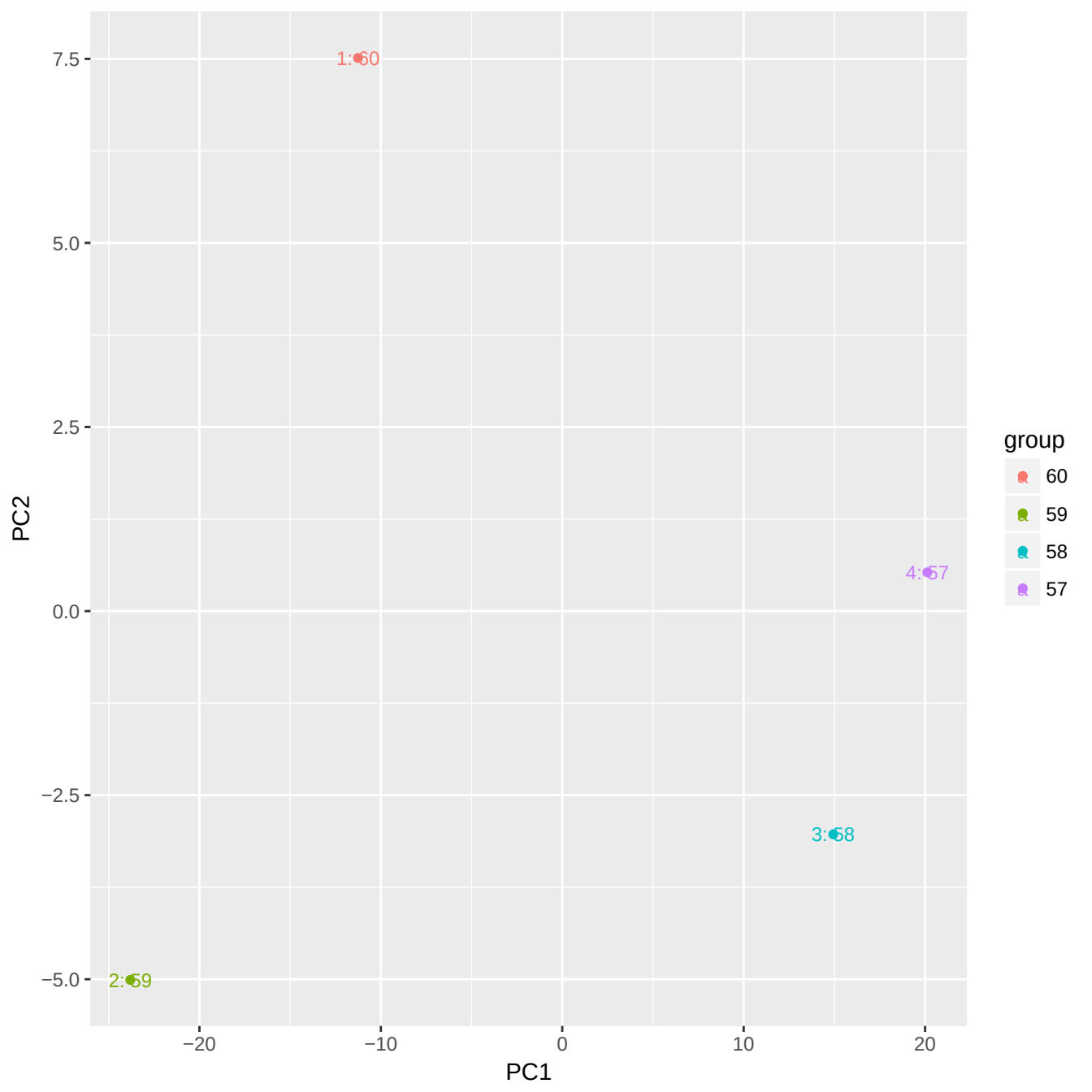
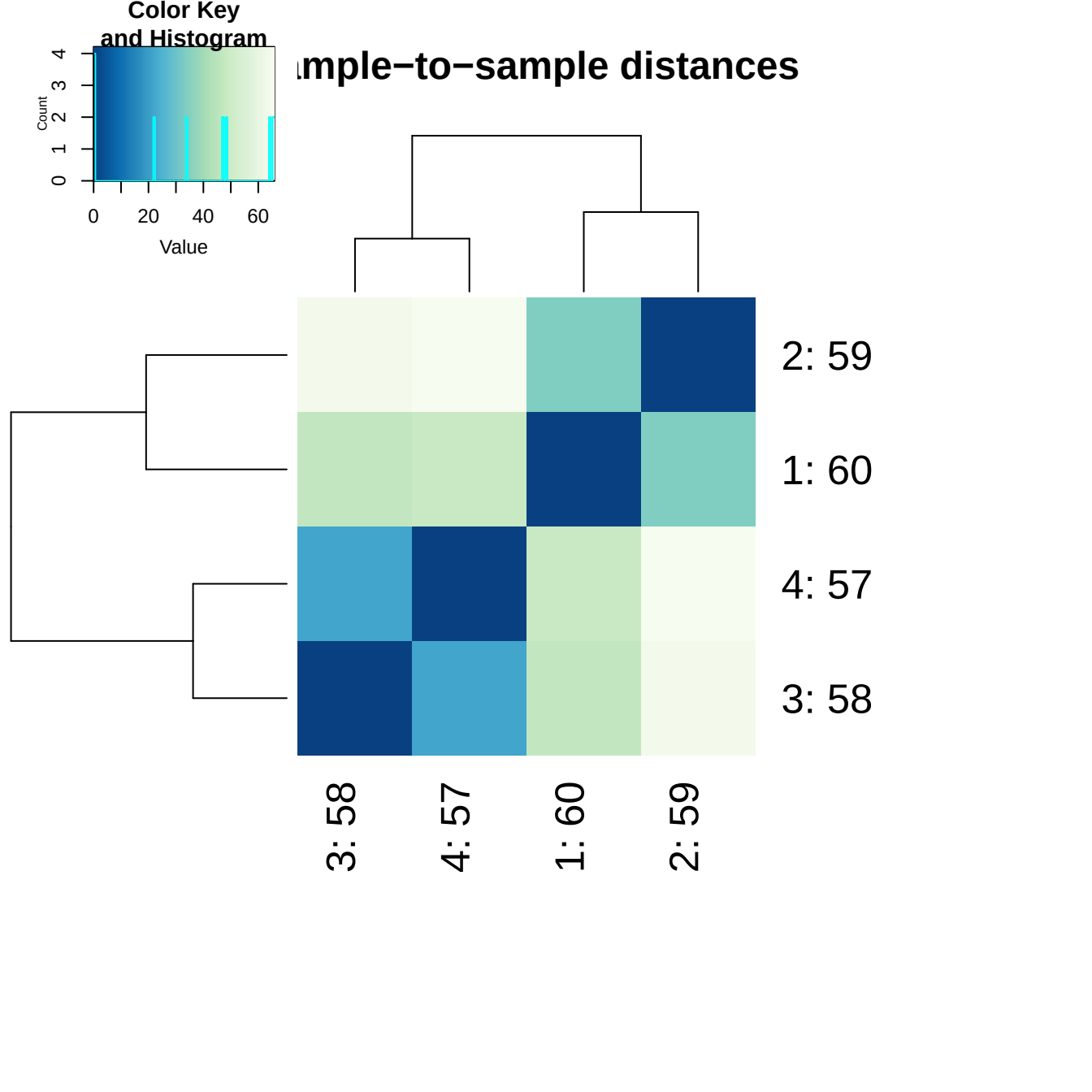
