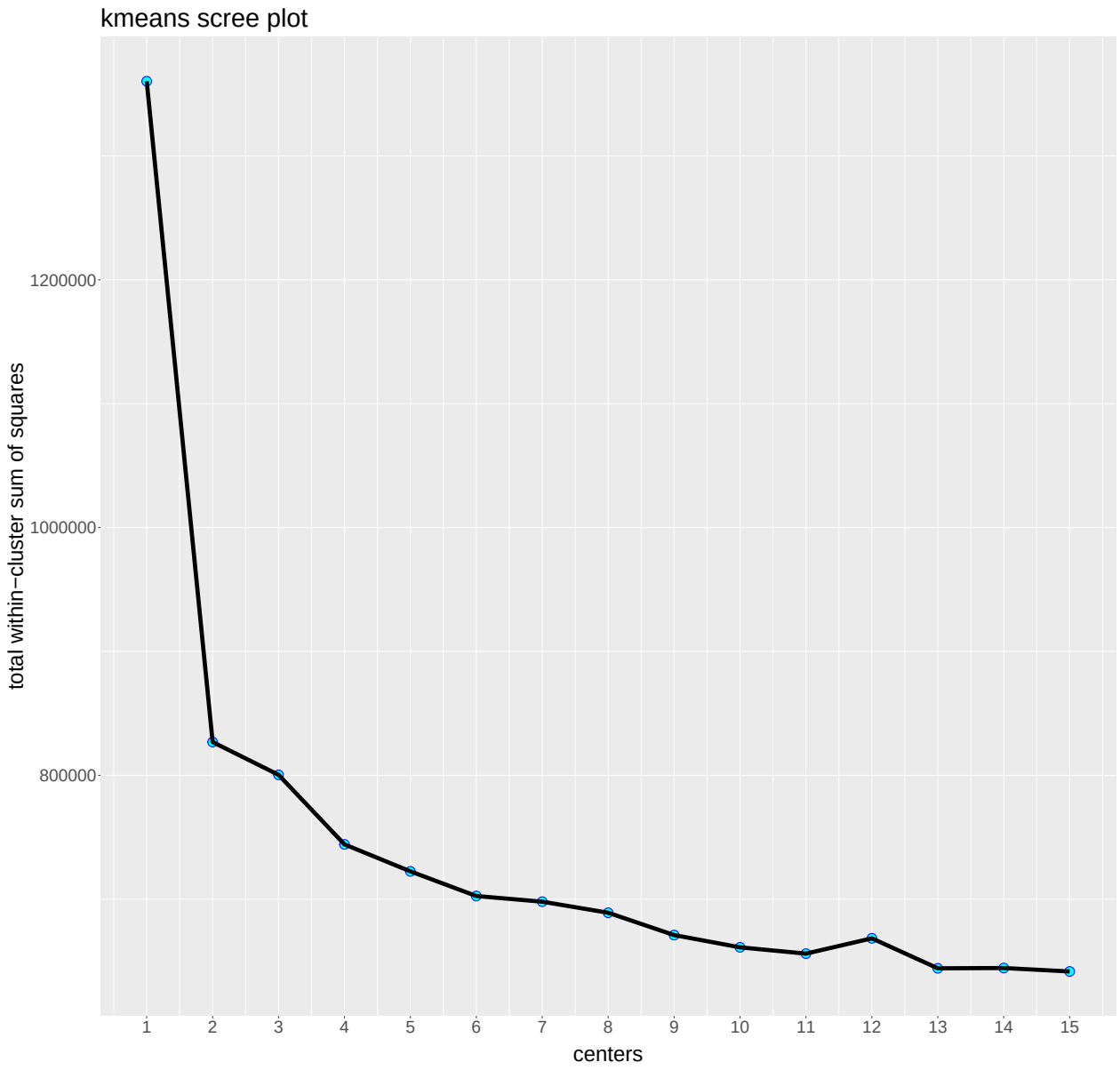
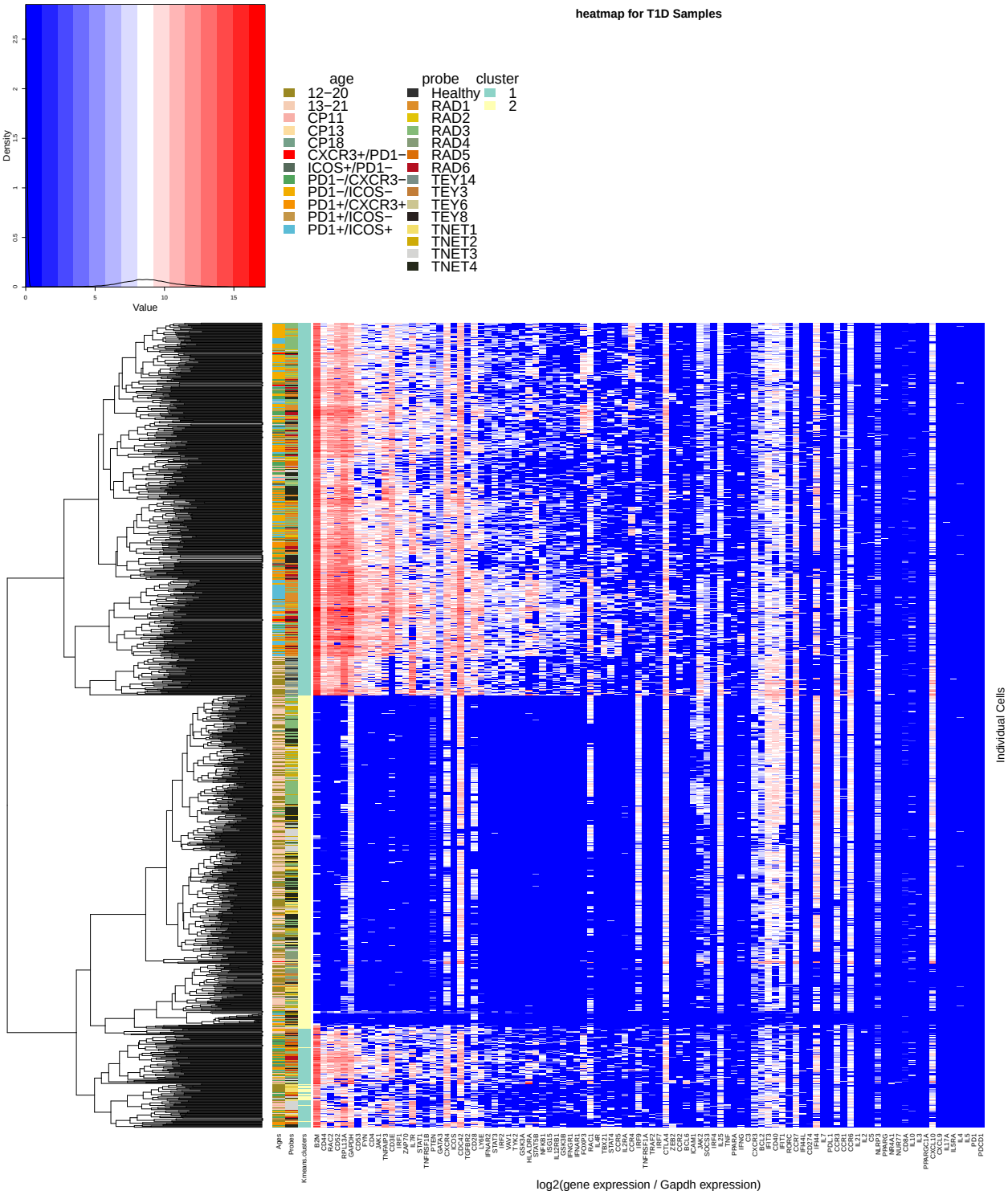
# T1D_analysis

```
No expression detected in 5/1291 cells
```

```
ctNorm[is.na(ctNorm)] <- 0
```

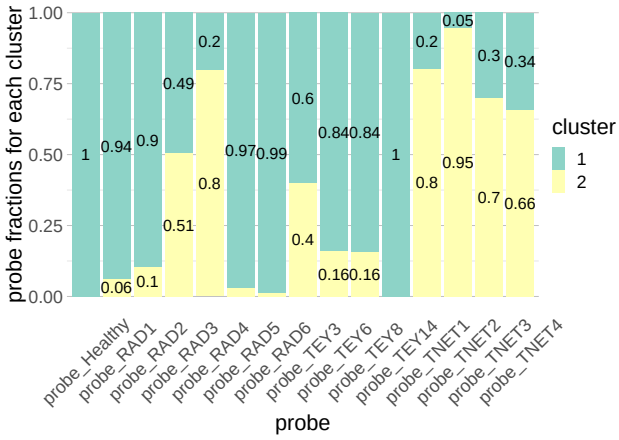


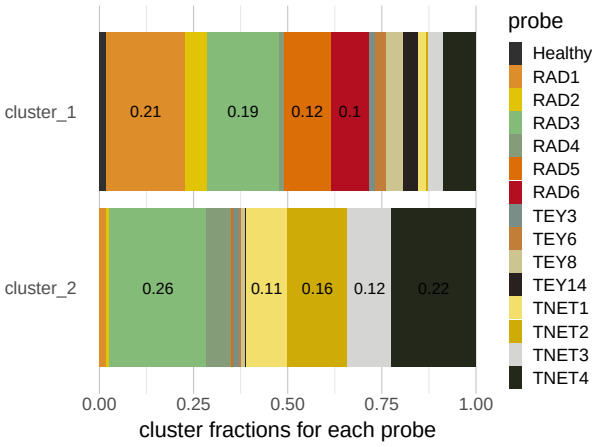


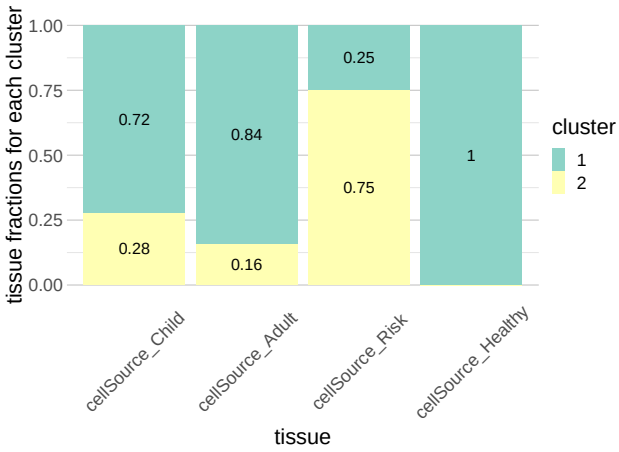

```
[1]
[1]
[1] Patient vs. Cluster
          probe_Healthy probe_RAD1 probe_RAD2 probe_RAD3 probe_RAD4
cluster_1            14        152         43        140          9
cluster_2             0         10          5        143         36
          probe_RAD5 probe_RAD6 probe_TEY3 probe_TEY6 probe_TEY8
```

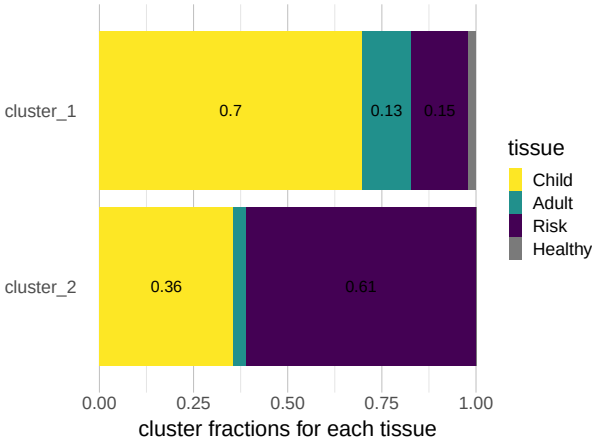
```
cluster_1         91         75         12         21         32
cluster_2          3          1          8          4          6
          probe_TEY14 probe_TNET1 probe_TNET2 probe_TNET3 probe_TNET4
cluster_1          30          15           5          28          64
cluster_2           0          61          89          65         124

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

data:  probeTable
X-squared = 521.83, df = NA, p-value = 0.0004998

[1]
[1]
[1] Cohort vs. Cluster
          cellSource_Child cellSource_Adult cellSource_Risk
cluster_1              510              95             112
cluster_2              198              18             339
          cellSource_Healthy
cluster_1                 14
cluster_2                  0

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

data:  sourceTable
X-squared = 299.74, df = NA, p-value = 0.0004998

[1]
[1]
[1] Marker vs. Cluster
          age_PD1+/ICOS+ age_PD1-/CXCR3- age_PD1-/ICOS- age_CP18 age_CP11
cluster_1            140             125            150        1       15
cluster_2              9              13              7       23       40
          age_PD1+/CXCR3+ age_13-21 age_12-20 age_PD1+/ICOS-
cluster_1             115        64        75             22
cluster_2               6       196       222             13
          age_ICOS+/PD1- age_CP13 age_CXCR3+/PD1-
cluster_1             14        2               8
cluster_2              2       22               2

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

data:  ageTable
X-squared = 625.02, df = NA, p-value = 0.0004998
```

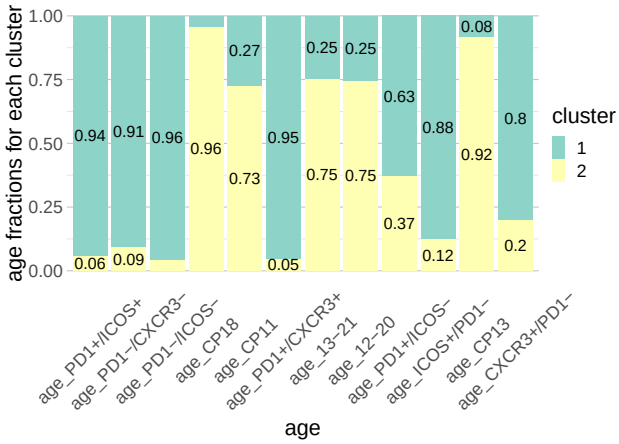

probe counts for each cluster
probe
cluster
1
2
value
Healthy RAD1 RAD2 RAD3 RAD4 RAD5 RAD6 TEY3 TEY6 TEY8 TEY14 TNET1 TNET2 TNET3 TNET4
14 152 43 140 9 91 75 12 21 32 30 15 5 28 64
0 10 5 143 36 3 1 8 4 6 0 61 89 65 124
tissue counts for each cluster
tissue
Child Adult Risk Healthy
510 95 112 14
198 18 339 0
age counts for each cluster
age
PD1+/ICOS+ PD1−/CXCR3− PD1−/ICOS− CP18 CP11 PD1+/CXCR3+ 13−21 12−20 PD1+/ICOS− ICOS+/PD1− CP13 CXCR3+/PD1−
140 125 150 1 15 115 64 75 22 14 2 8
9 13 7 23 40 6 196 222 13 2 22 2

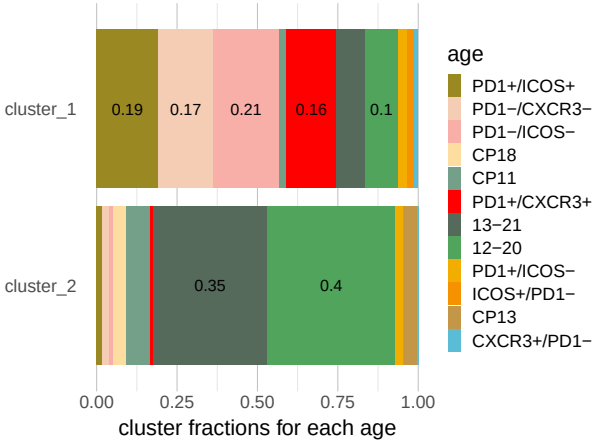

probe fractions for each cluster
1.00
0.75
0.50
0.25
0.00
1 0.94 0.9 0.49 0.2 0.97 0.99 0.6 0.84 0.84 1 0.2 0.05 0.3 0.34
0.06 0.1 0.51 0.8 0.4 0.16 0.16 0.8 0.95 0.7 0.66
probe_Healthy
probe_RAD1
probe_RAD2
probe_RAD3
probe_RAD4
probe_RAD5
probe_RAD6
probe_TEY3
probe_TEY6
probe_TEY8
probe_TEY14
probe_TNET1
probe_TNET2
probe_TNET3
probe_TNET4
probe
cluster
1
2

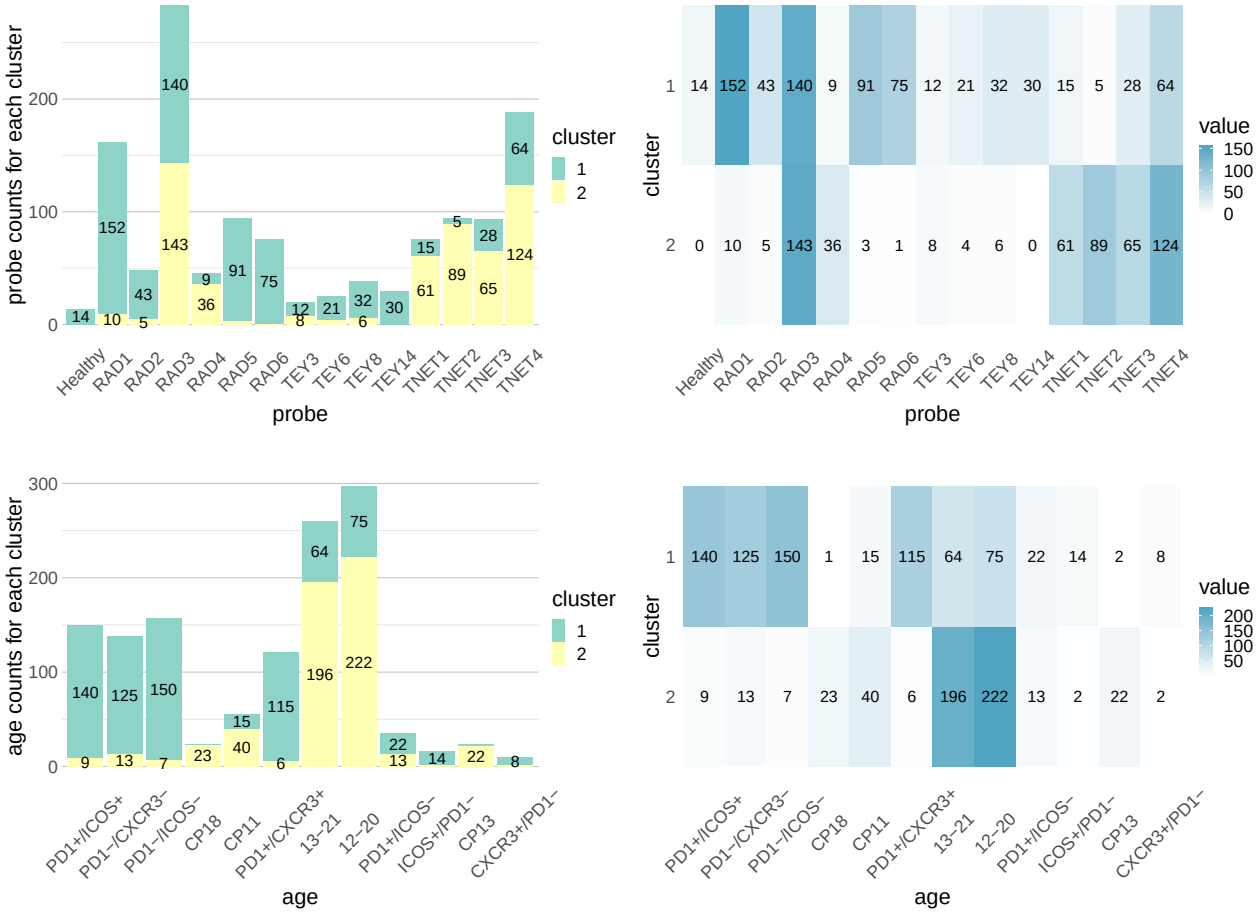

cluster_1
cluster_2
0.21 0.19 0.12 0.1
0.26 0.11 0.16 0.12 0.22
0.00 0.25 0.50 0.75 1.00
cluster fractions for each probe
probe
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4

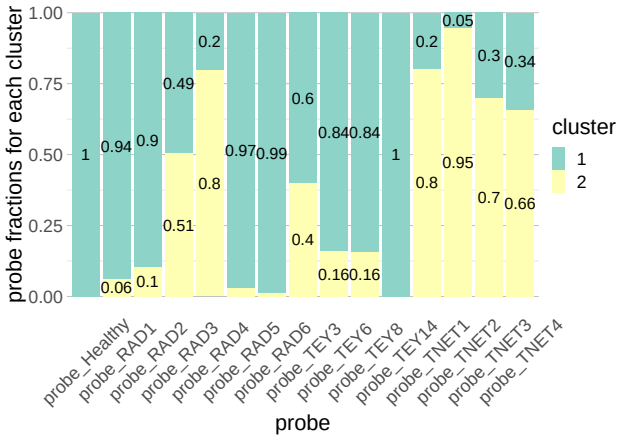

tissue fractions for each cluster
1.00
0.75
0.50
0.25
0.00
0.72 0.84 0.25 1
0.28 0.16 0.75
cellSource_Child
cellSource_Adult
cellSource_Risk
cellSource_Healthy
tissue
cluster
1
2

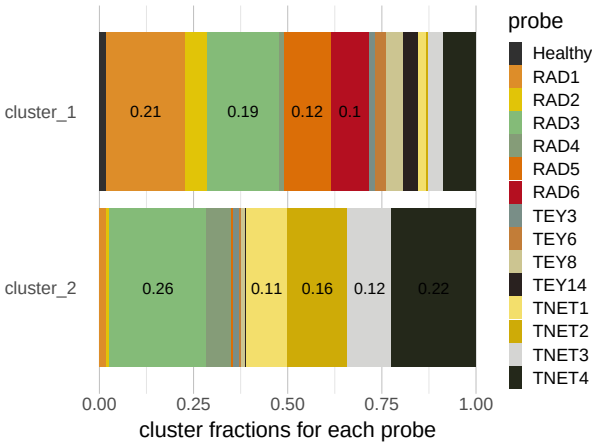

cluster_1
cluster_2
0.7 0.13 0.15
0.36 0.61
0.00 0.25 0.50 0.75 1.00
cluster fractions for each tissue
tissue
Child
Adult
Risk
Healthy

