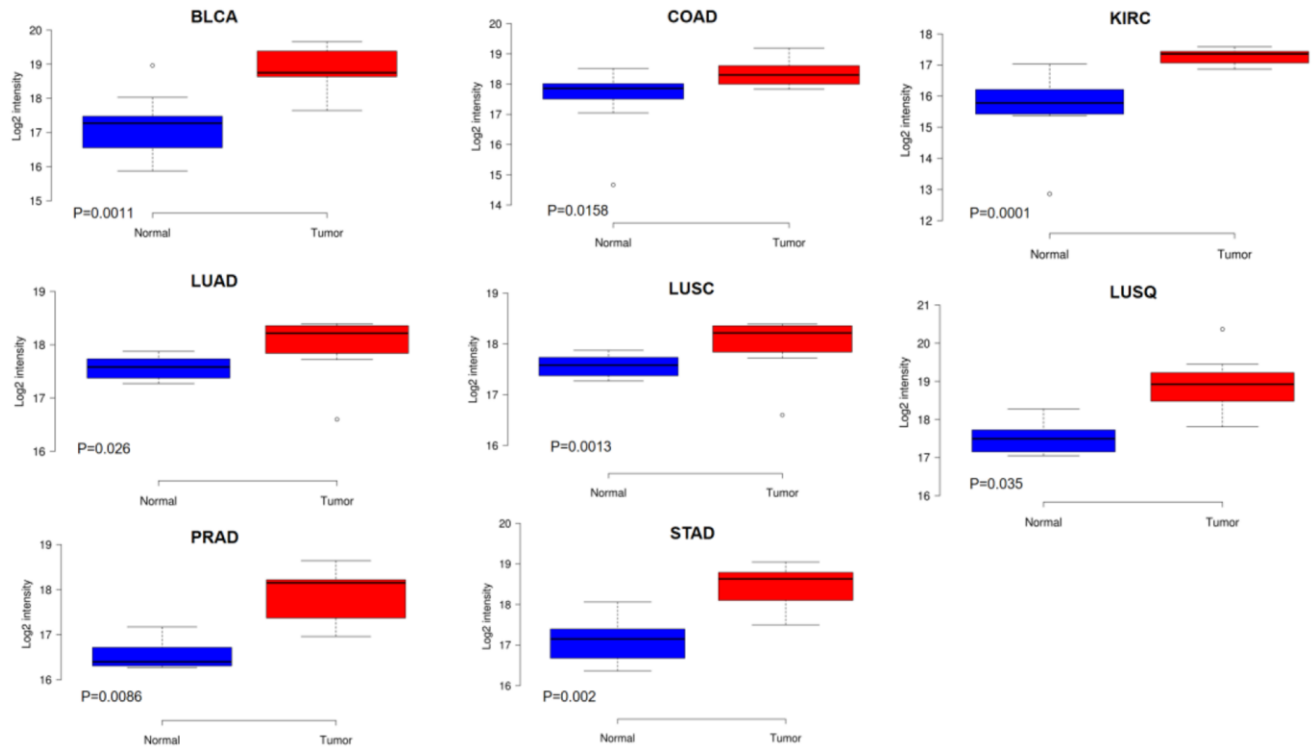
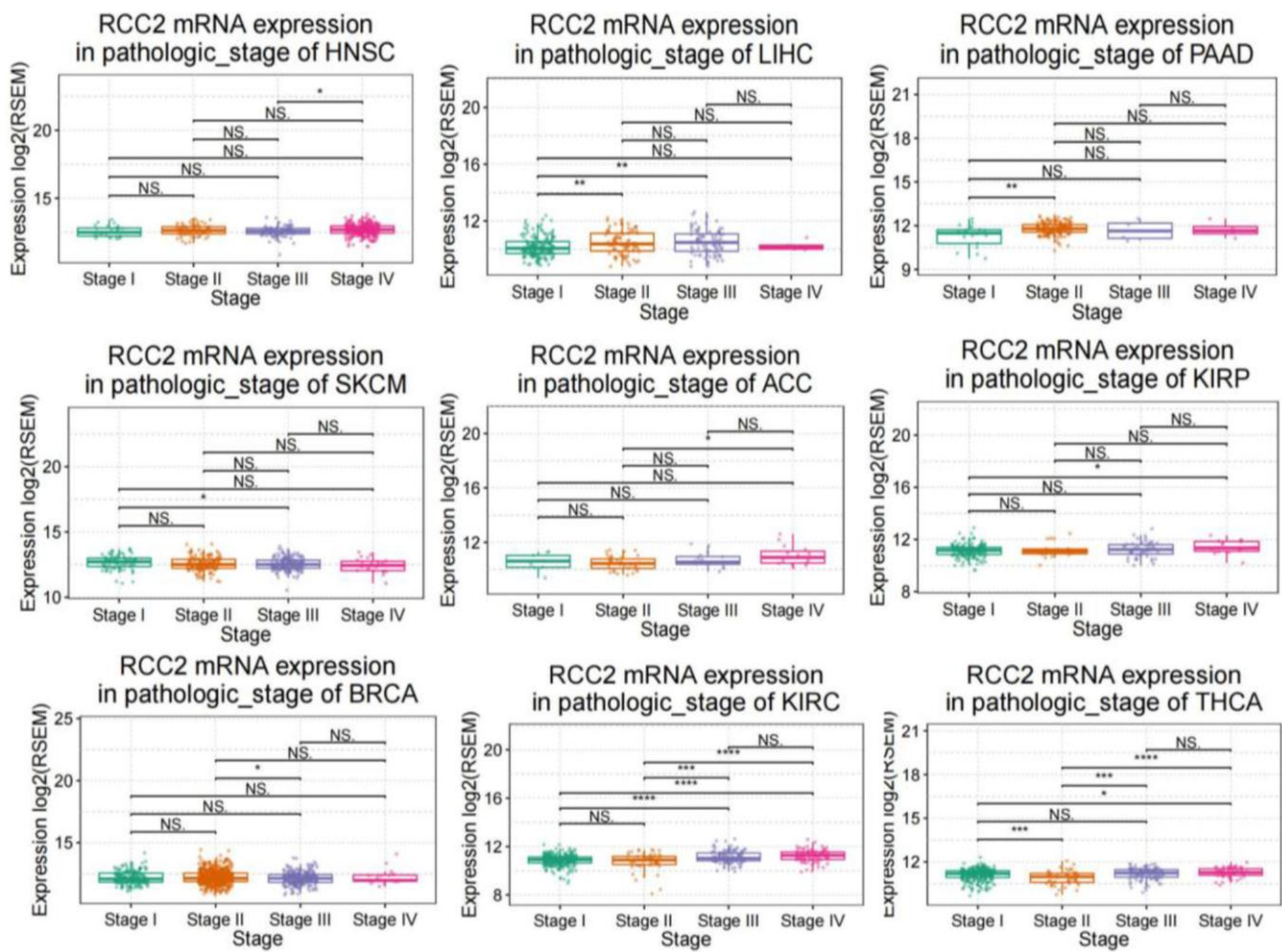


