

# Rauch2019\_to\_heatmap

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```
library(biomaRt)
library(ComplexHeatmap)
knitr::opts_chunk$set(echo = TRUE, dev = c("pdf"), fig.path = "Rauch2019_to_heatmap/", fig.dim = c(4, 8))
```

## Load count data from GEO and convert gene ids

```
read.geo <- function(file_url) {
  con <- gzcon(url(file_url))
  txt <- readLines(con)
  return(read.delim(textConnection(txt), header=T))
}
```

```
rauch_file = "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE113nnn/GSE113253/suppl/GSE113253%5FGeneExpr%5FAT%5FData.txt"
expr = read.geo(rauch_file)
#head(expr)
dim(expr)
```

```
## [1] 17475    72
```

## Match Rauch genes

```
mart <- biomaRt::useMart(biomart = "ensembl",
  dataset = "hsapiens_gene_ensembl",
  host = "ensembl.org")
```

```
## Warning: Ensembl will soon enforce the use of https.
## Ensure the 'host' argument includes "https://"
```

```
#look for GO filter
head(searchFilters(mart = mart, pattern = ".ef.eq"), n=20)
```

```
##                                name
## 37                with_refseq_mrna
## 38    with_refseq_mrna_predicted
```

```
## 39          with_refseq_ncrna
## 40  with_refseq_ncrna_predicted
## 41          with_refseq_peptide
## 42  with_refseq_peptide_predicted
## 96          refseq_mrna
## 97          refseq_mrna_predicted
## 98          refseq_ncrna
## 99          refseq_ncrna_predicted
## 100         refseq_peptide
## 101  refseq_peptide_predicted
##
##                                     description
## 37                                     With RefSeq mRNA ID(s)
## 38                                     With RefSeq mRNA predicted ID(s)
## 39                                     With RefSeq ncRNA ID(s)
## 40                                     With RefSeq ncRNA predicted ID(s)
## 41                                     With RefSeq peptide ID(s)
## 42                                     With RefSeq peptide predicted ID(s)
## 96                                     RefSeq mRNA ID(s) [e.g. NM_000014]
## 97  RefSeq mRNA predicted ID(s) [e.g. XM_003118719]
## 98                                     RefSeq ncRNA ID(s) [e.g. NR_000005]
## 99  RefSeq ncRNA predicted ID(s) [e.g. XR_001736900]
## 100                                     RefSeq peptide ID(s) [e.g. NP_000005]
## 101 RefSeq peptide predicted ID(s) [e.g. XP_003118767]
```

```
head(searchAttributes(mart = mart, pattern = ".ef.eq"), n=20)
```

```
##                                     name                                     description
## 22          transcript_mane_select          RefSeq match transcript (MANE Select)
## 23 transcript_mane_plus_clinical RefSeq match transcript (MANE Plus Clinical)
## 84          refseq_mrna                                     RefSeq mRNA ID
## 85          refseq_mrna_predicted          RefSeq mRNA predicted ID
## 86          refseq_ncrna                                     RefSeq ncRNA ID
## 87          refseq_ncrna_predicted          RefSeq ncRNA predicted ID
## 88          refseq_peptide                                     RefSeq peptide ID
## 89          refseq_peptide_predicted          RefSeq peptide predicted ID
##
##          page
## 22 feature_page
## 23 feature_page
## 84 feature_page
## 85 feature_page
## 86 feature_page
## 87 feature_page
## 88 feature_page
## 89 feature_page
```

```
ens = getBM(c("external_gene_name", "ensembl_gene_id", "refseq_mrna"),
            filters = "refseq_mrna",
            values = expr$RefSeqID,
            mart = mart)
```

```
nrow(ens) #15644 id found
```

```
## [1] 15529
```

```
length(unique(ens$ensembl_gene_id)) #15619 unique ensembl ids
```

```
## [1] 15514
```

```
length(unique(ens$refseq_mrna)) #14589 unique refseqIDs
```

```
## [1] 14441
```

```
nc_ens = getBM(c("external_gene_name", "ensembl_gene_id", "refseq_ncrna"),  
              filters = "refseq_ncrna",  
              values = expr$RefSeqID,  
              mart = mart)
```

```
nrow(nc_ens) #2487 ncrna
```

```
## [1] 2533
```

```
length(unique(nc_ens$ensembl_gene_id)) #2478 unique ensembl ids
```

```
## [1] 2524
```

```
length(unique(nc_ens$refseq_ncrna)) #2300 unique refseqIDs
```

```
## [1] 2328
```

```
#First combine mRNA and ncRNA  
colnames(ens) = c("gene_name", "gene", "RefSeqID")  
colnames(nc_ens) = c("gene_name", "gene", "RefSeqID")  
ids = rbind(ens, nc_ens)  
dim(ids)
```

