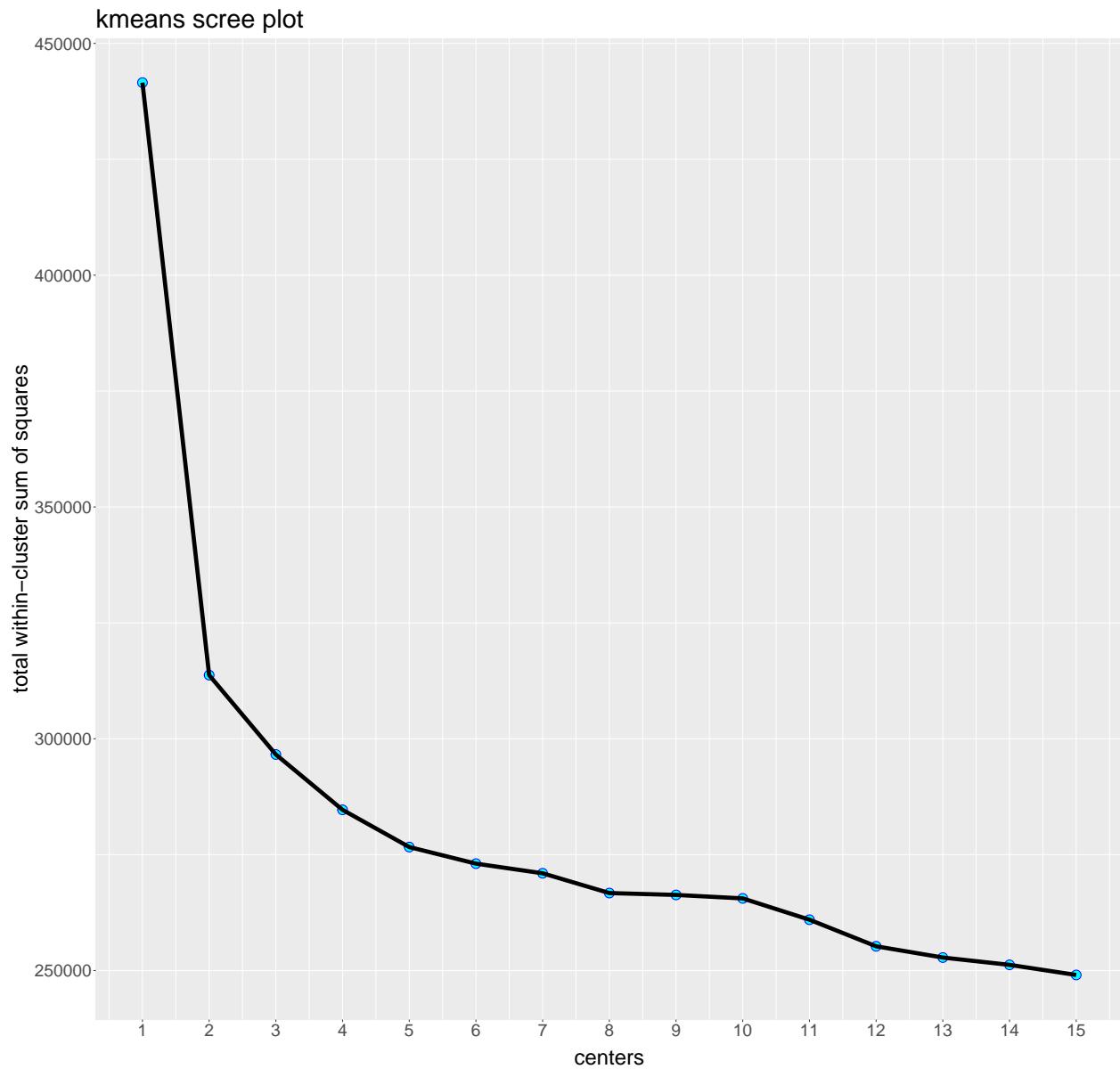
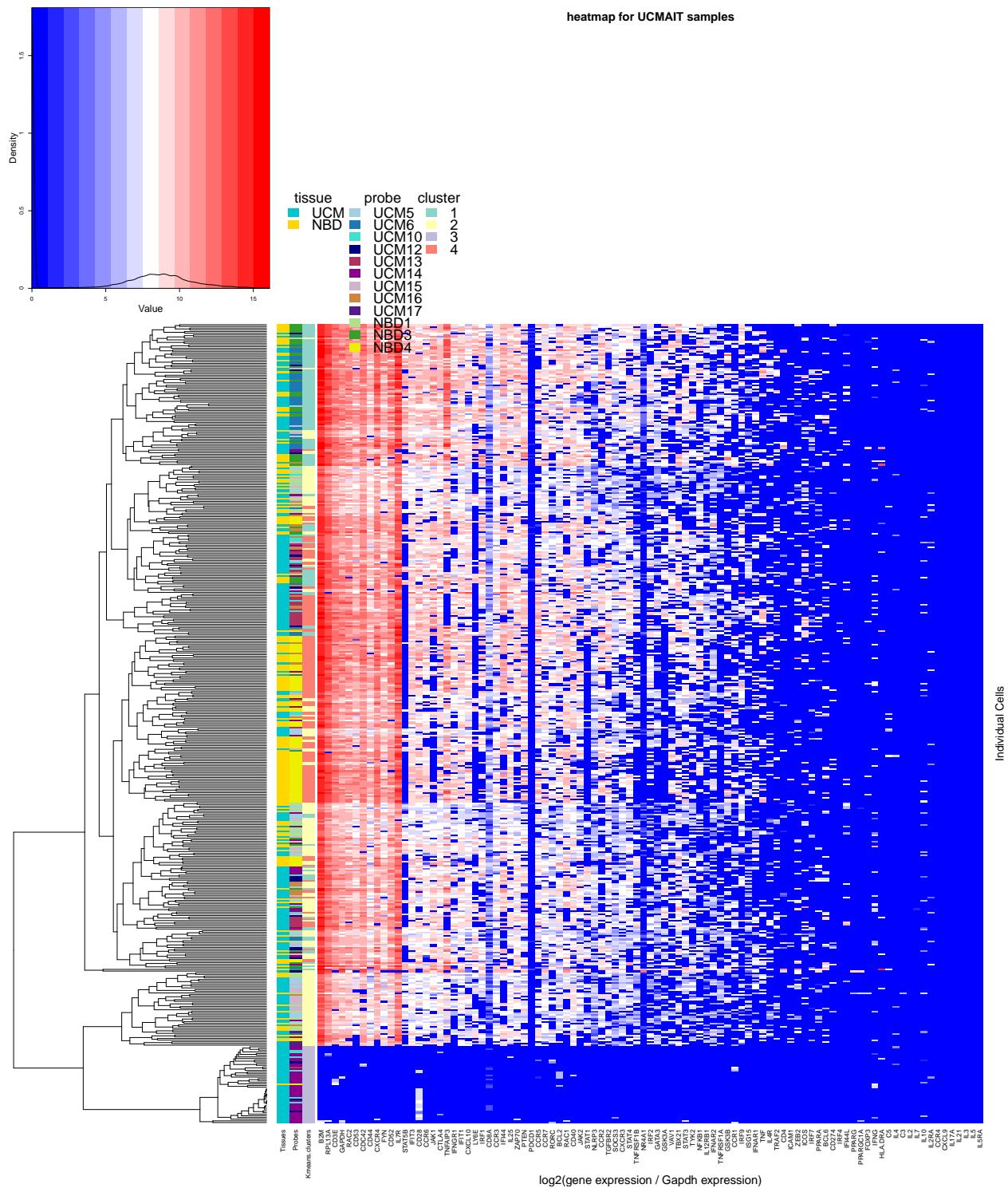


# UC-MAIT analysis (blood only)

No expression detected in 22/497 cells





	0	2	10	4	23
	probe_UCM14	probe_UCM15	probe_UCM16	probe_UCM17	probe_NBD1
cluster_1	6	1	6	0	1
cluster_2	19	28	11	5	46
cluster_3	35	0	0	0	0
cluster_4	5	1	13	0	1
	probe_NBD3	probe_NBD4			
cluster_1	43	0			
cluster_2	5	12			
cluster_3	0	1			
cluster_4	0	82			

