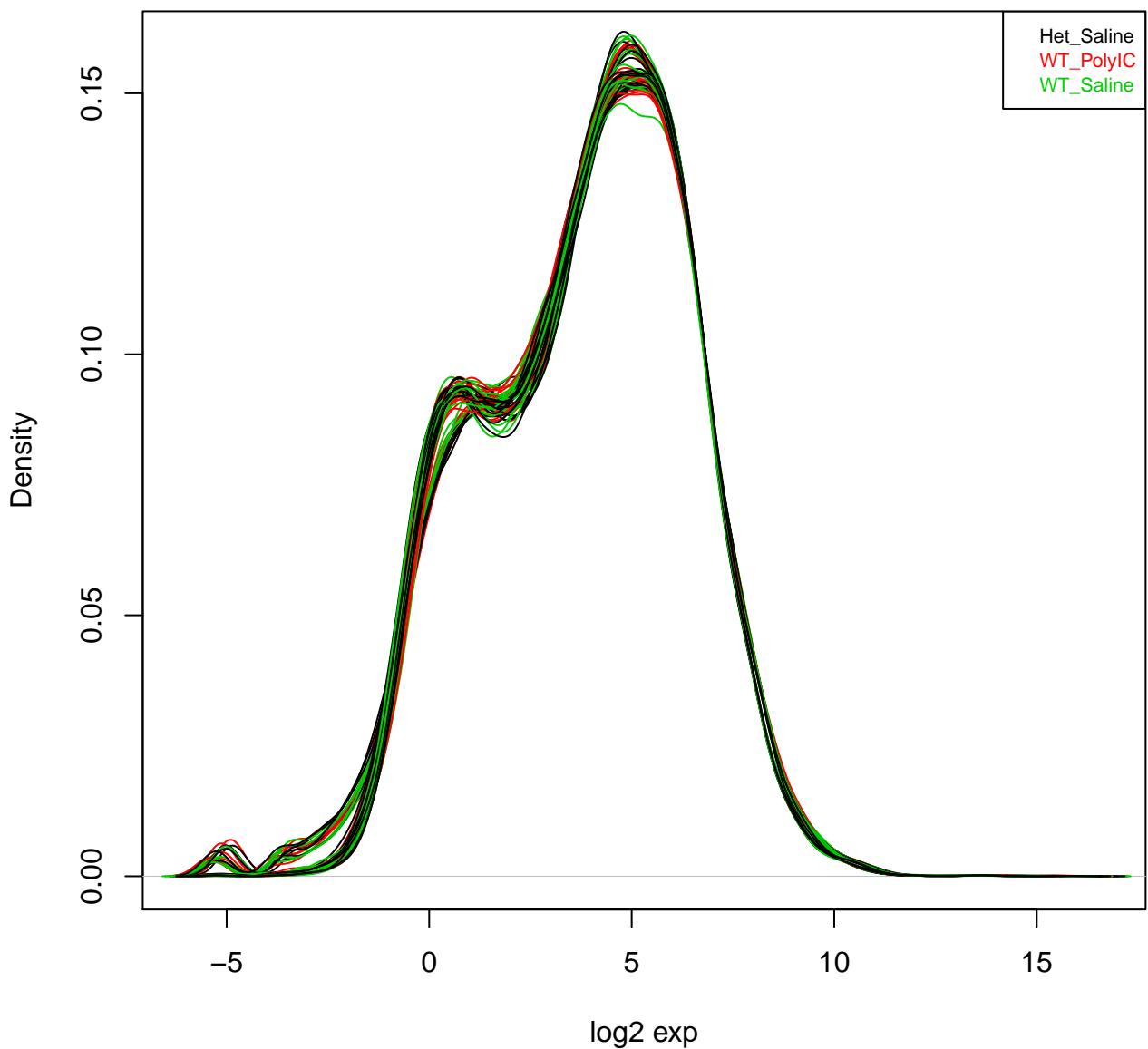
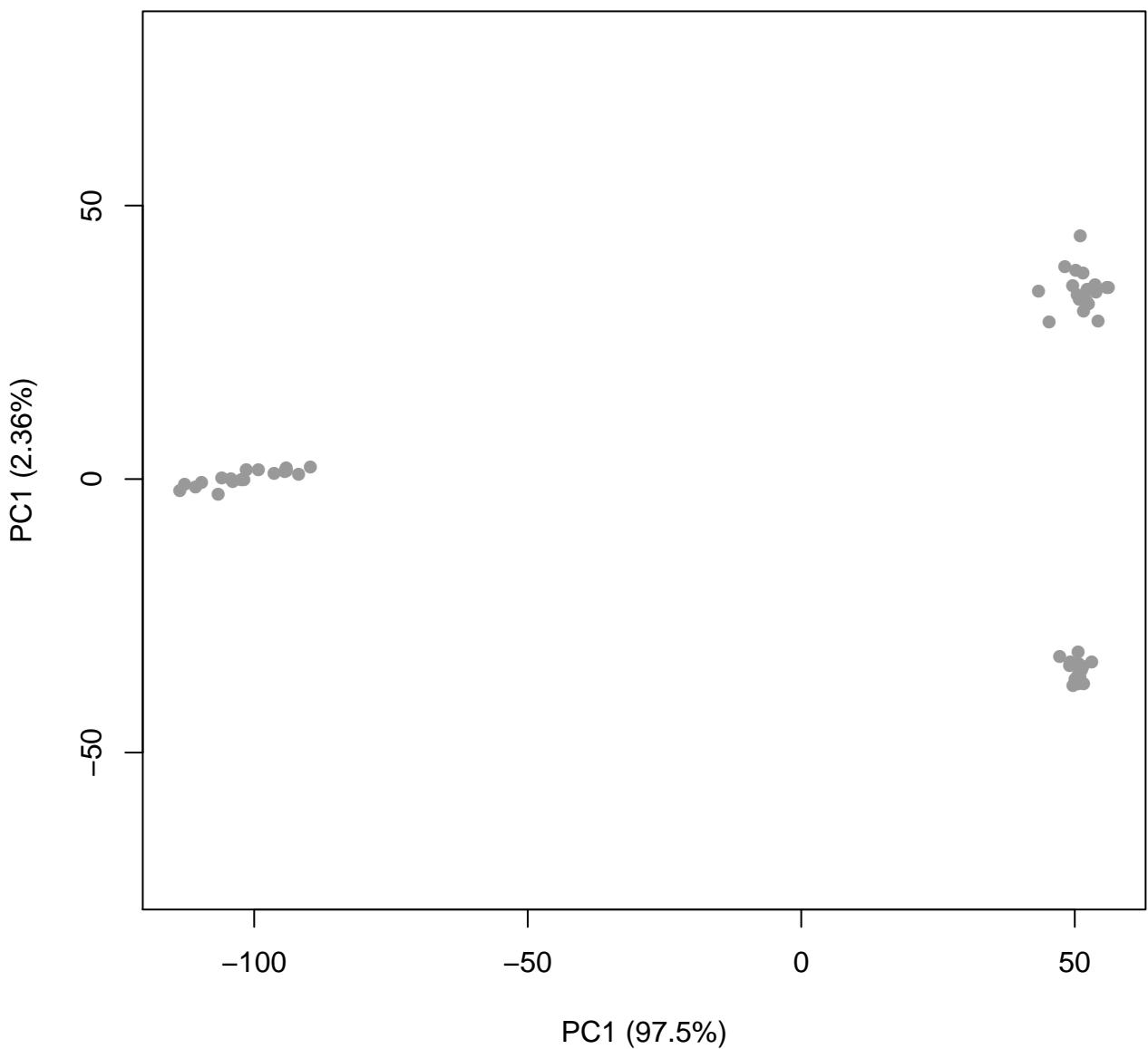