```
## [1] 18062      3
```

```
#Add ensembl Id column  
nexpr = merge(expr, ids, by="RefSeqID", all=F)  
dim(nexpr) #18132
```

```
## [1] 18062      74
```

```
head(nexpr)
```

```
##   RefSeqID  chr   start      end strand Length Copies  
## 1 NM_000014 chr12  9220304  9268558    -    4615      1  
## 2 NM_000015 chr8   18248755 18258723    +    1313      1  
## 3 NM_000017 chr12 121163571 121177811    +    1905      1  
## 4 NM_000019 chr11 107992258 108018891    +    2120      1  
## 5 NM_000020 chr12  52301202  52317145    +    4251      1  
## 6 NM_000021 chr14  73603143  73690399    +    6076      1
```

```

##                                     Annotation.Divergence
## 1                                A2M|A2MD|CPAMD5|FWP007|S863-7|-|12p13.31|protein-coding
## 2                                NAT2|AAC2|NAT-2|PNAT|-|8p22|protein-coding
## 3                                ACADS|ACAD3|SCAD|-|12q24.31|protein-coding
## 4                                ACAT1|ACAT|MAT|T2|THIL|-|11q22.3|protein-coding
## 5 ACVRL1|ACVRLK1|ALK-1|ALK1|HHT|HHT2|ORW2|SKR3|TSR-I|-|12q13.13|protein-coding
## 6                                PSEN1|AD3|FAD|PS-1|PS1|S182|-|14q24.3|protein-coding
## RNA_14dOb_AT_rep1 RNA_7dOb_AT_rep1 RNA_3dOb_AT_rep1 RNA_1dOb_AT_rep1
## 1                                16                                33                                46                                35
## 2                                0                                0                                0                                1
## 3                                94                                84                                61                                70
## 4                                400                               318                               243                               287
## 5                                632                               337                               266                               293
## 6                                962                               596                               500                               610
## RNA_4hOb_AT_rep1 RNA_Msc_AT_rep1 RNA_4hAd_AT_rep1 RNA_1dAd_AT_rep1
## 1                                1                                2                                4                                3
## 2                                0                                0                                0                                5
## 3                                53                               65                               125                               56
## 4                                223                              313                              534                              212
## 5                                497                              250                              472                              166
## 6                                419                              632                              1004                             500
## RNA_3dAd_AT_rep1 RNA_7dAd_AT_rep1 RNA_14dAd_AT_rep1 RNA_14dOb_AT_rep2
## 1                                15                               244                               325                               143
## 2                                0                                7                                1                                0
## 3                                69                               283                               198                               38
## 4                                216                              799                              484                              155
## 5                                146                              680                              374                              453
## 6                                591                              1510                             543                              440
## RNA_7dOb_AT_rep2 RNA_3dOb_AT_rep2 RNA_1dOb_AT_rep2 RNA_4hOb_AT_rep2
## 1                                72                               53                               36                               13
## 2                                1                                0                                0                                0
## 3                                72                               38                               45                               49
## 4                                211                              128                              167                              187
## 5                                415                              246                              290                              603
## 6                                627                              454                              524                              514
## RNA_Msc_AT_rep2 RNA_4hAd_AT_rep2 RNA_1dAd_AT_rep2 RNA_3dAd_AT_rep2
## 1                                4                                10                               7                                79
## 2                                0                                0                                1                                1
## 3                                21                               26                               35                               28
## 4                                182                              