Full\_analysisx8\_aug2020.R

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2020-08-19

# Meta Deg manuscript ###  
# 13APR2020, v2 to remove Smillie parts; reorganize to show meta with singles  
# 1MAY2020, got list of datasets and sample from KULeuven. a lot of overlap in GSE16879, GSE59071, GSE73661  
# 15May2020, fix symbols to remove any ///  
# can only use 1 set because controls used completely overlap (12 in GSE73661 contain 11 from GES59071, 6 in GSE16879   
# are in the 11 and 12 from other). Cannot use same samples as it messes up variance estimate of controls (GY message)  
# will use only GSE73661  
# 17JUNE2020- x10, remove GSE42911 because ages <18  
# 10July2020 drop GSE22619- some uninflamed  
# 11July202- remove ileal sample from 97012  
# 4Aug2020-add sample size plot  
#13Aug2020-remove GSE97012- ibd and non-ibd were processed separatly acc to methods- probable reason for so many deg  
  
rm(list=ls())  
require(limma);require(Biobase);require(BiocGenerics);require(ggplot2)

## Loading required package: limma

## Loading required package: Biobase

## 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 object is masked from 'package:limma':  
##   
## plotMA

## 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, which.max, which.min

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

## Loading required package: ggplot2

wd= setwd('C:\\Users/bryan.linggi/Box Sync/PMED\_Data(bryan.linggi@robartsinc.com 2)/Projects/')  
source('C:/Users/bryan.linggi/Box Sync/PMED\_Data(bryan.linggi@robartsinc.com 2)/Code\_General/DEGfunctions\_v01.R')  
#load previous run  
  
  
# # include methods like descriptions   
# & We performed a search in NCBI Gene expressed Omnibus (GEO) for microarray datasets using the search terms[ (((ulcerative colitis) AND "Homo sapiens"[porgn] AND "gse"[Filter])) AND (((("expression profiling by array"[dataSet Type]))) AND "gse"[Filter]) AND ("gse"[Filter])]   
# & which resulted in 85 datasets. We excluded datasets that did not contain normal and uc patients,those only containing onlyediatric patietns, < 10 total samples, was uninflamed samples only, or those that were from the same cohort, or those that did not contain data in intesity values (exclude thoset that have been Z transformed), resulting in 14 datasets.  
# & Each dataset was dowloaded from GEO using GEOquery to create and ExpressionSet containing the intensity values, phenotype data (metadata), and gene feature information. datasets were already normalized and log2 transformed, with the exception of GSE97012, which was   
#... quantile normalized, and GSE16879, with was log2 transormed  
# genes were annotated in R using the annotation databases indicated in the GEO description. All probesets were retained (did not exclude those without gene symbols) with the execption of GSE97012, in which we removed genes with PREDICTED or Unknown or Control != 0)  
  
# Get DEG datasets, output from DEGout codes#####  
#gse16=readRDS('GSE16879/Output/GSE16879\_coloncontrol\_DEG.rds')#redid 23mar2020 to include all probes, (before had removed na symbol, but had not done same in other datasets)  
#gse22= readRDS('GSE22619/Output/GSE22619\_DEG.RDS')  
gse38=readRDS('GSE38713/Output/GSE38713\_DEG.rds')  
#gse59=readRDS('GSE59071/Output/GSE59071\_DEG.RDS')  
gse73=readRDS('GSE73661/Output/GSE73661\_DEG.rds')  
gse87=readRDS('GSE87466/Output/GSE87466\_DEG.RDS')  
gse9452=readRDS('GSE9452/Output/GSE9452\_DEG.RDS')  
#gse97=readRDS('GSE97012/Output/GSE97012\_DEG\_noIleum.rds')  
gse53=readRDS('GSE53306/Output/GSE53306\_DEGrds')  
#gse48=readRDS('GSE48634/Output/GSE48634\_DEGrds')#uninflamed  
gse47=readRDS('GSE47908/Output/GSE47908\_DEGrds')  
#gse42=readRDS('GSE42911/Output/GSE42911\_DEGrds')  
#gse36=readRDS('GSE36807/Output/GSE36807\_DEGrds') # is uninflamed acc to paper  
gse133= readRDS('GSE13367/Output/GSE13367\_DEGrds')  
gse114=readRDS('GSE114527/Output/GSE114527\_DEGrds')# , is agilent, cant get in in , tried a lot, # is illumina looks ok as geo download 23mar2020  
  
  
# R: 10 datasets matched the search criteria . below is NOT updated to 10 samples  
#...  
###note , check the above to gse files to make sure didnt drop anything in cleaning-done  
  
  
# #gse105= readRDS('GSE105074/Output/GSE105074\_DEG\_rect\_rcrds')# is uninflamed, do not use  
#   
#   
par(mfrow=c(1,1))  
gse=list( 'GSE13367'=gse133,# 11 datasets  
 'GSE9452'= gse9452,  
   
 # 'GSE22619'=gse22,  
 'GSE53306'=gse53,  
 'GSE38713'=gse38,  
 'GSE47908'=gse47,   
 # 'GSE42911'=gse42,  
   
 # 'GSE97012'=gse97,  
 'GSE73661'=gse73,  
 'GSE114527'=gse114,  
 'GSE87466'=gse87 )  
   
  
  
# # # NOTE: GSE105074, GSE48634 is uninflamed, removed from V9 to get GSE14  
# # #  
# saveRDS(gse,'../MetaProjects/MetaDEG\_v01/Output/GSE14.rds')  
  
#gse=readRDS('../MetaProjects/MetaDEG\_v01/Output/GSE14.rds')# get saved 14 datasets (has toptable, topconfect output, and pdata in each list) (saved previously as list)  
require(data.table)

## Loading required package: data.table

gsett=sapply(gse, function(x) (x$toptable) )#   
sapply(gse,function(x) colnames(x$toptable))

## $GSE13367  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE9452  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE53306  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE38713  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE47908  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE73661  
## [1] "featureData.ds..PROBEID" "featureData.ds..SYMBOL"   
## [3] "logFC" "CI.L"   
## [5] "CI.R" "AveExpr"   
## [7] "t" "P.Value"   
## [9] "adj.P.Val" "B"   
## [11] "Cd"   
##   
## $GSE114527  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE87466  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"

for (j in 1:length(gsett)){  
 colnames(gsett[[j]])[grep('symbol',tolower(colnames(gsett[[j]])))]='SYMBOL'}  
  
# Info on datasets#####  
pdata= print(sapply(gse,function(x) summary(pData(x$input))))#used either Disease or INDC, use this to create summary table

## $GSE13367  
## INDC INFLSTS LOC ANTREG SPEC VISIT   
## Normal:10 Inflamed : 8 Unknown:18 Colon:18 RNA:18 NA's:18   
## UC : 8 Uninflamed: 0   
## NA's :10   
##   
##   
##   
##   
## SUBJID PROJ   
## GSM337490: 1 GSE13367:18   
## GSM337492: 1   
## GSM337494: 1   
## GSM337495: 1   
## GSM337496: 1   
## GSM337498: 1   
## (Other) :12   
##   
## $GSE9452  
## Description Disease Segment INFLSTS   
## colonic\_mucosa\_inflamation\_119:1 Normal:5 Colon :3 Inflamed :8   
## colonic\_mucosa\_inflamation\_125:1 UC :8 Left Colon:8 Normal :5   
## colonic\_mucosa\_inflamation\_76 :1 Sigmoid :2 Uninflamed:0   
## colonic\_mucosa\_inflamation\_93 :1   
## colonic\_mucosa\_inflamation\_94 :1   
## colonic\_mucosa\_inflamation\_95 :1   
## (Other) :7   
##   
## $GSE53306  
## SUBJID VISIT INDC LOC ANTREG SPEC   
## 1 : 1 PostRelapse: 0 Normal:12 Unknown:24 Colon:24 RNA:24   
## 2 : 1 Remission : 0 UC :12   
## 4 : 1 Screening :12   
## 5 : 1 NA's :12   
## 6 : 1   
## (Other): 7   
## NA's :12   
## PROJ   
## GSE53306:24   
##   
##   
##   
##   
##   
##   
##   
## $GSE38713  
## Description SampleID DiseaseActivity DiseaseLocation  
## b105 : 1 GSM948550: 1 Active:15 -- :13   
## b106 : 1 GSM948551: 1 Normal:13 Left-sided colitis: 8   
## B137+ : 1 GSM948552: 1 Pancolitis : 7   
## b138 : 1 GSM948553: 1   
## b143 : 1 GSM948554: 1   
## b146 : 1 GSM948555: 1   
## (Other):22 (Other) :22   
## evolutiontime gender treatment   
## -- :13 female:19 -- :13   
## 7 : 3 male : 9 5-ASA : 4   
## 0 : 2 Azathioprine : 8   
## 13 : 2 No treatment : 2   
## 3 : 2 Systemic steroids: 1   
## 1 : 1   
## (Other): 5   
## long   
## Human colon biopsies from non-inflammatory control :13   
## Human colon biopsies from UC patient in remission (involved mucosa) : 0   
## Human colon biopsies from UC patient with active disease (involved mucosa) :15   
## Human colon biopsies from UC patient with active disease (non-involved mucosa): 0   
##   
##   
##   
## InflammationStatus Disease Project   
## Inflamed :15 Active:15 Length:28   
## Normal :13 Normal:13 Class :character   
## Uninflamed: 0 Mode :character   
##   
##   
##   
##   
##   
## $GSE47908  
## INDC DISLOC LOC ANTREG SPEC   
## Normal :15 Left :20 Left Colon:54 Colon:54 RNA:54   
## UC :39 Normal :15   
## UCwithDysplasia: 0 Pancolitis:19   
##   
##   
##   
##   
## VISIT SUBJID PROJ   
## NA:54 GSM1162227: 1 GSE47908:54   
## GSM1162228: 1   
## GSM1162229: 1   
## GSM1162230: 1   
## GSM1162231: 1   
## GSM1162232: 1   
## (Other) :48   
##   
## $GSE73661  
## title Treatment mayoendosubscore Subject   
## Bp069\_Active UC W0\_IFX\_43: 1 CO :12 0 : 0 7 : 2   
## Bp073\_Control\_2 : 1 IFX :23 1 : 0 1 : 1   
## Bp075\_Control\_3 : 1 plac\_plac: 3 2 :21 10 : 1   
## Bp076\_Control\_4 : 1 vdz\_plac : 4 3 :46 11 : 1   
## Bp077\_Control\_7 : 1 vdz\_vdz4w:20 CO:12 12 : 1   
## Bp079\_Active UC W0\_IFX\_5 : 1 vdz\_vdz8w: 4 13 : 1   
## (Other) :73 vdz4w :13 (Other):72   
## Tissue Visit Response4\_6\_52 Treatment2  
## colonic mucosal biopsy:79 W0 :67 :14 control :12   
## CO :12 NR:40 inflx :23   
## W10 : 0 R :25 placebo : 3   
## W12 : 0 vedo :37   
## W14 : 0 vedo-plac: 4   
## W16 : 0   
## (Other): 0   
## Disease Response\_visit Response\_Vedo\_WK6 Response\_Vedo\_WK12  
## Length:79 Length:79 Mode :logical Mode :logical   
## Class :character Class :character FALSE:73 FALSE:76   
## Mode :character Mode :character TRUE :6 TRUE :3   
##   
##   
##   
##   
## Response\_Vedo\_WK52  
## Mode :logical   
## FALSE:66   
## TRUE :13   
##   
##   
##   
##   
##   
## $GSE114527  
## tissue:ch1 INDC LOC ANTREG SPEC VISIT   
## intestine:21 Normal: 6 Rectum:21 Colon:21 RNA:21 Day0:15   
## UC :15 Day3: 0   
## NA's: 6   
##   
##   
##   
##   
## SUBJID PROJ TRT RESP RESPTYP   
## GSM3143535: 1 GSE114527:21 Glucocorticoids:15 N :6 Unknown:21   
## GSM3143536: 1 Normal : 6 Y :9   
## GSM3143537: 1 NA's:6   
## GSM3143538: 1   
## GSM3143539: 1   
## GSM3143543: 1   
## (Other) :15   
##   
## $GSE87466  
## Description Disease DiseaseExtent Segment   
## 1014 : 1 Normal:21 -- :21 Colon:108   
## 1015 : 1 UC :87 Extensive:27   
## 1016 : 1 Limited :60   
## 1017 : 1   
## 1019 : 1   
## 1020 : 1   
## (Other):102

fdata= print(sapply(gse,function(x) summary(fData(x$input))))#

## $GSE13367  
## PROBEID ENTREZID SYMBOL   
## 1007\_s\_at: 1 10730 : 26 YME1L1 : 26   
## 1053\_at : 1 3514 : 19 IGKC : 19   
## 117\_at : 1 3077 : 15 HFE : 15   
## 121\_at : 1 3500 : 15 IGHG1 : 15   
## 1255\_g\_at: 1 3493 : 14 CFLAR : 14   
## 1294\_at : 1 (Other):44252 (Other):44252   
## (Other) :54669 NA's :10334 NA's :10334   
## GENENAME   
## YME1 like 1 ATPase : 26   
## immunoglobulin kappa constant : 19   
## homeostatic iron regulator : 15   
## immunoglobulin heavy constant gamma 1 (G1m marker): 15   
## CASP8 and FADD like apoptosis regulator : 14   
## (Other) :44252   
## NA's :10334   
##   
## $GSE9452  
## PROBEID ENTREZID SYMBOL   
## 1007\_s\_at: 1 10730 : 26 YME1L1 : 26   
## 1053\_at : 1 3514 : 19 IGKC : 19   
## 117\_at : 1 3077 : 15 HFE : 15   
## 121\_at : 1 3500 : 15 IGHG1 : 15   
## 1255\_g\_at: 1 3493 : 14 CFLAR : 14   
## 1294\_at : 1 (Other):44252 (Other):44252   
## (Other) :54669 NA's :10334 NA's :10334   
## GENENAME   
## YME1 like 1 ATPase : 26   
## immunoglobulin kappa constant : 19   
## homeostatic iron regulator : 15   
## immunoglobulin heavy constant gamma 1 (G1m marker): 15   
## CASP8 and FADD like apoptosis regulator : 14   
## (Other) :44252   
## NA's :10334   
##   
## $GSE53306  
## PROBEID ENTREZID SYMBOL   
## ILMN\_1343291: 1 2543 : 9 GAGE1 : 9   
## ILMN\_1651209: 1 5339 : 8 PLEC : 8   
## ILMN\_1651228: 1 1756 : 7 DMD : 7   
## ILMN\_1651229: 1 54768 : 7 HYDIN : 7   
## ILMN\_1651235: 1 5733 : 7 PTGER3 : 7   
## ILMN\_1651236: 1 (Other):25842 (Other):25842   
## (Other) :26452 NA's : 578 NA's : 578   
## GENENAME   
## G antigen 1 : 9   
## family with sequence similarity 86, member A pseudogene: 8   
## plectin : 8   
## dystrophin : 7   
## HYDIN axonemal central pair apparatus protein : 7   
## (Other) :25841   
## NA's : 578   
##   
## $GSE38713  
## PROBEID ENTREZID SYMBOL   
## 1007\_s\_at: 1 10730 : 26 YME1L1 : 26   
## 1053\_at : 1 3514 : 19 IGKC : 19   
## 117\_at : 1 3077 : 15 HFE : 15   
## 121\_at : 1 3500 : 15 IGHG1 : 15   
## 1255\_g\_at: 1 3493 : 14 CFLAR : 14   
## 1294\_at : 1 (Other):44252 (Other):44252   
## (Other) :54669 NA's :10334 NA's :10334   
## GENENAME   
## YME1 like 1 ATPase : 26   
## immunoglobulin kappa constant : 19   
## homeostatic iron regulator : 15   
## immunoglobulin heavy constant gamma 1 (G1m marker): 15   
## CASP8 and FADD like apoptosis regulator : 14   
## (Other) :44252   
## NA's :10334   
##   
## $GSE47908  
## PROBEID ENTREZID SYMBOL   
## 1007\_s\_at: 1 10730 : 26 YME1L1 : 26   
## 1053\_at : 1 3514 : 19 IGKC : 19   
## 117\_at : 1 3077 : 15 HFE : 15   
## 121\_at : 1 3500 : 15 IGHG1 : 15   
## 1255\_g\_at: 1 3493 : 14 CFLAR : 14   
## 1294\_at : 1 (Other):44252 (Other):44252   
## (Other) :54669 NA's :10334 NA's :10334   
## GENENAME   
## YME1 like 1 ATPase : 26   
## immunoglobulin kappa constant : 19   
## homeostatic iron regulator : 15   
## immunoglobulin heavy constant gamma 1 (G1m marker): 15   
## CASP8 and FADD like apoptosis regulator : 14   
## (Other) :44252   
## NA's :10334   
##   
## $GSE73661  
## featureData.ds..PROBEID featureData.ds..SYMBOL  
## 7896738: 1 LINC00965: 26   
## 7896740: 1 LOC728323: 15   
## 7896742: 1 DUX4 : 12   
## 7896744: 1 CT47A10 : 11   
## 7896746: 1 RNU2-1 : 11   
## 7896748: 1 GUSBP2 : 10   
## (Other):25287 (Other) :25208   
##   
## $GSE114527  
## PROBEID ENTREZID SYMBOL   
## ILMN\_1343291: 1 2543 : 14 GAGE1 : 14   
## ILMN\_1651209: 1 54768 : 10 HYDIN : 10   
## ILMN\_1651228: 1 1756 : 8 DMD : 8   
## ILMN\_1651229: 1 5339 : 8 PLEC : 8   
## ILMN\_1651235: 1 143162 : 7 BDNF : 7   
## ILMN\_1651236: 1 (Other):28539 (Other):28539   
## (Other) :29371 NA's : 791 NA's : 791   
## GENENAME   
## G antigen 1 : 14   
## HYDIN axonemal central pair apparatus protein : 10   
## dystrophin : 8   
## family with sequence similarity 86, member A pseudogene: 8   
## plectin : 8   
## (Other) :28538   
## NA's : 791   
##   
## $GSE87466  
## PROBEID ENTREZID SYMBOL   
## 1007\_s\_at: 1 10730 : 26 YME1L1 : 26   
## 1053\_at : 1 3514 : 19 IGKC : 19   
## 117\_at : 1 3077 : 15 HFE : 15   
## 121\_at : 1 3500 : 15 IGHG1 : 15   
## 1255\_g\_at: 1 3493 : 14 CFLAR : 14   
## 1294\_at : 1 (Other):44252 (Other):44252   
## (Other) :54709 NA's :10374 NA's :10374   
## GENENAME   
## YME1 like 1 ATPase : 26   
## immunoglobulin kappa constant : 19   
## homeostatic iron regulator : 15   
## immunoglobulin heavy constant gamma 1 (G1m marker): 15   
## CASP8 and FADD like apoptosis regulator : 14   
## (Other) :44252   
## NA's :10374

adata= print(sapply(gse,function(x) annotation(x$input)))#

## $GSE13367  
## character(0)  
##   
## $GSE9452  
## character(0)  
##   
## $GSE53306  
## character(0)  
##   
## $GSE38713  
## character(0)  
##   
## $GSE47908  
## character(0)  
##   
## $GSE73661  
## [1] "hugene10sttranscriptcluster.db"  
##   
## $GSE114527  
## character(0)  
##   
## $GSE87466  
## [1] "hgu133plus2.db"

# length(unique(fData(gse$GSE97012$input)$SYMBOL))/ length((fData(gse$GSE97012$input)$SYMBOL))  
 # length(unique(fData(gse$GSE16879$input)$SYMBOL))/ length((fData(gse$GSE16879$input)$SYMBOL))  
 length(unique(fData(gse$GSE38713$input)$SYMBOL))/ length((fData(gse$GSE38713$input)$SYMBOL))

## [1] 0.3836305

# length(unique(fData(gse$GSE22619$input)$SYMBOL))/ length((fData(gse$GSE22619$input)$SYMBOL))  
   
 # length(intersect(fData(gse$GSE97012$input)$SYMBOL, fData(gse$GSE16879$input)$SYMBOL))  
 #length(setdiff(fData(gse$GSE97012$input)$SYMBOL, fData(gse$GSE16879$input)$SYMBOL))  
# length(setdiff(fData(gse$GSE16879$input)$SYMBOL,fData(gse$GSE97012$input)$SYMBOL))  
   
# compare 97012 to other  
 # deg97=gsett$GSE97012$SYMBOL[gsett$GSE97012$adj.P.Val<.05 & abs(gsett$GSE97012$logFC) > log2(1.5)]  
 # #deg16=gsett$GSE16879$SYMBOL[gsett$GSE16879$adj.P.Val<.05 & abs(gsett$GSE16879$logFC) > log2(1.5)]  
 # #ength(deg16)#7986  
 # length(intersect(deg97,deg16))#3147  
 # length(setdiff(deg97,deg16))#14048  
 # length(setdiff(deg16,deg97))#2023  
# pdata= print(sapply(gse,function(x) summary(x$input@phenodata$INDC)))  
# td= print(summary(pdata(gse$GSE73661$input))) # this one is comparintg on visit not disease  
  
  
  
# Volcano plots####  
#& volcano plots were produced with the R package 'EnhancedVolcano'  
require('EnhancedVolcano')

## Loading required package: EnhancedVolcano

## Loading required package: ggrepel

runit=T # to suppress printing  
  
if (runit){  
for (i in 1:length(gse)){  
dev.new()  
res1=gse[[i]]$toptable  
symix=grep('symbol',tolower(colnames(res1)))  
pl=EnhancedVolcano(res1,  
 lab = res1[,symix],  
 x = 'logFC',  
 y = 'P.Value',  
 xlim = c(-5, 8), title = names(gse)[[i]],subtitle = '')  
print(pl)  
}  
}  
i=8  
# Enrichment on individ, using toptable ####  
 #& Gene set enrichment analysis was performed with the Reactome Pathways database (reactome.org) using the the R packages  
 #... ReactomePA and clusterProfiler using genes that have abs(log2(FC) > 1.5 and adjusted pvalue (benjamini) < .05  
 # options\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  
lfc=log2(1.5)  
apv= .05  
 # \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  
  
 enrupTt= vector(mode = "list", length = length(gse))  
 enrdownTt=vector(mode = "list", length = length(gse))  
 #k=1  
 require(dplyr)

## Loading required package: dplyr

##   
## Attaching package: 'dplyr'

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

## The following object is masked from 'package:Biobase':  
##   
## combine

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

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

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

for (k in 1:length(gse)){  
 res1 =gse[[k]]$toptable  
 symix= grep('symbol',tolower(colnames(res1)))  
 apvix= grep('adj', tolower(colnames(res1)))  
 lfcix= grep('logfc' ,tolower(colnames(res1)))  
  
 ixfcup= res1[,lfcix] > lfc  
 ixfcdown= res1[,lfcix] < -lfc  
 ixp= res1[,apvix] < apv  
   
 if ( sum(ixfcup & ixp) >0 ){  
 enrupTt[[k]]= enrichuniv( res1[ ixfcup & ixp, symix],univ=res1[,symix] )  
 #tp=enrupTt[[k]][1:10,]  
 require(ggplot2)  
 # p= ggplot(tp, aes(x=reorder(Description,p.adjust), y=-log10(p.adjust)))+geom\_col()+  
 # theme(axis.text.x = element\_text(face="bold", color="993333",  
 # size=6, angle=45,vjust = 1, hjust=1))+ggtitle(paste('Up;', names(gse)[k]))  
 # plot(p)  
  
 enrdownTt[[k]]=enrichuniv(res1[ ixfcdown & ixp, symix],univ=res1[,symix] )  
 tp= enrdownTt[[k]][1:10,]  
 # q=ggplot(tp, aes(x=reorder(Description,p.adjust), y=-log10(p.adjust)))+geom\_col()+  
 # theme(axis.text.x = element\_text(face="bold", color="993333",  
 # size=6, angle=45,vjust = 1, hjust=1))+ggtitle(paste('Down;', names(gse)[k]))  
 # plot(q)  
 }}

## Loading required package: ReactomePA

##

## Registered S3 method overwritten by 'enrichplot':  
## method from  
## fortify.enrichResult DOSE

## ReactomePA v1.28.0 For help: https://guangchuangyu.github.io/ReactomePA  
##   
## If you use ReactomePA in published research, please cite:  
## Guangchuang Yu, Qing-Yu He. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. Molecular BioSystems 2016, 12(2):477-479

## Loading required package: clusterProfiler

## clusterProfiler v3.12.0 For help: https://guangchuangyu.github.io/software/clusterProfiler  
##   
## If you use clusterProfiler in published research, please cite:  
## Guangchuang Yu, Li-Gen Wang, Yanyan Han, Qing-Yu He. clusterProfiler: an R package for comparing biological themes among gene clusters. OMICS: A Journal of Integrative Biology. 2012, 16(5):284-287.