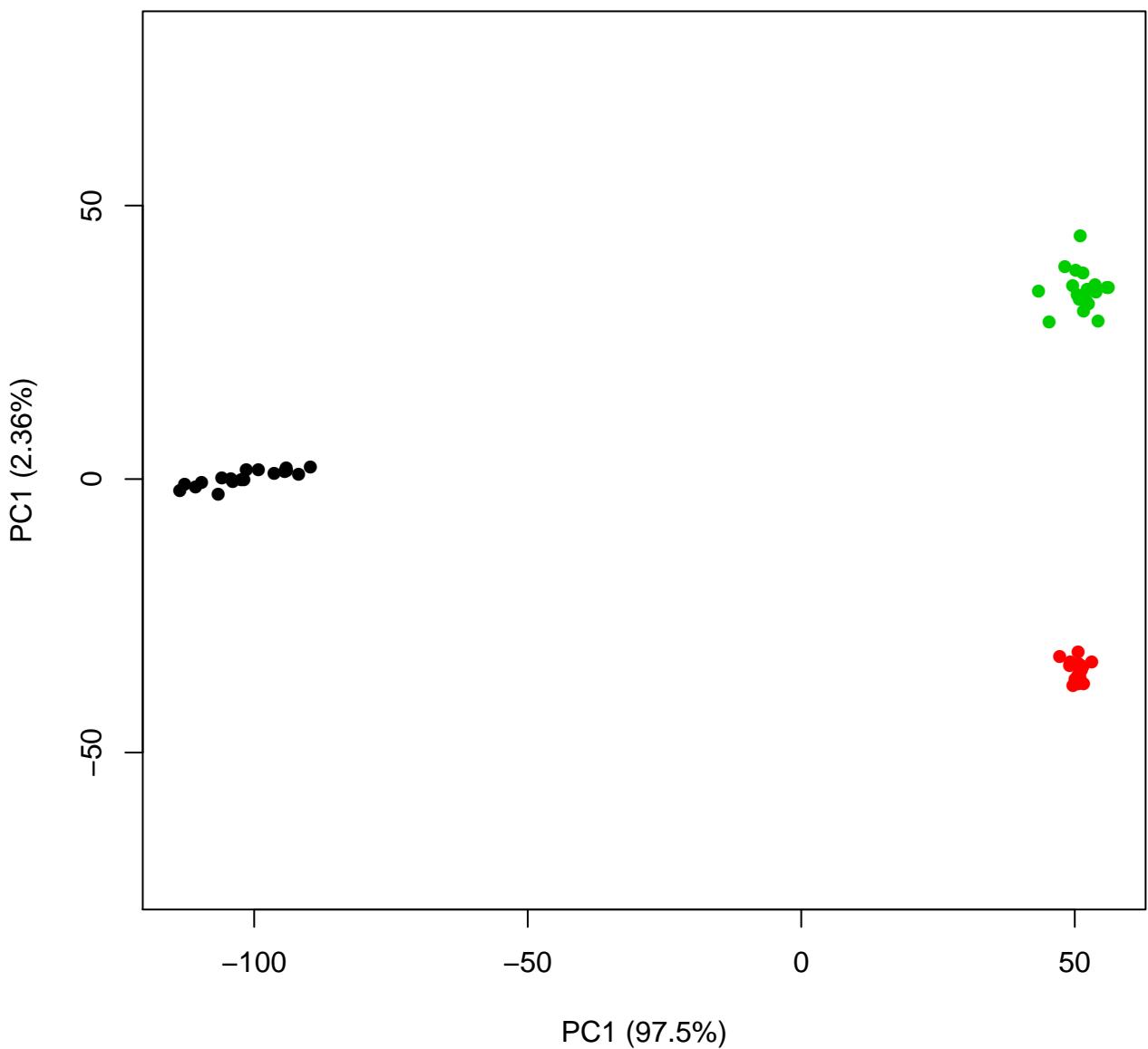
# Hist of Log2 Exp



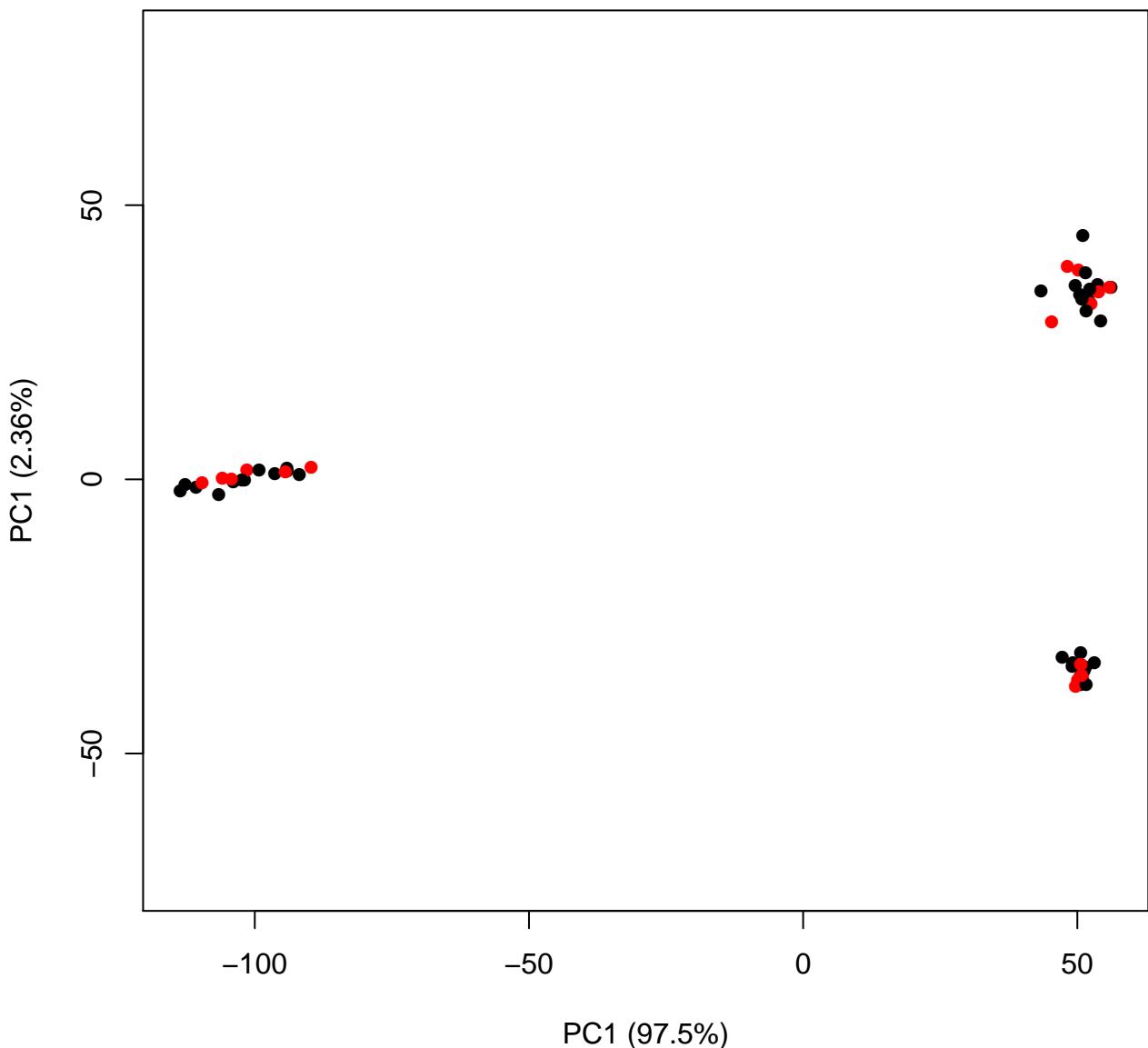
## MDS Plot



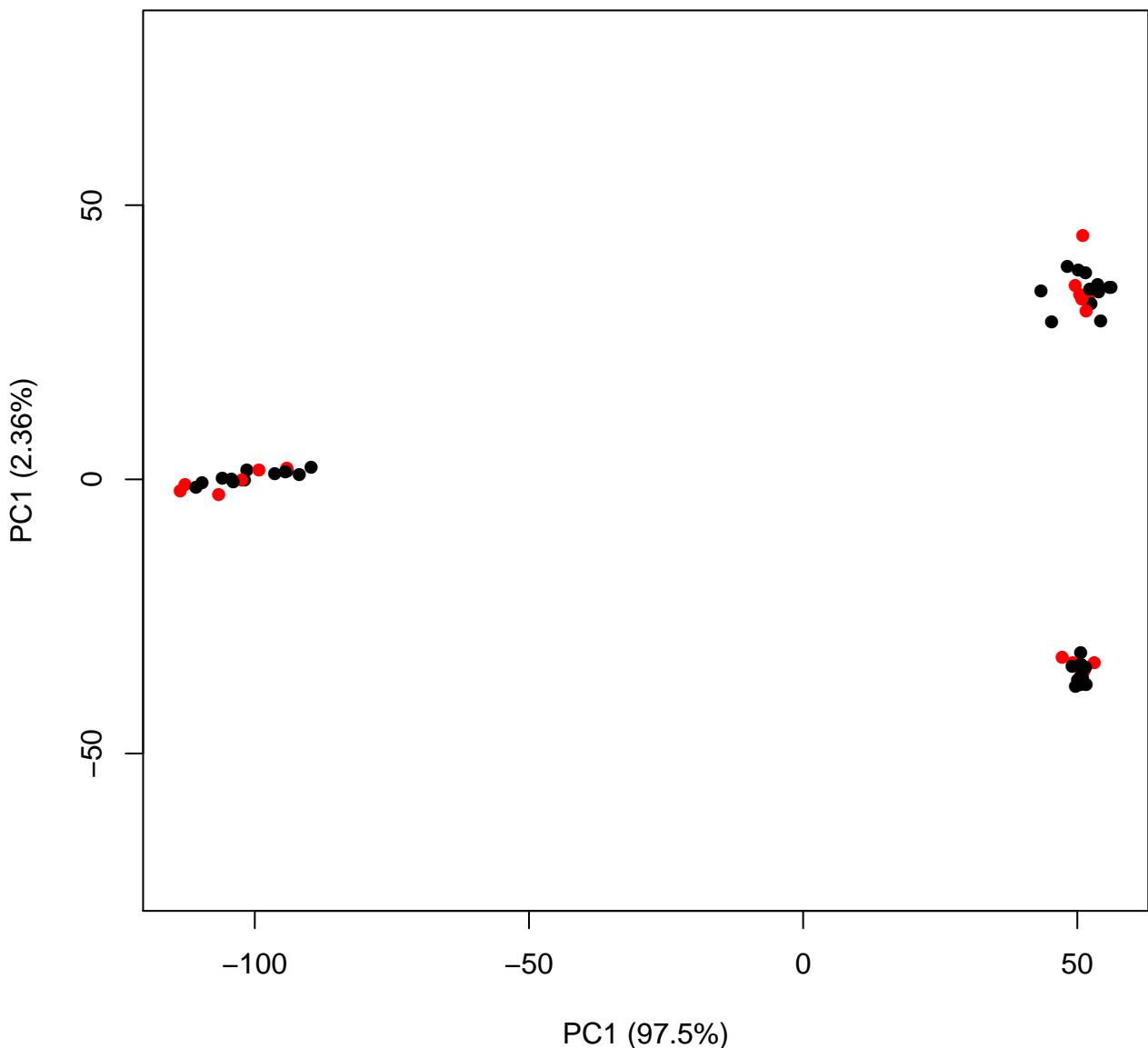
## MDS Plot by Region



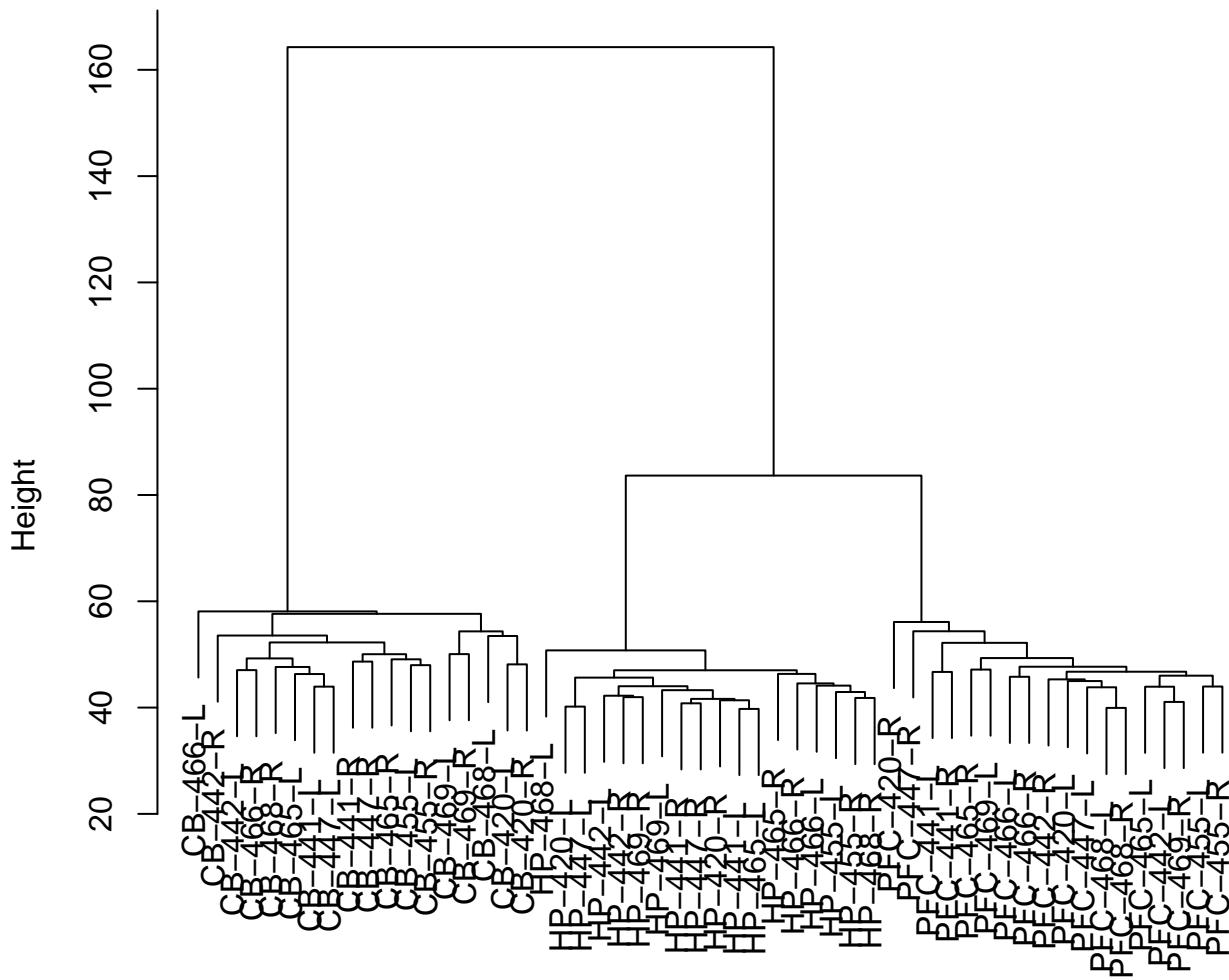
