FIGURE S1

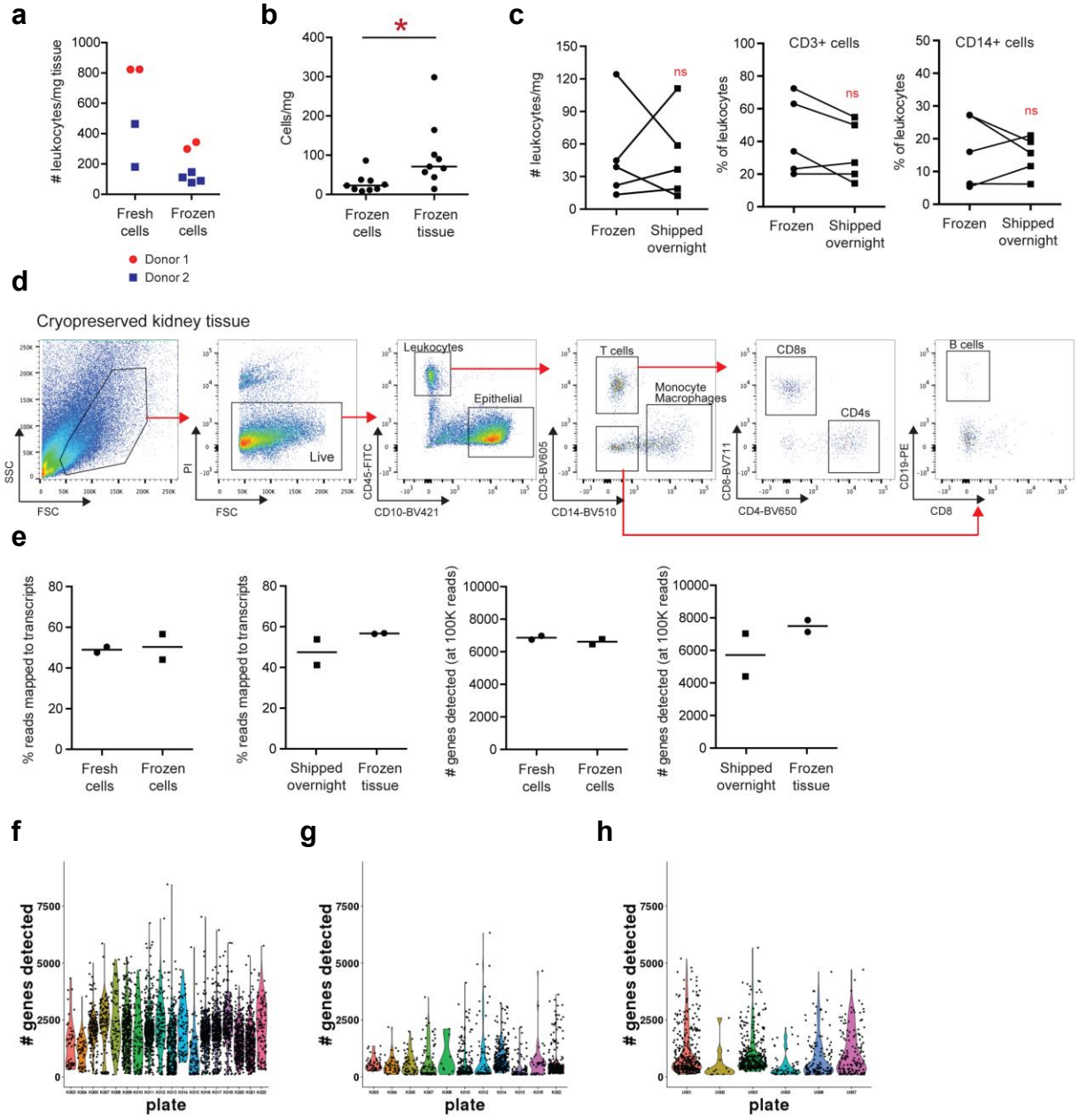

Figure S1. Analysis of cells obtained from cryopreserved viable kidney tissue. **a,** Leukocyte yields from kidney tissue samples processed fresh or after freeze/thaw. **b,** Leukocyte yields from kidney tissue samples cryopreserved either post-dissociation (frozen cells) or pre-dissociation (frozen tissue). n=9 segments pooled from 4 different donors. * p<0.01 by Mann-Whitney test. **c,** Cell yields and leukocyte frequencies from kidney samples either cryopreserved or shipped overnight on wet ice. Wilcoxon matched-pairs signed rank test. **d,** Example of flow cytometry analysis of cells from a cryopreserved lupus nephritis kidney biopsy. **e,** RNA-seq quality metrics of bulk leukocytes from kidney cells analyzed before (fresh cells) and after freeze/thaw (frozen cells), or obtained from kidney tissue shipped overnight or shipped after

tissue cryopreservation (frozen tissue). **f-h,** The distribution of the number of genes per cell on each processed 384-well plate, in kidney leukocytes (f), kidney epithelial cells (g) and urine leukocytes (h).

