

**Supplementary Figure 2. Heatmap of RNA-seq Analysis**

A-B. Heatmap of differentially expressed genes identified by RNA-seq analysis. 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 expression level of the gene, with red indicating high expression and blue indicating low expression. This heatmap illustrates the differences in gene expression patterns associated with high YBX1 expression, providing a foundation for subsequent pathway enrichment analysis.