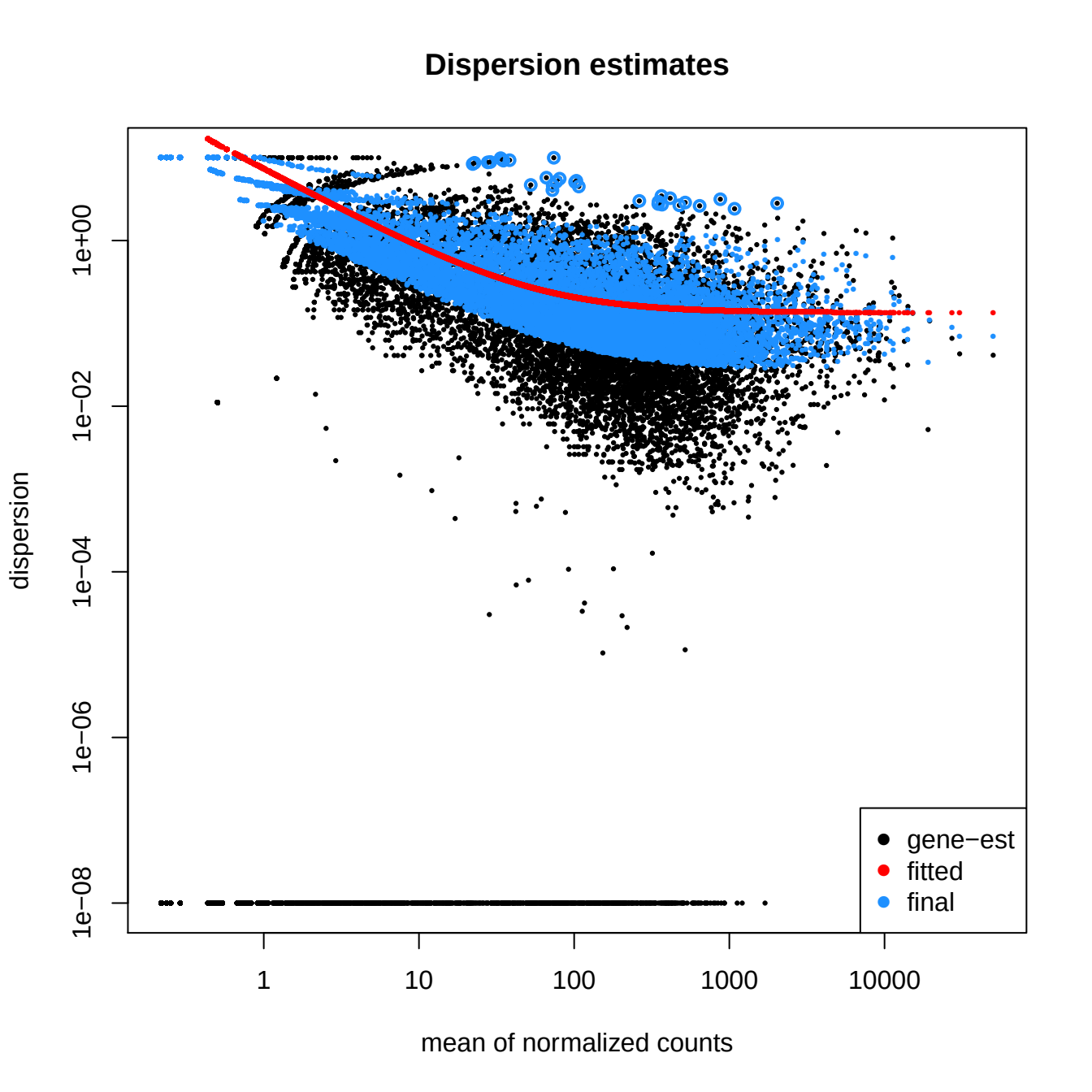
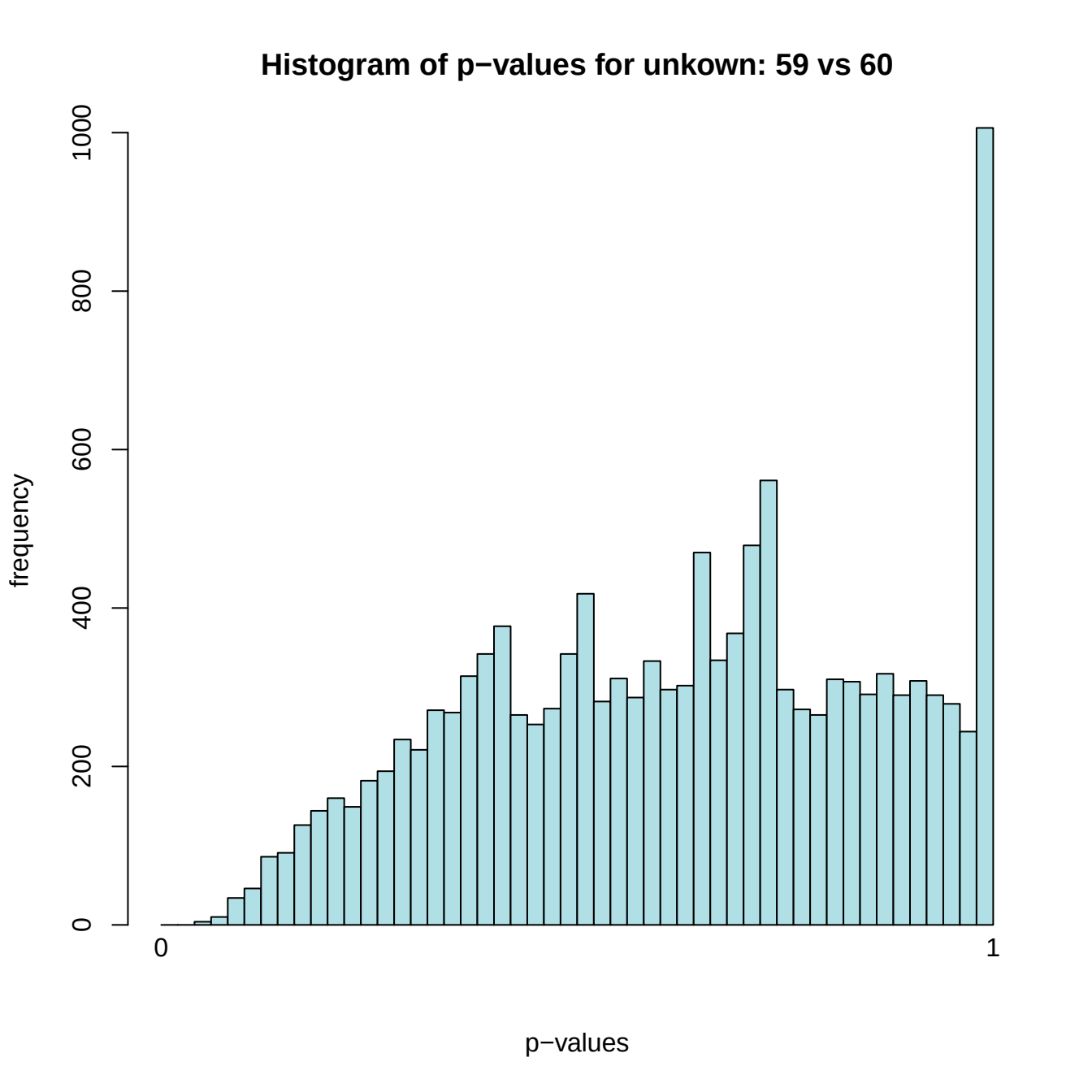
