Title: Mapping Immune Landscape in Clear Cell Renal Carcinoma by Single-Cell Genomics

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**Abstract**:

Human clear cell renal cell carcinoma (ccRCC) is one of the most immunologically distinct tumor types due to high levels of tumor-infiltrating immune cells including T cells, yet not every patient responds to immunotherapy. Interestingly, in contrast to other cancers, infiltration with cytotoxic CD8+ T cells is associated with poorer overall survival in ccRCC, suggesting that sub-populations of CD8+ and other immune cells may underlie this observation. To characterize the tumor immune microenvironment of ccRCC, we applied single-cell-RNA sequencing (SCRS) along with T-cell-receptor (TCR) sequencing to map the transcriptomic heterogeneity of 25,688 individual CD45+ lymphoid and myeloid cells in matched tumor and blood from patients with ccRCC. Will need to update based on new findings. This report represents the first such characterization of the ccRCC immune landscape using scRNA-seq. With further characterization and functional validation, these findings may identify novel sub-populations of immune cells amenable to therapeutic intervention.

**Introduction**

Clear cell renal cell carcinoma (ccRCC) is the most common type of renal cell carcinoma arising from epithelial cells of the proximal tubule of the kidney, comprising more than 70% of all renal cancers (1). ccRCC represents an immune sensitive tumor type well known for early advances in systemic immunotherapy using T cell proliferation cytokine IL-2 and interferon (IFN) -ɑ2b therapy (2). Recent novel immunotherapies targeting T cell checkpoints as standard of care has transformed the treatment paradigm of ccRCC (3,4). However, a substantial subset of renal cancer patients still do not respond to these therapies and patients who initially do can eventually progress (5,6). Cytotoxic tumor-infiltrating lymphocytes (TILs), in particular CD8+ T cells are key effectors of the adaptive anti-tumor immune response (7) and abundance of CD8+ T cells in solid cancers is generally associated with better survival in cancer patients (8–10). However, in RCC, immune cell abundance is inversely correlated with survival, specifically TILs (11–14). Biomarker analysis results from recent clinical trials comparing PD-1 blockade versus anti-angiogenic inhibitors and combination therapies in treatment-naïve ccRCC patients also supported the negative prognostic significance of T cell infiltrate in the absence of immunotherapy (15,16). Other abundant immune players in the ccRCC tumor microenvironment include monocytes, dendritic cells and tumor-associated macrophages (TAMs) (17) which are now being harnessed for discovery of novel gene programs but remain far less studied than T cells.

Quantifying and inferring immune cell abundance from transcriptional analysis of primary or metastasized bulk tumor samples is inadequate to provide a clear picture of the immune cell types (18,19). While these studies are suggestive, they lack single cell resolution for characterizing heterogeneous cell subpopulations that ultimately shape anti-tumor response, as has been demonstrated in breast cancer and melanoma (20,21). Single-cell methodologies including flow cytometry, immunohistochemistry, and mass cytometry (13,17,22) have revealed immune cell states in ccRCC but only as discrete phenotypes when in vivo they typically display diverse spectrum of differentiation or activation states. Also, these methods require use of antibody panels targeting known immune cell components, and by design are not capable of identifying novel sub-populations of cells. SCRS has enabled comprehensive characterization of heterogeneous lymphoid and myeloid immune cells in several cancers (23–26), providing an unbiased approach to profiling cells and enabling molecular classification of different subpopulations and identification of novel gene programs. Transcriptome mapping of T lymphocytes coupled with TCR sequencing allows additional measurement of clonal T cell response to cancer at an unprecedented depth (27,28).

Here, we report the single-cell mRNA profiling of the immune landscape in ccRCC mapping 25,688 of immune single cells (5’ gene expression and recombined V(D)J region of the T cell receptor) in matched samples of tumor and peripheral blood isolated from three treatment-naïve ccRCC patients. To these cells, we integrated an additional, 11,367 immune cells isolated from peripheral blood and renal parenchyma, providing controls to evaluate tumor-specific transcriptional and clonal changes in immune populations at the single-cell level. Analysis of tumor-infiltrating T cells demonstrated distinct expression changes compared to peripheral blood. Clonal structure of the T cells differed, with marked expansion seen in CD8+ T cells, but not CD4+ T cells and was associated with transcriptional patterning revealed by cell trajectory analysis. In myleloid cells, we observed an overall increase in macrophage populations with mixed polarization across patients. Will need to update with results. This represents the first such report of the immune landscape of ccRCC using SCRS for both transcriptional and clonal assessment.

