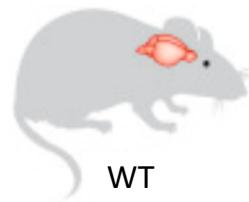


CCBR1045

Identification of a unique microglia signature associated with *Arf1*-knockout neurodegenerative mice

2020.4.21

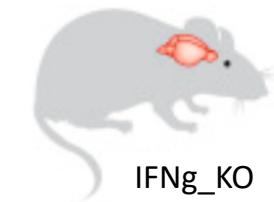
Da, Nathan



WT



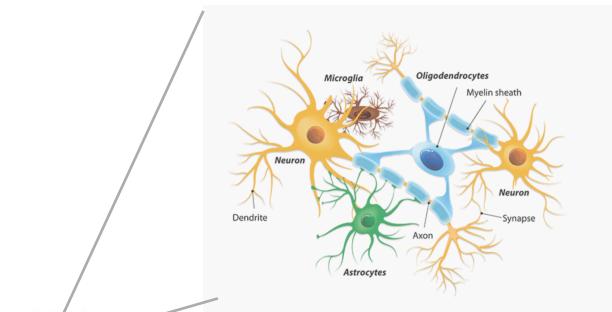
Arf1_KO



IFNg_KO

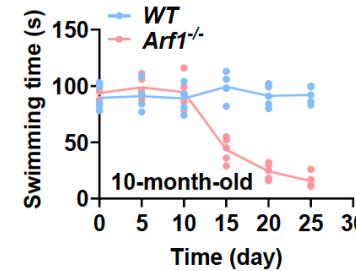
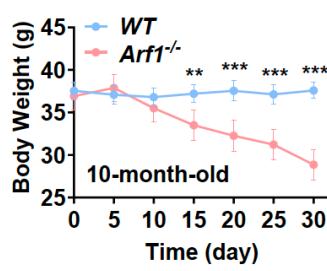
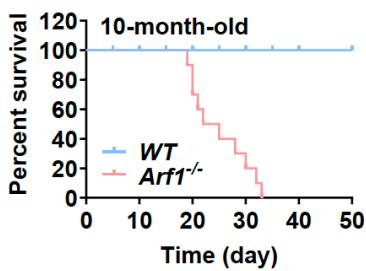
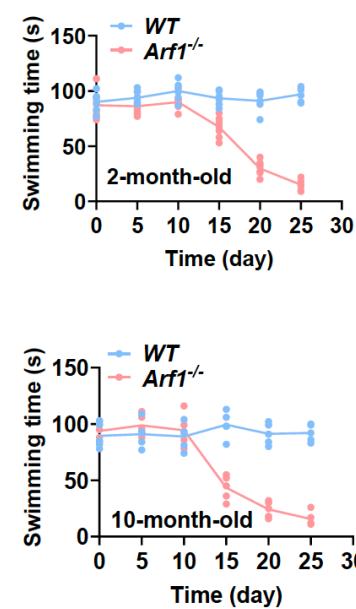
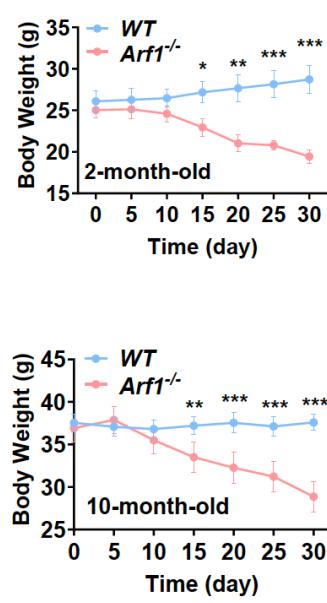
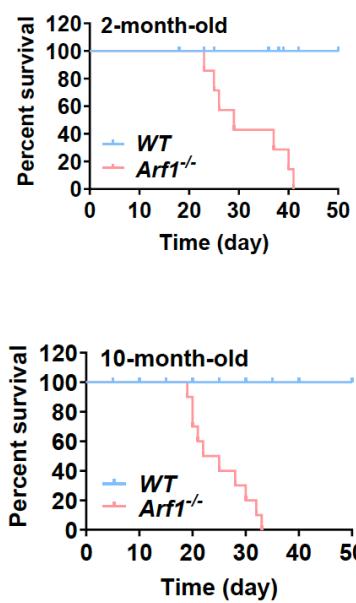
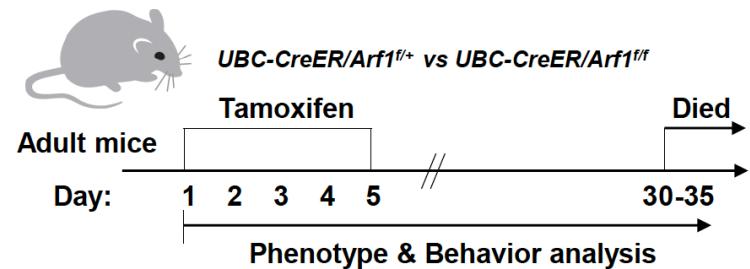


Arf1_IFNg_KO



Arf1 knock-down, ubiquitous | disease

Arf1 ablation induces neurodegenerative behaviors in adult mice



Arf1 knock-down, neuron | disease



Arf1 and IFNg knock-down, ubiquitous | normal



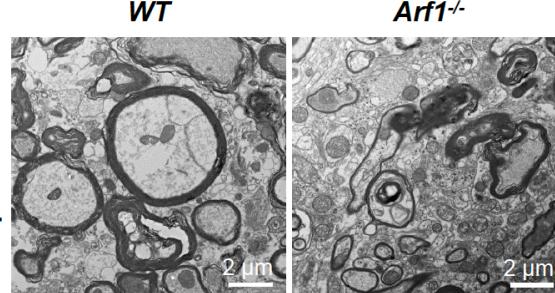
Guohao Wang

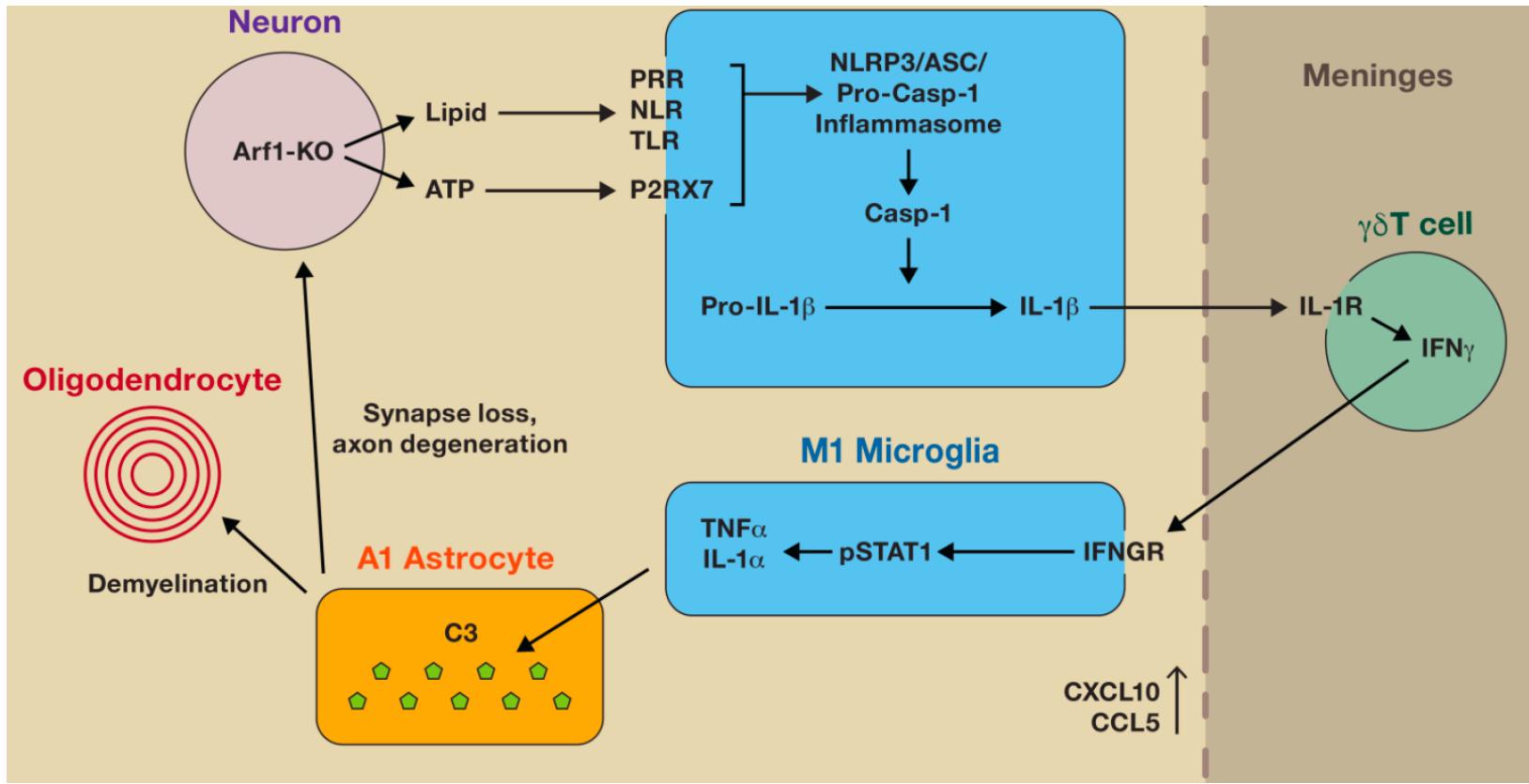
What do we know about Arf1

- *Arf1* is one of the most evolutionarily conserved genes between *Drosophila* and mouse, with an amino acid identity of 95.6% between the two species
- The ARF1 protein is localized to the Golgi apparatus and has a central role in intra-Golgi transport.
- Arf1-mediated lipid metabolism sustains cancer cells and its ablation induces anti-tumor immune responses in mice (Wang et al 2020)
- Arf1 regulates the initiation of myelination in the peripheral nervous system (Miyamoto et al 2018)

New findings

- Arf1 ablation induces neurodegenerative behaviors in adult mice
- Arf1 deficiency promotes demyelination, axon degeneration, synapse loss
- The slow traveling in the balance beam tests, poor neurological score, synapse loss, axon demyelination, and axon degeneration associated with Arf1-ablated mice were almost completely suppressed in IFN γ -deficient mice



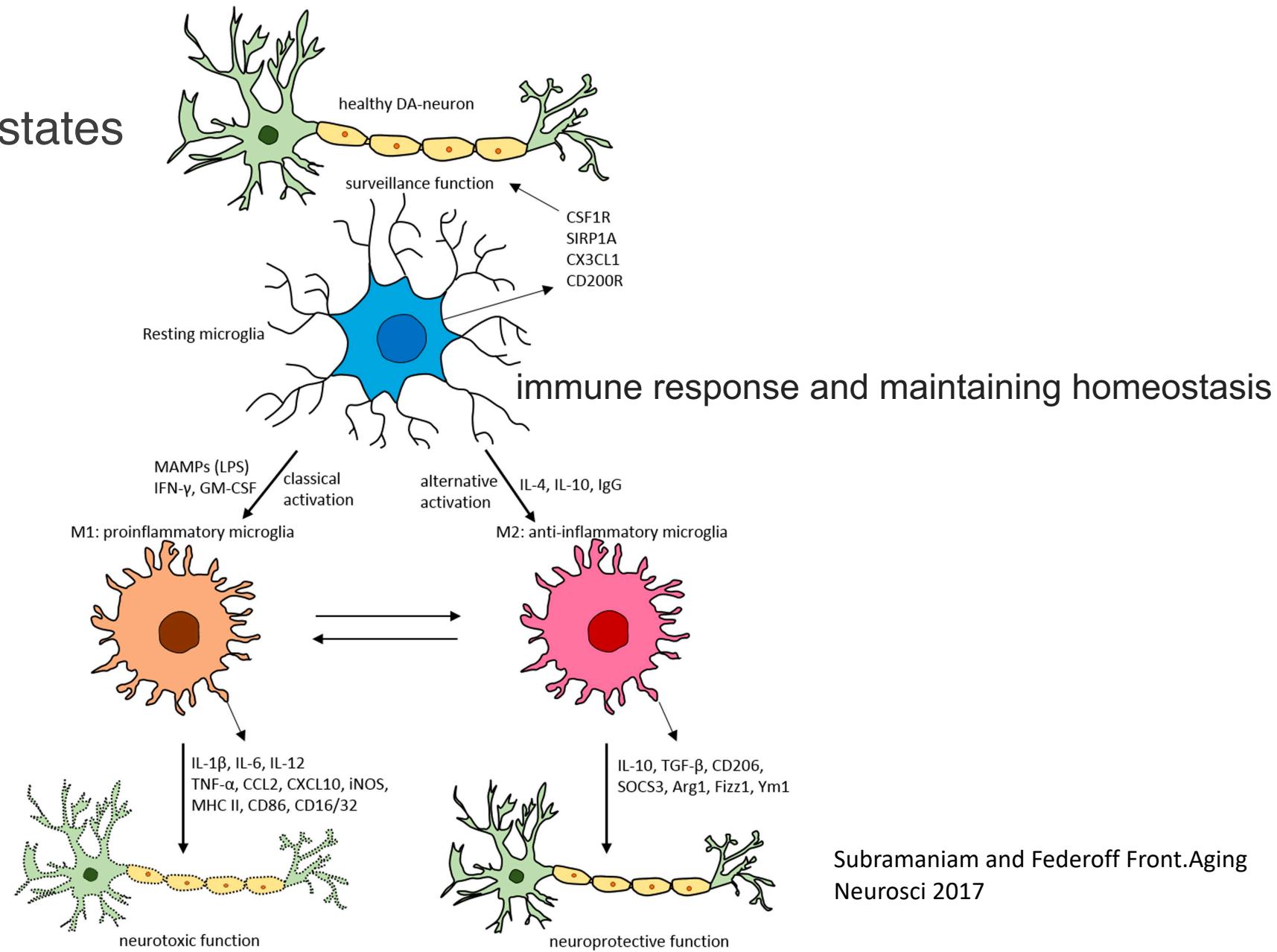


Guohao Wang

1. Knocking down Arf1 in neurons increases ROS and promotes the release of ATP, chemokines, and peroxidized lipids;
2. ATP and peroxidized lipids activate the inflammasome to produce IL-1 β in microglia;
3. Chemokines may help to recruit $\gamma\delta$ T cells to meninges; and the IL-1 β activates $\gamma\delta$ T cells to produce IFN γ , which enters parenchyma to activate a microglia-A1 astrocyte-C3 cascade;
4. Damage to neurons and oligodendrocytes, leading to neurodegeneration.

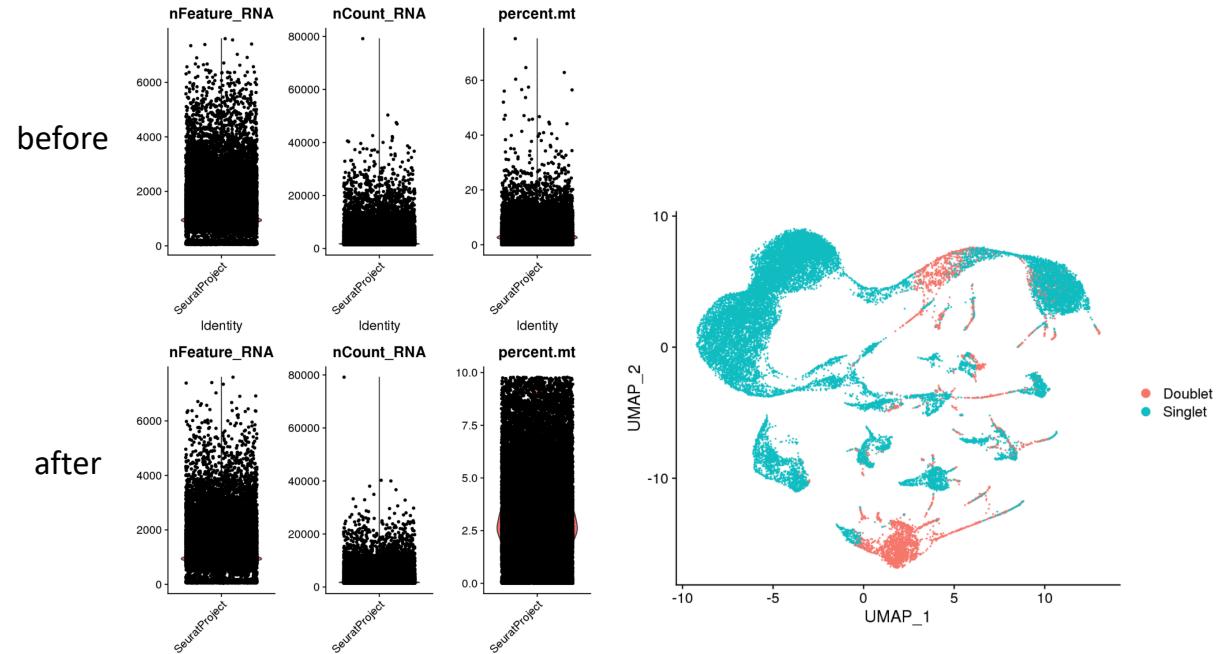
microglial polarization states

- Resting microglia state
- M1 pro-inflammatory state
- M2 anti-inflammatory state



pre-processing workflow

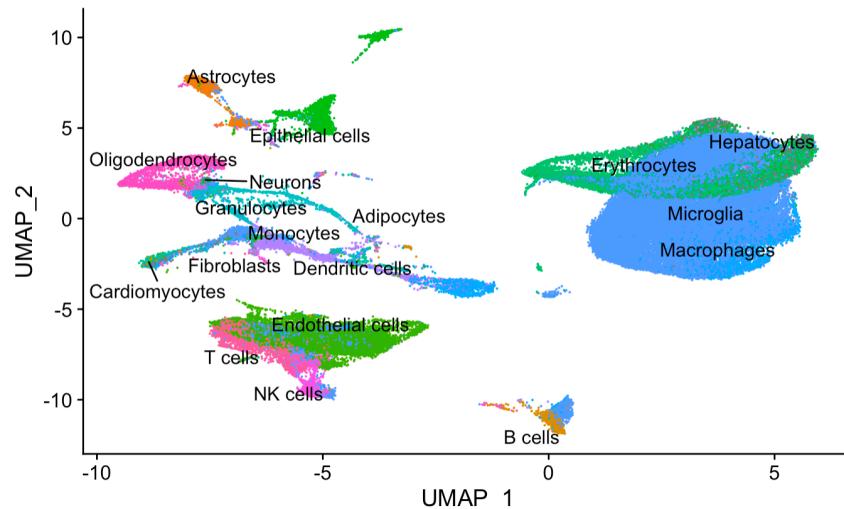
- Filtering out cells with nCount, nFeature, pct.mitochondria: mean absolute deviation (MAD) above 3
- Dimension reduction (PCA, URD), Clustering (Smart Local Moving) with resolution 0.2-1.2,
- Doublet removal(doubletFinder_v3), cell identity annotation (singleR)
- Integrate batches (four samples)



Sample	Estimated Number of Cells	Cells after filtering
WT	30,710	24,531
Arf1_KO	28,652	22,036
IFNg_KO	27,930	23,166
Arf1_IFNg_KO	28,695	23,484

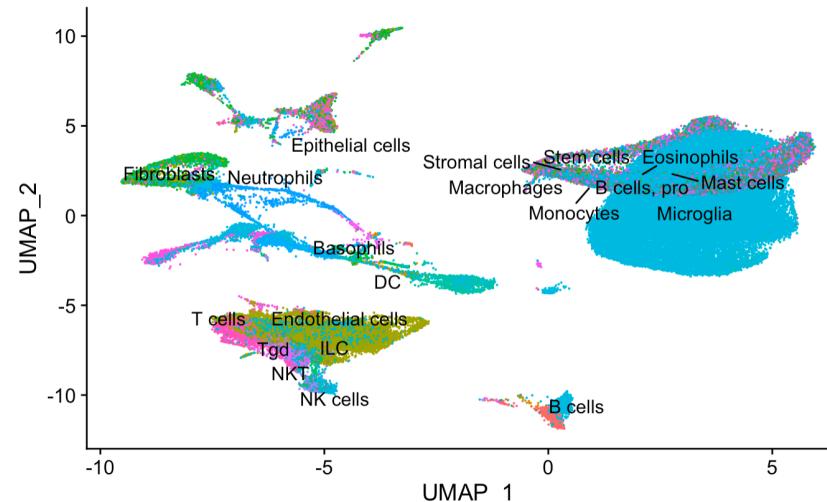
Comparison of cell identity annotation by three databases

mouseRNAseq_main



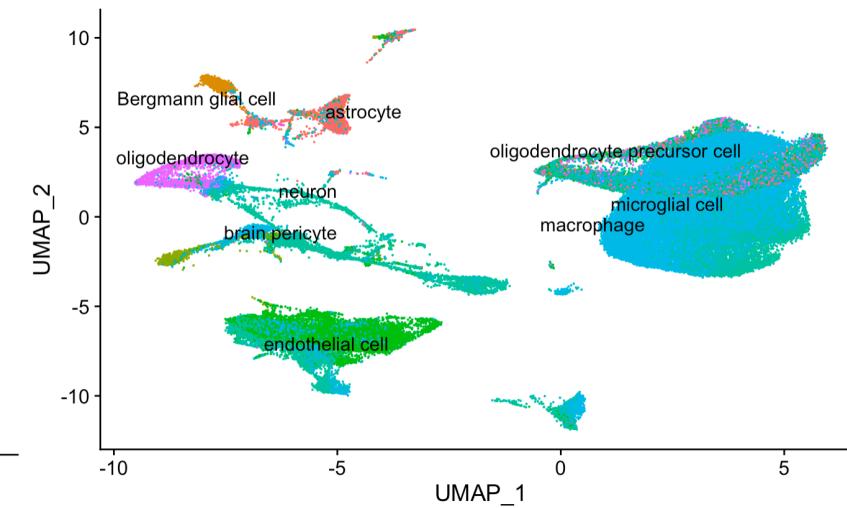
Microglia: 48,662

Immgen_main



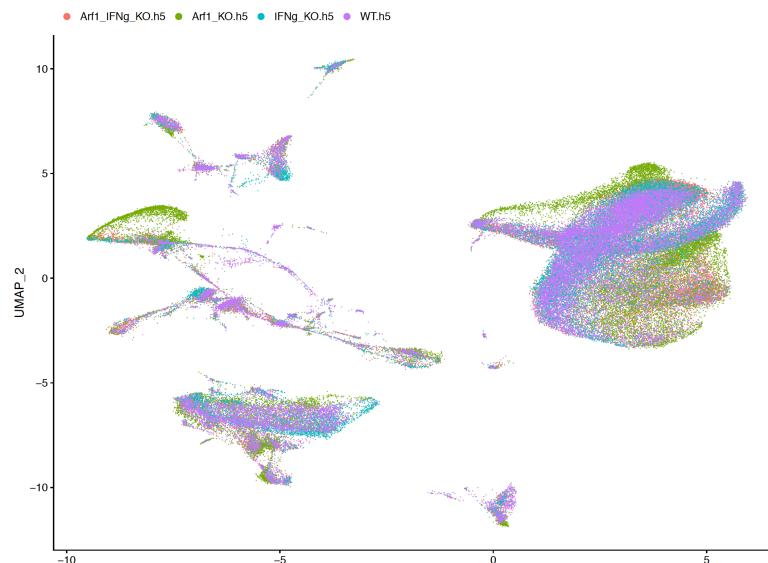
Microglia: 53,078

Tabulus Muris (mouse brain)

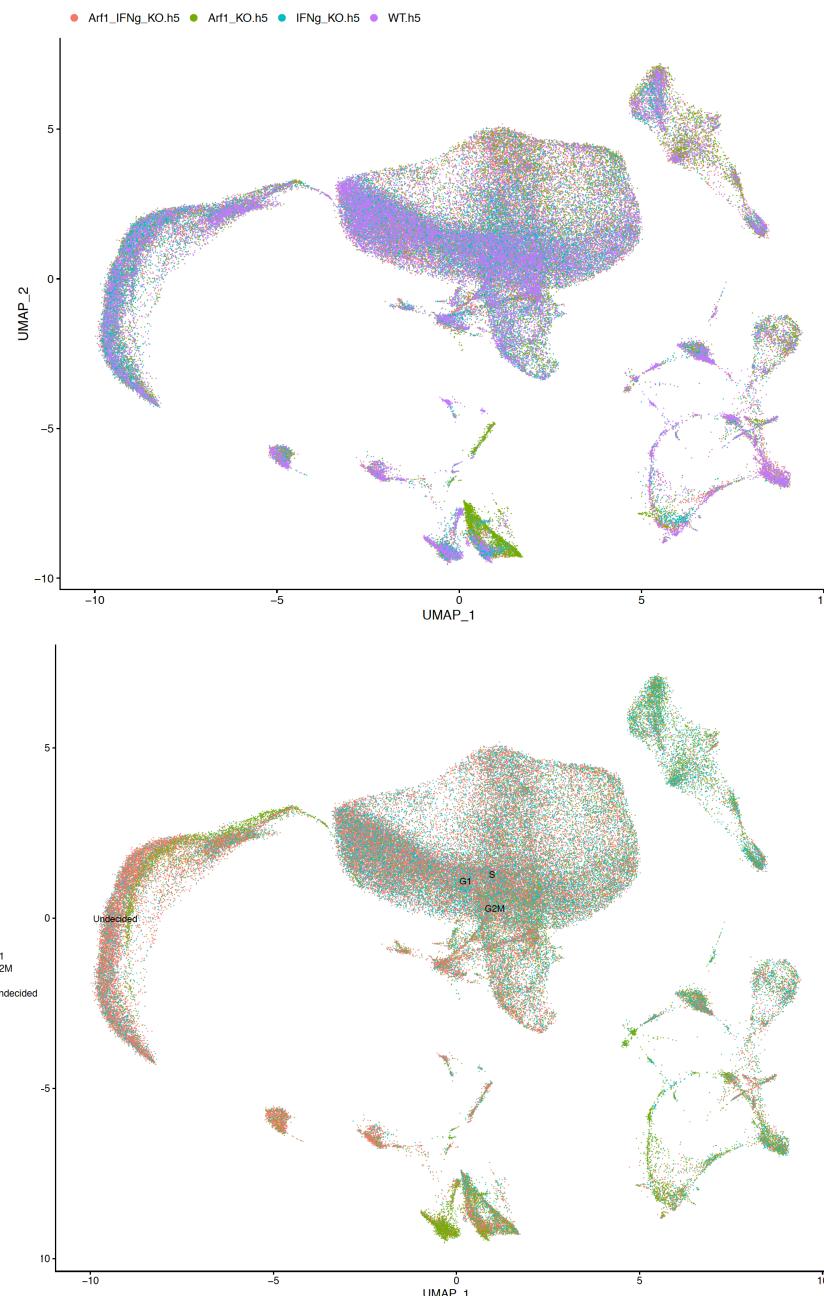


Microglial cell: 48,789

Before batch correction



Batch-corrected



Color by sample

Plotting all samples overlaid, colored by sample. Check to see if clustering behavior is tied to sample.