## MDS Plot by Genotype



## MDS Plot by Treatment

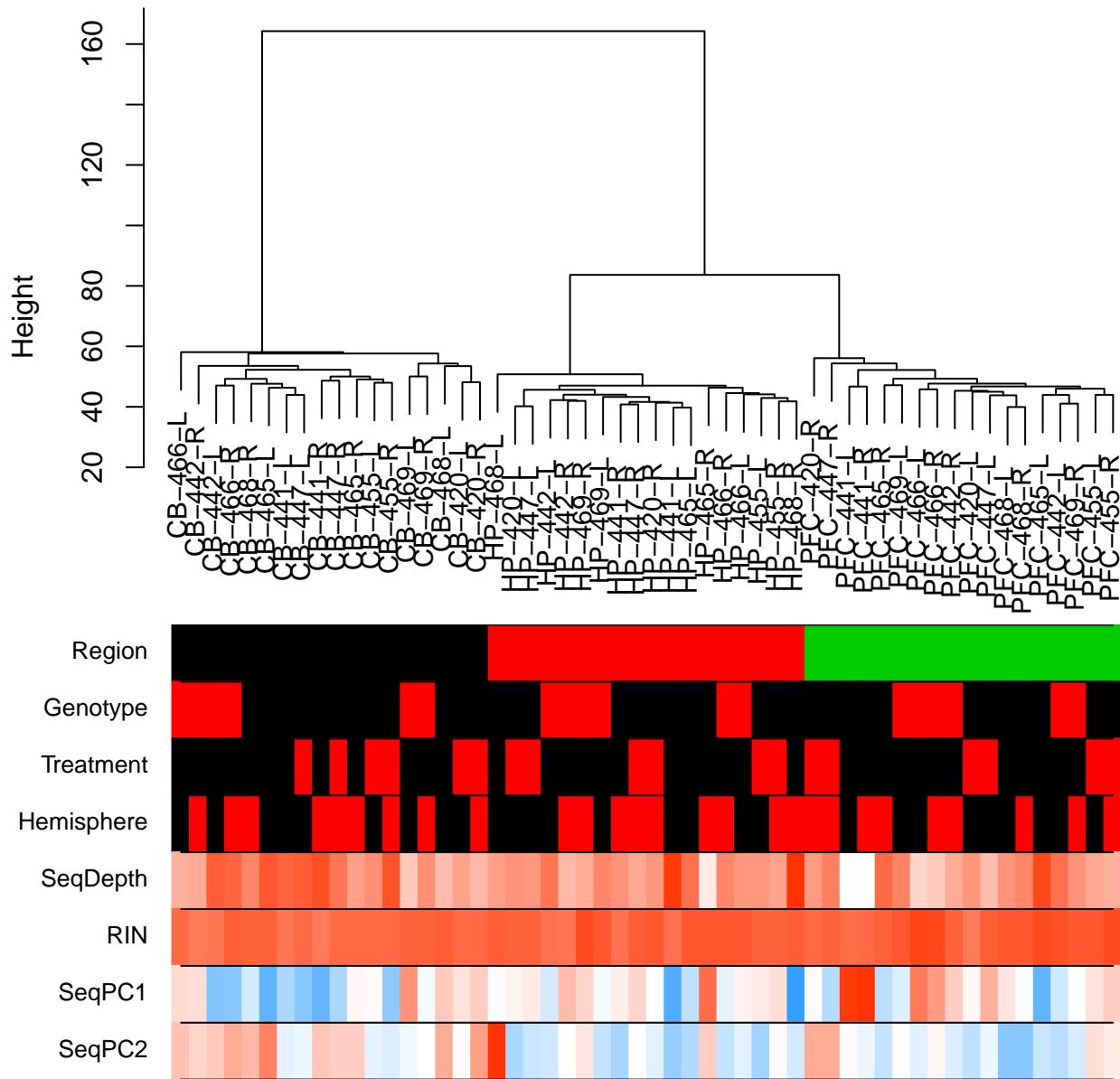


## Cluster Dendrogram

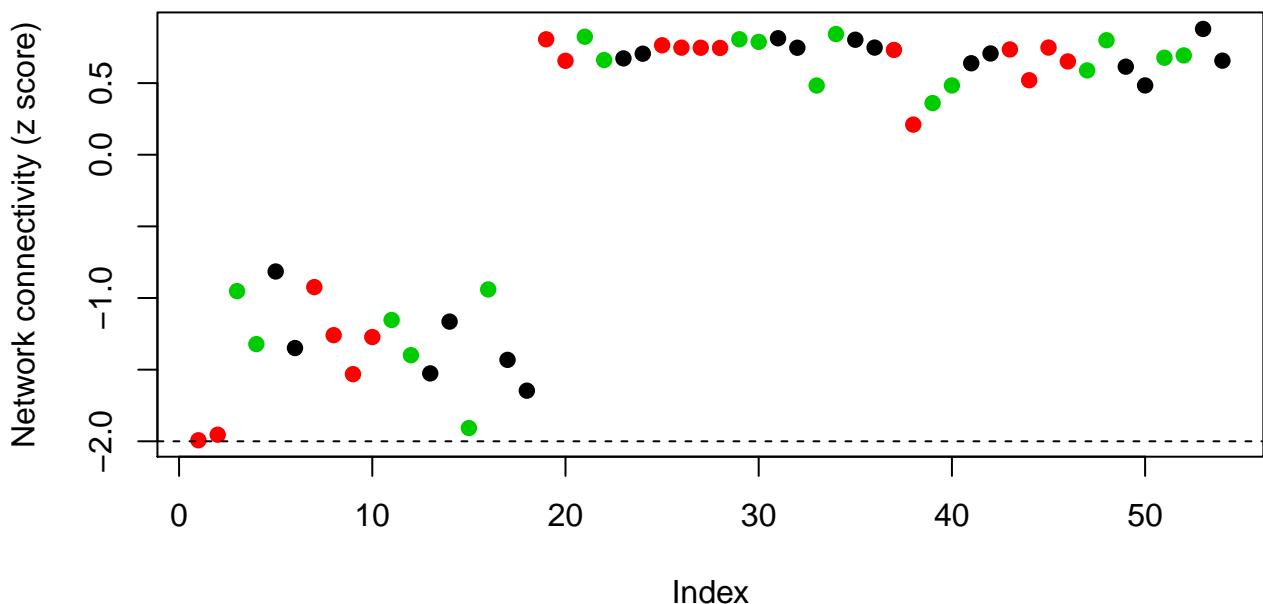


```
dist(t(datExpr.cpm))  
hclust (*, "average")
```

