

SUPPLEMENTARY DATA

Figure S1

Simulated dendrogram of four samples. A. Simulated dendrogram tree with four samples and 10 subgroups for each sample. B-C. Purity 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. Simulated dendrogram tree with ten samples and 10 subgroups for each sample. B. Purity tree cut results for the simulated tree at edge cutoffs of 0.2. C. ClusterMap results for the T cell sub-types across 12 patients. The cell sub-types are pre-defined in the original study and shown as the names of sub-groups. The purity tree cut results are shown in Table S1.

Figure S3

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 S4

CCA and scmap analysis and clustering for epithelial cell datasets as in Figure3, 4. A. t-SNE plot of clustered cells after CCA analysis. B. t-SNE plot with cells colored by sample after CCA analysis. C. Feature plot for identifying cell types after CCA analysis. D. t-SNE plot of CCA analysis. Cells of group 2 in estrus, defined as in Figure 4B are highlighted in green. E. scmap analysis that map cells in estrus to the sub-groups in diestrus at threshold 0.5 (left) and 0.7 (right). Cells are colored the same as their assigned sub-groups in Fig. 3A. F. scmap analysis that map cells in diestrus to the sub-groups in estrus at threshold 0.5. Cells are colored the same as their assigned sub-groups in Fig. 3B.

Figure S5

A. Pre-analysis for immune stimulated datasets. B. Circos plot of matched sub groups. C. Re-colored t-SNE plot based on the matching results of ClusterMap. D. scmap analysis result that map the cells in control sample to the sub-groups in stimulated sample at threshold 0.3. Cells are colored the same as their assigned sub-groups in A (right). E-F. Feature plot for identifying cell types.

Figure S6

ClusterMap analysis for the PBMC replicates datasets. A. Pre-analysis of PBMC 4K. B. Pre-analysis of PBMC 8K. C. Heat map of marker genes. D. Dendrogram of the hierarchical clustering of marker genes. E. Circos plot of the matched subgroups. F. ClusterMap results.

Figure S7

A-B. Re-colored t-SNE plot based on matching results for control and stimulated conditions. C. Re-colored t-SNE plot based on matching results for the combined dataset. D. t-SNE plot with cells colored by sample. E-F. Feature plots to identify cell types.

Figure S8

Compare brain cell dataset with epithelial dataset. A. Pre-analysis of brain cell dataset. B-C ClusterMap results that match brain cell sub-groups with the sub-groups in estrus phase of epithelial dataset (Fig. 3B). D. ClusterMap results that match brain cells with fake estrus dataset, in which any overlapped marker genes between the two datasets were removed.

Figure S9

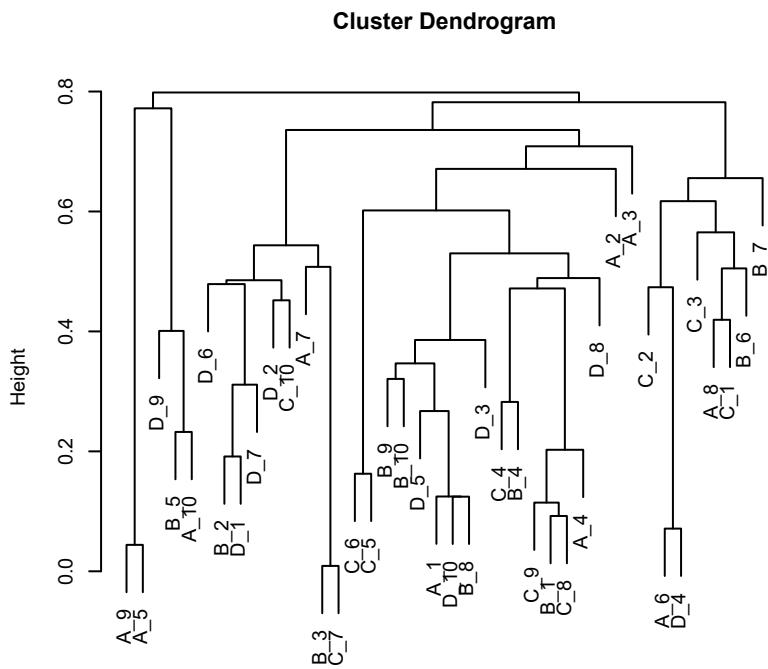
A,C. ClusterMap results between two patients of T cell sub-types. Only CD4 and CD8 T cells and the sub-types with more than 20 cells in a patient were used. B. Pre-defined T cell sub-types as in the original publication. The figure was downloaded from Zhang et al., 2018.

Table S1

The purity tree cut results of dendrogram shown in Fig. S2C.

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_1;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

