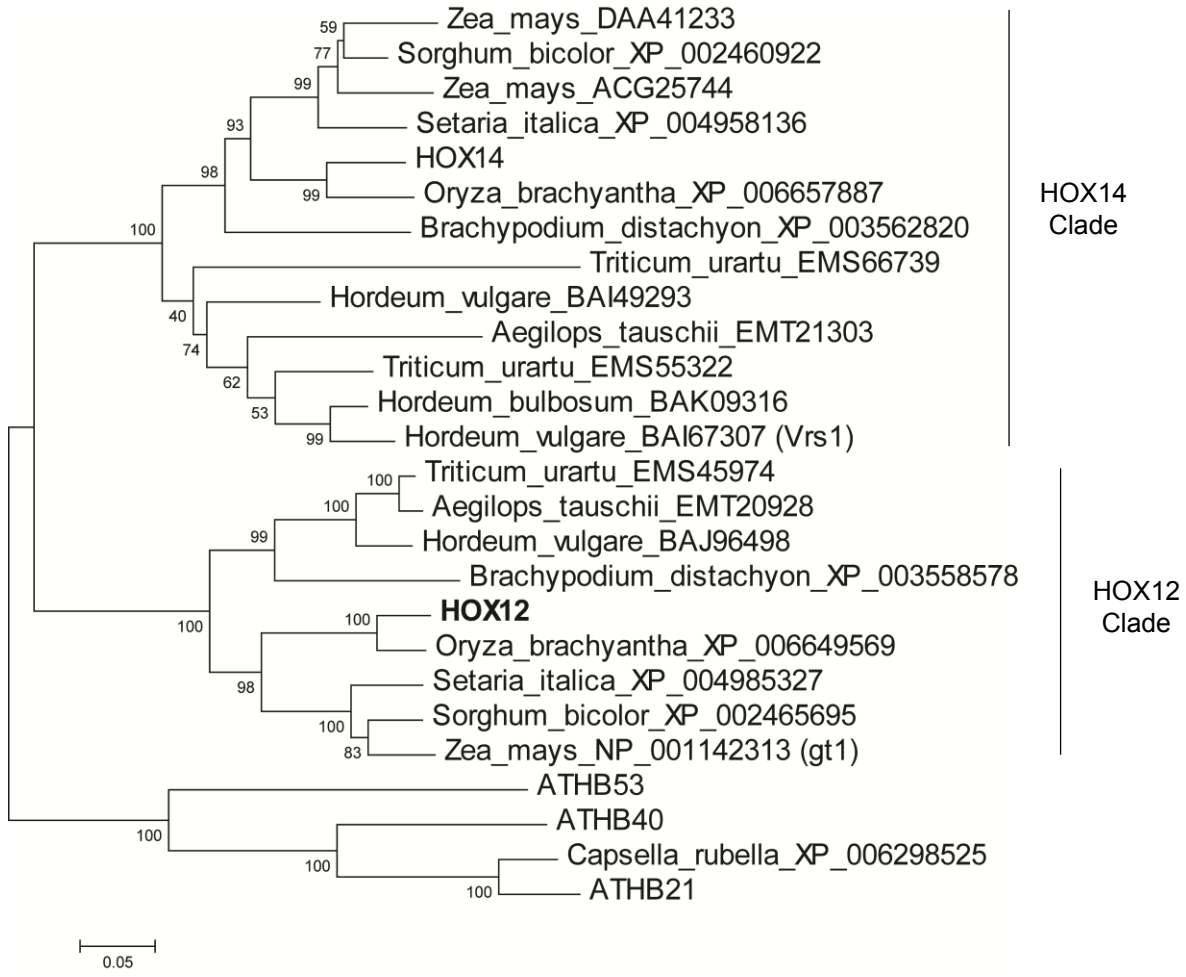
Supplemental Figure 1. Phenotypes of *Os01g0198500* Overexpression Transgenic Plants.

(A) Representative morphological phenotypes of *Os01g0198500* overexpression (*8500*-ox) transgenic plants (#2 and #6) at the mature stage. Bar = 20 cm.

(B) qRT-PCR analysis of the expression levels of *Os01g0198500* in *8500*-ox plants. The transcript level of *Os01g0198500* in the wild type was set as 1.0. Error bars indicate the SD (n = 3).

