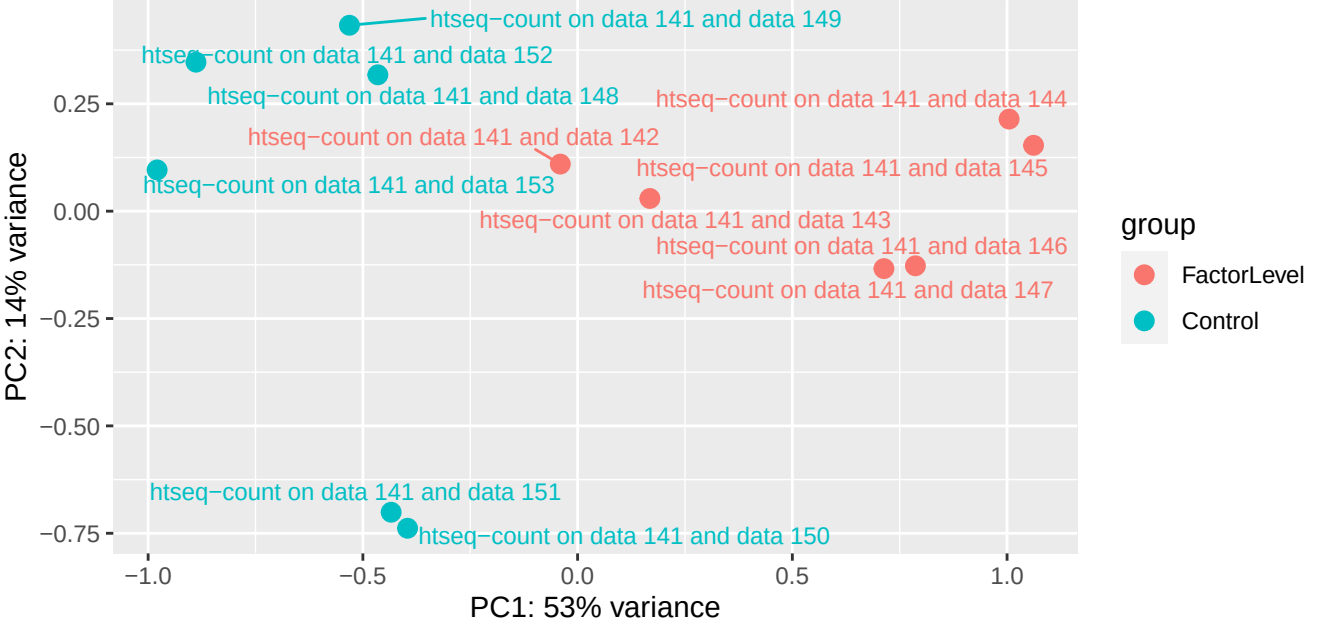
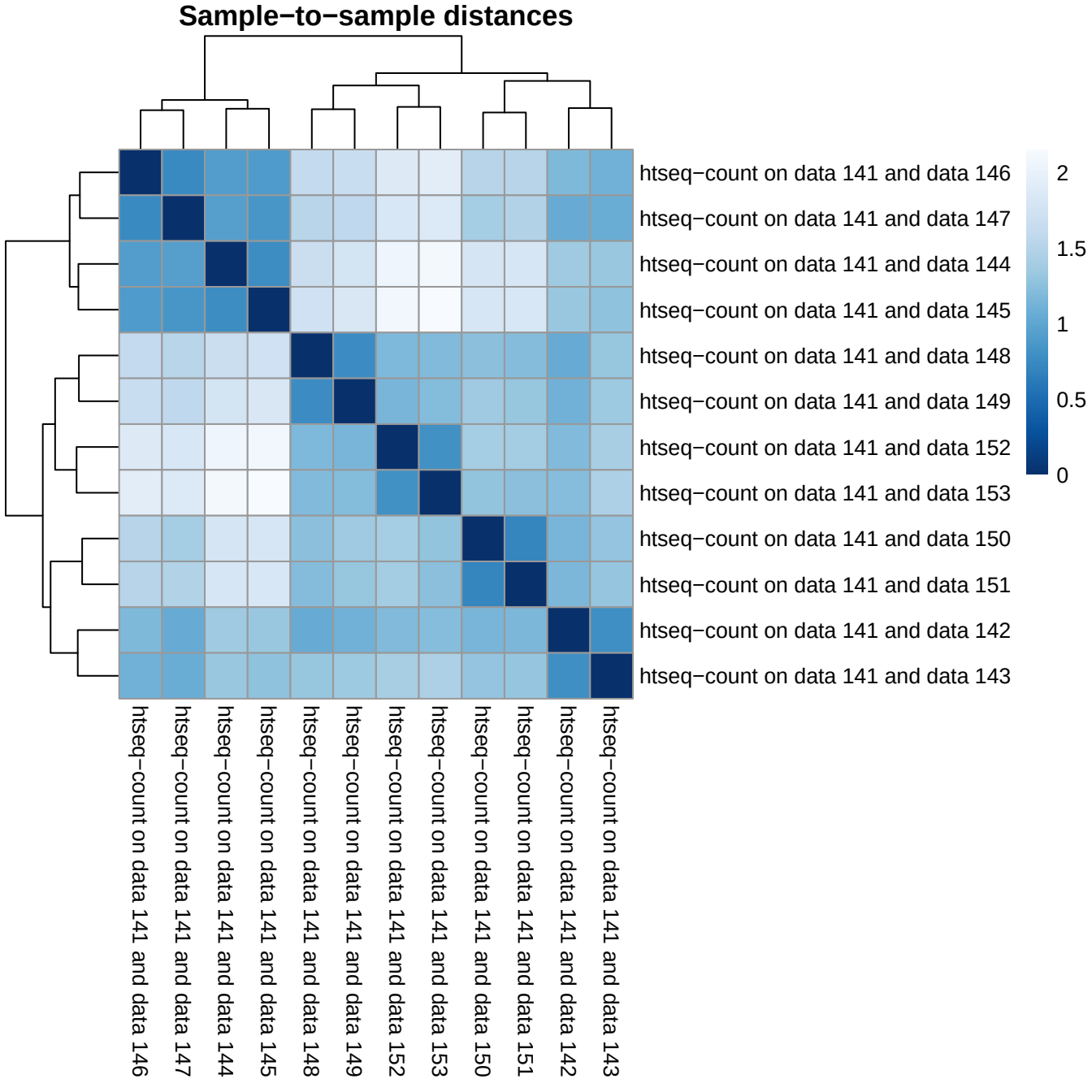
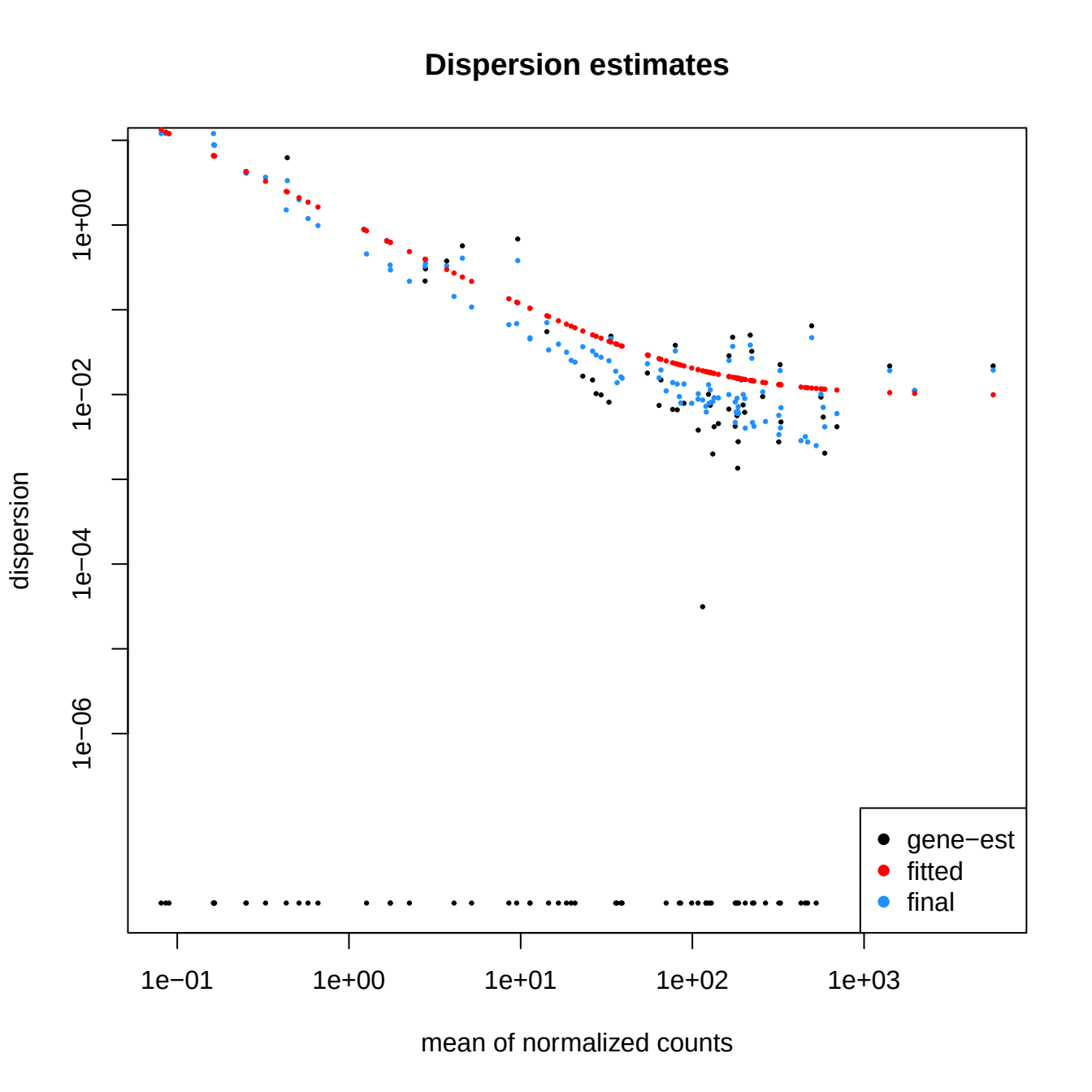
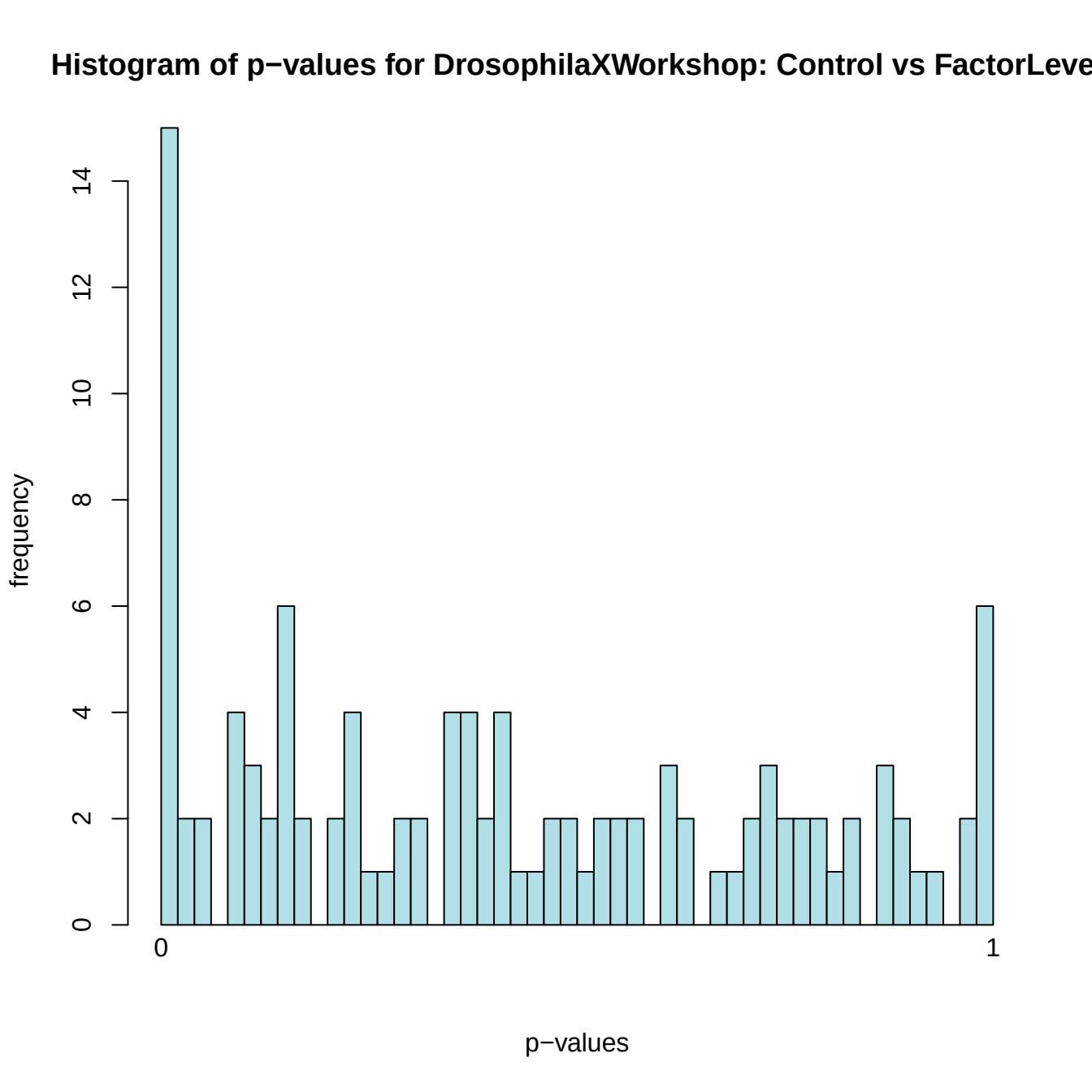
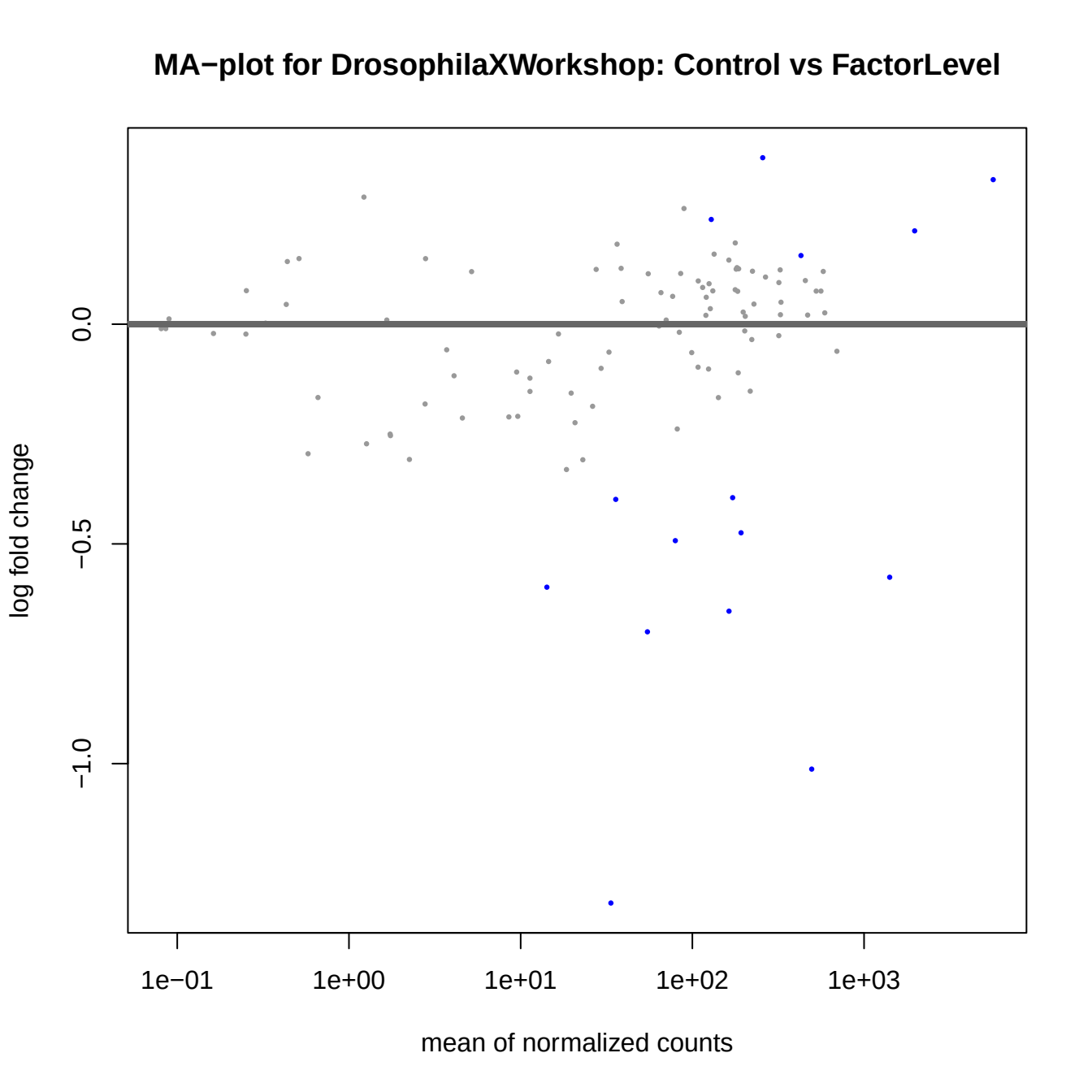

htseq−count on data 141 and data 149
htseq−count on data 141 and data 152
htseq−count on data 141 and data 148
