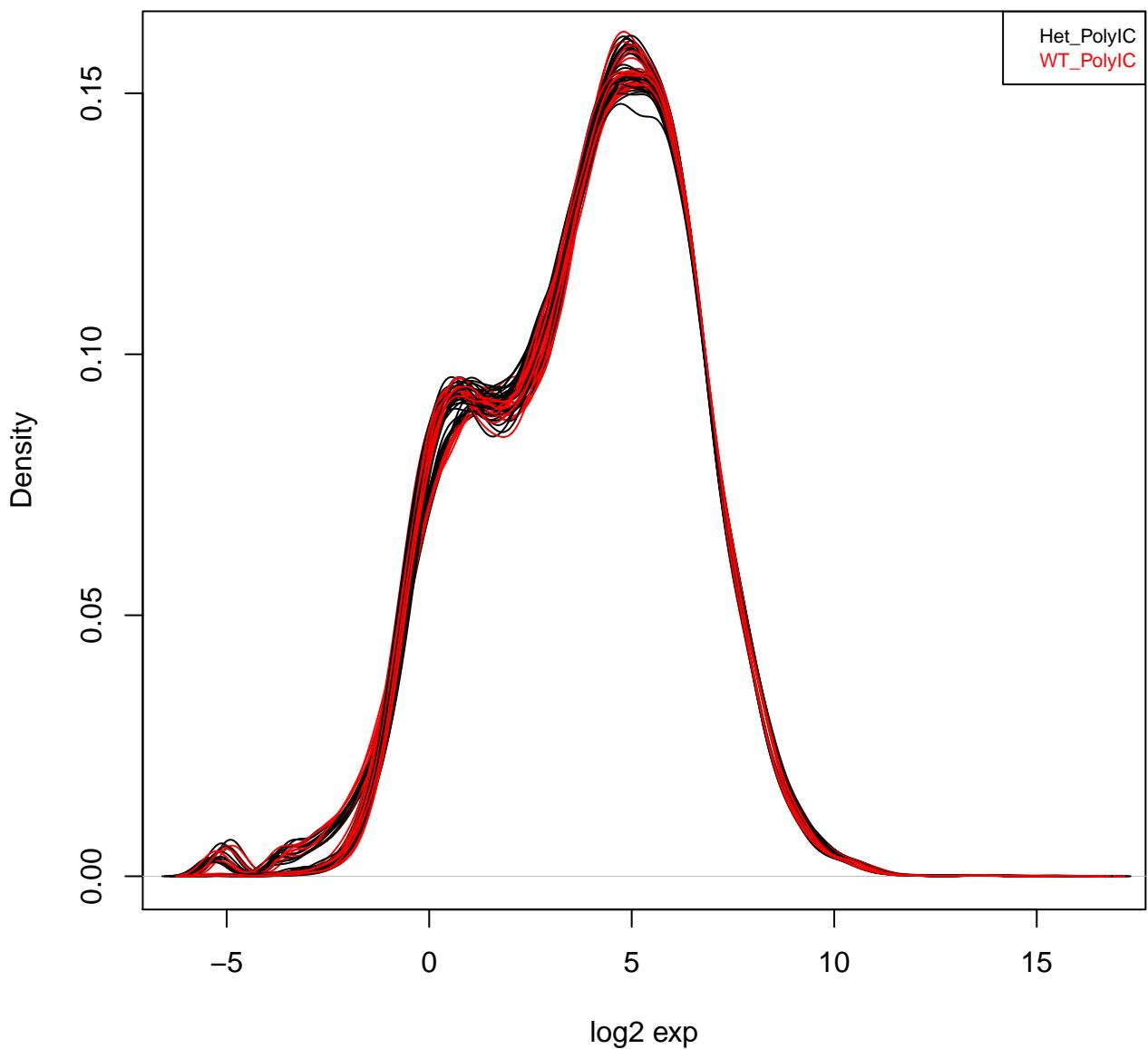
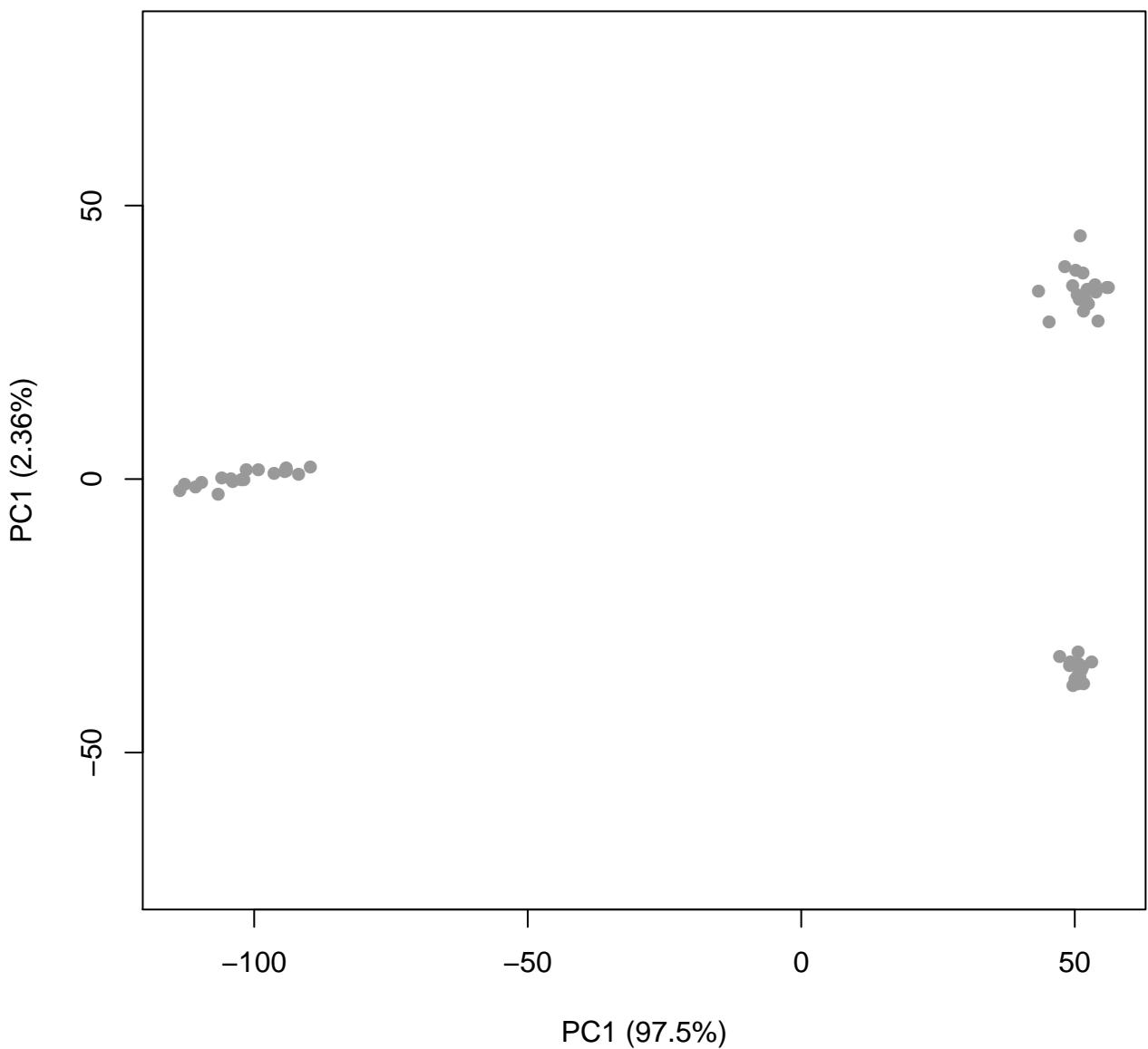


