R Notebook

**include dependencies**

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:data.table':  
##   
## between, first, last

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

##   
## Attaching package: 'purrr'

## The following object is masked from 'package:data.table':  
##   
## transpose

## Loading required package: S4Vectors

## Loading required package: stats4

## Loading required package: BiocGenerics

## Loading required package: parallel

##   
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':  
##   
## clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,  
## clusterExport, clusterMap, parApply, parCapply, parLapply,  
## parLapplyLB, parRapply, parSapply, parSapplyLB

## The following objects are masked from 'package:dplyr':  
##   
## combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':  
##   
## IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':  
##   
## anyDuplicated, append, as.data.frame, basename, cbind, colnames,  
## dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,  
## grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,  
## order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,  
## rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,  
## union, unique, unsplit, which.max, which.min

##   
## Attaching package: 'S4Vectors'

## The following objects are masked from 'package:dplyr':  
##   
## first, rename

## The following objects are masked from 'package:data.table':  
##   
## first, second

## The following objects are masked from 'package:base':  
##   
## expand.grid, I, unname

## Loading required package: IRanges

##   
## Attaching package: 'IRanges'

## The following object is masked from 'package:purrr':  
##   
## reduce

## The following objects are masked from 'package:dplyr':  
##   
## collapse, desc, slice

## The following object is masked from 'package:data.table':  
##   
## shift

## The following object is masked from 'package:grDevices':  
##   
## windows

## Loading required package: GenomicRanges

## Loading required package: GenomeInfoDb

## Loading required package: SummarizedExperiment

## Loading required package: MatrixGenerics

## Loading required package: matrixStats

##   
## Attaching package: 'matrixStats'

## The following object is masked from 'package:dplyr':  
##   
## count

##   
## Attaching package: 'MatrixGenerics'

## The following objects are masked from 'package:matrixStats':  
##   
## colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,  
## colCounts, colCummaxs, colCummins, colCumprods, colCumsums,  
## colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,  
## colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,  
## colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,  
## colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,  
## colWeightedMeans, colWeightedMedians, colWeightedSds,  
## colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,  
## rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,  
## rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,  
## rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,  
## rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,  
## rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,  
## rowWeightedMads, rowWeightedMeans, rowWeightedMedians,  
## rowWeightedSds, rowWeightedVars

## Loading required package: Biobase

## Welcome to Bioconductor  
##   
## Vignettes contain introductory material; view with  
## 'browseVignettes()'. To cite Bioconductor, see  
## 'citation("Biobase")', and for packages 'citation("pkgname")'.

##   
## Attaching package: 'Biobase'

## The following object is masked from 'package:MatrixGenerics':  
##   
## rowMedians

## The following objects are masked from 'package:matrixStats':  
##   
## anyMissing, rowMedians

## Loading required package: grid

## ========================================  
## ComplexHeatmap version 2.8.0  
## Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/  
## Github page: https://github.com/jokergoo/ComplexHeatmap  
## Documentation: http://jokergoo.github.io/ComplexHeatmap-reference  
##   
## If you use it in published research, please cite:  
## Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional   
## genomic data. Bioinformatics 2016.  
##   
## The new InteractiveComplexHeatmap package can directly export static   
## complex heatmaps into an interactive Shiny app with zero effort. Have a try!  
##   
## This message can be suppressed by:  
## suppressPackageStartupMessages(library(ComplexHeatmap))  
## ========================================

##

## clusterProfiler v4.0.5 For help: https://yulab-smu.top/biomedical-knowledge-mining-book/  
##   
## If you use clusterProfiler in published research, please cite:  
## T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo, and G Yu. clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. The Innovation. 2021, 2(3):100141. doi: 10.1016/j.xinn.2021.100141

##   
## Attaching package: 'clusterProfiler'

## The following object is masked from 'package:IRanges':  
##   
## slice

## The following object is masked from 'package:S4Vectors':  
##   
## rename

## The following object is masked from 'package:purrr':  
##   
## simplify

## The following object is masked from 'package:stats':  
##   
## filter

## DOSE v3.18.2 For help: https://guangchuangyu.github.io/software/DOSE  
##   
## If you use DOSE in published research, please cite:  
## Guangchuang Yu, Li-Gen Wang, Guang-Rong Yan, Qing-Yu He. DOSE: an R/Bioconductor package for Disease Ontology Semantic and Enrichment analysis. Bioinformatics 2015, 31(4):608-609