## Loading required package: org.Hs.eg.db

## Loading required package: AnnotationDbi

## Loading required package: stats4

## Loading required package: IRanges

## Loading required package: S4Vectors

##   
## 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 object is masked from 'package:base':  
##   
## expand.grid

##   
## Attaching package: 'IRanges'

## 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

##   
## Attaching package: 'AnnotationDbi'

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

##

#plot together  
# Compile up and down enriched pathways for individual into single table  
 #for Up  
 require(plyr)

## Loading required package: plyr

## ------------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.  
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:  
## library(plyr); library(dplyr)

## ------------------------------------------------------------------------------

##   
## Attaching package: 'plyr'

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

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

## The following objects are masked from 'package:dplyr':  
##   
## arrange, count, desc, failwith, id, mutate, rename, summarise,  
## summarize

a= sapply(enrupTt, length)  
 ix=which(a!=0)# some with 0, need to skip  
 enrupTt2 = enrupTt[ix]#  
 names(enrupTt2)=names(gse)[ix]#  
 allenrTtup = Reduce(function(x,y) merge(x,y,all.x=T,all.y=T,by='Description'),enrupTt2)

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in  
## the result  
  
## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in  
## the result

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in the result  
  
## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in the result

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x', 'GeneRatio.x', 'BgRatio.x',  
## 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y',  
## 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y',  
## 'Count.y' are duplicated in the result

allenrupTtsmall= allenrTtup[,c(1,grep('p.adjust',tolower(colnames(allenrTtup))))]  
 colnames(allenrupTtsmall)[2:ncol(allenrupTtsmall)]= names(gse)[ix]#  
 # feed above into plotting after adding meta results  
#   
# a=lapply(enrupTt2,function(x) x$Description[1:3])# get top x enr  
# b=unique(unlist((a))) # combine   
# c=allenrupTtsmall[allenrupTtsmall$Description %in% b,]  
# c$Mean=apply(c[,2:12],MARGIN = 1,function(x) mean(x, na.rm=T))  
#   
#   
# require(reshape2)  
# mc=melt(c)  
# # ggplot(mc, aes(x=Description,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
# # theme(axis.text.x = element\_text(  
# # color='black',size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Up')+facet\_grid(~variable)  
#   
# ggplot(mc, aes(x=variable,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
# theme(axis.text.x = element\_text(  
# color='black',size=10, angle=90,vjust = 1, hjust=1))+ggtitle('Up DEG')+facet\_wrap(~Description)+theme( strip.text.x = element\_text(  
# size = 12, color='black' ) )  
   
   
 # ggplot(mc, aes(x=variable,y=-log10(value), fill=(Description))) +geom\_bar(position = 'dodge',stat='identity')+  
 # theme(axis.text.x = element\_text(  
 # color="black",size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Up')  
 #   
 #down enriched   
 # rm(mc)  
 a=sapply(enrdownTt, length)  
 ix=which(a!=0)# some with 0, need to skip  
 enrTt2=enrdownTt[ix]#  
 names(enrTt2)=names(gse)[ix]#  
 allenrTt = Reduce(function(x,y) merge(x,y,all.x=T,all.y=T,by='Description'),enrTt2)

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in  
## the result

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in  
## the result

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in the result  
  
## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y' are duplicated in the result

## Warning in merge.data.frame(x, y, all.x = T, all.y = T, by = "Description"):  
## column names 'ID.x', 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x',  
## 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y',  
## 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x',  
## 'GeneRatio.x', 'BgRatio.x', 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x',  
## 'Count.x', 'ID.y', 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y',  
## 'qvalue.y', 'geneID.y', 'Count.y', 'ID.x', 'GeneRatio.x', 'BgRatio.x',  
## 'pvalue.x', 'p.adjust.x', 'qvalue.x', 'geneID.x', 'Count.x', 'ID.y',  
## 'GeneRatio.y', 'BgRatio.y', 'pvalue.y', 'p.adjust.y', 'qvalue.y', 'geneID.y',  
## 'Count.y' are duplicated in the result

allenr\_down\_Ttsmall=allenrTt[,c(1,grep('p.adjust',tolower(colnames(allenrTt))))]  
 colnames(allenr\_down\_Ttsmall)[2:ncol(allenr\_down\_Ttsmall)]= names(gse)[ix]#\*\*\*   
 # feed above into plotting after adding meta results  
   
   
#   
# # ggplot(mc, aes(x=Description,y=-log10(value), fill=(variable))) +geom\_bar(position = 'dodge',stat='identity')+theme\_linedraw()+  
# # theme(axis.text.x = element\_text(  
# # color='black',size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Down')  
# ggplot(mc, aes(x=variable,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
# theme(axis.text.x = element\_text(  
# color='black',size=10, angle=90,vjust = 1, hjust=1))+ggtitle('Down DEG')+facet\_wrap(~Description)+theme( strip.text.x = element\_text(  
# size = 8, color='black' ) )  
#   
#   
# # ggplot(mc, aes(x=variable,y=-log10(value), fill=(Description))) +geom\_bar(position = 'dodge',stat='identity')+  
# # theme(axis.text.x = element\_text(  
# # color="black",size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Down')  
#   
#   
#   
# # Run Meta Deg ######  
#check colnames  
sapply(gse,function(x) colnames(x$toptable))

## $GSE13367  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE9452  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE53306  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE38713  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE47908  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE73661  
## [1] "featureData.ds..PROBEID" "featureData.ds..SYMBOL"   
## [3] "logFC" "CI.L"   
## [5] "CI.R" "AveExpr"   
## [7] "t" "P.Value"   
## [9] "adj.P.Val" "B"   
## [11] "Cd"   
##   
## $GSE114527  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE87466  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"

for (j in 1:length(gsett)){  
colnames(gsett[[j]])[grep('symbol',tolower(colnames(gsett[[j]])))]='SYMBOL'  
}  
sapply(gsett,function(x) colnames(x))

## $GSE13367  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE9452  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE53306  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE38713  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE47908  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE73661  
## [1] "featureData.ds..PROBEID" "SYMBOL"   
## [3] "logFC" "CI.L"   
## [5] "CI.R" "AveExpr"   
## [7] "t" "P.Value"   
## [9] "adj.P.Val" "B"   
## [11] "Cd"   
##   
## $GSE114527  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"   
##   
## $GSE87466  
## [1] "PROBEID" "ENTREZID" "SYMBOL" "GENENAME" "logFC" "CI.L"   
## [7] "CI.R" "AveExpr" "t" "P.Value" "adj.P.Val" "B"   
## [13] "Cd"

# ^ 15may change symbols with /// to \_ to allow plotting output  
# also is a '.' SW-CL.36 17may  
  
test='CH /// CH'  
test2=gsub('[ /// ]','\_',test)  
  
for (i in 1:length(gse)){  
#print(gsub(' /// ','\_' ,gsett[[i]]$SYMBOL))  
 gsett[[i]]$SYMBOL= gsub(' /// ','\_' ,gsett[[i]]$SYMBOL)  
 # print(gsub('[.]','\_' ,gsett[[i]]$SYMBOL))  
 gsett[[i]]$SYMBOL= gsub('[.]','\_' ,gsett[[i]]$SYMBOL)  
  
 # print(gsub('[.]','\_' ,gsett[[i]]$SYMBOL))  
 gsett[[i]]$SYMBOL= gsub('[.]','\_' ,gsett[[i]]$SYMBOL)  
 gsett[[i]]$SYMBOL= gsub('[/]','\_' ,gsett[[i]]$SYMBOL)  
   
   
   
   
}  
  
# also is a '.' SW-CL.36  
  
  
  
#TEMP=data.frame(gsett$GSE42911$SYMBOL)  
  
# # & DEG metanalysis was perfomred using the R. Package 'MetavolcanoR' using the paramaters cvar=T, collaps=T (yes, is mispelled in code) , and metathr =0.1  
 pcriteria="P.Value"  
 foldchangecol='logFC'  
 genenamecol1="SYMBOL"  
 geneidcol=NULL  
 collaps=T  
 names(gsett)

## [1] "GSE13367" "GSE9452" "GSE53306" "GSE38713" "GSE47908" "GSE73661"   
## [7] "GSE114527" "GSE87466"

require(MetaVolcanoR)

## Loading required package: MetaVolcanoR

require(metafor)

## Loading required package: metafor

## Loading required package: Matrix

##   
## Attaching package: 'Matrix'

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

## Loading 'metafor' package (version 2.4-0). For an overview   
## and introduction to the package please type: help(metafor).

# meta\_degs\_rem <- rem\_mv(diffexp=gsett,  
# pcriteria=pcriteria,  
# foldchangecol=foldchangecol,  
# genenamecol=genenamecol1,  
# geneidcol=NULL,  
# collaps=T,  
# llcol='CI.L',  
# rlcol='CI.R',  
# vcol = NULL,  
# cvar=T,  
# metathr=0.1,  
# jobname="MetaVolcano",  
# outputfolder=".",  
# draw='HTML',  
# ncores=1)  
  
#saveRDS(meta\_degs\_rem,'C:\\Users/bryan.linggi/Box Sync/PMED\_Data(bryan.linggi@robartsinc.com 2)/MetaProjects/MetaDEG\_v01/Output/mremx8\_aug2020.rds')  
# # # # #load previous run  
meta\_degs\_rem=readRDS('../MetaProjects/MetaDEG\_v01/Output/mremx8\_aug2020.rds')  
  
#result tables  
mr=meta\_degs\_rem@metaresult  
#write.csv(mr,'../MetaProjects/MetaDEG\_v01/Output/mr.csv')  
#& the adjusted p value for meta results was calculated using the r p.adjust function with the parameter ('BH')  
mrinput= meta\_degs\_rem@input  
mr$adjP= p.adjust(mr$randomP,'BH')# add adjusted pvalue to table  
  
  
# Graph DEG from indiv and Meta  
  
# Meta analysisis and diagnositics ####  
sc=.75\*length(gse) # for Sign consistency variable, 8.25 for 11  
pthresh=.05#\*\*\*   
  
mrup= mr[mr$signcon >= sc & mr$adjP < pthresh & mr$randomSummary > log2(1.5),];nrow(mrup)

## [1] 946

mrdown= mr[mr$signcon <= -sc & mr$adjP < pthresh & mr$randomSummary < -log2(1.5),];nrow(mrdown)

## [1] 543

write.csv(mr,'../MetaProjects/MetaDEG\_v01/Output/mremresultx9-noileum.csv',row.names = F)  
summary(mrup)

## SYMBOL signcon randomSummary randomCi.lb   
## Length:946 Min. :6.00 Min. :0.5859 Min. :0.1516   
## Class :character 1st Qu.:8.00 1st Qu.:0.6980 1st Qu.:0.3586   
## Mode :character Median :8.00 Median :0.8574 Median :0.4448   
## Mean :7.65 Mean :1.0018 Mean :0.5335   
## 3rd Qu.:8.00 3rd Qu.:1.0987 3rd Qu.:0.6162   
## Max. :8.00 Max. :4.8627 Max. :2.6455   
## randomCi.ub randomP het\_QE het\_QEp   
## Min. :0.693 Min. :0.000e+00 Min. : 7.493 Min. :0.000000   
## 1st Qu.:1.027 1st Qu.:1.289e-06 1st Qu.: 54.678 1st Qu.:0.000000   
## Median :1.261 Median :2.607e-05 Median : 91.108 Median :0.000000   
## Mean :1.470 Mean :4.382e-04 Mean :112.848 Mean :0.001253   
## 3rd Qu.:1.619 3rd Qu.:2.582e-04 3rd Qu.:143.017 3rd Qu.:0.000000   
## Max. :7.080 Max. :1.305e-02 Max. :973.568 Max. :0.379406   
## het\_QM het\_QMp error rank   
## Min. : 6.163 Min. :0.000e+00 Mode :logical Min. : 12.0   
## 1st Qu.: 13.351 1st Qu.:1.289e-06 FALSE:946 1st Qu.: 548.2   
## Median : 17.685 Median :2.607e-05 Median :1092.5   
## Mean : 19.797 Mean :4.382e-04 Mean :1336.0   
## 3rd Qu.: 23.439 3rd Qu.:2.582e-04 3rd Qu.:1820.2   
## Max. :128.604 Max. :1.305e-02 Max. :7416.0   
## adjP   
## Min. :0.000e+00   
## 1st Qu.:2.224e-05   
## Median :2.519e-04   
## Mean :1.899e-03   
## 3rd Qu.:1.637e-03   
## Max. :3.897e-02

summary(mrdown)

## SYMBOL signcon randomSummary randomCi.lb   
## Length:543 Min. :-8.000 Min. :-4.2732 Min. :-5.7850   
## Class :character 1st Qu.:-8.000 1st Qu.:-1.0164 1st Qu.:-1.4630   
## Mode :character Median :-8.000 Median :-0.7774 Median :-1.1407   
## Mean :-7.737 Mean :-0.8988 Mean :-1.3030   
## 3rd Qu.:-8.000 3rd Qu.:-0.6574 3rd Qu.:-0.9606   
## Max. :-6.000 Max. :-0.5850 Max. :-0.7331   
## randomCi.ub randomP het\_QE het\_QEp   
## Min. :-2.7614 Min. :0.000e+00 Min. : 13.87 Min. :0.0000000   
## 1st Qu.:-0.5553 1st Qu.:2.740e-07 1st Qu.: 62.41 1st Qu.:0.0000000   
## Median :-0.4321 Median :9.526e-06 Median : 96.89 Median :0.0000000   
## Mean :-0.4946 Mean :4.174e-04 Mean :121.78 Mean :0.0002554   
## 3rd Qu.:-0.3527 3rd Qu.:1.581e-04 3rd Qu.:148.61 3rd Qu.:0.0000000   
## Max. :-0.1097 Max. :1.659e-02 Max. :735.16 Max. :0.0534833   
## het\_QM het\_QMp error rank   
## Min. : 5.74 Min. :0.000e+00 Mode :logical Min. : 7   
## 1st Qu.:14.27 1st Qu.:2.740e-07 FALSE:543 1st Qu.: 579   
## Median :19.60 Median :9.526e-06 Median :1044   
## Mean :21.29 Mean :4.174e-04 Mean :1331   
## 3rd Qu.:26.43 3rd Qu.:1.581e-04 3rd Qu.:1744   
## Max. :79.76 Max. :1.659e-02 Max. :9250   
## adjP   
## Min. :0.000e+00   
## 1st Qu.:6.320e-06   
## Median :1.126e-04   
## Mean :1.718e-03   
## 3rd Qu.:1.101e-03   
## Max. :4.718e-02

dput(colnames(mrup))

## c("SYMBOL", "signcon", "randomSummary", "randomCi.lb", "randomCi.ub",   
## "randomP", "het\_QE", "het\_QEp", "het\_QM", "het\_QMp", "error",   
## "rank", "adjP")

write.csv(mrup[1:10,c("SYMBOL", "signcon", "randomSummary", "randomCi.lb", "randomCi.ub",   
 "randomP", "adjP")],'../MetaProjects/MetaDEG\_v01/Output/mrup.csv',row.names = F)  
write.csv(mrdown[1:10,c("SYMBOL", "signcon", "randomSummary", "randomCi.lb", "randomCi.ub",   
 "randomP", "adjP")],'../MetaProjects/MetaDEG\_v01/Output/mrdown.csv',row.names = F)  
  
#if signcon filter not included  
# mrup\_noscfilter =mr[which(mr$adjP < pthresh & mr$randomSummary > log2(1.5)),]  
# mrdown\_noscfilter=mr[which(mr$adjP < pthresh & mr$randomSummary > log2(1.5)),]  
  
#prep meta data to match Smillie cuttoffs  
# lfc= log2(1.5) #log2(1) is 0  
# apv= .05  
# mr2 = mr[abs(mr$signcon)>sc & mr$adjP< pthresh,] # above use 05 for padj, but here trying to match to scrna?   
# mr2up = mr2[mr2$randomSummary > lfc,]  
# mr2down= mr2[mr2$randomSummary< -lfc,]# change this 30mar2020 to match scrna  
  
# done meta   
length(mr$SYMBOL[mr$error==F])

## [1] 27858

length(mrup$SYMBOL[mrup$signcon==length(gse)])

## [1] 760

# length(mrup$SYMBOL[mrup$signcon==12])  
# length(mrup$SYMBOL[mrup$signcon==11])  
  
length(mrdown$SYMBOL[mrdown$signcon==-length(gse)])

## [1] 464

# length(mrdown$SYMBOL[mrdown$signcon==-12])  
# length(mrdown$SYMBOL[mrdown$signcon==-11])  
#\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  
# Stats on individual by tt####  
# input is gse (list of gse lists)  
# output is table of tc deg  
#& Differential gene expression was determine using limma with abs(log2(FC) > 1.5 and adjust pvalue (benjamini) < .05  
lfc= log2(1.5) #log2(1) is 0  
apv= .05  
#  
DEGtable=data.frame(matrix(nrow=length(gsett)))  
unique=T  
for (i in 1:length(gsett)) {  
 In= gsett[[i]]  
 apval= In[which(In$adj.P.Val < apv),]  
 up= apval[which(apval$logFC > lfc ),]  
 down= apval[which(apval$logFC < -lfc ),]  
   
 rownames(DEGtable)[i]=names(gsett[i])  
 colnames(DEGtable)[1]='Up'  
 if (!unique){  
 ifelse( nrow(up) >0,DEGtable$Up [i] <- nrow(up), DEGtable$Up[i] <- 0)  
 ifelse( nrow(down) >0,DEGtable$Down[i] <- nrow(down), DEGtable$Down[i] <- 0)}  
   
 if (unique){  
 ifelse( nrow(up) >0,DEGtable$Up [i] <- length(unique(up$SYMBOL)), DEGtable$Up[i] <- 0)  
 ifelse( nrow(down) >0,DEGtable$Down[i] <- length(unique(down$SYMBOL)), DEGtable$Down[i] <- 0)}  
   
}  
  
  
  
  
summary(DEGtable$Up)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 369.0 489.2 1090.5 1235.1 1822.5 2442.0

summary(DEGtable$Down)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 110.0 383.2 942.0 999.0 1554.2 2098.0

#DEGtable$Sum=DEGtable$Up+DEGtable$Down  
# R Differential gene expression analysis was performed using R limma to compare UC patients to normal control patients, using the same settings to allow comparison acrross dattasets (lfc=log2(1.5), BH apv<.05. there was a wide range of   
  
print(DEGtable) ## fig 1

## Up Down  
## GSE13367 491 110  
## GSE9452 1582 1765  
## GSE53306 484 441  
## GSE38713 2442 2098  
## GSE47908 369 210  
## GSE73661 1688 1338  
## GSE114527 599 546  
## GSE87466 2226 1484

#add meta results  
DEGtable\_wMeta= rbind(DEGtable,c(nrow(mrup),nrow(mrdown)))  
# median(DEGtable$Up)/nrow(mrup)  
# median(DEGtable$Down)/nrow(mrdown)  
  
rownames(DEGtable\_wMeta)[length(gse)+1]='Meta-x8'  
DEGtable\_wMeta$Dataset= rownames(DEGtable\_wMeta)  
require(reshape2)

## Loading required package: reshape2

##   
## Attaching package: 'reshape2'

## The following objects are masked from 'package:data.table':  
##   
## dcast, melt

melt\_deg=melt(DEGtable\_wMeta)

## Using Dataset as id variables

melt\_deg$Dataset = factor(melt\_deg$Dataset,levels =DEGtable\_wMeta$Dataset)  
colnames(melt\_deg)=c('Dataset','Direction','Number')  
  
  
ggplot(melt\_deg, aes(y=Number, x=Dataset,fill=Direction))+geom\_bar(stat='identity')+theme\_light()+  
 theme(axis.text.x = element\_text(  
 color="black",size=10, angle=90,vjust = .5, hjust=1))+ggtitle('DEG')  
  
  
## add sample size vs deg  
DEGtable$Total = DEGtable$Up+DEGtable$Down  
DEGtable$SampleSize=c(18,13,24,28,54,79,21,108)#manually entered  
plot(DEGtable$SampleSize,DEGtable$Total)  
plot(DEGtable$SampleSize,DEGtable$Up)  
plot(DEGtable$SampleSize,DEGtable$Down)  
cor(DEGtable$SampleSize,DEGtable$Total,method = 'spearman')

## [1] 0.2142857

cor(DEGtable$SampleSize,DEGtable$Up,method = 'spearman')

## [1] 0.3095238

cor(DEGtable$SampleSize,DEGtable$Down,method = 'spearman')

## [1] 0.1428571

# #write.csv(DEGtable,'../MetaProjects/MetaDEG\_v01/Output/DEGtable.csv')  
#   
# the volcano plots for the individual datasets are provided in the supp material.   
  
#alculate Cohens D for meta results  
##source of calc, check with stats that this is correc,t using meta N values, but only after meta analysis  
#http://handbook-5-1.cochrane.org/chapter\_7/7\_7\_3\_2\_obtaining\_standard\_deviations\_from\_standard\_errors\_and.htm  
mr\_clean=mr[!is.na(mr$randomSummary),]  
N=524  
#for (i in 1:nrow(mr\_clean)){  
#   
# if (mr\_clean$randomSummary[i] > 0){  
# mr\_clean$Cd[i]=mr\_clean$randomSummary[i]/ abs(sqrt(N)\*(mr\_clean$randomCi.ub[i]-mr\_clean$randomCi.lb[i])/3.92) }  
# if (mr\_clean$randomSummary[i] < 0){  
# mr\_clean$Cd[i]=mr\_clean$randomSummary[i]/ abs(sqrt(N)\*(mr\_clean$randomCi.ub[i]-mr\_clean$randomCi.lb[i])/3.92) }   
#   
# }  
#   
# #test 2^, doesnt work because ci gets very big  
# mr\_clean2=mr[!is.na(mr$randomSummary),]  
# mr\_clean2[,3:5]= 2^mr\_clean2[,3:5]  
#   
# N=524  
# for (i in 1:nrow(mr\_clean2)){  
#   
# if (mr\_clean2$randomSummary[i] > 0){  
# mr\_clean2$Cd[i]=mr\_clean2$randomSummary[i]/ abs(sqrt(N)\*(mr\_clean2$randomCi.ub[i]-mr\_clean2$randomCi.lb[i])/3.92) }  
# if (mr\_clean2$randomSummary[i] < 0){  
# mr\_clean2$Cd[i]=mr\_clean2$randomSummary[i]/ abs(sqrt(N)\*(mr\_clean2$randomCi.ub[i]-mr\_clean2$randomCi.lb[i])/3.92) }   
#   
# }  
mrlfc= mr$randomSummary  
  
#& meta deg genes were retained that were regulated in the same direction in at least 75% of the datasets (at least 10)  
# and log2(1.5) fold change (randomsummary).   
  