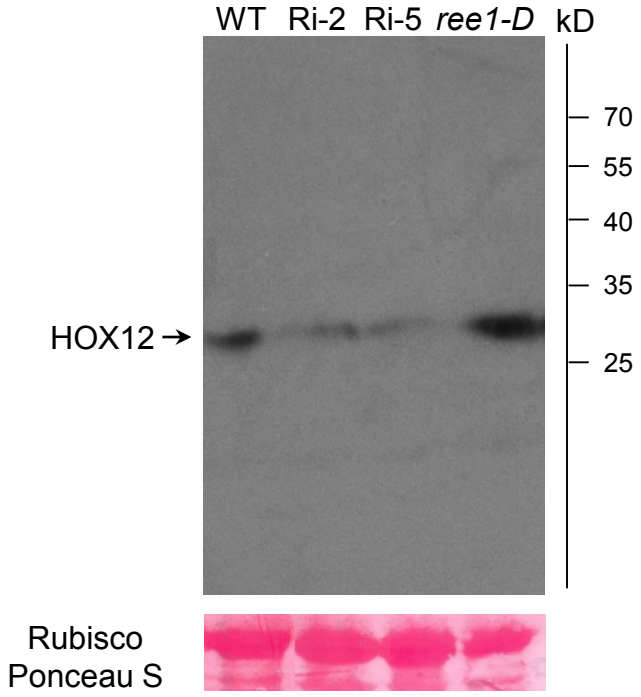


Supplemental Figure 2. Phenotypes of *Os01g0198600/HOX12* Overexpression Transgenic Plants.
(A) Representative morphological phenotypes of *HOX12* overexpression (*HOX12*-ox) transgenic plants (#7 and #12) at the mature stage. Bar = 20 cm.
(B) qRT-PCR analysis of the expression levels of *HOX12* in *HOX12*-ox plants. The transcript level of *HOX12* in the wild type was set as 1.0. Error bars indicate the SD (n = 3).



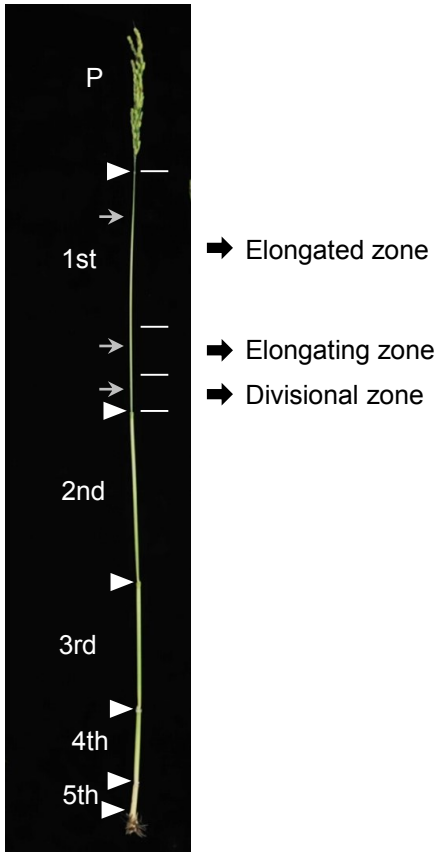
Supplemental Figure 3. A Phylogenetic Tree of the HOX12-like Proteins in Higher Plants.

Amino acid sequences of 25 HOX12 homologs were obtained from NCBI (http://www.ncbi.nlm.nih.gov/) and used to construct a bootstrap N-J phylogenetic tree. The evolutionary distances were computed using p-distance and pairwise deletions. Bootstrap analysis was performed with 1000 replicates.