htseq−count on data 141 and data 144
htseq−count on data 141 and data 142
htseq−count on data 141 and data 145
htseq−count on data 141 and data 153
htseq−count on data 141 and data 143
htseq−count on data 141 and data 146
htseq−count on data 141 and data 147
htseq−count on data 141 and data 151
htseq−count on data 141 and data 150
0.25
0.00
−0.25
−0.50
−0.75
−1.0
−0.5
0.0
0.5
1.0
PC2: 14% variance
PC1: 53% variance
group
FactorLevel
Control


Sample−to−sample distances
htseq−count on data 141 and data 146
htseq−count on data 141 and data 147
htseq−count on data 141 and data 144
htseq−count on data 141 and data 145
htseq−count on data 141 and data 148
htseq−count on data 141 and data 149
htseq−count on data 141 and data 152
htseq−count on data 141 and data 153
htseq−count on data 141 and data 150
htseq−count on data 141 and data 151
htseq−count on data 141 and data 142
htseq−count on data 141 and data 143
2
1.5
1
0.5
0


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


Histogram of p−values for DrosophilaXWorkshop: Control vs FactorLeve
frequency
0
2
4
6
8
10
12
14
0
1
p−values


MA−plot for DrosophilaXWorkshop: Control vs FactorLevel
log fold change
0.0
−0.5
−1.0
1e−01
1e+00
1e+01
1e+02
1e+03
mean of normalized counts