## Cluster Dendrogram

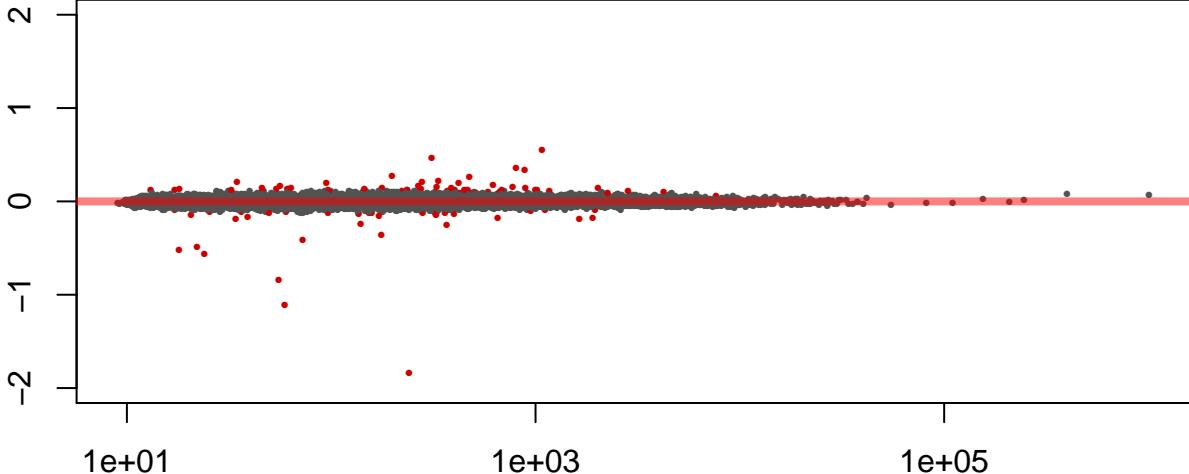


## Outlier detection



# all genotype

log fold change



mean expression

$\log_{10}(P.\text{adj})$

Gm15487

Gm9825

Tagap

Hmgaj1<sub>rs1</sub>

Gm14292

Pss41

D330041H02Rik

3110052H02Rik

Zfp766<sub>rs3</sub>

Prune1

Tsc2

Tagap1

Rnps1

Atp6v0c

Zfp766

Prune1

-2

-1

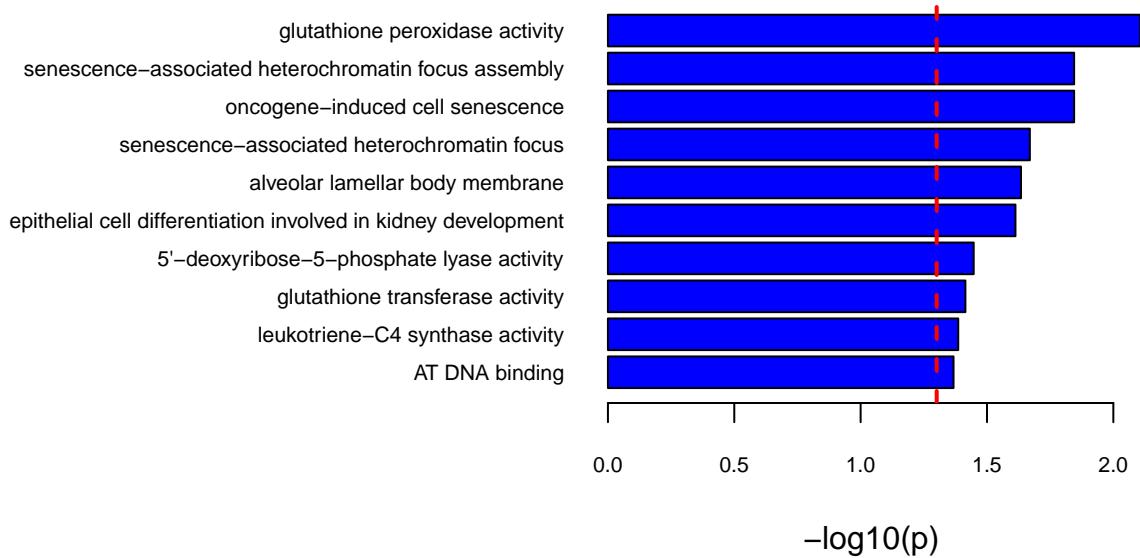
0

1

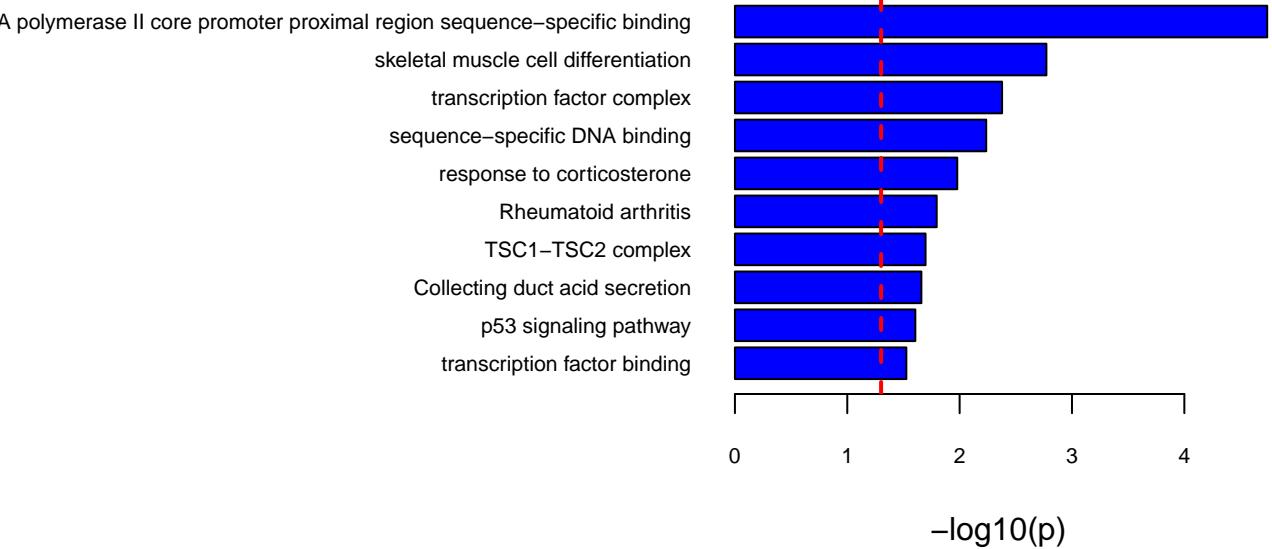
2

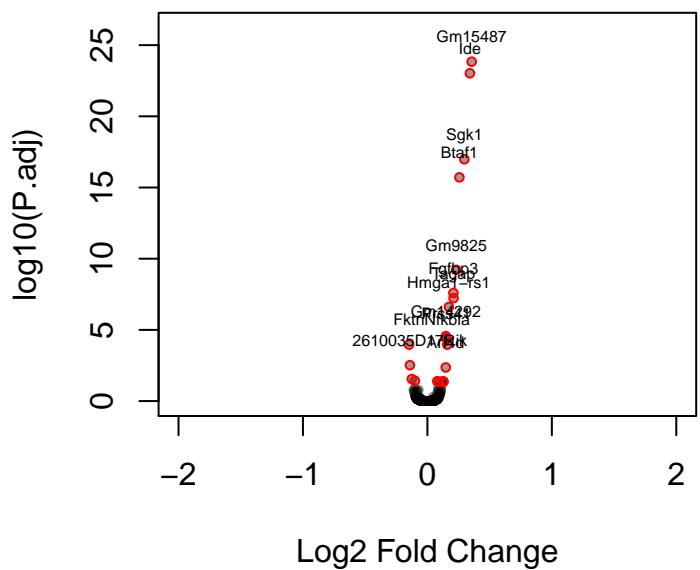
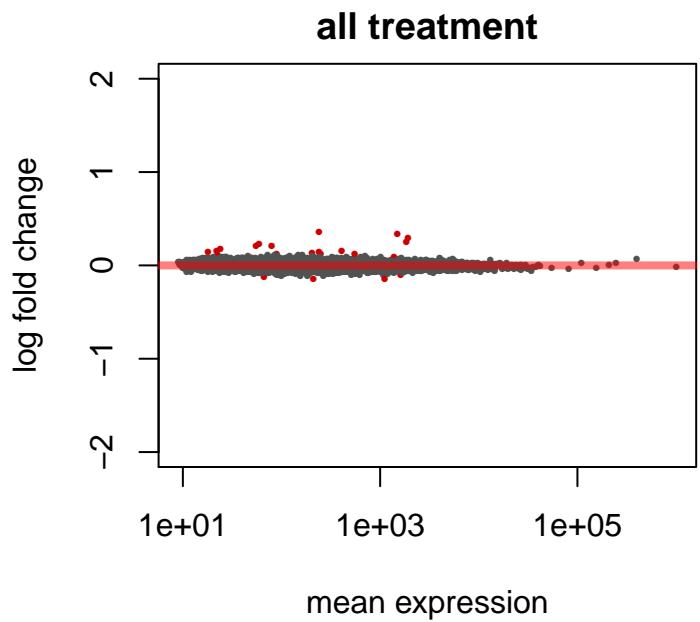
Log2 Fold Change

