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├── meta2d\_nfil3\_WT.txt

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├── meta2d\_hdac3\_WT.txt

└── meta2d\_hdac3\_KO.txt

Some progress and changes

1. **Get foldchange for each dependent gene list**

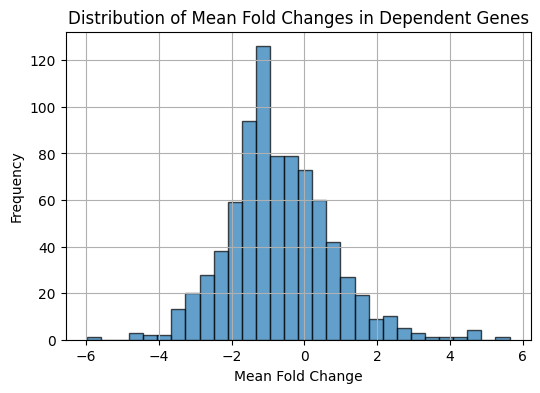
***Foldchange\_genelist\_get.ipynb***

(eg:Nr1d1) Input : *meta2d\_nr1d1\_KO.txt ,meta2d\_nr1d1\_KO.txt* - - - use ramp column

*nr1d1\_uniq\_ID.txt*

Output : nr1d1\_dependent\_genes\_with\_fold\_change.txt

Description:calculate original all gene foldchange based on ‘ramp’ column and then filter out genes by dependent genelist



*Nr1d1 distribution of gene foldchange*

1. **For each dependent gene list with foldchange file, perform GO, network**

Follow tutorial <https://yulab-smu.top/biomedical-knowledge-mining-book/enrichplot.html>

(eg:Nr1d1)

***go\_nr1d1.Rmd go\_nr1d1.Rmd go\_nr1d1.Rmd***

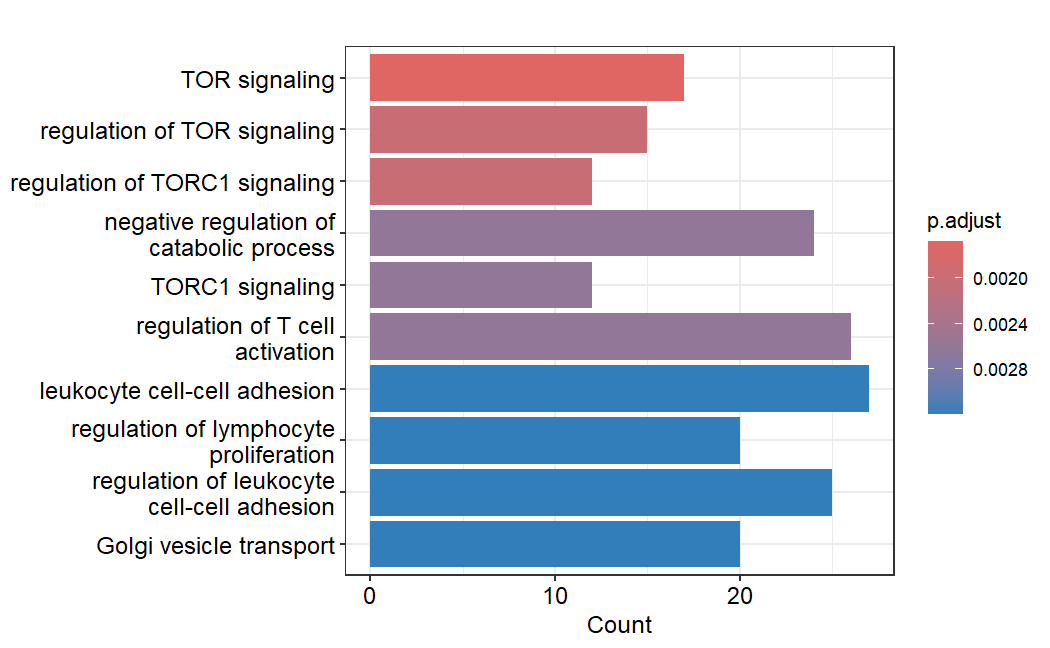
Input files needed :

*nr1d1\_dependent\_genes\_with\_fold\_change.txt hdac3\_dependent\_genes\_with\_fold\_change.txt hdac3\_dependent\_genes\_with\_fold\_change.txt*