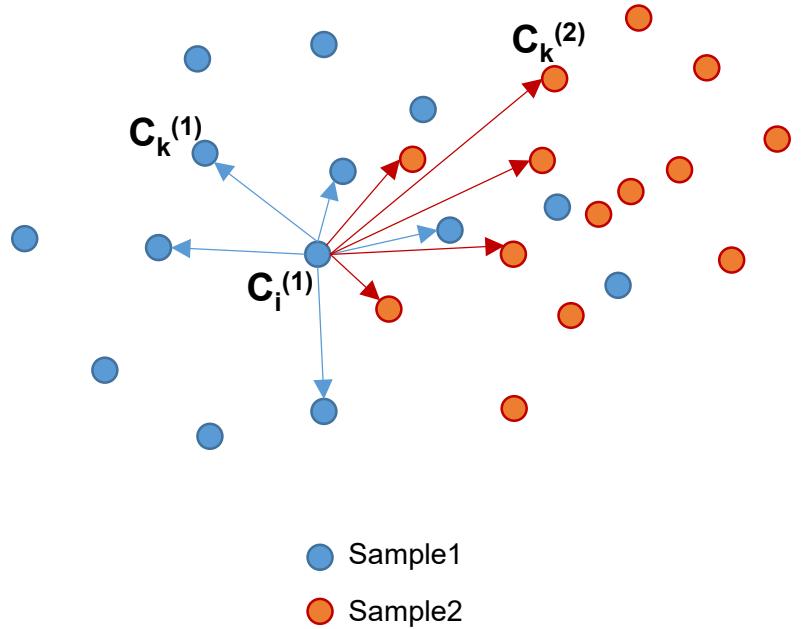
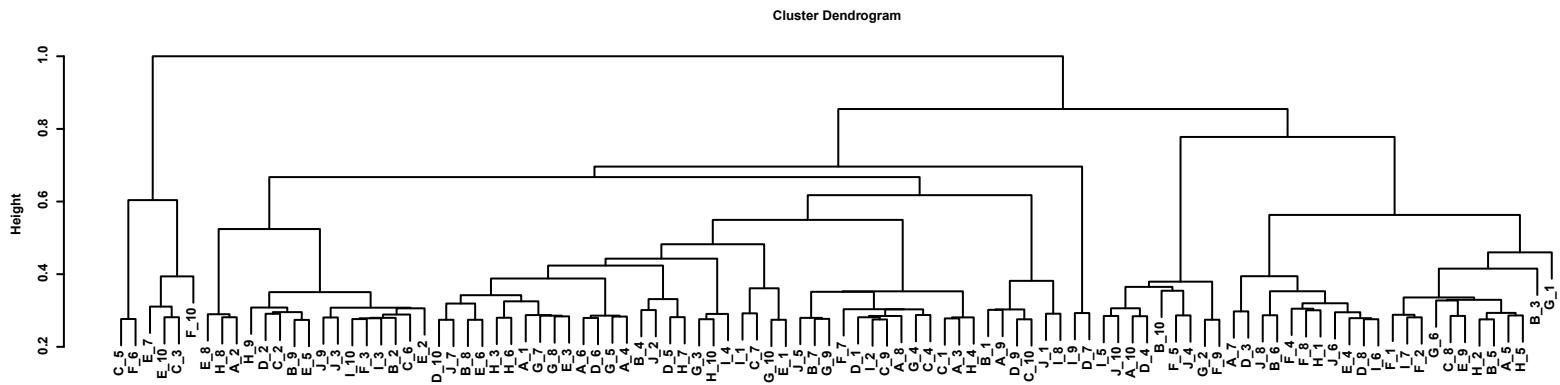


Figure S2

A



B

A	B	C	D	E	F	G	H	I	J	similarity	regroup
		C_5			F_6					0.72	1
			D_7				I_9			0.71	2
A_2				E_8			H_8			0.71	3
A_6;A_4			D_6			G_5				0.71	5
	B_4		D_5				H_7		J_2	0.67	6
A_1	B_8		D_10	E_6;E_3		G_7;G_8	H_3;H_6		J_7	0.66	7
A_8;A_3	B_7	C_9;C_4;C_1	D_1		F_7	G_9;G_4	H_4	I_2	J_5	0.65	8
	B_9;B_2	C_2;C_6	D_2	E_5;E_2	F_3		H_9	I_10;I_3	J_9;J_3	0.65	9
		C_7		E_1		G_10		I_1		0.64	10
A_10	B_10		D_4		F_5;F_9	G_2		I_5	J_10;J_4	0.62	11
A_9	B_1	C_10	D_9					I_8	J_1	0.62	12
		C_3		E_7;E_10	F_10					0.61	13
A_7;A_5	B_6;B_5;B_3	C_8	D_3;D_8	E_4;E_9	F_4;F_8;F_1;F_2	G_6;G_1	H_1;H_2;H_5	I_6;I_7	J_8;J_6	0.44	14

C

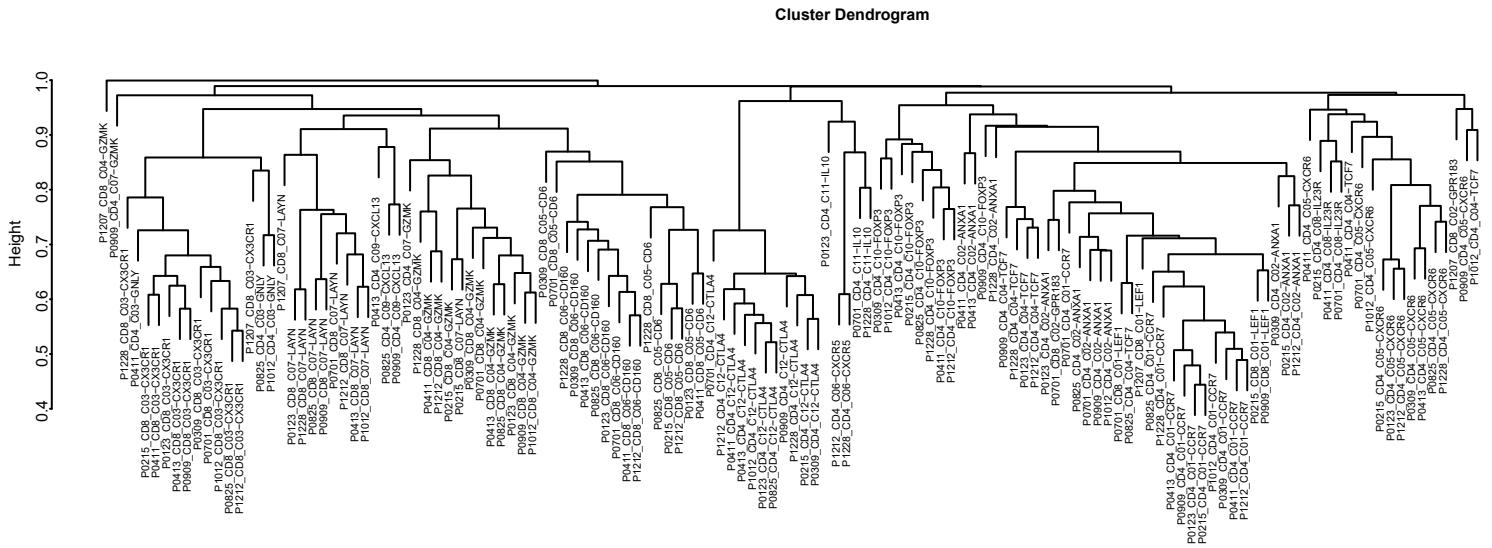
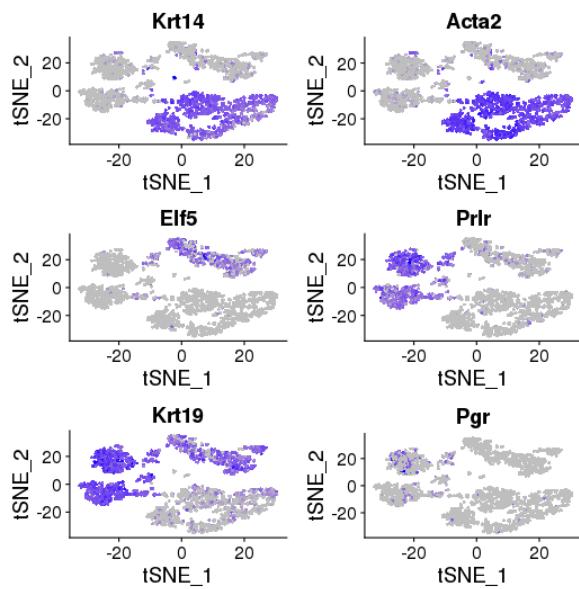