## Loading required package: AnnotationDbi

##   
## Attaching package: 'AnnotationDbi'

## The following object is masked from 'package:clusterProfiler':  
##   
## select

## The following object is masked from 'package:dplyr':  
##   
## select

##

#### Data Loading

*Only use relevant columns*

infected\_raw <- fread(file="data/GSE162323\_slam\_inf\_params.txt", check.names=TRUE)  
uninfected\_raw <- fread("data/GSE162323\_slam\_uninf\_params.txt", check.names=TRUE)  
infected\_1 = infected\_raw[,c(1, 3:8)]  
uninfected\_1 = uninfected\_raw[,c(1, 3:8)]

*Remove duplicate rows with median and merge uninfected and infected gene expression datasets*

infected\_dedup <- infected\_1 %>%  
 group\_by(gene.symbol) %>%  
 summarize(  
 one.hour.inf = as.integer(median(X1h.4sU.Readcount, na.rm=TRUE)),  
 two.hour.inf = as.integer(median(X2h.4sU.rep1.Readcount)),  
 three.hour.inf = as.integer(median(X3h.4sU.Readcount)),  
 four.hour.inf = as.integer(median(X4h.4sU.Readcount))  
 )  
  
uninfected\_dedup <- uninfected\_1 %>%  
 group\_by(gene.symbol) %>%  
 summarize(  
 one.hour.uninf = as.integer(median(X1h.4sU.Readcount, na.rm=TRUE)),  
 two.hour.uninf = as.integer(median(X2h.4sU.rep2.Readcount)),  
 three.hour.uninf = as.integer(median(X3h.4sU.Readcount)),  
 four.hour.uninf = as.integer(median(X4h.4sU.Readcount))  
 )  
  
cts\_merged <- merge(x=infected\_dedup, y=uninfected\_dedup, by="gene.symbol")  
cts <- cts\_merged[,-1]  
rownames(cts) <- cts\_merged[,1]

### PCA Plot

*Coldata*

coldata <- as.data.frame(names(cts))  
coldata$condition <- c("infected", "infected", "infected", "infected", "uninfected", "uninfected", "uninfected", "uninfected")

*Gene Expression Matrix*

dds <- DESeqDataSetFromMatrix(countData = cts,  
 colData = coldata,  
 design = ~ condition)

## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in  
## design formula are characters, converting to factors

dds <- DESeq(dds) #this is doing a lot of number crunching

## estimating size factors

## estimating dispersions

## gene-wise dispersion estimates

## mean-dispersion relationship

## final dispersion estimates

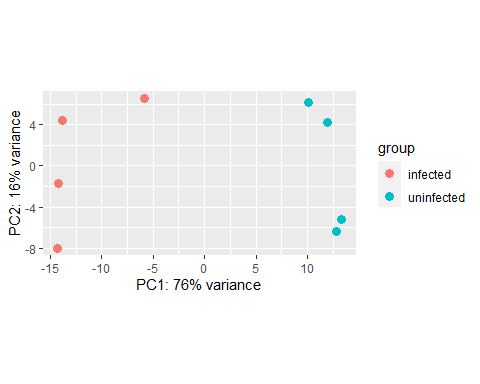
## fitting model and testing

res <- results(dds)  
vsd <- vst(dds, blind=FALSE)  
head(res)

## log2 fold change (MLE): condition uninfected vs infected   
## Wald test p-value: condition uninfected vs infected   
## DataFrame with 6 rows and 6 columns  
## baseMean log2FoldChange lfcSE stat pvalue padj  
## <numeric> <numeric> <numeric> <numeric> <numeric> <numeric>  
## 5S\_rRNA 0.649514 -2.712206 2.57137 -1.054773 0.291529 NA  
## 7SK 0.599757 -1.134343 2.71528 -0.417762 0.676121 NA  
## A1BG 0.736968 0.793627 2.59163 0.306227 0.759432 NA  
## A1BG-AS1 2.022509 2.321052 2.17927 1.065060 0.286849 NA  
## A1CF 0.882045 -0.712850 2.52134 -0.282726 0.777387 NA  
## A2M 0.922488 1.386869 2.06441 0.671799 0.501712 NA

*PCA Plot TODO: Correct axis (infected vs uninfected)*

plotPCA(vsd, intgroup=c("condition"))



### Volcano Plot

#### Some Extra Analysis

set.seed(9823249)  
deseq\_df <- res |>  
 as.data.frame() |>  
 tibble::rownames\_to\_column("Gene") |>  
 dplyr::mutate(threshold = padj < 0.05) |>  
 arrange(desc(log2FoldChange))  
  
head(deseq\_df, n=10)

