

Figure S1 Screening of PCD genes. (A) Venn plots of differentially expressed PCD genes in cancerous and paraneoplastic tissues in the TCGA-CRC cohort; (B) PCD genes with high prognostic impact in CRC patients assessed by random forest algorithm. DEGs, differentially expressed genes; LCD, lysosome-dependent cell death; PCD, programmed cell death; TCGA, The Cancer Genome Atlas; CRC, colorectal cancer.

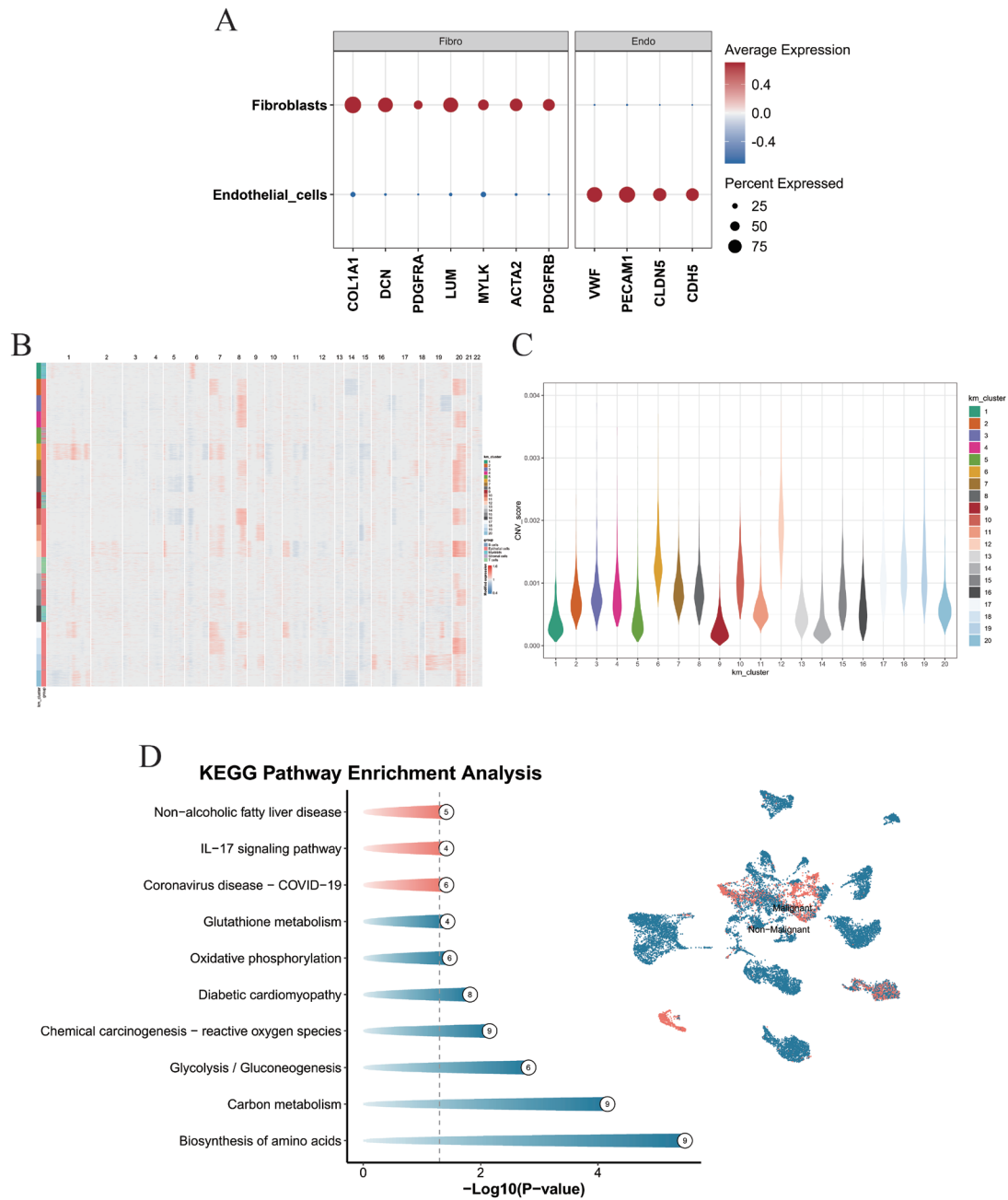


Figure S2 Identification of malignant epithelial cells. (A) Fibroblasts classic marker demonstrates the accuracy of our annotations; (B) distinguishing malignant cells from total epithelial cells by extrapolating large-scale CNV using immune cells as a reference; (C) CNV-score for each epithelial cell subpopulation; (D) KEGG enrichment analysis of differentially expressed genes in malignant and non-malignant