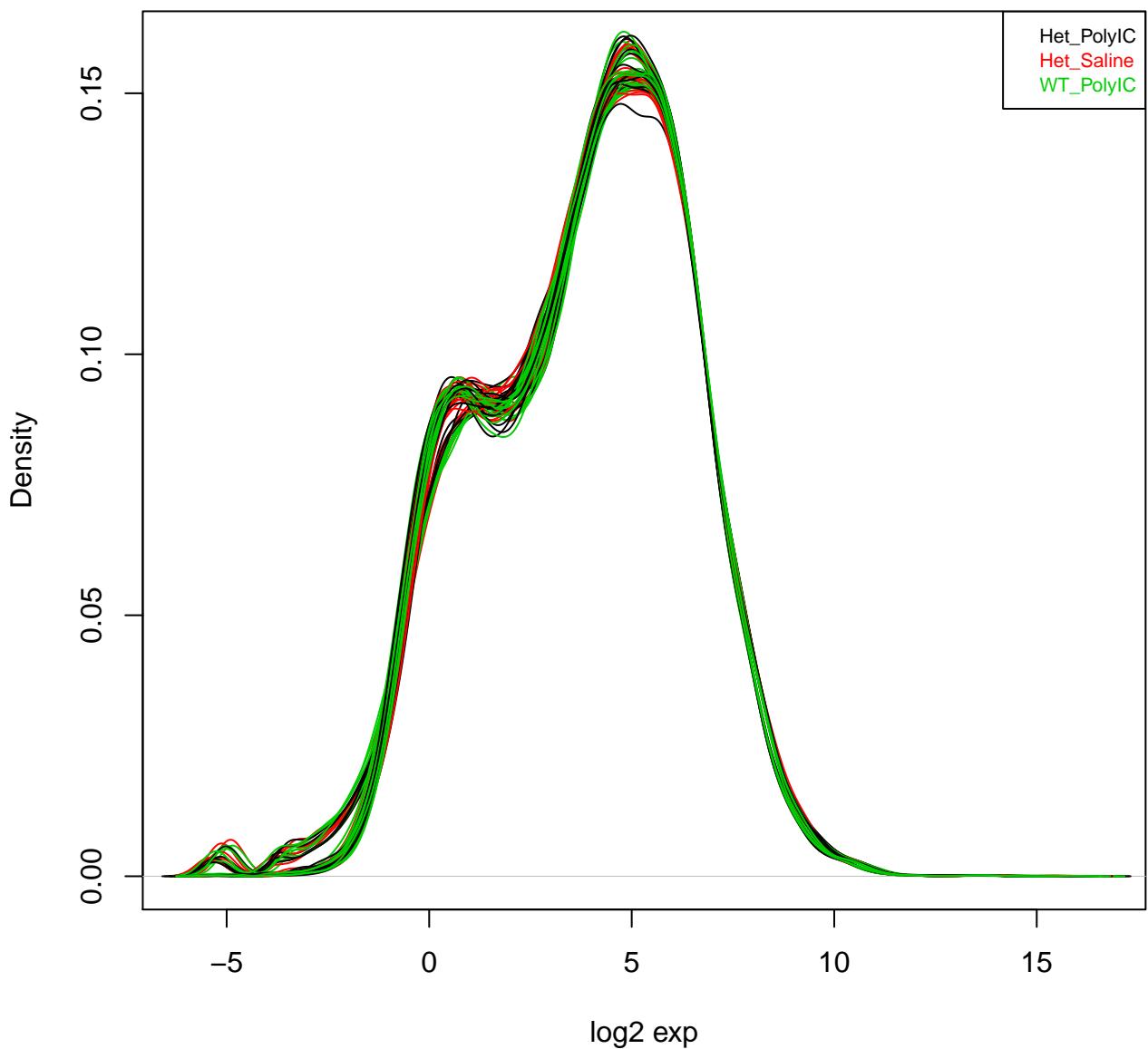
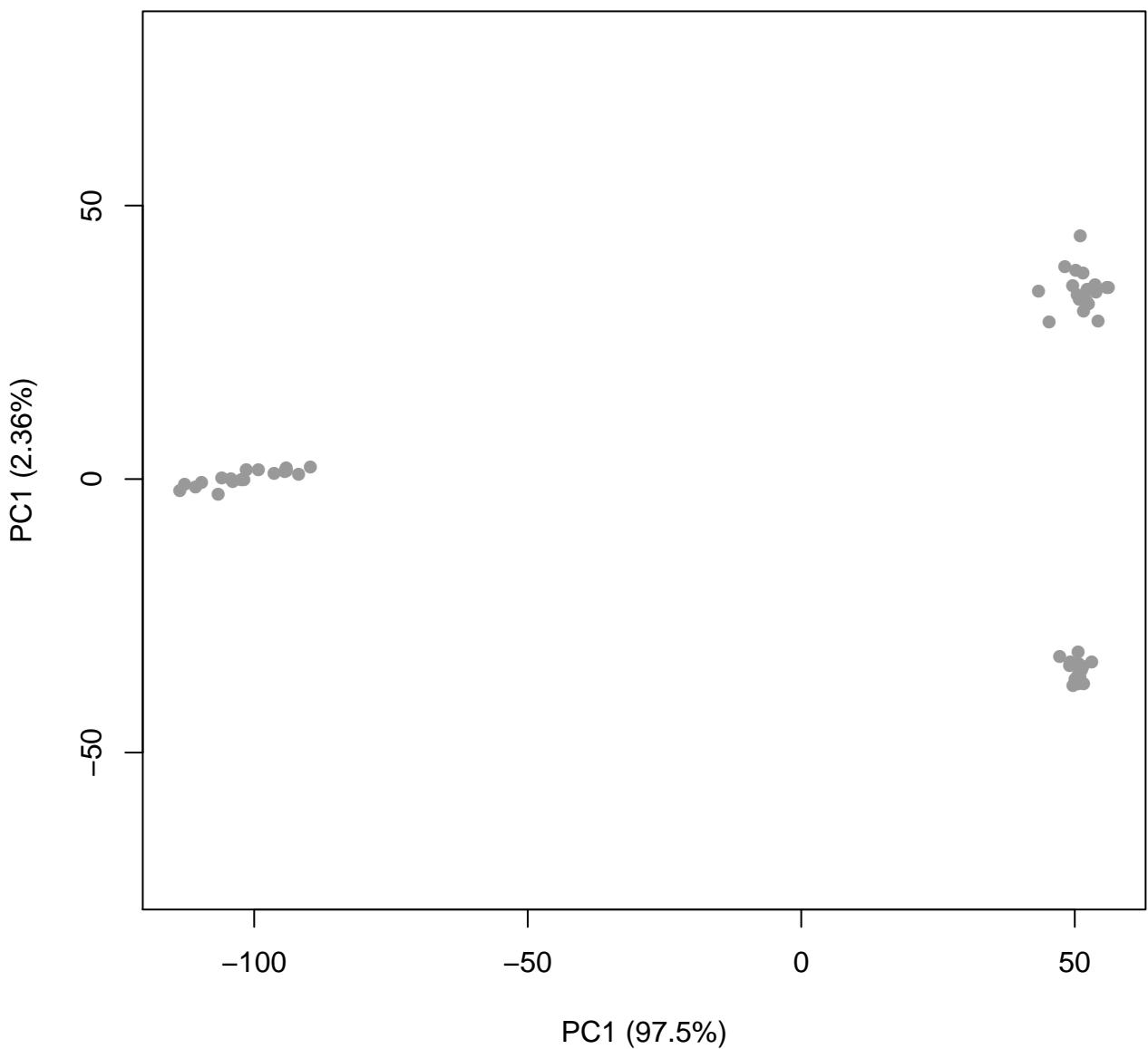