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

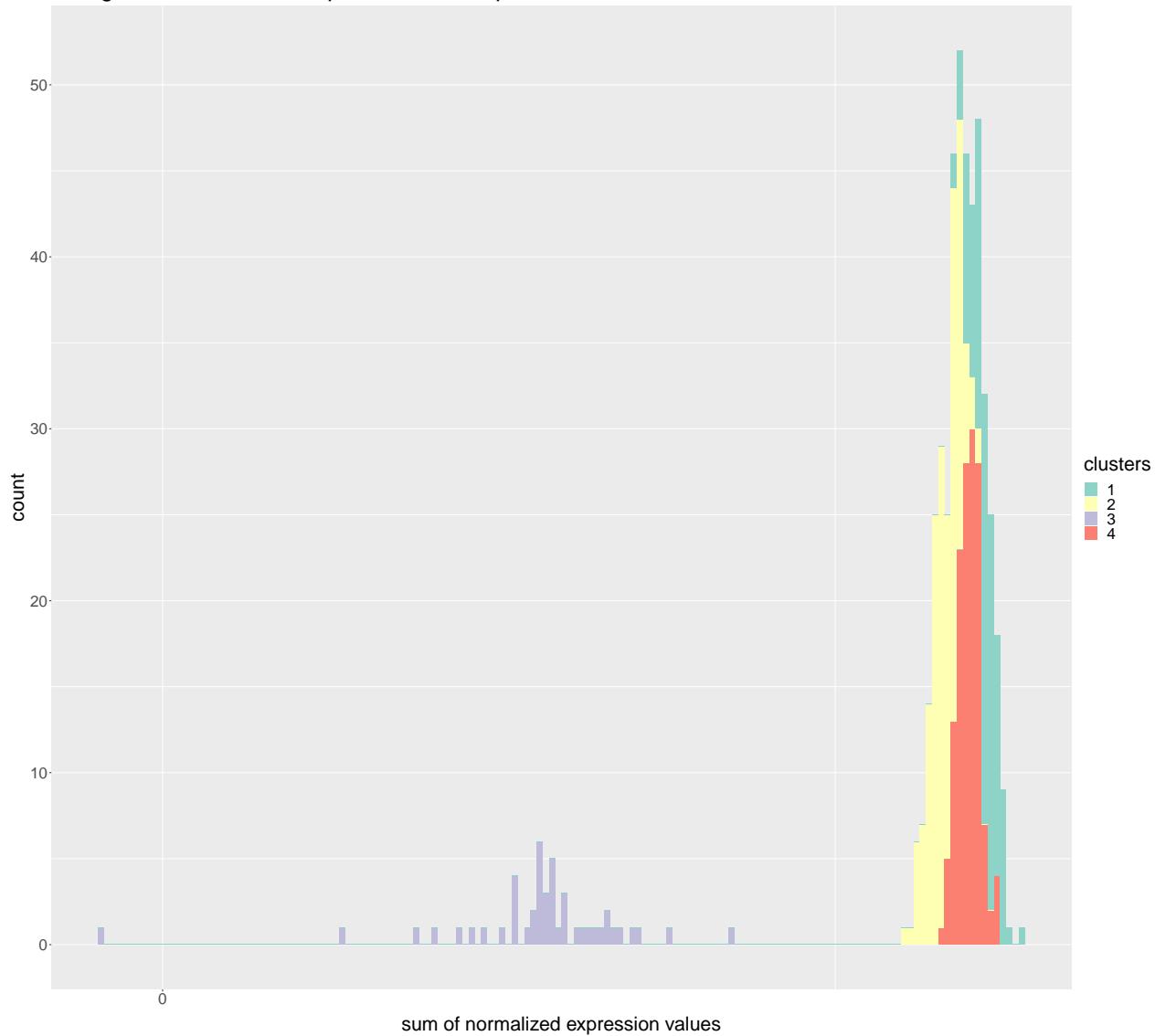
```
data: probeTable
X-squared = 730.51, df = NA, p-value = 0.0004998
```

```
[1]
[1]
[1] Tissue vs. Cluster
      cellSource_UCM cellSource_NBD
cluster_1        74        44
cluster_2       107        63
cluster_3        45        1
cluster_4        58       83
```

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

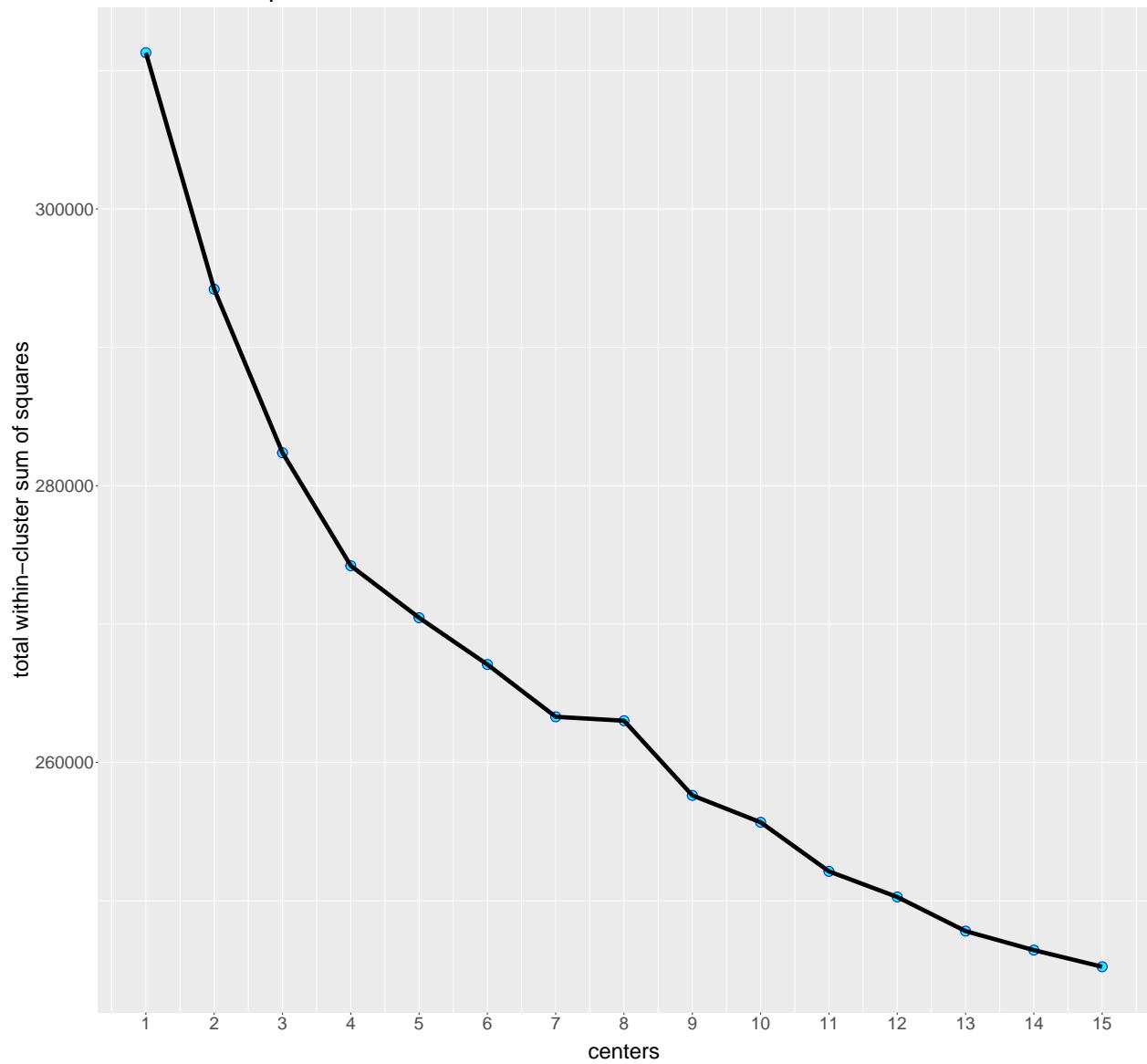
```
data: sourceTable
X-squared = 49.213, df = NA, p-value = 0.0004998
```

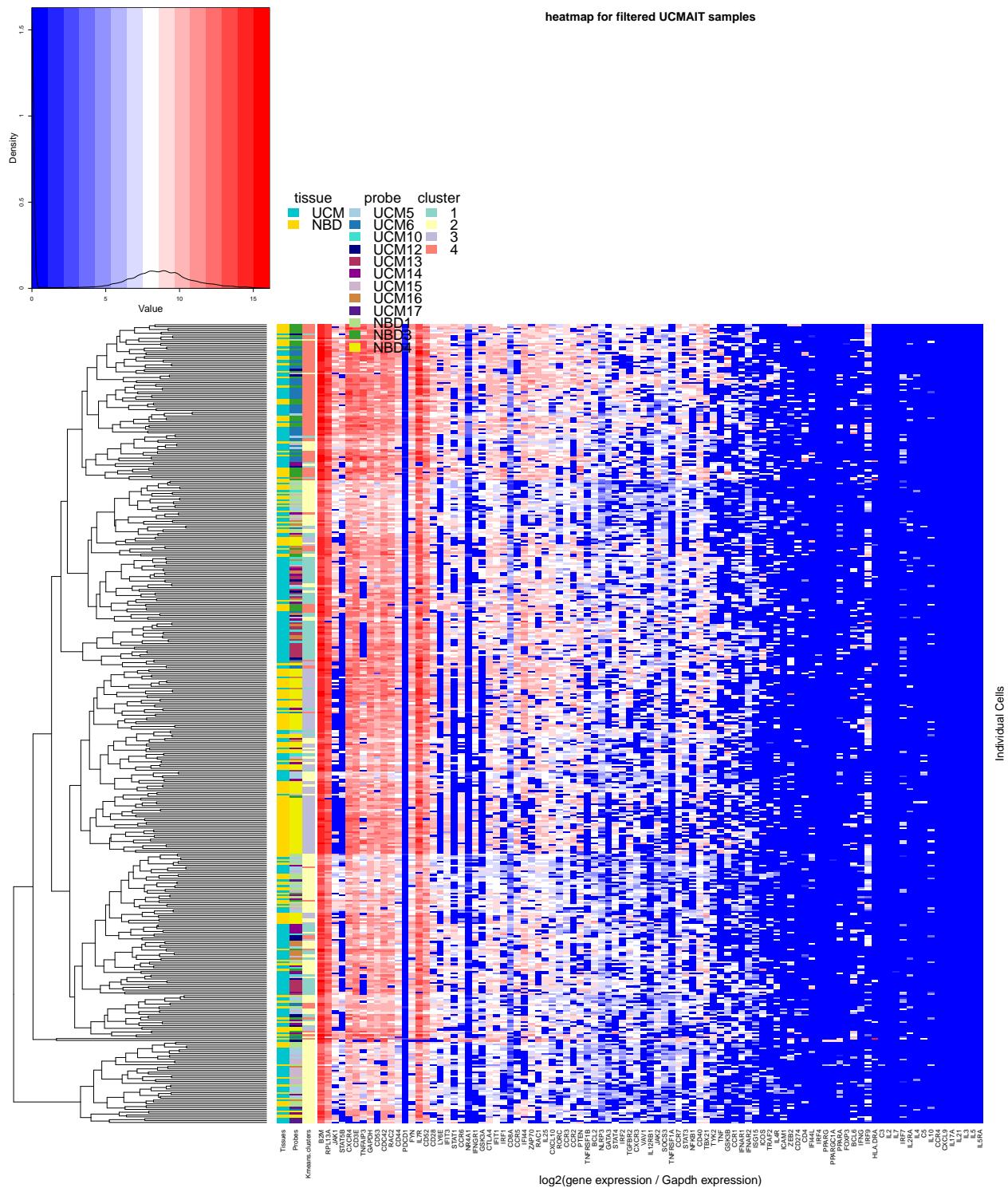
histogram of cumulative expression values per cell



