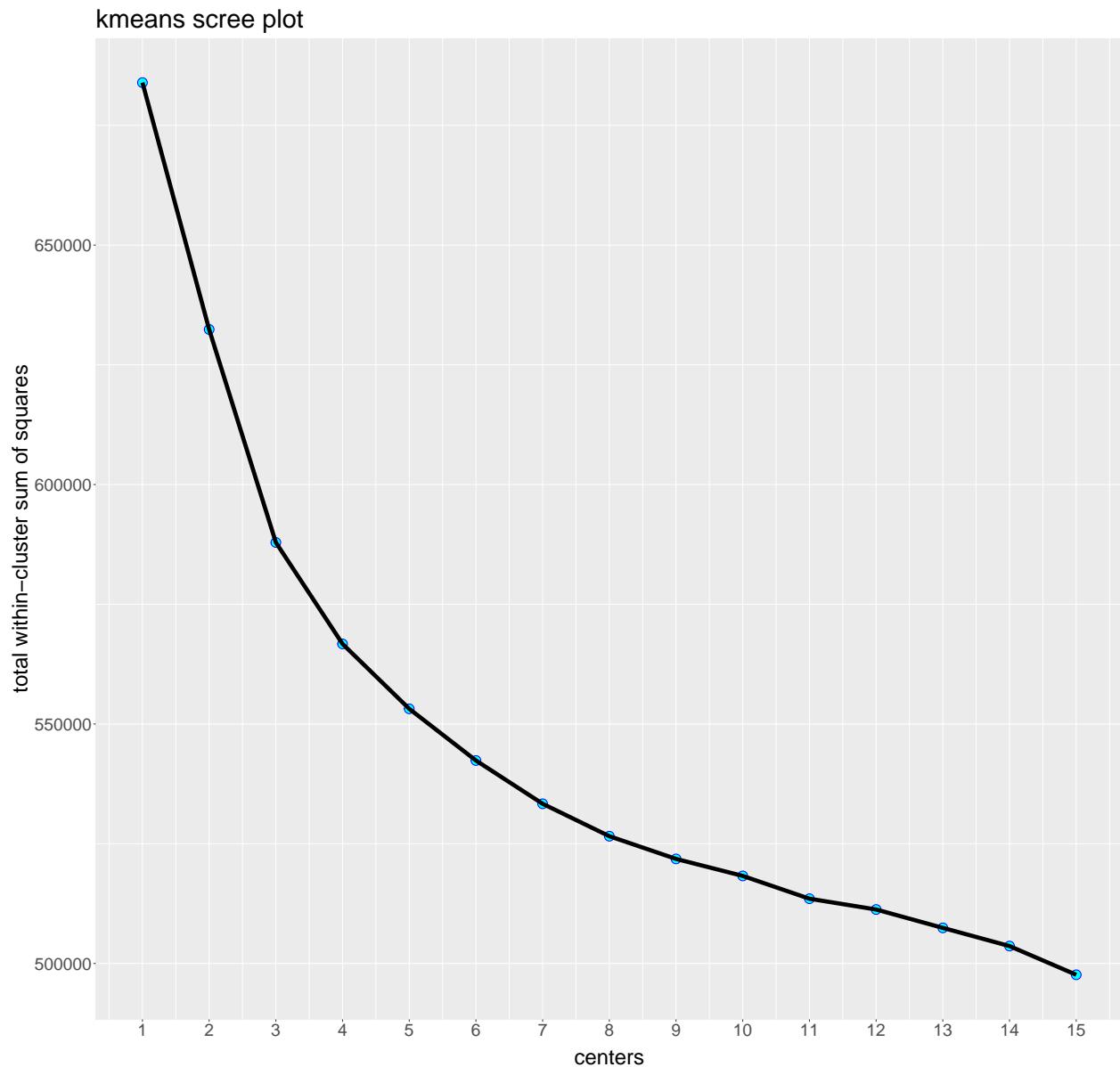
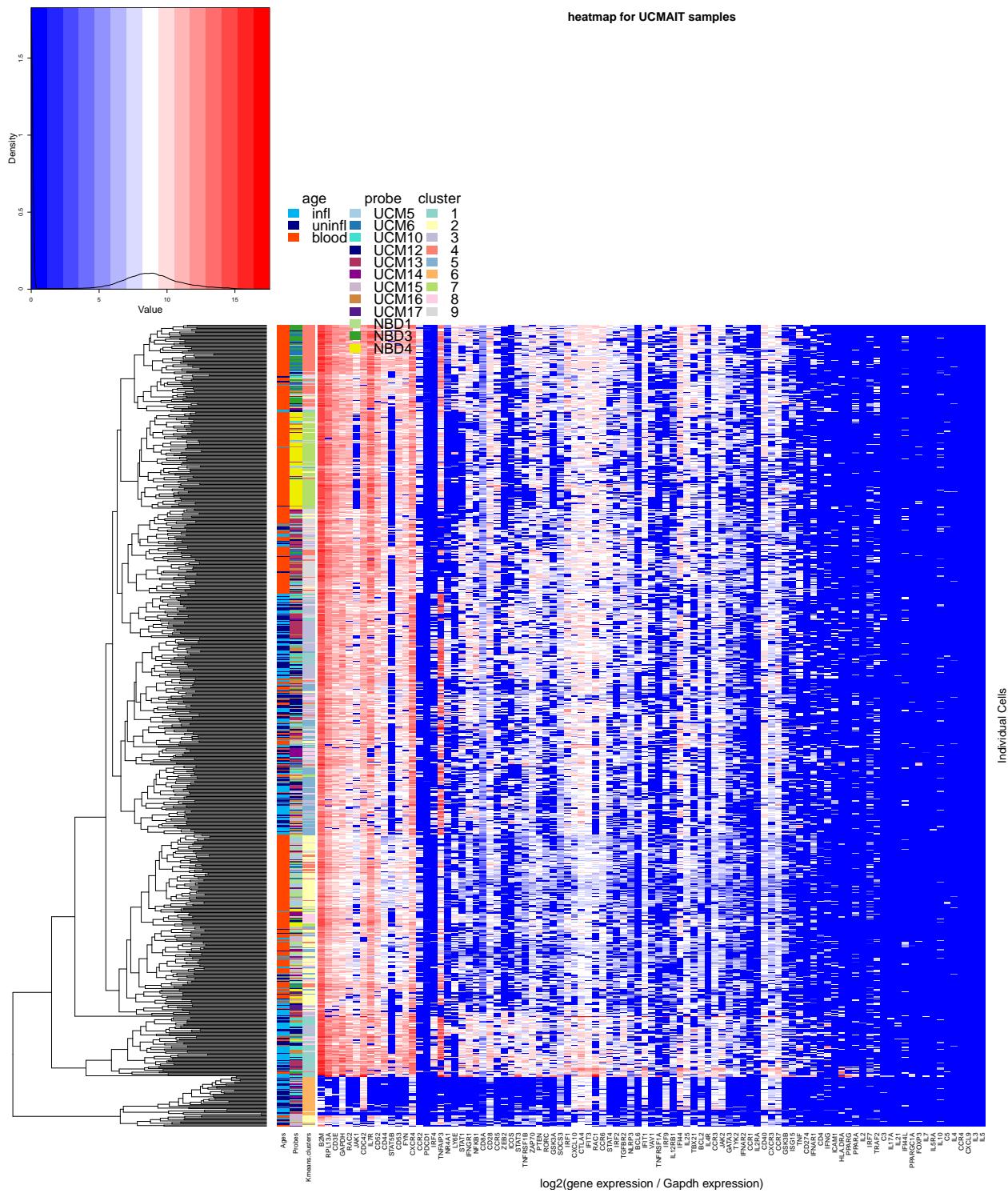


# UC-MAIT analysis (all together)

No expression detected in 15/796 cells





[1]

[1]

## [1] Probe vs. Cluster

probe\_UCM5 probe\_UCM6 probe\_UCM10 probe\_UCM12 probe\_UCM13

<i>cluster_1</i>	0	0	33	12	7
<i>cluster_2</i>	26	2	2	2	0
<i>cluster_3</i>	0	0	18	26	35

cluster_4	4	43	0	5	0
cluster_5	2	0	7	15	3
cluster_6	0	0	10	10	6
cluster_7	0	0	0	1	0
cluster_8	3	3	7	17	3
cluster_9	0	0	12	2	40
	probe_UCM14	probe_UCM15	probe_UCM16	probe_UCM17	probe_NBD1
cluster_1	3	0	14	0	0
cluster_2	10	25	7	7	37
cluster_3	1	3	22	2	0
cluster_4	0	2	4	0	2
cluster_5	9	27	21	4	4
cluster_6	7	5	0	0	0
cluster_7	0	1	5	0	0
cluster_8	22	4	6	5	4
cluster_9	3	1	15	0	1
	probe_NBD3	probe_NBD4			
cluster_1	1	0			
cluster_2	0	10			
cluster_3	0	0			
cluster_4	37	0			
cluster_5	3	1			
cluster_6	0	0			
cluster_7	1	81			
cluster_8	6	1			
cluster_9	0	1			

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

```
data: probeTable
X-squared = 1804.2, df = NA, p-value = 0.0004998
```

```
[1]
[1]
[1] Tissue vs. Cluster
      cellSource_blood cellSource_tissue
cluster_1           2            68
cluster_2          111           17
cluster_3           0           107
cluster_4          95            2
cluster_5          21            75
cluster_6           0            38
cluster_7          88            1
cluster_8          48            33
cluster_9          63            12
```

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

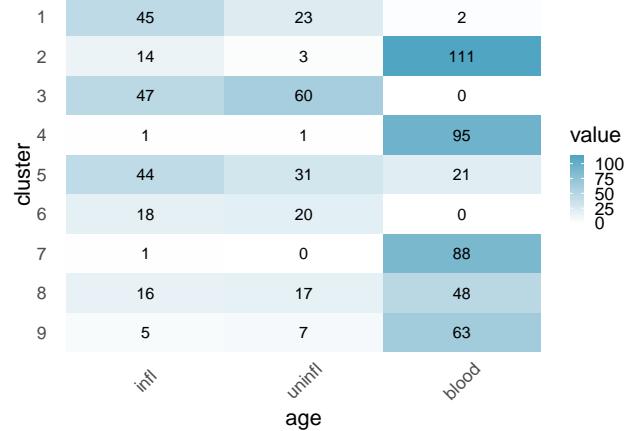
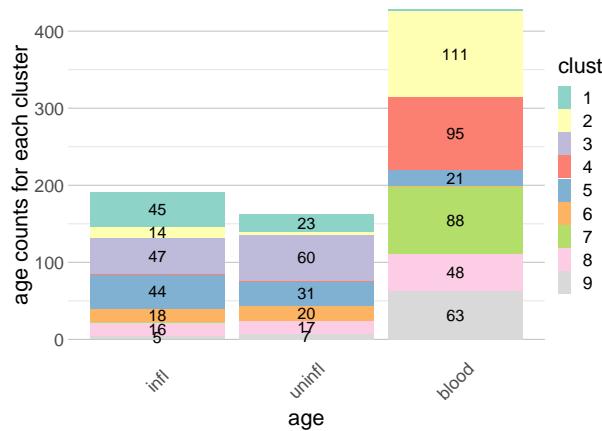
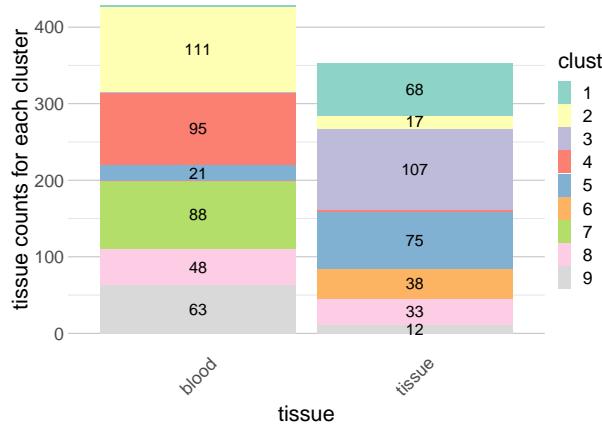
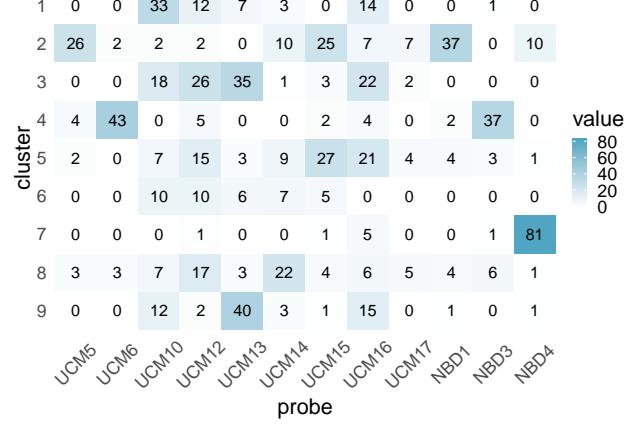
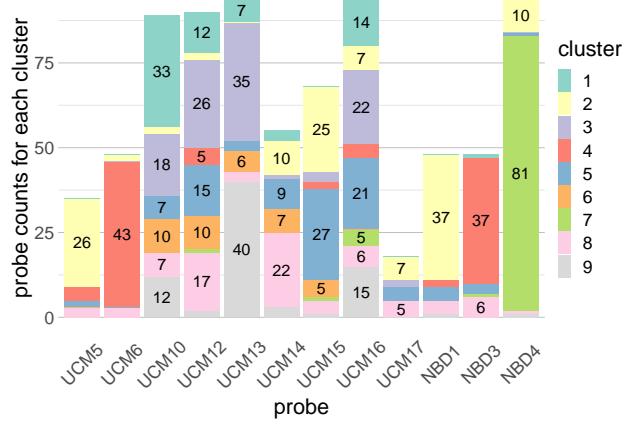
```
data: sourceTable
X-squared = 515.86, df = NA, p-value = 0.0004998
```