132                              141                              169
## 5                                137                              164                              141                               92
## 6                                461                              332                              429                              544
## RNA_7dAd_AT_rep2 RNA_14dAd_AT_rep2 NormAve_14dOb_AT NormAve_7dOb_AT
## 1                                87                               241                               27.15296                        14.3743007
## 2                                0                                1                                0.00000                        0.4836905
## 3                                69                               46                               37.87861                        51.5438970
## 4                                129                              113                              142.22175                       156.8964208
## 5                                176                              132                              152.59056                       111.5137496
## 6                                412                              344                              128.50301                       126.8021821
## NormAve_3dOb_AT NormAve_1dOb_AT NormAve_4hOb_AT NormAve_Msc_AT
## 1                                17.33151                       10.6282867                       2.096019                        0.9528313
## 2                                0.00000                        0.4658704                        0.000000                       0.0000000
## 3                                40.21529                       40.6135081                       36.123375                       28.2673477
## 4                                133.89332                      143.2903135                      130.305469                      153.4855229

```

## 5	95.82145	94.5386656	175.213282	59.5292008	
## 6	124.75326	127.6254037	103.990318	120.7083193	
##	NormAve_4hAd_AT	NormAve_1dAd_AT	NormAve_3dAd_AT	NormAve_7dAd_AT	
## 1	2.283874	1.569964	15.3726009	31.138377	
## 2	0.000000	2.779559	0.5843517	1.343623	
## 3	31.644259	31.325859	36.2246975	71.666008	
## 4	130.746541	109.731092	131.3394425	152.483468	
## 5	68.090147	48.534804	40.2604963	79.436826	
## 6	98.728292	102.838688	135.6891878	126.707020	
##	NormAve_14dAd_AT	SE_NormAve_14dOb_AT	SE_NormAve_7dOb_AT	SE_NormAve_3dOb_AT	
## 1	98.939672	24.150699	5.4420214	3.626557	
## 2	1.289227	0.000000	0.4836905	0.000000	
## 3	87.089223	4.851344	3.5374262	3.812424	
## 4	191.586850	21.167564	30.4784377	23.708674	
## 5	85.535117	23.847009	12.4855565	9.785129	
## 6	114.807143	8.603099	4.2704554	11.606132	
##	SE_NormAve_1dOb_AT	SE_NormAve_4hOb_AT	SE_NormAve_Msc_AT	SE_NormAve_4hAd_AT	
## 1	1.3502490	1.8112063	0.4635869	1.786549	
## 2	0.4658704	0.0000000	0.0000000	0.000000	
## 3	4.3399240	0.4455848	10.2526272	6.005934	
## 4	22.3270360	7.9558577	13.1916383	13.783312	
## 5	10.2175566	21.5404838	6.8629170	4.380814	
## 6	4.8046200	13.3486325	3.2815989	3.915243	
##	SE_NormAve_1dAd_AT	SE_NormAve_3dAd_AT	SE_NormAve_7dAd_AT	SE_NormAve_14dAd_AT	
## 1	0.8264017	10.8952403	4.488686	17.3623398	
## 2	1.5762916	0.5843517	1.343623	0.4069737	
## 3	2.2990178	13.6702576	3.213938	33.3112111	
## 4	4.6535347	9.0131424	37.486518	72.8776247	
## 5	3.8680241	7.0507377	1.192287	16.3799370	
## 6	8.7104565	1.6992329	1.441007	11.2834146	
##	log2FC_14dOb_AT	log2FC_7dOb_AT	log2FC_3dOb_AT	log2FC_1dOb_AT	log2FC_4hOb_AT
## 1	3.23119922	2.51470096	2.72168159	2.17666154	0.572698357
## 2	-0.06766609	0.32693694	0.07071751	0.36206679	0.001707546
## 3	0.37395909	0.77421856	0.44630260	0.45917686	0.301004953
## 4	-0.10085379	0.02797461	-0.18807170	-0.09574751	-0.232156116
## 5	1.30299981	0.86950341	0.65528641	0.63785703	1.498500442
## 6	0.09499176	0.07145753	0.04473431	0.07975398	-0.212428653
##	log2FC_4hAd_AT	log2FC_1dAd_AT	log2FC_3dAd_AT	log2FC_7dAd_AT	log2FC_14dAd_AT
## 1	0.5582999	0.3336399	2.5861296	3.40166499	4.78254845
## 2	-0.1659126	1.4959093	0.4102887	1.08709074	0.76950307
## 3	0.1537770	0.1166818	0.3104162	1.22082394	1.49641454
## 4	-0.2164207	-0.4710796	-0.2205064	0.01250962	0.33114933
## 5	0.1789347	-0.2892690	-0.5432919	0.39905632	0.50795641
## 6	-0.2911188	-0.2310917	0.1680315	0.06910237	-0.07960832
##	FDR_14dOb_AT	FDR_7dOb_AT	FDR_3dOb_AT	FDR_1dOb_AT	FDR_4hOb_AT
## 1	0.01171642	0.07351784	0.05453437	0.2524745	0.972016672
## 2	0.99740616	0.89818079	0.99762181	0.9998728	0.999832751
## 3	0.89814286	0.46729307	0.90911977	0.9998728	0.995661787
## 4	0.99740616	0.99999005	0.99161315	0.9998728	0.999832751
## 5	0.00001190	0.01601386	0.15900216	0.2537683	0.000000256
## 6	0.96872469	0.99211980	0.99762181	0.9998728	0.851497833
##	FDR_1dAd_AT	FDR_3dAd_AT	FDR_7dAd_AT	FDR_14dAd_AT	gene_name
## 1	0.8582632	0.02129693	0.001584163	0.000011100	A2M ENSG00000175899
## 2	0.4086935	0.65991606	0.439808117	0.498953892	NAT2 ENSG00000156006

```
## 3 0.9316638 0.72659071 0.015848373 0.002265622 ACADS ENSG000000122971
## 4 0.5023851 0.79610881 0.997577797 0.621191148 ACAT1 ENSG000000075239
## 5 0.6137406 0.15384275 0.293696904 0.151085181 ACVRL1 ENSG000000139567
## 6 0.4939214 0.56857076 0.840754065 0.851372831 PSEN1 ENSG000000080815
```

```
write.table(nexpr, "../03limma/rauch2019_gene_list.tab", sep="\t", row.names=FALSE)
```