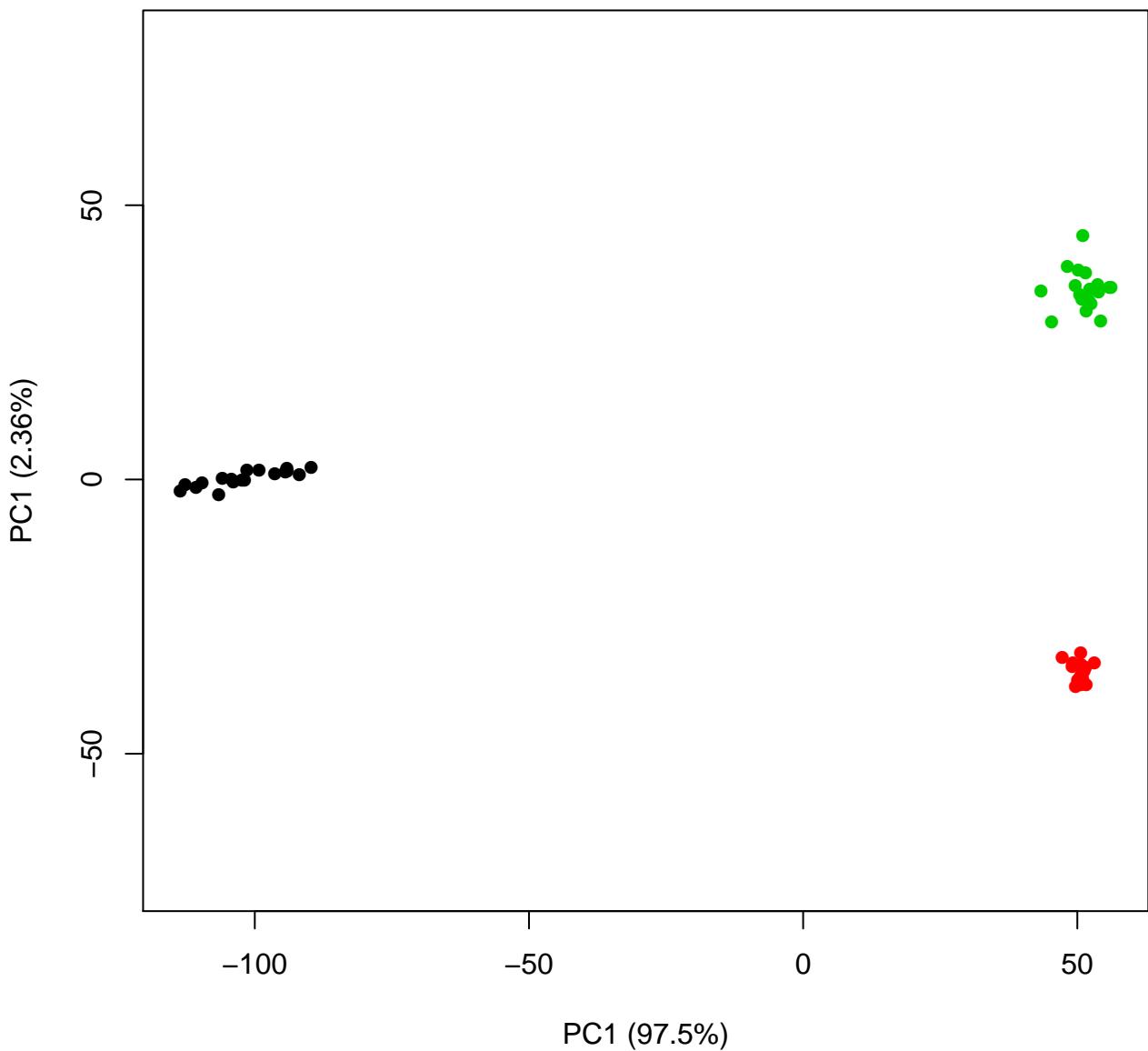
# Hist of Log2 Exp



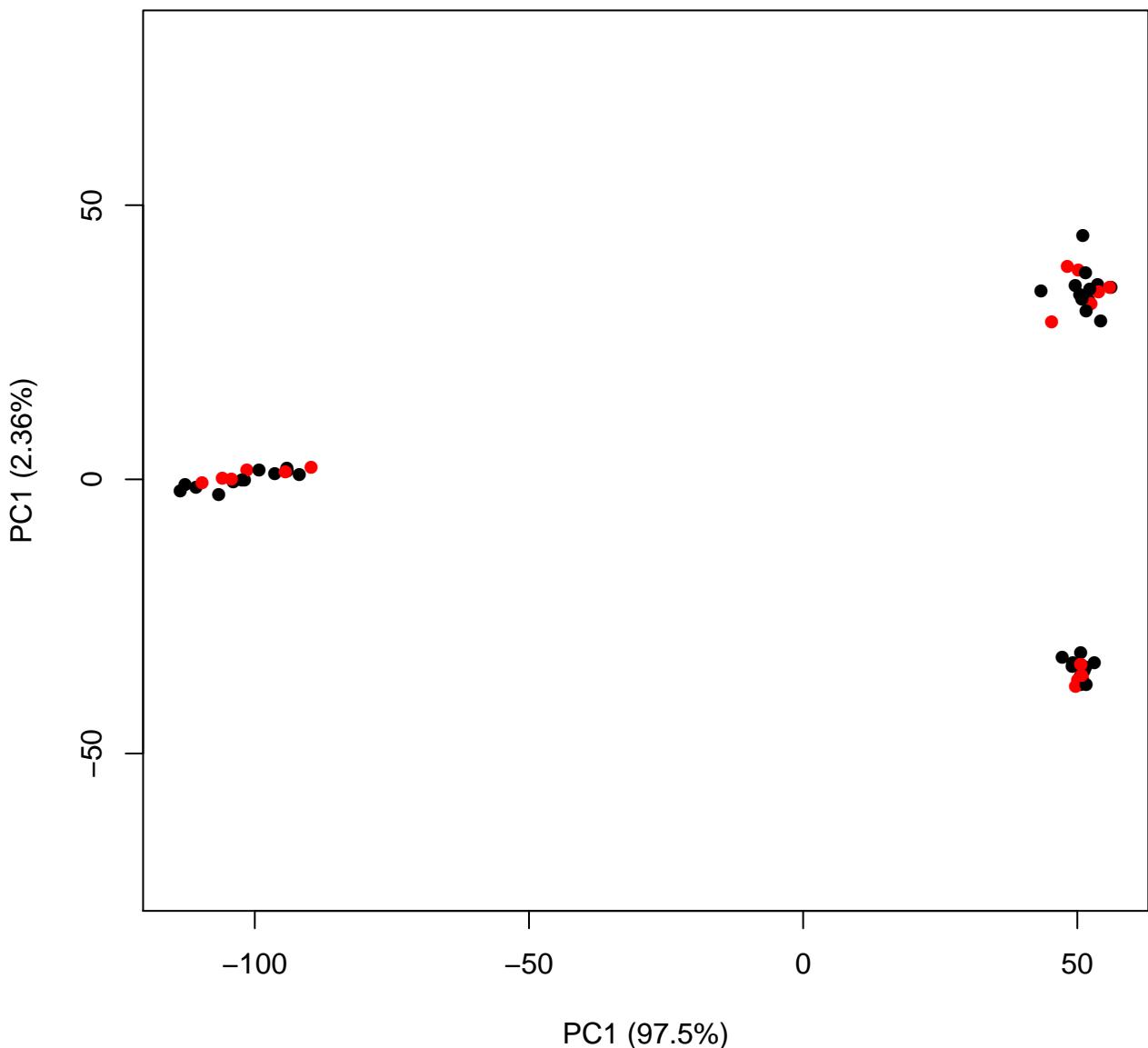
## MDS Plot



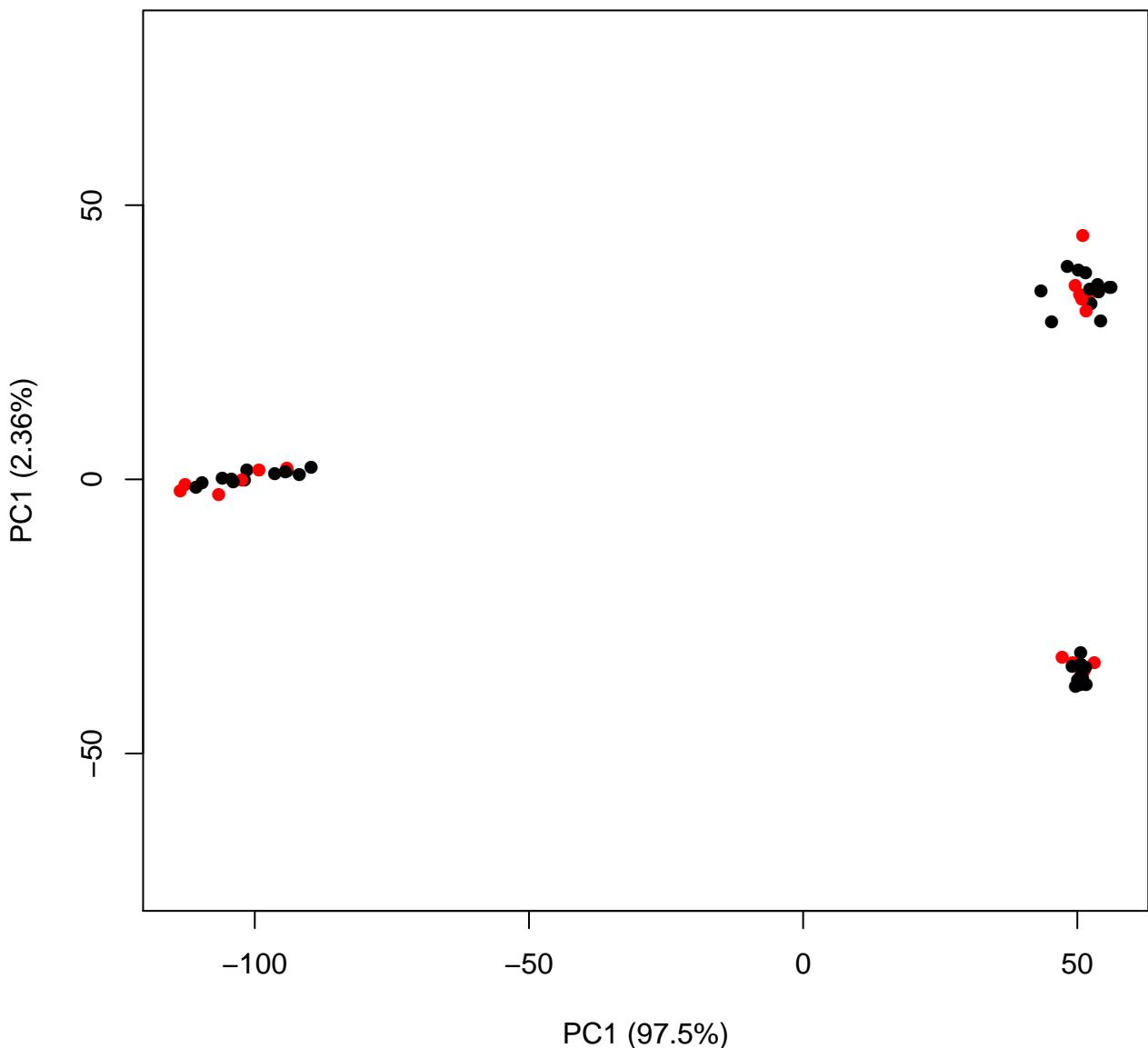
## MDS Plot by Region



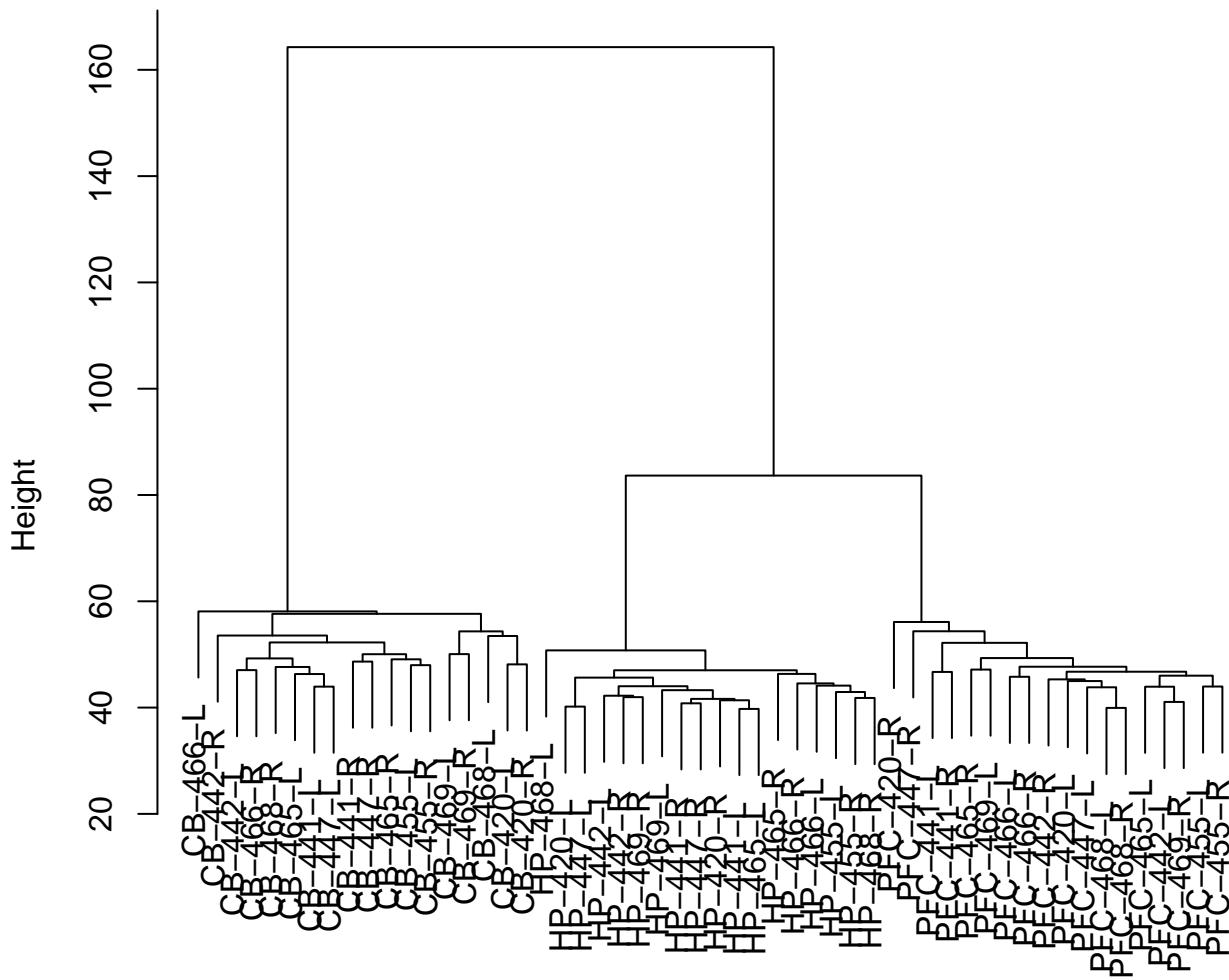