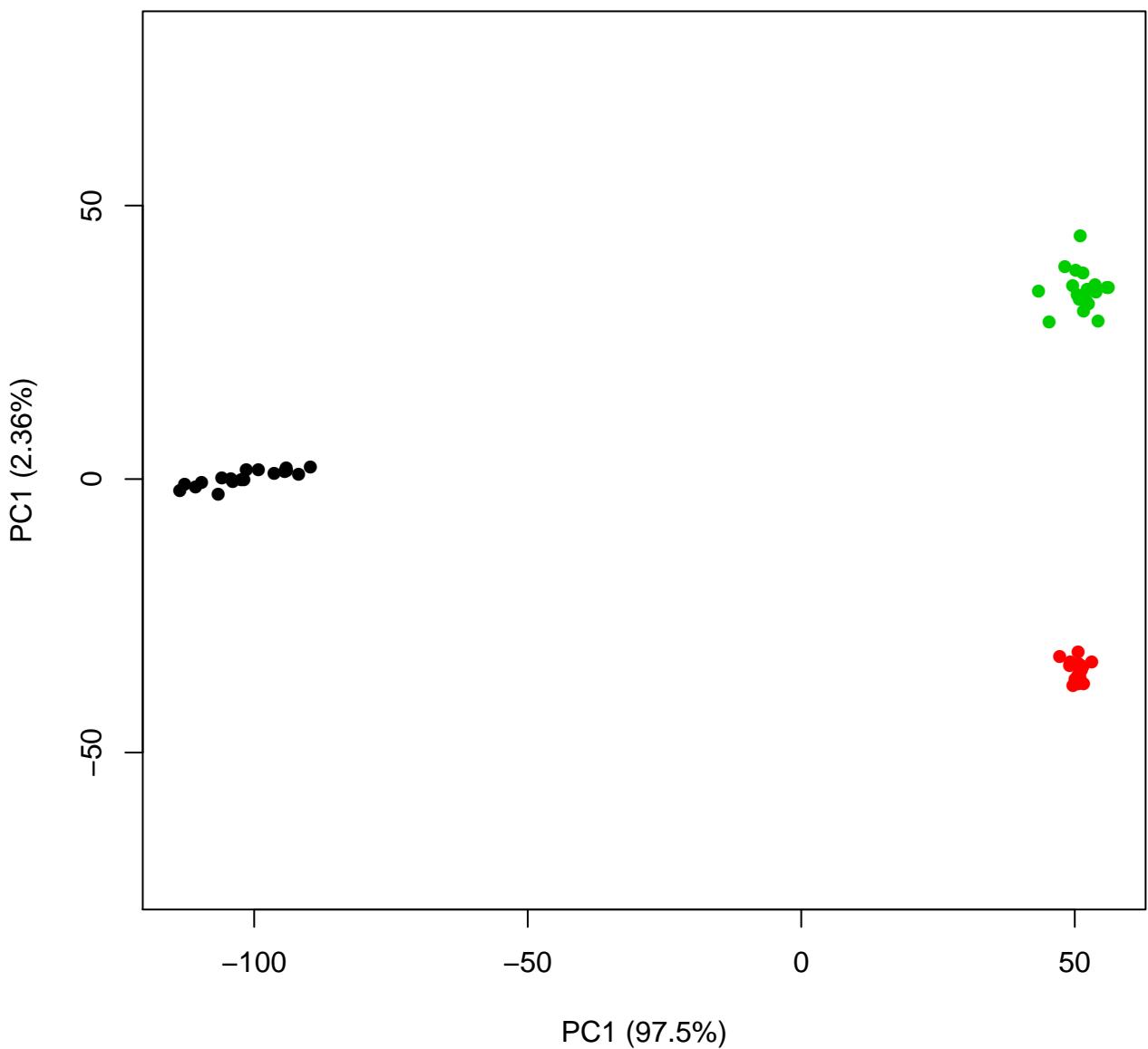
Hist of Log2 Exp



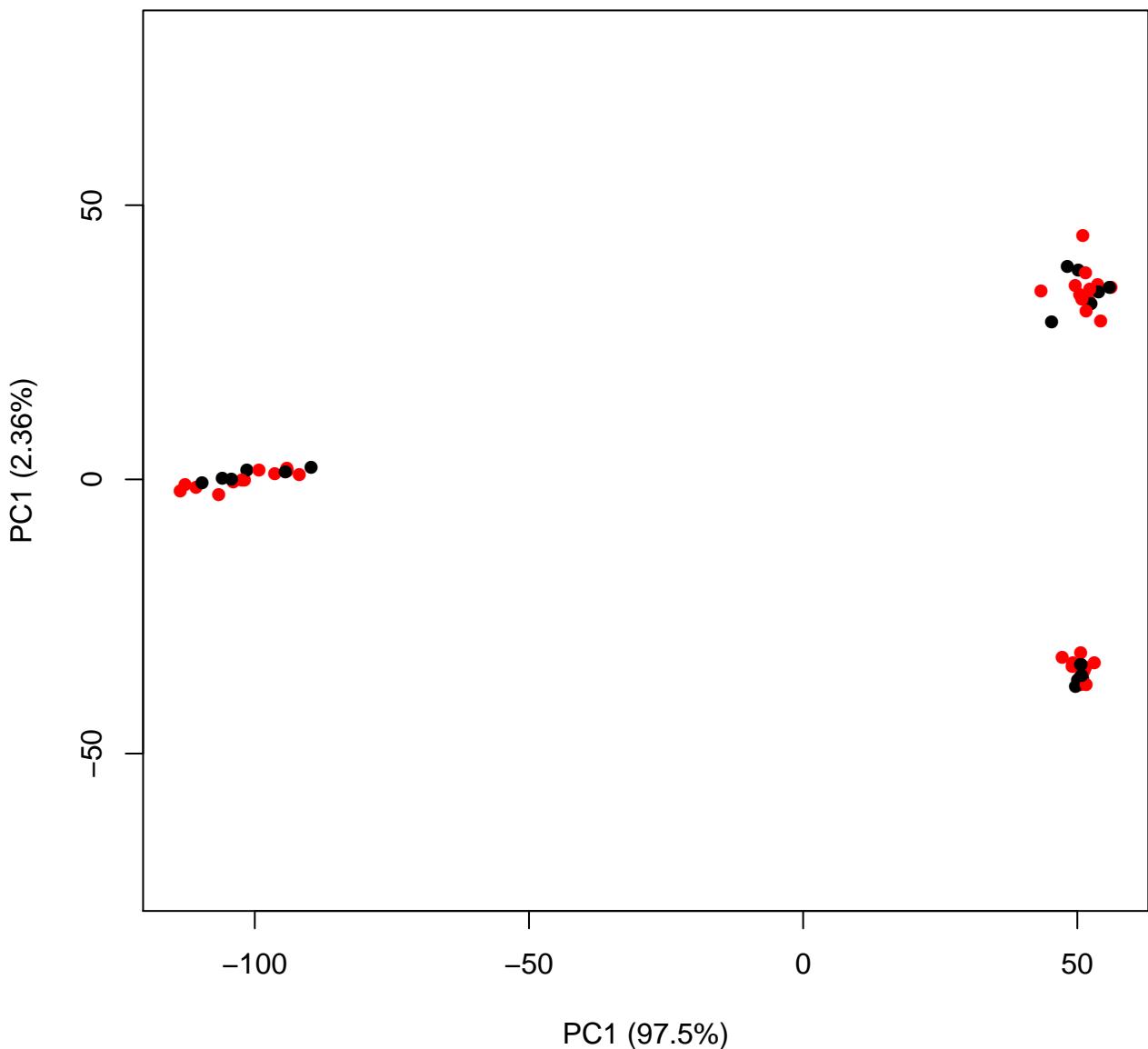
MDS Plot



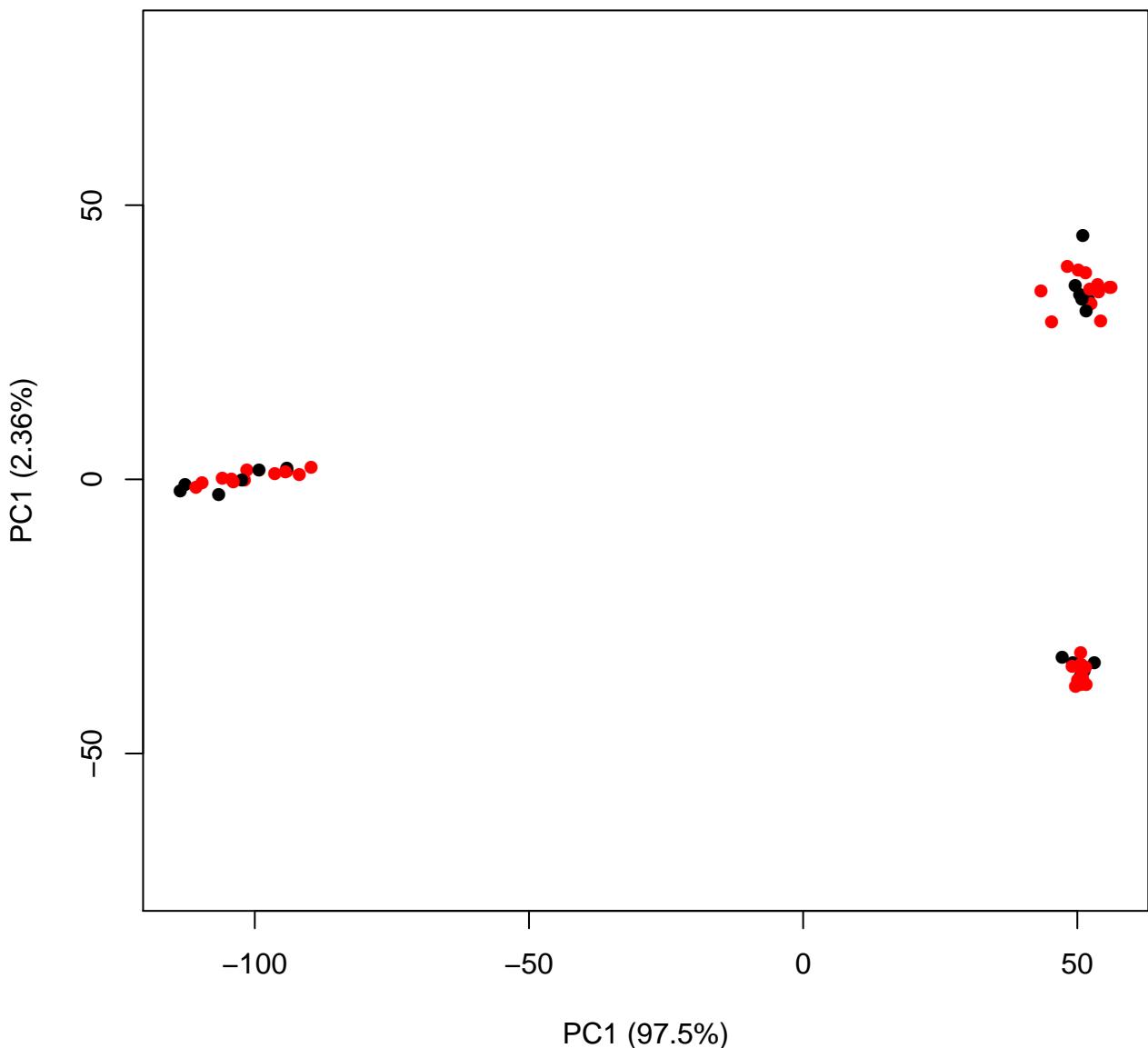
MDS Plot by Region



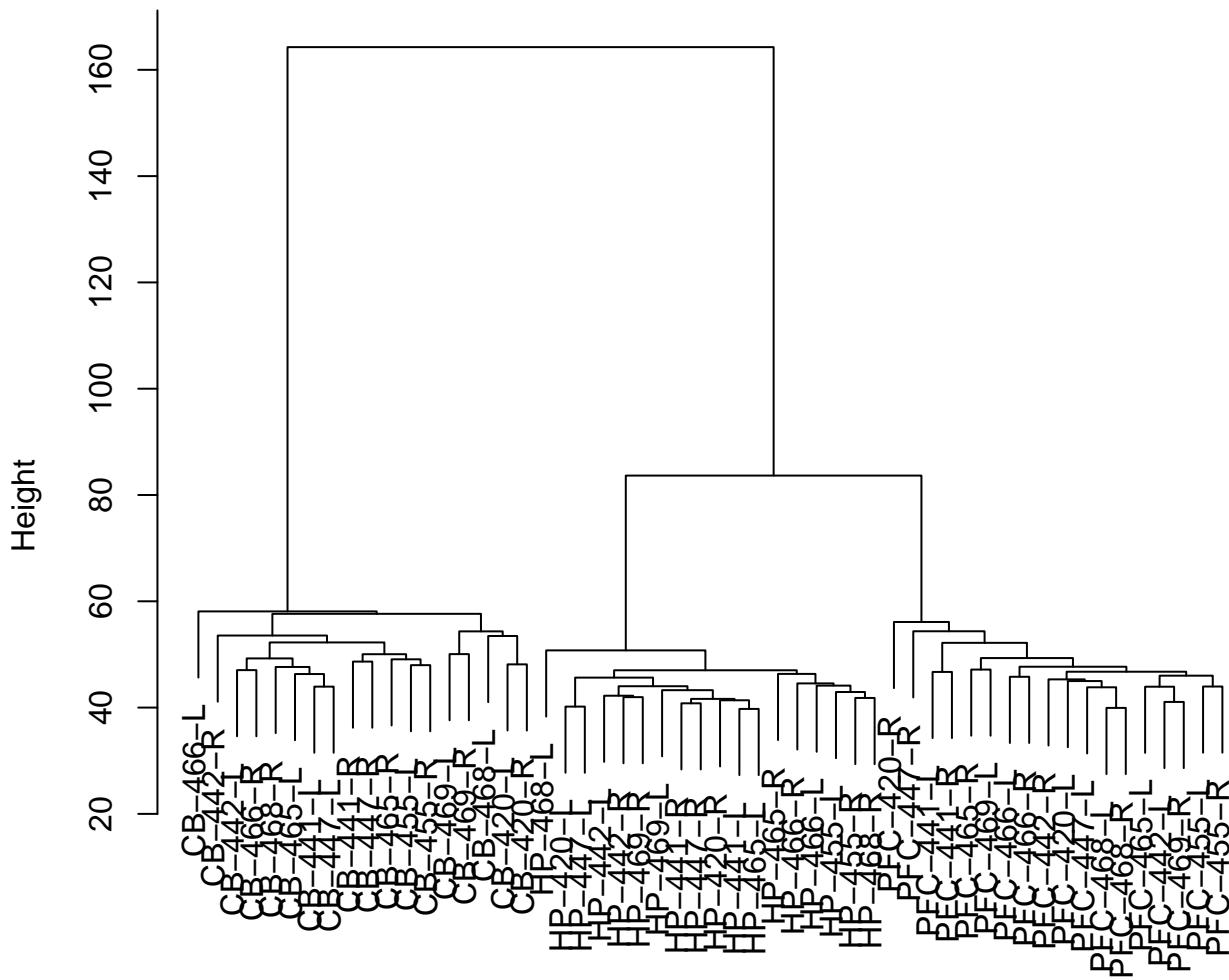
