

SUPPLEMENTARY DATA

Figure S1

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

Figure S2

A-B. Feature plot for identifying cell types. C-D. Gene ontology and pathway analysis for the new marker genes of groups in combined sample (Figure 4C) using Metascape. C. luminal progenitors groups 1 and 11. D. Basal groups 3 and 7.

Figure S3

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

Figure S4

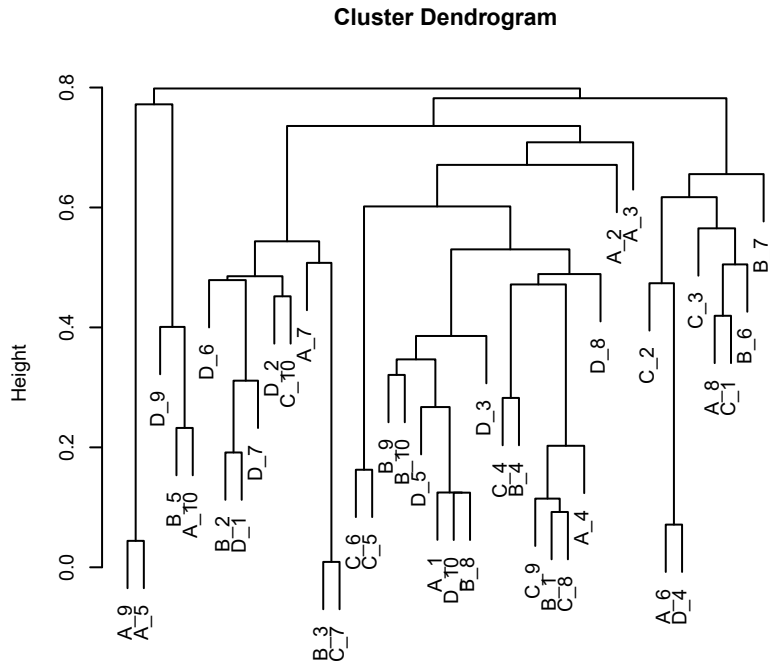
Analysis for PBMCs replicates. A. Pre-analysis of PBMC 4K. B. Pre-analysis of PBMC 8K. C. Heat map of marker genes. D. ClusterMap results. E-F. Feature plots to identify cell types.

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 with highlighted cells of group 2 and group 10, defined as in Figure 4.

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

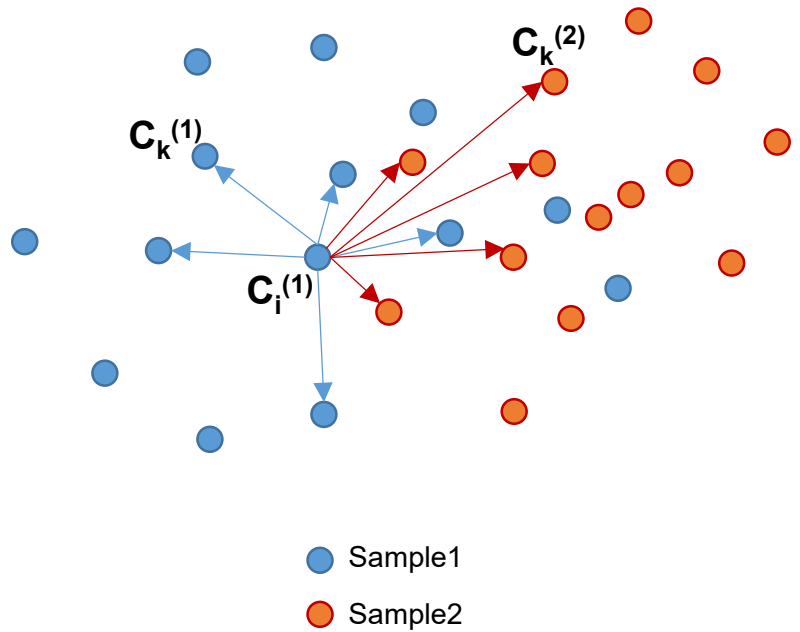
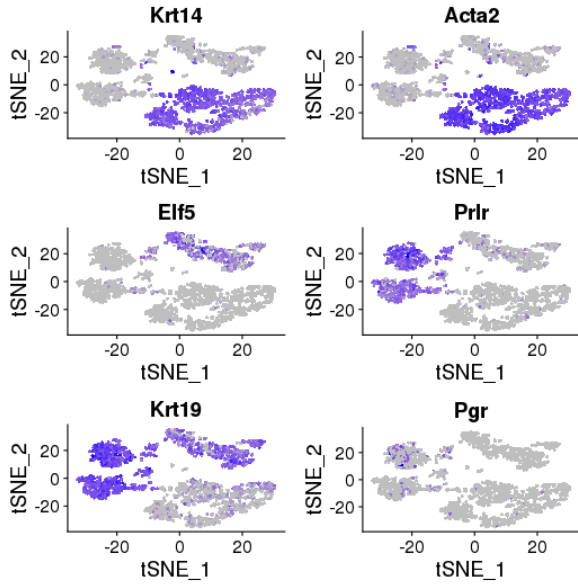


