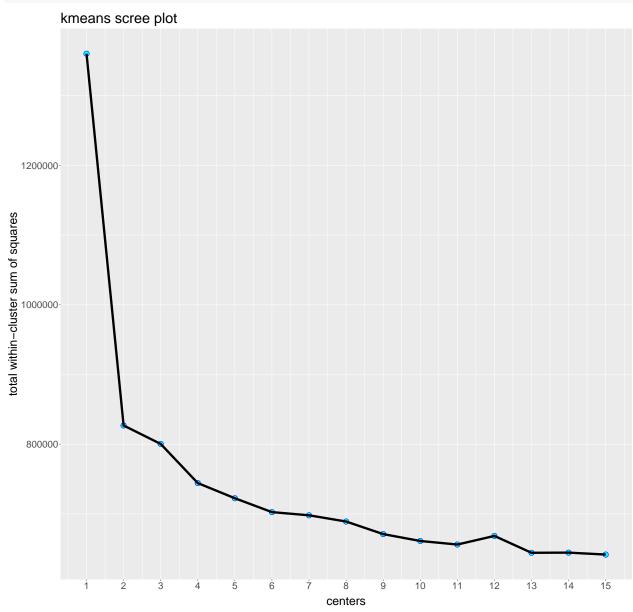
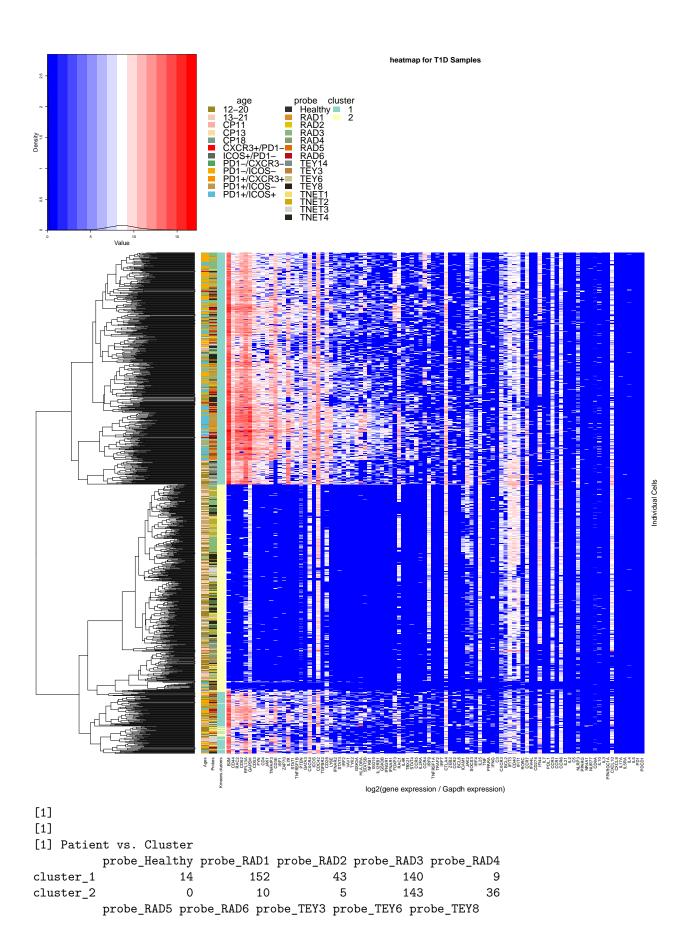
T1D_specific_analysis

No expression detected in 5/1291 cells

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





cluster_1	91	75	12	21	32
cluster_2	3	1	8	4	6
	probe_TEY14	<pre>probe_TNET1</pre>	<pre>probe_TNET2</pre>	<pre>probe_TNET3</pre>	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

