

Article title: **Genome-Wide Discovery of Natural Variation in Pre-mRNA Splicing and Prioritizing Causal Alternative Splicing to Salt Stress Response in Rice**

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The following Supporting Information is available for this article:

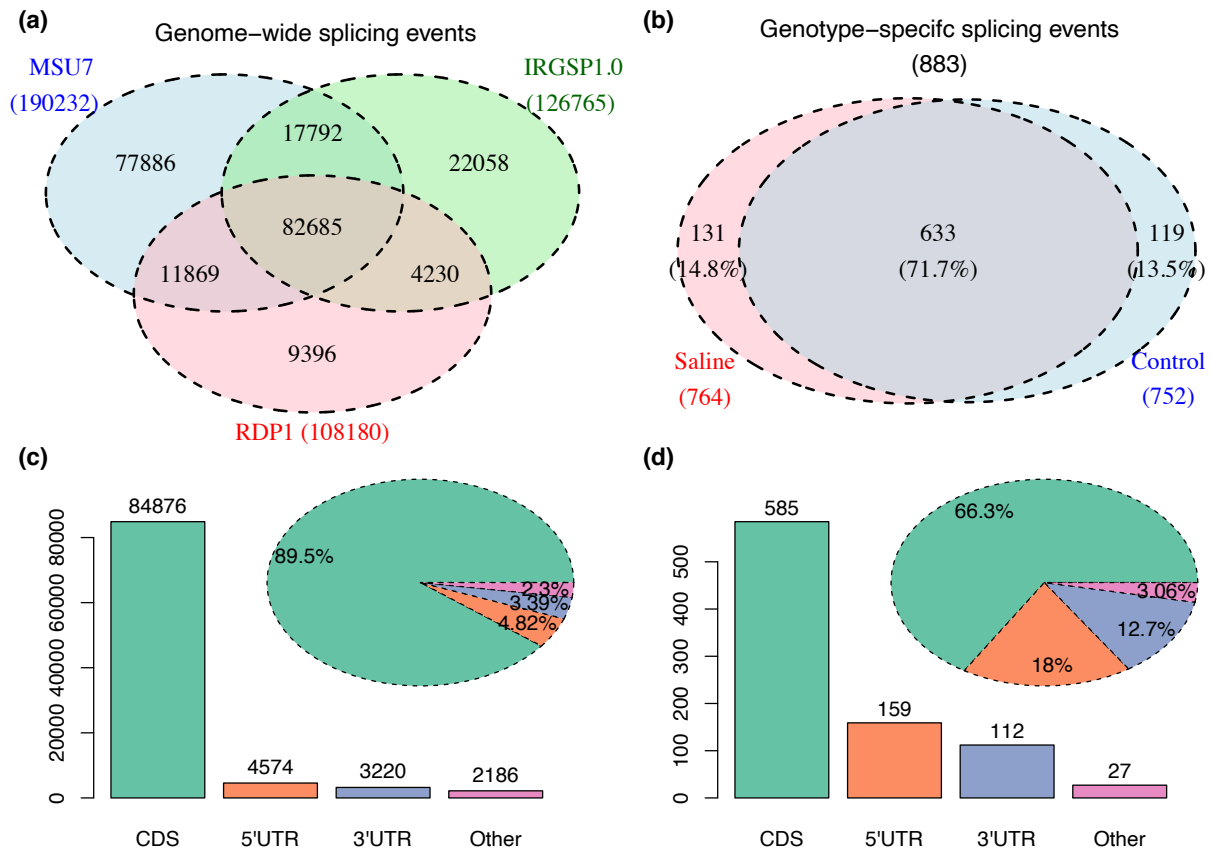


Figure S1. Splicing events identified by VaSP in RDP1 population. (a) Venn diagram of genome-wide splicing events identified in RDP1 (Rice Diversity Panel 1) population, annotated by MSU7 (<http://rice.plantbiology.msu.edu>) and by RAP-DB/IRGSP1.0 (<https://rapdb.dna.affrc.go.jp>). (b) Venn diagram of GSS events identified in control and salt stress conditions. (c) Distribution of genome-wide splicing events in different gene regions. (d) Distribution of GSS events in different gene regions. CDS, coding sequence; 5'UTR, 5 prime untranslated regions; 3'UTR, 3 prime untranslated regions; Other, unannotated or untranslated gene regions.

