

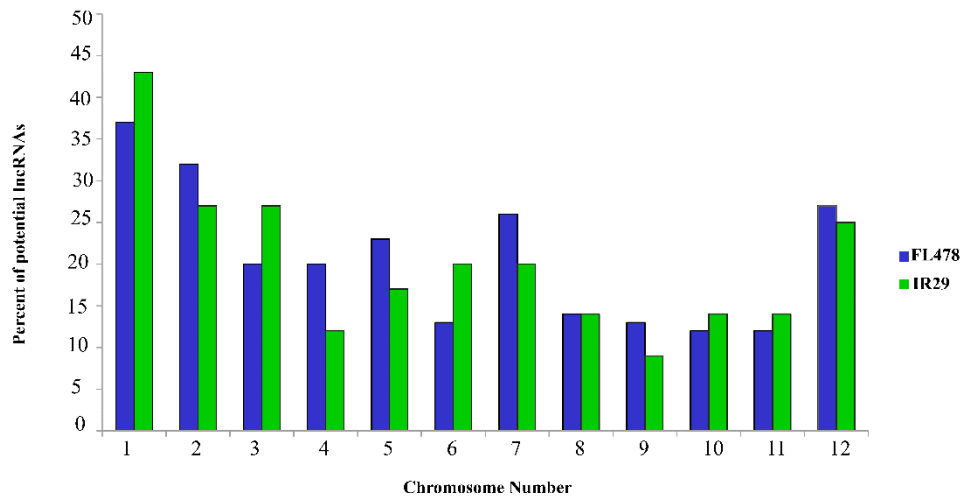


Fig. S1. Distribution of the expressed lncRNAs related to salt responses in each chromosome in the rice genotypes' roots.

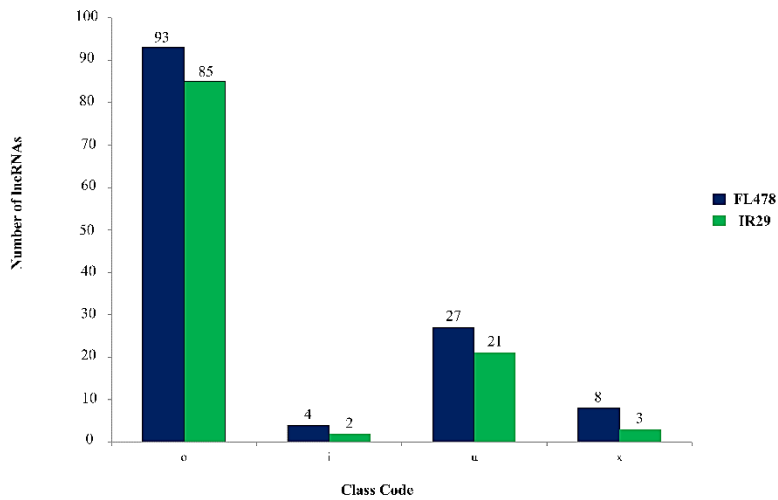


Fig. S2. The lncRNAs classification according to their position and orientation in the rice genome.

