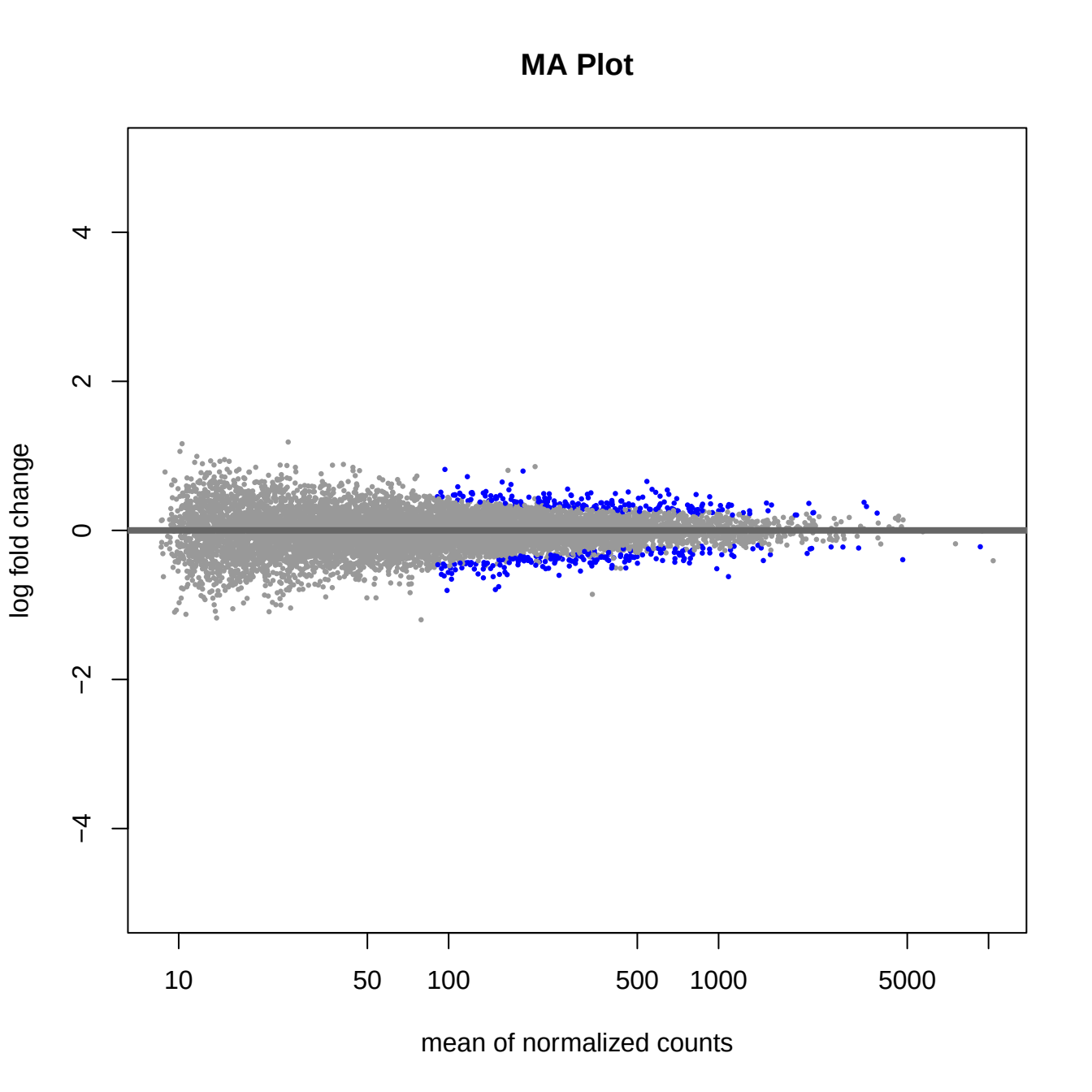
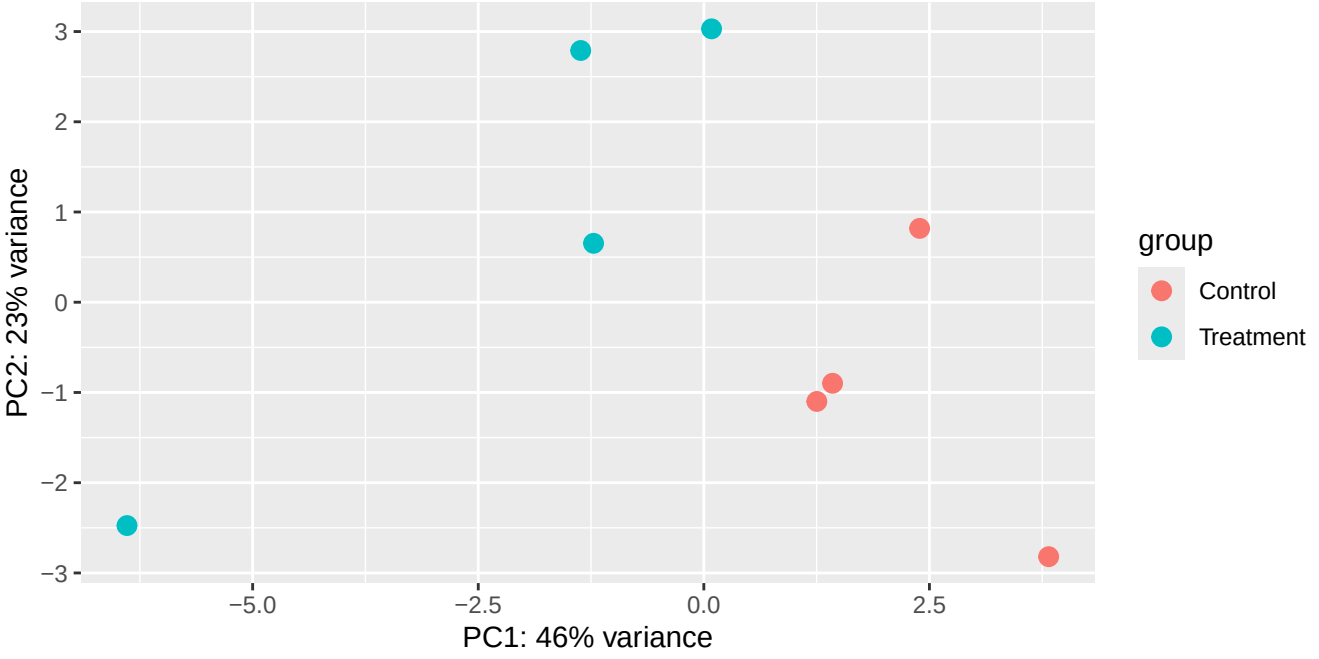
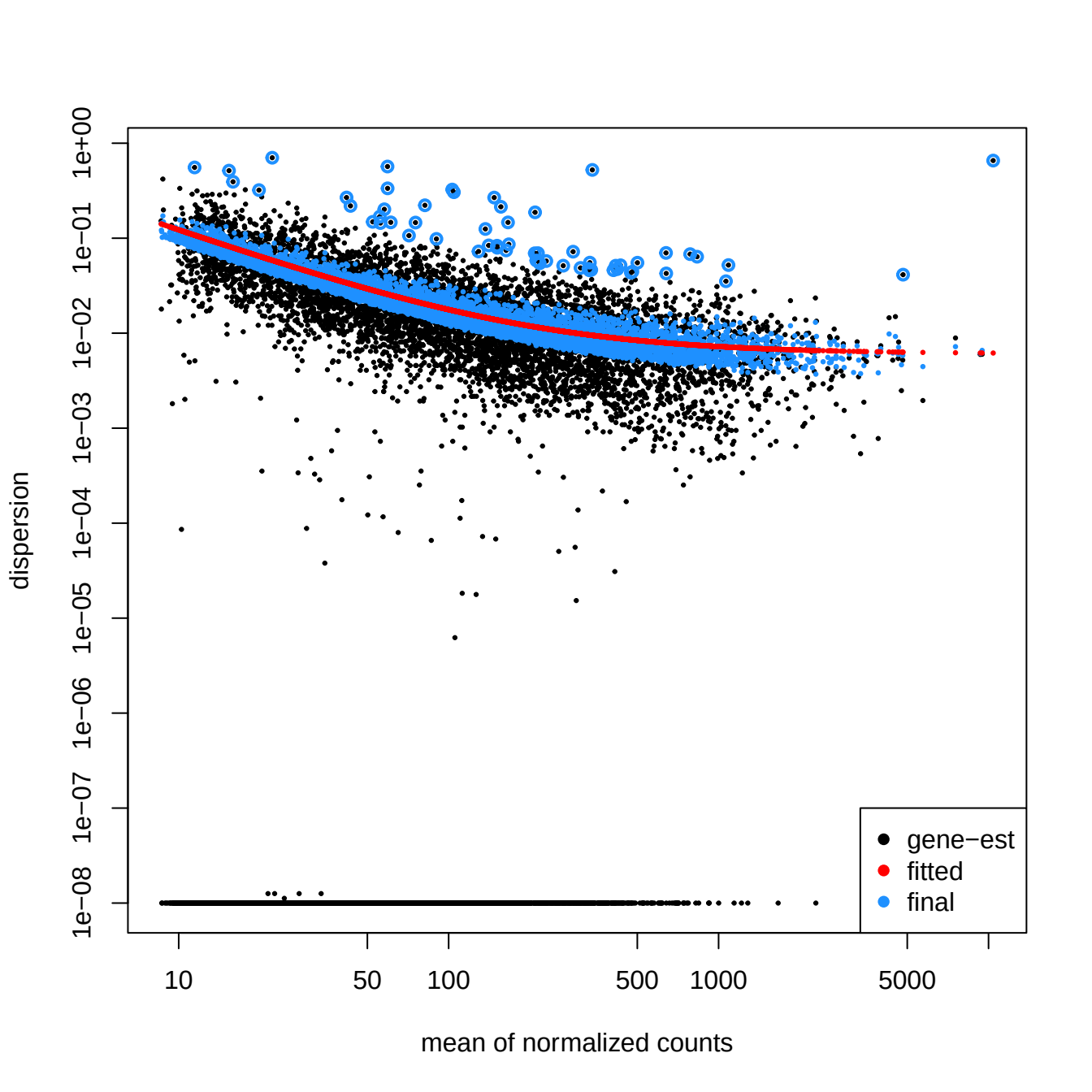
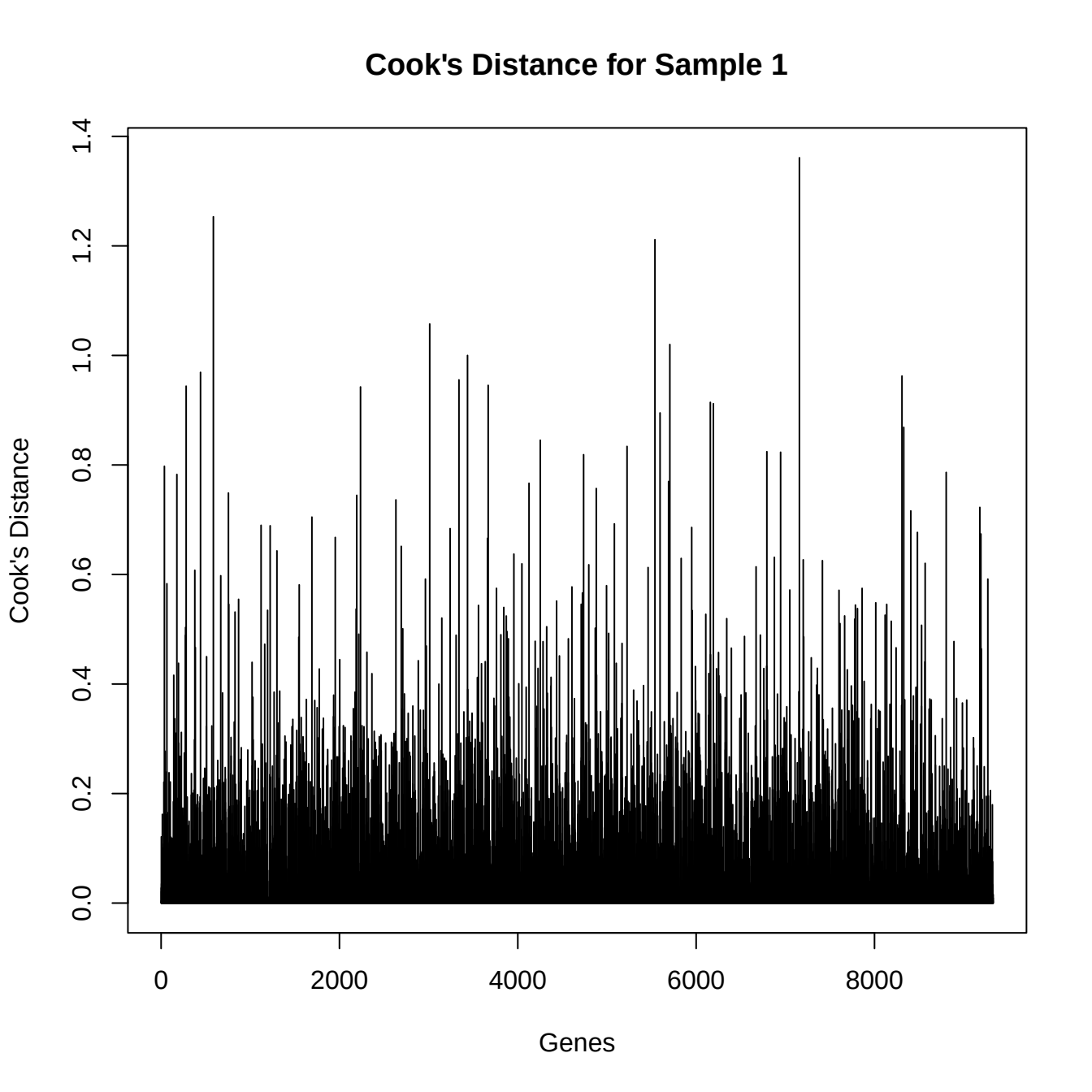
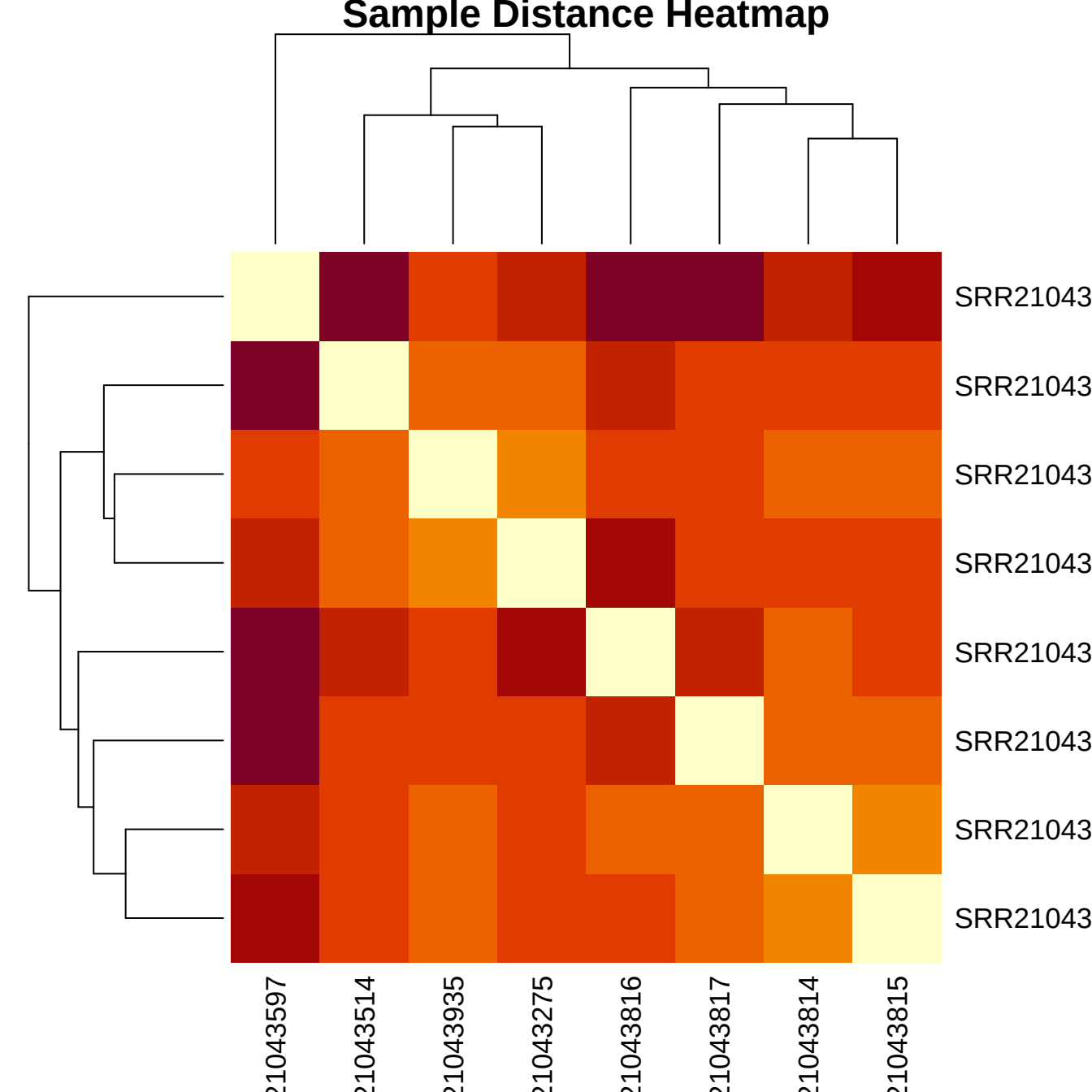

MA Plot
log fold change
4
2
0
−2
−4
10
50
100
500
1000
5000
mean of normalized counts


3
2
1
0
−1
−2
−3
PC2: 23% variance
−5.0
−2.5
0.0
2.5
PC1: 46% variance
group
Control
Treatment


dispersion
1e+00
1e−01
1e−02
1e−03
1e−04
1e−05
1e−06
1e−07
1e−08
10
50
100
500
1000
5000
mean of normalized counts
gene−est
fitted
final


Cook's Distance for Sample 1
Cook's Distance
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
2000
4000
6000
8000
Genes


Sample Distance Heatmap
SRR21043
SRR21043
SRR21043
SRR21043
SRR21043
SRR21043
SRR21043
SRR21043
21043597
21043514
21043935
21043275
21043816
21043817
21043814
21043815