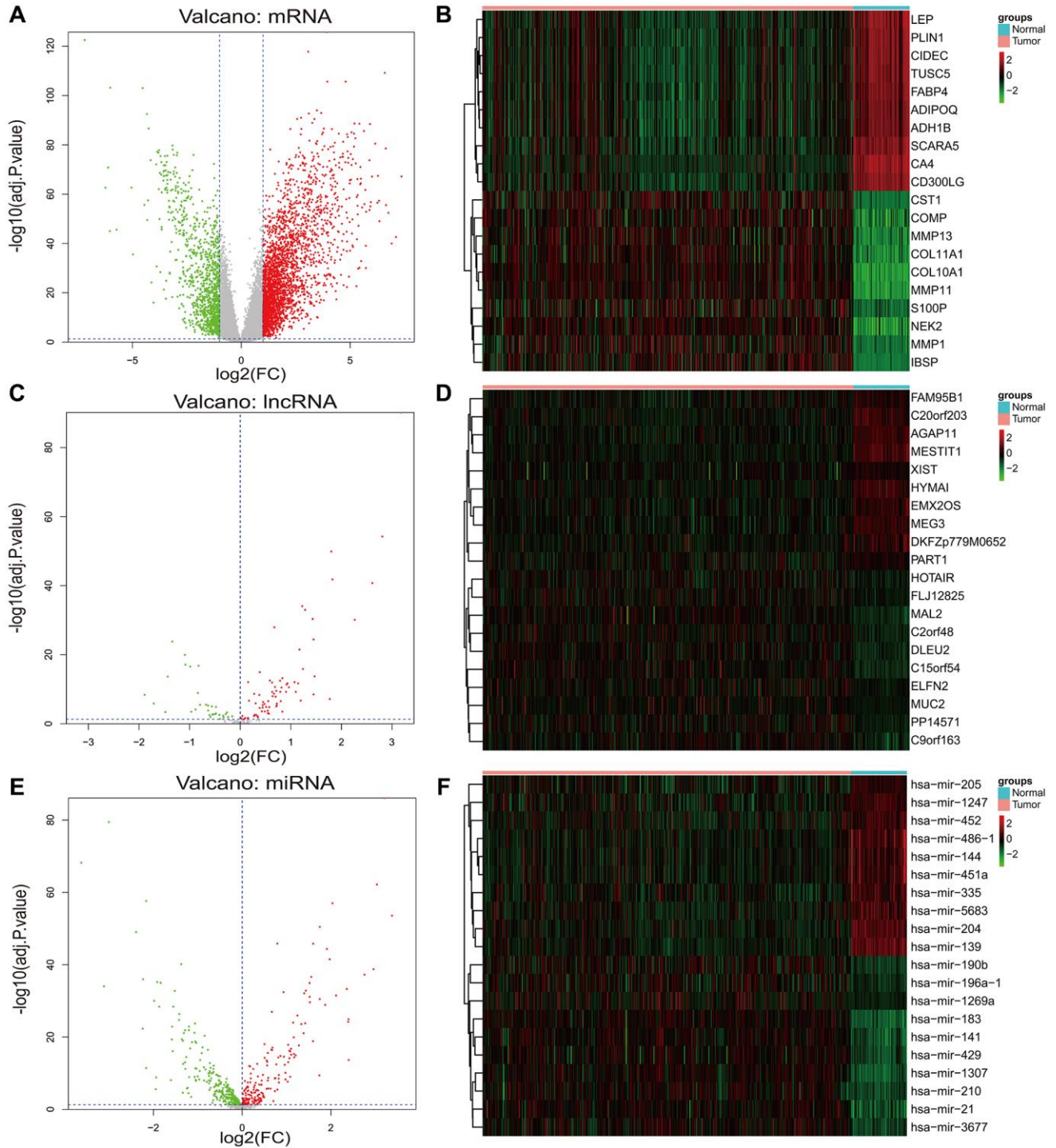
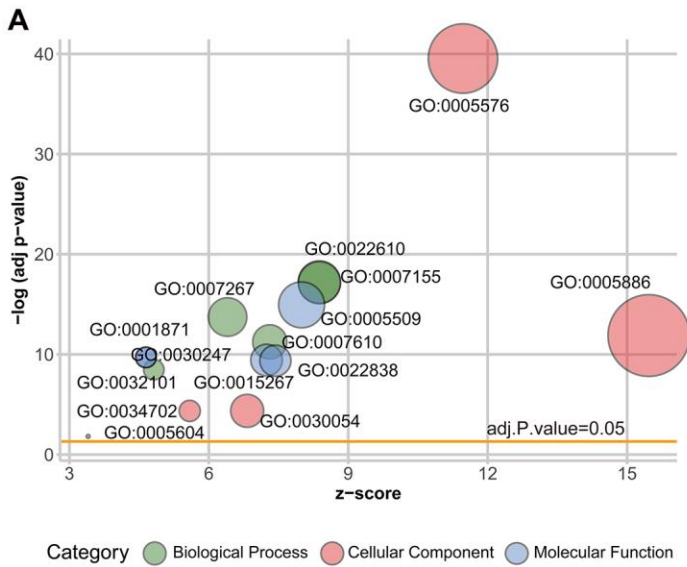


