

Fig. S1 Protein domain and gene structure analysis of *NAL11* and 28 homologous genes. Schematic diagram of *NAL11* proteins and 28 homologous proteins functional domain; Structural analysis of *NAL11* and 28 homologous genes based on their own genome annotation file GFF3; Exon - intron structure of the 28 homologous genes, with introns indicated by black lines, exons by yellow wedges, and upstream (5')/downstream (3') untranslated regions (UTRs) by green rectangles.

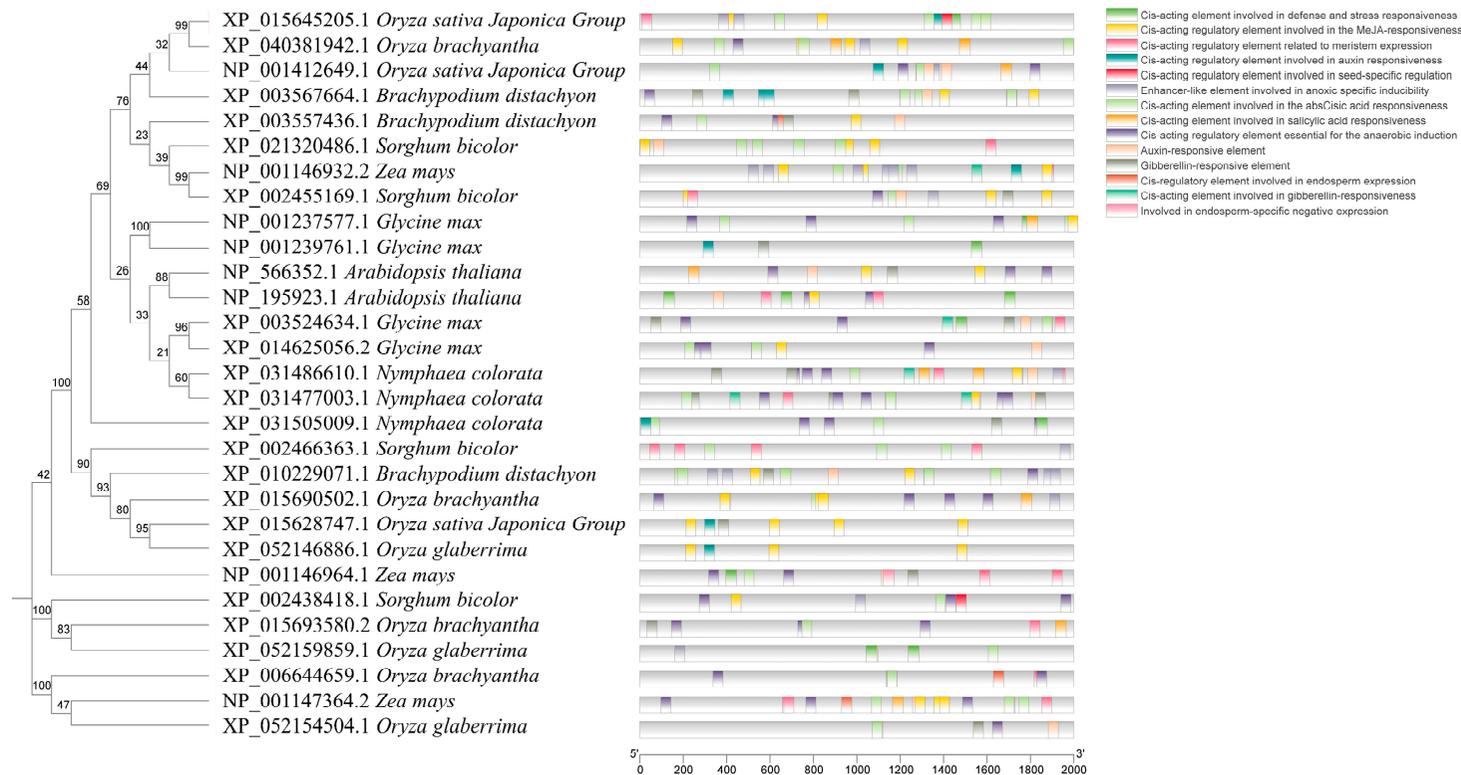
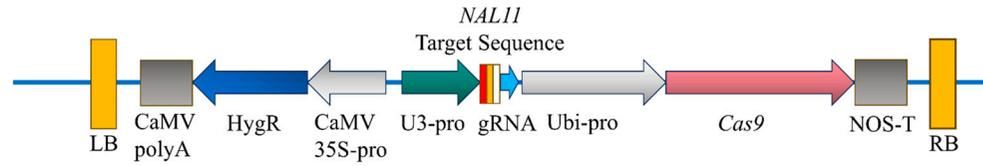
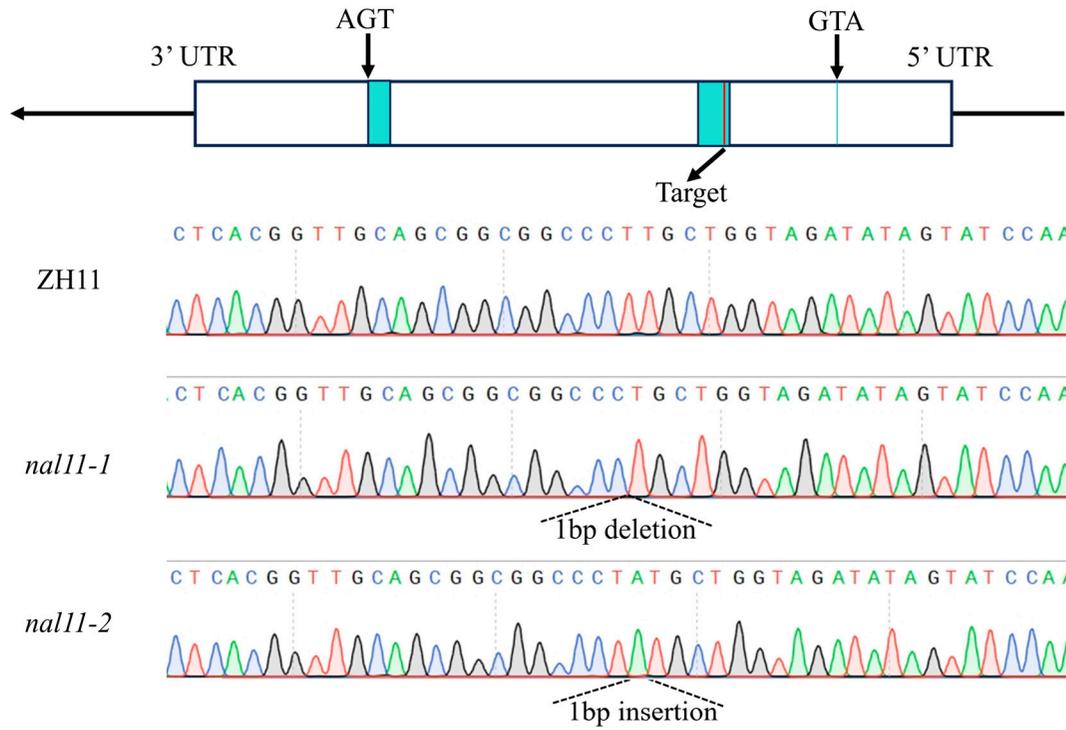


