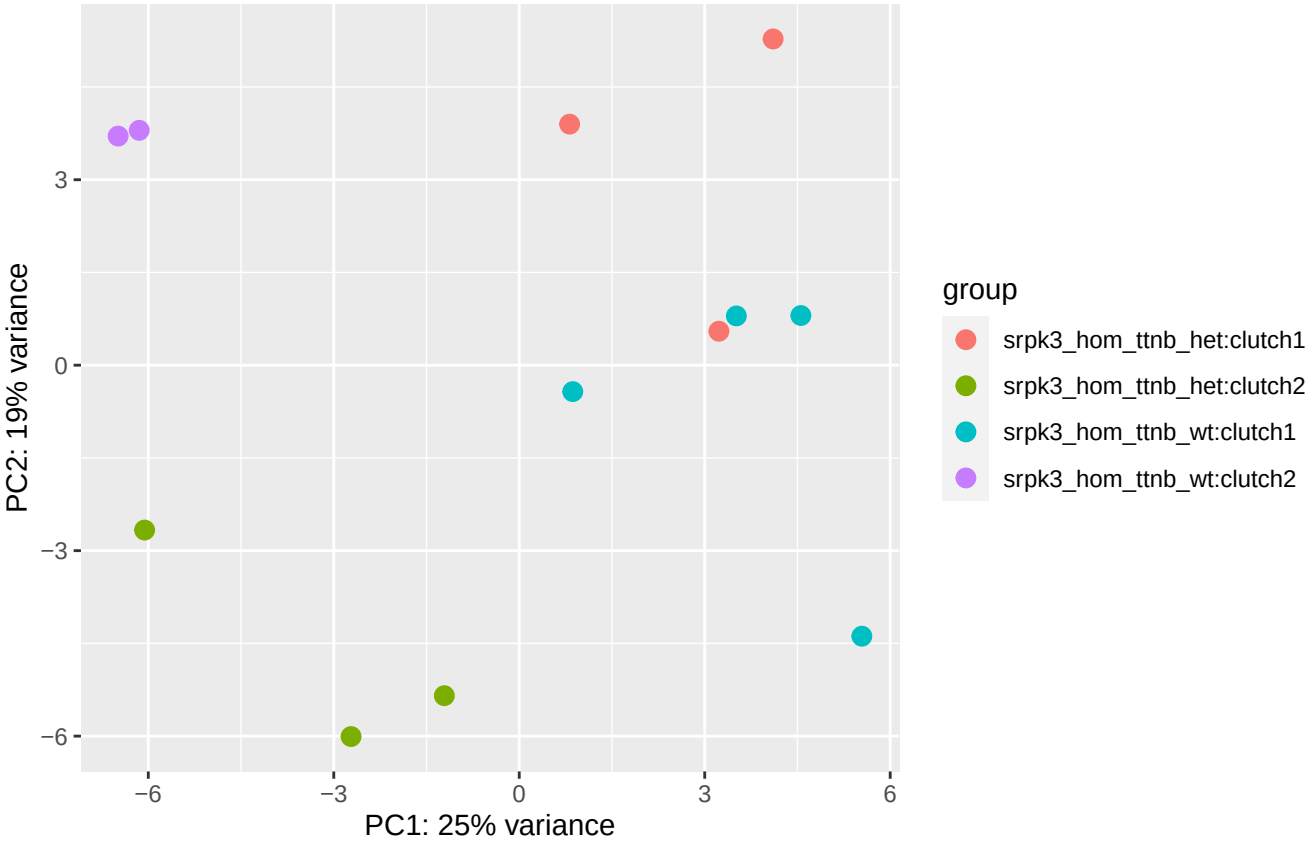
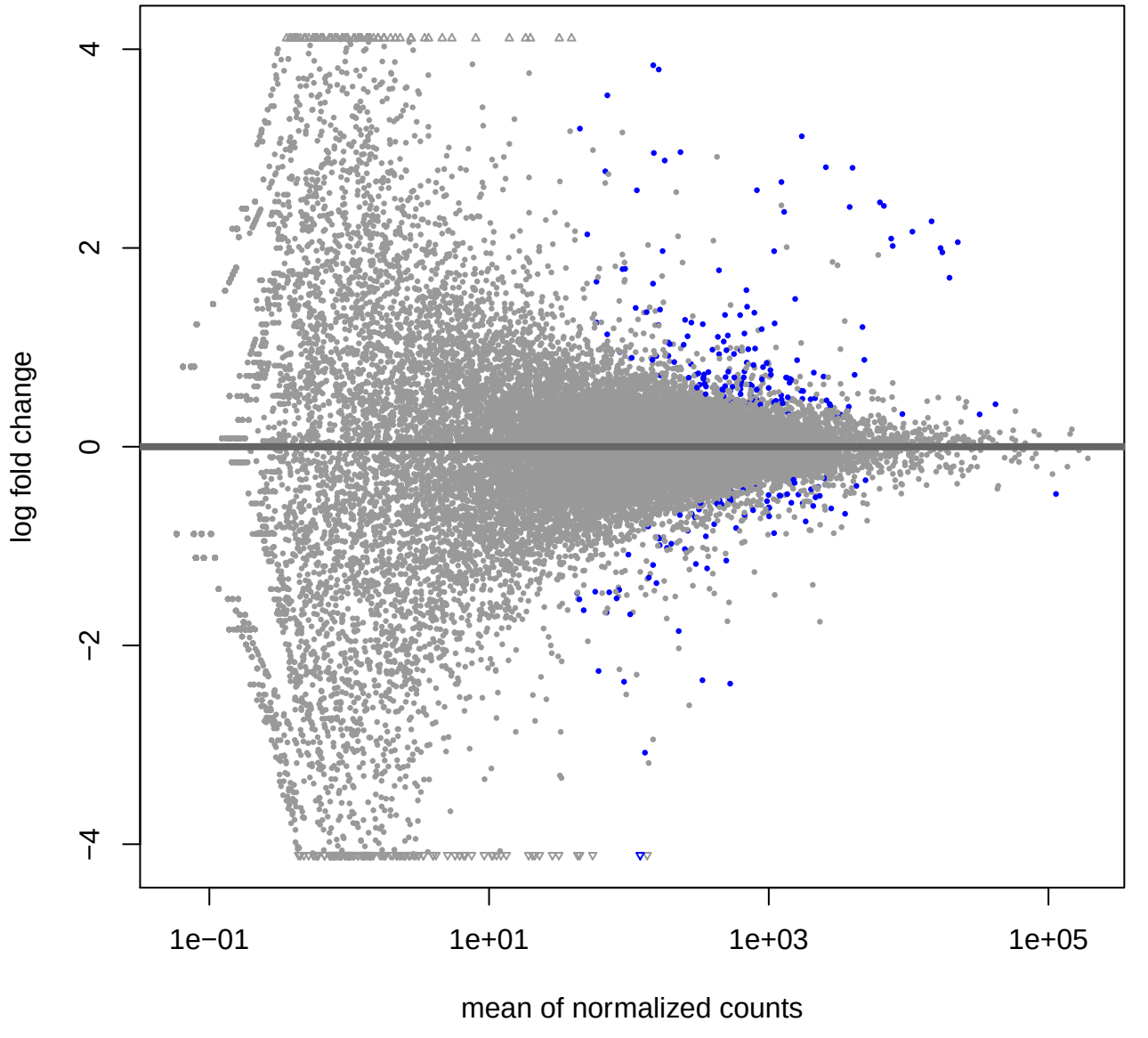
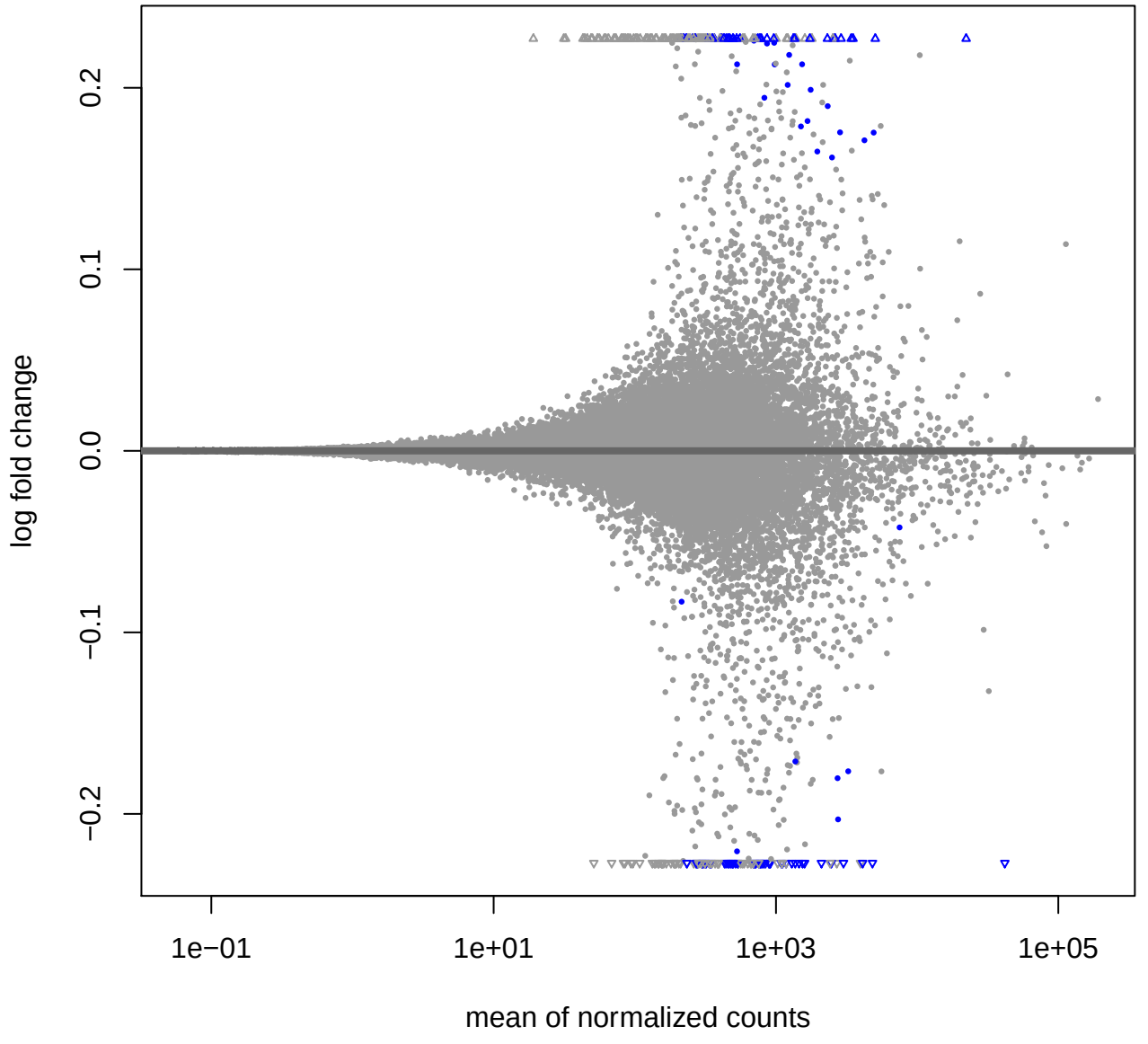