**Results**

*Single-cell expression profiling of immune cells in ccRCC.*

In order to define the immune microenvironment of human ccRCC, we obtained tumor and peripheral blood specimen of three treatment-naïve ccRCC patients and subject flow-sorted lymphoid and myeloid cells to SCRS. The general workflow for isolation and sequencing is available in Supplemental Figure 1. To these samples, we added immune cells from peripheral blood and normal renal parenchyma (21) to obtain an integrated UMAP projection of 22 clusters across 37,055 primary immune cells (Figure 1A). Across the three tissues, peripheral blood (n=21,160), tumor (n=12,239) and normal kidney (n=3,556), we a number of clusters with similar gene expression notably in Clusters 0, 1, 3 and 7 (Figure 1B). Despite the integration of sequencing runs to reduce tissue-type divergence, each tissue type had enrichment for clusters: peripheral blood formed the majority of Cluster 2, tumor tissues were enriched for Clusters 14, 17, 18, and 19, and normal kidney was enriched for Cluster 11. Using gene expression, we assigned cell lineages to each cluster using a three method approach: 1) examining expressions of canonical markers for T cells (*CD3E*, *CD8A*, *CD4*, and *IL7R* or CD127), B cells (*CD19* and *MS4A1*), myeloid cells (*CD14* and *FCGR3A* or CD16) and natural killer (NK) cells (*KLRD1* and *NKG7*) (Figure 1C), 2) correlations with pure-cell gene signatures derived from ENCODE (29) (Figure 1D), and 3) assigning clonotypes based on the TCR sequencing. Based on these approaches we annotated clusters as monocytes (Clusters 0, 5, 11, 12, and 16), CD4+ T Cells (Clusters 4, 6, 10, 13, 15, and 20), CD8+ T cells (Clusters 1, 8, 9 and 17), NK cells (Clusters 3 and 7), B cells (Cluster 2), macrophages (Mφ, Cluster 14) and dendritic cells (DC, Clusters 18 and 19) (Figure 1E). Based on these annotations, we also examined the relative proportion of cell types comprising the sequencing runs by tissue type (Figure 3E). We observed a decrease in CD4+ T cells and B cells comparing peripheral blood to normal kidney tissue or tumor (Figure 1E). Conversely and as expected, we also found an increase in CD8+ T cells and Mφ in ccRCC versus peripheral blood (Figure 1E).

*CD8+ T cells in ccRCC tumors exhibit a transcriptional continuum with distinct populations*

The presence of CD8+ T cells in the tumor microenvironment is recognized as key effectors in the anti-tumor immune response (30) and have been associated in with response to immunotherapy (31). Sub-clustering of CD8+ T cells revealed 8 distinct clusters (Figure 3A) with relative tissue-specific distribution (Figure 3B). To understand the distribution of these new CD8+ clusters along the UMAP, we first examined the relative percent of single-cells represented in each cluster by tissue type. Tissue-infiltrating CD8+ T cells (both tumor and normal kidney) comprised the majority of CD8\_0, CD8\_1, CD8\_3, CD8\_5, CD8\_6 and CD8\_7. Only Clusters CD8\_2 and CD8\_4 had increased relative levels of peripheral blood cells (Figure 3B). Going from right to left across the x-axis of the UMAP there is a change in tissue-specific contribution starting from peripheral blood (right) to kidney (middle) to increasing levels of ccRCC tumor CD8+ T cells (left) and may represent the process of tissue infiltration itself. Within SCRS literature, these is a concern for variations in cell cycle leading to increased heterogeneity or obscure subpopulations (32), however proliferation of CD8+ T cells is an important surrogate markers of anti-tumor immune response (cite). We next examined the variation in proliferative gene signatures, finding a similar distribution to the tissue-type with increasing cells in S or G2M phases from right to left, peaking with Cluster CD8\_6 (Figure 3C).

