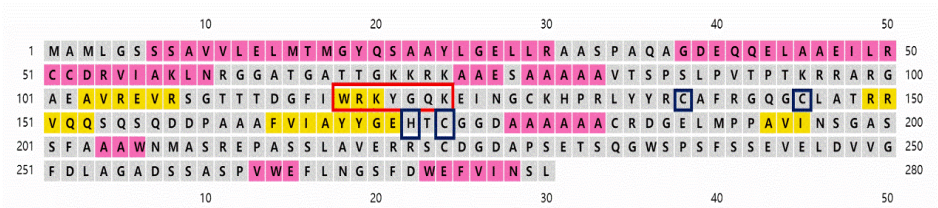
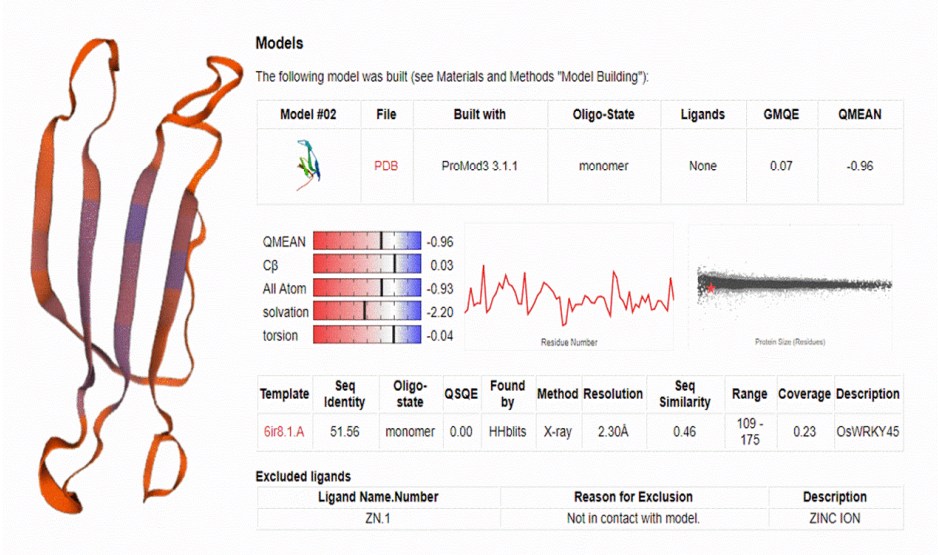


Supplementary Figure S1

A



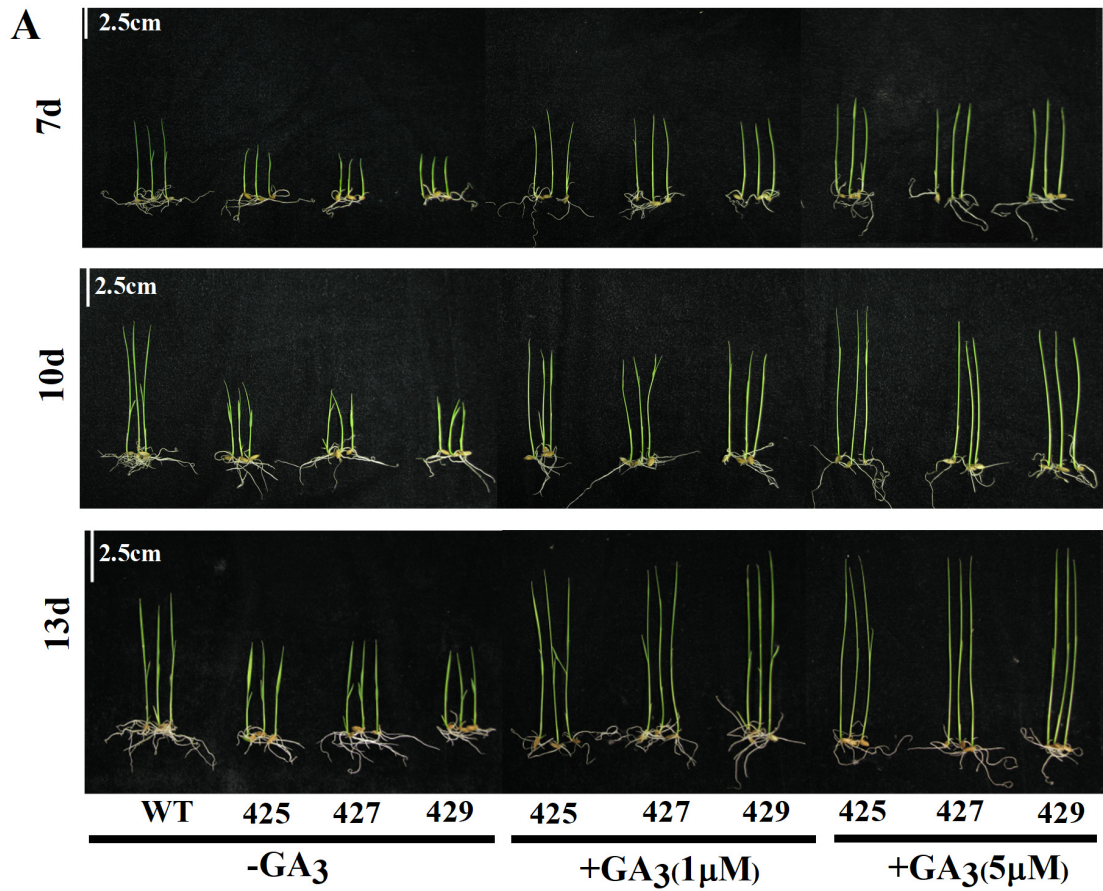
B



Supplementary Figure S1: Secondary and tertiary structures of OsWRKY21 protein

Predicted secondary structure of OsWRKY21 protein (1A). Rectangles with different colors represents protein secondary structure, pink: helix; yellow: strand; grey: coil. The sequences of the OsWRKY21 motif (WRKYGQK) and the C2HC domain (CX6CX26HX1C) are highlighted by the red and blue rectangles, respectively (1A). Predicted tertiary structure of OsWRKY21 contained a conserved zinc-finger structure widely distributed WRKY family (1B).

