

Read name: sample_tumor-RA

Mapping rate: 59.0%

Duplication rate: 30.8%

ContEst rate: 18.8%

Depth Quarter

Mapq	Min	1stQ	Median	Mean	3rdQ	Max
0	0.0	392.0	621.0	751.2	962.0	12544.0
20	0.0	391.0	620.0	750.1	960.0	12544.0
30	0.0	391.0	620.0	749.8	960.0	12544.0

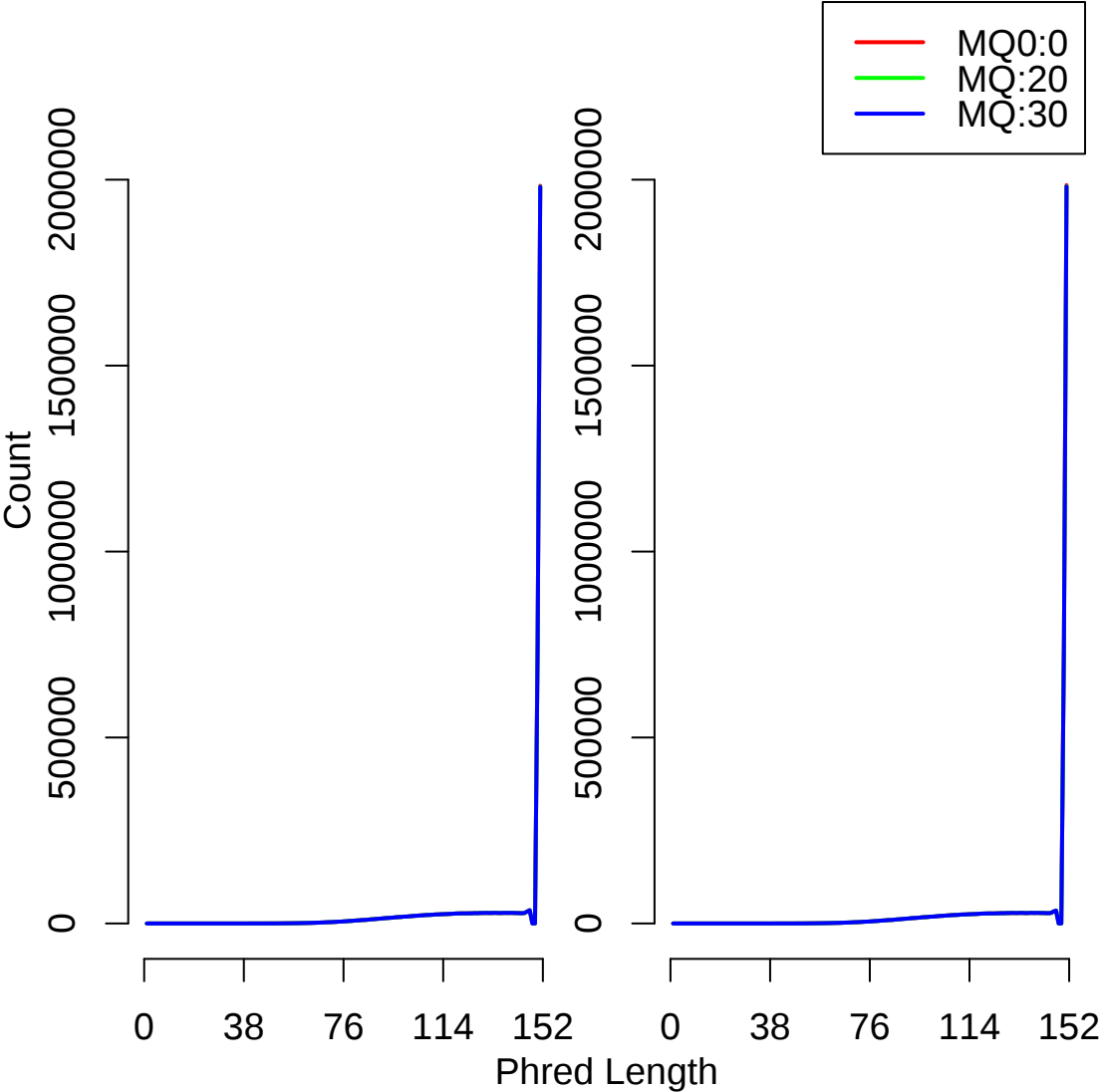
Depth Target Occupied

Mapq	Depth>=20	Depth>=100	Depth>=300
0	99.8	98.1	84.4
20	99.8	98.0	84.3
30	99.8	98.0	84.3