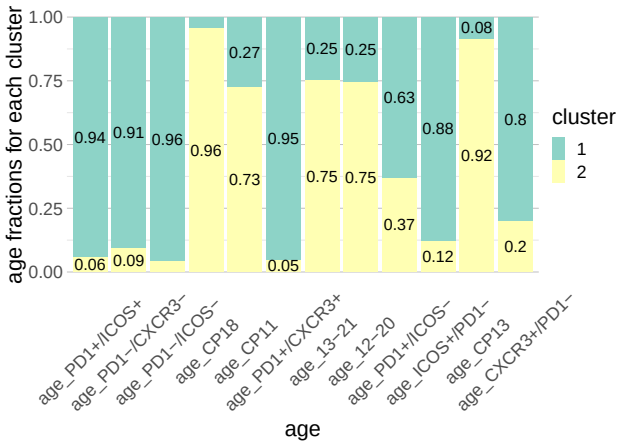

age fractions for each cluster
1.00
0.75
0.50
0.25
0.00
0.94 0.91 0.96 0.96 0.27 0.95 0.25 0.25 0.63 0.88 0.08 0.8
0.06 0.09 0.73 0.05 0.75 0.75 0.37 0.12 0.92 0.2
age_PD1+/ICOS+
age_PD1−/CXCR3−
age_PD1−/ICOS−
age_CP18
age_CP11
age_PD1+/CXCR3+
age_13−21
age_12−20
age_PD1+/ICOS−
age_ICOS+/PD1−
age_CP13
age_CXCR3+/PD1−
age
cluster
1
2

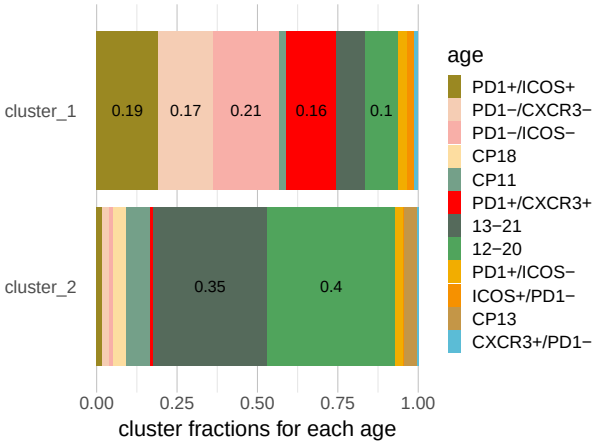

cluster_1
cluster_2
0.19 0.17 0.21 0.16 0.1
0.35 0.4
0.00 0.25 0.50 0.75 1.00
cluster fractions for each age
age
PD1+/ICOS+
PD1−/CXCR3−
PD1−/ICOS−
CP18
CP11
PD1+/CXCR3+
13−21
12−20
PD1+/ICOS−
ICOS+/PD1−
CP13
CXCR3+/PD1−

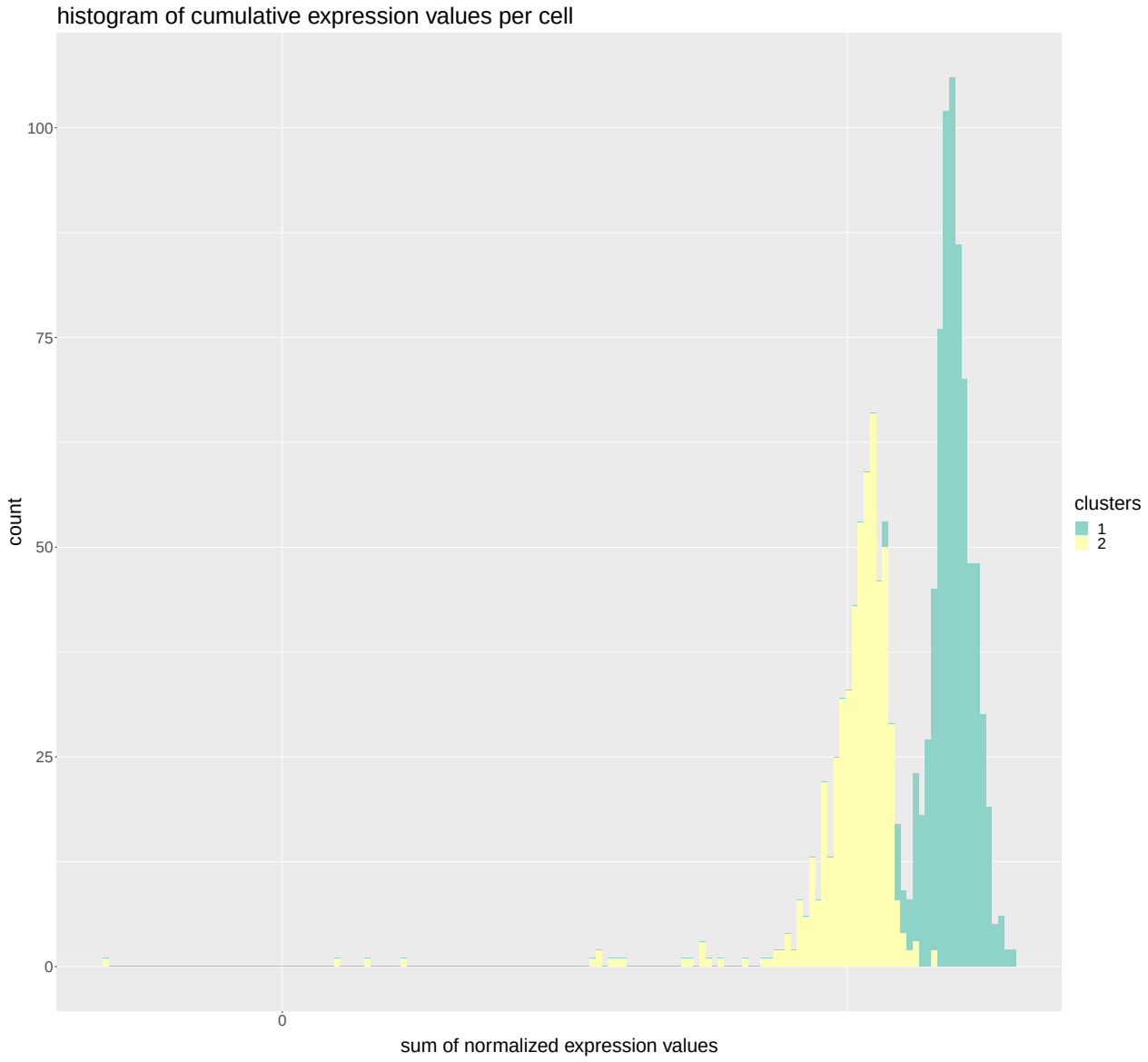

probe counts for each cluster
0
100
200
14
10
152
5
43
140
143
9
36
91
75
12
8
21
32
6
30
15
61
5
89
28
65
64
124
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4
probe
cluster
1
2
cluster
1
2
14 152 43 140 9 91 75 12 21 32 30 15 5 28 64
0 10 5 143 36 3 1 8 4 6 0 61 89 65 124
value
150
100
50
0
probe
age counts for each cluster
0
100
200
300
140
9
125
13
150
7
23
15
40
115
6
64
196
75
222
22
13
14
22
8
PD1+/ICOS+
PD1−/CXCR3−
PD1−/ICOS−
CP18
CP11
PD1+/CXCR3+
13−21
12−20
PD1+/ICOS−
ICOS+/PD1−
CP13
CXCR3+/PD1−
age
cluster
1
2
cluster
1
2
140 125 150 1 15 115 64 75 22 14 2 8
9 13 7 23 40 6 196 222 13 2 22 2
value
200
150
100
50
age


probe fractions for each cluster
1.00
0.75
0.50
0.25
0.00
1
0.94
0.06
0.9
0.1
0.49
0.51
0.2
0.8
0.97
0.99
0.6
0.4
0.84
0.16
0.84
0.16
1
0.2
0.8
0.05
0.95
0.3
0.7
0.34
0.66
probe_Healthy
probe_RAD1
probe_RAD2
probe_RAD3
probe_RAD4
probe_RAD5
probe_RAD6
probe_TEY3
probe_TEY6
probe_TEY8
probe_TEY14
probe_TNET1
probe_TNET2
probe_TNET3
probe_TNET4
probe
cluster
1
2

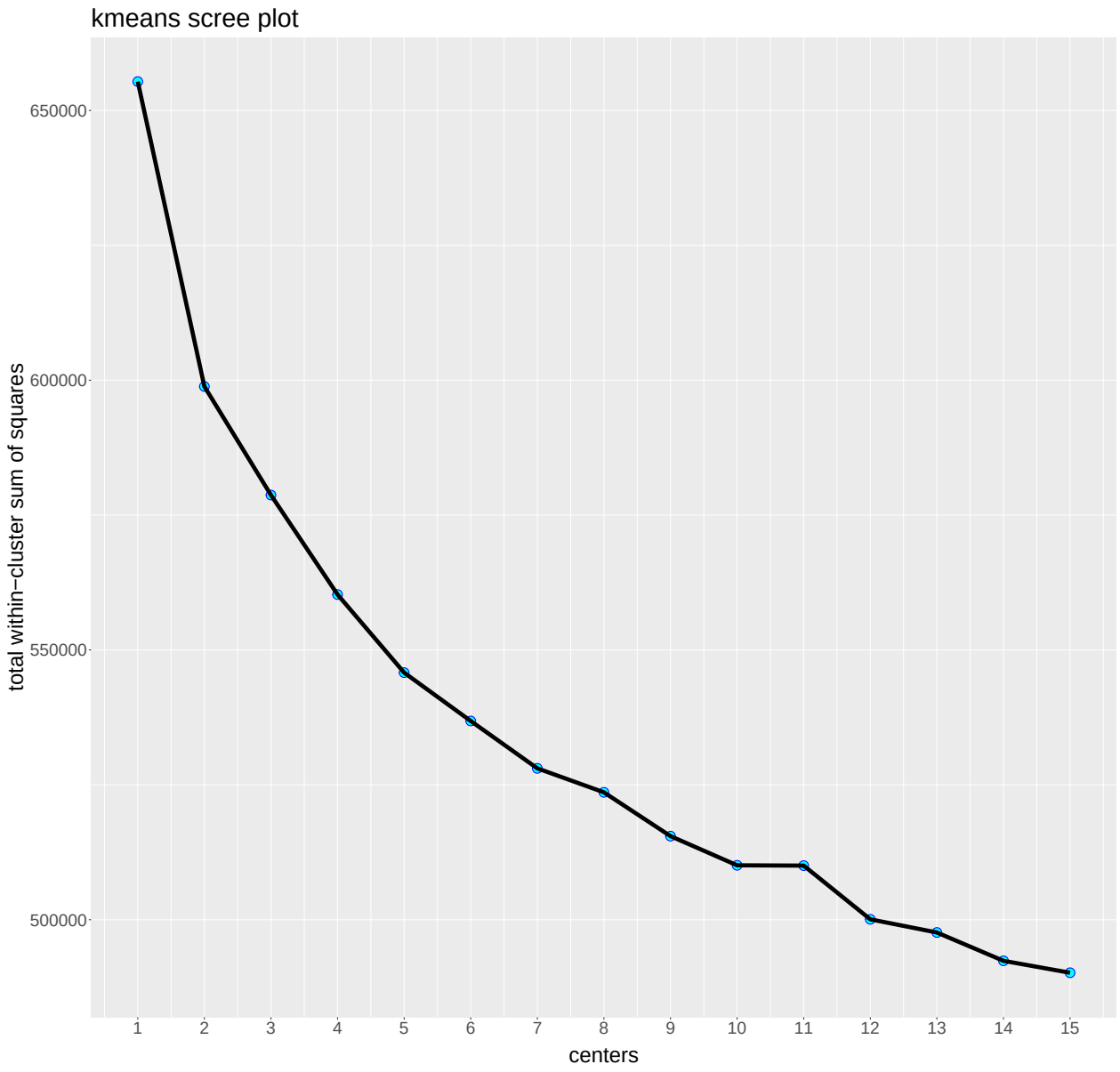

cluster_1
0.21
0.19
0.12
0.1
cluster_2
0.26
0.11
0.16
0.12
0.22
0.00
0.25
0.50
0.75
1.00
cluster fractions for each probe
probe
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4

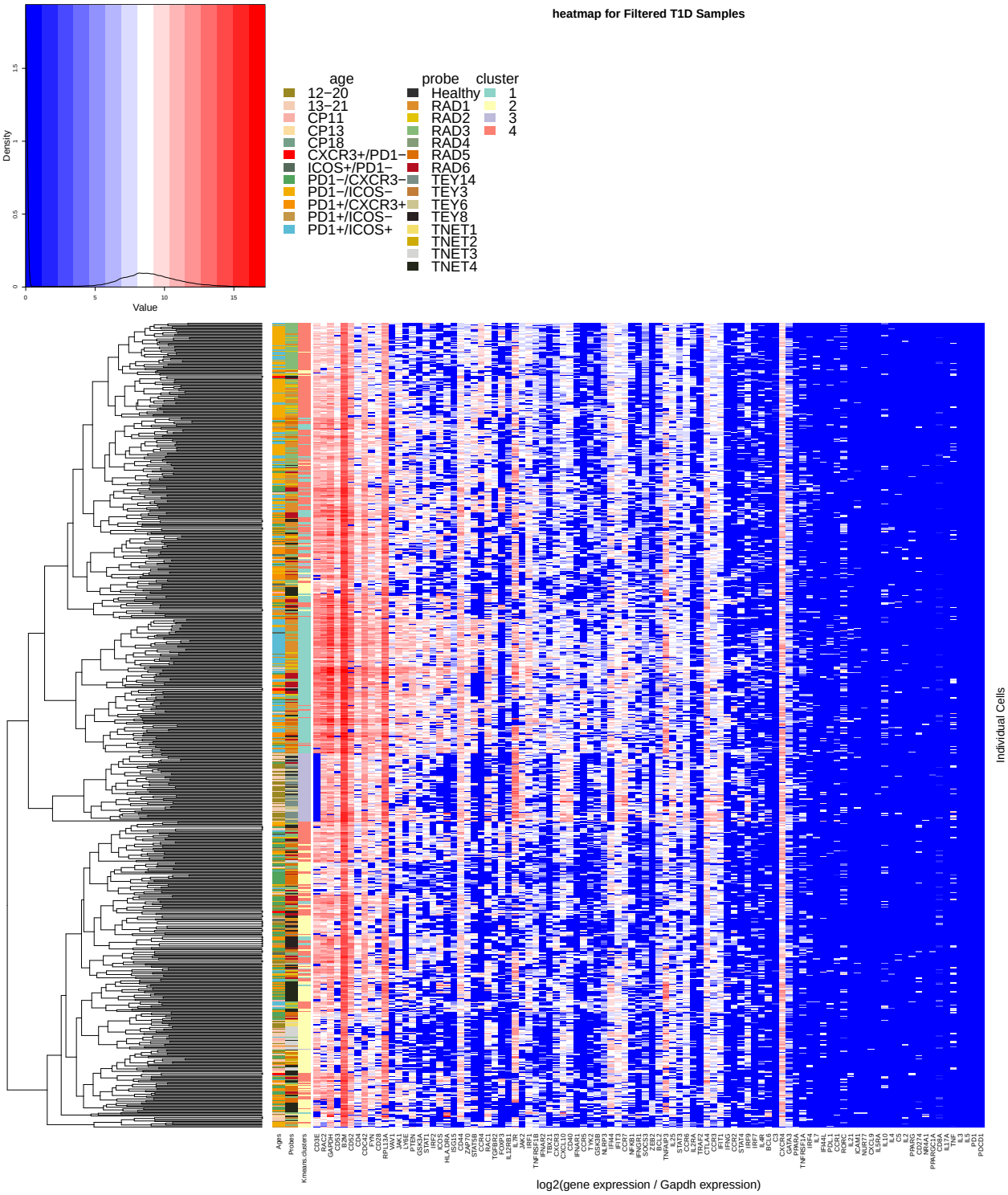

age fractions for each cluster
1.00
0.75
0.50
0.25
0.00
0.94
0.06
0.91
0.09
0.96
0.96
0.27
0.73
0.95
0.05
0.25
0.75
0.25
0.75
0.63
0.37
0.88
0.12
0.08
0.92
0.8
0.2
age_PD1+/ICOS+
age_PD1−/CXCR3−
age_PD1−/ICOS−
age_CP18
age_CP11
age_PD1+/CXCR3+
age_13−21
age_12−20
age_PD1+/ICOS−
age_ICOS+/PD1−
age_CP13
age_CXCR3+/PD1−
age
cluster
1
2


cluster_1
0.19
0.17
0.21
0.16
0.1
cluster_2
0.35
0.4
0.00
0.25
0.50
0.75
1.00
cluster fractions for each age
age
PD1+/ICOS+
PD1−/CXCR3−
PD1−/ICOS−
CP18
CP11
PD1+/CXCR3+
13−21
12−20
PD1+/ICOS−
ICOS+/PD1−
CP13
CXCR3+/PD1−




```
555 / 1286 cells were removed due to low gene expression (cluster ID of removed clusters: 2)
```


kmeans scree plot
650000
600000
550000
500000
total within−cluster sum of squares
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
centers

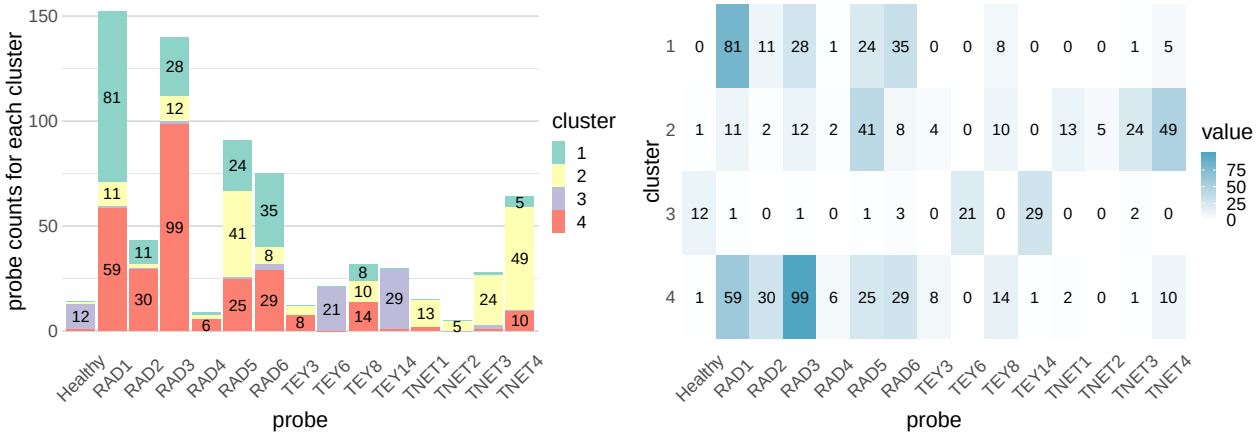


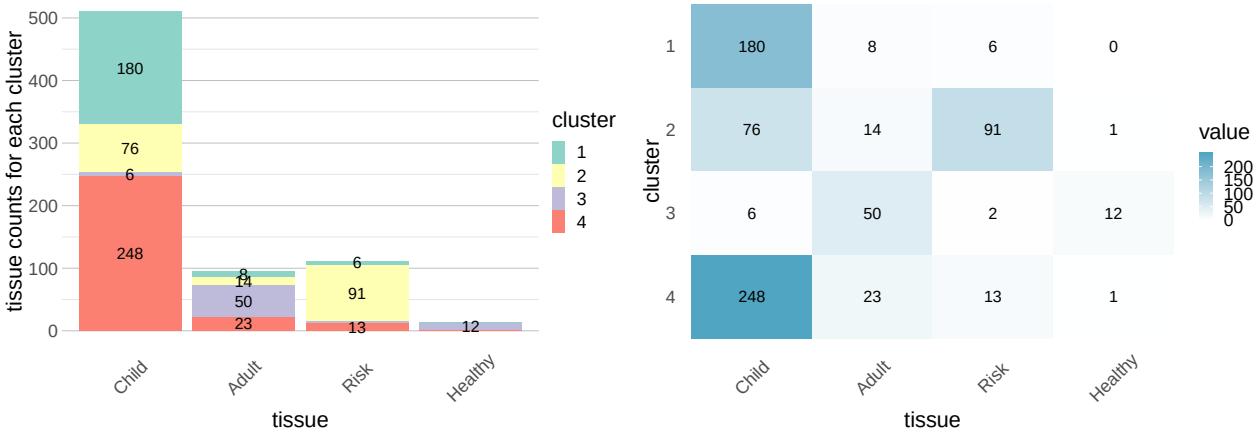

```
[1]
[1]
[1] Patient vs. Cluster
          probe_Healthy probe_RAD1 probe_RAD2 probe_RAD3 probe_RAD4
cluster_1             0         81         11         28          1
cluster_2             1         11          2         12          2
cluster_3            12          1          0          1          0
```

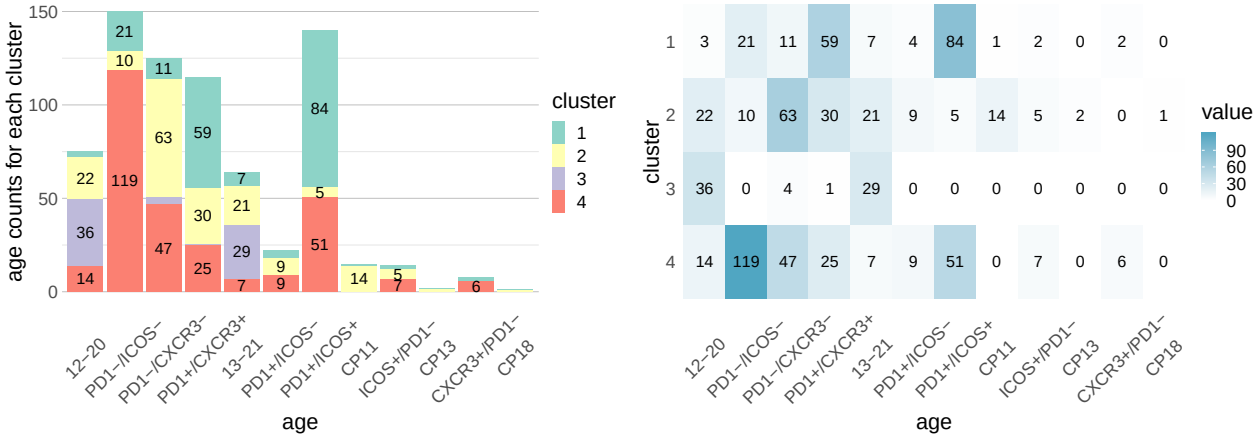
```
cluster_4             1         59         30         99          6
          probe_RAD5 probe_RAD6 probe_TEY3 probe_TEY6 probe_TEY8
cluster_1         24         35          0          0          8
cluster_2         41          8          4          0         10
cluster_3          1          3          0         21          0
cluster_4         25         29          8          0         14
          probe_TEY14 probe_TNET1 probe_TNET2 probe_TNET3 probe_TNET4
cluster_1           0           0           0           1           5
cluster_2           0          13           5          24          49
cluster_3          29           0           0           2           0
cluster_4           1           2           0           1          10

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

data:  probeTable
X-squared = 967.78, df = NA, p-value = 0.0004998

[1]
[1]
[1] Cohort vs. Cluster
          cellSource_Child cellSource_Adult cellSource_Risk
cluster_1              180               8              6
cluster_2               76              14             91
cluster_3                6              50              2
cluster_4              248              23             13
          cellSource_Healthy
cluster_1                  0
cluster_2                  1
cluster_3                 12
cluster_4                  1

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

data:  sourceTable
X-squared = 574.15, df = NA, p-value = 0.0004998

[1]
[1]
[1] Marker vs. Cluster
          age_12-20 age_PD1-/ICOS- age_PD1-/CXCR3- age_PD1+/CXCR3+
cluster_1         3             21              11              59
cluster_2        22             10              63              30
cluster_3        36              0               4               1
cluster_4        14            119              47              25
          age_13-21 age_PD1+/ICOS- age_PD1+/ICOS+ age_CP11 age_ICOS+/PD1-
cluster_1         7              4             84        1              2
cluster_2        21              9              5       14              5
cluster_3        29              0              0        0              0
cluster_4         7              9             51        0              7
          age_CP13 age_CXCR3+/PD1- age_CP18
cluster_1        0               2        0
cluster_2        2               0        1
```