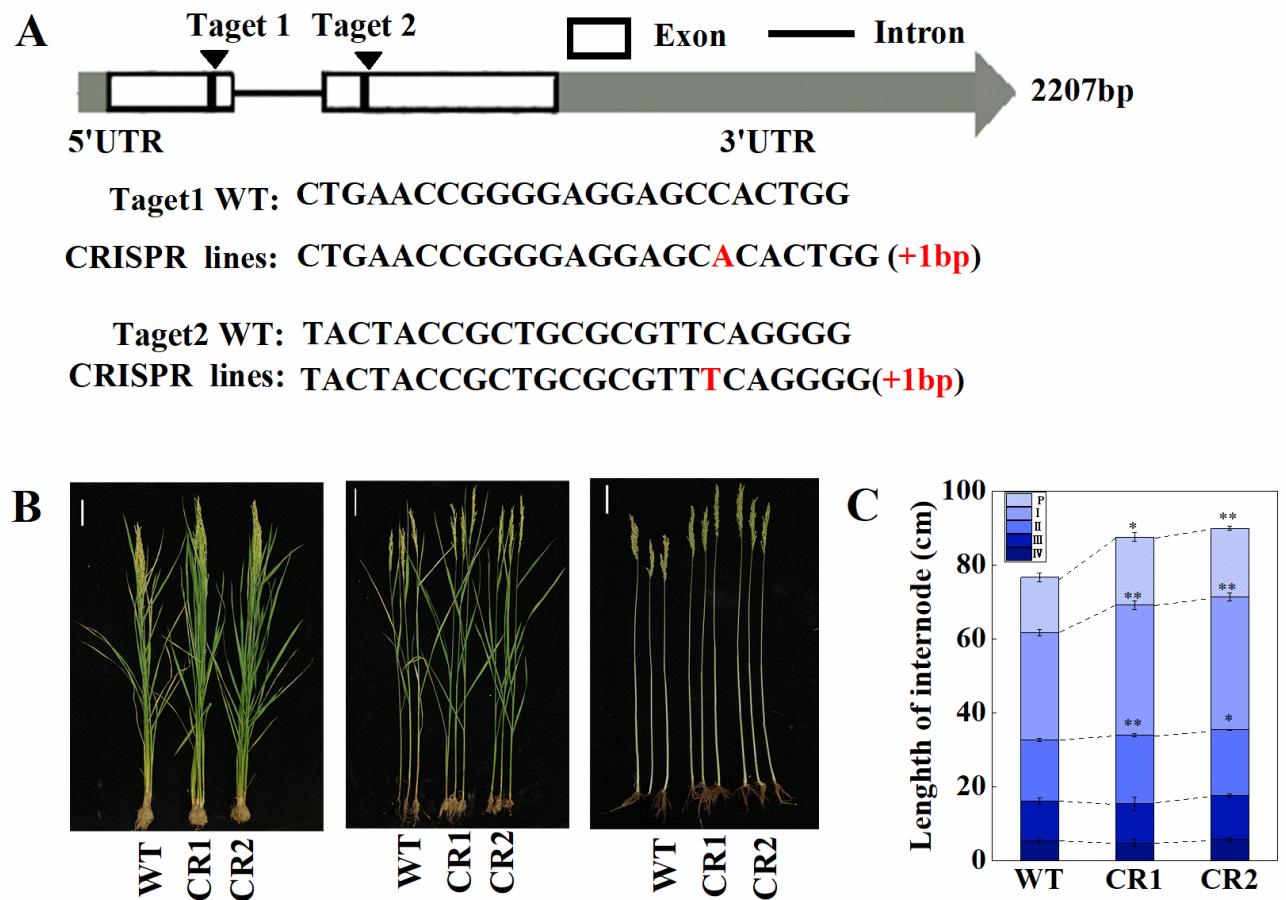
## Supplementary Figure S2



**Supplementary Figure S2: Phenotype of wild-type ZH11 and three OE lines treated without or with GA<sub>3</sub> at seedling stage**

Phenotype of wild-type ZH11 and three OE lines (425, 427 and 429) treated without or with 1 μmol/L GA<sub>3</sub> and 5 μmol/L at seedling stage

Supplementary Figure S3



Supplementary Figure S3: *OsWRKY21* gene editing site information and phenotype

Construct for editing of target genomic sites in rice and PCR detection of target sequences in two independent lines. The *OsWRKY21* gene model includes one exons separated by two introns (represented by the solid line) and Red mark as mutation site. (3A); Phenotype of wild-type ZH11 and two CRISPR lines (CR1 and CR2), bar= 25cm (3B) ;Lengths of the panicles and internodes of wild-type ZH11 and knockout mutant plants at heading stage. P, panicle; I, the uppermost internode; II, III, IV, the second, third, and fourth internodes counted from the up to bottom, respectively. (\* and \*\* indict  $p$ -value < 0.05 and 0.01, respectively,  $t$ -test,  $n = 15$ )(3C).