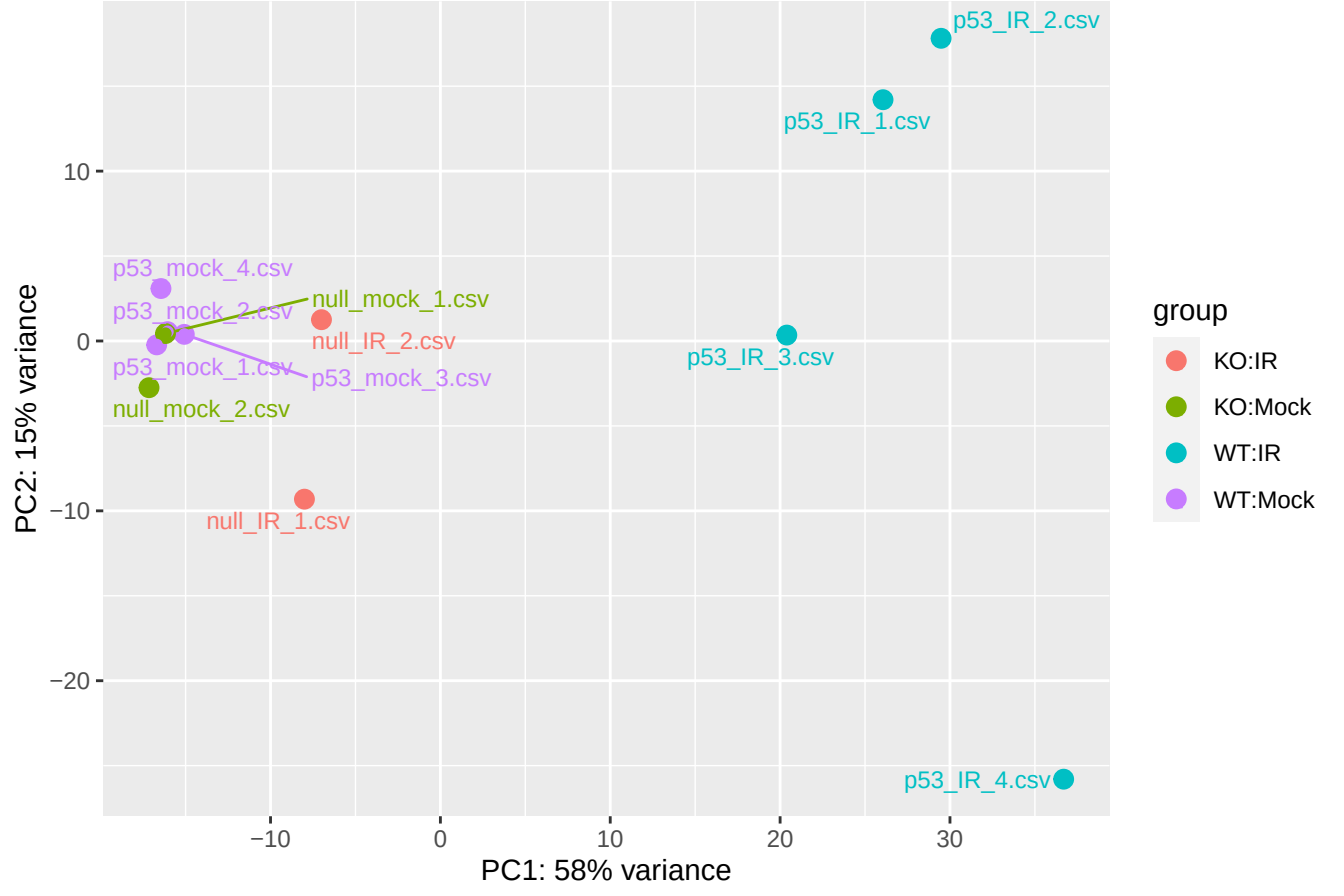
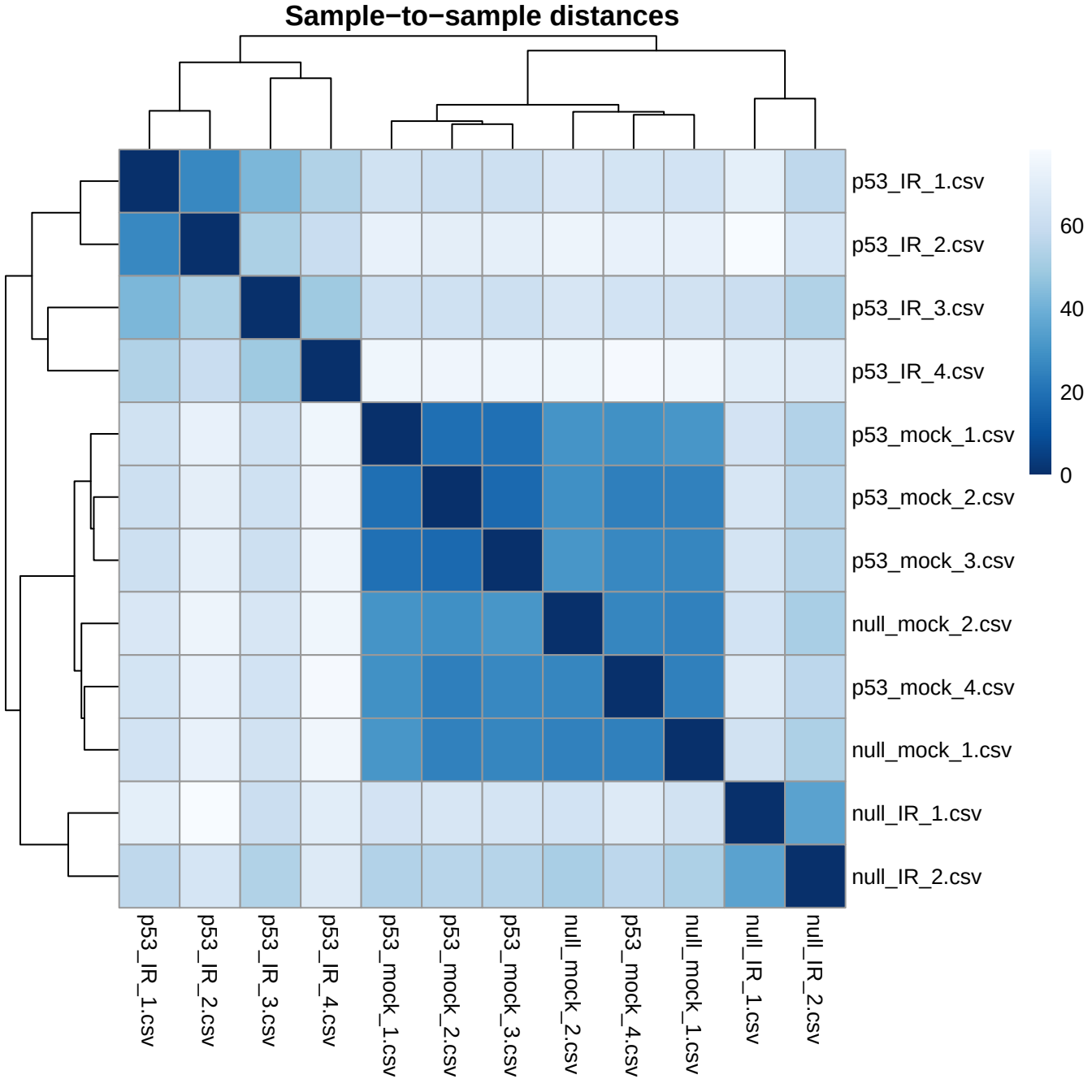
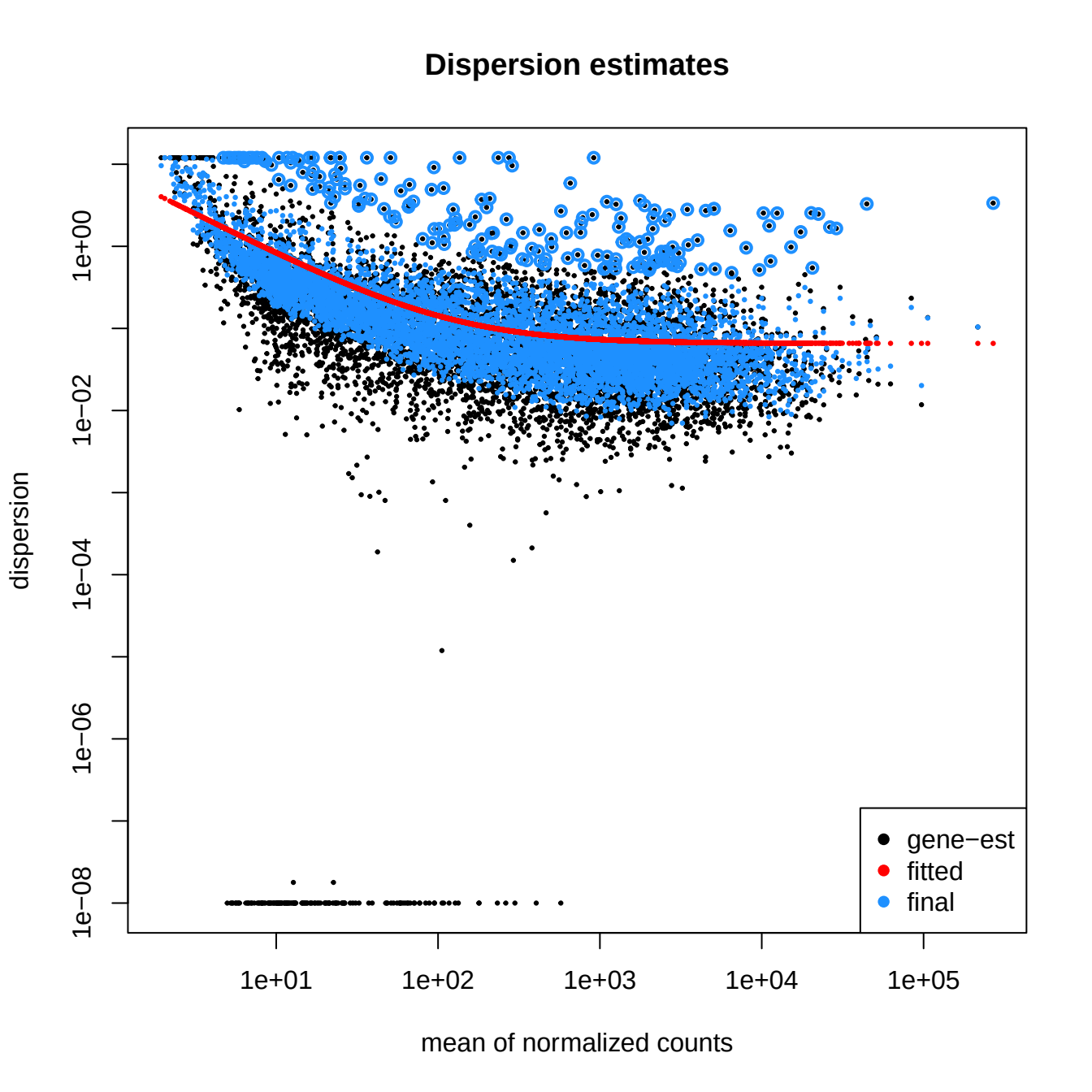
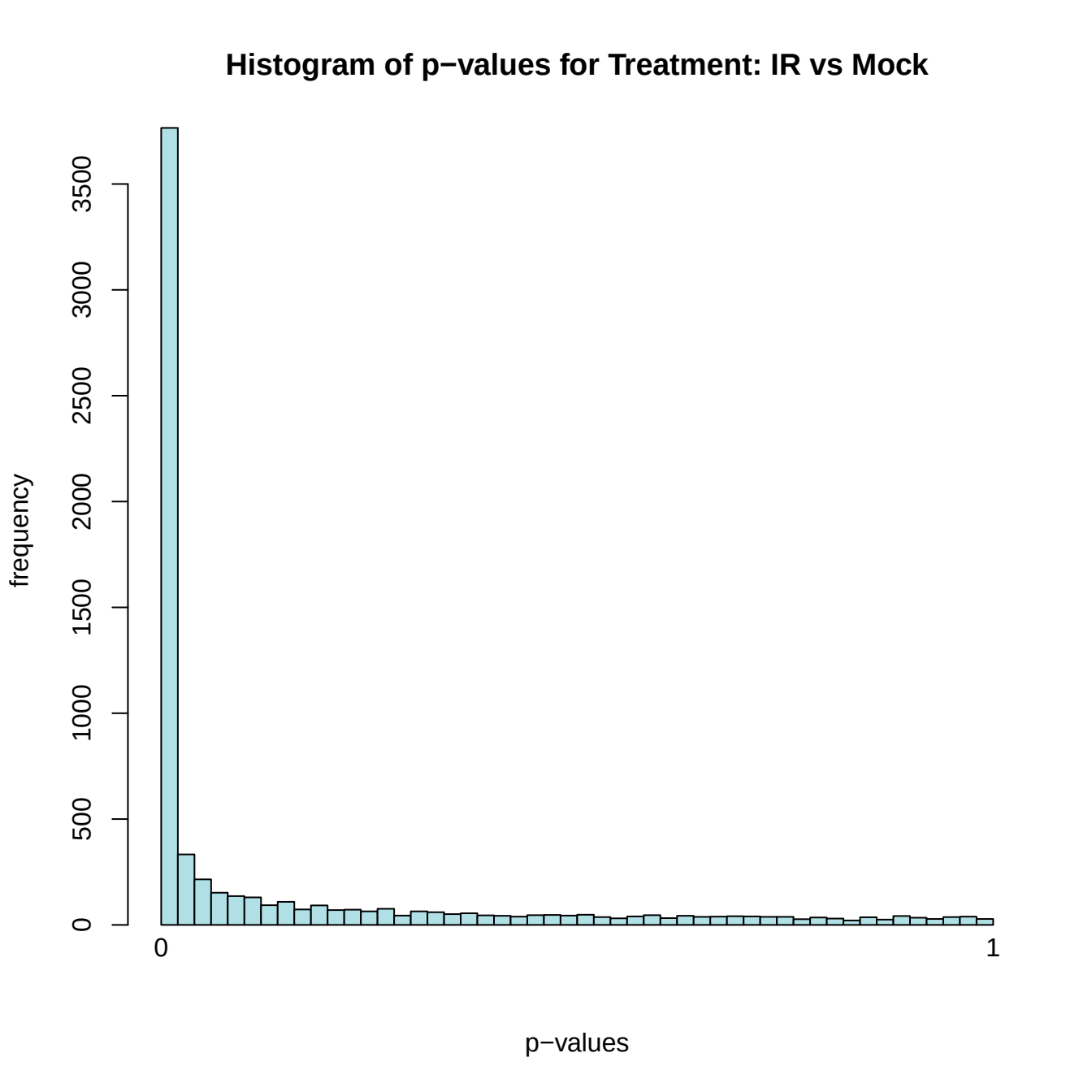
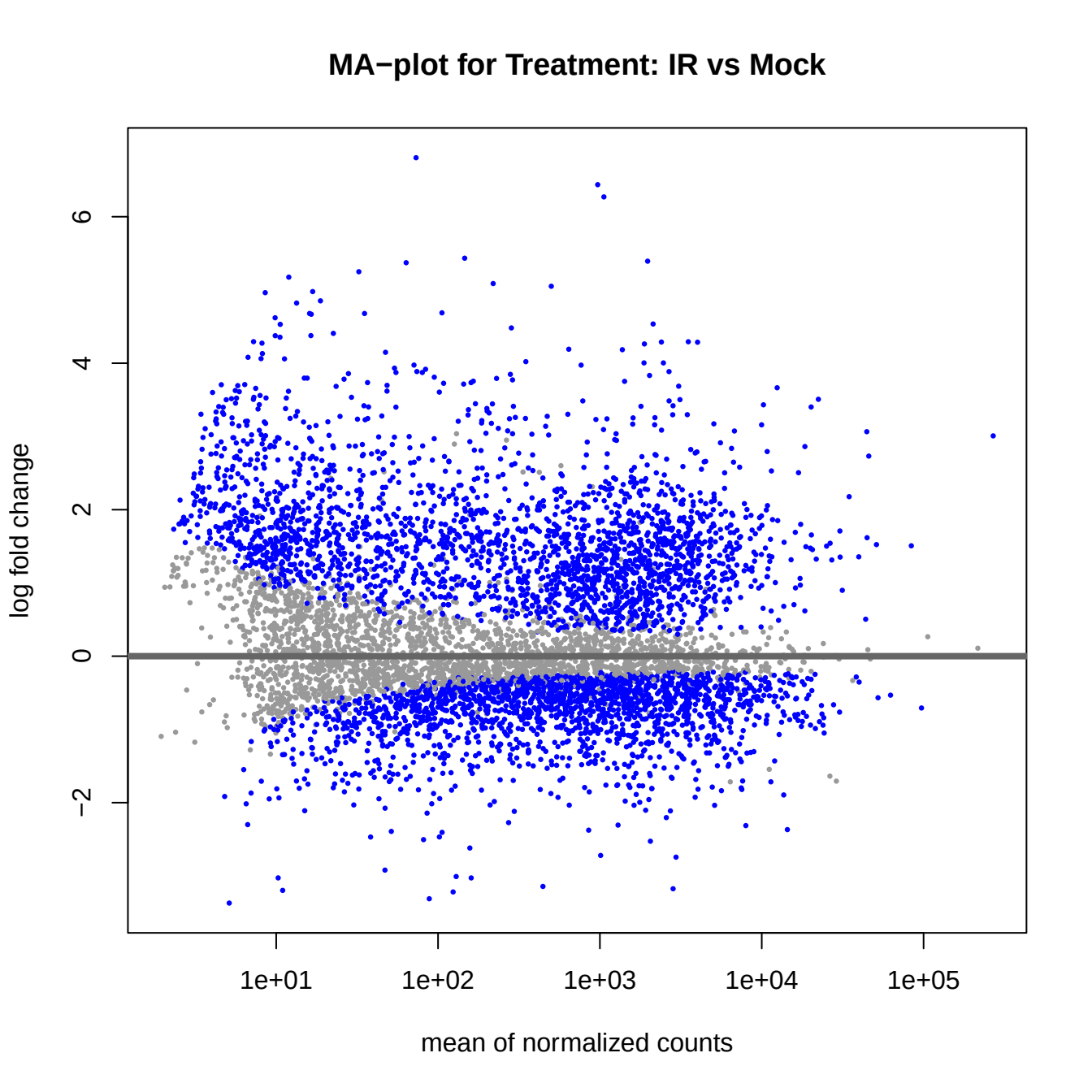

p53_IR_2.csv
p53_IR_1.csv
p53_mock_4.csv
null_mock_1.csv
p53_mock_2.csv
null_IR_2.csv
p53_IR_3.csv
p53_mock_1.csv
p53_mock_3.csv
null_mock_2.csv
null_IR_1.csv
p53_IR_4.csv
10
0
−10
−20
−10
0
10
20
30
PC2: 15% variance
PC1: 58% variance
group
KO:IR
KO:Mock
WT:IR
WT:Mock


Sample−to−sample distances
p53_IR_1.csv
p53_IR_2.csv
p53_IR_3.csv
p53_IR_4.csv
p53_mock_1.csv
p53_mock_2.csv
p53_mock_3.csv
null_mock_2.csv
p53_mock_4.csv
null_mock_1.csv
null_IR_1.csv
null_IR_2.csv
60
40
20
0


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


Histogram of p−values for Treatment: IR vs Mock
frequency
0
500
1000
1500
2000
2500
3000
3500
0
1
p−values


MA−plot for Treatment: IR vs Mock
log fold change
6
4
2
0
−2
1e+01
1e+02
1e+03
1e+04
1e+05
mean of normalized counts