

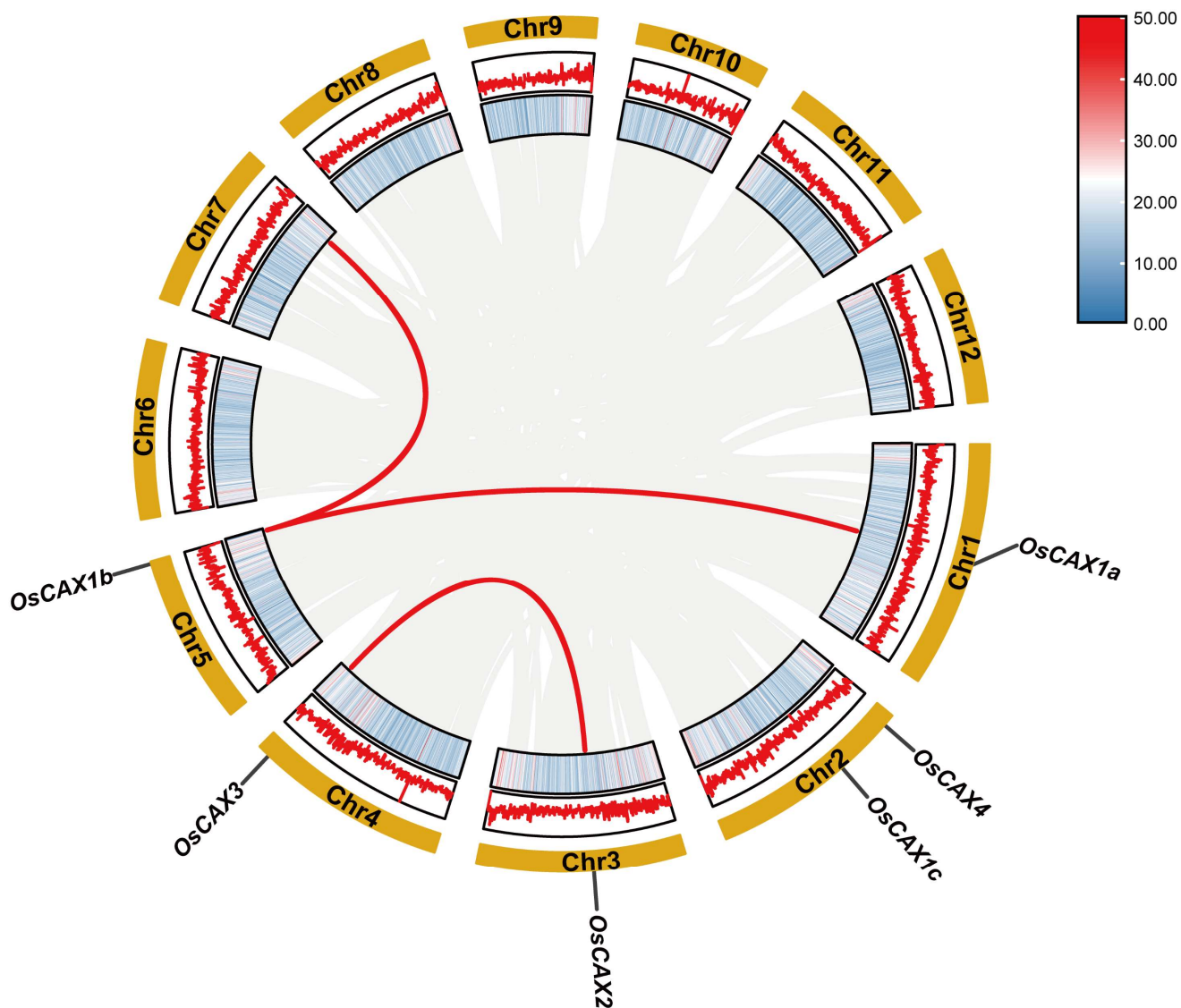
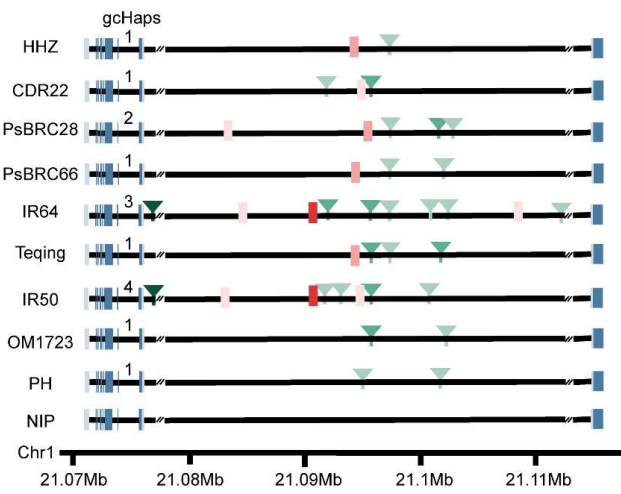
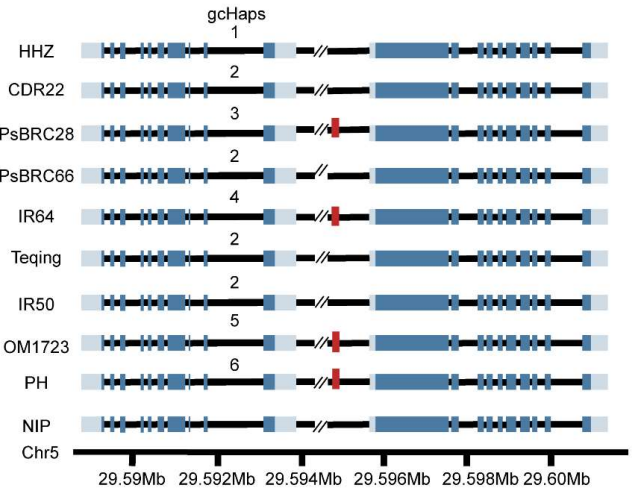