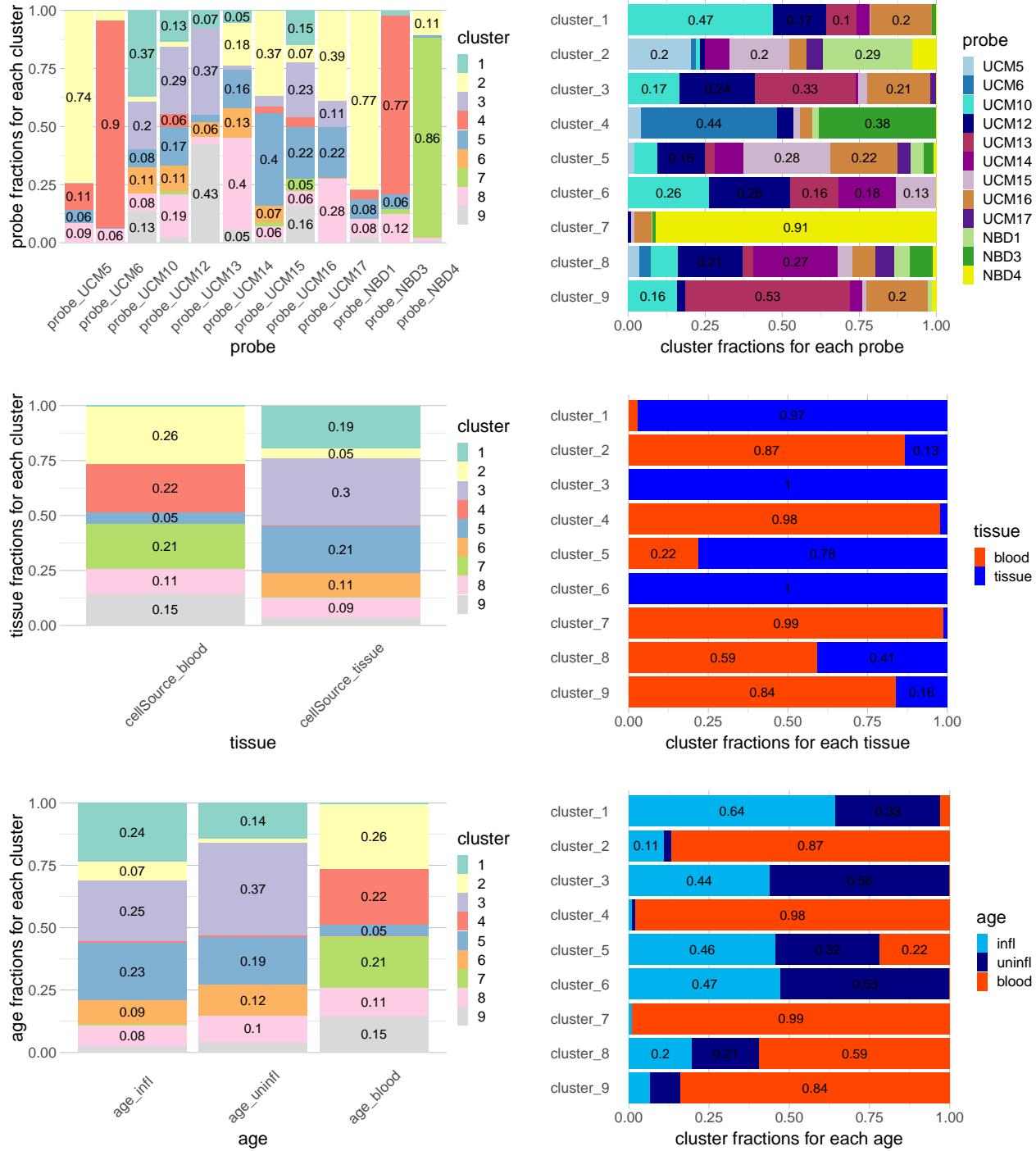
```
[1]
```

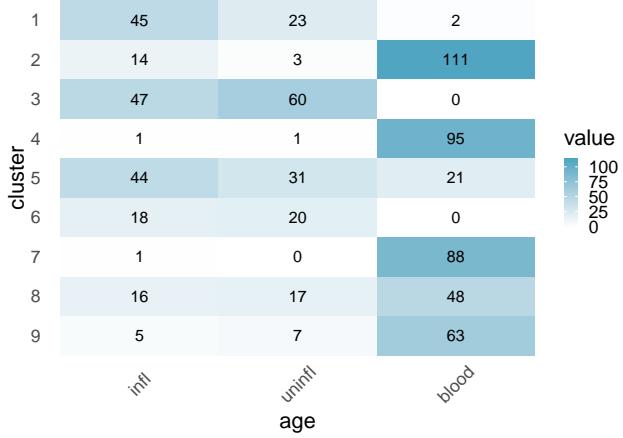
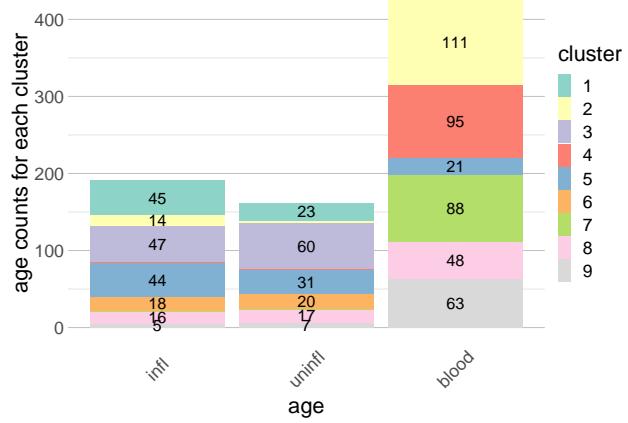
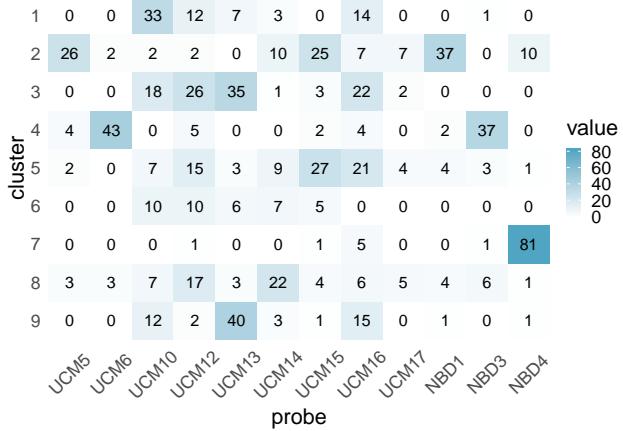
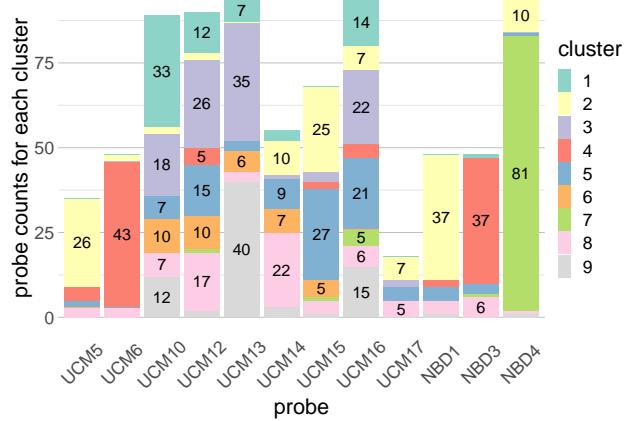
```
[1]
[1] age vs. Cluster
      age_infl age_uninfl age_blood
cluster_1     45        23        2
cluster_2     14         3       111
cluster_3     47        60        0
cluster_4      1         1       95
cluster_5     44        31       21
cluster_6     18        20        0
cluster_7      1         0       88
cluster_8     16        17       48
cluster_9      5         7       63

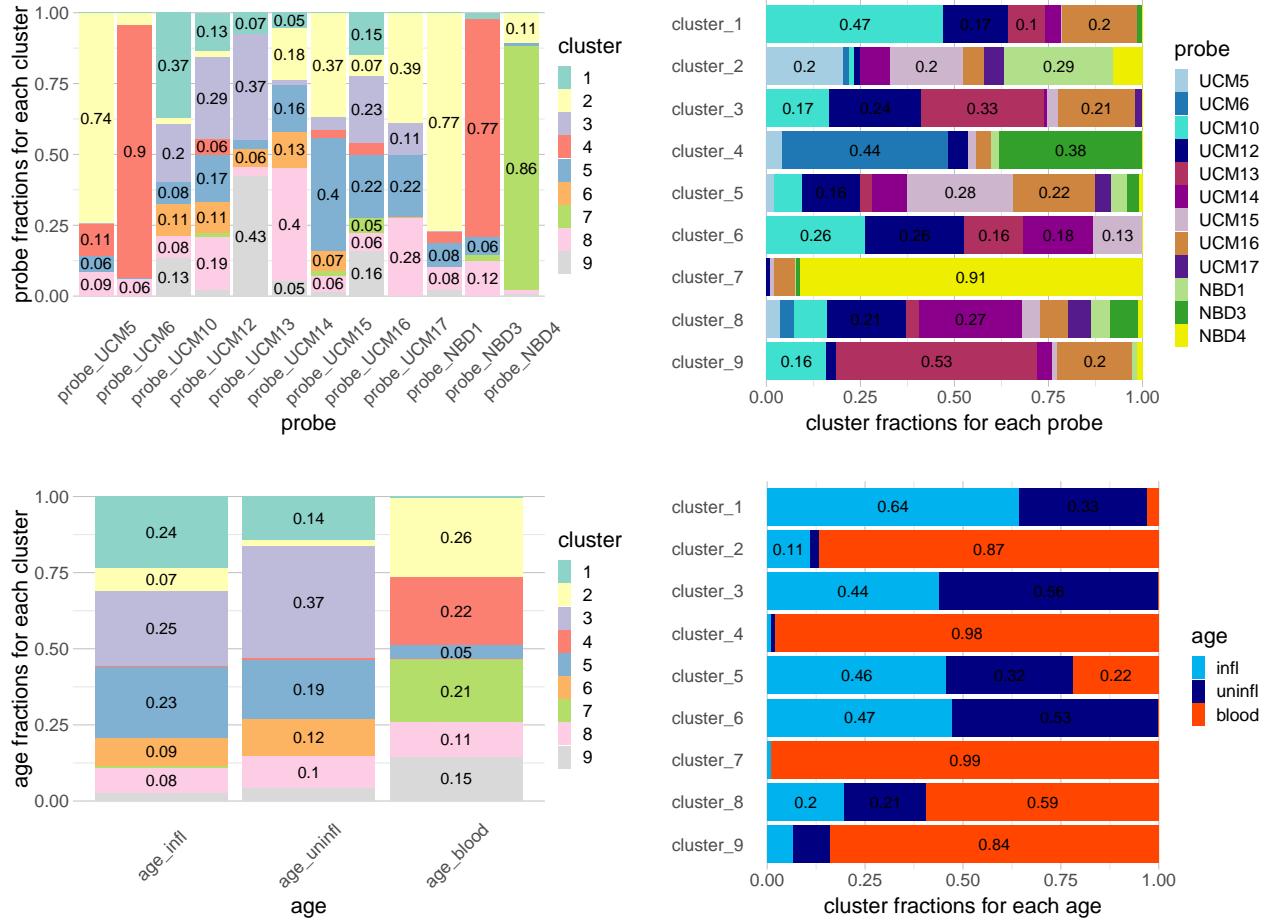
Pearson's Chi-squared test with simulated p-value (based on 2000
replicates)

data: ageTable
X-squared = 539.21, df = NA, p-value = 0.0004998
```

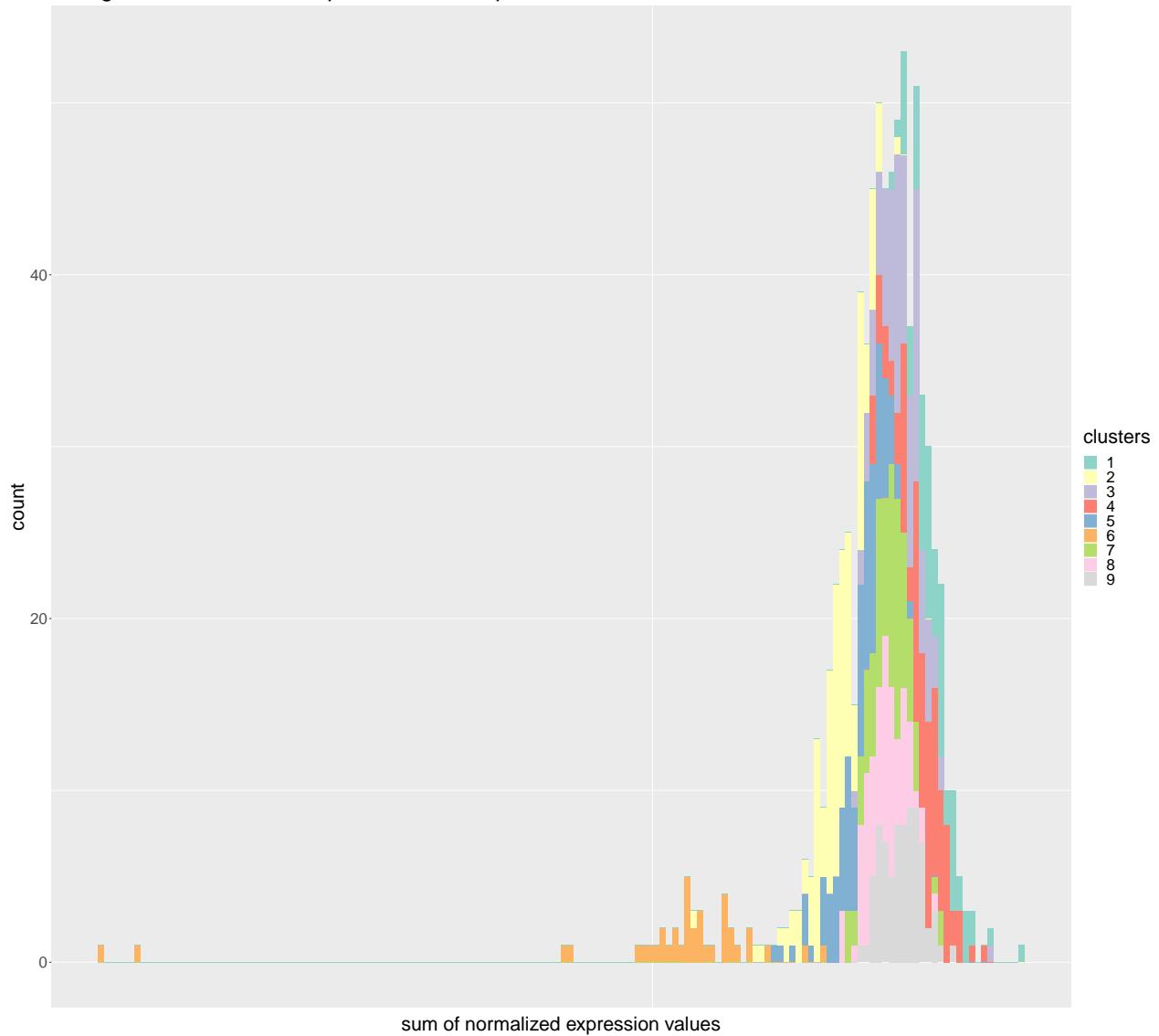






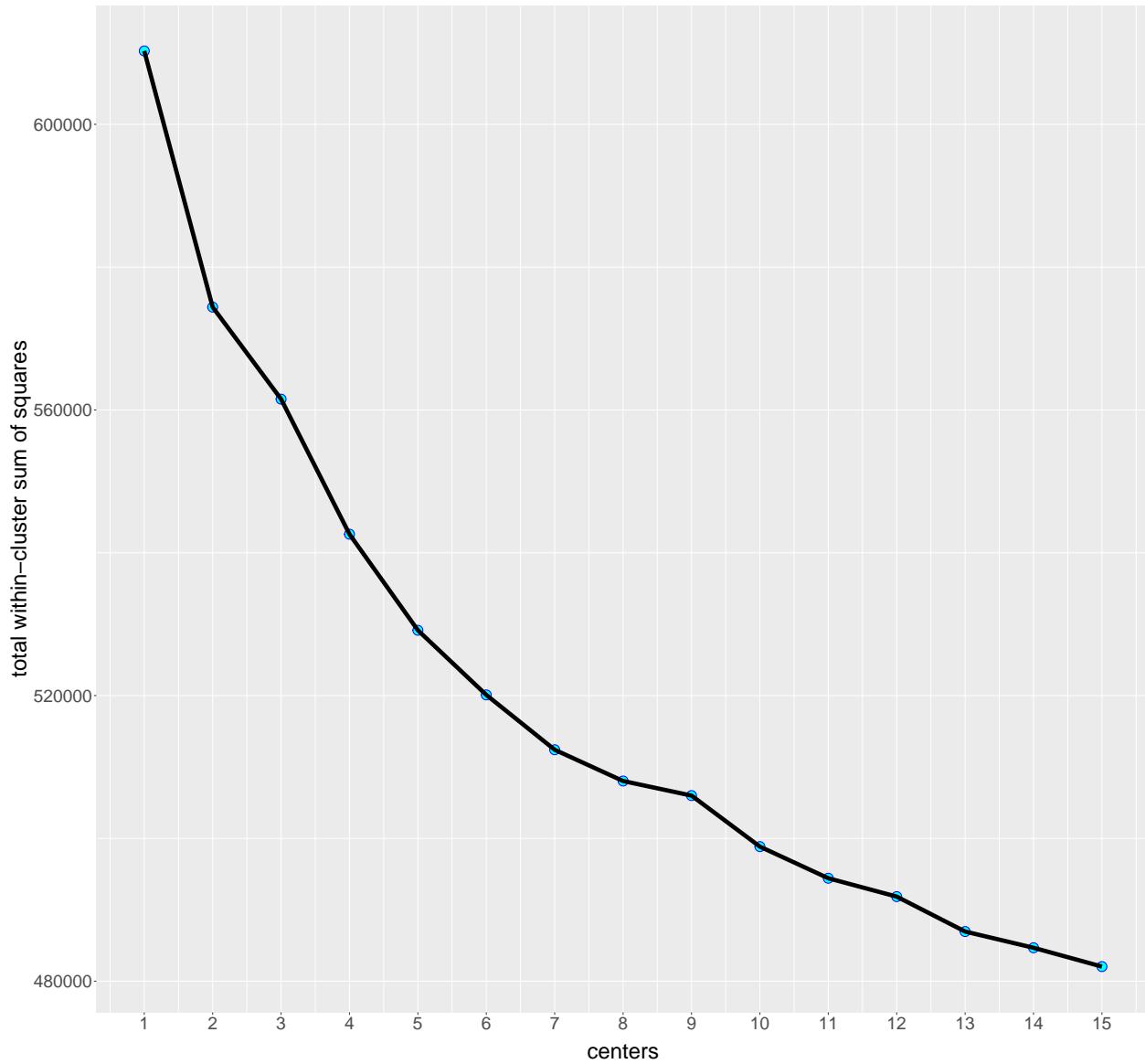


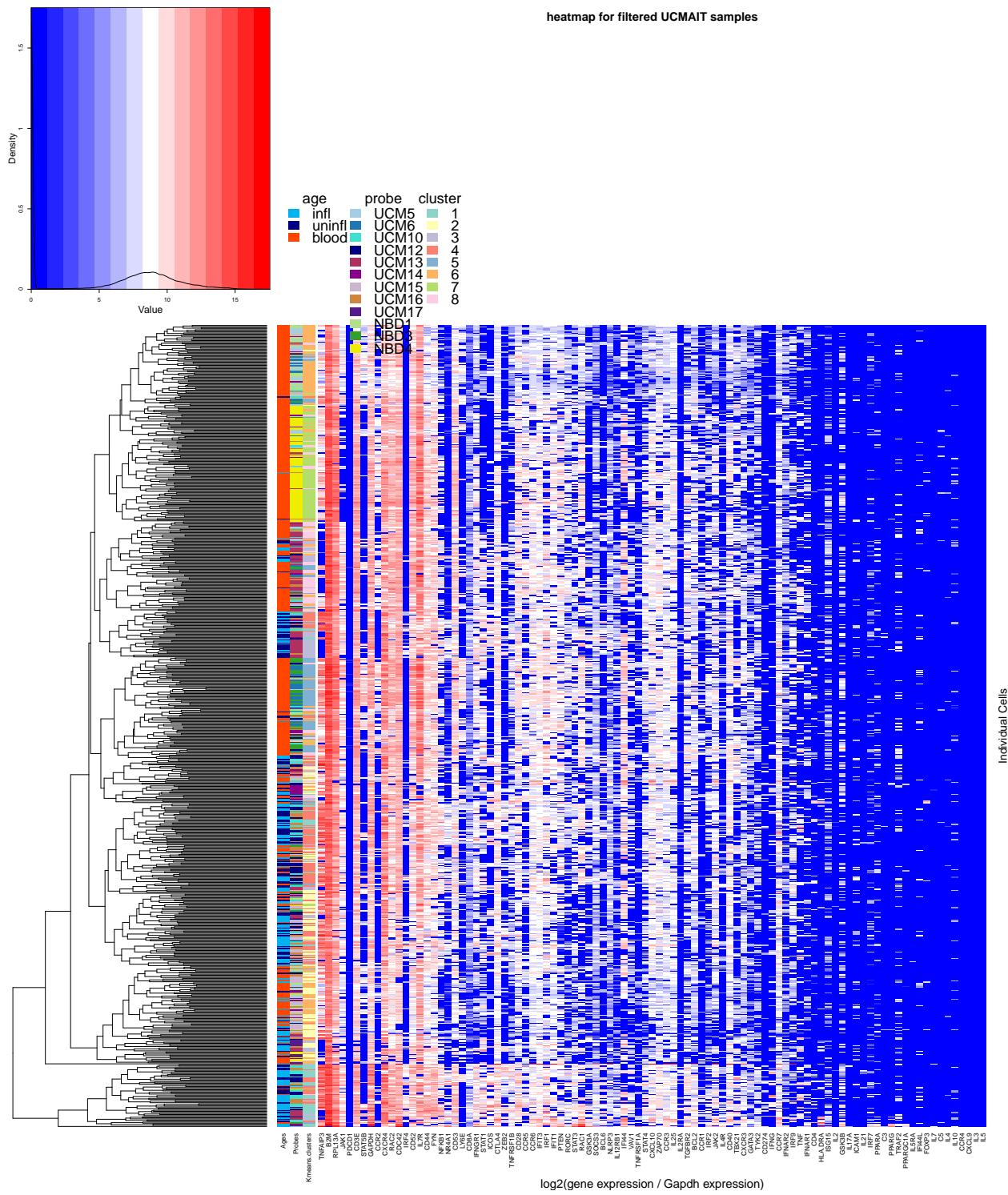
histogram of cumulative expression values per cell



