

Supplemental Figure.

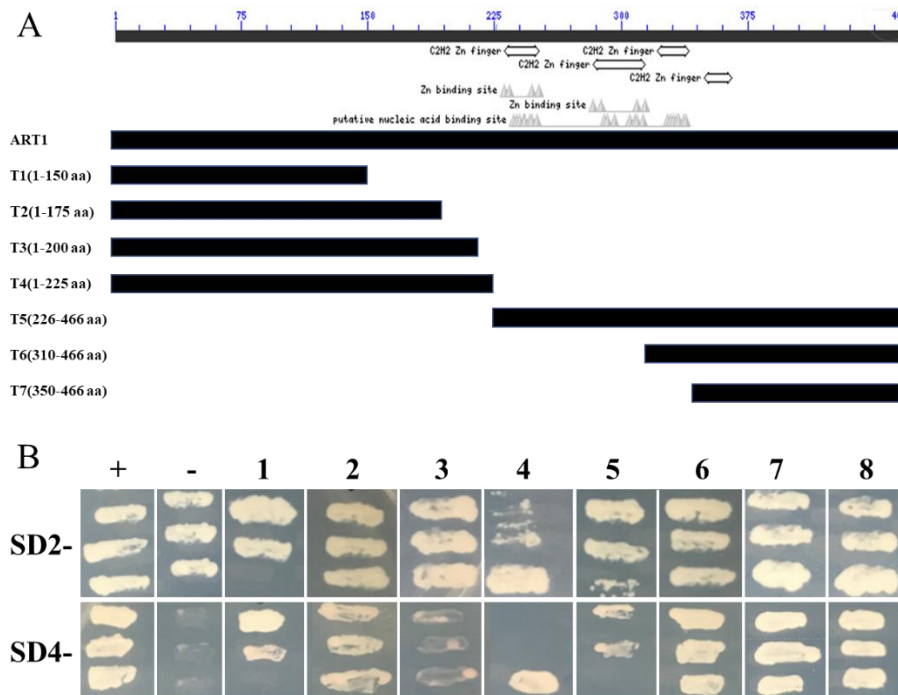


Figure S1. Transcriptional activation analysis of various truncated ART1s. (A) ART1 was truncated into different fragments, including T1 (1-150 aa), T2 (1-175 aa), T3 (1-200 aa), T4 (1-225 aa), T5 (226-466 aa), T6 (310-466 aa) and T7 (350-466 aa). (B) Identification of self-activation domain of ART. + : AD-T7 + BK-53, - : AD + BK, 1: ART1-BK + AD, 2: ART1-T1-BK + AD, 3: ART1-T2-BK + AD, 4: ART1-T3-BK + AD, 5: ART1-T4-BK + AD, 6: ART1-T5-BK + AD, 7: ART1-T6-BK + AD, 8: ART1-T7-BK + AD, the above pair of plasmids were co-transformed into yeast cells(AH109). The yeast colonies were grown on SD2- and SD4- medium plate. The plates were incubated at 30 °C for 3 d.