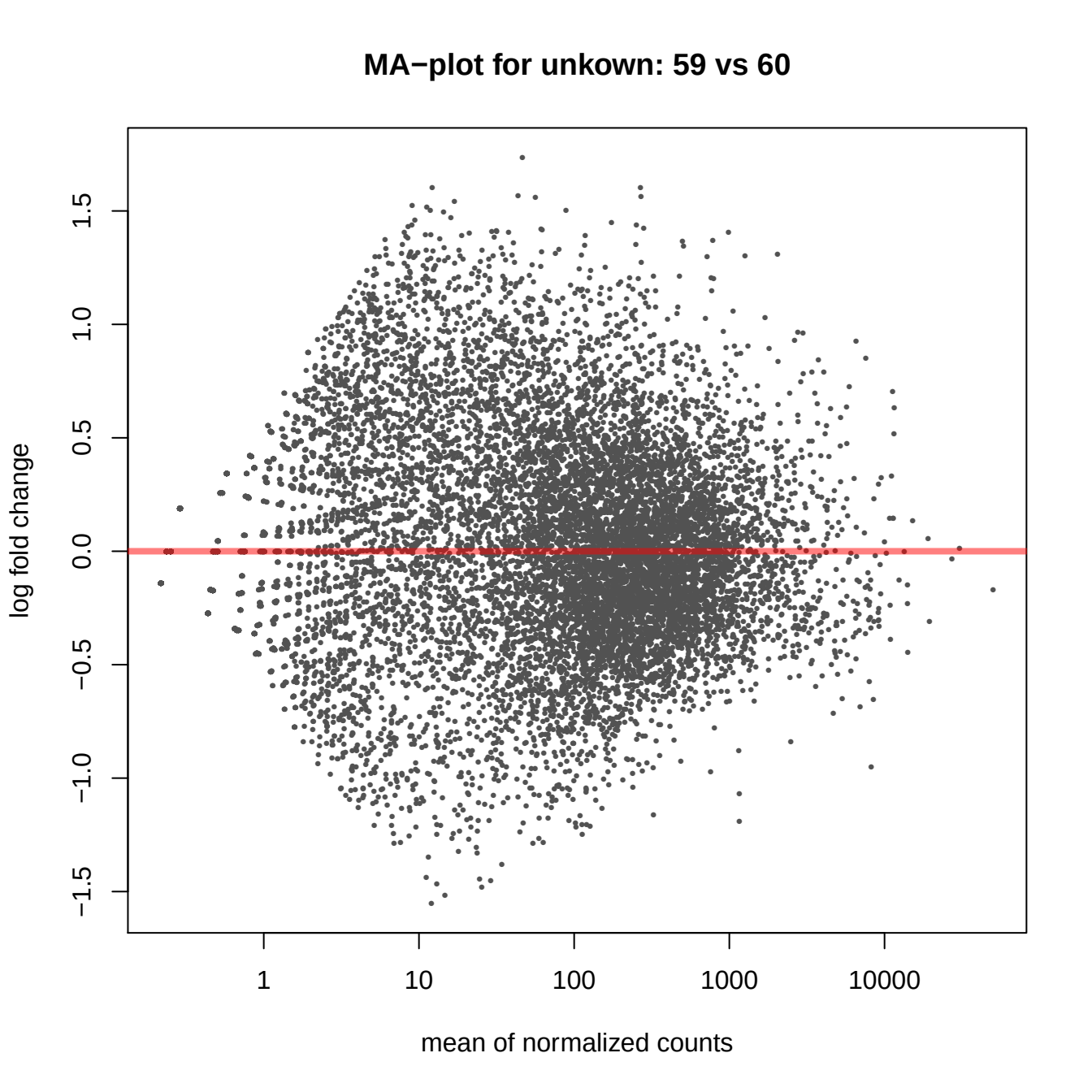
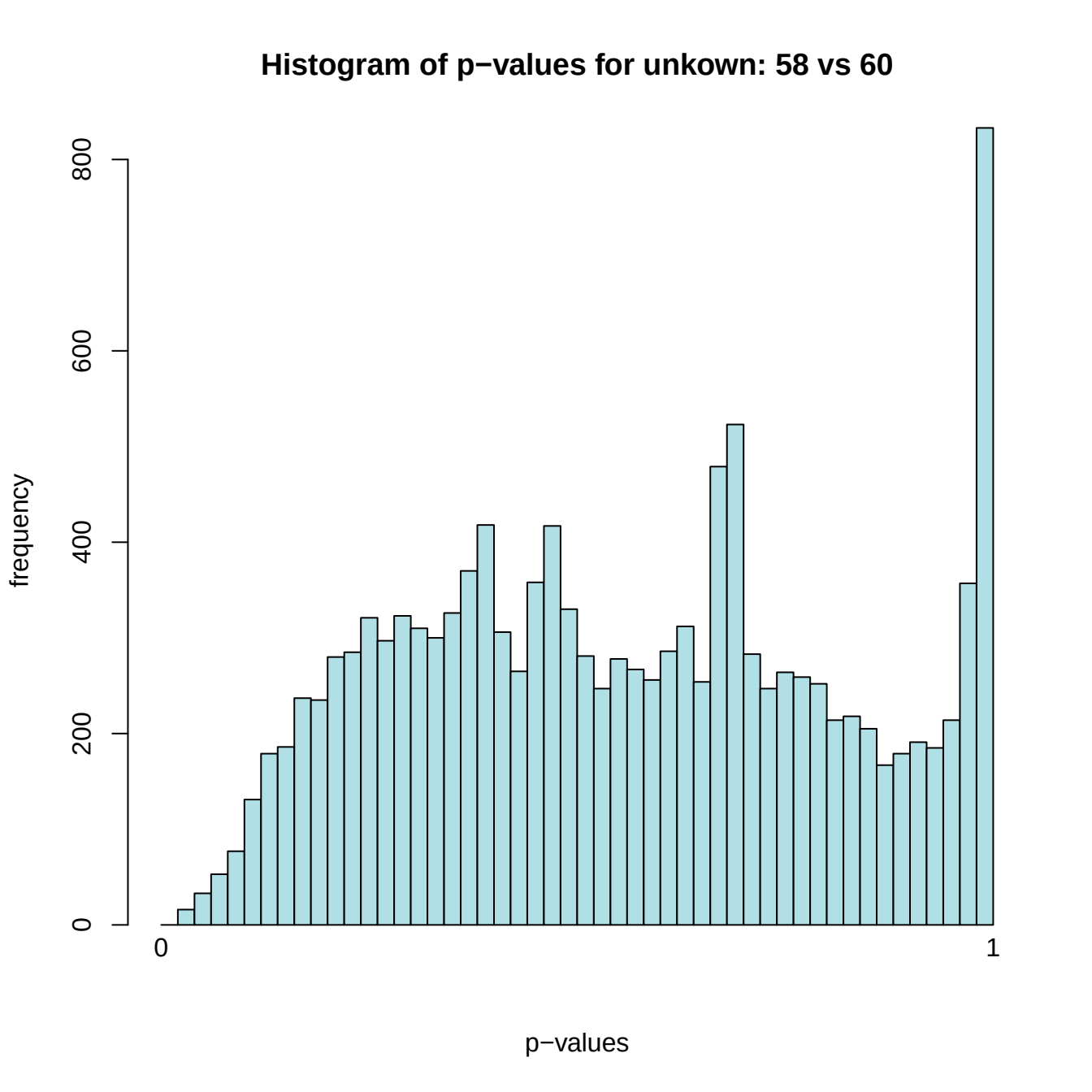