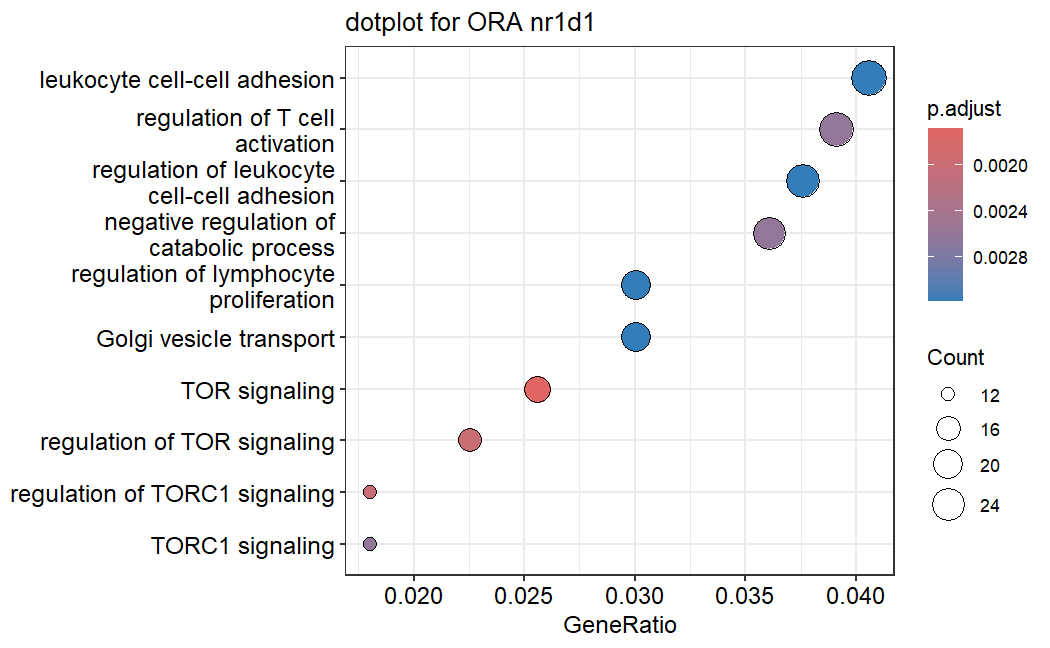
```{r}

*edo <- enrichGO(gene = names(gene\_list), OrgDb = org.Mm.eg.db, keyType = "ENTREZID", ont = "BP", pvalueCutoff = 0.05)*

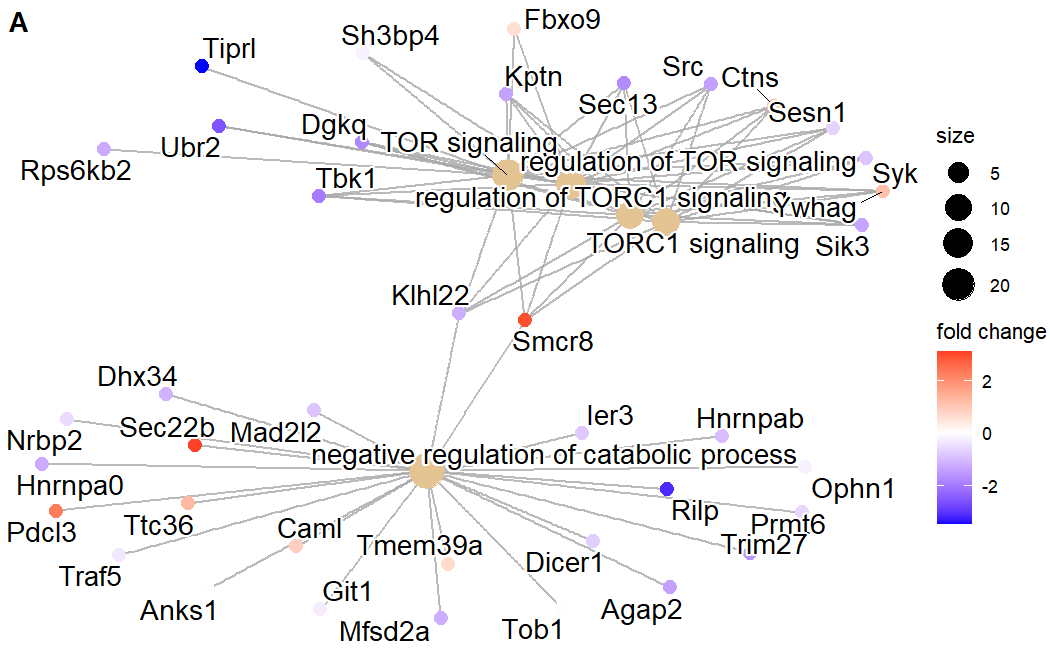
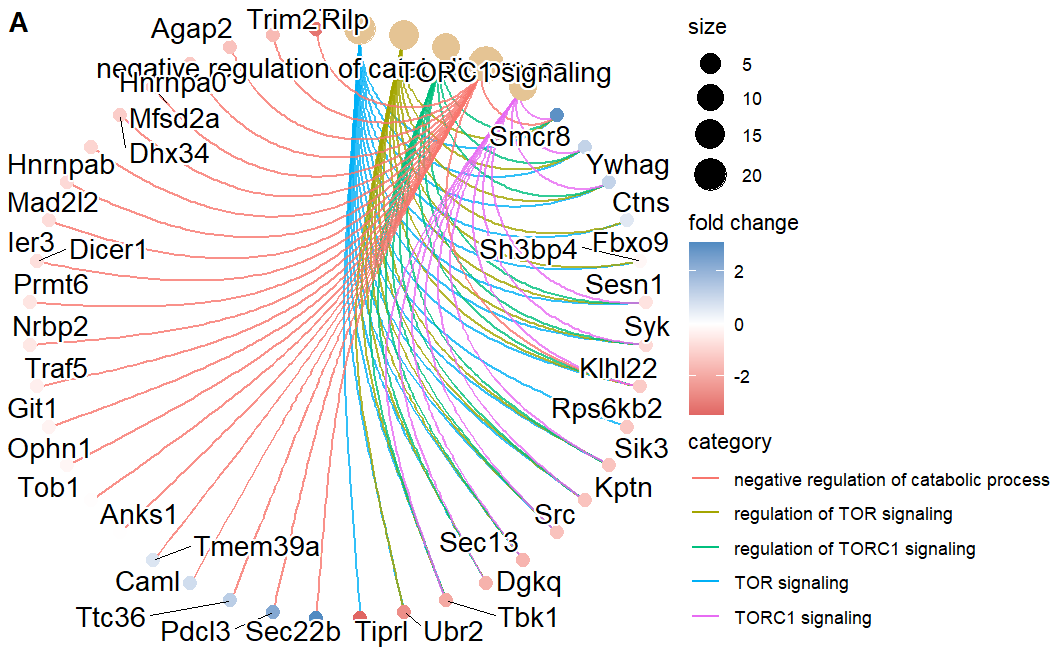
```