Figure S3

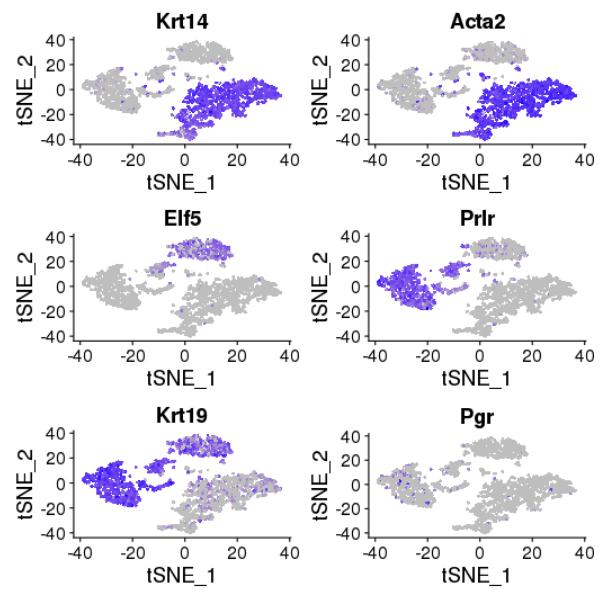
A

Diestrus (p7d)



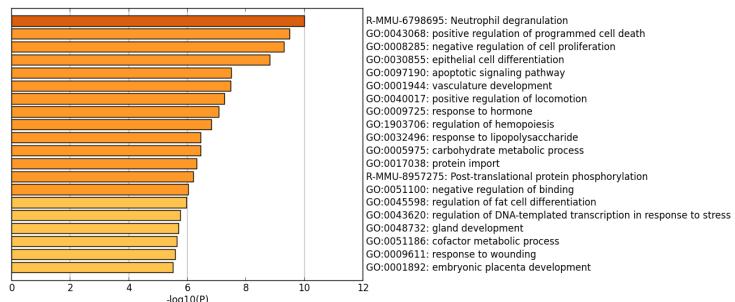
B

Estrus (p7e)

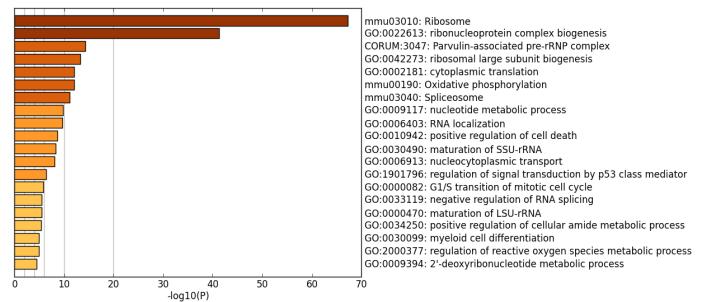


C

Luminal progenitors Group1

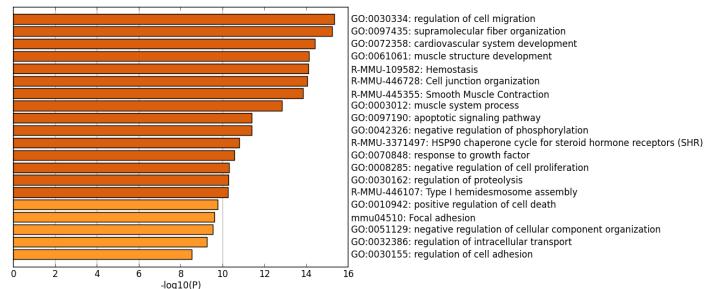


Luminal progenitors Group11, diestrus only



D

Basal Group 3, estrus enriched



Basal Group 7, diestrus

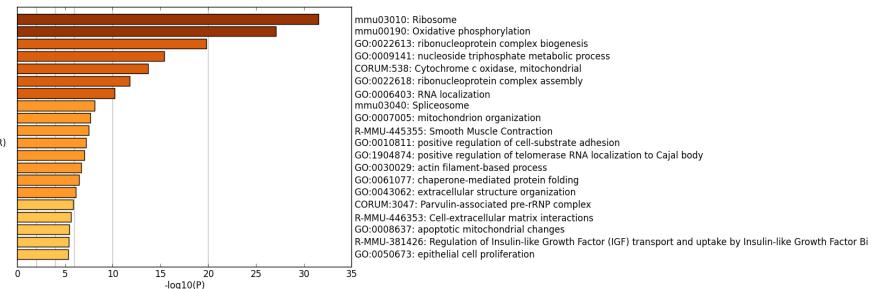
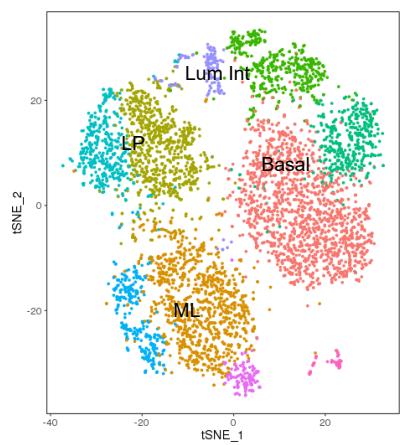
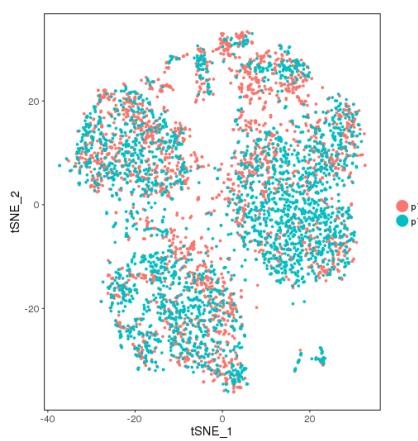


