

SUPPLEMENTARY DATA

Figure S1

Simulated dendrogram of four samples. A. Simulated dendrogram tree with four samples and 10 subgroups for each sample. B-C. ClusterMap tree cut results for the simulated tree at edge cutoffs of 0.1 and 0.2. D. Diagram of the separability calculation.

Figure S2

A-B. Feature plot for identifying cell types. The known markers for basal cells are Krt14, Acta2, Myl9, Sparc, Mylk, and Cxcl14. Luminal cells express Elf5, Prlr, Areg, Ly6d, Stc2, Krt19, and mature luminal express Pgr, Prlr, Cited1, Esrrb, and Cxcl15 (15). C-D. Gene ontology and pathway analysis for new marker genes of groups in combined samples (Figure 4C) using Metascape. C. luminal progenitors groups 1 and 11. D. Basal groups 3 and 7.

Figure S3

A. Pre-analysis for immune stimulated datasets. B. Circos plot of matched sub groups. C-D. Feature plot for identifying cell types.

Figure S4

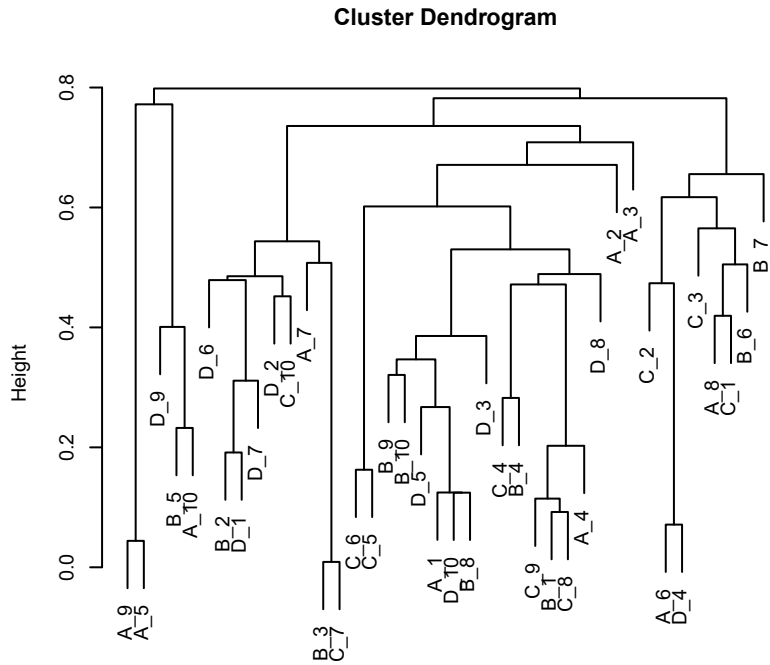
Analysis for PBMC replicates. A. Pre-analysis of PBMC 4K. B. Pre-analysis of PBMC 8K. C. Heat map of marker genes. D. ClusterMap results. E-F. Feature plots to identify cell types.

Figure S5

CCA analysis and clustering for epithelial cell datasets as in Figure3, 4. A. t-SNE plot of clustered cells. B. t-SNE plot with cells colored by sample. C. Feature plot for identifying cell types. D. t-SNE plot of CCA analysis. Cells of group 2 in estrus, defined as in Figure 4B are highlighted in green.

Figure S1

A



B

edge_cutoff = 0.1

	A	B	C	D	similarity	regroup
1	NA	B_3	C_7	NA	0.99	1
2	A_9;A_5	NA	NA	NA	0.96	2
3	A_6	NA	NA	D_4	0.93	3
4	A_1	B_8	NA	D_10	0.88	4
5	NA	NA	C_6;C_5	NA	0.84	5
6	NA	B_2	NA	D_1	0.81	6
7	A_4	B_1	C_9;C_8	NA	0.8	7
8	A_10	B_5	NA	NA	0.77	8
9	NA	B_4	C_4	NA	0.72	9
10	NA	B_9;B_10	NA	NA	0.68	10
11	NA	NA	C_10	D_2	0.55	11
12	A_8	B_6	C_3;C_1	NA	0.43	12
13	NA	NA	NA	D_9	NA	13
14	NA	NA	NA	D_6	NA	14
15	NA	NA	NA	D_7	NA	15
16	A_7	NA	NA	NA	NA	16
17	NA	NA	NA	D_5	NA	17
18	NA	NA	NA	D_3	NA	18
19	NA	NA	NA	D_8	NA	19
20	A_2	NA	NA	NA	NA	20
21	A_3	NA	NA	NA	NA	21
22	NA	NA	C_2	NA	NA	22
23	NA	B_7	NA	NA	NA	23

