

Supplementary Information

Single-cell transcriptional profiling of clear cell renal cell carcinoma reveals a tumor associated endothelial tip cell phenotype

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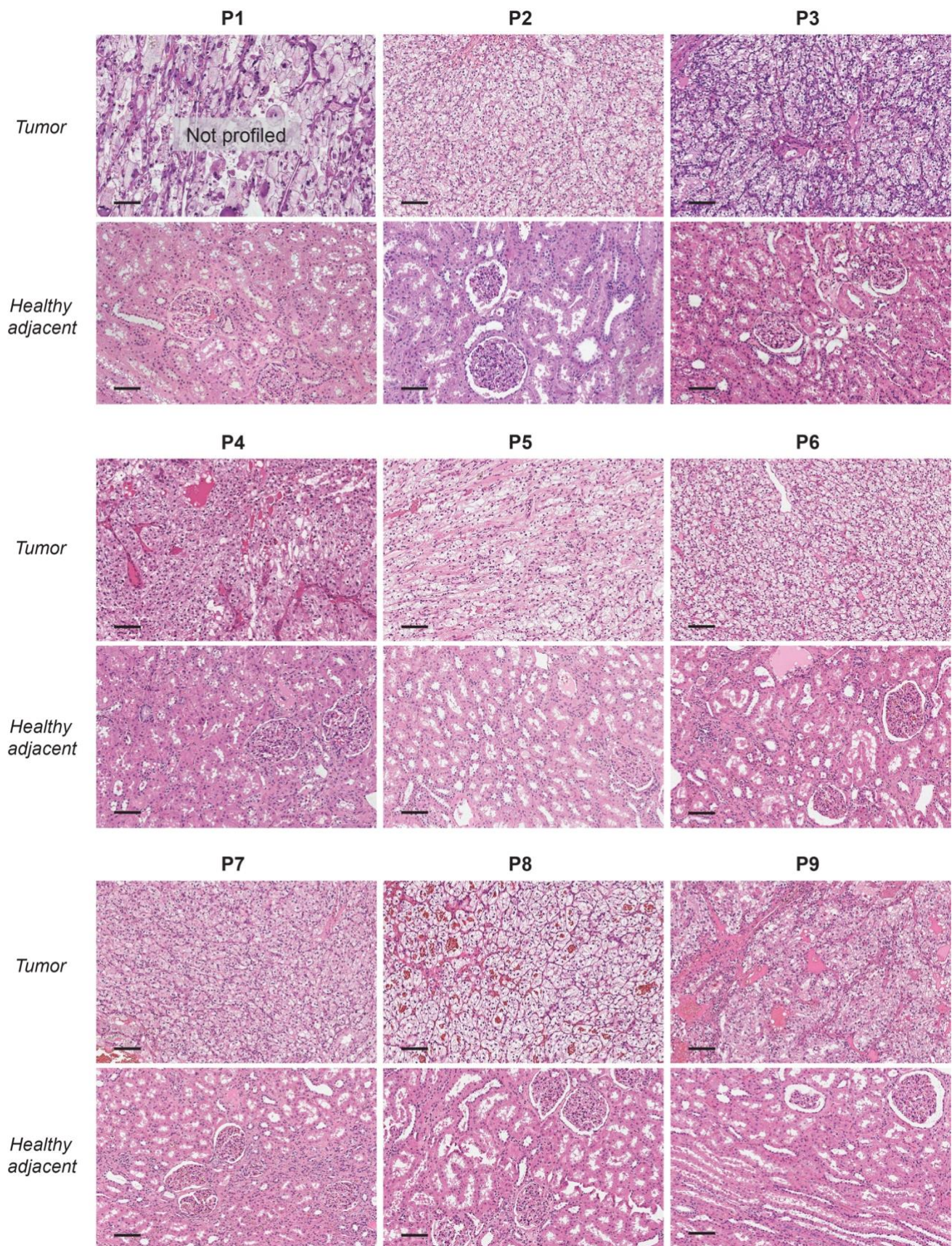
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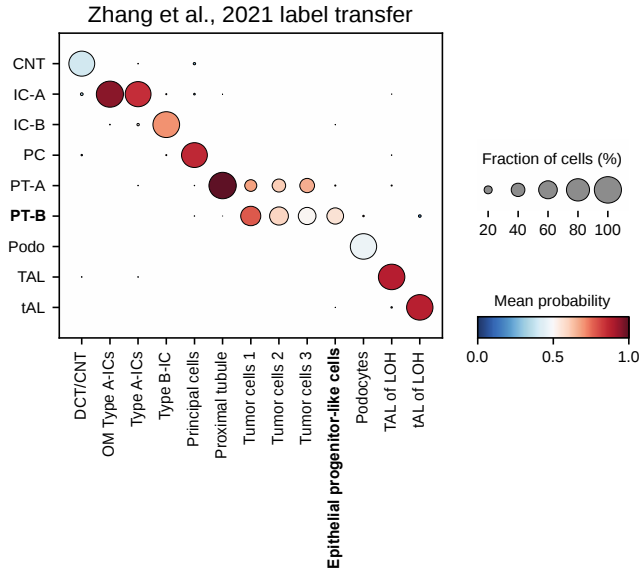
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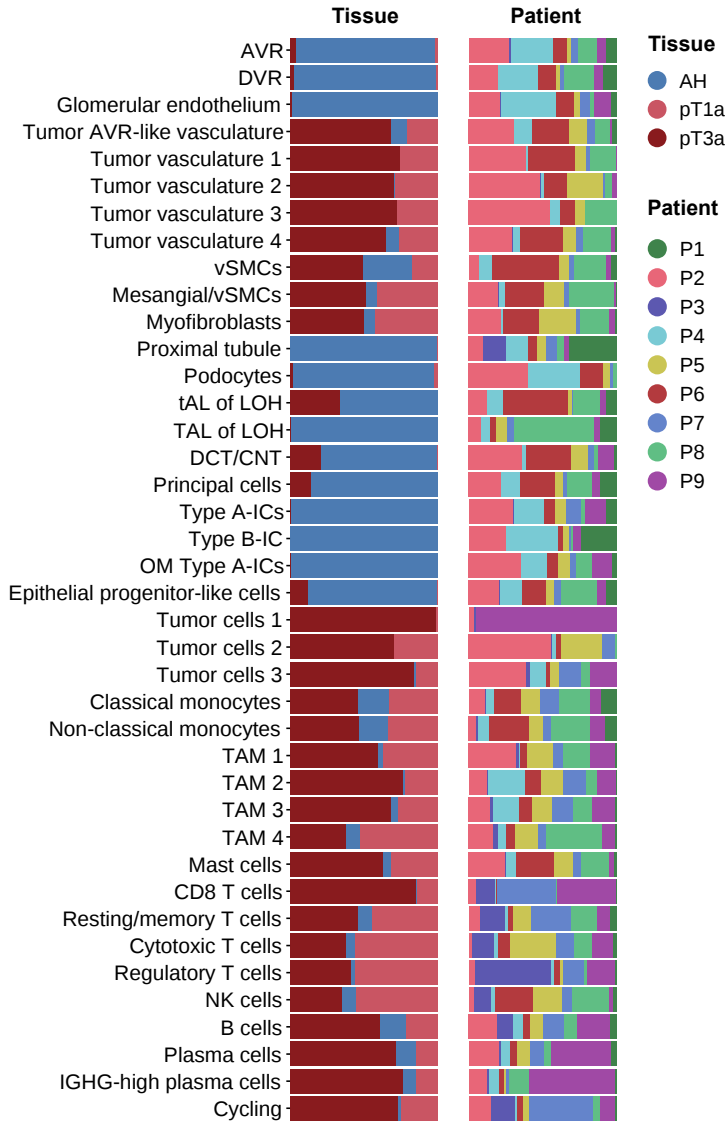