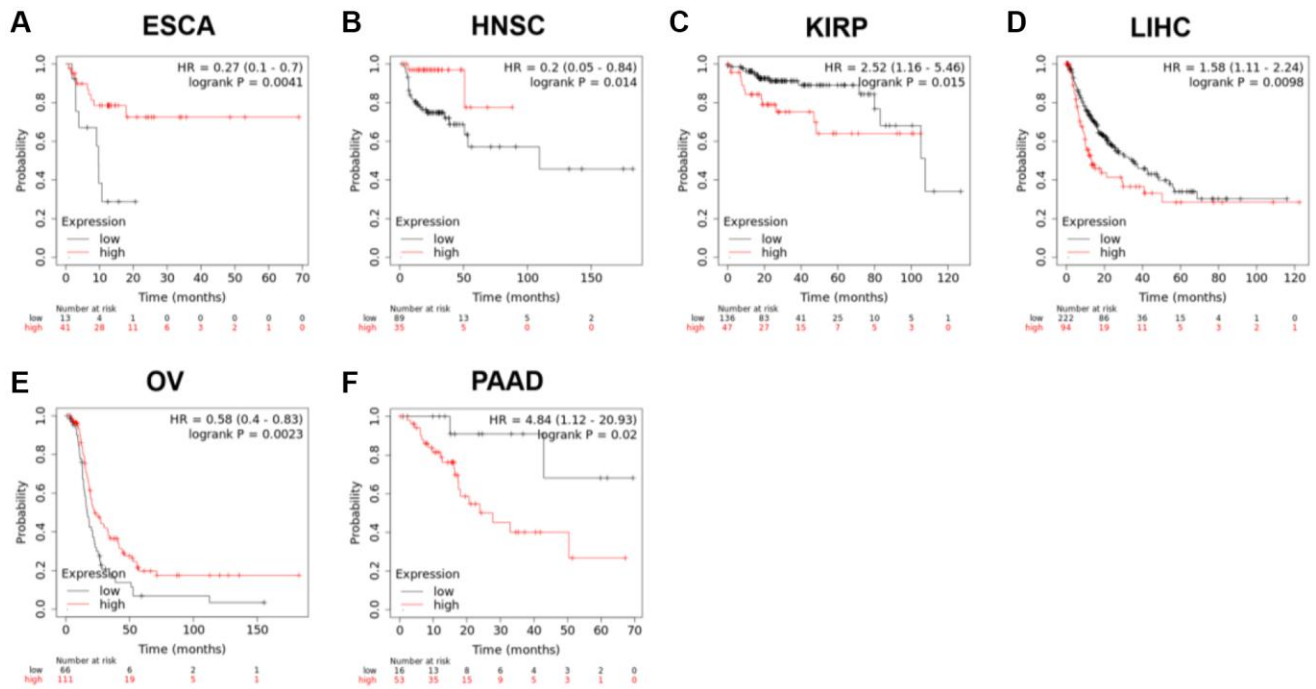
SUPPLEMENTARY FIGURES



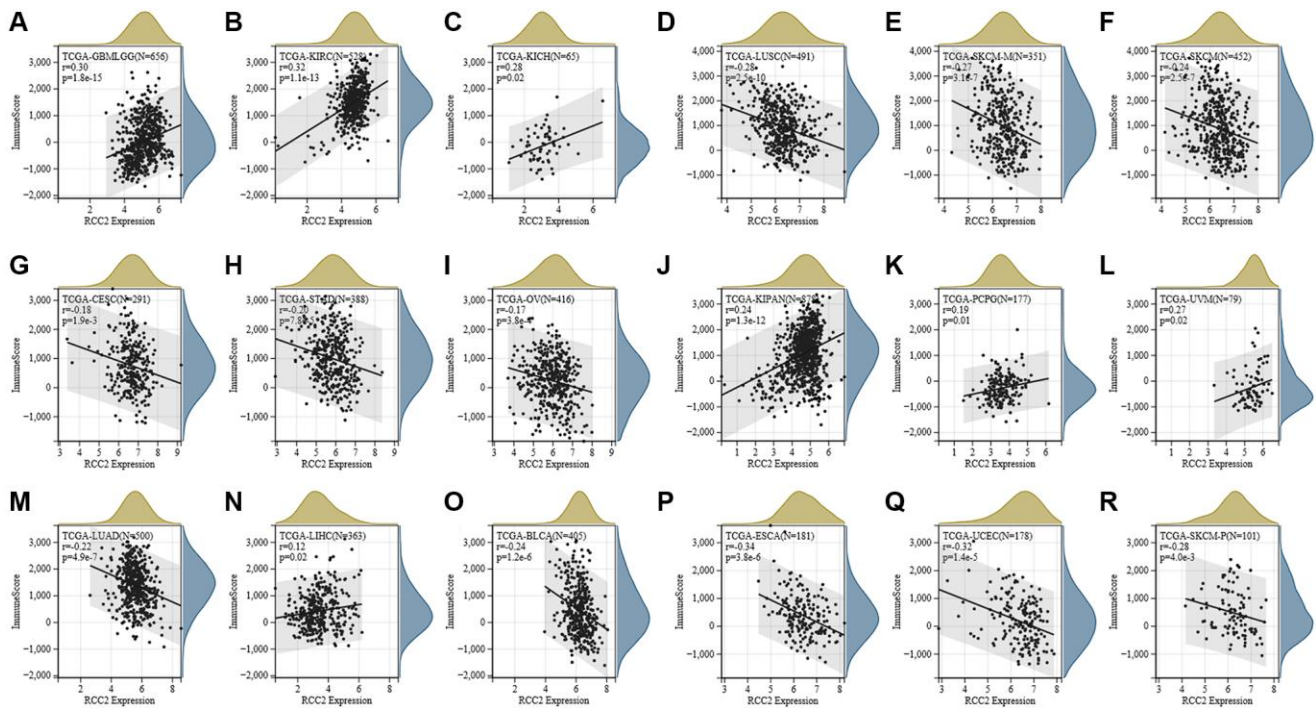
Supplementary Figure 2: RCC expression in proteomics data of 16 different cancer types with $p < 0.05$ were illustrated.