FIGURE S2

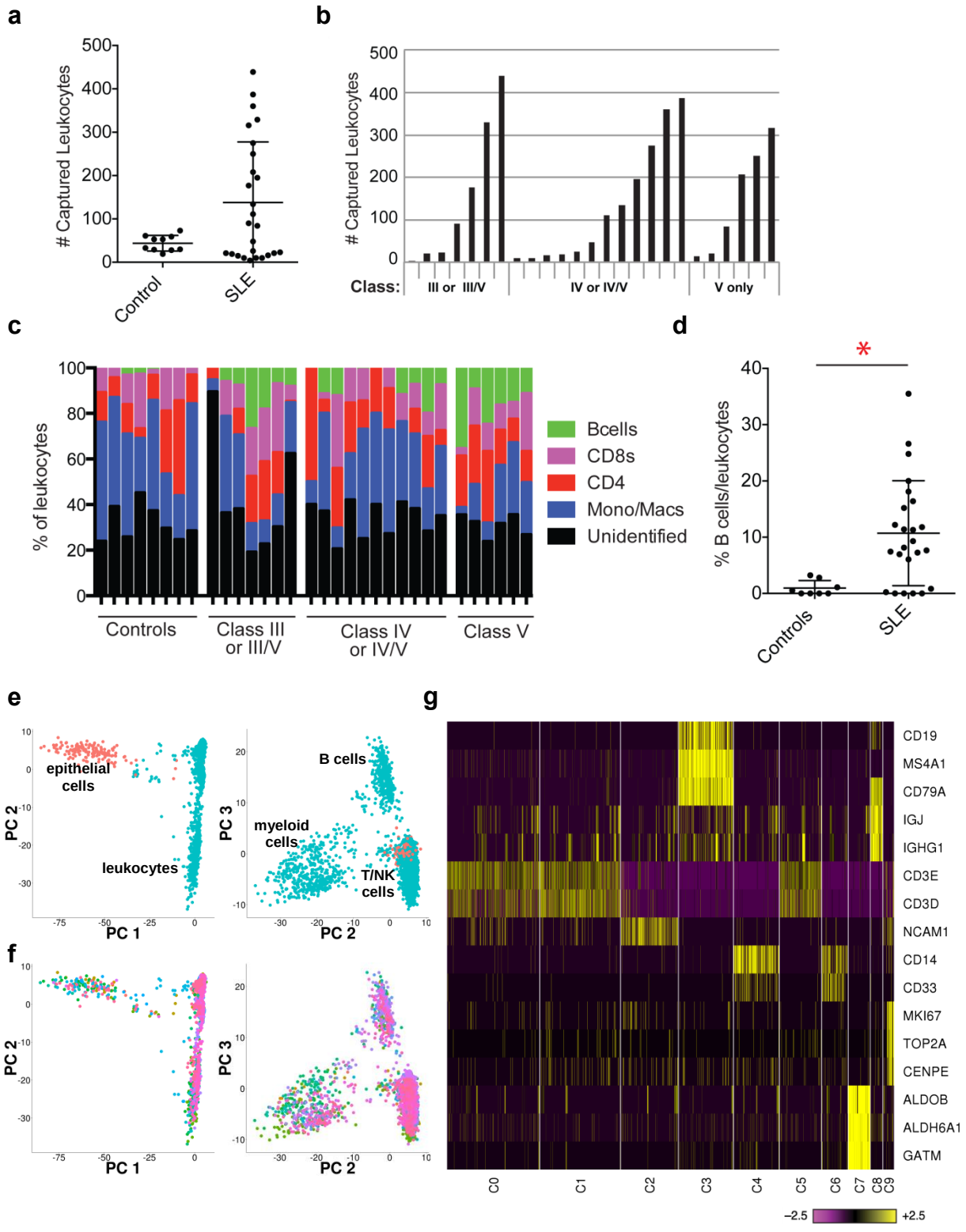

Figure S2. An overview of the isolated cells. **a-d,** Leukocyte yields and composition from LN kidney biopsies, as determined by flow cytometry. **a,** Number of leukocytes sorted as single cells from LN and control biopsy samples. **b,** Number of leukocytes sorted from LN biopsies

stratified by histologic glomerulonephritis class. **c,** Flow cytometric assessment of the proportion of leukocytes that are B cells, T cells, monocyte/macrophages, or other in biopsy samples. **d,** Percentage of B cells among leukocytes in biopsy samples. Mann-Whitney two-tailed U test ($p = 0.0031$). **e**, Projection of the gene expression data of kidney cells following principal component analysis (PCA), in the PC1-PC2 (left) and PC2-PC3 (right) planes. Cells are colored based on their identity as either leukocytes (cyan) or epithelial cells (pink), as determined by flow cytometry. The labeling of clusters in the PC2-PC3 plane is based on the identity of the leading genes in each principal component. **f,** Same as (e), except cells are colored based on the 384-well plate they were processed on. **g,** The expression of selected genes in the 10 low-resolution clusters; these were among the genes used to determine the putative lineage of each cell.