Fig. S2 Promoter prediction analysis of *NAL11* and 28 homologous genes, with introns indicated by black lines, exons by yellow wedges, and upstream (5')/downstream (3') untranslated regions (UTRs) by green rectangles. D, Distribution of various cis-elements in the promoters of 28 homologous genes. E, Color-coded patterns corresponding to each motif box.

A



B



| | | |
|----------------|--|-------|
| ZH11 | CTCACGGTTGCAGCGGCGGCCCTTGCTGGTAGATATAGTATCCAA | 45 bp |
| <i>nal11-1</i> | CTCACGGTTGCAGCGGCGGCCCT-GCTGGTAGATATAGTATCCAA | 44 bp |
| <i>nal11-2</i> | CTCACGGTTGCAGCGGCGGCCCTATGCTGGTAGATATAGTATCCAA | 46 bp |

C

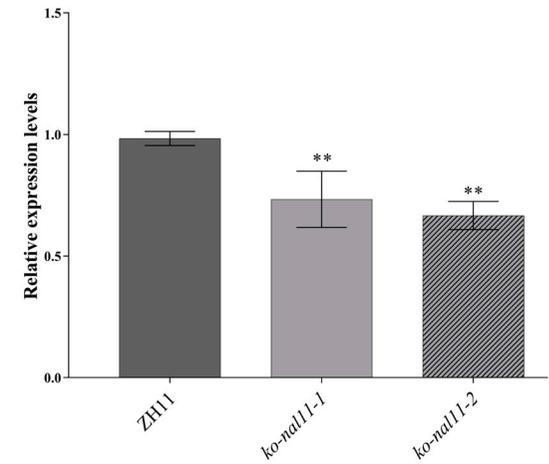


Fig. S3 A, Schematic of the CRISPR/Cas9 knockout vector cloning of *NAL11*. B, Gene structure diagram of *NAL11*. The UTRs and CDS are indicated by black and orange rectangles, respectively; the black arrows indicate the start (ATG) and stop codon (TGA). The red box indicates the location of the target. The green background fonts indicate the mutation site of *NAL11* in the three mutants. Sequence length is shown below. C, Expression levels of *NAL11* in transgenic lines and wild type. (Data are presented as mean \pm SD, $n = 3$; significant differences were determined by two-tailed Student's t-tests. $*P < 0.05$, $**P < 0.01$, ns, no significance).

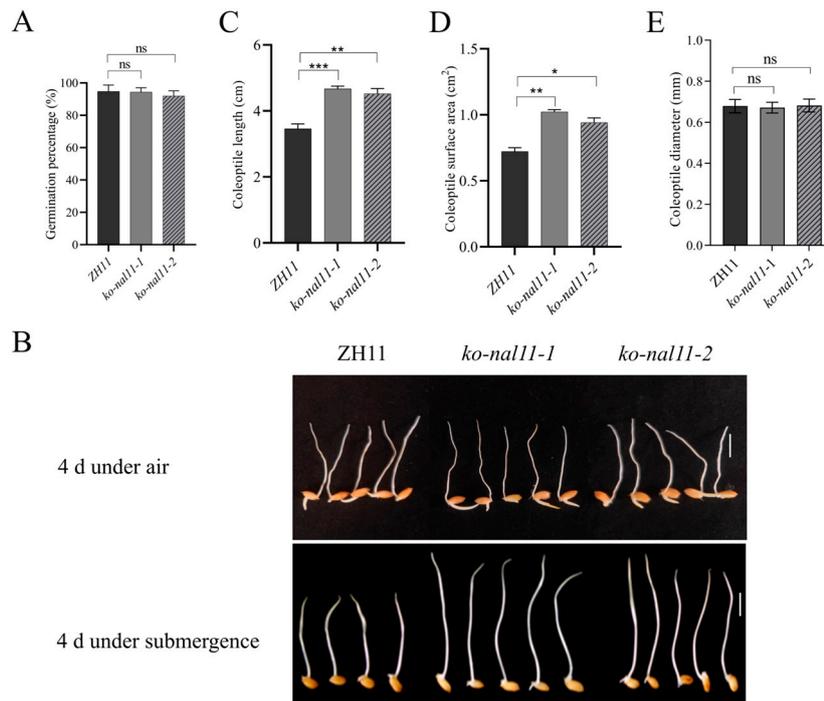


Fig. S4 *NAL11* regulates rice seedling emergence under submergence. A, Germination percentage after 4 d under normal conditions. B, Representative images of coleoptile length for both WT and knockout lines after 4 d under aerobic conditions and 4 d under submergence conditions. Scale bars, 1 cm. C, D, E, Average coleoptile length, coleoptile surface, and diameter of WT and knockout lines after 4 d under submergence, respectively. (Data are presented as mean \pm SD, $n = 5$; significant differences were determined by two-tailed Student's t-tests. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, ns, no significance).

