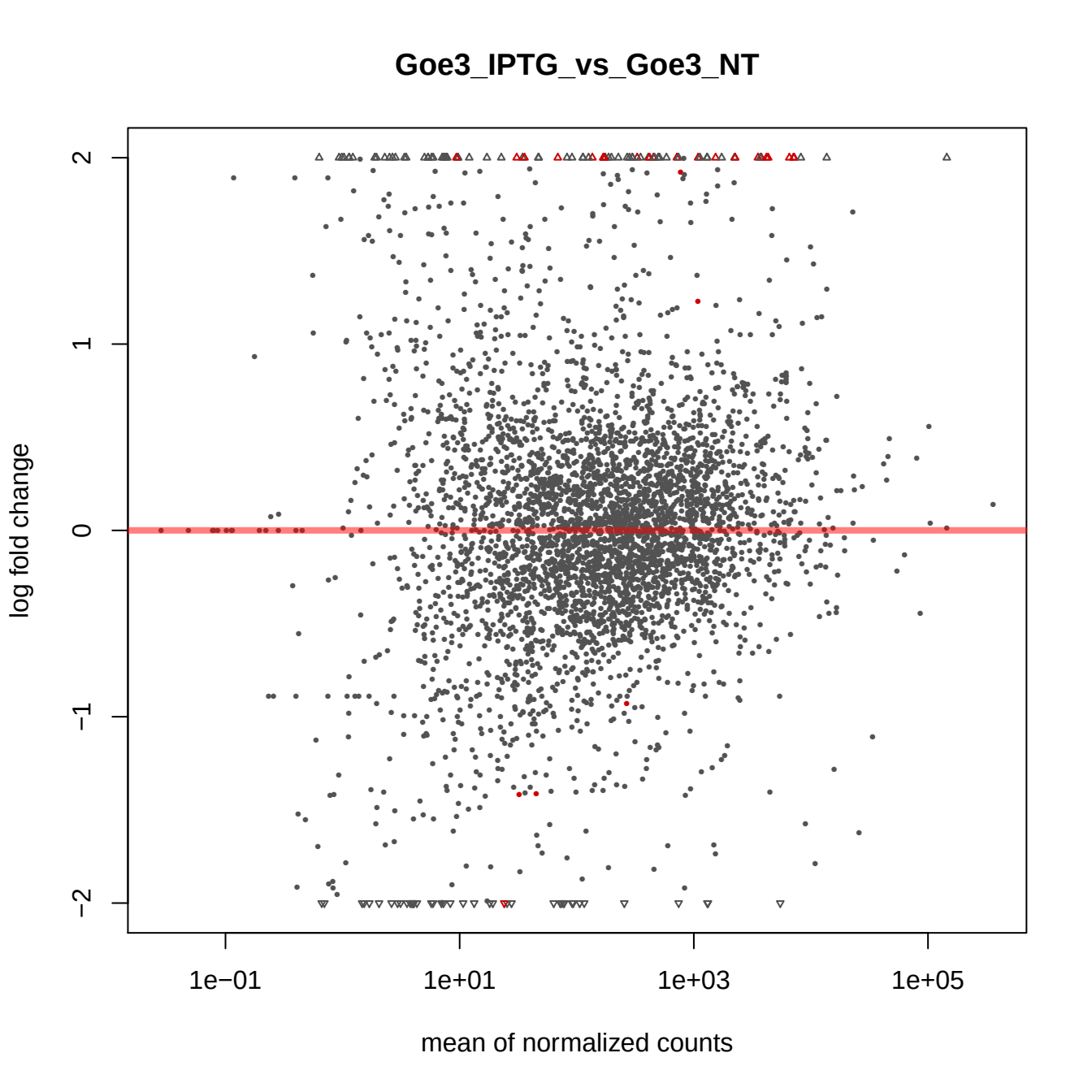
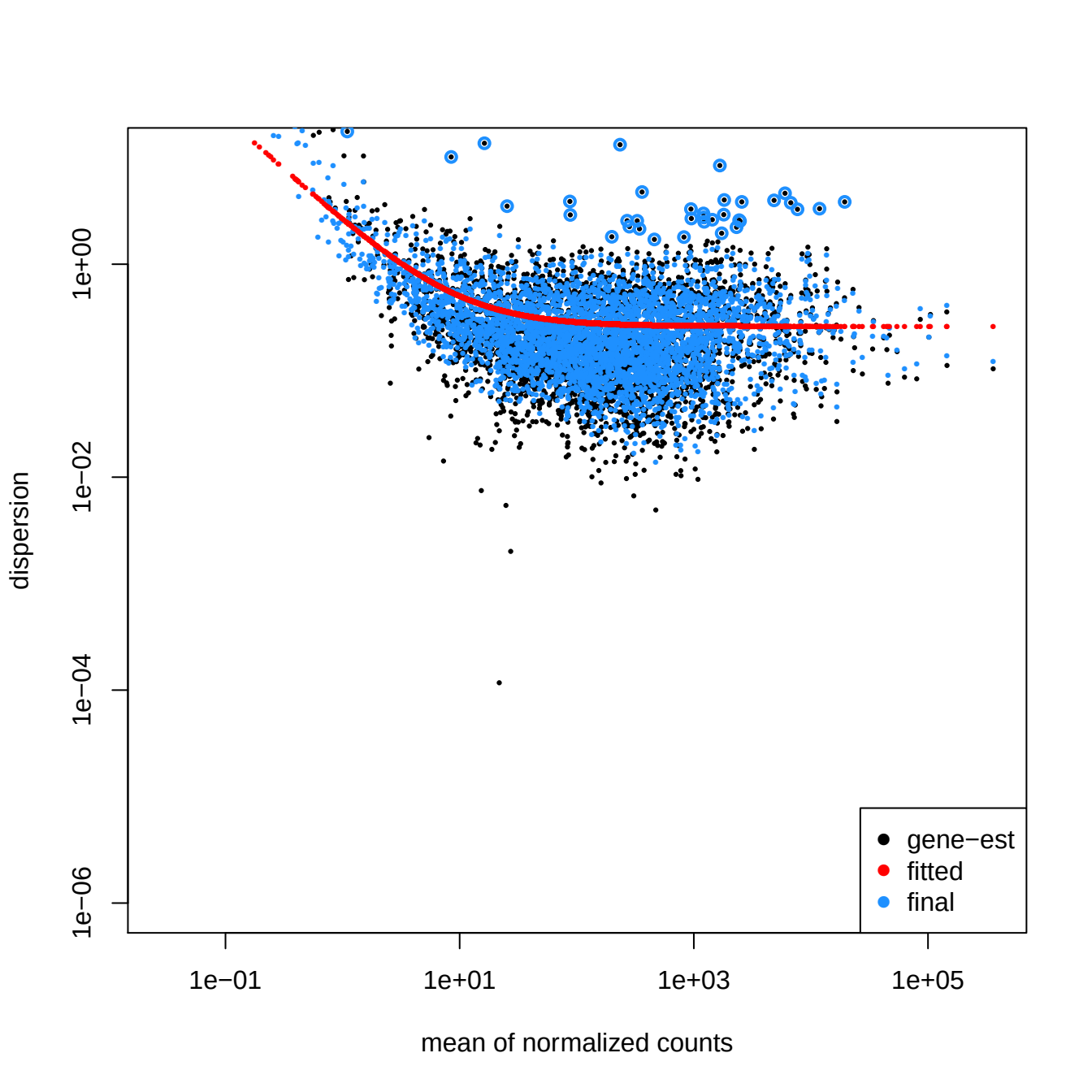
