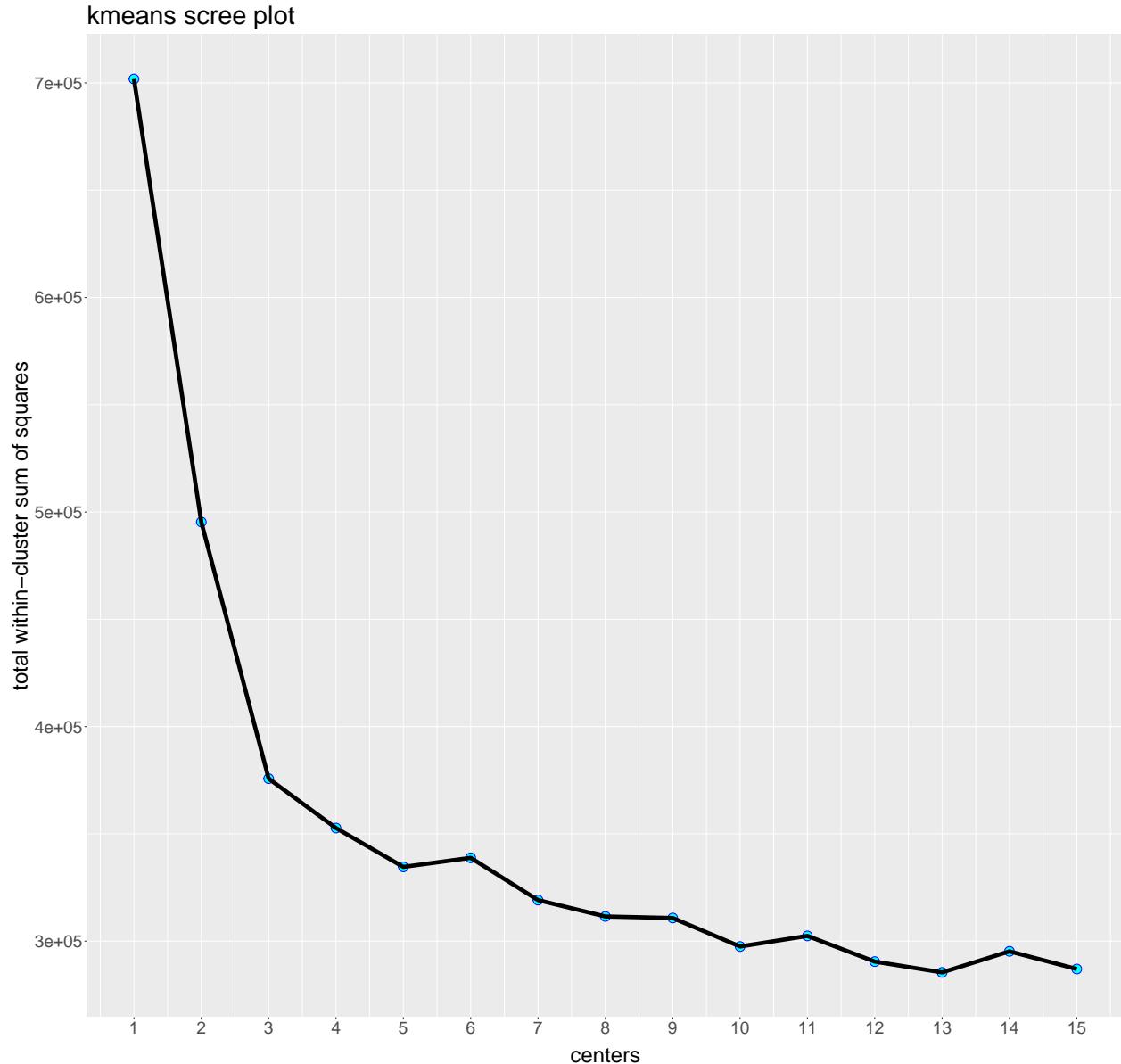
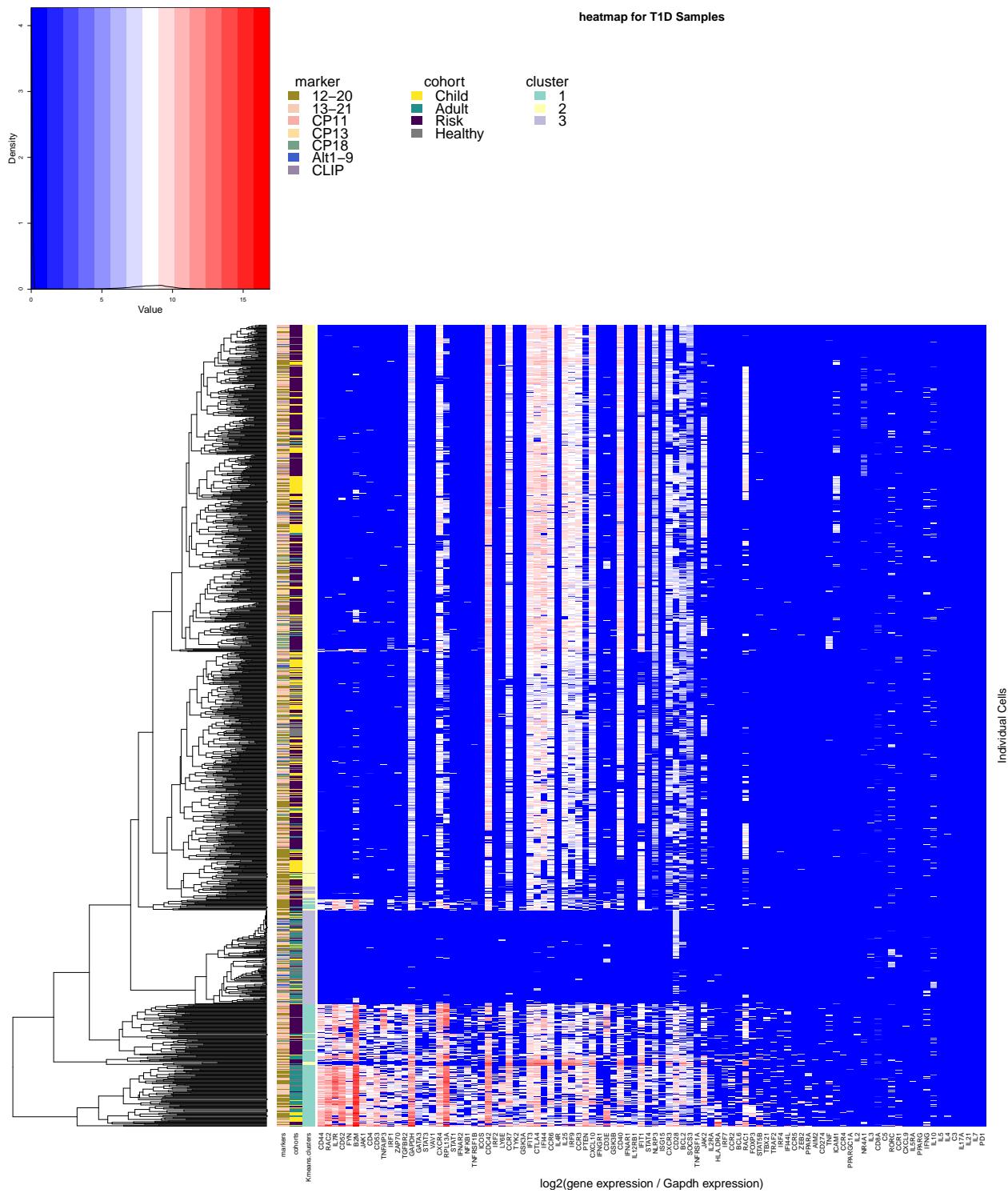


T1D_Tetramer_Cells_Analysis

No expression detected in 47/1950 cells

No expression detected in 19/1223 Tetramer cells





```
[1]  
[1]  
[1] Cohort vs. Cluster  
      cohort_Child cohort_Adult cohort_Risk cohort_Healthy  
cluster_1          22           65          86           15  
cluster_2         227           35         486          115  
cluster_3          20           55          22           56
```