46 / 475 cells were removed due to low gene expression (cluster ID of removed clusters: 3)

kmeans scree plot





[1]

[1]

[1] Probe vs. Cluster

	probe_UCM5	probe_UCM6	probe_UCM10	probe_UCM12	probe_UCM13
cluster_1	1	0	13	9	29
cluster_2	32	4	2	2	1
cluster_3	0	1	0	1	0

cluster_4	2	43	0	4	0
	probe_UCM14	probe_UCM15	probe_UCM16	probe_UCM17	probe_NBD1
cluster_1	12	1	15	0	2
cluster_2	17	28	9	5	45
cluster_3	0	1	4	0	0
cluster_4	1	0	2	0	1
	probe_NBD3	probe_NBD4			
cluster_1	0	1			
cluster_2	4	10			
cluster_3	1	83			
cluster_4	43	0			

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

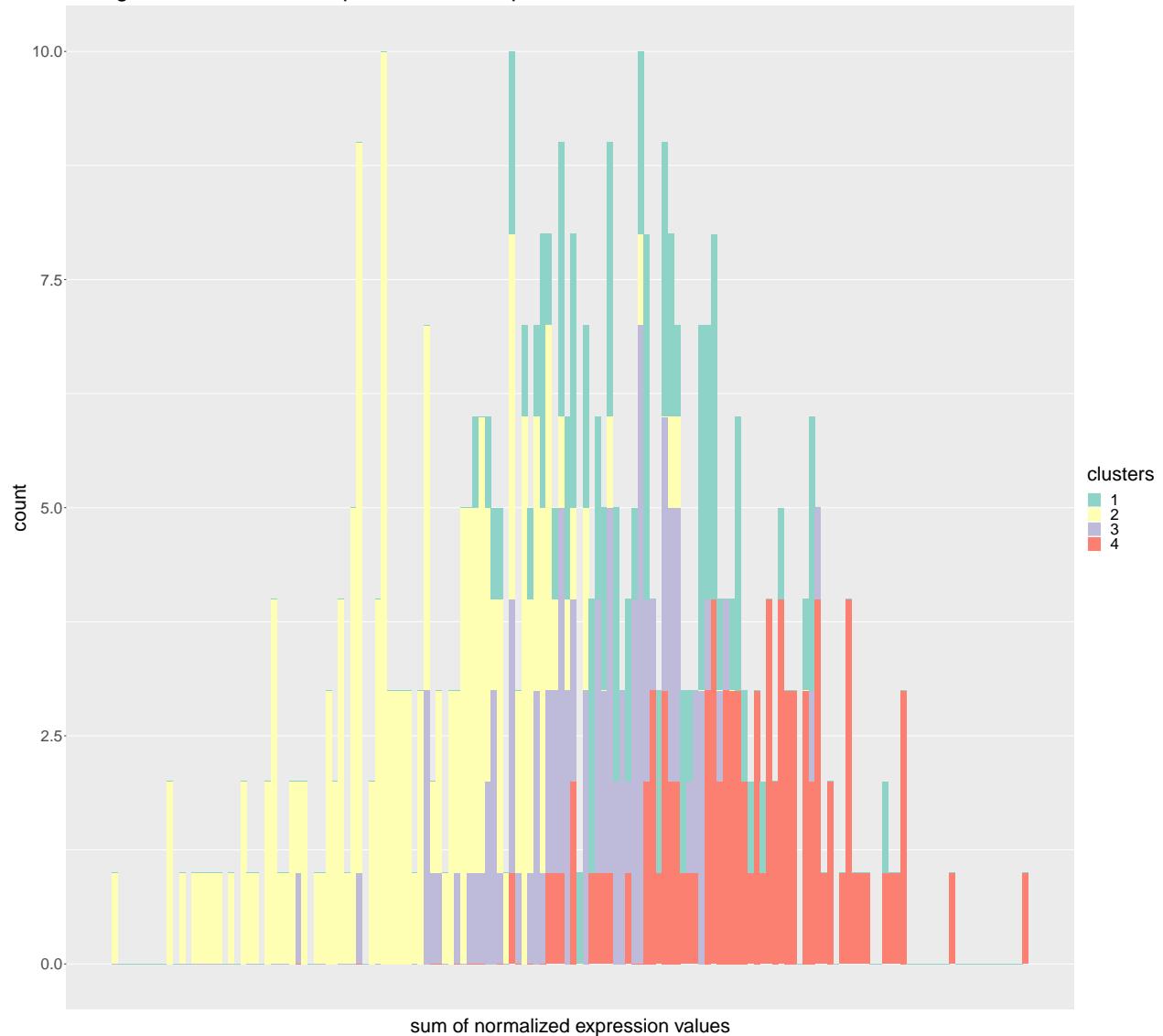
```
data: probeTable
X-squared = 879.63, df = NA, p-value = 0.0004998
```

```
[1]
[1]
[1] Tissue vs. Cluster
      cellSource_UCM cellSource_NBD
cluster_1          80            3
cluster_2         100           59
cluster_3           7           84
cluster_4          52           44
```

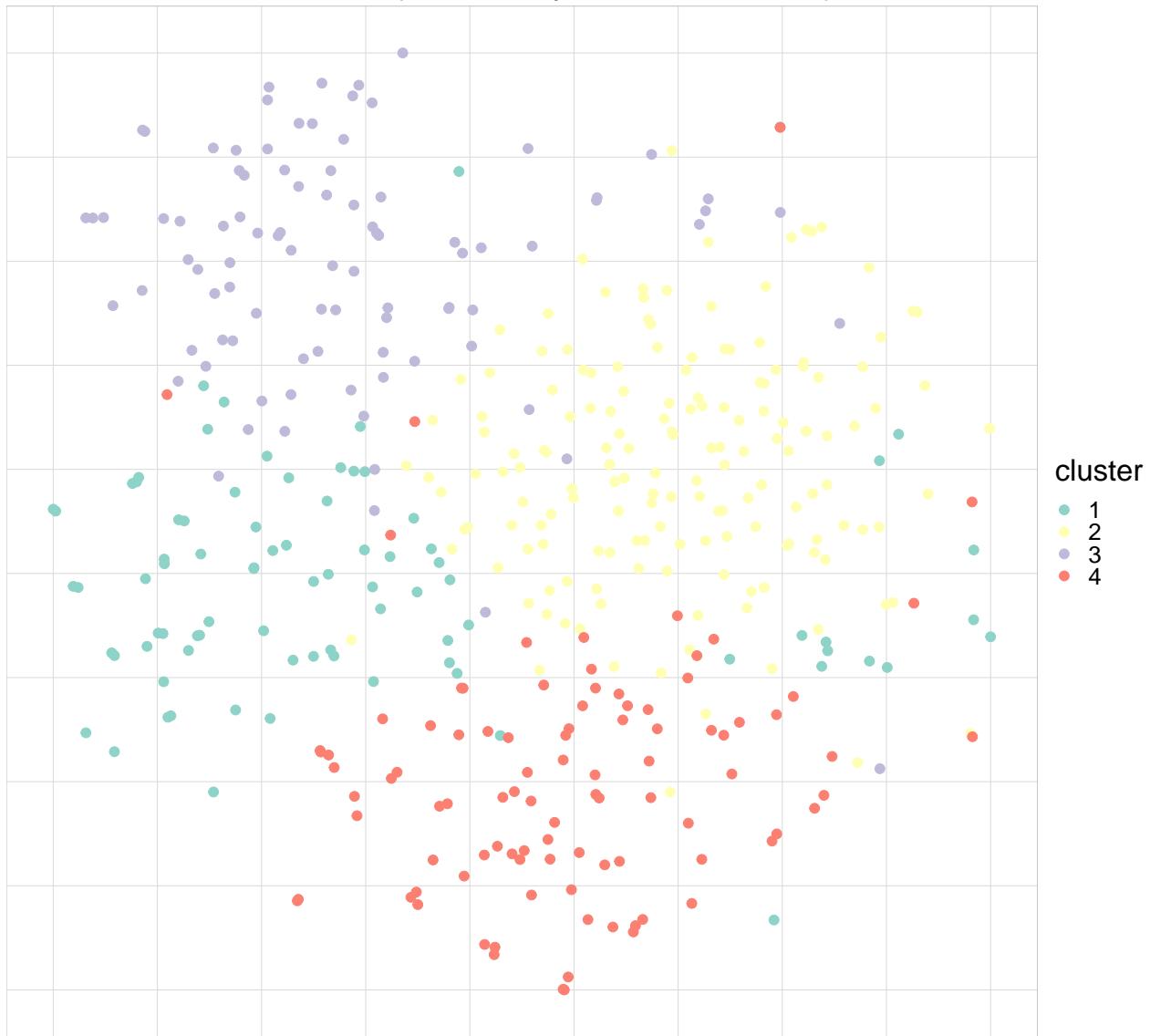
Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

```
data: sourceTable
X-squared = 144.11, df = NA, p-value = 0.0004998
```

