

Before Trimming

Reads #: 50,000

Total bases: 5,000,000

Reads Length: 100.00

After Trimming

Reads #: 40,252 (80.50 %)

Total bases: 3,664,693 (73.29 %)

Mean Reads Length: 91.04

Paired Reads #: 35,156 (87.34 %)

Paired total bases: 3,219,284 (87.85 %)

Unpaired Reads: 5,096 (12.66 %)

Unpaired total bases: 445,409 (12.15 %)

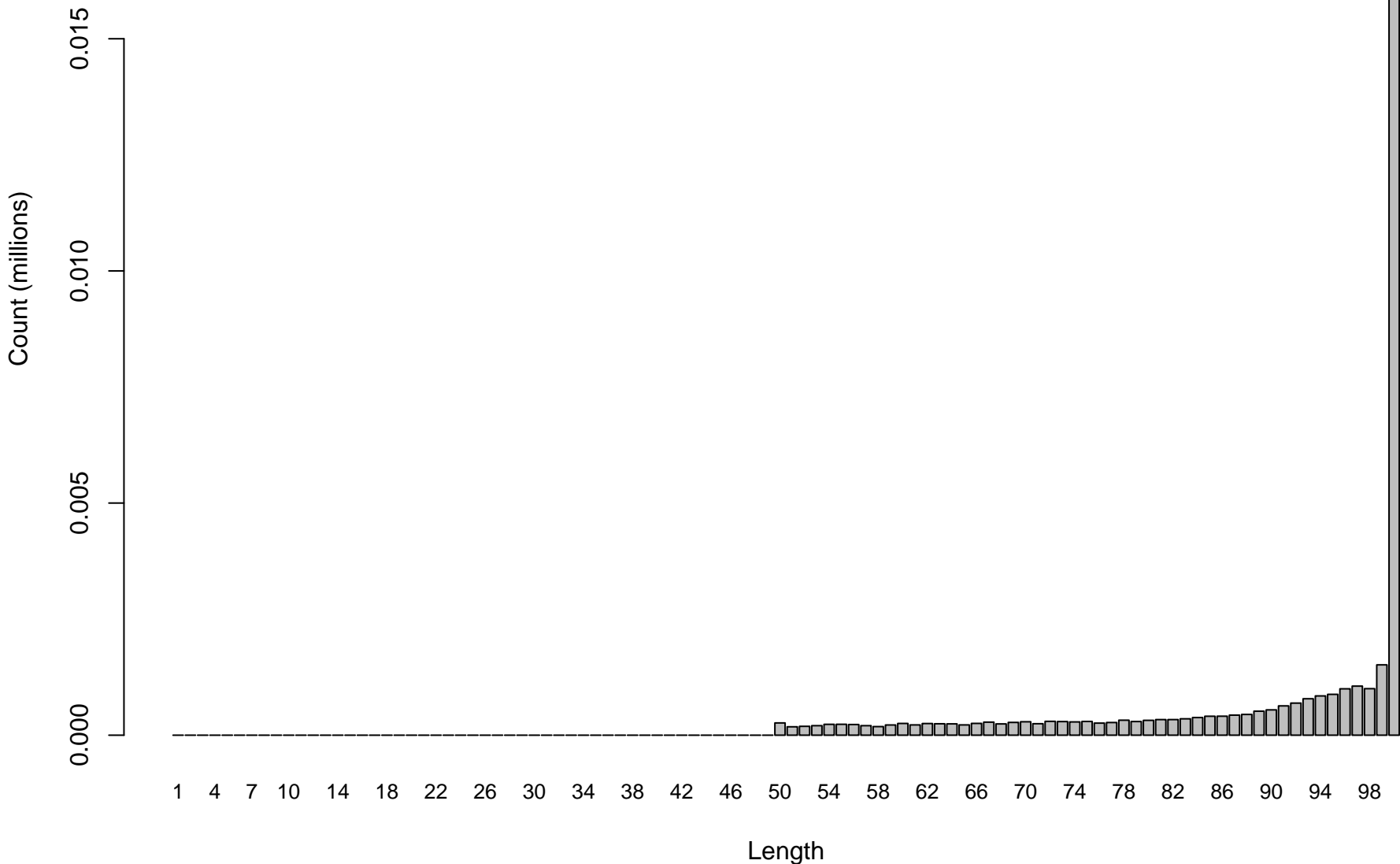
Reads with Adapters/Primers #: 39 (0.08 %)

