

Figure S1 GO and KEGG enrichment analysis based on differentially expressed genes between low LDCD activity cells and high LDCD activity cells in different cell types. (A) GO and KEGG enrichment analysis in high LDCD activity tumor cells. (B) GO and KEGG enrichment analysis in high LDCD activity neutrophil cells. (C) GO and KEGG enrichment analysis in high LDCD activity fibroblast cells. (D) GO and KEGG enrichment analysis in high LDCD activity T cells. (E) GO and KEGG enrichment analysis in high LDCD activity endothelial cells. (F) GO and KEGG enrichment analysis in high LDCD activity mast cells. (G) GO and KEGG enrichment analysis in high LDCD activity B cells. (H) GO and KEGG enrichment analysis in high LDCD activity epithelial cells.

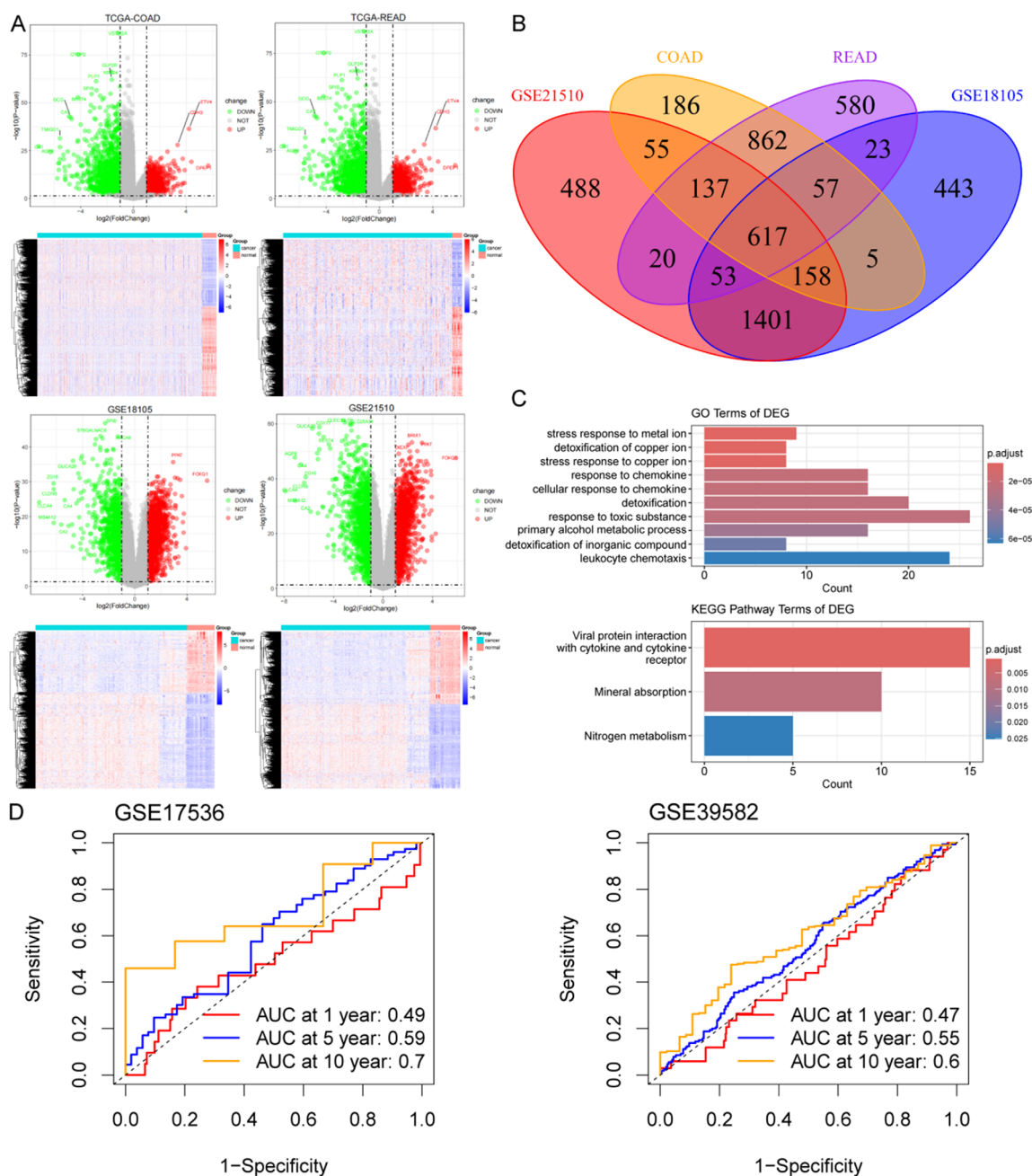


Figure S2 Differential expression analysis, functional enrichment analysis and ROC analysis based on the bulk dataset. (A) Volcano plot and heatmap of DEGs between cancer and normal samples in TCGA-COAD, TCGA-READ, GSE18105 and GSE21510. (B) Venn diagram displays the 617 key CRC-related genes on overlapping DEGs from TCGA-COAD, TCGA-READ, GSE18105 and GSE21510. (C) GO and KEGG enrichment analysis based on 617 key CRC-related genes. (D) ROC curves in the GSE17536 and GSE39582.