Figure S2

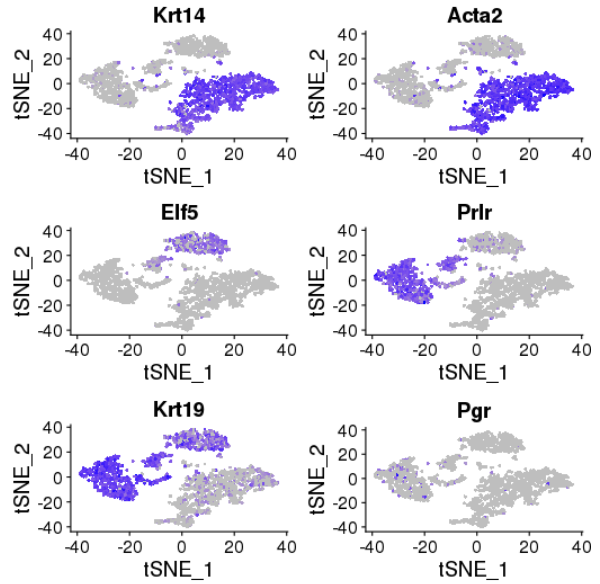
A

Diestrus (p7d)



B

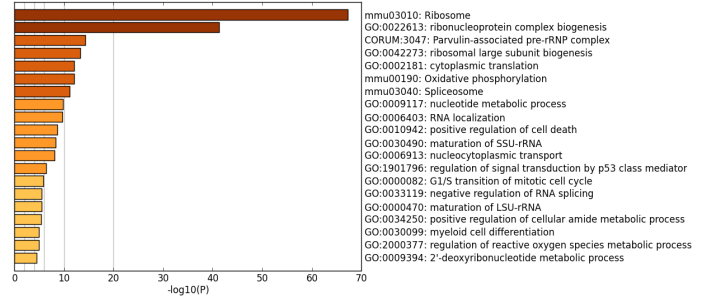
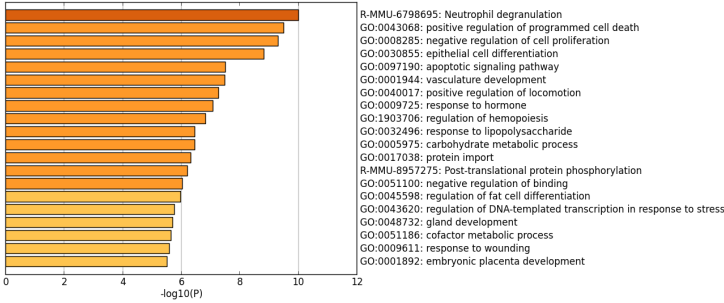
Estrus (p7e)