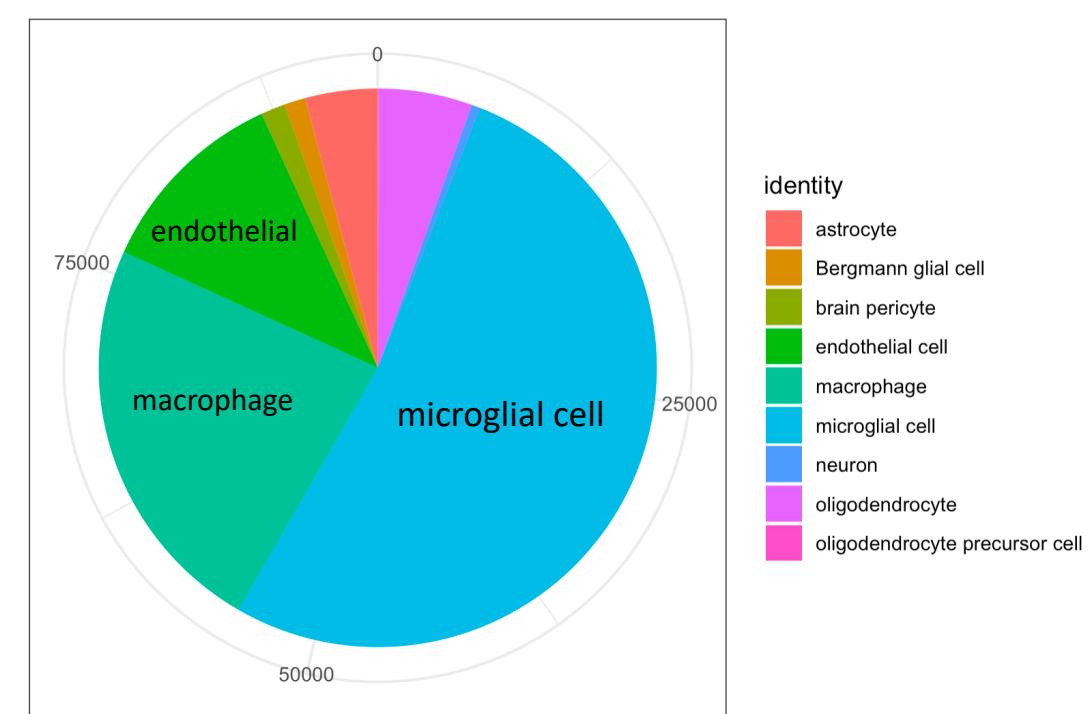
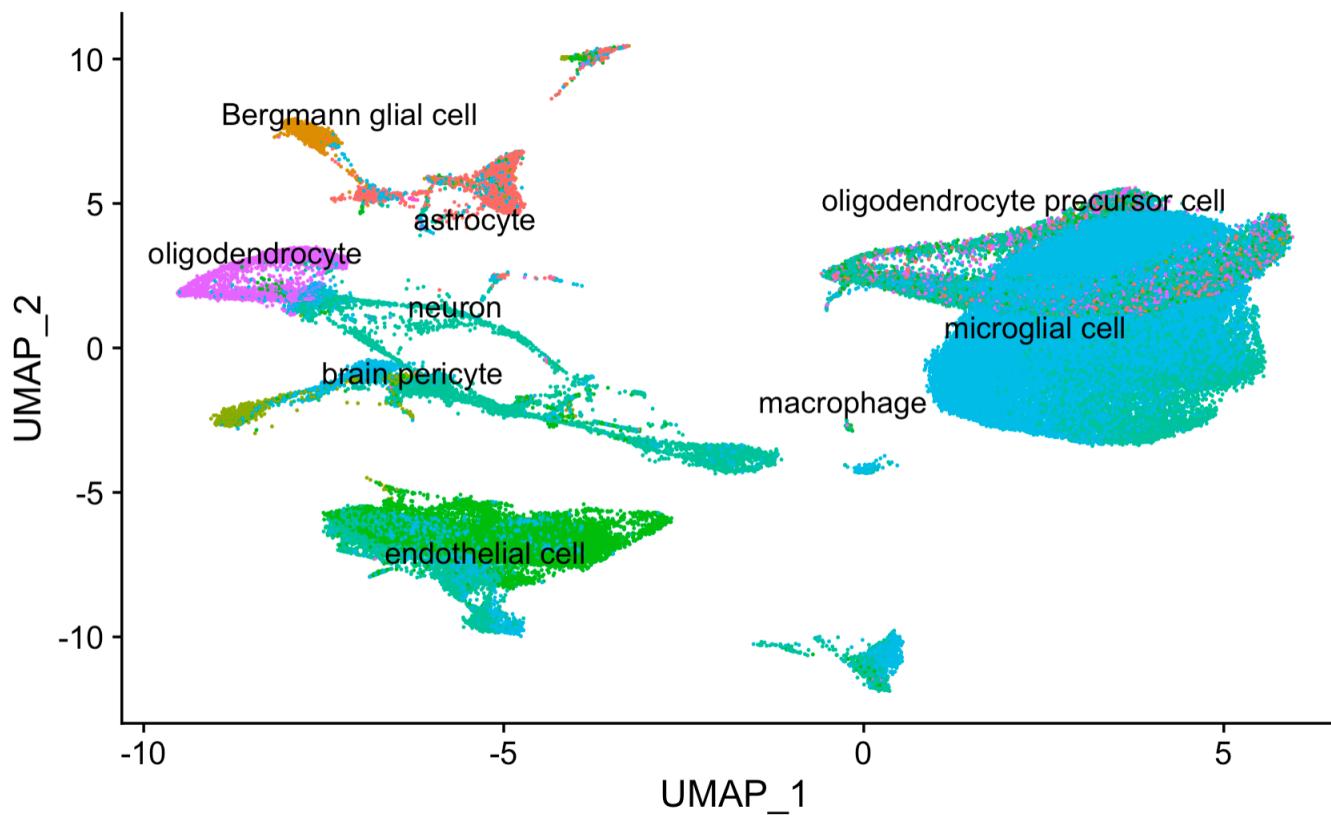
It looks like the four samples aren't separated before or after, which is expected.

Color by cell cycle

Plotting all samples overlaid, colored by phase. Check to see if clustering behavior is tied to cell cycle.

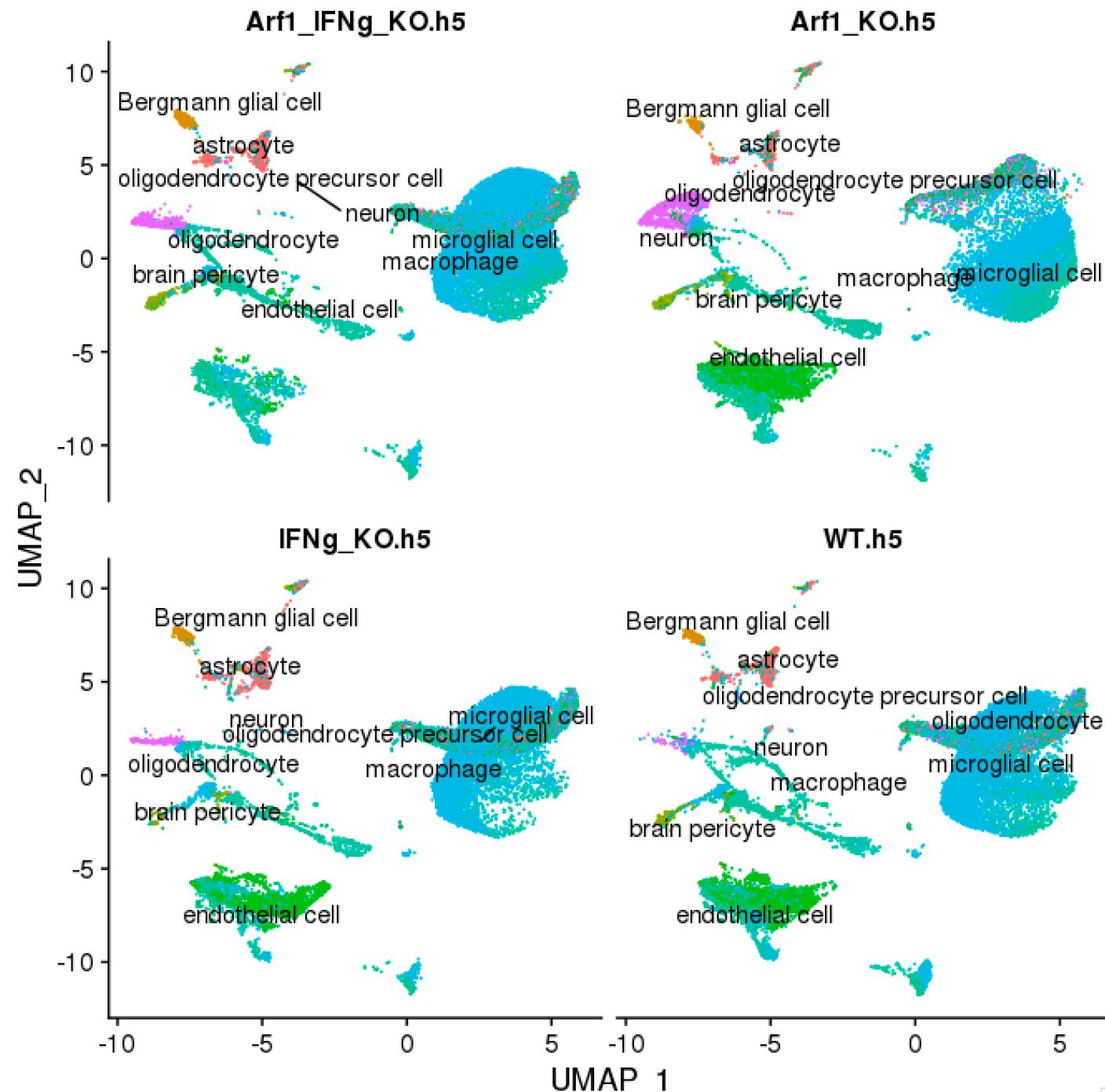
It looks like the microglial cluster(main cluster) isn't tied to cell cycle, good.

Cell identity annotation by Tabula Muris – over half of the cells are microglia

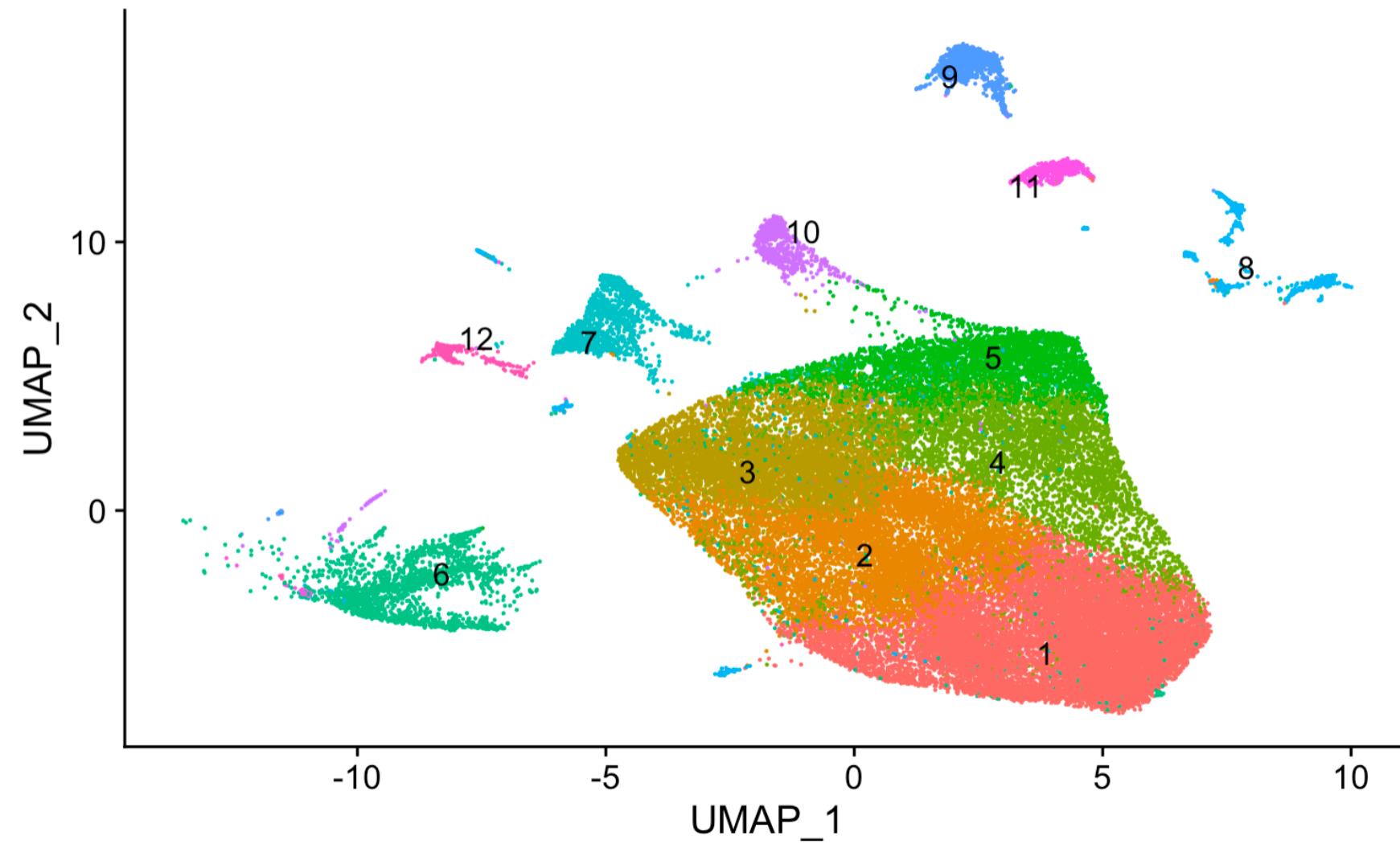


Cell identity and count by sample

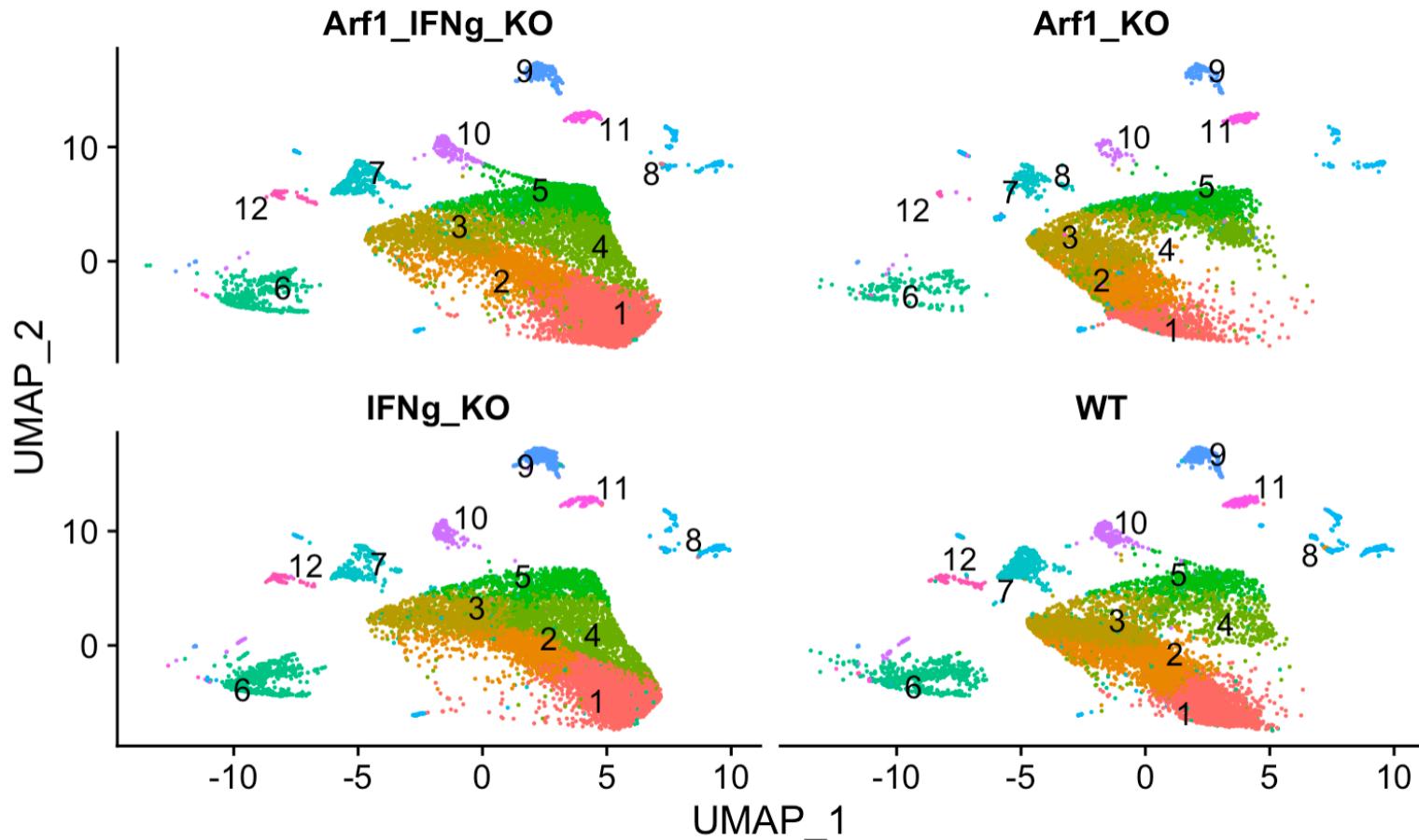
cell identity	Arf1_IFNg_KO.h5	Arf1_KO.h5	IFNg_KO.h5	WT.h5
astrocyte	1136	554	1177	1049
Bergmann glial cell	380	230	230	297
brain pericyte	461	349	241	266
endothelial cell	788	3473	3053	3276
macrophage	6387	6463	3853	5193
microglial cell	13238	7683	14105	13763
neuron	56	282	58	81
oligodendrocyte	1023	2988	438	602
oligodendrocyte precursor cell	15	14	11	4
Total	23484	22036	23166	24531



Only microglia cells – reshaped with 0.3 resolution into 12 microglia subclusters



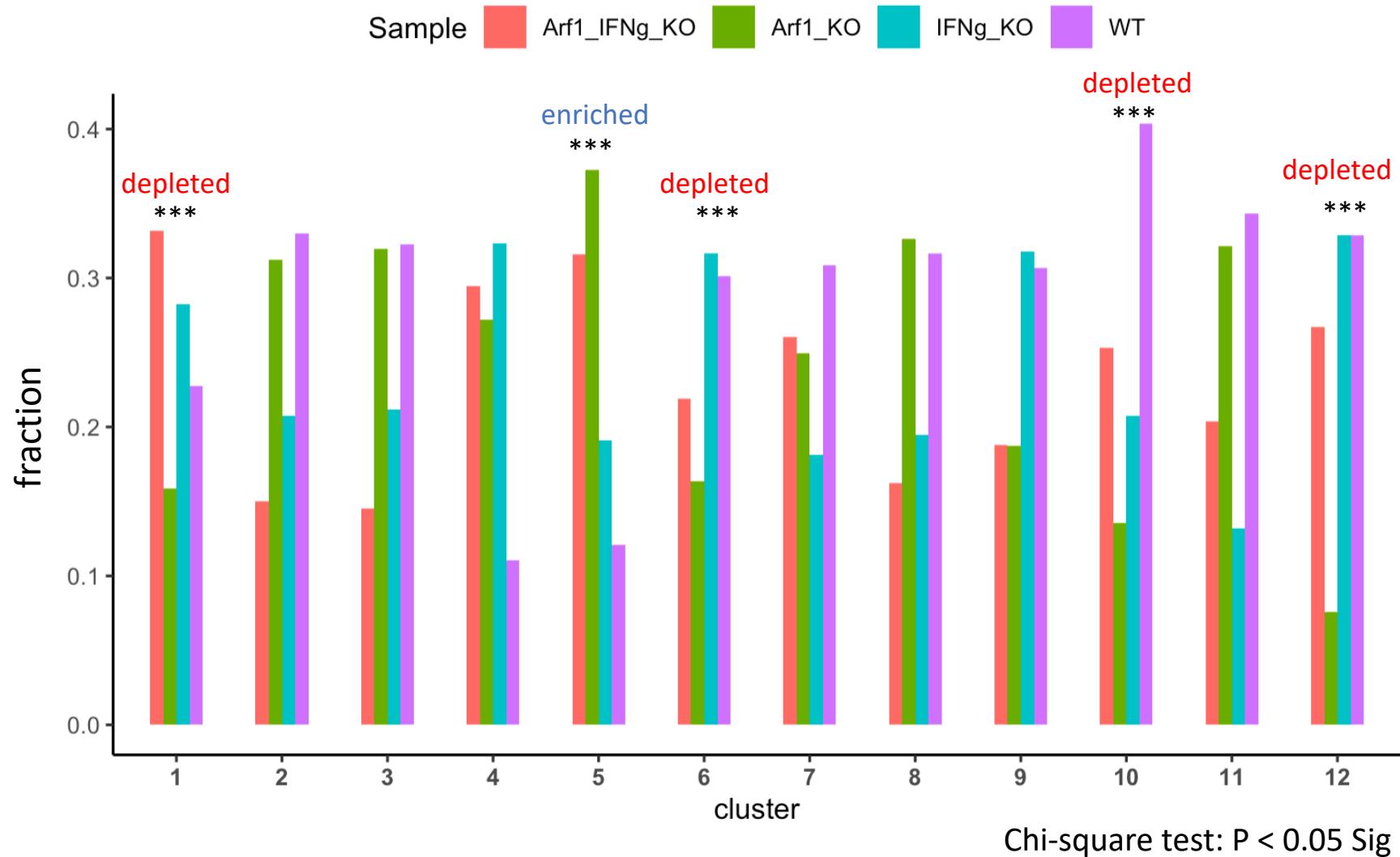
Only microglia cells – reshaped with 0.3 resolution into 12 microglia subclusters



Number of microglial cells for each cluster in each sample

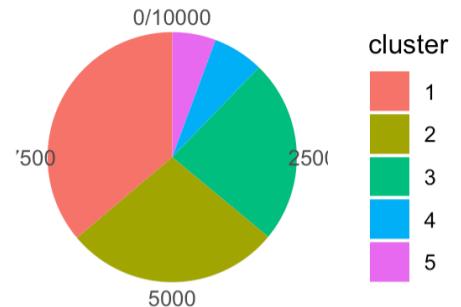
	Arf1_IFNg_KO	Arf1_KO	IFNg_KO	WT
1	4165	1990	3544	2855
2	1001	2080	1380	2198
3	844	1856	1230	1874
4	1392	1284	1527	522
5	1171	1380	707	447
6	412	308	596	567
7	317	304	221	376
8	169	340	203	330
9	171	170	289	279
10	172	92	141	274
11	111	175	72	187
12	74	21	91	91

