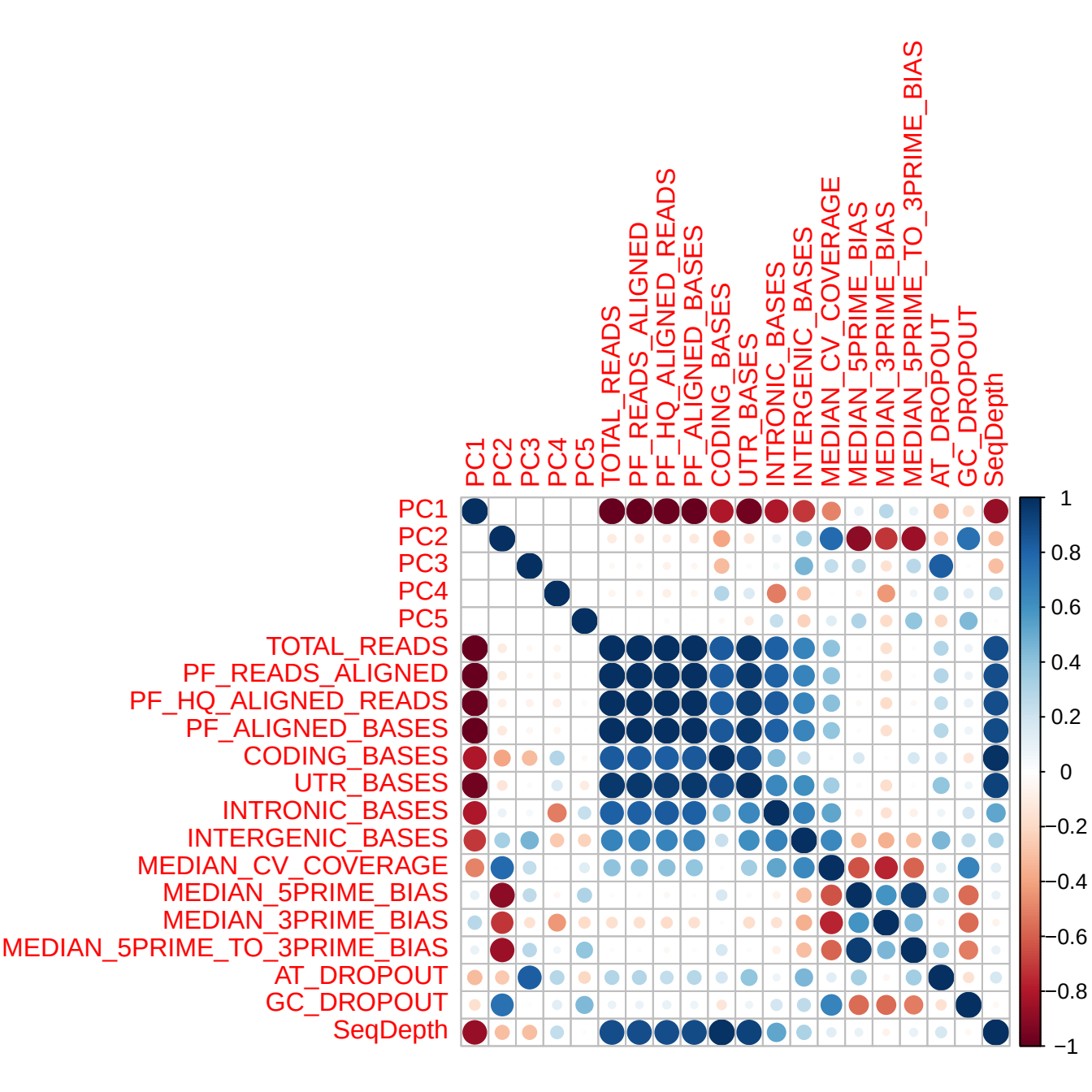
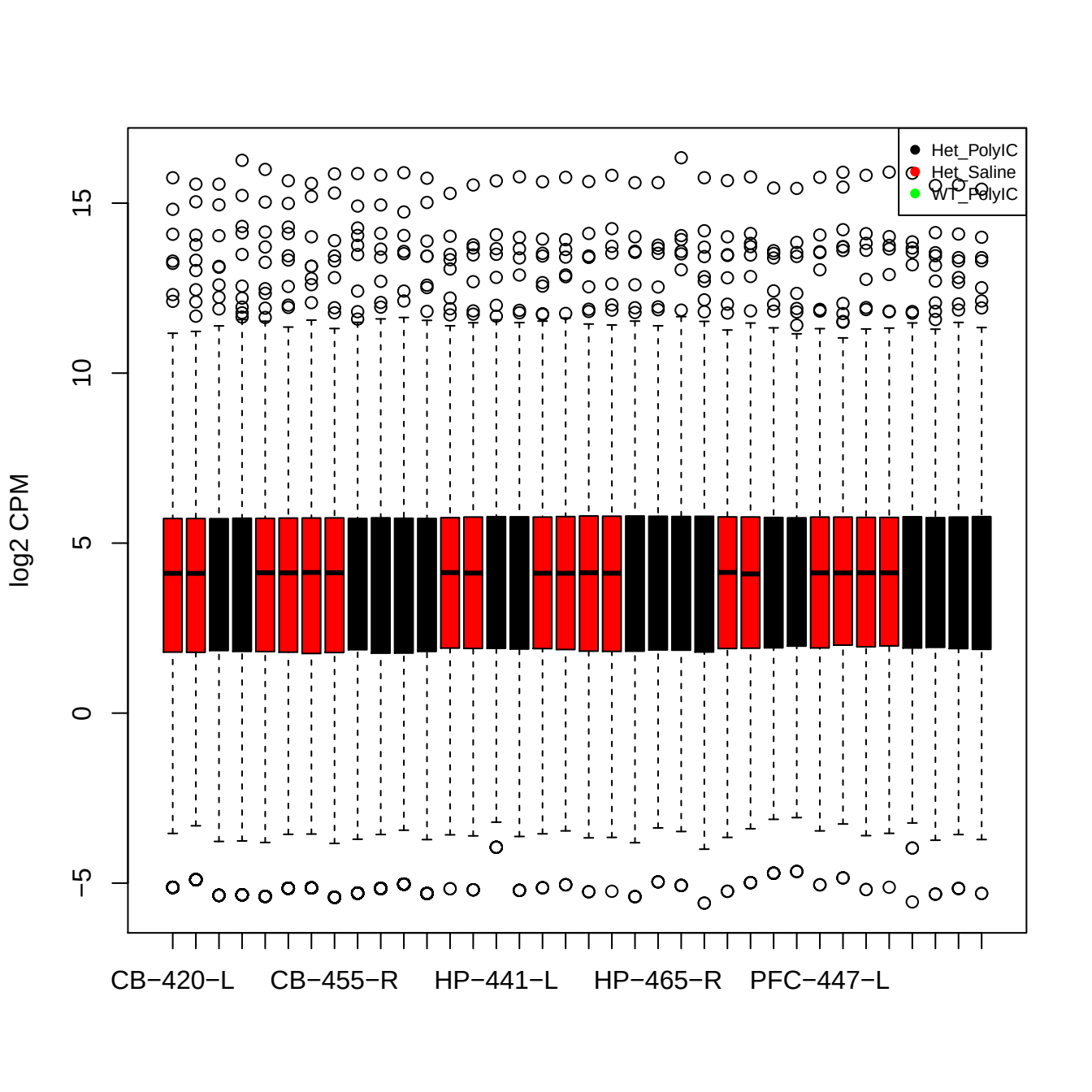
