Supplementary

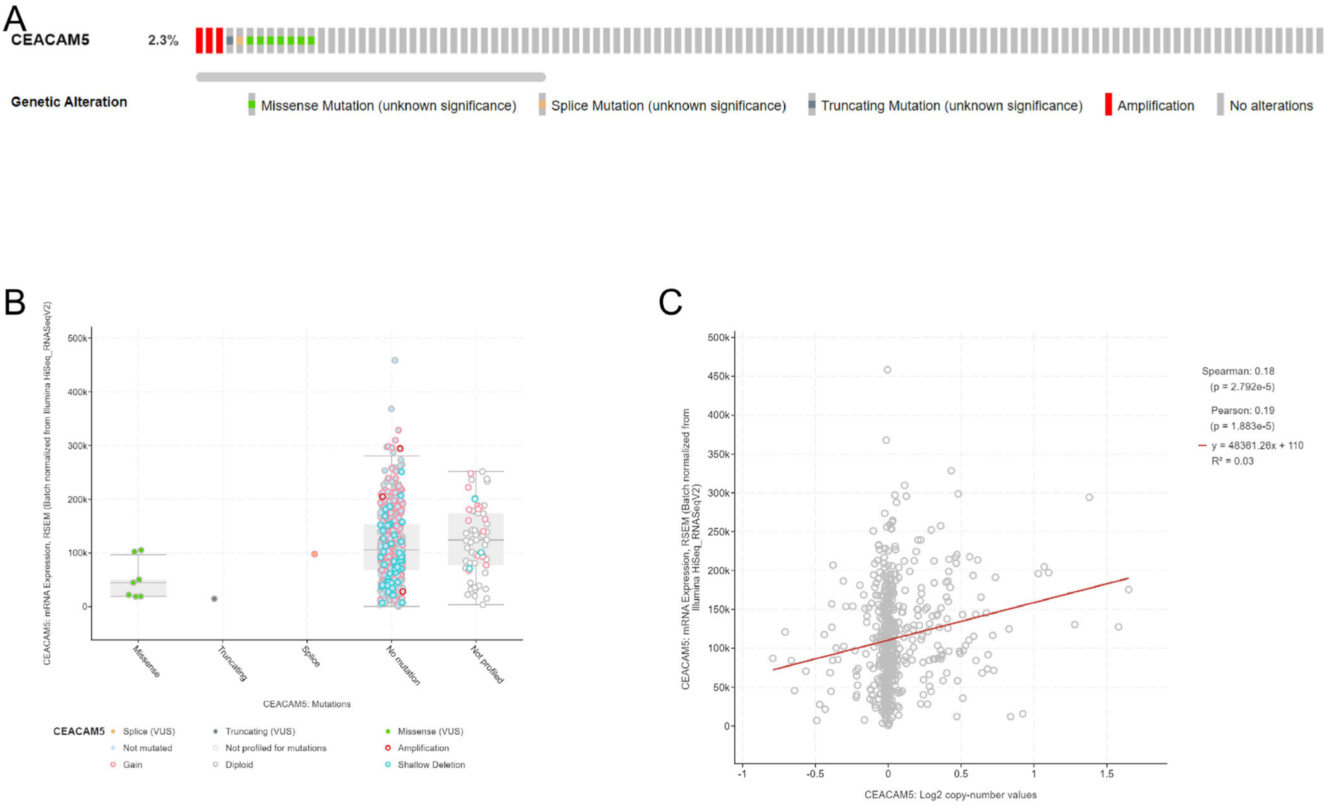

Figure S1 The genetic mutations and copy numbers of CEACAM5 in the TCGA-COAD dataset. (A) CEACAM5 genomic alteration of TCGA-COAD in the cBioPortal database. (B) Relationship between CEACAM5 genomic alteration and mRNA expression. (C) Relationship between CEACAM5 copy number and mRNA expression. RSEM, RNA-Seq by Expectation-Maximization; VUS, variant of uncertain significance; TCGA-COAD, The Cancer Genome Atlas colorectal adenocarcinoma; mRNA, messenger RNA.