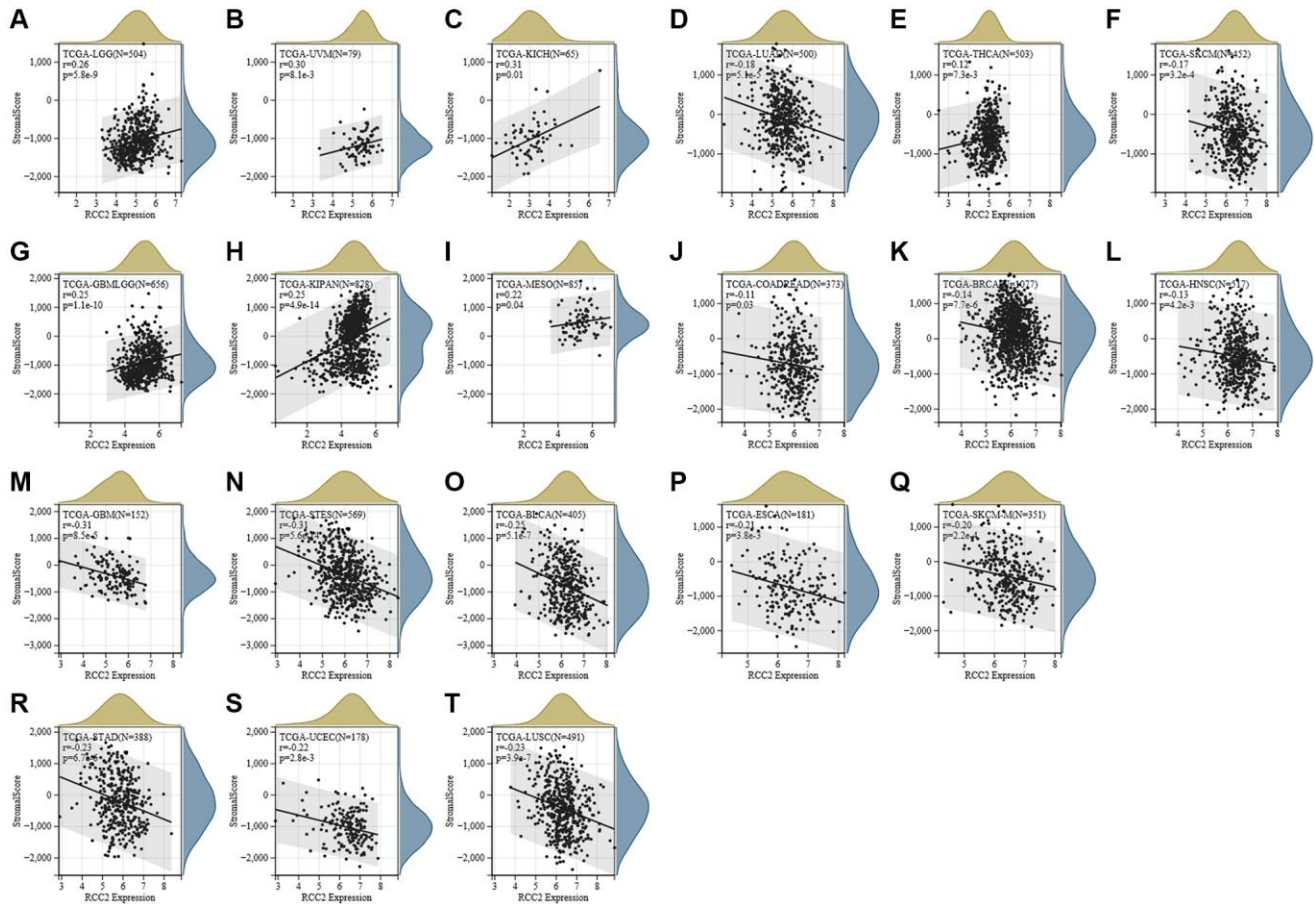
Supplementary Figure 2. RCC2 mRNA expression in pathologic stages of HNSC, LIHC, PAAD, SKCM, ACC, KIRP, BRCA, KIRC, and THCA.