FIGURE S3

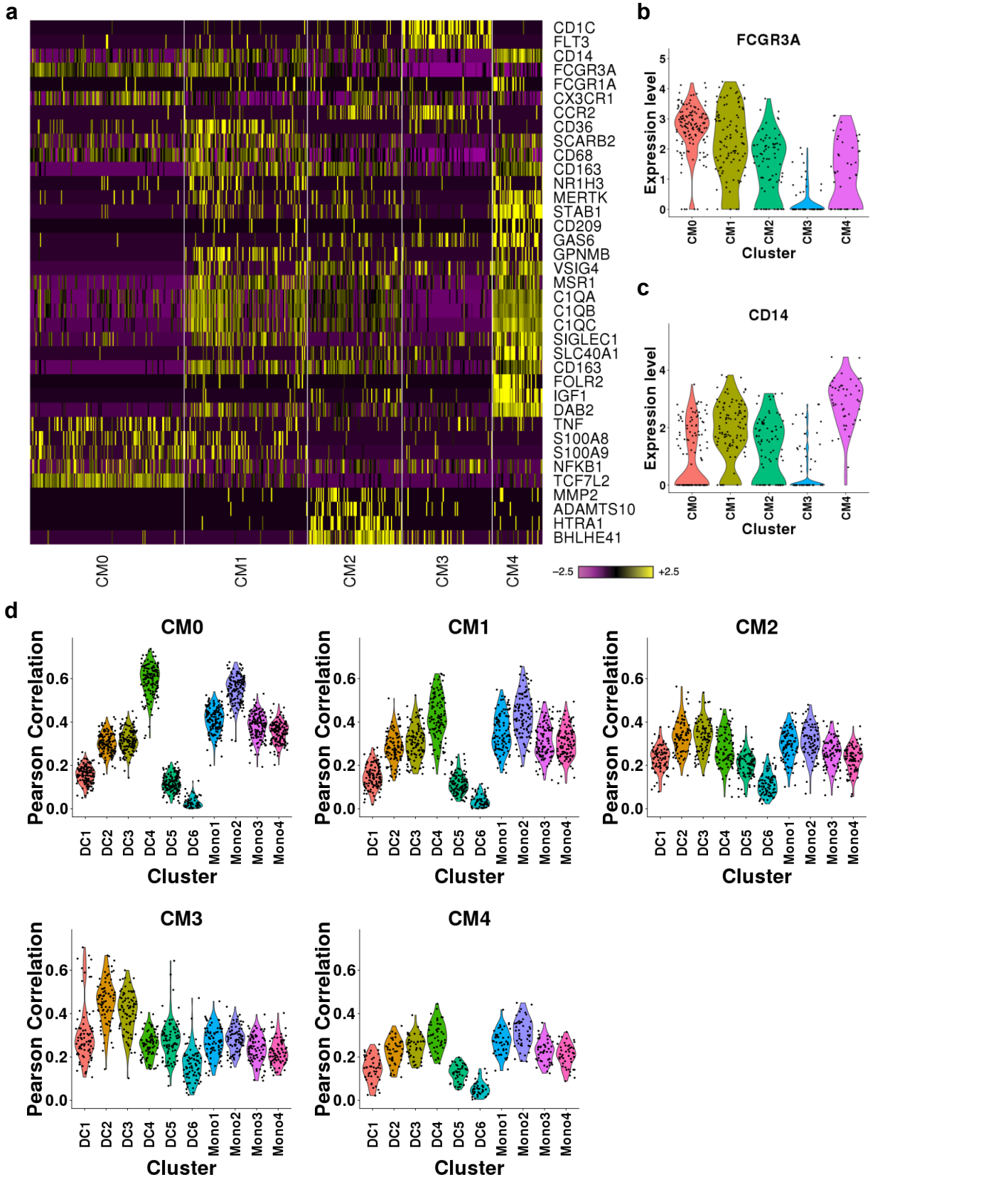
a
CD1C
FLT3
CD14
FCGR3A
FCGR1A
CX3CR1
CCR2
CD36
SCARB2
CD68
CD163
NR1H3
MERTK
STAB1
CD209
GAS6
GPNMB
VSIG4
MSR1
C1QA
C1QB
C1QC
SIGLEC1
SLC40A1
CD163
FOLR2
IGF1
DAB2
TNF
S100A8
S100A9
NFKB1
TCF7L2
MMP2
ADAMTS10
HTRA1
BHLHE41
CM0
CM1
CM2
CM3
CM4
−2.5
+2.5
b
FCGR3A
Expression level
Cluster
c
CD14
Expression level
Cluster
d
CM0
CM1
CM2
CM3
CM4
Pearson Correlation
DC1
DC2
DC3
DC4
DC5
DC6
Mono1
Mono2
Mono3
Mono4
Cluster