## MDS Plot by Genotype



## MDS Plot by Treatment

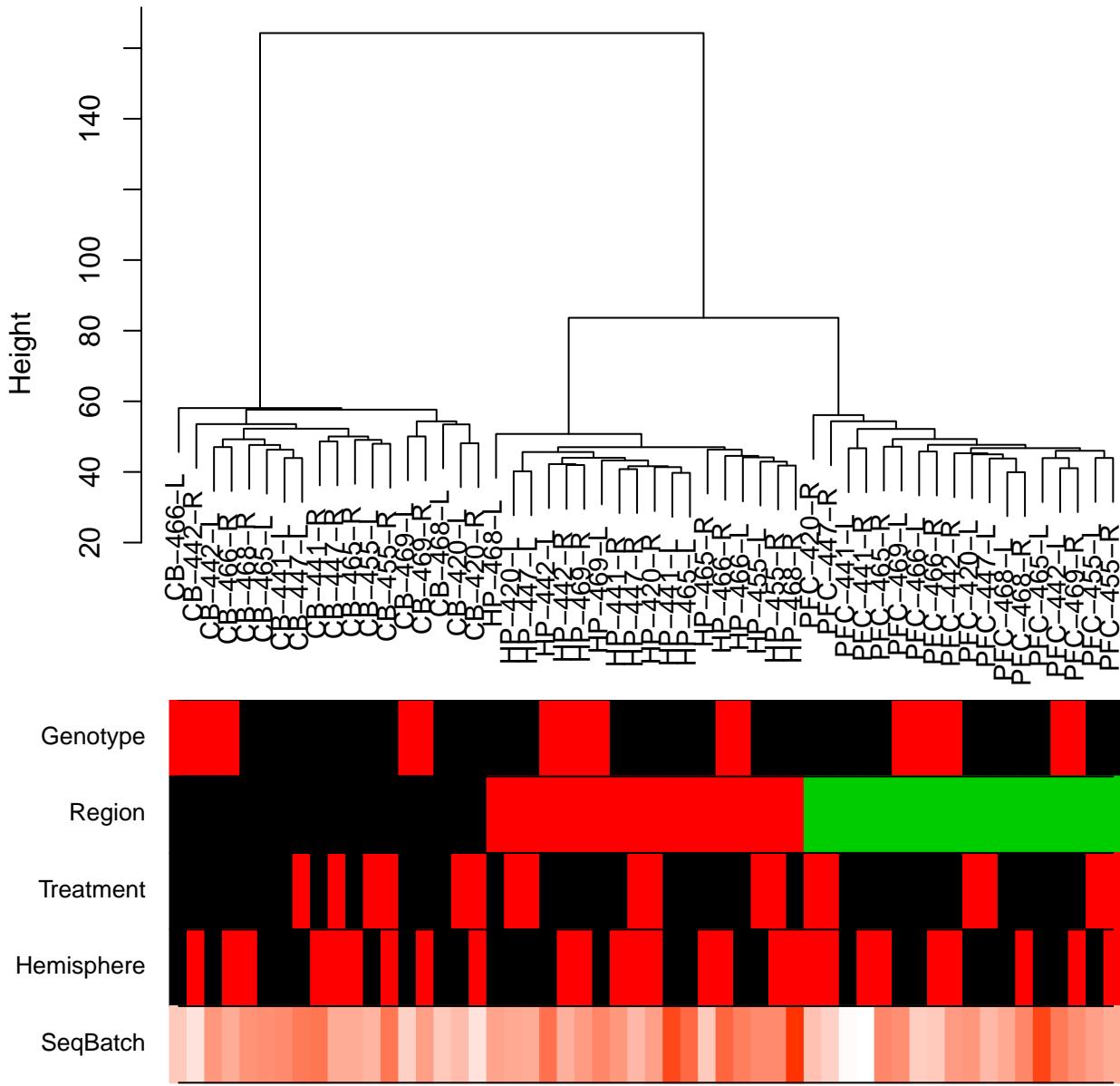


## Cluster Dendrogram

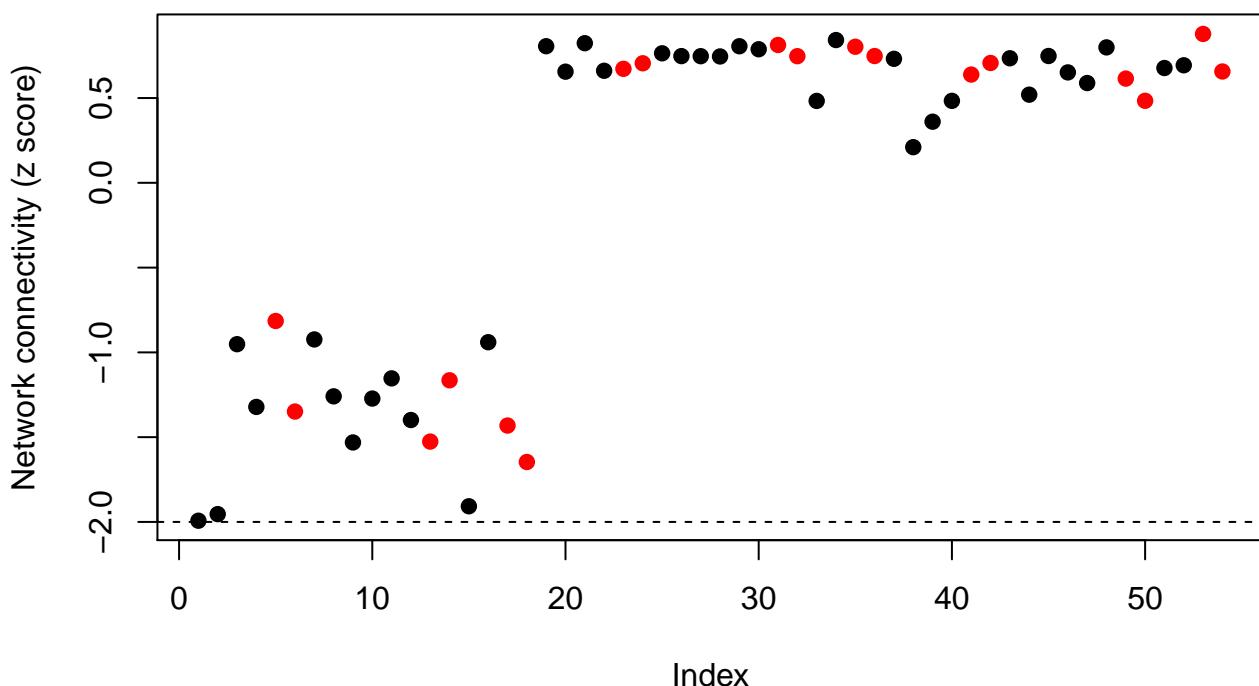


```
dist(t(datExpr.cpm))  
hclust (*, "average")
```