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

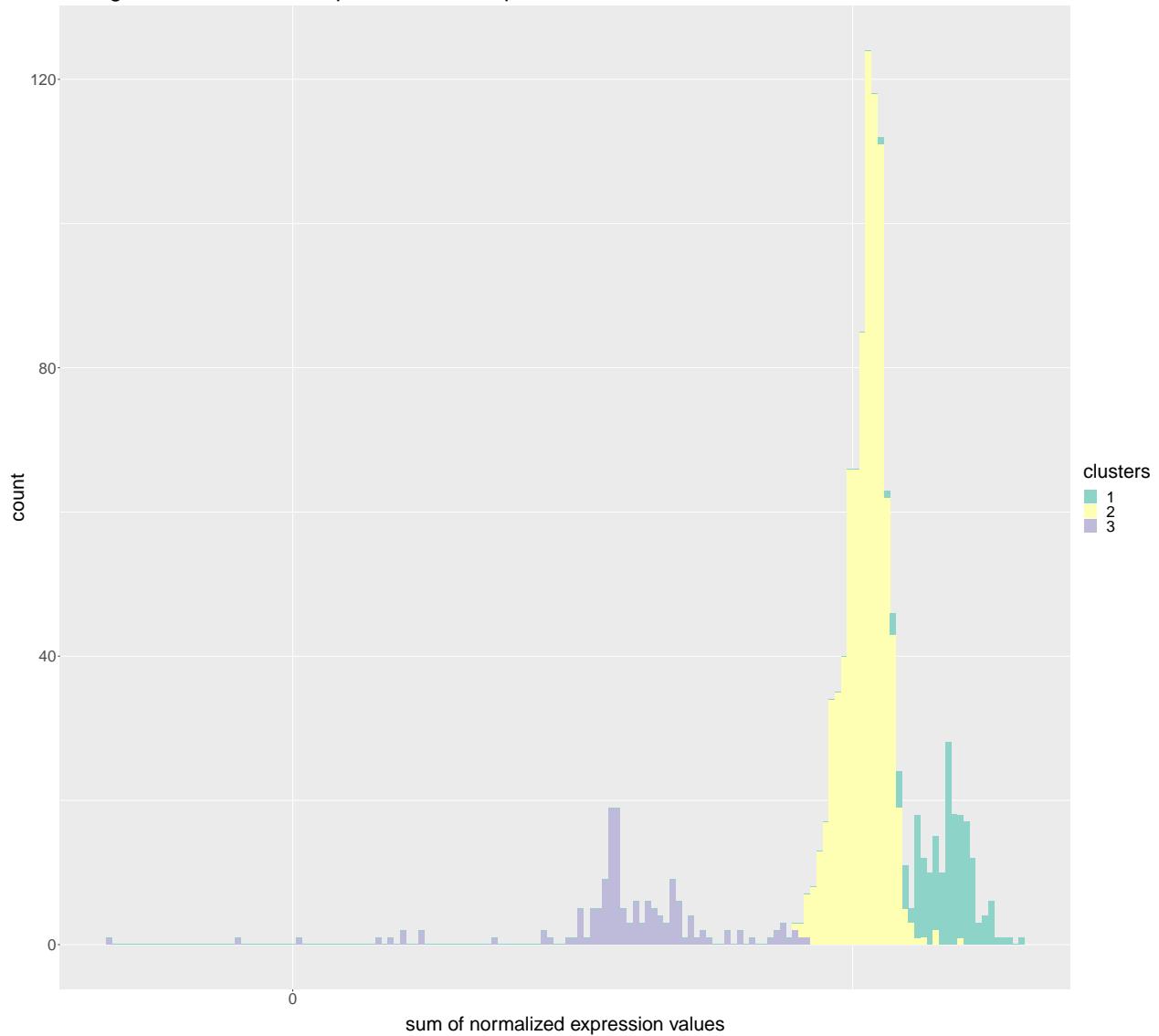
```
data: cohortTable  
X-squared = 306.17, df = NA, p-value = 0.0004998
```

```
[1]  
[1]  
[1] marker vs. Cluster  
      marker_12-20 marker_13-21 marker_CP11 marker_CP13 marker_CP18  
cluster_1        86          68          27          4          3  
cluster_2       271         253         102         94         83  
cluster_3        34          32          22         21         18  
      marker_Alt1-9 marker_CLIP  
cluster_1        0           0  
cluster_2       25          35  
cluster_3       23          3
```

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

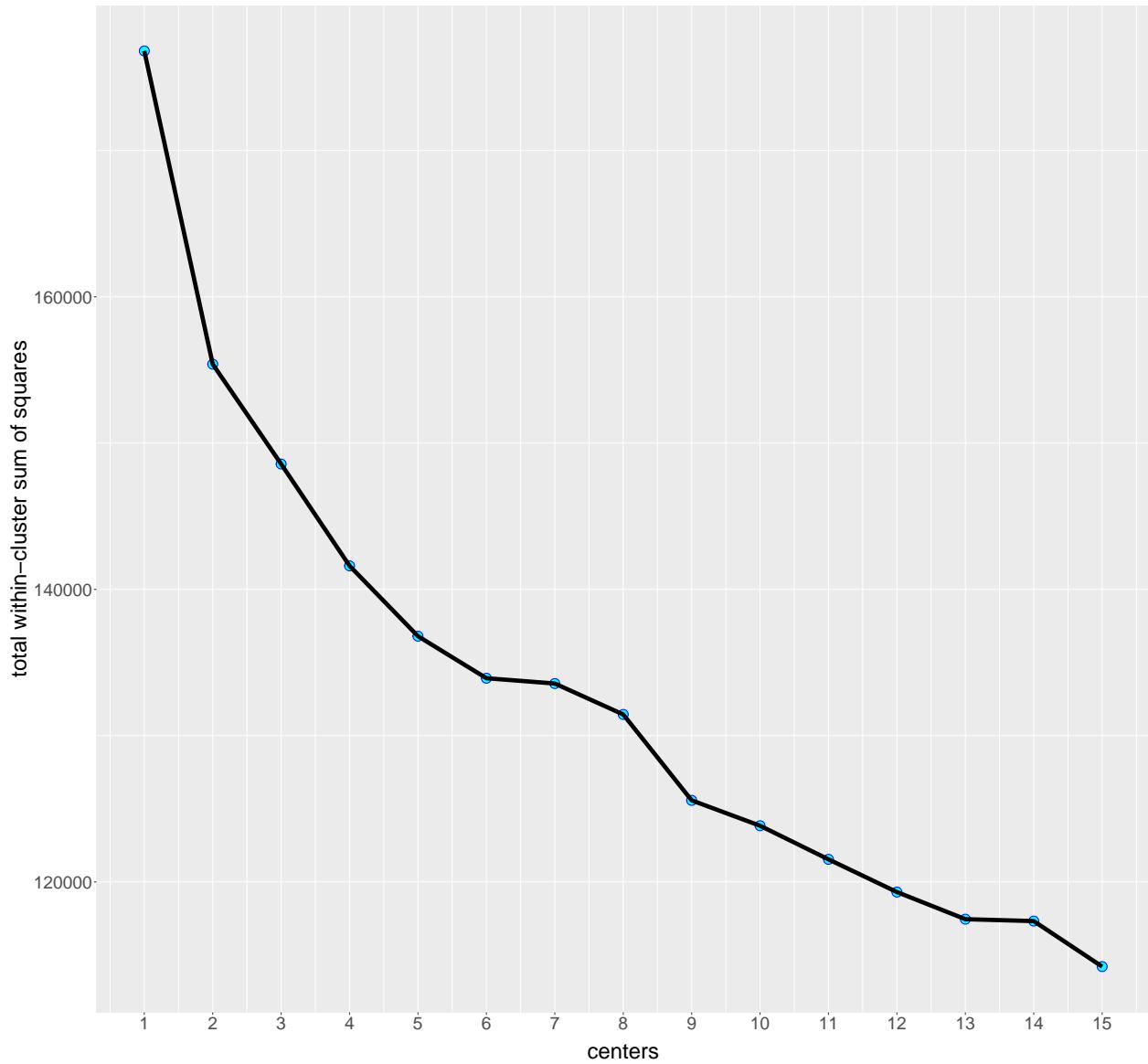
```
data: markerTable  
X-squared = 117.24, df = NA, p-value = 0.0004998
```

