Supplementary Figures and figure legends.

Figure S1

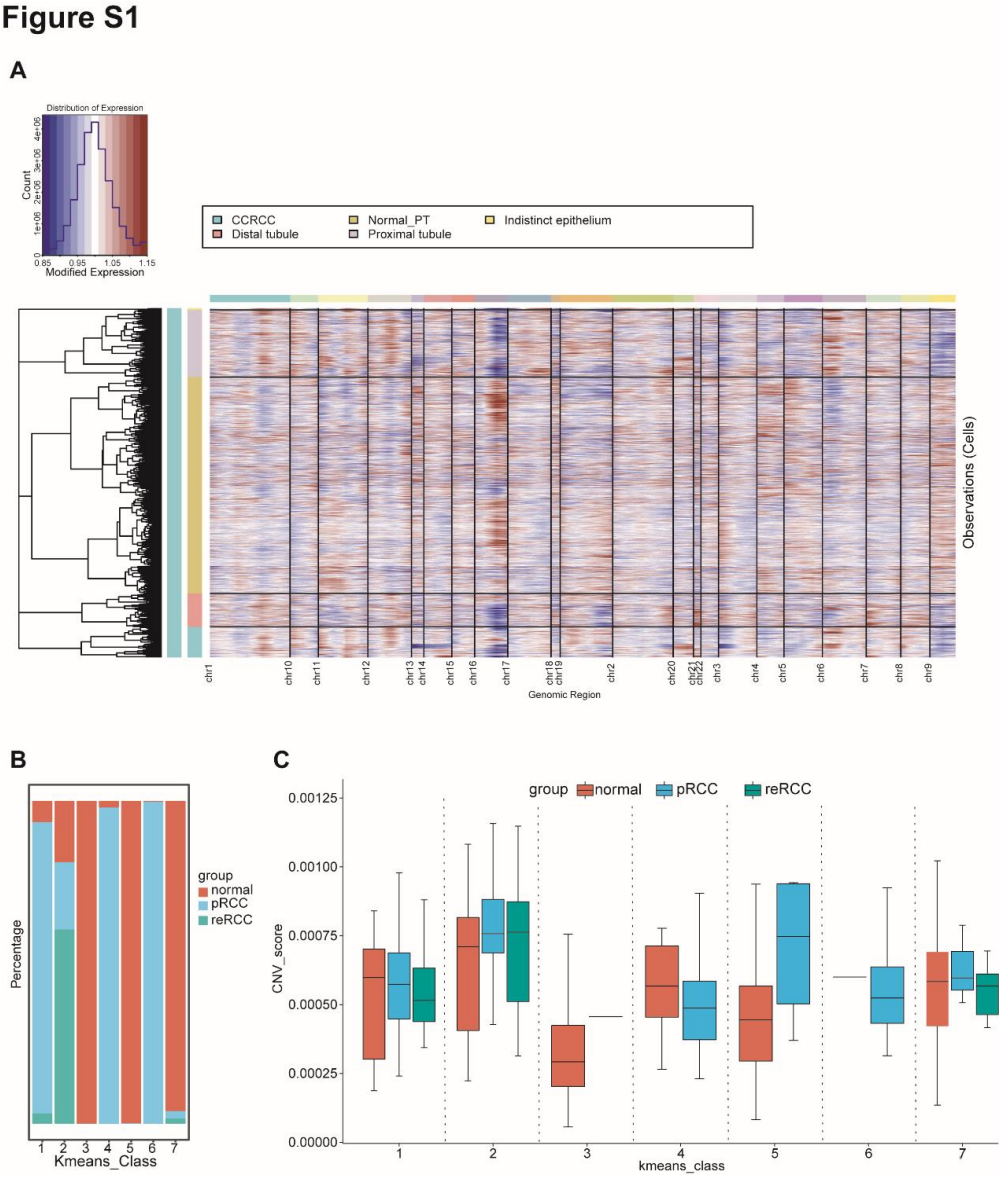

Figure S1 Detecting malignant cells using CNV analysis and kmeans clustering.