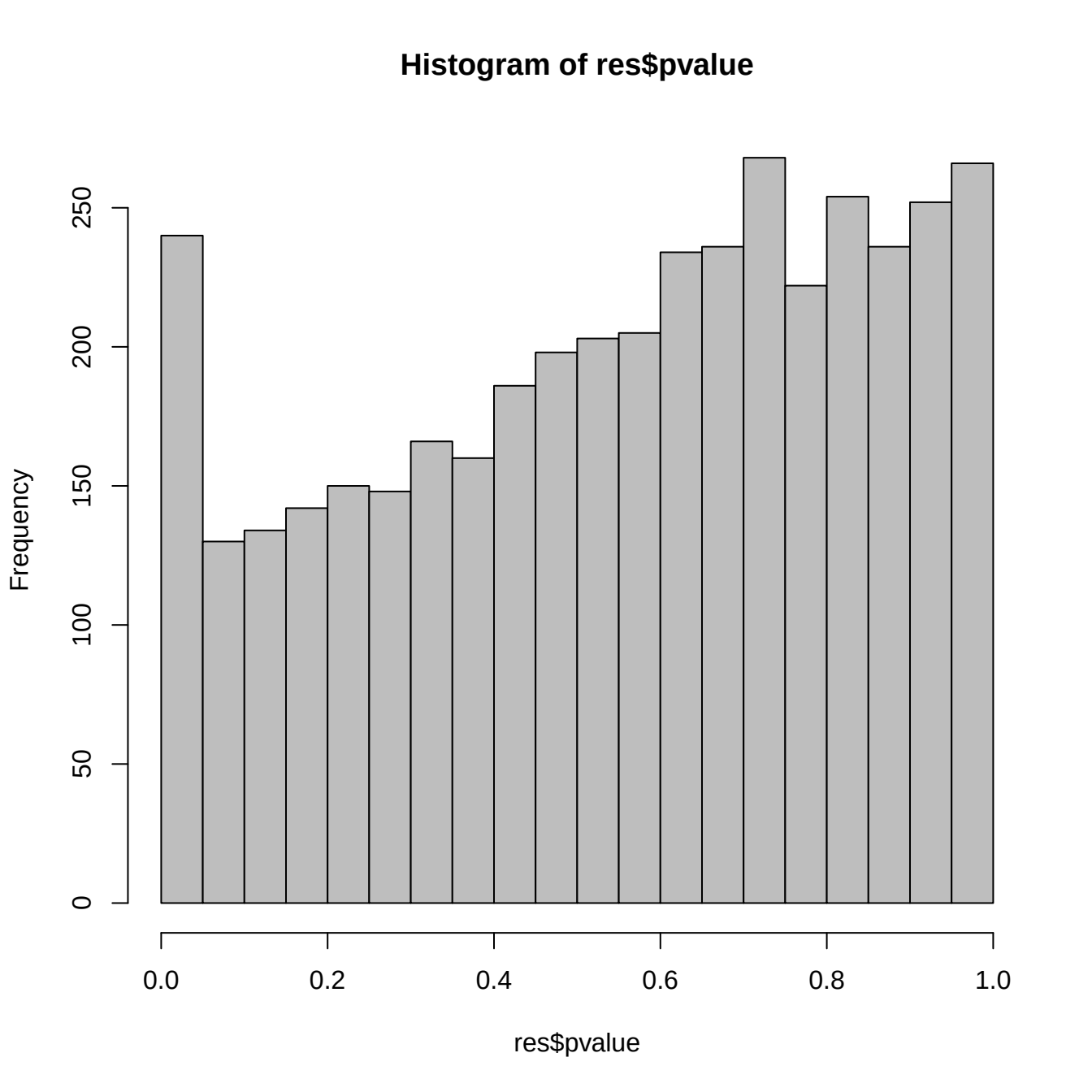