7.5
5.0
2.5
0.0
−2.5
−5.0
PC2
−20
−10
0
10
20
PC1
1:60
2:59
3:58
4:57
group
60
59
58
57

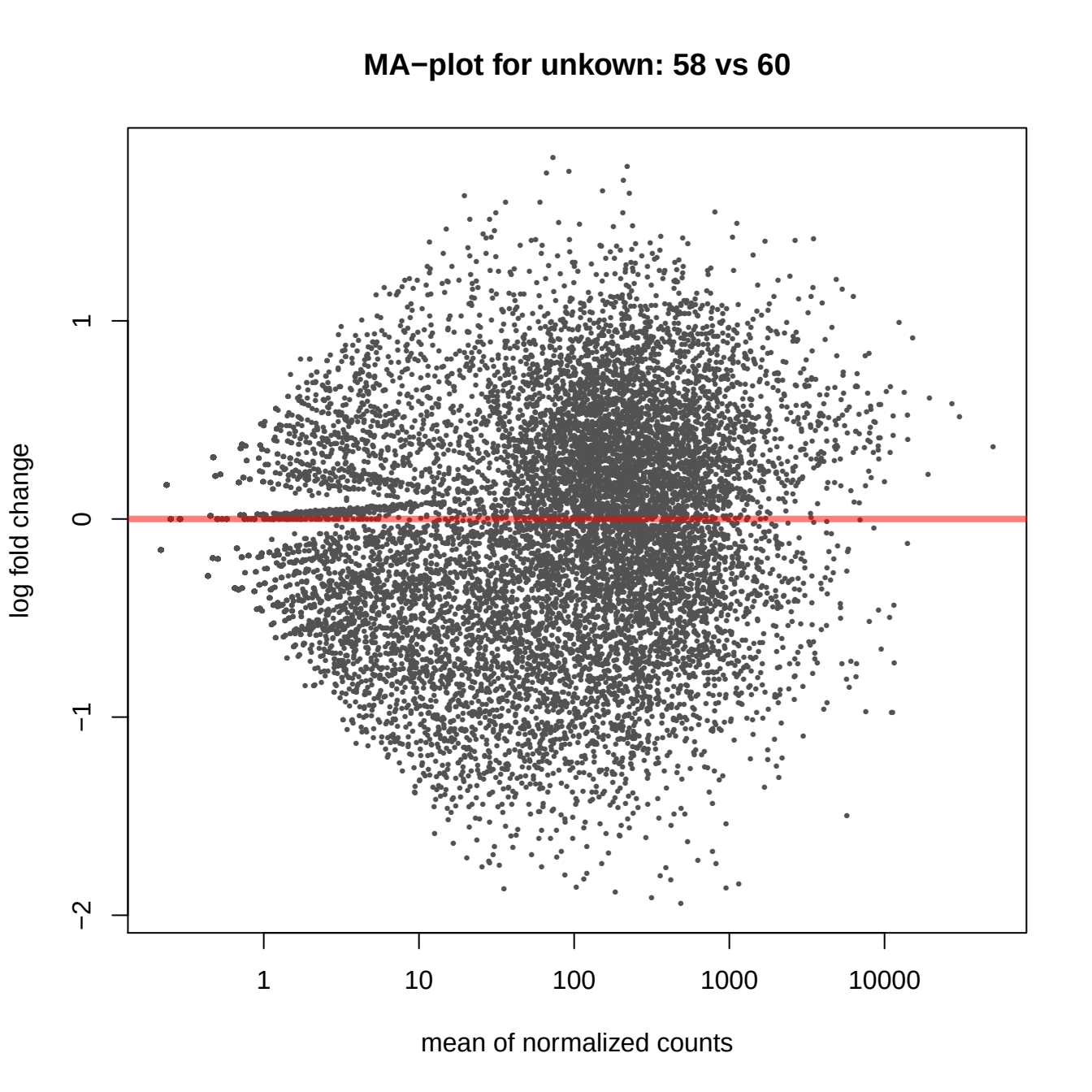

Color Key
and Histogram
Count
0
1
2
3
4
0
20
40
60
Value
ımple−to−sample distances
2: 59
1: 60
4: 57
3: 58
3: 58
4: 57
1: 60
2: 59

