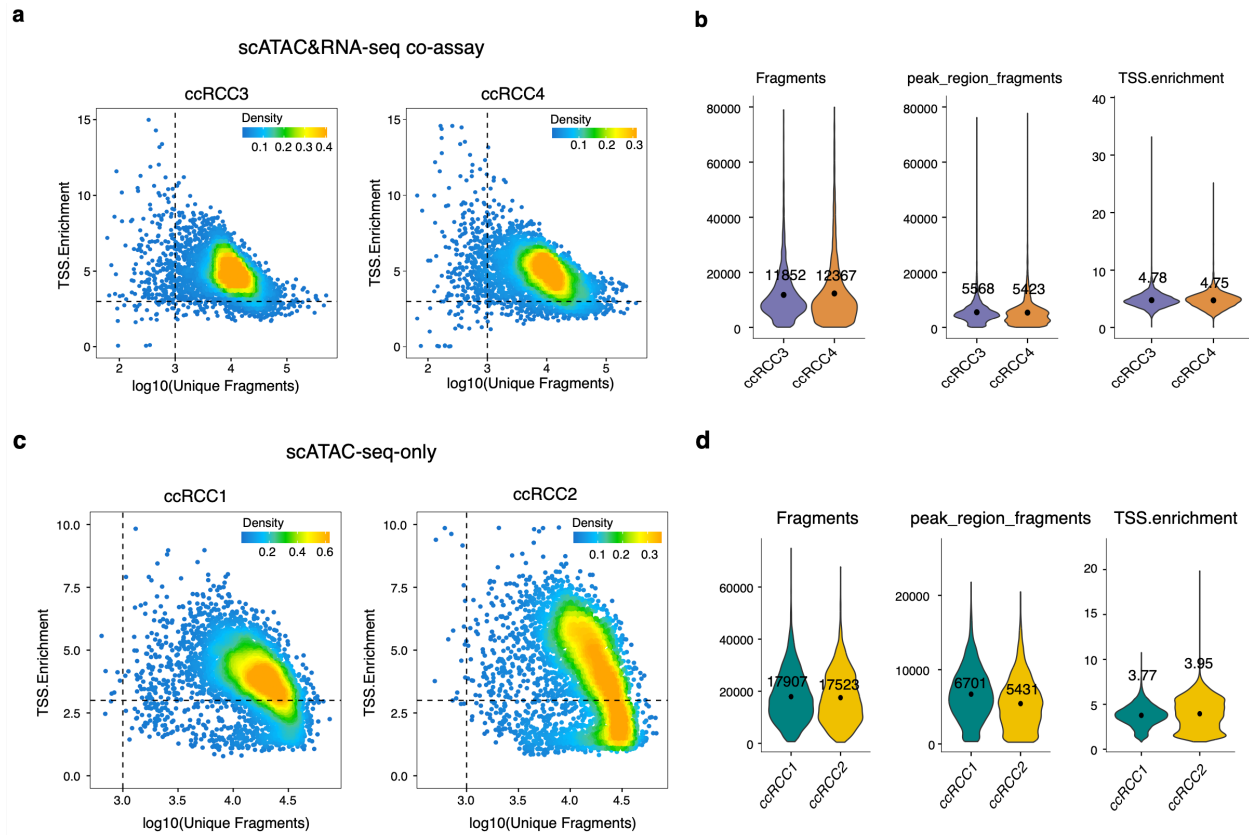
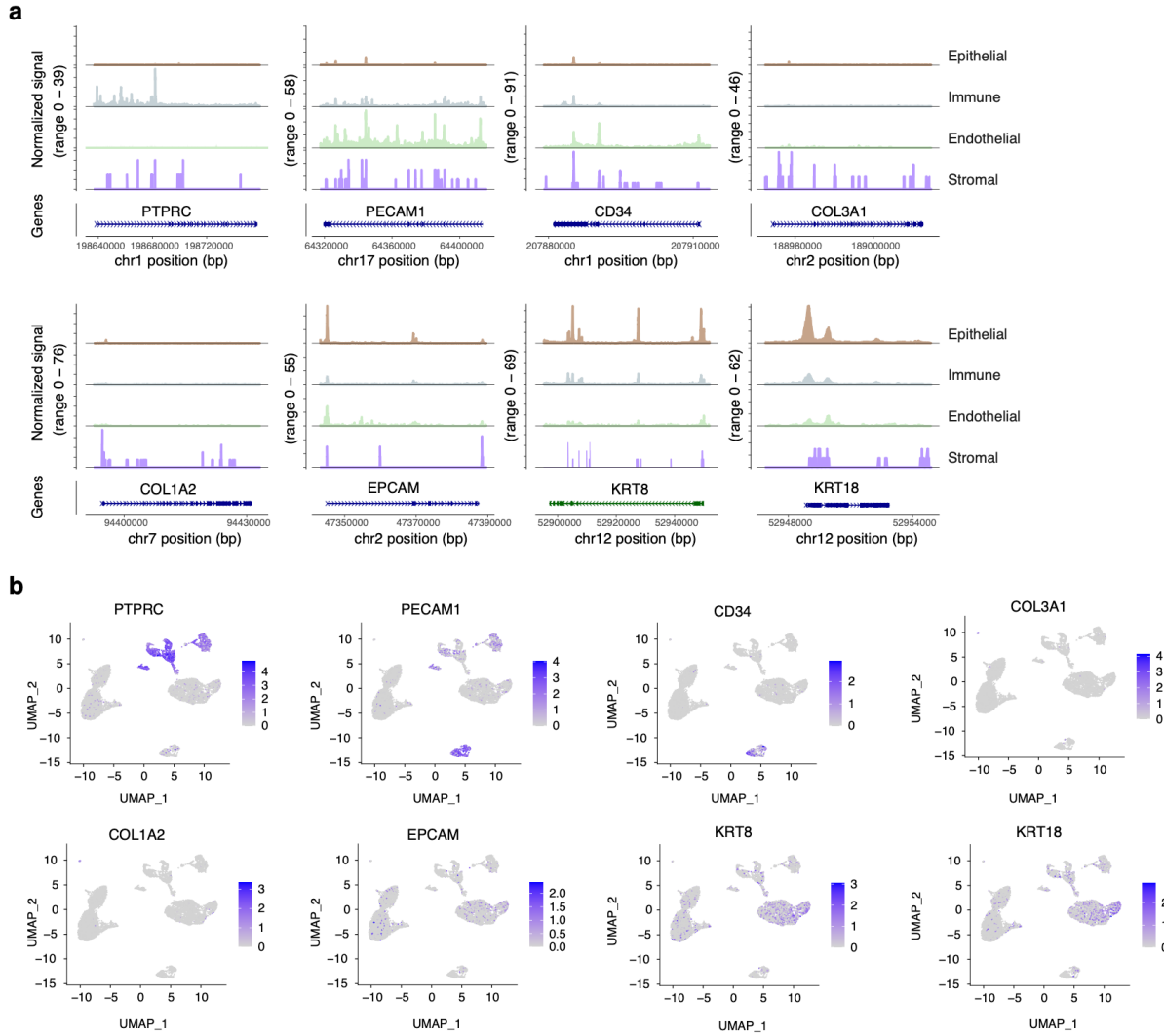


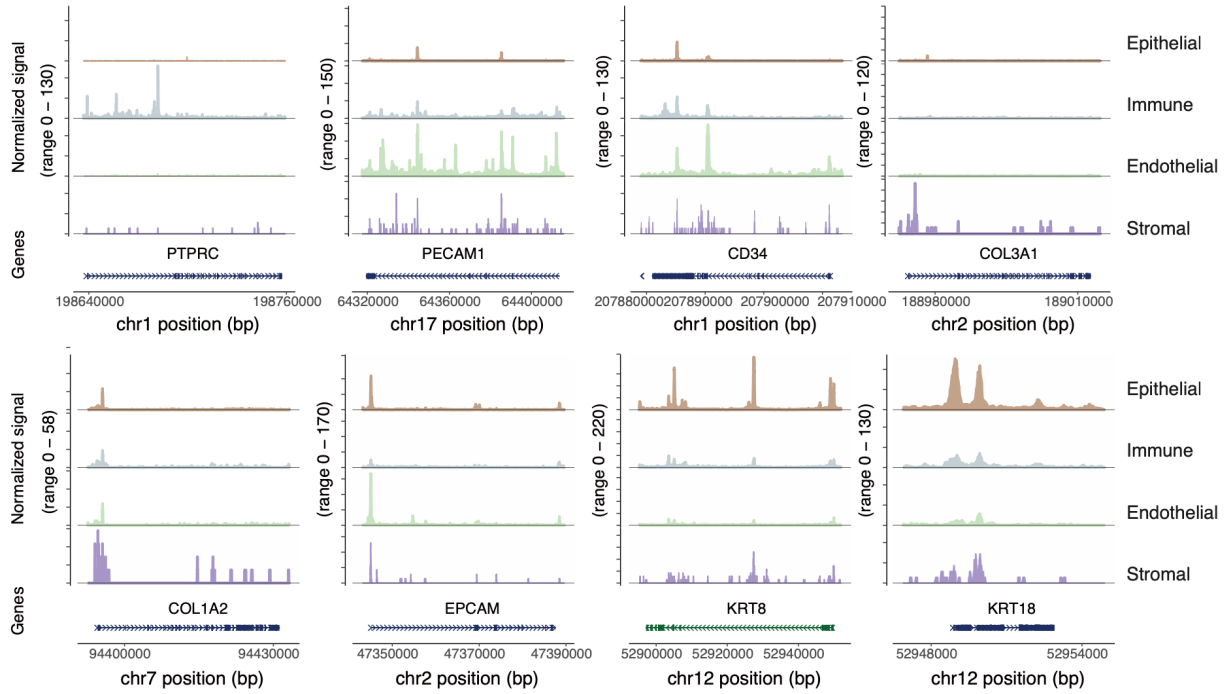
Supplementary Figures



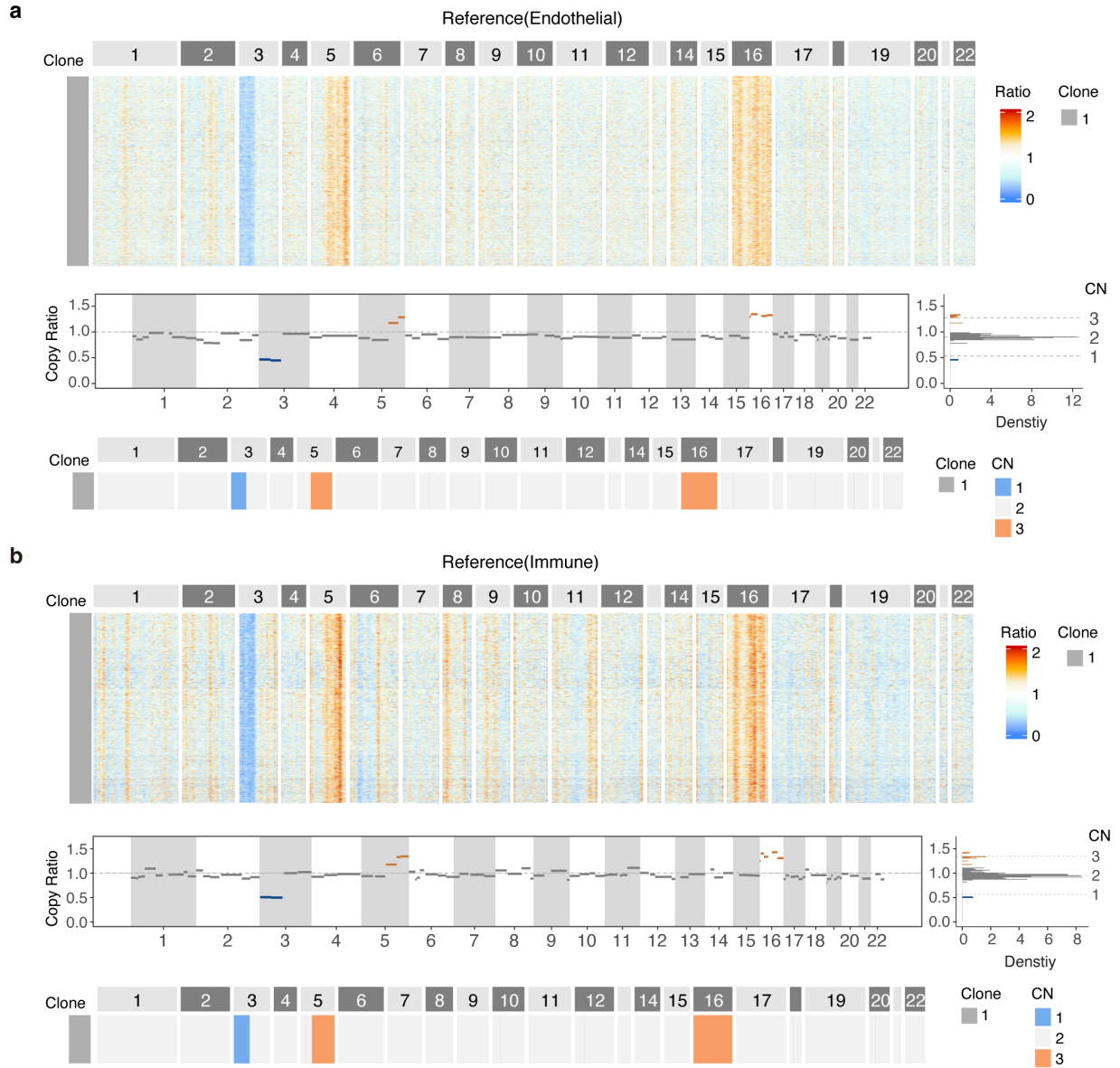
Supplementary Fig. 1 Data quality of scATAC&scRNA-seq co-assayed and scATAC-seq only data for ccRCC patients. (a) and (c) The number of unique ATAC-seq fragments in each single cell (each dot) compared with TSS enrichment of all fragments in that cell. Dashed lines represent cutoffs for filtering high-quality cells. Dots are colored by density. (b) and (d) Violin plots show the distribution of total fragment counts, the number of fragments located in peaks, and TSS enrichment values across individual samples.