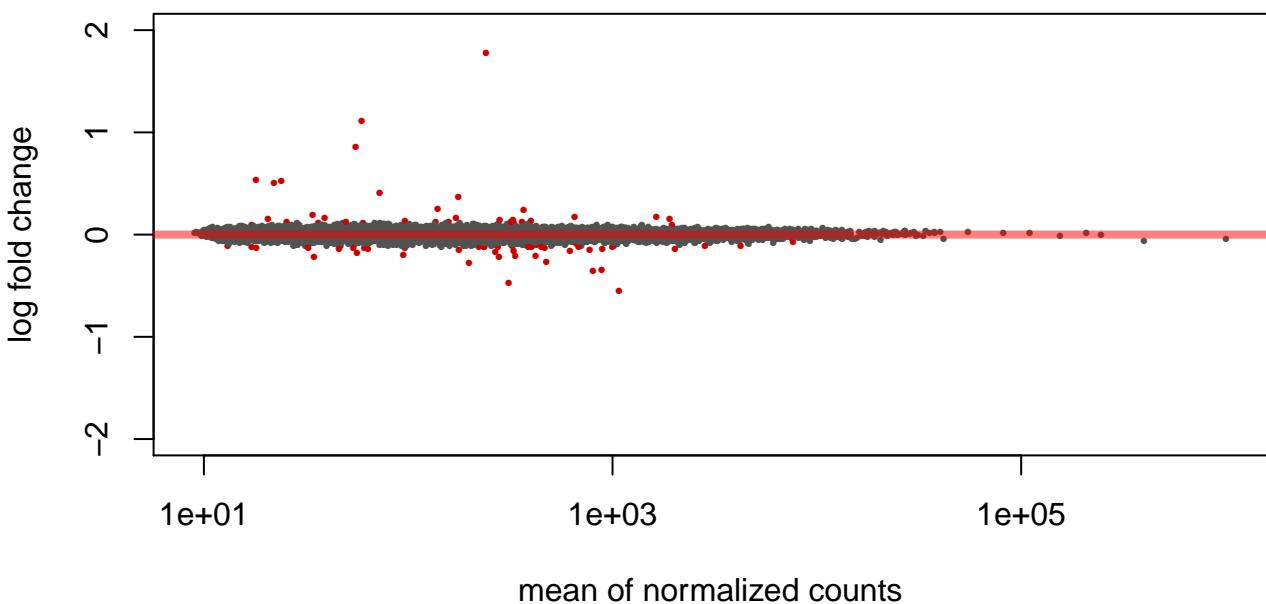
## Cluster Dendrogram



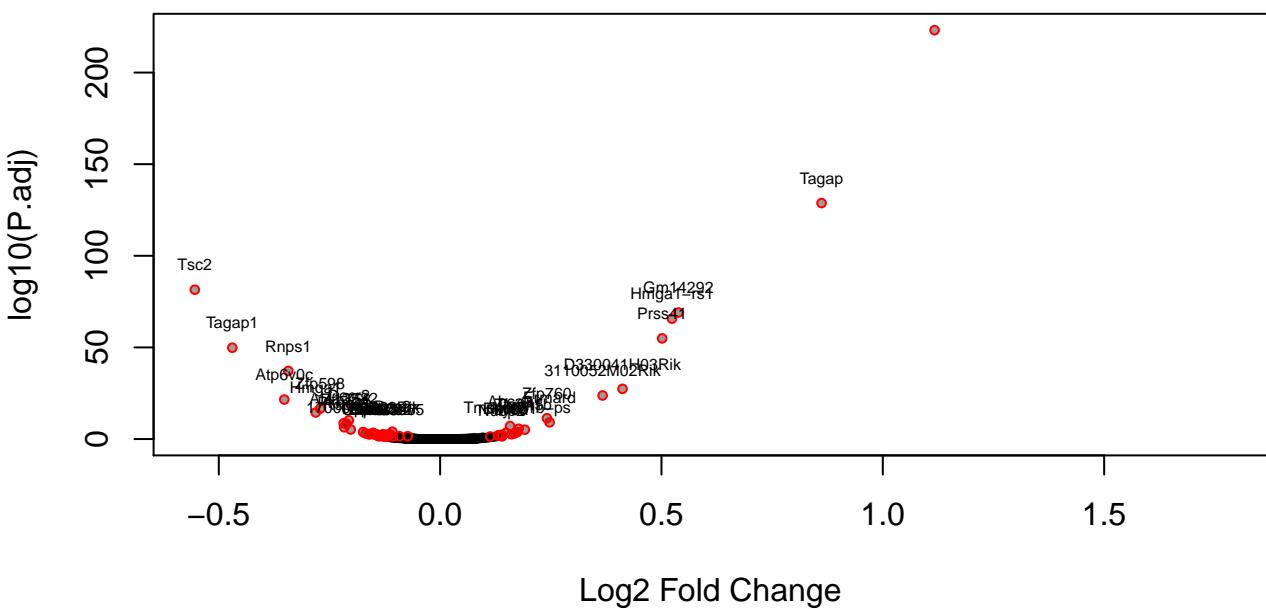
## Outlier detection



# all genotype

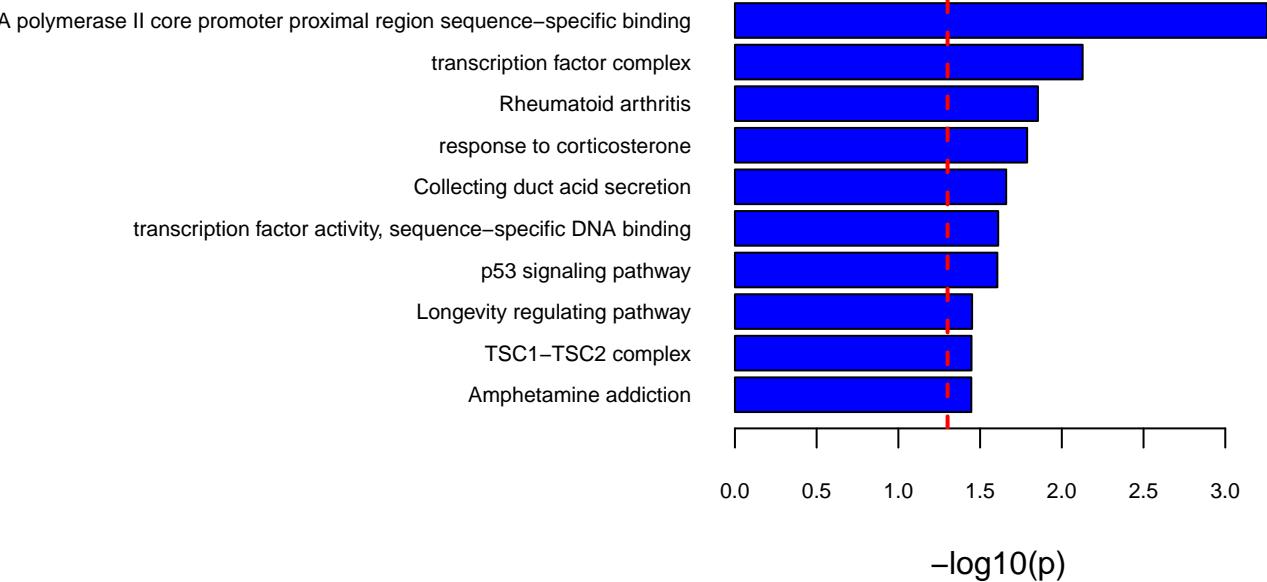


mean of normalized counts

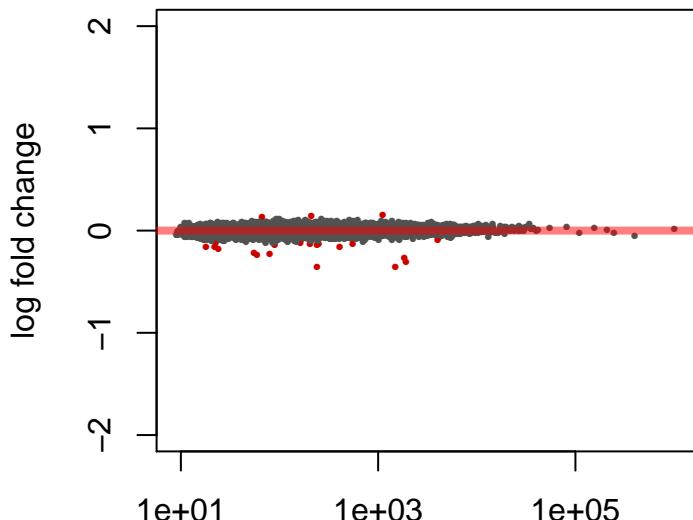


Log2 Fold Change

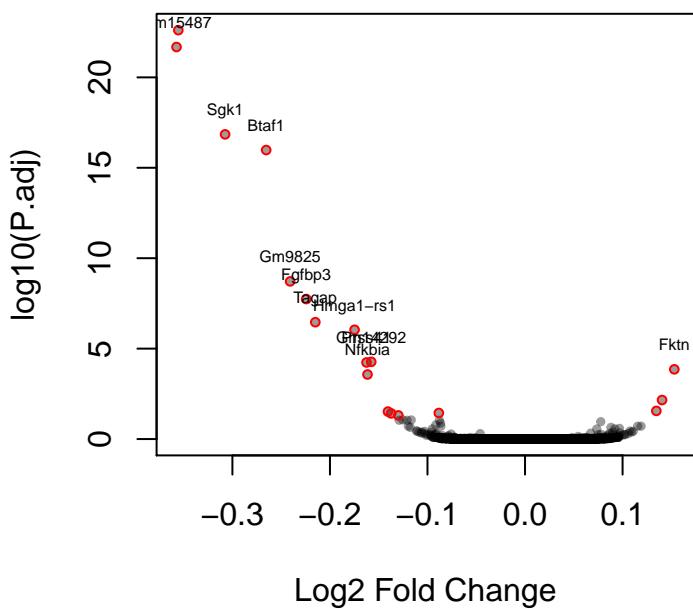
### GO downregulated genotype all



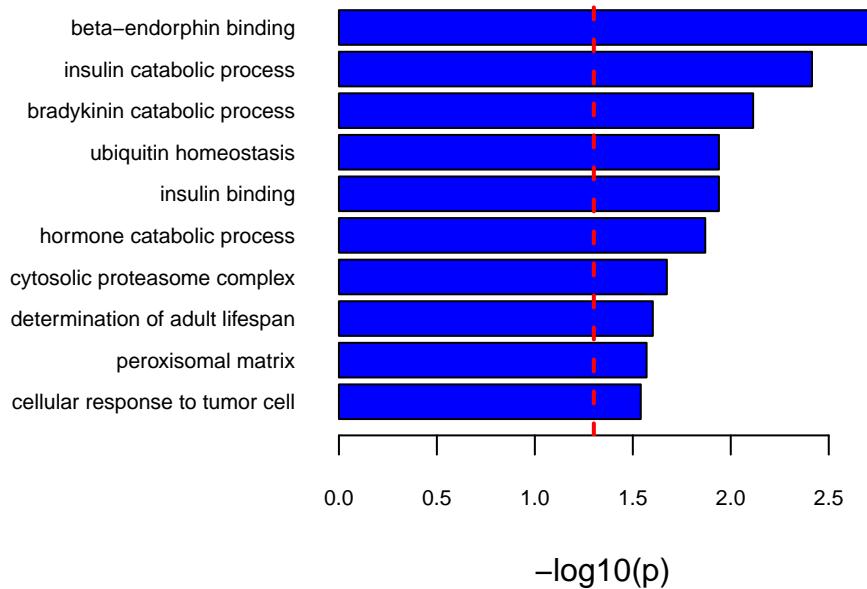
### all treatment



mean of normalized counts

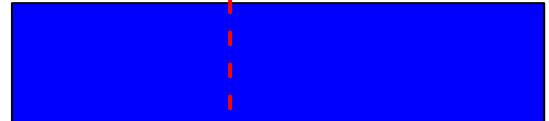


### GO downregulated treatment all

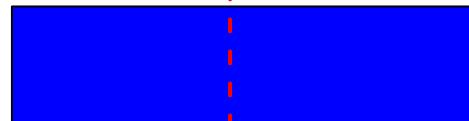


**GO upregulated treatment all**

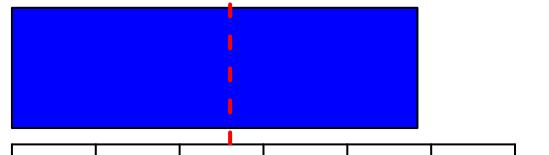
regulation of stress–activated MAPK cascade