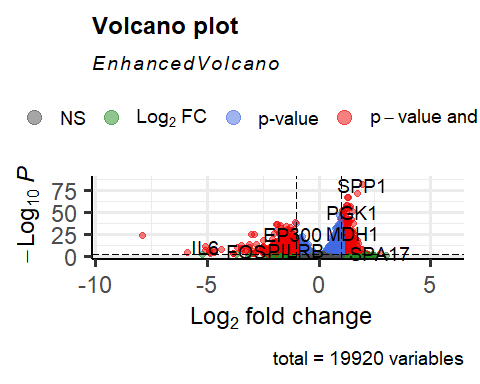
## Gene baseMean log2FoldChange lfcSE stat pvalue padj threshold  
## 1 LCK 3.485863 4.231088 1.331835 3.176887 0.001488651 NA NA  
## 2 CD7 3.003281 4.019607 2.257319 1.780700 0.074961537 NA NA  
## 3 GRM6 2.699829 3.859555 1.805952 2.137131 0.032587355 NA NA  
## 4 ABHD16B 1.979928 3.412723 2.028978 1.681991 0.092570644 NA NA  
## 5 C1orf95 1.979928 3.412723 2.028978 1.681991 0.092570644 NA NA  
## 6 VSIG8 1.963892 3.396306 1.804804 1.881814 0.059861329 NA NA  
## 7 SLC2A7 1.898840 3.355788 2.431937 1.379883 0.167622608 NA NA  
## 8 ANP32C 3.112576 3.302454 1.643594 2.009289 0.044506546 NA NA  
## 9 ACTG2 3.086690 3.297262 1.856547 1.776019 0.075729839 NA NA  
## 10 CD84 1.815817 3.291125 2.449052 1.343836 0.179001272 NA NA

volcano\_plot <- EnhancedVolcano::EnhancedVolcano(  
 deseq\_df,  
 lab = deseq\_df$Gene,  
 x = "log2FoldChange",  
 y = "padj",  
 pCutoff = 0.01  
)

## Registered S3 methods overwritten by 'ggalt':  
## method from   
## grid.draw.absoluteGrob ggplot2  
## grobHeight.absoluteGrob ggplot2  
## grobWidth.absoluteGrob ggplot2  
## grobX.absoluteGrob ggplot2  
## grobY.absoluteGrob ggplot2

## Warning: Ignoring unknown parameters: xlim, ylim

volcano\_plot

 ### clustProfiler GO

geneList <- deseq\_df[,3]  
names(geneList) = deseq\_df[,1]  
go\_res <- gseGO(  
 geneList = sort(geneList, decreasing = TRUE),  
 OrgDb = org.Hs.eg.db,  
 ont = "BP",  
 keyType = 'SYMBOL',  
 pvalueCutoff = 0.05,  
 verbose = FALSE  
)

## Warning in preparePathwaysAndStats(pathways, stats, minSize, maxSize, gseaParam, : There are ties in the preranked stats (9.54% of the list).  
## The order of those tied genes will be arbitrary, which may produce unexpected results.

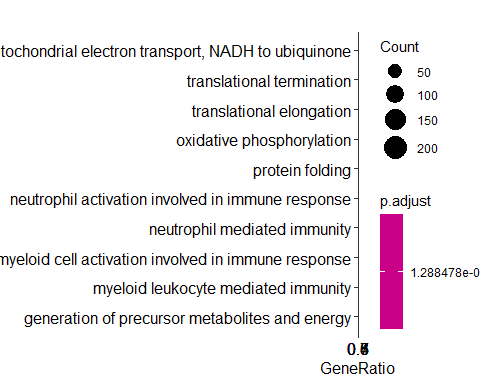
## Warning in fgseaMultilevel(...): For some pathways, in reality P-values are less  
## than 1e-10. You can set the `eps` argument to zero for better estimation.

head(go\_res, n=10)

