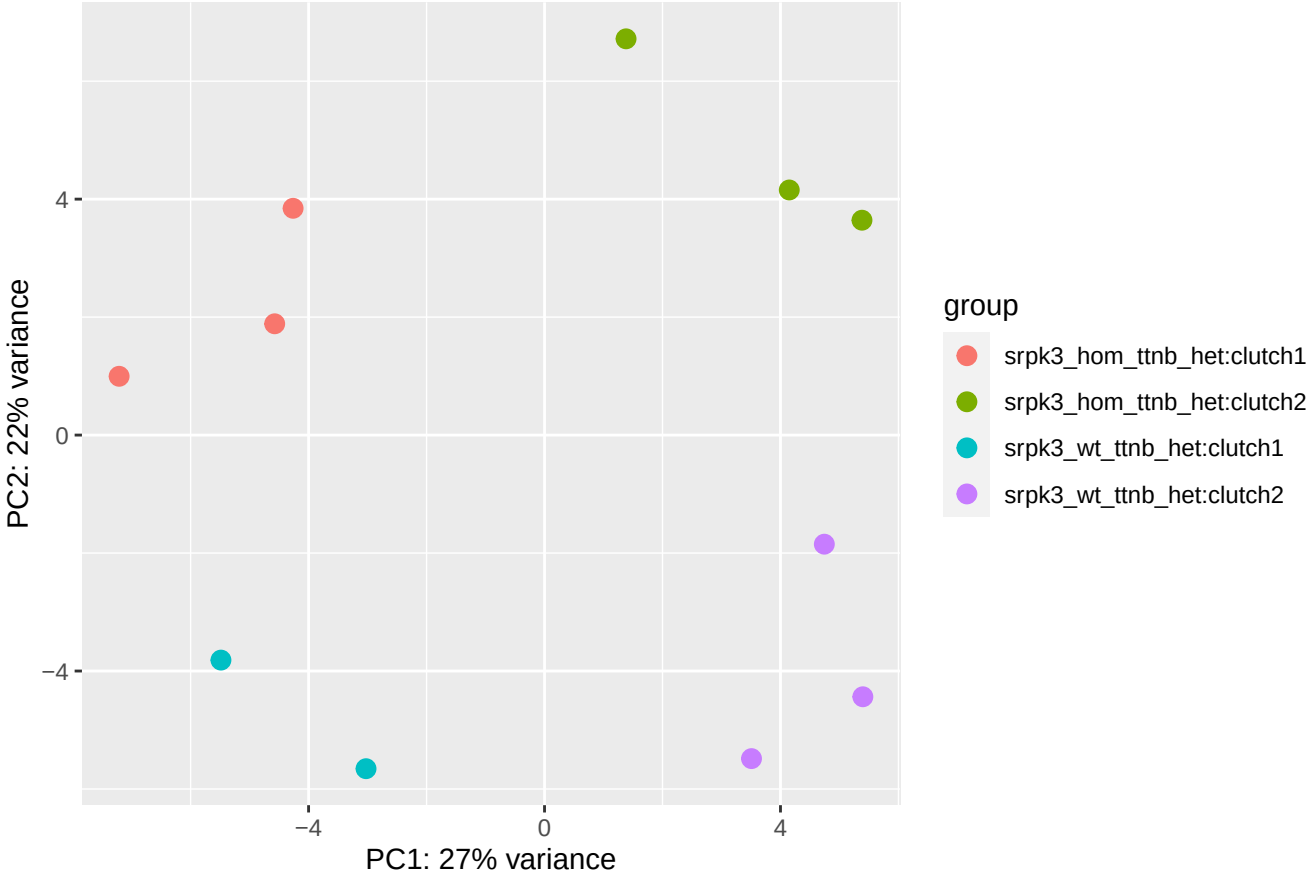
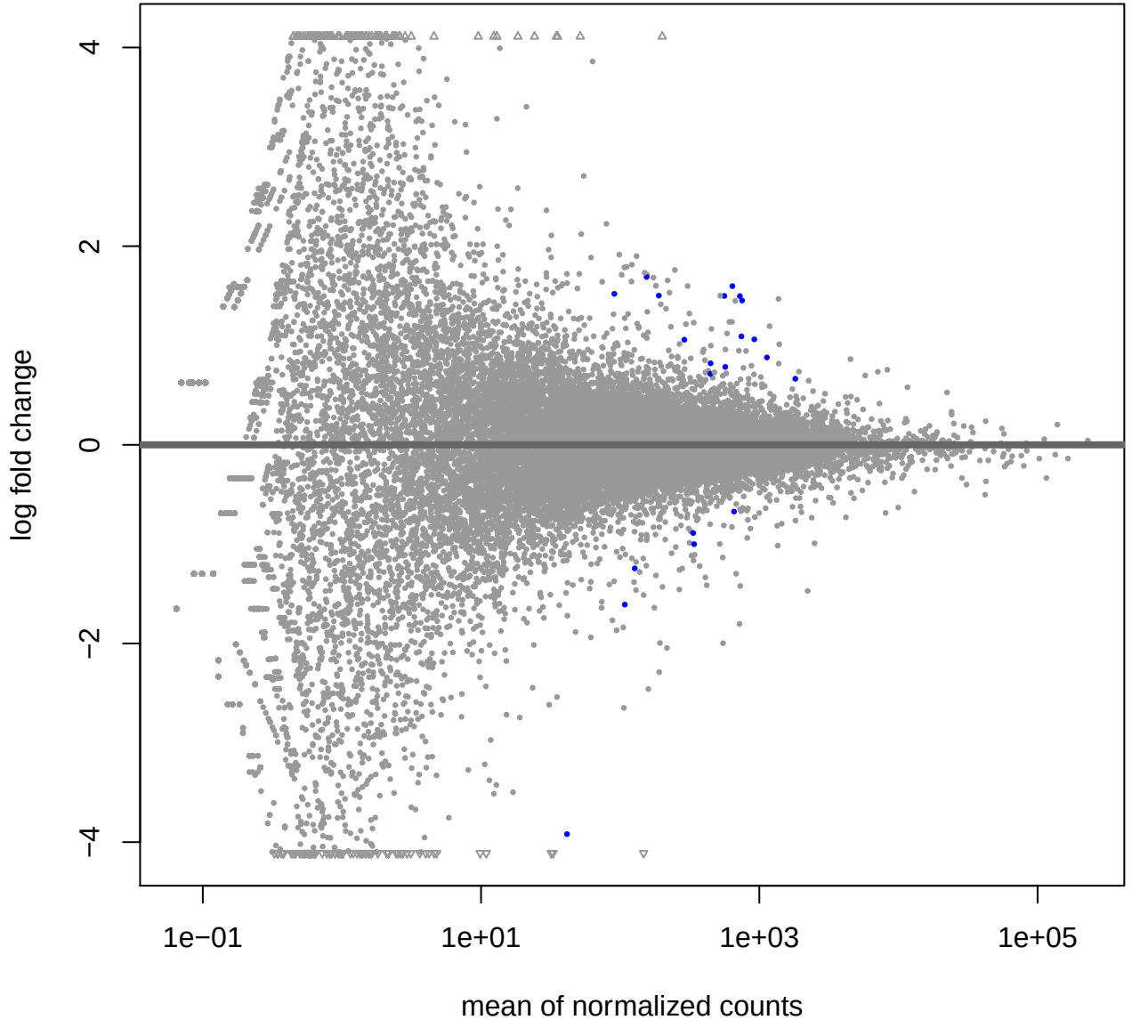
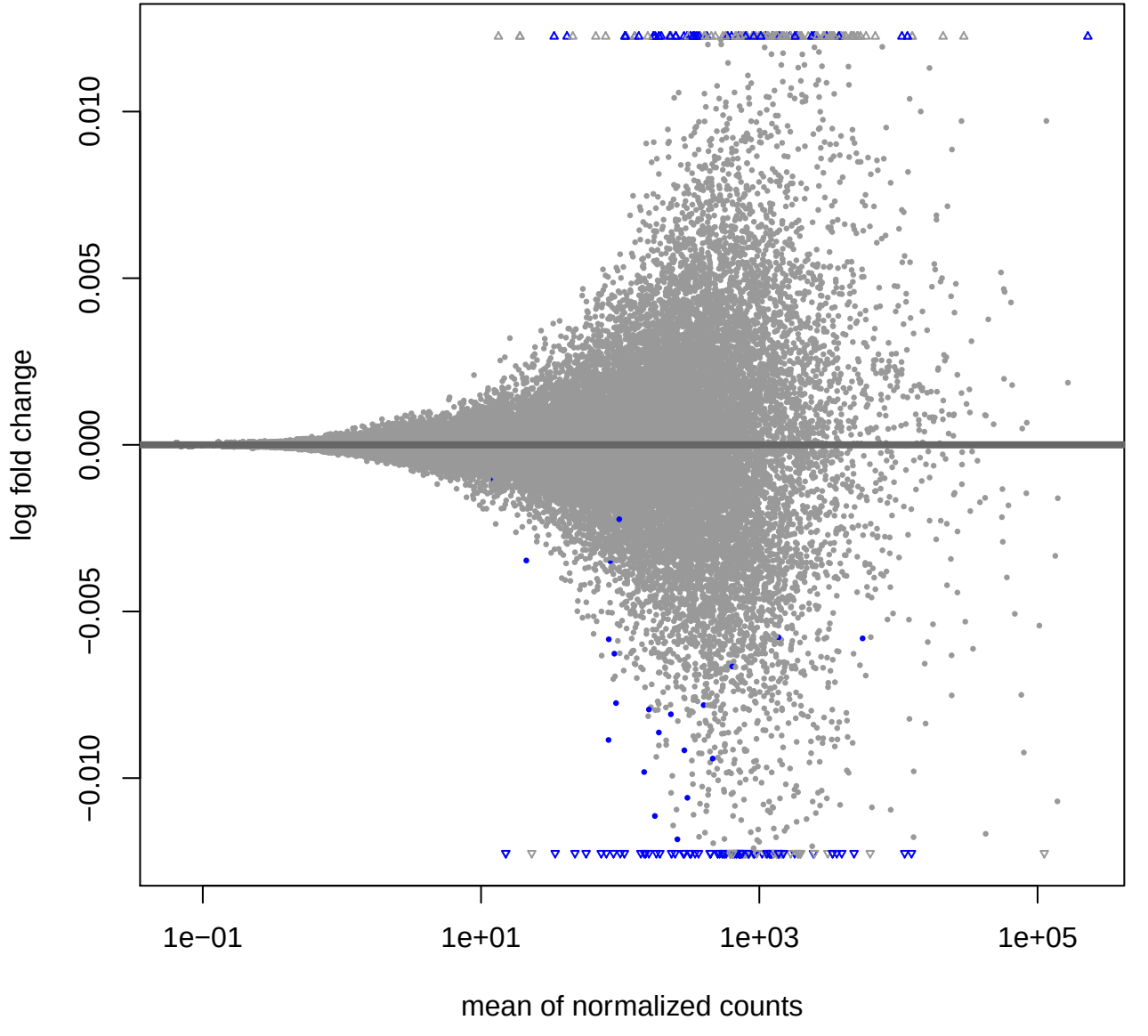