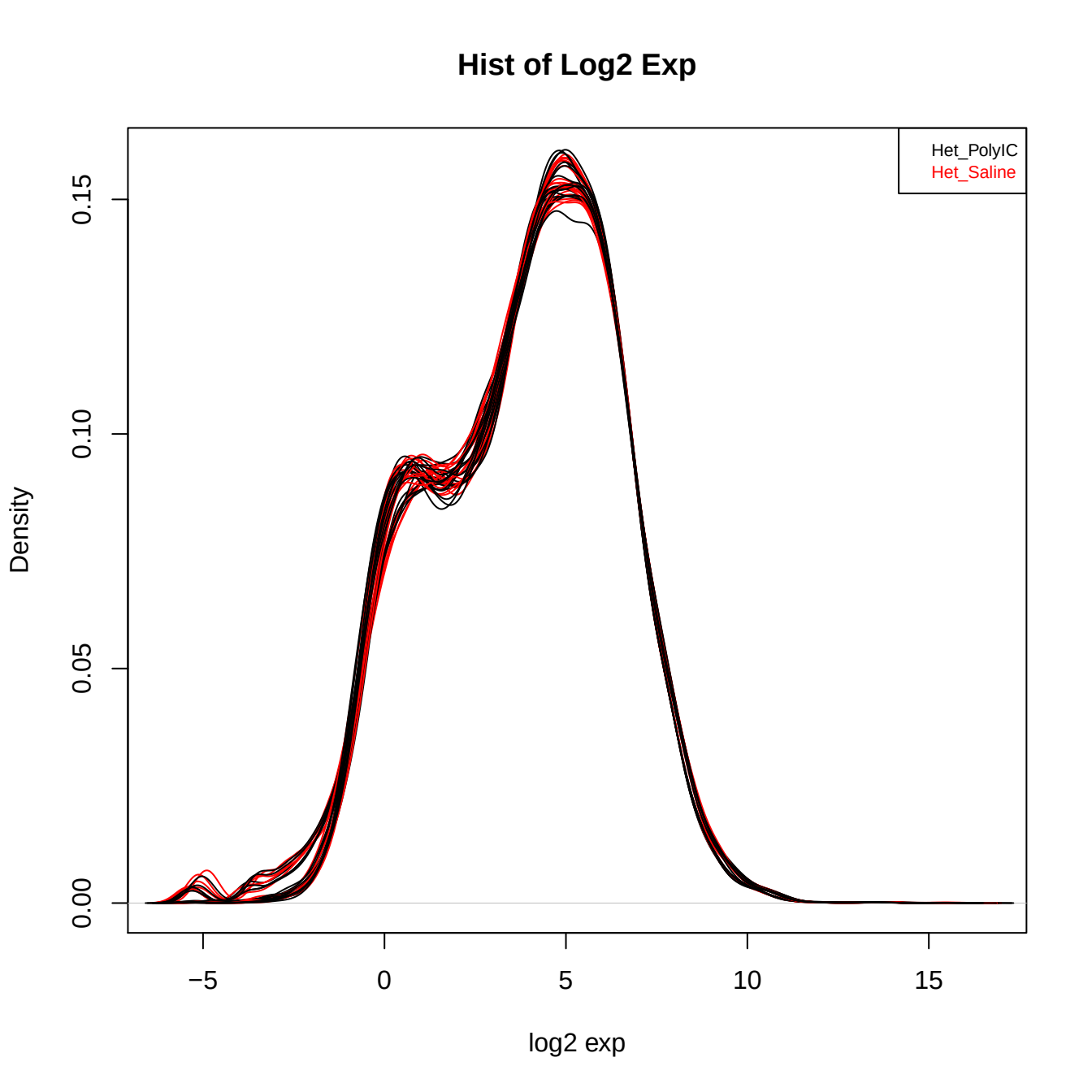
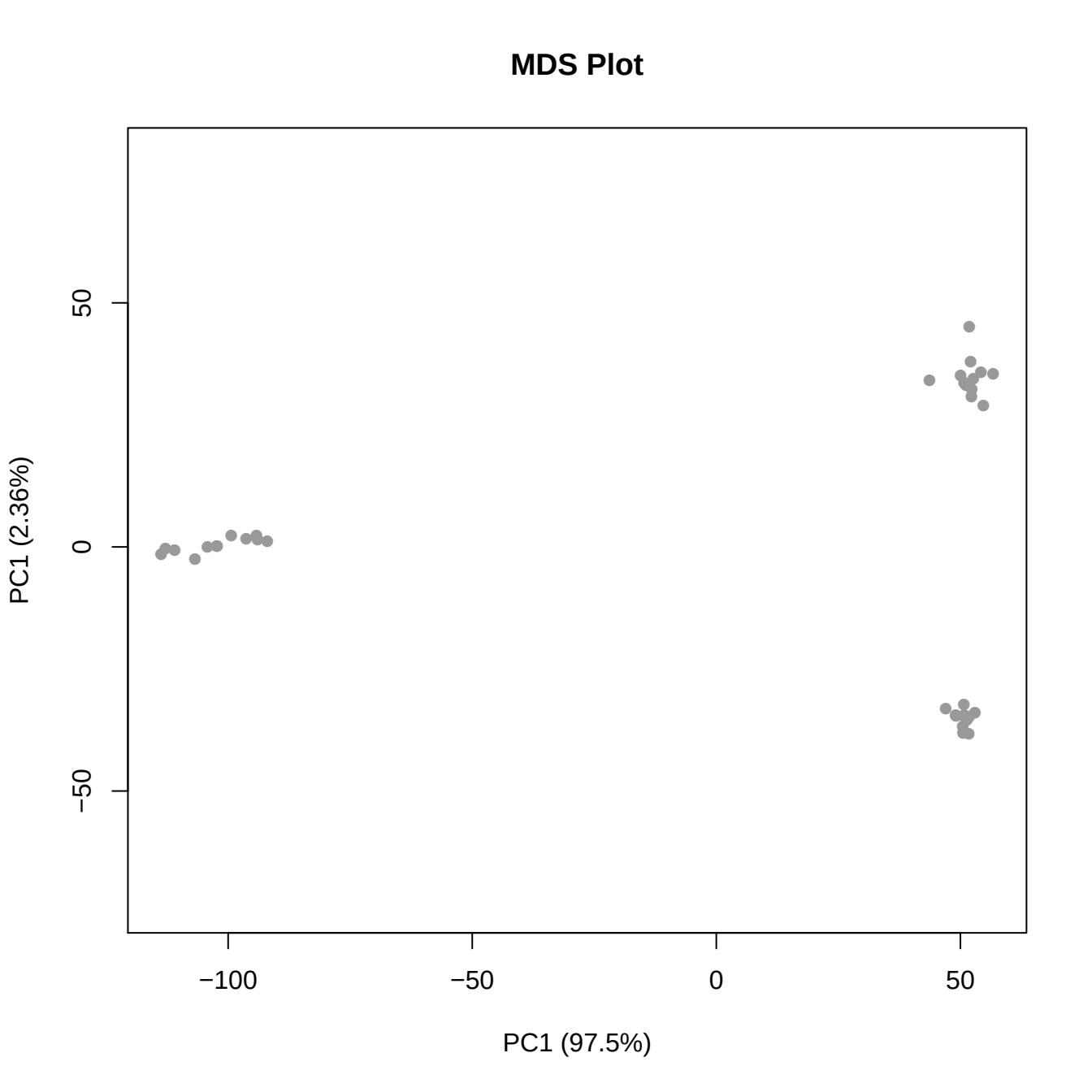