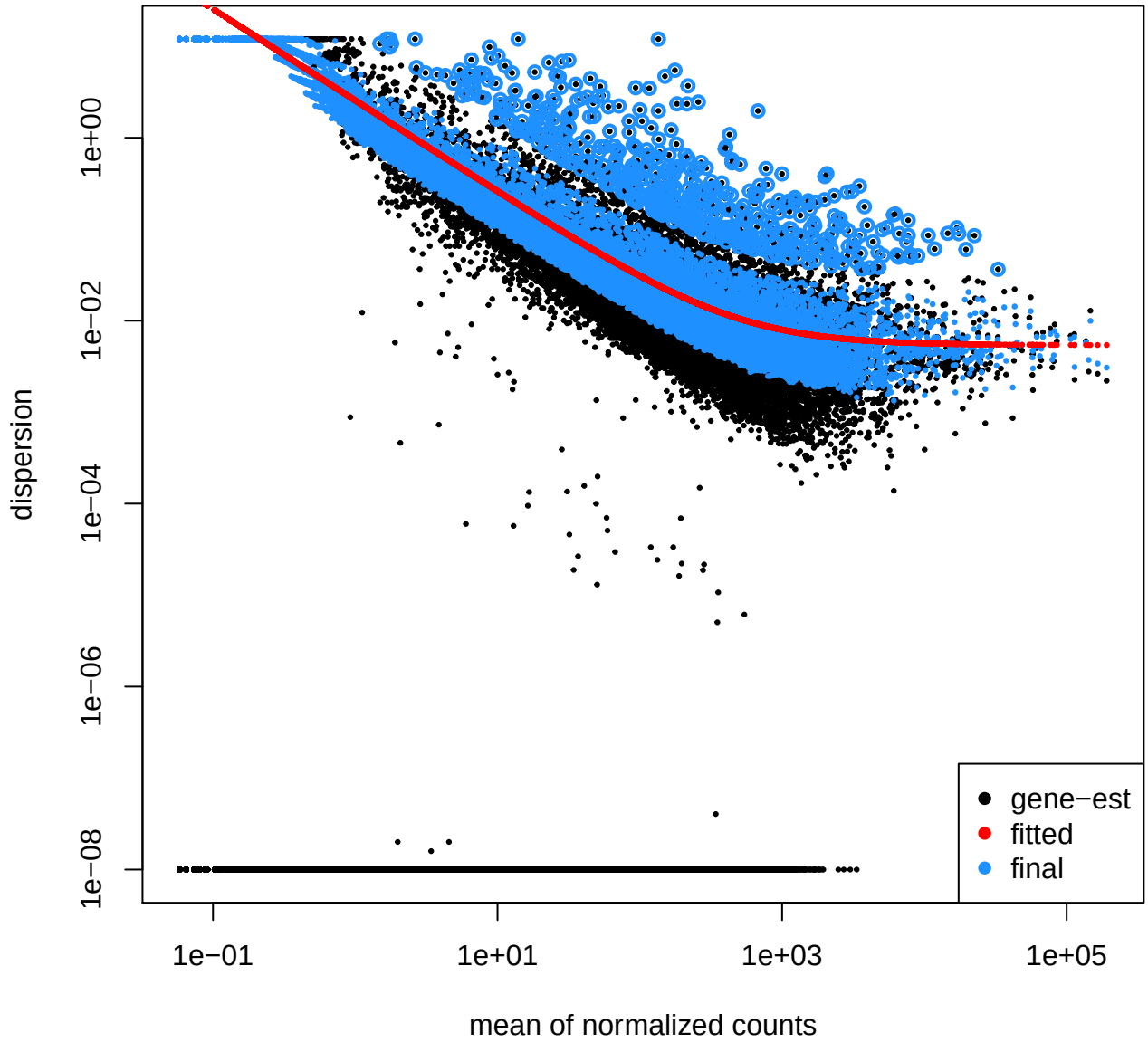

PC2: 19% variance
3
0
−3
−6
−6
−3
0
3
6
PC1: 25% variance
group
srpk3_hom_ttnb_het:clutch1
srpk3_hom_ttnb_het:clutch2
srpk3_hom_ttnb_wt:clutch1
srpk3_hom_ttnb_wt:clutch2


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


log fold change
0.2
0.1
0.0
−0.1
−0.2
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