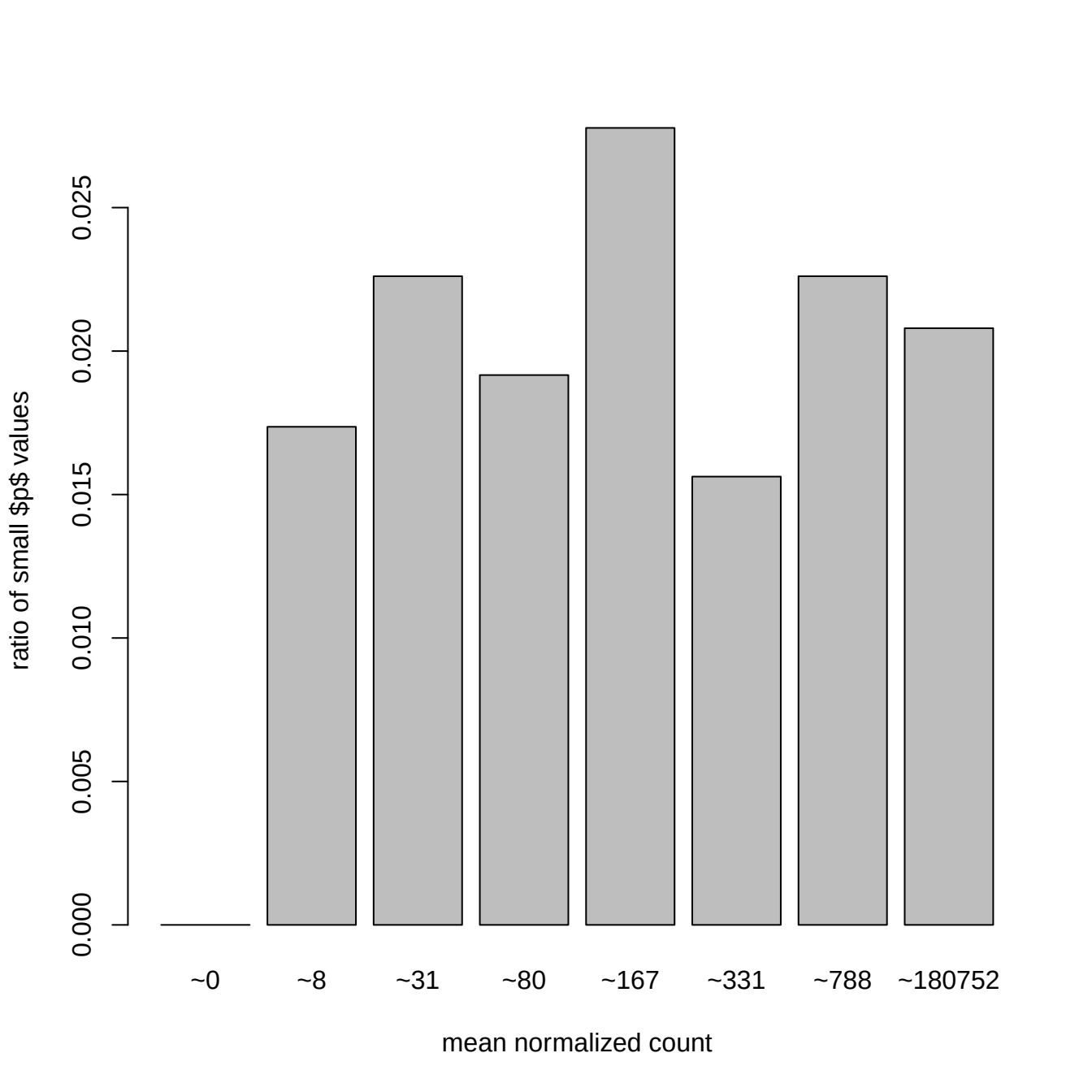
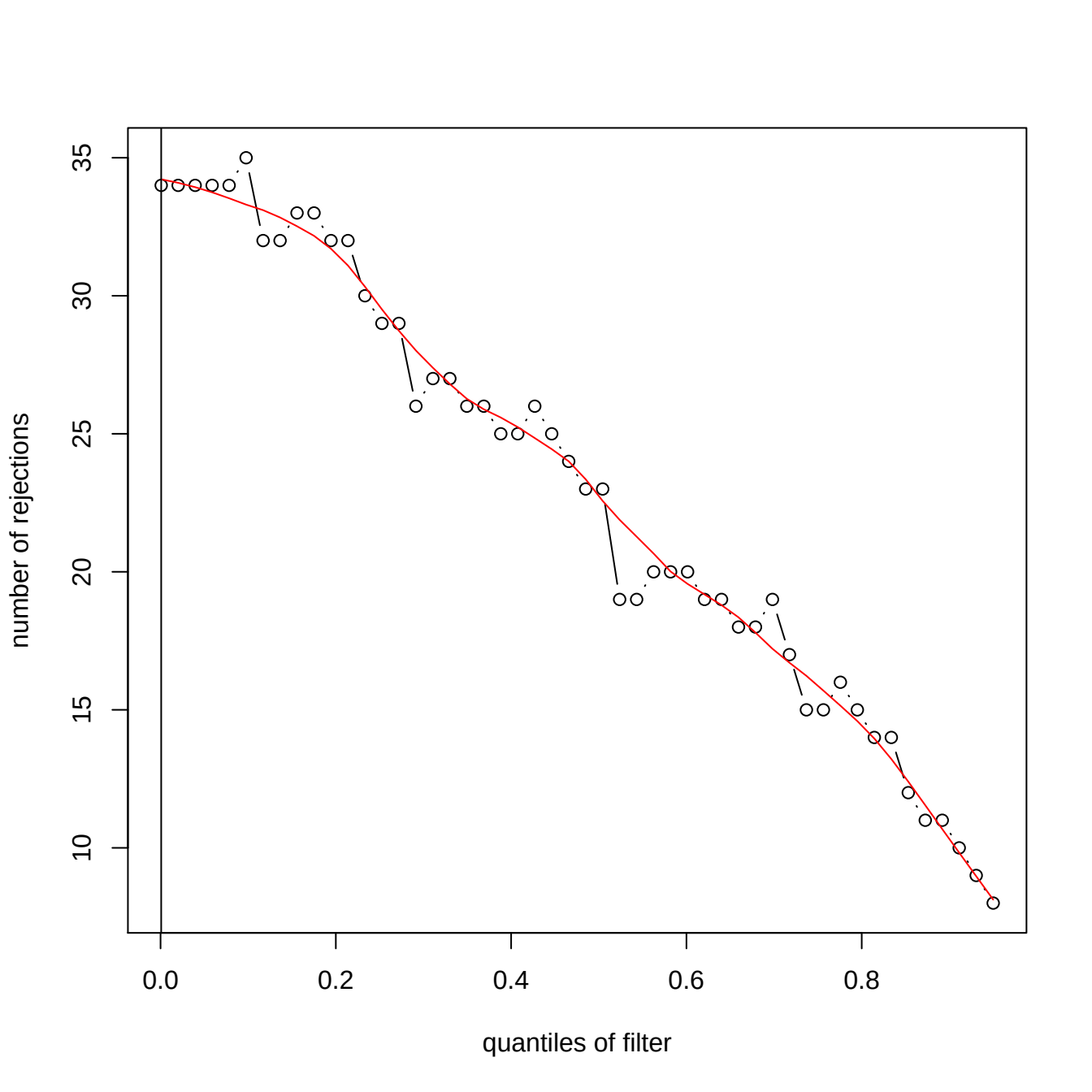