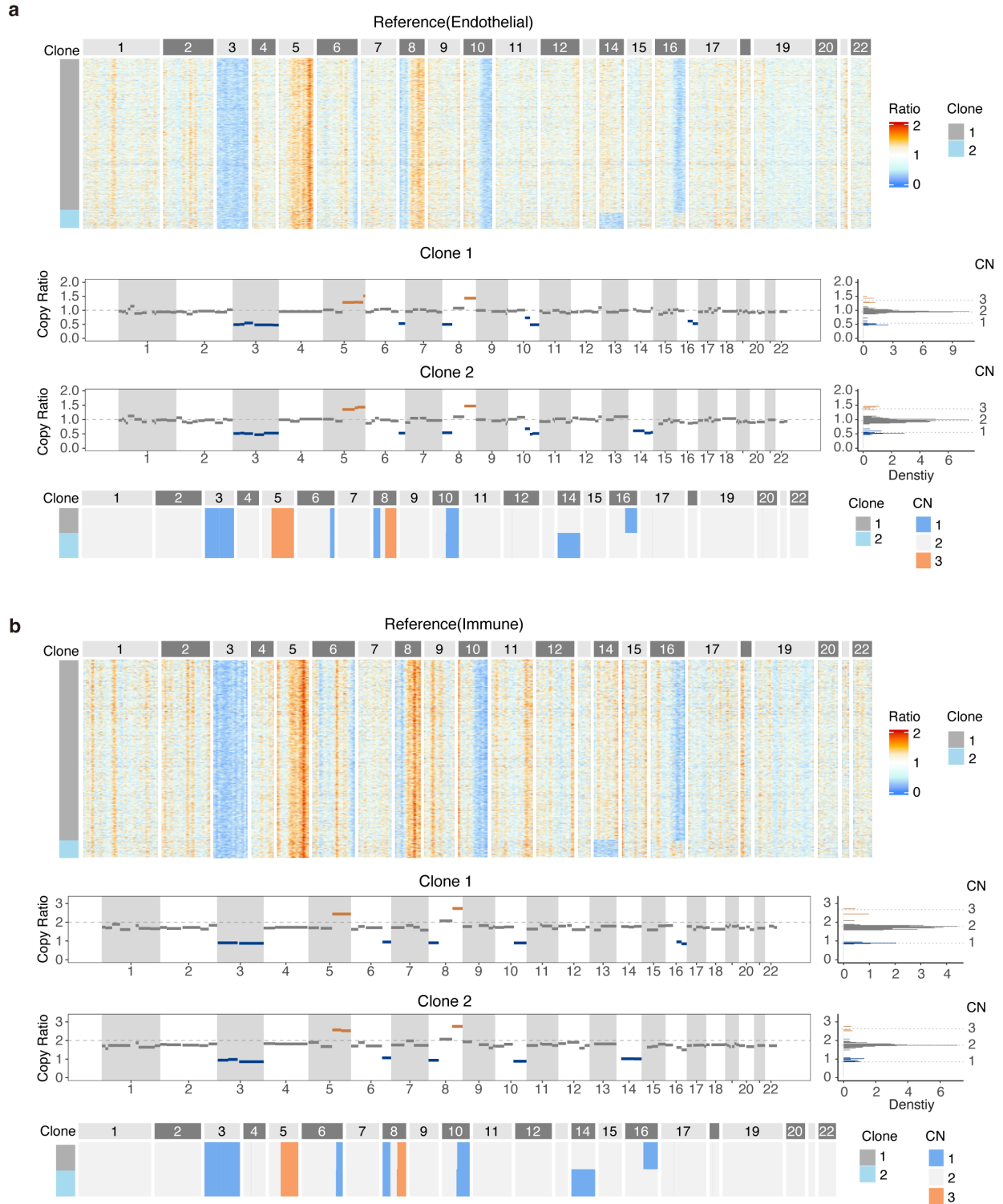
Supplementary Fig. 2 Cell annotation of scATAC&RNA-seq co-assayed data from two ccRCC patients. (a) Genome track of aggregate scATAC-seq signals across cells near the cell-type marker locus. Tracks are colored by cell type: epithelial, immune, endothelial, and stromal cells. (b) Expression levels of cell-type marker genes from scRNA-seq data.



Supplementary Fig. 3 Genome track of aggregate scATAC-seq signals across cells near the cell-type marker locus for scATAC-seq-only samples. Tracks are colored by cell type: epithelial, immune, endothelial, and stromal cells.

