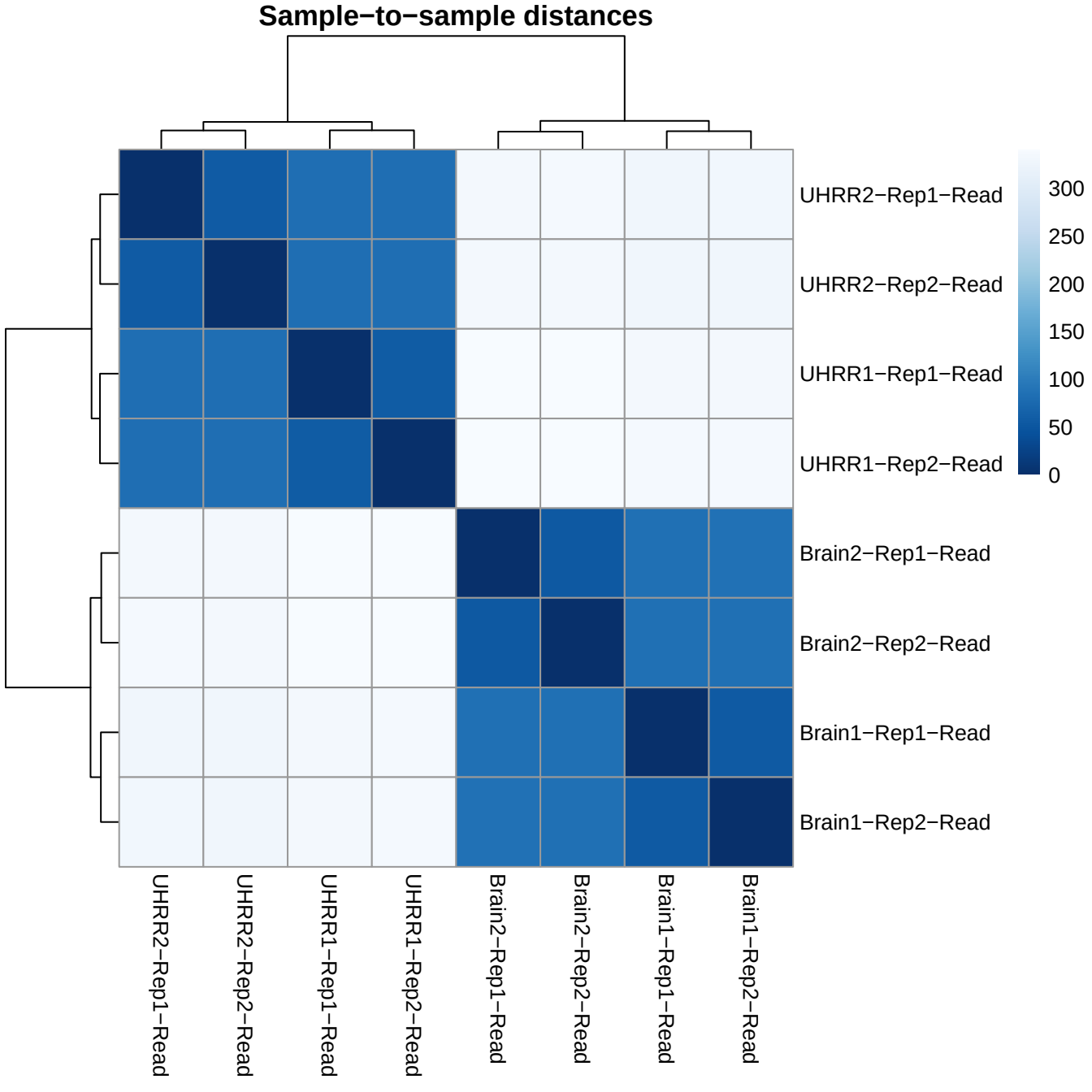
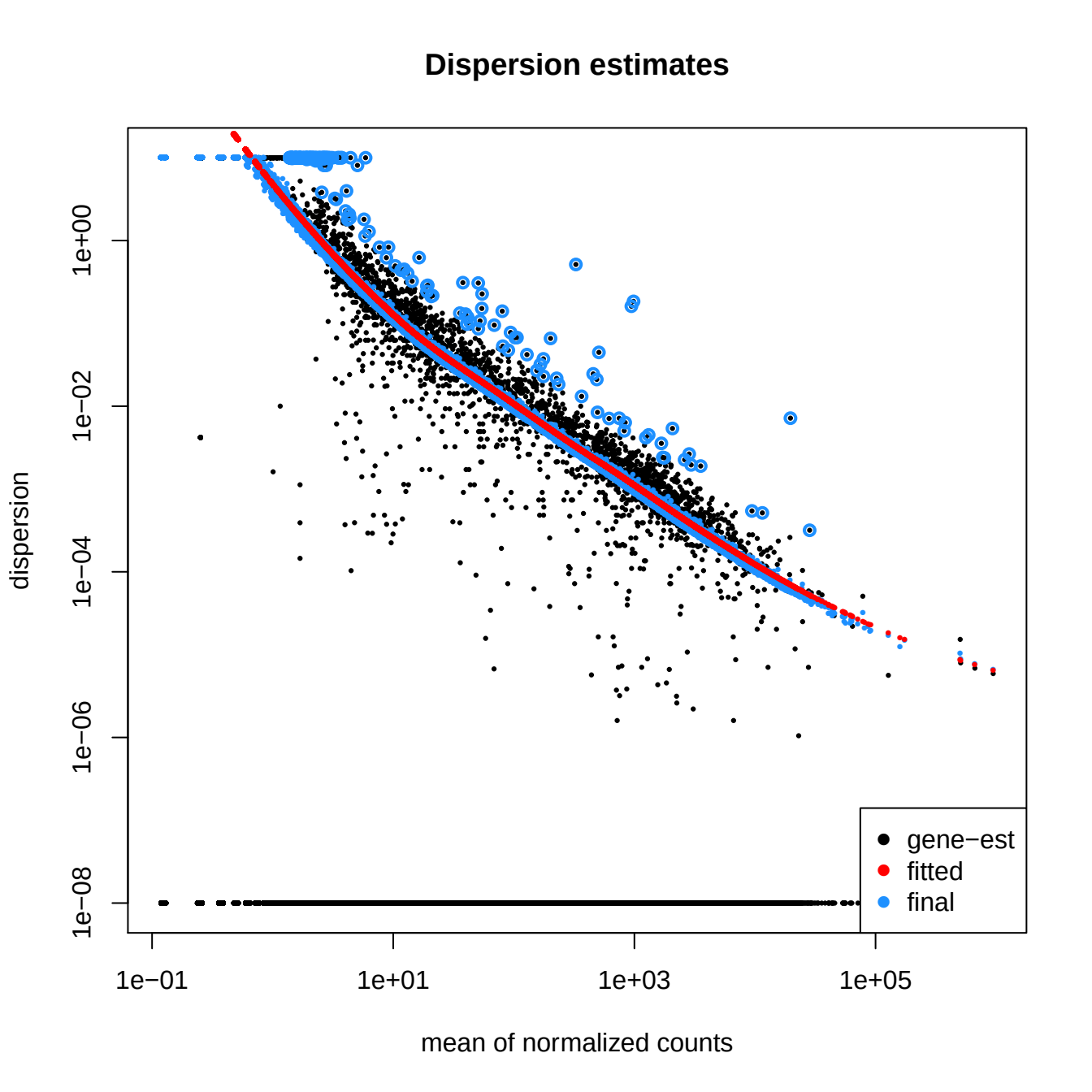
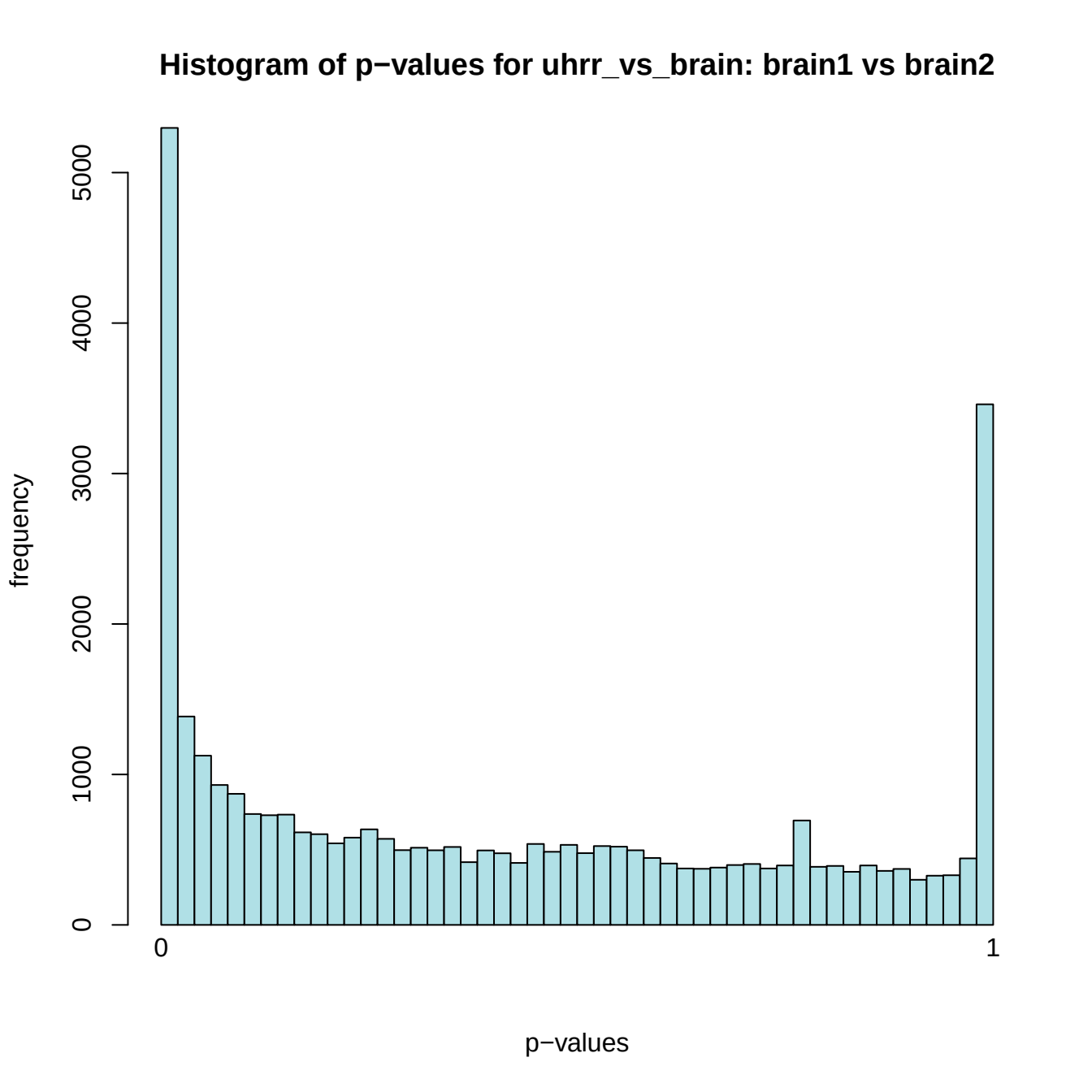
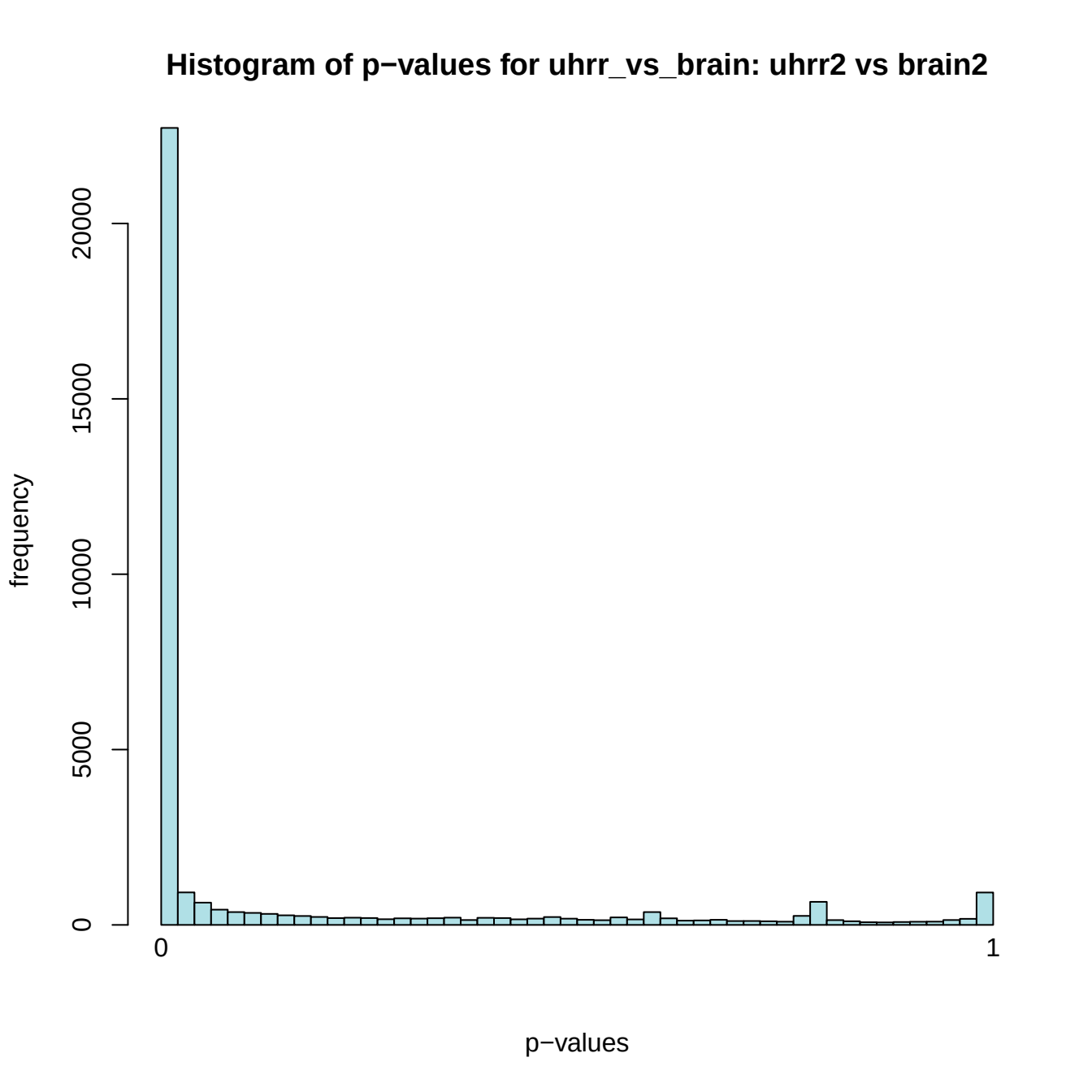
PC2: 0% variance
2
0
−2
Brain1−Rep1−Read
Brain1−Rep2−Read
Brain2−Rep2−Read
Brain2−Rep1−Read
UHRR2−Rep1−Read
UHRR2−Rep2−Read
UHRR1−Rep1−Read
UHRR1−Rep2−Read
−40
0
40
PC1: 100% variance
group
brain2
brain1
uhrr2
uhrr1