Supplementary figure S1. H&E staining histology slides for tissues analyzed in the study. Slides presented in pairs – tumor and healthy adjacent tissue staining for patient P1, P2 etc. All tumor samples present with WHO/ISUP differentiation grade II, except for P1 and P4, which are of grade IV. Note: tumor sample from patient P1 was not profiled due to low cell viability after dissociation. Scale bar – 100 μ m.

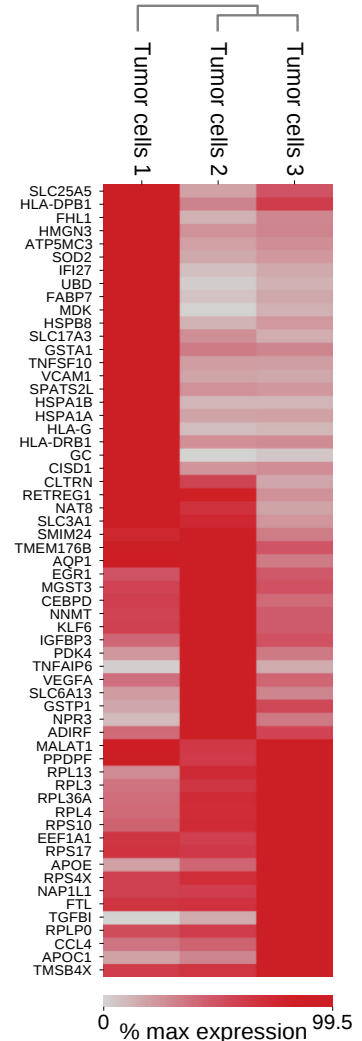
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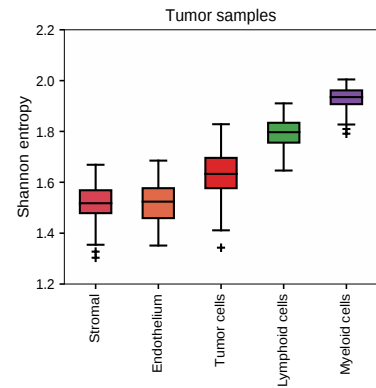
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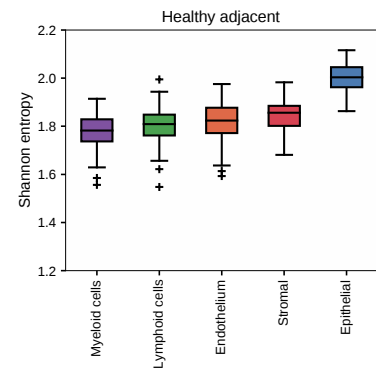
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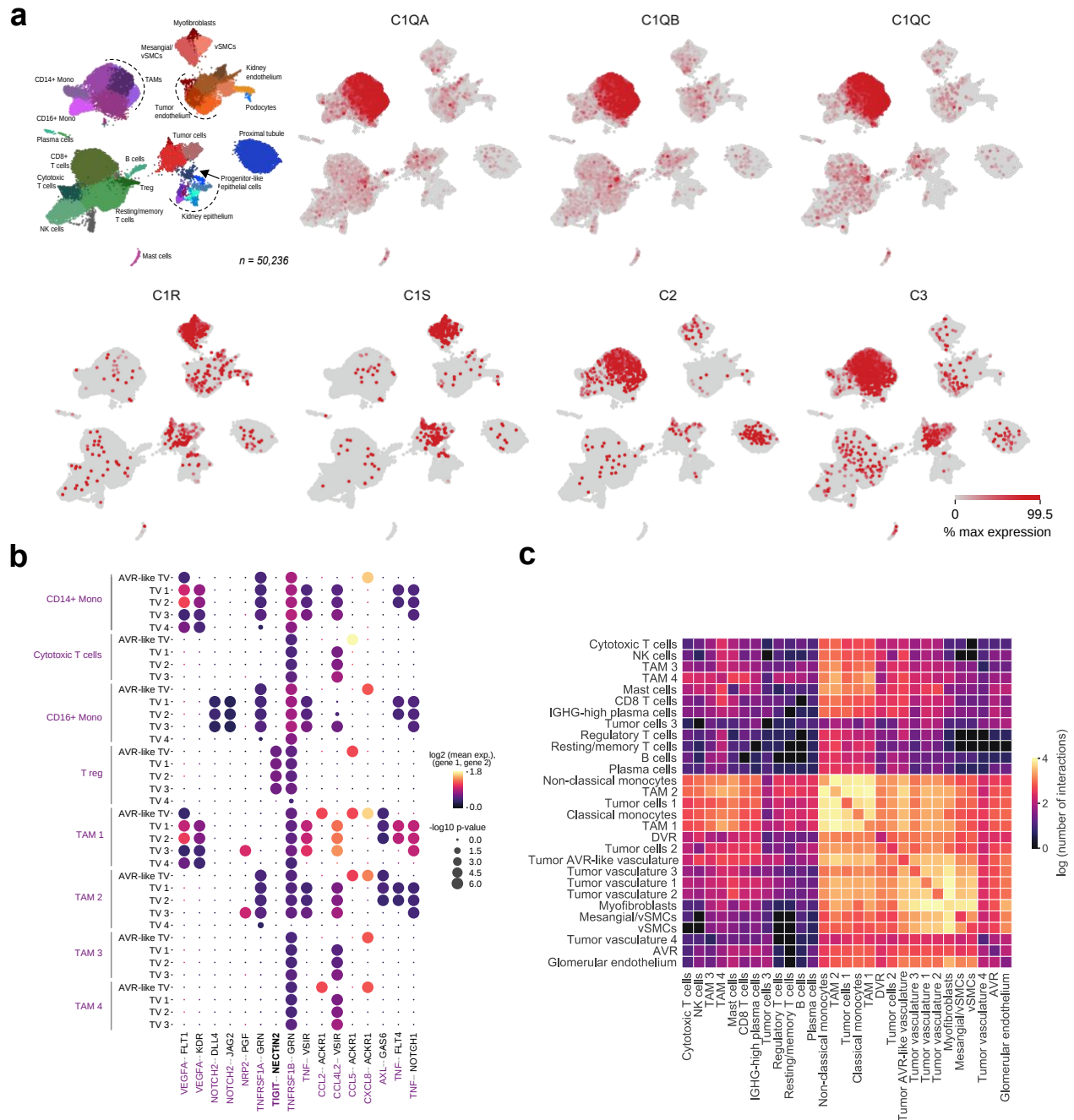
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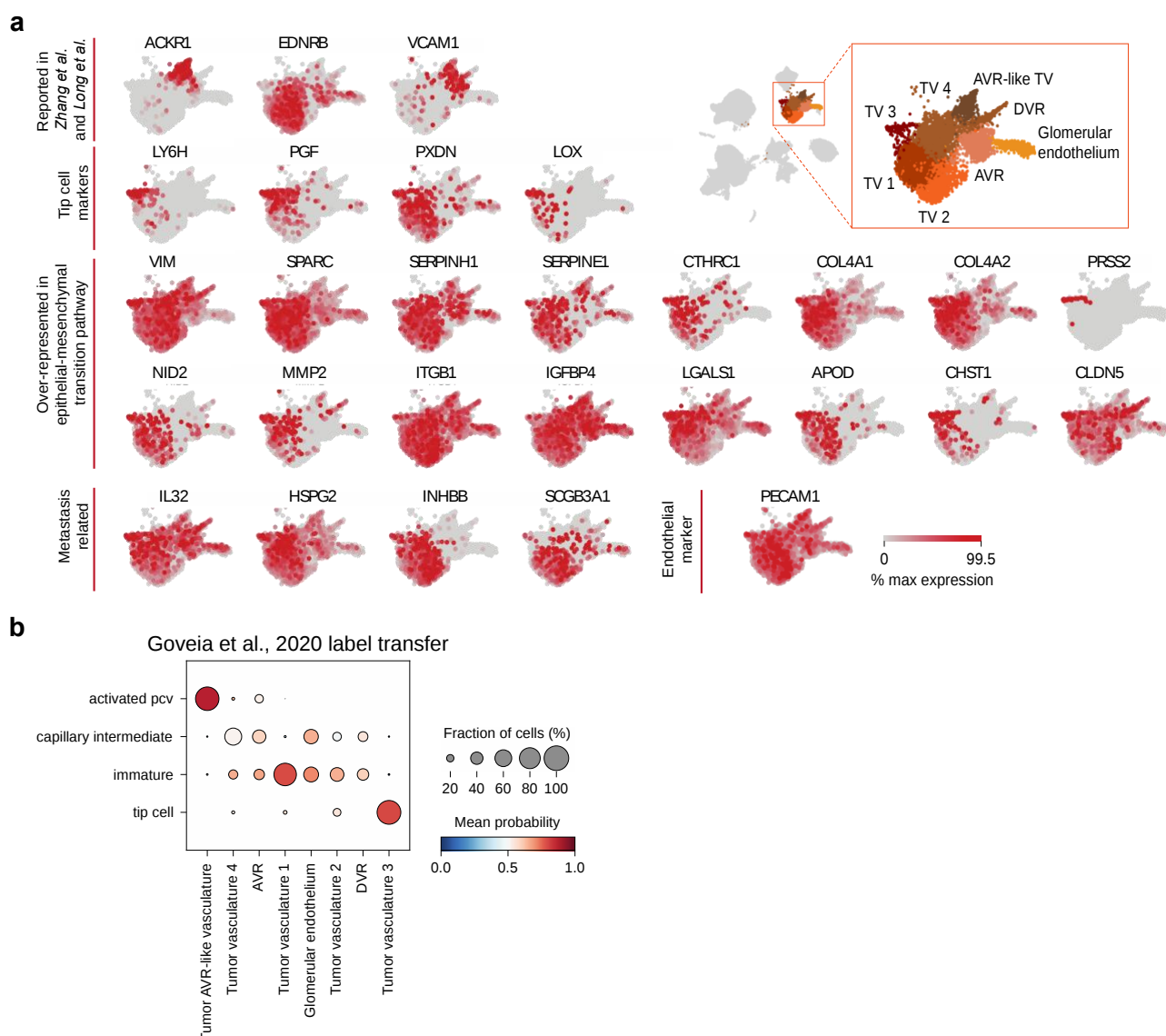
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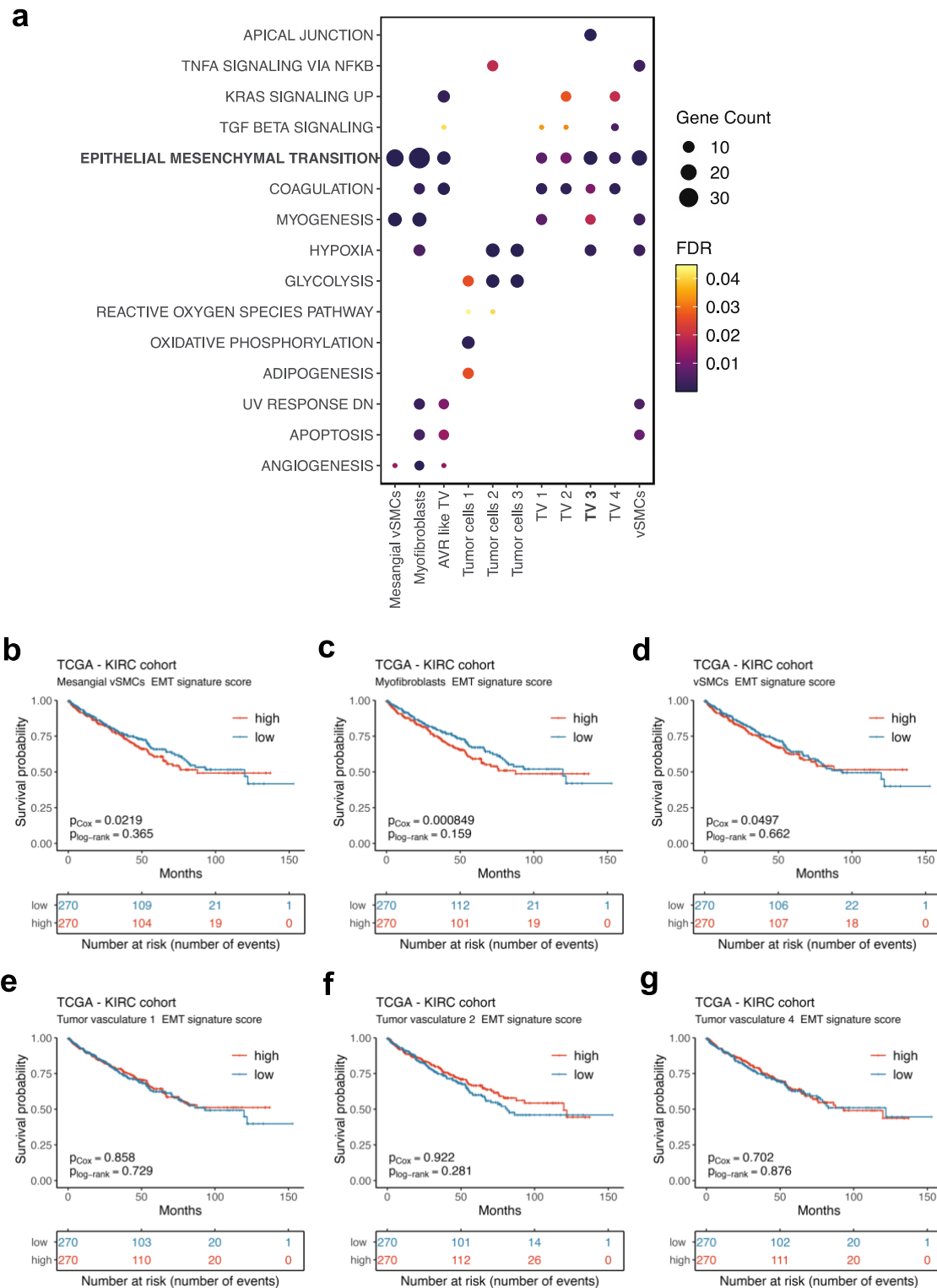
Supplementary figure S2. Cell composition and inter-patient variability in ccRCC. **a)** CellTypist model label transfer from Zhang et al. 2021 dataset. X-axis labels are cell populations from this study and y-axis labels are from Zhang et al., 2021. The annotation of cell types in both studies is in agreement and epithelial progenitor-like cell population is most similar to cell-of-origin 'PT-B' cell population from Zhang et al., 2021. **b)** Cell composition by disease stage and patient ID. Specialized epithelial and endothelial cells originate mostly from the healthy-adjacent tissues, while immune, tumor, endothelial and stromal cells are enriched in the tumor samples. Different types of cells are adequately represented by multiple samples, except for tumor cells 1 population, which appears specific to patient P9. **c)** Differential gene expression between tumor cell subpopulations. Only genes with Benjamini-Hochberg adjusted p-value <0.05 are shown. **d, e)** Tumor and healthy adjacent sample heterogeneity for broad cell group as measured by Shannon entropy. Lower entropy values indicate higher sample heterogeneity. AH – adjacent healthy.