38 / 781 cells were removed due to low gene expression (cluster ID of removed clusters: 6)

kmeans scree plot





[1]

[1]

[1] Probe vs. Cluster

	probe_UCM5	probe_UCM6	probe_UCM10	probe_UCM12	probe_UCM13
cluster_1	0	0	30	9	4
cluster_2	3	0	2	9	1
cluster_3	0	0	0	0	53

cluster_4	0	0	31	47	0
cluster_5	0	41	0	4	0
cluster_6	29	6	3	4	2
cluster_7	2	1	0	1	0
cluster_8	1	0	13	6	28
	probe_UCM14	probe_UCM15	probe_UCM16	probe_UCM17	probe_NBD1
cluster_1	5	0	8	0	0
cluster_2	13	34	21	6	5
cluster_3	1	0	1	6	0
cluster_4	2	3	37	2	0
cluster_5	0	0	3	0	0
cluster_6	16	22	3	4	41
cluster_7	0	2	4	0	0
cluster_8	11	2	17	0	2
	probe_NBD3	probe_NBD4			
cluster_1	0	0			
cluster_2	2	2			
cluster_3	0	0			
cluster_4	1	0			
cluster_5	42	0			
cluster_6	1	7			
cluster_7	2	84			
cluster_8	0	1			

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

```
data: probeTable
X-squared = 2156.3, df = NA, p-value = 0.0004998
```

```
[1]
[1]
[1] Tissue vs. Cluster
      cellSource_blood cellSource_tissue
cluster_1          0            56
cluster_2         29            69
cluster_3          1            60
cluster_4          2           121
cluster_5         89            1
cluster_6        134            4
cluster_7         95            1
cluster_8         78            3
```

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

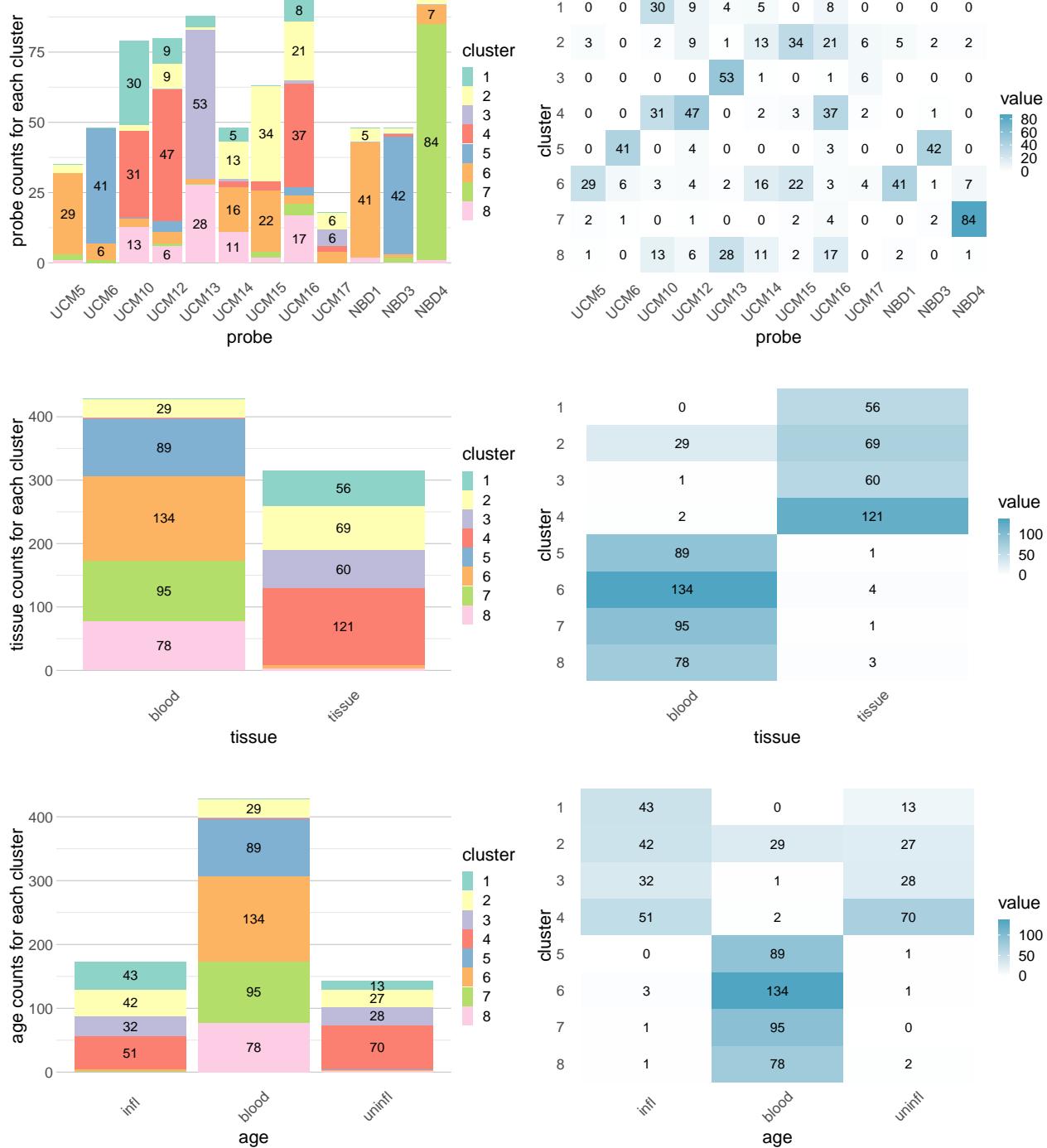
```
data: sourceTable
X-squared = 611.47, df = NA, p-value = 0.0004998
```

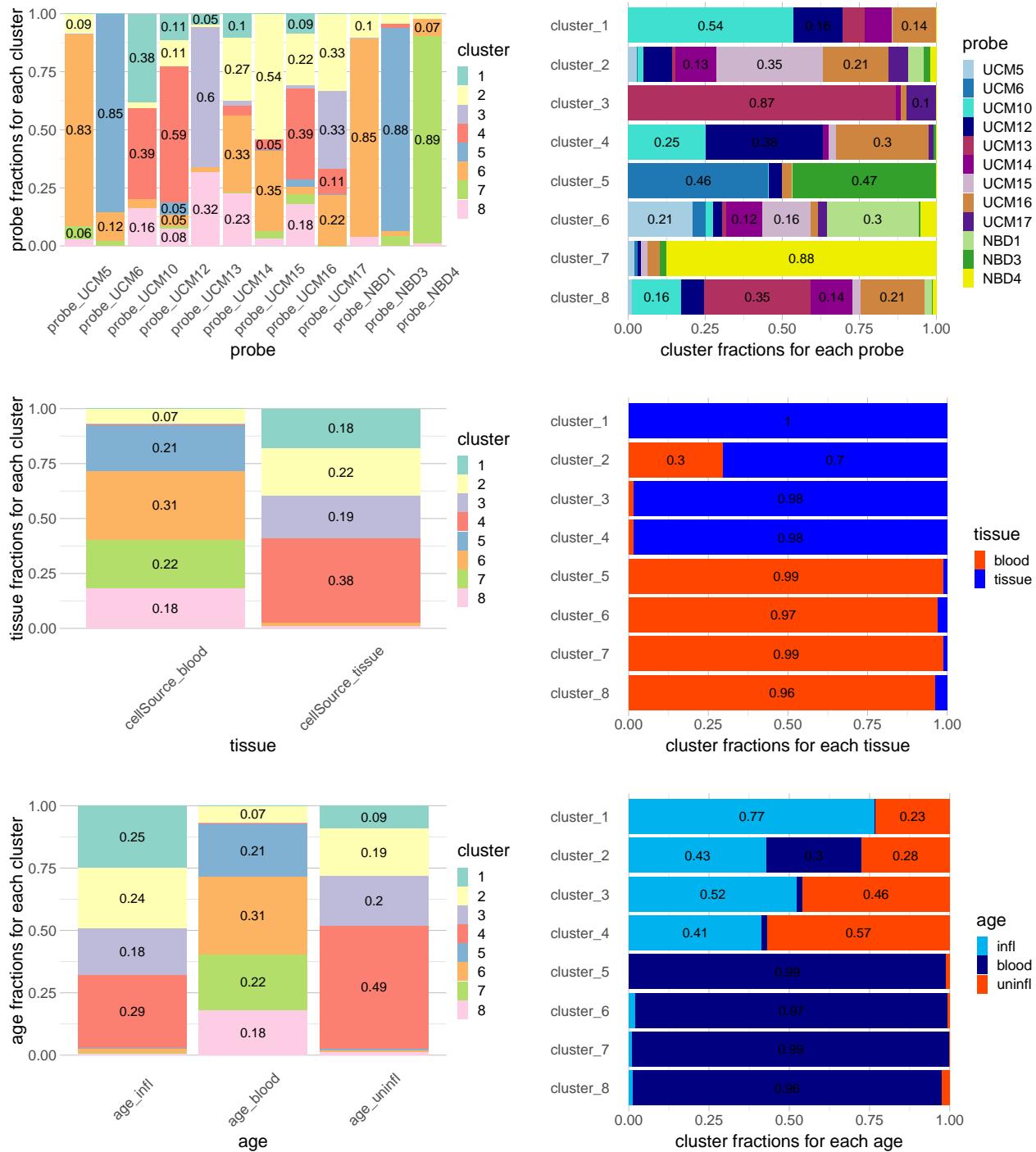
```
[1]
[1]
[1] age vs. Cluster
      age_infl age_blood age_uninfl
cluster_1       43        0        13
```

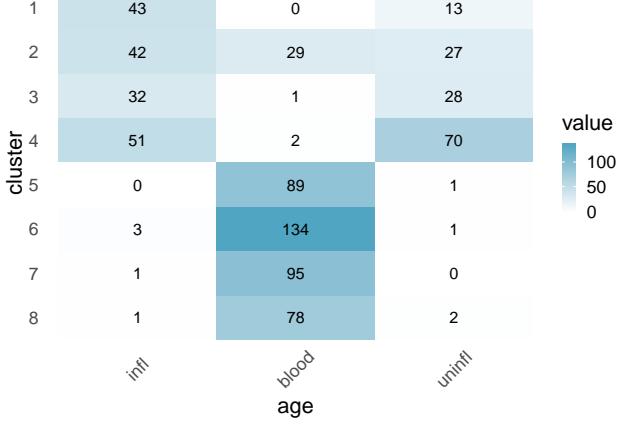
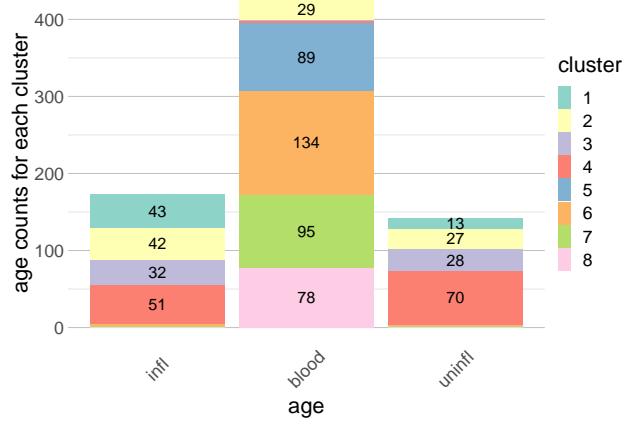
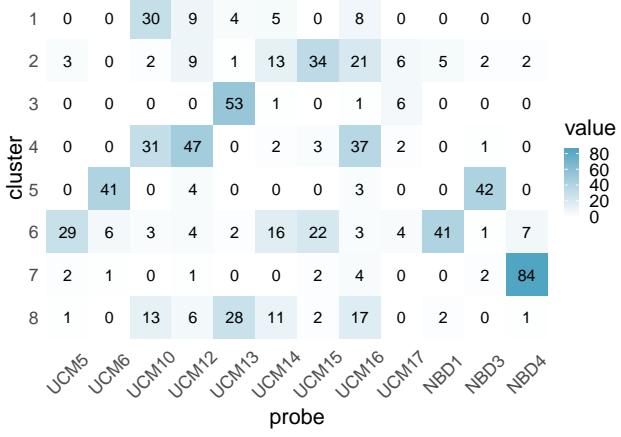
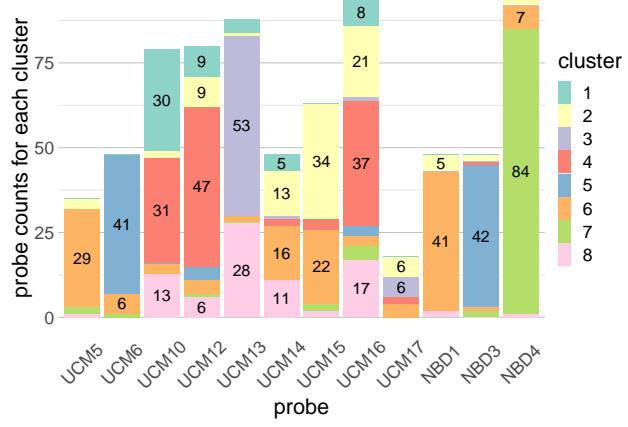
cluster_2	42	29	27
cluster_3	32	1	28
cluster_4	51	2	70
cluster_5	0	89	1
cluster_6	3	134	1
cluster_7	1	95	0
cluster_8	1	78	2

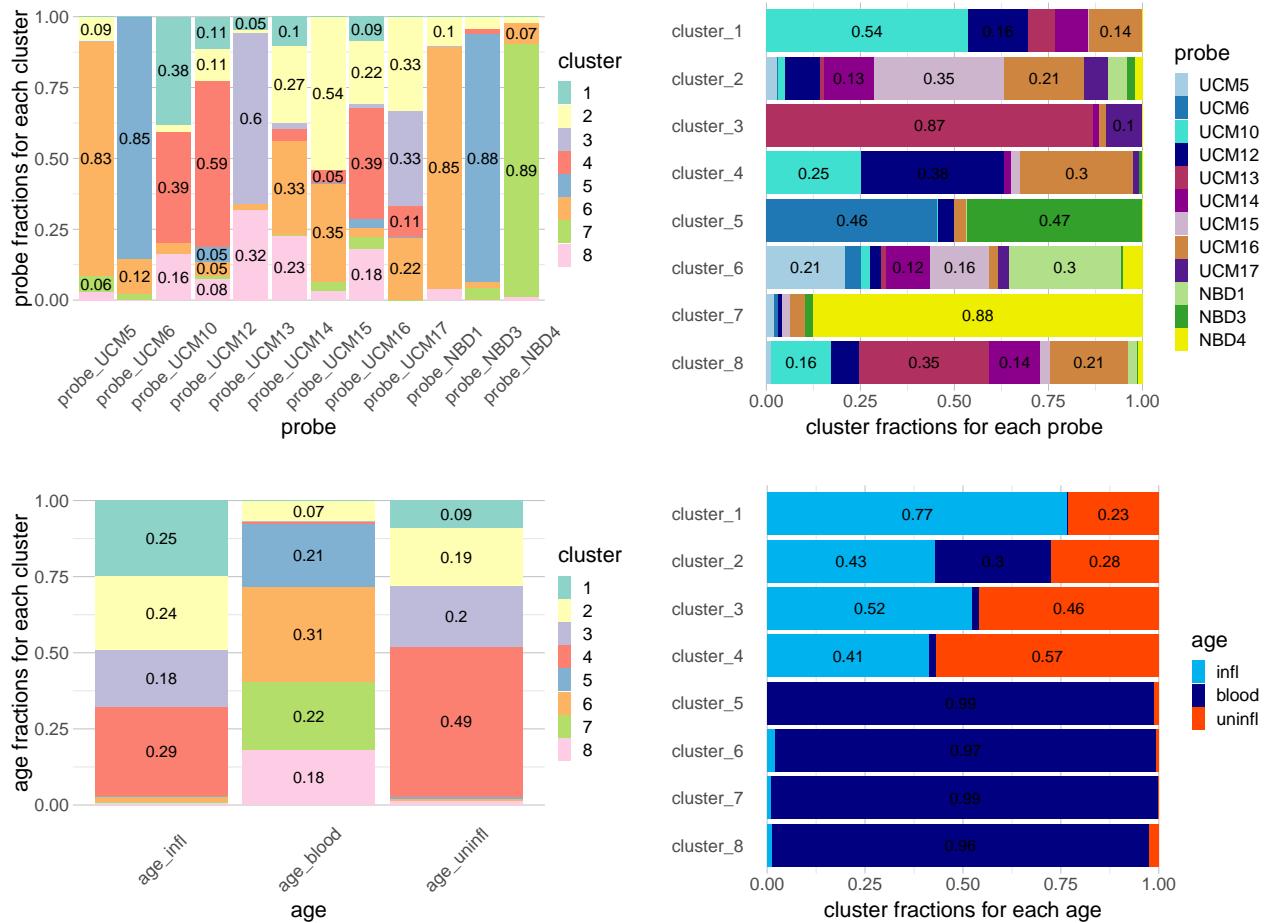
Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

```
data: ageTable  
X-squared = 657.41, df = NA, p-value = 0.0004998
```