data: sourceTable

X-squared = 299.74, df = NA, p-value = 0.0004998

- [1]
- [1]
- [1] Marker vs. Cluster

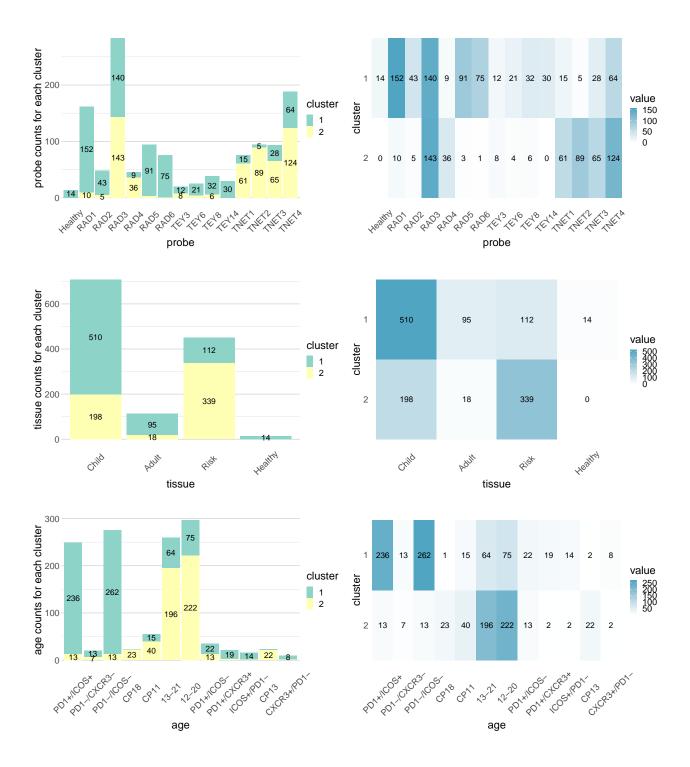
age_PD1+/ICOS+ age_PD1-/CXCR3- age_PD1-/ICOS- age_CP18 age_CP11 cluster_1 236 13 262 1 15 cluster_2 13 7 13 23 40

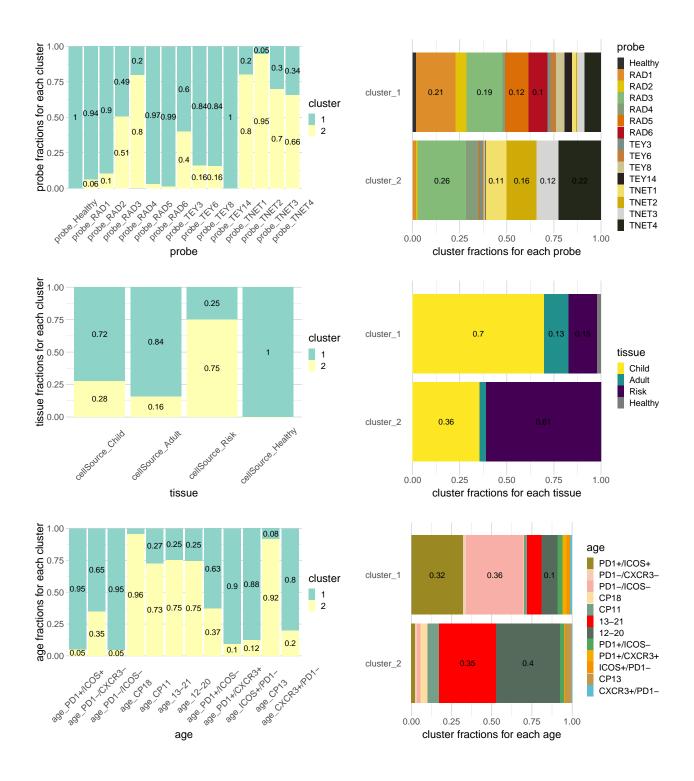
age_13-21 age_12-20 age_PD1+/ICOS- age_PD1+/CXCR3+