Figure S3. Focused analysis of kidney myeloid cells. **a,** The expression of selected genes over the 5 myeloid cell clusters. **b-c,** The expression of the canonical markers CD16 (FCGR3A) and CD14 on the 5 myeloid clusters. **d,** The distributions of the correlation values between individual cells and reference clusters in Villani *et al.* (DC1-DC6, Mono1-Mono4), shown separately for each of the 5 myeloid cell clusters identified here.

FIGURE S4

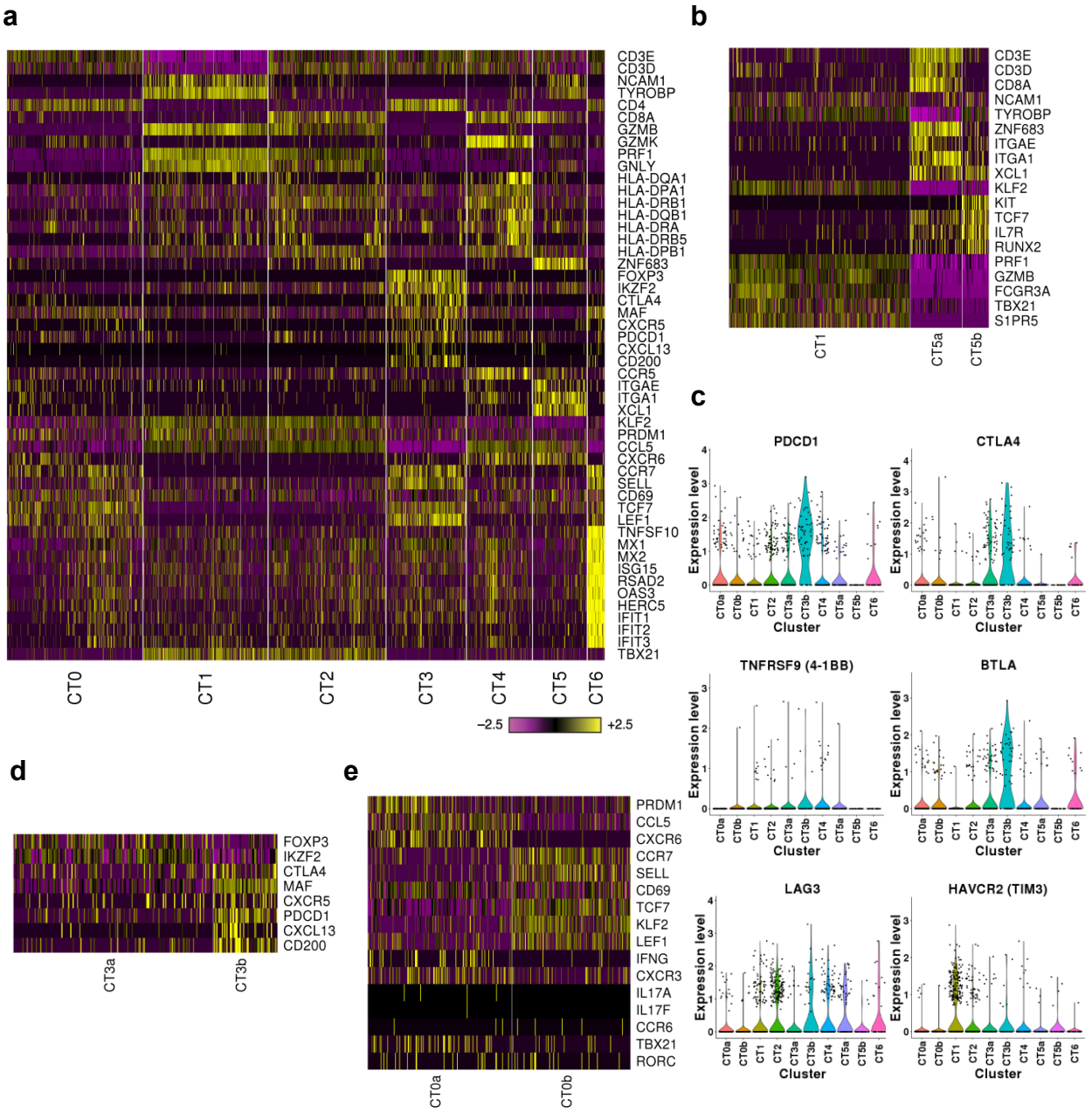

Figure S4. Focused analysis of kidney T cells and NK cells. **a,** The expression of selected genes across the 7 high-level T/NK cell clusters. **b,** The expression of selected genes across the two subclusters of cluster CT5, and in comparison to cluster CT1. **c,** The expression of genes associated with exhaustion, across the different T cell clusters. **d,** The expression of selected genes across the two subclusters of cluster CT3. **e,** The expression of selected genes across the two subclusters of cluster CT0a.