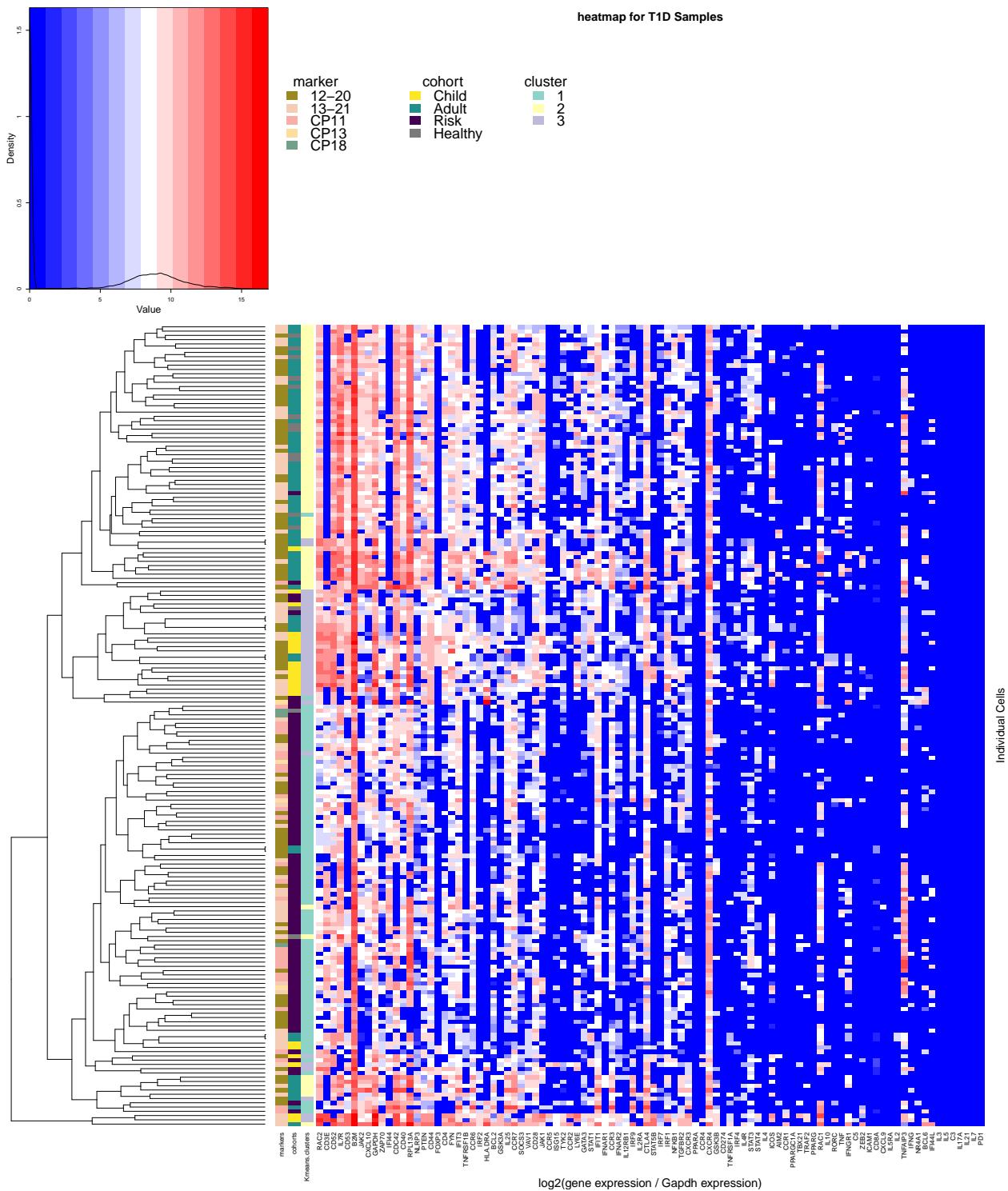
histogram of cumulative expression values per cell



1016 / 1204 cells were removed due to low gene expression (cluster ID of removed clusters: 2, 3)

kmeans scree plot





```
[1]
[1]
[1] Cohort vs. Cluster
      cohort_Child cohort_Adult cohort_Risk cohort_Healthy
cluster_1          2           5         77            2
cluster_2          1          51          3           12
cluster_3         19           9          6            1
```

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

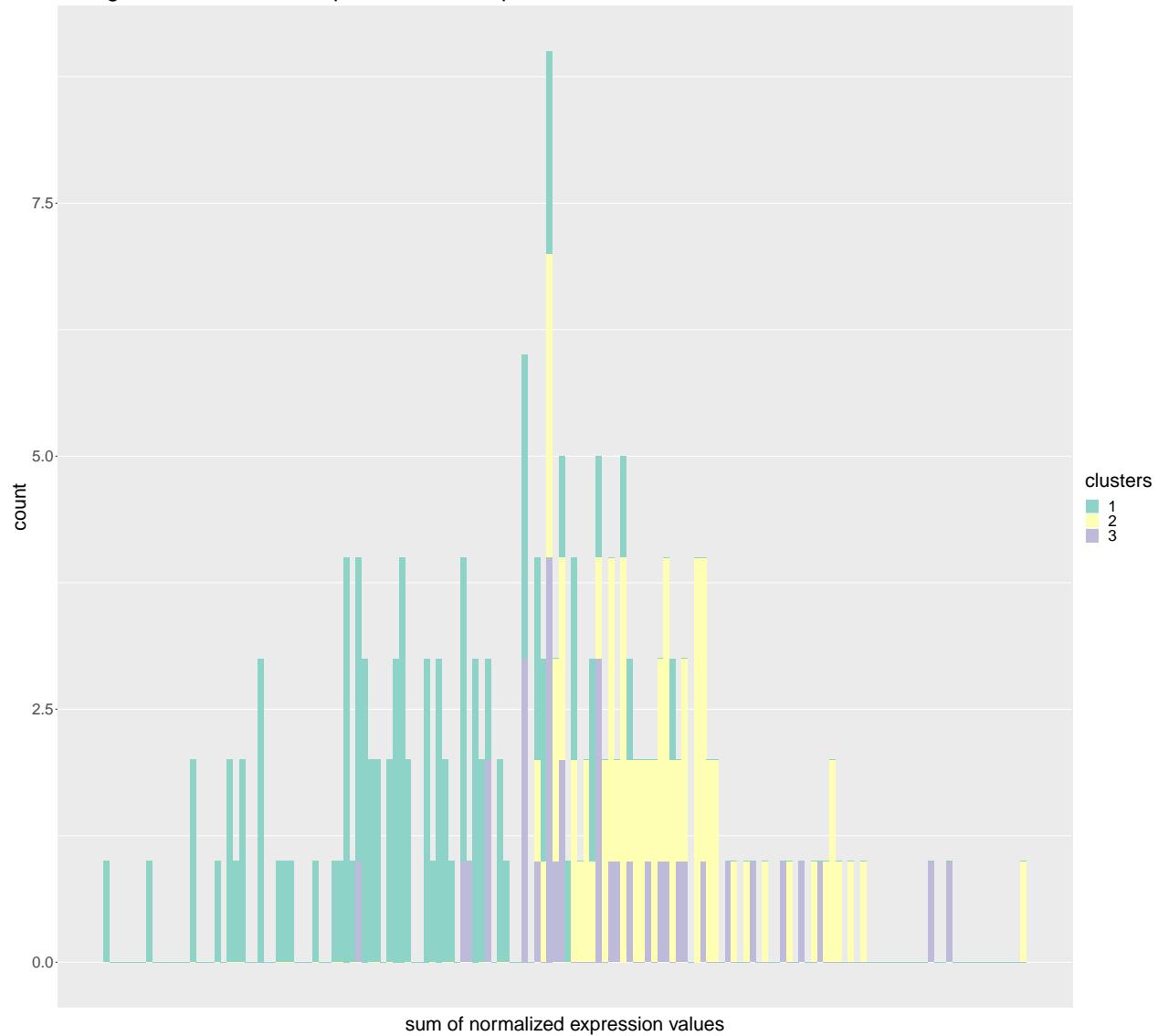
```
data: cohortTable  
X-squared = 201.61, df = NA, p-value = 0.0004998
```

```
[1]  
[1]  
[1] marker vs. Cluster  
      marker_12-20 marker_13-21 marker_CP11 marker_CP13 marker_CP18  
cluster_1          32        23        25         3         3  
cluster_2          37        29         1         0         0  
cluster_3          17        16         1         1         0
```

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

```
data: markerTable  
X-squared = 36.403, df = NA, p-value = 0.0004998
```