In order to better characterize the CD8+ clusters, we next used canonical and differential T cells markers to examine gene expression differences along the UMAP (Figure 3D) with several patterns. The first pattern was the discovery of a naïve *CCR7*+ *SELL*+ *TCF7*+ being seen in CD8\_4 (Figure 3D). Looking for effector CD8+ T cells, we next observed two populations of *IFNG*+ *PRF1*+ T cells, principally in CD8\_1 and CD8\_0 (Figure 3D). The latter also expressed negative immune checkpoint, such as *CTLA4*, *HAVCR2*, *PDCD1*, and *TIGIT* (Figure 3D). These negative immune checkpoints were expressed at more moderate levels in both CD8\_5 and CD8\_6, however, CD8\_6 exclusively expressed a number of proliferation markers, such as *CDK1*, *MKI67*, *STMN1*, and *TOP2A* (Figure 2D). In order to examine gene expression patterns above single or selected genes, we used slingshot (33) to building minimum spanning trees between clusters, generating curves based on the most varied genes (Figure 3E). We identified 5 distinct curves (labeled B1 to B5) with the origin in the *CCR7*+ *SELL*+ *TCF7*+ CD8\_4. With the exception of B1 extending into CD8\_2, the remining curves graphed along a similar trajectory with a common node of CD8\_1 and branching at distinct clusters with increased levels of tumor-infiltrating CD8+ T cells (Figure 3E). Although based on gene expression, these curves also varied by CD8+ clonotypes based on TCR sequencing, with the root having no clonal expansion and the B3, B4 and B5 curves terminating into regions with higher levels of clonal expansion compared to B1 or B3 (Figure 2E). This clonotype relationship was also observed in specific clonotype sequences (nucleotide and TCR genes) with overlapping clonotypes seen in subclusters CD8\_0, CD8\_6, CD8\_5 and CD8\_3 (Figure 3F). In contrast, CD8\_7 had minimal overlaping clonotypes with other subclusters (Figure 3F). This relationship was seen also independent of the individual patient sequenced (Supplemental Figure X). In order to assess possible functional differences based on these branching, we performed gene set enrichment analysis (Figure 3G). As expected based on the immune checkpoint inhibitors expression, Clusters CD8\_0 and CD8\_5 showed increased terminal differentiation and exhaustion (Figure 2G). Cytolytic gene enrichment was seen in CD8\_1, the PRF1+ IFNG+ population lacking immune checkpoints (Figure 3G). The highly proliferative CD8\_6 population was enriched for metabolic activity, such as the tricarboxylic acid cycle and glycolysis, and DNA repair (Figure 2G). The B2 curve termination cluster, CD8\_2, has preferential enrichment of cytokine signaling, such as IL-2/STAT5, TGFβ, and type 1 interferons (Figure 3H). With immune checkpoint inhibitor responsiveness associated with distinct CD8+ T cell populations (21), we next examined enrichment of signatures associated with response or nonresponse to anti-PD-1 therapies (Figure 3H). Using the ordinal construction of the trajectories, we created a pseudotime variable for cells, allowing us to see the difference in the enrichment along the curves. This approach allowed us to see an overall enrichment in responsiveness to anti-PD-1 at the terminal points of B2 and midpoints of B3, B4 and B5, corresponding to cells in CD8\_1 (Figure 3H, blue lines). Likewise, we observed an overall increase in gene expression associated with no response or progression was observed at the terminal points of B3, B4, and B5 (Figure 3H, red lines). Concluding thought.

*Single-cell CD4+ T cell characterization in ccRCC finds disparate intratumoral with common endpoints.*

CD4+ T cells can target the tumor cells in various ways, either directly through cytolytic mechanisms or indirectly by modulating the tumor immune microenvironment. While CD4+ helper T cells promote T cell priming and both the effector and memory functions of CD8+ T cells, regulatory CD4+ T cells play key role for dampening responses from immune system against cancer. Subclustering of CD4+ T cells revealed 9 distinct clusters (Figure 4A), with a similar pattern to tissue distribution of predominantly peripheral blood CD4+ T cells on the right leading to tissue-infiltrating CD4+ T cells on the left (Figure 4B). The CD4\_8 was comprised solely of peripheral blood cells from the heathy donor and was eliminated from the remaining analysis. Like the CD8+ T cells, we next examined the canonical and differential T cells markers differences along the UMAP (Figure 4C). The first pattern that emerged was a naïve *CCR7*+ *SELL*+ *TCF7*+ being seen in CD4\_1 and CD4\_3 (Figure 4C). Within the tumor-infiltrating CD4\_4 cluster, we observed increased expression of the Th1 driver *TBX21* (T-bet), activation marker *LAG3* and *NR4A2* and cytokine expression (Figure 4C). Both CD4\_5 and CD4\_7 had expression of regulatory T (Tregs) cell markers (Figure 4C), with higher levels of *FOXP3*, *IL2RA* (CD25), *CTLA4* and *TNFRSF18* (GITR) in the tumor-predominant CD4\_5 (Figure 4C).

The pro- and anti-tumor role of CD4 T cell landscape within ccRCC remains relatively unexplored. Constructing the cell trajectory curves based on the CD4+ subclustering, we observed two origin points of the *CCR7*+ *SELL*+ *TCF7*+ Clusters CD4\_1 and CD4\_3 leading to a common CD4\_4 termination (Figure 4D). Unlike the other CD4+ T cells, the curve generated for Tregs was divergent, starting at CD4\_5 through CD4\_7 and into CD4\_4 (Figure 4D). This likely represents a distinct expression pattern for Tregs (shared by CD4\_5 and CD4\_7) compared to other tumor-infiltrating CD4+ T cells. In addition, compared to the CD8+ subclustering, modest clonal expansion was seen in CD4\_4 and CD4\_5 and was not a clear pattern for cell trajectory. With the common termination point for the curves at Cluster CD4\_4, we next wanted to examine if there were common markers for CD4+ T cell infiltration in ccRCC by comparing tumor-infiltering to peripheral-blood CD4+ T cells. Within tumor-infiltrating CD4+ T cell, 203 genes adjusted p-value < 0.05, log-fold change ≥ 0.5 and ∆ cell percent > 10% (Supplemental Table 4). Upregulated within the tumor-infiltrating CD4+ T cells were heat shock proteins (*HSPA1A* and *HSPA1B*), Jun and FOS constituents (*FOS*, *JUN*, *JUNB*), MHC-II molecules (HLA-DRB), and secreting molecules (*CCL5*, *GZMA*, *GZMK*) (Figure 4E). Several of the upregulated genes are shared across all the tumor-predominant CD4 Clusters (Figure 4E), however each cluster also had unique expression markers. Both CD4\_2 and CD4\_4 had increased levels of *IFNG*, but CD4\_2 was enriched for heat shock proteins, while CD4\_4 had cytotoxic component and there was expression of *CD8A*, which likely represents modest contamination of CD8+ T cells (Figure 4E). The tumor-infiltrating Tregs, CD4\_5, had high levels of *CTLA4*, GITR (*TNFRSF18*) and *TIGIT*. In addition CD4\_5 had the highly-specific expression *CCR8* and *LAYN*, corresponding to previous reports (34,35). The CD4\_6 cluster had increased expression of the IL-6 cytokine, *OSM6*, and *AREG* and *SOCS3*, downstream of interleukin signaling (Figure 4B). The differential expression closely matched the pathway analysis, with CD4\_4 enriched for cytolytic and type I interferon signaling (Figure 4F). The CD4\_5 and CD4\_7 Treg cluster had preferential enrichment for metabolic pathways, with high levels of terminal differentiation in tumor-infiltrated CD4\_5 (Figure 4F). The *OSM*-high CD4\_6 was enriched for IL-6/JAK/STAT3 signaling and inflammatory response genes.

