**We have provided the main code and labeled the figure order. Some of the figures are from online mapping sites.**

**Figure 2B**

#install.packages("ggpubr")

library(ggpubr)

inputFile="geneExp.txt"

setwd("C:\\LY9.panDiff")

data=read.table(inputFile, header=T, sep="\t", check.names=F)

gene=colnames(data)[2]

colnames(data)[2]="expression"

Normal=data[data[,"Type"]=="Normal",]

NormalNum=table(Normal[,"CancerType"])

NormalNum=NormalNum[NormalNum>=5]

NormalCacner=names(NormalNum)

data=data[which(data[,"CancerType"] %in% NormalCacner),]

p=ggboxplot(data, x="CancerType", y="expression", color="Type",

 xlab="",

 ylab=paste0(gene," expression"),

 palette = c("green","red") )

p=p+rotate\_x\_text(60)

pdf(file="boxplot.pdf", width=7.5, height=5)

p+stat\_compare\_means(aes(group=Type),

 method="wilcox.test",

 symnum.args=list(cutpoints = c(0, 0.001, 0.01, 0.05, 1), symbols = c("\*\*\*", "\*\*", "\*", " ")),

 label = "p.signif")

dev.off()

**Figure 4A**

#if (!requireNamespace("BiocManager", quietly = TRUE))

# install.packages("BiocManager")

#BiocManager::install("limma")

#install.packages("beeswarm")

#引用包

library(limma)

library(beeswarm)

inputFile="symbol.txt"

gene="LY9"

yMin=0

yMax=200

setwd("C:\\LY9.geneDiff")

rt=read.table(inputFile,sep="\t",header=T,check.names=F)

rt=as.matrix(rt)

rownames(rt)=rt[,1]

exp=rt[,2:ncol(rt)]

dimnames=list(rownames(exp),colnames(exp))

data=matrix(as.numeric(as.matrix(exp)),nrow=nrow(exp),dimnames=dimnames)

data=avereps(data)

data=data[rowMeans(data)>0,]

group=sapply(strsplit(colnames(data),"\\-"),"[",4)

group=sapply(strsplit(group,""),"[",1)

tumor=data[,group==0]

tumorNum=ncol(tumor)

normalNum=ncol(data)-tumorNum

Type=c(rep(1,normalNum),rep(2,tumorNum))

rt=rbind(expression=data[gene,],Type=Type)

rt=as.matrix(t(rt))

wilcoxTest=wilcox.test(expression ~ Type, data=rt)

pvalue=wilcoxTest$p.value

if(pvalue<0.001){

 pvalue="<0.001"

}else{

 pvalue=paste0("=",sprintf("%.03f",pvalue))

}

pdf(file="diff.pdf",width=6,height=5)

par(mar = c(4,6,3,3))

labels=c("Normal","Tumor")

boxplot(expression ~ Type, data = rt,names=labels,xlab="",

 ylab = paste(gene," expression",sep=""),

 cex.main=1.5, cex.lab=1.3, cex.axis=1.2,ylim=c(yMin,yMax),outline = FALSE)

beeswarm(expression ~ Type, data = rt, col = c("blue","red"),lwd=0.1,

 pch = 16, add = TRUE, corral="wrap")

ySeg=yMax\*0.94

segments(1,ySeg, 2,ySeg);segments(1,ySeg, 1,ySeg\*0.96);segments(2,ySeg, 2,ySeg\*0.96)

text(1.5,ySeg\*1.05,labels=paste("p",pvalue,sep=""),cex=1.2)

dev.off()

**Figure 4B**

#if (!requireNamespace("BiocManager", quietly = TRUE))

# install.packages("BiocManager")

#BiocManager::install("limma")