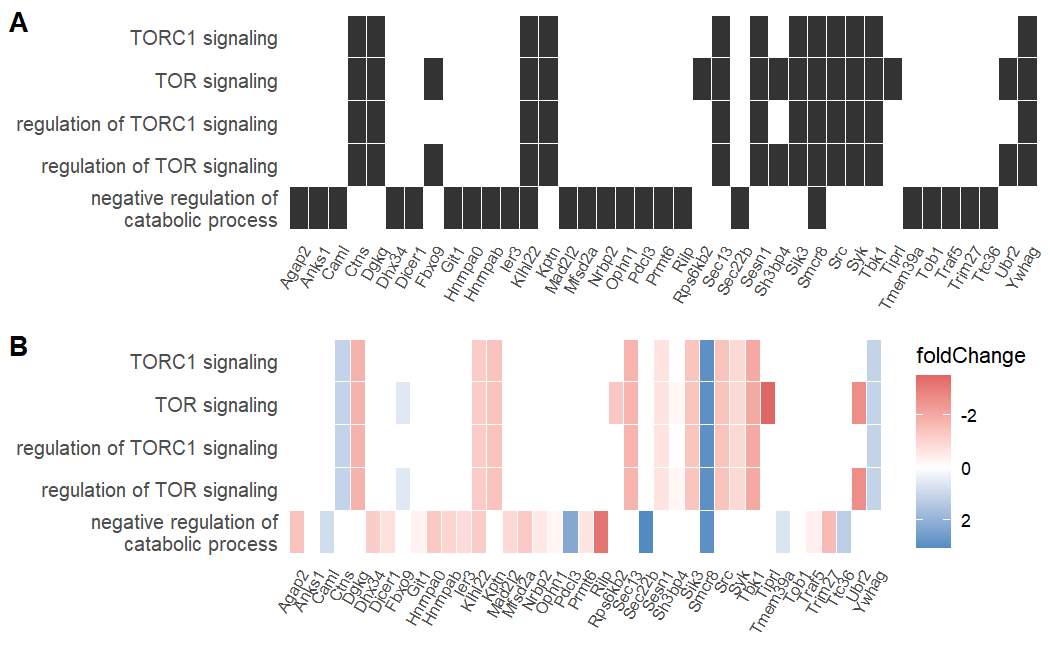
*Bar plot of 10 go terms*



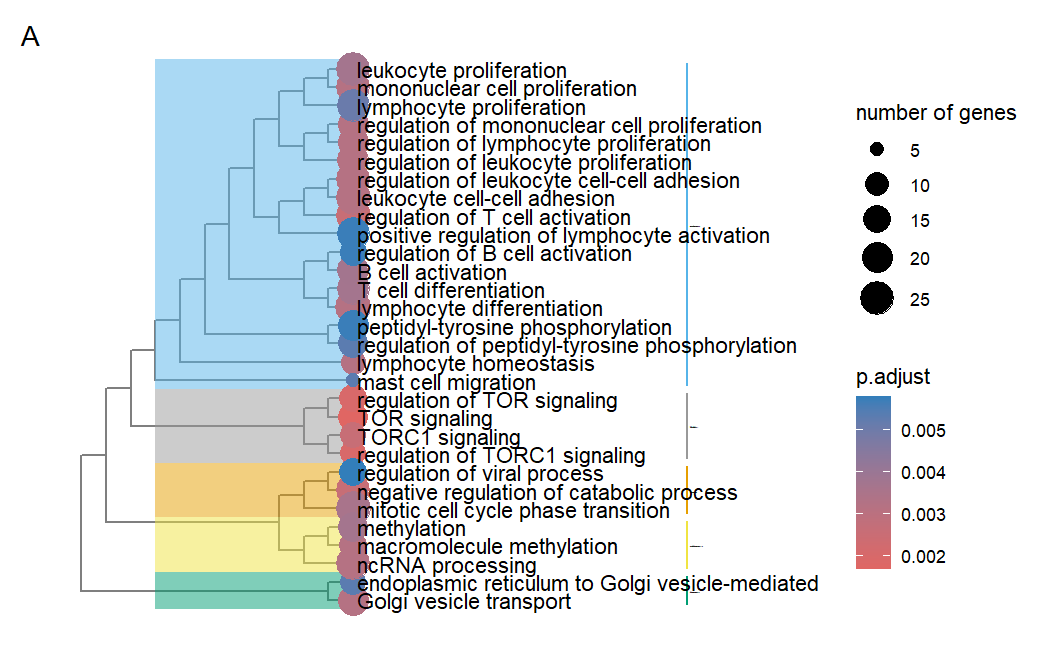
*Dot plot of 10 go terms*

**

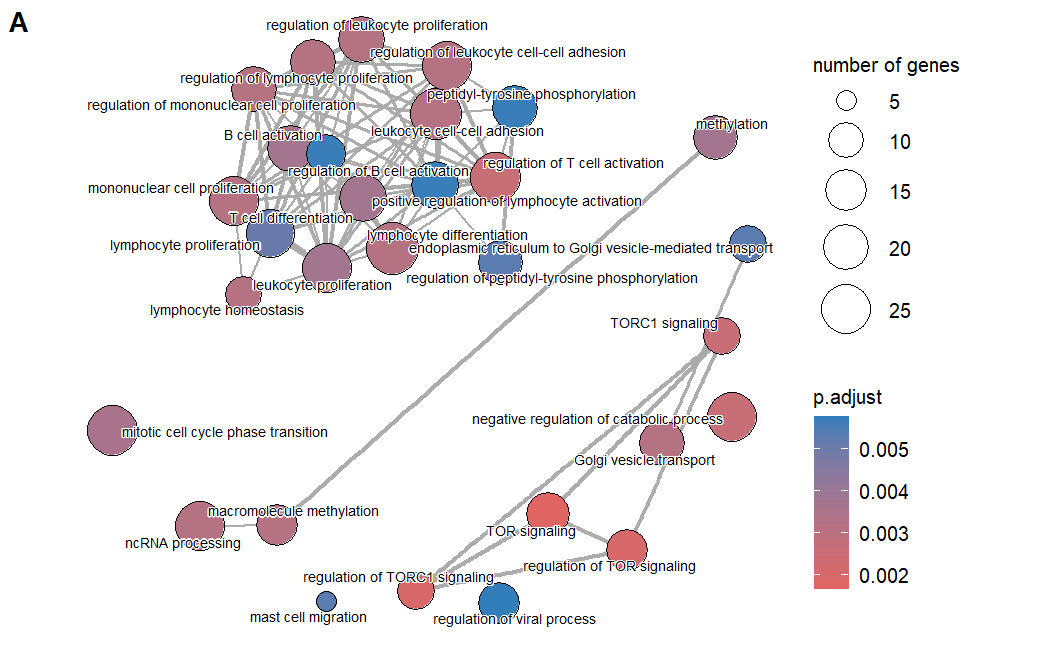
*Gene - concept network*