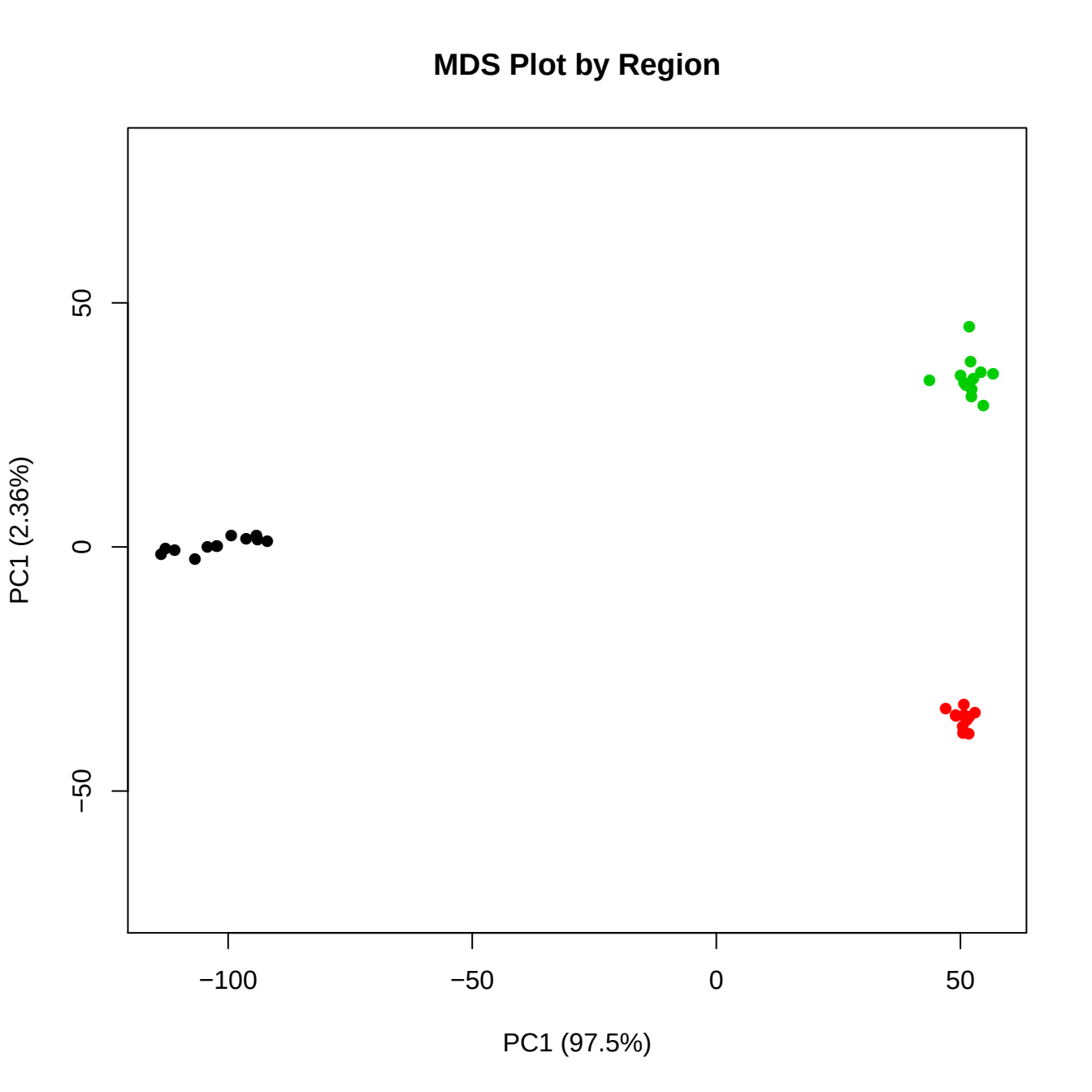
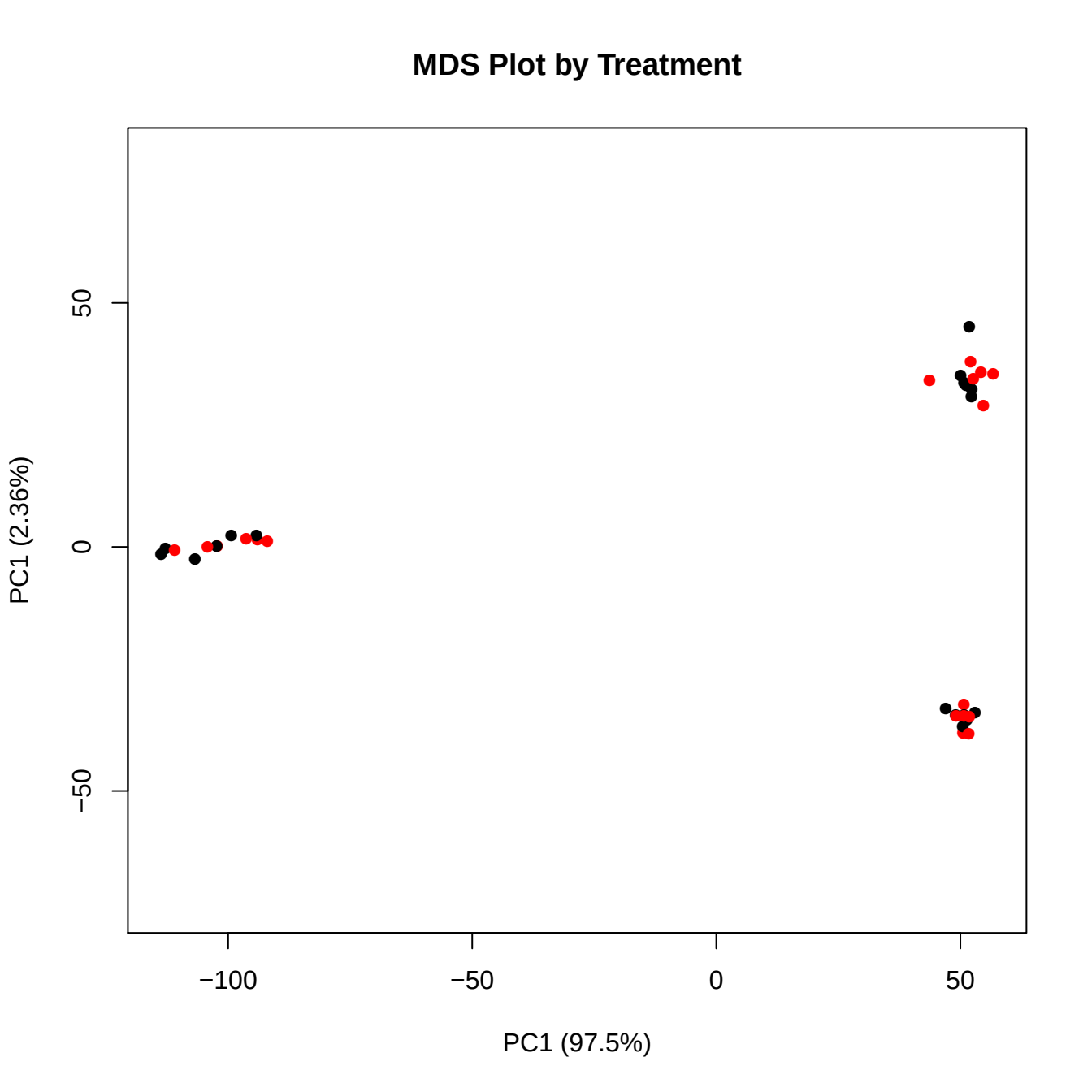