*Prominent infiltration of macrophages in ccRCC have transcriptional divergence.*

With the previous observation of an overall increase in macrophages and decreased monocytes in integrated UMAP (Figure 1E), we next focused on differential analyses of the myeloid populations (Figure 5A). Across monocytes, macrophages and dendritic cells, subclustering found 20 distinct clusters (Figure 5A). Tissue-specific distribution was observed, with the majority tumor-infiltrating myeloid cells in subclusters 0, 3, 7, 8 and 15 (Figure 5B). In contrast, both normal kidney parenchyma and peripheral blood were comprised of a majority of monocytic subclusters (Figure 5B). Populations were assigned using canonical markers and in addition to the previously described singleR approach with macrophage subclusters (0, 3, 7, 13 and 14) identified using markers such as *CD1C*, *CLECL10A* (CD301), *FCER1A*, and *MSR1* (Figure 5C). In total, we observed a decreased the proportion in CD14+ monocytes in tissue-infiltrating myeloid cells compared to peripheral blood and an increase in macrophages (Figure 5D). Normal renal parenchyma had a variable increased in CD14- CD16- monocytes, which was not significant. As previously seen, we found a small number of DC (subclusters 15, 16, and 19) with distinct expression profiles associated with conventional DC 1, plasmacytoid DC, and monocyte-derived DCs, respectively (Supplemental Figure X).

Next we isolated the five macrophage subclusters, relabeling them tumor-associated macrophage 1 (TAM\_1), TAM\_2, TAM\_3, resident macrophage (rM) and peripheral macrophage (pM) based on the relative percent of cells derived from the respective tissue (Figure 3E). Although similar expression, these five clusters had distinct expression patterns. For example, the X+ X+ TAM\_1 expressed increased levels of chemokines and cytokines, like *CCL3*, *CCL4*, *CXCL2*, and *IL10*; X+ X+ TAM\_2 subcluster expressed the apolipoprotein gene *APOE*, lysosomal lipase (*LIPA*), and ferroportin (*SLC40A1*); and X+ X TAM\_3 had high levels of *CD1C*, *IL1R2*, and Langerhin (*CD207*), a marker of the skin-resident Langerhan cells (Figure 5F). The pM subcluster had the highest level of the cell adhesion molecules *CLEC10A*, *SELL* (CD62L), and *ITGB7*, which can dimerize with *ITGA4* (CD49d) or *ITGAE* (CD103). Like the CD8+ T cells, we built cell trajectories based on varied genes find two distinct curves converging into TAM\_3 and pM (Figure 5G). In order to assess potential functional differences for the macrophages, we performed gene set enrichment analysis (Figure 5H). As previously observed in single-cell data (cite here), no subclusters was distinctly M1 or M2 polarized. For example, TAM\_1 had enrichment for gene sets commonly associated with the M2 macrophage compartment, such has angiogenesis and the production of lipid mediators, while also having the highest levels of TNFɑ signaling enrichment, a common M1 macrophage characteristic. Across the three TAM subclusters, modest enrichment in both type 1 and type 2 interferon signaling was observed (Figure 5H). The non-TAM subclusters, rM and pM had relatively lower levels of enrichment with the exception of proinflammatory signaling and glycolysis, respectively (Figure 5H). Concluding thought

**Discussion**

With the improved understanding on how immunotherapies work, the phenotypic and functional profile of immune cells in the tumor microenvironment is now well known to influence prognosis and disease outcome. Comprehensive knowledge of gene expression signatures to fully understand the roles of specific immune populations in cancer is of high biological relevance; not only in identifying dysregulated immune determinants of cancer progression but also as a useful tool for the selection of patients, evaluating the likelihood of benefit from immunotherapy and further identifying clinically significant subpopulations.