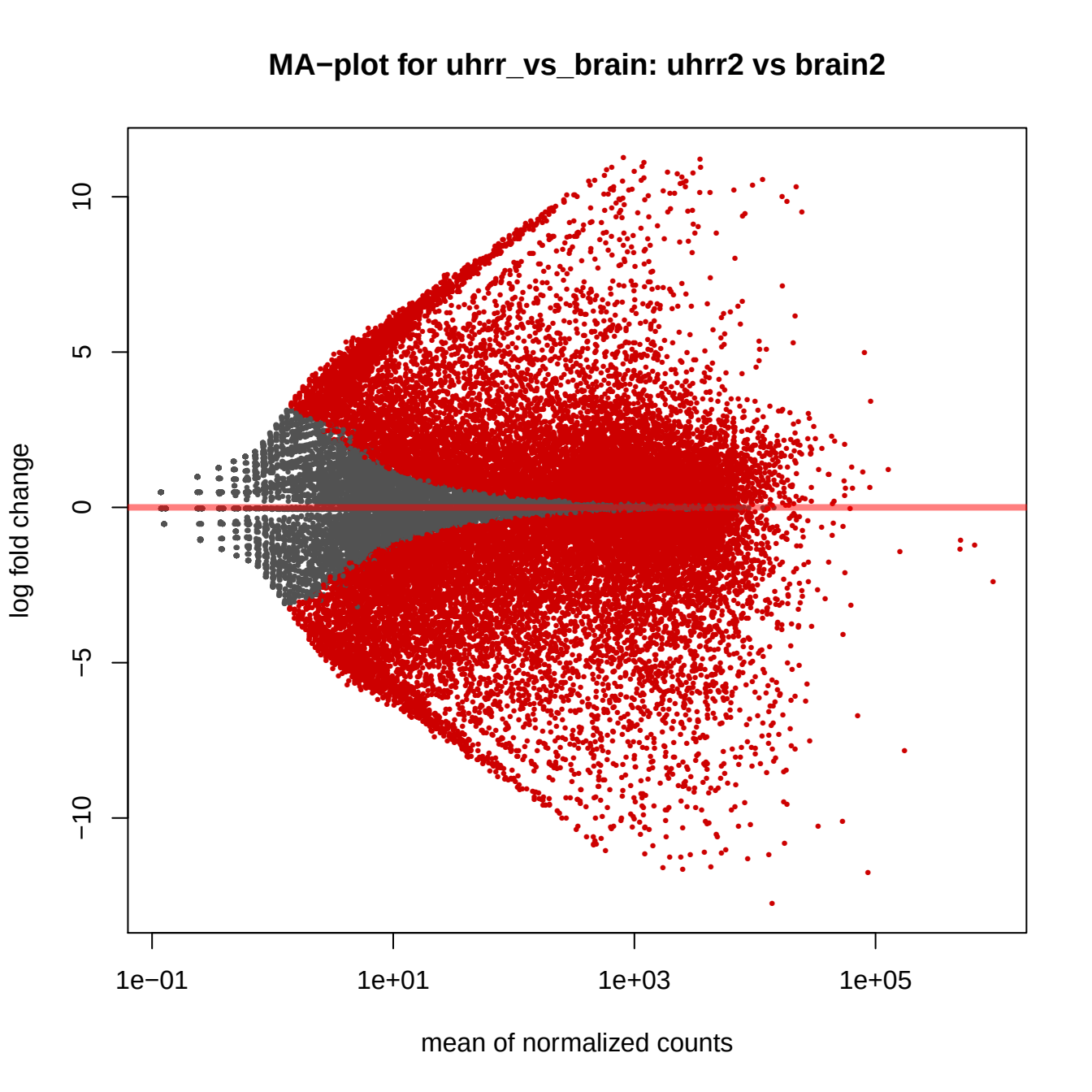

Sample−to−sample distances
UHRR2−Rep1−Read
UHRR2−Rep2−Read
UHRR1−Rep1−Read
UHRR1−Rep2−Read
Brain2−Rep1−Read
Brain2−Rep2−Read
Brain1−Rep1−Read
Brain1−Rep2−Read
300
250
200
150
100
50
0