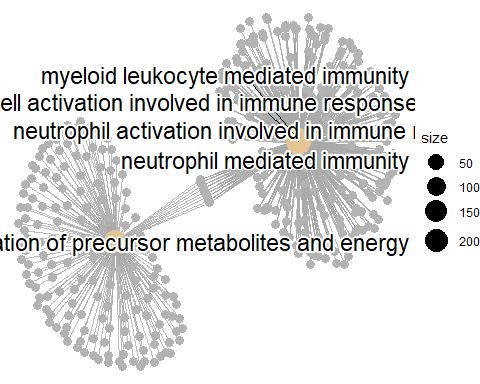
## ID Description  
## GO:0002275 GO:0002275 myeloid cell activation involved in immune response  
## GO:0002283 GO:0002283 neutrophil activation involved in immune response  
## GO:0002444 GO:0002444 myeloid leukocyte mediated immunity  
## GO:0002446 GO:0002446 neutrophil mediated immunity  
## GO:0006091 GO:0006091 generation of precursor metabolites and energy  
## GO:0006119 GO:0006119 oxidative phosphorylation  
## GO:0006120 GO:0006120 mitochondrial electron transport, NADH to ubiquinone  
## GO:0006414 GO:0006414 translational elongation  
## GO:0006415 GO:0006415 translational termination  
## GO:0006457 GO:0006457 protein folding  
## setSize enrichmentScore NES pvalue p.adjust qvalues  
## GO:0002275 468 0.3583013 1.964671 1e-10 1.288478e-08 1.029062e-08  
## GO:0002283 421 0.4010586 2.208797 1e-10 1.288478e-08 1.029062e-08  
## GO:0002444 475 0.3496213 1.918329 1e-10 1.288478e-08 1.029062e-08  
## GO:0002446 433 0.3821367 2.098519 1e-10 1.288478e-08 1.029062e-08  
## GO:0006091 442 0.4142780 2.288052 1e-10 1.288478e-08 1.029062e-08  
## GO:0006119 103 0.6541312 3.003821 1e-10 1.288478e-08 1.029062e-08  
## GO:0006120 45 0.7818669 3.088561 1e-10 1.288478e-08 1.029062e-08  
## GO:0006414 125 0.5788764 2.743235 1e-10 1.288478e-08 1.029062e-08  
## GO:0006415 100 0.6610471 3.003169 1e-10 1.288478e-08 1.029062e-08  
## GO:0006457 204 0.5092289 2.587248 1e-10 1.288478e-08 1.029062e-08  
## rank leading\_edge  
## GO:0002275 4686 tags=44%, list=24%, signal=35%  
## GO:0002283 4686 tags=48%, list=24%, signal=37%  
## GO:0002444 4686 tags=44%, list=24%, signal=34%  
## GO:0002446 4686 tags=46%, list=24%, signal=36%  
## GO:0006091 3391 tags=37%, list=17%, signal=32%  
## GO:0006119 3091 tags=66%, list=16%, signal=56%  
## GO:0006120 2718 tags=80%, list=14%, signal=69%  
## GO:0006414 5485 tags=71%, list=28%, signal=52%  
## GO:0006415 4522 tags=73%, list=23%, signal=57%  
## GO:0006457 5876 tags=62%, list=30%, signal=44%  
## core\_enrichment  
## GO:0002275 