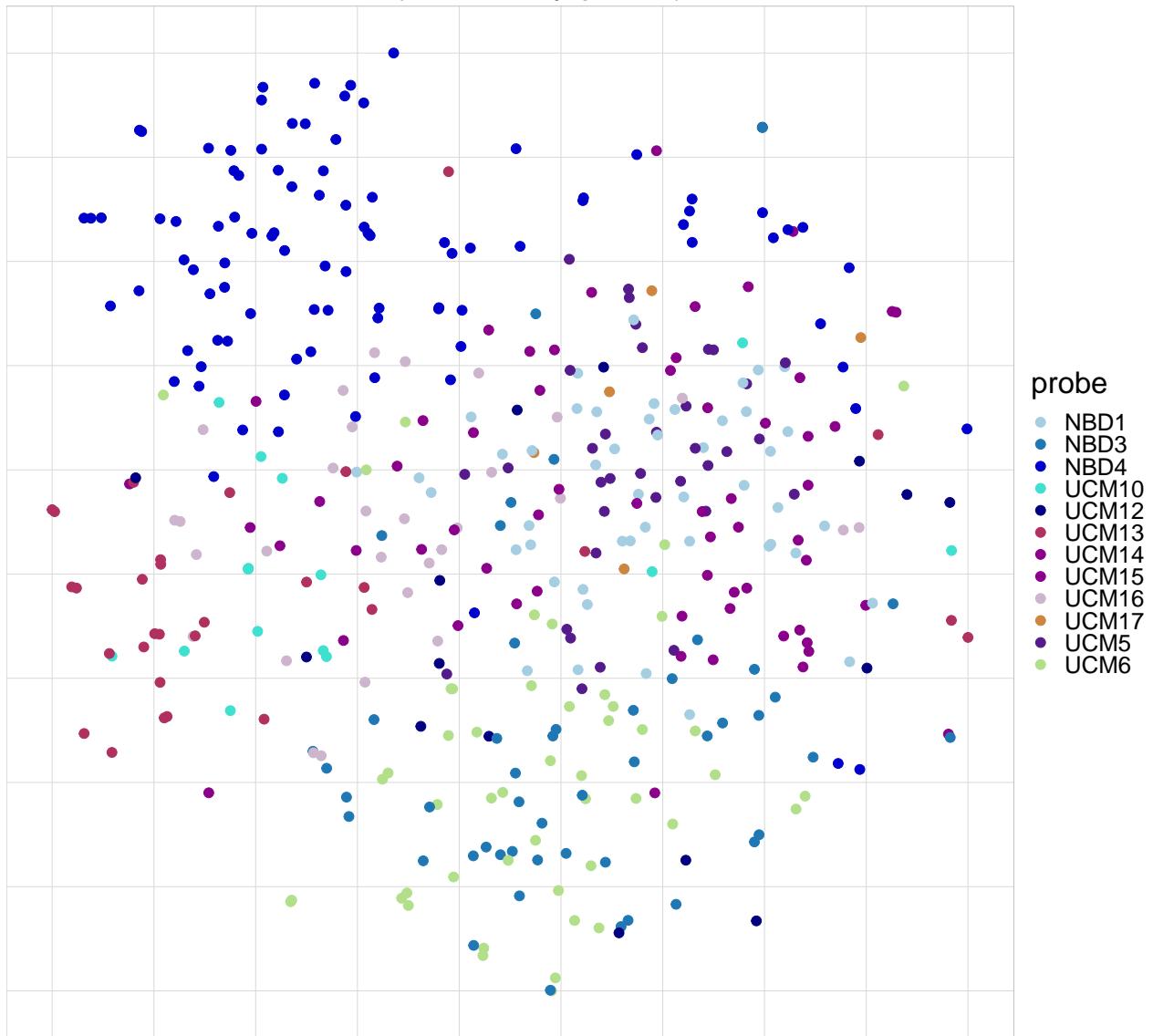
histogram of cumulative expression values per cell



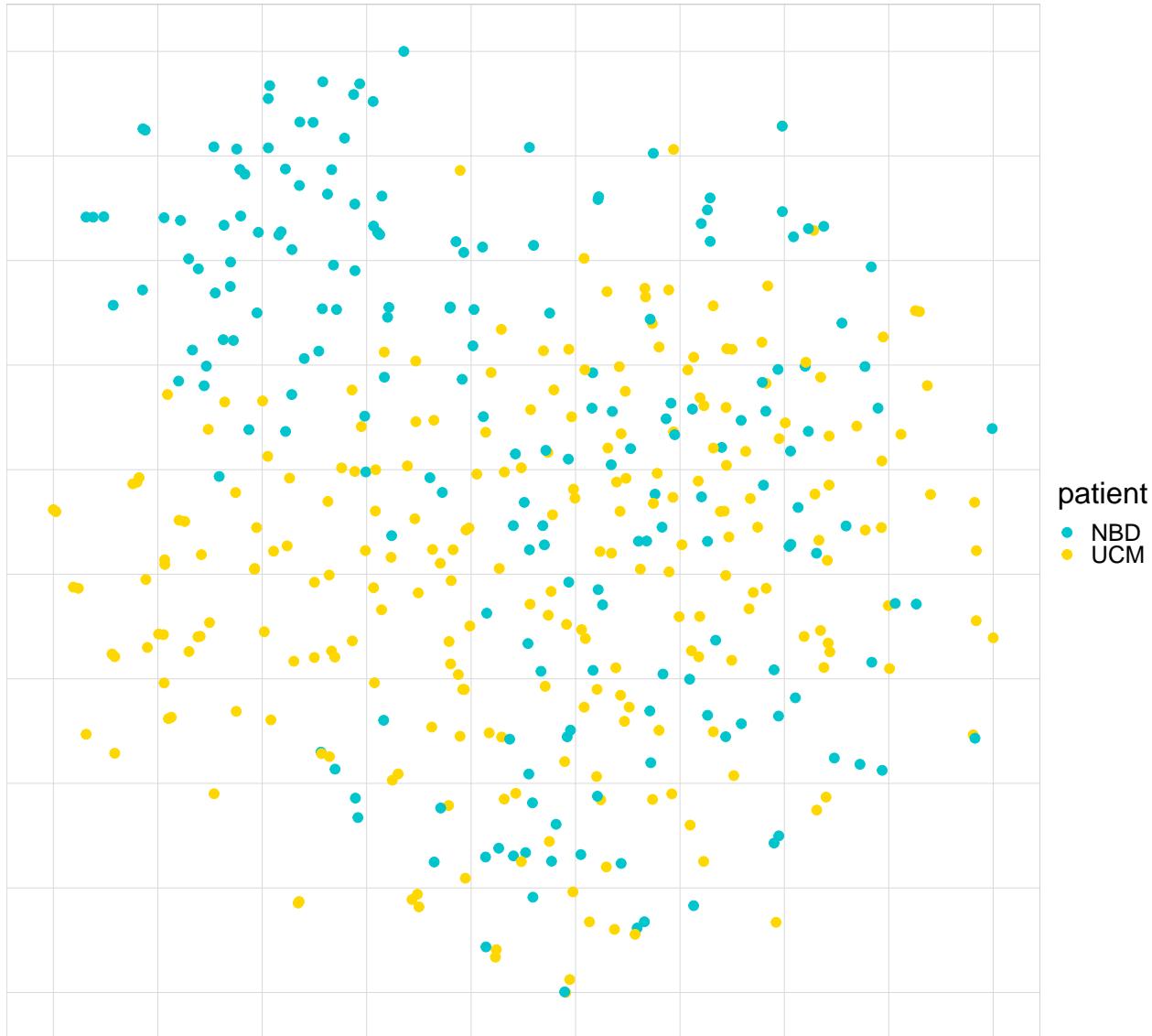
t-SNE between tissues (colored by kmeans.cluster)



t-SNE between tissues (colored by probe)



