Supplementary Figure S1 — heatmap of METTL family members across cancer types.

Rows (top to bottom): METTL1, METTL10, METTL11B, METTL12, METTL13, METTL14, METTL15, METTL16, METTL17, METTL18, METTL21A, METTL21B, METTL21EP, METTL22, METTL23, METTL24, METTL25, METTL2A, METTL2B, METTL3, METTL4, METTL5, METTL6, METTL7A, METTL7B, METTL8, METTL9

Columns (left to right): BLCA, BRCA, CESC, COAD, GBM, HNSC, KIRC, KIRP, LAML, LGG, LIHC, LUAD, LUSC, OV, PAAD, READ, SARC, SKCM, STAD, UCEC

Legend:
* p < 0.05
** p < 0.01
*** p < 0.001
**** p < 0.0001

Hazard Ratio < -0.3
Not Significant
Hazard Ratio > 0.3

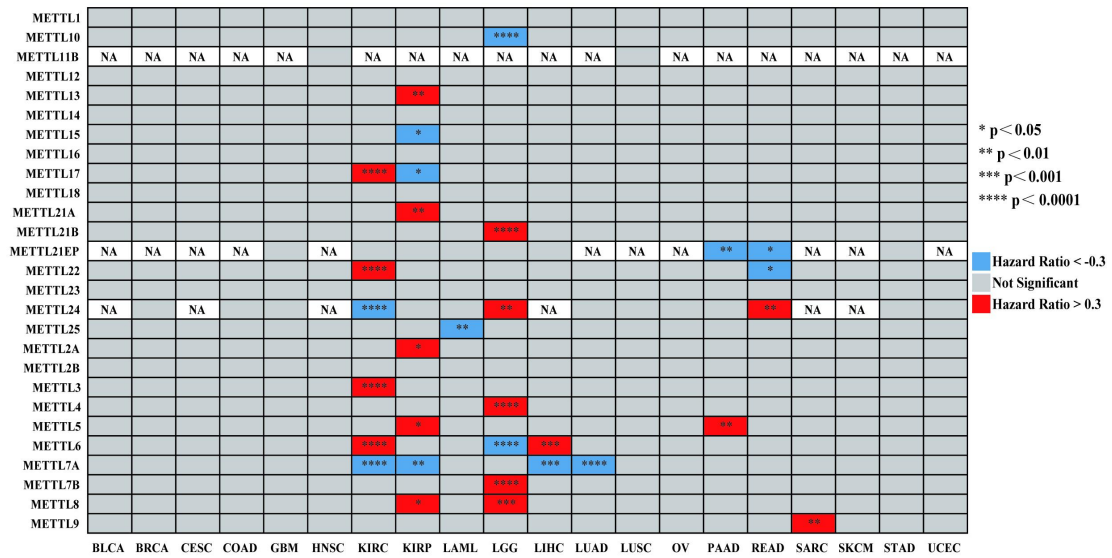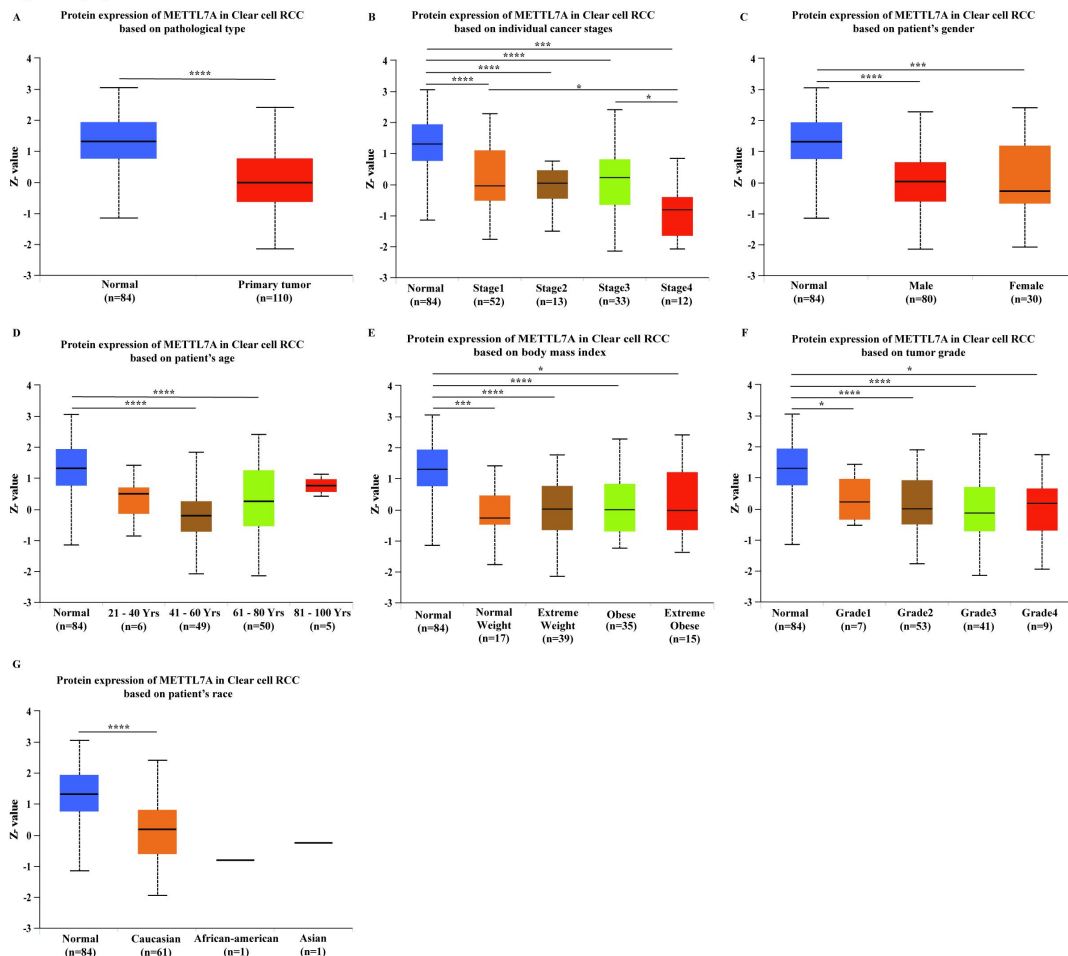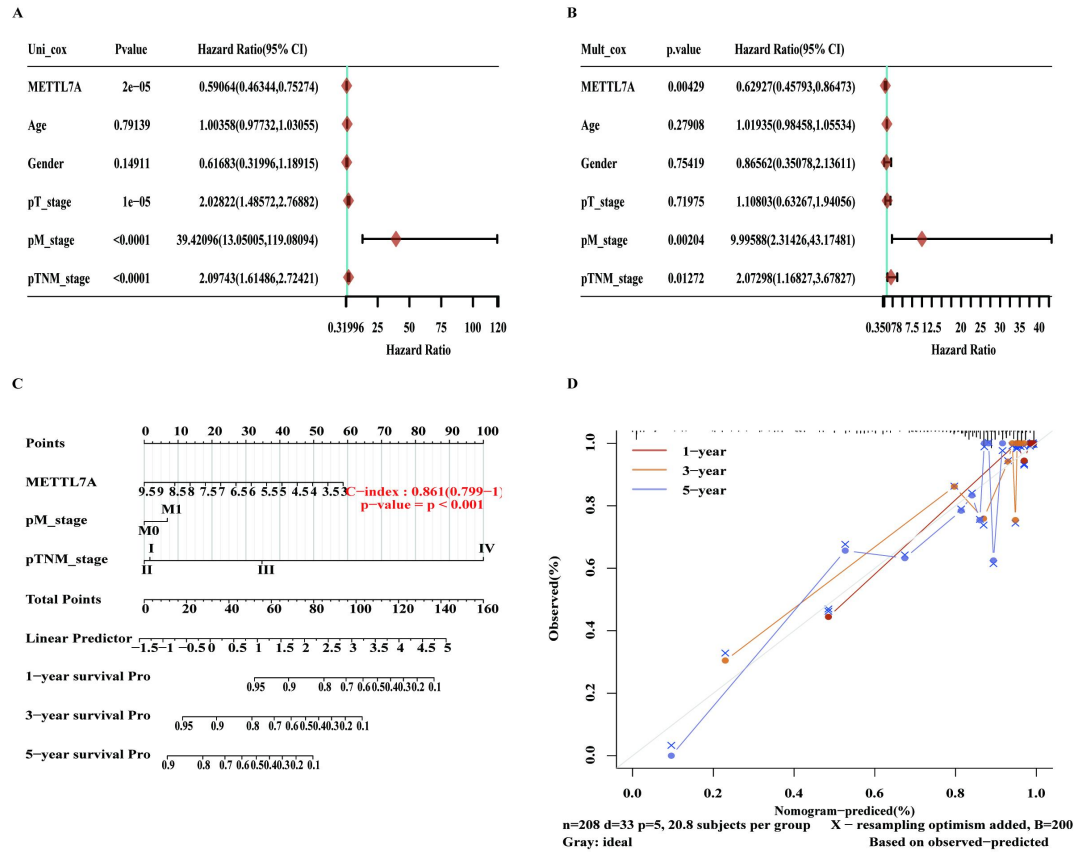**SUPPLEMENTARY FIGURE S1** Our previous study demonstrated that METTL family members were highly associated with the risk of renal cancer, rather than other cancers, as analyzed using univariate Cox regression analysis.