#use other volcano plotter  
require(EnhancedVolcano)  
# # all genes!!  
# EnhancedVolcano(mr,  
# lab = mr$SYMBOL,  
# x = 'randomSummary',  
# y = 'adjP',# is the column used   
# xlim = c(-5, 8), title = 'Meta11',subtitle = '',transcriptLabSize = 2,  
# pCutoff = .05,FCcutoff = log2(1.5), drawConnectors = F)  
  
#use other volcano plotter  
require(EnhancedVolcano)  
#genes with signcon filter  
mrsc=mr[abs(mr$signcon)>sc,]  
EnhancedVolcano(mrsc,  
 lab = mrsc$SYMBOL,  
 x = 'randomSummary',  
 y = 'adjP',  
 xlim = c(-4.2, 5),ylim=c(0,25), title = 'Metax8',subtitle = '',transcriptLabSize = 2,  
 pCutoff = .05,FCcutoff = log2(1.5), drawConnectors = F)  
  
mrsc=mr[abs(mr$signcon)>sc,]  
#no y axis limit  
EnhancedVolcano(mrsc,  
 lab = mrsc$SYMBOL,  
 x = 'randomSummary',  
 y = 'adjP',  
 xlim = c(-4.2, 5), title = 'Metax8',subtitle = '',transcriptLabSize = 2,  
 pCutoff = .05,FCcutoff = log2(1.5), drawConnectors = F)  
length(mr$SYMBOL[mr$error=='FALSE'])

## [1] 27858

a=print(sum(abs(mrsc$randomSummary) >log2(1.5) & !mrsc$adjP<.05))# logfc only

## [1] 4

b=print(sum((mrsc$adjP<.05) & !abs(mrsc$randomSummary) >log2(1.5)))# p only

## [1] 3020

c=print(sum(abs(mrsc$randomSummary) >log2(1.5) & mrsc$adjP<.05)) # log and p

## [1] 1280

d=print(sum( abs(mrsc$randomSummary) < log2(1.5) & !mrsc$adjP<.05))# neither

## [1] 113

a+b+c+d

## [1] 4417

#diagnostics  
  
hist( mr$signcon ,breaks = 25)  
hist((mr$randomSummary),breaks = 100)  
hist(-log10(mr$adjP) ,breaks=20000)  
#combo=merge(mrinput,mr)  
  
  
head(mrup,10)

## SYMBOL signcon randomSummary randomCi.lb randomCi.ub randomP het\_QE  
## 12 LCN2 8 3.308605 2.205978 4.411232 4.073577e-09 275.39866  
## 15 DUOXA2 8 3.309076 2.165940 4.452211 1.398444e-08 267.89540  
## 22 PI3 8 2.932324 1.927112 3.937535 1.081325e-08 178.14602  
## 23 CXCL8 8 2.839833 1.879191 3.800476 6.872643e-09 92.98878  
## 37 MMP3 8 3.731084 2.244917 5.217250 8.629127e-07 192.04647  
## 49 REG3A 8 4.211572 2.412897 6.010247 4.448880e-06 200.62997  
## 50 CHI3L1 8 3.595713 2.112534 5.078892 2.018172e-06 356.43356  
## 53 MMP7 8 2.232241 1.459154 3.005328 1.520123e-08 80.08280  
## 56 DUOX2 8 3.648986 2.119876 5.178096 2.908873e-06 306.46967  
## 58 MMP9 8 1.864532 1.268392 2.460673 8.780778e-10 62.48654  
## het\_QEp het\_QM het\_QMp error rank adjP  
## 12 1.075459e-55 34.58825 4.073577e-09 FALSE 12 1.798442e-07  
## 15 4.276972e-54 32.18950 1.398444e-08 FALSE 15 5.159982e-07  
## 22 4.798381e-35 32.68927 1.081325e-08 FALSE 22 4.143544e-07  
## 23 3.007020e-17 33.57052 6.872643e-09 FALSE 23 2.790934e-07  
## 37 5.537815e-38 24.21204 8.629127e-07 FALSE 37 1.603671e-05  
## 49 8.441976e-40 21.06101 4.448880e-06 FALSE 49 6.069388e-05  
## 50 5.168104e-73 22.57767 2.018172e-06 FALSE 50 3.211140e-05  
## 53 1.324975e-14 32.02741 1.520123e-08 FALSE 53 5.535634e-07  
## 56 2.511144e-62 21.87575 2.908873e-06 FALSE 56 4.324193e-05  
## 58 4.803220e-11 37.57848 8.780778e-10 FALSE 58 4.863119e-08

head(mrdown,10)

## SYMBOL signcon randomSummary randomCi.lb randomCi.ub randomP het\_QE  
## 7 AQP8 -8 -4.273211 -5.784976 -2.761446 3.022897e-08 161.29145  
## 11 CLDN8 -8 -3.225811 -4.276521 -2.175100 1.773154e-09 132.32221  
## 21 HMGCS2 -8 -3.014245 -4.055931 -1.972558 1.416431e-08 324.69701  
## 30 UGT2A3 -8 -2.385681 -3.156366 -1.614996 1.302132e-09 157.37488  
## 34 GUCA2B -8 -2.431126 -3.231408 -1.630845 2.615797e-09 68.98257  
## 35 PCK1 -8 -2.858842 -3.891095 -1.826590 5.693910e-08 110.11500  
## 44 TRPM6 -8 -2.113062 -2.795482 -1.430641 1.288091e-09 109.79932  
## 60 CHP2 -8 -2.238064 -3.033353 -1.442775 3.475238e-08 125.80324  
## 81 ANPEP -8 -1.525100 -1.981993 -1.068208 6.056896e-11 31.26082  
## 83 ADH1C -8 -2.099642 -2.869436 -1.329849 8.997911e-08 100.99353  
## het\_QEp het\_QM het\_QMp error rank adjP  
## 7 1.715486e-31 30.69277 3.022897e-08 FALSE 7 9.918948e-07  
## 11 2.055881e-25 36.20828 1.773154e-09 FALSE 11 8.773804e-08  
## 21 3.192878e-66 32.16467 1.416431e-08 FALSE 21 5.205662e-07  
## 30 1.144212e-30 36.81011 1.302132e-09 FALSE 30 6.680440e-08  
## 34 2.371404e-12 35.45076 2.615797e-09 FALSE 34 1.228851e-07  
## 35 8.691592e-21 29.46488 5.693910e-08 FALSE 35 1.701942e-06  
## 44 1.010624e-20 36.83125 1.288091e-09 FALSE 44 6.632836e-08  
## 60 4.726910e-24 30.42222 3.475238e-08 FALSE 60 1.111518e-06  
## 81 5.565073e-05 42.80204 6.056896e-11 FALSE 81 4.807209e-09  
## 83 6.725366e-19 28.57843 8.997911e-08 FALSE 83 2.519234e-06

#playing around   
#other genes without high sigcon?  
#sum(is.na(mrinput[grep(ea,mrinput$SYMBOL),2:53]))>0  
# w\_up= mr[mr$signcon >4 & mr$signcon < 8 & mr$adjP > .9 ,]  
# k=1  
# w\_up2=data.frame(matrix(nrow = 1,ncol = 13))  
# ea=w\_up$SYMBOL[1]  
# ea  
# for (ea in w\_up$SYMBOL){  
# if (sum(is.na(mrinput[grep(ea,mrinput$SYMBOL),2:53]))==0)  
# {  
# w\_up2[k,]= w\_up[w\_up$SYMBOL %in% ea,]  
# w\_up2$SYMBOL[k]=as.character(ea)  
# k=k+1  
# }  
#   
# }  
# #w\_down=mr[mr$signcon >-7 & mr$signcon < -4 ,]  
# require(MetaVolcanoR)  
# for (gene in w\_up2$SYMBOL)  
# {pl=draw\_forest(remres=meta\_degs\_rem,  
# gene=gene,  
# genecol=genenamecol1,  
# foldchangecol=foldchangecol,  
# llcol="CI.L",  
# rlcol="CI.R",  
# jobname="MetaVolcano",  
# outputfolder="../../MetaProjects/MetaDEG\_v01/Output/Forests",  
# draw="PDF")  
# print(pl)}  
#8 plot forests ##  
# & forest plots were created in using the metavolcanor function with a adjusted p value of <0.05 and at least 11 with the same direction  
  
#plot.new();meta\_degs\_rem@MetaVolcano  
pcriteria="P.Value"  
foldchangecol='logFC'  
genenamecol1="SYMBOL"  
getwd()

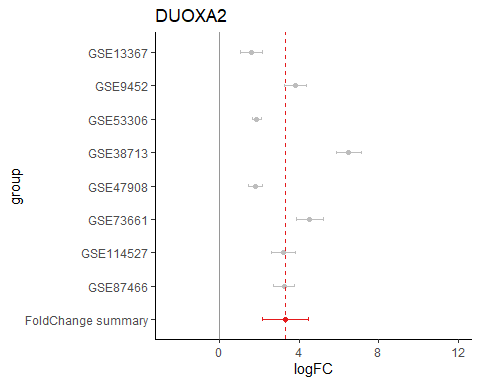
## [1] "C:/Users/bryan.linggi/Box Sync/PMED\_Data(bryan.linggi@robartsinc.com 2)/Projects"

##up  
source('../MetaProjects/MetaDEG\_v01/Code/draw\_forest\_mod.R')  
for (i in 1:2){  
 require(MetaVolcanoR);require(dplyr)  
   
 pl=draw\_forest\_mod(remres=meta\_degs\_rem,  
 gene=mrup$SYMBOL[i],  
 genecol=genenamecol1,  
 foldchangecol=foldchangecol,  
 llcol="CI.L",  
 rlcol="CI.R",  
 jobname="MetaVolcano",  
 outputfolder="../MetaProjects/MetaDEG\_v01/Output/Forests",  
 draw="PDF",xlim=c(-2.5,12))  
 print(pl)  
 print(mrup$SYMBOL[i])  
 #print( min(mrinput[mrinput$SYMBOL %in% mrup$SYMBOL[i], grep('logFC',colnames(mrinput))],na.rm=T))  
   
 print( max(mrinput[mrinput$SYMBOL %in% mrup$SYMBOL[i], grep('logFC',colnames(mrinput))],na.rm=T))  
 print( min(mrinput[mrinput$SYMBOL %in% mrup$SYMBOL[i], grep('logFC',colnames(mrinput))]))  
   
   
}

## [1] "LCN2"  
## [1] 5.425762  
## [1] 1.545532

## [1] "DUOXA2"  
## [1] 6.497016  
## [1] 1.608536

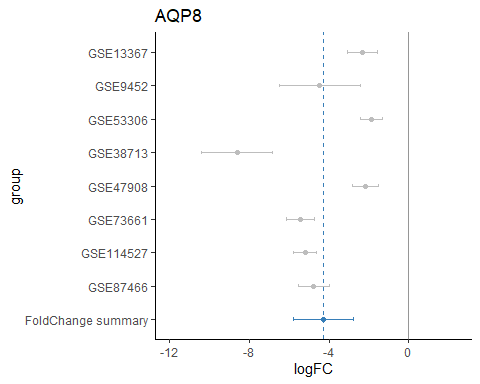
draw\_forest



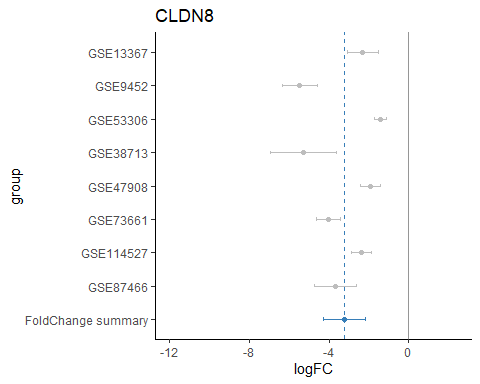
## function (remres, gene = "MMP9", genecol = "Symbol", foldchangecol = "Log2FC",   
## llcol = "CI.L", rlcol = "CI.R", jobname = "MetaVolcano",   
## outputfolder = ".", draw = "PDF")   
## {  
## if (!draw %in% c("PDF", "HTML")) {  
## stop("Oops! Seems like you did not provide a right 'draw' parameter. \n Try 'PDF' or 'HTML'")  
## }  
## if (is(remres) != "MetaVolcano") {  
## stop("Oops! Please, provide a MetaVolcano object as input")  
## }  
## rem <- sremres <- merge(remres@metaresult, remres@input,   
## by = genecol) %>% dplyr::filter(!!rlang::sym(genecol) ==   
## gene)  
## if (nrow(sremres) == 0) {  
## stop(paste("Oops! Seems that", gene, "is not in the",   
## "provided REM result"))  
## }  
## stds <- unique(unlist(regmatches(colnames(sremres), regexec("\_\\d+$",   
## colnames(sremres)))))  
## if (is.null(remres@inputnames)) {  
## message("We recomend providing a character vector with the names\n\t of the input studies")  
## stds <- setNames(stds, paste("study\_", seq\_along(stds)))  
## }  
## else {  
## stds <- setNames(stds, remres@inputnames)  
## }  
## edat <- Reduce(rbind, lapply(names(stds), function(sn) {  
## std <- dplyr::select(sremres, dplyr::matches(paste0(genecol,   
## "|", stds[sn], "$")))  
## colnames(std) <- gsub("\_\\d+$", "", colnames(std))  
## std[["group"]] <- sn  
## std  
## }))  
## if (!all(c(genecol, foldchangecol, llcol, rlcol) %in% colnames(edat))) {  
## stop("Oops! Please, check the match among the provided parameters\n and the colnames of the remres@metaresult and remres@input")  
## }  
## edat <- dplyr::select(edat, c(!!rlang::sym(genecol), !!rlang::sym(foldchangecol),   
## !!rlang::sym(llcol), !!rlang::sym(rlcol), group))  
## sdat <- data.frame(genecol = unique(edat[[genecol]]), foldchangecol = sremres[["randomSummary"]],   
## llcol = sremres[["randomCi.lb"]], rlcol = sremres[["randomCi.ub"]],   
## group = "FoldChange summary")  
## colnames(sdat) <- c(genecol, foldchangecol, llcol, rlcol,   
## "group")  
## dat <- rbind(edat, sdat)  
## dat[["class"]] <- ifelse(grepl("summary", dat[["group"]]),   
## "FoldChange summary", "Study")  
## sumfc <- dplyr::filter(dat, grepl("summary", class))[[foldchangecol]]  
## maxfc <- max(dat[[rlcol]])  
## minfc <- min(dat[[llcol]])  
## if (sumfc > 0) {  
## sumcol <- "#E41A1C"  
## minlim <- -maxfc  
## maxlim <- maxfc  
## }  
## else {  
## sumcol <- "#377EB8"  
## minlim <- minfc  
## maxlim <- -minfc  
## }  
## gg <- ggplot(dat, aes(x = group, y = !!rlang::sym(foldchangecol),   
## color = class)) + geom\_point() + geom\_errorbar(aes(ymin = !!rlang::sym(llcol),   
## ymax = !!rlang::sym(rlcol), width = 0.1, color = class)) +   
## scale\_color\_manual(values = c(sumcol, "#bdbdbd")) + scale\_x\_discrete(limits = rev(dat[["group"]])) +   
## theme\_classic() + ggtitle(unique(edat[[genecol]])) +   
## geom\_hline(yintercept = 0, linetype = "solid", size = 0.05,   
## color = "#969696") + geom\_hline(yintercept = sumfc,   
## linetype = "dashed", size = 0.1, color = sumcol) + theme(legend.position = "none") +   
## scale\_y\_continuous(limits = c(minlim, maxlim)) + coord\_flip()  
## if (draw == "PDF") {  
## pdf(paste0(normalizePath(outputfolder), "/Forestplot\_",   
## unique(edat[[genecol]]), "\_", jobname, ".pdf"), width = 4,   
## height = 5)  
## plot(gg)  
## dev.off()  
## }  
## else if (draw == "HTML") {  
## htmlwidgets::saveWidget(as\_widget(ggplotly(gg)), paste0(normalizePath(outputfolder),   
## "/Forestplot\_", unique(edat[[genecol]]), jobname,   
## ".html"))  
## }  
## return(gg)  
## }  
## <bytecode: 0x0000000033e7e850>  
## <environment: namespace:MetaVolcanoR>

##down  
for (i in 1:2){#\*\*\* Numbers%@#@$  
 pl=draw\_forest\_mod(remres=meta\_degs\_rem,  
 gene=mrdown$SYMBOL[i],  
 genecol=genenamecol1,  
 foldchangecol=foldchangecol,  
 llcol="CI.L",  
 rlcol="CI.R",  
 jobname="MetaVolcano",  
 outputfolder="../MetaProjects/MetaDEG\_v01/Output/Forests",  
 draw="PDF",xlim=c(-12, 2.5))  
 print(mrdown$SYMBOL[i])  
 print( min(mrinput[mrinput$SYMBOL %in% mrdown$SYMBOL[i], grep('logFC',colnames(mrinput))],na.rm=T))  
  
 print( max(mrinput[mrinput$SYMBOL %in% mrdown$SYMBOL[i], grep('logFC',colnames(mrinput))],na.rm=T))  
 print(pl)  
 # print(mrdown[i,])  
 # print(mrinput[mrinput$SYMBOL %in% mrdown$SYMBOL[i],])  
}

## [1] "AQP8"  
## [1] -8.614498  
## [1] -1.849549

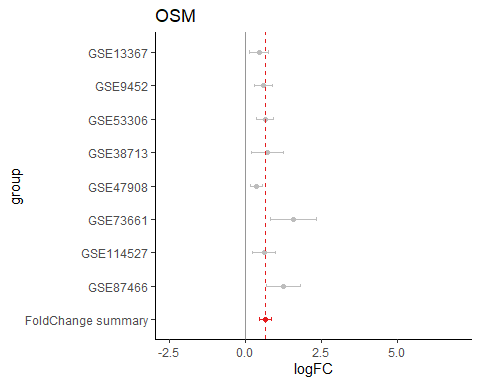


## [1] "CLDN8"  
## [1] -5.4705  
## [1] -1.402534

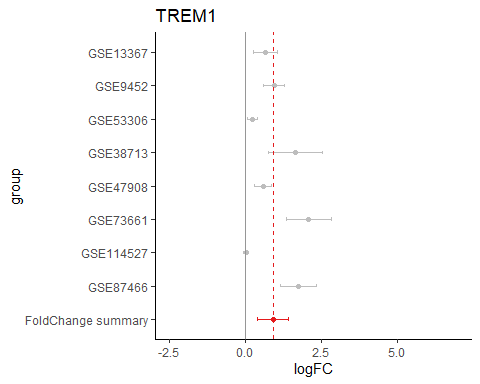


require(MetaVolcanoR)  
  
# Selected forests ####  
genes=c('OSM','TREM1','IL13RA2','IL1RN')  
#genes=c('CMTM2','C5AR1','FGF2','GK','HGF','IL1RN','LILRA2','NAMPT','PAPPA','SNCA','SOD2','STEAP4',"ZBED3")  
for (ea in genes){  
pl=draw\_forest\_mod(remres=meta\_degs\_rem,  
 gene=ea,  
 genecol=genenamecol1,  
 foldchangecol=foldchangecol,  
 llcol="CI.L",  
 rlcol="CI.R",  
 jobname="MetaVolcano",  
 outputfolder="../MetaProjects/MetaDEG\_v01/Output/Forests",  
 draw="PDF",xlim=c(-2.5,7))  
print(pl)  
print(ea)  
print( (mrup[mrup$SYMBOL %in% ea, grep('randomSummary',colnames(mrup))]))  
print( (mrup[mrup$SYMBOL %in% ea, grep('randomCi.lb',colnames(mrup))]))  
print( (mrup[mrup$SYMBOL %in% ea, grep('randomCi.ub',colnames(mrup))]))  
  
  
print( min(mrinput[mrinput$SYMBOL %in% ea, grep('logFC',colnames(mrinput))],na.rm=T))  
print( max(mrinput[mrinput$SYMBOL %in% ea, grep('logFC',colnames(mrinput))],na.rm=T))  
print('----------------------------------------------------------------------')  
# print(mrup[mrup$SYMBOL %in% ea,])  
# print(mrinput[mrinput$SYMBOL %in% ea,])  
}

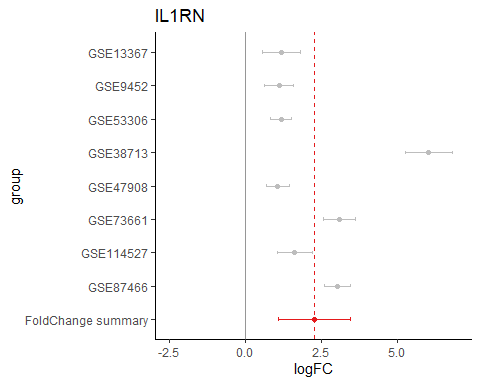
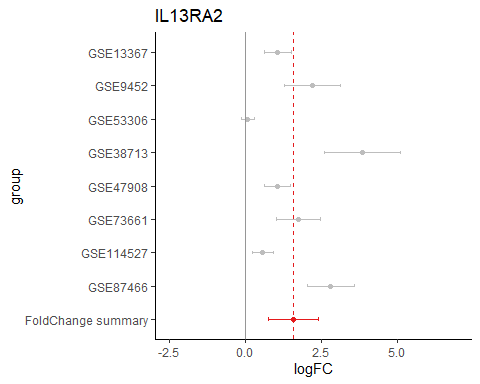
## [1] "OSM"  
## [1] 0.6513943  
## [1] 0.4450584  
## [1] 0.8577303  
## [1] 0.3398937  
## [1] 1.571981  
## [1] "----------------------------------------------------------------------"



## [1] "TREM1"  
## [1] 0.9087541  
## [1] 0.3998045  
## [1] 1.417704  
## [1] 0.009130152  
## [1] 2.068913  
## [1] "----------------------------------------------------------------------"



## [1] "IL13RA2"  
## [1] 1.575262  
## [1] 0.7527671  
## [1] 2.397757  
## [1] 0.07105807  
## [1] 3.853197  
## [1] "----------------------------------------------------------------------"



## [1] "IL1RN"  
## [1] 2.266435  
## [1] 1.085242  
## [1] 3.447628  
## [1] 1.058444  
## [1] 6.034659  
## [1] "----------------------------------------------------------------------"

# ranges of selected from input- replace 'sel' for other genes  
sel='IL1RN'  
mrinput[mrinput$SYMBOL %in% sel, grep('logFC',colnames(mrinput))]

## logFC\_1 logFC\_2 logFC\_3 logFC\_4 logFC\_5 logFC\_6 logFC\_7 logFC\_8  
## 464 1.178132 1.09925 1.166689 6.034659 1.058444 3.082634 1.618514 3.017758

min(mrinput[mrinput$SYMBOL %in% sel, grep('logFC',colnames(mrinput))],na.rm=T)

## [1] 1.058444

max(mrinput[mrinput$SYMBOL %in% sel, grep('logFC',colnames(mrinput))],na.rm=T)

## [1] 6.034659

# Enrichment analysis meta #####  
  
require(vctrs)

## Loading required package: vctrs

require(clusterProfiler)  
require(ReactomePA)  
  
#&Gene set enrichment analysis was performed with the Reactome Pathways database (reactome.org) using the the R packages  
#... ReactomePA and clusterProfiler using genes that have abs(log2(FC) > 1.5 and adjusted pvalue (benjamini) < .05  
  
# we next used the meta13 dataset DEG lists (selected on criteria above) to identify reactome enriched pathways, as was performed for the individual datasets.  
  
menrUp=enrichuniv(mrup$SYMBOL,univ = mr$SYMBOL)# mrup and mrdown defined above (line 247)  
menrDown=enrichuniv(mrdown$SYMBOL, univ=mr$SYMBOL)  
#& tables were created with the top 10 (lowest p.adjust) for enriched reactome pathways  
#get genes in meta enriched  
for(i in 1:20){  
print(menrUp$Description[i])  
idsplit=unlist(strsplit(menrUp$geneID[i],'/'))  
out=bitr(idsplit,fromType = 'ENTREZID',toType = 'SYMBOL',OrgDb="org.Hs.eg.db")  
print(out)  
}