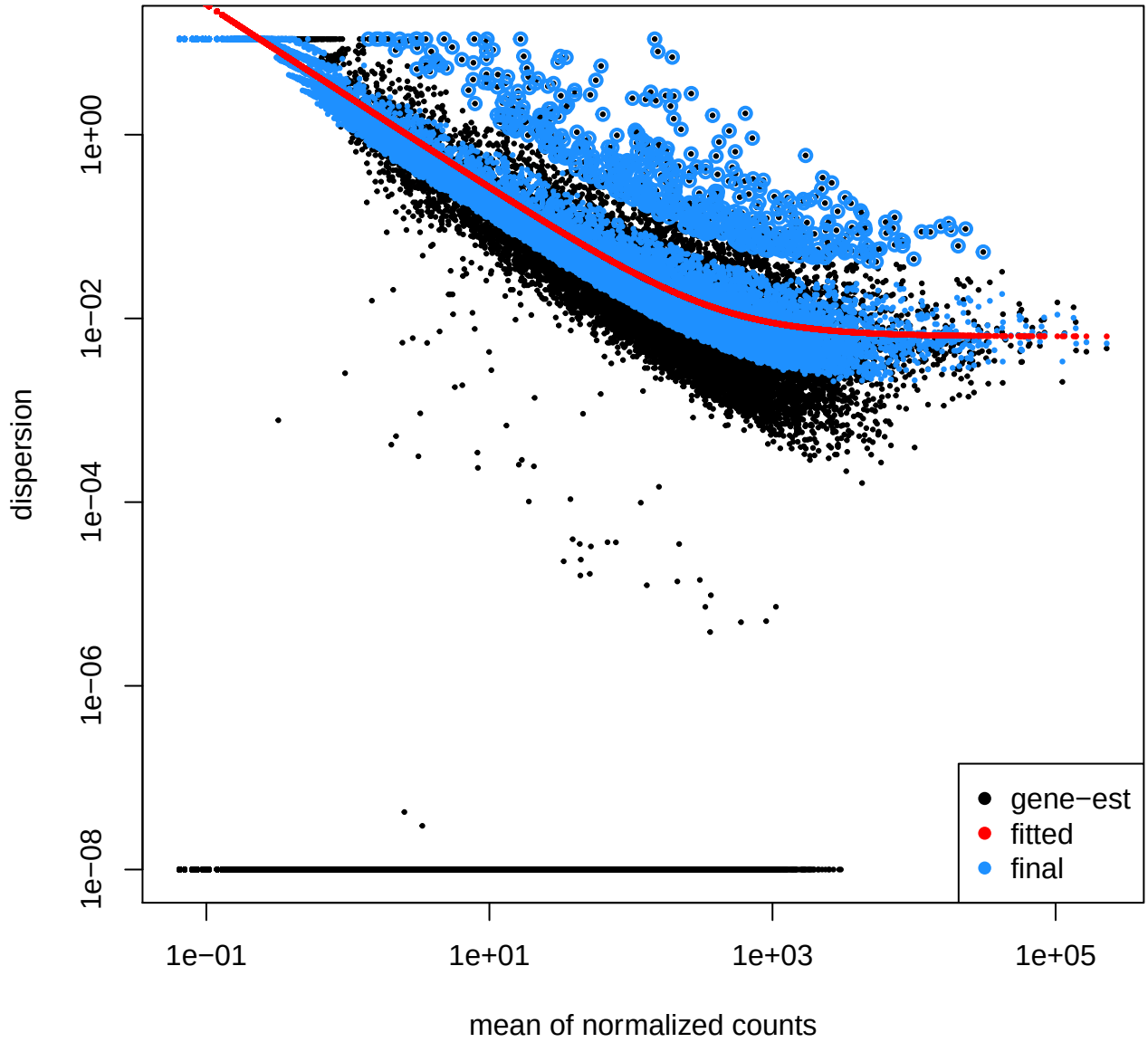

PC2: 22% variance
4
0
−4
−4
0
4
PC1: 27% variance
group
srpk3_hom_ttnb_het:clutch1
srpk3_hom_ttnb_het:clutch2
srpk3_wt_ttnb_het:clutch1
srpk3_wt_ttnb_het:clutch2


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


log fold change
0.010
0.005
0.000
−0.005
−0.010
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