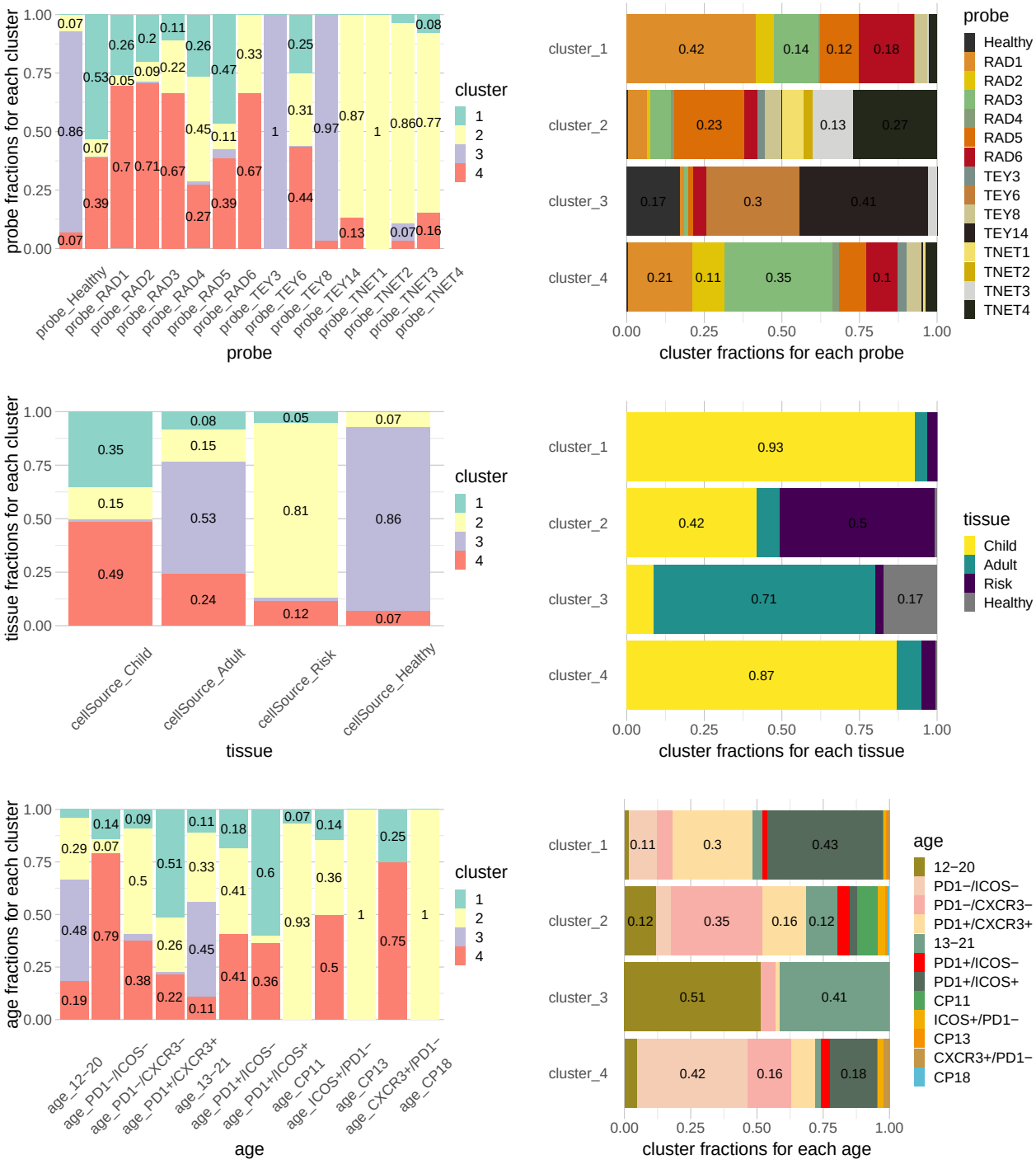
```
cluster_3        0               0        0
cluster_4        0               6        0
```

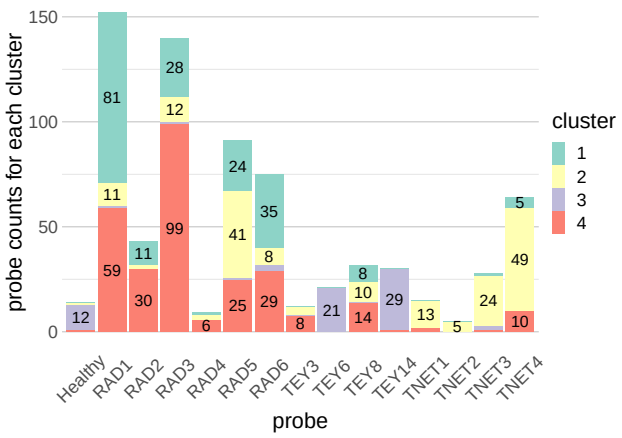
```
    Pearson's Chi-squared test with simulated p-value (based on 2000
    replicates)

data:  ageTable
X-squared = 606.23, df = NA, p-value = 0.0004998
```

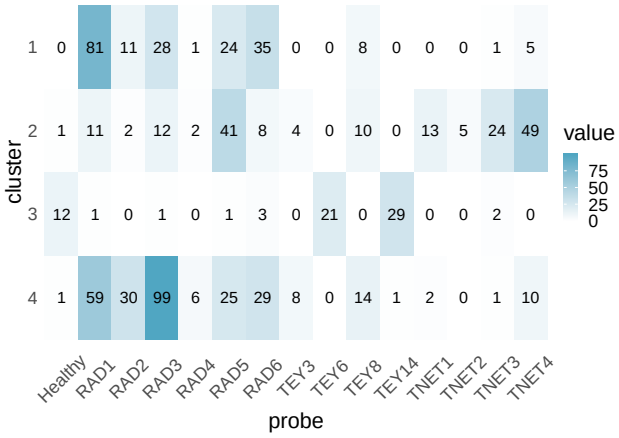


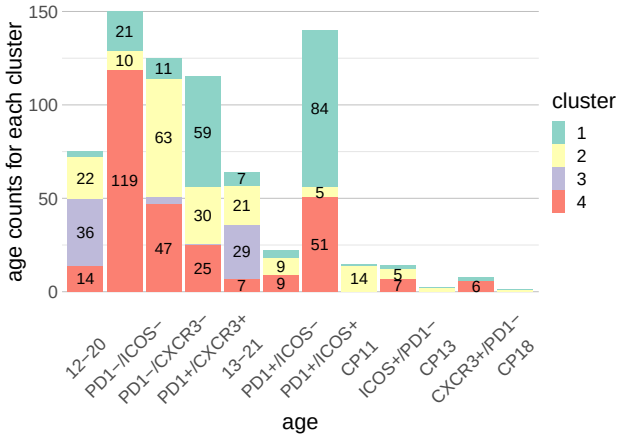



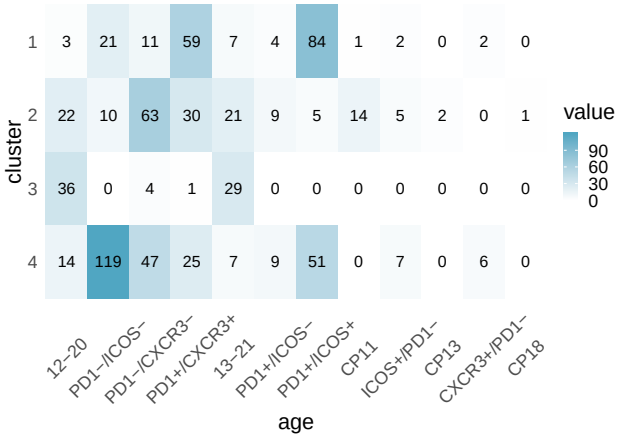



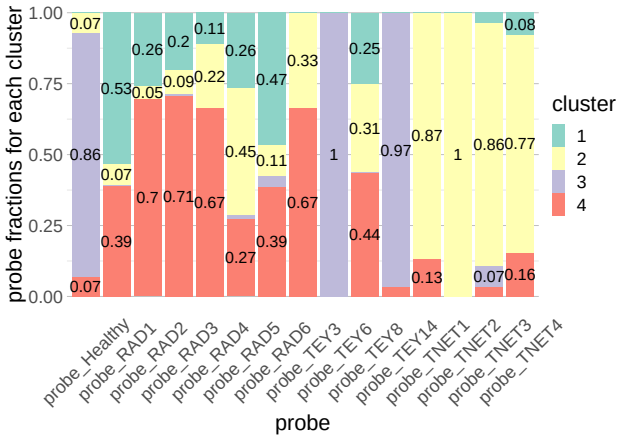

probe fractions for each cluster
probe
cluster
1
2
3
4
probe_Healthy
probe_RAD1
probe_RAD2
probe_RAD3
probe_RAD4
probe_RAD5
probe_RAD6
probe_TEY3
probe_TEY6
probe_TEY8
probe_TEY14
probe_TNET1
probe_TNET2
probe_TNET3
probe_TNET4
cluster fractions for each probe
probe
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4
cluster_1
cluster_2
cluster_3
cluster_4
tissue fractions for each cluster
tissue
cellSource_Child
cellSource_Adult
cellSource_Risk
cellSource_Healthy
cluster fractions for each tissue
tissue
Child
Adult
Risk
Healthy
age fractions for each cluster
age
age_12−20
age_PD1−/ICOS−
age_PD1−/CXCR3−
age_PD1+/CXCR3+
age_13−21
age_PD1+/ICOS−
age_PD1+/ICOS+
age_CP11
age_ICOS+/PD1−
age_CP13
age_CXCR3+/PD1−
age_CP18
cluster fractions for each age
age
12−20
PD1−/ICOS−
PD1−/CXCR3−
PD1+/CXCR3+
13−21
PD1+/ICOS−
PD1+/ICOS+
CP11
ICOS+/PD1−
CP13
CXCR3+/PD1−
CP18

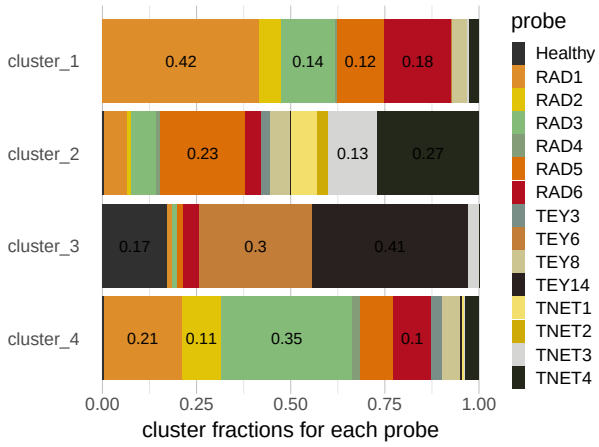

probe counts for each cluster
150
100
50
0
81
11
59
30
28
12
99
11
6
24
41
25
35
8
29
8
21
8
10
14
29
13
5
24
5
49
10
12
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4
probe
cluster
1
2
3
4

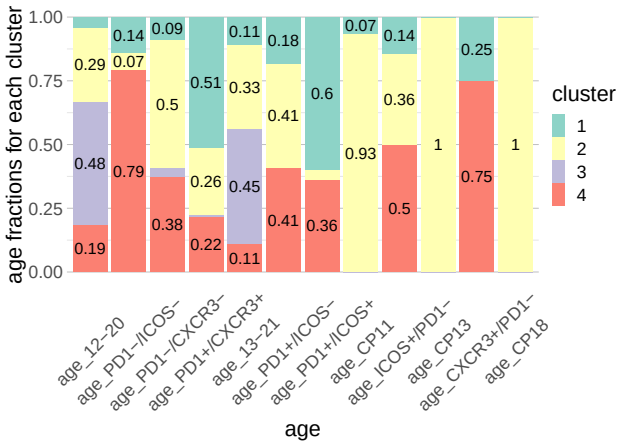

cluster
1 0 81 11 28 1 24 35 0 0 8 0 0 0 1 5
2 1 11 2 12 2 41 8 4 0 10 0 13 5 24 49
3 12 1 0 1 0 1 3 0 21 0 29 0 0 2 0
4 1 59 30 99 6 25 29 8 0 14 1 2 0 1 10
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4
probe
value
75
50
25
0

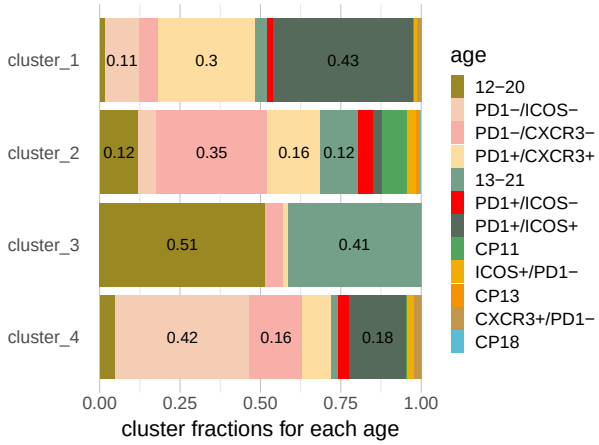

age counts for each cluster
150
100
50
0
22
36
14
21
10
119
11
63
47
59
30
25
7
21
29
7
9
9
84
5
51
14
5
7
6
12–20
PD1−/ICOS−
PD1−/CXCR3−
PD1+/CXCR3+
13–21
PD1+/ICOS−
PD1+/ICOS+
CP11
ICOS+/PD1−
CP13
CXCR3+/PD1−
CP18
age
cluster
1
2
3
4

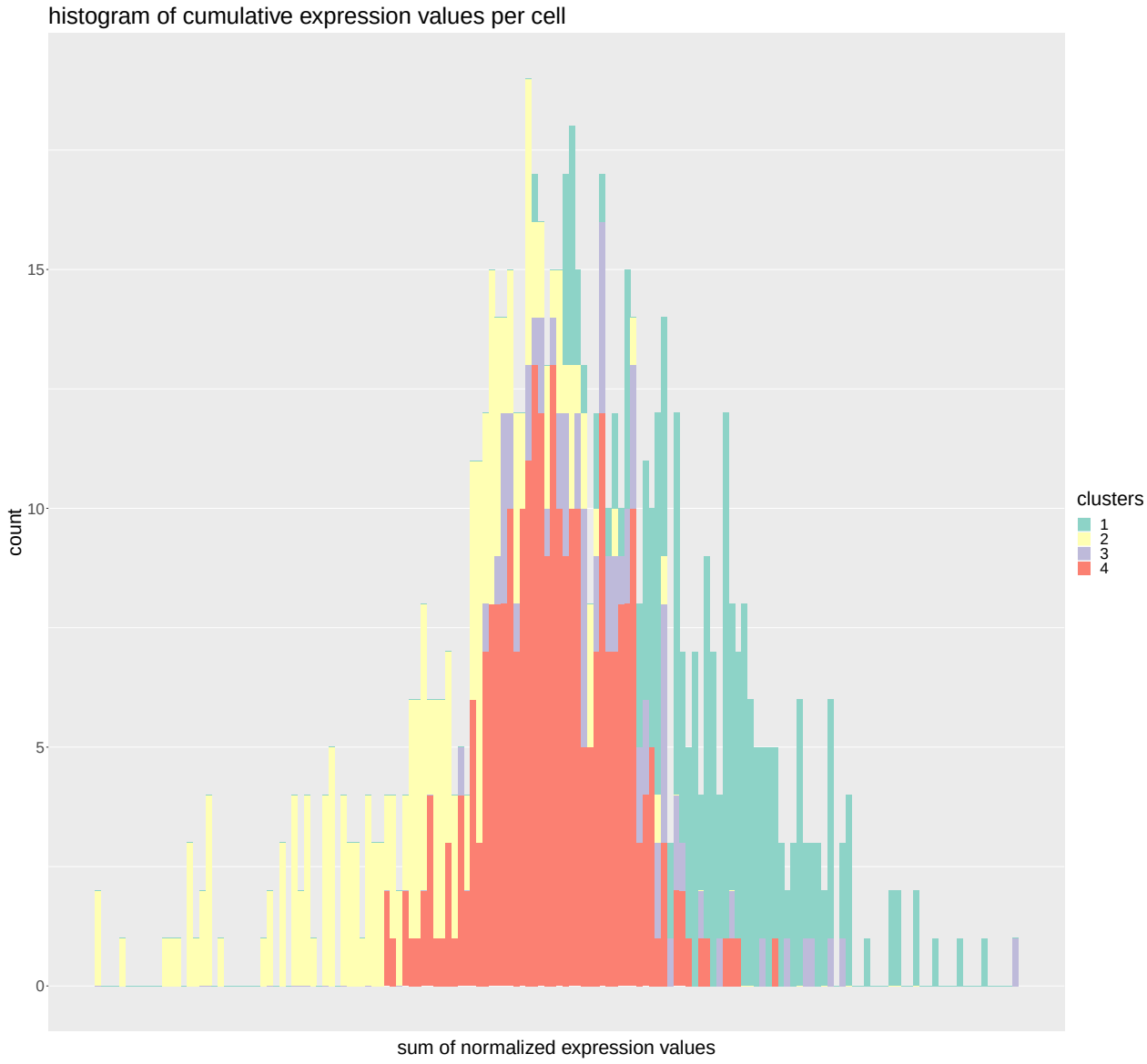

cluster
1 3 21 11 59 7 4 84 1 2 0 2 0
2 22 10 63 30 21 9 5 14 5 2 0 1
3 36 0 4 1 29 0 0 0 0 0 0 0
4 14 119 47 25 7 9 51 0 7 0 6 0
12–20
PD1−/ICOS−
PD1−/CXCR3−
PD1+/CXCR3+
13–21
PD1+/ICOS−
PD1+/ICOS+
CP11
ICOS+/PD1−
CP13
CXCR3+/PD1−
CP18
age
value
90
60
30
0


probe fractions for each cluster
1.00
0.75
0.50
0.25
0.00
probe_Healthy
probe_RAD1
probe_RAD2
probe_RAD3
probe_RAD4
probe_RAD5
probe_RAD6
probe_TEY3
probe_TEY6
probe_TEY8
probe_TEY14
probe_TNET1
probe_TNET2
probe_TNET3
probe_TNET4
probe
cluster
1
2
3
4


cluster_1
cluster_2
cluster_3
cluster_4
0.42
0.14
0.12
0.18
0.23
0.13
0.27
0.17
0.3
0.41
0.21
0.11
0.35
0.1
0.00
0.25
0.50
0.75
1.00
cluster fractions for each probe
probe
Healthy
RAD1
RAD2
RAD3
RAD4
RAD5
RAD6
TEY3
TEY6
TEY8
TEY14
TNET1
TNET2
TNET3
TNET4