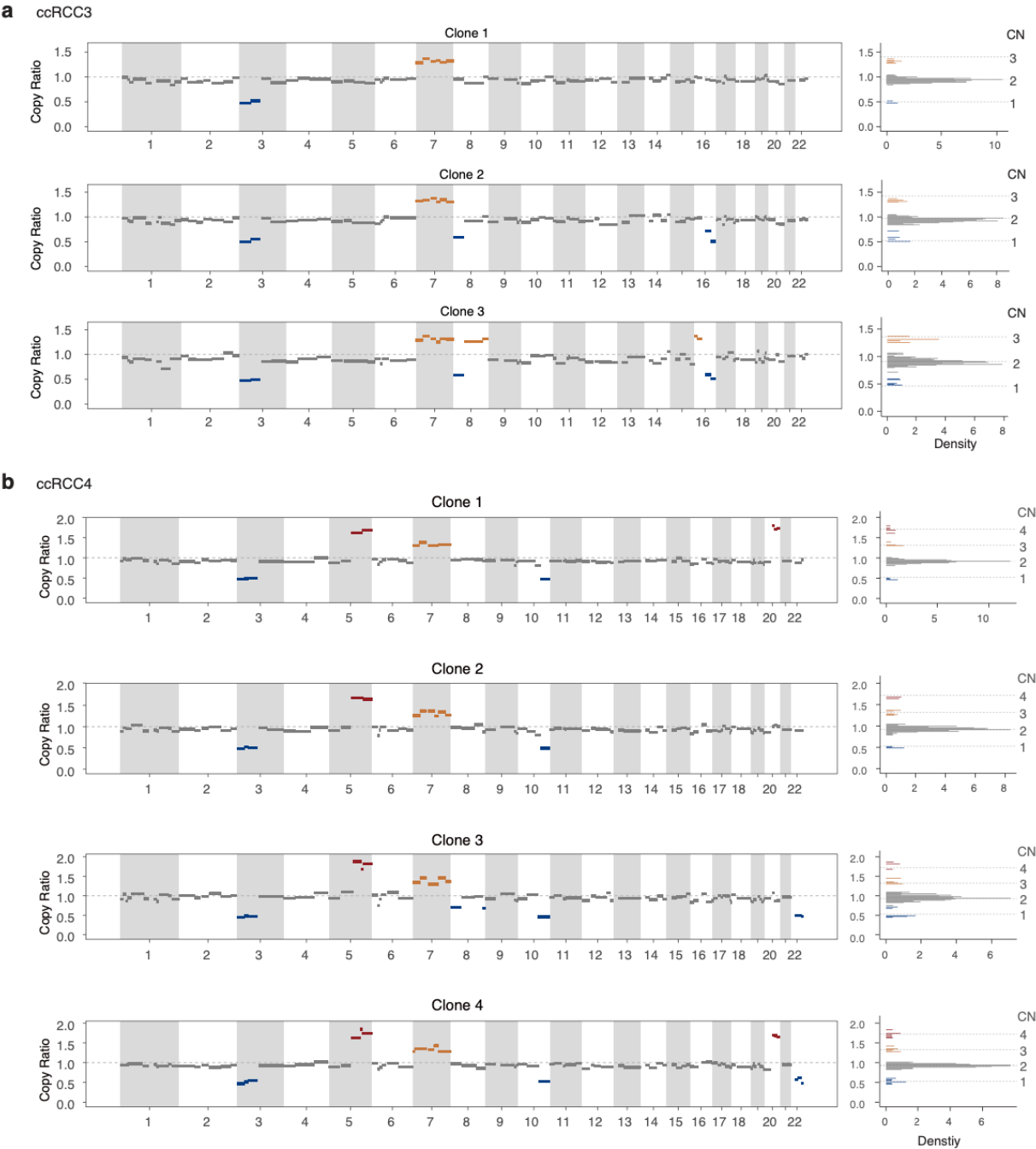


Supplementary Fig. 4 Validation of TeaCNV robustness using different reference cells in ccRCC1. Absolute CNs of epithelial cells were inferred using endothelial cells (**a**) and immune cells (**b**) as references. The panels include: a heatmap displaying the copy ratio of epithelial cells relative to the reference (top), a genome-wide segmentation of copy ratios for clones (middle left) with the corresponding copy ratio histogram (middle right), and a heatmap of inferred clonal absolute CN profiles (bottom).