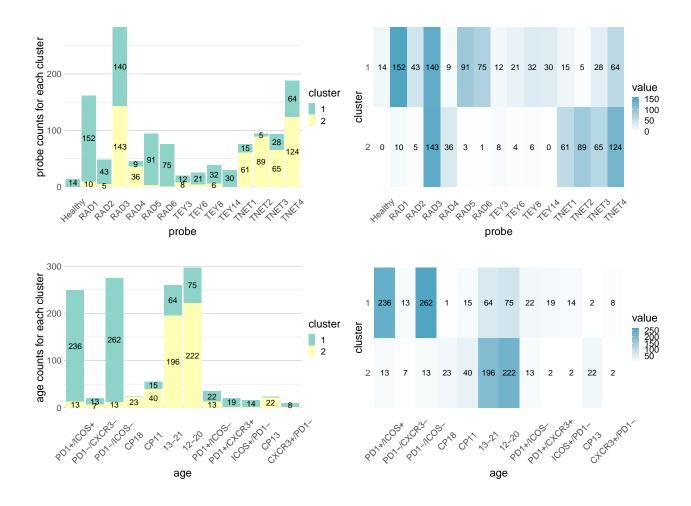
cluster_1 14 2 8 cluster_2 2 22 2

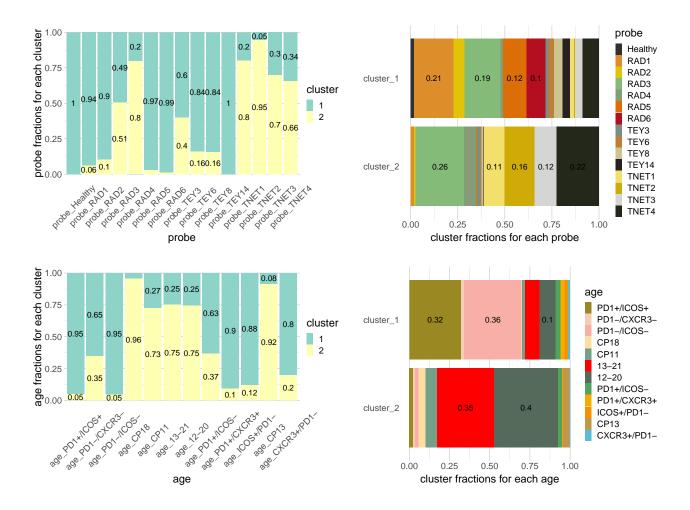
data: ageTable

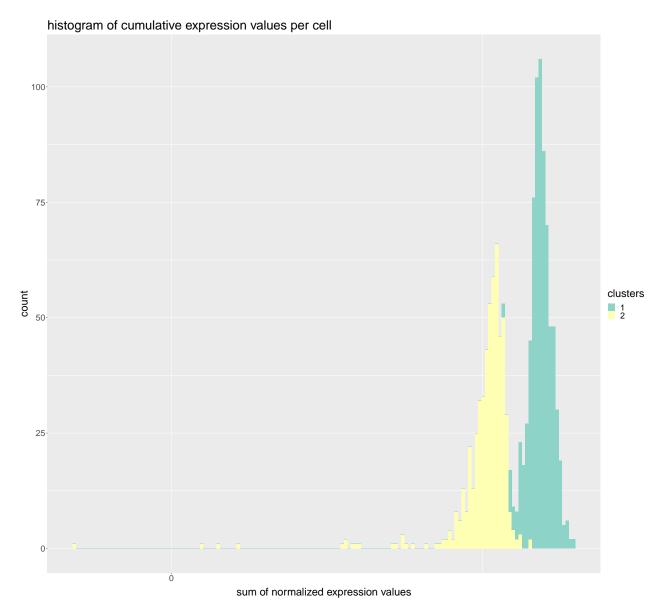
X-squared = 631.36, df = NA, p-value = 0.0004998