```
nexpr = read.delim("../03limma/rauch2019_gene_list.tab", header = T)
dim(nexpr); colnames(nexpr)
```

```
## [1] 18062 74
```

```
## [1] "RefSeqID" "chr" "start"
## [4] "end" "strand" "Length"
## [7] "Copies" "Annotation.Divergence" "RNA_14dOb_AT_rep1"
## [10] "RNA_7dOb_AT_rep1" "RNA_3dOb_AT_rep1" "RNA_1dOb_AT_rep1"
## [13] "RNA_4hOb_AT_rep1" "RNA_Msc_AT_rep1" "RNA_4hAd_AT_rep1"
## [16] "RNA_1dAd_AT_rep1" "RNA_3dAd_AT_rep1" "RNA_7dAd_AT_rep1"
## [19] "RNA_14dAd_AT_rep1" "RNA_14dOb_AT_rep2" "RNA_7dOb_AT_rep2"
## [22] "RNA_3dOb_AT_rep2" "RNA_1dOb_AT_rep2" "RNA_4hOb_AT_rep2"
## [25] "RNA_Msc_AT_rep2" "RNA_4hAd_AT_rep2" "RNA_1dAd_AT_rep2"
## [28] "RNA_3dAd_AT_rep2" "RNA_7dAd_AT_rep2" "RNA_14dAd_AT_rep2"
## [31] "NormAve_14dOb_AT" "NormAve_7dOb_AT" "NormAve_3dOb_AT"
## [34] "NormAve_1dOb_AT" "NormAve_4hOb_AT" "NormAve_Msc_AT"
## [37] "NormAve_4hAd_AT" "NormAve_1dAd_AT" "NormAve_3dAd_AT"
## [40] "NormAve_7dAd_AT" "NormAve_14dAd_AT" "SE_NormAve_14dOb_AT"
## [43] "SE_NormAve_7dOb_AT" "SE_NormAve_3dOb_AT" "SE_NormAve_1dOb_AT"
## [46] "SE_NormAve_4hOb_AT" "SE_NormAve_Msc_AT" "SE_NormAve_4hAd_AT"
## [49] "SE_NormAve_1dAd_AT" "SE_NormAve_3dAd_AT" "SE_NormAve_7dAd_AT"
## [52] "SE_NormAve_14dAd_AT" "log2FC_14dOb_AT" "log2FC_7dOb_AT"
## [55] "log2FC_3dOb_AT" "log2FC_1dOb_AT" "log2FC_4hOb_AT"
## [58] "log2FC_4hAd_AT" "log2FC_1dAd_AT" "log2FC_3dAd_AT"
## [61] "log2FC_7dAd_AT" "log2FC_14dAd_AT" "FDR_14dOb_AT"
## [64] "FDR_7dOb_AT" "FDR_3dOb_AT" "FDR_1dOb_AT"
## [67] "FDR_4hOb_AT" "FDR_4hAd_AT" "FDR_1dAd_AT"
## [70] "FDR_3dAd_AT" "FDR_7dAd_AT" "FDR_14dAd_AT"
## [73] "gene_name" "gene"
```

```
nexpr = nexpr[!duplicated(nexpr$gene_name),]
rownames(nexpr) = nexpr$gene_name
dim(nexpr)
```

```
## [1] 16579 74
```

```
expr = nexpr[grepl("^NormAve_(14|3|1|Msc)", colnames(nexpr))]
head(expr)
```

```
## NormAve_14dOb_AT NormAve_3dOb_AT NormAve_1dOb_AT NormAve_Msc_AT
## A2M 27.15296 17.33151 10.6282867 0.9528313
## NAT2 0.00000 0.00000 0.4658704 0.0000000
## ACADS 37.87861 40.21529 40.6135081 28.2673477
```

```
## ACAT1      142.22175      133.89332      143.2903135      153.4855229
## ACVRL1     152.59056      95.82145      94.5386656      59.5292008
## PSEN1      128.50301      124.75326      127.6254037      120.7083193
##           NormAve_1dAd_AT NormAve_3dAd_AT NormAve_14dAd_AT
## A2M        1.569964      15.3726009      98.939672
## NAT2        2.779559      0.5843517      1.289227
## ACADS       31.325859      36.2246975      87.089223
## ACAT1      109.731092      131.3394425      191.586850
## ACVRL1     48.534804      40.2604963      85.535117
## PSEN1      102.838688      135.6891878      114.807143
```

```
colnames(expr) = gsub("NormAve_", "", colnames(expr))
head(as.matrix(expr))
```

