#ssgsea and genes correlation analysis

library(GSVA)

library(tidyverse)

library(ggpubr)

library(ggplot2)

library(pheatmap)

GSE39582\_series\_tumor<-read.csv("bindgeo\_exp.csv",header = T,row.names = 1,sep = ",")

library(tidyverse)

cellMarker1 <- read.delim("1.txt", header = F, sep = "\t") #

cellMarker1 <- cellMarker1 %>% column\_to\_rownames("V1") %>% t()

a <- cellMarker1

a[1:5,1:5]

a <- a[1:nrow(a), ]

set <- colnames(a)

geneSet <- list()

for (i in set) {

x <- as.character(a[,i])

x <- x[nchar(x)!=0]

x <- as.character(x)

geneSet[[i]] <-x

}

library(GSVA)

GSE39582\_series\_tumor=as.matrix(GSE39582\_series\_tumor)

gsva\_matrix1 <- gsva(GSE39582\_series\_tumor, geneSet, method='ssgsea', kcdf='Gaussian', abs.ranking=TRUE)

res <- gsva\_matrix1

pheatmap(res, show\_colnames = F)

group\_list <- read.csv("group.csv",header = T,row.names = 1,sep = ",")

annotation <- data.frame(group\_list)

rownames(annotation) <- colnames(res)

resm<-res

for(i in colnames(res)){

resm[,i]<-(res[,i]-min(res[,1]))/max(res[,i]-min(res[,i]))

}

pheatmap(res,

show\_colnames = F,

annotation\_col = annotation,

fontsize = 10,

)

dt<-resm%>%t()%>%as.data.frame()%>%

rownames\_to\_column("sample")%>%

gather(key = cell\_type,

value = value,-sample)

head(dt)

dtt<-dt%>%

group\_by(sample)%>%

mutate(proportion=round(value/sum(value),3))

head(dtt)

dtt$cell\_type<-factor(dtt$cell\_type,levels = unique(rownames(res)))

mytheme<-theme(axis.title = element\_text(size=12),

axis.text.x = element\_blank(),

axis.ticks.x = element\_blank(),

plot.title = element\_text(size = 13,

hjust = 0.5,

face = "bold"),

legend.text = element\_text(size = 10),

legend.position = "bottom")

library(paletteer)

d\_palettes<-palettes\_d\_names

col<-paletteer\_d("khroma::smoothrainbow",n=28)

p<-ggplot(dtt,

aes(x=cell\_type,y=proportion,fill=cell\_type))+

geom\_boxplot(color="black",alpha=0.6,outlier.shape = 21,outlier.size = 1.2)+

scale\_fill\_manual(values = col)+

labs(x="cell type",y="proportion")+

theme\_bw()+mytheme

p

write.table(dtt,file="dtt.csv",sep=",",quote=T,row.names=T)

rest<-t(res)

write.table(rest,file="rest.csv",sep=",",quote=T,row.names=T)

#然后加上分组和列

dtt<-read.csv("dtt.csv",header = T,row.names = 1,sep = ",")

colnames(dtt)

library(tidyverse)

p1<-ggplot(dtt,

aes(x=cell\_type,y=proportion,fill=group))+

geom\_boxplot(color="black",alpha=0.6,outlier.shape = 21,outlier.size = 1.2)+

scale\_fill\_manual(values = c("#4979b6","#d9352a"))+

labs(x="cell type",y="proportion")+

theme\_bw()+mytheme+theme(axis.text.x = element\_text(angle=45))

p1

library(ggsignif)

pvalues <- sapply(dtt$cell\_type, function(x) {

res <- wilcox.test(as.numeric(proportion) ~ group, data = subset(dtt, cell\_type == x)) #两组，wilcox.test或t.test；多组，kruskal.test或aov(one-way ANOVA test)

res$p.value

})

pv <- data.frame(gene = dtt$cell\_type, pvalue = pvalues)

pv$sigcode <- cut(pv$pvalue, c(0,0.0001, 0.001, 0.01, 0.05, 1),

labels=c('\*\*\*\*','\*\*\*', '\*\*', '\*', 'ns'))

p.box <- ggplot(dtt, aes(x=cell\_type, y=proportion, color=group, fill=group)) +

geom\_boxplot(alpha = .5) + #半透明

theme\_classic() + #或theme\_bw()

scale\_fill\_brewer(palette = "Set1") + #按类填充颜色

scale\_color\_brewer(palette = "Set1") + #按类给边框着色

theme(axis.text.x = element\_text(colour="black", size = 11,

#名太挤，旋转45度

angle = 90, hjust = .5, vjust = .5)) +

geom\_text(aes(x=gene, y=max(dtt$proportion) \* 1.1,

label = pv$sigcode),

data=pv,

inherit.aes=F)

p.box

library(ggcorrplot)

library(tidyr)

exp<-read.csv("bindgeo\_exp.csv",row.names = 1)

re<-read.csv("res.csv",row.names = 1)

mygene <- c("RRM2","DLGAP5",'KIF11') #定义你的目的基因

nc = t(rbind(re,exp[mygene,])) ;#将你的目的基因匹配到表达矩阵---行名匹配--注意大小写

m = rcorr(nc)$r[1:nrow(re),(ncol(nc)-length(mygene)+1):ncol(nc)]

##计算p值

p = rcorr(nc)$P[1:nrow(re),(ncol(nc)-length(mygene)+1):ncol(nc)]

head(p)

tmp <- matrix(case\_when(as.vector(p) < 0.01 ~ "\*\*",

as.vector(p) < 0.05 ~ "\*",

TRUE ~ ""), nrow = nrow(p))

##绘制热图

library(pheatmap)

p1 <- pheatmap(t(m),

display\_numbers =t(tmp),

angle\_col =45,

color = colorRampPalette(c("#92b7d1", "white", "#d71e22"))(100),

border\_color = "white",

cellwidth = 20,

cellheight = 20,

width = 7,

height=9.1,

treeheight\_col = 0,

treeheight\_row = 0)