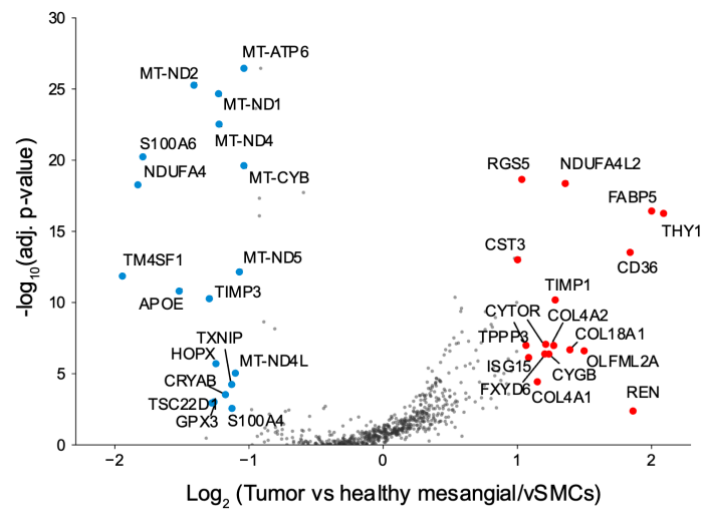
Supplementary figure S3. Expression of complement system genes and cell-cell communication analysis. **a)** Expression of complement system molecules C1QA, C1QB and C1QC is specific to tumor associated macrophages, while C1R, C1S are expressed by tumor and stromal cells. **b)** Cell-cell communication analysis between immune cells and tumor vasculature reveal immunosuppressive TIGIT-NECTIN2 interaction between tumor vasculature and regulatory T cells. **c)** Count matrix of all major cell-cell interactions observed within the TME of ccRCC



Supplementary figure S4. Tumor endothelial cell characterization. **a)** Expression of metastasis associated genes, tip-cell markers and genes overlapping with epithelial-mesenchymal transition pathway in tumor vasculature. The tip-cell markers are mostly enriched in tumor vasculature 3 population, while other genes are expressed in multiple tumor vasculature populations in heterogeneous manner. Previously reported markers *ACKR1*, *EDNRB* and *VCAM1* are not expressed in tumor vasculature 3. **b)** CellTypist model label transfer from Goveia et al. 2020 dataset. X-axis labels are cell populations from this study and y-axis labels are from Goveia et al., 2020. This analysis suggests that tumor vasculature populations in our study represent immature vessels described by Goveia et al. 2020, and Tumor vasculature 3 population represents the tip cell phenotype. AVR – ascending vasa recta, DVR – descending vasa recta, pcv – post-capillary vein, TV – tumor vasculature.



Supplementary figure S5. MSigDB Hallmark pathway overrepresentation analysis. **a)** Cell type signature overrepresentation analysis reveals enrichment of epithelial-mesenchymal transition (EMT) in tumor vasculature and stromal cell populations. **b-g)** None of the stromal and tumor vasculature signature genes overlapping with EMT correlate with overall survival in the TCGA KIRC cohort (except for tumor AVR-like vasculature and tip-like tumor vasculature 3, as shown in Figure 4b-c).



