Supplementary figure legends

Supplementary figure 1. (A-B) KEGG and GO pathway were enriched in CD39$^+$CD8$^+$ T cell

score high group. (C) Correlation of CD39$^+$CD8$^+$ T cells score and effector/exhausted markers

from TCGA.

Supplementary figure 2. Representative staining pictures of immune cells.

(A) Representative pictures of B cell= B cells, CD4= CD4$^+$ T cells, Th1= type 1 T helper cells,

Th2= type 2 T helper cells, CD8=CD8$^+$ T cells, NK= nature killer cells, Treg= regulatory T cells.

(B) Representative pictures of DC= dendritic cells, M1=M1 macrophages, M2=M2

macrophages, Mast= mast cells, Neut= neutrophils.

Supplementary figure 3. (A) Representative staining pictures of VEGFA$^+$ cells.(B)

Comparison of the VEGFA$^+$ cells between high/low percentage of CD39$^+$CD8$^+$ T cells

(n=85).** $p < 0.01$. (C) High percentage of CD39$^+$CD8$^+$ T cells was associated with high

proportion of VEGFA$^+$ cells (n=85, Spearman's r=0.3646, p=0.0006).

Supplementary Table 1. Clinical characteristics of non-metastatic ccRCC.

Supplementary Table 2. Clinical characteristics of metastatic ccRCC.

Supplementary Table 3. Immunohistochemistry (IHC) antibodies.

Supplementary Table 4. Flow cytometry (FCM) antibodies.

Supplementary Table 5. Gene list of signature.

Supplementary Table 6. Clinical characteristics of 48 ccRCC patients.

Supplementary methods