### GO downregulated genotype all

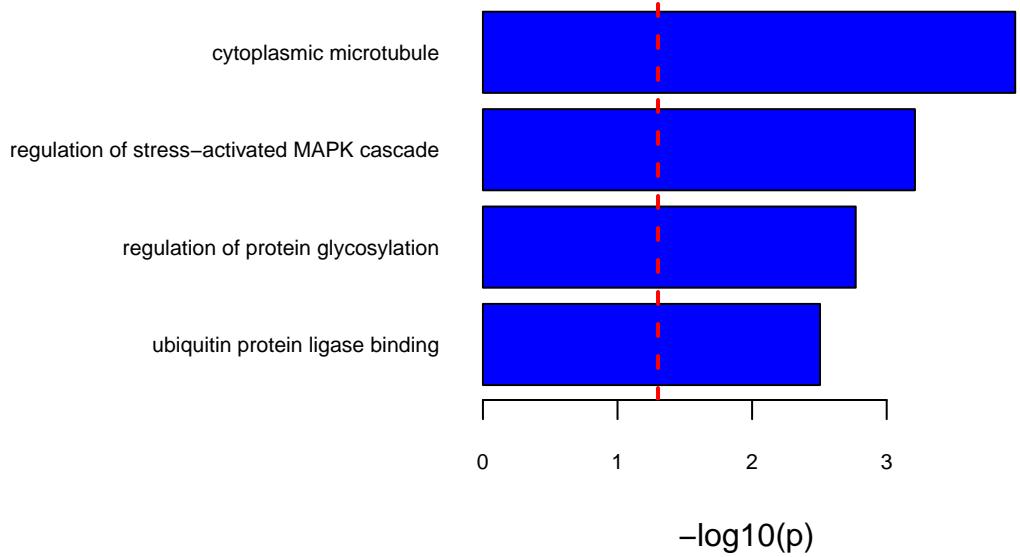


### GO upregulated genotype all

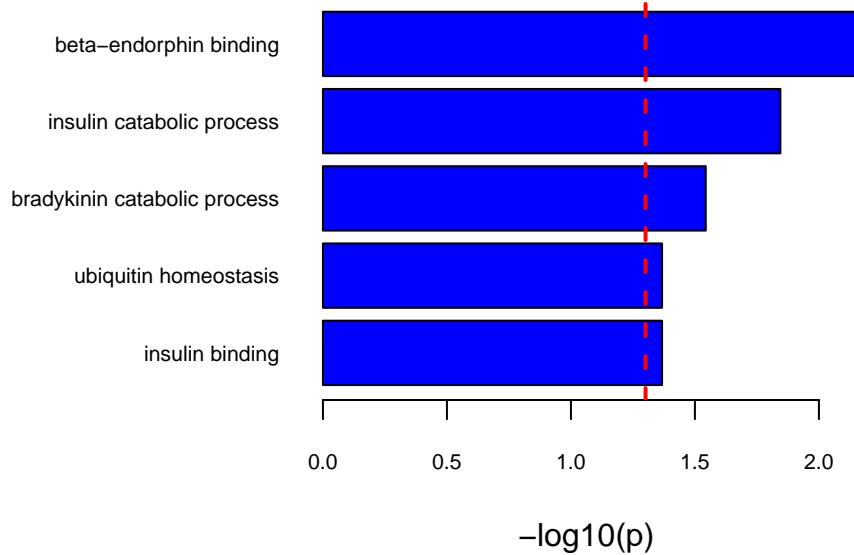




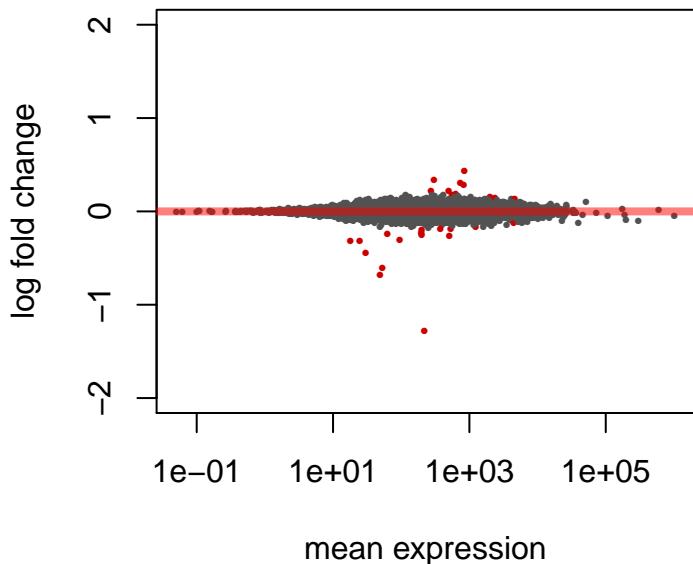
GO downregulated treatment all



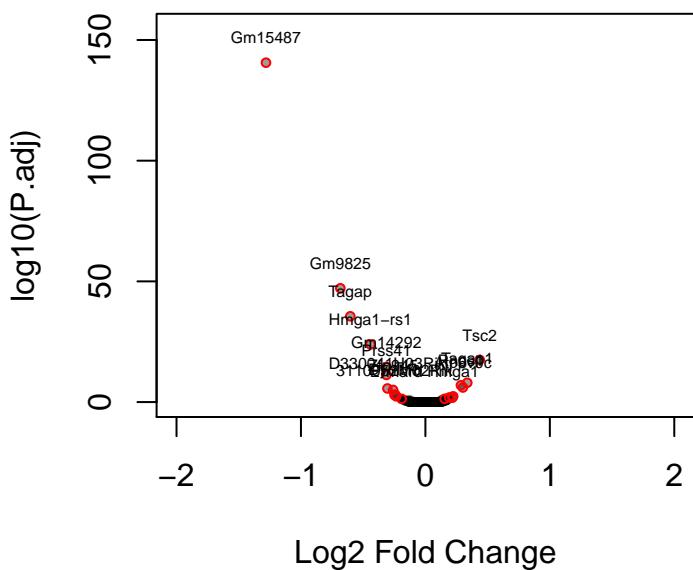
GO upregulated treatment all



### cbl genotype

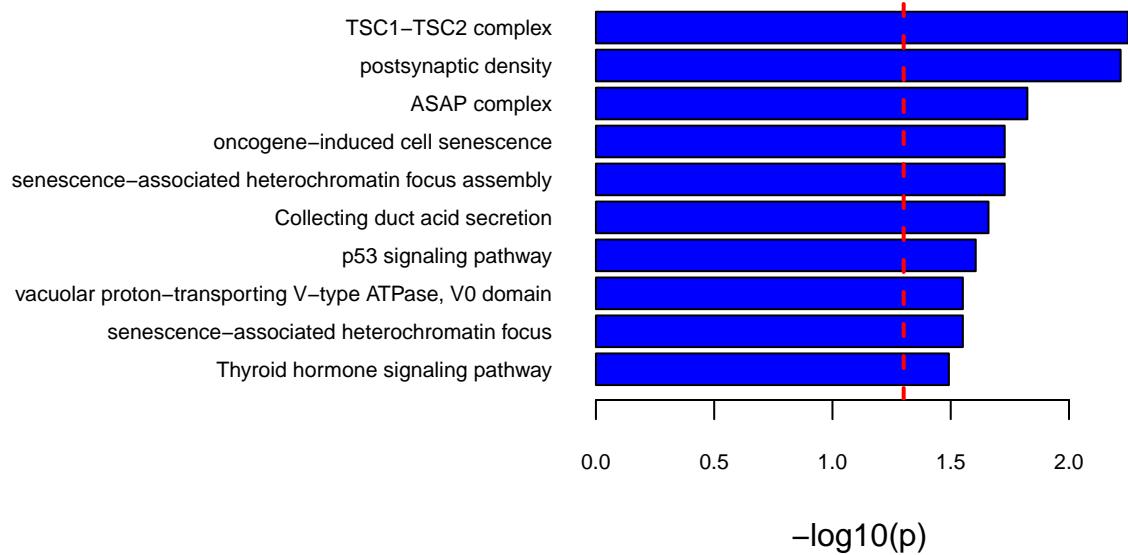


mean expression

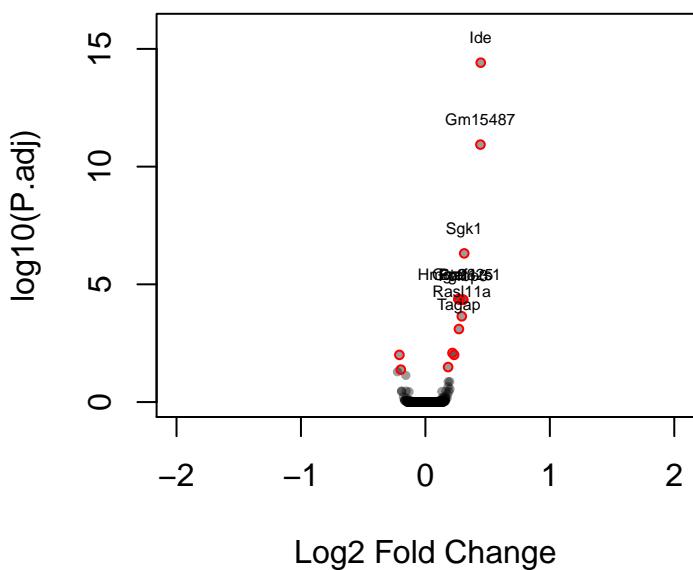
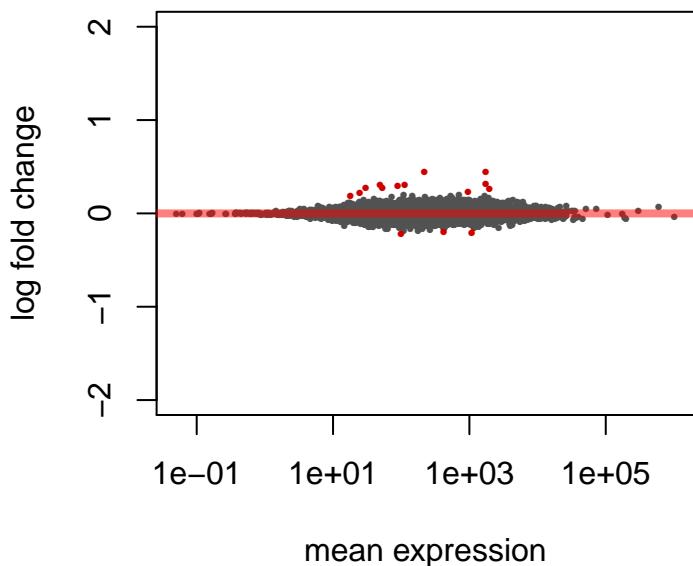


