

Figure S1: Figure depicts the number of lncRNAs present on the telomeric region of each chromosome in rice genotype (a) IR64 and (b) Pokkali.

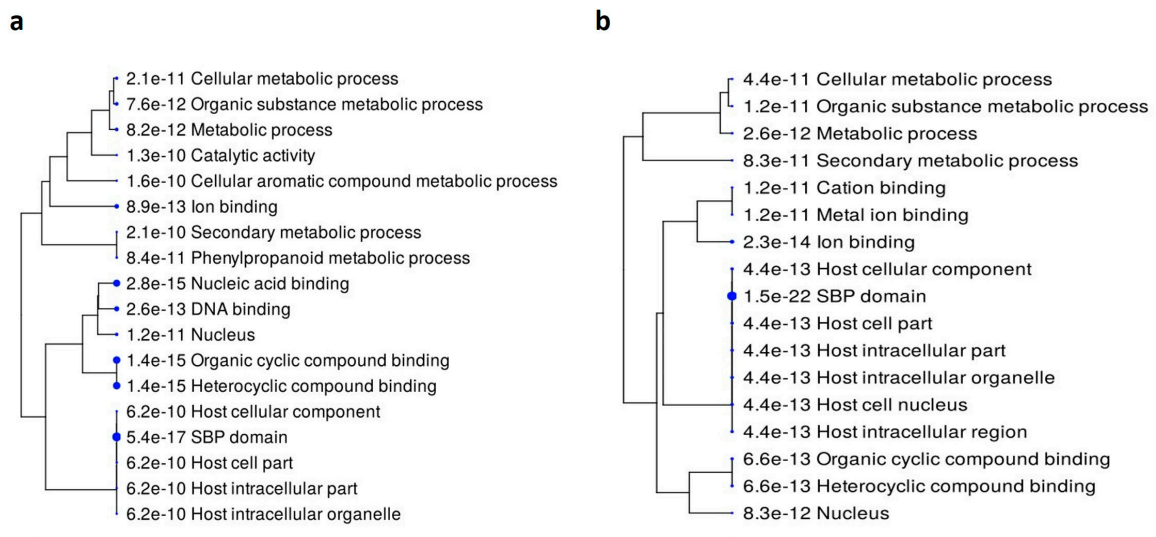


Figure S2: A hierarchical clustering tree summarizes the correlation among significant pathways in (a) IR64 and (b) Pokkali. Pathways with many shared genes are clustered together. Bigger dots indicate more significant *p*-values.

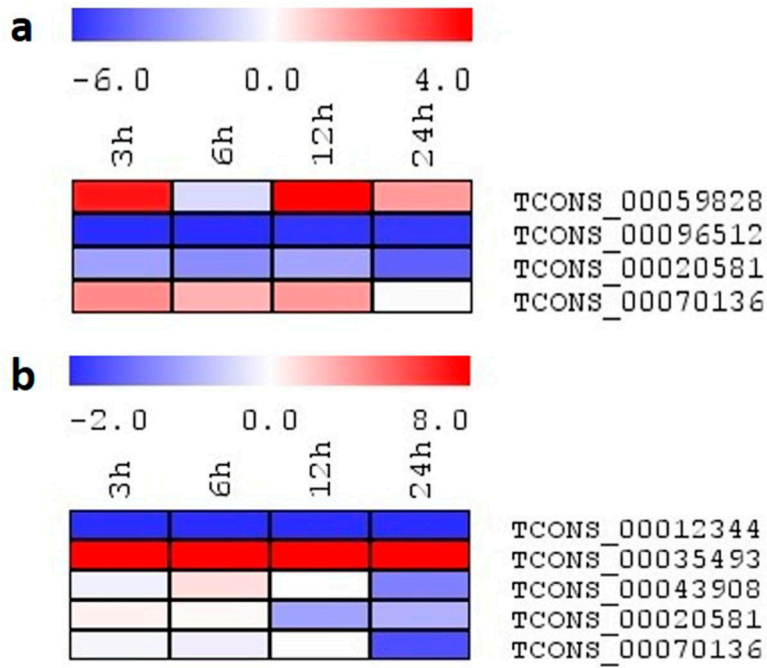


Figure S3 (a,b): The heatmap has been generated based on the log2 fold-change values showing differential expression of lncRNAs in rice genotypes (a) IR64 and (b) Pokkali exposed to ABA at 0, 3, 6, 12, and 24 h.