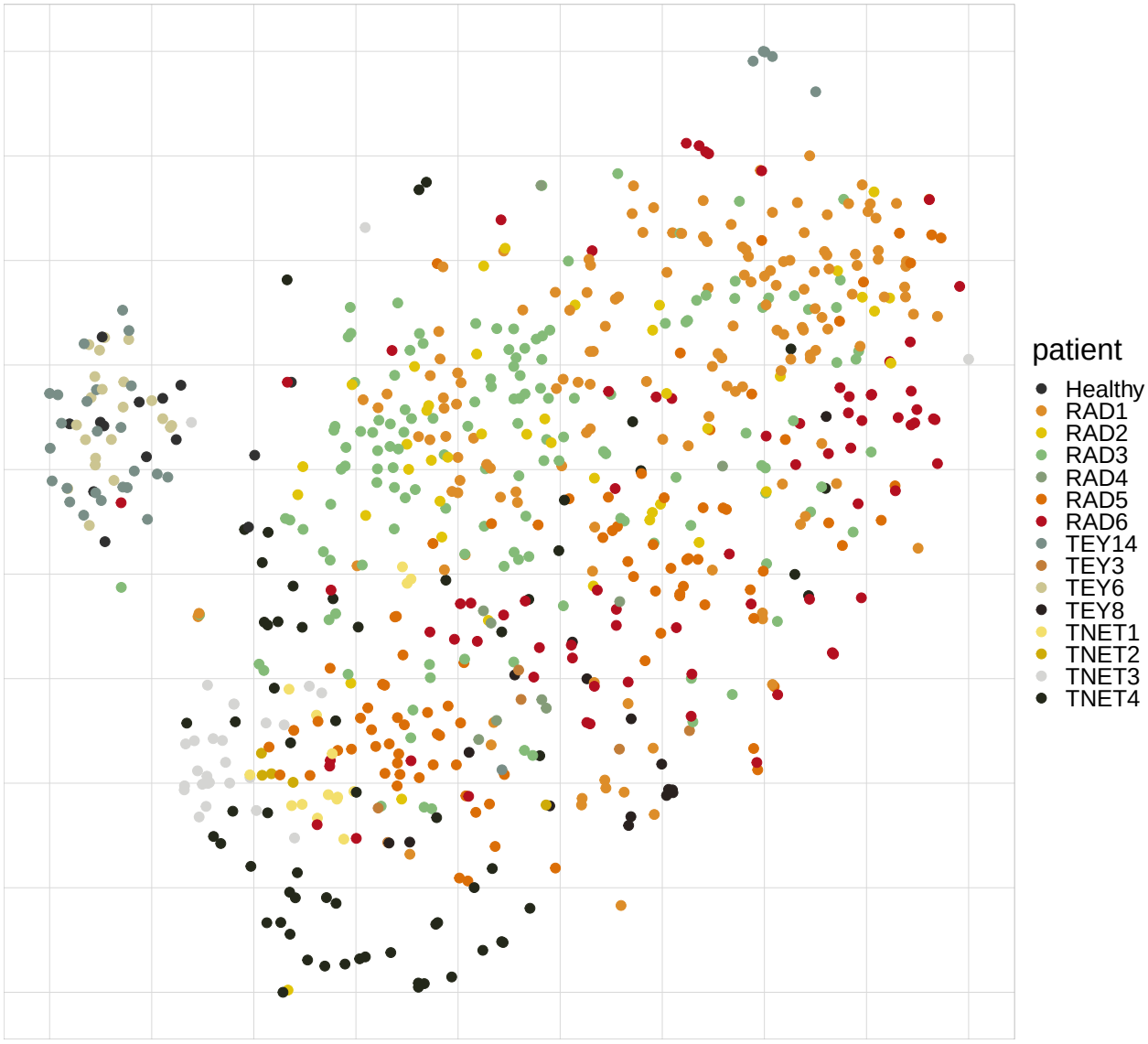

age fractions for each cluster
1.00
0.75
0.50
0.25
0.00
age_12−20
age_PD1−/ICOS−
age_PD1−/CXCR3−
age_PD1+/CXCR3+
age_13−21
age_PD1+/ICOS−
age_PD1+/ICOS+
age_CP11
age_ICOS+/PD1−
age_CP13
age_CXCR3+/PD1−
age_CP18
age
cluster
1
2
3
4


cluster_1
cluster_2
cluster_3
cluster_4
0.11
0.3
0.43
0.12
0.35
0.16
0.12
0.51
0.41
0.42
0.16
0.18
0.00
0.25
0.50
0.75
1.00
cluster fractions for each age
age
12−20
PD1−/ICOS−
PD1−/CXCR3−
PD1+/CXCR3+
13−21
PD1+/ICOS−
PD1+/ICOS+
CP11
ICOS+/PD1−
CP13
CXCR3+/PD1−
CP18

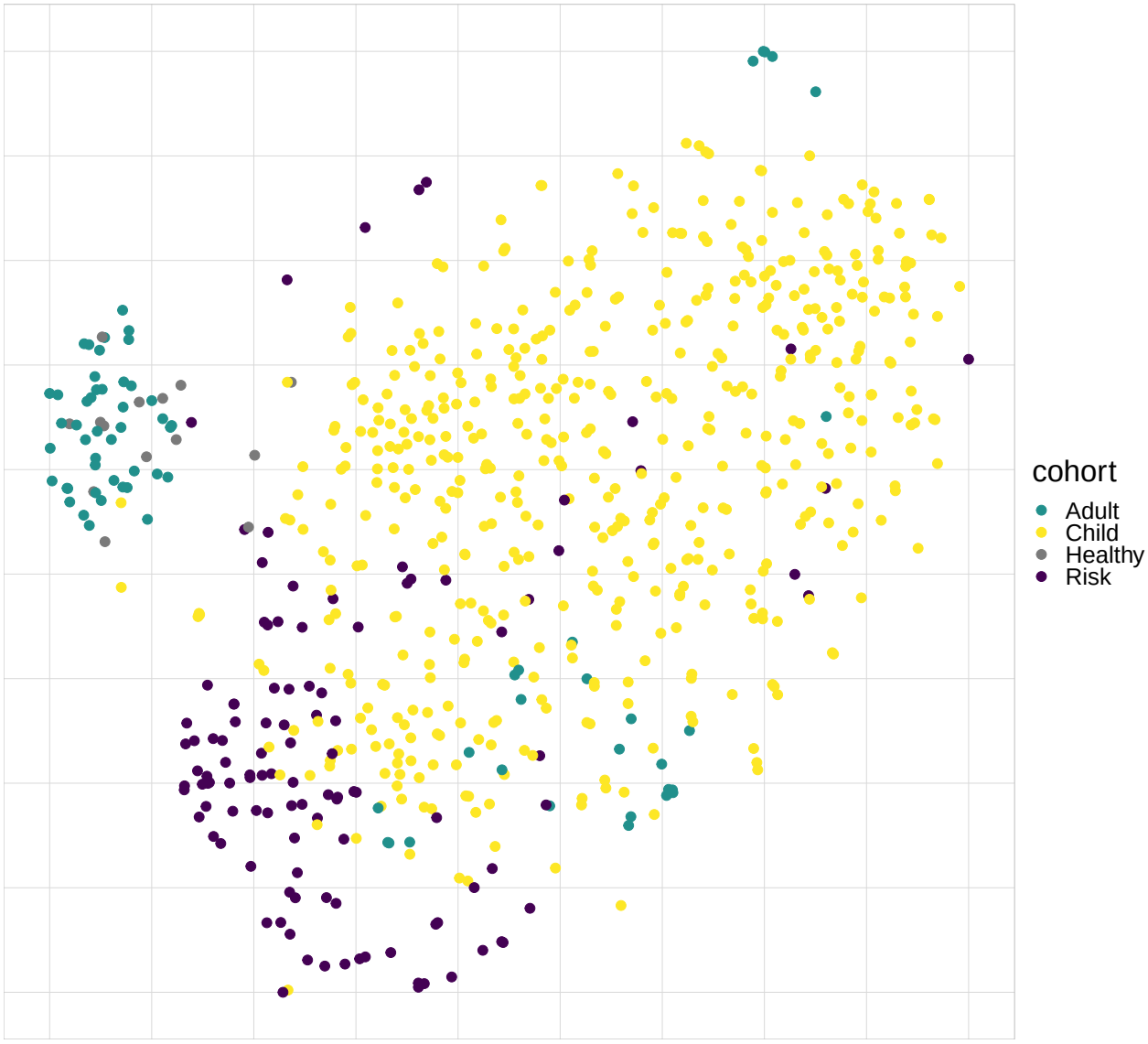

histogram of cumulative expression values per cell
count
15
10
5
0
sum of normalized expression values
clusters
1
2
3
4