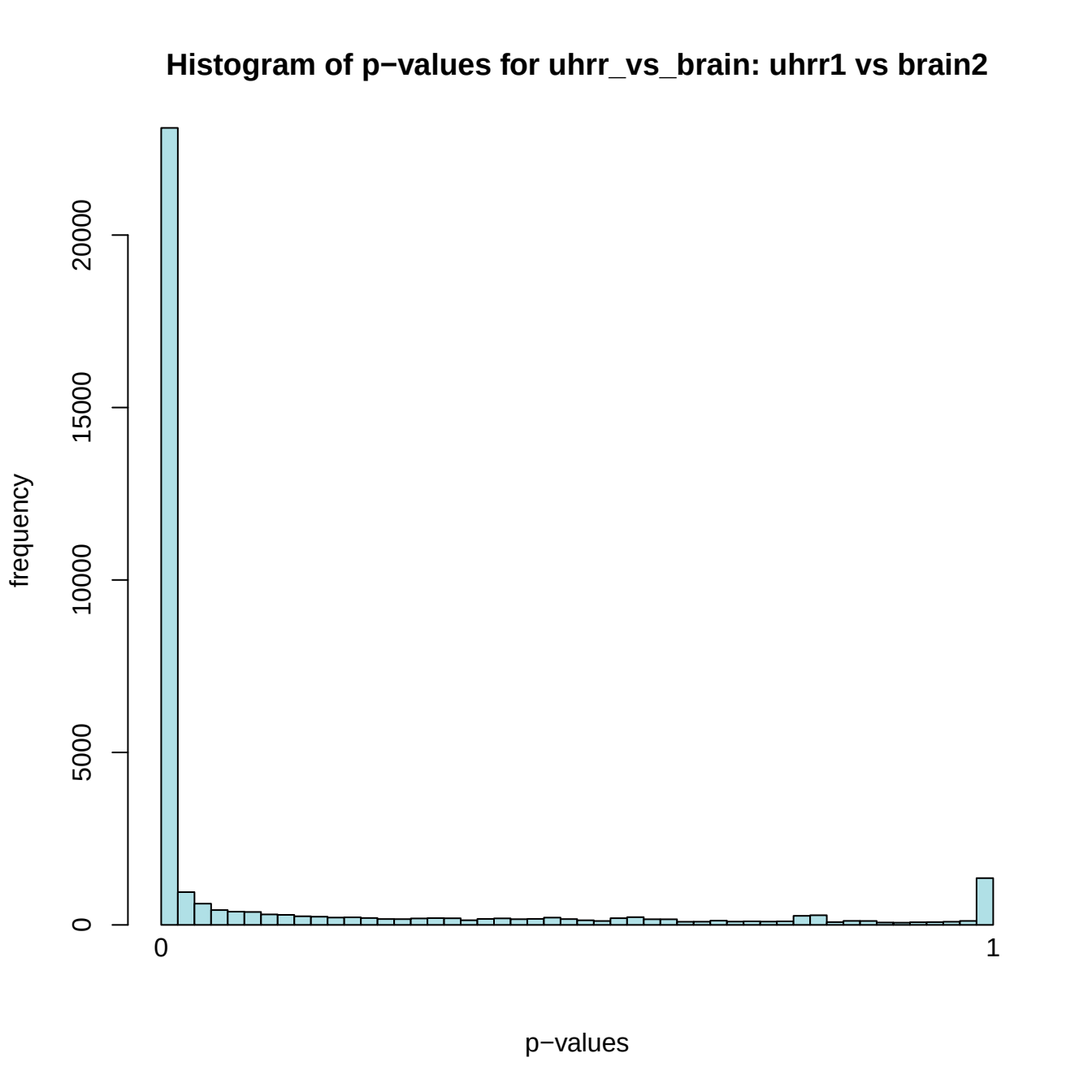

Dispersion estimates
dispersion
1e+00
1e−02
1e−04
1e−06
1e−08
1e−01
1e+01
1e+03
1e+05
mean of normalized counts
gene−est
fitted
final

