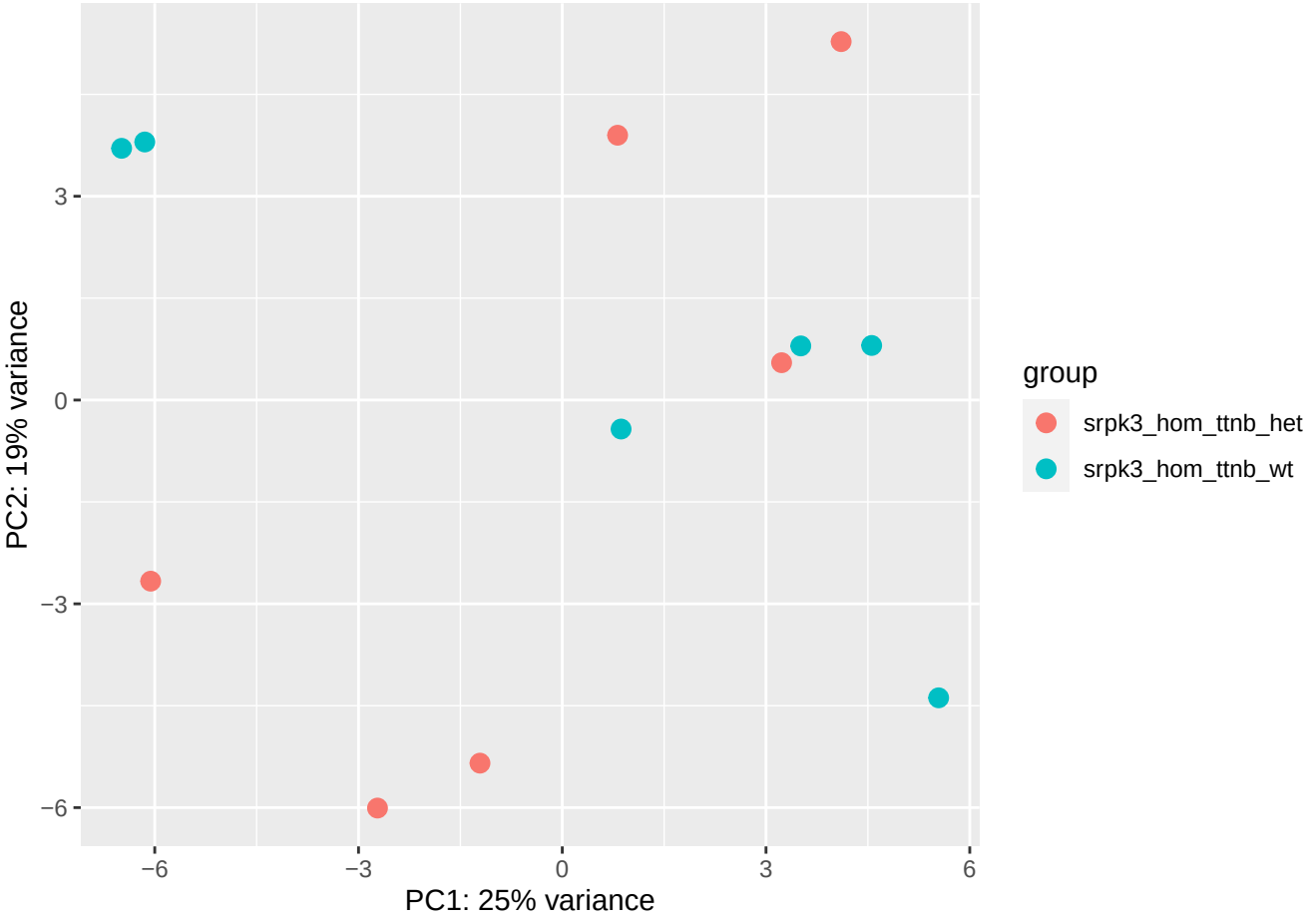
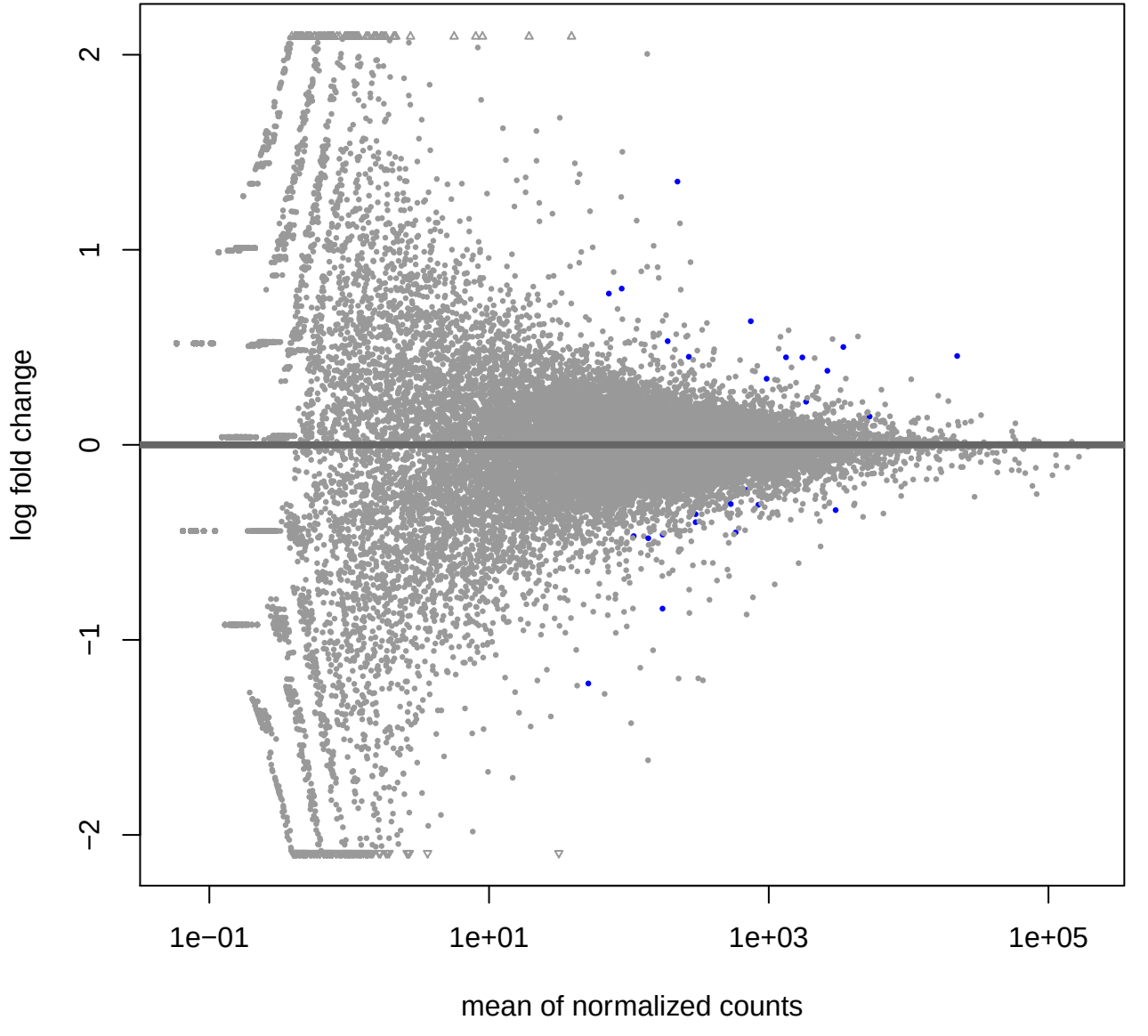
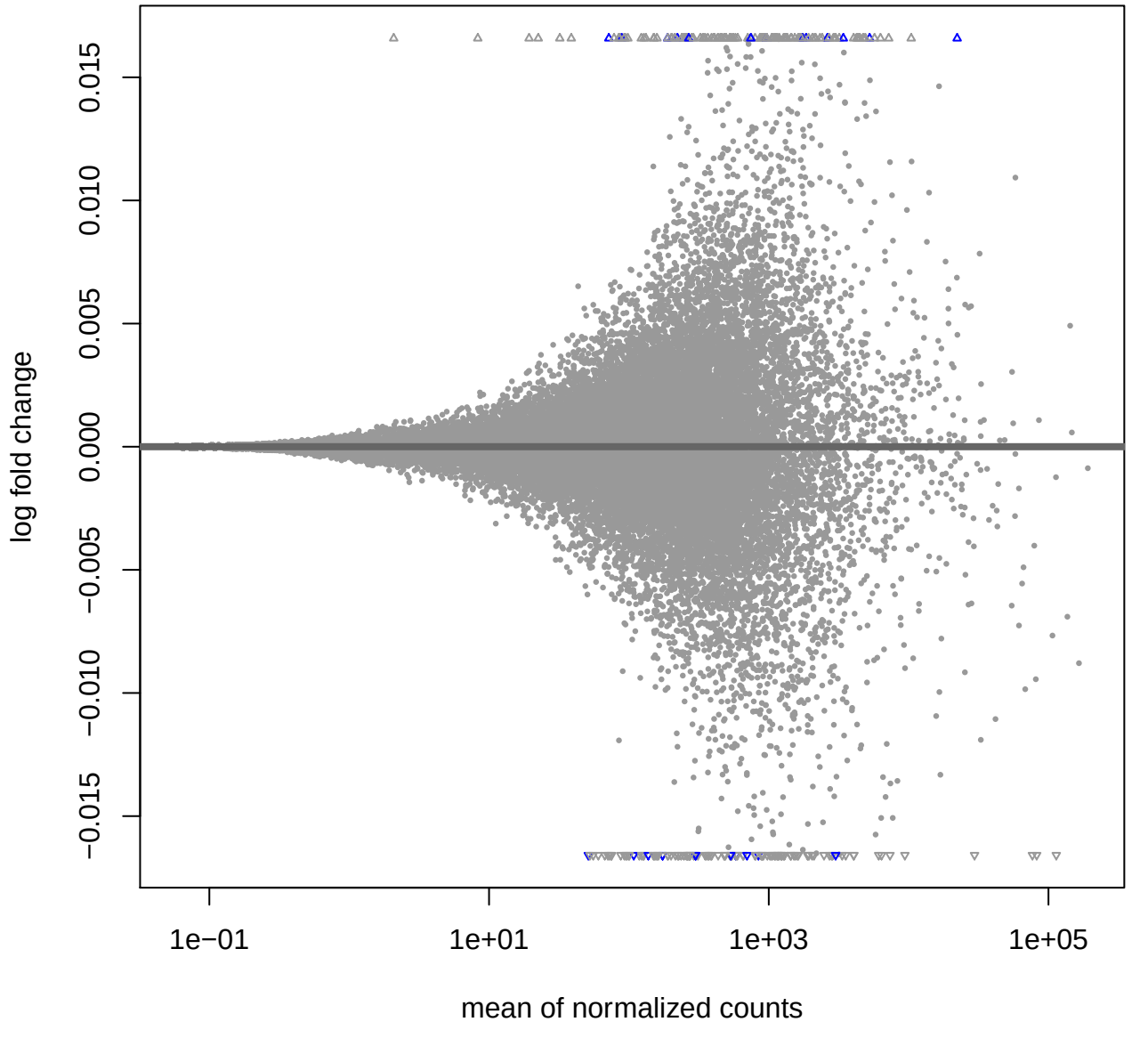
