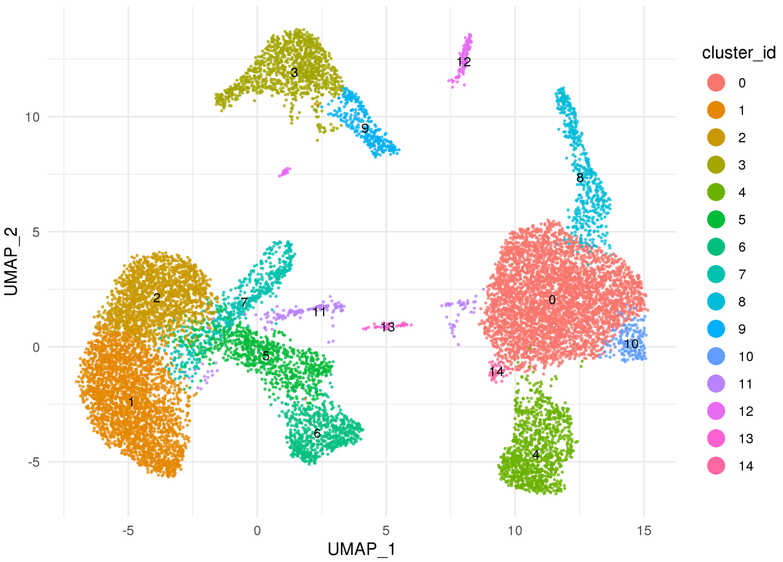
pipeline_seurat.py: summary report

Interferon beta stimulated vs control PBMCs (Seurat example dataset)

Sansom group

November 5, 2020



Sample: integrated

Run specs: no. components: 20, cluster resolution: 0.6, cluster algorithm: leiden, de test: wilcox

Code: `https://github.com/sansomlab/tenx`

Contents

1 Introduction

The core of the data analysis was performed using Seurat and scanpy:

- The construction of the nearest neighbor graph, clustering and UMAP computation were performed using scanpy (or scvelo for use of hnswlib).
- The differential expression analysis was performed using Seurat.
- The geneset analysis was performed using gsfisher
- Please see https://github/sansomlab/tenx for more details.

The key parameter choices used for this analysis were:

- The number of pca components: 20
- The number of nearest neighbors: 20
- The distance metric used for the nearest neighbor graph: euclidean
- The method used for construction of the nearest neighbor graph: hnsw
- The resolution of the clustering: 0.6
- The clustering algorithm: leiden
- The differential expression test: wilcox

1.1 Optional tasks

This table summarises the status of the optional tasks. Tasks set to "True" were run.

task	run
explore_hvg_and_cell_cycle	True
singleR	True
jackstraw	False
compare_clusters	True
characterise_markers	True
top_marker_heatmap	True
extra_cluster_marker_plots	True
diffusionmap	True
phate	True
paga	True
velocity	False
knownmarkers	False
marker_report	True
exprsreport	False
genesets	True
cellbrowser	False

2 Visualisation of clusters and factors of interest

2.1 umap.mindist_0 plot colored by cluster_id

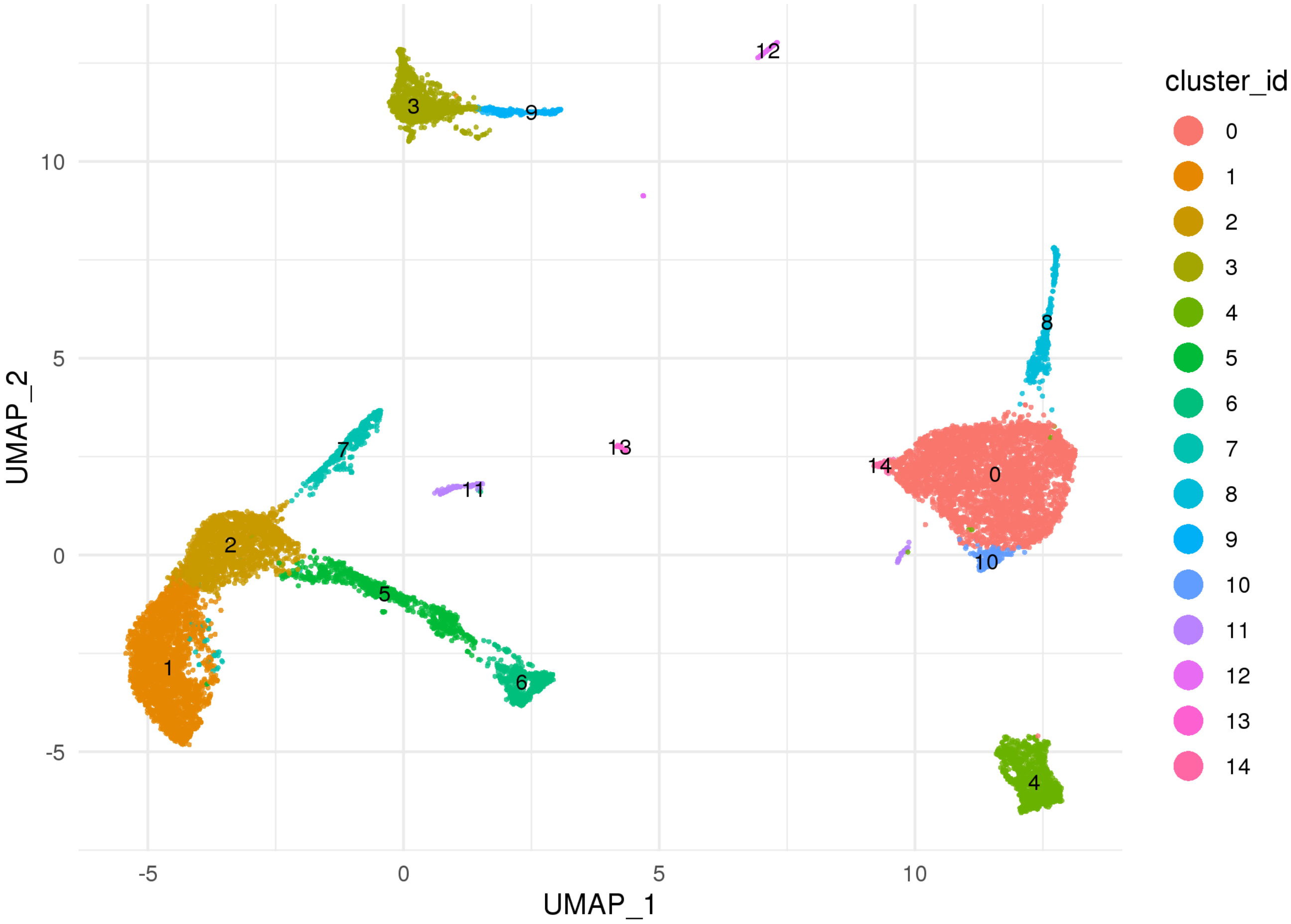


Figure 1: umap.mindist_0 plot colored by cluster_id

2.2 umap.mindist_0.1 plot colored by cluster_id

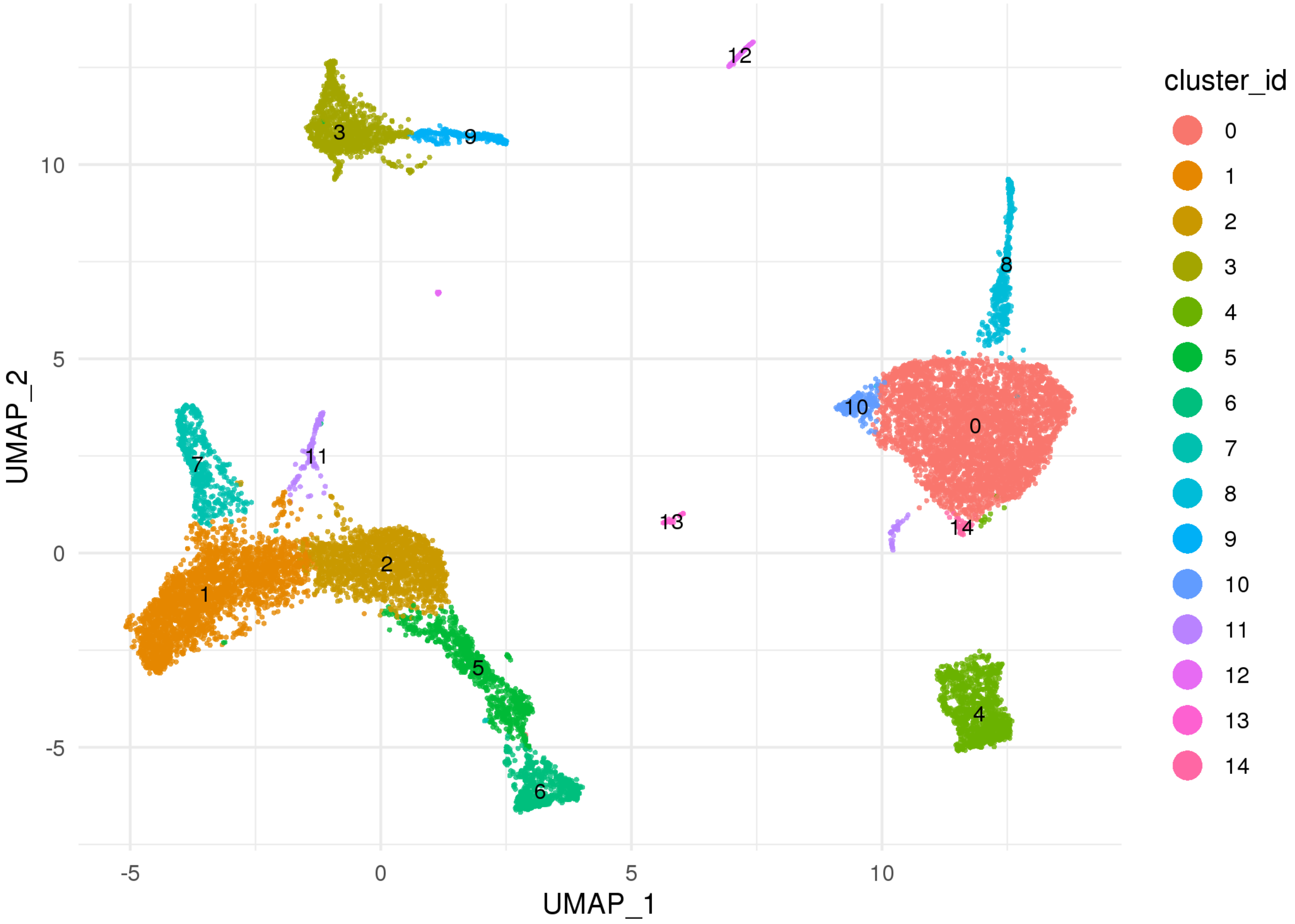


Figure 2: umap.mindist_0.1 plot colored by cluster_id

2.3 umap.mindist_0.3 plot colored by cluster_id

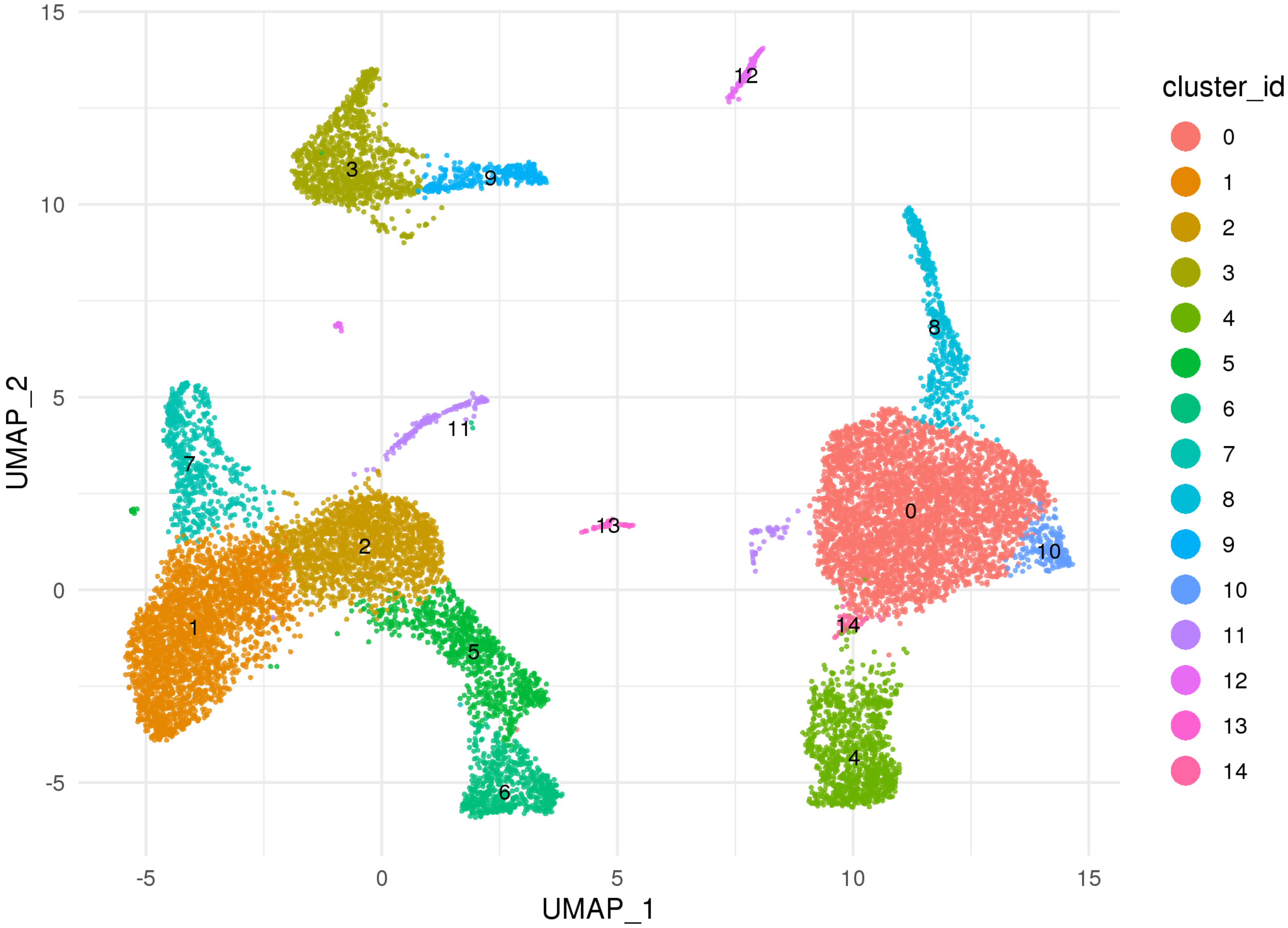


Figure 3: umap.mindist_0.3 plot colored by cluster_id

2.4 umap.mindist_0.5 plot colored by cluster_id

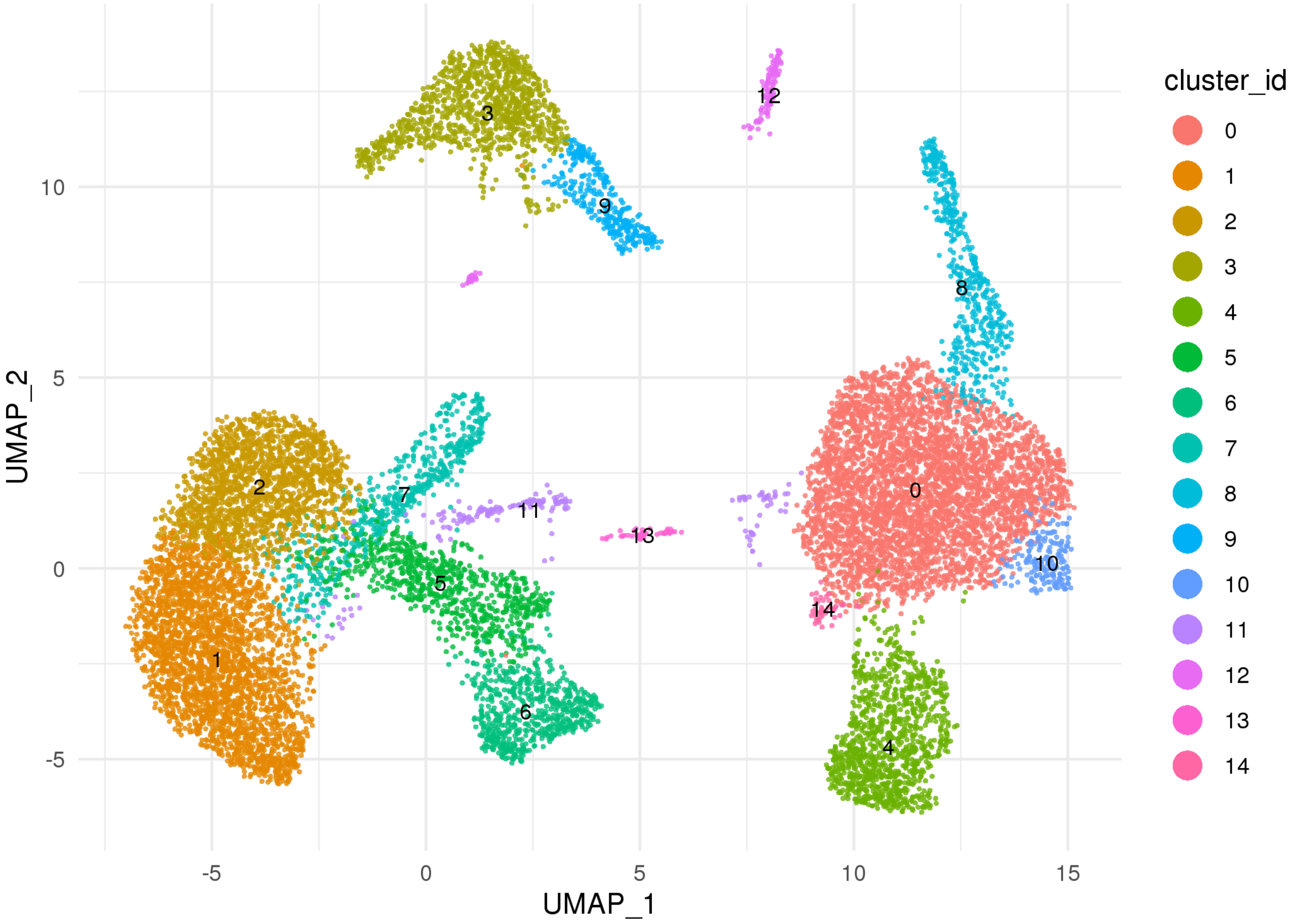


Figure 4: umap.mindist_0.5 plot colored by cluster_id

2.5 umap.mindist_0.7 plot colored by cluster_id

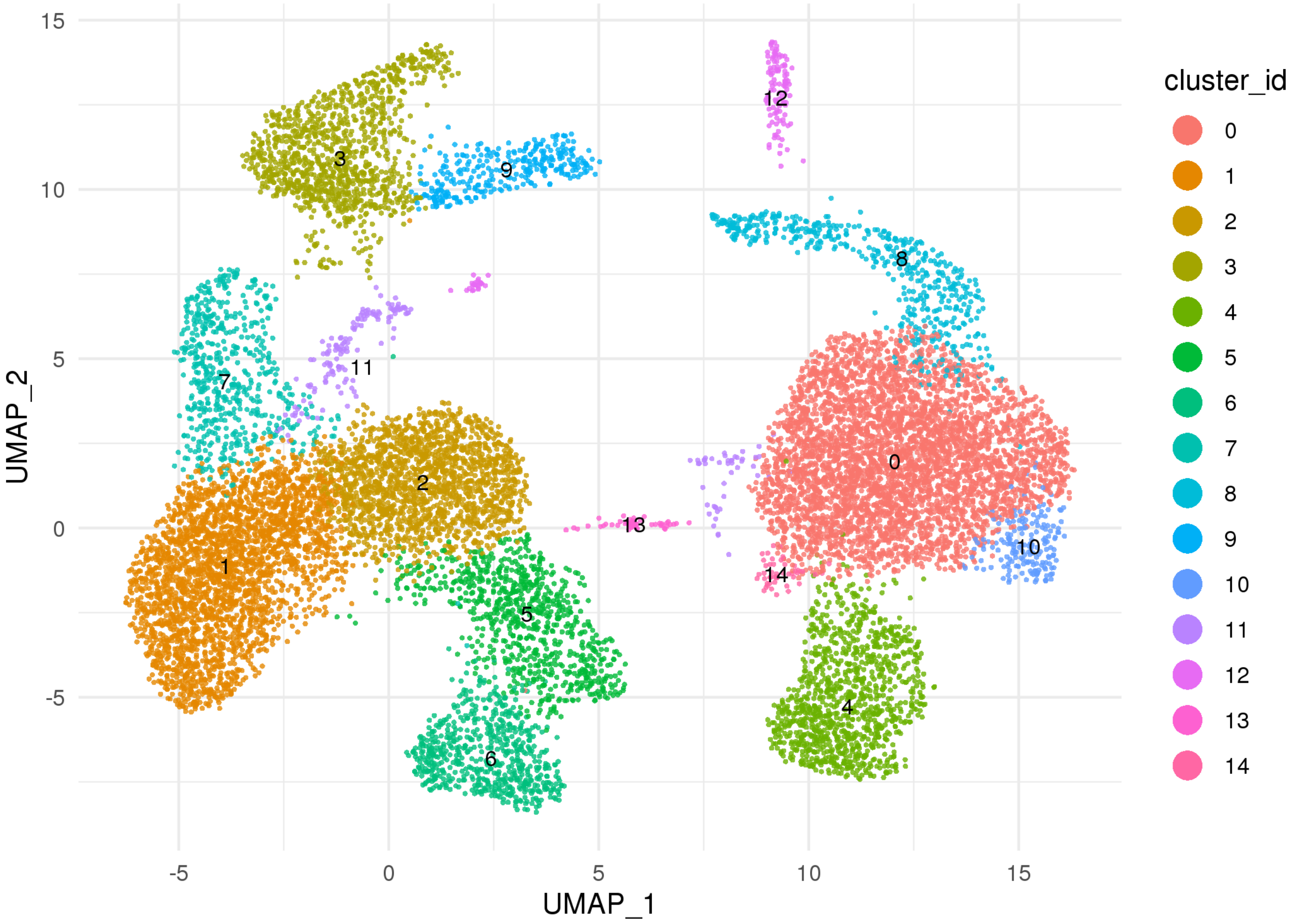


Figure 5: umap.mindist_0.7 plot colored by cluster_id

2.6 umap plot colored by nCount_RNA

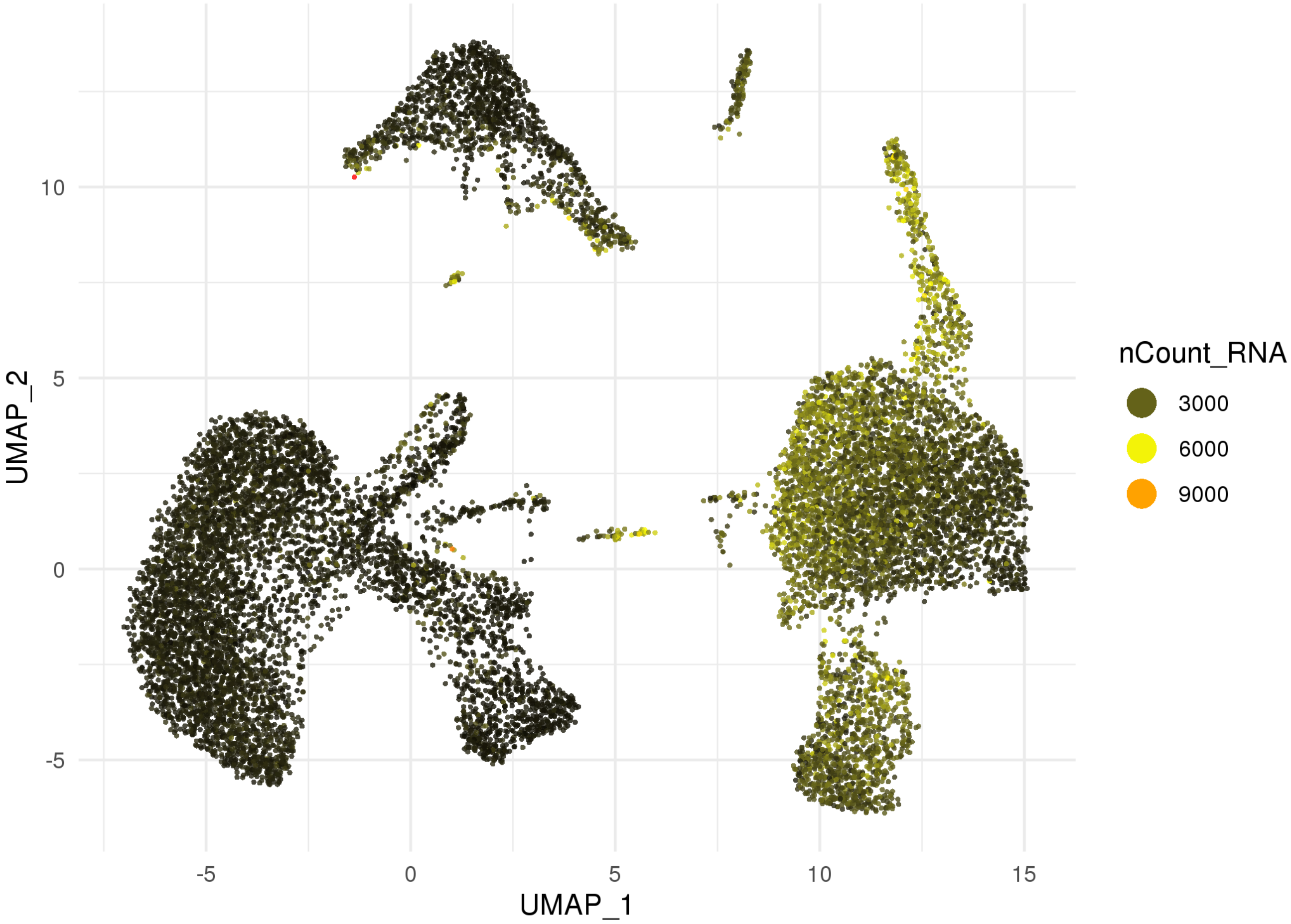


Figure 6: umap plot colored by nCount_RNA

2.7 umap plot colored by stim

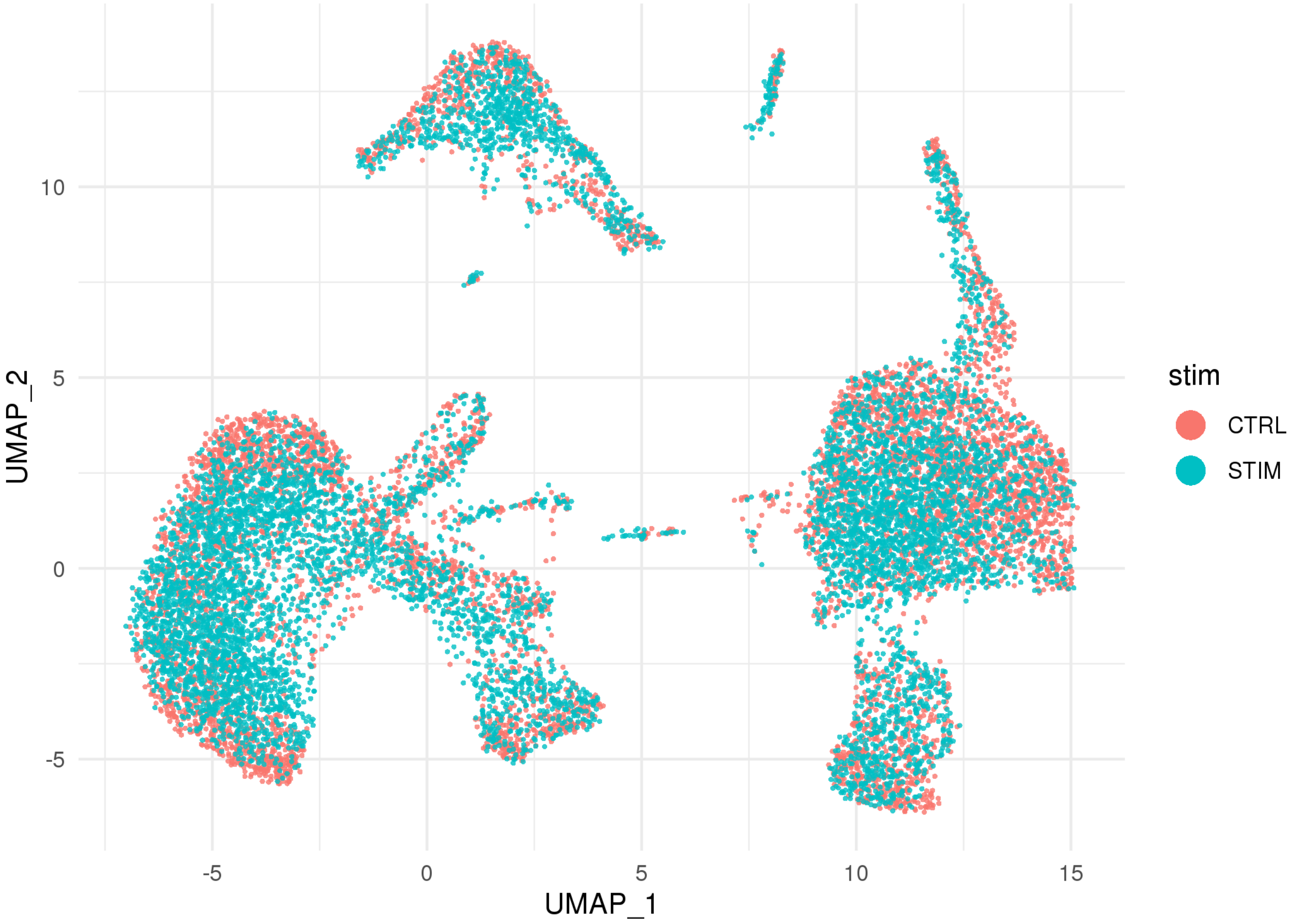


Figure 7: umap plot colored by stim

3 singleR

See the singleR paper and bioconductor package for more information.

3.1 HumanPrimaryCellAtlasData

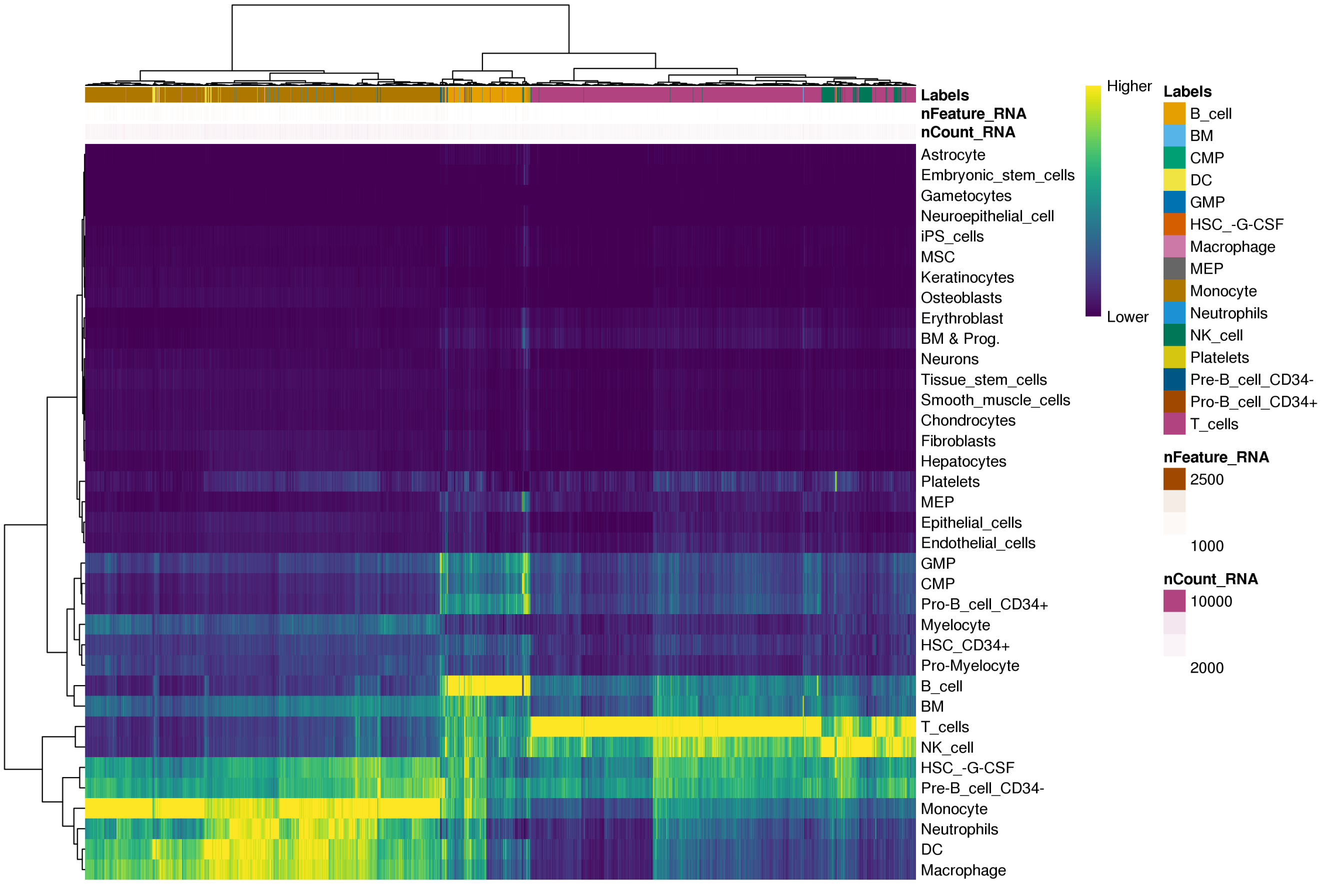


Figure 8: singleR predictions (HumanPrimaryCellAtlasData)

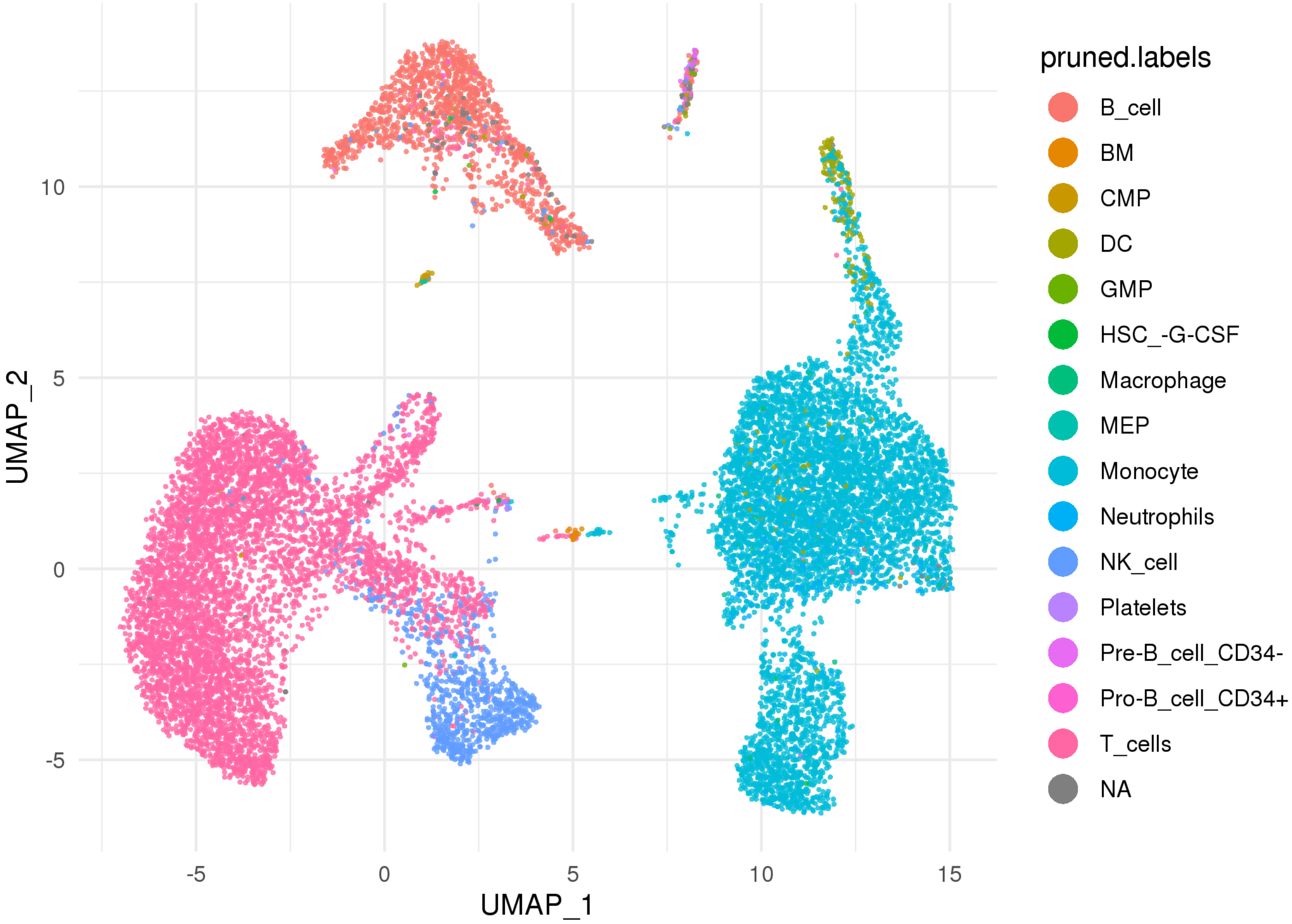


Figure 9: pruned singleR predictions (HumanPrimaryCellAtlasData)

3.2 DatabaseImmuneCellExpressionData

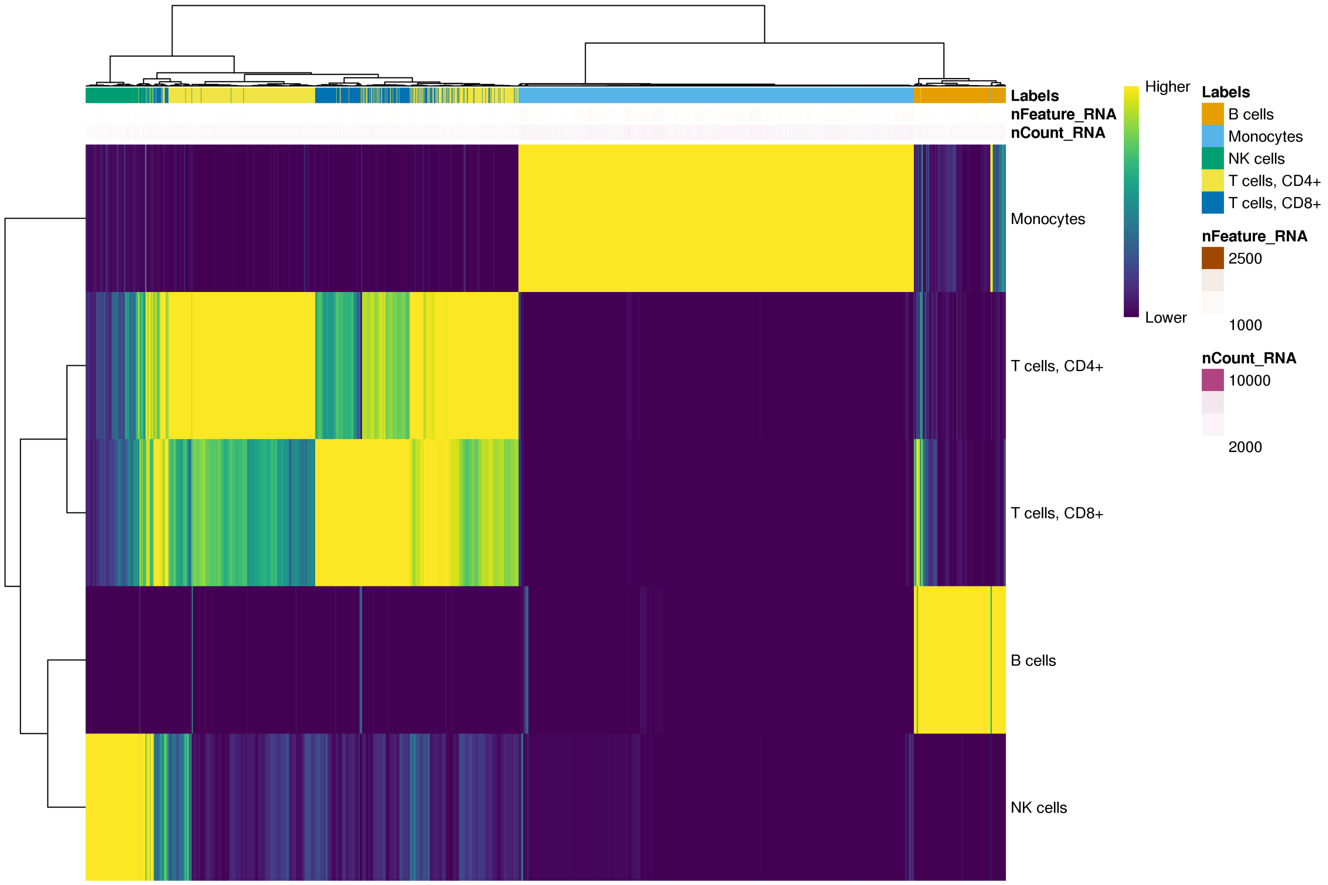


Figure 10: singleR predictions (DatabaseImmuneCellExpressionData)

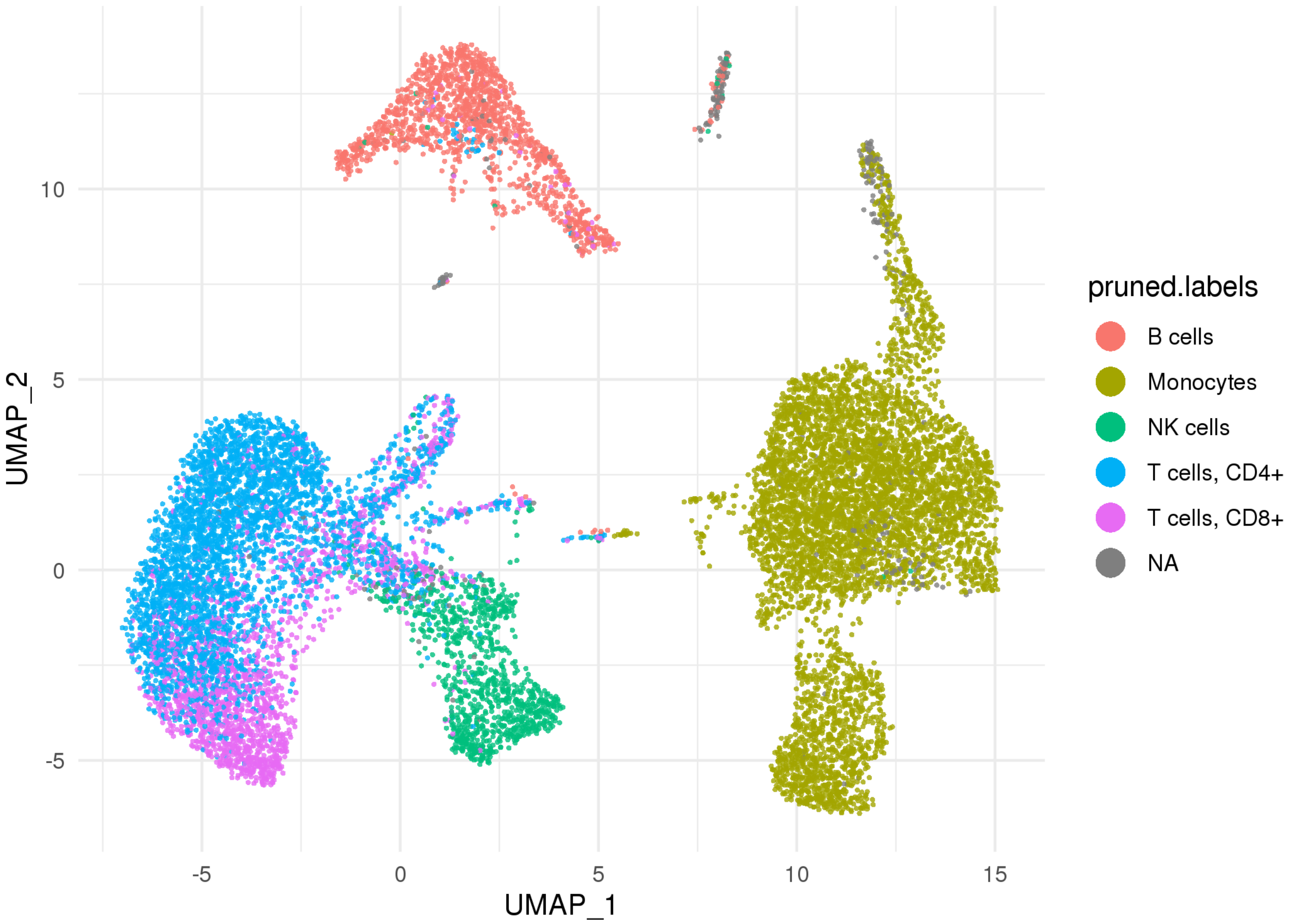


Figure 11: pruned singleR predictions (DatabaseImmuneCellExpressionData)

3.3 MonacoImmuneData

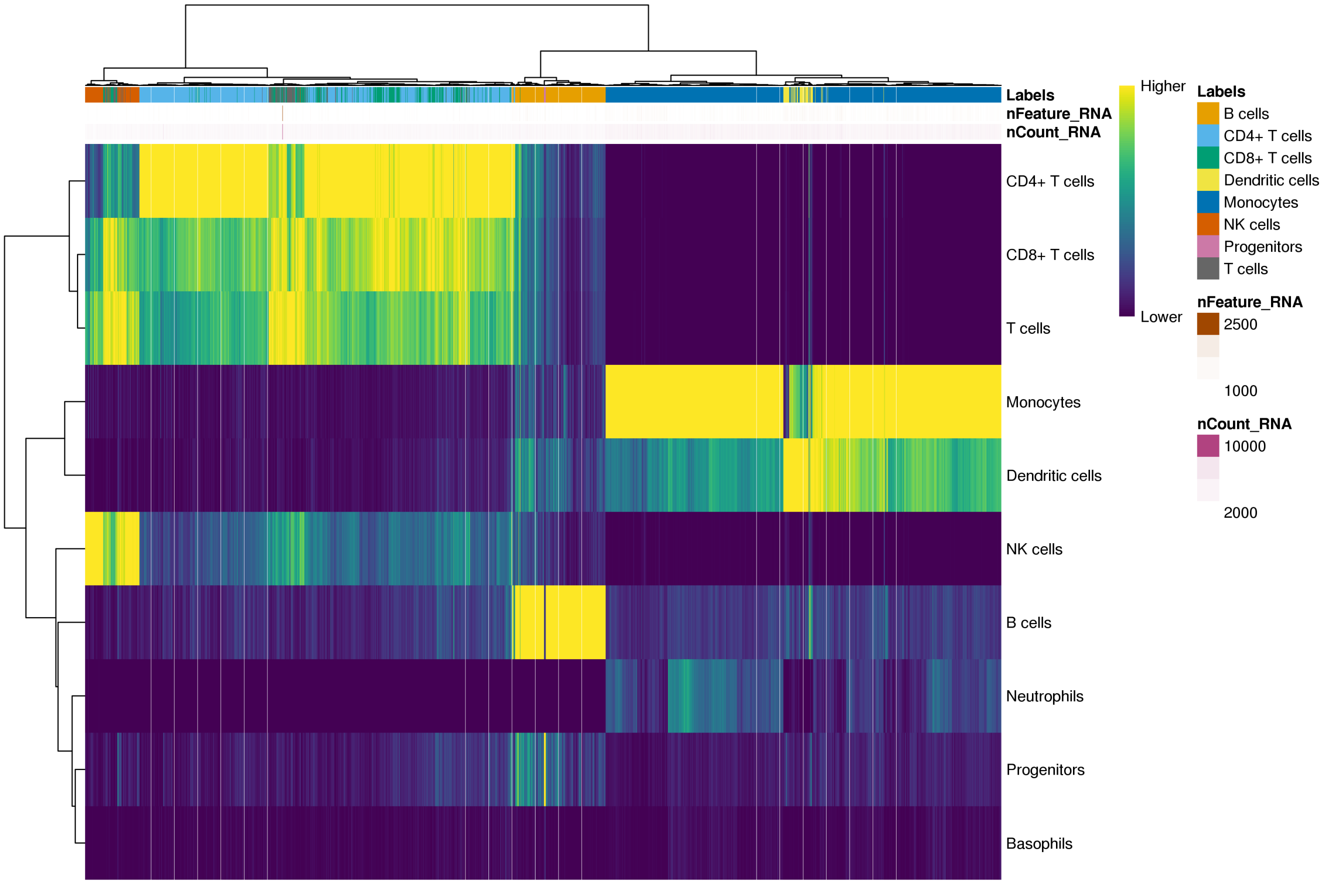


Figure 12: singleR predictions (MonacoImmuneData)

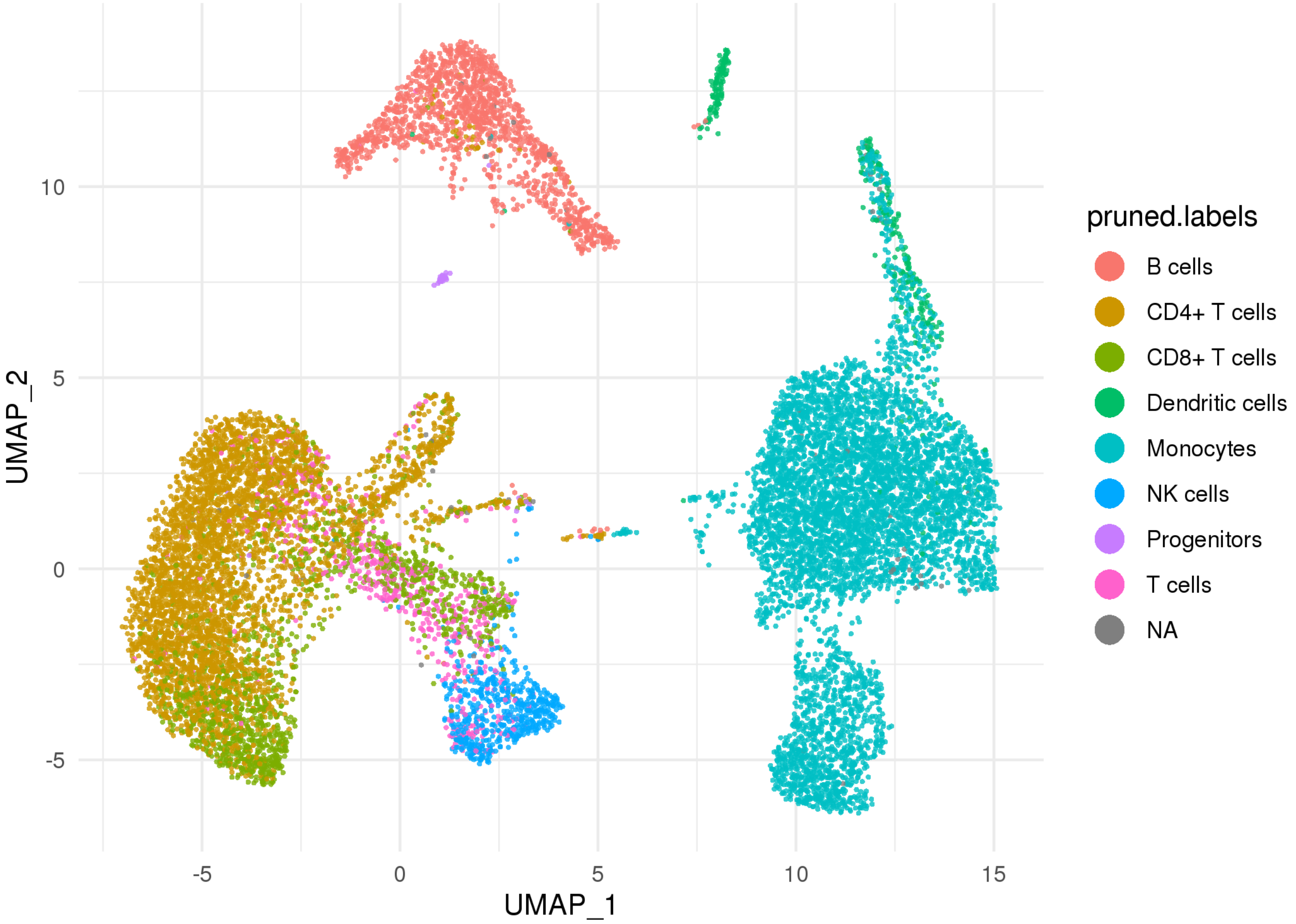


Figure 13: pruned singleR predictions (MonacoImmuneData)

4 Plots of summary statistics

Plots of summary statistics (e.g. cell number) by factor of interest (e.g. cluster)

4.1 Overall numbers of cells per cluster

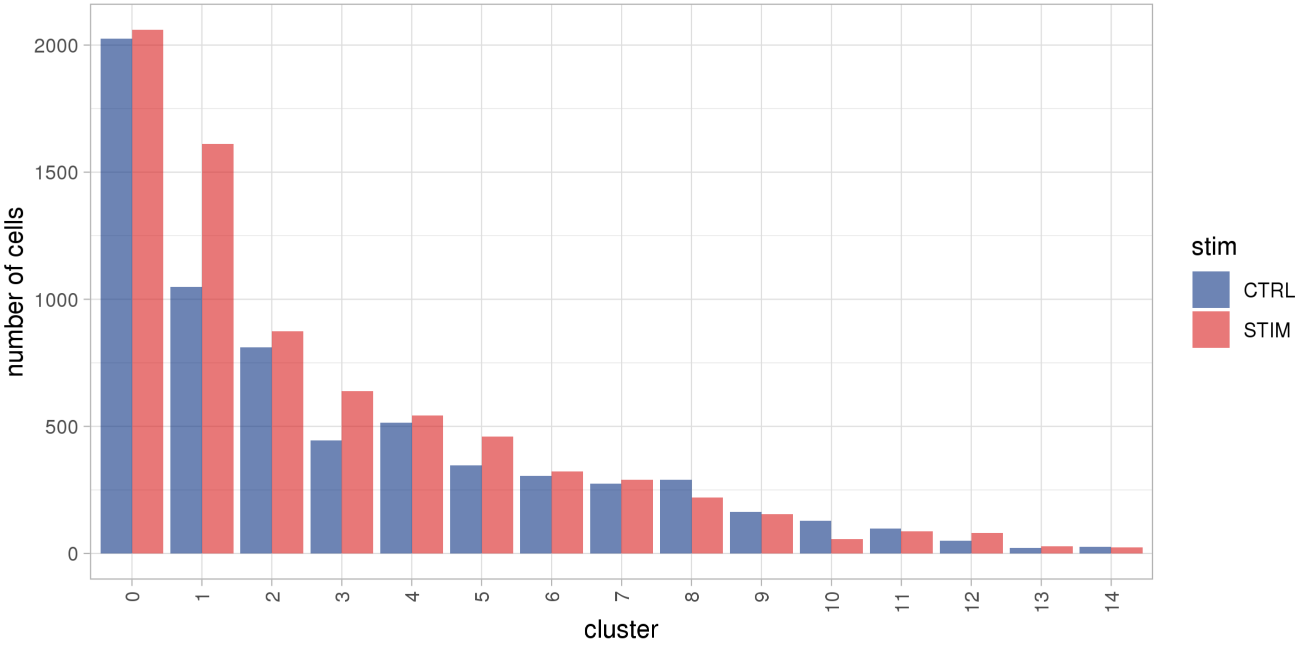


Figure 14: Overall numbers of cells per cluster

4.2 Percentage of cells per cluster

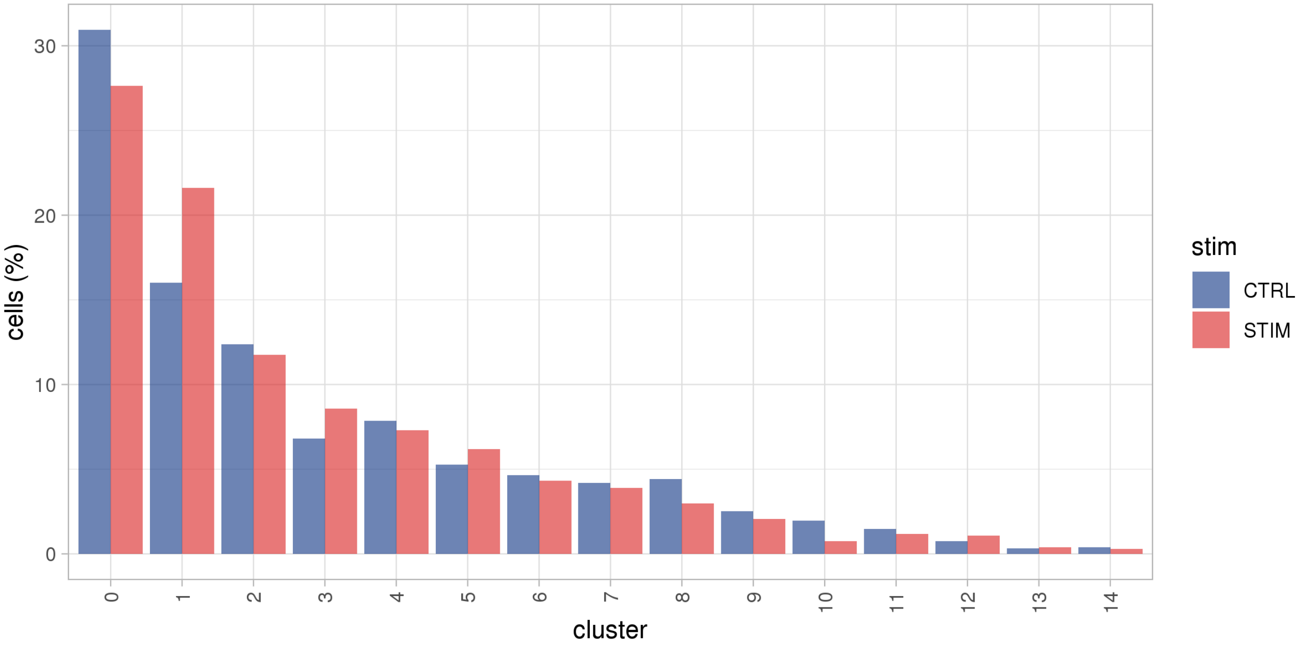


Figure 15: Percentage of cells per cluster

4.3 Composition of clusters by stimulation

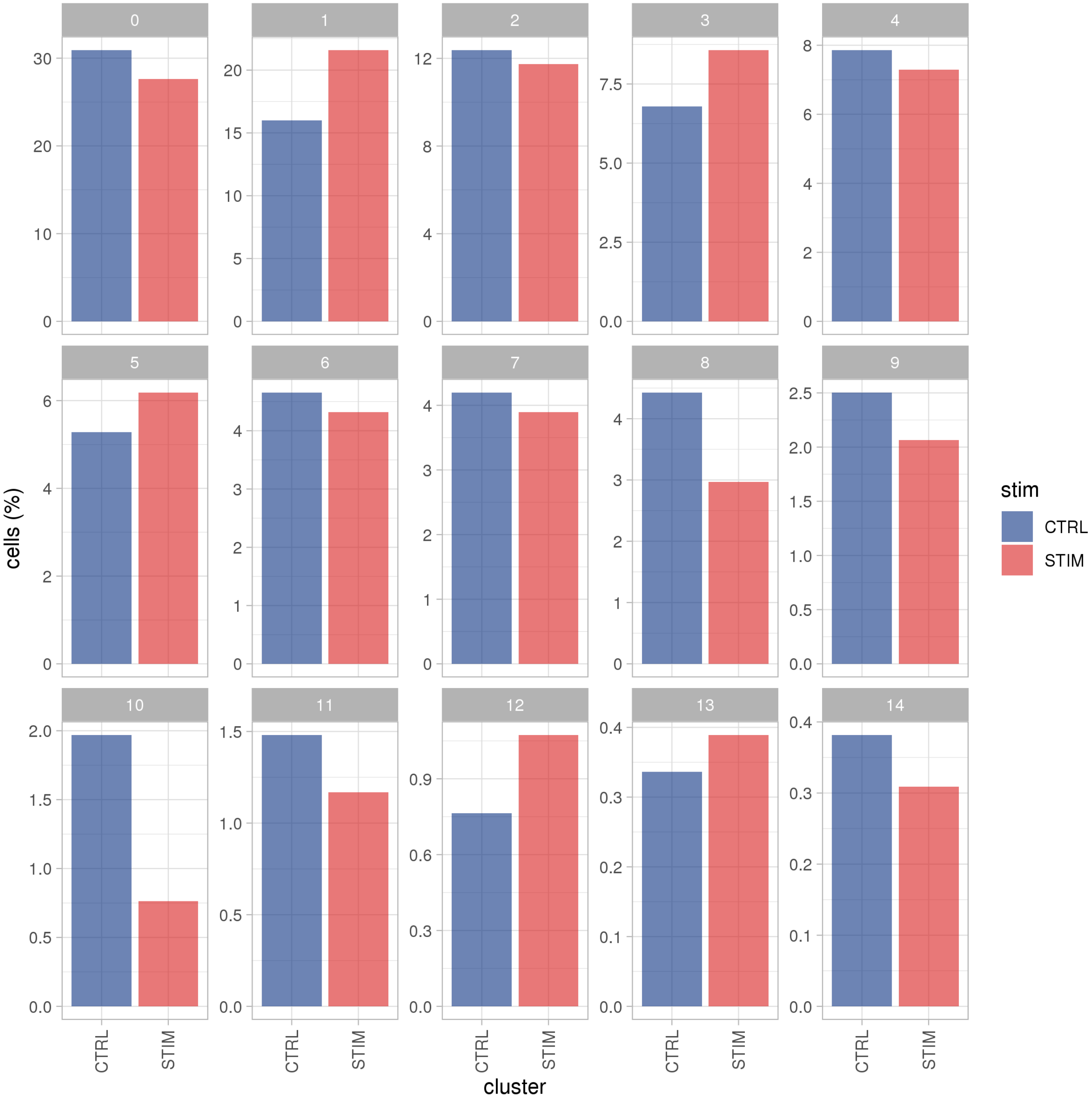


Figure 16: Composition of clusters by stimulation

4.4 Number of genes per cell per cluster

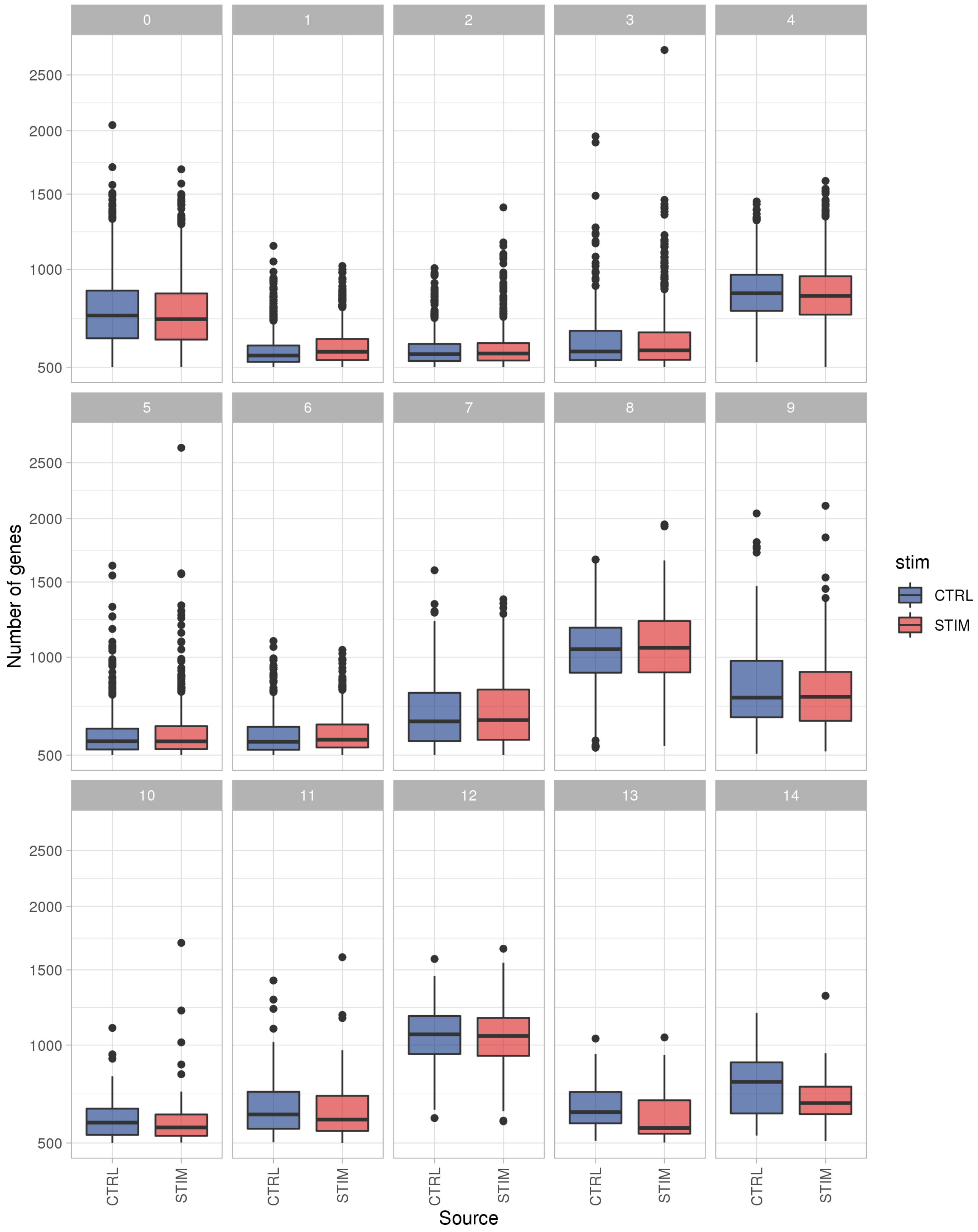


Figure 17: Number of genes per cell per cluster

4.5 Number of umi per cell per cluster

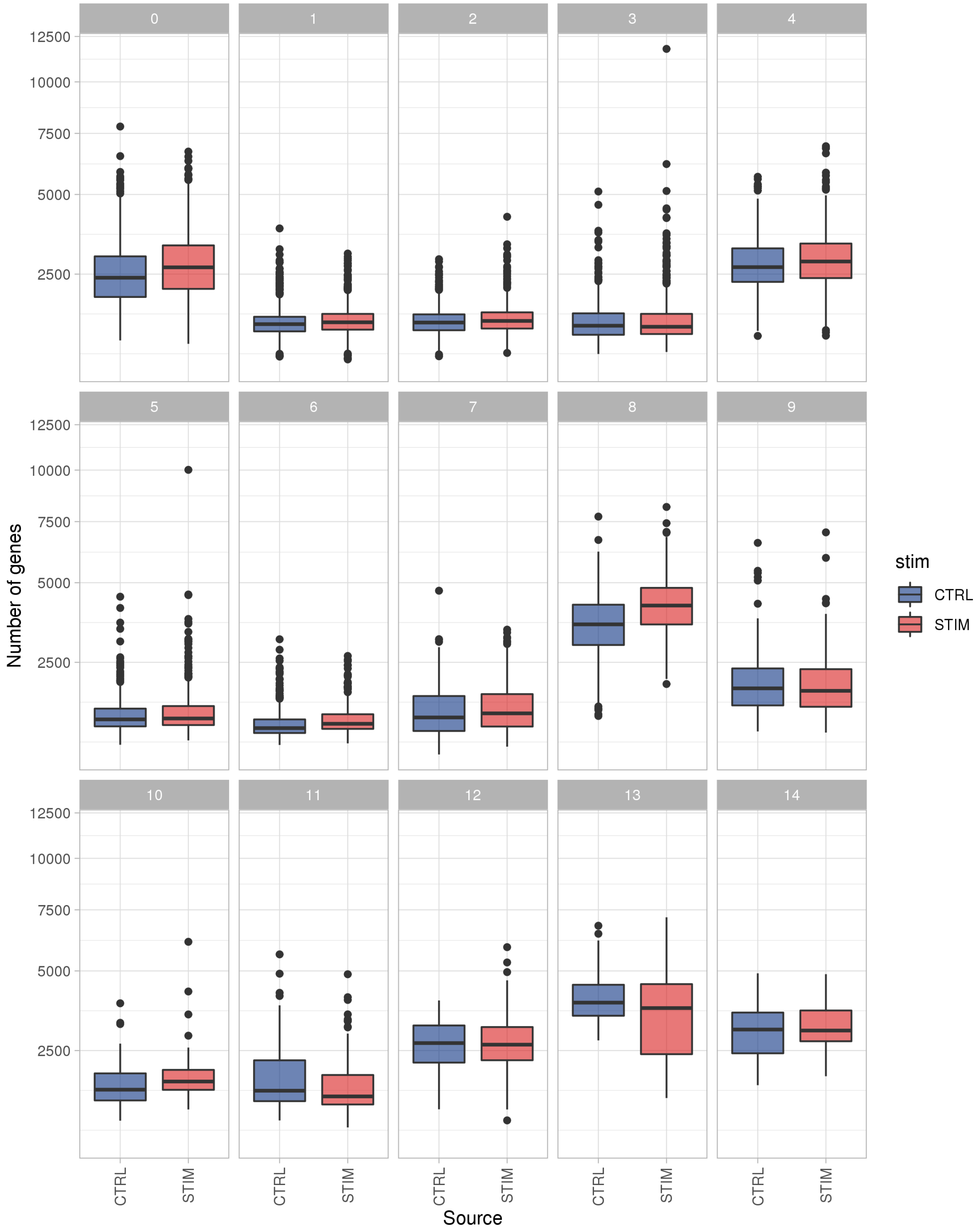


Figure 18: Number of umi per cell per cluster

5 Cluster dissimilarity

5.1 Dissimilarity by gene expression

The distances between the clusters was assessed using the "BuildClusterTree" function in the Seurat package, which "constructs a phylogenetic tree relating the "average" cell from each identity class".

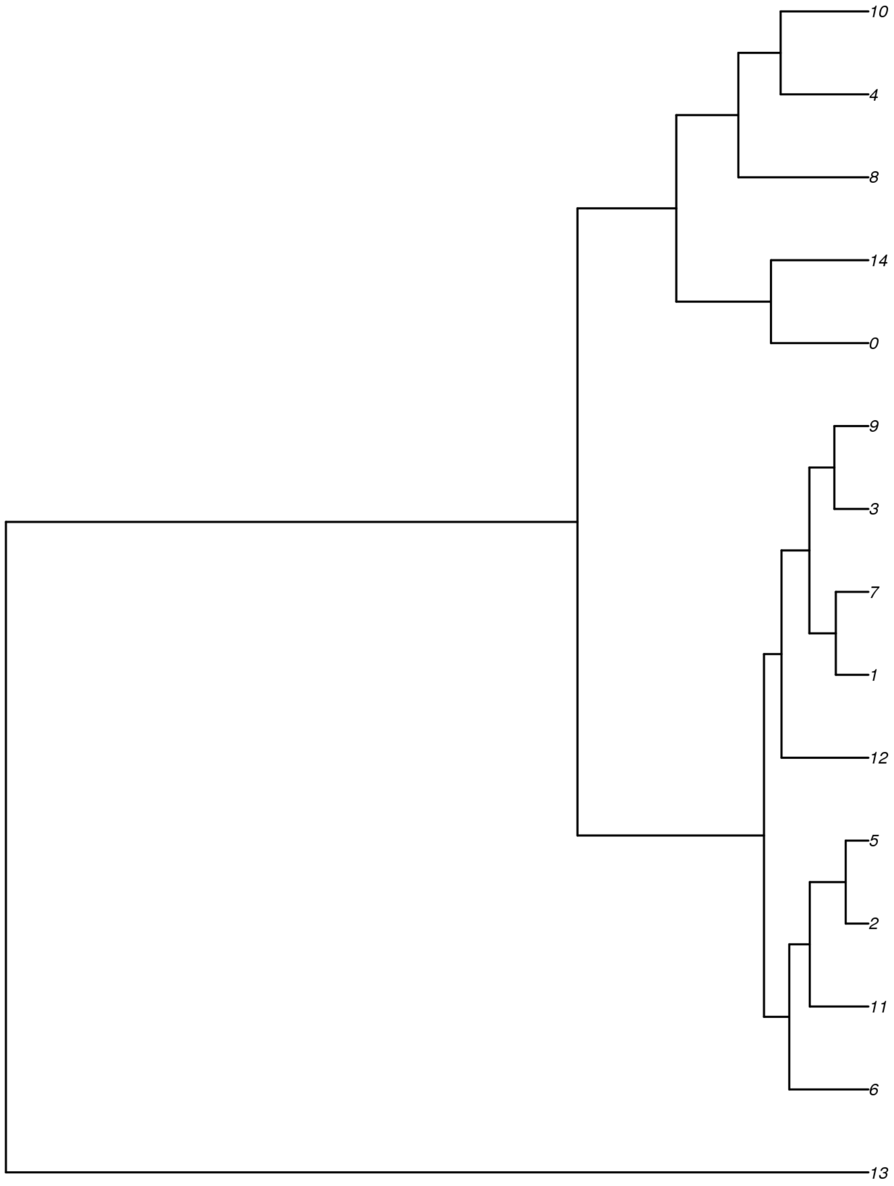


Figure 19: Visualisation of inter-cluster distances (cluster average, gene-based)

6 Cluster resolution analysis

The clustree algorithm is used to compare the different clustering resolutions.

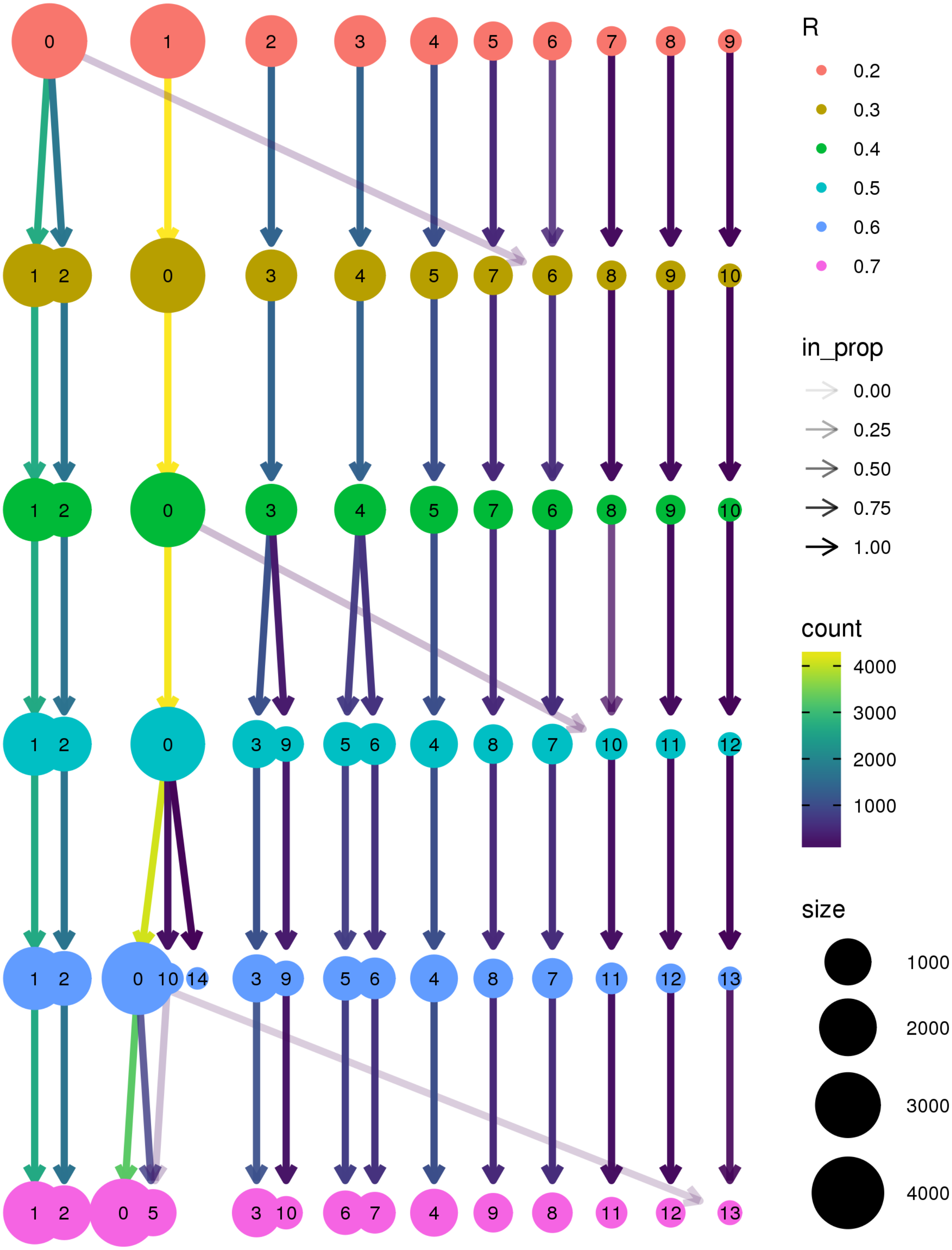


Figure 20: The relationships between the clusters identified at different resolutions

7 Diffusion map

7.0.1 Diffusion map plots (first 3 dimensions, different rotations) colored by cluster

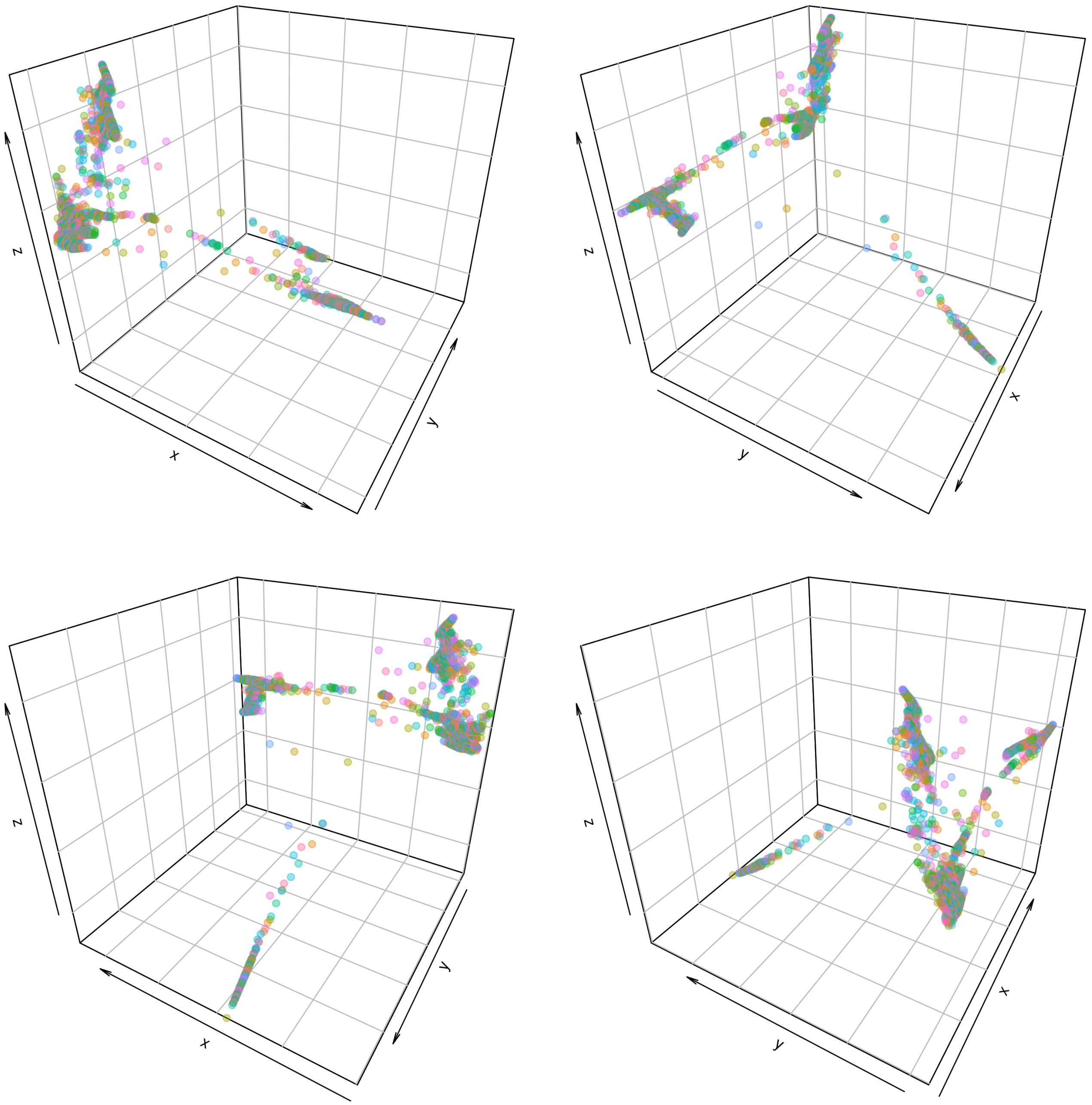


Figure 21: Diffusion map plots (first 3 dimensions, different rotations) colored by cluster

8 Phate maps

See: https://www.nature.com/articles/s41587-019-0336-3.

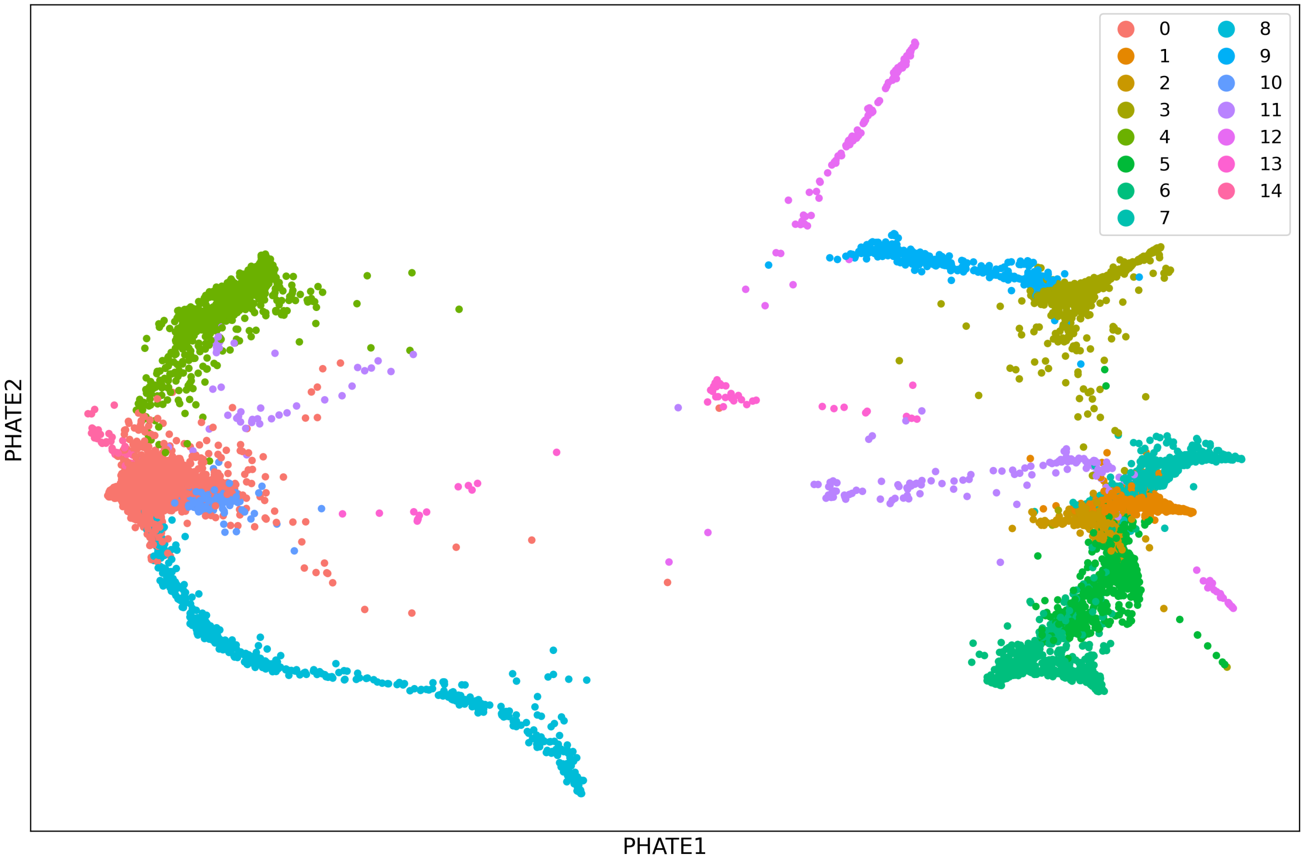


Figure 22: 2D Phate map

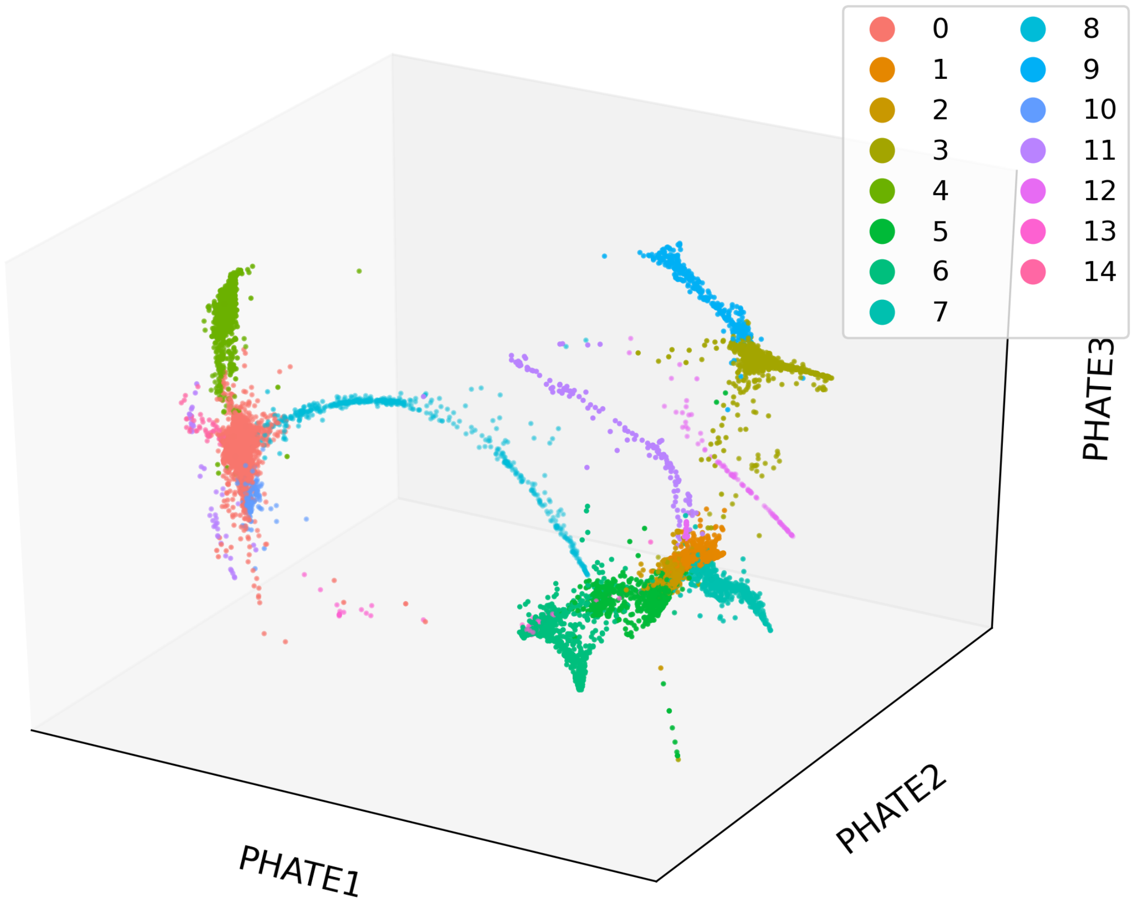


Figure 23: 3D Phate map

9 Partion-based graph abstraction (PAGA)

The original method is described here: PAGA

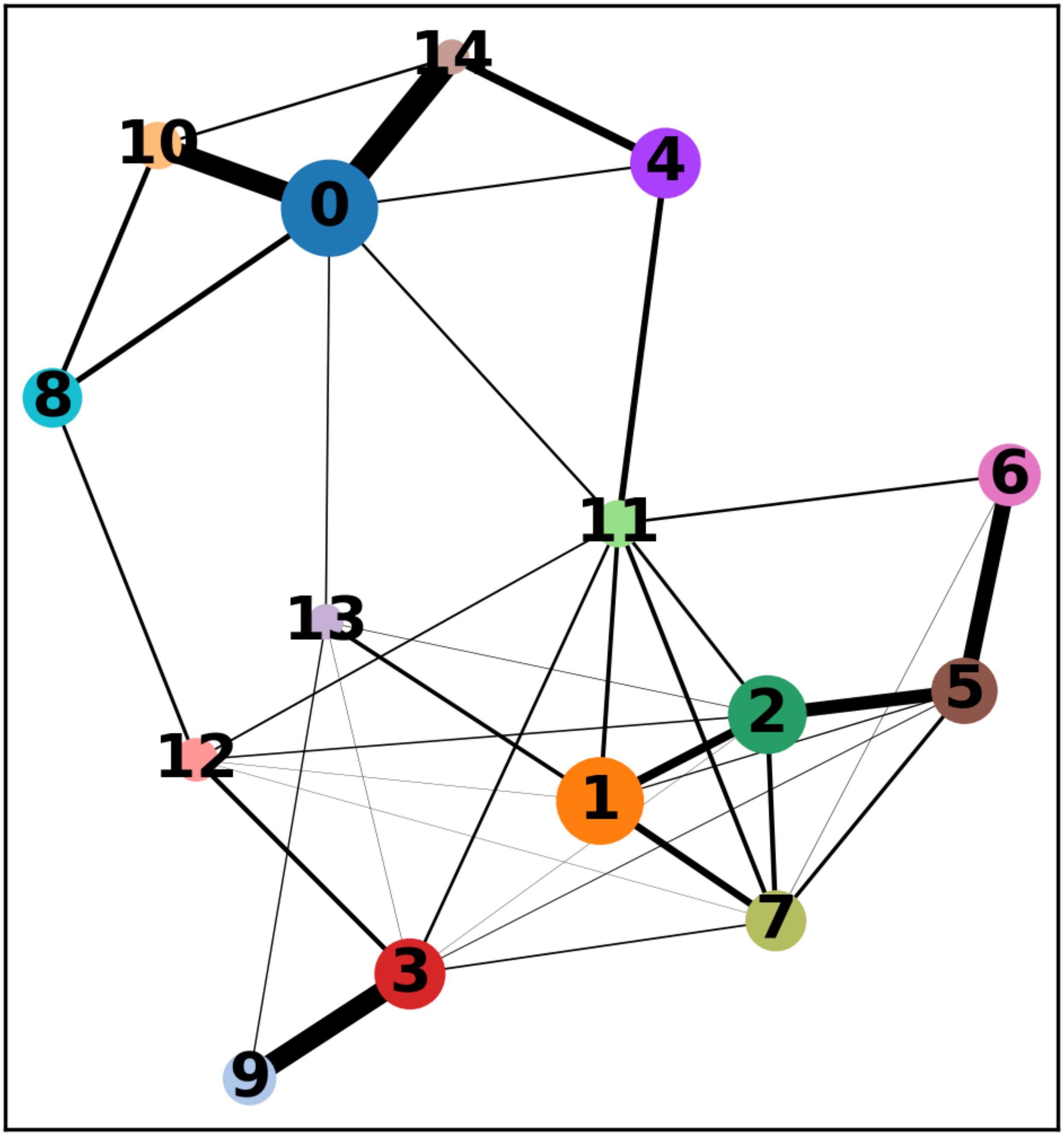


Figure 24: PAGA graph

9.1 UMAP

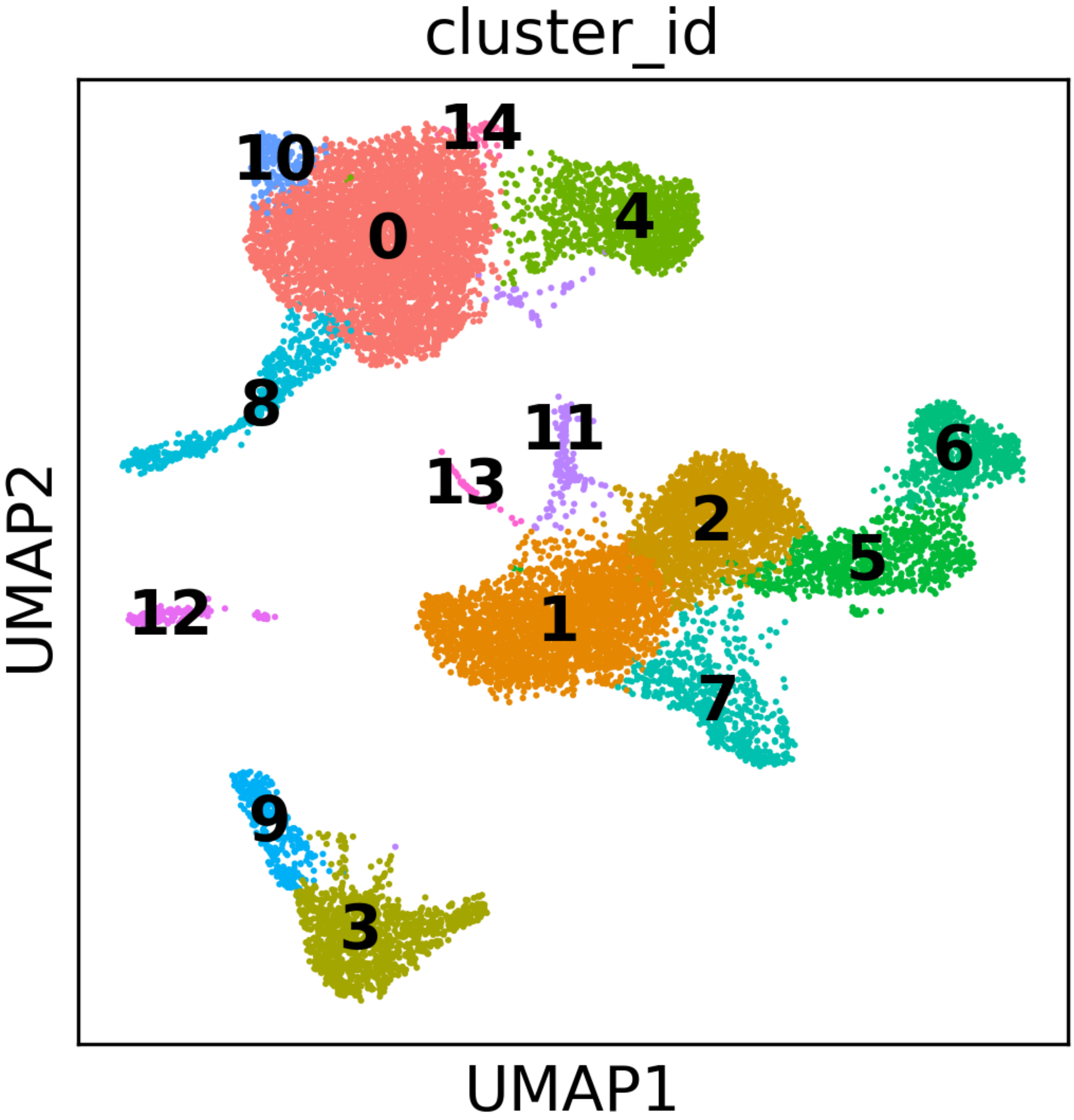


Figure 25: PAGA initialised UMAP

9.2 Force directed graphs

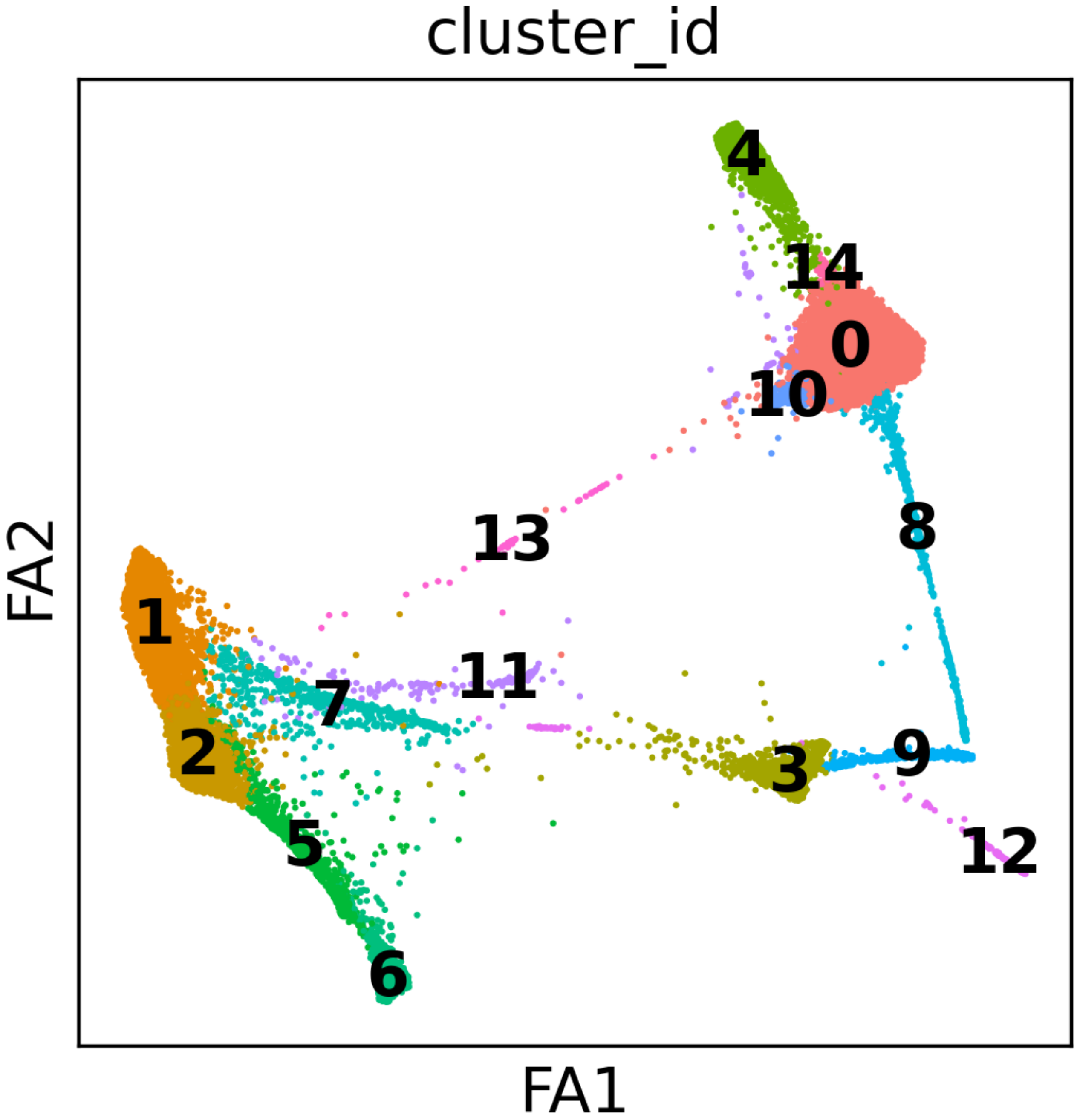


Figure 26: Force atlas 2 (FA2) force directed graph

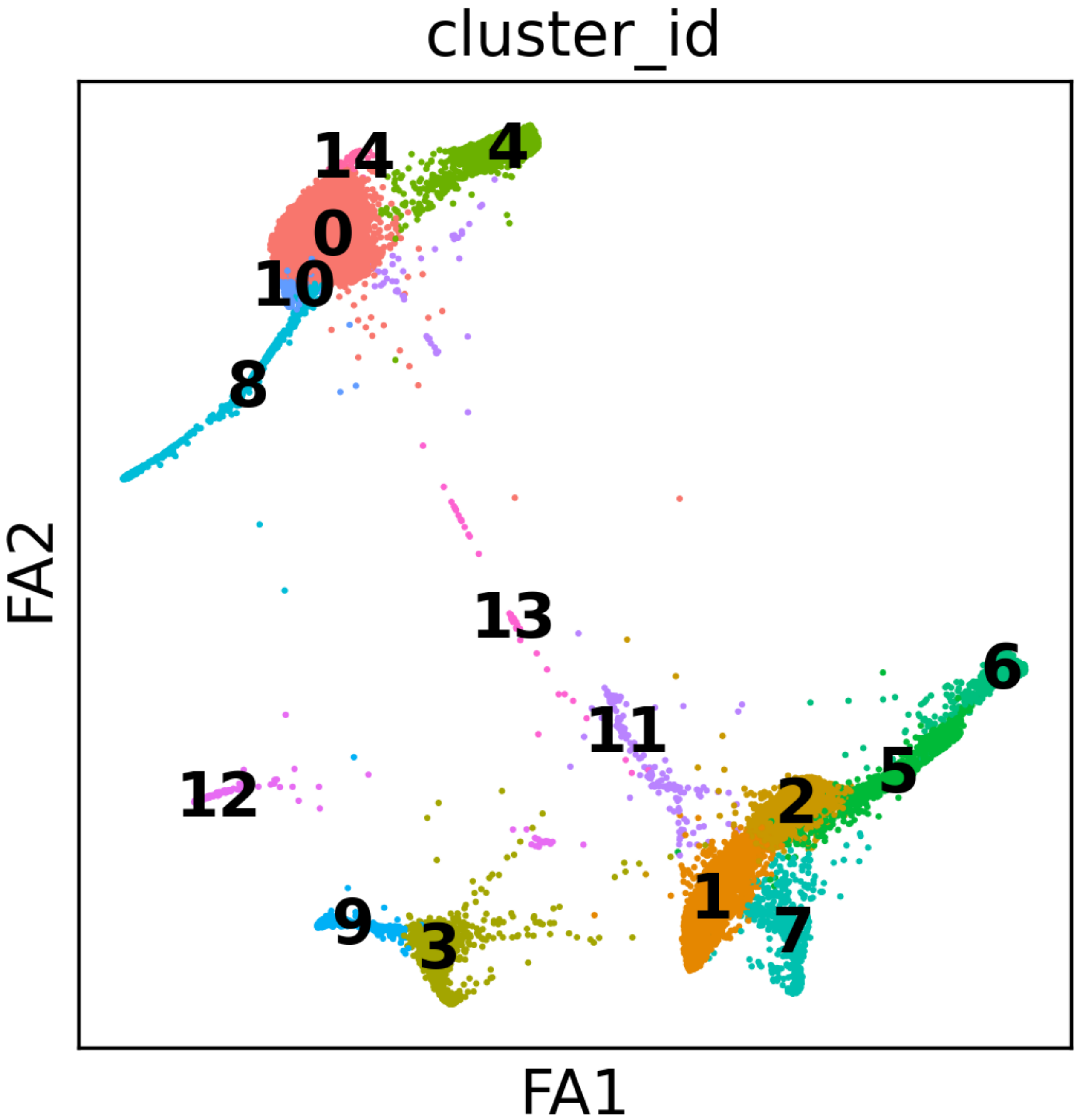


Figure 27: PAGA initialised FA2 force directed graph

10 Identification of cluster marker genes

Cluster marker genes were identified using the Seurat FindMarkers routine and the wilcox test. A summary table containing all of the significant markers for all of the clusters (based on BH adjusted p value) is available separately.