MDS Plot by Genotype



MDS Plot by Treatment

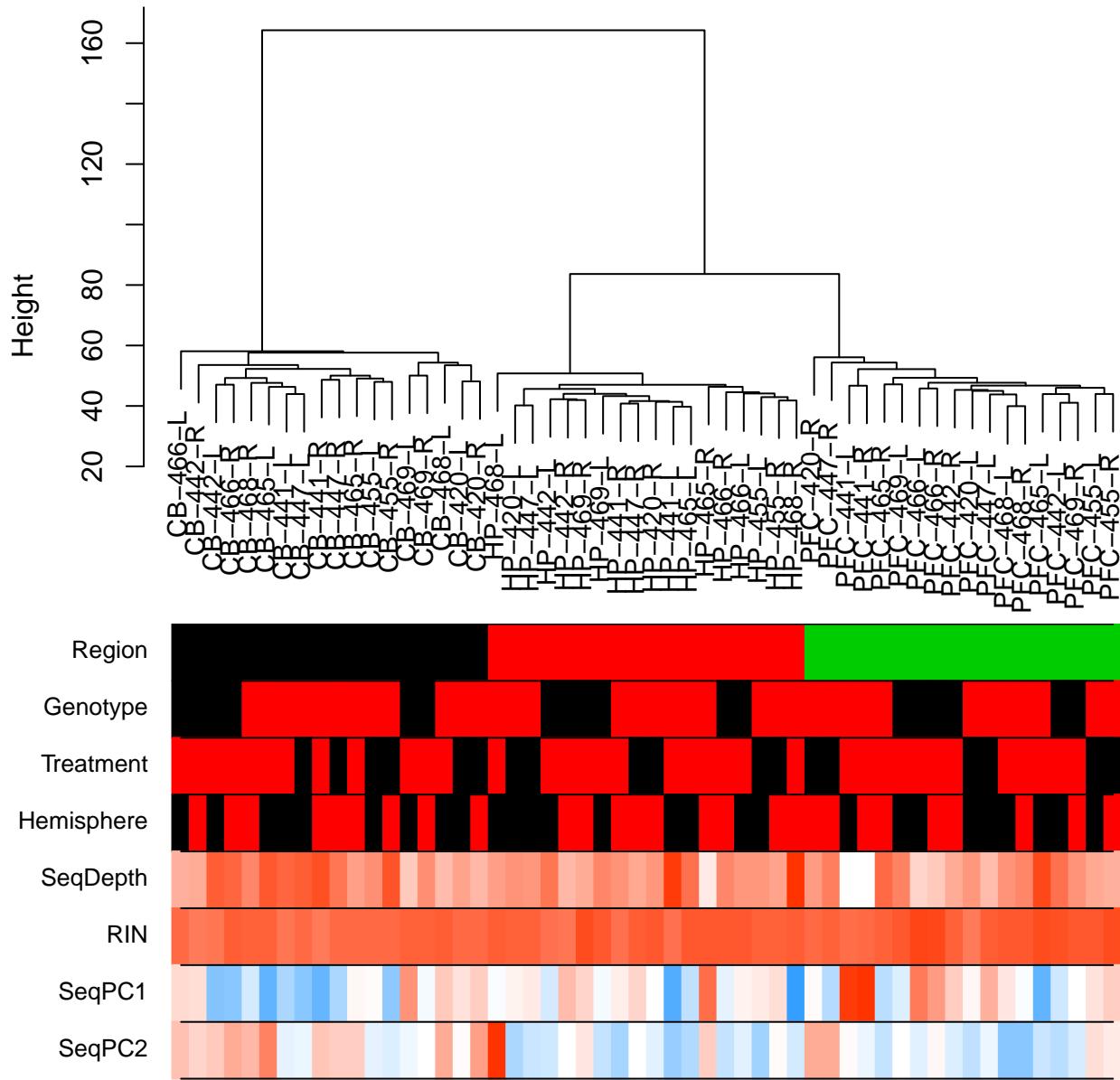


Cluster Dendrogram

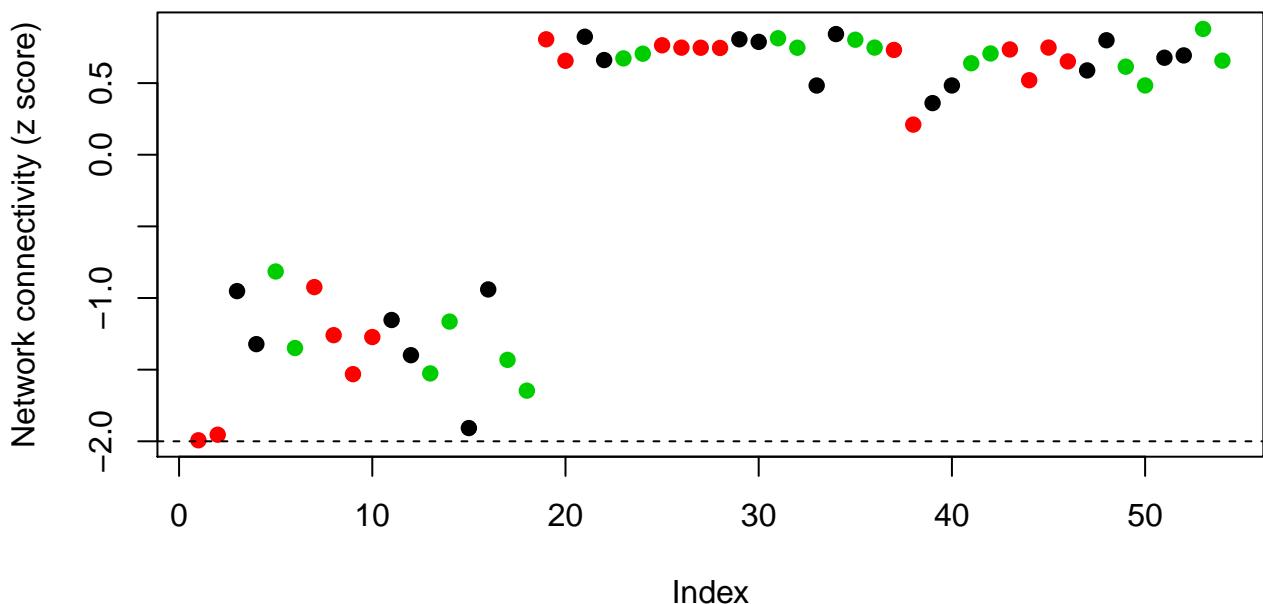


```
dist(t(datExpr.cpm))  
hclust (*, "average")
```

