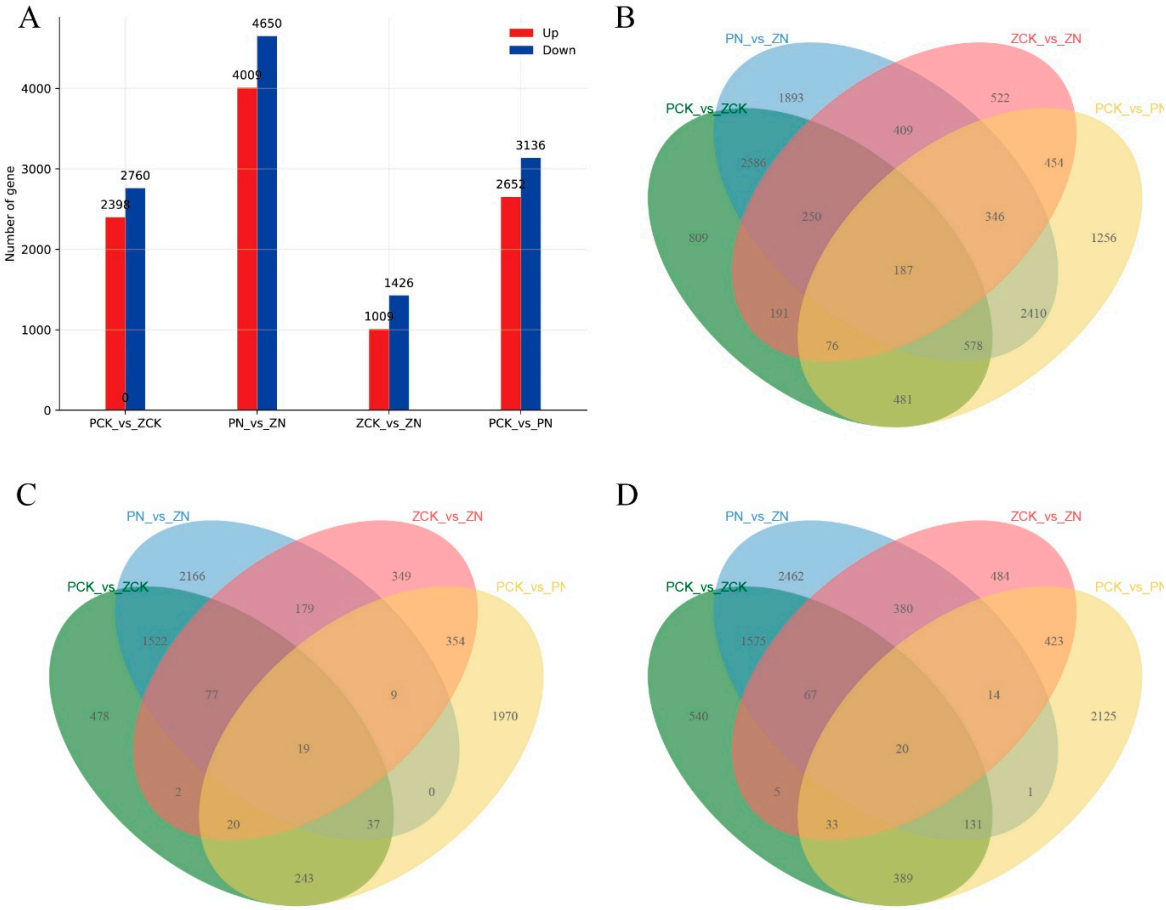
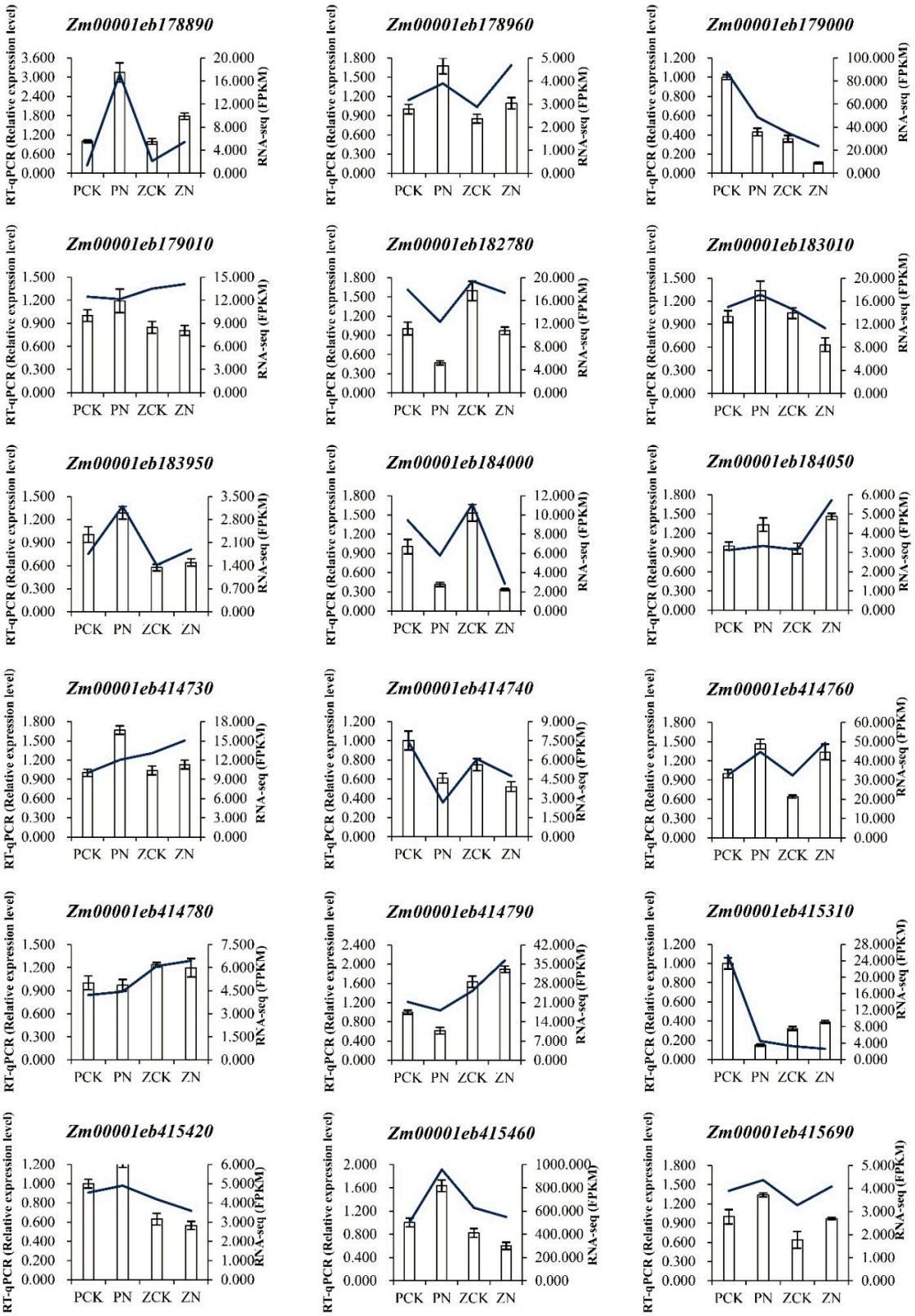
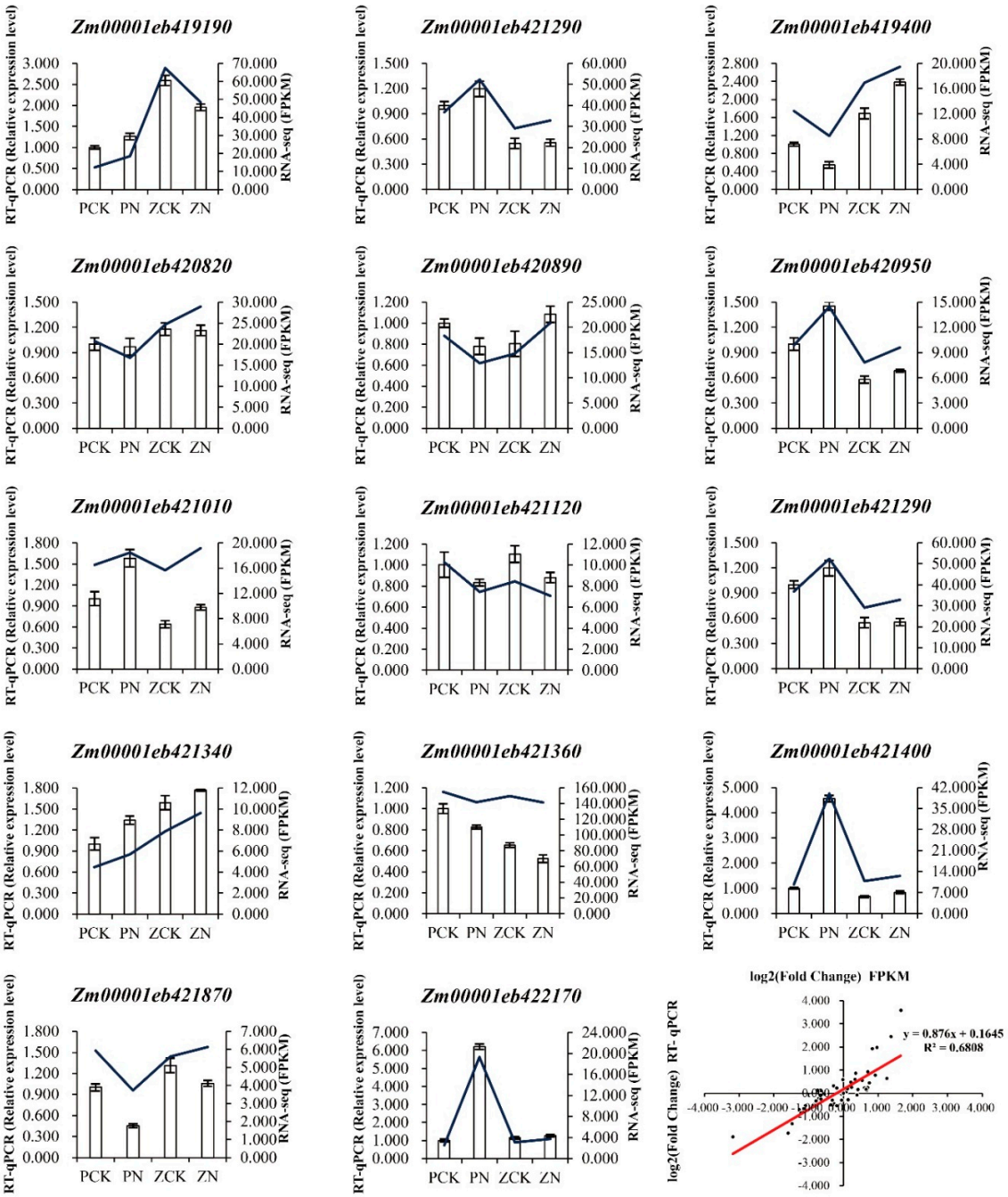
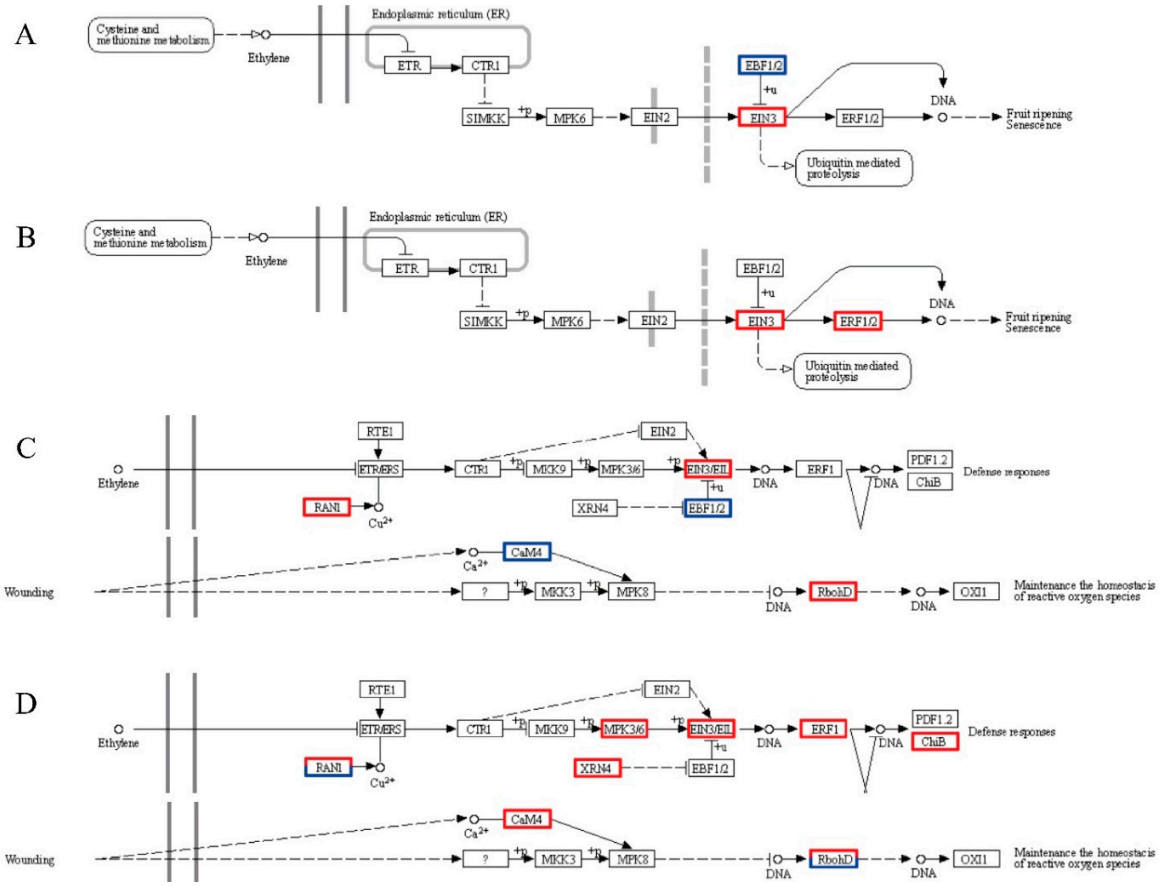


Supplementary Figure S1 Differential gene expression analysis under salt stress conditions. (**A)** Quantitative distribution of up-regulated and down-regulated DEGs across comparative groups, illustrating the magnitude of transcriptional changes. **(B-D)** Venn diagram analysis of DEG overlap: Total