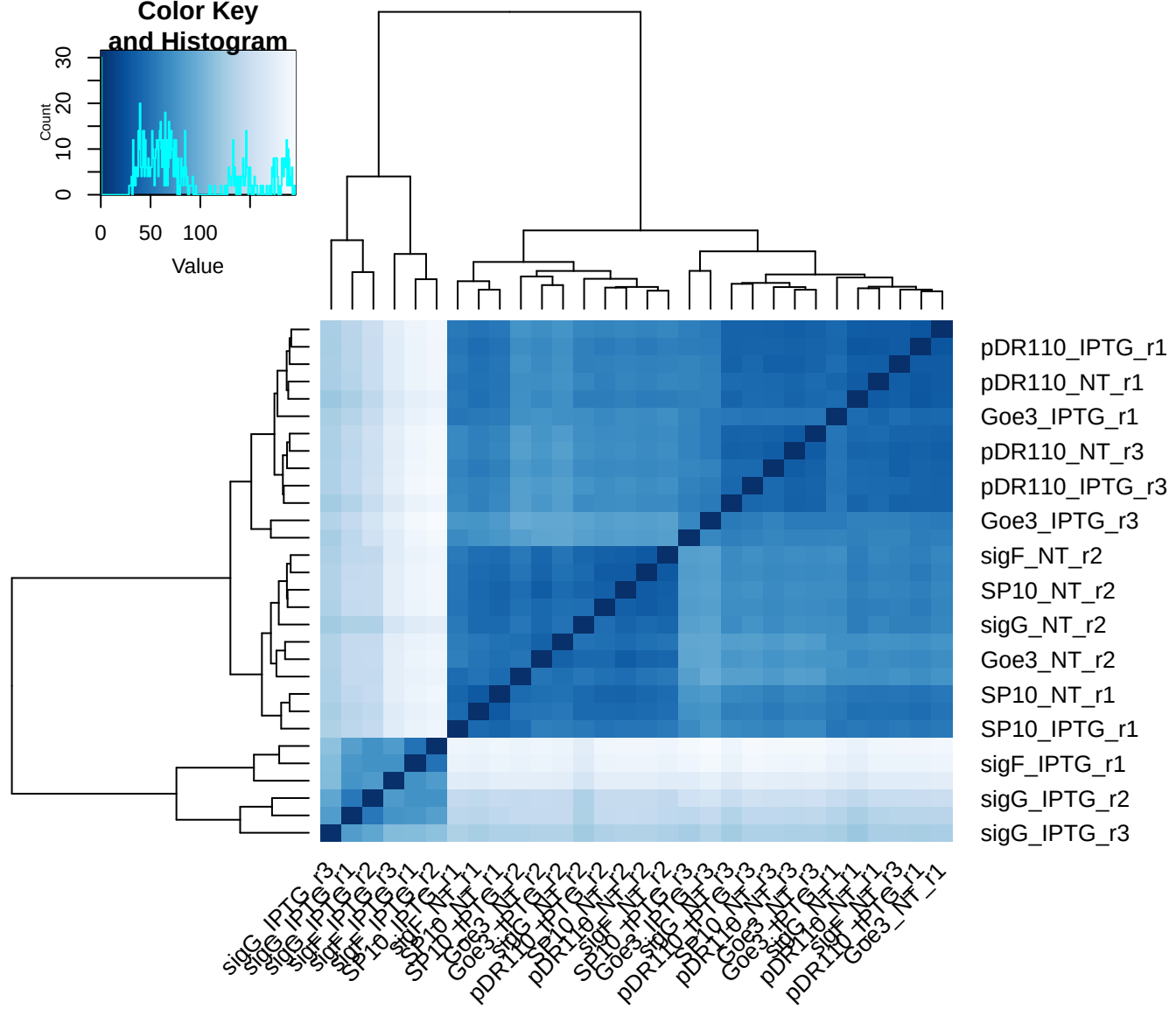