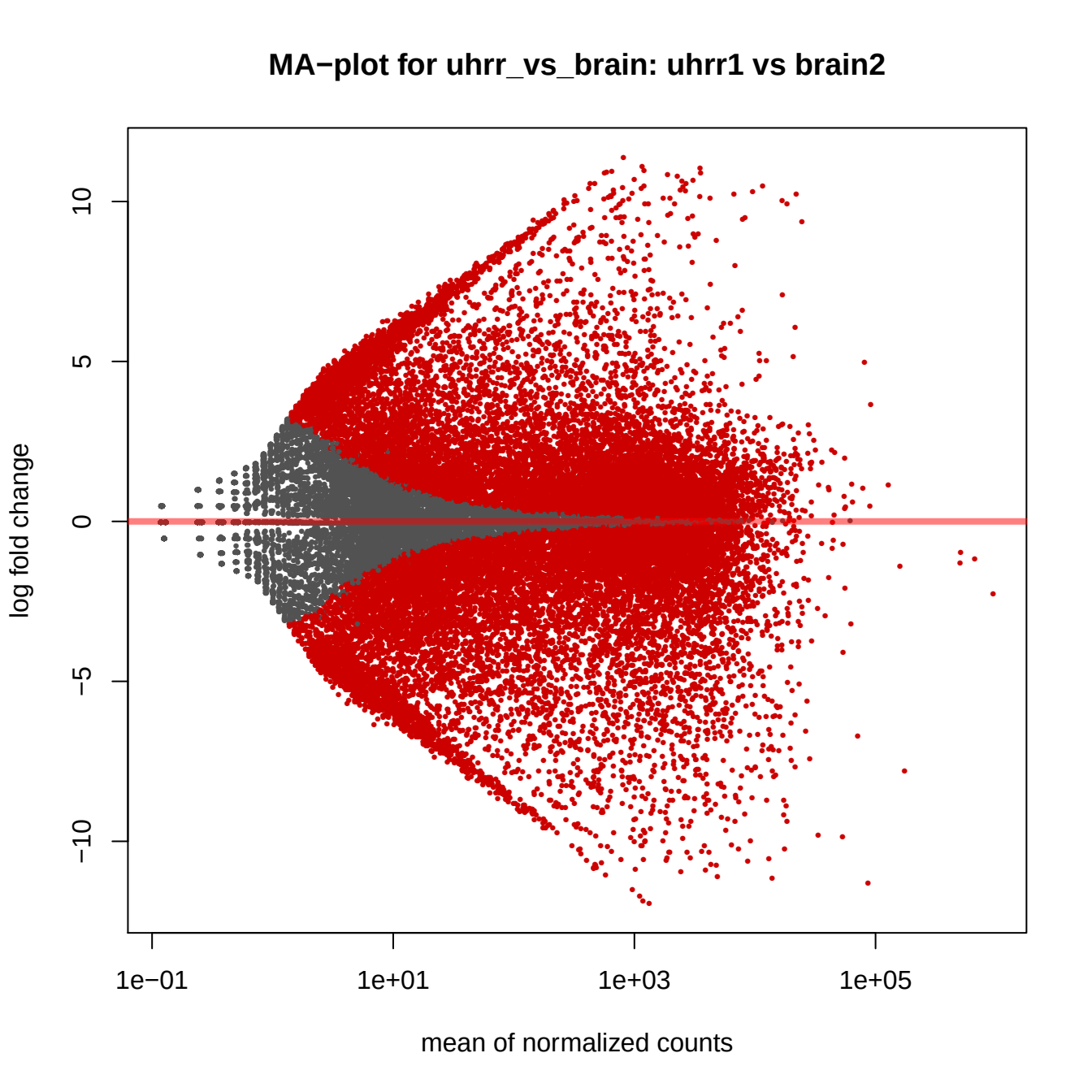

Histogram of p−values for uhrr_vs_brain: brain1 vs brain2
frequency
0
1000
2000
3000
4000
5000
0
1
p−values

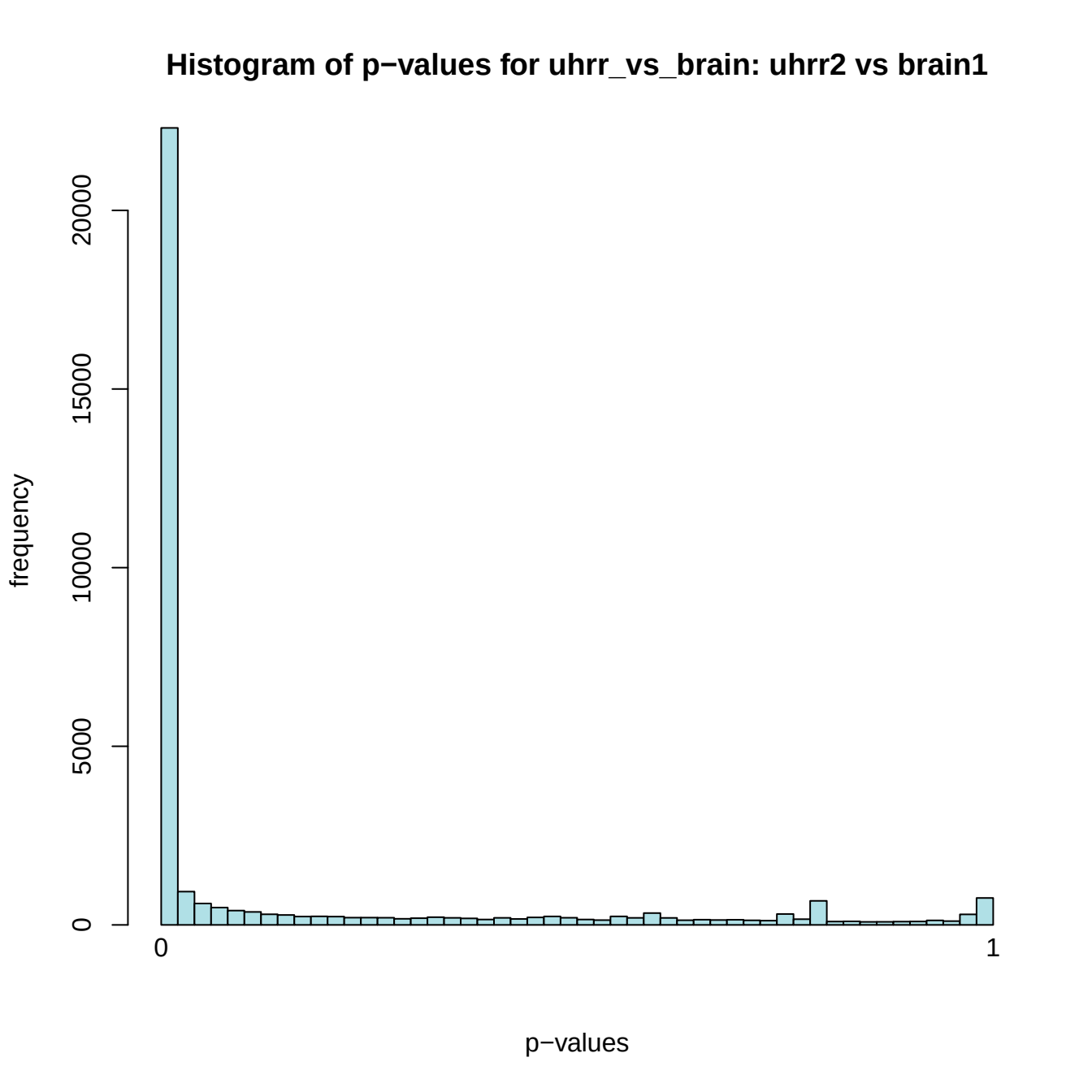
MA−plot for uhrr_vs_brain: brain1 vs brain2
log fold change
4
2
0
−2
−4
−6
1e−01
1e+01
1e+03
1e+05
mean of normalized counts