Arf1_KO is enriched in Cluster 5

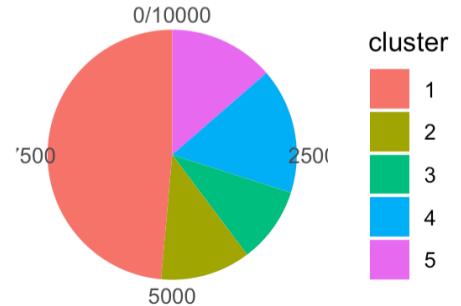


Proportion of cells for each cluster across samples

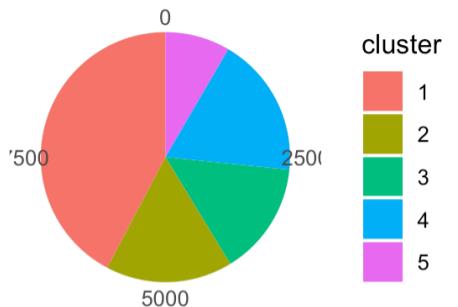
WT



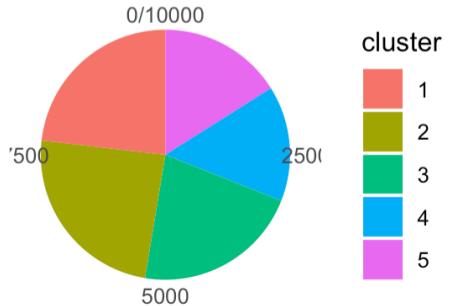
Arf1_IFNg_KO



IFNg_KO

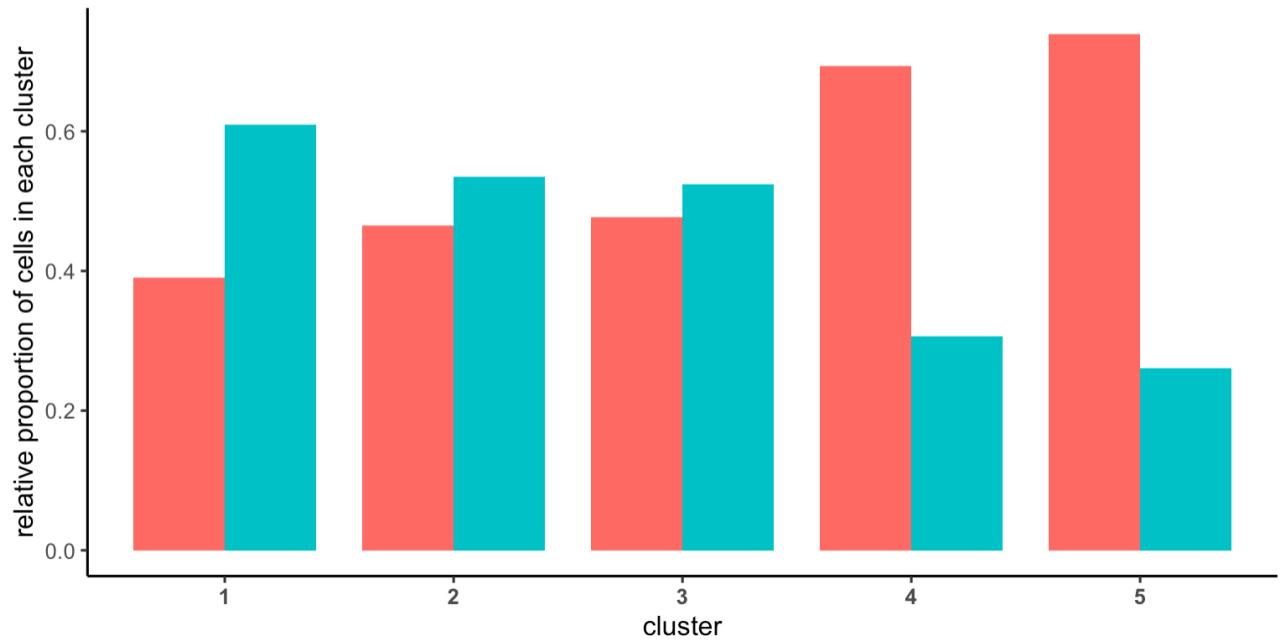


Arf1_KO

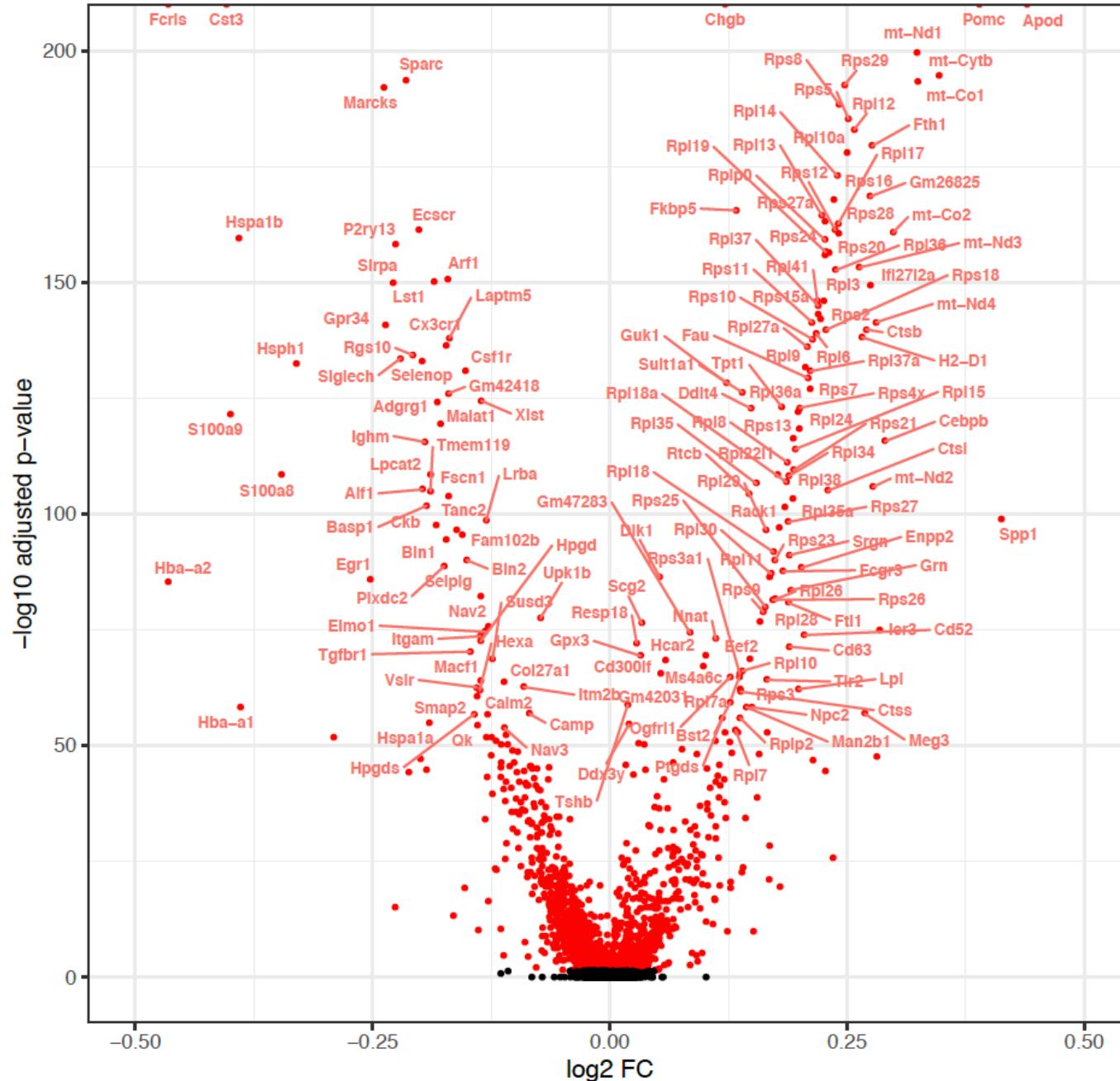


significantly higher proportion of cells in Arf1-KO cluster 5

SampleName Arf1_KO WT

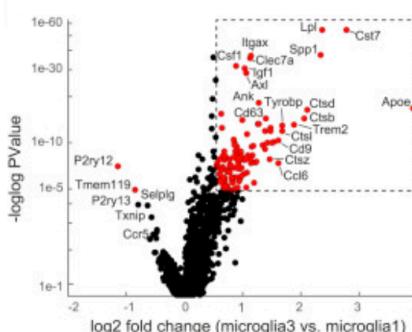


Arf1–WT

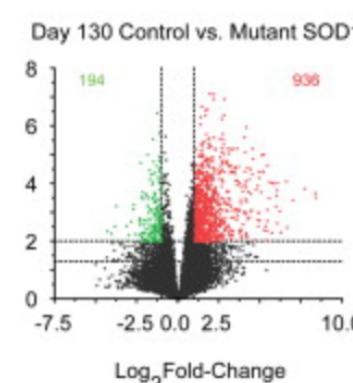


Curating published data to create a set of dysregulated genes in neurodegeneration

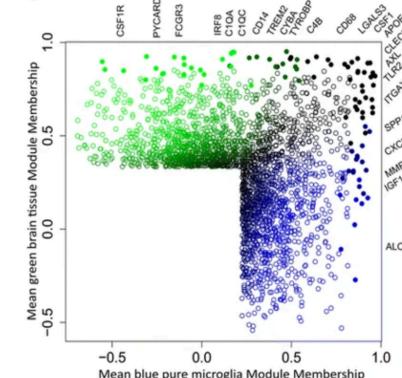
conditions	Model	Sequencing tech	source
multiple sclerosis	Mouse (EAE)	Nanostring	Kraseman et al., 2017
Amyotrophic lateral sclerosis (ALS)	Mouse (SODG93A)	Bulk RNA-seq	Chiu et al., 2013
Alzheimer's disease (AD)	Mouse	Single cell RNAseq	Keren-Shaul et al. 2017
aging	mouse	Bulk RNA-seq	Holtman et al., 2015



Alzheimer's disease (AD)

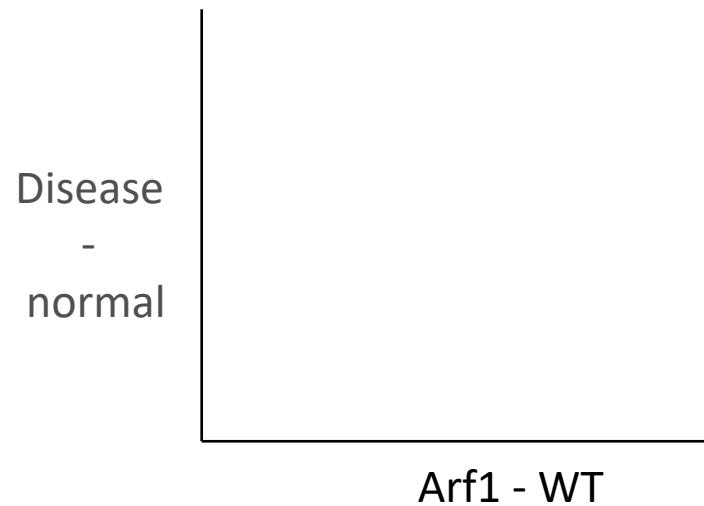


Amyotrophic lateral sclerosis (ALS)

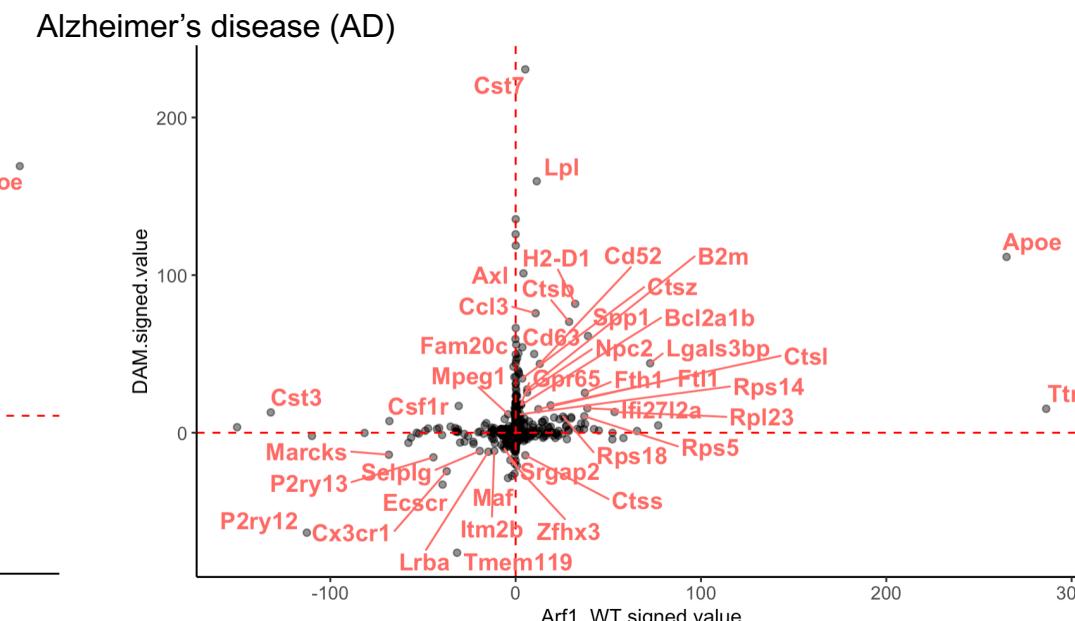
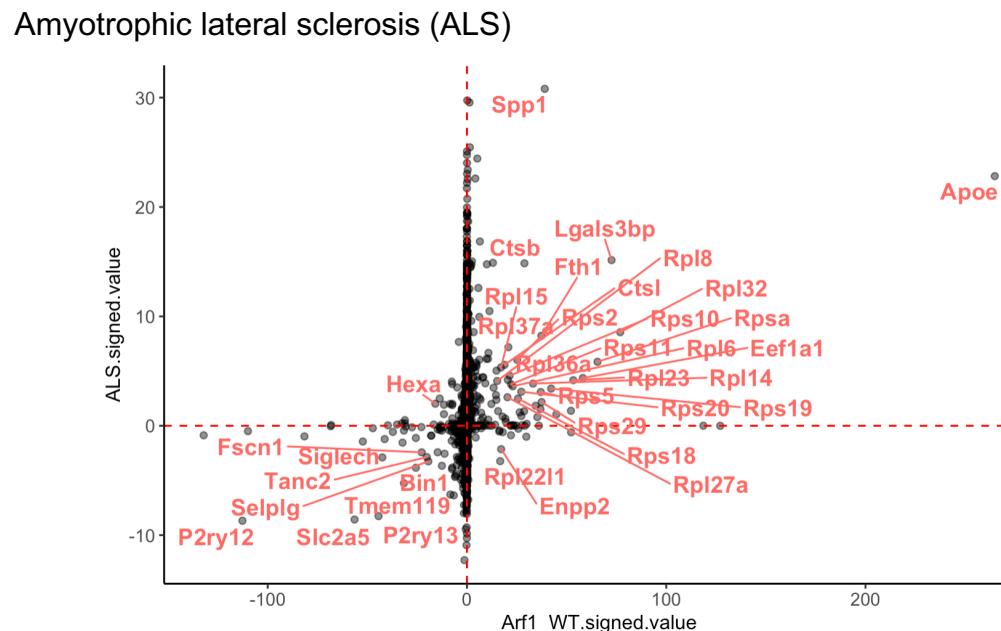
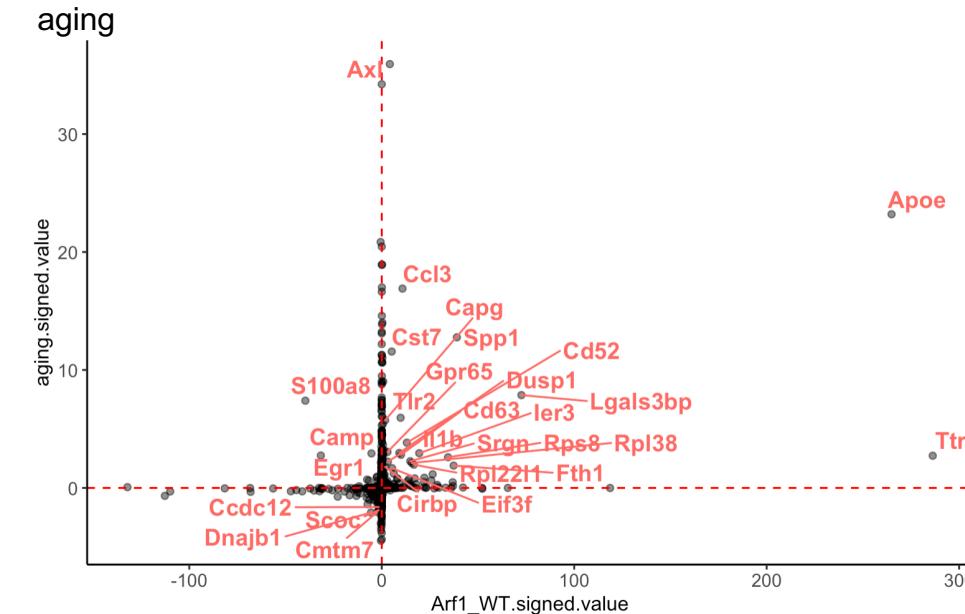
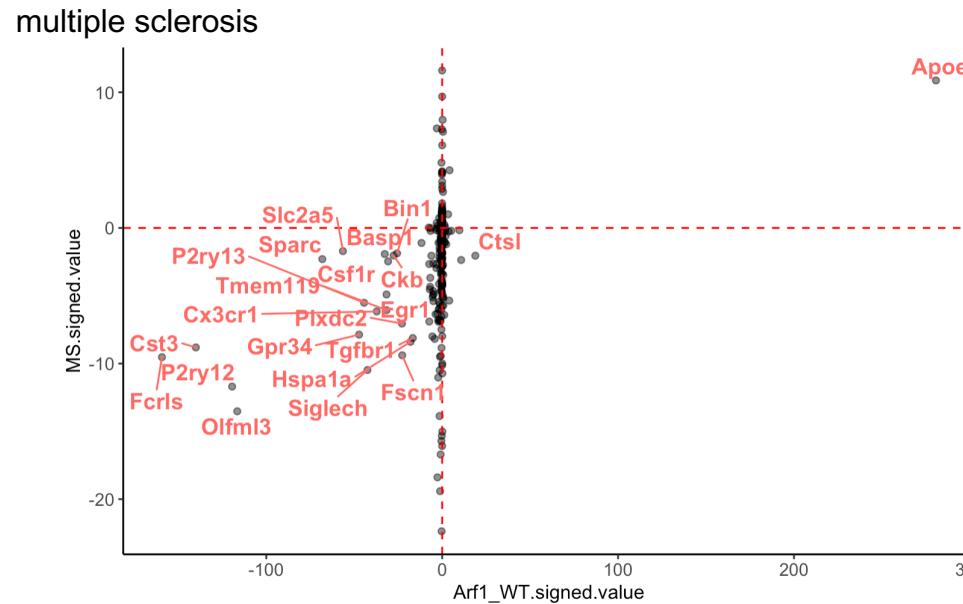


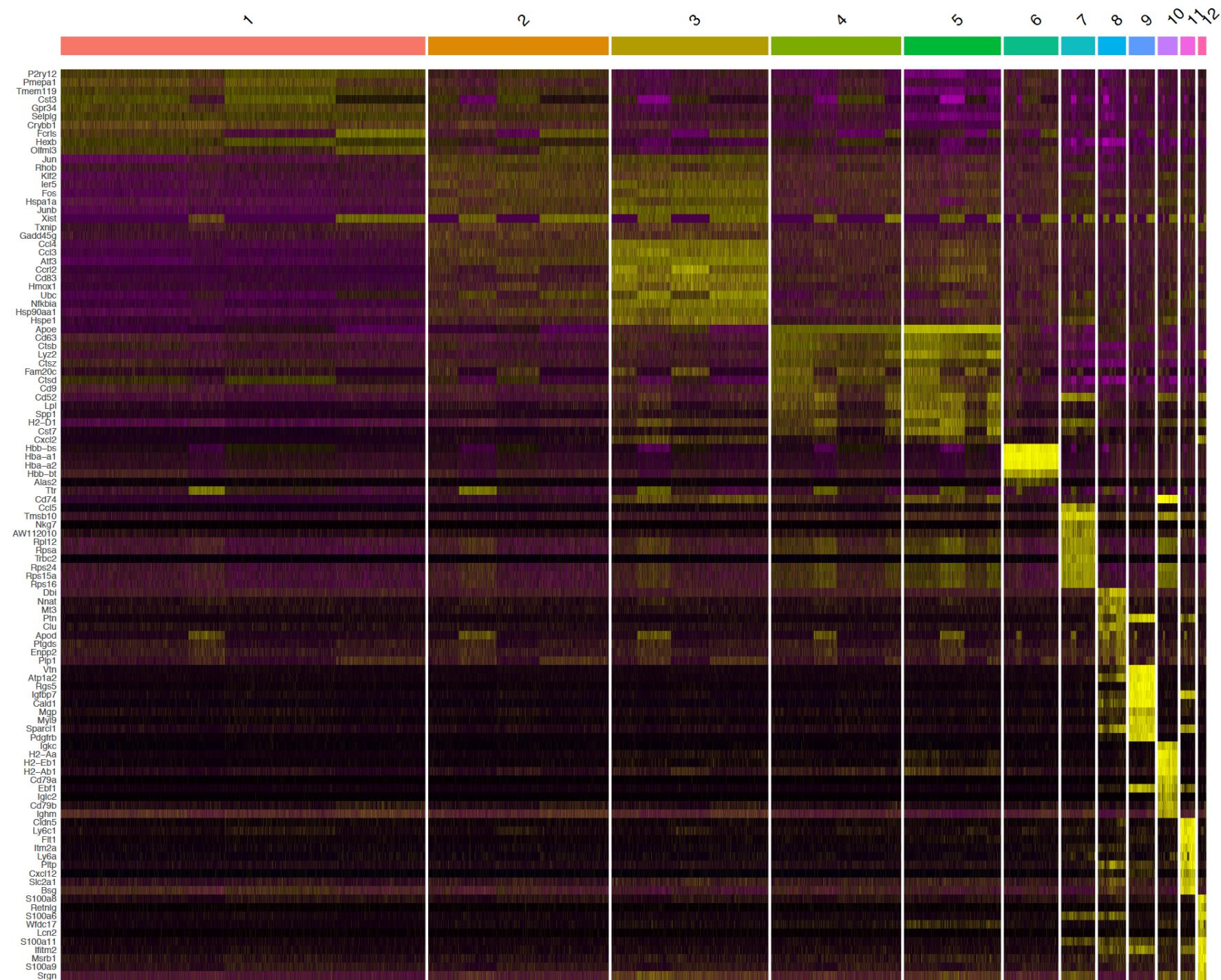
aging

Signed.value = sign(logFC) * log10(Pvalue) * abs(logFC) * -1



Top differentially expressed genes in Arf1-WT include some of the well-known neurodegenerative disease risk genes





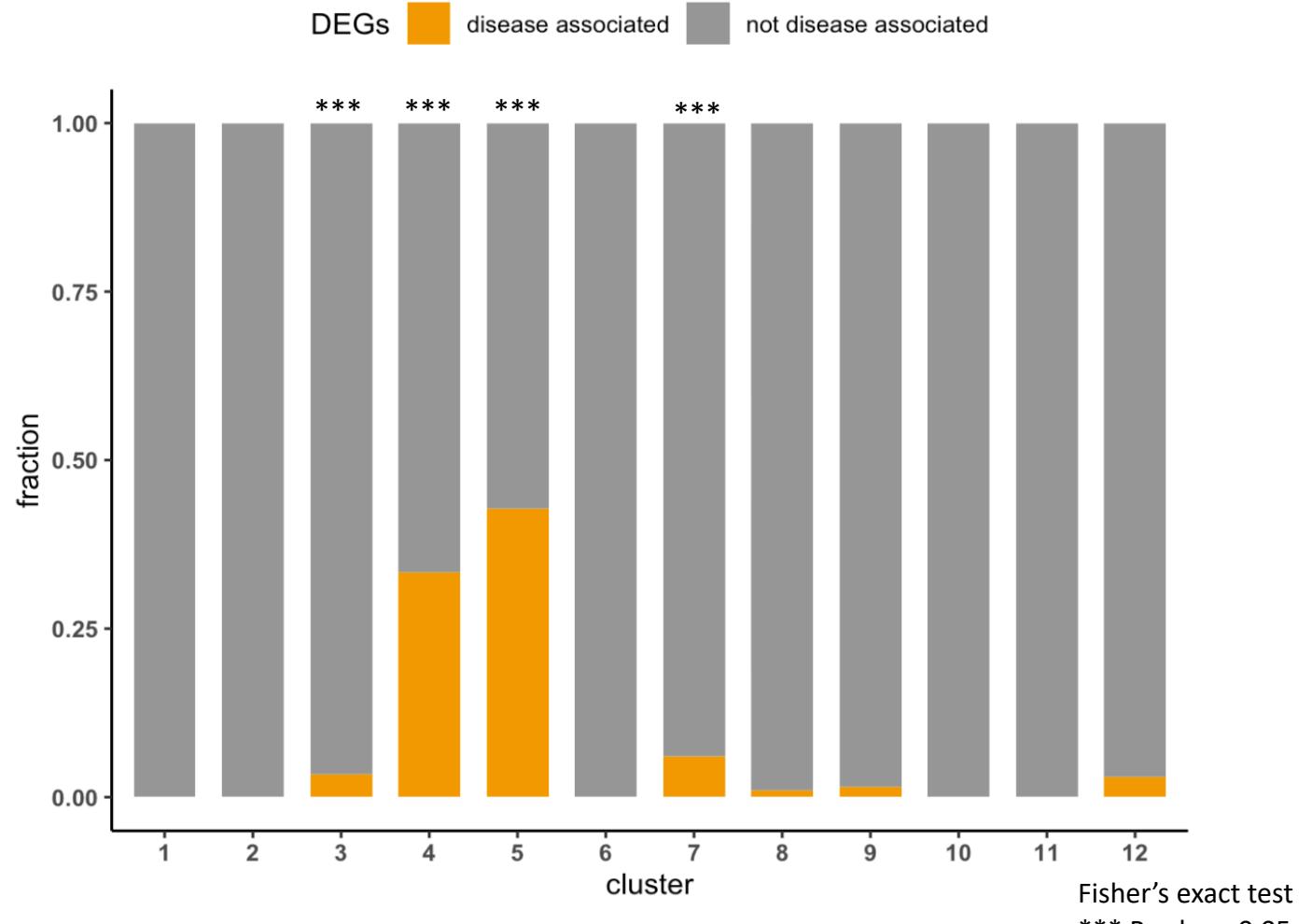
Markers (top 10 by average fold change)
for each microglia subcluster

Does cluster5 DEGs have an over-representation of neurodegenerative disease-associated genes?