```
##           14d0b_AT  3d0b_AT  1d0b_AT  Msc_AT  1dAd_AT  3dAd_AT
## A2M      27.15296  17.33151  10.6282867  0.9528313  1.569964  15.3726009
## NAT2      0.00000  0.00000  0.4658704  0.0000000  2.779559  0.5843517
## ACADS     37.87861  40.21529  40.6135081  28.2673477  31.325859  36.2246975
## ACAT1    142.22175  133.89332  143.2903135  153.4855229  109.731092  131.3394425
## ACVRL1   152.59056  95.82145  94.5386656  59.5292008  48.534804  40.2604963
## PSEN1    128.50301  124.75326  127.6254037  120.7083193  102.838688  135.6891878
##           14dAd_AT
## A2M      98.939672
## NAT2      1.289227
## ACADS     87.089223
## ACAT1    191.586850
## ACVRL1    85.535117
## PSEN1    114.807143
```

## Get GO terms

```
mart <- biomaRt::useMart(biomart = "ensembl",
  dataset = "hsapiens_gene_ensembl",
  host = "https://jan2019.archive.ensembl.org")
```

```
ribogen = biomaRt::getBM(c("external_gene_name", "ensembl_gene_id", "go_linkage_type"),
  filters = "go",
  values = c("GO:0042254"),
  mart = mart)
length(unique(ribogen$ensembl_gene_id)) #104
```

```
## [1] 104
```

```
norp_ribogen = ribogen[!grepl("^M?RP", ribogen$external_gene_name),]
length(unique(norp_ribogen$ensembl_gene_id)) #96
```

```
## [1] 96
```

```
translation = getBM(c("external_gene_name", "ensembl_gene_id"),
  filters = "go",
  values = "GO:0006412",
  mart = mart)
nrow(translation)
```

```
## [1] 378
```

```
norp_trans = translation[!grepl("^M?RP", translation$external_gene_name),]
nrow(norp_trans) #165 non RP translation genes
```

```
## [1] 213
```

```
cyt_ribosome = biomaRt::getBM(c("external_gene_name", "ensembl_gene_id", "go_linkage_type"),
  filters = "go",
  values = c("GO:0022625", "GO:0022627"),
  mart = mart)
length(unique(cyt_ribosome$ensembl_gene_id)) #120 cytosolic ribosome genes
```

```
## [1] 120
```

## Format and scale

```
summary(expr)
```

```
##      14dOb_AT      3dOb_AT      1dOb_AT      Msc_AT
## Min.   : 0.000   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
## 1st Qu.: 5.579   1st Qu.: 5.627   1st Qu.: 5.311   1st Qu.: 5.201
## Median : 43.653   Median : 43.431   Median : 42.872   Median : 42.669
## Mean   : 94.209   Mean   : 98.007   Mean   : 97.880   Mean   : 97.261
## 3rd Qu.: 116.957   3rd Qu.: 114.978   3rd Qu.: 115.157   3rd Qu.: 116.175
## Max.   :3022.468   Max.   :4099.242   Max.   :4111.197   Max.   :3906.684
##      1dAd_AT      3dAd_AT      14dAd_AT
## Min.   : 0.00   Min.   : 0.000   Min.   : 0.00
## 1st Qu.: 4.58   1st Qu.: 4.911   1st Qu.: 5.09
## Median : 41.86   Median : 40.703   Median : 40.62
## Mean   : 95.61   Mean   : 95.679   Mean   : 103.35
## 3rd Qu.: 116.22   3rd Qu.: 114.661   3rd Qu.: 118.55
## Max.   :3975.81   Max.   :3726.408   Max.   :3356.06
```

```
zs = t(scale(t(log2(expr+1))))
summary(zs)
```

```
##      14dOb_AT      3dOb_AT      1dOb_AT      Msc_AT
## Min.   : -2.1956   Min.   : -2.18913   Min.   : -2.25413   Min.   : -2.23658
## 1st Qu.: -0.5558   1st Qu.: -0.62725   1st Qu.: -0.58529   1st Qu.: -0.71234
## Median : 0.0249   Median : 0.00870   Median : -0.00264   Median : -0.02407
## Mean   : 0.0245   Mean   : 0.00521   Mean   : -0.00433   Mean   : 0.00385
```



```
## 3rd Qu.: 0.5845 3rd Qu.: 0.64558 3rd Qu.: 0.58224 3rd Qu.: 0.72255
## Max. : 2.2678 Max. : 2.26779 Max. : 2.26779 Max. : 2.26779
## NA's :63 NA's :63 NA's :63 NA's :63
## 1dAd_AT 3dAd_AT 14dAd_AT
## Min. :-2.20081 Min. :-2.21494 Min. :-2.23591
## 1st Qu.: -0.84725 1st Qu.: -0.77747 1st Qu.: -0.91375
## Median : -0.13928 Median : -0.02881 Median : -0.00407
## Mean : -0.05784 Mean : 0.00198 Mean : 0.02664
## 3rd Qu.: 0.76707 3rd Qu.: 0.79843 3rd Qu.: 0.96528
## Max. : 2.26779 Max. : 2.26779 Max. : 2.26779
## NA's :63 NA's :63 NA's :63
```

