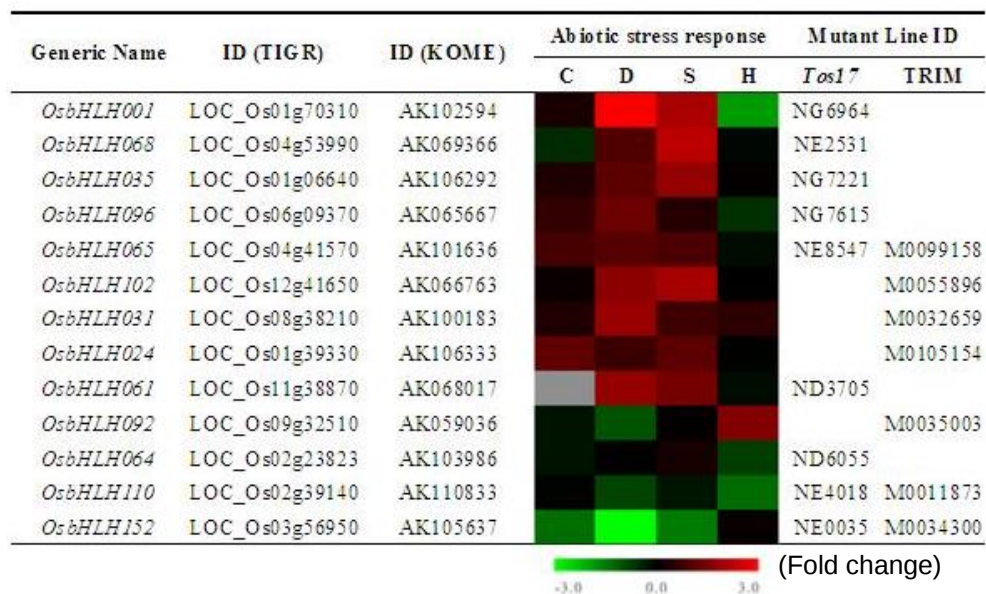
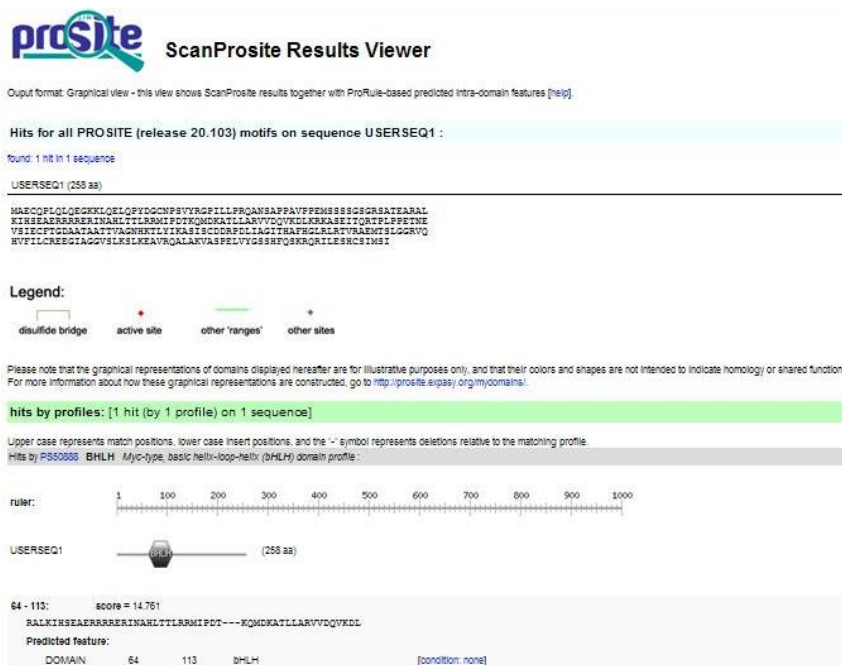




**Fig. S1** Abiotic stress-responsive *OsbHLHs*. The fold change among each *OsbHLH* gene under different abiotic stresses is calculated as a ratio normalizing the data to it corresponding nontreated control. Red and green colors represent up- and downregulation, respectively. C, cold stress; D, drought stress; S, salt stress; and H, heat stress.