regulation of protein glycosylation



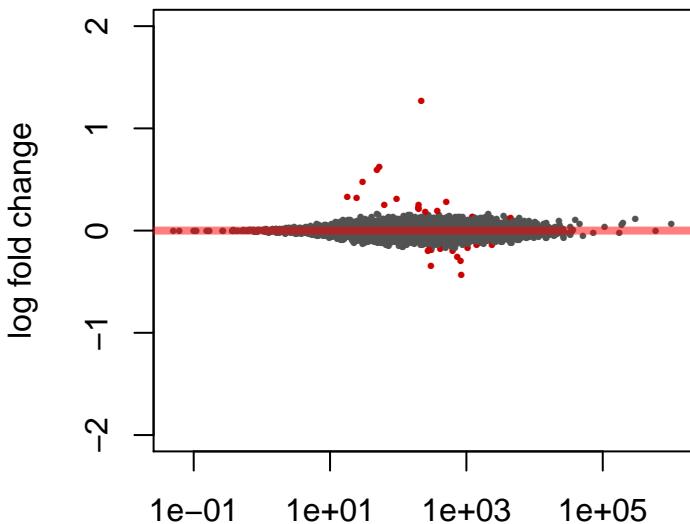
protein localization to microtubule



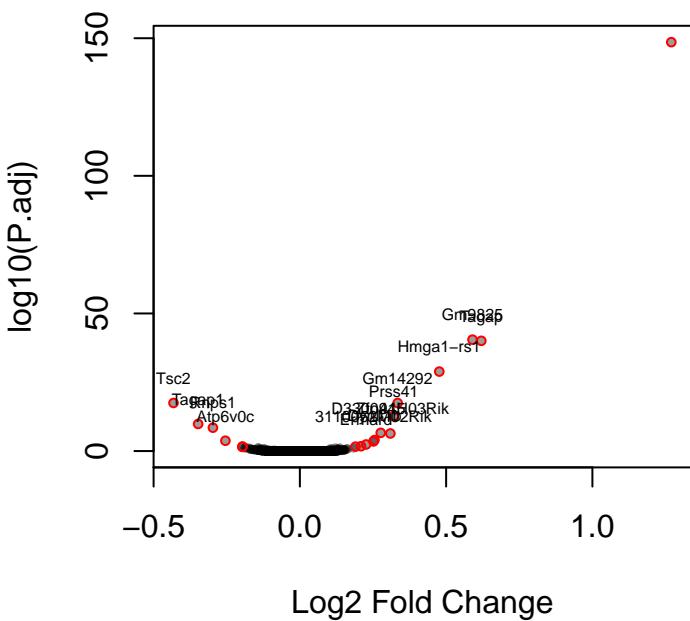
0.0 0.5 1.0 1.5 2.0 2.5 3.0

$-\log_{10}(p)$

### cbl genotype

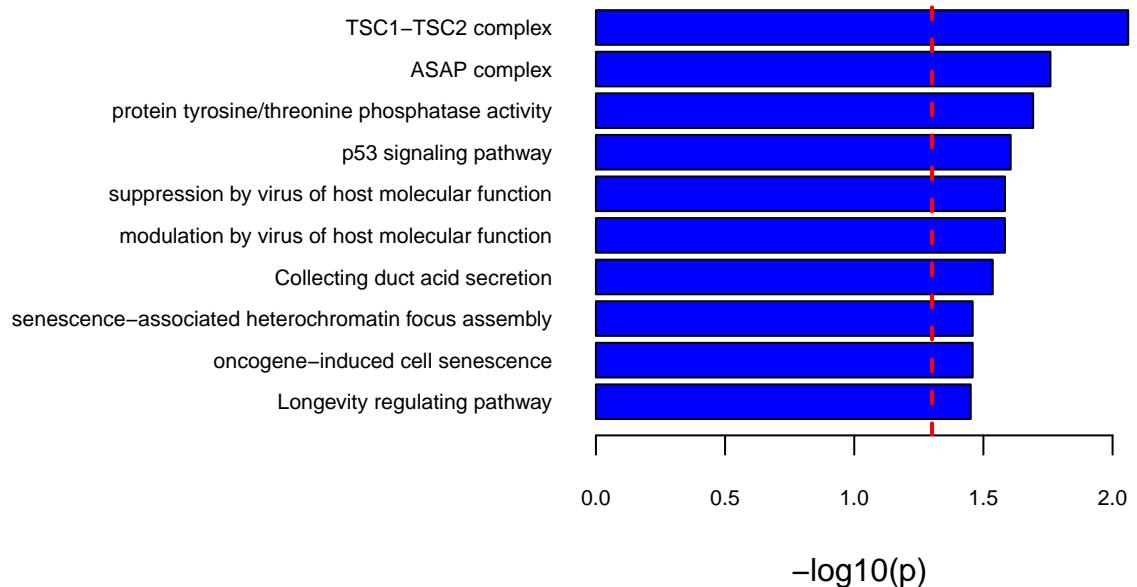


mean of normalized counts

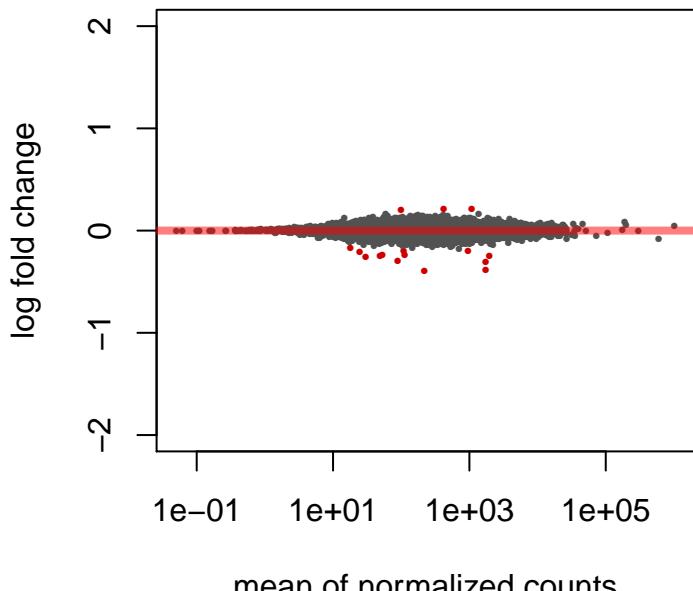


Log2 Fold Change

