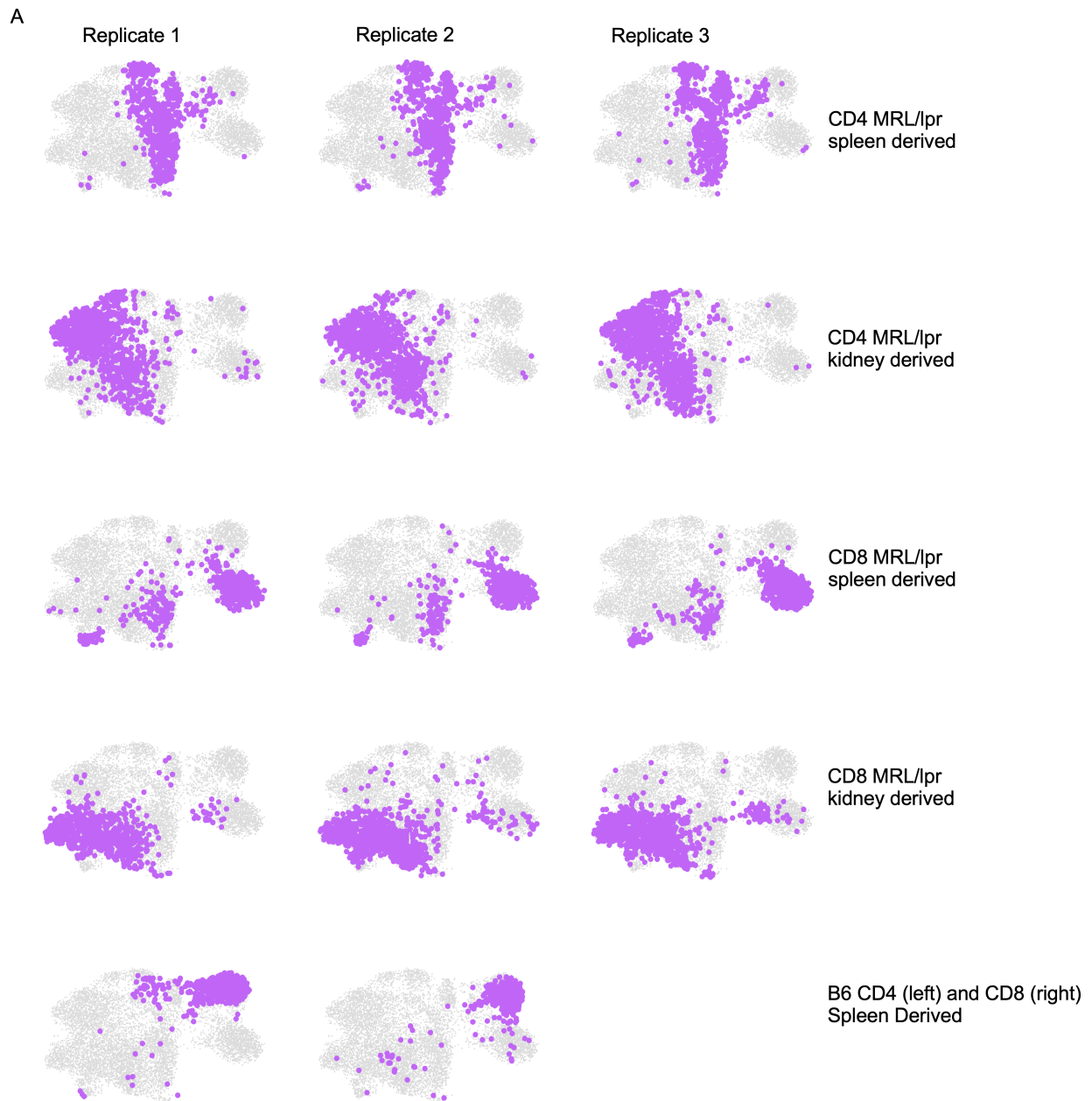
