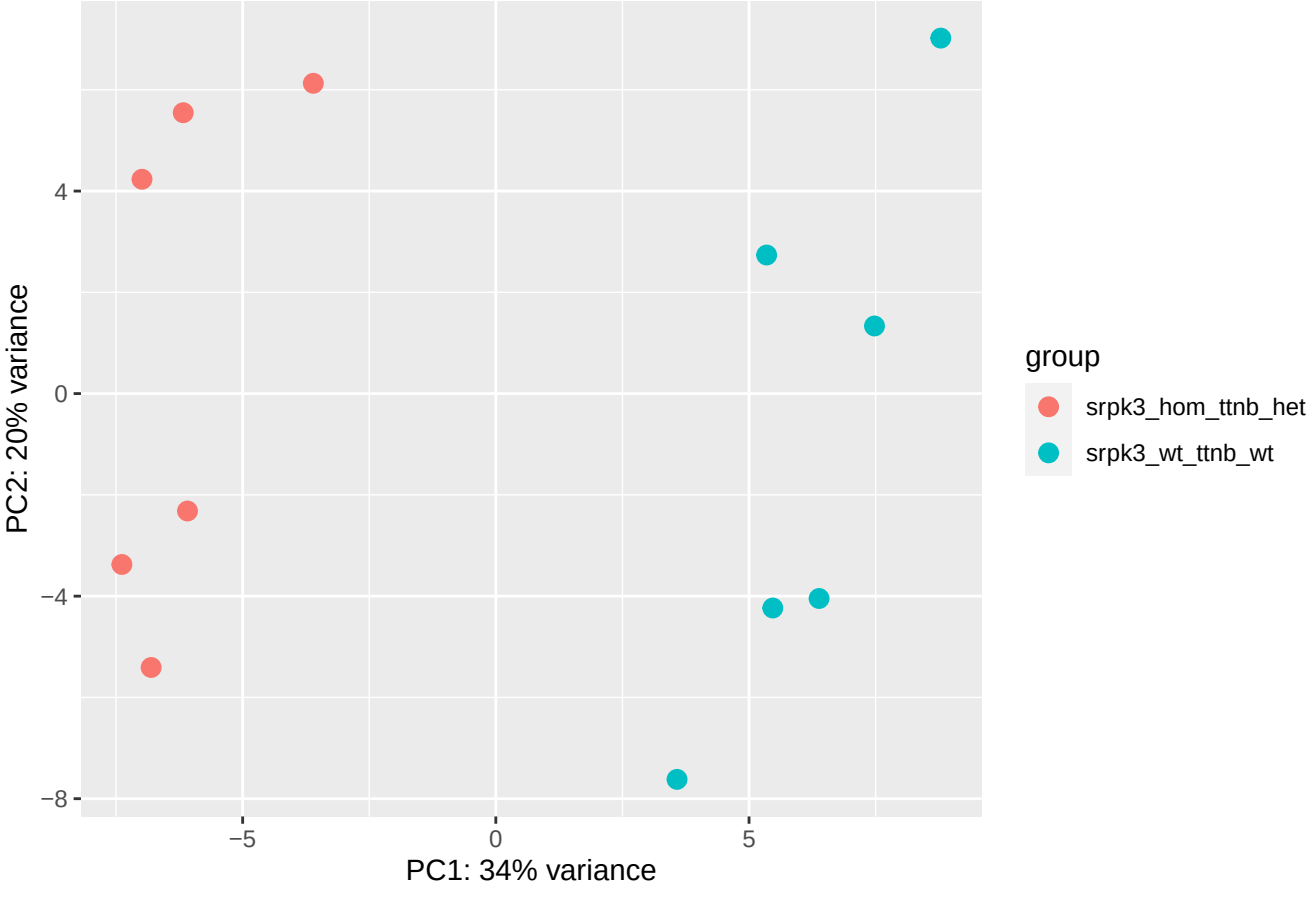
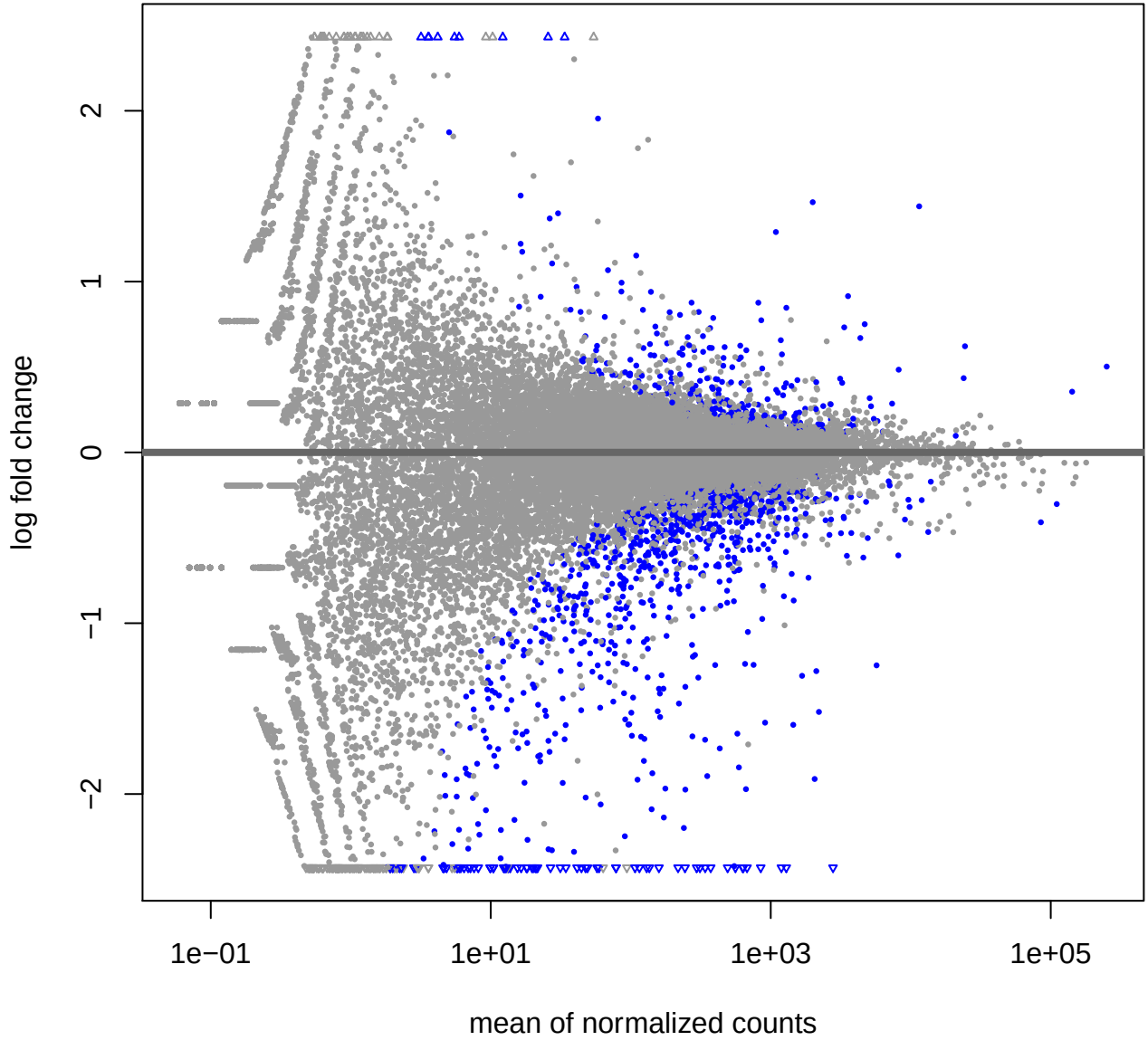
