Full\_analysisx8\_20AUG2020-v1.R

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# Full Analysis  
# Meta Deg manuscript ###  
### Versions  
# 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  
# 20AUG2020-v1 -update to remove GSE9452 from enrichment top pathways because is 0 and chosing by alphebetics, also clean  
  
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  
  
# 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  
  
   
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 )  
   
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 dataset #####  
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"

# Volcano plots ####  
#& volcano plots were produced with the R package 'EnhancedVolcano'  
require('EnhancedVolcano')

## Loading required package: EnhancedVolcano

## Loading required package: ggrepel

runit=F # 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)  
}  
}  
  
# 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 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] )  
 require(ggplot2)  
 enrdownTt[[k]]=enrichuniv(res1[ ixfcdown & ixp, symix],univ=res1[,symix] )  
 tp= enrdownTt[[k]][1:10,]  
 }}

## 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 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: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  
  
 #down enriched   
 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  
   
   
# 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).

#comment out if loading previous run  
# 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/mremresultx8.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")

#export top 10 up and down DEG  
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)  
  
# get counts  
length(mr$SYMBOL[mr$error==F])

## [1] 27858

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

## [1] 760

length(mrdown$SYMBOL[mrdown$signcon==-length(gse)])

## [1] 464

#\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  
# 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 #collapse probesets to gene level  
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) ##

## 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)))  
# compare deg ind to meta  
median(DEGtable$Up)/nrow(mrup)

## [1] 1.152748

median(DEGtable$Down)/nrow(mrdown)

## [1] 1.734807

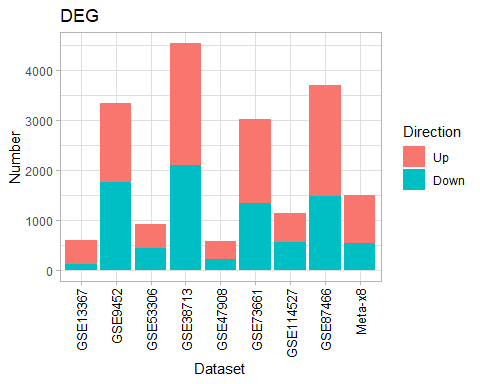
rownames(DEGtable\_wMeta)[length(gse)+1]='Meta-x8'  
DEGtable\_wMeta$Dataset= rownames(DEGtable\_wMeta)  
require(reshape2)

## Loading required package: reshape2

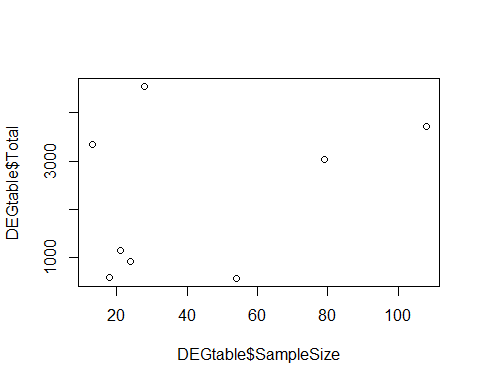
melt\_deg=melt(DEGtable\_wMeta)

## Using Dataset as id variables

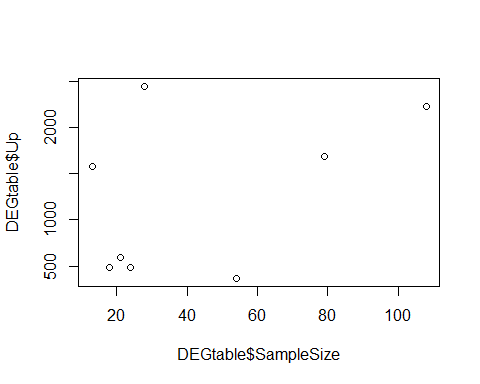
melt\_deg$Dataset = factor(melt\_deg$Dataset,levels =DEGtable\_wMeta$Dataset)  
colnames(melt\_deg)=c('Dataset','Direction','Number')  
  
  
ggplot(melt\_deg, aes(y=Number, x=Dataset,fill=Direction))+geom\_bar(stat='identity')+theme\_light()+  
 theme(axis.text.x = element\_text(  
 color="black",size=10, angle=90,vjust = .5, hjust=1))+ggtitle('DEG')