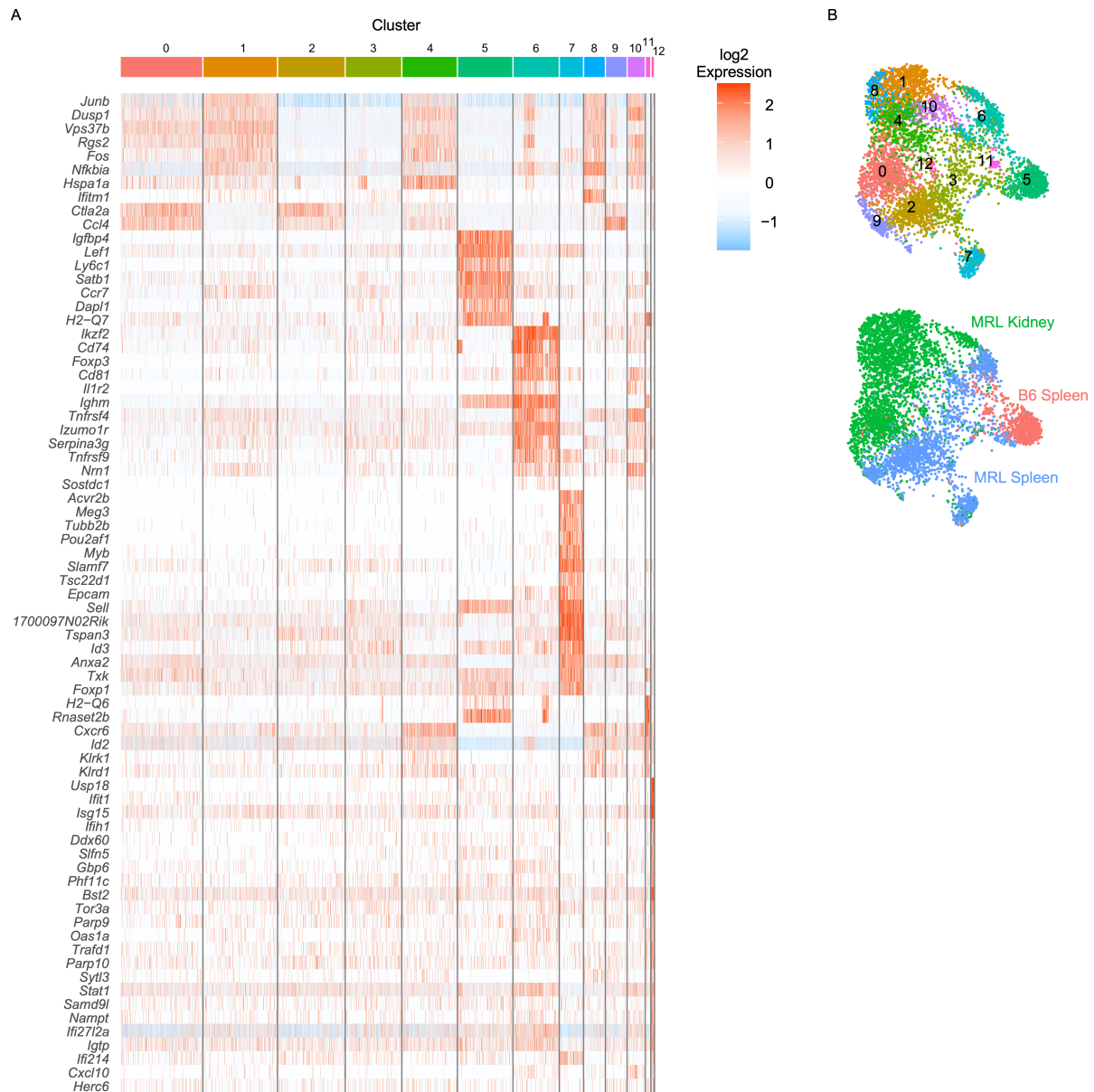


