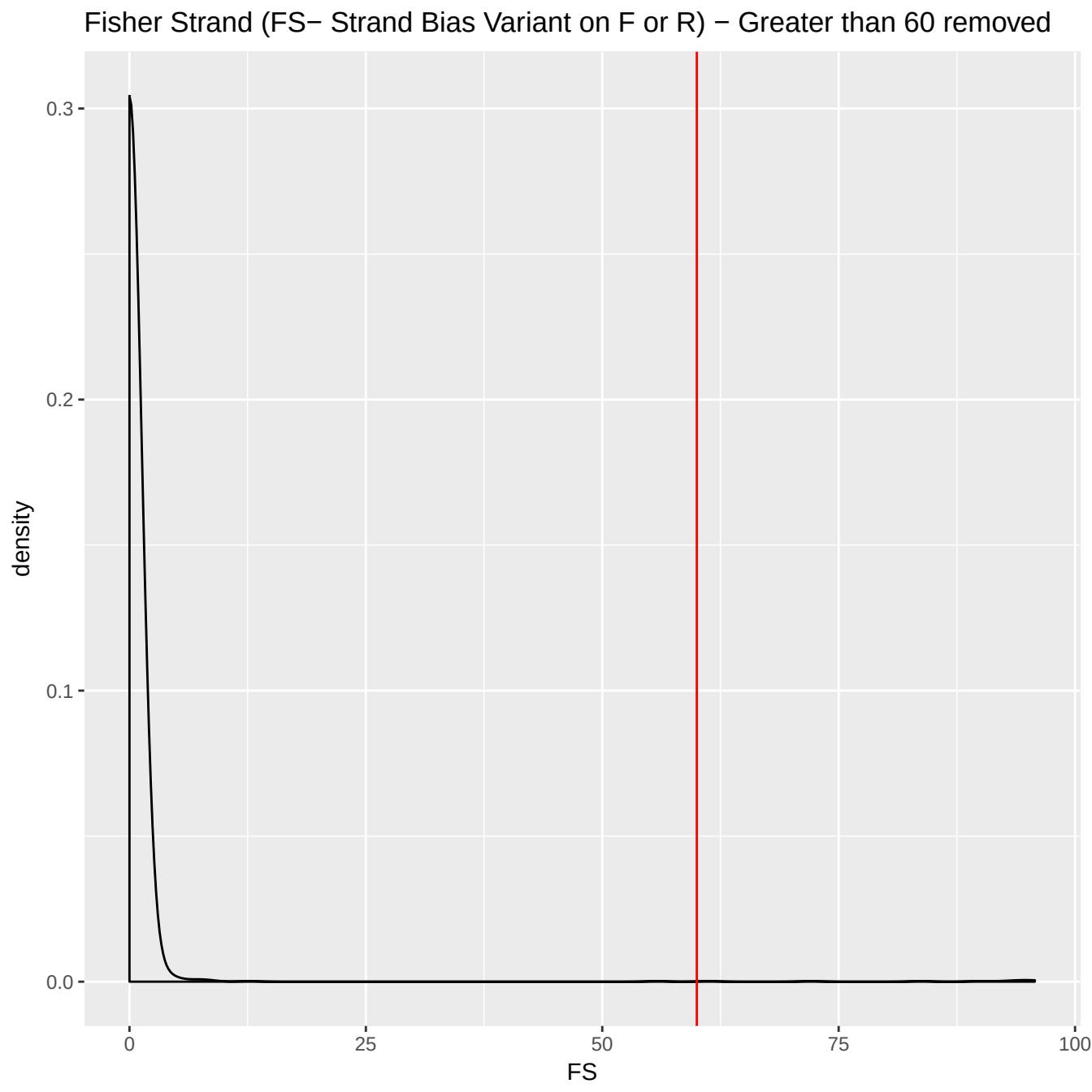
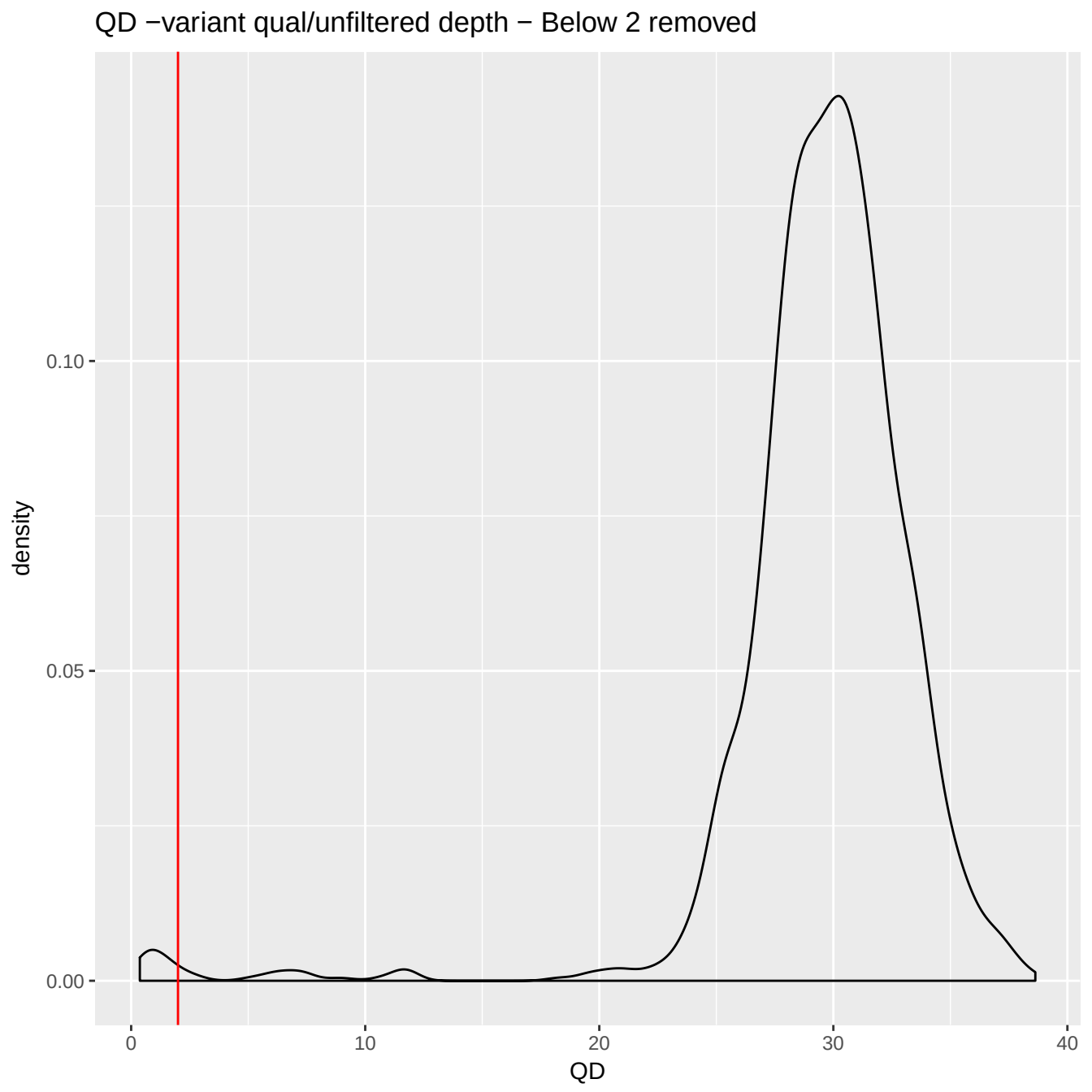
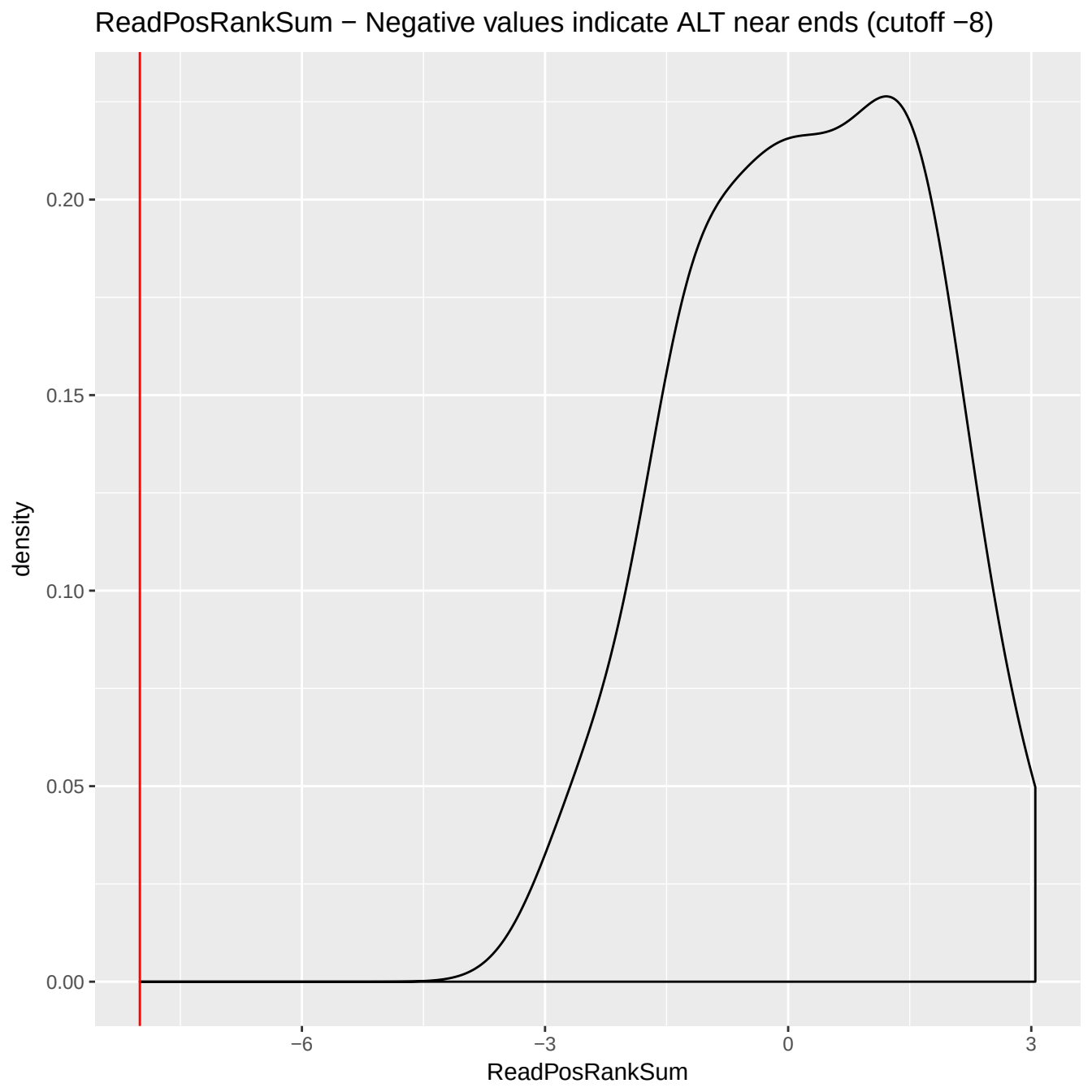
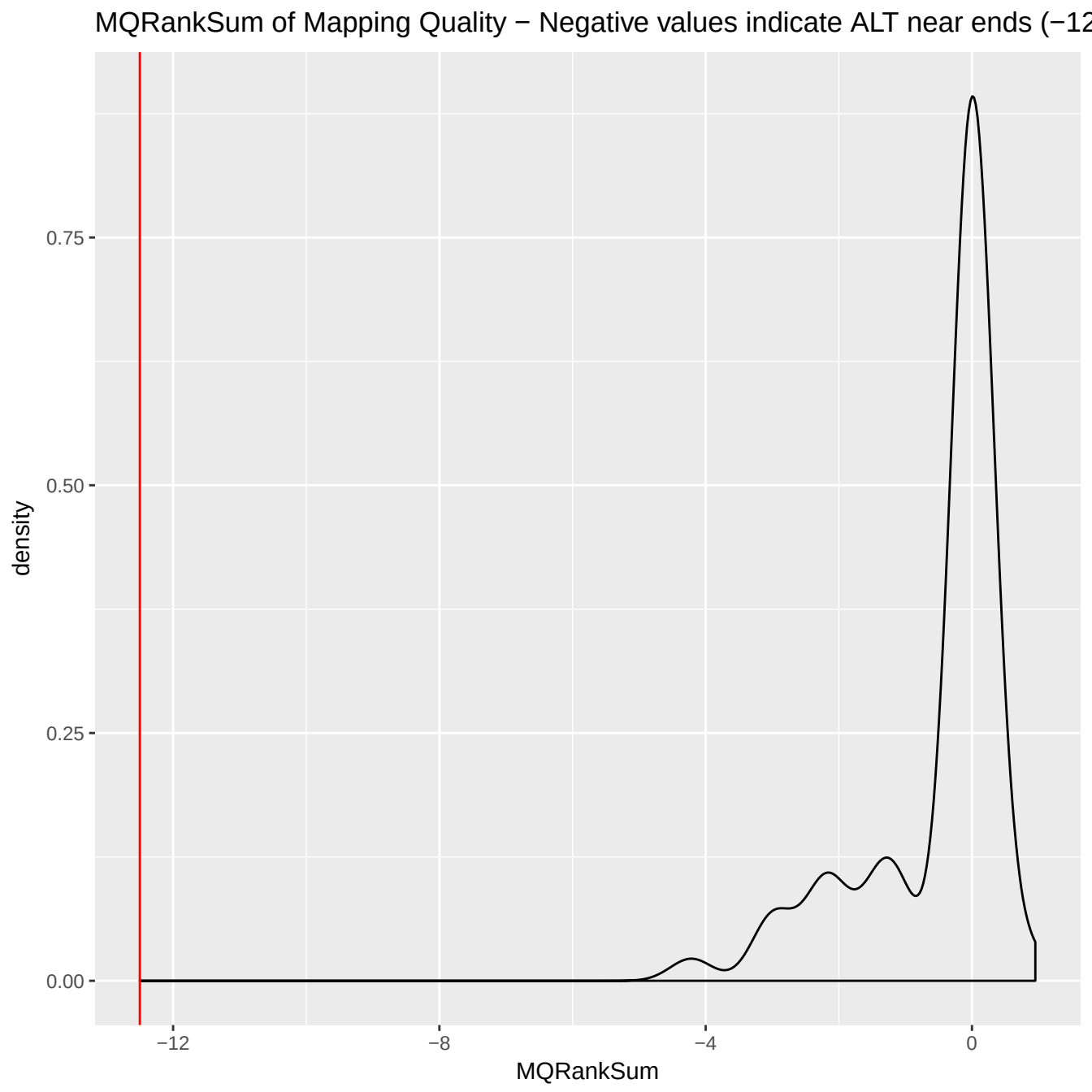