## [1] "Interleukin-4 and Interleukin-13 signaling"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 240 ALOX5  
## 2 301 ANXA1  
## 3 604 BCL6  
## 4 6347 CCL2  
## 5 6356 CCL11  
## 6 6367 CCL22  
## 7 1052 CEBPD  
## 8 1278 COL1A2  
## 9 3576 CXCL8  
## 10 6624 FSCN1  
## 11 3082 HGF  
## 12 3091 HIF1A  
## 13 7184 HSP90B1  
## 14 3383 ICAM1  
## 15 3552 IL1A  
## 16 3553 IL1B  
## 17 3569 IL6  
## 18 3598 IL13RA2  
## 19 51561 IL23A  
## 20 3662 IRF4  
## 21 3687 ITGAX  
## 22 3689 ITGB2  
## 23 3717 JAK2  
## 24 3718 JAK3  
## 25 3934 LCN2  
## 26 4312 MMP1  
## 27 4313 MMP2  
## 28 4314 MMP3  
## 29 4318 MMP9  
## 30 4582 MUC1  
## 31 4843 NOS2  
## 32 5008 OSM  
## 33 5743 PTGS2  
## 34 9021 SOCS3  
## 35 6772 STAT1  
## 36 6774 STAT3  
## 37 7040 TGFB1  
## 38 7076 TIMP1  
## 39 7133 TNFRSF1B  
## 40 7291 TWIST1  
## 41 7412 VCAM1  
## 42 7431 VIM  
## 43 6935 ZEB1  
## [1] "Signaling by Interleukins"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 240 ALOX5  
## 2 301 ANXA1  
## 3 604 BCL6  
## 4 834 CASP1  
## 5 6347 CCL2  
## 6 6348 CCL3  
## 7 6351 CCL4  
## 8 6356 CCL11  
## 9 6363 CCL19  
## 10 6364 CCL20  
## 11 6367 CCL22  
## 12 1230 CCR1  
## 13 729230 CCR2  
## 14 941 CD80  
## 15 942 CD86  
## 16 1052 CEBPD  
## 17 1278 COL1A2  
## 18 1439 CSF2RB  
## 19 1441 CSF3R  
## 20 2919 CXCL1  
## 21 2920 CXCL2  
## 22 3576 CXCL8  
## 23 3627 CXCL10  
## 24 1846 DUSP4  
## 25 2357 FPR1  
## 26 6624 FSCN1  
## 27 2534 FYN  
## 28 3055 HCK  
## 29 3082 HGF  
## 30 3091 HIF1A  
## 31 7184 HSP90B1  
## 32 3383 ICAM1  
## 33 3552 IL1A  
## 34 3553 IL1B  
## 35 3554 IL1R1  
## 36 3557 IL1RN  
## 37 3559 IL2RA  
## 38 3569 IL6  
## 39 3575 IL7R  
## 40 3587 IL10RA  
## 41 3598 IL13RA2  
## 42 3601 IL15RA  
## 43 8809 IL18R1  
## 44 50615 IL21R  
## 45 51561 IL23A  
## 46 11009 IL24  
## 47 9466 IL27RA  
## 48 90865 IL33  
## 49 3635 INPP5D  
## 50 11213 IRAK3  
## 51 3662 IRF4  
## 52 3687 ITGAX  
## 53 3689 ITGB2  
## 54 3717 JAK2  
## 55 3718 JAK3  
## 56 3934 LCN2  
## 57 3936 LCP1  
## 58 4067 LYN  
## 59 1326 MAP3K8  
## 60 4312 MMP1  
## 61 4313 MMP2  
## 62 4314 MMP3  
## 63 4318 MMP9  
## 64 4478 MSN  
## 65 4582 MUC1  
## 66 4843 NOS2  
## 67 5008 OSM  
## 68 9180 OSMR  
## 69 5293 PIK3CD  
## 70 8503 PIK3R3  
## 71 5698 PSMB9  
## 72 5724 PTAFR  
## 73 5743 PTGS2  
## 74 5778 PTPN7  
## 75 8767 RIPK2  
## 76 6196 RPS6KA2  
## 77 6283 S100A12  
## 78 9021 SOCS3  
## 79 6648 SOD2  
## 80 6772 STAT1  
## 81 6774 STAT3  
## 82 6775 STAT4  
## 83 7040 TGFB1  
## 84 7076 TIMP1  
## 85 7133 TNFRSF1B  
## 86 7291 TWIST1  
## 87 7412 VCAM1  
## 88 7431 VIM  
## 89 6935 ZEB1  
## [1] "Extracellular matrix organization"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 8754 ADAM9  
## 2 8038 ADAM12  
## 3 8728 ADAM19  
## 4 9510 ADAMTS1  
## 5 9509 ADAMTS2  
## 6 11096 ADAMTS5  
## 7 56999 ADAMTS9  
## 8 633 BGN  
## 9 960 CD44  
## 10 1277 COL1A1  
## 11 1278 COL1A2  
## 12 1281 COL3A1  
## 13 1282 COL4A1  
## 14 1284 COL4A2  
## 15 1289 COL5A1  
## 16 1290 COL5A2  
## 17 1291 COL6A1  
## 18 1292 COL6A2  
## 19 1293 COL6A3  
## 20 1294 COL7A1  
## 21 1295 COL8A1  
## 22 1303 COL12A1  
## 23 1306 COL15A1  
## 24 80781 COL18A1  
## 25 1508 CTSB  
## 26 1513 CTSK  
## 27 1514 CTSL  
## 28 1634 DCN  
## 29 2200 FBN1  
## 30 5654 HTRA1  
## 31 3383 ICAM1  
## 32 3384 ICAM2  
## 33 3673 ITGA2  
## 34 3678 ITGA5  
## 35 8516 ITGA8  
## 36 3683 ITGAL  
## 37 3687 ITGAX  
## 38 3689 ITGB2  
## 39 3791 KDR  
## 40 3910 LAMA4  
## 41 3915 LAMC1  
## 42 3918 LAMC2  
## 43 4015 LOX  
## 44 4016 LOXL1  
## 45 4017 LOXL2  
## 46 4053 LTBP2  
## 47 4060 LUM  
## 48 8174 MADCAM1  
## 49 4312 MMP1  
## 50 4313 MMP2  
## 51 4314 MMP3  
## 52 4316 MMP7  
## 53 4318 MMP9  
## 54 4319 MMP10  
## 55 4321 MMP12  
## 56 4811 NID1  
## 57 64175 P3H1  
## 58 5118 PCOLCE  
## 59 5175 PECAM1  
## 60 5351 PLOD1  
## 61 7837 PXDN  
## 62 5054 SERPINE1  
## 63 6678 SPARC  
## 64 6696 SPP1  
## 65 7040 TGFB1  
## 66 7076 TIMP1  
## 67 7077 TIMP2  
## 68 3371 TNC  
## 69 7412 VCAM1  
## 70 1462 VCAN  
## 71 7450 VWF  
## [1] "Interleukin-10 signaling"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 6347 CCL2  
## 2 6348 CCL3  
## 3 6351 CCL4  
## 4 6363 CCL19  
## 5 6364 CCL20  
## 6 6367 CCL22  
## 7 1230 CCR1  
## 8 729230 CCR2  
## 9 941 CD80  
## 10 942 CD86  
## 11 2919 CXCL1  
## 12 2920 CXCL2  
## 13 3576 CXCL8  
## 14 3627 CXCL10  
## 15 2357 FPR1  
## 16 3383 ICAM1  
## 17 3552 IL1A  
## 18 3553 IL1B  
## 19 3554 IL1R1  
## 20 3557 IL1RN  
## 21 3569 IL6  
## 22 3587 IL10RA  
## 23 5724 PTAFR  
## 24 5743 PTGS2  
## 25 6774 STAT3  
## 26 7076 TIMP1  
## 27 7133 TNFRSF1B  
## [1] "Neutrophil degranulation"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 51816 ADA2  
## 2 240 ALOX5  
## 3 64333 ARHGAP9  
## 4 23250 ATP11A  
## 5 684 BST2  
## 6 718 C3  
## 7 719 C3AR1  
## 8 728 C5AR1  
## 9 960 CD44  
## 10 963 CD53  
## 11 1604 CD55  
## 12 22918 CD93  
## 13 11314 CD300A  
## 14 1116 CHI3L1  
## 15 1378 CR1  
## 16 1508 CTSB  
## 17 1075 CTSC  
## 18 1512 CTSH  
## 19 2919 CXCL1  
## 20 3579 CXCR2  
## 21 1536 CYBB  
## 22 8560 DEGS1  
## 23 1794 DOCK2  
## 24 79930 DOK3  
## 25 2207 FCER1G  
## 26 2212 FCGR2A  
## 27 2215 FCGR3B  
## 28 2219 FCN1  
## 29 2268 FGR  
## 30 2357 FPR1  
## 31 2358 FPR2  
## 32 11010 GLIPR1  
## 33 9535 GMFG  
## 34 3310 HSPA6  
## 35 3683 ITGAL  
## 36 3687 ITGAX  
## 37 3689 ITGB2  
## 38 3934 LCN2  
## 39 11026 LILRA3  
## 40 79888 LPCAT1  
## 41 4057 LTF  
## 42 4069 LYZ  
## 43 4311 MME  
## 44 4318 MMP9  
## 45 4332 MNDA  
## 46 3071 NCKAP1L  
## 47 10562 OLFM4  
## 48 5175 PECAM1  
## 49 5315 PKM  
## 50 5328 PLAU  
## 51 5329 PLAUR  
## 52 10549 PRDX4  
## 53 5724 PTAFR  
## 54 5788 PTPRC  
## 55 5768 QSOX1  
## 56 11031 RAB31  
## 57 6278 S100A7  
## 58 6279 S100A8  
## 59 6280 S100A9  
## 60 6282 S100A11  
## 61 6283 S100A12  
## 62 6286 S100P  
## 63 6402 SELL  
## 64 5265 SERPINA1  
## 65 12 SERPINA3  
## 66 6317 SERPINB3  
## 67 140885 SIRPA  
## 68 6515 SLC2A3  
## 69 6556 SLC11A1  
## 70 6590 SLPI  
## 71 2040 STOM  
## 72 10312 TCIRG1  
## 73 6947 TCN1  
## 74 353376 TICAM2  
## 75 7077 TIMP2  
## 76 7097 TLR2  
## 77 11322 TMC6  
## 78 7130 TNFAIP6  
## 79 7133 TNFRSF1B  
## 80 81567 TXNDC5  
## 81 7305 TYROBP  
## 82 8876 VNN1  
## [1] "Integrin cell surface interactions"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 960 CD44  
## 2 1277 COL1A1  
## 3 1278 COL1A2  
## 4 1281 COL3A1  
## 5 1282 COL4A1  
## 6 1284 COL4A2  
## 7 1289 COL5A1  
## 8 1290 COL5A2  
## 9 1291 COL6A1  
## 10 1292 COL6A2  
## 11 1293 COL6A3  
## 12 1294 COL7A1  
## 13 1295 COL8A1  
## 14 80781 COL18A1  
## 15 2200 FBN1  
## 16 3383 ICAM1  
## 17 3384 ICAM2  
## 18 3673 ITGA2  
## 19 3678 ITGA5  
## 20 8516 ITGA8  
## 21 3683 ITGAL  
## 22 3687 ITGAX  
## 23 3689 ITGB2  
## 24 3791 KDR  
## 25 4060 LUM  
## 26 8174 MADCAM1  
## 27 5175 PECAM1  
## 28 6696 SPP1  
## 29 3371 TNC  
## 30 7412 VCAM1  
## 31 7450 VWF  
## [1] "Assembly of collagen fibrils and other multimeric structures"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 1277 COL1A1  
## 2 1278 COL1A2  
## 3 1281 COL3A1  
## 4 1282 COL4A1  
## 5 1284 COL4A2  
## 6 1289 COL5A1  
## 7 1290 COL5A2  
## 8 1291 COL6A1  
## 9 1292 COL6A2  
## 10 1293 COL6A3  
## 11 1294 COL7A1  
## 12 1295 COL8A1  
## 13 1303 COL12A1  
## 14 1306 COL15A1  
## 15 80781 COL18A1  
## 16 1508 CTSB  
## 17 1514 CTSL  
## 18 3918 LAMC2  
## 19 4015 LOX  
## 20 4016 LOXL1  
## 21 4017 LOXL2  
## 22 4314 MMP3  
## 23 4316 MMP7  
## 24 4318 MMP9  
## 25 5118 PCOLCE  
## 26 7837 PXDN  
## [1] "Degradation of the extracellular matrix"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 8754 ADAM9  
## 2 9510 ADAMTS1  
## 3 11096 ADAMTS5  
## 4 56999 ADAMTS9  
## 5 960 CD44  
## 6 1277 COL1A1  
## 7 1278 COL1A2  
## 8 1281 COL3A1  
## 9 1282 COL4A1  
## 10 1284 COL4A2  
## 11 1289 COL5A1  
## 12 1290 COL5A2  
## 13 1291 COL6A1  
## 14 1292 COL6A2  
## 15 1293 COL6A3  
## 16 1294 COL7A1  
## 17 1295 COL8A1  
## 18 1303 COL12A1  
## 19 1306 COL15A1  
## 20 80781 COL18A1  
## 21 1508 CTSB  
## 22 1513 CTSK  
## 23 1514 CTSL  
## 24 1634 DCN  
## 25 2200 FBN1  
## 26 5654 HTRA1  
## 27 3915 LAMC1  
## 28 3918 LAMC2  
## 29 4312 MMP1  
## 30 4313 MMP2  
## 31 4314 MMP3  
## 32 4316 MMP7  
## 33 4318 MMP9  
## 34 4319 MMP10  
## 35 4321 MMP12  
## 36 4811 NID1  
## 37 6696 SPP1  
## 38 7076 TIMP1  
## 39 7077 TIMP2  
## [1] "Collagen degradation"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 8754 ADAM9  
## 2 1277 COL1A1  
## 3 1278 COL1A2  
## 4 1281 COL3A1  
## 5 1282 COL4A1  
## 6 1284 COL4A2  
## 7 1289 COL5A1  
## 8 1290 COL5A2  
## 9 1291 COL6A1  
## 10 1292 COL6A2  
## 11 1293 COL6A3  
## 12 1294 COL7A1  
## 13 1295 COL8A1  
## 14 1303 COL12A1  
## 15 1306 COL15A1  
## 16 80781 COL18A1  
## 17 1508 CTSB  
## 18 1513 CTSK  
## 19 1514 CTSL  
## 20 4312 MMP1  
## 21 4313 MMP2  
## 22 4314 MMP3  
## 23 4316 MMP7  
## 24 4318 MMP9  
## 25 4319 MMP10  
## 26 4321 MMP12  
## [1] "Collagen formation"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 9509 ADAMTS2  
## 2 1277 COL1A1  
## 3 1278 COL1A2  
## 4 1281 COL3A1  
## 5 1282 COL4A1  
## 6 1284 COL4A2  
## 7 1289 COL5A1  
## 8 1290 COL5A2  
## 9 1291 COL6A1  
## 10 1292 COL6A2  
## 11 1293 COL6A3  
## 12 1294 COL7A1  
## 13 1295 COL8A1  
## 14 1303 COL12A1  
## 15 1306 COL15A1  
## 16 80781 COL18A1  
## 17 1508 CTSB  
## 18 1514 CTSL  
## 19 3918 LAMC2  
## 20 4015 LOX  
## 21 4016 LOXL1  
## 22 4017 LOXL2  
## 23 4314 MMP3  
## 24 4316 MMP7  
## 25 4318 MMP9  
## 26 64175 P3H1  
## 27 5118 PCOLCE  
## 28 5351 PLOD1  
## 29 7837 PXDN  
## [1] "Interferon Signaling"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 684 BST2  
## 2 960 CD44  
## 3 4261 CIITA  
## 4 1958 EGR1  
## 5 2209 FCGR1A  
## 6 2633 GBP1  
## 7 2634 GBP2  
## 8 115361 GBP4  
## 9 115362 GBP5  
## 10 3113 HLA-DPA1  
## 11 3117 HLA-DQA1  
## 12 3119 HLA-DQB1  
## 13 3122 HLA-DRA  
## 14 3123 HLA-DRB1  
## 15 3127 HLA-DRB5  
## 16 3383 ICAM1  
## 17 2537 IFI6  
## 18 10437 IFI30  
## 19 3437 IFIT3  
## 20 8519 IFITM1  
## 21 10581 IFITM2  
## 22 10410 IFITM3  
## 23 3455 IFNAR2  
## 24 3659 IRF1  
## 25 3662 IRF4  
## 26 9636 ISG15  
## 27 3669 ISG20  
## 28 3717 JAK2  
## 29 4600 MX2  
## 30 4939 OAS2  
## 31 5724 PTAFR  
## 32 25939 SAMHD1  
## 33 9021 SOCS3  
## 34 6772 STAT1  
## 35 10346 TRIM22  
## 36 23650 TRIM29  
## 37 9246 UBE2L6  
## 38 7412 VCAM1  
## 39 54739 XAF1  
## [1] "ECM proteoglycans"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 633 BGN  
## 2 1277 COL1A1  
## 3 1278 COL1A2  
## 4 1281 COL3A1  
## 5 1282 COL4A1  
## 6 1284 COL4A2  
## 7 1289 COL5A1  
## 8 1290 COL5A2  
## 9 1291 COL6A1  
## 10 1292 COL6A2  
## 11 1293 COL6A3  
## 12 1634 DCN  
## 13 3673 ITGA2  
## 14 8516 ITGA8  
## 15 3687 ITGAX  
## 16 3910 LAMA4  
## 17 3915 LAMC1  
## 18 4060 LUM  
## 19 5054 SERPINE1  
## 20 6678 SPARC  
## 21 7040 TGFB1  
## 22 3371 TNC  
## 23 1462 VCAN  
## [1] "Interferon gamma signaling"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 960 CD44  
## 2 4261 CIITA  
## 3 2209 FCGR1A  
## 4 2633 GBP1  
## 5 2634 GBP2  
## 6 115361 GBP4  
## 7 115362 GBP5  
## 8 3113 HLA-DPA1  
## 9 3117 HLA-DQA1  
## 10 3119 HLA-DQB1  
## 11 3122 HLA-DRA  
## 12 3123 HLA-DRB1  
## 13 3127 HLA-DRB5  
## 14 3383 ICAM1  
## 15 10437 IFI30  
## 16 3659 IRF1  
## 17 3662 IRF4  
## 18 3717 JAK2  
## 19 4939 OAS2  
## 20 5724 PTAFR  
## 21 9021 SOCS3  
## 22 6772 STAT1  
## 23 10346 TRIM22  
## 24 23650 TRIM29  
## 25 7412 VCAM1  
## [1] "Chemokine receptors bind chemokines"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 51554 ACKR4  
## 2 6363 CCL19  
## 3 6364 CCL20  
## 4 6366 CCL21  
## 5 1230 CCR1  
## 6 729230 CCR2  
## 7 1236 CCR7  
## 8 2919 CXCL1  
## 9 2920 CXCL2  
## 10 6374 CXCL5  
## 11 6372 CXCL6  
## 12 3576 CXCL8  
## 13 4283 CXCL9  
## 14 3627 CXCL10  
## 15 6373 CXCL11  
## 16 10563 CXCL13  
## 17 3579 CXCR2  
## 18 7852 CXCR4  
## [1] "Cell surface interactions at the vascular wall"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 285 ANGPT2  
## 2 857 CAV1  
## 3 914 CD2  
## 4 960 CD44  
## 5 972 CD74  
## 6 8832 CD84  
## 7 1277 COL1A1  
## 8 1278 COL1A2  
## 9 2207 FCER1G  
## 10 2534 FYN  
## 11 3635 INPP5D  
## 12 3678 ITGA5  
## 13 3683 ITGAL  
## 14 3687 ITGAX  
## 15 3689 ITGB2  
## 16 4067 LYN  
## 17 4312 MMP1  
## 18 5175 PECAM1  
## 19 6401 SELE  
## 20 6402 SELL  
## 21 6403 SELP  
## 22 6404 SELPLG  
## 23 140885 SIRPA  
## 24 8140 SLC7A5  
## 25 9056 SLC7A7  
## 26 23657 SLC7A11  
## 27 7010 TEK  
## 28 7040 TGFB1  
## 29 7056 THBD  
## 30 54210 TREM1  
## [1] "Complement cascade"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 715 C1R  
## 2 716 C1S  
## 3 717 C2  
## 4 718 C3  
## 5 719 C3AR1  
## 6 722 C4BPA  
## 7 725 C4BPB  
## 8 728 C5AR1  
## 9 930 CD19  
## 10 1604 CD55  
## 11 629 CFB  
## 12 3426 CFI  
## 13 1191 CLU  
## 14 1378 CR1  
## 15 1380 CR2  
## 16 2219 FCN1  
## 17 8547 FCN3  
## 18 5648 MASP1  
## 19 710 SERPING1  
## [1] "Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 718 C3  
## 2 930 CD19  
## 3 947 CD34  
## 4 958 CD40  
## 5 11314 CD300A  
## 6 9976 CLEC2B  
## 7 1277 COL1A1  
## 8 1278 COL1A2  
## 9 1281 COL3A1  
## 10 2209 FCGR1A  
## 11 2213 FCGR2B  
## 12 3383 ICAM1  
## 13 3384 ICAM2  
## 14 8519 IFITM1  
## 15 3683 ITGAL  
## 16 3689 ITGB2  
## 17 3904 LAIR2  
## 18 11026 LILRA3  
## 19 10859 LILRB1  
## 20 11006 LILRB4  
## 21 8174 MADCAM1  
## 22 4277 MICB  
## 23 29992 PILRA  
## 24 6402 SELL  
## 25 114836 SLAMF6  
## 26 57823 SLAMF7  
## 27 54210 TREM1  
## 28 7305 TYROBP  
## 29 7412 VCAM1  
## [1] "Regulation of Complement cascade"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 715 C1R  
## 2 716 C1S  
## 3 717 C2  
## 4 718 C3  
## 5 719 C3AR1  
## 6 722 C4BPA  
## 7 725 C4BPB  
## 8 728 C5AR1  
## 9 930 CD19  
## 10 1604 CD55  
## 11 629 CFB  
## 12 3426 CFI  
## 13 1191 CLU  
## 14 1378 CR1  
## 15 1380 CR2  
## 16 710 SERPING1  
## [1] "Collagen biosynthesis and modifying enzymes"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 9509 ADAMTS2  
## 2 1277 COL1A1  
## 3 1278 COL1A2  
## 4 1281 COL3A1  
## 5 1282 COL4A1  
## 6 1284 COL4A2  
## 7 1289 COL5A1  
## 8 1290 COL5A2  
## 9 1291 COL6A1  
## 10 1292 COL6A2  
## 11 1293 COL6A3  
## 12 1294 COL7A1  
## 13 1295 COL8A1  
## 14 1303 COL12A1  
## 15 1306 COL15A1  
## 16 80781 COL18A1  
## 17 64175 P3H1  
## 18 5118 PCOLCE  
## 19 5351 PLOD1  
## [1] "Interferon alpha/beta signaling"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 684 BST2  
## 2 1958 EGR1  
## 3 2634 GBP2  
## 4 2537 IFI6  
## 5 3437 IFIT3  
## 6 8519 IFITM1  
## 7 10581 IFITM2  
## 8 10410 IFITM3  
## 9 3455 IFNAR2  
## 10 3659 IRF1  
## 11 3662 IRF4  
## 12 9636 ISG15  
## 13 3669 ISG20  
## 14 4600 MX2  
## 15 4939 OAS2  
## 16 25939 SAMHD1  
## 17 9021 SOCS3  
## 18 6772 STAT1  
## 19 54739 XAF1

for(i in 1:11){  
 print(menrDown$Description[i])  
 idsplit=unlist(strsplit(menrDown$geneID[i],'/'))  
 out=bitr(idsplit,fromType = 'ENTREZID',toType = 'SYMBOL',OrgDb="org.Hs.eg.db")  
 print(out)  
}