A. CNV analysis of epithelial cells.

B. Histogram showing the percentage of cell in kmeans class by groups.

C. Box plots showing the CNV score for kmeans class in each group.

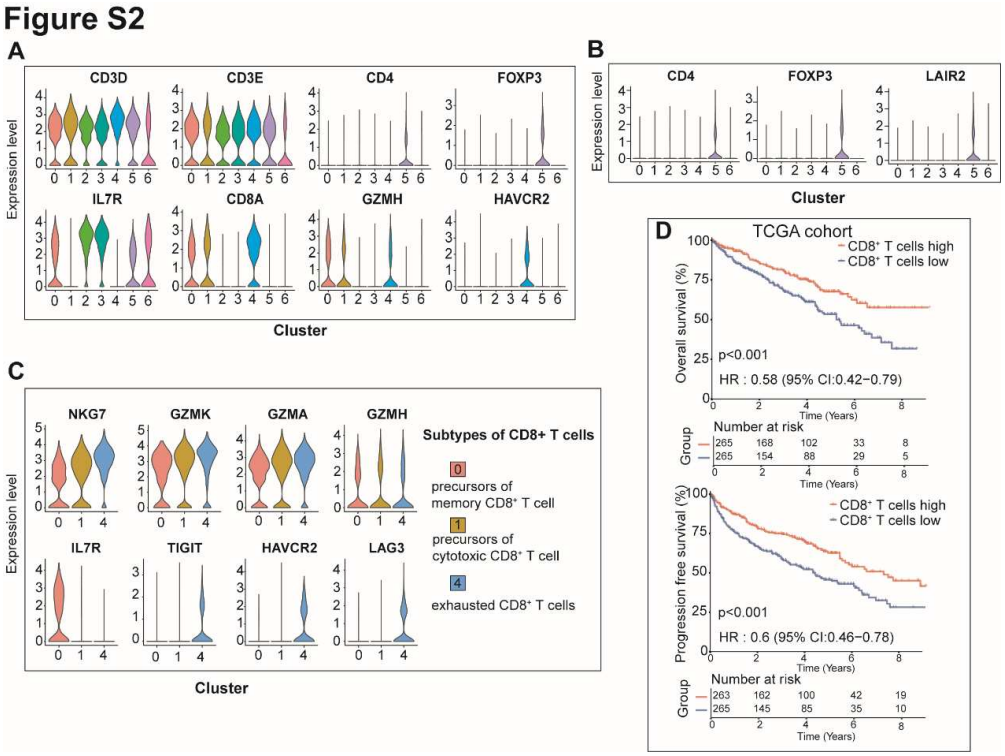

Figure S2

A. Violin plots showing the markers of subtypes of T cells.

B. Violin plots showing the markers of Tregs were specifically expressed in cluster5 of T cells.

C. Violin plots showing the genes of cytotoxicity were specifically expressed in $CD8^+$ T cells, and marker genes of 3 subtypes of $CD8^+$ T cells.

D. K-M curves showed a high infiltrating level of $CD8^+$T cells was significantly associated with longer overall survival and progression-free survival in RCC patients in the TCGA cohort.