t−SNE colored by kmeans.cluster

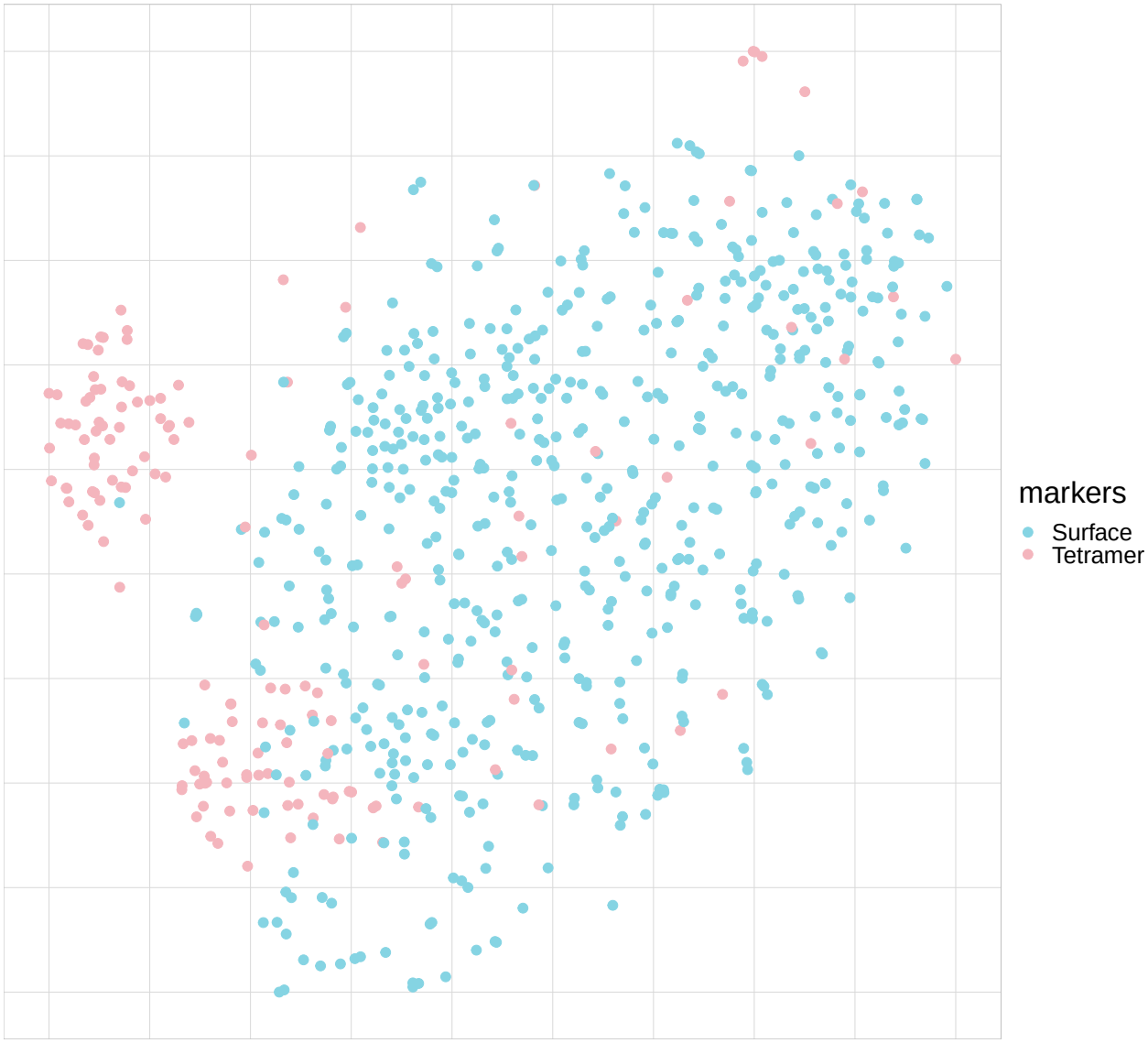
t−SNE colored by different patients



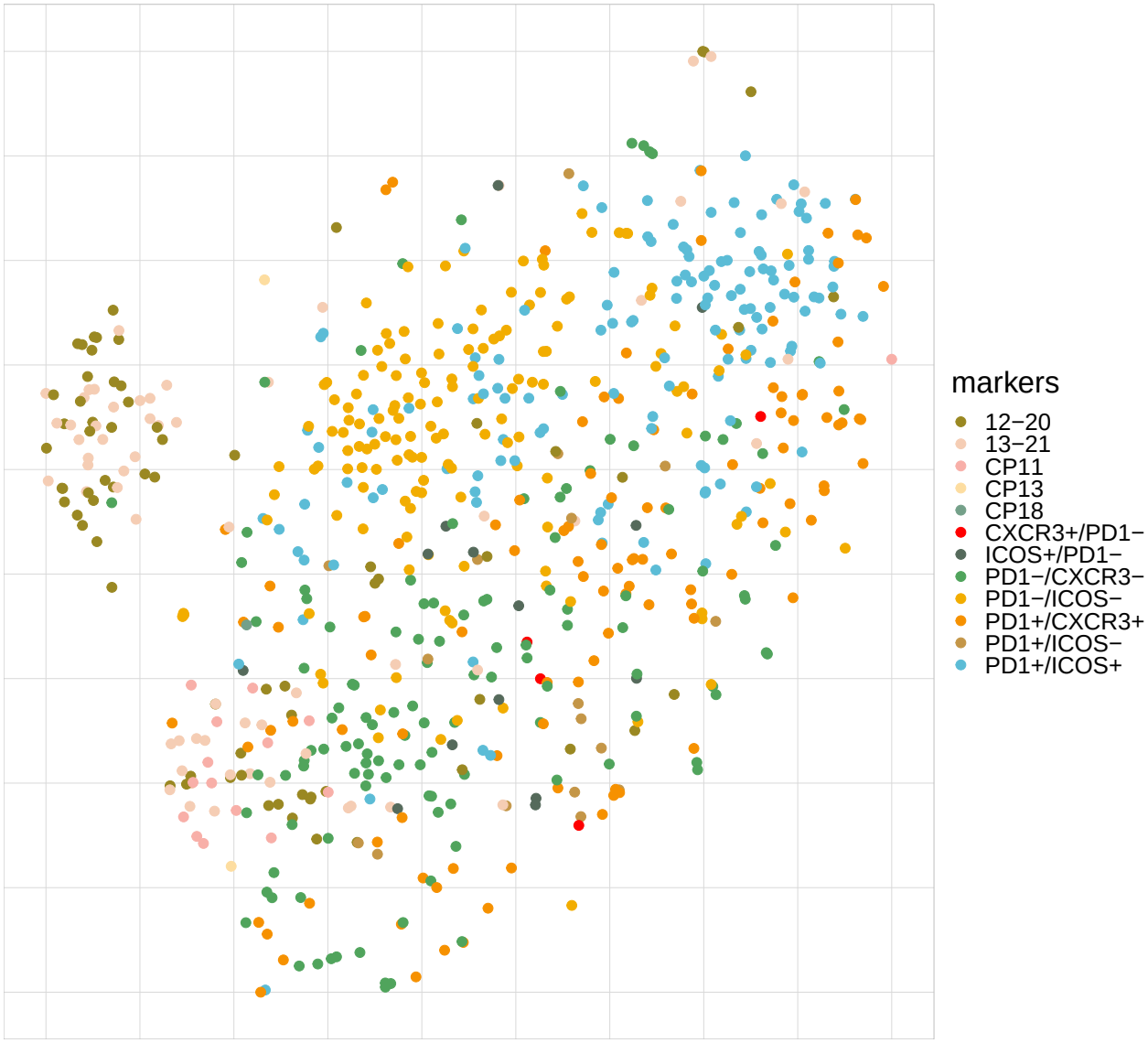
t−SNE colored by patient cohorts



t−SNE colored by different types of markers

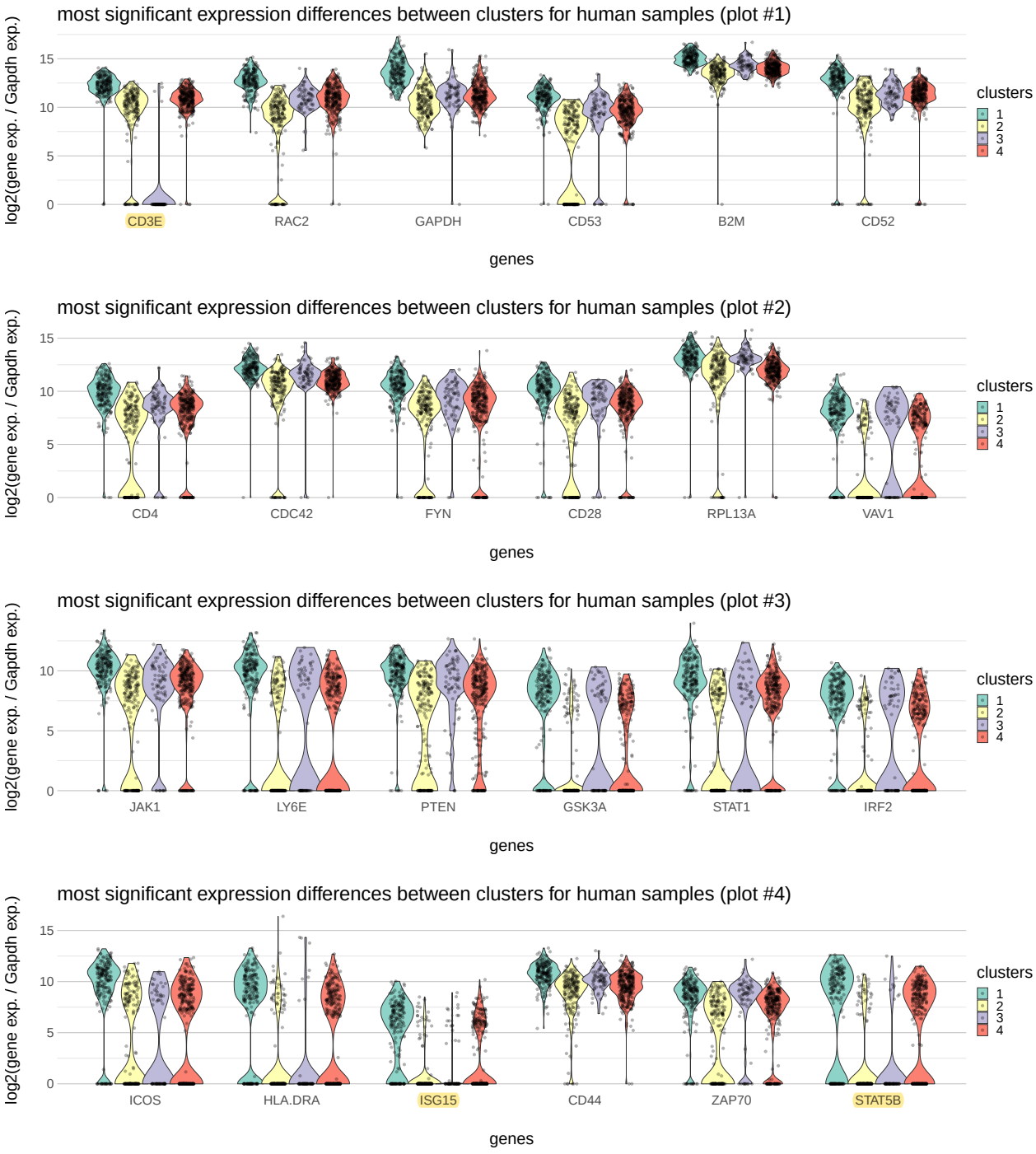


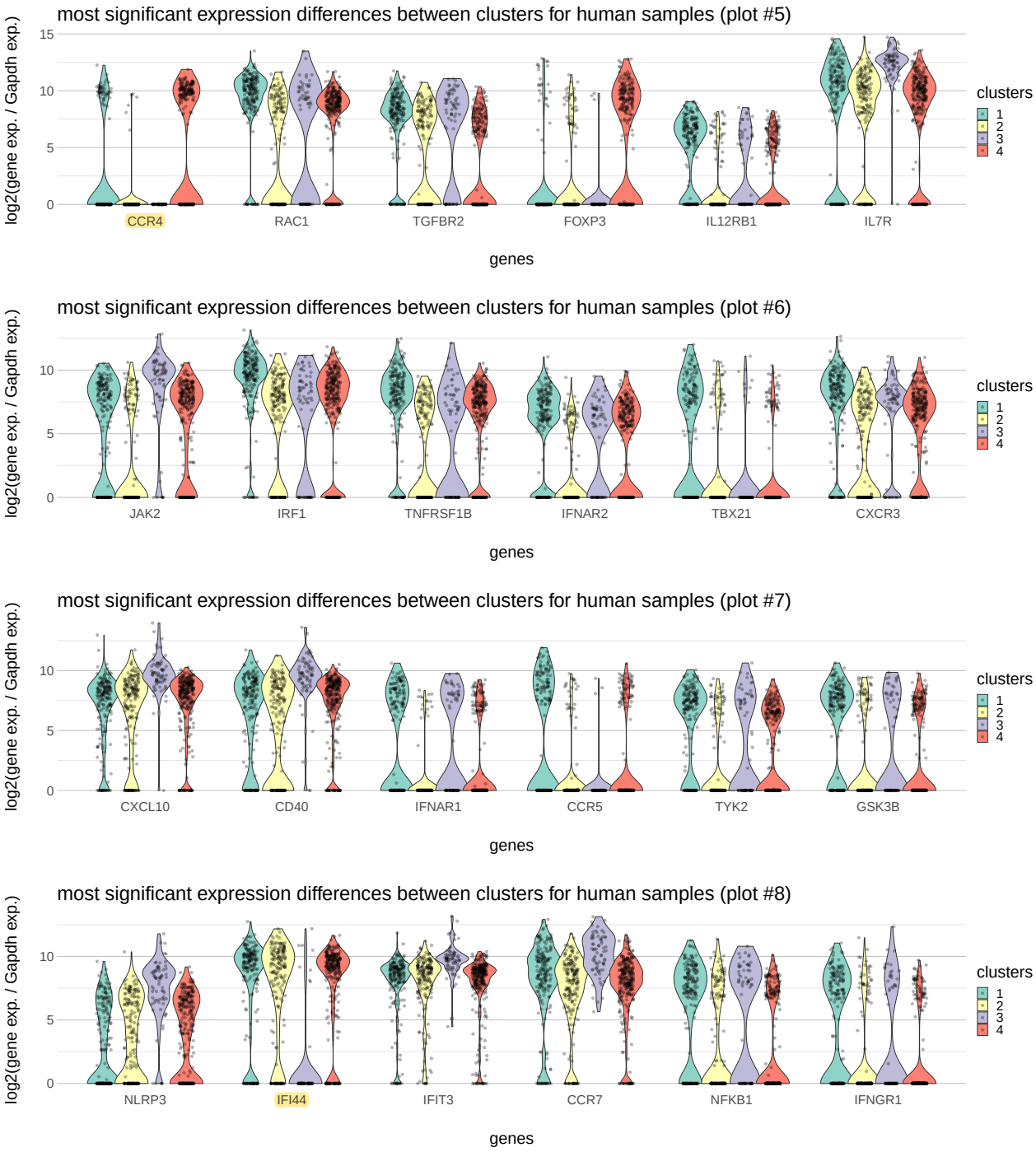
t−SNE colored by different markers

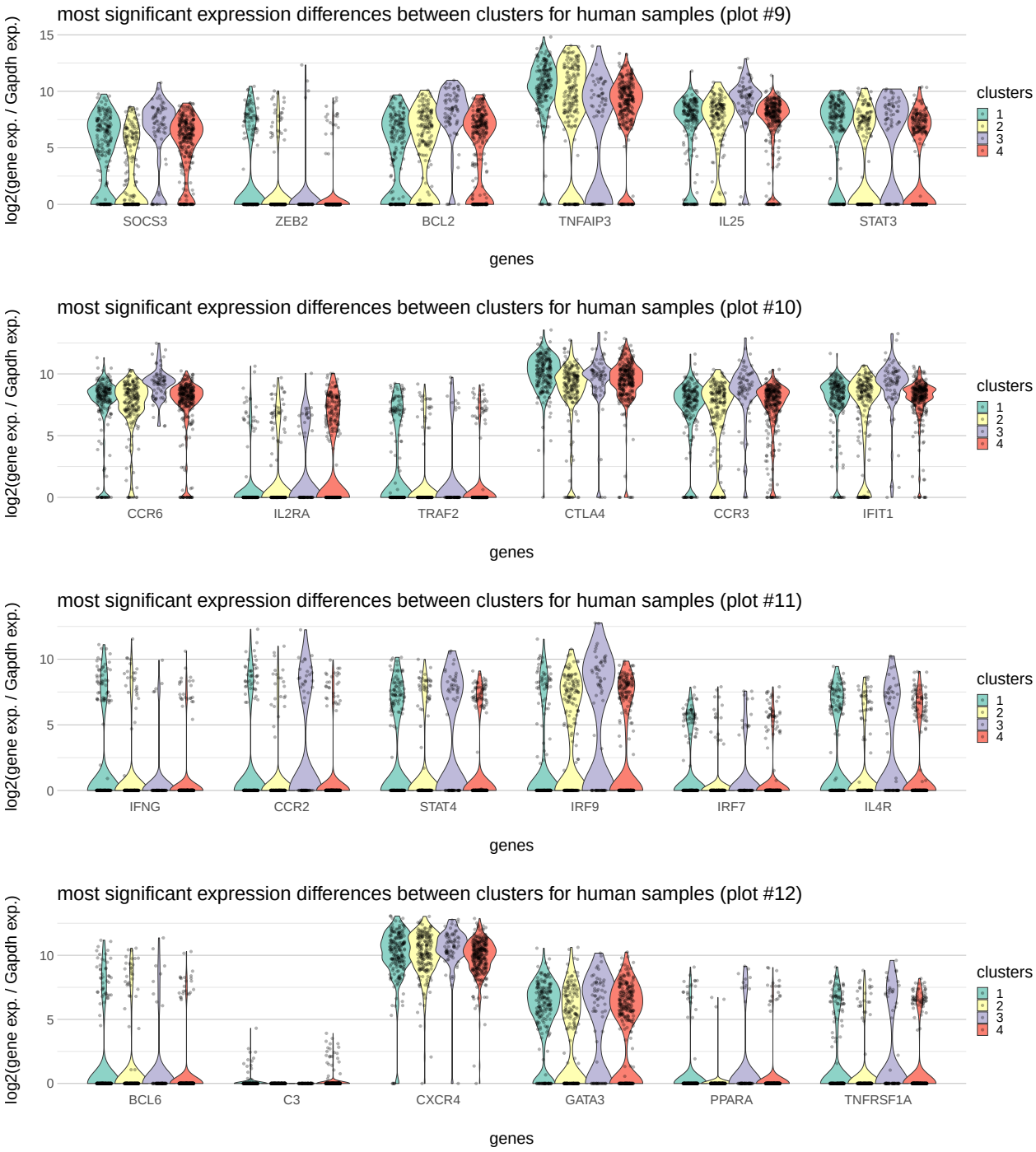


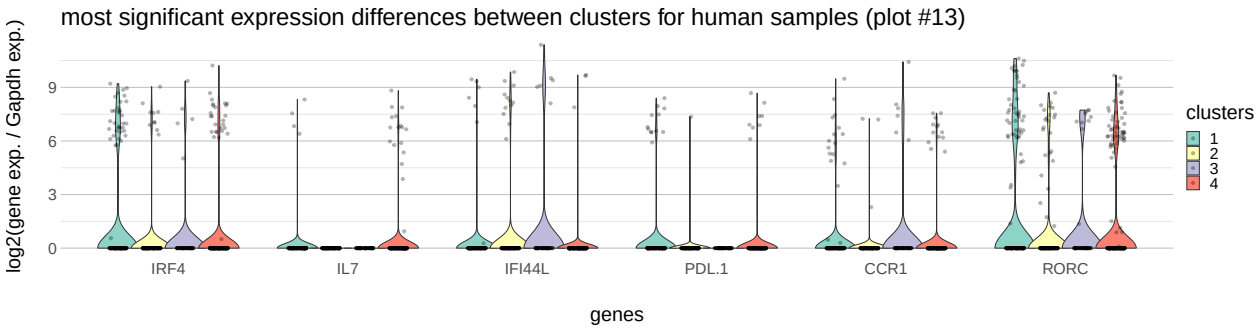

```
[1] Differentially expressed genes between clusters for human samples:
 [1] CD3E: 1.705e-78     RAC2: 2.047e-73     GAPDH: 3.469e-67
 [4] CD53: 4.727e-62     B2M: 1.146e-59      CD52: 9.399e-56
 [7] CD4: 1.985e-49      CDC42: 1.258e-48    FYN: 3.676e-44
[10] CD28: 1.376e-43     RPL13A: 1.599e-42   VAV1: 1.319e-41
[13] JAK1: 8.245e-40     LY6E: 1.65e-39      PTEN: 6.094e-37
[16] GSK3A: 6.88e-37     STAT1: 5.829e-36    IRF2: 5.006e-35
[19] ICOS: 8.374e-35     HLA.DRA: 1.072e-34  ISG15: 2.045e-34
[22] CD44: 1.567e-33     ZAP70: 4.435e-33    STAT5B: 2.905e-32
[25] CCR4: 5.321e-31     RAC1: 8.806e-31     TGFBR2: 9.311e-31
[28] FOXP3: 1.608e-30    IL12RB1: 3.323e-28  IL7R: 8.738e-28
[31] JAK2: 9.679e-28     IRF1: 3.508e-27     TNFRSF1B: 5.728e-27
[34] IFNAR2: 5.873e-25   TBX21: 1.364e-23    CXCR3: 1.248e-22
[37] CXCL10: 2.554e-21   CD40: 3.939e-21     IFNAR1: 5.235e-21
[40] CCR5: 1.535e-20     TYK2: 2.531e-20     GSK3B: 2.77e-20
[43] NLRP3: 1.281e-19    IFI44: 2.892e-19    IFIT3: 2.954e-18
```

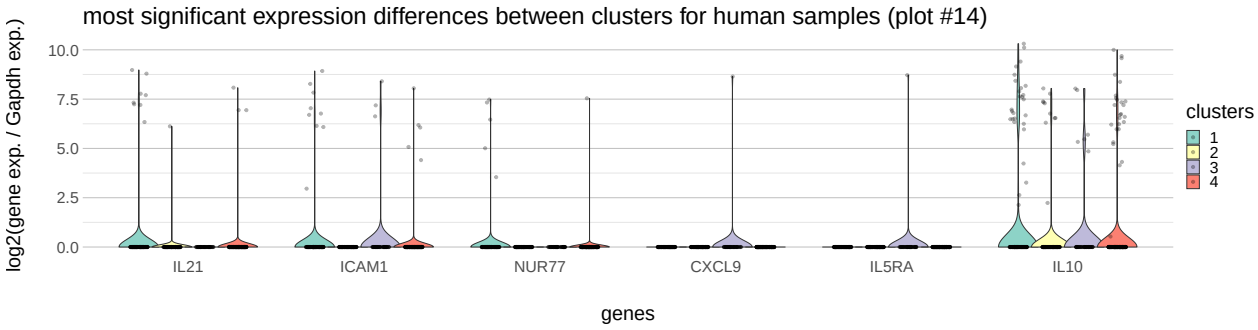
```
[46] CCR7: 3.111e-18     NFKB1: 2.327e-17    IFNGR1: 5.603e-17
[49] SOCS3: 6.359e-17    ZEB2: 2.782e-16     BCL2: 3.571e-16
[52] TNFAIP3: 2.572e-15  IL25: 8.536e-15     STAT3: 1.657e-14
[55] CCR6: 3.986e-14     IL2RA: 1.206e-13    TRAF2: 2.275e-11
[58] CTLA4: 2.87e-11     CCR3: 5.978e-11     IFIT1: 6.719e-11
[61] IFNG: 3.836e-09     CCR2: 6.39e-08      STAT4: 2.465e-07
[64] IRF9: 6.555e-07     IRF7: 1.005e-05     IL4R: 2.415e-05
[67] BCL6: 2.836e-05     C3: 6.957e-05       CXCR4: 6.957e-05
[70] GATA3: 0.0001186    PPARA: 0.0001369    TNFRSF1A: 0.0001578
[73] IRF4: 0.0006577     IL7: 0.0006947      IFI44L: 0.003539
[76] PDL.1: 0.005404     CCR1: 0.01362       RORC: 0.01552
[79] IL21: 0.01672       ICAM1: 0.01672      NUR77: 0.02002
[82] CXCL9: 0.02712      IL5RA: 0.02712      IL10: 0.04623
```

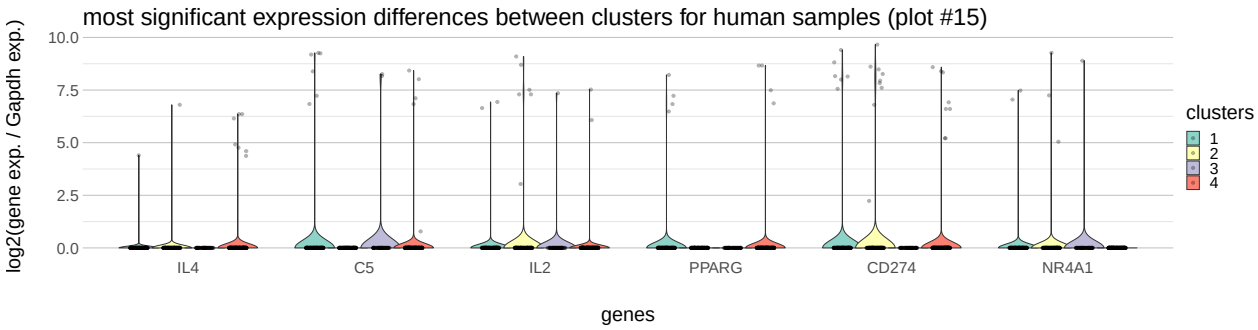

most significant expression differences between clusters for human samples (plot #1)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CD3E
RAC2
GAPDH
CD53
B2M
CD52
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #2)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CD4
CDC42
FYN
CD28
RPL13A
VAV1
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #3)
log2(gene exp. / Gapdh exp.)
10
5
0
JAK1
LY6E
PTEN
GSK3A
STAT1
IRF2
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #4)
log2(gene exp. / Gapdh exp.)
15
10
5
0
ICOS
HLA.DRA
ISG15
CD44
ZAP70
STAT5B
genes
clusters
1
2
3
4

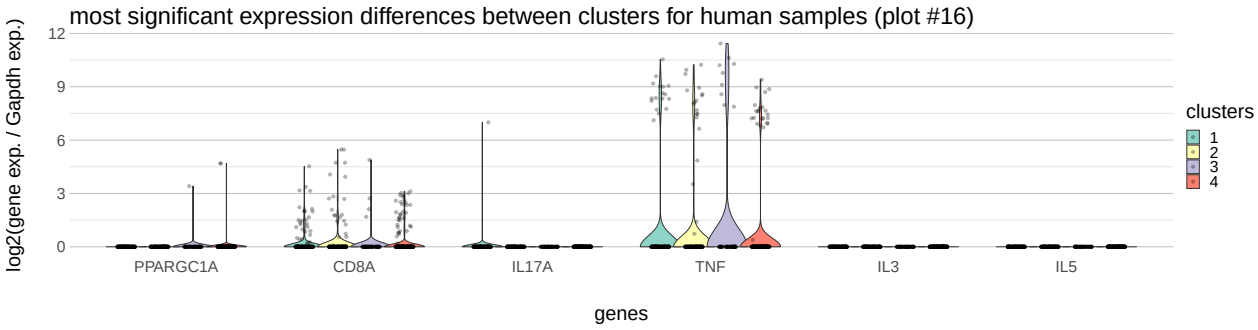

most significant expression differences between clusters for human samples (plot #5)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CCR4
RAC1
TGFBR2
FOXP3
IL12RB1
IL7R
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #6)
log2(gene exp. / Gapdh exp.)
10
5
0
JAK2
IRF1
TNFRSF1B
IFNAR2
TBX21
CXCR3
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #7)
log2(gene exp. / Gapdh exp.)
10
5
0
CXCL10
CD40
IFNAR1
CCR5
TYK2
GSK3B
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #8)
log2(gene exp. / Gapdh exp.)
10
5
0
NLRP3
IFI44
IFIT3
CCR7
NFKB1
IFNGR1
genes
clusters
1
2
3
4


most significant expression differences between clusters for human samples (plot #9)
log2(gene exp. / Gapdh exp.)
15
10
5
0
SOCS3
ZEB2
BCL2
TNFAIP3
IL25
STAT3
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #10)
log2(gene exp. / Gapdh exp.)
10
5
0
CCR6
IL2RA
TRAF2
CTLA4
CCR3
IFIT1
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #11)
log2(gene exp. / Gapdh exp.)
10
5
0
IFNG
CCR2
STAT4
IRF9
IRF7
IL4R
genes
clusters
1
2
3
4
most significant expression differences between clusters for human samples (plot #12)
log2(gene exp. / Gapdh exp.)
10
5
0
BCL6
C3
CXCR4
GATA3
PPARA
TNFRSF1A
genes
clusters
1
2
3
4



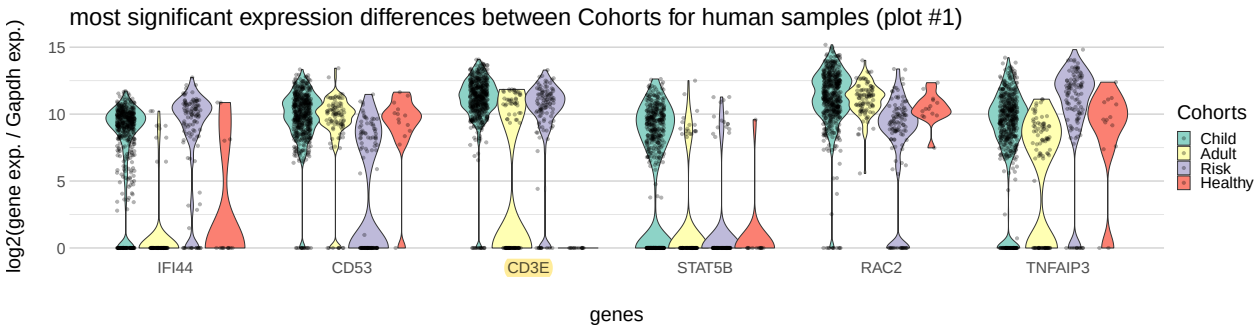



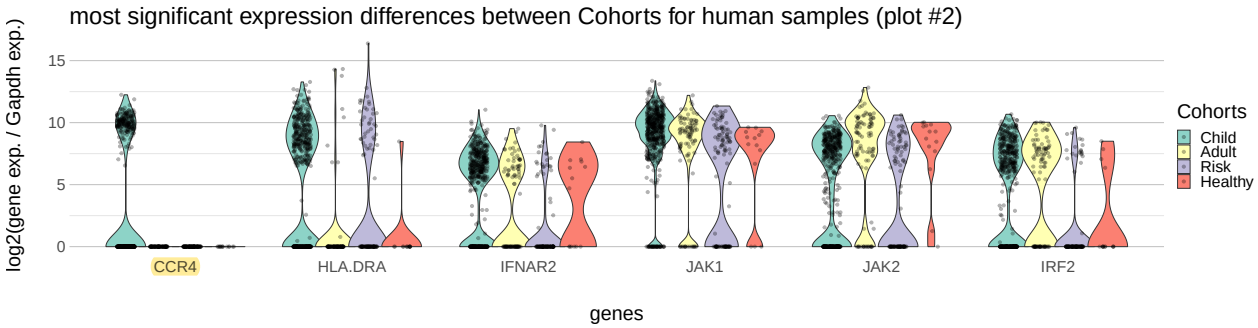



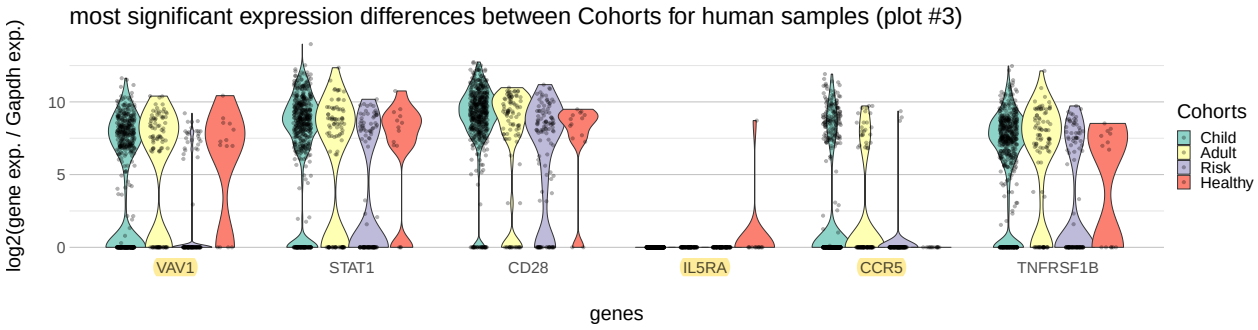



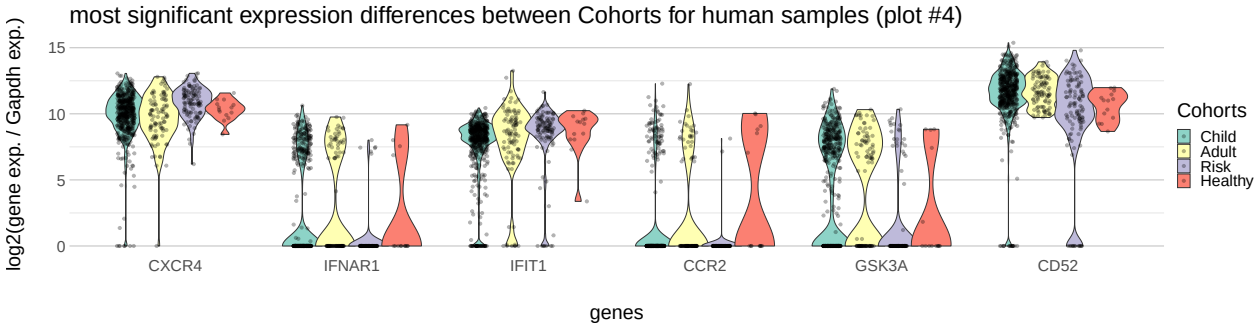

```
[1] Differentially expressed genes between Cohorts for human samples:
 [1] IFI44: 1.788e-35    CD53: 1.046e-31     CD3E: 6.064e-28
 [4] STAT5B: 9.982e-25   RAC2: 1.534e-24     TNFAIP3: 5.748e-23
 [7] CCR4: 7.084e-23     HLA.DRA: 5.297e-17  IFNAR2: 3.594e-13
[10] JAK1: 6.573e-13     JAK2: 8.796e-13     IRF2: 2.035e-12
[13] VAV1: 2.159e-11     STAT1: 3.59e-11     CD28: 4.329e-11
[16] IL5RA: 2.587e-10    CCR5: 2.199e-09     TNFRSF1B: 3.617e-09
[19] CXCR4: 7.742e-09    IFNAR1: 1.211e-08   IFIT1: 1.329e-08
[22] CCR2: 3.237e-08     GSK3A: 3.4e-08      CD52: 3.857e-08
[25] LY6E: 1.013e-07     BCL2: 1.647e-07     ISG15: 2.759e-07
```

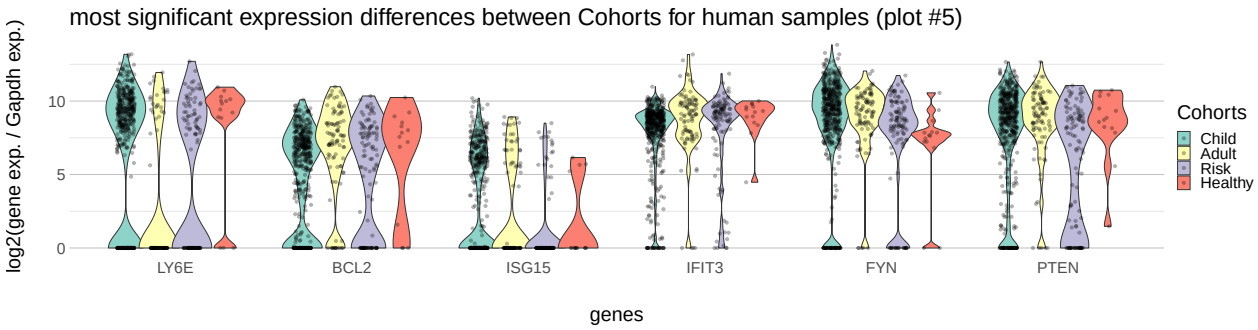
```
[28] IFIT3: 2.823e-07    FYN: 1.028e-06      PTEN: 1.632e-06
[31] FOXP3: 1.632e-06    IL7R: 6.206e-06     ZAP70: 1.667e-05
[34] NLRP3: 2.351e-05    CXCL10: 2.453e-05   SOCS3: 3.471e-05
[37] TNFRSF1A: 3.7e-05   PPARGC1A: 4.488e-05 BCL6: 7.433e-05
[40] ICOS: 8.929e-05     CD4: 9.405e-05      CD40: 0.0002526
[43] GAPDH: 0.0002728    PPARA: 0.0005246    C3: 0.0007997
[46] B2M: 0.0009622      IRF1: 0.001067      IRF9: 0.001067
[49] IL25: 0.004051      RPL13A: 0.005001    IL12RB1: 0.008475
[52] NR4A1: 0.008475     IL2RA: 0.01098      CD274: 0.01292
[55] CCR6: 0.01958       IRF7: 0.02546       IFI44L: 0.02546
[58] TRAF2: 0.03125      GSK3B: 0.03843      IL7: 0.03843
[61] PDL.1: 0.03843      RORC: 0.04007       RAC1: 0.04905
```