C

edge_cutoff = 0.2

	A	B	C	D	similarity	regroup
1	NA	B_3	C_7	NA	0.99	1
2	A_9;A_5	NA	NA	NA	0.96	2
3	A_6	NA	NA	D_4	0.93	3
4	NA	NA	C_6;C_5	NA	0.84	4
5	A_4	B_1	C_9;C_8	NA	0.8	5
6	NA	B_4	C_4	NA	0.72	6
7	A_1	B_9;B_10;B_8	NA	D_5;D_10;D_3	0.61	7
8	A_10	B_5	NA	D_9	0.6	8
9	NA	B_2	C_10	D_6;D_1;D_7;D_2	0.51	9
10	A_8	B_6	C_3;C_1	NA	0.43	10
11	A_7	NA	NA	NA	NA	11
12	NA	NA	NA	D_8	NA	12
13	A_2	NA	NA	NA	NA	13
14	A_3	NA	NA	NA	NA	14
15	NA	NA	C_2	NA	NA	15
16	NA	B_7	NA	NA	NA	16

D

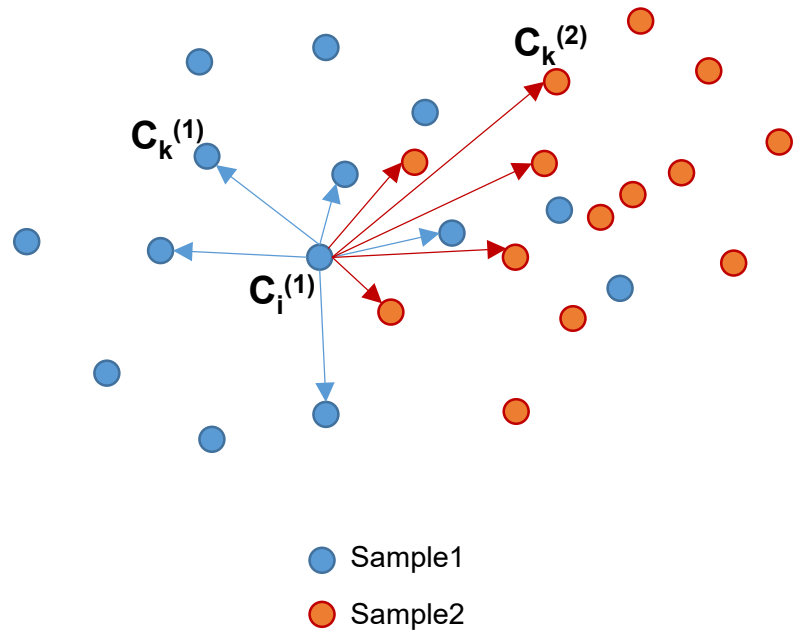
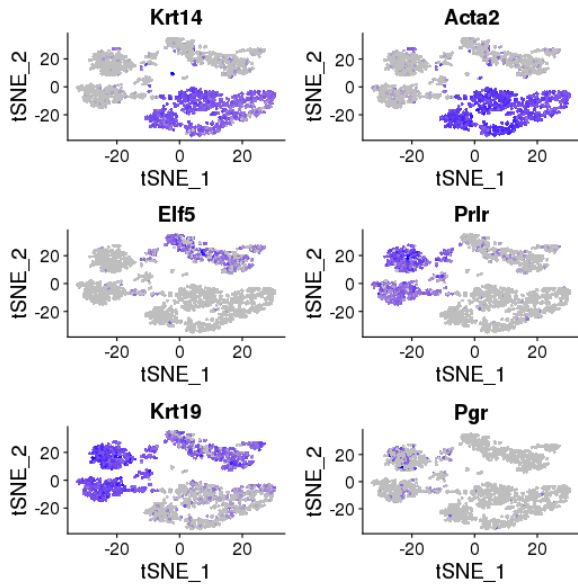