https://dx.doi.org/10.21037/jgo-24-43

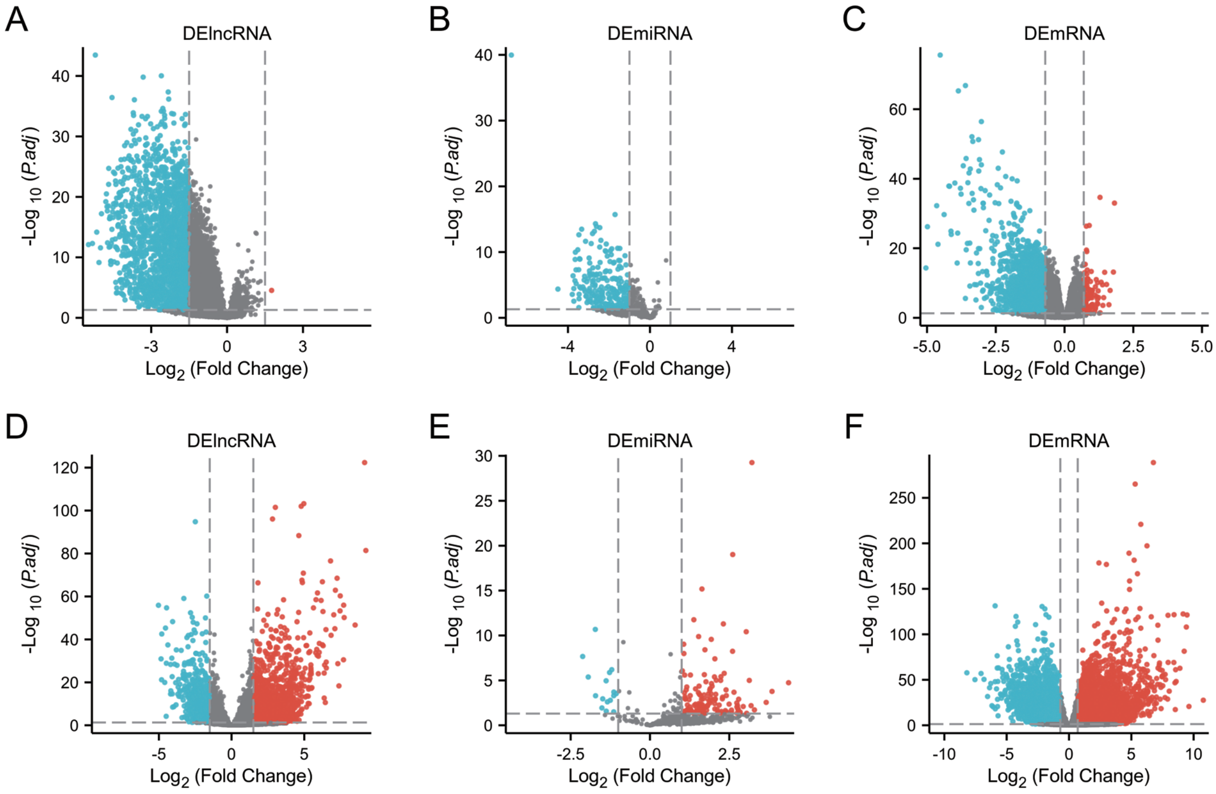

Figure S2 Volcano plots of differential analysis. (A-C) Volcano plots of differential genes between the high- and low-expression groups of CEACAM5. (D-F) Volcano plots of differential genes between colon cancer and paracancerous tissues (red represents upregulated genes, blue represents downregulated genes, and grey represents non-significant genes). P.adj, adjusted P value; DE, differentially expressed; lncRNA, long non-coding RNAs; miRNA, microRNA; mRNA, messenger RNA.