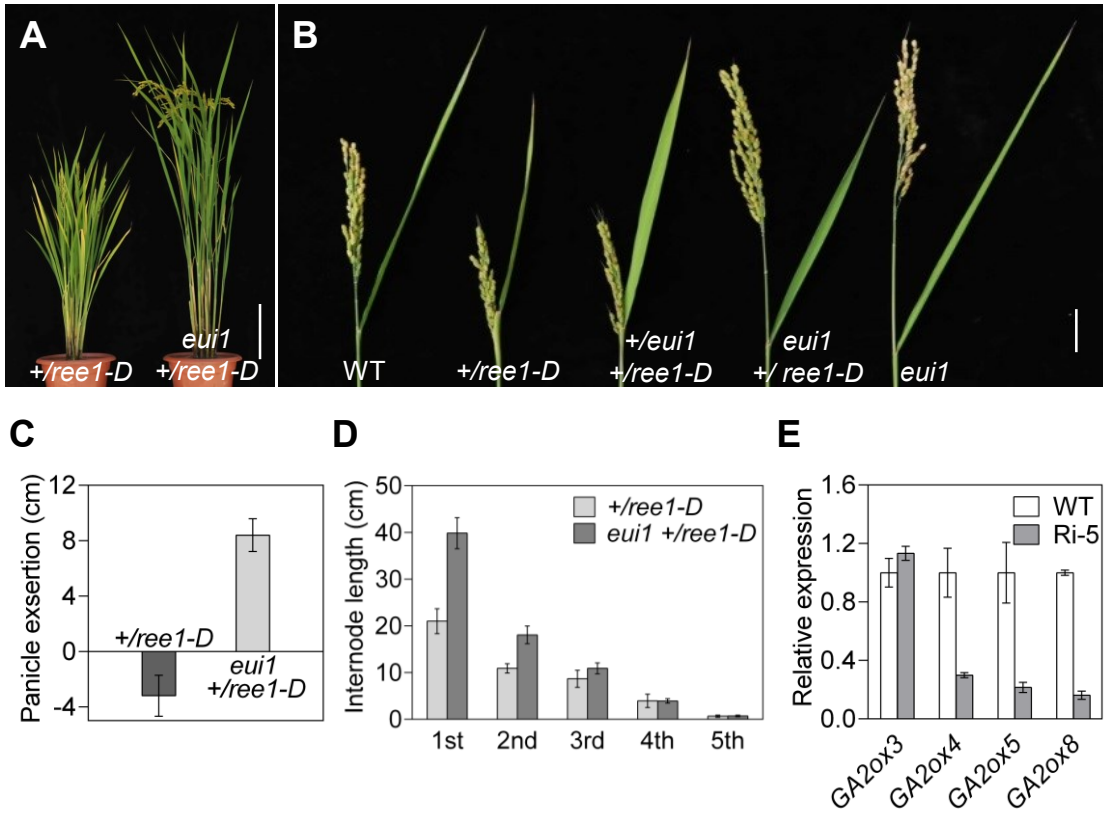


Supplemental Figure 4. Specificity of the Rice HOX12 Monoclonal Antibody.

Immunoblotting of protein from roots of the wild type (WT), *HOX12* knockdown (Ri-2, Ri-5) and *ree1-D* plants showed a specific band of expected size of HOX12. The immunoblots were developed with anti-HOX12 in SDS-PAGE. Ponceau S stained Rubisco large subunit serves as a loading control.



Supplemental Figure 5. Representative Stem of a *HOX12$_{Pro}$:GUS* Plant.
The divisional, elongating and elongated zones are shown in the 1st (uppermost) internode. The white triangles indicate the nodes. The thin gray arrows indicate the regions used for GUS staining. P, panicle.



Supplemental Figure 6. *EUI1* Is Required for HOX12 to Regulate Panicle Exsertion.

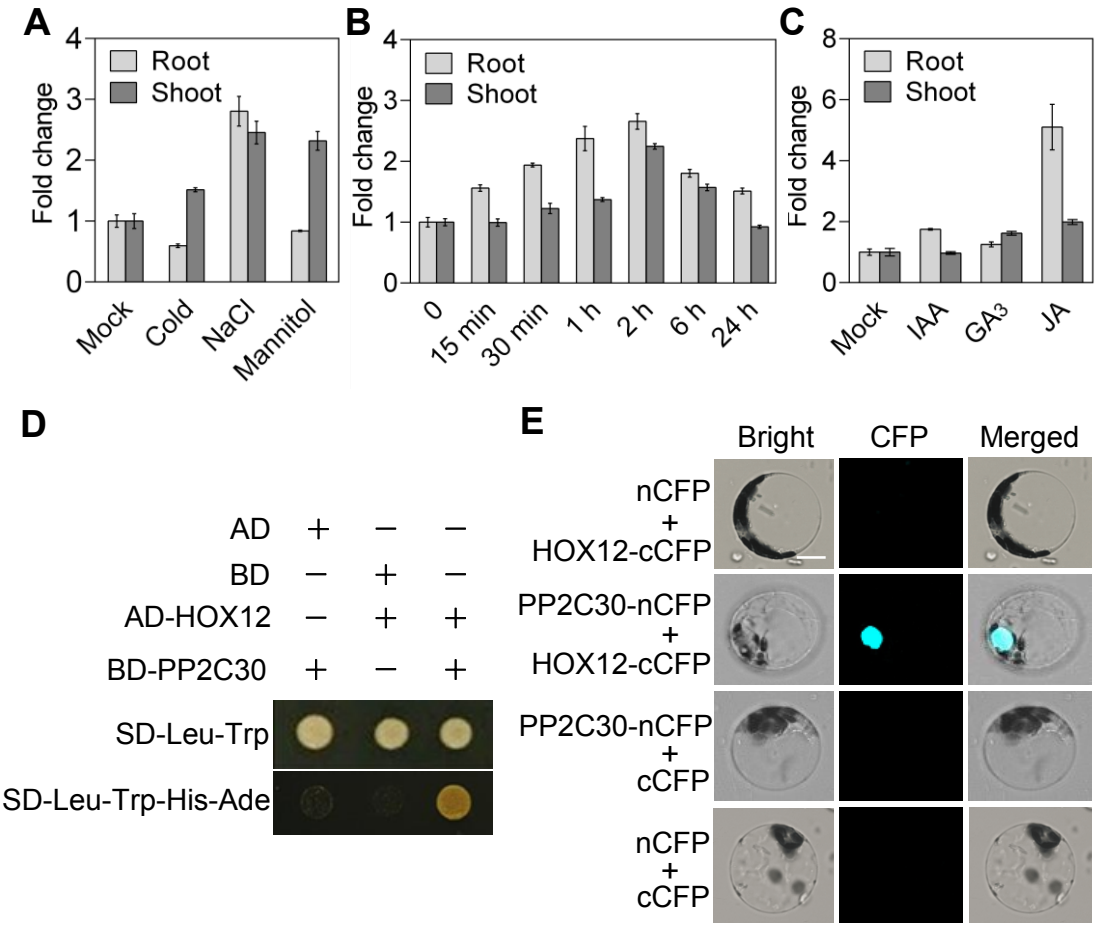
(A) Morphological phenotype of *eui1 +/ree1-D* at mature stage. Bar = 20 cm.