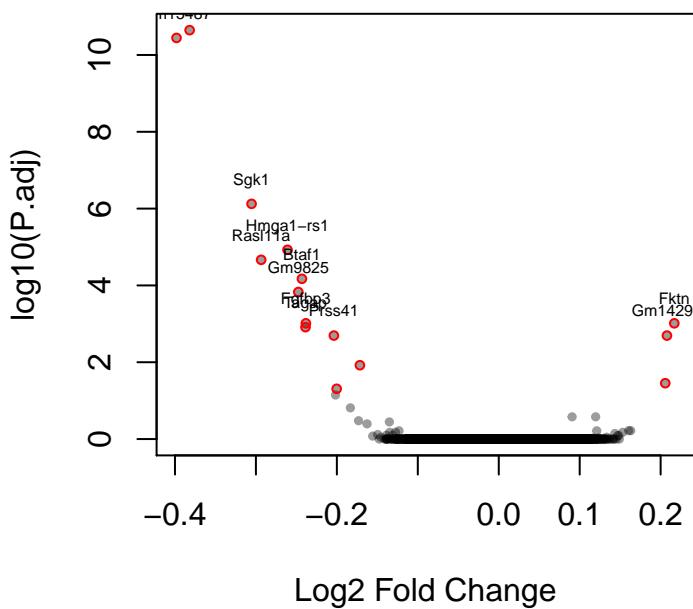
### GO downregulated genotype cbl



### cbl treatment

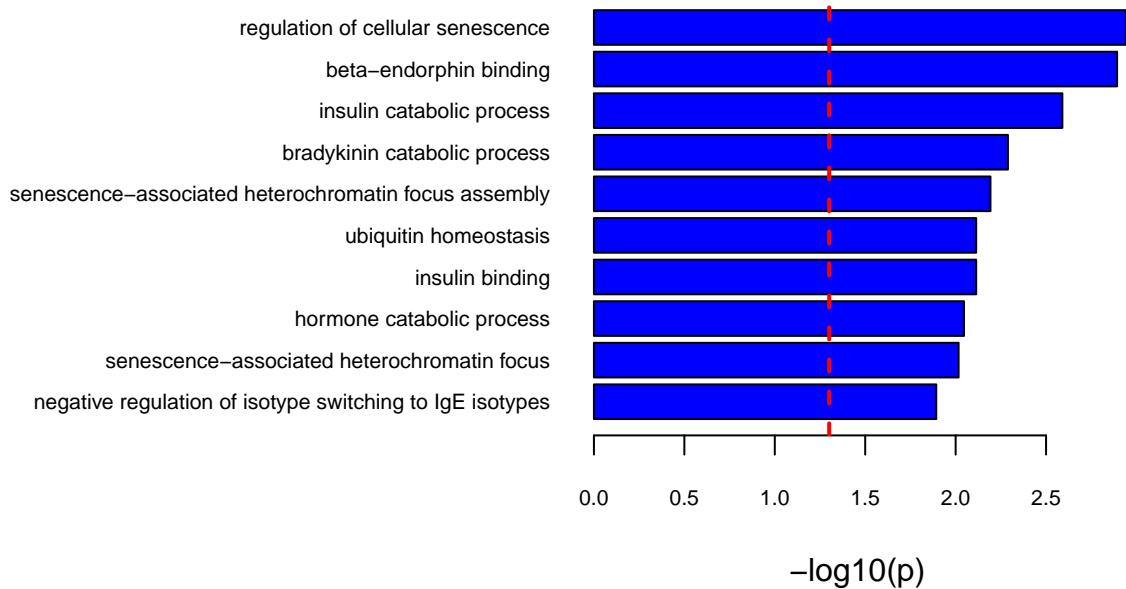


mean of normalized counts

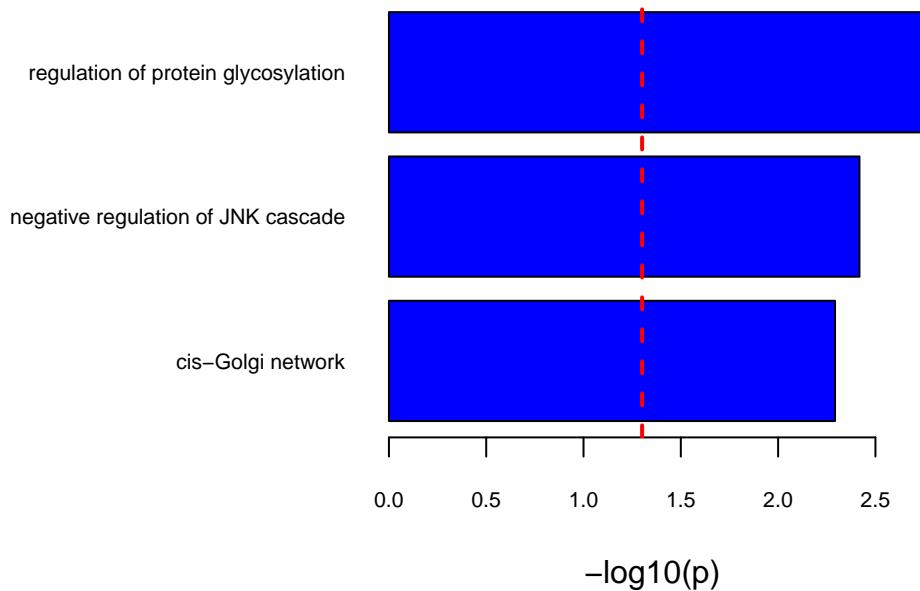


Log2 Fold Change

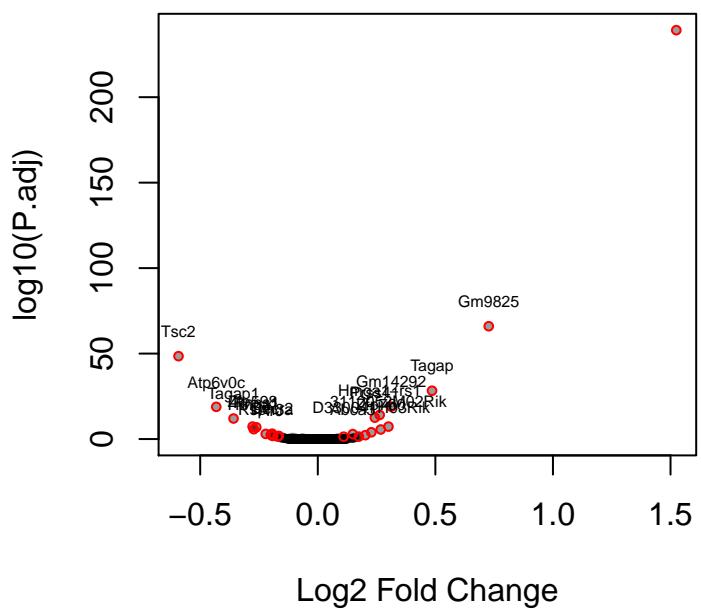
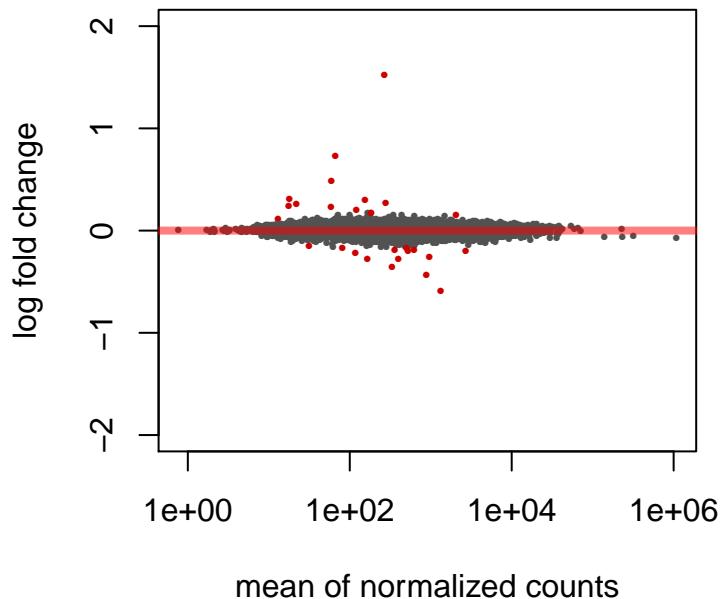
### GO downregulated treatment cbl