Key parameters are:

- Differential expression methods: wilcox
- Testing limited to genes with a log fold change of > 0.25
- Testing limited to genes detected in a minimum fraction of 0.1 of cells
- Conservation factor applied: stim

11 Top cluster marker genes

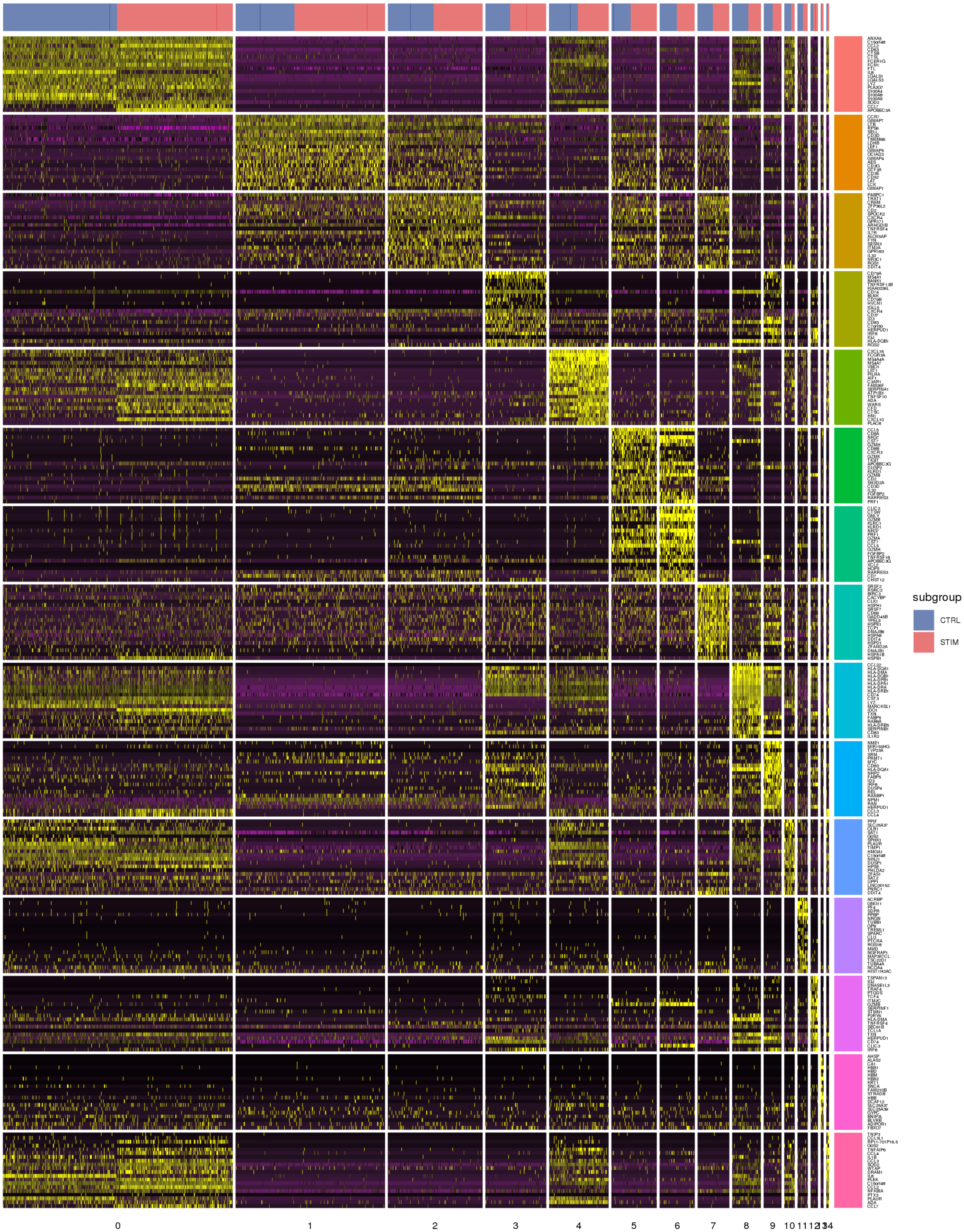


Figure 28: Heatmap of the top cluster-specific genes (based on differential expression analysis)

12 Marker genes by cluster

12.0.1 Summary of numbers of DE genes per-cluster

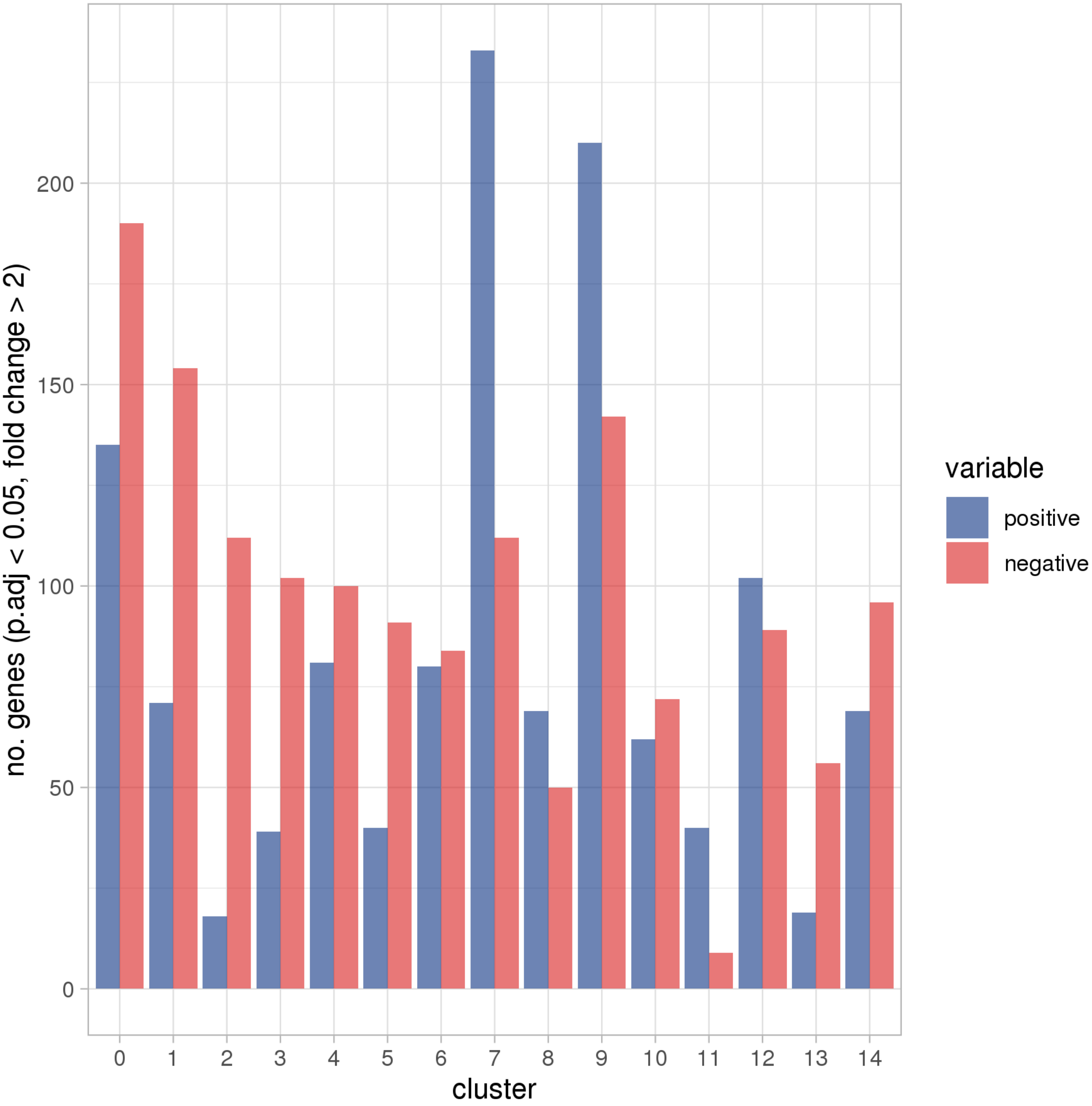


Figure 29: Numbers of differentially expressed genes (adjusted p-value < 0.05, fold change > 2) per cluster

12.1 Cluster 0: summary plots

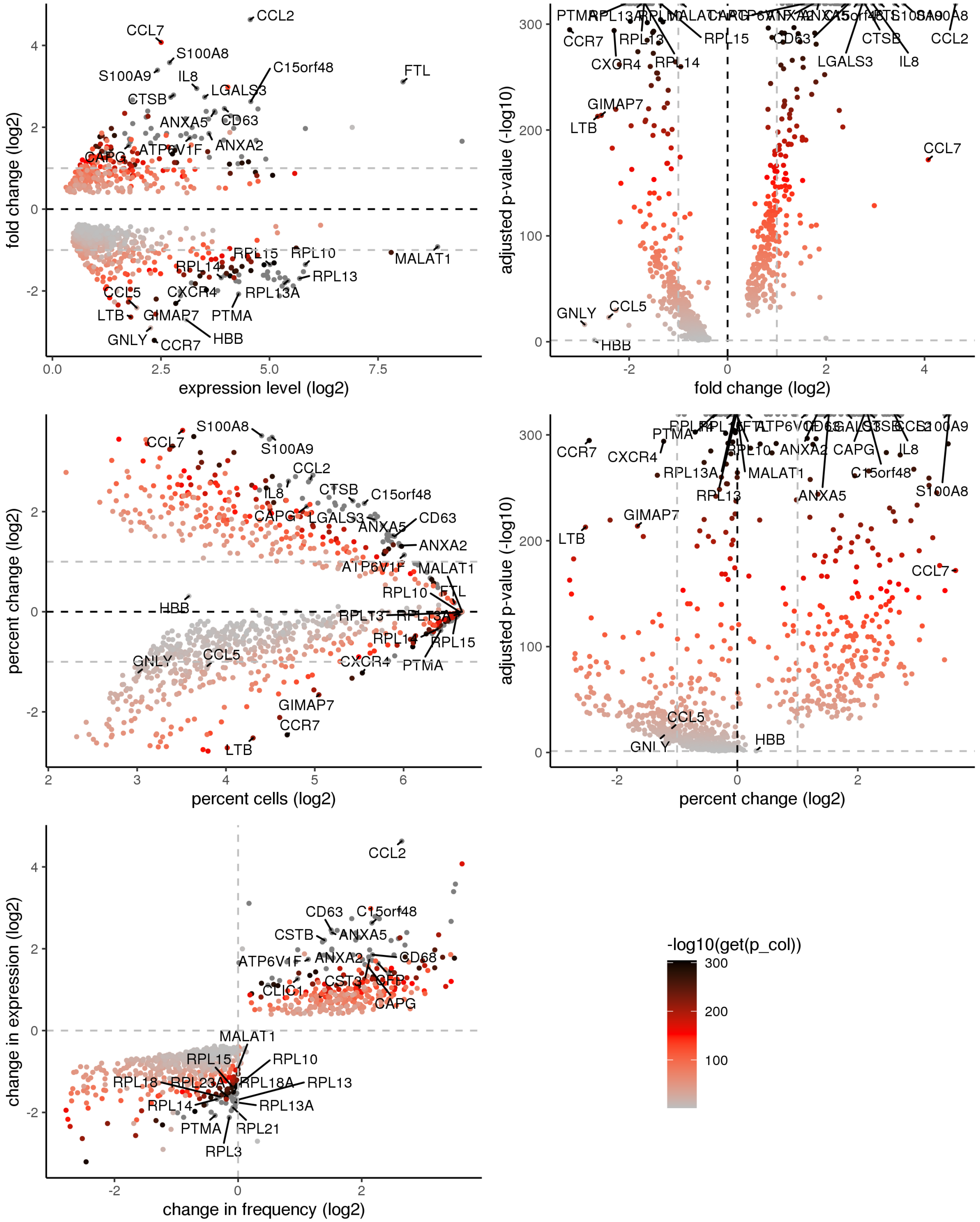
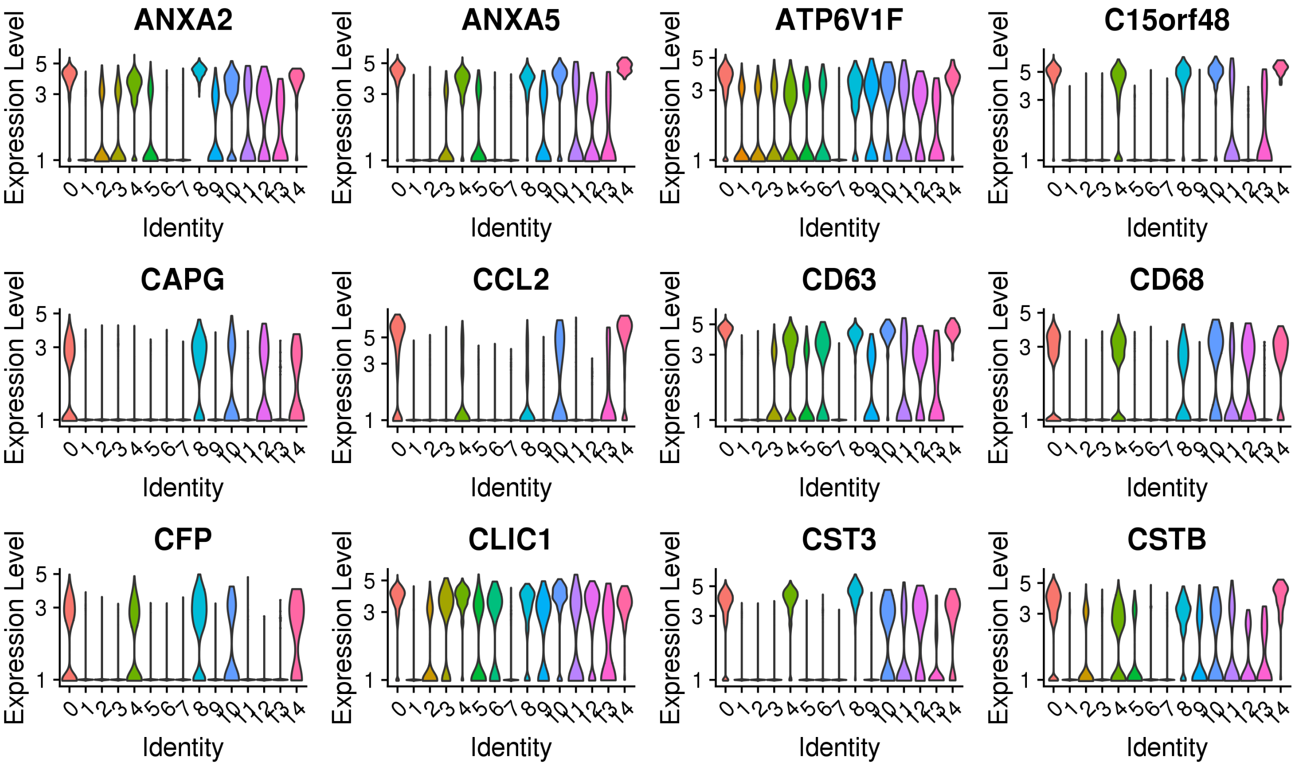
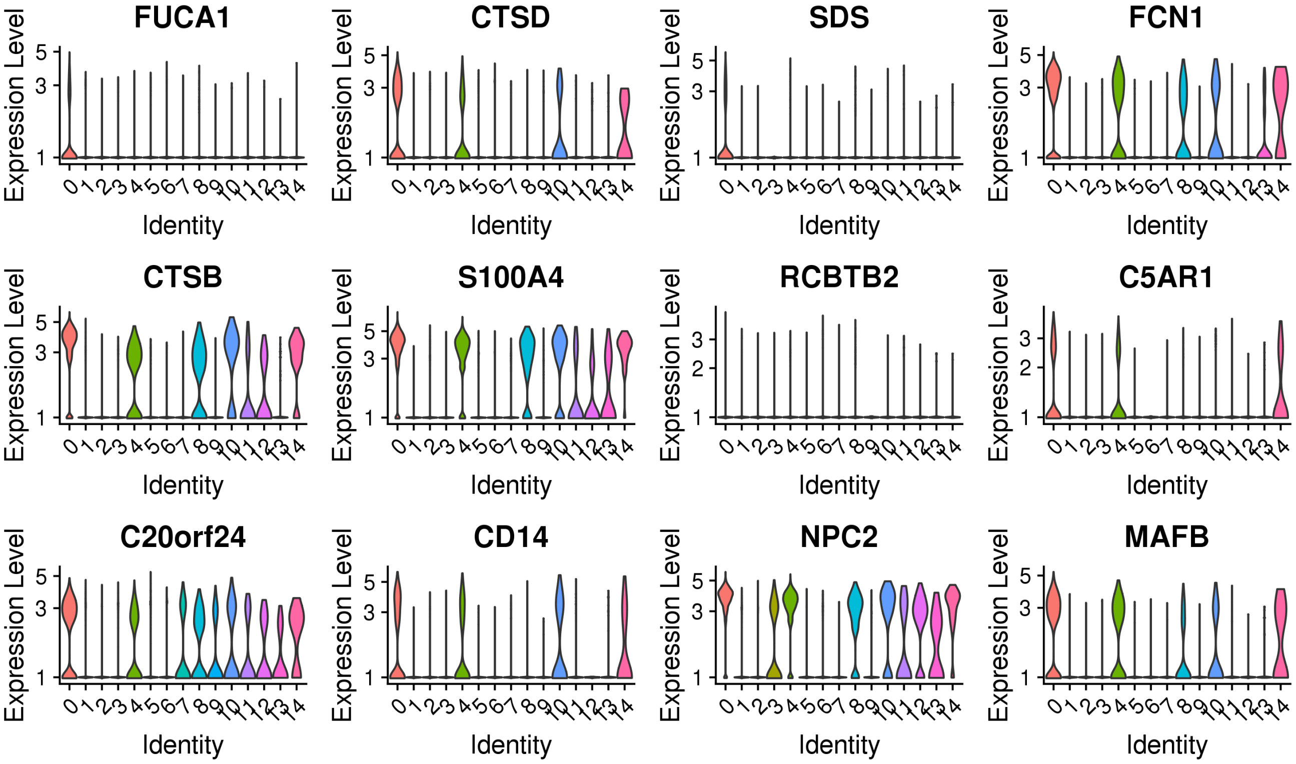


Figure 30: Differential expression summary plots for cluster 0

12.2 Cluster 0 violin plots: positive marker genes

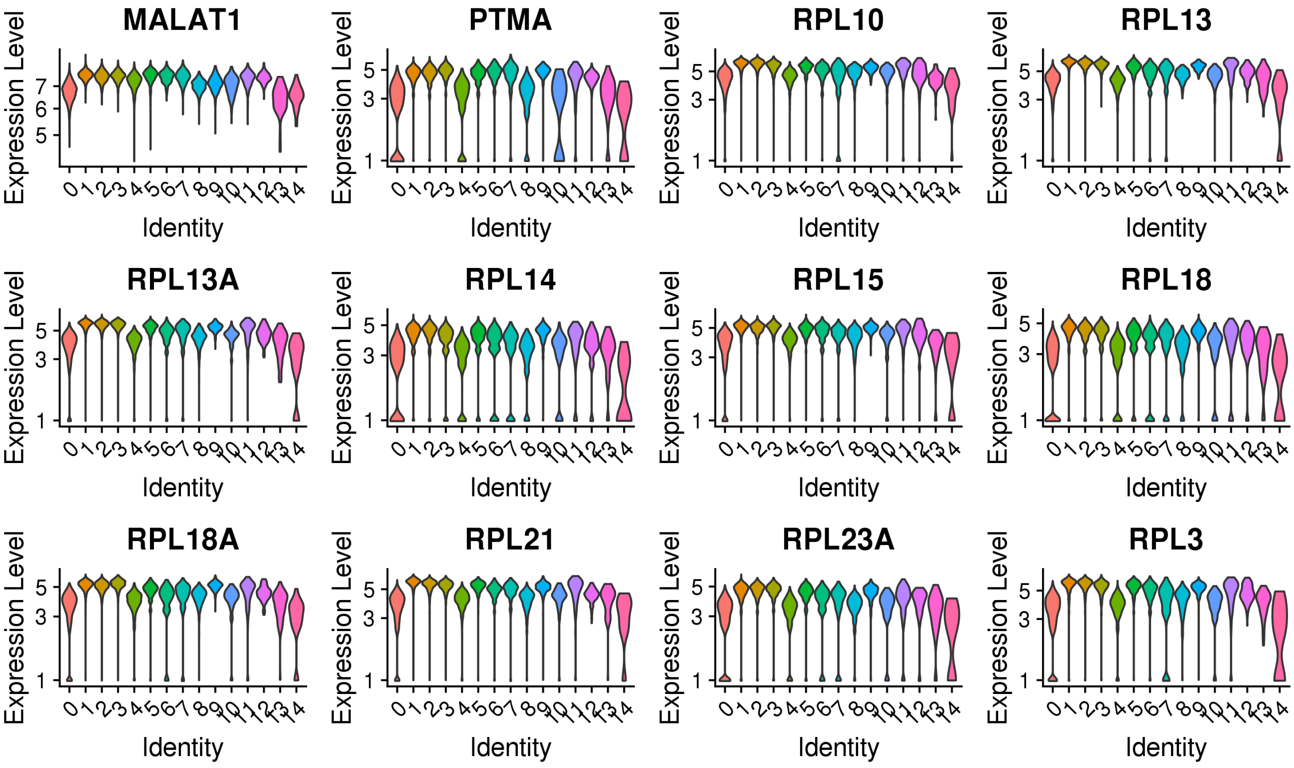


(a) Top positive marker genes ordered by p-value, cluster: 0

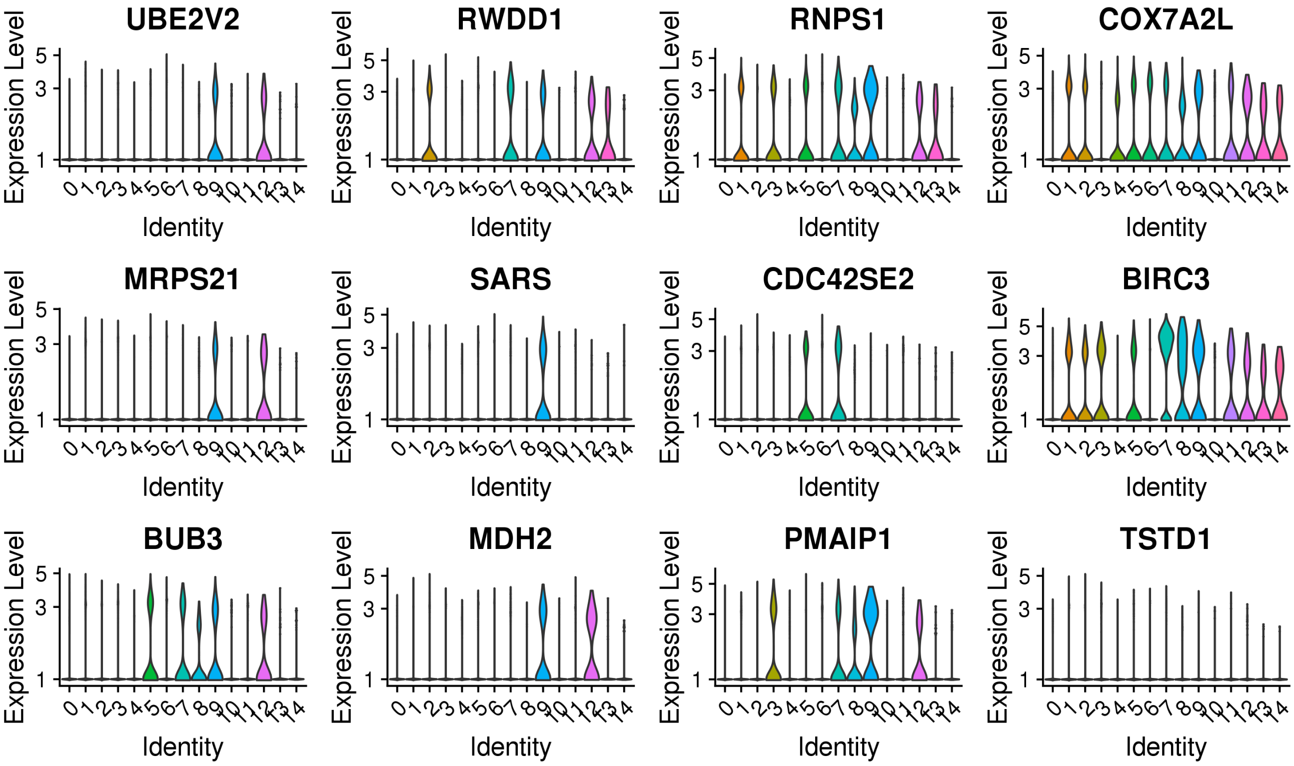


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 0

12.3 Cluster 0 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 0



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 0

12.4 Cluster 1: summary plots

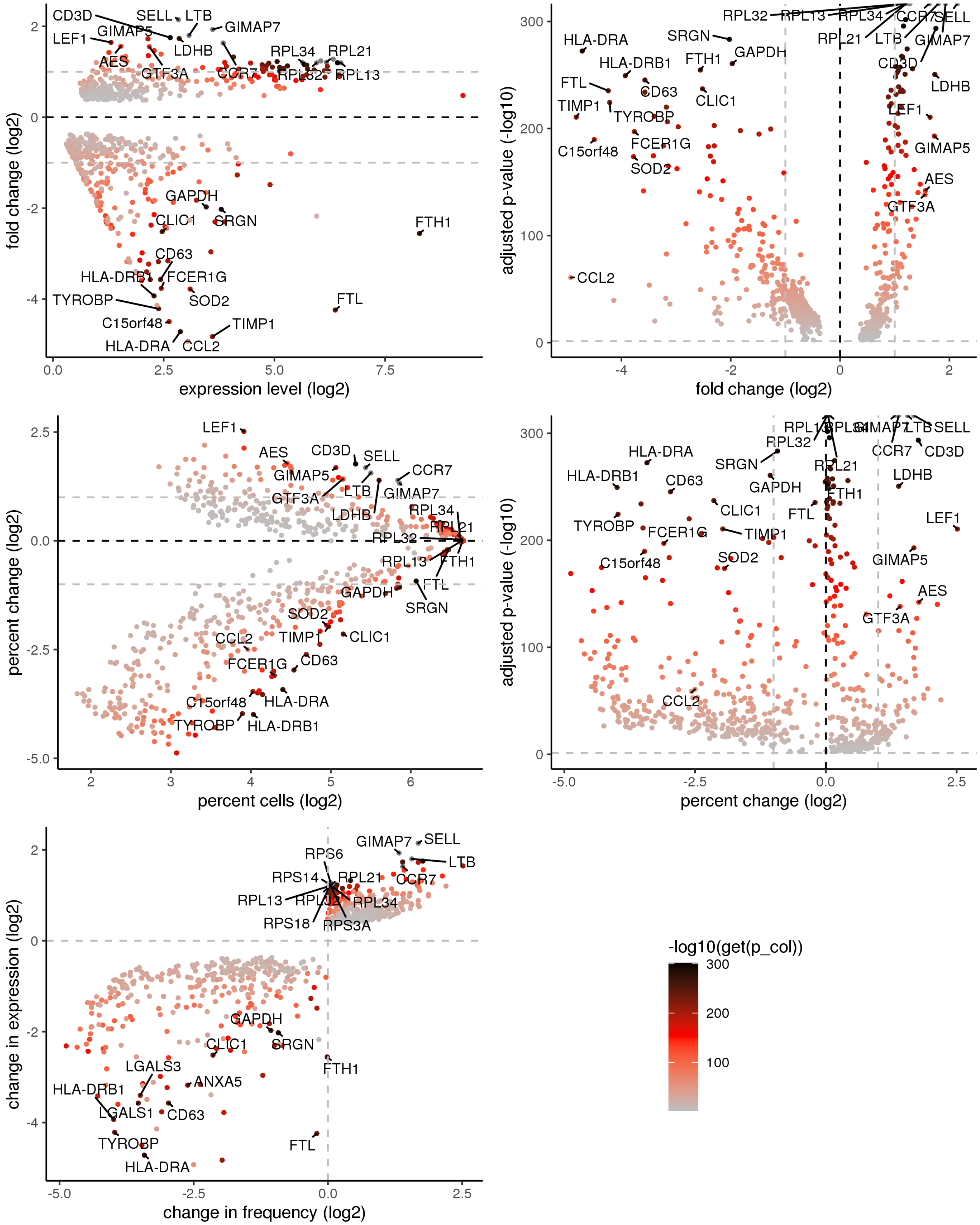
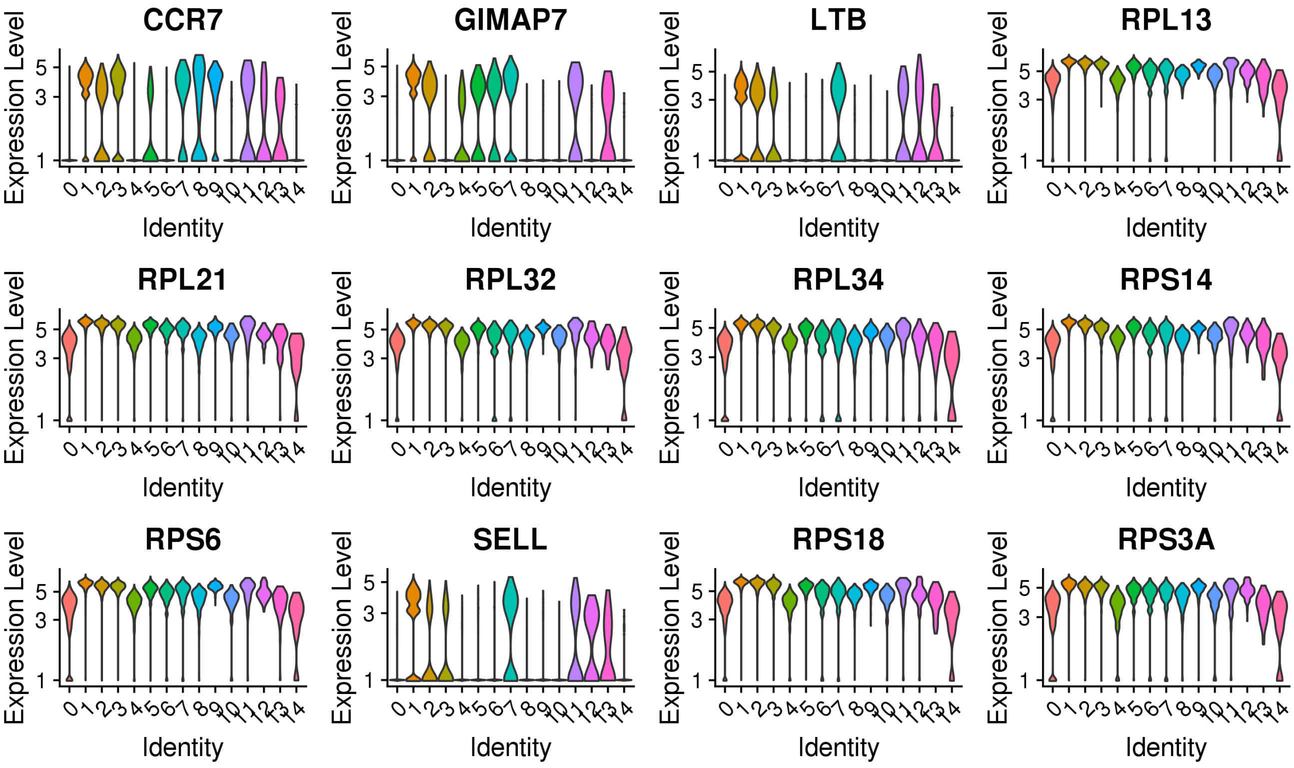
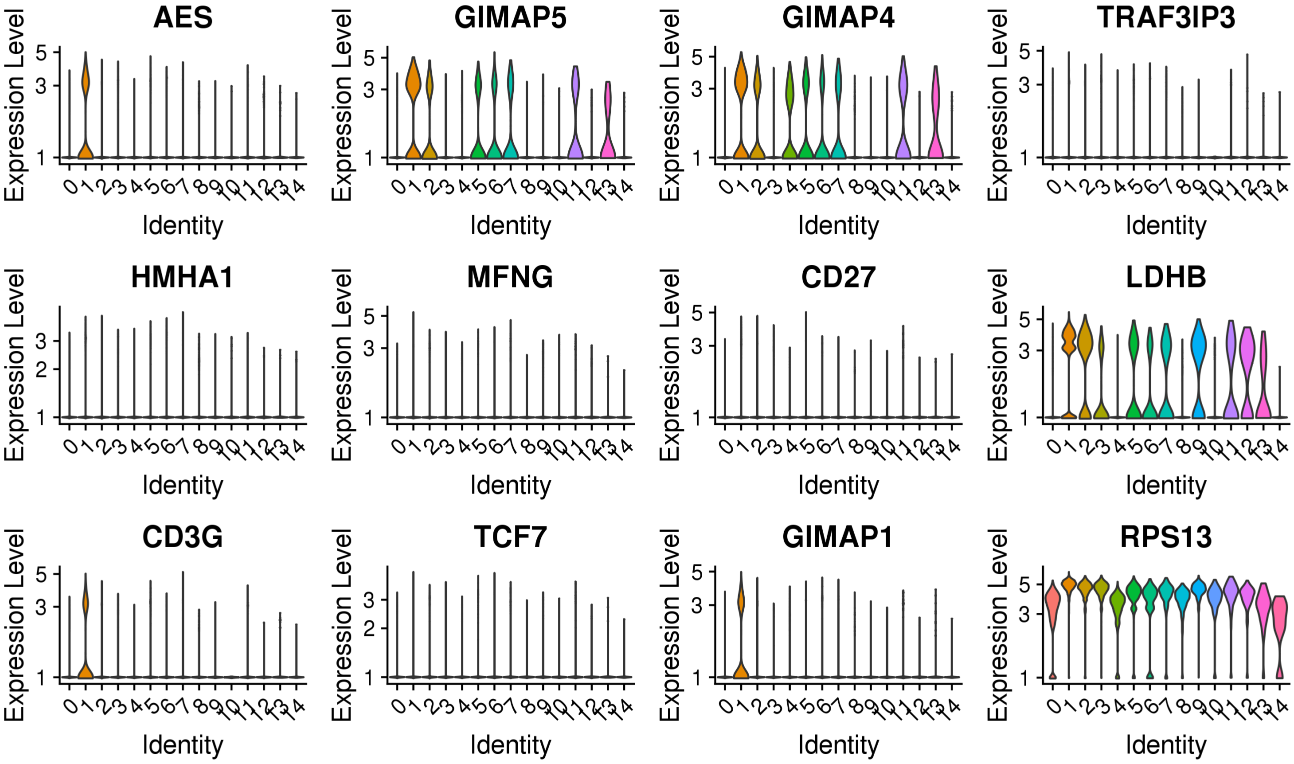


Figure 33: Differential expression summary plots for cluster 1

12.5 Cluster 1 violin plots: positive marker genes

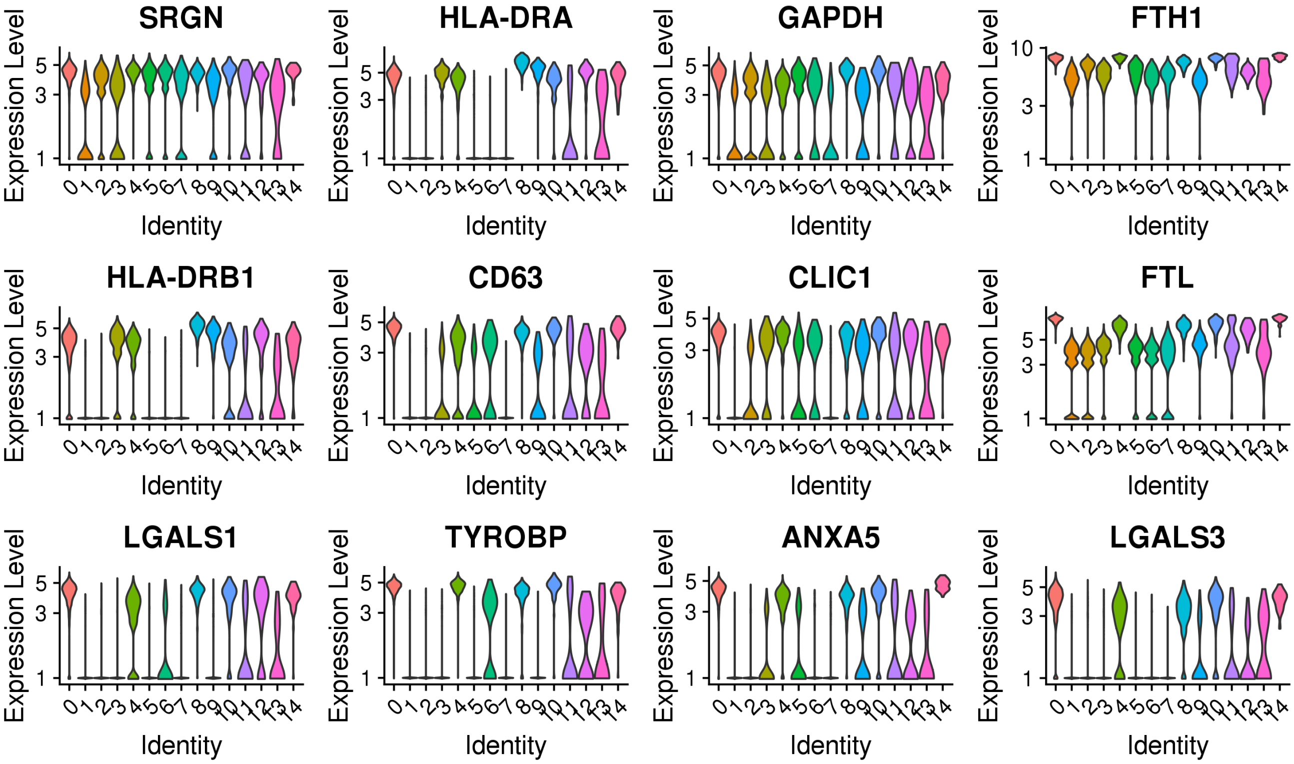


(a) Top positive marker genes ordered by p-value, cluster: 1

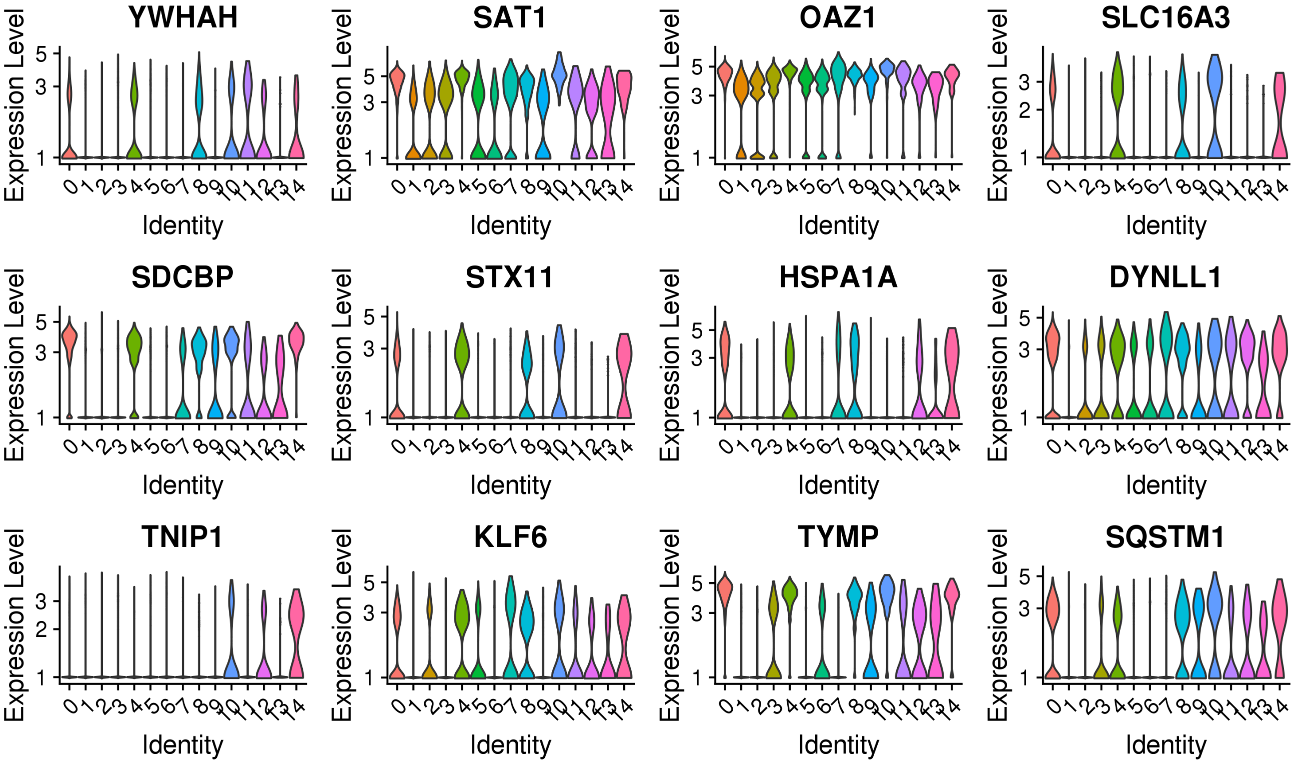


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 1

12.6 Cluster 1 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 1



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 1

12.7 Cluster 2: summary plots

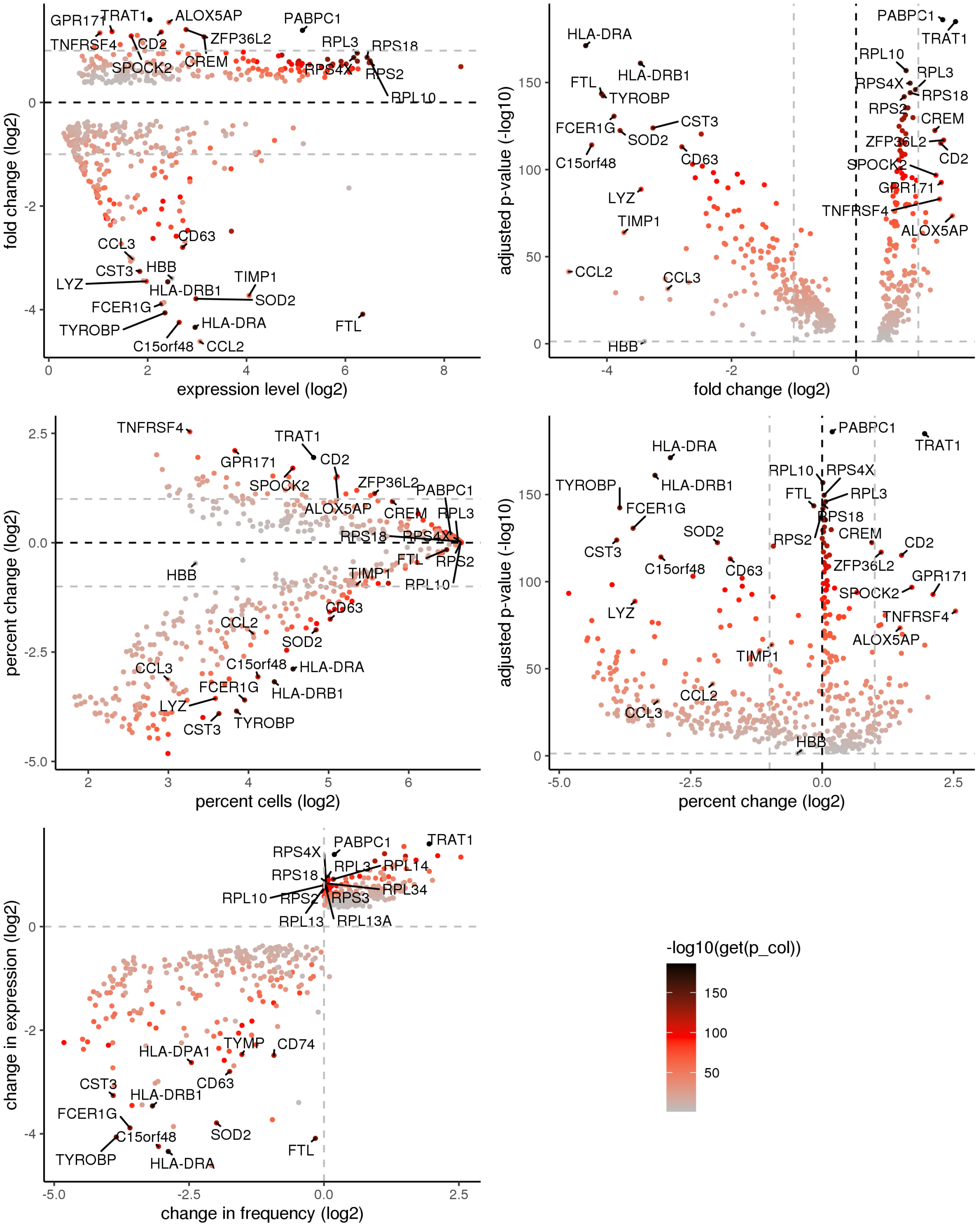
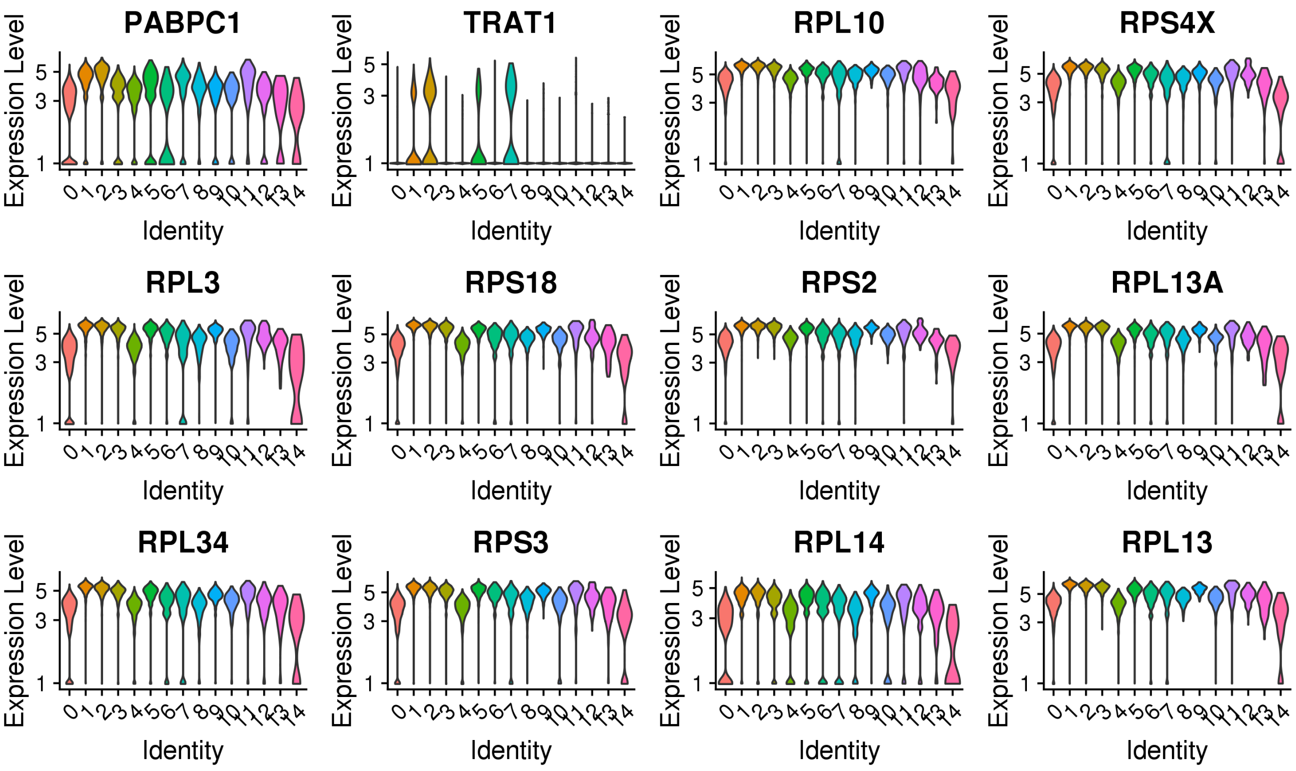
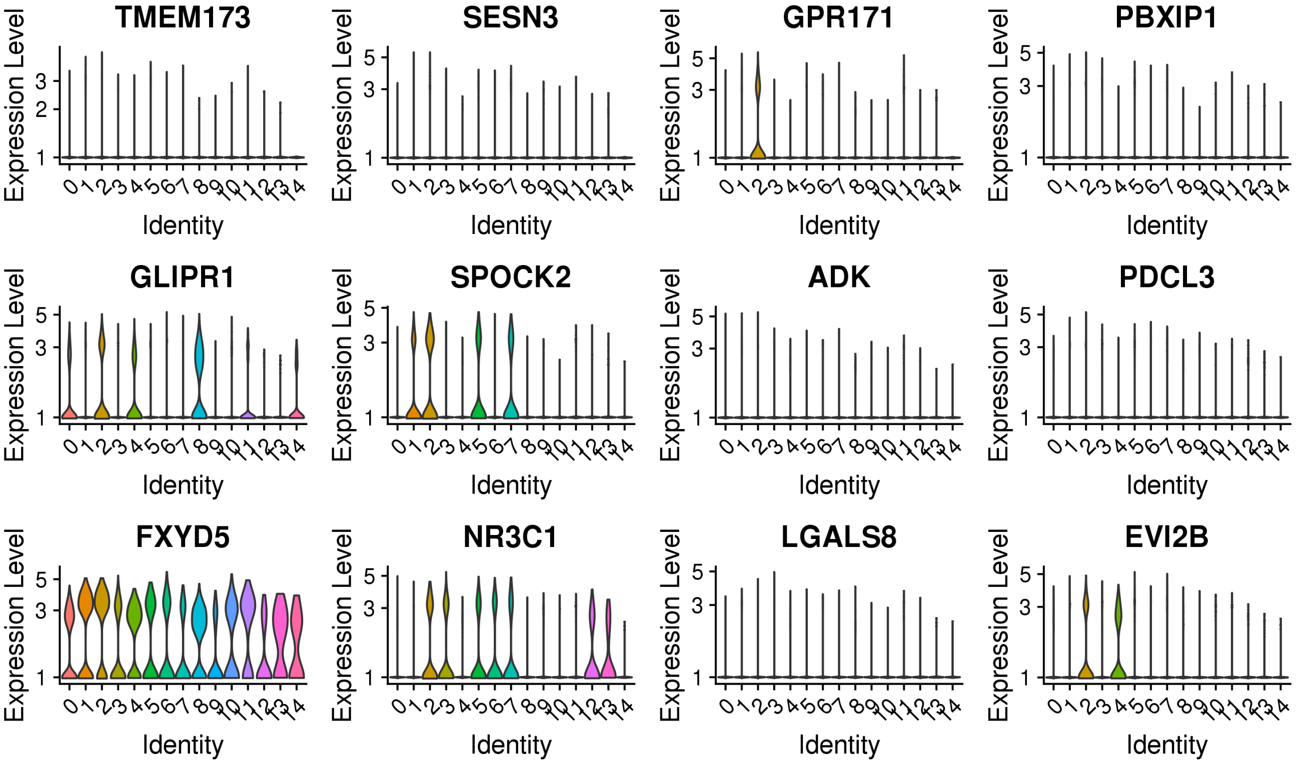


Figure 36: Differential expression summary plots for cluster 2

12.8 Cluster 2 violin plots: positive marker genes

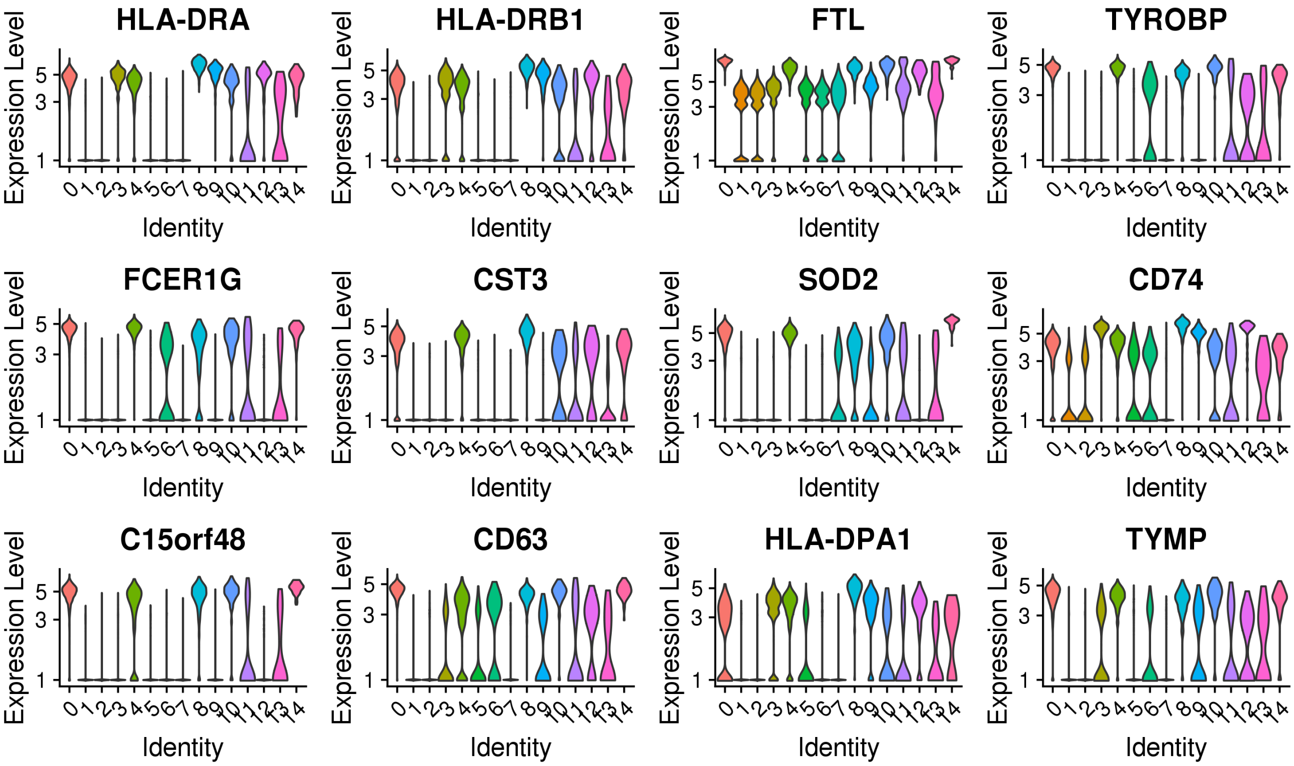


(a) Top positive marker genes ordered by p-value, cluster: 2

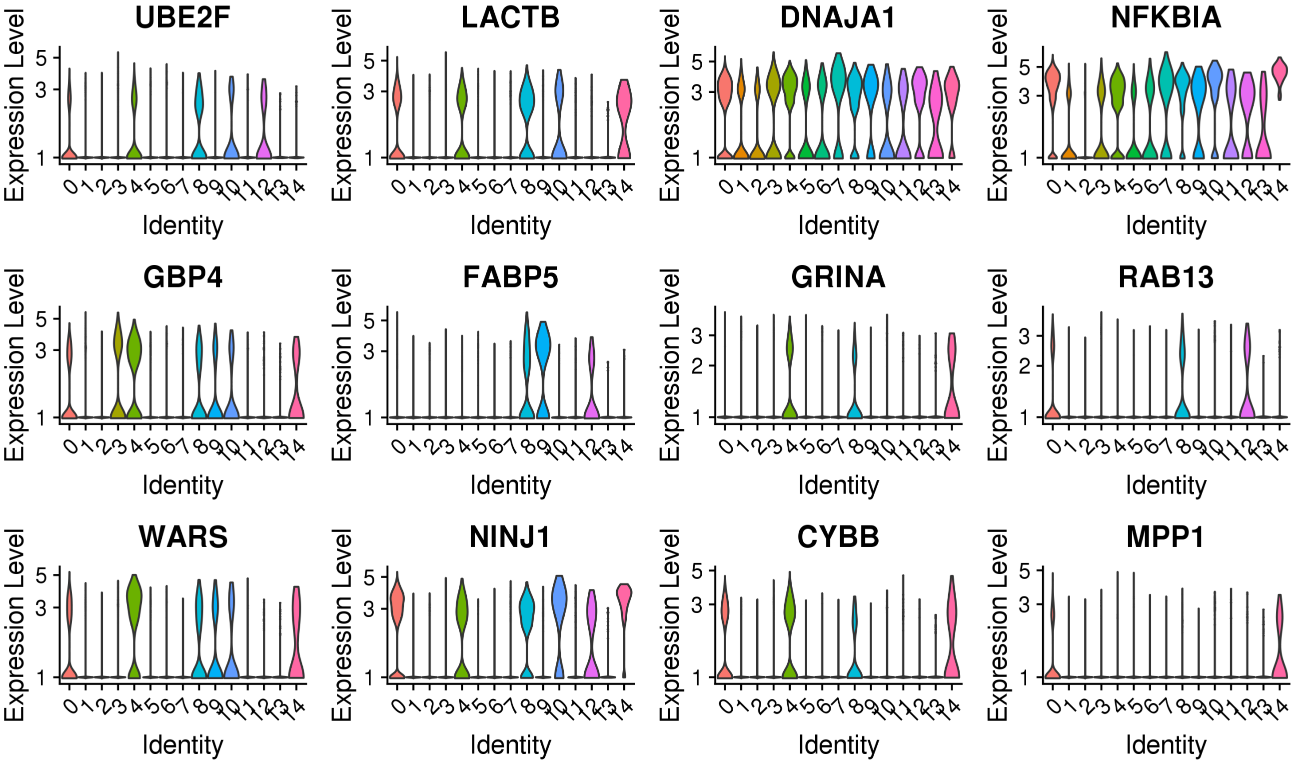


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 2

12.9 Cluster 2 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 2



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 2

12.10 Cluster 3: summary plots

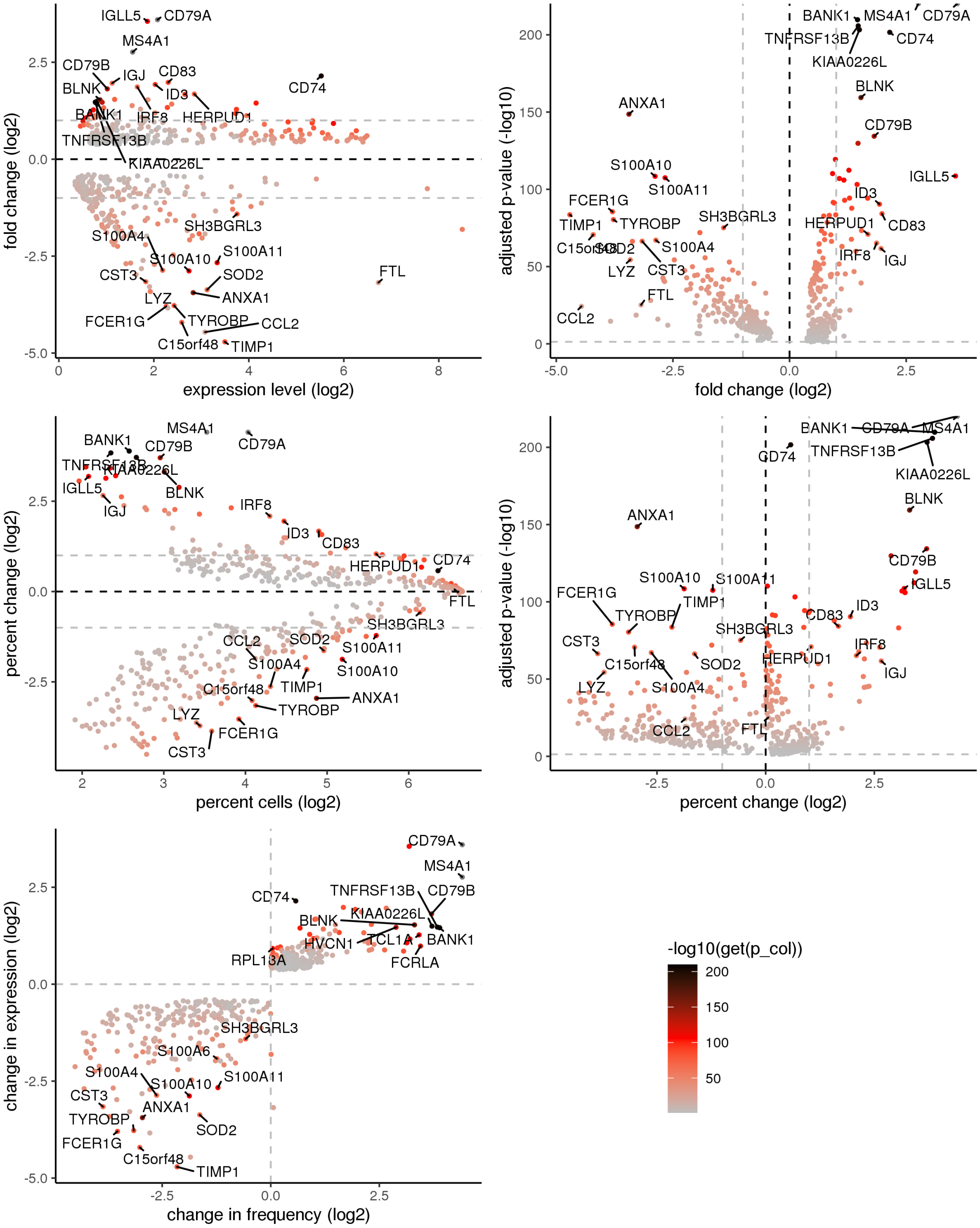
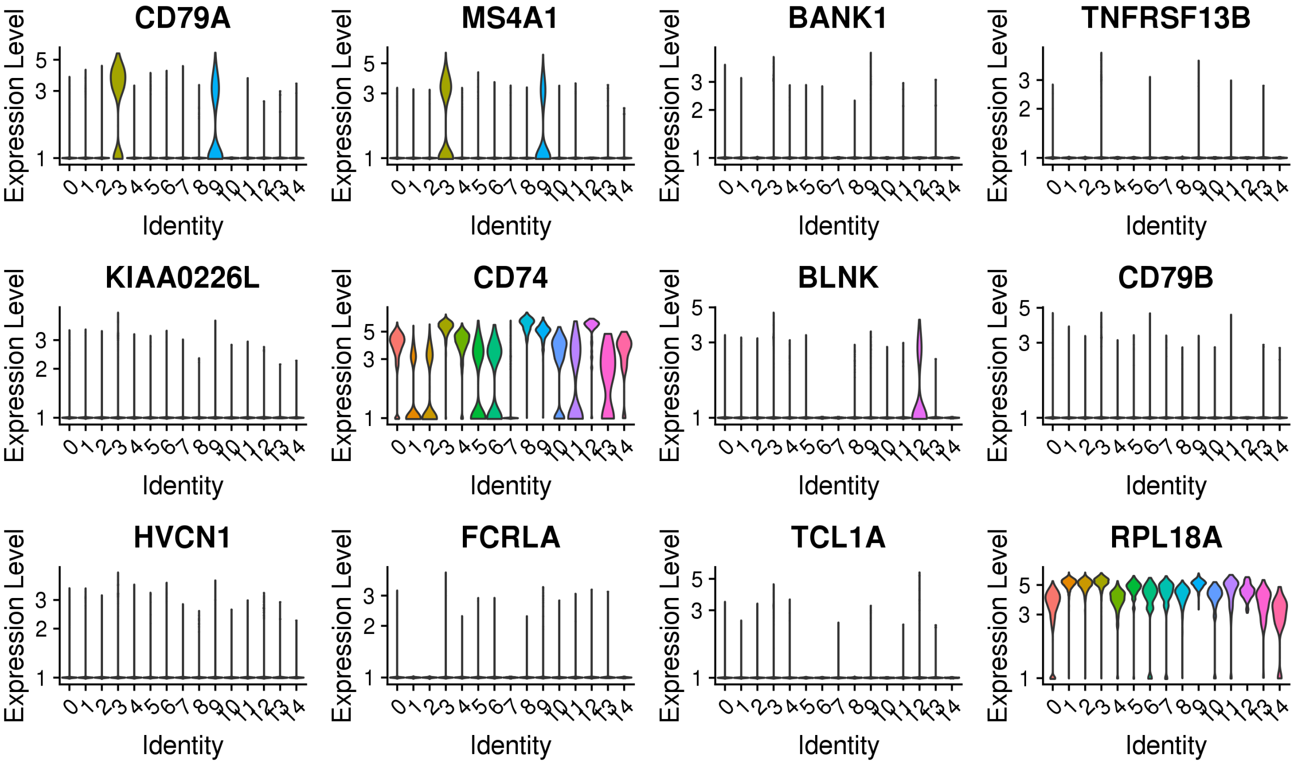
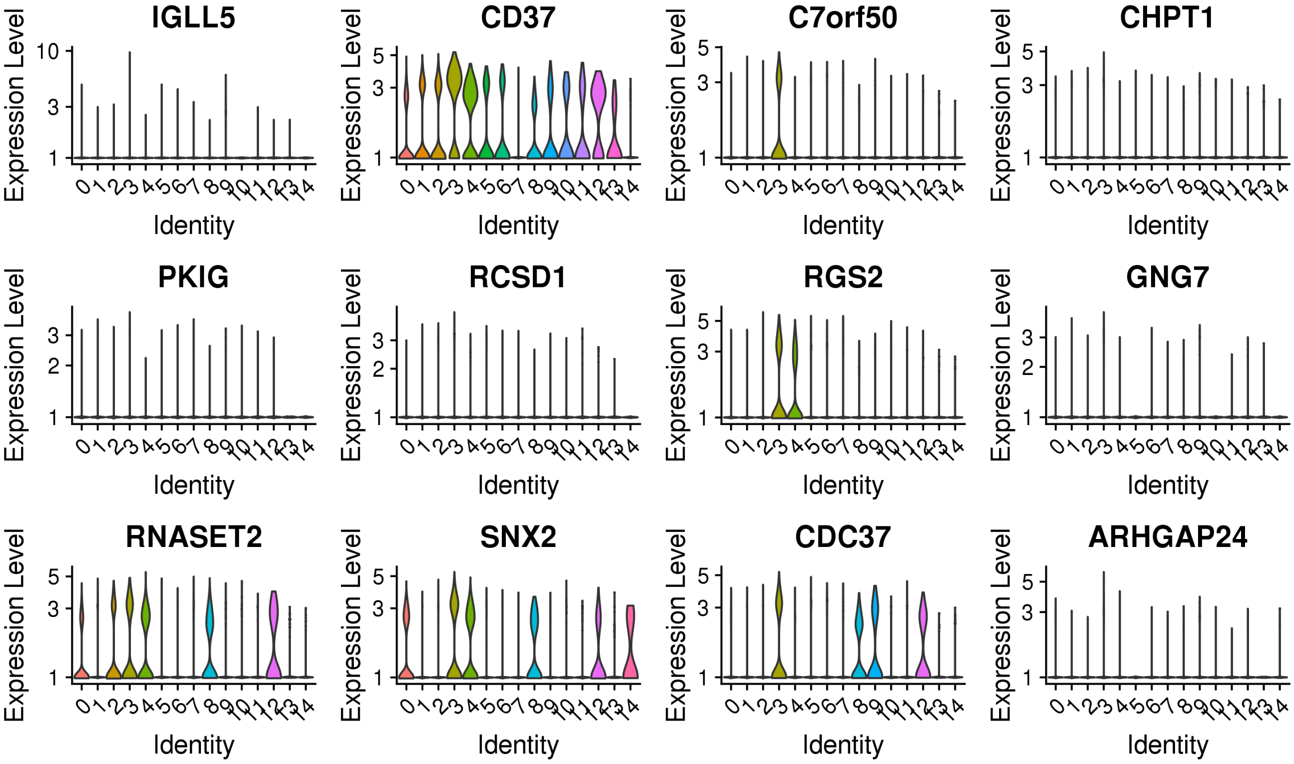


Figure 39: Differential expression summary plots for cluster 3

12.11 Cluster 3 violin plots: positive marker genes

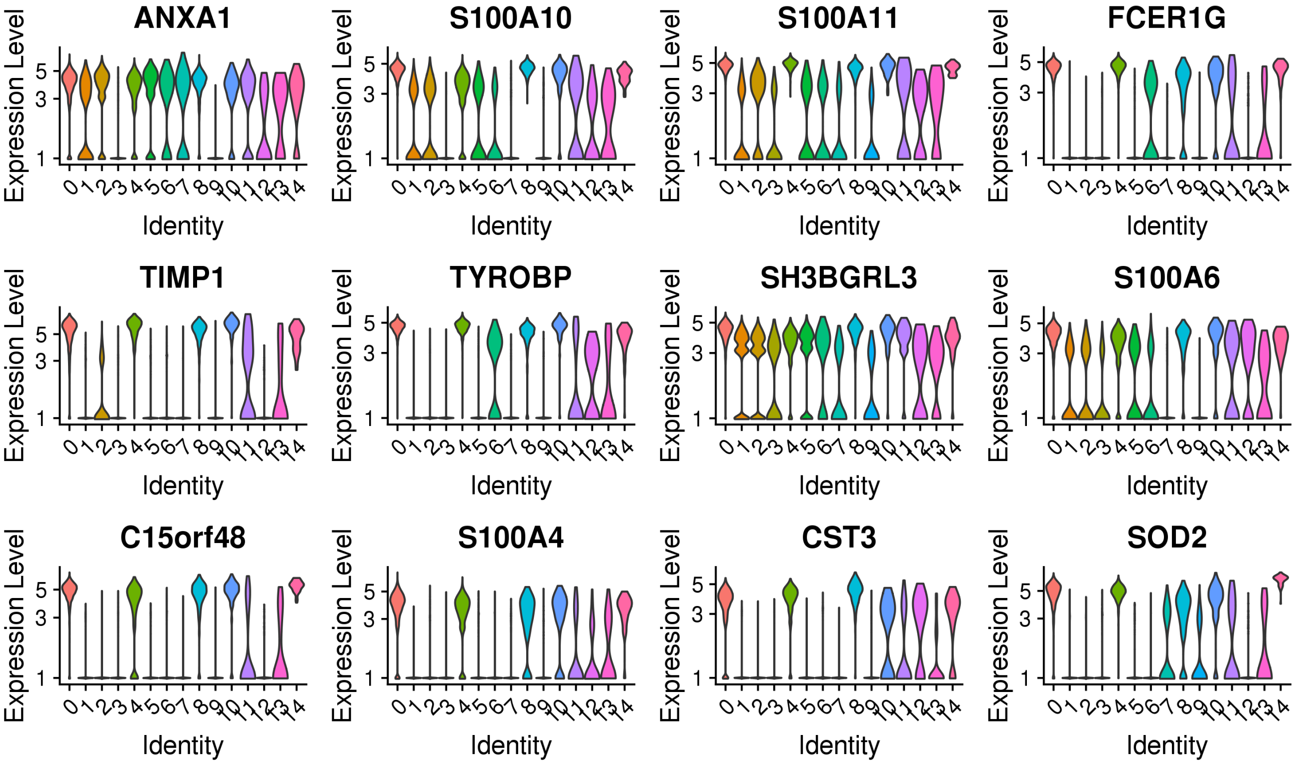


(a) Top positive marker genes ordered by p-value, cluster: 3

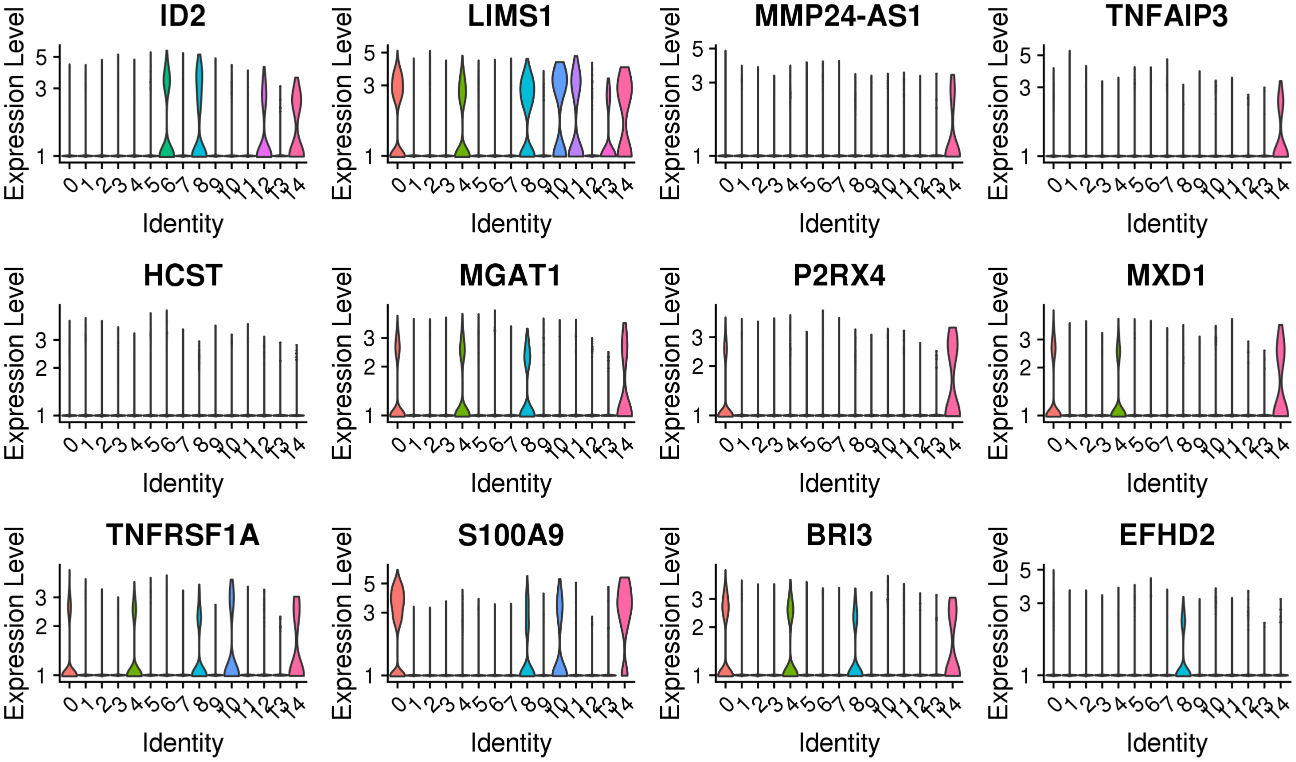


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 3

12.12 Cluster 3 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 3



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 3

12.13 Cluster 4: summary plots

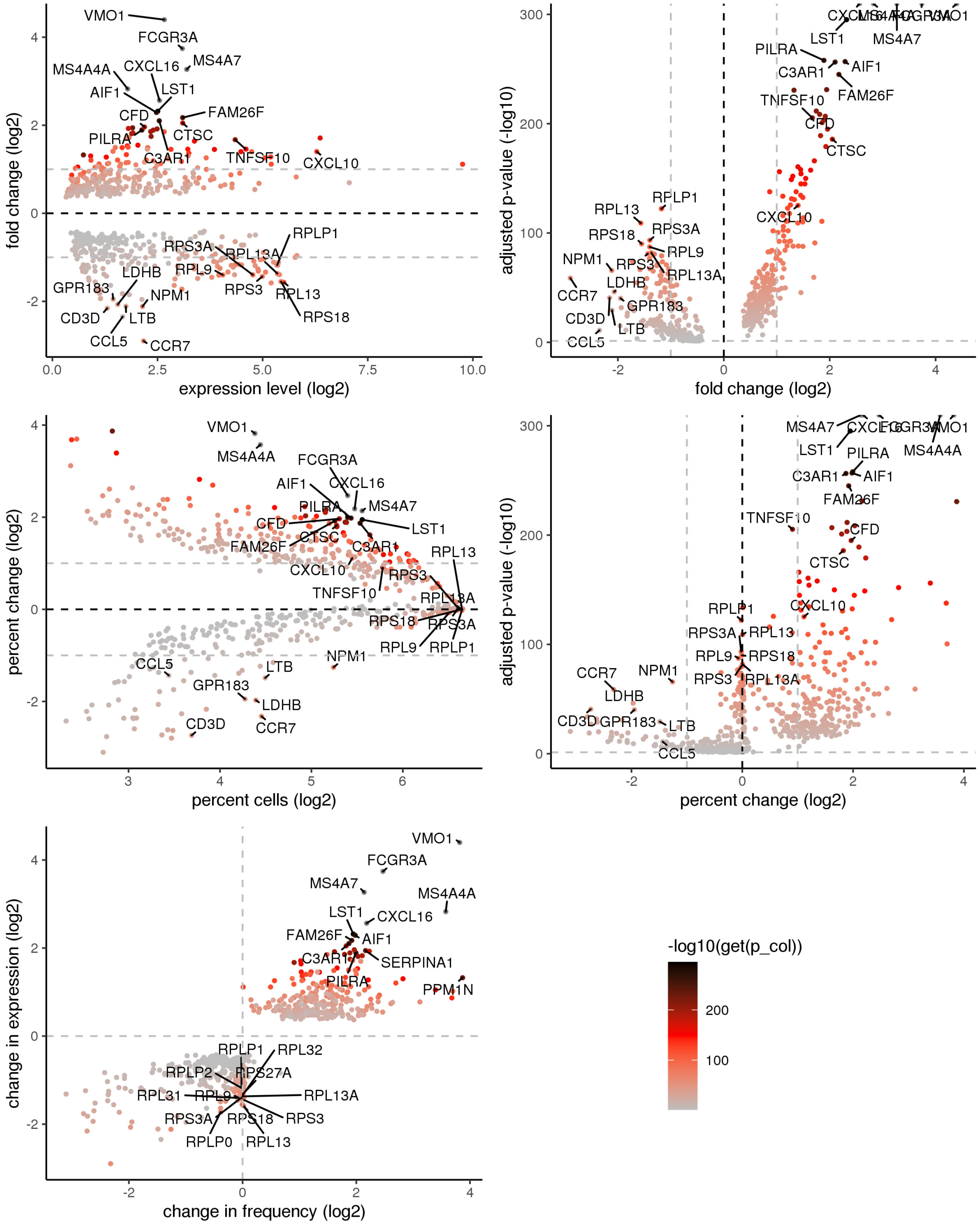
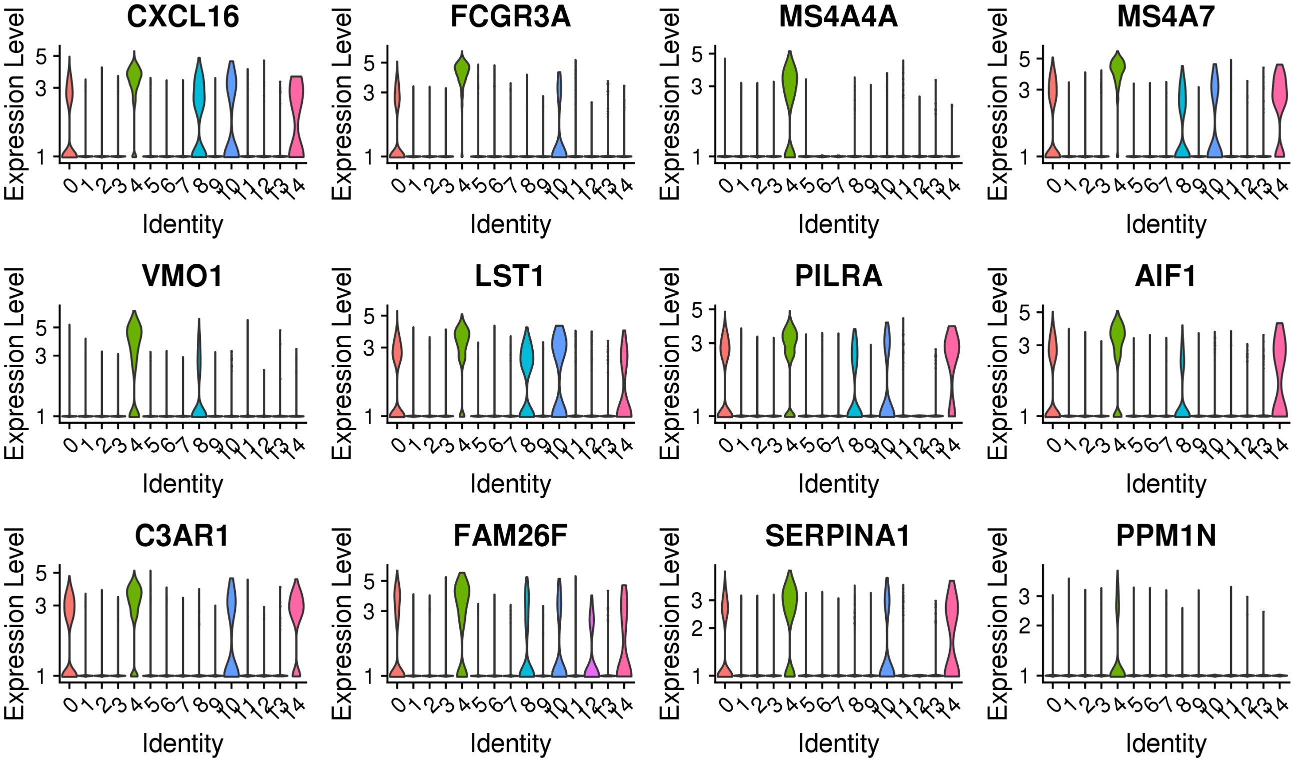
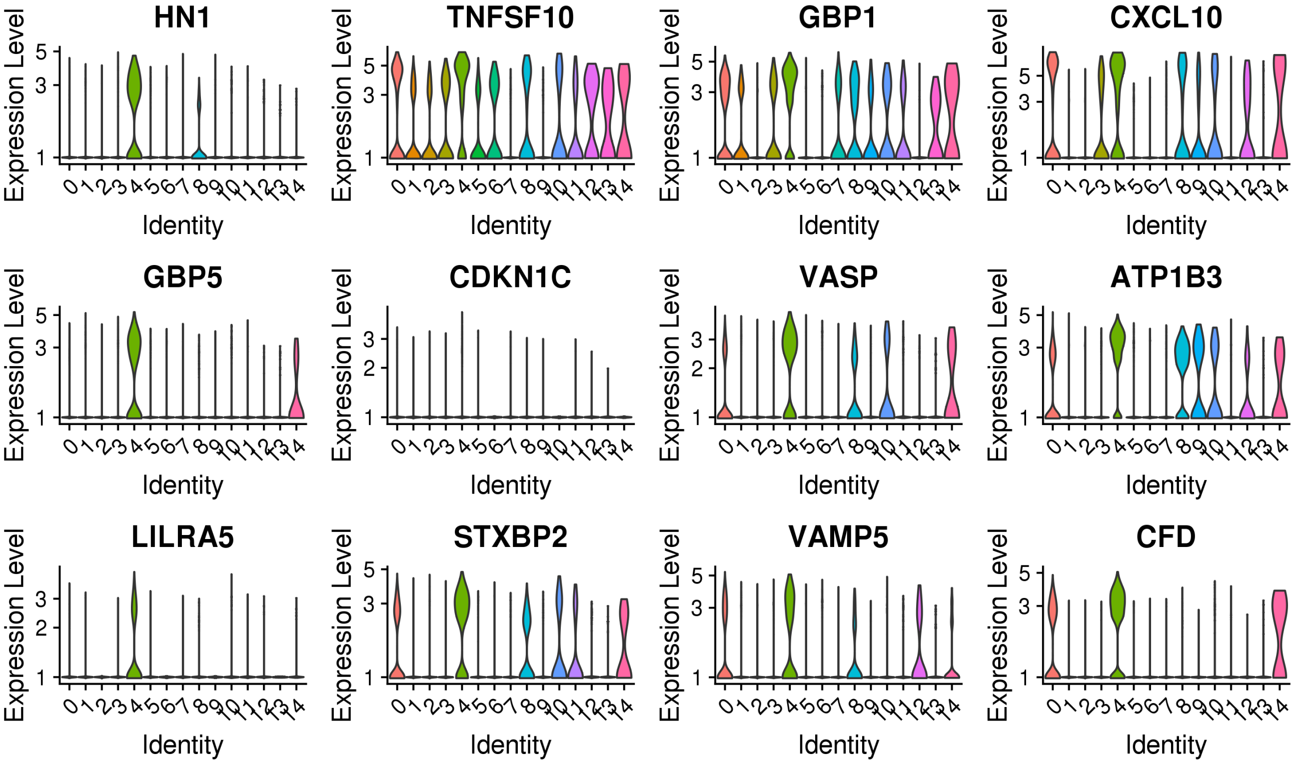


Figure 42: Differential expression summary plots for cluster 4

12.14 Cluster 4 violin plots: positive marker genes

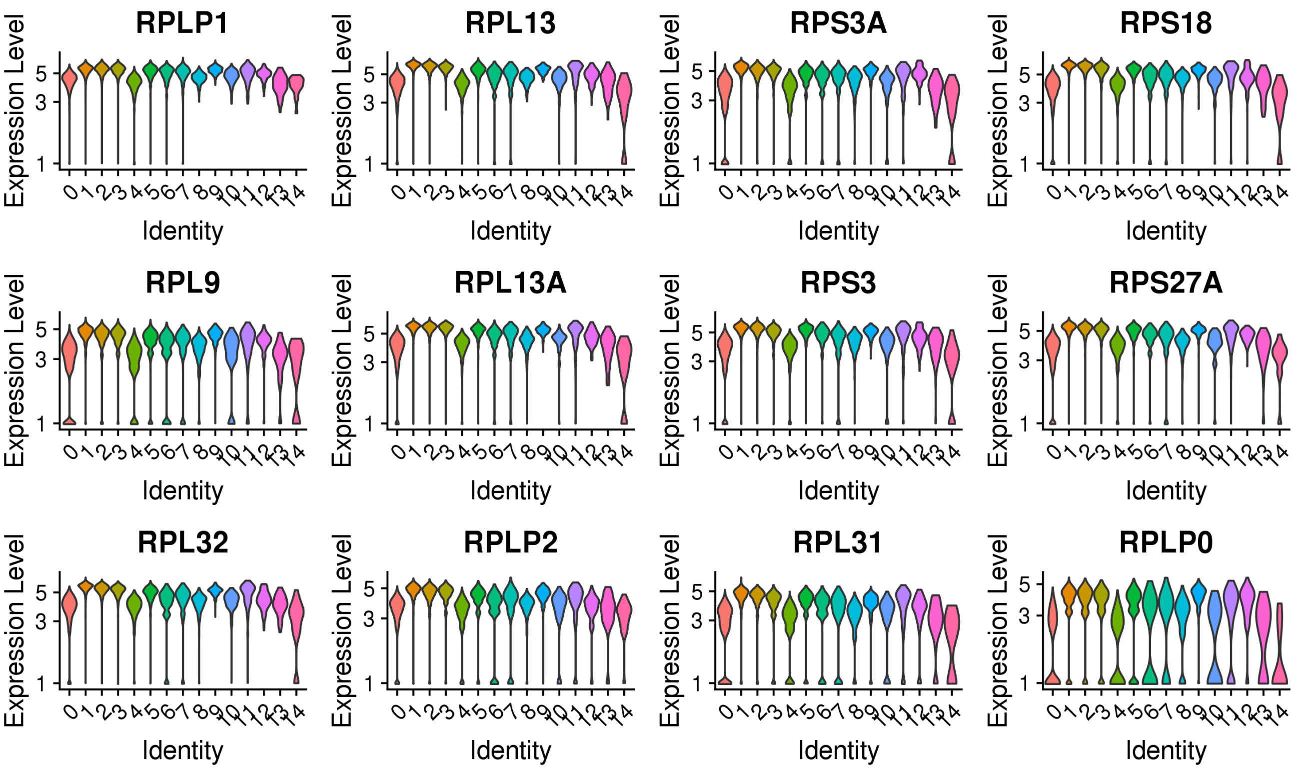


(a) Top positive marker genes ordered by p-value, cluster: 4

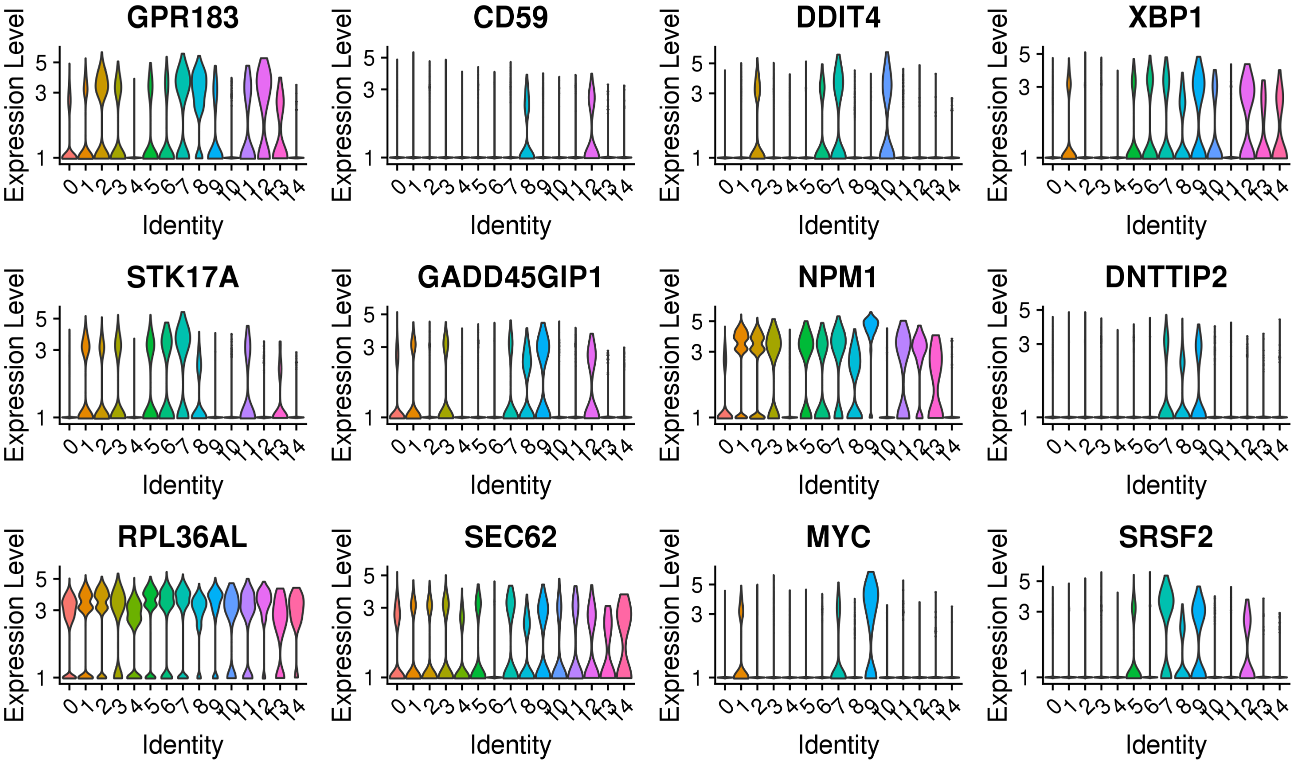


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 4

12.15 Cluster 4 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 4



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 4

12.16 Cluster 5: summary plots

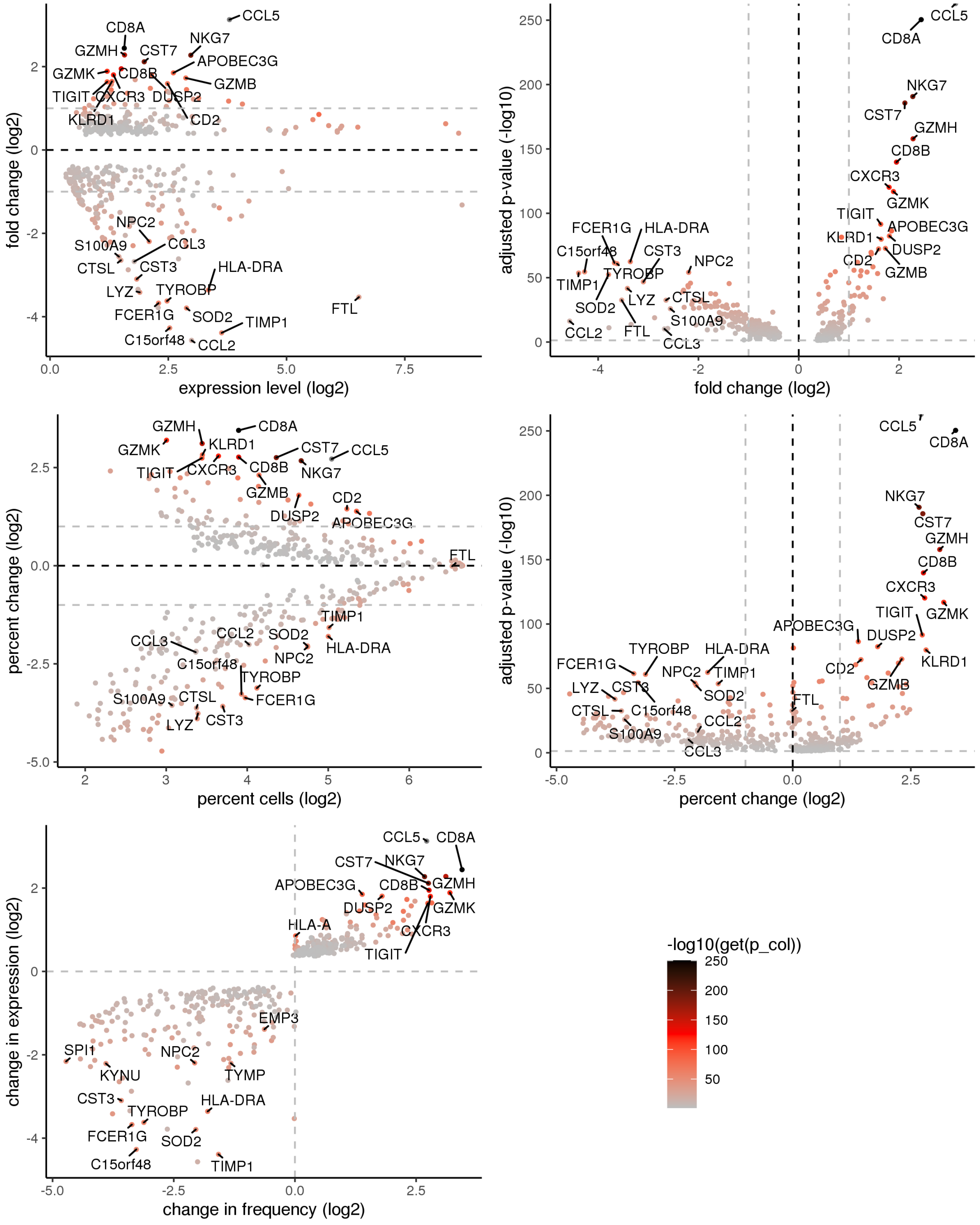
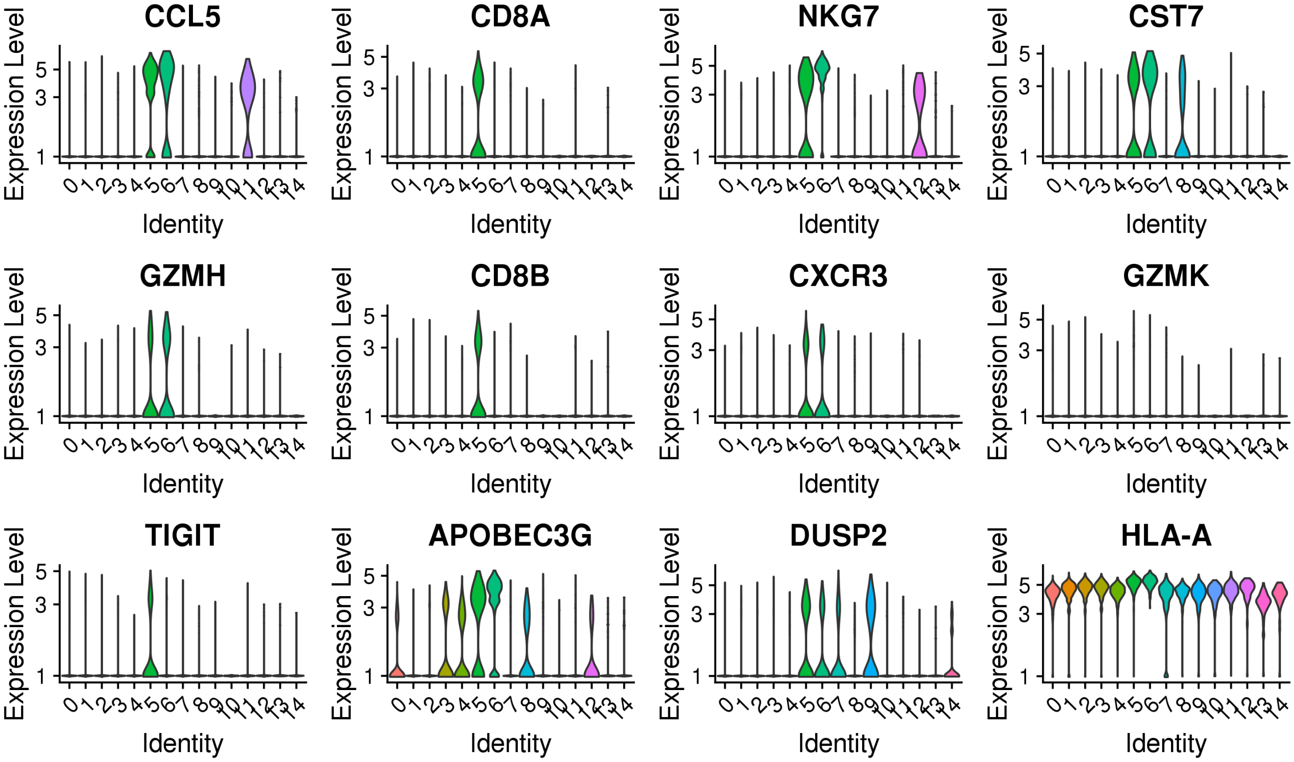
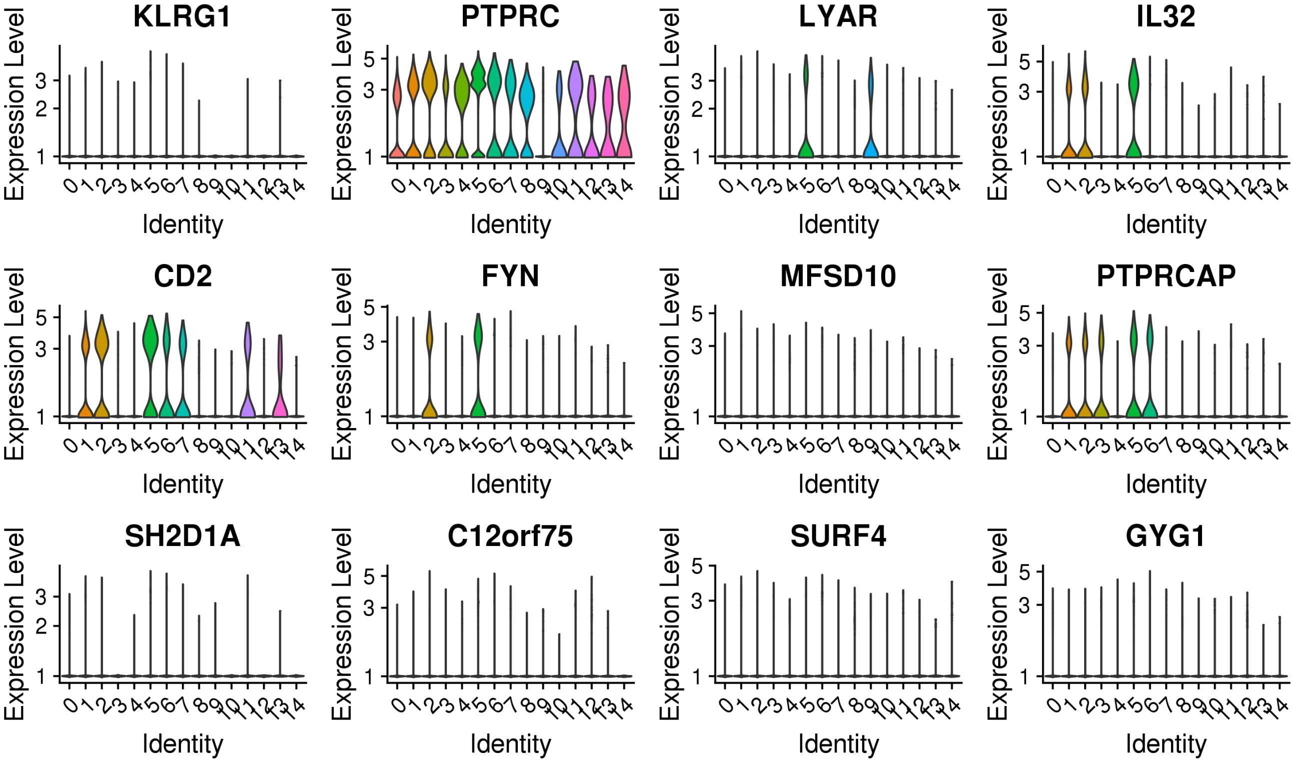


Figure 45: Differential expression summary plots for cluster 5

12.17 Cluster 5 violin plots: positive marker genes

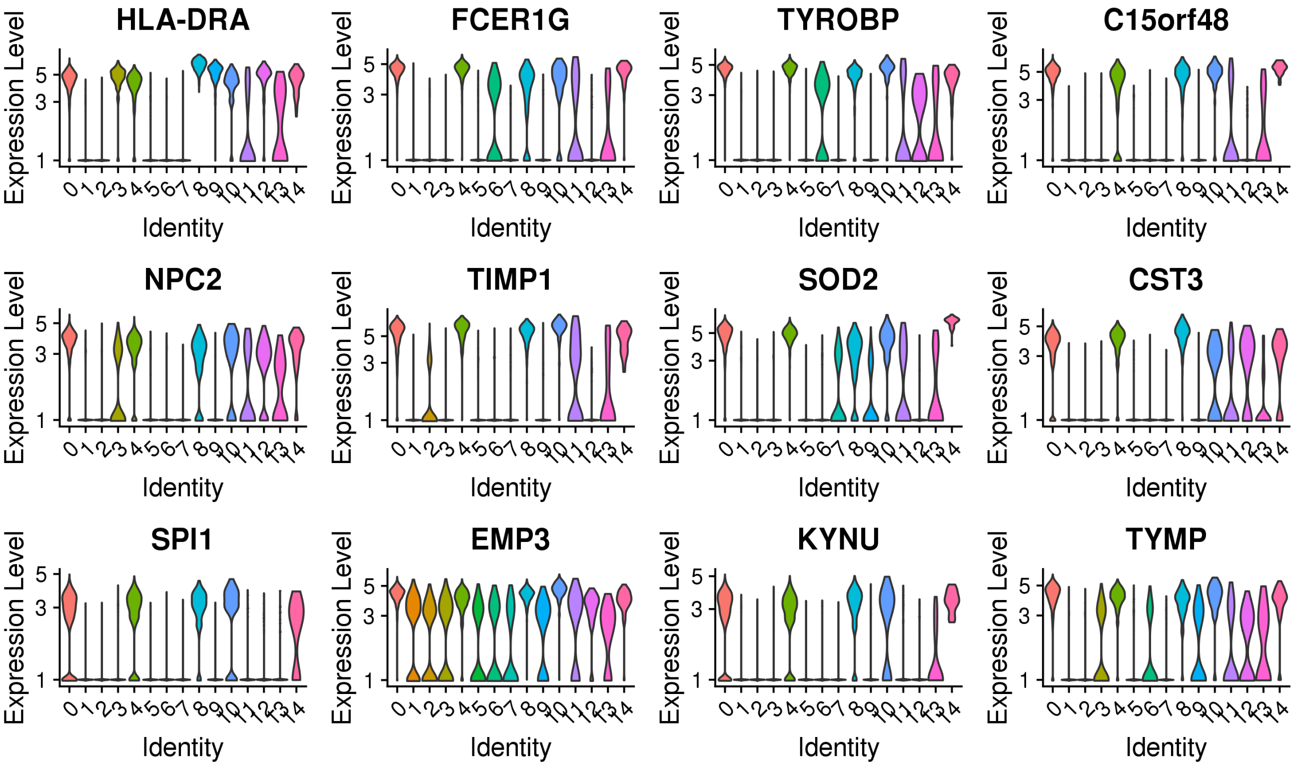


(a) Top positive marker genes ordered by p-value, cluster: 5

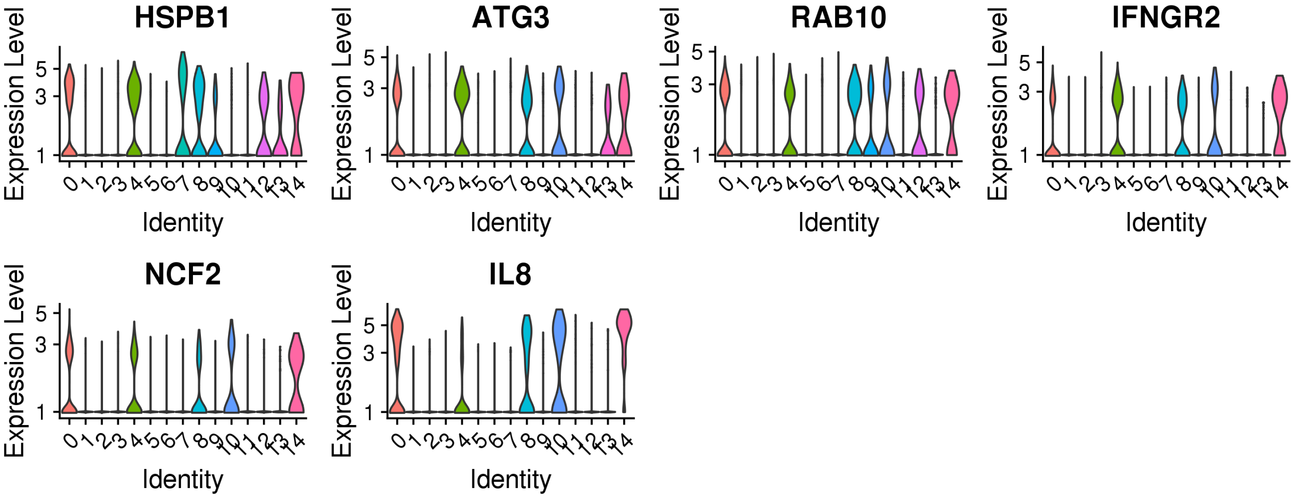


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 5

12.18 Cluster 5 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 5



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 5

12.19 Cluster 6: summary plots

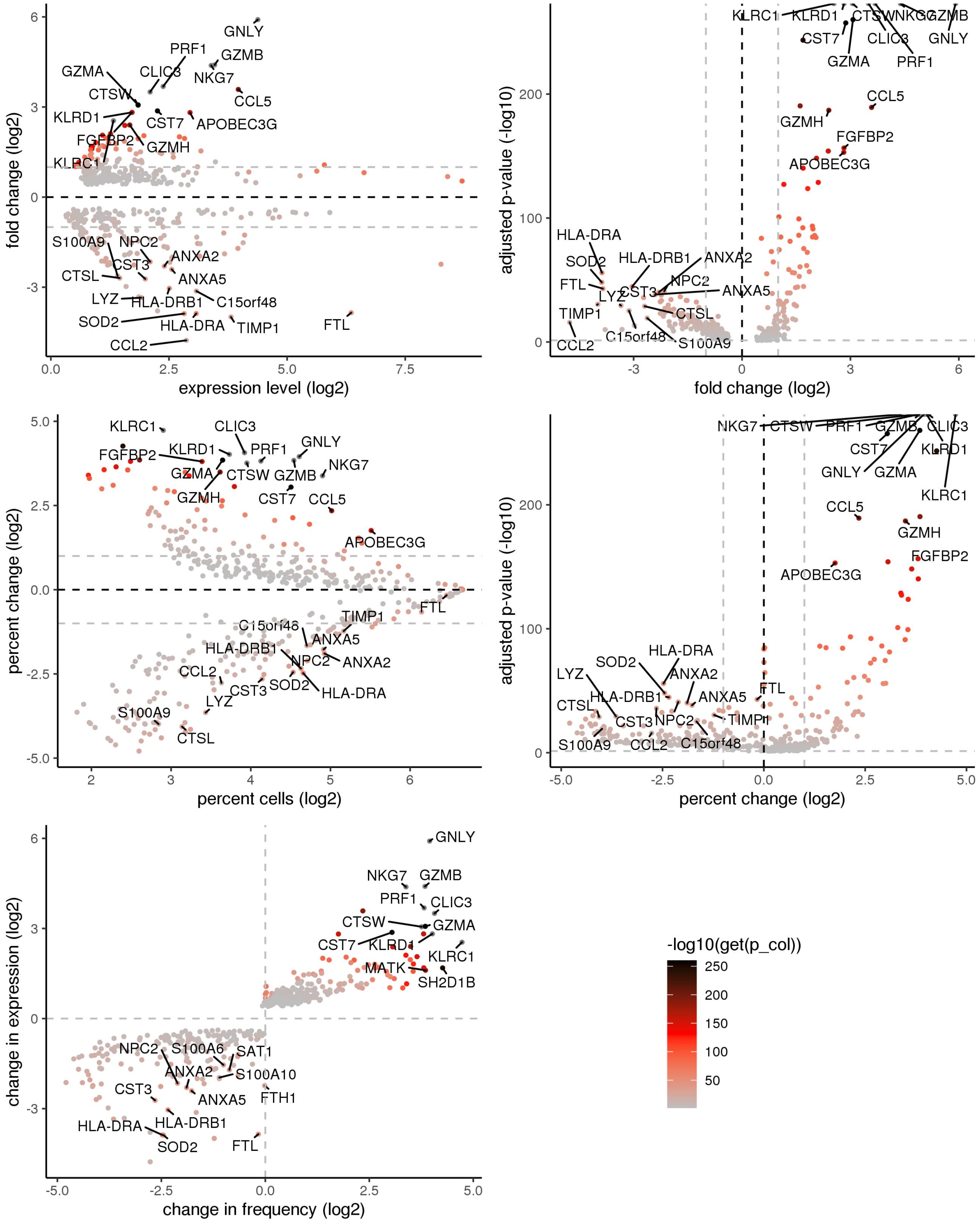
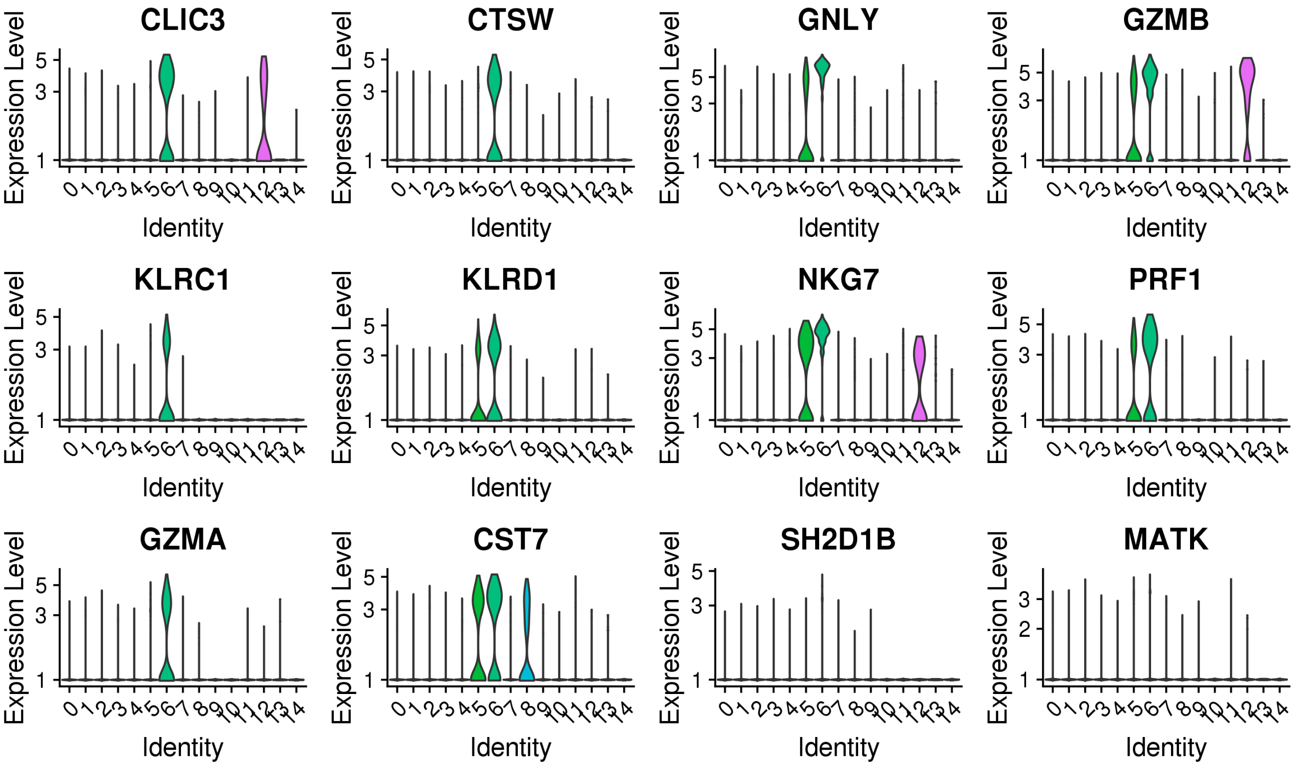
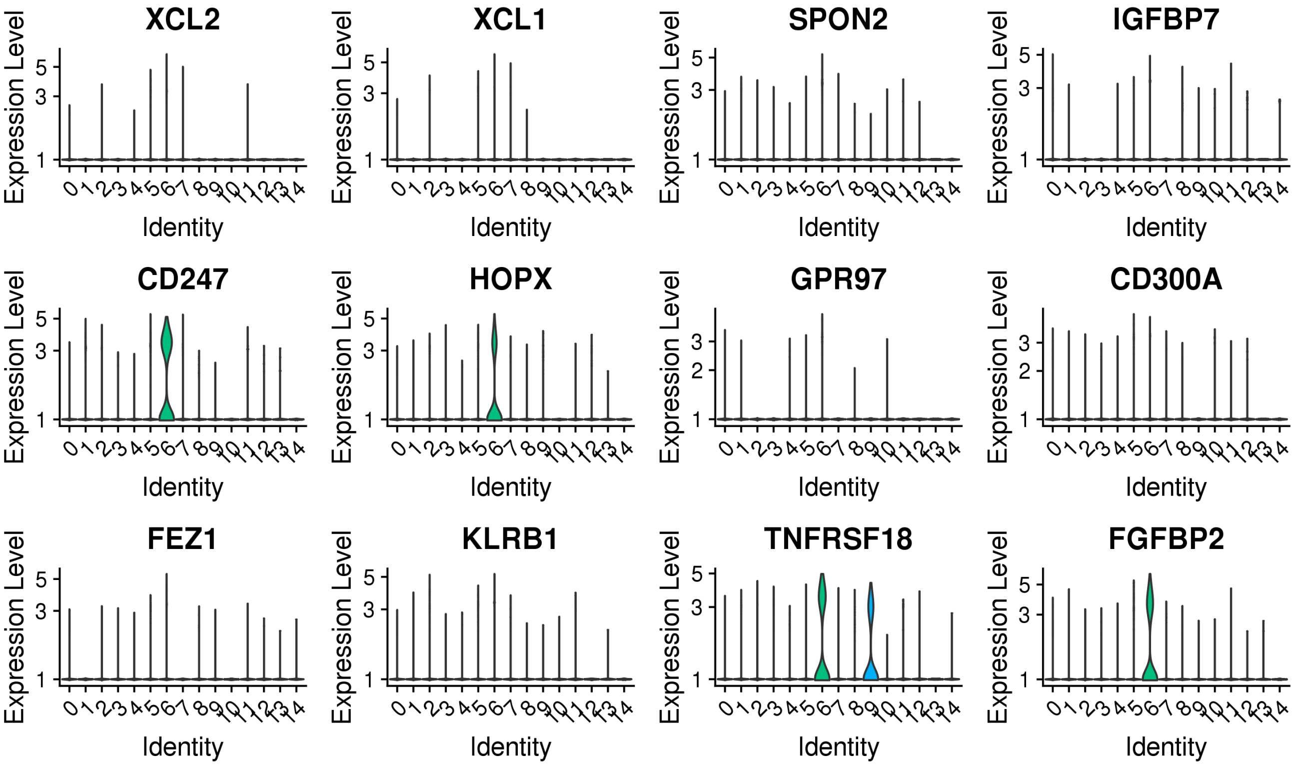