DEGs (B), Up-regulated DEGs (C), and Down-regulated DEGs (D), demonstrating the shared and unique stress-responsive genes between different genotype-treatment comparisons.


Zm00001eb178890
Zm00001eb178960
Zm00001eb179000
Zm00001eb179010
Zm00001eb182780
Zm00001eb183010
Zm00001eb183950
Zm00001eb184000
Zm00001eb184050
Zm00001eb414730
Zm00001eb414740
Zm00001eb414760
Zm00001eb414780
Zm00001eb414790
Zm00001eb415310
Zm00001eb415420
Zm00001eb415460
Zm00001eb415690
RT-qPCR (Relative expression level)
RNA-seq (FPKM)
PCK PN ZCK ZN



Supplementary Figure S2 Validation of DEGs by quantitative RT-PCR. Expression patterns of 32 candidate genes were verified, with normalization to the Actin reference gene. Data represent means ± SEM (n=3 biological replicates). Bar plots (left axis) show RT-qPCR results while connected lines (right axis) display corresponding RNA-seq expression levels. Treatment groups: PCK, PN, ZCK, ZN. Correlation analysis between qPCR and RNA-seq data, demonstrating high consistency between both methods.



Supplementary Figure S3 Plant hormone signal transduction and MAPK signaling pathways regulating salt tolerance in different comparison groups. **(A, B)** Plant hormone signal transduction pathway. **(C, D)** MAPK signaling pathway - plant.

Note: Panels (A, C) correspond to the ZCK vs ZN comparison (Zheng58), while panels (B, D) correspond to the PCK vs PN comparison (PH4CV).