## [1] "Biological oxidations"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 55902 ACSS2  
## 2 124 ADH1A  
## 3 126 ADH1C  
## 4 130 ADH6  
## 5 8824 CES2  
## 6 23491 CES3  
## 7 134147 CMBL  
## 8 1555 CYP2B6  
## 9 1573 CYP2J2  
## 10 29785 CYP2S1  
## 11 1576 CYP3A4  
## 12 8529 CYP4F2  
## 13 66002 CYP4F12  
## 14 1593 CYP27A1  
## 15 2948 GSTM4  
## 16 4128 MAOA  
## 17 10 NAT2  
## 18 9971 NR1H4  
## 19 1836 SLC26A2  
## 20 6817 SULT1A1  
## 21 6799 SULT1A2  
## 22 7358 UGDH  
## 23 7360 UGP2  
## 24 54658 UGT1A1  
## 25 54576 UGT1A8  
## 26 54600 UGT1A9  
## 27 79799 UGT2A3  
## [1] "Phase I - Functionalization of compounds"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 55902 ACSS2  
## 2 124 ADH1A  
## 3 126 ADH1C  
## 4 130 ADH6  
## 5 8824 CES2  
## 6 23491 CES3  
## 7 134147 CMBL  
## 8 1555 CYP2B6  
## 9 1573 CYP2J2  
## 10 29785 CYP2S1  
## 11 1576 CYP3A4  
## 12 8529 CYP4F2  
## 13 66002 CYP4F12  
## 14 1593 CYP27A1  
## 15 4128 MAOA  
## 16 9971 NR1H4  
## [1] "Metallothioneins bind metals"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 4493 MT1E  
## 2 4494 MT1F  
## 3 4495 MT1G  
## 4 4496 MT1H  
## 5 4499 MT1M  
## 6 4501 MT1X  
## [1] "Fatty acid metabolism"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 10449 ACAA2  
## 2 34 ACADM  
## 3 35 ACADS  
## 4 26027 ACOT11  
## 5 51 ACOX1  
## 6 8309 ACOX2  
## 7 80221 ACSF2  
## 8 23600 AMACR  
## 9 1374 CPT1A  
## 10 1376 CPT2  
## 11 1384 CRAT  
## 12 54677 CROT  
## 13 1573 CYP2J2  
## 14 8529 CYP4F2  
## 15 2053 EPHX2  
## 16 3248 HPGD  
## 17 283927 NUDT7  
## 18 5264 PHYH  
## 19 22949 PTGR1  
## 20 6584 SLC22A5  
## [1] "Response to metal ions"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 4493 MT1E  
## 2 4494 MT1F  
## 3 4495 MT1G  
## 4 4496 MT1H  
## 5 4499 MT1M  
## 6 4501 MT1X  
## [1] "Reversible hydration of carbon dioxide"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 759 CA1  
## 2 760 CA2  
## 3 762 CA4  
## 4 766 CA7  
## 5 771 CA12  
## [1] "Peroxisomal lipid metabolism"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 51 ACOX1  
## 2 8309 ACOX2  
## 3 23600 AMACR  
## 4 1384 CRAT  
## 5 54677 CROT  
## 6 283927 NUDT7  
## 7 5264 PHYH  
## [1] "SLC-mediated transmembrane transport"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 23382 AHCYL2  
## 2 682 BSG  
## 3 6505 SLC1A1  
## 4 6519 SLC3A1  
## 5 8671 SLC4A4  
## 6 340024 SLC6A19  
## 7 6549 SLC9A2  
## 8 9058 SLC13A2  
## 9 6566 SLC16A1  
## 10 6575 SLC20A2  
## 11 6583 SLC22A4  
## 12 6584 SLC22A5  
## 13 1836 SLC26A2  
## 14 1811 SLC26A3  
## 15 55532 SLC30A10  
## 16 206358 SLC36A1  
## 17 55089 SLC38A4  
## 18 55630 SLC39A4  
## 19 283375 SLC39A5  
## 20 23446 SLC44A1  
## 21 6717 SRI  
## [1] "Pyruvate metabolism and Citric Acid (TCA) cycle"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 682 BSG  
## 2 81889 FAHD1  
## 3 10873 ME3  
## 4 25874 MPC2  
## 5 5160 PDHA1  
## 6 5164 PDK2  
## 7 5166 PDK4  
## 8 6566 SLC16A1  
## 9 8801 SUCLG2  
## [1] "Nuclear Receptor transcription pathway"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 3172 HNF4A  
## 2 3174 HNF4G  
## 3 9971 NR1H4  
## 4 8856 NR1I2  
## 5 2494 NR5A2  
## 6 5468 PPARG  
## 7 7068 THRB  
## 8 7421 VDR  
## [1] "Glucuronidation"

## 'select()' returned 1:1 mapping between keys and columns

## ENTREZID SYMBOL  
## 1 7358 UGDH  
## 2 7360 UGP2  
## 3 54658 UGT1A1  
## 4 54576 UGT1A8  
## 5 54600 UGT1A9  
## 6 79799 UGT2A3

#plot Enr with Individual#####  
#Compile up and down enriched pathways for individual into single table  
  
#for Up   
require(plyr)  
#from indiv output :   
head(enrupTt2)

