**G:\01、各刊资料\FBL\1. 稿件内容\2. 已接受待发表文章\4. 已排PDF\FBL20331\FBL20331-PDF\FBL20331-production-2\Supplementary material\FBL20331-new Supplementary Material\Supplementary Figure1.tif**

**Supplementary Figure 1. Enrichment analysis and somatic mutation features.** (A) The bar chart represents the top 20 enrichment pathways. (B) Network interaction diagram of the top 20 signaling pathways. (C) Somatic mutation classification of CFRGs. (D) Types of CFRG variants. (E) SNV class of CFRGs. (D, E) TMB level of CRC samples. (F and G) The number and classification of mutations per sample. (H) Top 15 mutated genes in CRC samples.

G:\01、各刊资料\FBL\1. 稿件内容\2. 已接受待发表文章\4. 已排PDF\FBL20331\FBL20331-PDF\FBL20331-production-2\Supplementary material\FBL20331-new Supplementary Material\Supplementary Figure2.tif

**Supplementary Figure 2. Analysis of clinical correlations in the CFRG-based risk panel.** (A) Heatmap showing correlations between the risk score and clinical features. \*p<0.05, \*\*p<0.01, \*\*\*P < 0.001. Variations in survival between high- and low-risk patients depicted by the KM curve based on age (B), gender (C and D), M state (E), N state (F and G), T state (H), and stage (I and J).

G:\01、各刊资料\FBL\1. 稿件内容\2. 已接受待发表文章\4. 已排PDF\FBL20331\FBL20331-PDF\FBL20331-production-2\Supplementary material\FBL20331-new Supplementary Material\Supplementary Figure3.tif

**Supplementary Figure 3. Comparative analysis of the functional characteristics between different risk groups.** (A) The five signaling pathways with significant enrichment in high-risk patients, as determined by GSVA. (B) The five signaling pathways with significant enrichment in low-risk patients, as determined by GSVA. (C) A waterfall diagram illustrating gene mutations in the low-risk group. (D) Waterfall chart showing gene mutations in the high-risk patients. (E) The KM survival curve illustrates the grouping of patients based on the combination of the risk score and the TMB. (F) Scatter plots showing risk scores and dryness indices.

G:\01、各刊资料\FBL\1. 稿件内容\2. 已接受待发表文章\4. 已排PDF\FBL20331\FBL20331-PDF\FBL20331-production-2\Supplementary material\FBL20331-new Supplementary Material\Supplementary Figure4.tif

**Supplementary Figure 4 Analysis of the survival and expression of 7 hub CFSRGs.** KM survival analysis and paired violin plots displayed the survival prognosis and differential expression of 7 hub CFSRGs with CRC patients. (A) *CCNF*; (B) *CXCL11*; (C) *EPHB2*; (D) *EREG*; (E) *MMP3*; (F) *STC2*; (G) *TIMP1*. (H) ROC analysis of STC2. (I) ROC analysis of TIMP1. (J) 7 CFSRGs were detected in normal intestinal epithelial cells and LOVO cells using qRT-PCR. Asterisks (\*) denotes significant differences, \**p*<0.05, \*\**p*<0.01, \*\*\**P* < 0.001.