Figure S2

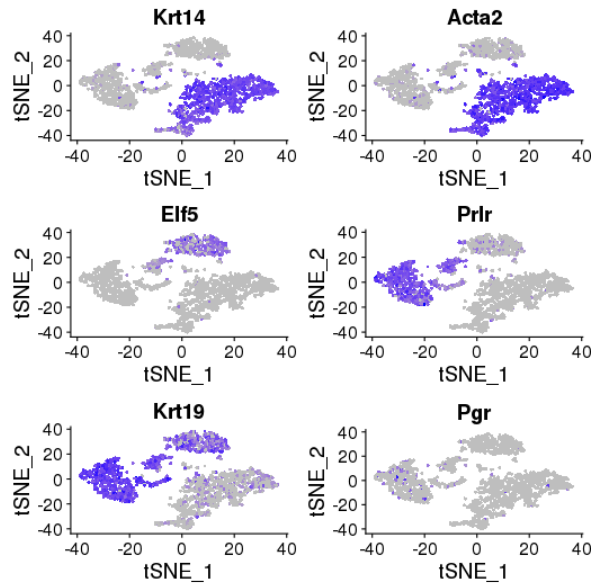
A

Diestrus (p7d)



B

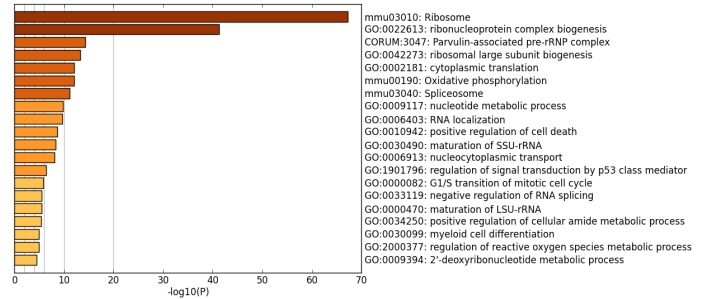
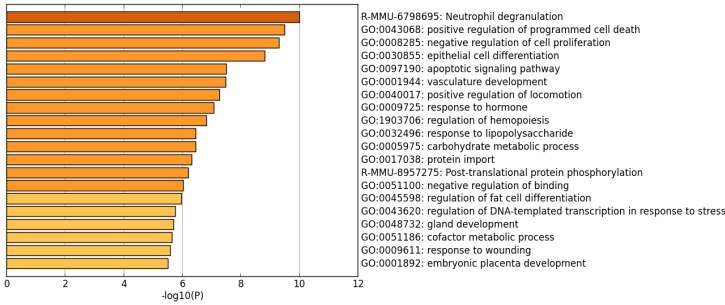
Estrus (p7e)



C

luminal progenitors Group1

luminal progenitors Group11, diestrus only