C

luminal progenitors Group1

luminal progenitors Group11, diestrus only



D

Basal Group 3, estrus enriched

Basal Group 7, diestrus

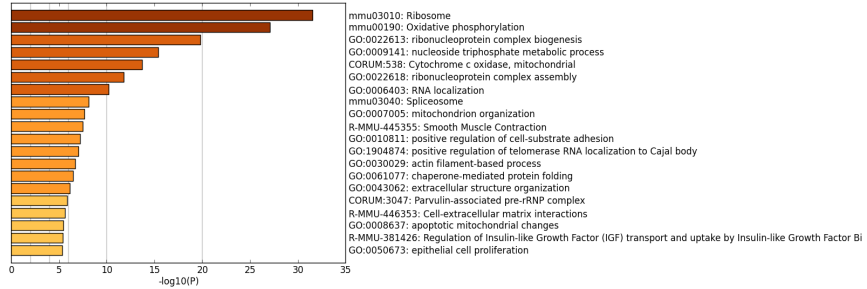
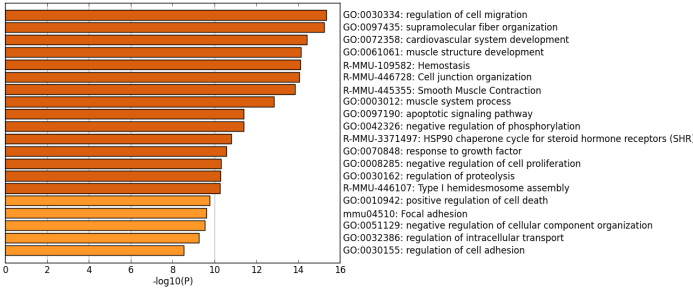
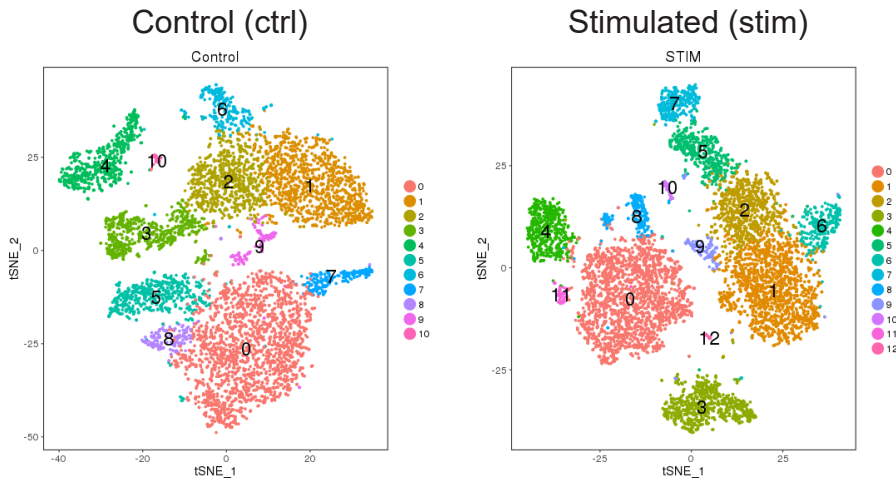
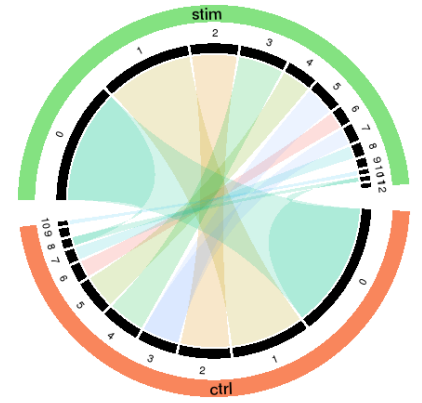