(B) Panicle exsertion of the *eui1 +/ree1-D* plants. WT, Nipponbare. Bar = 5 cm.

(C) Quantification of panicle exsertion of the *eui1 +/ree1-D* plants. Error bars indicate the SD (n = 15).

(D) Individual internode lengths of the *eui1 +/ree1-D* plants. Error bars indicate the SD (n = 15).

(E) qRT-PCR analysis of the expression levels of *GA2ox3*, *GA2ox4*, *GA2ox5*, and *GA2ox8* in the uppermost internodes of WT and Ri-5 plants. The transcript level of *GA2ox3*, *GA2ox4*, *GA2ox5*, and *GA2ox8* in the wild type was set as 1.0. Error bars indicate the SD (n = 3).


A
Root
Shoot
Fold change
Mock
Cold
NaCl
Mannitol
B
Root
Shoot
Fold change
0
15 min
30 min
1 h
2 h
6 h
24 h
C
Root
Shoot
Fold change
Mock
IAA
GA3
JA
D
AD
BD
AD-HOX12
BD-PP2C30
SD-Leu-Trp
SD-Leu-Trp-His-Ade
E
Bright
CFP
Merged
nCFP + HOX12-cCFP
PP2C30-nCFP + HOX12-cCFP
PP2C30-nCFP + cCFP
nCFP + cCFP

Supplemental Figure 7. *HOX12* Expression Is Regulated by Environmental and Hormonal Stimuli.

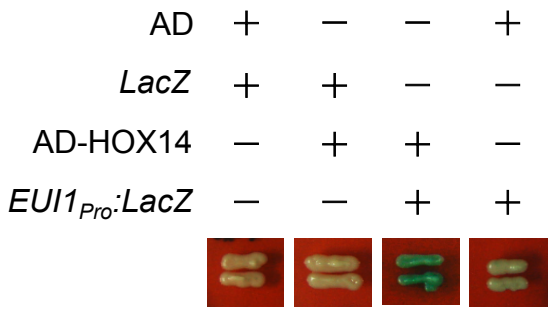
(A) qRT-PCR analysis of HOX12 transcripts in 2-week-old wild-type plants treated for 2 h with the specified agents. The transcript level of *HOX12* in untreated seedlings was set as 1.0. Error bars indicate the SD (n = 3).

(B) Expression of *HOX12* in wild-type roots and shoots after exposure to ABA for 15 min, 30 min, 1 h, 2 h, 6 h, or 24 h. The transcript level of *HOX12* in untreated seedlings was set as 1.0. Error bars indicate the SD (n = 3).

(C) qRT-PCR analysis of *HOX12* expression after treatment with exogenous IAA, GA_3, or JA. The transcript level of *HOX12* in untreated seedlings was set as 1.0. Error bars indicate the SD (n = 3).

(D) Y2H assay for the interaction of HOX12 and the PP2C30. Yeast cells cotransformed with HOX12 fused to the GAL4 activation domain (AD-HOX12) and PP2C30 fused to the GAL4 binding domain (BD-PP2C30) were grown on selective media (right column). Coexpression of AD-HOX12/BD (middle column) and AD/BD-PP2C30 (left column) was used as negative controls.

(E) HOX12 interacted with PP2C30 in the BiFC system. The C-terminal part of CFP was fused with HOX12 (HOX12-cCFP), while the N-terminal part of CFP was fused with PP2C30 (PP2C30-nCFP). Bar = 10 μm.



Supplemental Figure 8. Yeast One-Hybrid Assay Testing the Binding of HOX14 to the *EUI1* Promoter.

Yeast cells containing *EUI1*$_{Pro}$*:LacZ* were transformed with HOX14 fused with the activation domain (AD) and grown on medium containing X-Gal. Co-expression of AD/*LacZ*, AD-HOX14/*LacZ*, and AD/*EUI1*$_{Pro}$*:LacZ* was used as negative controls.