Supplementary figure S6. Volcano plot of differentially expressed genes between tumor originating and healthy-adjacent originating cells in mesangial/vSMC population. Genes with fold-change of 2 and adjusted p-value < 0.05 are highlighted and considered significant. The asymmetry of the central position of the volcano plot is due to difference in cell size with tumor cells having higher fraction of non-zero genes. This effect was not corrected to maintain consistency in differential gene expression analysis performed.

Table 1. Cluster annotation by top 25 DEGs.

Cluster No in Supp. Table S2	Annotation	Top 25 genes and references
0	Tumor vasculature 1	PLVAP ¹⁻³ , SPRY1, SPARC, PLPP1, COL4A1 ⁴ , VWA1, SPARCL1 ^{5,6} , VWF ^{2,4,7} , HSPG2 ² , PLPP3 ⁴ , GNG11, COL4A2 ⁴ , RGCC, RBP7, IGFBP7 ⁴ , TIMP3 ⁸ , RAMP2 ⁸ , IFI27, EGFL7 ⁹ , FLT1 ^{1,2} , RAMP3, ESAM, INSR ⁴ , GSN, A2M
1	Tumor vasculature 2	IGFBP3 ¹⁰ , ENPP2 ⁷ , RBP7, ESM1, SPARCL1 ^{5,6} , FLT1 ^{1,2} , A2M, PLVAP ¹⁻³ , SPRY1, STC1, ANGPT2, INSR ⁴ , PRSS23, PLPP3 ⁴ , VWF ^{2,4,7} , PLPP1, GNG11, PECAM1 ^{1,2,8} , SPARC, EFNB2 ¹¹ , GJA1, TIMP3 ⁸ , IGFBP7 ⁴ , IFI27, EPAS1 ¹²
2	Proximal tubule	MIOX ^{8,13} , ALDOB ⁸ , MT1G ^{8,13} , GATM ^{8,13} , GSTA2 ⁸ , GSTA1 ⁸ , ASS1 ^{8,14} , FABP1 ⁸ , NAT8 ⁸ , GPX3 ^{8,14} , PDZK1IP1 ^{2,8,13} , PCK1 ⁸ , MT1H ⁸ , RBP4 ⁸ , DCXR ⁸ , HPD ⁸ , SUCLG1 ⁸ , ECHS1 ⁸ , FBP1 ⁸ , UGT2B7 ⁸ , BBOX1 ⁸ , GLYAT ⁸ , RIDA ⁸ , PEPD ⁸ , CYB5A ⁸
3	Plasma cells	IGHA1 ^{15,16} , IGLC3 ¹⁶ , IGHM ¹⁶ , IGLC2 ^{15,16} , JCHAIN ¹⁶ , IGKC ¹⁶ , MZB1 ^{15,16} , SSR4, DERL3, SEC11C, FKBP11, CD79A ^{15,16} , HERPUD1, PRDX4, HSP90B1, XBP1, FKBP2, ITM2C, DNAAF1, CD27, SELENOS, ATF4, LMAN2, SDF2L1, SSR3
4	TAM 1	CCL3L1, CCL3 ^{2,17,18} , IL1B ^{2,19,20} , CXCL8 ^{17,20,21} , IER3, CCL4L2, TNF ^{19,20} , CXCL3 ¹⁷ , CXCL2 ¹⁷ , MS4A7, BCL2A1, C1QC ²² , PLAUR, C1QA ^{20,22,23} , HLA-DRA ²⁰ , GPR183, EIF4E, C1QB ^{20,22} , CD83, NFKBIA, HLA-DPA1 ²⁰ , HLA-DPB1 ²⁰ , CCL20 ² , CD74 ^{20,23} , HLA-DQB1 ²⁰
5	Principal cells	FXYD4 ^{11,13} , AQP2 ^{8,11,24} , AQP3 ^{8,11,24} , GDF15, WFDC2, EPCAM, HSD11B2 ^{11,13} , KRT19 ¹³ , TACSTD2, CLU ²⁵ , CDH16, SLPI ¹³ , AIF1L, ELF3, DEFB1 ¹⁴ , CLDN4 ^{8,26} , ATP1B1, RASD1, FOLR1, S100A2, COBLL1, GSTM3, RALBP1, SPINT2, CD24
6	vSMCs	TAGLN ^{11,13,27} , ACTA2 ^{11,13,27} , MYL9, ADIRF, TPM2, RGS5, CALD1, C11orf96, PLN, REN, MYH11 ^{11,13} , MGP, RERGL ¹¹ , BGN, PPP1R14A, PLAC9, CSRP2, SOD3, DSTN, RGS16, NOTCH3 ²⁷ , IGFBP7, MFGE8, MYLK, CCL2
7	Glomerular endothelium	IGFBP5 ^{4,8,28} , EMCN ^{8,11,13} , CRHBP ^{2,8} , PLAT ^{8,11} , SOST ^{2,8} , SLC9A3R2 ^{8,28} , EHD3 ^{8,11} , MGP ⁸ , PLPP3 ⁸ , RNASE1 ⁸ , IFI27 ⁸ , TGFB2 ⁸ , FCN3 ⁸ , PLPP1 ⁸ , ID1 ⁸ , RAMP2 ⁸ , GNG11 ⁸ , IFITM3 ⁸ , ADGRF5 ⁸ , PTPRB ⁸ , SLC14A1 ⁸ , EPAS1 ⁸ , MEIS2 ⁸ , TIMP3 ⁸ , APP ⁸
8	Classical monocytes (CD14+)	S100A9 ^{15,20,29} , S100A8 ^{15,20,29} , LYZ ²⁹ , G0S2, FCN1 ¹⁵ , IL1B, EREG, THBS1, CXCL8, S100A12 ^{15,29} , VCAN ^{15,29} , PLAUR, CXCL2, BCL2A1, CTSS, AREG, C5AR1, NAMPT, PPIF, LST1, NLRP3, IER3, SOD2, CEBPB, ATP2B1-AS1
9	Mast cells	TPSB2 ⁸ , TPSAB1 ^{8,20} , CPA3 ⁸ , AREG ⁸ , CD69 ⁸ , CTSG ⁸ , MS4A2 ⁸ , LMNA ⁸ , LTC4S ⁸ , HPGDS ⁸ , RGS13 ⁸ , RHEX, RGS2, KIT ²⁰ , HPGD, VWA5A, SRGN, FOSB, CPM, GATA2, NFKBIA, GPR65, ANXA1, LMO4, PPP1R15A
10	Distal convoluted tubule/connecting tubule	DEFB1 ^{11,14} , CALB1 ^{11,13,30} , HSD11B2, KLK1 ¹¹ , KNG1, ATP1B1, TMEM52B ¹³ , CA12, MAL, WFDC2 ⁸ , SLC12A3 ^{11,13,30} , RHCG ⁸ , GDF15, NFE2L2 ⁸ , EPCAM, CDH16, HMGCS2, FXYD2 ^{11,14} , SERPINA5, CA2, KCNJ1 ^{1,31} , KRT19, MTRNR2L8, EMX1, CLDN4 ⁸