PC1
PC2
PC3
PC4
PC5
TOTAL_READS
PF_READS_ALIGNED
PF_HQ_ALIGNED_READS
PF_ALIGNED_BASES
CODING_BASES
UTR_BASES
INTRONIC_BASES
INTERGENIC_BASES
MEDIAN_CV_COVERAGE
MEDIAN_5PRIME_BIAS
MEDIAN_3PRIME_BIAS
MEDIAN_5PRIME_TO_3PRIME_BIAS
AT_DROPOUT
GC_DROPOUT
SeqDepth
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

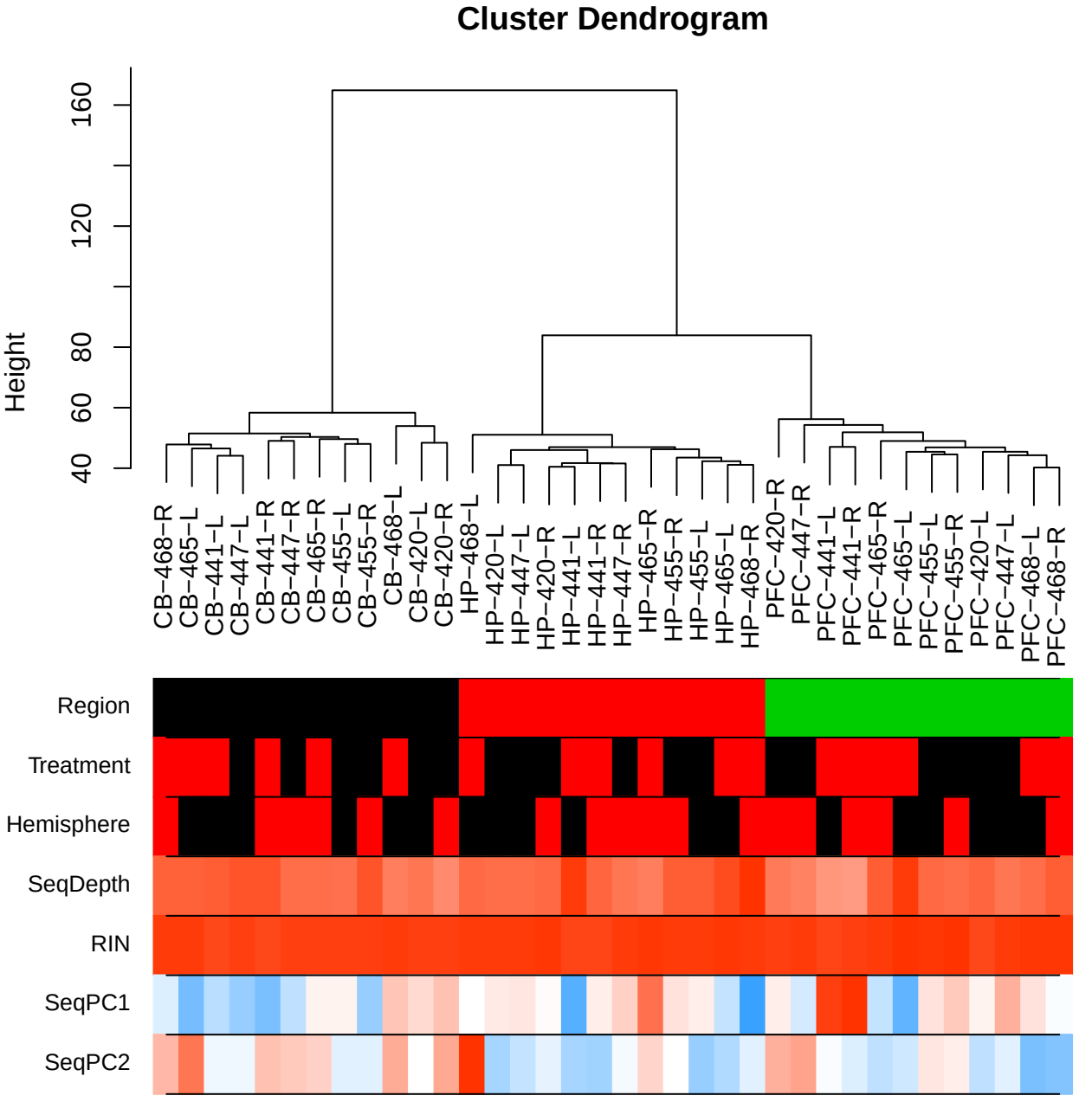

Het_PolyIC
Het_Saline
WT_PolyIC
log2 CPM
15
10
5
0
−5
CB−420−L
CB−455−R
HP−441−L
HP−465−R
PFC−447−L