Goe3_IPTG_vs_Goe3_NT
log fold change
2
1
0
−1
−2
1e−01
1e+01
1e+03
1e+05
mean of normalized counts

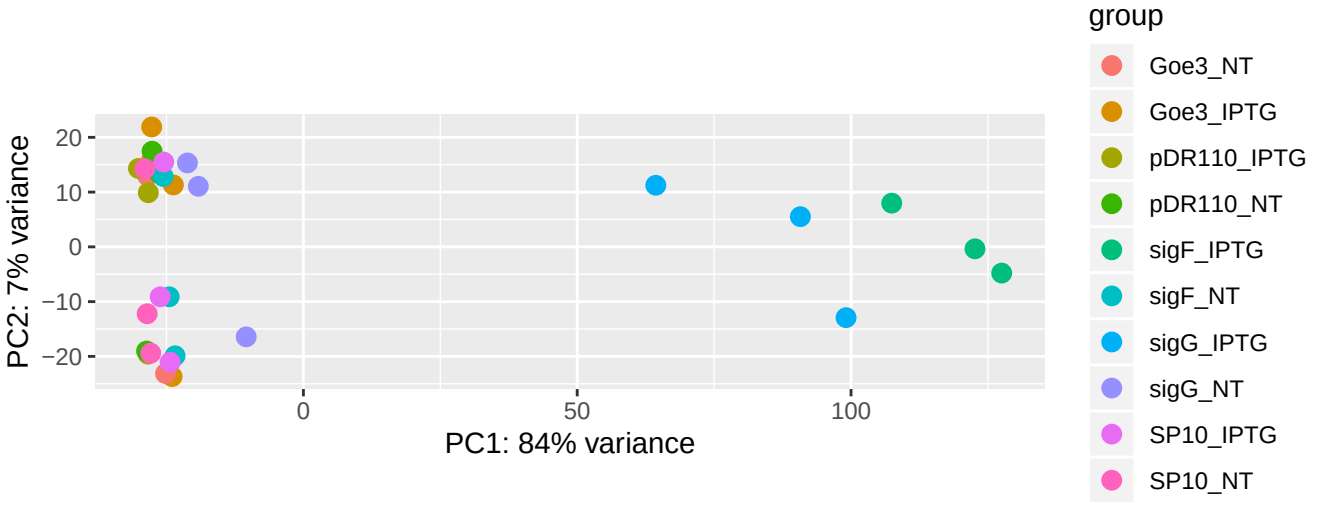

dispersion
1e+00
1e−02
1e−04
1e−06
1e−01
1e+01
1e+03
1e+05
mean of normalized counts
gene−est
fitted
final

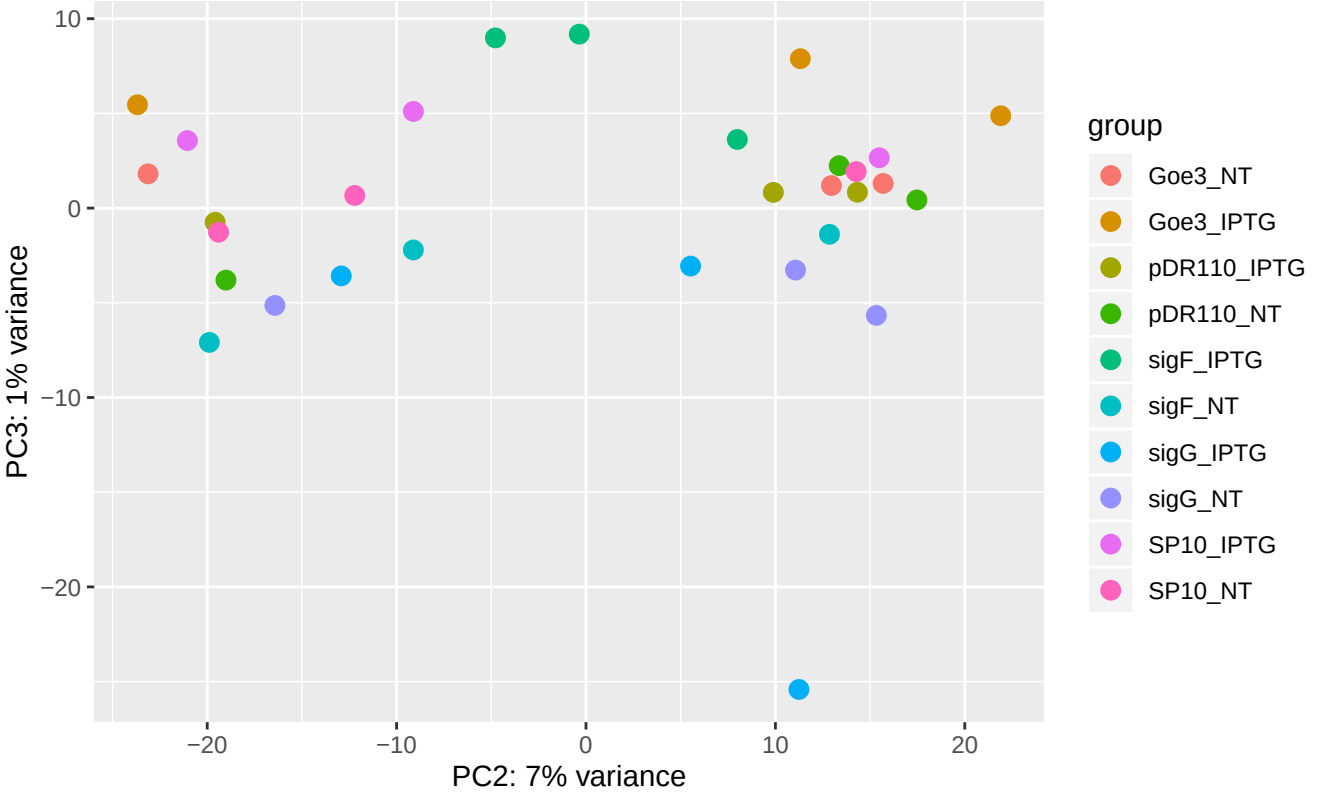

Histogram of res$pvalue
Frequency
0
50
100
150
200
250
0.0
0.2
0.4
0.6
0.8
1.0
res$pvalue