```
#create vector for ordering
order = apply(zs, 1, cor, y=1:ncol(zs)) #uses pearson correlation
head(order)
```

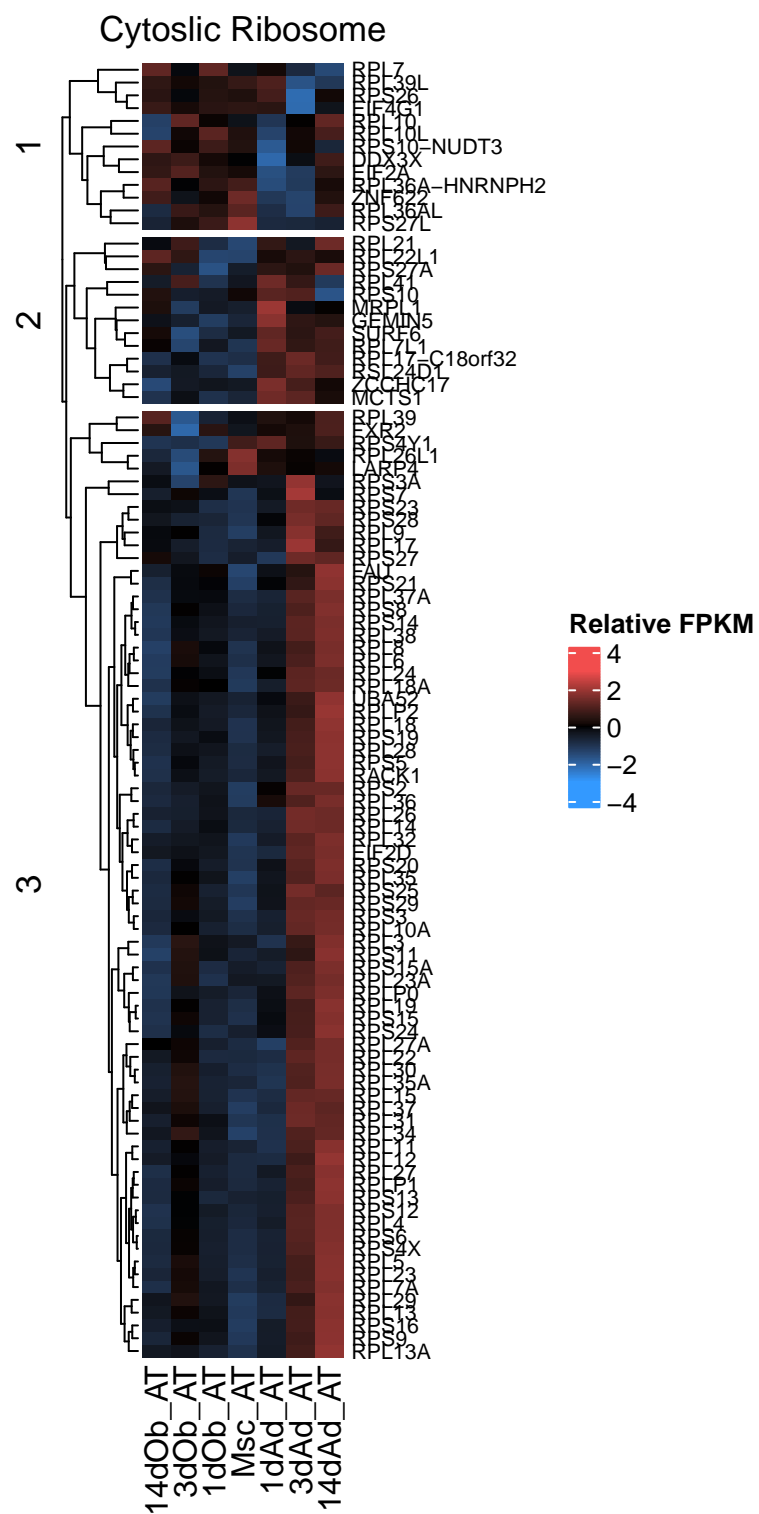
```
## A2M NAT2 ACADS ACAT1 ACVRL1 PSEN1
## 0.1168593 0.6658657 0.4310559 0.2687754 -0.6956949 -0.3277898
```