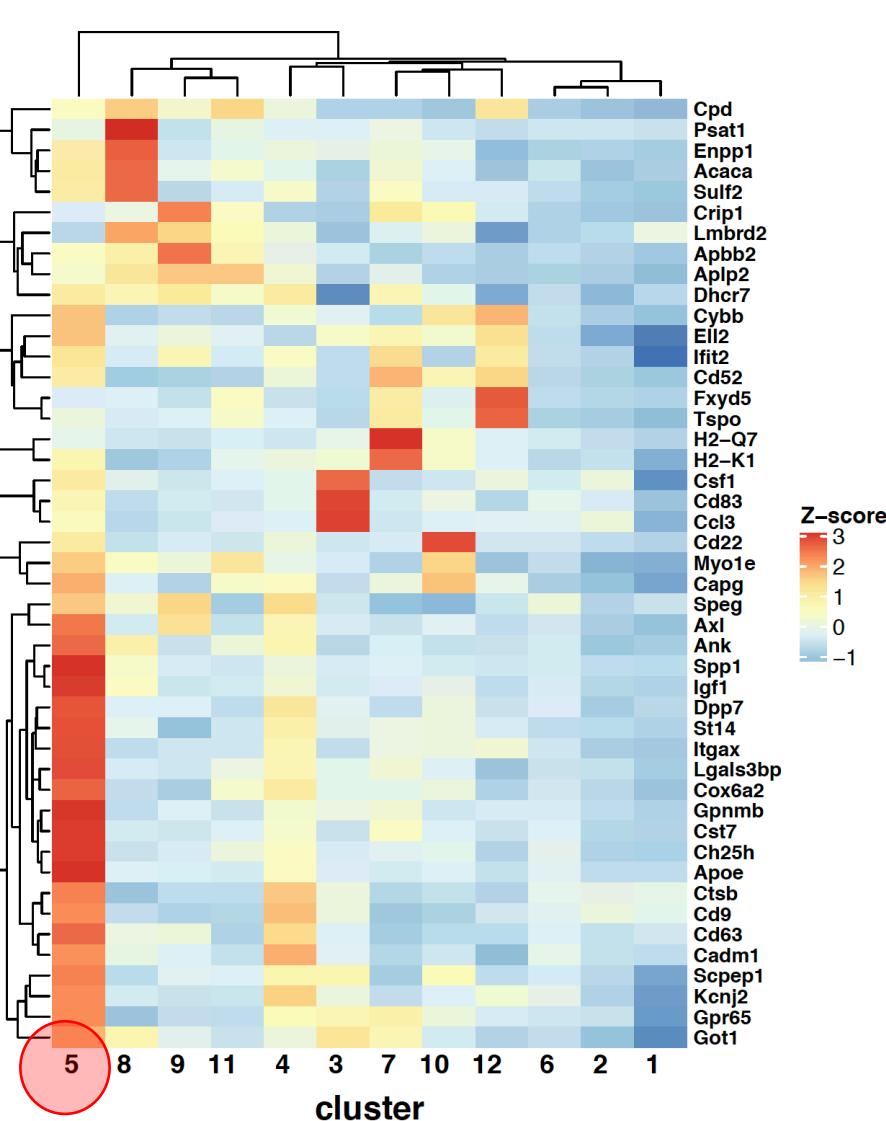
Commonly dysregulated genes in neurodegeneration:

- Up-regulated
- Down-regulated

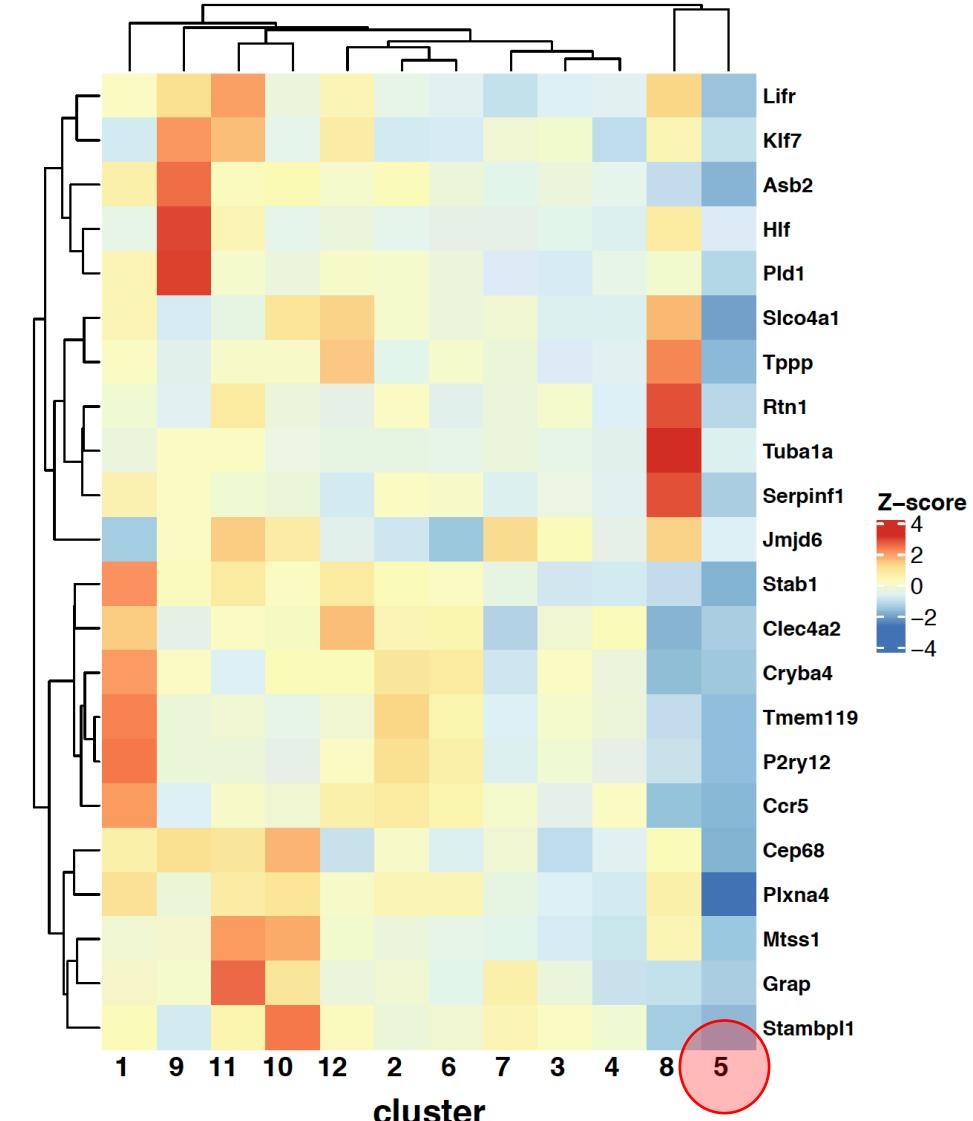
Cpd	Lifr
Psat1	Klf7
Enpp1	Axb2
Acaca	Hif
Sulf2	Pld1
Crip1	Sico4a1
Lmbrd2	Tppp
Appb2	Rtn1
Apfp2	Tuba1a
Dhcr7	Serpinf1
Cybb	Jmjdc6
Eif2	Stab1
Ifit2	Clec4a2
Cd52	Cryba4
Fxyd5	Tmem119
Tspo	P2ry12
H2-Q7	Ccr5
H2-K1	Cep68
Csf1	Plxna4
Cd83	Mtss1
Ccl3	Grap
Cd22	Stambpl1
Myo1e	
Capg	
Spag	
Axl	
Ank	
Spp1	
Igf1	
Dpp7	
St14	
Itgax	
Lgals3bp	
Cox6a2	
Gpnmb	
Cst7	
Ch25h	
Apoe	
Ctsb	
Cd9	
Cd63	
Cadm1	
Sccep1	
Kcnj2	
Gpr65	
Got1	



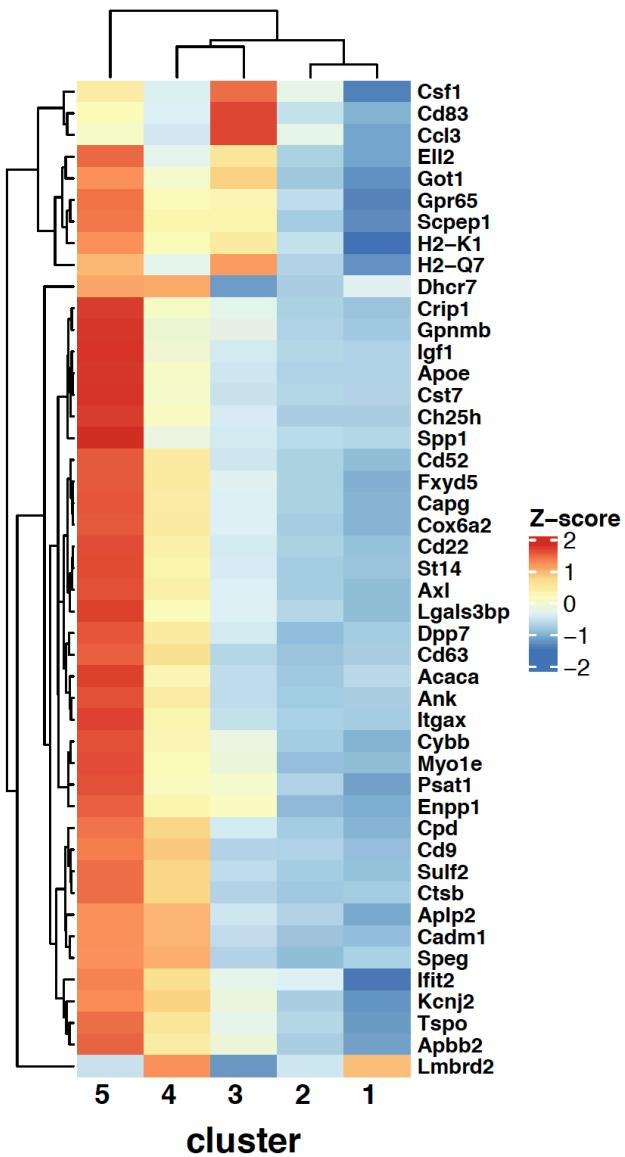
Up-regulated genes in neurodegeneration



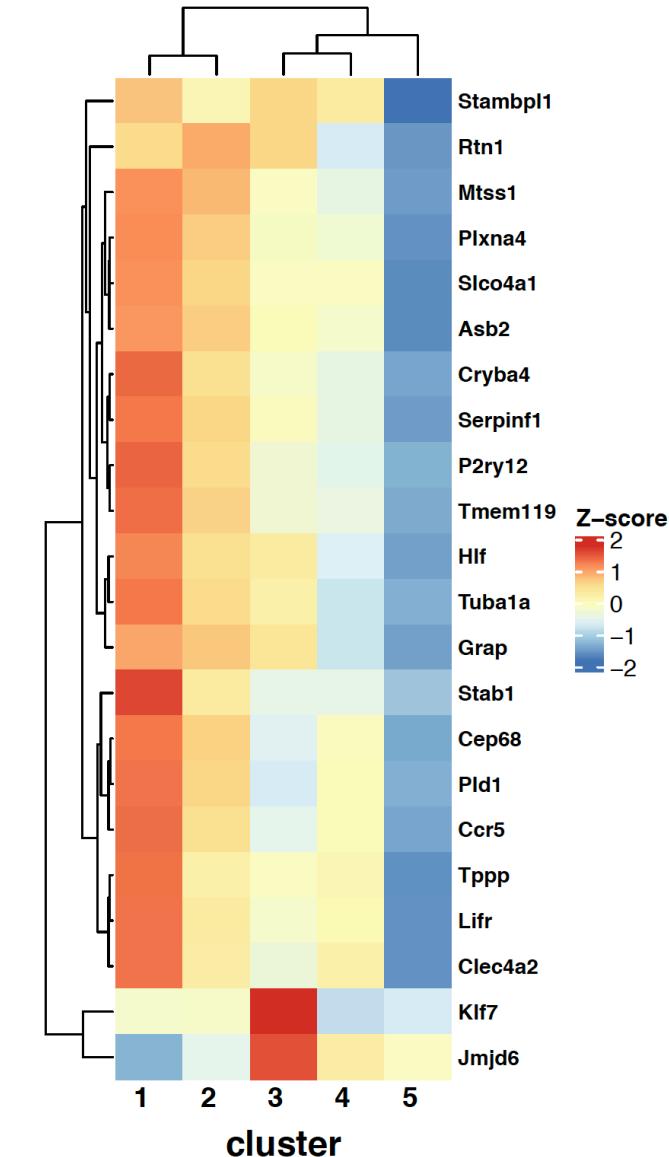
Down-regulated genes in neurodegeneration

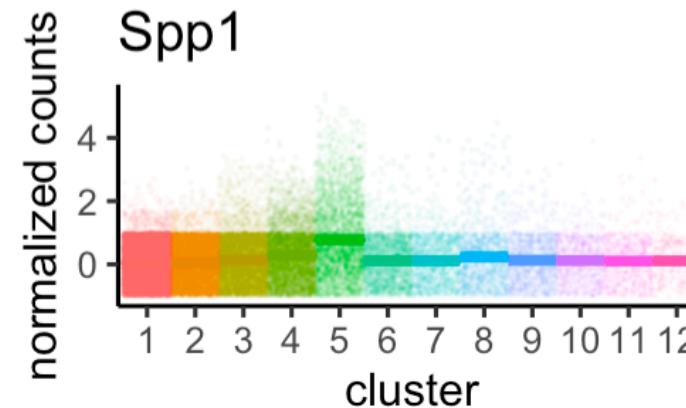
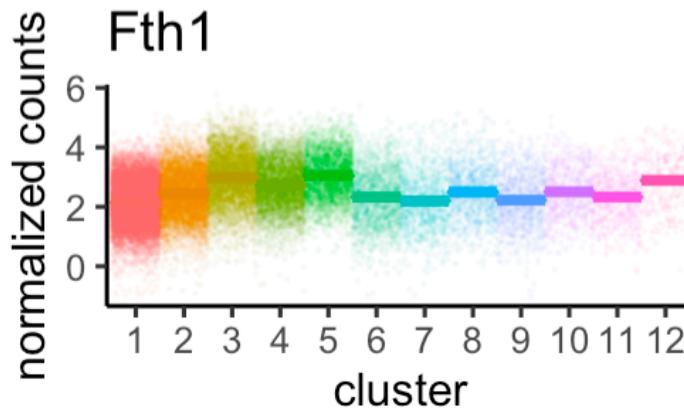
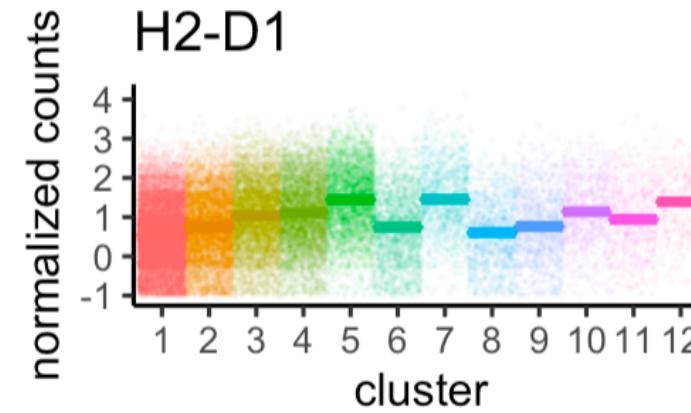
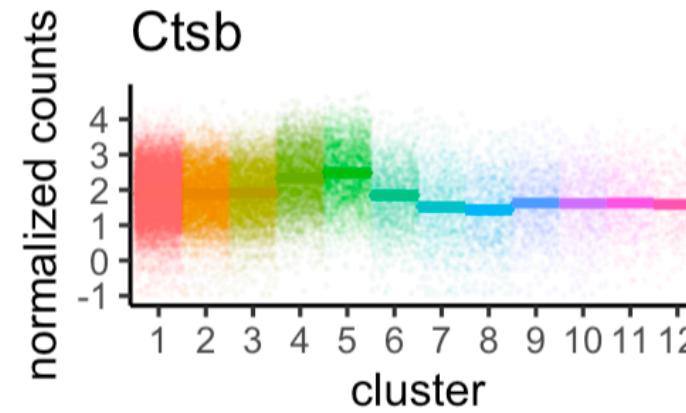
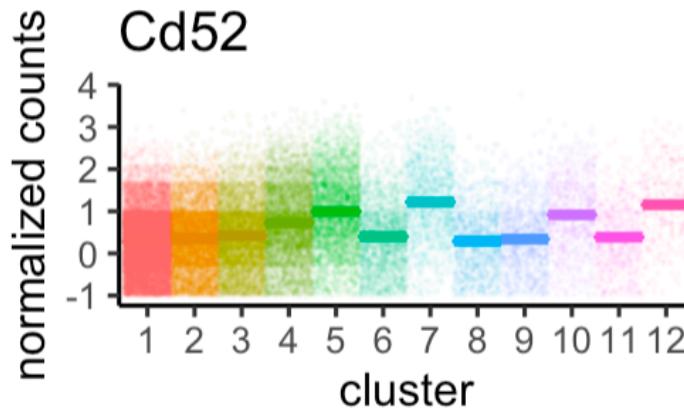
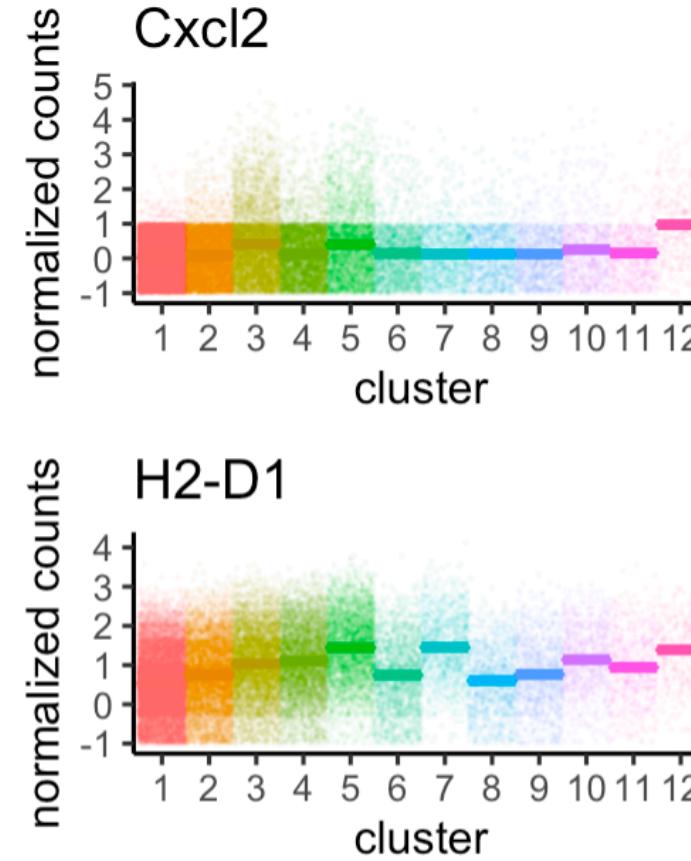
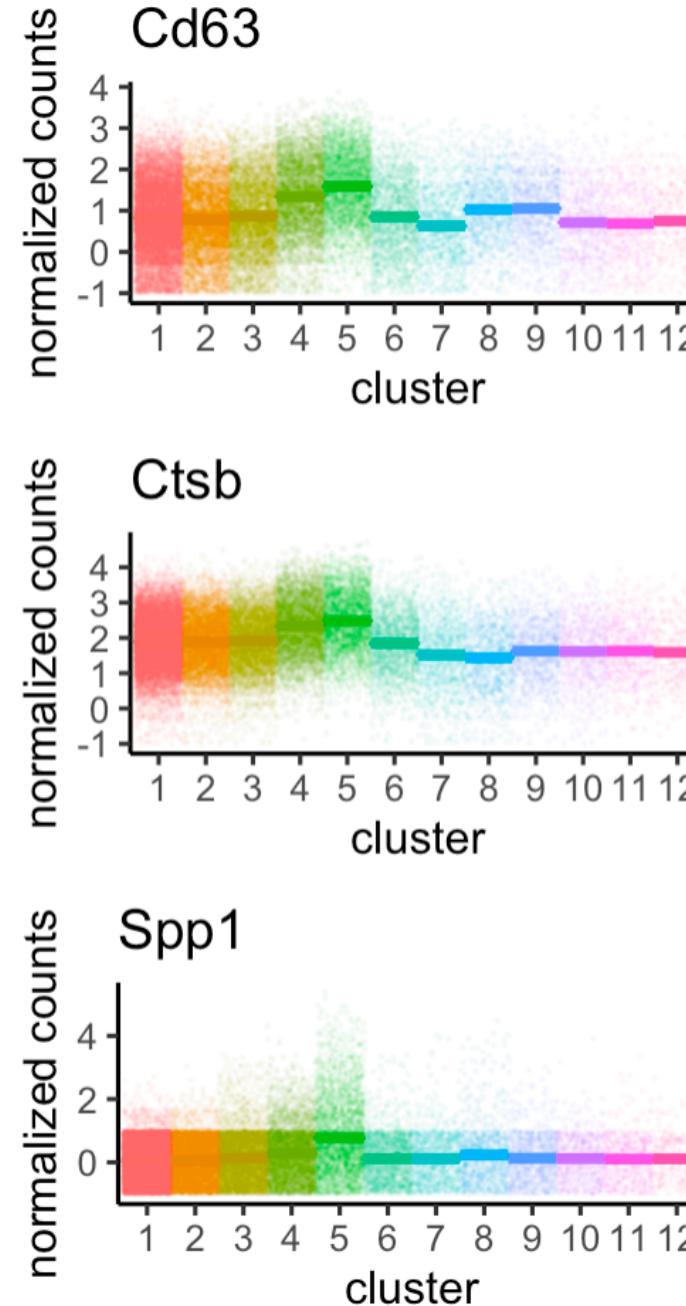
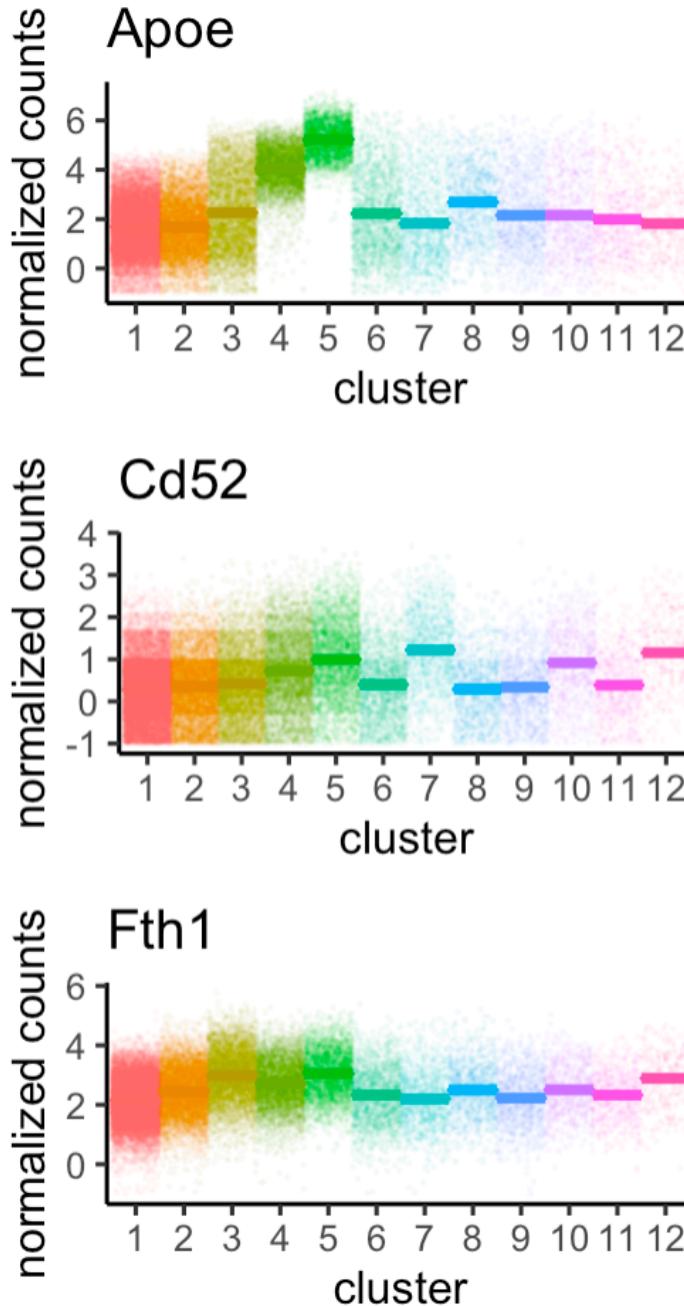