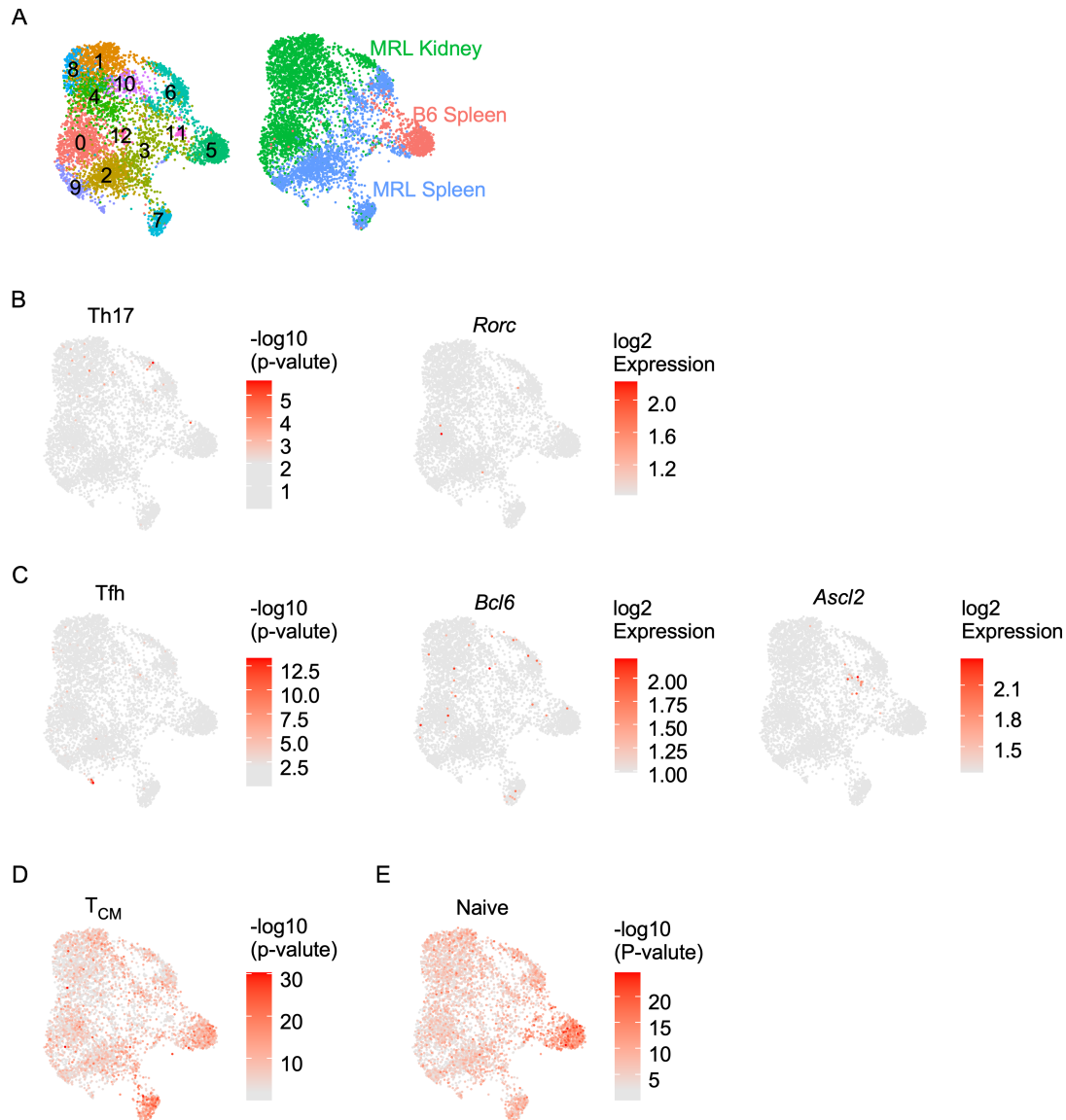
Supplemental Data:



Supplemental Figure 1: *Analytics methodology* (A) Cell source determined using HTO for each of the 14 individual sorted populations was overlaid on the UMAP projection (as per Fig 1B) and organized based on replicates to exhibit the equal contribution of each replicate to the observed clusters.

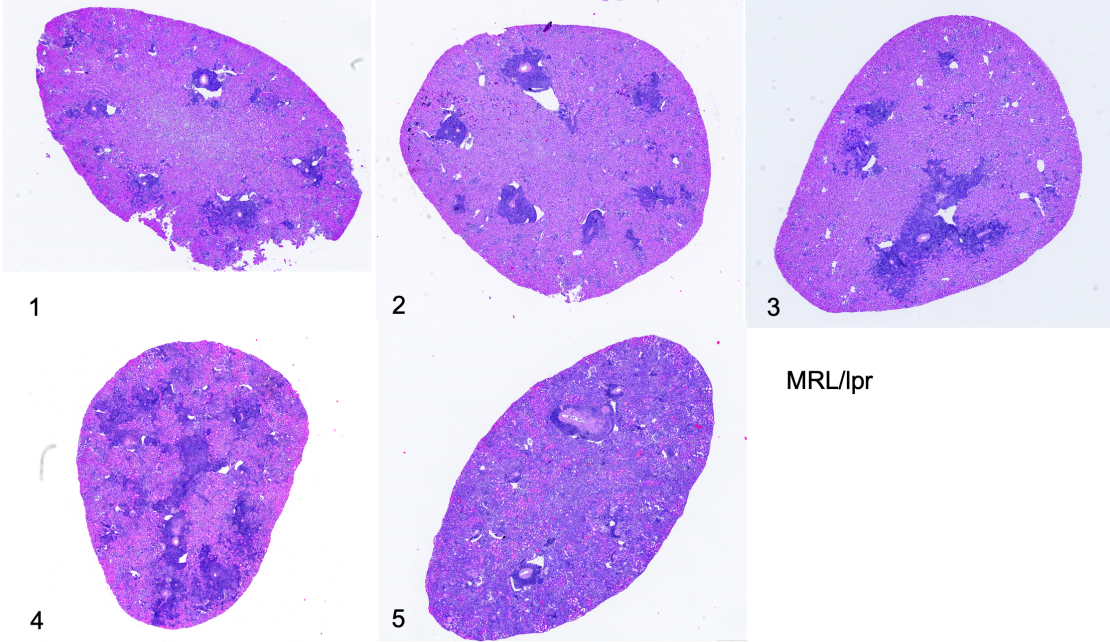


Supplemental Figure 2: *Top DEGs associated with CD4 T cell clusters.* (A) Heat map shows top (Fold change > 1 and FDR < 0.01) significant differentially expressed genes (rows) associated with the 13 CD4 clusters and their expression at the single cell level (columns), colored according to expression level. (B) With UMAP projection of CD4 T cells from Main-seq outlining 13 clusters, and overlay of cell source as determined by HTO (as defined in Figure 2).