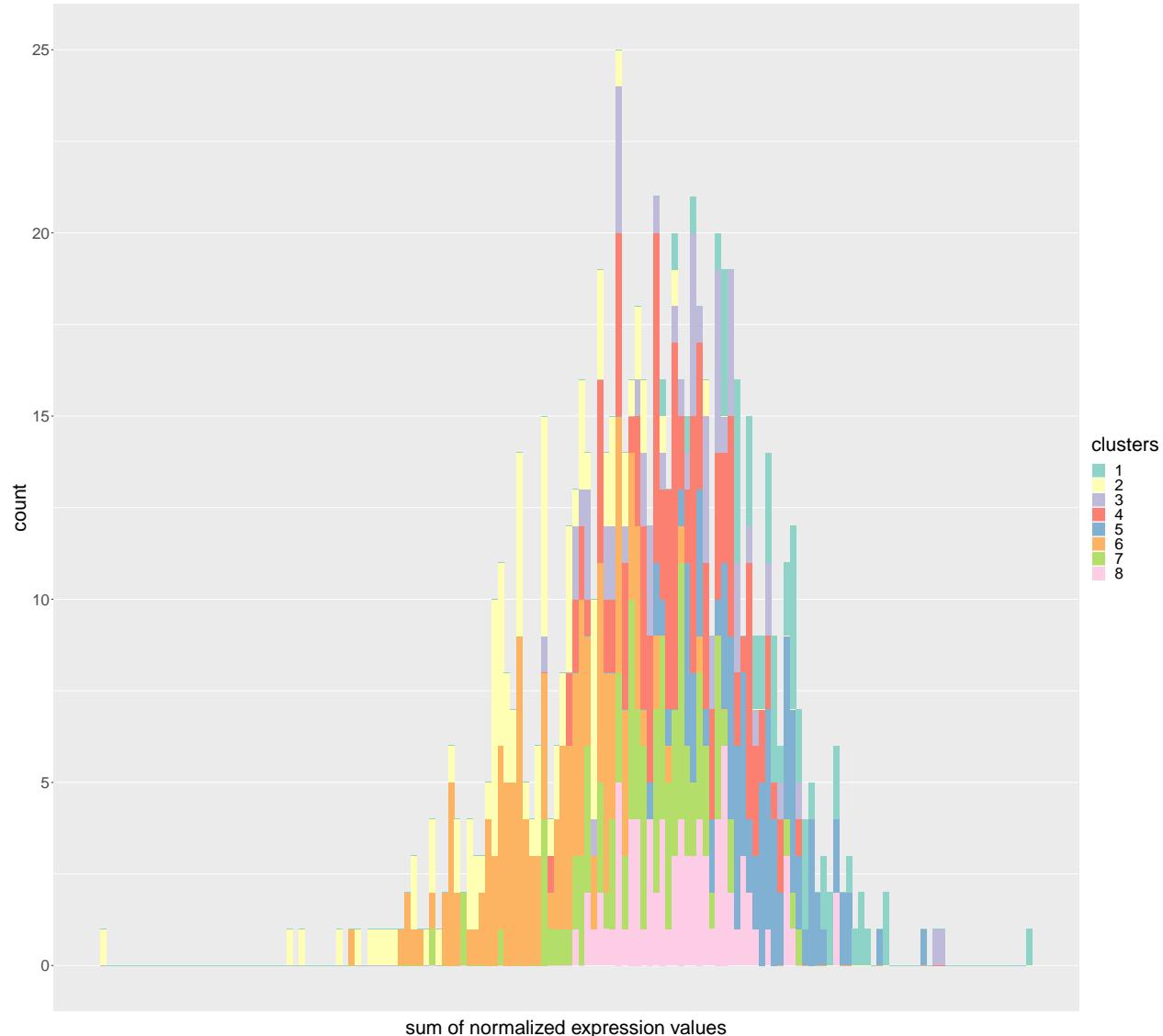




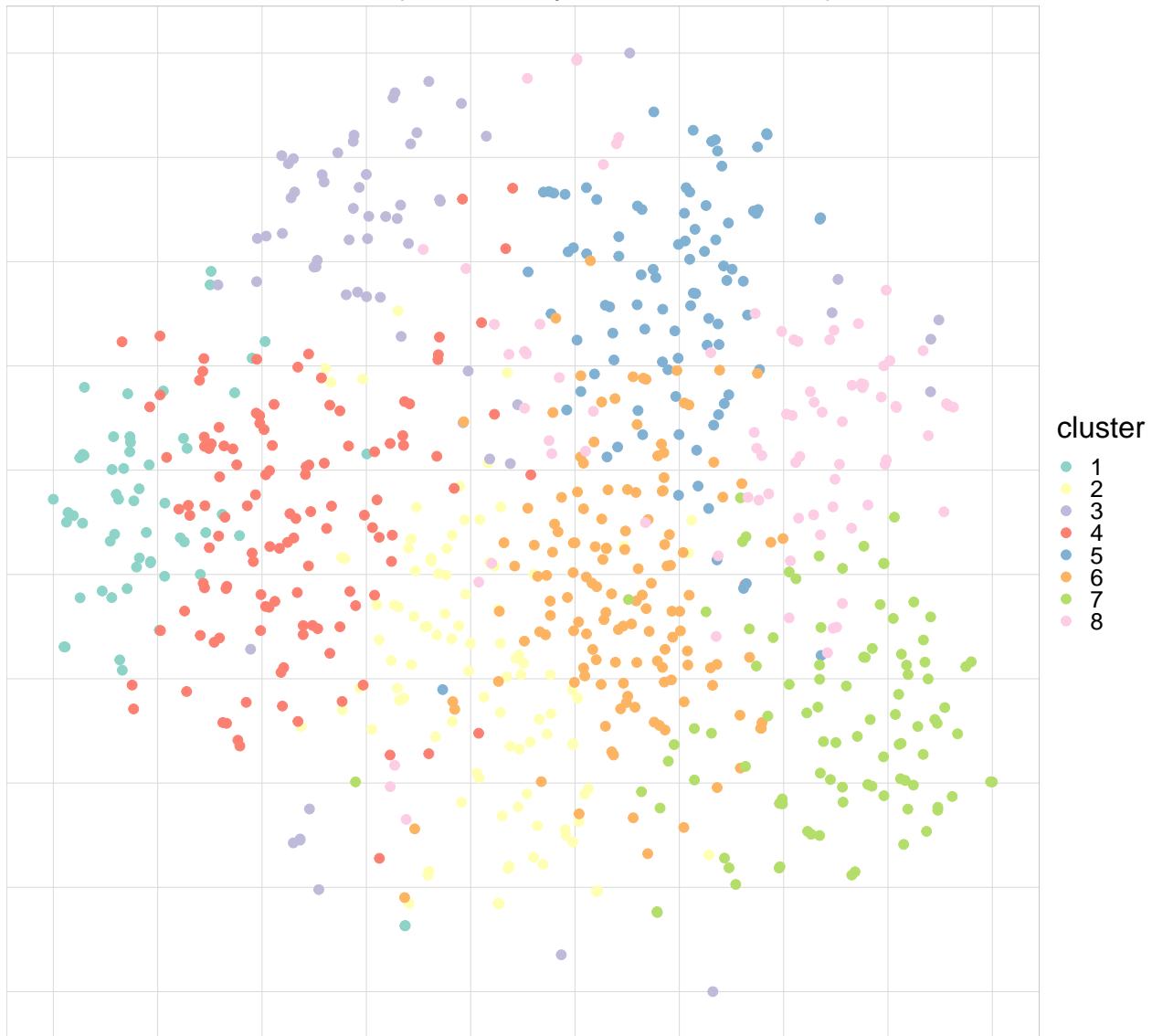




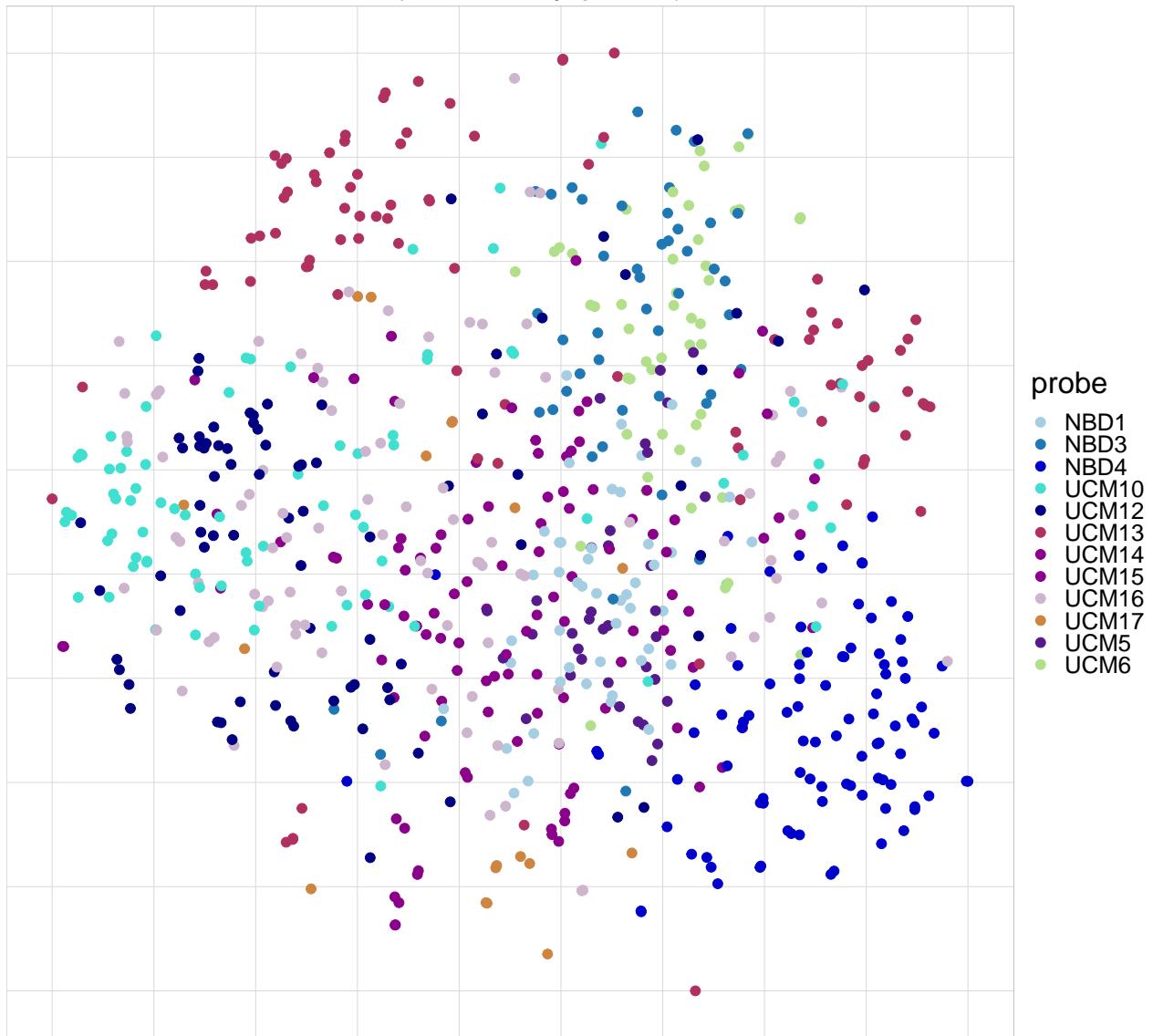
histogram of cumulative expression values per cell



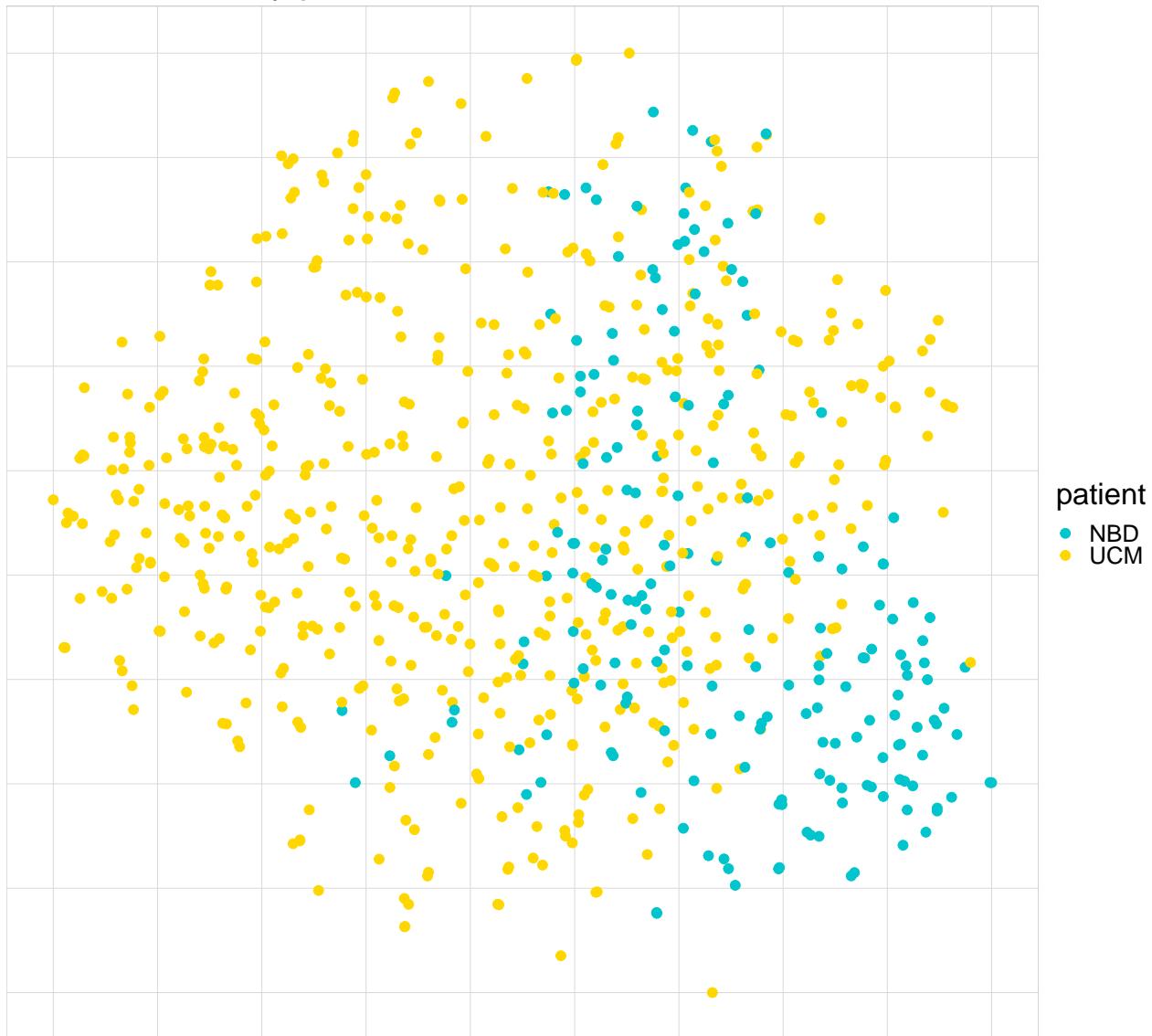
t-SNE between tissues (colored by kmeans.cluster)



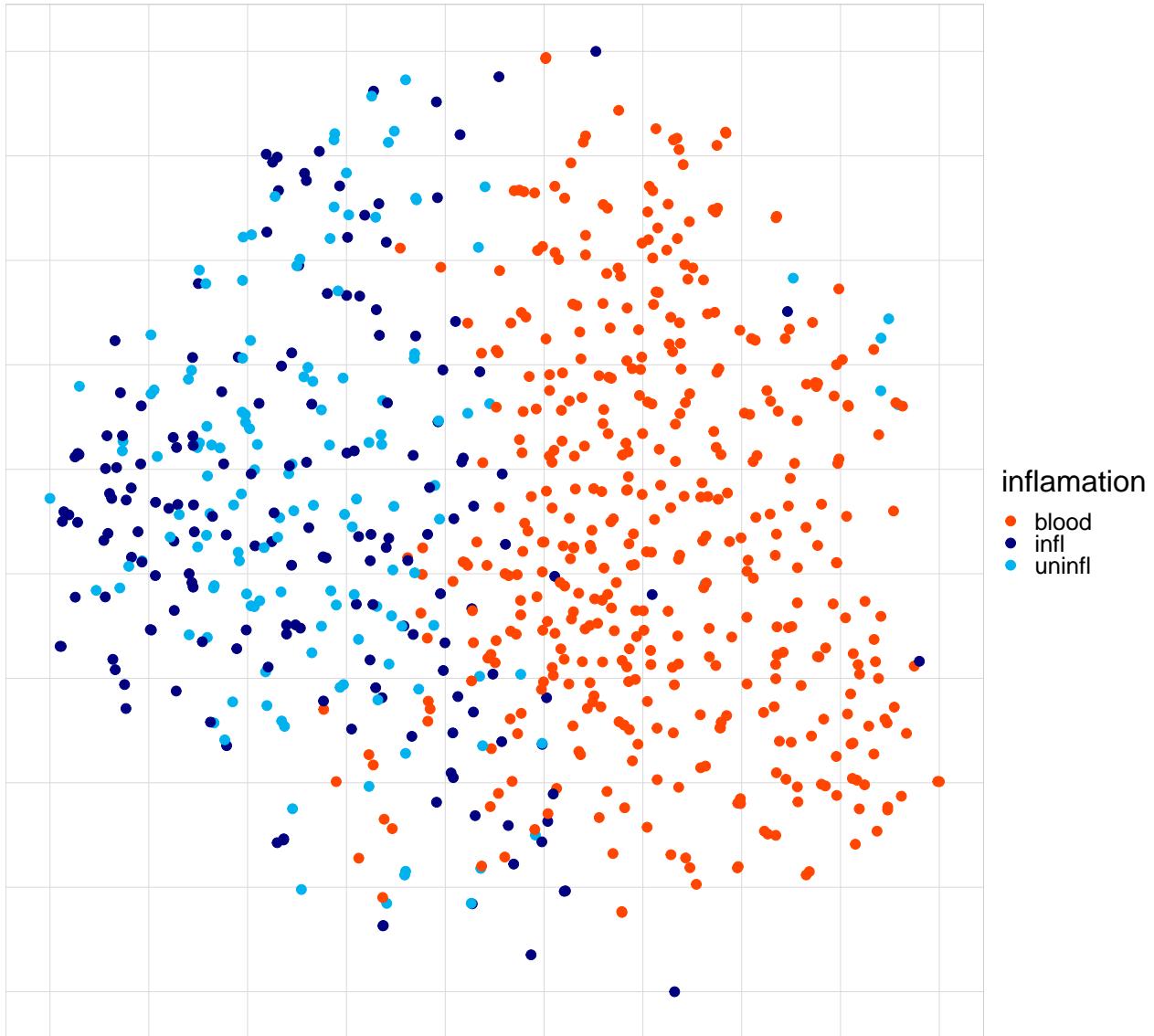
t-SNE between tissues (colored by probe)