Fig. S1 Collinearity relationship analysis of the *OsCAX* gene family. The red lines represent the four homologous gene pairs in *Oryza sativa*.

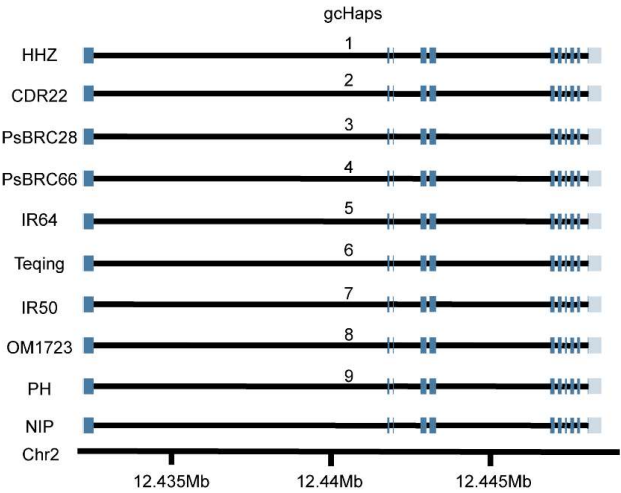
a. *OsCAX1a*



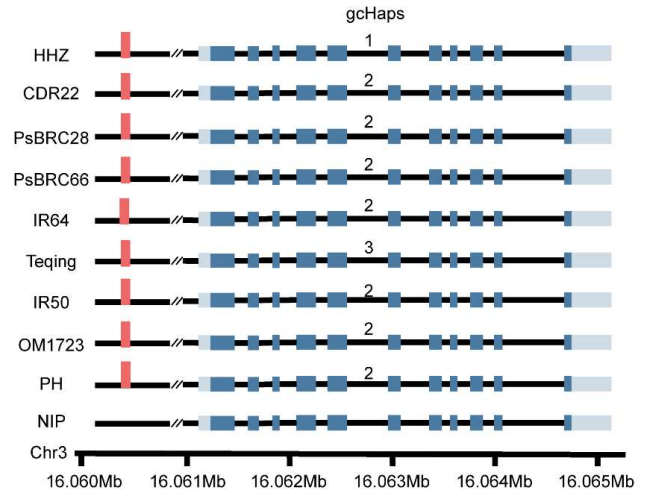
b. *OsCAX1b*



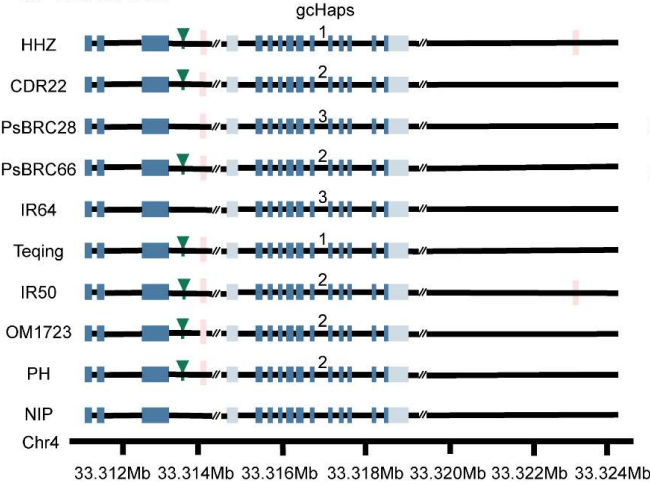
c. *OsCAX1c*



d. *OsCAX2*



e. *OsCAX3*



f. *OsCAX4*

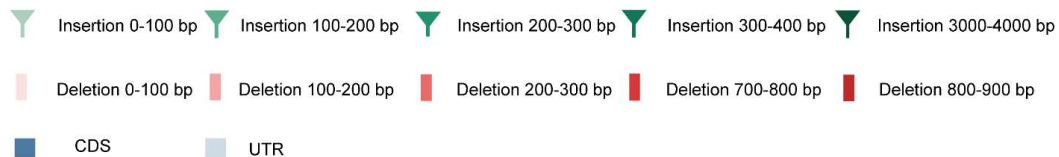
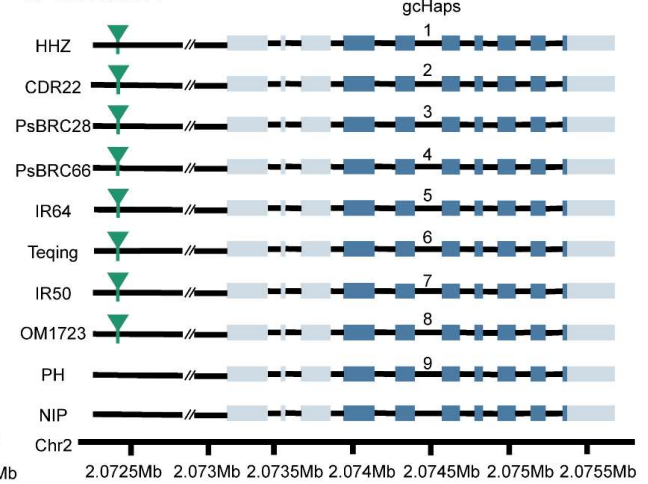