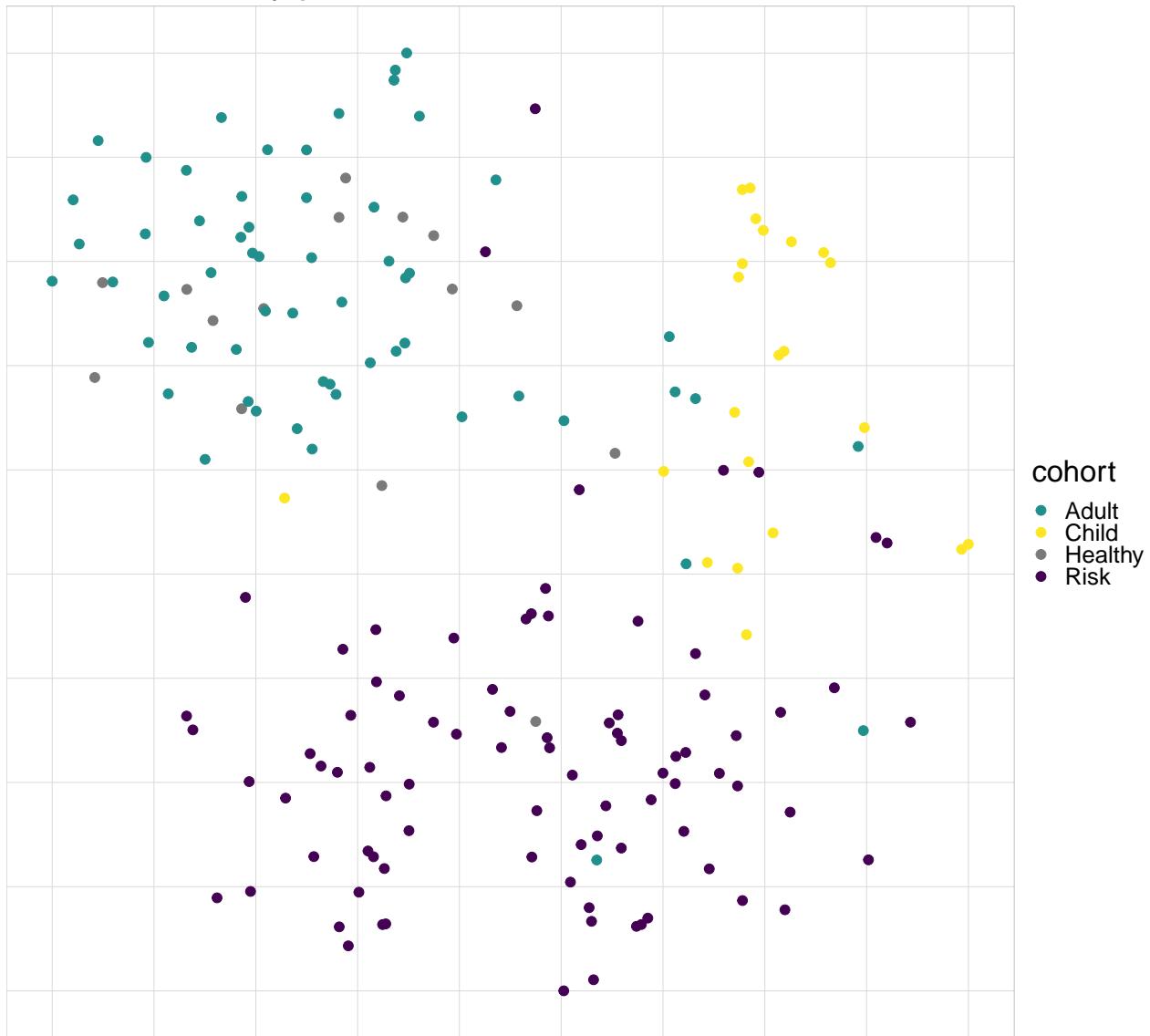
histogram of cumulative expression values per cell



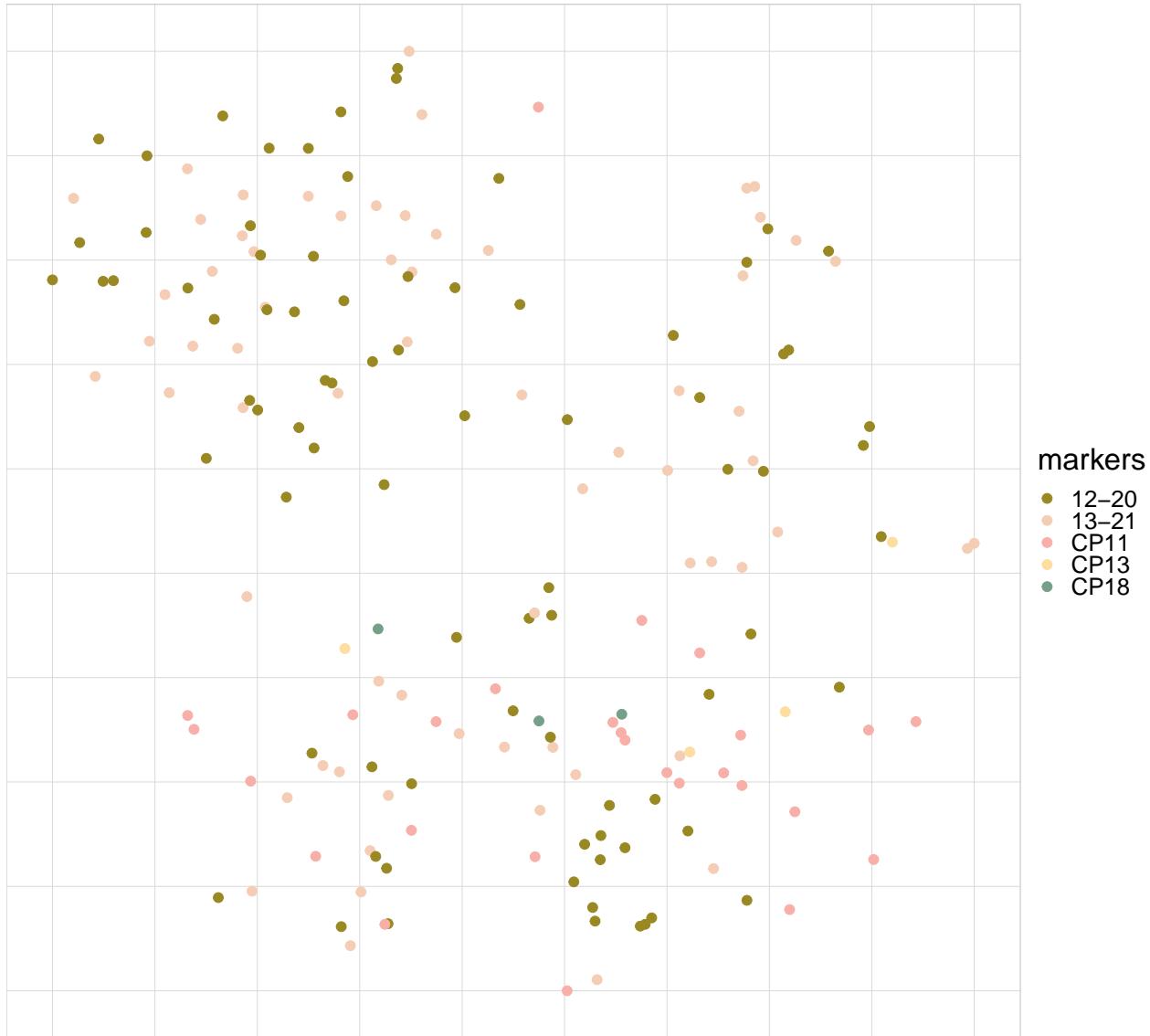
t-SNE colored by kmeans.cluster



t-SNE colored by patient cohorts



t-SNE colored by different markers

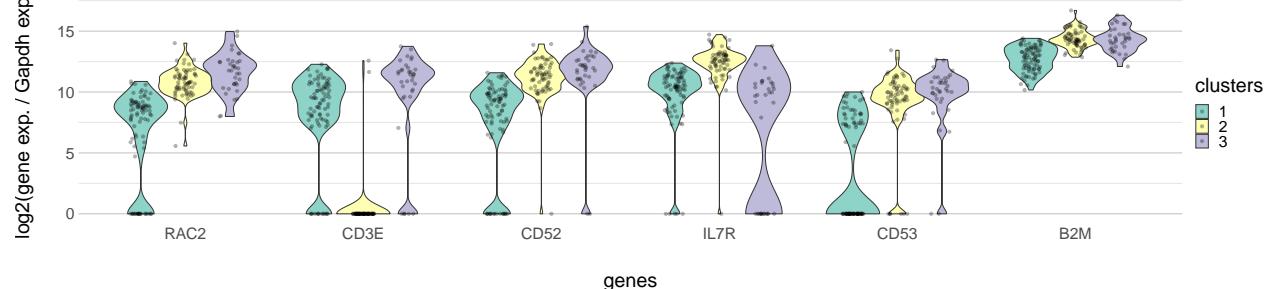


[1] Differentially expressed genes between clusters for human samples:

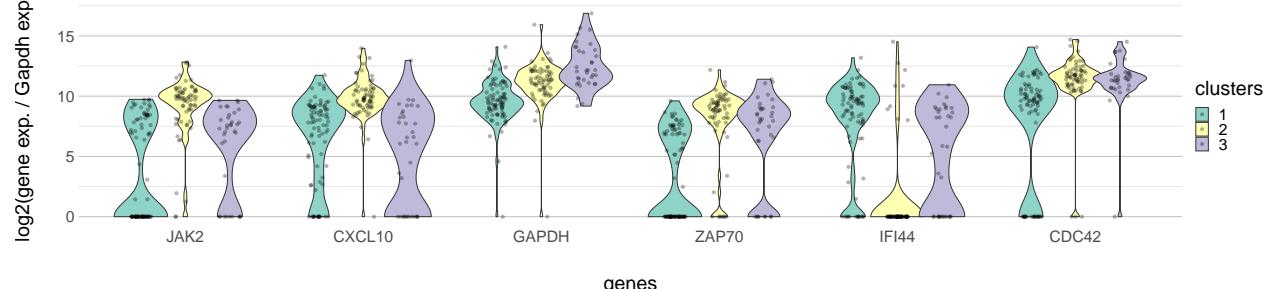
[1]	RAC2: 1.654e-23	CD3E: 2.013e-20	CD52: 2.381e-20
[4]	IL7R: 6.41e-20	CD53: 9.744e-20	B2M: 2.301e-19
[7]	JAK2: 9.489e-17	CXCL10: 5.796e-15	GAPDH: 9.534e-15
[10]	ZAP70: 9.534e-15	IFI44: 1.184e-13	CDC42: 1.218e-13
[13]	CD40: 1.218e-13	RPL13A: 1.218e-13	NLRP3: 1.697e-13
[16]	PTEN: 1.008e-12	CD44: 4.569e-12	FOXP3: 1.02e-11
[19]	CD4: 1.032e-11	FYN: 9.767e-11	IFIT3: 1.339e-10
[22]	TNFRSF1B: 4.799e-10	CCR6: 6.237e-10	IRF2: 2.028e-09
[25]	HLA.DRA: 2.332e-09	BCL2: 3.6e-09	GSK3A: 3.987e-09
[28]	IL25: 1.143e-08	CCR7: 1.527e-08	SOCS3: 2.301e-08
[31]	VAV1: 3.444e-08	CD28: 1.029e-07	JAK1: 1.868e-07
[34]	CCR5: 2.306e-07	ISG15: 2.306e-07	TYK2: 2.895e-07
[37]	CCR2: 3.607e-07	LY6E: 4.655e-07	GATA3: 4.66e-07
[40]	STAT1: 5.162e-07	IFIT1: 6.05e-07	IFNAR1: 7.311e-07
[43]	CCR3: 8.332e-07	IFNAR2: 8.332e-07	IL12RB1: 9.118e-07

[46]	IRF9: 9.118e-07	IL2RA: 1.47e-05	CTLA4: 1.538e-05
[49]	STAT5B: 4.369e-05	IRF7: 5.515e-05	IRF1: 6.291e-05
[52]	NFKB1: 0.0001096	TGFBR2: 0.0001309	CXCR3: 0.0001612
[55]	PPARA: 0.0002202	CCR4: 0.0002202	CXCR4: 0.0003704
[58]	GSK3B: 0.0007099	CD274: 0.001519	TNFRSF1A: 0.001965
[61]	IRF4: 0.002797	IL4R: 0.005615	STAT3: 0.009402
[64]	STAT4: 0.01043	IL4: 0.0169	ICOS: 0.03201

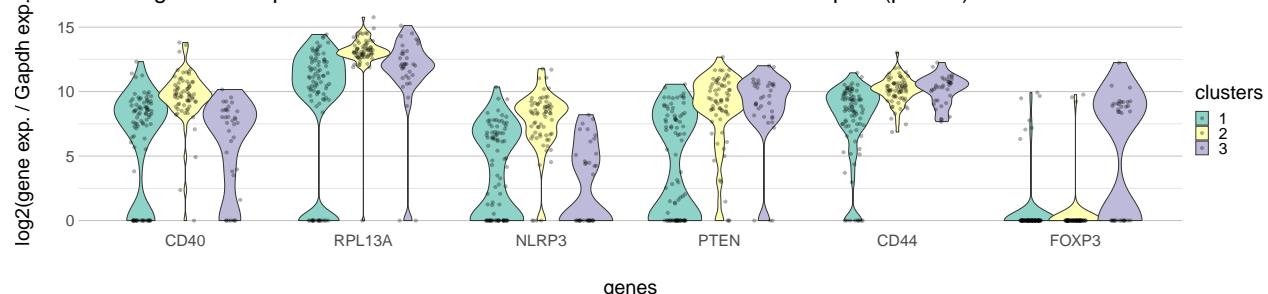
most significant expression differences between clusters for human samples (plot #1)



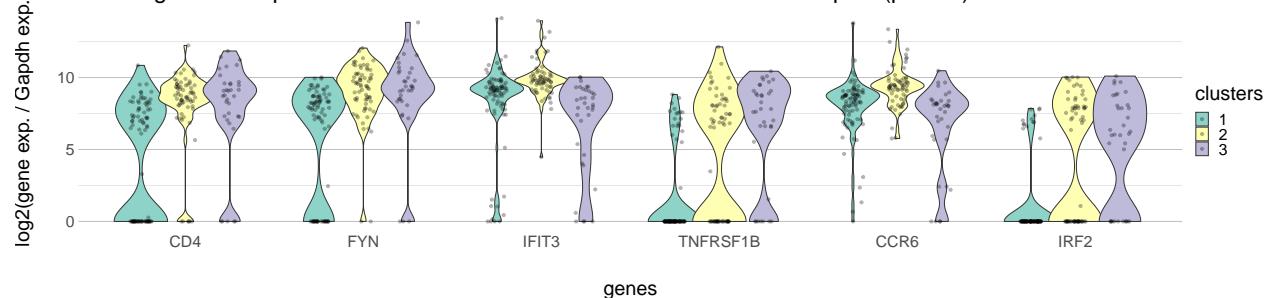
most significant expression differences between clusters for human samples (plot #2)

