RNF45, BP, heatmap

hguo

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Heatmap for BP terms

```
### this block perform z-score calculations
library("microbenchmark")
library("matrixStats")

## the GO terms for biological processes (BP)
GOcategory.file <- read.csv("../Data/human.bp.term.csv",header=TRUE, stringsAsFactors=F)
bp.go.cat <- GOcategory.file$GO.term
bp.dim <- length(bp.go.cat)
conn.dim <- 20
hspin <- matrix(as.numeric(unlist(read.table("human.rnf43.all.bp.txt", header=F, sep=","))), nrow=bp.dim
obs <- c(hspin)

perm <- c()
for (i in 1:100) {
    name <- paste("ms02.human", "/", "rnf43.heatmap", "/", "ms02.", i, ".bp.matrix.csv", sep="")
    mat <- matrix(as.numeric(unlist(read.table(name, header=F, sep=","))), nrow=bp.dim, ncol=conn.dim)
    perm <- rbind(perm, c(mat))
}

mean <- colMeans(perm)
std <- colSds(perm)

zscore <- round((obs - mean)/std, 3)

z <- matrix(zscore, nrow=bp.dim, ncol=conn.dim)

write.table(z, file="human.rnf43.all.bp.z.csv", sep=",", row.names=F, col.names=F, quote=F)

library('gplots')
```

```
##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##     lowess
```
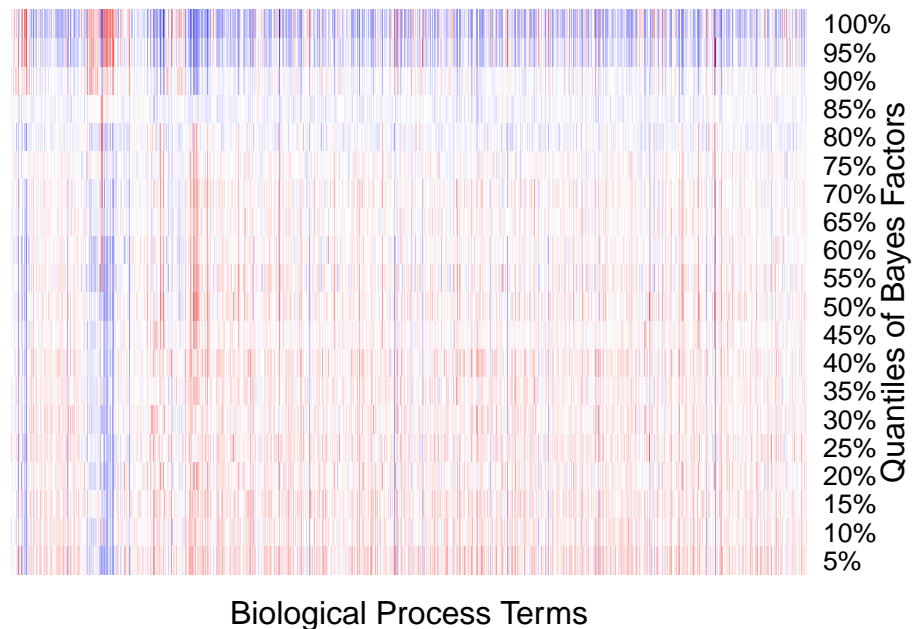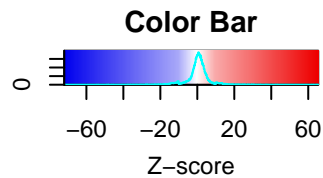
```
z <- t(z)

rownames(z) <- c("5%","10%","15%","20%","25%","30%","35%","40%","45%","50%",
                 "55%","60%","65%","70%","75%","80%","85%","90%","95%","100%")

colnames(z) <- bp.go.cat

colors = c(seq(min(z),-10.1,length=100),seq(-9.9,9.9,length=100),seq(10.1,max(z),length=100))
```

```
#colors = c(seq(min(z), max(z), length=300))
my_palette <- colorRampPalette(c("blue2", "white", "red2"))(n = 299)

#png(filename = "09.rnf43.bp.hm.new.png",width=6, height=5.5, res=1200, unit="in")
heatmap.2(z, col=my_palette, breaks=colors, dendrogram='none', Rowv=F, Colv=F,