## t-SNE colored by patient

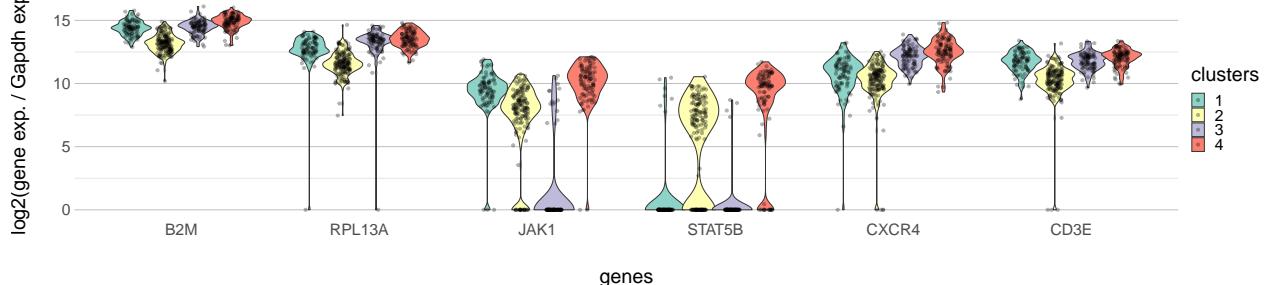


[1] Differentially expressed genes between clusters for human samples:

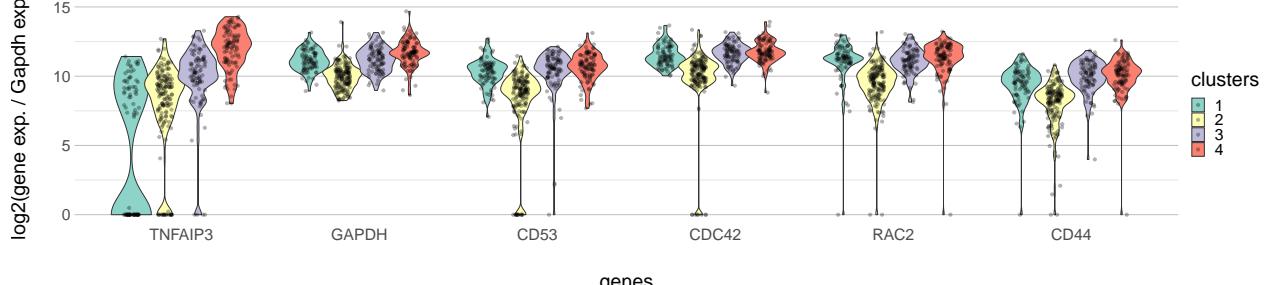
[1]	B2M: 6.95e-51	RPL13A: 5.2e-50	JAK1: 4.722e-48
[4]	STAT5B: 3.694e-44	CXCR4: 7.461e-44	CD3E: 2.41e-42
[7]	TNFAIP3: 1.542e-40	GAPDH: 3.316e-37	CD53: 3.597e-36
[10]	CDC42: 3.888e-36	RAC2: 1.452e-35	CD44: 1.959e-34
[13]	PDCD1: 1.058e-33	FYN: 4.043e-32	IL7R: 6.278e-31
[16]	CD52: 2.791e-29	CD28: 1.127e-27	LY6E: 3.368e-26
[19]	IFIT3: 2.306e-25	STAT1: 1.395e-24	CCR6: 1.683e-23
[22]	NR4A1: 2.411e-22	IFNGR1: 4.267e-22	GSK3A: 1.015e-20
[25]	CTLA4: 1.093e-20	IFIT1: 6.911e-20	IRF1: 1.133e-18
[28]	CD8A: 2.005e-18	CCR5: 8.908e-18	IFI44: 2.838e-17
[31]	ZAP70: 4.816e-16	RAC1: 5.556e-16	IL25: 9.729e-16
[34]	CXCL10: 2.912e-15	RORC: 1.707e-14	CCR3: 1.018e-13
[37]	CCR2: 1.373e-13	PTEN: 7.788e-13	TNFRSF1B: 7.788e-13
[40]	BCL2: 1.122e-12	NLRP3: 1.342e-12	GATA3: 1.93e-11
[43]	STAT4: 1.952e-10	IRF2: 3.113e-10	TGFBR2: 8.393e-10

[46]	CXCR3:	5.578e-09	VAV1:	1.084e-08	IL12RB1:	3.908e-08
[49]	JAK2:	4.193e-08	SOCS3:	4.193e-08	TNFRSF1A:	1.164e-07
[52]	CCR7:	1.59e-07	STAT3:	2.525e-07	NFKB1:	1.192e-06
[55]	CD40:	2.666e-06	TBX21:	1.053e-05	TYK2:	1.215e-05
[58]	TNF:	0.0007985	GSK3B:	0.001491	CCR1:	0.002194
[61]	IFNAR1:	0.003302	IFNAR2:	0.005243	ISG15:	0.01308
[64]	ICOS:	0.01634	TRAF2:	0.03186	IL4R:	0.04279

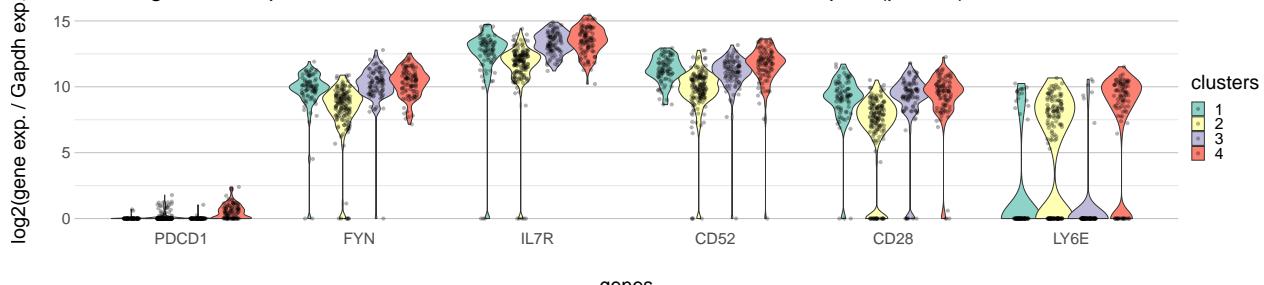
most significant expression differences between clusters for human samples (plot #1)



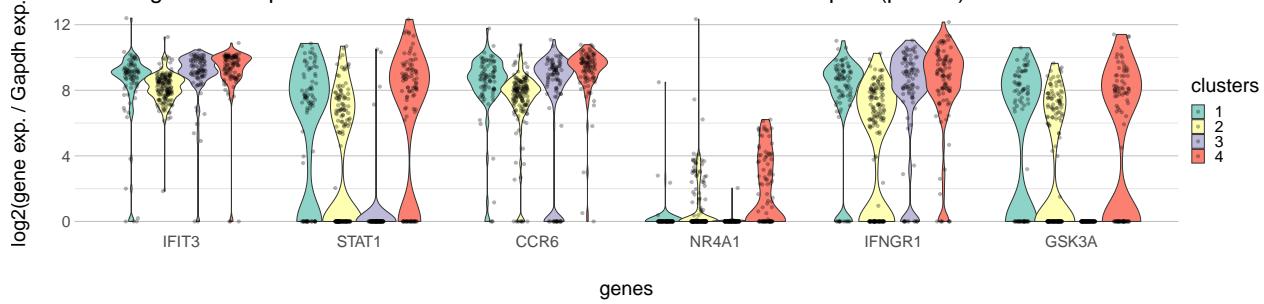
most significant expression differences between clusters for human samples (plot #2)