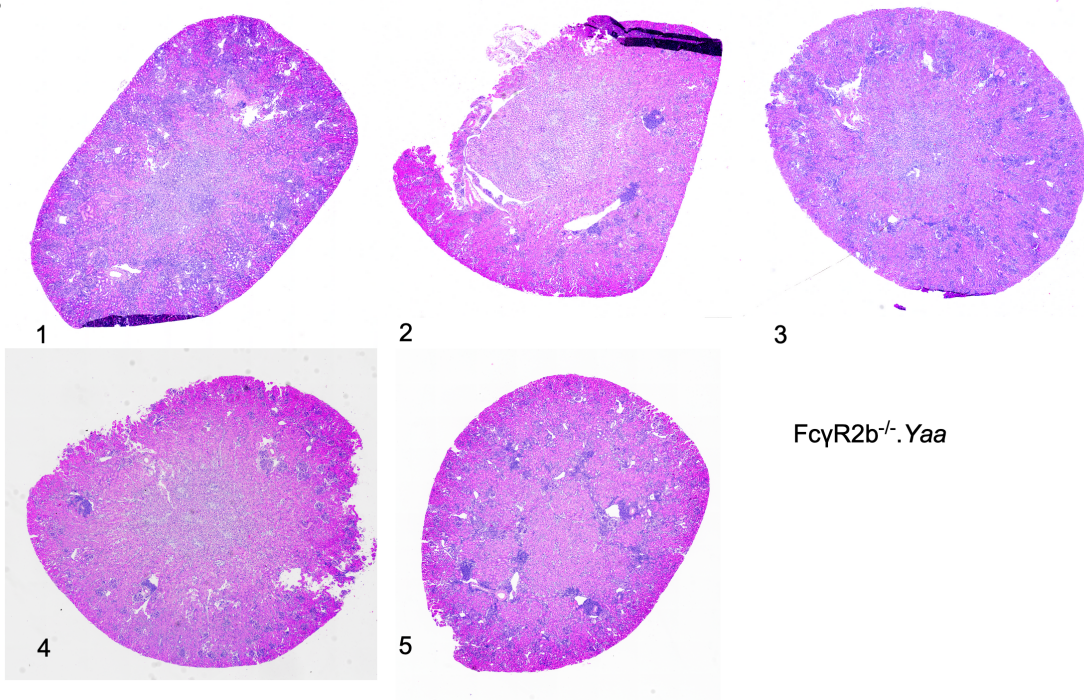


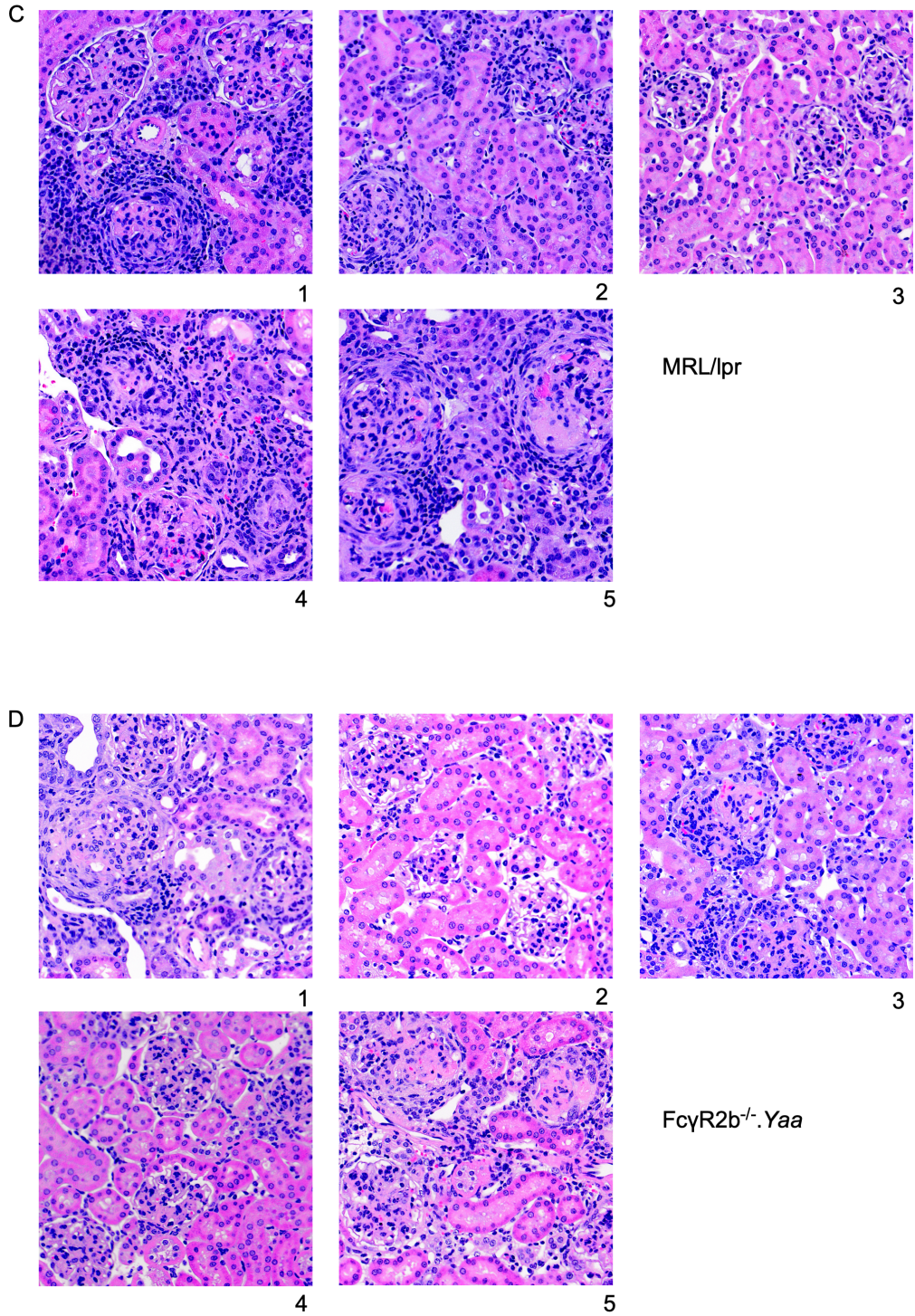
Supplemental Figure 3: GSEA and gene expression mapping identifies clusters and cells with a naïve and T_{CM} signature but not Th17 or Tfh populations. GSEA performed in each cell by Wilcox-test using published reference signature genes (Table S1) and related TF expression is mapped onto the (A) CD4 UMAP and HTO defined cell source to identify CD4 T cell phenotypes. (B) Th17 gene signature and associated TF *Rorc*; (C) Tfh gene signature and associated transcription factors *Bcl6* and *Ascl2*; and gene signatures for (D) T_{CM} and (E) naïve populations.