Log2 Fold Change

### GO upregulated genotype cbl



### cbl treatment



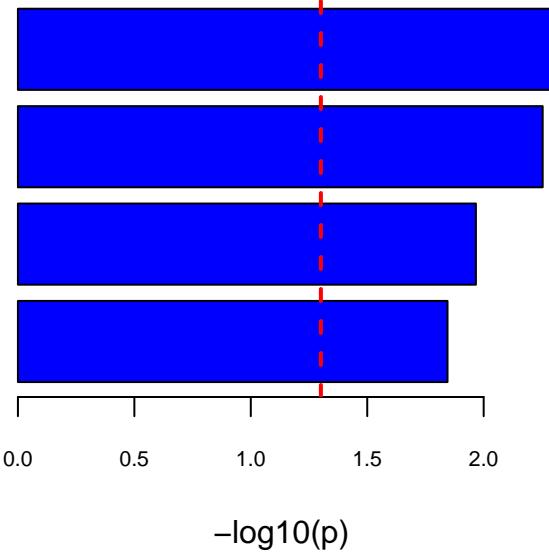
### GO downregulated treatment cbl

regulation of protein glycosylation

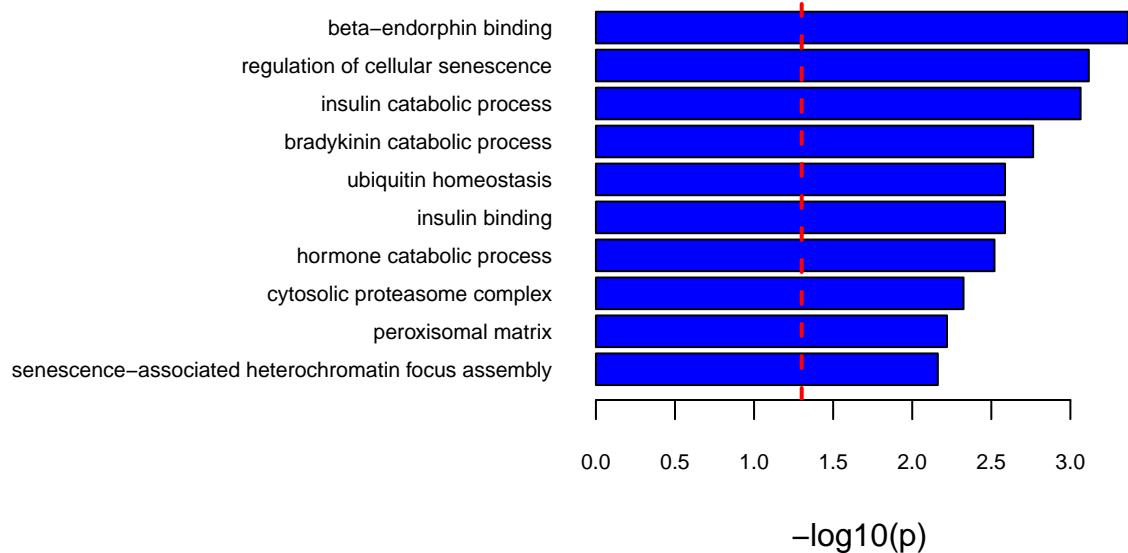
protein O-linked mannosylation

negative regulation of JNK cascade

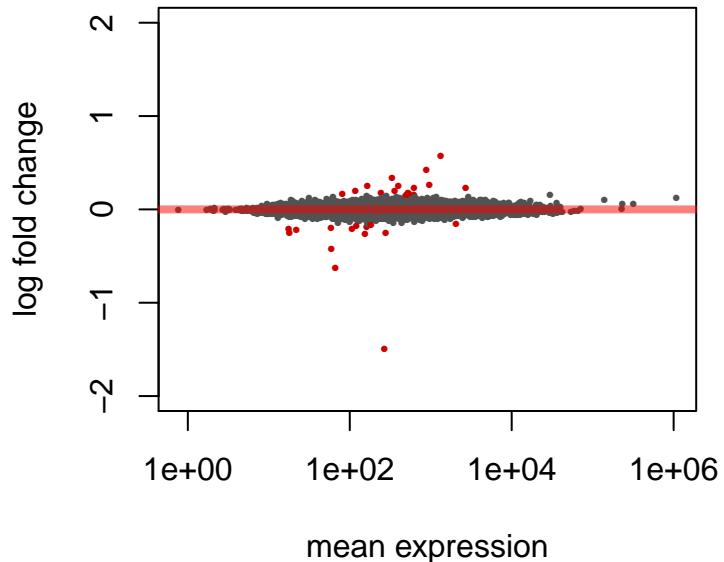
cis-Golgi network



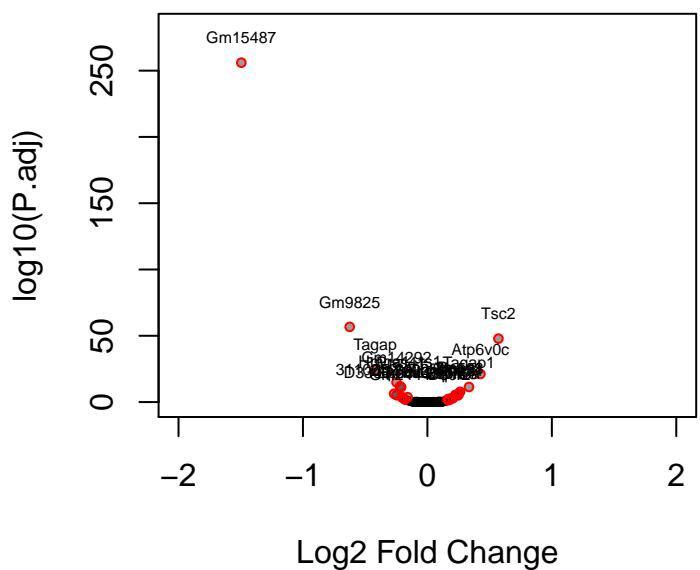