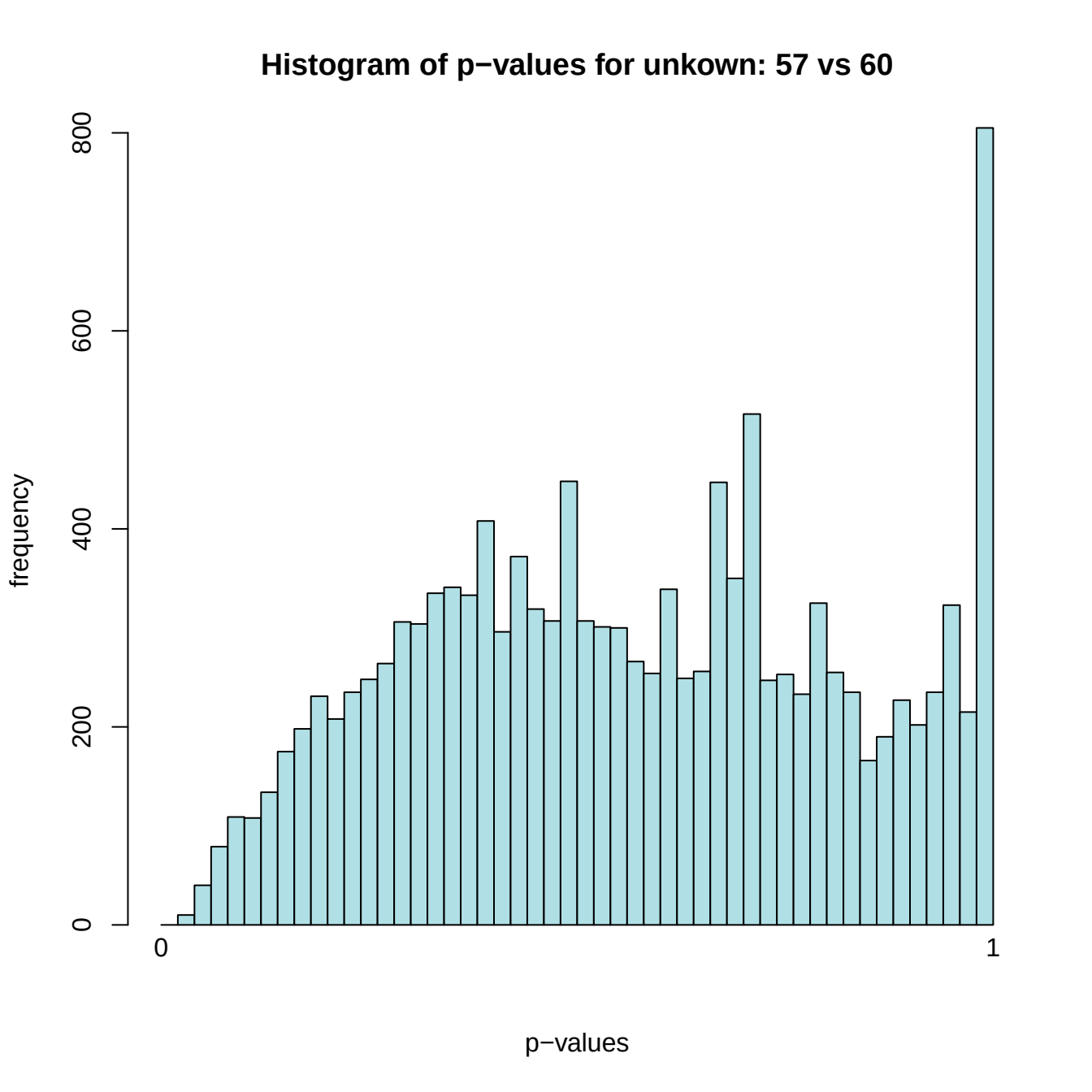

Dispersion estimates
dispersion
1e+00
1e−02
1e−04
1e−06
1e−08
1
10
100
1000
10000
mean of normalized counts
gene−est
fitted
final

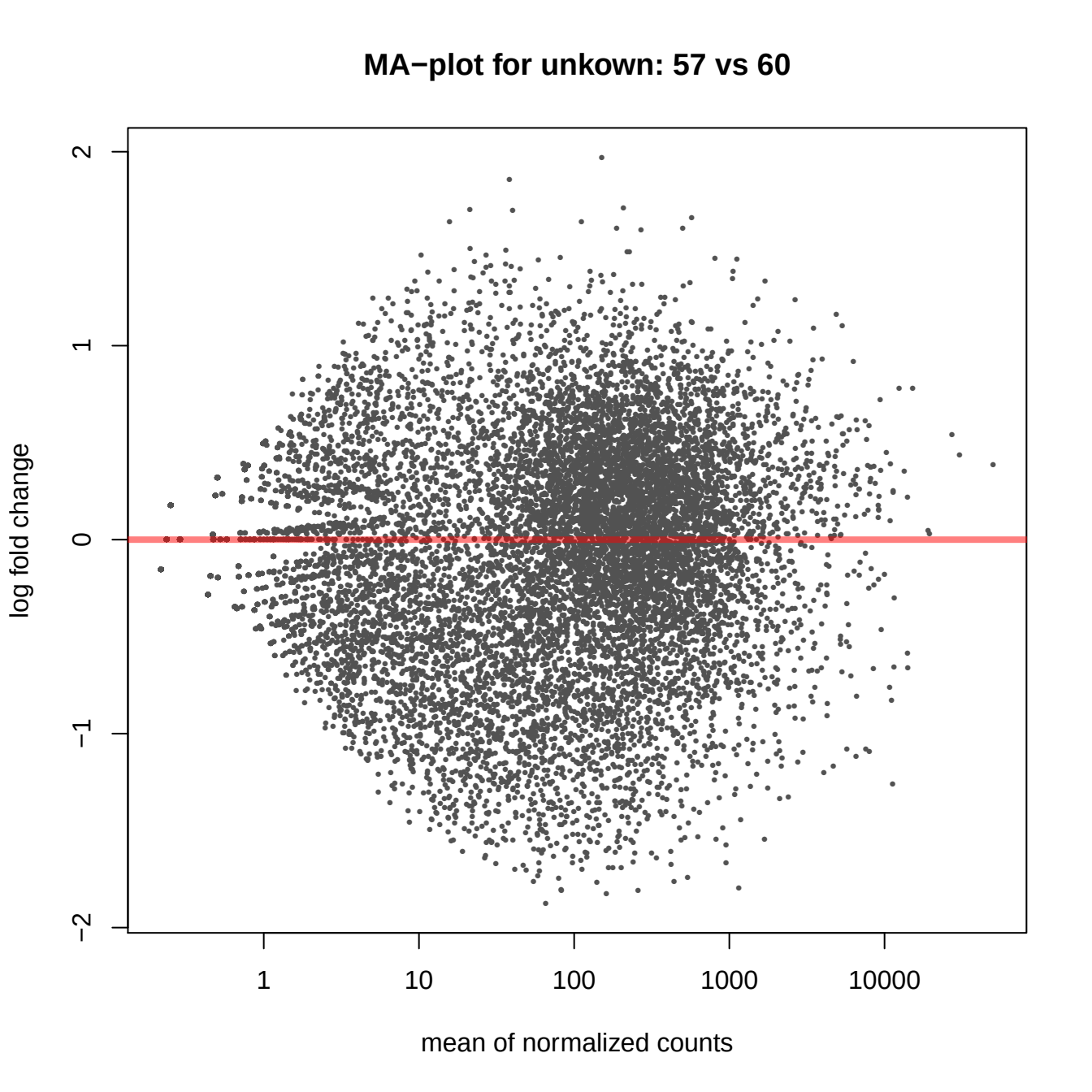

Histogram of p−values for unkown: 59 vs 60
frequency
0
200
400
600
800
1000
0
1
p−values