D

Basal Group 3, estrus enriched

Basal Group 7, diestrus

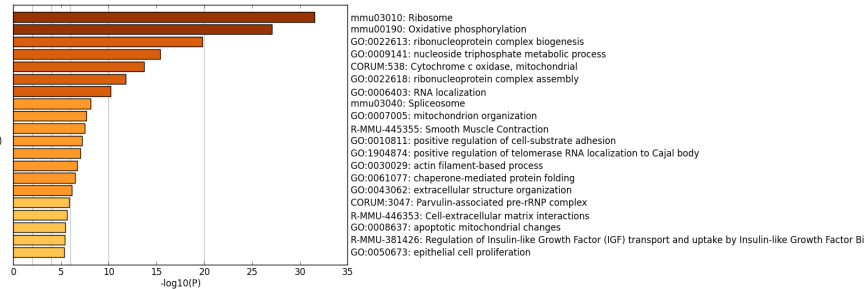
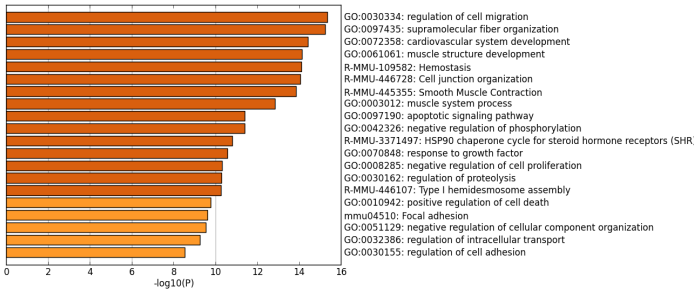
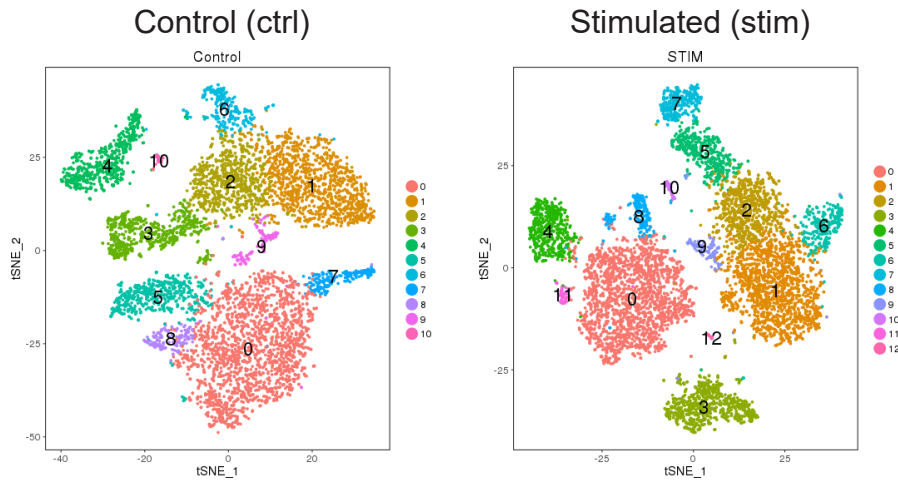
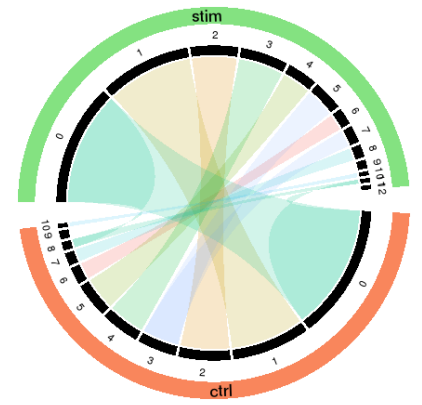