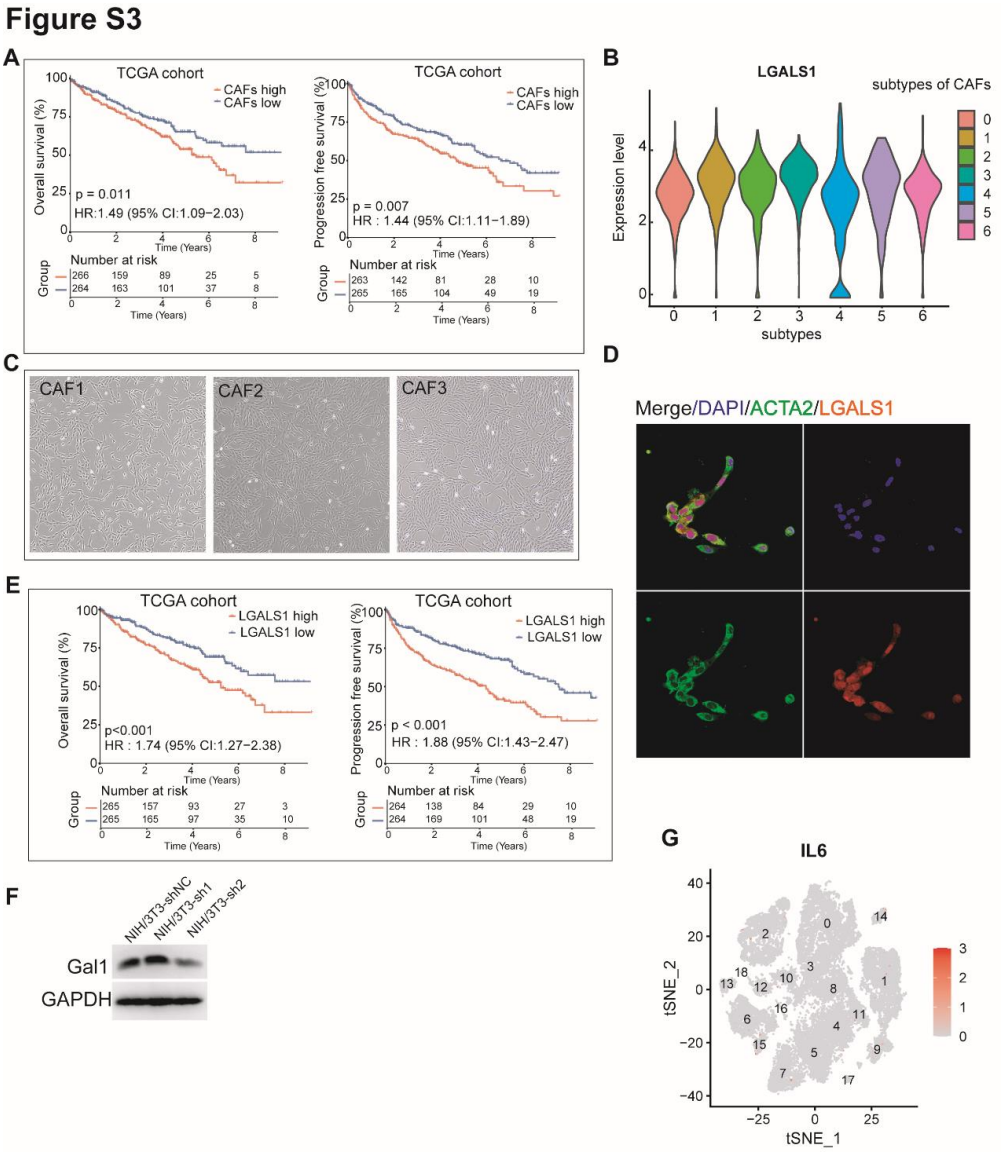

Figure S3

A. K-M curves showed a high infiltrating level of CAFs was significantly associated with poorer overall survival and progression-free survival in RCC patients in the TCGA cohort.

B. LGALS1 expressed high in 7 subclusters of CAFs.

C. Isolating and culturing primary CAFs from RCC patients

D. Multiplexed immunofluorescent staining of α-SMA and Gal-1 in primary CAFs.

E. K-M curves showed a high expression level of Gal-1 was significantly associated with poorer overall survival and progression-free survival in RCC patients in the

TCGA cohort.

F. Establishing and validating knocking down Gal1 in NIH/3T3 cell lines.

G. tSNE plot showing IL6 expressed extremely low in all cell types in RCC.