**

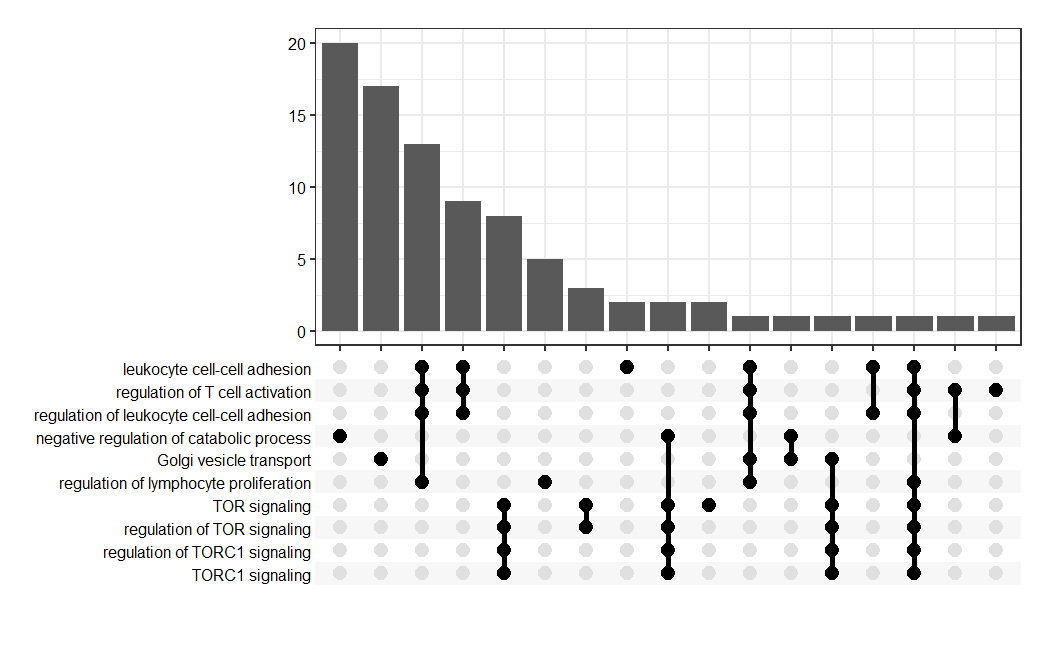
*Heatmap-like functional classification*

**

*Tree plot*

**

*Enrichment Map*

**

*Upset plot*

1. **Compare 3 gene lists without foldchange**

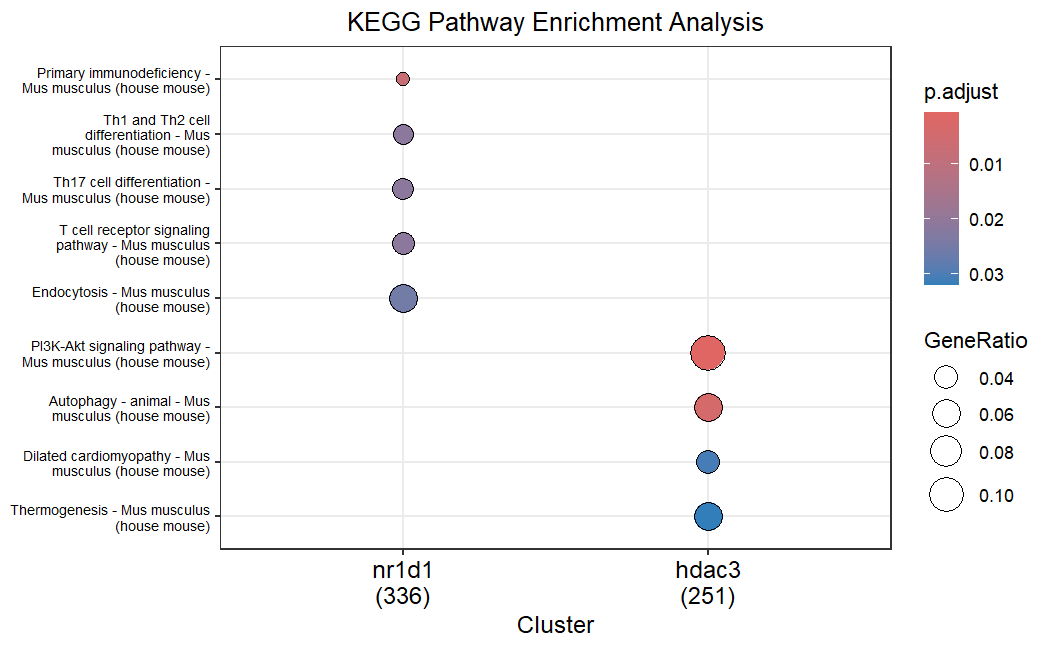
*Follow tutorial* [*https://yulab-smu.top/biomedical-knowledge-mining-book/clusterprofiler-comparecluster.html*](https://yulab-smu.top/biomedical-knowledge-mining-book/clusterprofiler-comparecluster.html)