Figure S4

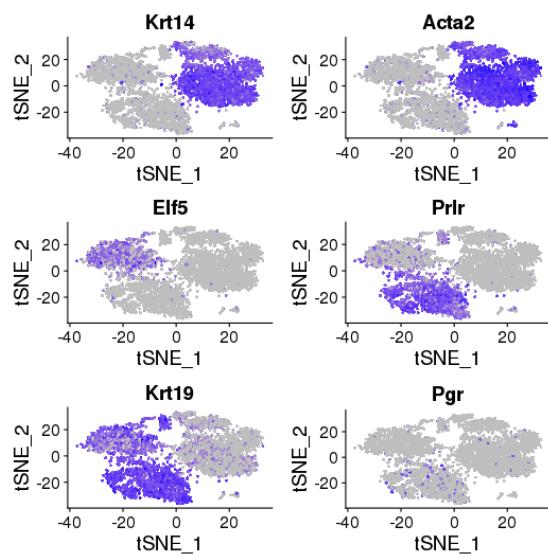
A CCA analysis, clustering results



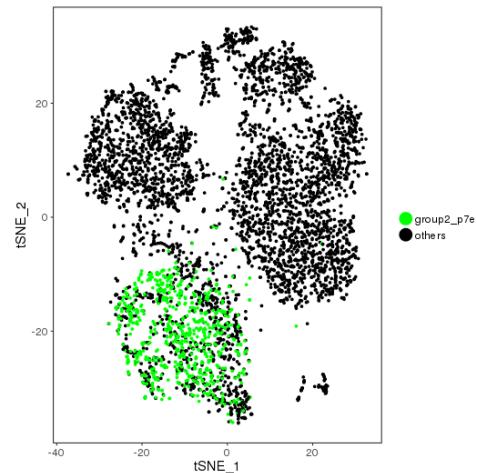
B CCA analysis, colored by sample



C



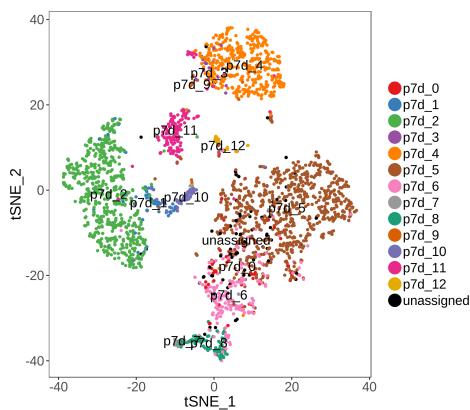
D



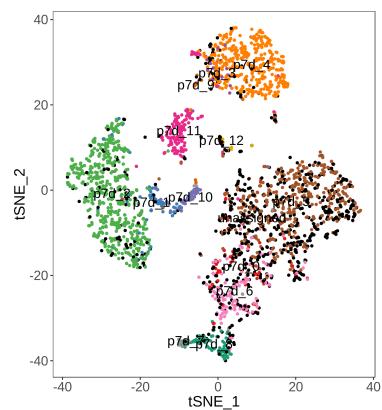
E

scmap Estrus (p7e) to Diestrus (p7d)

threshold=0.5



threshold=0.7



F

scmap Diestrus (p7d) to Estrus (p7e)

threshold=0.5

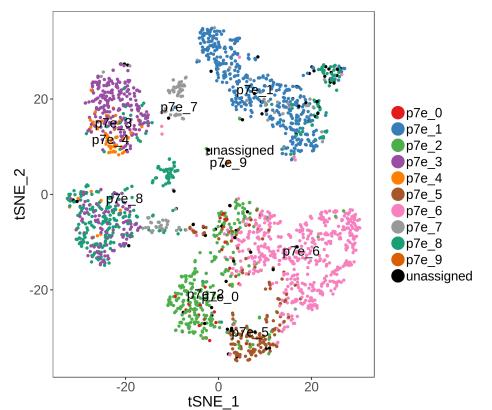
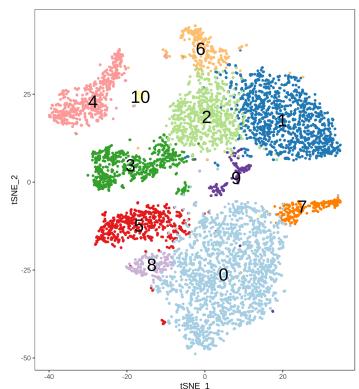


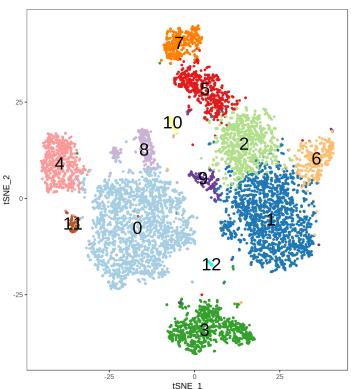
Figure S5

A

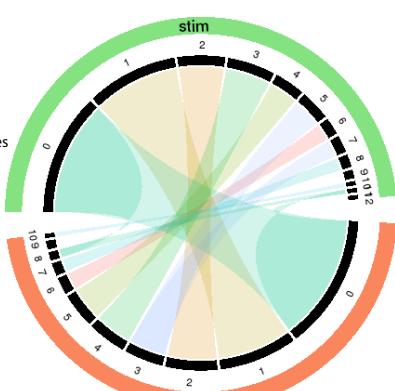
pre-analysis
Control (ctrl)



pre-analysis
Stimulated (stim)

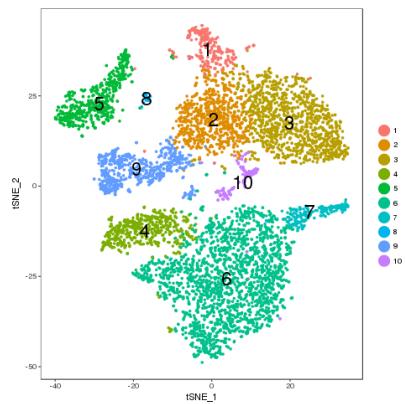


B

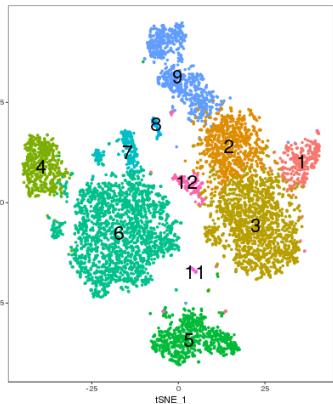


C

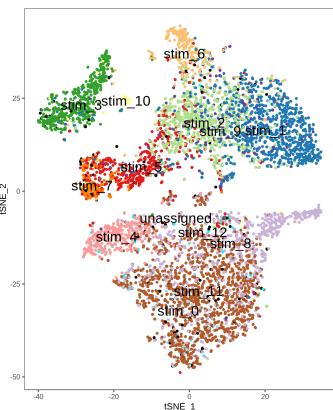
Control (ctrl)