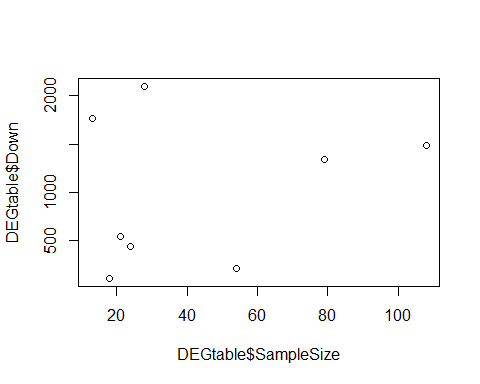
## add sample size vs deg  
DEGtable$Total = DEGtable$Up+DEGtable$Down  
DEGtable$SampleSize=c(18,13,24,28,54,79,21,108)#manually entered  
plot(DEGtable$SampleSize,DEGtable$Total)



plot(DEGtable$SampleSize,DEGtable$Up)



plot(DEGtable$SampleSize,DEGtable$Down)



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

## [1] 0.2142857

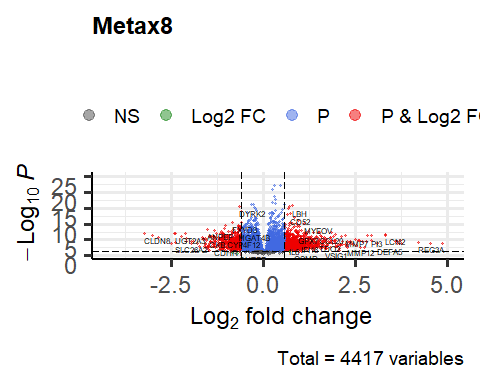
cor(DEGtable$SampleSize,DEGtable$Up,method = 'spearman')

## [1] 0.3095238

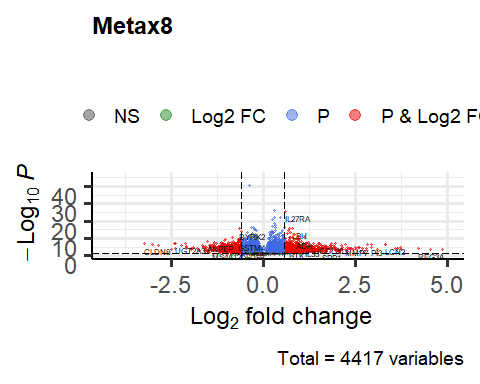
cor(DEGtable$SampleSize,DEGtable$Down,method = 'spearman')

## [1] 0.1428571

# Volcano plot meta results ####  
#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

#count numbers in each group on volcano plot  
fcandp=print(sum(abs(mrsc$randomSummary) >log2(1.5) & mrsc$adjP<.05)) # log and p