epithelia. Fibro, fibroblasts; Endo, endothelial cells; CNV, copy number variation; KEGG, Kyoto Encyclopedia of Genes and Genomes; IL-17, interleukin-17; COVID-19, coronavirus disease 2019.

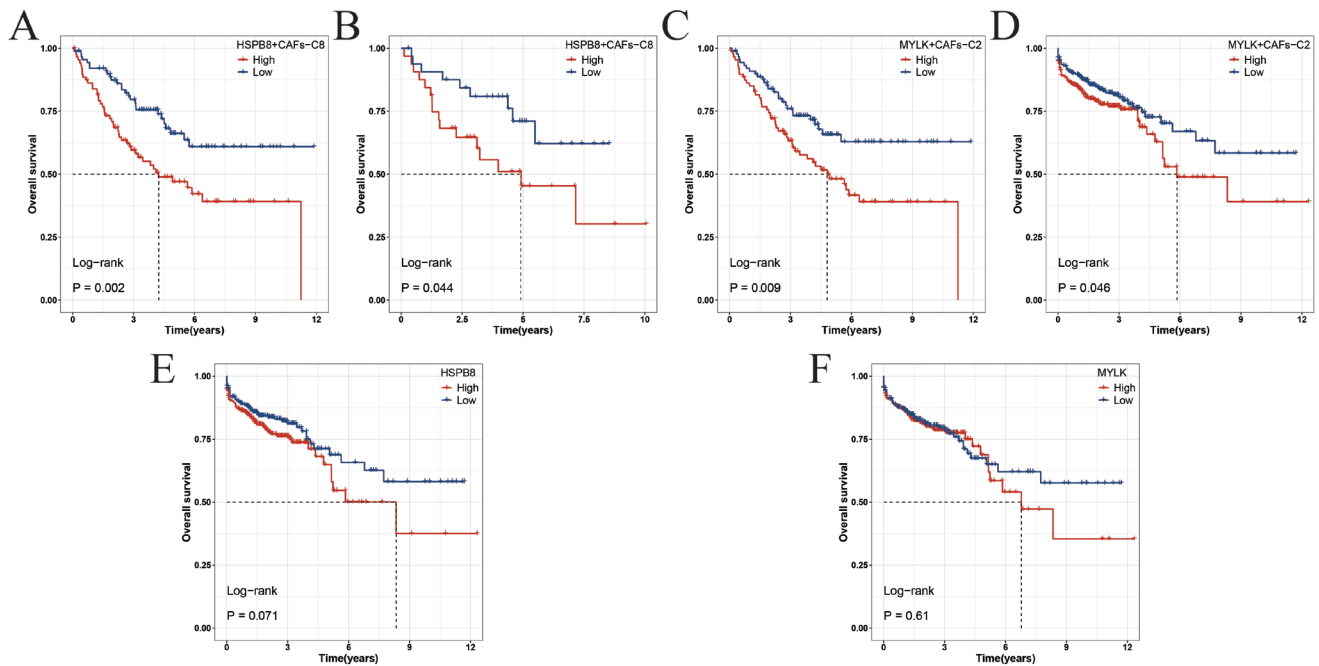


Figure S3 Exploring key factors affecting the prognosis of CRC patients. (A,B) Overall survival curves of CRC patients with high and low HSPB8⁺ CAFs subpopulation MYLK scoring groups in GSE17536 (A), GSE29621 (B); (C,D) overall survival curves of CRC patients with high and low MYLK⁺ CAFs subpopulation GSVA scoring groups in GSE17536 (C), TCGA-CRC (D); (E) survival curves between patients with high and low HSPB8 expression in the TCGA-CRC cohort; (F) survival curves between patients with high and low MYLK expression in the TCGA-CRC cohort. CAFs, cancer-associated fibroblasts; CRC, colorectal cancer; GSVA, gene set variation analysis; TCGA, The Cancer Genome Atlas.