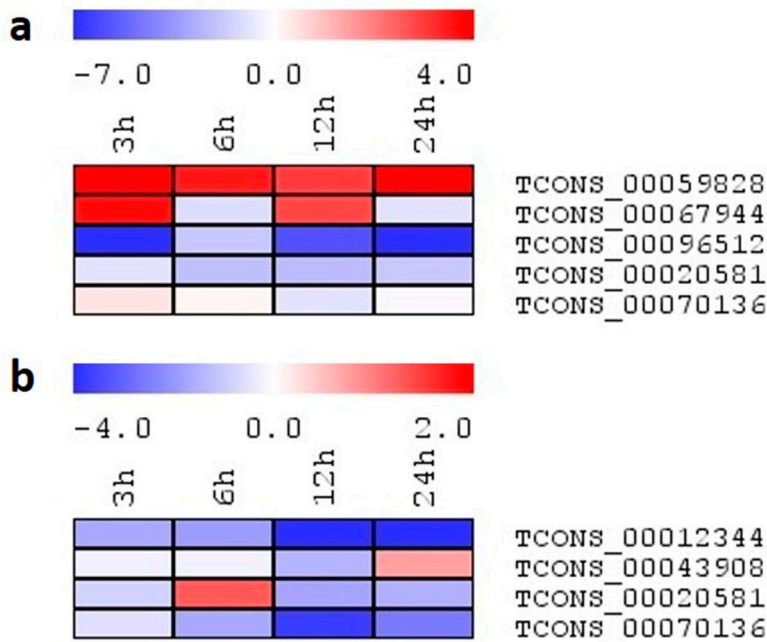


Figure S4 a,b): The heatmap has been generated based on the log2 fold-change values showing differential expression of lncRNAs in rice genotypes (a) IR64 and (b) Pokkali exposed to SA at 0, 3, 6, 12, and 24 h.

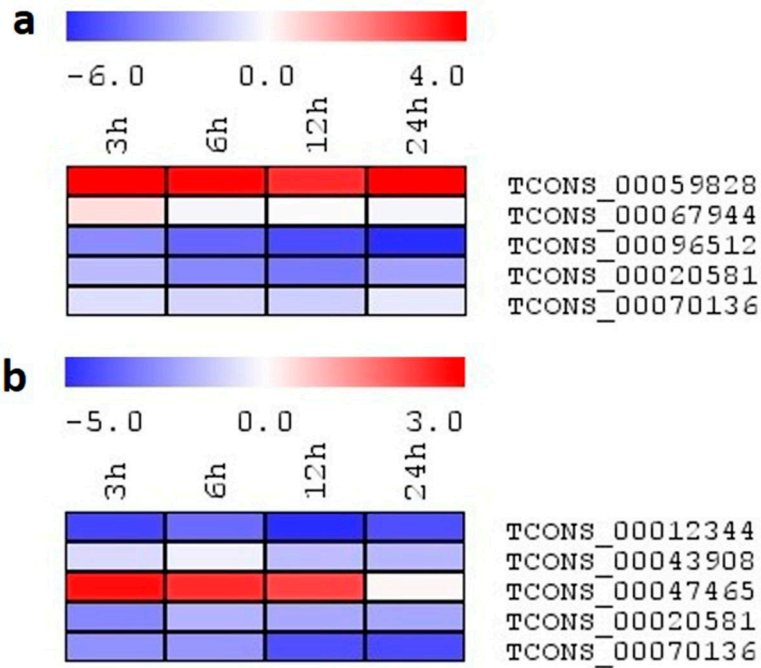


Figure S5 (a,b): The heatmap has been generated based on the log2 fold-change values showing differential expression of lncRNAs in rice genotypes (a) IR64 and (b) Pokkali exposed to JA at 0, 3, 6, 12, and 24 h.