CD84/S100A9/CEACAM6/ANXA2/LBP/DSG1/NMI/DOCK2/CR1/HSPA1A/TCN1/MAGT1/FCAR/LYZ/TUBB/FABP5/PGRMC1/PSMA2/PPBP/HMGB1/PSMB1/SLC2A5/SDCBP/PSAP/MIF/PSMB7/TNFAIP6/CD63/SLPI/CYBA/B2M/FGL2/CEACAM8/DYNLT1/CD44/OLFM4/S100A11/SVIP/ARPC5/PSMA5/PRDX4/HPSE/SRP14/PSMD14/HSP90AA1/ACTR2/MGST1/AHSG/STOM/ANXA3/FUCA2/PNP/HLA-B/RAP1B/NPC2/VAMP8/XRCC5/HSP90AB1/SUCNR1/PSMC2/PPIA/CTSS/CAP1/EEF1A1/ERP44/ATP6V1D/PRSS3/CYSTM1/CD59/IDH1/SERPINB1/TBC1D10C/GGH/PSMD12/QPCT/GNS/QSOX1/ATP6V0C/MGAM/HSPA8/HK3/CCT8/TUBB4B/XRCC6/LAMTOR2/ILF2/CMTM6/TIMP2/RAB7A/CAT/GRN/MLEC/SELL/CCT2/ACTR10/PSMD1/PSMC3/SERPINA3/CREG1/SERPINA1/RAB5C/PGAM1/COMMD9/LAMP2/FTH1/BST1/DDOST/GCA/GLA/PA2G4/CD58/HEXB/PSMD2/RAB44/A1BG/RAB18/CST3/CPNE3/DYNLL1/ATP6AP2/GM2A/NRAS/HRNR/PLAU/CTSH/CD68/CD55/GOLGA7/FTL/S100A13/APRT/CTSC/HMOX2/LGALS9/RETN/CD47/AGA/JUP/PPIE/PKM/ALDOA/SNAP23/TNFRSF1B/CPNE1/LGALS3/GPI/ASAH1/S100A8/LAMP1/KCNAB2/ADAM10/FUCA1/PRAM1/SURF4/APEH/PRDX6/DIAPH1/ITGAL/PSMD7/SERPINB6/GSTP1/RAB37/MILR1/TRAPPC1/IFI35/GLB1/TMEM179B/PRCP/PIGR/CSTB/MME/RAP1A/PKP1/CD177/CFD/GUSB/GYG1/IQGAP2/SPTAN1/ACLY/COPB1/GDI2/P2RX1/RAC1/SNAP29/OSTF1/VCP/SIRPB1/PSMD6/HLA-C/IMPDH2/PTGES2/NCSTN/SCAMP1/RAB5B/PGM2/TMEM30A/BST2/VCL/NIT2/PSMD3/RAB10/CYB5R3/COTL1/PRTN3/SLCO4C1/PSEN1/LAMTOR3  
## GO:0002283 S100A9/CEACAM6/ANXA2/DSG1/DOCK2/CR1/HSPA1A/TCN1/MAGT1/FCAR/LYZ/TUBB/FABP5/PGRMC1/PSMA2/PPBP/HMGB1/PSMB1/SLC2A5/SDCBP/PSAP/MIF/PSMB7/TNFAIP6/CD63/SLPI/CYBA/B2M/FGL2/CEACAM8/DYNLT1/CD44/OLFM4/S100A11/SVIP/ARPC5/PSMA5/PRDX4/HPSE/SRP14/PSMD14/HSP90AA1/ACTR2/MGST1/AHSG/STOM/ANXA3/FUCA2/PNP/HLA-B/RAP1B/NPC2/VAMP8/XRCC5/HSP90AB1/PSMC2/PPIA/CTSS/CAP1/EEF1A1/ERP44/ATP6V1D/PRSS3/CYSTM1/CD59/IDH1/SERPINB1/TBC1D10C/GGH/PSMD12/QPCT/GNS/QSOX1/ATP6V0C/MGAM/HSPA8/HK3/CCT8/TUBB4B/XRCC6/LAMTOR2/ILF2/CMTM6/TIMP2/RAB7A/CAT/GRN/MLEC/SELL/CCT2/ACTR10/PSMD1/PSMC3/SERPINA3/CREG1/SERPINA1/RAB5C/PGAM1/COMMD9/LAMP2/FTH1/BST1/DDOST/GCA/GLA/PA2G4/CD58/HEXB/PSMD2/RAB44/A1BG/RAB18/CST3/CPNE3/DYNLL1/ATP6AP2/GM2A/NRAS/HRNR/PLAU/CTSH/CD68/CD55/GOLGA7/FTL/APRT/CTSC/HMOX2/RETN/CD47/AGA/JUP/PPIE/PKM/ALDOA/SNAP23/TNFRSF1B/CPNE1/LGALS3/GPI/ASAH1/S100A8/LAMP1/KCNAB2/ADAM10/FUCA1/PRAM1/SURF4/APEH/PRDX6/DIAPH1/ITGAL/PSMD7/SERPINB6/GSTP1/RAB37/TRAPPC1/GLB1/TMEM179B/PRCP/PIGR/CSTB/MME/RAP1A/PKP1/CD177/CFD/GUSB/GYG1/IQGAP2/SPTAN1/ACLY/COPB1/GDI2/P2RX1/RAC1/SNAP29/OSTF1/VCP/SIRPB1/PSMD6/HLA-C/IMPDH2/PTGES2/NCSTN/SCAMP1/RAB5B/PGM2/TMEM30A/BST2/VCL/NIT2/PSMD3/RAB10/CYB5R3/COTL1/PRTN3/SLCO4C1/PSEN1/LAMTOR3  