*Have questions for this part, I notice 3 gene lists not overlapped*

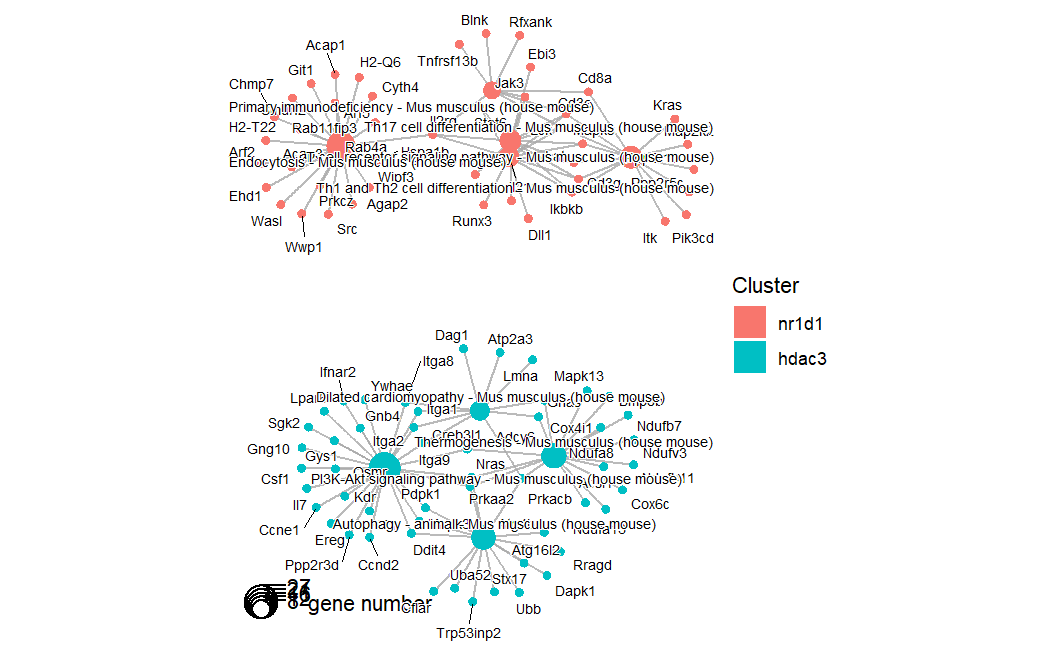
***compare.Rmd***

Input files needed: *nr1d1\_uniq\_ID.txt hdac3\_uniq\_ID.txt nfil3\_uniq\_ID.txt*