Cluster Dendrogram

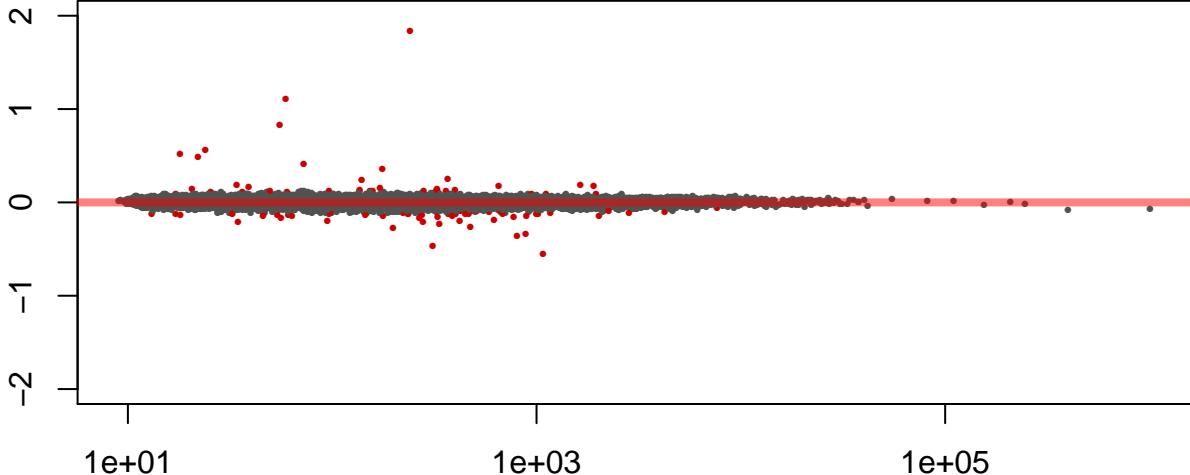


Outlier detection



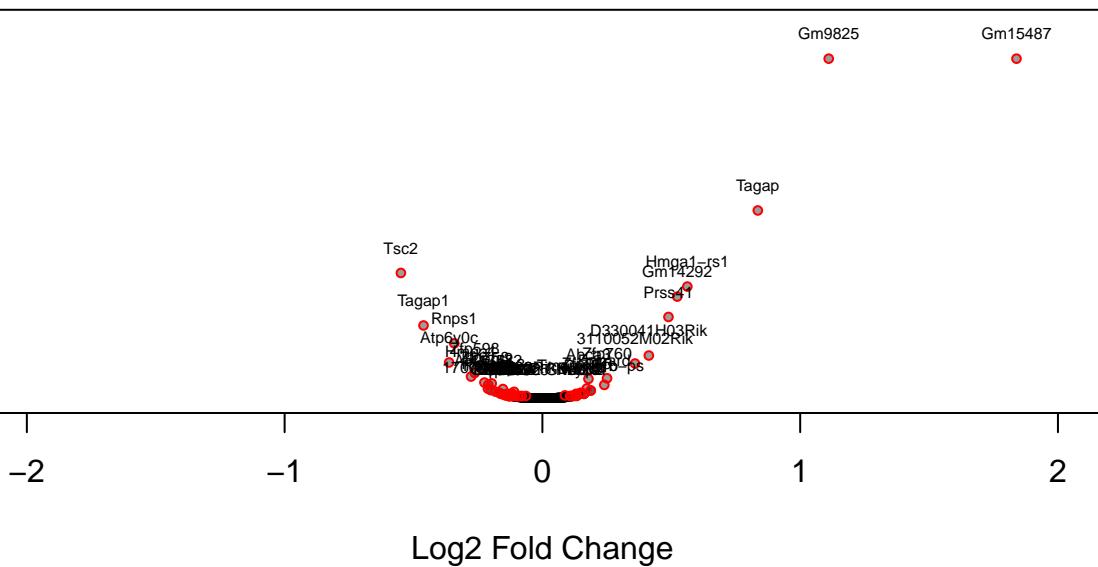
all genotype

log fold change

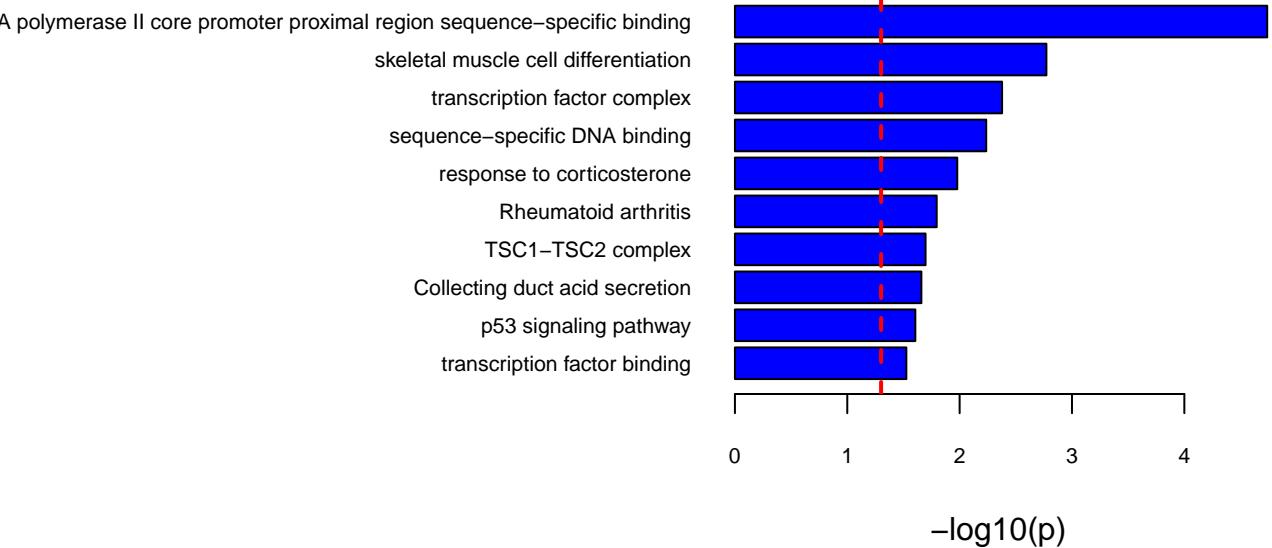


mean expression

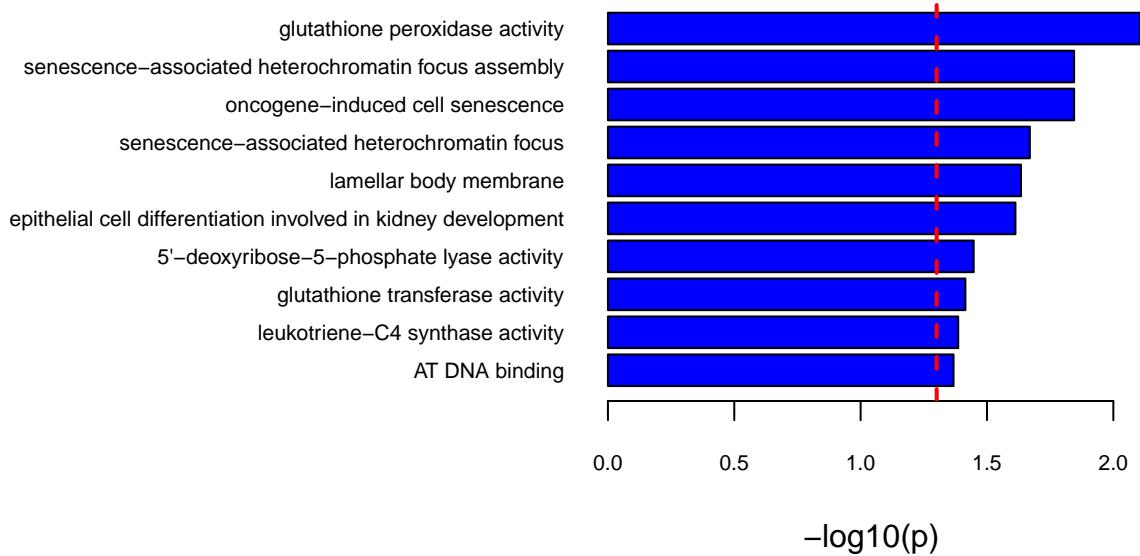
$\log_{10}(P.\text{adj})$



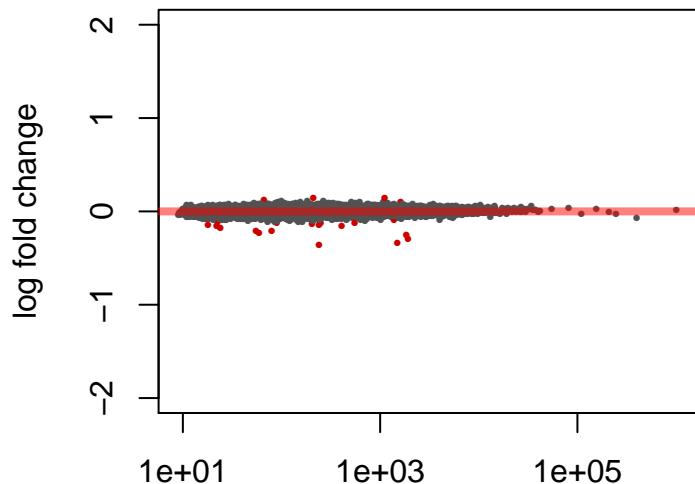
GO downregulated genotype all



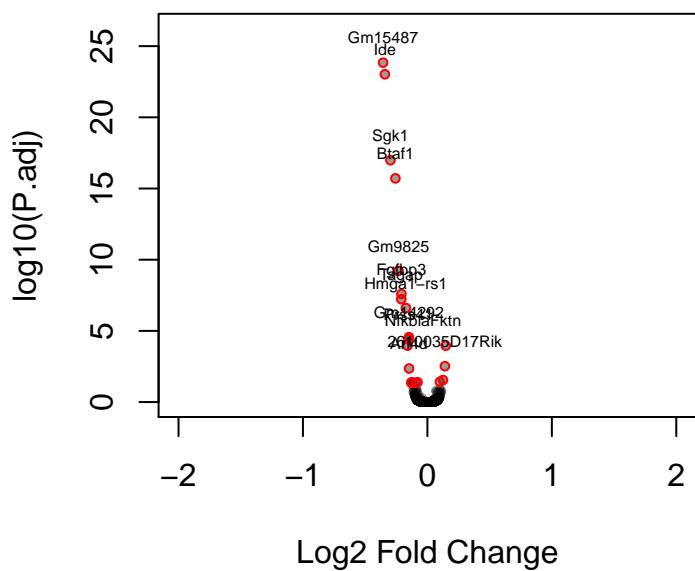
GO upregulated genotype all