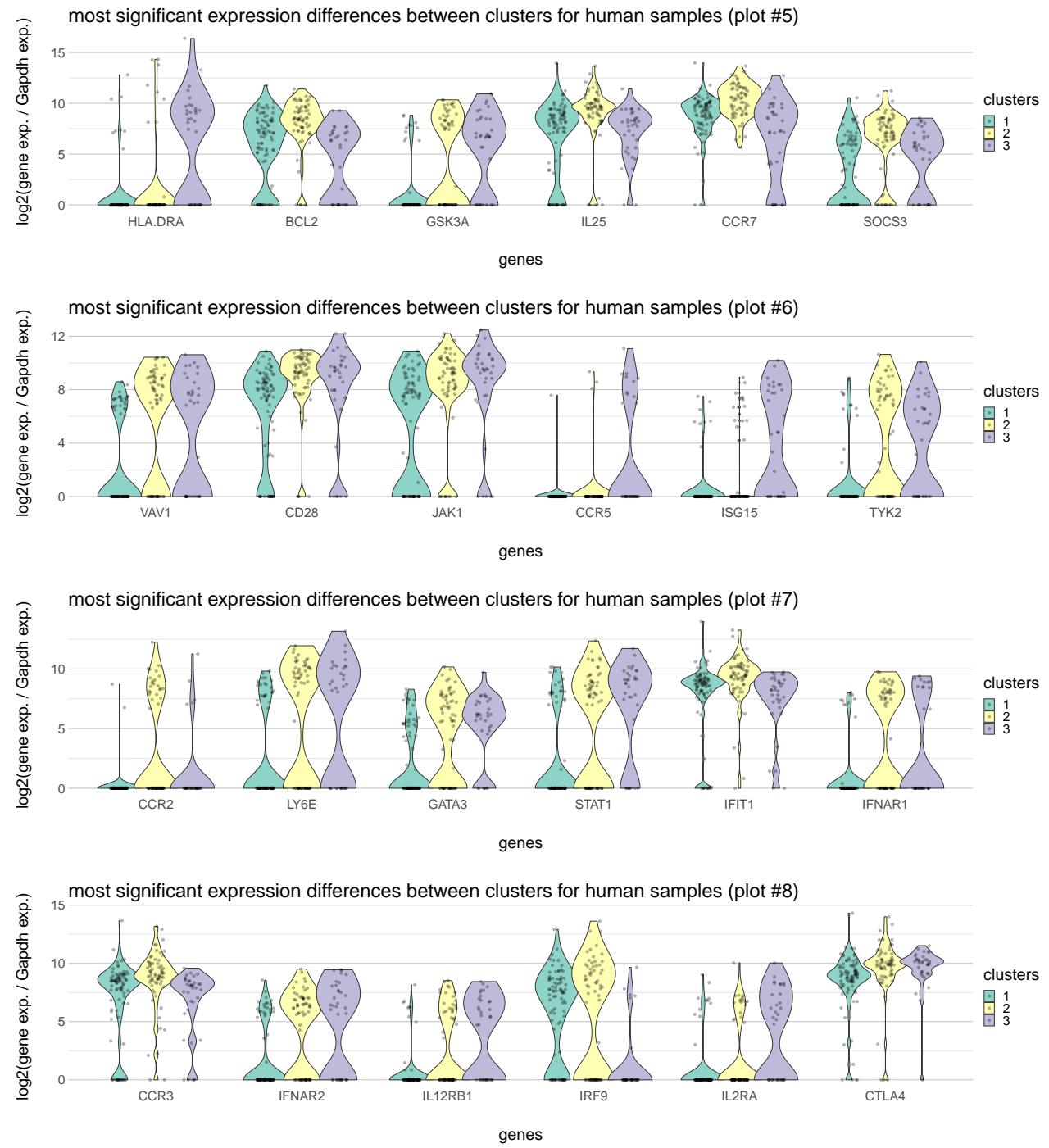


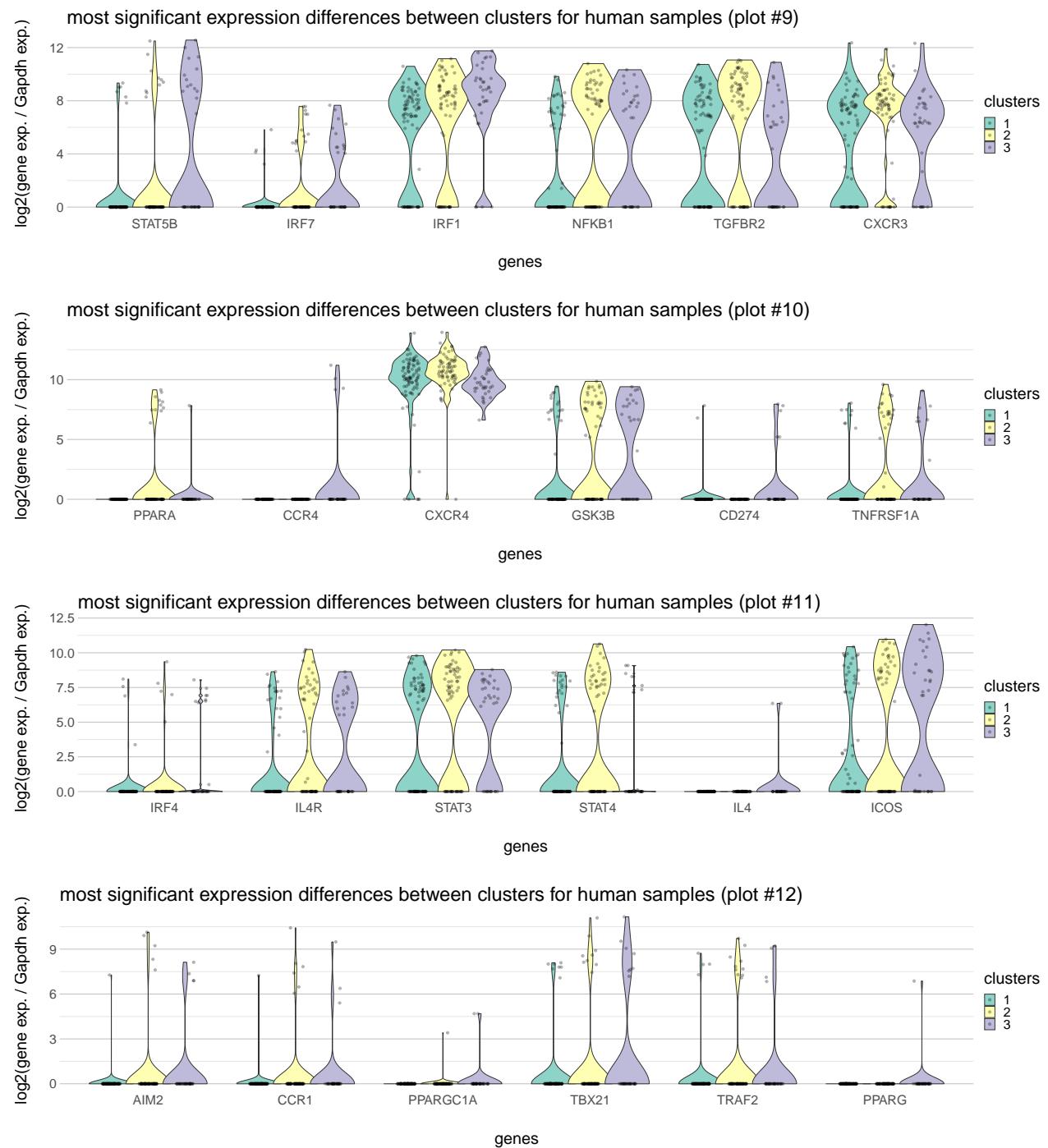
most significant expression differences between clusters for human samples (plot #3)

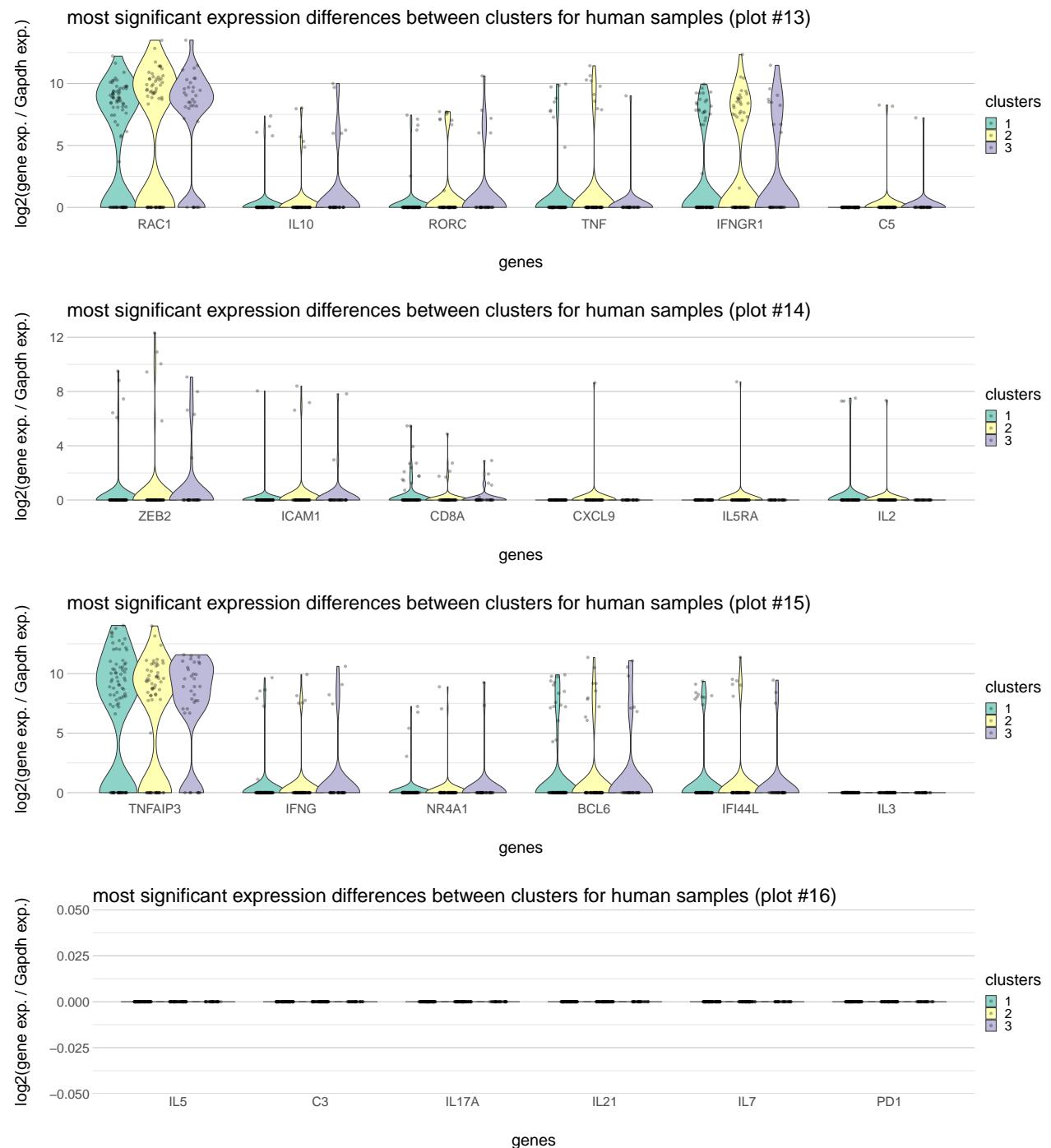


most significant expression differences between clusters for human samples (plot #4)