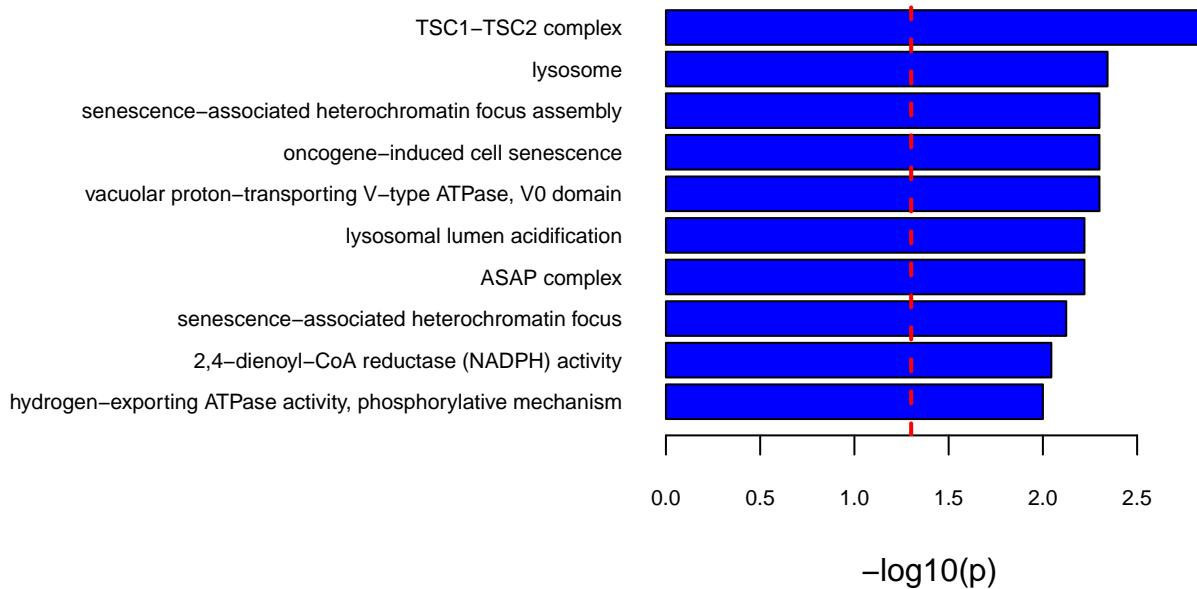
**GO upregulated treatment cbl**



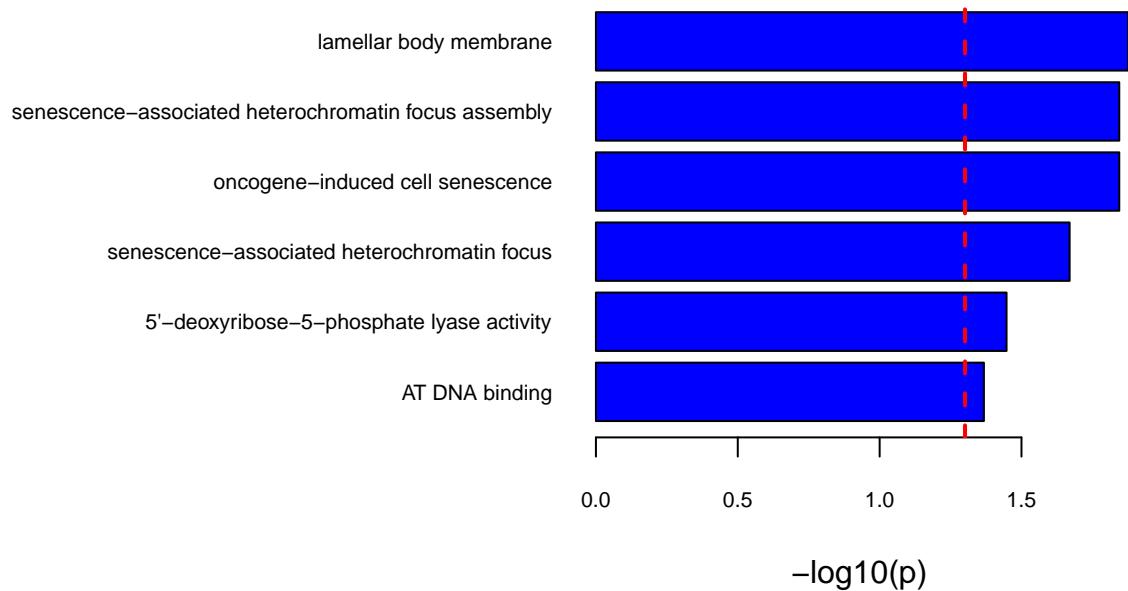
### hc genotype

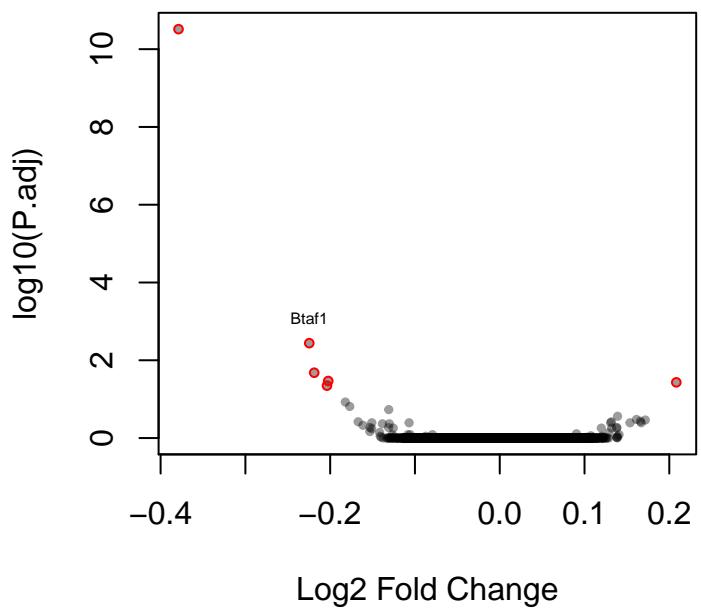
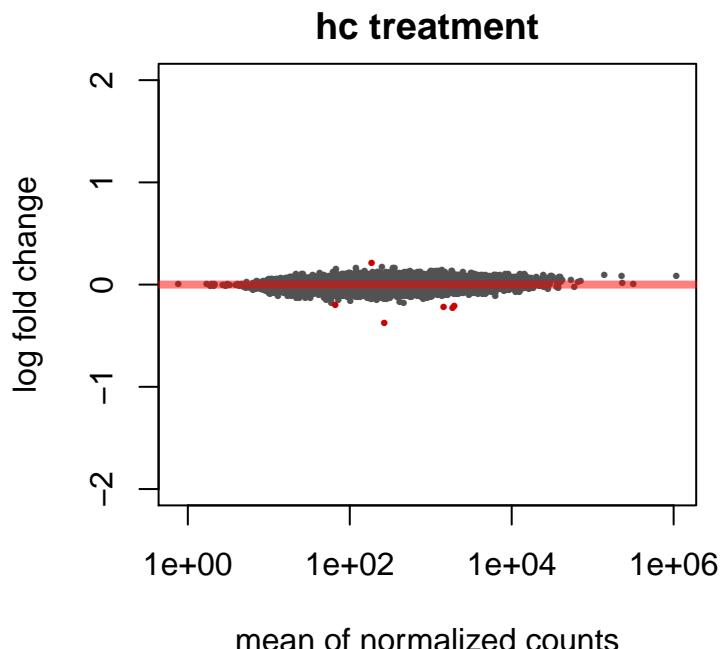