Up-regulated genes in neurodegeneration



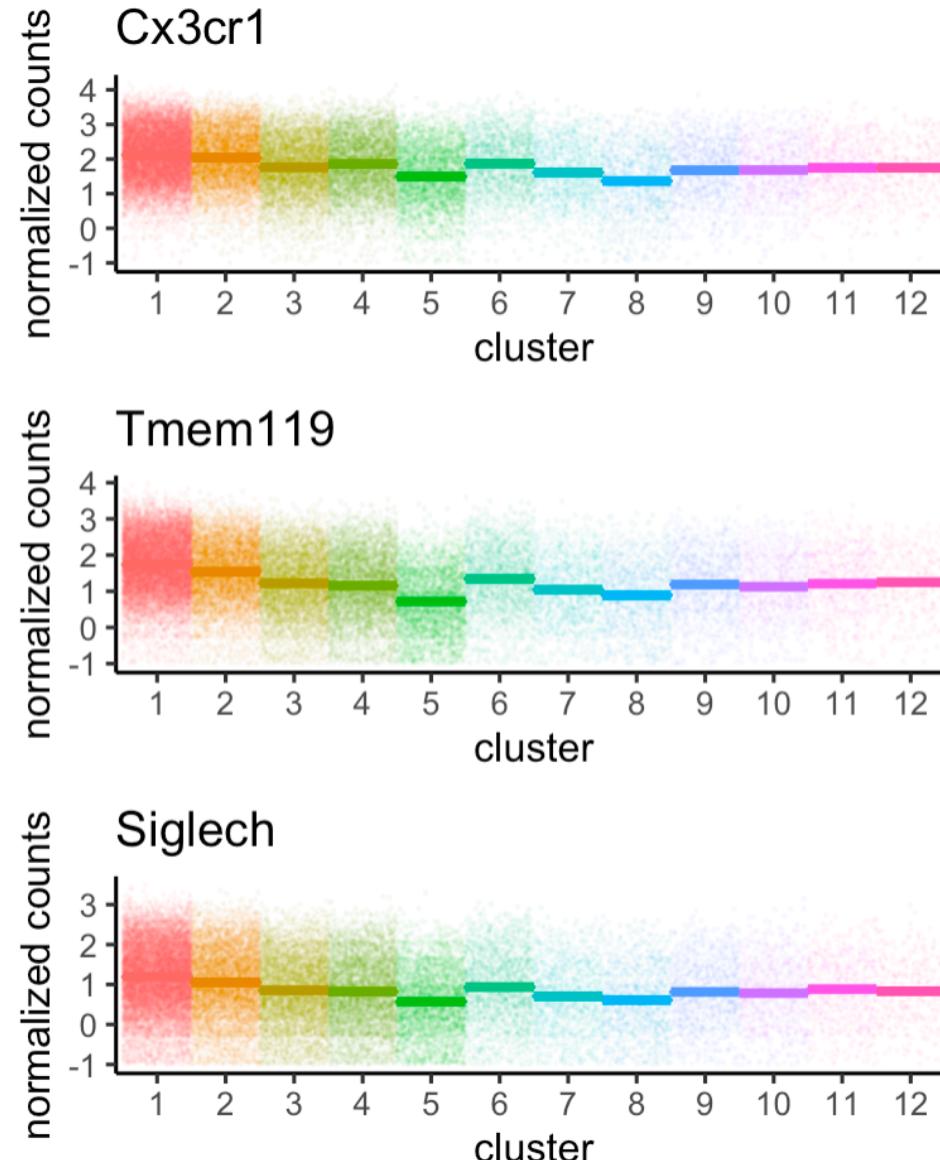
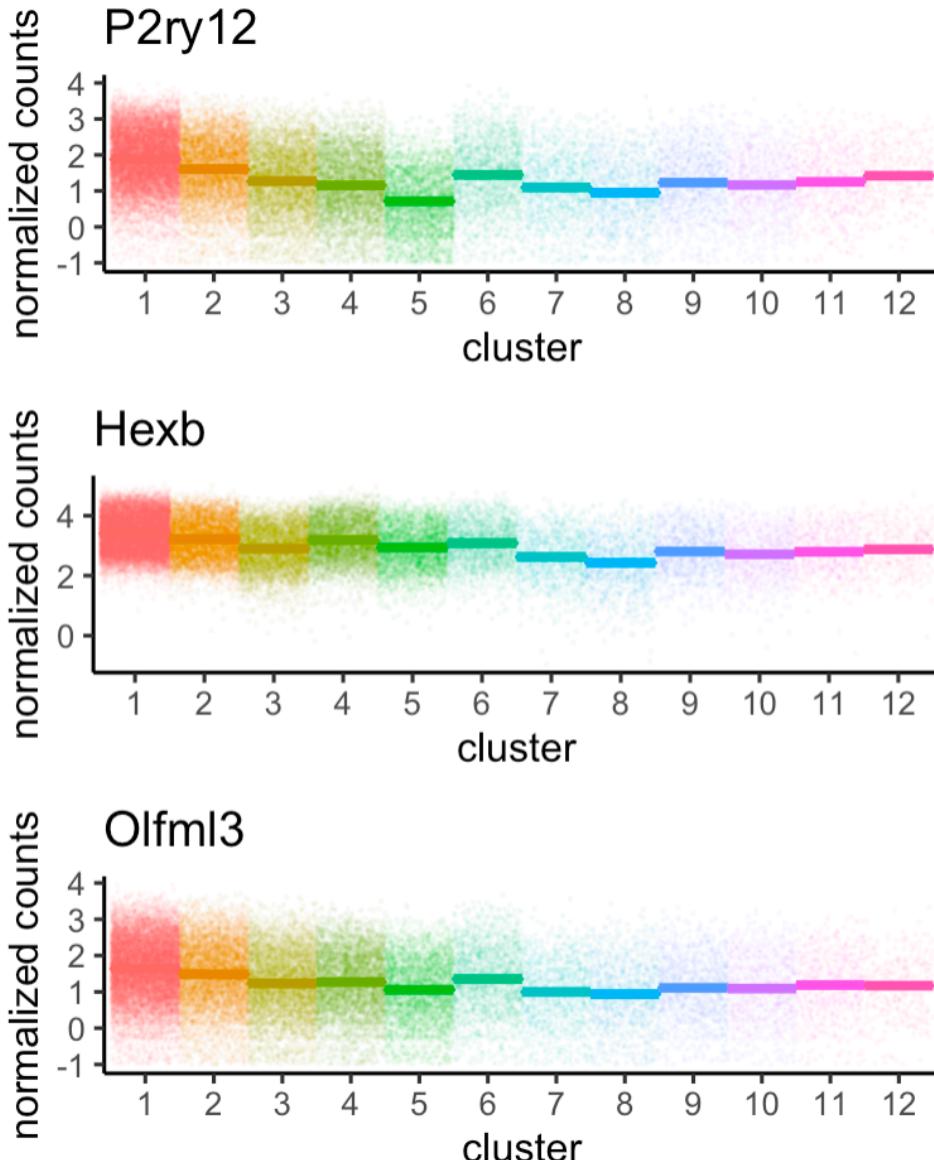
Down-regulated genes in neurodegeneration



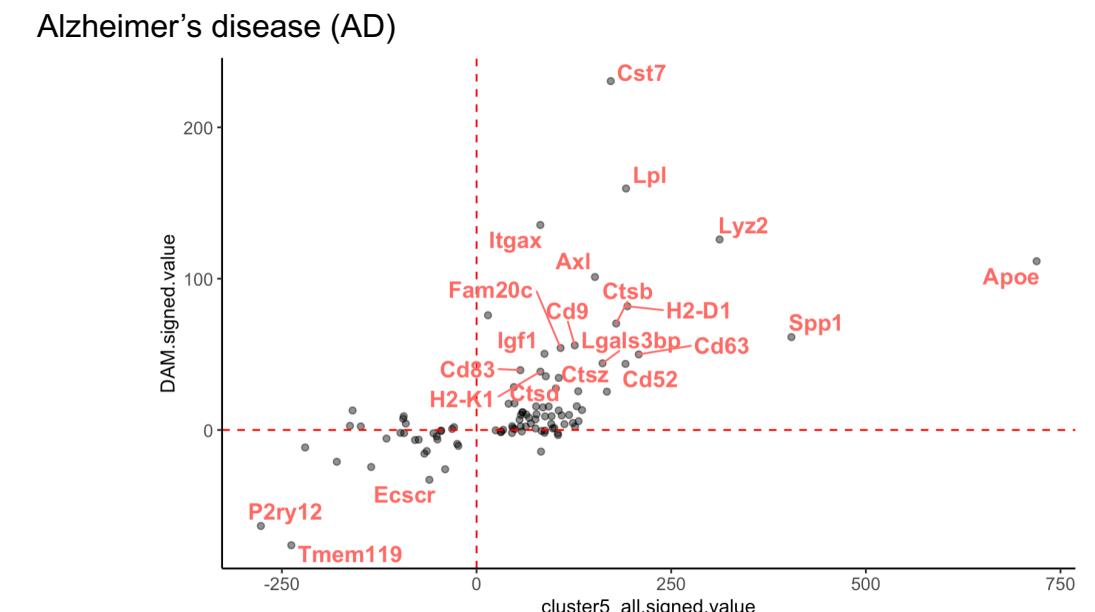
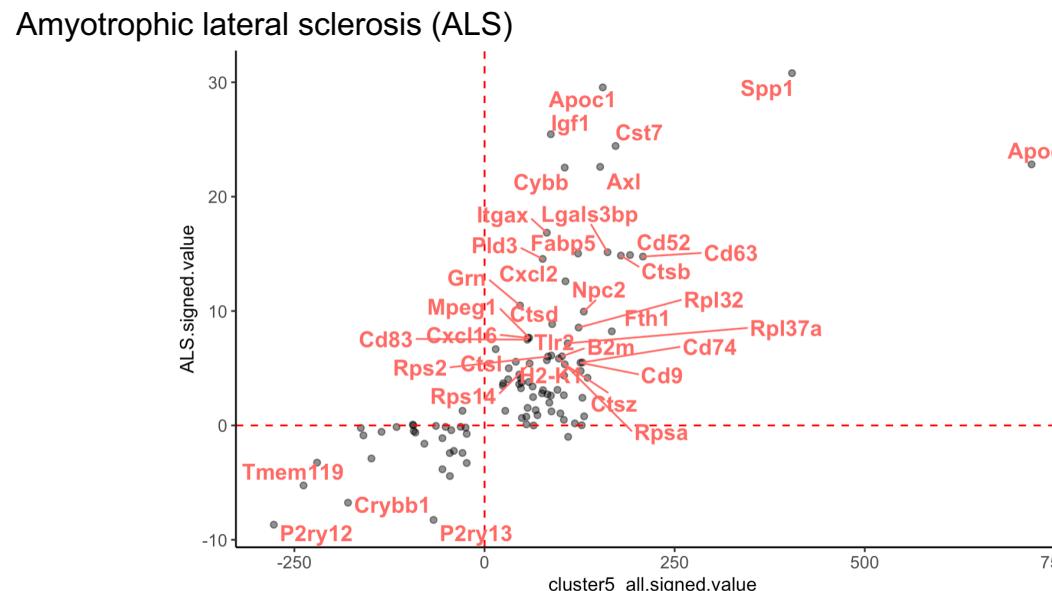
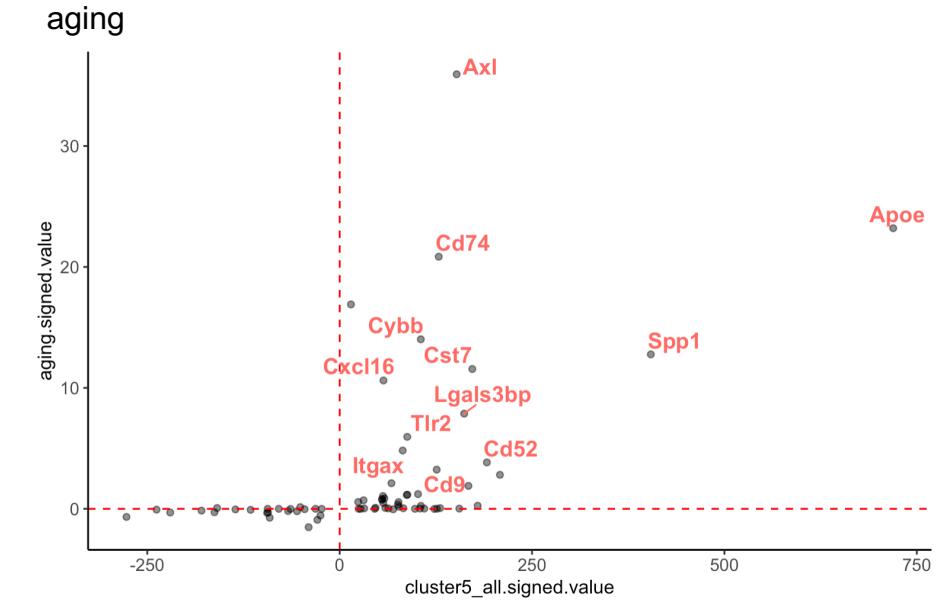
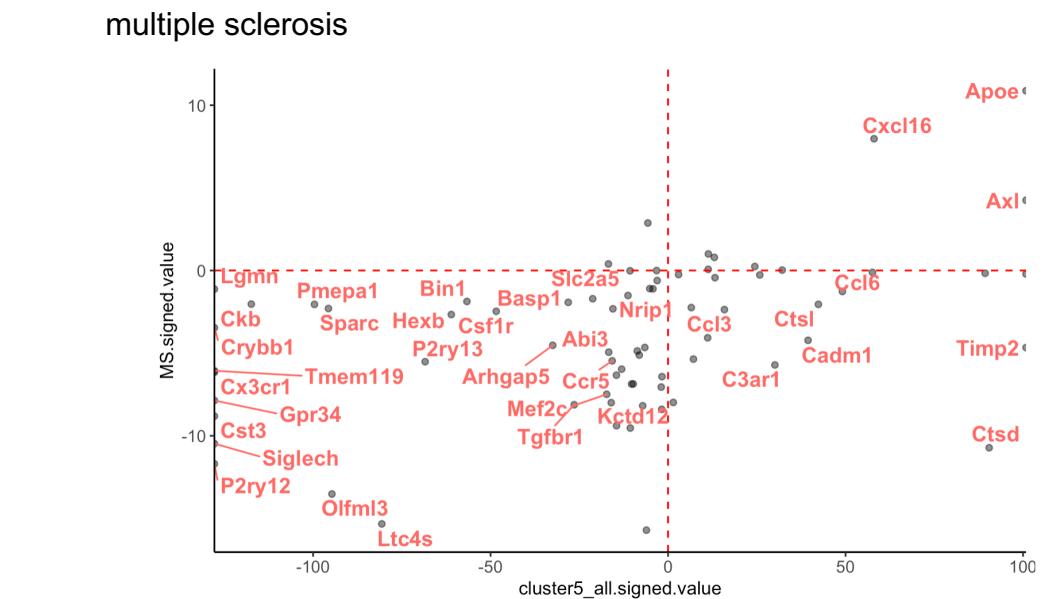


- Top markers for Cluster 5 include many known disease risk factors
- An increase in expression from Cluster 1 to Cluster 5

Top marker of Cluster 1 include mostly “microglial marker genes”

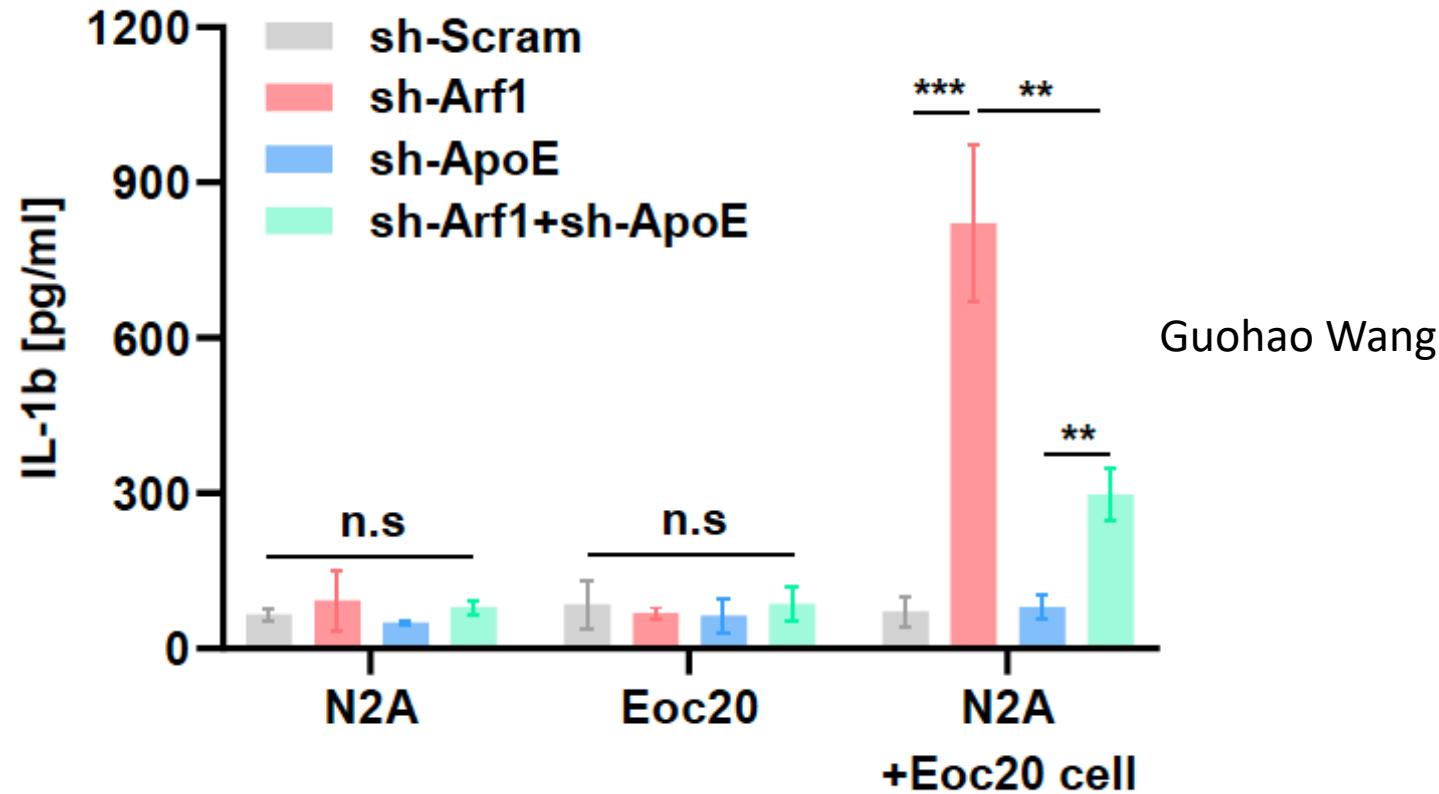


Top markers in both Cluster 5 include some of the well-known neurodegenerative disease risk genes



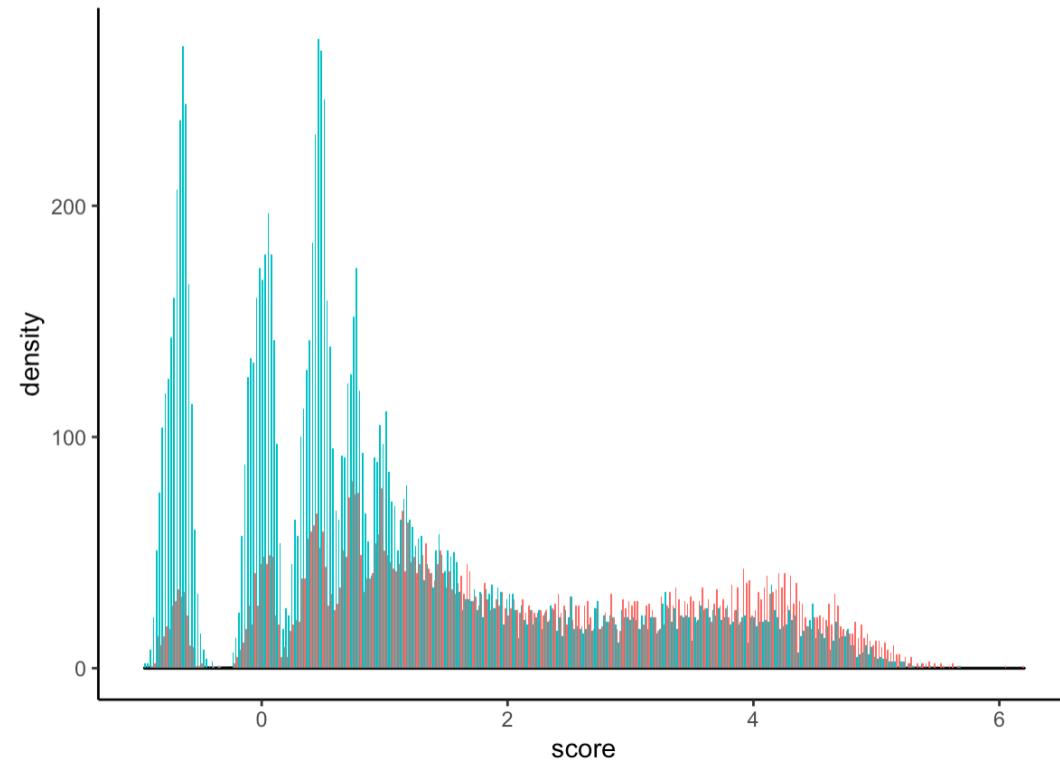
Increased IL-1 β in neuron (N2A) and microglia (Eoc20) co-culture can be significantly suppressed by knocking down *ApoE* (sh-ApoE).

interleukin-1 β :
proinflammatory cytokines

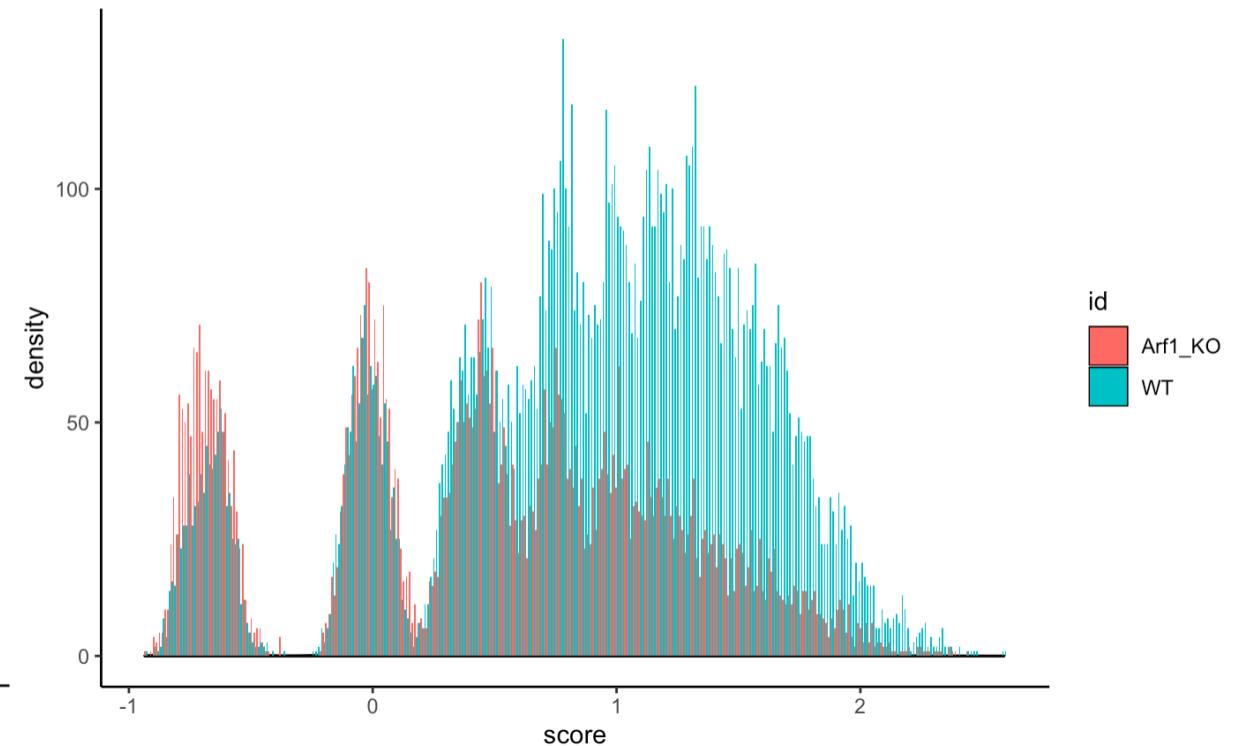


ApoE-mediated lipid transportation is important for IL-1 β induction in microglia

