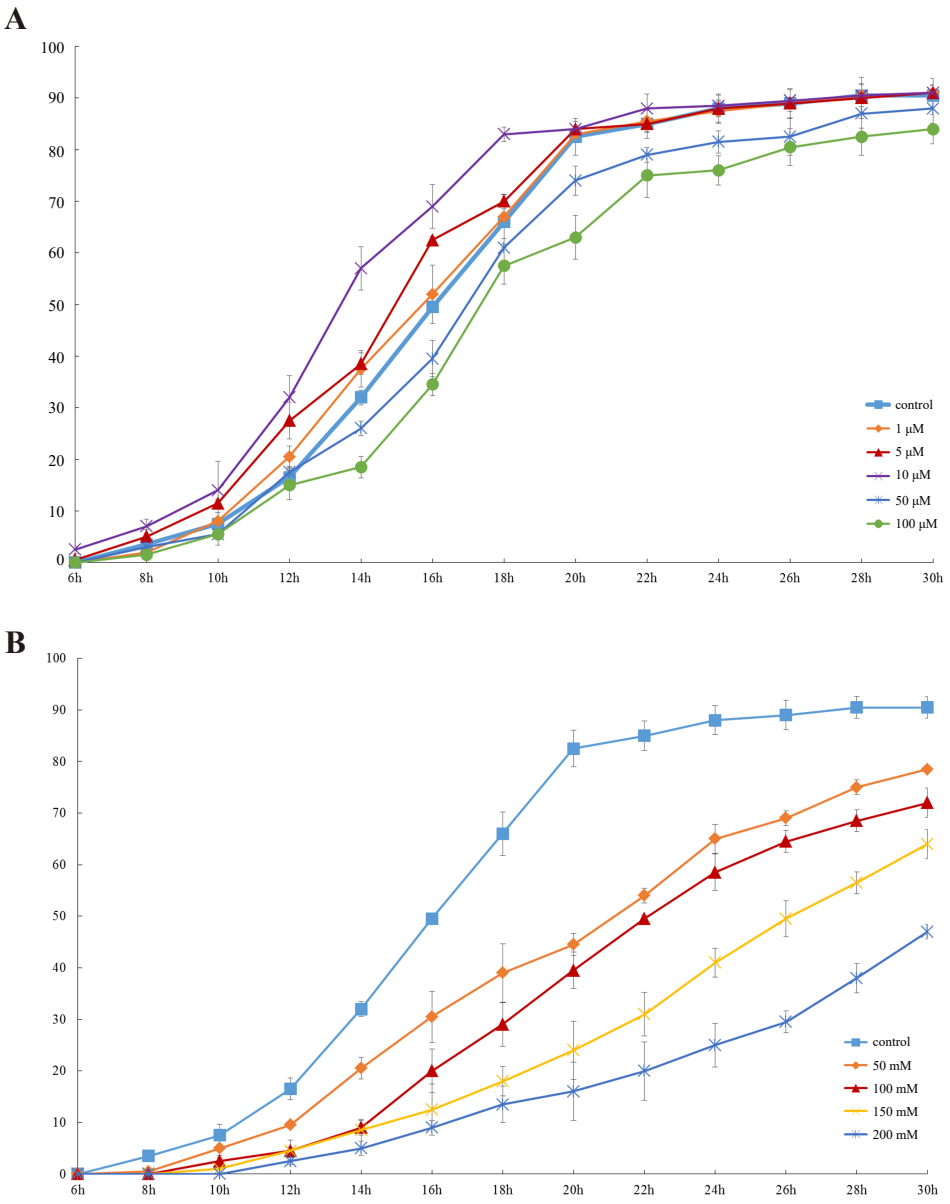
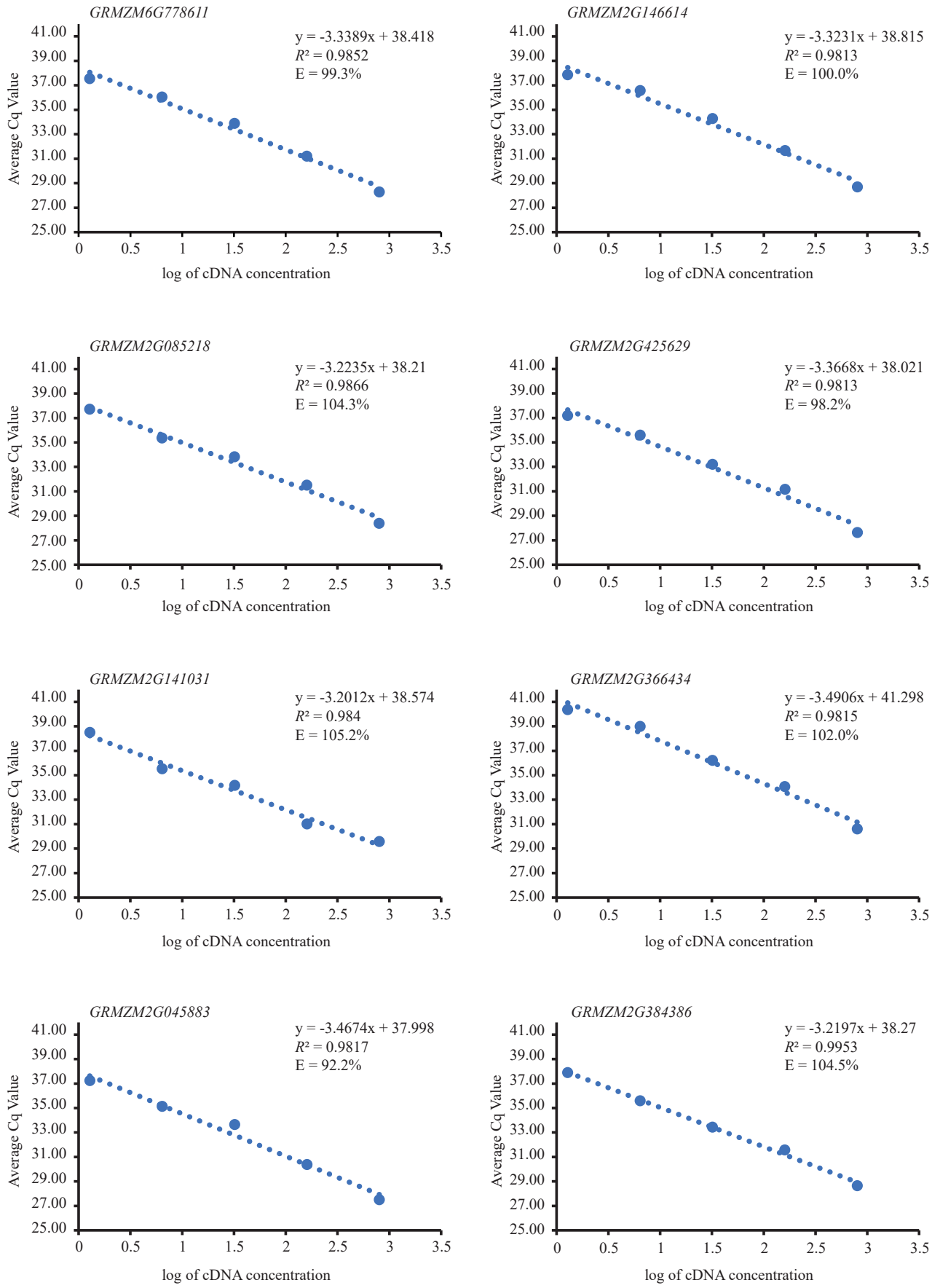
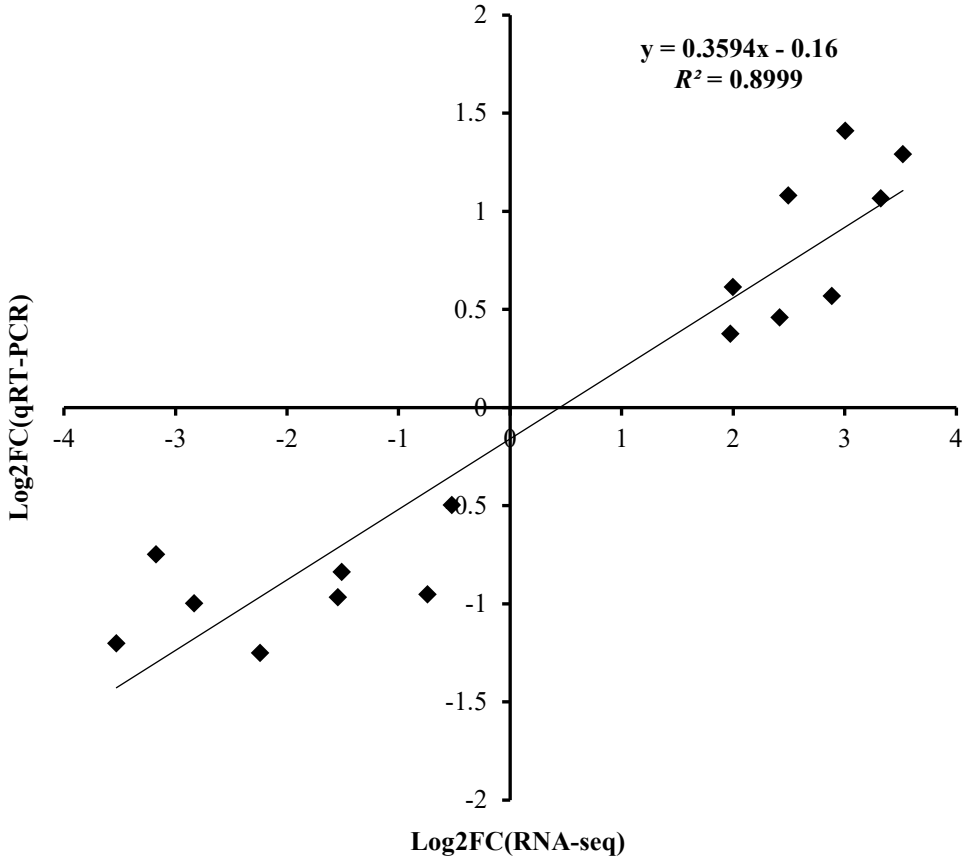


Supplementary Fig. 1. The effect of melatonin and NaCl treatments on the germination percentage of maize seeds. (A) The germination percentage of maize seeds under different concentrations of exogenous melatonin. (B) The germination percentage of maize seeds under different concentrations of NaCl. Data show means ± SD of three biological replicates.

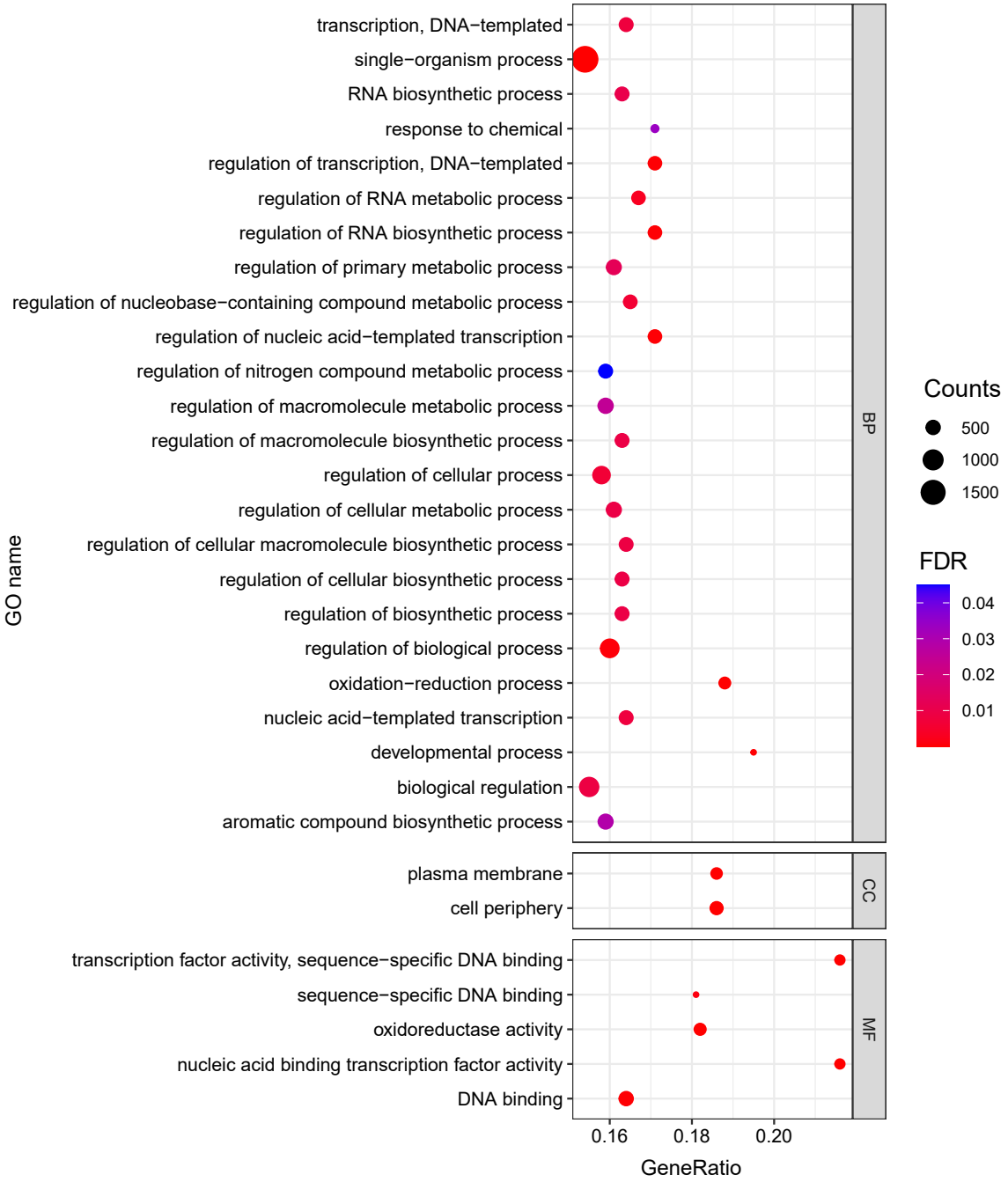
