QC stats

Before Trimming

Reads #: 100,000

Total bases: 25,100,000

Reads Length: 251.00

After Trimming

Reads #: 81,894 (81.89 %)

Total bases: 15,946,538 (63.53 %)

Mean Reads Length: 194.72

Paired Reads #: 69,538 (84.91 %)

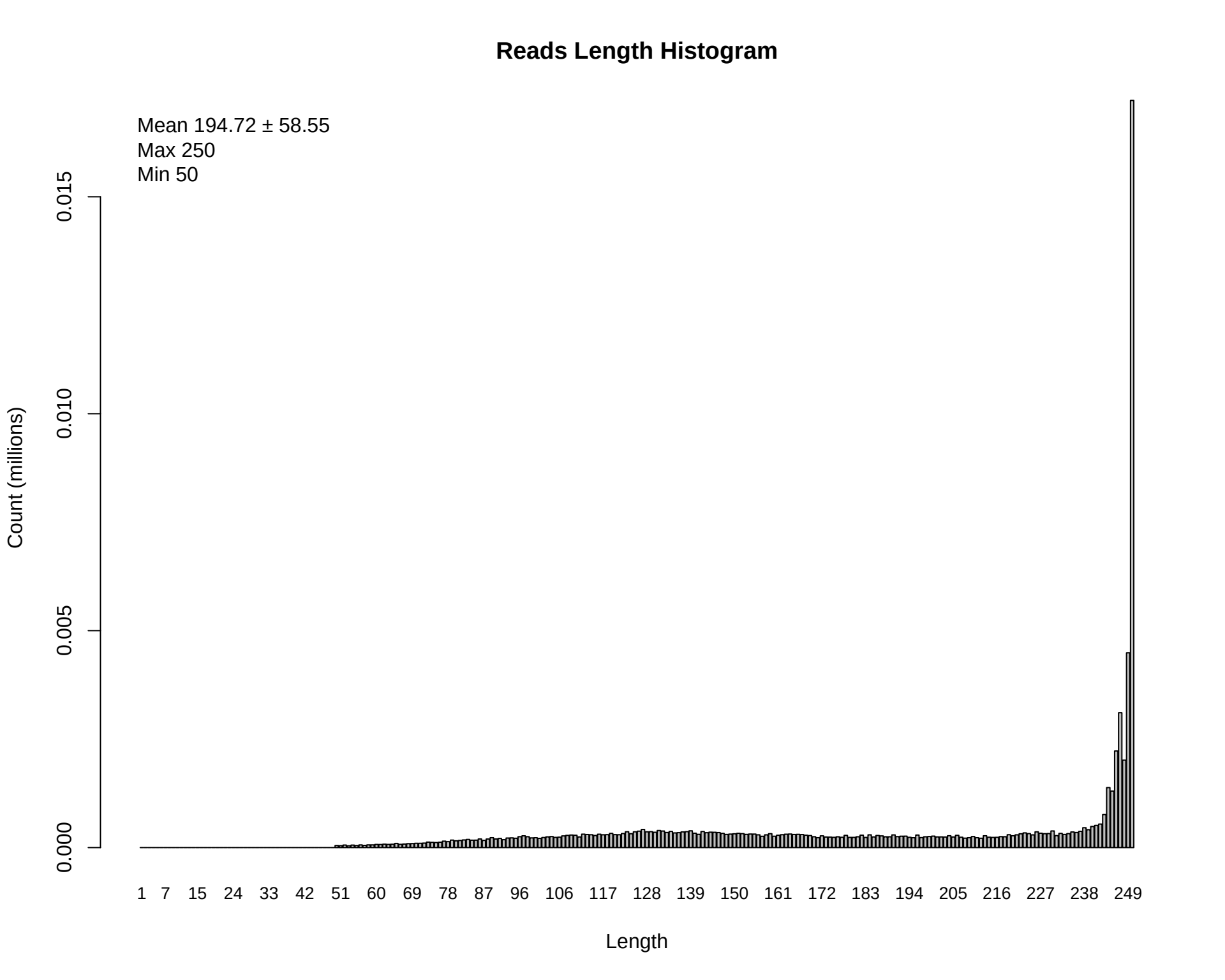
Paired total bases: 13,492,008 (84.61 %)