A

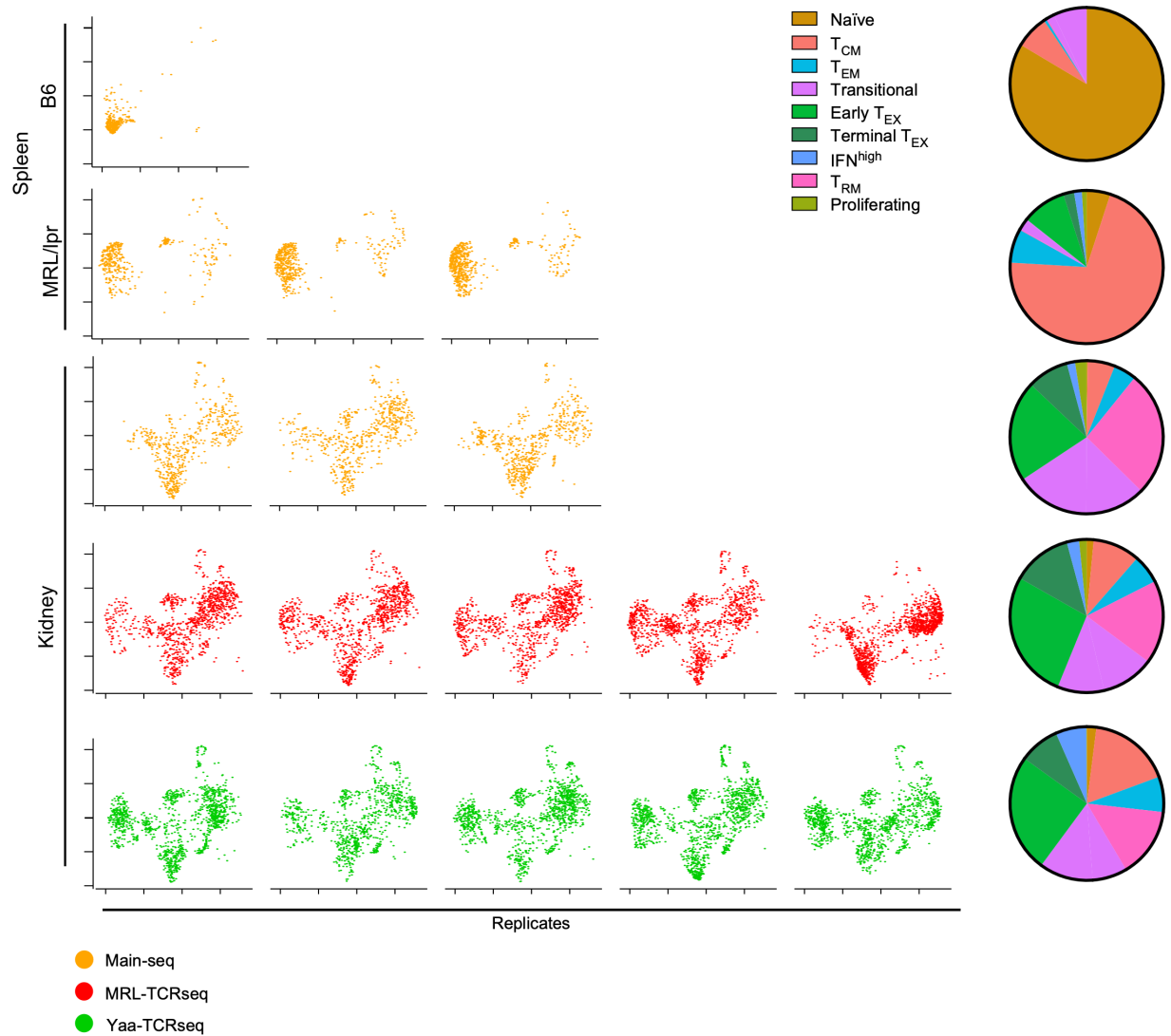


B





Supplemental Figure 4: H&E stained cross section of kidneys from mice analyzed in (A) cohort 2 (MRL-TCRseq), and (B) cohort 3 (Yaa-TCRseq), with high resolution 20x images of representative glomeruli for (C) cohort 2 mice (MRL-TCRseq), and (D) cohort 3 (Yaa-TCRseq). Associated disease scoring is included in Supplemental Table 2.

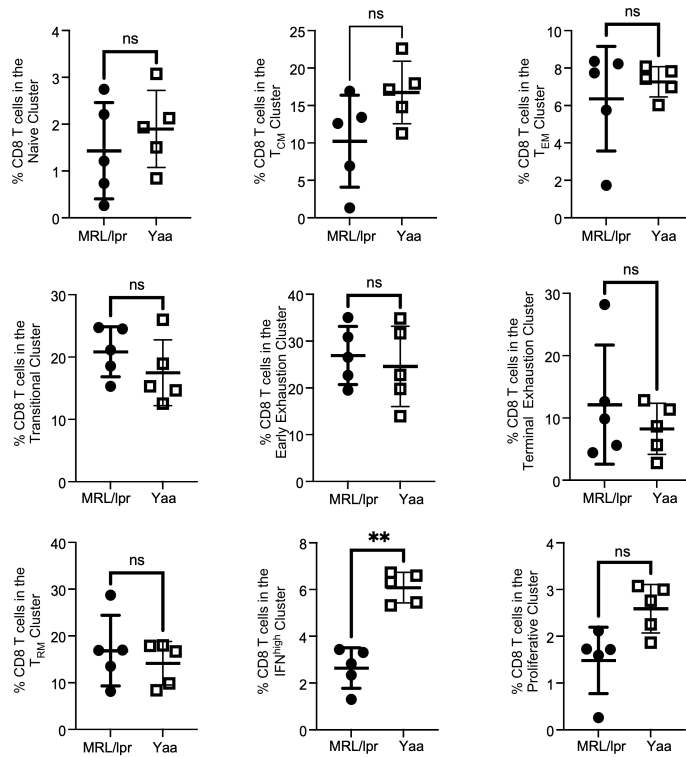


Supplemental Figure 5: *Cluster contribution by mouse and cohort.* Mouse by mouse contribution to combined CD8 UMAP cluster as defined in Figure 5. Each row of UMAP plots represents a single source and origin. The cohort derivation of each UMAP plot is color-coded according to the legend. Pie charts to the right represent relative phenotypically-identified cluster distribution of T cells within combined cells from each source/origin.