Supplementary Fig. 2. Morphology of germinating maize seeds at 18 h after various treatments. Scale bar, 1 cm. control: water-treated seeds germinated in water; NaCl: water-treated seeds germinated in 100 mM NaCl; NaCl+MT: 10 μM melatonin (MT)-treated seeds germinated in 100 mM NaCl.



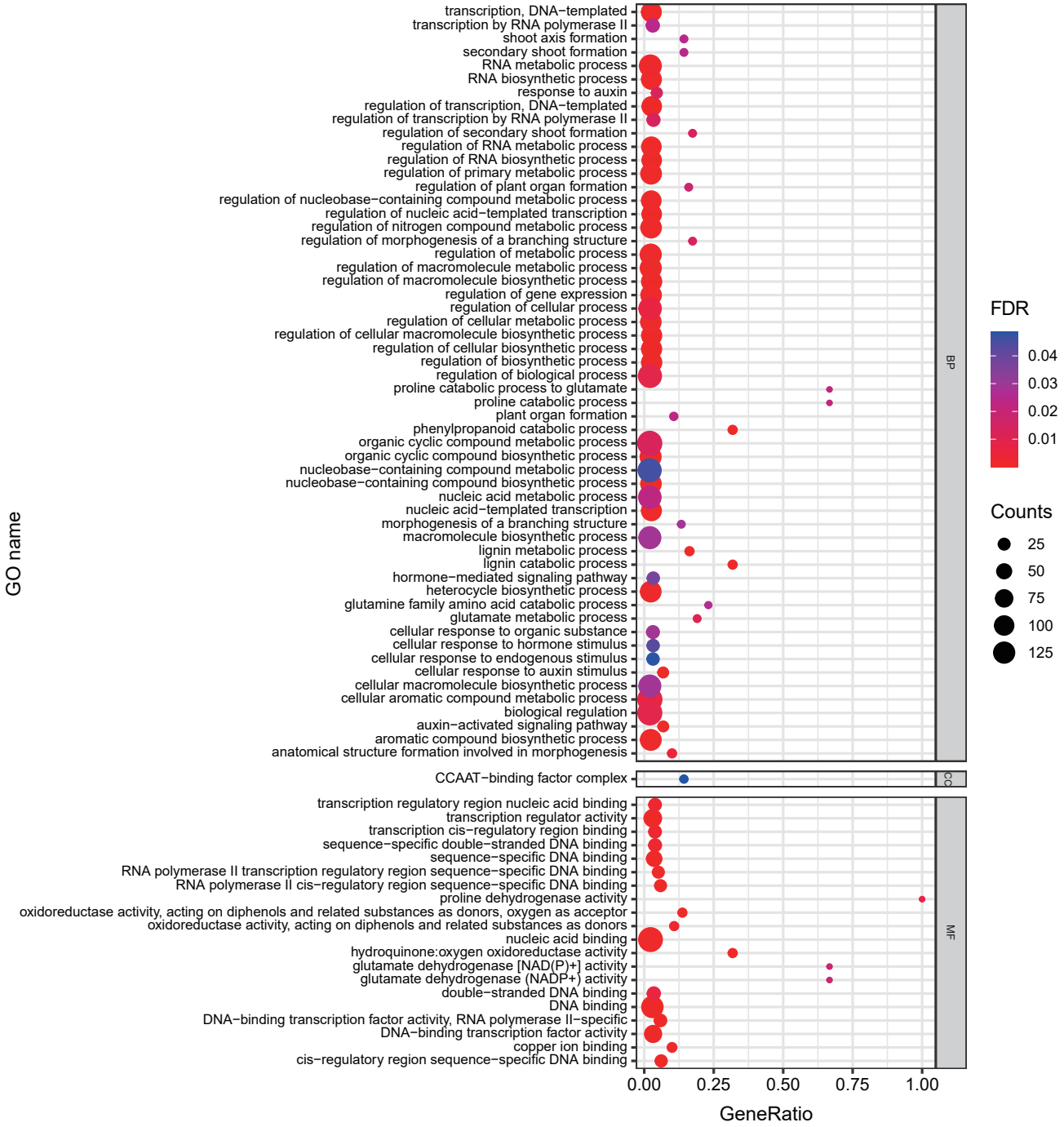
Supplementary Fig. 3. Standard curves and primer efficiency of eight select genes from DEGs in RNA-seq data. The PCR efficiency (E; %) for each primer pair was calculated as E = (10-1/A − 1) × 