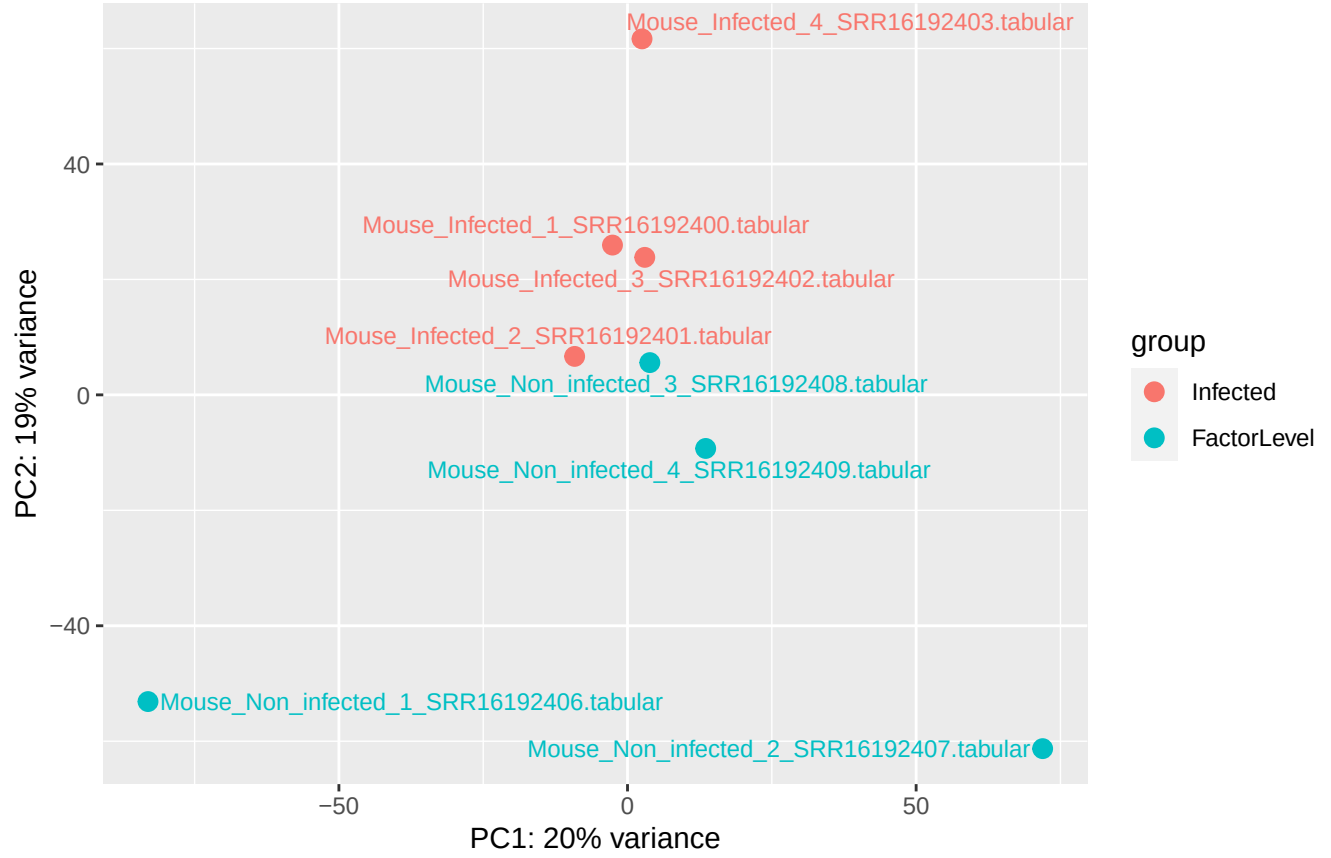
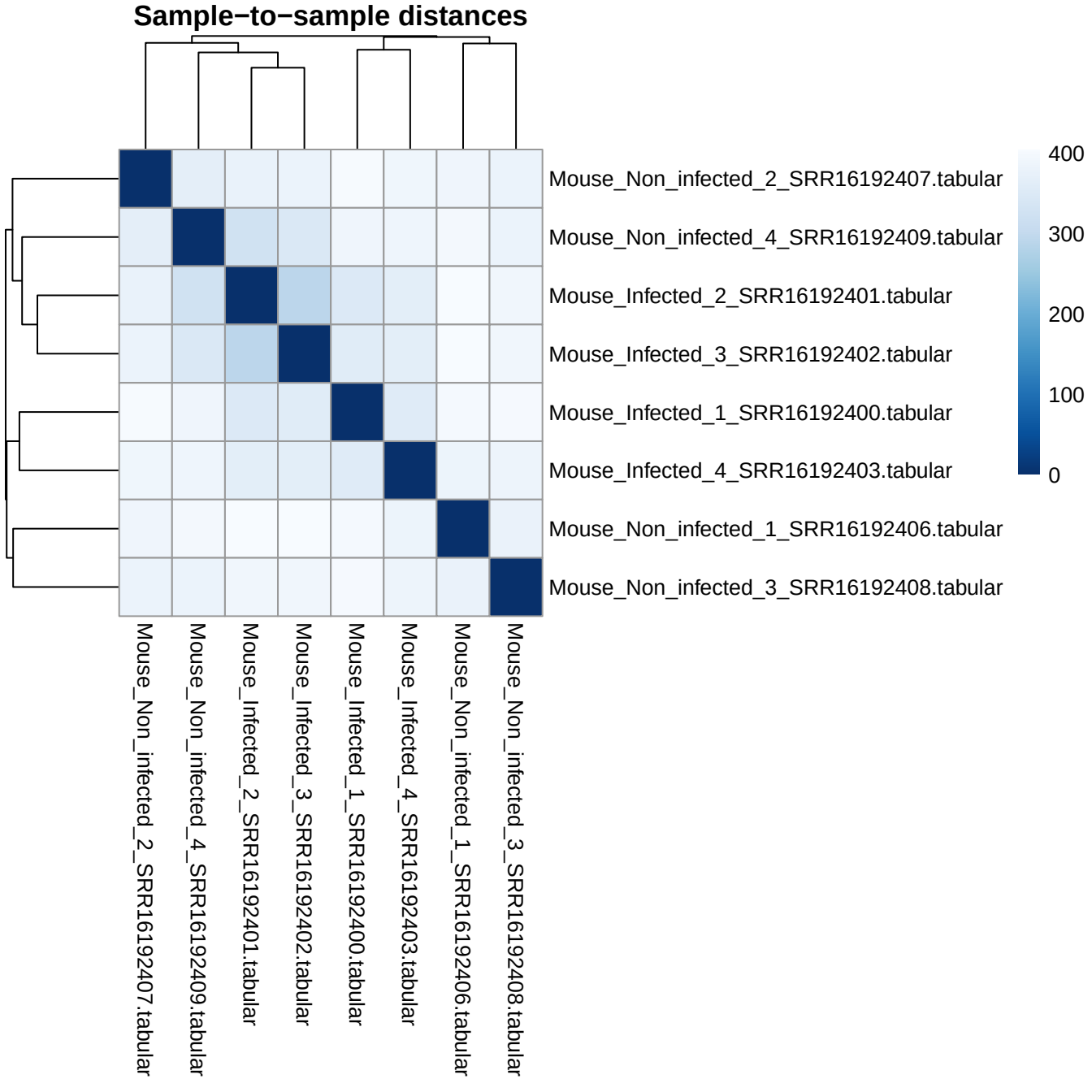
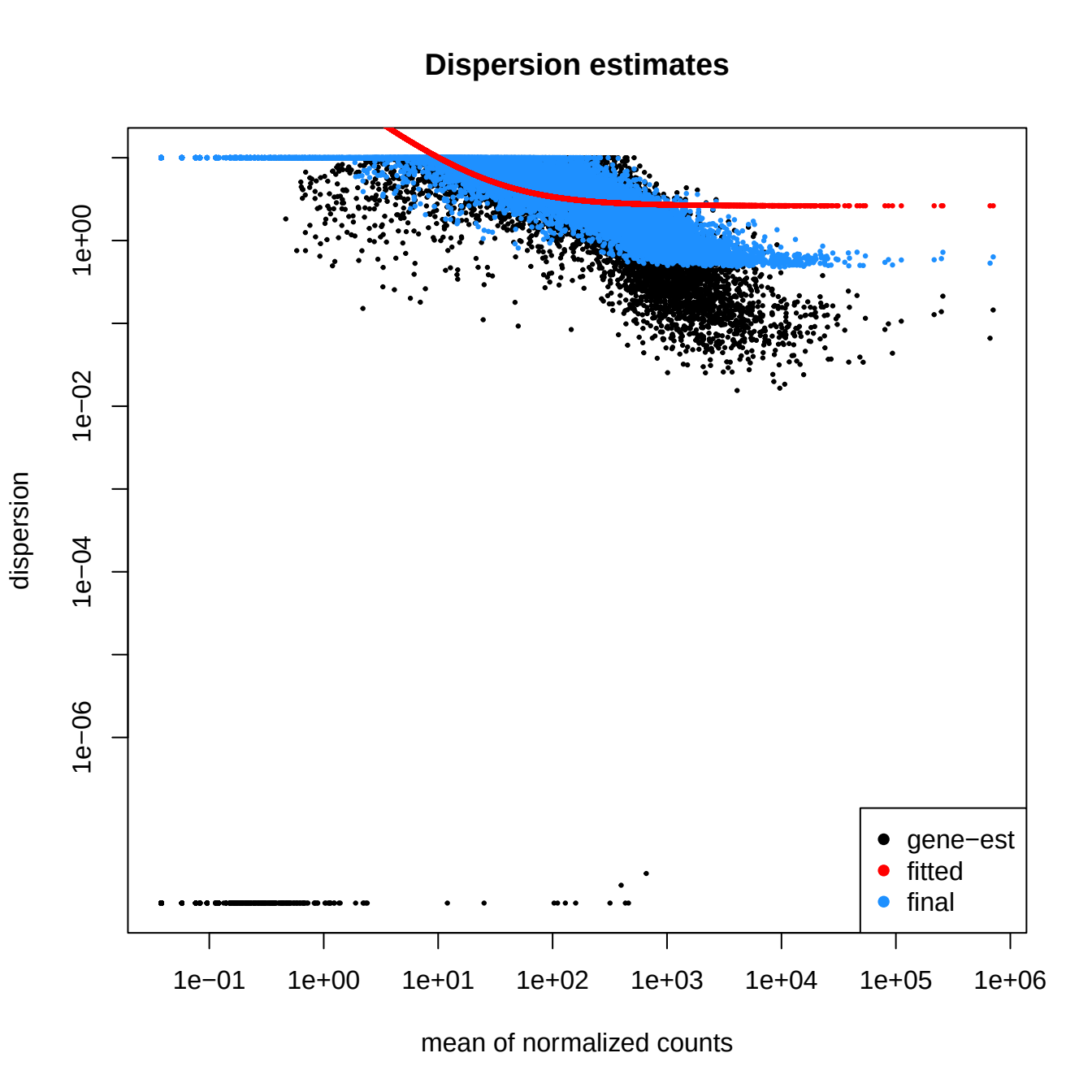
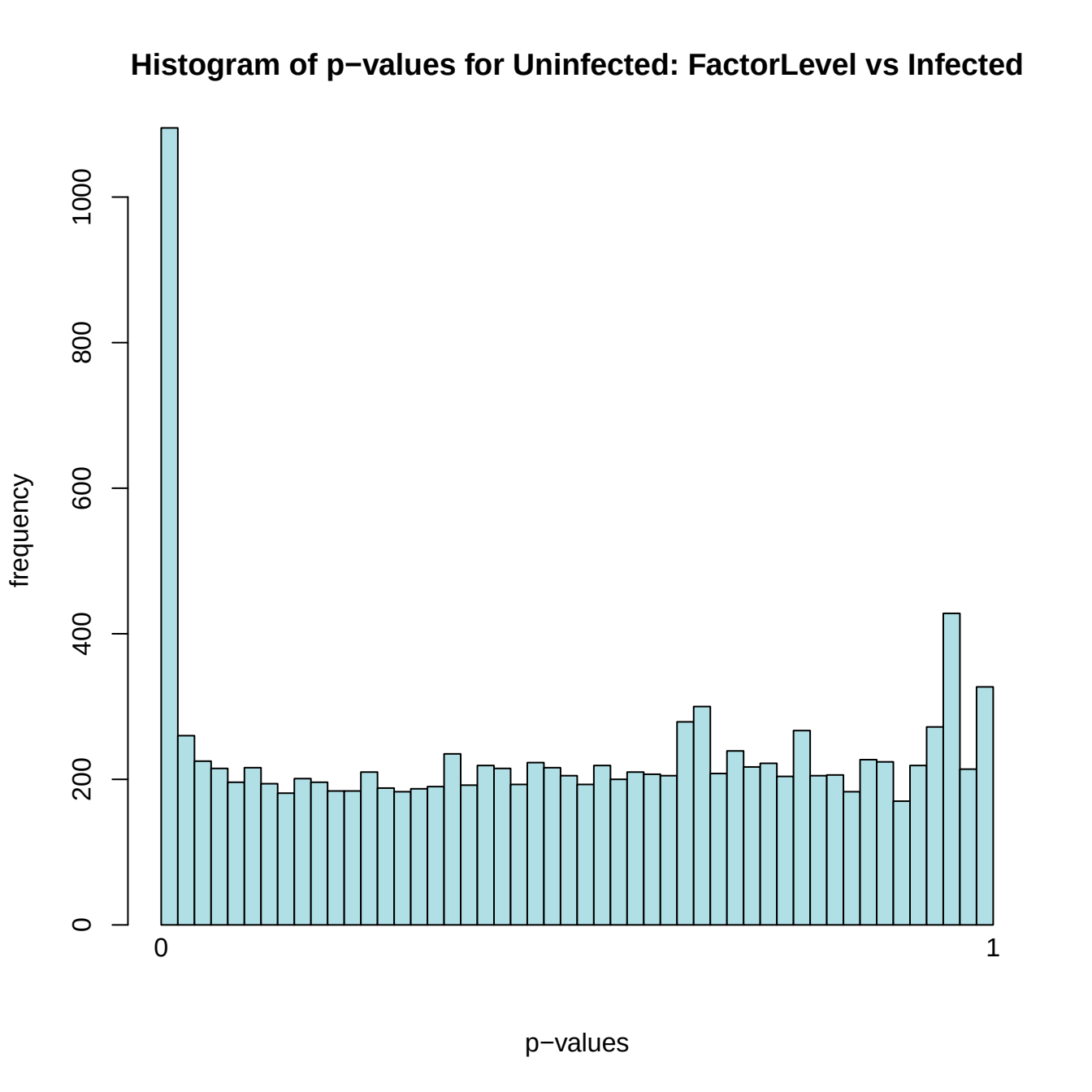
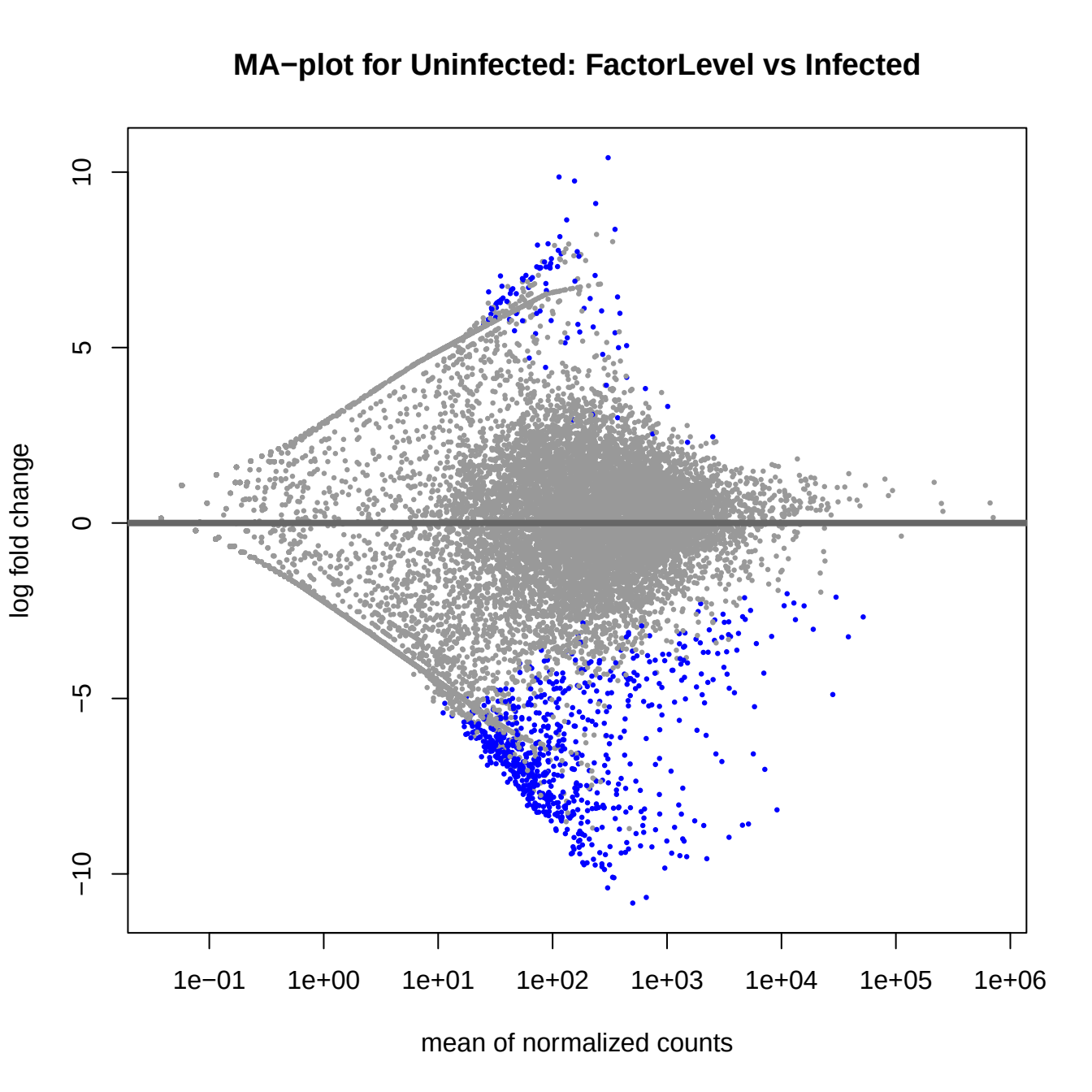

Mouse_Infected_4_SRR16192403.tabular