11	Mesangial/vSMCs	RGS5, BGN ^{25,32,33} , REN ³⁴ , PLAC9, ADIRF, IGFBP7, CALD1 ³³ , MGP ¹³ , MYL9 ³³ , NDUFA4L2, HIGD1B, TPM2, ID3, FABP4, NOTCH3, CD36 ³⁵ , PDGFRB ^{11,13,27} , C11orf96, CSRP2, FRZB, TAGLN ¹¹ , TPPP3, THY1 ³⁰ , COL1A2, LHFPL6
12	Mast cells	TPSB2 ⁸ , TPSAB1 ^{8,20} , CPA3 ⁸ , CTSG ⁸ , CD69 ⁸ , AREG ⁸ , HPGDS ⁸ , RHEX, MS4A2 ⁸ , HPGD, VWA5A, CCL2, RGS13 ⁸ , RGS2, LTC4S, SRGN, ANXA1, LMNA, GPR65, KIT ²⁰ , ALOX5AP, PPP1R15A, LAPTM4A, FCER1A, AC020571.1
13	Cycling	HIST1H4C, STMN1 ⁸ , HMGB2 ³⁶ , PCLAF, UBE2C ^{8,36} , HMGN2, TUBB, CKS1B, MKI67 ^{8,23,36} , TUBA1B, H2AFV, H2AFZ, CENPF ³⁶ , PTTG1, TYMS ^{8,36} , RRM2 ³⁶ , HMGB1, PCNA ³⁶ , DUT, CLSPN ³⁶ , NUSAP1 ³⁶ , GZMK, GZMA, CXCL13, DEK
14	IGHG-high plasma cells	IGKC ¹⁶ , IGHG3, IGHG1, IGLC2 ^{15,16} , IGHG4, IGLC3 ¹⁶ , JCHAIN ¹⁶ , MZB1 ^{15,16} , IGHG, IGHG2, SSR4, SEC11C, XBP1, CD79A ^{15,16} , FKBP11, DERL3, HSP90B1, ITM2C, PRDX4, FAM30A, ERLEC1, SPCS1, IGHM, DNAAF1, KLF13
15	Non-classical monocytes (CD16+)	LST1 ³⁷ , SMIM25, FCN1 ¹⁵ , AIF1 ³⁷ , G0S2, LYPD2 ³⁸ , COTL1, SAT1, FCER1G, CTSS ³⁷ , BCL2A1, IL1B, LILRB2 ¹⁵ , PLAUR, FCGR3A ^{20,37,39} , C5AR1, TYROBP, MS4A7, TIMP1, NAP1L1, POU2F2, IFI30, STXBP2, CALHM6, NEAT1
16	Descending vasa recta	TIMP3 ⁸ , CLDN5 ^{2,13} , AQP1 ^{2,11,40} , SLC9A3R2 ²⁸ , TM4SF1, IFI27, RAMP2 ⁸ , RBP7, SLC14A1 ^{11,13,40} , DEPP1, ID1 ² , CRIP2, SERPINE2 ² , PPP1R14A, SRP14, PALMD ¹³ , FAM107A, PLPP1, ICAM2, RNASE1, SSUH2, KCTD12, S100A6, ABI3BP, IFITM3 ⁸
17	Proximal tubule	MT1G ^{8,13} , ALDOB ⁸ , MT1H ⁸ , GPX3 ^{8,14} , FABP1 ⁸ , PDZK1IP1 ^{2,8,13} , MIOX ^{8,13} , HPD ⁸ , MT1X ⁸ , CXCL14 ⁸ , ASS1 ^{8,14} , GATM ⁸ , NAT8 ⁸ , MT1F ⁸ , GSTA1 ⁸ , SUCLG1 ⁸ , SMIM24 ⁸ , FXD2 ^{8,13} , RBP5 ⁸ , RIDA ⁸ , MT1E ⁸ , SPP1 ⁸ , UGT2B7 ⁸ , LGALS2 ⁸ , ALB
18	Tumor vasculature 3	LY6H, CLDN5 ^{2,13} , PGF, COL4A1 ⁴ , APOD, SPARC ⁴¹ , COL4A2 ⁴ , HSPG2 ² , CHST1, TNFRSF4, PXDN, VWF ^{2,4,7} , LAMA4, GNG11, CCDC85B, PECAM1 ^{1,2,8} , SPARCL1 ² , PRSS2, FSCN1 ⁴ , SPRY1, CRIP2, LXN, ICAM2, TCF4, CD93
19	Tumor cells 1	FABP7 ⁴² , GC, CD24 ^{43,44} , ANXA4, SLC17A3 ^{2,23} , NDRG1 ⁴⁵ , UBD, PLIN2 ⁴⁶ , CRYAB ²³ , CLU ²³ , SPATS2L, FHL1, MDK, HLA-G, MGST2, GSTA1, HMGN3, CISD1, ATP1B1, NNMT ² , SLC13A1, CXCL14, SOD2 ²³ , HSPB8, VCAM1 ²³
20	Outer medulla type A intercalated cells	SPINK1 ⁸ , TMEM213 ^{8,13} , ATP6V1G3 ^{11,36,47} , SLC4A1 ^{1,11,13} , DEFB1, ATP6V0D2 ^{11,13,36} , RTN4 ⁸ , CKB ⁸ , RHCG ⁸ , EPCAM, SMIM6, ATP6AP2 ^{8,13} , MAL ⁸ , FAM24B ⁸ , CA12 ⁸ , LGALS3, HSD11B2, C12orf75 ¹³ , ADGRF5 ^{11,13,47} , ATP6V0B ⁸ , BSG, DHRS7, ATP6V0A4, CLCNKB ^{1,11} , ATP1B1 Also positive for marker SLC26A7 ⁴⁸
21	Myofibroblasts	COL1A1 ⁴⁹ , COL1A2 ⁴⁹ , TIMP1 ⁴⁹ , MGP ⁸ , TAGLN ⁸ , COL3A1 ⁴⁹ , ACTA2 ^{1,8,49} , BGN ^{8,10} , FN1, TPM2 ⁸ , DCN ¹⁰ , CALD1 ^{8,10} , MYL9 ⁸ , IGFBP7 ⁸ , POSTN, RGS5 ⁸ , LUM ⁴⁹ , COL6A2 ⁸ , SPARC ^{8,10} , PLAC9 ⁸ , COL4A2, AEBP1, COL6A1 ¹⁰ , PPP1R14A, COL4A1