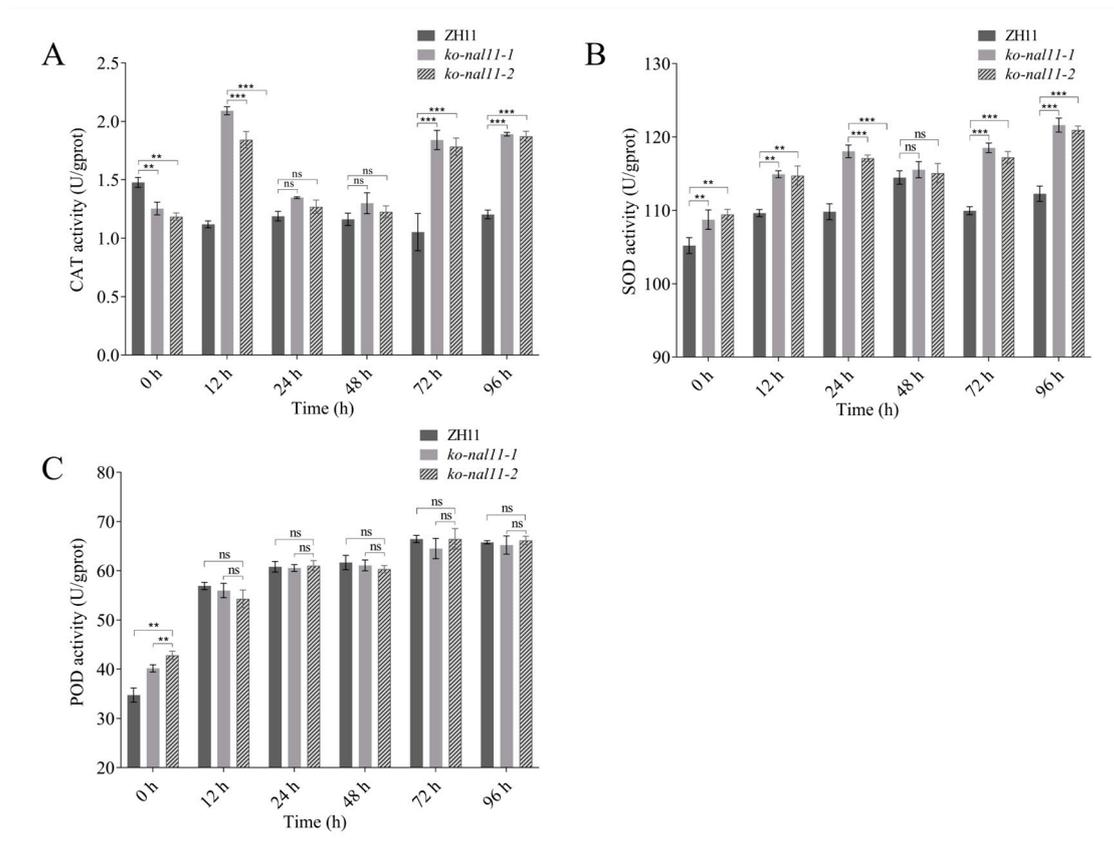


Fig. S5. Analysis of CAT, SOD and POD activity of WT and transgenic plants under normal and submergence conditions. A. CAT activity. B. SOD activity. C. POD activity. (Data are presented as mean±SD, $n = 5$; significant differences were determined by two-tailed Student's t-tests. $**P < 0.01$, $***P < 0.001$, ns, no significance).