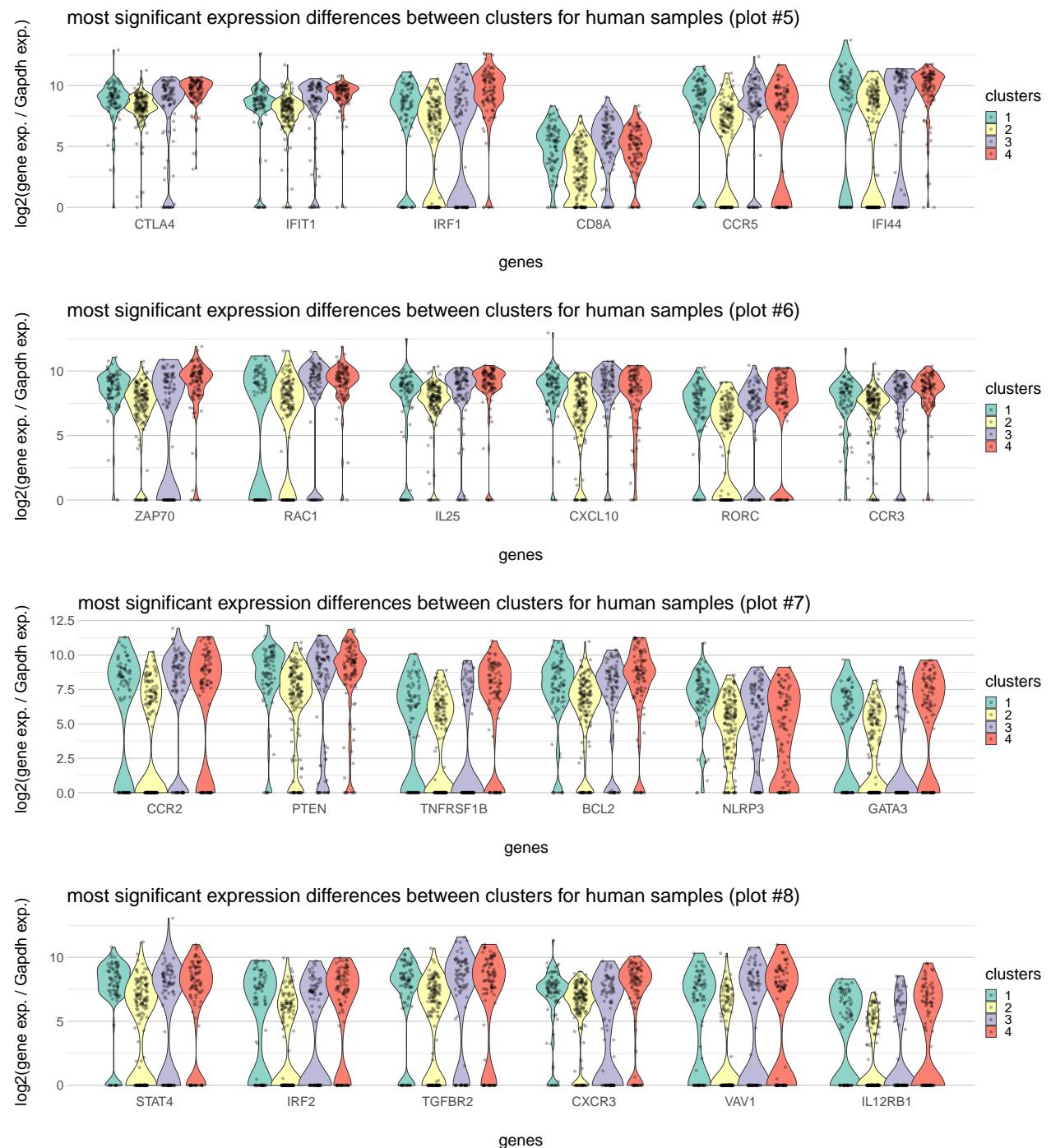


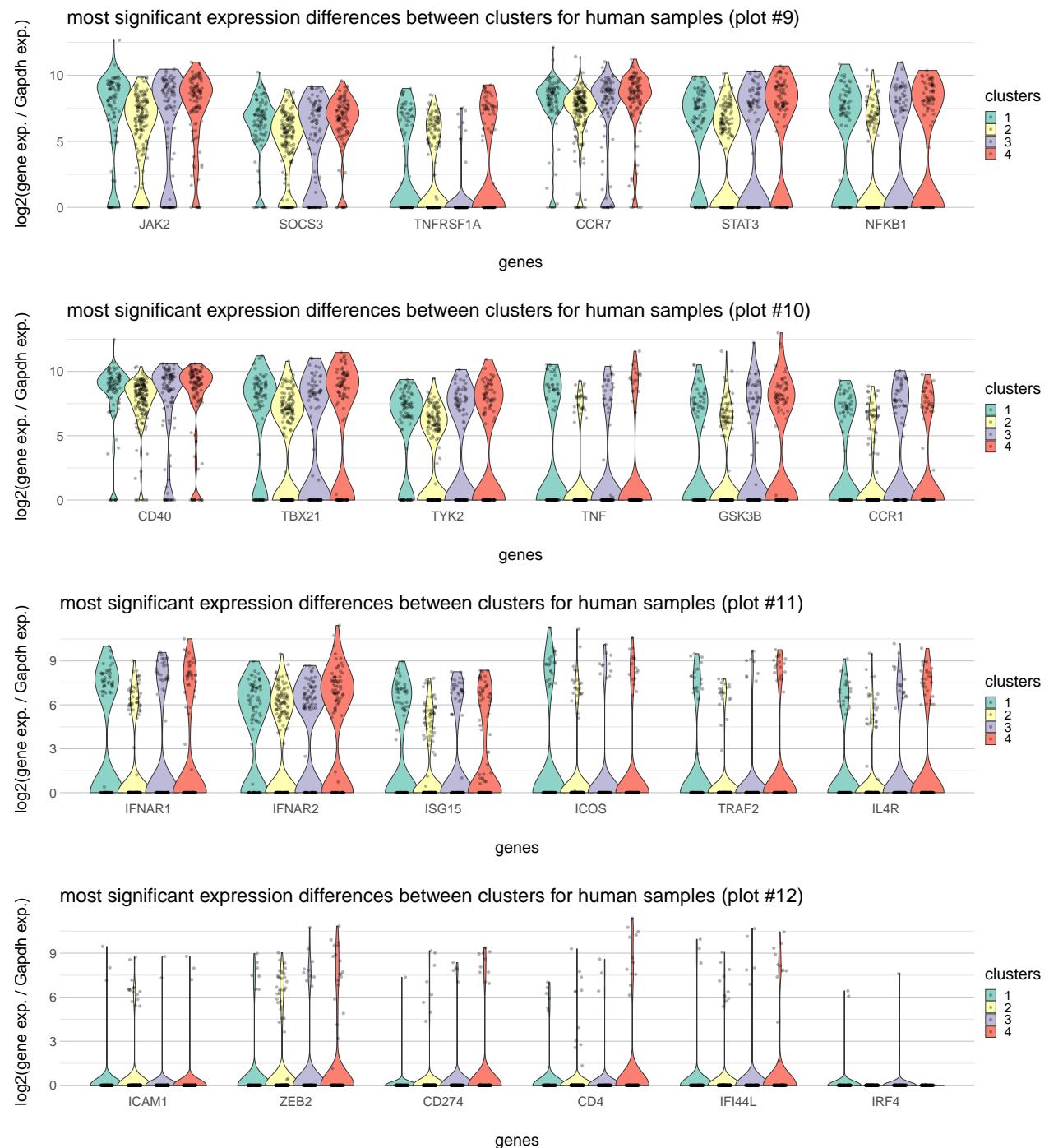
most significant expression differences between clusters for human samples (plot #3)

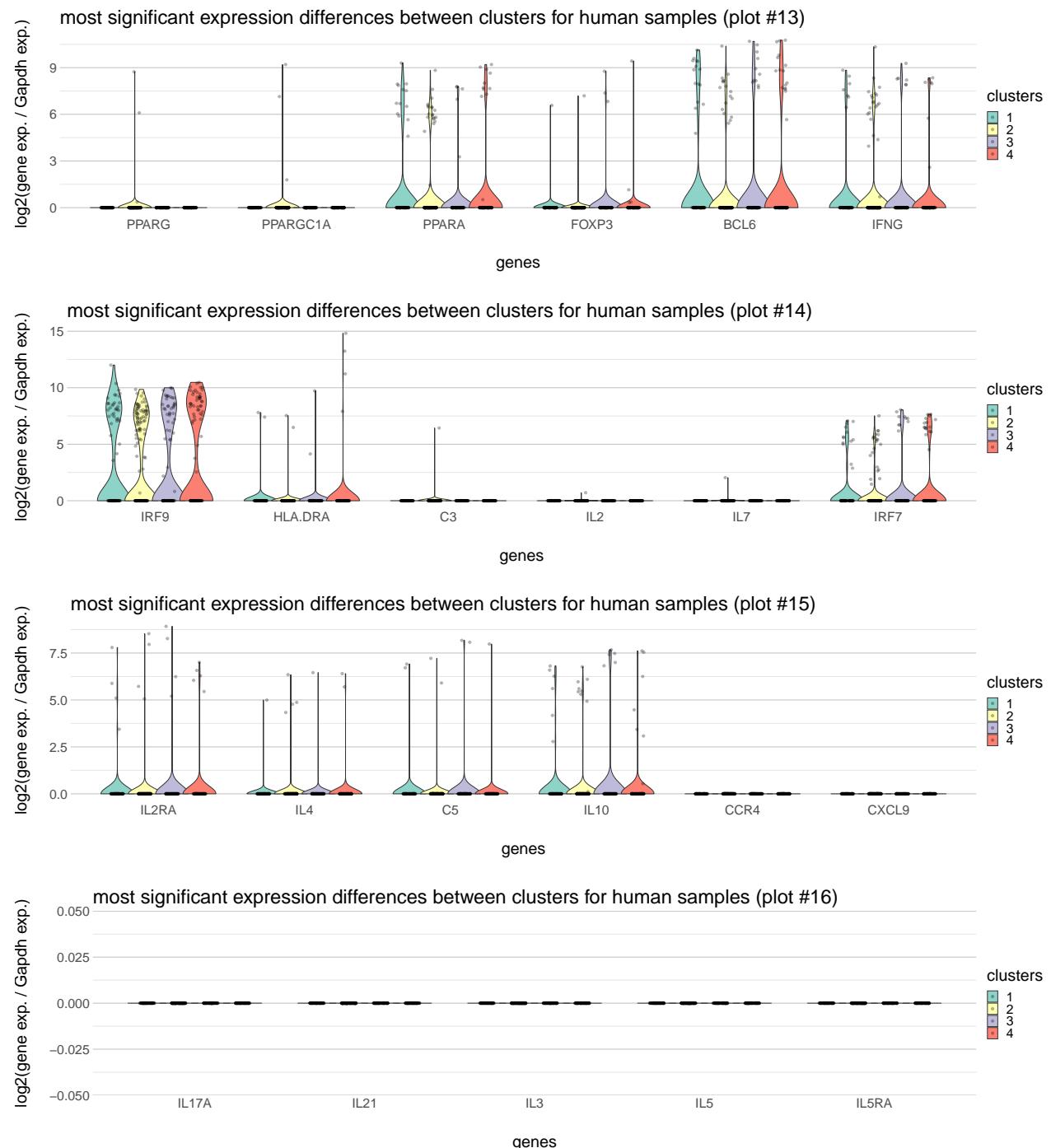


most significant expression differences between clusters for human samples (plot #4)