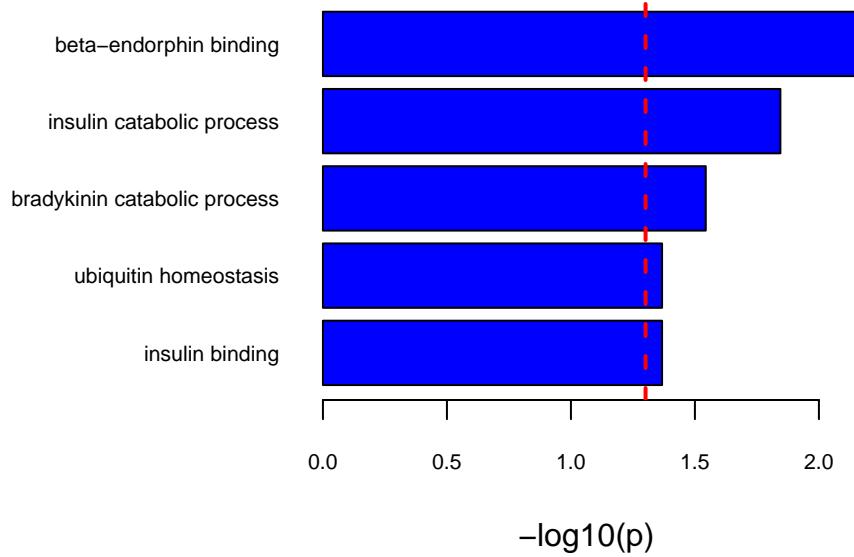
all treatment



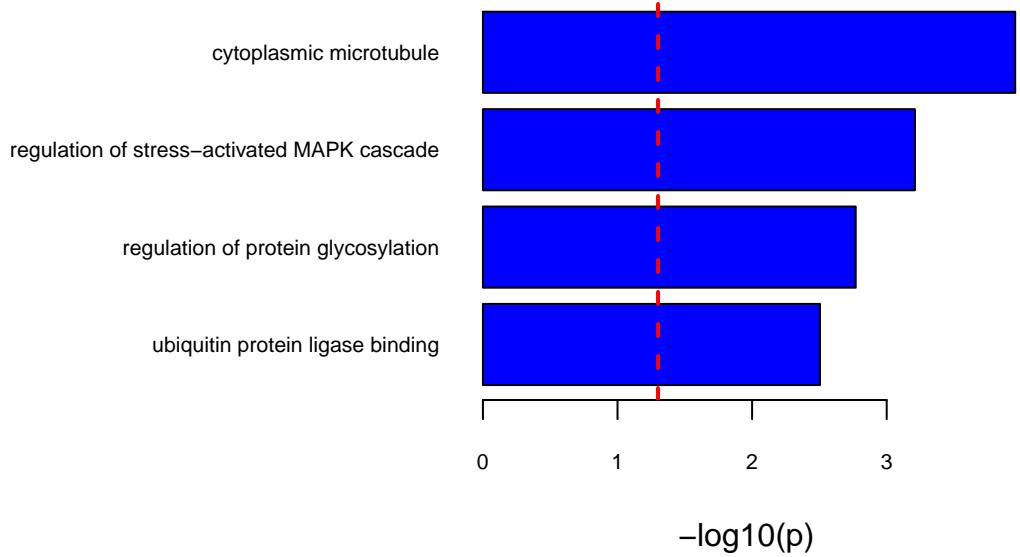
mean expression



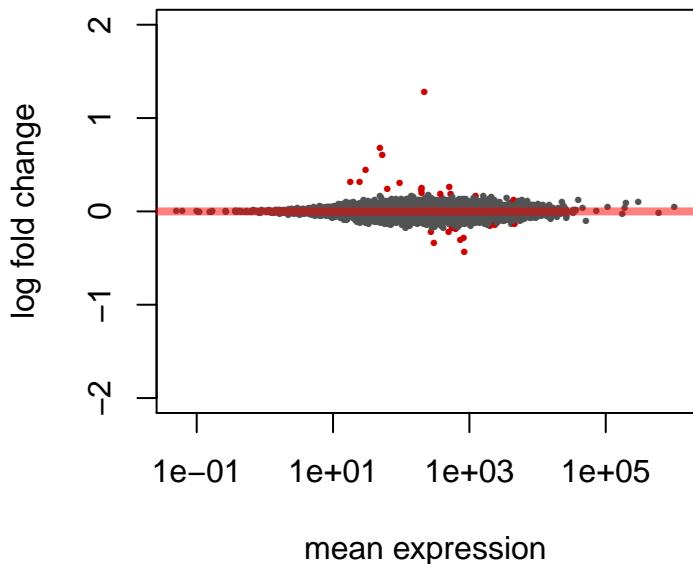
GO downregulated treatment all



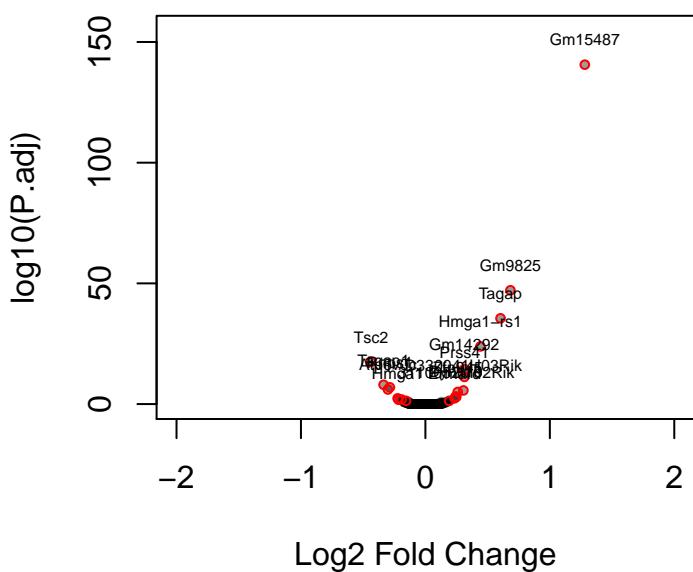
GO upregulated treatment all



cbl genotype

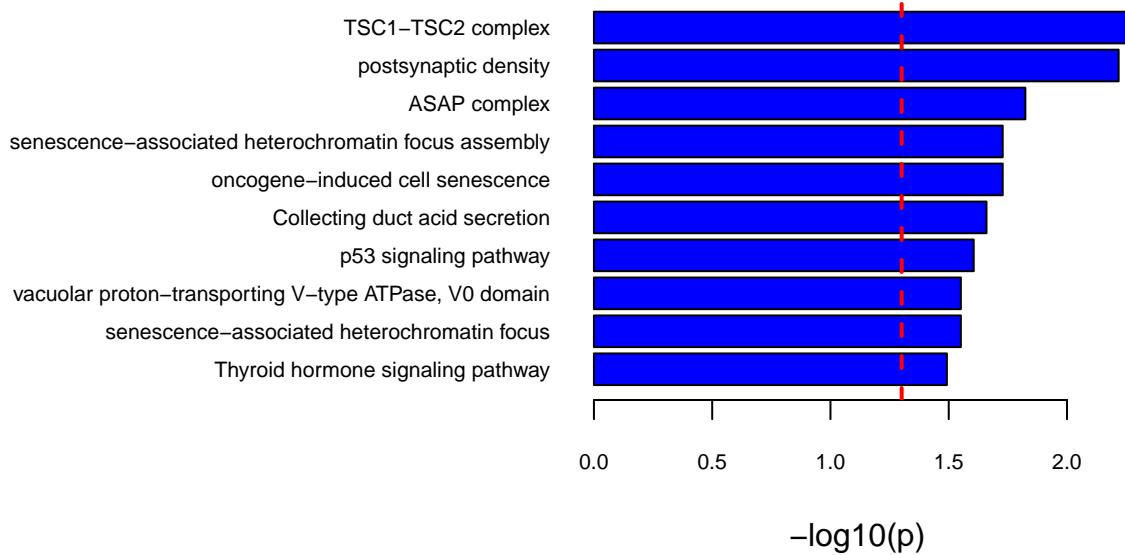


mean expression

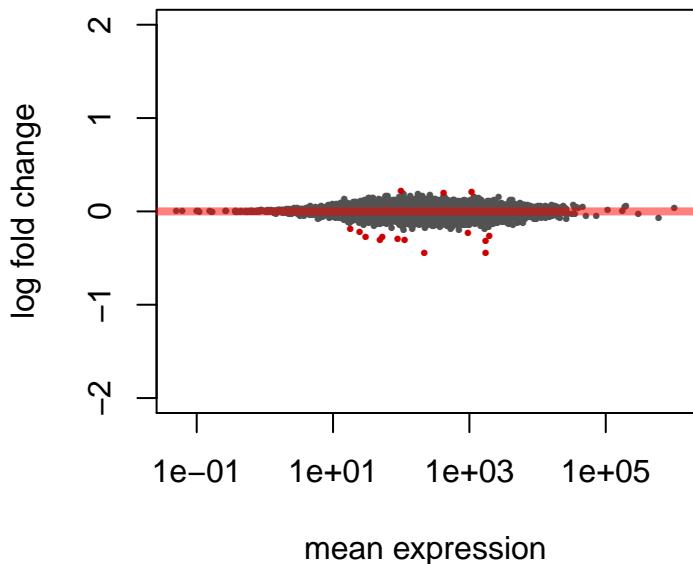


Log2 Fold Change

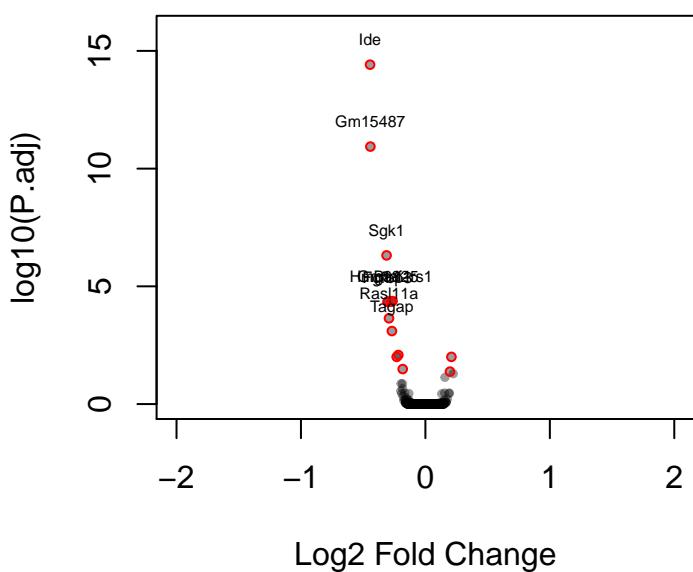