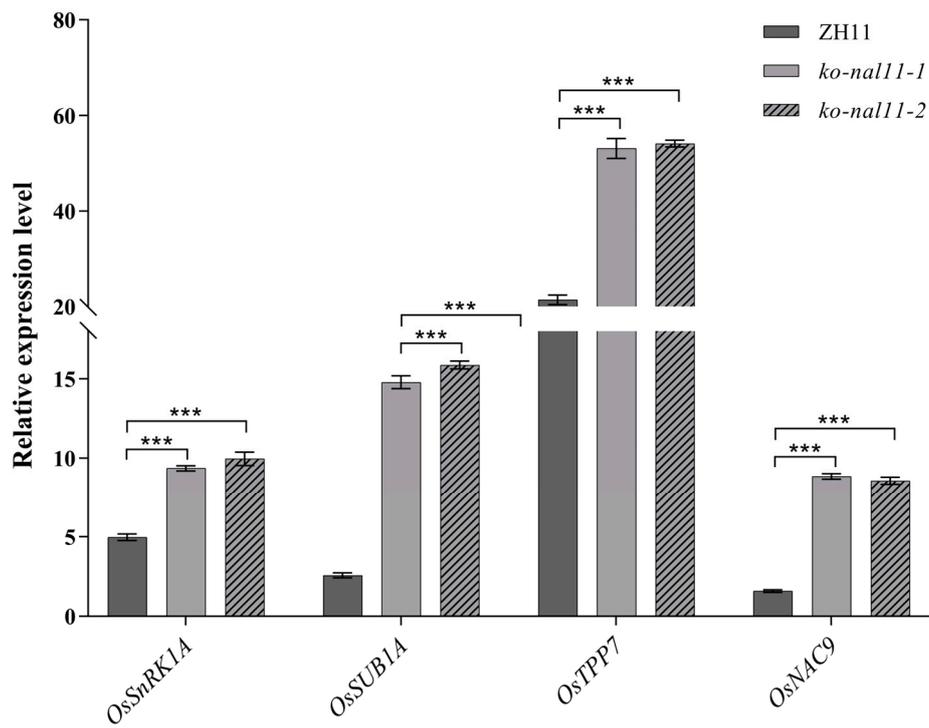


Fig. S6 Transcript accumulation of stress-related genes in seeds after 48 h of submergence treatment. A. *OsSnRK1A*. B. *OsSUB1A*. C. *OsTPP7*. D. *OsNAC9*. (Data are presented as mean \pm SD, $n = 3$; Asterisks indicate significant differences between transgenic lines and WT using t-test. $***P < 0.001$).