## $GSE13367  
## ID  
## R-HSA-1474244 R-HSA-1474244  
## R-HSA-1474228 R-HSA-1474228  
## R-HSA-1442490 R-HSA-1442490  
## R-HSA-2022090 R-HSA-2022090  
## R-HSA-1474290 R-HSA-1474290  
## R-HSA-2243919 R-HSA-2243919  
## R-HSA-6798695 R-HSA-6798695  
## R-HSA-216083 R-HSA-216083  
## R-HSA-977606 R-HSA-977606  
## R-HSA-449147 R-HSA-449147  
## R-HSA-6785807 R-HSA-6785807  
## R-HSA-76002 R-HSA-76002  
## R-HSA-166658 R-HSA-166658  
## R-HSA-983695 R-HSA-983695  
## R-HSA-381426 R-HSA-381426  
## R-HSA-1592389 R-HSA-1592389  
## R-HSA-114604 R-HSA-114604  
## R-HSA-375276 R-HSA-375276  
## R-HSA-380108 R-HSA-380108  
## R-HSA-202733 R-HSA-202733  
## R-HSA-8957275 R-HSA-8957275  
## R-HSA-3000178 R-HSA-3000178  
## R-HSA-2022870 R-HSA-2022870  
## R-HSA-202427 R-HSA-202427  
## R-HSA-202433 R-HSA-202433  
## R-HSA-1650814 R-HSA-1650814  
## R-HSA-8948216 R-HSA-8948216  
## R-HSA-373076 R-HSA-373076  
## R-HSA-6803157 R-HSA-6803157  
## R-HSA-202430 R-HSA-202430  
## R-HSA-5686938 R-HSA-5686938  
## R-HSA-418594 R-HSA-418594  
## R-HSA-500792 R-HSA-500792  
## R-HSA-388841 R-HSA-388841  
## R-HSA-168898 R-HSA-168898  
## R-HSA-210990 R-HSA-210990  
## R-HSA-166663 R-HSA-166663  
## R-HSA-389948 R-HSA-389948  
## R-HSA-5668599 R-HSA-5668599  
## R-HSA-71240 R-HSA-71240  
## R-HSA-983705 R-HSA-983705  
## R-HSA-1793185 R-HSA-1793185  
## R-HSA-76005 R-HSA-76005  
## R-HSA-2214320 R-HSA-2214320  
## R-HSA-75892 R-HSA-75892  
## R-HSA-3000170 R-HSA-3000170  
## R-HSA-76009 R-HSA-76009  
## R-HSA-1630316 R-HSA-1630316  
## R-HSA-3000171 R-HSA-3000171  
## R-HSA-114608 R-HSA-114608  
## R-HSA-451927 R-HSA-451927  
## R-HSA-416476 R-HSA-416476  
## R-HSA-352230 R-HSA-352230  
## Description  
## R-HSA-1474244 Extracellular matrix organization  
## R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-1442490 Collagen degradation  
## R-HSA-2022090 Assembly of collagen fibrils and other multimeric structures  
## R-HSA-1474290 Collagen formation  
## R-HSA-2243919 Crosslinking of collagen fibrils  
## R-HSA-6798695 Neutrophil degranulation  
## R-HSA-216083 Integrin cell surface interactions  
## R-HSA-977606 Regulation of Complement cascade  
## R-HSA-449147 Signaling by Interleukins  
## R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-76002 Platelet activation, signaling and aggregation  
## R-HSA-166658 Complement cascade  
## R-HSA-983695 Antigen activates B Cell Receptor (BCR) leading to generation of second messengers  
## R-HSA-381426 Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)  
## R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-114604 GPVI-mediated activation cascade  
## R-HSA-375276 Peptide ligand-binding receptors  
## R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-202733 Cell surface interactions at the vascular wall  
## R-HSA-8957275 Post-translational protein phosphorylation  
## R-HSA-3000178 ECM proteoglycans  
## R-HSA-2022870 Chondroitin sulfate biosynthesis  
## R-HSA-202427 Phosphorylation of CD3 and TCR zeta chains  
## R-HSA-202433 Generation of second messenger molecules  
## R-HSA-1650814 Collagen biosynthesis and modifying enzymes  
## R-HSA-8948216 Collagen chain trimerization  
## R-HSA-373076 Class A/1 (Rhodopsin-like receptors)  
## R-HSA-6803157 Antimicrobial peptides  
## R-HSA-202430 Translocation of ZAP-70 to Immunological synapse  
## R-HSA-5686938 Regulation of TLR by endogenous ligand  
## R-HSA-418594 G alpha (i) signalling events  
## R-HSA-500792 GPCR ligand binding  
## R-HSA-388841 Costimulation by the CD28 family  
## R-HSA-168898 Toll-like Receptor Cascades  
## R-HSA-210990 PECAM1 interactions  
## R-HSA-166663 Initial triggering of complement  
## R-HSA-389948 PD-1 signaling  
## R-HSA-5668599 RHO GTPases Activate NADPH Oxidases  
## R-HSA-71240 Tryptophan catabolism  
## R-HSA-983705 Signaling by the B Cell Receptor (BCR)  
## R-HSA-1793185 Chondroitin sulfate/dermatan sulfate metabolism  
## R-HSA-76005 Response to elevated platelet cytosolic Ca2+  
## R-HSA-2214320 Anchoring fibril formation  
## R-HSA-75892 Platelet Adhesion to exposed collagen  
## R-HSA-3000170 Syndecan interactions  
## R-HSA-76009 Platelet Aggregation (Plug Formation)  
## R-HSA-1630316 Glycosaminoglycan metabolism  
## R-HSA-3000171 Non-integrin membrane-ECM interactions  
## R-HSA-114608 Platelet degranulation   
## R-HSA-451927 Interleukin-2 family signaling  
## R-HSA-416476 G alpha (q) signalling events  
## R-HSA-352230 Amino acid transport across the plasma membrane  
## GeneRatio BgRatio pvalue p.adjust qvalue  
## R-HSA-1474244 41/313 300/9781 1.614754e-15 8.945740e-13 7.699829e-13  
## R-HSA-1474228 24/313 140/9781 1.235284e-11 3.421735e-09 2.945176e-09  
## R-HSA-1442490 16/313 64/9781 1.005068e-10 1.856026e-08 1.597530e-08  
## R-HSA-2022090 15/313 60/9781 3.917839e-10 5.426207e-08 4.670476e-08  
## R-HSA-1474290 16/313 89/9781 1.758125e-08 1.948002e-06 1.676696e-06  
## R-HSA-2243919 8/313 18/9781 3.329629e-08 2.741494e-06 2.359675e-06  
## R-HSA-6798695 39/313 469/9781 3.463982e-08 2.741494e-06 2.359675e-06  
## R-HSA-216083 15/313 84/9781 5.442362e-08 3.768836e-06 3.243934e-06  
## R-HSA-977606 11/313 45/9781 1.161273e-07 7.148281e-06 6.152710e-06  
## R-HSA-449147 36/313 437/9781 1.547042e-07 8.570613e-06 7.376948e-06  
## R-HSA-6785807 16/313 104/9781 1.711141e-07 8.617929e-06 7.417674e-06  
## R-HSA-76002 25/313 258/9781 7.296624e-07 3.368608e-05 2.899448e-05  
## R-HSA-166658 11/313 56/9781 1.243705e-06 5.300096e-05 4.561929e-05  
## R-HSA-983695 8/313 32/9781 5.407966e-06 2.140009e-04 1.841961e-04  
## R-HSA-381426 15/313 121/9781 6.805005e-06 2.403614e-04 2.068853e-04  
## R-HSA-1592389 8/313 33/9781 6.941847e-06 2.403614e-04 2.068853e-04  
## R-HSA-114604 8/313 34/9781 8.827782e-06 2.876818e-04 2.476152e-04  
## R-HSA-375276 18/313 177/9781 1.401297e-05 4.312881e-04 3.712208e-04  
## R-HSA-380108 9/313 48/9781 1.750712e-05 5.104709e-04 4.393755e-04  
## R-HSA-202733 15/313 133/9781 2.163628e-05 5.993249e-04 5.158544e-04  
## R-HSA-8957275 13/313 104/9781 2.563319e-05 6.266221e-04 5.393498e-04  
## R-HSA-3000178 11/313 76/9781 2.703668e-05 6.266221e-04 5.393498e-04  
## R-HSA-2022870 6/313 20/9781 2.714608e-05 6.266221e-04 5.393498e-04  
## R-HSA-202427 6/313 20/9781 2.714608e-05 6.266221e-04 5.393498e-04  
## R-HSA-202433 7/313 30/9781 3.468628e-05 7.686479e-04 6.615951e-04  
## R-HSA-1650814 10/313 67/9781 4.791701e-05 1.021001e-03 8.788019e-04  
## R-HSA-8948216 8/313 44/9781 6.520743e-05 1.337960e-03 1.151617e-03  
## R-HSA-373076 23/313 303/9781 1.069470e-04 2.116022e-03 1.821315e-03  
## R-HSA-6803157 10/313 74/9781 1.138820e-04 2.175538e-03 1.872542e-03  
## R-HSA-202430 5/313 17/9781 1.464675e-04 2.704766e-03 2.328062e-03  
## R-HSA-5686938 5/313 18/9781 1.975219e-04 3.529907e-03 3.038282e-03  
## R-HSA-418594 26/313 383/9781 2.362846e-04 4.067399e-03 3.500915e-03  
## R-HSA-500792 28/313 427/9781 2.422819e-04 4.067399e-03 3.500915e-03  
## R-HSA-388841 9/313 67/9781 2.618233e-04 4.266179e-03 3.672010e-03  
## R-HSA-168898 14/313 151/9781 3.357415e-04 5.314309e-03 4.574163e-03  
## R-HSA-210990 4/313 12/9781 4.154352e-04 6.319629e-03 5.439468e-03  
## R-HSA-166663 5/313 21/9781 4.334764e-04 6.319629e-03 5.439468e-03  
## R-HSA-389948 5/313 21/9781 4.334764e-04 6.319629e-03 5.439468e-03  
## R-HSA-5668599 5/313 23/9781 6.800844e-04 9.660687e-03 8.315202e-03  
## R-HSA-71240 4/313 14/9781 7.985165e-04 1.105945e-02 9.519157e-03  
## R-HSA-983705 11/313 111/9781 8.272712e-04 1.117825e-02 9.621408e-03  
## R-HSA-1793185 7/313 50/9781 9.835919e-04 1.297405e-02 1.116710e-02  
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## R-HSA-1630316 11/313 124/9781 2.047944e-03 2.363668e-02 2.034470e-02  
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## Description  
## R-HSA-449147 Signaling by Interleukins  
## R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-1474244 Extracellular matrix organization  
## R-HSA-6798695 Neutrophil degranulation  
## R-HSA-877300 Interferon gamma signaling  
## R-HSA-913531 Interferon Signaling  
## R-HSA-1236975 Antigen processing-Cross presentation  
## R-HSA-6783783 Interleukin-10 signaling  
## R-HSA-216083 Integrin cell surface interactions  
## R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-1442490 Collagen degradation  
## R-HSA-202733 Cell surface interactions at the vascular wall  
## R-HSA-909733 Interferon alpha/beta signaling  
## R-HSA-1474290 Collagen formation  
## R-HSA-1236974 ER-Phagosome pathway  
## R-HSA-983170 Antigen Presentation: Folding, assembly and peptide loading of class I MHC  
## R-HSA-2022090 Assembly of collagen fibrils and other multimeric structures  
## R-HSA-3000178 ECM proteoglycans  
## R-HSA-2132295 MHC class II antigen presentation  
## R-HSA-76002 Platelet activation, signaling and aggregation  
## R-HSA-977606 Regulation of Complement cascade  
## R-HSA-198933 Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell  
## R-HSA-166658 Complement cascade  
## R-HSA-381426 Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)  
## R-HSA-114608 Platelet degranulation   
## R-HSA-1650814 Collagen biosynthesis and modifying enzymes  
## R-HSA-202427 Phosphorylation of CD3 and TCR zeta chains  
## R-HSA-3299685 Detoxification of Reactive Oxygen Species  
## R-HSA-202430 Translocation of ZAP-70 to Immunological synapse  
## R-HSA-76005 Response to elevated platelet cytosolic Ca2+  
## R-HSA-166663 Initial triggering of complement  
## R-HSA-2243919 Crosslinking of collagen fibrils  
## R-HSA-114604 GPVI-mediated activation cascade  
## R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-3000171 Non-integrin membrane-ECM interactions  
## R-HSA-8957275 Post-translational protein phosphorylation  
## R-HSA-447115 Interleukin-12 family signaling  
## R-HSA-389948 PD-1 signaling  
## R-HSA-8948216 Collagen chain trimerization  
## R-HSA-202433 Generation of second messenger molecules  
## R-HSA-983169 Class I MHC mediated antigen processing & presentation  
## R-HSA-3000170 Syndecan interactions  
## R-HSA-3000480 Scavenging by Class A Receptors  
## R-HSA-5686938 Regulation of TLR by endogenous ligand  
## R-HSA-1059683 Interleukin-6 signaling  
## R-HSA-1566948 Elastic fibre formation  
## R-HSA-388841 Costimulation by the CD28 family  
## R-HSA-174143 APC/C-mediated degradation of cell cycle proteins  
## R-HSA-453276 Regulation of mitotic cell cycle  
## R-HSA-176814 Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins  
## R-HSA-8984722 Interleukin-35 Signalling  
## R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-168898 Toll-like Receptor Cascades  
## R-HSA-3000157 Laminin interactions  
## R-HSA-195258 RHO GTPase Effectors  
## R-HSA-2173782 Binding and Uptake of Ligands by Scavenger Receptors  
## R-HSA-381119 Unfolded Protein Response (UPR)  
## R-HSA-2029480 Fcgamma receptor (FCGR) dependent phagocytosis  
## R-HSA-176409 APC/C:Cdc20 mediated degradation of mitotic proteins  
## R-HSA-5602498 MyD88 deficiency (TLR2/4)  
## R-HSA-166786 Creation of C4 and C2 activators  
## R-HSA-983695 Antigen activates B Cell Receptor (BCR) leading to generation of second messengers  
## R-HSA-381038 XBP1(S) activates chaperone genes  
## R-HSA-112409 RAF-independent MAPK1/3 activation  
## R-HSA-202403 TCR signaling  
## R-HSA-5694530 Cargo concentration in the ER  
## R-HSA-416700 Other semaphorin interactions  
## R-HSA-1236977 Endosomal/Vacuolar pathway  
## R-HSA-2029481 FCGR activation  
## R-HSA-5603041 IRAK4 deficiency (TLR2/4)  
## R-HSA-9020956 Interleukin-27 signaling  
## R-HSA-451927 Interleukin-2 family signaling  
## R-HSA-176408 Regulation of APC/C activators between G1/S and early anaphase  
## R-HSA-381070 IRE1alpha activates chaperones  
## R-HSA-8874081 MET activates PTK2 signaling  
## R-HSA-204005 COPII-mediated vesicle transport  
## R-HSA-2022870 Chondroitin sulfate biosynthesis  
## R-HSA-186797 Signaling by PDGF  
## R-HSA-9020591 Interleukin-12 signaling  
## R-HSA-8851680 Butyrophilin (BTN) family interactions  
## R-HSA-179419 APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint  
## R-HSA-877312 Regulation of IFNG signaling  
## R-HSA-141424 Amplification of signal from the kinetochores  
## R-HSA-141444 Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal  
## R-HSA-264876 Insulin processing  
## R-HSA-2980736 Peptide hormone metabolism  
## R-HSA-2129379 Molecules associated with elastic fibres  
## R-HSA-194315 Signaling by Rho GTPases  
## R-HSA-5668599 RHO GTPases Activate NADPH Oxidases  
## R-HSA-6783589 Interleukin-6 family signaling  
## R-HSA-69618 Mitotic Spindle Checkpoint  
## R-HSA-202424 Downstream TCR signaling  
## R-HSA-446652 Interleukin-1 family signaling  
## R-HSA-2555396 Mitotic Metaphase and Anaphase  
## R-HSA-8877330 RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs)  
## R-HSA-8875878 MET promotes cell motility  
## R-HSA-174184 Cdc20:Phospho-APC/C mediated degradation of Cyclin A  
## R-HSA-2467813 Separation of Sister Chromatids  
## R-HSA-166016 Toll Like Receptor 4 (TLR4) Cascade  
## R-HSA-2500257 Resolution of Sister Chromatid Cohesion  
## R-HSA-140534 Caspase activation via Death Receptors in the presence of ligand  
## R-HSA-391160 Signal regulatory protein family interactions  
## R-HSA-75892 Platelet Adhesion to exposed collagen  
## R-HSA-69273 Cyclin A/B1/B2 associated events during G2/M transition  
## R-HSA-375276 Peptide ligand-binding receptors  
## R-HSA-2029482 Regulation of actin dynamics for phagocytic cup formation  
## R-HSA-5678895 Defective CFTR causes cystic fibrosis  
## R-HSA-1433557 Signaling by SCF-KIT  
## R-HSA-2514853 Condensation of Prometaphase Chromosomes  
## R-HSA-68882 Mitotic Anaphase  
## R-HSA-1236978 Cross-presentation of soluble exogenous antigens (endosomes)  
## R-HSA-196849 Metabolism of water-soluble vitamins and cofactors  
## R-HSA-446203 Asparagine N-linked glycosylation  
## R-HSA-2871809 FCERI mediated Ca+2 mobilization  
## R-HSA-352230 Amino acid transport across the plasma membrane  
## GeneRatio BgRatio pvalue p.adjust qvalue  
## R-HSA-449147 114/1034 437/9781 4.730038e-21 5.562524e-18 4.725059e-18  
## R-HSA-6785807 48/1034 104/9781 1.774301e-20 1.043289e-17 8.862168e-18  
## R-HSA-1474244 88/1034 300/9781 5.607711e-20 2.198223e-17 1.867269e-17  
## R-HSA-6798695 115/1034 469/9781 6.373703e-19 1.873869e-16 1.591749e-16  
## R-HSA-877300 41/1034 87/9781 4.365660e-18 1.026803e-15 8.722130e-16  
## R-HSA-913531 58/1034 191/9781 2.896136e-14 5.218617e-12 4.432928e-12  
## R-HSA-1236975 39/1034 98/9781 3.106320e-14 5.218617e-12 4.432928e-12  
## R-HSA-6783783 25/1034 44/9781 5.955236e-14 8.754196e-12 7.436209e-12  
## R-HSA-216083 34/1034 84/9781 7.849032e-13 1.025607e-10 8.711967e-11  
## R-HSA-1474228 43/1034 140/9781 4.347119e-11 5.112212e-09 4.342543e-09  
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## R-HSA-983170 15/1034 25/9781 2.457284e-09 1.730436e-07 1.469910e-07  
## R-HSA-2022090 24/1034 60/9781 2.501481e-09 1.730436e-07 1.469910e-07  
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## R-HSA-174184 16/1034 71/9781 2.544605e-03 3.085006e-02 2.620543e-02  
## R-HSA-2467813 32/1034 182/9781 2.605344e-03 3.126413e-02 2.655716e-02  
## R-HSA-166016 24/1034 125/9781 2.669677e-03 3.171253e-02 2.693805e-02  
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## R-HSA-1236977 567/1514/3107/3133/3134/3135  
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## R-HSA-8851680 10385/11119/11118/10384/30835/7498  
## R-HSA-179419 701/890/991/996/983/4085/4751/5684/5690/5696/5698/5699/5707/5720/5721/23198/11065  
## R-HSA-877312 3458/3459/3716/3717/9021/6772  
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## R-HSA-2980736 59272/183/1359/1363/30001/56605/60412/10640/54536/3479/3624/4311/4644/5122/7941/5873/90701/9789/60559  
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## R-HSA-2555396 9212/332/699/701/991/996/1058/1062/1063/23122/6249/26271/11004/57082/4085/10403/83540/5347/5520/5527/5684/5690/5696/5698/5699/5707/5720/5721/23198/9232/151246/348235/57405/11065  
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## R-HSA-174184 701/890/991/996/983/4085/5684/5690/5696/5698/5699/5707/5720/5721/23198/11065  
## R-HSA-2467813 9212/332/699/701/991/996/1058/1062/1063/23122/6249/11004/57082/4085/10403/83540/5347/5527/5684/5690/5696/5698/5699/5707/5720/5721/23198/9232/151246/348235/57405/11065  
## R-HSA-166016 330/695/841/929/1846/1848/3146/11213/3684/3689/23643/1326/9261/57162/5336/8767/6196/6283/6285/353376/7096/7097/7099/7323  
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## R-HSA-391160 961/2533/2885/140885/8935/7305  
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## R-HSA-69273 890/891/9133/994/983/2305/5347/5520  
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## R-HSA-449147 R-HSA-449147 Signaling by Interleukins  
## R-HSA-6783783 R-HSA-6783783 Interleukin-10 signaling  
## R-HSA-380108 R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-6785807 R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-6798695 R-HSA-6798695 Neutrophil degranulation  
## R-HSA-1442490 R-HSA-1442490 Collagen degradation  
## R-HSA-375276 R-HSA-375276 Peptide ligand-binding receptors  
## R-HSA-373076 R-HSA-373076 Class A/1 (Rhodopsin-like receptors)  
## R-HSA-6803157 R-HSA-6803157 Antimicrobial peptides  
## R-HSA-1592389 R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-75205 R-HSA-75205 Dissolution of Fibrin Clot  
## R-HSA-5668599 R-HSA-5668599 RHO GTPases Activate NADPH Oxidases  
## R-HSA-1474228 R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-8956321 R-HSA-8956321 Nucleotide salvage  
## R-HSA-74217 R-HSA-74217 Purine salvage  
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## R-HSA-380108 13/318 43/9464 8.042764e-10 2.171546e-07 2.091119e-07  
## R-HSA-6785807 18/318 99/9464 3.926113e-09 7.950379e-07 7.655920e-07  
## R-HSA-6798695 39/318 455/9464 5.616629e-08 9.098939e-06 8.761941e-06  
## R-HSA-1442490 10/318 62/9464 3.623967e-05 4.892356e-03 4.711158e-03  
## R-HSA-375276 16/318 158/9464 7.894203e-05 8.809551e-03 8.483272e-03  
## R-HSA-373076 22/318 266/9464 8.700791e-05 8.809551e-03 8.483272e-03  
## R-HSA-6803157 9/318 58/9464 1.215775e-04 1.094198e-02 1.053672e-02  
## R-HSA-1592389 6/318 31/9464 4.964512e-04 3.464751e-02 3.336427e-02  
## R-HSA-75205 4/318 12/9464 4.999350e-04 3.464751e-02 3.336427e-02  
## R-HSA-5668599 5/318 21/9464 5.417981e-04 3.464751e-02 3.336427e-02  
## R-HSA-1474228 13/318 134/9464 5.560711e-04 3.464751e-02 3.336427e-02  
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## Description  
## R-HSA-1474244 Extracellular matrix organization  
## R-HSA-449147 Signaling by Interleukins  
## R-HSA-6798695 Neutrophil degranulation  
## R-HSA-216083 Integrin cell surface interactions  
## R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-1474290 Collagen formation  
## R-HSA-913531 Interferon Signaling  
## R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-202733 Cell surface interactions at the vascular wall  
## R-HSA-1442490 Collagen degradation  
## R-HSA-2022090 Assembly of collagen fibrils and other multimeric structures  
## R-HSA-877300 Interferon gamma signaling  
## R-HSA-1236975 Antigen processing-Cross presentation  
## R-HSA-6783783 Interleukin-10 signaling  
## R-HSA-983705 Signaling by the B Cell Receptor (BCR)  
## R-HSA-1650814 Collagen biosynthesis and modifying enzymes  
## R-HSA-909733 Interferon alpha/beta signaling  
## R-HSA-3000178 ECM proteoglycans  
## R-HSA-381426 Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)  
## R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-1236974 ER-Phagosome pathway  
## R-HSA-381070 IRE1alpha activates chaperones  
## R-HSA-8957275 Post-translational protein phosphorylation  
## R-HSA-3000171 Non-integrin membrane-ECM interactions  
## R-HSA-977606 Regulation of Complement cascade  
## R-HSA-983695 Antigen activates B Cell Receptor (BCR) leading to generation of second messengers  
## R-HSA-3000157 Laminin interactions  
## R-HSA-381119 Unfolded Protein Response (UPR)  
## R-HSA-166658 Complement cascade  
## R-HSA-76002 Platelet activation, signaling and aggregation  
## R-HSA-381038 XBP1(S) activates chaperone genes  
## R-HSA-983170 Antigen Presentation: Folding, assembly and peptide loading of class I MHC  
## R-HSA-1236978 Cross-presentation of soluble exogenous antigens (endosomes)  
## R-HSA-8874081 MET activates PTK2 signaling  
## R-HSA-3000170 Syndecan interactions  
## R-HSA-5362768 Hh mutants that don't undergo autocatalytic processing are degraded by ERAD  
## R-HSA-8948216 Collagen chain trimerization  
## R-HSA-114604 GPVI-mediated activation cascade  
## R-HSA-5358346 Hedgehog ligand biogenesis  
## R-HSA-198933 Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell  
## R-HSA-174143 APC/C-mediated degradation of cell cycle proteins  
## R-HSA-453276 Regulation of mitotic cell cycle  
## R-HSA-5387390 Hh mutants abrogate ligand secretion  
## R-HSA-176409 APC/C:Cdc20 mediated degradation of mitotic proteins  
## R-HSA-176814 Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins  
## R-HSA-8875878 MET promotes cell motility  
## R-HSA-451927 Interleukin-2 family signaling  
## R-HSA-2022870 Chondroitin sulfate biosynthesis  
## R-HSA-5678895 Defective CFTR causes cystic fibrosis  
## R-HSA-5668541 TNFR2 non-canonical NF-kB pathway  
## R-HSA-5621481 C-type lectin receptors (CLRs)  
## R-HSA-8984722 Interleukin-35 Signalling  
## R-HSA-166663 Initial triggering of complement  
## R-HSA-114608 Platelet degranulation   
## R-HSA-69278 Cell Cycle, Mitotic  
## R-HSA-350562 Regulation of ornithine decarboxylase (ODC)  
## R-HSA-76005 Response to elevated platelet cytosolic Ca2+  
## R-HSA-176408 Regulation of APC/C activators between G1/S and early anaphase  
## R-HSA-162909 Host Interactions of HIV factors  
## R-HSA-2173782 Binding and Uptake of Ligands by Scavenger Receptors  
## R-HSA-174178 APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1  
## R-HSA-174184 Cdc20:Phospho-APC/C mediated degradation of Cyclin A  
## R-HSA-2871809 FCERI mediated Ca+2 mobilization  
## R-HSA-446203 Asparagine N-linked glycosylation  
## R-HSA-179419 APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint  
## R-HSA-75205 Dissolution of Fibrin Clot  
## R-HSA-447115 Interleukin-12 family signaling  
## R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-446652 Interleukin-1 family signaling  
## R-HSA-1168372 Downstream signaling events of B Cell Receptor (BCR)  
## R-HSA-1566948 Elastic fibre formation  
## R-HSA-202433 Generation of second messenger molecules  
## R-HSA-174154 APC/C:Cdc20 mediated degradation of Securin  
## R-HSA-202403 TCR signaling  
## R-HSA-202427 Phosphorylation of CD3 and TCR zeta chains  
## R-HSA-174113 SCF-beta-TrCP mediated degradation of Emi1  
## R-HSA-1793185 Chondroitin sulfate/dermatan sulfate metabolism  
## R-HSA-1059683 Interleukin-6 signaling  
## R-HSA-2029481 FCGR activation  
## R-HSA-9020956 Interleukin-27 signaling  
## R-HSA-202430 Translocation of ZAP-70 to Immunological synapse  
## R-HSA-453279 Mitotic G1-G1/S phases  
## R-HSA-388841 Costimulation by the CD28 family  
## R-HSA-5619084 ABC transporter disorders  
## R-HSA-2132295 MHC class II antigen presentation  
## R-HSA-8941858 Regulation of RUNX3 expression and activity  
## R-HSA-180534 Vpu mediated degradation of CD4  
## R-HSA-349425 Autodegradation of the E3 ubiquitin ligase COP1  
## R-HSA-69601 Ubiquitin Mediated Degradation of Phosphorylated Cdc25A  
## R-HSA-69610 p53-Independent DNA Damage Response  
## R-HSA-69613 p53-Independent G1/S DNA damage checkpoint  
## R-HSA-389948 PD-1 signaling  
## R-HSA-202424 Downstream TCR signaling  
## R-HSA-5607764 CLEC7A (Dectin-1) signaling  
## R-HSA-2243919 Crosslinking of collagen fibrils  
## R-HSA-3000480 Scavenging by Class A Receptors  
## R-HSA-1630316 Glycosaminoglycan metabolism  
## R-HSA-5621480 Dectin-2 family  
## R-HSA-9020702 Interleukin-1 signaling  
## R-HSA-3858494 Beta-catenin independent WNT signaling  
## R-HSA-180585 Vif-mediated degradation of APOBEC3G  
## R-HSA-8854050 FBXL7 down-regulates AURKA during mitotic entry and in early mitosis  
## R-HSA-211733 Regulation of activated PAK-2p34 by proteasome mediated degradation  
## R-HSA-69017 CDK-mediated phosphorylation and removal of Cdc6  
## R-HSA-68827 CDT1 association with the CDC6:ORC:origin complex  
## R-HSA-9604323 Negative regulation of NOTCH4 signaling  
## R-HSA-68867 Assembly of the pre-replicative complex  
## R-HSA-68886 M Phase  
## R-HSA-2454202 Fc epsilon receptor (FCERI) signaling  
## R-HSA-4608870 Asymmetric localization of PCP proteins  
## R-HSA-8939902 Regulation of RUNX2 expression and activity  
## R-HSA-8878159 Transcriptional regulation by RUNX3  
## R-HSA-204005 COPII-mediated vesicle transport  
## R-HSA-112409 RAF-independent MAPK1/3 activation  
## R-HSA-4086400 PCP/CE pathway  
## R-HSA-75815 Ubiquitin-dependent degradation of Cyclin D  
## R-HSA-194315 Signaling by Rho GTPases  
## R-HSA-2555396 Mitotic Metaphase and Anaphase  
## R-HSA-9020958 Interleukin-21 signaling  
## R-HSA-8939236 RUNX1 regulates transcription of genes involved in differentiation of HSCs  
## R-HSA-69541 Stabilization of p53  
## R-HSA-169911 Regulation of Apoptosis  
## R-HSA-512988 Interleukin-3, Interleukin-5 and GM-CSF signaling  
## R-HSA-194840 Rho GTPase cycle  
## R-HSA-68949 Orc1 removal from chromatin  
## R-HSA-3299685 Detoxification of Reactive Oxygen Species  
## R-HSA-1169091 Activation of NF-kappaB in B cells  
## R-HSA-352230 Amino acid transport across the plasma membrane  
## R-HSA-69620 Cell Cycle Checkpoints  
## R-HSA-2467813 Separation of Sister Chromatids  
## R-HSA-68882 Mitotic Anaphase  
## R-HSA-166786 Creation of C4 and C2 activators  
## R-HSA-5676590 NIK-->noncanonical NF-kB signaling  
## R-HSA-5658442 Regulation of RAS by GAPs  
## R-HSA-69615 G1/S DNA Damage Checkpoints  
## R-HSA-15869 Metabolism of nucleotides  
## R-HSA-4641257 Degradation of AXIN  
## R-HSA-174084 Autodegradation of Cdh1 by Cdh1:APC/C  
## R-HSA-8948751 Regulation of PTEN stability and activity  
## R-HSA-5607761 Dectin-1 mediated noncanonical NF-kB signaling  
## R-HSA-983169 Class I MHC mediated antigen processing & presentation  
## R-HSA-382556 ABC-family proteins mediated transport  
## R-HSA-8852276 The role of GTSE1 in G2/M progression after G2 checkpoint  
## R-HSA-450408 AUF1 (hnRNP D0) binds and destabilizes mRNA  
## R-HSA-1433557 Signaling by SCF-KIT  
## R-HSA-168898 Toll-like Receptor Cascades  
## R-HSA-912631 Regulation of signaling by CBL  
## R-HSA-6803157 Antimicrobial peptides  
## R-HSA-453274 Mitotic G2-G2/M phases  
## R-HSA-140534 Caspase activation via Death Receptors in the presence of ligand  
## R-HSA-1433559 Regulation of KIT signaling  
## R-HSA-2214320 Anchoring fibril formation  
## R-HSA-75892 Platelet Adhesion to exposed collagen  
## R-HSA-1234176 Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha  
## R-HSA-69563 p53-Dependent G1 DNA Damage Response  
## R-HSA-69580 p53-Dependent G1/S DNA damage checkpoint  
## R-HSA-4641258 Degradation of DVL  
## R-HSA-351202 Metabolism of polyamines  
## R-HSA-69002 DNA Replication Pre-Initiation  
## R-HSA-69481 G2/M Checkpoints  
## R-HSA-69052 Switching of origins to a post-replicative state  
## R-HSA-446219 Synthesis of substrates in N-glycan biosythesis  
## R-HSA-446193 Biosynthesis of the N-glycan precursor (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein  
## R-HSA-416700 Other semaphorin interactions  
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## R-HSA-1474290 9509/1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/1307/80781/85301/10491/1508/1514/3691/3909/3918/4015/4016/4017/4314/4316/4318/64175/55214/5033/5034/5118/5351/8985/5479/7837/871  
## R-HSA-913531 8086/103/684/818/960/4261/5610/1973/2209/2210/2633/2634/115361/115362/3113/3119/3122/3123/3126/3127/3133/3134/3383/2537/10437/3430/3437/8519/10581/10410/3455/3459/3659/3662/3665/10379/9636/3669/3716/3717/3836/3838/3837/4599/4600/4734/23636/4939/4940/5371/5696/5724/5770/8480/25939/6396/9021/6772/6773/81603/6737/10346/23650/10475/7318/9246/7412/54739  
## R-HSA-1474228 2/101/8754/8751/6868/9510/11096/56999/388743/960/1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/1307/80781/1508/1511/1513/1514/1634/2200/5045/3339/5654/3909/3912/3915/3918/4312/4313/4314/4316/4318/4319/4321/4327/64386/4811/5645/6696/7076/7077  
## R-HSA-202733 285/857/914/960/961/962/972/8832/83692/634/4680/1277/1278/90952/2207/2534/2734/2885/2995/3676/3678/3683/3684/3685/3687/3689/58494/83700/120425/3932/4067/4282/4312/5175/5196/10544/6383/9672/6401/6402/6403/6404/140885/8140/23428/23657/9123/7010/7040/7056/8797/8795/54210  
## R-HSA-1442490 8754/6868/1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/1307/80781/1508/1513/1514/5045/4312/4313/4314/4316/4318/4319/4321/4327/5645  
## R-HSA-2022090 1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/80781/85301/1508/1514/3691/3909/3918/4015/4016/4017/4314/4316/4318/5118/7837  
## R-HSA-877300 818/960/4261/2209/2210/2633/2634/115361/115362/3113/3119/3122/3123/3126/3127/3133/3134/3383/10437/3459/3659/3662/3665/10379/3716/3717/4939/4940/5371/5724/5770/9021/6772/81603/6737/10346/23650/10475/7412  
## R-HSA-1236975 695/811/1514/1536/2209/2210/3133/3134/3685/23643/4360/9902/653361/4688/4689/2923/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9554/29927/10952/6890/6891/6892/7096/7097/7099  
## R-HSA-6783783 6347/6351/6364/1230/729230/1234/942/2919/2920/3576/3627/2357/3383/3552/3553/3554/3557/3587/3716/5724/5743/6774/7076/7133  
## R-HSA-983705 695/808/930/973/974/27071/2534/2885/3708/4067/10892/4772/84876/80228/118788/5293/5336/5530/5534/5579/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/10125/25780/5966/6850/7409  
## R-HSA-1650814 9509/1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/1307/80781/85301/10491/64175/55214/5033/5034/5118/5351/8985/5479/871  
## R-HSA-909733 103/684/2634/3133/3134/2537/3430/3437/8519/10581/10410/3455/3659/3662/3665/10379/9636/3669/3716/4599/4600/4939/4940/5696/5770/25939/9021/6772/6773/54739  
## R-HSA-3000178 375790/633/1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1634/3339/3673/8516/3680/3685/3687/3909/3910/3912/3913/3915/4060/5802/5054/6678/7040/3371/1462  
## R-HSA-381426 348/8542/718/720/813/3491/10970/1511/5611/56975/2200/2266/11167/7184/3481/3488/3489/3490/3912/3913/3915/3956/4240/4312/4313/54587/5034/5069/255738/10130/5768/5954/6383/5265/51246/8404/6696/7076/54972/3371/1462/64856/7466  
## R-HSA-380108 51554/6364/1230/729230/1234/1236/2826/2919/2920/2921/6374/6372/3576/4283/3627/6373/6387/10563/58191/3579/7852/10663/5196  
## R-HSA-1236974 695/811/3133/3134/23643/2923/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9554/29927/10952/6890/6891/6892/7096/7097/7099  
## R-HSA-381070 4189/51726/5611/9695/2081/55033/3309/10525/11015/56005/10954/10130/5526/10113/22872/6734/58477/6745/84447/7094/7466/7494/10897  
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## R-HSA-3000171 87/375790/1277/1278/1281/1282/1284/1289/1290/50509/4921/3339/3673/3685/3691/3909/3910/3912/3913/3915/3918/6383/9672/7040/3371  
## R-HSA-977606 712/713/715/716/717/718/719/720/722/725/728/930/1604/966/975/629/3078/3426/1191/1378/710  
## R-HSA-983695 695/808/930/973/974/27071/2534/2885/3708/4067/84876/80228/118788/5293/5336/6850/7409  
## R-HSA-3000157 1282/1284/1294/80781/3339/3673/3685/3691/3909/3910/3912/3913/3915/3918/4811/22795  
## R-HSA-381119 440/811/6347/10488/90993/64764/3576/4189/51726/5611/9695/1965/8894/2081/55033/7184/3309/10525/11015/56005/10954/10130/5526/10113/22872/6734/58477/6745/84447/7094/7466/7494/10897  
## R-HSA-166658 712/713/715/716/717/718/719/720/722/725/728/930/1604/966/975/629/3078/3426/1191/1378/2219/8547/5648/710  
## R-HSA-76002 2/87/308/54518/409/808/813/7123/1191/1277/1278/1893/2149/2151/2207/2266/2534/2768/9630/2769/2771/59345/10681/2791/2885/3082/3309/3481/3708/3932/3937/4067/10916/7873/22915/5099/78991/10630/5175/5196/5294/8503/23533/5336/5341/5579/5583/5770/5768/5874/5880/10125/391/6403/5265/12/5054/710/6678/5552/6850/7040/7076/7078/7094/54495/54863/7409/7424/7450  
## R-HSA-381038 4189/51726/5611/9695/55033/10525/11015/56005/10954/10130/5526/10113/22872/6734/58477/6745/84447/7094/7466/7494/10897  
## R-HSA-983170 811/821/3133/3134/3309/2923/6396/10802/9632/9871/22872/6890/6891/6892  
## R-HSA-1236978 2209/2210/4360/9902/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198  
## R-HSA-8874081 1277/1278/1281/1289/1290/50509/85301/3082/3673/3909/3910/3912/3913/3915/3918  
## R-HSA-3000170 87/1277/1278/1281/1289/1290/50509/3673/3685/3691/6383/9672/7040/3371  
## R-HSA-5362768 51009/27248/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/6469/84447/7415  
## R-HSA-8948216 1277/1278/1281/1282/1284/1289/1290/50509/1291/1292/1293/1294/1295/1303/7373/1306/1307/80781/85301  
## R-HSA-114604 1277/1278/2207/2534/3932/3937/4067/10630/5294/8503/23533/5336/5880/391/6850/7409  
## R-HSA-5358346 6868/51009/27248/5034/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/6469/84447/7415  
## R-HSA-198933 718/915/930/958/975/4345/11314/146722/9976/1277/1278/1281/2209/2213/3133/3134/3383/3384/8519/3676/3683/3689/120425/3903/353514/10859/11006/8174/4277/5819/56654/29992/6402/89790/57823/54210/7305/7412  
## R-HSA-174143 6790/9212/701/890/891/991/246184/996/983/26271/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
## R-HSA-453276 6790/9212/701/890/891/991/246184/996/983/26271/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
## R-HSA-5387390 51009/27248/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/6469/84447/7415  
## R-HSA-176409 701/890/891/991/246184/996/983/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
## R-HSA-176814 701/890/891/991/246184/996/983/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
## R-HSA-8875878 1277/1278/1281/1289/1290/50509/85301/2885/3082/3673/3909/3910/3912/3913/3915/3918/84951  
## R-HSA-451927 1438/1439/2885/84868/3559/3563/3601/50615/3716/3717/3718/3932/5293/8503/6772/6774/6775/6850  
## R-HSA-2022870 633/79586/54480/50515/55501/51363/22856/55790/55454/1634/1462  
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## R-HSA-5668541 330/939/958/4050/4791/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/7133/8771/3604/4982/608/944/8741/10673/9966  
## R-HSA-5621481 808/841/30835/50856/26253/64581/2207/2534/3384/3553/3708/4067/10892/4582/4585/4586/727897/4772/4791/5336/5530/5534/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/6850  
## R-HSA-8984722 821/3572/9466/3716/3717/6772/6774/6775  
## R-HSA-166663 712/713/715/716/717/718/720/629/2219/8547/5648  
## R-HSA-114608 2/87/308/808/813/7123/1191/1893/2266/3082/3309/3481/10916/7873/22915/5099/78991/5175/5196/5341/5768/5874/6403/5265/12/5054/710/6678/5552/7040/7076/7078/7094/54495/54863/7424/7450  
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## R-HSA-176408 701/890/891/991/246184/996/983/26271/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/11065  
## R-HSA-162909 8086/8907/8905/130340/163/60489/920/1794/9844/2534/3055/3159/3836/3837/3932/4869/23636/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/8480/5905/6396  
## R-HSA-2173782 348/8542/811/9332/1277/1278/1281/1282/1284/3039/3043/7184/10808/10525/5648/6678  
## R-HSA-174178 6790/9212/991/246184/996/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
## R-HSA-174184 701/890/991/246184/996/983/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/11065  
## R-HSA-2871809 695/808/2207/2885/3702/3708/3937/4067/4772/5336/5530/5534/6850/7409  
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## R-HSA-75205 302/5327/5328/5329/5269/5271/5054/5270  
## R-HSA-447115 302/821/1265/9446/3572/3594/51561/9466/3716/3717/3936/4282/4478/5034/5306/5721/6648/6772/6774/6775  
## R-HSA-1592389 80781/1511/1513/5045/4312/4313/4314/4316/4318/4319/64386/5645/7076/7077  
## R-HSA-446652 240/834/1511/3552/3553/3554/3557/10068/8809/90865/3654/3656/11213/5604/1326/4791/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/5778/5784/8767/6283/6774  
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## R-HSA-1566948 2202/30008/11117/84034/2192/10516/2200/5045/3678/8516/3685/4015/4016/4017/4053/4237/7040  
## R-HSA-202433 915/920/2533/3113/3119/3122/3123/3126/3127/3702/3932/3937/7454  
## R-HSA-174154 991/246184/996/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198/9232/11065  
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## R-HSA-174113 991/26271/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198  
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## R-HSA-2029481 2209/2212/2268/2534/3055/4067/6850  
## R-HSA-9020956 821/3572/9466/3716/3717/6772/6774  
## R-HSA-202430 915/920/3113/3119/3122/3123/3126/3127/3932  
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## R-HSA-388841 10000/151888/915/920/942/29126/1493/2534/2885/3113/3119/3122/3123/3126/3127/3932/4067/1326/8503/5526/57761/7409  
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## R-HSA-69610 993/5682/5684/5686/5687/5690/5693/5696/5698/5699/5701/5704/5707/5718/10213/5720/5721/23198  
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## R-HSA-1474244 R-HSA-1474244  
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## R-HSA-1474228 R-HSA-1474228  
## R-HSA-216083 R-HSA-216083  
## R-HSA-418594 R-HSA-418594  
## R-HSA-6803157 R-HSA-6803157  
## R-HSA-1592389 R-HSA-1592389  
## R-HSA-2022090 R-HSA-2022090  
## R-HSA-76005 R-HSA-76005  
## R-HSA-1474290 R-HSA-1474290  
## R-HSA-114608 R-HSA-114608  
## R-HSA-3000178 R-HSA-3000178  
## R-HSA-381426 R-HSA-381426  
## R-HSA-8957275 R-HSA-8957275  
## R-HSA-71240 R-HSA-71240  
## R-HSA-168898 R-HSA-168898  
## R-HSA-75892 R-HSA-75892  
## R-HSA-202733 R-HSA-202733  
## R-HSA-8948216 R-HSA-8948216  
## R-HSA-5686938 R-HSA-5686938  
## R-HSA-352230 R-HSA-352230  
## R-HSA-1650814 R-HSA-1650814  
## R-HSA-114604 R-HSA-114604  
## R-HSA-166663 R-HSA-166663  
## R-HSA-210991 R-HSA-210991  
## R-HSA-186797 R-HSA-186797  
## R-HSA-913531 R-HSA-913531  
## Description  
## R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-375276 Peptide ligand-binding receptors  
## R-HSA-449147 Signaling by Interleukins  
## R-HSA-1442490 Collagen degradation  
## R-HSA-373076 Class A/1 (Rhodopsin-like receptors)  
## R-HSA-6798695 Neutrophil degranulation  
## R-HSA-500792 GPCR ligand binding  
## R-HSA-6783783 Interleukin-10 signaling  
## R-HSA-166658 Complement cascade  
## R-HSA-977606 Regulation of Complement cascade  
## R-HSA-1474244 Extracellular matrix organization  
## R-HSA-76002 Platelet activation, signaling and aggregation  
## R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-216083 Integrin cell surface interactions  
## R-HSA-418594 G alpha (i) signalling events  
## R-HSA-6803157 Antimicrobial peptides  
## R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-2022090 Assembly of collagen fibrils and other multimeric structures  
## R-HSA-76005 Response to elevated platelet cytosolic Ca2+  
## R-HSA-1474290 Collagen formation  
## R-HSA-114608 Platelet degranulation   
## R-HSA-3000178 ECM proteoglycans  
## R-HSA-381426 Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)  
## R-HSA-8957275 Post-translational protein phosphorylation  
## R-HSA-71240 Tryptophan catabolism  
## R-HSA-168898 Toll-like Receptor Cascades  
## R-HSA-75892 Platelet Adhesion to exposed collagen  
## R-HSA-202733 Cell surface interactions at the vascular wall  
## R-HSA-8948216 Collagen chain trimerization  
## R-HSA-5686938 Regulation of TLR by endogenous ligand  
## R-HSA-352230 Amino acid transport across the plasma membrane  
## R-HSA-1650814 Collagen biosynthesis and modifying enzymes  
## R-HSA-114604 GPVI-mediated activation cascade  
## R-HSA-166663 Initial triggering of complement  
## R-HSA-210991 Basigin interactions  
## R-HSA-186797 Signaling by PDGF  
## R-HSA-913531 Interferon Signaling  
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## R-HSA-375276 24/242 177/9781 8.797814e-12 1.794754e-09 1.608302e-09  
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## R-HSA-6798695 34/242 469/9781 1.365817e-08 1.194114e-06 1.070061e-06  
## R-HSA-500792 32/242 427/9781 1.737506e-08 1.329192e-06 1.191106e-06  
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## R-HSA-166658 10/242 56/9781 9.355586e-07 5.725619e-05 5.130801e-05  
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## R-HSA-1442490 13  
## R-HSA-373076 27  
## R-HSA-6798695 34  
## R-HSA-500792 32  
## R-HSA-6783783 10  
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## R-HSA-977606 9  
## R-HSA-1474244 23  
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## R-HSA-2022090 9  
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## R-HSA-3000178 9  
## R-HSA-381426 11  
## R-HSA-8957275 10  
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## Description  
## R-HSA-1474244 Extracellular matrix organization  
## R-HSA-449147 Signaling by Interleukins  
## R-HSA-6785807 Interleukin-4 and Interleukin-13 signaling  
## R-HSA-6783783 Interleukin-10 signaling  
## R-HSA-216083 Integrin cell surface interactions  
## R-HSA-6798695 Neutrophil degranulation  
## R-HSA-1474228 Degradation of the extracellular matrix  
## R-HSA-3000178 ECM proteoglycans  
## R-HSA-913531 Interferon Signaling  
## R-HSA-380108 Chemokine receptors bind chemokines  
## R-HSA-202733 Cell surface interactions at the vascular wall  
## R-HSA-877300 Interferon gamma signaling  
## R-HSA-3000171 Non-integrin membrane-ECM interactions  
## R-HSA-1442490 Collagen degradation  
## R-HSA-2022090 Assembly of collagen fibrils and other multimeric structures  
## R-HSA-166658 Complement cascade  
## R-HSA-909733 Interferon alpha/beta signaling  
## R-HSA-198933 Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell  
## R-HSA-1474290 Collagen formation  
## R-HSA-977606 Regulation of Complement cascade  
## R-HSA-381426 Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)  
## R-HSA-8957275 Post-translational protein phosphorylation  
## R-HSA-76002 Platelet activation, signaling and aggregation  
## R-HSA-3000157 Laminin interactions  
## R-HSA-3000170 Syndecan interactions  
## R-HSA-388841 Costimulation by the CD28 family  
## R-HSA-8874081 MET activates PTK2 signaling  
## R-HSA-375276 Peptide ligand-binding receptors  
## R-HSA-76005 Response to elevated platelet cytosolic Ca2+  
## R-HSA-114608 Platelet degranulation   
## R-HSA-168898 Toll-like Receptor Cascades  
## R-HSA-373076 Class A/1 (Rhodopsin-like receptors)  
## R-HSA-389948 PD-1 signaling  
## R-HSA-5621480 Dectin-2 family  
## R-HSA-1650814 Collagen biosynthesis and modifying enzymes  
## R-HSA-8875878 MET promotes cell motility  
## R-HSA-6811558 PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling  
## R-HSA-75205 Dissolution of Fibrin Clot  
## R-HSA-114604 GPVI-mediated activation cascade  
## R-HSA-199418 Negative regulation of the PI3K/AKT network  
## R-HSA-2219530 Constitutive Signaling by Aberrant PI3K in Cancer  
## R-HSA-202427 Phosphorylation of CD3 and TCR zeta chains  
## R-HSA-2173782 Binding and Uptake of Ligands by Scavenger Receptors  
## R-HSA-202430 Translocation of ZAP-70 to Immunological synapse  
## R-HSA-416700 Other semaphorin interactions  
## R-HSA-983695 Antigen activates B Cell Receptor (BCR) leading to generation of second messengers  
## R-HSA-166058 MyD88:MAL(TIRAP) cascade initiated on plasma membrane  
## R-HSA-168188 Toll Like Receptor TLR6:TLR2 Cascade  
## R-HSA-166016 Toll Like Receptor 4 (TLR4) Cascade  
## R-HSA-2029481 FCGR activation  
## R-HSA-168179 Toll Like Receptor TLR1:TLR2 Cascade  
## R-HSA-181438 Toll Like Receptor 2 (TLR2) Cascade  
## R-HSA-2022870 Chondroitin sulfate biosynthesis  
## R-HSA-500792 GPCR ligand binding  
## R-HSA-8948216 Collagen chain trimerization  
## R-HSA-983170 Antigen Presentation: Folding, assembly and peptide loading of class I MHC  
## R-HSA-1236975 Antigen processing-Cross presentation  
## R-HSA-1566948 Elastic fibre formation  
## R-HSA-202433 Generation of second messenger molecules  
## R-HSA-166663 Initial triggering of complement  
## R-HSA-381070 IRE1alpha activates chaperones  
## R-HSA-2219528 PI3K/AKT Signaling in Cancer  
## R-HSA-5602498 MyD88 deficiency (TLR2/4)  
## R-HSA-8877330 RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs)  
## R-HSA-2243919 Crosslinking of collagen fibrils  
## R-HSA-3000480 Scavenging by Class A Receptors  
## R-HSA-75892 Platelet Adhesion to exposed collagen  
## R-HSA-1592389 Activation of Matrix Metalloproteinases  
## R-HSA-9006934 Signaling by Receptor Tyrosine Kinases  
## R-HSA-112409 RAF-independent MAPK1/3 activation  
## R-HSA-352230 Amino acid transport across the plasma membrane  
## R-HSA-381038 XBP1(S) activates chaperone genes  
## R-HSA-451927 Interleukin-2 family signaling  
## R-HSA-5603041 IRAK4 deficiency (TLR2/4)  
## R-HSA-381119 Unfolded Protein Response (UPR)  
## R-HSA-5260271 Diseases of Immune System  
## R-HSA-5602358 Diseases associated with the TLR signaling cascade  
## R-HSA-6783589 Interleukin-6 family signaling  
## R-HSA-416476 G alpha (q) signalling events  
## R-HSA-2132295 MHC class II antigen presentation  
## R-HSA-210990 PECAM1 interactions  
## R-HSA-512988 Interleukin-3, Interleukin-5 and GM-CSF signaling  
## R-HSA-1793185 Chondroitin sulfate/dermatan sulfate metabolism  
## R-HSA-446652 Interleukin-1 family signaling  
## R-HSA-2129379 Molecules associated with elastic fibres  
## R-HSA-447115 Interleukin-12 family signaling  
## R-HSA-1630316 Glycosaminoglycan metabolism  
## R-HSA-5668599 RHO GTPases Activate NADPH Oxidases  
## R-HSA-373755 Semaphorin interactions  
## R-HSA-186797 Signaling by PDGF  
## R-HSA-975138 TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation  
## R-HSA-418594 G alpha (i) signalling events  
## R-HSA-168181 Toll Like Receptor 7/8 (TLR7/8) Cascade  
## R-HSA-975155 MyD88 dependent cascade initiated on endosome  
## R-HSA-9020958 Interleukin-21 signaling  
## R-HSA-9020591 Interleukin-12 signaling  
## R-HSA-5686938 Regulation of TLR by endogenous ligand  
## R-HSA-194138 Signaling by VEGF  
## R-HSA-6803157 Antimicrobial peptides  
## R-HSA-168643 Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways  
## R-HSA-2214320 Anchoring fibril formation  
## R-HSA-194840 Rho GTPase cycle  
## R-HSA-168138 Toll Like Receptor 9 (TLR9) Cascade  
## R-HSA-622312 Inflammasomes  
## R-HSA-1433557 Signaling by SCF-KIT  
## R-HSA-1059683 Interleukin-6 signaling  
## R-HSA-9009391 Non-genomic estrogen signaling  
## R-HSA-5684996 MAPK1/MAPK3 signaling  
## R-HSA-8950505 Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation  
## R-HSA-166166 MyD88-independent TLR4 cascade   
## R-HSA-937061 TRIF(TICAM1)-mediated TLR4 signaling   
## R-HSA-983705 Signaling by the B Cell Receptor (BCR)  
## R-HSA-168142 Toll Like Receptor 10 (TLR10) Cascade  
## R-HSA-168176 Toll Like Receptor 5 (TLR5) Cascade  
## R-HSA-975871 MyD88 cascade initiated on plasma membrane  
## R-HSA-5669034 TNFs bind their physiological receptors  
## R-HSA-912526 Interleukin receptor SHC signaling  
## R-HSA-389359 CD28 dependent Vav1 pathway  
## R-HSA-71240 Tryptophan catabolism  
## R-HSA-3906995 Diseases associated with O-glycosylation of proteins  
## R-HSA-389356 CD28 co-stimulation  
## R-HSA-389357 CD28 dependent PI3K/Akt signaling  
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## R-HSA-6798695 154664/101/240/196527/302/64333/23250/51411/684/718/719/728/960/963/1604/968/22918/4680/1116/338339/23601/1265/23406/1378/83716/1508/1512/2919/3577/3579/1536/8560/1794/2204/2207/2212/2219/2268/2357/2358/25801/11010/2760/9535/53831/3043/10855/3683/3684/3685/3687/3689/8514/3934/11026/79888/116844/4057/4069/8972/4282/4311/4318/64386/4332/23218/3071/10562/4973/5175/5315/5328/5329/4860/10549/5724/5788/25797/5768/11031/6279/6280/6282/6283/6286/6402/5265/12/1992/6317/5269/10326/6515/6556/6590/2040/10312/6947/7077/7097/7130/7133/7305/201294/8876  
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## R-HSA-3000171 87/375790/1277/1278/1281/1282/1284/1289/1290/4921/2247/2335/3339/3673/3685/3690/3691/3910/3911/3912/3913/3915/3918/7040/3371  
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## R-HSA-198933 718/911/930/933/947/958/975/4345/10666/342510/29121/1277/1278/1281/2209/2213/2214/3134/3383/3384/3385/8519/3676/3683/3689/11024/11026/353514/10859/11006/6402/114836/57823/54210/7305/7412  
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## R-HSA-977606 715/716/717/718/719/721/722/725/728/930/1604/975/629/3075/3078/3426/1191/1378/1380/710  
## R-HSA-381426 8542/718/721/813/2153/54757/56975/2200/2335/11167/7184/3488/3490/3569/3912/3913/3915/3956/4240/4312/4313/5034/5069/10130/5768/5954/5265/51246/8404/6696/7076/3371/1462/64856/7466  
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## R-HSA-76002 2/87/308/54518/813/135228/1191/1277/1278/2149/2151/2153/2207/83706/2335/2534/2769/2771/59345/2791/3082/3309/3671/3690/3708/3937/4067/10916/7873/22915/10630/5175/8503/23533/5336/5341/5579/5583/5768/5880/11069/10125/388/6403/5265/12/5054/710/6678/5552/7040/7042/7043/7076/7078/7409/7450  
## R-HSA-3000157 1282/1284/1294/3339/3673/3685/3691/3910/3911/3912/3913/3915/3918/4811/22795  
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## R-HSA-114608 2/87/308/813/135228/1191/2153/83706/2335/3082/3309/3671/3690/10916/7873/22915/5175/5341/5768/6403/5265/12/5054/710/6678/5552/7040/7042/7043/7076/7078/7450  
## R-HSA-168898 330/695/4064/1508/1513/1846/1848/1849/2353/7184/3656/11213/3684/3689/23643/5606/1326/9261/4791/4792/64127/5336/8767/6196/6279/6280/6283/6285/6288/7096/7097/7099/10333/51311/81793  
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## R-HSA-1650814 9509/1277/1278/1281/1282/1284/1289/1290/1291/1292/1293/1294/1303/7373/1306/5033/5034/5118/5351/871  
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## R-HSA-6811558 374/930/940/941/942/2069/2247/2252/2534/1839/3082/29851/8870/3556/9173/90865/3667/3815/3084/5156/5159/118788/8503/5305/5880/7409  
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## R-HSA-983695 695/930/933/973/27071/2534/3708/4067/80228/118788/5336/7409  
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## R-HSA-168179 695/1846/1848/1849/2353/3656/11213/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7096/7097/7099/10333  
## R-HSA-181438 695/1846/1848/1849/2353/3656/11213/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7096/7097/7099/10333  
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## R-HSA-8950505 302/1265/3458/3936/4282/4478/5721/5055/6648/6775  
## R-HSA-166166 330/1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099  
## R-HSA-937061 330/1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099  
## R-HSA-983705 695/84433/930/933/973/27071/2534/3708/4067/4792/80228/118788/5336/5579/5698/5699/5721/10125/25780/5966/7409  
## R-HSA-168142 1846/1848/1849/2353/3656/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/81793  
## R-HSA-168176 1846/1848/1849/2353/3656/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/81793  
## R-HSA-975871 1846/1848/1849/2353/3656/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/81793  
## R-HSA-5669034 939/7133/3604/4982/608/944/10673/9966  
## R-HSA-912526 1438/1439/3559/3563/3635/3717/3718/8503  
## R-HSA-389359 940/941/942/2534/7409  
## R-HSA-71240 3620/8564/8942/8140/6999  
## R-HSA-3906995 9510/9509/9507/11096/56999/81792/4582/4585/727897/140453/4854/10417/7058/221981  
## R-HSA-389356 10000/940/941/942/2534/4067/1326/8503/7409  
## R-HSA-389357 10000/940/941/942/2534/1326/8503  
## Count  
## R-HSA-1474244 100  
## R-HSA-449147 126  
## R-HSA-6785807 51  
## R-HSA-6783783 30  
## R-HSA-216083 38  
## R-HSA-6798695 105  
## R-HSA-1474228 48  
## R-HSA-3000178 34  
## R-HSA-913531 55  
## R-HSA-380108 24  
## R-HSA-202733 41  
## R-HSA-877300 32  
## R-HSA-3000171 25  
## R-HSA-1442490 26  
## R-HSA-2022090 24  
## R-HSA-166658 23  
## R-HSA-909733 25  
## R-HSA-198933 36  
## R-HSA-1474290 29  
## R-HSA-977606 20  
## R-HSA-381426 35  
## R-HSA-8957275 32  
## R-HSA-76002 57  
## R-HSA-3000157 15  
## R-HSA-3000170 14  
## R-HSA-388841 23  
## R-HSA-8874081 14  
## R-HSA-375276 42  
## R-HSA-76005 33  
## R-HSA-114608 32  
## R-HSA-168898 35  
## R-HSA-373076 58  
## R-HSA-389948 11  
## R-HSA-5621480 12  
## R-HSA-1650814 20  
## R-HSA-8875878 15  
## R-HSA-6811558 26  
## R-HSA-75205 8  
## R-HSA-114604 13  
## R-HSA-199418 27  
## R-HSA-2219530 21  
## R-HSA-202427 10  
## R-HSA-2173782 14  
## R-HSA-202430 9  
## R-HSA-416700 9  
## R-HSA-983695 12  
## R-HSA-166058 23  
## R-HSA-168188 23  
## R-HSA-166016 28  
## R-HSA-2029481 7  
## R-HSA-168179 23  
## R-HSA-181438 23  
## R-HSA-2022870 9  
## R-HSA-500792 70  
## R-HSA-8948216 14  
## R-HSA-983170 10  
## R-HSA-1236975 23  
## R-HSA-1566948 14  
## R-HSA-202433 11  
## R-HSA-166663 9  
## R-HSA-381070 14  
## R-HSA-2219528 23  
## R-HSA-5602498 6  
## R-HSA-8877330 6  
## R-HSA-2243919 8  
## R-HSA-3000480 8  
## R-HSA-75892 7  
## R-HSA-1592389 11  
## R-HSA-9006934 70  
## R-HSA-112409 9  
## R-HSA-352230 11  
## R-HSA-381038 13  
## R-HSA-451927 13  
## R-HSA-5603041 6  
## R-HSA-381119 20  
## R-HSA-5260271 9  
## R-HSA-5602358 9  
## R-HSA-6783589 9  
## R-HSA-416476 38  
## R-HSA-2132295 25  
## R-HSA-210990 6  
## R-HSA-512988 13  
## R-HSA-1793185 13  
## R-HSA-446652 26  
## R-HSA-2129379 11  
## R-HSA-447115 14  
## R-HSA-1630316 24  
## R-HSA-5668599 8  
## R-HSA-373755 15  
## R-HSA-186797 14  
## R-HSA-975138 19  
## R-HSA-418594 59  
## R-HSA-168181 19  
## R-HSA-975155 19  
## R-HSA-9020958 5  
## R-HSA-9020591 12  
## R-HSA-5686938 7  
## R-HSA-194138 21  
## R-HSA-6803157 18  
## R-HSA-168643 13  
## R-HSA-2214320 6  
## R-HSA-194840 25  
## R-HSA-168138 19  
## R-HSA-622312 7  
## R-HSA-1433557 11  
## R-HSA-1059683 5  
## R-HSA-9009391 16  
## R-HSA-5684996 40  
## R-HSA-8950505 10  
## R-HSA-166166 19  
## R-HSA-937061 19  
## R-HSA-983705 21  
## R-HSA-168142 17  
## R-HSA-168176 17  
## R-HSA-975871 17  
## R-HSA-5669034 8  
## R-HSA-912526 8  
## R-HSA-389359 5  
## R-HSA-71240 5  
## R-HSA-3906995 14  
## R-HSA-389356 9  
## R-HSA-389357 7