t-SNE colored by patient



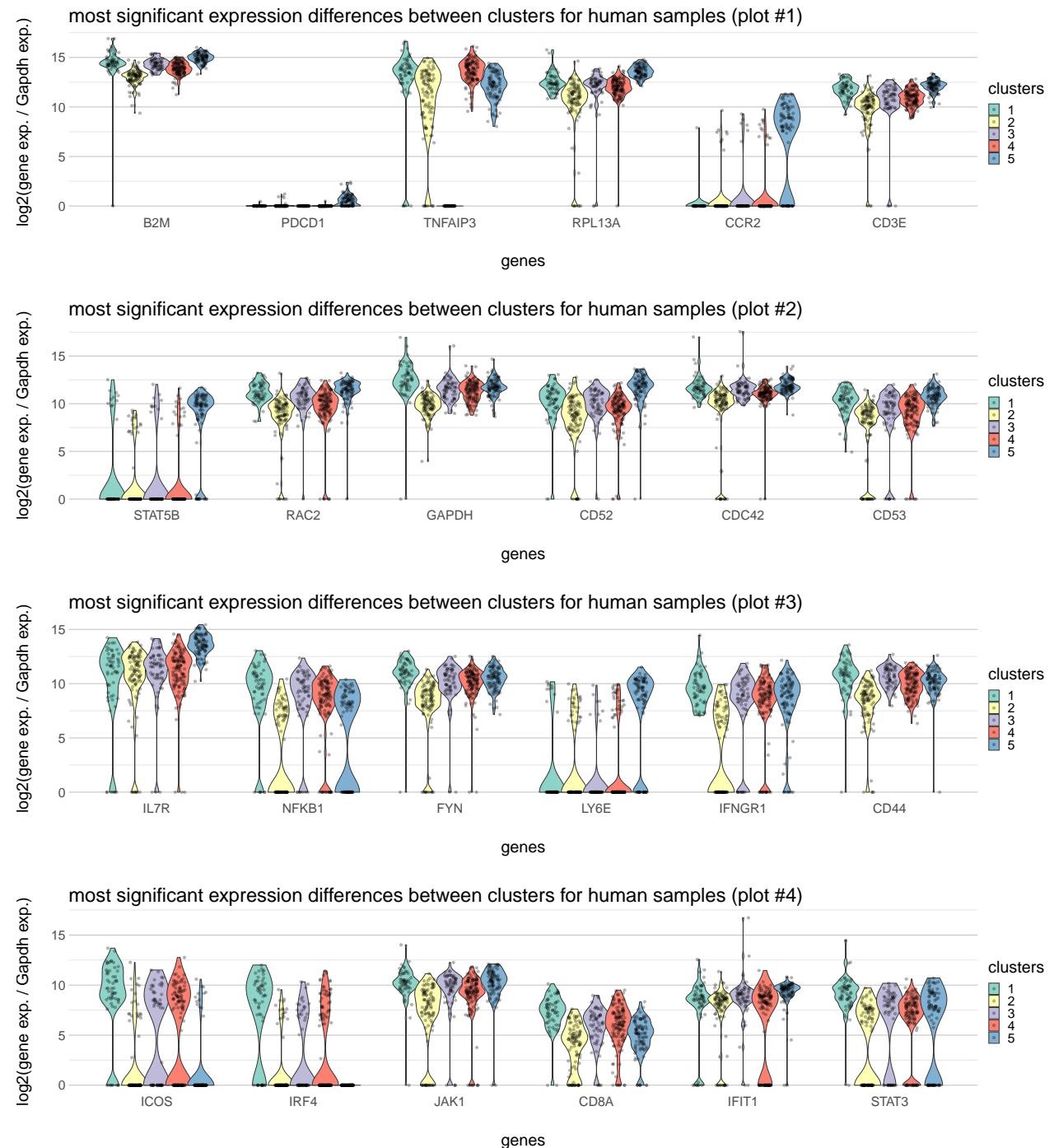
## t-SNE colored by inflamed site

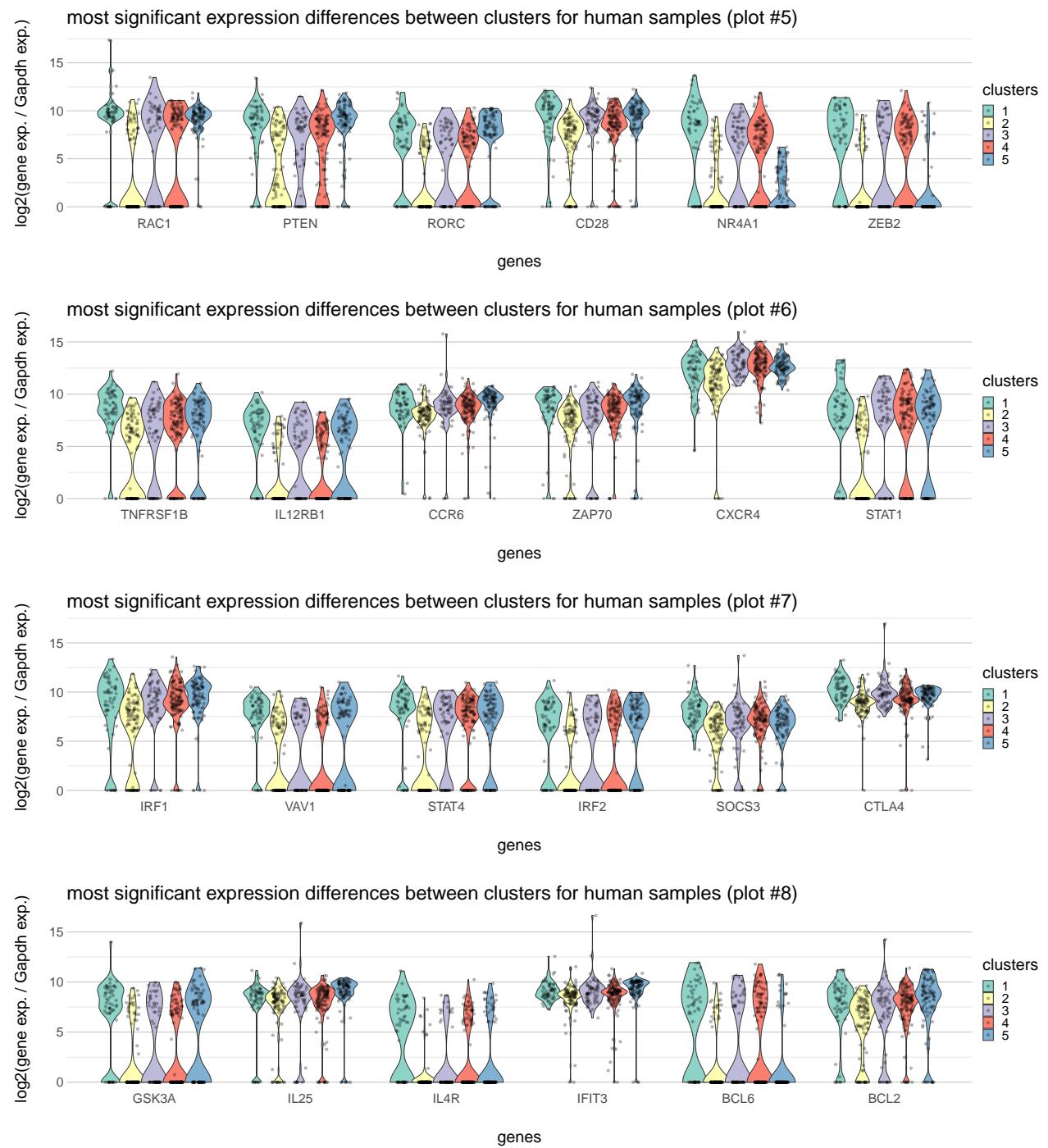


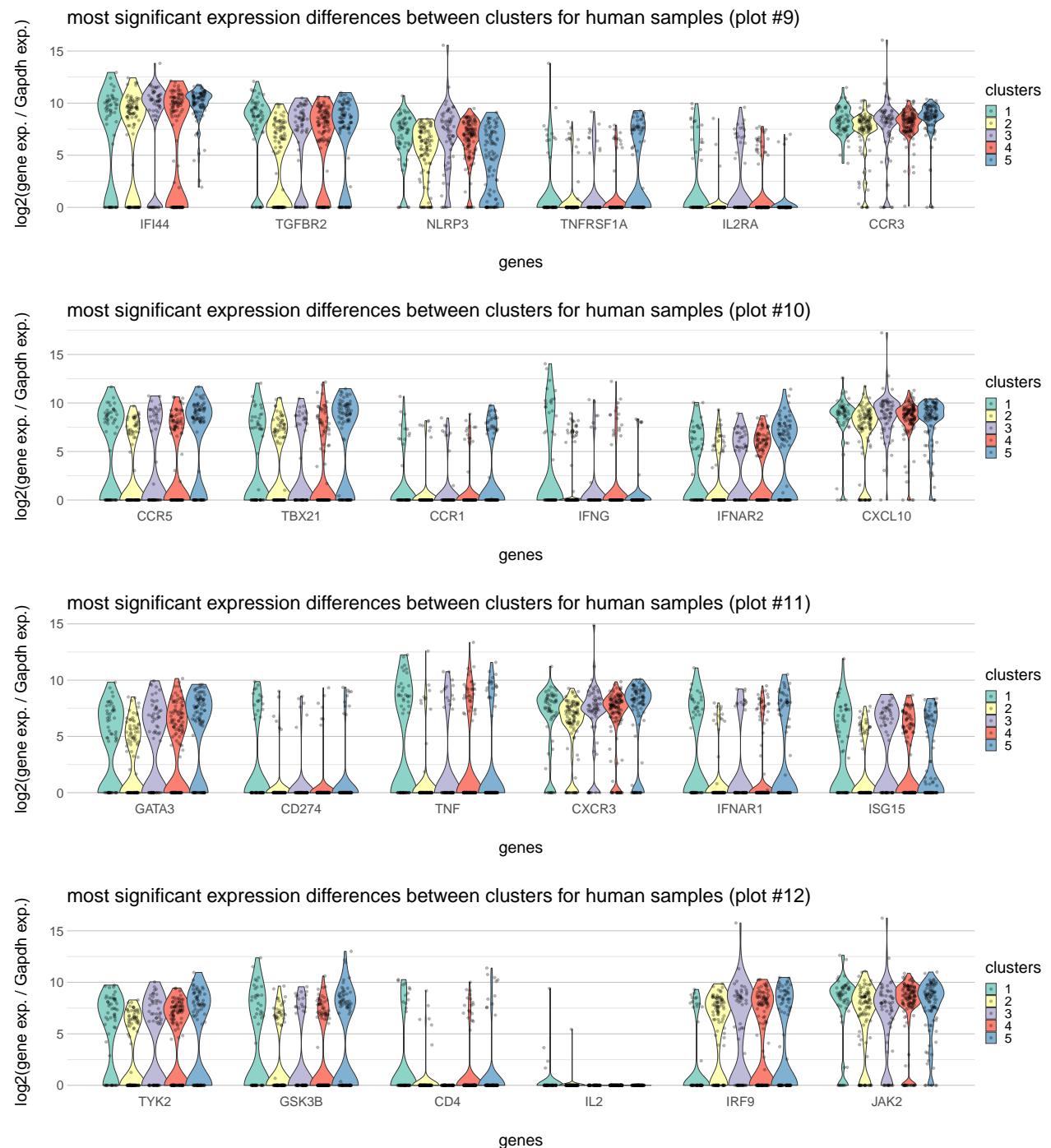
[1] Differentially expressed genes between clusters for human samples:

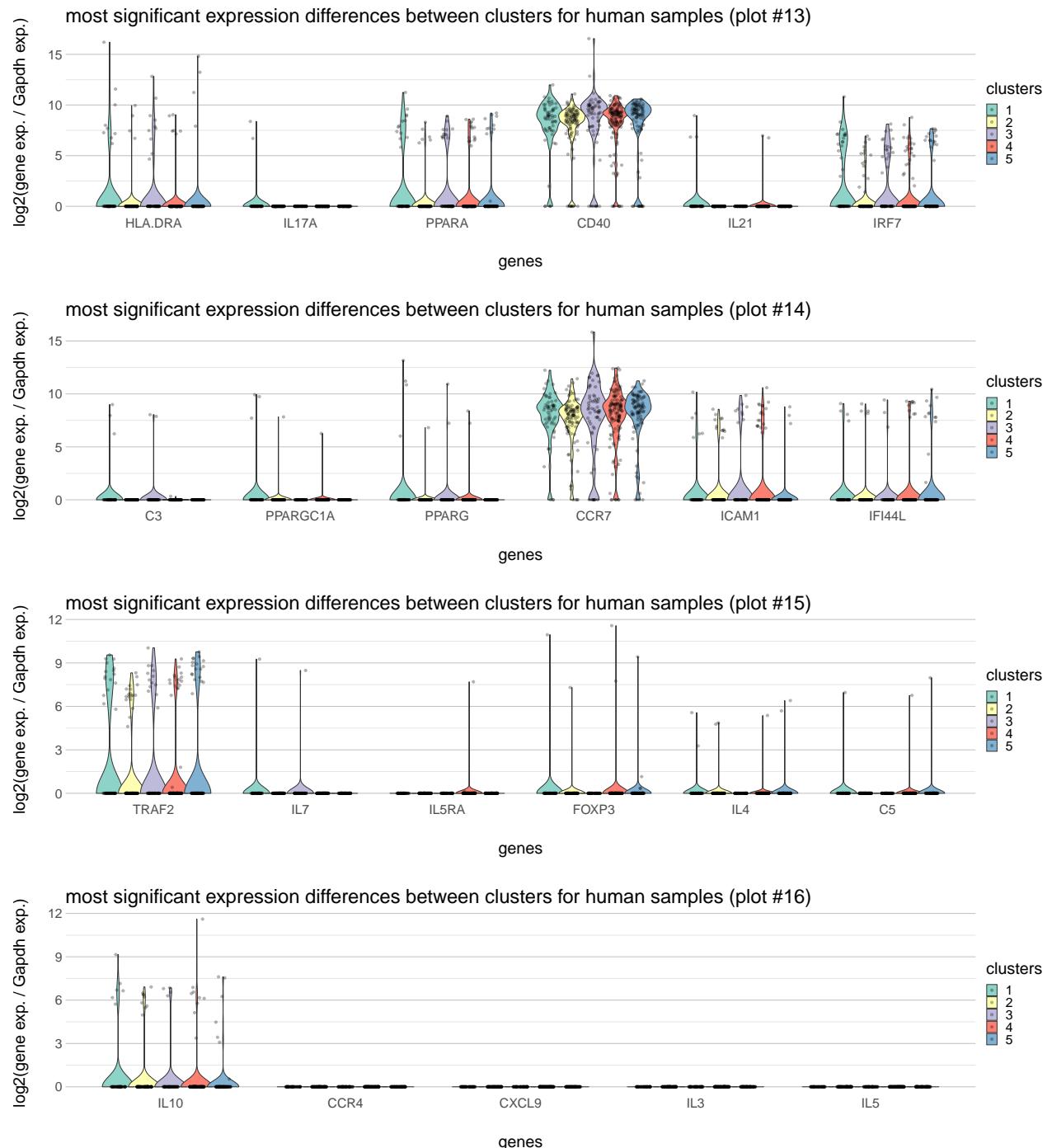
[1]	B2M: 1.757e-50	PDCD1: 1.757e-50	TNFAIP3: 2.323e-45
[4]	RPL13A: 4.171e-44	CCR2: 1.466e-37	CD3E: 1.523e-36
[7]	STAT5B: 2.085e-34	RAC2: 2.085e-34	GAPDH: 5.46e-34
[10]	CD52: 1.375e-30	CDC42: 2.81e-29	CD53: 6.181e-28
[13]	IL7R: 1.101e-27	NFKB1: 3.275e-27	FYN: 9.77e-27
[16]	LY6E: 8.48e-25	IFNGR1: 9.145e-25	CD44: 1.063e-24
[19]	ICOS: 1.21e-24	IRF4: 1.438e-23	JAK1: 7.065e-23
[22]	CD8A: 5.261e-22	IFIT1: 5.809e-19	STAT3: 5.809e-19
[25]	RAC1: 6.651e-19	PTEN: 1.173e-18	RORC: 1.619e-18
[28]	CD28: 5.474e-18	NR4A1: 1.004e-17	ZEB2: 5.535e-16
[31]	TNFRSF1B: 5.034e-15	IL12RB1: 1.906e-14	CCR6: 2.196e-14
[34]	ZAP70: 2.763e-14	CXCR4: 2.877e-14	STAT1: 4.588e-14
[37]	IRF1: 9.241e-14	VAV1: 1.602e-13	STAT4: 1.067e-11
[40]	IRF2: 1.067e-11	SOCS3: 2.835e-11	CTLA4: 5.44e-11
[43]	GSK3A: 8.348e-11	IL25: 1.188e-10	IL4R: 1.85e-10

[46] IFIT3:	2.433e-10	BCL6:	2.433e-10	BCL2:	4.707e-10
[49] IFI44:	7.139e-10	TGFBR2:	1.213e-09	NLRP3:	2.003e-09
[52] TNFRSF1A:	4.833e-09	IL2RA:	1.383e-08	CCR3:	2.172e-07
[55] CCR5:	4.002e-07	TBX21:	5.93e-07	CCR1:	1.575e-06
[58] IFNG:	5.568e-06	IFNAR2:	8.8e-06	CXCL10:	9.731e-06
[61] GATA3:	9.731e-06	CD274:	9.731e-06	TNF:	1.867e-05
[64] CXCR3:	2.908e-05	IFNAR1:	4.18e-05	ISG15:	0.0001249
[67] TYK2:	0.0003459	GSK3B:	0.0003572	CD4:	0.0004208
[70] IL2:	0.0005236	IRF9:	0.0008145	JAK2:	0.001897
[73] HLA.DRA:	0.003577	IL17A:	0.01208	PPARA:	0.01882
[76] CD40:	0.02174	IL21:	0.02352	IRF7:	0.02352
[79] C3:	0.03177	PPARGC1A:	0.03735	PPARG:	0.04485





