**Availability of data and materials**

The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

**Supplemental figure legends**

**Table S1**

Table showing RCC patient data including clinical parameters and status

**Figure S1**

A.-E. Dotplot showing differences in cytokine profiles between the tumor (T) and adjacent healthy renal tissue (H) samples. Overall, tumor displayed higher levels of most of the cytokines compared to the healthy counterparts. Non-parametric Mann-Whitney U test was used with a 95% confidence level. Error bars indicate the median and range. ns=non-significant.

**Figure S2**

1. Dotplot showing that CD3+ T cell dominant (CD3high) tumor samples have an increased abundance of CD3+ T cells than NK cell dominant (NKhigh) tumors, and that NK cell dominant tumors are more enriched with NK cells compared to the CD3high counterparts. Non-parametric Mann-Whitney U test was used with a 95% confidence level. Error bars indicate the median and range. \*\*\*\*, p<0.0001.
2. Scatterplot showing two subgroups (PD1\_hi (pink) and PD1\_lo (green)) based on the CD4+ T cell PD-1 and CD8+ T cell PD-1 expressions. Blue dots (NA) indicate samples that have been excluded from the analysis.
3. Scatterplot showing Kruskal-Wallis test comparing the absolute amount of lymphocytes from all events and the different cytokine clusters (hi, int, lo). Benjamini-Hochberg multiple correction with a family-wise alpha threshold and confidence level of 0.05 were used. ns=non-significant.
4. Correlation plot using Spearman rank correlation across the tumor cytokines, including other clinical parameters and immune cell subsets such as lymphocyte quantity (lymph), WHO ISUP 2016 tumor grading (WHO-ISUP), presence of necrosis (necrosis), age, sex, and dominance (CD3high or NKhigh). Statistically significant cytokines with a false discovery rate (FDR) < 0.05 are shown. Overall, strong positive correlations were observed across the tumoral cytokine expressions.

**Figure S3**

1. Heatmap of the adjacent healthy renal tissue samples (n=24) expressing a total of 42 cytokines, including the clinical parameters such as gender, and RCC subtype. Unsupervised Euclidean distance clustering and ward.D2 linkage methods were used. Like the RCC tumors, the healthy adjacent tissue samples were grouped using three main clusters according to the high (hi), intermediate (int) and low (lo) cytokine expression profiles. No differences were observed between the clinical parameters. NAs refer to outlier samples excluded from the analysis or with missing clinical data.
2. Correlation plot using Spearman rank correlation across the healthy adjacent renal tissue sample cytokine profiles. Statistically significant cytokines with a false discovery rate (FDR) < 0.05 are shown. Strong positive correlations were observed across most of the healthy sample cytokine expressions. Although IL-8 did not show any correlation in the tumor samples, negative correlations were observed between IL-8 and a few cytokines (IL-3, b-NGF and VEGF).

**Figure S4**

1. Scatterplots showing Spearman’s correlation between the expression of various cytokines: (i) MIG, (ii) IL-16 and (iii) IL-1Ra and NK cell abundance.
2. Boxplots showing expressions between (i) IP-10 (p=0.2), (ii) IL-16 (p=0.1), (iii) IL-1Ra (p=0.2) and Dominance (CD3+ T cell or NK cell dominant tumors).