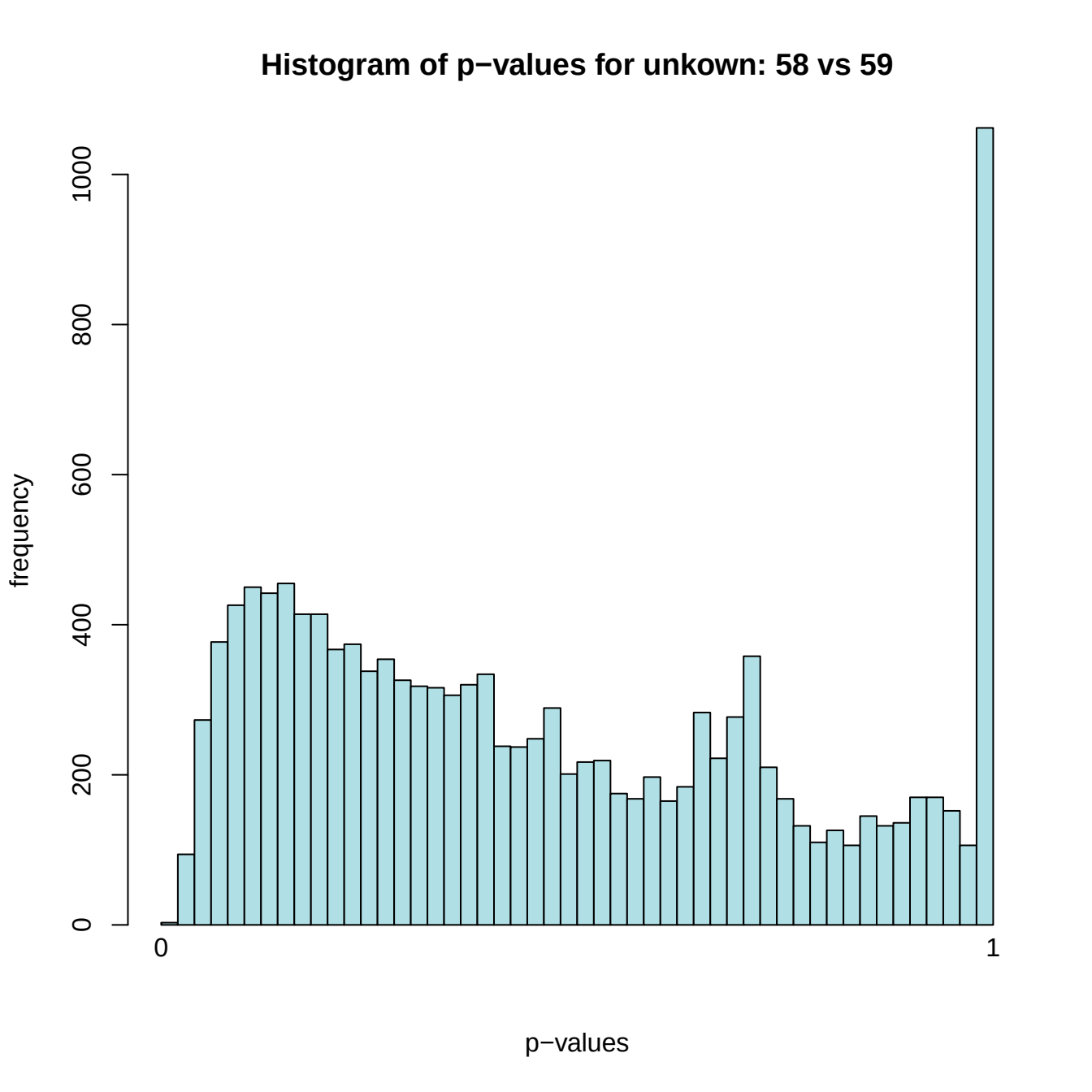

MA−plot for unkown: 59 vs 60
log fold change
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
1
10
100
1000
10000
mean of normalized counts

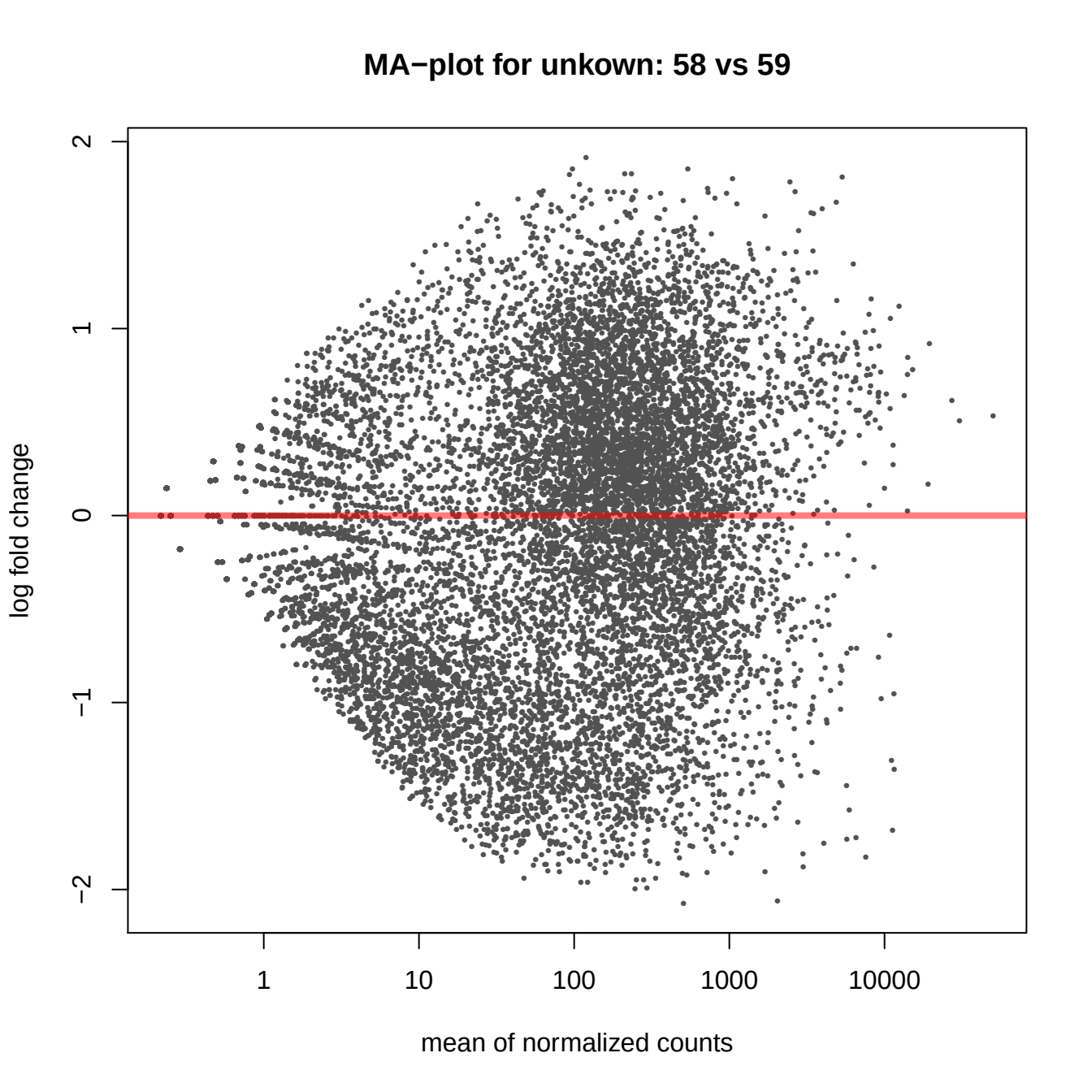

Histogram of p−values for unkown: 58 vs 60
frequency
0
200
400
600
800
0
1
p−values

