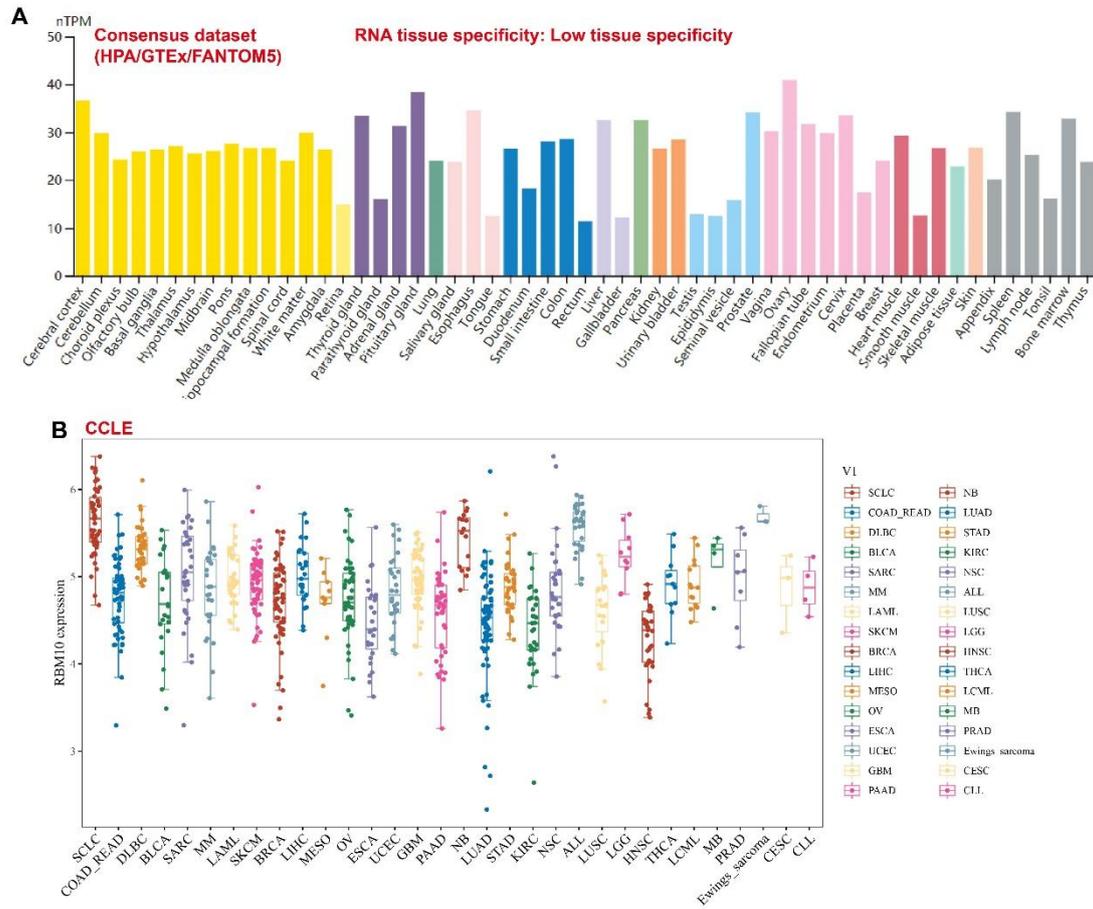
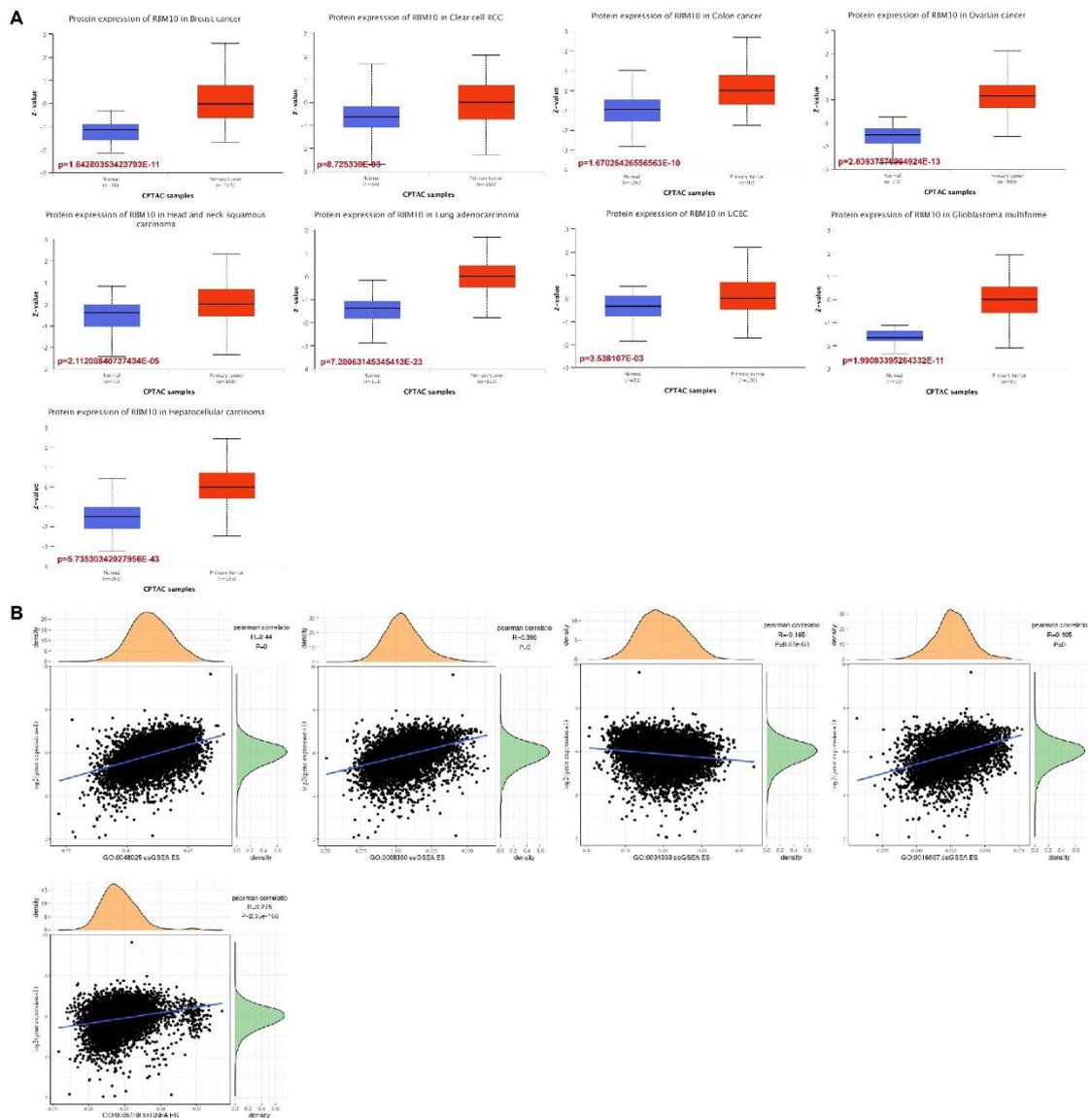


