

**Supplementary Figure 3. Heatmap and Volcano Plot of RNA-seq Analysis**

A. Data were obtained by comparing colorectal cancer (CRC) samples with high and low YBX1 expression groups, and genes with significant differential expression (p-value < 0.05) were selected. Each column in the heatmap represents a sample, and each row represents a gene. The color intensity reflects the gene's expression level, with red indicating high expression and blue indicating low expression. This heatmap shows the differences in gene expression patterns associated with high YBX1 expression, providing a foundation for subsequent pathway enrichment analysis.
B. A volcano plot used to reveal the gene expression differences between the YBX1 high-expression and low-expression groups. Each point represents a gene, with the x-axis indicating the log2 fold change in gene expression and the y-axis indicating the statistical significance (-log10 p-value). Red and blue points represent genes that are significantly upregulated and downregulated, respectively, while gray points represent genes with non-significant expression differences. This volcano plot shows the potential impact of high YBX1 expression on different signaling pathways and cellular processes, providing a basis for subsequent functional enrichment analysis.