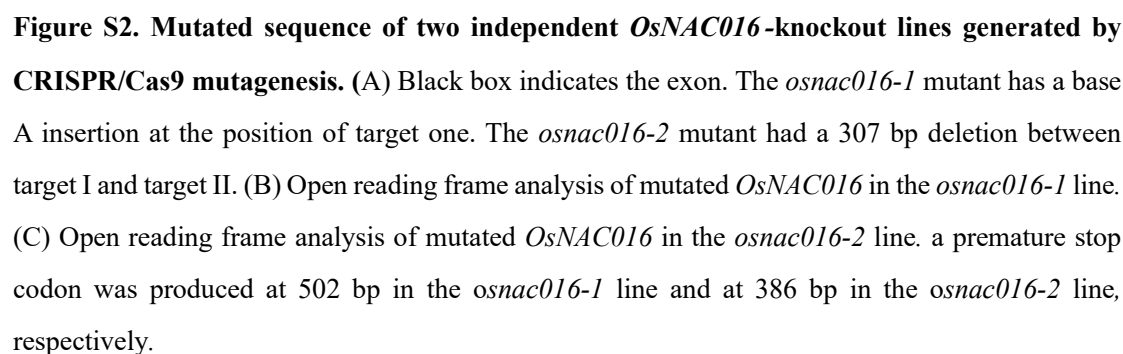


Figure S2. Mutated sequence of two independent *OsNAC016*-knockout lines generated by CRISPR/Cas9 mutagenesis. (A) Black box indicates the exon. The *osnac016-1* mutant has a base A insertion at the position of target one. The *osnac016-2* mutant had a 307 bp deletion between target I and target II. (B) Open reading frame analysis of mutated *OsNAC016* in the *osnac016-1* line. (C) Open reading frame analysis of mutated *OsNAC016* in the *osnac016-2* line. a premature stop codon was produced at 502 bp in the *osnac016-1* line and at 386 bp in the *osnac016-2* line, respectively.

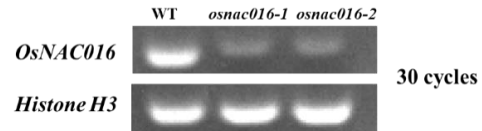


Figure S3. Transcript level of *OsNAC016* in roots of the wild-type and *osnac016* plants. The expression level of *OsNAC016* in the roots of 5-d-old rice seedlings were determined by semi-quantitative RT-PCR. *Histone H3* was used as an internal standard.

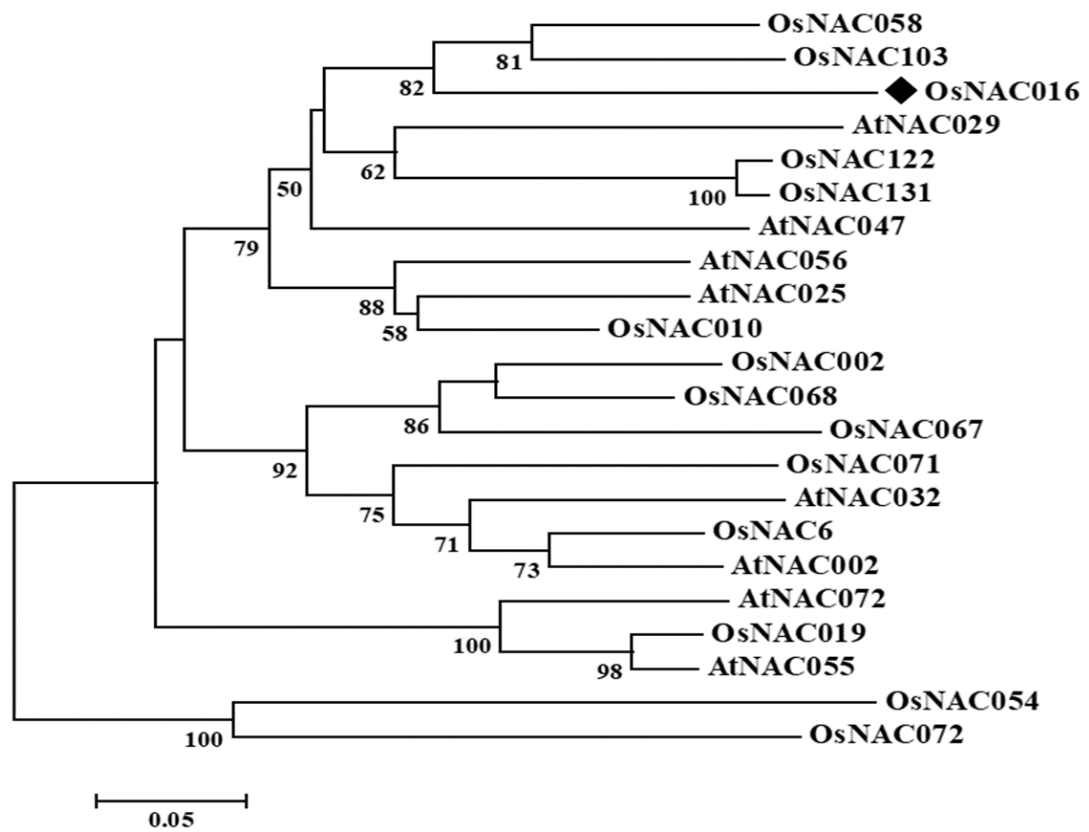


Figure S4. Phylogenetic tree analysis of *OsNAC016*. Homologs sharing with more than 40% identity to *OsNAC016* were used to construct the phylogenetic tree. Multiple sequence alignment was performed using the MEGA 6.0 and the phylogenetic tree was created.