### GO upregulated treatment cbl



### hc genotype

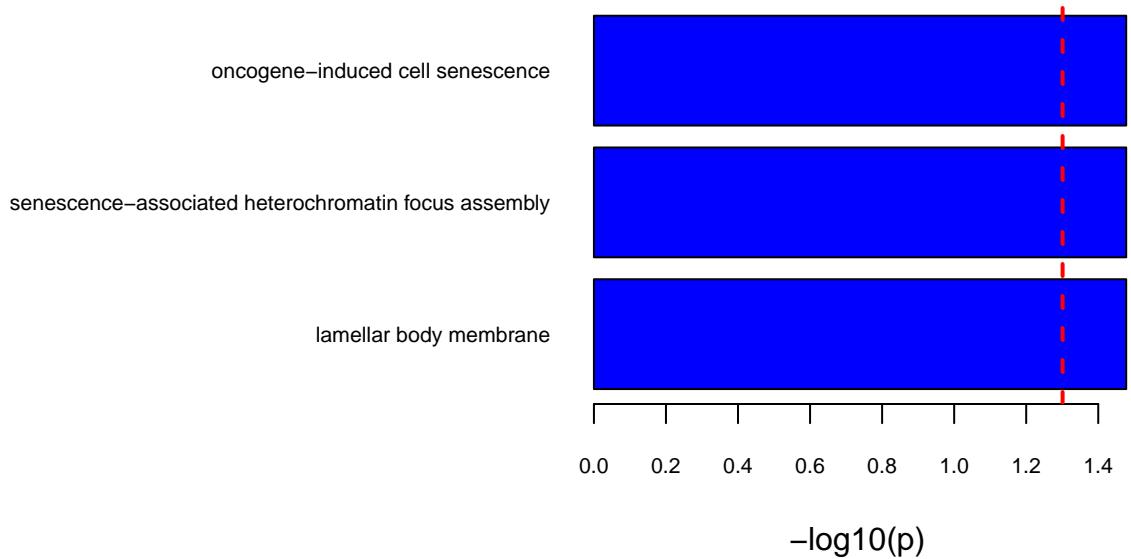


mean expression

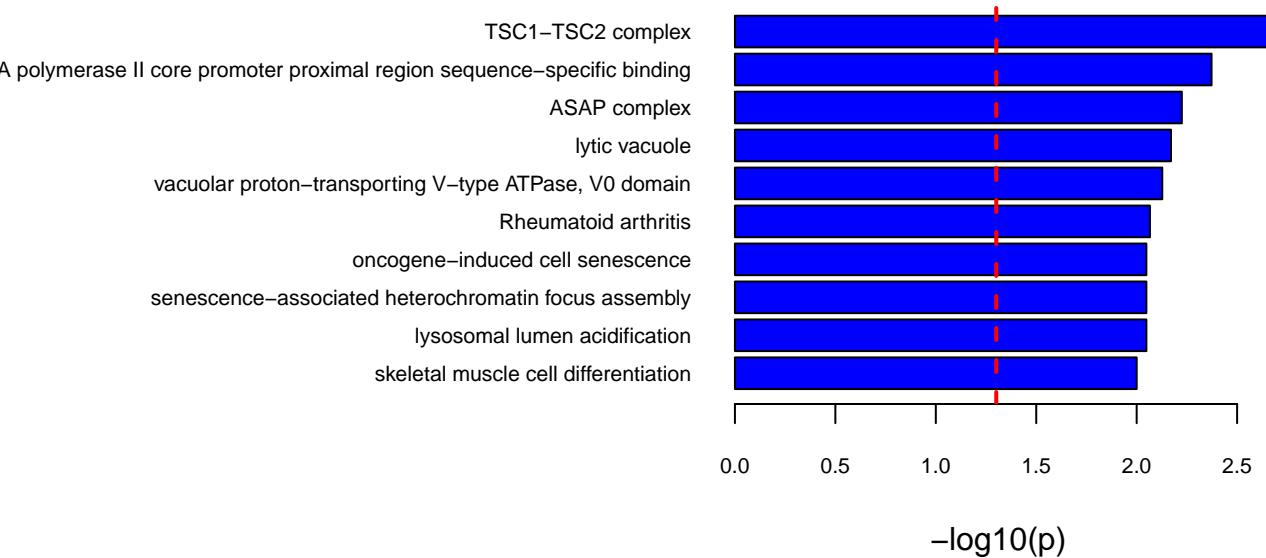


Log2 Fold Change

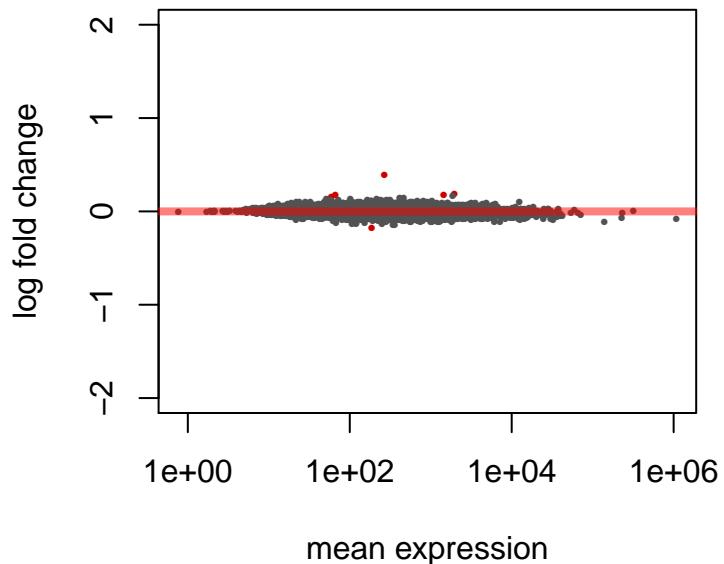
GO downregulated genotype hc



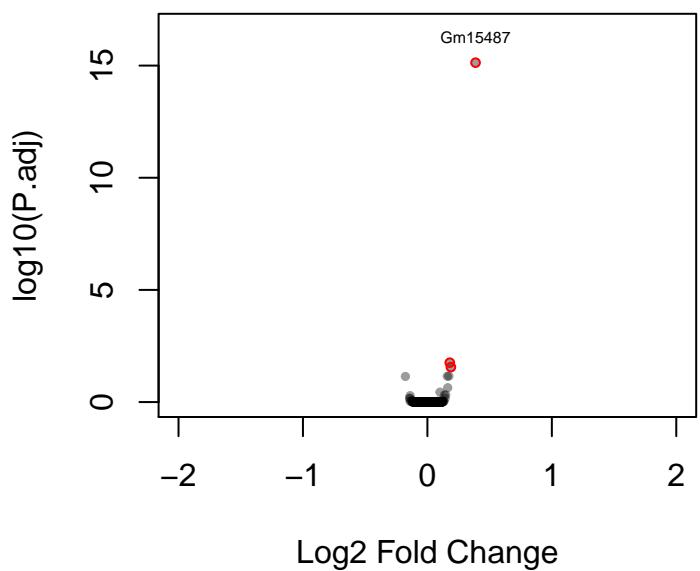
GO upregulated genotype hc



### hc treatment

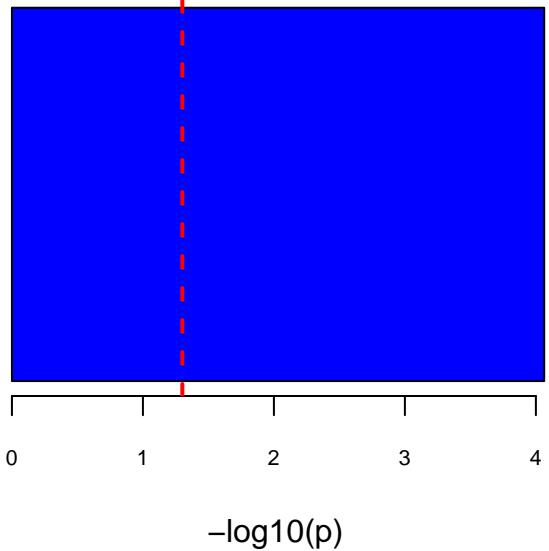


Gm15487

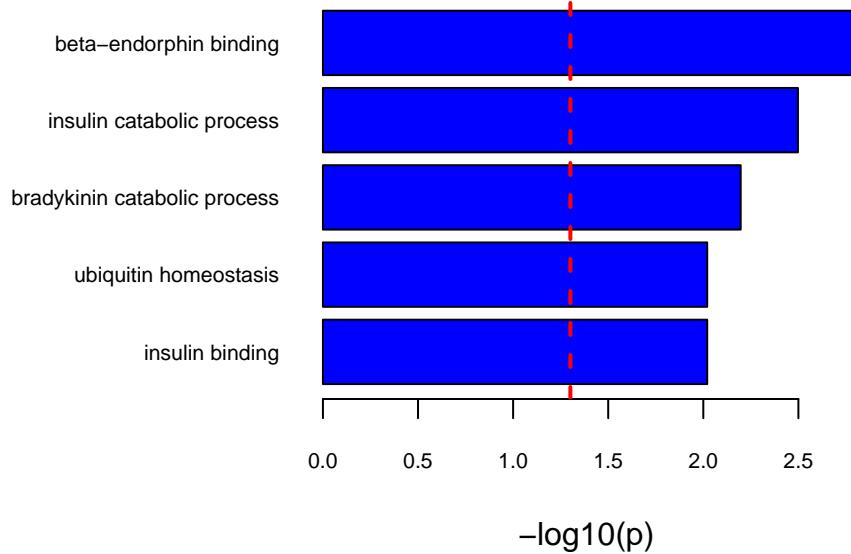