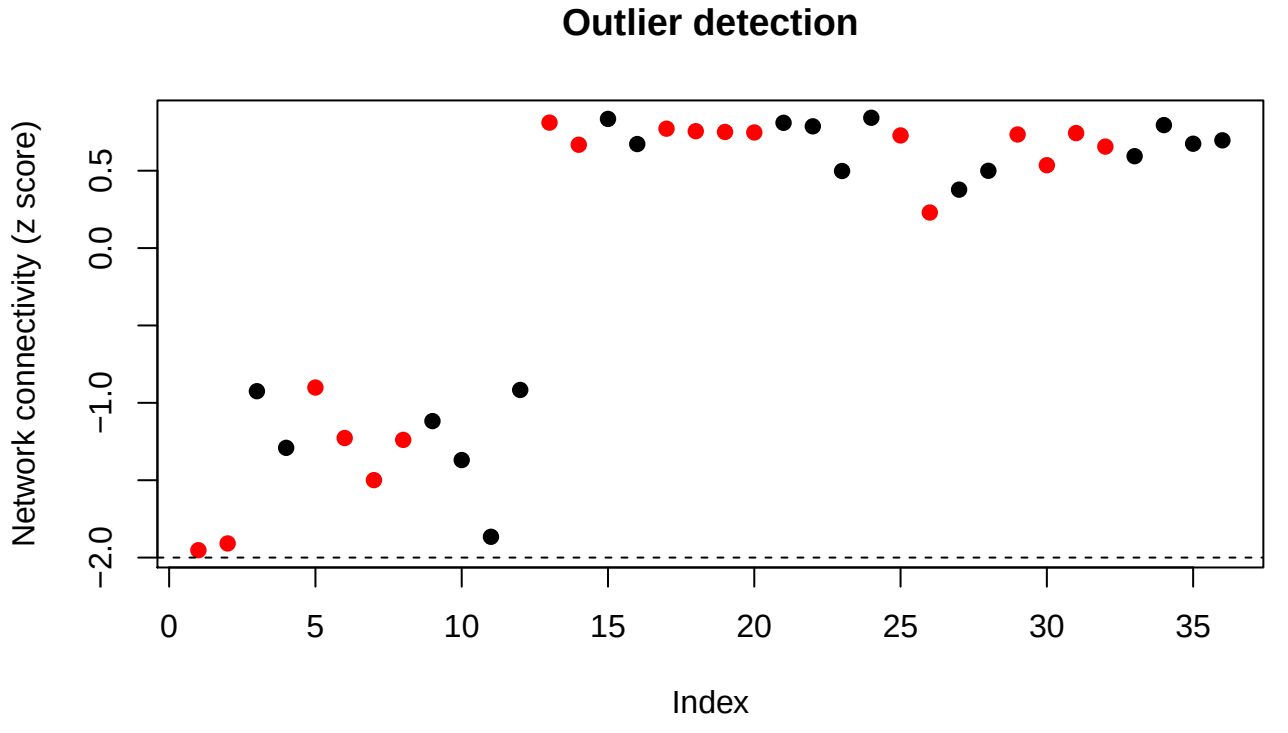

Hist of Log2 Exp
Het_PolyIC
Het_Saline
Density
0.00
0.05
0.10
0.15
−5
0
5
10
15
log2 exp

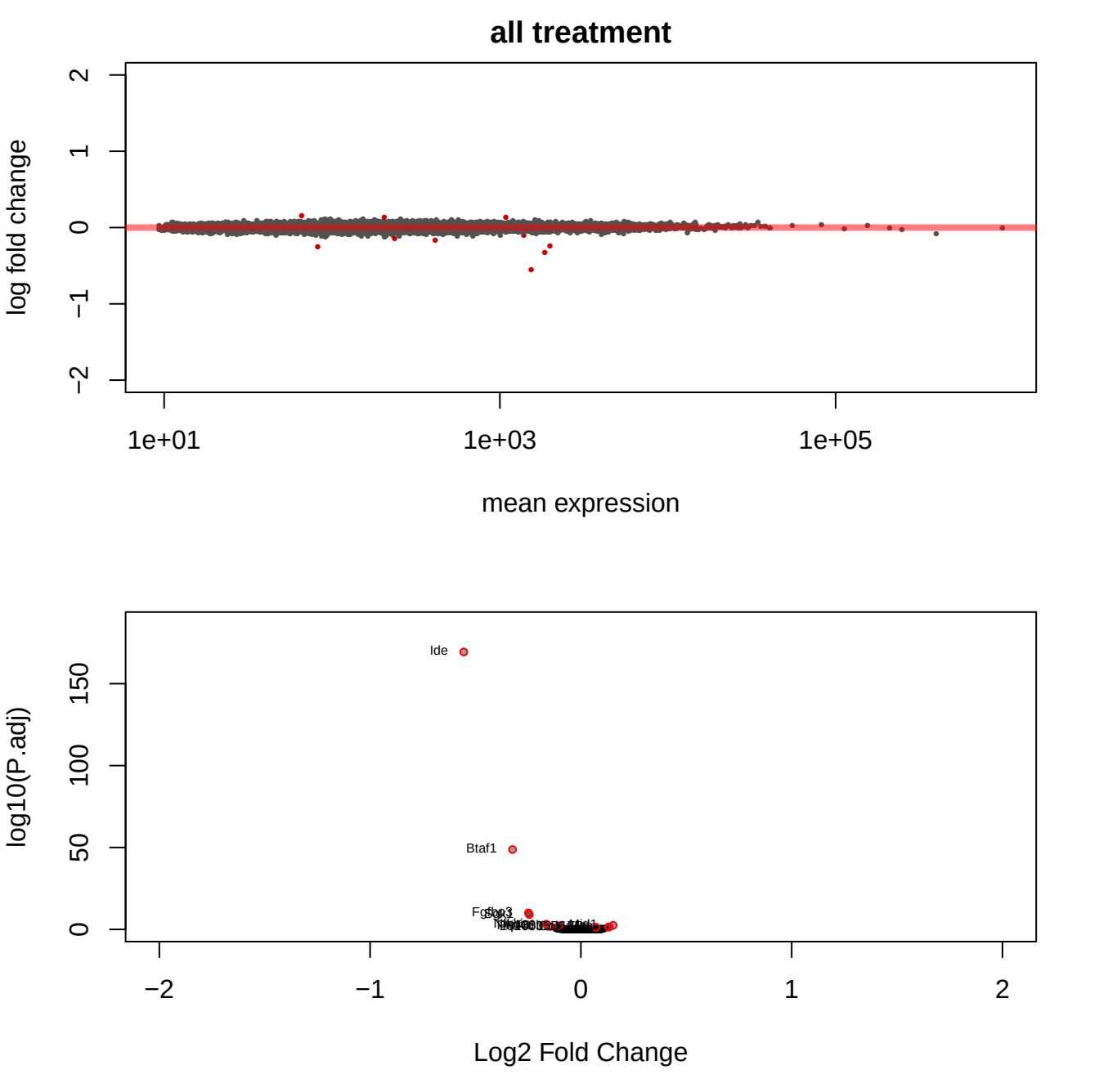

MDS Plot
PC1 (2.36%)
50
0
−50
−100
−50
0
50
PC1 (97.5%)

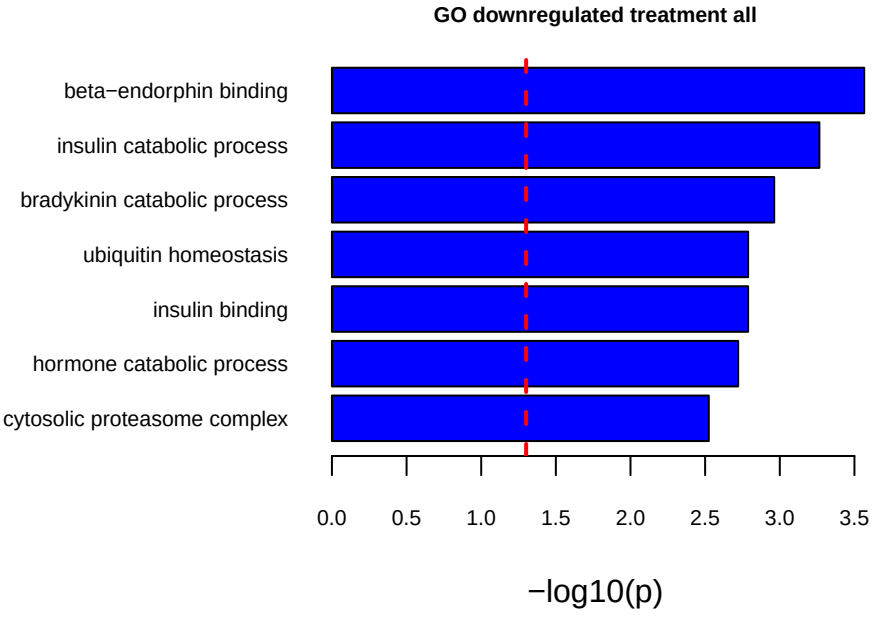

MDS Plot by Region
PC1 (2.36%)
50
0
−50
−100
−50
0
50
PC1 (97.5%)