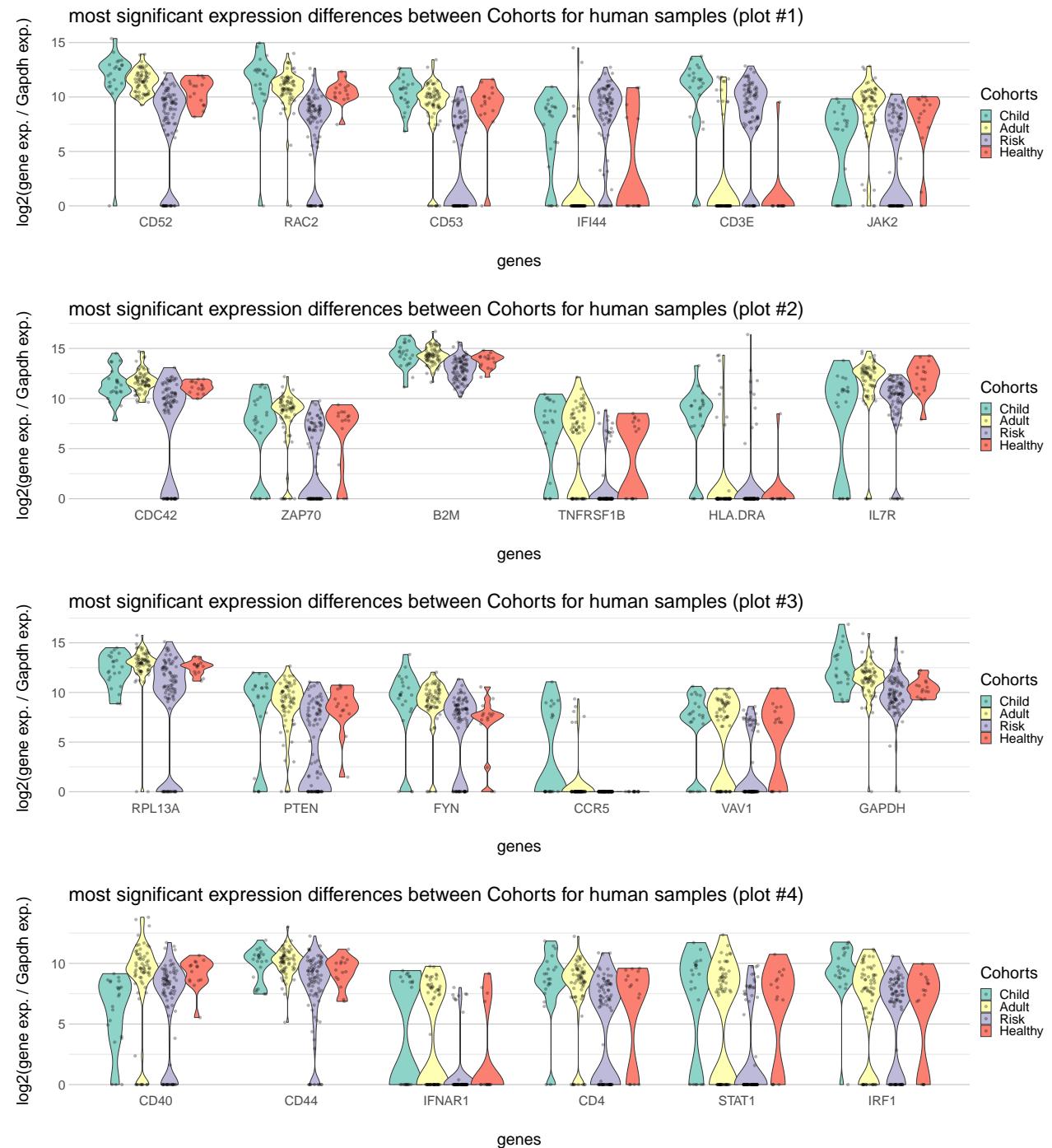


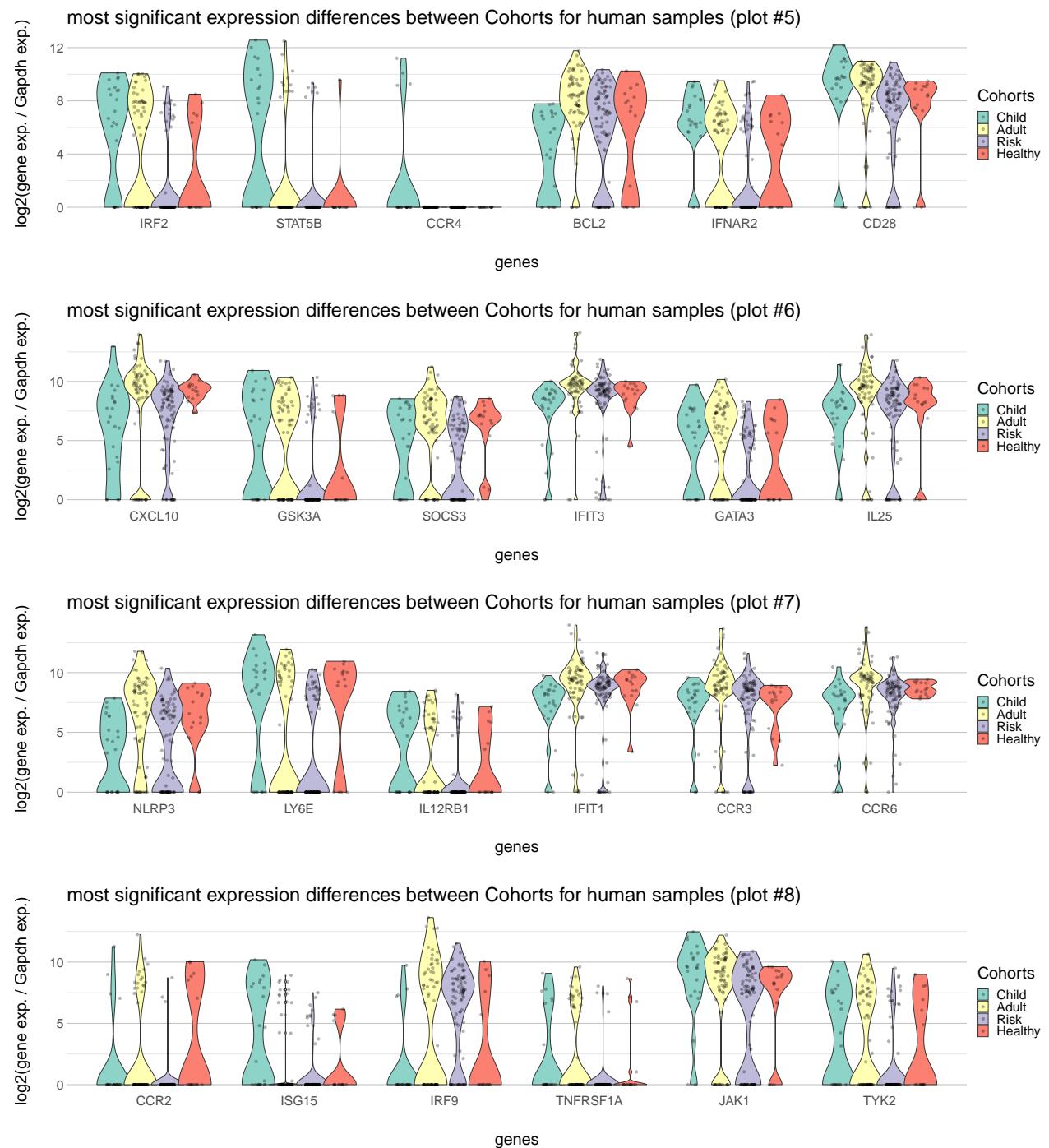


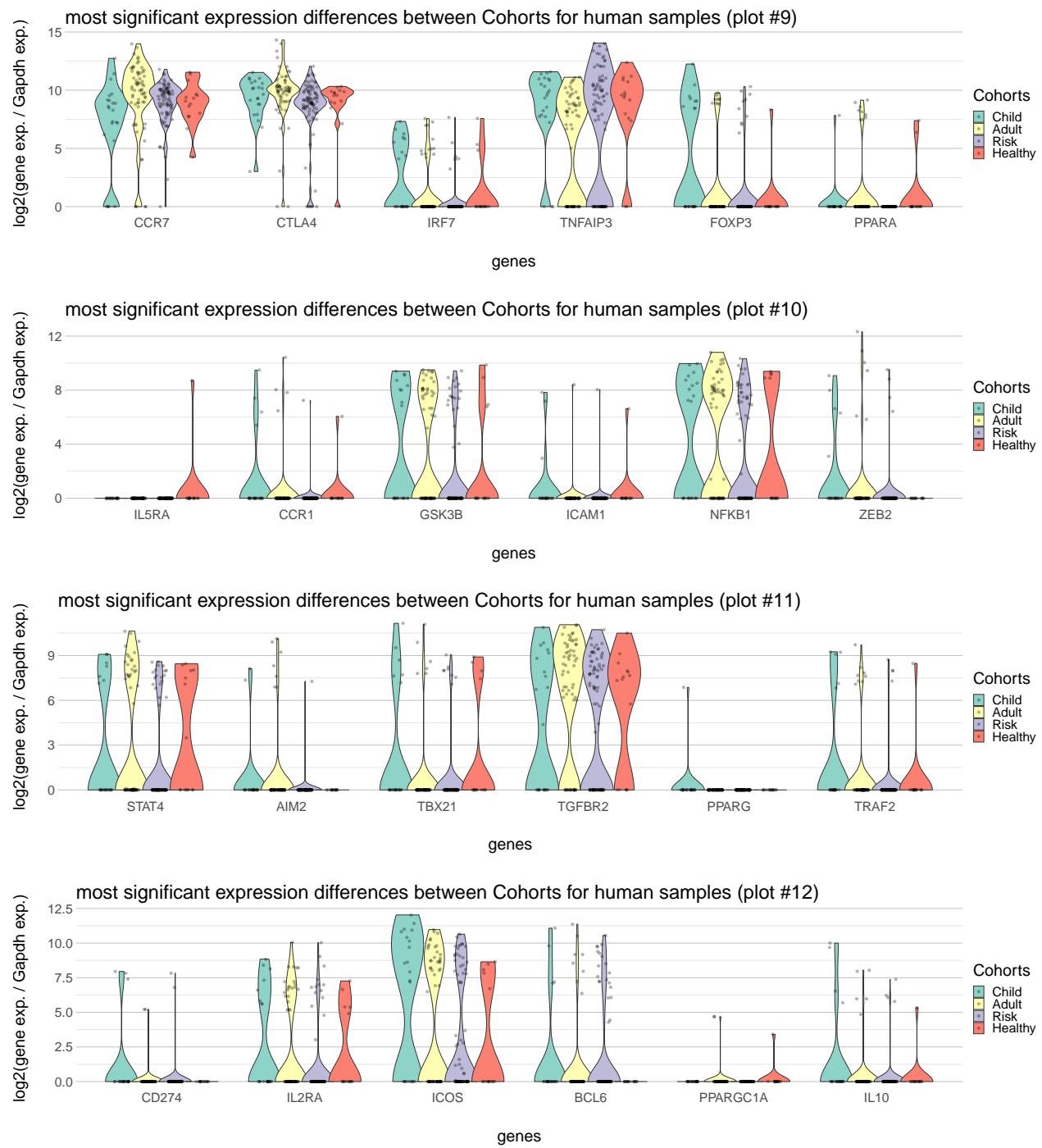


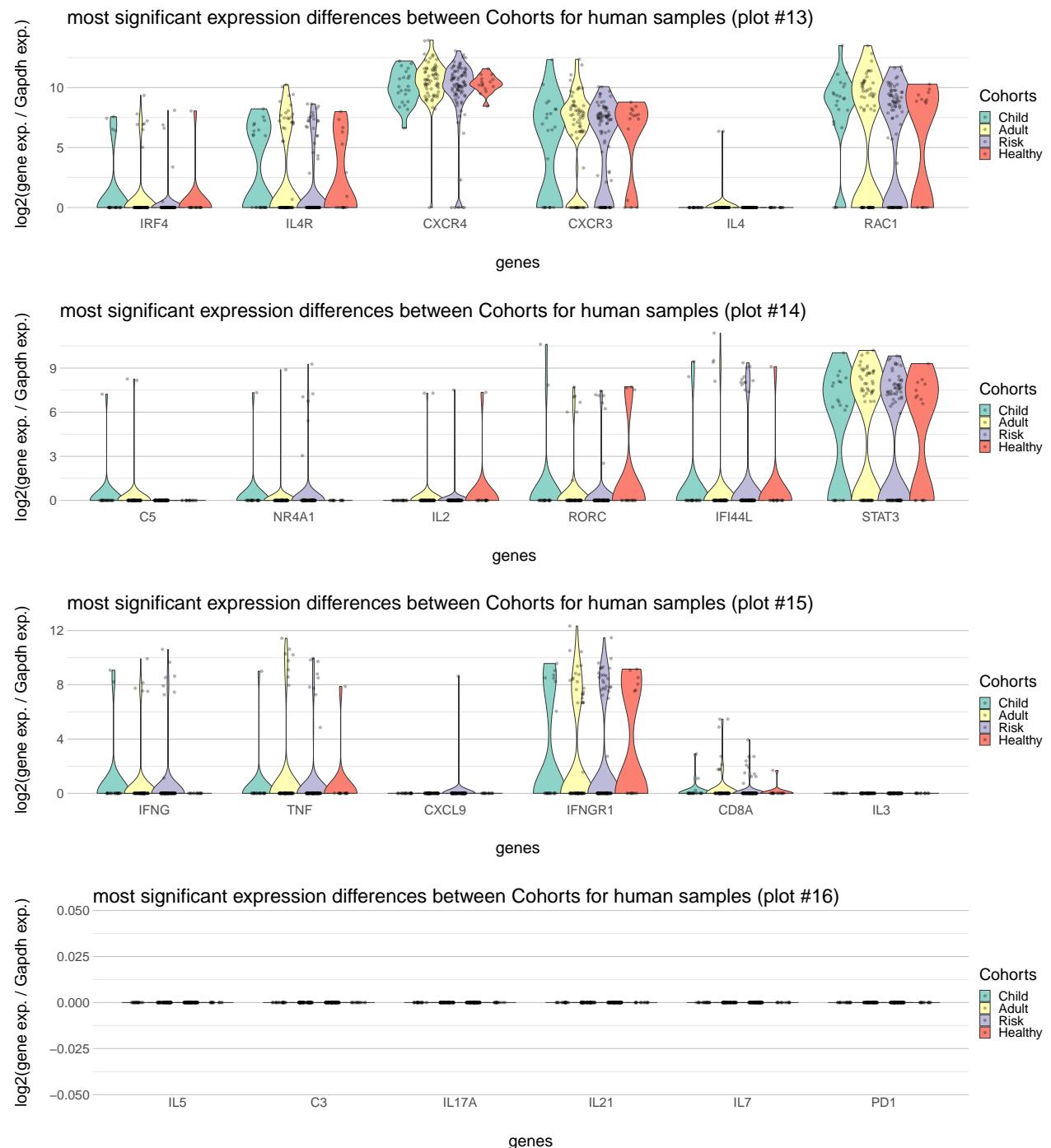
```
[1] Differentially expressed genes between Cohorts for human samples:
[1] CD52: 2.315e-19      RAC2: 1.141e-18      CD53: 3.774e-17
[4] IFI44: 3.62e-16      CD3E: 5.656e-14      JAK2: 2.158e-13
[7] CDC42: 4.486e-13     ZAP70: 4.834e-12     B2M: 6.066e-12
[10] TNFRSF1B: 1.013e-11   HLA.DRA: 5.642e-11    IL7R: 2e-10
[13] RPL13A: 8.296e-09     PTEN: 8.979e-09      FYN: 8.979e-09
[16] CCR5: 2.042e-08       VAV1: 3.348e-08     GAPDH: 6.018e-08
[19] CD40: 1.002e-07       CD44: 2.121e-07     IFNAR1: 4.002e-07
[22] CD4: 4.817e-07        STAT1: 7.691e-07    IRF1: 8.209e-07
[25] IRF2: 9.422e-07       STAT5B: 1.972e-06   CCR4: 3.289e-06
```

[28]	BCL2:	3.765e-06	IFNAR2:	4.101e-06	CD28:	5.059e-06
