

Figure S1. Synteny analysis of SSs between rice and other genomes. Each rice chromosome is displayed in a different color. Duplicated gene pairs are displayed and linked using lines with that color. (A) *Arabidopsis*, (B) barley, (C) maize, (D) sorghum, (E) soybeans, and (F) wheat.

Figure S2. Expression profiles of duplications across different growth stages.

Figure S3. Expression profiles of *OsSS* genes. (A) Expression related to specific tissues in the flowering stage. (B) Expression related to the *OsZip58-1* mutant line. (C) Expression related to the *gif1* mutant.

Figure S4. Putative miRNA targets of *OsSS* genes. The predicted targets are connected by solid lines.

Figure S5. Haplotype analysis of *OsSSIV-2*. (A) Structural representation of *OsSSIV-2* and upstream promoter region. (B) *OsSSIV-2* SNPs and haplotype groups in 137 rice accessions. SNP positions are given relative to the start of the 5'UTR. Hap: haplotype. (C) Association of phenotype with haplotype; different letters indicate significant AC differences between haplotypes (ANOVA, Duncan test). (D) Haplotype network variation of *OsSSIV-2*. The circle size represents the number of accessions in each Hap, and the number of transverse lines between each Hap represents the number of nucleotide variations. (E). SNP 2 haplotype relationship with AC. Tej: Temperate Japonica; Trj: Tropical Japonica; Ind: Indica; Aus: Aus; and Adm: Admixture rice varieties. (ANOVA and Student's *t*-test, ** $p < 0.01$, *** $p < 0.001$.)

Figure S6. Haplotype analysis of *OsGBSSI*. (A) Structural representation of *OsGBSSI* and upstream promoter region. (B) *OsGBSSI* SNPs and haplotype groups in 137 rice accessions. SNP positions are given relative to the start of the 5'UTR. Hap: haplotype. (C) Association of phenotype with haplotype; different letters indicate significant AC differences between haplotypes (ANOVA, Duncan test). (D) Haplotype network variation of *OsGBSSI*. The circle size represents the number of accessions in each Hap, and the number of transverse lines between each Hap represents the number of nucleotide variations. (ANOVA, *** $p < 0.001$).

Figure S7. Haplotype analysis of *OsGBSSII*. (A) Structural representation of *OsGBSSII* and upstream

promoter region. **(B)** *OsGBSSII* SNPs and haplotype groups in 137 rice accessions. SNP positions are given relative to the start of the 5'UTR. Hap: haplotype. **(C)** Association of phenotype with haplotype; different letters indicate significant AC differences between haplotypes (ANOVA, Duncan test). **(D)** Haplotype network variation of *OsGBSSII*. The circle size represents the number of accessions in each Hap, and the number of transverse lines between each Hap represents the number of nucleotide variations. **(E)** SNP 1 haplotype relationship with AC. Tej: Temperate *Japonica*; Trj: Tropical *Japonica*; Ind: *Indica*; Aus: Aus; and Adm: Admixture rice varieties. (ANOVA and Student's *t*-test, ****p* < 0.001).