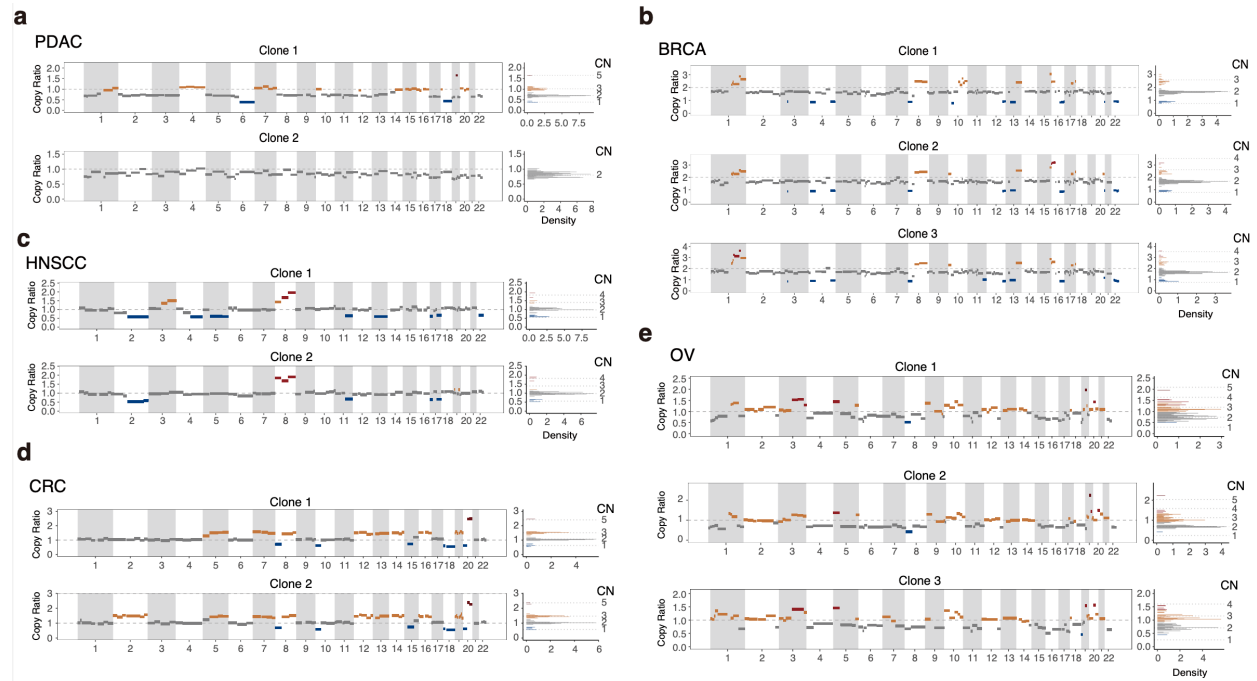


Supplementary Fig. 5 Validation of TeaCNV robustness using different reference cells in ccRCC2. Absolute CNs of epithelial cells were inferred using endothelial cells (**a**) and immune cells (**b**) as references. The panels include: a heatmap displaying the copy ratio of epithelial cells

relative to the reference (top), a genome-wide segmentation of copy ratios for clones (middle left) with the corresponding copy ratio histogram (middle right), and a heatmap of inferred clonal absolute CN profiles (bottom).



Supplementary Fig. 6 The chromosomal segmental estimation for ccRCC3 (a) and ccRCC4 (b). Relative copy number profiles of each subclone (left) and the corresponding distribution of absolute copy number states (right).



Supplementary Fig. 7 The chromosomal segmental estimation for PDAC (a), BRCA (b), HNSCC (c), CRC (d) and OV (e) samples. Relative copy number profiles of each subclone (left) and the corresponding distribution of absolute copy number states (right).