100%. The cDNA concentration in 1:1, 1:5, 1:25, 1:125, and 1:625 dilutions was 800, 160, 32, 6.4, 1.28ng/μl, respectively, while the Log (cDNA in ng/reaction) for the 1:1, 1:5, 1:25, 1:125, and 1:625 dilutions were 2.90309, 2.20412, 1.50515, 0.80618, and 0.10721, respectively.



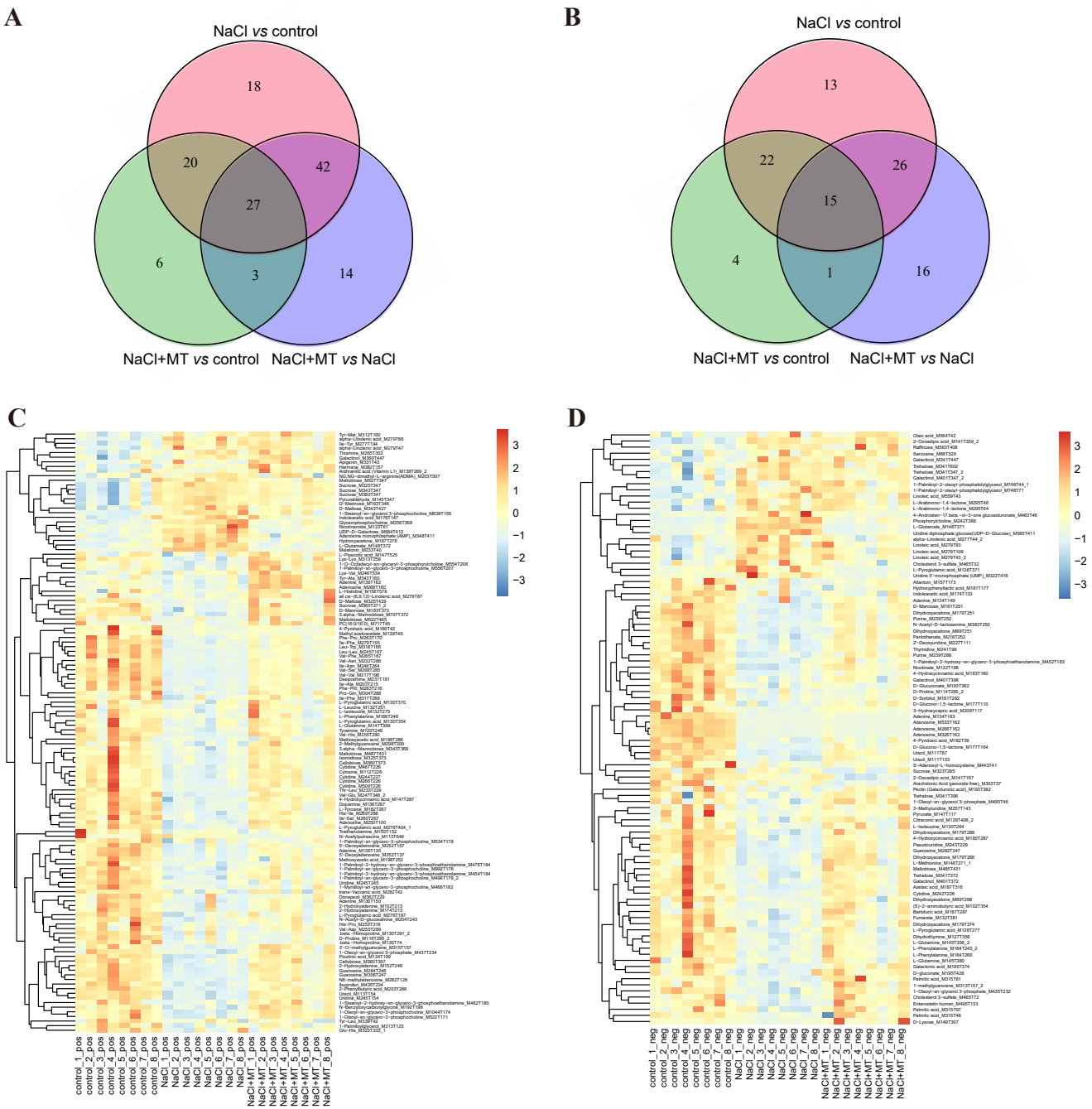
Supplementary Fig. 4. qRT-PCR validation of DEGs from the RNA-seq data. Each point represents a selected DEG from the RNA-seq data. The x-axis indicated the gene expression fold change (FC) from