Figure S3

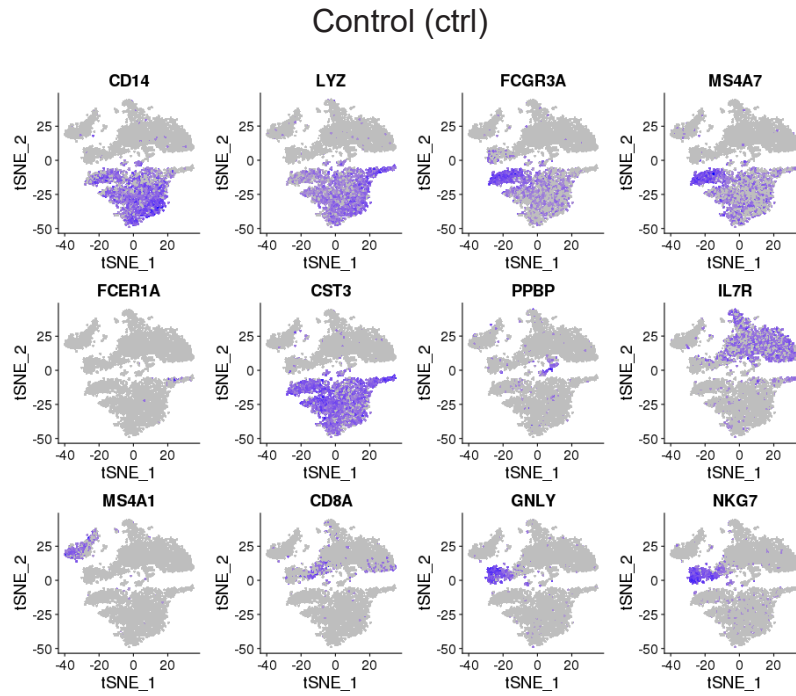
A



B



C



D

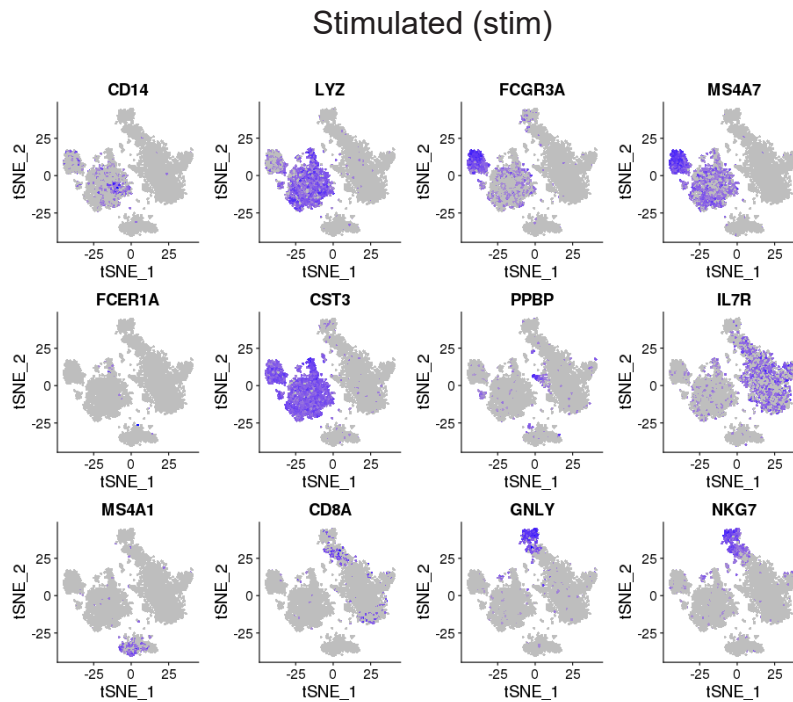
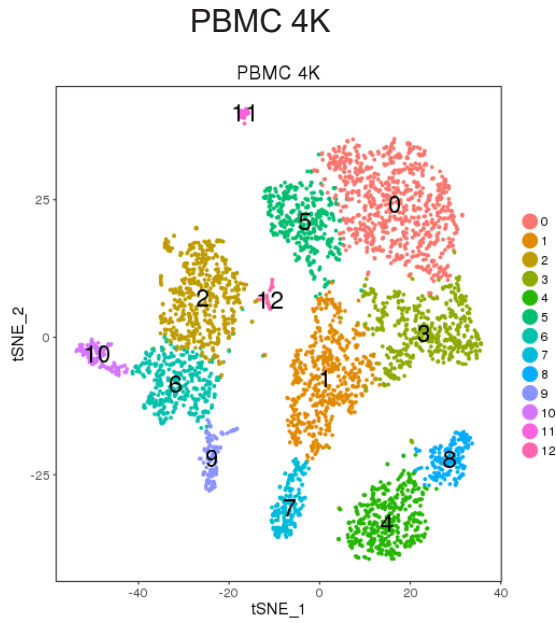
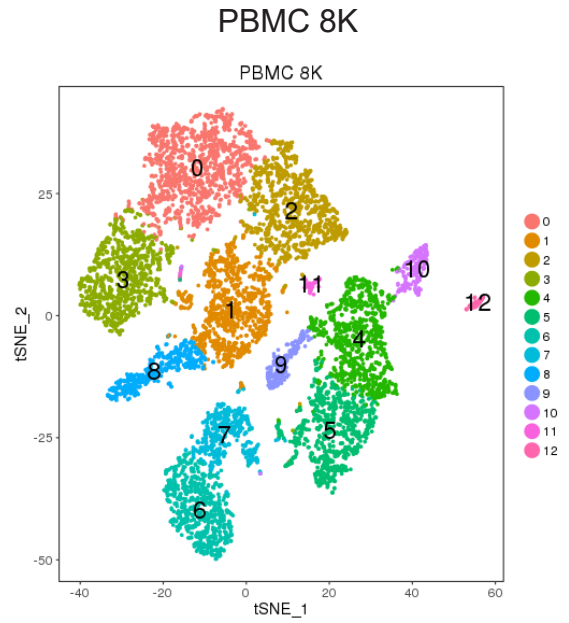


