



Figure S1 The standard PRISMA flow diagram of the screened samples in this study. We obtained 514 and 585 samples from TCGA-COAD dataset and GSE39582 dataset, respectively. Then, incomplete clinical information, non-primary solid tumors, follow-up days <30, and normal tissue sequencing data were sequentially removed. Finally, 417 samples in TCGA-COAD dataset and 556 samples in GSE39582 were selected for subsequent studies. TCGA, The Cancer Genome Atlas; COAD, colon adenocarcinoma; n, numbers.