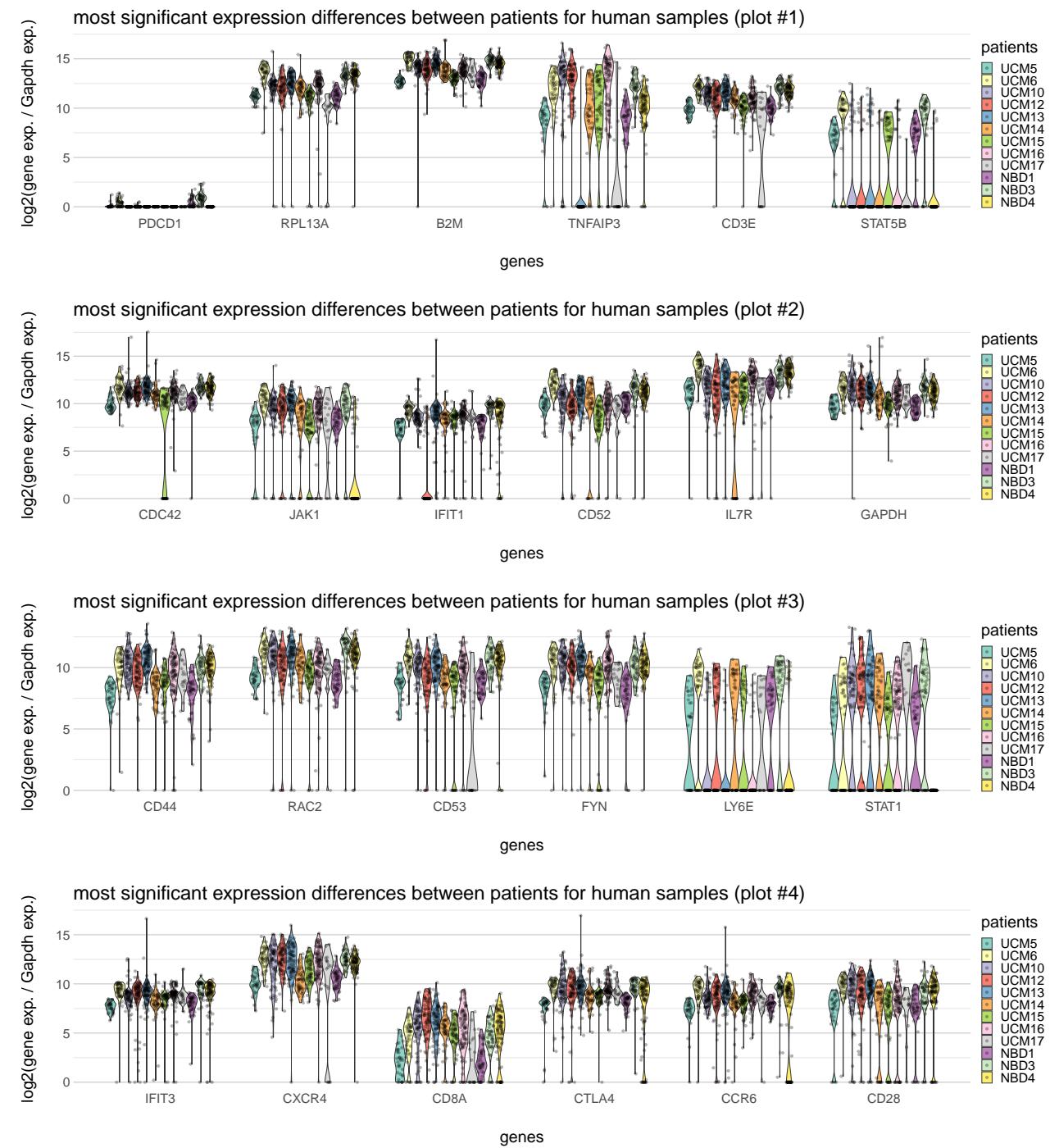


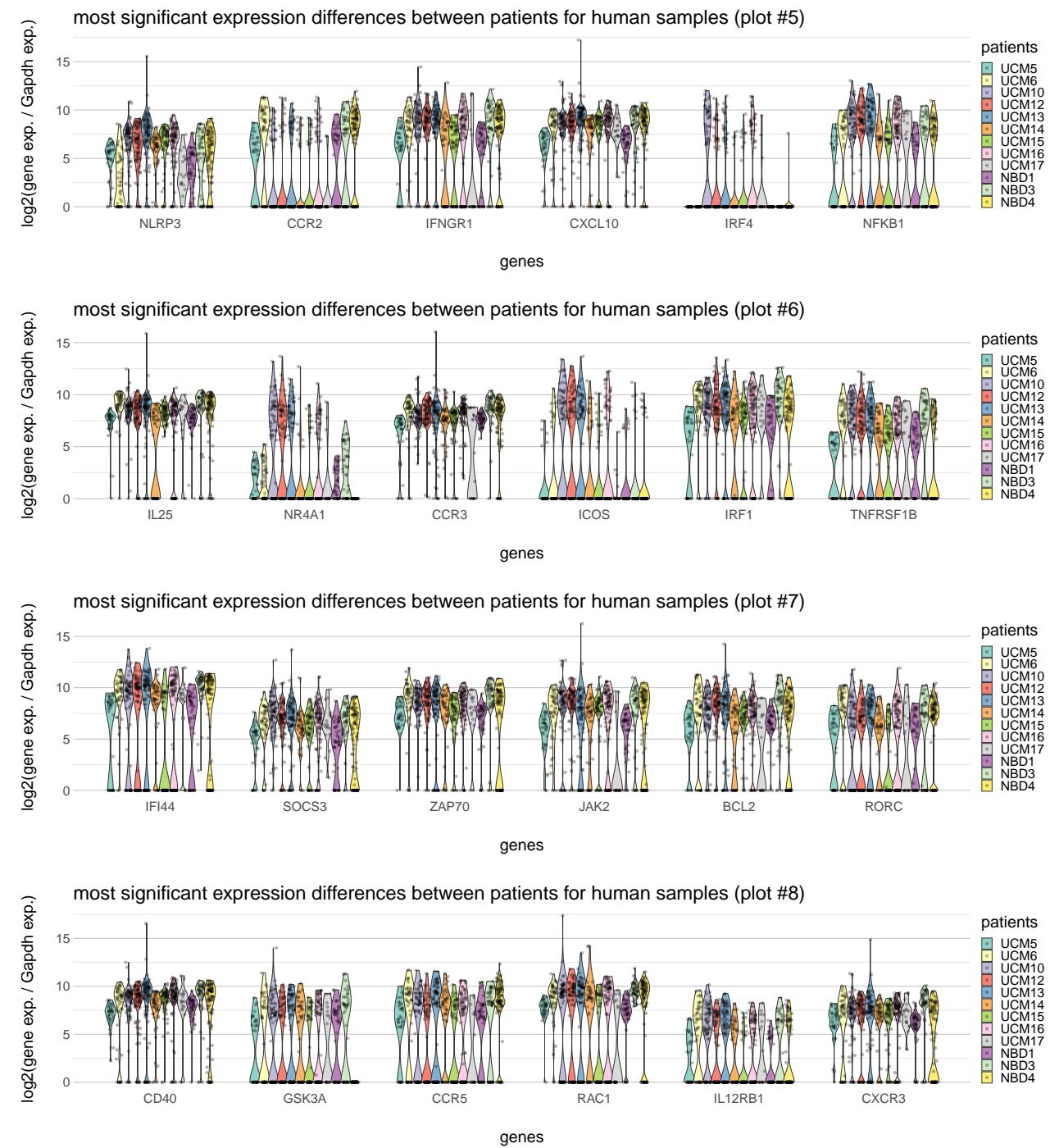


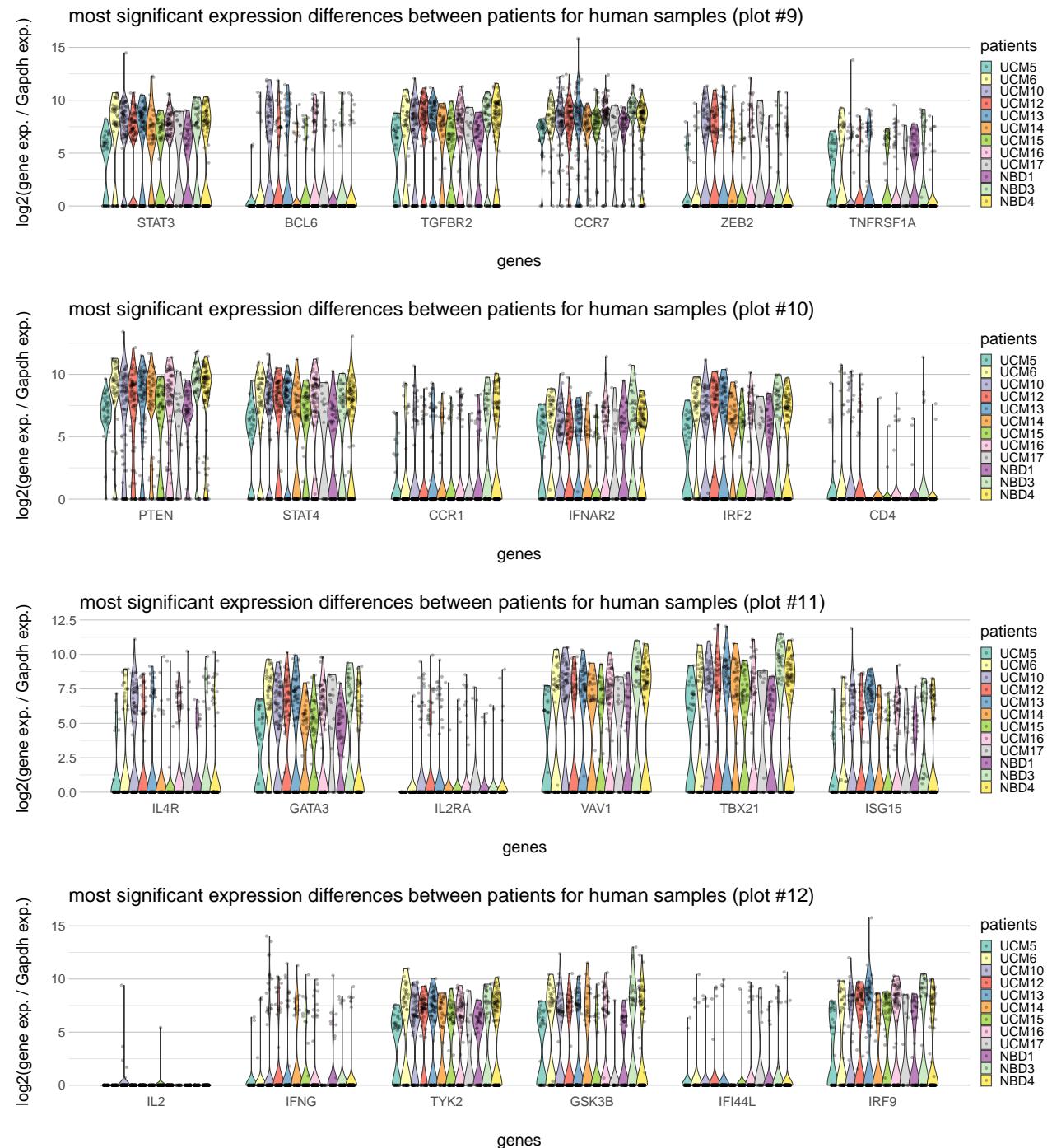
[1] Differentially expressed genes between patients for human samples:

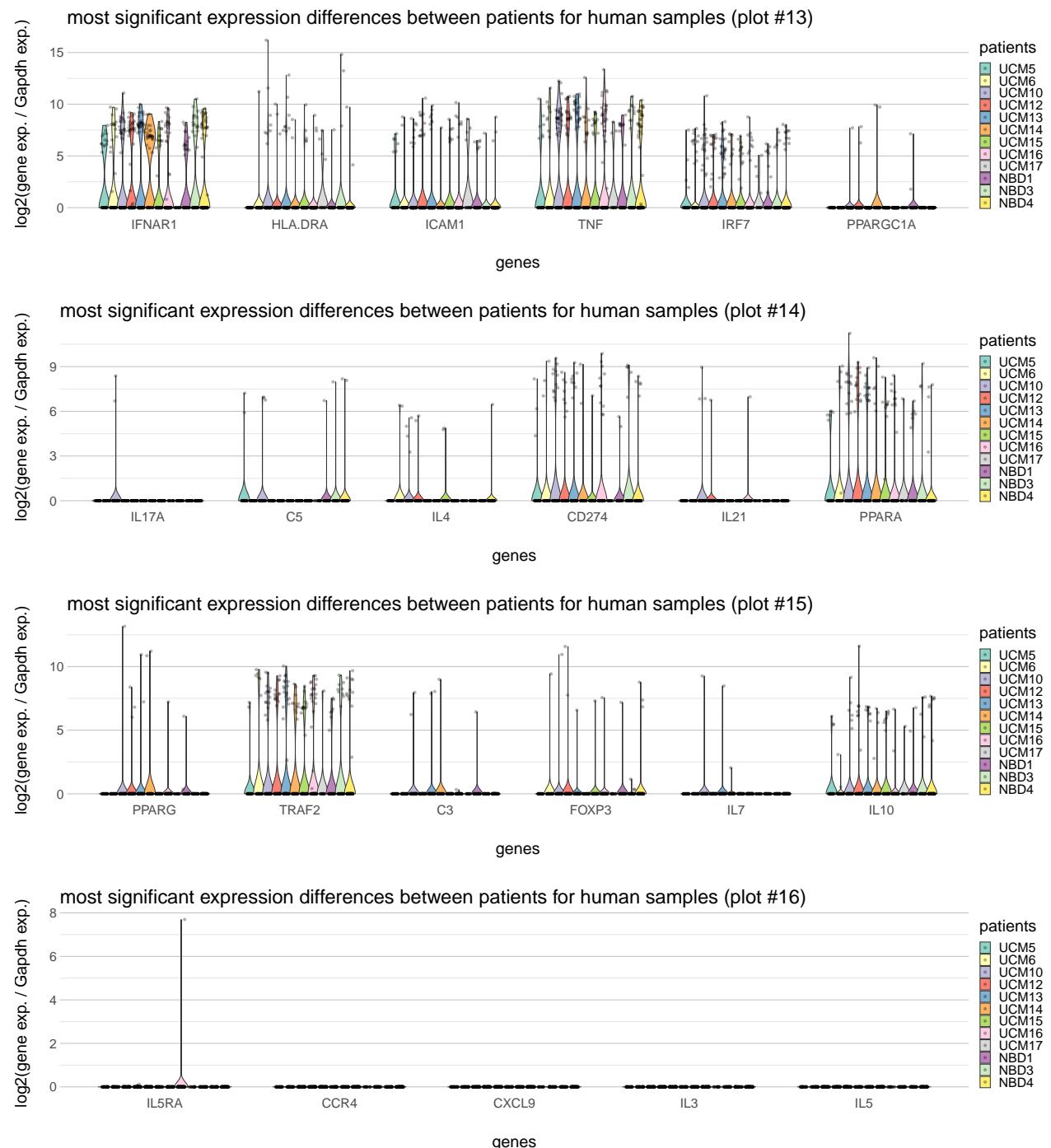
- |                       |                   |                   |
|-----------------------|-------------------|-------------------|
| [1] PDCD1: 1.313e-90  | RPL13A: 1.535e-77 | B2M: 3.93e-77     |
| [4] TNFAIP3: 2.43e-72 | CD3E: 2.919e-61   | STAT5B: 8.759e-57 |
| [7] CDC42: 1.24e-53   | JAK1: 1.206e-52   | IFIT1: 1.555e-52  |
| [10] CD52: 8.635e-50  | IL7R: 2.712e-49   | GAPDH: 5.973e-49  |
| [13] CD44: 6.704e-46  | RAC2: 2.92e-43    | CD53: 5.199e-42   |
| [16] FYN: 6.31e-42    | LY6E: 3.235e-41   | STAT1: 3.432e-37  |
| [19] IFIT3: 3.201e-36 | CXCR4: 1.819e-35  | CD8A: 2.611e-34   |
| [22] CTLA4: 4.105e-33 | CCR6: 9.961e-31   | CD28: 1.227e-30   |
| [25] NLRP3: 2.002e-30 | CCR2: 9.477e-27   | IFNGR1: 4.679e-26 |

[28]	CXCL10:	1.017e-25	IRF4:	2.317e-25	NFKB1:	5.485e-25
[31]	IL25:	5.648e-24	NR4A1:	1.253e-23	CCR3:	5.981e-23
[34]	ICOS:	2.365e-21	IRF1:	1.963e-20	TNFRSF1B:	1.681e-19
[37]	IFI44:	7.793e-19	SOCS3:	1.76e-17	ZAP70:	2.564e-17
[40]	JAK2:	8.342e-17	BCL2:	2.16e-15	RORC:	2.39e-15
[43]	CD40:	2.39e-15	GSK3A:	3.684e-15	CCR5:	7.567e-15
[46]	RAC1:	1.503e-14	IL12RB1:	5.904e-14	CXCR3:	1.56e-13
[49]	STAT3:	1.688e-13	BCL6:	1.478e-12	TGFBR2:	2.798e-12
[52]	CCR7:	6.447e-12	ZEB2:	1.174e-11	TNFRSF1A:	2.421e-11
[55]	PTEN:	1.874e-10	STAT4:	4.063e-09	CCR1:	5.533e-09
[58]	IFNAR2:	1.278e-07	IRF2:	1.329e-07	CD4:	2.986e-07
[61]	IL4R:	4.462e-07	GATA3:	2.36e-06	IL2RA:	5.031e-06
[64]	VAV1:	7.873e-06	TBX21:	1.027e-05	ISG15:	4.829e-05
[67]	IL2:	0.0002954	IFNG:	0.001	TYK2:	0.001318
[70]	GSK3B:	0.002007	IFI44L:	0.00719	IRF9:	0.01977
[73]	IFNAR1:	0.01993	HLA.DRA:	0.01993	ICAM1:	0.02974