Despite immunotherapy being a mainstay of treatment for advanced and treatment-naive ccRCC (3,36,37), ccRCC tumors have numerous counterintuitive immune findings compared with other immunotherapy-responsive tumors (38). For example, unlike other tumors that respond to immune checkpoint blockade, ccRCC has a relatively low tumor mutational load, which is thought to drive T-cell infiltration (18,39), and is not associated with response to anti-PD-1 therapy (14). Despite this low mutational burden, ccRCC has the highest T cell infiltration score among tumor types within the TCGA (40). Similarly, therapeutic response to anti-PD-1 therapy have been correlated with HLA heterozygosity in lung cancers and melanoma (41), which does not seem to be the case for ccRCC (14). Taken together, these disparate findings suggest a more complex interrelationship of the immune compartment for ccRCC tumors. While a few recent studies have explored human ccRCC at a single-cell level (42–45), the technique has not yet been applied to tumor-infiltrating immune cells to characterize the global transcriptional immune and T cell receptor landscape along with underlying mechanisms contributing to this unique tumor environment.

T cells are recognized as key effectors of the adaptive anti-tumor immune response. Several studies have demonstrated association of these cells with an unfavorable response to therapy and poor patient survival in ccRCC (6,12). In a comprehensive study, T cells represented the dominant lymphocytic population in most ccRCC cases, B cells were rarely detected (22), consistent with our findings of increased CD4+ and CD8+ T cells (Figure 1). We find that the blood CD8+ T cells are non-heterogeneous and poorly reflect tumor-infiltrating CD8+ T cell transcriptional profiles (Figure 2A,D). Organizing the structure of the CD8+ T cell manifold, we found four distinct branches that may represented transcriptional states upon tumor-infiltration, two associated with a PD-1+ TIM-3+ exhausted subcluster, a proliferative subcluster, and a fourth with the higher levels of cytokine signaling (Figure 2E,G). The latter cluster, CD8\_7 was also unique with minimal overlap in clonotypes compared to the other tumor-infiltrating predominant subcluster. Recent single-cell analyses in melanoma showed CD8+ T cells with lower activation and exhausted expression patterns were associated with improved anti-PD-1 responses (21). These responsive T cells had had minimal shared clonotypes, similar to CD8\_7 (21). Other studies have found the ccRCC tumors polyclonal CD8+ T cells with an “immune-regulated” phenotype and lower cytotoxicity compared to tumors with oligoclonal CD8+ T cell (46). Recently, CD39, upregulated in CD8\_0 and CD8\_6, was linked with a PD-1+ TIM-3+ CD8+ T cell subset, that was predictive of worse overall survival for ccRCC patients (47). However, patients with the a CD39+ PD-1+ TIM-3+ CD8+ T cells also had improved responses to the multi-tyrosine kinase inhibitor, sunitinib, suggesting that evaluation of exhausted phenotype for CD8+ T cells may help in clinical decision making or therapy selection (47). This similar exhausted CD8+ T cell phenotype have been associated with advanced histological features and increased risk of disease progression (40,46,47), increased dysfunctional DC (6), and increased macrophage populations (17).

Controversy surrounds the role of myeloid populations in ccRCC tumor prognosis and progression. This may, in part, be a result of transcriptional and phenotypic plasticity of tumor-infiltrating myeloid cells (17,24). Our analysis demonstrated distinct CD16+ myeloid population derived within tumor compared to peripheral blood or normal renal parenchyma and an overall increased in tumor-associated macrophages (Figure 5A, D). M2 markers, like CD163 and CD204, has been associated with poor overall survival (17,48) and were the highest in the TAM\_1 and TAM\_2 subclusters (Figure 5G). This is despite no clear identification of canonical M1 or M2 macrophages subclusters (Figure 5I). The increased immunogenicity of ccRCC has been tied to upregulation of the antigen presenting machinery expression through MHC-I (40). What is most APC like? Although several distinct DC populations were detected and there was a trend for increase in conventional DC1 subsets (subcluster 15) within ccRCC, further analysis was limited by the total number of DCs isolated.

Need to add more on the topics of subsequent figures

In addition to our observations and signature development, we provide a valuable data resource in hope to further gain insight into biomarkers and therapeutic targets in ccRCC.

**Methods**

*Subject Details and Tissue Collection*

Fresh blood and primary clear cell renal cell carcinoma (ccRCC) samples were obtained from the University of Iowa Tissue Procurement Core and GUMER repository through the Holden Comprehensive Cancer Center from subjects providing written consent approved by the University of Iowa ethics board committee. The patients were males with an age range of 67 to 74 years old. Tumor grades were histologically determined by a pathologist. Primary tumor stage for Patient 1 and Patient 2 were reported as pT1b without extension, while Patient 3 was reported as pT3a with vascular invasion into renal vein. Three ccRCC tumor specimens paired with individual blood samples were used in the study. Will need IRB FOR publication