Discarded reads #: 9,748 (19.50 %)

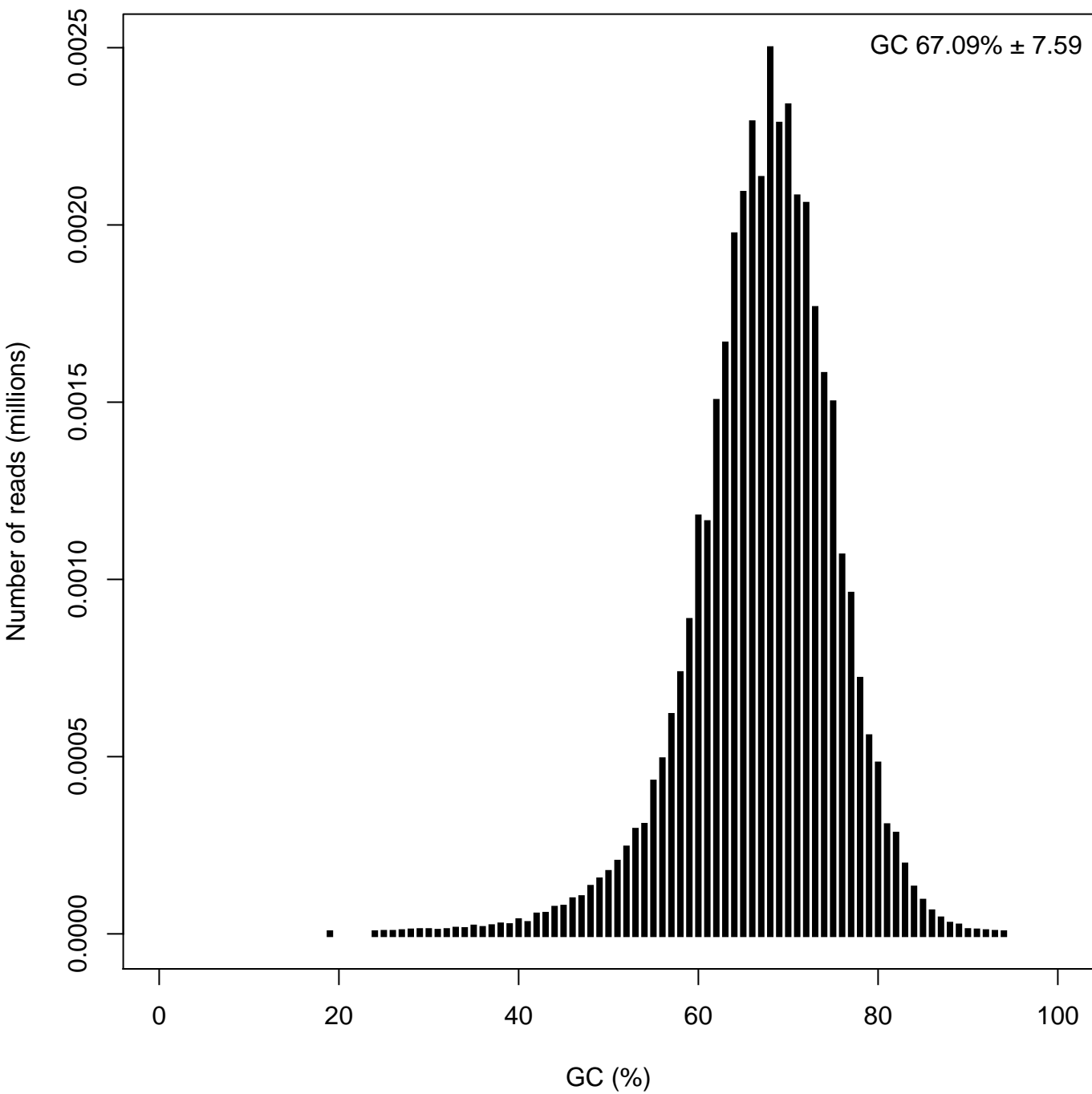
Discarded bases: 1,335,307 (26.71 %)