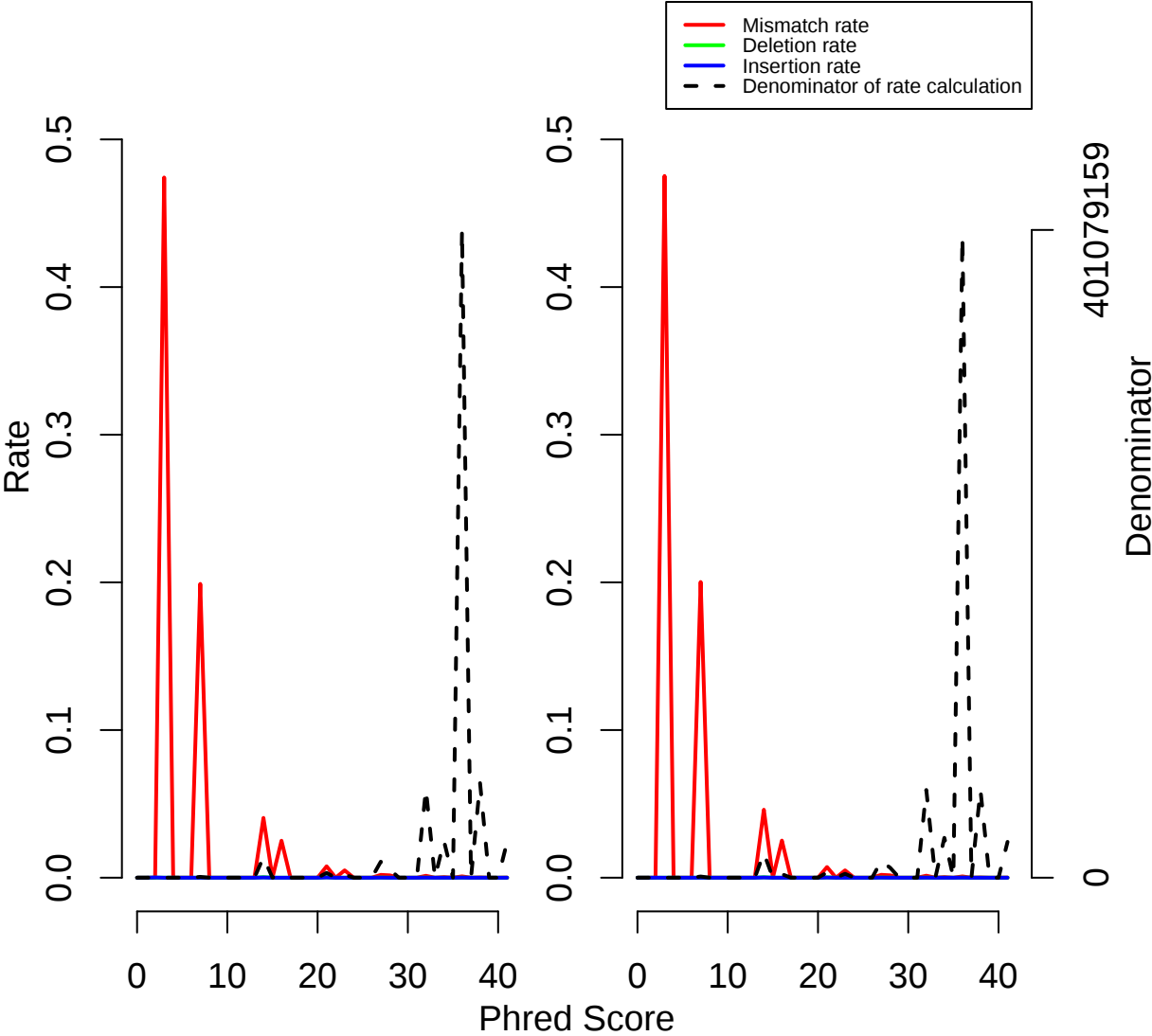
Depth Uniformity

Mapq	Depth>=0.1*Average	Depth>=0.2*Average	Depth>=0.5*Average
0	98.8	95.8	76.7
20	98.7	95.8	76.7
30	98.7	95.8	76.7

