A picture containing many, person, bunch, person

Description automatically generated

**Supplemental Figure 1:** Workflow for SCRS of isolated lymphoid and myeloid immune cell populations from ccRCC subjects and computational analysis. SCRS data across ccRCC and data derived from 10x Genomics and EGAS00001002325 were integrated using SCTtransform approach to form a UMAP of 37,055, acting as a basis for subclustering and further analysis by cell type.

A picture containing implement, stationary, colorful, computer

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**Supplemental Figure 2:** Top clonotypes for CD8+ T cells for each patient by proportion in each subcluster.

A picture containing sitting, table, screen, computer

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**Supplemental Figure 3: A**. UMAP subclustering of CD4+ T cells (original clusters 4, 6, 10, 13, 15, and 20). **B**. Normalized correlation values for predicted immune cell phenotypes based on the SingleR R package for selected subclusters. **C**. . Percent of cells expressing canonical immune cell markers across the UMAP.

A picture containing television, screen, monitor, sitting

Description automatically generated

**Supplemental Figure 4:** Z-transformed normalized enrichment scores from ssGSEA for MHC-related gene sets in the C5 library of the Molecular Signature Database by APC/Myeloid subcluster.