Stimulated (stim)

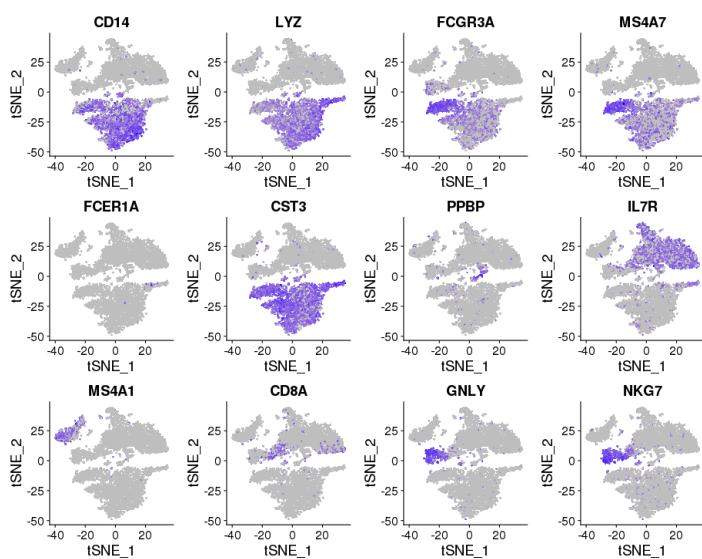


D scmap Control (ctrl) to Stimulated (stim)
threshold=0.3



E

Control (ctrl)



F

Stimulated (stim)