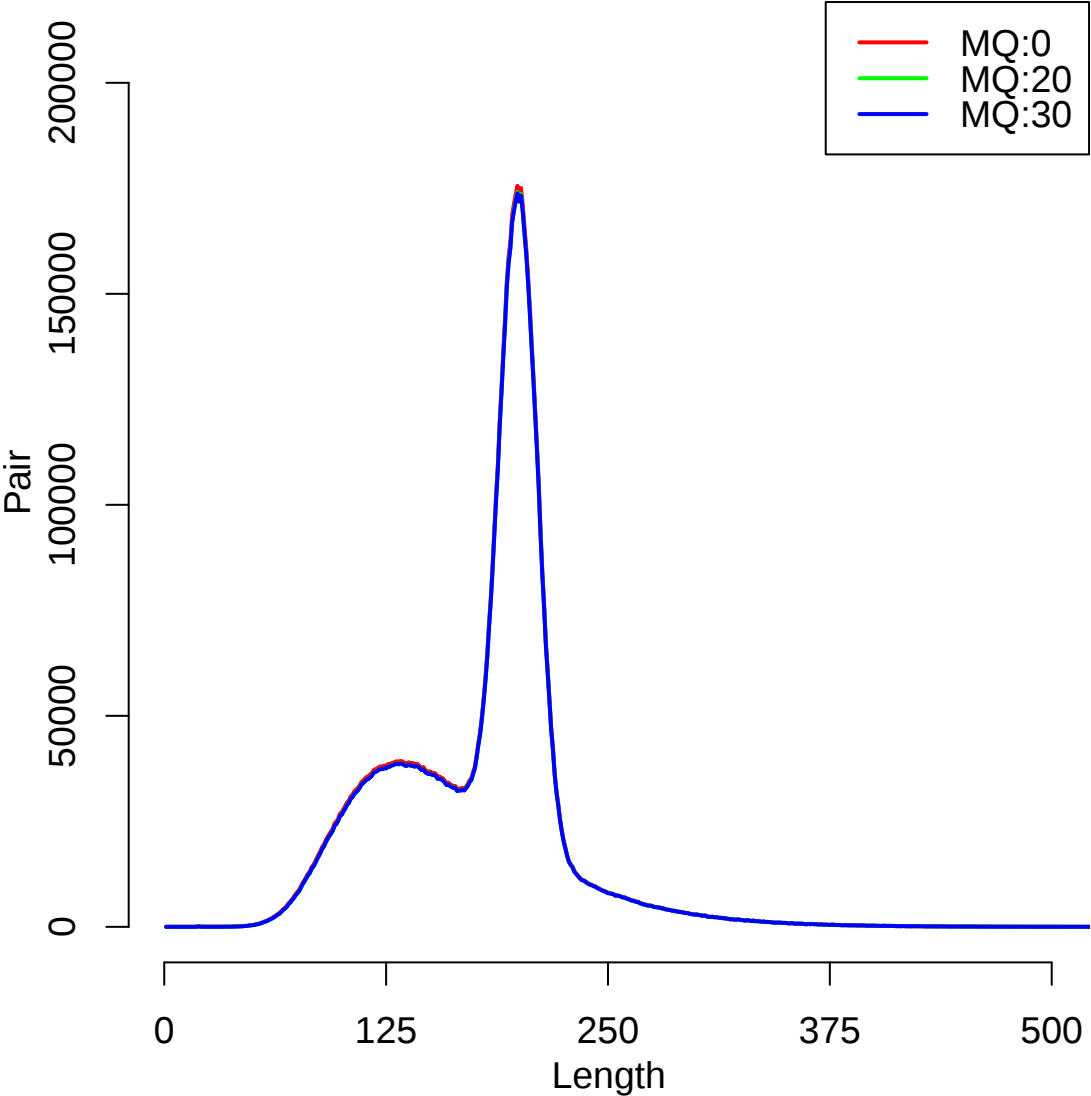
Read Length Distribution



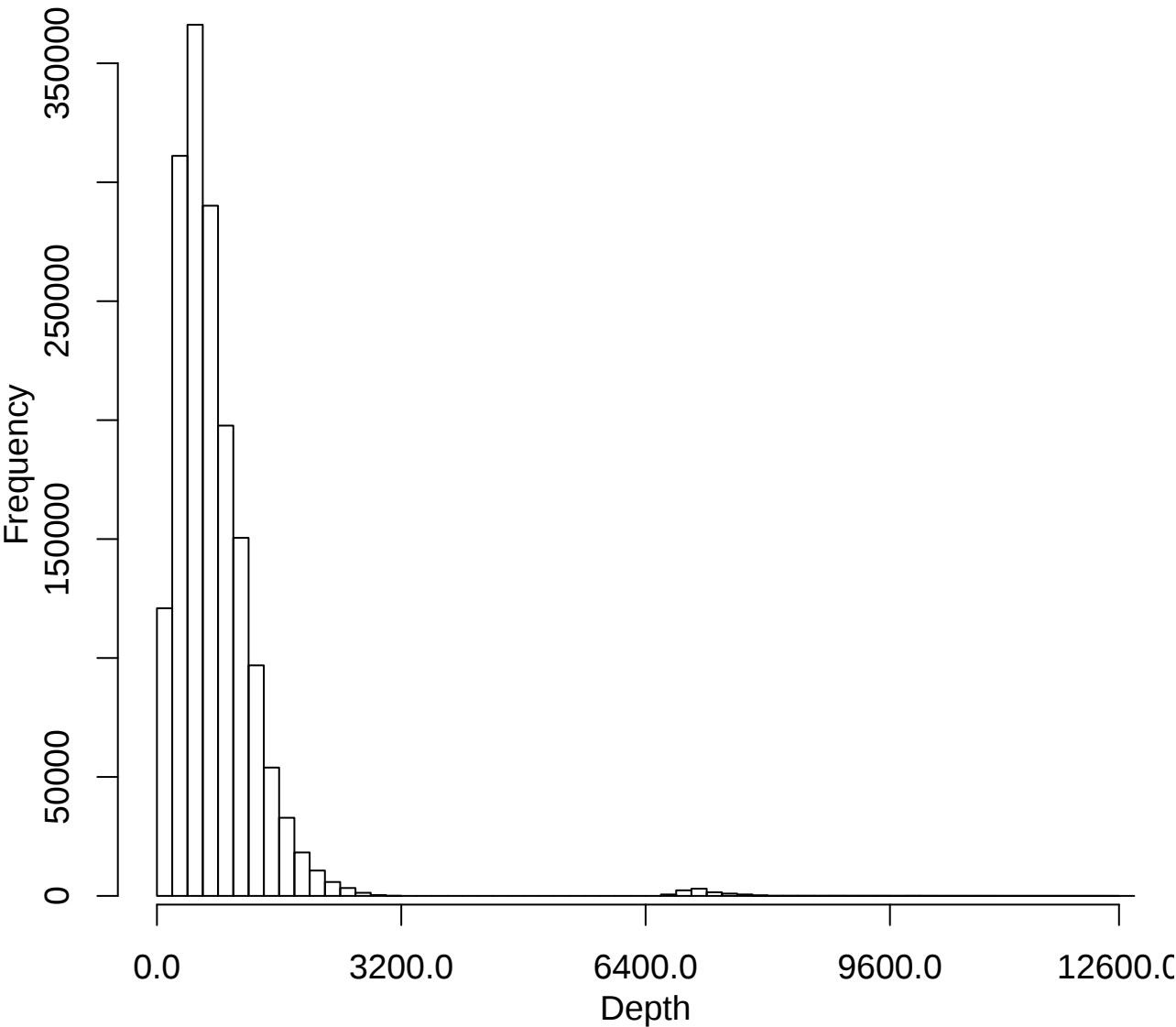
Mismatch Rate on Phred Score



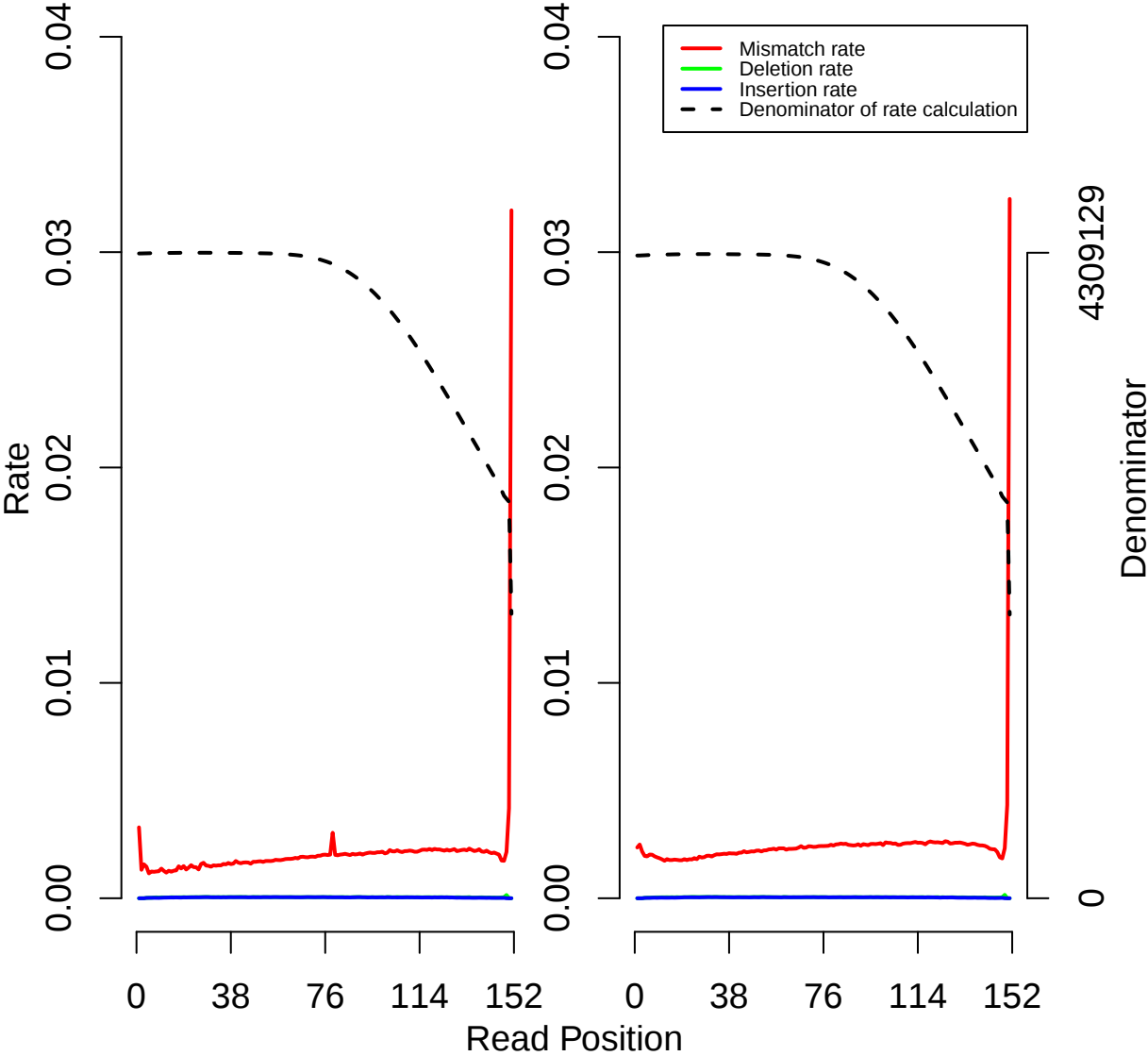
Insert Length Distribution



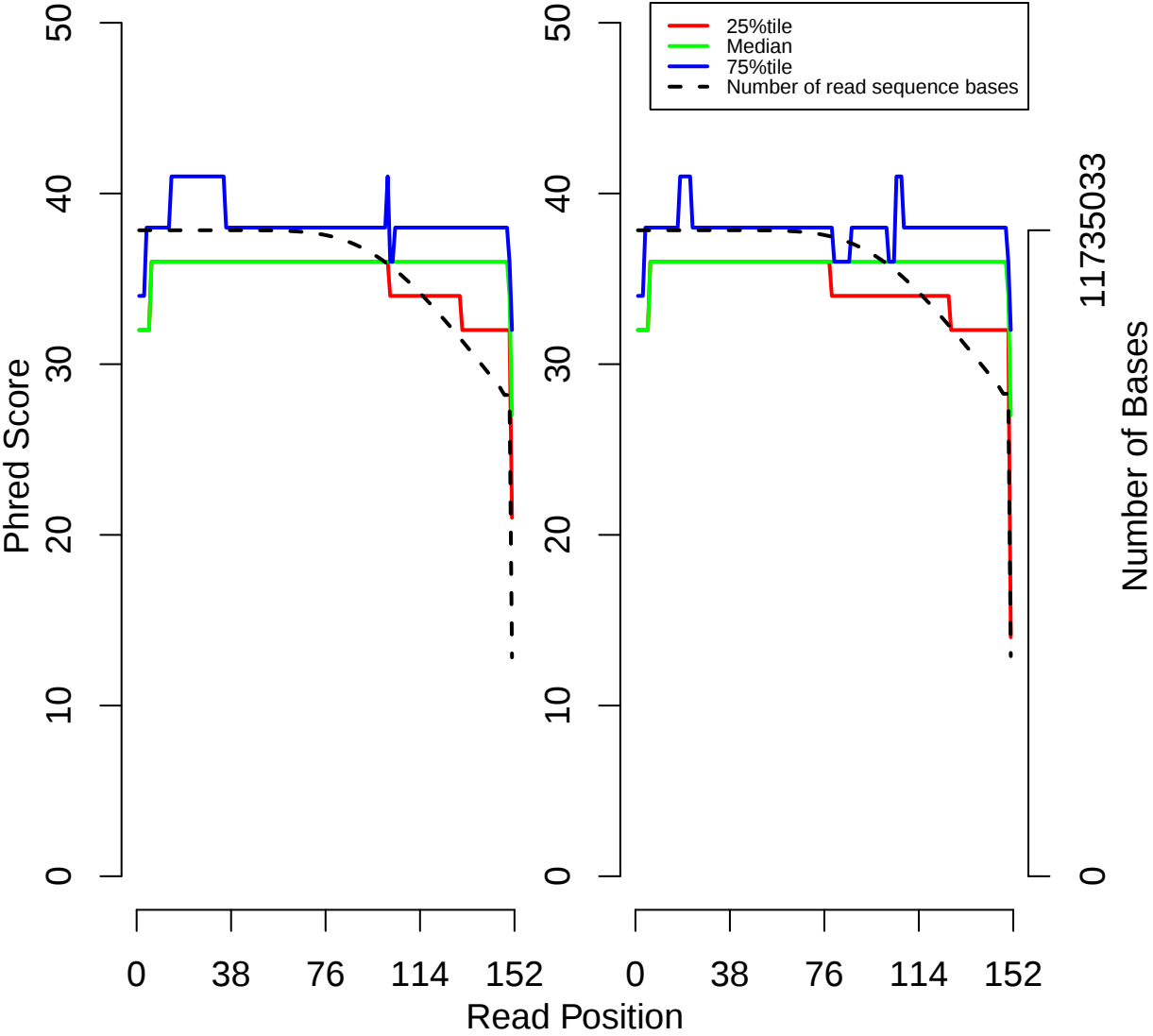
Depth Frequency Histogram



