

Figure S1: Flow chart of this research.

First, we applied Spearman correlation analysis and identified 6,268 ERGs (E3-related genes) in colon cancer samples based on 240 E3s (E3 ubiquitin ligases) from the TCGA and GTEx datasets. Then, WGCNA and Limma analysis were used to identify meaningful ERGs between tumor and normal tissues respectively and 409 intersecting genes were identified. Based on the overlapping ERGs evaluated, we identified distinct prognostic subtypes using consensus clustering and revealed that the best number of clusters was two; these clusters were denominated A and B. We performed survival analysis, immune cell abundance,

immune function and GSVA to clarify the differences between the two clusters. To further study the potential mechanisms of these two tumor clusters, we identified 800 DEGs (differentially expressed genes) between clusters A and B via Limma analysis. Moreover, univariate Cox regression analysis and integrated machine learning algorithms were used to construct the prognostic model. We also evaluated the E3-related risk model in terms of survival analysis, drug sensitivity and other factors. The correlation between the immune response and the prognostic model was also assessed.

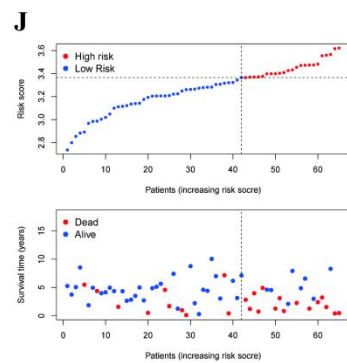
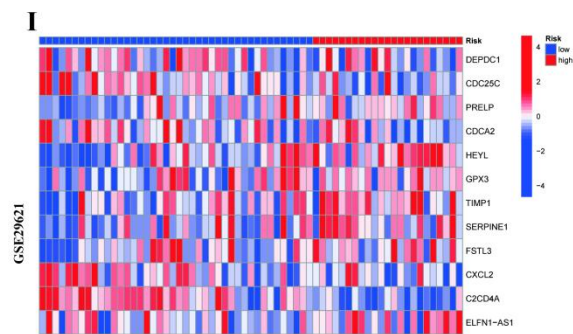
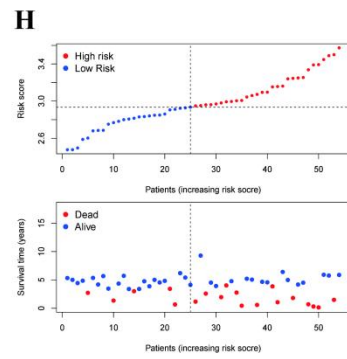
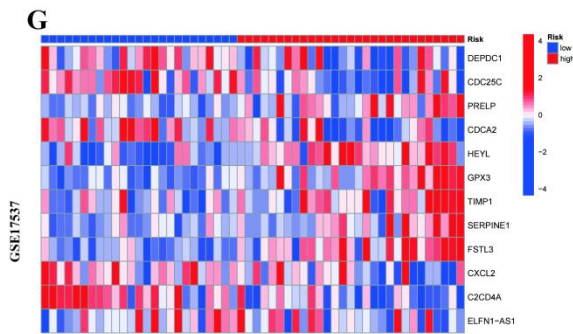
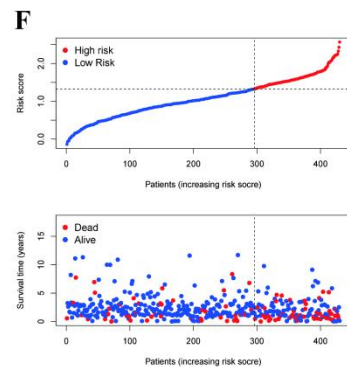
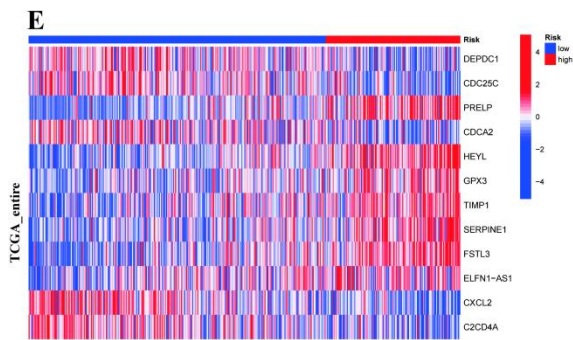
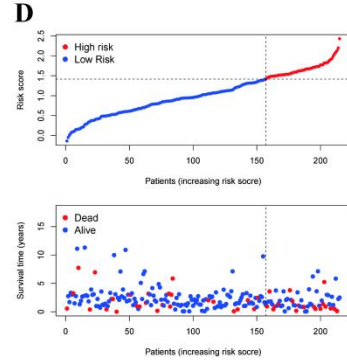
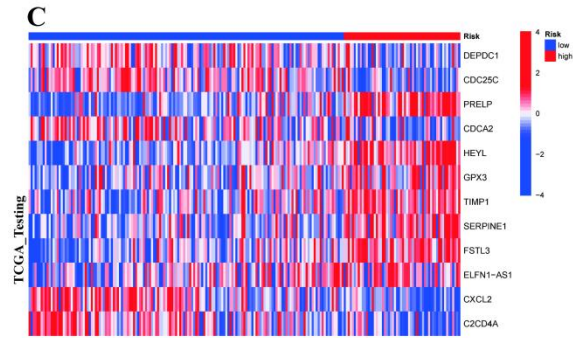
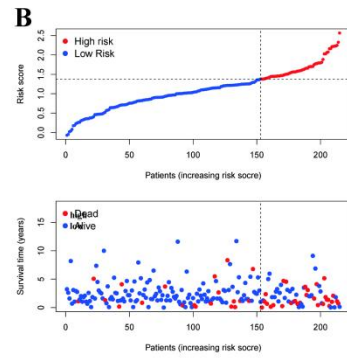
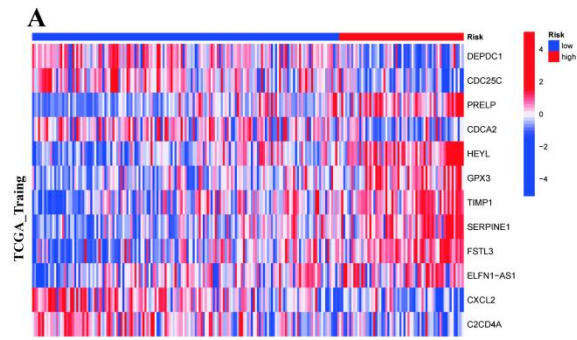


Figure S2: Further validation of the OS-associated prognostic risk model for colon cancer. (A, B) The distributions of the prognostic model, survival status, and expression profile of risk genes in the training dataset. The distributions of the prognostic model, survival status, and expression profile of risk genes in the TCGA Testing dataset (C,D), TCGA entire dataset (E,F), GSE17537 (G,H) and GSE29621 (I,J).