*Tumor Dissociation and Isolation of Mononuclear Cells*

Renal tumor samples were dissociated into single cells by a semi-automated combined mechanical/enzymatic process. The tumor tissue was cut into pieces of (2-3mm) in size and transferred to C Tubes (Miltenyi Biotech, Bergisch Gladbach, Germany) containing a mix of Enzymes H, R and A (Tumor Dissociation Kit, human; Miltenyi Biotech). Mechanical dissociation was accomplished by performing three consecutive automated steps on the gentleMACS Dissociator (h\_tumor\_01, h\_tumor\_02 and h\_tumor\_03). To allow for enzymatic digestion, the C tube was rotated continuously for 30 min at 37°C, after the first and second mechanical dissociation step (49). Cells from fresh tumor specimens were incubated with FcR blocking reagent (StemCell Technologies, Vancouver, Canada) for 10 min at 40C and labelled with 1ug/ml of the FITC anti-human CD45 antibody (BioLegend, San Diego, CA) per 107 cells for 20 min at 40C. CD45+ cells were isolated using the EasySepTM FITC Positive Selection Kit (StemCell Technologies). Alternatively, mononuclear cells (MNCs) from whole peripheral blood of paired subjects were isolated using SepMate Tubes (StemCell Technologies) by density gradient centrifugation. Cells were then viably frozen in 5% DMSO in RPMI complemented with 95% FBS. Cryopreserved cells were resuscitated for flow cytometry analyses by rapid thawing and slow dilution.

*Cell Sorting for Single-Cell RNA sequencing*

Viable immune (CD45+ Hoechst-) single cell suspensions generated from three ccRCC tumor samples and blood were FACS sorted on a FACS ARIA sorter (BD Biosciences) for lymphoid and myeloid cells (Ratio 3:1). The cells were sorted into ice cold Dulbecco’s PBS + 0.04% non-acetylated BSA (New England BioLabs, Ipswitch, MA). Sorted cells were then counted and assessed viability MoxiGoII counter (Orflo Technologies, Ketchum, ID) ensuring that cells were re-suspended at 1000 cells/ul with a viability >90%.

Library Preparation, Single-Cell 5’ and TCR Sequencing

Single-cell library preparation was carried out as per the 10X Genomics Chromium Single Cell 5' Library and Gel Bead Kit v2 #1000014 (10x Genomics, Pleasanton, CA). Cell suspensions were loaded onto a Chromium Single-Cell Chip along with the reverse transcription (RT) master mix and single cell 5′ gel beads, aiming for 7,500 cells per channel. Following generation of single-cell gel bead-in-emulsions (GEMs), reverse transcription was performed using a C1000 Touch Thermal Cycler (Bio-Rad Laboratories, Hercules, CA); 13 cycles were used for cDNA amplification. Amplified cDNA was purified using SPRIselect beads (Beckman Coulter, Lane Cove, NSW, Australia) as per the manufacturer’s recommended parameters. Post-cDNA amplification reaction QC and quantification was performed on the Agilent 2100 Bioanalyzer using the DNA High Sensitivity chip. For input into the gene expression library construction, 50ng cDNA and 14 cycles was used. To obtain TCR repertoire profile, VDJ enrichment was carried out as per the Chromium Single Cell V(D)J Enrichment Kit, Human T Cell #1000005 (10x Genomics) using the same input sample. Sequencing libraries were generated with unique sample indices (SI) for each sample and quantified. Libraries were sequenced on an Illumina HiSeq 4000 using a 150-pair-end sequencing kit. Gene expression FASTQ files were aligned to the human genome (GRCh38) using the CellRanger v2.2 pipeline, while clonotype sequencing was aligned to the vdj\_GRCh38\_alts\_ensembl genome build provided by the manufacturer.

*Incorporation of other SCRS data sets*

SCRS and TCR sequencing data processed using Cell Ranger v2.2 for healthy donor peripheral blood immune cells were acquired from the 10x Genomics website on 6/20/2020. Filtered gene matrix and contig annotations were used in the incorporation of the uniform manifold approximation and project (UMAP). Total number of cells from healthy peripheral blood control were 7,726. SCRS of normal immune populations in the kidney were derived previously published data (42). Gene expression matrices were downloaded from the EGAS00001002325 and filtered for normal renal parenchyma cells using the provided cell manifest for the samples RCC1, RCC2, and RCC3. These processed using the procedure as described above to form a UMAP. Immune cells were identified using canonical markers for lineage and were then isolated. Isolated immune cells for normal renal parenchyma were: RCC1 (n=1,011), RCC2 (n=888), and RCC3 (n=1,757).

*SCRS Integration*

Initial processing of cells isolated from ccRCC patients; Patient 1 (n=10,694), Patient 2 (n=5,174) and Patient 3 (n=9,805) were processed and integrated with the above samples using the Seurat R package (v3.0.2) (50,51). Samples were normalized using the *SCTtransform* approach (52) with default settings. Preparation for integration used 3,000 anchor features and *PrepSCTIntegration*. The integration of sequencing runs occurred with the SCT-transformed data. The dimensional reduction to form the UMAP utilized the top 30 calculated dimensions and a resolution of 0.7. Data characteristics by sequencing run can be found in Supplemental Table 1. Cell type subclustering used the SCTtransform approach as described above, but integrating the data across samples instead of individual sequencing runs. The adjusted dimensional inputs for the subclustering analysis can be found in Supplemental Table 2.