## GO:0002444 CD84/S100A9/CEACAM6/ANXA2/DSG1/DOCK2/CR1/HSPA1A/TCN1/MAGT1/FCAR/LYZ/TUBB/FABP5/PGRMC1/PSMA2/HLA-E/PPBP/HMGB1/PSMB1/SLC2A5/SDCBP/PSAP/MIF/PSMB7/TNFAIP6/CD63/SLPI/CYBA/B2M/FGL2/CEACAM8/DYNLT1/CD44/OLFM4/S100A11/SVIP/ARPC5/PSMA5/PRDX4/HPSE/SRP14/PSMD14/HSP90AA1/ACTR2/MGST1/AHSG/STOM/ANXA3/FUCA2/PNP/HLA-B/RAP1B/NPC2/VAMP8/XRCC5/HSP90AB1/PSMC2/PPIA/CTSS/CAP1/EEF1A1/ERP44/ATP6V1D/PRSS3/CYSTM1/CD59/IDH1/SERPINB1/TBC1D10C/GGH/PSMD12/QPCT/GNS/QSOX1/ATP6V0C/MGAM/HSPA8/HK3/CCT8/TUBB4B/XRCC6/LAMTOR2/ILF2/CMTM6/TIMP2/RAB7A/CAT/GRN/MLEC/SELL/CCT2/ACTR10/PSMD1/PSMC3/SERPINA3/CREG1/SERPINA1/RAB5C/PGAM1/COMMD9/LAMP2/FTH1/BST1/DDOST/GCA/GLA/PA2G4/CD58/HEXB/PSMD2/RAB44/A1BG/RAB18/CST3/CPNE3/DYNLL1/ATP6AP2/GM2A/NRAS/HRNR/PLAU/CTSH/CD68/CD55/GOLGA7/FTL/FCGR2B/S100A13/APRT/CTSC/HMOX2/LGALS9/RETN/CD47/AGA/JUP/PPIE/PKM/ALDOA/SNAP23/TNFRSF1B/CPNE1/LGALS3/GPI/ASAH1/TUSC2/S100A8/LAMP1/KCNAB2/ADAM10/FUCA1/PRAM1/SURF4/APEH/PRDX6/DIAPH1/ITGAL/PSMD7/SERPINB6/GSTP1/RAB37/MILR1/TRAPPC1/DDX21/GLB1/TMEM179B/PRCP/PIGR/CSTB/MME/RAP1A/PKP1/CD177/CFD/GUSB/GYG1/IQGAP2/SPTAN1/ACLY/COPB1/GDI2/P2RX1/RAC1/SNAP29/OSTF1/VCP/SIRPB1/PSMD6/HLA-C/IMPDH2/PTGES2/NCSTN/SCAMP1/RAB5B/PGM2/TMEM30A/BST2/VCL/NIT2/PSMD3/RAB10/CYB5R3/COTL1/PRTN3/SLCO4C1/PSEN1/LAMTOR3  
## GO:0002446 S100A9/CEACAM6/ANXA2/DSG1/DOCK2/CR1/HSPA1A/TCN1/MAGT1/FCAR/LYZ/TUBB/FABP5/PGRMC1/PSMA2/PPBP/HMGB1/PSMB1/SLC2A5/SDCBP/PSAP/MIF/PSMB7/TNFAIP6/CD63/SLPI/CYBA/B2M/FGL2/CEACAM8/DYNLT1/CD44/OLFM4/S100A11/SVIP/ARPC5/PSMA5/PRDX4/HPSE/SRP14/PSMD14/HSP90AA1/ACTR2/MGST1/AHSG/STOM/ANXA3/FUCA2/PNP/HLA-B/RAP1B/NPC2/VAMP8/XRCC5/HSP90AB1/PSMC2/PPIA/CTSS/CAP1/EEF1A1/ERP44/ATP6V1D/PRSS3/CYSTM1/CD59/IDH1/SERPINB1/TBC1D10C/GGH/PSMD12/QPCT/GNS/QSOX1/ATP6V0C/MGAM/HSPA8/HK3/CCT8/TUBB4B/XRCC6/LAMTOR2/ILF2/CMTM6/TIMP2/RAB7A/CAT/GRN/MLEC/SELL/CCT2/ACTR10/PSMD1/PSMC3/SERPINA3/CREG1/SERPINA1/RAB5C/PGAM1/COMMD9/LAMP2/FTH1/BST1/DDOST/GCA/GLA/PA2G4/CD58/HEXB/PSMD2/RAB44/A1BG/RAB18/CST3/CPNE3/DYNLL1/ATP6AP2/GM2A/NRAS/HRNR/PLAU/CTSH/CD68/CD55/GOLGA7/FTL/APRT/CTSC/HMOX2/RETN/CD47/AGA/JUP/PPIE/PKM/ALDOA/SNAP23/TNFRSF1B/CPNE1/LGALS3/GPI/ASAH1/TUSC2/S100A8/LAMP1/KCNAB2/ADAM10/FUCA1/PRAM1/SURF4/APEH/PRDX6/DIAPH1/ITGAL/PSMD7/SERPINB6/GSTP1/RAB37/TRAPPC1/GLB1/TMEM179B/PRCP/PIGR/CSTB/MME/RAP1A/PKP1/CD177/CFD/GUSB/GYG1/IQGAP2/SPTAN1/ACLY/COPB1/GDI2/P2RX1/RAC1/SNAP29/OSTF1/VCP/SIRPB1/PSMD6/HLA-C/IMPDH2/PTGES2/NCSTN/SCAMP1/RAB5B/PGM2/TMEM30A/BST2/VCL/NIT2/PSMD3/RAB10/CYB5R3/COTL1/PRTN3/SLCO4C1/PSEN1/LAMTOR3  