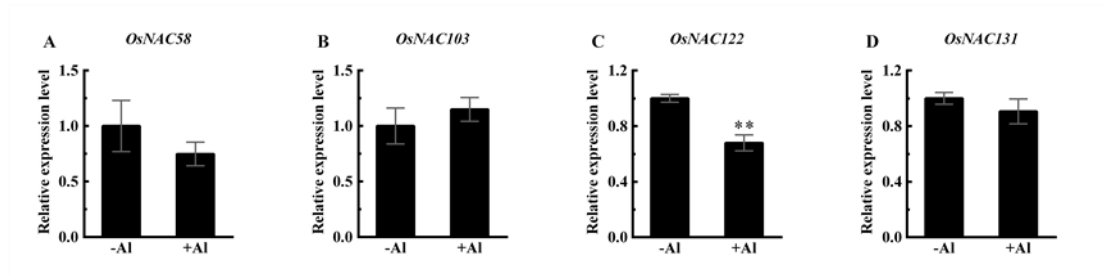


Figure S5. Expression analysis of four OsNAC016 homologous genes in roots. (A-D) Rice seedlings (5-d-old) were subjected to a solution containing 0 or 30 μ M AlCl_3 for 8 h. Histone H3 was used as an internal standard. Data are means \pm SD ($n = 3$). Asterisks indicates significant differences ($P < 0.01$, Tukey's test).

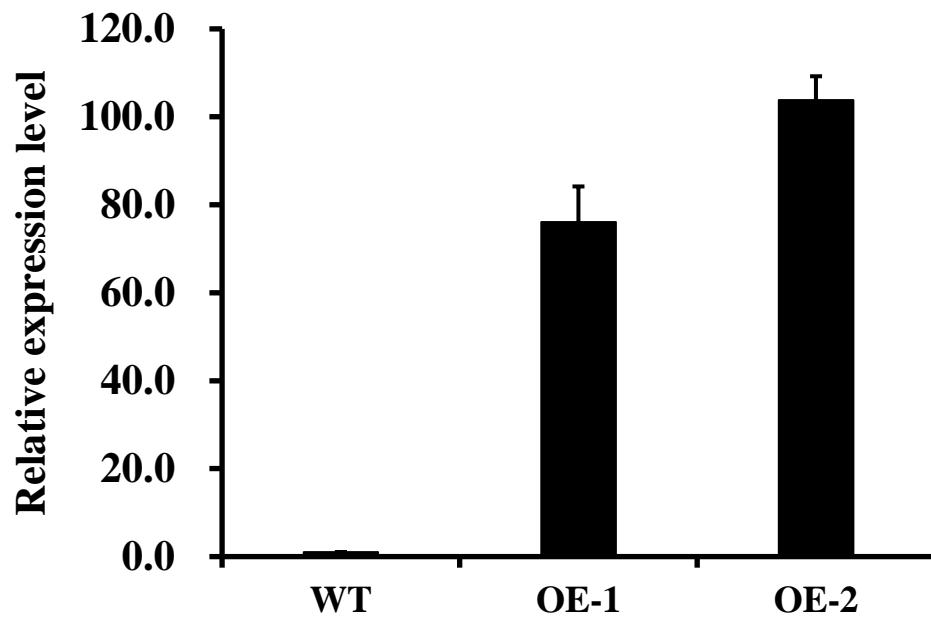


Figure S6. Relative expression levels of *OsNAC016* in the *OsNAC016*-overexpression lines (OE-1, OE-2) in roots. Data are means \pm SD of three biological replicates.