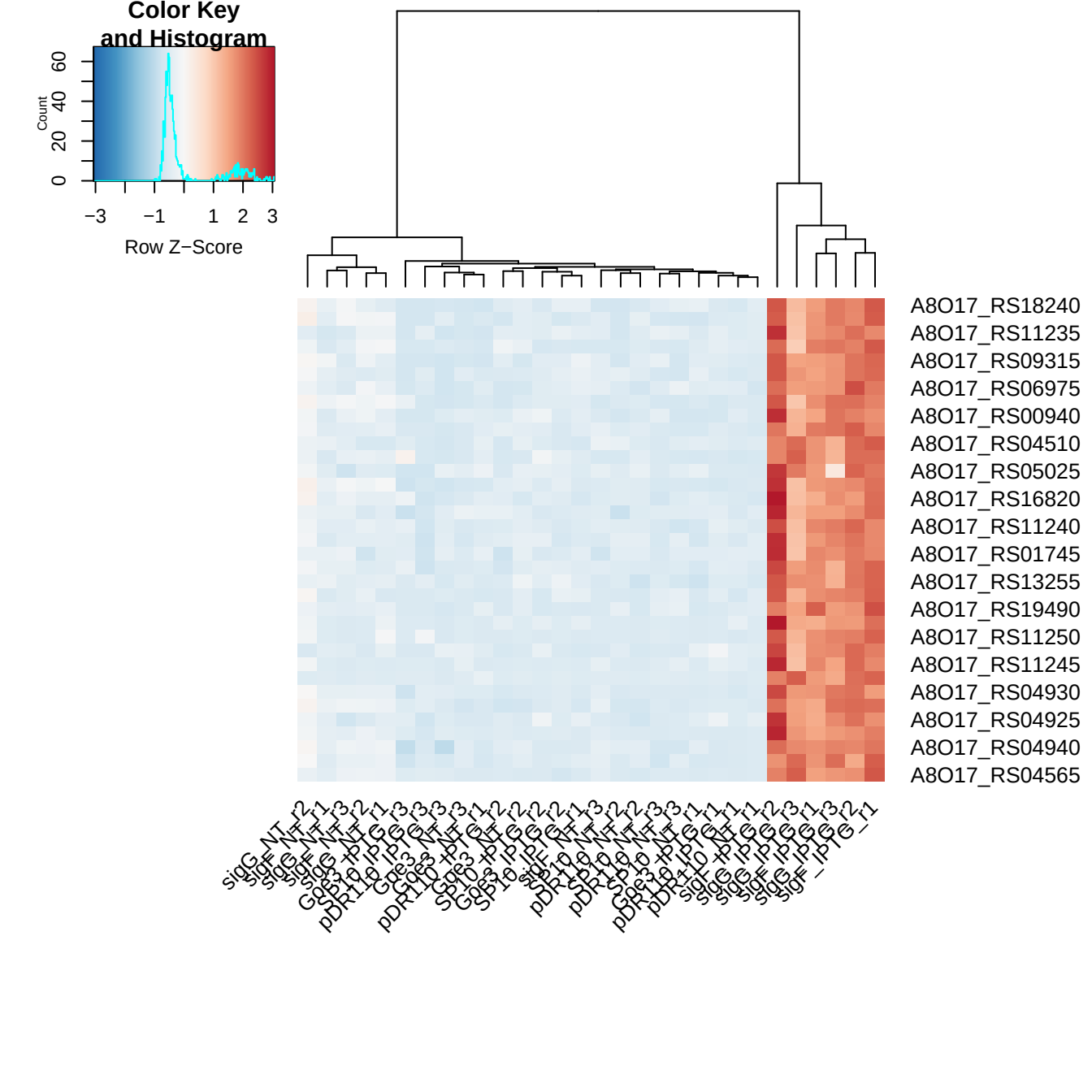

ratio of small p values
0.000
0.005
0.010
0.015
0.020
0.025
~0
~8
~31
~80
~167
~331
~788
~180752
mean normalized count