RNA-seq data, while the y-axis indicated the gene expression fold change determined by qRT-PCR.



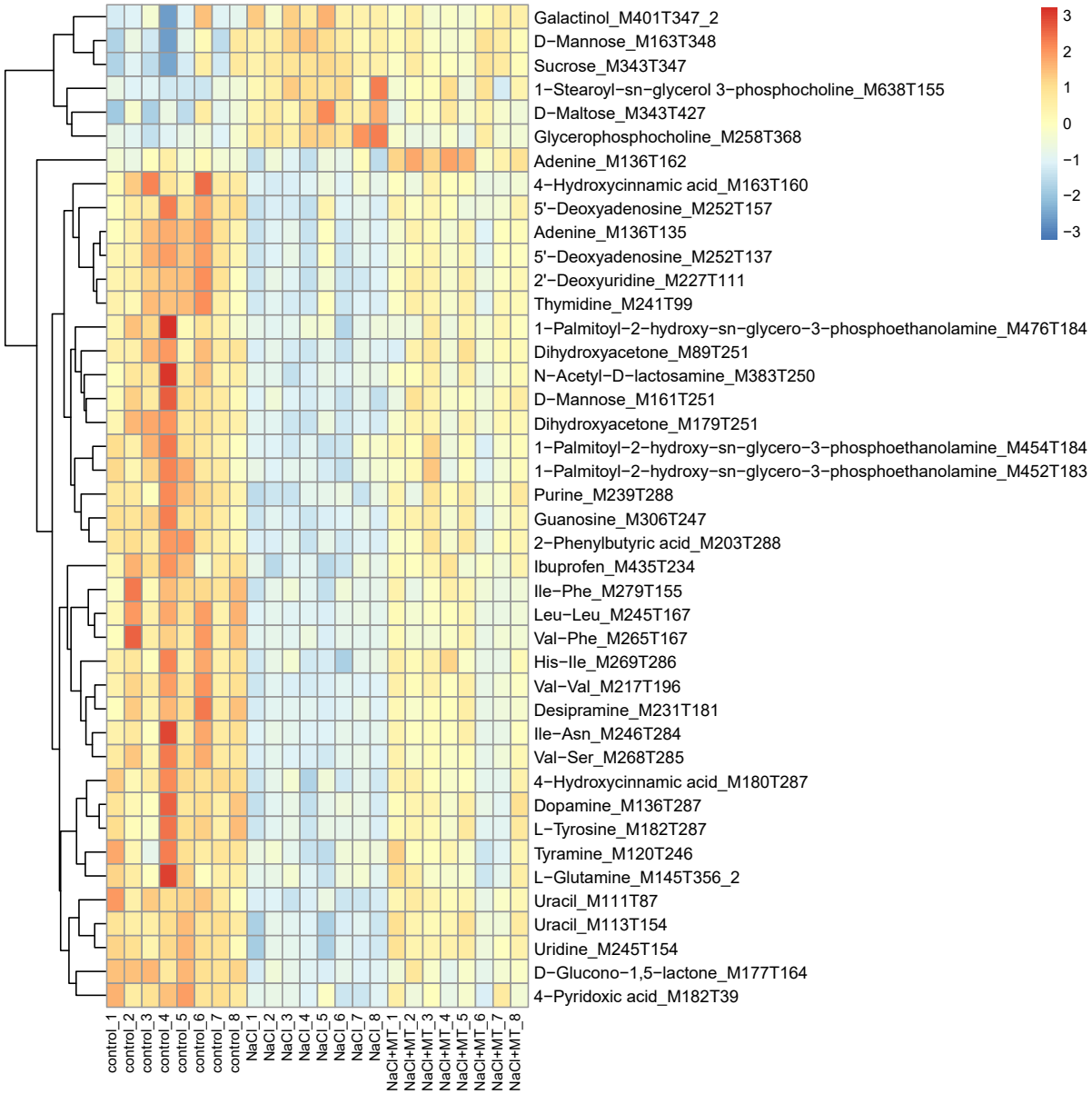
Supplementary Fig. 5. GO enrichment analysis of all DEGs under three pairwise comparisons of NaCl *vs* control, NaCl+MT *vs* control and NaCl+MT *vs* NaCl. The most significant enriched GO terms with more than 200 DEGs and an FDR < 0.05 were shown. BP, CC and MF indicated biological process, cellular component, molecular function, respectively.



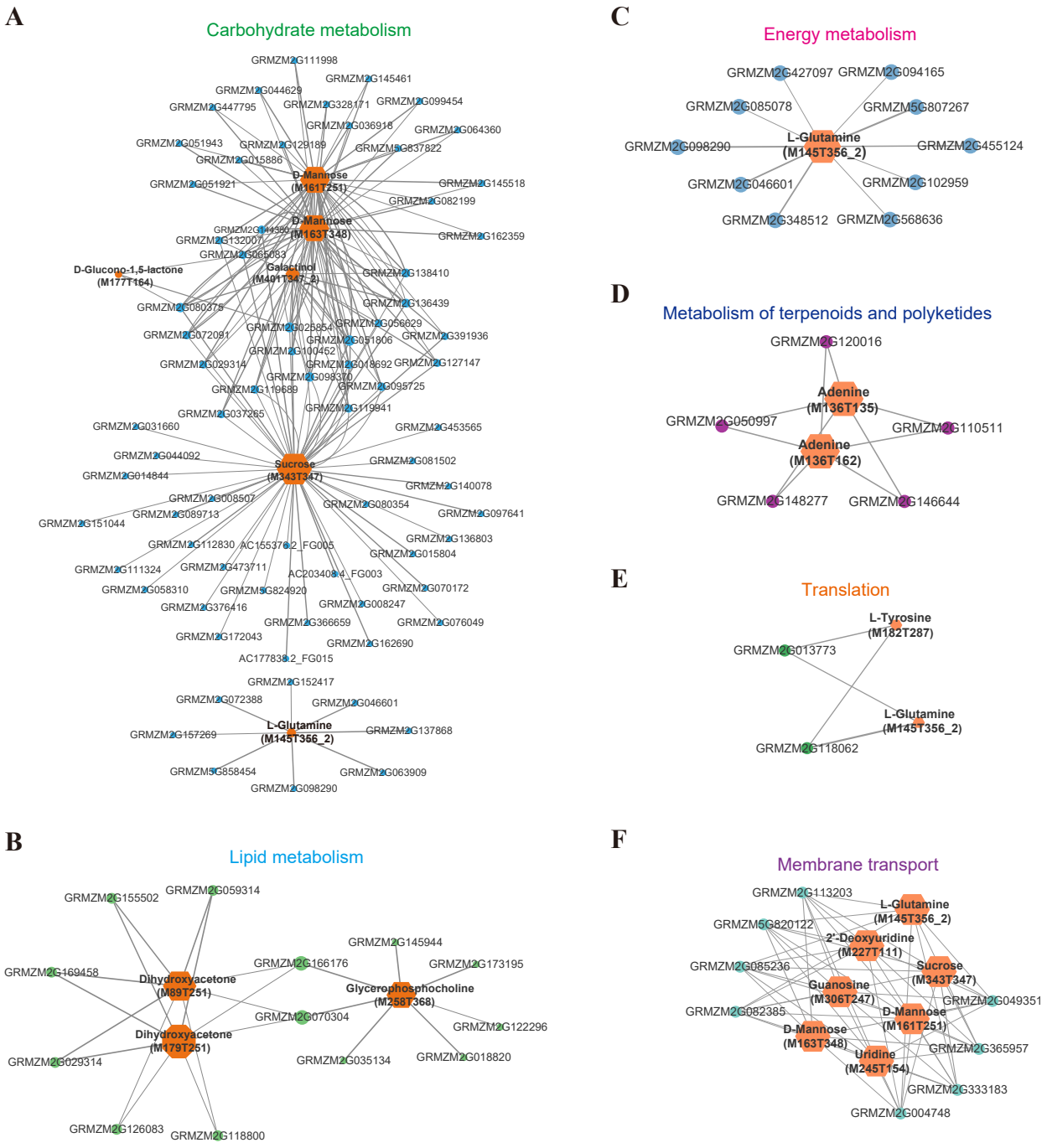