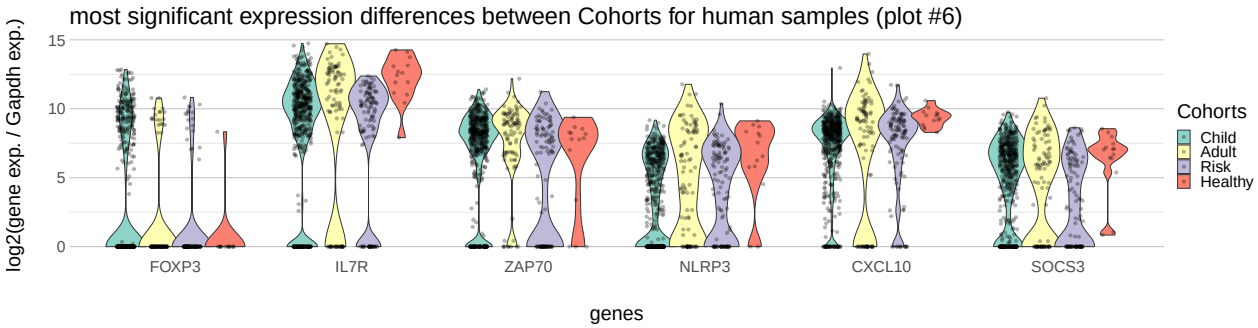

most significant expression differences between Cohorts for human samples (plot #1)
log2(gene exp. / Gapdh exp.)
15
10
5
0
IFI44
CD53
CD3E
STAT5B
RAC2
TNFAIP3
genes
Cohorts
Child
Adult
Risk
Healthy

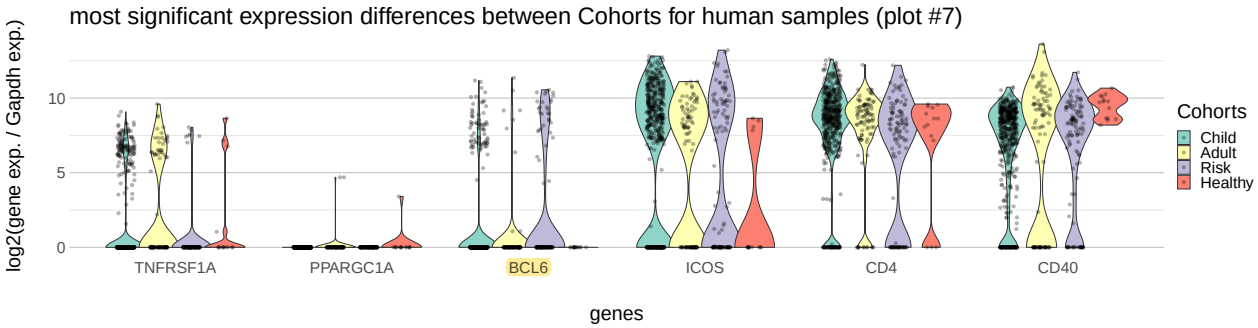

most significant expression differences between Cohorts for human samples (plot #2)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CCR4
HLA.DRA
IFNAR2
JAK1
JAK2
IRF2
genes
Cohorts
Child
Adult
Risk
Healthy

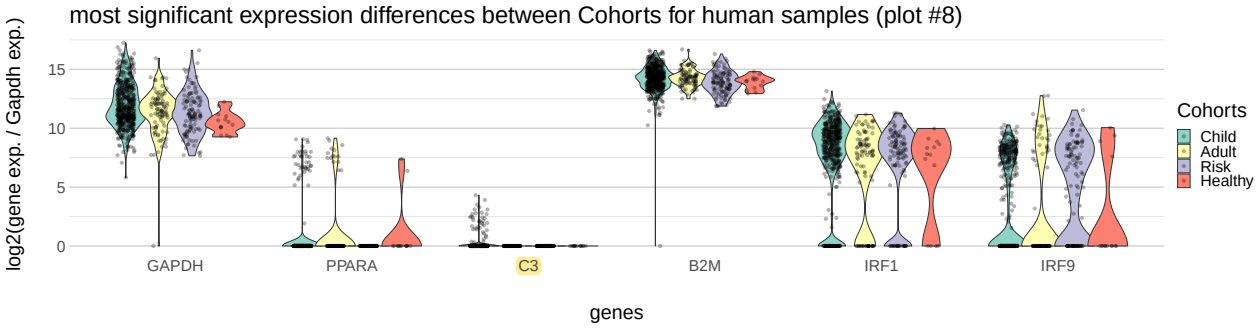

most significant expression differences between Cohorts for human samples (plot #3)
log2(gene exp. / Gapdh exp.)
10
5
0
VAV1
STAT1
CD28
IL5RA
CCR5
TNFRSF1B
genes
Cohorts
Child
Adult
Risk
Healthy

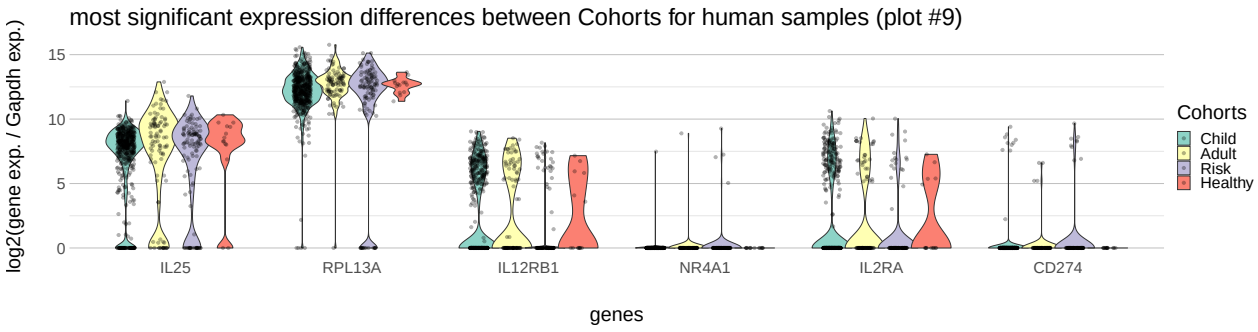

most significant expression differences between Cohorts for human samples (plot #4)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CXCR4
IFNAR1
IFIT1
CCR2
GSK3A
CD52
genes
Cohorts
Child
Adult
Risk
Healthy

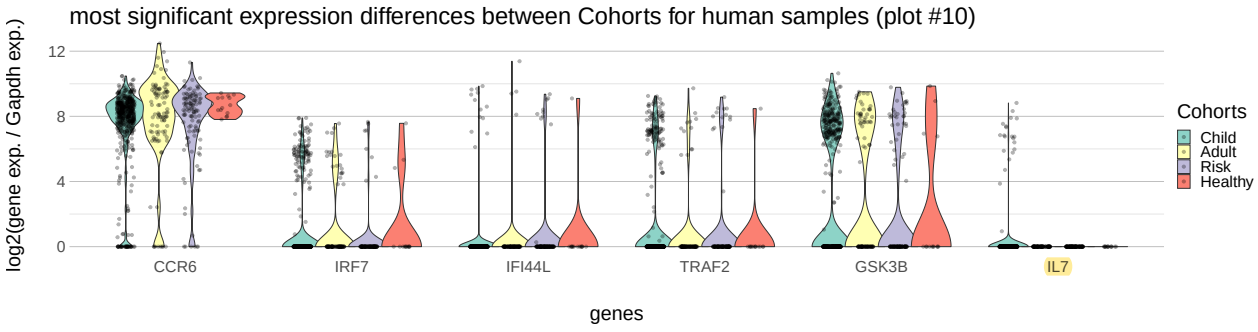

most significant expression differences between Cohorts for human samples (plot #5)
log2(gene exp. / Gapdh exp.)
0
5
10
LY6E
BCL2
ISG15
IFIT3
FYN
PTEN
genes
Cohorts
Child
Adult
Risk
Healthy

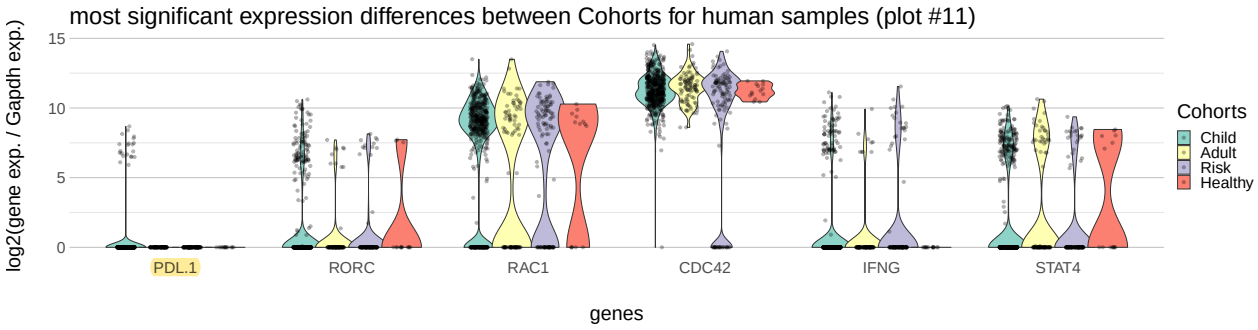

most significant expression differences between Cohorts for human samples (plot #6)
log2(gene exp. / Gapdh exp.)
0
5
10
15
FOXP3
IL7R
ZAP70
NLRP3
CXCL10
SOCS3
genes
Cohorts
Child
Adult
Risk
Healthy

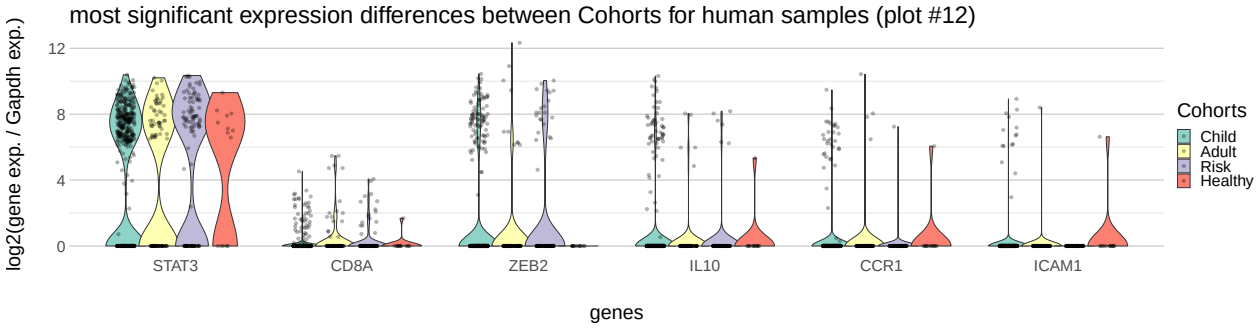

most significant expression differences between Cohorts for human samples (plot #7)
log2(gene exp. / Gapdh exp.)
0
5
10
TNFRSF1A
PPARGC1A
BCL6
ICOS
CD4
CD40
genes
Cohorts
Child
Adult
Risk
Healthy

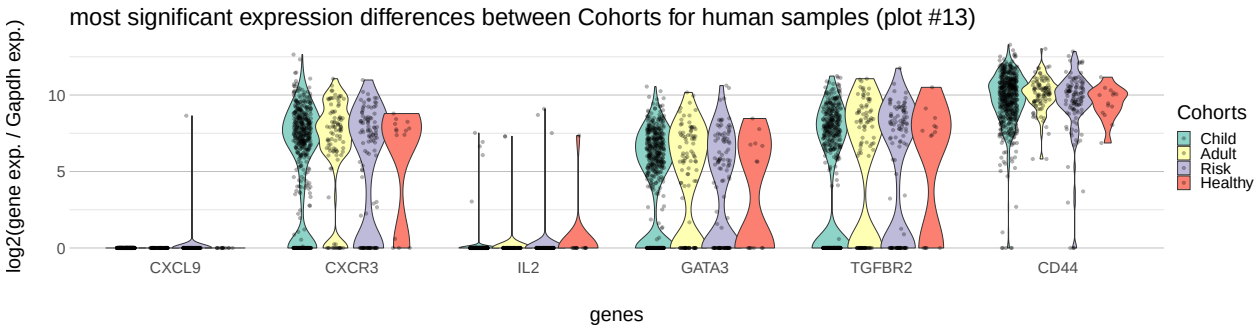

most significant expression differences between Cohorts for human samples (plot #8)
log2(gene exp. / Gapdh exp.)
0
5
10
15
GAPDH
PPARA
C3
B2M
IRF1
IRF9
genes
Cohorts
Child
Adult
Risk
Healthy

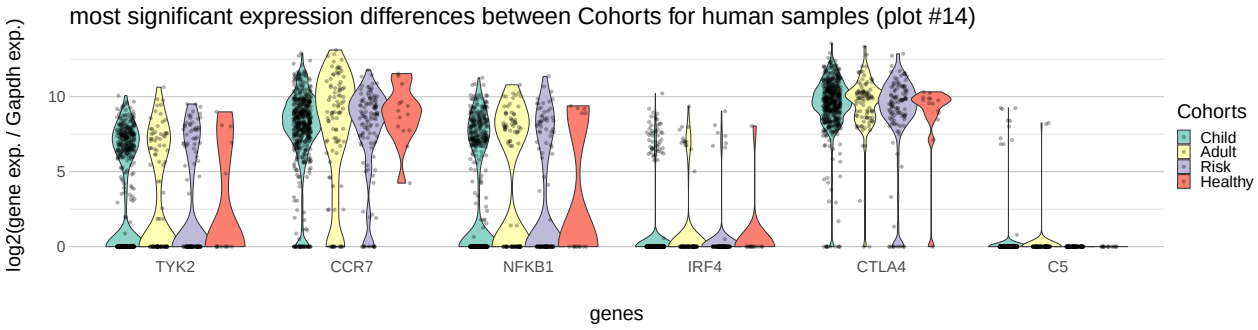

most significant expression differences between Cohorts for human samples (plot #9)
log2(gene exp. / Gapdh exp.)
15
10
5
0
IL25
RPL13A
IL12RB1
NR4A1
IL2RA
CD274
genes
Cohorts
Child
Adult
Risk
Healthy

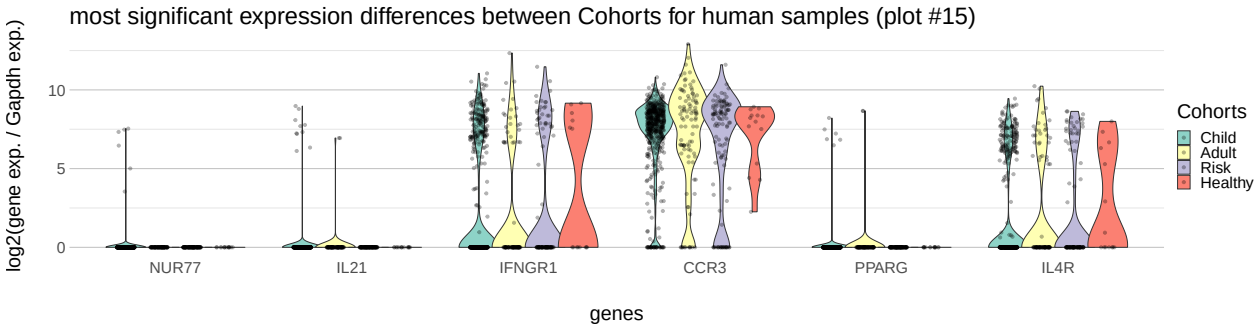

most significant expression differences between Cohorts for human samples (plot #10)
log2(gene exp. / Gapdh exp.)
12
8
4
0
CCR6
IRF7
IFI44L
TRAF2
GSK3B
IL7
genes
Cohorts
Child
Adult
Risk
Healthy

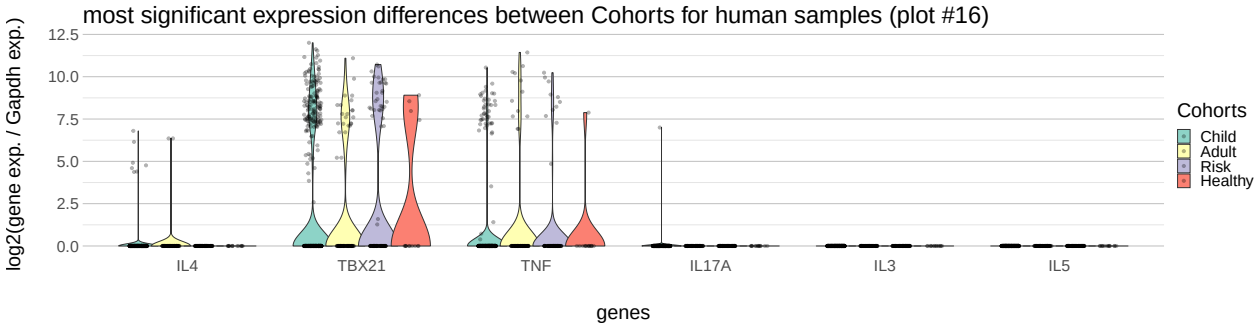

most significant expression differences between Cohorts for human samples (plot #11)
log2(gene exp. / Gapdh exp.)
15
10
5
0
PDL.1
RORC
RAC1
CDC42
IFNG
STAT4
genes
Cohorts
Child
Adult
Risk
Healthy


most significant expression differences between Cohorts for human samples (plot #12)
log2(gene exp. / Gapdh exp.)
12
8
4
0
STAT3
CD8A
ZEB2
IL10
CCR1
ICAM1
genes
Cohorts
Child
Adult
Risk
Healthy



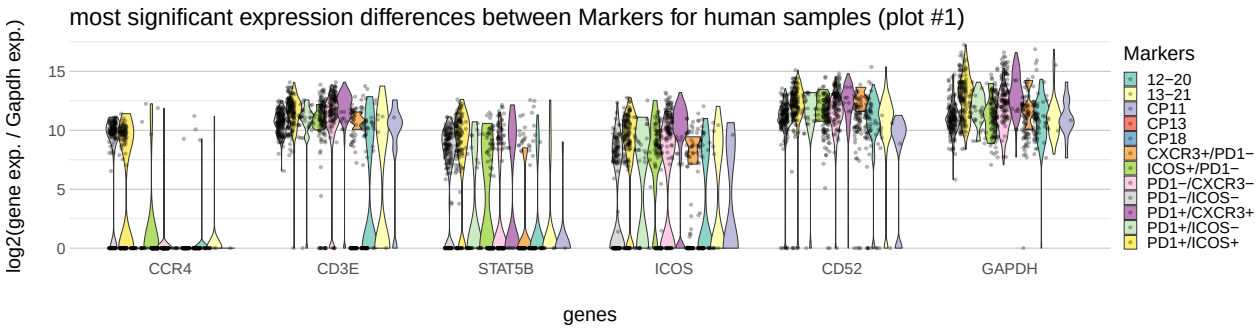



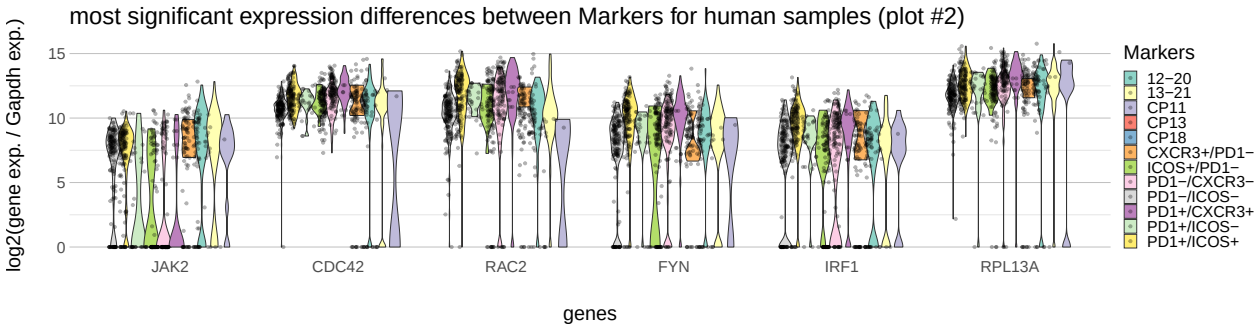



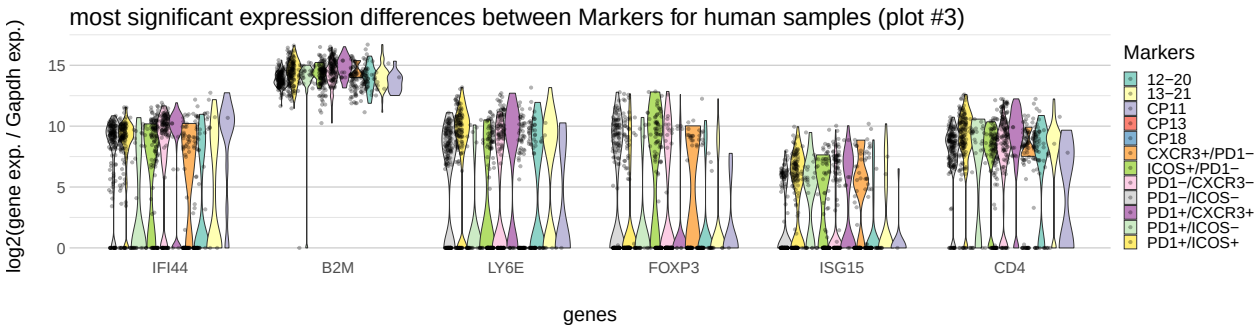



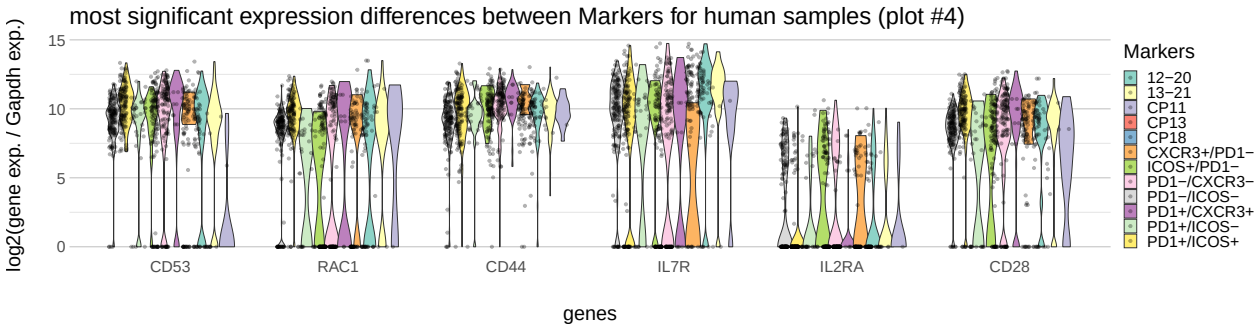

```
[1] Differentially expressed genes between Markers for human samples:
 [1] CCR4: 2.004e-69     CD3E: 9.791e-37     STAT5B: 1.996e-30
 [4] ICOS: 3.614e-30     CD52: 5.4e-27       GAPDH: 1.22e-26
 [7] JAK2: 9.202e-26     CDC42: 1.943e-22    RAC2: 2.59e-22
[10] FYN: 4.427e-21      IRF1: 5.023e-19     RPL13A: 1.169e-18
[13] IFI44: 2.916e-17    B2M: 5.249e-17      LY6E: 2.115e-15
[16] FOXP3: 8.913e-14    ISG15: 1.31e-13     CD4: 1.74e-13
[19] CD53: 4.433e-13     RAC1: 5.932e-13     CD44: 8.131e-13
[22] IL7R: 1.536e-12     IL2RA: 1.536e-12    CD28: 2.793e-12
[25] HLA.DRA: 4.703e-12  IFIT3: 7.541e-12    CCR7: 1.162e-11
```