Figure 48: Differential expression summary plots for cluster 6

12.20 Cluster 6 violin plots: positive marker genes

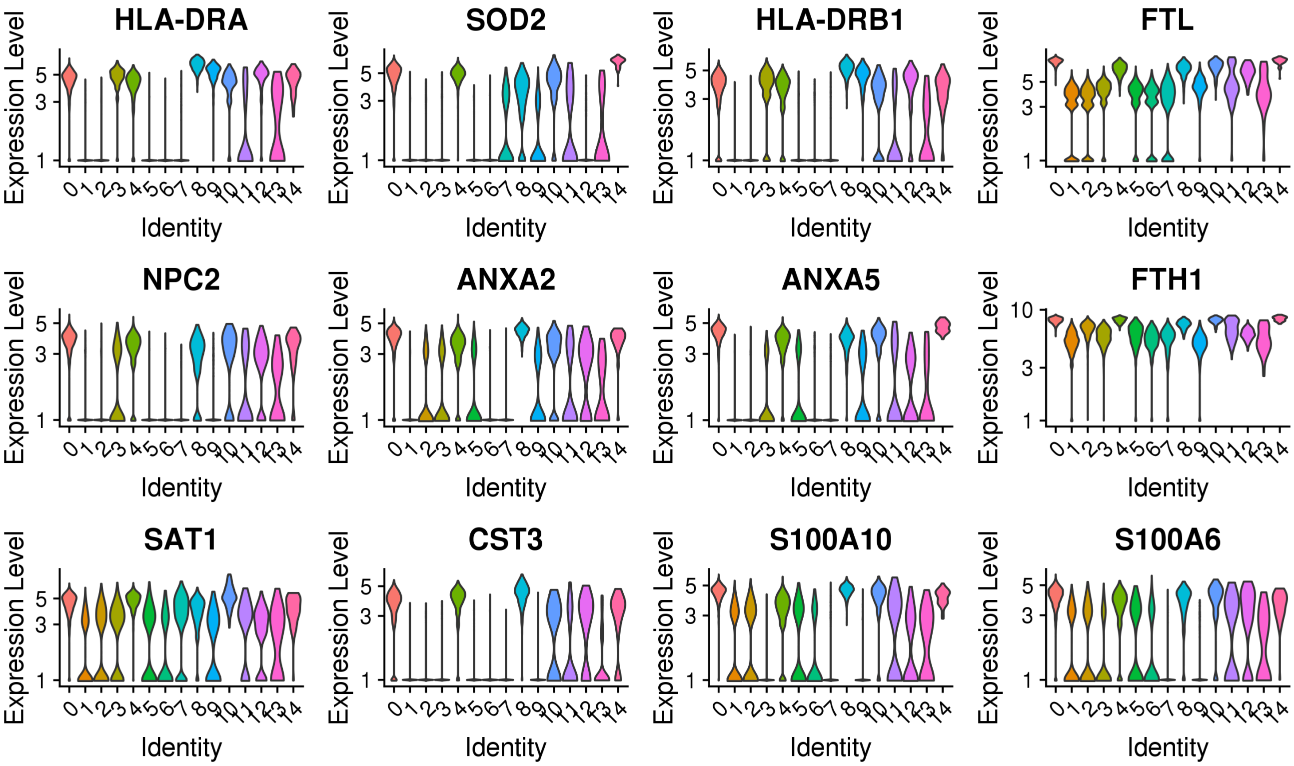


(a) Top positive marker genes ordered by p-value, cluster: 6

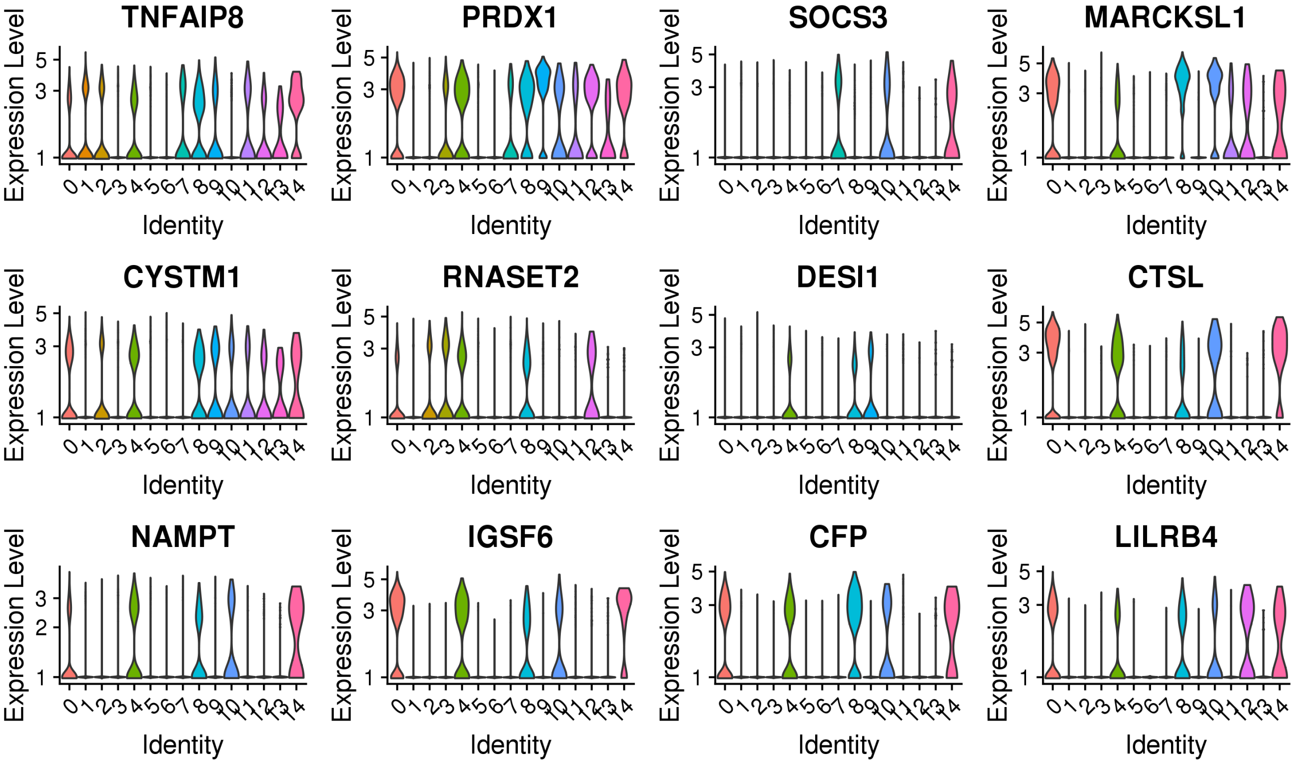


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 6

12.21 Cluster 6 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 6



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 6

12.22 Cluster 7: summary plots

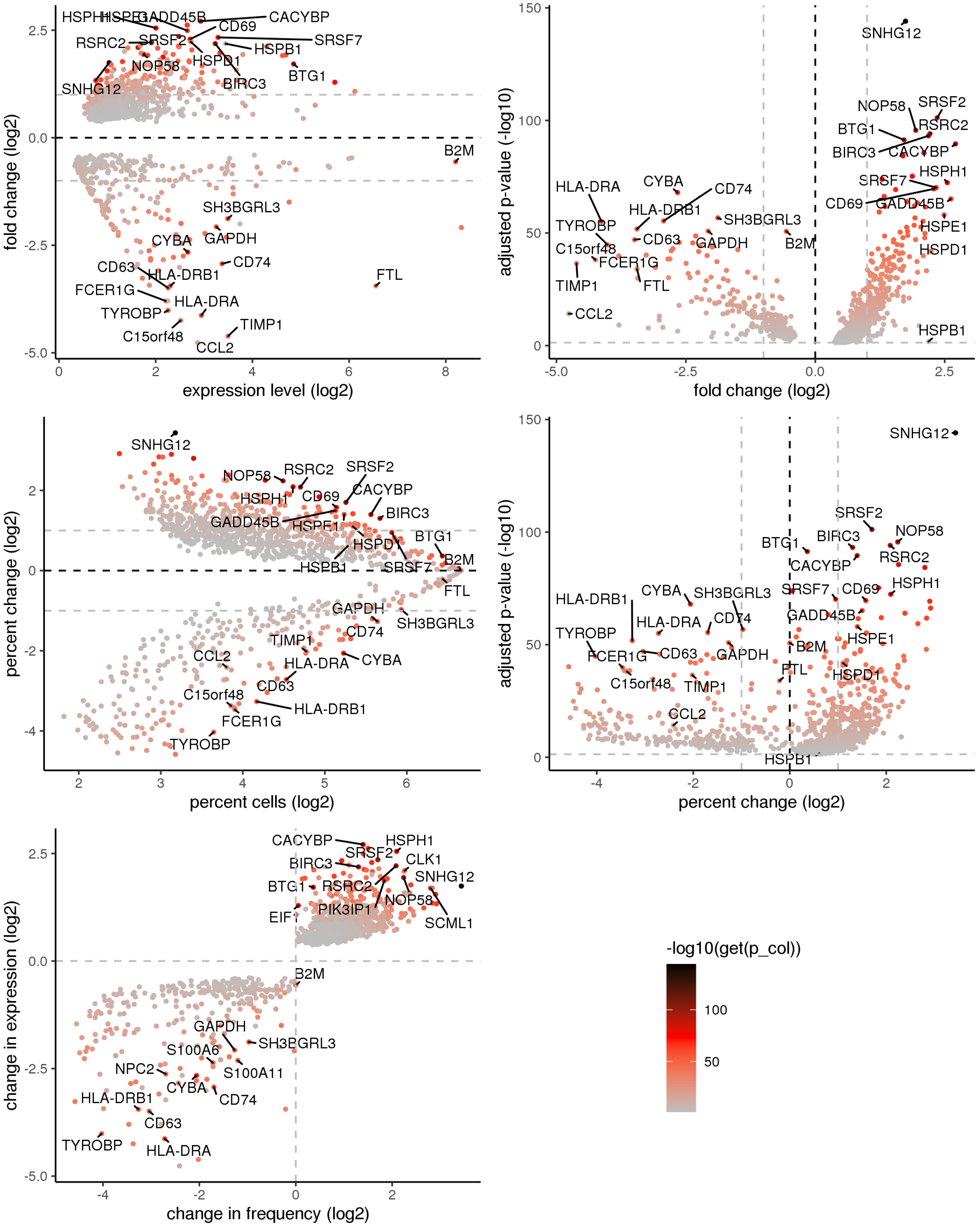
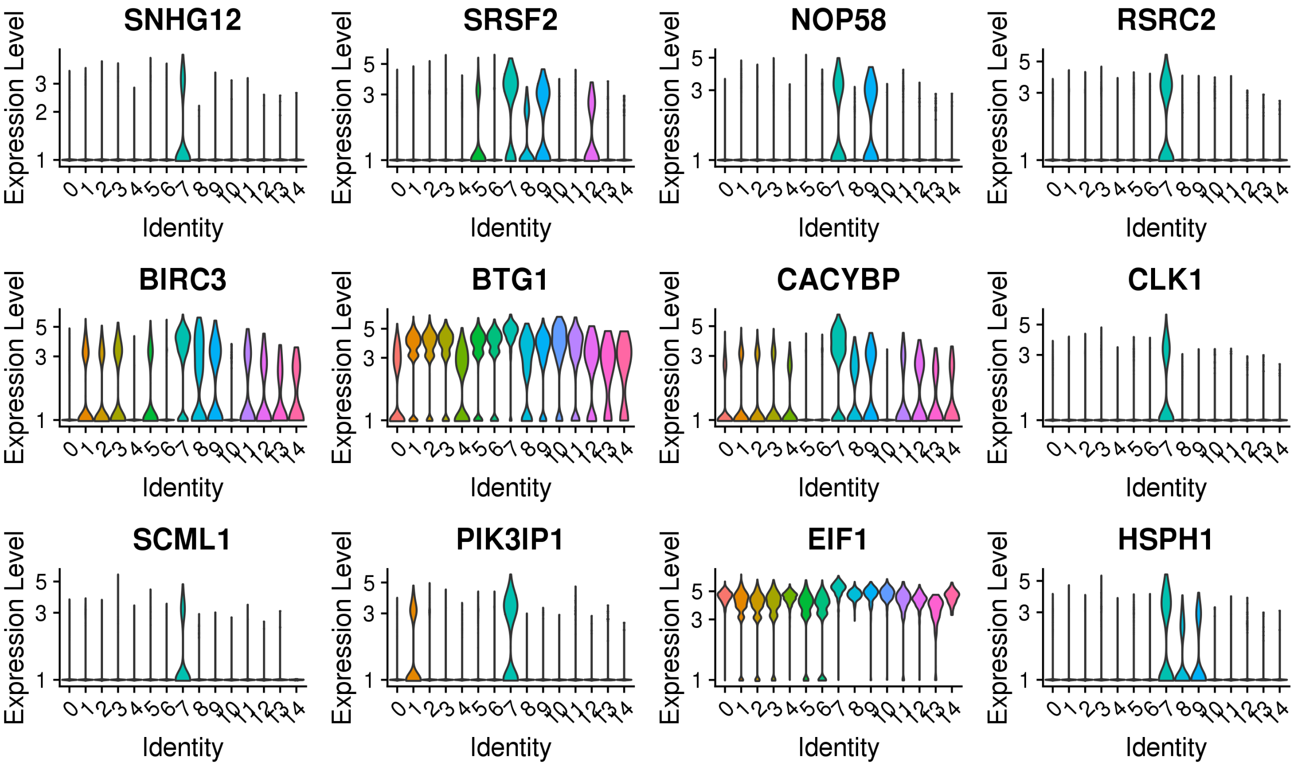
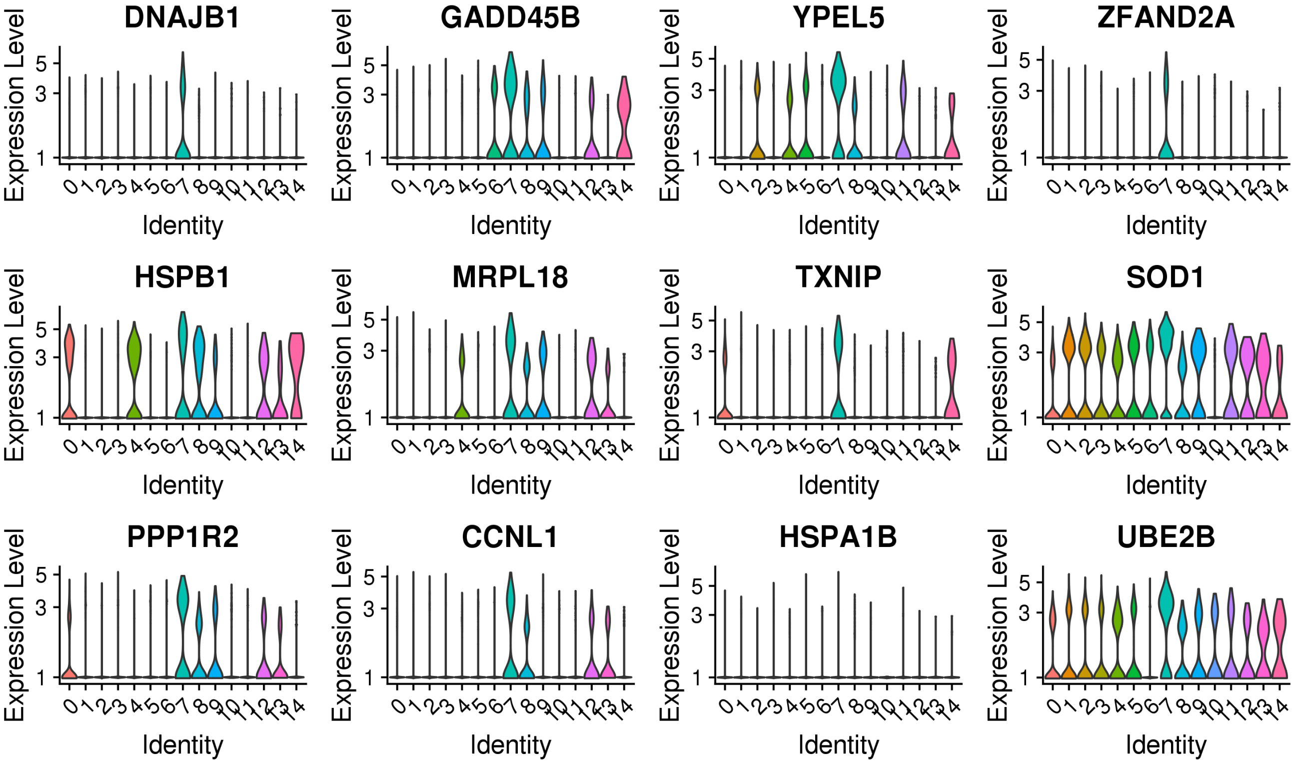


Figure 51: Differential expression summary plots for cluster 7

12.23 Cluster 7 violin plots: positive marker genes

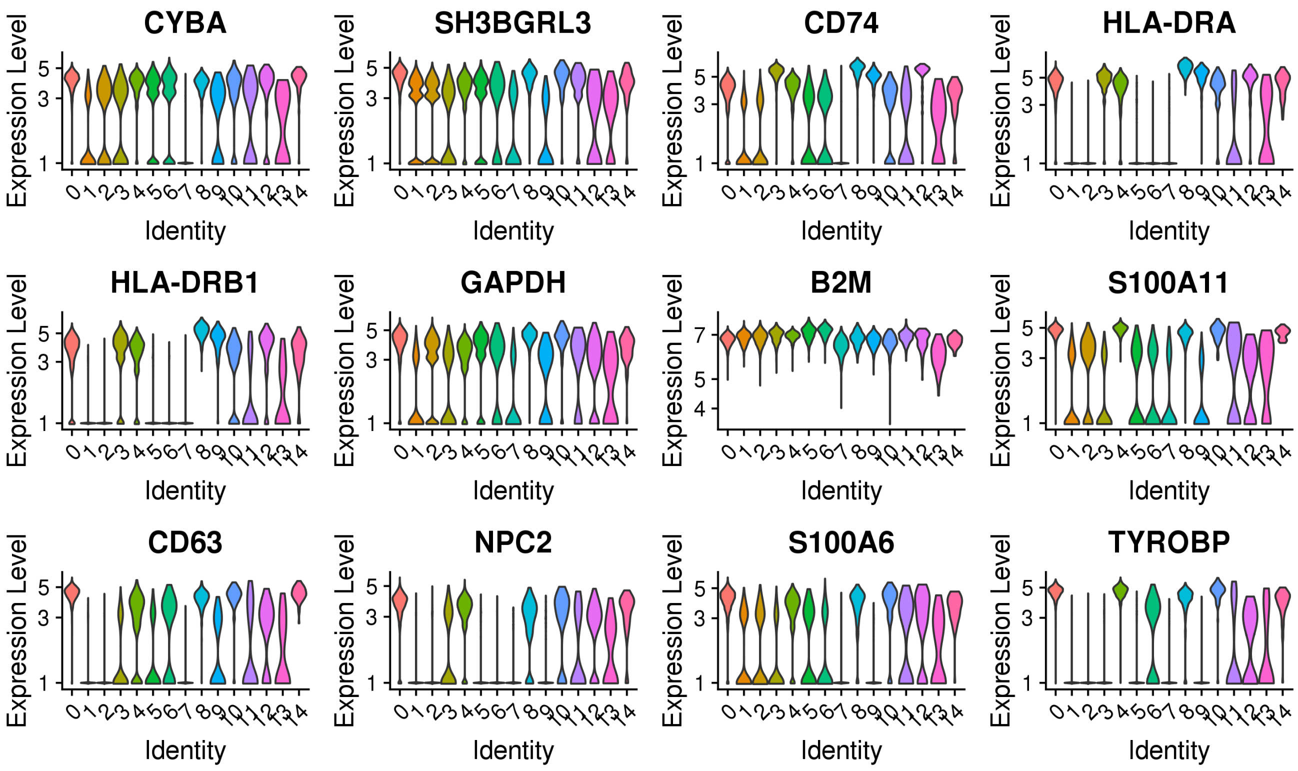

SNHG12 SRSF2 NOP58 RSRC2 BIRC3 BTG1 CACYBP CLK1 SCML1 PIK3IP1 EIF1 HSPH1

(a) Top positive marker genes ordered by p-value, cluster: 7

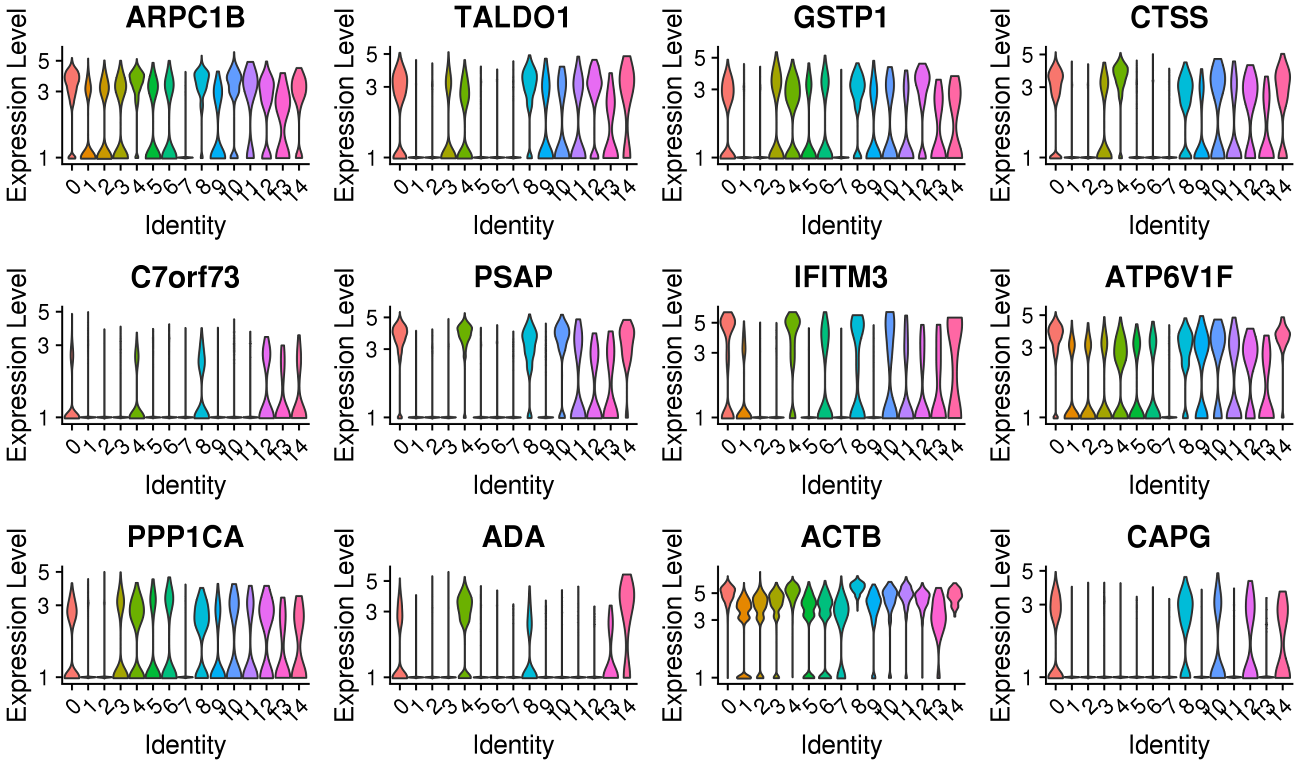

DNAJB1 GADD45B YPEL5 ZFAND2A HSPB1 MRPL18 TXNIP SOD1 PPP1R2 CCNL1 HSPA1B UBE2B

(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 7

12.24 Cluster 7 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 7



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 7

12.25 Cluster 8: summary plots

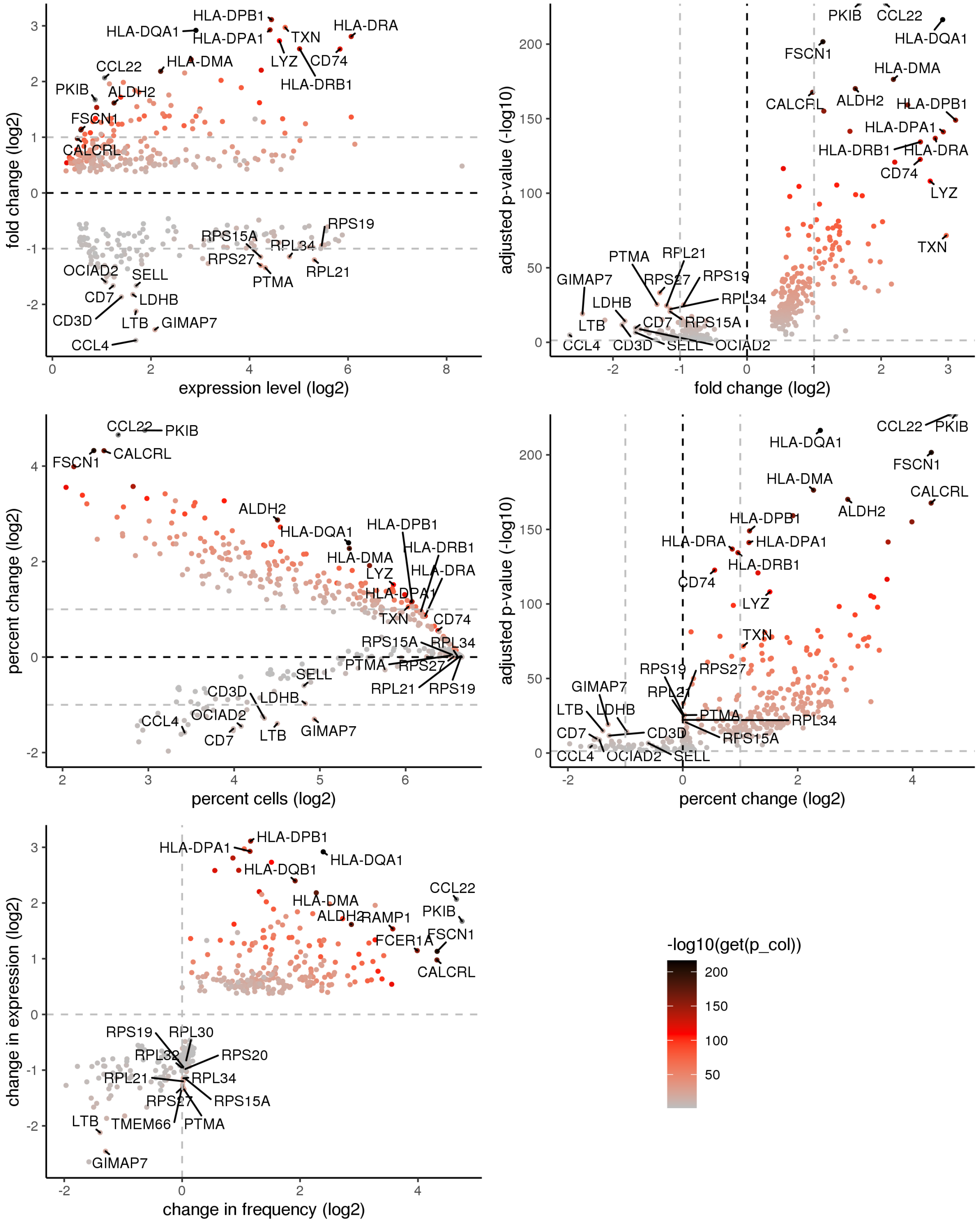
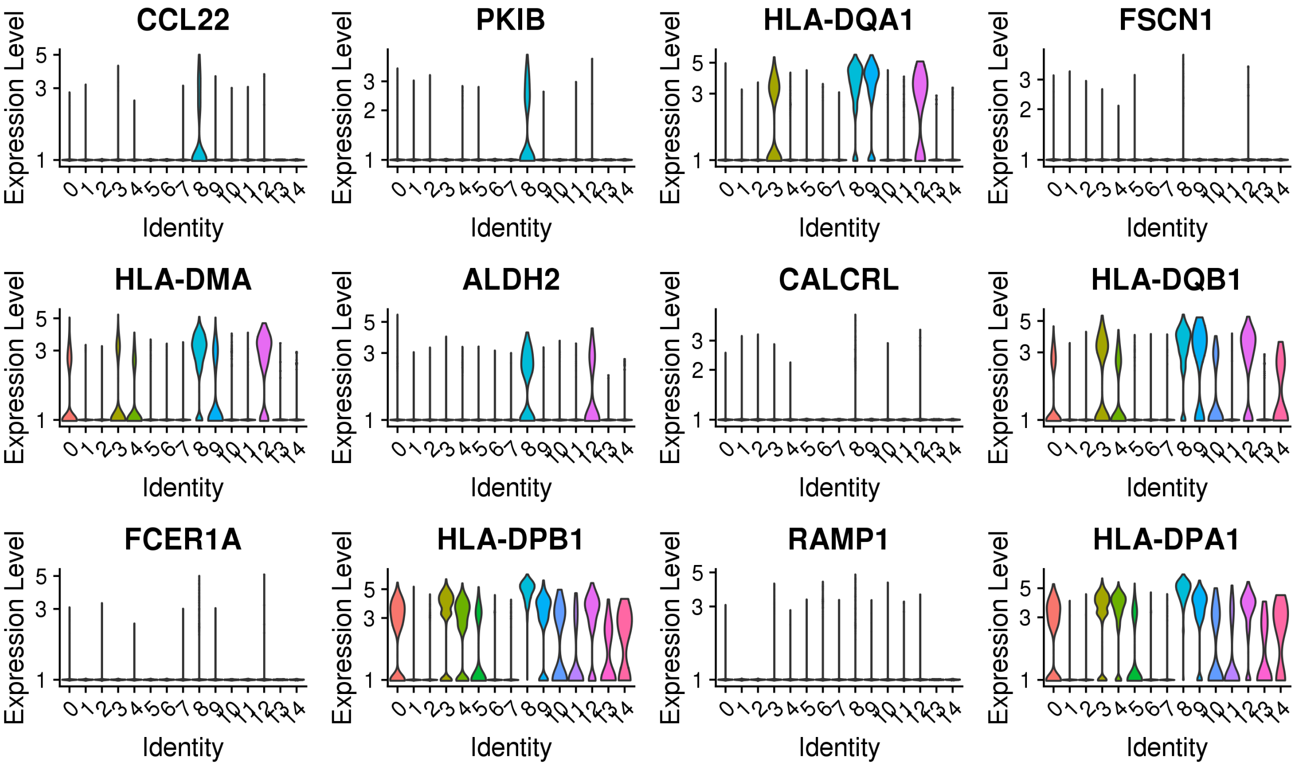
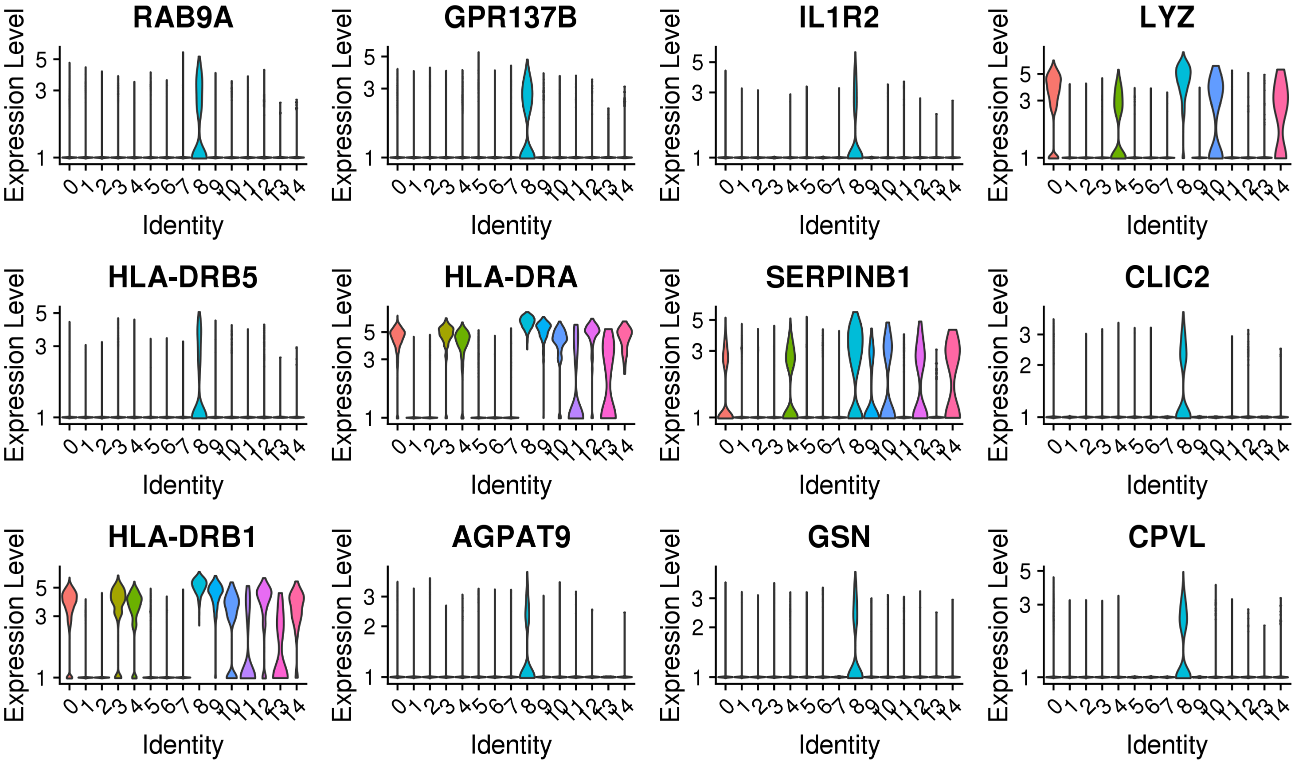


Figure 54: Differential expression summary plots for cluster 8

12.26 Cluster 8 violin plots: positive marker genes

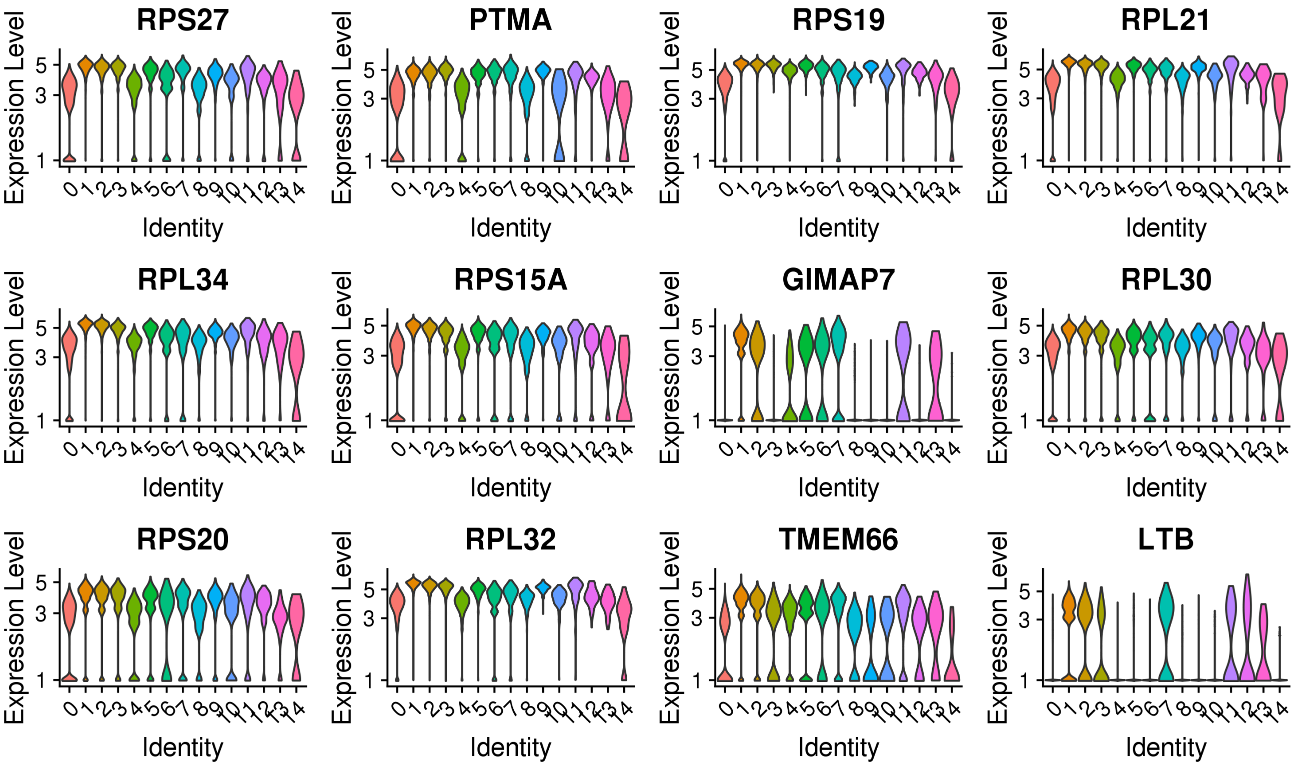


(a) Top positive marker genes ordered by p-value, cluster: 8

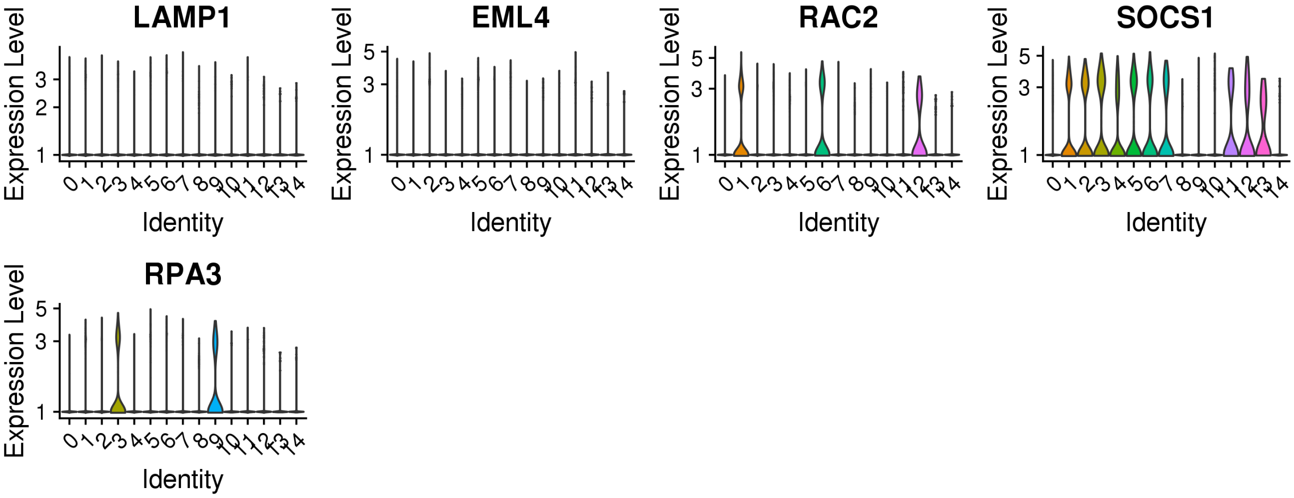


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 8

12.27 Cluster 8 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 8



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 8

12.28 Cluster 9: summary plots

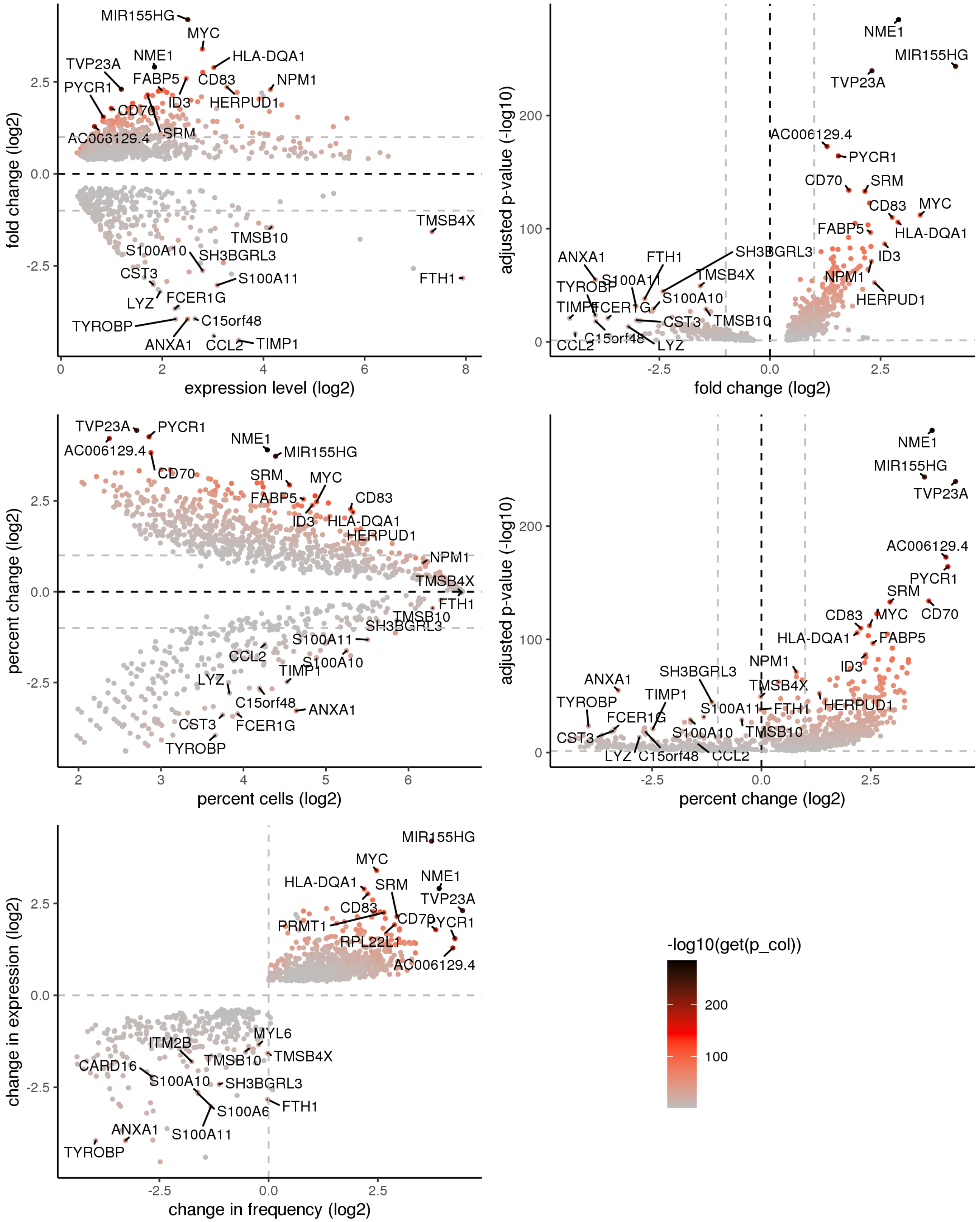
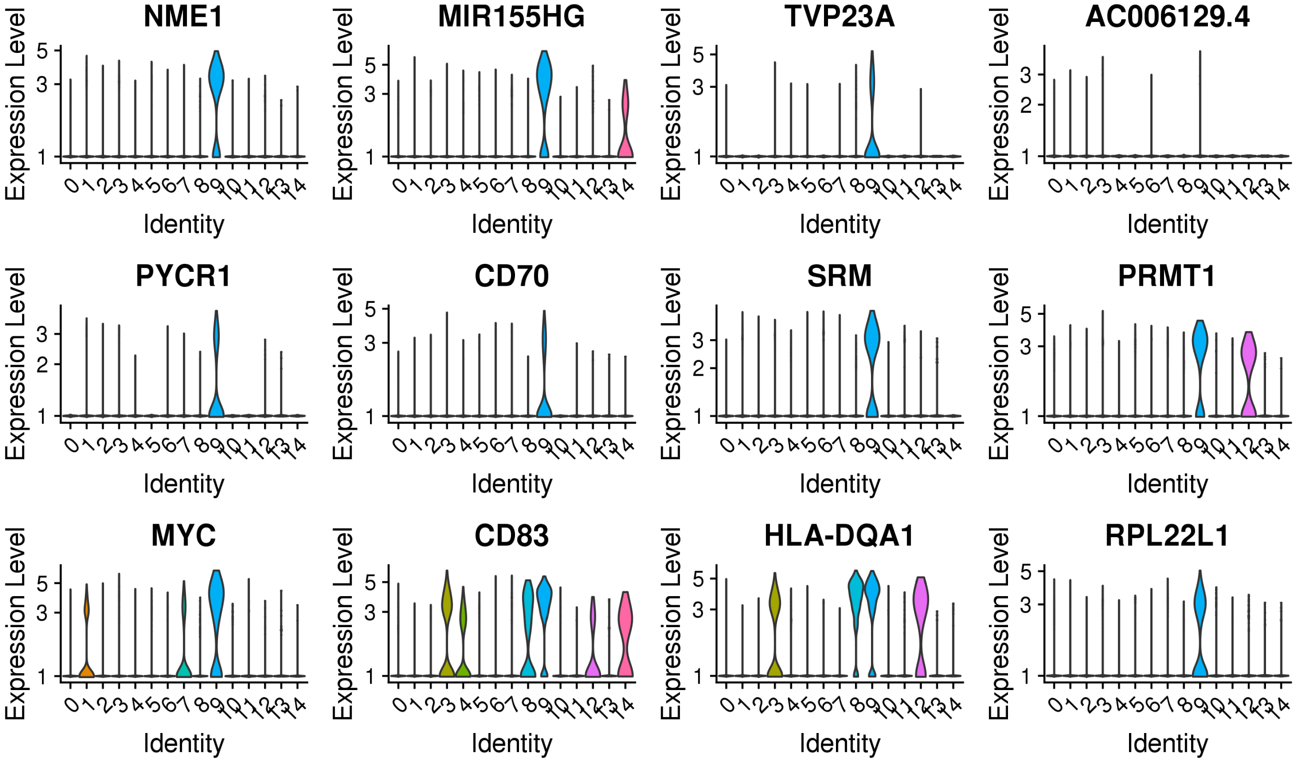
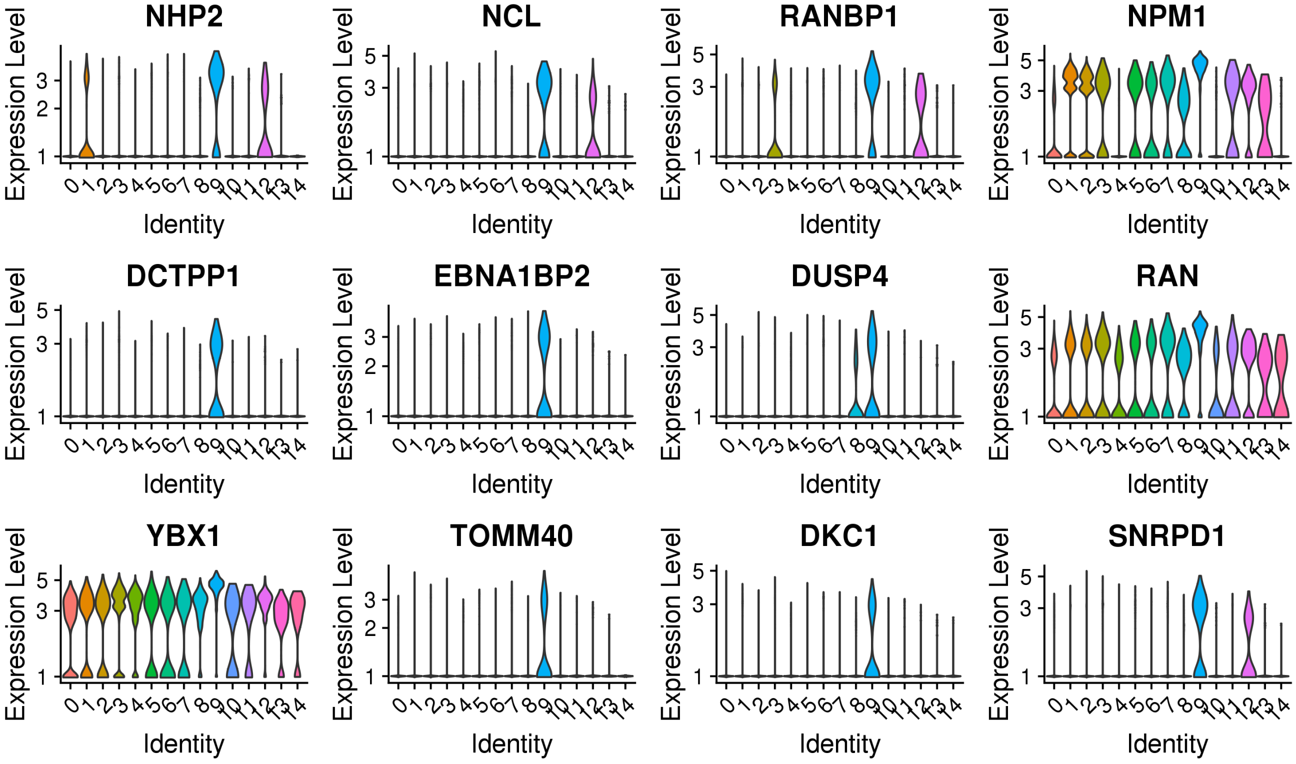


Figure 57: Differential expression summary plots for cluster 9

12.29 Cluster 9 violin plots: positive marker genes

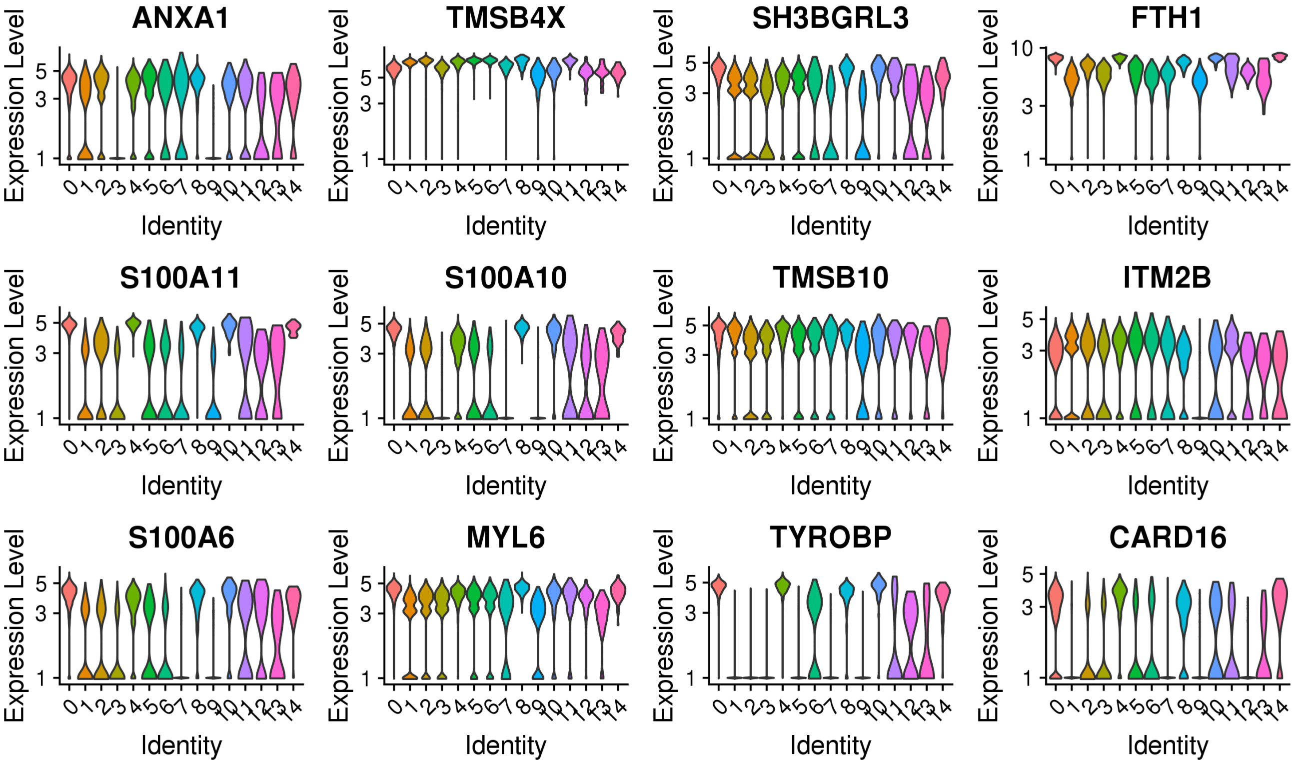


(a) Top positive marker genes ordered by p-value, cluster: 9



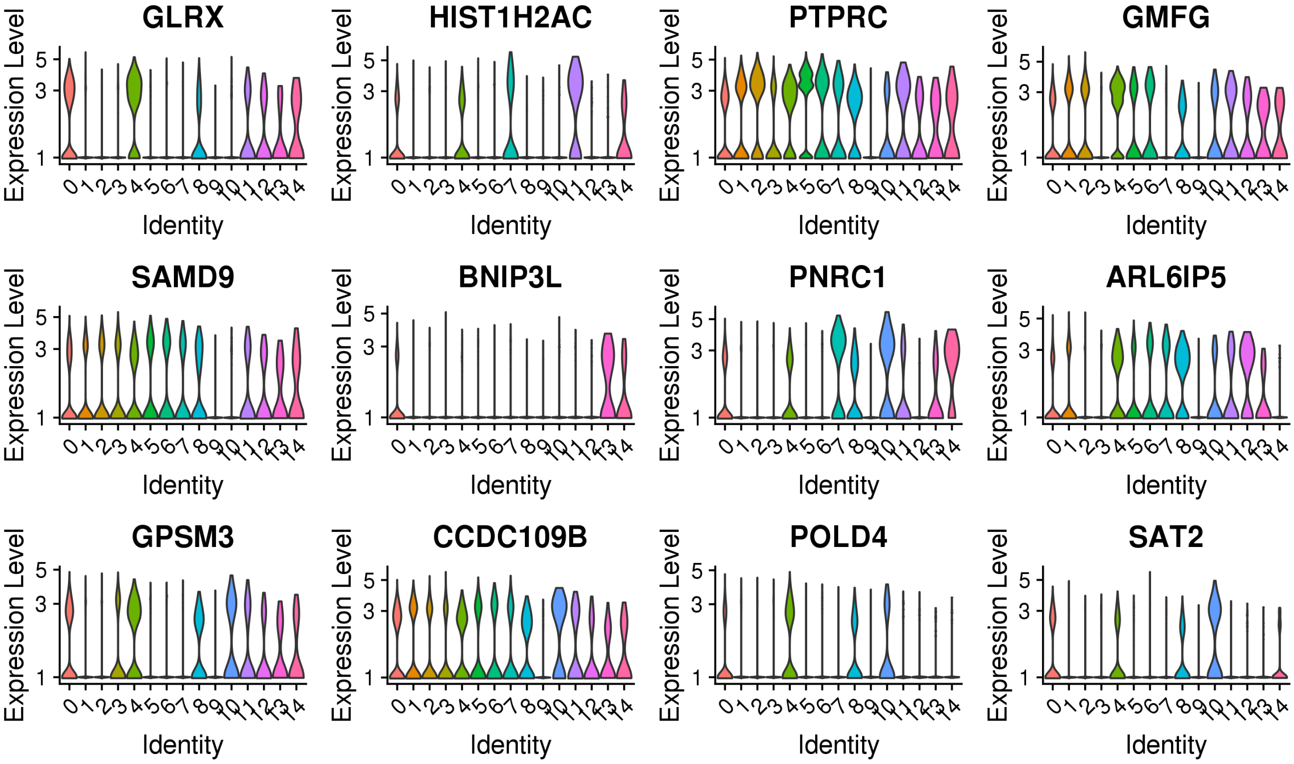
(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 9

12.30 Cluster 9 violin plots: negative marker genes



ANXA1
TMSB4X
SH3BGRL3
FTH1
S100A11
S100A10
TMSB10
ITM2B
S100A6
MYL6
TYROBP
CARD16

(a) Top negative marker genes ordered by p-value, cluster: 9



GLRX
HIST1H2AC
PTPRC
GMFG
SAMD9
BNIP3L
PNRC1
ARL6IP5
GPSM3
CCDC109B
POLD4
SAT2

(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 9

12.31 Cluster 10: summary plots

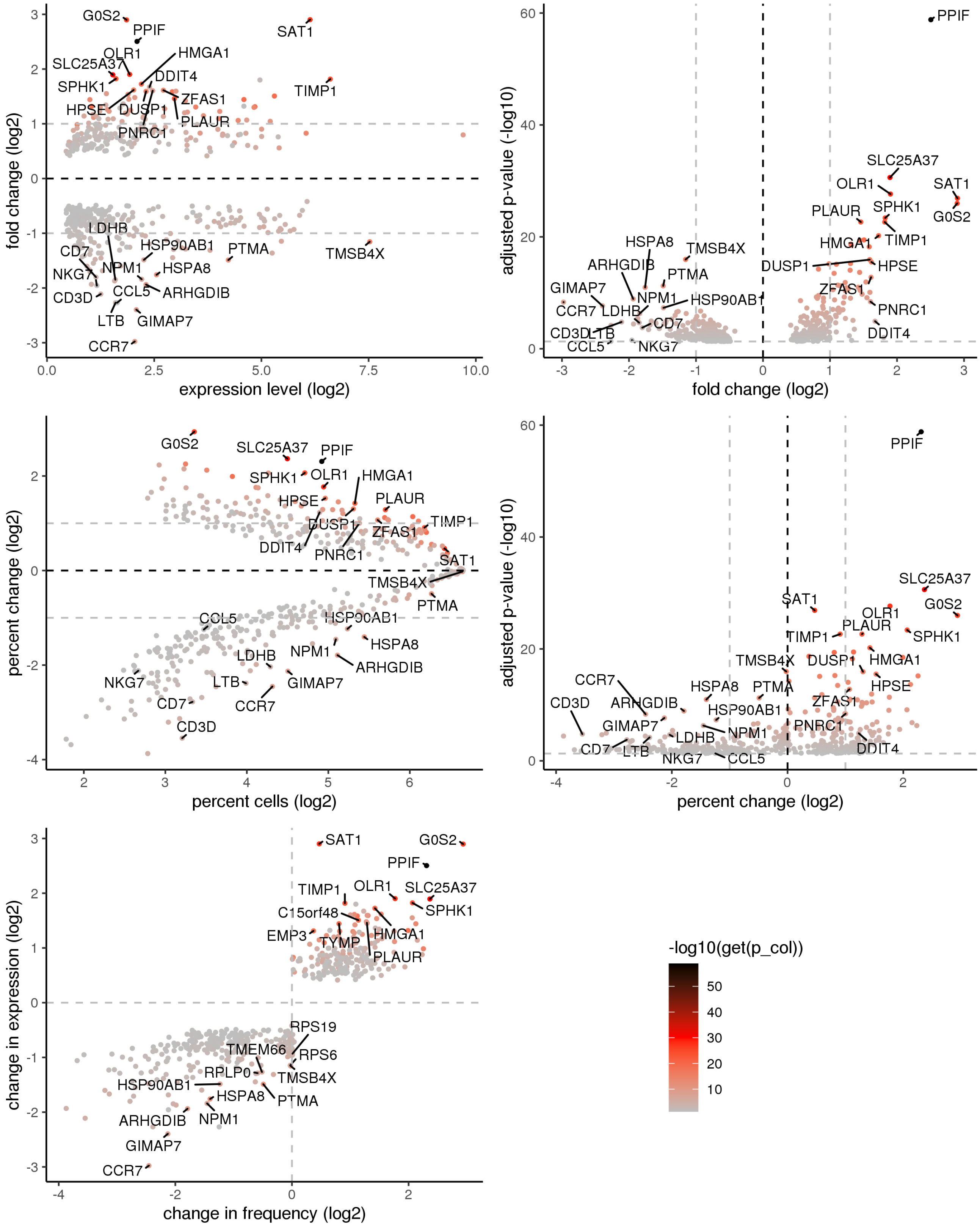
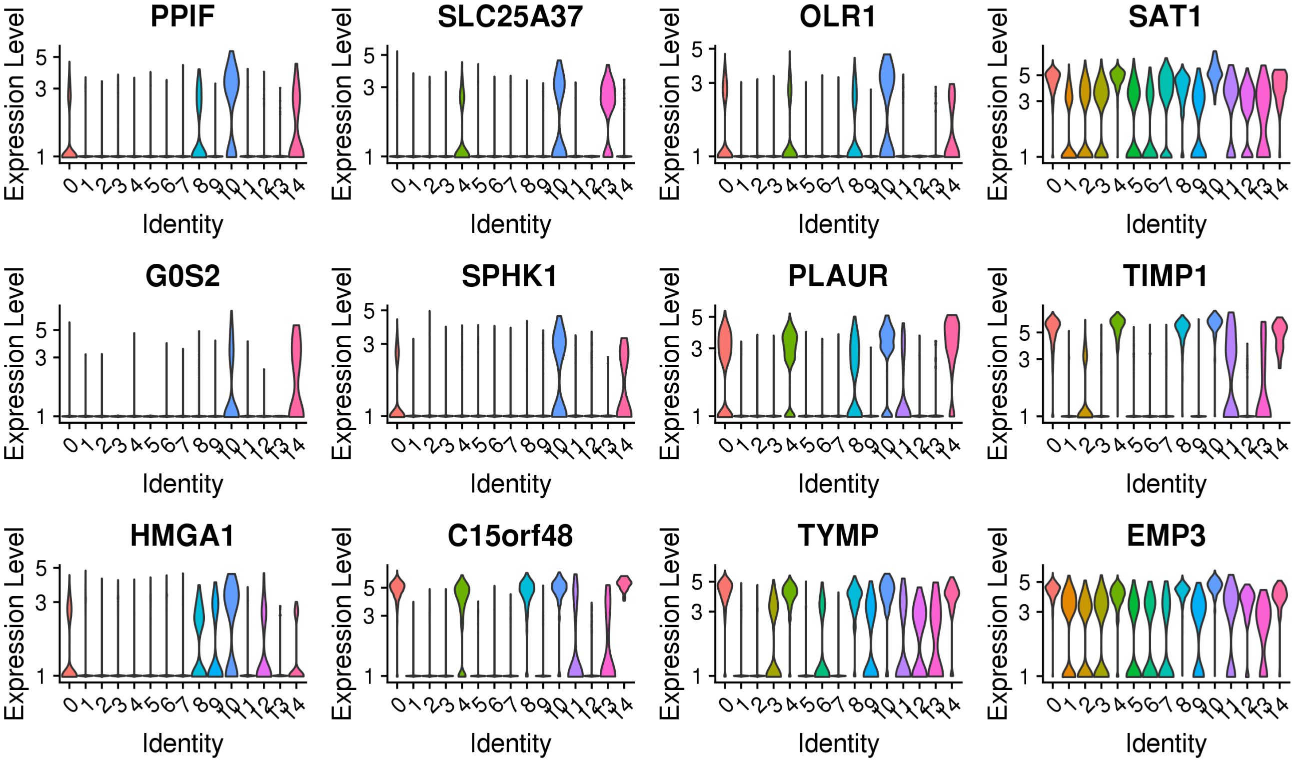
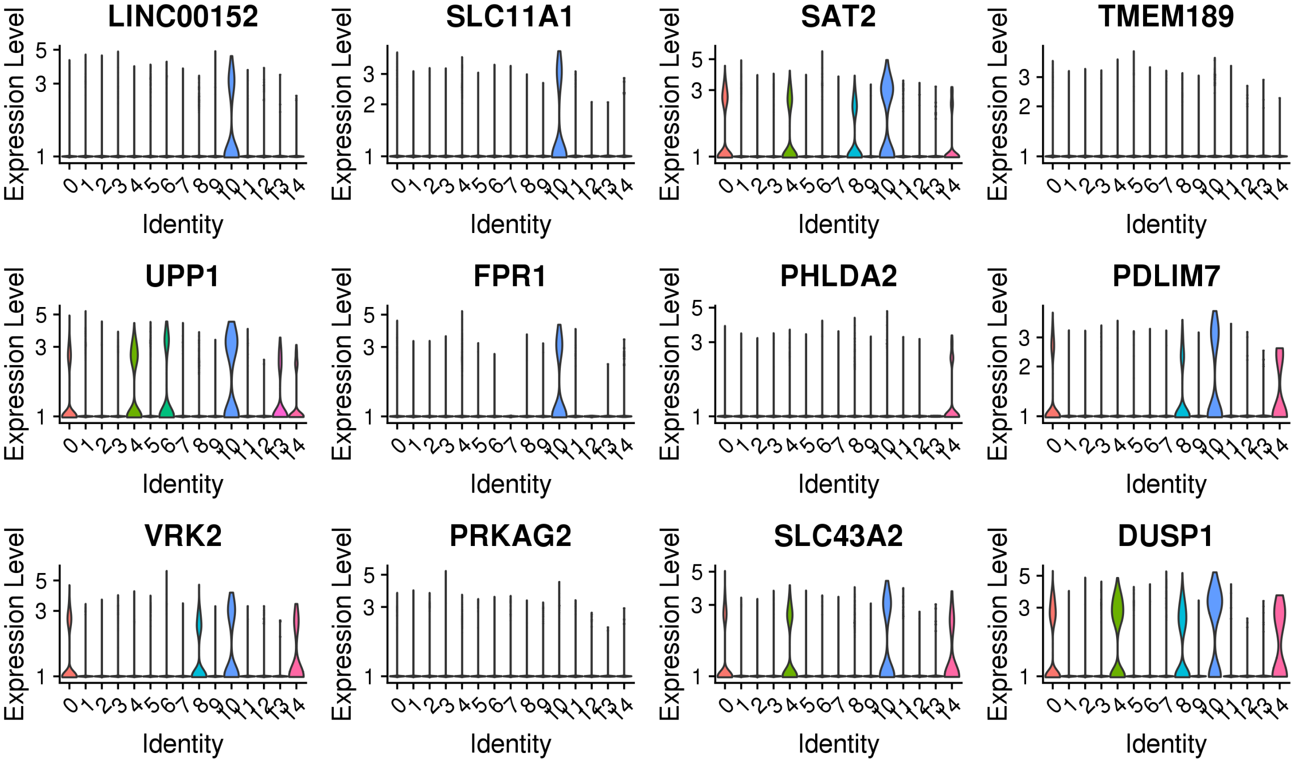


Figure 60: Differential expression summary plots for cluster 10

12.32 Cluster 10 violin plots: positive marker genes

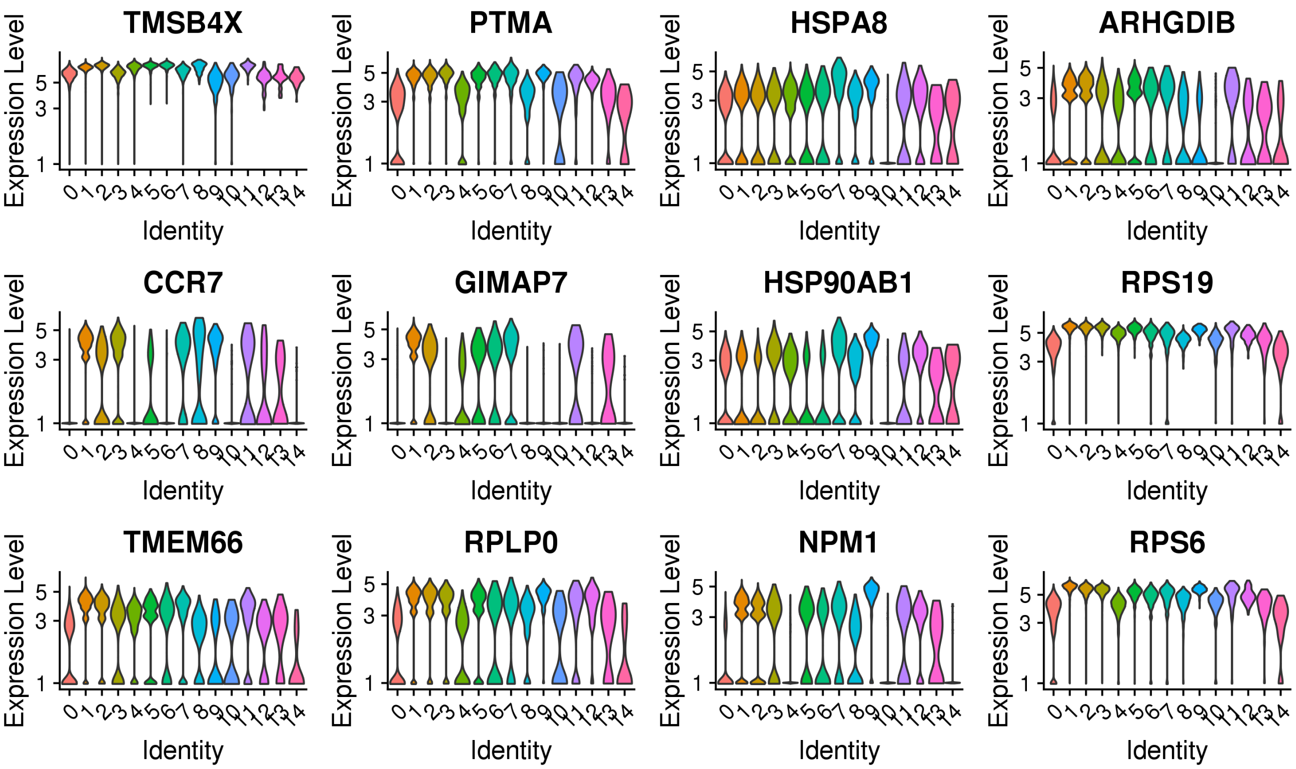


(a) Top positive marker genes ordered by p-value, cluster: 10

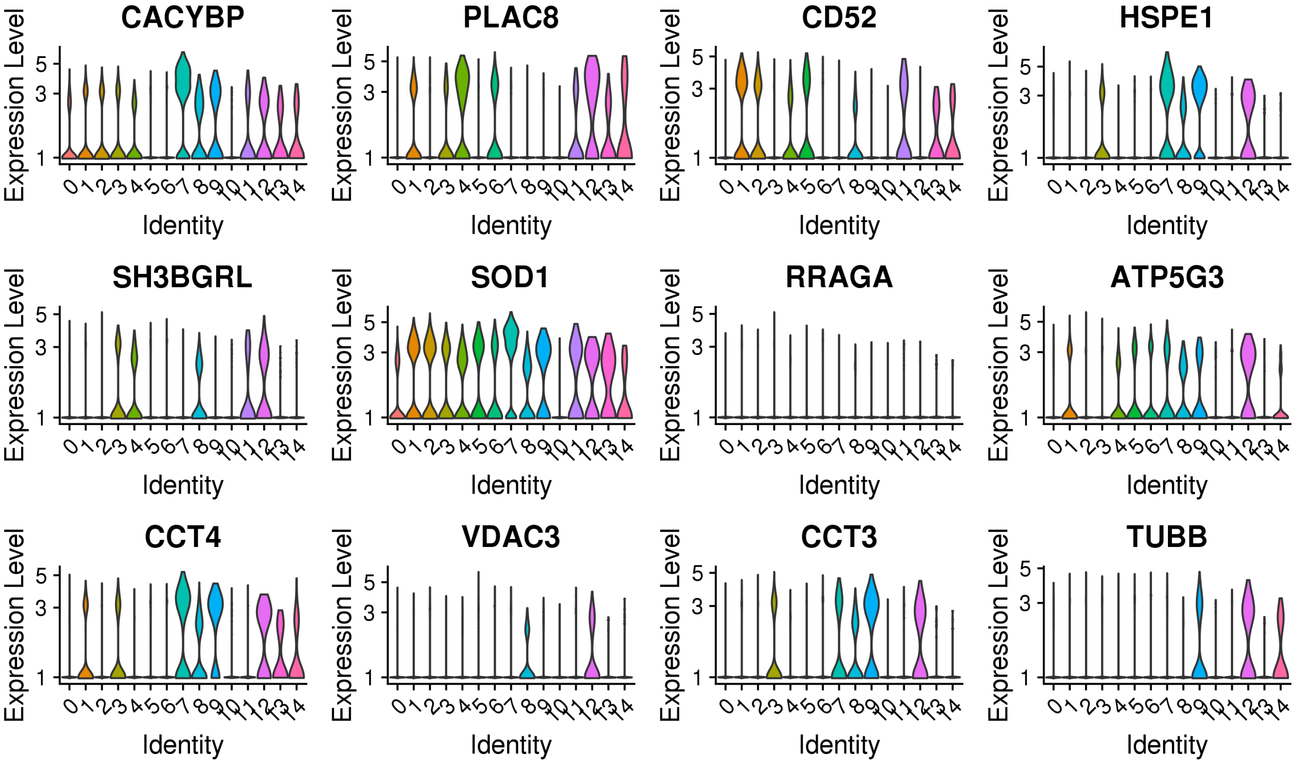


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 10

12.33 Cluster 10 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 10



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 10

12.34 Cluster 11: summary plots

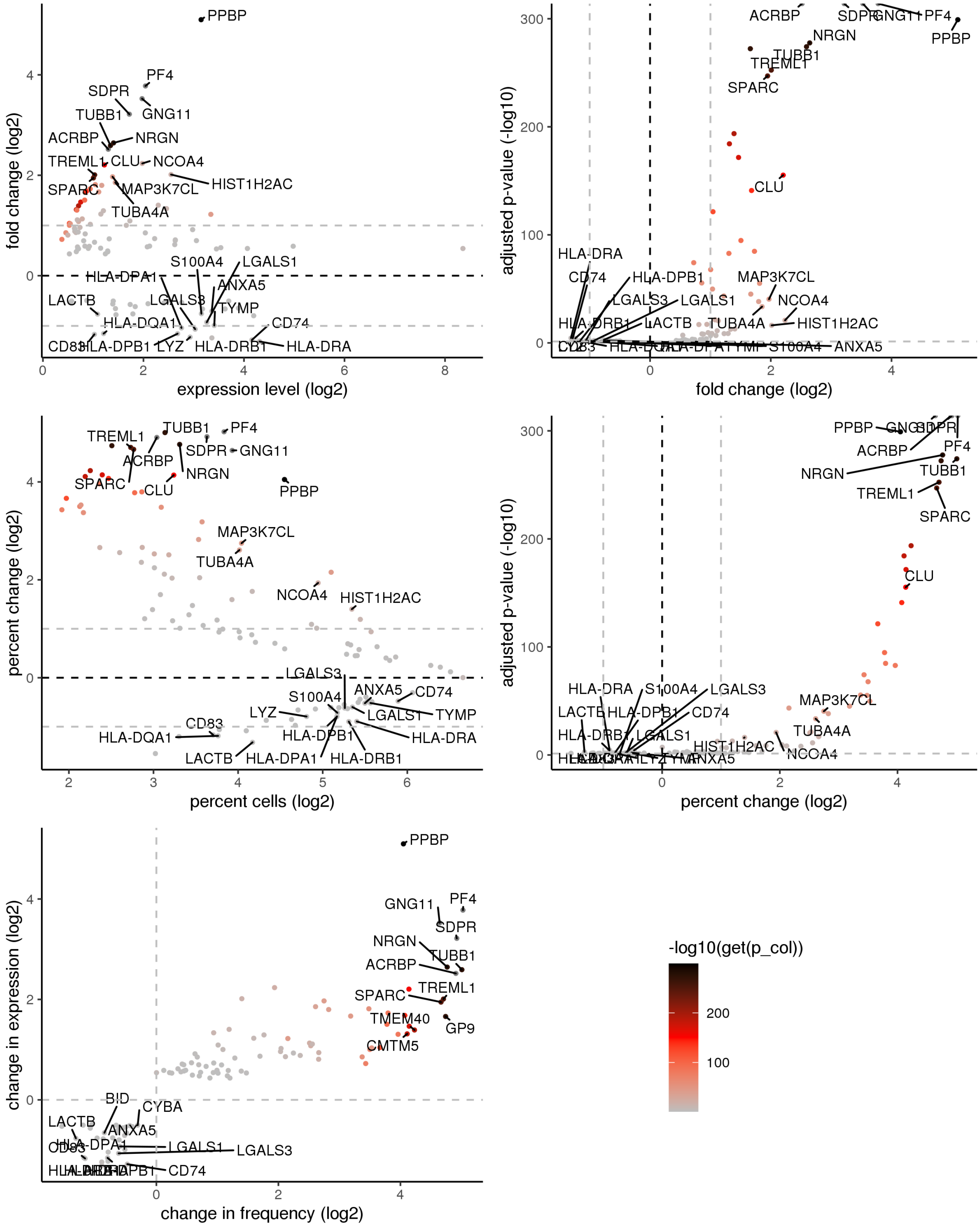
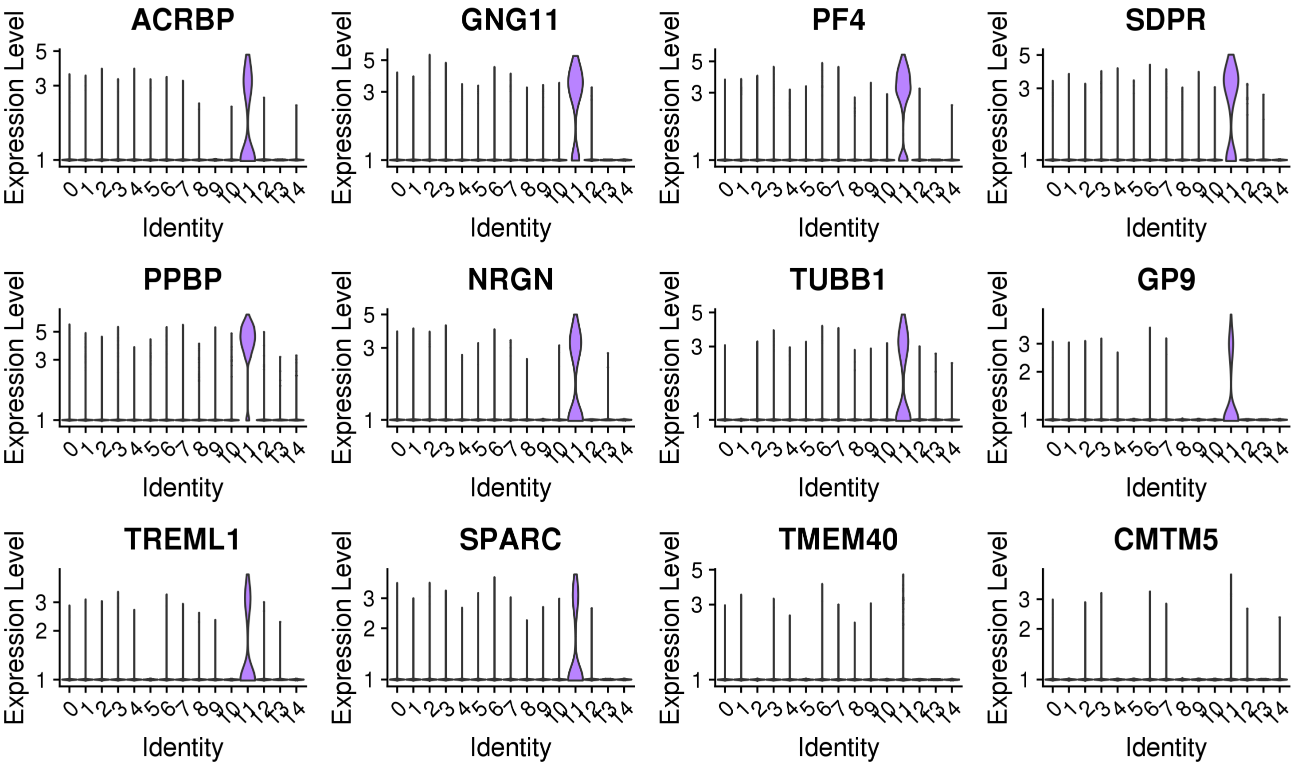
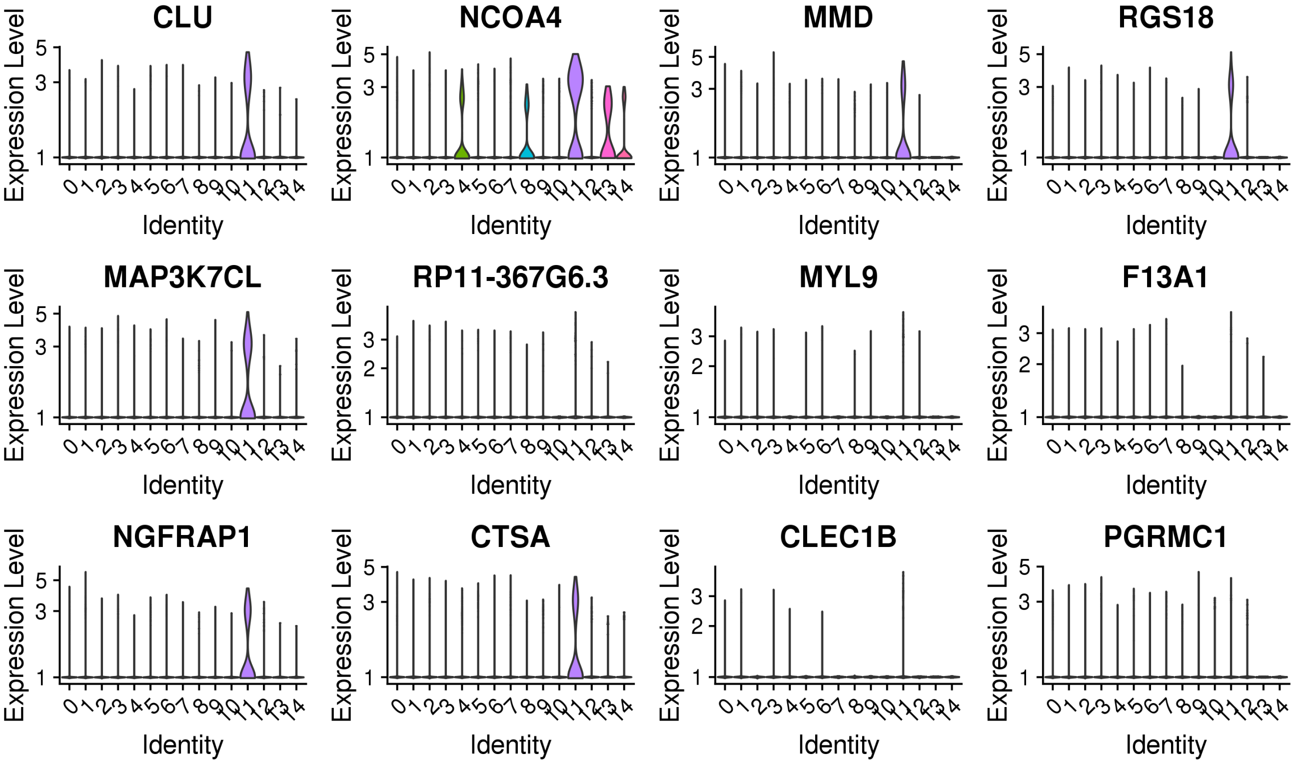


Figure 63: Differential expression summary plots for cluster 11

12.35 Cluster 11 violin plots: positive marker genes

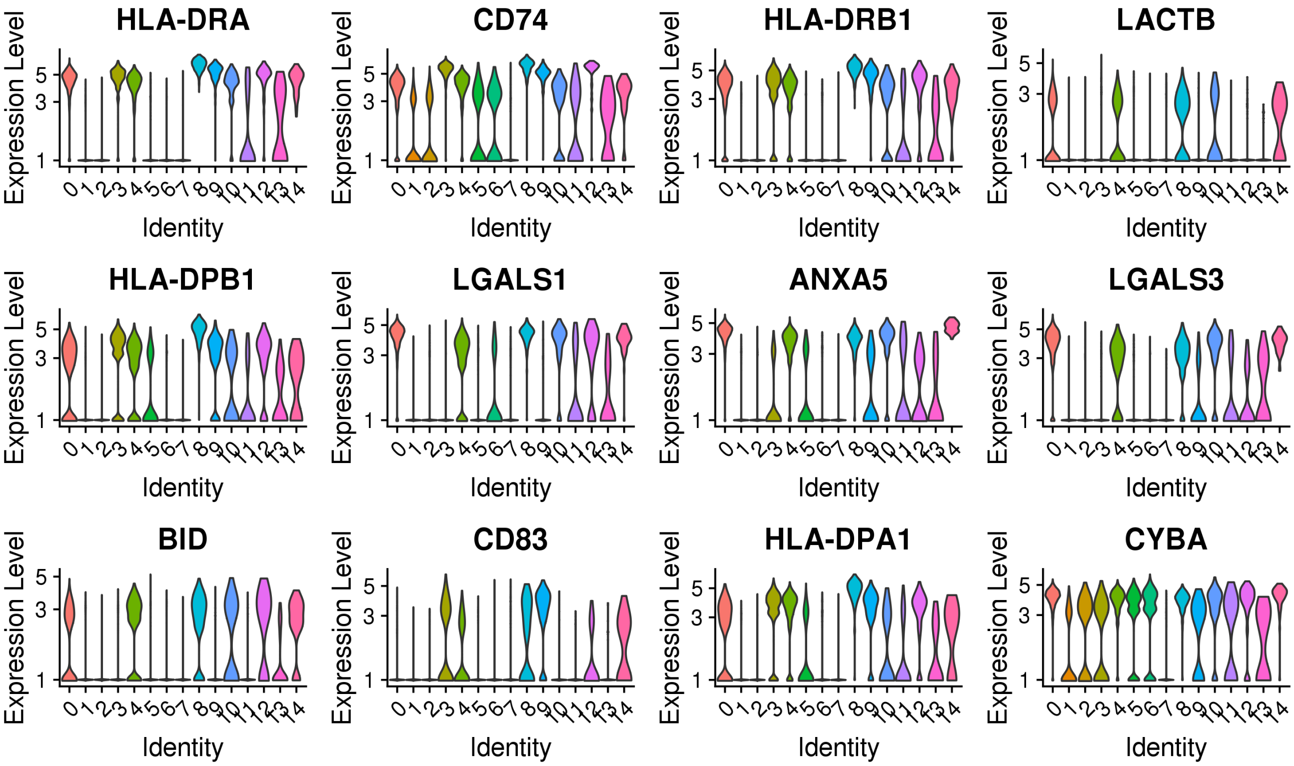


(a) Top positive marker genes ordered by p-value, cluster: 11

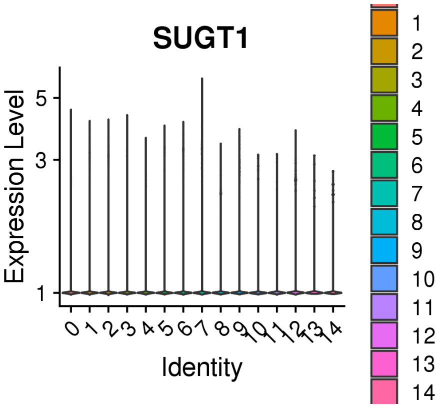


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 11

12.36 Cluster 11 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 11



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 11

12.37 Cluster 12: summary plots

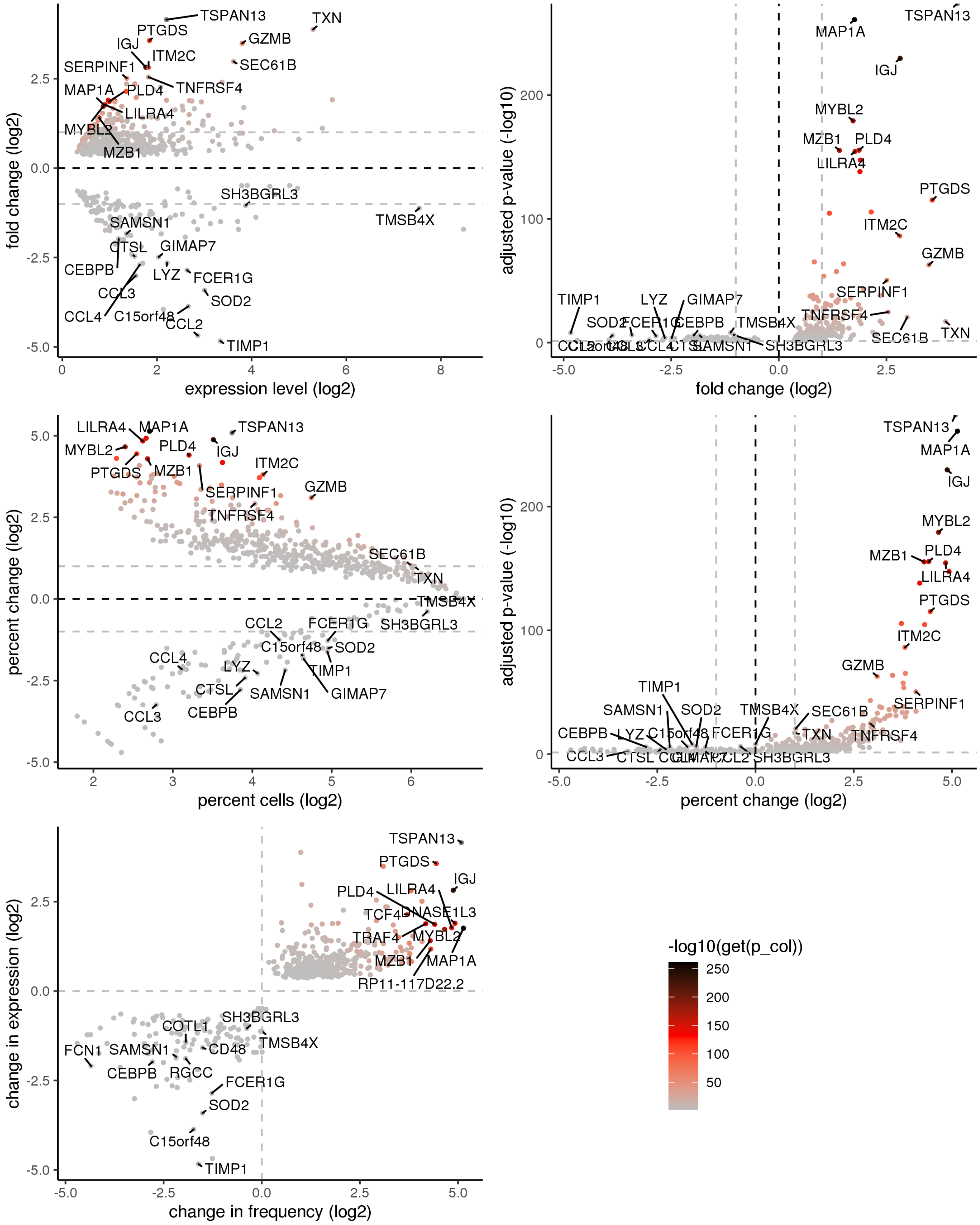
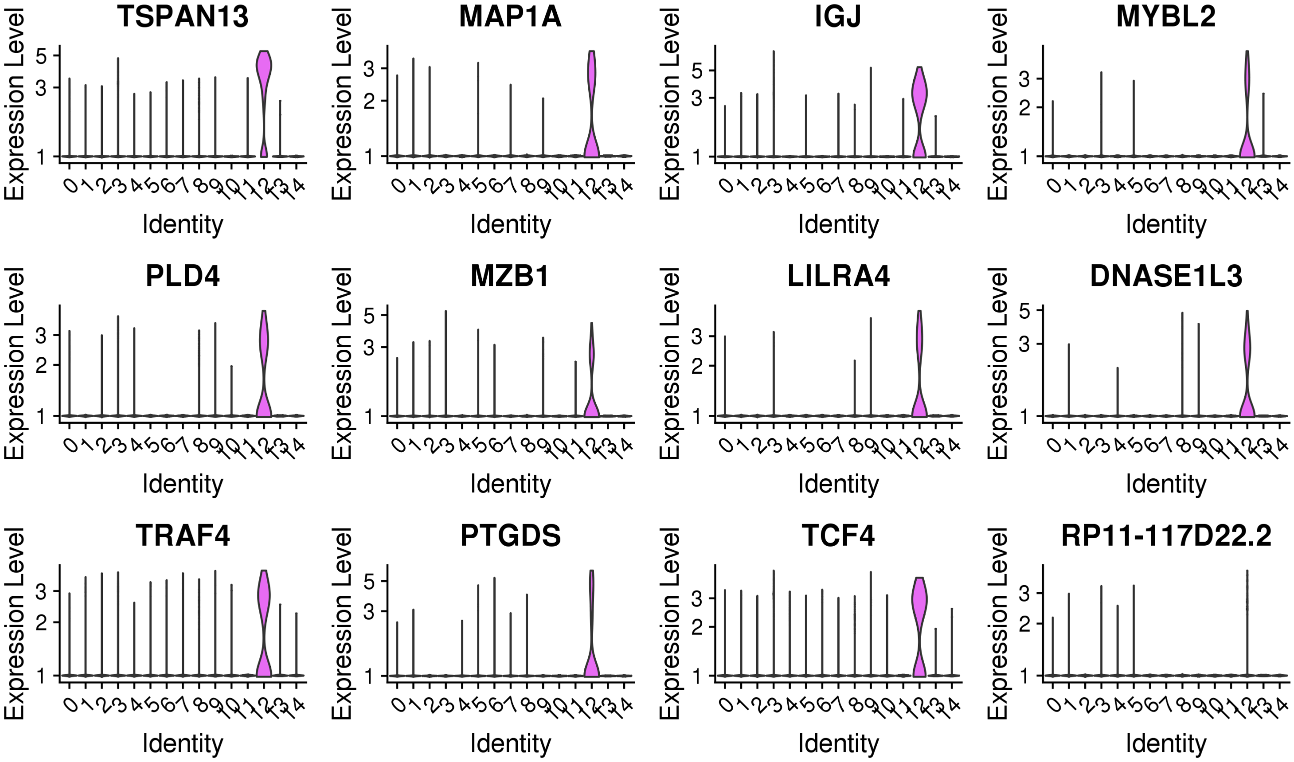
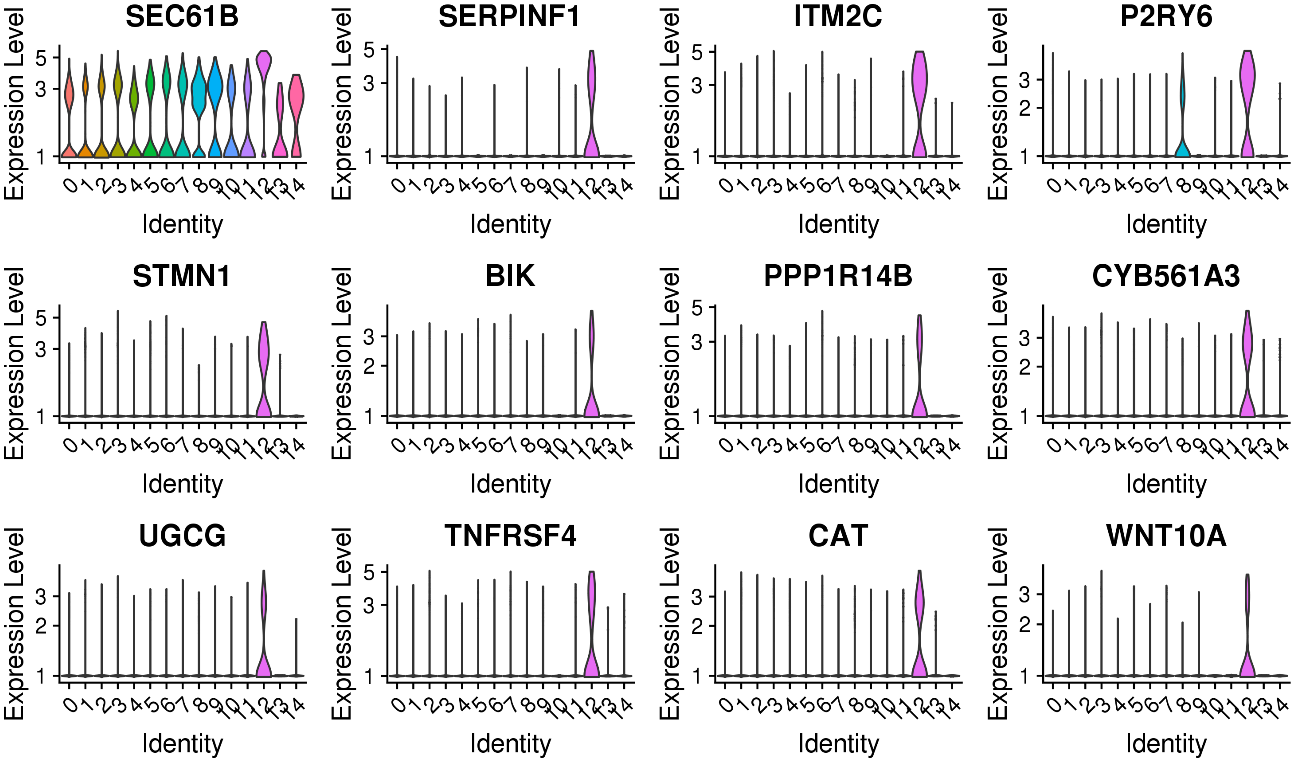