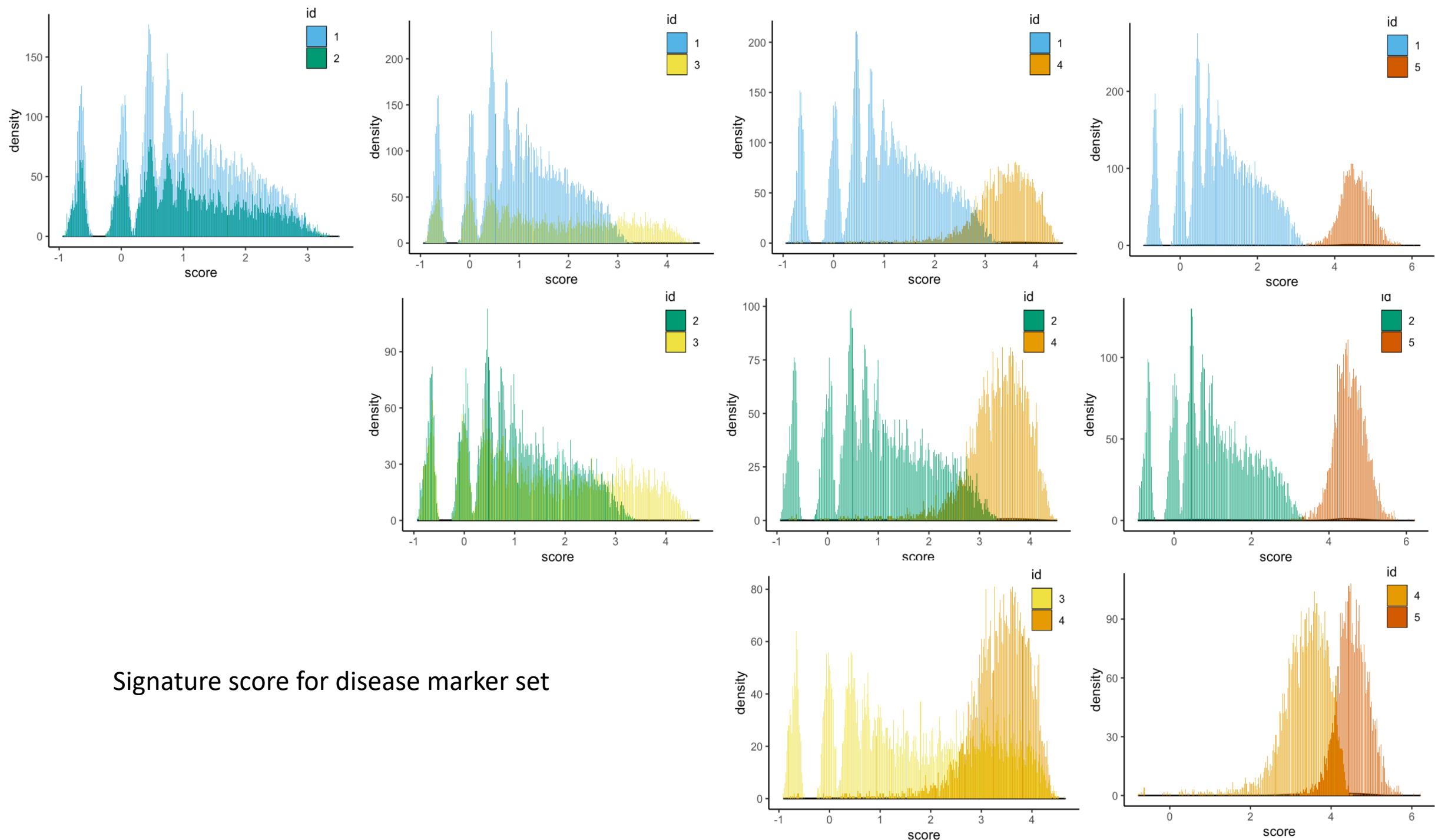
Signature score for disease marker set

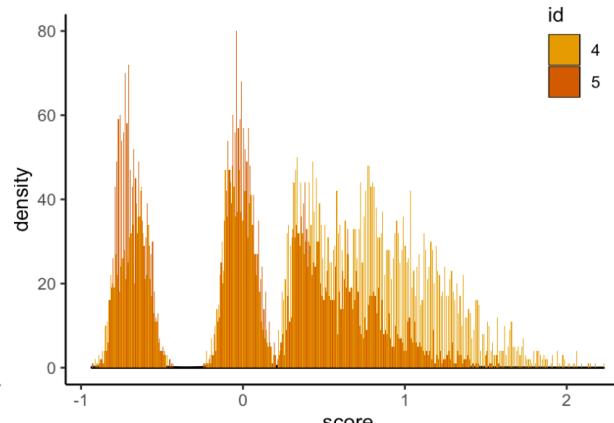
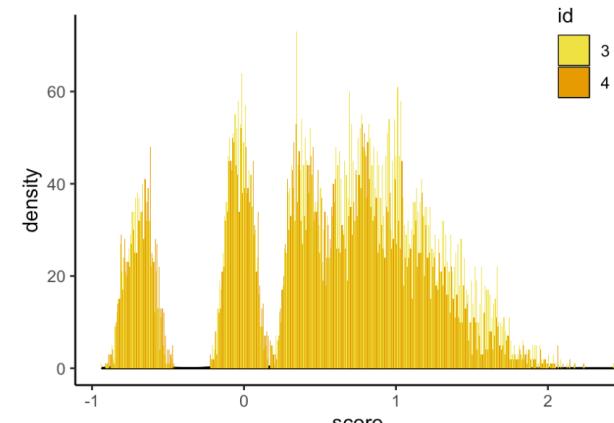
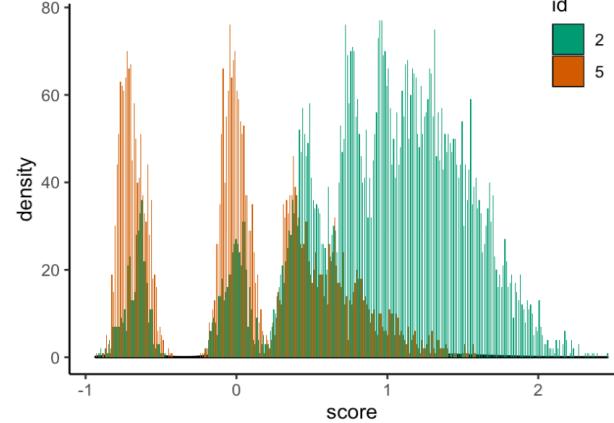
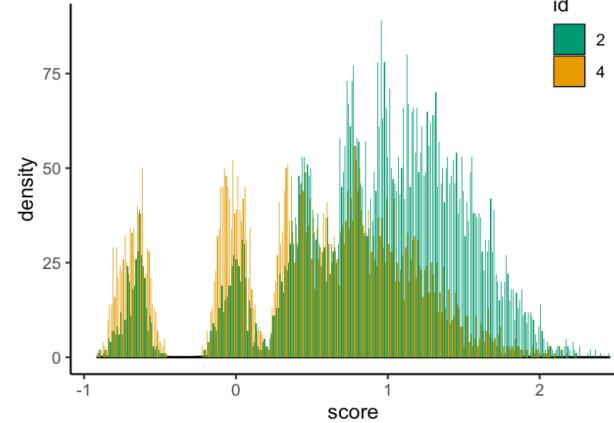
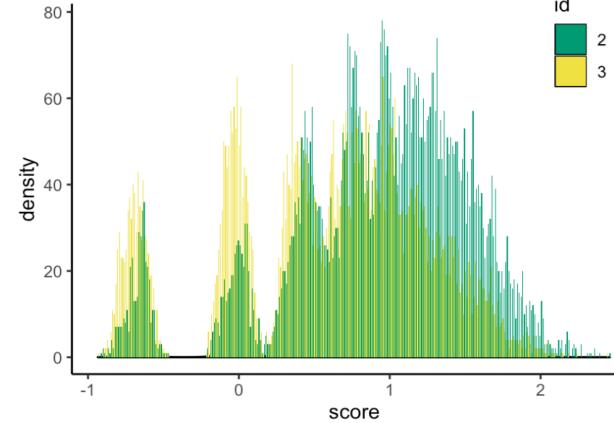
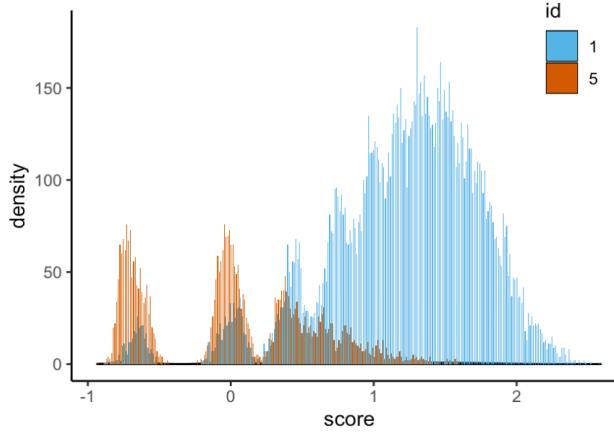
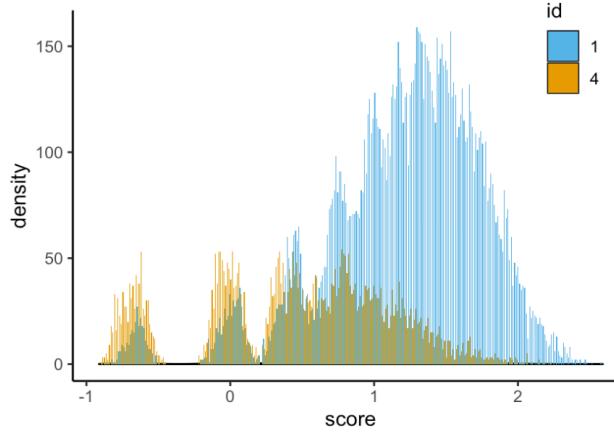
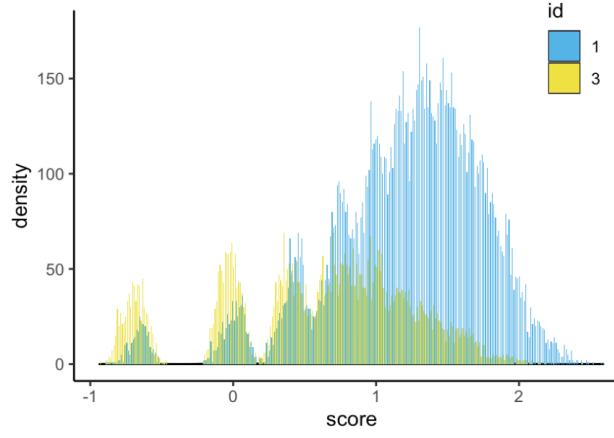
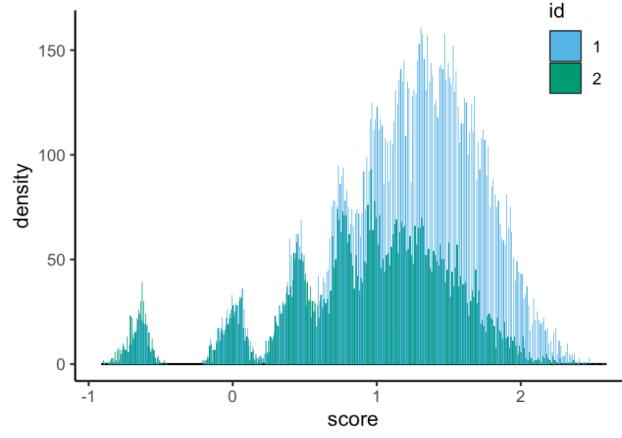


Signature score for homeostatic gene set



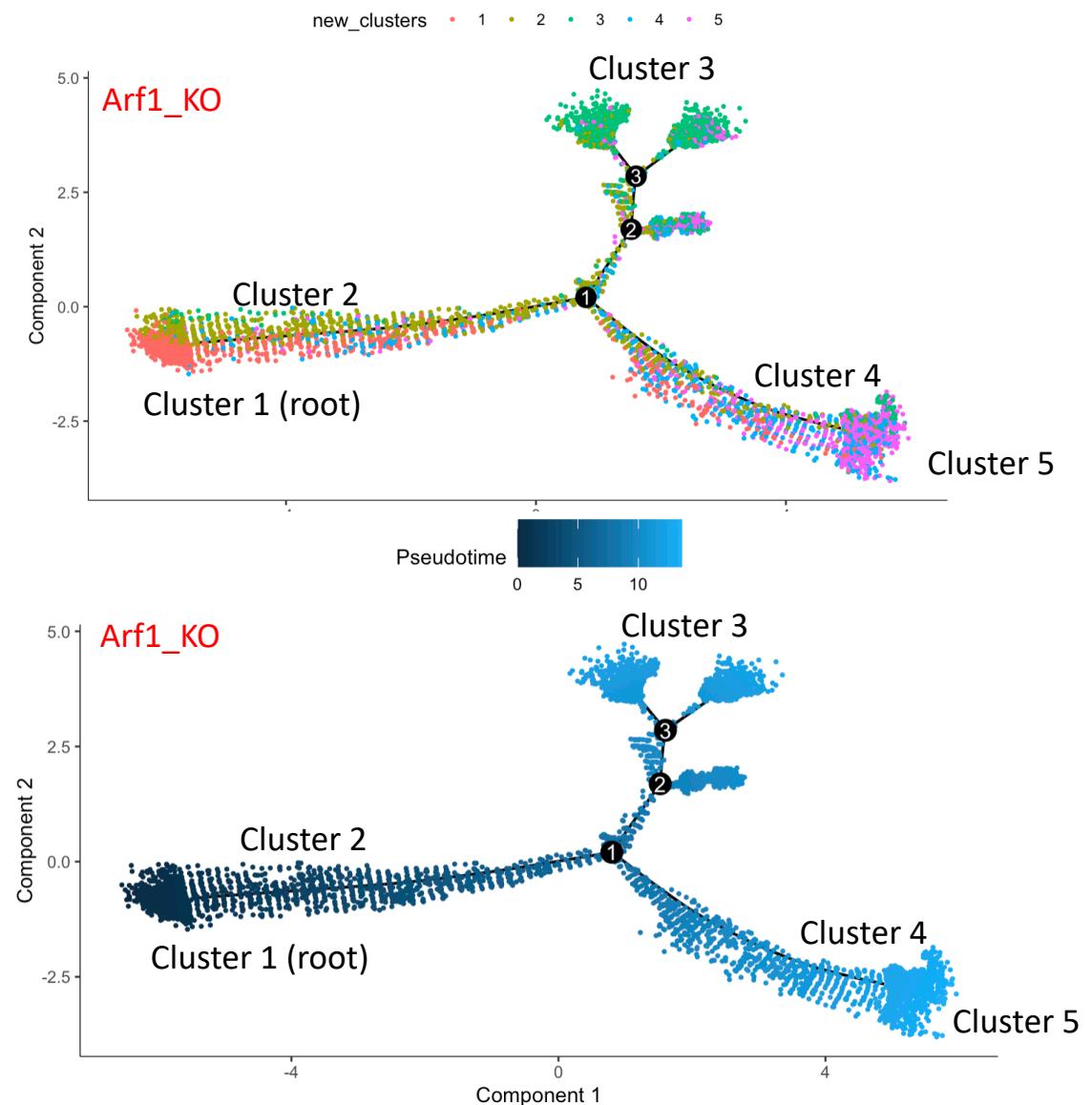
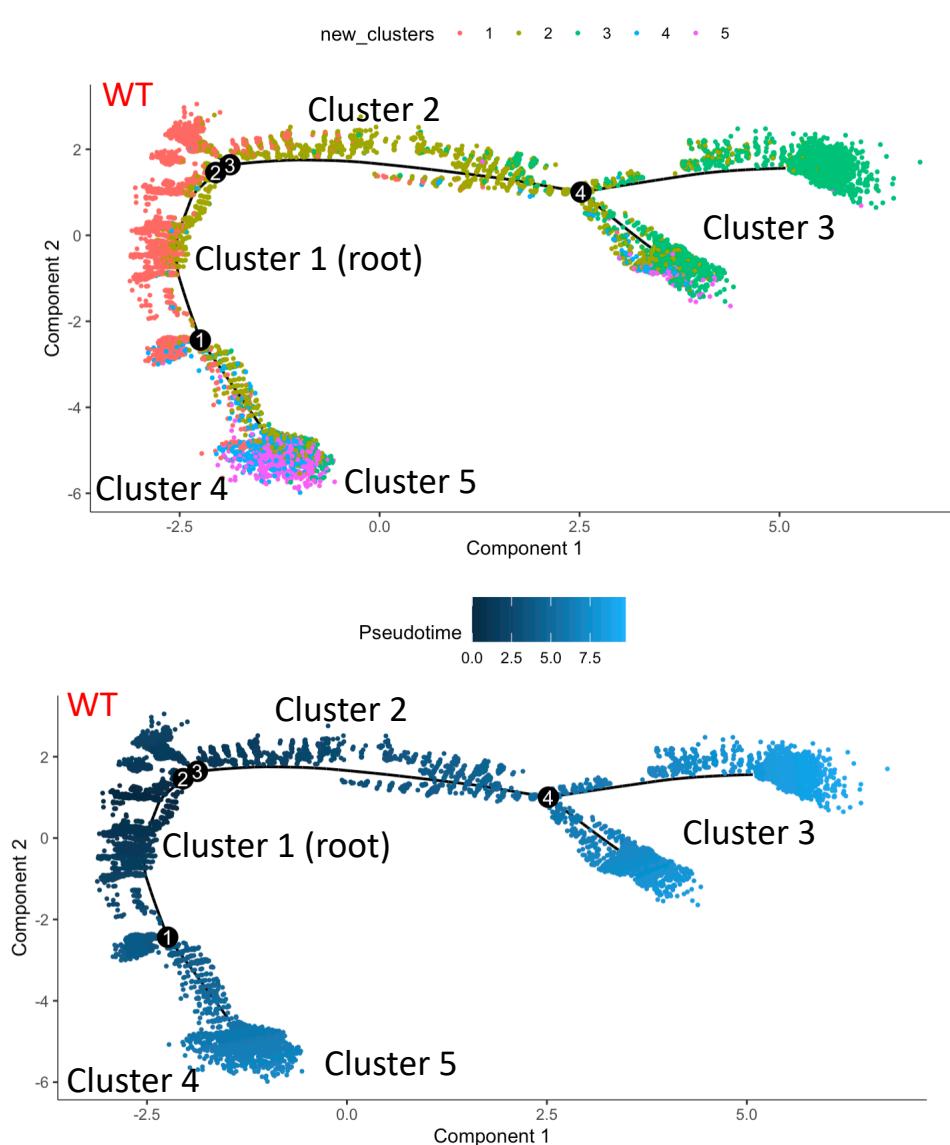
“Add Signature Score” aggregate individual marker score (AddModuleScore) from a gene list – a template created by Maggie on Palantir



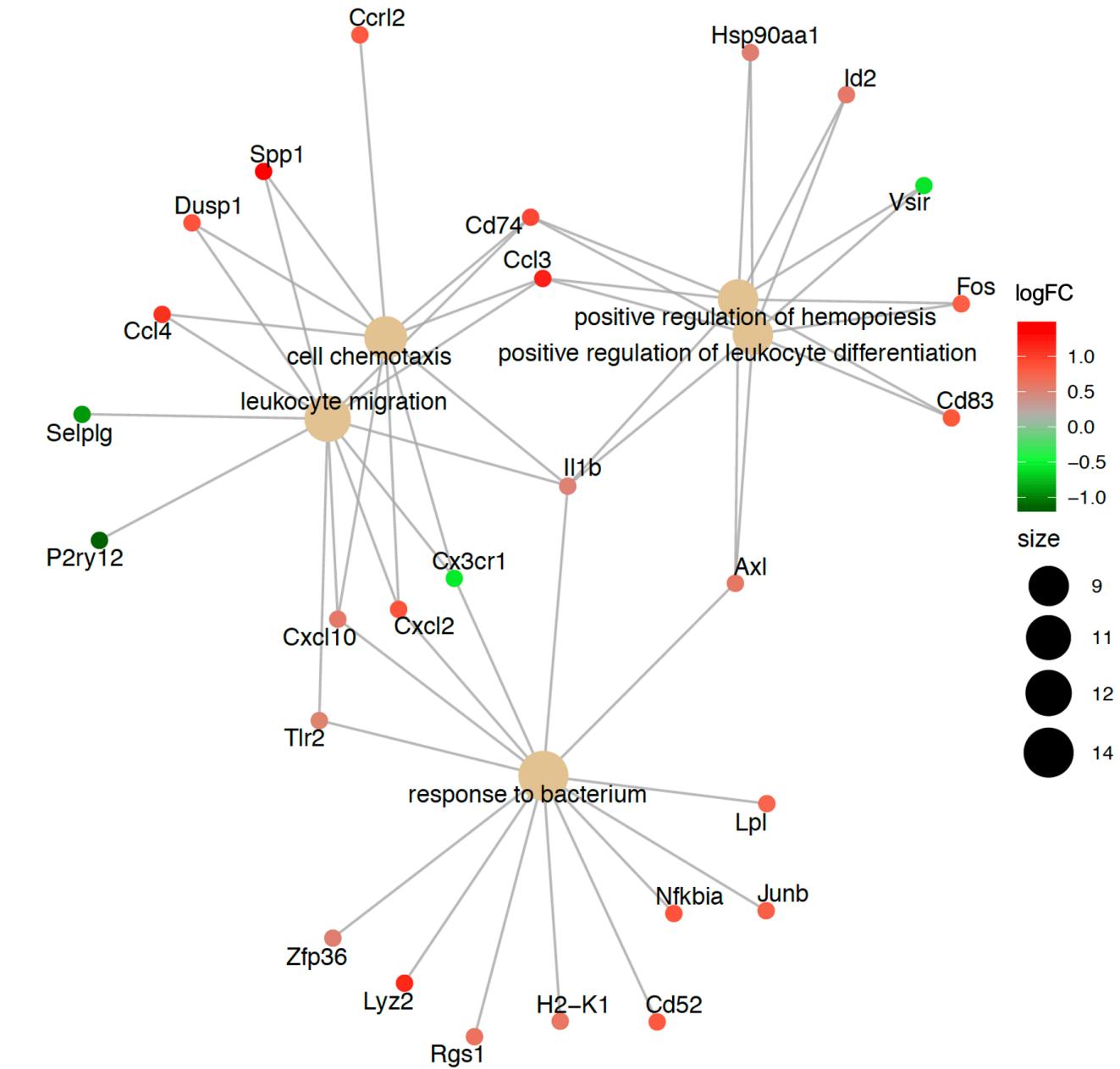
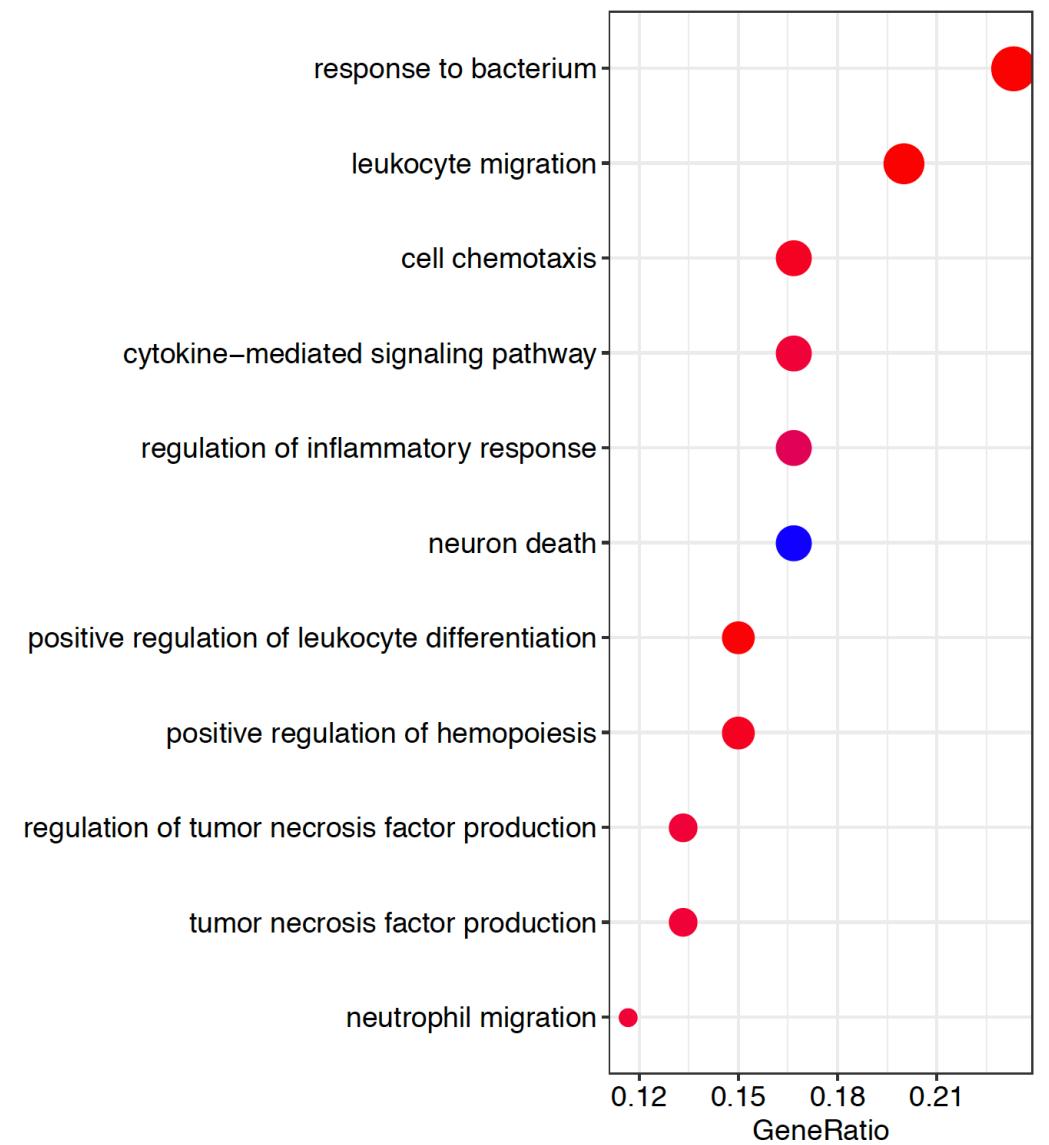


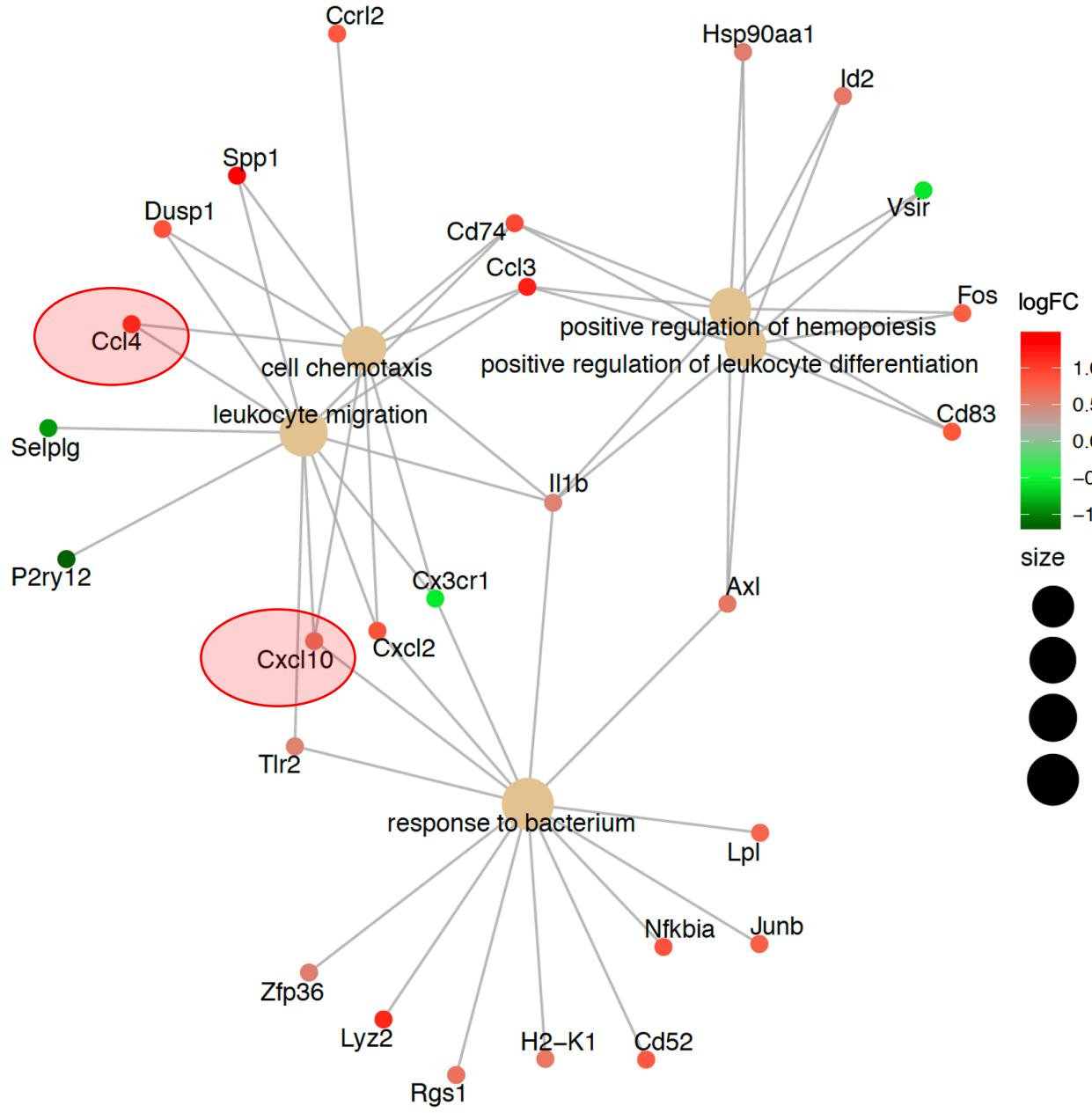
Signature score for homeostatic gene set