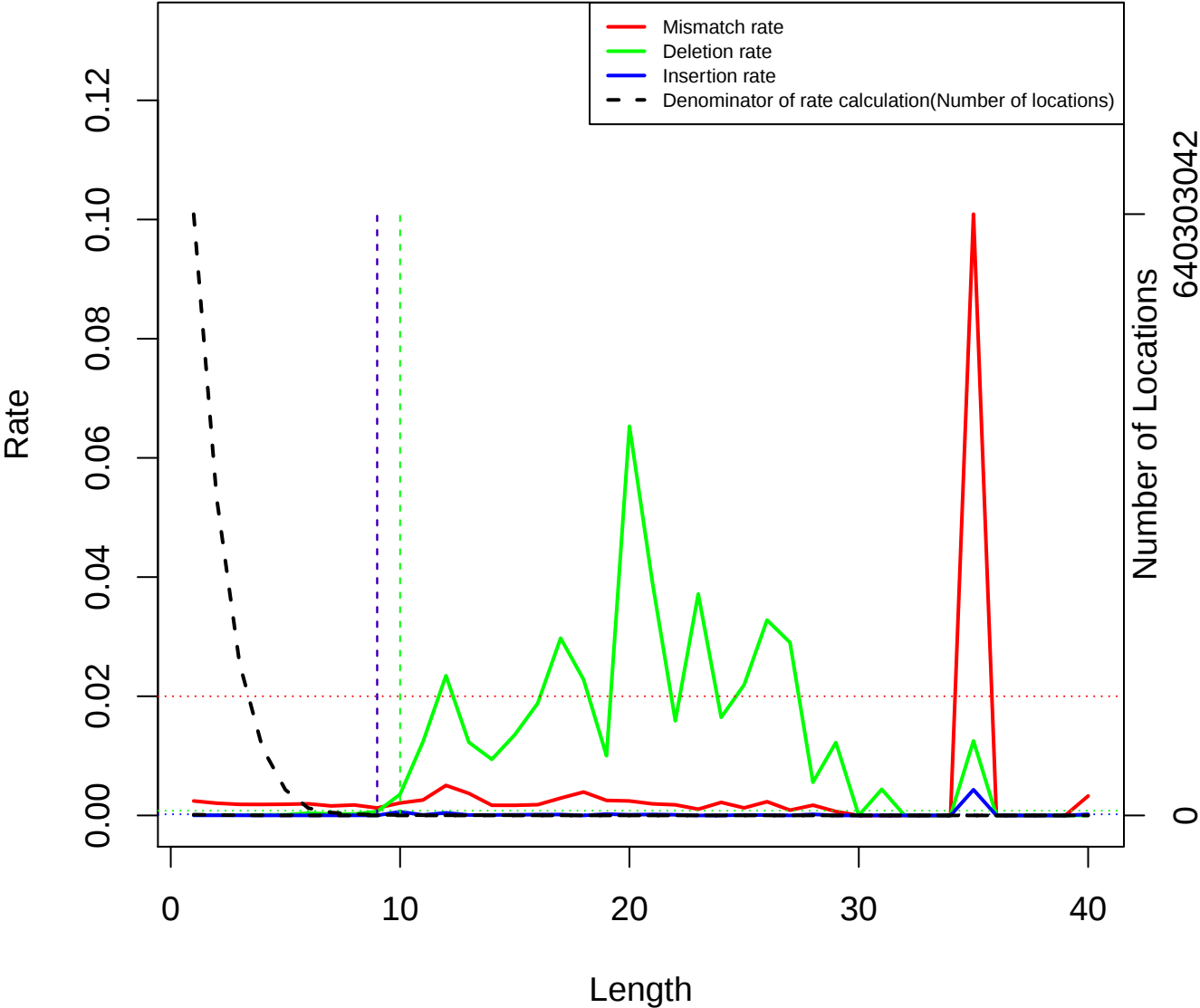
Mismatch Rate on Read Position



Phred Score Distribution on Read Position



Mismatch Rate on Homopolymer Length



The dotted line shows the respective Max – permissive rate,and the dashed line shows the respective Cutoff length.