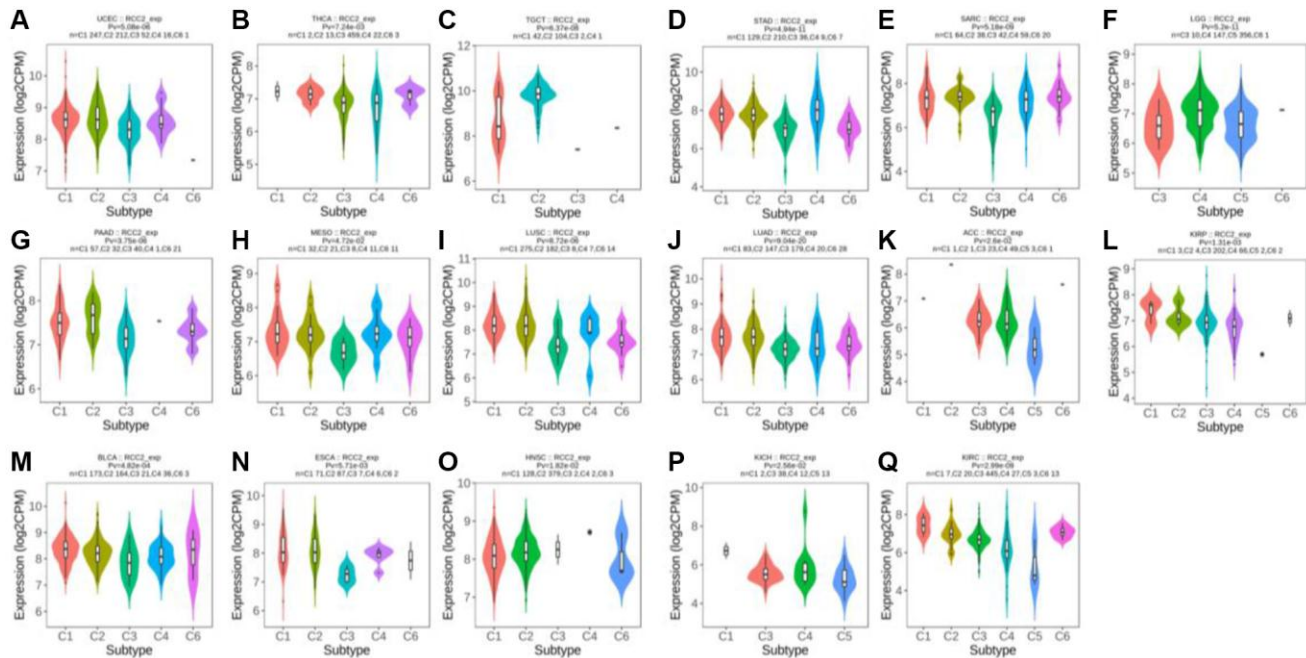
Supplementary Figure (A-F) Relationship between RCC2 expression and overall survival (OS) in TCGA cancer. Only tumor types with logrank < 0.05 were displayed.