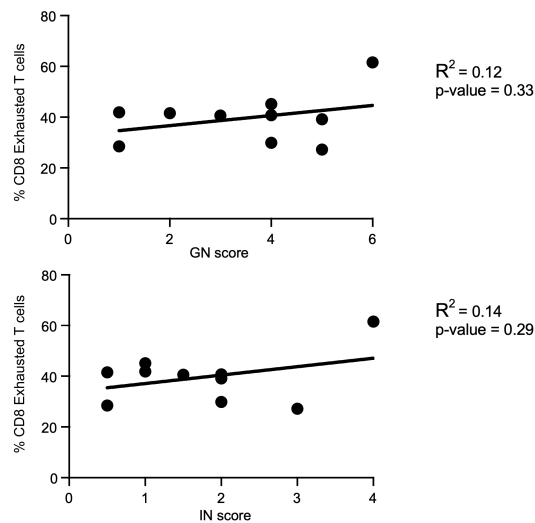
A



B

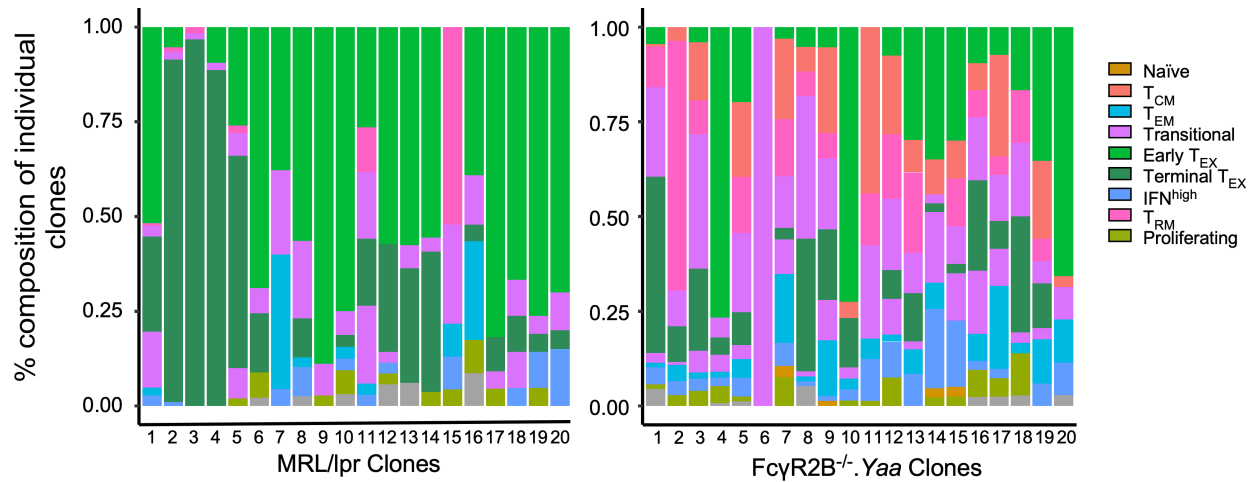


C



Supplemental Figure 6: *CD8 Cluster distribution does not differ by mouse model or based on histologic disease.* (A) Pie charts represent relative phenotypically-identified cluster distribution of CD8 T cells defined in Figure 5 for each mouse assessed in cohort 2 and 3. (B) Dot plot represents percent of CD8 T cells from MRL/lpr and FcγR2B^{-/-}.Yaa (Yaa) models in each outlined cluster. Statistics were determined using Two-way Anova with repeat measures corrected for multiple comparisons using Bonferroni adjustment (**

indicates p-value <0.01). (C) Linear regression analysis of % exhausted T cells in each mouse and corresponding histologic disease score, either glomerulonephritis (GN) or interstitial nephritis (IN), with no analysis reaching statistical significance.



Supplemental Figure 7. *Progeny of the same T cell transition between different clusters within the kidney suggesting dynamic progression between T cell states.* Bar graphs represent the top 20 CD8 T cell clones from the MRL/lpr (left panel) and FcγR2B^{-/-}.Yaa (right panel) models with the relative distribution of these clones within the putative T cell clusters as defined in Fig. 8 B/C.