Reads Length Histogram

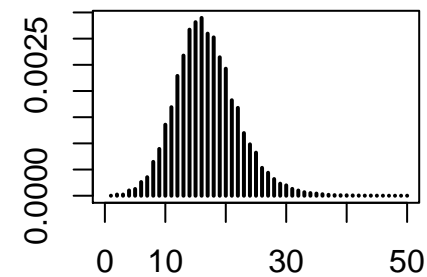
Mean 91.04 ± 13.62
Max 100
Min 50



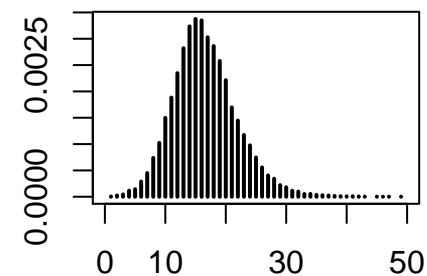
Reads GC content



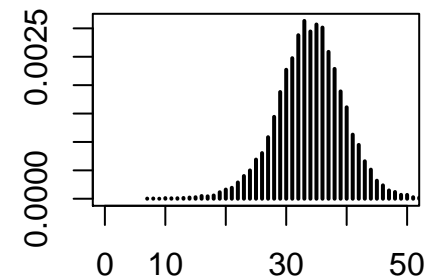
A 16.59% \pm 5.23



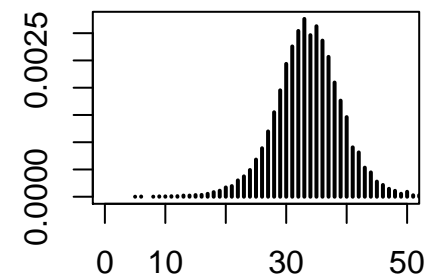
T 16.31% \pm 5.29



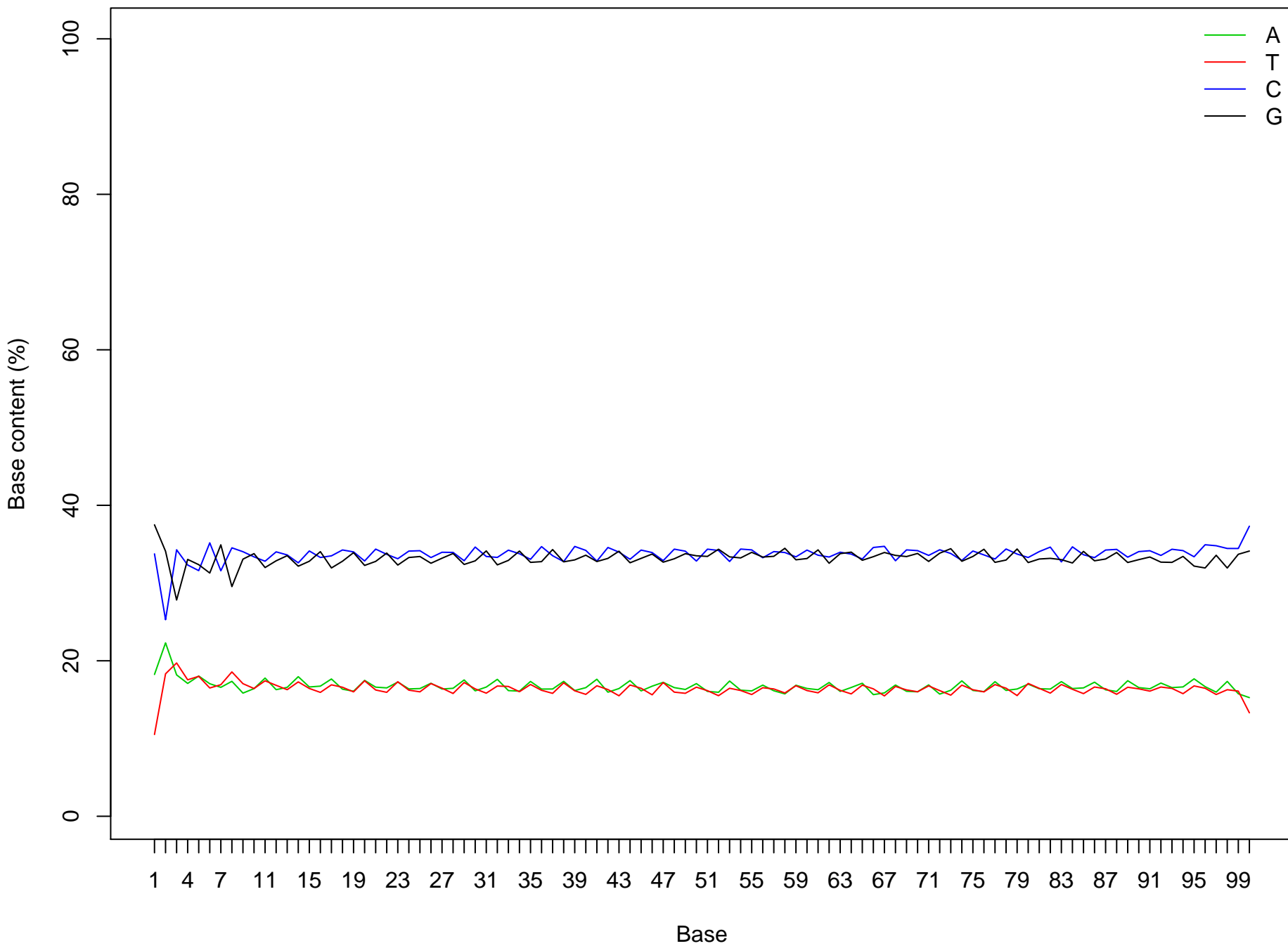
C 33.70% \pm 5.52



G 33.39% \pm 5.44