Figure S3

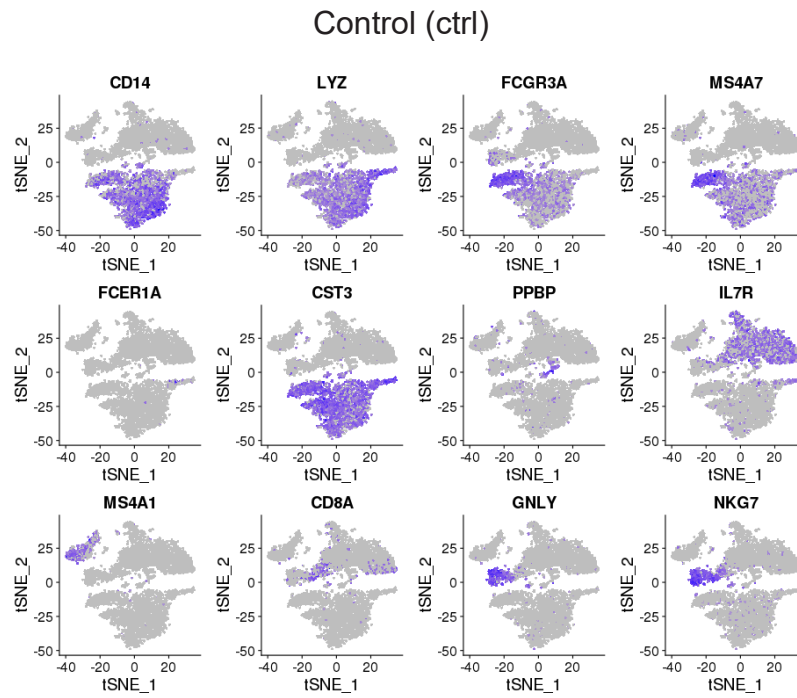
A



B



C



D

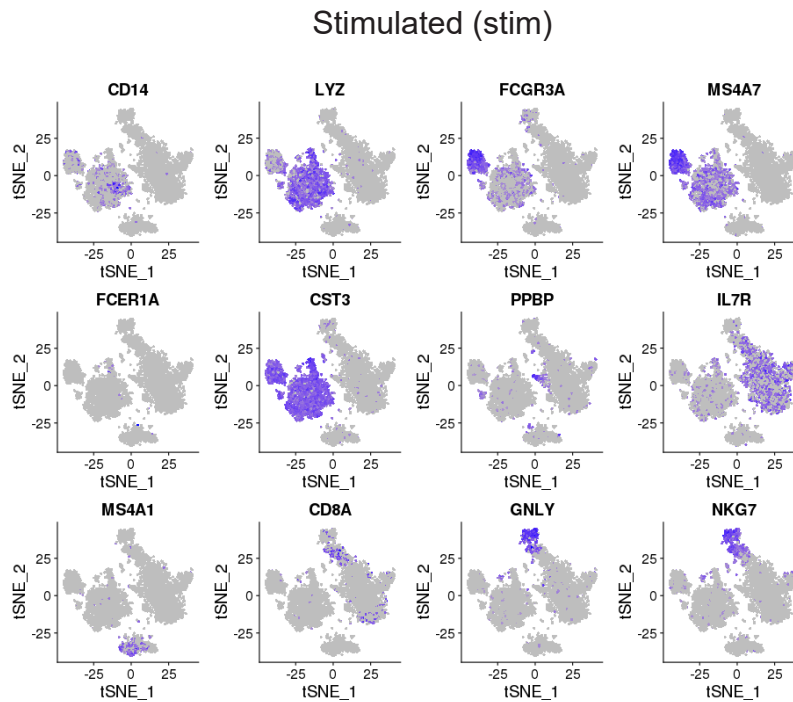
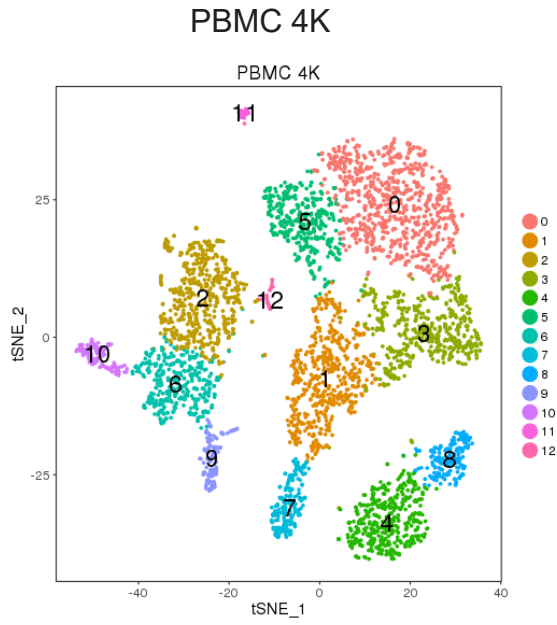
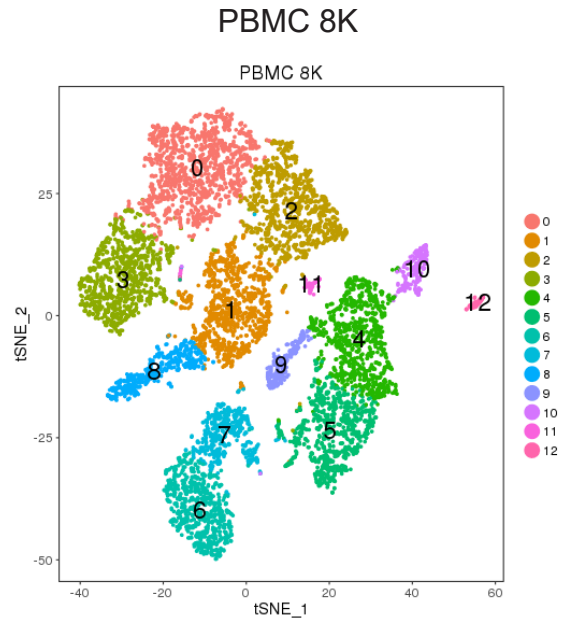