Figure 66: Differential expression summary plots for cluster 12

12.38 Cluster 12 violin plots: positive marker genes

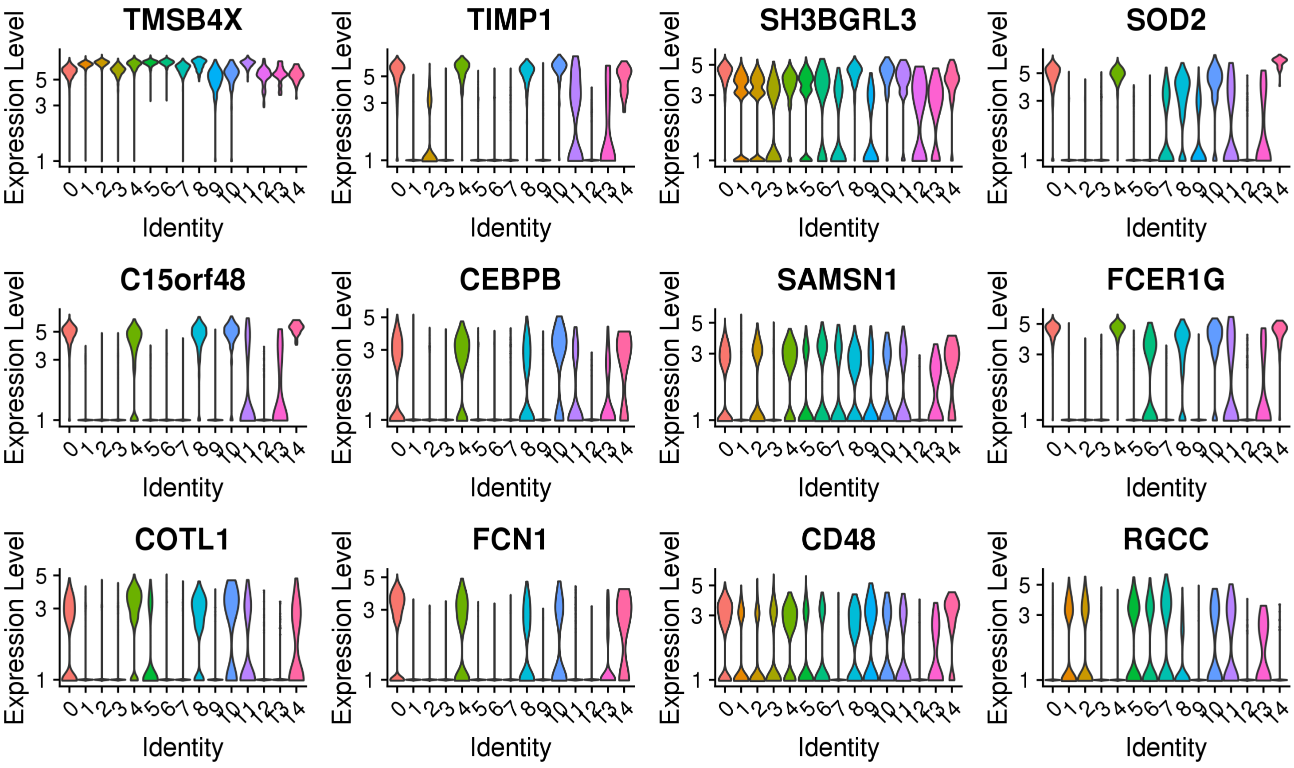


(a) Top positive marker genes ordered by p-value, cluster: 12

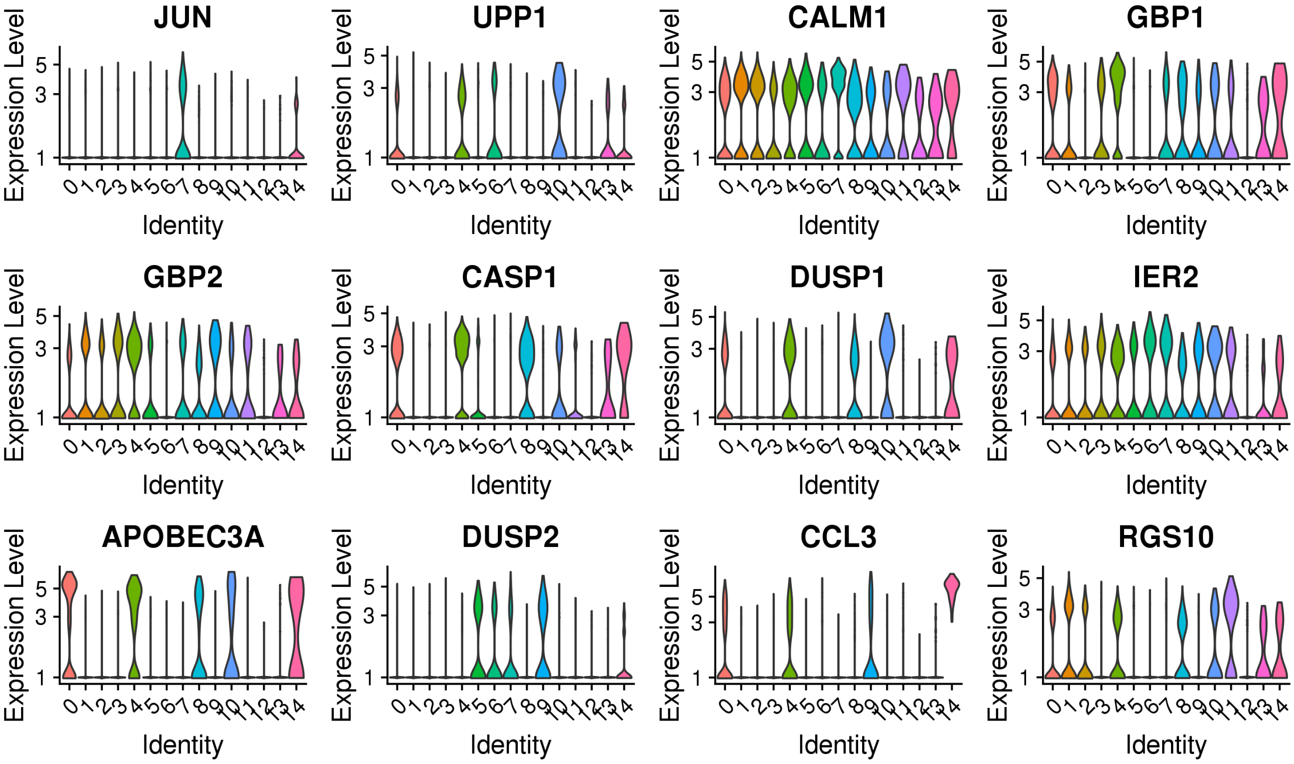


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 12

12.39 Cluster 12 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 12



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 12

12.40 Cluster 13: summary plots

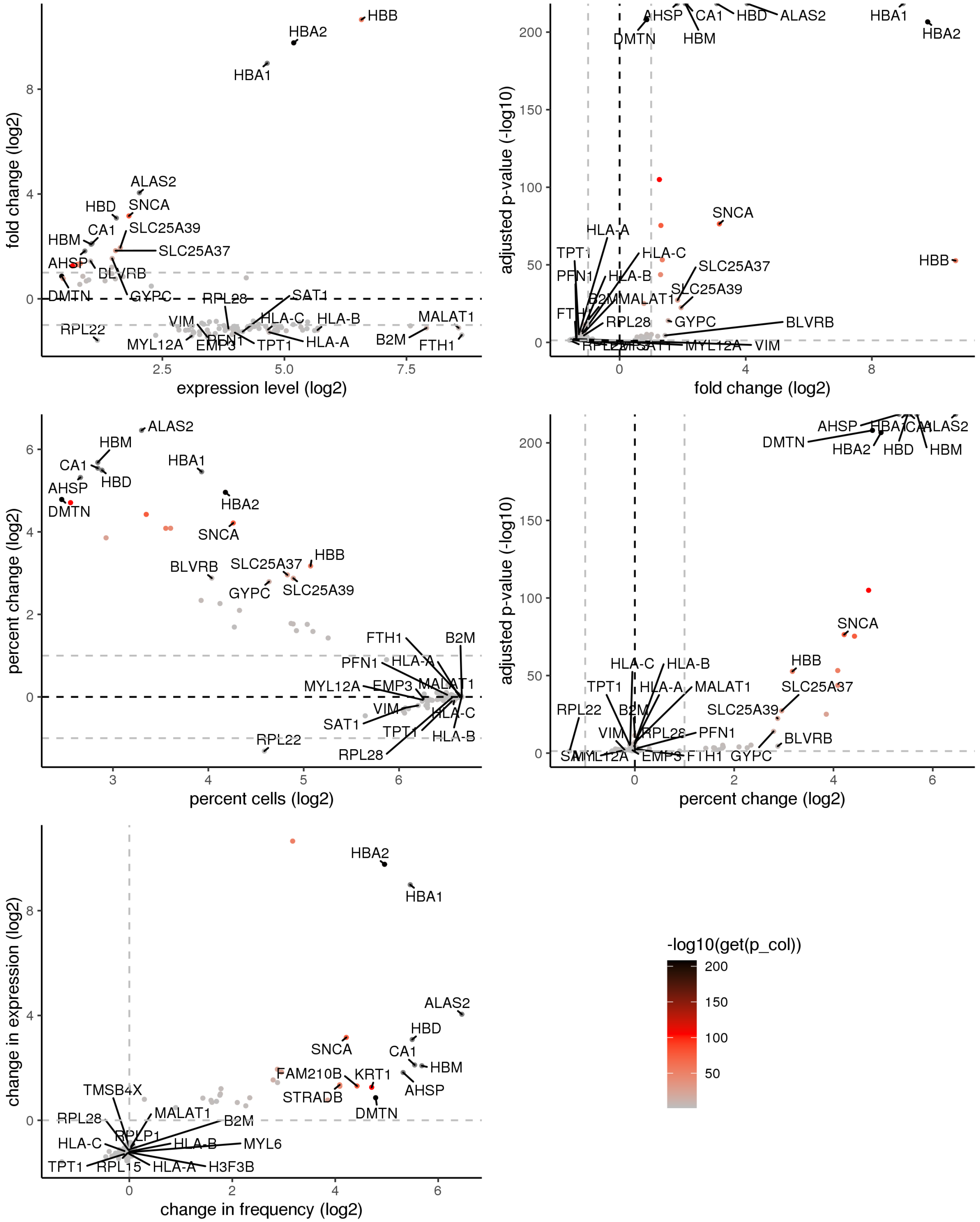
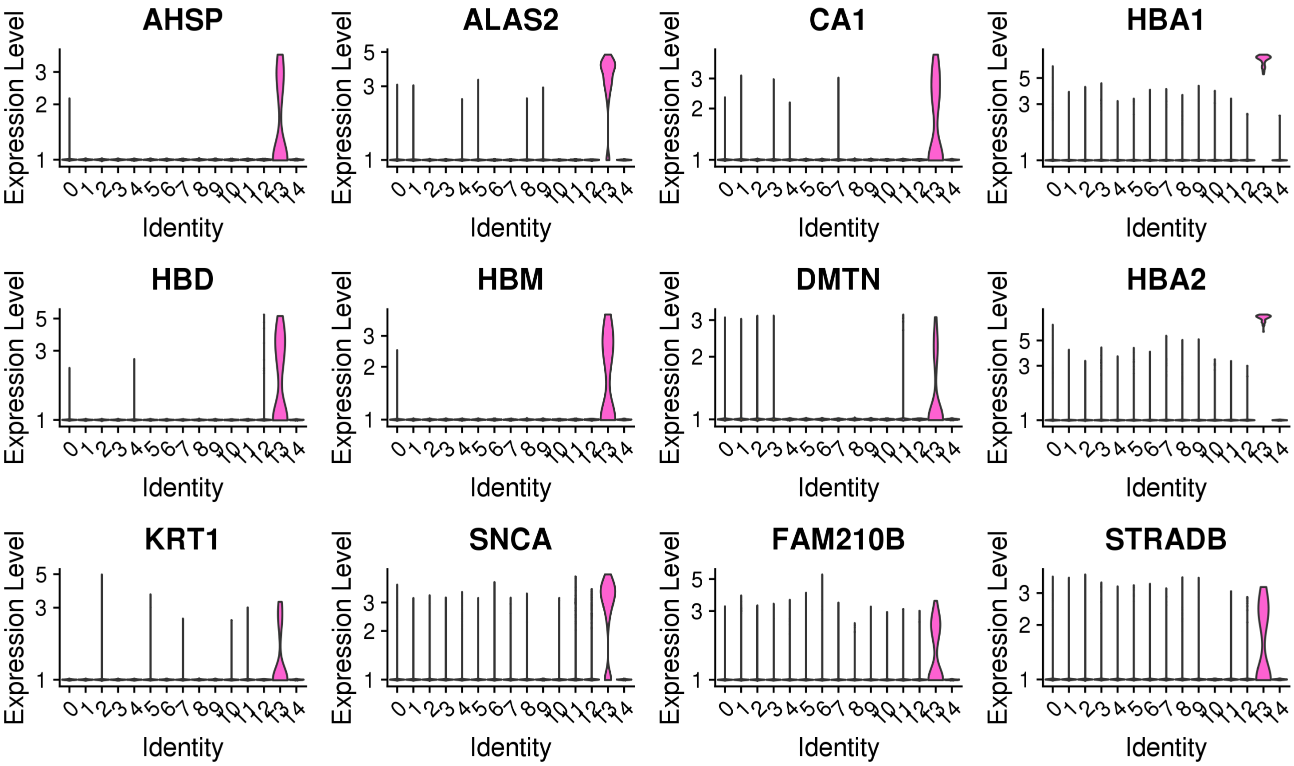
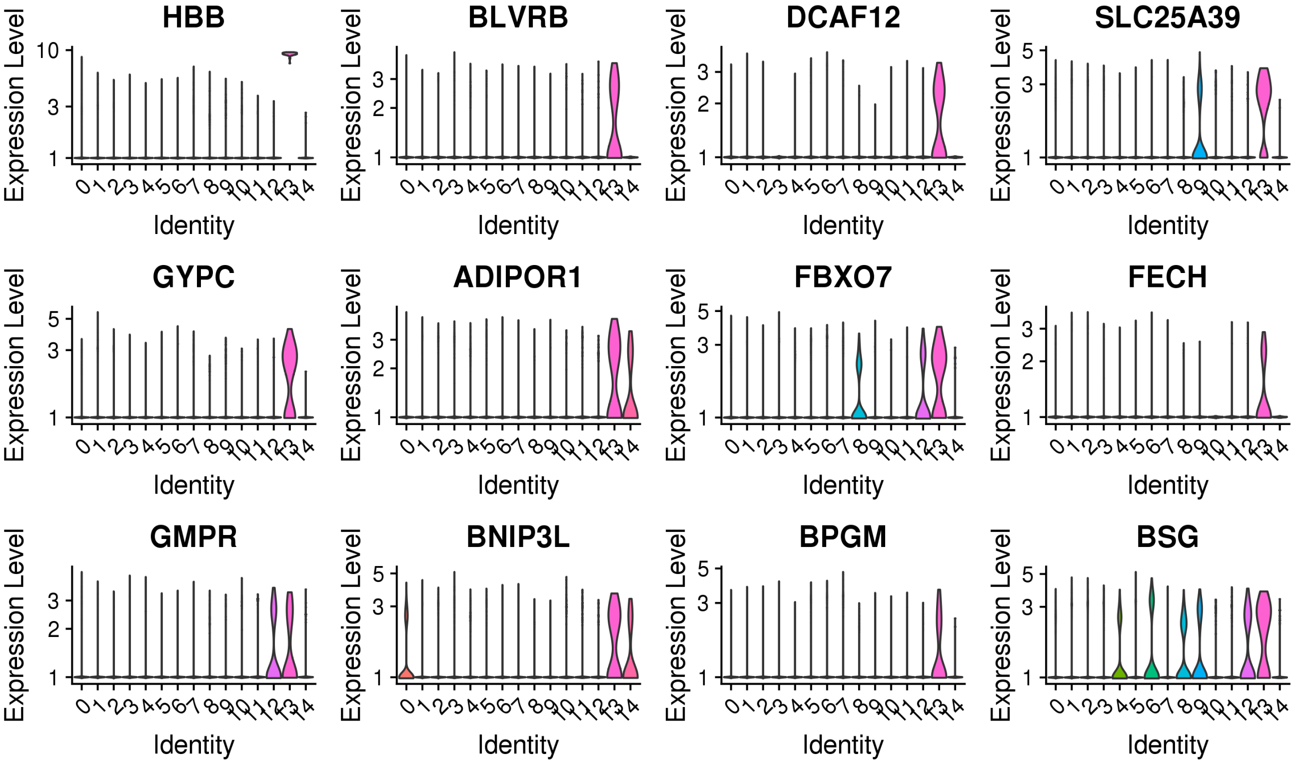


Figure 69: Differential expression summary plots for cluster 13

12.41 Cluster 13 violin plots: positive marker genes

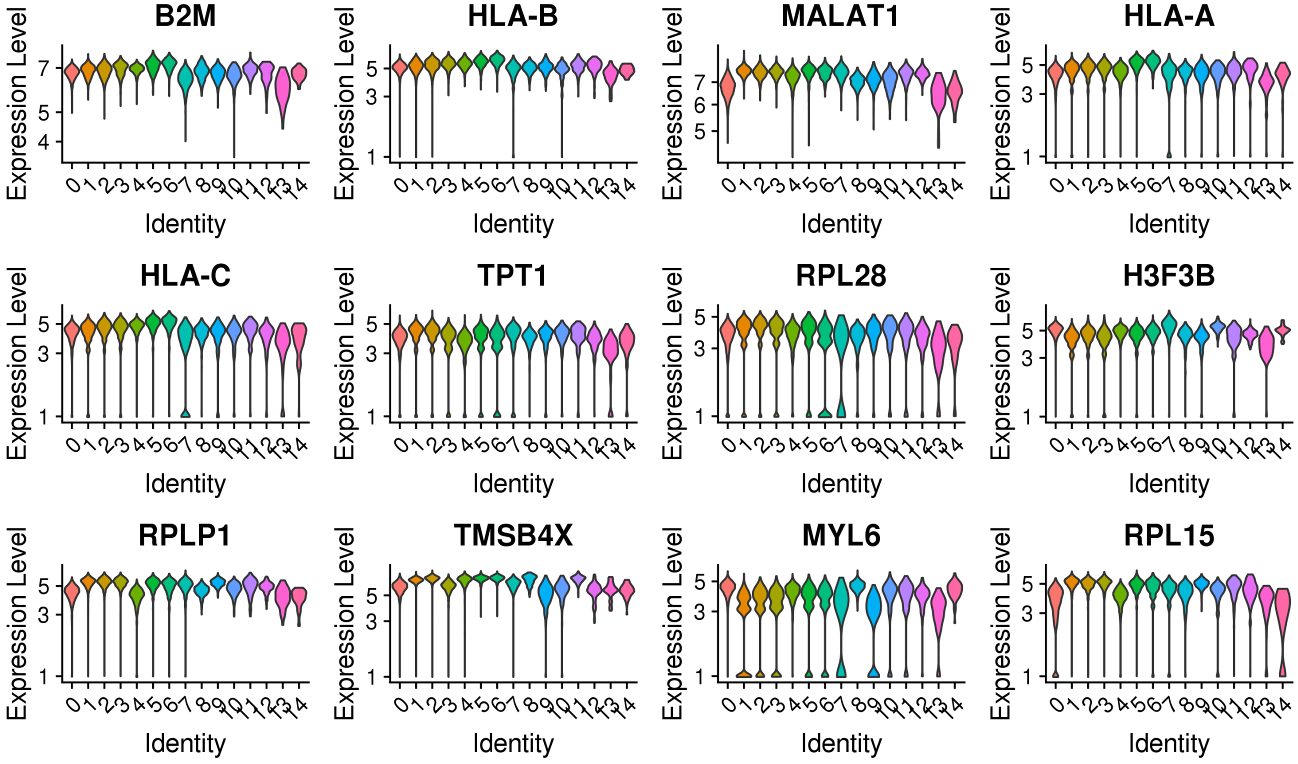


(a) Top positive marker genes ordered by p-value, cluster: 13

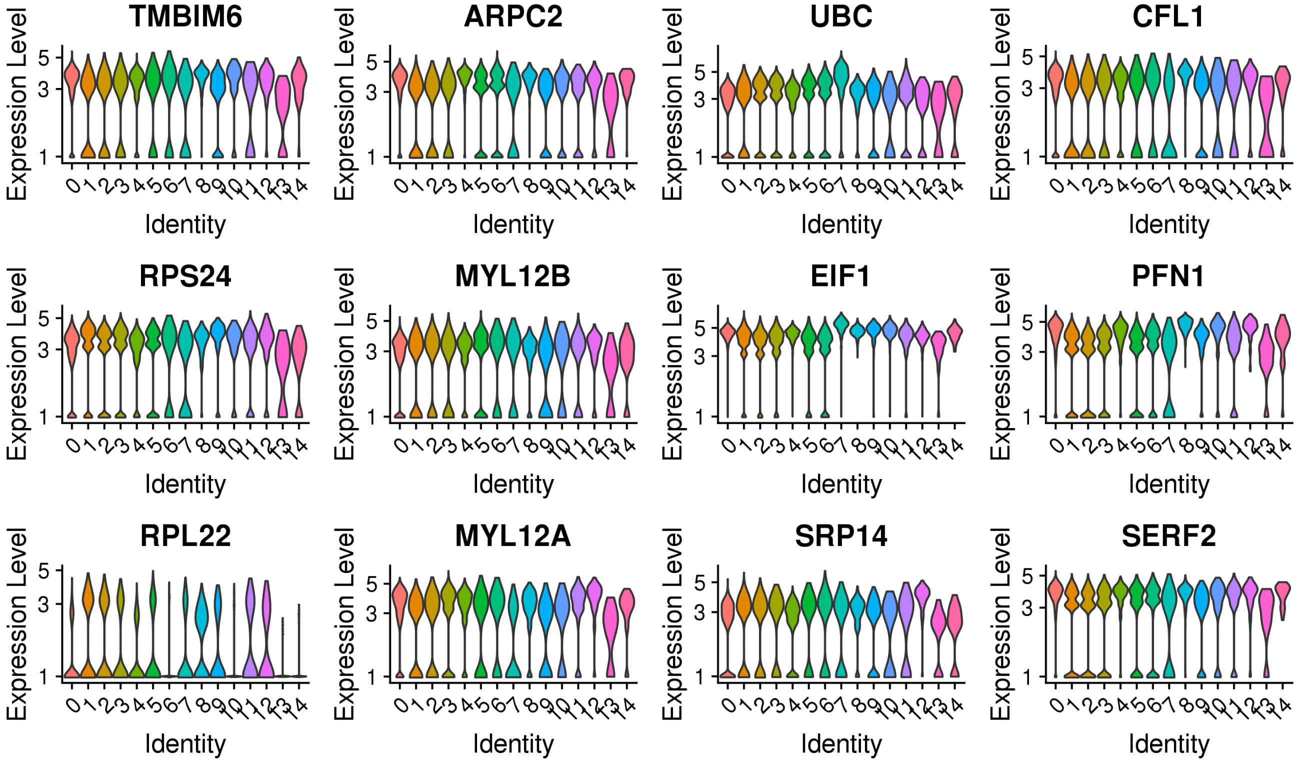


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 13

12.42 Cluster 13 violin plots: negative marker genes


B2M, HLA-B, MALAT1, HLA-A, HLA-C, TPT1, RPL28, H3F3B, RPLP1, TMSB4X, MYL6, RPL15

(a) Top negative marker genes ordered by p-value, cluster: 13


TMBIM6, ARPC2, UBC, CFL1, RPS24, MYL12B, EIF1, PFN1, RPL22, MYL12A, SRP14, SERF2

(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 13

12.43 Cluster 14: summary plots

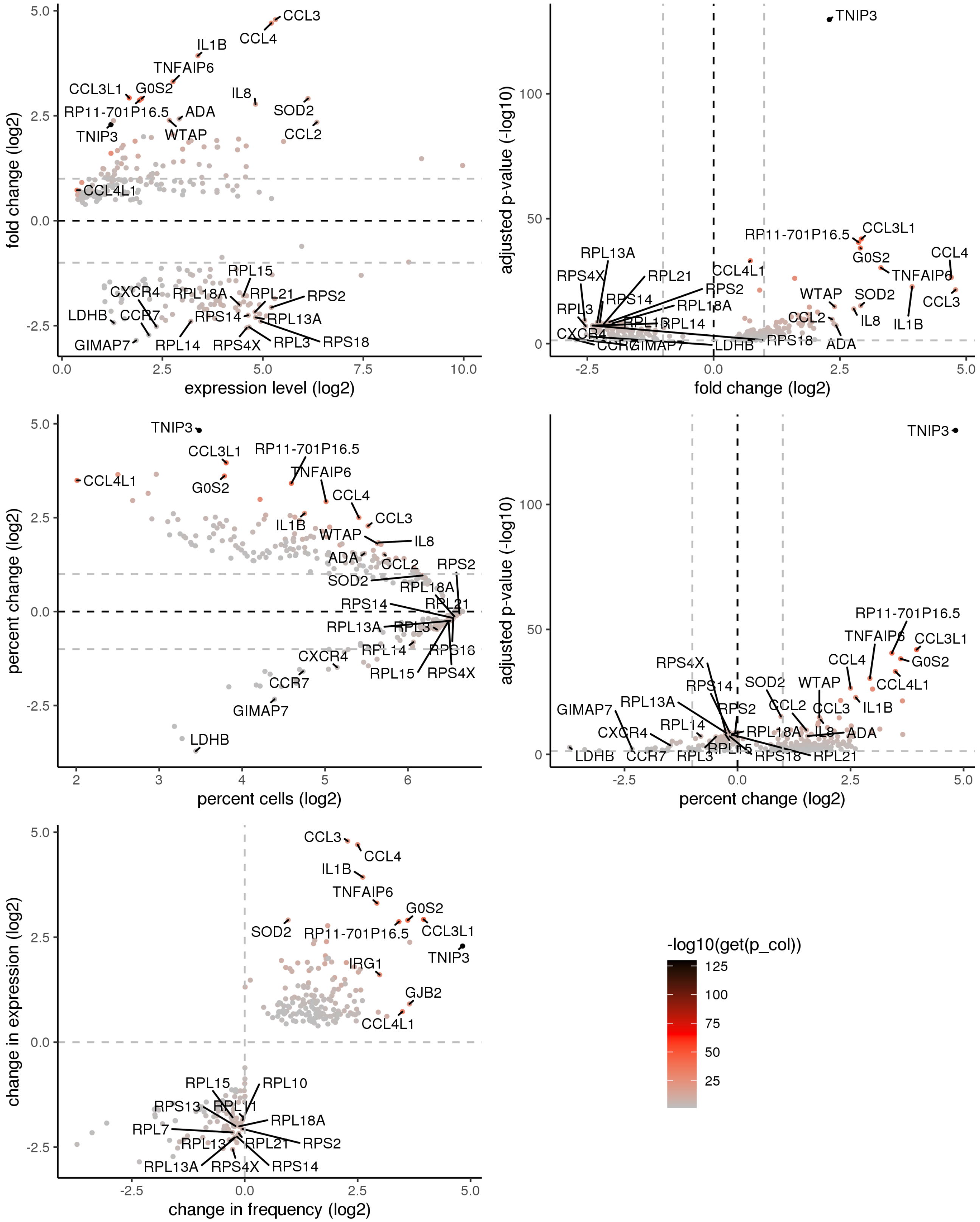
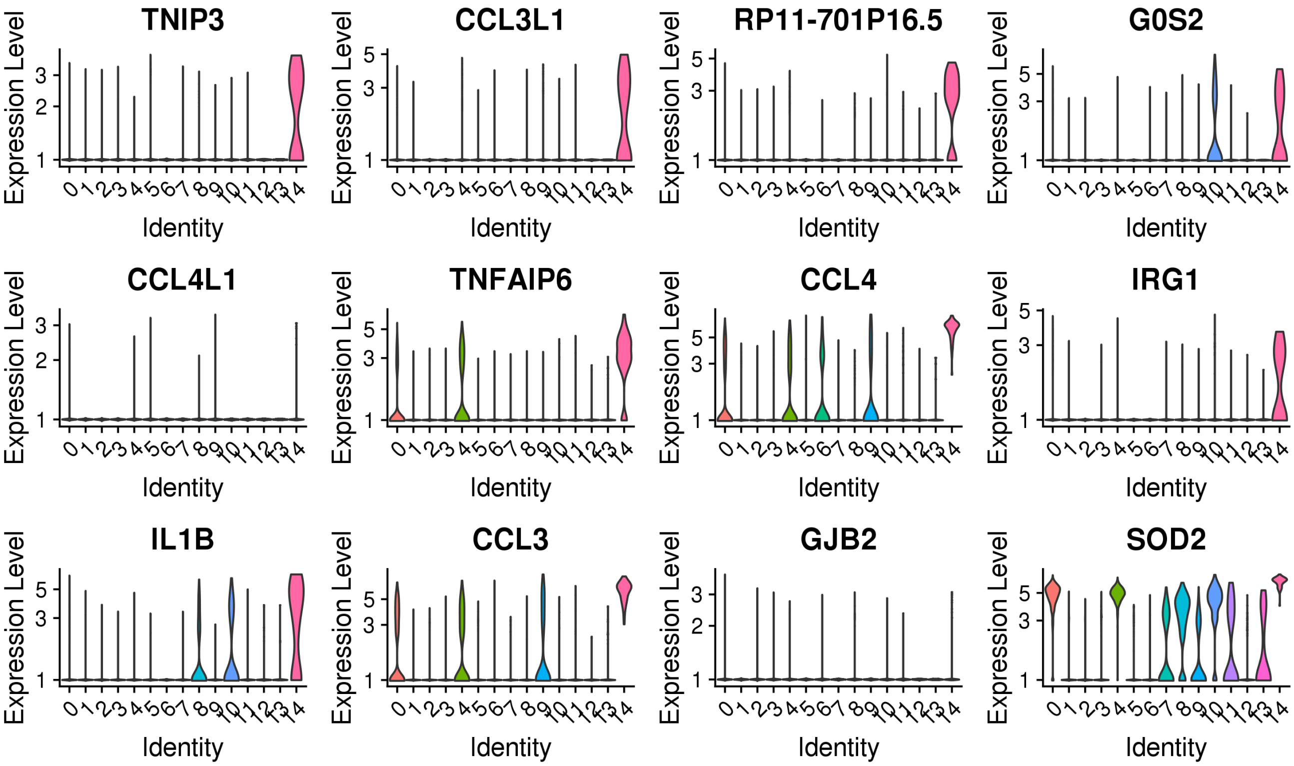
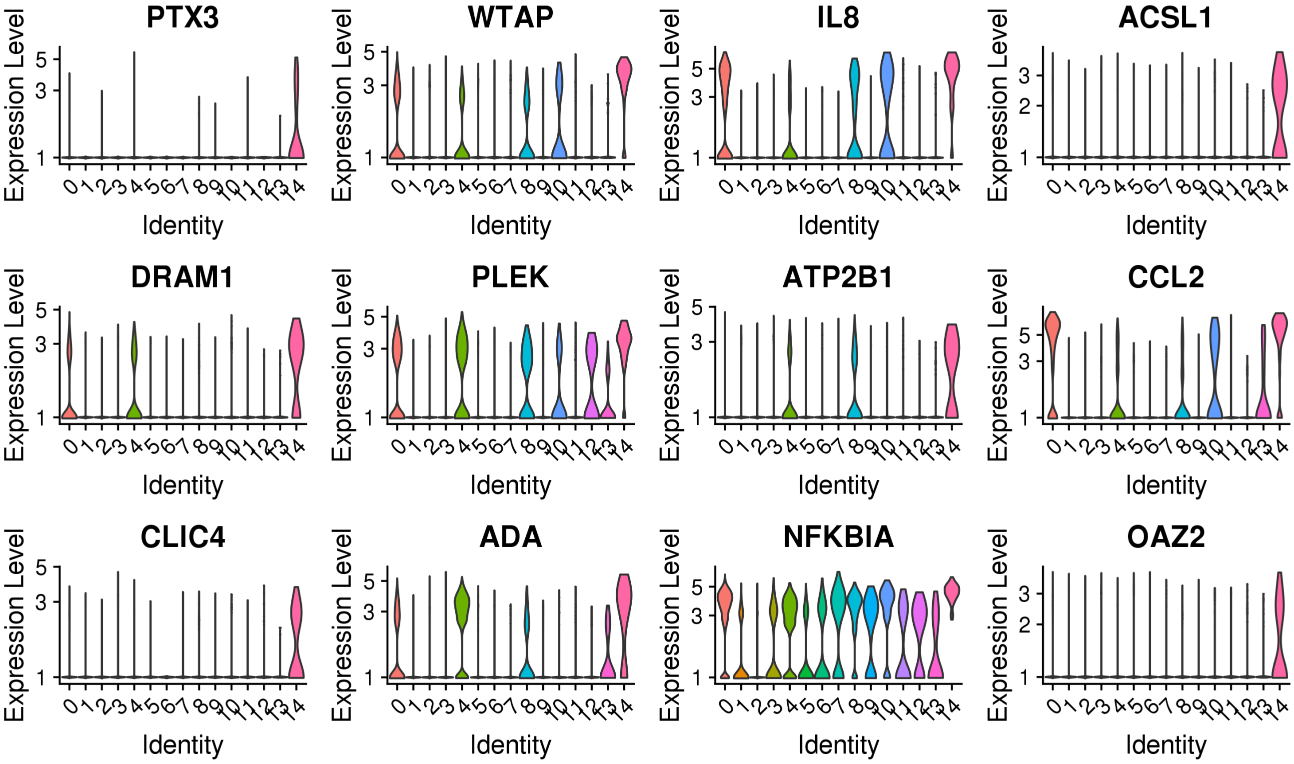


Figure 72: Differential expression summary plots for cluster 14

12.44 Cluster 14 violin plots: positive marker genes

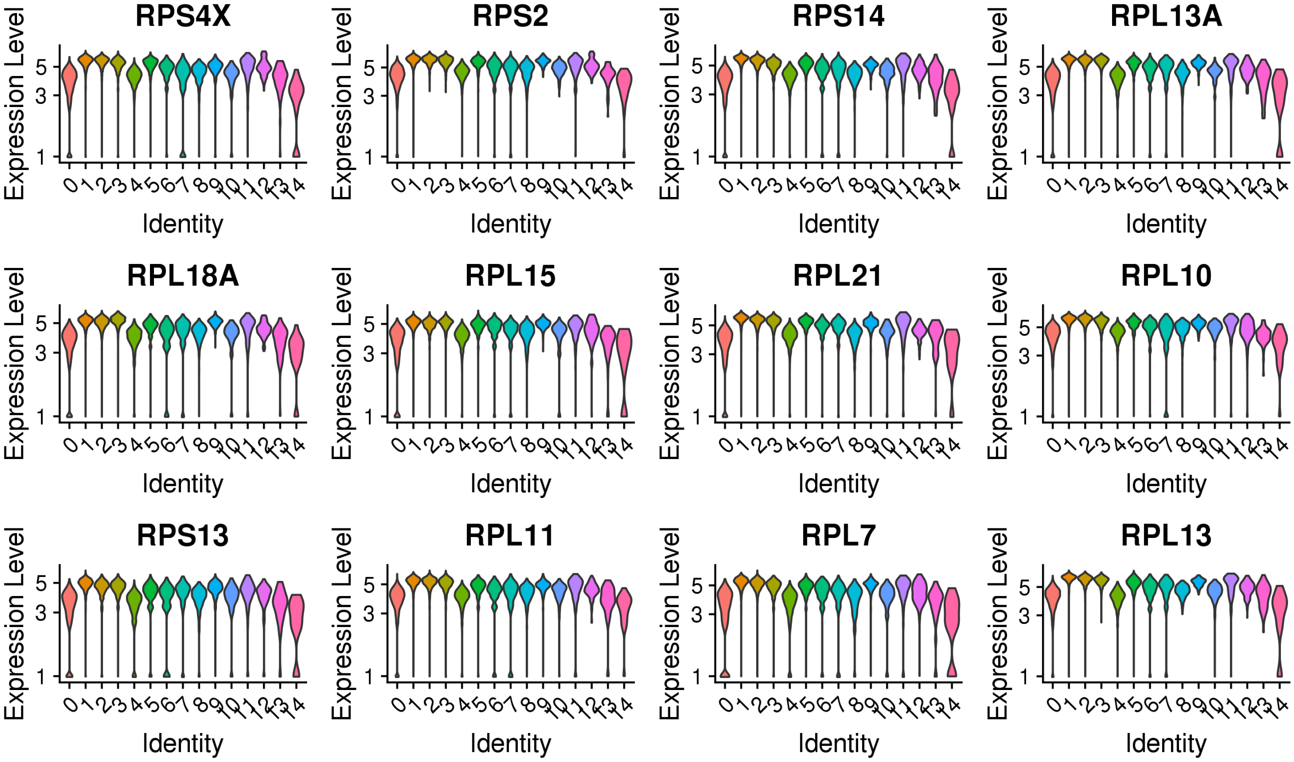


(a) Top positive marker genes ordered by p-value, cluster: 14

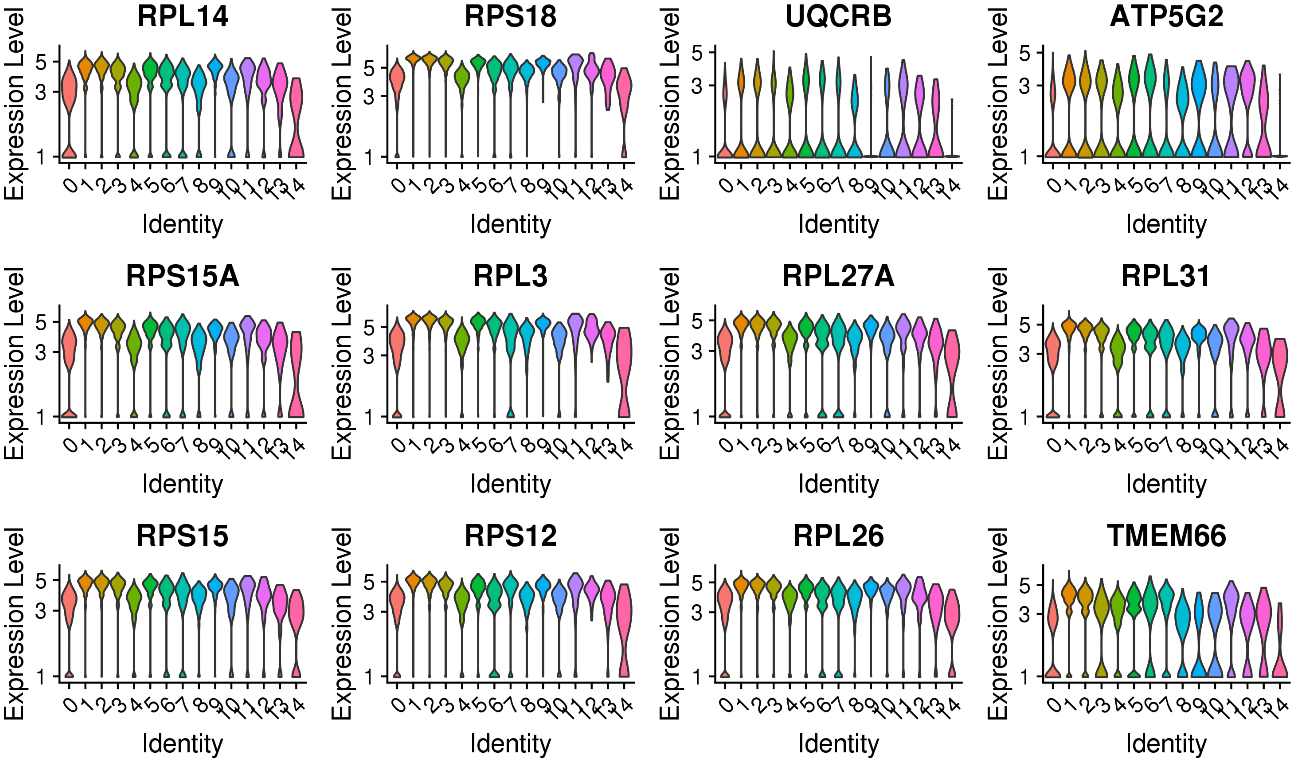


(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 14

12.45 Cluster 14 violin plots: negative marker genes



(a) Top negative marker genes ordered by p-value, cluster: 14



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 14

13 Geneset analysis

A hypergeometric test is used to test for the enrichment of GO, KEGG and msigdb genesets amongst the positive marker genes for each cluster. The full results are available as a separate xlsx document.

13.1 GO.BP

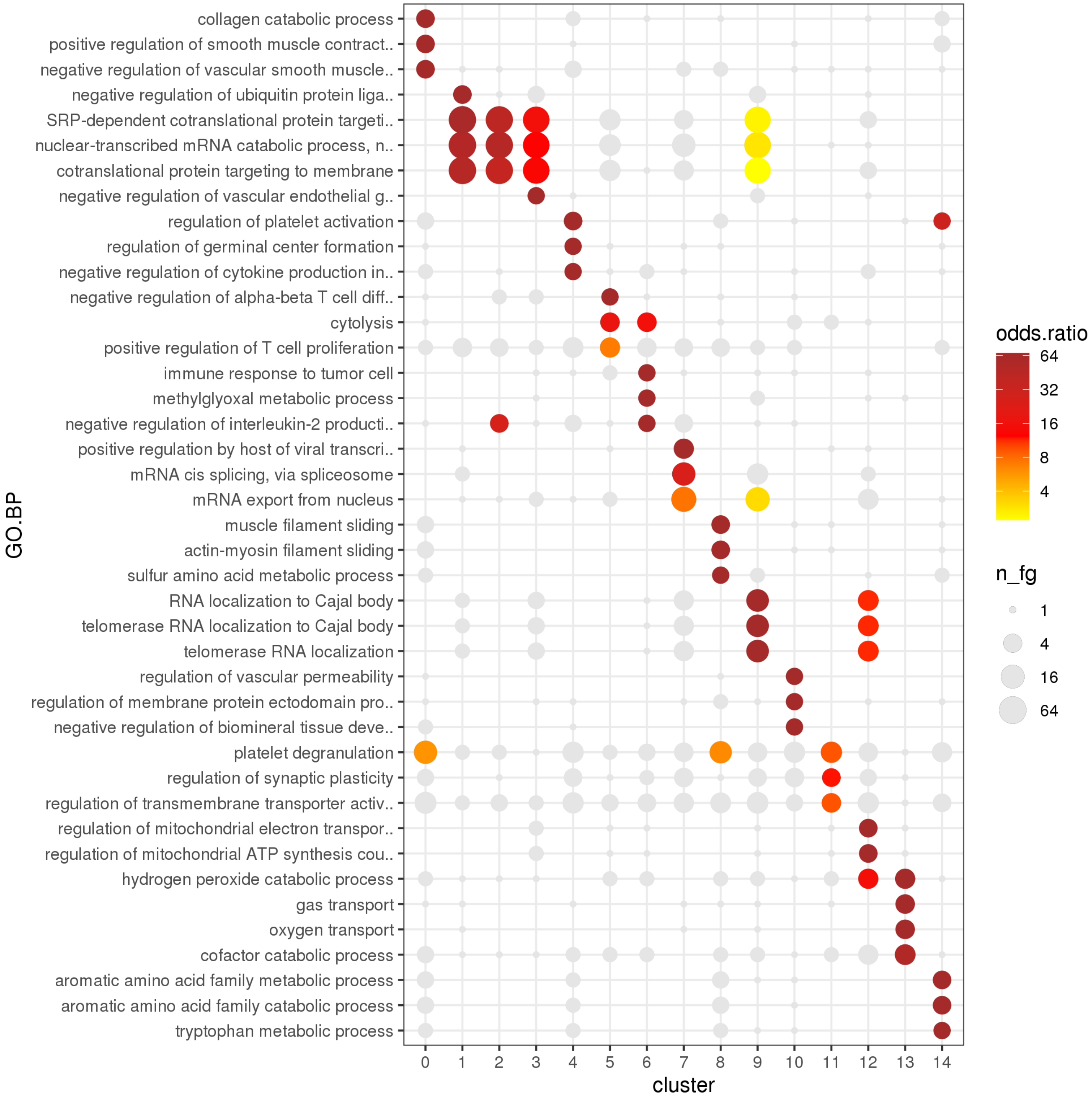


Figure 75: Heatmap of the top GO.BP genesets

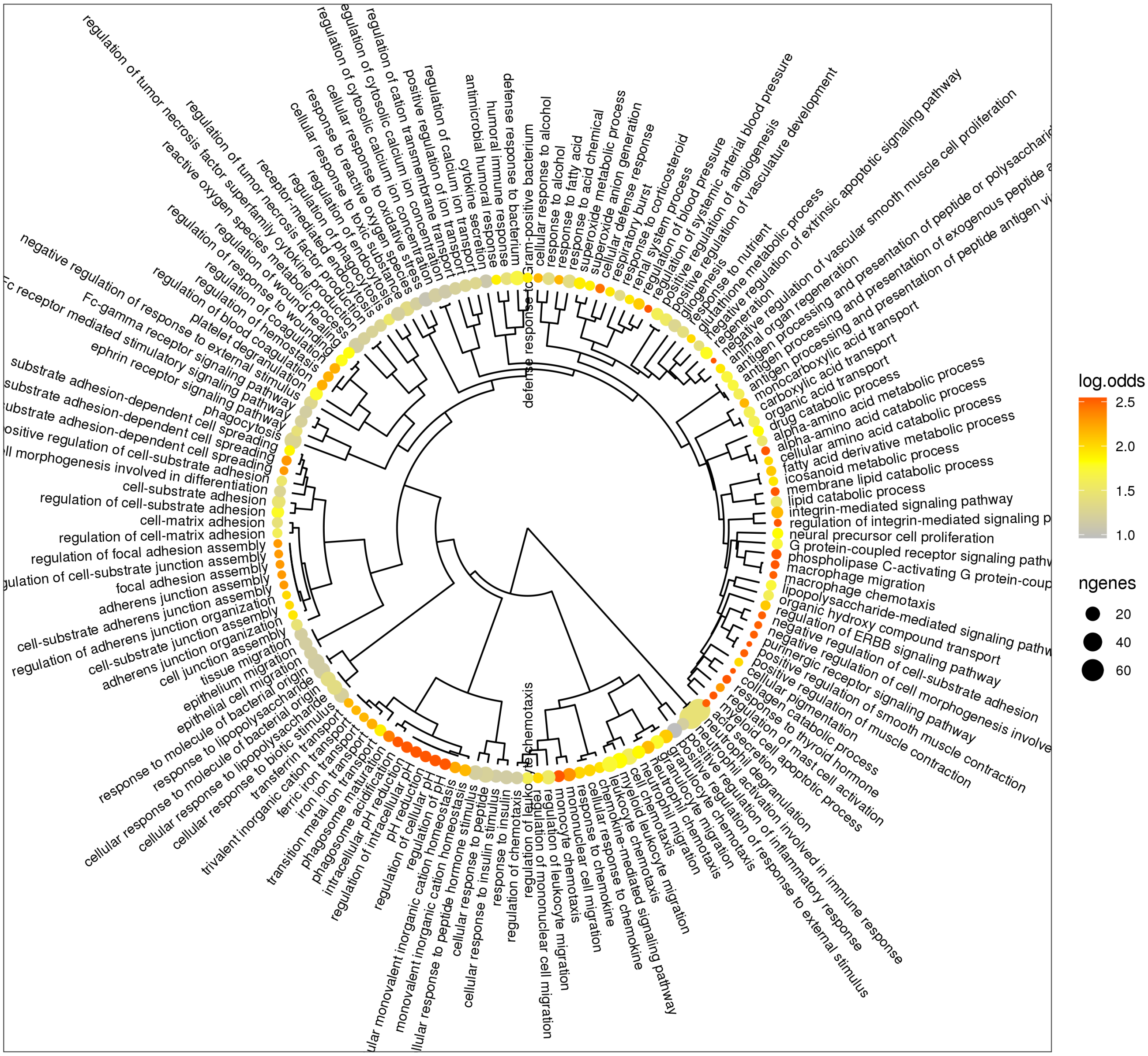


Figure 76: Cluster 0 GO.BP genesets clustered by similarity between over-represented genes.

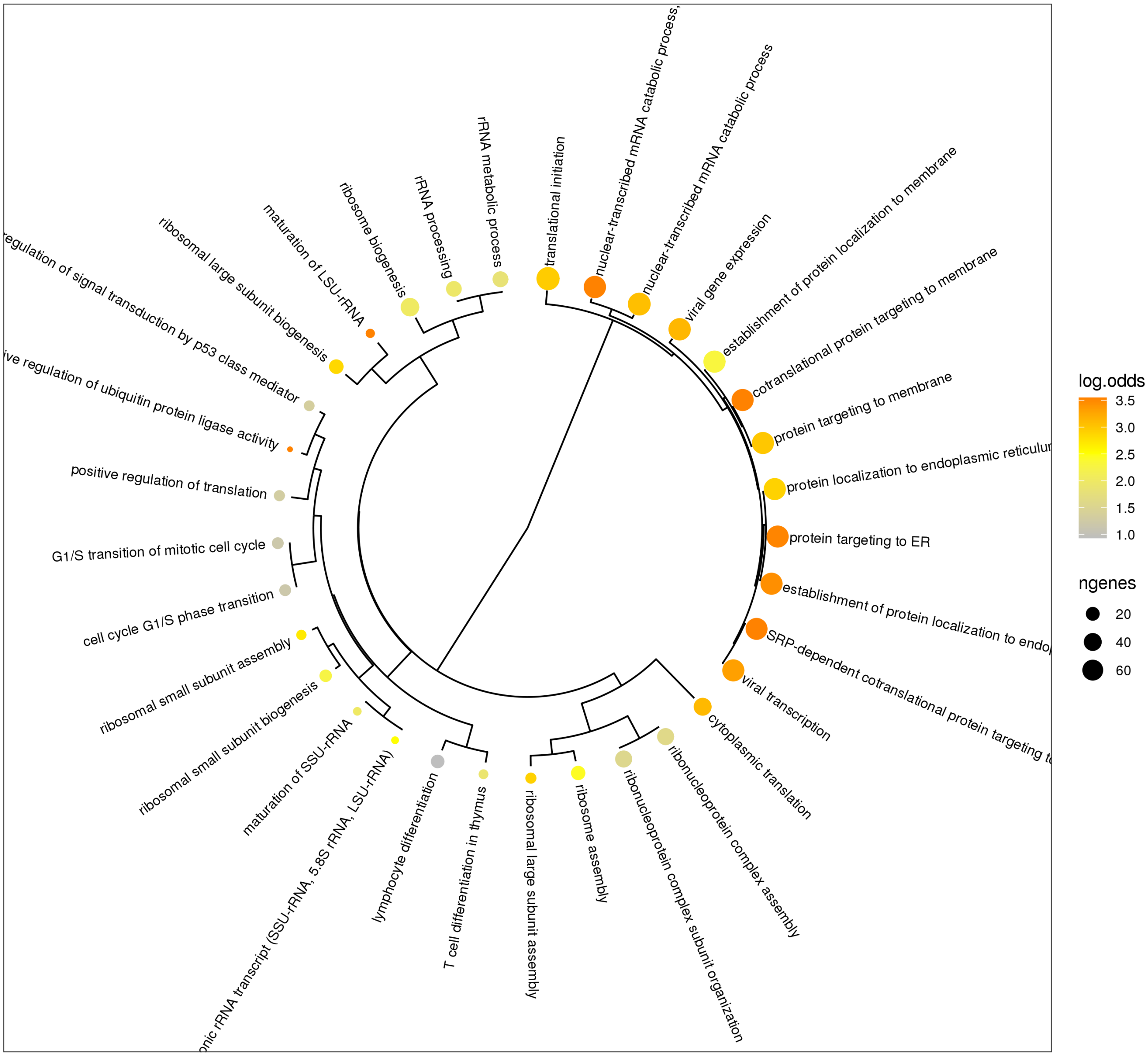


Figure 77: Cluster 1 GO.BP genesets clustered by similarity between over-represented genes.

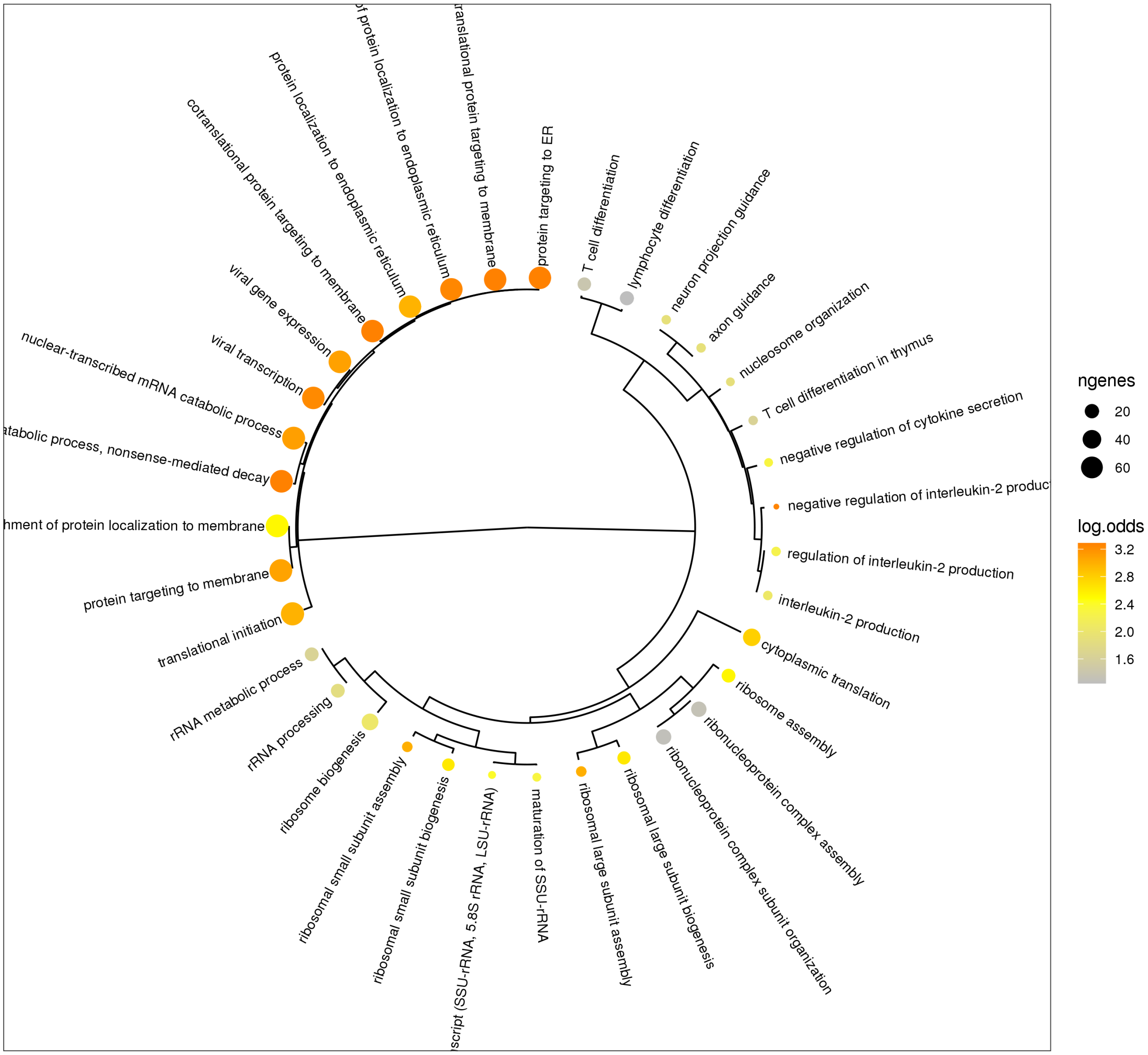


Figure 78: Cluster 2 GO.BP genesets clustered by similarity between over-represented genes.

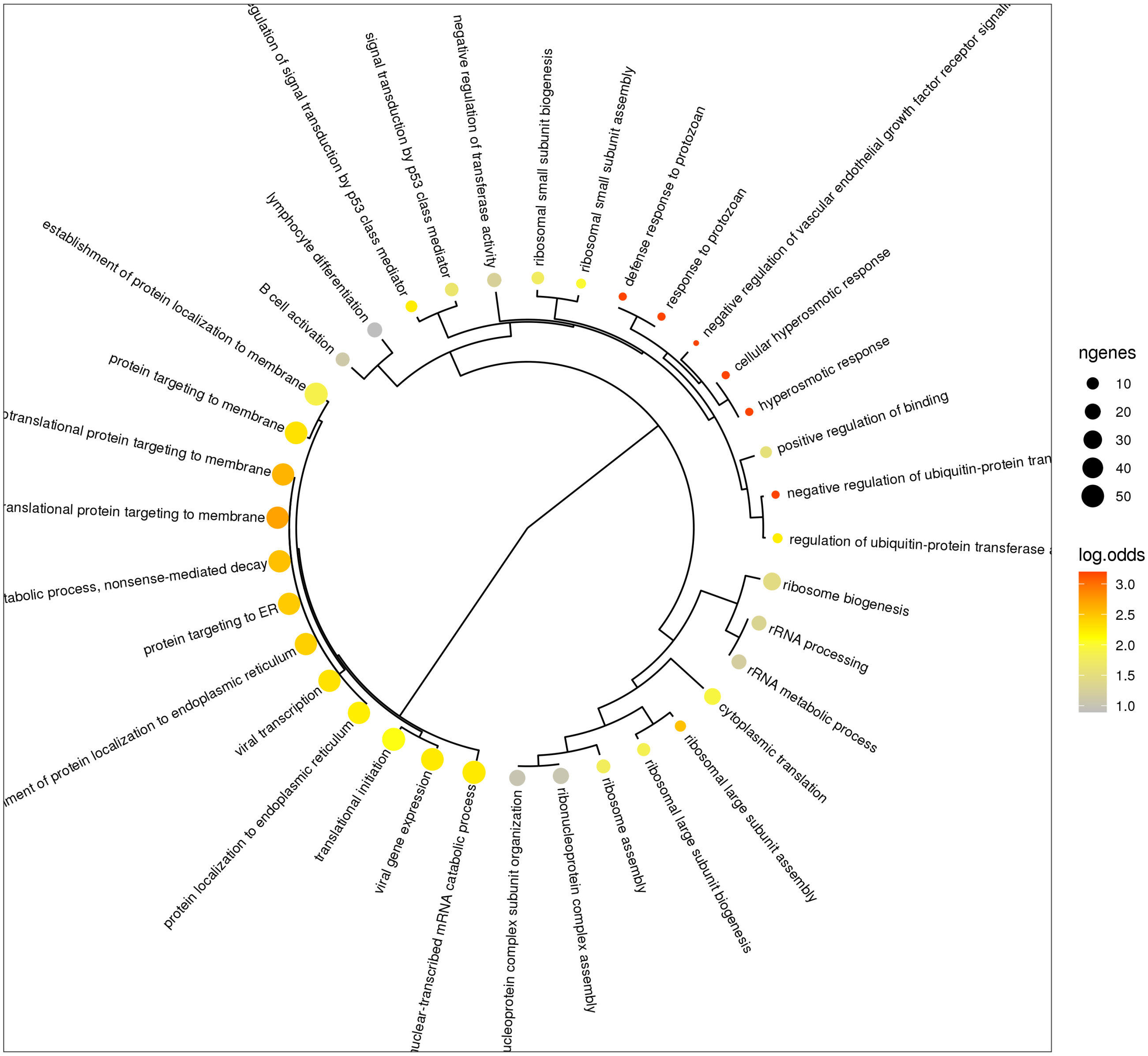


Figure 79: Cluster 3 GO.BP genesets clustered by similarity between over-represented genes.

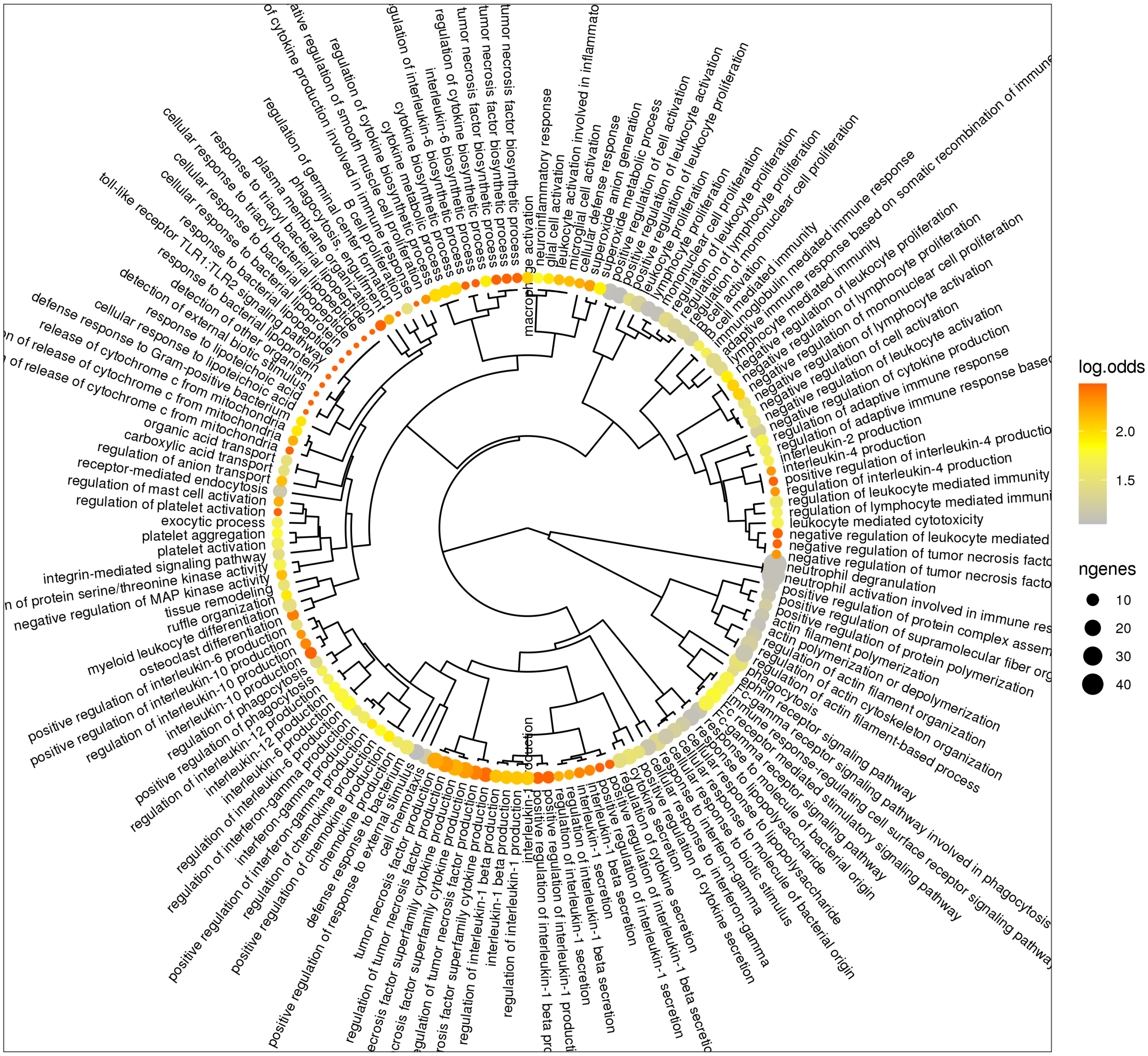


Figure 80: Cluster 4 GO.BP genesets clustered by similarity between over-represented genes.

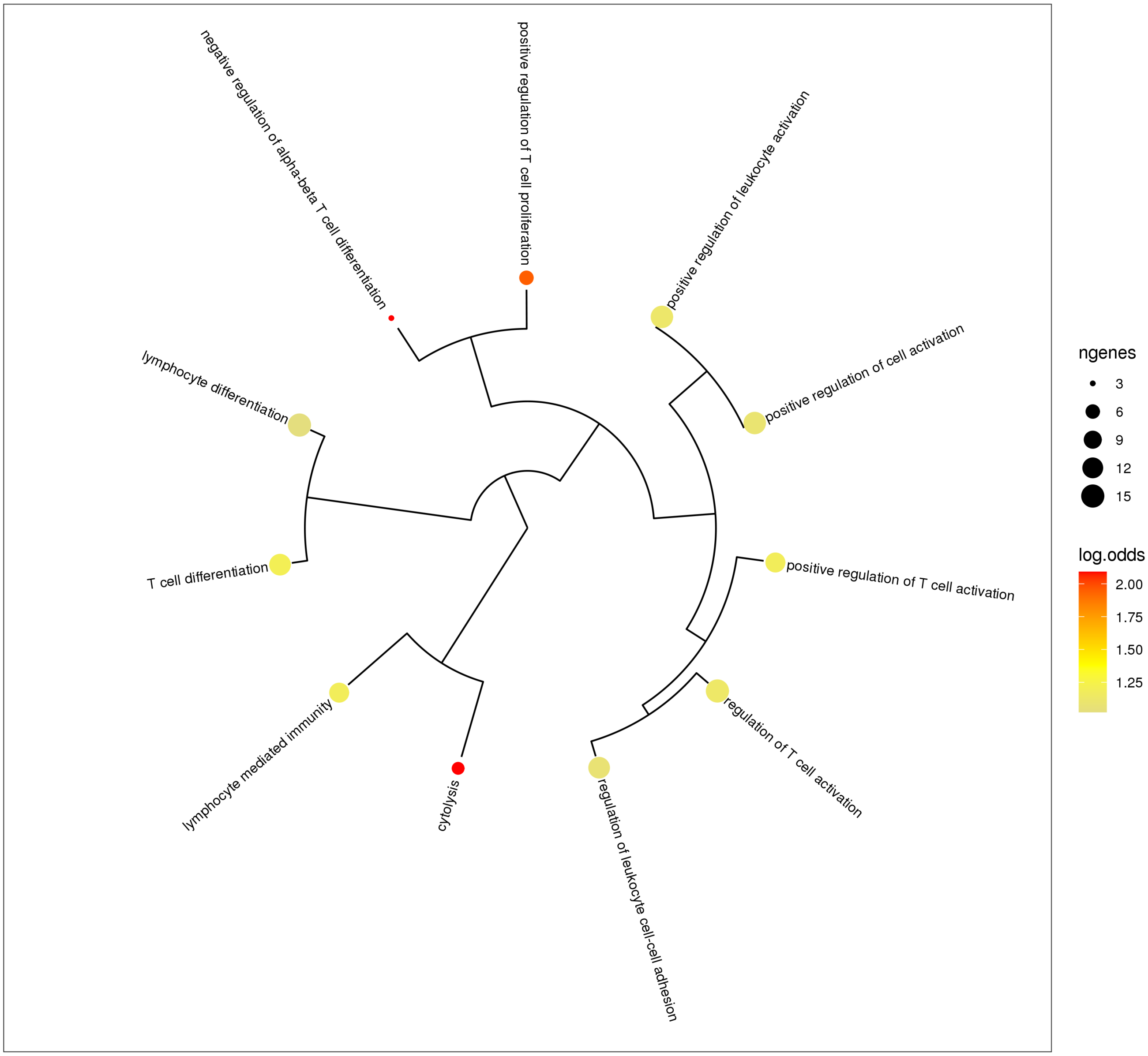


Figure 81: Cluster 5 GO.BP genesets clustered by similarity between over-represented genes.

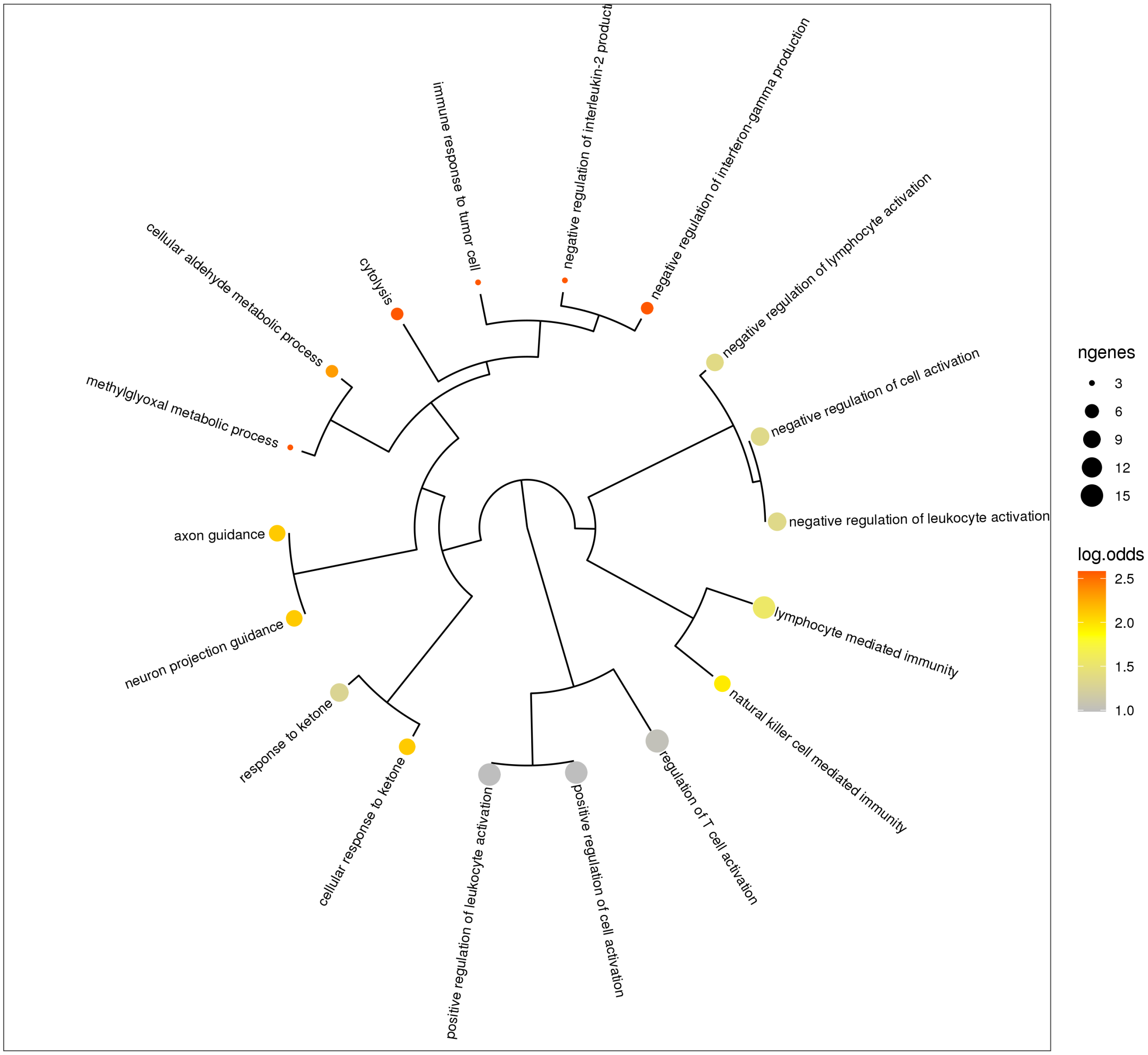


Figure 82: Cluster 6 GO.BP genesets clustered by similarity between over-represented genes.

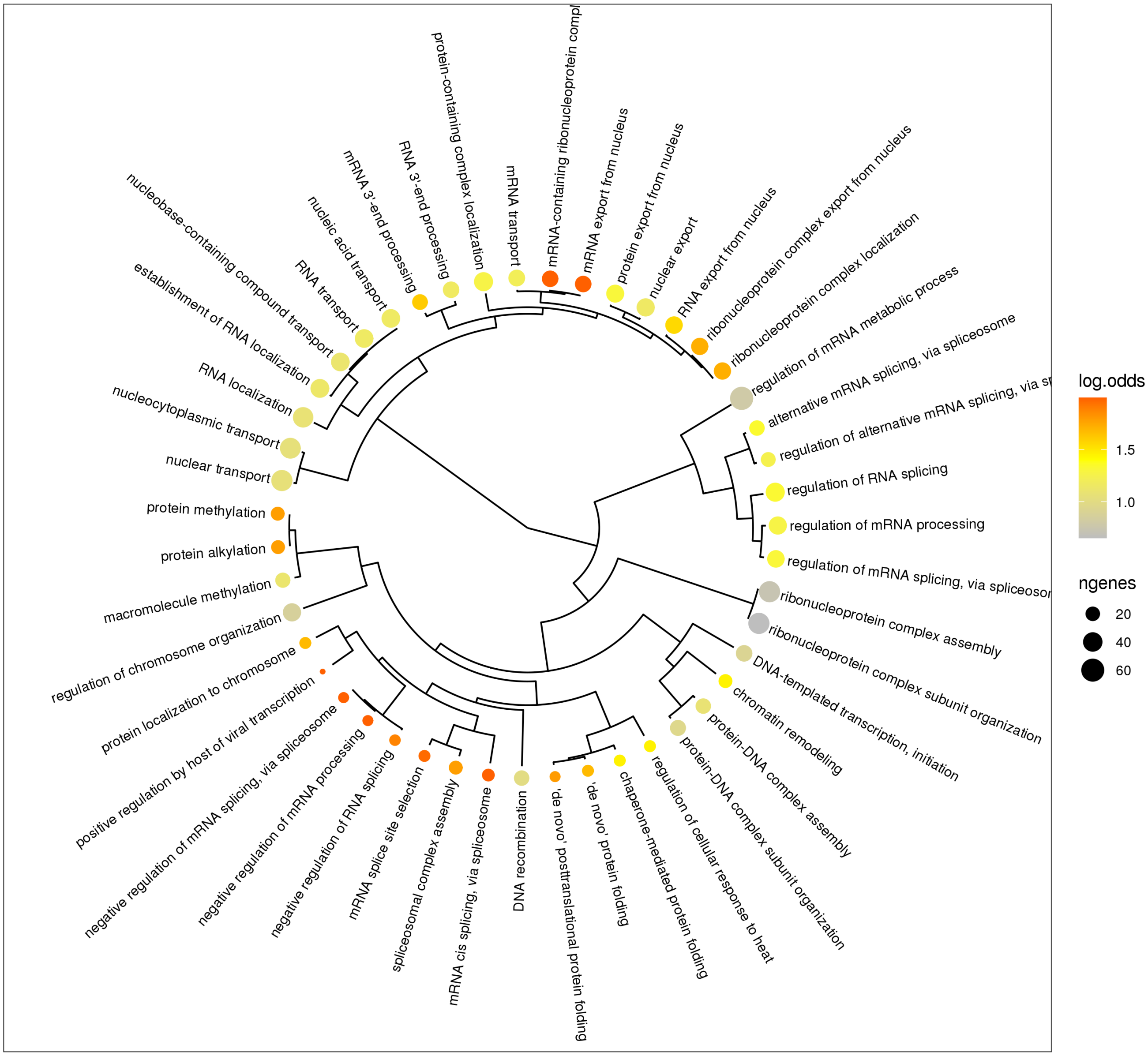


Figure 83: Cluster 7 GO.BP genesets clustered by similarity between over-represented genes.

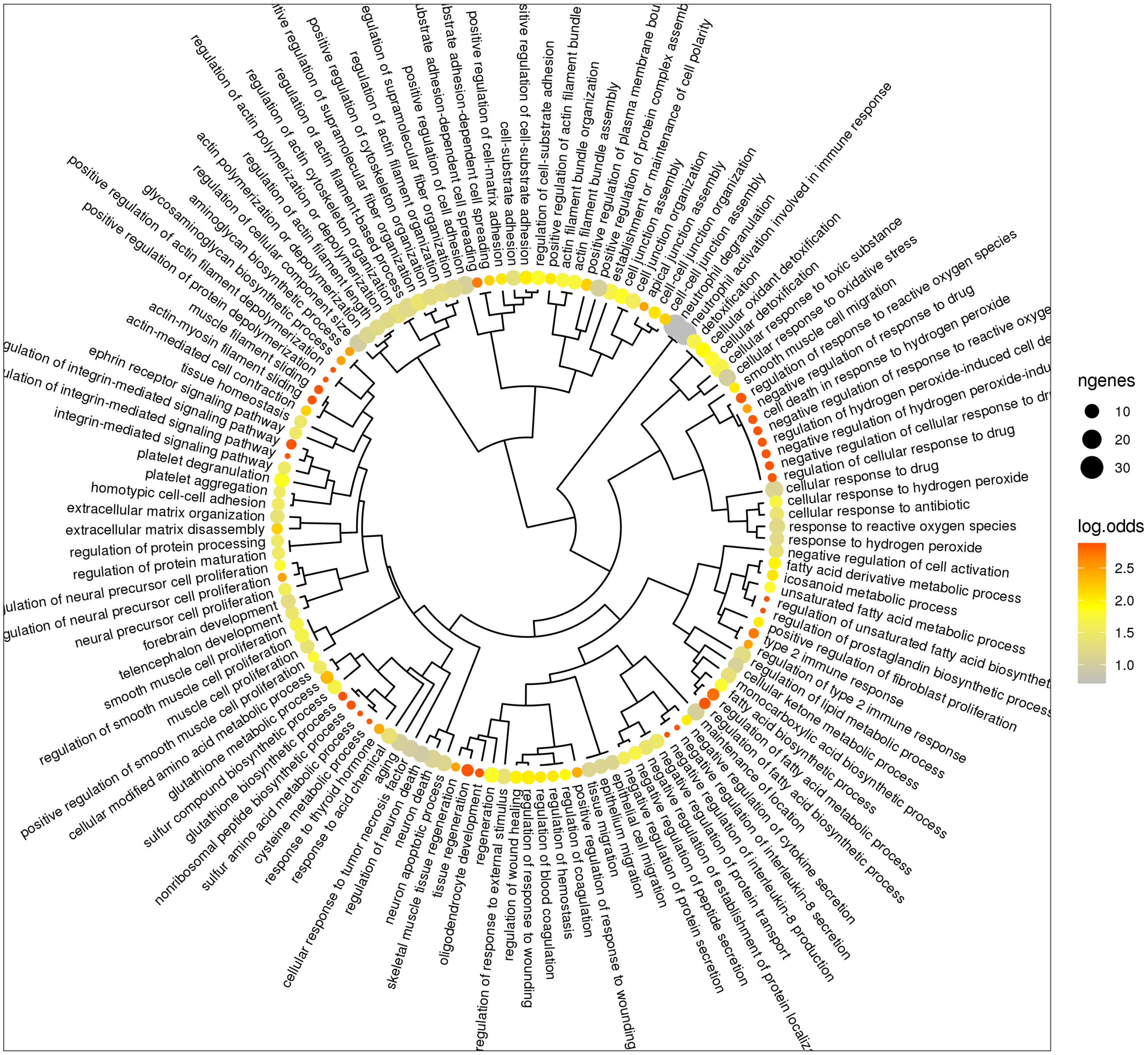


Figure 84: Cluster 8 GO.BP genesets clustered by similarity between over-represented genes.

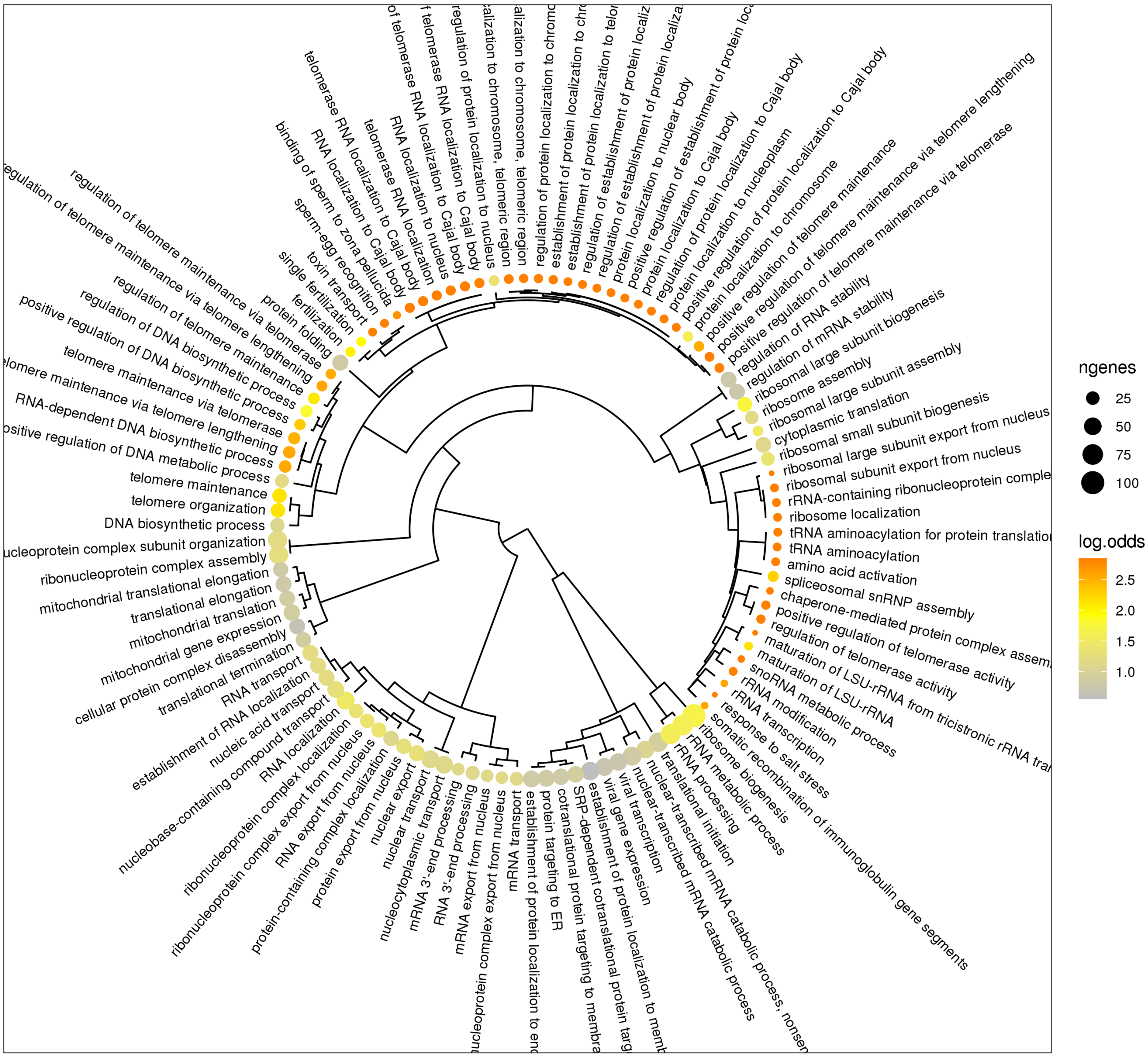


Figure 85: Cluster 9 GO.BP genesets clustered by similarity between over-represented genes.

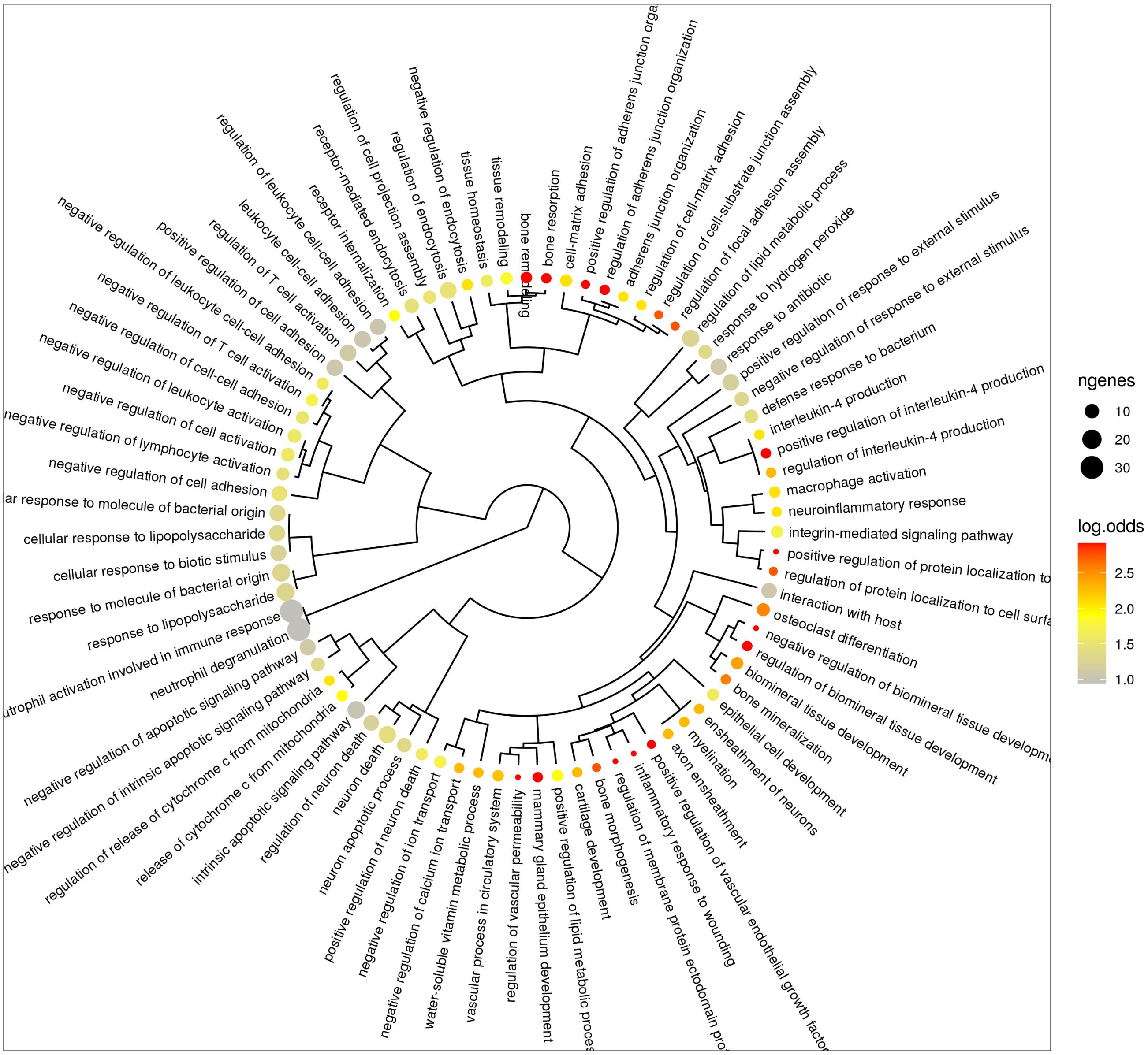


Figure 86: Cluster 10 GO.BP genesets clustered by similarity between over-represented genes.

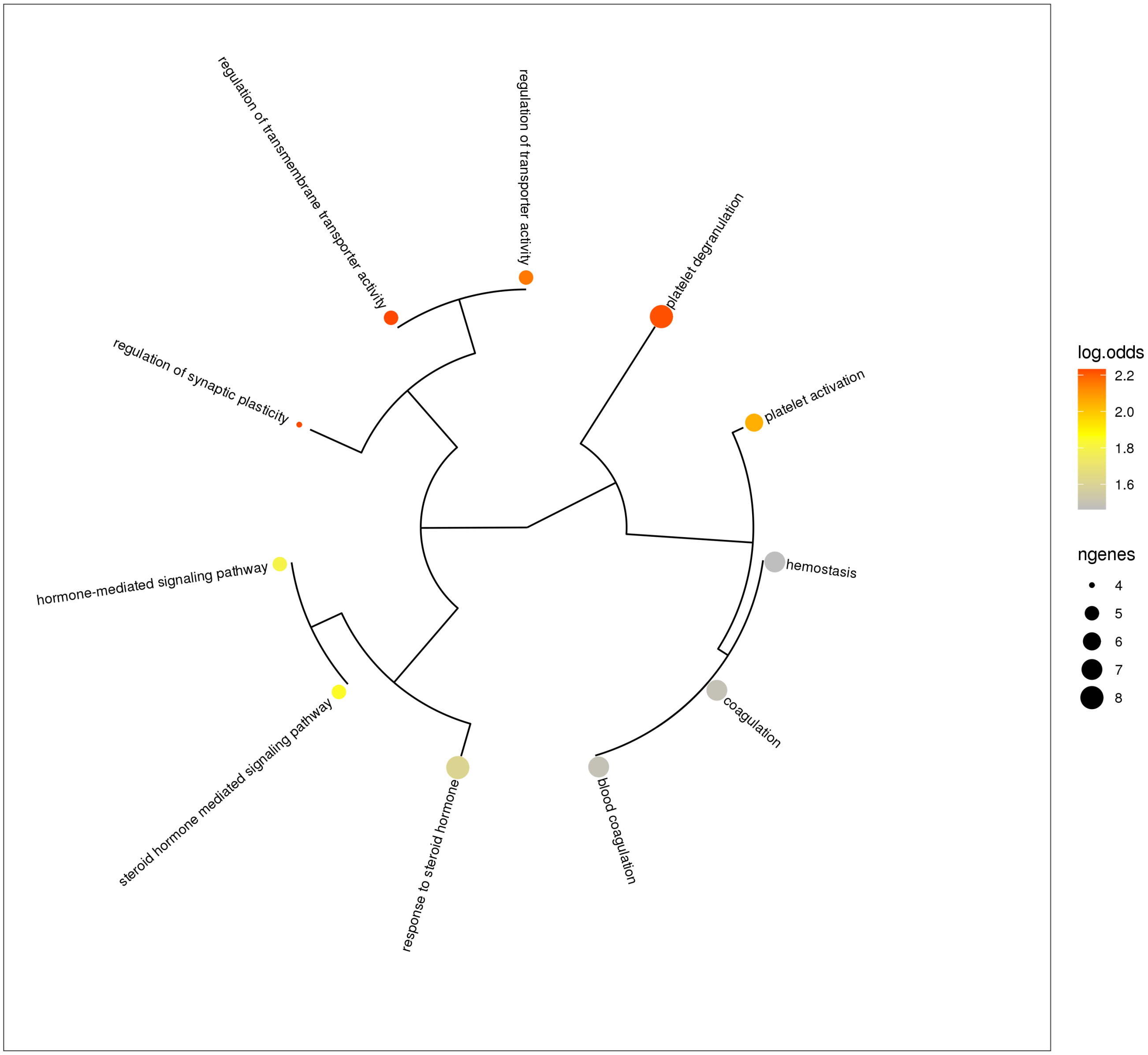


Figure 87: Cluster 11 GO.BP genesets clustered by similarity between over-represented genes.

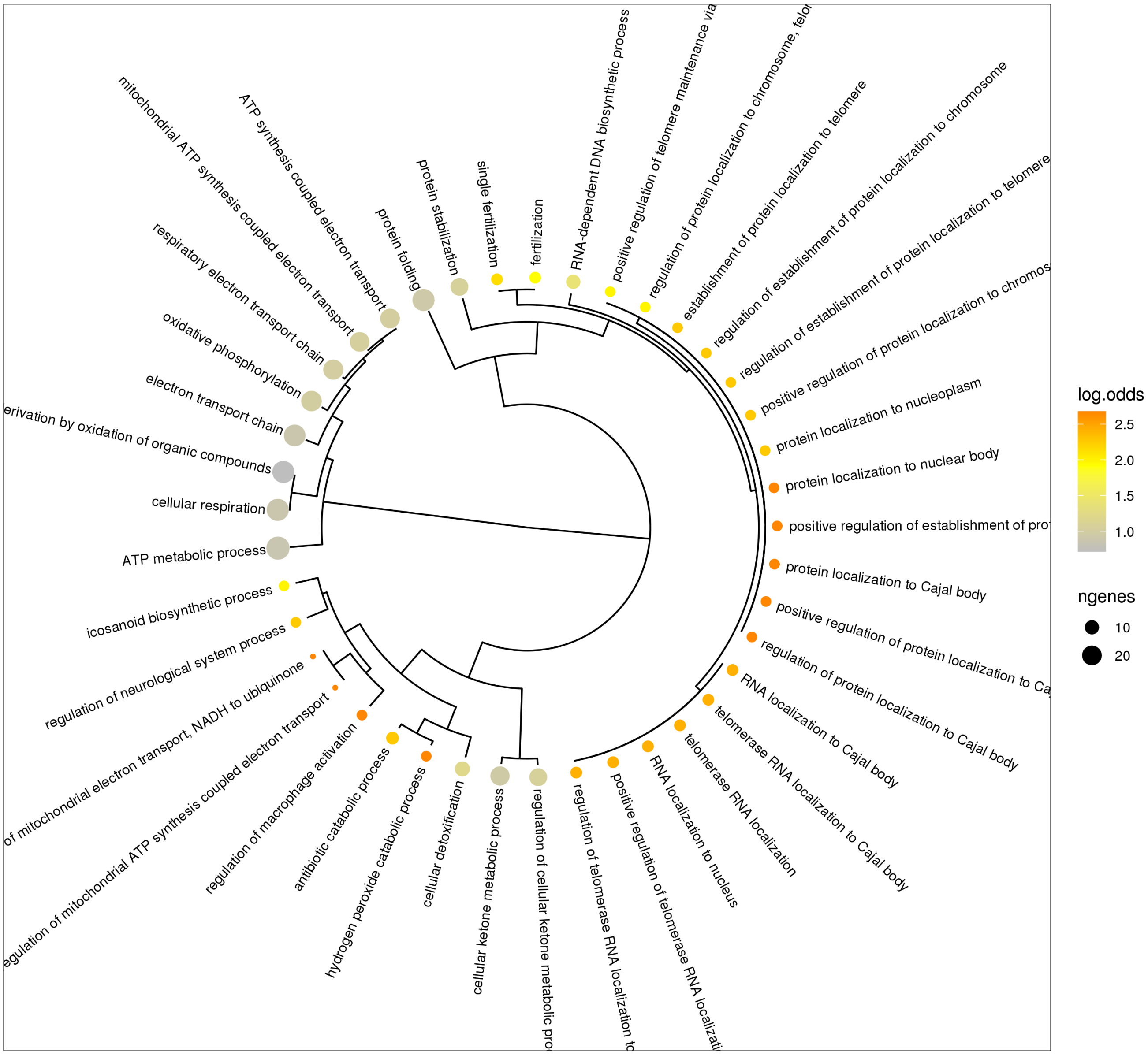


Figure 88: Cluster 12 GO.BP genesets clustered by similarity between over-represented genes.

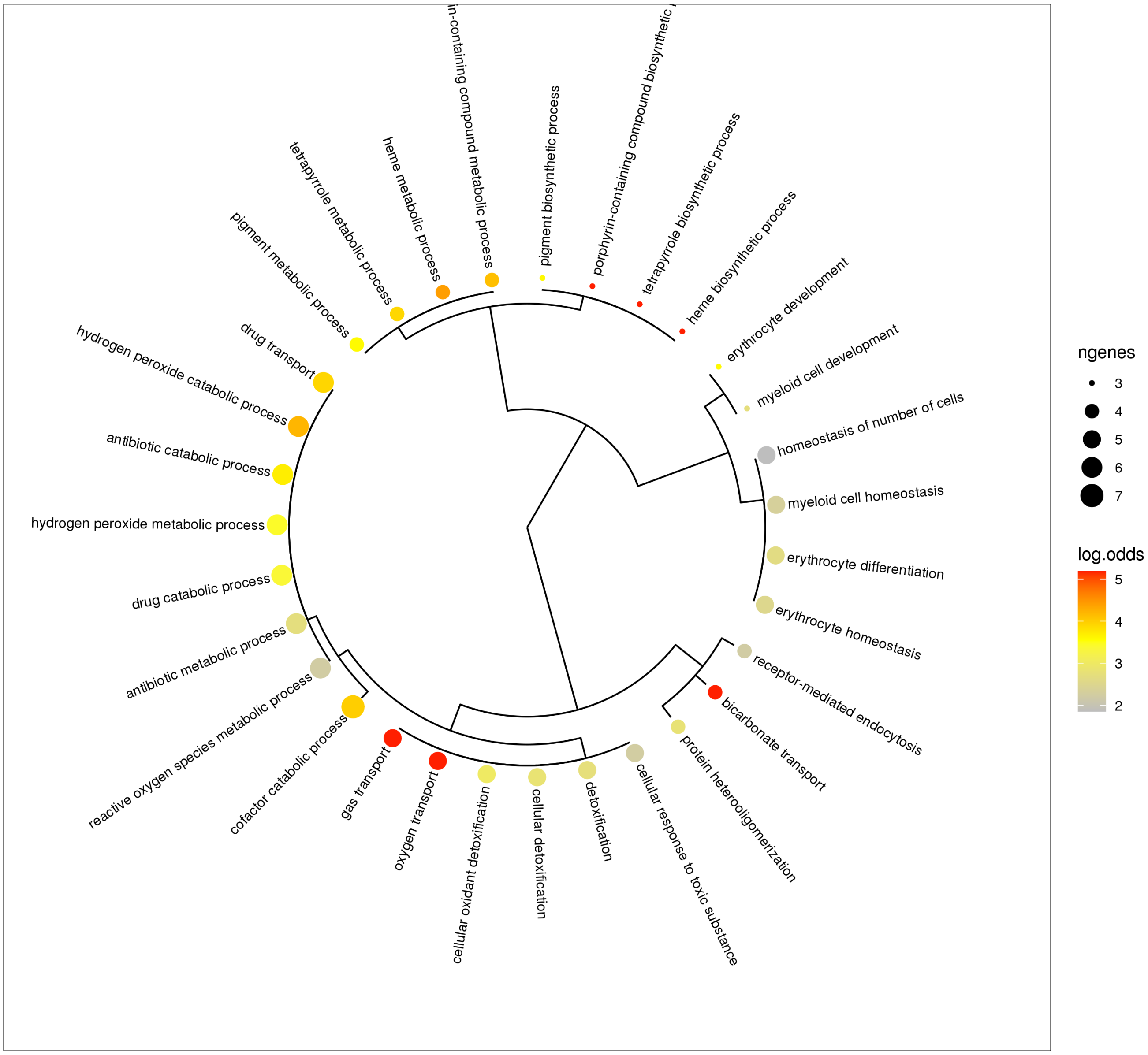


Figure 89: Cluster 13 GO.BP genesets clustered by similarity between over-represented genes.

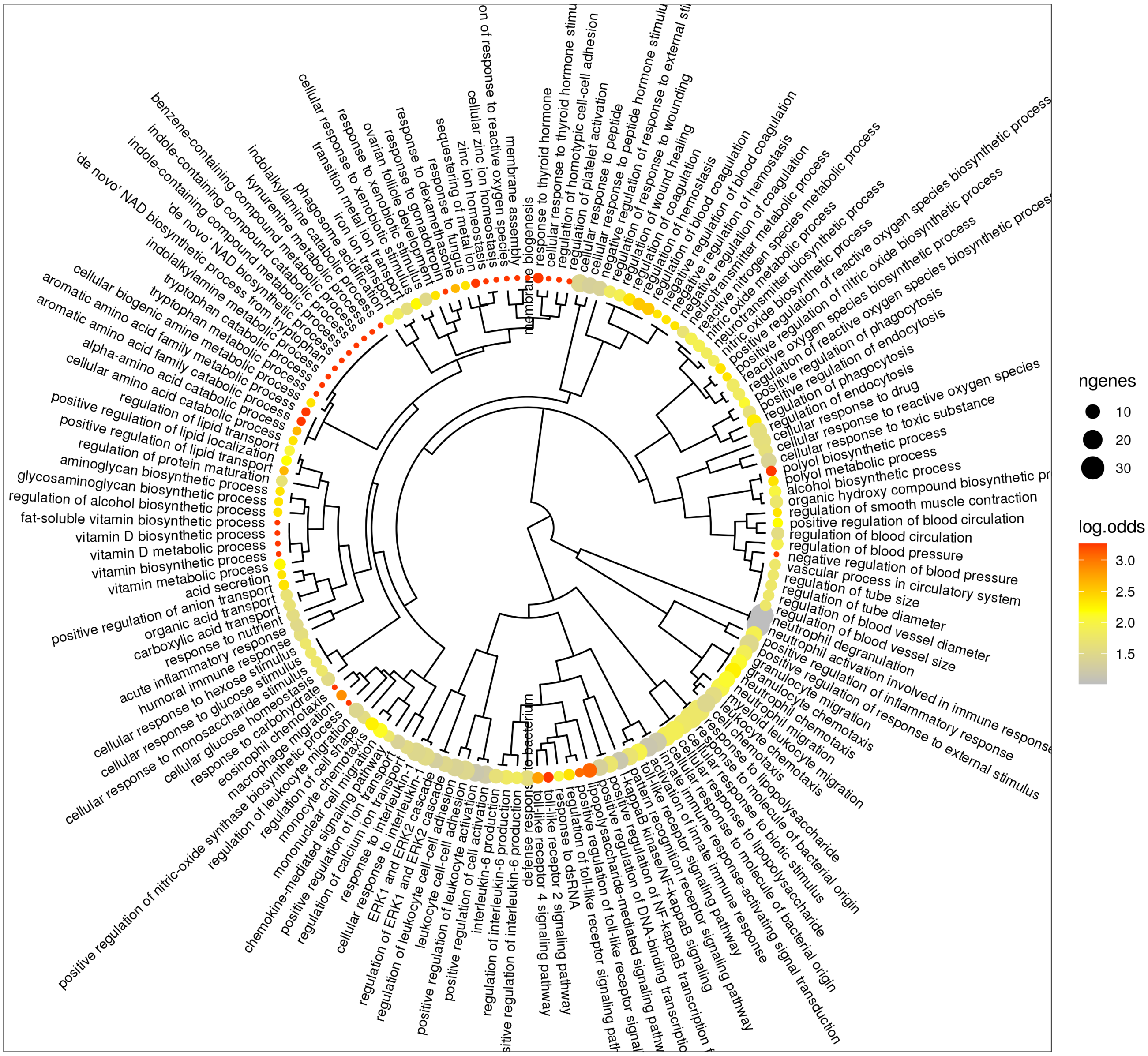


Figure 90: Cluster 14 GO.BP genesets clustered by similarity between over-represented genes.