## [1] 1280

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

## [1] 4

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

## [1] 3020

none=print(sum( abs(mrsc$randomSummary) < log2(1.5) & !mrsc$adjP<.05))# neither

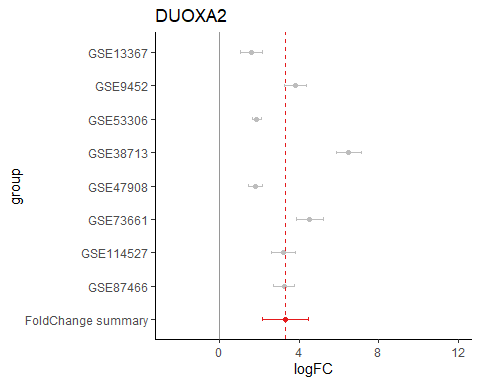
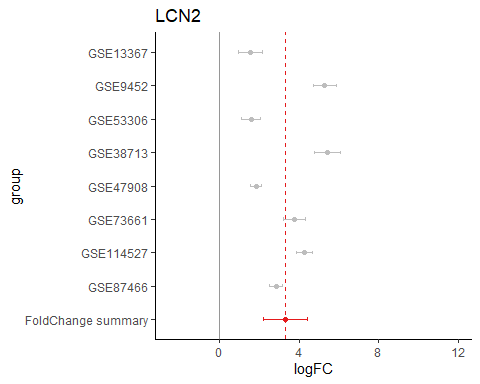
## [1] 113

total=(fcandp+fconly+ponly+none)  
  
#diagnostics  
#   
# hist( mr$signcon ,breaks = 25)  
# hist((mr$randomSummary),breaks = 100)  
# hist(-log10(mr$adjP) ,breaks=20000)  
# #combo=merge(mrinput,mr)  
#   
#   
# head(mrup,10)  
# head(mrdown,10)  
  
# Forest plots ####  
#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') # mod allows manual pick of axis length  
for (i in 1:2){  
 require(MetaVolcanoR);require(dplyr)  
   
 pl=draw\_forest\_mod(remres=meta\_degs\_rem,  
 gene=mrup$SYMBOL[i],  
 genecol=genenamecol1,  
 foldchangecol=foldchangecol,  
 llcol="CI.L",  
 rlcol="CI.R",  
 jobname="MetaVolcano",  
 outputfolder="../MetaProjects/MetaDEG\_v01/Output/Forests",  
 draw="PDF",xlim=c(-2.5,12))  
 #output stats  
 print(pl)  
 print(mrup$SYMBOL[i])  
 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



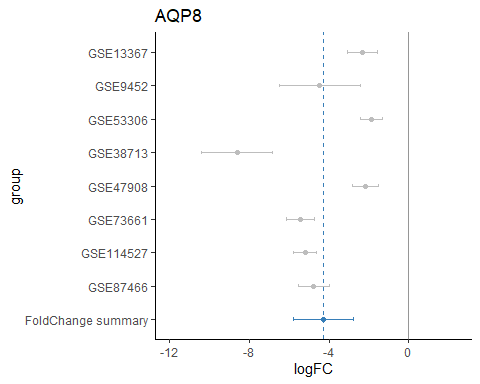
## [1] "DUOXA2"  
## [1] 6.497016  
## [1] 1.608536

draw\_forest

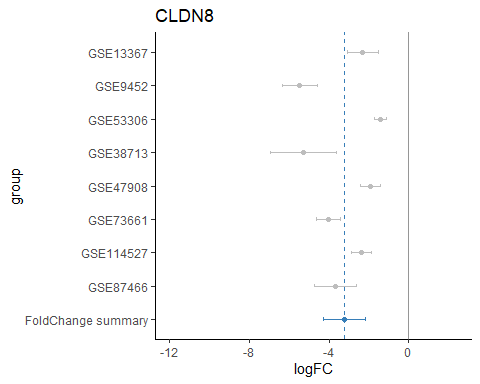
## function (remres, gene = "MMP9", genecol = "Symbol", foldchangecol = "Log2FC",   
## llcol = "CI.L", rlcol = "CI.R", jobname = "MetaVolcano",   
## outputfolder = ".", draw = "PDF")   
## {  
## if (!draw %in% c("PDF", "HTML")) {  
## stop("Oops! Seems like you did not provide a right 'draw' parameter. \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: 0x00000000298fa7b0>  
## <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