FIGURE S5

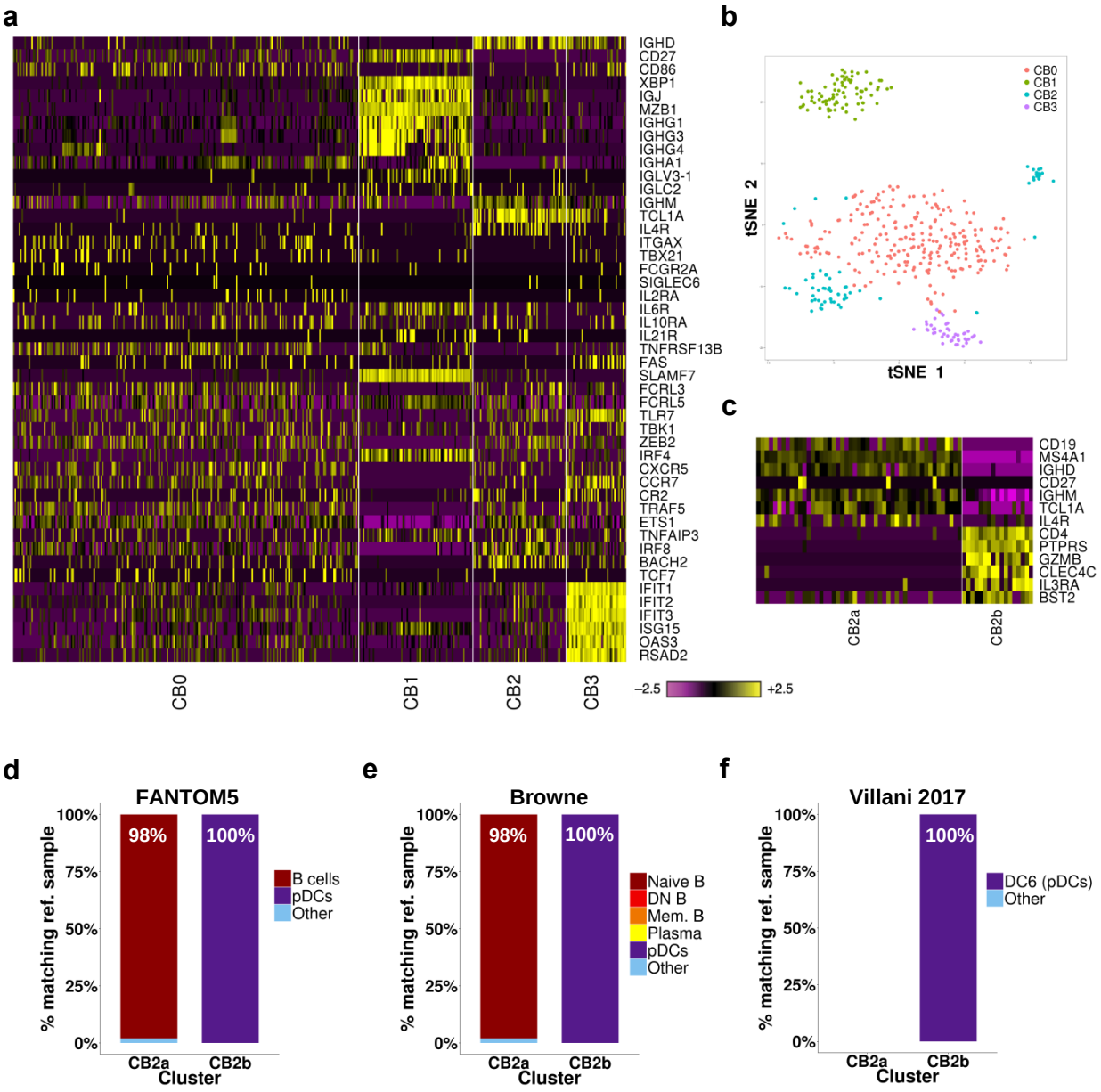

Figure S5. Focused analysis of kidney B cells. **a,** The expression of selected genes, across the 4 high-level B cell clusters. **b,** A tSNE projection of all B cells. Note that the cells of cluster CB2 (in cyan) occupy two main and separate regions in the tSNE1-tSNE2 plane. **c,** The expression of selected genes, across the two subclusters of cluster CB2. **d-f,** The results of classifying the CB2 cells by correlating their gene expression with that of 3 sets of reference samples – FANTOM5 (d), 13 immune cell populations sorted from healthy individuals (Browne *et al.*; e), and the clusters identified in Villani *et al.