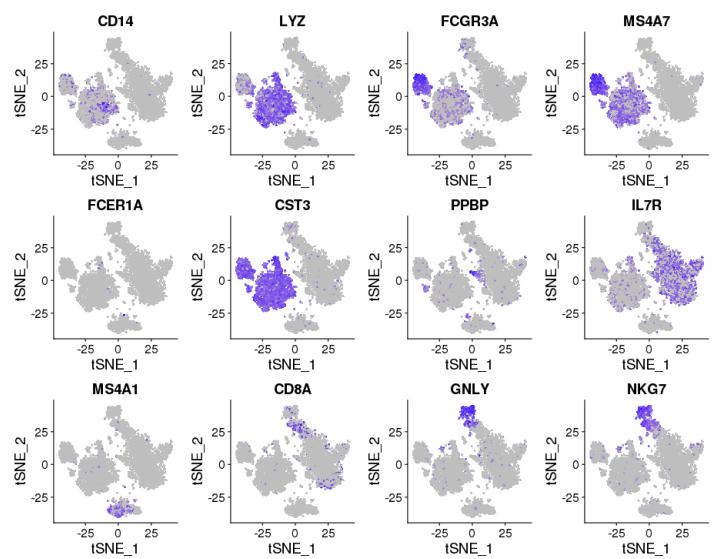


Figure S6

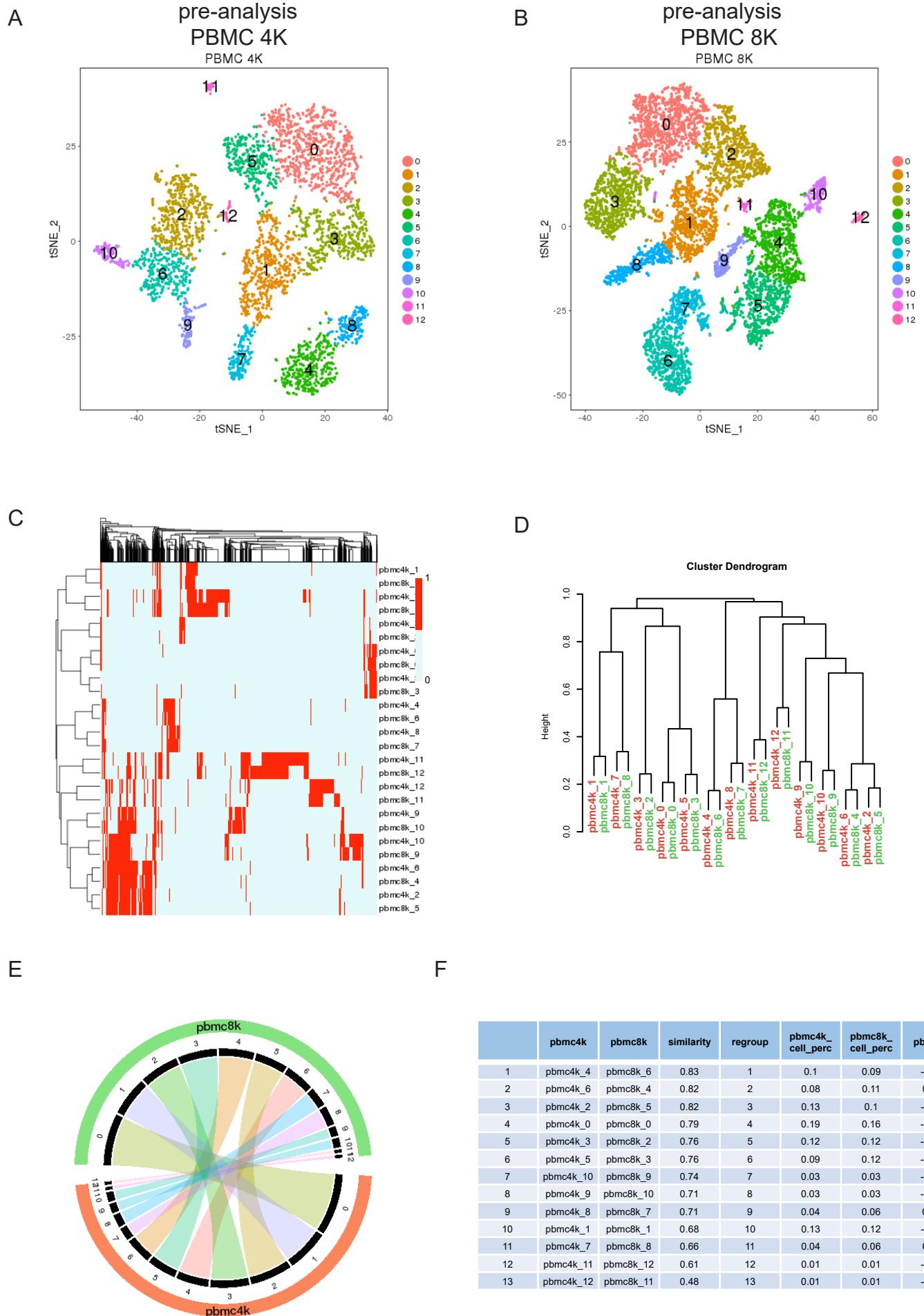


Figure S7

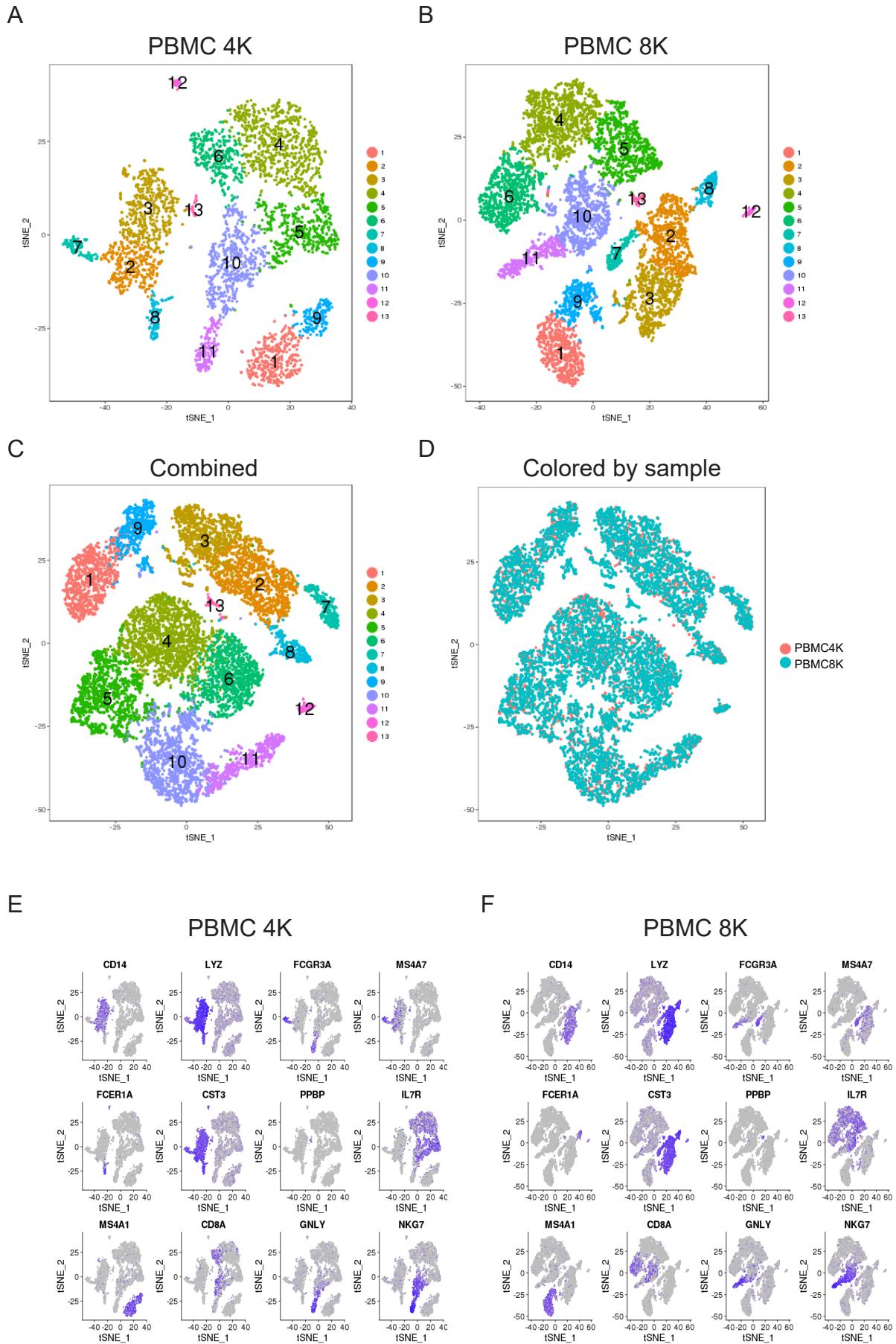
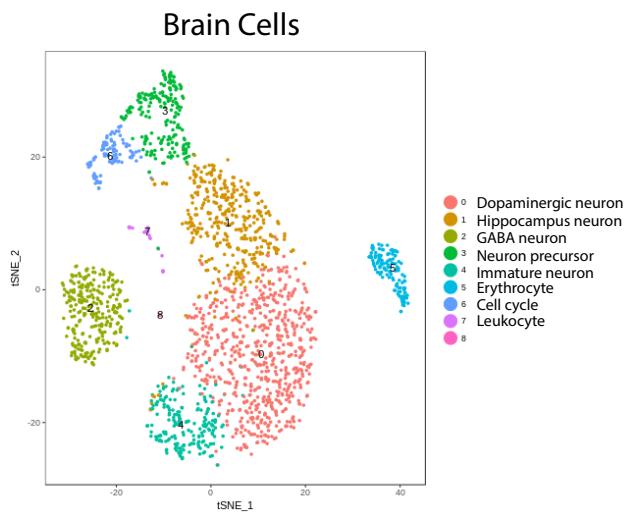
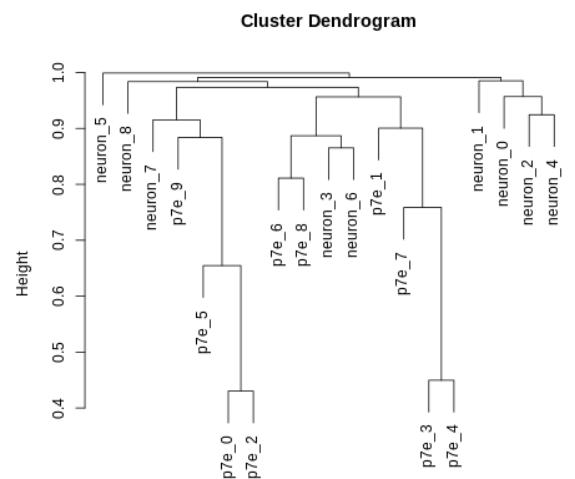