## Figures S1~S13



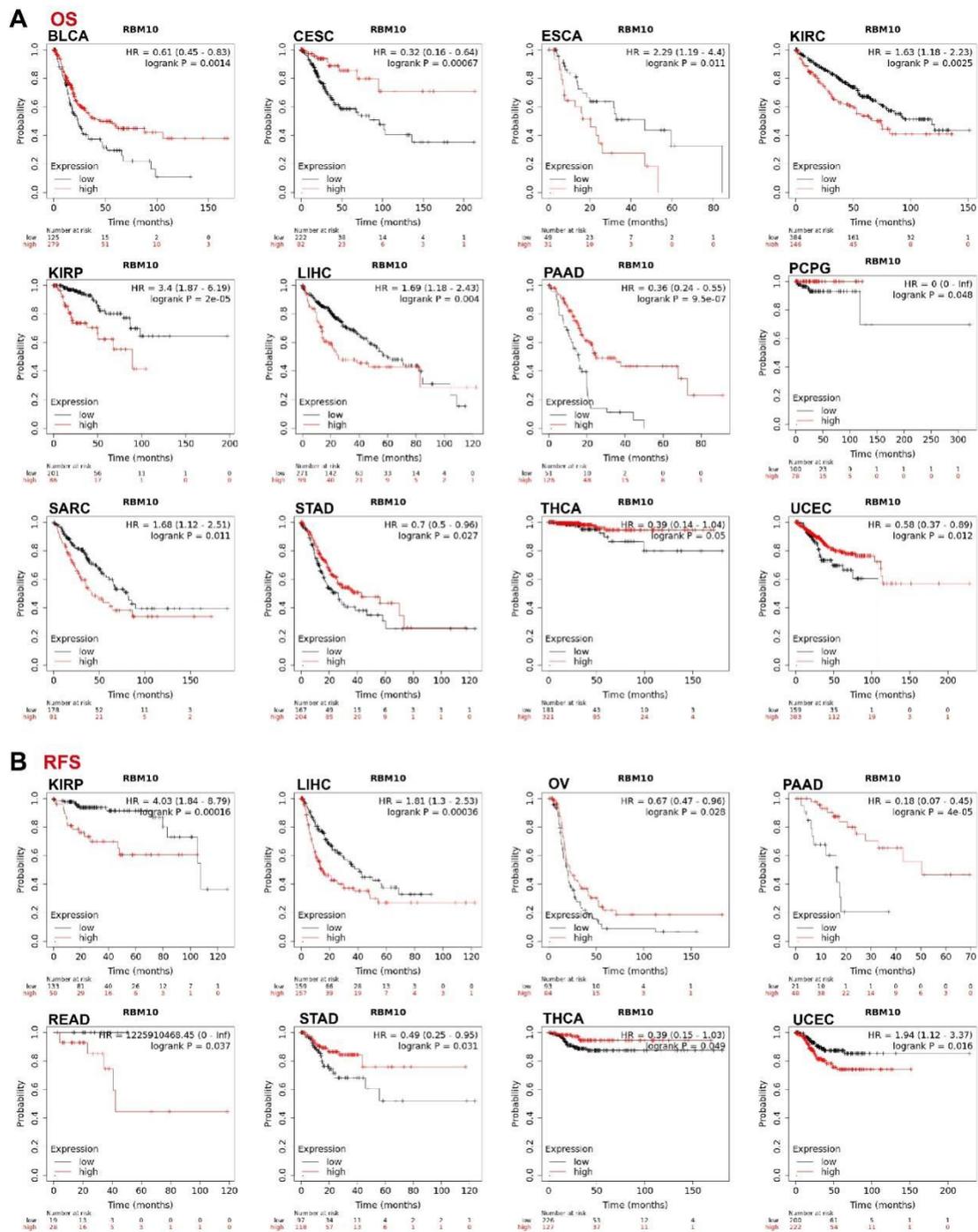
**Figure S1 RBM10 mRNA expression in human normal tissues and different cancer cells (A)** RBM10 mRNA expression in various normal tissues was analyzed using HPA/GTEX/FANTOM5 database. **(B)** The mRNA expression level of RBM10 in various cancer cells was analyzed from the data of CCL database.