22	Tumor cells 2	NNMT ² , NDUFA4L2 ^{2,23,50} , CD24 ^{43,44} , VEGFA ²³ , PDK4, CRYAB ²³ , ANGPTL4 ^{2,51} , PLIN2 ⁴⁶ , CLU ²³ , TMEM176B, NDRG1 ⁴⁵ , TMEM176A, RARRES2, HILPDA, BNIP3 ⁵² , ANXA4, RNASET2, CYB5A, CCDC146, KRT8, CCND1 ⁵² , ENO1, CXCL14, KRT18, EGR1
23	Thick ascending limb of LOH	DEFB1 ^{8,11} , UMOD ^{11,14,30} , PCP4 ⁸ , FXYD2 ^{8,14,31} , KNG1 ^{8,13} , CKB ⁸ , GSTM3 ⁸ , MPC1 ⁸ , LDHB ⁸ , PEBP1 ⁸ , MRPS6 ⁸ , PPP1R1A ⁸ , CYSTM1, BEX3, SLC25A5 ⁸ , SLC12A1 ^{8,11,14} , CBR1, ATP5F1A ⁸ , SLC25A4 ⁸ , CD24 ⁸ , TCIM, ATP5MC3 ⁸ , UQCERS1 ⁸ , PRDX2 ⁸ , MAL
24	Tumor AVR-like vasculature	ACKR1 ^{1,2,8} , VWF ^{2,4,7} , RNASE1 ⁸ , CLU ² , IFI27 ⁸ , TFF3, CD59, HYAL2 ⁸ , RAMP3 ⁸ , FKBP1A, FN1, TM4SF1 ⁸ , IFITM3 ⁸ , PTGDS, PECAM1 ^{1,2,8} , ADIRF, DNASE1L3 ^{2,13} , S100A6, IGFBP4 ⁸ , SLCO2A1 ¹³ , ECSCR, FAM167B, RAMP2 ⁸ , IL33, TGM2
25	Regulatory T cells	LTB, TNFRSF18 ^{23,53} , IL32, BATF ⁵³ , TIGIT ^{53,54} , CARD16, CORO1B, TNFRSF4 ^{53,54} , TRAC ²³ , TRBC1, S100A4, LINC01943, FOXP3 ^{23,53,54} , CD3D ^{41,53} , LAIR2, AC133644.2, LINC02195, CD27, CTLA4 ^{53,54} , PMAIP1, TBC1D4, DUSP4, CYTIP, SPOCK2, ICA1
26	Thick ascending limb of LOH	UMOD ^{11,14,30} , DEFB1 ^{8,11} , KNG1 ^{8,13} , SLC12A1 ^{8,11,14} , ATP1A1, ATP1B1, S100A2, CLDN10, SFRP1, KCNJ1 ^{8,11} , CA12, MAL, CKB ⁸ , TMEM52B, CDH16, UCHL1, GSTM3, PCP4 ⁸ , SERPINA5, CLCNKB, TSPAN8, MPC1 ⁸ , SPP1, MTRNR2L8, EGF
27	Tumor cells 3	FABP7 ⁴² , NDUFA4L2 ^{2,23,50} , CD24 ^{43,44} , NNMT ² , BNIP3 ⁵² , HILPDA, CRYAB ²³ , PLIN2 ⁴⁶ , LDHA ⁵² , RARRES2, ANGPTL4 ^{2,51} , ANXA4, GAPDH, ENO1, TPM1, NDRG1 ⁴⁵ , CLU ²³ , TPI1, VDAC1, SERPINA1, TMEM176A, NUPR1, KRT18, VEGFA ²³ , EGLN3 ⁵⁵
28	Tumor vasculature 4	PLVAP ¹⁻³ , GNG11, SPARC, RBP7, SPRY1, HSPG2 ² , VWF ^{2,4,7} , IFI27, RAMP2 ⁸ , PLPP1, COL4A1 ⁸ , SPARCL1 ^{5,6} , IGFBP7 ⁴ , TIMP3 ⁸ , MTRNR2L8, EGFL7 ⁹ , INSR ⁴ , GSN, RAMP3, ESM1, VWA1, IFITM3 ⁸ , ECSCR, TCF4, SLC9A3R2
29	Podocytes	PTGDS ⁸ , DCN ⁸ , NPHS2 ^{8,11,13} , EMCN, IGFBP5, TNNT2 ⁸ , IGFBP2 ⁸ , HTRA1 ⁸ , PCOLCE2 ⁸ , CTGF, PLAT, PODXL ^{8,13,56} , TPPP3 ⁸ , MYL9 ⁸ , CRHBP, APOD ⁸ , MME ⁸ , HPGD, CLIC5 ^{8,13,56} , TCF21 ^{8,56} , CDKN1C ^{11,47} , SLC9A3R2, ID1, BST2 ⁸ , AIF1 ⁸
30	TAM 2	APOC1 ³⁹ , APOE ^{20,23,39} , C1QB ^{20,22} , C1QA ^{20,22,23} , C1QC ²² , CTSD ³⁹ , HLA-DRA ²⁰ , TYROBP, TREM2 ⁵⁴ , HLA-DPA1 ²⁰ , HLA-DQA1 ²⁰ , HLA-DRB1 ²⁰ , FCER1G, PSAP, HLA-DPB1 ²⁰ , LYZ, HLA-DQB1 ²⁰ , CTSB, GPNMB ^{23,39} , NPC2, CST3, CD68 ^{1,2,54} , CD74 ^{20,23} , HLA-DRB5 ²⁰ , CFD
31	CD8 T cells	DUSP4 ⁴¹ , GZMK ^{41,53} , CST7, LYST, CCL5 ⁵³ , TRBC2, CD8B ⁵³ , CD3D ^{41,53} , RGS1, CD27 ⁴¹ , CREM ⁴¹ , RGS2 ⁴¹ , NKG7 ⁵³ , TRAC ⁵³ , TNFRSF9 ^{41,53} , CD8A ^{41,53} , TRBC1, HSP90AA1 ⁴¹ , GZMA ²³ , SRSF7, CD2, PMAIP1, CMC1, RUNX3 ⁵⁷ , SYTL3
32	Type A intercalated cells	ATP6V1G3 ^{11,36,47} , DEFB1, TMEM213 ^{8,13} , C12orf75 ⁸ , SPINK1 ⁸ , CKB ⁸ , FXYD2 ⁸ , MAL ⁸ , ATP6V0D2 ^{11,13,36} , FAM24B ⁸ , SMIM6, NUPR2, LGALS3 ⁸ , CYSTM1 ⁸ , CA12 ⁸ , CLCNKB ^{1,11} , RTN4 ⁸ , SLC25A5 ⁸ , SLC25A39 ⁸ , BSG ⁸ ,