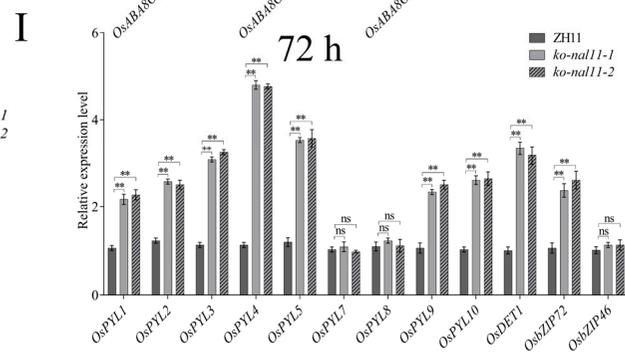
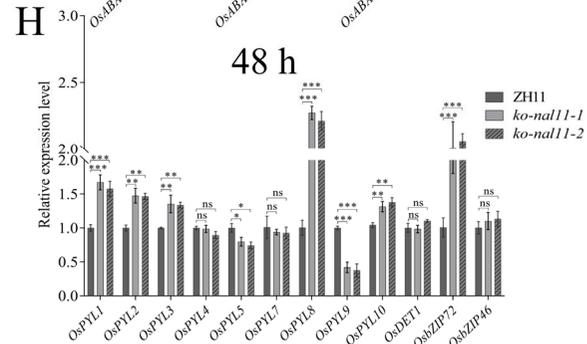
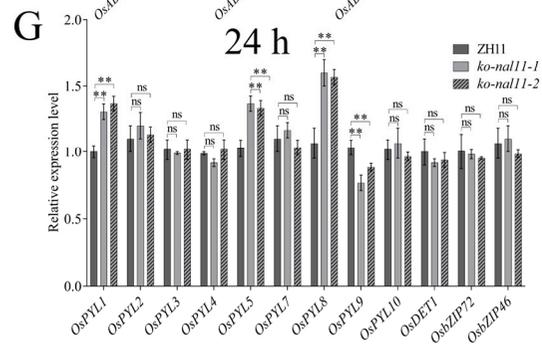
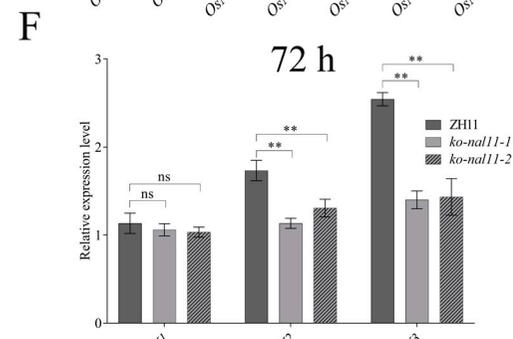
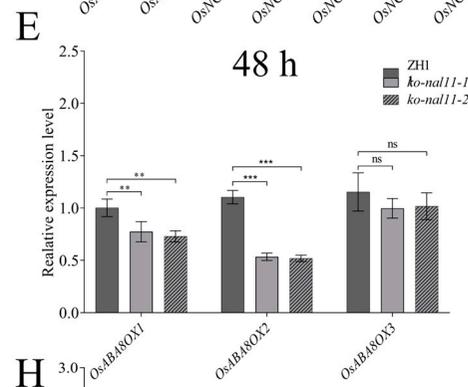
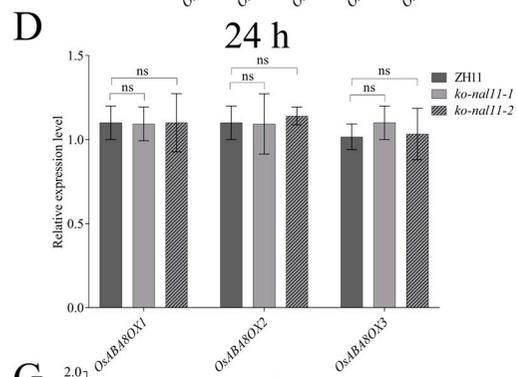
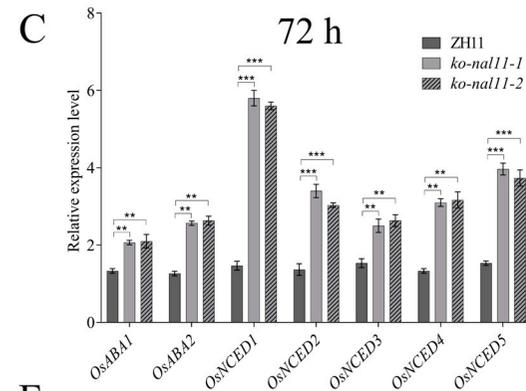
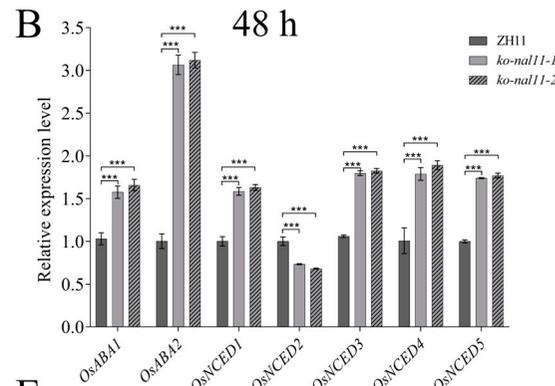
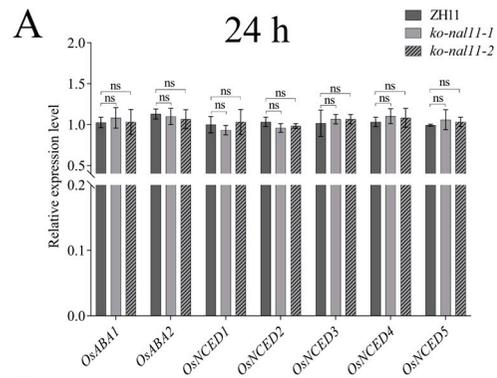


Fig. S7 *NAL11* is involved in the ABA signaling pathway. A-C qRT-PCR of ABA biosynthesis-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. D-F qRT-PCR of ABA catabolism-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. G-I qRT-PCR of ABA signal transduction-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. (Data are presented as mean \pm SD, $n = 5$; significant differences were determined by two-tailed Student's t-tests. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, ns, no significance).