#install.packages("ggpubr")

library("limma")

library("ggpubr")

inputFile="symbol.txt"

gene="LY9"

setwd("C:\\LY9.genePairDiff")

rt=read.table(inputFile,sep="\t",header=T,check.names=F)

rt=as.matrix(rt)

rownames(rt)=rt[,1]

exp=rt[,2:ncol(rt)]

dimnames=list(rownames(exp),colnames(exp))

data=matrix(as.numeric(as.matrix(exp)),nrow=nrow(exp),dimnames=dimnames)

data=avereps(data)

data=data[rowMeans(data)>0,]

group=sapply(strsplit(colnames(data),"\\-"),"[",4)

group=sapply(strsplit(group,""),"[",1)

normal=data[,group!=0]

tumor=data[,group==0]

normal=rbind(normal,gene=normal[gene,])

normal=as.matrix(t(normal[c("gene",gene),]))

rownames(normal)=gsub("(.\*?)\\-(.\*?)\\-(.\*?)\\-(.\*?)\\-.\*","\\1\\-\\2\\-\\3",rownames(normal))

normal=avereps(normal)

tumor=rbind(tumor,gene=tumor[gene,])

tumor=as.matrix(t(tumor[c("gene",gene),]))

rownames(tumor)=gsub("(.\*?)\\-(.\*?)\\-(.\*?)\\-(.\*?)\\-.\*","\\1\\-\\2\\-\\3",rownames(tumor))

tumor=avereps(tumor)

samSample=intersect(row.names(normal),row.names(tumor))

normal=normal[samSample,]

tumor=tumor[samSample,]

data=cbind(normal,tumor)

data=as.data.frame(data[,c(1,3)])

colnames(data)=c("Normal","Tumor")

pdf(file="pairDiff.pdf",width=5.5,height=5)

ggpaired(data, cond1 = "Normal", cond2 = "Tumor",fill = "condition", palette = "jco",

 xlab="",ylab = paste0(gene," expression"))+

 stat\_compare\_means(paired = TRUE, label = "p.format", label.x = 1.35)

dev.off()

**Figure 4C**

#install.packages("survival")

#install.packages("survminer")

library(survival)

library(survminer)

inputFile="expTime.txt"

gene="LY9"

setwd("C:\\LY9.geneSur")

#读取输入文件

rt=read.table(inputFile,header=T,sep="\t",check.names=F)

rt$futime=rt$futime/365

a=ifelse(rt[,gene]<=median(rt[,gene]),"Low","High")

diff=survdiff(Surv(futime, fustat) ~a,data = rt)

pValue=1-pchisq(diff$chisq,df=1)

fit=survfit(Surv(futime, fustat) ~ a, data = rt)

if(pValue<0.001){

 pValue="p<0.001"

}else{

 pValue=paste0("p=",sprintf("%.03f",pValue))

}

titleName=gene

surPlot=ggsurvplot(fit,

 data=rt,

 conf.int=TRUE,

 pval=pValue,

 pval.size=6,

 risk.table=T,

 #ncensor.plot = TRUE,

 legend.labs=c("high","low"),

 legend.title=titleName,

 xlab="Time(years)",

 break.time.by = 1,

 risk.table.title="",

 palette=c("red", "blue"),

 risk.table.height=.25)

pdf(file=paste0("sur.",gene,".pdf"), width = 6.5, height = 5.5,onefile = FALSE)

print(surPlot)

dev.off()

**Figure 4D-I**

#if (!requireNamespace("BiocManager", quietly = TRUE))

# install.packages("BiocManager")

#BiocManager::install("limma")