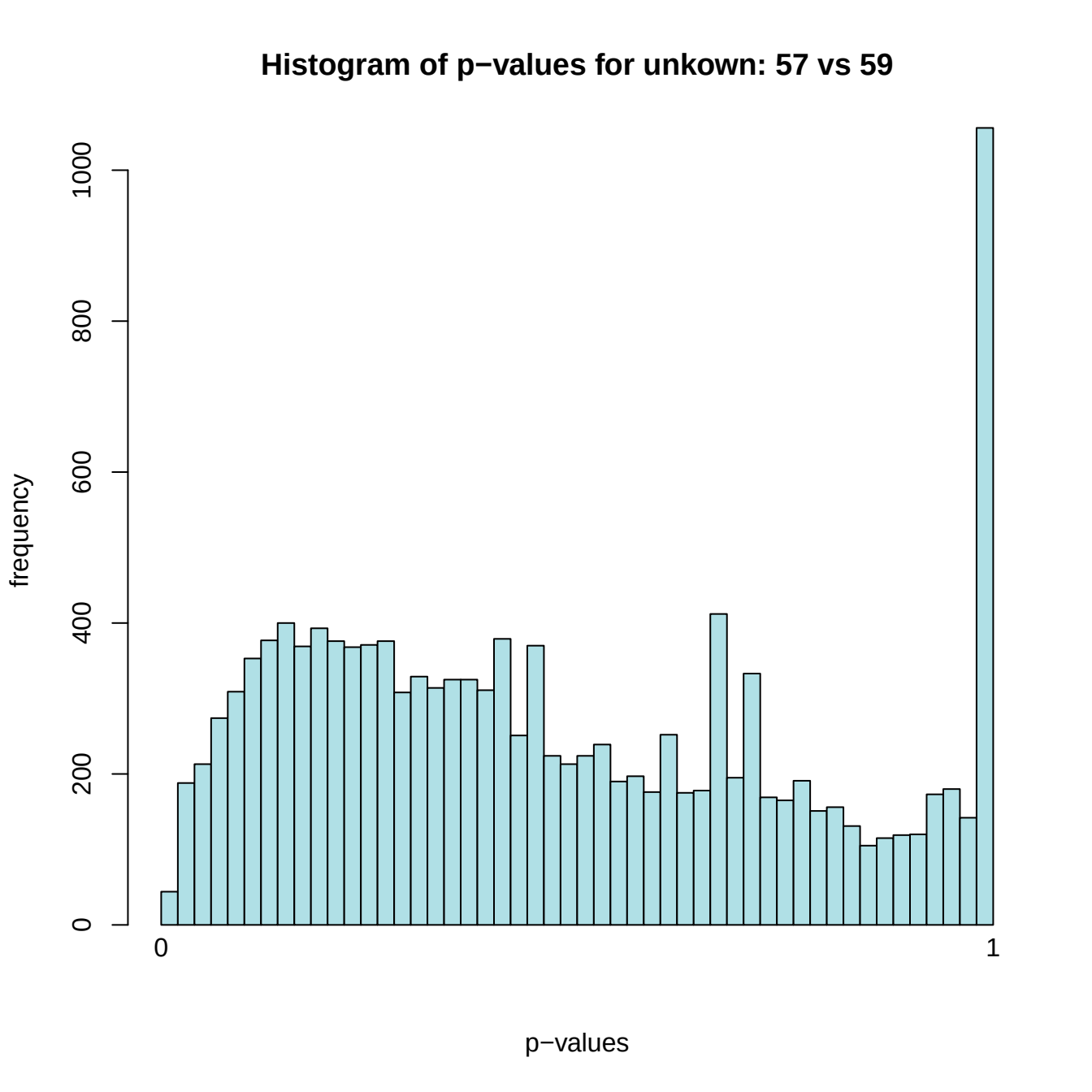

MA−plot for unkown: 58 vs 60
log fold change
1
0
−1
−2
1
10
100
1000
10000
mean of normalized counts

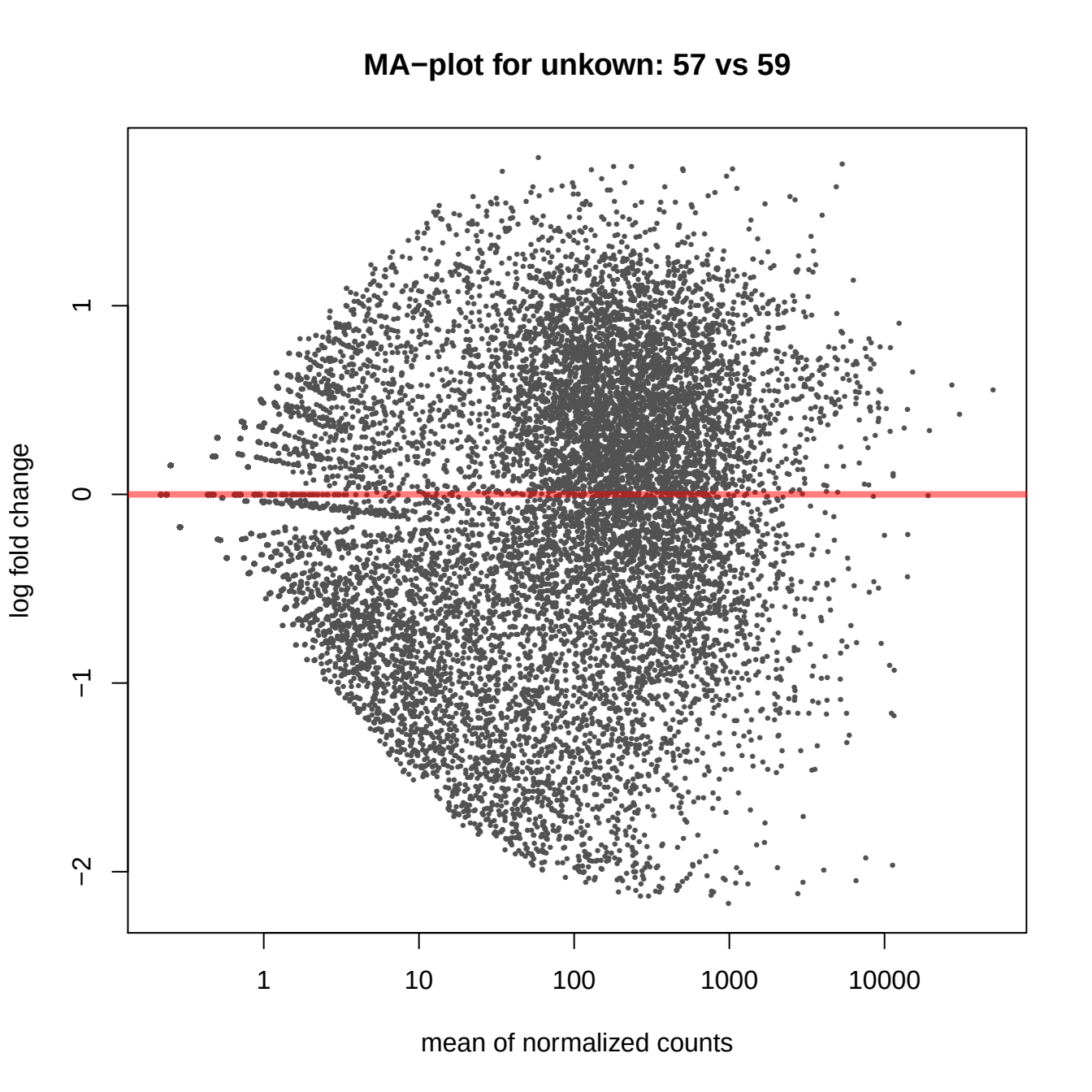

Histogram of p−values for unkown: 57 vs 60
frequency
0
200
400
600
800
0
1
p−values

