

QC stats

Before Trimming

Reads: 50000

Total bases: 5000000

Reads Length: 100.00

After Trimming

Reads: 40343 (80.69 %)

Total bases: 3672219 (73.44 %)

Mean Reads Length: 91.02

Paired Reads: 35214 (87.29 %)

Paired total bases: 3224338 (87.80 %)

Unpaired Reads: 5129 (12.71 %)

Unpaired total bases: 447881 (12.20 %)

Discarded reads: 9657 (19.31 %)

Trimmed bases: 1327781 (26.56 %)

Reads Filtered by length cutoff (50 bp): 8946 (17.89 %)

Bases Filtered by length cutoff: 248963 (4.98 %)

Reads Filtered by continuous base "N" (2): 711 (1.42 %)

Bases Filtered by continuous base "N": 62380 (1.25 %)

Reads Filtered by low complexity ratio (0.8): 0 (0.00 %)

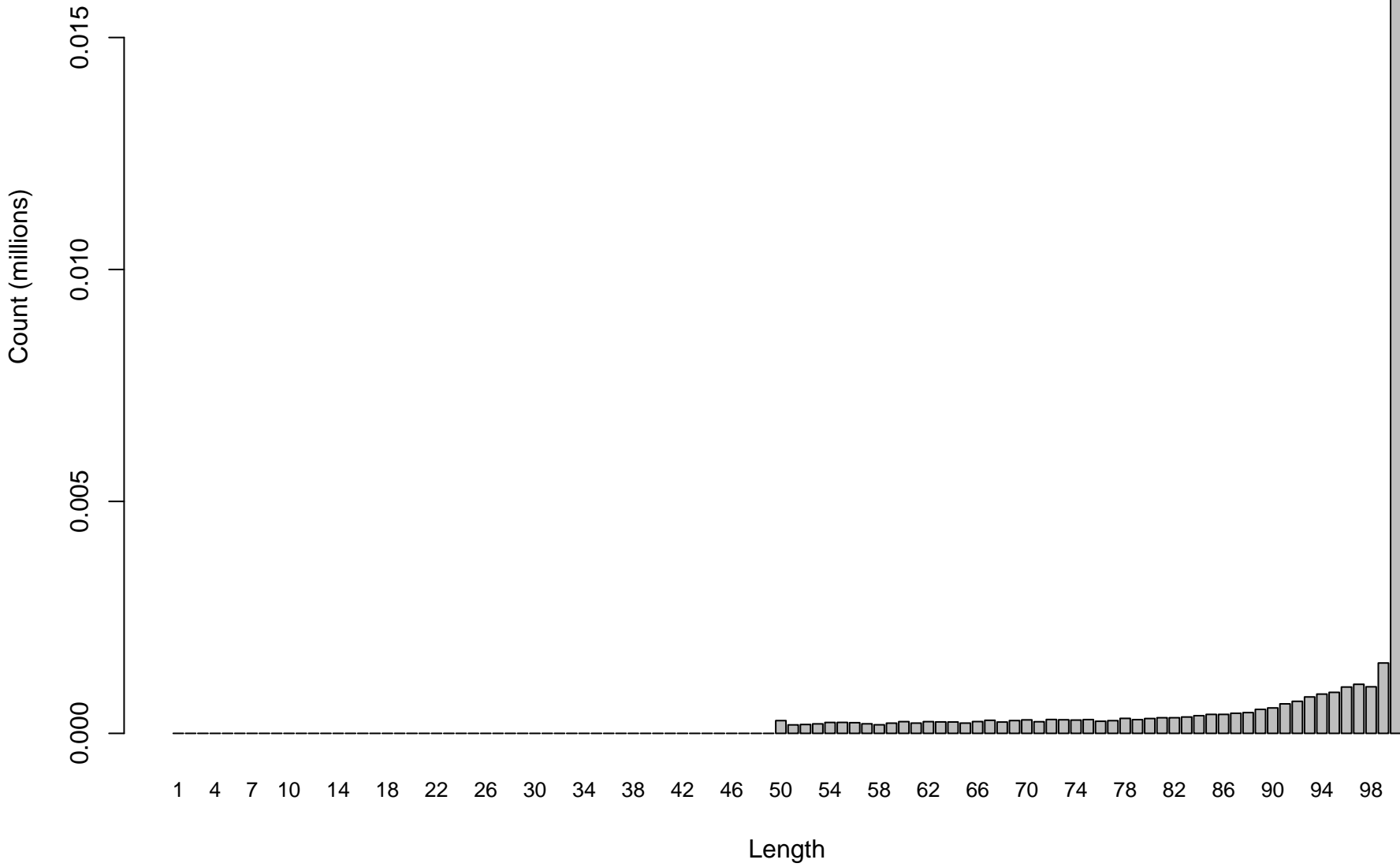
Bases Filtered by low complexity ratio: 0 (0.00 %)