Trajectory analysis (pseudotime) shows Cluster3 has a different fate than Cluster4, 5 (1000 most variable genes across clusters)

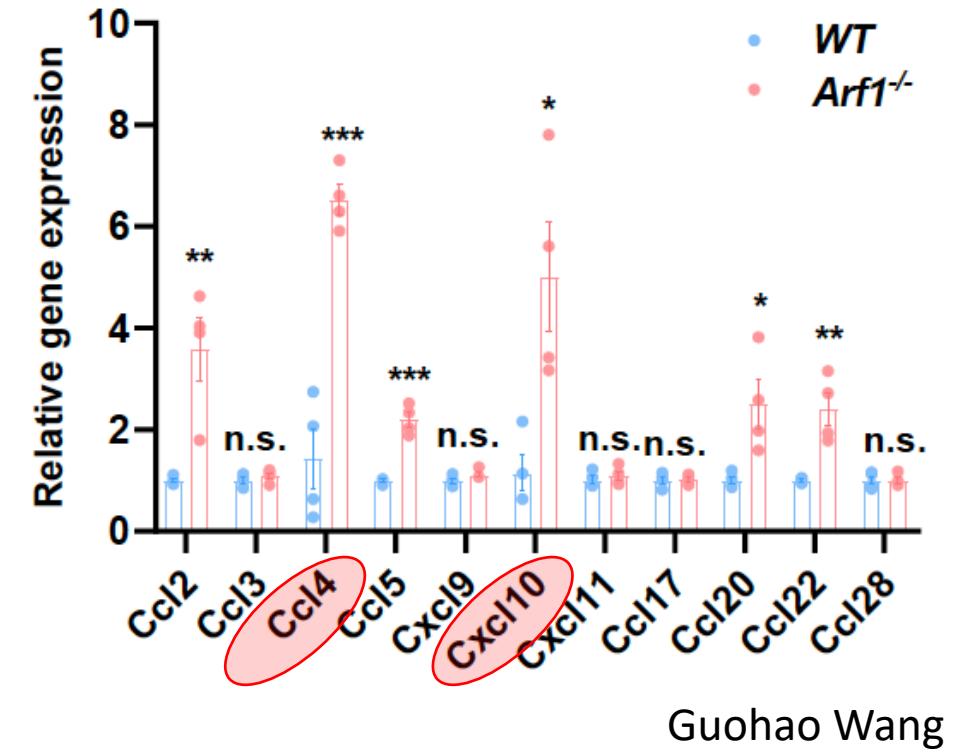


Cluster5 - enriched pathways





several chemokines were significantly increased in Arf1-ablated mice



Guohao Wang

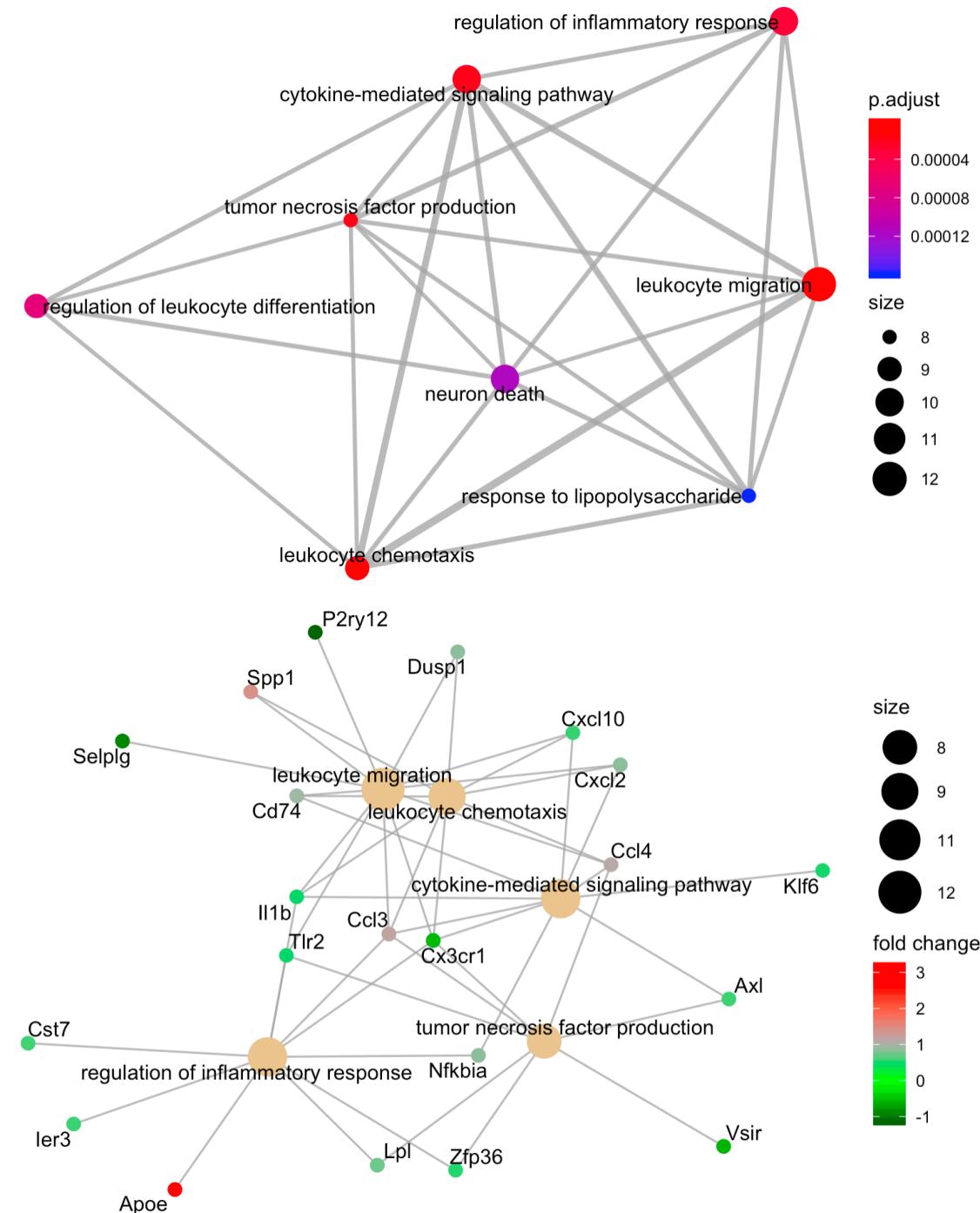
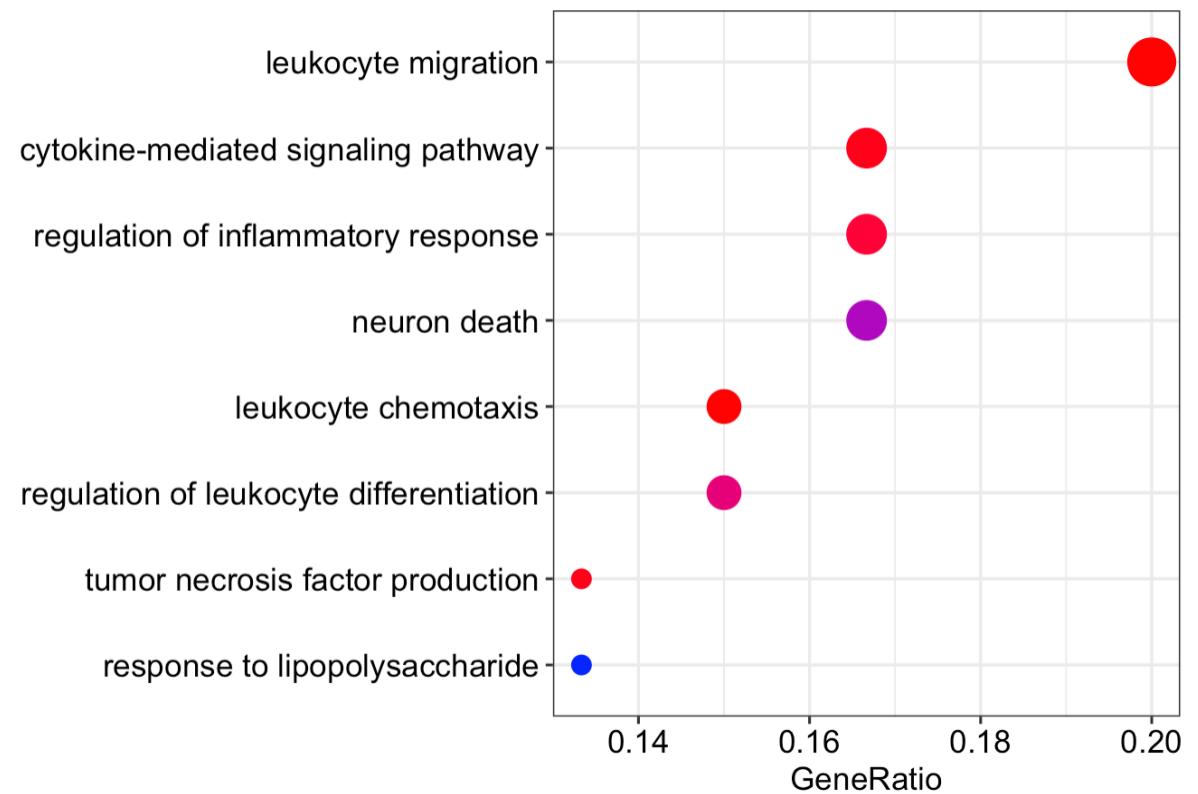
Summary

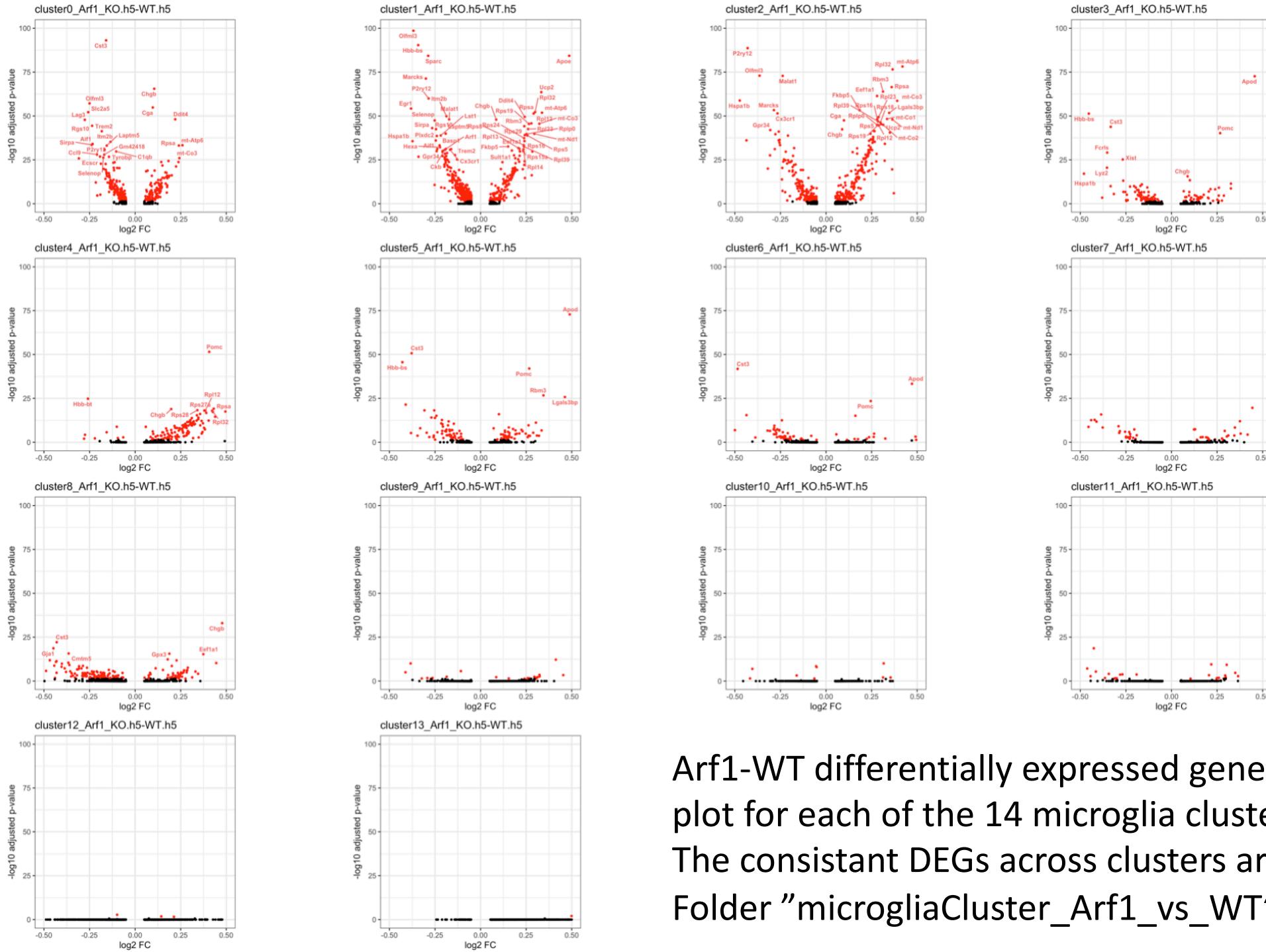
- Arf1 KO shows similar microglia gene dysregulation signature to AD, ALS, MS.
- A microglia subtype - microglia Cluster 5 is identified and is strongly associated with Arf1-deficient neurodegeneration. Cluster 5 markers include some of the previously known neurodegenerative risk factors *Apoe*, *Cd63*, *Cxcl2*, *Cd52*, *Ctsb*, *H2-D1*, *Fth1*, and *Spp1*
- Cluster 5 is also characterized by down-regulation of several microglia homeostatic genes, including *P2ry12*, *P2ry13*, *Tmem119*, *Selplg*, *Cx3cr1*, *Hexb*, and *Siglech*
- Cluster1 has the opposite expression in “disease markers” and “homeostatic markers” compared to Cluster 5. Cluster 2 and Cluster 4 has “in-between” expression for these genes, and may represent transitional state from homeostatic to pro-inflammatory state.
- The pathogenic phenotype of Arf1 knock-out is associated with a shift in the distribution of number of cells from Cluster 1 to Cluster 5. Arf1-KO microglia cells are depleted in Cluster1 and enriched in Cluster 5 compared to three other samples. Percentage of cells in Cluster 5 for WT (5%), for Arf1_KO(15%).

Supplementary

Cluster5 - enriched pathways

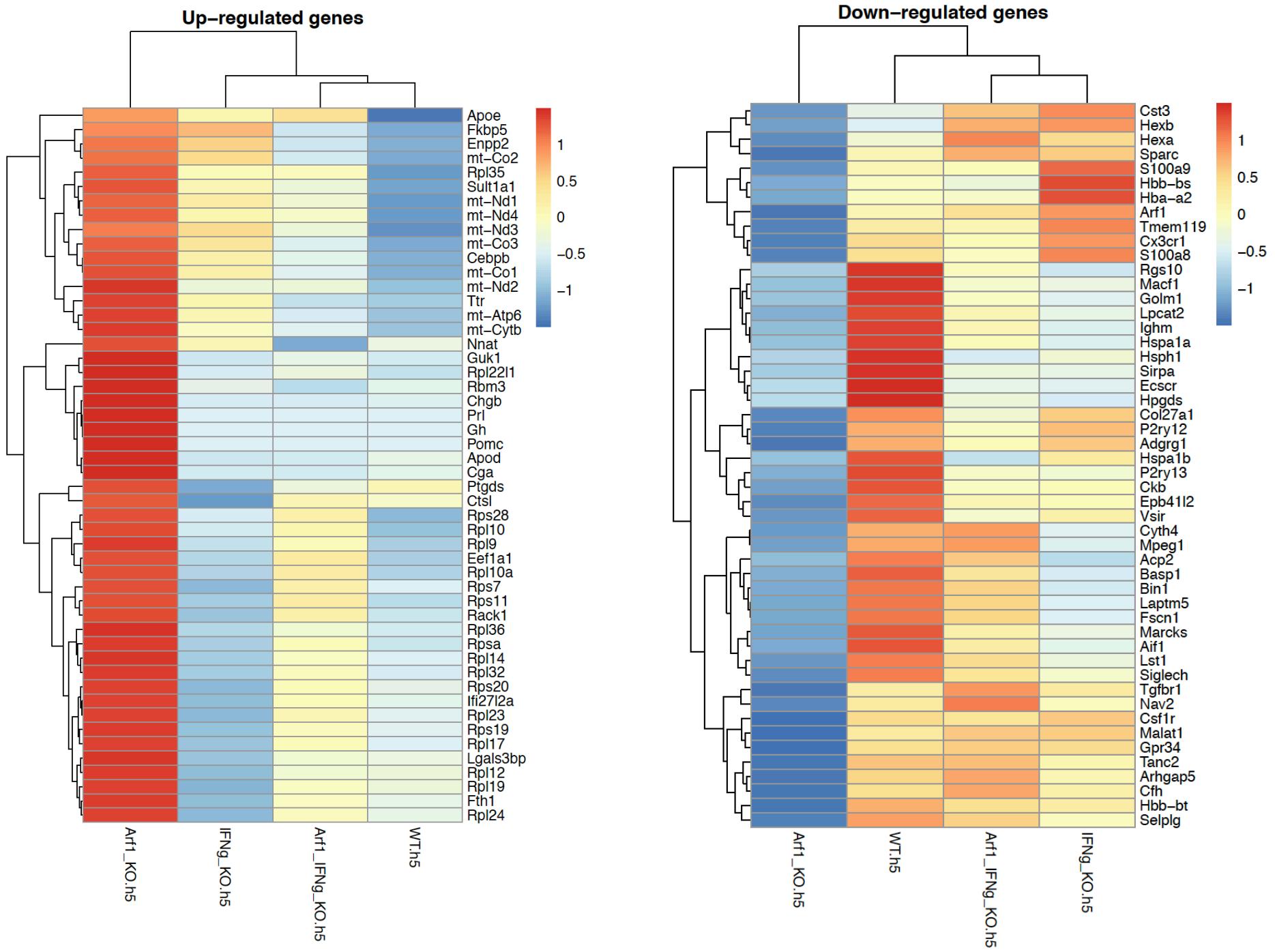
From file: myCluster5_cluster1_deg_ORA



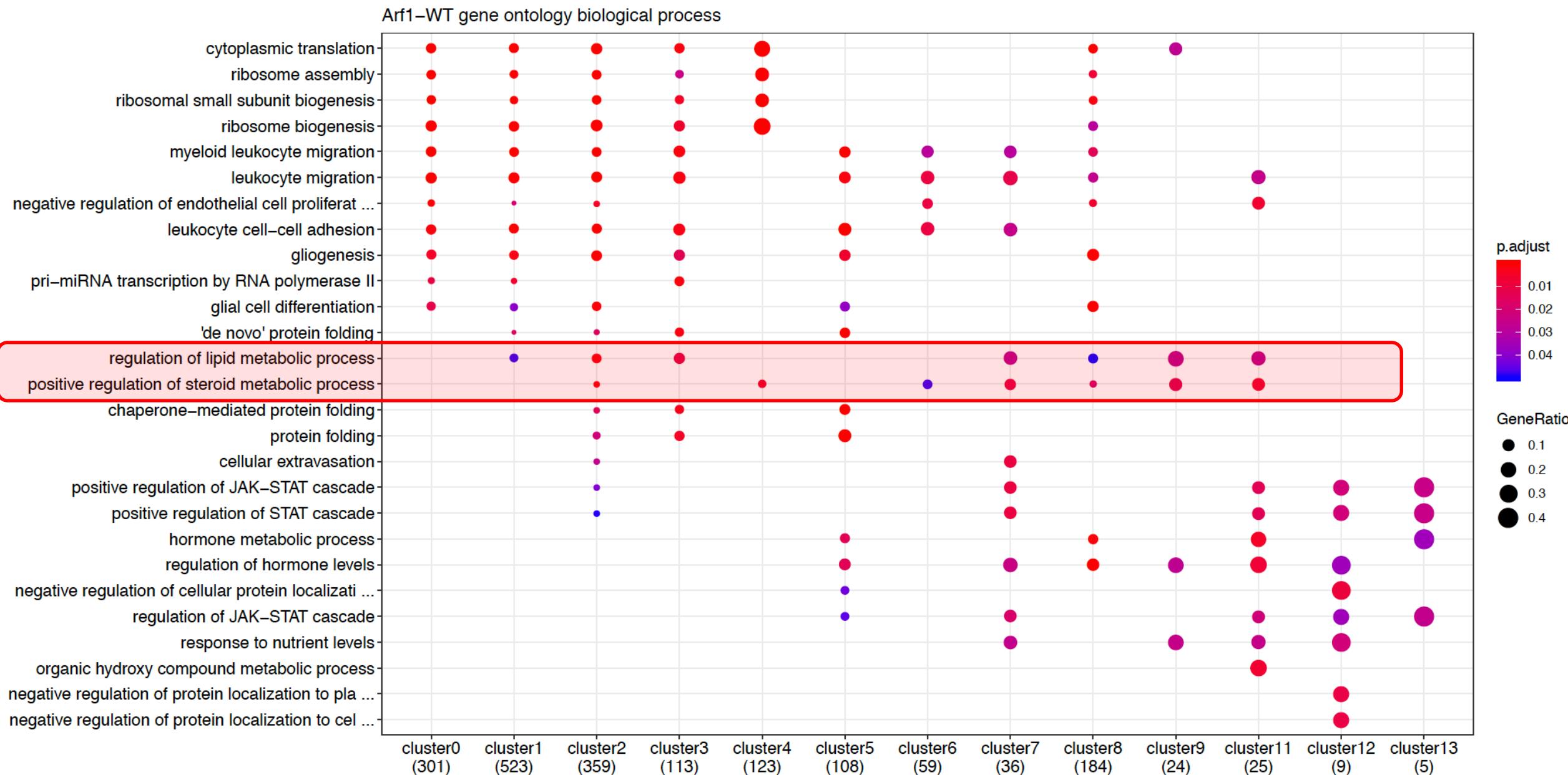


Arf1-WT differentially expressed genes volcano plot for each of the 14 microglia clusters
The consistant DEGs across clusters are in
Folder "microgliaCluster_Arf1_vs_WT"

Up and down-regulated genes in Arf1 vs. all



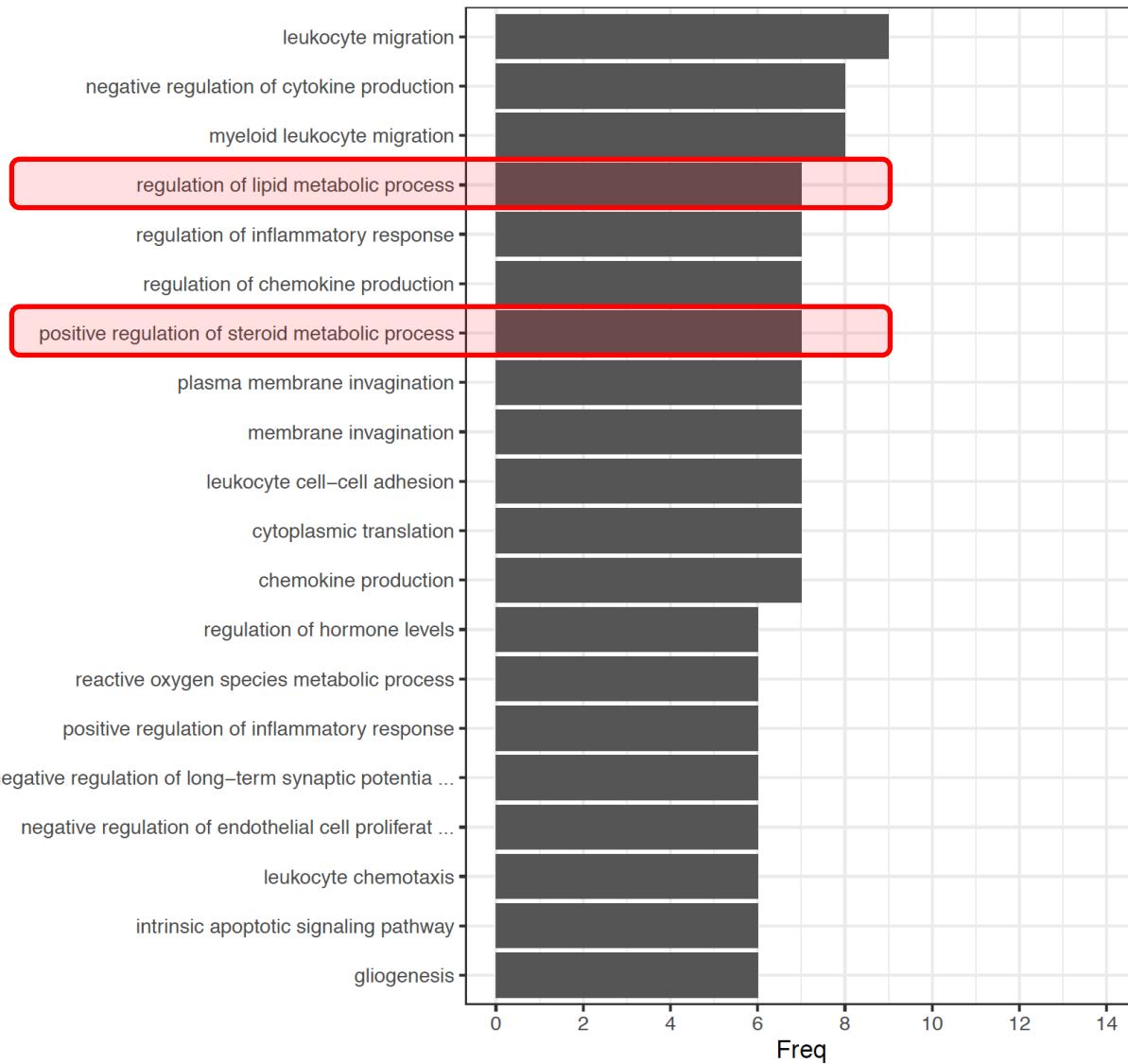
Overlap of significantly over-represented processes in Arf1-WT for each microglial cluster