**Figure S2 The protein expression of RBM10 in pan-cancer and a single-gene GO analysis of RBM10 (A) RBM10 protein level in different tumors and normal adjacent tissues through CPTAC database. (B) SangerBox showed the positively association between RBM10 expression and each analysis result.**



**Figure S3 The correlation between RBM10 and different molecular subtypes in pan-cancer** (A) The expression of RBM10 was significantly associated with molecular subtypes in BRCA, HNSC, KIRP, LGG, READ, OV, LUSC and PRAD. (B) RBM10 expression was no associated with molecular subtypes in ACC, COAD, ESCA, GBM, LIHC, PCPG and SKCM. (C) The expression level of RBM10 was no associated with tumor stages in BLCA, BRCA, CESC, CHOL, COAD, DLBC, ESCA, HNSC, KIRC, KIRP, LUAD, LUSC, READ, STAD, TGCT, THCA and UCEC.



**Figure S4 The prognosis analysis of RBM10 in tumors. (A~B)** The correlation analysis of RBM10 expression with overall survival (OS, **A**) and relapse free survival (RFS, **B**) in patients with different cancer types from TCGA database of Kaplan-Meier plotter. The median RBM10 expression was used to classify patients into high expression and low expression groups.  $p < 0.05$  was statistically significant.

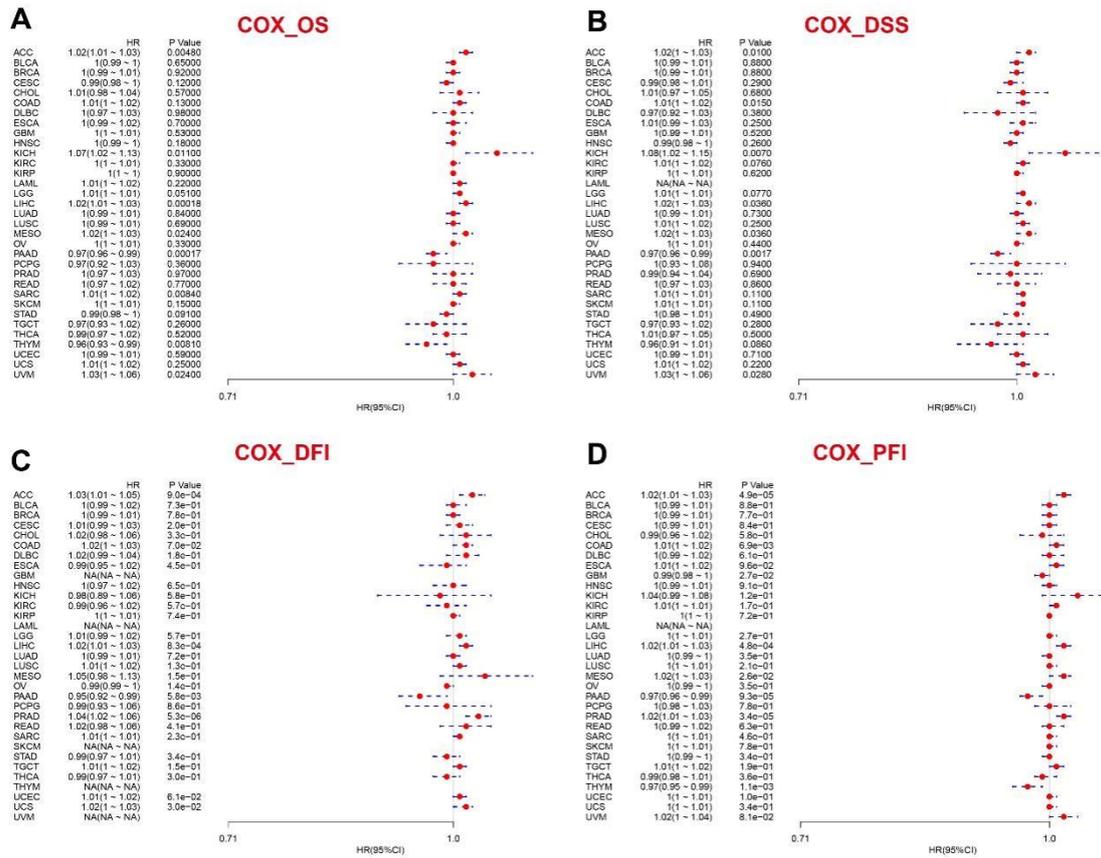
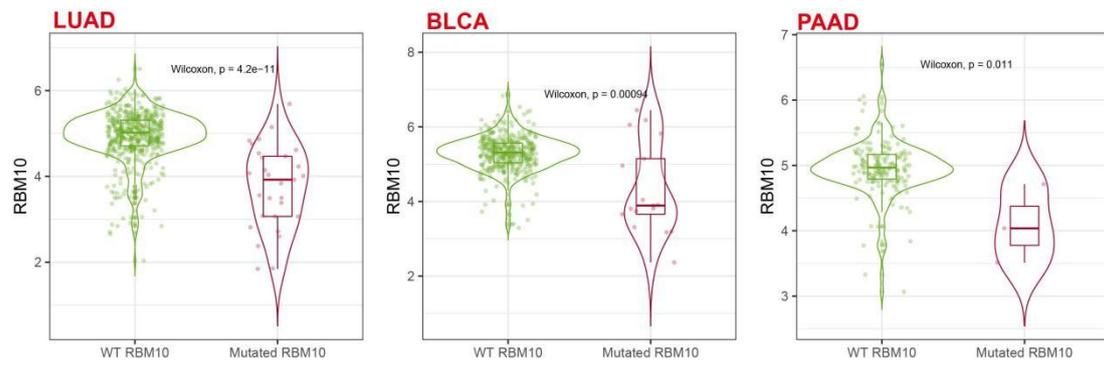


