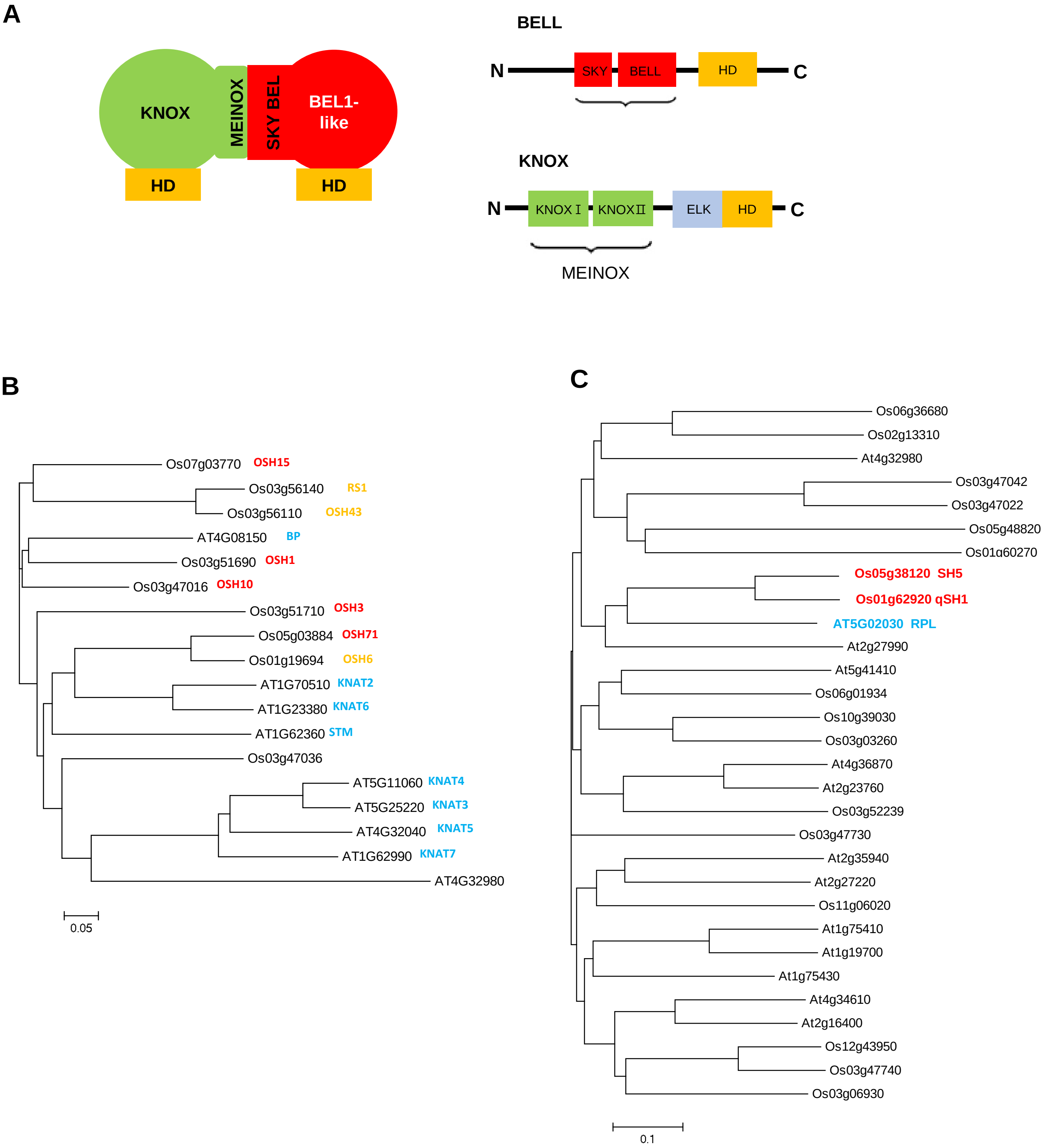
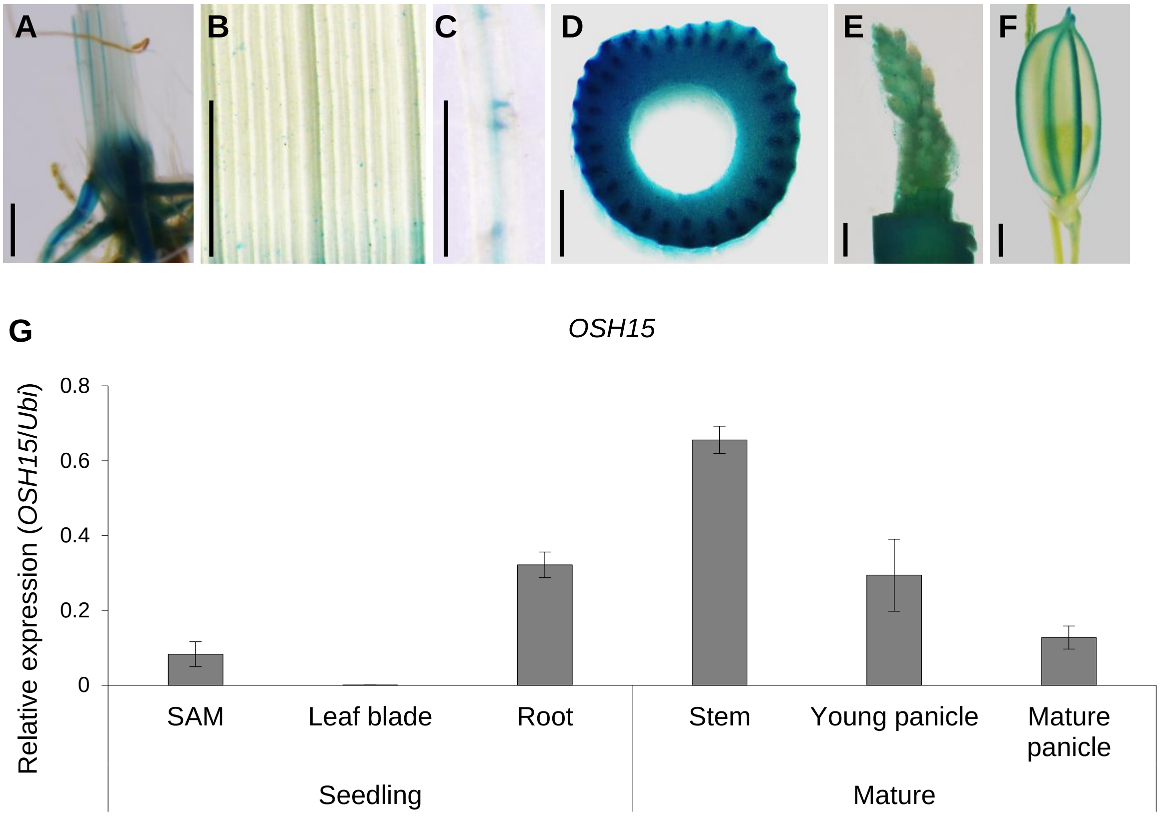
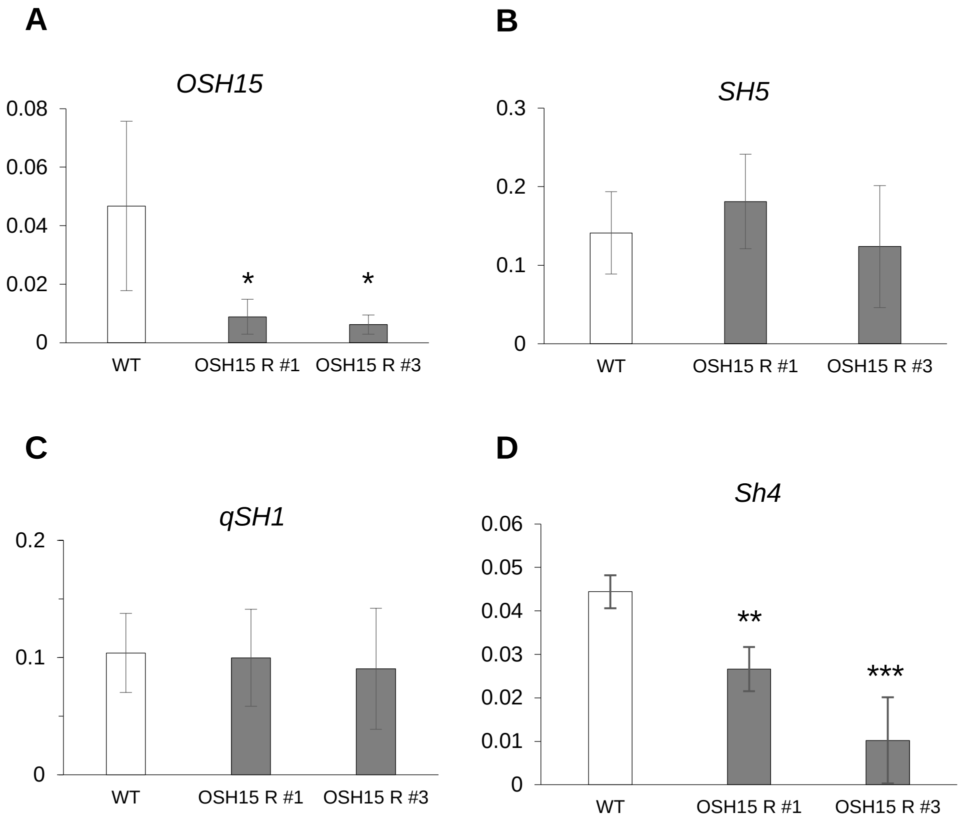


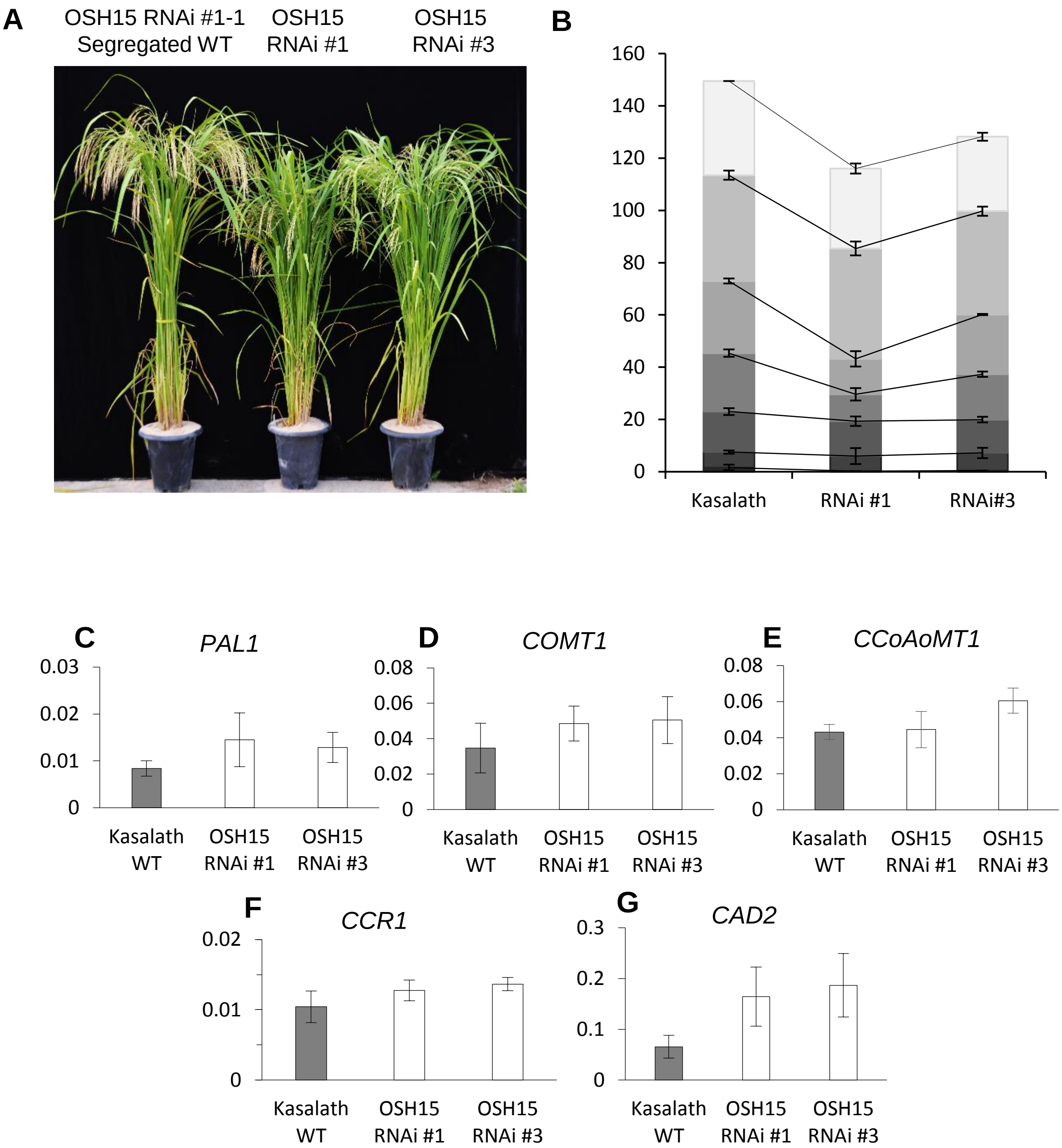
Supplemental Figure 1. Phylogenetic analysis and schematic diagram of TALE-HD members. A, Schematic diagrams of TALE-HD complex. B, Phylogenetic tree of KNOX protein from rice and Arabidopsis. C, Phylogenetic