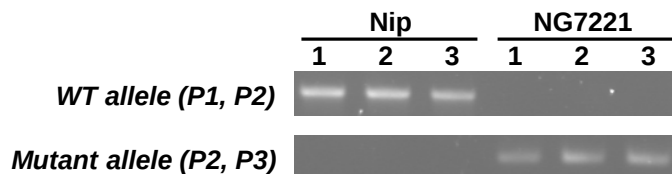
A



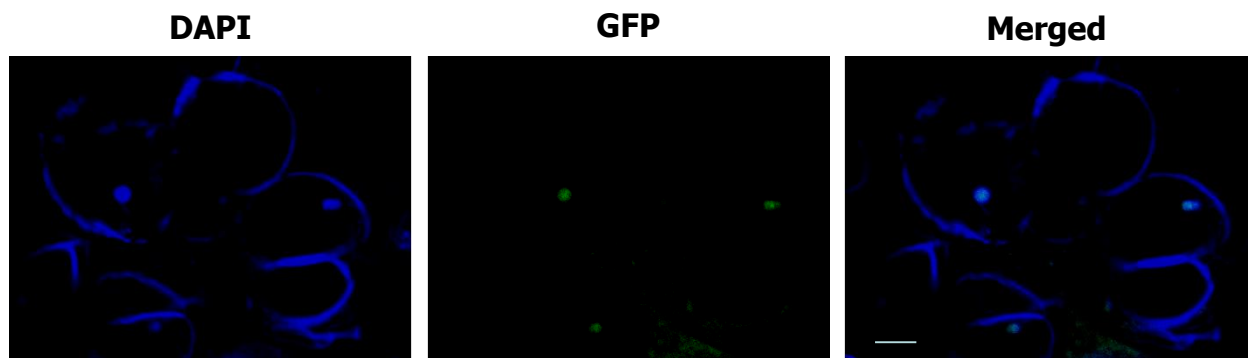
B



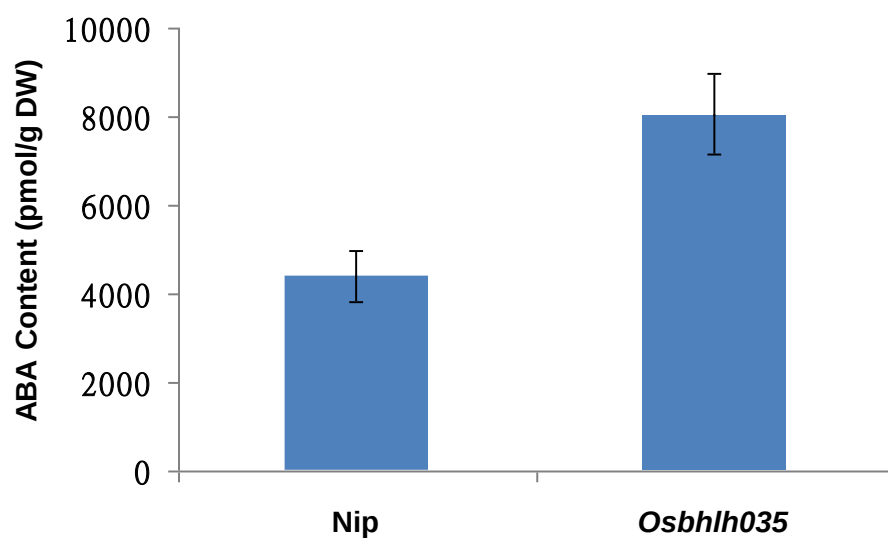
C



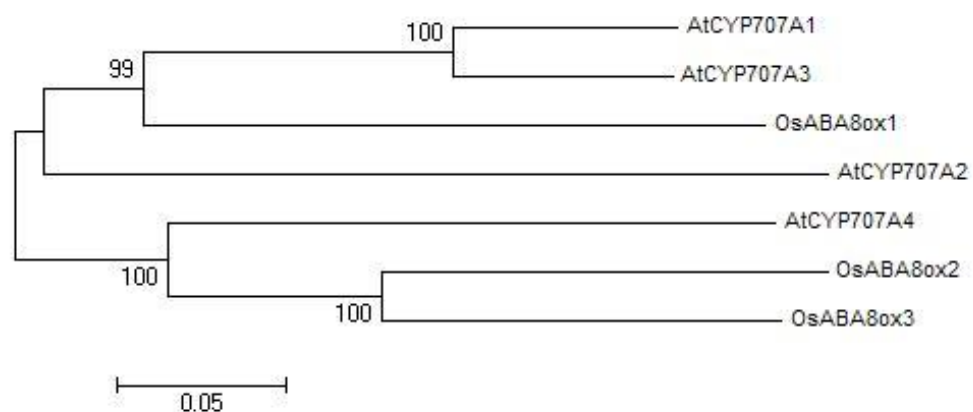
**Fig. S2** Prediction of the conserved domains in OsbHLH035 and characterization of the NG7221 mutant line. (A) The ScanProsite tool in ExPASy (<http://www.expasy.org/>) predicts the presence of a typical bHLH domain (residues 64 to 113) in OsbHLH035. (B) Based on its annotation in the rice *Tos17* insertion mutant database (<https://tos.nias.affrc.go.jp/>), NG7221 is a single retrotransposon insertional line. (C) The identification of homozygous NG7221 mutants via PCR genotyping of gDNA. The primer positions and sequences are shown in Fig. 1A and Supplementary Table 1, respectively. Arabic numbers in (C) represent three independent biological replicates within each genotype.



**Fig. S3** GFP-fused OsbHLH035 protein is predominantly localized to the nucleus in rice calli. The husk-removed seeds harboring *OsbHLH035::GFP-OsbHLH035* were placed on callus induction medium (Tran and Sanan-Mishra 2015) for 7 days and then the calli were subjected to GFP visualization by a confocal microscope. Scale bars, 10  $\mu\text{m}$ .



**Fig. S4** The endogenous ABA contents in both germinating WT and *Osbhlh035* seeds. The husk-removed seeds were grown on basal medium for 2 days and then subjected to ABA ELISAs.



**Fig. S5** Phylogenetic analysis of AtCYP707As and OsABA8oxs using the neighbor-joining method. Numbers next to the descendant indicate confidence values based on the bootstrap method.