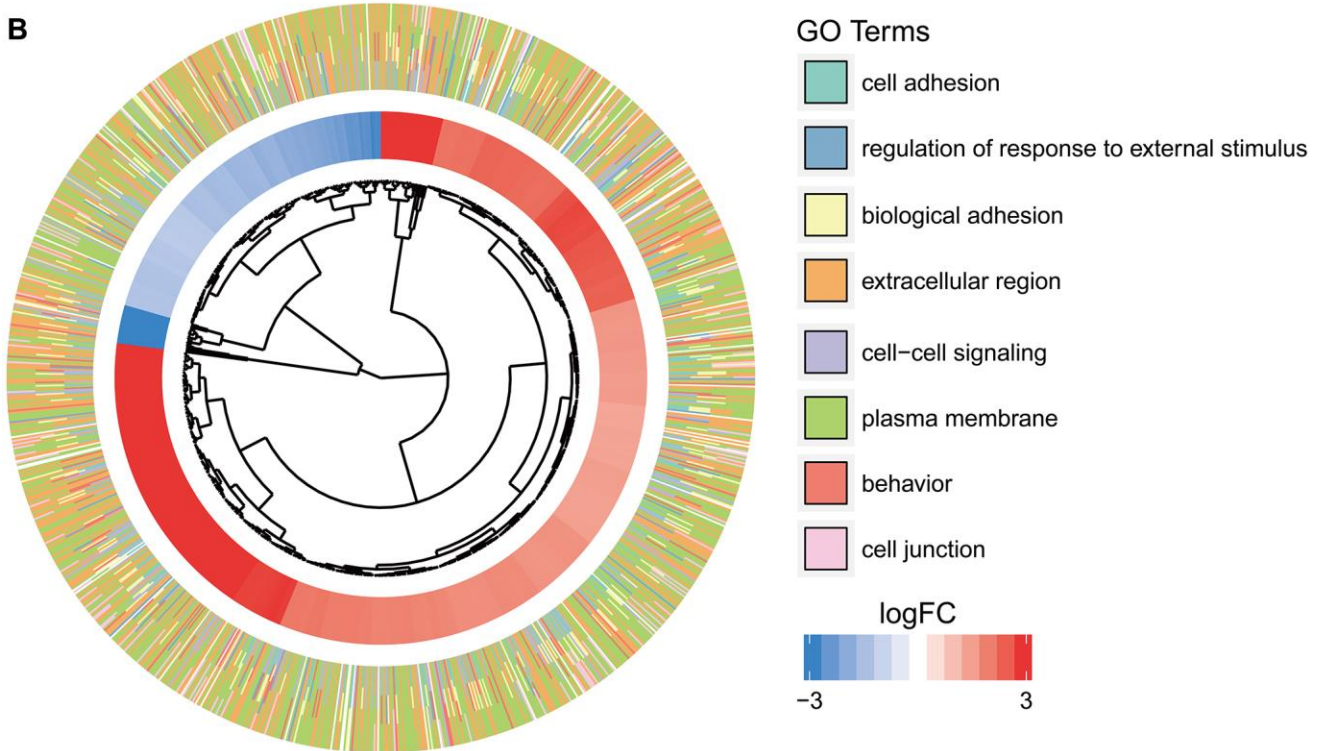
SUPPLEMENTARY FIGURES



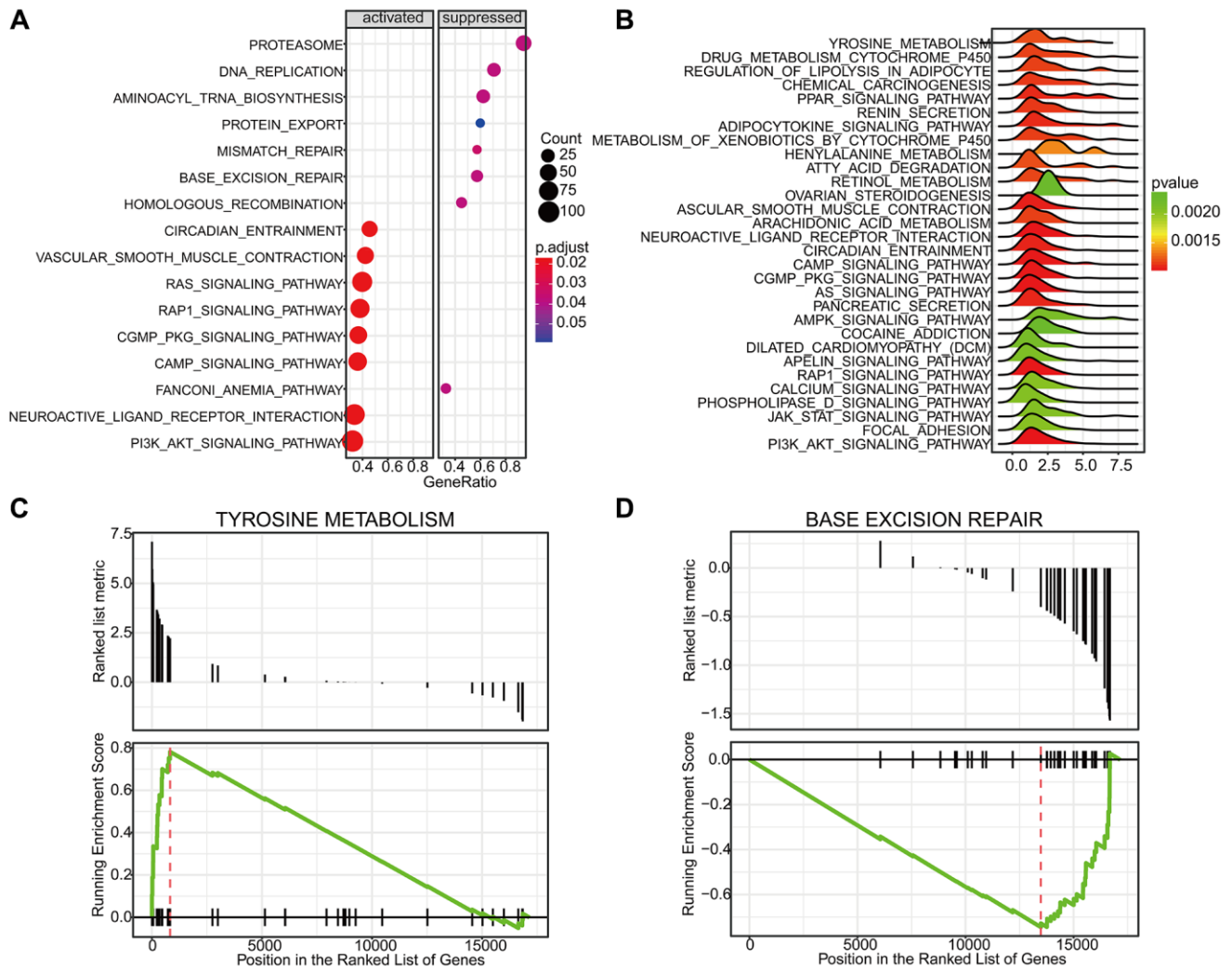
Supplementary Figure 1. Illustration of differentially expressed mRNAs, lncRNAs and miRNAs. (A, B) The volcano plot and heatmaps of differentially expressed mRNAs; (C, D) The volcano plot and heatmaps of differential lncRNAs; (E, F) The volcano plot and heatmaps of differential miRNAs. Red spots stand for up-regulated genes, while green spots stand for down-regulated genes.



ID	Description
GO:0007155	cell adhesion
GO:0022610	biological adhesion
GO:0007267	cell-cell signaling
GO:0007610	behavior
GO:0032101	regulation of response to external stimulus
GO:0005576	extracellular region
GO:0005886	plasma membrane
GO:0030054	cell junction
GO:0034702	ion channel complex
GO:0005604	basement membrane
GO:0005509	calcium ion binding
GO:0030247	polysaccharide binding
GO:0001871	pattern binding
GO:0015267	channel activity
GO:0022838	substrate specific channel activity



Supplementary Figure 2. Significant GO enrichment results. (A) The top 5 biological process (green), cellular component (red), and molecular functions (blue). (B) Significant GO terms and the corresponding enriched genes. Color bar from -3 to 3 represents \log_2 FC value.



Supplementary Figure 3. GSEA enrichment pathways. (A) Dotplot of significant pathways. (B) Joyplot of significant pathways. (C) Up-regulated tyrosine metabolism pathway. (D) Down-regulated base excision repair pathway. Count, the number of genes enriched in a pathway; GeneRatio, the percentage of significantly enriched genes in all genes.