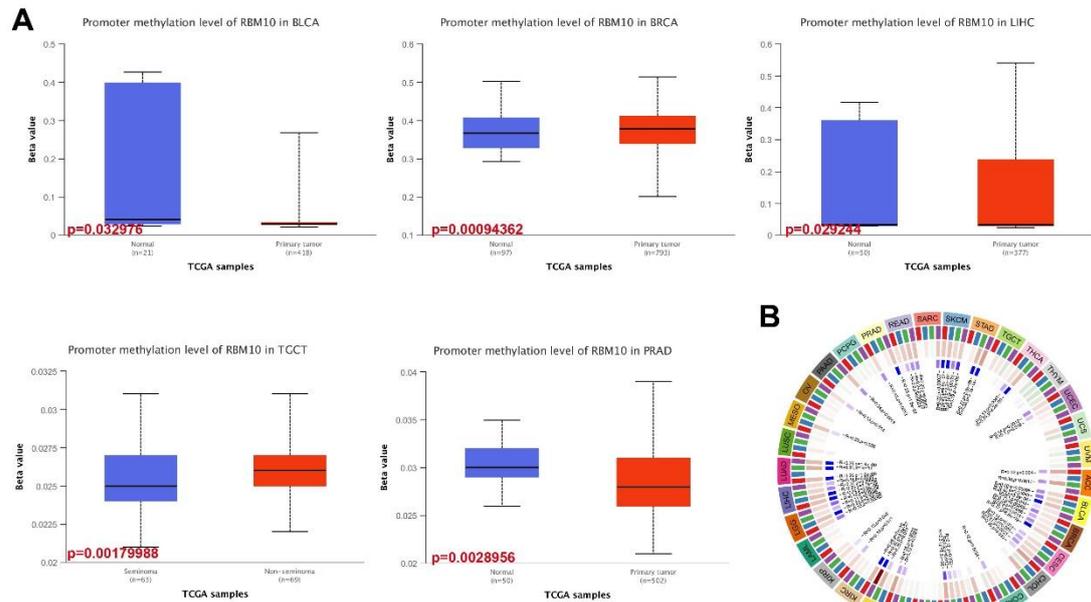
Figure S5 (A~D) Forest map showed the univariate cox regression results of RBM10 for OS (A), DSS(B), DFI(C) and PFI(D) in multiple cancers.