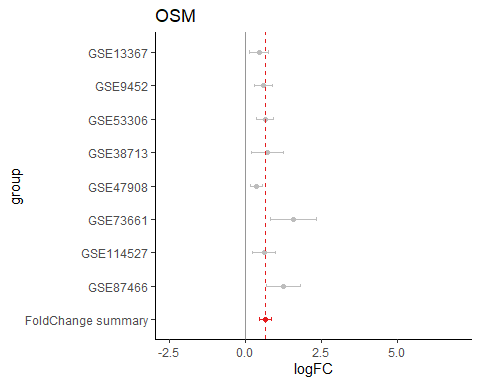


## [1] "CLDN8"  
## [1] -5.4705  
## [1] -1.402534

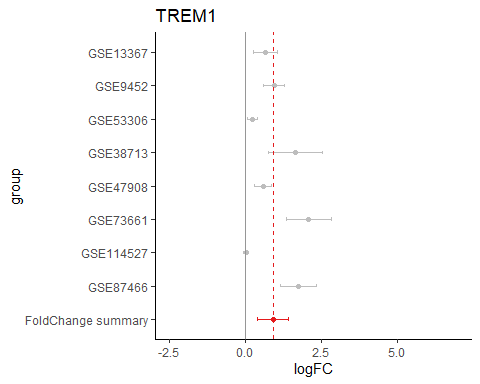


require(MetaVolcanoR)  
  
# Selected forests ####  
genes=c('OSM','TREM1','IL13RA2','IL1RN')  
#genes=c('CMTM2','C5AR1','FGF2','GK','HGF','IL1RN','LILRA2','NAMPT','PAPPA','SNCA','SOD2','STEAP4',"ZBED3")  
for (ea in genes){  
pl=draw\_forest\_mod(remres=meta\_degs\_rem,  
 gene=ea,  
 genecol=genenamecol1,  
 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('----------------------------------------------------------------------')  
}

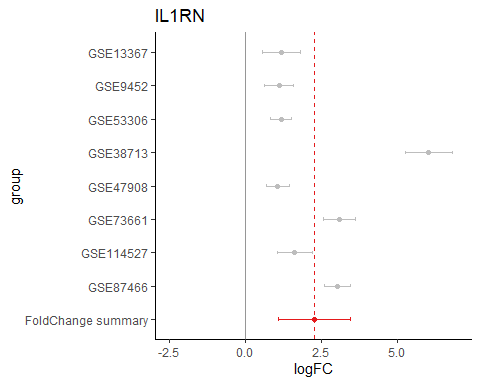
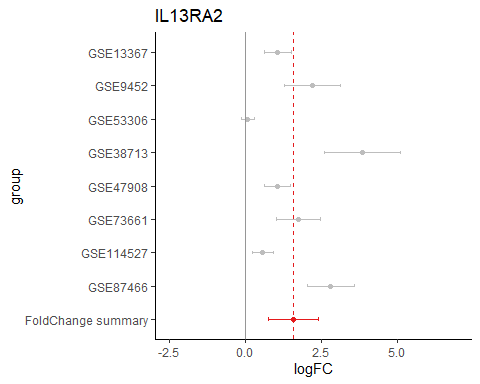
## [1] "OSM"  
## [1] 0.6513943  
## [1] 0.4450584  
## [1] 0.8577303  
## [1] 0.3398937  
## [1] 1.571981  
## [1] "----------------------------------------------------------------------"



## [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)  
  
menrUp=enrichuniv(mrup$SYMBOL,univ = mr$SYMBOL)# mrup and mrdown defined above   
menrDown=enrichuniv(mrdown$SYMBOL, univ=mr$SYMBOL)  
#& tables were created with the top 10 (lowest p.adjust) for enriched reactome pathways  
  