13.2 GO.MF

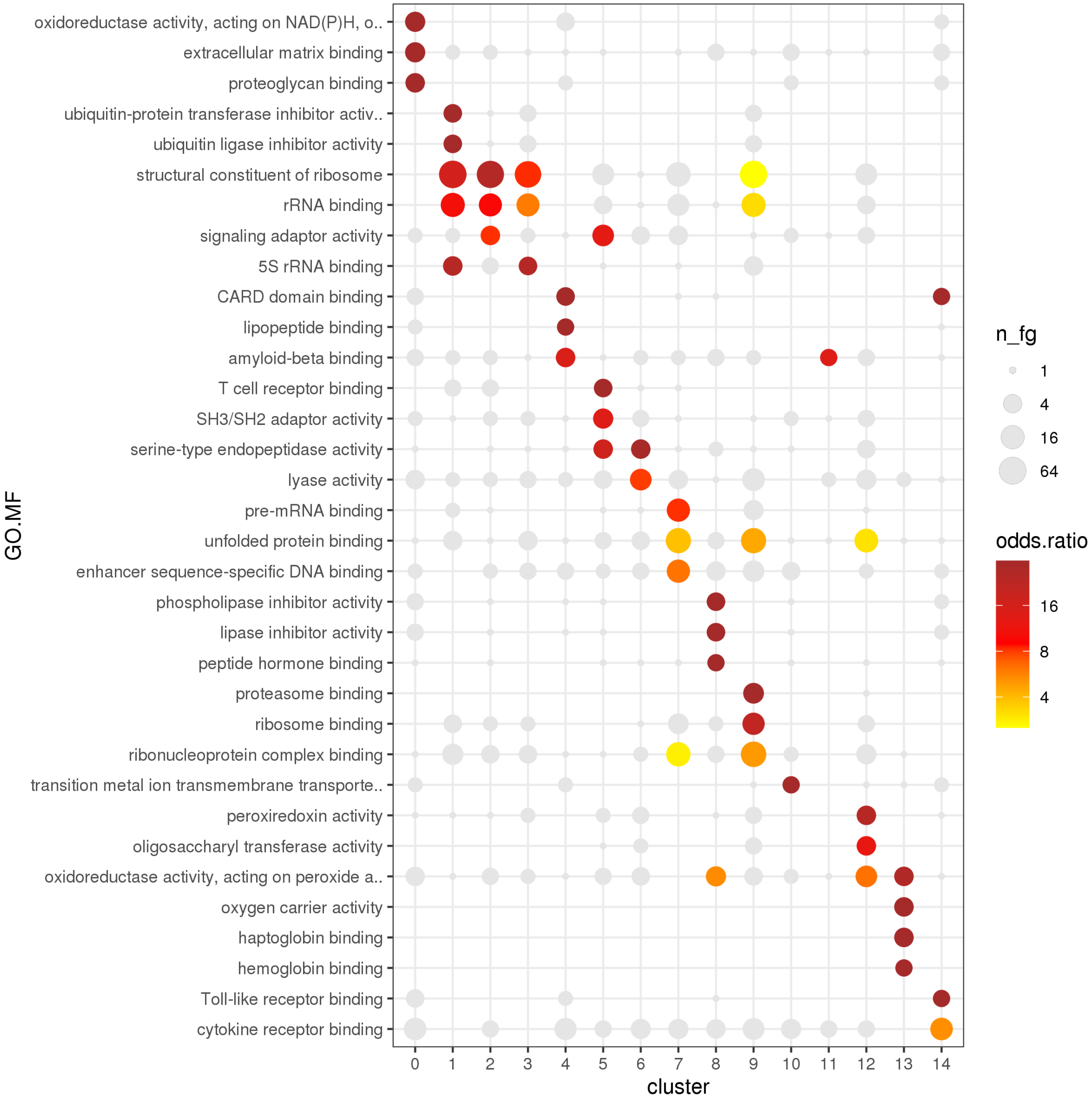


Figure 91: Heatmap of the top GO.MF genesets

13.3 GO.CC

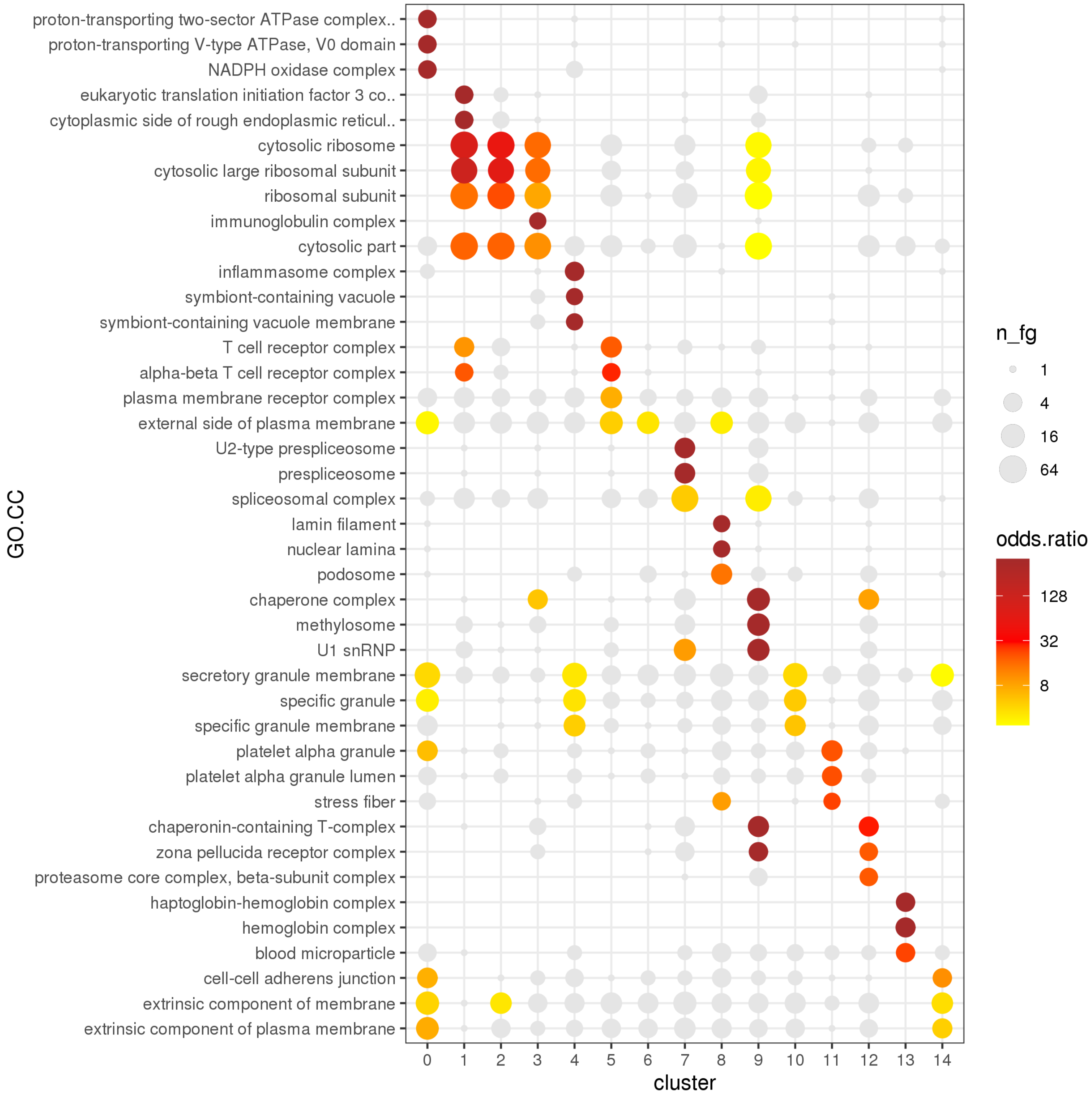


Figure 92: Heatmap of the top GO.CC genesets

13.4 KEGG

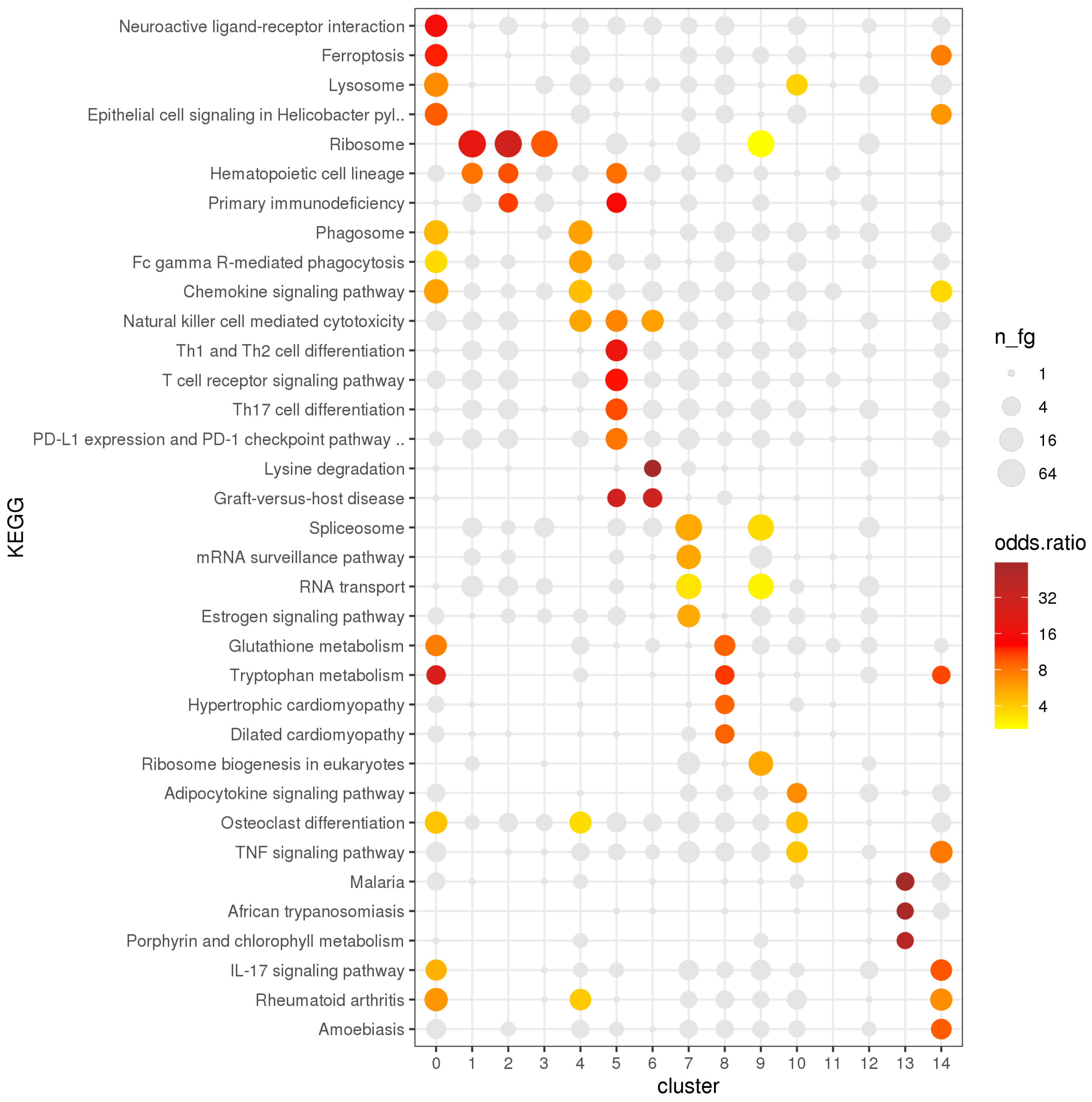


Figure 93: Heatmap of the top KEGG genesets

13.5 msigdb_biocarta

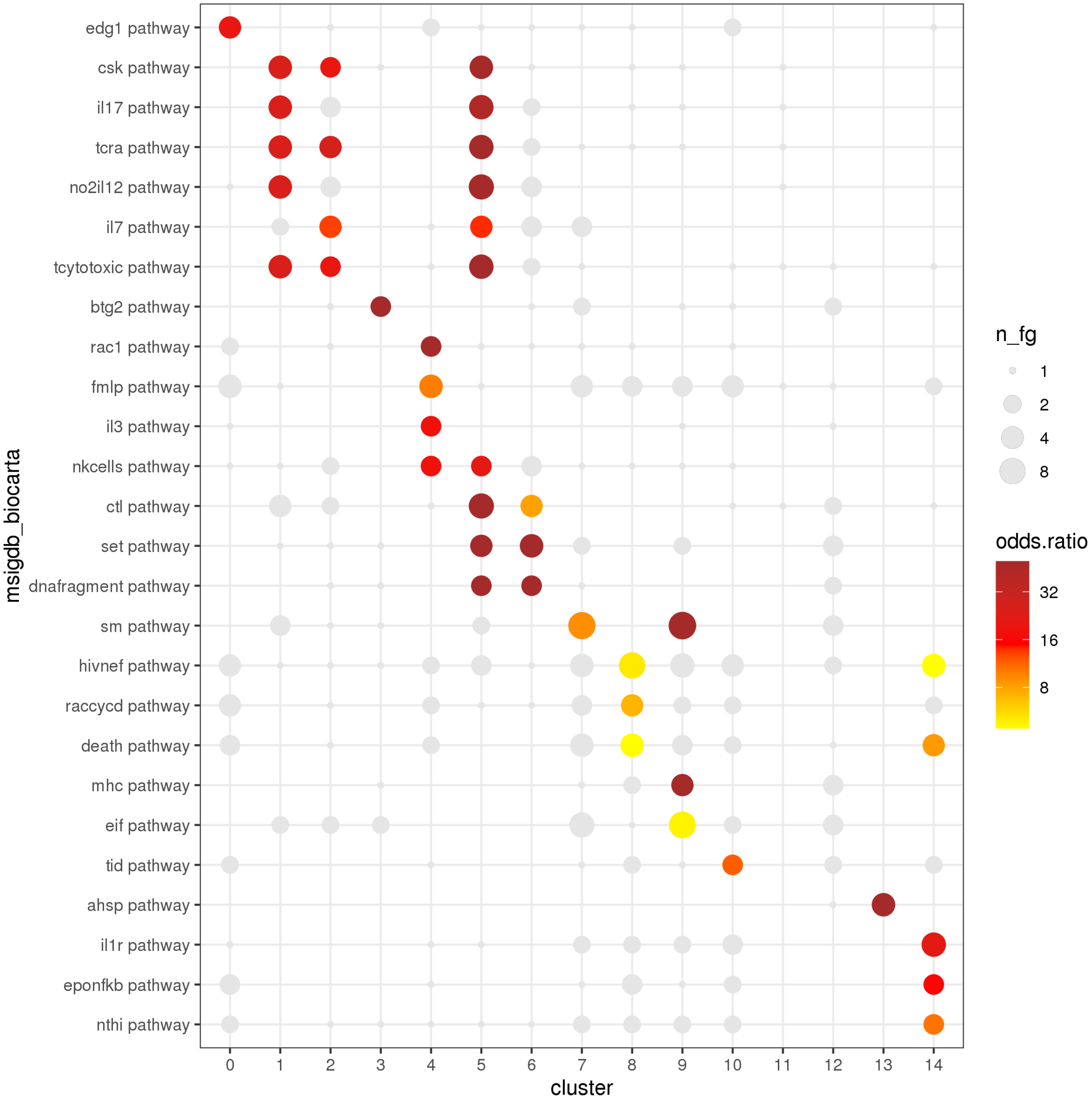


Figure 94: Heatmap of the top msigdb_biocarta genesets

13.6 msigdb_reactome

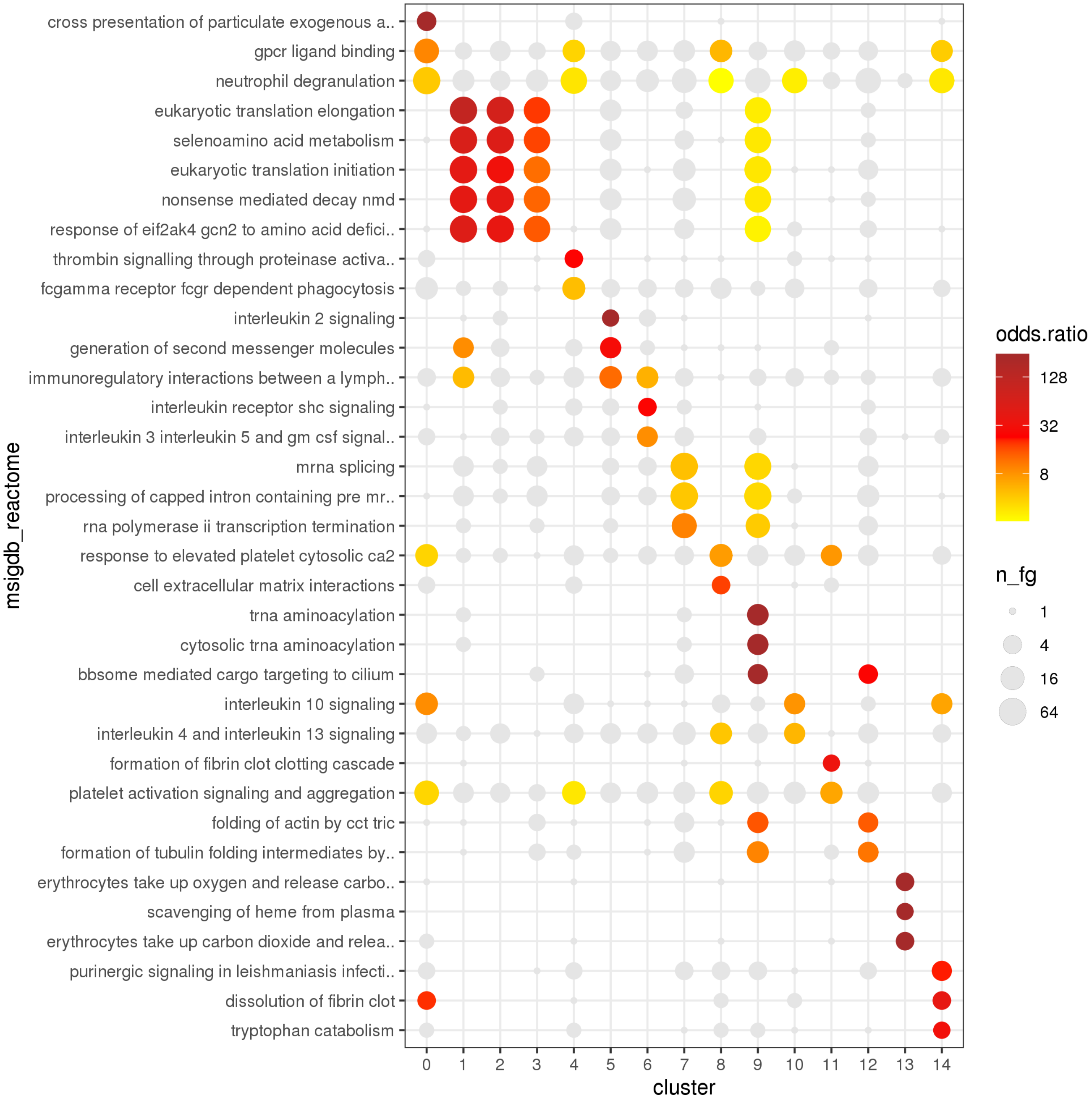


Figure 95: Heatmap of the top msigdb_reactome genesets

13.7 msigdb__canonical__pathways

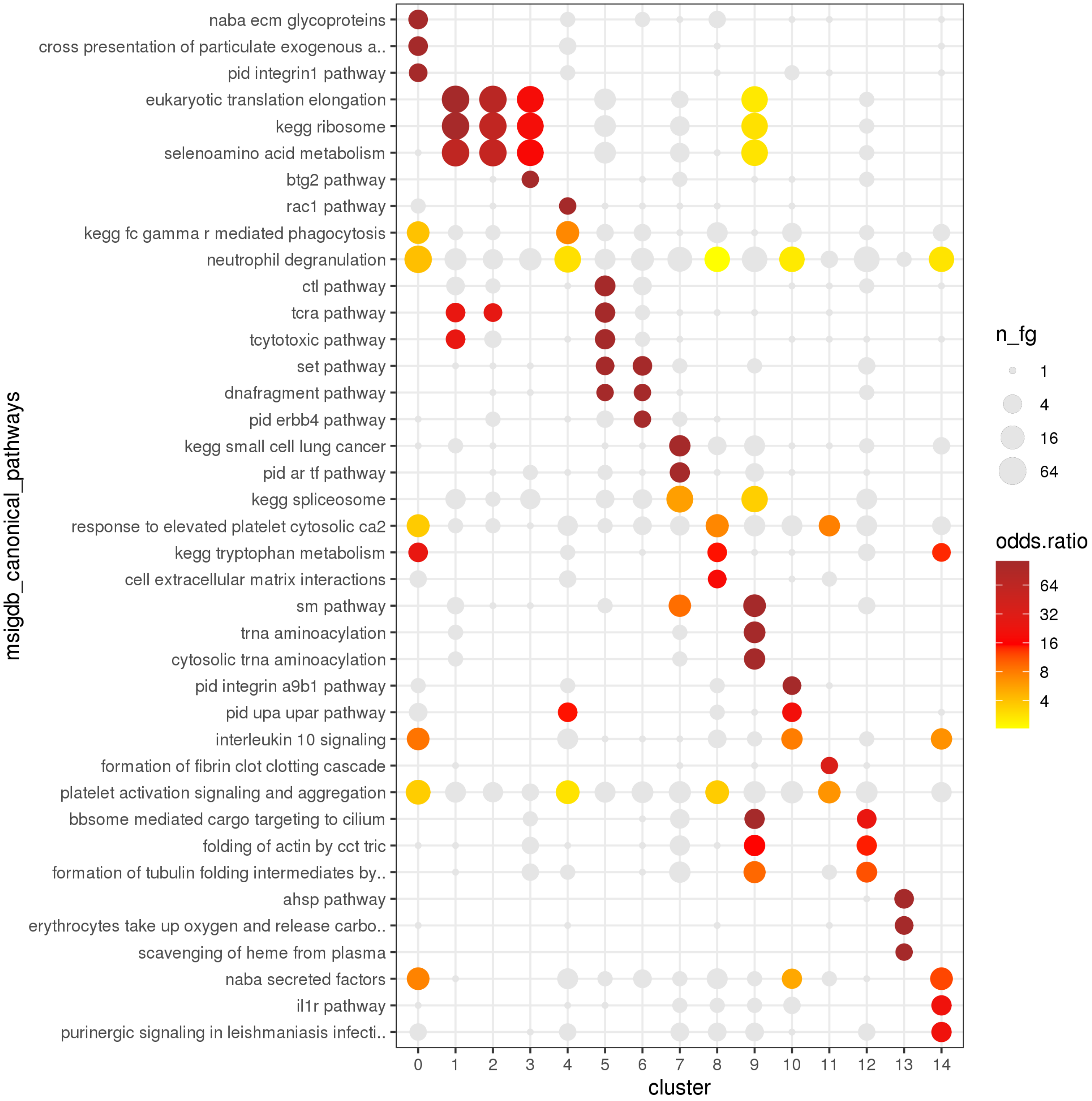


Figure 96: Heatmap of the top msigdb__canonical__pathways genesets

13.8 msigdb_tf_motifs

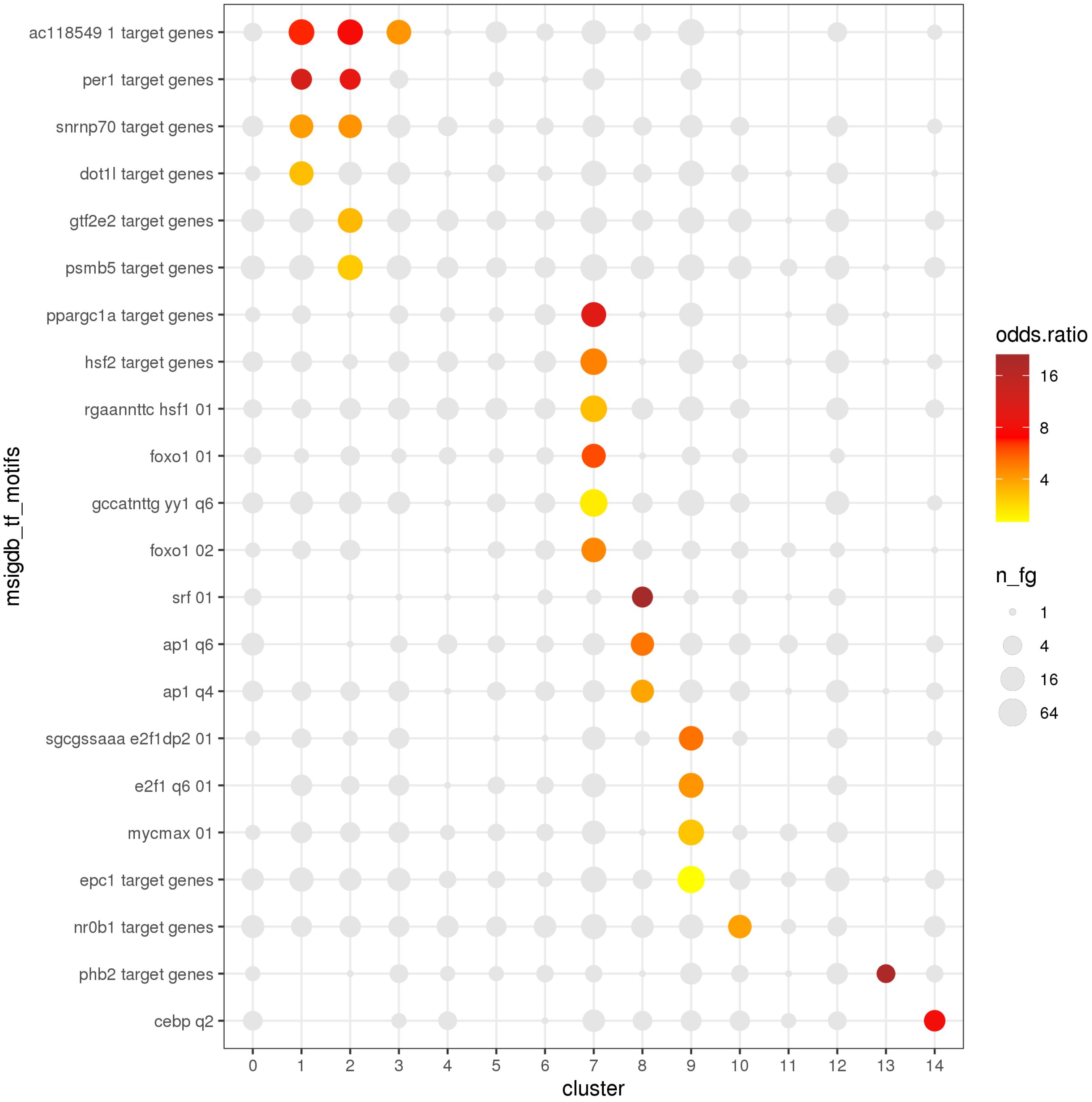


Figure 97: Heatmap of the top msigdb_tf_motifs genesets

13.9 msigdb_immunological_signatures

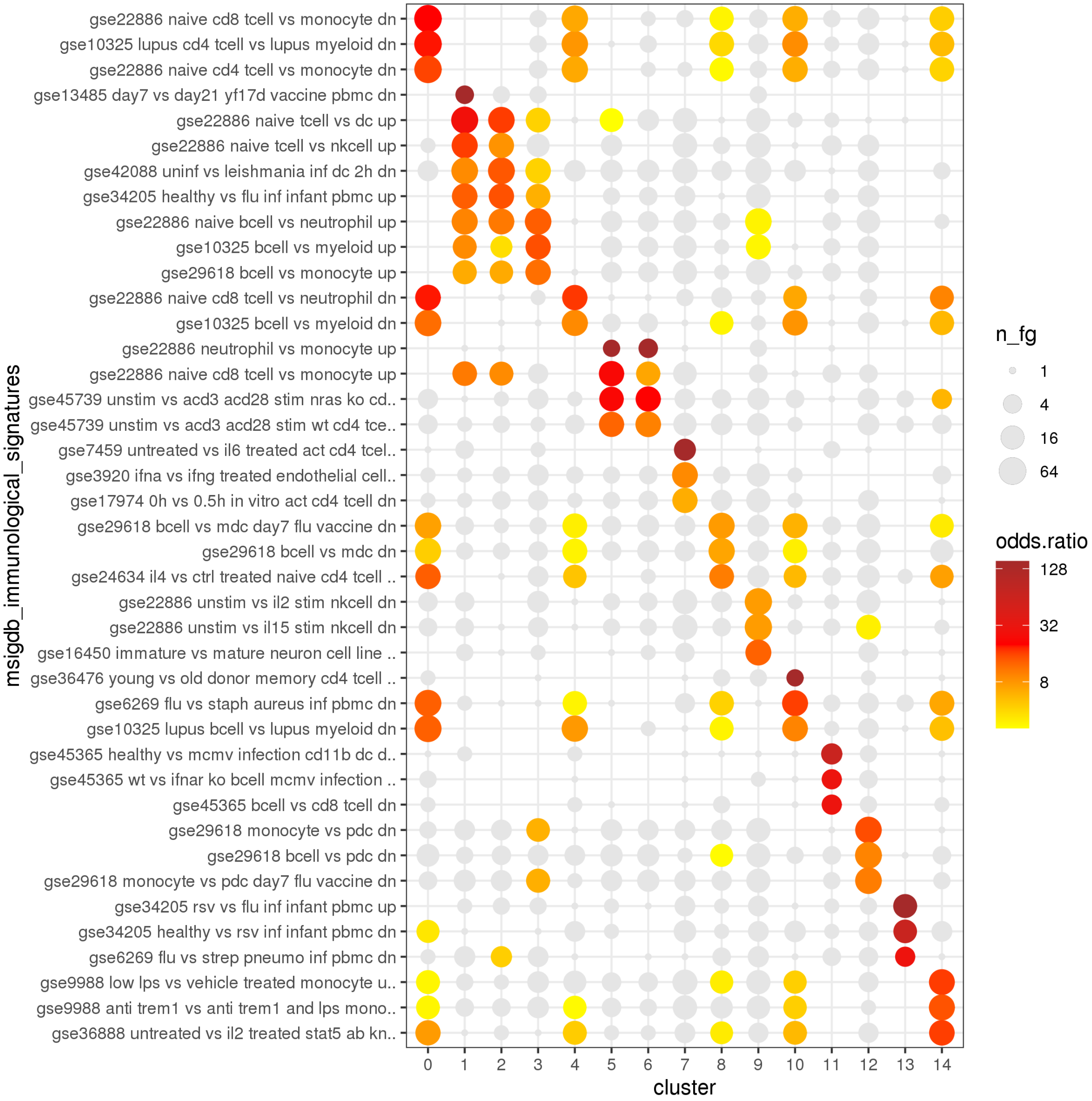


Figure 98: Heatmap of the top msigdb_immunological_signatures genesets

13.10 Top genesets by cluster

The table lists the top (filtered by nominal p value) genesets by cluster.

cluster	type	description	p.val	p.adj	n__fg	odds.ratio	n.clust
0	GO.BP	neutrophil activation involved in immune resp..	2.46e-15	9.3e-13	68	4.23	5
0	GO.BP	neutrophil degranulation	2.46e-15	9.3e-13	68	4.23	5
0	GO.BP	myeloid leukocyte migration	9.87e-09	2.18e-06	24	6.28	3
0	GO.BP	cell chemotaxis	1.97e-08	4.12e-06	28	4.92	3
0	GO.BP	leukocyte chemotaxis	3.17e-08	6.3e-06	24	5.7	2
0	GO.MF	oxidoreductase activity, acting on NAD(P)H, o..	2.32e-05	0.00164	6	Inf	1
0	GO.MF	extracellular matrix binding	2.32e-05	0.00164	6	Inf	1
0	GO.MF	G protein-coupled receptor binding	2.42e-05	0.00165	16	4.79	1
0	GO.MF	chemokine activity	0.000102	0.00497	7	17.4	2
0	GO.MF	proteoglycan binding	0.000138	0.00637	5	Inf	1
0	GO.CC	secretory granule membrane	1.73e-08	9.76e-07	35	3.98	4
0	GO.CC	tertiary granule	2.52e-07	1.19e-05	24	4.81	3
0	GO.CC	lysosomal membrane	1.31e-06	5.41e-05	33	3.23	1
0	GO.CC	lytic vacuole membrane	1.31e-06	5.41e-05	33	3.23	1
0	GO.CC	tertiary granule lumen	5.66e-06	0.000198	11	11.1	2
0	KEGG	Lysosome	3.43e-08	9.5e-06	21	6.81	2
0	KEGG	Chemokine signaling pathway	1.13e-07	2.61e-05	22	5.71	3
0	KEGG	Neuroactive ligand-receptor interaction	4.56e-07	6.32e-05	12	15.2	1
0	KEGG	Phagosome	8.92e-07	0.000103	22	4.75	2
0	KEGG	Ferroptosis	1.32e-06	0.00013	12	12.1	2
0	msigdb__biocarta	edg1 pathway	0.00356	0.0185	4	19.7	1
0	msigdb__reactome	neutrophil degranulation	7.12e-15	4.8e-13	67	4.15	5
0	msigdb__reactome	gpcr ligand binding	3.63e-11	2.17e-09	25	9.41	4
0	msigdb__reactome	class a 1 rhodopsin like receptors	7.88e-10	4.5e-08	21	9.93	3
0	msigdb__reactome	peptide ligand binding receptors	9.54e-09	5.12e-07	16	13.7	3
0	msigdb__reactome	ros and rns production in phagocytes	2.08e-06	8.98e-05	11	13.9	1
0	msigdb__canonical__pathways	neutrophil degranulation	7.12e-15	6.66e-13	67	4.15	5
0	msigdb__canonical__pathways	gpcr ligand binding	3.63e-11	2.97e-09	25	9.41	4
0	msigdb__canonical__pathways	class a 1 rhodopsin like receptors	7.88e-10	6.19e-08	21	9.93	3
0	msigdb__canonical__pathways	peptide ligand binding receptors	9.54e-09	6.82e-07	16	13.7	3
0	msigdb__canonical__pathways	kegg lysosome	1.75e-08	1.21e-06	21	7.27	2
0	msigdb__immunological__signatures	gse22886 naive cd8 tcell vs monocyte dn	6.84e-41	3.13e-36	75	20	5
0	msigdb__immunological__signatures	gse10325 lupus cd4 tcell vs lupus myeloid dn	2.14e-39	4.89e-35	73	19.3	5
0	msigdb__immunological__signatures	gse22886 naive cd4 tcell vs monocyte dn	6.7e-36	1.02e-31	71	15.9	5
0	msigdb__immunological__signatures	gse34156 tlr1 tlr2 ligand vs nod2 and tlr1 tl..	2.79e-33	2.55e-29	66	15.6	5
0	msigdb__immunological__signatures	gse22886 naive tcell vs monocyte dn	7.59e-33	5.78e-29	68	14	5
1	GO.BP	nuclear-transcribed mRNA catabolic process, n..	4.03e-48	3.2e-44	71	51.4	4
1	GO.BP	SRP-dependent cotranslational protein targeti..	1.91e-47	1.01e-43	68	62.4	4
1	GO.BP	cotranslational protein targeting to membrane	1.77e-46	5.63e-43	69	49.3	4
1	GO.BP	protein targeting to ER	2.46e-43	5.59e-40	69	34.1	4
1	GO.BP	establishment of protein localization to endo..	1.27e-42	2.51e-39	69	31.6	4
1	GO.MF	structural constituent of ribosome	8.38e-38	7.73e-35	74	16.6	4
1	GO.MF	rRNA binding	1.35e-09	4.17e-07	20	10.4	4
1	GO.MF	mRNA 5'-UTR binding	6.67e-05	0.00402	8	13.3	1
1	GO.MF	5S rRNA binding	0.000719	0.0191	5	24.7	2
1	GO.MF	ubiquitin-protein transferase inhibitor activ..	0.000828	0.0193	4	Inf	1
1	GO.CC	cytosolic ribosome	5.63e-52	1.11e-48	71	92.6	4
1	GO.CC	cytosolic part	4.72e-38	2.34e-35	73	17.5	4
1	GO.CC	ribosomal subunit	4.06e-37	1.61e-34	75	15.3	4
1	GO.CC	cytosolic large ribosomal subunit	8.38e-34	2.37e-31	45	130	4
1	GO.CC	large ribosomal subunit	3.18e-20	5.25e-18	46	10.5	4
1	KEGG	Ribosome	7.34e-39	5.08e-36	72	19.4	4
1	KEGG	Hematopoietic cell lineage	0.000379	0.0103	8	7.98	3
1	msigdb__biocarta	csk pathway	0.000719	0.00565	5	24.7	3
1	msigdb__biocarta	il17 pathway	0.000719	0.00565	5	24.7	2
1	msigdb__biocarta	tcra pathway	0.000719	0.00565	5	24.7	3
1	msigdb__biocarta	no2il12 pathway	0.000719	0.00565	5	24.7	2
1	msigdb__biocarta	tcytotoxic pathway	0.000719	0.00565	5	24.7	3
1	msigdb__reactome	eukaryotic translation elongation	3.03e-52	3.99e-49	70	114	4
1	msigdb__reactome	eukaryotic translation initiation	1.46e-50	1.28e-47	76	46	4
1	msigdb__reactome	selenoamino acid metabolism	2.82e-48	1.24e-45	69	63.6	4
1	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	1.57e-46	4.6e-44	68	54.5	4
1	msigdb__reactome	nonsense mediated decay nmd	1.86e-46	4.9e-44	70	45.2	4
1	msigdb__canonical__pathways	eukaryotic translation elongation	3.03e-52	5.95e-49	70	114	4
1	msigdb__canonical__pathways	eukaryotic translation initiation	1.46e-50	1.49e-47	76	46	4
1	msigdb__canonical__pathways	kegg ribosome	1.51e-50	1.49e-47	68	109	4
1	msigdb__canonical__pathways	selenoamino acid metabolism	2.82e-48	1.39e-45	69	63.6	4
1	msigdb__canonical__pathways	response of eif2ak4 gcn2 to amino acid defici..	1.57e-46	5.62e-44	68	54.5	4
1	msigdb__tf__motifs	ac118549 1 target genes	1.73e-11	4.69e-08	32	6.64	3
1	msigdb__tf__motifs	snrnp70 target genes	9.34e-05	0.022	16	4.07	2

1	msigdb__tf__motifs	dot1l target genes	0.000139	0.0264	19	3.35	1
1	msigdb__tf__motifs	per1 target genes	0.000293	0.0454	7	11.6	2
1	msigdb__immunological__signatures	gse22886 naive tcell vs dc up	1.27e-35	1.45e-31	60	26.3	4
1	msigdb__immunological__signatures	gse2405 0h vs 24h a phagocytophilum stim neut..	9.17e-24	1.75e-20	71	7.04	4
1	msigdb__immunological__signatures	gse2405 0h vs 9h a phagocytophilum stim neutr..	2.76e-23	4.66e-20	67	7.37	4
1	msigdb__immunological__signatures	gse3720 unstim vs pma stim vd2 gammadelta tce..	4.37e-22	6.44e-19	43	15.3	4
1	msigdb__immunological__signatures	gse22886 naive tcell vs nkcell up	1.06e-21	1.35e-18	41	16.5	2
2	GO.BP	nuclear-transcribed mRNA catabolic process, n..	3.76e-49	5.97e-45	66	48.2	4
2	GO.BP	SRP-dependent cotranslational protein targeti..	1.45e-46	5.63e-43	64	42.9	4
2	GO.BP	cotranslational protein targeting to membrane	1.64e-45	4.33e-42	65	36	4
2	GO.BP	protein targeting to ER	1.08e-41	1.56e-38	64	27.1	4
2	GO.BP	nuclear-transcribed mRNA catabolic process	1.18e-41	1.56e-38	68	22.4	4
2	GO.MF	structural constituent of ribosome	1.63e-41	3.01e-38	65	25.4	4
2	GO.MF	rRNA binding	2.21e-07	4.64e-05	14	9.64	4
2	GO.MF	signaling adaptor activity	0.00326	0.0482	5	8.26	2
2	GO.CC	cytosolic ribosome	1.04e-49	1.03e-46	65	55.8	4
2	GO.CC	ribosomal subunit	1.56e-39	1.03e-36	65	21.7	4
2	GO.CC	cytosolic part	7.15e-37	2.36e-34	65	17.8	4
2	GO.CC	cytosolic large ribosomal subunit	3.08e-33	7.62e-31	42	68.3	4
2	GO.CC	large ribosomal subunit	3.38e-24	6.09e-22	42	16.9	4
2	KEGG	Ribosome	3.91e-43	5.42e-40	65	29.1	4
2	KEGG	Hematopoietic cell lineage	0.000703	0.0165	6	9.95	3
2	KEGG	Primary immunodeficiency	0.00163	0.0297	5	11	2
2	msigdb__biocarta	tcra pathway	0.0014	0.00955	4	26.3	3
2	msigdb__biocarta	il7 pathway	0.00375	0.0189	4	13.2	2
2	msigdb__biocarta	stathmin pathway	0.00784	0.0346	4	8.77	3
2	msigdb__biocarta	csk pathway	0.00852	0.0354	3	19.6	3
2	msigdb__biocarta	tcytotoxic pathway	0.00852	0.0354	3	19.6	3
2	msigdb__reactome	eukaryotic translation elongation	2.83e-53	7.45e-50	67	71.5	4
2	msigdb__reactome	selenoamino acid metabolism	1.04e-49	6.86e-47	65	55.8	4
2	msigdb__reactome	nonsense mediated decay nmd	1.95e-48	1.03e-45	66	44.9	4
2	msigdb__reactome	eukaryotic translation initiation	1.13e-47	4.24e-45	70	32.5	4
2	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	8.16e-47	2.68e-44	65	40.9	4
2	msigdb__canonical__pathways	eukaryotic translation elongation	2.83e-53	1.11e-49	67	71.5	4
2	msigdb__canonical__pathways	selenoamino acid metabolism	1.04e-49	8.2e-47	65	55.8	4
2	msigdb__canonical__pathways	kegg ribosome	1.51e-49	9.89e-47	64	60.1	4
2	msigdb__canonical__pathways	nonsense mediated decay nmd	1.95e-48	1.09e-45	66	44.9	4
2	msigdb__canonical__pathways	eukaryotic translation initiation	1.13e-47	4.93e-45	70	32.5	4
2	msigdb__tf__motifs	ac118549 1 target genes	3.71e-12	2.01e-08	29	7.66	3
2	msigdb__tf__motifs	psmb5 target genes	1.27e-05	0.0075	27	3.1	1
2	msigdb__tf__motifs	gtf2e2 target genes	1.38e-05	0.0075	23	3.45	1
2	msigdb__tf__motifs	snrnp70 target genes	6.21e-05	0.0198	15	4.29	2
2	msigdb__tf__motifs	per1 target genes	0.000304	0.0458	7	9.33	2
2	msigdb__immunological__signatures	gse42088 uninf vs leishmania inf dc 2h dn	8.15e-29	3.73e-25	55	14	3
2	msigdb__immunological__signatures	gse22886 naive tcell vs dc up	3.07e-27	1.02e-23	48	16.7	4
2	msigdb__immunological__signatures	gse2405 0h vs 9h a phagocytophilum stim neutr..	5.92e-21	7.12e-18	57	7.29	4
2	msigdb__immunological__signatures	gse2405 0h vs 24h a phagocytophilum stim neut..	9.65e-20	9.59e-17	59	6.43	4
2	msigdb__immunological__signatures	gse42088 uninf vs leishmania inf dc 4h dn	1.46e-19	1.39e-16	45	9.08	3
3	GO.BP	SRP-dependent cotranslational protein targeti..	7.2e-26	4.57e-23	48	15.2	4
3	GO.BP	cotranslational protein targeting to membrane	1.16e-24	7.07e-22	48	13.4	4
3	GO.BP	nuclear-transcribed mRNA catabolic process, n..	6.55e-24	3.85e-21	48	12.5	4
3	GO.BP	protein targeting to ER	3.41e-23	1.87e-20	48	11.7	4
3	GO.BP	nuclear-transcribed mRNA catabolic process	7.33e-23	3.86e-20	53	9.49	4
3	GO.MF	structural constituent of ribosome	6.72e-20	4.13e-17	49	8.37	4
3	GO.MF	rRNA binding	9.83e-06	0.000825	14	5.95	4
3	GO.MF	5S rRNA binding	0.00176	0.0307	4	24.5	2
3	GO.MF	kinase regulator activity	0.00251	0.0391	10	3.67	1
3	GO.CC	cytosolic ribosome	4.61e-27	1.02e-24	49	16.3	4
3	GO.CC	cytosolic part	1.8e-24	3.56e-22	54	10.5	4
3	GO.CC	ribosomal subunit	1.69e-19	2.57e-17	50	7.85	4
3	GO.CC	cytosolic large ribosomal subunit	4.16e-17	4.85e-15	30	16	4
3	GO.CC	large ribosomal subunit	7.22e-11	5.96e-09	30	6.2	4
3	KEGG	Ribosome	1.06e-21	4.92e-19	50	9.48	4
3	msigdb__biocarta	btg2 pathway	0.00283	0.017	3	Inf	1
3	msigdb__reactome	eukaryotic translation elongation	1.54e-29	1.62e-27	51	18.8	4
3	msigdb__reactome	selenoamino acid metabolism	2.76e-28	2.79e-26	50	17.5	4
3	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	1.47e-26	1.43e-24	50	14.7	4
3	msigdb__reactome	eukaryotic translation initiation	9.28e-26	8.72e-24	53	12.1	4
3	msigdb__reactome	nonsense mediated decay nmd	2.22e-25	2.01e-23	50	13.2	4
3	msigdb__canonical__pathways	eukaryotic translation elongation	1.54e-29	2.23e-27	51	18.8	4
3	msigdb__canonical__pathways	kegg ribosome	3.16e-29	4.44e-27	50	19.2	4
3	msigdb__canonical__pathways	selenoamino acid metabolism	2.76e-28	3.74e-26	50	17.5	4
3	msigdb__canonical__pathways	response of eif2ak4 gcn2 to amino acid defici..	1.47e-26	1.92e-24	50	14.7	4
3	msigdb__canonical__pathways	eukaryotic translation initiation	9.28e-26	1.18e-23	53	12.1	4
3	msigdb__tf__motifs	ac118549 1 target genes	2.03e-06	0.00163	22	4.23	3

3	msigdb__immunological__signatures	gse22886 naive bcell vs neutrophil up	5.09e-25	1.16e-21	49	13.3	4
3	msigdb__immunological__signatures	gse10325 bcell vs myeloid up	1.15e-16	6.48e-14	30	14.8	4
3	msigdb__immunological__signatures	gse29618 bcell vs monocyte up	1.84e-16	9.87e-14	33	11.5	3
3	msigdb__immunological__signatures	gse10325 lupus bcell vs lupus myeloid up	9.14e-16	4.35e-13	32	11.1	5
3	msigdb__immunological__signatures	gse10325 lupus cd4 tcell vs lupus bcell dn	9.98e-14	3.56e-11	27	11.5	4
4	GO.BP	regulation of tumor necrosis factor superfami..	8.74e-10	2.48e-07	20	9.71	2
4	GO.BP	regulation of tumor necrosis factor productio..	1.81e-09	4.8e-07	19	9.96	2
4	GO.BP	tumor necrosis factor superfamily cytokine pr..	1.85e-09	4.81e-07	20	9.01	2
4	GO.BP	tumor necrosis factor production	3.89e-09	9.5e-07	19	9.19	2
4	GO.BP	phagocytosis	8.98e-09	2.01e-06	31	4.47	3
4	GO.MF	CARD domain binding	0.000438	0.0144	4	Inf	2
4	GO.MF	cytokine activity	0.000978	0.022	9	4.94	3
4	GO.MF	amyloid-beta binding	0.00102	0.0222	5	14.9	2
4	GO.MF	lipid transporter activity	0.00102	0.0222	5	14.9	1
4	GO.MF	SH3 domain binding	0.00154	0.0279	10	4.03	1
4	GO.CC	tertiary granule	2.23e-08	1.23e-06	23	5.84	3
4	GO.CC	secretory granule membrane	8.52e-06	0.000268	26	3.29	4
4	GO.CC	inflammasome complex	6.28e-05	0.0015	5	Inf	1
4	GO.CC	primary lysosome	0.000223	0.0042	19	3.09	2
4	GO.CC	azurophil granule	0.000223	0.0042	19	3.09	2
4	KEGG	Phagosome	2.25e-07	4.23e-05	20	5.71	2
4	KEGG	Fc gamma R-mediated phagocytosis	1.35e-05	0.000848	14	5.74	2
4	KEGG	Chemokine signaling pathway	2.78e-05	0.00153	16	4.49	3
4	KEGG	Natural killer cell mediated cytotoxicity	0.000133	0.00485	11	5.58	3
4	KEGG	NOD-like receptor signaling pathway	0.000156	0.00539	17	3.49	2
4	msigdb__biocarta	fmlp pathway	0.00241	0.015	5	9.95	1
4	msigdb__biocarta	rac1 pathway	0.00304	0.0172	3	Inf	1
4	msigdb__biocarta	il3 pathway	0.0109	0.0404	3	17.8	1
4	msigdb__biocarta	nkcells pathway	0.0109	0.0404	3	17.8	2
4	msigdb__reactome	neutrophil degranulation	7.39e-08	3.81e-06	48	2.9	5
4	msigdb__reactome	fcgamma receptor fcgr dependent phagocytosis	5.41e-05	0.00169	14	4.77	1
4	msigdb__reactome	leishmania infection	0.000106	0.00297	18	3.48	3
4	msigdb__reactome	cell surface interactions at the vascular wal..	0.000214	0.00527	11	5.15	1
4	msigdb__reactome	parasite infection	0.000334	0.00764	11	4.78	2
4	msigdb__canonical__pathways	neutrophil degranulation	7.39e-08	4.92e-06	48	2.9	5
4	msigdb__canonical__pathways	kegg fc gamma r mediated phagocytosis	2.54e-06	0.000125	14	7.19	2
4	msigdb__canonical__pathways	kegg chemokine signaling pathway	4.11e-05	0.0015	16	4.29	3
4	msigdb__canonical__pathways	fcgamma receptor fcgr dependent phagocytosis	5.41e-05	0.0018	14	4.77	2
4	msigdb__canonical__pathways	leishmania infection	0.000106	0.00316	18	3.48	3
4	msigdb__immunological__signatures	gse10325 lupus cd4 tcell vs lupus myeloid dn	9.53e-19	8.38e-16	47	8.03	5
4	msigdb__immunological__signatures	gse10325 lupus bcell vs lupus myeloid dn	4.08e-18	3.38e-15	46	7.82	5
4	msigdb__immunological__signatures	gse10325 bcell vs myeloid dn	4.14e-18	3.38e-15	42	9.03	5
4	msigdb__immunological__signatures	gse22886 naive cd8 tcell vs neutrophil dn	6.42e-18	4.81e-15	31	17.1	4
4	msigdb__immunological__signatures	gse22886 naive cd8 tcell vs monocyte dn	9.91e-17	5.8e-14	47	6.68	5
5	GO.BP	cytolysis	0.000532	0.0153	5	17.6	2
5	GO.BP	regulation of T cell activation	0.00081	0.0199	15	3.11	5
5	GO.BP	T cell differentiation	0.00102	0.0234	13	3.35	2
5	GO.BP	positive regulation of leukocyte activation	0.00131	0.0276	14	3.06	4
5	GO.BP	positive regulation of cell activation	0.00165	0.0316	14	2.97	4
5	GO.MF	signaling adaptor activity	8.15e-06	0.000717	9	12.9	2
5	GO.MF	SH3/SH2 adaptor activity	0.000235	0.00986	6	14.1	1
5	GO.MF	molecular adaptor activity	0.000241	0.0099	13	4.09	1
5	GO.MF	T cell receptor binding	0.000253	0.0101	4	Inf	1
5	GO.MF	serine-type endopeptidase activity	0.000532	0.0169	5	17.6	2
5	GO.CC	T cell receptor complex	6.94e-06	0.000229	8	19	2
5	GO.CC	external side of plasma membrane	5.31e-05	0.00131	14	4.63	4
5	GO.CC	plasma membrane receptor complex	0.000125	0.00273	9	7.14	1
5	GO.CC	alpha-beta T cell receptor complex	0.00114	0.015	4	27.9	2
5	GO.CC	immunological synapse	0.00483	0.0405	6	5.28	3
5	KEGG	T cell receptor signaling pathway	2.87e-07	4.42e-05	12	12.5	1
5	KEGG	Th1 and Th2 cell differentiation	5.56e-07	7e-05	10	18	1
5	KEGG	Th17 cell differentiation	7.62e-06	0.000528	10	10.3	1
5	KEGG	PD-L1 expression and PD-1 checkpoint pathway ..	2.87e-05	0.00153	10	7.98	1
5	KEGG	Natural killer cell mediated cytotoxicity	5.1e-05	0.00236	10	7.18	3
5	msigdb__biocarta	tcr pathway	1.78e-07	1.89e-05	10	24	3
5	msigdb__biocarta	ctl pathway	4.83e-07	3.41e-05	7	Inf	2
5	msigdb__biocarta	il12 pathway	3.45e-06	0.000104	7	49.7	2
5	msigdb__biocarta	no2il12 pathway	3.45e-06	0.000104	7	49.7	2
5	msigdb__biocarta	tcra pathway	3.91e-06	0.000104	6	Inf	3
5	msigdb__reactome	immunoregulatory interactions between a lymph..	2.87e-07	1.4e-05	12	12.5	3
5	msigdb__reactome	generation of second messenger molecules	2.12e-06	9.01e-05	8	28.5	2
5	msigdb__reactome	costimulation by the cd28 family	7e-05	0.00207	9	8.04	1
5	msigdb__reactome	dap12 signaling	8.76e-05	0.00248	6	21.2	1
5	msigdb__reactome	pd 1 signaling	0.00017	0.00433	5	35.1	2
5	msigdb__canonical__pathways	pid cd8 tcr downstream pathway	9.32e-10	7.18e-08	12	43.7	2

5	msigdb__canonical__pathways	pid il12 2pathway	5.29e-08	3.59e-06	13	13.6	1
5	msigdb__canonical__pathways	tcr pathway	1.78e-07	1.11e-05	10	24	1
5	msigdb__canonical__pathways	kegg t cell receptor signaling pathway	2.87e-07	1.71e-05	12	12.5	1
5	msigdb__canonical__pathways	immunoregulatory interactions between a lymph..	2.87e-07	1.71e-05	12	12.5	3
5	msigdb__immunological__signatures	gse22886 naive cd8 tcell vs monocyte up	2.23e-20	2.37e-17	31	22.8	4
5	msigdb__immunological__signatures	gse45739 unstim vs acd3 acd28 stim wt cd4 tce..	3.61e-16	1.85e-13	30	12.6	2
5	msigdb__immunological__signatures	gse3039 nkt cell vs alphaalpha cd8 tcell dn	1.99e-15	9.17e-13	29	12.1	4
5	msigdb__immunological__signatures	gse45739 unstim vs acd3 acd28 stim nras ko cd..	2.32e-15	1.06e-12	23	22.2	3
5	msigdb__immunological__signatures	gse22886 naive tcell vs monocyte up	9.88e-15	4.03e-12	24	16.9	4
6	GO.BP	lymphocyte mediated immunity	3.1e-05	0.00198	15	4.74	3
6	GO.BP	axon guidance	0.000215	0.00843	8	8.23	2
6	GO.BP	neuron projection guidance	0.000215	0.00843	8	8.23	2
6	GO.BP	cellular response to ketone	0.000215	0.00843	8	8.23	1
6	GO.BP	natural killer cell mediated immunity	0.000404	0.0132	8	7.05	1
6	GO.MF	lyase activity	9.87e-05	0.00497	9	7.97	1
6	GO.MF	serine-type endopeptidase activity	0.000305	0.0113	5	30.5	2
6	GO.CC	external side of plasma membrane	0.00163	0.0195	12	3.39	4
6	KEGG	Natural killer cell mediated cytotoxicity	0.000112	0.00432	11	5.71	3
6	KEGG	Graft-versus-host disease	0.000305	0.0092	5	30.5	2
6	KEGG	Lysine degradation	0.00289	0.0441	3	Inf	1
6	msigdb__biocarta	set pathway	5.76e-05	0.000939	5	Inf	2
6	msigdb__biocarta	dnafragment pathway	0.00289	0.017	3	Inf	2
6	msigdb__biocarta	ctl pathway	0.01	0.0386	4	8.1	2
6	msigdb__reactome	immunoregulatory interactions between a lymph..	0.000246	0.00582	10	5.65	3
6	msigdb__reactome	interleukin 3 interleukin 5 and gm csf signal..	0.000468	0.01	7	8.61	1
6	msigdb__reactome	interleukin receptor shc signaling	0.00181	0.0277	4	24.3	1
6	msigdb__canonical__pathways	pid il2 stat5 pathway	3.14e-05	0.00118	7	21.5	2
6	msigdb__canonical__pathways	set pathway	5.76e-05	0.0019	5	Inf	2
6	msigdb__canonical__pathways	kegg natural killer cell mediated cytotoxicit..	0.000112	0.00332	11	5.71	3
6	msigdb__canonical__pathways	pid cd8 tcr downstream pathway	0.000215	0.00548	8	8.23	2
6	msigdb__canonical__pathways	immunoregulatory interactions between a lymph..	0.000246	0.00603	10	5.65	3
6	msigdb__immunological__signatures	gse45739 unstim vs acd3 acd28 stim nras ko cd..	1.82e-18	1.57e-15	30	20.5	3
6	msigdb__immunological__signatures	gse45739 unstim vs acd3 acd28 stim wt cd4 tce..	1.13e-15	5.28e-13	34	9.81	2
6	msigdb__immunological__signatures	gse26495 naive vs pd1low cd8 tcell dn	1.64e-11	3.74e-09	28	7.51	2
6	msigdb__immunological__signatures	gse3039 nkt cell vs alphaalpha cd8 tcell dn	2.31e-11	5.14e-09	26	8.25	4
6	msigdb__immunological__signatures	gse24634 teff vs tconv day7 in culture up	1.16e-08	1.45e-06	16	11.4	3
7	GO.BP	mRNA export from nucleus	2.65e-07	4.48e-05	27	7.57	2
7	GO.BP	mRNA-containing ribonucleoprotein complex exp..	2.65e-07	4.48e-05	27	7.57	2
7	GO.BP	ribonucleoprotein complex localization	6.83e-07	9.43e-05	30	5.62	2
7	GO.BP	ribonucleoprotein complex export from nucleus	6.83e-07	9.43e-05	30	5.62	2
7	GO.BP	RNA export from nucleus	2.1e-06	0.000257	31	4.75	2
7	GO.MF	unfolded protein binding	2.01e-05	0.00154	30	3.88	3
7	GO.MF	pre-mRNA binding	0.000103	0.00497	15	8.29	1
7	GO.MF	DNA-binding transcription activator activity,..	0.000256	0.0101	31	2.88	1
7	GO.MF	enhancer sequence-specific DNA binding	0.000318	0.0113	15	6.21	1
7	GO.MF	heat shock protein binding	0.000351	0.0122	21	3.88	1
7	GO.CC	spliceosomal complex	2.13e-11	1.83e-09	61	4.84	2
7	GO.CC	nuclear speck	5.86e-09	3.63e-07	68	3.29	1
7	GO.CC	catalytic step 2 spliceosome	1.57e-08	9.17e-07	35	6.6	2
7	GO.CC	U2-type spliceosomal complex	7.26e-08	3.6e-06	33	6.21	2
7	GO.CC	precatalytic spliceosome	9.31e-06	0.000279	21	7.01	2
7	KEGG	Spliceosome	7.22e-11	2.5e-08	53	5.4	2
7	KEGG	mRNA surveillance pathway	1.65e-05	0.000955	23	5.49	1
7	KEGG	RNA transport	4.62e-05	0.00221	33	3.26	2
7	KEGG	Estrogen signaling pathway	0.00141	0.0282	13	5.37	1
7	msigdb__biocarta	sm pathway	0.000772	0.00584	11	9.07	2
7	msigdb__reactome	processing of capped intron containing pre mr..	2.12e-12	1.39e-10	75	4.28	2
7	msigdb__reactome	mrna splicing	2.32e-12	1.49e-10	69	4.67	2
7	msigdb__reactome	rna polymerase ii transcription termination	1.43e-08	7.5e-07	29	9.79	2
7	msigdb__reactome	transport of mature transcript to cytoplasm	1.71e-07	8.47e-06	26	8.74	2
7	msigdb__reactome	attenuation phase	7.37e-05	0.00213	12	19.8	1
7	msigdb__canonical__pathways	processing of capped intron containing pre mr..	2.12e-12	1.94e-10	75	4.28	2
7	msigdb__canonical__pathways	mrna splicing	2.32e-12	2.07e-10	69	4.67	2
7	msigdb__canonical__pathways	kegg spliceosome	2.73e-11	2.28e-09	53	5.74	2
7	msigdb__canonical__pathways	rna polymerase ii transcription termination	1.43e-08	1e-06	29	9.79	2
7	msigdb__canonical__pathways	transport of mature transcript to cytoplasm	1.71e-07	1.08e-05	26	8.74	2
7	msigdb__tf__motifs	hsf2 target genes	1.83e-08	3.31e-05	44	4.7	1
7	msigdb__tf__motifs	ppargc1a target genes	2.32e-07	0.000314	24	10.1	1
7	msigdb__tf__motifs	rgaannttc hsf1 01	1.6e-06	0.00163	45	3.33	1
7	msigdb__tf__motifs	gccatnttg yy1 q6	2.1e-06	0.00163	65	2.55	1
7	msigdb__tf__motifs	yy1 02	4.47e-05	0.0151	32	3.36	1
7	msigdb__immunological__signatures	gse3920 ifna vs ifng treated endothelial cell..	2.81e-10	5.28e-08	37	9.02	1
7	msigdb__immunological__signatures	gse17974 0h vs 0.5h in vitro act cd4 tcell dn	2.46e-07	2.16e-05	30	6.32	1
7	msigdb__immunological__signatures	gse41867 day8 vs day15 lcmv clone13 effector ..	2.46e-07	2.16e-05	30	6.32	1
7	msigdb__immunological__signatures	gse17974 2.5h vs 72h il4 and anti il12 act cd..	3.13e-07	2.64e-05	41	4.1	1

7	msigdb__immunological__signatures	gse17974 ctrl vs act il4 and anti il12 0.5h c..	6.18e-07	4.84e-05	34	4.79	1
8	GO.BP	cellular response to toxic substance	3.35e-07	5.37e-05	19	5.3	4
8	GO.BP	tissue regeneration	9.52e-06	0.000808	7	21.2	1
8	GO.BP	regulation of actin cytoskeleton organization	1.21e-05	0.000988	20	3.71	2
8	GO.BP	regeneration	1.51e-05	0.00117	12	6.16	2
8	GO.BP	cell junction assembly	1.51e-05	0.00117	12	6.16	2
8	GO.MF	amide binding	1.69e-06	0.00024	16	5.56	1
8	GO.MF	actin filament binding	3.24e-06	0.000344	15	5.61	1
8	GO.MF	glutathione peroxidase activity	6.75e-05	0.00402	6	18.1	1
8	GO.MF	peptide binding	9.18e-05	0.00497	12	4.81	2
8	GO.MF	phospholipase inhibitor activity	0.000105	0.00497	4	Inf	1
8	GO.CC	podosome	8.38e-06	0.000268	8	14.6	1
8	GO.CC	cell-substrate adherens junction	0.000436	0.00745	27	2.31	4
8	GO.CC	focal adhesion	0.000436	0.00745	27	2.31	4
8	GO.CC	cell-substrate junction	0.000436	0.00745	27	2.31	4
8	GO.CC	cell cortex	0.000444	0.00746	15	3.23	1
8	KEGG	Glutathione metabolism	6.38e-05	0.00276	8	9.1	2
8	KEGG	Salmonella infection	7.83e-05	0.00329	21	3.05	2
8	KEGG	Fluid shear stress and atherosclerosis	0.000327	0.00928	11	4.39	3
8	KEGG	Transcriptional misregulation in cancer	0.000571	0.0144	11	4.03	1
8	KEGG	Apoptosis	0.000667	0.0159	13	3.42	1
8	msigdb__biocarta	hivnef pathway	0.000476	0.00537	9	5.13	2
8	msigdb__biocarta	raccycd pathway	0.00874	0.0356	4	7.16	1
8	msigdb__biocarta	death pathway	0.0134	0.0458	5	4.49	2
8	msigdb__reactome	response to elevated platelet cytosolic ca2	7.64e-07	3.4e-05	14	7.26	3
8	msigdb__reactome	gpcr ligand binding	4.7e-05	0.00159	12	5.27	4
8	msigdb__reactome	platelet activation signaling and aggregation	6.6e-05	0.00202	17	3.61	4
8	msigdb__reactome	leishmania infection	0.000117	0.00325	15	3.77	3
8	msigdb__reactome	ephb mediated forward signaling	0.000181	0.00457	8	7.28	3
8	msigdb__canonical__pathways	response to elevated platelet cytosolic ca2	7.64e-07	4.06e-05	14	7.26	3
8	msigdb__canonical__pathways	gpcr ligand binding	4.7e-05	0.00166	12	5.27	4
8	msigdb__canonical__pathways	platelet activation signaling and aggregation	6.6e-05	0.00214	17	3.61	4
8	msigdb__canonical__pathways	leishmania infection	0.000117	0.00344	15	3.77	3
8	msigdb__canonical__pathways	ephb mediated forward signaling	0.000181	0.00477	8	7.28	3
8	msigdb__tf__motifs	srf 01	9.52e-06	0.00646	7	21.2	1
8	msigdb__tf__motifs	ap1 q6	1.78e-05	0.00877	14	5	1
8	msigdb__tf__motifs	ap1 q4	0.00026	0.0428	13	3.87	1
8	msigdb__immunological__signatures	gse29618 bcell vs mdc day7 flu vaccine dn	2.58e-17	1.73e-14	41	7.6	5
8	msigdb__immunological__signatures	gse29618 bcell vs mdc dn	2.68e-17	1.78e-14	44	6.92	4
8	msigdb__immunological__signatures	gse24634 il4 vs ctrl treated naive cd4 tcell ..	2.95e-13	9.62e-11	25	10.2	5
8	msigdb__immunological__signatures	gse22886 naive tcell vs dc dn	8.79e-12	2.11e-09	32	5.85	3
8	msigdb__immunological__signatures	gse22886 naive cd8 tcell vs dc dn	2.5e-11	5.53e-09	33	5.36	6
9	GO.BP	ribosome biogenesis	1.41e-20	6.2e-18	101	5.41	4
9	GO.BP	rRNA metabolic process	1.45e-14	5.36e-12	74	4.93	4
9	GO.BP	rRNA processing	1.34e-13	4.85e-11	69	4.88	4
9	GO.BP	RNA localization	4.5e-10	1.32e-07	53	4.43	2
9	GO.BP	ribonucleoprotein complex assembly	2.79e-09	6.92e-07	62	3.47	5
9	GO.MF	ribonucleoprotein complex binding	2.26e-07	4.64e-05	33	4.98	2
9	GO.MF	structural constituent of ribosome	5.27e-07	9.11e-05	70	2.51	4
9	GO.MF	unfolded protein binding	2.16e-06	0.000284	30	4.51	3
9	GO.MF	ribosome binding	6.64e-05	0.00402	11	21.1	1
9	GO.MF	translation factor activity, RNA binding	7.6e-05	0.00425	24	3.88	1
9	GO.CC	preribosome	1.14e-10	9.02e-09	33	10.9	1
9	GO.CC	chaperone complex	3.23e-07	1.49e-05	14	Inf	3
9	GO.CC	catalytic step 2 spliceosome	4.84e-07	2.18e-05	32	4.83	2
9	GO.CC	ribosomal subunit	1.23e-06	5.39e-05	73	2.37	4
9	GO.CC	spliceosomal complex	2.27e-06	8.83e-05	46	3.03	2
9	KEGG	Spliceosome	2.44e-07	4.23e-05	45	3.57	2
9	KEGG	Ribosome	1.27e-06	0.00013	62	2.58	4
9	KEGG	Ribosome biogenesis in eukaryotes	3.46e-06	0.000266	25	5.41	1
9	KEGG	RNA transport	3.36e-05	0.00167	38	2.86	2
9	msigdb__biocarta	sm pathway	2.76e-06	0.000104	12	Inf	2
9	msigdb__biocarta	eif pathway	0.00535	0.0258	10	4.78	1
9	msigdb__biocarta	mhc pathway	0.0142	0.0472	4	Inf	1
9	msigdb__reactome	translation	6.91e-12	4.32e-10	110	2.86	4
9	msigdb__reactome	rrna processing	7.86e-12	4.81e-10	80	3.58	4
9	msigdb__reactome	processing of capped intron containing pre mr..	1.15e-09	6.42e-08	67	3.4	2
9	msigdb__reactome	mrna splicing	5.98e-09	3.28e-07	59	3.49	2
9	msigdb__reactome	metabolism of amino acids and derivatives	3.34e-07	1.59e-05	74	2.49	4
9	msigdb__canonical__pathways	translation	6.91e-12	6.03e-10	110	2.86	4
9	msigdb__canonical__pathways	rrna processing	7.86e-12	6.71e-10	80	3.58	4
9	msigdb__canonical__pathways	processing of capped intron containing pre mr..	1.15e-09	8.67e-08	67	3.4	2
9	msigdb__canonical__pathways	mrna splicing	5.98e-09	4.35e-07	59	3.49	2
9	msigdb__canonical__pathways	metabolism of amino acids and derivatives	3.34e-07	1.96e-05	74	2.49	4
9	msigdb__tf__motifs	mycmax 01	2.87e-05	0.013	33	3.22	1

9	msigdb__tf__motifs	sgcgssaaa e2f1dp2 01	3.24e-05	0.0135	21	5.08	1
9	msigdb__tf__motifs	e2f1 q6 01	3.74e-05	0.0145	24	4.23	1
9	msigdb__tf__motifs	epc1 target genes	4.03e-05	0.0146	56	2.26	1
9	msigdb__immunological__signatures	gse22886 unstim vs il2 stim nkcell dn	4.2e-17	2.63e-14	66	7.55	1
9	msigdb__immunological__signatures	gse22886 unstim vs il15 stim nkcell dn	4.2e-17	2.63e-14	66	7.55	2
9	msigdb__immunological__signatures	gse37532 treg vs tconv pparg ko cd4 tcell fro..	4.77e-15	2.09e-12	63	6.44	1
9	msigdb__immunological__signatures	gse24634 treg vs tconv post day3 il4 conversi..	7.35e-14	2.69e-11	51	7.92	3
9	msigdb__immunological__signatures	gse21927 spleen c57bl6 vs el4 tumor balbc mon..	1.2e-13	4.23e-11	67	5.08	1
10	GO.BP	osteoclast differentiation	2.01e-05	0.00144	8	12.8	2
10	GO.BP	bone remodeling	4.85e-05	0.00277	6	23.8	1
10	GO.BP	neutrophil activation involved in immune resp..	5.19e-05	0.00292	31	2.57	5
10	GO.BP	neutrophil degranulation	5.19e-05	0.00292	31	2.57	5
10	GO.BP	regulation of endocytosis	6.53e-05	0.0035	14	4.41	3
10	GO.MF	transition metal ion transmembrane transporte..	0.00149	0.0276	3	Inf	1
10	GO.CC	secretory granule membrane	2.8e-06	0.000105	22	3.97	4
10	GO.CC	specific granule	0.000104	0.00236	12	4.88	3
10	GO.CC	specific granule membrane	0.00096	0.0134	8	5.33	2
10	GO.CC	membrane raft	0.00357	0.0332	13	2.77	2
10	GO.CC	membrane microdomain	0.00357	0.0332	13	2.77	2
10	KEGG	Osteoclast differentiation	0.000636	0.0155	10	4.47	3
10	KEGG	TNF signaling pathway	0.00155	0.0292	9	4.24	2
10	KEGG	Adipocytokine signaling pathway	0.00181	0.0306	6	6.79	1
10	KEGG	Lysosome	0.00279	0.0435	9	3.79	2
10	msigdb__biocarta	tid pathway	0.0125	0.0441	3	11.7	1
10	msigdb__reactome	neutrophil degranulation	4.44e-05	0.00154	31	2.6	5
10	msigdb__reactome	interleukin 10 signaling	0.000148	0.00388	8	8.01	3
10	msigdb__reactome	interleukin 4 and interleukin 13 signaling	0.00096	0.0169	8	5.33	2
10	msigdb__canonical__pathways	neutrophil degranulation	4.44e-05	0.0016	31	2.6	5
10	msigdb__canonical__pathways	interleukin 10 signaling	0.000148	0.00405	8	8.01	3
10	msigdb__canonical__pathways	pid integrin a9b1 pathway	0.000168	0.0045	4	Inf	1
10	msigdb__canonical__pathways	pid upa upar pathway	0.000327	0.00755	5	19.7	2
10	msigdb__canonical__pathways	kegg amyotrophic lateral sclerosis als	0.000593	0.012	6	9.52	1
10	msigdb__tf__motifs	nr0b1 target genes	9.09e-05	0.022	15	3.98	1
10	msigdb__immunological__signatures	gse6269 flu vs staph aureus inf pbmc dn	2.7e-23	4.66e-20	39	16.4	5
10	msigdb__immunological__signatures	gse10325 lupus bcell vs lupus myeloid dn	1.07e-16	6.16e-14	35	9.59	5
10	msigdb__immunological__signatures	gse10325 lupus cd4 tcell vs lupus myeloid dn	6.1e-16	3.03e-13	35	8.8	5
10	msigdb__immunological__signatures	gse34156 untreated vs 6h tlr1 tlr2 ligand tre..	7.38e-16	3.59e-13	32	10.1	5
10	msigdb__immunological__signatures	gse34156 tlr1 tlr2 ligand vs nod2 and tlr1 tl..	8.75e-15	3.6e-12	33	8.42	5
11	GO.BP	platelet degranulation	1.84e-05	0.00137	8	9.21	3
11	GO.BP	platelet activation	0.000424	0.0138	6	7.76	2
11	GO.BP	regulation of transmembrane transporter activ..	0.000645	0.0178	5	9.32	1
11	GO.BP	response to steroid hormone	0.000647	0.0178	8	5.01	1
11	GO.BP	regulation of transporter activity	0.000847	0.0206	5	8.65	3
11	GO.MF	amyloid-beta binding	0.00346	0.0497	3	14.1	2
11	GO.CC	platelet alpha granule	2.07e-07	9.99e-06	8	20.4	2
11	GO.CC	platelet alpha granule lumen	6.15e-06	0.000206	6	21.1	1
11	GO.CC	stress fiber	0.00131	0.0164	3	23.5	2
11	GO.CC	contractile actin filament bundle	0.00131	0.0164	3	23.5	2
11	GO.CC	sarcomere	0.00174	0.0205	5	7.11	1
11	msigdb__reactome	platelet activation signaling and aggregation	1.09e-05	0.000409	11	6.44	4
11	msigdb__reactome	response to elevated platelet cytosolic ca2	5e-05	0.00164	8	7.78	3
11	msigdb__reactome	formation of fibrin clot clotting cascade	0.000677	0.0133	3	35.3	1
11	msigdb__reactome	neurotransmitter receptors and postsynaptic s..	0.0036	0.0476	4	7.96	1
11	msigdb__canonical__pathways	platelet activation signaling and aggregation	1.09e-05	0.00046	11	6.44	4
11	msigdb__canonical__pathways	response to elevated platelet cytosolic ca2	5e-05	0.00174	8	7.78	3
11	msigdb__canonical__pathways	formation of fibrin clot clotting cascade	0.000677	0.013	3	35.3	1
11	msigdb__canonical__pathways	neurotransmitter receptors and postsynaptic s..	0.0036	0.0427	4	7.96	1
11	msigdb__immunological__signatures	gse45365 healthy vs mcmv infection cd11b dc d..	9.87e-10	1.64e-07	8	67.9	1
11	msigdb__immunological__signatures	gse9006 healthy vs type 1 diabetes pbmc at dx..	4.31e-08	4.67e-06	14	8.66	1
11	msigdb__immunological__signatures	gse11057 pbmc vs mem cd4 tcell up	5.32e-07	4.23e-05	10	10.9	6
11	msigdb__immunological__signatures	gse45365 wt vs ifnar ko bcell mcmv infection ..	1.77e-06	0.000119	6	29.6	1
11	msigdb__immunological__signatures	gse45365 bcell vs cd8 tcell dn	1.77e-06	0.000119	6	29.6	1
12	GO.BP	antibiotic catabolic process	0.000192	0.00782	8	9.74	2
12	GO.BP	protein folding	0.000272	0.0101	26	2.54	2
12	GO.BP	RNA localization to Cajal body	0.000324	0.0114	7	11.3	2
12	GO.BP	telomerase RNA localization to Cajal body	0.000324	0.0114	7	11.3	2
12	GO.BP	telomerase RNA localization	0.000324	0.0114	7	11.3	2
12	GO.MF	unfolded protein binding	0.000435	0.0144	18	3.07	3
12	GO.MF	oxidoreductase activity, acting on peroxide a..	0.000457	0.0148	9	6.27	3
12	GO.MF	peroxiredoxin activity	0.000773	0.0193	5	24.2	1
12	GO.MF	peptide binding	0.00102	0.0222	13	3.54	2
12	GO.MF	antioxidant activity	0.00122	0.0243	10	4.44	3
12	GO.CC	chaperonin-containing T-complex	0.000154	0.00314	6	29.1	2
12	GO.CC	chaperone complex	0.00076	0.0116	7	8.51	3
12	GO.CC	peptidase complex	0.00295	0.0294	15	2.73	1

12	GO.CC	zona pellucida receptor complex	0.00379	0.0343	4	19.3	2
12	GO.CC	proteasome core complex, beta-subunit complex	0.00379	0.0343	4	19.3	1
12	msigdb__reactome	formation of tubulin folding intermediates by..	0.000324	0.00748	7	11.3	2
12	msigdb__reactome	folding of actin by cct tric	0.000525	0.0109	6	14.6	2
12	msigdb__reactome	bbsome mediated cargo targeting to cilium	0.000773	0.014	5	24.2	2
12	msigdb__reactome	detoxification of reactive oxygen species	0.0014	0.0226	9	4.87	3
12	msigdb__canonical__pathways	formation of tubulin folding intermediates by..	0.000324	0.00755	7	11.3	2
12	msigdb__canonical__pathways	folding of actin by cct tric	0.000525	0.0108	6	14.6	2
12	msigdb__canonical__pathways	bbsome mediated cargo targeting to cilium	0.000773	0.0134	5	24.2	2
12	msigdb__canonical__pathways	detoxification of reactive oxygen species	0.0014	0.0216	9	4.87	3
12	msigdb__canonical__pathways	kegg glycerolipid metabolism	0.00379	0.0443	4	19.3	1
12	msigdb__immunological__signatures	gse29618 monocyte vs pdc dn	3.28e-25	8.32e-22	50	15	2
12	msigdb__immunological__signatures	gse29618 bcell vs pdc dn	3.51e-23	5.72e-20	56	9.58	2
12	msigdb__immunological__signatures	gse29618 monocyte vs pdc day7 flu vaccine dn	6.06e-22	8.4e-19	51	10.2	2
12	msigdb__immunological__signatures	gse29618 pdc vs mdc up	7.53e-18	5.46e-15	46	8.16	2
12	msigdb__immunological__signatures	gse29618 bcell vs pdc day7 flu vaccine dn	3.8e-17	2.48e-14	48	7.12	3
13	GO.BP	gas transport	1.27e-09	3.47e-07	5	Inf	1
13	GO.BP	oxygen transport	1.27e-09	3.47e-07	5	Inf	1
13	GO.BP	cofactor catabolic process	2.79e-09	6.92e-07	7	54.4	1
13	GO.BP	hydrogen peroxide catabolic process	1.62e-08	3.53e-06	6	67.1	2
13	GO.BP	drug transport	5.15e-08	9.85e-06	6	50.5	1
13	GO.MF	oxygen carrier activity	1.27e-09	4.17e-07	5	Inf	1
13	GO.MF	haptoglobin binding	1.27e-09	4.17e-07	5	Inf	1
13	GO.MF	oxygen binding	7.51e-09	1.98e-06	5	318	1
13	GO.MF	molecular carrier activity	5.43e-07	9.11e-05	5	53.8	1
13	GO.MF	organic acid binding	8.53e-07	0.000131	6	26.9	1
13	GO.CC	hemoglobin complex	1.31e-10	9.98e-09	6	400	1
13	GO.CC	haptoglobin-hemoglobin complex	1.27e-09	8.1e-08	5	Inf	1
13	GO.CC	blood microparticle	1.24e-05	0.00036	5	23.2	1
13	GO.CC	endocytic vesicle lumen	0.00017	0.00336	3	45.2	1
13	GO.CC	inclusion body	0.002	0.0233	3	15.1	1
13	KEGG	Malaria	5.44e-06	0.000397	4	62.3	1
13	KEGG	African trypanosomiasis	9.81e-05	0.004	3	60.1	1
13	KEGG	Porphyrin and chlorophyll metabolism	0.00017	0.00573	3	45.2	1
13	msigdb__biocarta	ahsp pathway	1.27e-09	2.69e-07	5	Inf	1
13	msigdb__reactome	erythrocytes take up oxygen and release carbo..	8.17e-08	4.13e-06	4	Inf	1
13	msigdb__reactome	erythrocytes take up carbon dioxide and relea..	4.04e-07	1.86e-05	4	247	1
13	msigdb__reactome	scavenging of heme from plasma	5.08e-06	0.000209	3	Inf	1
13	msigdb__reactome	metabolism of porphyrins	4.96e-05	0.00164	3	89.9	1
13	msigdb__reactome	binding and uptake of ligands by scavenger re..	0.000397	0.00887	3	30.2	1
13	msigdb__canonical__pathways	ahsp pathway	1.27e-09	9.4e-08	5	Inf	1
13	msigdb__canonical__pathways	erythrocytes take up oxygen and release carbo..	8.17e-08	5.35e-06	4	Inf	1
13	msigdb__canonical__pathways	erythrocytes take up carbon dioxide and relea..	4.04e-07	2.3e-05	4	247	1
13	msigdb__canonical__pathways	scavenging of heme from plasma	5.08e-06	0.000232	3	Inf	1
13	msigdb__canonical__pathways	metabolism of porphyrins	4.96e-05	0.00174	3	89.9	1
13	msigdb__tf__motifs	phb2 target genes	0.000165	0.0289	4	19.2	1
13	msigdb__immunological__signatures	gse34205 rsv vs flu inf infant pbmc up	3.7e-27	1.13e-23	19	154	1
13	msigdb__immunological__signatures	gse34205 healthy vs rsv inf infant pbmc dn	1.11e-20	1.26e-17	17	69.5	2
13	msigdb__immunological__signatures	gse6269 flu vs strep pneumo inf pbmc dn	6.17e-07	4.84e-05	6	28.9	2
13	msigdb__immunological__signatures	gse21546 sap1a ko vs sap1a ko and elk1 ko ant..	1.63e-05	0.000779	5	21.6	1
13	msigdb__immunological__signatures	gse21379 tfh vs non tfh sap ko cd4 tcell up	7.76e-05	0.00285	5	14.7	1
14	GO.BP	response to molecule of bacterial origin	2.68e-10	8.5e-08	27	5.86	4
14	GO.BP	response to lipopolysaccharide	2.68e-10	8.5e-08	27	5.86	4
14	GO.BP	cellular response to molecule of bacterial or..	8.21e-09	1.89e-06	20	6.66	4
14	GO.BP	cellular response to lipopolysaccharide	8.21e-09	1.89e-06	20	6.66	4
14	GO.BP	myeloid leukocyte migration	1.9e-08	4.03e-06	18	7.15	3
14	GO.MF	cytokine receptor binding	3.83e-05	0.00253	12	5.3	1
14	GO.MF	chemokine activity	0.000877	0.02	5	10.6	2
14	GO.MF	CCR chemokine receptor binding	0.000877	0.02	5	10.6	2
14	GO.MF	chemokine receptor binding	0.00109	0.0229	6	7.12	2
14	GO.MF	cytokine activity	0.0012	0.0243	8	4.79	3
14	GO.CC	cell-cell adherens junction	0.000877	0.0125	5	10.6	2
14	GO.CC	extrinsic component of membrane	0.00243	0.0266	9	3.74	3
14	GO.CC	tertiary granule	0.00267	0.0281	11	3.15	3
14	GO.CC	secretory granule membrane	0.00409	0.0361	15	2.46	4
14	GO.CC	extrinsic component of plasma membrane	0.00584	0.0459	6	4.57	2
14	KEGG	TNF signaling pathway	2.01e-06	0.000174	12	7.83	2
14	KEGG	IL-17 signaling pathway	1.1e-05	0.000725	9	9.81	2
14	KEGG	Rheumatoid arthritis	1.51e-05	0.000909	11	6.73	3
14	KEGG	Tuberculosis	5.48e-05	0.00245	13	4.65	3
14	KEGG	Amoebiasis	0.000128	0.00478	7	9.41	1
14	msigdb__biocarta	il1r pathway	2.88e-05	0.000557	6	21.4	1
14	msigdb__biocarta	death pathway	0.00516	0.0255	4	8.44	2
14	msigdb__biocarta	eponfkb pathway	0.0059	0.0278	3	15.7	1
14	msigdb__biocarta	nthi pathway	0.011	0.0404	3	10.5	1

14	msigdb__biocarta	hivnef pathway	0.0129	0.045	5	4.41	2
14	msigdb__reactome	neutrophil degranulation	1.76e-05	0.000651	30	2.78	5
14	msigdb__reactome	purinergic signaling in leishmaniasis infecti..	2.88e-05	0.00104	6	21.4	1
14	msigdb__reactome	signaling by interleukins	4.61e-05	0.00158	25	2.87	3
14	msigdb__reactome	toll like receptor cascades	5.18e-05	0.00168	12	5.09	1
14	msigdb__reactome	class a 1 rhodopsin like receptors	0.000136	0.00369	10	5.46	3
14	msigdb__canonical__pathways	naba secreted factors	8.38e-08	5.4e-06	12	12.1	3
14	msigdb__canonical__pathways	neutrophil degranulation	1.76e-05	0.000727	30	2.78	5
14	msigdb__canonical__pathways	il1r pathway	2.88e-05	0.00114	6	21.4	1
14	msigdb__canonical__pathways	purinergic signaling in leishmaniasis infecti..	2.88e-05	0.00114	6	21.4	1
14	msigdb__canonical__pathways	kegg nod like receptor signaling pathway	3.74e-05	0.00139	8	9.62	1
14	msigdb__tf__motifs	cebp q2	9.97e-05	0.0225	8	7.87	1
14	msigdb__immunological_signatures	gse9988 low lps vs vehicle treated monocyte u..	3.46e-24	7.19e-21	38	16.6	4
14	msigdb__immunological_signatures	gse9988 anti trem1 vs anti trem1 and lps mono..	6.64e-24	1.32e-20	40	14.5	4
14	msigdb__immunological_signatures	gse9988 anti trem1 vs low lps monocyte dn	2.54e-22	4e-19	40	12.5	3
14	msigdb__immunological_signatures	gse9988 anti trem1 vs lps monocyte dn	3.41e-22	5.19e-19	41	11.8	2
14	msigdb__immunological_signatures	gse36888 untreated vs il2 treated stat5 ab kn..	7.74e-22	1.01e-18	34	16.5	5

Table 1: The top (lowest p-value) genesets found (uniquely) in each cluster

14 With-in cluster comparison of conditions

Genes differentially expressed between the conditions within each cluster were identified. Full results are avaliable as a tab delimited text file.

Key parameters are:

- Conservation factor: None

	ncells_CTRL	ncells_STIM	n_de_genes
0	2026	2060	1026
1	1048	1610	322
2	811	875	302
3	445	639	525
4	515	543	870
5	346	461	365
6	305	322	508
7	275	290	489
8	290	221	1096
9	164	154	483
10	129	57	809
11	97	87	412
12	50	80	869
13	22	29	47
14	25	23	471

Table 2: summary of clusters by condition

14.1 Number of cells within each cluster

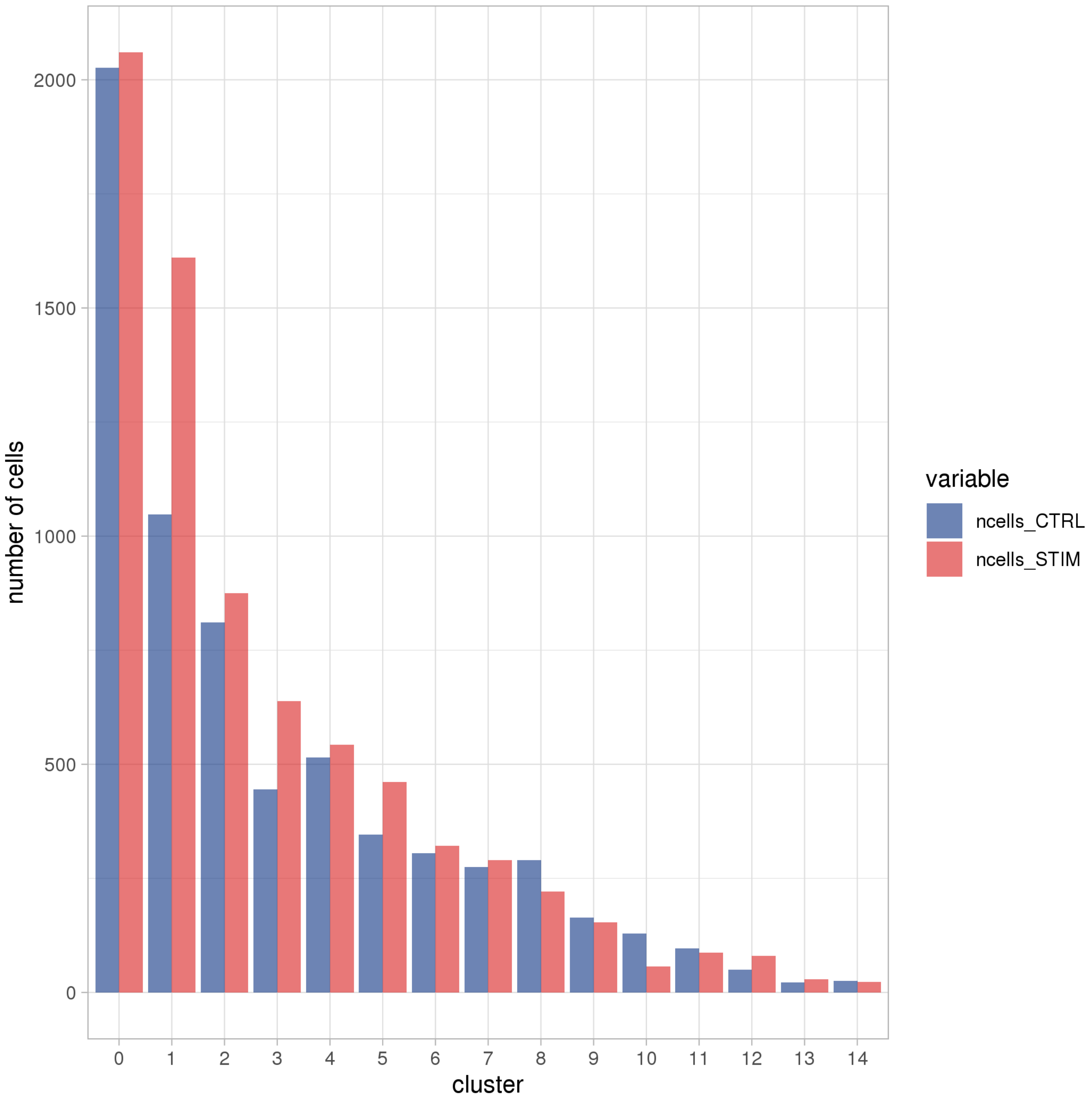


Figure 99: The numbers of cells of each condition found in the clusters

14.2 Summary of the top within-cluster differentially expressed genes

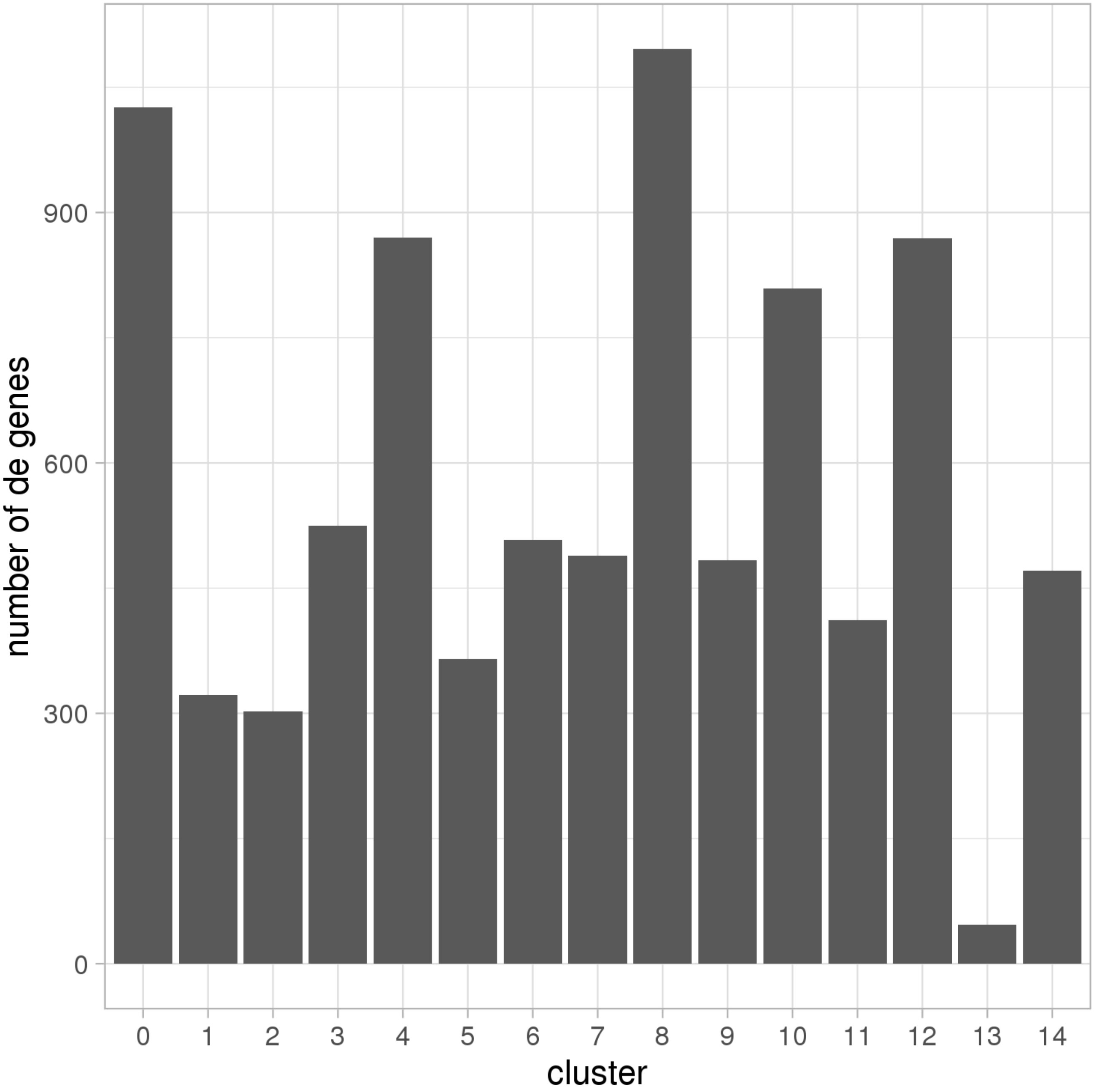


Figure 100: Numbers of genes differential expressed between the conditions within each clusters

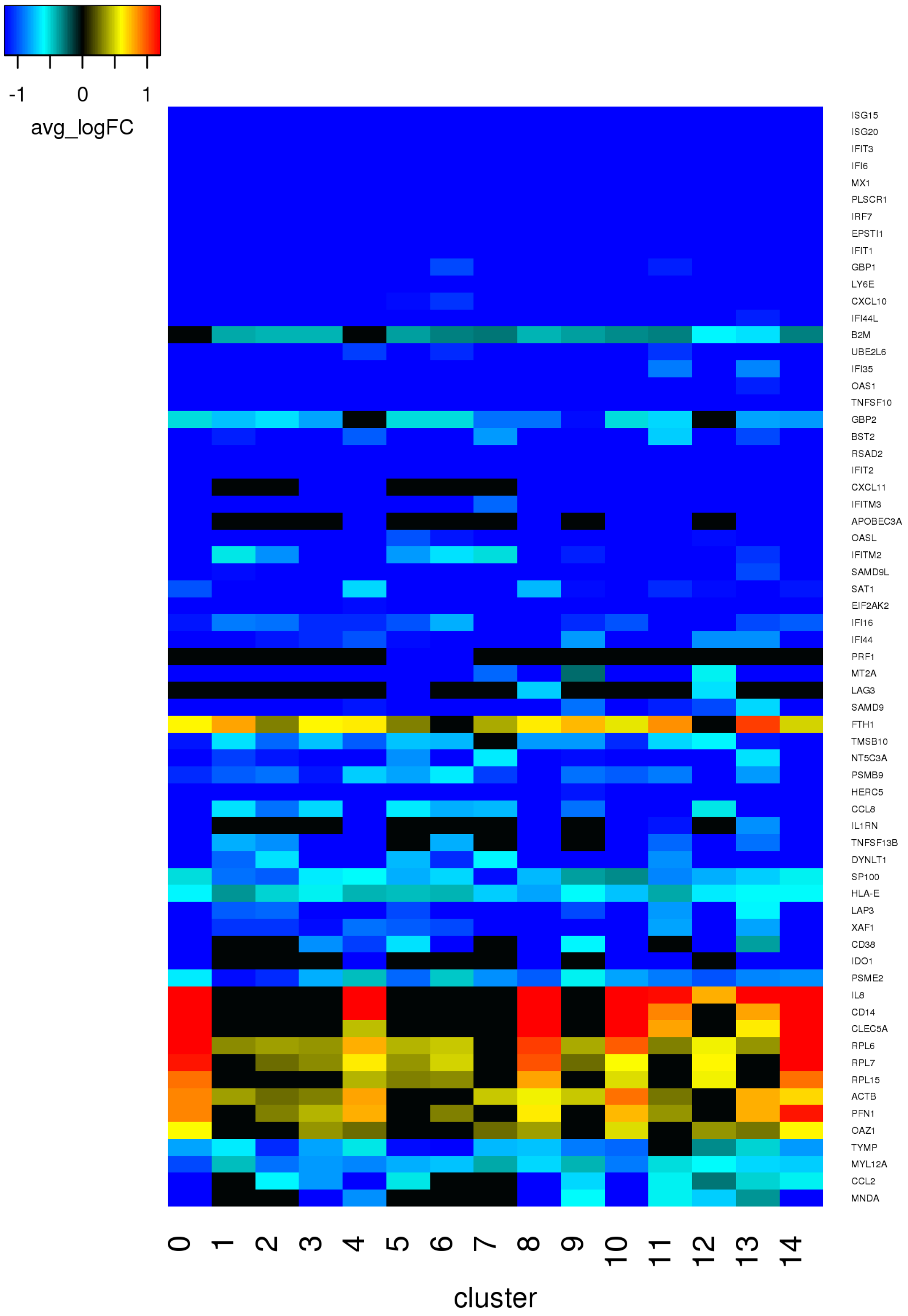


Figure 101: Genes differential expressed between the conditions within one or more clusters

14.3 Summary of differentially expressed genes per cluster

14.3.1 Summary of numbers of DE genes per-cluster

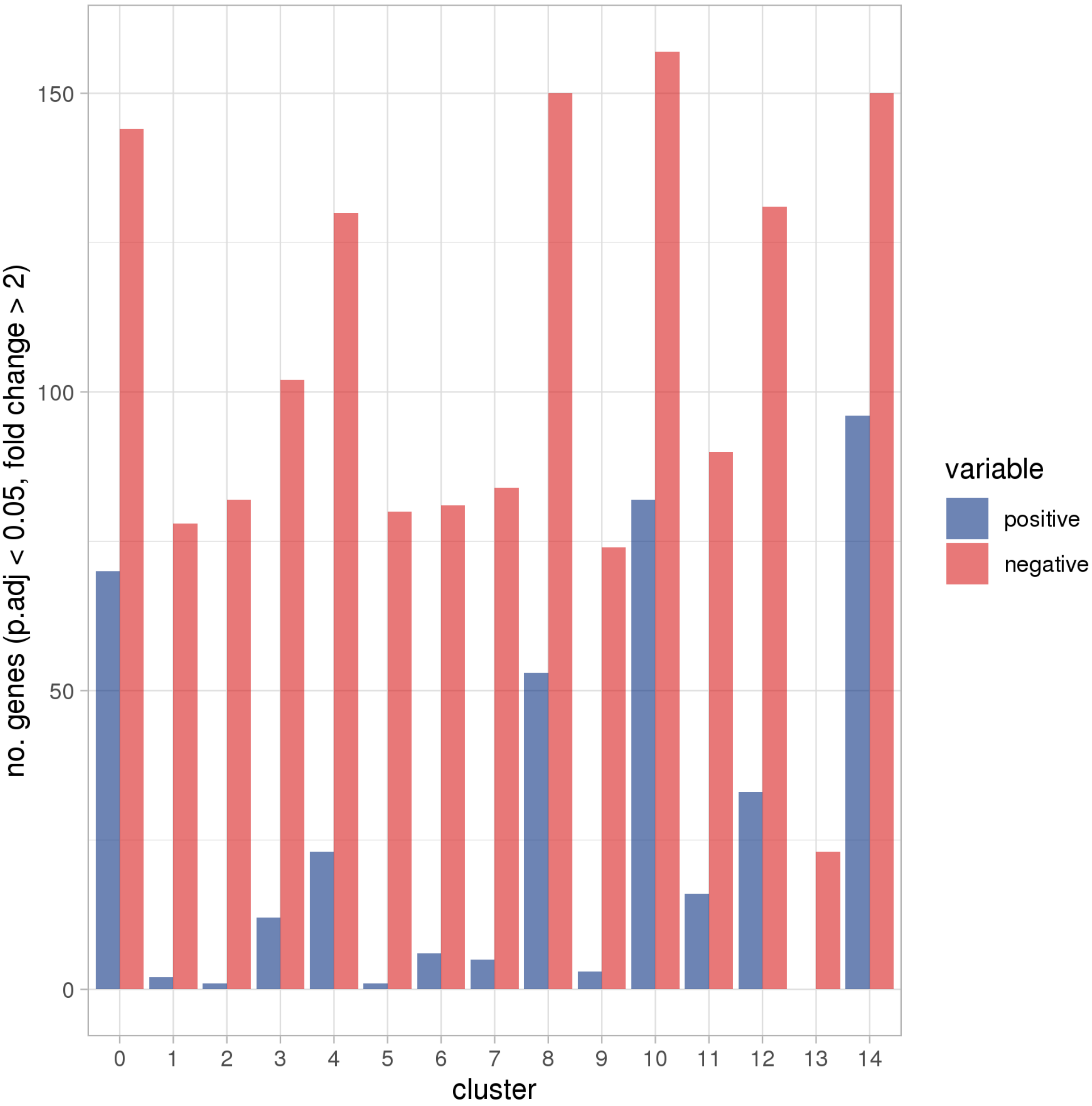


Figure 102: Numbers of differentially expressed genes (adjusted p-value < 0.05, fold change > 2) per cluster

14.4 Cluster 0: summary plots

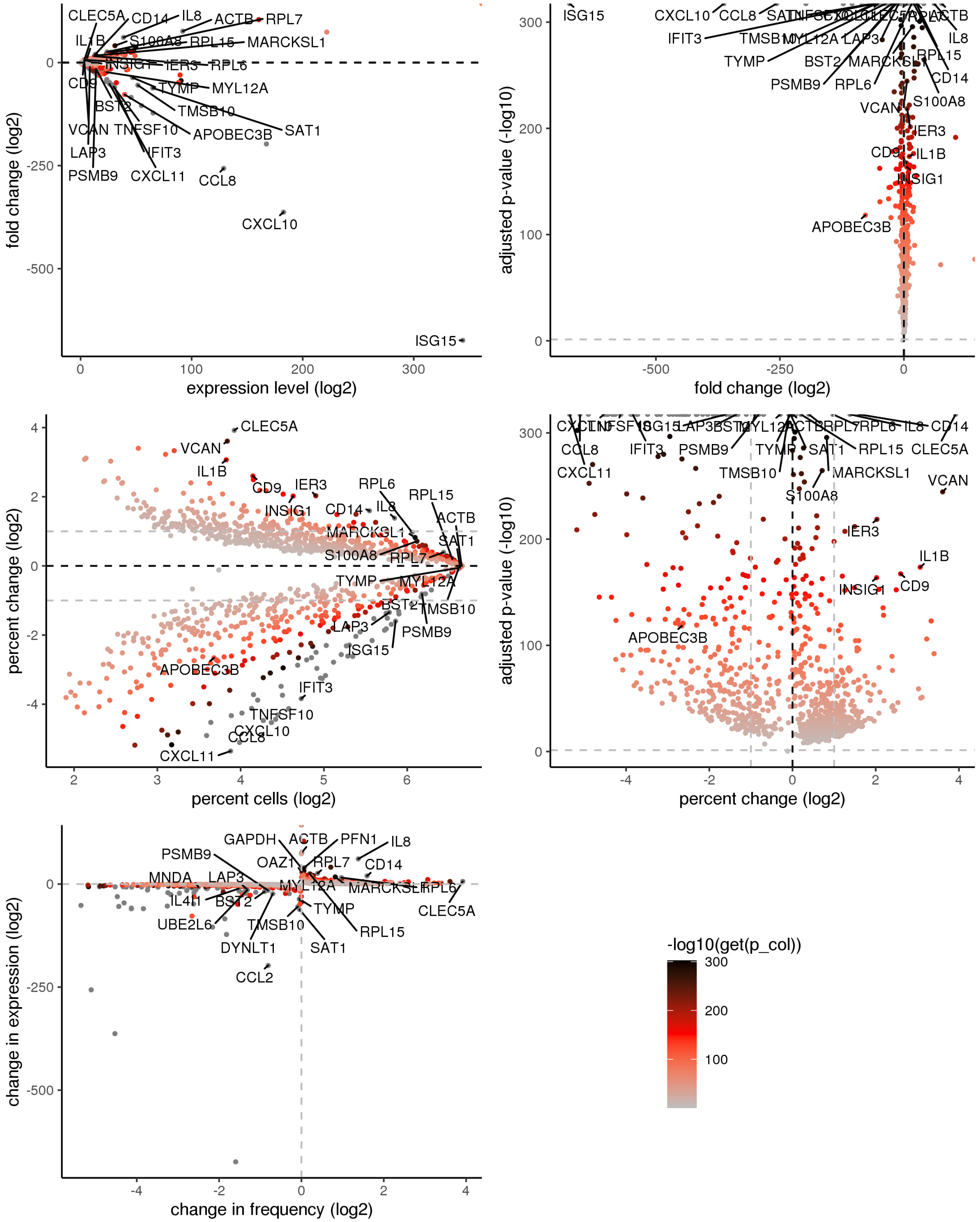
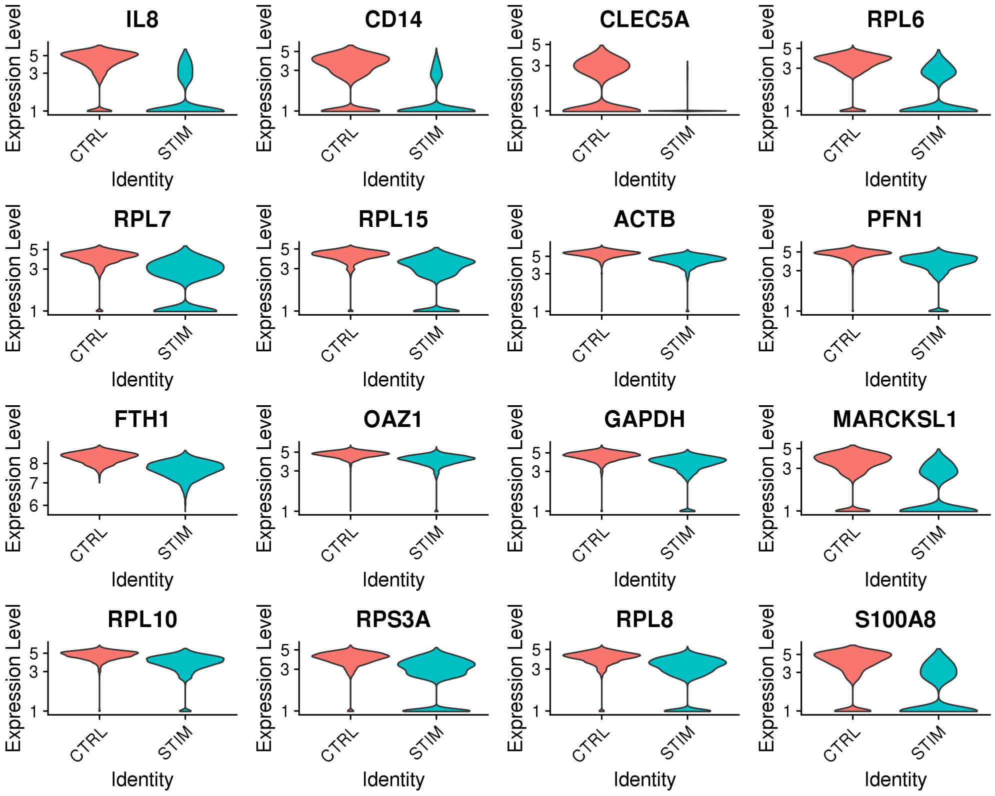
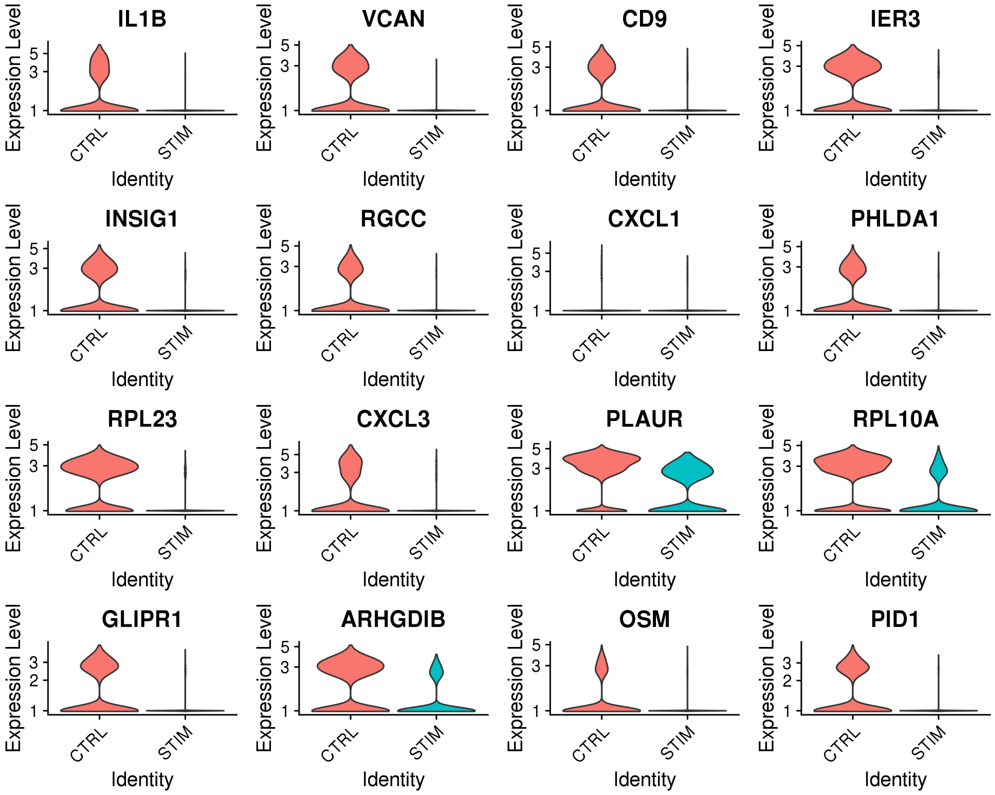