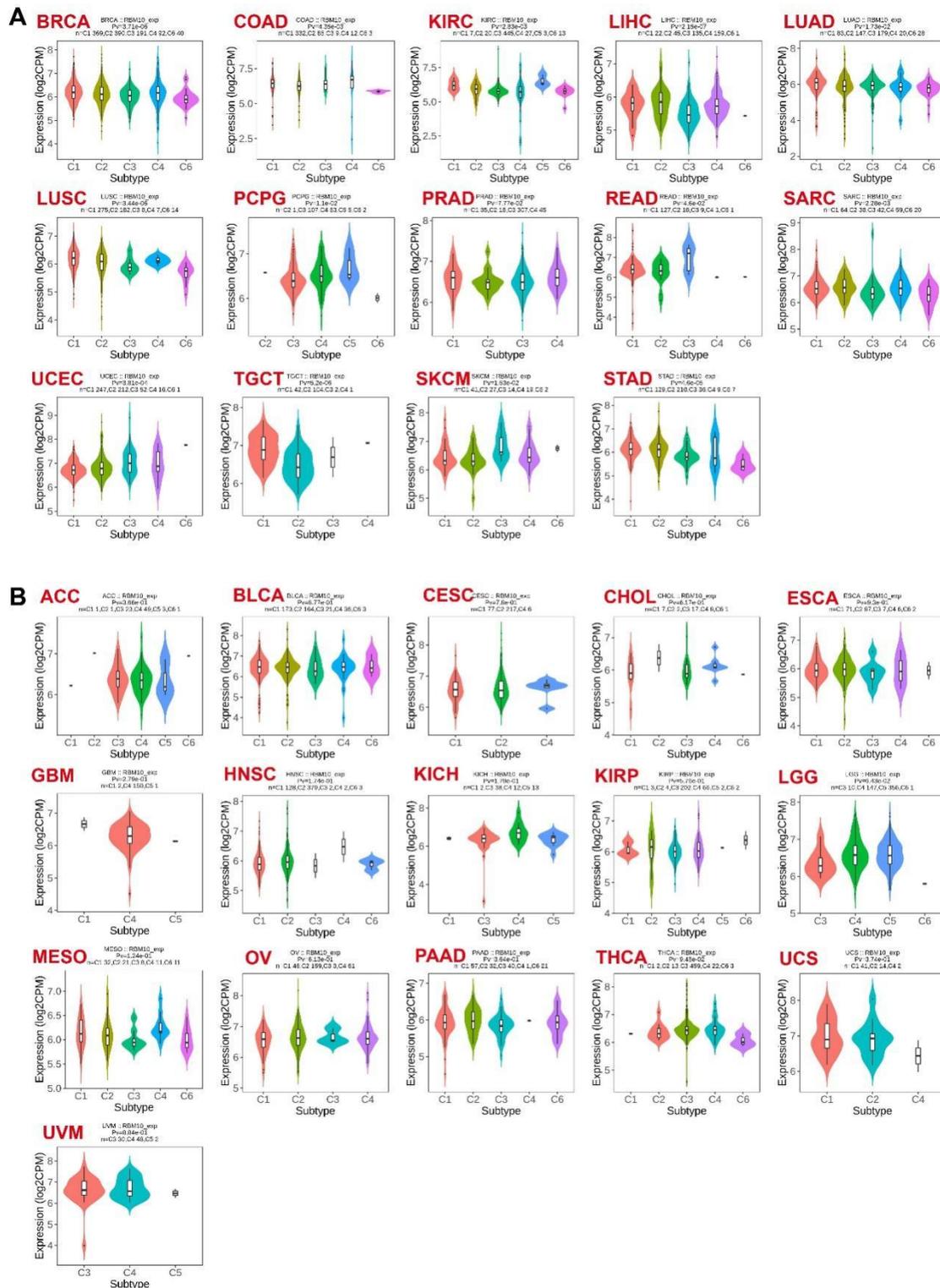
**Figure S6 The expression level of RBM10 in the patients with RBM10 wild type (RBM10 WT) or RBM10 mutation (RBM10 Mut) of LUAD, BLCA and PAAD.**



bubbles represented negative correlation, red bubbles represented positive correlation; and the darker the color, the higher the correlation. Bubble size was positively correlated with FDR. Black outline indicates  $FDR < 0.05$ . **(B)** A significant difference correlation between RBM10 mRNA levels and CNV in ACC, BLCA, CESC, ESCA, HNSC, KIRP, LGG, LUAD, LUSC, OV, PRAD, STAD and UCS. **(C)** There was no correlation between RBM10 mRNA expression and CNV among other human tumors.