Read name: sample_normal-RA

Mapping rate: 81.6%

Duplication rate: 32.8%

Depth Quarter

Mapq	Min	1stQ	Median	Mean	3rdQ	Max
0	0.0	381.0	584.0	632.9	835.0	3126.0
20	0.0	380.0	583.0	631.9	834.0	3126.0
30	0.0	380.0	583.0	631.7	834.0	3126.0

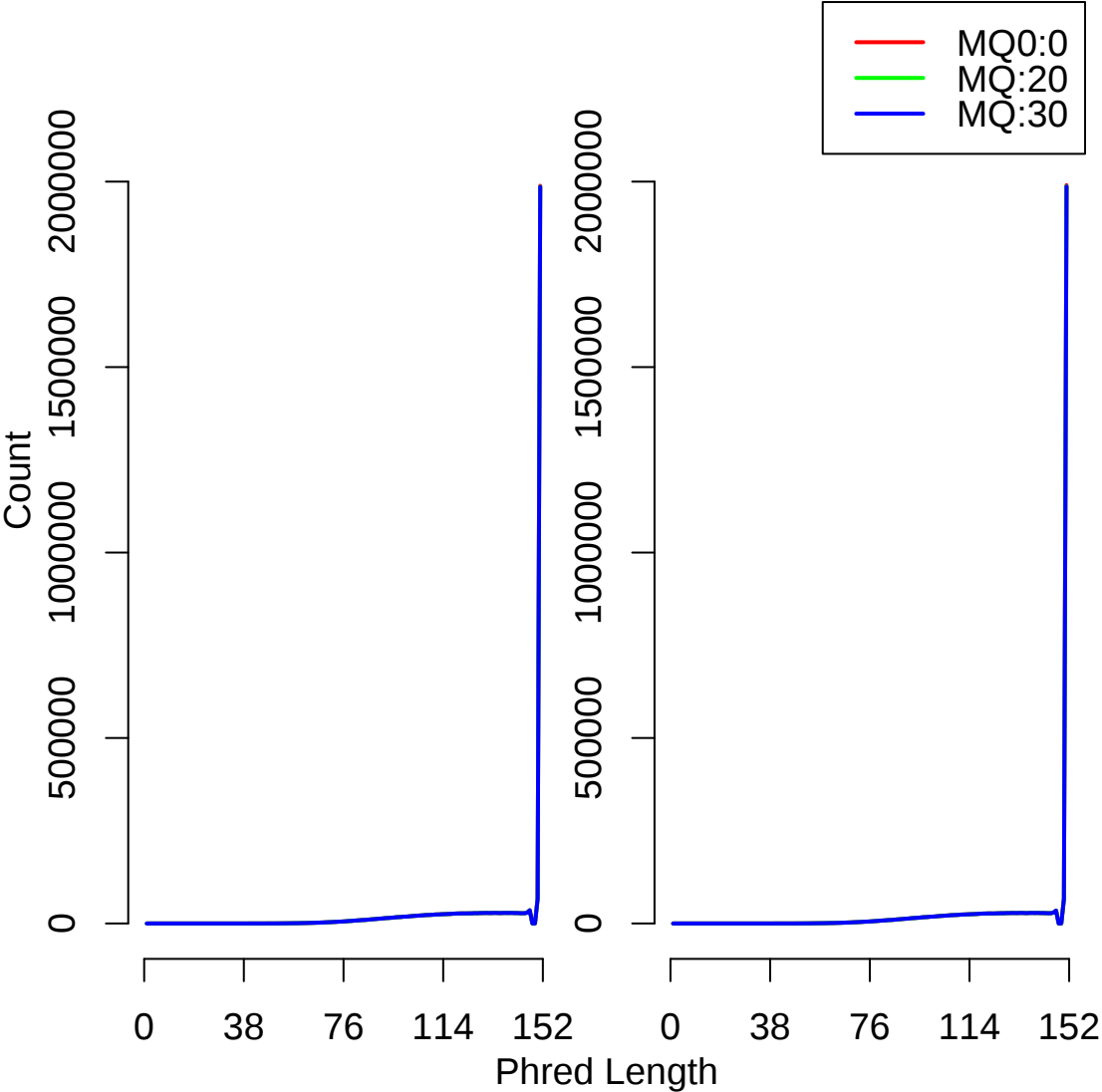
Depth Target Occupied

Mapq	Depth>=20	Depth>=100	Depth>=300
0	99.8	98.0	83.7
20	99.8	98.0	83.6
30	99.8	98.0	83.6