Figure 103: Differential expression summary plots for cluster 0

14.5 Cluster 0 violin plots: positively differentially expressed genes

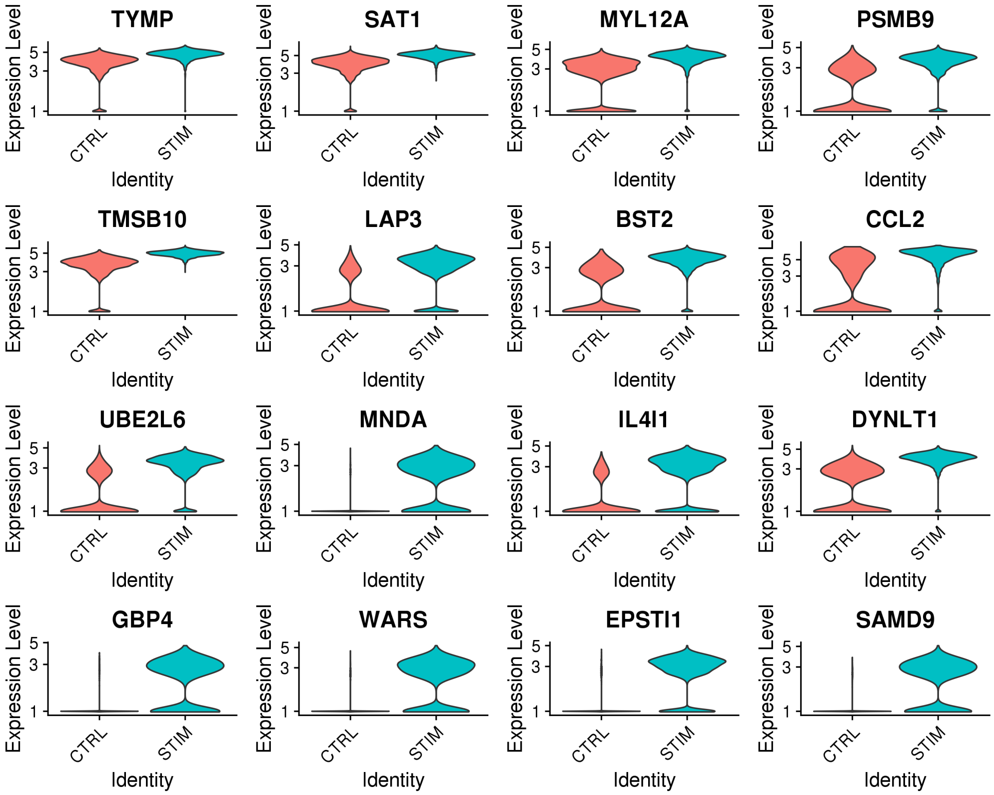


(a) Top positively differentially expressed genes ordered by p-value, cluster: 0

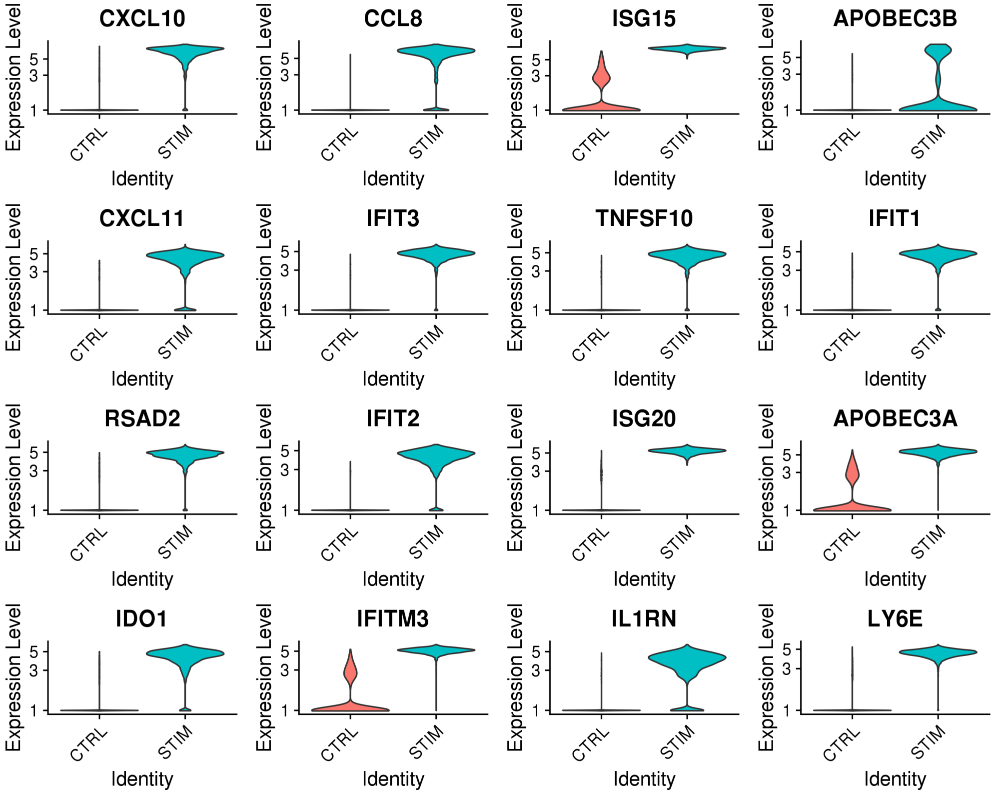


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 0

14.6 Cluster 0 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 0



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 0

14.7 Cluster 1: summary plots

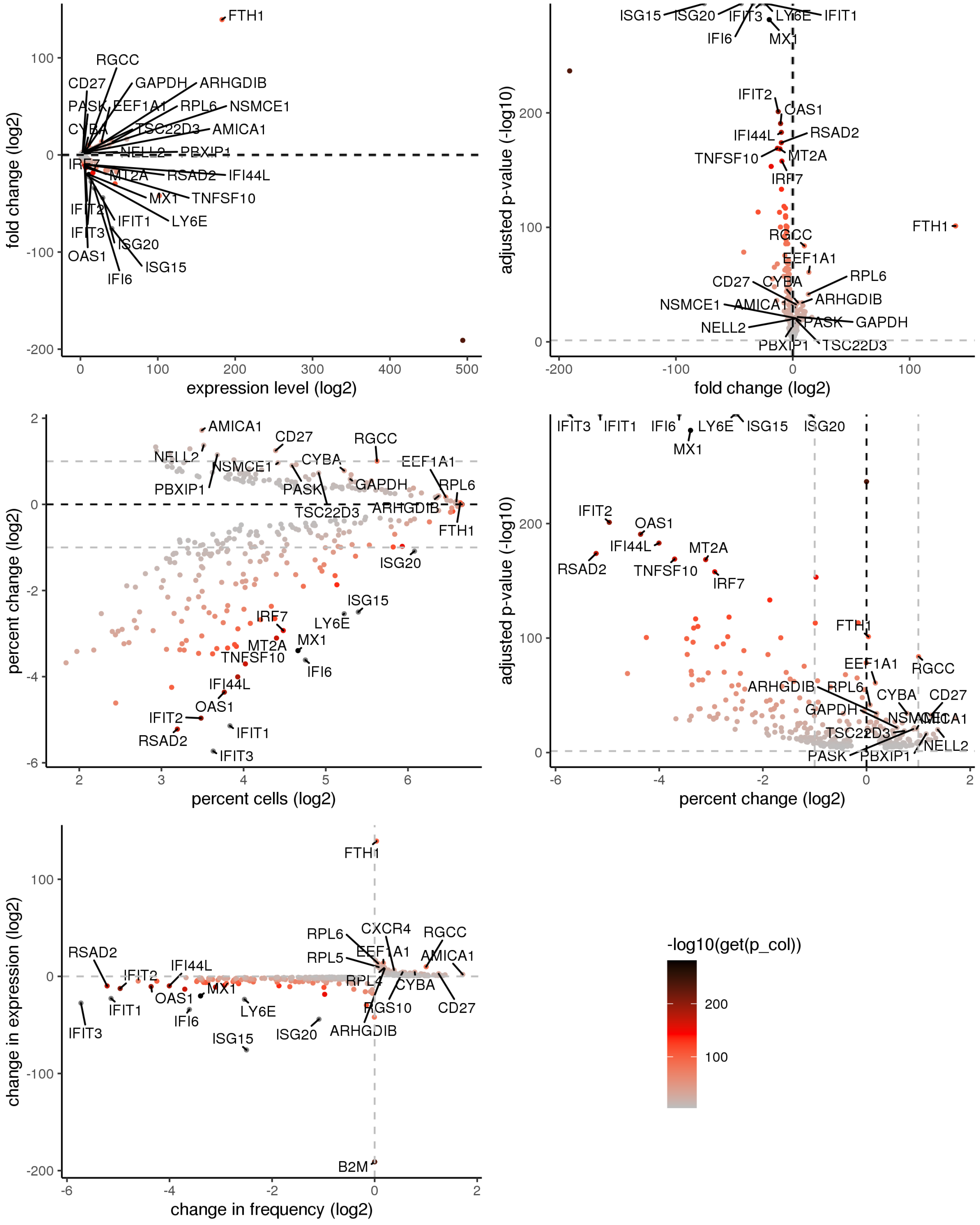
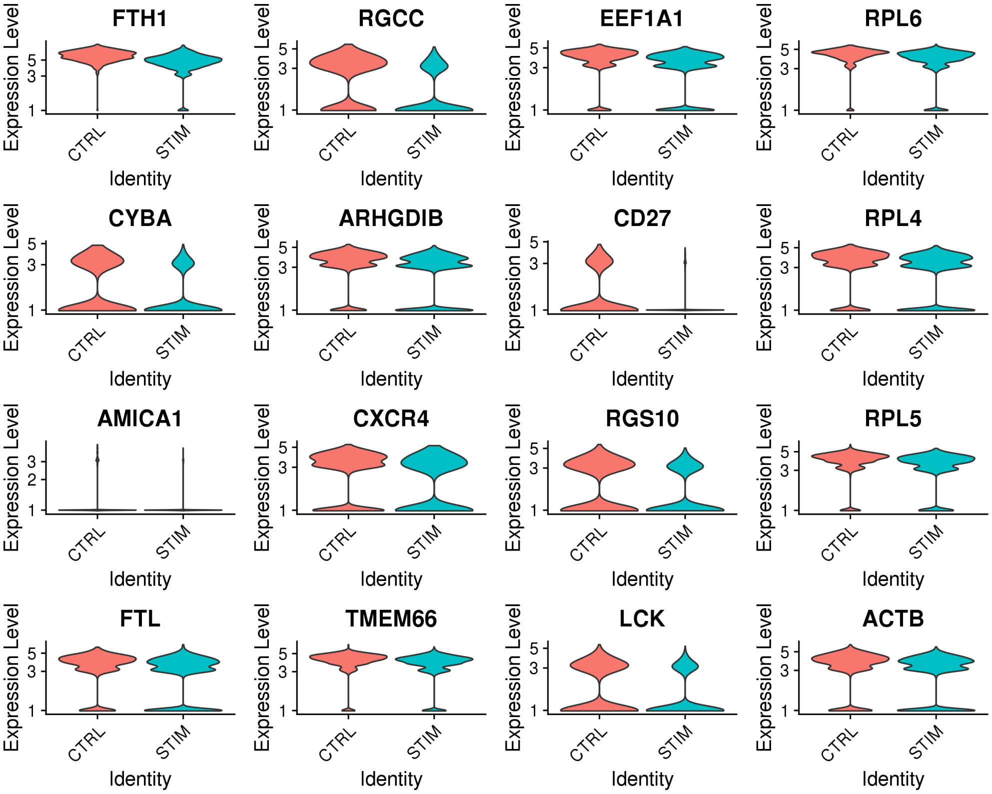
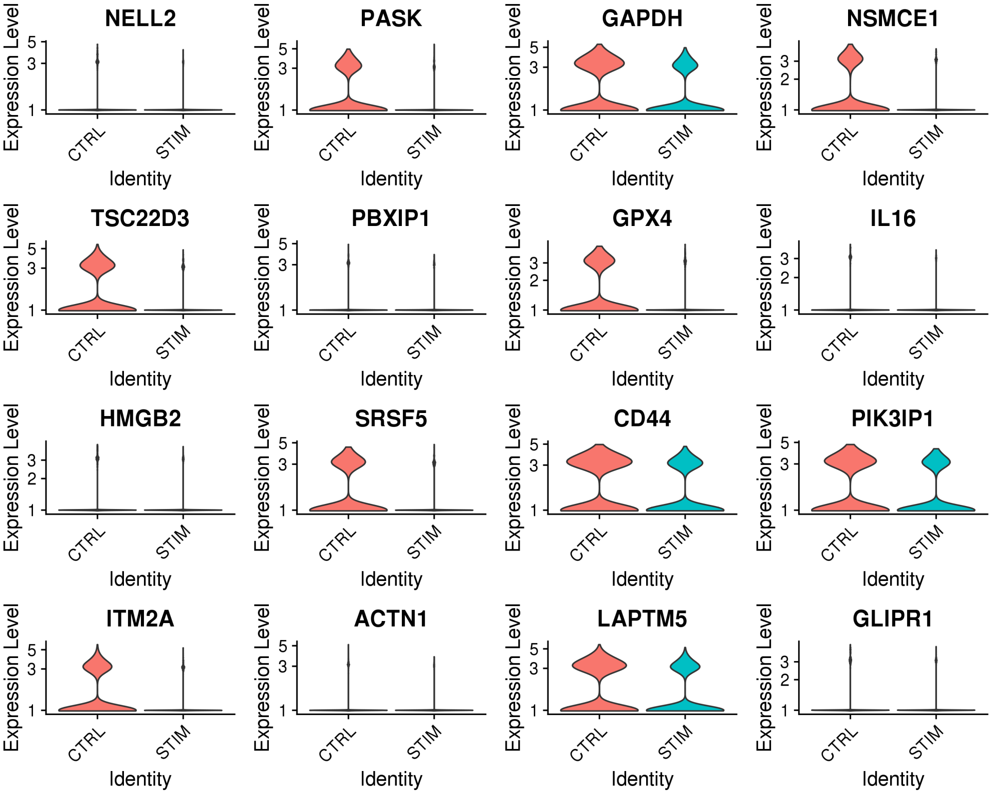


Figure 106: Differential expression summary plots for cluster 1

14.8 Cluster 1 violin plots: positively differentially expressed genes

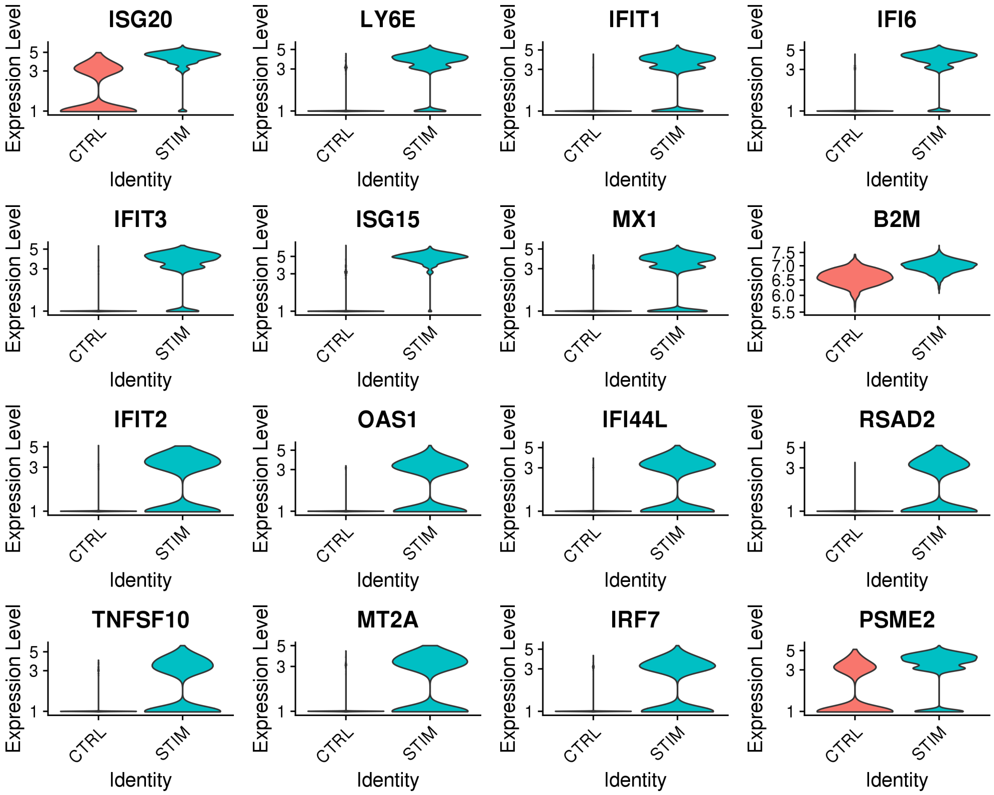


(a) Top positively differentially expressed genes ordered by p-value, cluster: 1

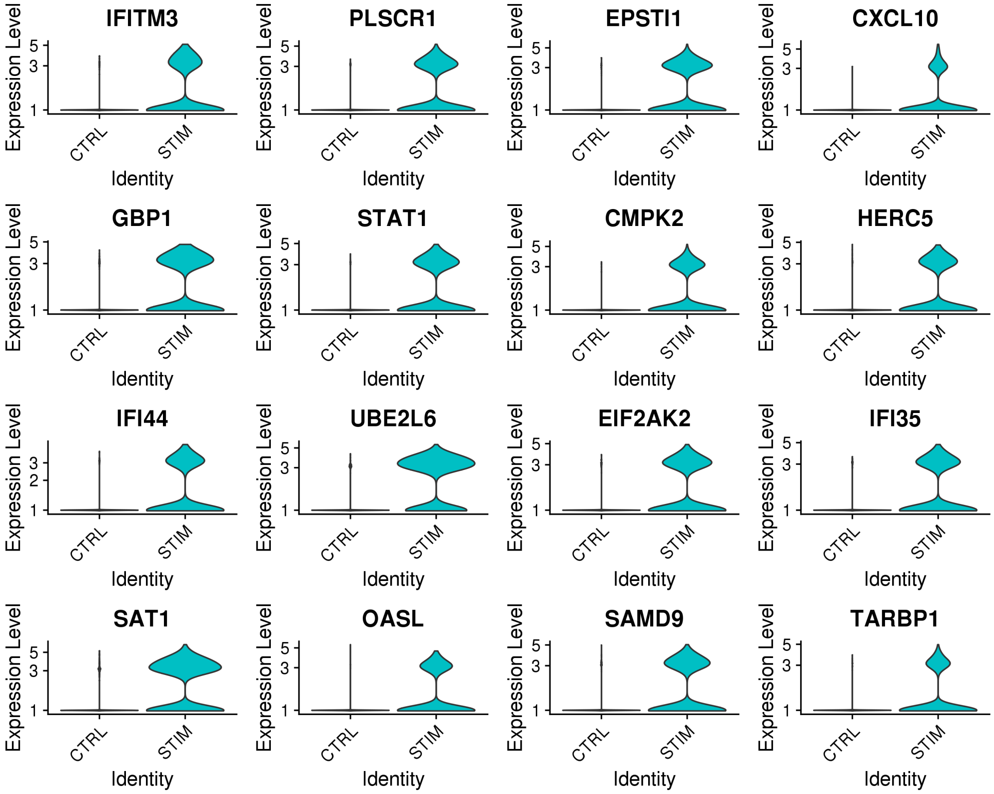


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 1

14.9 Cluster 1 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 1



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 1

14.10 Cluster 2: summary plots

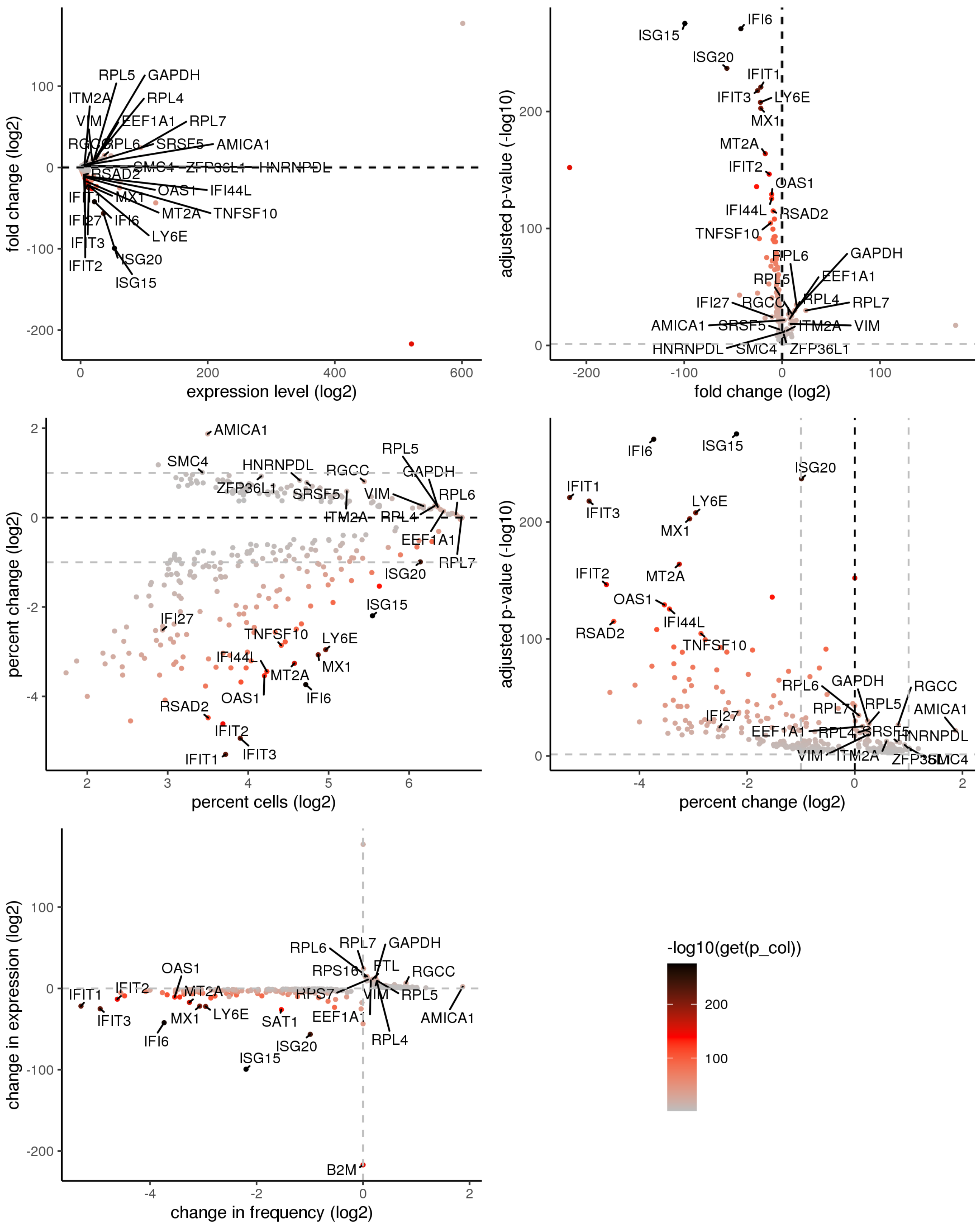
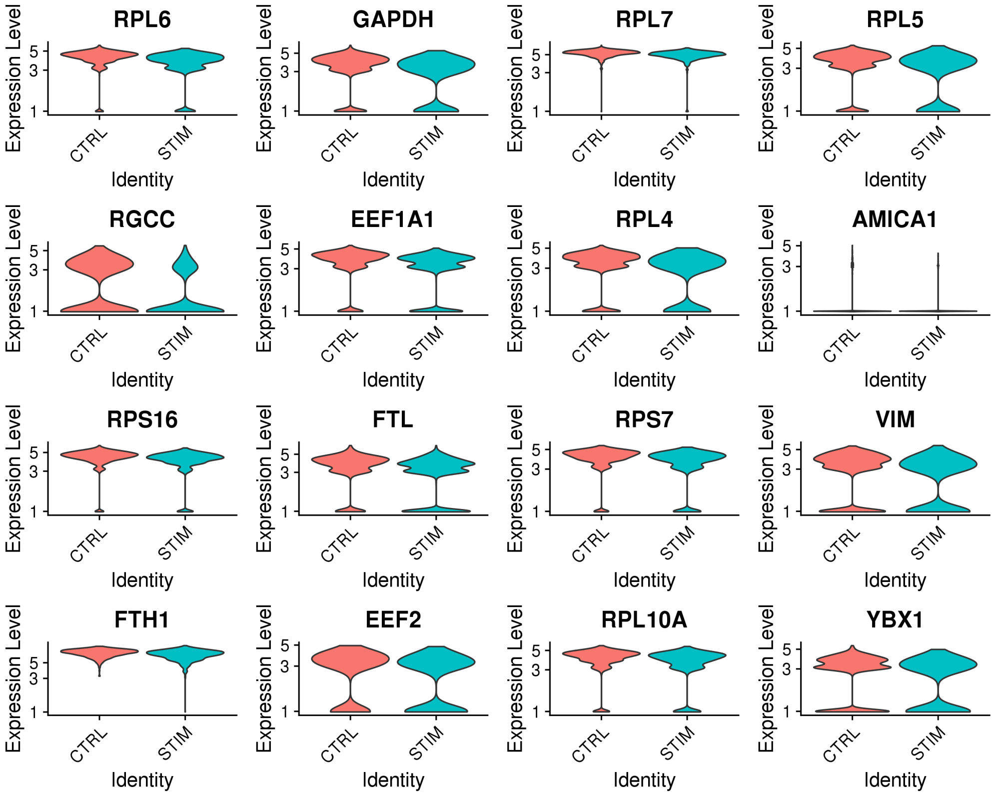
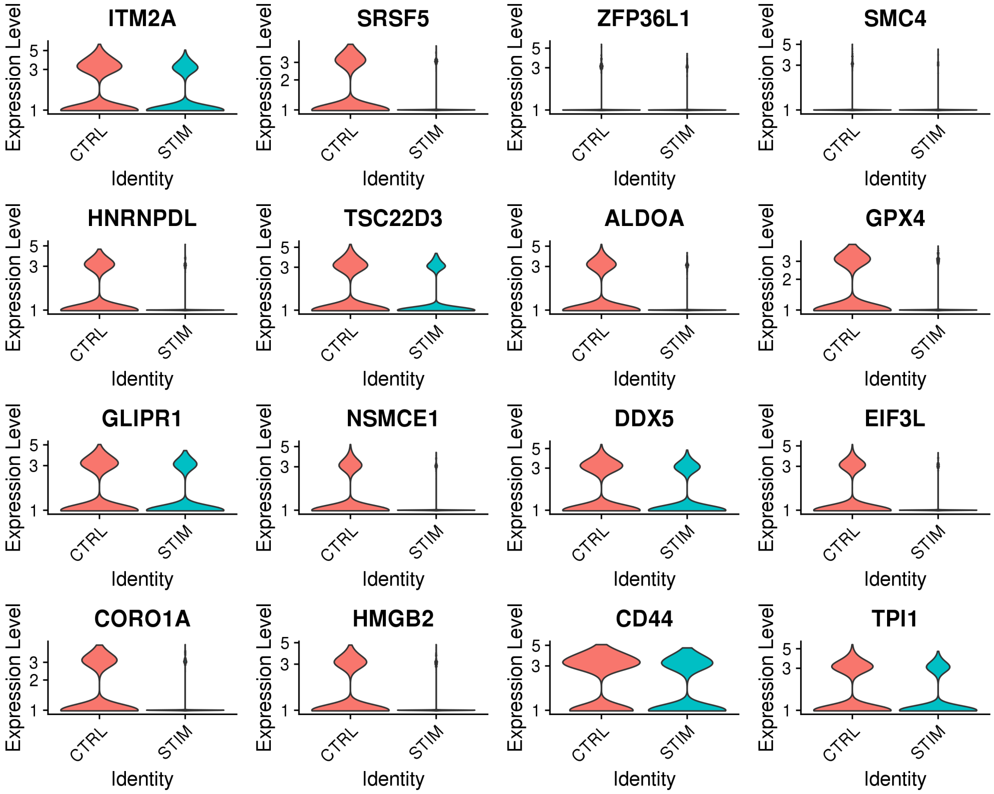


Figure 109: Differential expression summary plots for cluster 2

14.11 Cluster 2 violin plots: positively differentially expressed genes

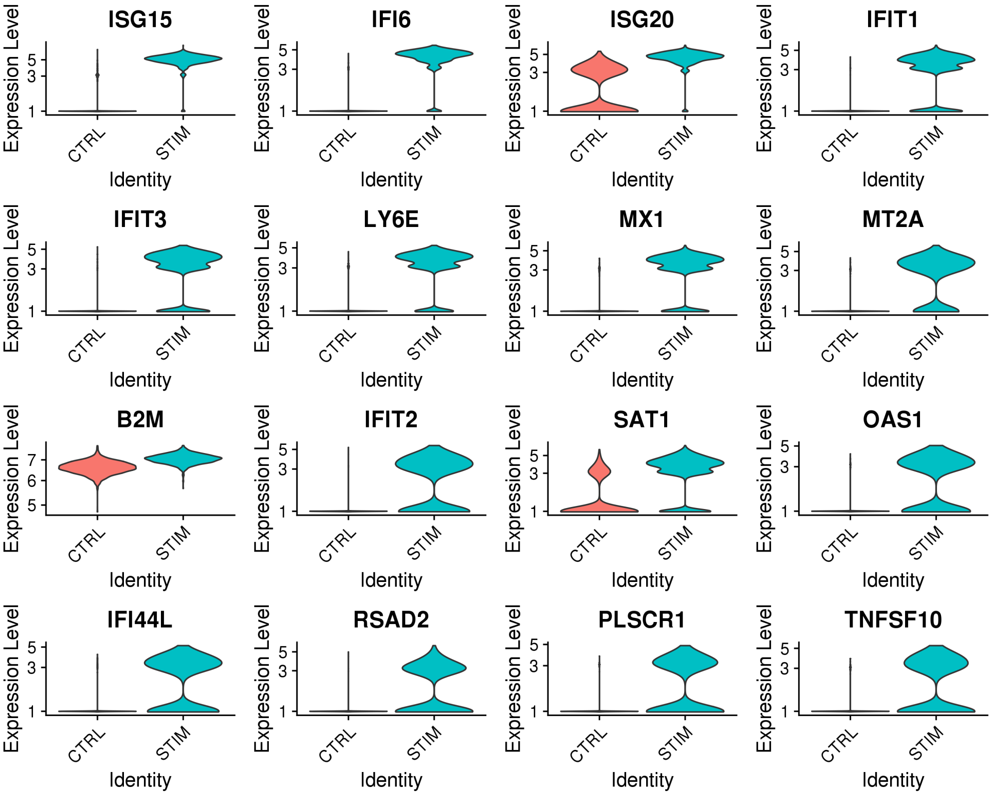


(a) Top positively differentially expressed genes ordered by p-value, cluster: 2

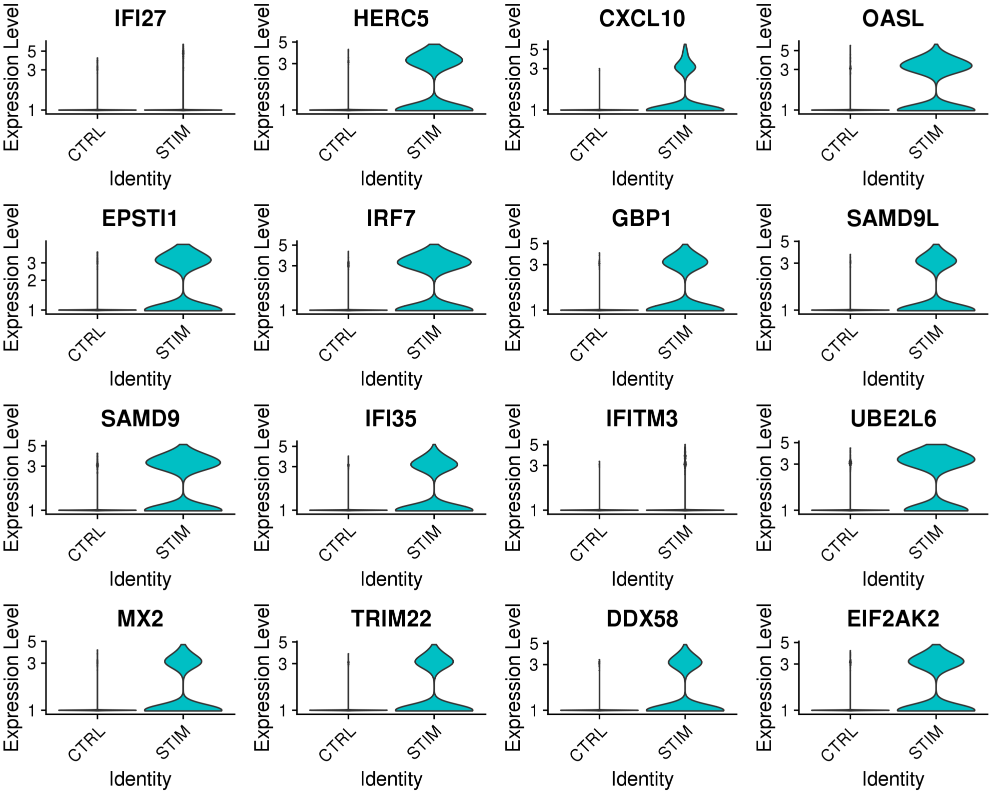


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 2

14.12 Cluster 2 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 2



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 2

14.13 Cluster 3: summary plots

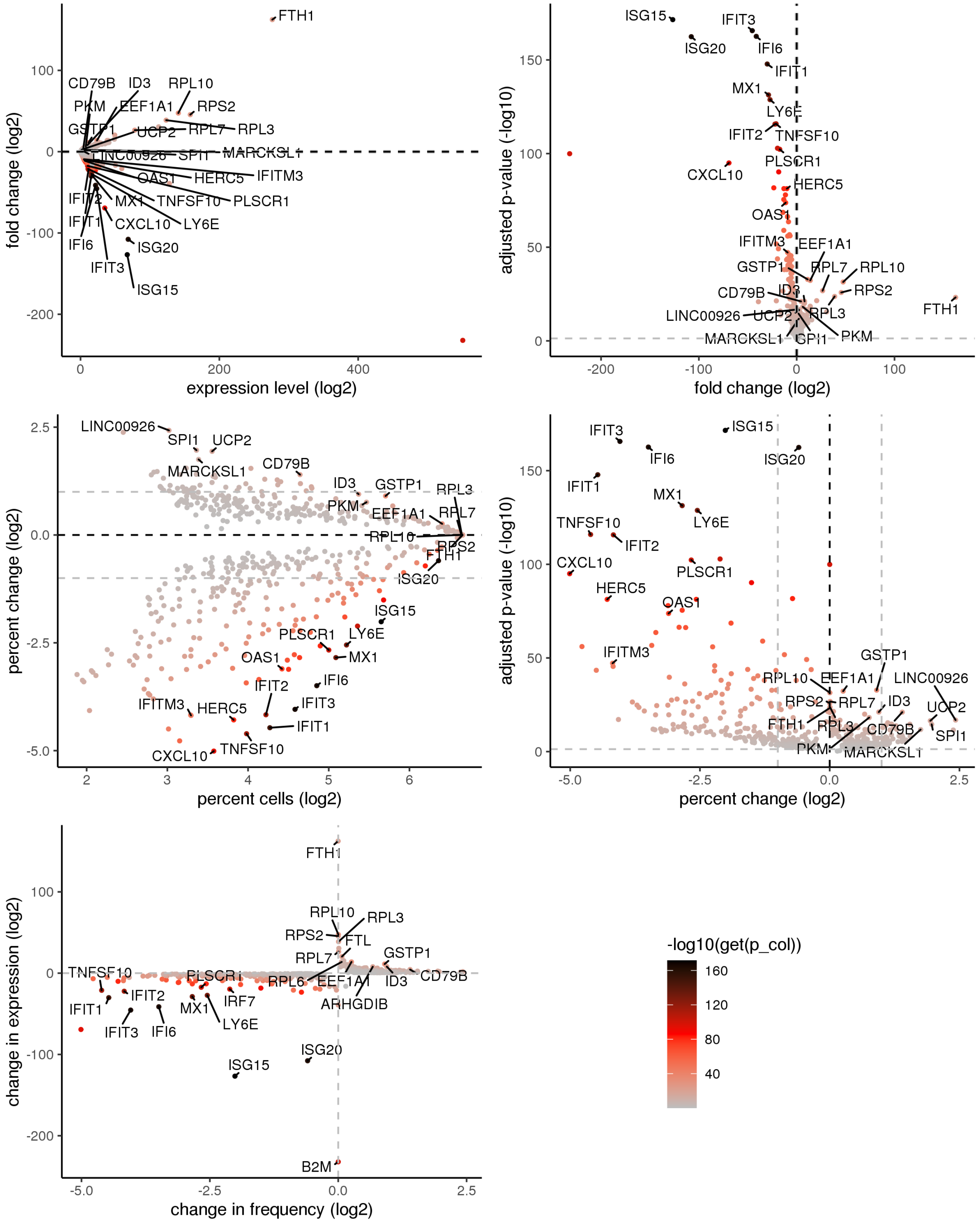
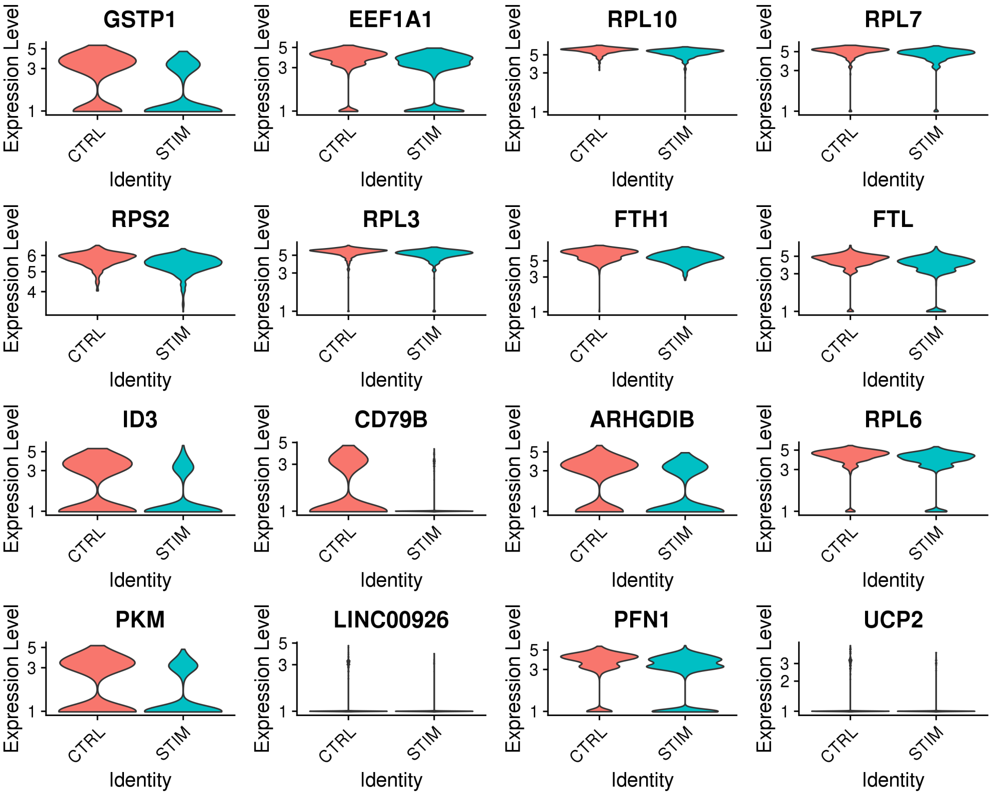
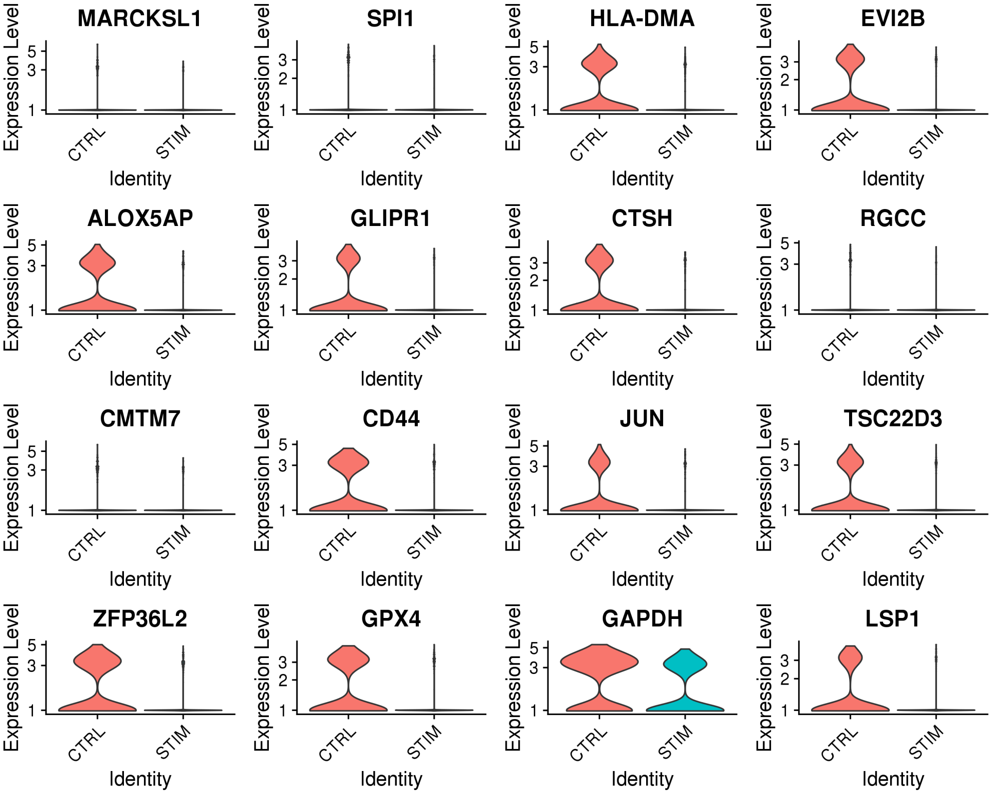


Figure 112: Differential expression summary plots for cluster 3

14.14 Cluster 3 violin plots: positively differentially expressed genes

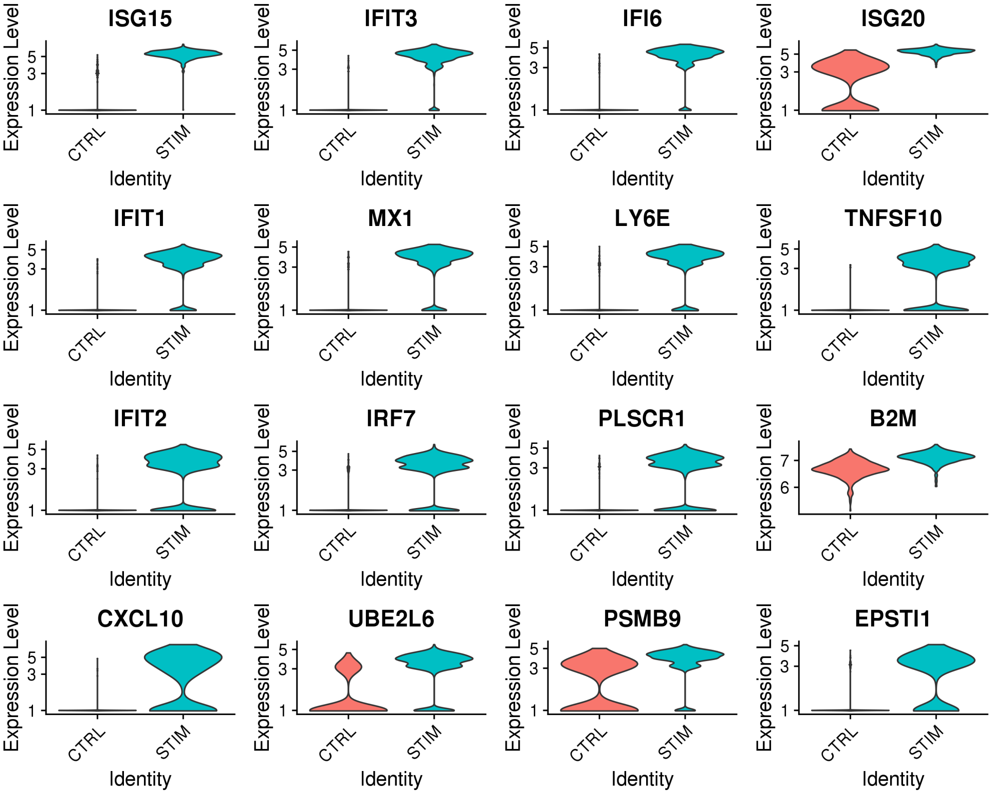


(a) Top positively differentially expressed genes ordered by p-value, cluster: 3

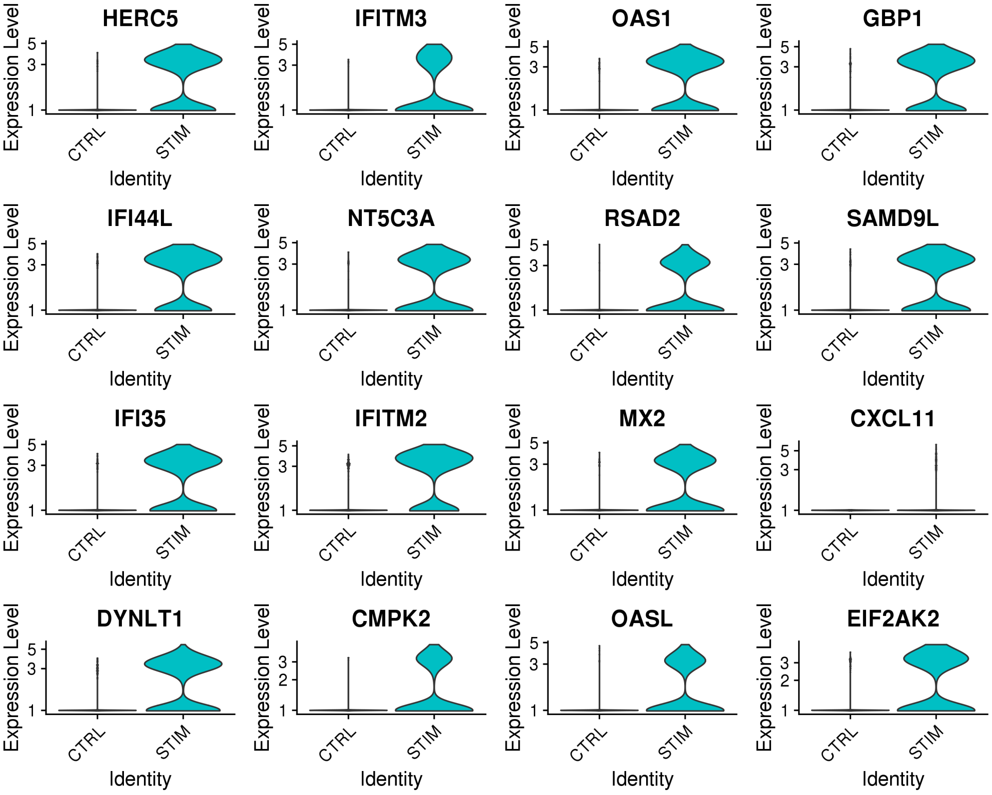


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 3

14.15 Cluster 3 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 3



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 3

14.16 Cluster 4: summary plots

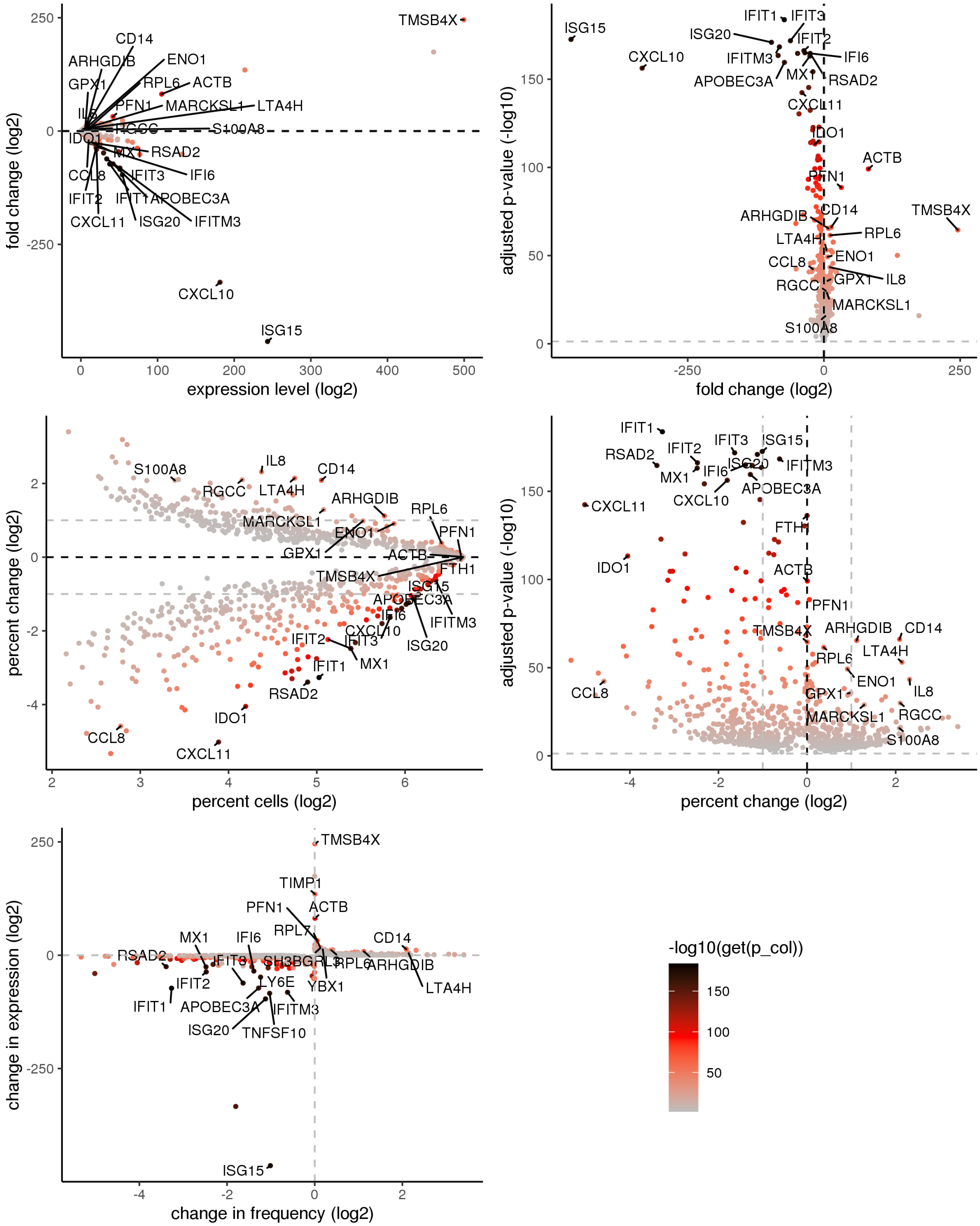
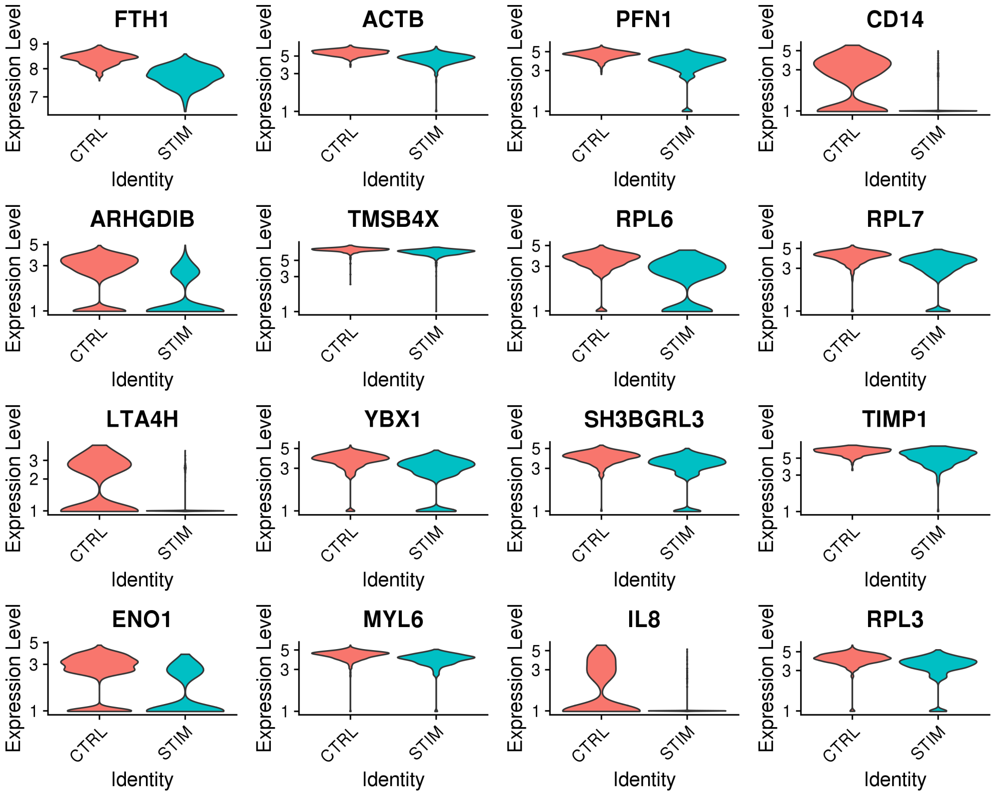
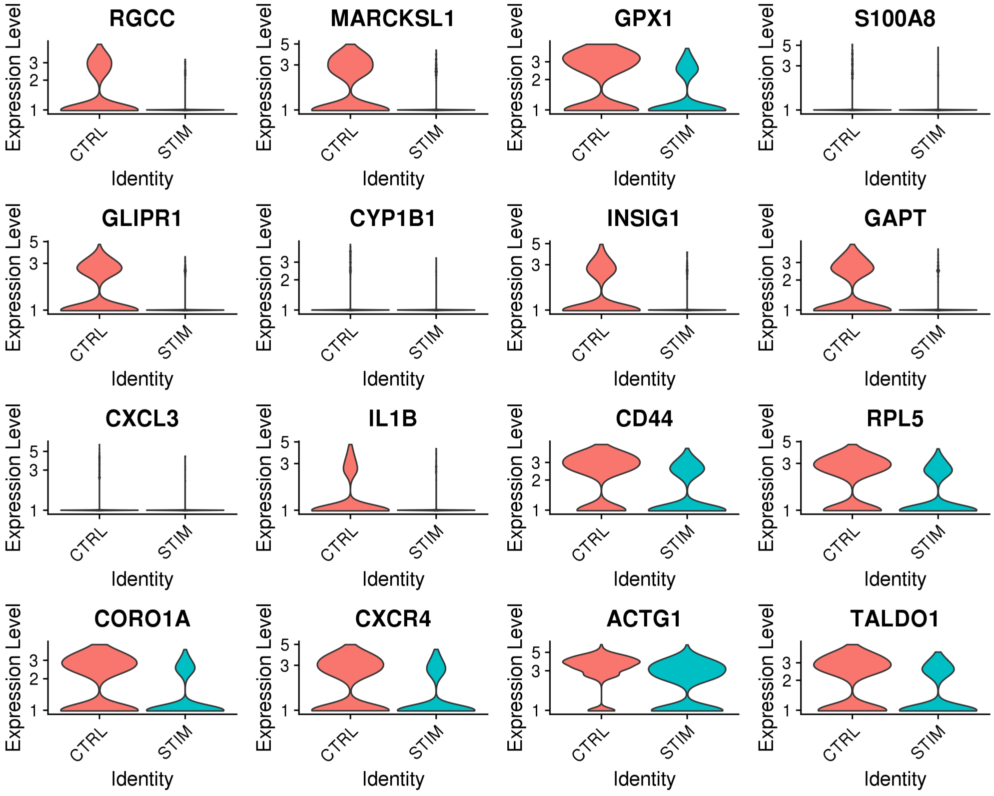


Figure 115: Differential expression summary plots for cluster 4

14.17 Cluster 4 violin plots: positively differentially expressed genes

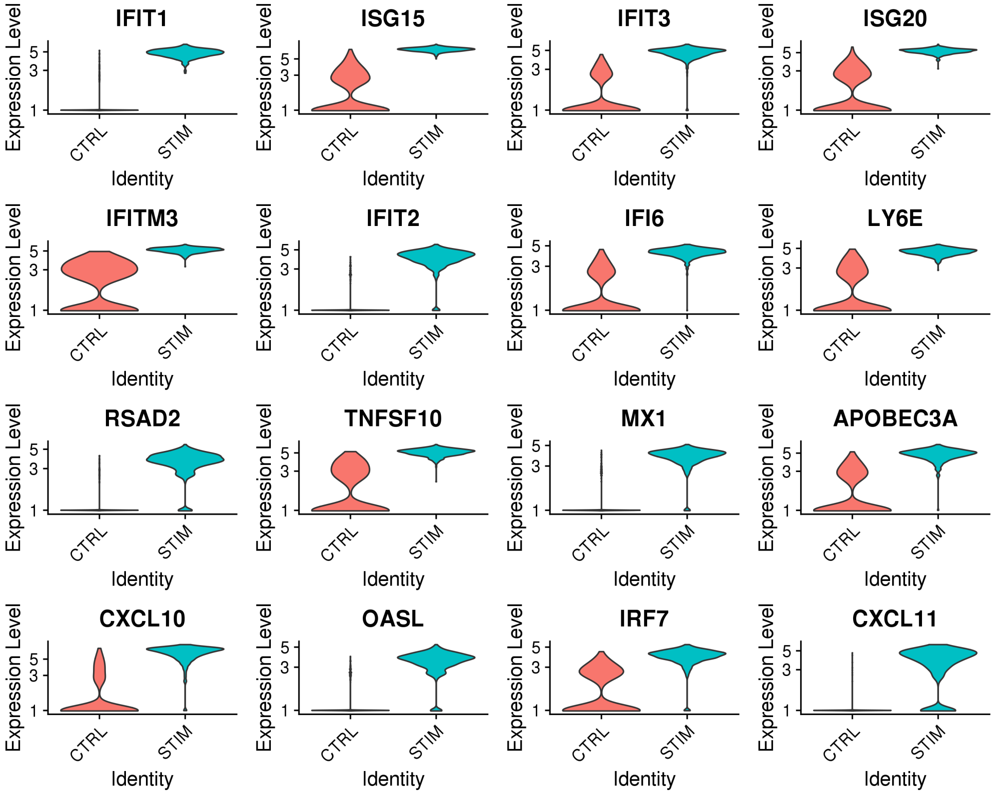


(a) Top positively differentially expressed genes ordered by p-value, cluster: 4

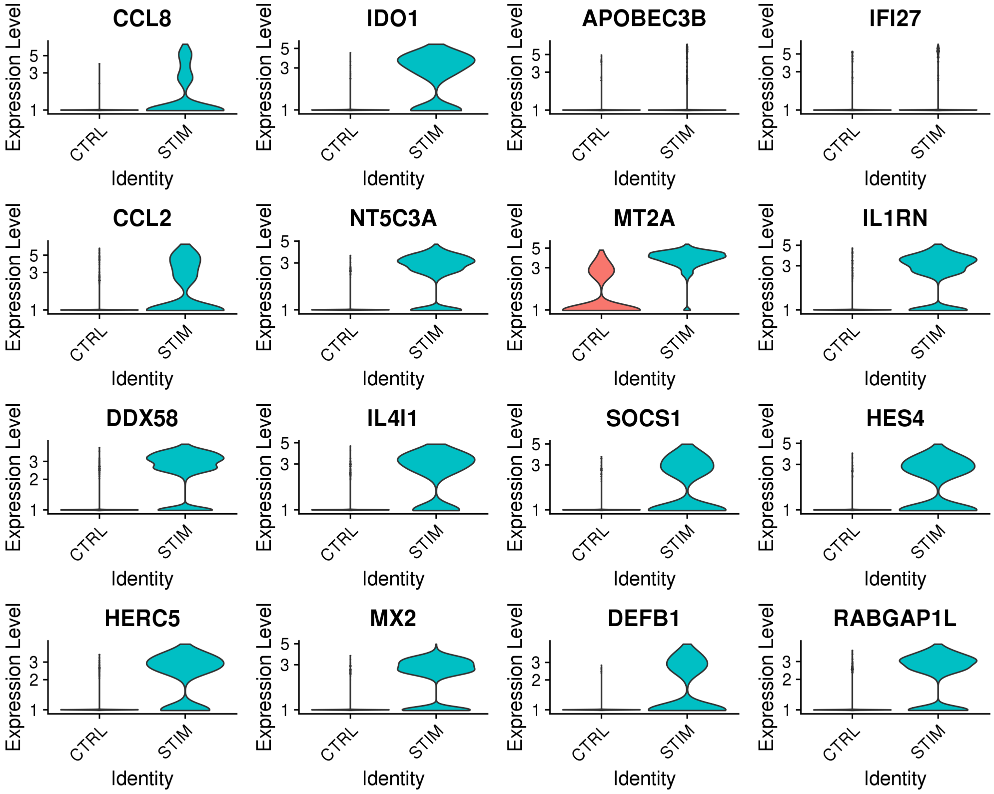


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 4

14.18 Cluster 4 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 4



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 4

14.19 Cluster 5: summary plots

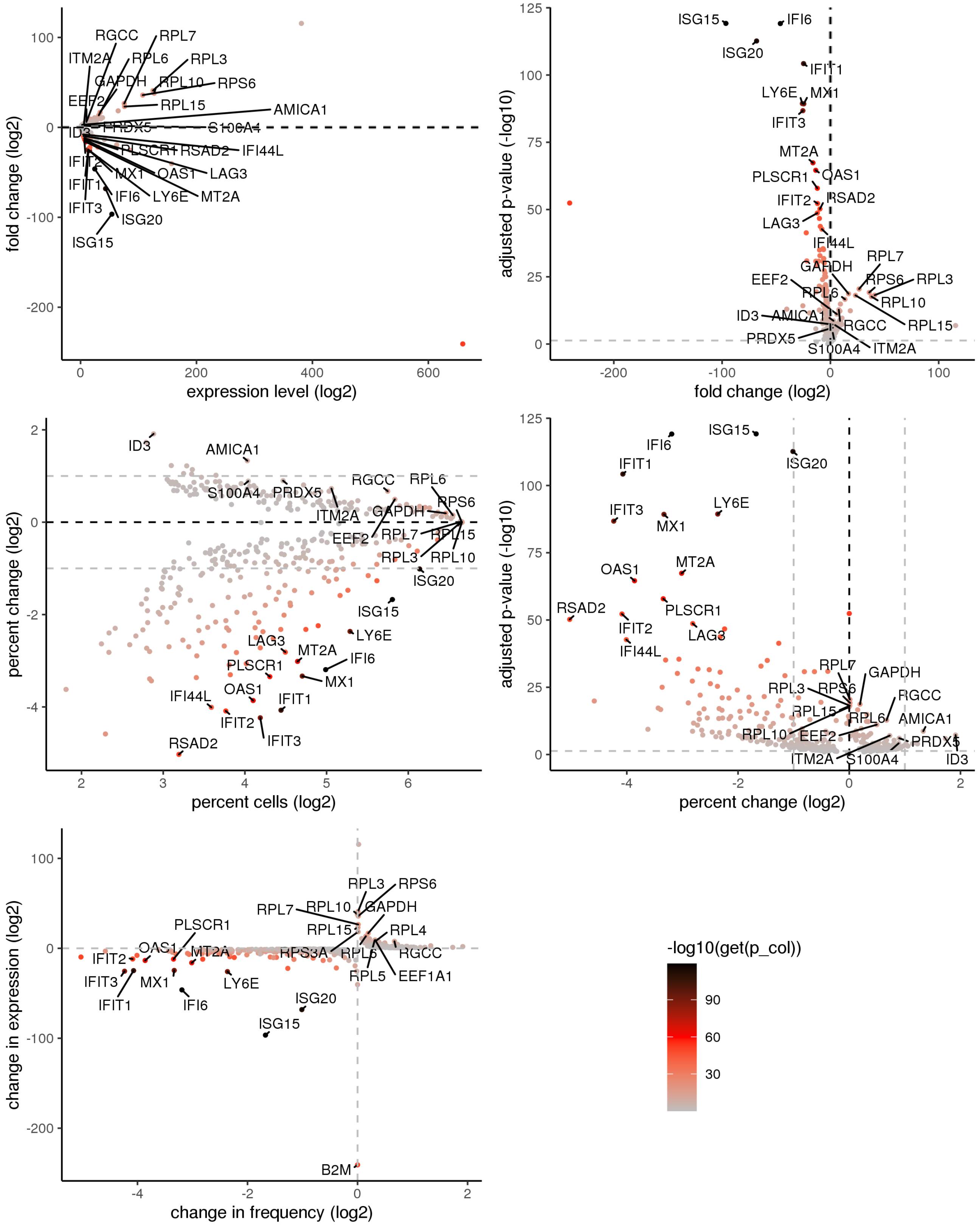
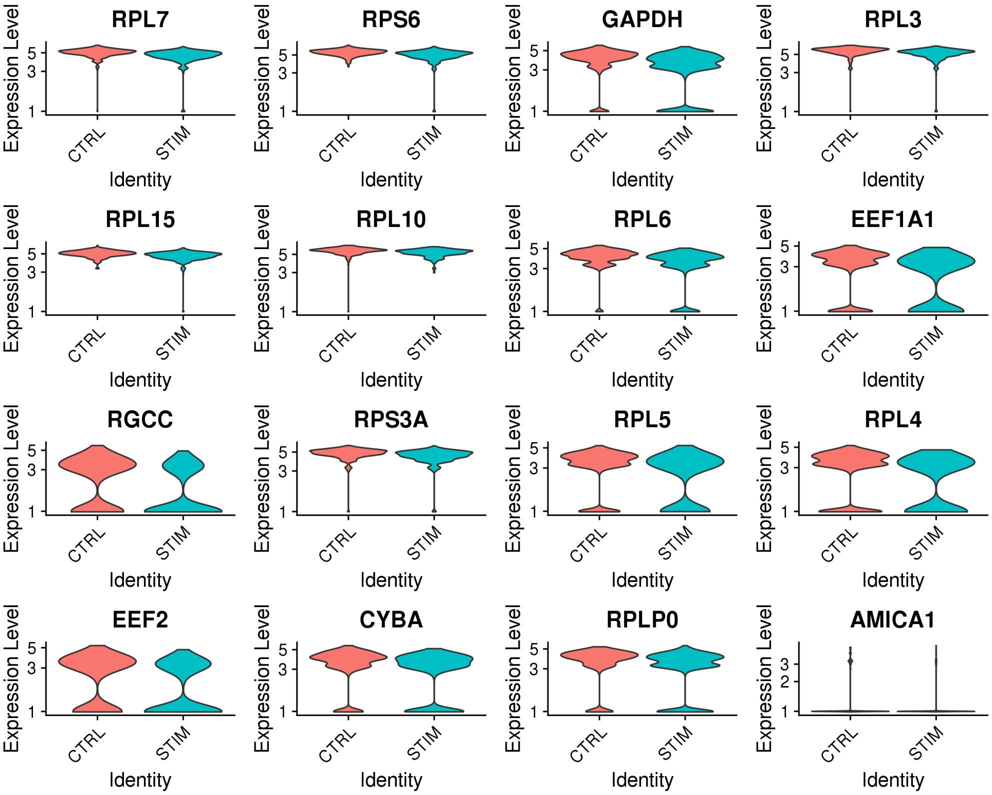
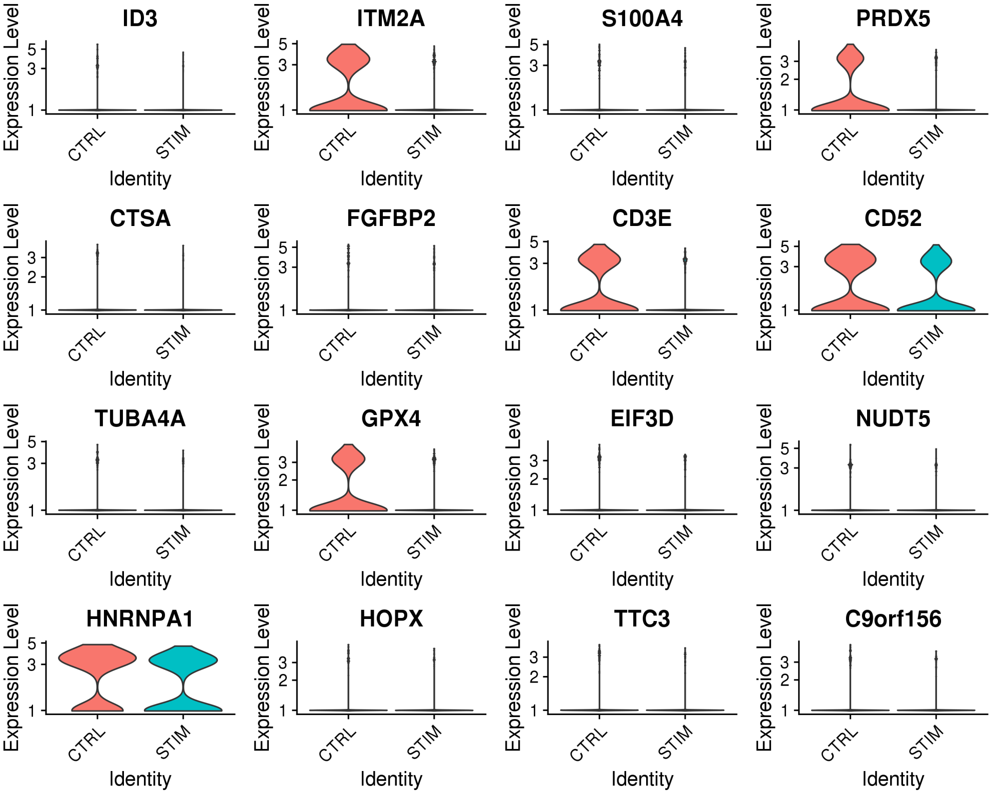


Figure 118: Differential expression summary plots for cluster 5

14.20 Cluster 5 violin plots: positively differentially expressed genes

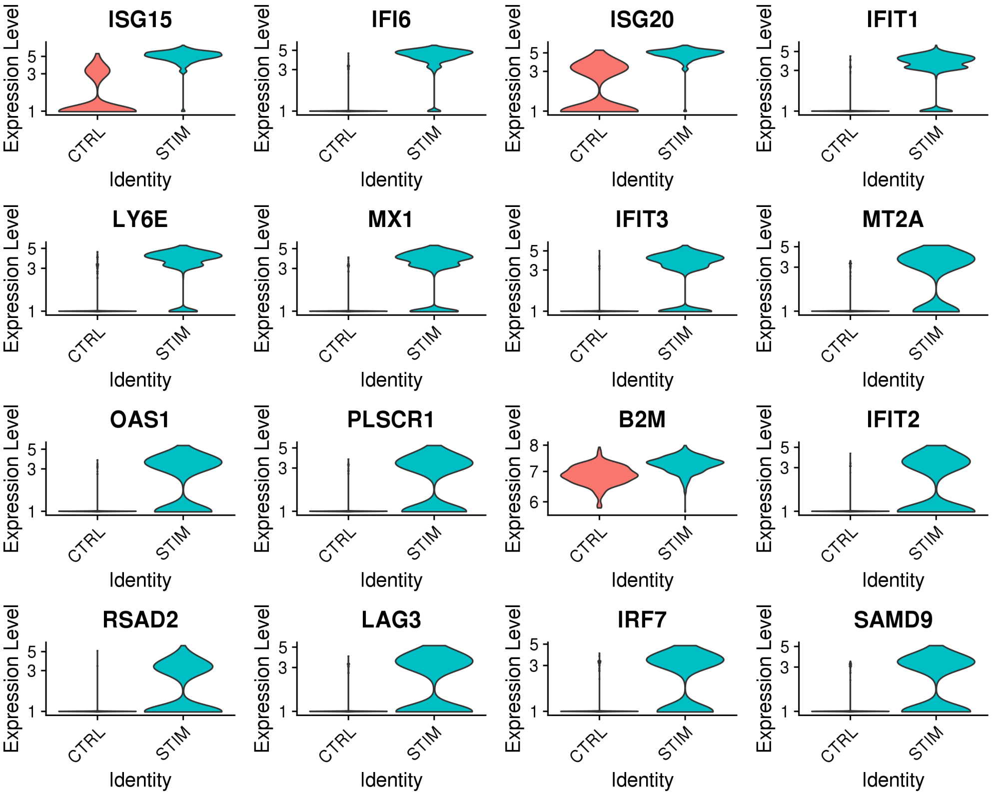


(a) Top positively differentially expressed genes ordered by p-value, cluster: 5

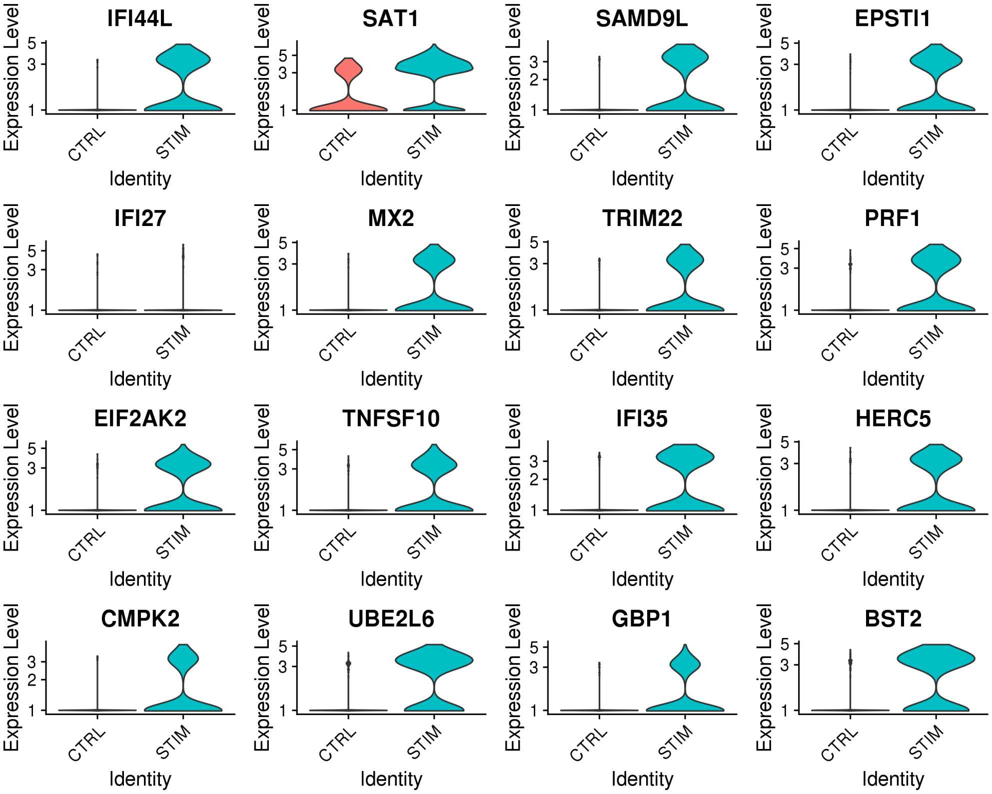


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 5

14.21 Cluster 5 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 5



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 5

14.22 Cluster 6: summary plots

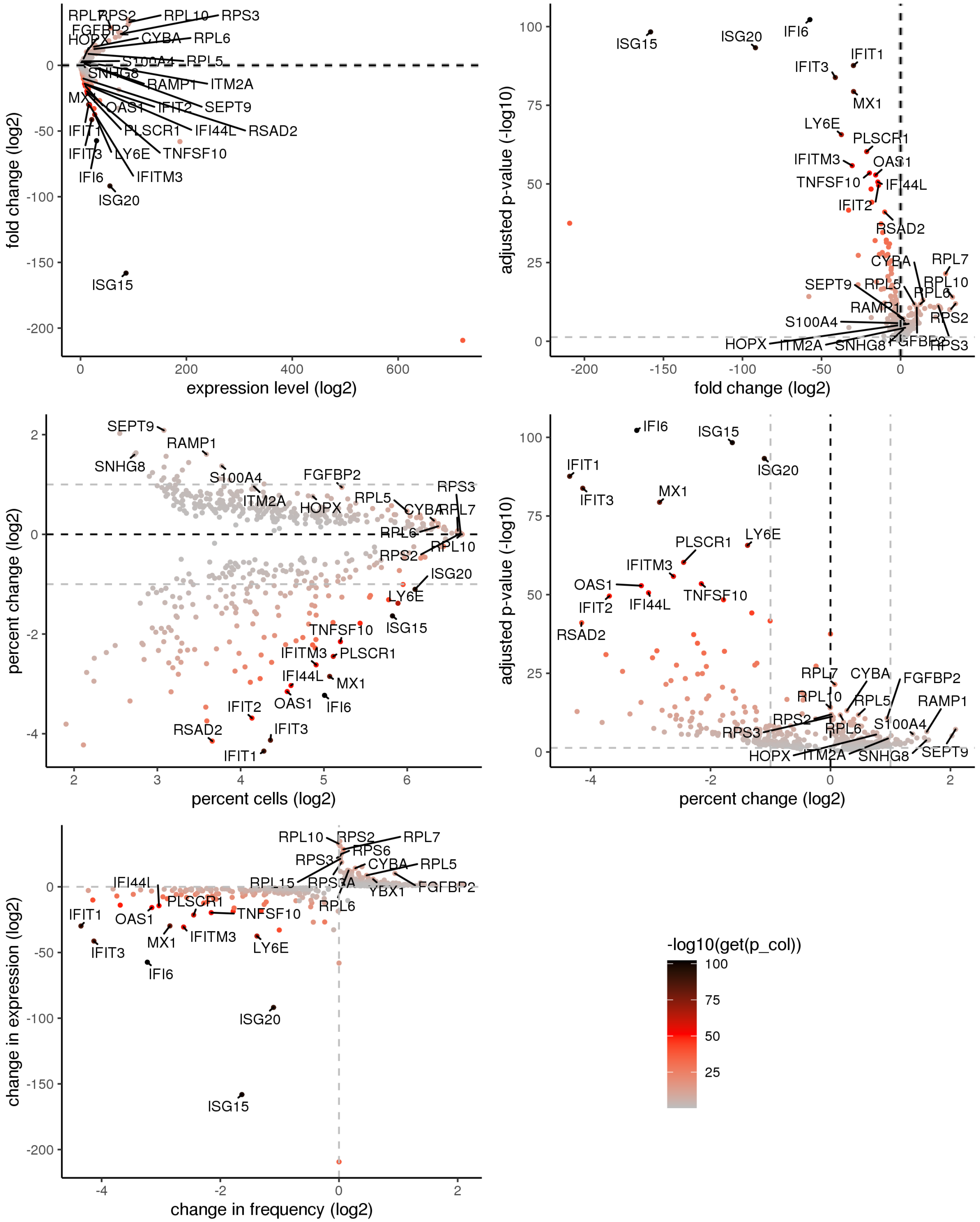
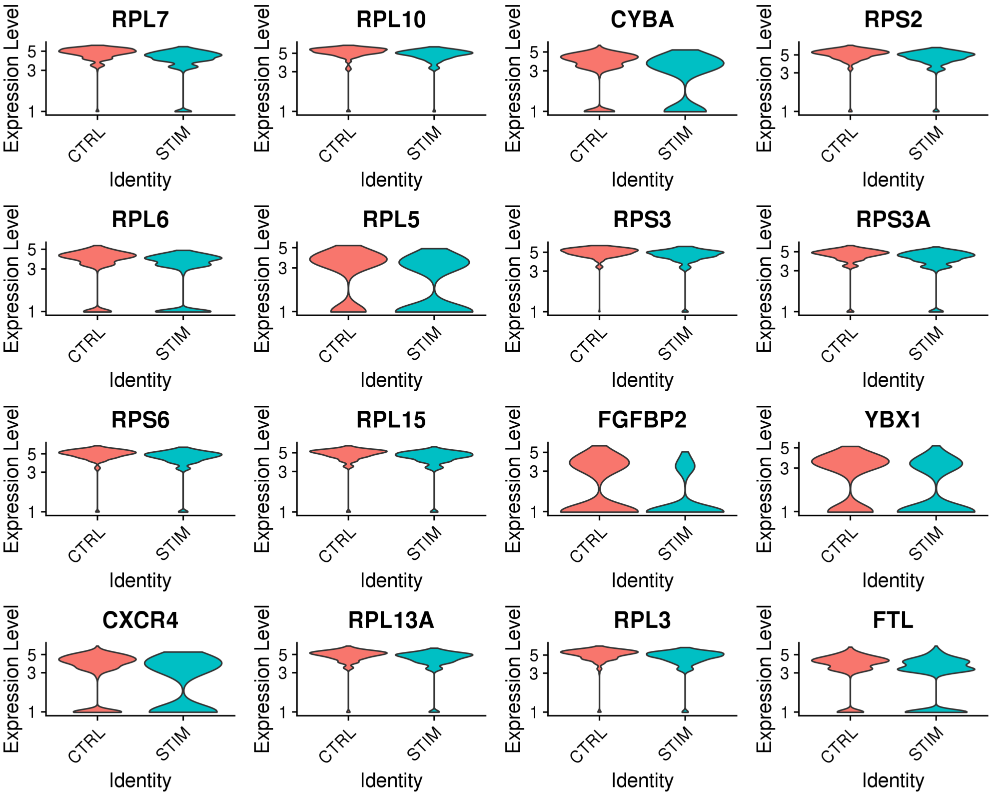
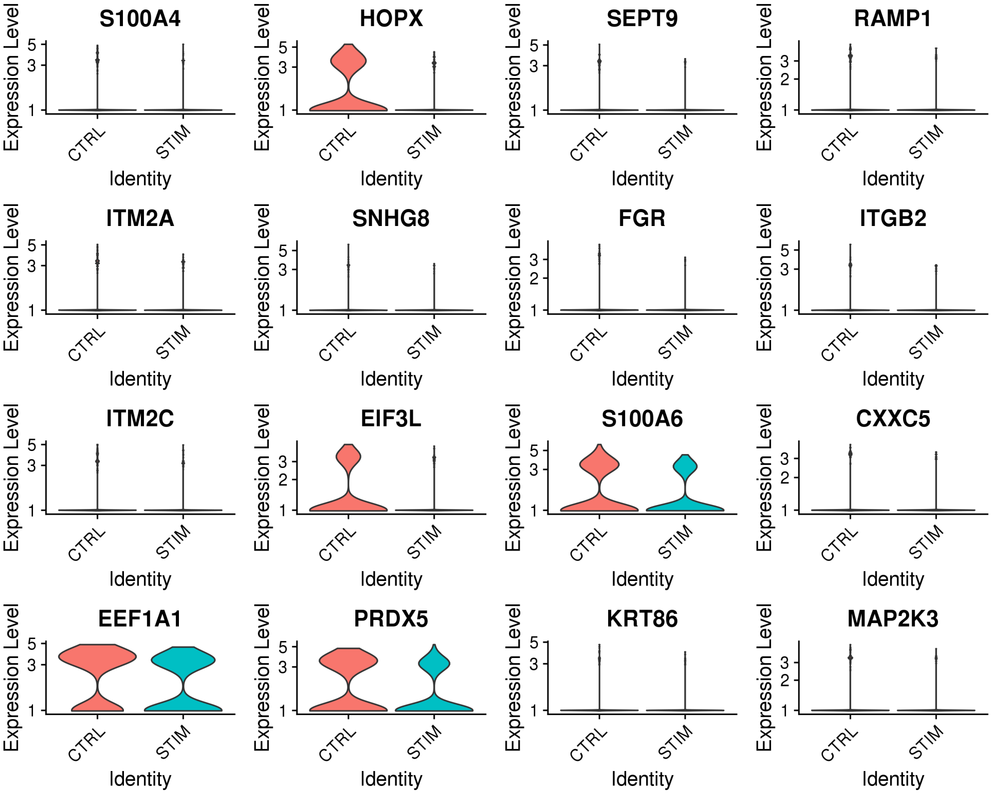


Figure 121: Differential expression summary plots for cluster 6

14.23 Cluster 6 violin plots: positively differentially expressed genes

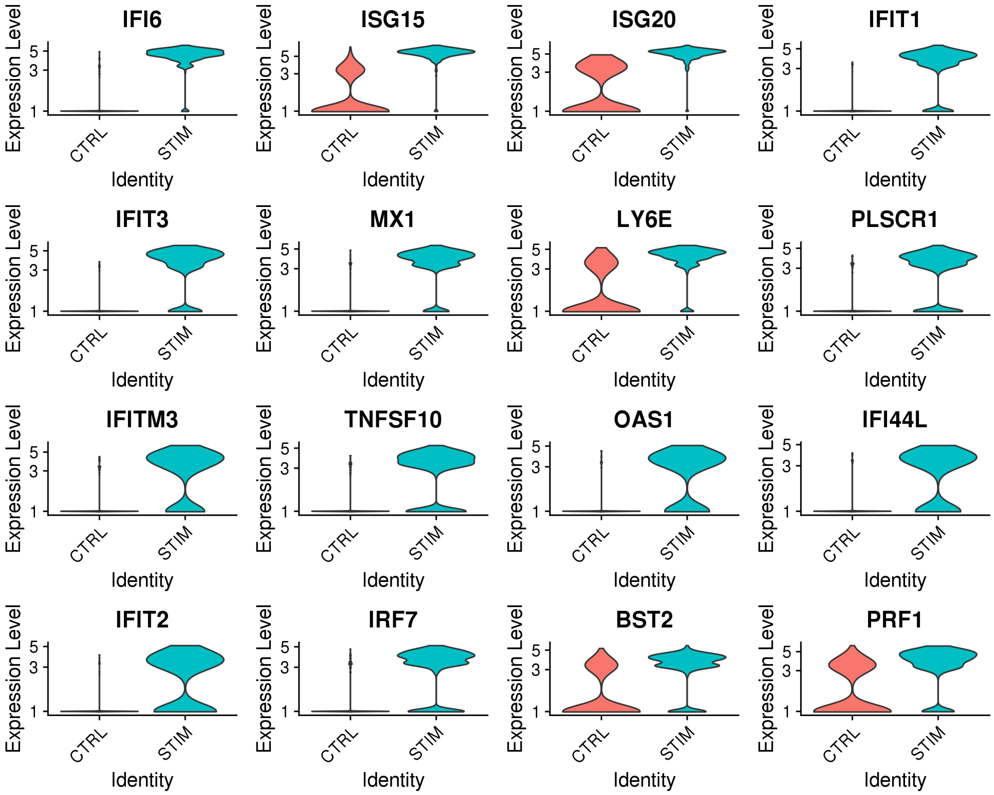


(a) Top positively differentially expressed genes ordered by p-value, cluster: 6

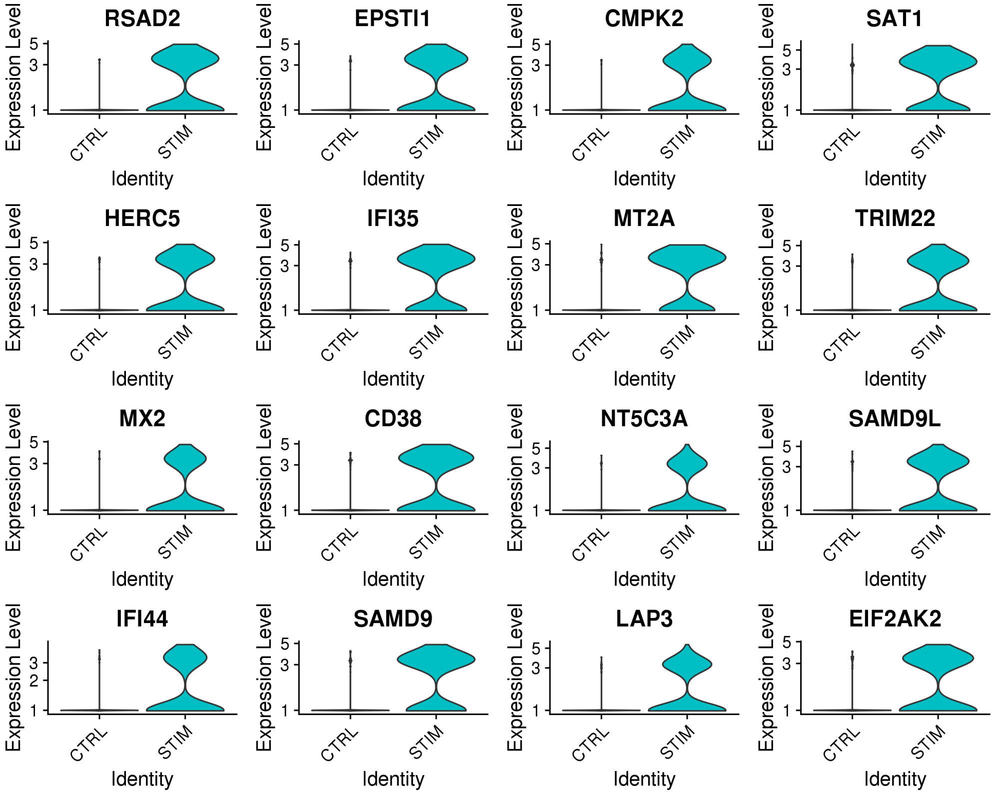


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 6

14.24 Cluster 6 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 6



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 6

14.25 Cluster 7: summary plots

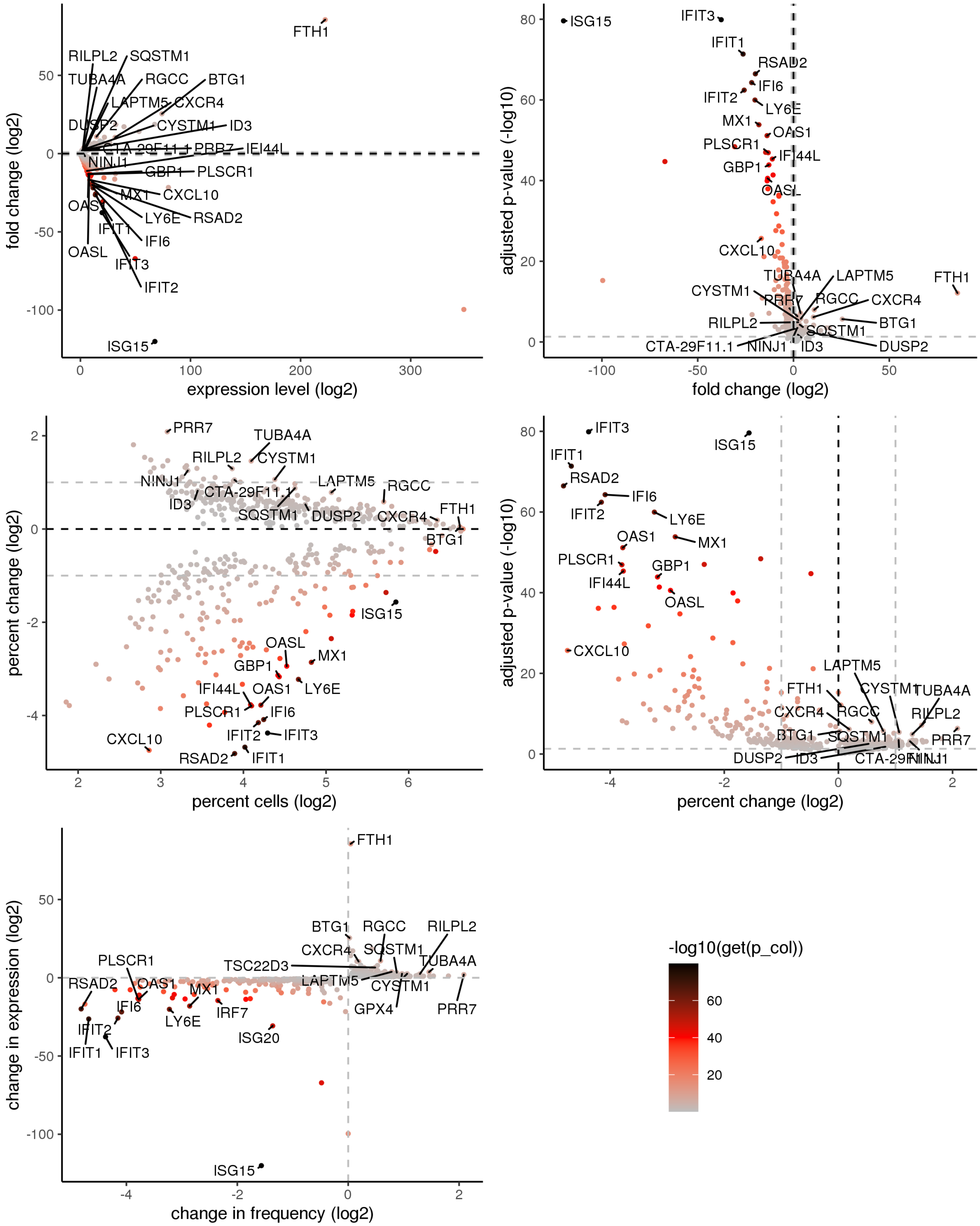
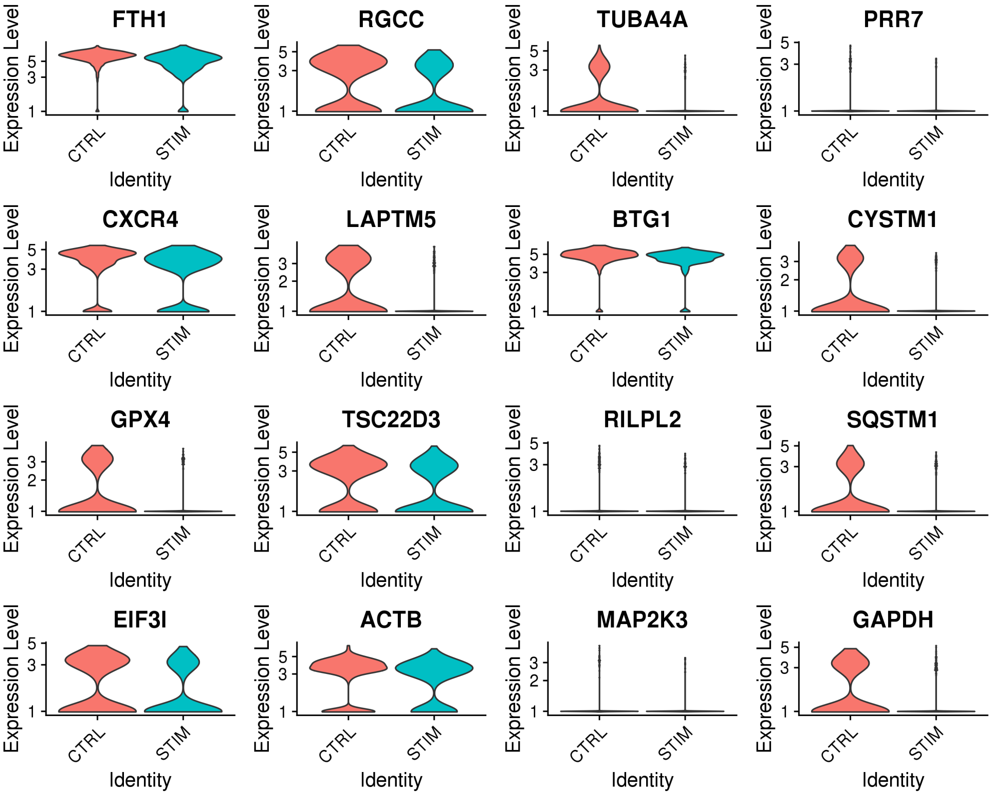
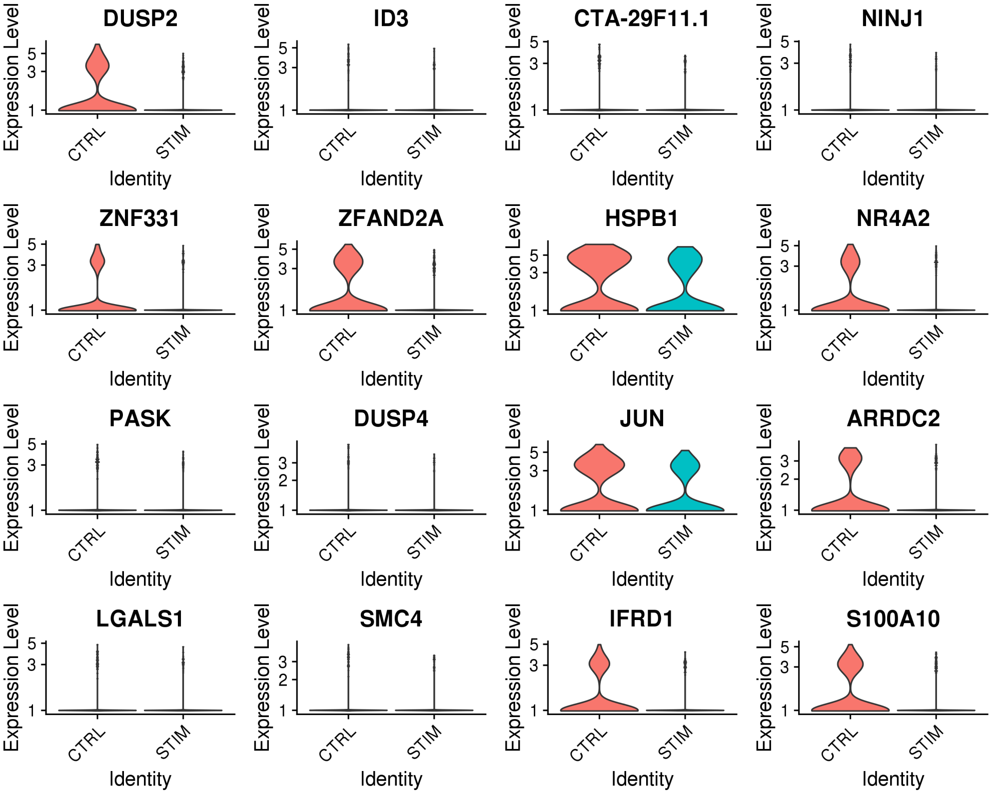


Figure 124: Differential expression summary plots for cluster 7

14.26 Cluster 7 violin plots: positively differentially expressed genes

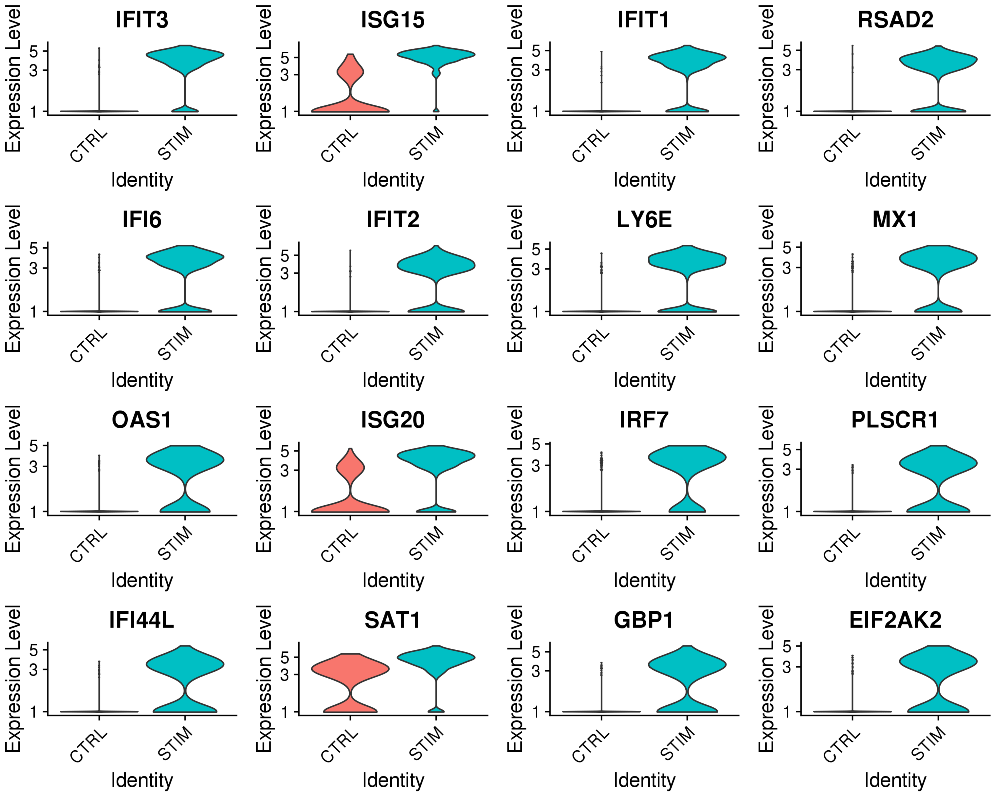


(a) Top positively differentially expressed genes ordered by p-value, cluster: 7

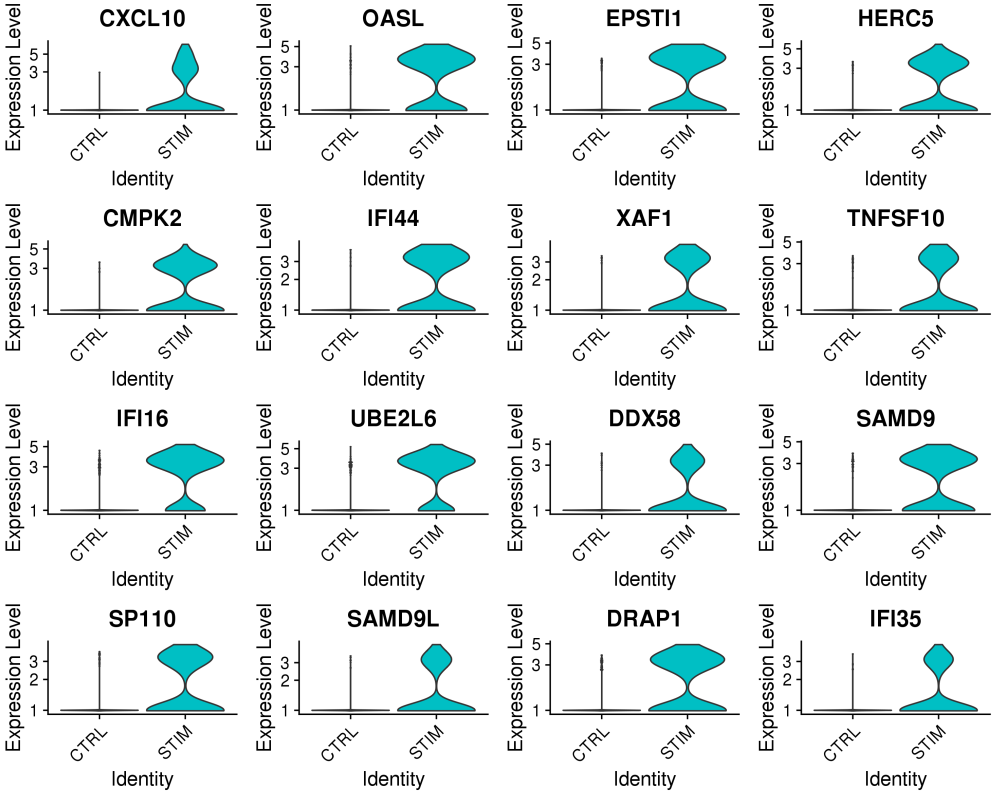


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 7

14.27 Cluster 7 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 7



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 7

14.28 Cluster 8: summary plots

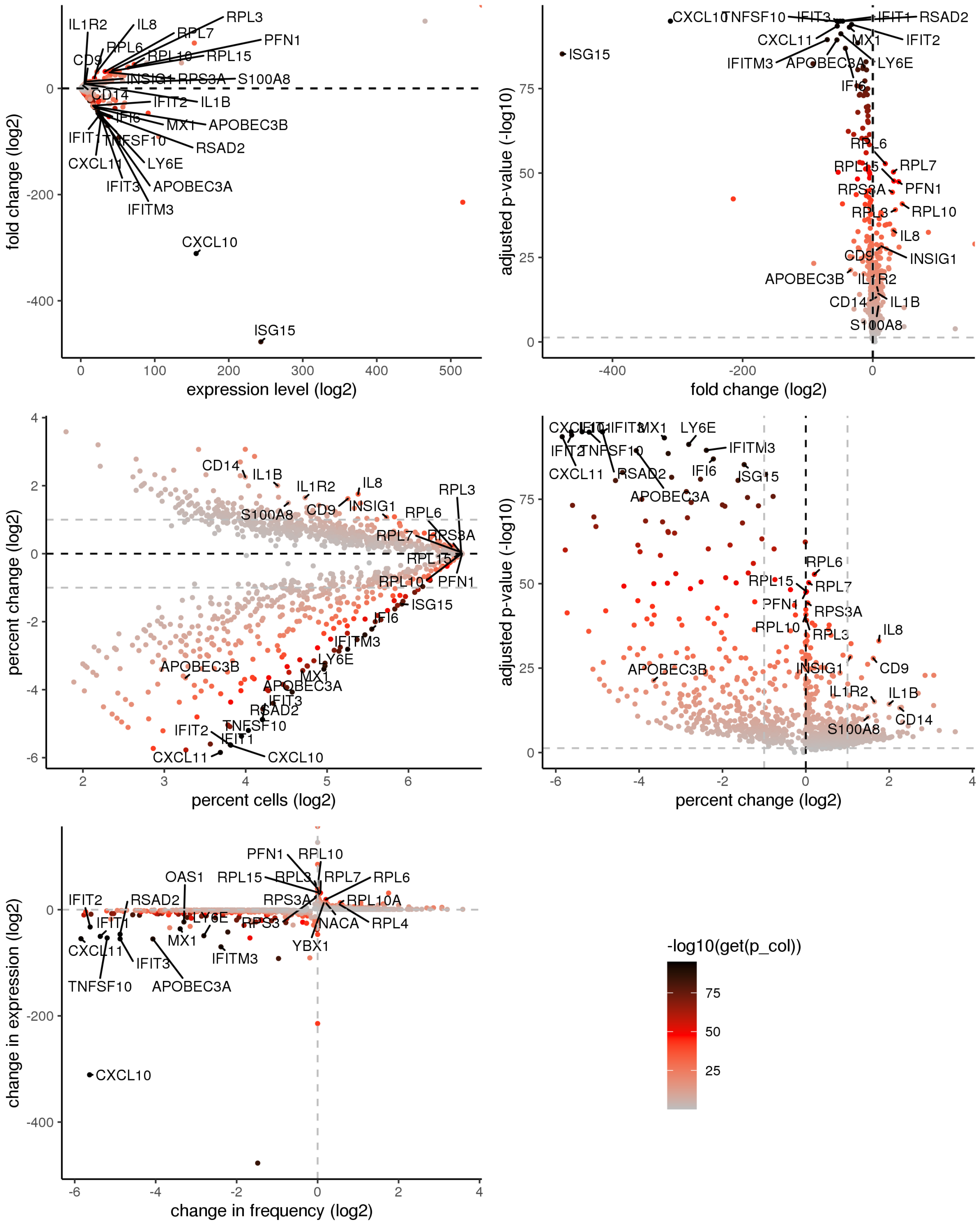
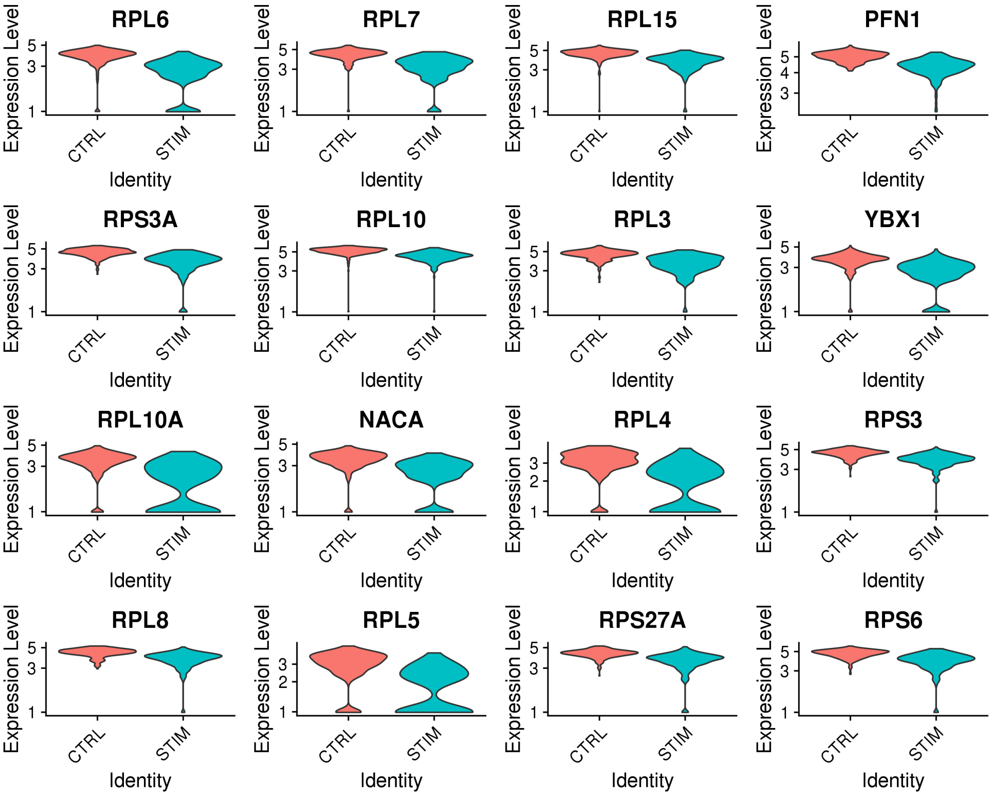
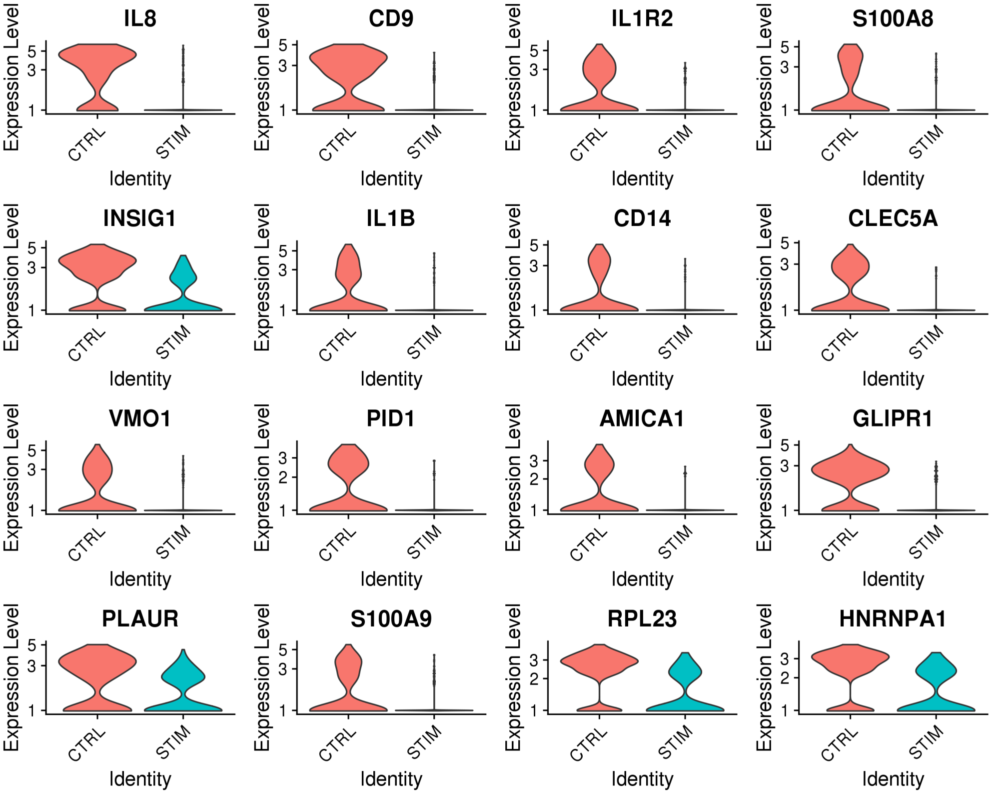