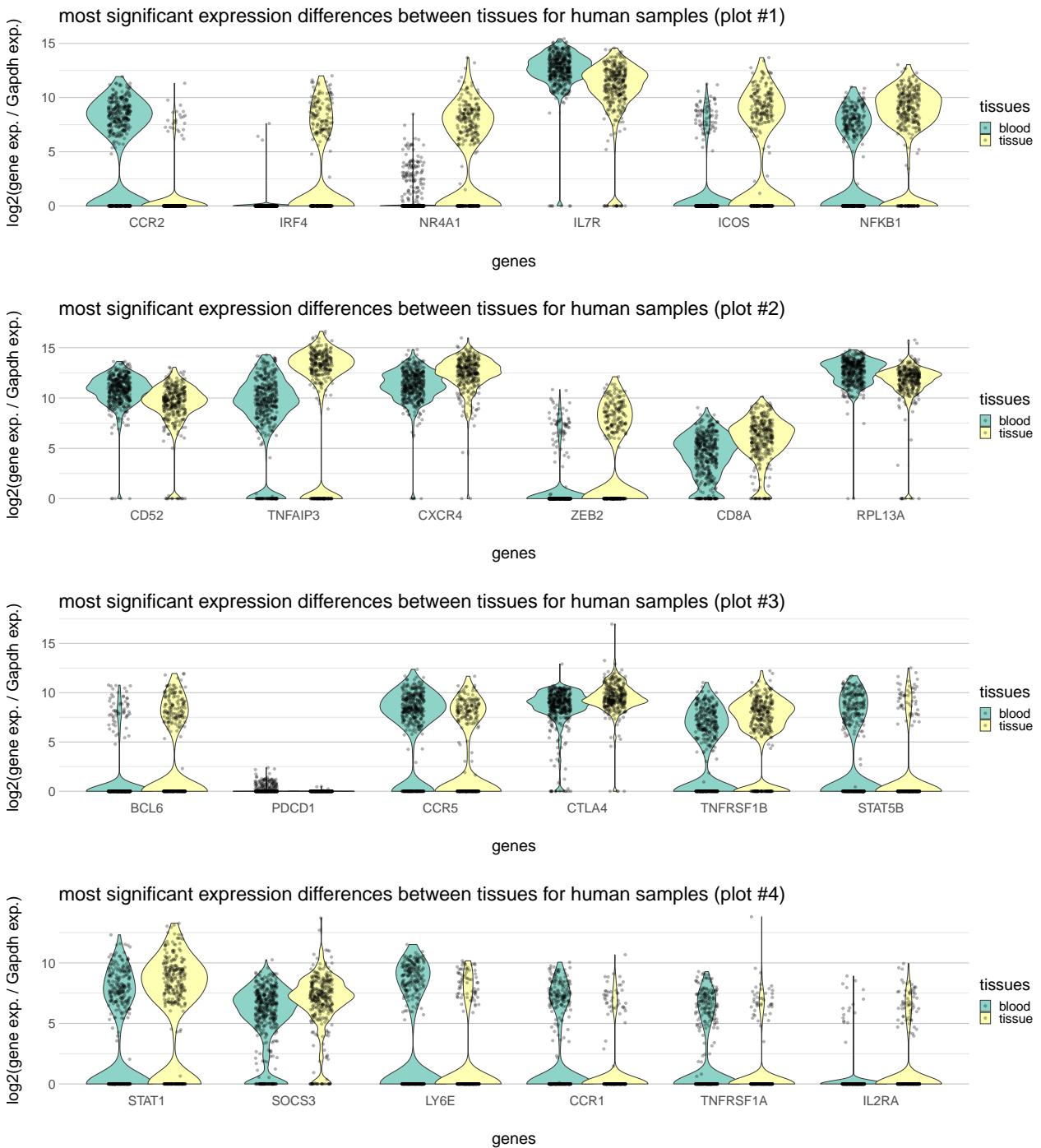
[1] Differentially expressed genes between tissues for human samples:

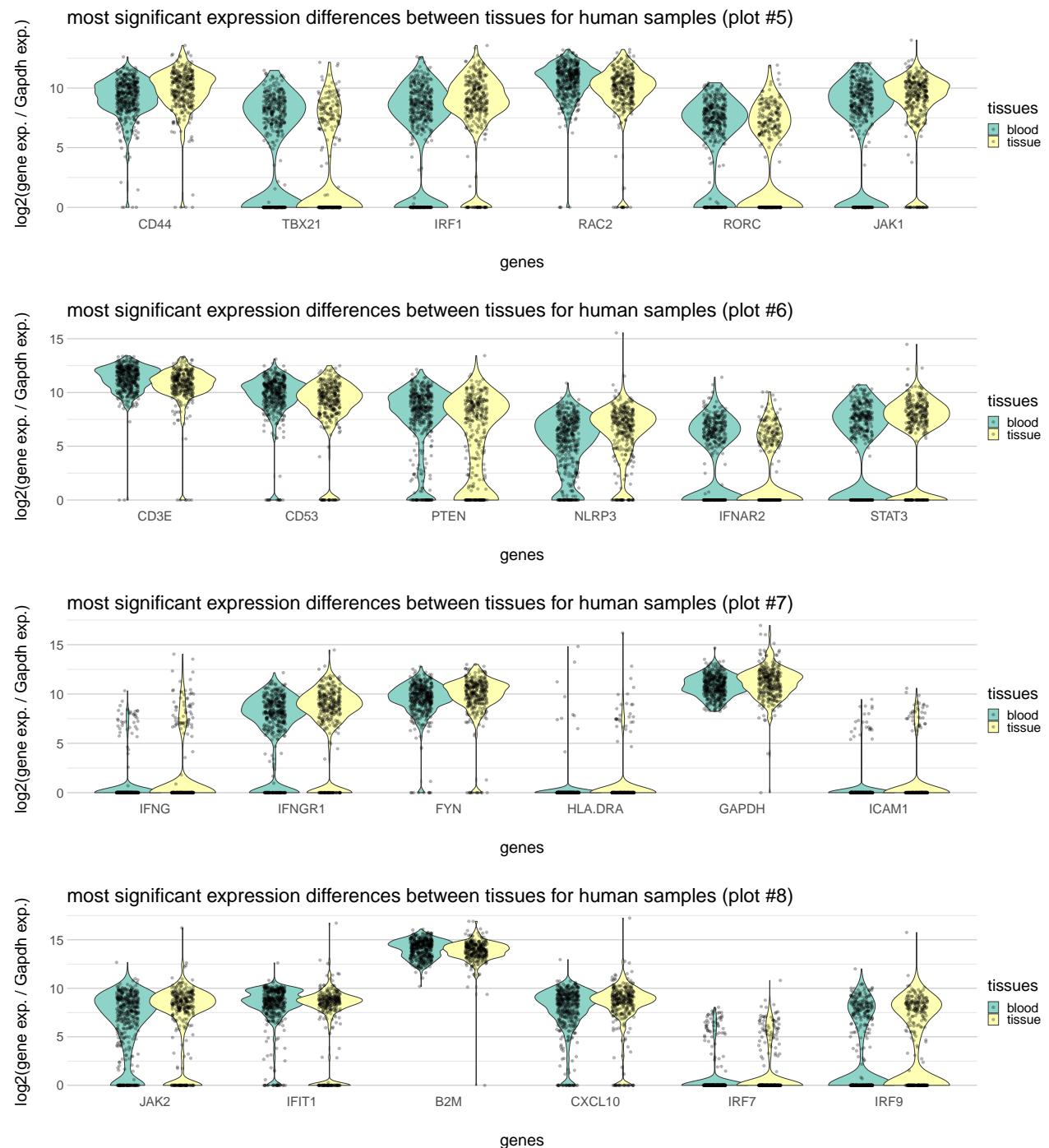
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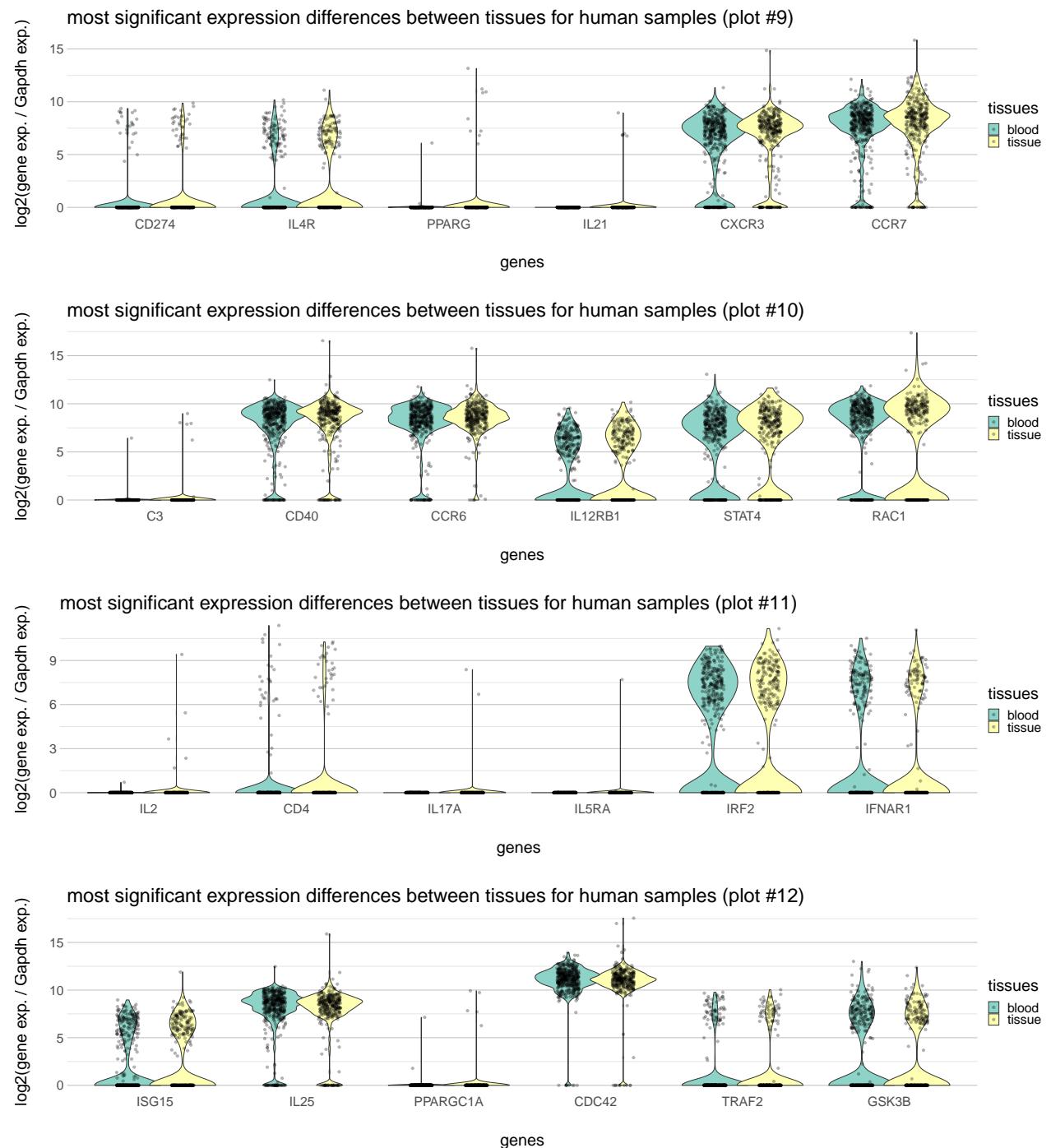
[1] CCR2: 3.834e-50    IRF4: 4.268e-45    NR4A1: 7.104e-36
[4] IL7R: 1e-33        ICOS: 4.964e-29    NFKB1: 4.977e-29
[7] CD52: 3.762e-28    TNFAIP3: 4.889e-27   CXCR4: 6.399e-27
[10] ZEB2: 2.228e-26   CD8A: 1.984e-21    RPL13A: 3.407e-19
[13] BCL6: 6.454e-19   PDCD1: 1.019e-18   CCR5: 4.825e-16
[16] CTLA4: 5.289e-14  TNFRSF1B: 1.037e-13  STAT5B: 3.048e-13
[19] STAT1: 1.459e-12  SOCS3: 1.505e-12   LY6E: 4.751e-12
[22] CCR1: 1.044e-11   TNFRSF1A: 2.022e-11  IL2RA: 2.354e-11
[25] CD44: 1.331e-09   TBX21: 2.097e-09   IRF1: 3.631e-09