  
#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  
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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  
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## R-HSA-3000157 11  
## R-HSA-195258 47  
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## R-HSA-983695 11  
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## R-HSA-112409 9  
## R-HSA-202403 25  
## R-HSA-5694530 11  
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## R-HSA-1236977 6  
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## R-HSA-9020591 13  
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## R-HSA-877312 6  
## R-HSA-141424 20  
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## R-HSA-264876 9  
## R-HSA-2980736 19  
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## R-HSA-202424 20  
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## R-HSA-2555396 34  
## R-HSA-8877330 5  
## R-HSA-8875878 11  
## R-HSA-174184 16  
## R-HSA-2467813 32  
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## R-HSA-2500257 23  
## R-HSA-140534 6  
## R-HSA-391160 6  
## R-HSA-75892 6  
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## R-HSA-5678895 14  
## R-HSA-1433557 11  
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## R-HSA-68882 33  
## R-HSA-1236978 12  
## R-HSA-196849 23  
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## R-HSA-2871809 9  
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## ID Description  
## 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  
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## R-HSA-877300 R-HSA-877300  
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## R-HSA-2173782 R-HSA-2173782  
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## R-HSA-446203 R-HSA-446203  
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## R-HSA-75205 R-HSA-75205  
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## R-HSA-446652 R-HSA-446652  
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## R-HSA-1566948 R-HSA-1566948  
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## R-HSA-174113 R-HSA-174113  
## R-HSA-1793185 R-HSA-1793185  
## R-HSA-1059683 R-HSA-1059683  
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## R-HSA-69610 R-HSA-69610  
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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  
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## 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-5260271 R-HSA-5260271  
## R-HSA-5602358 R-HSA-5602358  
## R-HSA-6783589 R-HSA-6783589  
## R-HSA-416476 R-HSA-416476  
## R-HSA-2132295 R-HSA-2132295  
## R-HSA-210990 R-HSA-210990  
## R-HSA-512988 R-HSA-512988  
## R-HSA-1793185 R-HSA-1793185  
## R-HSA-446652 R-HSA-446652  
## R-HSA-2129379 R-HSA-2129379  
## R-HSA-447115 R-HSA-447115  
## R-HSA-1630316 R-HSA-1630316  
## R-HSA-5668599 R-HSA-5668599  
## R-HSA-373755 R-HSA-373755  
## R-HSA-186797 R-HSA-186797  
## R-HSA-975138 R-HSA-975138  
## R-HSA-418594 R-HSA-418594  
## R-HSA-168181 R-HSA-168181  
## R-HSA-975155 R-HSA-975155  
## R-HSA-9020958 R-HSA-9020958  
## R-HSA-9020591 R-HSA-9020591  
## R-HSA-5686938 R-HSA-5686938  
## R-HSA-194138 R-HSA-194138  
## R-HSA-6803157 R-HSA-6803157  
## R-HSA-168643 R-HSA-168643  
## R-HSA-2214320 R-HSA-2214320  
## R-HSA-194840 R-HSA-194840  
## R-HSA-168138 R-HSA-168138  
## R-HSA-622312 R-HSA-622312  
## R-HSA-1433557 R-HSA-1433557  
## R-HSA-1059683 R-HSA-1059683  
## R-HSA-9009391 R-HSA-9009391  
## R-HSA-5684996 R-HSA-5684996  
## R-HSA-8950505 R-HSA-8950505  
## R-HSA-166166 R-HSA-166166  
## R-HSA-937061 R-HSA-937061  
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## R-HSA-168142 R-HSA-168142  