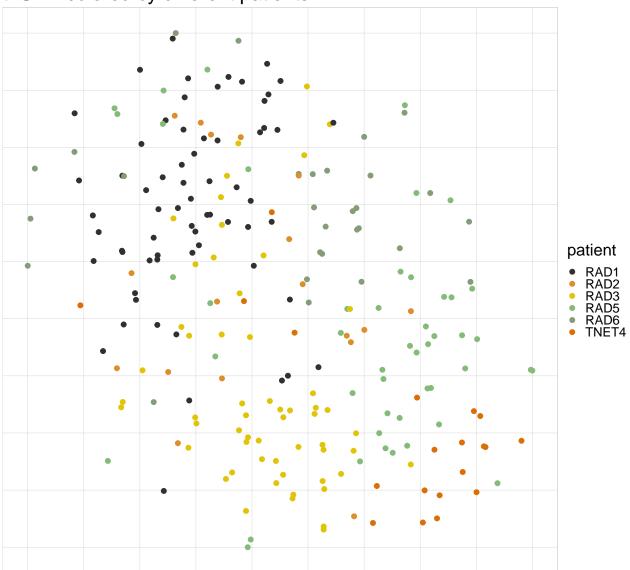




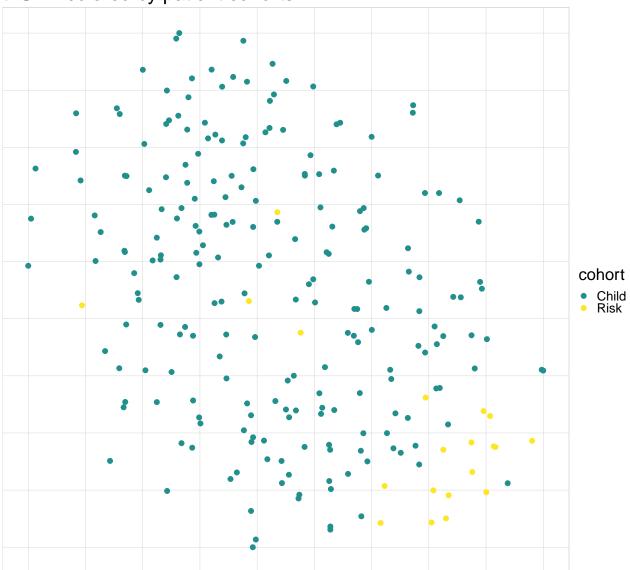


/ 1286 cells were removed due to low gene expression (cluster ID of removed clusters: 2)