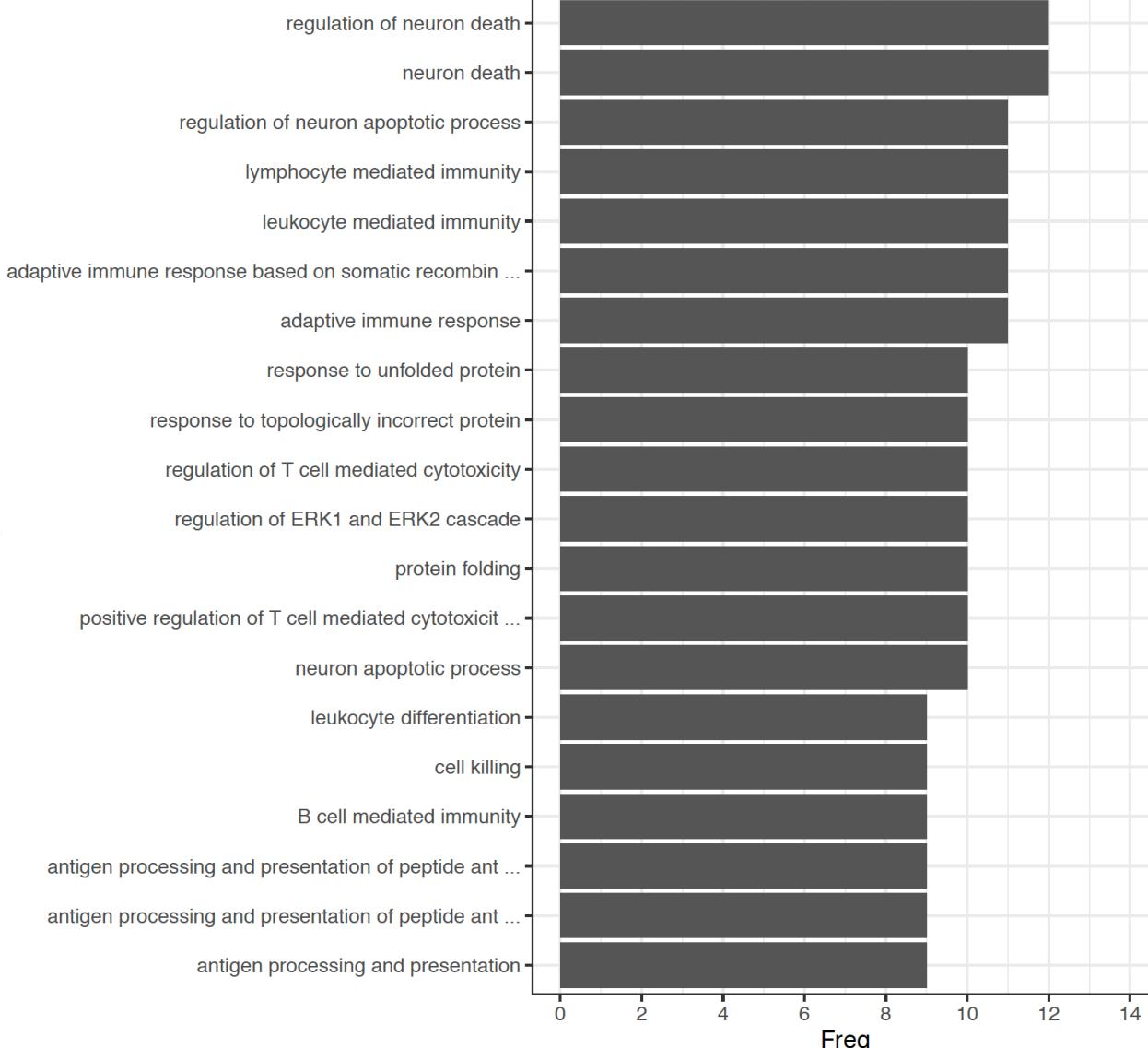
Most frequent biological processes in different sample comparisons

biological process

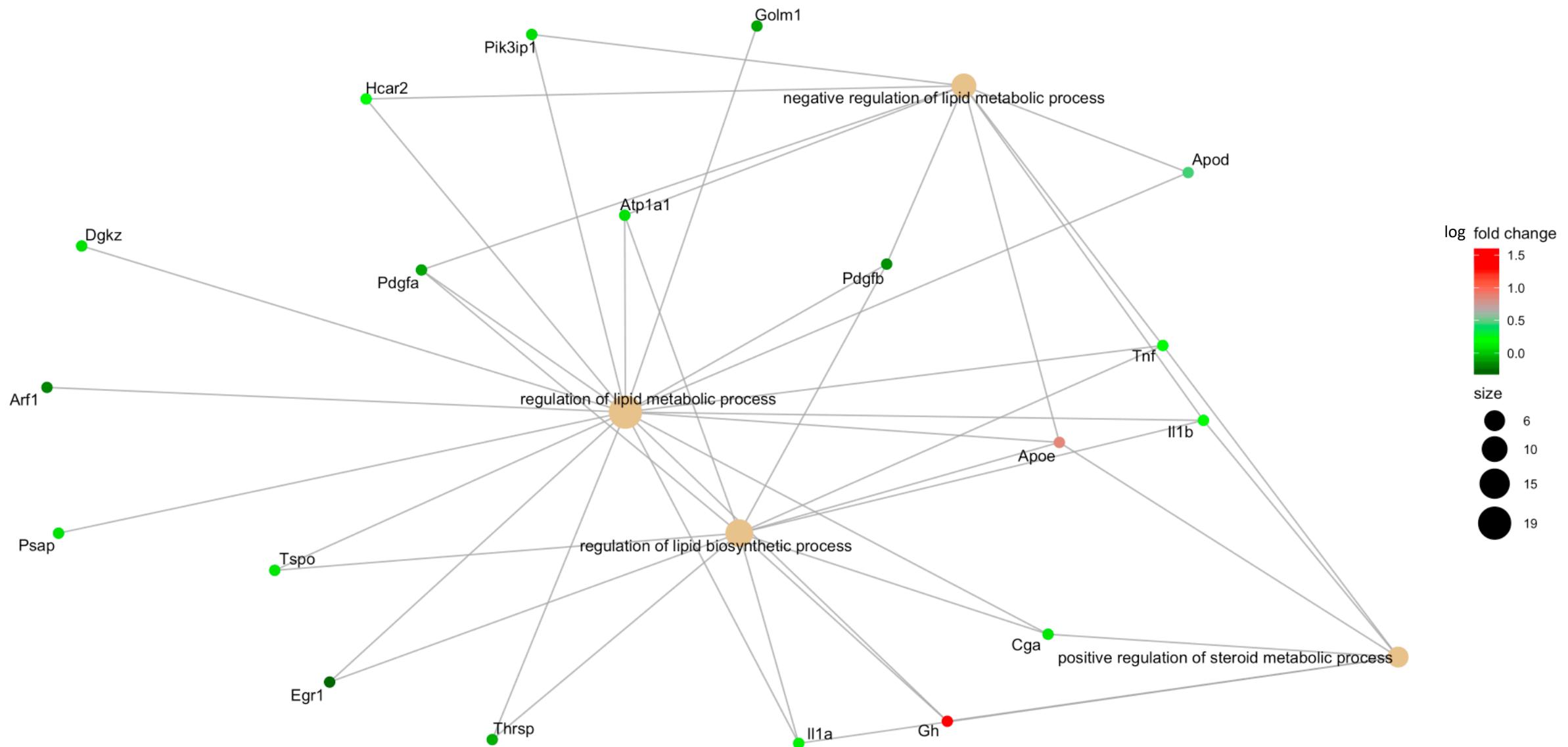
Arf1-WT : top enriched biological process



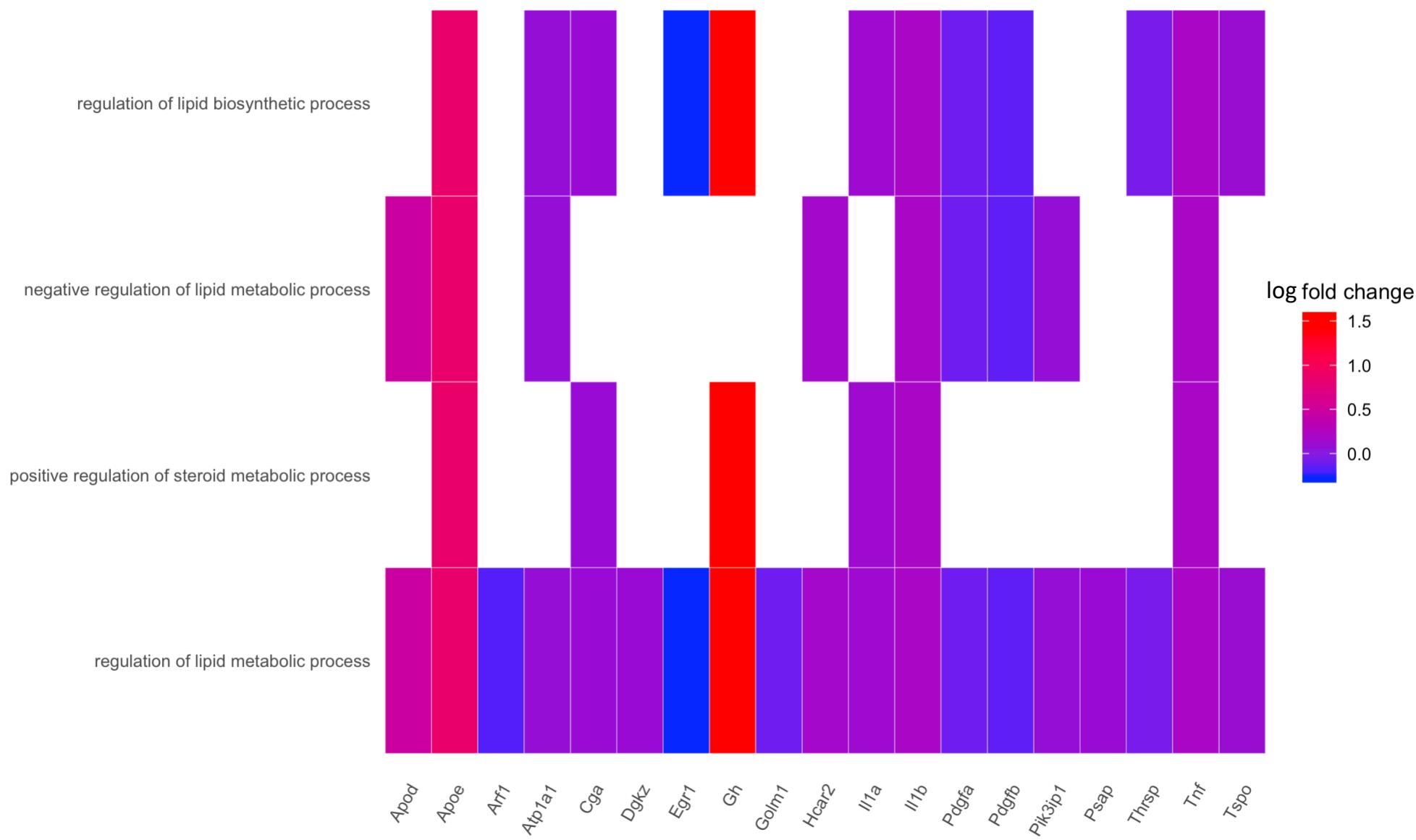
Arf1_IFNg-WT : top enriched biological process



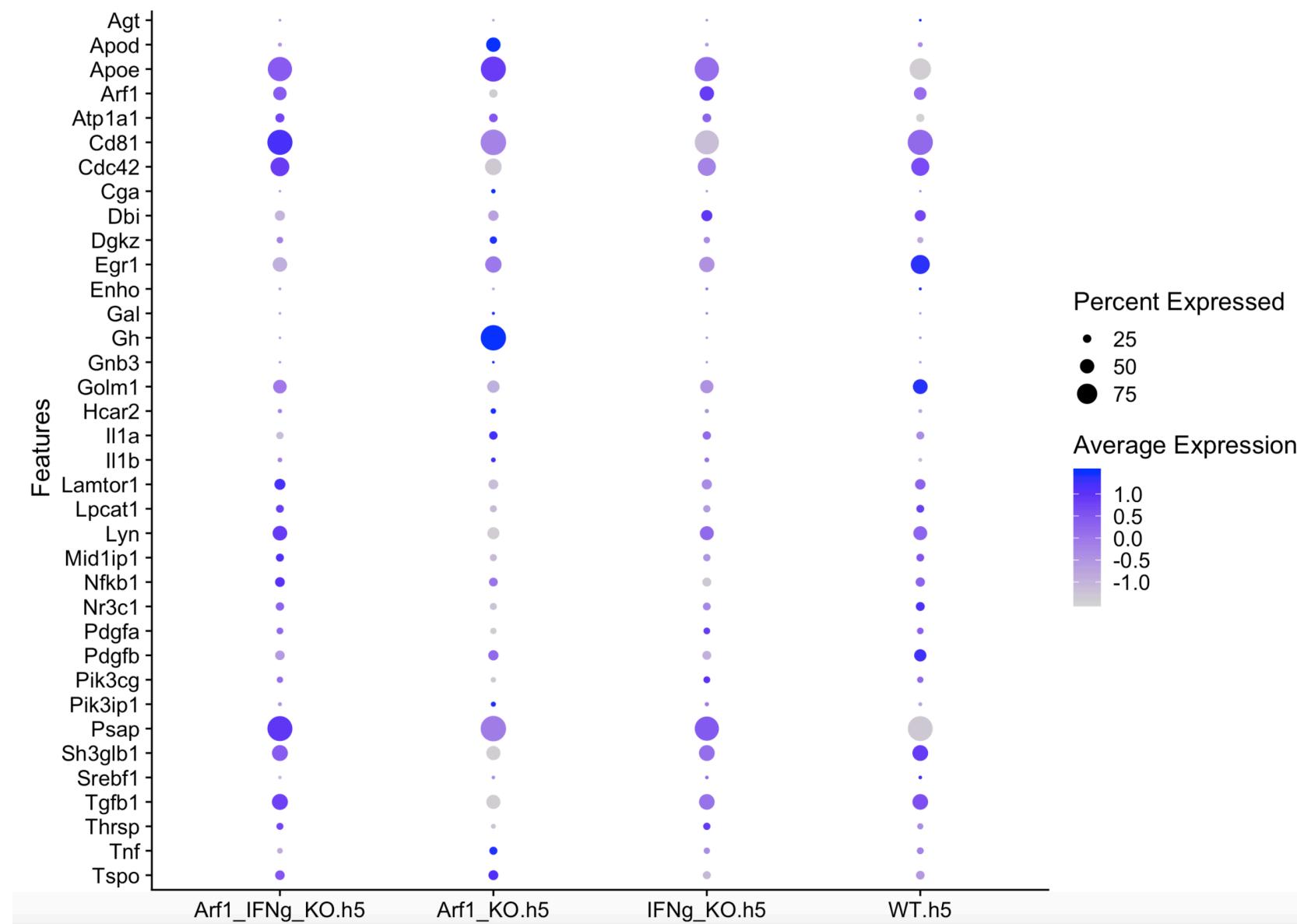
lipid metabolic process network



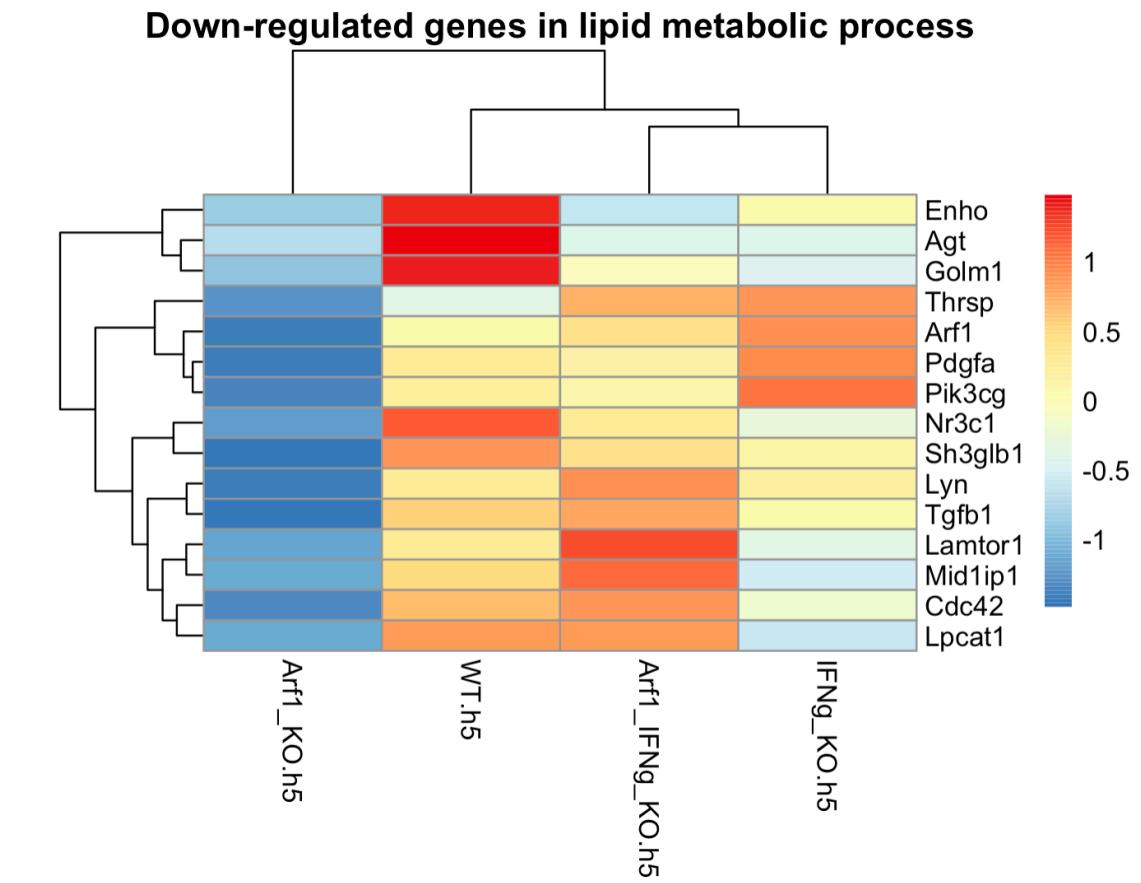
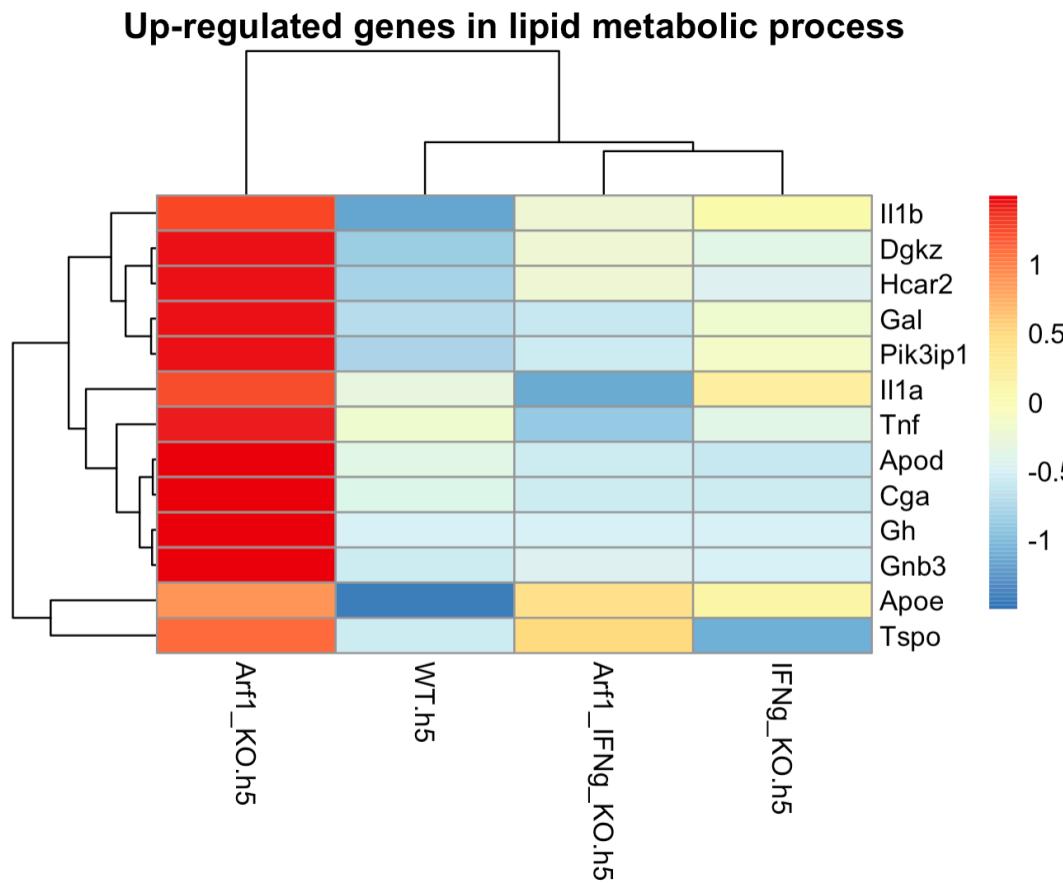
Differentially expressed genes in the lipid metabolic process



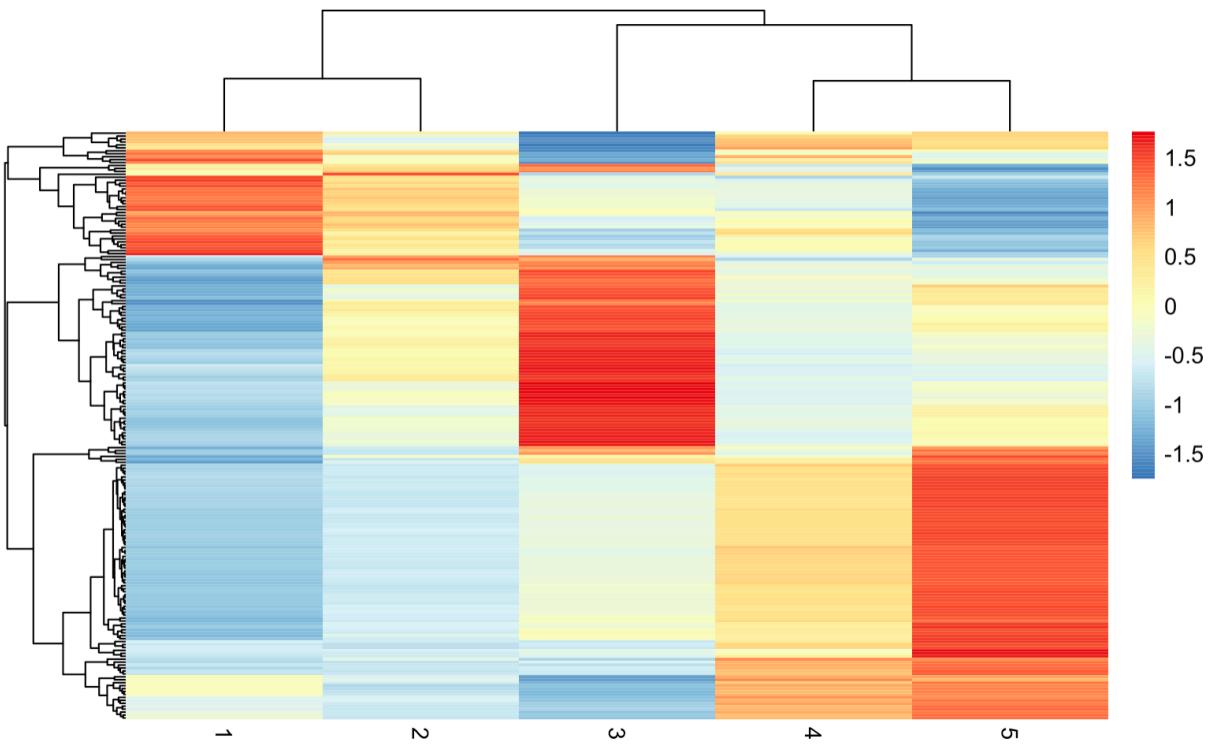
Differentially expressed genes in the lipid metabolic process – across samples



Differentially expressed genes in the lipid metabolic process – across samples



Top 500 most variable genes (mean expression) cluster1 - 5



PCA cluster1 - 5