Figure S4

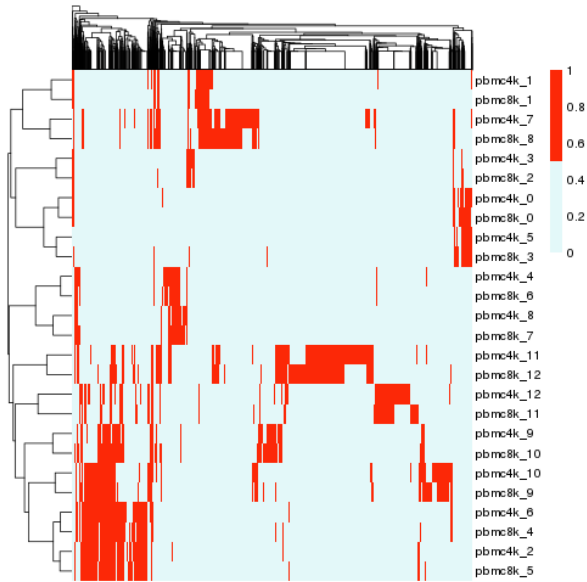
A



B



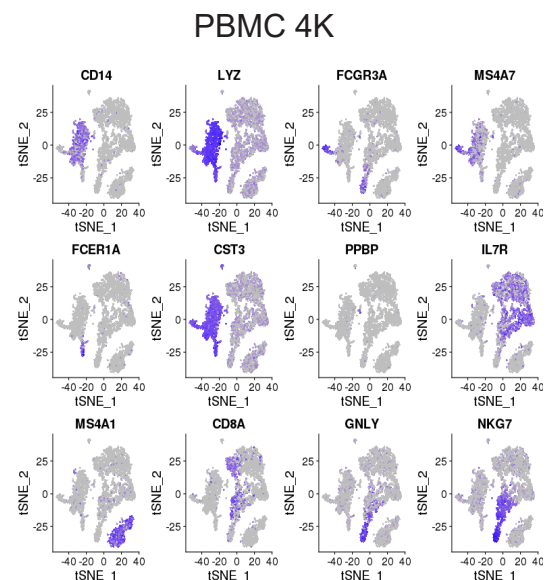
C



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