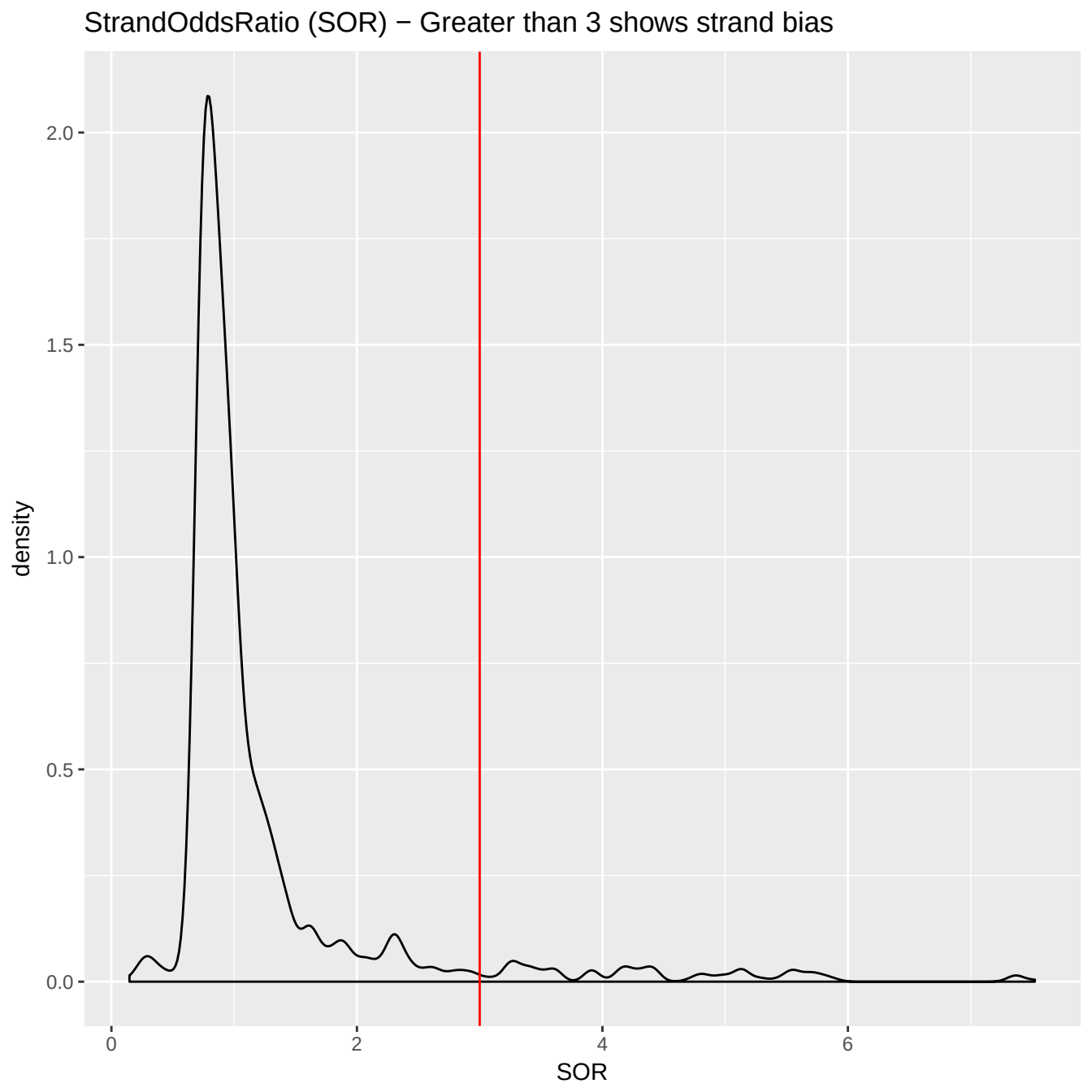
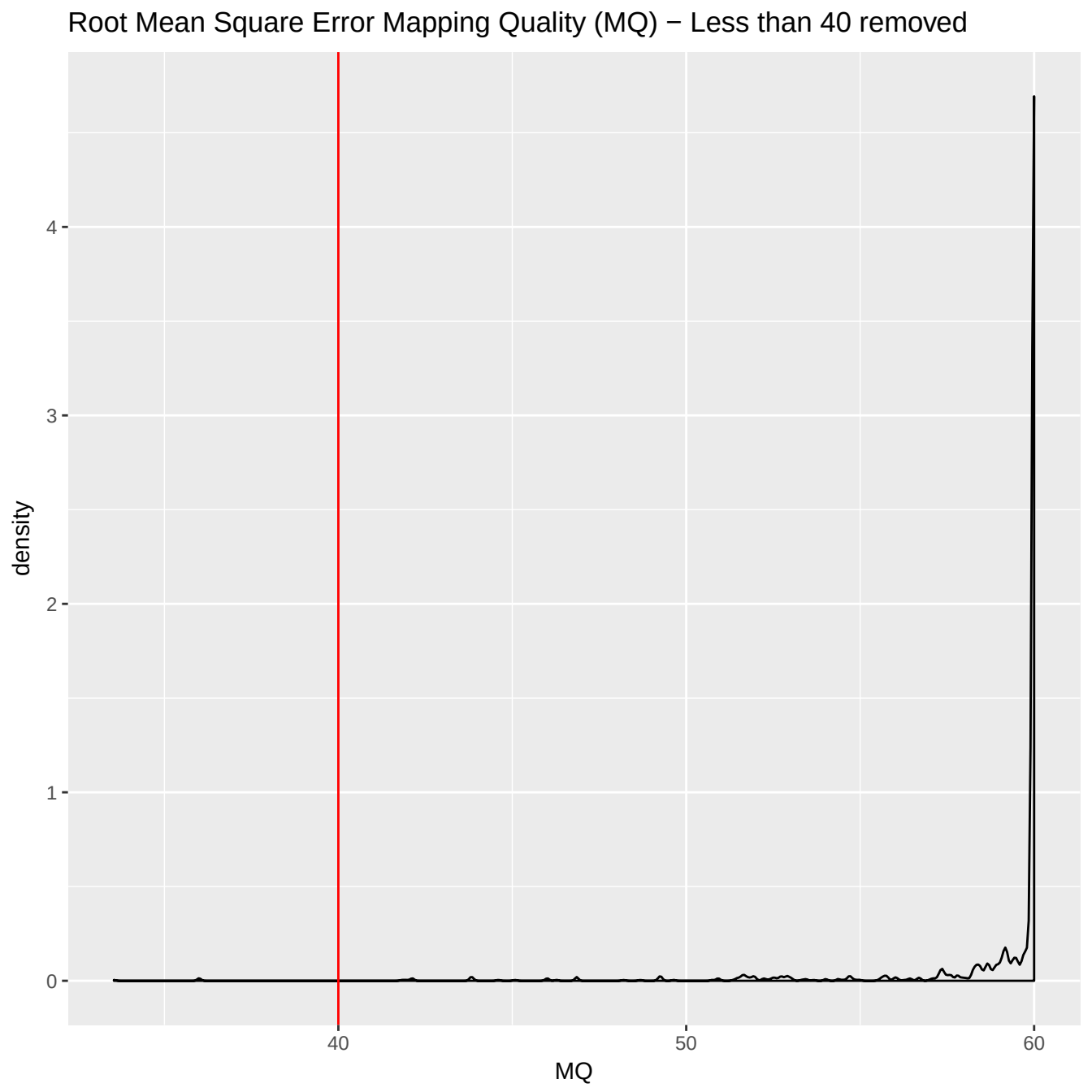

Fisher Strand (FS− Strand Bias Variant on F or R) − Greater than 60 removed