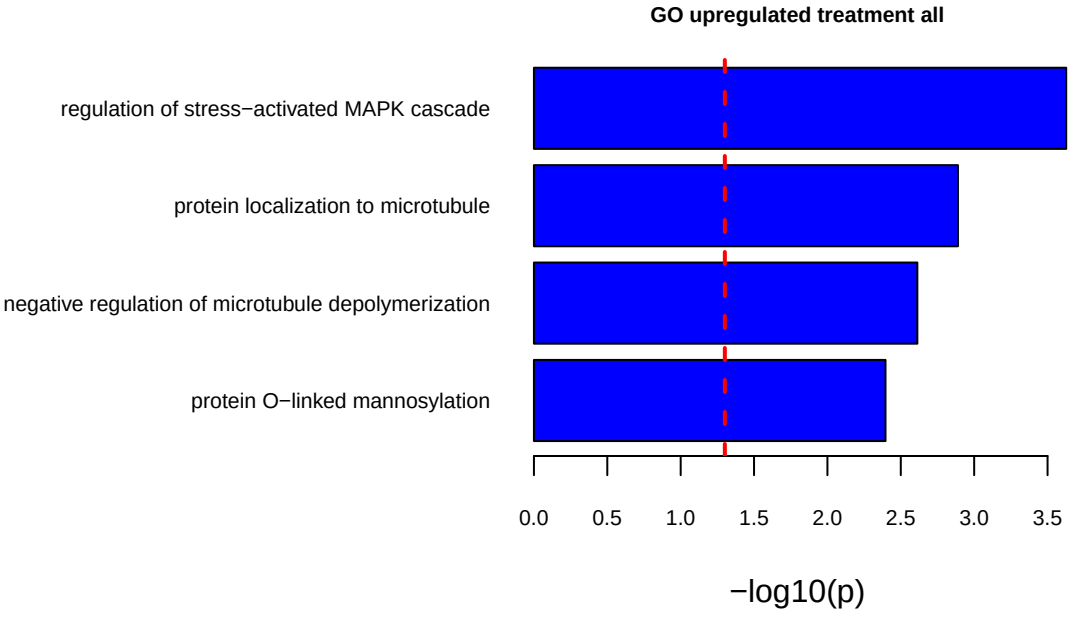

MDS Plot by Treatment
PC1 (2.36%)
50
0
−50
−100
−50
0
50
PC1 (97.5%)

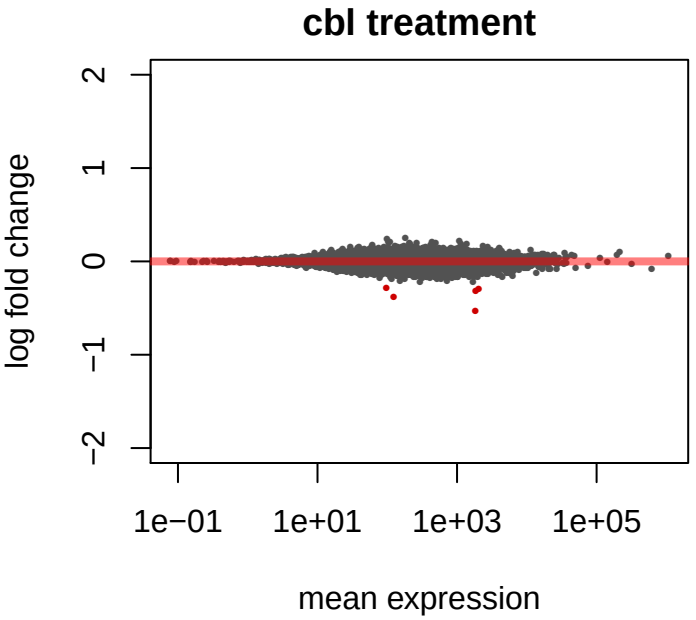

Cluster Dendrogram
Height
40
60
80
120
160
CB−468−R
CB−465−L
CB−441−L
CB−447−L
CB−441−R
CB−447−R
CB−465−R
CB−455−L
CB−455−R
CB−468−L
CB−420−L
CB−420−R
HP−468−L
HP−420−L
HP−447−L
HP−420−R
HP−441−L
HP−441−R
HP−447−R
HP−465−R
HP−455−R
HP−455−L
HP−465−L
HP−468−R
PFC−420−R
PFC−447−R
PFC−441−L
PFC−441−R
PFC−465−R
PFC−465−L
PFC−455−L
PFC−455−R
PFC−420−L
PFC−447−L
PFC−468−L
PFC−468−R
Region
Treatment
Hemisphere
SeqDepth
RIN
SeqPC1
SeqPC2

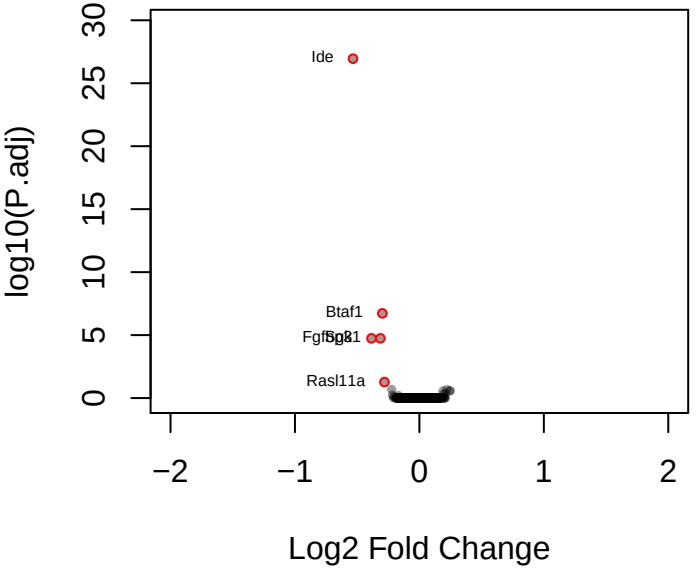

Outlier detection
Network connectivity (z score)
−2.0
−1.0
0.0
0.5
0
5
10
15
20
25
30
35
Index