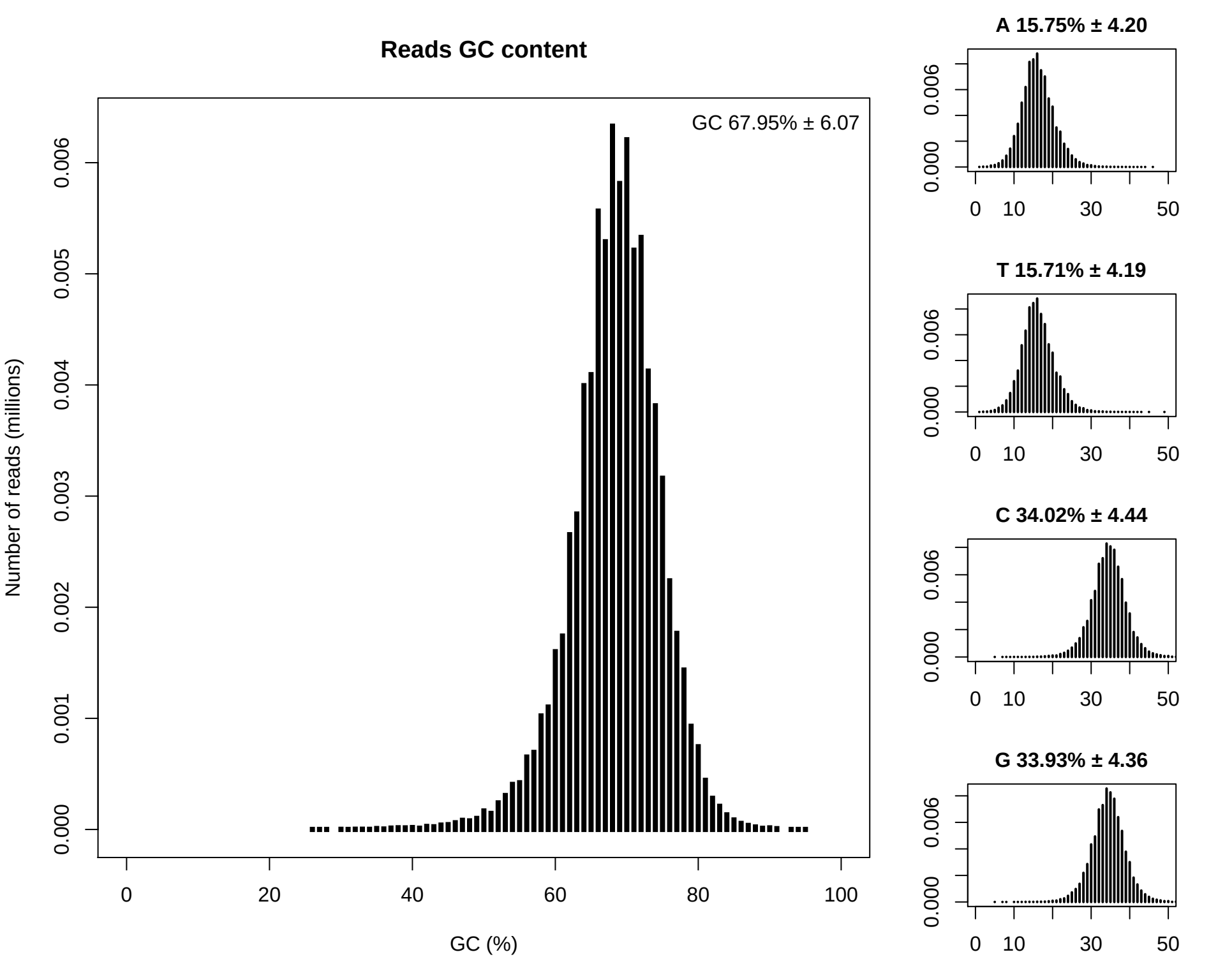
Unpaired Reads: 12,356 (15.09 %)