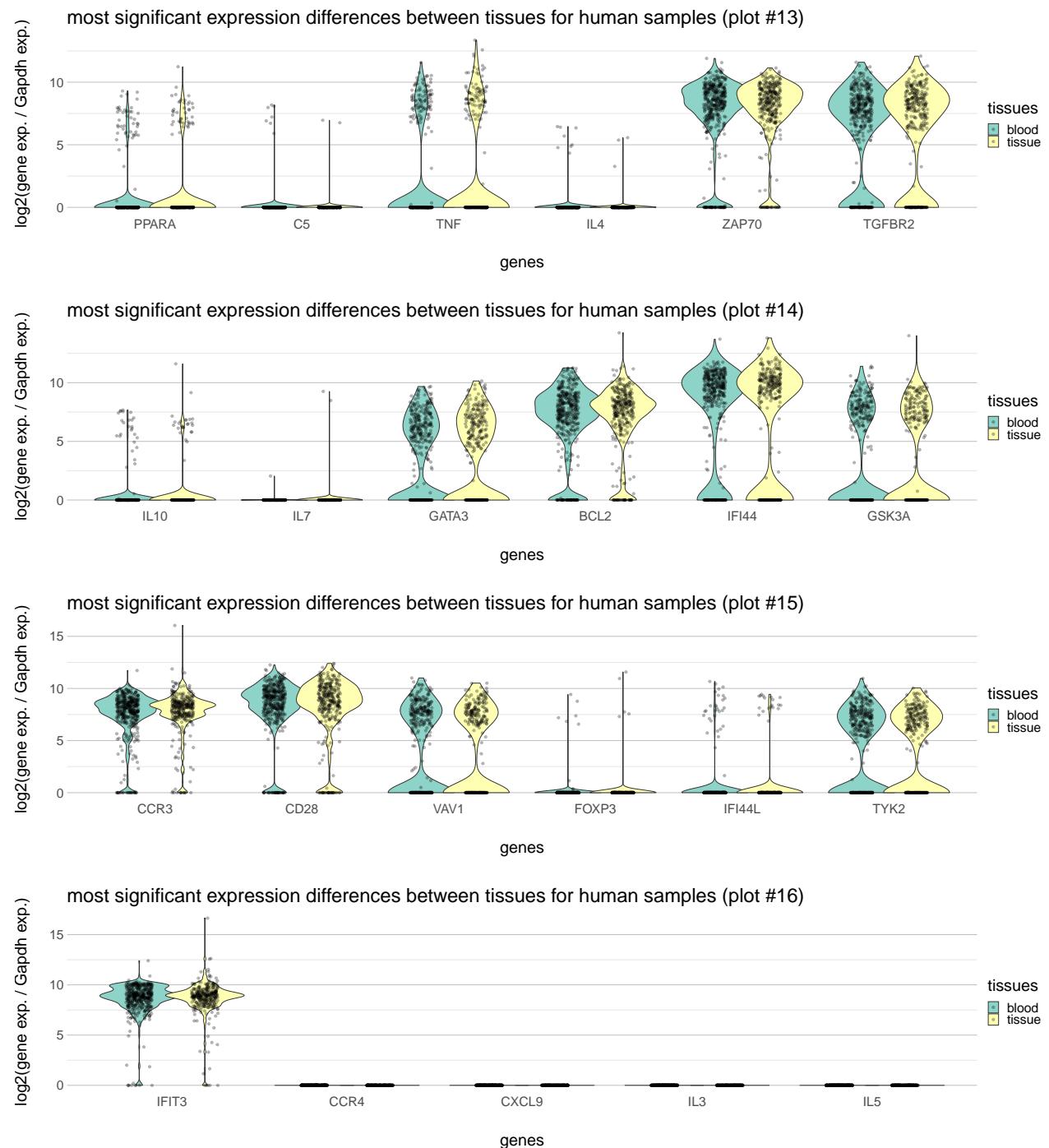
```

[28]	RAC2:	6.236e-09	RORC:	1.236e-08	JAK1:	2.019e-08
[31]	CD3E:	2.648e-08	CD53:	3.304e-08	PTEN:	3.304e-08
[34]	NLRP3:	4.265e-08	IFNAR2:	2.331e-07	STAT3:	2.415e-07
[37]	IFNG:	1.422e-06	IFNGR1:	1.028e-05	FYN:	3.032e-05
[40]	HLA.DRA:	4.561e-05	GAPDH:	0.0001395	ICAM1:	0.0003246
[43]	JAK2:	0.001304	IFIT1:	0.001346	B2M:	0.002136
[46]	CXCL10:	0.002414	IRF7:	0.002621	IRF9:	0.003657
[49]	CD274:	0.007612	IL4R:	0.008887	PPARG:	0.01326
[52]	IL21:	0.01568	CXCR3:	0.01601	CCR7:	0.01665
[55]	C3:	0.03271	CD40:	0.03967	CCR6:	0.04226





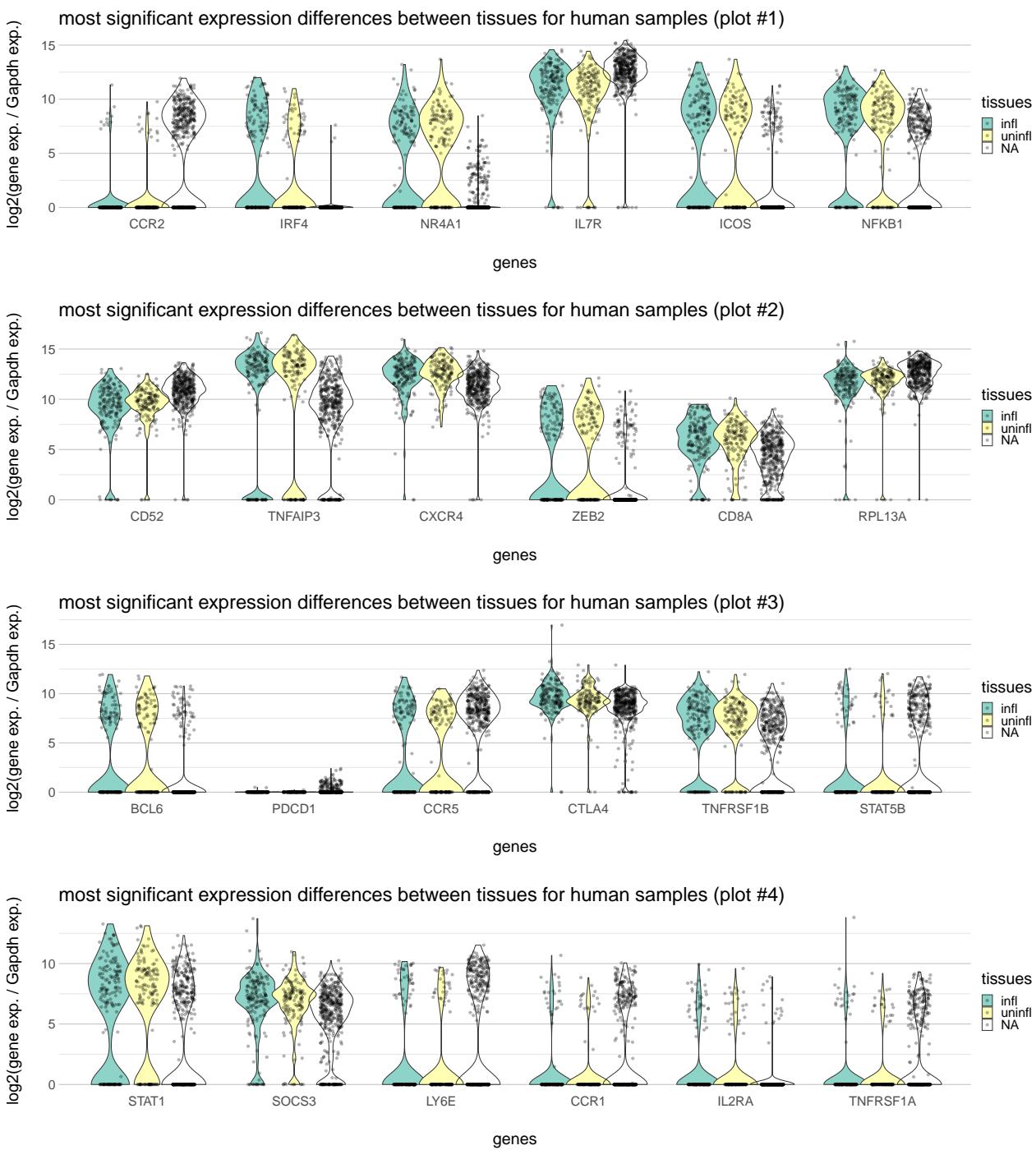


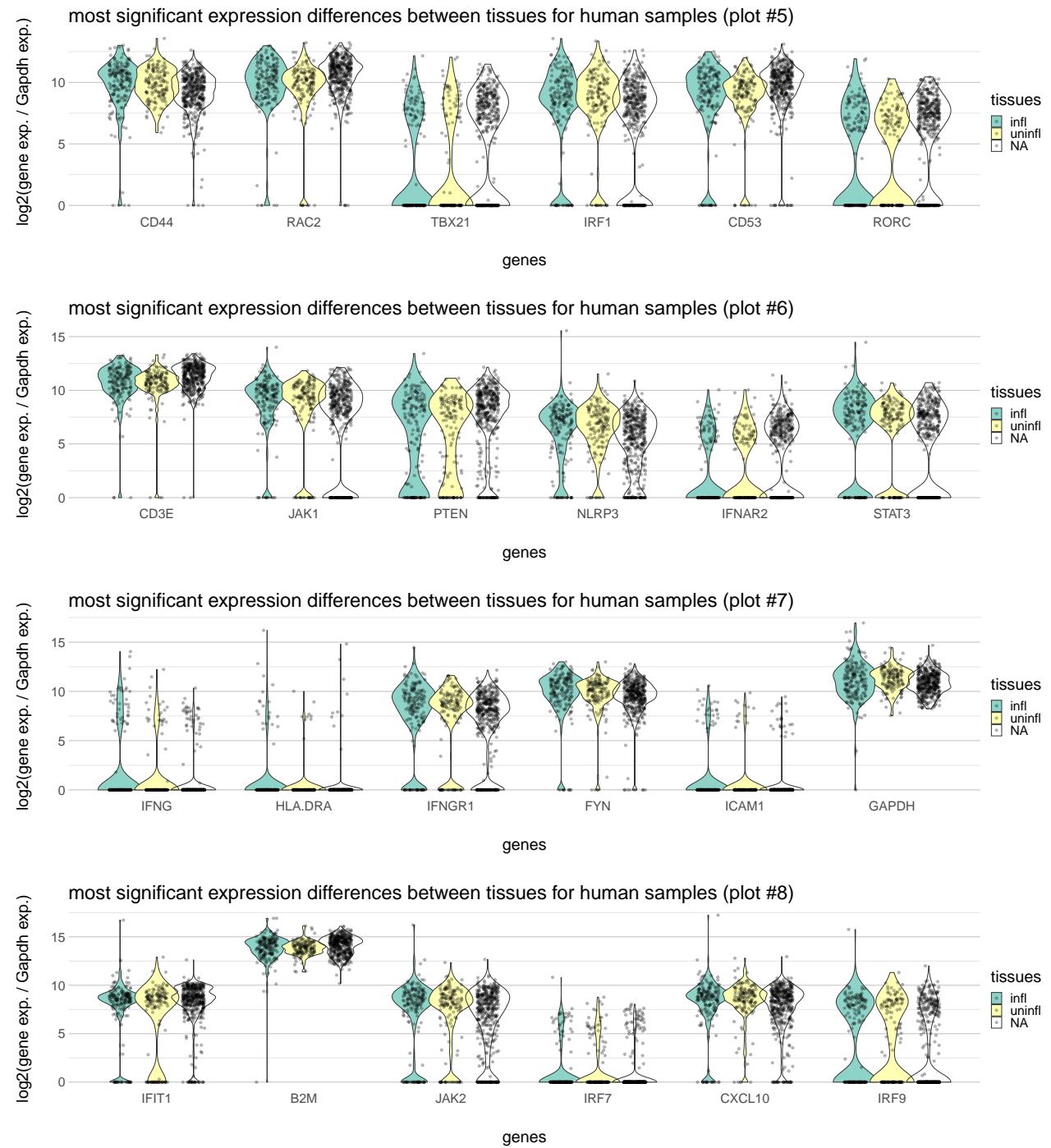


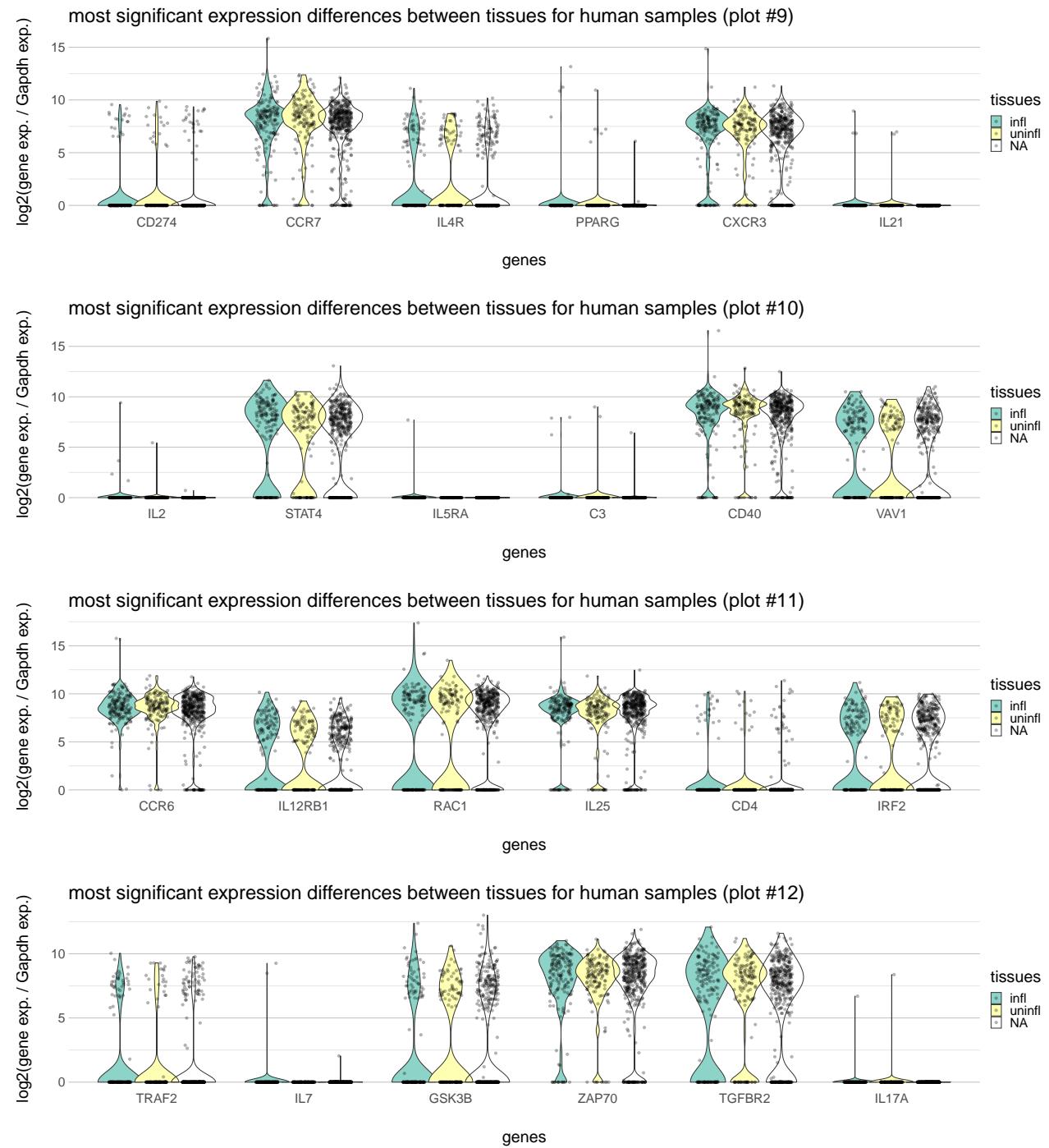
[1] Differentially expressed genes between tissues for human samples:

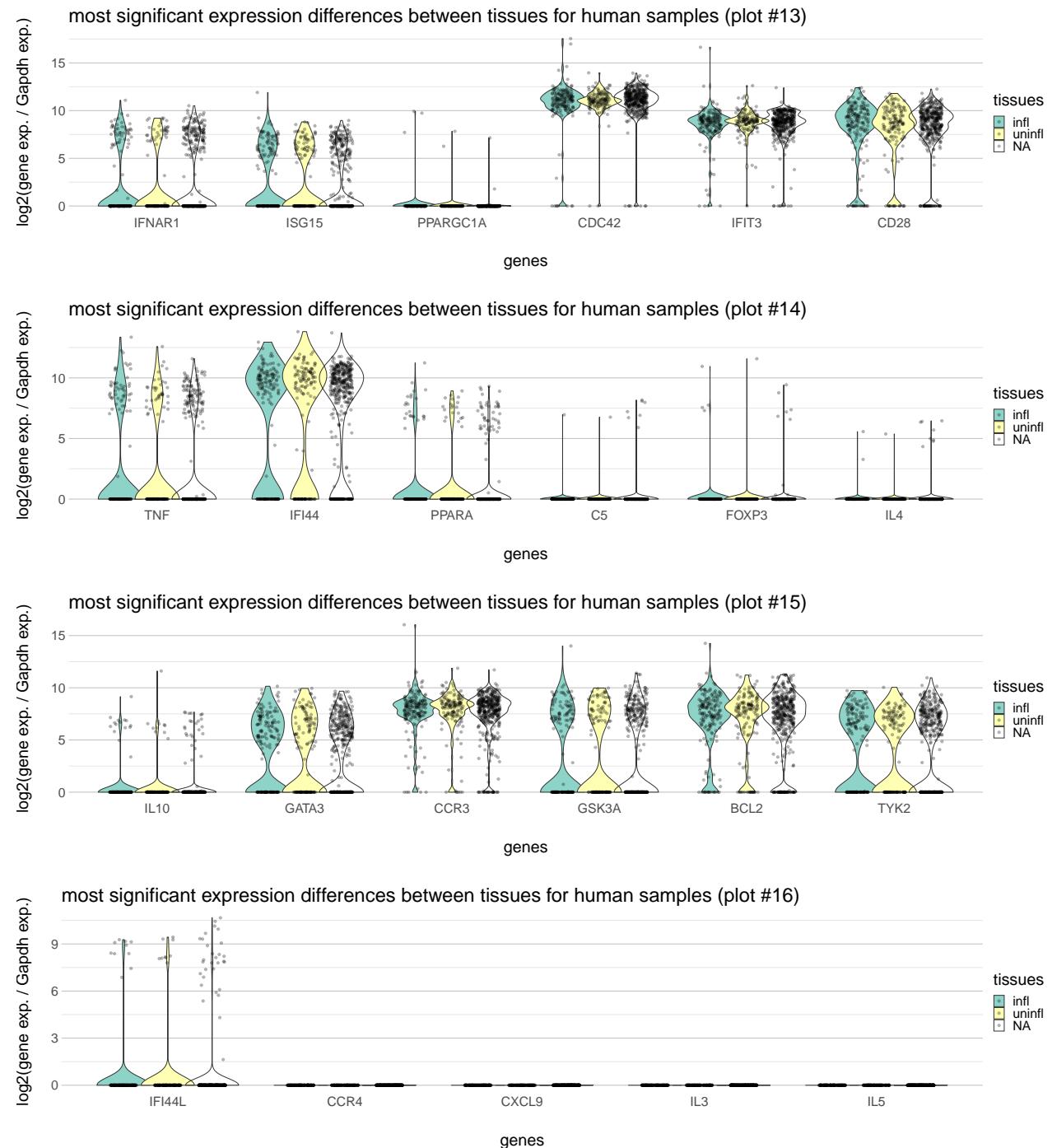
- |                       |                         |                         |
|-----------------------|-------------------------|-------------------------|
| [1] CCR2: 6.864e-49   | [1] IRF4: 7.057e-47     | [1] NR4A1: 8.646e-36    |
| [4] IL7R: 2.398e-33   | [1] ICOS: 4.672e-28     | [1] NFKB1: 6.668e-28    |
| [7] CD52: 5.314e-27   | [1] TNFAIP3: 5.36e-26   | [1] CXCR4: 5.36e-26     |
| [10] ZEB2: 2.472e-25  | [1] CD8A: 2.294e-20     | [1] RPL13A: 1.732e-18   |
| [13] BCL6: 6.456e-18  | [1] PDCD1: 1.168e-17    | [1] CCR5: 4.894e-15     |
| [16] CTLA4: 1.361e-13 | [1] TNFRSF1B: 8.977e-13 | [1] STAT5B: 1.627e-12   |
| [19] STAT1: 6.519e-12 | [1] SOCS3: 1.143e-11    | [1] LY6E: 3.037e-11     |
| [22] CCR1: 8.313e-11  | [1] IL2RA: 1.605e-10    | [1] TNFRSF1A: 1.674e-10 |
| [25] CD44: 4.142e-09  | [1] RAC2: 9.296e-09     | [1] TBX21: 1.586e-08    |

[28]	IRF1: 2.634e-08	CD53: 7.192e-08	RORC: 7.354e-08
[31]	CD3E: 1.016e-07	JAK1: 1.074e-07	PTEN: 1.73e-07
[34]	NLRP3: 2.935e-07	IFNAR2: 1.074e-06	STAT3: 1.186e-06
[37]	IFNG: 2.204e-06	HLA.DRA: 1.921e-05	IFNGR1: 3.567e-05
[40]	FYN: 5.754e-05	ICAM1: 0.0001428	GAPDH: 0.0002261
[43]	IFIT1: 0.002587	B2M: 0.003168	JAK2: 0.005725
[46]	IRF7: 0.005822	CXCL10: 0.006832	IRF9: 0.01425
[49]	CD274: 0.02432	CCR7: 0.02916	IL4R: 0.03346
[52]	PPARG: 0.03348		









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[1] Differentially expressed genes between phenotypes for human samples:
[1] PDCD1: 9.322e-22   JAK1: 4.533e-17   CCR2: 4.286e-16
[4] IL7R: 1.322e-14    STAT1: 1.792e-12   RPL13A: 4.021e-12
[7] IRF4: 4.756e-12    ICOS: 4.994e-12   CD52: 3.058e-10
[10] CCR1: 5.473e-09   NLRP3: 2.314e-07   NFKB1: 1.345e-06
[13] ZEB2: 2.577e-06   CCR5: 3.124e-06   NR4A1: 4.551e-06
[16] CD8A: 5.726e-06   CD53: 9.705e-06   BCL6: 2.134e-05
[19] IFIT1: 3.092e-05   SOCS3: 3.654e-05   CD3E: 3.979e-05
[22] GSK3A: 6.37e-05   IFNAR2: 0.0001017  STAT5B: 0.0006666
[25] TNFRSF1B: 0.000693 B2M: 0.0007045  CTLA4: 0.0007111
```

[28]	RAC1: 0.0007111	IL12RB1: 0.003017	PTEN: 0.003672
[31]	RAC2: 0.0037	STAT3: 0.0037	STAT4: 0.004436
[34]	CDC42: 0.004871	IL2RA: 0.005232	TBX21: 0.005984
[37]	RORC: 0.0134	CXCR3: 0.01379	LY6E: 0.01433
[40]	GATA3: 0.01464	PPARA: 0.01464	CCR3: 0.01662
[43]	IFIT3: 0.01693	IL25: 0.0411	ICAM1: 0.04251