Reads Trimmed by quality (5.0): 29802 (59.60 %)

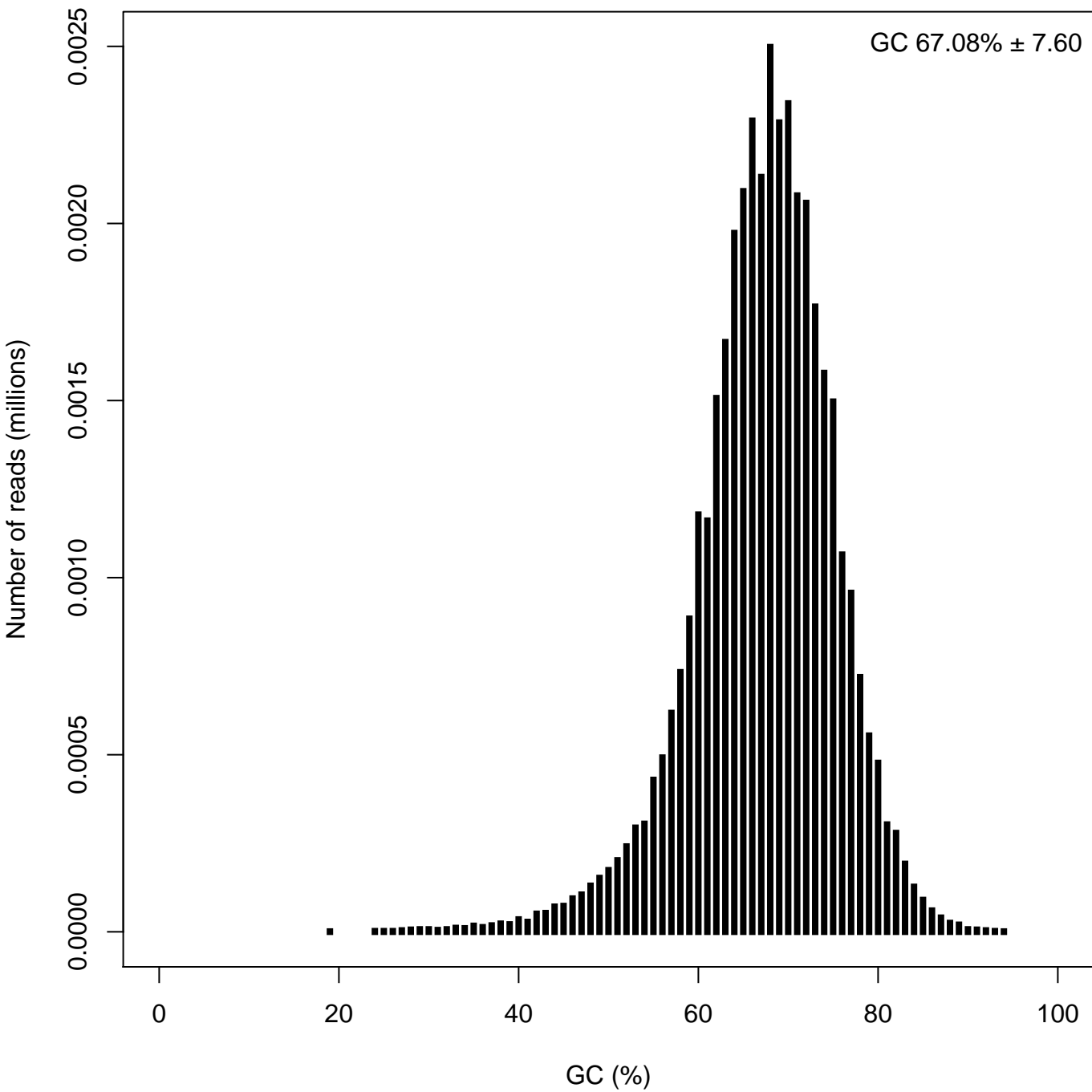
Bases Trimmed by quality: 1016438 (20.33 %)