## R-HSA-168176 R-HSA-168176  
## R-HSA-975871 R-HSA-975871  
## R-HSA-5669034 R-HSA-5669034  
## R-HSA-912526 R-HSA-912526  
## R-HSA-389359 R-HSA-389359  
## R-HSA-71240 R-HSA-71240  
## R-HSA-3906995 R-HSA-3906995  
## R-HSA-389356 R-HSA-389356  
## R-HSA-389357 R-HSA-389357  
## 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  
## GeneRatio BgRatio pvalue p.adjust qvalue  
## R-HSA-1474244 100/1032 292/9974 3.010638e-29 3.465244e-26 3.070850e-26  
## R-HSA-449147 126/1032 437/9974 1.761290e-28 1.013623e-25 8.982581e-26  
## R-HSA-6785807 51/1032 105/9974 2.238078e-23 8.586758e-21 7.609464e-21  
## R-HSA-6783783 30/1032 45/9974 1.405379e-19 4.043978e-17 3.583716e-17  
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## R-HSA-6798695 105/1032 461/9974 1.357737e-15 2.604591e-13 2.308152e-13  
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## R-HSA-1442490 26/1032 64/9974 2.248899e-10 1.848916e-08 1.638484e-08  
## R-HSA-2022090 24/1032 60/9974 1.623643e-09 1.245875e-07 1.104077e-07  
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## R-HSA-114604 13/1032 33/9974 1.144286e-05 3.333745e-04 2.954318e-04  
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## R-HSA-2219530 21/1032 74/9974 1.187520e-05 3.333745e-04 2.954318e-04  
## R-HSA-202427 10/1032 21/9974 1.632524e-05 4.473893e-04 3.964701e-04  
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## R-HSA-202430 9/1032 18/9974 2.686063e-05 6.870352e-04 6.088409e-04  
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## R-HSA-166058 23/1032 92/9974 4.413750e-05 1.058380e-03 9.379218e-04  
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## R-HSA-166016 28/1032 125/9974 5.934064e-05 1.393900e-03 1.235254e-03  
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## R-HSA-983170 10/1032 25/9974 1.027209e-04 2.111282e-03 1.870989e-03  
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## R-HSA-168176 17/1032 83/9974 4.367737e-03 4.371535e-02 3.873993e-02  
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## R-HSA-186797 1281/1282/1284/1289/1290/1291/1292/1293/5156/5159/6696/6772/6776/7058  
## R-HSA-975138 1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099/51311  
## R-HSA-418594 375790/183/301/187/718/719/728/6351/9560/6363/6364/6366/1230/729230/1233/1235/1236/2919/2920/2921/6374/6372/3576/4283/3627/6373/10563/58191/3577/3579/7852/643/2357/2358/2771/59345/2791/1880/338442/8843/3339/3352/3708/3838/3949/4023/7804/56923/53829/5142/23236/5368/5577/5996/5999/8490/6004/1901/6288  
## R-HSA-168181 1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099/51311  
## R-HSA-975155 1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099/51311  
## R-HSA-9020958 50615/3718/6772/6775/6776  
## R-HSA-9020591 302/1265/3458/3717/3936/4282/4478/5034/5721/5055/6648/6775  
## R-HSA-5686938 23643/6279/6280/7096/7097/7099/10333  
## R-HSA-194138 10000/857/1003/1536/9844/2321/2534/3685/3690/3708/3791/9261/653361/4688/4689/3071/8829/8828/5579/8877/7409  
## R-HSA-6803157 729230/1235/1191/1670/1671/100289462/3934/4057/4069/5266/5320/5068/6039/6279/6280/6556/7096/7097  
## R-HSA-168643 9447/330/834/837/3656/4210/4791/22861/114548/64127/24145/8767/7128  
## R-HSA-2214320 1277/1278/1282/1284/1294/3918  
## R-HSA-194840 2/64333/9824/55843/83478/9938/9411/257106/57514/397/50650/9459/1123/1894/221472/64857/57580/5880/5924/388/399/57381/23380/117289/7409  
## R-HSA-168138 1846/1848/1849/2353/3656/23643/5606/1326/9261/4791/4792/64127/8767/6196/6283/6285/6288/7099/51311  
## R-HSA-622312 9447/834/4210/4791/22861/114548/24145  
## R-HSA-1433557 2534/10750/2887/3717/3815/4067/4318/8503/6772/6776/7409  
## R-HSA-1059683 3569/3572/3717/9021/6772  
## R-HSA-9009391 10000/374/857/858/2069/2353/2771/59345/2791/1839/4313/4314/4316/4318/8503/8877  
## R-HSA-5684996 54518/374/1438/1439/1843/1846/1848/1849/11221/2069/2247/2252/2335/2534/1839/3082/3559/3563/3569/3572/3667/3690/3717/3718/3815/3084/5156/5159/8682/5698/5699/5721/10156/64926/5924/10125/25780/53358/7010/7450  
## 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'  
  