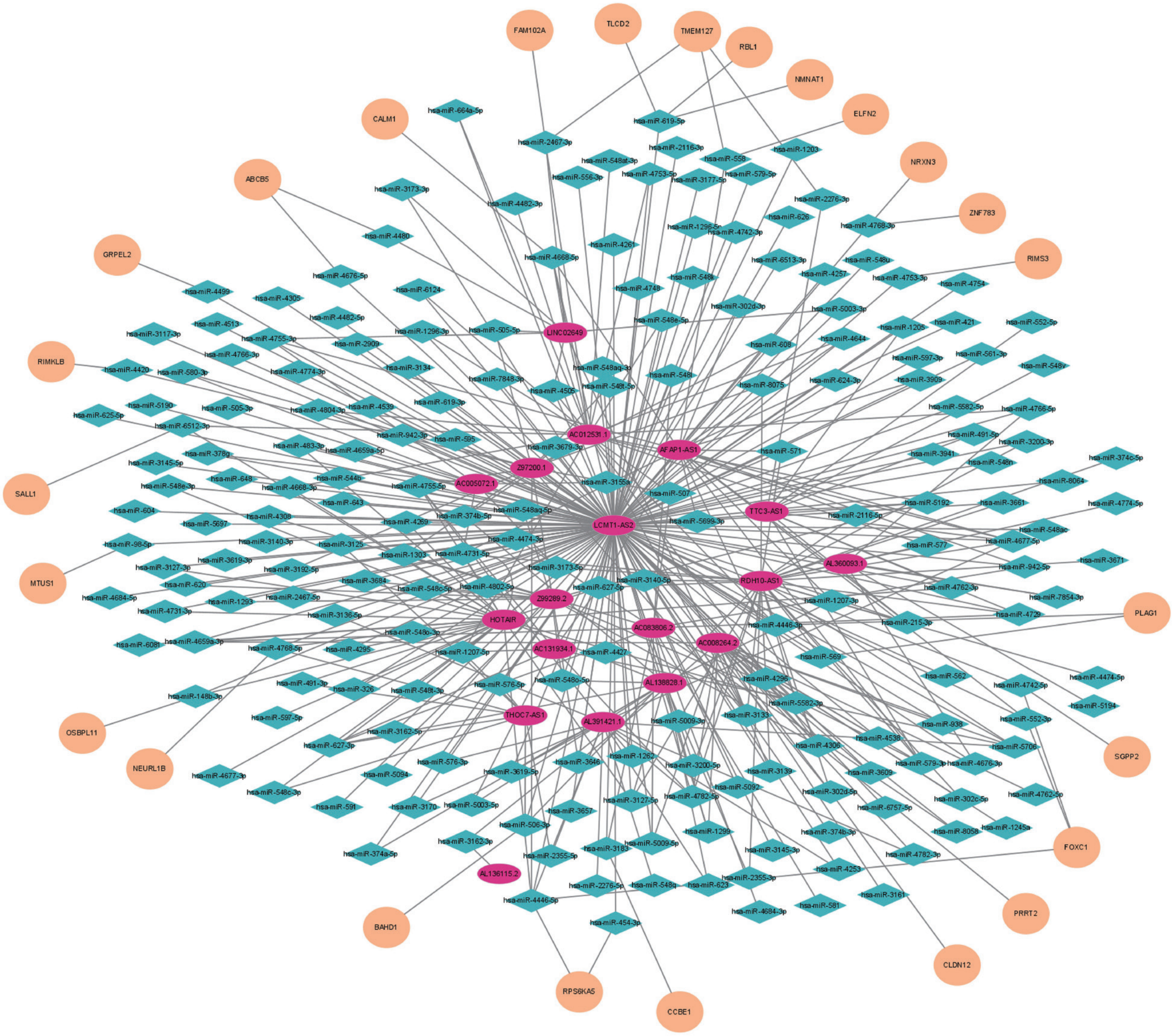

Figure S3 ceRNA networks diagram of 18 lncRNA-177 miRNAs-25 mRNAs. ceRNA, competitive endogenous RNA; lncRNA, long non-coding RNA; miRNA, microRNA; mRNA, messenger RNA.