* (f). For each of the 2 subclusters in CB2, the bars denote the percentage of cells most similar to each of the reference samples. For readability, only relevant reference samples are specified, and the rest are collapsed into an “other” category. Note that the reference samples in Villani *et al.* do not include B cells, and therefore are not relevant for the classification of the cells in cluster CB2a.

FIGURE S6

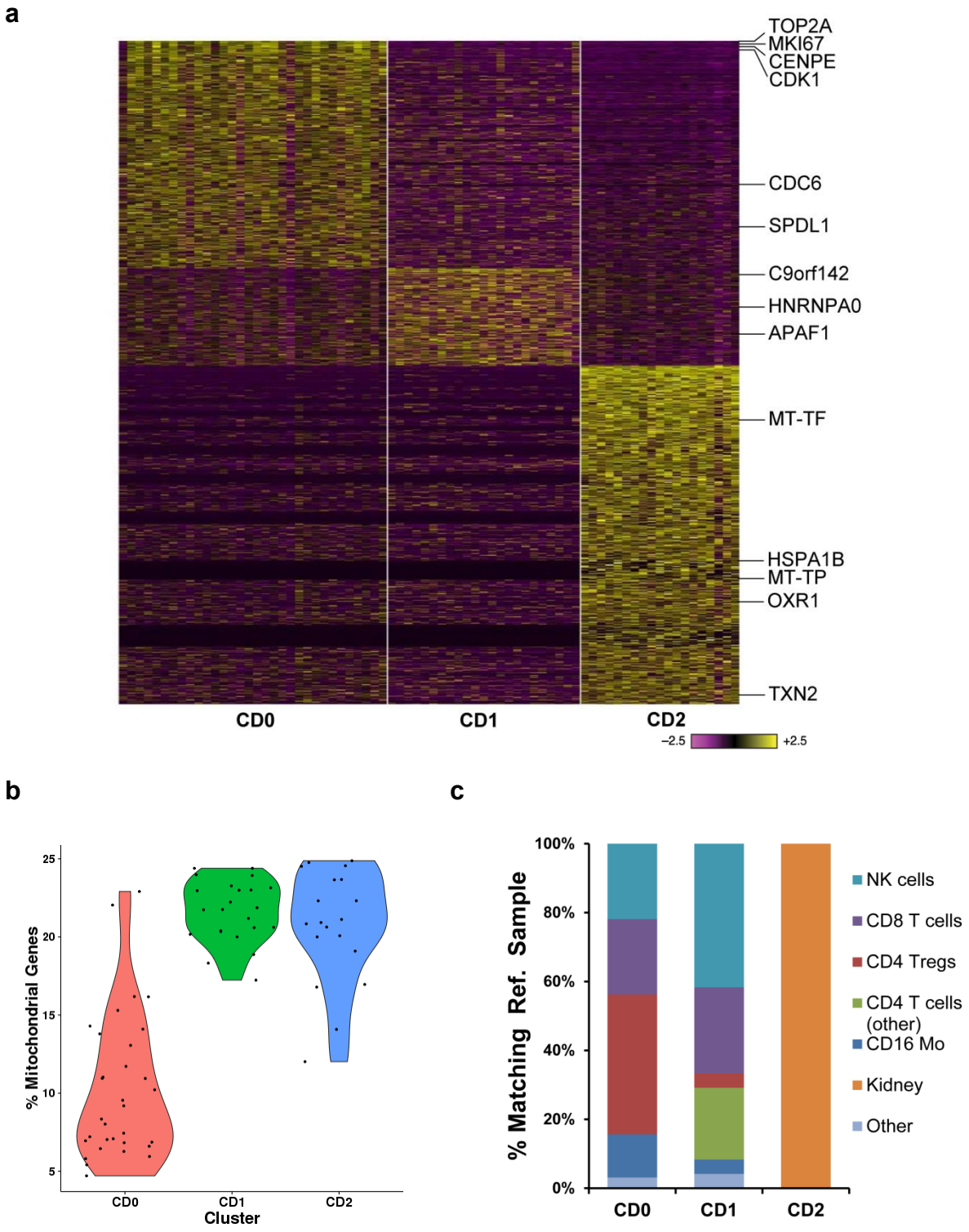

Figure S6. Focused analysis of cluster C9. **a,** The identification of 3 subclusters, the first of which pertains to cells undergoing mitosis. **b,** The percentage of mitochondrial genes detected

in each subcluster. **c,** Classification results for each subcluster, comparing the cells of cluster C9 to reference samples found in FANTOM5.

