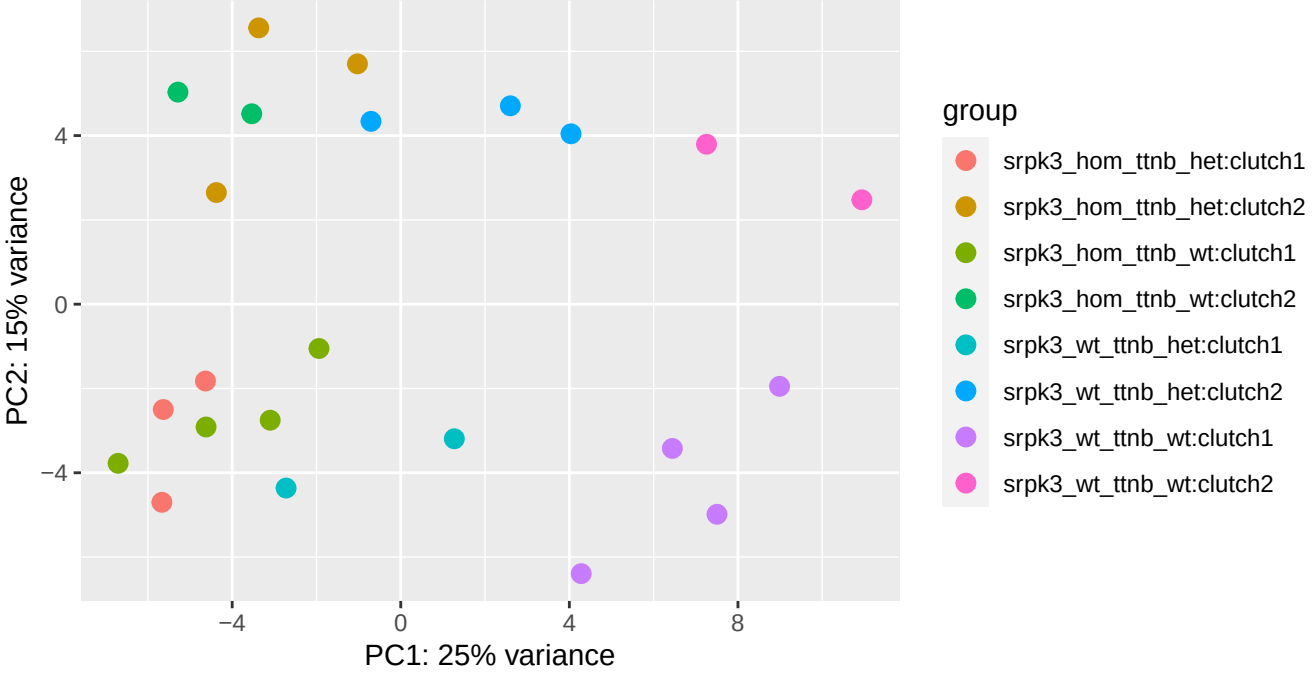
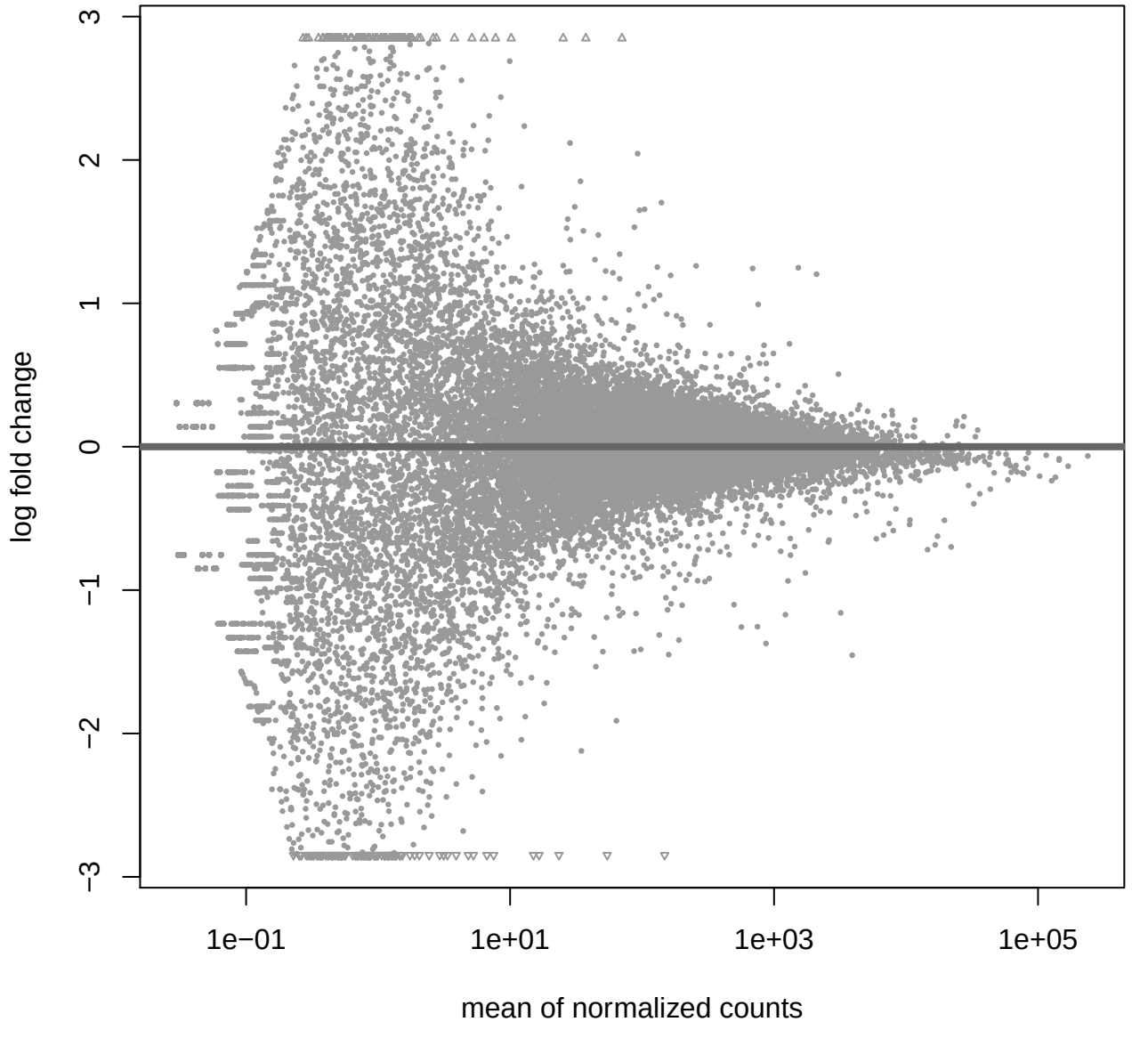
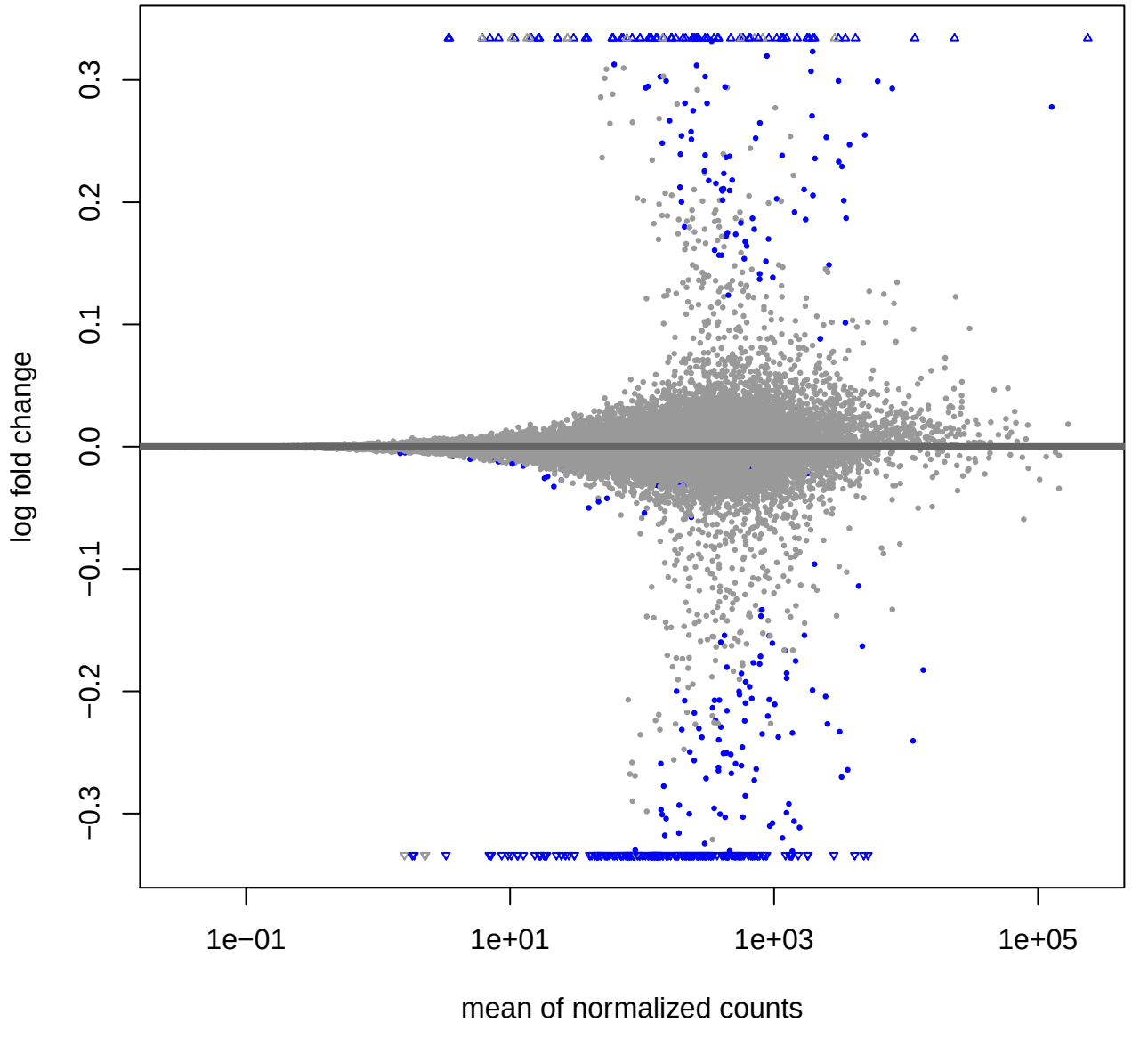
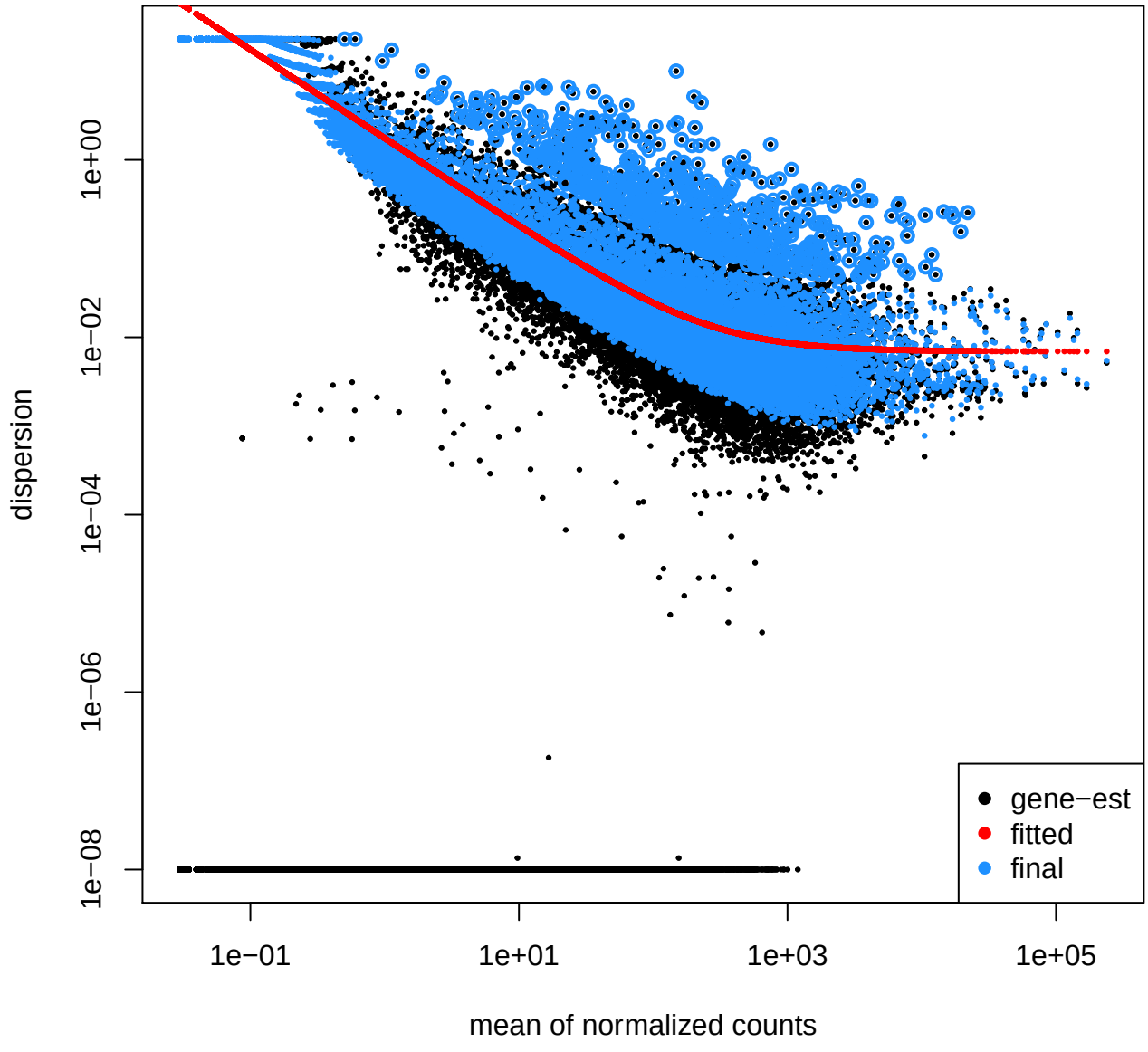

group
srpk3_hom_ttnb_het:clutch1
srpk3_hom_ttnb_het:clutch2
srpk3_hom_ttnb_wt:clutch1
srpk3_hom_ttnb_wt:clutch2
srpk3_wt_ttnb_het:clutch1
srpk3_wt_ttnb_het:clutch2
srpk3_wt_ttnb_wt:clutch1
srpk3_wt_ttnb_wt:clutch2
PC2: 15% variance
PC1: 25% variance
4
0
−4
−4
0
4
8


log fold change
3
2
1
0
−1
−2
−3
1e−01
1e+01
1e+03
1e+05
mean of normalized counts


log fold change
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
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