https://dx.doi.org/10.21037/jgo-24-43

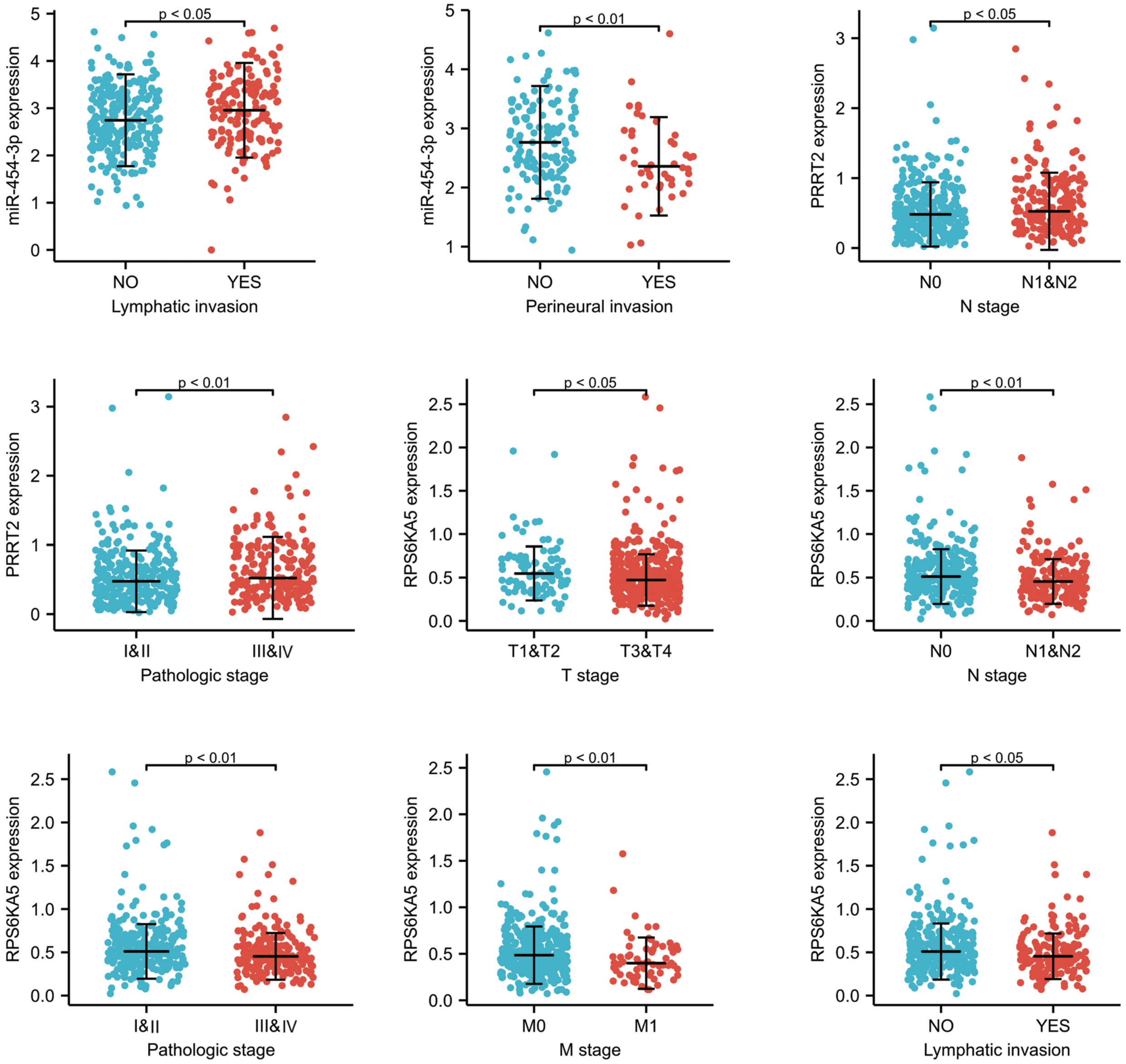

Figure S4 Correlation analysis between gene expression levels and clinical pathological factors.