#install.packages("ggpubr")

options(stringsAsFactors=F)

library(limma)

library(ggpubr)

inputFile="symbol.txt"

cliFile="clinical.txt"

gene="LY9"

setwd("C:\\LY9.geneCliCor")

rt=read.table(inputFile,sep="\t",header=T,check.names=F)

rt=as.matrix(rt)

rownames(rt)=rt[,1]

exp=rt[,2:ncol(rt)]

dimnames=list(rownames(exp),colnames(exp))

data=matrix(as.numeric(as.matrix(exp)),nrow=nrow(exp),dimnames=dimnames)

data=avereps(data)

data=data[rowMeans(data)>0,]

group=sapply(strsplit(colnames(data),"\\-"),"[",4)

group=sapply(strsplit(group,""),"[",1)

group=gsub("2","1",group)

data=data[,group==0]

data=rbind(data,gene=data[gene,])

exp=as.matrix(t(data[c("gene",gene),]))

rownames(exp)=gsub("(.\*?)\\-(.\*?)\\-(.\*?)\\-(.\*?)\\-.\*","\\1\\-\\2\\-\\3",rownames(exp))

exp=avereps(exp)

cli=read.table(cliFile,sep="\t",header=T,check.names=F,row.names=1)

samSample=intersect(row.names(exp),row.names(cli))

exp=exp[samSample,]

cli=cli[samSample,]

rt=cbind(exp,cli)

for(clinical in colnames(rt[,3:ncol(rt)])){

 data=rt[c(gene,clinical)]

 colnames(data)=c("gene","clinical")

 data=data[(data[,"clinical"]!="unknow"),]

 group=levels(factor(data$clinical))

 data$clinical=factor(data$clinical, levels=group)

 comp=combn(group,2)

 my\_comparisons=list()

 for(i in 1:ncol(comp)){my\_comparisons[[i]]<-comp[,i]}

 boxplot=ggboxplot(data, x="clinical", y="gene", color="clinical",

 xlab=clinical,

 ylab=paste(gene,"expression"),

 legend.title=clinical,

 add = "jitter")+

 stat\_compare\_means(comparisons = my\_comparisons)

 pdf(file=paste0(clinical,".pdf"),width=5.5,height=5)

 print(boxplot)

 dev.off()

}

**Spearman correlation analysis**

library(limma)

library(reshape2)

library(ggpubr)

library(ggExtra)

corFilter=0.2

pvalueFilter=0.01

gene="LY9"

expFile="diffGeneExp.txt"

miExpFile="miRNAmatrix.txt"

mirnaFile="miRNA.txt"

setwd("C:\\SingleGene\\15.miRNAcor")

rt=read.table(expFile, header=T, sep="\t", check.names=F)

rt=as.matrix(rt)

rownames(rt)=rt[,1]

exp=rt[,2:ncol(rt)]

dimnames=list(rownames(exp),colnames(exp))

data=matrix(as.numeric(as.matrix(exp)),nrow=nrow(exp),dimnames=dimnames)

data=avereps(data)

data=data[gene,,drop=F]

group=sapply(strsplit(colnames(data),"\\-"), "[", 4)

group=sapply(strsplit(group,""), "[", 1)

group=gsub("2", "1", group)

conData=data[,group==1,drop=F]

treatData=data[,group==0,drop=F]

logFC=mean(treatData)-mean(conData)

geneExp=data[,group==0,drop=F]

rt1=read.table(miExpFile, header=T, sep="\t", check.names=F)

rt1=as.matrix(rt1)

rownames(rt1)=rt1[,1]

exp1=rt1[,2:ncol(rt1)]

dimnames1=list(rownames(exp1),colnames(exp1))

miRNA=matrix(as.numeric(as.matrix(exp1)), nrow=nrow(exp1), dimnames=dimnames1)

miRNA=avereps(miRNA)

miRNA=miRNA[rowMeans(miRNA)>0,]

miList=read.table(mirnaFile, header=F, sep="\t", check.names=F)

sameMirna=intersect(row.names(miRNA), as.vector(miList[,1]))

miRNA=miRNA[sameMirna,]

miRNA=log2(miRNA+1)

group=sapply(strsplit(colnames(miRNA),"\\-"), "[", 4)

group=sapply(strsplit(group,""), "[", 1)

group=gsub("2", "1", group)

miRNAtumor=miRNA[,group==0]

conNum=length(group[group==1])