FIGURE S7

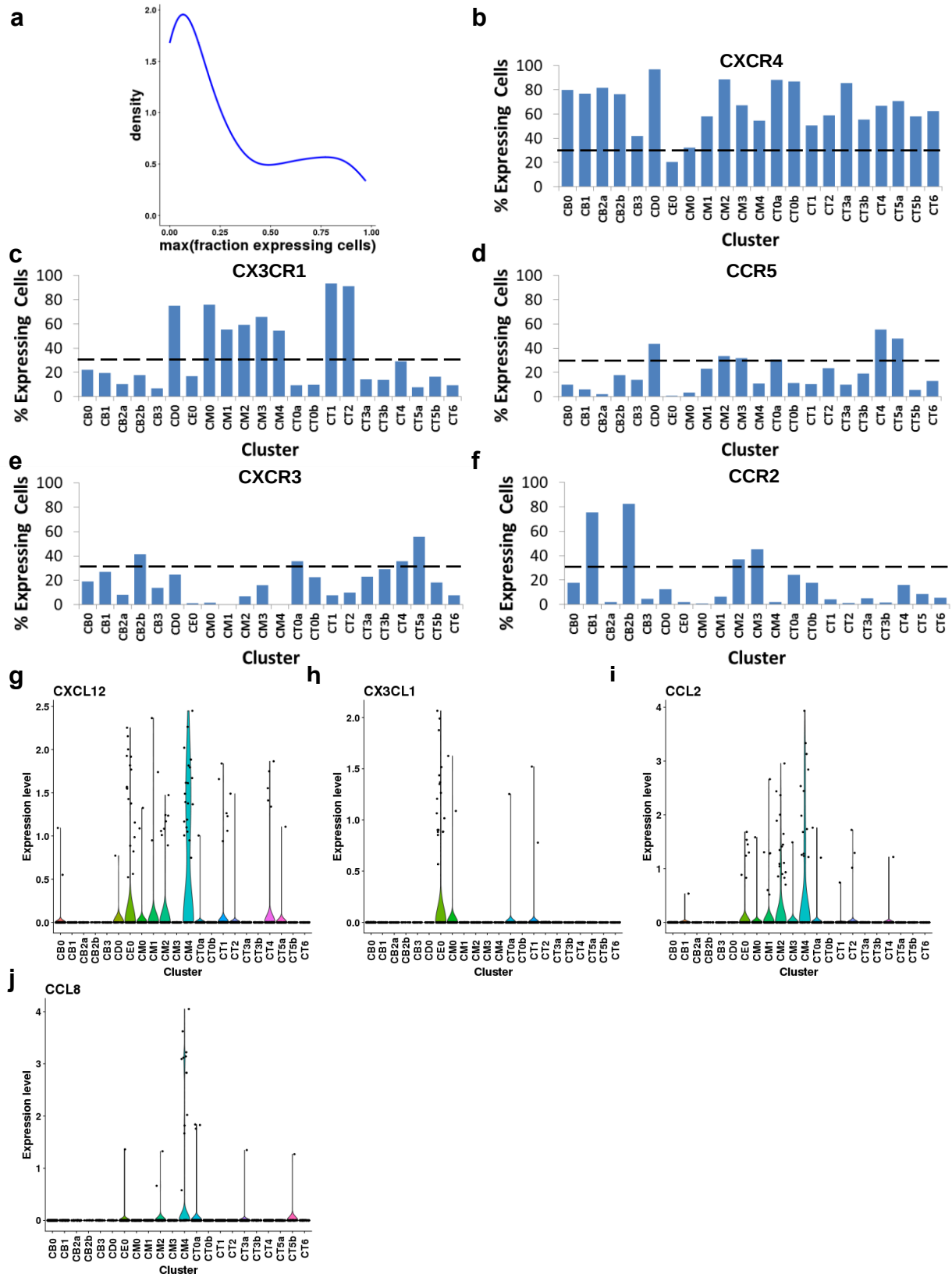
a
density
max(fraction expressing cells)
b
CXCR4
% Expressing Cells
Cluster
c
CX3CR1
d
CCR5
e
CXCR3
f
CCR2
g
CXCL12
h
CX3CL1
i
CCL2
j
CCL8
Expression level
CB0 CB1 CB2a CB2b CB3 CD0 CE0 CM0 CM1 CM2 CM3 CM4 CT0a CT0b CT1 CT2 CT3a CT3b CT4 CT5a CT5b CT6

Figure S7. Analysis of chemokine and cytokine networks. **a,** The distribution of the maximum fraction of expressing cells (taken over all clusters for each receptor), for all receptors. Based on this distribution, a threshold of 0.3 was chosen to define frequently expressed receptors. **b-f,** The percentage of cells expressing selected chemokine receptors, specified for each cluster. **g-j,** The distribution of expression levels of selected chemokines, for each cluster.