1. ***KEGG***

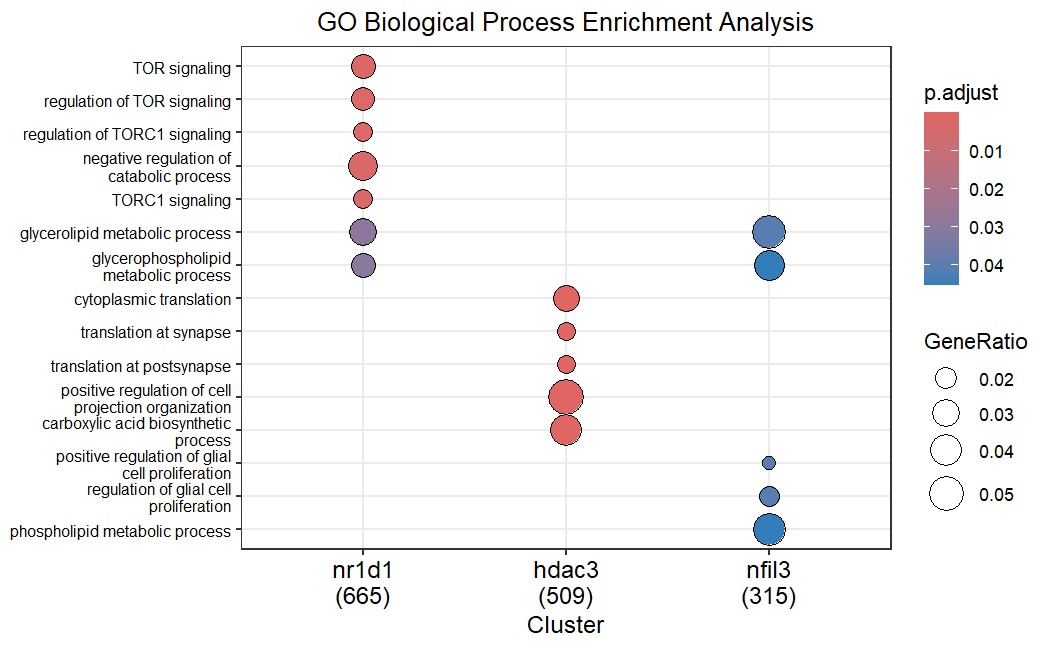
**

when I use KEGG, nfil3 group not shown in the graph, I think this make sense. Enriched terms very few with KEGG.

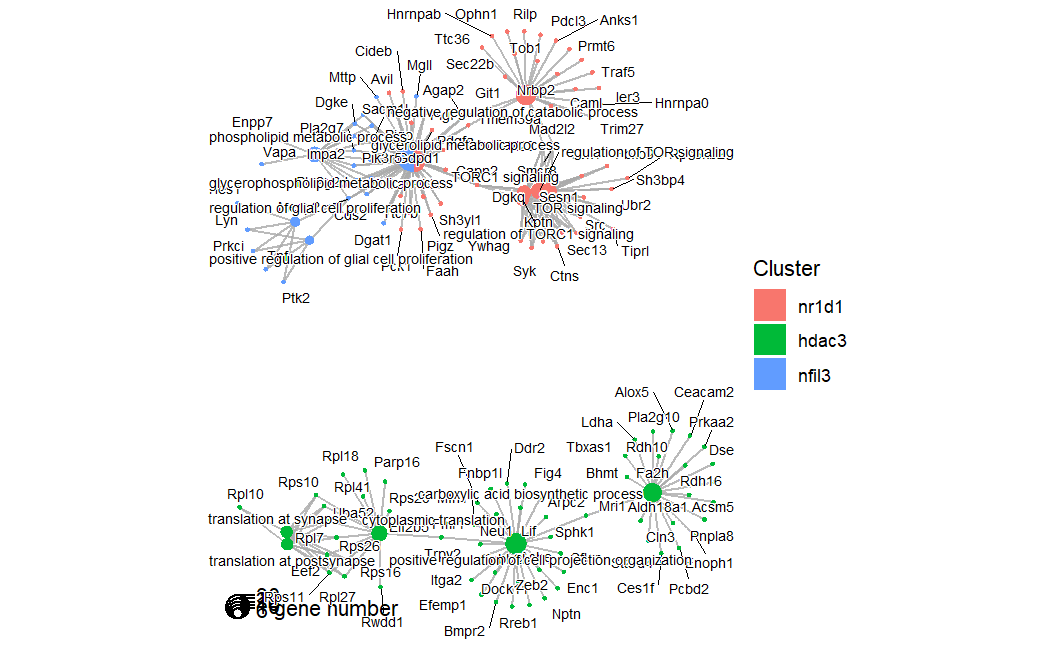
******

While the go term network looks like there is no overlap between 2 groups which is weird. No genes in 2 groups share same go term.