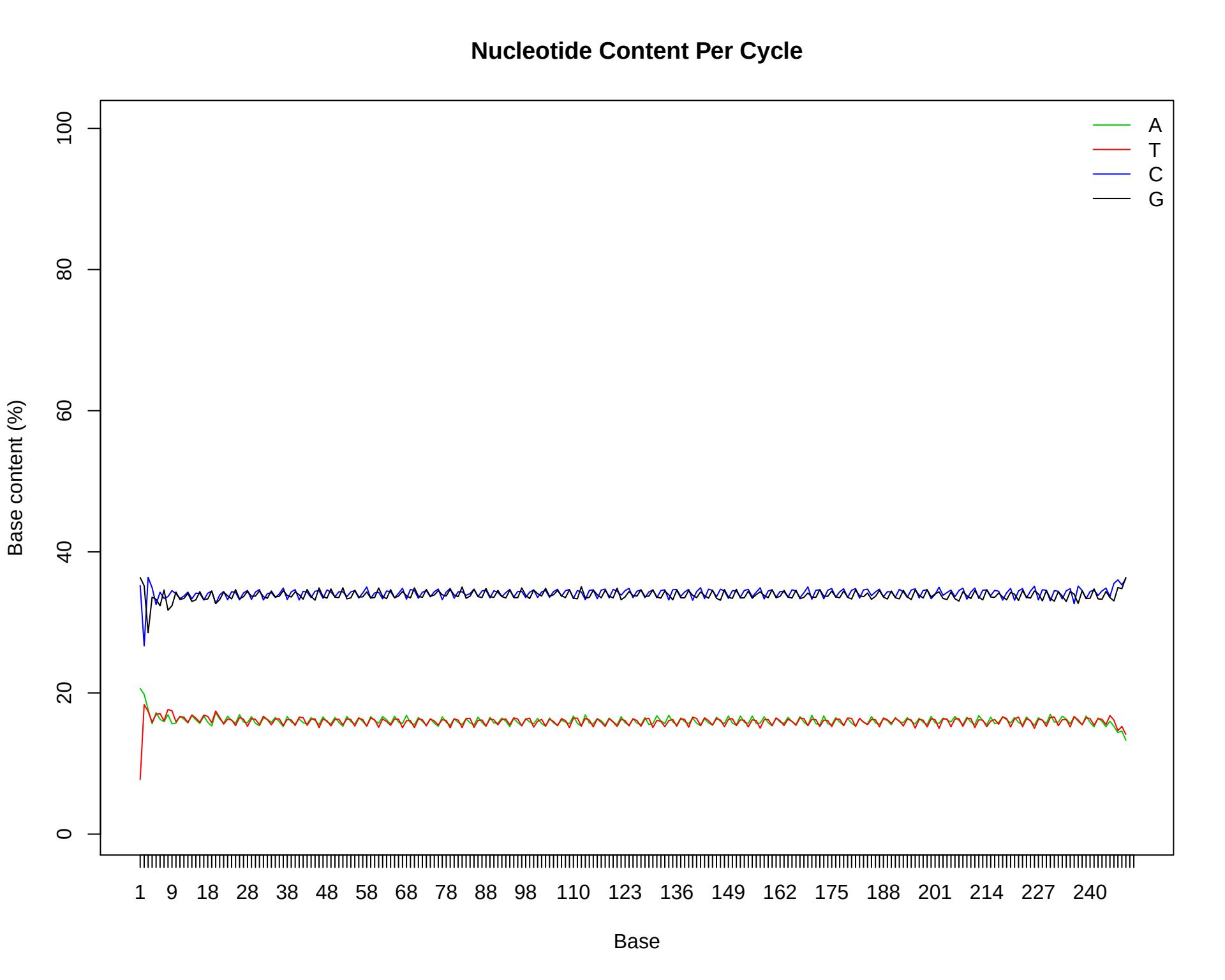
Unpaired total bases: 2,454,530 (15.39 %)