FIGURE S8

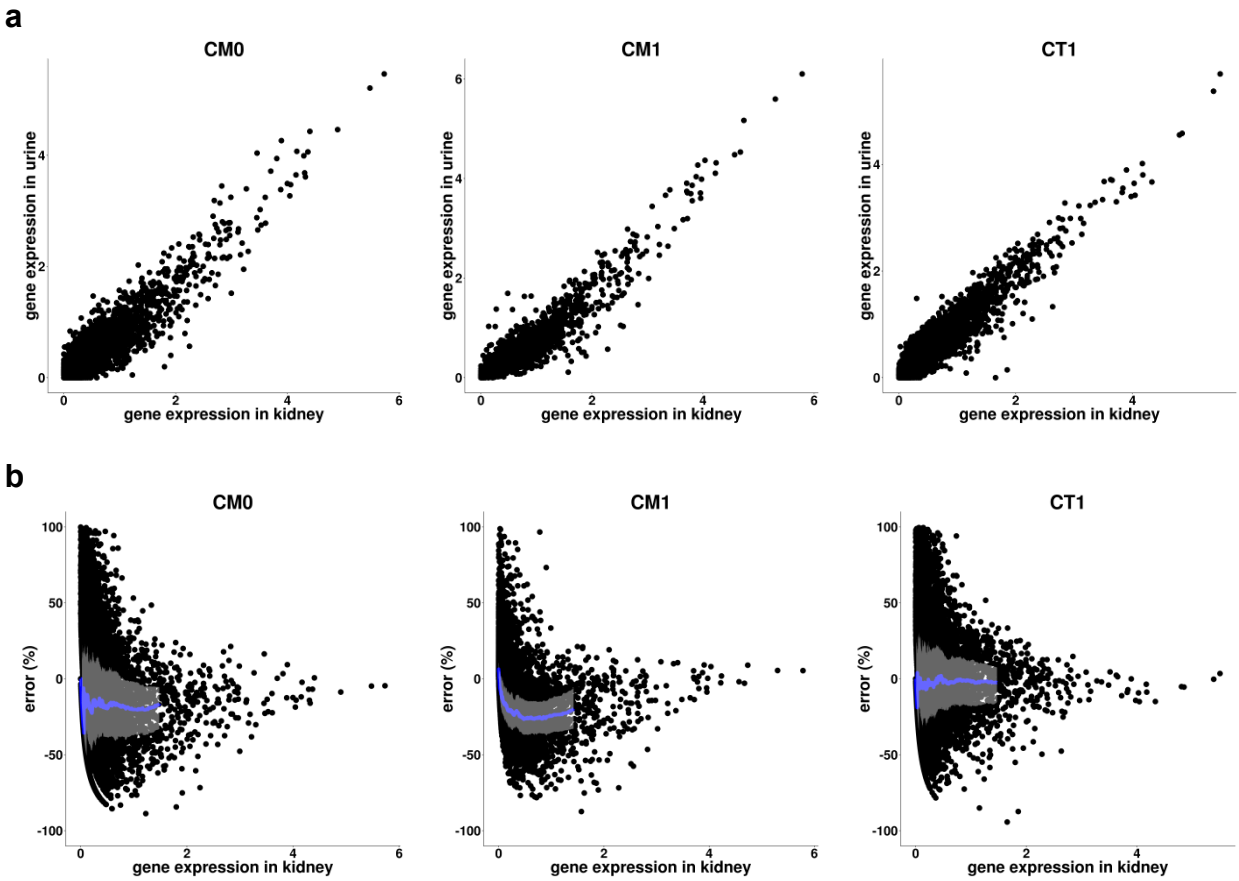

Figure S8. Analysis of urine cells. **a,** A comparison of gene expression in kidney (x axis) and urine (y axis), for 3 of the clusters represented in both. **b,** The relative error (in percent) predicting kidney gene expression using urine gene expression, as a function of the gene expression level in the kidney. The blue line represents a moving window median (window size of 500 points); the shaded area represents the interquartile range, computed using the same moving window.