

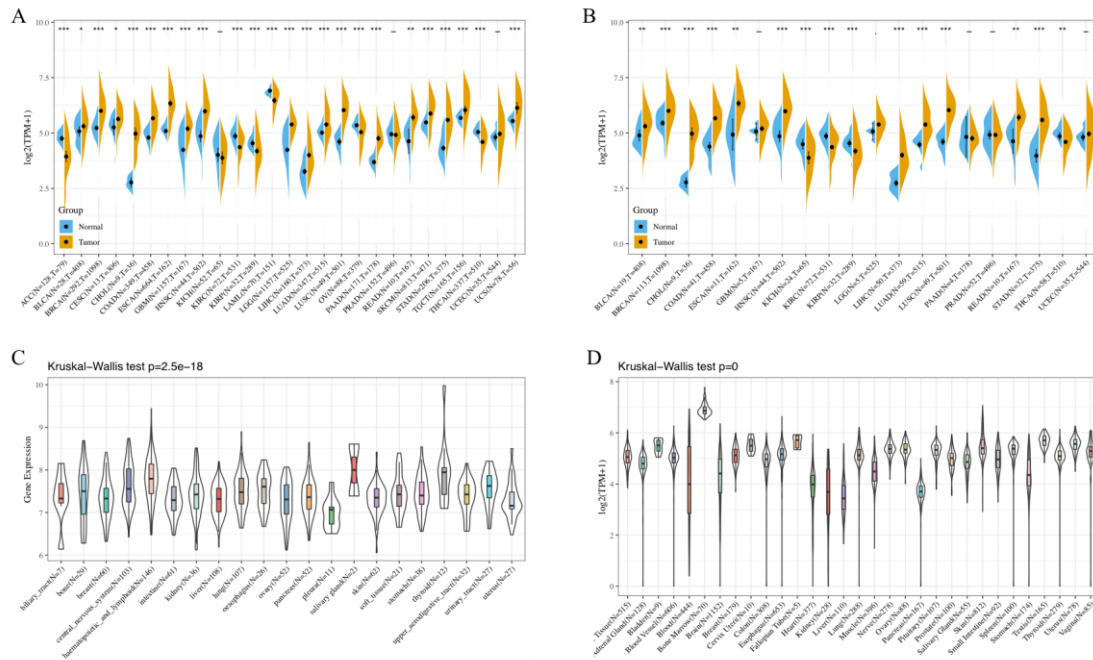


Figure S1 PRKDC mRNA levels in different normal and tumor tissues. (A) PRKDC mRNA expression in normal tissues and in tumor samples from TCGA and GTEx databases. (B) PRKDC mRNA levels in normal tissues from TCGA database. (C) PRKDC mRNA levels in tumor cell lines from CCLE database. (D) PRKDC mRNA levels in normal tissues and in tumor samples from the GTEx database.

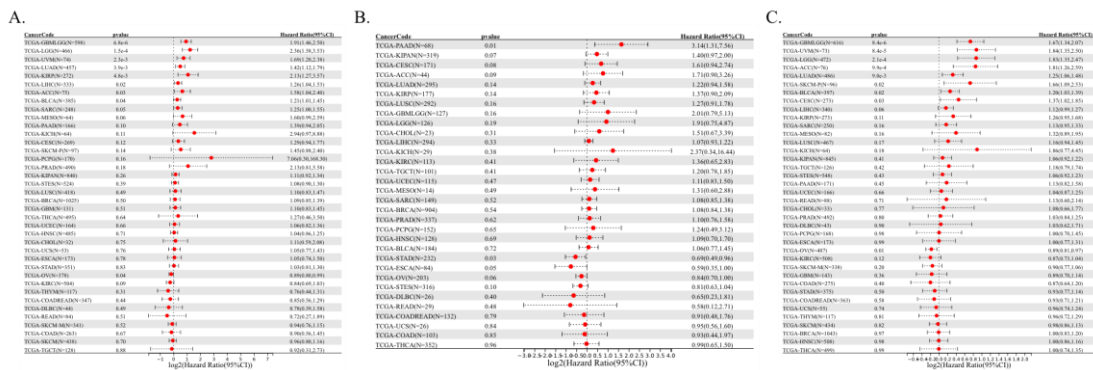


Figure S2. Survival analysis comparing the effect of high and low expression of PRKDC on overall survival in different cancers from TCGA, TARGET, and GTEx datasets. (C-E) Forest map showing the results of univariate Cox regression analysis of the role of PRKDC in DFI, DSS, and PFI in pan-cancer samples. Overall survival (OS) analysis stratified by SETD2 mutation status in the whole TCGA cohort. j Disease-free survival (DFS) analysis stratified by SETD2 mutation status in TCGA. k Disease-free survival (DFS) analysis stratified by SETD2 mutation status in TCGA.

the total incidence of deletions or insertions in repeating sequences per million base pair. $p < 0.05$ was considered significant. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$ and **** $p < 0.0001$.