## GO:0006091 AKR1C4/GAPDHS/PGK2/PGAM4/MCHR1/ALDH1A1/GLRX/AK9/MDH1/SNCA/UQCRHL/PGK1/SLC25A18/CYCS/ADH5/BDH2/NDUFB6/NDUFB1/NDUFA5/COX6C/NDUFA4/CBFA2T3/NDUFB8/GLRX2/NDUFA2/UQCR10/AOX1/KL/ENO1/HMGB1/NDUFAF2/ACAT1/GCGR/SDHB/COX6A1/TPI1/NDUFA6/PARK7/PGAM2/NDUFA12/CYBA/NUP37/COX5B/CHCHD2/ALDH2/UQCRQ/MTFR1/COX7C/ETFA/NDUFB5/CALM1/AKR1B1/NDUFB2/SDHD/IDO1/NDUFA1/NDUFS6/COX17/QDPR/NDUFA9/FH/COX8A/COX11/PRKAG1/NDUFAB1/NDUFB10/COX7B/PHGDH/NDUFC2-KCTD14/UQCRH/NDUFB4/PDHB/GHITM/MAOB/UQCR11/IDH1/CYB5B/PRELID1/G6PD/RBKS/RDH16/NDUFC1/NDUFA7/CDK1/COX7A2/SUCLA2/IDH3B/ASIP/CISD1/COX6B1/DLD/DGUOK/GPX2/HK3/NDUFA8/NDUFS5/NDUFS4/UGP2/NDUFA11/CCNB1/ETFB/SORBS1/NDUFB11/NDUFB3/COX7A2L/CAT/SUCLG2/SHMT2/NDUFS1/BLOC1S1/NDUFS8/LEPR/NDUFB9/BID/NDUFA3/UQCRB/SDHA/PGAM1/GCK/XDH/UQCRC1/NDUFV2/IDH3A/MDH2/NDUFS2/NDUFB7/LYRM7/FBP1/MRAP2/ASPH/CYC1/IMMP2L/EIF6/PDHA1/IDH3G/NDUFS7/ACO1/ETFDH/CHCHD10/COA6/SUCLG1/COX4I1/AKR1A1/HMGCS2/STOML2/IDH2/MSH2/RPE/PPP1CA/P4HA2/ALDH4A1/NQO2/NUP93/TRAP1/PGD/SLC4A1/ENPP1/APP/PPP1CB/SEC13/NDUFS3/PKM/ALDOA/GPI/AKR7A2  
## GO:0006119 SNCA/UQCRHL/CYCS/NDUFB6/NDUFB1/NDUFA5/COX6C/NDUFA4/NDUFB8/NDUFA2/UQCR10/COX6A1/NDUFA6/PARK7/NDUFA12/COX5B/CHCHD2/UQCRQ/COX7C/NDUFB5/NDUFB2/SDHD/NDUFA1/NDUFS6/NDUFA9/COX8A/NDUFAB1/NDUFB10/COX7B/NDUFC2-KCTD14/UQCRH/NDUFB4/GHITM/UQCR11/NDUFC1/NDUFA7/CDK1/COX7A2/COX6B1/DLD/DGUOK/NDUFA8/NDUFS5/NDUFS4/NDUFA11/CCNB1/NDUFB11/NDUFB3/COX7A2L/SHMT2/NDUFS1/NDUFS8/NDUFB9/BID/NDUFA3/UQCRB/SDHA/UQCRC1/NDUFV2/NDUFS2/NDUFB7/CYC1/NDUFS7/CHCHD10/COA6/COX4I1/STOML2/MSH2  
## GO:0006120 SNCA/NDUFB6/NDUFB1/NDUFA5/NDUFA4/NDUFB8/NDUFA2/NDUFA6/PARK7/NDUFA12/NDUFB5/NDUFB2/NDUFA1/NDUFS6/NDUFA9/NDUFAB1/NDUFB10/NDUFC2-KCTD14/NDUFB4/NDUFC1/NDUFA7/DLD/NDUFA8/NDUFS5/NDUFS4/NDUFA11/NDUFB11/NDUFB3/NDUFS1/NDUFS8/NDUFB9/NDUFA3/NDUFV2/NDUFS2/NDUFB7/NDUFS7  
## GO:0006414 