```
length(order)
```

```
## [1] 16579
```

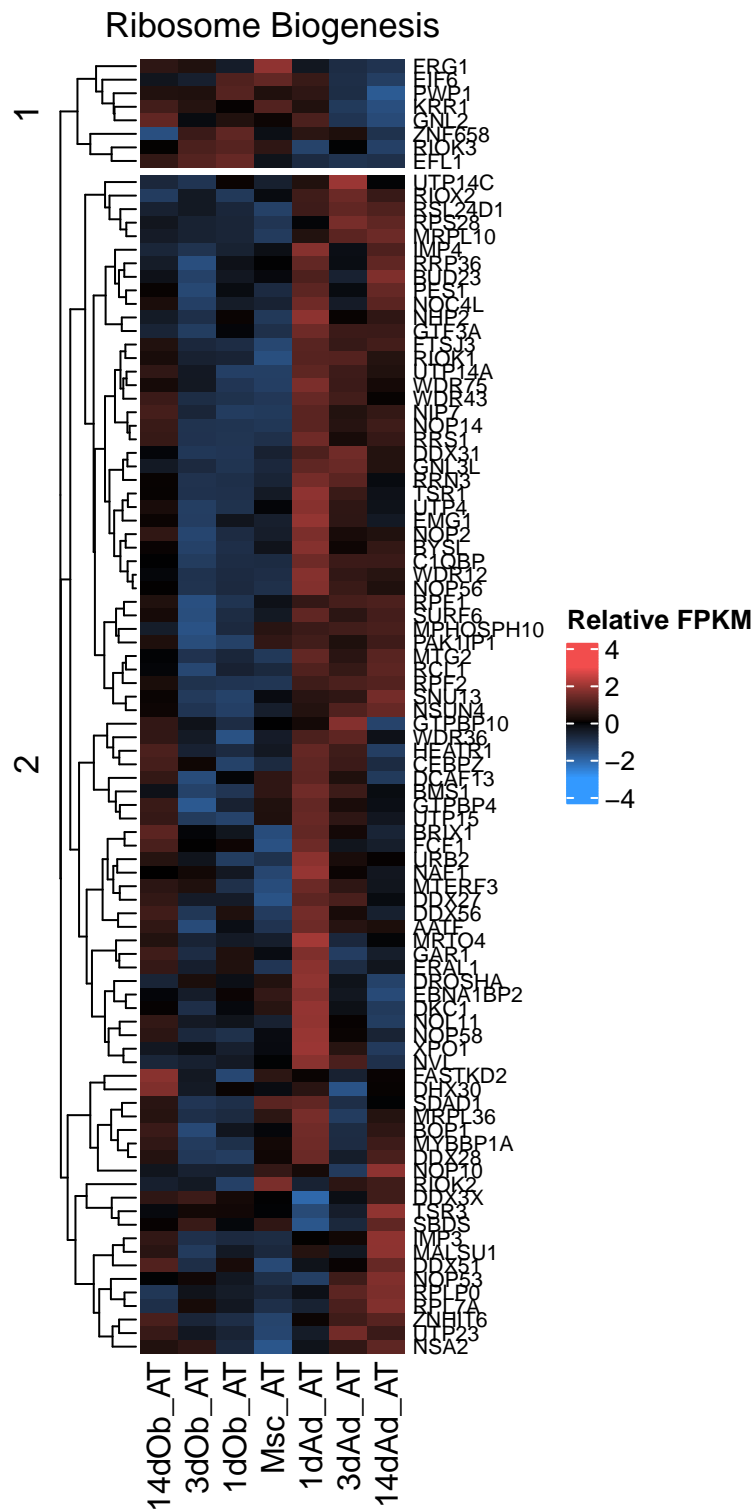
## Supp Figure 6c - Ribosomal Proteins