GO downregulated genotype cbl



cbl treatment

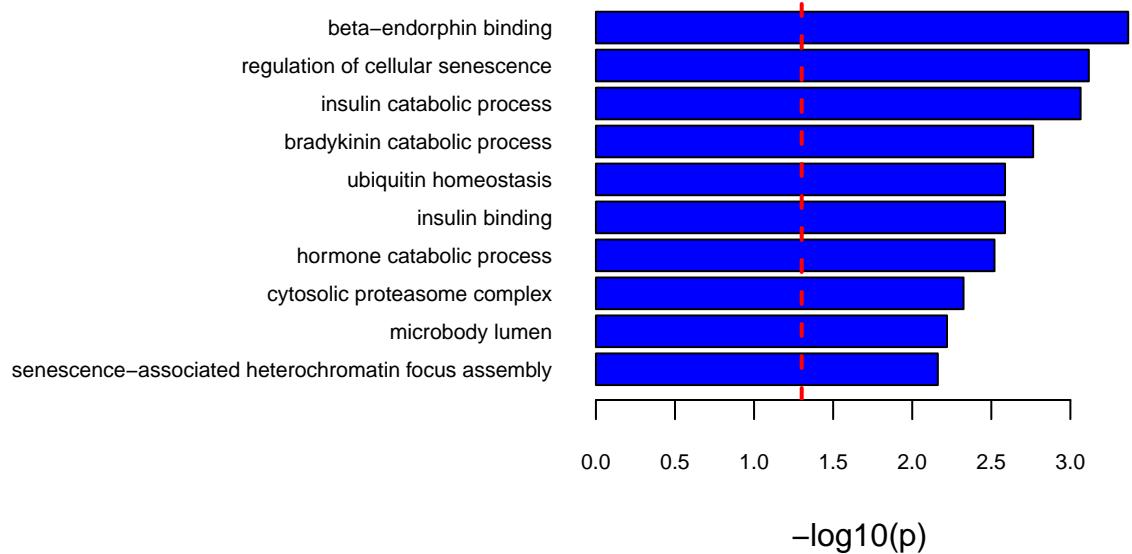


mean expression



Log2 Fold Change

GO downregulated treatment cbl



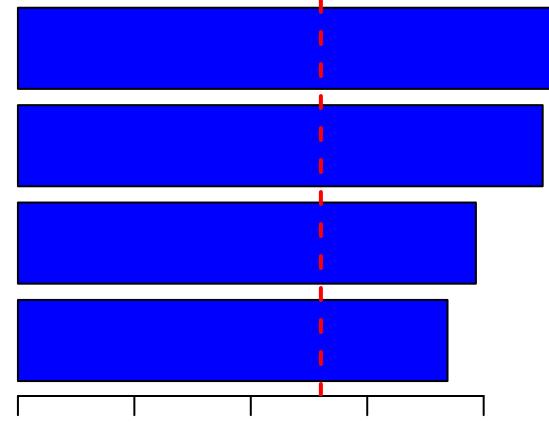
GO upregulated treatment cbl

regulation of protein glycosylation

protein O-linked mannosylation

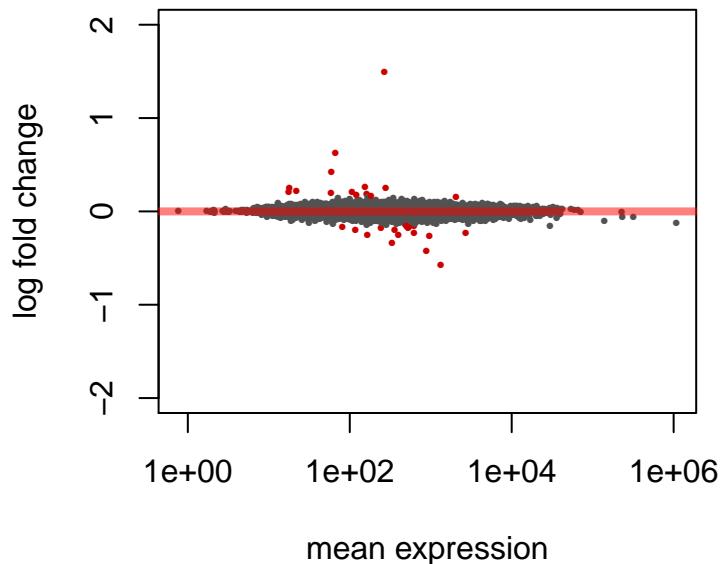
negative regulation of JNK cascade

cis-Golgi network

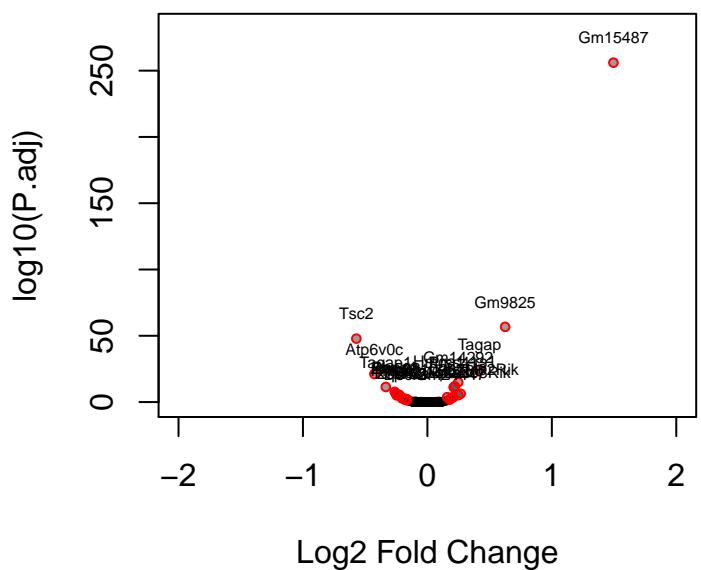