density
0.3
0.2
0.1
0.0
0
25
50
75
100
FS

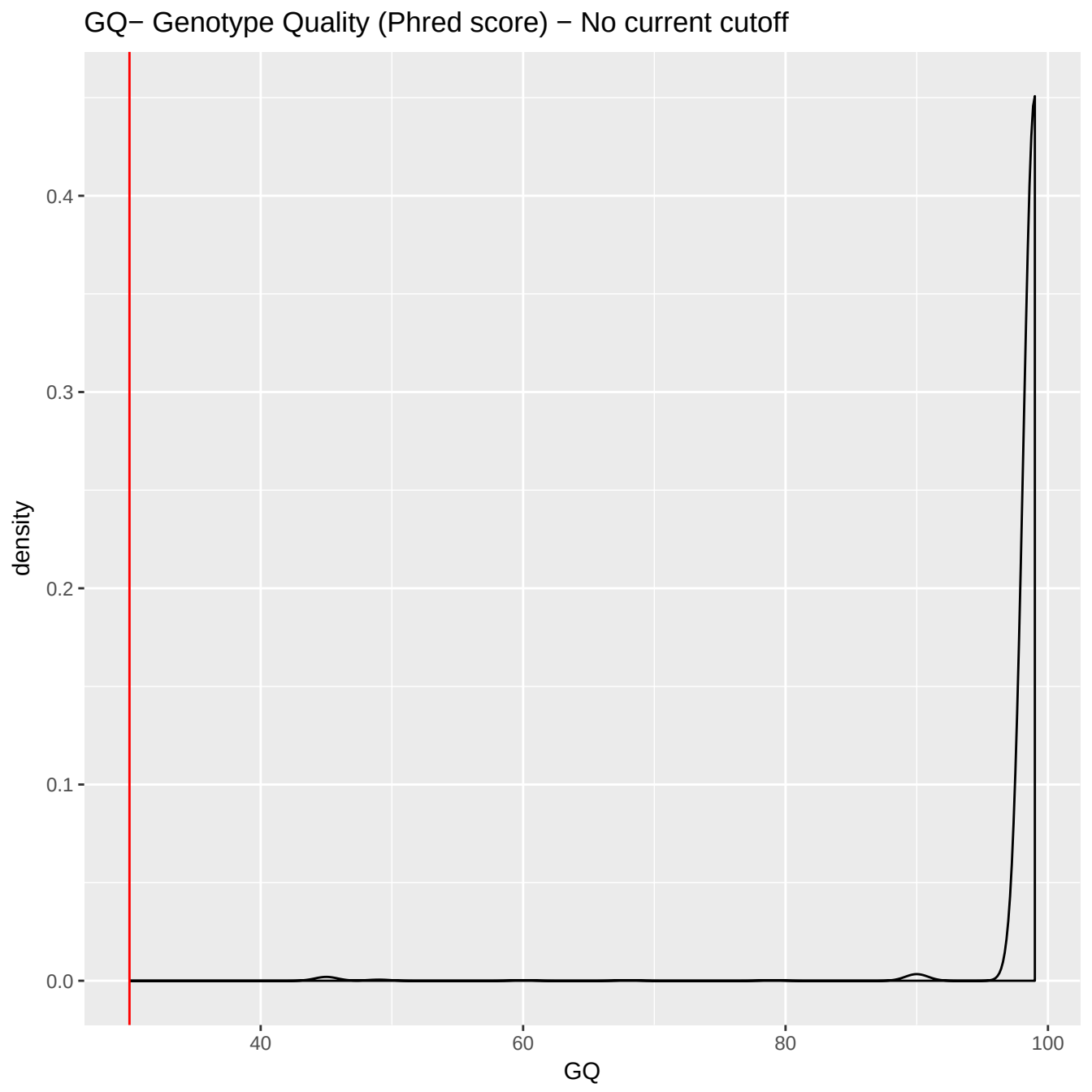

QD −variant qual/unfiltered depth − Below 2 removed
density
0.10
0.05
