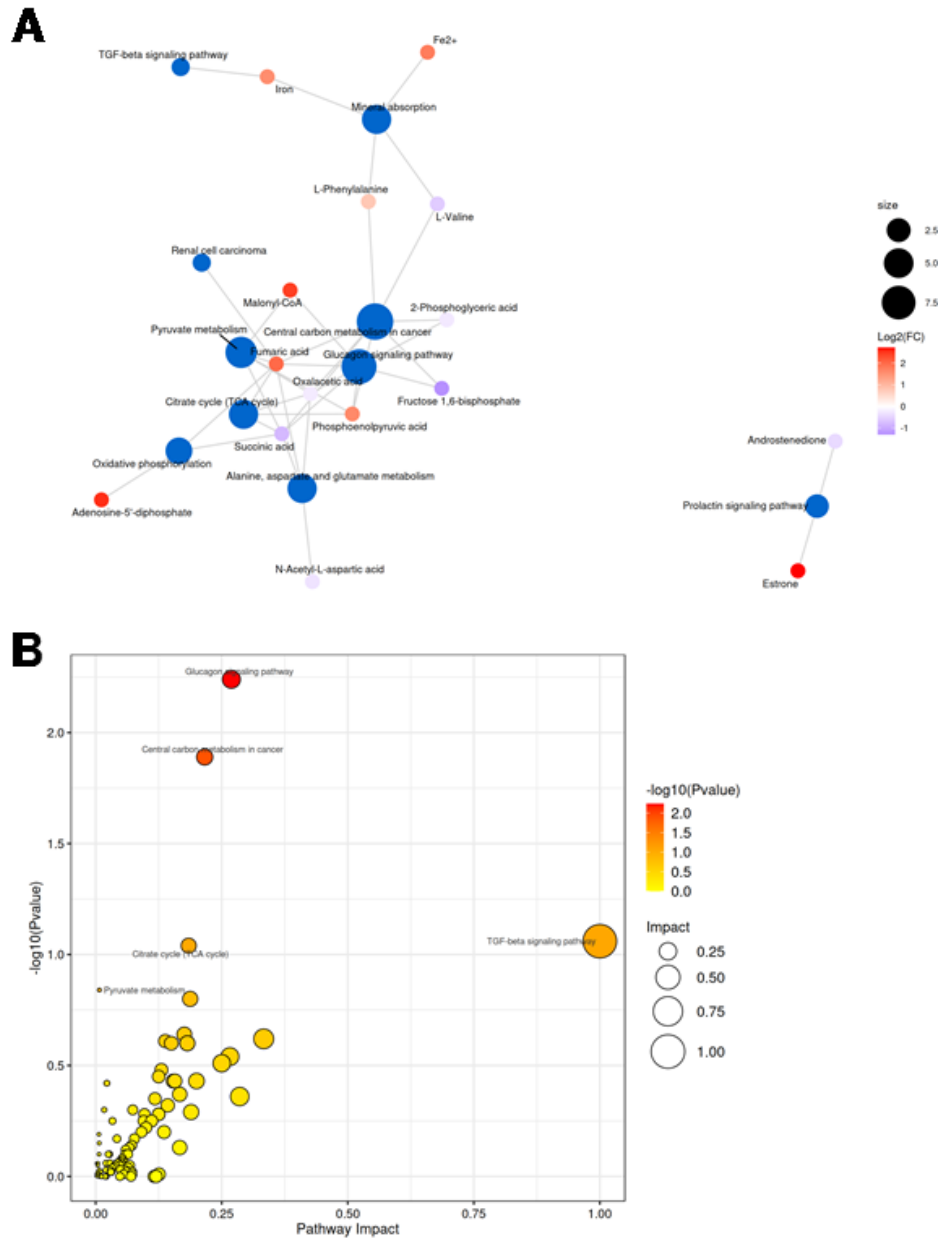
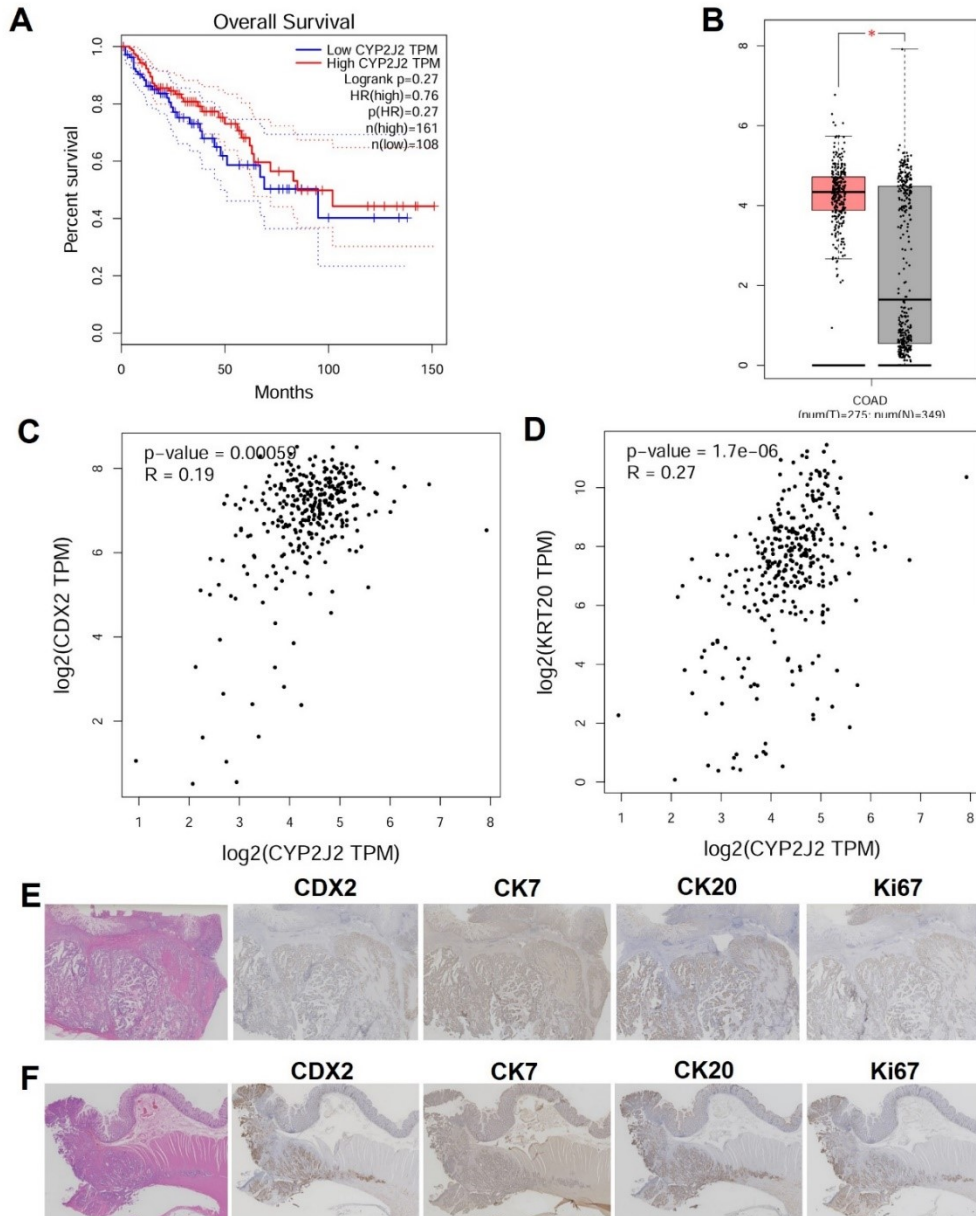


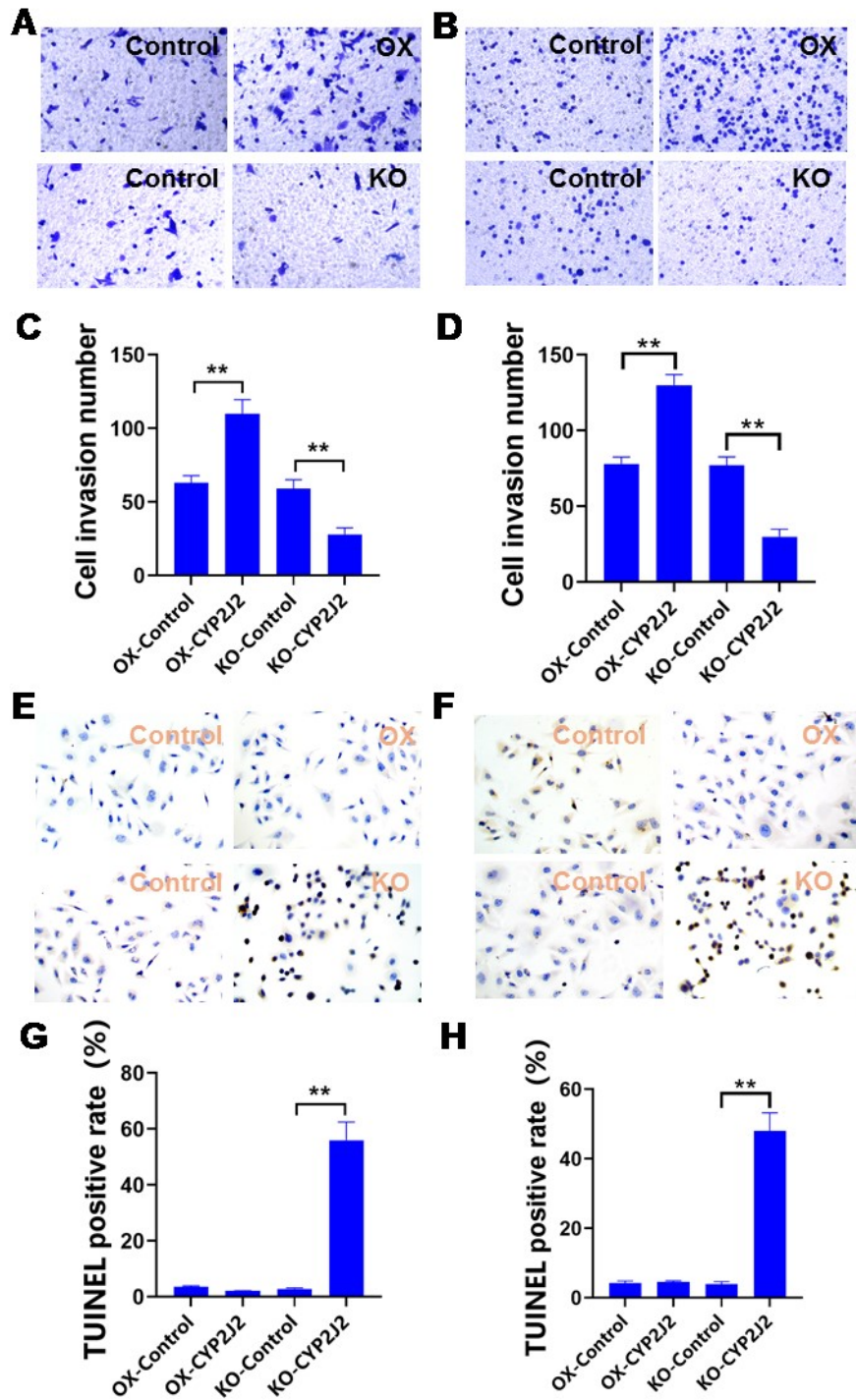
**Supplementary Figure S1.** Differential metabolomics analysis of colorectal cancer and adjacent normal tissues. **A** – Heatmap of differential metabolites levels: Color coding: represents metabolite expression levels in different samples. Red: High expression. Blue: Low expression. White: Moderate expression. Sample grouping: The top color bar indicates sample grouping. Red: colorectal cancer tissues. Blue: adjacent normal tissues. Clustering analysis: The dendrogram on the left shows the similarity among metabolites. **B** – Volcano plot: X-axis ( $\log_2(\text{FC})$ ): logarithmic value of fold change in metabolite expression between colorectal cancer tissues and adjacent tissues. Y-axis ( $-\log_{10}(p\text{-value})$ ): statistical significance; higher values indicate greater significance. Point colors: Red: upregulated metabolites. Blue: downregulated metabolites. Gray: non-significant metabolites (ns). Point size (VIP): represents the importance of metabolites in distinguishing between the two sample groups. Larger points indicate higher VIP values and greater importance



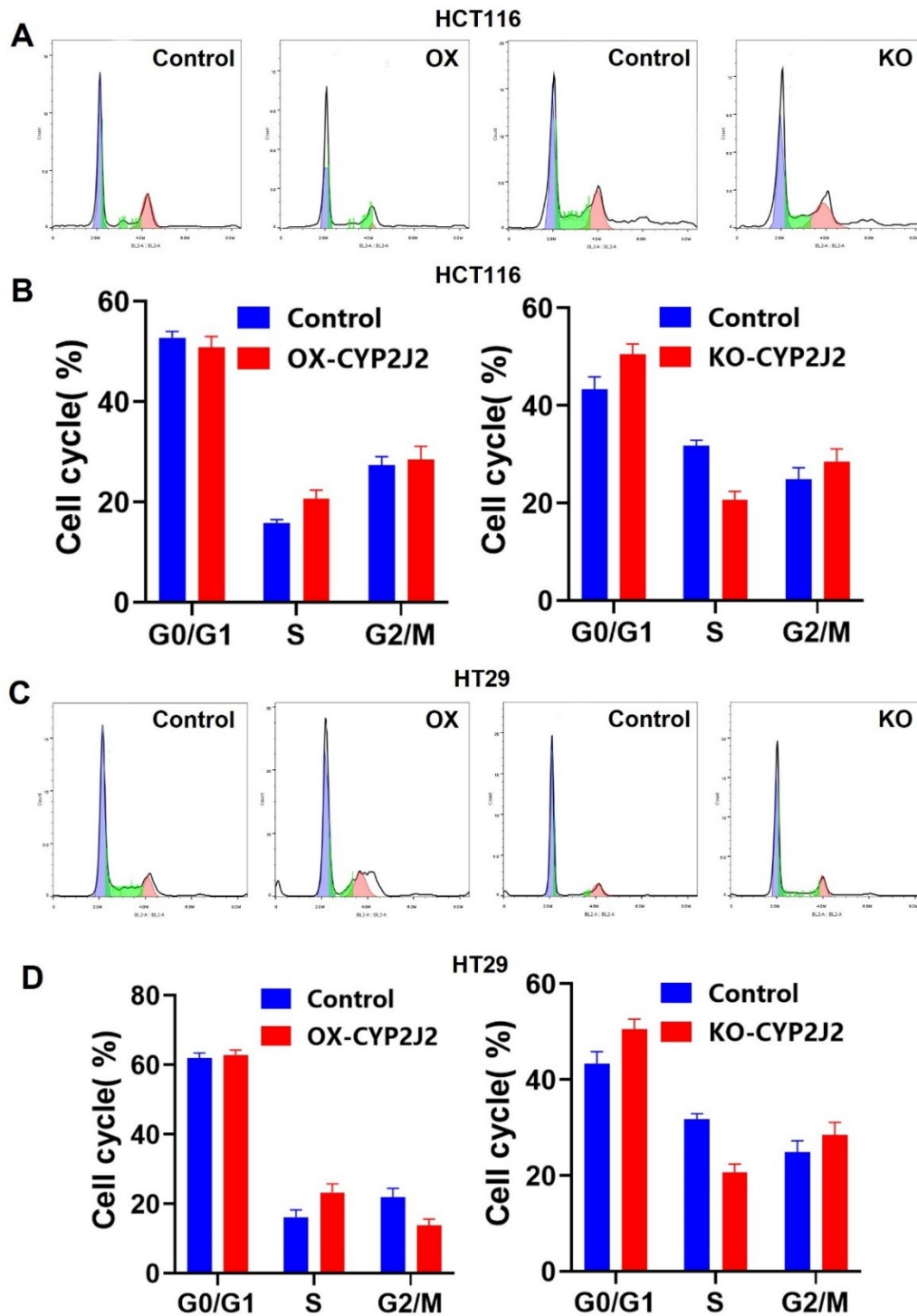
**Supplementary Figure S2.** Biological function analysis of differential metabolites. **A** – Network diagram of enrichment analysis: Nodes: represent different metabolic pathways or biological processes. Node color: colored based on  $\log_2(\text{FC})$  values; red indicates upregulation, blue indicates downregulation. Node size: indicates the number of differential metabolites in the pathway; larger nodes contain more differential metabolites. Edges: represent the relationships among pathways. **B** – Bubble plot of enrichment analysis: X-axis (pathway impact): measure of the proportion of differentially expressed metabolites in the pathway. Y-axis ( $-\log_{10}(p\text{-value})$ ): statistical significance; higher values indicate greater significance. Bubble color: represents  $-\log_{10}(p\text{-value})$ ; darker colors indicate higher significance. Bubble size: indicates the number of differential metabolites in the pathway



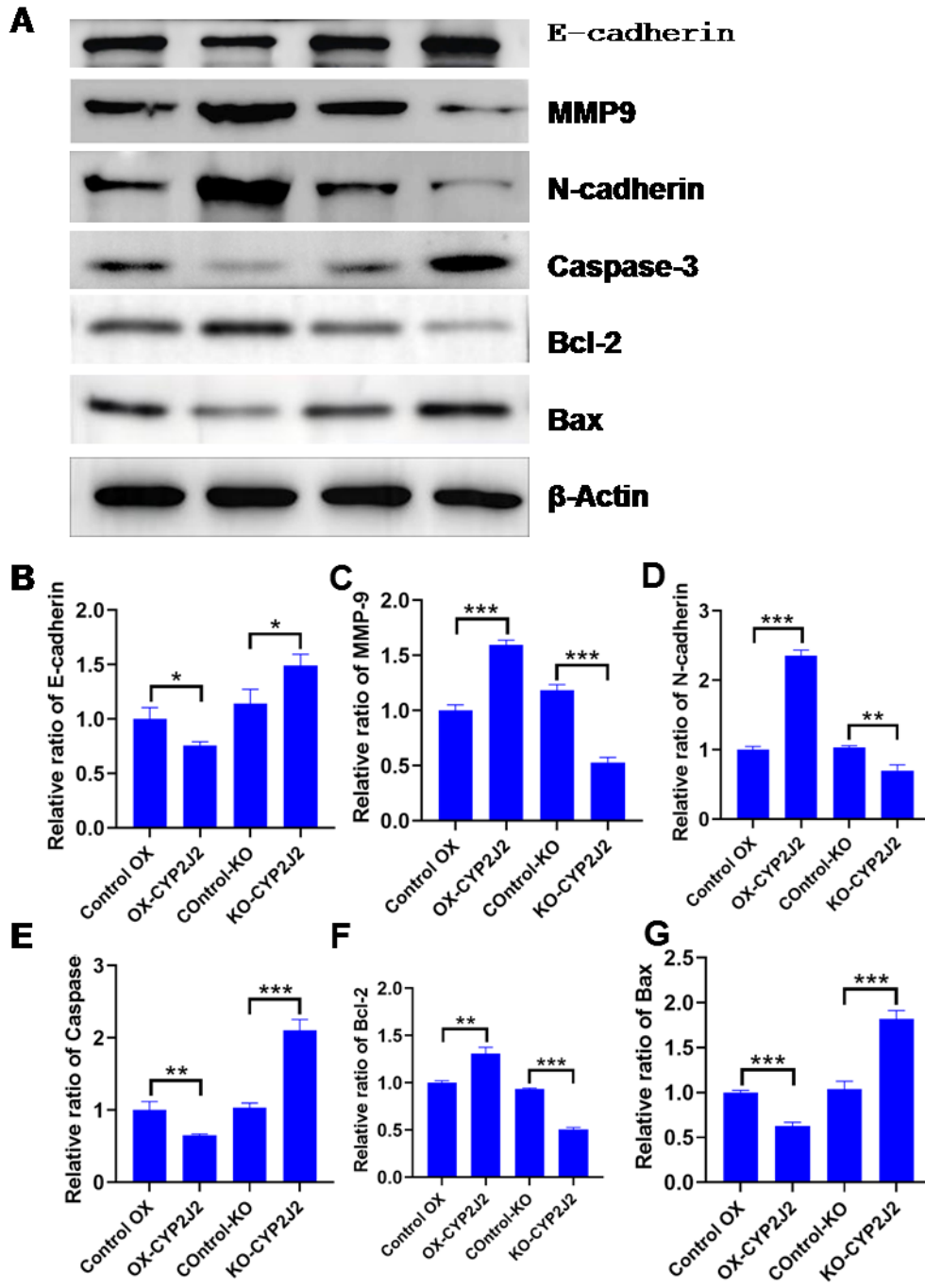
**Supplementary Figure S3.** Relationship between CYP2J2 gene expression and colorectal cancer. **A** – Survival curve: Blue line: represents the survival curve of the low CYP2J2 expression group. Red line: represents the survival curve of the high CYP2J2 expression group. Logrank p-value: statistical significance of the comparison between the two survival curves. HR (high): hazard ratio of the high expression group. p(HR): Statistical significance of the hazard ratio. n(high) and n(low): sample numbers in high and low expression groups. **B** – Box