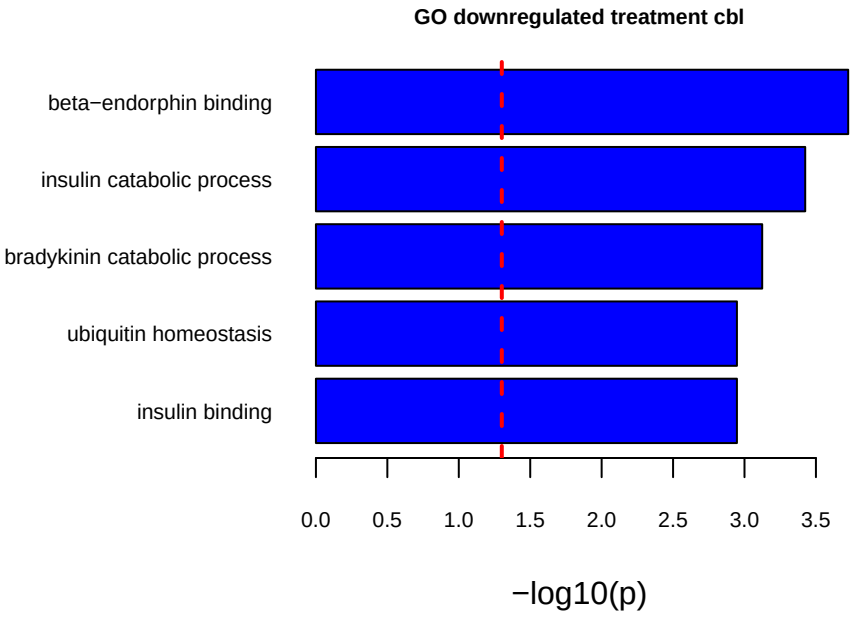

all treatment
log fold change
2
1
0
−1
−2
1e+01
1e+03
1e+05
mean expression
log10(P.adj)
150
100
50
0
Ide
Btaf1
−2
−1
0
1
2
Log2 Fold Change

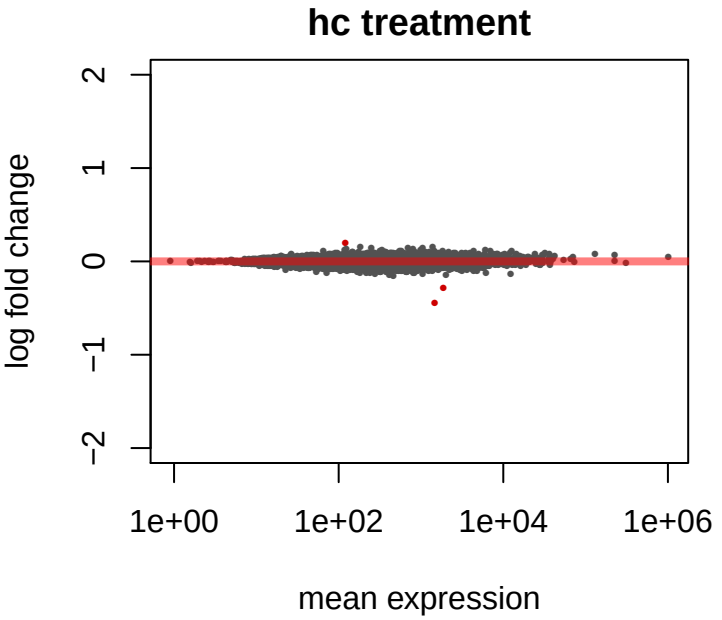

GO downregulated treatment all
beta−endorphin binding
insulin catabolic process
bradykinin catabolic process
ubiquitin homeostasis
insulin binding
hormone catabolic process
cytosolic proteasome complex
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−log10(p)

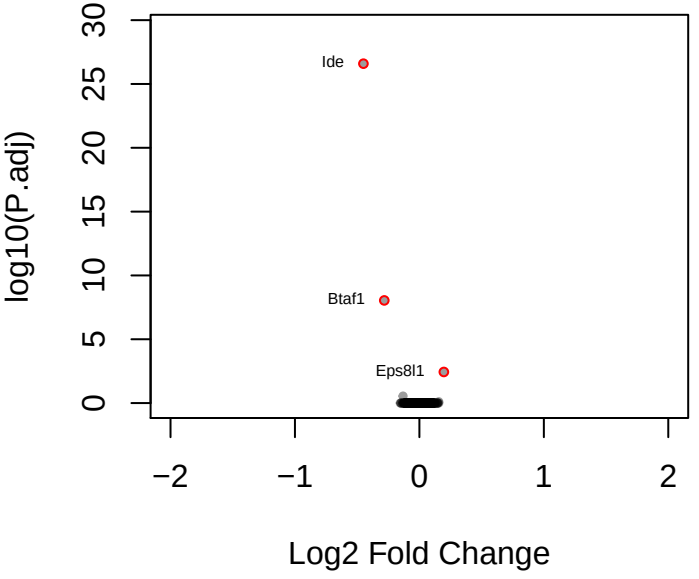

GO upregulated treatment all
regulation of stress−activated MAPK cascade
protein localization to microtubule
negative regulation of microtubule depolymerization
protein O−linked mannosylation
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−log10(p)

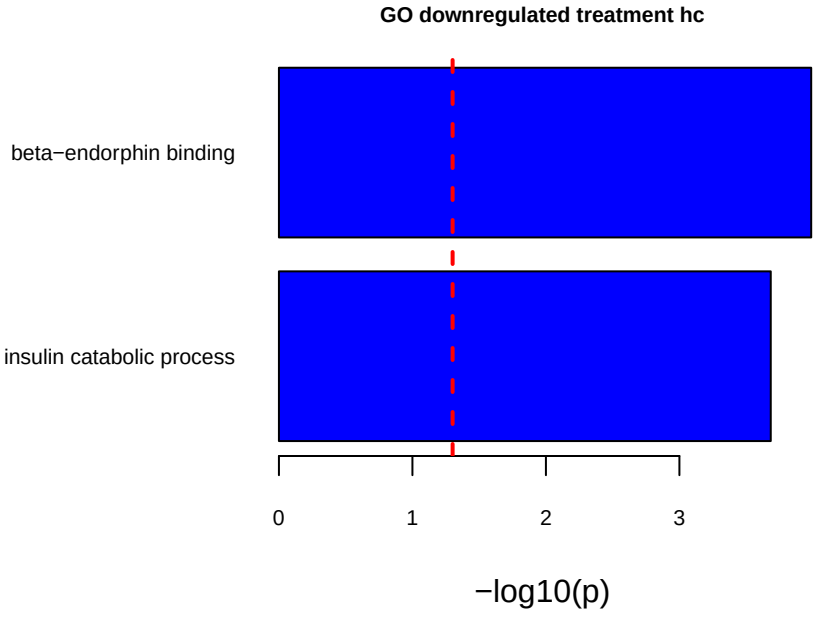

cbl treatment
log fold change
2
1
0
−1
−2
1e−01
1e+01
1e+03
1e+05
mean expression