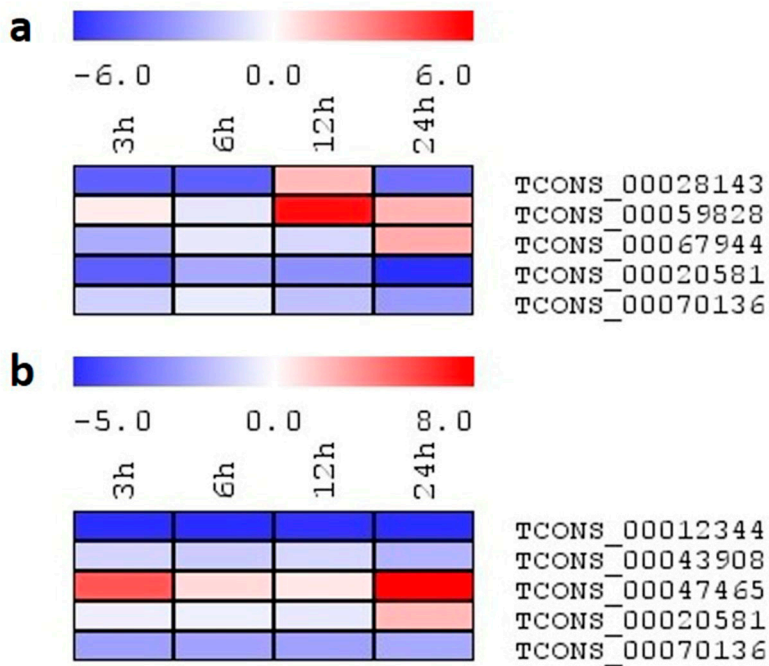


Figure S6 (a,b): The heatmap has been generated based on the log2 fold-change values showing differential expression of lncRNAs in rice genotypes (a) IR64 and (b) Pokkali exposed to ET at 0, 3, 6, 12, and 24 h.

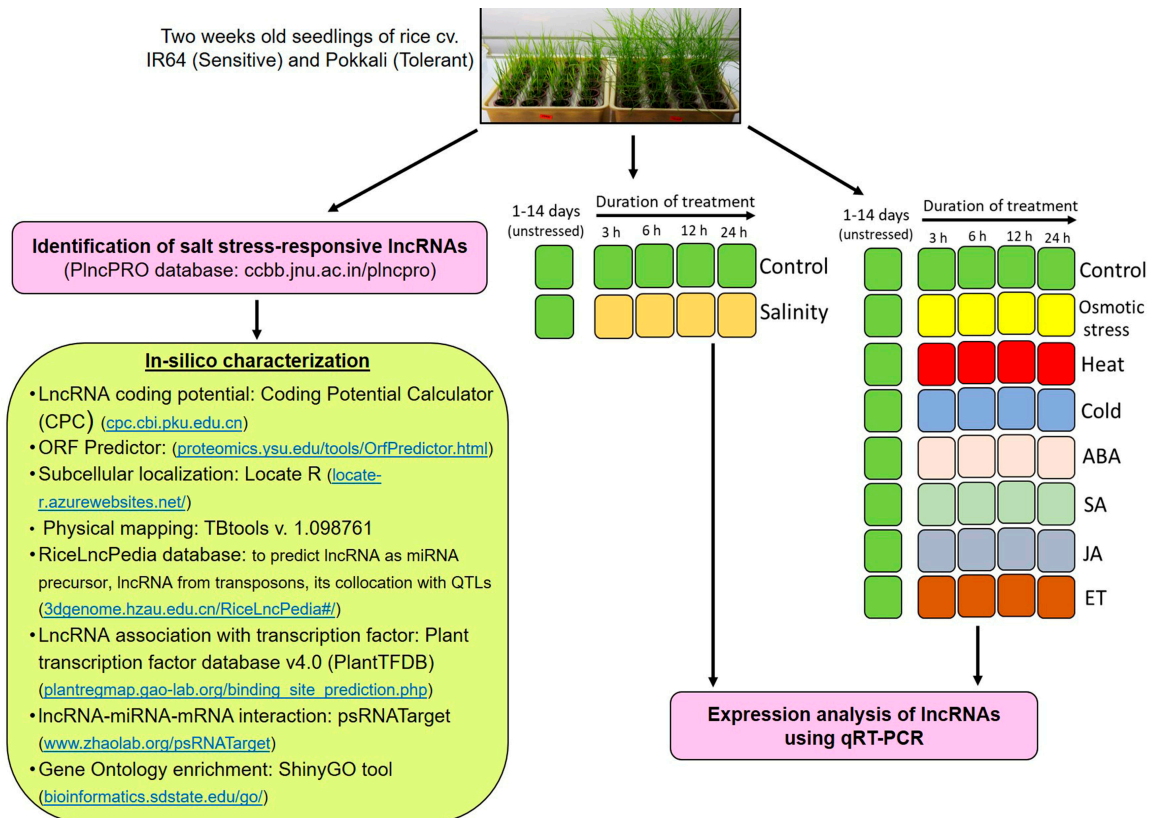


Figure S7: Schematic representation of the workflow and steps involved in the experiment.