DPH3P1/MRPS28/MRPL13/MRPS18C/MRPL22/EIF5AL1/SRP9/MRPL47/MRPL39/MRPL42/MRPL27/MRPL18/MRPL20/MRPL11/MRPL33/MRPL40/EEF1A1/MRPL24/MRPS33/MRPL1/MRPL49/EIF5A/MRPL9/CHCHD1/MRPL2/MRPS17/MRPS10/MRPL19/MRPL50/MRPL23/MRPL54/MRPS14/MRPS22/MRPL16/MRPS23/MRPL41/MRPL3/MRPL15/MRPS24/MRPS11/MRPL37/MRPL32/RPL30/MRPL45/MRPL36/MRPL55/MRPS18A/MRPL17/MRPS18B/MRPS9/MRPL46/MRPL28/MRPL52/EEF1A2/AURKAIP1/TRNAU1AP/MRPL48/MRPL35/MRPL30/MRPS21/TSFM/MRPS35/DAP3/GADD45GIP1/DPH5/MRPS15/OXA1L/MRPL51/MRPS16/MRPS31/MRPS36/GFM1/USP16/MRPL34/EIF4A3/MRPL14/MRPS7/MRPS12/DIO2/DPH2/MRPL53/MRPS26/MRPL4/DNAJC24/DPH3/MRPS34/MRPS27/ERAL1/MRPL21  
## GO:0006415 MRPS28/MRPL13/MRPS18C/MRPL22/EIF5AL1/MRPL47/MRPL39/MRPL42/MRPL27/MRPL18/MRPL20/MRPL11/MRPL33/MRPL40/MRPL24/MRPS33/MRPL1/MRPL49/EIF5A/MRPL9/CHCHD1/MRPL2/MRPS17/MRPS10/MRPL19/MRPL50/MRPL23/MRPL54/MRPS14/MRPS22/MRPL16/MRPS23/MRPL41/MRPL3/MRPL15/MRPS24/MRPS11/MRPL37/ABCE1/MRPL32/GFM2/N6AMT1/MRPL45/MRPL36/MRPL55/TRMT112/MRPS18A/MRPL17/MRPS18B/MRPS9/MRPL46/OGFOD1/MRPL28/MRPL52/AURKAIP1/MRPL48/MRPL35/MRPL30/MRPS21/APEH/MRPS35/DAP3/GADD45GIP1/MRPS15/OXA1L/MRPL51/MRPS16/MRPS31/MRPS36/MRPL34/MRPL14/MRPS7/MRPS12  
## GO:0006457 PPIAL4G/PPIAL4D/UNC45B/HSPA1A/PFDN4/GNAT1/B2M/PPIL3/CALR/PFDN2/HSP90B1/PRDX4/VBP1/HSP90AA1/PDIA6/MPDU1/CWC27/PPIH/HSPA1L/HSP90AB1/PDCL3/PPIA/GANAB/GNB3/PSMC1/ERP44/PDIA3/TTC1/FKBP1A/PPIB/QSOX1/HSPA8/DNAJC19/CCT8/DNAJB8/CANX/HSPB6/PFDN1/HSPA2/GRN/CRYAB/MLEC/CCT2/GNAI3/ERP27/RUVBL2/GRPEL1/CD74/DNAJA1/FKBP1B/PPIAL4F/HSPD1/HSPA13/MKKS/HSPB1/HSPBP1/HSP90B2P/ATF6/PDCD5/CCT5/PPIC/CLU/LMAN1/AHSA1/HSP90AB4P/GNB4/PRKCSH/PDIA4/PPID/TBCA/NUDCD2/TRAP1/PPIE/UNC45A/TCP1/RAD23B/DNAJC10/LMAN2L/HSPH1/HSPA5/ERP29/NUDC/FKBP8/DNLZ/PDIA5/CCT3/GNAI2/CCT7/PTGES3/TBCE/DERL1/FKBP5/CHCHD4/CCT4/BAG2/ZMYND10/FKBP4/DNAJB6/DNAJC7/VCP/CCT6A/PFDN5/SDF2L1/HSPA9/DNAJB11/SDF2/PPIF/DFFA/DNAJC24/UGGT1/CCT6B/PDIA2/GNB1/RP2/PDRG1/SGTB/TOR1A/HSPA1B/ST13P4/CHORDC1/CSNK2A1/WFS1/SIL1/ALG12/DNAJC3/GNAT2/PPIL1

#### Dot Plot

dotplot(go\_res, showCategory=10)

 #### CNet Plot

cnetplot(go\_res, node\_label="category",   
 cex\_label\_category = 1.2)



For the gene ontology using clusterProfiler we looked at the biological processes domain. Many of the genes that are being expressed are related to the immune response.

### clustProfiler Disease Ontology