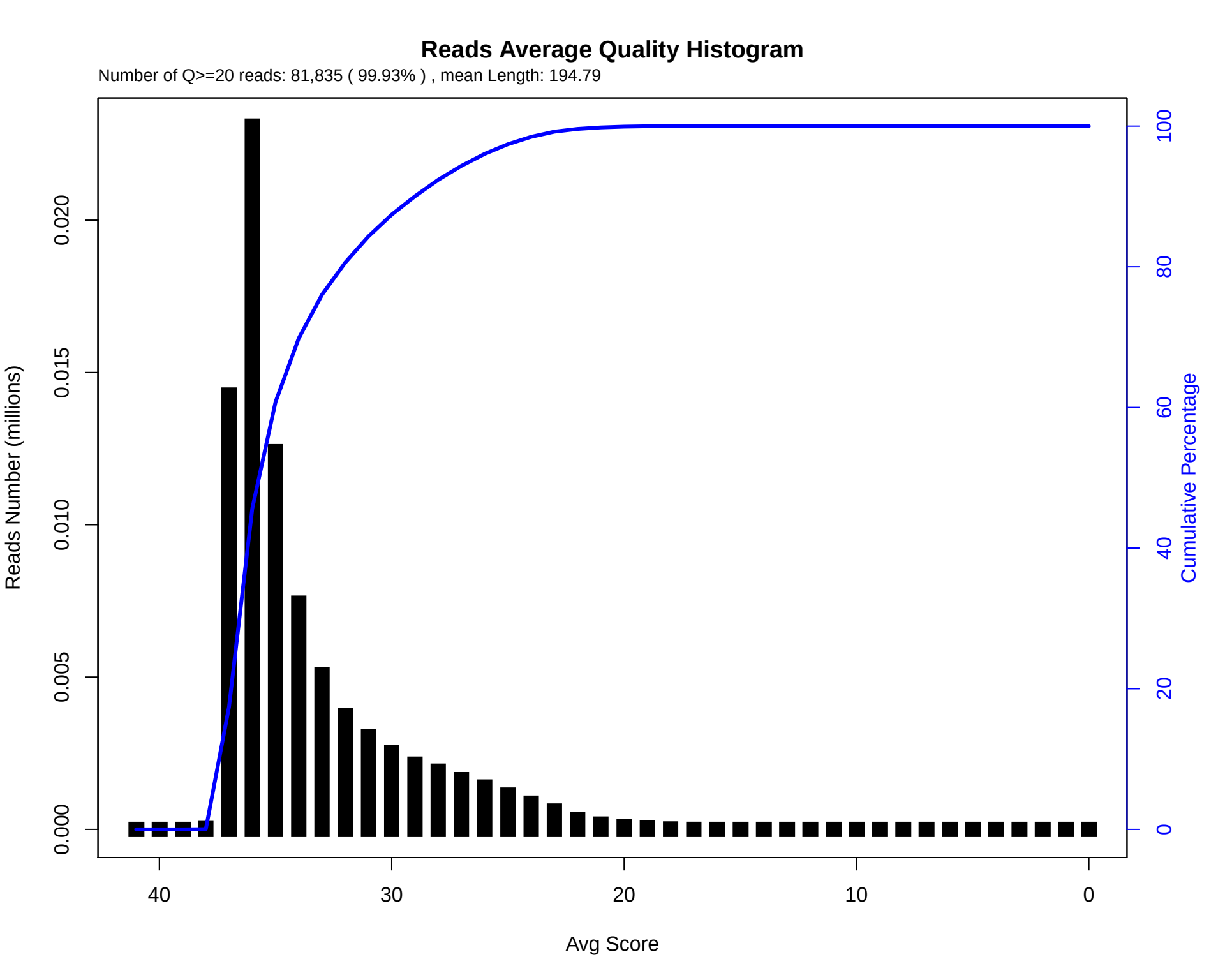
Discarded reads #: 18,106 (18.11 %)