Fig. S2 Comparison of the nine parents of the HHZ IL population for SVs in intron/exon/UTR regions, gcHaps, PAVs, and CNVs at six CAX genes.

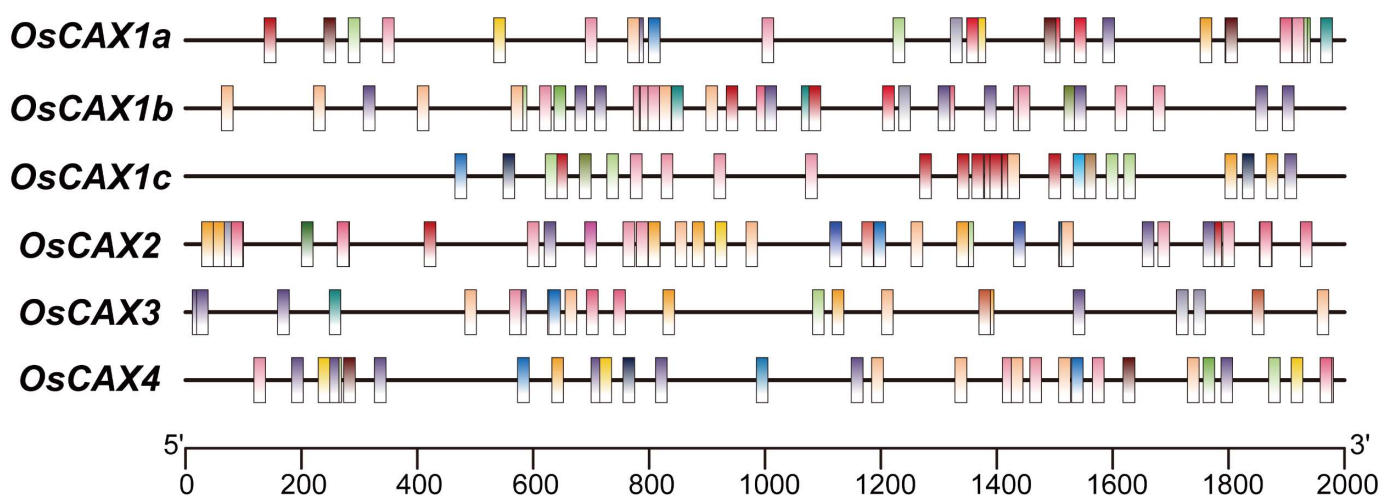


Fig. S3 Promoter cis-regulatory element analysis of the *OsCAX* gene family in Nipponbare (*Geng*). Different color boxes represent different cis-regulatory elements. Some cis-regulatory element may overlap with others.

