rm(list=ls())

library(gplots)

#library('Cairo')

args <- commandArgs(trailingOnly = TRUE)

if (length(args) < 4) {

stop('Your input arguments is wrong!\n

args1:\t the RPKM file\n

args2:\t column of first sample\n

args3:\t column of last sample\n

args4:\t the out directory\n\n')

}

infile <- args[1]

i <- args[2]

j <- args[3]

outdir <- args[4]

data <- read.table(file=infile,header=T,sep='\t',comment.char='')

columnName <- colnames(data)

#Data <- data[,i:j]

Data <- log(data[,i:j]+1,2)

CorData <- cor(data[,i:j])

CorData <- cor(log(data[,i:j]+1,2))

CorData <- CorData^2

setwd(outdir)

cat(c("Sample","\t"),file="Sample\_correlation.txt")

write.table(CorData,file="Sample\_correlation.txt",

append=T,quote=F,sep='\t')

png(file='Sample\_correlation.png',pointsize =20,width=1600,height=1600,)

par(mar=c(7.1,1.1,0,3.1),omi=c(2.3,0,0.1,2.3))

heatmap.2(CorData,col=cm.colors(256), #heat.colors bluered(256) greenred(256) cm.colors(256)

#Rowv=FALSE,

#Colv=FALSE,# don't cluster the heatmap

trace='none',revC=F,#dendrogram='none',

#hclustfun = hclust,

na.rm = F,

#ColSideColors = patientcolors,

#RowSideColors=RowCol,

main='Sample Correlation',cex.main=6,

cexRow=1.5,

font.lab = 2,font.axis = 2,

notecex=3,cexCol=1.5,

#scale = "row",

scale = 'none',

#labRow = rownames(X),

#labCol = colnames(Data),

symkey=FALSE,key=T,keysize=1,density.info = "none"

)

dev.off()