1. ***GO***



*Go enrichment Compare 3 groups (dotplot)*

******

*Go enrichment Compare 3 groups(network)*

**4. Scrnaseq, dependent\_genes**

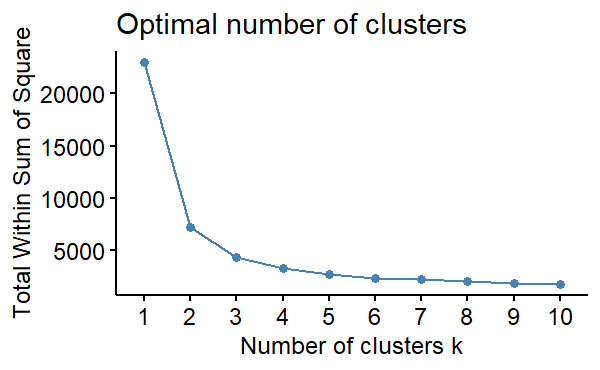
Combine 3 dependent genelists

Filter scrnaseq data *atlas\_mean.txt* by combined genes: *# 1530*

***scseq\_2.Rmd***

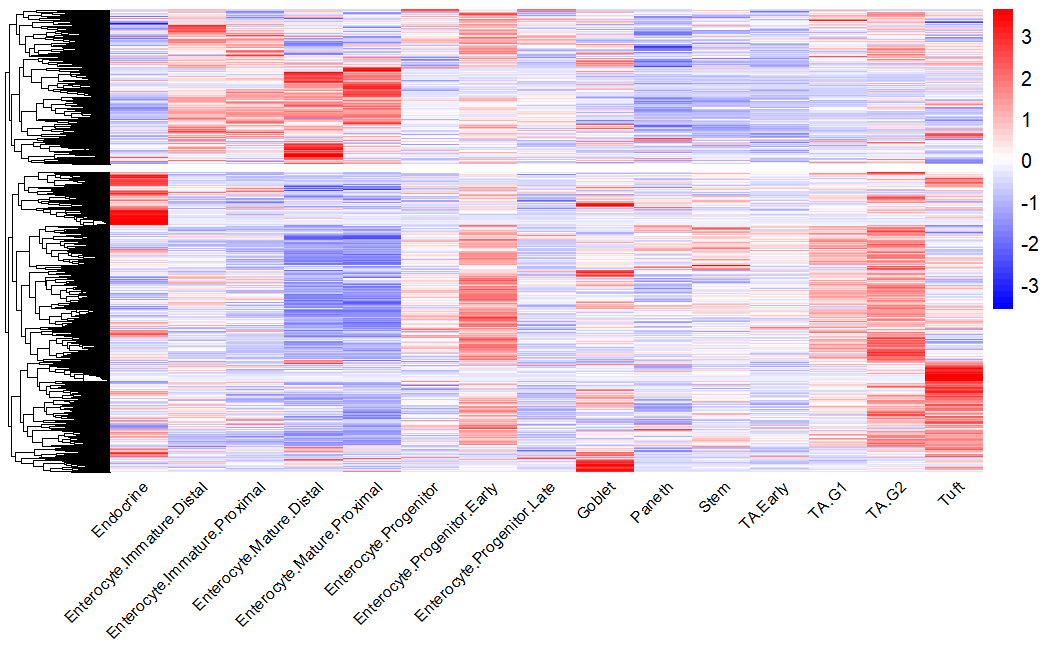
Q: I pre-define the cluster of genes based on gene expression levels among cell types.

Use elbow plot to find optimal k ->2, and then plot heatmap based on cluster 2

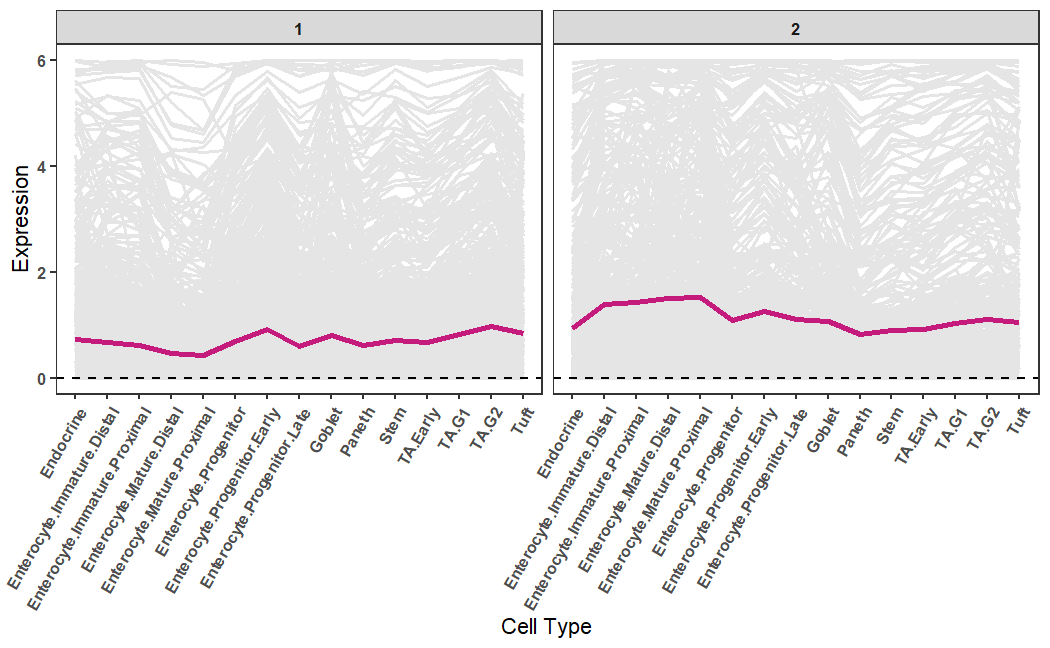


*Elbow plot*

A little confused by this heatmap of 2 clusters



*Heatmap of 2 clusters based on rows(genes)*

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*gene expression trends*

**Some visualizations of the percentage and counts :**