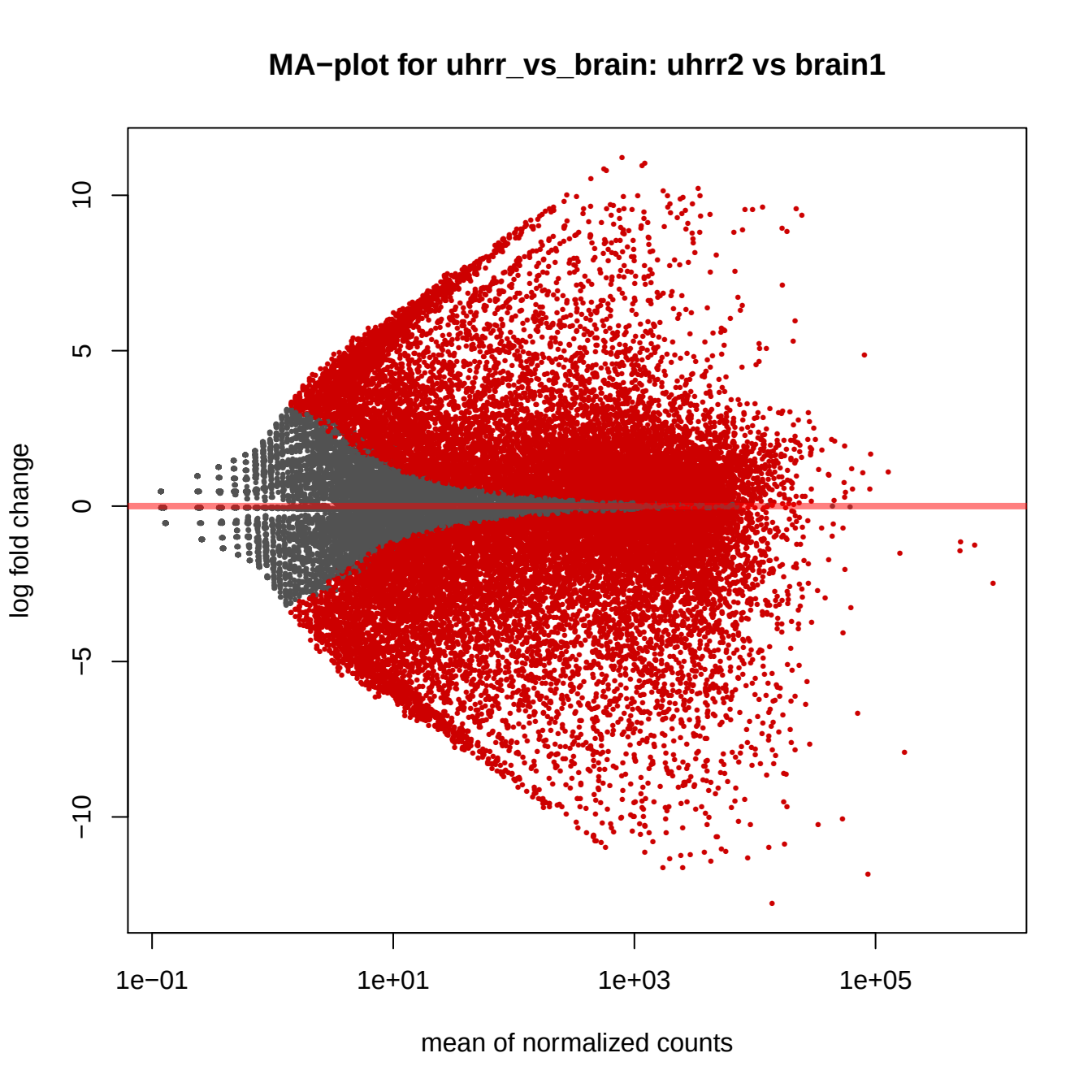

Histogram of p−values for uhrr_vs_brain: uhrr2 vs brain2
frequency
0
5000
10000
15000
20000
0
1
p−values

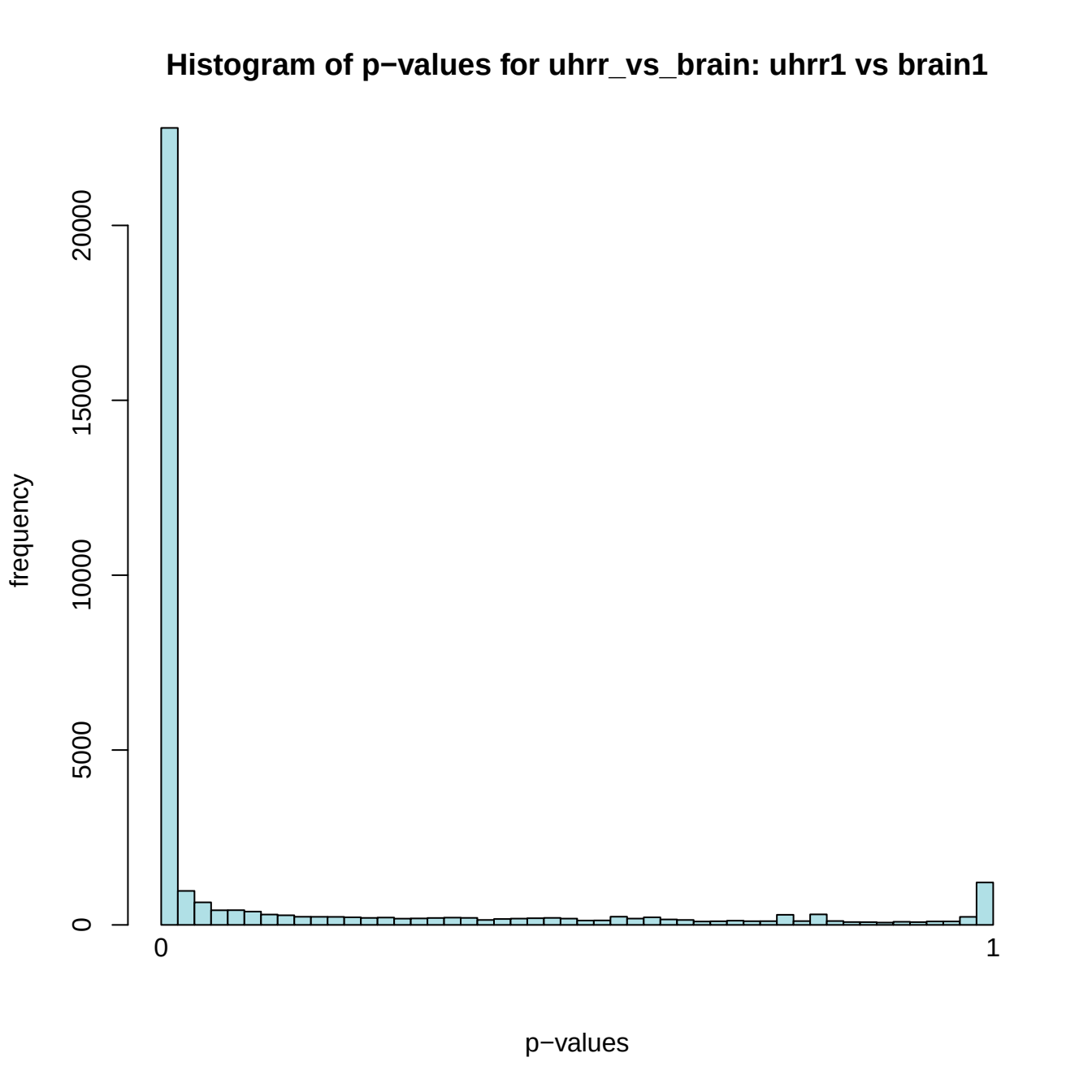

MA−plot for uhrr_vs_brain: uhrr2 vs brain2
log fold change
10
5
0
−5
−10
1e−01
1e+01
1e+03
1e+05
mean of normalized counts