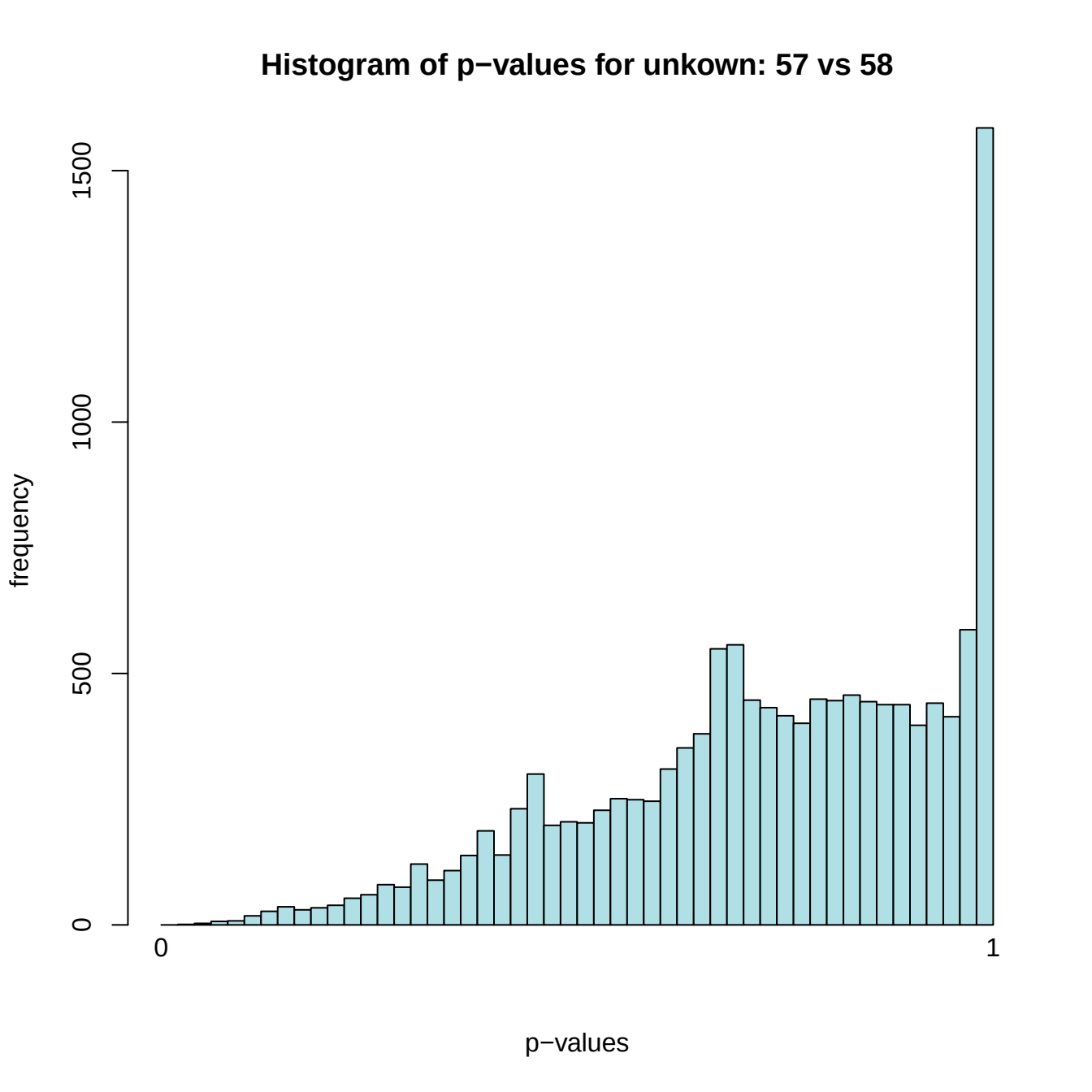

MA−plot for unkown: 57 vs 60
log fold change
2
1
0
−1
−2
1
10
100
1000
10000
mean of normalized counts

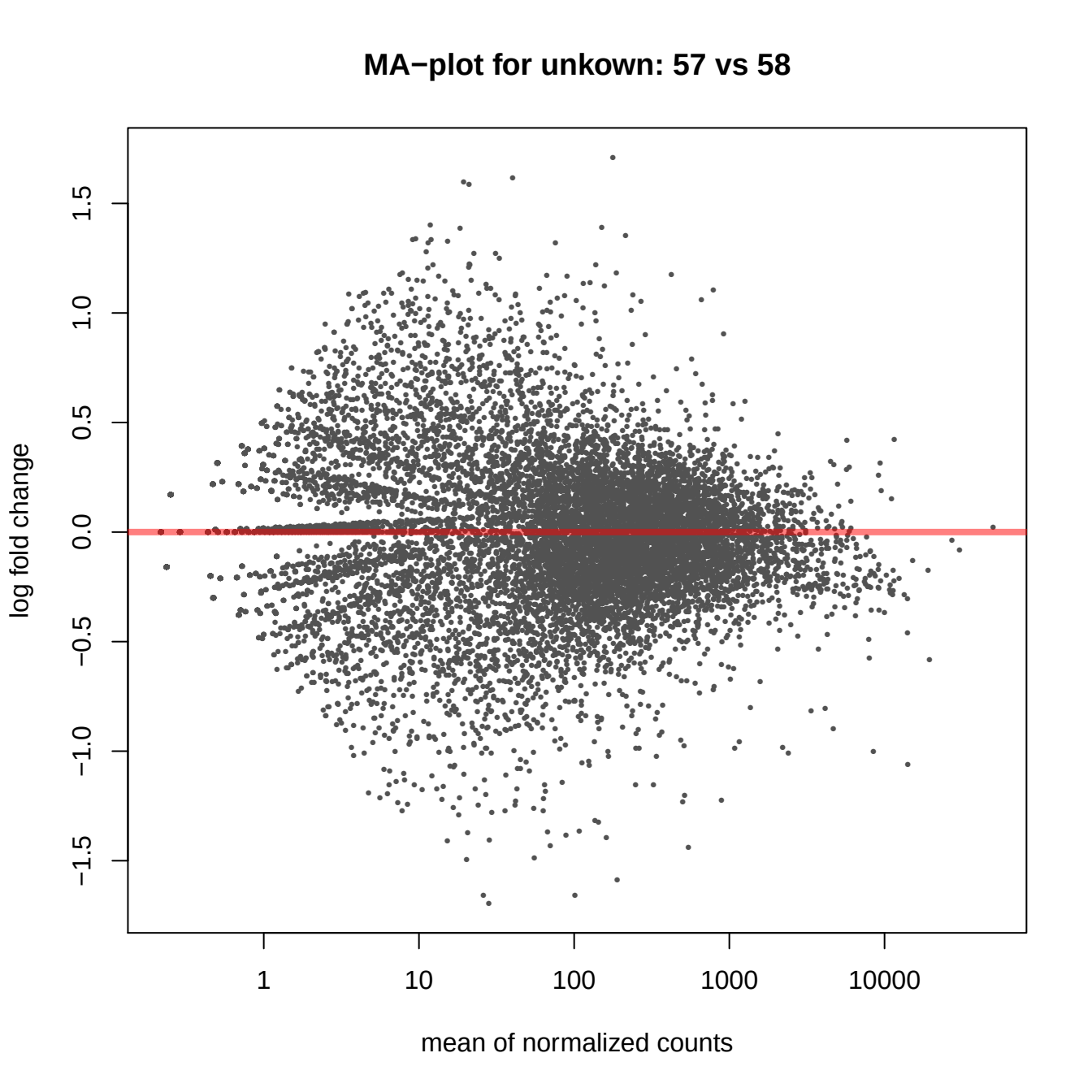

Histogram of p−values for unkown: 58 vs 59
frequency
0
200
400
600
800
1000
0
1
p−values


MA−plot for unkown: 58 vs 59
log fold change
2
1
0
−1
−2
1
10
100
1000
10000
mean of normalized counts


Histogram of p−values for unkown: 57 vs 59
frequency
0
200
400
600
800
1000
0
1
p−values


MA−plot for unkown: 57 vs 59
log fold change
1
0
−1
−2
1
10
100
1000
10000
mean of normalized counts


Histogram of p−values for unkown: 57 vs 58
frequency
0
500
1000
1500
0
1
p−values


MA−plot for unkown: 57 vs 58
log fold change
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
1
10
100
1000
10000
mean of normalized counts