*SCRS Data Analysis and Visualizations*

The schex R package (v1.1.5) was used to visualize mRNA expression of lineage-specific or highly differential markers by converting the UMAP manifold into hexbin quantifications of the proportion of single-cells with the indicated gene expressed. Default bins across all cells was 80 and 40 for subcluster analyses, unless otherwise indicated in the figure legend. Differential gene expression utilized the Wilcoxon rank sum test on count-level mRNA data. For differential gene expression across clusters or subclusters, *FindAllMarkers* function in the Seurat package using the log-fold change threshold > 0.25, minimum group percentage = 10%, and the pseudocount = 0.1. Differential comparisons between condition utilized the *FindMarkers* function in Seurat, without filtering and a pseudocount = 0.1. Multiple hypothesis correction was reported using the Bonferroni method. Cell cycle regression was performed in Seurat using the *CellCycleScoring* function and genes derived from Nestorowa et alia (53). Genes were isolated by calling *cc.genes.updated.2019* in R.

Cell type identification utilized the SingleR (v1.0.1) R package (54) with correlations of the single-cell expression values with transcriptional profiles from pure cell populations in the ENCODE (29). In addition to correlations, canonical markers for cell lineages (Supplemental Table 3) and corresponding TCR sequences were used. Gene set enrichment analysis was performed using the escape R package (v0.99.0). Gene sets were derived from the Hallmark library of the Molecular Signature Database and from previous publications (21,24). Enrichment for anti-PD-1 therapy response was derived from Sade-Feldmen et alia to develop gene signatures for the CD8\_B (nonresponsive) and CD8\_G (responsive) single-cell populations(21). Differential enrichment analysis was performed using the *getSignificance* function in escape that is based on the limma R package linear fit model. TCR analysis utilized our previously described scRepertoire R package (v0.99.3) (55) with clonotype being defined as the combination of the gene components of the VDJ and the nucleotide sequence for both chains and assigned on the integrated Seurat object. Cell trajectory analysis used the slingshot (v1.6.0) R package (33) with default settings for the *slingshot* function and using the embedding from the subclustering for each cell type. Inferred start and end clusters were applied in the CD8+ T cell trajectory based on gene expression markers. Ranked importance of genes were calculated using the top 300 variable genes and rsample (v0.0.9) and tidymodels (v0.1.0) R packages were used to generate random forest model based on a training data set of 75% of the cells. The *rand\_forest* function in the parsnip (v0.1.1) R package was used, with mtry set to 200, trees to 1400, and minimum number of data points in a node equal to 15 across all cell types. The code for all analysis is available at <https://github.com/ncborcherding/ccRCC>.

Mass Cytometry Analysis

Flow cytometry standard files were downloaded for 78 samples utilizing a previously-defined tumor-associated macrophage panel (17). Subsequent loading and analyses of the data was based on the accompanying published methods (17). These files were loaded into R using the flowCore (v2.0.1) R package. Protein signal was arcsinh transformed using a cofactor of 5, filtered for previously identified myeloid cells, and up to 2,000 cells were randomly selected for each sample using the *sample* function with *set.seed* of 123. After the transformation and filtering, 127,880 myeloid cells were subjected to t-SNE based embedding using the Rtsne (v0.1.5) package using only the defined cell markers. Clusters were defined using the R implementation of the PhenoGraph algorithm (56) in the Rphenograph R package (v0.99.1) with the k set at 100. Marker expression visualization utilized a normalized intensity between 0 and 1. Further data visualization utilized ggplot2 (v3.3.1) and pheatmap (v1.0.12).

*Machine Learning Modeling*

The renal clear cell carcinoma (KIRC) log2 gene expression data from the downloaded from the University of California Santa Cruz Xena Browser and filtered for only primary tumor samples. To the expression data, updated clinical information was assigned by tumor barcode (57). Gene signatures from subcluster analysis were generated by filtering differential gene expression results for genes with > 0.5 log-fold change and 15% difference in cell expression. Training and testing sample cohorts were divided using the *sample* function with *set.seed* set to 123, splitting the data into 1:1 ratio. The caret (v6.0-86) R package was used to generate random forest models, using the repeated cross-validation method splitting the data into 10 groups and repeating a total of 16 times and recursive feature selection to optimize feature selection for 1, 5, 10, 15, and 20 features. Generated models were then used to predict survival in the testing cohort and testing parameters were then calculated. Survival analyses utilized the survival (3.1-12) and survMiner (v0.4.7) R packages. Edit if changes.