Figure S8

A



B



C

neuron	p7e	similarity	regroup
neuron_7	p7e_0;p7e_2;p7e_5;p7e_9	0.08	1
neuron_3;neuron_6	p7e_1;p7e_3;p7e_4;p7e_6;p7e_7;p7e_8	0.04	2
neuron_0;neuron_1;neuron_2;neuron_4	NA	0.01	3
neuron_5	NA	NA	4
neuron_8	NA	NA	5

D

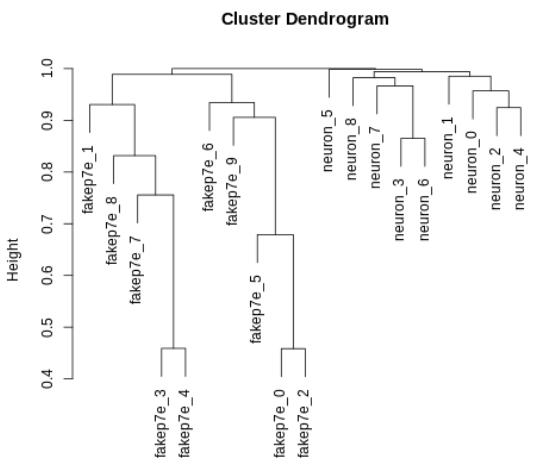
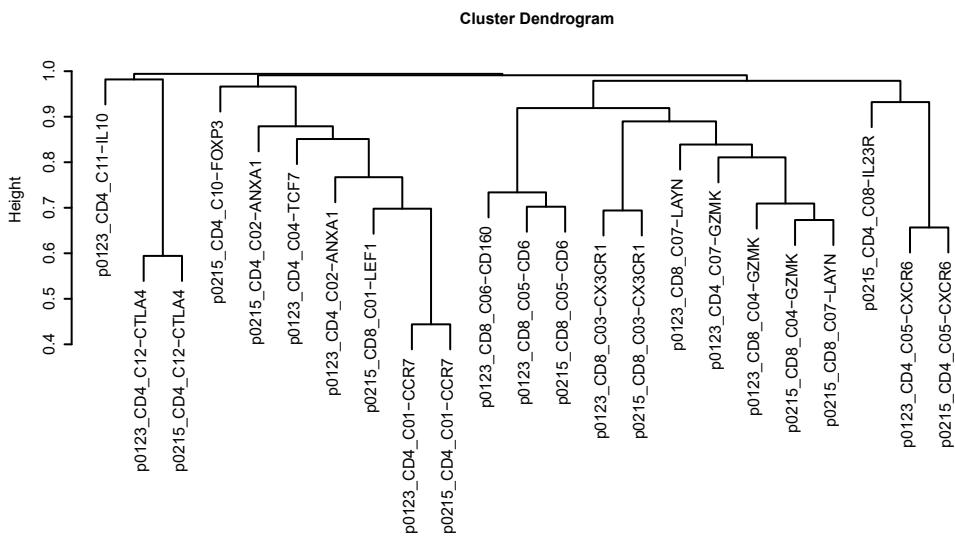
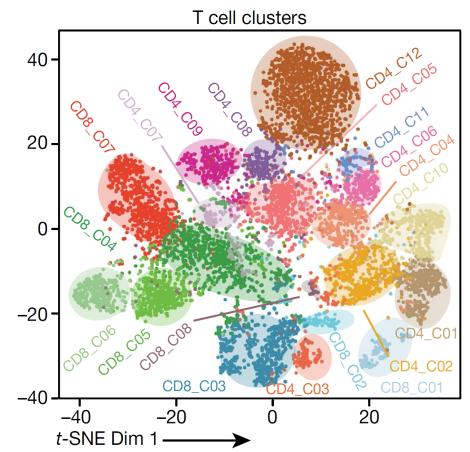


Figure S9

A



B



C

p0123	p0215	similarity	regroup
p0123_CD4_C01-CCR7	p0215_CD4_C01-CCR7	0.56	1
p0123_CD4_C12-CTLA4	p0215_CD4_C12-CTLA4	0.41	2
p0123_CD4_C05-CXCR6	p0215_CD4_C05-CXCR6	0.34	3
p0123_CD8_C03-CX3CR1	p0215_CD8_C03-CX3CR1	0.31	4
p0123_CD8_C04-GZMK	p0215_CD8_C04-GZMK;p0215_CD8_C07-LAYN	0.29	5
p0123_CD8_C05-CD6;p0123_CD8_C06-CD160	p0215_CD8_C05-CD6	0.27	6
p0123_CD4_C02-ANXA1	NA	NA	7
p0123_CD4_C04-TCF7	NA	NA	8
p0123_CD4_C07-GZMK	NA	NA	9
p0123_CD4_C11-IL10	NA	NA	10
p0123_CD8_C07-LAYN	NA	NA	11
NA	p0215_CD4_C02-ANXA1	NA	12
NA	p0215_CD4_C08-IL23R	NA	13
NA	p0215_CD4_C10-FOXP3	NA	14
NA	p0215_CD8_C01-LEF1	NA	15