Figure S4

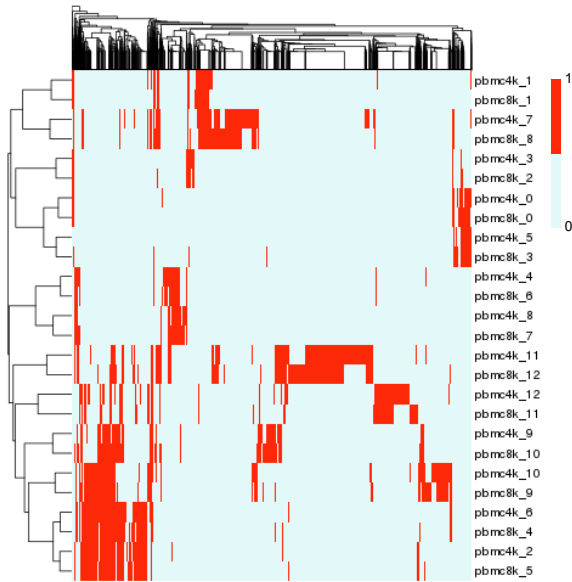
A



B



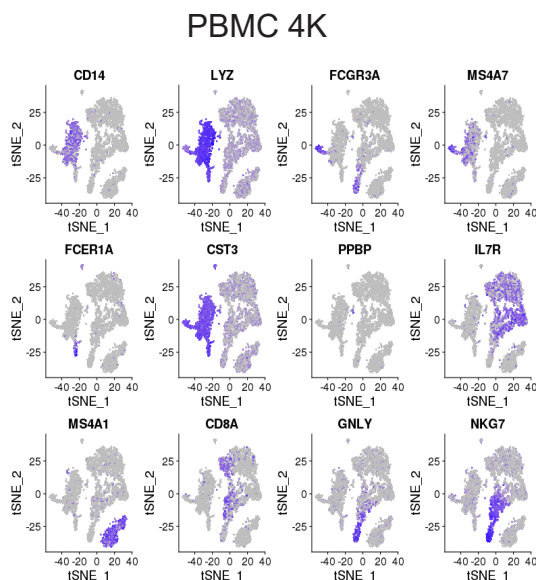
C



D

	pbmc4k	pbmc8k	similarity	regroup	pbmc4k_cell_perc	pbmc8k_cell_perc	pbmc4k.vs.pbmc8k_separability
1	pbmc4k_4	pbmc8k_6	0.83	1	0.1	0.09	-0.09
2	pbmc4k_6	pbmc8k_4	0.82	2	0.08	0.11	0.03
3	pbmc4k_2	pbmc8k_5	0.82	3	0.13	0.1	-0.01
4	pbmc4k_0	pbmc8k_0	0.79	4	0.19	0.16	-0.02
5	pbmc4k_3	pbmc8k_2	0.76	5	0.12	0.12	-0.08
6	pbmc4k_5	pbmc8k_3	0.76	6	0.09	0.12	-0.07
7	pbmc4k_10	pbmc8k_9	0.74	7	0.03	0.03	-0.08
8	pbmc4k_9	pbmc8k_10	0.71	8	0.03	0.03	-0.01
9	pbmc4k_8	pbmc8k_7	0.71	9	0.04	0.06	0.05
10	pbmc4k_1	pbmc8k_1	0.68	10	0.13	0.12	-0.08
11	pbmc4k_7	pbmc8k_8	0.66	11	0.04	0.06	0.05
12	pbmc4k_11	pbmc8k_12	0.61	12	0.01	0.01	-0.08
13	pbmc4k_12	pbmc8k_11	0.48	13	0.01	0.01	-0.02