Mouse_Infected_1_SRR16192400.tabular
Mouse_Infected_3_SRR16192402.tabular
Mouse_Infected_2_SRR16192401.tabular
Mouse_Non_infected_3_SRR16192408.tabular
Mouse_Non_infected_4_SRR16192409.tabular
Mouse_Non_infected_1_SRR16192406.tabular
Mouse_Non_infected_2_SRR16192407.tabular
40
0
−40
−50
0
50
PC2: 19% variance
PC1: 20% variance
group
Infected
FactorLevel


Sample−to−sample distances
Mouse_Non_infected_2_SRR16192407.tabular
Mouse_Non_infected_4_SRR16192409.tabular
Mouse_Infected_2_SRR16192401.tabular
Mouse_Infected_3_SRR16192402.tabular
Mouse_Infected_1_SRR16192400.tabular
Mouse_Infected_4_SRR16192403.tabular
Mouse_Non_infected_1_SRR16192406.tabular
Mouse_Non_infected_3_SRR16192408.tabular
400
300
200
100
0


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


Histogram of p−values for Uninfected: FactorLevel vs Infected
frequency
0
200
400
600
800
1000
0
1
p−values


MA−plot for Uninfected: FactorLevel vs Infected
log fold change
10
5
0
−5
−10
1e−01
1e+00
1e+01
1e+02
1e+03
1e+04
1e+05
1e+06
mean of normalized counts