tree of BEL1-like homeobox (BLH) subfamily genes from rice and Arabidopsis. Phylogenetic analyses were conducted with ClustalX and MEGA5.1. Full-length amino acid residues were used. Tree was generated by Neighbor-joining method.



Supplemental Figure 2. Expression patterns of *OSH15*. A to C, GUS expression in SAM, leaf, and root at seedling stage. Bars = 2 mm. D to F, GUS expression in stem, young panicle, and mature spikelet. Bars = 5 mm. G, Endogenous expression of *OSH15* in various tissues. n = 4.



Supplemental Figure 3. Expression of shattering-related genes in young panicles (1-3 cm) from ‘Kasalath’ WT and *OSH15* RNAi Lines #1 and #3. (n = 4; *, $P<0.05$, **; $P<0.01$; ***, $P<0.001$).



Supplemental Figure 4. Analysis of *OSH15* ‘Kasalath’ RNAi transgenic plants. A, Phenotypic comparisons between WT and transgenics. B, Schematic representation of internode elongation patterns for WT and RNAi plants. n = 5. C to G, Expression patterns for *PAL1*(C), *COMT1* (D), *CCoAoMT1* (E), *CCT1* (F), and *CAD2* (G) in IM before heading stage, when WT internode was approximately 5 cm long. n = 4.