A — Protein expression of METTL7A in Clear cell RCC based on pathological type
Normal (n=84), Primary tumor (n=110); ****

B — Protein expression of METTL7A in Clear cell RCC based on individual cancer stages
Normal (n=84), Stage1 (n=52), Stage2 (n=13), Stage3 (n=33), Stage4 (n=12)

C — Protein expression of METTL7A in Clear cell RCC based on patient's gender
Normal (n=84), Male (n=80), Female (n=30)

D — Protein expression of METTL7A in Clear cell RCC based on patient's age
Normal (n=84), 21 - 40 Yrs (n=6), 41 - 60 Yrs (n=49), 61 - 80 Yrs (n=50), 81 - 100 Yrs (n=5)

E — Protein expression of METTL7A in Clear cell RCC based on body mass index
Normal (n=84), Normal Weight (n=17), Extreme Weight (n=39), Obese (n=35), Extreme Obese (n=15)

F — Protein expression of METTL7A in Clear cell RCC based on tumor grade
Normal (n=84), Grade1 (n=7), Grade2 (n=53), Grade3 (n=41), Grade4 (n=9)

G — Protein expression of METTL7A in Clear cell RCC based on patient's race
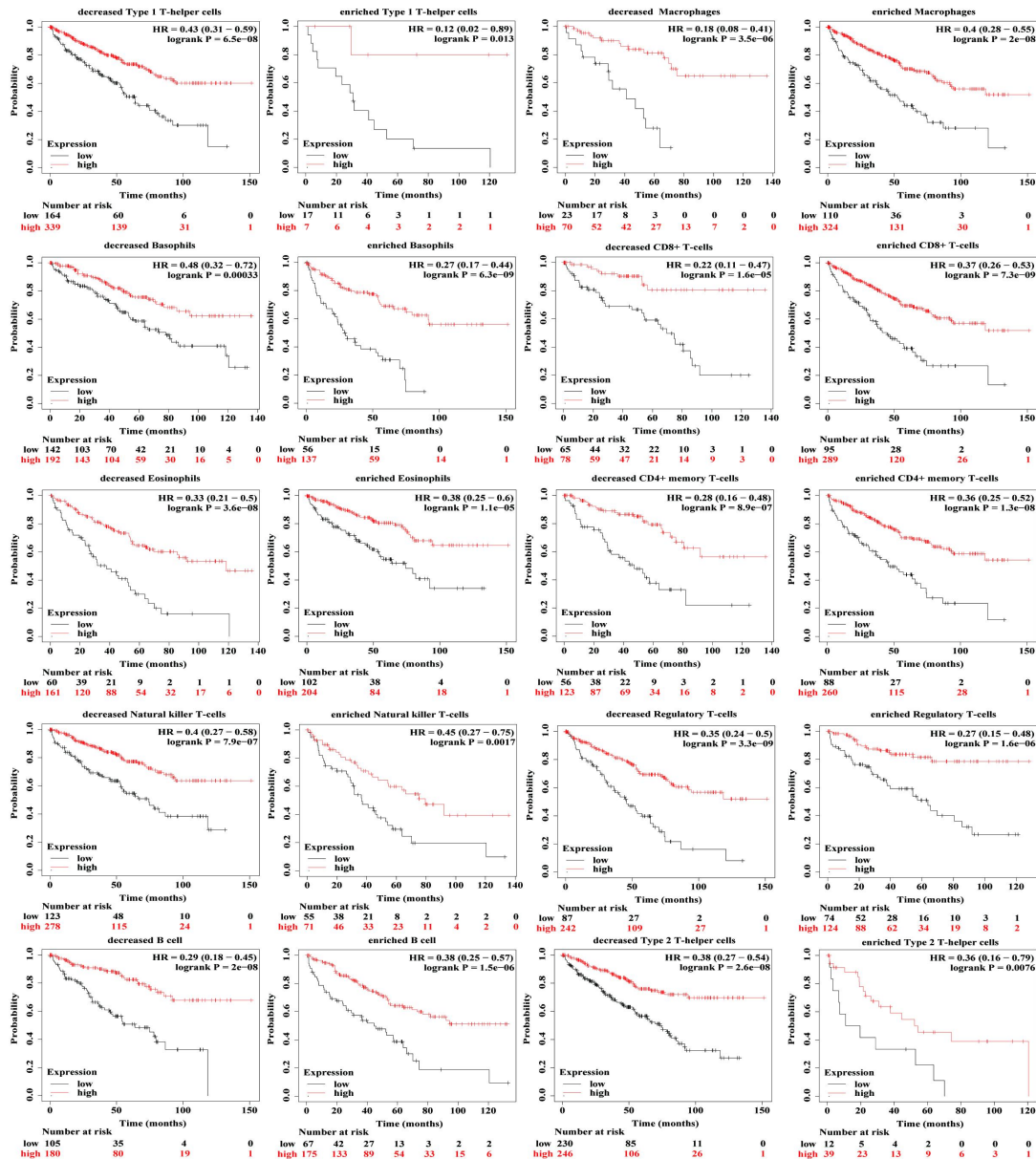Normal (n=84), Caucasian (n=61), African-american (n=1), Asian (n=1)

SUPPLEMENTARY FIGURE S2 Box plots showed the protein expression of METTL7A among different kidney renal clear cell carcinoma (KIRC) patient groups. Analysis was shown for protein expression of METTL7A between (A) normal tissues and primary tumors, different (B) cancer stages, (C) races, (D) sex, (E) ages, (F) body mass indexs (BMI), (G) and grades.

SUPPLEMENTARY FIGURE S3 METTL7A as one potential independent prognostic factor in renal papillary cell carcinoma (KIRP). (A, B) By univariate and multivariate Cox regression analysis, METTL7A was identified as a putative independent prognostic factor for KIRP. (C, D) The nomogram revealed that METTL7A could predict the 1-, 3-, and 5-year survival rates of KIRP patients when combined with other clinical markers.

SUPPLEMENTARY FIGURE S4 METTL7A might influence the overall survival of KIRC patients by controlling immune cell infiltration. Kaplan-Meier survival curve of METTL7A in KIRC patients with immune cell infiltration at high or low levels.