ATCTAATCATTAATTGTCAAAAAGACATTGAGCACATCATCCTCCCTCGTTGCTGCACATACAATT
 GAGATATTTTATTTTCTTCAACTCTAAACTACAATTTTCTCATTTTCCGTTAGCACACTATACAAA
 TTGTTAAATAGTATTATGTTTTTTTTTCAAAAAGTGTATATATAAAATTTCTTTAAATAAATTTA
 TCTTTAAAGTTTATTATAAATTAATTATATGCTAATGTCTTATCTCACTTTATGTGTGCTTGAAAAG
 CTAACCAAATTGTGCTGATTTGAATTAAGCCCGAGTCACTCGCATATGAGTAGTCCTATTTGTT
 ACGGTCTCACATGCGAATGATTTAGCTTCCTTATACTATACTCTTTTCGTAACAAAATATAATAA
 CCTACTACTGGAACATAAAACCTGTTTAGATTCTTAATACTTGACGGAGCGTGGGGCTCCTCAC
 CGGGAGACCGCGCGGGCCCTTTGCCGGTTCGGCCGGGGCGCTAAGTGAGGTTCTAAGCC
 CTTGATCTGTGGAATGGTTTCGCGAGAGAGTAAATGCACAAGA CACG GCGG ATGTAGACAGGTT
 C GGGCCG CTGAGAAGCGTAATACCCTACTCCTGTGTTCTGGTGGATCTGTGTATGAAGGAGTTA
 CAAAGAGCTGGAGAGCAAGAGAGTTTCGAACTCTAGAGACCCTCTCCCTACTCTTTTTCCCAGTC
 CCCTCTTTTTCTTTTCCCCCGTCCGTCAGTCCGTCAGTCCCCCTCTTGGTAGGCAT GGTCTC
 CTTTTATATCTCAAGGGGATACCACATACACCATTTCTACCTACCCTTCTTTTGGGTGG GGACCC
 ATCCTACTTTGACCAAAACTTGGCTTGACCTTCGTCTGACACCGGGATAACCCTGTCTCCCTC
 ATTAATGGGCGGAGATTTGCAATGGCTGCCGTCCGAAT GGGCTCCGATGGGATGGGTCATACC
 AACCTCCACTCCGCCGGAAGCA GGTGCAACGTGGAAG CACG GTTGTGTTGCTGATGACGCGACC
 GCGTCAGACCAGTCACAGACCGGTATTCTTGTCAC CACG TGTGAGTTAGCATGCTA CACG
 TCTGCCCTTCTTCATACAATGACTTCCTTGCAATGGTTGCGATGAAGCCTGGAATGTATCTAGCC
 GGGGCTGACGTGCCAACTCCAGGAGTCCC CACG CCGGCTCCGGCTAGGGACGAGTGCCTGGAG
 GCTCTCATCATTCCGACGGGACGGGGCGAGGCGTGTGTCA GGGCGCTGTTGCCCCCTAACCCG
 CGATCTGACCGGTCTGTGACCGGTACACACTGCGACCGAT CACG GACTAGATAAGCATGTGCT
 ACGCTGCATTAATGCGGCGTGAGACGCTCGTCCAACCCGCAATAAACGCGGTTAGGTGAGCG
 CCGCTGTGCTCATCTAACCACAC CACG TGGCGCAAACCCTCAGGGGGTTCGGGGCGCCCCAGC
 CCTCGGGGACGAAACGGGAGC GGGCGACCCCTCGGGGAGATAGAGGGAGGGGCGGCCTCAT
 CACCCTC GGGCCCGACCCCCCGAGGGGGTCAGGC CACG TGGGTGACCGCGGCTGCCCAAAC
 CTCTAGTCAAGATATCCCC GGTCCCATGTACCGACAATACTAATAAGATAAATCTTATCCGAC
 ACG GAAAGAGATCCTCTTACCTACTTGTGTGTCAGTTGAATTACTGATATATAAACCAACAACAA
 AGTAGGATTAATTCATATATCAGTGACAACCTACACAGTTAGGTCAAAGGATCCGCTTCCATCCG
 GCACTAGGTTGGGAGTATTACCATACAAGCTTCCCTTGCTGCCTGCTGCTGGCCACTCCTTGTGT
 CCACTGTCCACAGATACAACTCCATTCGTAATTTTCGTAC GGGCGTCGGGTACATCTAGTGC
 AGG CACGAA CACGTACAGACTCCCCTGATTTTTGGATCTATTTAAGCCGAGCTGAGTGAACCAA
 TTGGCCACC

Figure S7: Cis-acting element analysis of *OsFRDL4* promoter.

NAC TFs of cis-acting element: CACG.

ART1 TF of cis-acting element: [GGN(T/g/a/C)V(C/A/g)S(C/G)].