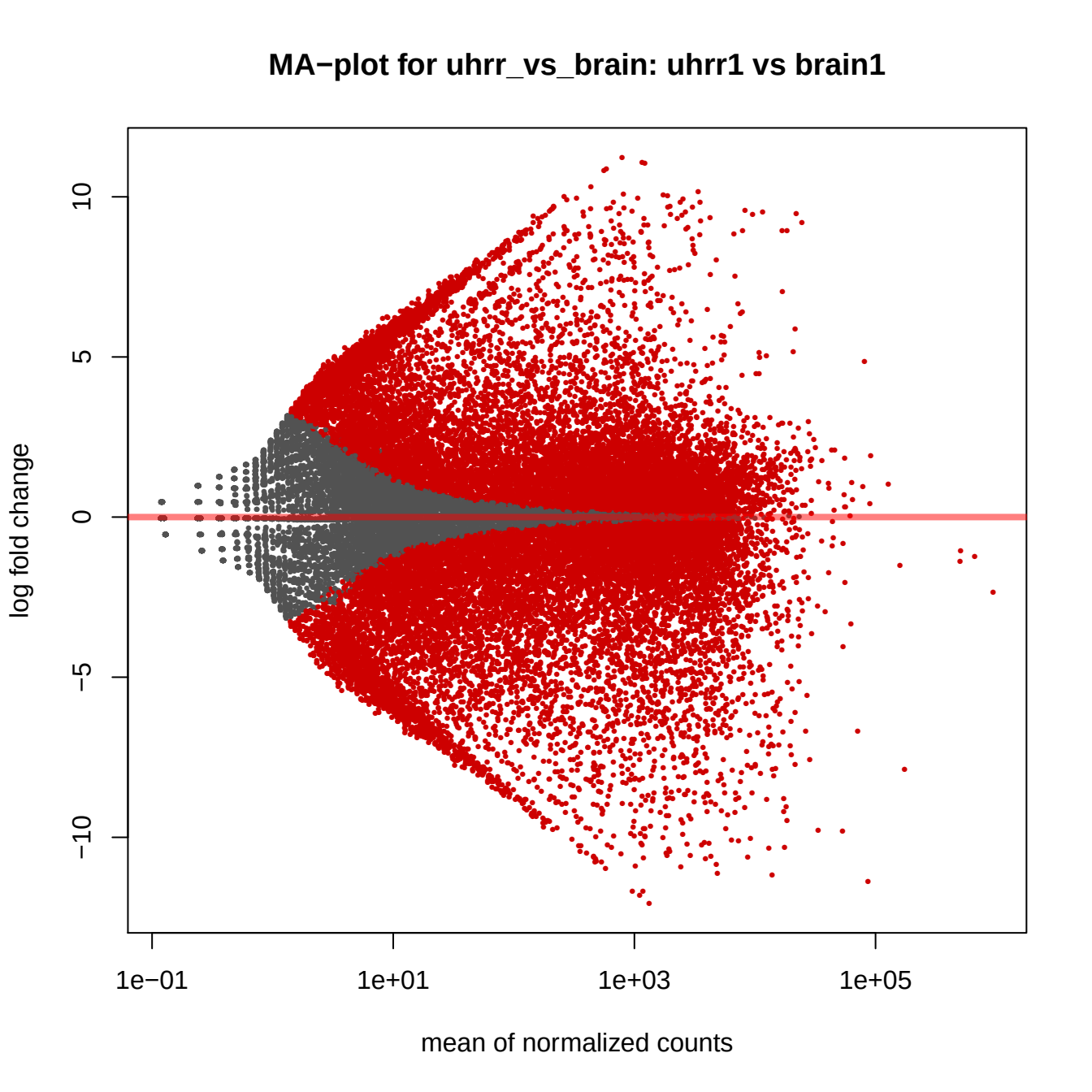

Histogram of p−values for uhrr_vs_brain: uhrr1 vs brain2
frequency
0
5000
10000
15000
20000
0
1
p−values