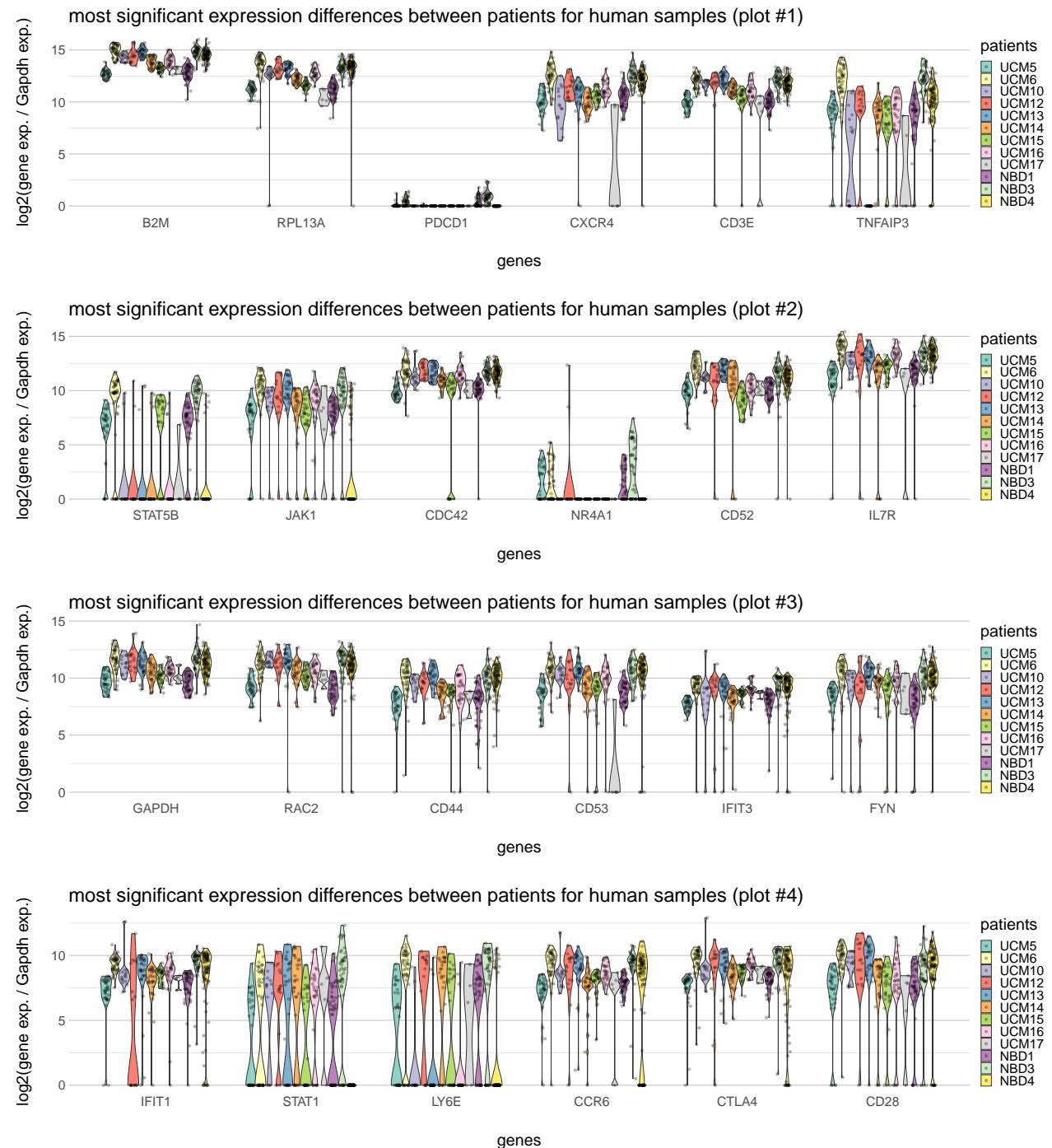


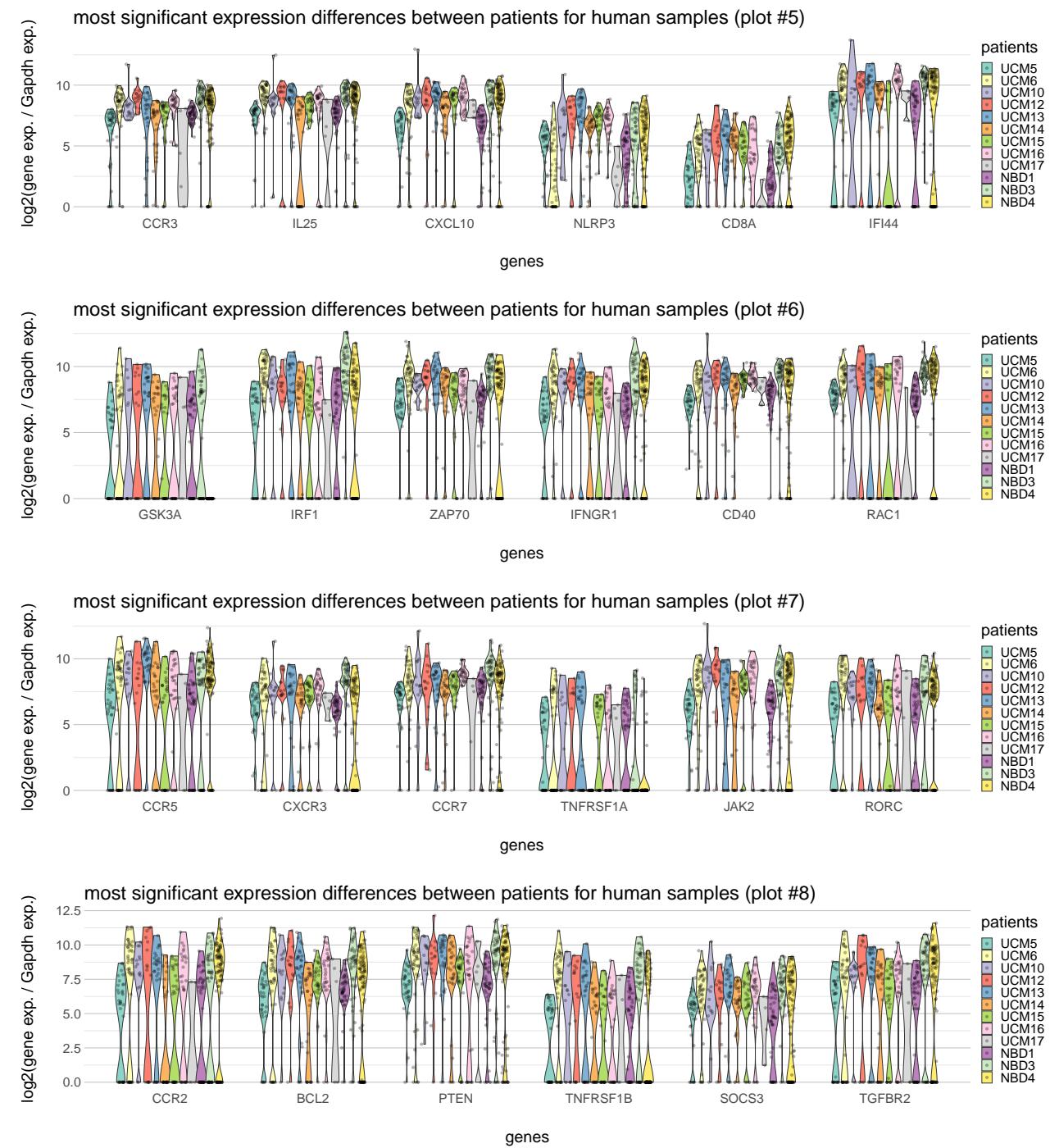


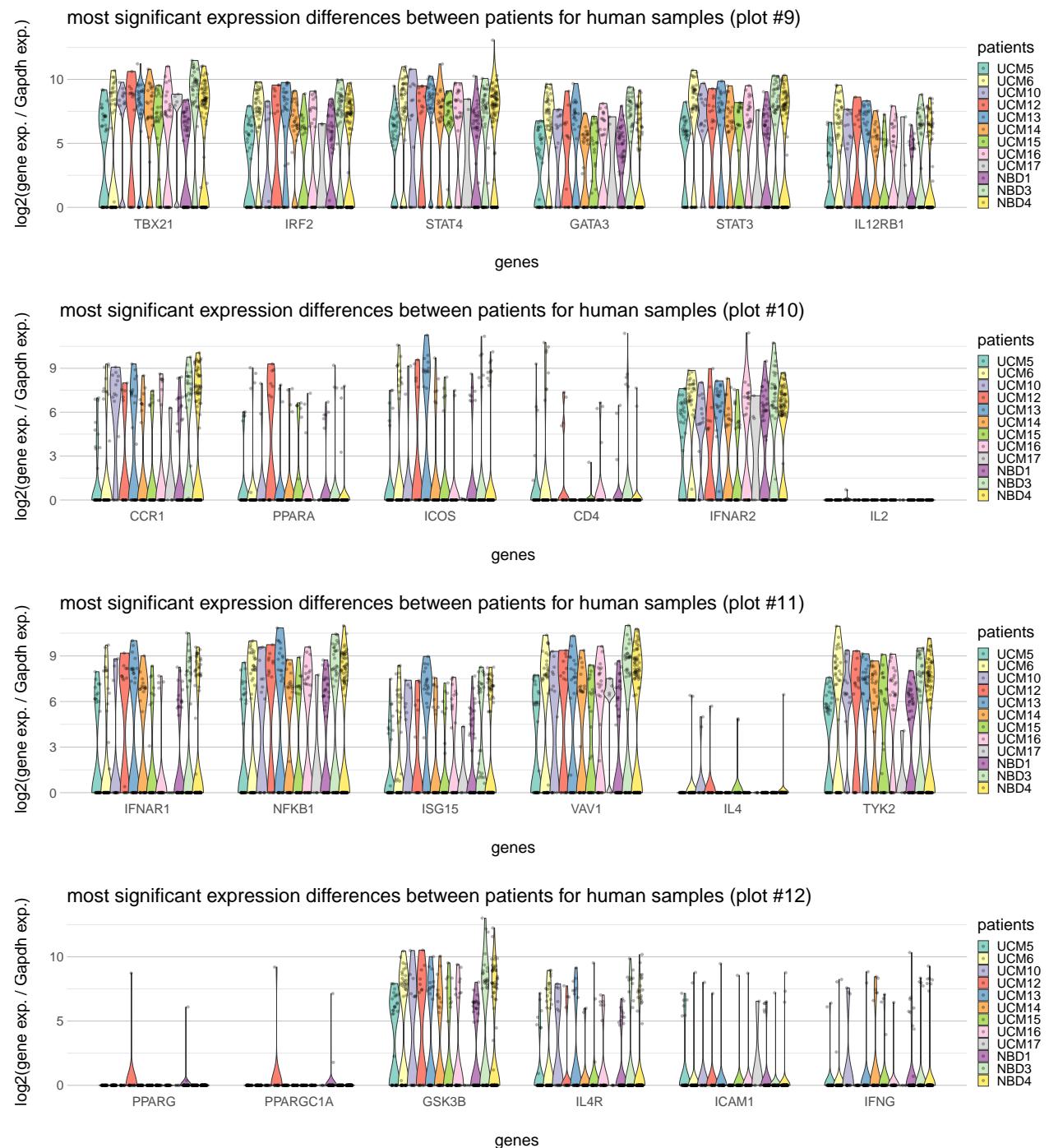
[1] Differentially expressed genes between patients for human samples:

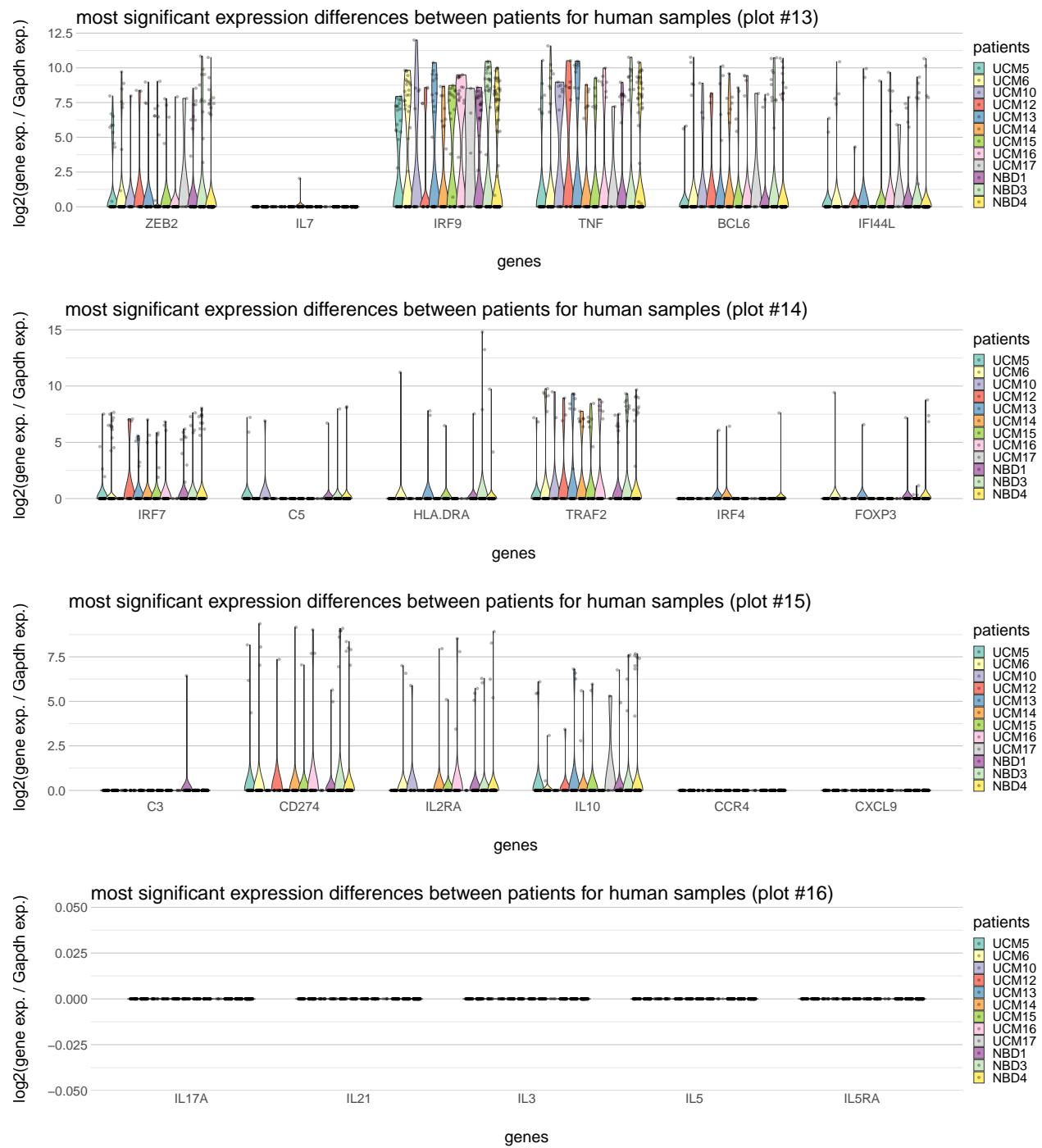
[1] B2M: 1.945e-53	RPL13A: 1.532e-51	PDCD1: 1.63e-47
[4] CXCR4: 3.595e-45	CD3E: 1.212e-44	TNFAIP3: 7.734e-44
[7] STAT5B: 1.298e-41	JAK1: 3.816e-38	CDC42: 7.141e-38
[10] NR4A1: 6.515e-36	CD52: 8.854e-36	IL7R: 3.265e-35
[13] GAPDH: 1.086e-33	RAC2: 1.125e-33	CD44: 5.845e-32
[16] CD53: 1.694e-30	IFIT3: 4.742e-29	FYN: 5.213e-29
[19] IFIT1: 2.19e-27	STAT1: 3.563e-25	LY6E: 2.144e-24
[22] CCR6: 9.751e-24	CTLA4: 1.433e-23	CD28: 1.721e-22
[25] CCR3: 2.168e-20	IL25: 9.456e-19	CXCL10: 2.321e-18

[28]	NLRP3:	2.607e-18	CD8A:	1.3e-17	IFI44:	2.194e-17
[31]	GSK3A:	1.738e-15	IRF1:	3.129e-15	ZAP70:	9.394e-14
[34]	IFNGR1:	1.304e-12	CD40:	1.861e-12	RAC1:	2.85e-12
[37]	CCR5:	2.614e-11	CXCR3:	4.749e-11	CCR7:	1.077e-10