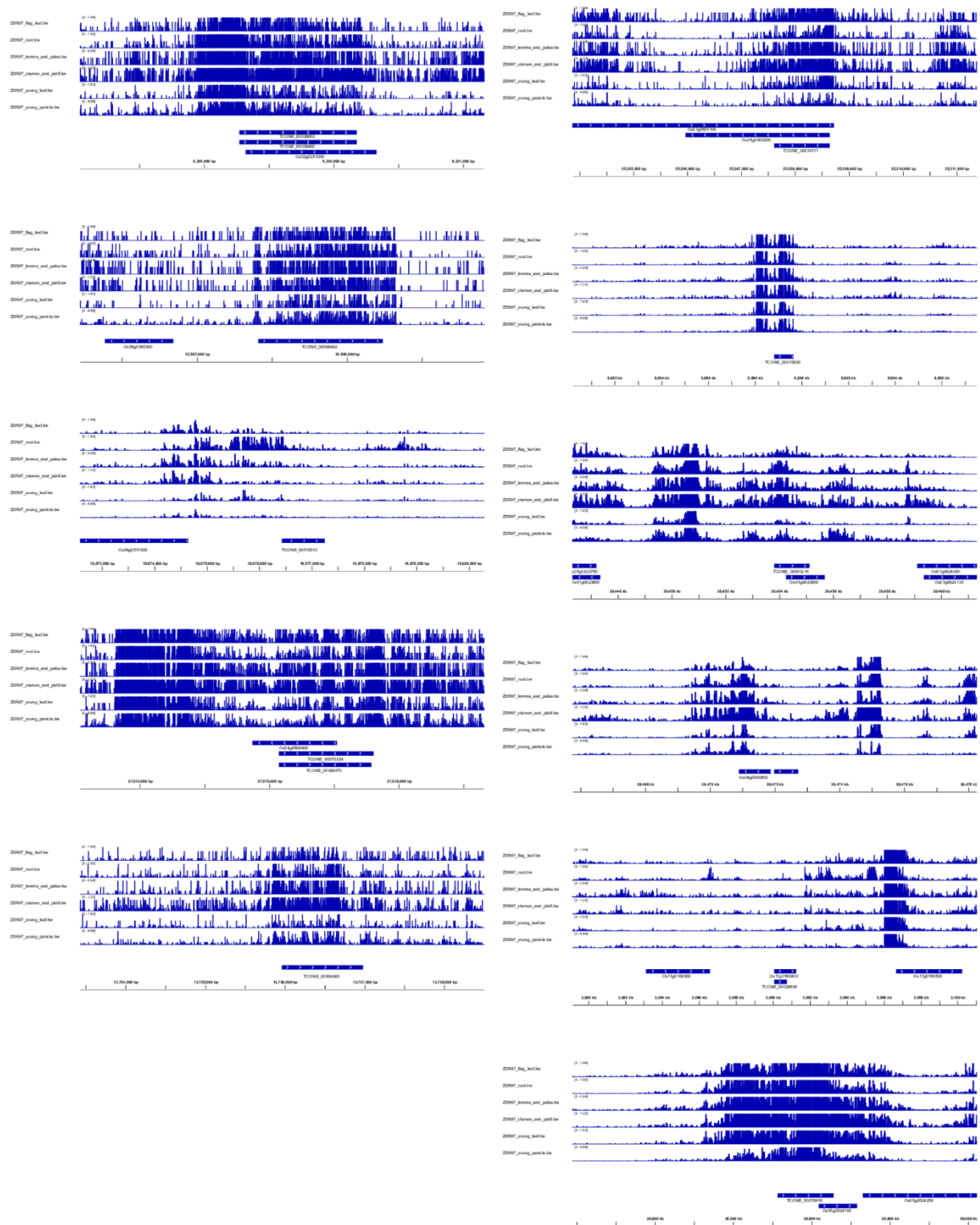


Fig. S3. ATAC-seq levels on the genomic regions of all the 11 DE-lncRNAs in 6 tissues.

