**Supplementary Materials and Methods**

Tissue specificity entropy calculation

RPKM values were provided by the GTEx consortium for 56318 genes across 9647 samples from adipose tissue, adrenal gland, bladder, blood, blood vessel, bone marrow, brain, breast, cervix uteri, colon, esophagus, fallopian tube, heart, kidney, liver, lung, muscle, nerve, ovary, pancreas, pituitary, prostate, salivary gland, skin, small intestine, spleen, stomach, testis, thyroid, uterus, and vagina. The average RPKM for each of the 56318 reference transcripts in each tissue type was computed, resulting in 31 total RPKM values for each gene. All of the 9647 RPKM values for each of the 56318 transcripts were retained as a null distribution of expression values. For each gene then, an entropy value was computed. The entropy value for a gene across tissue types was computed by fitting the 9647 RPKM null distribution values for the gene into a normal distribution. The normal distribution was broken up into 10,000 contiguous ranges to estimate the probability of a value occurring in any of the ranges. The probability (p) of observing each of the 31 average RPKM values given the real observed ranges of expression of the gene across all the 9647 samples was computed using the discretized normal distribution constructed above. The entropy of each gene across the 31 tissue types was then was a cumulative $-p*\ln(p)$ of the probability p of each of the 31 average RPKM values. RPKM values were converted into TPM.
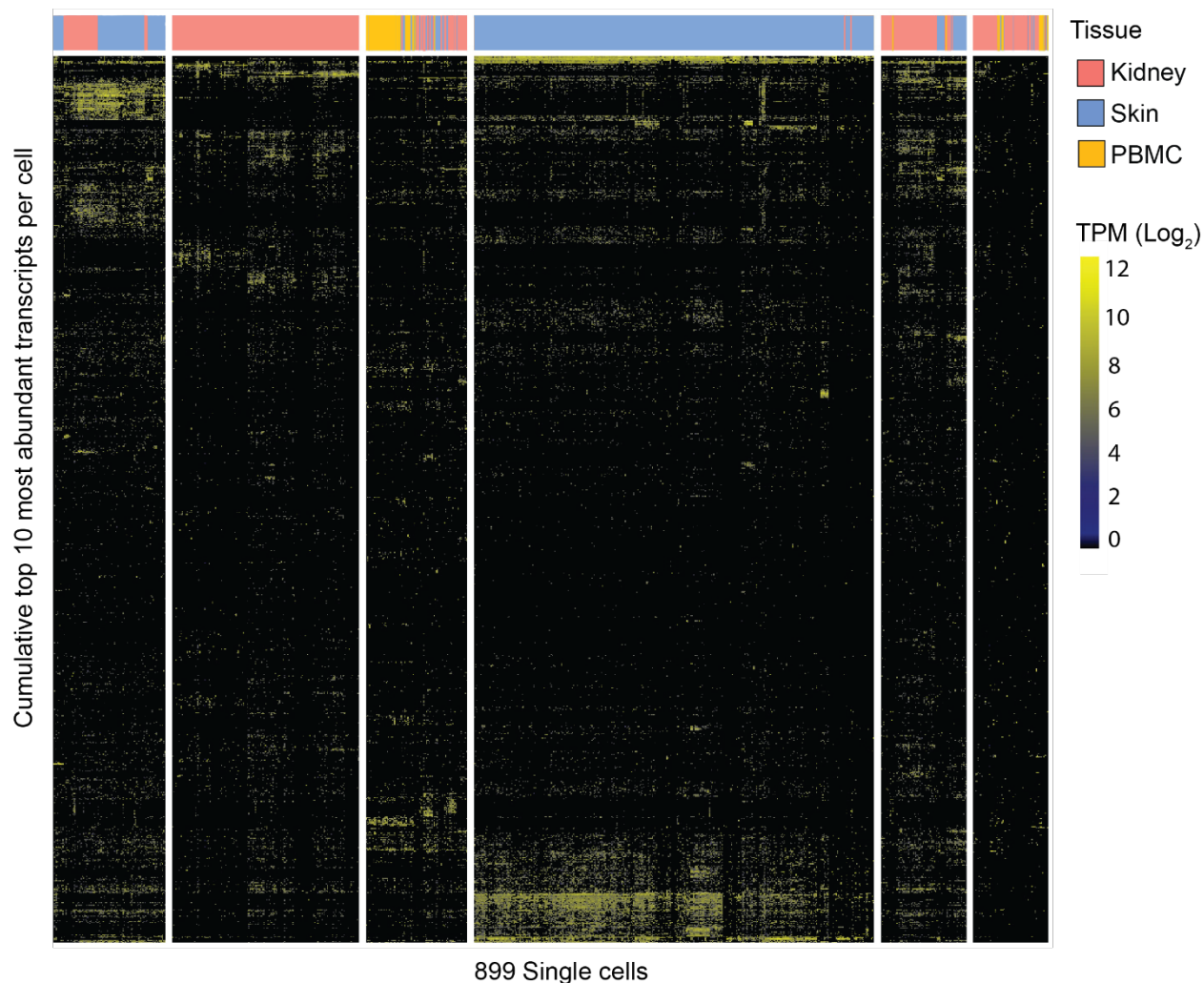
Supplemental Figure 1. Unsupervised hierarchical clustering of single-cell datasets from skin, kidney and PBMC. Each column represents a single cell each row a single gene from a cumulative list of the top 10 most abundant transcripts per cell excluding mitochondrially encoded genes, ribosomal proteins, and *HLA* genes.

Supplemental Table 1. Kidney-specifically expressed genes absent in scRNA-seq.

Gene symbol	Kidney GTEx average TPM	Single cell average TPM	Entropy	3' UTR % GC	3' UTR length
REN	391.3	0.0	0.7	58	359
CRYAA	303.4	0.0	0.6	65	735
NPHS2	237.0	0.0	0.5	46	913
SLC9A3	161.2	0.0	0.3	81	73
NPHS1	81.6	0.0	0.3	53	682
CYP27B1	75.7	0.0	0.5	66	201
HOXB8	69.4	0.0	0.5	56	1164
SLC30A2	47.9	0.0	0.3	57	2054
MAPK15	38.1	0.0	0.4	67	384
LBP	35.7	0.0	0.3	50	399
SLC34A3	33.2	0.0	0.4	68	603
CLEC18A	29.3	0.0	0.4	58	775

Supplemental Table 5. Patient clinical scores.

METRO patient ID	2634	2644	5324	2726	2732	5288	5563	5594	5596	5552
ISN/RPS Class	IV/V	V	IV	III	III/V	V	III	IV	III	III/V
Activity index	0	0	5	3	3	0	2	10	4	2
Chronicity index	2	1	8	1	3	0	2	5	1	1
Glomerular IgG deposition	2	3	3	2	2	2	3	3	3	1
Proteinuria	N.D.	1.1	6	2.3	2.4	1.4	8.41	9.065	2.35	0.76
eGFR (m/min/1.73m^2)	>60	>60	34	>60	>60	>60	>60	25.6	N.D.	>60
IFN response score	249	250	302	239	221	233	301	258	188	66