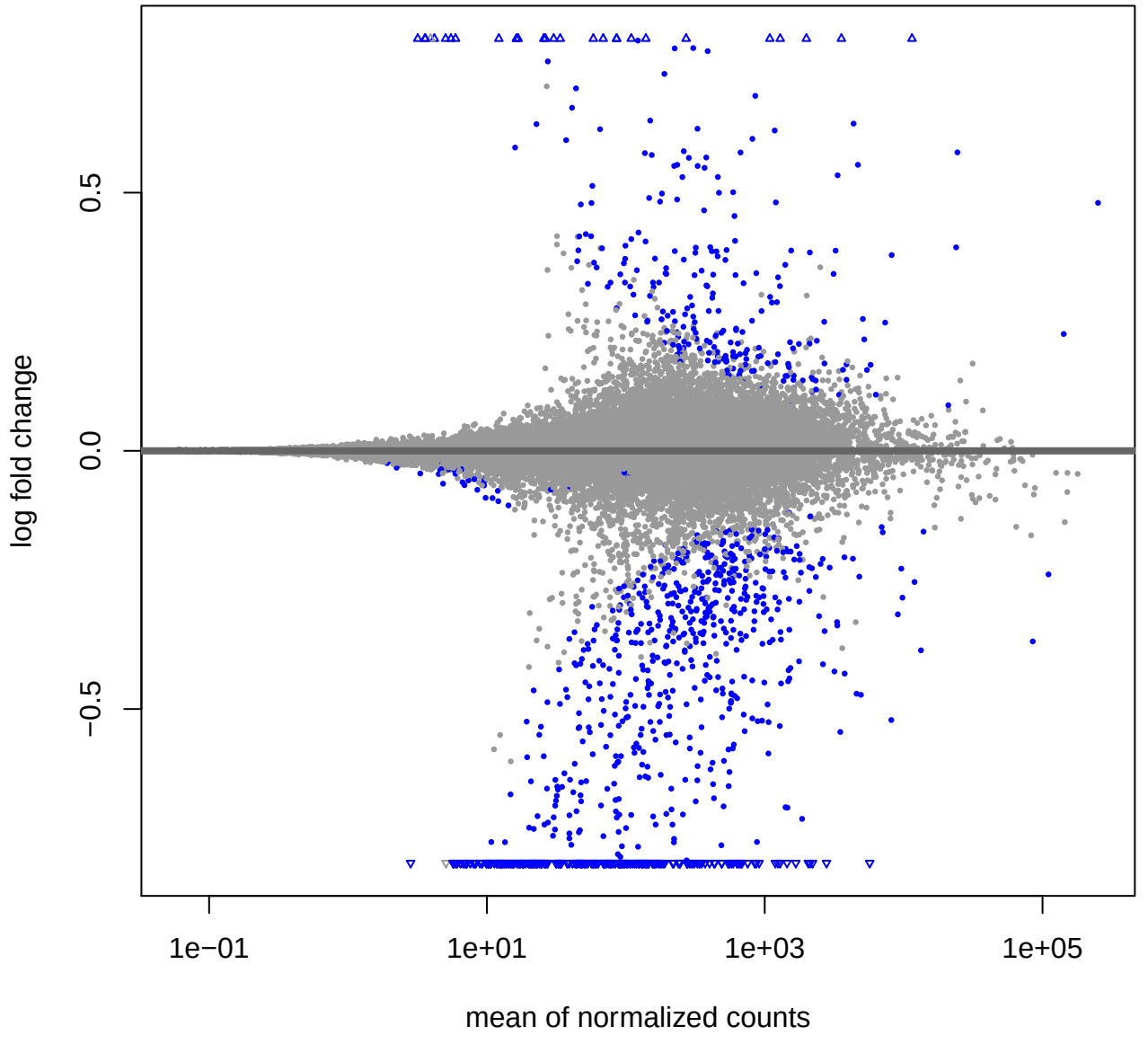
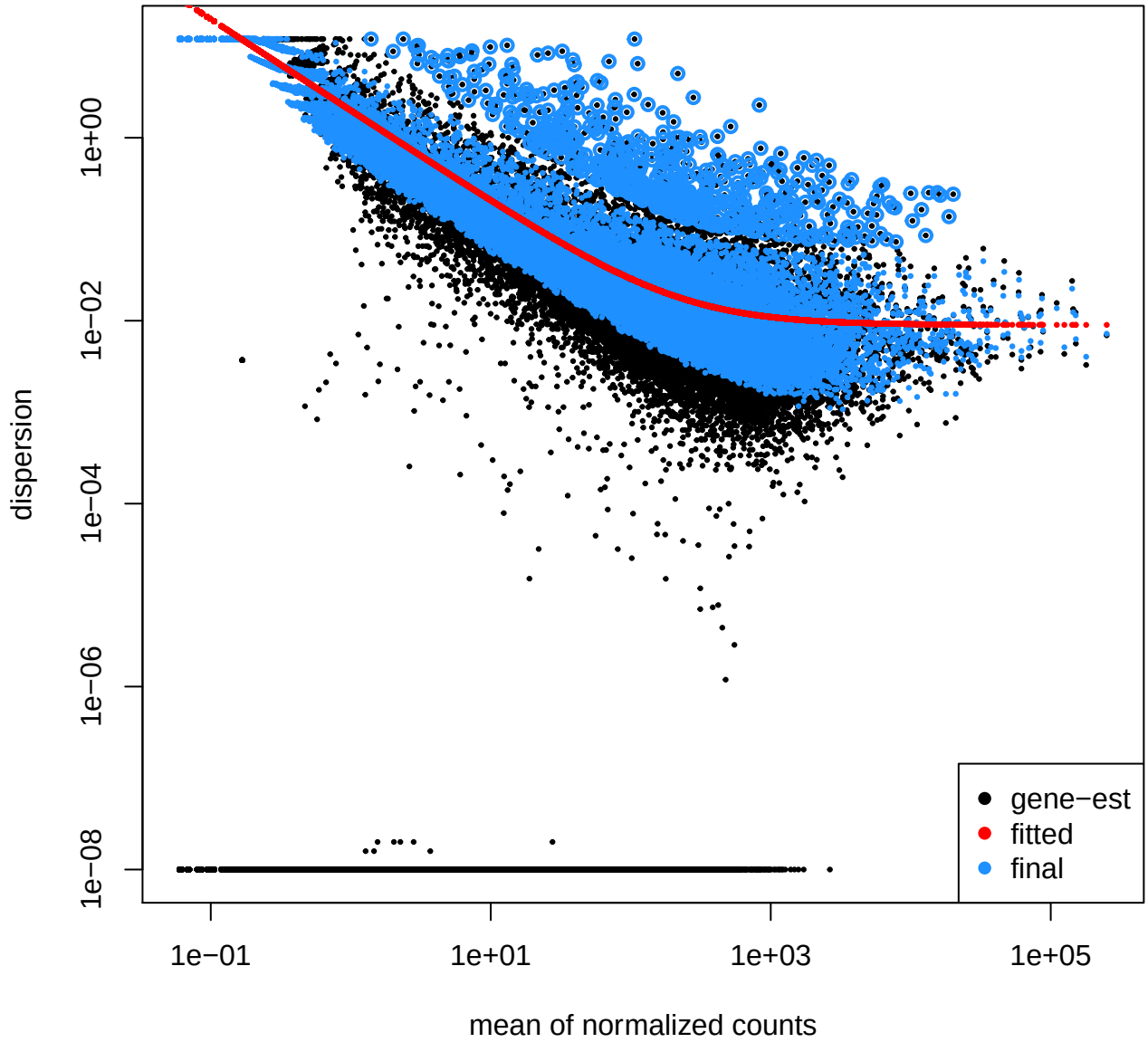

PC2: 20% variance
4
0
−4
−8
−5
0
5
PC1: 34% variance
group
srpk3_hom_ttnb_het
srpk3_wt_ttnb_wt


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


log fold change
0.5
0.0
−0.5
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