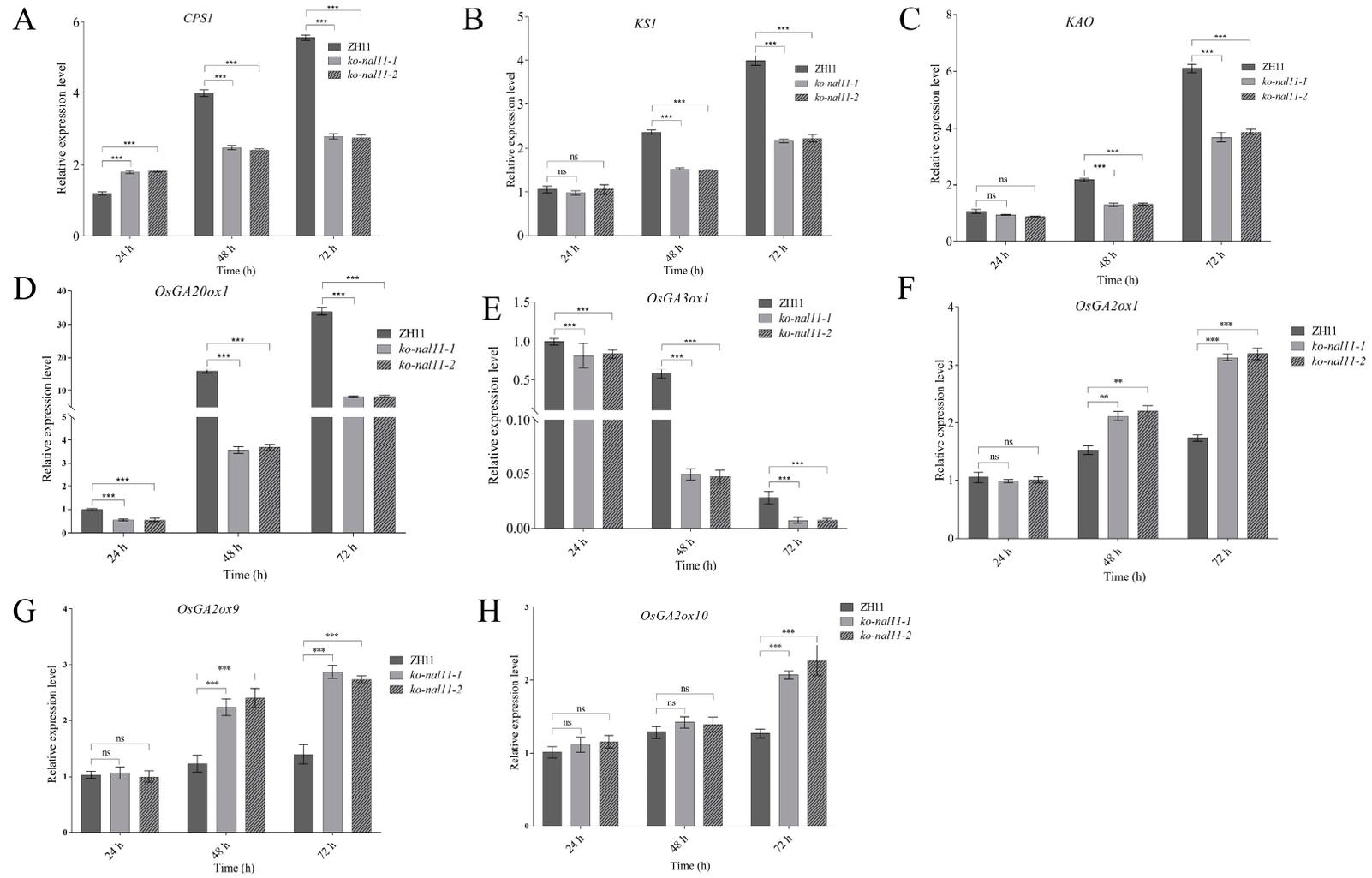


Fig. S8 *NAL11* is involved in the GA signaling pathway. A-E qRT-PCR of GA biosynthesis-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. F-H qRT-PCR of GA catabolism-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. (Data are presented as mean \pm SD, $n = 5$; significant differences were determined by two-tailed Student's t-tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, ns, no significance).