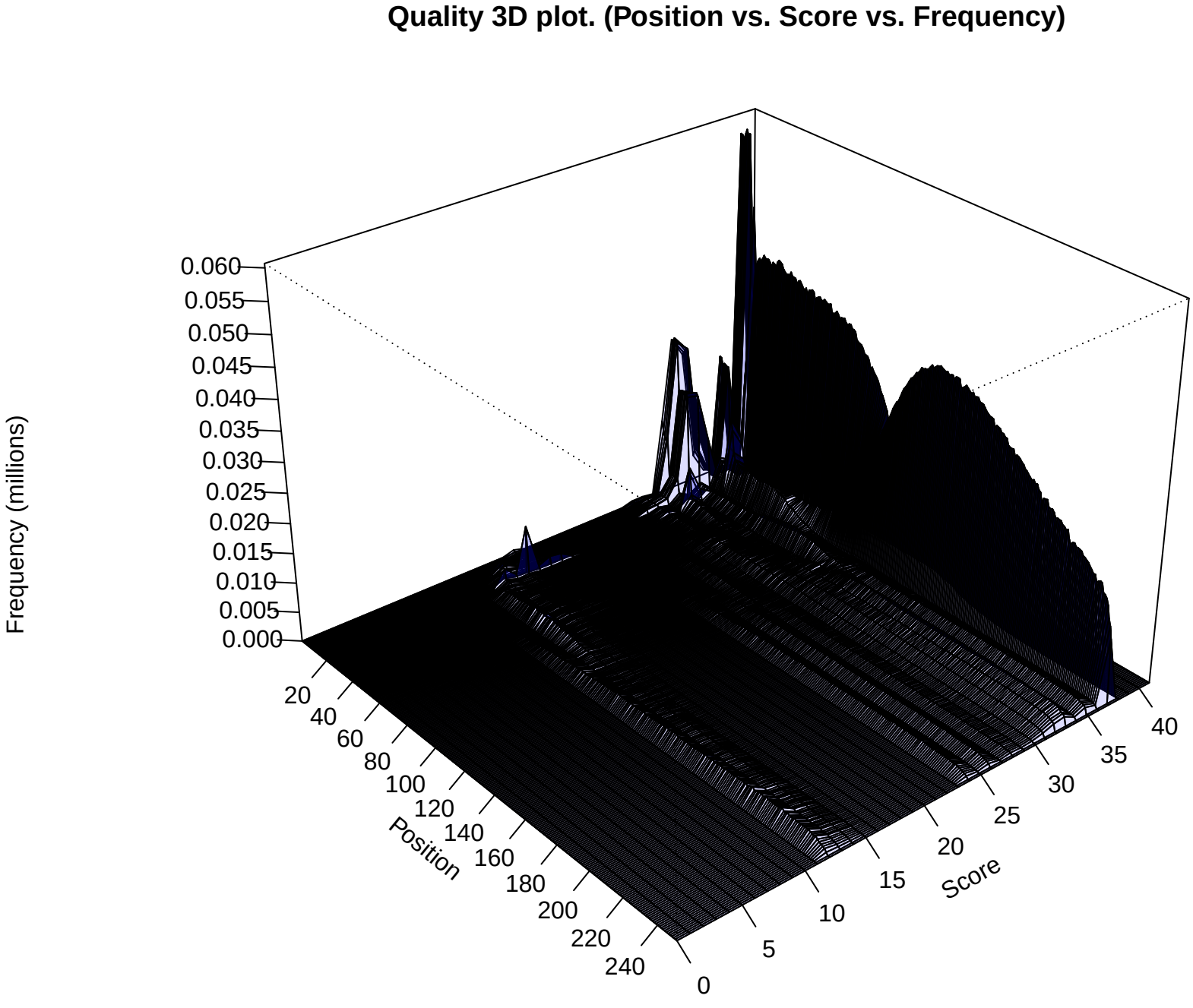
Discarded bases: 9,153,462 (36.47 %)