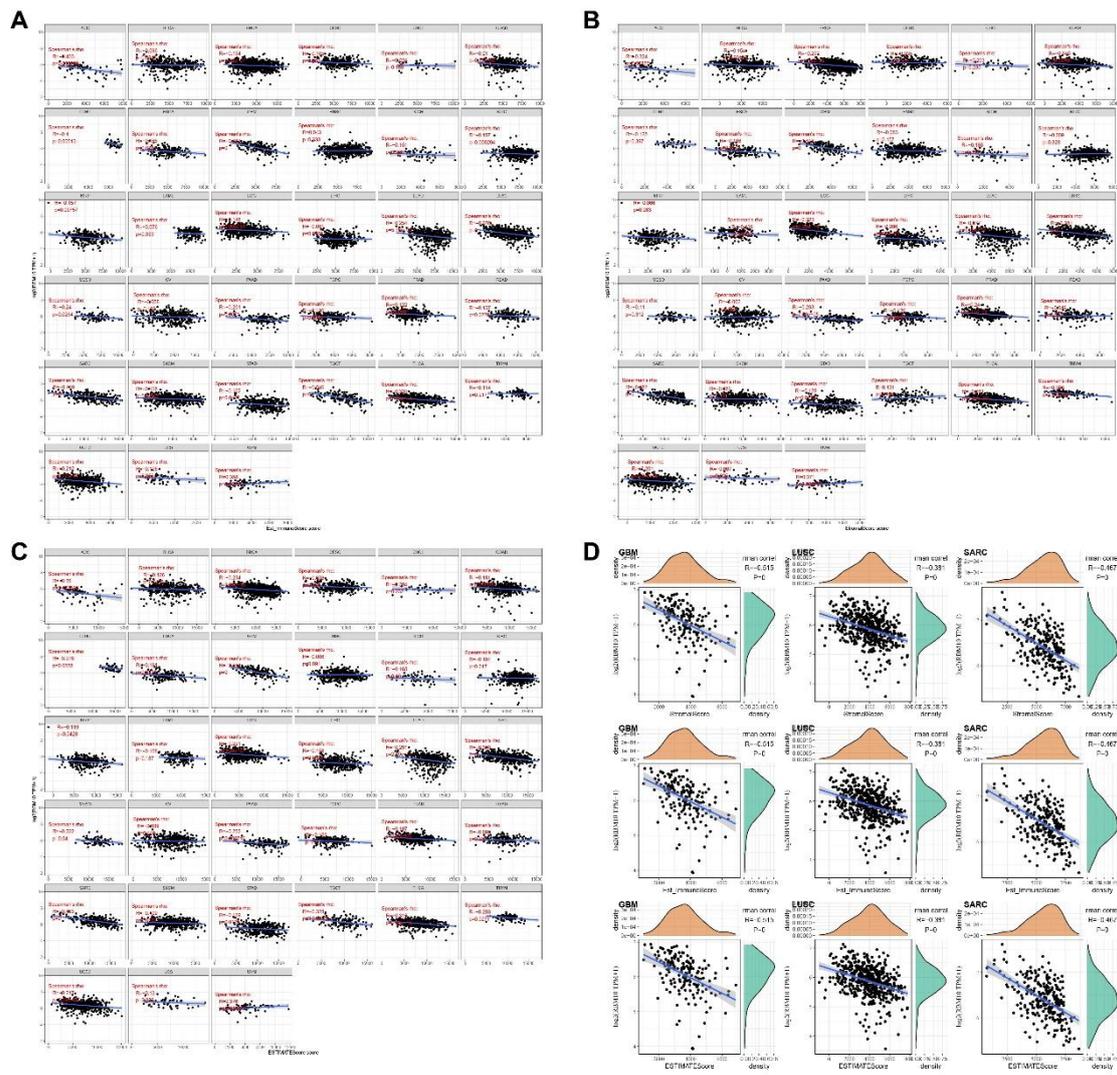


**Figure S8 The promoter methylation level of RBM10 in various cancers (A) The promoter methylation level of RBM10 in BLCA, BRCA, LIHC, TGCT and PRAD. (B) The correlation between RBM10 expression and the level of DNMT genes in across different cancer types was investigated via SangerBox database. The red color: DNMT1, the blue color: DNMT2, the green color: DNMT3A, the purple: DNMT3B.**



**Figure S9 Relationship between RBM10 expression and different immune subtypes in human tumor (A)** The violin diagram showed that RBM10 is significantly associated with different immune subtypes in BRCA, COAD, KIRC, LIHC, LUAD, LUSC, PCPG, PRAD, READ, SARC, UCEC, TGCT, SKCM and STAD using TISIDB. **(B)** There was not differ significantly between RBM10

expression and immune subtypes in ACC, BLCA, CESC, CHOL, ESCA, GBM, HNSC, KICH, KIRP, LGG, MESO, OV, PAAD, THCA, UCS and UVM.



**Figure S10 RBM10 expression was related to TME (A)** The correlation of RBM10 expression with ImmuneScore in pan-cancer through Sangerbox. **(B)** The association between RBM10 level and StromaScore in different cancer types based on the SangerBox website. **(C)** The relationship of RBM10 expression with ESTIMATEScore across multiple cancer types using SangerBox. **(D)** The top three tumors that were most significantly related.