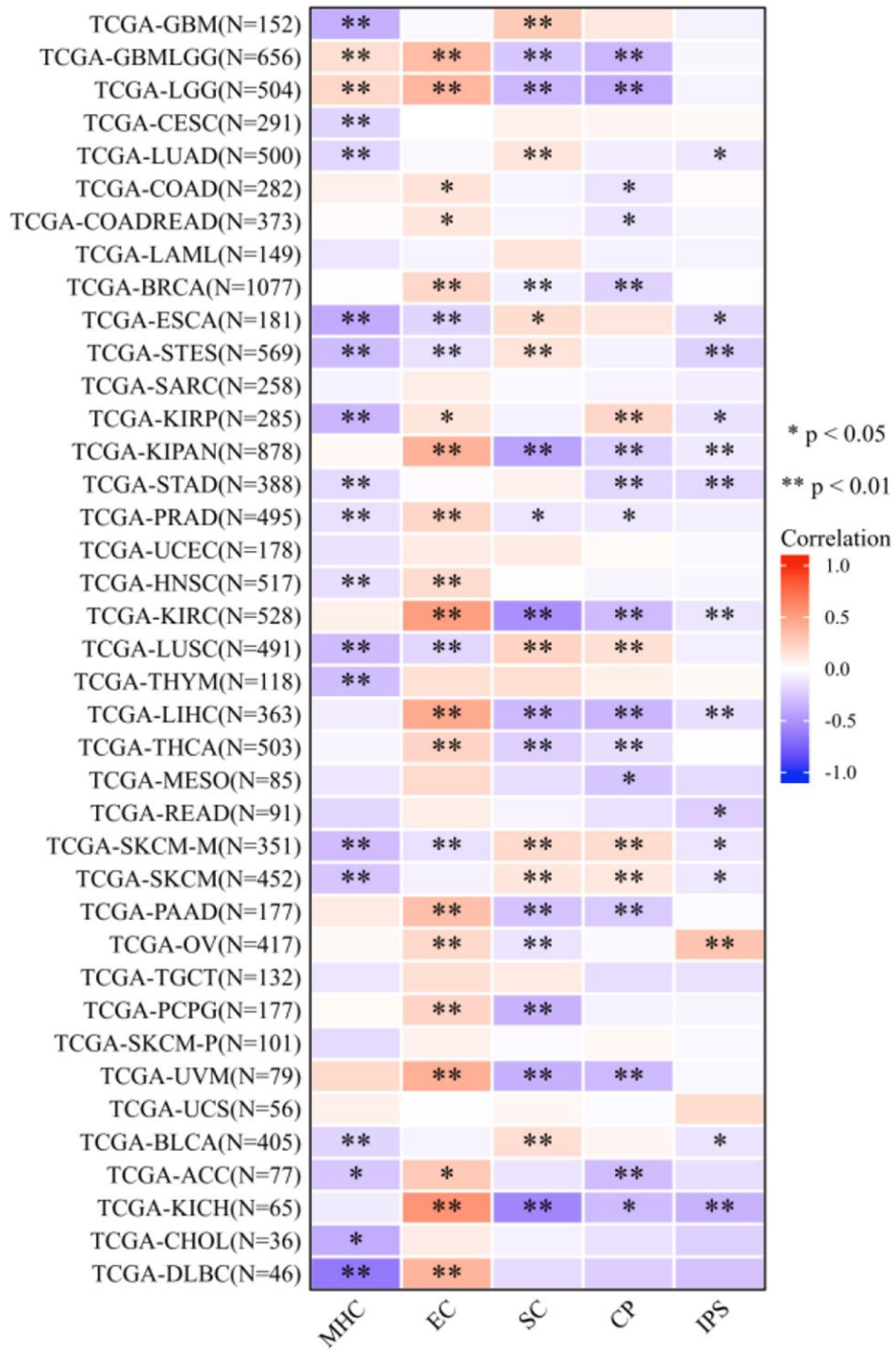
Supplementary Figure (A-R) Correlation of RCC2 expression with immune scores.



Supplementary Figure 5 (T) Correlation of RCC2 expression with stromal scores.



Supplementary Figure 6: Expression levels of RCC2 in different types of tumor immune subtypes (A-Q). (A) USCC. (B) THCA. (C) TGCT. (D) STAD. (E) SARC. (F) LGG. (G) PAAD. (H) MESO. (I) LUSC. (J) LUAD. (K) ACC. (L) KIPAN. (M) BLCA. (N) ESCA. (O) HNSC. (P) KICH. (Q) KIRC.



Supplementary Figure 7. Correlation of RCC2 expression with MHC, EC, SC, CP, and IPS scores in cancer. Abbreviations: MHC major histocompatibility complex; EC effector cells; SC suppressor cells; CP checkpoints; IPS immunophenoscore.