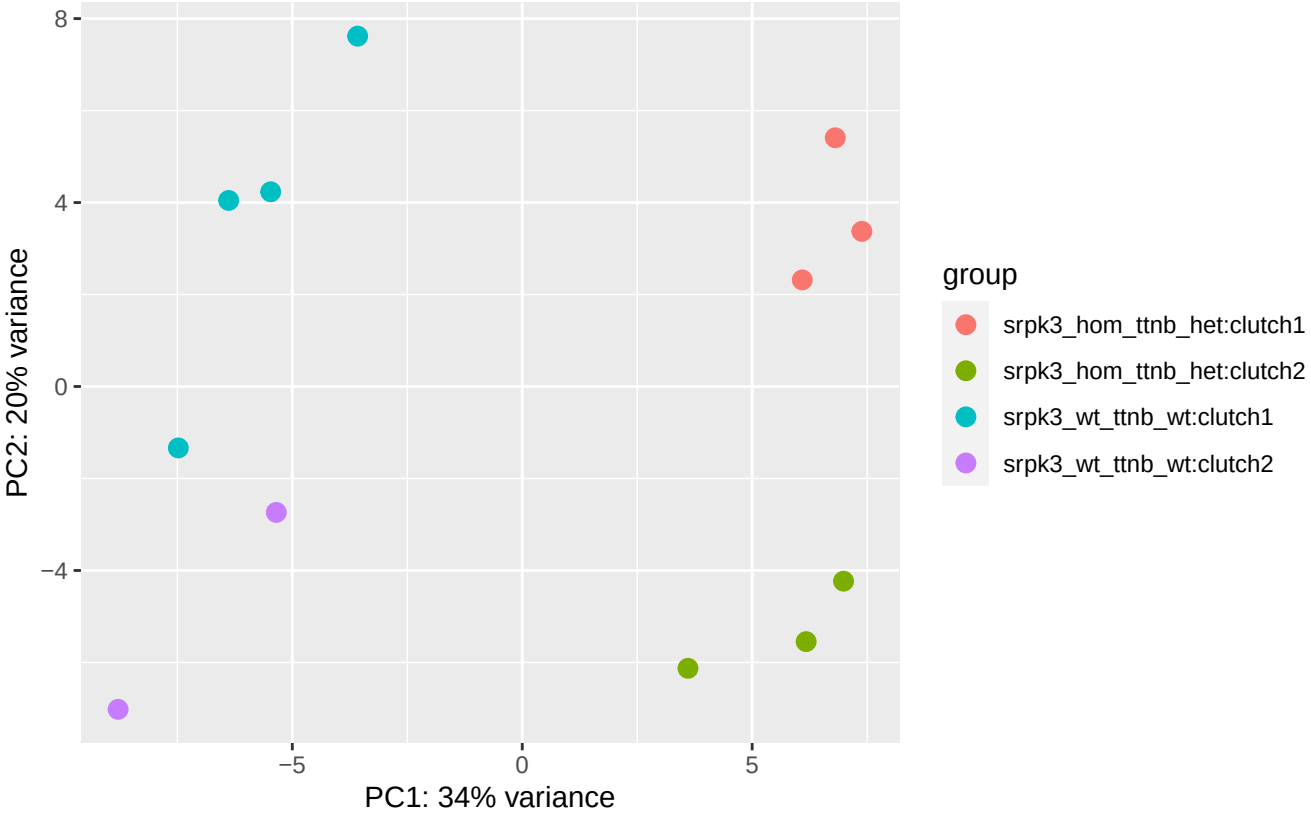
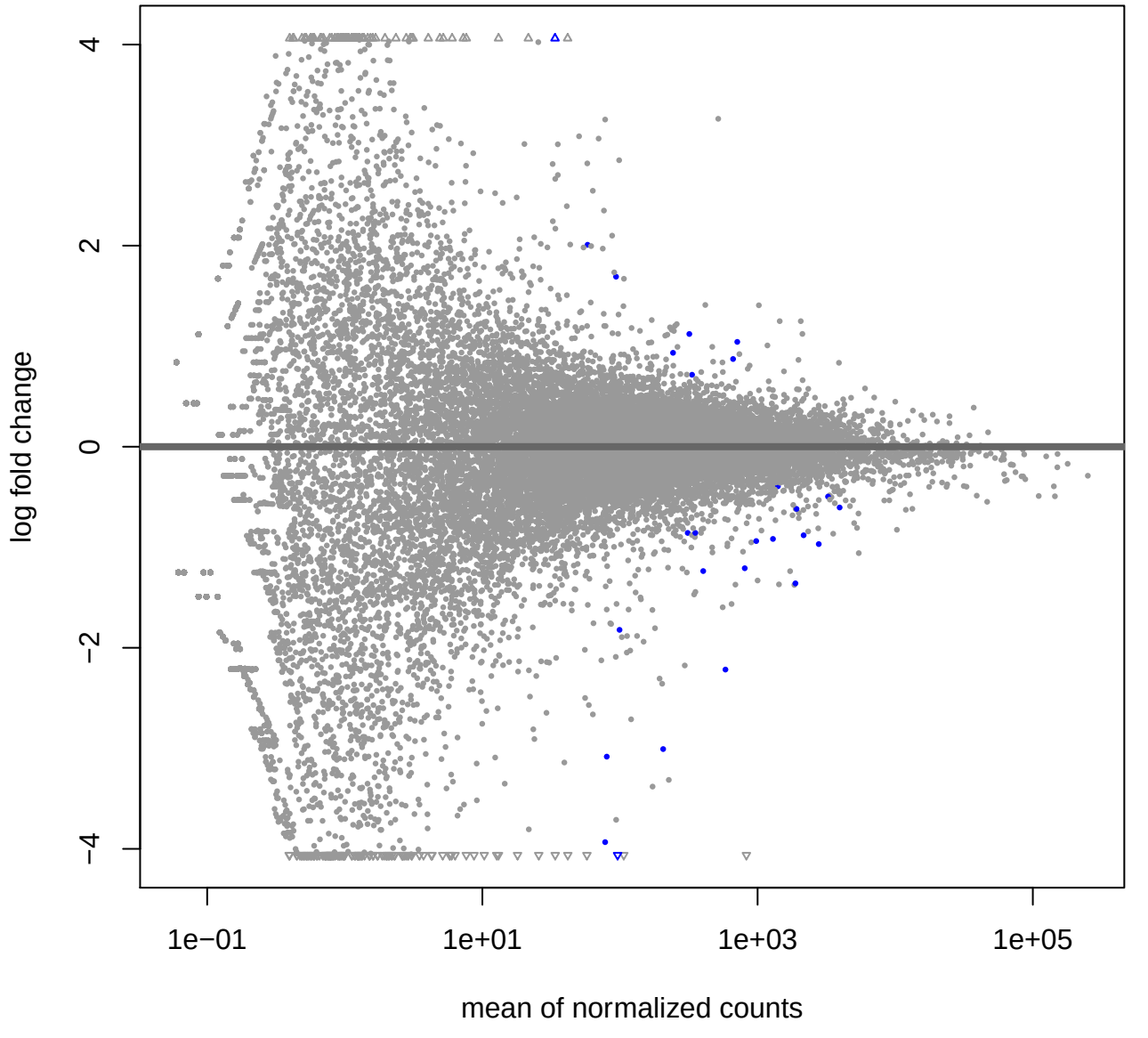
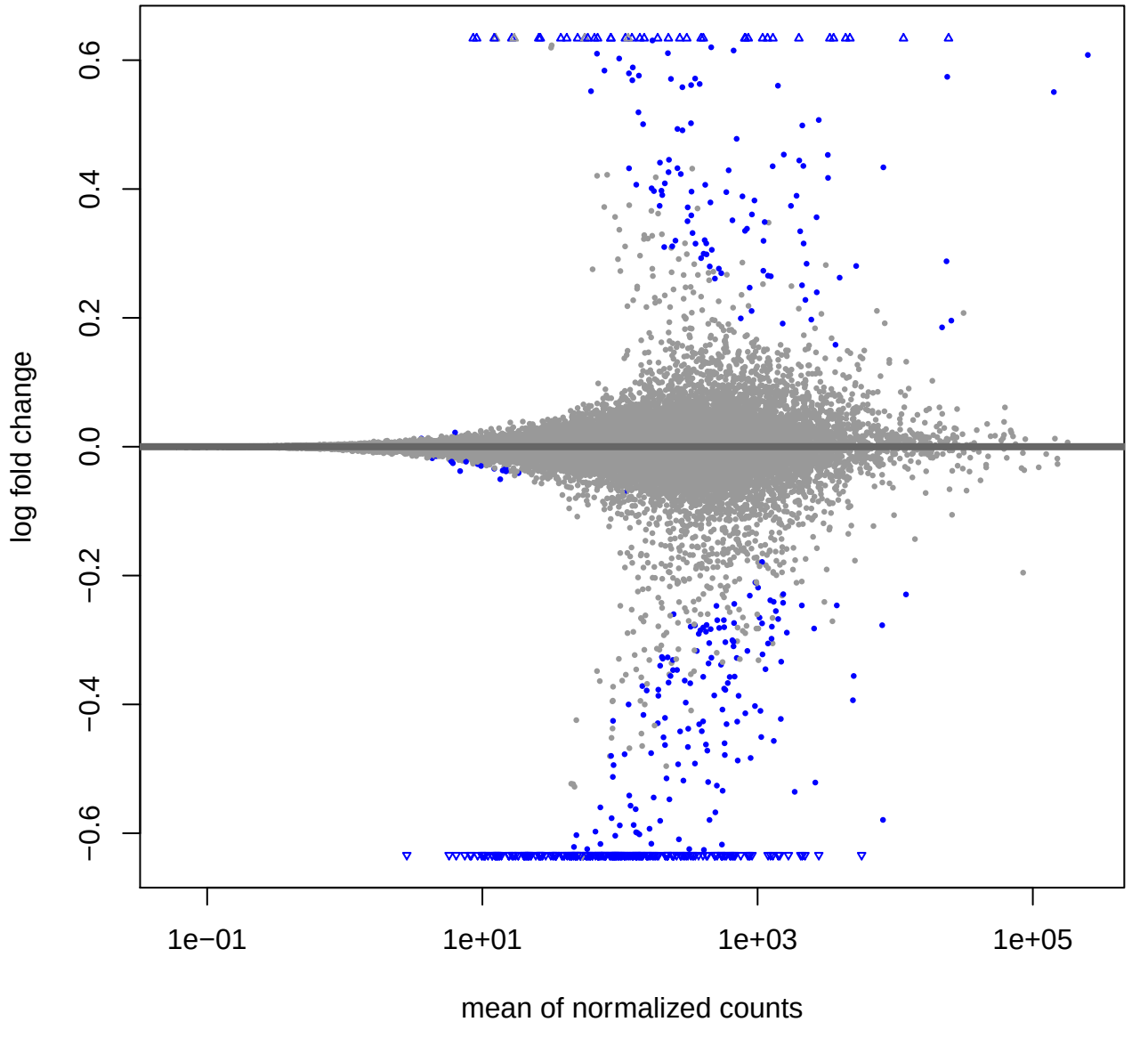
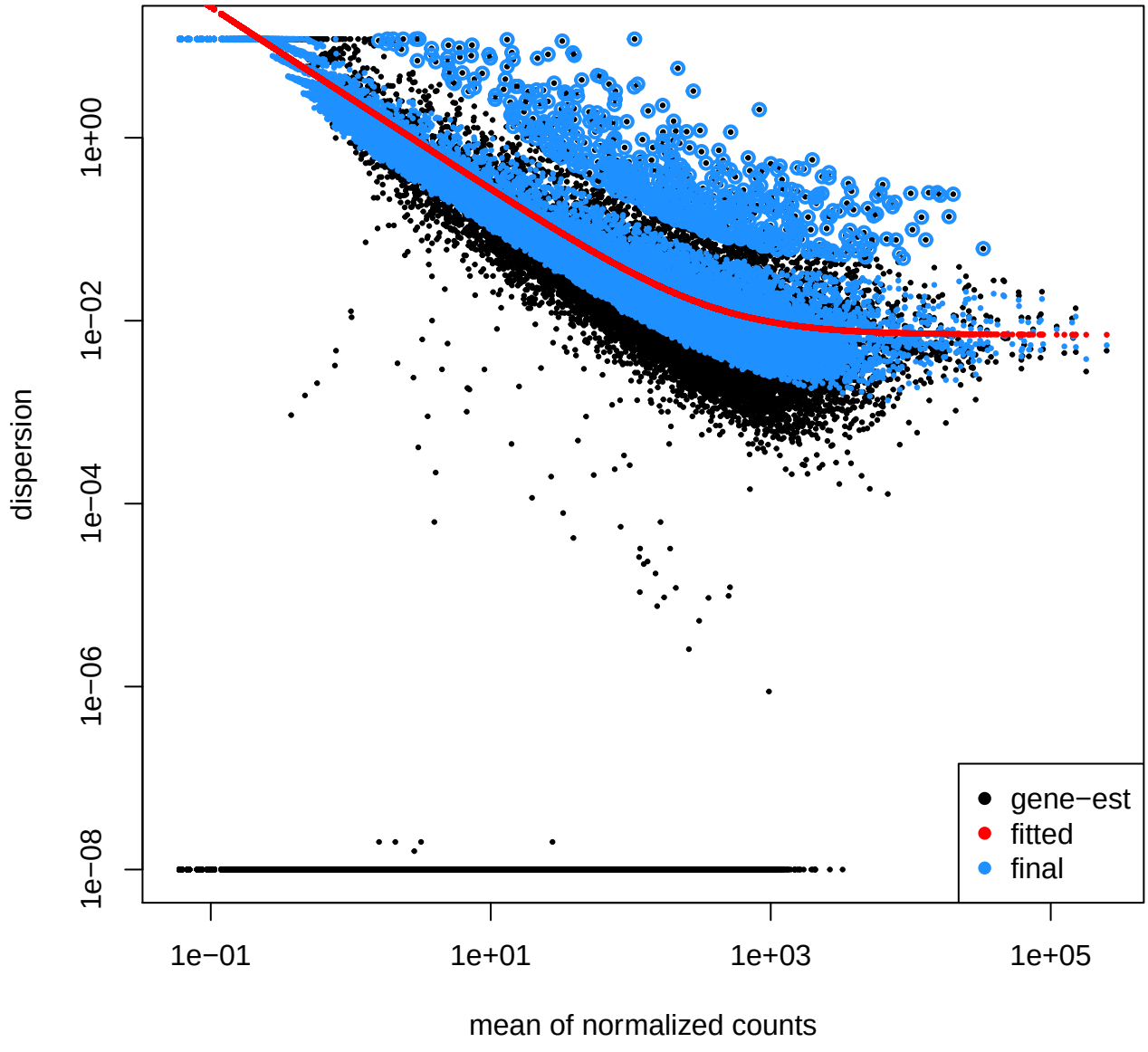

8
4
0
−4
PC2: 20% variance
−5
0
5
PC1: 34% variance
group
srpk3_hom_ttnb_het:clutch1
srpk3_hom_ttnb_het:clutch2
srpk3_wt_ttnb_wt:clutch1
srpk3_wt_ttnb_wt:clutch2


log fold change
4
2
0
−2
−4
1e−01
1e+01
1e+03
1e+05
mean of normalized counts


log fold change
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
1e−01
1e+01
1e+03
1e+05
mean of normalized counts


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