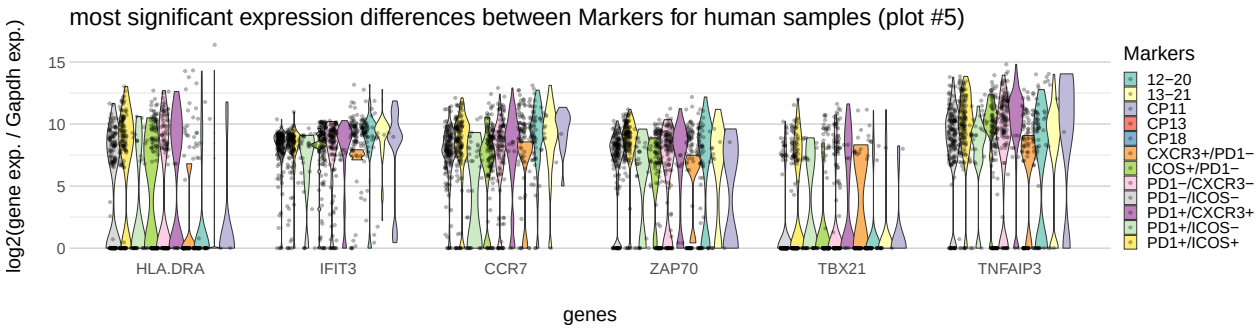
```
[28] ZAP70: 2.297e-11    TBX21: 2.297e-11    TNFAIP3: 2.297e-11
[31] VAV1: 6.081e-11     STAT1: 7.538e-11    NR4A1: 9.983e-11
[34] PTEN: 1.69e-10      IFIT1: 6.649e-10    IFNAR2: 2.003e-09
[37] C3: 2.003e-09       TGFBR2: 2.365e-09   CD40: 2.365e-09
[40] SOCS3: 1.901e-08    IL25: 2.002e-08     GSK3A: 8.909e-08
[43] BCL2: 1.015e-07     CCR5: 1.043e-07     STAT3: 1.458e-07
[46] IRF9: 1.458e-07     TNFRSF1B: 1.462e-07 TYK2: 1.462e-07
[49] ZEB2: 3.623e-07     IRF2: 3.886e-07     CCR3: 4.715e-06
[52] BCL6: 4.731e-06     PPARG: 4.745e-06    CCR6: 6.126e-06
[55] CXCR3: 1.04e-05     JAK1: 1.54e-05      IL21: 1.919e-05
[58] NFKB1: 3.129e-05    CTLA4: 4.066e-05    CXCR4: 7.938e-05
[61] GSK3B: 9.776e-05    IL12RB1: 0.0001289  CXCL10: 0.0001289
[64] NLRP3: 0.0002977    IFNGR1: 0.0002977   PPARA: 0.002193
[67] GATA3: 0.002479     IFNAR1: 0.002538    CD274: 0.002944
[70] TRAF2: 0.004186     PPARGC1A: 0.007719  IFI44L: 0.01045
[73] ICAM1: 0.01795      IFNG: 0.02452       IL4R: 0.02543
[76] IRF7: 0.02616       PDL.1: 0.03137
```

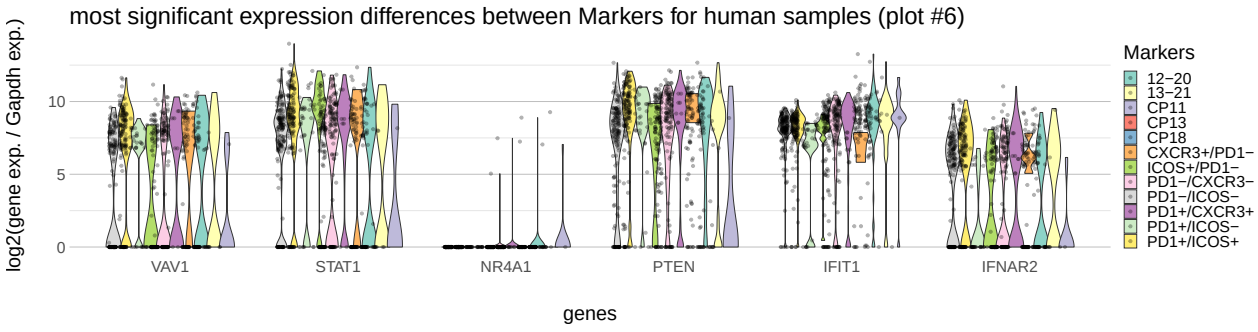

most significant expression differences between Markers for human samples (plot #1)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CCR4
CD3E
STAT5B
ICOS
CD52
GAPDH
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

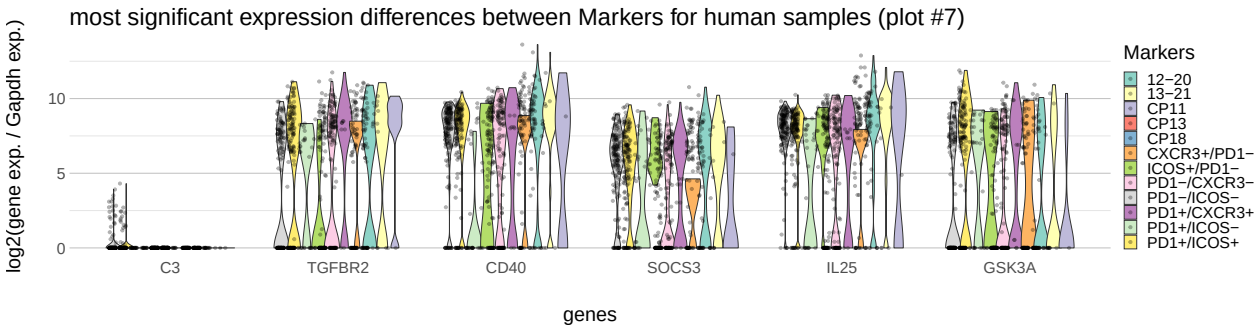

most significant expression differences between Markers for human samples (plot #2)
log2(gene exp. / Gapdh exp.)
15
10
5
0
JAK2
CDC42
RAC2
FYN
IRF1
RPL13A
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

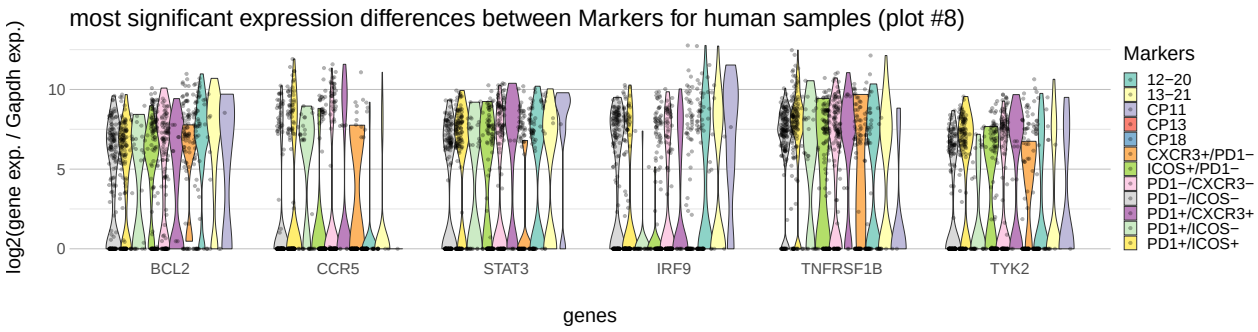

most significant expression differences between Markers for human samples (plot #3)
log2(gene exp. / Gapdh exp.)
15
10
5
0
IFI44
B2M
LY6E
FOXP3
ISG15
CD4
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

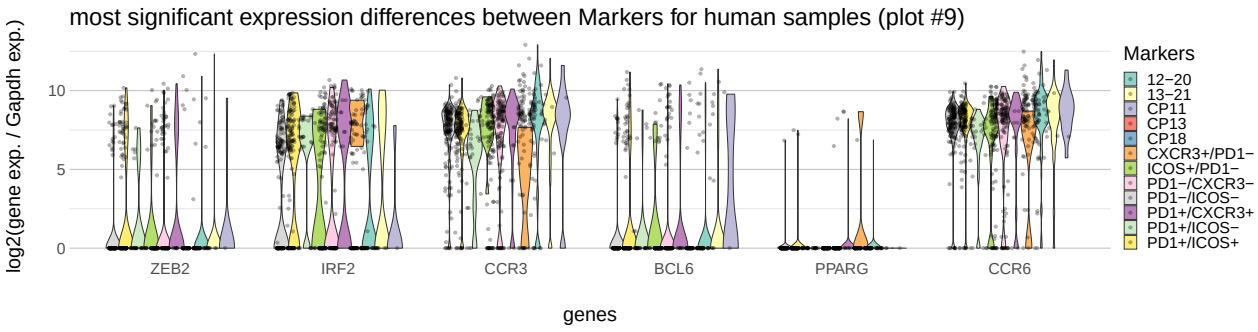

most significant expression differences between Markers for human samples (plot #4)
log2(gene exp. / Gapdh exp.)
15
10
5
0
CD53
RAC1
CD44
IL7R
IL2RA
CD28
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

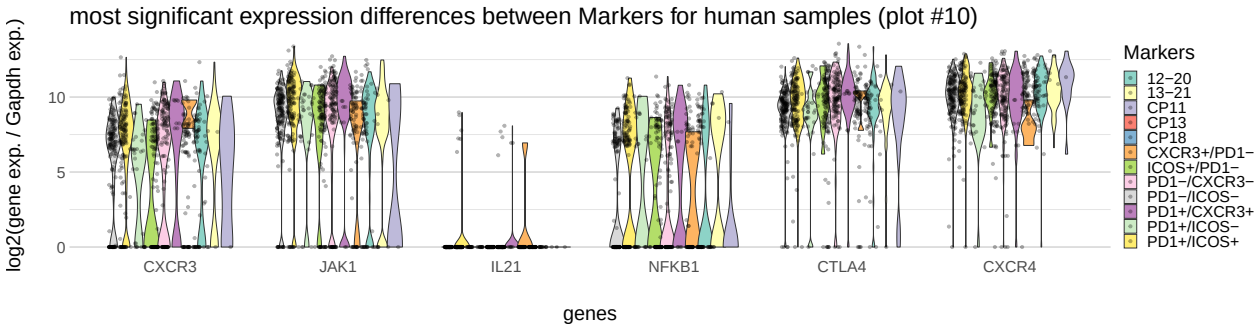

most significant expression differences between Markers for human samples (plot #5)
log2(gene exp. / Gapdh exp.)
15
10
5
0
HLA.DRA
IFIT3
CCR7
ZAP70
TBX21
TNFAIP3
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

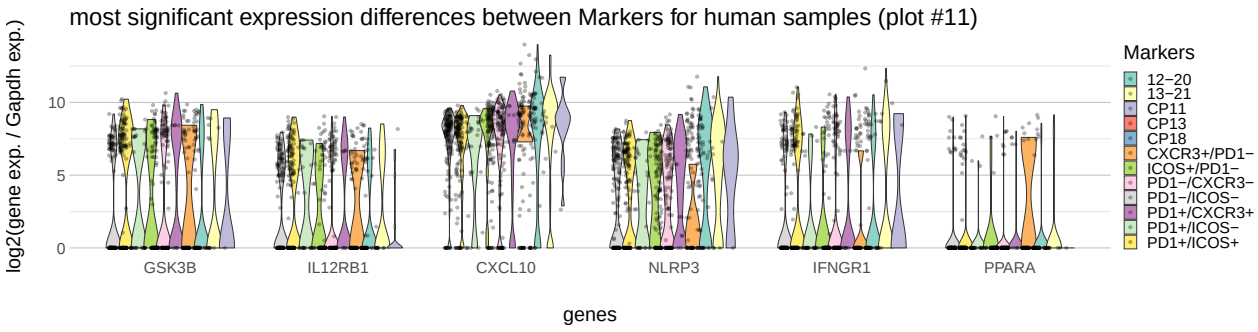

most significant expression differences between Markers for human samples (plot #6)
log2(gene exp. / Gapdh exp.)
10
5
0
VAV1
STAT1
NR4A1
PTEN
IFIT1
IFNAR2
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

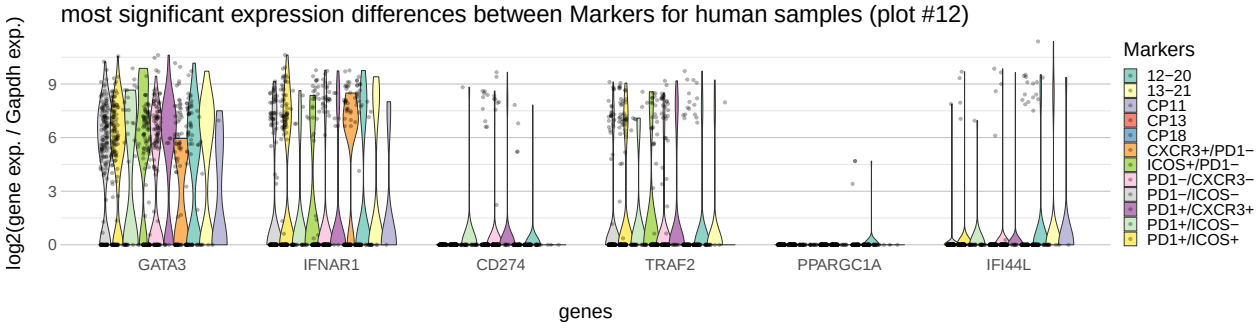

most significant expression differences between Markers for human samples (plot #7)
log2(gene exp. / Gapdh exp.)
10
5
0
C3
TGFBR2
CD40
SOCS3
IL25
GSK3A
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

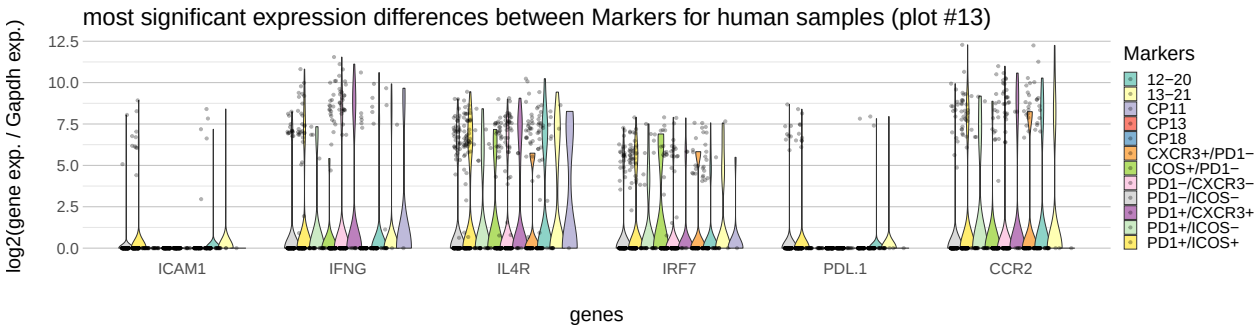

most significant expression differences between Markers for human samples (plot #8)
log2(gene exp. / Gapdh exp.)
10
5
0
BCL2
CCR5
STAT3
IRF9
TNFRSF1B
TYK2
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

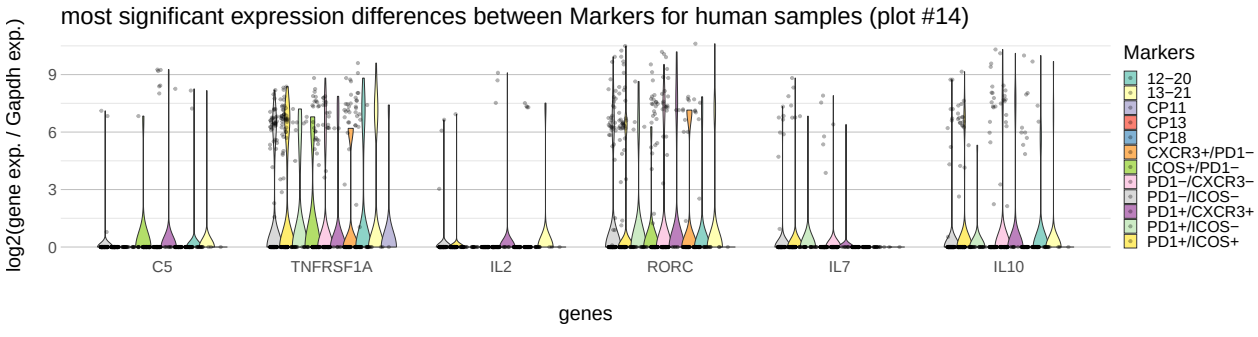

most significant expression differences between Markers for human samples (plot #9)
log2(gene exp. / Gapdh exp.)
10
5
0
ZEB2
IRF2
CCR3
BCL6
PPARG
CCR6
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

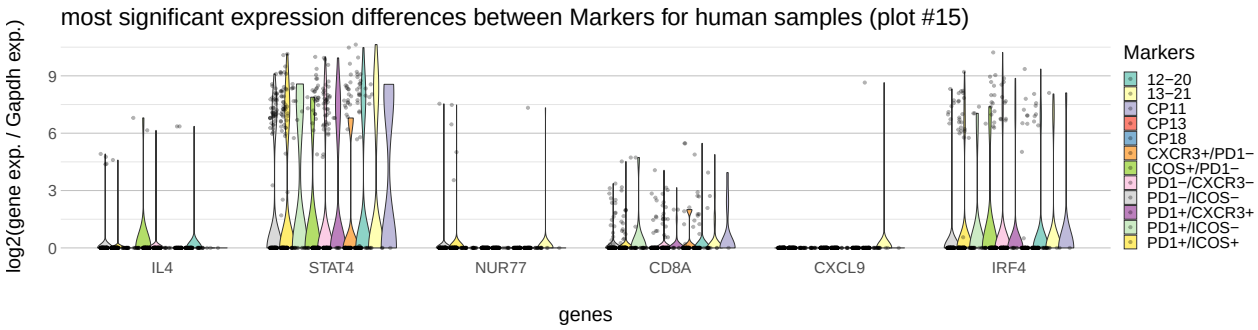

most significant expression differences between Markers for human samples (plot #10)
log2(gene exp. / Gapdh exp.)
10
5
0
CXCR3
JAK1
IL21
NFKB1
CTLA4
CXCR4
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+

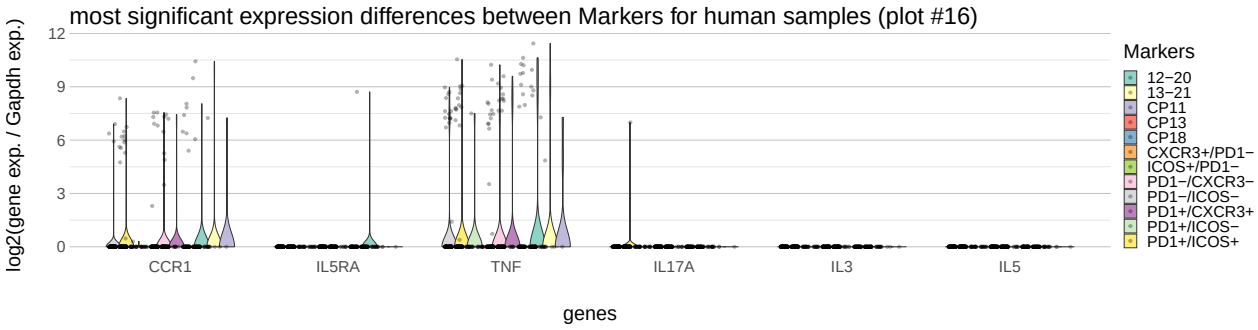

most significant expression differences between Markers for human samples (plot #11)
log2(gene exp. / Gapdh exp.)
10
5
0
GSK3B
IL12RB1
CXCL10
NLRP3
IFNGR1
PPARA
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+


most significant expression differences between Markers for human samples (plot #12)
log2(gene exp. / Gapdh exp.)
9
6
3
0
GATA3
IFNAR1
CD274
TRAF2
PPARGC1A
IFI44L
genes
Markers
12−20
13−21
CP11
CP13
CP18
CXCR3+/PD1−
ICOS+/PD1−
PD1−/CXCR3−
PD1−/ICOS−
PD1+/CXCR3+
PD1+/ICOS−
PD1+/ICOS+