          trace='none', offsetRow = 0, offsetCol = 0,
          xlab="Biological Process Terms", ylab="Quantiles of Bayes Factors",
          margins = c(2,3.5), key.title = "Color Bar", key.xlab="Z-score", key.ylab=NA,
          revC = T,
          labCol = NA, #labRow =,
          #srtCol=45, adjCol=c(1,0),
          #lmat=rbind(c(0,3,4), c(2,1,0)), lwid=c(1.5,4,2),
          scale="none", symbreaks=T, symm=F, symkey = F)
```
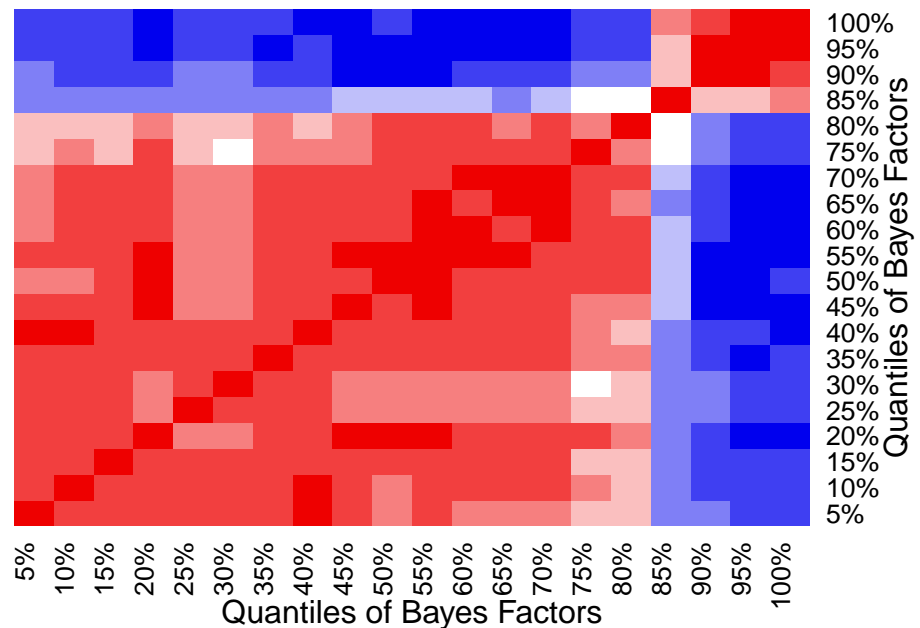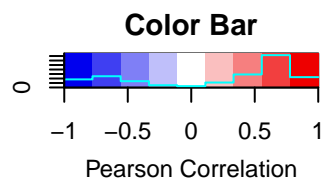


```
#dev.off()
```

```
#correlations to quantile 20 (95%-100%) genes
y.val <- c()
for (i in 1:20) {
  y.val2 <- c()
  for (j in 1:20) {
    cor.val <- cor.test(z[j,], z[i,])
    y.val2 <- rbind(y.val2, cor.val$estimate)
  }
  y.val <- cbind(y.val, y.val2)
}
```

```r
rownames(y.val) <- c("5%","10%","15%","20%","25%","30%","35%","40%","45%","50%",
                     "55%","60%","65%","70%","75%","80%","85%","90%","95%","100%")
colnames(y.val) <- c("5%","10%","15%","20%","25%","30%","35%","40%","45%","50%",
                     "55%","60%","65%","70%","75%","80%","85%","90%","95%","100%")
my_palette2 <- colorRampPalette(c("blue2", "white", "red2"))(9)
#png(filename = "09.rnf43.tumor.bp.cor.matrix.png",width=6, height=5.5, res=1200, unit="in")
heatmap.2(y.val, col=my_palette2, dendrogram='none', Rowv=F, Colv=F,
          trace='none', offsetRow = 0, offsetCol = 0,
          xlab="Quantiles of Bayes Factors", ylab="Quantiles of Bayes Factors",
          margins = c(3.5,3.5), key.title = "Color Bar", key.xlab="Pearson Correlation", key.ylab=NA,
          revC = T,
          #labCol = NA, #labRow =,
          #srtCol=45, adjCol=c(1,0),
          #lmat=rbind(c(0,3,4), c(2,1,0)), lwid=c(1.5,4,2),
          scale="none", symbreaks=T, symm=F, symkey = F)
```



```r
#dev.off()
```