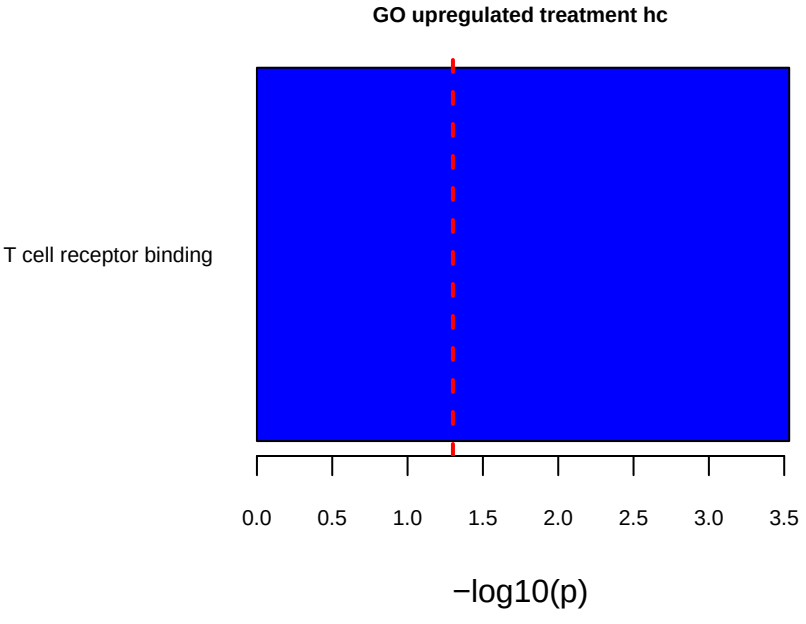

log10(P.adj)
30
25
20
15
10
5
0
Ide
Btaf1
Fgfbp1
Rasl11a
−2
−1
0
1
2
Log2 Fold Change

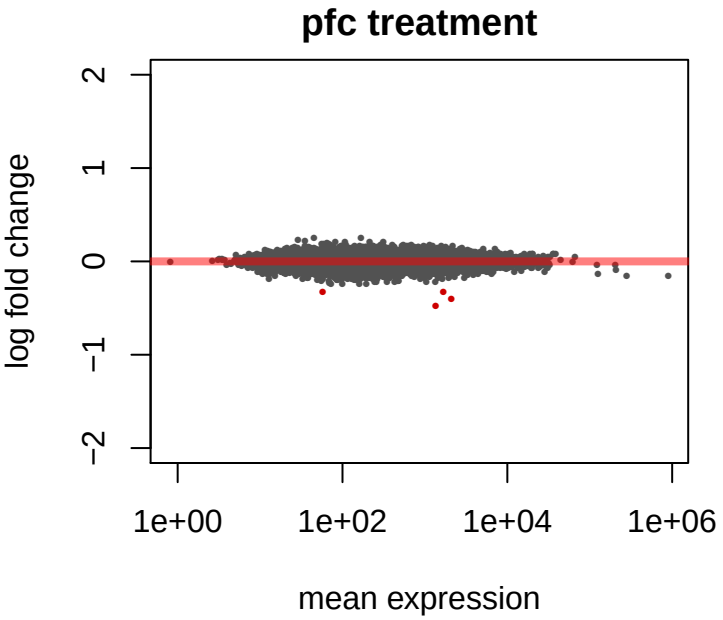

GO downregulated treatment cbl
beta−endorphin binding
insulin catabolic process
bradykinin catabolic process
ubiquitin homeostasis
insulin binding
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−log10(p)

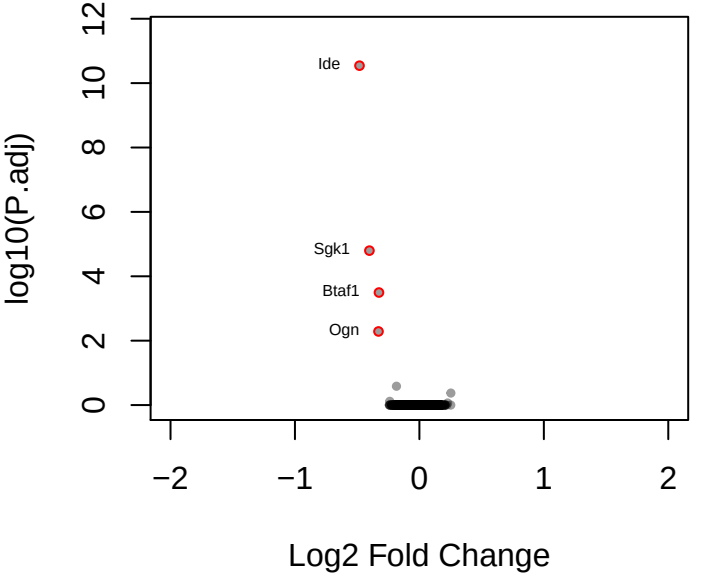

hc treatment
log fold change
2
1
0
−1
−2
1e+00
1e+02
1e+04
1e+06
mean expression

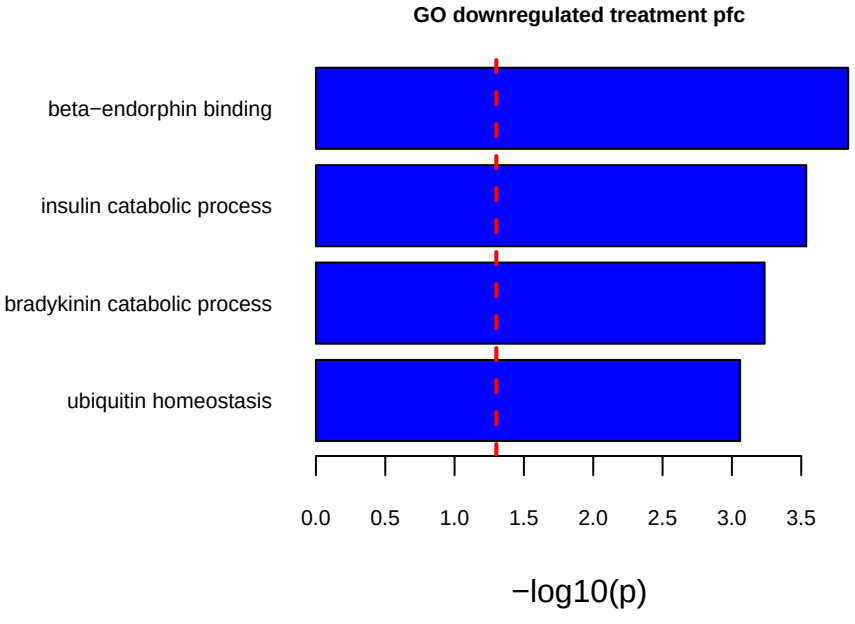

log10(P.adj)
30
25
20
15
10
5
0
Ide
Btaf1
Eps8l1
−2
−1
0
1
2
Log2 Fold Change


GO downregulated treatment hc
beta−endorphin binding
insulin catabolic process
0
1
2
3
−log10(p)


GO upregulated treatment hc
T cell receptor binding
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−log10(p)


pfc treatment
log fold change
2
1
0
−1
−2
1e+00
1e+02
1e+04
1e+06
mean expression


log10(P.adj)
12
10
8
6
4
2
0
Ide
Sgk1
Btaf1
Ogn
−2
−1
0
1
2
Log2 Fold Change


GO downregulated treatment pfc
beta−endorphin binding
insulin catabolic process
bradykinin catabolic process
ubiquitin homeostasis
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−log10(p)