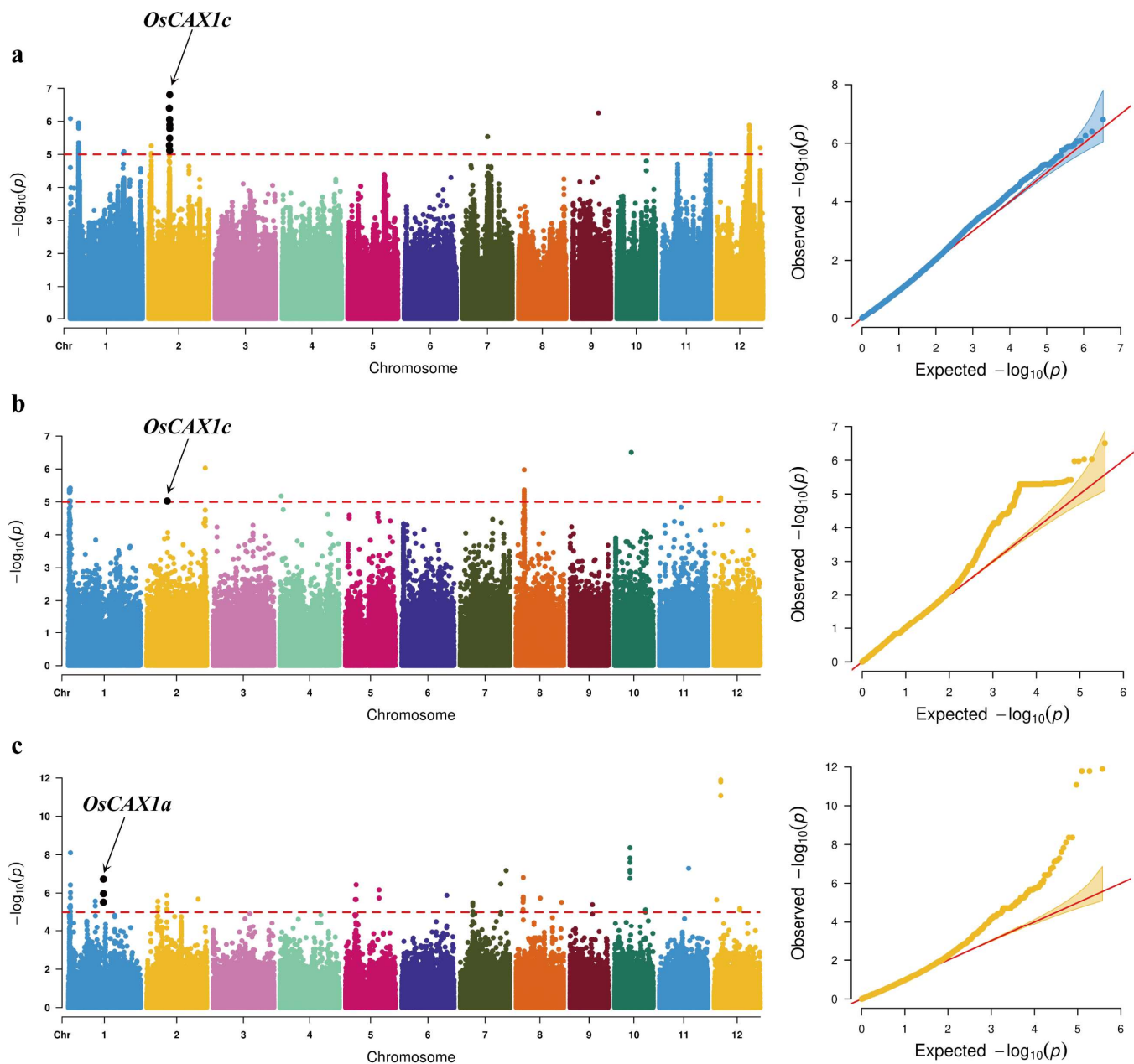


Fig. S4 GWAS of loci associated with germination stage and agronomic traits under salt tolerance in 3KRG and HHZ ILs, respectively, the Manhattan plots and quantile-quantile (Q-Q) plots depicting the GWAS results for three indexes (a. IR48h, b. PL, c. HD) using Mixed Linear Model (MLM). And the horizontal dashed lines indicate the significance threshold of $P = 1.0E-5$, while the x-axis represents the physical locations across the 12 rice chromosomes, with black points indicating the regions where CAX-genes are identified. IR48h: 48 hours imbibition rate, PL: panicle length, HD: days to heading.