### Neoantigen

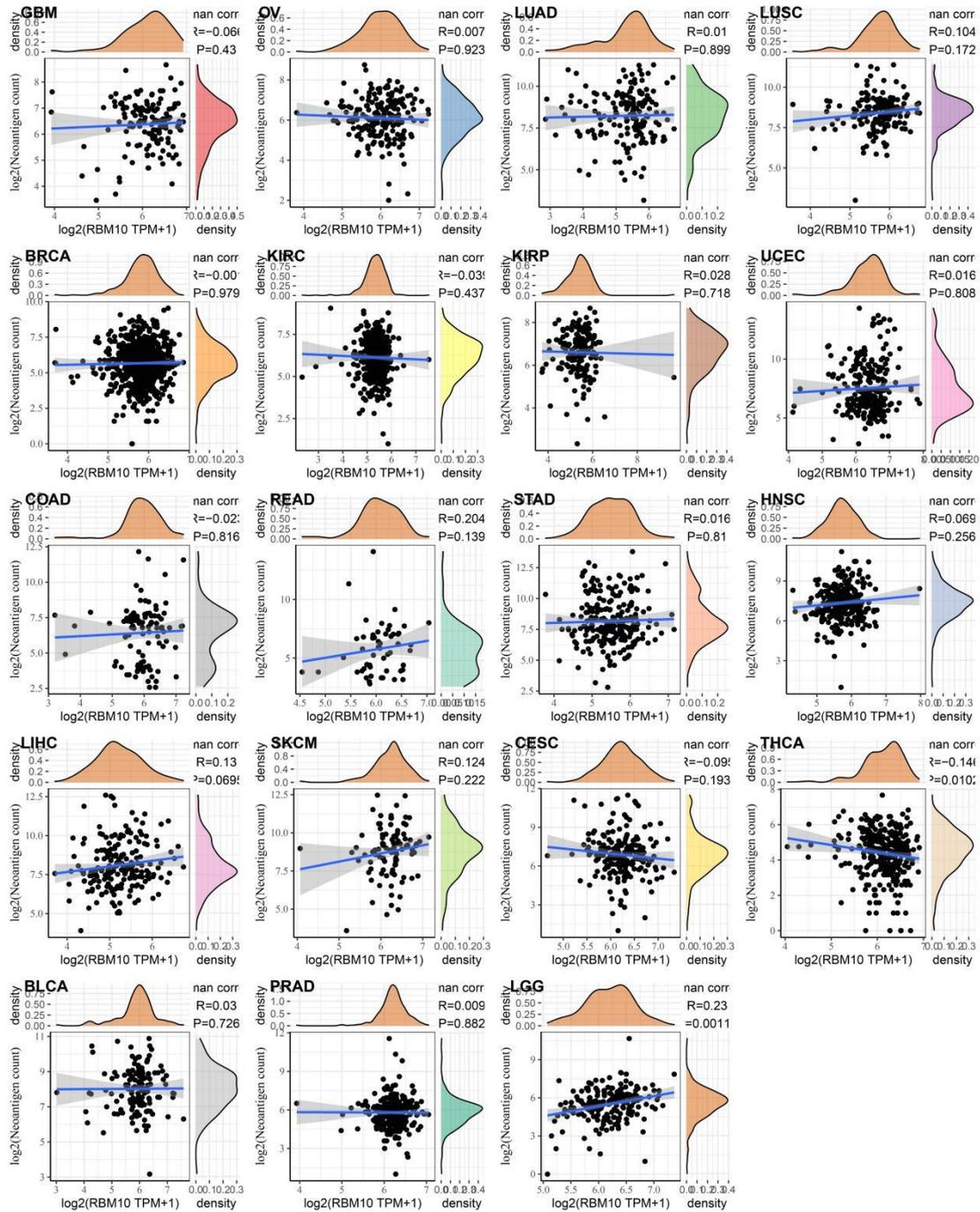
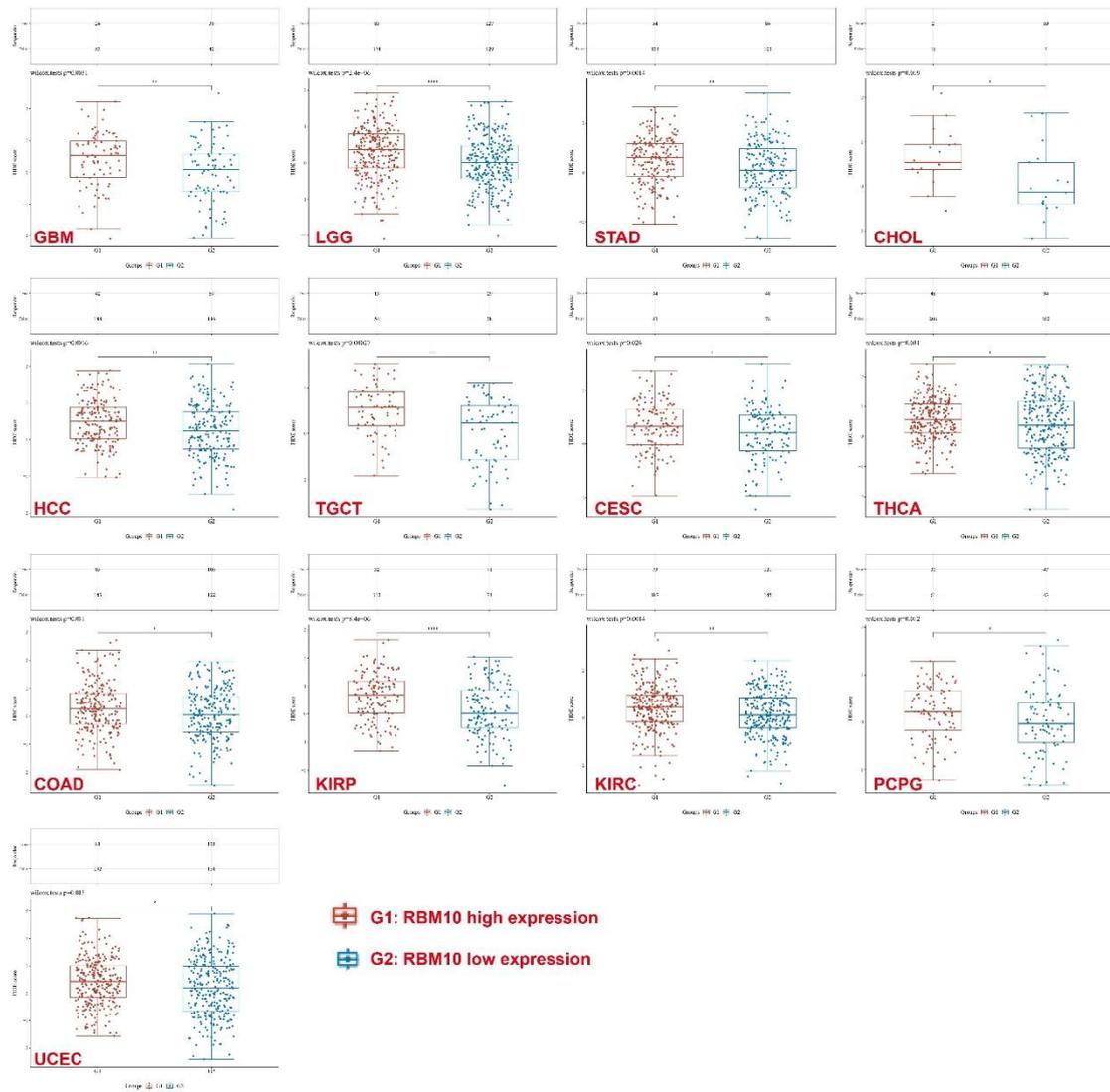
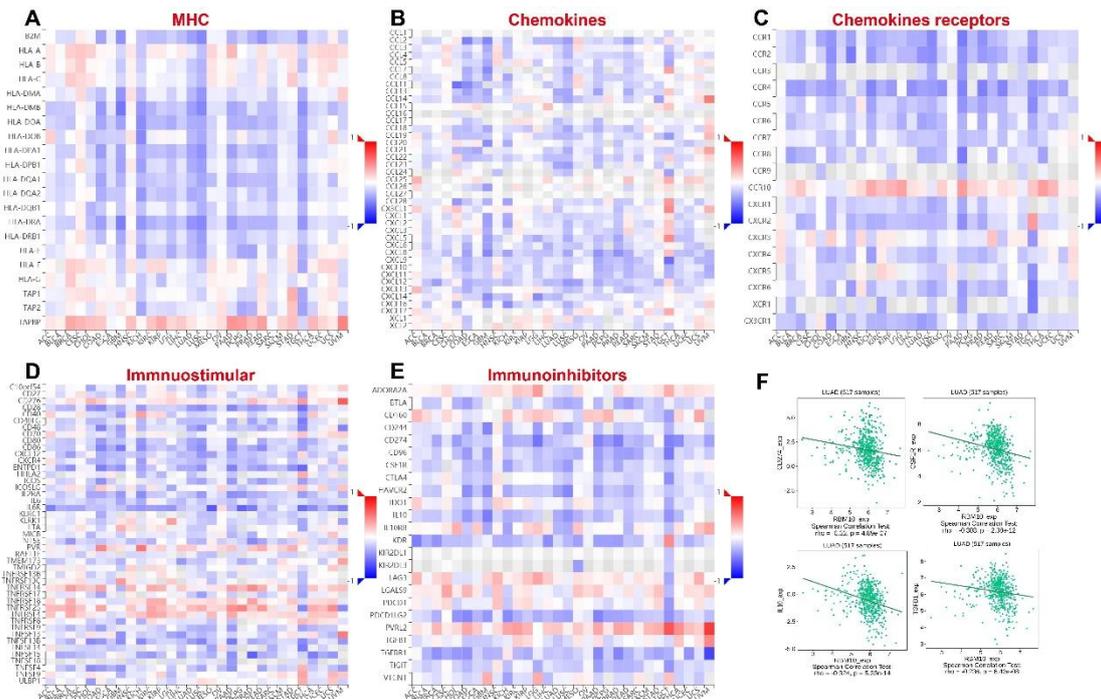


Figure S11 The relationship between RBM10 expression and neoantigens.



**Figure S12 TIDE score of high and low RBM10 expression groups in GBM, TGCT, CESC, THCA, COAD, KIRP, KIRC, PCPG and UCEC. G1, RBM10 high expression: red color; G2, RBM10 low expression: blue color.**



**Figure S13 The correlation of RBM10 expression with immunorelation-related genes (A~E)** Heatmaps indicated the association of RBM10 expression with MHC(A), chemokines(B), chemokines receptors(C), immunostimulars(D) and immuoinhibitors(E). (F) Scatter plots showed that RBM10 was negatively correlated with PD-L1(CD274), CSF1R, IL-10 and TGFB1 in LUAD.