Table S1

	P0123	P0215	P0309	P0411	P0413	P0701	P0825	P0909	P1012	P1207	P1212	P1228	similarity	regroup
1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	P1212_CD4_C06-CXCR5	P1228_CD4_C06-CXCR5	0.39	1
2	NA	NA	NA	NA	NA	P0701_CD8_C01-LEF1	P0825_CD4_C04-TCF7	NA	NA	NA	NA	NA	0.37	2
3	P0123_CD4_C01-CCR7	P0215_CD4_C01-CCR7	P0309_CD4_C01-CCR7	P0411_CD4_C01-CCR7	P0413_CD4_C01-CCR7	NA	P0825_CD4_C01-CCR7	P0909_CD4_C01-CCR7	P1012_CD4_C01-CCR7	NA	P1212_CD4_C01-CCR7	P1228_CD4_C01-CCR7	0.35	3
4	NA	P0215_CD8_C01-LEF1	NA	NA	NA	NA	NA	P0909_CD8_C01-LEF1	NA	NA	NA	NA	0.35	4
5	NA	NA	NA	NA	NA	P0701_CD4_C02-ANXA1	P0825_CD4_C02-ANXA1	P0909_CD4_C02-ANXA1	P1012_CD4_C02-ANXA1	NA	NA	NA	0.29	5
6	P0123_CD4_C12-CTLA4	P0215_CD4_C12-CTLA4	P0309_CD4_C12-CTLA4	P0411_CD4_C12-CTLA4	P0413_CD4_C12-CTLA4	P0701_CD4_C12-CTLA4	P0825_CD4_C12-CTLA4	P0909_CD4_C12-CTLA4	P1012_CD4_C12-CTLA4	NA	P1212_CD4_C12-CTLA4	P1228_CD4_C12-CTLA4	0.27	6
7	P0123_CD4_C02-ANXA1	NA	NA	NA	NA	P0701_CD8_C02-GPR183	NA	NA	NA	NA	NA	NA	0.26	7
8	P0123_CD4_C04-TCF7	NA	NA	NA	NA	NA	NA	P0909_CD4_C04-TCF7	NA	NA	P1212_CD4_C04-TCF7	P1228_CD4_C04-TCF7	0.23	8
9	NA	NA	NA	NA	NA	P0701_CD4_C11-IL10	NA	NA	NA	NA	NA	P1228_CD4_C11-IL10	0.2	9
10	NA	P0215_CD4_C02-ANXA1	P0309_CD4_C02-ANXA1	NA	NA	NA	NA	NA	NA	NA	P1212_CD4_C02-ANXA1	NA	0.18	10
11	P0123_CD4_C07-GZMK;P012	P0215_CD8_C04-GZMK;P021	P0309_CD8_C04-GZMK	P0411_CD8_C04-GZMK	P0413_CD8_C04-GZMK	P0701_CD8_C04-GZMK	P0825_CD8_C04-GZMK	P0909_CD8_C04-GZMK	P1012_CD8_C04-GZMK	NA	P1212_CD8_C04-GZMK	P1228_CD8_C04-GZMK	0.15	11

	3_CD8_C04-GZMK	5_CD8_C07-LAYN												
12	P0123_CD8_C03-CX3CR1	P0215_CD8_C03-CX3CR1	P0309_CD8_C03-CX3CR1	P0411_CD4_GNLY;P0411_CD8_C03-CX3CR1	P0413_CD8_C03-CX3CR1	P0701_CD8_C03-CX3CR1	P0825_CD4_GNLY;P0825_CD8_C03-CX3CR1	P0909_CD8_C03-CX3CR1	P1012_CD4_GNLY;P1012_CD8_C03-CX3CR1	P1207_CD8_C03-CX3CR1	P1212_CD8_C03-CX3CR1	P1228_CD8_C03-CX3CR1	0.14	12
13	P0123_CD8_C07-LAYN	NA	NA	NA	P0413_CD8_C07-LAYN	P0701_CD8_C07-LAYN	P0825_CD8_C07-LAYN	P0909_CD8_C07-LAYN	P1012_CD8_C07-LAYN	P1207_CD8_C07-LAYN	P1212_CD8_C07-LAYN	P1228_CD8_C07-LAYN	0.14	13
14	NA	NA	NA	P0411_CD4_C02-ANXA1	P0413_CD4_C02-ANXA1	NA	NA	NA	NA	NA	NA	NA	0.13	14
15	P0123_CD8_C05-CD6;P0123_CD8_C06-CD160	P0215_CD8_C05-CD6	P0309_CD8_C05-CD6	P0411_CD8_C05-CD6;P0411_CD8_C06-CD160	P0413_CD8_C05-CD160	P0701_CD8_CD6;P0701_CD8_C06-CD160	P0825_CD8_CD6;P0825_CD8_C06-CD160	NA	NA	NA	P1212_CD8_CD6;P1212_CD8_C06-CD160	P1228_CD8_CD6;P1228_CD8_C06-CD160	0.13	15
16	NA	NA	NA	NA	P0413_CD4_C09-CXCL13	NA	P0825_CD4_C09-CXCL13	P0909_CD4_C09-CXCL13	NA	NA	NA	NA	0.12	16
17	NA	P0215_CD4_C10-FOXP3	P0309_CD4_C10-FOXP3	P0411_CD4_C10-FOXP3	P0413_CD4_C10-FOXP3	NA	P0825_CD4_C10-FOXP3	NA	P1012_CD4_C10-FOXP3	NA	P1212_CD4_C10-FOXP3	P1228_CD4_C10-FOXP3	0.11	17
18	NA	P0215_CD4_C08-IL23R	NA	P0411_CD4_C08-IL23R	NA	P0701_CD4_C08-IL23R	NA	NA	NA	NA	NA	NA	0.11	18
19	P0123_CD4_C05-CXCR6	P0215_CD4_C05-CXCR6	P0309_CD4_C05-CXCR6	P0411_CD4_C04-TCF7	P0413_CD4_C05-CXCR6	P0701_CD4_C05-CXCR6	P0825_CD4_C05-CXCR6	NA	P1012_CD4_C05-CXCR6	NA	P1212_CD4_C05-CXCR6	P1228_CD4_C05-CXCR6	0.08	19
20	NA	NA	NA	NA	NA	NA	NA	P0909_CD4_C05-CXCR6	P1012_CD4_C04-TCF7	P1207_CD8_C02-GPR183	NA	NA	0.05	20

21	P0123_CD4_ C11-IL10	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	21
22	NA	NA	NA	P0411_CD4_ C05-CXCR6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	22
23	NA	NA	NA	NA	NA	P0701_CD4_ C01-CCR7	NA	NA	NA	NA	NA	NA	NA	NA	23
24	NA	NA	NA	NA	NA	NA	NA	P0909_CD4_ C07-GZMK	NA	NA	NA	NA	NA	NA	24
25	NA	NA	NA	NA	NA	NA	NA	P0909_CD4_ C10-FOXP3	NA	NA	NA	NA	NA	NA	25
26	NA	NA	NA	NA	NA	NA	NA	P1207_CD8_ C01-LEF1	NA	NA	NA	NA	NA	NA	26
27	NA	NA	NA	NA	NA	NA	NA	P1207_CD8_ C04-GZMK	NA	NA	NA	NA	NA	NA	27
28	NA	NA	NA	NA	NA	NA	NA	P1228_CD4_ C02-ANXA1	NA	NA	NA	NA	NA	NA	28