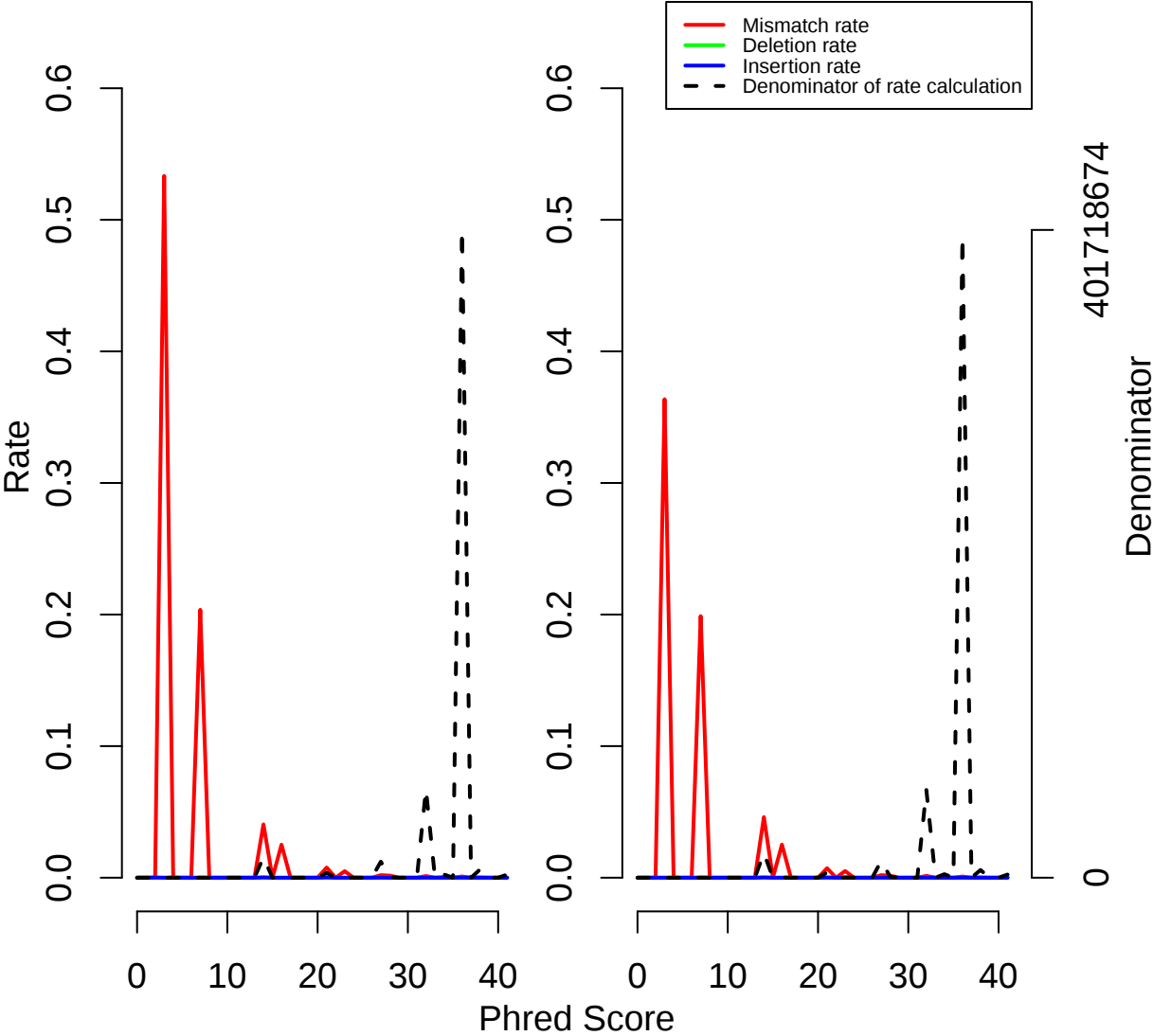
Depth Uniformity

Mapq	Depth>=0.1*Average	Depth>=0.2*Average	Depth>=0.5*Average
0	99.0	96.9	81.9
20	99.0	96.9	81.9
30	99.0	96.8	81.9