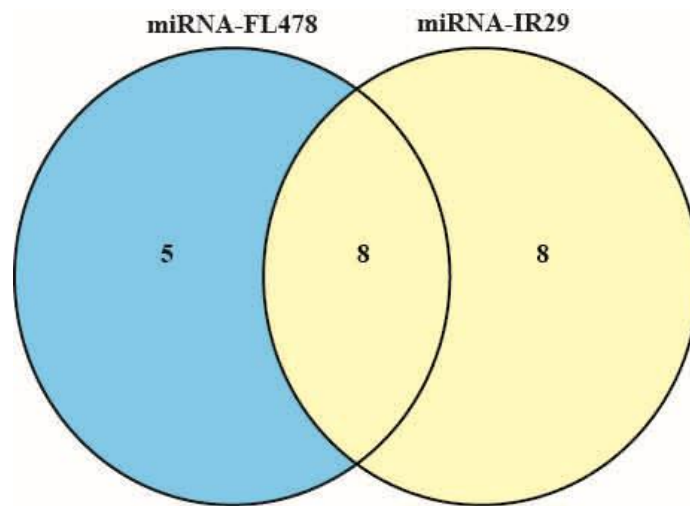


Fig. S4. A Venn diagram showing potential target miRNAs in the studied contrasting genotypes.

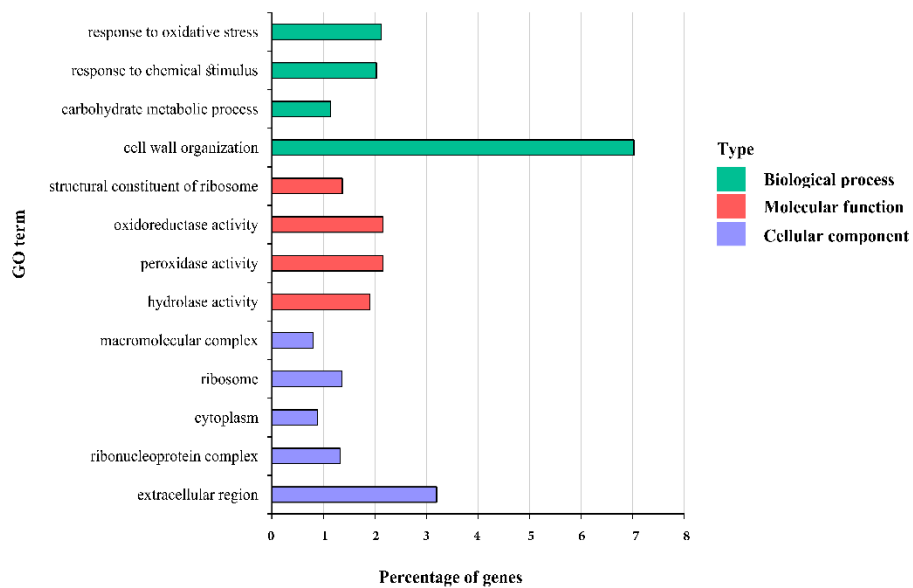


Fig. S5. The gene ontology (GO) enrichment analysis for target genes in the M39 module.

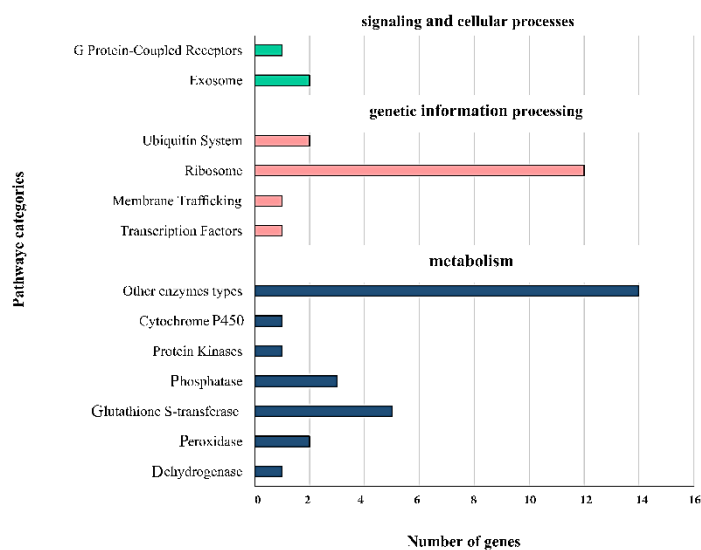


Fig. S6. Distribution of the KEGG pathways for target genes in the M39 module into three main categories.