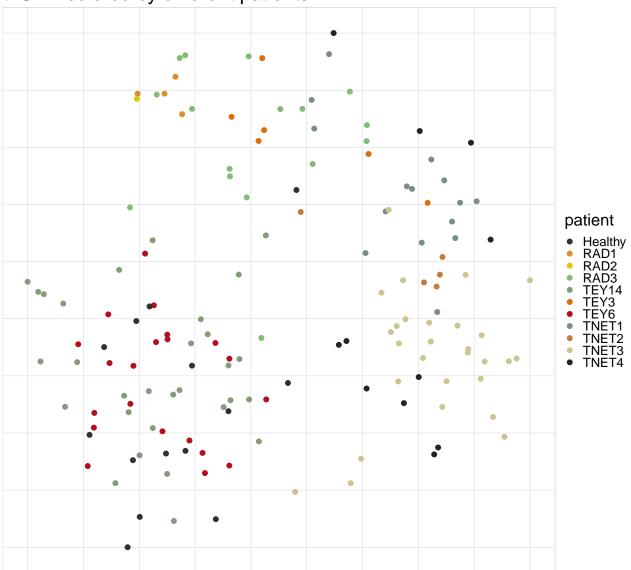
t-SNE colored by different patients



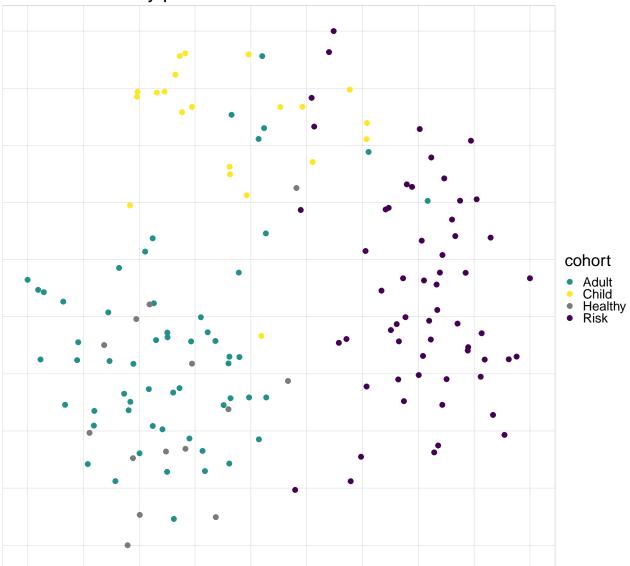
t-SNE colored by patient cohorts



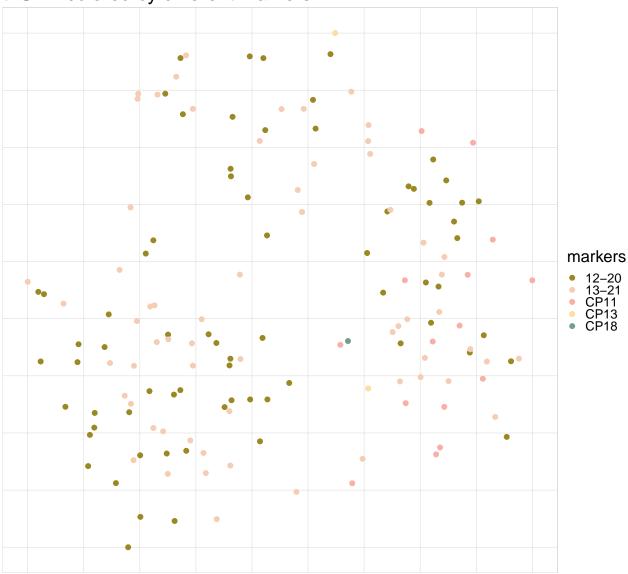
t-SNE colored by different patients



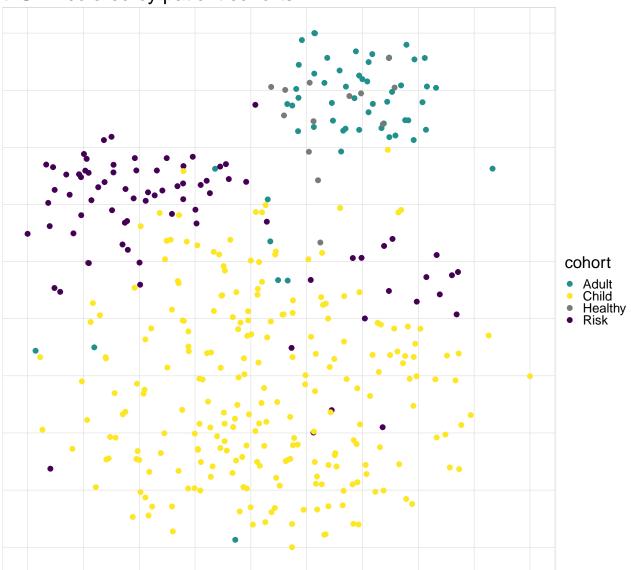
t-SNE colored by patient cohorts



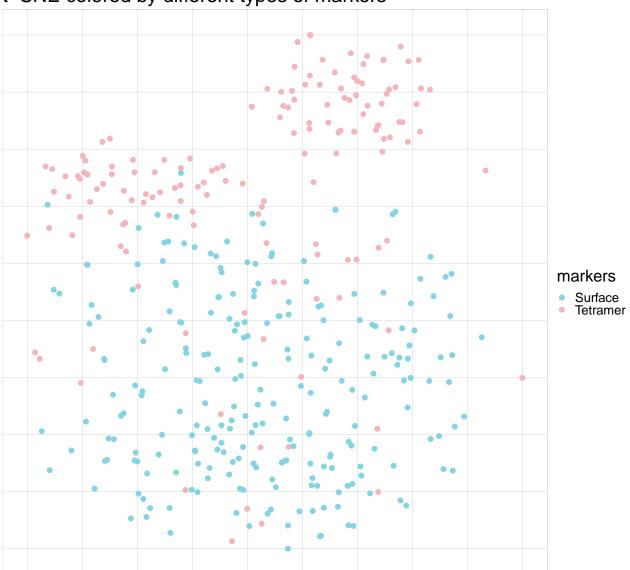
t-SNE colored by different markers



t-SNE colored by patient cohorts



t-SNE colored by different types of markers



t-SNE colored by different markers

