Differential Expression Analysis: Heatmaps

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June 10, 2019

## Differential Expression Analysis: Heatmaps for Ozburn RNA-Seq

library(superheat)  
  
geneCounts=read.csv("Unique\_DEG\_ETOH(CNO)\_0.05.csv")  
geneCounts=geneCounts[which(!duplicated(geneCounts[,1])),]  
row.names(geneCounts)=geneCounts[,1]  
geneNames=row.names(geneCounts)  
geneCounts=geneCounts[,2:dim(geneCounts)[2]]  
geneCounts=as.matrix(geneCounts)  
  
#Scales by converting your data to a [0,1] quantile-preserving scale, or simply by mean-centering.  
#So not enabled here.   
  
tiff("1431 DEGs Unique to EtOH (CNO).tiff", units="px")  
superheat(geneCounts,  
 scale= FALSE,  
 pretty.order.cols = FALSE,  
 pretty.order.rows = FALSE,  
 heat.pal = c("red", "light gray", "blue"),  
 heat.pal.values = c(0, 0.5, 1.322),  
 heat.lim = c(-2.05, 2.05),  
 row.dendrogram = FALSE,  
 col.dendrogram = FALSE,  
 title = "1431 DEGs Unique to EtOH(CNO)",  
 title.size = 12,  
 row.title= "Genes",  
 row.title.size = 12,  
 column.title = "Treatment Groups",  
 column.title.size = 12,  
 bottom.label.text.size = 10,  
 grid.hline = TRUE,  
 grid.vline = TRUE,  
 grid.hline.col = "white",  
 grid.vline.col = "white",  
 grid.hline.size = 1,  
 grid.vline.size = 1,  
 legend.height = 0.4,  
 legend.width = 4,  
 legend.text.size = 30,  
 bottom.label.text.angle = 90,  
 padding = 1  
   
)  
dev.off()