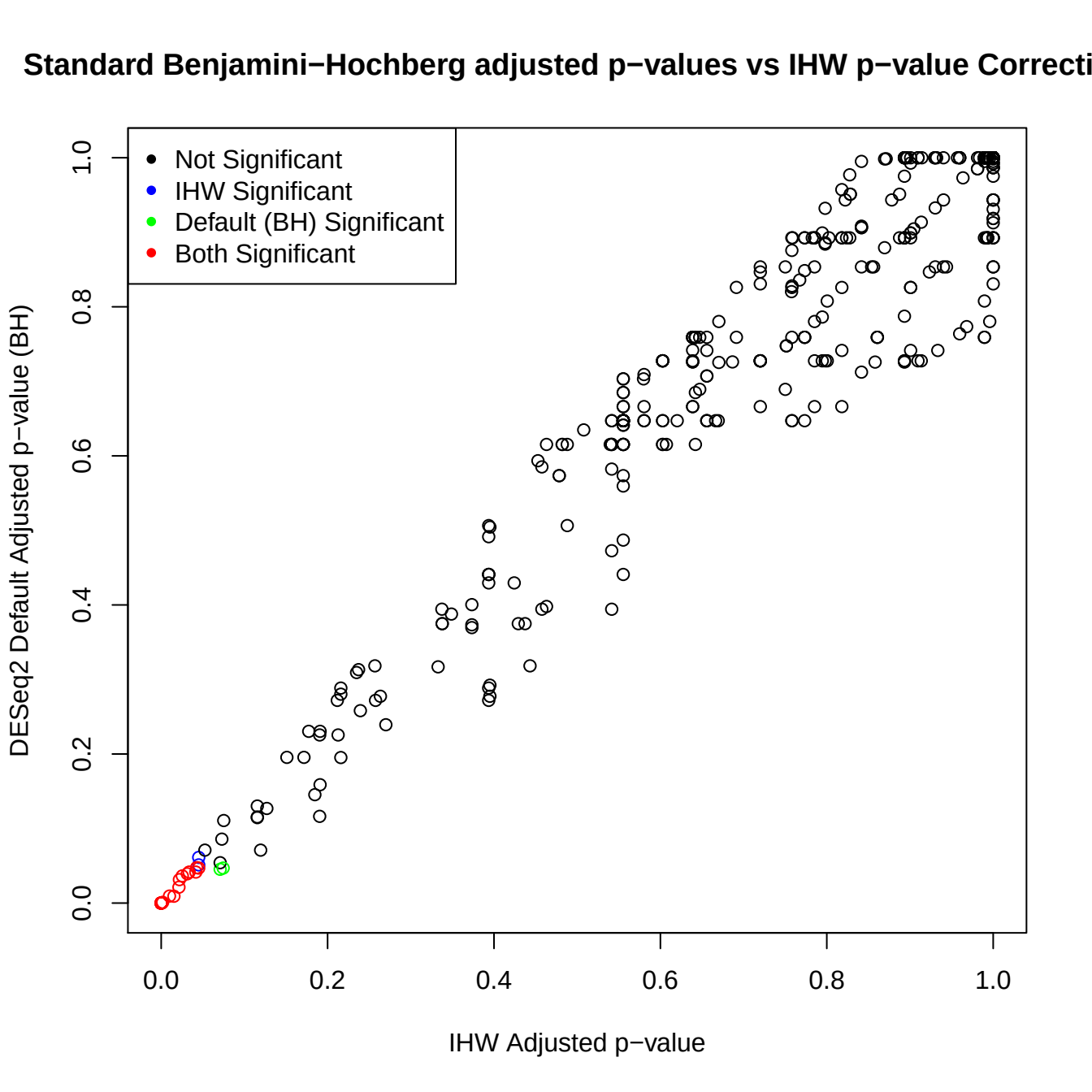

number of rejections
10
15
20
25
30
35
0.0
0.2
0.4
0.6
0.8
quantiles of filter

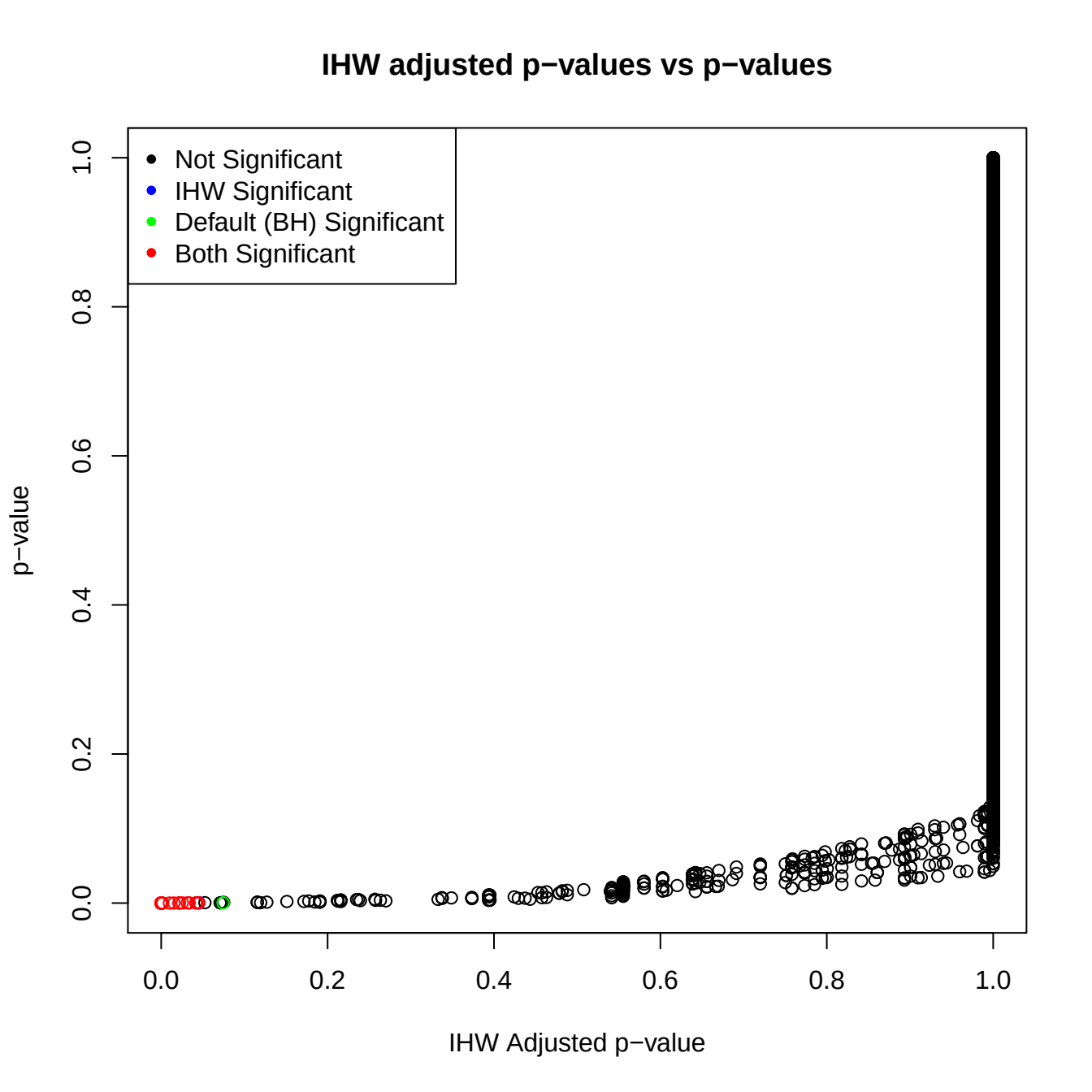

Color Key
and Histogram
Count
0
10
20
30
0
50
100
Value
pDR110_IPTG_r1
pDR110_NT_r1
Goe3_IPTG_r1
pDR110_NT_r3
pDR110_IPTG_r3
Goe3_IPTG_r3
sigF_NT_r2
SP10_NT_r2
sigG_NT_r2
Goe3_NT_r2
SP10_NT_r1
SP10_IPTG_r1
sigF_IPTG_r1
sigG_IPTG_r2
sigG_IPTG_r3