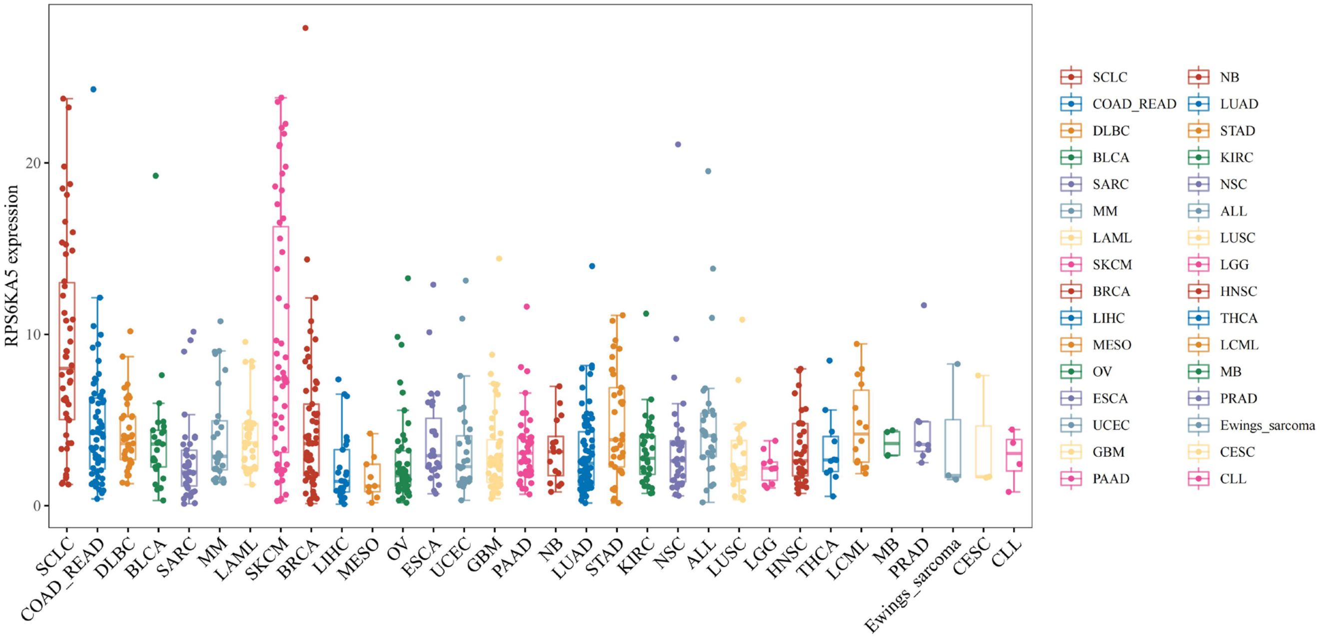

Figure S5 The *RPS6KA5* expression level of different cancer cell lines in the CCLE database (the x-axis represents different sample groups; the y-axis represents the distribution of gene expression). *RPS6KA5*, ribosomal protein S6 kinase A5; CCLE, Cancer Cell Line Encyclopedia.

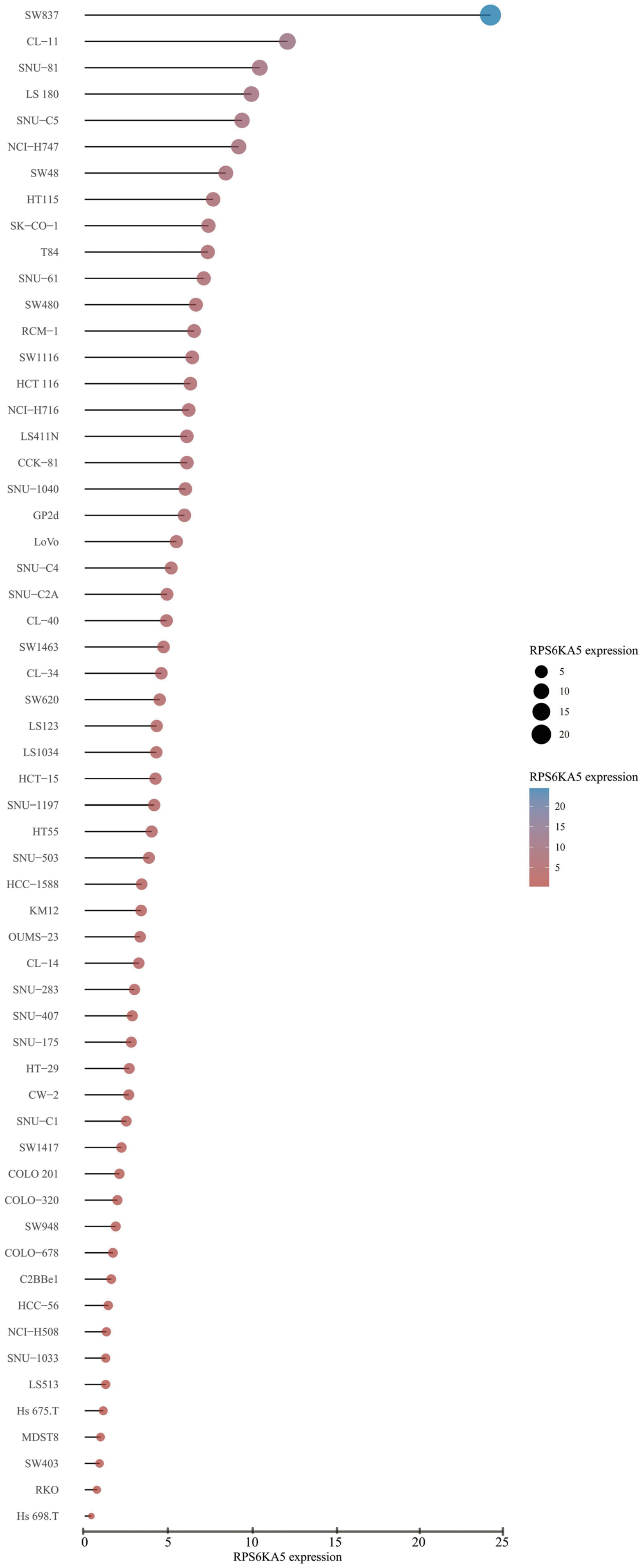

Figure S6 The distribution of *RPS6KA5* expression in different colorectal cancer cell lines in the CCLE database (the x-axis represents the status of gene expression, the y-axis represents different cell lines, the size of the dots in the figure indicates the level of expression, and different colors also signify the level of expression). *RPS6KA5*, ribosomal protein S6 kinase A5; CCLE, Cancer Cell Line Encyclopedia.