ATL3	KIAA1078	Mki67
ATP10A	KIAA1189	Ndrq4
ATP2B2	KIAA1729	Kif4
AV249152	KIAA1971	Osbp13
AW555355	KIF2	Ccnb2
B230312A22RIK	KIFAP3	Endod1
B3GALT5	KLF7	Birc5
B4GALT1	LASS6	Endod1
B4GALT5	LCHN	Cnn3
B830008J18RIK	LDHB	Fads2
B930095G15RIK	LEF1	Srxn1
BACE2	LENG10	Kif11
BAIAP2L1	LEPROTL1	S100a4
BARD1	LETMD1	Zbtb32
BB557941	LGTN	Lacc1
BC010981	LIAS	Pbk
BC023744	LISCH7	8-Mar
BC046404	LKAP	Tnfsf14
BC068157	LNPEP	Gm3924
BCL2L1	LOC129293	Endod1
BCL2L15	LOC143903	Bmp7
BCL6B	LPAAT-e	Gm34221
BCMO1	LRRC5	Ctla2b
BEND6	LRRN3	Alcam
BMPR2	LT44H	Myo1f
BNIP3	LTB	Plek
BRCA2	LY96	Optn
BSPRY	LYPLAL1	Srxn1
BTBD10.LOC100047893	MAGEH1	Gstt3
C130057M05RIK	MAL	Gm5593
C1QL3	MAML2	Ccnb1
C230098O21RIK	MAN1C1	Zdhhc2
C76533	MDS2	Bub1
C77545	MEST	Jdp2
C80258	MGC15763	Tmem2
CABLES1	MGC17330	8030451A03Rik
CALCB	MMS19L	Chrd1
CALD1	MPHOSPH9	Cdca8
CAMK2N1	MRPL1	Soat2
CAMK4	MSL3L1	S100a6
CAPSL	MTRF1	Atp1b1
CAR13	MTUS1	Morn4
CAR6	MYB	Klrc1
CAV1	MYC	Spag5
CAV2	NDE1	Tjp2
CCDC112	NDFIP1	Igfbp4
CCDC122	NDUFB5	Ccna2
CCDC21	NELL2	Ampd1
CCDC34	NGFRAP1	Runx2
CCL1	NKX3-1	Stfa3
CCL27A	NOG	Igfbp4
CCR8	NRCAM	Gm17619
CD200R4	NUCB2	Tshz2
CD34	PCSK5	Gpm6a
CD70	PDK1	Ncapp
CD93	PHEMX	Tk1
CDC14A	PIK3CD	Kitl
CDC14A.LOC100047731	PLAC8	Morc1
CDC25C	RAC2	Dtl
CDK6	RAPGEF6	Aifm2
CENPA	RASA2	Gm36401
CENPI	RASA4	Adam19
CENPP	RIN3	Stil
CETN4	RNU22	Kif14
CHAC1	SAMHD1	Igfbp4
CHST10	SP110	Ccnb1
CHST12	STK4	Gzmk
CIAPIN1	STX16	Proser2
CILP2	SUMF2	Ccna2
CKAP2	T3JAM	Rragd
CLDN12	TM4SF8	Pawr
CLEC4D	TPP2	Pif1
CNNM2	TTC11	Ccnf
CNRIP1	USP52	Esco2
CNTLN	VPS35	2810417H13Rik
COCH	WDR42A	Gna15
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COPZ2	ZNF291	
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D3ERTD751E.GM9529		
D430033H22RIK		
D5WSU178E		

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DLG2
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DNAJC12
DNAJC25
DPYSL3
DRAM1
DSC2
DSCAM
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DXERTD242E
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GPR97
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HHAT
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MYADM
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NDC80
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NEBL
NEK2
NEK7
NIPA2

NKG7
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NOL7
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NRP1
NT5DC2
NUF2
OLFM1
OSBPL3
PAQR4
PDCD1LG2
PF4
PGK1
PGLYRP1
PGM2
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PHACTR4
PHLPP1
PIK3CG
PKM2
PLEK
PLEKHB2
PLEKHF1
PLEKHO2
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SPRY2

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TNFSF11
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TOX
TPI1
TPX2
TRAM1
TRIB3
TRPS1
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TTC39C
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TYMS.TYMS.PS
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UGP2
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TNFSF14
TRAPPC1
TRAPPC4
TRPT1
TSEN2
TSGA14

Supplemental Table 2:

Experimental Mice used

Main-seq

Background	Mouse number	Age at Sacrifice	Proteinuria	Gender
MRL/lpr	1	21 weeks	4	F
MRL/lpr	2	21 weeks	2.5	F
MRL/lpr	3	21 weeks	1	F
C57Bl/6	4	8 weeks	0	F

MRL-TCRseq

Background	Mouse number	Age at Sacrifice	Proteinuria	Gender	GN score	IN Score
MRL/lpr	1	20.5 weeks	4	F	3.5	1.5
MRL/lpr	2	21 weeks	2.5	F	3	1.5
MRL/lpr	3	21 weeks	1	F	2	1
MRL/lpr	4	25.5 weeks	4	F	5	2.5
MRL/lpr	5	25.5 weeks	4	F	6	3

Yaa-TCRseq

Background	Mouse number	Age at Sacrifice	Proteinuria	Gender	GN score	IN Score
<i>FcyR2b^{-/-}.Yaa</i>	1	23.5 weeks	4	M	5	2
<i>FcyR2b^{-/-}.Yaa</i>	2	24 weeks	4	M	2	0.5
<i>FcyR2b^{-/-}.Yaa</i>	3	23.5 weeks	2.5	M	4	1
<i>FcyR2b^{-/-}.Yaa</i>	4	23.5 weeks	3	M	3	0.5
<i>FcyR2b^{-/-}.Yaa</i>	5	23 weeks	2	M	4	2