#select top 3 from each dataset (unless there are 0 enriched)  
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)

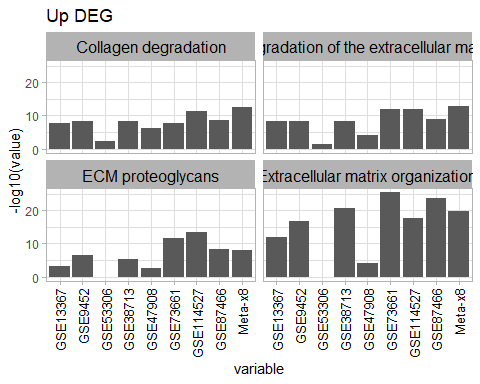
## Using Description as id variables

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

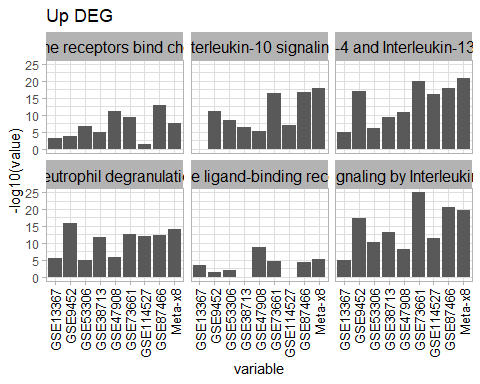
## [1] "Chemokine receptors bind chemokines"   
## [2] "Collagen degradation"   
## [3] "Degradation of the extracellular matrix"   
## [4] "ECM proteoglycans"   
## [5] "Extracellular matrix organization"   
## [6] "Interleukin-10 signaling"   
## [7] "Interleukin-4 and Interleukin-13 signaling"  
## [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)  
  
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);require(dplyr)  
#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'  
  
  
topDs=list()  
k=3  
dput(colnames(enr\_ind\_meta))

## c("Description", "GSE13367", "GSE9452", "GSE53306", "GSE38713",   
## "GSE47908", "GSE73661", "GSE114527", "GSE87466", "Meta-x8")

## !!remove GSE9452 bc has 0 enriched  
for (k in c(2,4:10)){  
 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("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   
# shorten names for plotting  
c$Description=c("Biological oxidations", #1  
 "Citric acid cycle (TCA cycle)",#2  
 "Fatty acid metabolism", #3  
 "Glucuronidation", #4  
 "Phase I - Functionalization of compounds", #5  
 "Phase II - Conjugation of compounds", #6  
 "Respiratory electron transport", #7  
 "Respiratory electron transport, ATP ...", #8  
 "Response to metal ions", #9  
 "SLC-mediated transmembrane transport", #10  
 "The citric acid (TCA) cycle and respiratory ...") #11  
  
rm(enr\_ind\_meta)  
require(reshape2)  
mc=melt(c)

## Using Description as id variables

#group pathways for plotting  
mc$Description=factor(mc$Description)  
levels(mc$Description)

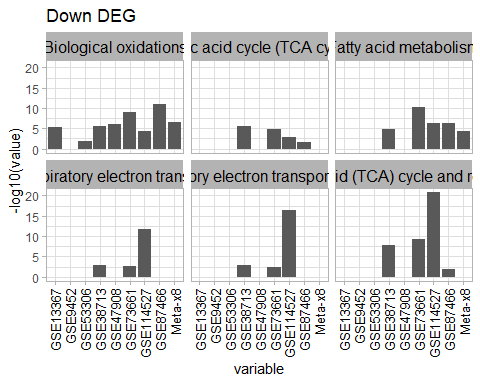
## [1] "Biological oxidations"   
## [2] "Citric acid cycle (TCA cycle)"   
## [3] "Fatty acid metabolism"   
## [4] "Glucuronidation"   
## [5] "Phase I - Functionalization of compounds"   
## [6] "Phase II - Conjugation of compounds"   
## [7] "Respiratory electron transport"   
## [8] "Respiratory electron transport, ATP ..."   
## [9] "Response to metal ions"   
## [10] "SLC-mediated transmembrane transport"   
## [11] "The citric acid (TCA) cycle and respiratory ..."