Figure 127: Differential expression summary plots for cluster 8

14.29 Cluster 8 violin plots: positively differentially expressed genes

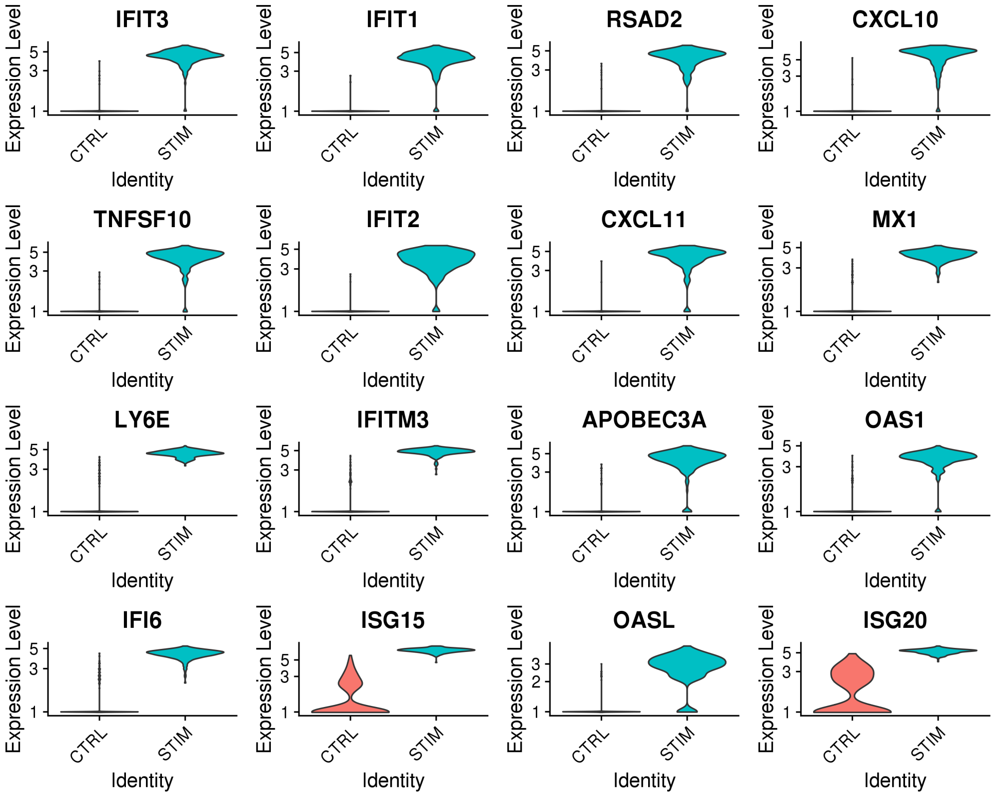


(a) Top positively differentially expressed genes ordered by p-value, cluster: 8

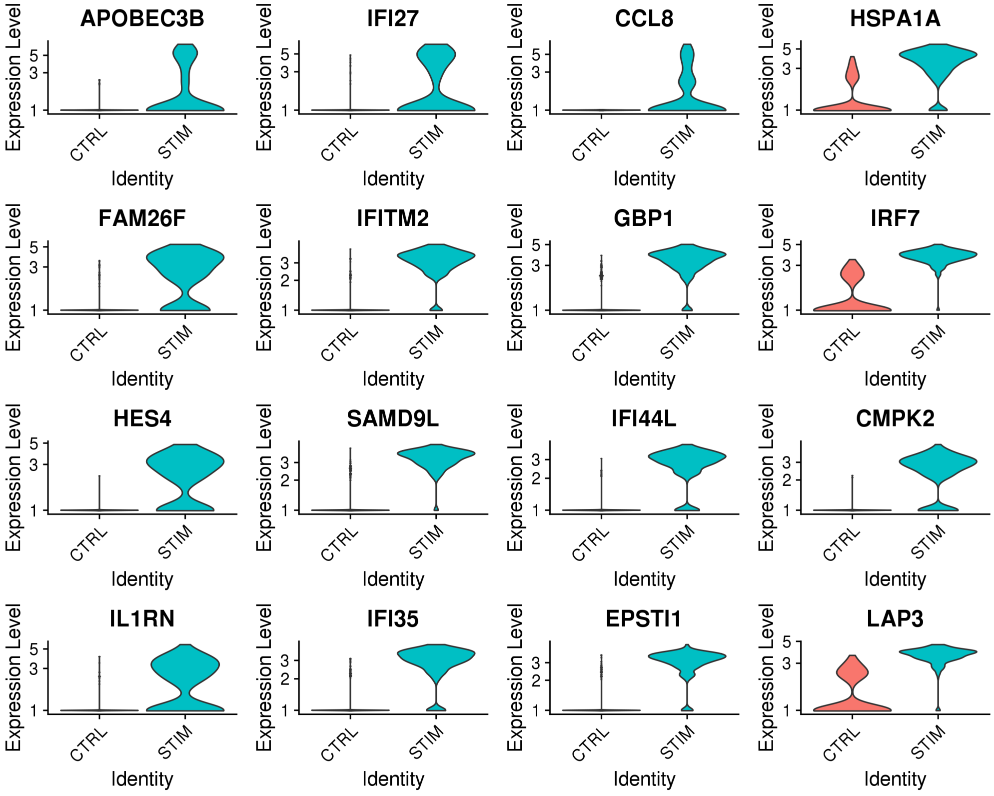


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 8

14.30 Cluster 8 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 8



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 8

14.31 Cluster 9: summary plots

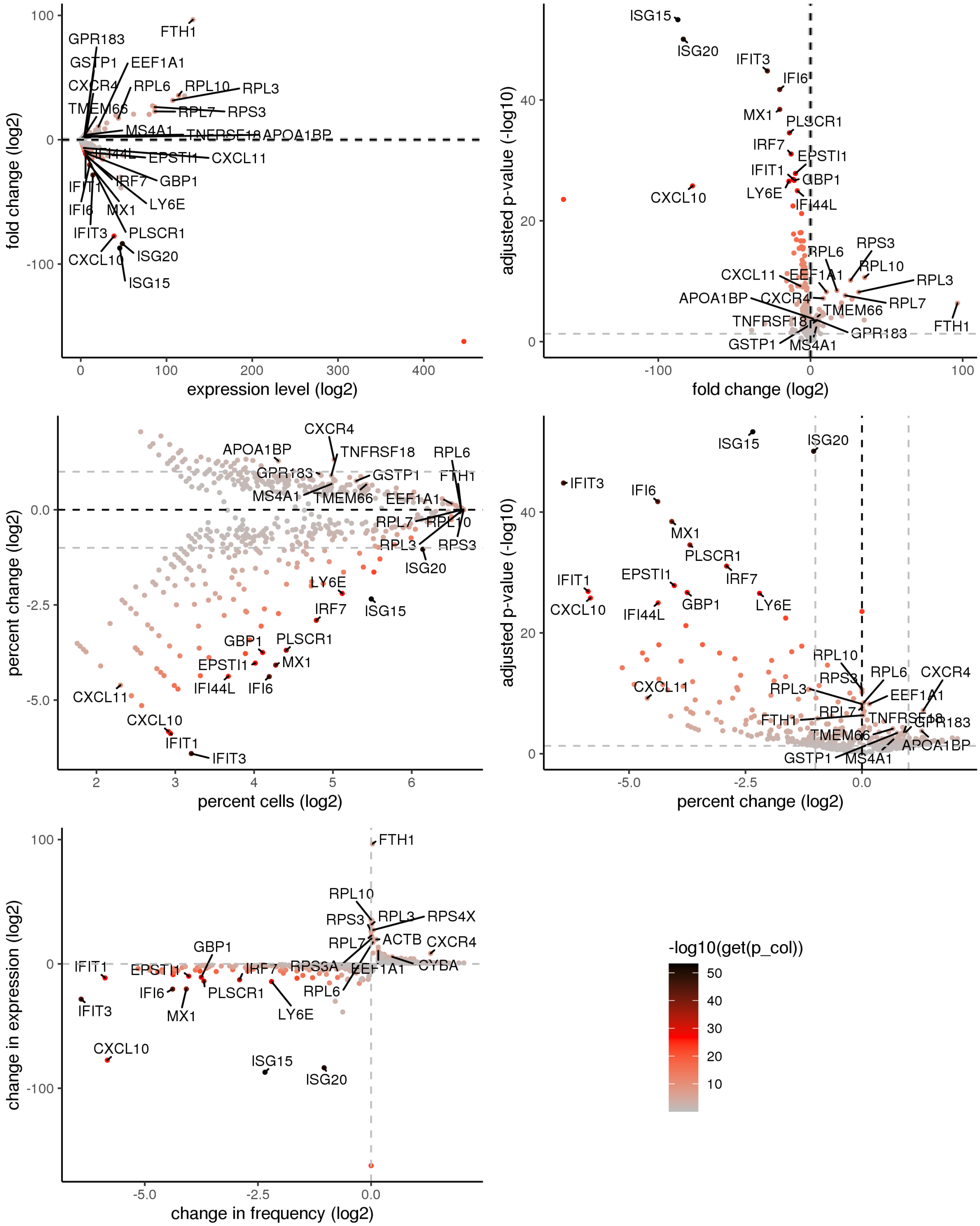
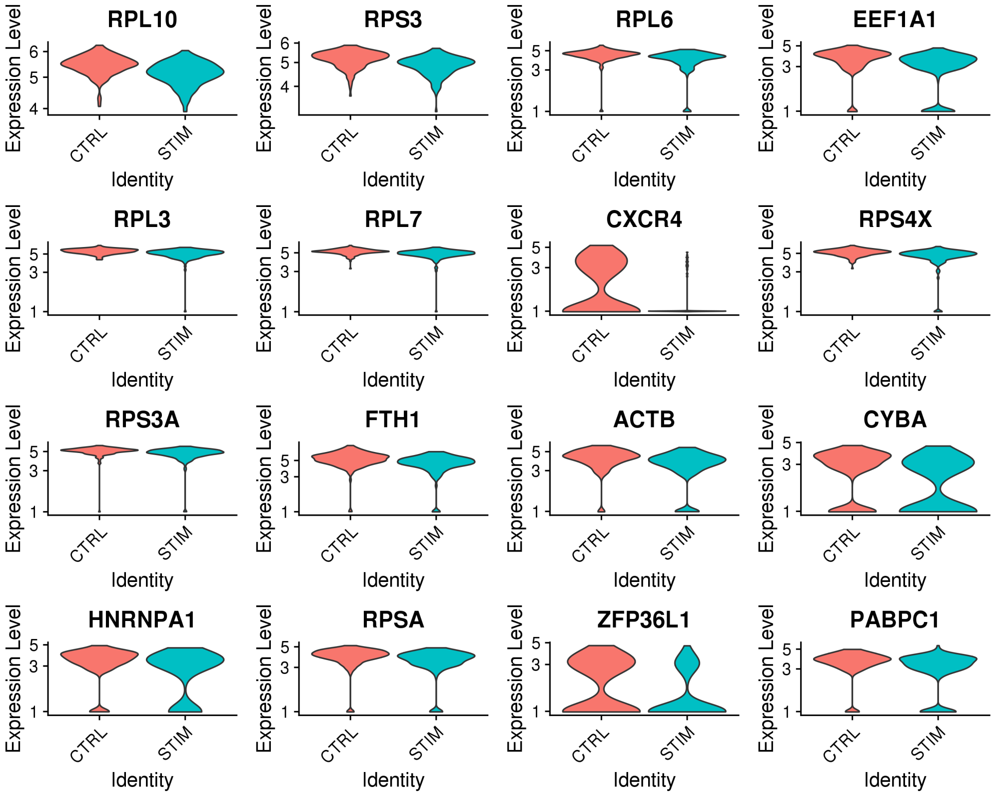
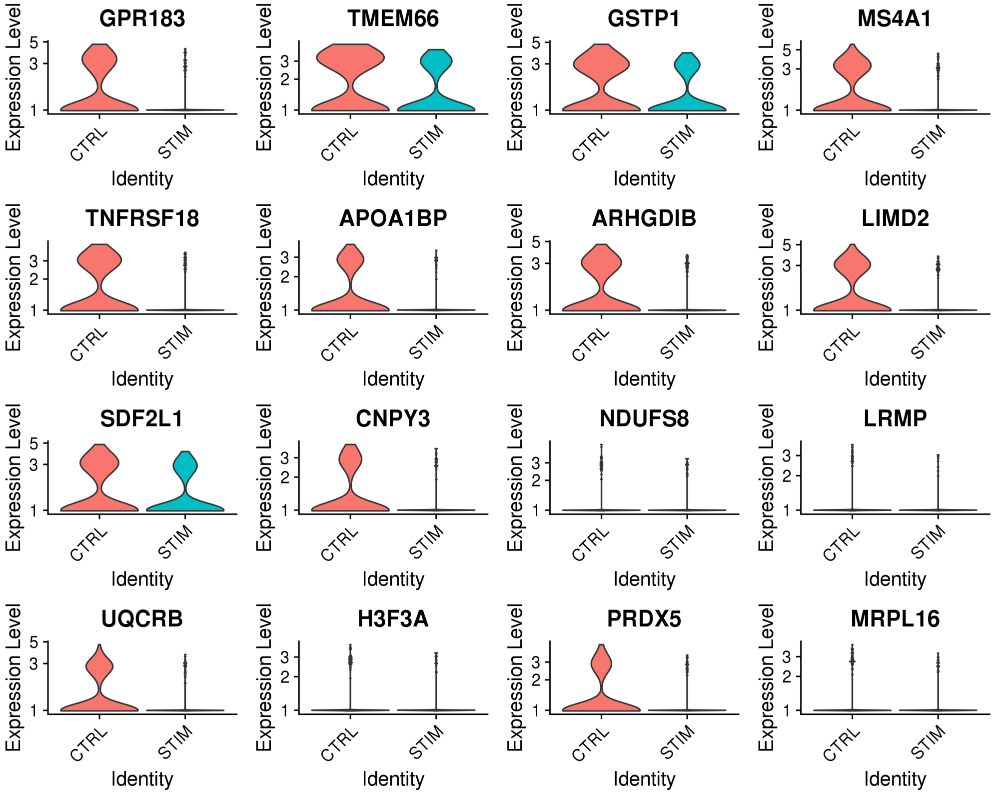


Figure 130: Differential expression summary plots for cluster 9

14.32 Cluster 9 violin plots: positively differentially expressed genes

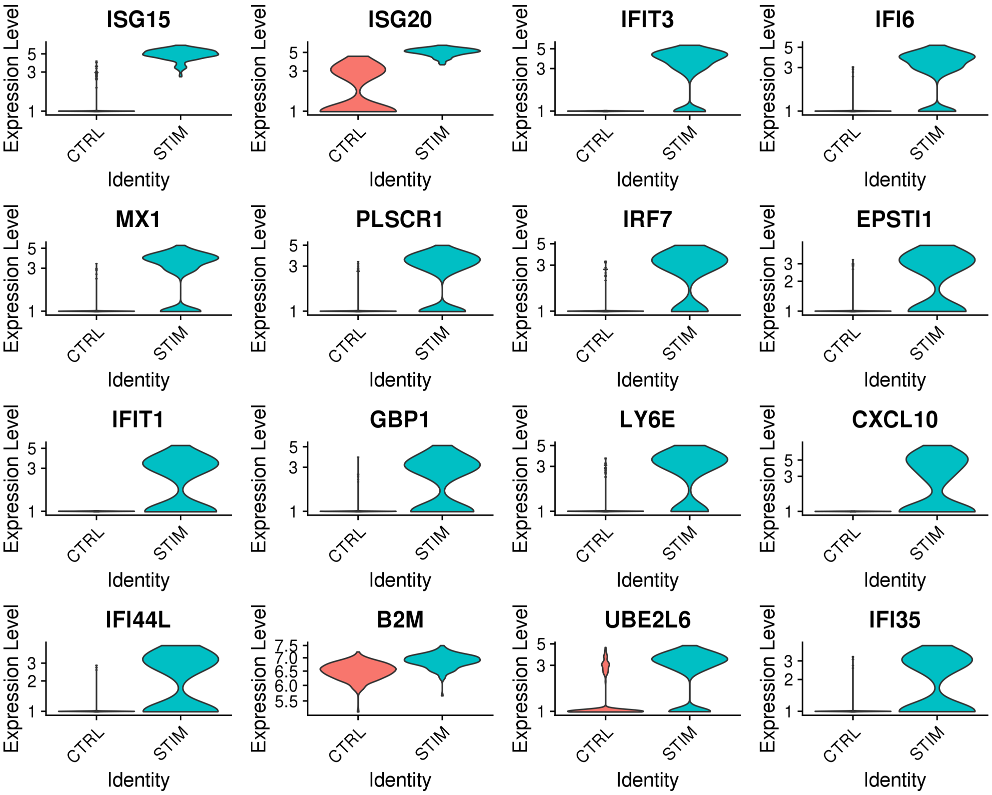


(a) Top positively differentially expressed genes ordered by p-value, cluster: 9

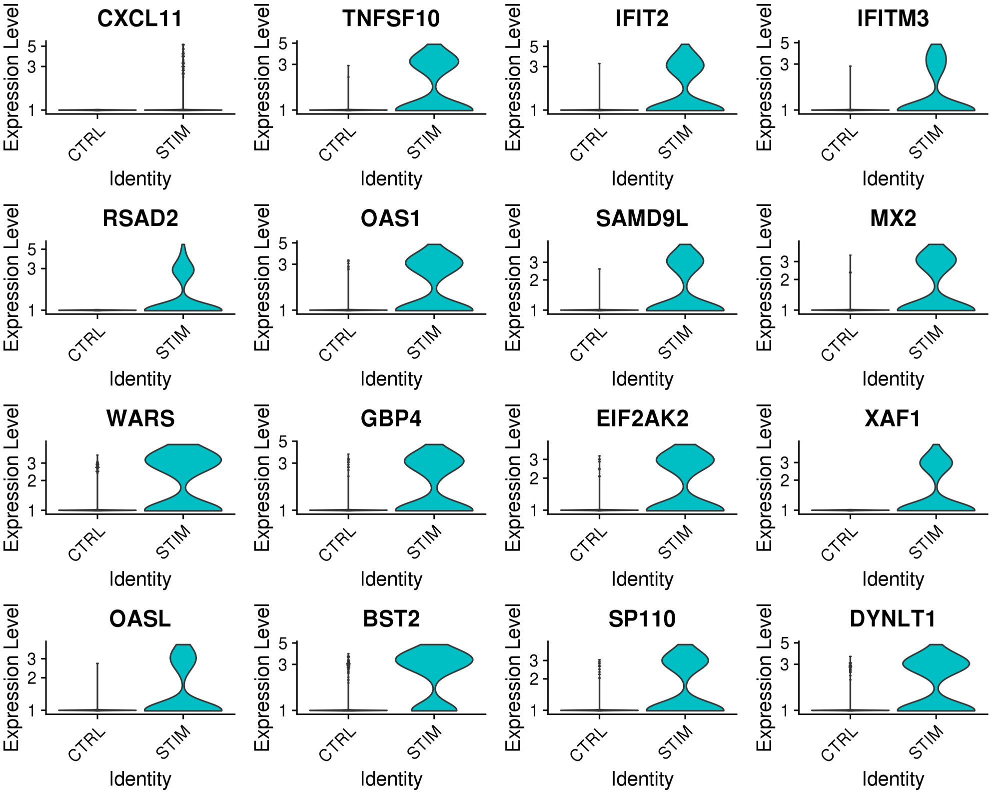


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 9

14.33 Cluster 9 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 9



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 9

14.34 Cluster 10: summary plots

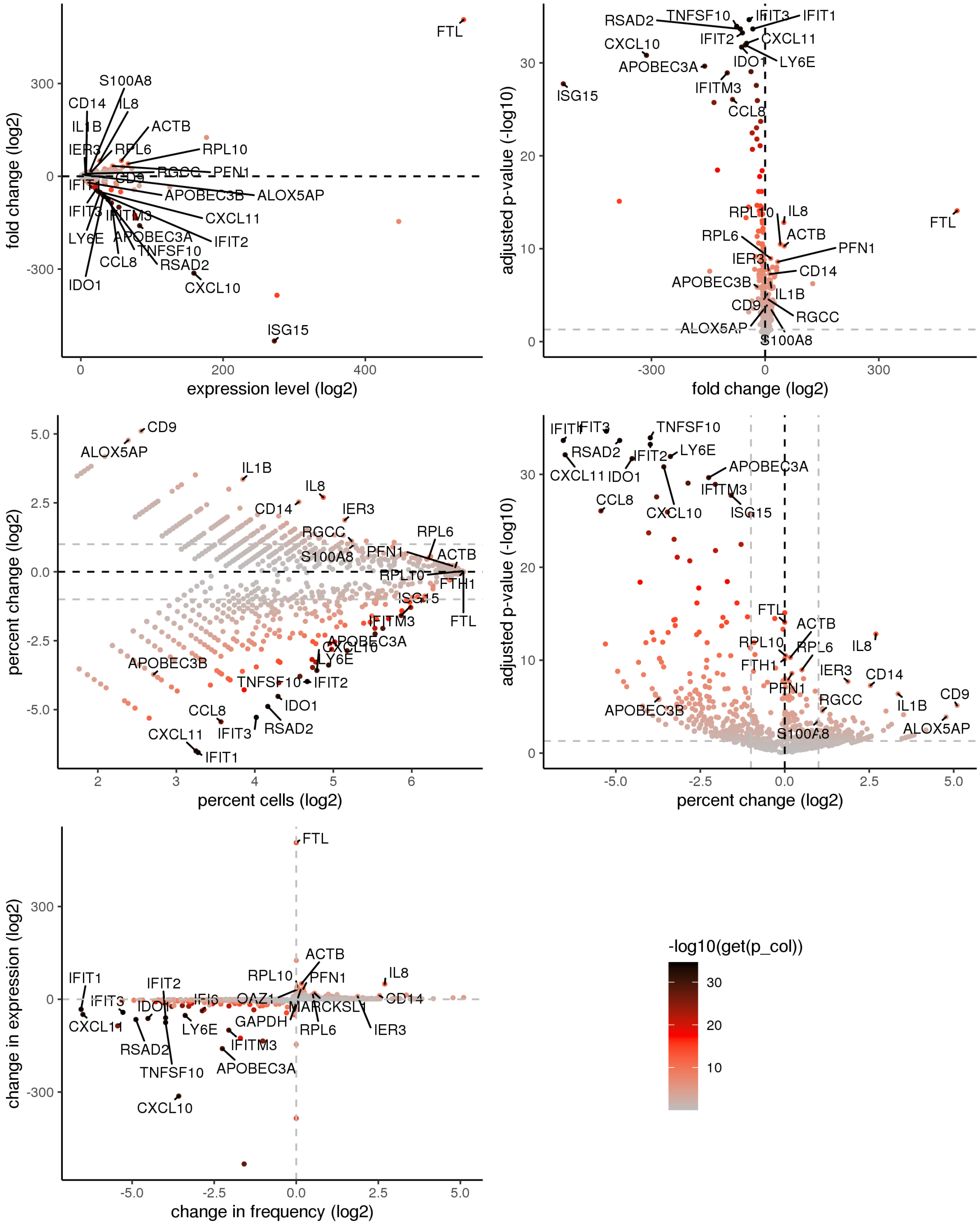
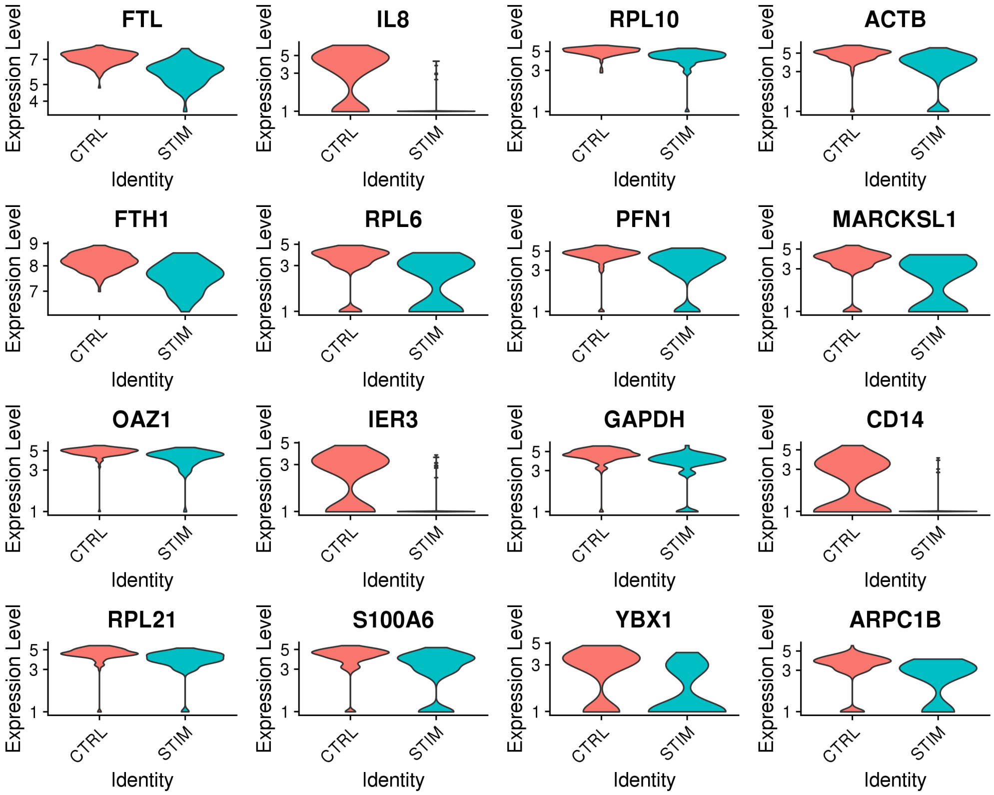
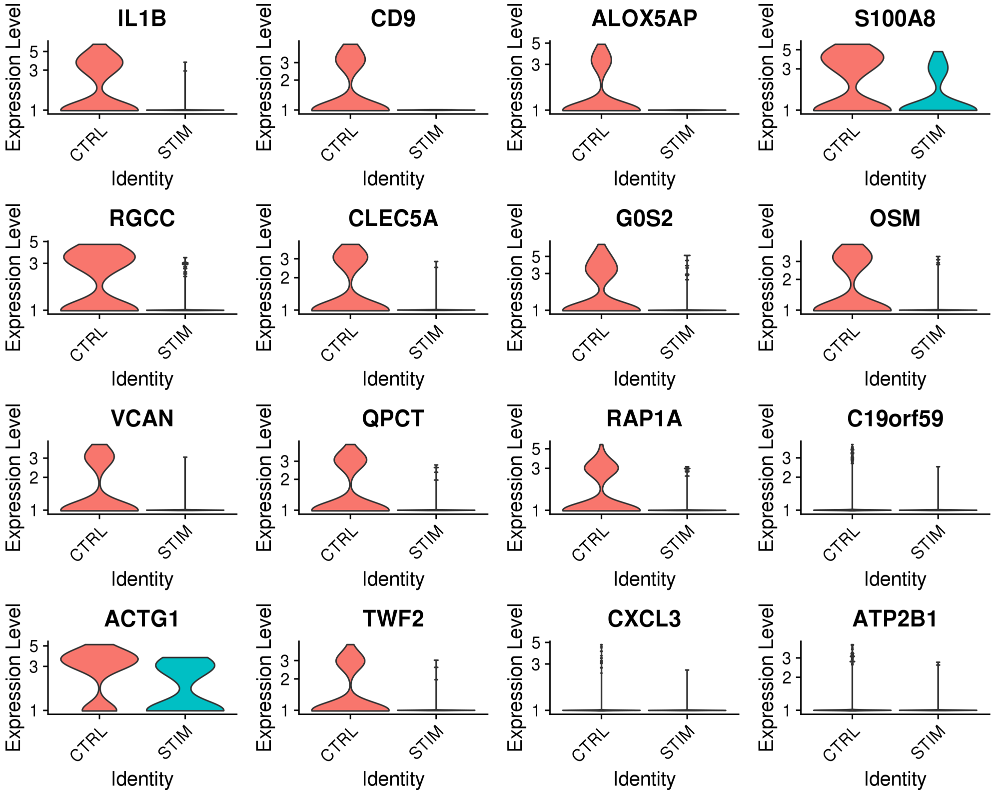


Figure 133: Differential expression summary plots for cluster 10

14.35 Cluster 10 violin plots: positively differentially expressed genes

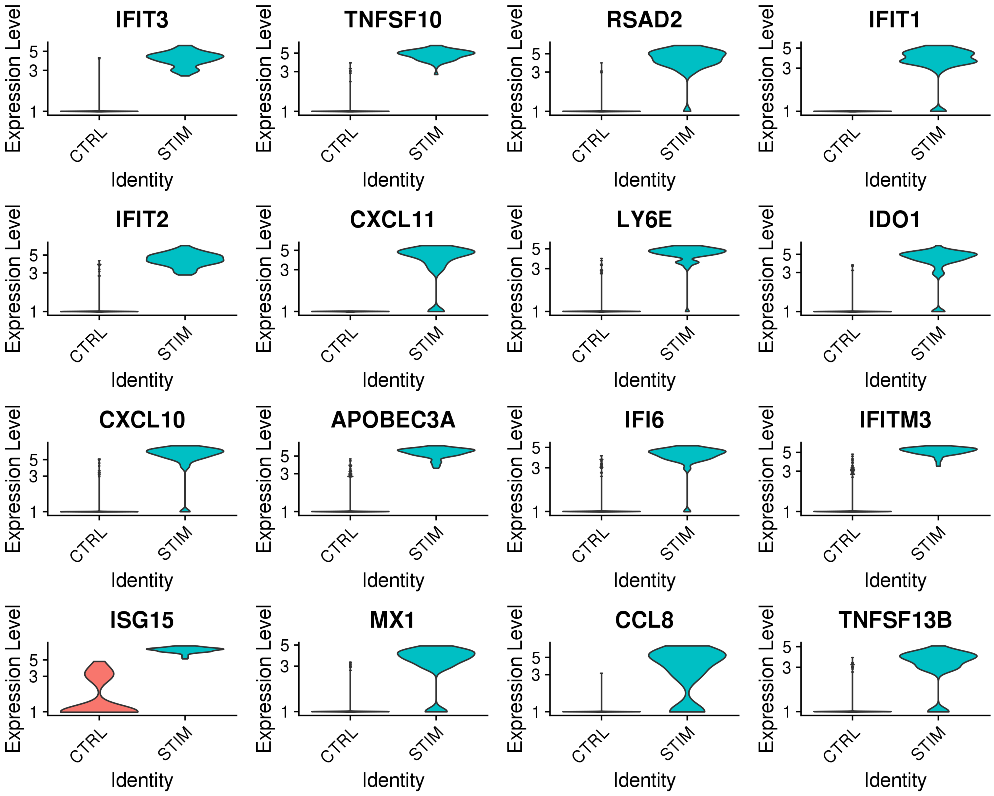


(a) Top positively differentially expressed genes ordered by p-value, cluster: 10

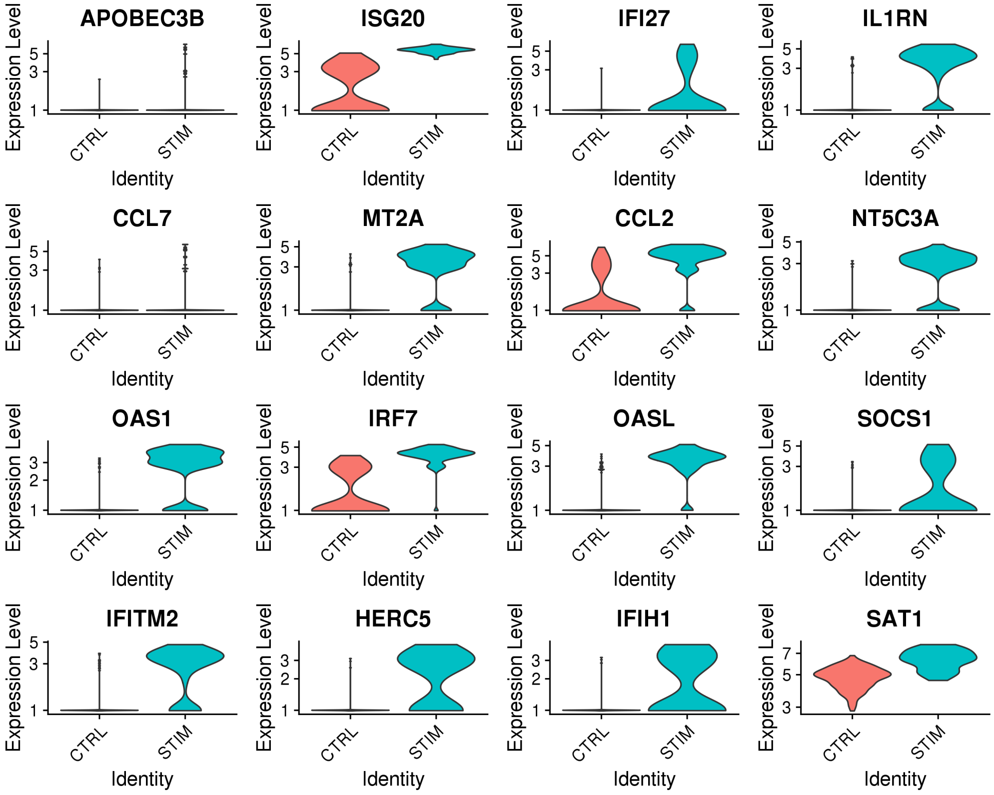


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 10

14.36 Cluster 10 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 10



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 10

14.37 Cluster 11: summary plots

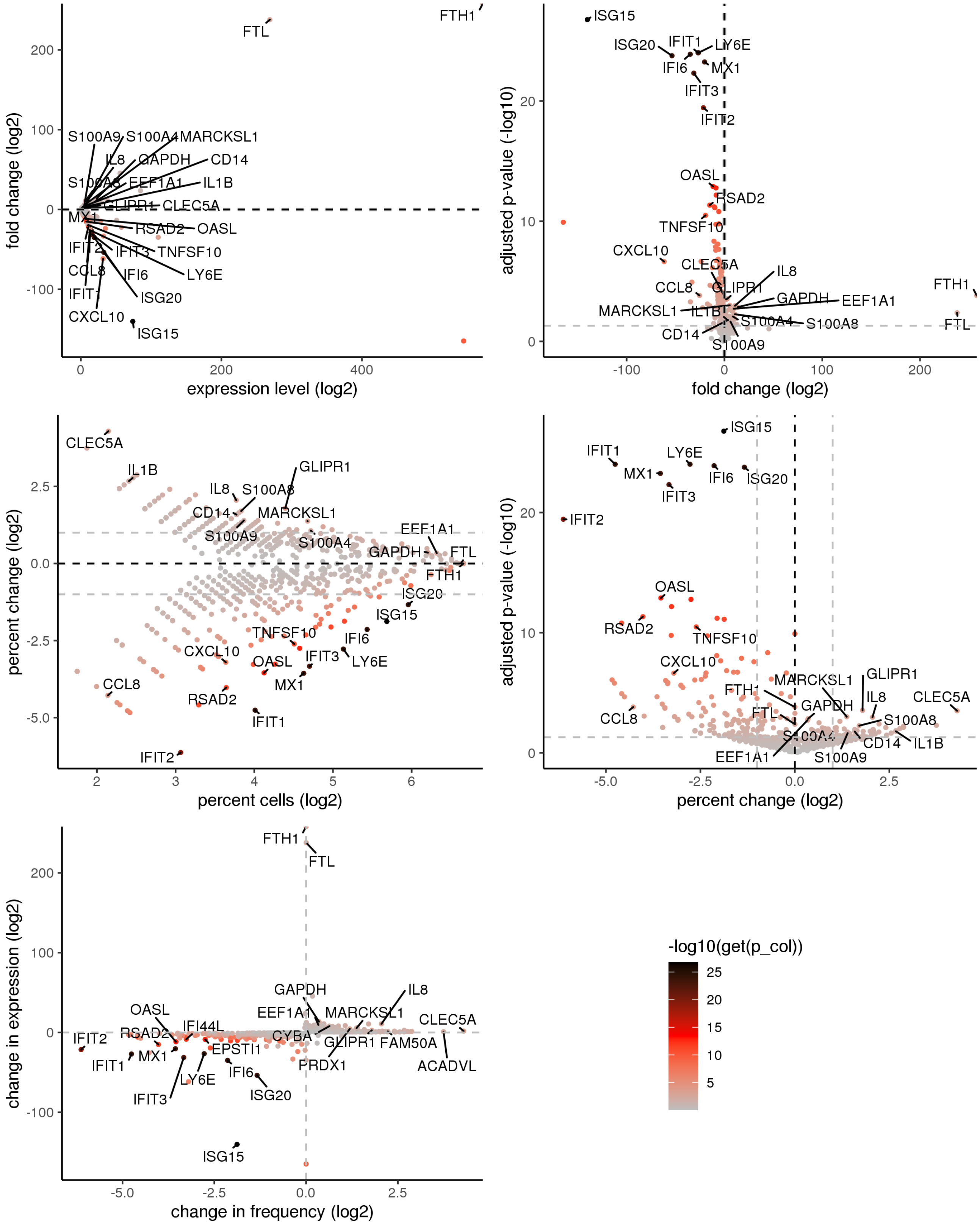
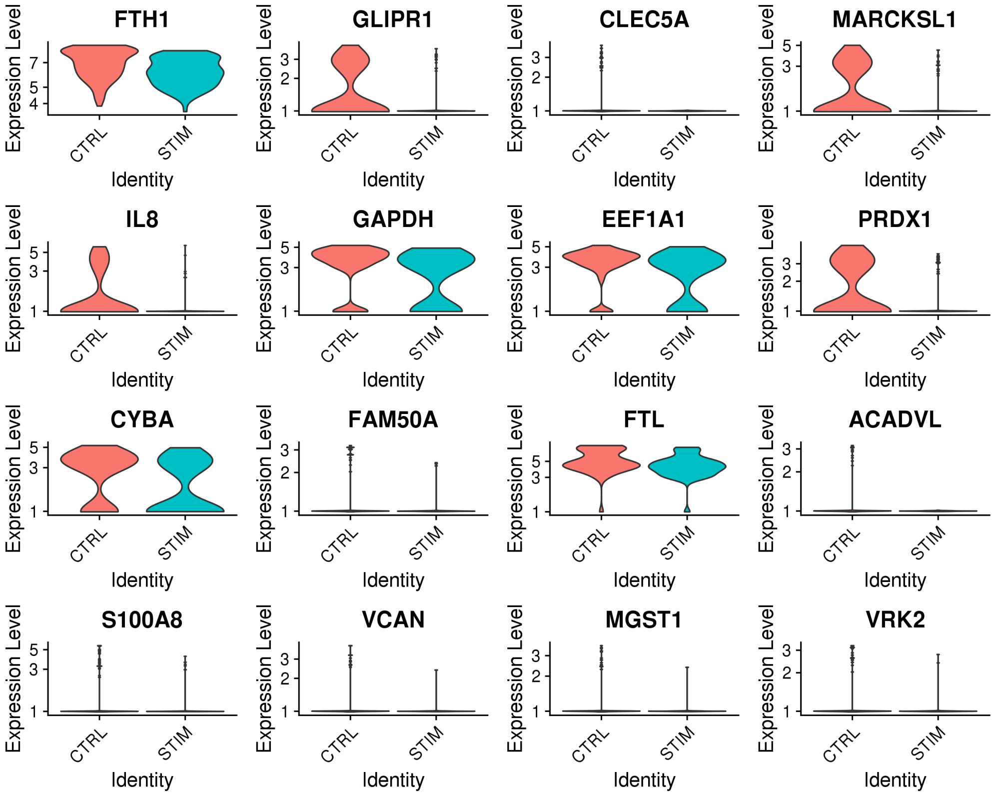
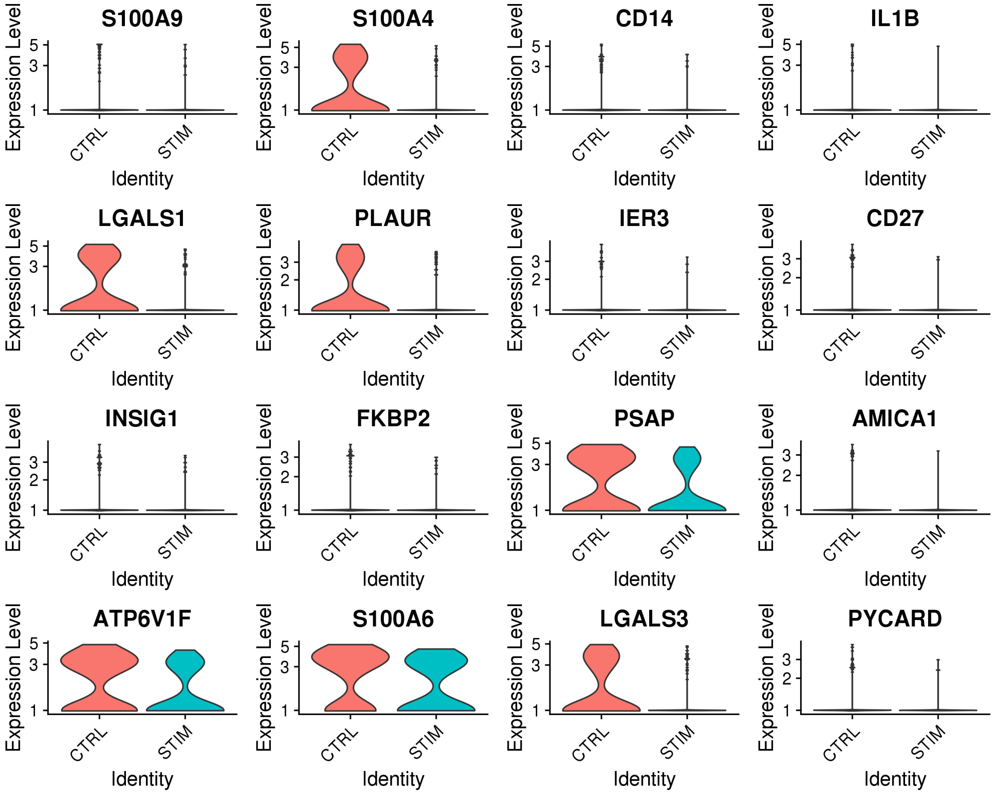


Figure 136: Differential expression summary plots for cluster 11

14.38 Cluster 11 violin plots: positively differentially expressed genes

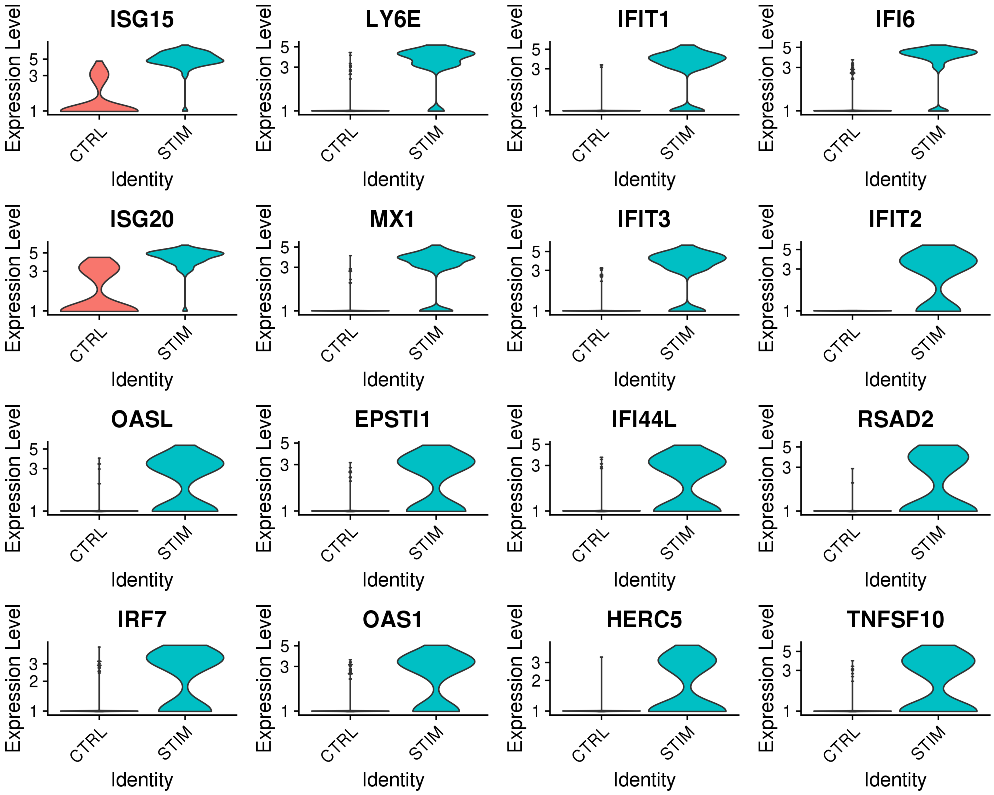


(a) Top positively differentially expressed genes ordered by p-value, cluster: 11

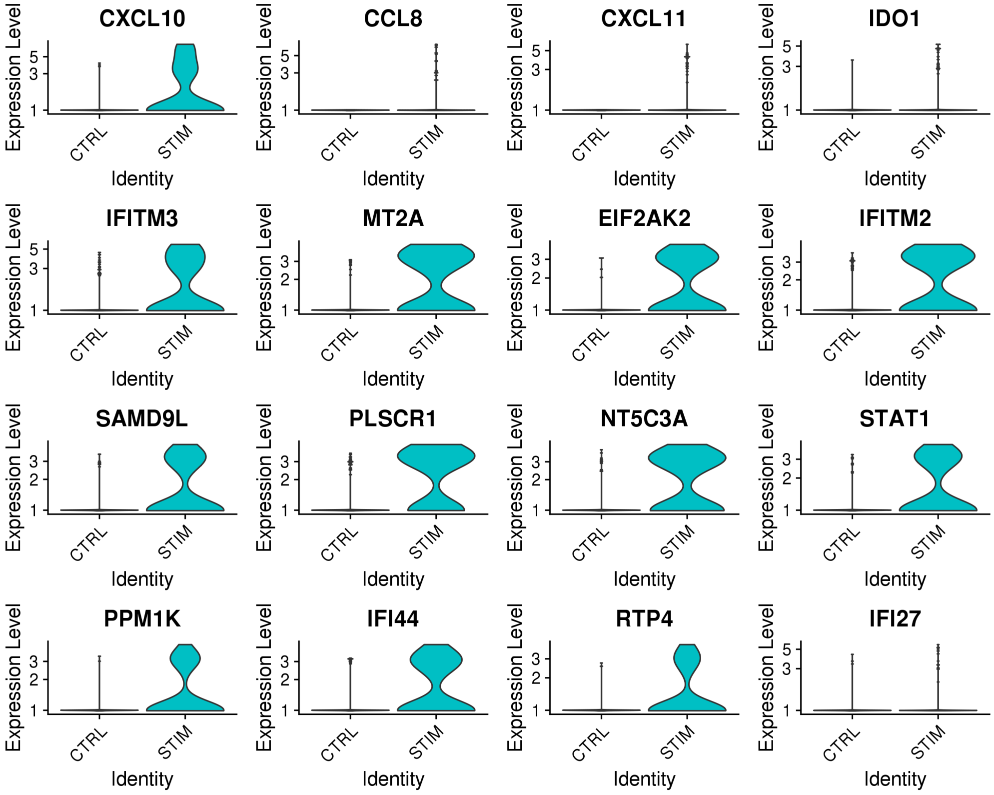


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 11

14.39 Cluster 11 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 11



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 11

14.40 Cluster 12: summary plots

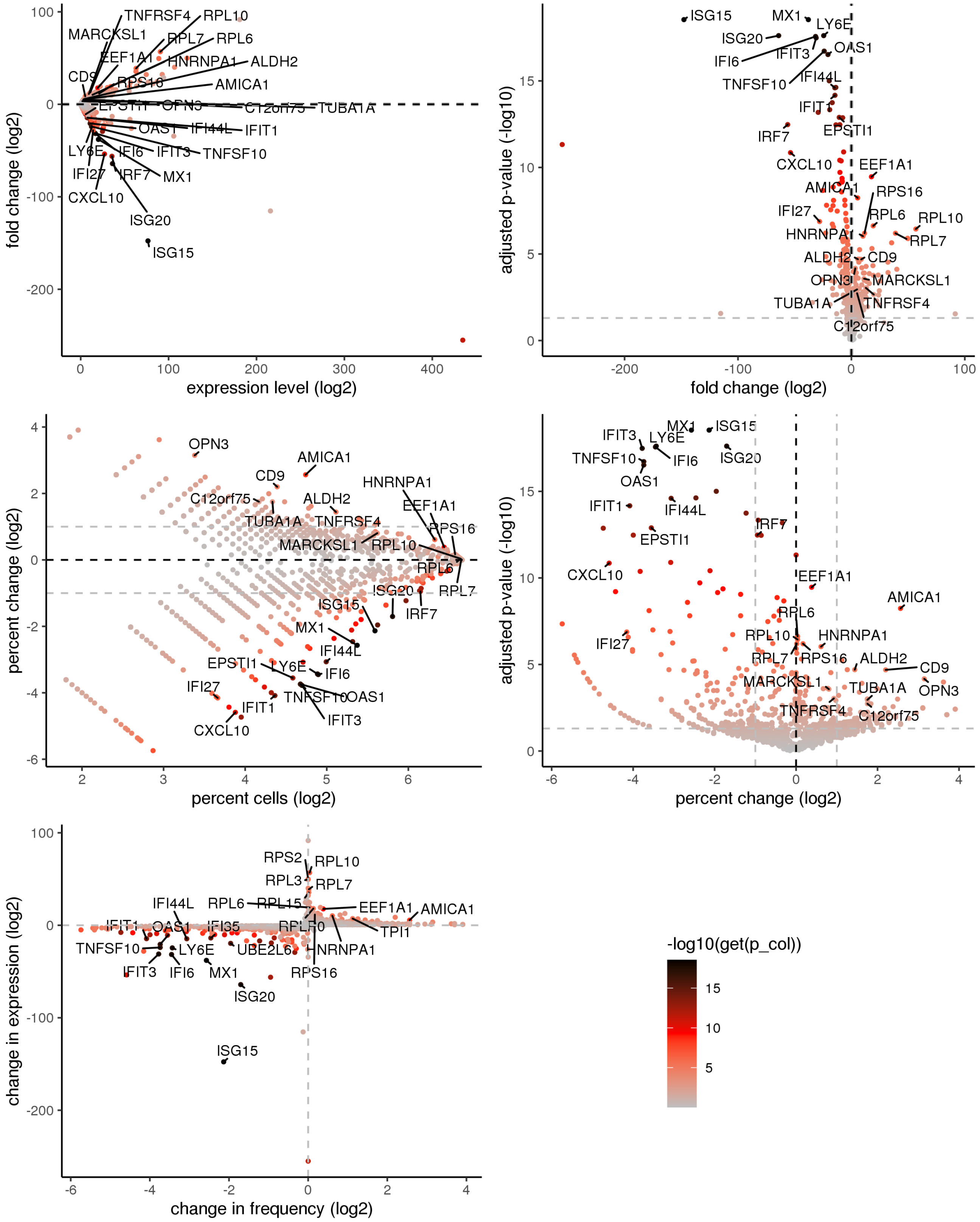
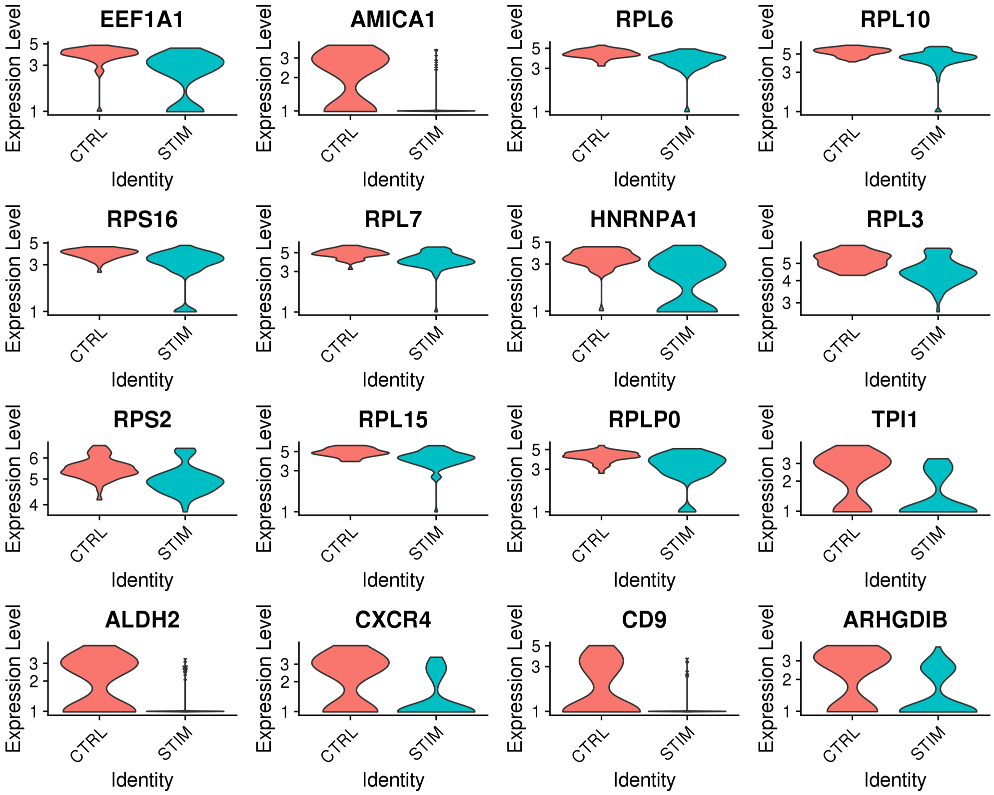
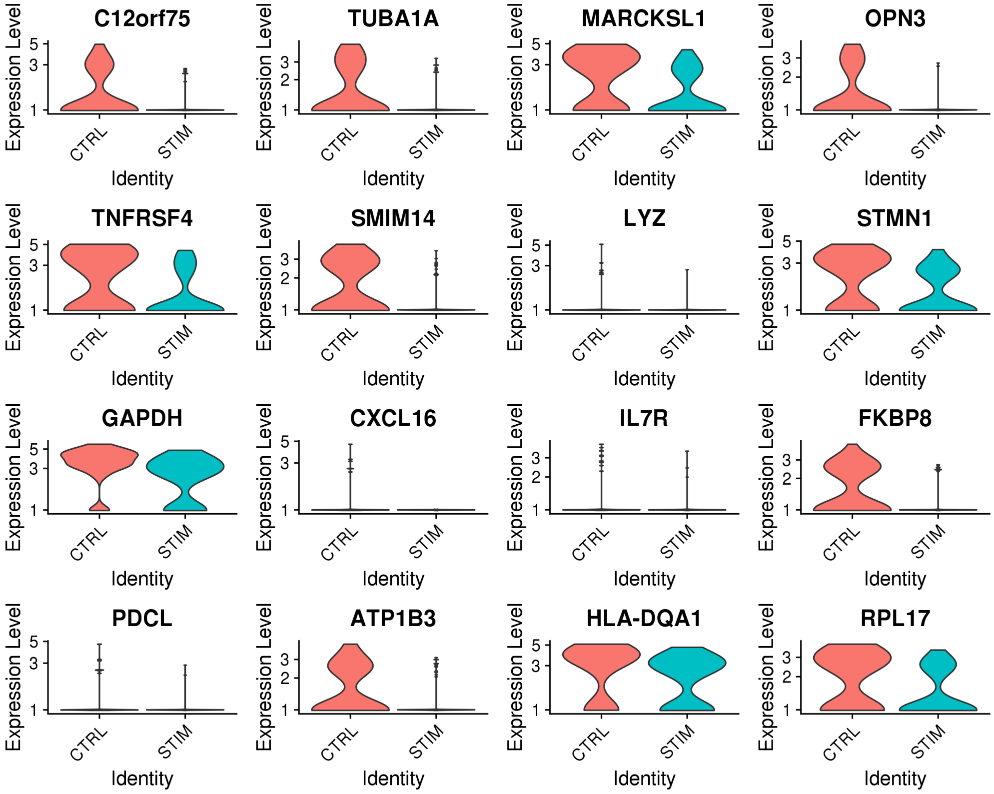


Figure 139: Differential expression summary plots for cluster 12

14.41 Cluster 12 violin plots: positively differentially expressed genes

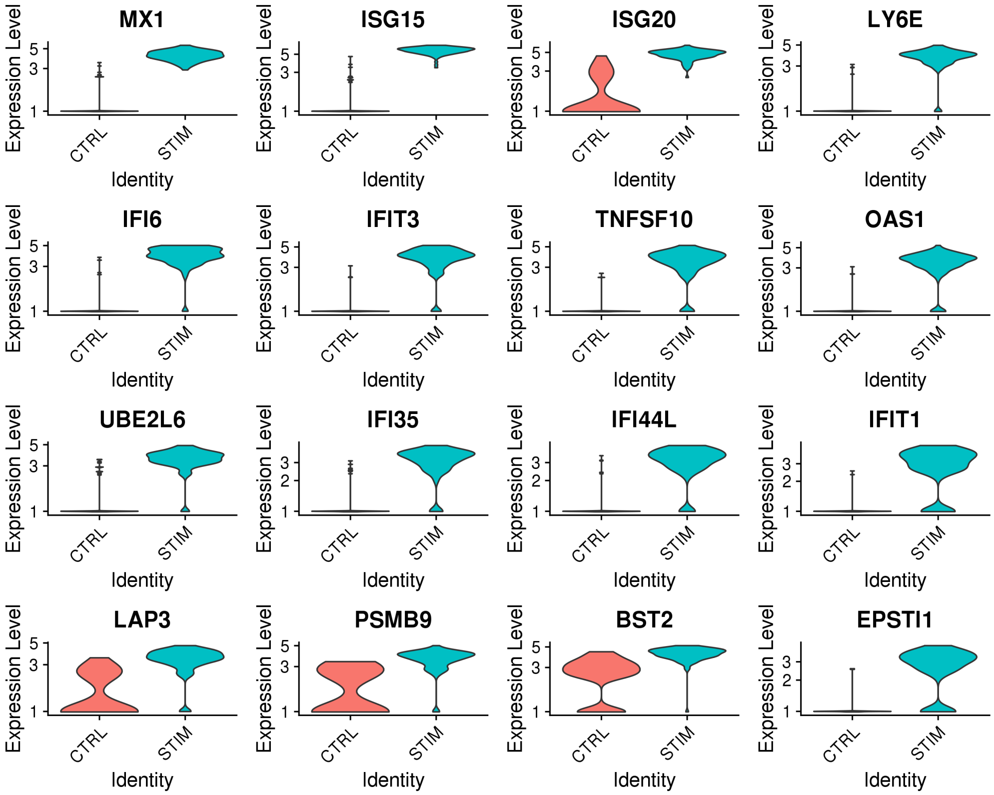


(a) Top positively differentially expressed genes ordered by p-value, cluster: 12

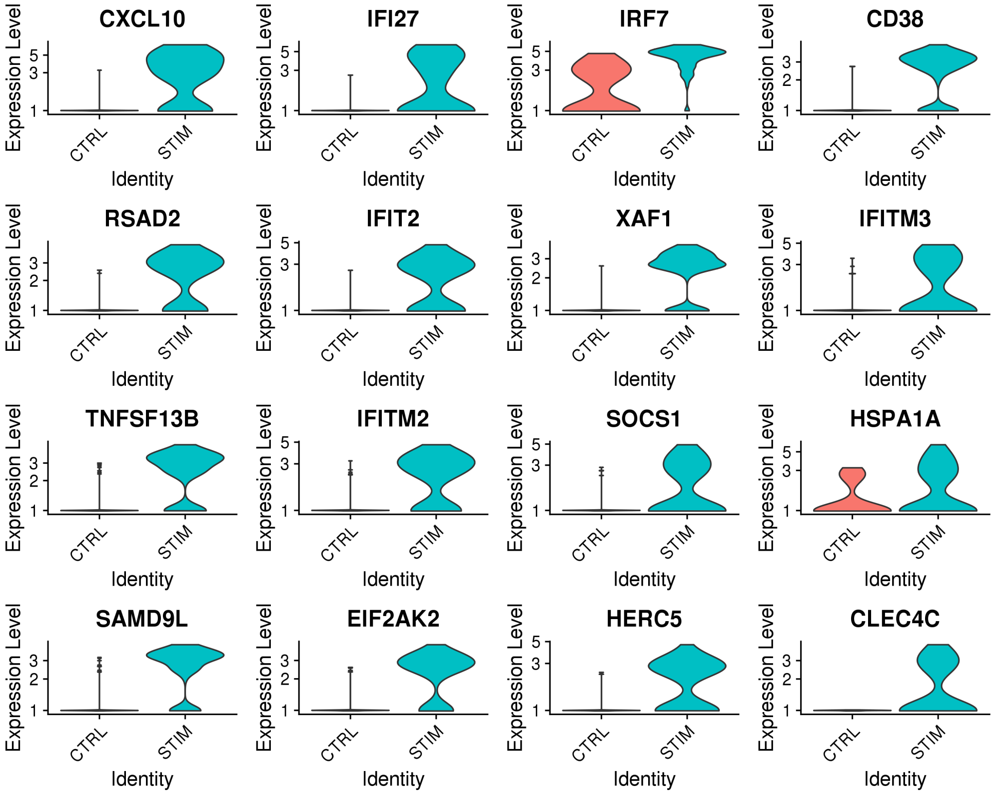


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 12

14.42 Cluster 12 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 12



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 12

14.43 Cluster 13: summary plots

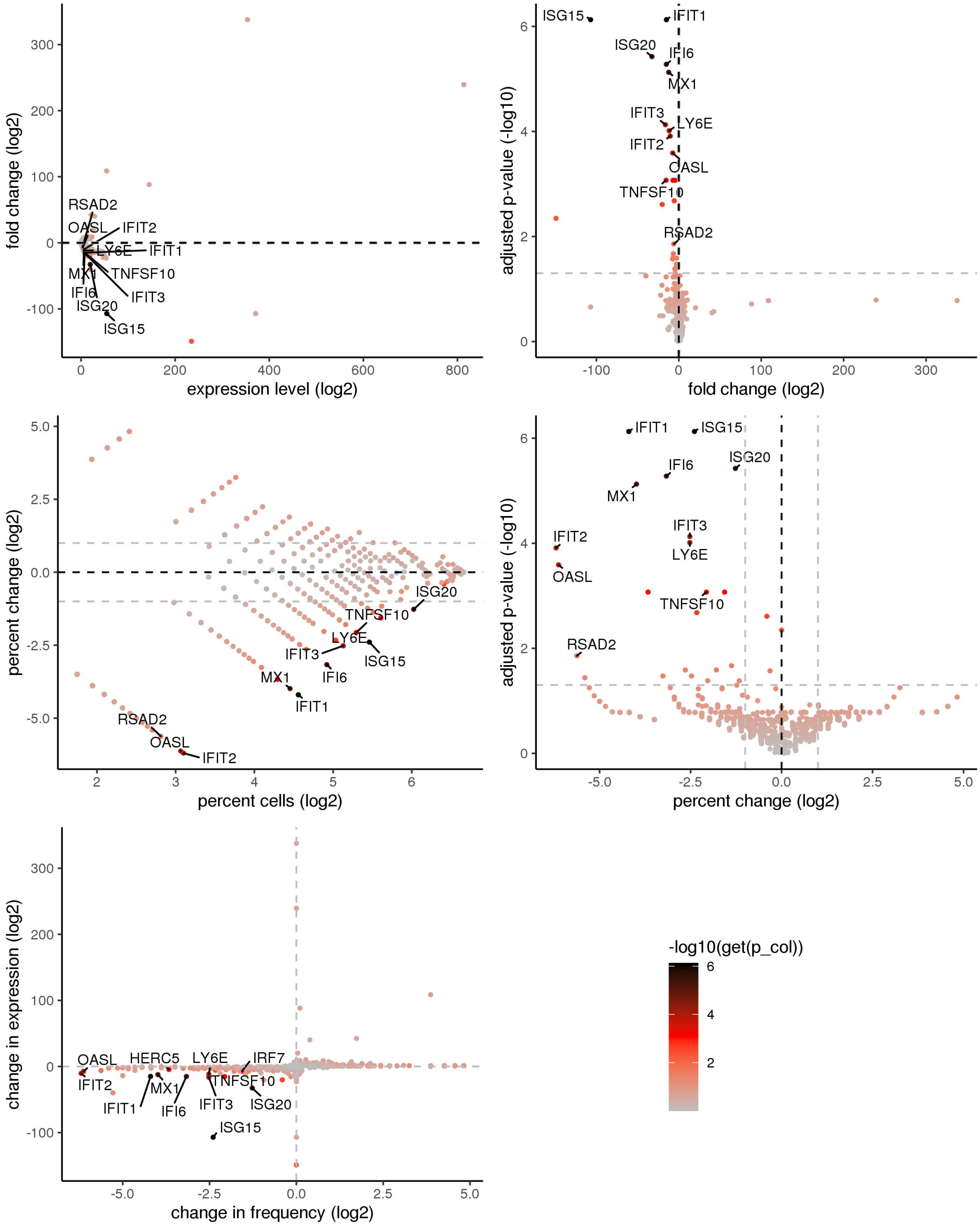
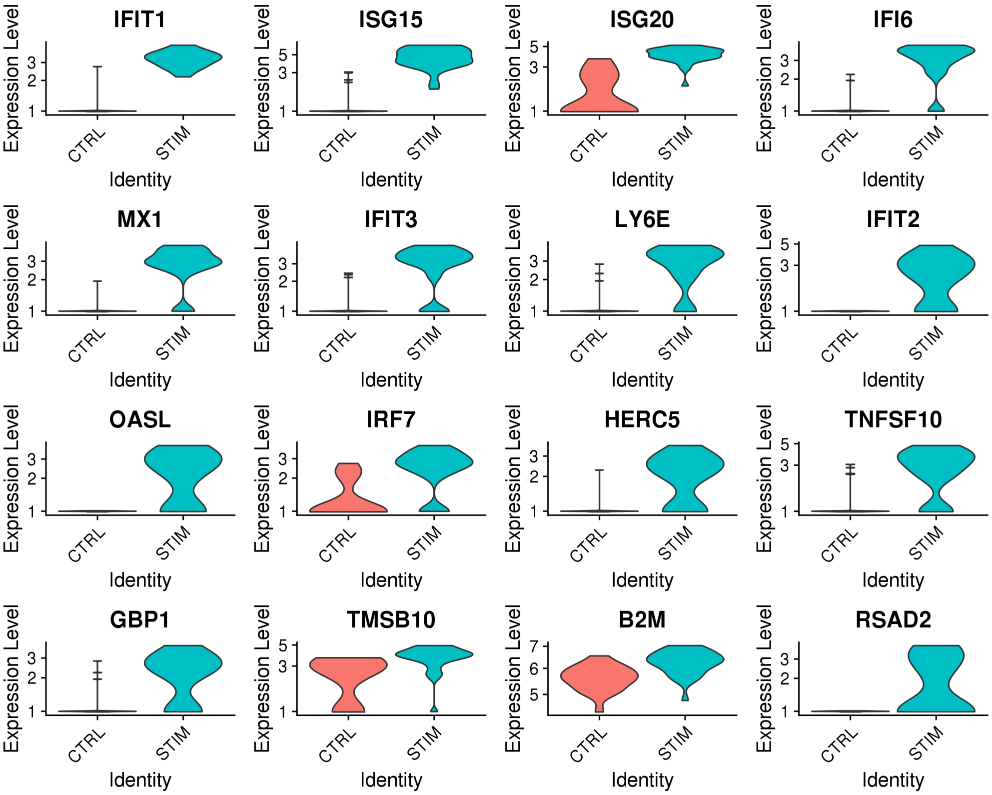


Figure 142: Differential expression summary plots for cluster 13

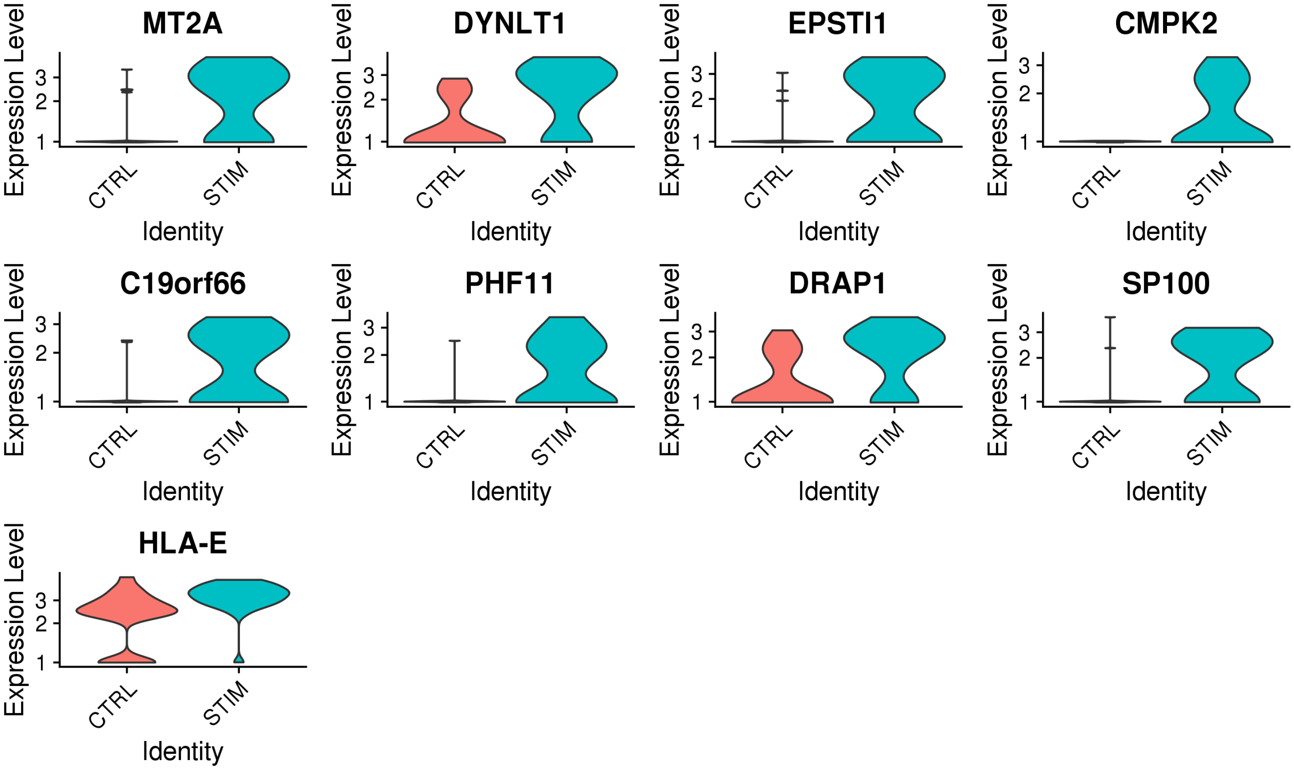
14.44 Cluster 13 violin plots: positively differentially expressed genes

No significant genes

14.45 Cluster 13 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 13



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 13

14.46 Cluster 14: summary plots

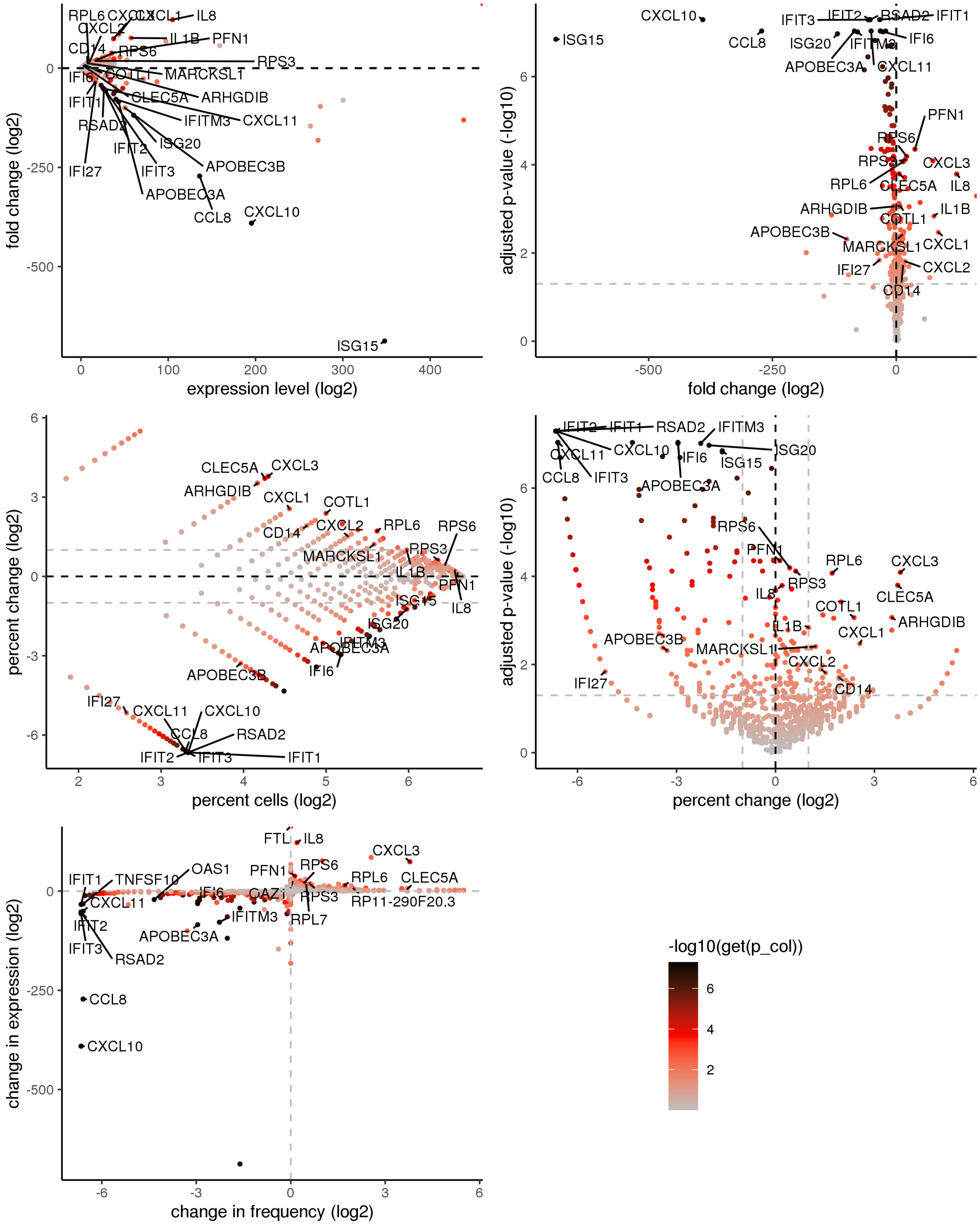
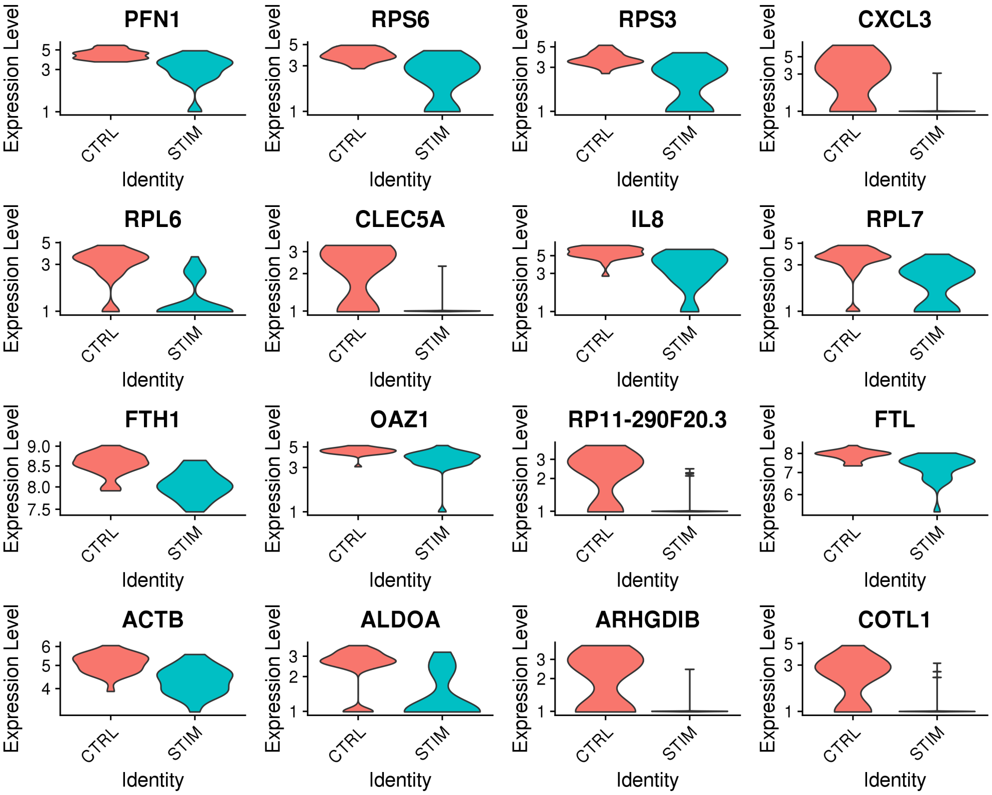
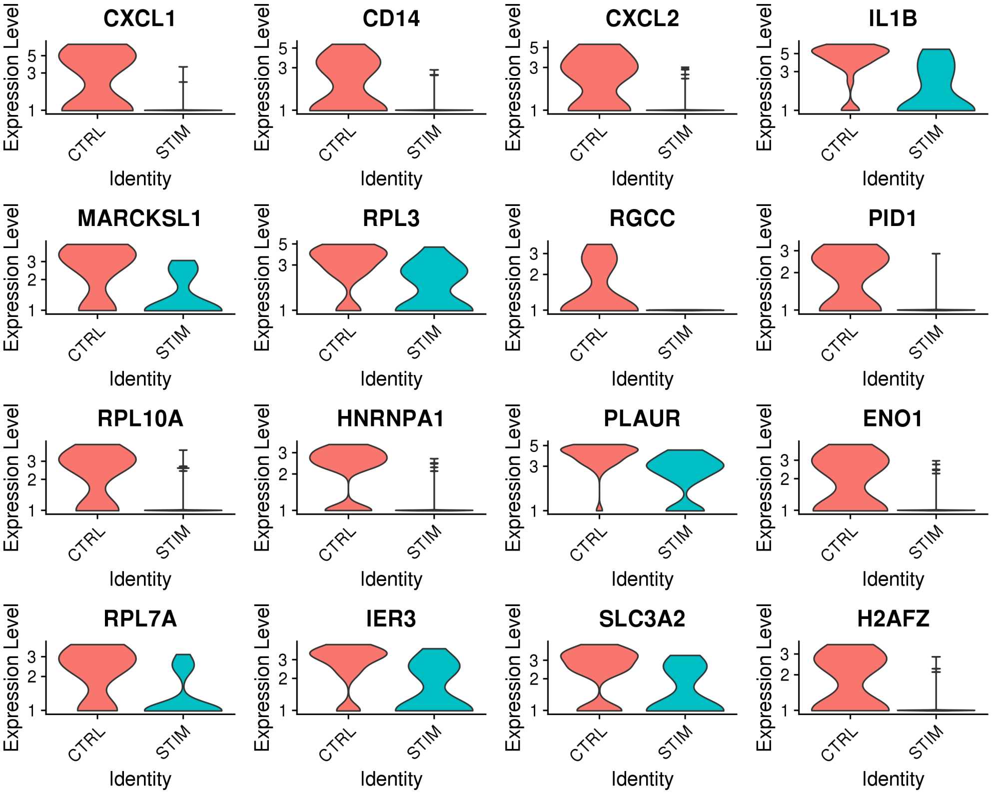


Figure 144: Differential expression summary plots for cluster 14

14.47 Cluster 14 violin plots: positively differentially expressed genes

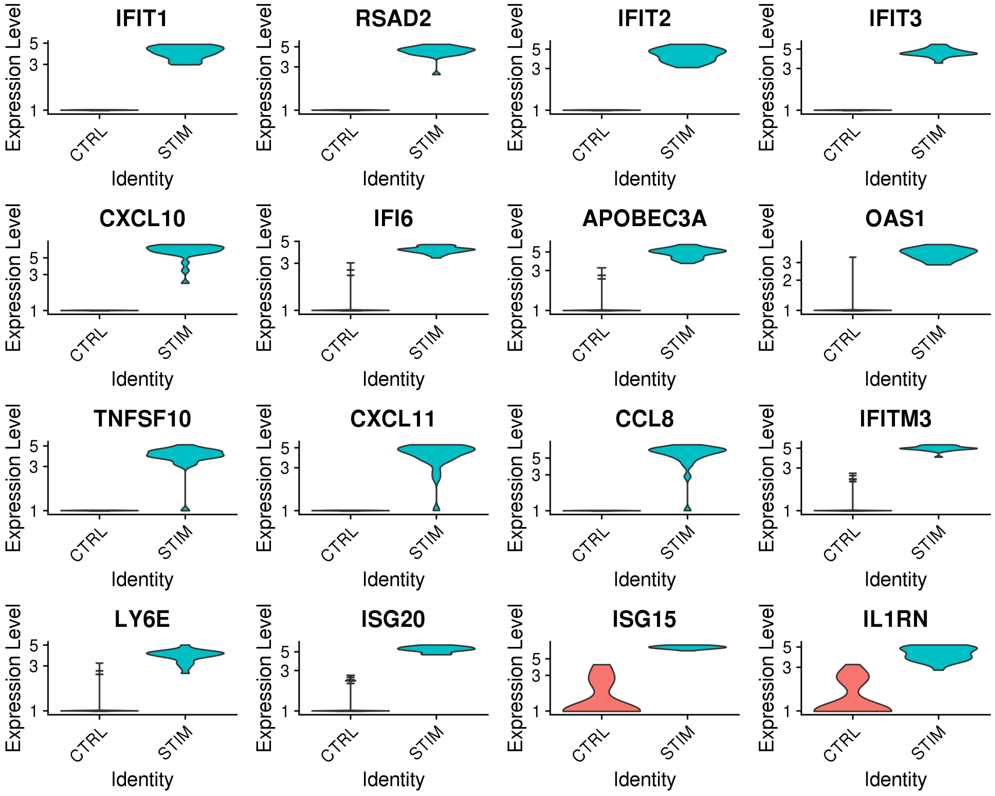


(a) Top positively differentially expressed genes ordered by p-value, cluster: 14

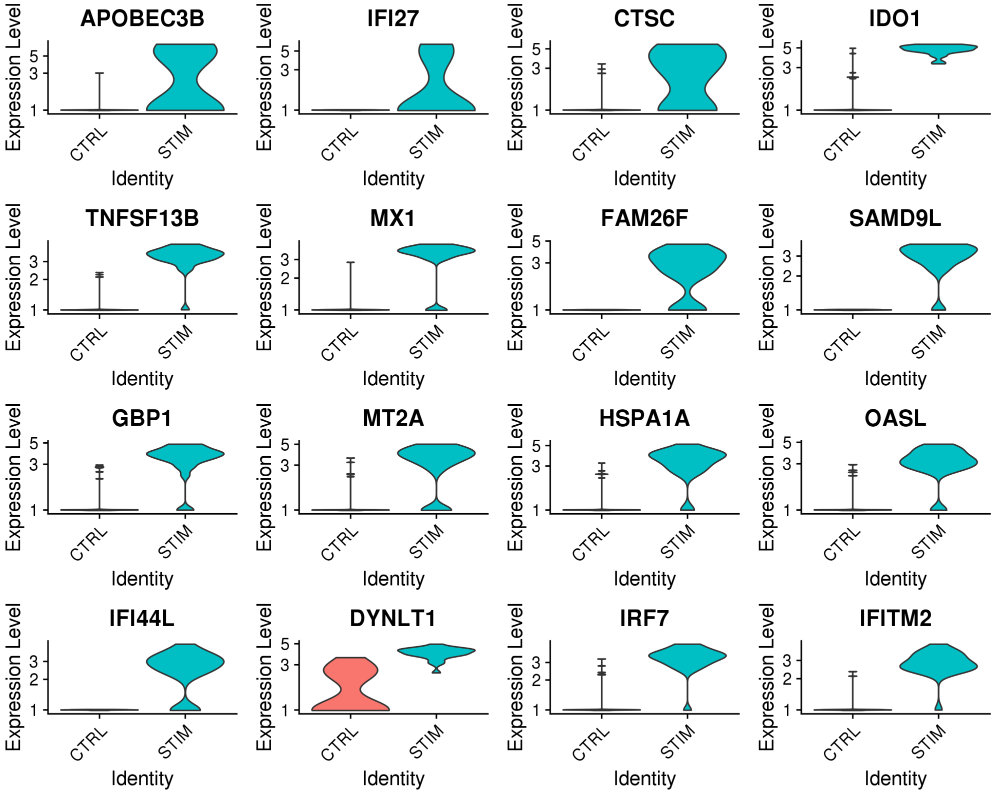


(b) Additional positively differentially expressed genes ordered by fold change, cluster: 14

14.48 Cluster 14 violin plots: negatively differentially expressed genes



(a) Top negatively differentially expressed genes ordered by p-value, cluster: 14



(b) Additional negatively differentially expressed genes ordered by fold change, cluster: 14

15 Geneset enrichment analysis of within-cluster differentially expressed genes

A hypergeometric test is used to test for the enrichment of GO, KEGG and msigdb genesets amongst the positive marker genes for each cluster. The full results are available as a separate xlsx document.

15.1 GO.BP

Figure 147: Heatmap of the top GO.BP genesets

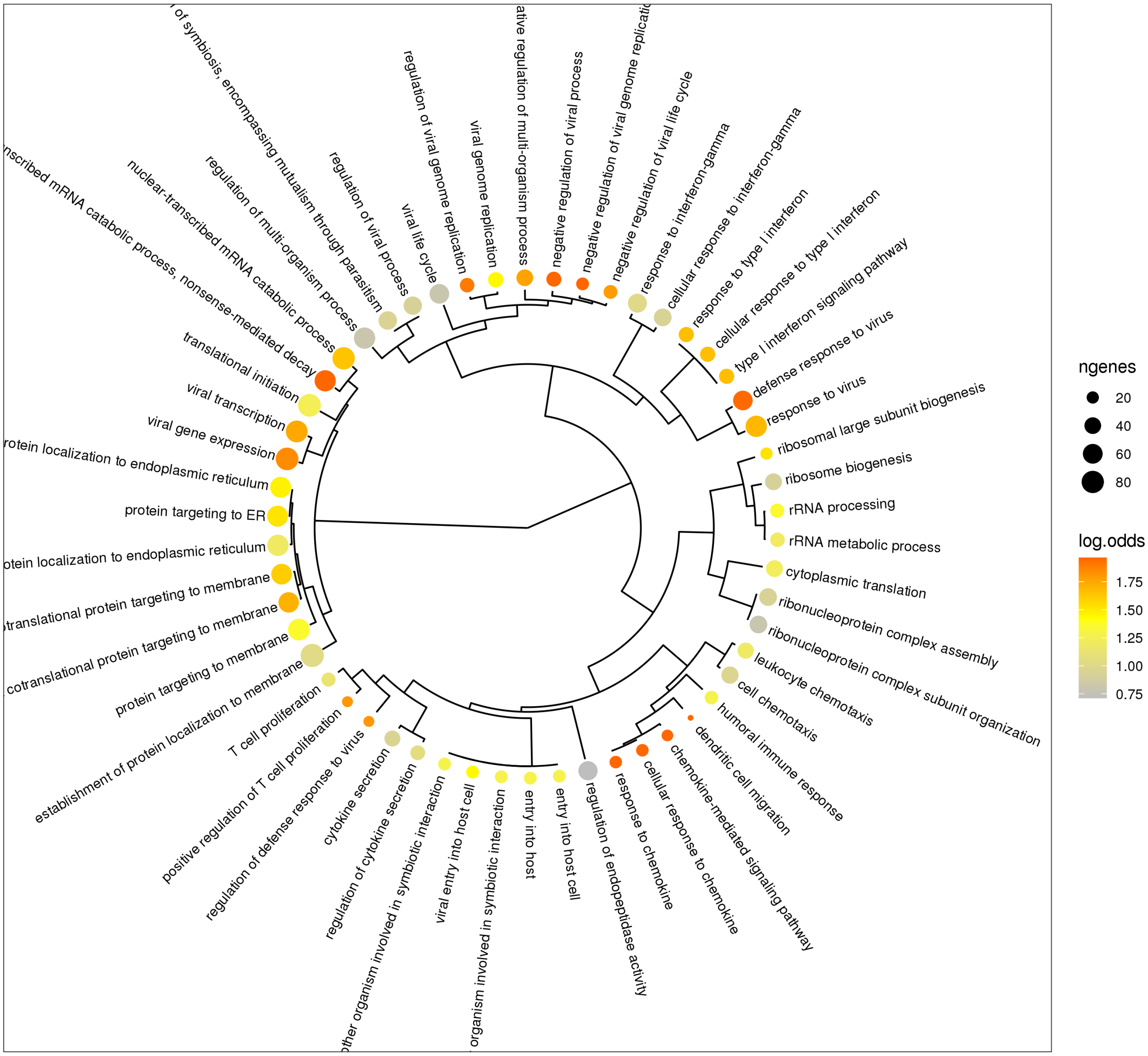


Figure 148: Cluster 0 GO.BP genesets clustered by similarity between over-represented genes.

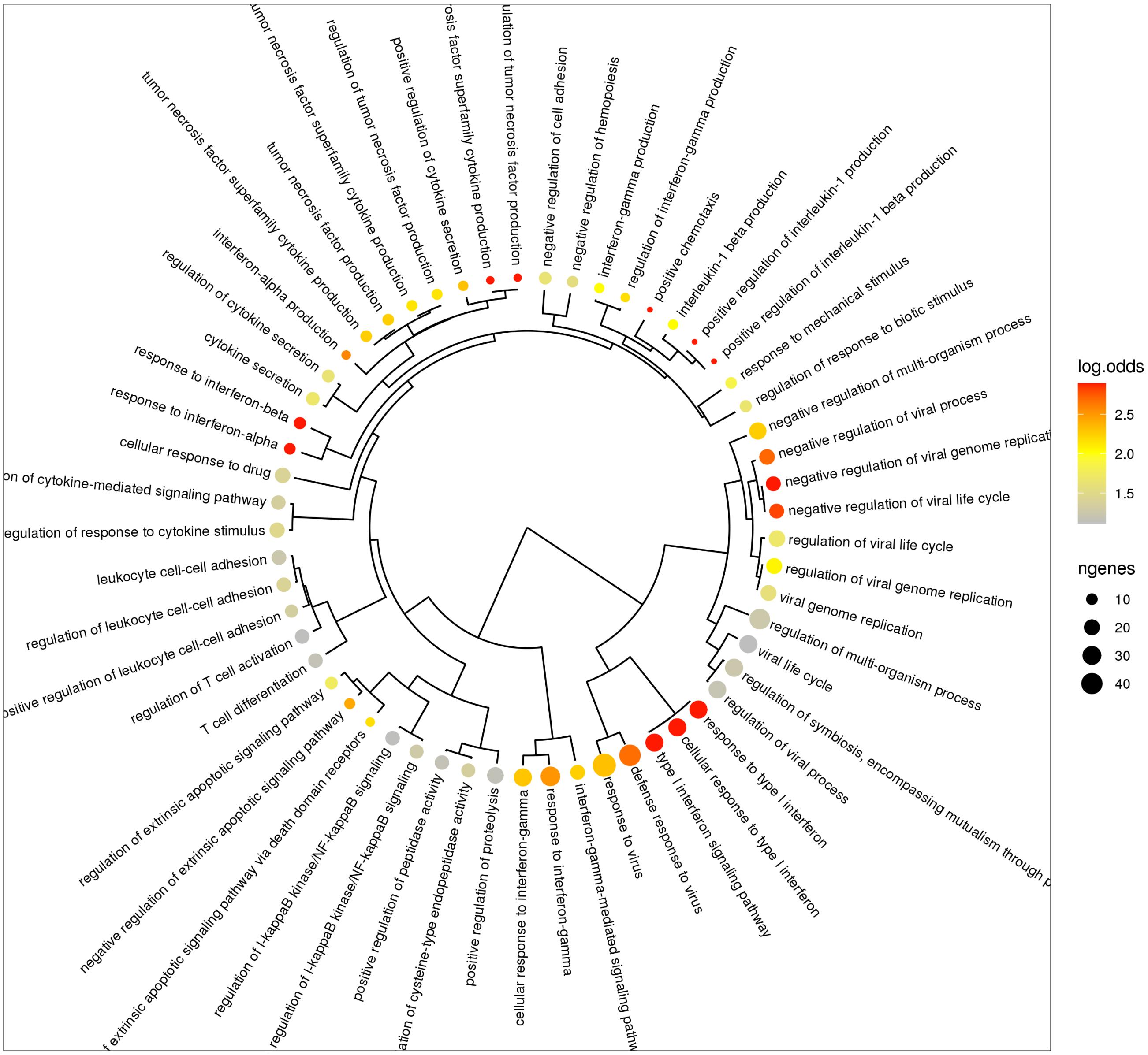


Figure 149: Cluster 1 GO.BP genesets clustered by similarity between over-represented genes.

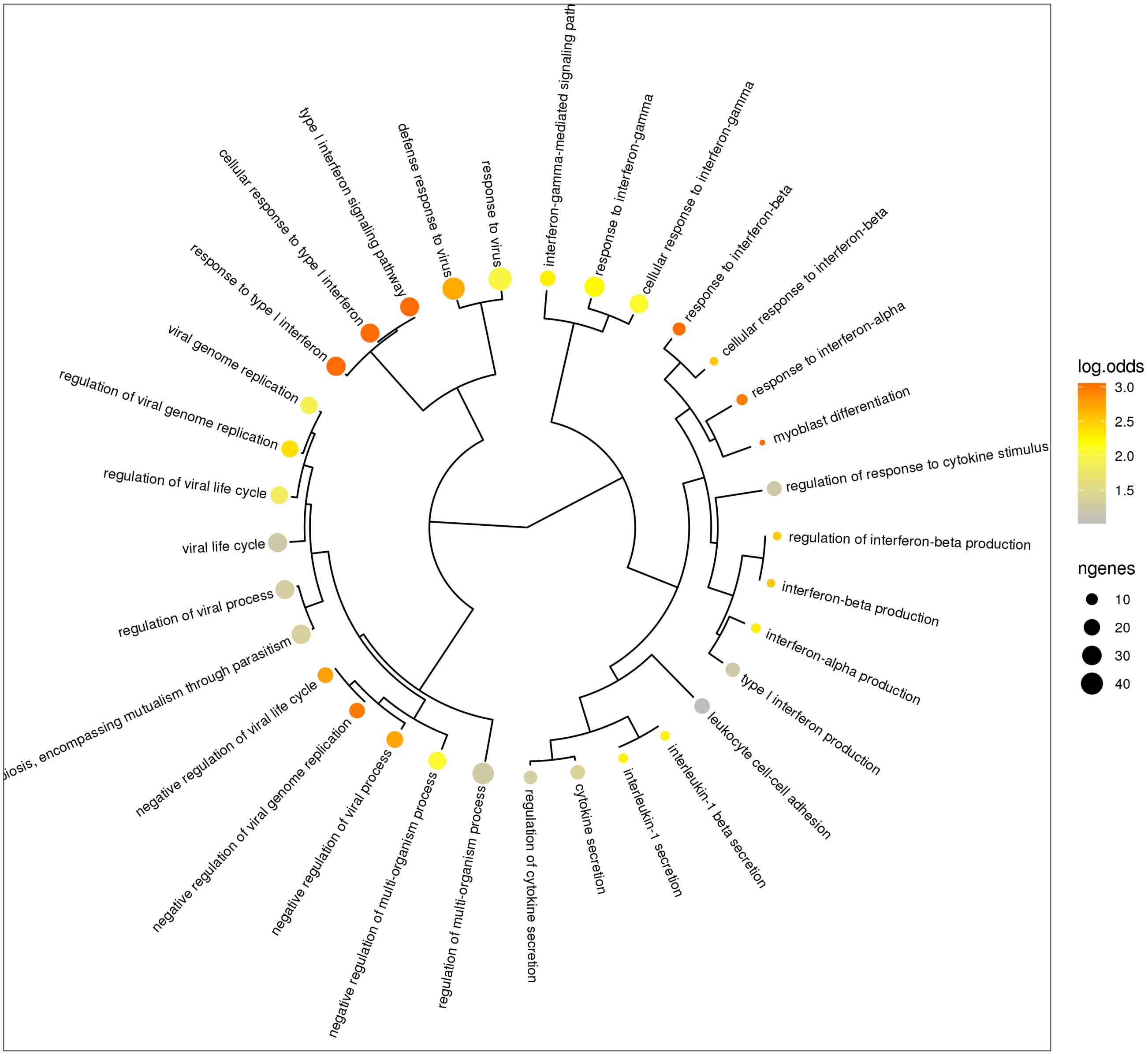


Figure 150: Cluster 2 GO.BP genesets clustered by similarity between over-represented genes.

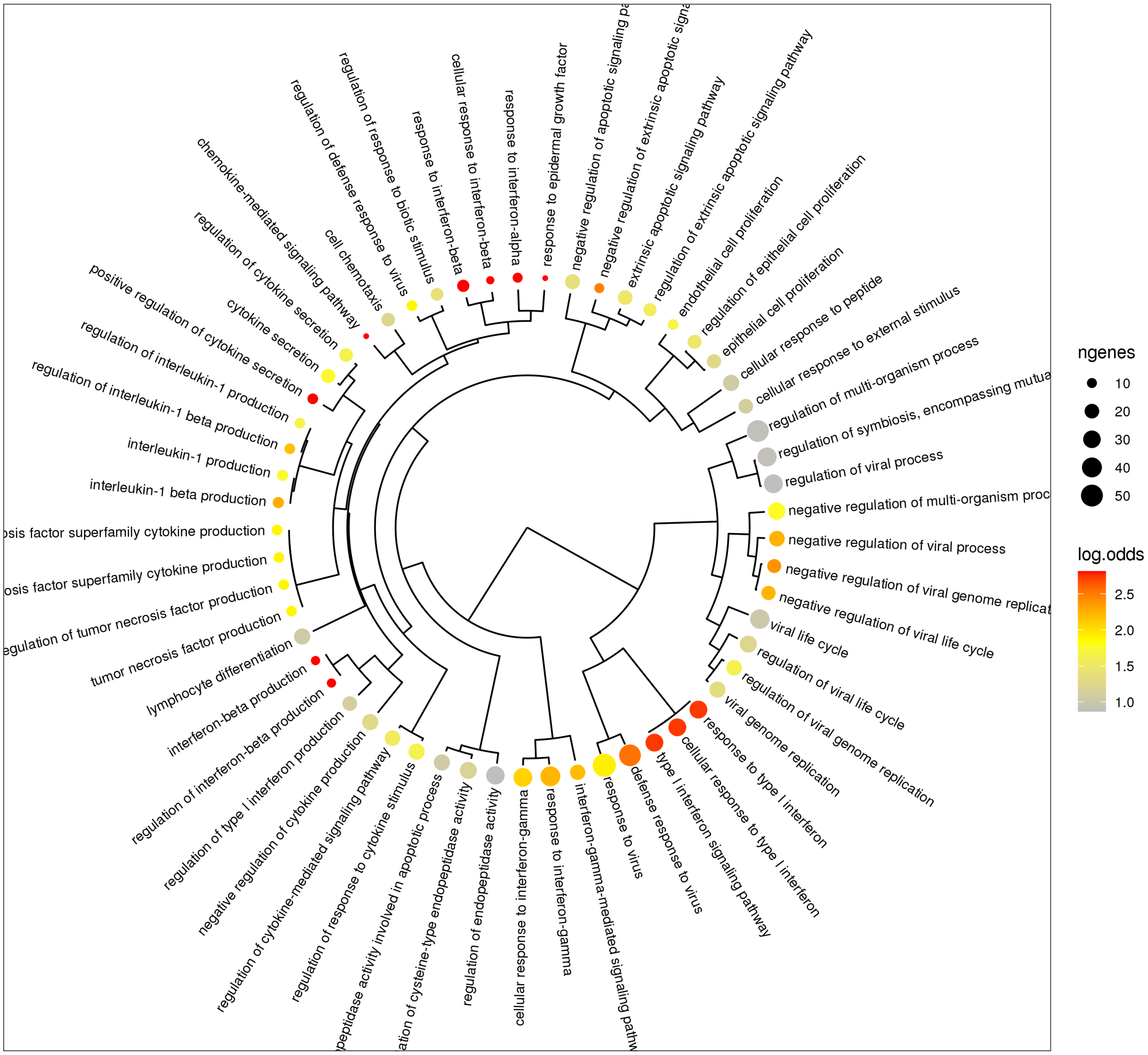


Figure 151: Cluster 3 GO.BP genesets clustered by similarity between over-represented genes.

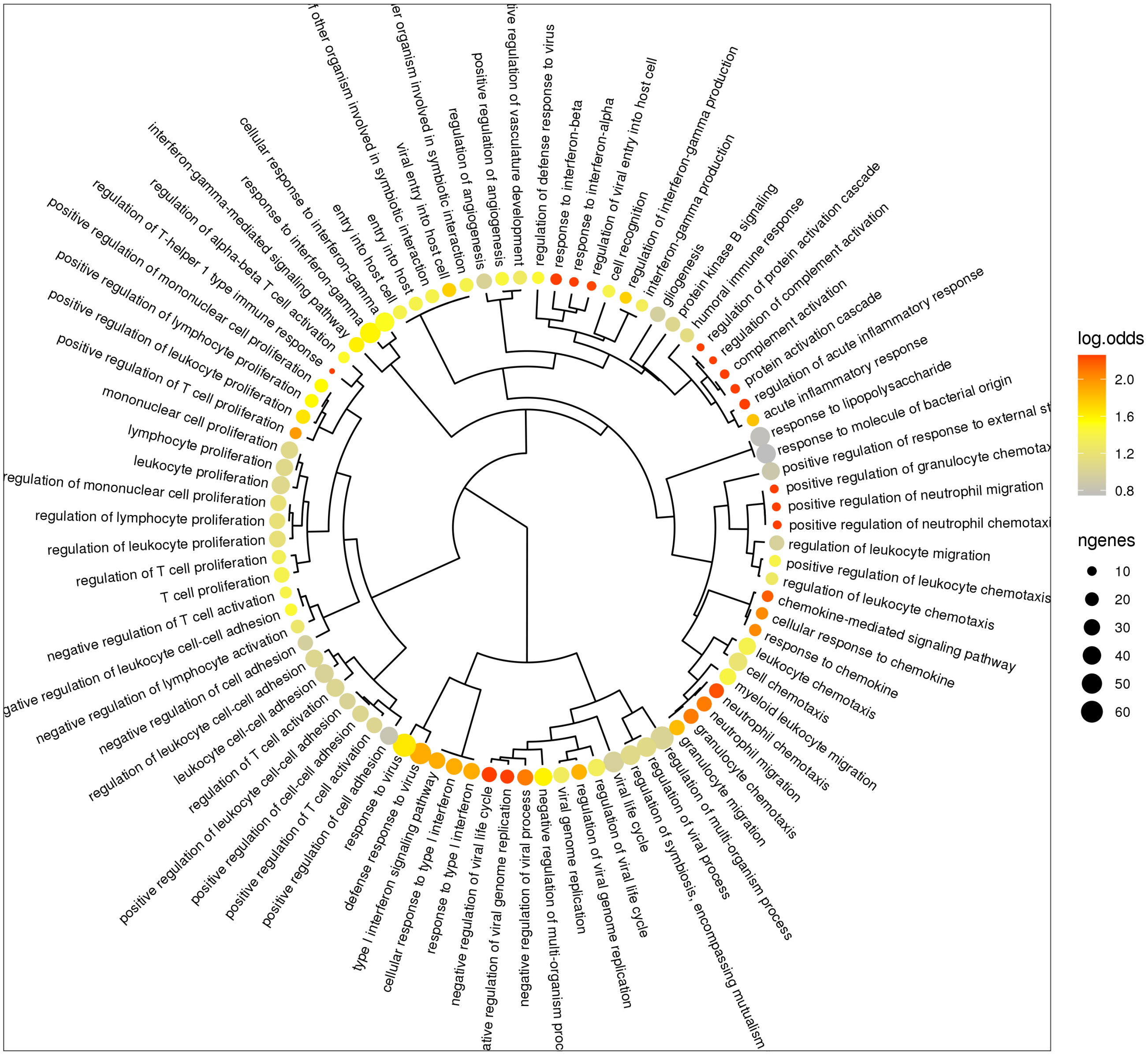


Figure 152: Cluster 4 GO.BP genesets clustered by similarity between over-represented genes.

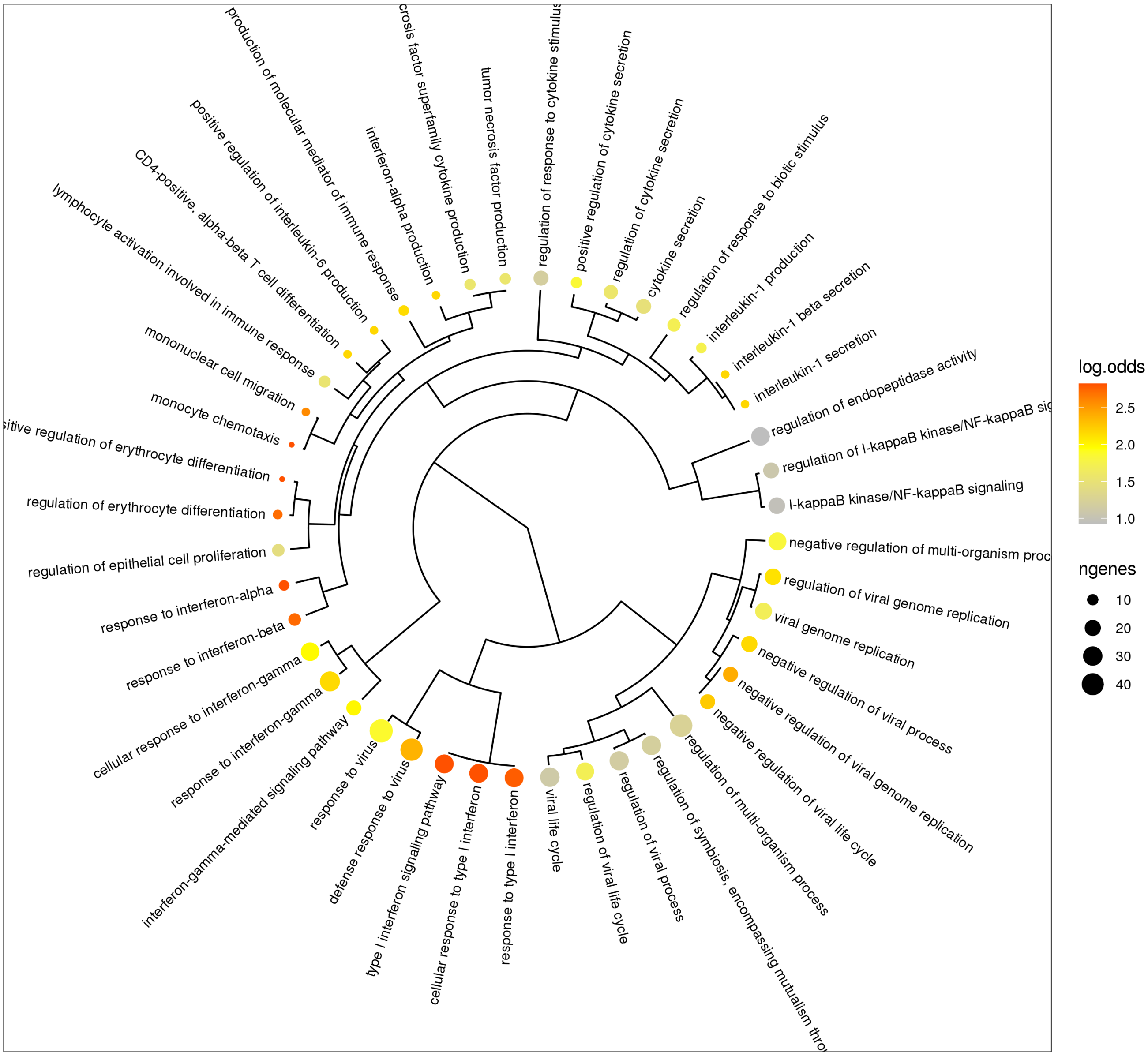


Figure 153: Cluster 5 GO.BP genesets clustered by similarity between over-represented genes.