E



F

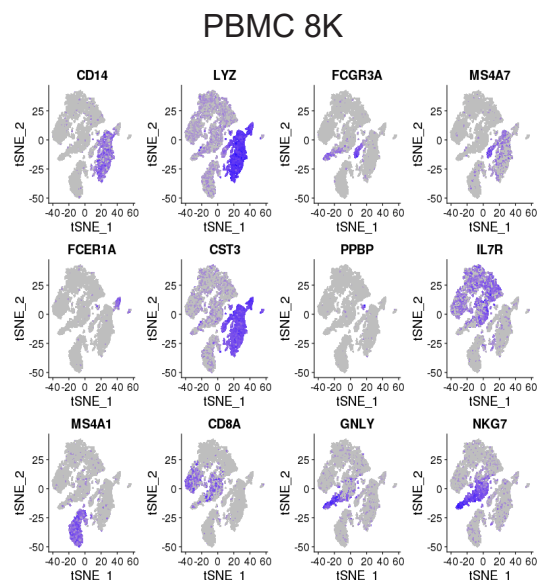
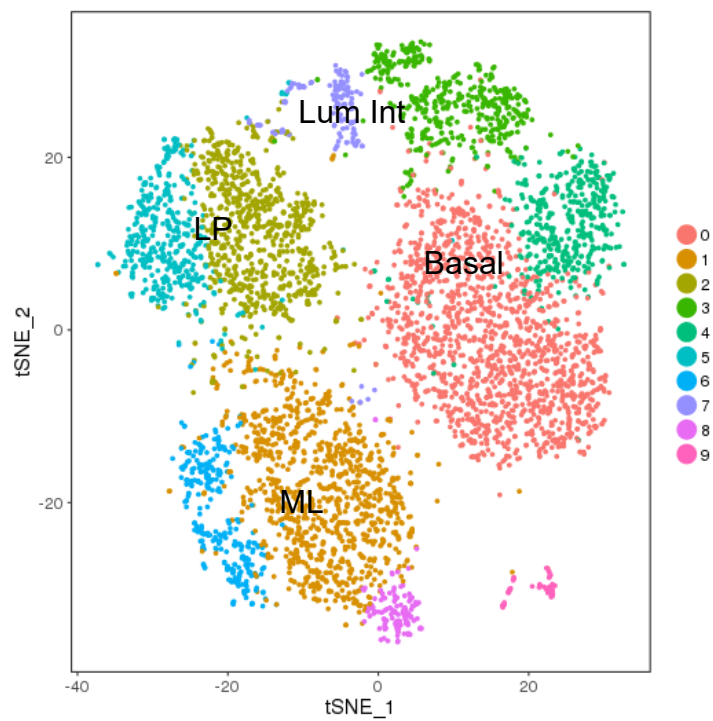
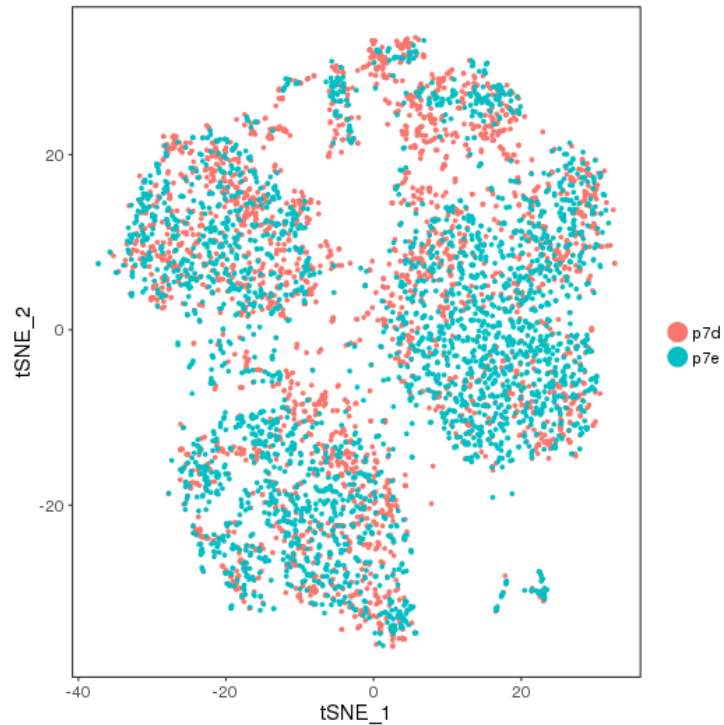


Figure S5

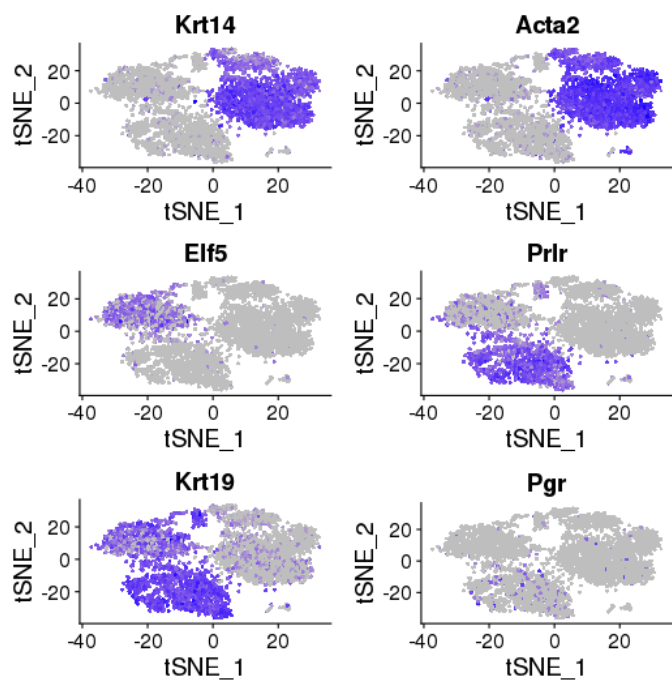
A



B



C



D