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

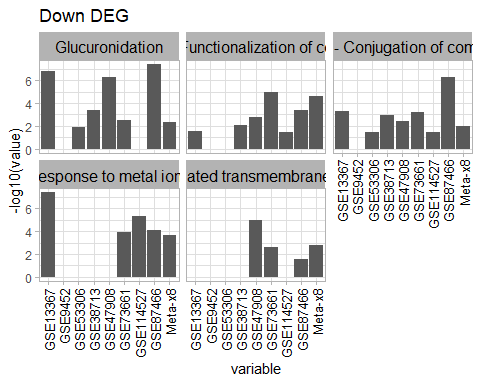
## c("Biological oxidations", "Citric acid cycle (TCA cycle)", "Fatty acid metabolism",   
## "Glucuronidation", "Phase I - Functionalization of compounds",   
## "Phase II - Conjugation of compounds", "Respiratory electron transport",   
## "Respiratory electron transport, ATP ...", "Response to metal ions",   
## "SLC-mediated transmembrane transport", "The citric acid (TCA) cycle and respiratory ..."  
## )

# check for changes   
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(1,2,3,7,8,11)]]='Metabolism'  
mc$Desc\_Group[mc$Description %in% levels(mc$Description)[c(4,5,6,9,10)]]='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 27 rows containing missing values (geom\_bar).



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



#get genes in meta enriched to give examples of genes enriched in list ( in the meta deg not the indiv)  
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

#   
# PCA of input datasets ####  
syms=as.character(unique(mrinput$SYMBOL))  
  
#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'  
  
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  
  
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)

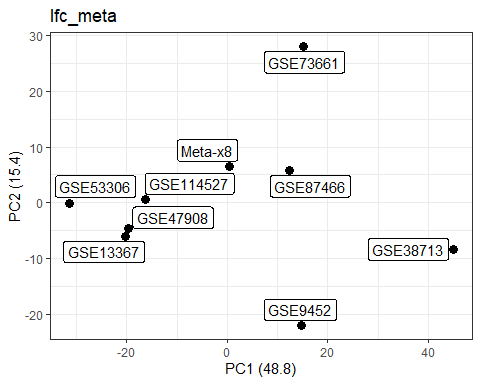
## PC1 PC2 sample  
## GSE13367 -20.23376 -6.00261812 GSE13367  
## GSE9452 14.82152 -22.01051412 GSE9452  
## GSE53306 -31.33187 -0.05150668 GSE53306  
## GSE38713 44.96627 -8.36454109 GSE38713  
## GSE47908 -19.73985 -4.52710293 GSE47908  
## GSE73661 15.23116 28.01060872 GSE73661

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"

# Correlation by selected genes (genes defined above (OSM, TREM etc)) ####  
# # #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

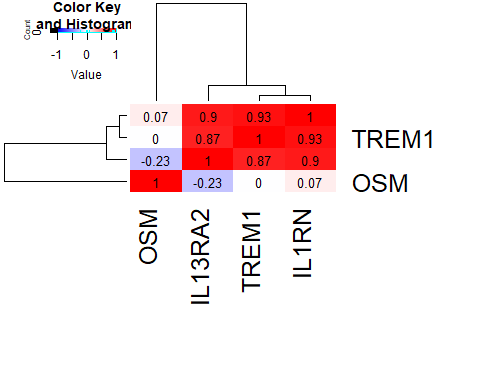
##   
## Attaching package: 'gplots'

## 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\_aug20\_2020v1.Rdata')