$-\log_{10}(p)$

hc genotype

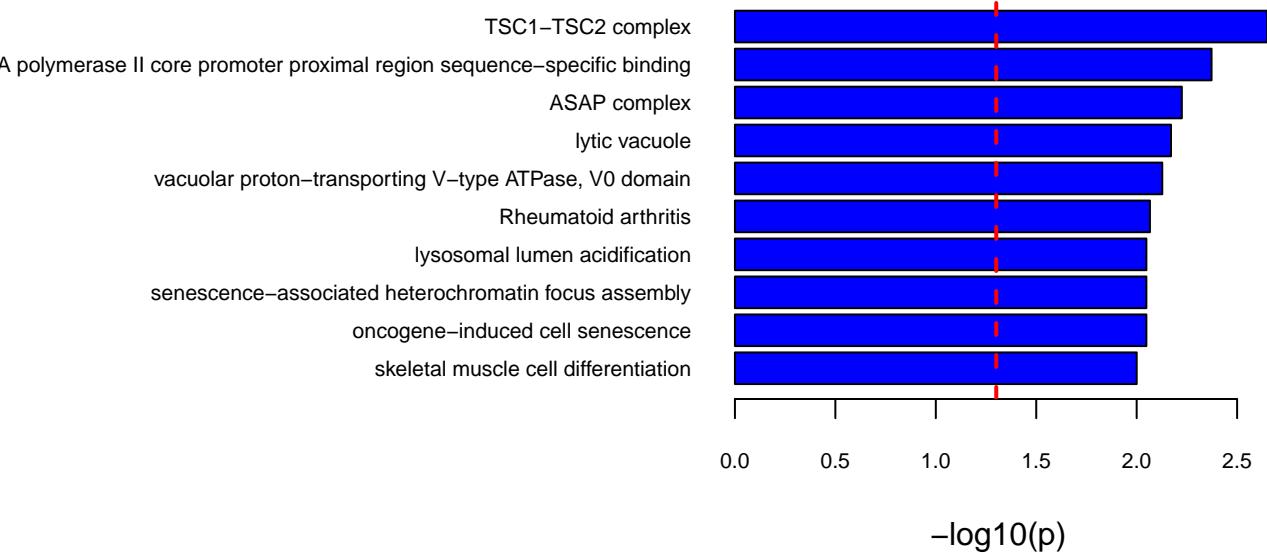


mean expression



Log2 Fold Change

GO downregulated genotype hc



GO upregulated genotype hc

senescence–associated heterochromatin focus assembly



oncogene–induced cell senescence



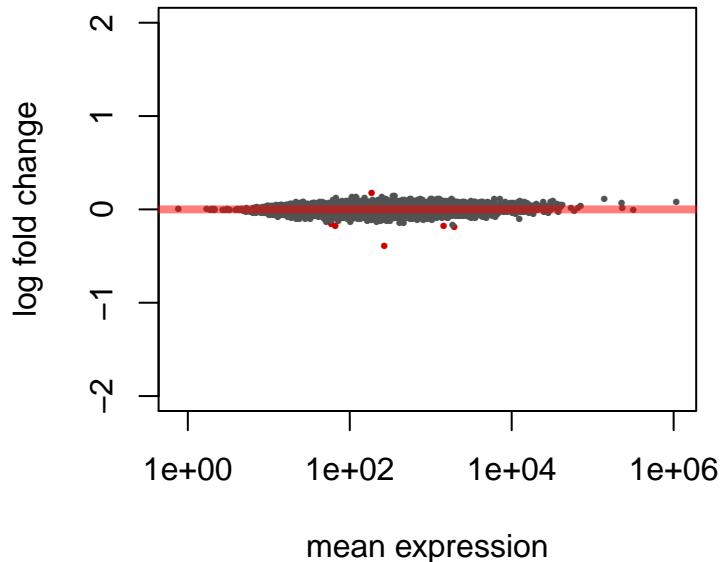
alveolar lamellar body membrane



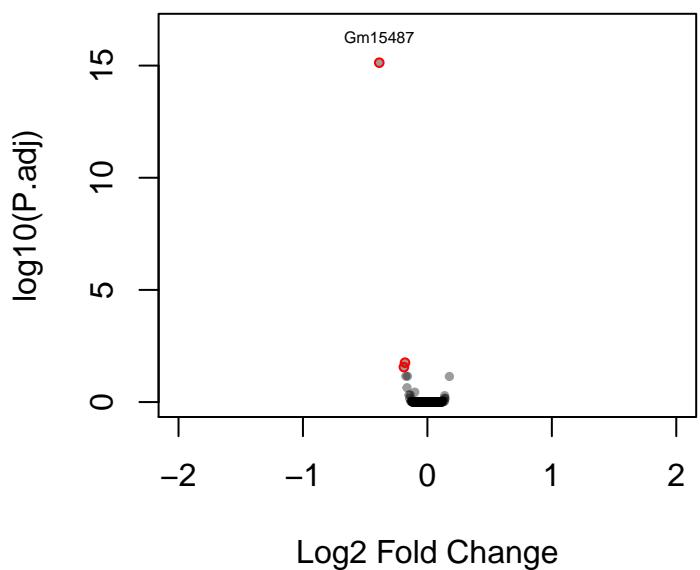
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4

