

Figure S1: Assessment of clinical features and the immune landscape associated with CAFs in the TCGA and GSE17536 cohort. (A) Correlations of different TME cell types with stromal, immune and ESTIMATE scores as well as tumor purity in the TCGA cohort. (B) Various TME cell abundances in the GSE17436 cohort were shown in the heat map. (C) Correlations of different TME cell types with stromal, immune and ESTIMATE scores as well as tumor purity in the GSE17536 cohort;

Figure S2: The network topology in WGCNA. (A) and (B) show the soft thresholds in the TCGA and GSE17536 cohort, respectively;

Figure S3: COMP-related biological processes were enriched by (A) GO and (B) KEGG analyses;

Figure S4: K-M plots for high- and low-COMP expression subgroups of (A) TCGA, (B) GSE17536, (C) GSE39582, (D) GSE41258 and (E) the combined-GEO cohorts;

Figure S5: Assessment of the 22 immune cell fractions in the low- and high-COMP expression subgroups by the CIBERSORT algorithm. (A) Association between CAFs, stromal score, immune score, tumor purity, and COMP expression. (B) Different infiltrating patterns of 22 immune cells across different COMP subgroups in TCGA and GSE17536. (B) Estimation of the 22 immune cell fractions in the low- and high-COMP expression subgroups in the (C) TCGA and (D) GSE17536 datasets;

Figure S6: Correlation of COMP with somatic mutations. (A) The landscape of somatic mutations showed the top 15 genes exhibiting the highest mutation frequency. (B) Twelve genes more frequently mutated in the high-COMP subgroup were input in GSCA database as a gene set, and the association between the abundance of naïve CD8<sup>+</sup> T cells, CD8<sup>+</sup> T cells, macrophages and the gene set mutation level was exhibited. (C) The correlation between COMP expression and TMB. (D) COMP expression in patients with MSS/MSI-L and MSI-H;

Figure S7: The correlations between COMP expression and putative immunotherapy response in external cohorts. The correlations between COMP expression and the TIDE score, the proportions of patients with putative immunotherapy response in two COMP expression subgroups, and the comparisons of COMP expression between distinct responses in the (A) GSE17536, (B) GSE39582 and (C) GSE41258 cohorts. R, responder; NR, non-responder. (D) Evaluation of COMP expression in anti-PD-L1 responders versus non-responders and ROC curves of COMP expression in the IMvigor210 cohort. (E) K-M plots for aRCC patients treated with the combination of avelumab and axitinib versus sunitinib alone in the whole JAVELIN Renal cohort.