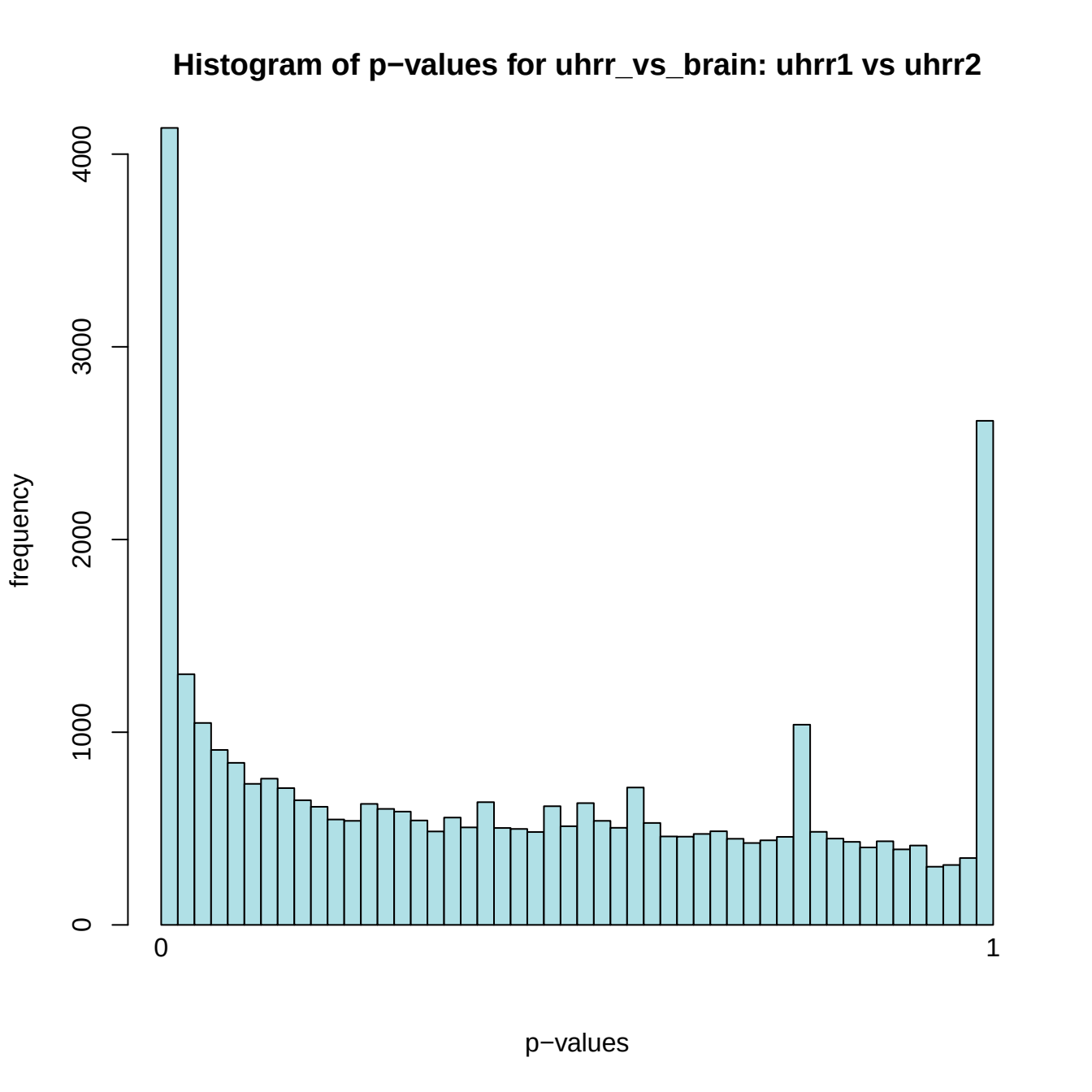

MA−plot for uhrr_vs_brain: uhrr1 vs brain2
log fold change
10
5
0
−5
−10
1e−01
1e+01
1e+03
1e+05
mean of normalized counts

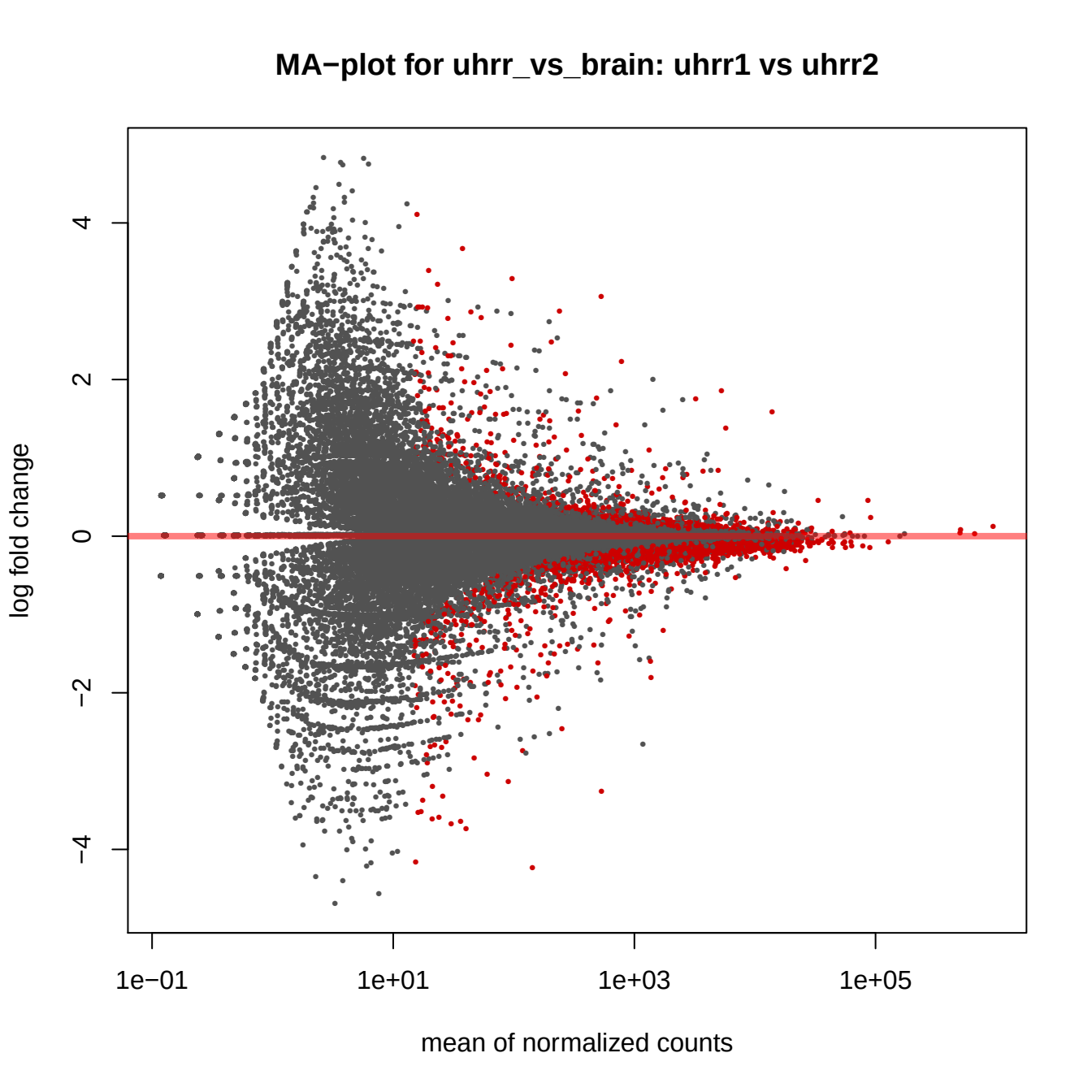

Histogram of p−values for uhrr_vs_brain: uhrr2 vs brain1
frequency
0
5000
10000
15000
20000
0
1
p−values


MA−plot for uhrr_vs_brain: uhrr2 vs brain1
log fold change
10
5
0
−5
−10
1e−01
1e+01
1e+03
1e+05
mean of normalized counts


Histogram of p−values for uhrr_vs_brain: uhrr1 vs brain1
frequency
0
5000
10000
15000
20000
0
1
p−values


MA−plot for uhrr_vs_brain: uhrr1 vs brain1
log fold change
10
5
0
−5
−10
1e−01
1e+01
1e+03
1e+05
mean of normalized counts


Histogram of p−values for uhrr_vs_brain: uhrr1 vs uhrr2
frequency
0
1000
2000
3000
4000
0
1
p−values


MA−plot for uhrr_vs_brain: uhrr1 vs uhrr2
log fold change
4
2
0
−2
−4
1e−01
1e+01
1e+03
1e+05
mean of normalized counts