0.00
0
10
20
30
40
QD

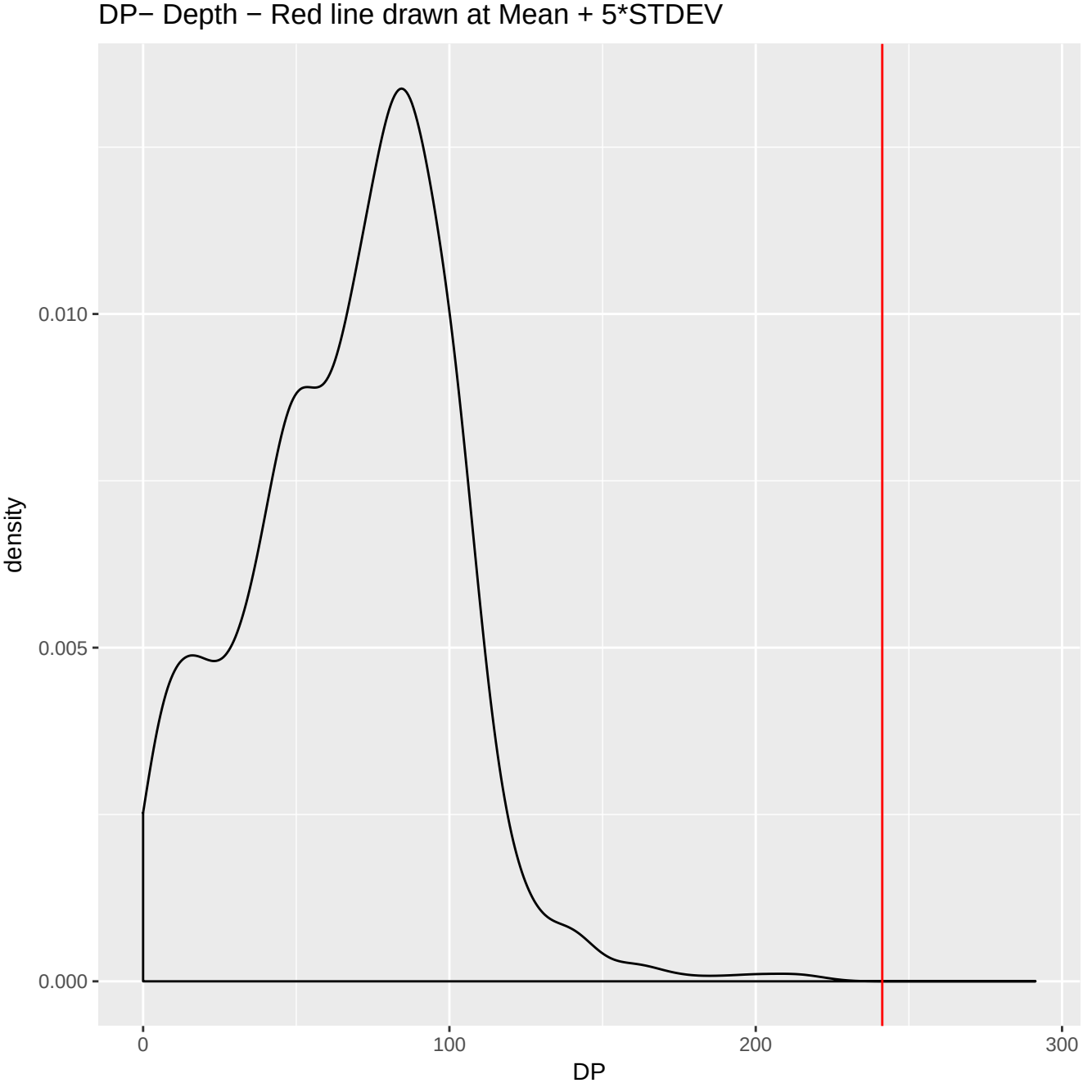

ReadPosRankSum − Negative values indicate ALT near ends (cutoff −8)
density
0.20
0.15
0.10
0.05
0.00
−6
−3
0
3
ReadPosRankSum


MQRankSum of Mapping Quality − Negative values indicate ALT near ends (−12
density
0.75
0.50
0.25
0.00
−12
−8
−4
0
MQRankSum


StrandOddsRatio (SOR) − Greater than 3 shows strand bias
density
2.0
1.5
1.0
0.5
0.0
0
2
4
6
SOR


Root Mean Square Error Mapping Quality (MQ) − Less than 40 removed
density
0
1
2
3
4
40
50
60
MQ


GQ− Genotype Quality (Phred score) − No current cutoff
density
0.4
0.3
0.2
0.1
0.0
40
60
80
100
GQ


DP− Depth − Red line drawn at Mean + 5*STDEV
density
0.010
0.005
0.000
0
100
200
300
DP

Depth Statistics

	mean	SD	mean_plus_5xSD
1	68.979102642901	34.4658349960375	241.308277623089