enr\_ind\_meta= merge(allenrupTtsmall,menrUp[,c('Description','p.adjust')],all.y=T,all.x=T,by='Description')  
colnames(enr\_ind\_meta)[ncol(enr\_ind\_meta)]='Meta-x8'  
#rownames(enr\_ind\_meta)=enr\_ind\_meta$Description  
#   
# # pca of this data  
# #PCA  
# #convert NA to 0  
# data=t(enr\_ind\_meta[,2:11])  
# data=-log10(data)  
# data[is.na(data)] <- 0  
#   
# summary(data)  
# # metadata  
#   
# #xtabs(~Response+treatment,pd)  
# pca\_data=prcomp(data,scale. = F)  
# pca\_data\_perc=round(100\*pca\_data$sdev^2/sum(pca\_data$sdev^2),1)  
#   
# df\_pca\_data = data.frame(PC1 = pca\_data$x[,1], PC2 = pca\_data$x[,2],  
# sample = rownames(data)  
# )#!!!!! adjust var names  
#   
# head(df\_pca\_data)  
# require(pcaExplorer)  
# ggplot(df\_pca\_data,aes(PC1,PC2))+geom\_point(size=3)+#!!!!! adjust var names  
# labs(x=paste0("PC1 (",pca\_data\_perc[1],")"), y=paste0("PC2 (",pca\_data\_perc[2],")"))+ggrepel::geom\_label\_repel(aes(label = sample))+theme\_bw()+  
# ggtitle('Enrichment, Up regulated genes ')  
#   
# #--  
  
topDs=list()  
k=3  
for (k in 2:(length(gse)+1)){  
x= enr\_ind\_meta[,c(1,k)]  
y= x %>% arrange(x[,2])   
topDs=c(topDs,y$Description[1:3])  
}  
  
c=enr\_ind\_meta[enr\_ind\_meta$Description %in% topDs,]  
require(reshape2)  
mc=melt(c)