Supplementary Fig. 6. GO enrichment analysis of genes targeted by differently expressed miRNAs under three pairwise comparisons of NaCl *vs* control, NaCl+MT *vs* control and NaCl+MT *vs* NaCl. The significant enriched GO terms with an FDR < 0.05 were shown. BP, CC and MF indicated biological process, cellular component, molecular function, respectively.



Supplementary Fig. 7. Cluster analysis of all differentially expressed metabolites in maize germinating seeds under three pairwise comparisons of NaCl *vs* control, NaCl+MT *vs* control and NaCl+MT *vs* NaCl. (A-B) Vern diagram showing differential metabolites, including 130 positive ions (A) and 97 negative ions (B) among NaCl *vs* control, NaCl +MT *vs* control and NaCl *vs* NaCl comparisons. (C-D) Heatmap showing the relative levels of 130 positive ions (C) and 97 negative ions (D) among three different comparisons.



Supplementary Fig. 8. Cluster analysis of 42 overlapped differential metabolites (27 positive ions and 15 negative ions) among three pairwise comparisons of NaCl *vs* control, NaCl+MT *vs* control and NaCl+MT *vs* NaCl. Heatmap showing the relative levels of 42 overlapped differential metabolites among three different comparisons.



Supplementary Fig. 9. Gene-metabolite correlation network showing the other six co-enriched KEGG pathways of 42 overlapped differently metabolites and 3059 differently expressed genes among three pairwise comparisons of NaCl *vs* control, NaCl+MT *vs* control and NaCl+MT *vs* NaCl. (A) Pathway of carbohydrate metabolism. (B) Pathway of lipid metabolism. (C) Pathway of energy metabolism. (D) Pathway of terpenoid and polyketide metabolism. (E) Pathway of translation. (F) Pathway of membrane transport. The gene-metabolite pairs are connected within the network by edges. The correlation levels of network are indicated by the width of edges. Orange hexagon nodes indicate differentially metabolites. Colorful round nodes indicate differently expressed genes. The size of nodes indicates the degree of connection between the genes and metabolites.