### GO downregulated genotype hc

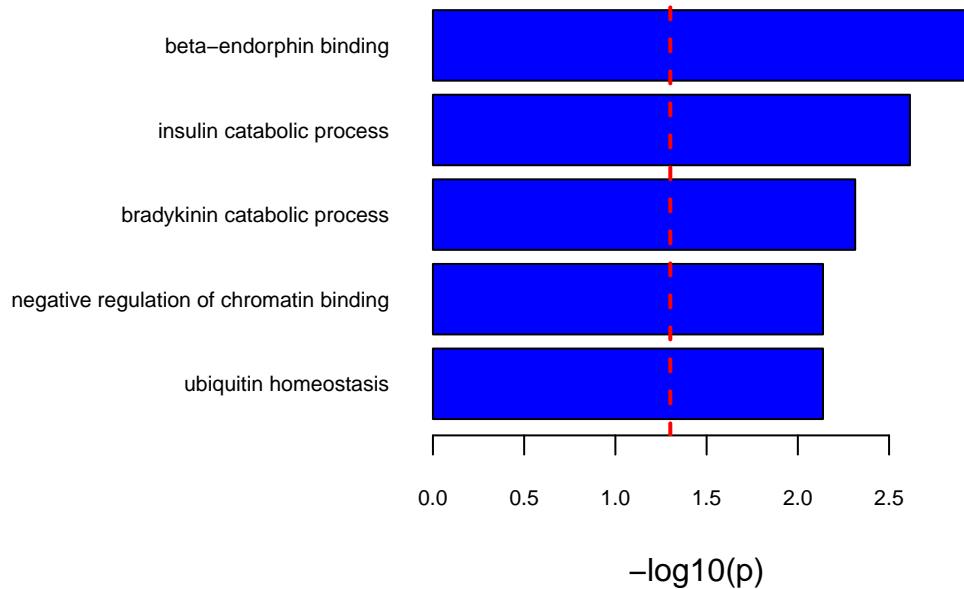


### GO upregulated genotype hc



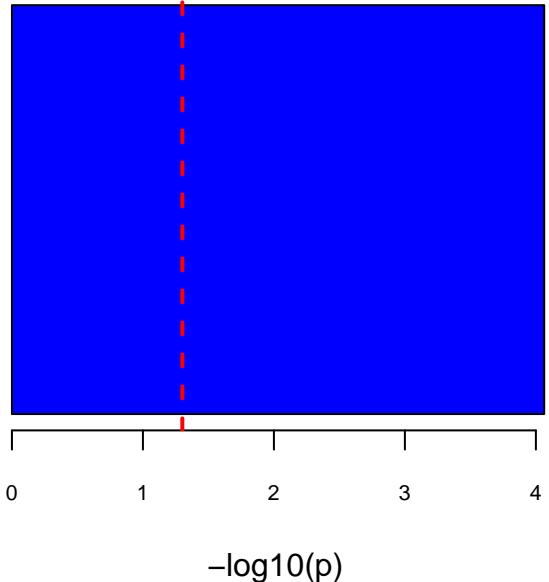


### GO downregulated treatment hc

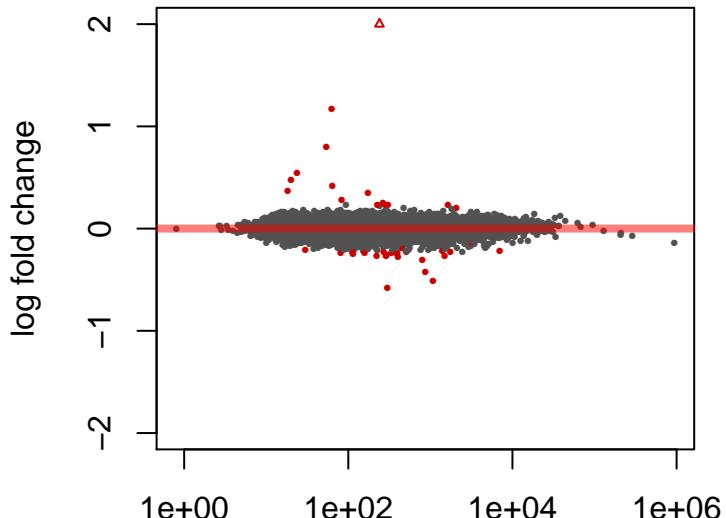


**GO upregulated treatment hc**

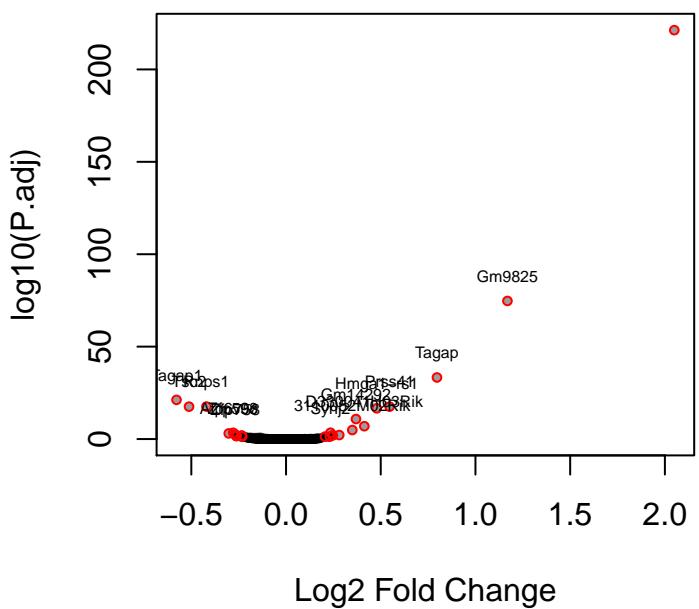
epithelial cell proliferation involved in prostatic bud elongation



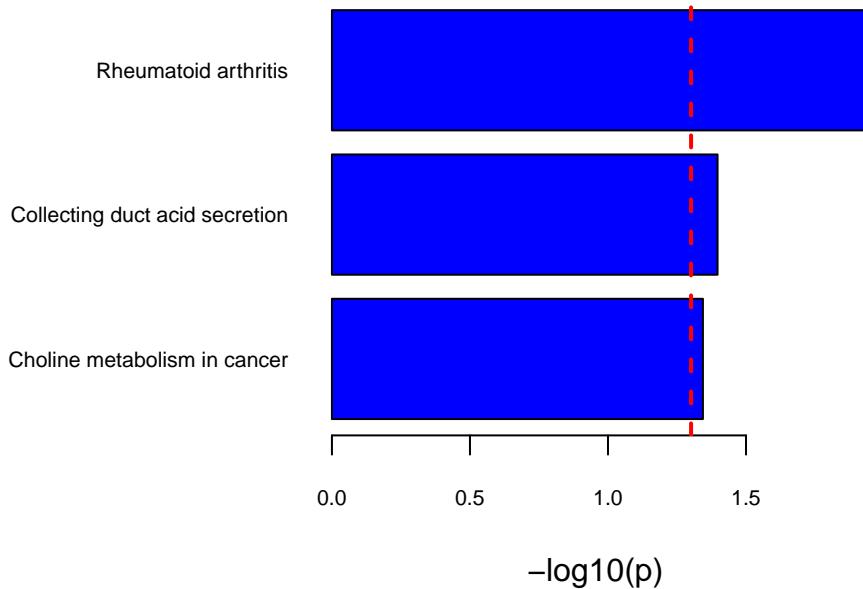
### pfc genotype



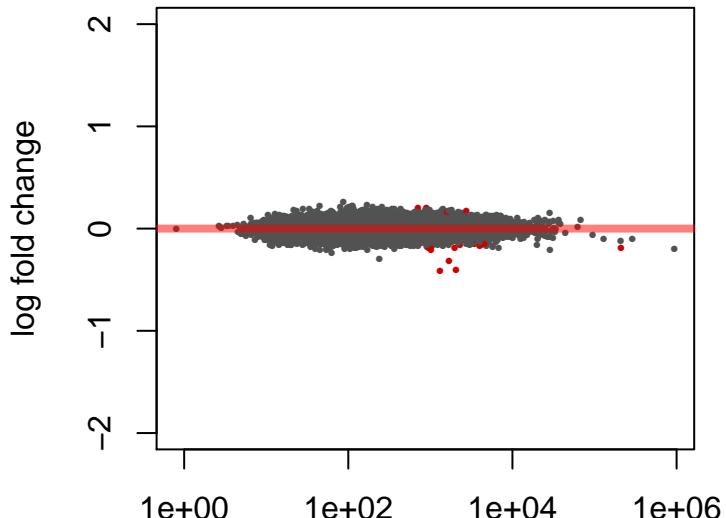
mean of normalized counts



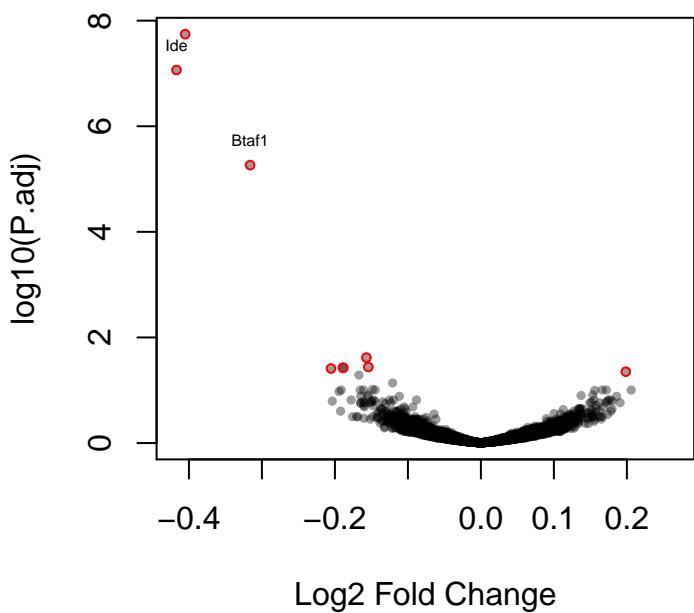
### GO downregulated genotype pfc



### pfc treatment

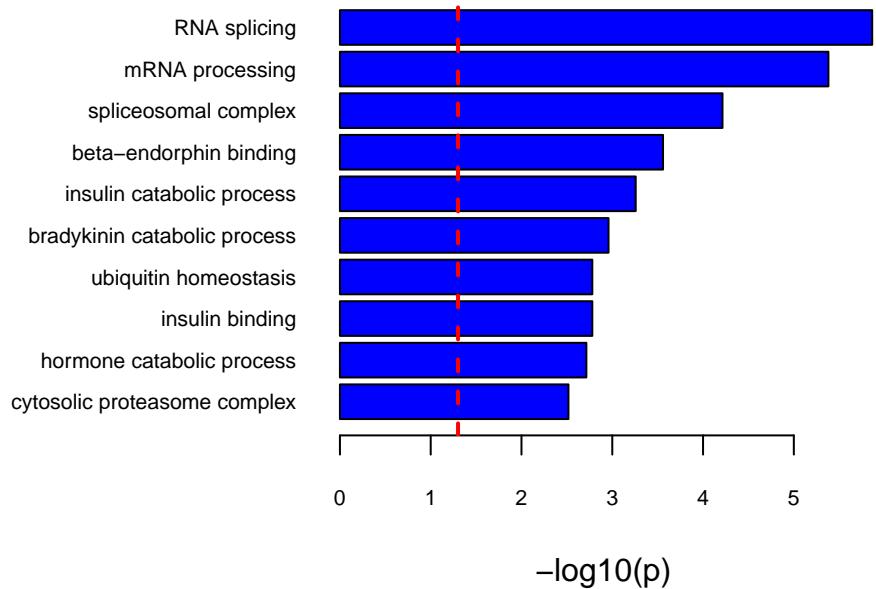


mean of normalized counts



Log2 Fold Change

### GO downregulated treatment pfc



**GO upregulated treatment pfc**