treatNum=length(group[group==0])

sampleType=c(rep("Normal",conNum), rep("Tumor",treatNum))

colnames(miRNAtumor)=gsub("(.\*?)\\-(.\*?)\\-(.\*?)\\-(.\*?)\\-.\*", "\\1\\-\\2\\-\\3-\\4", colnames(miRNAtumor))

sameSample=intersect(colnames(miRNAtumor), colnames(geneExp))

miRNAtumor=miRNAtumor[,sameSample,drop=F]

geneExp=geneExp[,sameSample,drop=F]

y=as.numeric(geneExp[gene,])

outTab=data.frame()

for(i in row.names(miRNAtumor)){

 if(sd(miRNAtumor[i,])>0.01){

 #miRNA

 miLogFC=mean(miRNA[i,((conNum+1):ncol(miRNA))])-mean(miRNA[i,1:conNum])

 test=wilcox.test(miRNA[i,] ~ sampleType)

 diffPvalue=test$p.value

 x=as.numeric(miRNAtumor[i,])

 corT=cor.test(x, y, method="spearma")

 cor=corT$estimate

 pvalue=corT$p.value

 outTab=rbind(outTab,cbind(Gene=gene, miRNA=i, cor, pvalue, logFC=miLogFC, diffPval=diffPvalue))

 if((cor< -corFilter) & (pvalue<pvalueFilter)){

 df1=as.data.frame(cbind(x,y))

 p1=ggplot(df1, aes(x, y)) +

 xlab(paste0(i, " expression")) + ylab(paste0(gene, " expression"))+

 geom\_point() + geom\_smooth(method="lm",formula = y ~ x) + theme\_bw()+

 stat\_cor(method = 'spearman', aes(x =x, y =y))

 p2=ggMarginal(p1, type="density", xparams=list(fill = "orange"), yparams=list(fill = "blue"))

 pdf(file=paste0("cor.",i,".pdf"), width=5.2, height=5)

 print(p2)

 dev.off()

 rt=data.frame(Expression=miRNA[i,], Type=sampleType)

 group=levels(factor(rt$Type))

 rt$Type=factor(rt$Type, levels=group)

 comp=combn(group,2)

 my\_comparisons=list()

 for(k in 1:ncol(comp)){my\_comparisons[[k]]<-comp[,k]}

 boxplot=ggboxplot(rt, x="Type", y="Expression", color="Type",

 xlab="",

 ylab=paste0(i, " expression"),

 legend.title="Type",

 palette = c("blue","red"),

 add = "jitter")+

 stat\_compare\_means(comparisons = my\_comparisons)

 pdf(file=paste0("diff.",i,".pdf"),width=5,height=4.5)

 print(boxplot)

 dev.off()

 }

 }

}

outTab=outTab[order(as.numeric(as.vector(outTab[,"cor"]))),]

write.table(file="net.network.txt",outTab,sep="\t",quote=F,row.names=F)

miNode=data.frame(Node=unique(as.vector(outTab[,"miRNA"])), Type="miRNA")

geneNode=data.frame(Node=unique(as.vector(outTab[,"Gene"])), Type="Gene")

nodeOut=rbind(miNode, geneNode)

write.table(nodeOut, file="net.node.txt", sep="\t", quote=F, row.names=F)

outTab=outTab[((as.numeric(as.vector(outTab[,"cor"])) < -corFilter) & (as.numeric(as.vector(outTab[,"pvalue"])) < pvalueFilter)),]

write.table(file="cor.sig.txt",outTab,sep="\t",quote=F,row.names=F)

corMirna=unique(as.vector(outTab[,"miRNA"]))

corMirnaExp=miRNA[corMirna,,drop=F]

corMirnaExp=rbind(ID=colnames(corMirnaExp), corMirnaExp)

write.table(corMirnaExp, file="cor.MirnaExp.txt", sep="\t", quote=F, col.names=F)