[31]	CXCL10:	5.27e-06	GSK3A:	5.27e-06	SOCS3:	5.27e-06
[34]	IFIT3:	5.349e-06	GATA3:	7.586e-06	IL25:	8.146e-06
[37]	NLRP3:	1.004e-05	LY6E:	2.087e-05	IL12RB1:	3.179e-05
[40]	IFIT1:	3.893e-05	CCR3:	4.451e-05	CCR6:	5.276e-05
[43]	CCR2:	6.512e-05	ISG15:	8.543e-05	IRF9:	0.0001941
[46]	TNFRSF1A:	0.0003596	JAK1:	0.0004551	TYK2:	0.0006821
[49]	CCR7:	0.0007021	CTLA4:	0.001065	IRF7:	0.001365
[52]	TNFAIP3:	0.005047	FOXP3:	0.006733	PPARA:	0.006896
[55]	IL5RA:	0.01483	CCR1:	0.02803	GSK3B:	0.02956
[58]	ICAM1:	0.03185	NFKB1:	0.04812	ZEB2:	0.04856









```
[1] Differentially expressed genes between Markers for human samples:
[1] RAC2: 0.001132    CD52: 0.001132    CD53: 0.001132
[4] IFI44: 0.001681    PTEN: 0.002176    BCL6: 0.002982
[7] CD4: 0.003058     B2M: 0.01783      ISG15: 0.03355
[10] TNFRSF1B: 0.03595   IL7R: 0.04237
```