plot: Red box: represents the expression level of the CYP2J2 gene in colorectal cancer tissues. Gray box: represents the expression level of the CYP2J2 gene in adjacent normal tissues. Asterisk (\*): indicates statistical significance of the expression differences between the two groups. **C** – Scatter plots: X-axis ( $\log_2(\text{CYP2J2 TPM})$ ): represents CYP2J2 gene expression levels. Y-axis (Figure C:  $\log_2(\text{CDX2 TPM})$ ): represents marker genes CDX2 and CK20 expression levels, respectively. p-value: Significance of the correlation between the two gene expression levels. R: Correlation coefficient between the expression levels of the two genes. **D, E** – Pathological analysis: Markers: levels of CDX2, CK7, CK20, and Ki67 compared between high and low CYP2J2 expression groups



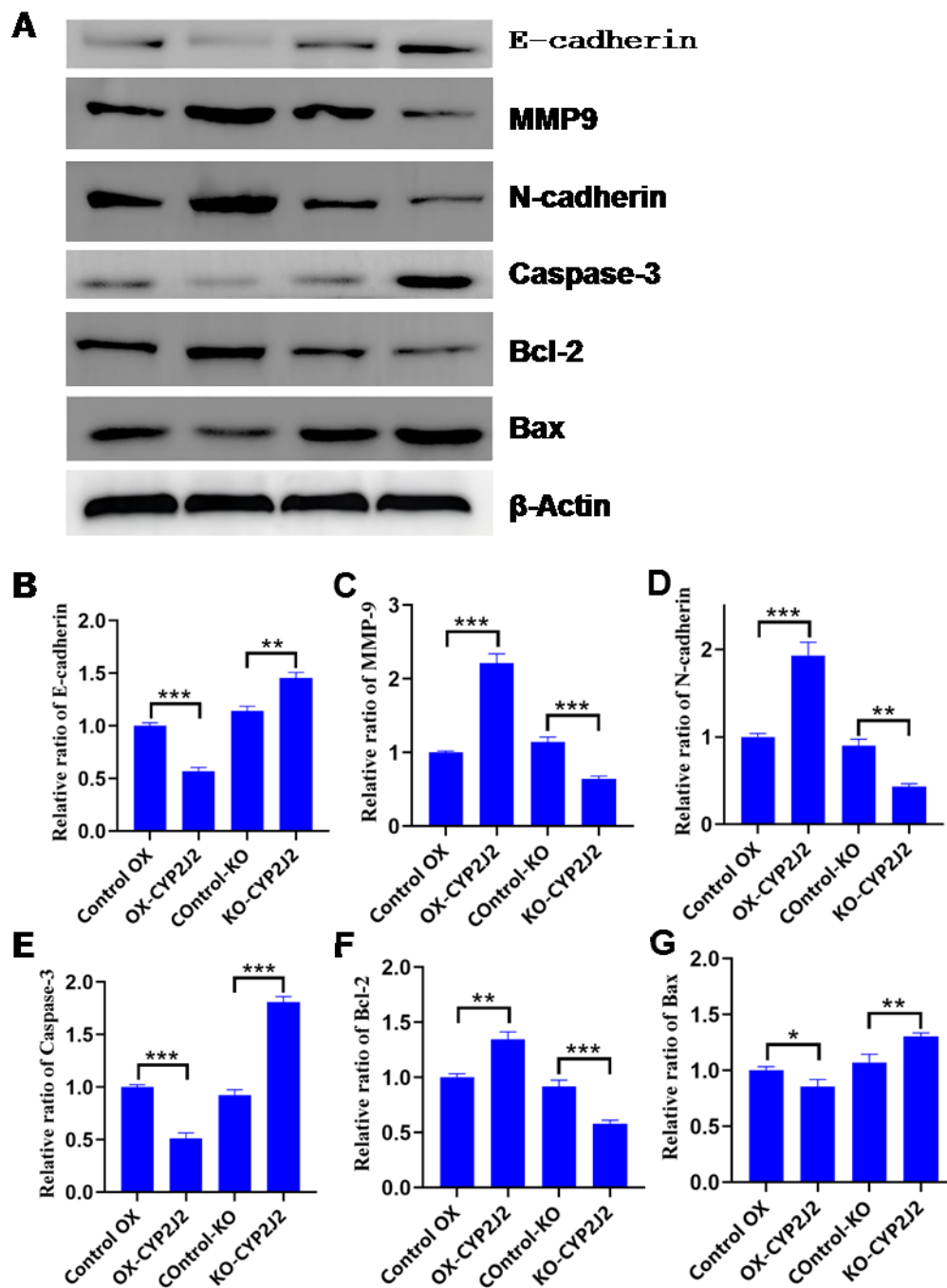
**Supplementary Figure S4.** CYP2J2 promotes colorectal cancer cell growth. **A–D** – Cell invasion assays: Groups: control, OX (overexpression of CYP2J2), KO (knockdown of CYP2J2). Bar charts (**E, F**): display the number of invasive cells in different treatment groups. \*\*Indicates highly statistically significant differences compared to the control group. **E–H** – TUNEL apoptosis assays: Groups: control, OX-CYP2J2 (overexpression of CYP2J2), KO-CYP2J2 (knockdown of CYP2J2)



**Supplementary Figure S5.** CYP2J2 promotes colorectal cancer cell cycle progression. **A** – HCT116 cell cycle analysis: Distributions: cell cycle phase distributions for control, OX (overexpression of CYP2J2), and KO (knockdown of CYP2J2) groups. **B** – HCT116 cell cycle percentage: Bar chart. **C** – HT29 cell cycle analysis. **D** – HT29 cell cycle percentage bar chart. Colors: blue bars for control group percentages, red bars for CYP2J2-modulated groups. Cell cycle stages: G0/G1 (resting phase), S (DNA synthesis phase), G2/M (cell division phase)



Supplementary Figure S6. CYP2J2 promotes key gene expression for cell proliferation in HCT116 cells



Supplementary Figure S7. CYP2J2 promotes key gene expression for cell proliferation in HT29 cells