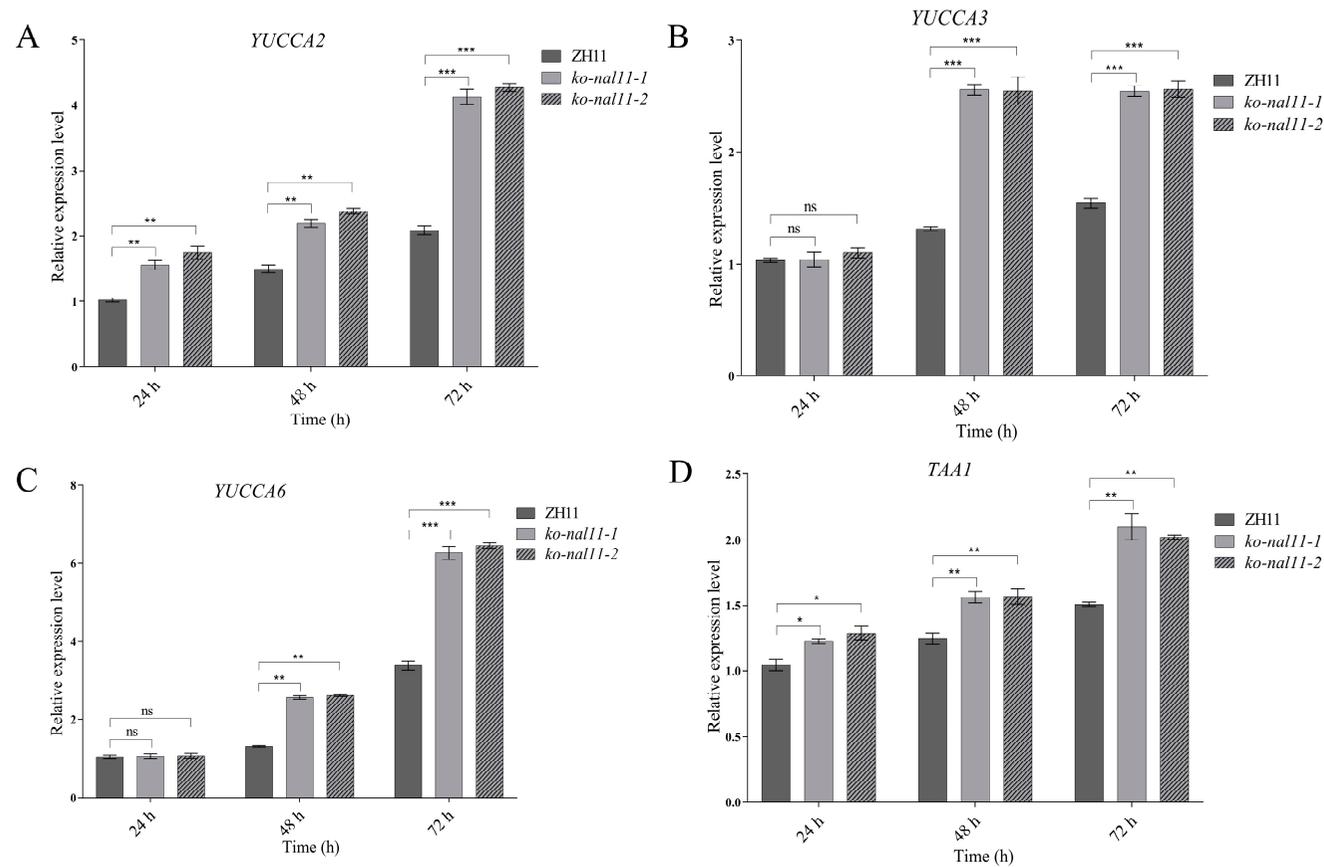


Fig. S9 *NAL11* is involved in the auxin signaling pathway. A-E qRT-PCR of auxin biosynthesis-related genes in the WT and knockout lines at 24 h, 48 h, and 72 h after submergence. (Data are presented as mean \pm SD, $n = 5$; significant differences were determined by two-tailed Student's t-tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, ns, no significance).