$-\log_{10}(p)$

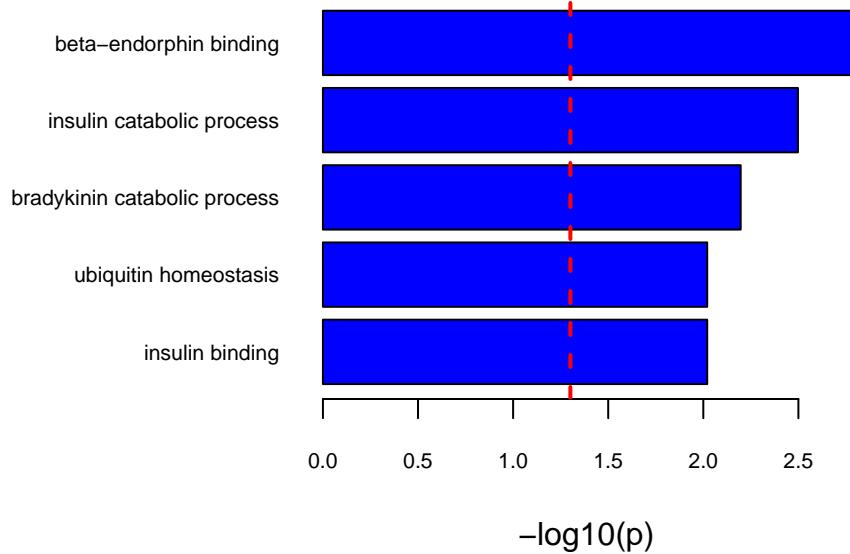
hc treatment



Gm15487

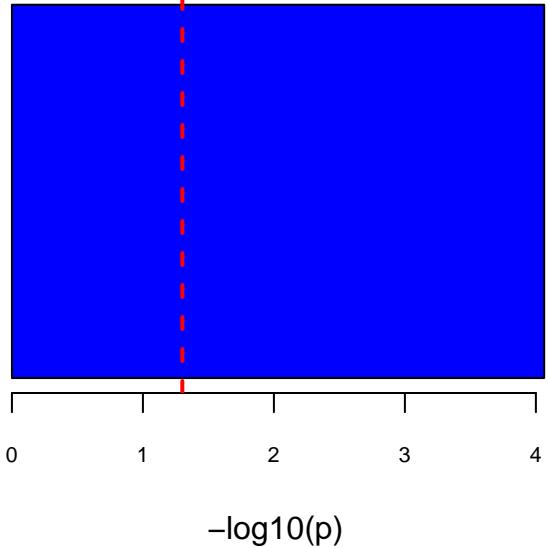


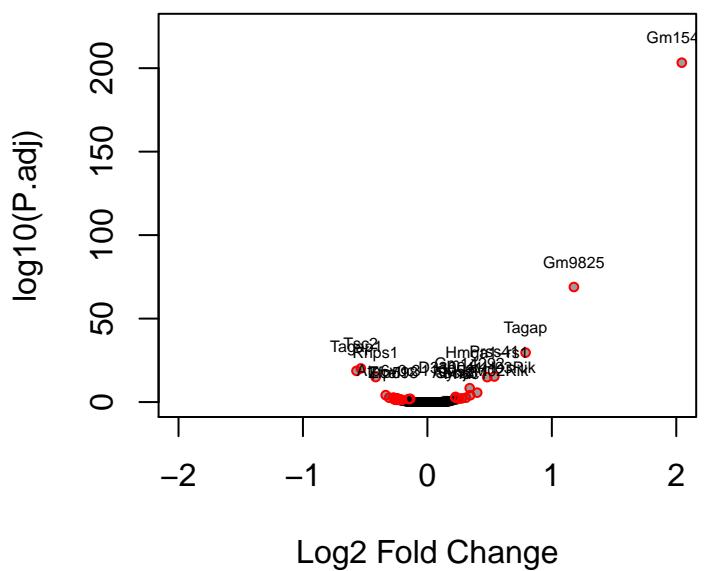
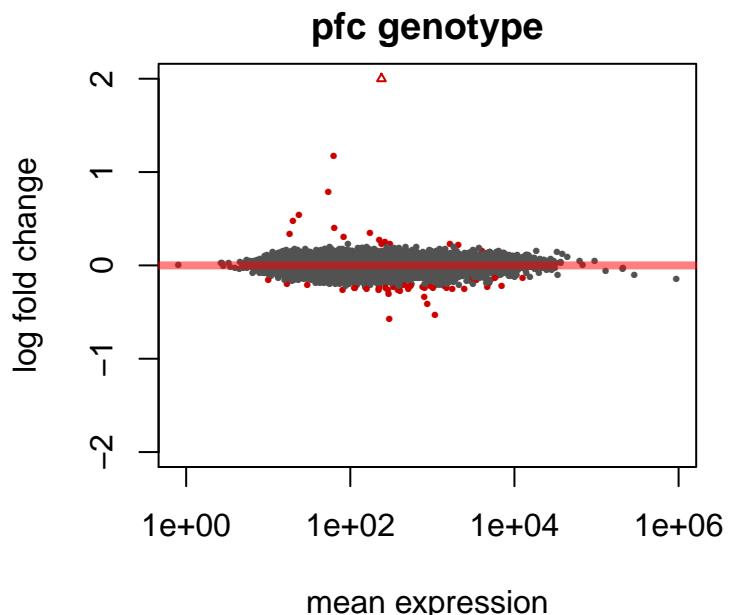
GO downregulated treatment hc



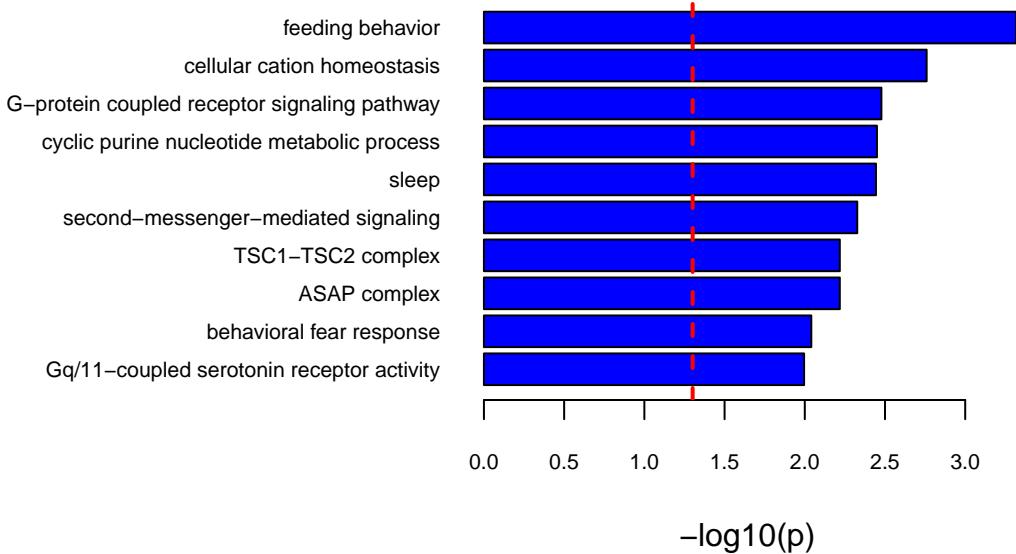
GO upregulated treatment hc

epithelial cell proliferation involved in prostatic bud elongation

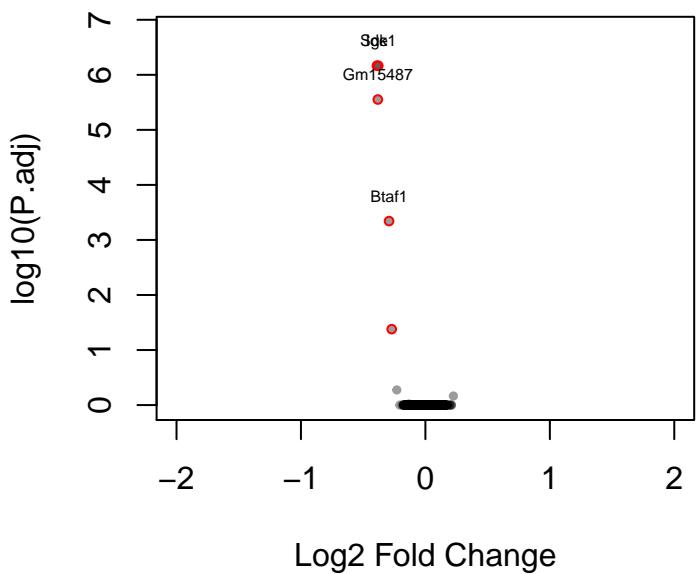
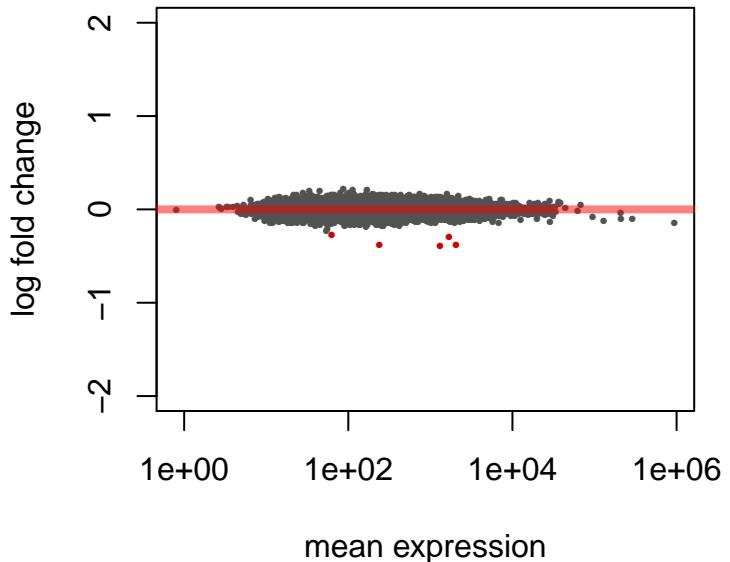




GO downregulated genotype pfc



pfc treatment



GO downregulated treatment pfc

