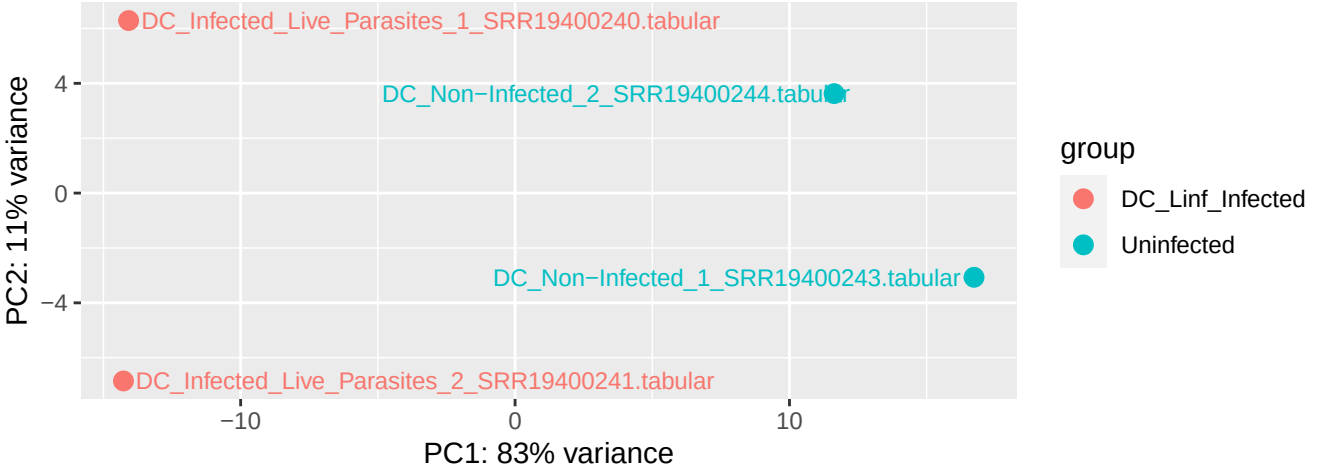
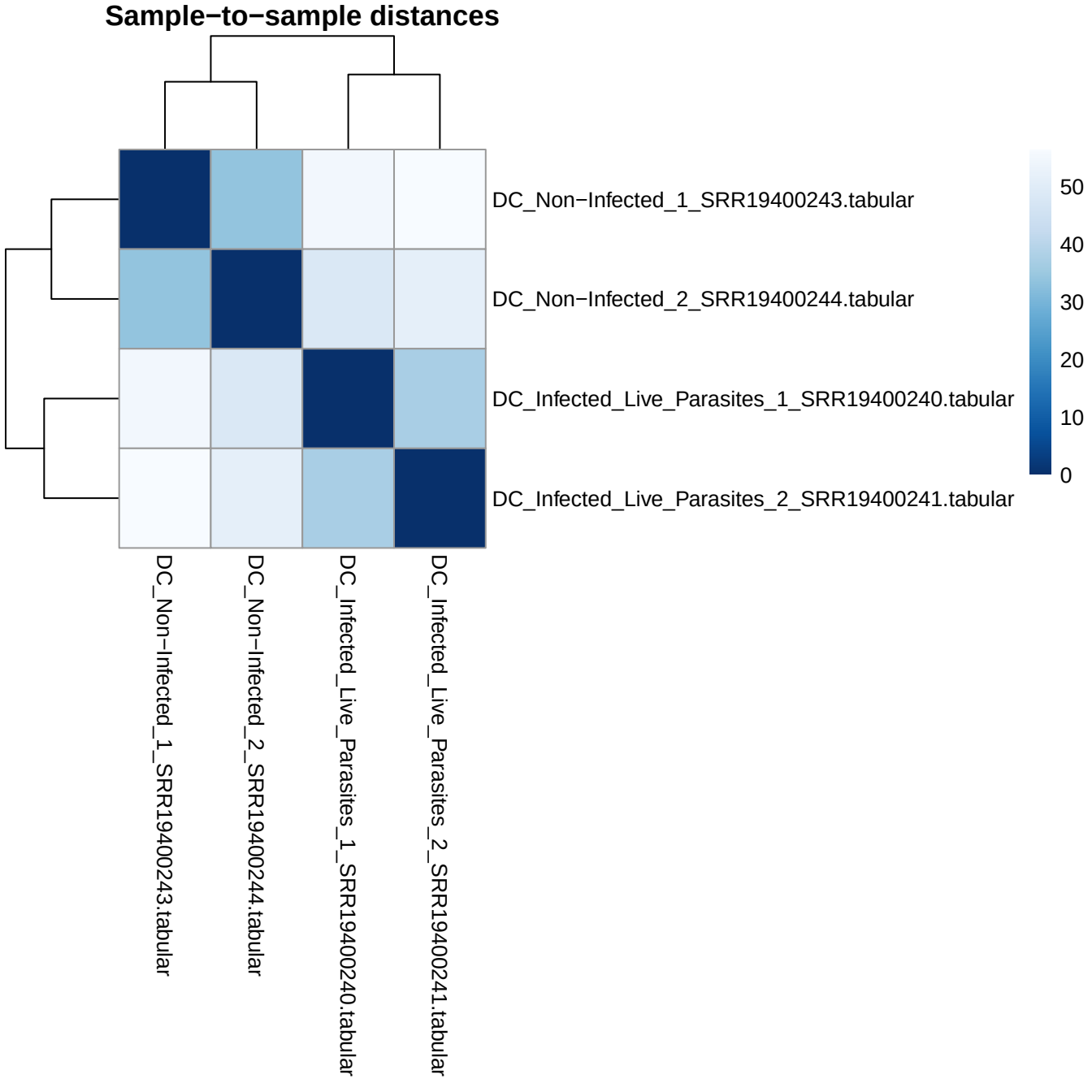
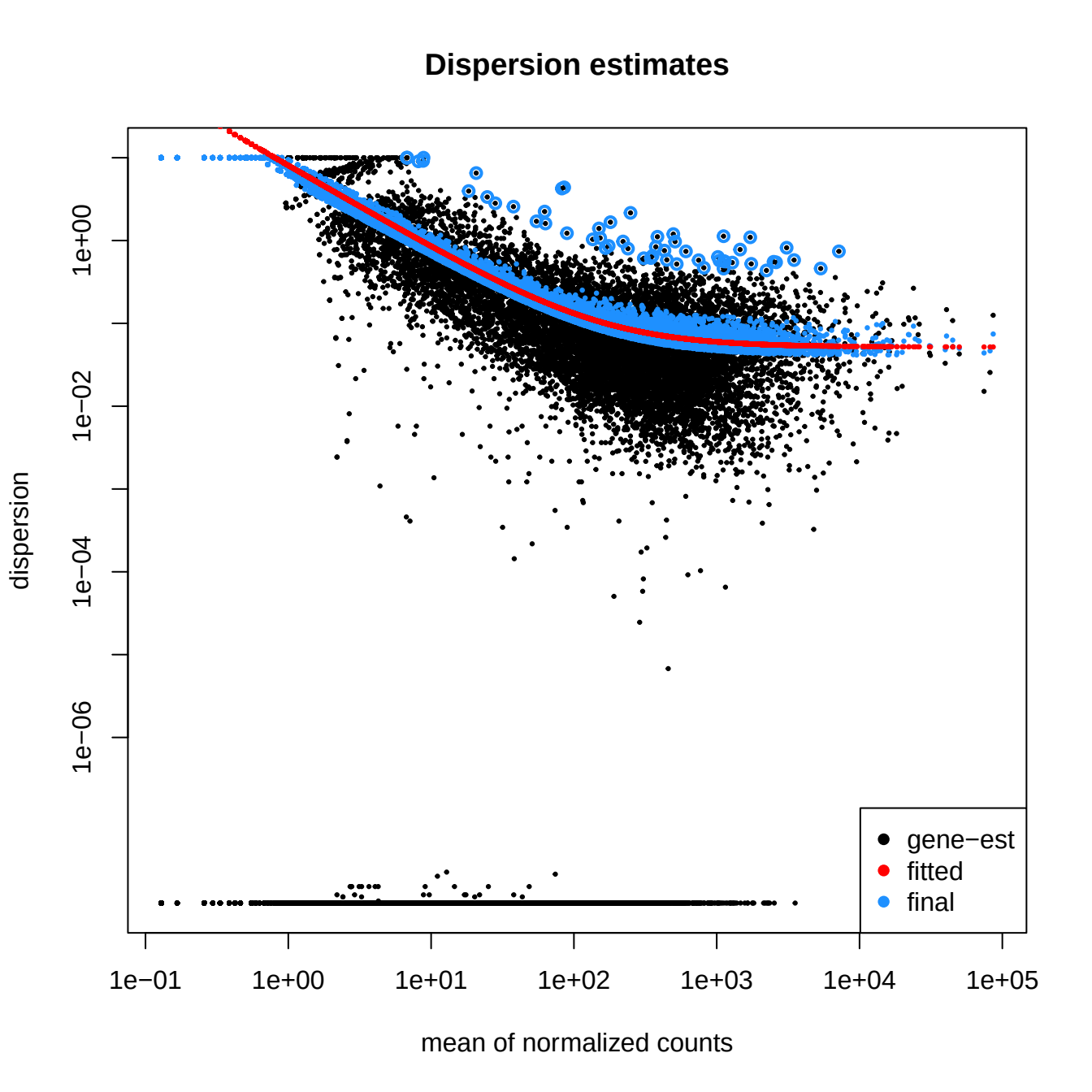
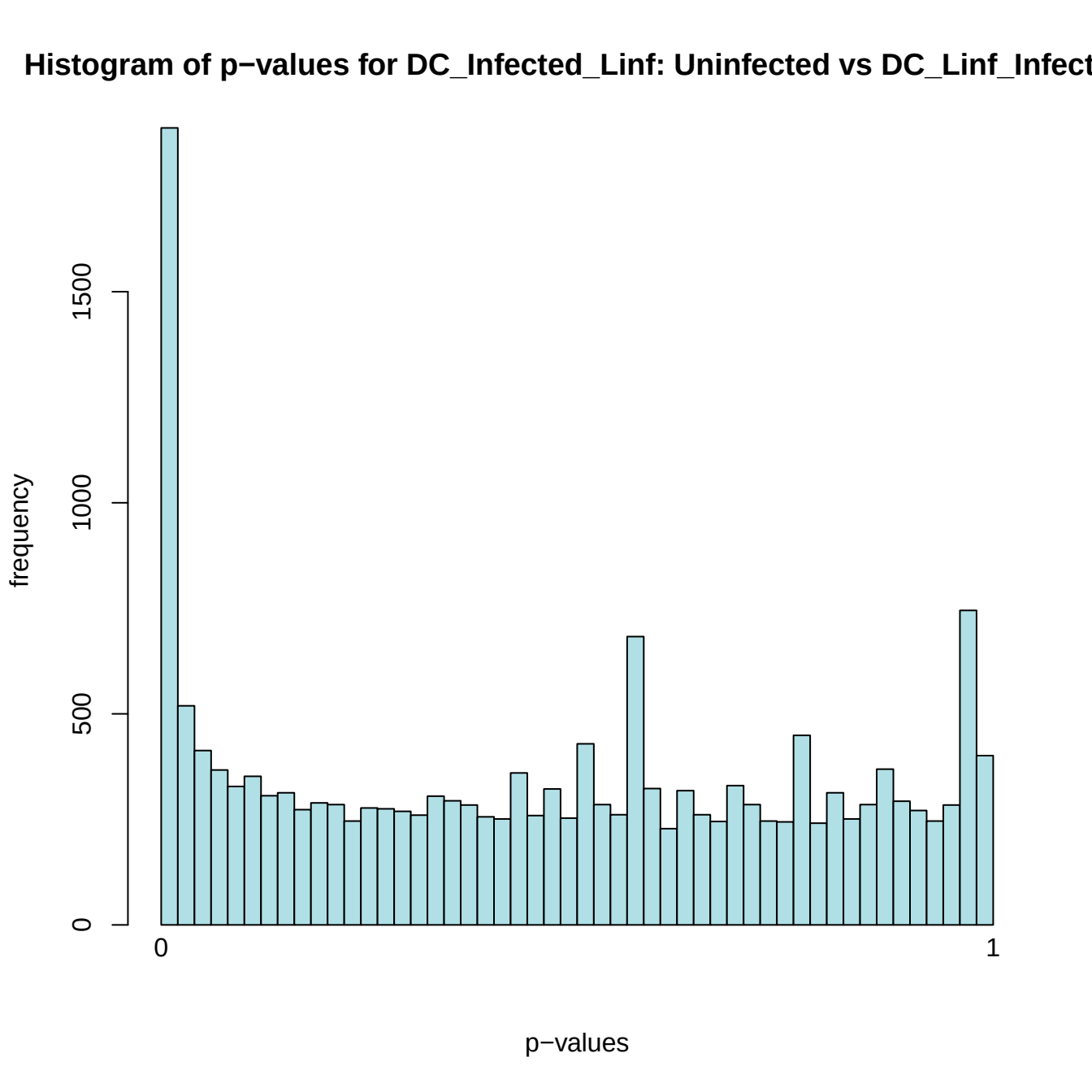
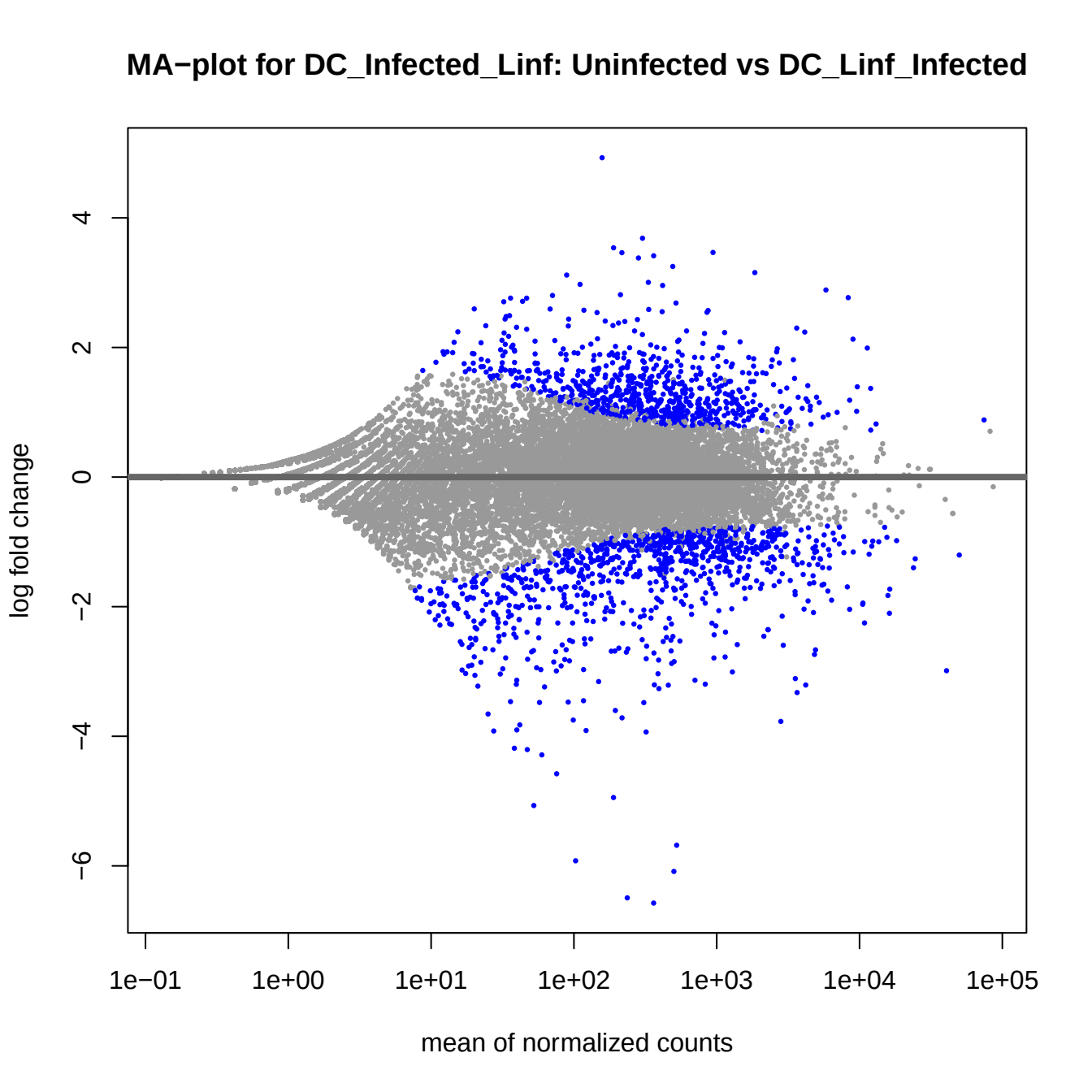

DC_Infected_Live_Parasites_1_SRR19400240.tabular
DC_Non−Infected_2_SRR19400244.tabular
DC_Non−Infected_1_SRR19400243.tabular
DC_Infected_Live_Parasites_2_SRR19400241.tabular
4
0
−4
PC2: 11% variance
−10
0
10
PC1: 83% variance
group
DC_Linf_Infected
Uninfected


Sample−to−sample distances
DC_Non−Infected_1_SRR19400243.tabular
DC_Non−Infected_2_SRR19400244.tabular
DC_Infected_Live_Parasites_1_SRR19400240.tabular
DC_Infected_Live_Parasites_2_SRR19400241.tabular
50
40
30
20
10
0
DC_Non−Infected_1_SRR19400243.tabular
DC_Non−Infected_2_SRR19400244.tabular
DC_Infected_Live_Parasites_1_SRR19400240.tabular
DC_Infected_Live_Parasites_2_SRR19400241.tabular


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
mean of normalized counts
gene−est
fitted
final


Histogram of p−values for DC_Infected_Linf: Uninfected vs DC_Linf_Infect
frequency
0
500
1000
1500
0
1
p−values


MA−plot for DC_Infected_Linf: Uninfected vs DC_Linf_Infected
log fold change
4
2
0
−2
−4
−6
1e−01
1e+00
1e+01
1e+02
1e+03
1e+04
1e+05
mean of normalized counts