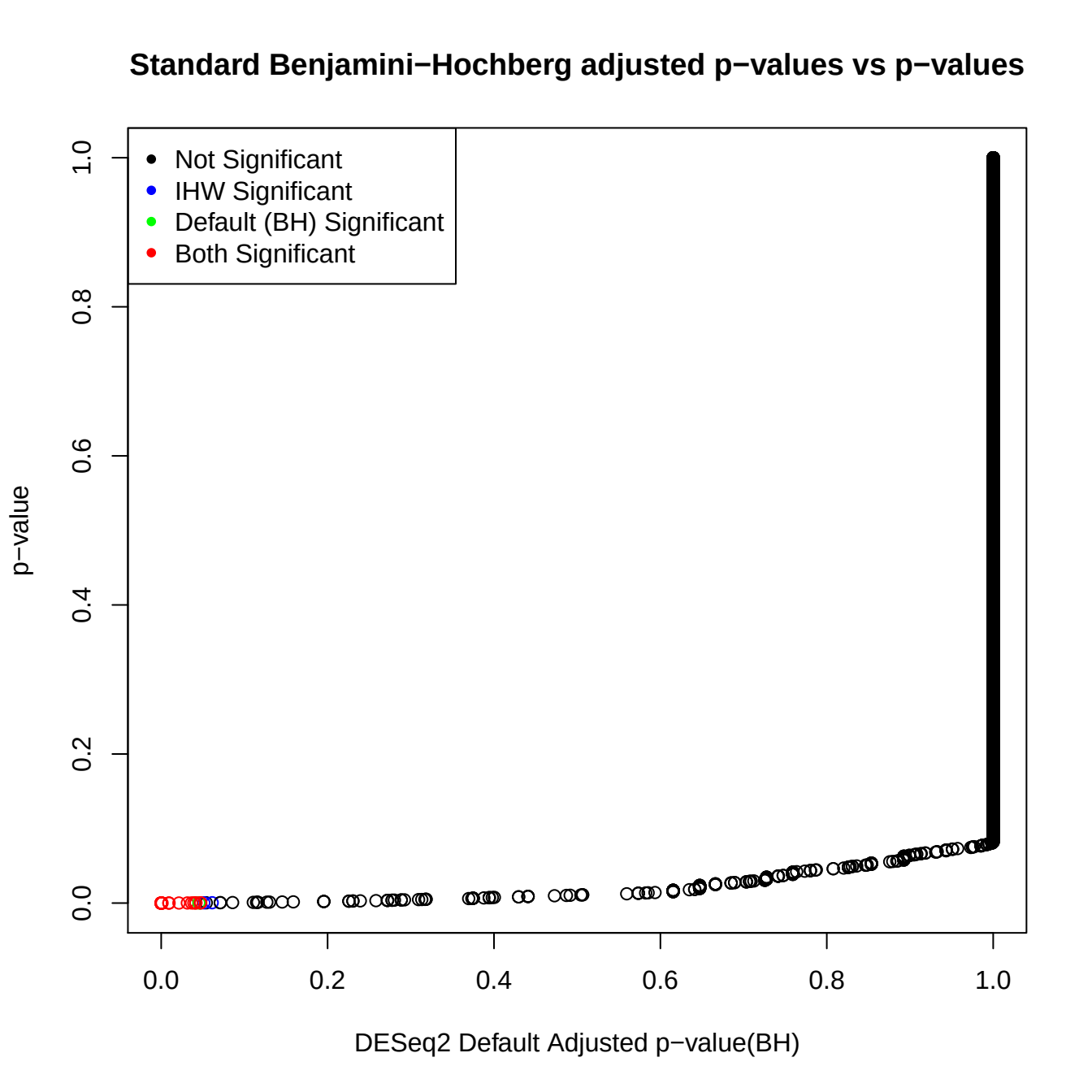

group
Goe3_NT
Goe3_IPTG
pDR110_IPTG
pDR110_NT
sigF_IPTG
sigF_NT
sigG_IPTG
sigG_NT
SP10_IPTG
SP10_NT
PC2: 7% variance
20
10
0
−10
−20
0
50
100
PC1: 84% variance


10
0
−10
−20
PC3: 1% variance
−20
−10
0
10
20
PC2: 7% variance
group
Goe3_NT
Goe3_IPTG
pDR110_IPTG
pDR110_NT
sigF_IPTG
sigF_NT
sigG_IPTG
sigG_NT
SP10_IPTG
SP10_NT


Color Key
and Histogram
Count
0
20
40
60
−3
−1
1
2
3
Row Z−Score
A8O17_RS18240
A8O17_RS11235
A8O17_RS09315
A8O17_RS06975
A8O17_RS00940
A8O17_RS04510
A8O17_RS05025
A8O17_RS16820
A8O17_RS11240
A8O17_RS01745
A8O17_RS13255
A8O17_RS19490
A8O17_RS11250
A8O17_RS11245
A8O17_RS04930
A8O17_RS04925
A8O17_RS04940
A8O17_RS04565
sigG_NT_r2
sigF_NT_r1
sigG_NT_r3
sigF_NT_r2
sigG_NT_r1
sigF_NT_r3
G0e3 +IPTG r3
SP10 +IPTG r3
pDR110 +IPTG r3
G0e3 +IPTG r1
pDR110 +IPTG r2
G0e3 +IPTG r2
SP10 +IPTG r1
SP10 +IPTG r2
sigF_NT_r3
pDR110 NT r1
pDR110 NT r2
SP10 NT r2
pDR110 NT r3
SP10 NT r3
G0e3 +IPTG r1
pDR110 +IPTG r1
sigF +IPTG r1
sigG +IPTG r2
sigG +IPTG r3
sigF +IPTG r3
sigG +IPTG r1
sigF _IPTG_r1


Standard Benjamini−Hochberg adjusted p−values vs IHW p−value Correcti
Not Significant
IHW Significant
Default (BH) Significant
Both Significant
DESeq2 Default Adjusted p−value (BH)
IHW Adjusted p−value
0.0
0.2
0.4
0.6
0.8
1.0


IHW adjusted p−values vs p−values
Not Significant
IHW Significant
Default (BH) Significant
Both Significant
p−value
0.0
0.2
0.4
0.6
0.8
1.0
IHW Adjusted p−value


Standard Benjamini−Hochberg adjusted p−values vs p−values
Not Significant
IHW Significant
Default (BH) Significant
Both Significant
p−value
0.0
0.2
0.4
0.6
0.8
1.0
DESeq2 Default Adjusted p−value(BH)