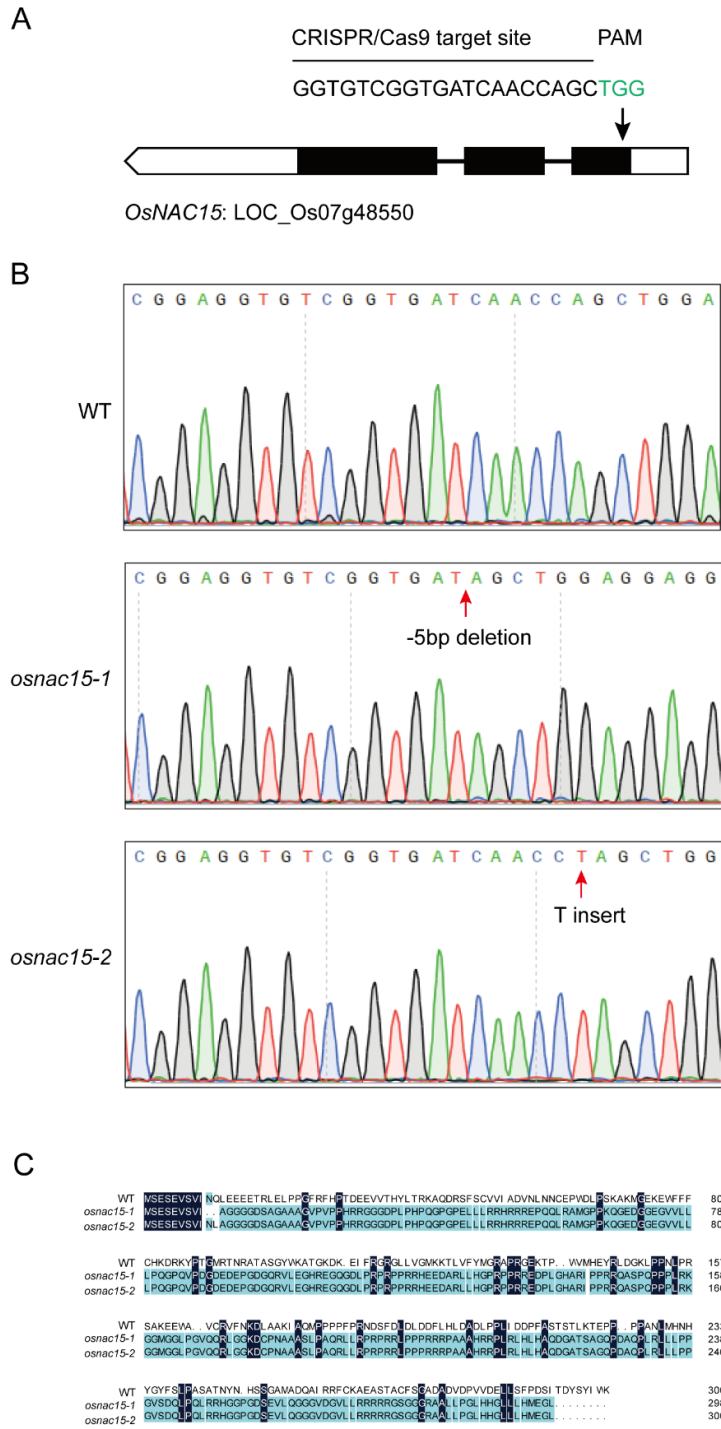


**Figure S1.** Phylogenetic analysis of OsNAC15. Phylogenetic analysis of OsNAC15 in rice (*Oryza sativa*) (A) and other species mainly including *Zea mays*, *Triticum aestivum*, *Hordeum vulgare*, *Miscanthus lutarioriparius*, *Panicum hallii* and *Sorghum bicolor* (B). Phylogenetic trees were constructed by neighbor-joining method and bootstrap values from 1000 replicates. The red triangle indicates OsNAC15. The black circles indicate other NAC proteins. Numbers on each branch represent the bootstrap percentage. (C) Multiple sequence alignment of NAC proteins. Sequence under the black bar represent the NAM domain.



**Figure S2.** Molecular characterization of *osnac15* mutants. **(A)** Schematic presentation of the gene structure of *OsNAC15* and CRISPR/Cas9 editing site. Black boxes: exons. PAM: protospacer adjacent motif. Top part: Sanger sequencing chromatograph of the CRISPR/Cas9 target site in the homozygous mutants of *osnac15*. The letter in green represented the PAM sequence. **(B)** The specific deletion and insertion of bases in the *osnac15* mutant lines are indicated by red arrows. **(C)** Protein sequence alignment of *OsNAC15* in the WT and *osnac15* mutant lines.