*Statistical Analysis*

Statistical Analyses were performed in R (v4.0.1). Two-sample significance testing utilized Welch’s T test, with significance testing for more than three samples utilizing one-way analysis of variance (ANOVA) with Tukey honest significance determination for correcting multiple comparisons. Two-proportion Z-tests was performed using the total number of cells in each condition as the number of trials and without a prior for proportion.

**Acknowledgments**

We thank Michael Knudson, Rita Sigmund, Joe Galbraith, Janice Cook-Granroth, Bethany Kilburg and Celeste Charchalac from University of Iowa Carver College of Medicine, Tissue Procurement Core (TPC) and Genito-Urologic Tissue Repository (GUMER) for receiving biological samples and clinical data. We thank Justin Fishbaugh, Heath Vignes and Michael Shey from the University of Iowa Flow Cytometry Facility. We thank Kevin Knudtson, Mary Boes, Garry Hauser and Mari Eyestone from the Iowa Institute of Human Genetics (IIHG) Genomics Division for planning and assisting use of Next Gen Sequencing (NGS) platforms, Diana Kolb from the IIHG Bioinformatics Division and the University of Iowa High Performance Computing (HPC) facility.

**Funding**

Funding for this project was provided by Rock ‘N’ Ride Foundation (PI: Y.Z.) and from the National Institute of Health under the R01 CA200673 (PI: W.Z.), R01 CA203834 (PI: W.Z.), K08 CA226391 (PI: R.W.J) and F30 CA206255 (PI: N.B.). The flow cytometry and sequencing **facilities are funded in part, by the National Cancer Institute of the National Institutes of Health under Award Number P30CA086862. The** FACSAria Fusion high-speed cell sorter was supported with funds from **the National Center for Research Resources of the National Institutes of Health under Award Number 1 S10 OD016199-01A1.** The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

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Supervision: YZ, WZ, RWJ

**Declaration of interests**

Dr. Russell W. Jenkins has a financial interest in XSphera Biosciences Inc., a company focused on using ex vivo profiling technology to deliver functional, precision immune-oncology solutions for patients, providers, and drug development companies. Dr. Jenkins’ interests were reviewed and are managed by Massachusetts General Hospital and Partners HealthCare in accordance with their conflict of interest policies.

**Data and materials availability:**

Quantified gene expression counts and V(D)J T cell receptor sequences for single-cell RNA sequencing are available at the Gene Expression Omnibus (GEO) at [GSE121638](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE121638). Code for the analysis and visualizations are available at <https://github.com/ncborcherding/ccRCC>

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**Figures**

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**Figure 1: Single-cell sequencing results for immune cells in ccRCC.** A. UMAP of 37,055 primary immune cells of peripheral blood, normal renal parenchyma and tumor-infiltrating ccRCC patients. **B**. Distribution of cells by tissue type, peripheral blood (blue), tumor (red), and kidney (light blue). Arrows indicated potential enriched or unique immune cells populations for tissue type. **C**. Percent of cells expressing canonical immune cell markers across the UMAP. **D**. Normalized correlation values for predicted immune cell phenotypes based on the SingleR R package for each cluster. **E**. UMAP demonstrating inferred immune cell types in ccRCC, clusters are colored by cell type and proportion of single-cell per sequencing run by tissue type. P values based on one-way ANOVA; lack of p-values equates to value > 0.05.

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**Figure 3: Single-cell CD4+ T cell characterization in ccRCC finds disparate intratumoral with common endpoints.** **A**. UMAP subclustering of CD4+ T cells (original clusters 4, 6, 10, 13, 15, and 20). **B**. UMAP distribution of single cells by tissue type with relative percent of cells by tissue in each cluster. **C**. Percent of cells expressing selected markers for myeloid and macrophage markers. **D**. Proportion of assigned cell types compared to total antigen presenting cells by tissue type. **E**. Macrophage subclusters: TAM\_1 (n=), TAM\_2 (n=), TAM\_3 (n=), pM (n=), and rM (n=) with relative percent of cells by tissue in each cluster. F. Differential expression markers for macrophage subclusters. **G**. Macrophage UMAP overlaid with slingshot-based (33) cell trajectories starting at rM and TAM\_2 and proceeding into pM. Smaller UMAP shows pseudotime created by the cell trajectories. **H**. Z-transformed normalized enrichment scores from ssGSEA for selected gene sets by subcluster.

CD4+ UMAP of subclusters (upper panel) and clonotype frequency (lower panel) overlaid with slingshot-based (33) cell trajectory starting from CD4\_1 (root 1) and CD4\_1 (root 2) with relative pseudotime for all curves calculated using slingshot. **E**. Percentage difference (∆ percent of cells) and log-fold change based on the Wilcoxon rank sum test results for differential gene expression comparing TI to PB CD4+ T cells in ccRCC patients (left panel), colored points indicate adjusted p-values < 0.05. Right panel includes top 10 markers for TI-predominant CD4+ subclusters. Size of points are relative percent of cells in cluster expressing the indicated mRNA species. **F**. Z-transformed normalized enrichment scores from ssGSEA for selected gene sets by subcluster.