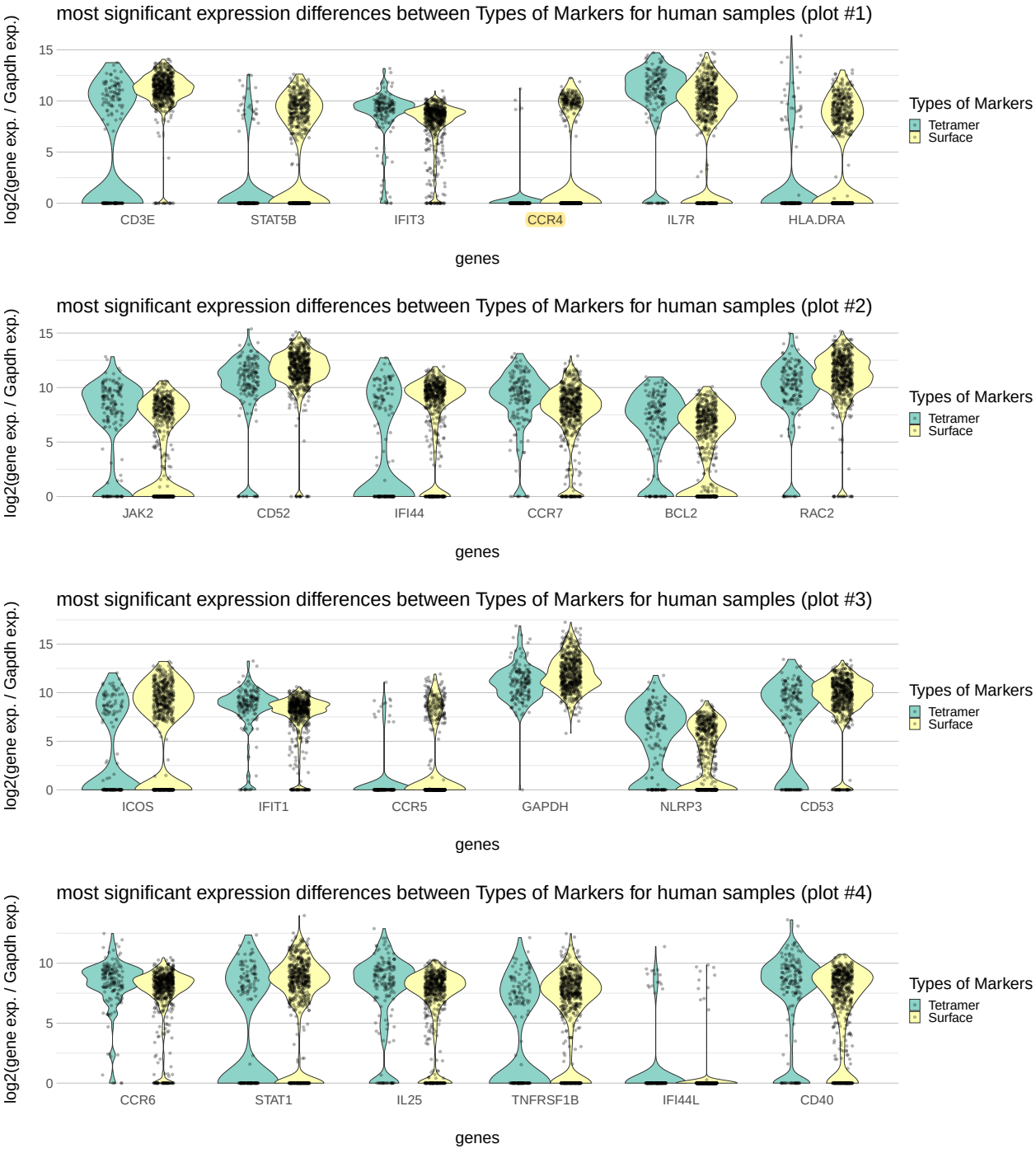



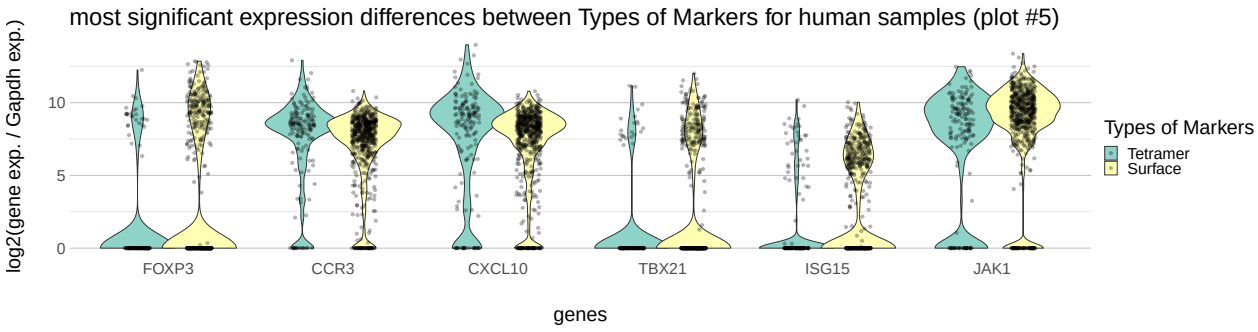



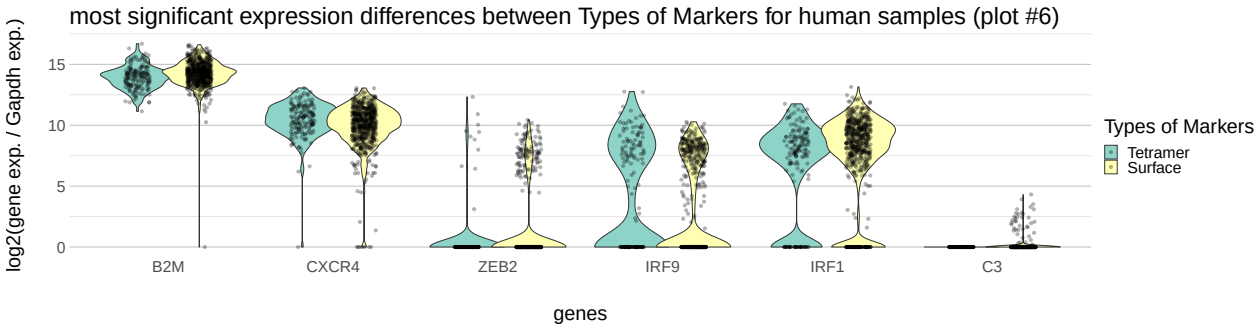



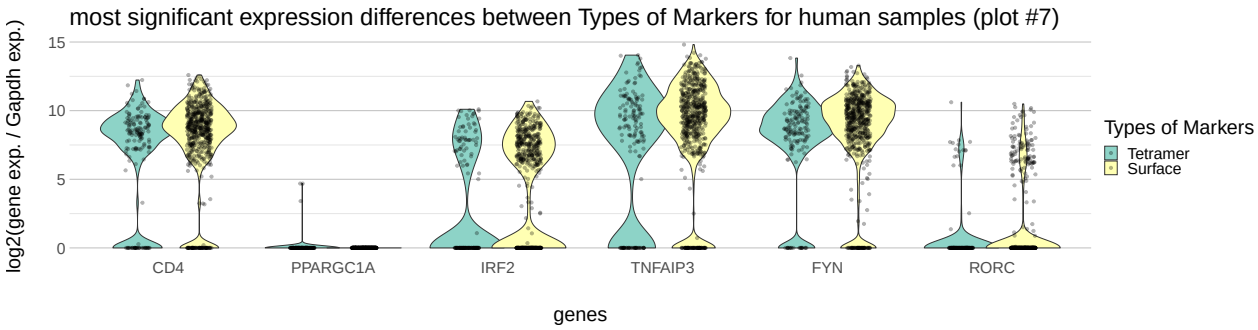

```
[1] Differentially expressed genes between Types of Markers for human samples:
 [1] CD3E: 7.834e-28     STAT5B: 1.355e-14   IFIT3: 1.485e-13
 [4] CCR4: 6.513e-13     IL7R: 8.901e-13     HLA.DRA: 1.92e-11
 [7] JAK2: 6.124e-11     CD52: 1.373e-10     IFI44: 4.402e-10
[10] CCR7: 3.345e-09     BCL2: 7.1e-09       RAC2: 7.744e-09
[13] ICOS: 2.453e-08     IFIT1: 3.655e-08    CCR5: 5.697e-08
[16] GAPDH: 1.791e-07    NLRP3: 6.187e-07    CD53: 8.713e-07
[19] CCR6: 1.16e-06      STAT1: 1.349e-06    IL25: 1.43e-06
[22] TNFRSF1B: 2.812e-06 IFI44L: 1.025e-05   CD40: 1.028e-05
[25] FOXP3: 1.14e-05     CCR3: 2.241e-05     CXCL10: 2.531e-05
```

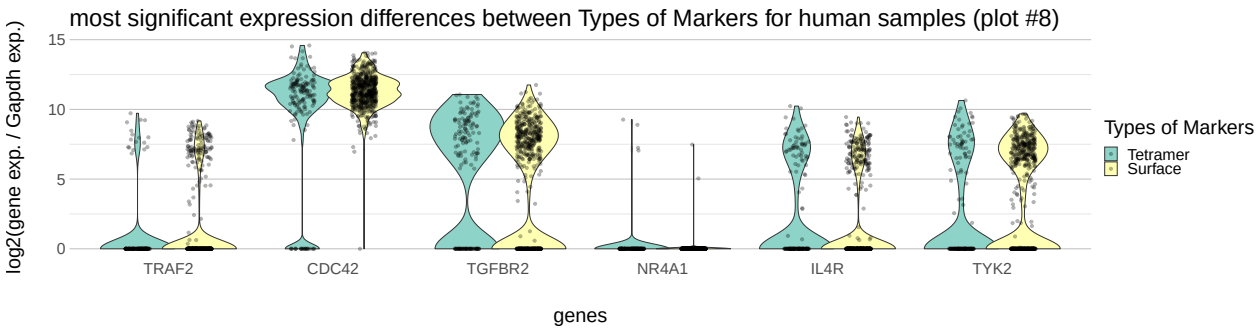
```
[28] TBX21: 2.606e-05    ISG15: 9.883e-05    JAK1: 0.0001365
[31] B2M: 0.0002118      CXCR4: 0.0009804    ZEB2: 0.0009929
[34] IRF9: 0.001112      IRF1: 0.001773      C3: 0.001773
[37] CD4: 0.002256       PPARGC1A: 0.002256  IRF2: 0.002438
[40] TNFAIP3: 0.003139   FYN: 0.003956       RORC: 0.008583
[43] TRAF2: 0.009596     CDC42: 0.01225      TGFBR2: 0.01326
[46] NR4A1: 0.01374      IL4R: 0.01755       TYK2: 0.01902
[49] IFNAR2: 0.01989     IL7: 0.0284         GSK3A: 0.04139
[52] LY6E: 0.04783
```

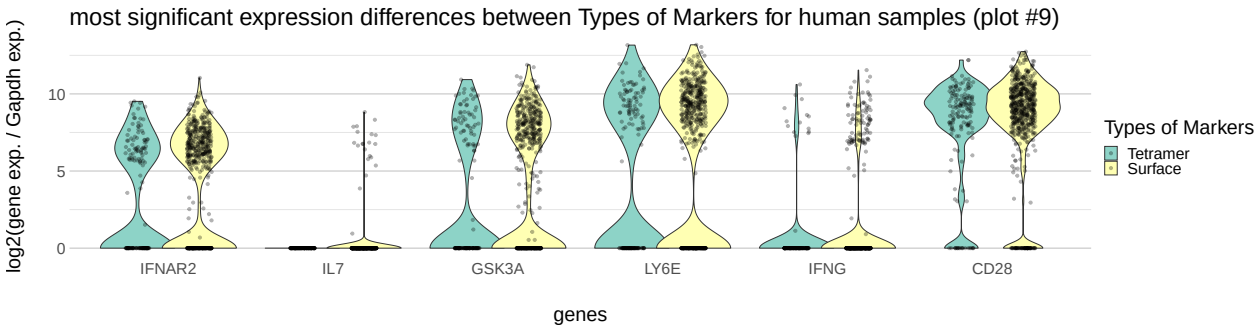


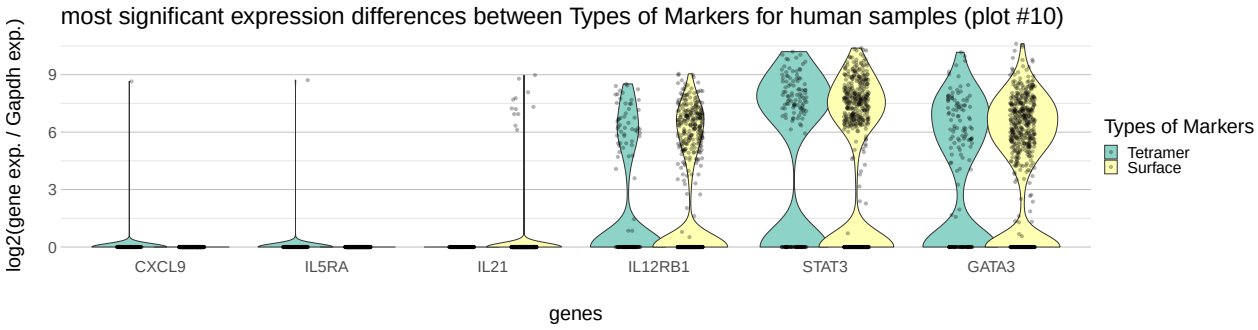

most significant expression differences between Types of Markers for human samples (plot #5)
log2(gene exp. / Gapdh exp.)
0
5
10
FOXP3
CCR3
CXCL10
TBX21
ISG15
JAK1
genes
Types of Markers
Tetramer
Surface

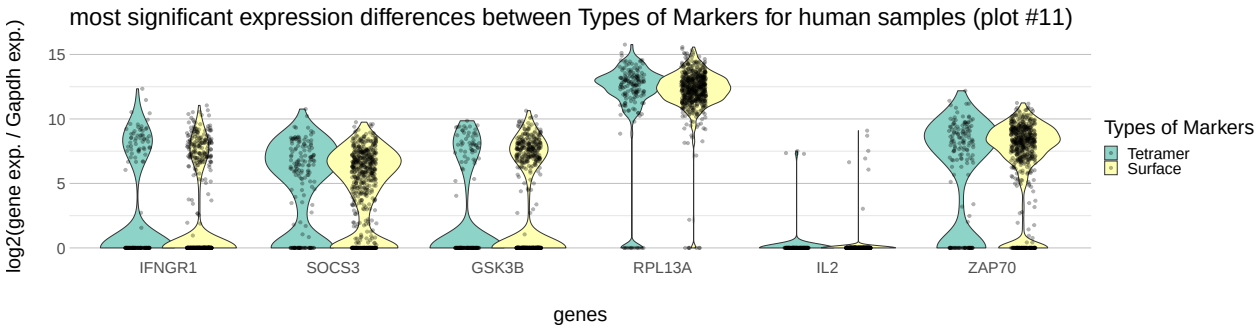

most significant expression differences between Types of Markers for human samples (plot #6)
log2(gene exp. / Gapdh exp.)
0
5
10
15
B2M
CXCR4
ZEB2
IRF9
IRF1
C3
genes
Types of Markers
Tetramer
Surface

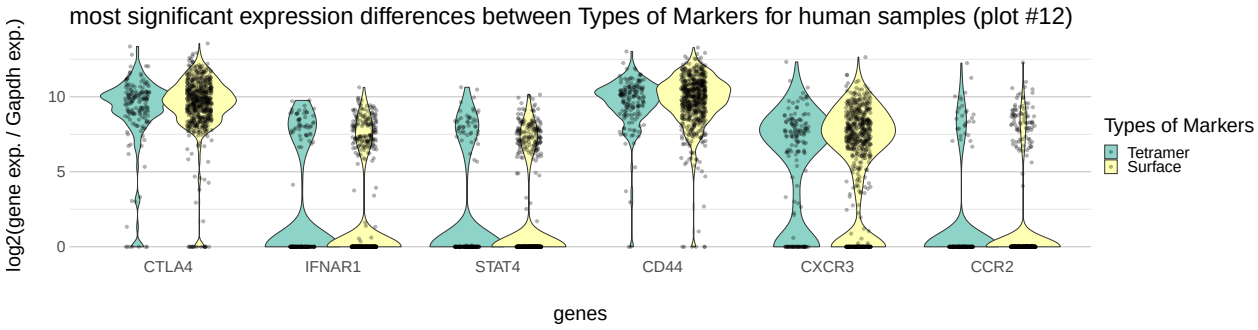

most significant expression differences between Types of Markers for human samples (plot #7)
log2(gene exp. / Gapdh exp.)
0
5
10
15
CD4
PPARGC1A
IRF2
TNFAIP3
FYN
RORC
genes
Types of Markers
Tetramer
Surface

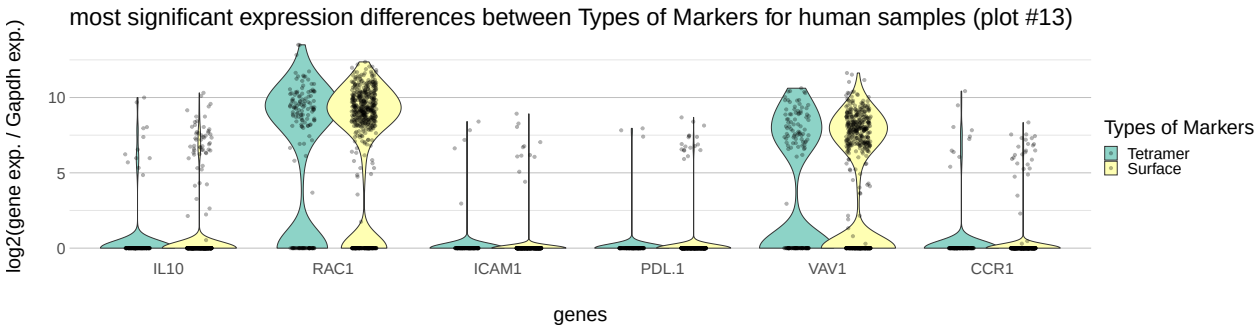

most significant expression differences between Types of Markers for human samples (plot #8)
log2(gene exp. / Gapdh exp.)
0
5
10
15
TRAF2
CDC42
TGFBR2
NR4A1
IL4R
TYK2
genes
Types of Markers
Tetramer
Surface

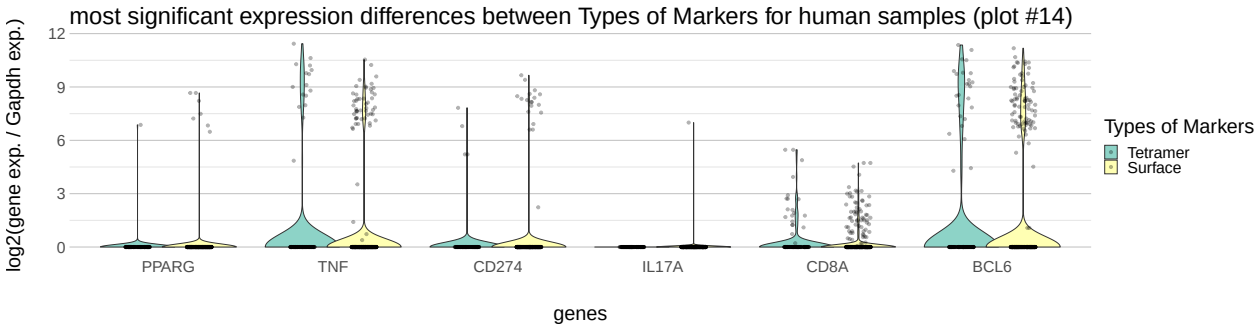

most significant expression differences between Types of Markers for human samples (plot #9)
log2(gene exp. / Gapdh exp.)
10
5
0
IFNAR2
IL7
GSK3A
LY6E
IFNG
CD28
genes
Types of Markers
Tetramer
Surface

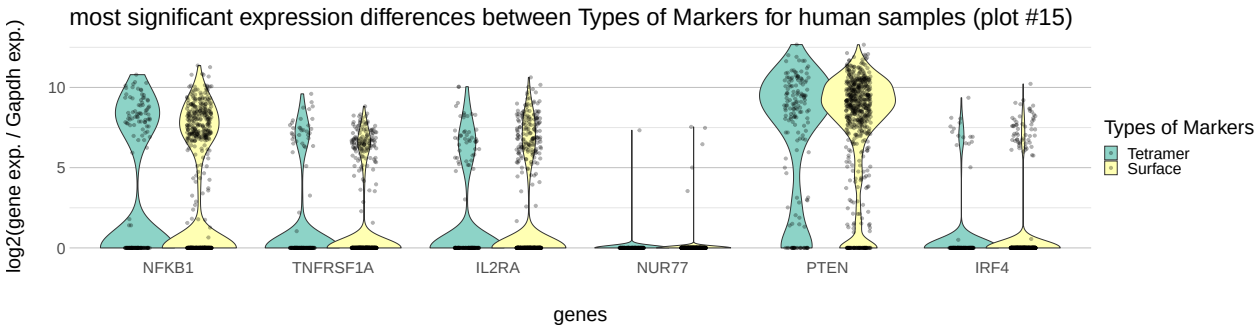

most significant expression differences between Types of Markers for human samples (plot #10)
log2(gene exp. / Gapdh exp.)
9
6
3
0
CXCL9
IL5RA
IL21
IL12RB1
STAT3
GATA3
genes
Types of Markers
Tetramer
Surface

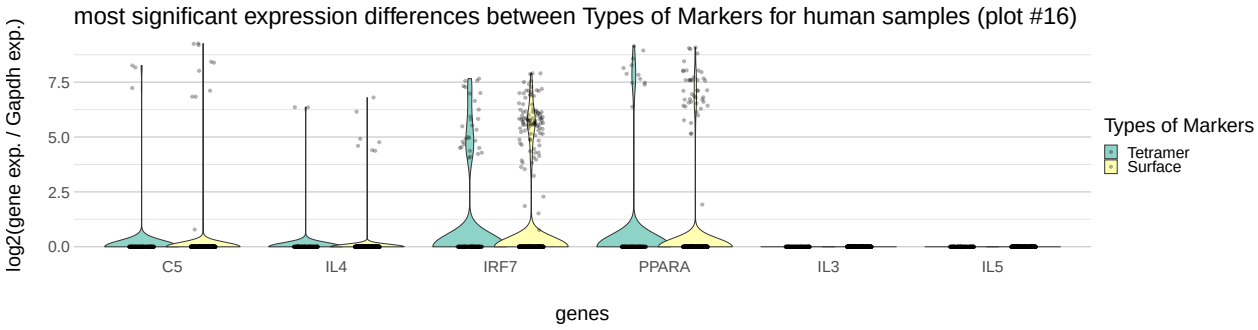

most significant expression differences between Types of Markers for human samples (plot #11)
log2(gene exp. / Gapdh exp.)
15
10
5
0
IFNGR1
SOCS3
GSK3B
RPL13A
IL2
ZAP70
genes
Types of Markers
Tetramer
Surface


most significant expression differences between Types of Markers for human samples (plot #12)
log2(gene exp. / Gapdh exp.)
10
5
0
CTLA4
IFNAR1
STAT4
CD44
CXCR3
CCR2
genes
Types of Markers
Tetramer
Surface


most significant expression differences between Types of Markers for human samples (plot #13)
log2(gene exp. / Gapdh exp.)
10
5
0
IL10
RAC1
ICAM1
PDL.1
VAV1
CCR1
genes
Types of Markers
Tetramer
Surface


most significant expression differences between Types of Markers for human samples (plot #14)
log2(gene exp. / Gapdh exp.)
12
9
6
3
0
PPARG
TNF
CD274
IL17A
CD8A
BCL6
genes
Types of Markers
Tetramer
Surface


most significant expression differences between Types of Markers for human samples (plot #15)
log2(gene exp. / Gapdh exp.)
10
5
0
NFKB1
TNFRSF1A
IL2RA
NUR77
PTEN
IRF4
genes
Types of Markers
Tetramer
Surface


most significant expression differences between Types of Markers for human samples (plot #16)
log2(gene exp. / Gapdh exp.)
7.5
5.0
2.5
0.0
C5
IL4
IRF7
PPARA
IL3
IL5
genes
Types of Markers
Tetramer
Surface