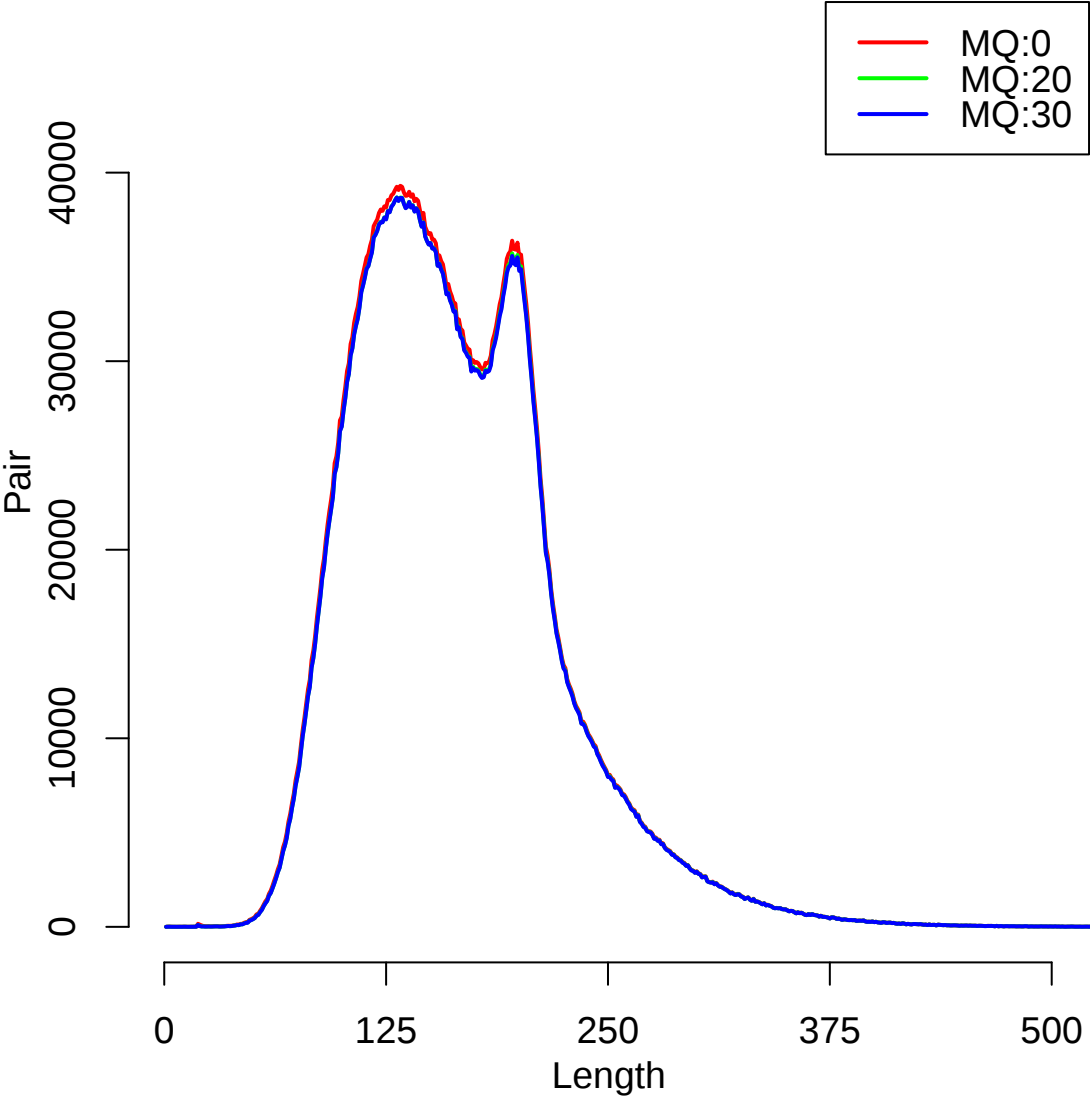
Read Length Distribution



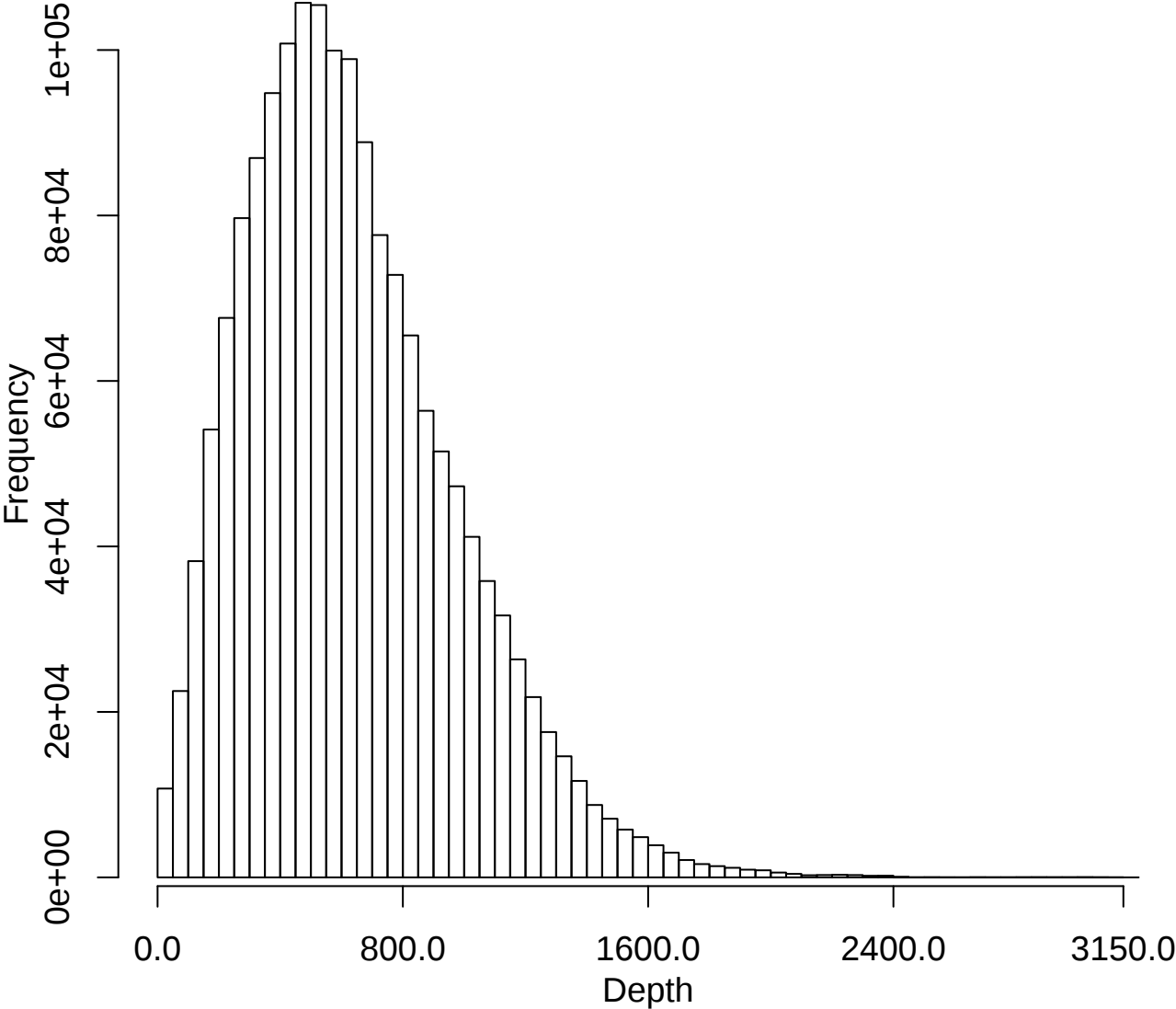
Mismatch Rate on Phred Score



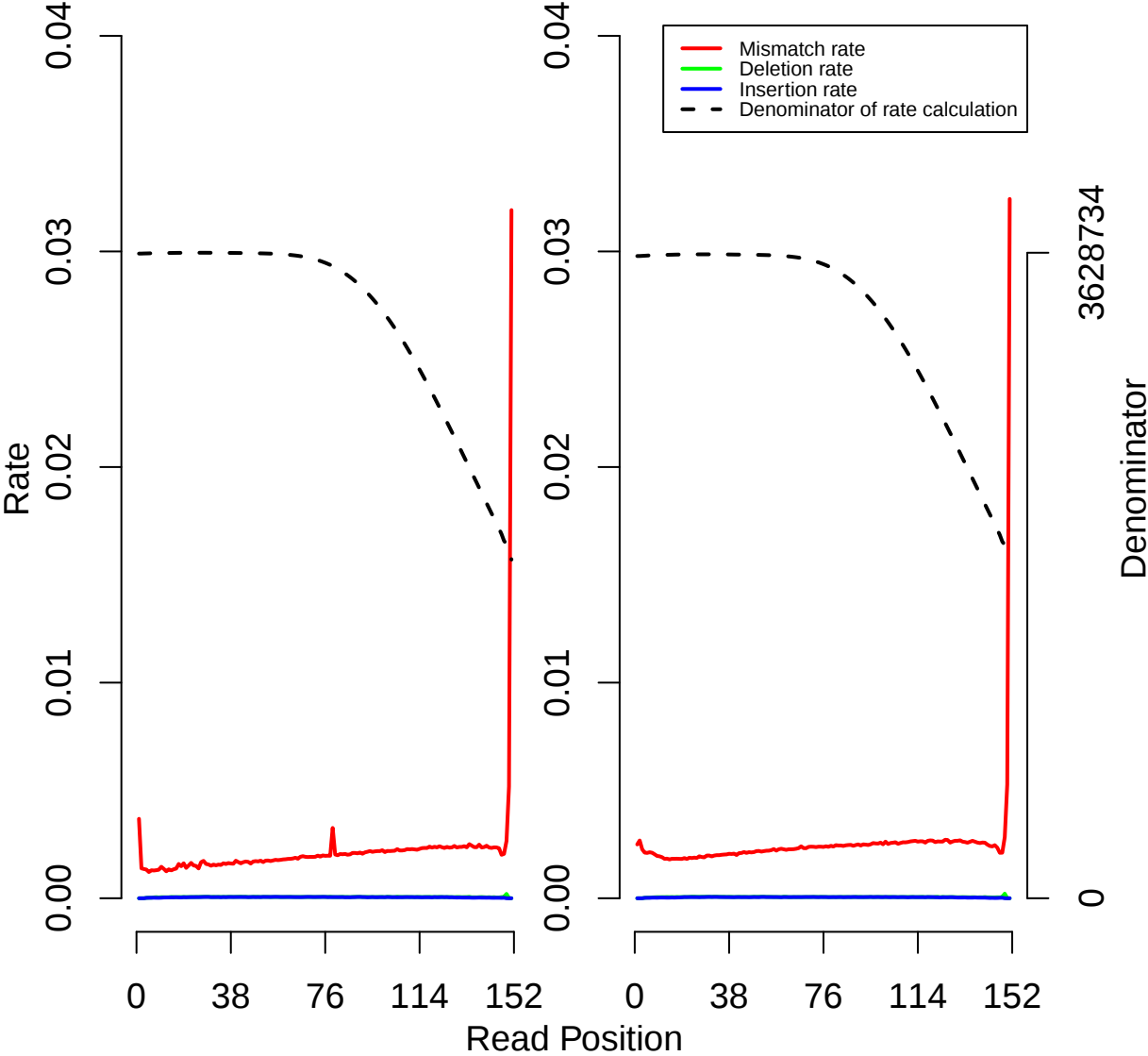
Insert Length Distribution



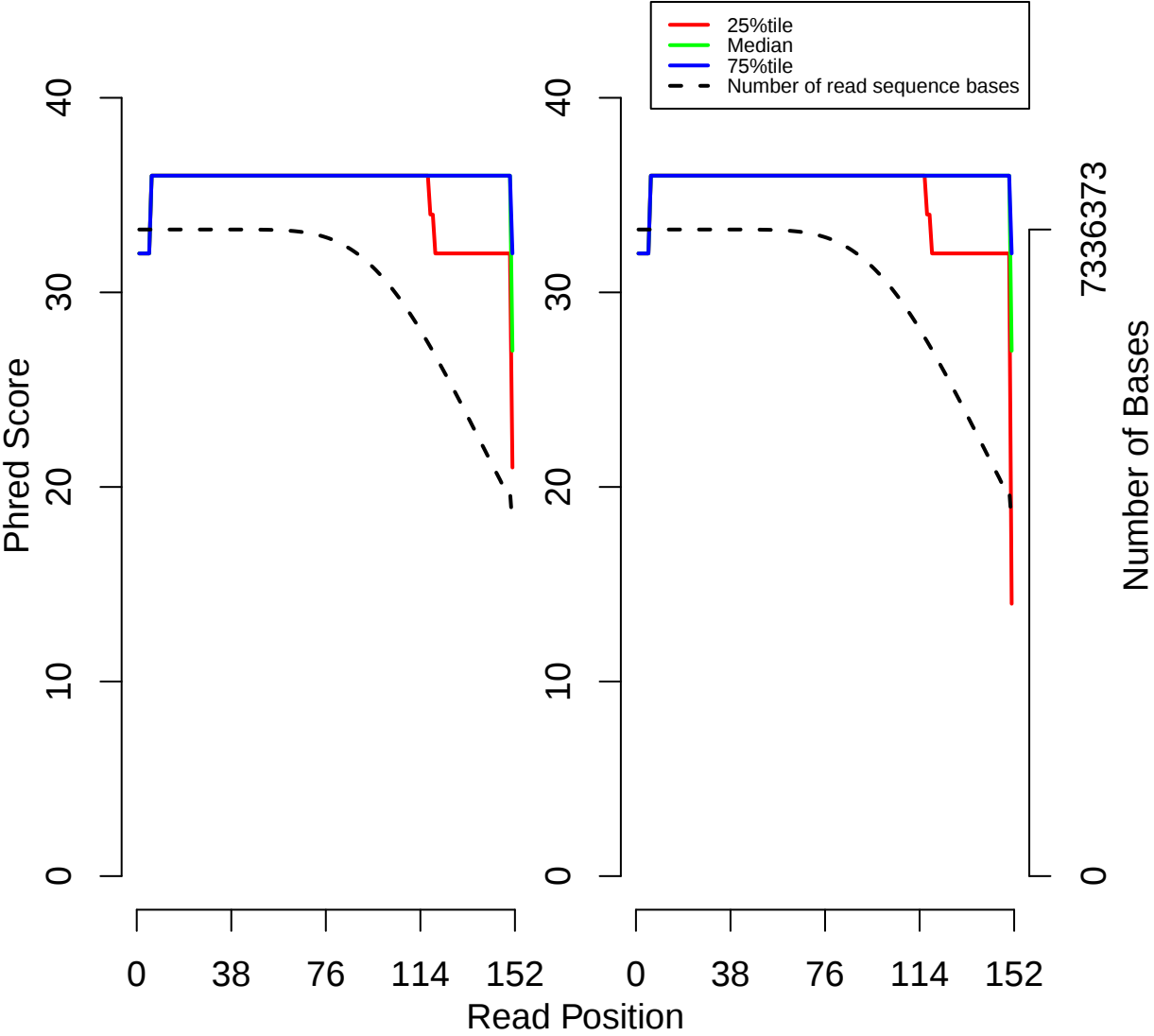
Depth Frequency Histogram