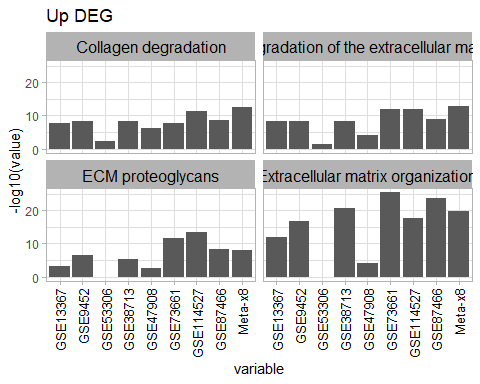
## Using Description as id variables

mc$Description=factor(mc$Description)  
levels(mc$Description)

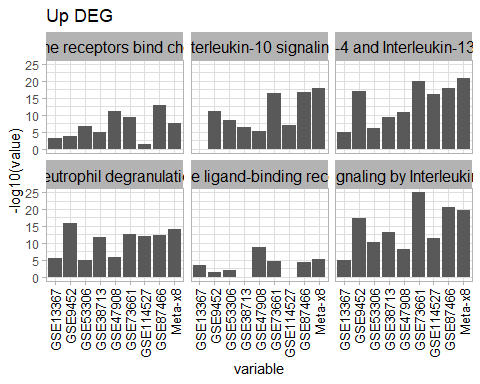
## [1] "Chemokine receptors bind chemokines"   
## [2] "Collagen degradation"   
## [3] "Degradation of the extracellular matrix"   
## [4] "ECM proteoglycans"   
## [5] "Extracellular matrix organization"   
## [6] "Interleukin-10 signaling"   
## [7] "Interleukin-4 and Interleukin-13 signaling"  
## [8] "Neutrophil degranulation"   
## [9] "Peptide ligand-binding receptors"   
## [10] "Signaling by Interleukins"

mc$Desc\_Group= 'Other'   
#check for changes  
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(1,6,7,8,9,10)]]='Immune\_Signaling'  
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(2,3,4,5)]]='ECM'  
#mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(10)]]='Neut'  
mc$Desc\_Group=factor(mc$Desc\_Group)  
# ggplot(mc, aes(x=Description,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
# theme(axis.text.x = element\_text(  
# color='black',size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Up')+facet\_grid(~variable)  
for (g in levels(mc$Desc\_Group)){  
 temp=mc%>% filter(mc$Desc\_Group %in% g)  
p=ggplot(temp, aes(x=variable,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
 theme(axis.text.x = element\_text(  
 color='black',size=10, angle=90,vjust = .5, hjust=1))+ggtitle('Up DEG')+facet\_wrap(~Description)+theme( strip.text.x = element\_text(  
 size = 12, color='black' ) )   
print(p)  
}

## Warning: Removed 2 rows containing missing values (geom\_bar).



## Warning: Removed 3 rows containing missing values (geom\_bar).



rm(enr\_ind\_meta)  
  
#for down--- ---  
require(plyr)  
#from indiv output :   
head(allenr\_down\_Ttsmall)

## Description GSE13367 GSE9452 GSE53306  
## 1 Abacavir transport and metabolism NA NA NA  
## 2 Beta-oxidation of very long chain fatty acids NA NA NA  
## 3 Bile acid and bile salt metabolism NA NA NA  
## 4 Biological oxidations 4.055148e-06 NA 0.01531844  
## 5 Branched-chain amino acid catabolism NA NA NA  
## 6 Cap-dependent Translation Initiation NA NA NA  
## GSE38713 GSE47908 GSE73661 GSE114527 GSE87466  
## 1 NA NA 1.281976e-02 NA NA  
## 2 NA NA 1.880374e-02 NA 6.044757e-03  
## 3 NA NA NA NA 1.946222e-02  
## 4 3.090294e-06 1.039131e-06 1.110401e-09 5.973875e-05 8.371041e-12  
## 5 2.261422e-03 NA 5.656039e-03 NA 4.576960e-02  
## 6 NA NA NA 2.056957e-06 NA

enr\_ind\_meta= merge(allenr\_down\_Ttsmall,menrDown[,c('Description','p.adjust')],all.y=T,all.x=T,by='Description')  
colnames(enr\_ind\_meta)[ncol(enr\_ind\_meta)]='Meta-x8'  
  
#rownames(enr\_ind\_meta)=enr\_ind\_meta$Description  
# #PCA  
# #convert NA to 0  
# data=t(enr\_ind\_meta[,2:13])  
# data=-log10(data)  
# data[is.na(data)] <- 0  
#   
# summary(data)  
# # metadata  
#   
# #xtabs(~Response+treatment,pd)  
# pca\_data=prcomp(data,scale. = F)  
# pca\_data\_perc=round(100\*pca\_data$sdev^2/sum(pca\_data$sdev^2),1)  
#   
# df\_pca\_data = data.frame(PC1 = pca\_data$x[,1], PC2 = pca\_data$x[,2],  
# sample = rownames(data)  
# )#!!!!! adjust var names  
#   
# head(df\_pca\_data)  
# require(pcaExplorer)  
# ggplot(df\_pca\_data,aes(PC1,PC2))+geom\_point(size=3)+#!!!!! adjust var names  
# labs(x=paste0("PC1 (",pca\_data\_perc[1],")"), y=paste0("PC2 (",pca\_data\_perc[2],")"))+ggrepel::geom\_label\_repel(aes(label = sample))+theme\_bw()+  
# ggtitle('Enrichment, Downregulated genes ')  
#   
# #--  
topDs=list()  
k=3  
for (k in 2:ncol(enr\_ind\_meta)){  
 x= enr\_ind\_meta[,c(1,k)]  
 y= x %>% arrange(x[,2])   
 topDs=c(topDs,y$Description[1:3])  
}  
  
c=enr\_ind\_meta[enr\_ind\_meta$Description %in% topDs,]  
#shorten some descriptions so fit in plot  
dput(c$Description)

## c("Abacavir transport and metabolism", "Beta-oxidation of very long chain fatty acids",   
## "Bile acid and bile salt metabolism", "Biological oxidations",   
## "Citric acid cycle (TCA cycle)", "Fatty acid metabolism", "Glucuronidation",   
## "Phase I - Functionalization of compounds", "Phase II - Conjugation of compounds",   
## "Respiratory electron transport", "Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.",   
## "Response to metal ions", "SLC-mediated transmembrane transport",   
## "The citric acid (TCA) cycle and respiratory electron transport"  
## )

# check for changes   
c$Description=c("Abacavir transport and metabolism", "Beta-oxidation of very long chain fatty acids",   
 "Bile acid and bile salt metabolism", "Biological oxidations",   
 "Citric acid cycle (TCA cycle)", "Fatty acid metabolism", "Glucuronidation",   
 "Phase I - Functionalization of compounds", "Phase II - Conjugation of compounds",   
 "Respiratory electron transport", "Respiratory electron transport,...",   
 "Response to metal ions", "SLC-mediated transmembrane transport",   
 "The citric acid (TCA) cycle and respiratory electron transport")  
  
# c$Description=c("Abacavir transport and metabolism", "Beta-oxidation of very long chain fatty acids",   
# "Bile acid and bile salt metabolism", "Biological oxidations",   
# "Chromatin modifying enzymes", "Chromatin organization", "Citric acid cycle (TCA cycle)",   
# "DNA Repair", "Fatty acid metabolism", "Glucuronidation", "Metallothioneins bind metals",   
# "Phase II - Conjugation of compounds", "Respiratory electron transport",   
# "Respiratory electron transport, ATP synthesis ...",   
# "Response to metal ions", "SLC-mediated transmembrane transport",   
# "The citric acid (TCA) cycle and ..."  
  
rm(enr\_ind\_meta)  
require(reshape2)  
mc=melt(c)

## Using Description as id variables

# ggplot(mc, aes(x=Description,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
# theme(axis.text.x = element\_text(  
# color='black',size=6, angle=45,vjust = 1, hjust=1))+ggtitle('Up')+facet\_grid(~variable)  
  
#group pathways for plotting  
mc$Description=factor(mc$Description)  
levels(mc$Description)

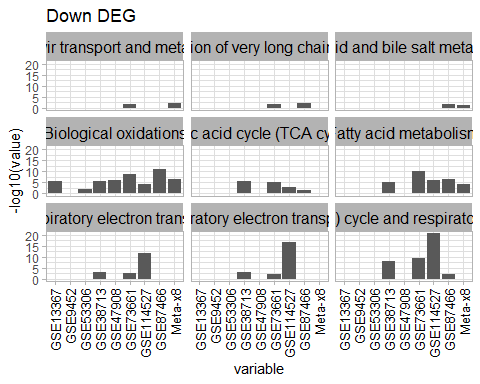
## [1] "Abacavir transport and metabolism"   
## [2] "Beta-oxidation of very long chain fatty acids"   
## [3] "Bile acid and bile salt metabolism"   
## [4] "Biological oxidations"   
## [5] "Citric acid cycle (TCA cycle)"   
## [6] "Fatty acid metabolism"   
## [7] "Glucuronidation"   
## [8] "Phase I - Functionalization of compounds"   
## [9] "Phase II - Conjugation of compounds"   
## [10] "Respiratory electron transport"   
## [11] "Respiratory electron transport,..."   
## [12] "Response to metal ions"   
## [13] "SLC-mediated transmembrane transport"   
## [14] "The citric acid (TCA) cycle and respiratory electron transport"

mc$Desc\_Group= 'Other' #todo: check if still same #  
dput(levels(mc$Description))

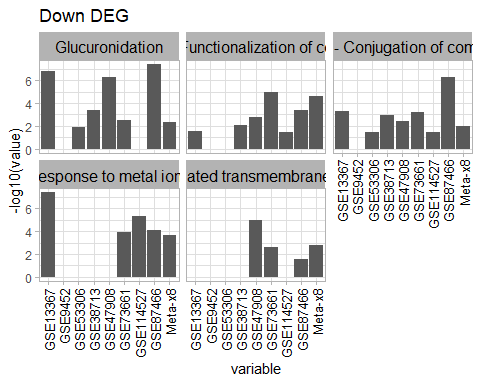
## c("Abacavir transport and metabolism", "Beta-oxidation of very long chain fatty acids",   
## "Bile acid and bile salt metabolism", "Biological oxidations",   
## "Citric acid cycle (TCA cycle)", "Fatty acid metabolism", "Glucuronidation",   
## "Phase I - Functionalization of compounds", "Phase II - Conjugation of compounds",   
## "Respiratory electron transport", "Respiratory electron transport,...",   
## "Response to metal ions", "SLC-mediated transmembrane transport",   
## "The citric acid (TCA) cycle and respiratory electron transport"  
## )

# c("Abacavir transport and metabolism",metab  
# "Beta-oxidation of very long chain fatty acids", -metabolism  
# # "Bile acid and bile salt metabolism",meta  
# "Biological oxidations", metab  
# # "Citric acid cycle (TCA cycle)", metab  
# "Fatty acid metabolism",metab  
# "Glucuronidation", -mod  
# # "Phase I - Functionalization of compounds",-mod  
# "Phase II - Conjugation of compounds",-mod  
# # "Respiratory electron transport",met  
# "Respiratory electron transport,...", metab  
# # "Response to metal ions",-response to external  
# "SLC-mediated transmembrane transport", transport  
# # "The citric acid (TCA) cycle and respiratory electron transport", metab  
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(1:6,10,11,14)]]='Metabolism'  
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(7,8,9,12,13)]]='Transport and modification'  
  
  
#mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(10)]]='Neut'  
mc$Desc\_Group=factor(mc$Desc\_Group)  
  
  
for (g in levels(mc$Desc\_Group)){  
 temp=mc%>% filter(mc$Desc\_Group %in% g)  
 p=ggplot(temp, aes(x=variable,y= -log10(value))) + geom\_bar(position = 'dodge',stat='identity')+theme\_light()+  
 theme(axis.text.x = element\_text(  
 color='black',size=10, angle=90,vjust = .5, hjust=1))+ggtitle('Down DEG')+facet\_wrap(~Description)+theme( strip.text.x = element\_text(  
 size = 12, color='black' ) )   
 print(p)  
}

## Warning: Removed 48 rows containing missing values (geom\_bar).



## Warning: Removed 14 rows containing missing values (geom\_bar).



#   
#   
# #find enrichemnt values from individual from selected pathways 'path;  
# path='Signaling by Interleukins'  
# max(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12],na.rm=T)  
# min(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12], na.rm=T)  
# median(as.numeric(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12]), na.rm=T)  
#   
# # for Interleukin-4 and Interleukin-13 signaling, the range was .41 (gse97012) to 2.43 e -21 (gse59071) with a median of 1.074e-15.  
# path='Interleukin-4 and Interleukin-13 signaling'  
# max(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12],na.rm=T)  
# min(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12], na.rm=T)  
# median(as.numeric(allenrupTtsmall[allenrupTtsmall$Description %in% path,2:12]), na.rm=T)  
#   
# # Down enriched  
#   
# menrDown$Description[menrDown$p.adjust<.05]  
# menrDown2= menrDown[1:20,]  
# # for the down regulated genes, the meta set had 16 enriched pathways, with the top 2 being 'Metallothioneins bind metals' (padj 0.0001490929) and "Fatty acid metabolism" (padj 0.0002756628)  
# # the range of the p.adj for met bind metals for individual datasets (excluding those w 0 deg) was between .92 (for GSE53306) and 6.63e-7 (for gse114527) (median of 1.46 e-5)  
#   
# path='Metallothioneins bind metals'  
# max(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12],na.rm=T)  
# min(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12], na.rm=T)  
# median(as.numeric(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12]), na.rm=T)  
#   
# # for Fatty acid metabolism in the individual datasets, the range is .95(gse97012) to 1.67e-12 (gse59071), with a median of 1.13e-5  
# path='Fatty acid metabolism'  
# max(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12],na.rm=T)  
# min(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12], na.rm=T)  
# median(as.numeric(allenr\_down\_Ttsmall[allenr\_down\_Ttsmall$Description %in% path,2:12]), na.rm=T)  
  
# Clustering of input datasets ####  
# what datasets have similar expression changes, do genes like osm and il13ra and trem1 all behave same in each datasets?  
# use cohens D, have them all calculated in toptable already, need to cross check calcs with Lenny/GY  
  
syms=as.character(unique(mrinput$SYMBOL))  
  
# gsett3=list()  
# for (k in 1:length(gsett)){  
# temp=gsett[[k]]  
# t2= temp[ match(syms , temp$SYMBOL),c("SYMBOL",'Cd')]  
# gsett3[[k]]=t2[!is.na(t2$SYMBOL),]  
# colnames(gsett3[[k]])[2]=paste('Cd',k,sep="")  
# }  
#   
# merged <- Reduce(function(x,y) merge(x,y,by='SYMBOL',all.y=F), gsett3)  
  
#use just fc  
gsett\_lfc=list()  
for (k in 1:length(gsett)){  
 temp=gsett[[k]]  
 t2= temp[ match(syms , temp$SYMBOL),c("SYMBOL",'logFC')]  
 gsett\_lfc[[k]]=t2[!is.na(t2$SYMBOL),]  
 colnames(gsett\_lfc[[k]])[2]=paste('logFC',k,sep="")  
}  
  
merged\_lfc <- Reduce(function(x,y) merge(x,y,by='SYMBOL',all.y=F), gsett\_lfc)  
colnames(merged\_lfc)[2:ncol(merged\_lfc)]=names(gse)  
#add meta   
mrtemp=mr[mr$SYMBOL %in% syms,c('randomSummary','SYMBOL')]  
merged\_lfc\_meta= merge(merged\_lfc,mrtemp ,all.y = F, by='SYMBOL')  
colnames(merged\_lfc\_meta)[ncol(merged\_lfc\_meta)]='Meta-x8'  
# colnames(merged\_lfc)=names(gse)  
# #use just pval  
# gsett\_pval=list()  
# for (k in 1:length(gsett)){  
# temp=gsett[[k]]  
# t2= temp[ match(syms , temp$SYMBOL),c("SYMBOL",'P.Value')]  
# gsett\_pval[[k]]=t2[!is.na(t2$SYMBOL),]  
# colnames(gsett\_pval[[k]])[2]=paste('pval',k,sep="")  
# }  
#   
# merged\_pval <- Reduce(function(x,y) merge(x,y,by='SYMBOL',all.y=F), gsett\_pval)  
#   
# colnames(merged\_pval)=names(gse)  
#   
# #use just pval up  
# gsett\_pvalup=list()  
# for (k in 1:length(gsett)){  
# temp=gsett[[k]]  
# t2= temp[ match(syms, temp$SYMBOL) ,c("SYMBOL",'P.Value','logFC')]  
# t3= t2[t2$logFC > 0,]  
# gsett\_pvalup[[k]]=t3[!is.na(t3$SYMBOL),]  
# colnames(gsett\_pvalup[[k]])[2]=paste('pval',k,sep="")  
# }  
#   
# merged\_pvalup <- Reduce(function(x,y) merge(x,y,by='SYMBOL',all.y=F), gsett\_pvalup)  
# colnames(merged\_pvalup)=names(gse)  
#   
# #use just pval down  
# gsett\_pvaldown=list()  
# for (k in 1:length(gsett)){  
# temp=gsett[[k]]  
# t2= temp[ match(syms, temp$SYMBOL) ,c("SYMBOL",'P.Value','logFC')]  
# t3= t2[t2$logFC < 0,]  
# gsett\_pvaldown[[k]]=t3[!is.na(t3$SYMBOL),]  
# colnames(gsett\_pvaldown[[k]])[2]=paste('logfc',k,sep="")  
# }  
#   
# merged\_pvaldown<- Reduce(function(x,y) merge(x,y,by='SYMBOL',all.y=F), gsett\_pvaldown)  
# colnames(merged\_pvaldown)=names(gse)  
  
#check  
# f=8  
# sym='IL13RA2'  
# gsett[[f]]$Cd[gsett[[f]]$SYMBOL %in% sym][1] == mergedCd[mergedCd$SYMBOL %in% sym, f+1]  
# # works! finally--------  
  
#run clustering   
  
data=data.frame(t(merged\_lfc\_meta[,2:ncol(merged\_lfc\_meta)])) # pick dataset  
colnames(data)=as.character(merged\_lfc\_meta$SYMBOL)  
#PCA  
#convert NA to 0  
data[is.na(data)] <- 0  
#summary(data)  
# metadata  
  
#xtabs(~Response+treatment,pd)  
pca\_data=prcomp(data,scale. = F)  
pca\_data\_perc=round(100\*pca\_data$sdev^2/sum(pca\_data$sdev^2),1)  
  
df\_pca\_data = data.frame(PC1 = pca\_data$x[,1], PC2 = pca\_data$x[,2],  
 sample = rownames(data)  
 )#!!!!! adjust var names  
  
head(df\_pca\_data)

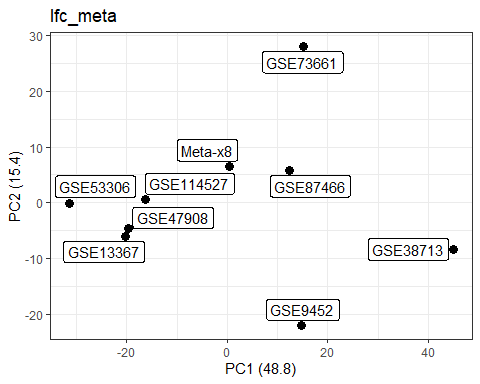
## PC1 PC2 sample  
## GSE13367 -20.23376 -6.00261812 GSE13367  
## GSE9452 14.82152 -22.01051412 GSE9452  
## GSE53306 -31.33187 -0.05150668 GSE53306  
## GSE38713 44.96627 -8.36454109 GSE38713  
## GSE47908 -19.73985 -4.52710293 GSE47908  
## GSE73661 15.23116 28.01060872 GSE73661

require(pcaExplorer)

## Loading required package: pcaExplorer

## Error: package or namespace load failed for 'pcaExplorer' in loadNamespace(i, c(lib.loc, .libPaths()), versionCheck = vI[[i]]):  
## namespace 'htmltools' 0.4.0 is already loaded, but >= 0.4.0.9003 is required

ggplot(df\_pca\_data,aes(PC1,PC2))+geom\_point(size=3)+#!!!!! adjust var names  
 labs(x=paste0("PC1 (",pca\_data\_perc[1],")"), y=paste0("PC2 (",pca\_data\_perc[2],")"))+ggrepel::geom\_label\_repel(aes(label = sample))+theme\_bw()+  
 ggtitle('lfc\_meta')



names(gse)

## [1] "GSE13367" "GSE9452" "GSE53306" "GSE38713" "GSE47908" "GSE73661"   
## [7] "GSE114527" "GSE87466"

#   
# ## Ward Hierarchical Clustering  
# d <- dist(data, method = "euclidean") # distance matrix  
# fit <- hclust(d, method="ward.D")  
# plot(fit) # display dendogram  
# groups <- cutree(fit, k=5) # cut tree into 5 clusters  
# # draw dendogram with red borders around the 5 clusters  
# rect.hclust(fit, k=5, border="red")  
#   
# # heatmap  
# require(heatmap3)  
# data=sapply(data,as.numeric)  
# #colnames(data)=names(gse)  
# #convert NA to 0  
# data[is.na(data)] <- 0  
# rownames(data)=colnames(merged\_lfc\_meta)[2:15]  
# str(data)  
# heatmap(t(data),scale='row',col=colorRampPalette(c("blue",  
# "white", "red"))(1024))  
#   
# #Correlation analysis, by dataset####   
# #uses 'data' from above   
# # require('DGCA')  
# # dd=ddcorAll(mr\_clean)  
# cor\_DS\_mrclean\_genesets=data.frame(cor(t(data)))  
# heatmap3(cor\_DS\_mrclean\_genesets,scale='none')  
#   
#   
# # #rev, by gene  
#   
cormr\_gen\_sp=data.frame(cor(data,method = 'spearman'))  
# # #genes from above  
c2=cormr\_gen\_sp[rownames(cormr\_gen\_sp)%in% genes,colnames(cormr\_gen\_sp) %in% genes]  
c2=(sapply(c2,as.numeric))  
rownames(c2)=colnames(c2)  
  
require(gplots)

## Loading required package: gplots

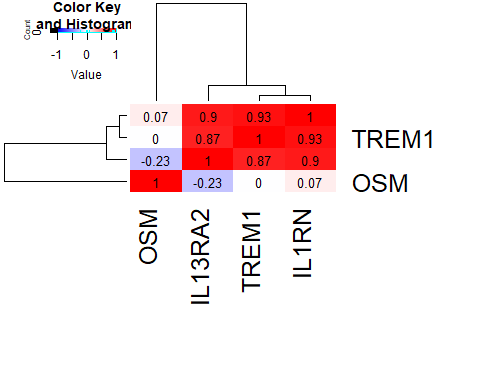
##   
## Attaching package: 'gplots'

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

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

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

heatmap.2(c2,margins=c(12,9),col=colorRampPalette(c("blue", "white", "red"))(1024),scale='none', notecol="black", cellnote = round(c2,2),trace='none')



save.image('../MetaProjects/MetaDEG\_v01/Output/mremx8\_aug13\_2020.Rdata')