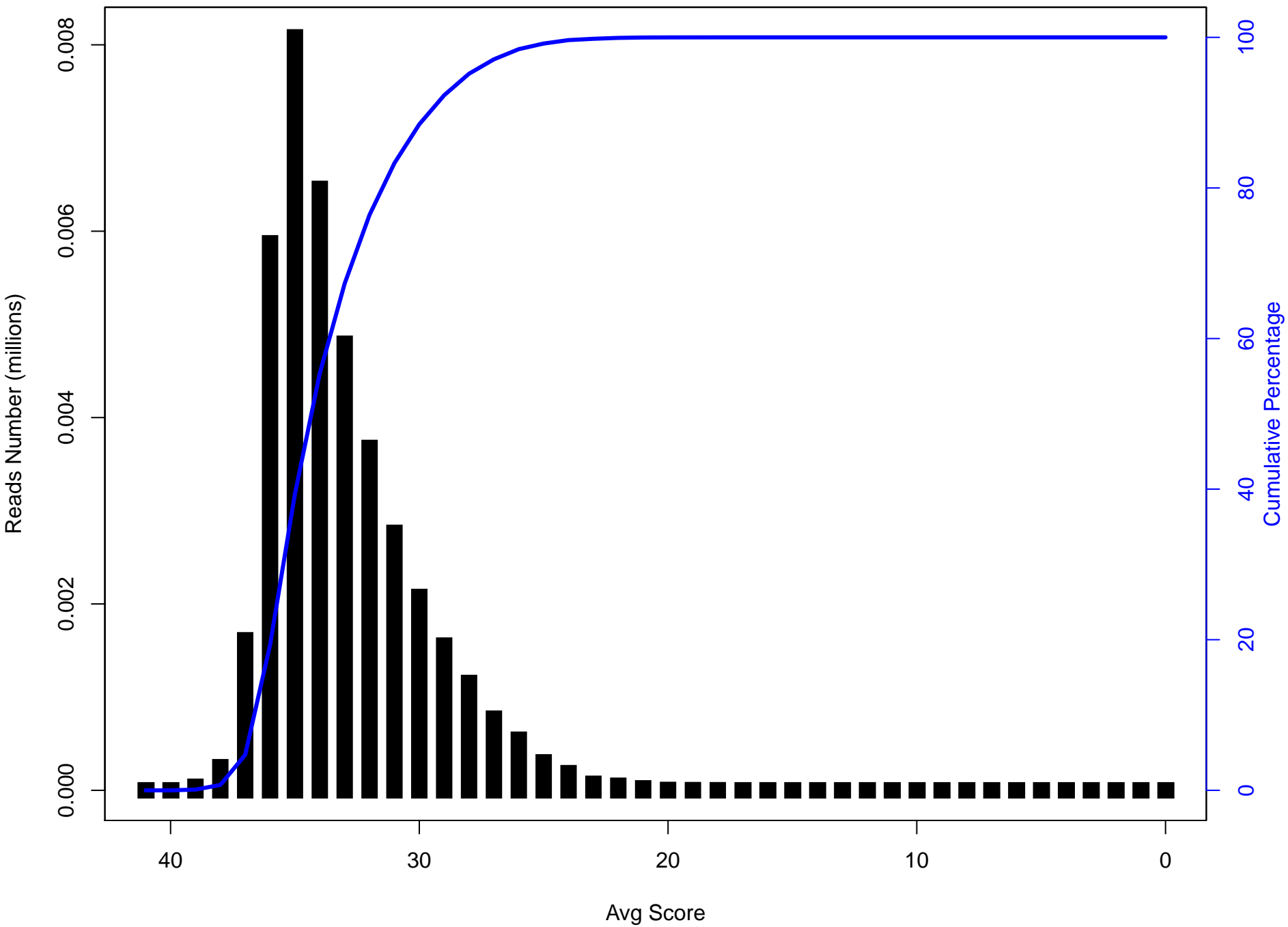


Nucleotide Content Per Cycle

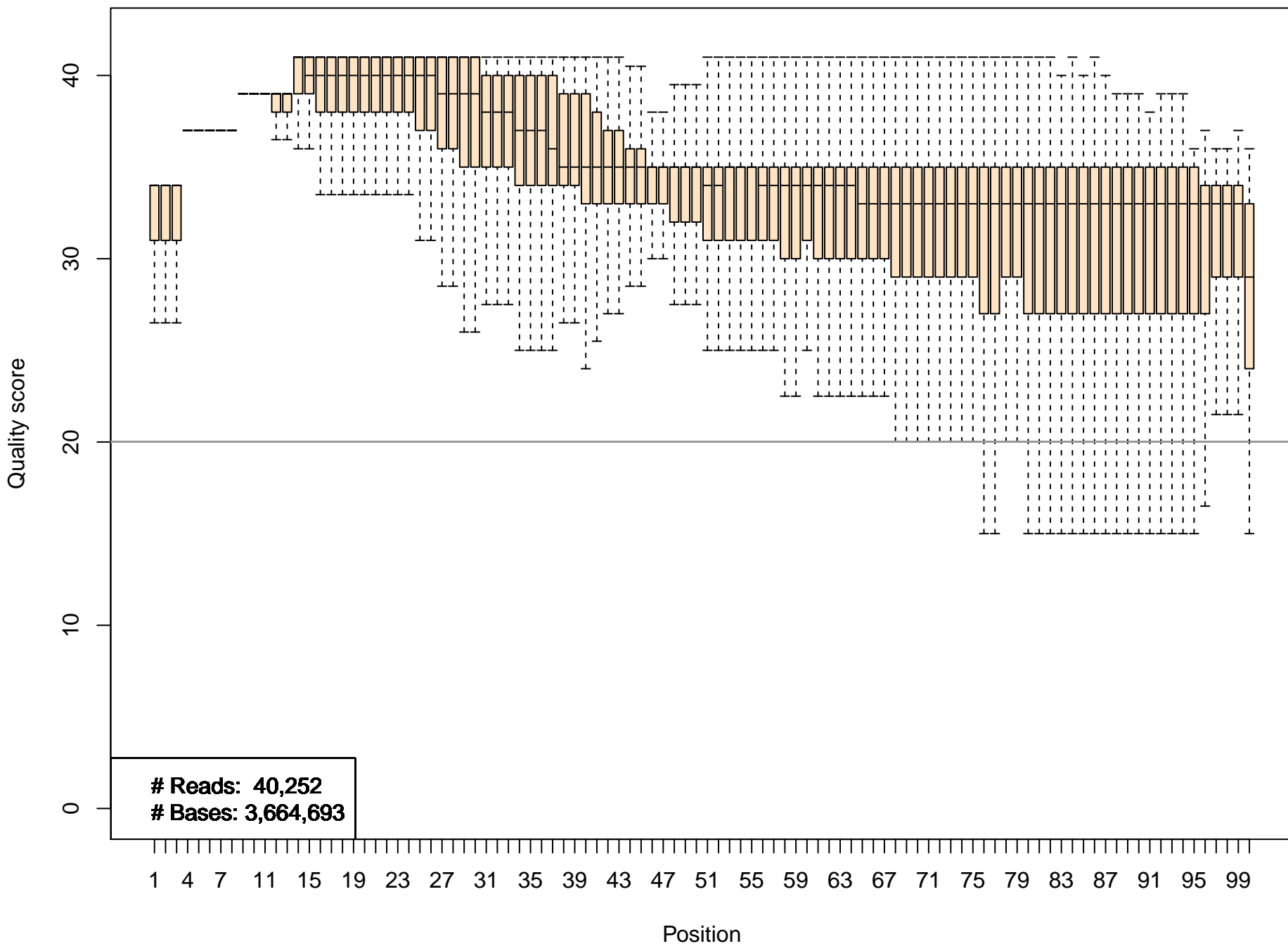


Reads Average Quality Histogram

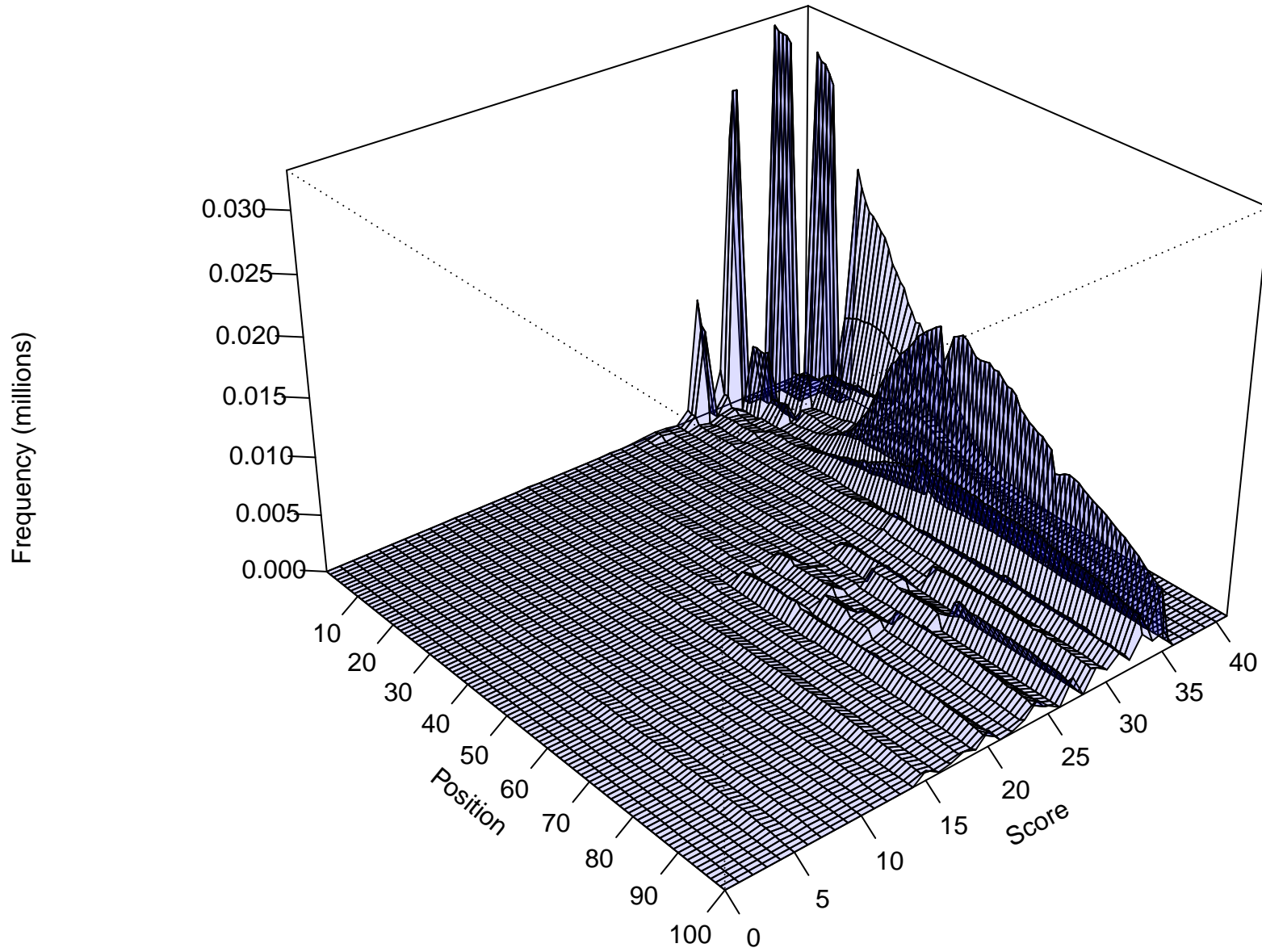
Number of Q>=20 reads: 40,249 (99.99%) , mean Length: 91.05



Quality Boxplot Per Cycle



Quality 3D plot. (Position vs. Score vs. Frequency)



Quality report