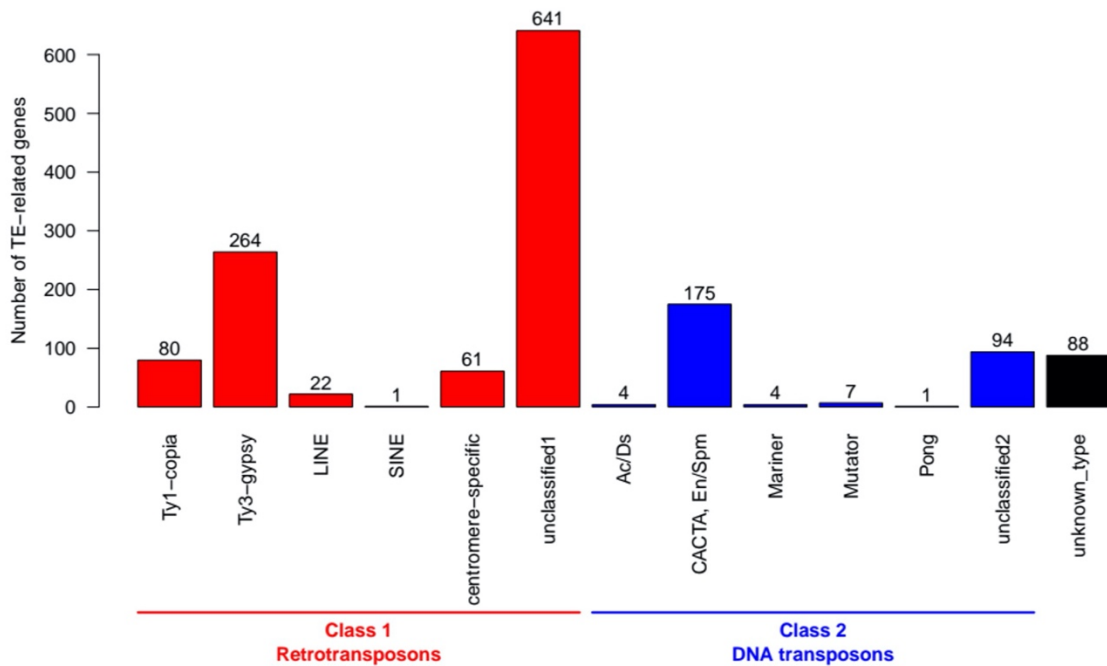


Figure S2. Different types of TE (transposable element)-related genes with splice site mutations.

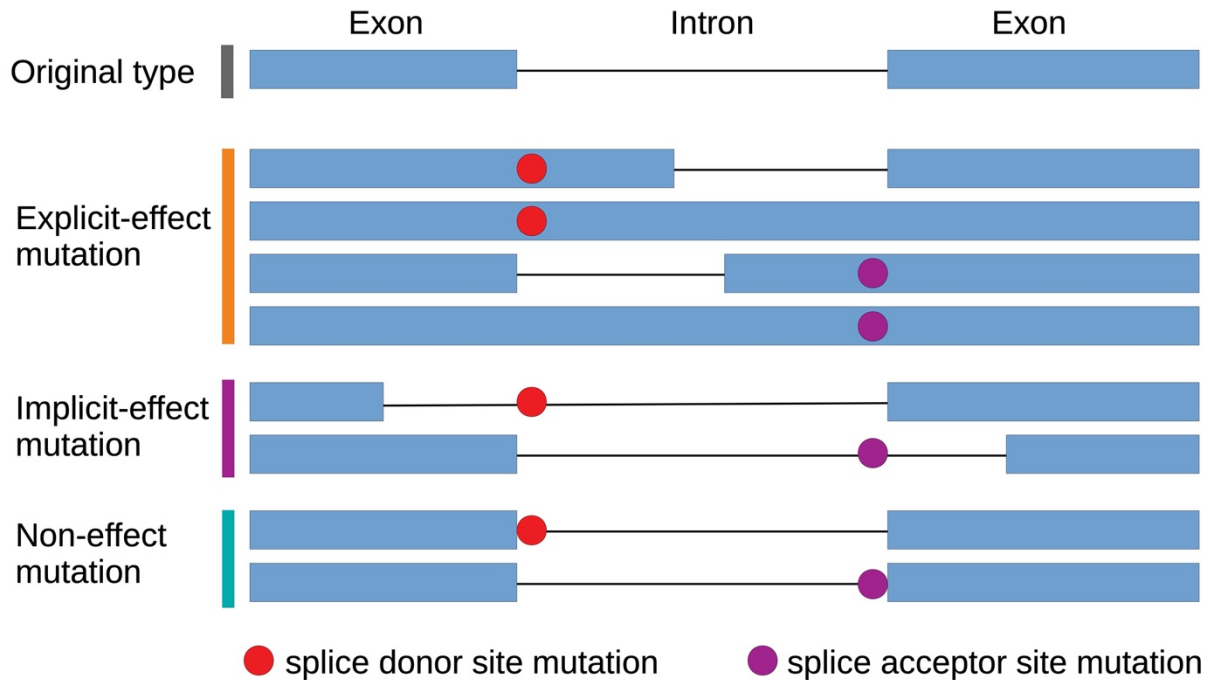


Figure S3. Classification of splice site mutations. Based on functions in pre-mRNA splicing regulation, splice site mutations (either in splice donor site or in acceptor site) can be classified into three types: explicit-effect, implicit-effect, and non-effect mutations.

Table S1. Detailed information of explicit-effect (ex) and implicit-effect (im) of splice site mutations in our dataset. (see separate file)