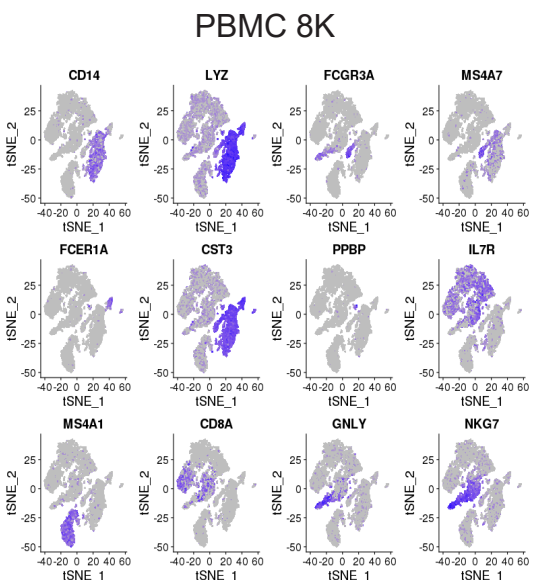
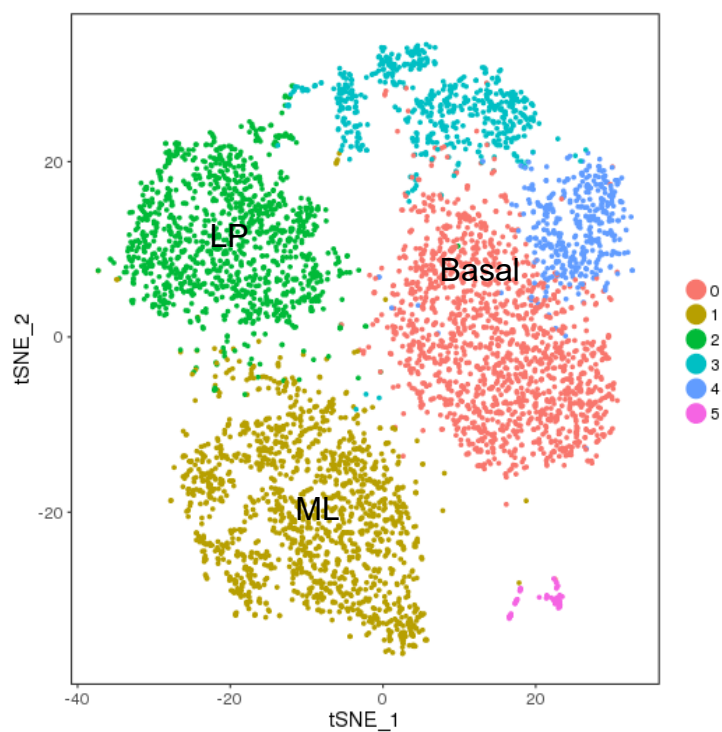
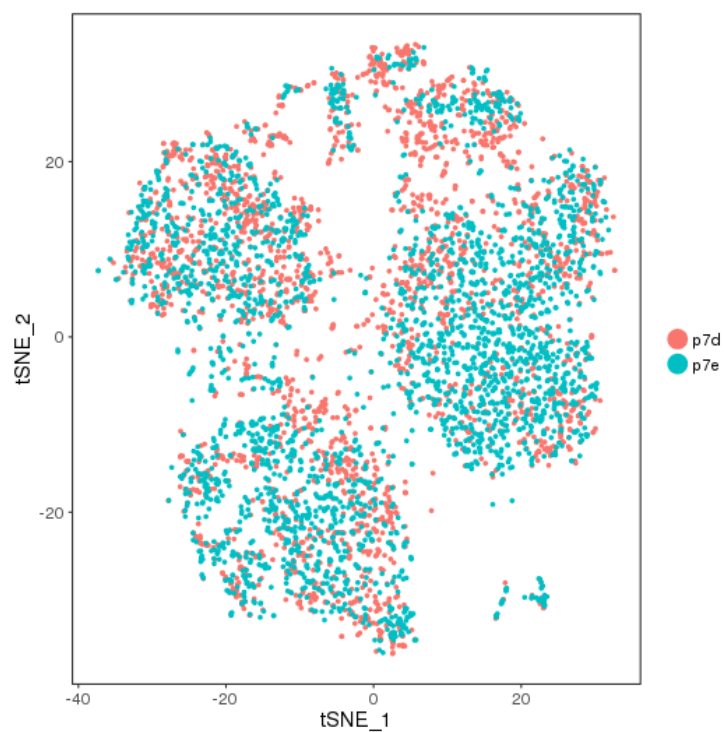


Figure S5

A



B



C