### GO downregulated treatment hc

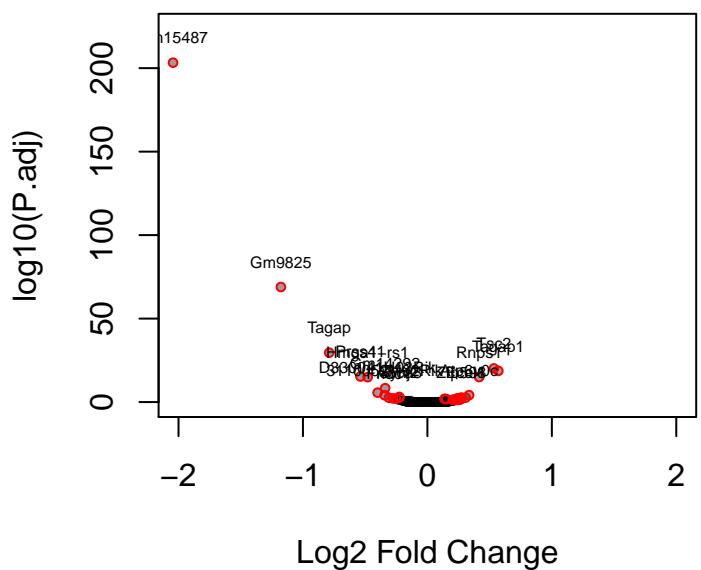
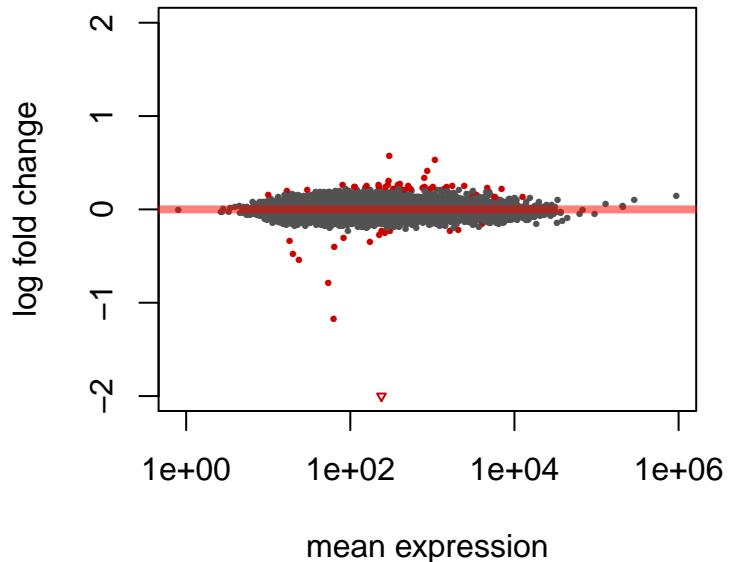
regulation of cell proliferation involved in tissue homeostasis



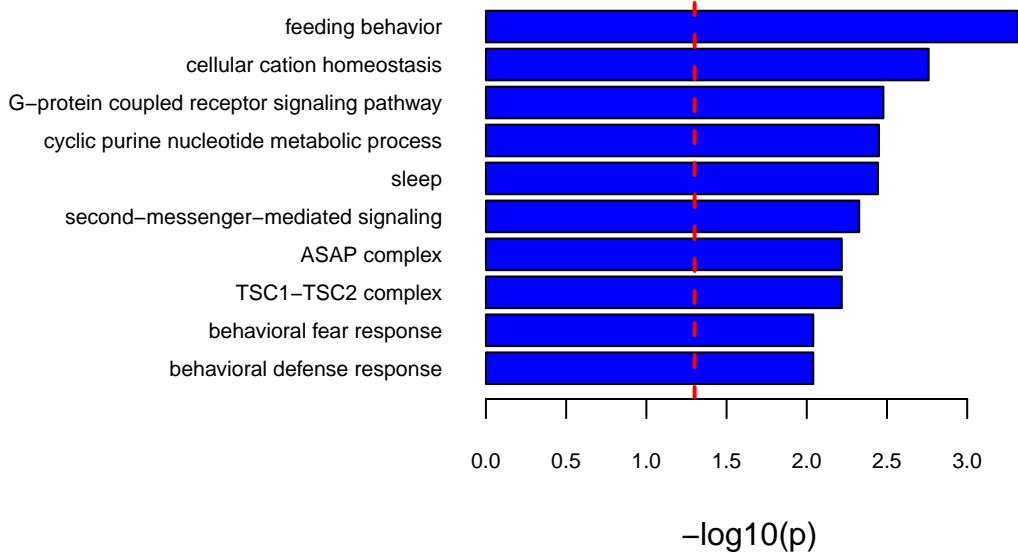
**GO upregulated treatment hc**



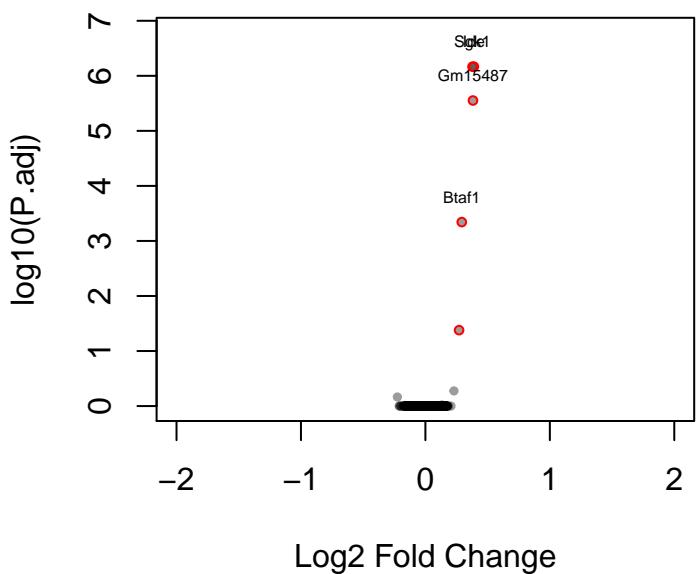
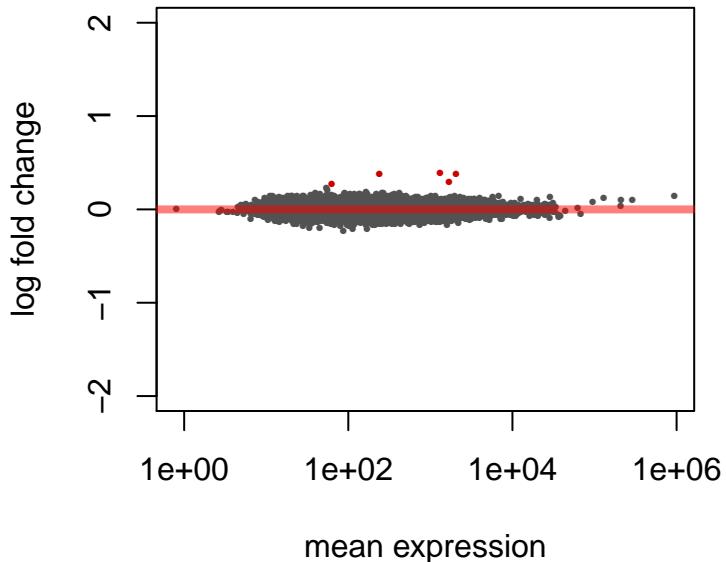
### pfc genotype



### GO upregulated genotype pfc



### pfc treatment



GO upregulated treatment pfc