```
Heatmap(as.matrix(zs[rownames(zs) %in% cyt_ribosome$external_gene_name,]),
  cluster_columns = F,
  name="Relative FPKM",
  column_title = "Cytosolic Ribosome",
  col=circlize::colorRamp2(c(-3,0,3),c(rgb(0.2,0.6,1),rgb(0,0,0),rgb(0.95,0.3,0.3))),
  show_row_names = T, row_names_gp = gpar(fontsize=8),
  row_dend_reorder = order[rownames(zs) %in% cyt_ribosome$external_gene_name],
  row_split=3
)
```



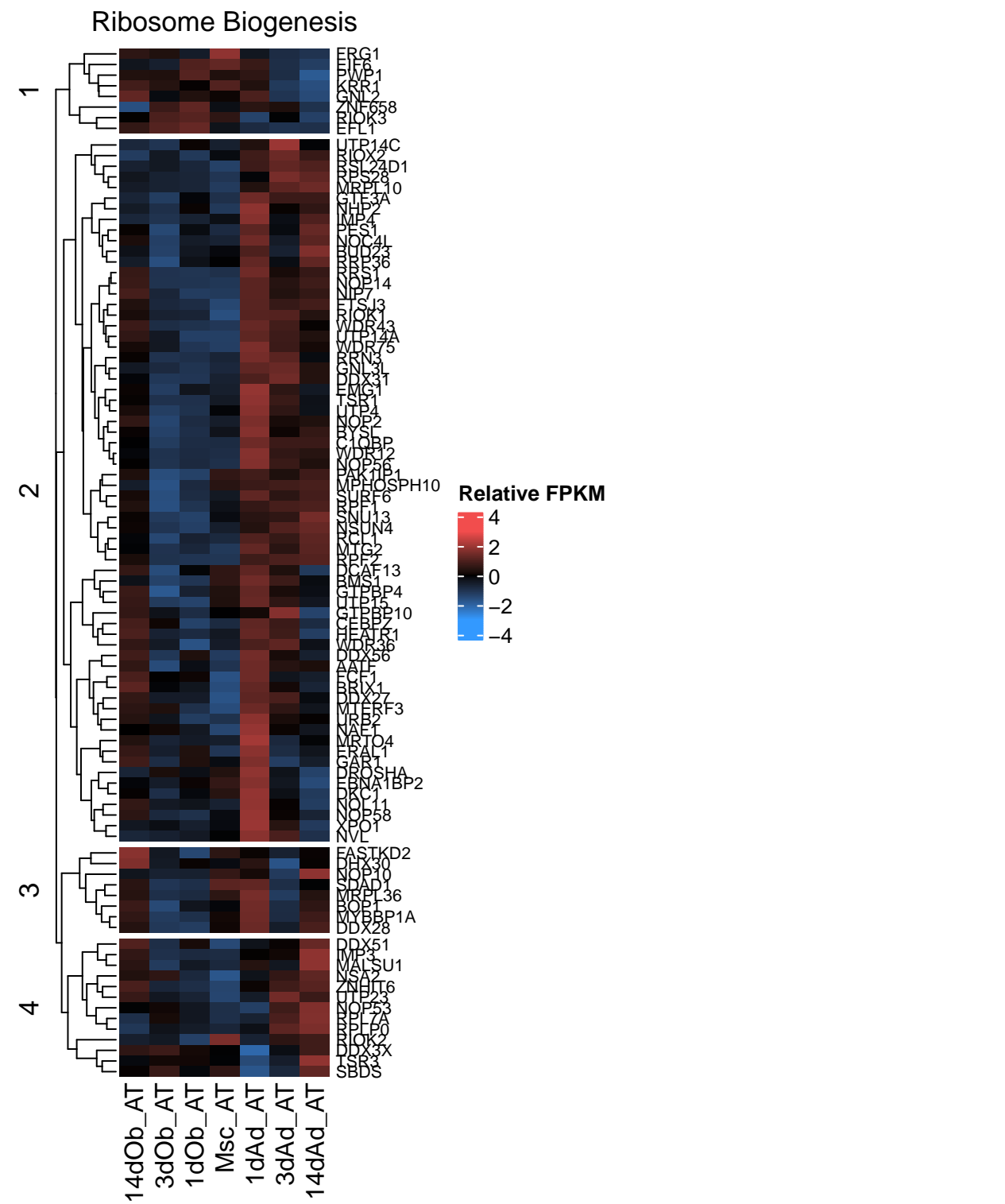
Do translation genes also increase expr. in Rauch2019?

```
Heatmap(as.matrix(zs[rownames(zs) %in% ribogen$external_gene_name,]),
        cluster_columns = F,
        name="Relative FPKM",
        column_title = "Ribosome Biogenesis",
        col=circlize::colorRamp2(c(-3,0,3),c(rgb(0.2,0.6,1),rgb(0,0,0),rgb(0.95,0.3,0.3))),
        show_row_names = T, row_names_gp = gpar(fontsize=8),
        row_dend_reorder = order[rownames(zs) %in% ribogen$external_gene_name],
        row_split=2
    )
```



```
Heatmap(as.matrix(zs[rownames(zs) %in% ribogen$external_gene_name,]),
        cluster_columns = F,
        name="Relative FPKM",
        column_title = "Ribosome Biogenesis",
        col=circlize::colorRamp2(c(-3,0,3),c(rgb(0.2,0.6,1),rgb(0,0,0),rgb(0.95,0.3,0.3))),
```

```
show_row_names = T, row_names_gp = gpar(fontsize=8),
row_dend_reorder = order[rownames(zs) %in% ribogen$external_gene_name],
row_split=4
)
```



Large part of ribosome biogenesis genes peak 4h after Diff onset, but the top cluster has higher expression later in diff.

Translation cluster 2 and 3 have later adipogenic specific activation, including RPs and elongation factors.

```
Heatmap(as.matrix(zs[rownames(zs) %in% translation$external_gene_name,]),
        cluster_columns = F,
        name="Relative FPKM",
        column_title = "Translation",
        col=circlize::colorRamp2(c(-3,0,3),c(rgb(0.2,0.6,1),rgb(0,0,0),rgb(0.95,0.3,0.3))),
        show_row_names = T, row_names_gp = gpar(fontsize=8),
        row_dend_reorder = order[rownames(zs) %in% translation$external_gene_name],
        row_split=3
    )
```



```
show_row_names = T, row_names_gp = gpar(fontsize=8),
row_dend_reorder = order[rownames(zs) %in% translation$external_gene_name],
row_split=4
)
```