[40]	TNFRSF1A:	2.668e-10	JAK2:	8.832e-10	RORC:	1.173e-09
[43]	CCR2:	1.555e-09	BCL2:	2.079e-09	PTEN:	4.543e-08
[46]	TNFRSF1B:	4.79e-08	SOCS3:	1.483e-07	TGFBR2:	1.59e-07
[49]	TBX21:	9.073e-07	IRF2:	2.414e-06	STAT4:	7.956e-06
[52]	GATA3:	1.077e-05	STAT3:	1.214e-05	IL12RB1:	2.67e-05
[55]	CCR1:	5.562e-05	PPARA:	0.002584	ICOS:	0.003578
[58]	CD4:	0.003667	IFNAR2:	0.004918	IL2:	0.005465
[61]	IFNAR1:	0.01214	NFKB1:	0.01258	ISG15:	0.0126
[64]	VAV1:	0.01612	IL4:	0.03388	TYK2:	0.03807









```
[1] Differentially expressed genes between phenotypes for human samples:
[1] JAK1: 4.895e-11    CXCR4: 6.649e-11    TNFAIP3: 1.267e-08
[4] PDCD1: 1.49e-06    STAT1: 8.044e-06    GSK3A: 4.114e-05
[7] TNFRSF1A: 0.002469 CCR3: 0.008939    RPL13A: 0.01058
[10] CD44: 0.01058     IFIT1: 0.01058     NLRP3: 0.01058
[13] RAC1: 0.0116      IFIT3: 0.01433     CCR1: 0.01659
[16] GATA3: 0.03945    IL12RB1: 0.03945   PPARA: 0.03945
```