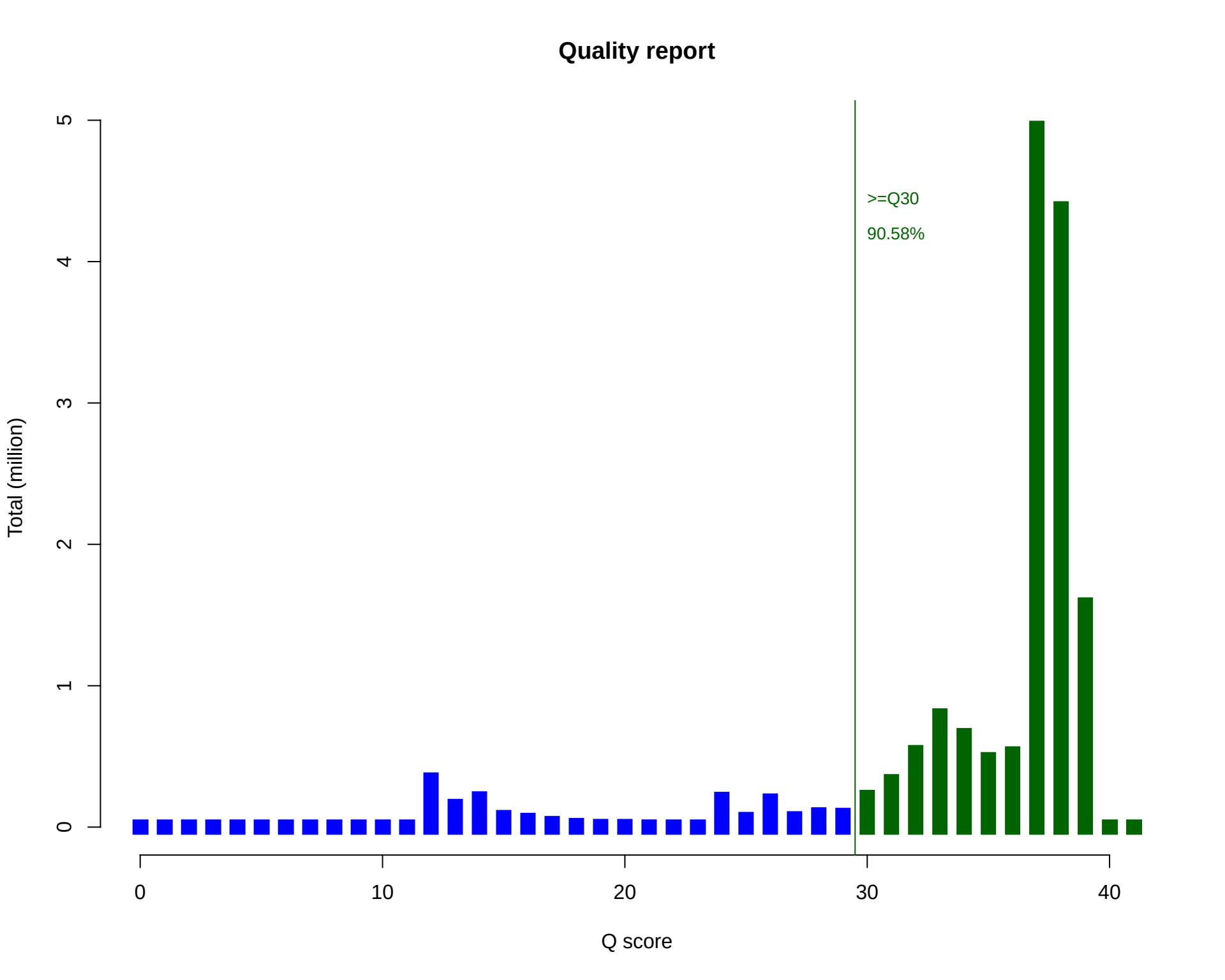

Reads Length Histogram
Mean 194.72 ± 58.55
Max 250
Min 50
Count (millions)
0.000
0.005
0.010
0.015
1 7 15 24 33 42 51 60 69 78 87 96 106 117 128 139 150 161 172 183 194 205 216 227 238 249
Length


Reads GC content
GC 67.95% ± 6.07
Number of reads (millions)
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0
20
40
60
80
100
GC (%)
A 15.75% ± 4.20
T 15.71% ± 4.19
C 34.02% ± 4.44
G 33.93% ± 4.36
0.000
0.006
0
10
30
50


Nucleotide Content Per Cycle
Base content (%)
0
20
40
60
80
100
A
T
C
G
1
9
18
28
38
48
58
68
78
88
98
110
123
136
149
162
175
188
201
214
227
240
Base


Reads Average Quality Histogram
Number of Q>=20 reads: 81,835 (99.93%) , mean Length: 194.79
Reads Number (millions)
0.000
0.005
0.010
0.015
0.020
Cumulative Percentage
0
20
40
60
80
100
40
30
20
10
0
Avg Score


Quality 3D plot. (Position vs. Score vs. Frequency)
Frequency (millions)
0.060
0.055
0.050
0.045
0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
Position
20
40
60
80
100
120
140
160
180
200
220
240
Score
0
5
10
15
20
25
30
35
40


Quality report
>=Q30
90.58%
Total (million)
0
1
2
3
4
5
0
10
20
30
40
Q score