		HOXB-AS3, ERP27 ¹³ , COX7A1, SLC4A1 ^{1,11,13} , ADGRF5 ^{11,13,47}
33	B cells	CD79A ^{15,16,23} , CD37 ¹⁶ , IGHM, IGKC, MS4A1 ^{15,16} , LTB ¹⁶ , BANK1, IGHD, LINC01781, LINC00926, CD83, RALGPS2, FAM30A, CD52, BIRC3, EEF1B2, RPS5, POU2F2, SPIB, RPL32, RPL18A, LINC01857, RPS8, CD79B ^{15,16} , CD55
34	Thin ascending limb of LOH	WFDC2, S100A2 ⁵⁸ , SLPI, SOD3, PAPP2 ⁵⁹ , MMP7, DEFB1, ITM2C, TACSTD2 ¹³ , MAL, SLC12A1 ¹³ , PCSK1N, IGFBP6, CLDN10 ^{13,58} , S100A6 ⁵⁸ , UMOD ^{13,58} , CLU ¹⁴ , TSPAN8 ¹³ , CA12, MUC1, CD24, CLDN3, ATP1A1, KRT7, EPCAM
35	Ascending vasa recta	DNASE1L3 ^{2,13} , IGFBP5 ²⁸ , RNASE1 ⁸ , RAMP3 ⁸ , EMCN ^{8,13} , CAVIN2 ⁸ , IFI27 ⁸ , ID1, TMEM88, RAMP2 ⁸ , SLC9A3R2 ²⁸ , CA4, GNG11 ⁸ , IFITM3 ⁸ , FAM167B, ENG ⁸ , TIMP3 ⁸ , TM4SF1 ⁸ , PLPP3, HYAL2 ⁸ , PCAT19, IGFBP4 ⁸ , PLAT ⁸ , MEIS2 ⁸ , GIMAP7
36	Type B intercalated cells	KRT7 ⁸ , WFDC2 ⁸ , ATP6V1G3 ^{11,36,47} , TMEM213 ^{8,13} , S100A2 ⁸ , CD9 ⁸ , CA12 ⁸ , MTRNR2L12, DEFB1, TSPAN8 ⁸ , MAL ⁸ , RARRES2 ⁸ , CDA ⁸ , ATP6V0B ⁸ , ATP6V0D2 ^{8,11,13} , ATP6AP2 ⁸ , LGALS3 ⁸ , ATP6V0A4 ⁸ , ATP6V1B1 ^{8,11} , MTRNR2L10, SMIM24 ⁸ , EPCAM, CKB, MTRNR2L1, MTRNR2L8 Also positive for markers: SLC26A4 ^{11,13,60} , HMX2 ¹¹ , SPINK8 ¹¹
37	TAM 3	HLA-DPB1 ²⁰ , HLA-DPA1 ²⁰ , APOC1 ³⁹ , CST3, HLA-DRA ²⁰ , TYROBP, AIF1, HLA-DQA1 ²⁰ , C1QA ^{20,22,23} , HLA-DQB1 ²⁰ , C1QB ^{20,22} , CD74 ^{20,23} , MS4A6A, C1orf162, FTL, LYZ, RGS10, NPC2, CD68 ^{1,2,54} , LST1, C1QC ²² , SAT1, IER3, HLA-DMA ²⁰ , HLA-DRB1 ²⁰
38	Epithelial progenitor-like cells	CRYAB ⁸ , SLPI ⁸ , MMP7 ⁸ , CLU ^{8,61} , CLDN4 ⁸ , WFDC2 ⁸ , TACSTD2 ⁸ , CD24 ^{8,58,61} , CTGF, CLDN3 ⁸ , NUPR1, MT1E, ELF3 ⁸ , EGOT, TPM1 ^{8,58} , KRT19, MAL ⁸ , PIGR, S100A13 ⁸ , SPINT2 ⁸ , SOX4 ⁶¹ , RASD1, ATF3, MT1X, BCAM ⁸
39	Cytotoxic T cells	XCL1 ⁵³ , XCL2 ⁵³ , KLRB1 ⁶² , TRDC, KLRC1, KRT86, CD7, KLRD1 ⁶² , HOPX ⁵³ , GNLY ^{53,62} , CCL4 ⁵³ , KRT81, CCL5 ⁵³ , ZNF683 ⁵³ , LINC01871, CTSW ⁶² , HCST, IL2RB, AREG, ZFP36L2, BTG1, REL, FAM177A1, MATK, CMC1
40	TAM 4	C1QB ^{20,22} , C1QA ^{20,22,23} , C1QC ²² , SELENOP ²⁰ , FOLR2 ^{20,23} , RNASE1, HLA-DPA1 ²⁰ , CD14, HLA-DRA ²⁰ , MS4A6A, MS4A7, HLA-DRB1 ²⁰ , AIF1, HMOX1, MS4A4A ²⁰ , TYROBP, HLA-DPB1 ²⁰ , NPC2, CD74 ^{20,23} , HLA-DQA1 ²⁰ , CST3, HLA-DQB1 ²⁰ , FCGRT, SLC40A1 ^{21,39} , FCER1G, PLTP ²⁰ , BLVRB
41	NK cells	GNLY ⁶³ , GZMB ⁶³ , FGFBP2, NKG7 ⁶³ , KLRD1 ⁶³ , KLRB1 ⁵³ , PRF1 ⁶³ , GZMH ⁶³ , SPON2 ⁶³ , PLAC8, CLIC3, KLRF1 ⁶³ , CD247 ⁶³ , AREG, GZMM, HOPX, CST7 ⁶³ , TRDC, CMC1 ⁶³ , ARL4C, CTSW, CCL4 ⁶³ , PTGDS ⁶³ , GZMA ⁶³ , EFHD2
42	Resting/memory T cells	IL7R ^{23,53} , CD52 ⁵³ , LTB ⁶⁴ , KLRB1 ⁵³ , ZFP36L2 ⁴¹ , RPS29, CD48, CXCR4 ⁴¹ , LYAR, BTG1, ANXA1, STK4, RPS27, EML4, PPP2R5C, RPS3, ACAP1, RPS15A, SPOCK2, ISG20, FYN, CD3D ^{41,53} , PDE4B, CD2, RPLP2

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