Supplemental Table 1. Primers used in this study

Primer name	Sequence (5' to 3')
OSH15 pro GUS F	GTTAACTCACGACCTCACTGAACTAG
OSH15 pro GUS R	TCTAGACCTCCTCCTCCAAGATTCC
OSH15 3’UTR RNAi F	ACCCACAGAATGCTGCTGCA
OSH15 3’UTR RNAi R	GGGGTACCAACATTACTGGAGAACTATAAGCC
OSH15 real time F	GAGAGAGAGCCTAGCTGCTA
OSH15 real time R	CGTGACCGTGGTACTGCGA
OSH15 RNA in situ F	ACCCACAGAATGCTGCTGCA
OSH15 RNA in situ R	AACATTACTGGAGAACTATAAGCC
OSH15 FL_F	GTTAAC GAGAGAGAGCCTAGCTG
OSH15 FL_R	GGTACCCGAACCGAGGCGGTACATTC
SH5 FL F	GTTAACATGTCGTCCGCCGCGGGGGGA
SH5 FL R	GGTACCACCAACAAAGTCATGGAGC
qSH1 FL F	GTTAACATGTCGTCCGCCGCTGGGGG
qSH1 FL R	GGTACCCCCGACAAAATCATGCAGCA
1D-03912 L	TCACCCATGCATATCAACAG
1D-03912 RS	CCTCCTCCAAGATTCCCAA
OsCOMT1 F	CCTCGCCCTCATGAACCA
OsCOMT1 R	CGTCCAGGACTGCGTCCTTA
CAD2 F	GCGAGTGCCATCCGTGCAA
CAD2 R	GAGCTGATCACCGTCACGT
CCoAoMT1 F	AACCTGCTGCTGAAGCTCATC
CCoAoMT1 R	GGTGGCGAGGAGGGAGTAG
CCR1 F	CTCATCCGTGGCTACCACGTC
CCR1 R	GGGTAGGACTTCTTGGTGCC
PAL1 F	AGGAGCTCGGCTGCGTATT
PAL1 R	ATGCCGAGGAACACCTTGTT
Ubi_real_Ko_F	AACCAGCTGAGGCCCAAGA
Ubi_real_Ko_R	ACGATTGATTTAACCAGTCCATGA

Supplemental Table 2. Primers used in ChIP assay

Primer name	Sequence (5' to 3')
CAD2 ChIP_F1	ACCCTATGGTAACAAGGTTATG
CAD2 ChIP_R1	TCCATAACCCTAACAGATTCCC
CAD2 ChIP_F2	GGGAATCTGTTAGGGTTATGGA
CAD2 ChIP_R2	TATACCCATAGGTGTCCCCTTG
CAD2 ChIP_F3	GGTTGTAGGGCTATTACCTGAC
CAD2 ChIP_R3	CTCGGTTATTACGTTCACTATCC
CAD2 ChIP_F4	GGATAGTGAACGTAATAACCGAG
CAD2 ChIP_R4	CTATTCAACTACTTTATCCGTATC
CAD2 ChIP_F5	GATACGGATAAAGTAGTTGAATAG
CAD2 ChIP_R5	GTTAGTAGTAGGACAAGTAGTG
CAD2 ChIP_F6	CTCAGTCACGACCCGTCCAAC
CAD2 ChIP_R6	CCAATGGATGGATCGGATTC
CAD2 ChIP_F7	CAACTACACCCTCAGGTATGAT
CAD2 ChIP_R7	AGTTGTACTCGAGGCAGATG
CAD2 ChIP_F8	CTCCATTCGATCCATTCCAC
CAD2 ChIP_R8	TGTGGAGCCAGGCAACTAGC
CAD2 ChIP_F9	TGTGTGAGACTCTGACGACTTGTC
CAD2 ChIP_R9	CATATATTGCGAGGCCGAATTT
Ehd1 ChIP_F1	CGTCATGATCATATCAACGG
Ehd1 ChIP_R1	GTAAATACTATATACGACAGG
Ehd1 ChIP_F2	CTGTGTCTACCTTGCACTAC
Ehd1 ChIP_R2	TGCATGATGCATGGAATGCG
Ehd1 ChIP_F3	TCATTAACTATATATGGTGCAC
Ehd1 ChIP_R3	ATTATTATAACCTAATTAGGAG
Ehd1 ChIP_F4	ACTACACACGTGTCCATGCA
Ehd1 ChIP_R4	ACTGACTGAACTTAAATAGTAG
Ehd1 ChIP_F5	AAAGATGATCAGCTCTGTGG
Ehd1 ChIP_R5	TACCCTCCAAGACTTCGATT