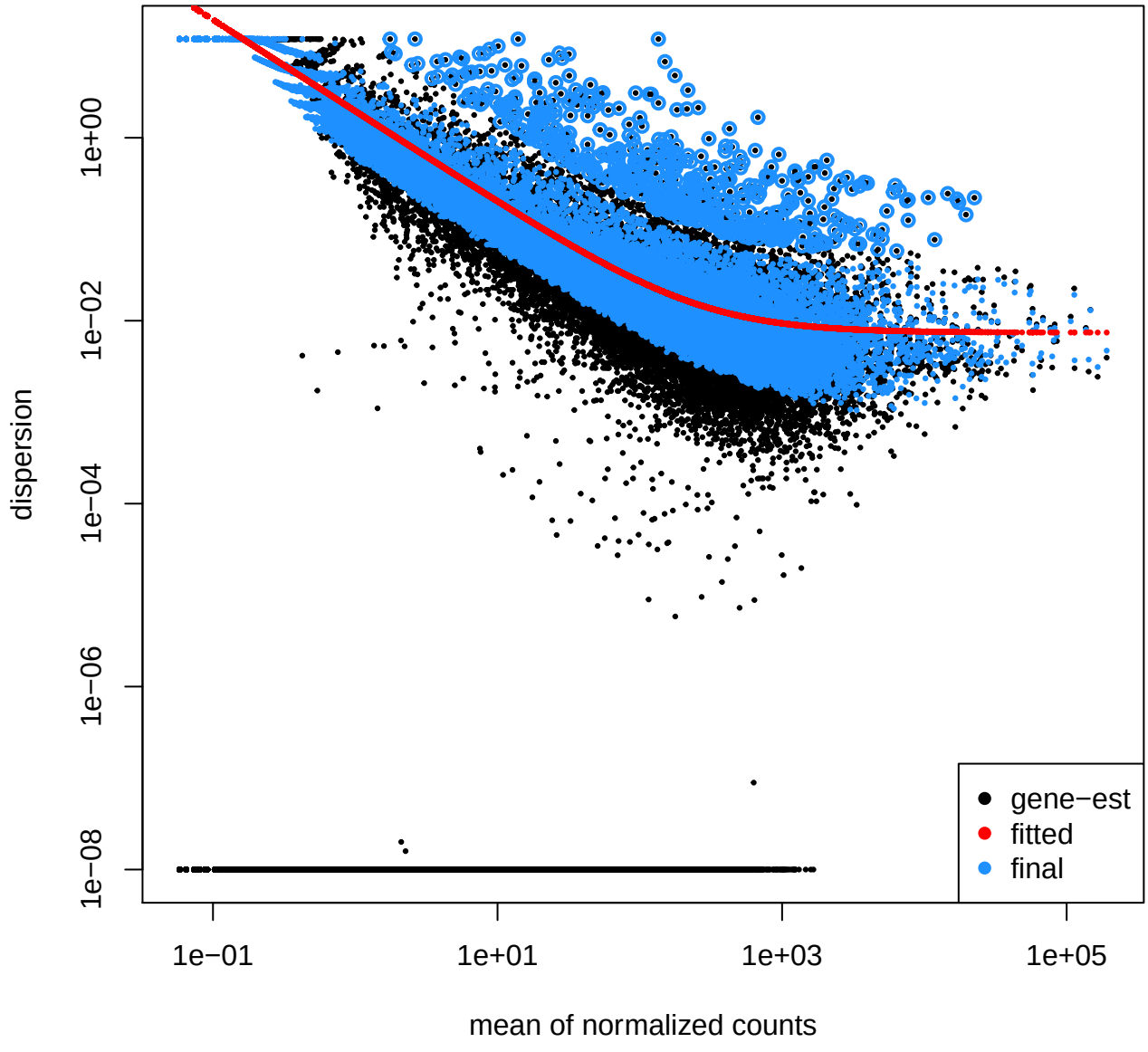

PC2: 19% variance
3
0
−3
−6
−6
−3
0
3
6
PC1: 25% variance
group
srpk3_hom_ttnb_het
srpk3_hom_ttnb_wt


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


log fold change
0.015
0.010
0.005
0.000
−0.005
−0.010
−0.015
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