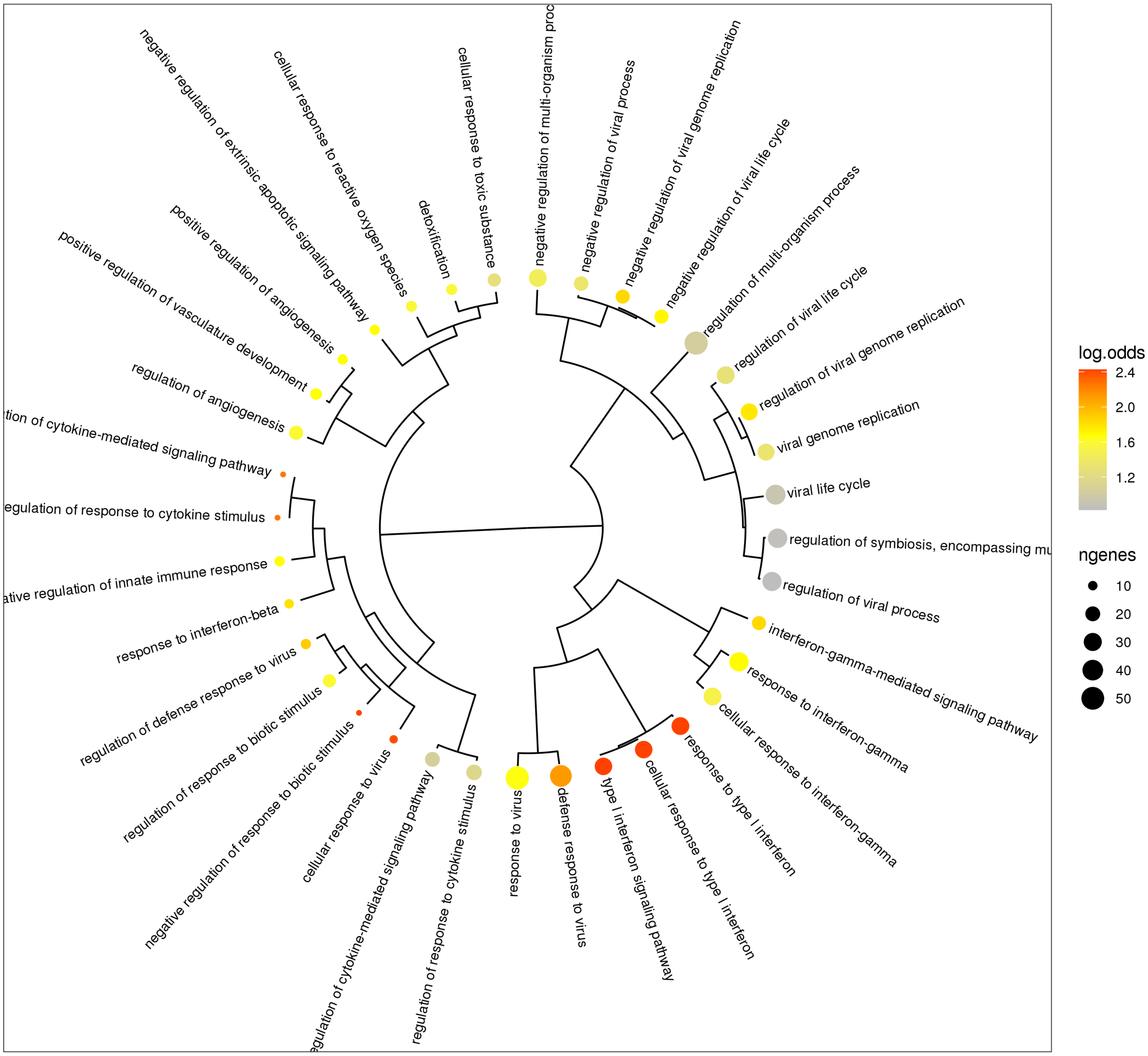


Figure 154: Cluster 6 GO.BP genesets clustered by similarity between over-represented genes.

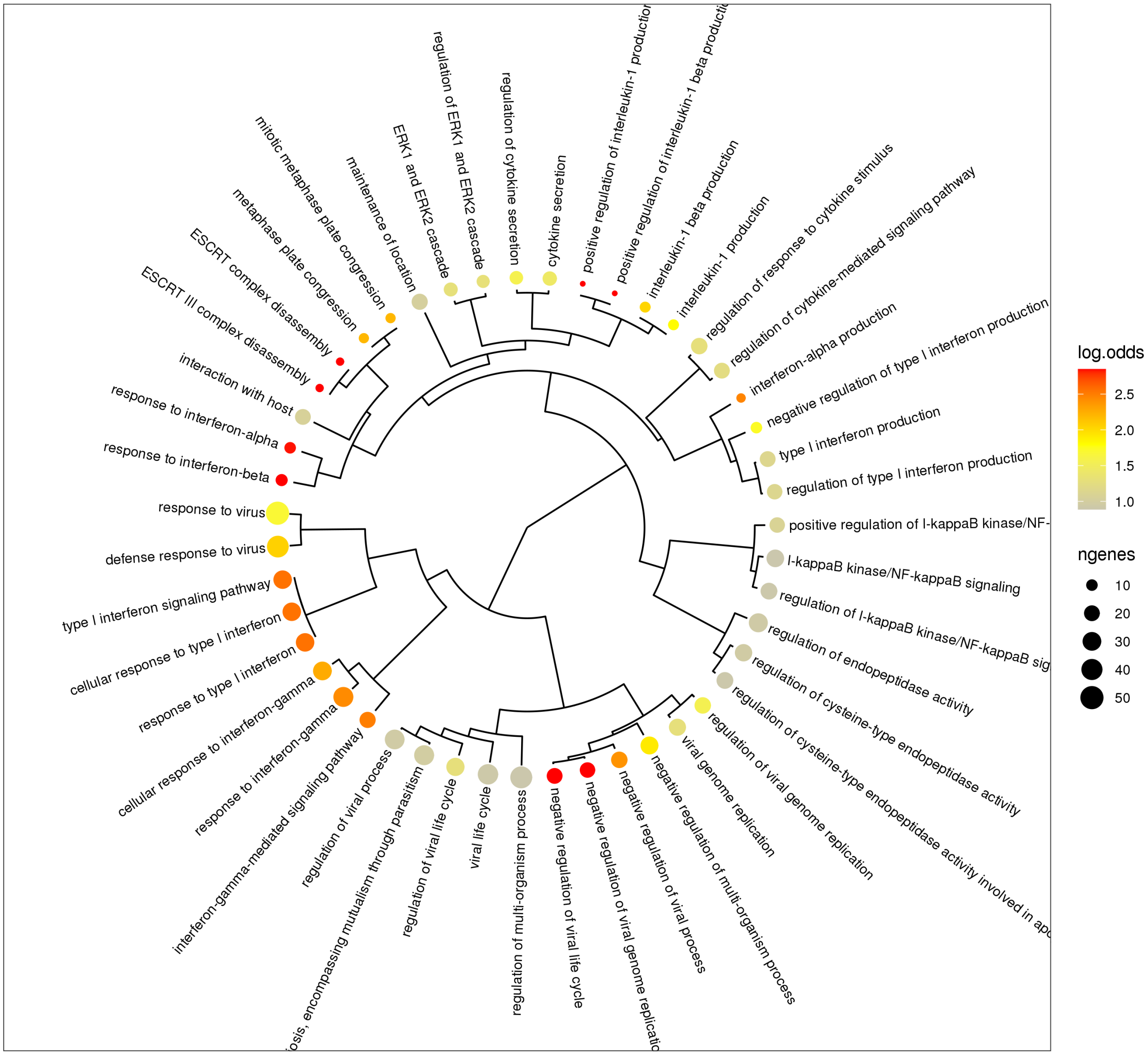


Figure 155: Cluster 7 GO.BP genesets clustered by similarity between over-represented genes.

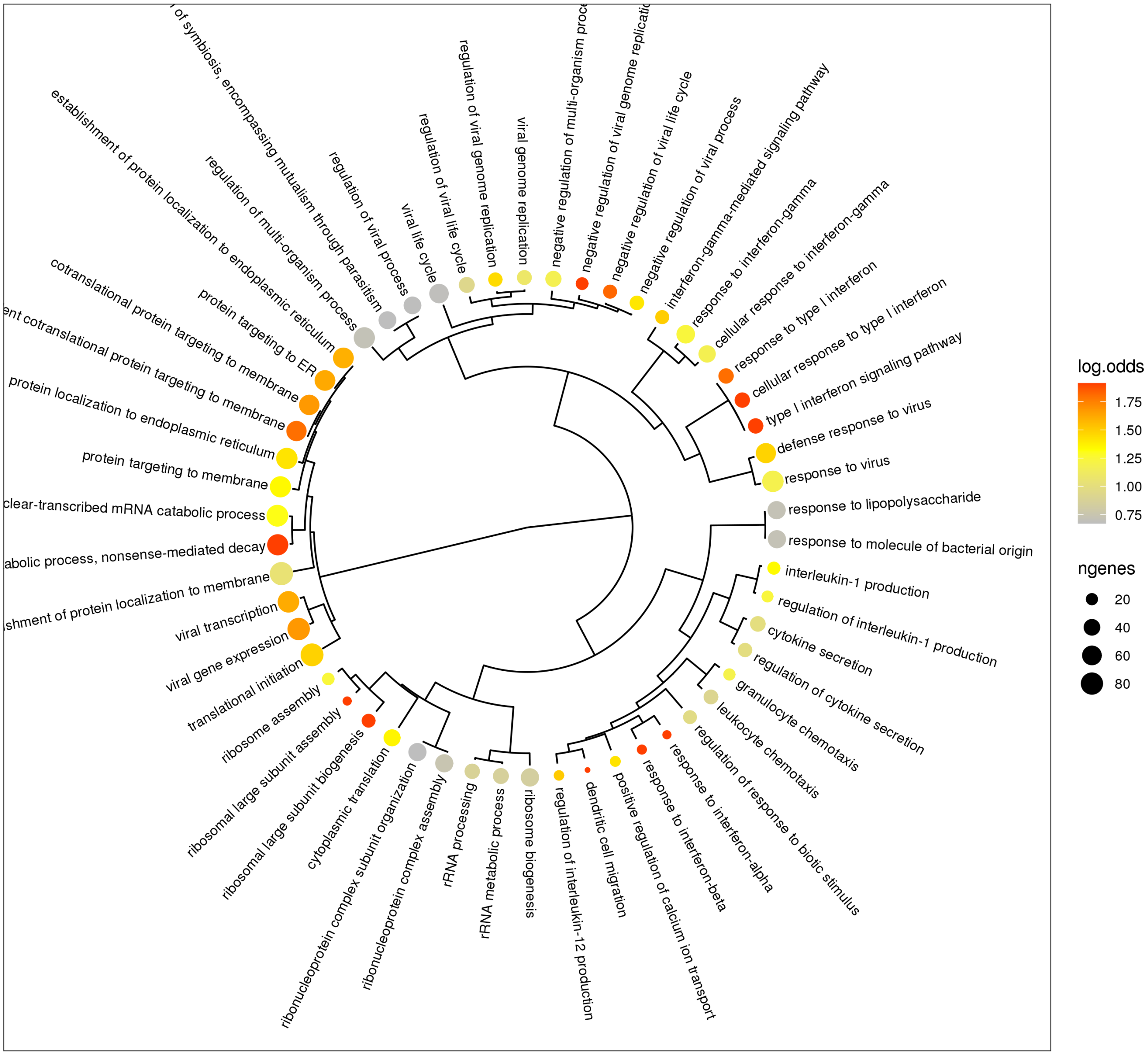


Figure 156: Cluster 8 GO.BP genesets clustered by similarity between over-represented genes.

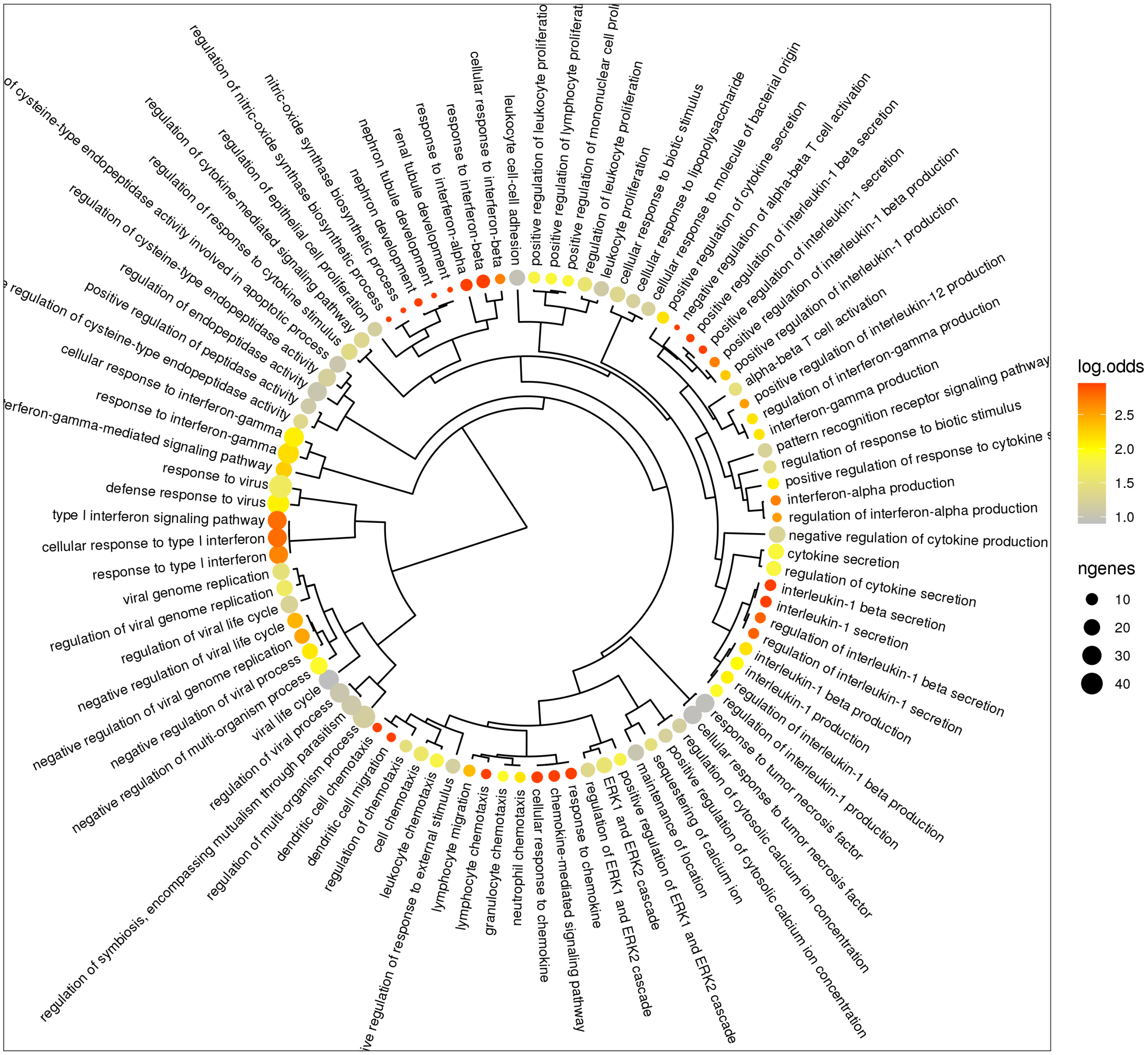


Figure 157: Cluster 9 GO.BP genesets clustered by similarity between over-represented genes.

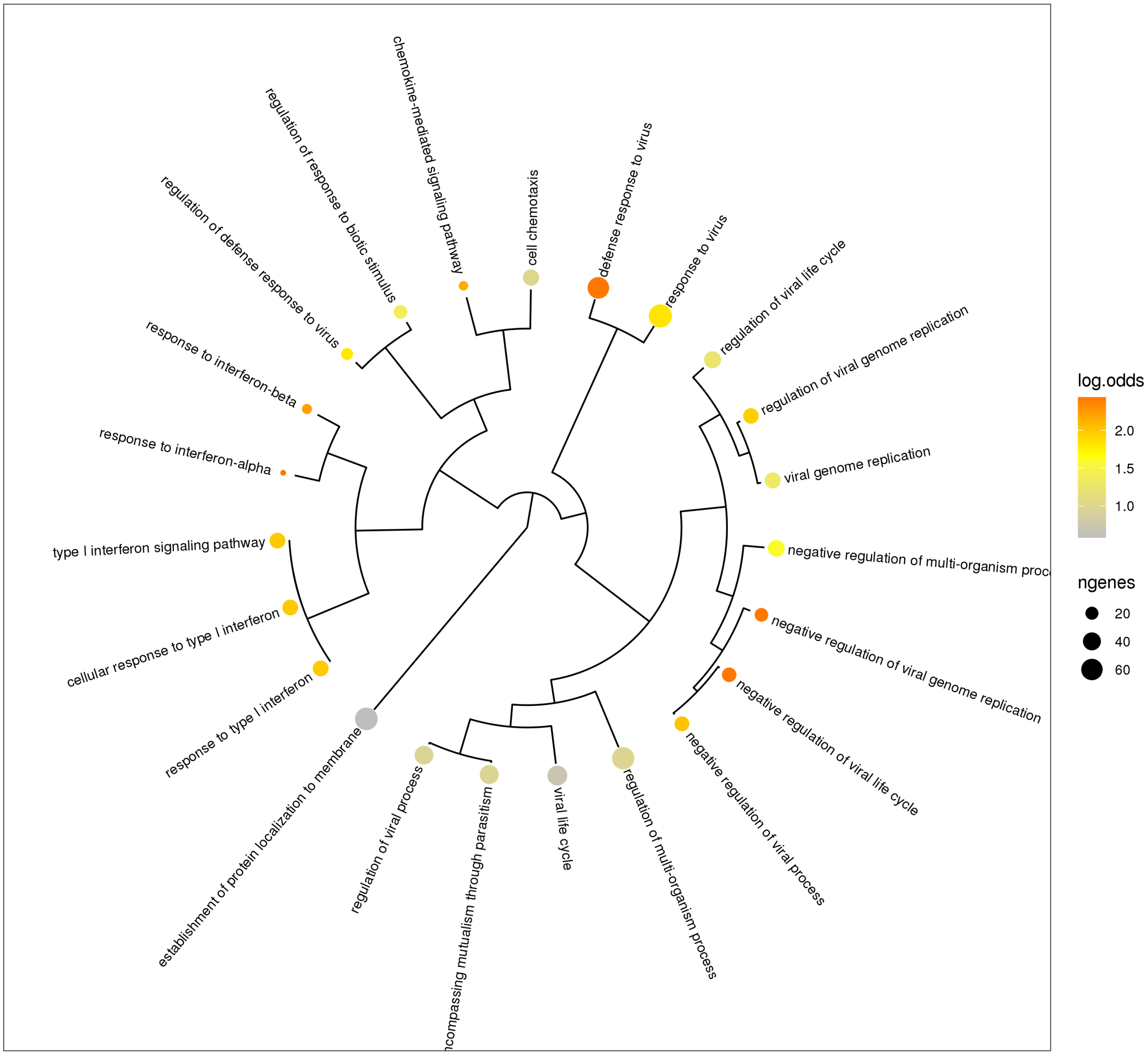


Figure 158: Cluster 10 GO.BP genesets clustered by similarity between over-represented genes.

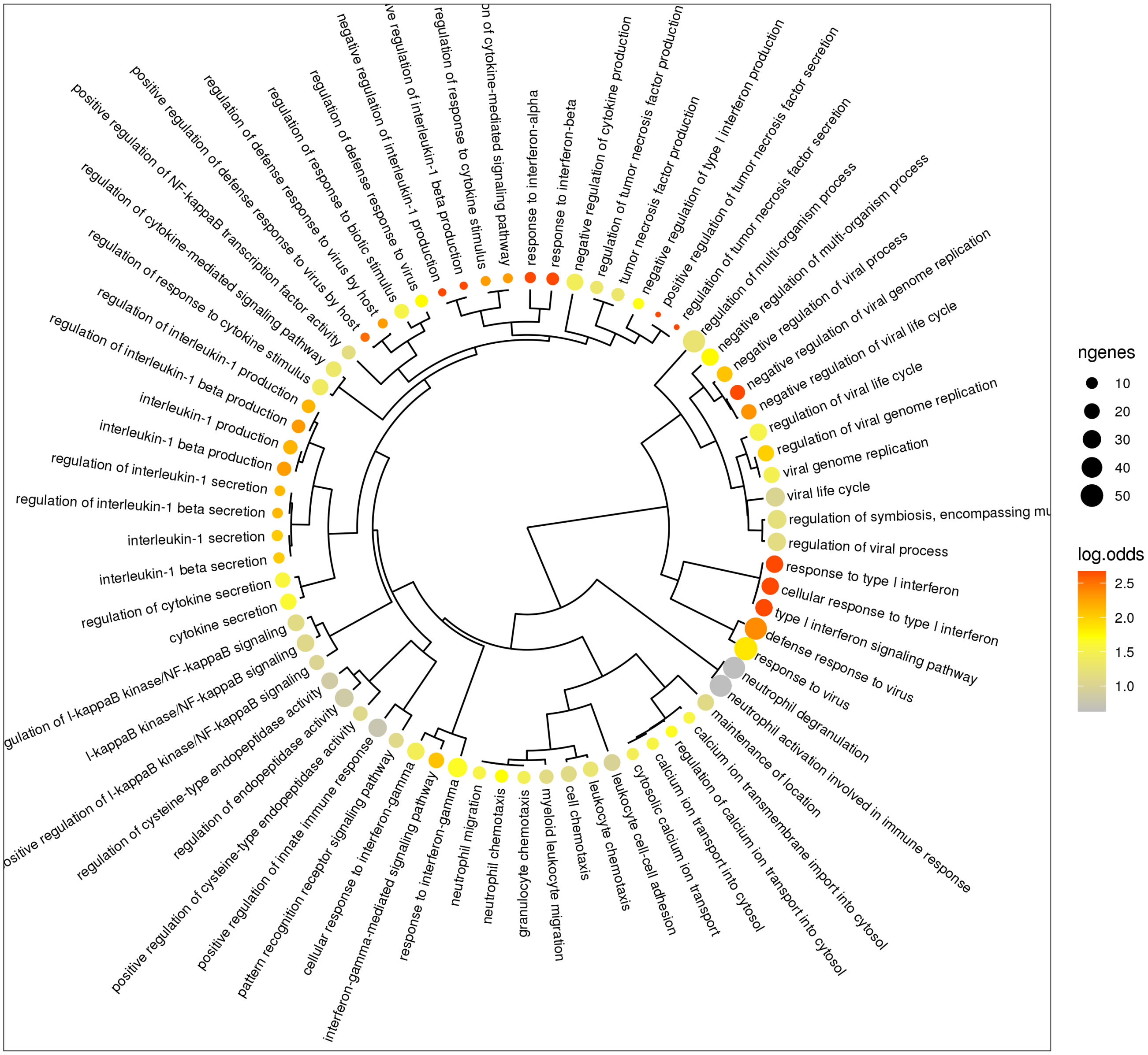


Figure 159: Cluster 11 GO.BP genesets clustered by similarity between over-represented genes.

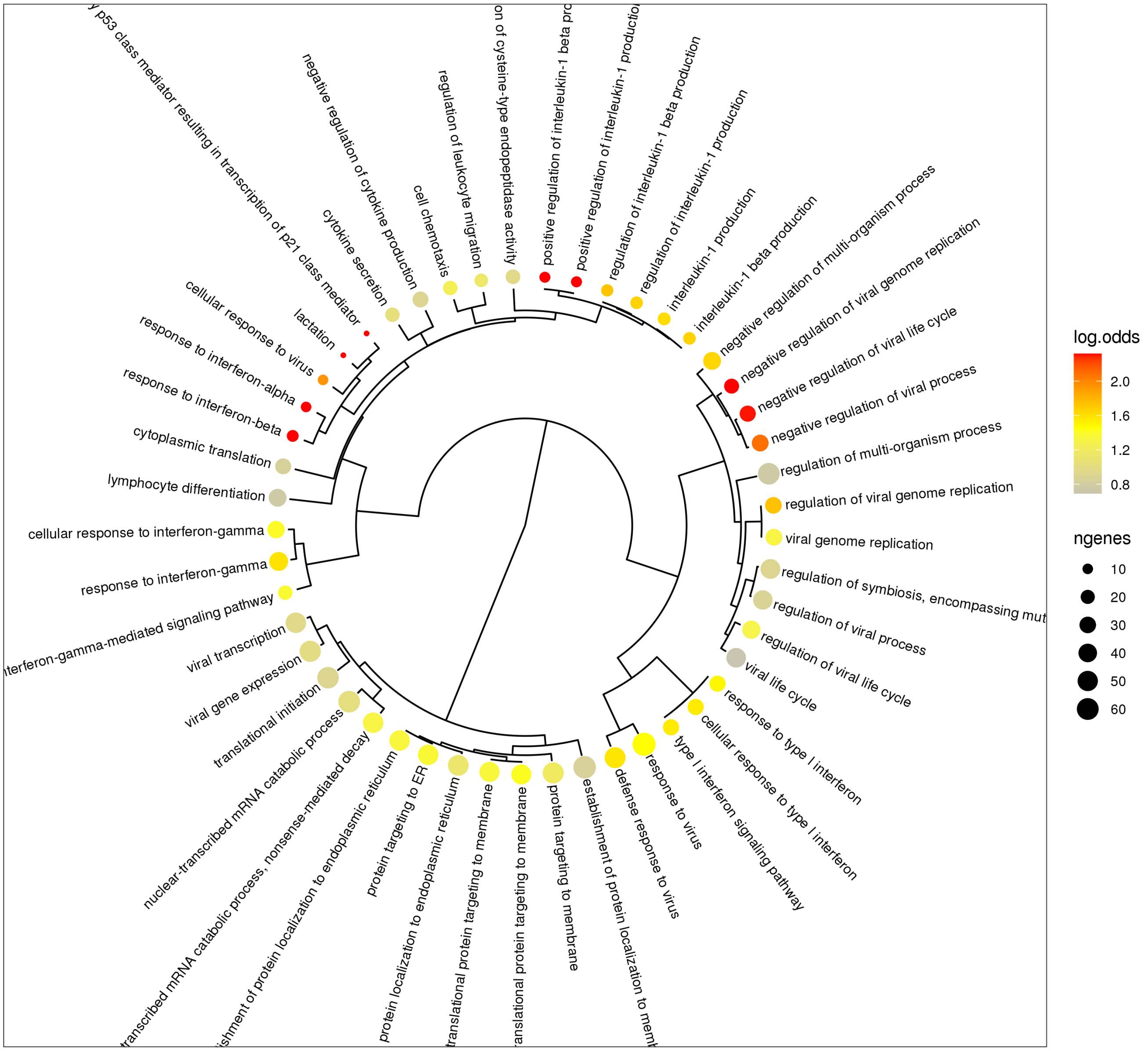


Figure 160: Cluster 12 GO.BP genesets clustered by similarity between over-represented genes.

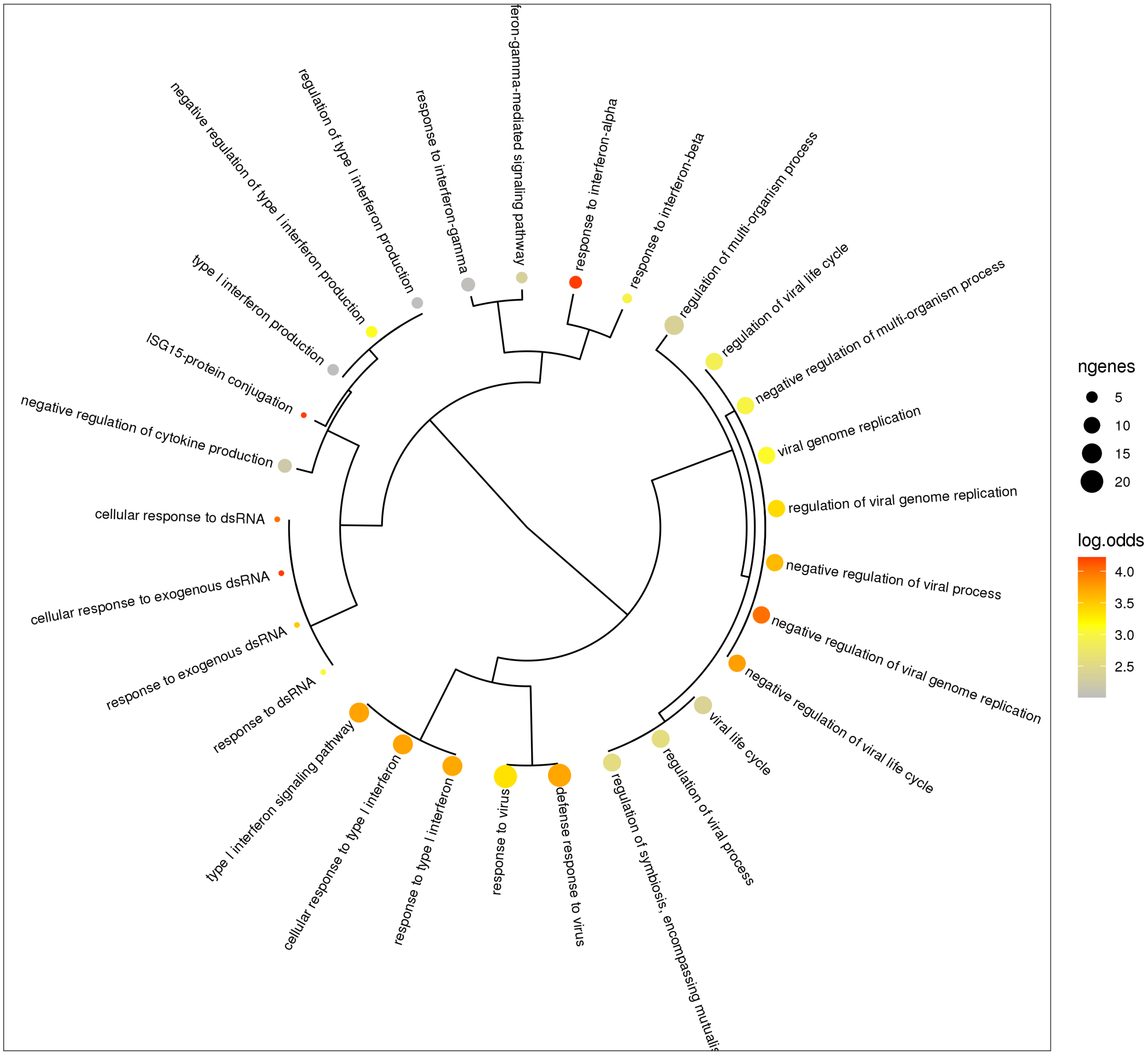


Figure 161: Cluster 13 GO.BP genesets clustered by similarity between over-represented genes.

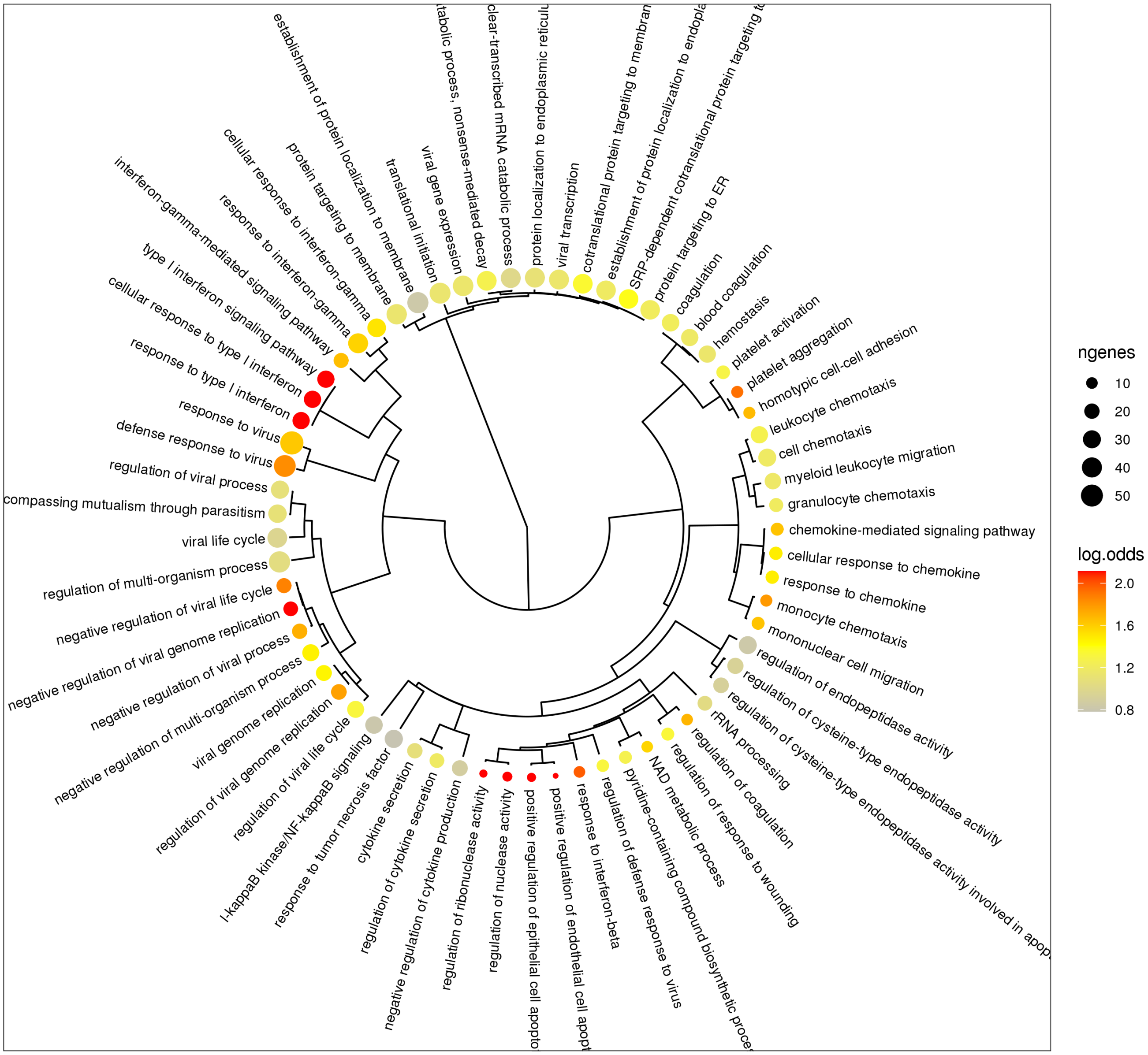


Figure 162: Cluster 14 GO.BP genesets clustered by similarity between over-represented genes.

15.2 GO.MF

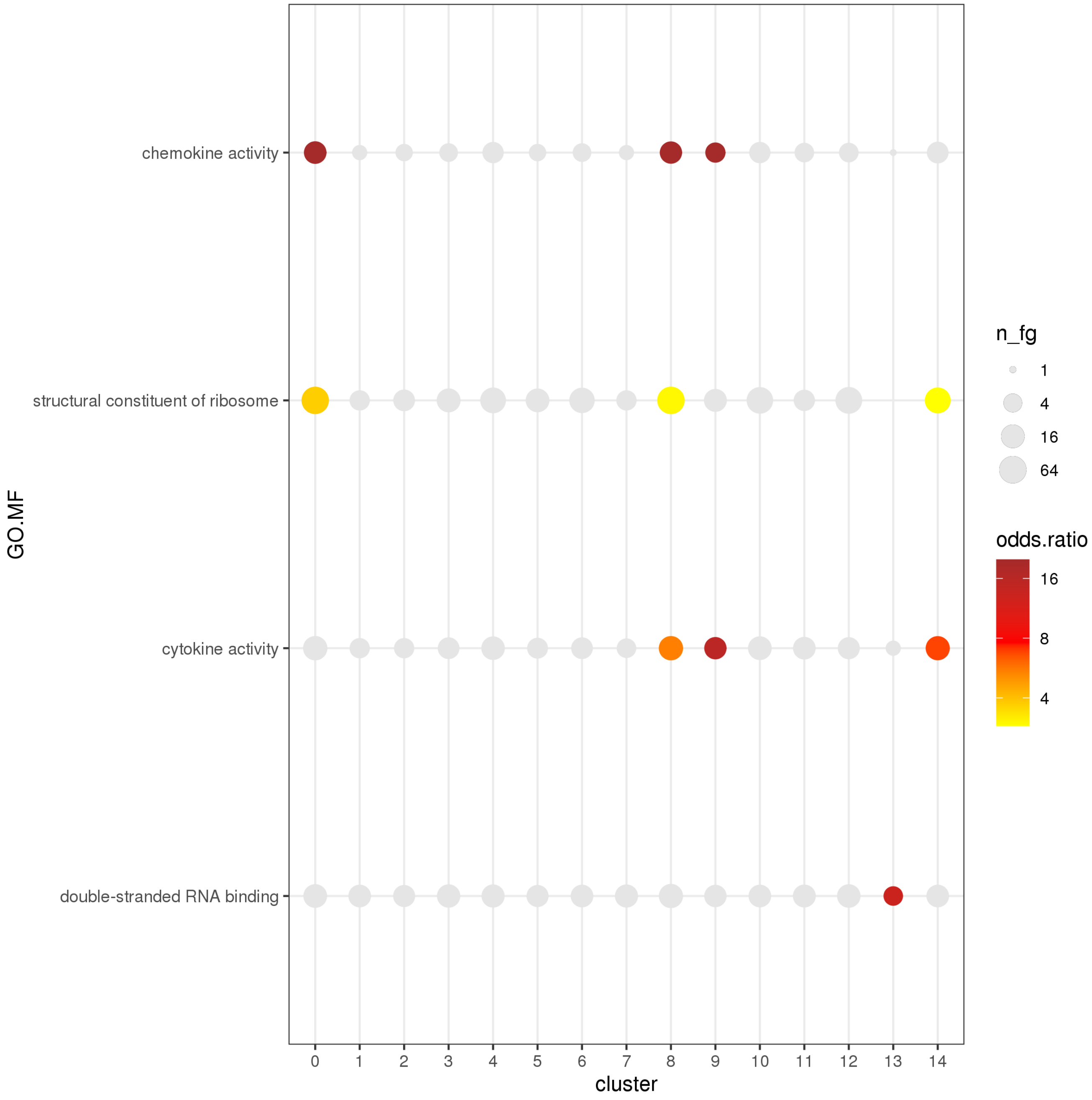


Figure 163: Heatmap of the top GO.MF genesets

15.3 GO.CC

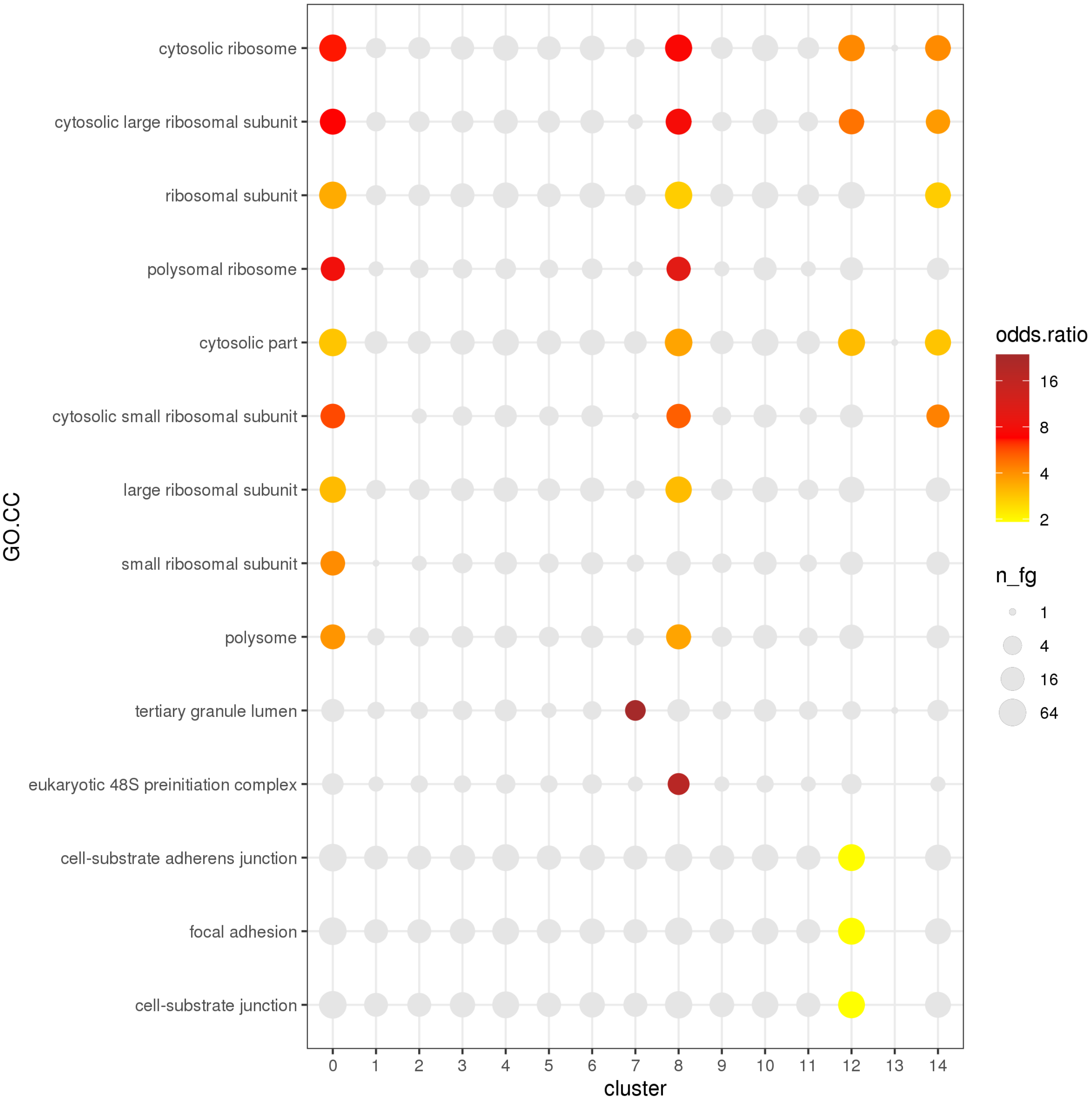


Figure 164: Heatmap of the top GO.CC genesets

15.4 KEGG

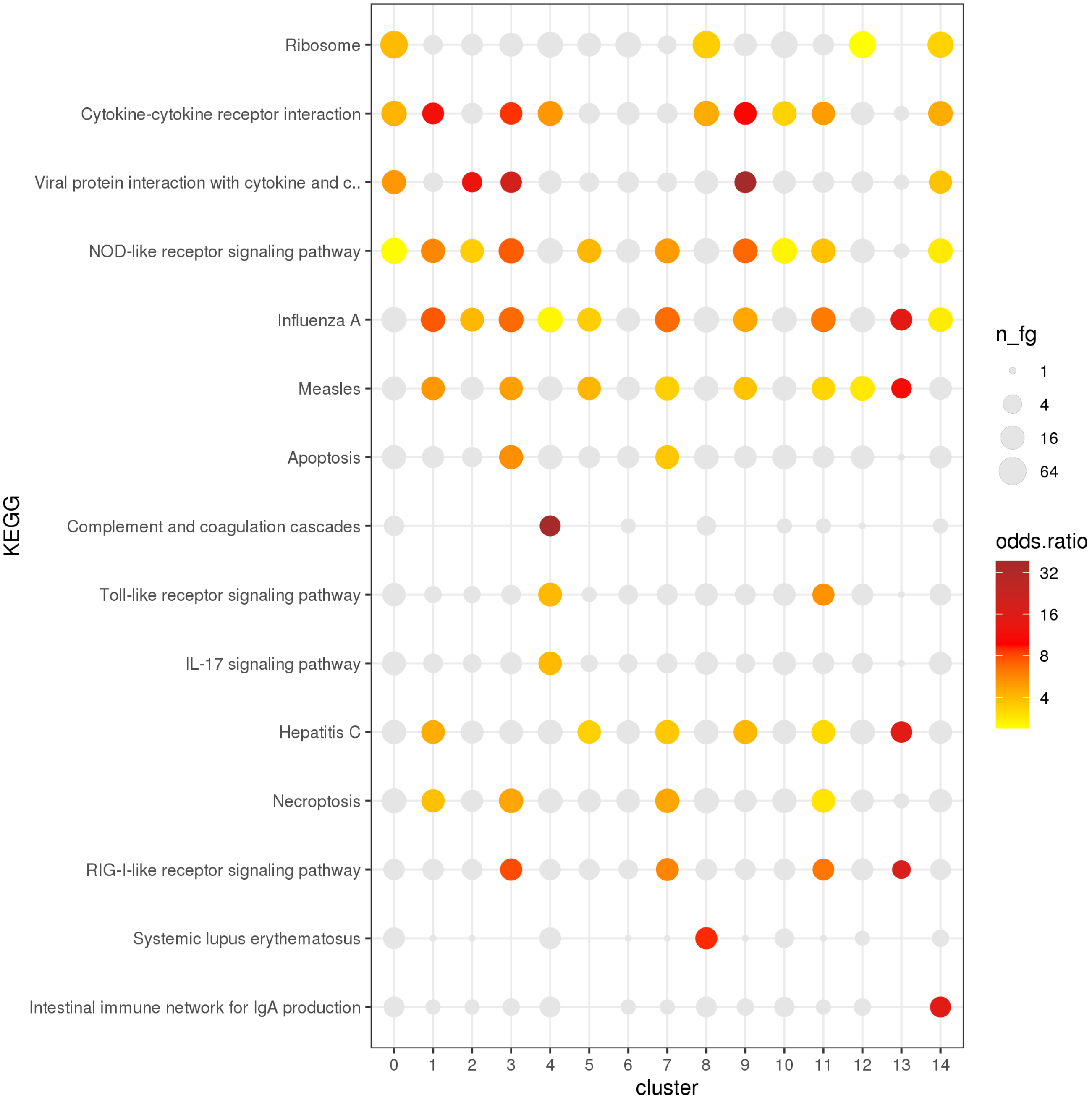


Figure 165: Heatmap of the top KEGG genesets

15.5 msigdb_biocarta

no significant genesets for:
msigdb_biocarta

Figure 166: Heatmap of the top msigdb_biocarta genesets

15.6 msigdb_reactome

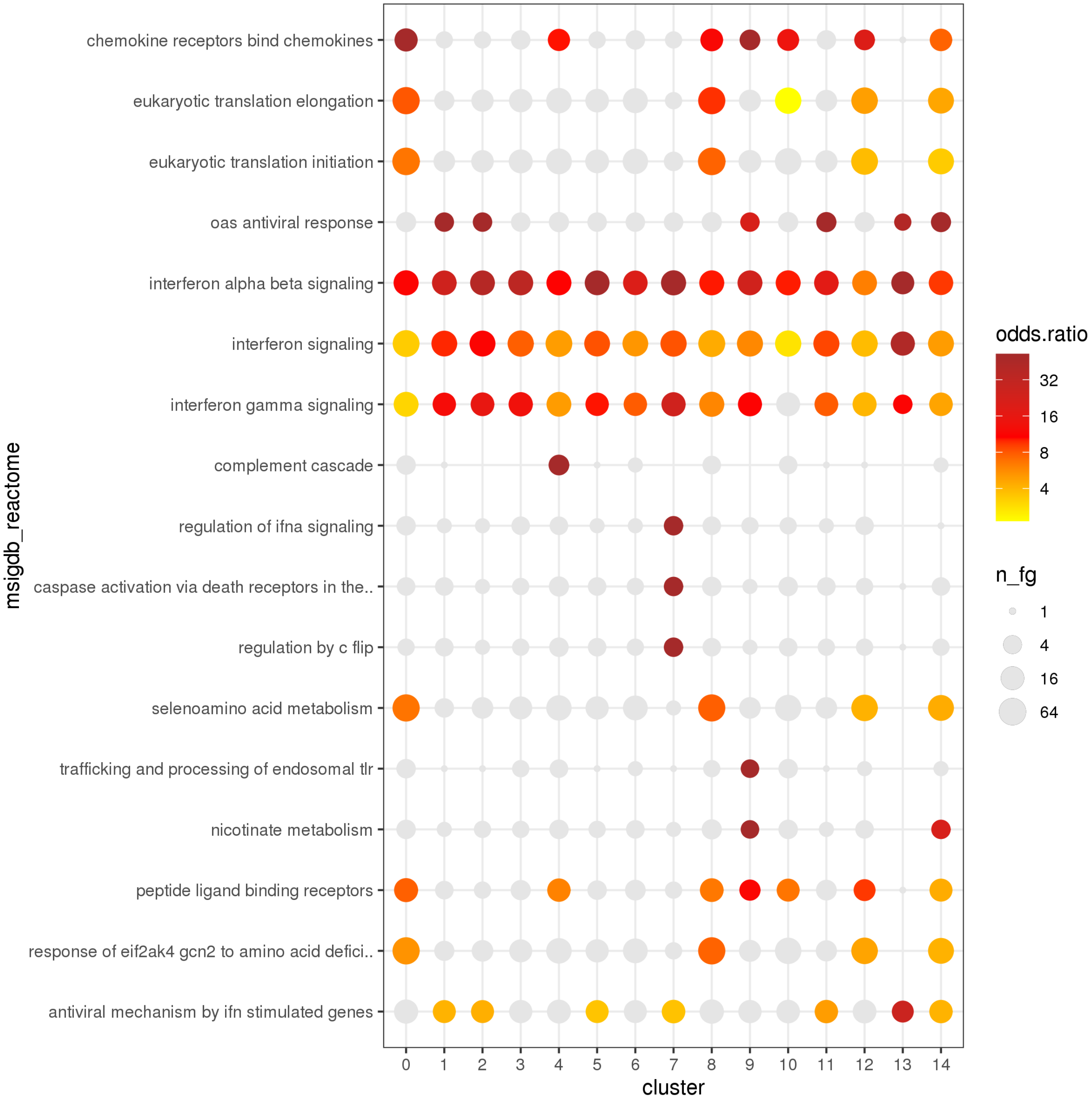


Figure 167: Heatmap of the top msigdb_reactome genesets

15.7 msigdb__canonical__pathways

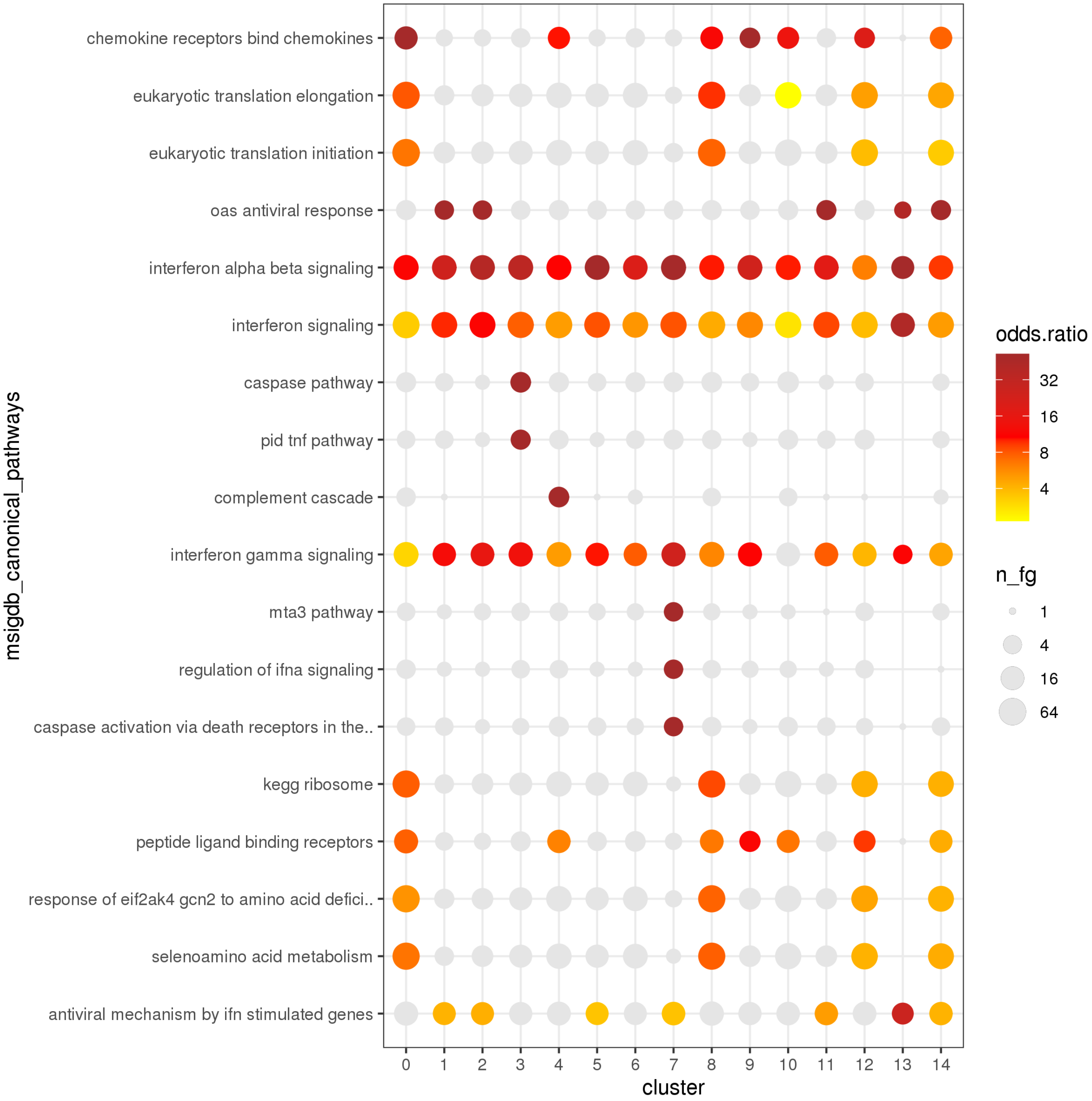


Figure 168: Heatmap of the top msigdb__canonical__pathways genesets

15.8 msigdb__tf__motifs

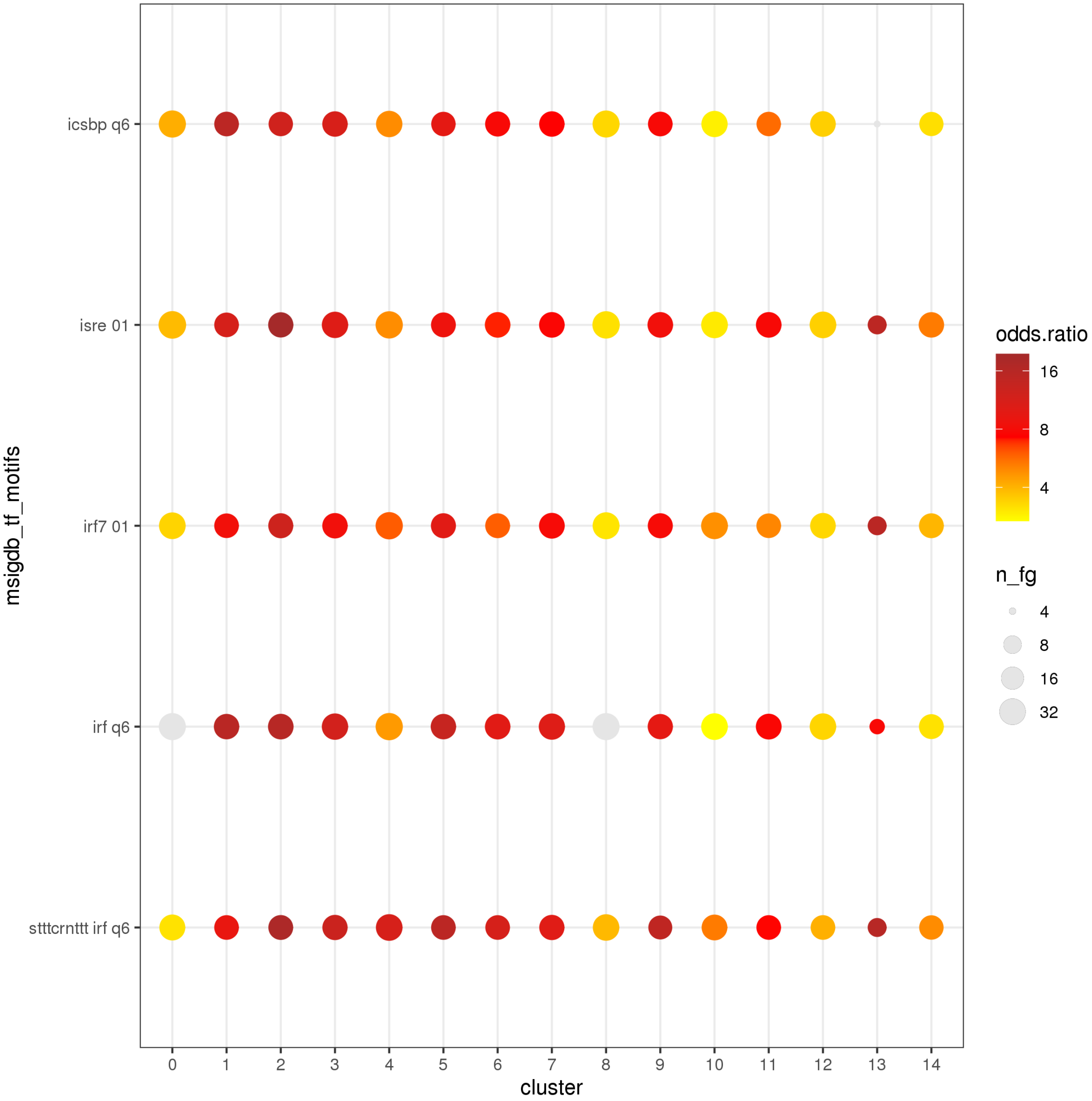


Figure 169: Heatmap of the top msigdb__tf__motifs genesets

15.9 msigdb_immunological_signatures

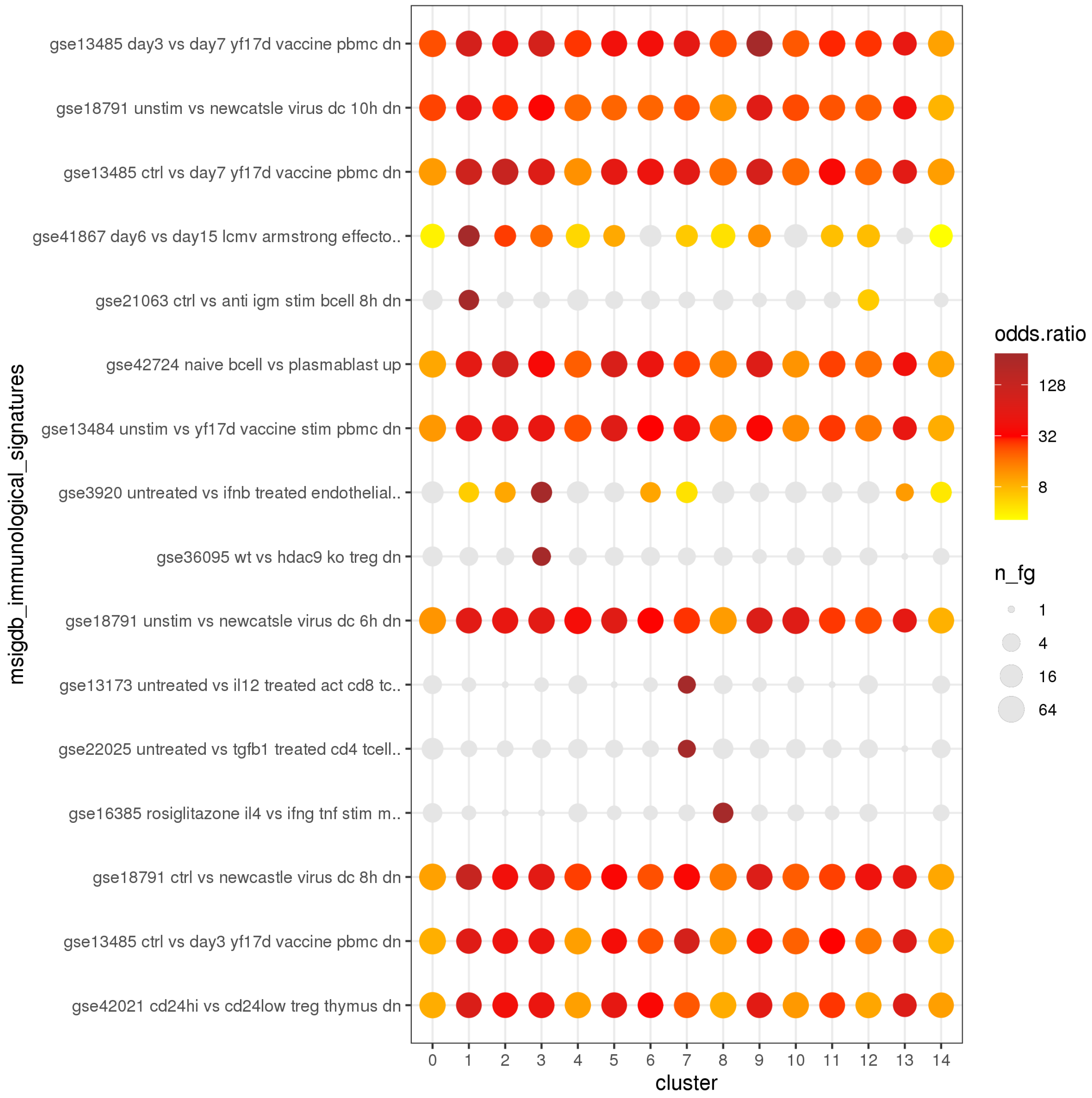


Figure 170: Heatmap of the top msigdb_immunological_signatures genesets

15.10 Top genesets by cluster

The table lists the top (filtered by nominal p value) genesets by cluster.

cluster	type	description	p.val	p.adj	n__fg	odds.ratio	n.clust
0	GO.BP	viral gene expression	7.42e-15	7.81e-12	83	6.33	4
0	GO.BP	nuclear-transcribed mRNA catabolic process, n..	9.58e-14	5.55e-11	71	7.15	4
0	GO.BP	viral transcription	5.54e-13	2.61e-10	76	5.75	4
0	GO.BP	nuclear-transcribed mRNA catabolic process	7.39e-13	3.37e-10	81	5.18	4
0	GO.BP	response to virus	6.12e-12	2.3e-09	72	5.42	15
0	GO.MF	structural constituent of ribosome	9.24e-09	2.32e-05	69	3.74	3
0	GO.MF	chemokine activity	0.000112	0.0421	12	Inf	3
0	GO.CC	cytosolic ribosome	2.27e-12	3.72e-09	66	6.61	4
0	GO.CC	cytosolic large ribosomal subunit	2.53e-08	1.04e-05	41	6.87	4
0	GO.CC	ribosomal subunit	3.44e-08	1.14e-05	71	3.39	3
0	GO.CC	cytosolic part	1.8e-07	4.94e-05	79	2.86	4
0	GO.CC	large ribosomal subunit	2.31e-05	0.00399	47	3.05	2
0	KEGG	Ribosome	4.96e-09	5.62e-06	67	4	4
0	KEGG	Cytokine-cytokine receptor interaction	8.33e-05	0.0061	29	4.19	9
0	KEGG	Viral protein interaction with cytokine and c..	0.000825	0.0302	18	5.15	5
0	KEGG	NOD-like receptor signaling pathway	0.00148	0.0432	36	2.45	10
0	msigdb__reactome	eukaryotic translation initiation	2.74e-14	7.86e-12	77	6.68	4
0	msigdb__reactome	eukaryotic translation elongation	8.44e-14	2.08e-11	67	8.07	5
0	msigdb__reactome	influenza infection	3.01e-13	6.48e-11	77	5.83	4
0	msigdb__reactome	selenoamino acid metabolism	1.21e-12	2.32e-10	67	6.72	4
0	msigdb__reactome	nonsense mediated decay nmd	2.14e-12	3.8e-10	70	6.02	4
0	msigdb__canonical__pathways	eukaryotic translation initiation	2.74e-14	1.1e-11	77	6.68	4
0	msigdb__canonical__pathways	eukaryotic translation elongation	8.44e-14	2.93e-11	67	8.07	5
0	msigdb__canonical__pathways	influenza infection	3.01e-13	9.14e-11	77	5.83	4
0	msigdb__canonical__pathways	kegg ribosome	3.11e-13	9.14e-11	65	7.81	4
0	msigdb__canonical__pathways	selenoamino acid metabolism	1.21e-12	3.19e-10	67	6.72	4
0	msigdb__tf__motifs	isre 01	3.88e-06	0.000537	43	3.86	15
0	msigdb__tf__motifs	icsbp q6	5.7e-06	0.000717	39	4.13	14
0	msigdb__tf__motifs	ac118549 1 target genes	6.9e-05	0.00716	46	2.82	3
0	msigdb__tf__motifs	irf7 01	9.99e-05	0.00976	35	3.38	15
0	msigdb__tf__motifs	gtf2e2 target genes	0.000179	0.0167	57	2.3	1
0	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	3.89e-25	9.26e-23	91	22.7	15
0	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	7.22e-25	1.66e-22	111	10.8	15
0	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 10h dn	1.57e-22	2.63e-20	80	24.6	15
0	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	6.72e-21	9.59e-19	91	11.3	15
0	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	8.4e-20	1.05e-17	85	11.6	15
1	GO.BP	response to virus	2.14e-19	1.49e-15	49	10.2	15
1	GO.BP	defense response to virus	5.88e-19	3.27e-15	41	14.5	15
1	GO.BP	response to interferon-gamma	1.12e-14	1.04e-11	33	12.4	14
1	GO.BP	response to type I interferon	8.14e-14	4.92e-11	27	18.2	15
1	GO.BP	type I interferon signaling pathway	8.14e-14	4.92e-11	27	18.2	15
1	KEGG	Influenza A	5.25e-08	1.7e-05	21	7.53	10
1	KEGG	NOD-like receptor signaling pathway	2.28e-06	0.000369	19	5.71	10
1	KEGG	Measles	2.98e-05	0.00282	16	5.16	8
1	KEGG	Hepatitis C	9.34e-05	0.00655	16	4.41	6
1	KEGG	Cytokine-cytokine receptor interaction	9.53e-05	0.00655	9	11.4	9
1	msigdb__reactome	interferon signaling	2.93e-15	9.46e-13	38	9.95	15
1	msigdb__reactome	interferon alpha beta signaling	6.79e-14	1.75e-11	25	25.1	15
1	msigdb__reactome	interferon gamma signaling	8.8e-08	6.49e-06	16	12.4	14
1	msigdb__reactome	antiviral mechanism by ifn stimulated genes	0.000387	0.0168	14	4.13	7
1	msigdb__reactome	oas antiviral response	0.000423	0.0182	5	Inf	6
1	msigdb__canonical__pathways	interferon signaling	2.93e-15	1.32e-12	38	9.95	15
1	msigdb__canonical__pathways	interferon alpha beta signaling	6.79e-14	2.47e-11	25	25.1	15
1	msigdb__canonical__pathways	interferon gamma signaling	8.8e-08	8.95e-06	16	12.4	14
1	msigdb__canonical__pathways	kegg cytokine cytokine receptor interaction	0.000346	0.0185	8	10.1	8
1	msigdb__canonical__pathways	antiviral mechanism by ifn stimulated genes	0.000387	0.0205	14	4.13	7
1	msigdb__tf__motifs	irf q6	3.2e-13	8.86e-10	27	15.6	13
1	msigdb__tf__motifs	icsbp q6	2.24e-11	1.67e-08	23	15.3	14
1	msigdb__tf__motifs	isre 01	2.44e-10	9.2e-08	23	11.5	15
1	msigdb__tf__motifs	stttcrnttt irf q6	1.87e-09	5.01e-07	23	9.14	15
1	msigdb__tf__motifs	irf7 01	4.68e-09	1.14e-06	23	8.31	15
1	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	3.65e-44	2.29e-40	67	107	15
1	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	6.49e-41	2.9e-37	67	53.3	15
1	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	1.85e-40	6.43e-37	65	61.5	15
1	msigdb__immunological__signatures	gse21546 wt vs sap1a ko dp thymocytes up	2.97e-39	7.76e-36	66	44.8	15
1	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.85e-38	6.37e-35	59	90.8	15
2	GO.BP	defense response to virus	6.55e-20	6.08e-16	41	15.1	15
2	GO.BP	response to type I interferon	4.07e-16	7.07e-13	29	22.1	15
2	GO.BP	response to virus	8.58e-16	1.41e-12	45	7.44	15
2	GO.BP	type I interferon signaling pathway	1.88e-15	2.49e-12	28	21.2	15

2	GO.BP	cellular response to type I interferon	1.88e-15	2.49e-12	28	21.2	15
2	KEGG	Influenza A	8.3e-05	0.0061	17	4.08	10
2	KEGG	NOD-like receptor signaling pathway	0.000296	0.0149	17	3.48	10
2	KEGG	Viral protein interaction with cytokine and c..	0.00104	0.0342	6	12.6	5
2	msigdb__reactome	interferon signaling	2.28e-17	2.94e-14	40	11.2	15
2	msigdb__reactome	interferon alpha beta signaling	2.78e-16	1.44e-13	26	39.2	15
2	msigdb__reactome	interferon gamma signaling	1.39e-09	1.47e-07	18	15.8	14
2	msigdb__reactome	antiviral mechanism by ifn stimulated genes	0.000247	0.0114	14	4.28	7
2	msigdb__reactome	oas antiviral response	0.000277	0.0125	5	Inf	6
2	msigdb__canonical__pathways	interferon signaling	2.28e-17	3.6e-14	40	11.2	15
2	msigdb__canonical__pathways	interferon alpha beta signaling	2.78e-16	1.93e-13	26	39.2	15
2	msigdb__canonical__pathways	interferon gamma signaling	1.39e-09	2.04e-07	18	15.8	14
2	msigdb__canonical__pathways	naba secreted factors	0.000185	0.0117	8	11.3	11
2	msigdb__canonical__pathways	antiviral mechanism by ifn stimulated genes	0.000247	0.0141	14	4.28	7
2	msigdb__tf__motifs	irf q6	2.89e-14	1.62e-10	28	15.9	13
2	msigdb__tf__motifs	isre 01	3.9e-14	1.62e-10	26	19.6	15
2	msigdb__tf__motifs	stttcrnttt irf q6	7.76e-13	1.29e-09	24	17.9	15
2	msigdb__tf__motifs	irf7 01	7.01e-12	7.28e-09	25	12.5	15
2	msigdb__tf__motifs	icsbp q6	1.56e-10	6.84e-08	22	12.2	14
2	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	1.88e-48	1.02e-43	69	126	15
2	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	4.72e-48	1.02e-43	70	96.3	15
2	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	1.02e-45	1.06e-41	71	55.9	15
2	msigdb__immunological__signatures	gse21546 wt vs sap1a ko dp thymocytes up	1.68e-42	8.77e-39	68	46.2	15
2	msigdb__immunological__signatures	gse37533 pparg1 foxp3 vs foxp3 transduced cd4..	9.14e-41	3.58e-37	70	31.9	15
3	GO.BP	defense response to virus	7.73e-18	3.07e-14	49	12.7	15
3	GO.BP	response to virus	1.85e-15	2.49e-12	57	6.79	15
3	GO.BP	response to interferon-gamma	4.11e-13	2.12e-10	40	9.24	14
3	GO.BP	response to type I interferon	1.92e-12	7.86e-10	31	15.5	15
3	GO.BP	type I interferon signaling pathway	1.92e-12	7.86e-10	31	15.5	15
3	KEGG	NOD-like receptor signaling pathway	1.98e-08	1.05e-05	27	7.41	10
3	KEGG	Influenza A	1.34e-07	3.64e-05	25	6.83	10
3	KEGG	Necroptosis	2.53e-05	0.0025	21	4.65	4
3	KEGG	Apoptosis	3.34e-05	0.00303	18	5.46	2
3	KEGG	Herpes simplex virus 1 infection	0.000146	0.00947	22	3.57	3
3	msigdb__reactome	interferon signaling	2.22e-13	5.2e-11	45	7.69	15
3	msigdb__reactome	interferon alpha beta signaling	2.51e-13	5.63e-11	28	34.9	15
3	msigdb__reactome	interferon gamma signaling	8.05e-09	6.72e-07	22	13.5	14
3	msigdb__canonical__pathways	interferon signaling	2.22e-13	7.36e-11	45	7.69	15
3	msigdb__canonical__pathways	interferon alpha beta signaling	2.51e-13	7.98e-11	28	34.9	15
3	msigdb__canonical__pathways	interferon gamma signaling	8.05e-09	9.33e-07	22	13.5	14
3	msigdb__canonical__pathways	pid caspase pathway	4.21e-05	0.00299	10	24	2
3	msigdb__canonical__pathways	caspase pathway	0.000204	0.0124	7	Inf	1
3	msigdb__tf__motifs	irf q6	4.03e-12	4.78e-09	33	11.8	13
3	msigdb__tf__motifs	isre 01	1.5e-11	1.38e-08	33	10.3	15
3	msigdb__tf__motifs	stttcrnttt irf q6	4.54e-10	1.64e-07	26	12.9	15
3	msigdb__tf__motifs	icsbp q6	6.14e-10	1.96e-07	27	11.1	14
3	msigdb__tf__motifs	irf7 01	6.83e-09	1.62e-06	27	8.35	15
3	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	2.9e-39	7.76e-36	78	73	15
3	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	1.59e-37	2.7e-34	77	53.9	15
3	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	1.59e-36	2.26e-33	79	37	15
3	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	8.87e-35	9.12e-32	70	64.2	15
3	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.39e-34	2.16e-31	67	91.8	15
4	GO.BP	response to virus	4.63e-14	3.22e-11	69	5.14	15
4	GO.BP	defense response to virus	5.8e-14	3.84e-11	57	6.68	15
4	GO.BP	response to interferon-gamma	1.34e-10	4.11e-08	52	4.88	14
4	GO.BP	cellular response to interferon-gamma	1.04e-08	2.06e-06	44	4.52	13
4	GO.BP	negative regulation of viral process	1.97e-08	3.59e-06	29	7.99	15
4	KEGG	Cytokine-cytokine receptor interaction	9.05e-06	0.00103	24	5.1	9
4	KEGG	Complement and coagulation cascades	0.000618	0.025	7	Inf	1
4	KEGG	Toll-like receptor signaling pathway	0.000711	0.0269	17	4.03	2
4	KEGG	Influenza A	0.00105	0.0342	28	2.54	10
4	KEGG	IL-17 signaling pathway	0.00143	0.0426	15	4.06	1
4	msigdb__reactome	interferon signaling	3.17e-11	4.81e-09	55	4.95	15
4	msigdb__reactome	interferon alpha beta signaling	3.66e-09	3.56e-07	28	10.8	15
4	msigdb__reactome	interferon gamma signaling	4.64e-06	0.000282	26	4.98	14
4	msigdb__reactome	peptide ligand binding receptors	0.000126	0.00625	16	6.07	7
4	msigdb__reactome	chemokine receptors bind chemokines	0.000324	0.0142	11	10.4	7
4	msigdb__canonical__pathways	interferon signaling	3.17e-11	6.72e-09	55	4.95	15
4	msigdb__canonical__pathways	interferon alpha beta signaling	3.66e-09	4.9e-07	28	10.8	15
4	msigdb__canonical__pathways	naba secreted factors	2.1e-06	0.00018	18	11.4	11
4	msigdb__canonical__pathways	interferon gamma signaling	4.64e-06	0.000389	26	4.98	14
4	msigdb__canonical__pathways	kegg cytokine cytokine receptor interaction	8.82e-05	0.0059	22	4.19	8
4	msigdb__tf__motifs	stttcrnttt irf q6	2.41e-11	1.67e-08	35	11.4	15
4	msigdb__tf__motifs	irf7 01	1.22e-09	3.61e-07	40	6	15
4	msigdb__tf__motifs	isre 01	1.82e-08	3.88e-06	40	4.86	15

4	msigdb__tf__motifs	irf q6	4.1e-08	8.11e-06	40	4.58	13
4	msigdb__tf__motifs	icsbp q6	2.92e-07	5.16e-05	33	4.9	14
4	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	6.25e-38	1.18e-34	93	39.3	15
4	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	1.98e-35	2.34e-32	96	22.6	15
4	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	4.05e-34	3.39e-31	95	20.1	15
4	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	4.77e-34	3.93e-31	89	26.7	15
4	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	3.09e-33	2.1e-30	108	12.2	15
5	GO.BP	defense response to virus	5.97e-17	1.98e-13	41	10.7	15
5	GO.BP	type I interferon signaling pathway	1.93e-14	1.58e-11	28	18.9	15
5	GO.BP	cellular response to type I interferon	1.93e-14	1.58e-11	28	18.9	15
5	GO.BP	response to virus	2.95e-14	2.16e-11	45	6.53	15
5	GO.BP	response to type I interferon	7.83e-14	4.92e-11	28	16.2	15
5	KEGG	NOD-like receptor signaling pathway	6.1e-05	0.00513	18	4.11	10
5	KEGG	Measles	0.000238	0.0126	15	4.13	8
5	KEGG	Influenza A	0.000375	0.0174	17	3.46	10
5	KEGG	Herpes simplex virus 1 infection	0.000879	0.0316	16	3.24	3
5	KEGG	Hepatitis C	0.000924	0.0316	15	3.39	6
5	msigdb__reactome	interferon alpha beta signaling	3.23e-16	1.52e-13	26	52.4	15
5	msigdb__reactome	interferon signaling	4.91e-14	1.33e-11	38	8.28	15
5	msigdb__reactome	interferon gamma signaling	2.52e-07	1.71e-05	16	10.4	14
5	msigdb__reactome	antiviral mechanism by ifn stimulated genes	0.000953	0.0367	14	3.58	7
5	msigdb__canonical__pathways	interferon alpha beta signaling	3.23e-16	2.05e-13	26	52.4	15
5	msigdb__canonical__pathways	interferon signaling	4.91e-14	1.87e-11	38	8.28	15
5	msigdb__canonical__pathways	interferon gamma signaling	2.52e-07	2.38e-05	16	10.4	14
5	msigdb__canonical__pathways	naba ecm affiliated	2.85e-05	0.00211	9	17.2	1
5	msigdb__canonical__pathways	naba secreted factors	0.000827	0.0369	8	7.6	11
5	msigdb__tf__motifs	irf q6	1.12e-12	1.55e-09	27	13.6	13
5	msigdb__tf__motifs	stttcrnttt irf q6	2.19e-11	1.67e-08	23	15.2	15
5	msigdb__tf__motifs	irf7 01	1.44e-10	6.66e-08	25	9.98	15
5	msigdb__tf__motifs	isre 01	1.33e-09	3.8e-07	24	8.67	15
5	msigdb__tf__motifs	icsbp q6	2.45e-09	6.35e-07	22	9.67	14
5	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	2.43e-45	2.18e-41	72	68.3	15
5	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	5.62e-45	4.4e-41	70	82.4	15
5	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	1.5e-39	4.26e-36	64	58.9	15
5	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	5.14e-37	8.05e-34	59	66.6	15
5	msigdb__immunological__signatures	gse21546 wt vs sap1a ko dp thymocytes up	5.97e-36	7.79e-33	64	32.6	15
6	GO.BP	defense response to virus	5.21e-14	3.54e-11	45	8.37	15
6	GO.BP	response to virus	3.8e-12	1.45e-09	52	5.24	15
6	GO.BP	response to type I interferon	5.74e-11	1.86e-08	29	12.2	15
6	GO.BP	type I interferon signaling pathway	1.68e-10	4.87e-08	28	11.7	15
6	GO.BP	cellular response to type I interferon	1.68e-10	4.87e-08	28	11.7	15
6	msigdb__reactome	interferon alpha beta signaling	1.46e-10	1.89e-08	24	20	15
6	msigdb__reactome	interferon signaling	4.38e-09	4.19e-07	37	5.23	15
6	msigdb__reactome	interferon gamma signaling	1.19e-05	0.000699	16	7.85	14
6	msigdb__canonical__pathways	interferon alpha beta signaling	1.46e-10	2.66e-08	24	20	15
6	msigdb__canonical__pathways	interferon signaling	4.38e-09	5.77e-07	37	5.23	15
6	msigdb__canonical__pathways	interferon gamma signaling	1.19e-05	0.000968	16	7.85	14
6	msigdb__canonical__pathways	naba secreted factors	0.000212	0.0127	12	7.3	11
6	msigdb__tf__motifs	irf q6	6.1e-10	1.96e-07	28	10.1	13
6	msigdb__tf__motifs	stttcrnttt irf q6	9.1e-09	2.04e-06	23	11.5	15
6	msigdb__tf__motifs	isre 01	1.65e-08	3.6e-06	28	7.03	15
6	msigdb__tf__motifs	icsbp q6	4e-08	8.11e-06	25	7.8	14
6	msigdb__tf__motifs	irf7 01	7.02e-07	0.000117	24	5.97	15
6	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	4.61e-35	5.07e-32	72	50.6	15
6	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	5.99e-34	4.82e-31	70	48.9	15
6	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	2.18e-31	1.2e-28	69	32	15
6	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	5.39e-29	2.26e-26	61	41.7	15
6	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	1.81e-27	5.99e-25	60	32.7	15
7	GO.BP	defense response to virus	9.47e-15	9.09e-12	43	7.84	15
7	GO.BP	response to interferon-gamma	1.67e-14	1.45e-11	35	11.4	14
7	GO.BP	response to virus	1.98e-13	1.1e-10	50	5.4	15
7	GO.BP	response to type I interferon	9.14e-13	3.98e-10	29	12.9	15
7	GO.BP	type I interferon signaling pathway	9.14e-13	3.98e-10	29	12.9	15
7	GO.CC	tertiary granule lumen	0.000213	0.0259	7	23.7	1
7	KEGG	Influenza A	1.67e-08	1.05e-05	25	6.74	10
7	KEGG	NOD-like receptor signaling pathway	1.17e-06	0.00022	23	5	10
7	KEGG	Necroptosis	1.17e-05	0.00127	20	4.61	4
7	KEGG	Hepatitis C	0.000142	0.00946	19	3.63	6
7	KEGG	RIG-I-like receptor signaling pathway	0.000198	0.0118	12	5.85	4
7	msigdb__reactome	interferon alpha beta signaling	4.58e-17	4.73e-14	29	51.6	15
7	msigdb__reactome	interferon signaling	9.13e-16	3.93e-13	45	8.24	15
7	msigdb__reactome	interferon gamma signaling	2.81e-11	4.4e-09	21	24.5	14
7	msigdb__reactome	antiviral mechanism by ifn stimulated genes	0.000306	0.0137	17	3.65	7
7	msigdb__reactome	regulation of ifna signaling	0.000639	0.0256	5	Inf	1
7	msigdb__canonical__pathways	interferon alpha beta signaling	4.58e-17	5.83e-14	29	51.6	15

7	msigdb__canonical__pathways	interferon signaling	9.13e-16	5.36e-13	45	8.24	15
7	msigdb__canonical__pathways	interferon gamma signaling	2.81e-11	6.13e-09	21	24.5	14
7	msigdb__canonical__pathways	kegg rig i like receptor signaling pathway	0.000198	0.0123	12	5.85	4
7	msigdb__canonical__pathways	antiviral mechanism by ifn stimulated genes	0.000306	0.017	17	3.65	7
7	msigdb__tf__motifs	irf q6	6.98e-13	1.29e-09	32	10.4	13
7	msigdb__tf__motifs	stttcrnttt irf q6	1.24e-10	6.07e-08	26	10.2	15
7	msigdb__tf__motifs	irf7 01	1.84e-10	7.64e-08	29	7.89	15
7	msigdb__tf__motifs	isre 01	5.79e-10	1.96e-07	28	7.6	15
7	msigdb__tf__motifs	icsbp q6	1.8e-09	4.98e-07	27	7.31	14
7	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	1.52e-42	8.68e-39	76	43.5	15
7	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	5.92e-39	1.43e-35	66	64.5	15
7	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.66e-36	3.71e-33	62	59.9	15
7	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	6.52e-36	8.34e-33	71	25.4	15
7	msigdb__immunological__signatures	gse18791 ctrl vs newcastle virus dc 8h dn	1.05e-34	1.05e-31	64	35.5	15
8	GO.BP	nuclear-transcribed mRNA catabolic process, n..	7.12e-17	1.98e-13	71	6.78	4
8	GO.BP	viral gene expression	1.82e-16	3.38e-13	81	5.37	4
8	GO.BP	translational initiation	7.57e-15	7.81e-12	85	4.41	4
8	GO.BP	viral transcription	1.54e-14	1.39e-11	74	5.04	4
8	GO.BP	SRP-dependent cotranslational protein targeti..	2.07e-14	1.6e-11	64	6.06	4
8	GO.MF	structural constituent of ribosome	1.23e-08	2.32e-05	70	2.99	3
8	GO.MF	cytokine activity	2.53e-05	0.0159	21	5.47	3
8	GO.MF	chemokine activity	9.73e-05	0.0421	11	19.9	3
8	GO.CC	cytosolic ribosome	3.72e-16	1.22e-12	65	7.26	4
8	GO.CC	cytosolic part	1.51e-11	1.65e-08	80	3.54	4
8	GO.CC	cytosolic large ribosomal subunit	6.05e-11	4.97e-08	41	7.62	4
8	GO.CC	ribosomal subunit	8.04e-08	2.4e-05	72	2.71	3
8	GO.CC	polysomal ribosome	3.84e-07	9.51e-05	22	10	2
8	KEGG	Ribosome	7.5e-10	1.7e-06	68	3.46	4
8	KEGG	Cytokine-cytokine receptor interaction	4.93e-06	0.000657	29	4.43	9
8	KEGG	Systemic lupus erythematosus	0.00102	0.0341	10	9.03	1
8	msigdb__reactome	eukaryotic translation initiation	2.04e-19	5.27e-16	78	7.51	4
8	msigdb__reactome	eukaryotic translation elongation	1.09e-18	1.87e-15	66	9.68	5
8	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	6.92e-17	5.95e-14	67	7.5	4
8	msigdb__reactome	selenoamino acid metabolism	1.16e-16	7.51e-14	65	7.72	4
8	msigdb__reactome	nonsense mediated decay nmd	1.29e-15	5.1e-13	70	6.06	4
8	msigdb__canonical__pathways	eukaryotic translation initiation	2.04e-19	7.78e-16	78	7.51	4
8	msigdb__canonical__pathways	eukaryotic translation elongation	1.09e-18	2.76e-15	66	9.68	5
8	msigdb__canonical__pathways	kegg ribosome	2.36e-17	3.6e-14	64	8.69	4
8	msigdb__canonical__pathways	response of eif2ak4 gcn2 to amino acid defici..	6.92e-17	7.54e-14	67	7.5	4
8	msigdb__canonical__pathways	selenoamino acid metabolism	1.16e-16	9.87e-14	65	7.72	4
8	msigdb__tf__motifs	stttcrnttt irf q6	3.06e-06	0.000446	34	3.91	15
8	msigdb__tf__motifs	isre 01	5.6e-06	0.000717	41	3.15	15
8	msigdb__tf__motifs	icsbp q6	6.01e-06	0.000745	38	3.33	14
8	msigdb__tf__motifs	irf7 01	1.97e-05	0.0023	37	3.09	15
8	msigdb__tf__motifs	ac118549 1 target genes	4.95e-05	0.00534	46	2.49	3
8	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	1.31e-37	2.29e-34	112	17.3	15
8	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	1.07e-32	6.82e-30	91	22.4	15
8	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	2.74e-32	1.68e-29	103	13.6	15
8	msigdb__immunological__signatures	gse18791 ctrl vs newcastle virus dc 8h dn	2.73e-30	1.34e-27	93	15.2	15
8	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	2.15e-29	9.57e-27	96	12.6	15
9	GO.BP	defense response to virus	3.46e-15	4.18e-12	41	7.84	15
9	GO.BP	type I interferon signaling pathway	6.28e-15	6.99e-12	29	16.3	15
9	GO.BP	cellular response to type I interferon	6.28e-15	6.99e-12	29	16.3	15
9	GO.BP	response to interferon-gamma	9.4e-15	9.09e-12	37	8.87	14
9	GO.BP	response to type I interferon	2.19e-14	1.64e-11	29	14.5	15
9	GO.MF	cytokine activity	2.46e-06	0.00213	11	15.8	3
9	GO.MF	chemokine activity	4.9e-05	0.0264	6	Inf	3
9	KEGG	NOD-like receptor signaling pathway	2.81e-08	1.06e-05	22	6.91	10
9	KEGG	Viral protein interaction with cytokine and c..	2.78e-06	0.00042	9	38.5	5
9	KEGG	Influenza A	3.4e-06	0.000481	21	4.59	10
9	KEGG	Cytokine-cytokine receptor interaction	5.36e-06	0.000676	12	10.3	9
9	KEGG	Hepatitis C	7.28e-05	0.00569	17	4.09	6
9	msigdb__reactome	interferon alpha beta signaling	1.76e-15	6.5e-13	27	24.1	15
9	msigdb__reactome	interferon signaling	5.65e-13	1.17e-10	42	5.83	15
9	msigdb__reactome	interferon gamma signaling	2.16e-09	2.15e-07	20	11	14
9	msigdb__reactome	chemokine receptors bind chemokines	9.32e-06	0.000559	7	Inf	7
9	msigdb__reactome	peptide ligand binding receptors	0.000168	0.00818	8	11.4	7
9	msigdb__canonical__pathways	interferon alpha beta signaling	1.76e-15	8.97e-13	27	24.1	15
9	msigdb__canonical__pathways	interferon signaling	5.65e-13	1.6e-10	42	5.83	15
9	msigdb__canonical__pathways	interferon gamma signaling	2.16e-09	3e-07	20	11	14
9	msigdb__canonical__pathways	chemokine receptors bind chemokines	9.32e-06	0.000773	7	Inf	7
9	msigdb__canonical__pathways	kegg cytokine cytokine receptor interaction	2.02e-05	0.00159	11	9.45	8
9	msigdb__tf__motifs	irf q6	3.35e-11	2.08e-08	26	9.62	13
9	msigdb__tf__motifs	isre 01	3.5e-11	2.08e-08	28	8.32	15
9	msigdb__tf__motifs	stttcrnttt irf q6	2.36e-10	9.2e-08	20	14.6	15

9	msigdb__tf__motifs	irf7 01	6.93e-10	2.13e-07	25	7.9	15
9	msigdb__tf__motifs	icsbp q6	3.82e-09	9.62e-07	23	7.8	14
9	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	4.86e-48	1.02e-43	71	89.4	15
9	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	1.09e-47	1.71e-43	72	72.7	15
9	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.48e-44	1.73e-40	61	299	15
9	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	2.83e-41	1.36e-37	62	76.1	15
9	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	7.17e-41	2.99e-37	69	34.4	15
10	GO.BP	defense response to virus	1.68e-16	3.38e-13	61	11.7	15
10	GO.BP	response to virus	1.99e-14	1.58e-11	72	6.16	15
10	GO.BP	negative regulation of viral life cycle	1.61e-07	2.32e-05	25	12.1	15
10	GO.BP	response to type I interferon	2.35e-07	3.16e-05	30	7.31	15
10	GO.BP	type I interferon signaling pathway	2.35e-07	3.16e-05	30	7.31	15
10	KEGG	NOD-like receptor signaling pathway	0.000934	0.0316	32	2.58	10
10	KEGG	Cytokine-cytokine receptor interaction	0.00137	0.0414	21	3.36	9
10	msigdb__reactome	interferon alpha beta signaling	7.16e-08	5.44e-06	28	10.2	15
10	msigdb__reactome	interferon signaling	4.23e-05	0.00228	45	2.75	15
10	msigdb__reactome	peptide ligand binding receptors	0.000664	0.0264	14	6.69	7
10	msigdb__reactome	eukaryotic translation elongation	0.000726	0.0286	47	2.15	5
10	msigdb__reactome	chemokine receptors bind chemokines	0.000999	0.0382	10	14.3	7
10	msigdb__canonical__pathways	interferon alpha beta signaling	7.16e-08	7.48e-06	28	10.2	15
10	msigdb__canonical__pathways	interferon signaling	4.23e-05	0.00299	45	2.75	15
10	msigdb__canonical__pathways	naba secreted factors	0.000341	0.0183	18	5.18	11
10	msigdb__canonical__pathways	peptide ligand binding receptors	0.000664	0.0307	14	6.69	7
10	msigdb__canonical__pathways	eukaryotic translation elongation	0.000726	0.0331	47	2.15	5
10	msigdb__tf__motifs	irf7 01	7.56e-07	0.000123	36	4.81	15
10	msigdb__tf__motifs	stttcrnttt irf q6	4.29e-06	0.000574	29	5.28	15
10	msigdb__tf__motifs	isre 01	0.000121	0.0117	35	3	15
10	msigdb__tf__motifs	maml1 target genes	0.000239	0.0219	29	3.24	1
10	msigdb__tf__motifs	icsbp q6	0.000313	0.0277	32	2.91	14
10	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	3.26e-32	1.96e-29	87	69.6	15
10	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	4.78e-30	2.31e-27	100	18	15
10	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	4.5e-25	1.07e-22	80	21	15
10	msigdb__immunological__signatures	gse18791 ctrl vs newcastle virus dc 8h dn	2.59e-24	5.44e-22	78	20.4	15
10	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 10h dn	4.22e-24	8.62e-22	75	23.5	15
11	GO.BP	defense response to virus	2.33e-20	3.24e-16	48	10.8	15
11	GO.BP	response to virus	6.8e-17	1.98e-13	53	6.44	15
11	GO.BP	response to type I interferon	5.35e-13	2.57e-10	26	14.5	15
11	GO.BP	type I interferon signaling pathway	5.35e-13	2.57e-10	26	14.5	15
11	GO.BP	cellular response to type I interferon	5.35e-13	2.57e-10	26	14.5	15
11	KEGG	Influenza A	2.32e-08	1.05e-05	24	6.21	10
11	KEGG	NOD-like receptor signaling pathway	2.39e-05	0.00246	21	3.8	10
11	KEGG	Cytokine-cytokine receptor interaction	4.89e-05	0.00427	15	4.96	9
11	KEGG	RIG-I-like receptor signaling pathway	0.000578	0.0243	9	6.37	4
11	KEGG	Hepatitis C	0.000585	0.0243	17	3.18	6
11	msigdb__reactome	interferon signaling	1.95e-16	1.12e-13	42	8.84	15
11	msigdb__reactome	interferon alpha beta signaling	7.67e-13	1.52e-10	24	17.7	15
11	msigdb__reactome	interferon gamma signaling	1.97e-07	1.41e-05	18	7.82	14
11	msigdb__reactome	antiviral mechanism by ifn stimulated genes	2.92e-05	0.00162	16	4.93	7
11	msigdb__reactome	oas antiviral response	5.1e-05	0.00269	6	Inf	6
11	msigdb__canonical__pathways	interferon signaling	1.95e-16	1.49e-13	42	8.84	15
11	msigdb__canonical__pathways	interferon alpha beta signaling	7.67e-13	2.09e-10	24	17.7	15
11	msigdb__canonical__pathways	naba secreted factors	6.98e-08	7.4e-06	16	11.5	11
11	msigdb__canonical__pathways	interferon gamma signaling	1.97e-07	1.95e-05	18	7.82	14
11	msigdb__canonical__pathways	antiviral mechanism by ifn stimulated genes	2.92e-05	0.00214	16	4.93	7
11	msigdb__tf__motifs	irf q6	5.49e-11	3.04e-08	29	7.62	13
11	msigdb__tf__motifs	isre 01	8.71e-11	4.52e-08	28	7.8	15
11	msigdb__tf__motifs	stttcrnttt irf q6	9.11e-09	2.04e-06	23	7.22	15
11	msigdb__tf__motifs	icsbp q6	2.31e-07	4.17e-05	22	5.66	14
11	msigdb__tf__motifs	irf7 01	4.48e-07	7.74e-05	23	5.04	15
11	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	5.16e-46	6.47e-42	77	36.5	15
11	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	3.76e-40	1.23e-36	73	25	15
11	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	3.93e-40	1.23e-36	72	26.4	15
11	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	1.03e-38	2.39e-35	68	28.7	15
11	msigdb__immunological__signatures	gse21546 wt vs sap1a ko dp thymocytes up	4.43e-38	9.24e-35	71	22.6	15
12	GO.BP	response to virus	3.59e-14	2.56e-11	69	4.29	15
12	GO.BP	defense response to virus	1.43e-12	6.13e-10	54	4.82	15
12	GO.BP	negative regulation of viral life cycle	1.44e-10	4.31e-08	28	10.1	15
12	GO.BP	negative regulation of viral process	1.47e-10	4.34e-08	31	8.12	15
12	GO.BP	response to interferon-gamma	3.18e-10	8.94e-08	42	4.88	14
12	GO.CC	cytosolic ribosome	1.69e-10	1.11e-07	50	4.18	4
12	GO.CC	cytosolic part	3.85e-09	1.81e-06	62	3.04	4
12	GO.CC	cytosolic large ribosomal subunit	3.48e-08	1.14e-05	33	4.75	4
12	GO.CC	cell-substrate adherens junction	0.000146	0.0192	58	1.95	1
12	GO.CC	focal adhesion	0.000146	0.0192	58	1.95	1
12	KEGG	Ribosome	7.45e-06	0.000889	52	2.39	4

12	KEGG	Measles	0.000495	0.022	23	2.83	8
12	msigdb__reactome	eukaryotic translation elongation	6.96e-12	1.2e-09	50	4.89	5
12	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	1.09e-11	1.75e-09	51	4.67	4
12	msigdb__reactome	eukaryotic translation initiation	1.09e-10	1.45e-08	56	3.83	4
12	msigdb__reactome	selenoamino acid metabolism	1.69e-10	2.13e-08	50	4.18	4
12	msigdb__reactome	srp dependent cotranslational protein targeti..	4.15e-10	4.82e-08	55	3.67	4
12	msigdb__canonical__pathways	eukaryotic translation elongation	6.96e-12	1.66e-09	50	4.89	5
12	msigdb__canonical__pathways	response of eif2ak4 gcn2 to amino acid defici..	1.09e-11	2.44e-09	51	4.67	4
12	msigdb__canonical__pathways	eukaryotic translation initiation	1.09e-10	2.04e-08	56	3.83	4
12	msigdb__canonical__pathways	selenoamino acid metabolism	1.69e-10	3e-08	50	4.18	4
12	msigdb__canonical__pathways	kegg ribosome	3.59e-10	5.95e-08	47	4.28	4
12	msigdb__tf__motifs	isre 01	1.2e-06	0.000184	35	3.47	15
12	msigdb__tf__motifs	irf q6	2.56e-06	0.00038	34	3.36	13
12	msigdb__tf__motifs	icsbp q6	1.3e-05	0.00159	28	3.47	14
12	msigdb__tf__motifs	stttcrnttt irf q6	1.63e-05	0.00194	23	4.09	15
12	msigdb__tf__motifs	irf7 01	2.13e-05	0.00245	28	3.33	15
12	msigdb__immunological__signatures	gse18791 ctrl vs newcastle virus dc 8h dn	4.65e-39	1.17e-35	76	46.8	15
12	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	2.21e-35	2.56e-32	83	18.4	15
12	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	1.09e-34	1.07e-31	83	17.1	15
12	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	1.61e-34	1.53e-31	76	23.3	15
12	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.3e-33	1.58e-30	71	27.1	15
13	GO.BP	defense response to virus	1.46e-21	4.05e-17	21	41	15
13	GO.BP	response to virus	7.16e-19	3.32e-15	21	28.5	15
13	GO.BP	type I interferon signaling pathway	1.23e-16	2.84e-13	15	41.9	15
13	GO.BP	cellular response to type I interferon	1.23e-16	2.84e-13	15	41.9	15
13	GO.BP	response to type I interferon	1.82e-16	3.38e-13	15	40.5	15
13	GO.MF	double-stranded RNA binding	0.000112	0.0421	5	13.3	1
13	KEGG	Influenza A	1.44e-07	3.64e-05	9	14.7	10
13	KEGG	Hepatitis C	5.87e-07	0.000121	8	14.9	6
13	KEGG	Measles	6.44e-05	0.00521	6	10.9	8
13	KEGG	RIG-I-like receptor signaling pathway	0.00022	0.0121	4	17.5	4
13	KEGG	Herpes simplex virus 1 infection	0.000335	0.0162	6	7.76	3
13	msigdb__reactome	interferon signaling	7.65e-22	3.95e-18	21	42.6	15
13	msigdb__reactome	interferon alpha beta signaling	1.08e-16	7.51e-14	14	52	15
13	msigdb__reactome	antiviral mechanism by ifn stimulated genes	2.34e-10	2.88e-08	10	27.1	7
13	msigdb__reactome	negative regulators of ddx58 ifih1 signaling	3.07e-05	0.00168	5	18.3	1
13	msigdb__reactome	ddx58 ifih1 mediated induction of interferon ..	0.00016	0.00787	5	12.1	2
13	msigdb__canonical__pathways	interferon signaling	7.65e-22	5.83e-18	21	42.6	15
13	msigdb__canonical__pathways	interferon alpha beta signaling	1.08e-16	9.87e-14	14	52	15
13	msigdb__canonical__pathways	antiviral mechanism by ifn stimulated genes	2.34e-10	4.06e-08	10	27.1	7
13	msigdb__canonical__pathways	negative regulators of ddx58 ifih1 signaling	3.07e-05	0.00223	5	18.3	1
13	msigdb__canonical__pathways	ddx58 ifih1 mediated induction of interferon ..	0.00016	0.0103	5	12.1	2
13	msigdb__tf__motifs	stttcrnttt irf q6	8.06e-08	1.56e-05	9	15.9	15
13	msigdb__tf__motifs	irf7 01	9.84e-08	1.86e-05	9	15.5	15
13	msigdb__tf__motifs	isre 01	1.19e-07	2.2e-05	9	15.1	15
13	msigdb__tf__motifs	irf1 01	4.15e-06	0.000565	7	13.9	11
13	msigdb__tf__motifs	irf q6	0.000335	0.0293	6	7.76	13
13	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	5.42e-30	2.57e-27	28	64.2	15
13	msigdb__immunological__signatures	gse13485 ctrl vs day3 yf17d vaccine pbmc dn	3.92e-29	1.68e-26	25	72.6	15
13	msigdb__immunological__signatures	gse21927 spleen c57bl6 vs 4t1 tumor balbc mon..	8.41e-29	3.4e-26	28	57	15
13	msigdb__immunological__signatures	gse42021 cd24hi vs cd24low treg thymus dn	2.07e-28	7.83e-26	24	73.5	15
13	msigdb__immunological__signatures	gse18791 unstim vs newcatsle virus dc 6h dn	3.79e-28	1.38e-25	26	59.7	15
14	GO.BP	defense response to virus	1.23e-15	1.91e-12	49	6.26	15
14	GO.BP	response to virus	2.73e-15	3.46e-12	57	5.05	15
14	GO.BP	response to type I interferon	4.02e-11	1.33e-08	27	8.71	15
14	GO.BP	type I interferon signaling pathway	4.02e-11	1.33e-08	27	8.71	15
14	GO.BP	cellular response to type I interferon	4.02e-11	1.33e-08	27	8.71	15
14	GO.MF	cytokine activity	1.22e-07	0.000154	20	6.83	3
14	GO.MF	structural constituent of ribosome	2.83e-06	0.00213	37	2.89	3
14	GO.CC	cytosolic ribosome	3.24e-09	1.77e-06	38	4.14	4
14	GO.CC	cytosolic part	4.06e-07	9.51e-05	44	2.88	4
14	GO.CC	ribosomal subunit	5.53e-06	0.00114	38	2.73	3
14	GO.CC	cytosolic large ribosomal subunit	9.61e-06	0.00186	23	3.78	4
14	GO.CC	cytosolic small ribosomal subunit	0.000111	0.0159	15	4.38	3
14	KEGG	Ribosome	1.75e-07	3.96e-05	38	3.33	4
14	KEGG	Cytokine-cytokine receptor interaction	1.57e-06	0.000274	23	4.45	9
14	KEGG	NOD-like receptor signaling pathway	0.000192	0.0117	24	2.8	10
14	KEGG	Intestinal immune network for IgA production	0.000215	0.0121	7	15.1	1
14	KEGG	Influenza A	0.000373	0.0174	22	2.77	10
14	msigdb__reactome	interferon signaling	6.03e-11	8.41e-09	39	4.99	15
14	msigdb__reactome	eukaryotic translation elongation	2.84e-10	3.41e-08	39	4.6	5
14	msigdb__reactome	interferon alpha beta signaling	5.39e-10	6.05e-08	23	9.37	15
14	msigdb__reactome	selenoamino acid metabolism	7.49e-10	8.23e-08	39	4.37	4
14	msigdb__reactome	response of eif2ak4 gcn2 to amino acid defici..	1.89e-09	1.91e-07	39	4.16	4
14	msigdb__canonical__pathways	interferon signaling	6.03e-11	1.18e-08	39	4.99	15

14	msigdb__canonical__pathways	eukaryotic translation elongation	2.84e-10	4.82e-08	39	4.6	5
14	msigdb__canonical__pathways	interferon alpha beta signaling	5.39e-10	8.4e-08	23	9.37	15
14	msigdb__canonical__pathways	selenoamino acid metabolism	7.49e-10	1.14e-07	39	4.37	4
14	msigdb__canonical__pathways	response of eif2ak4 gcn2 to amino acid defici..	1.89e-09	2.66e-07	39	4.16	4
14	msigdb__tf__motifs	isre 01	2.21e-08	4.59e-06	27	5.28	15
14	msigdb__tf__motifs	stttcrnttt irf q6	9.57e-07	0.000153	22	4.89	15
14	msigdb__tf__motifs	irf7 01	3.7e-06	0.00053	24	3.96	15
14	msigdb__tf__motifs	irf1 01	4.64e-05	0.00507	20	3.68	11
14	msigdb__tf__motifs	irf q6	5.44e-05	0.00579	24	3.13	13
14	msigdb__immunological__signatures	gse13485 ctrl vs day7 yf17d vaccine pbmc dn	7.53e-32	4.32e-29	78	10.5	15
14	msigdb__immunological__signatures	gse42724 naive bcell vs plasmablast up	1.38e-28	5.46e-26	72	9.81	15
14	msigdb__immunological__signatures	gse13485 day3 vs day7 yf17d vaccine pbmc dn	2.47e-26	6.75e-24	65	10.1	15
14	msigdb__immunological__signatures	gse37533 pparg1 foxp3 vs foxp3 transduced cd4..	4.05e-25	9.61e-23	68	8.46	15
14	msigdb__immunological__signatures	gse13484 unstim vs yf17d vaccine stim pbmc dn	5.01e-25	1.18e-22	66	8.84	15

Table 3: The top (lowest p-value) genesets found (uniquely) in each cluster