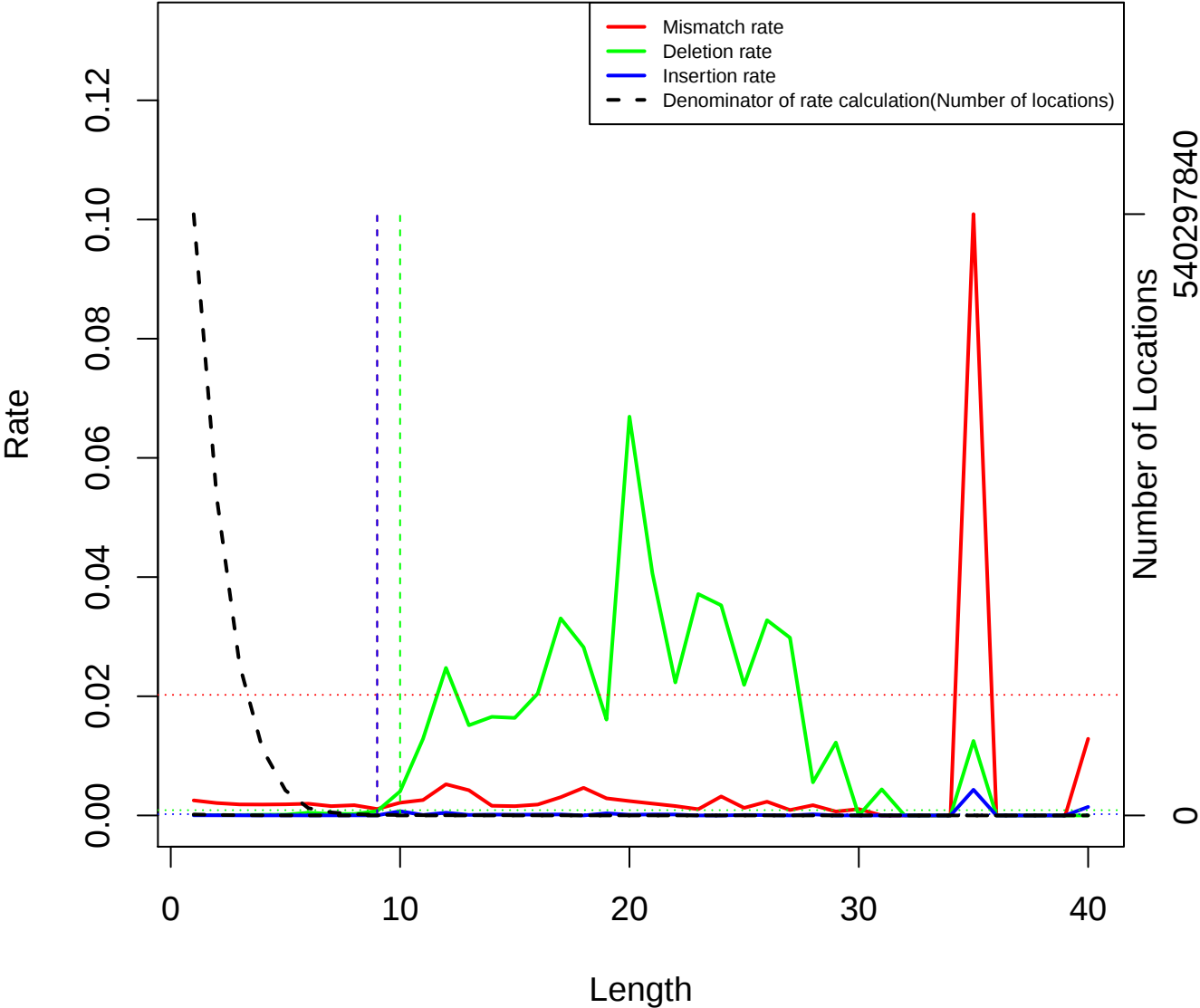
Mismatch Rate on Read Position



Phred Score Distribution on Read Position



Mismatch Rate on Homopolymer Length



The dotted line shows the respective Max – permissive rate,and the dashed line shows the respective Cutoff length.