Reads Length Histogram

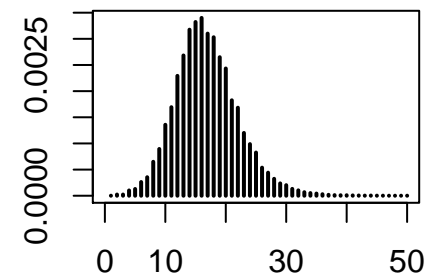
Mean 91.02 ± 13.64
Max 100
Min 50



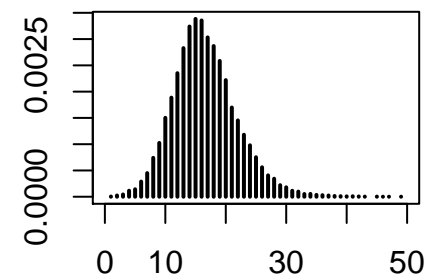
Reads GC content



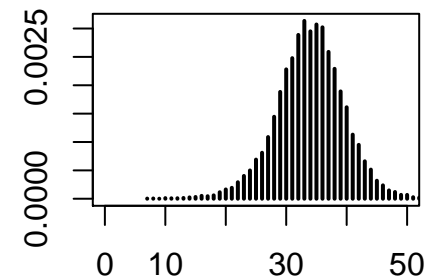
A 16.60% \pm 5.24



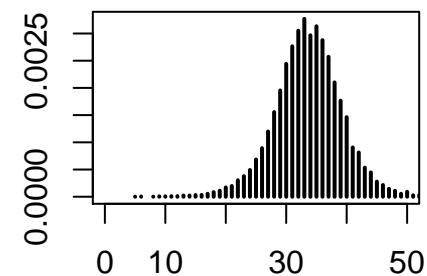
T 16.32% \pm 5.29



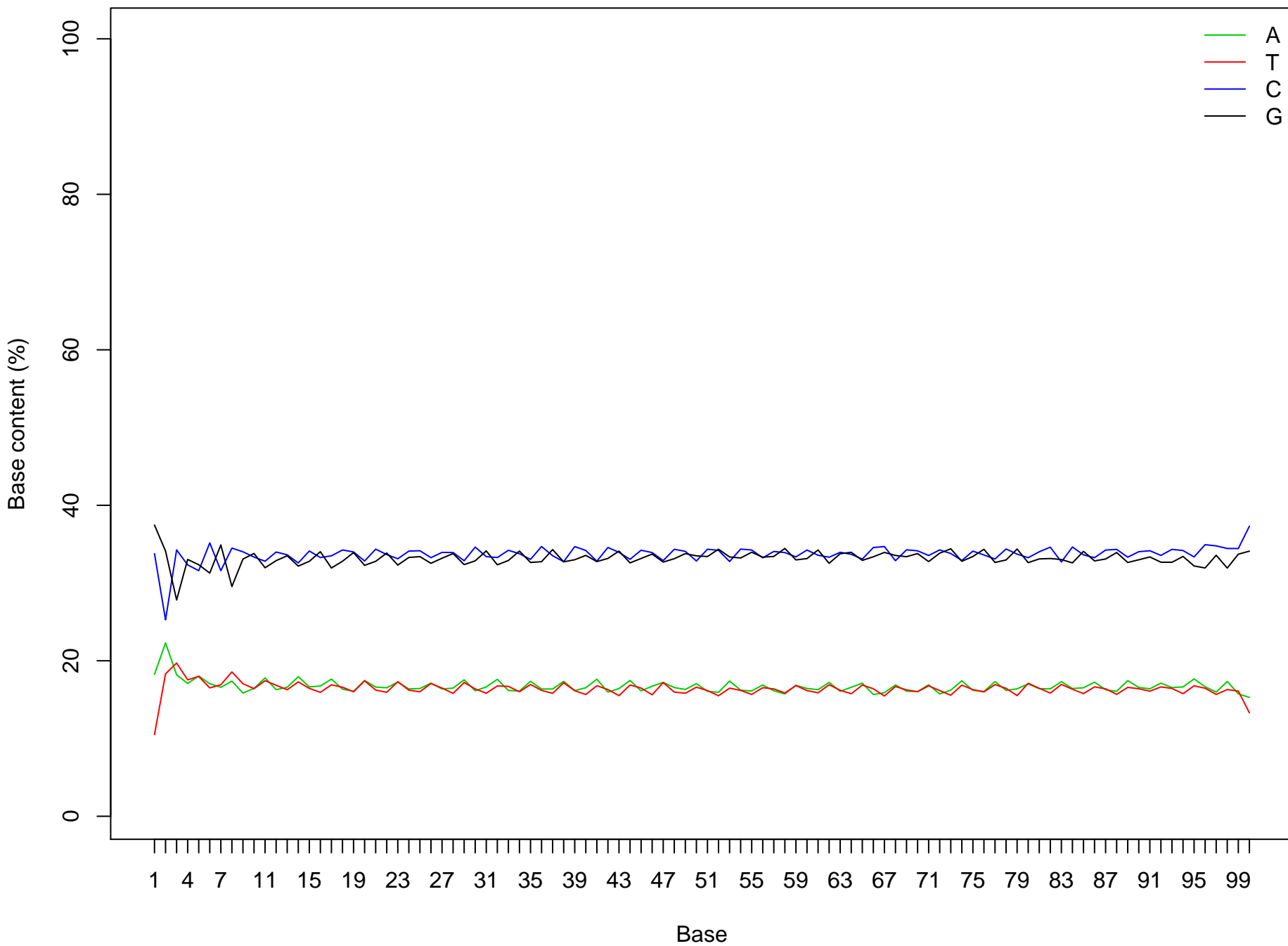
C 33.69% \pm 5.53



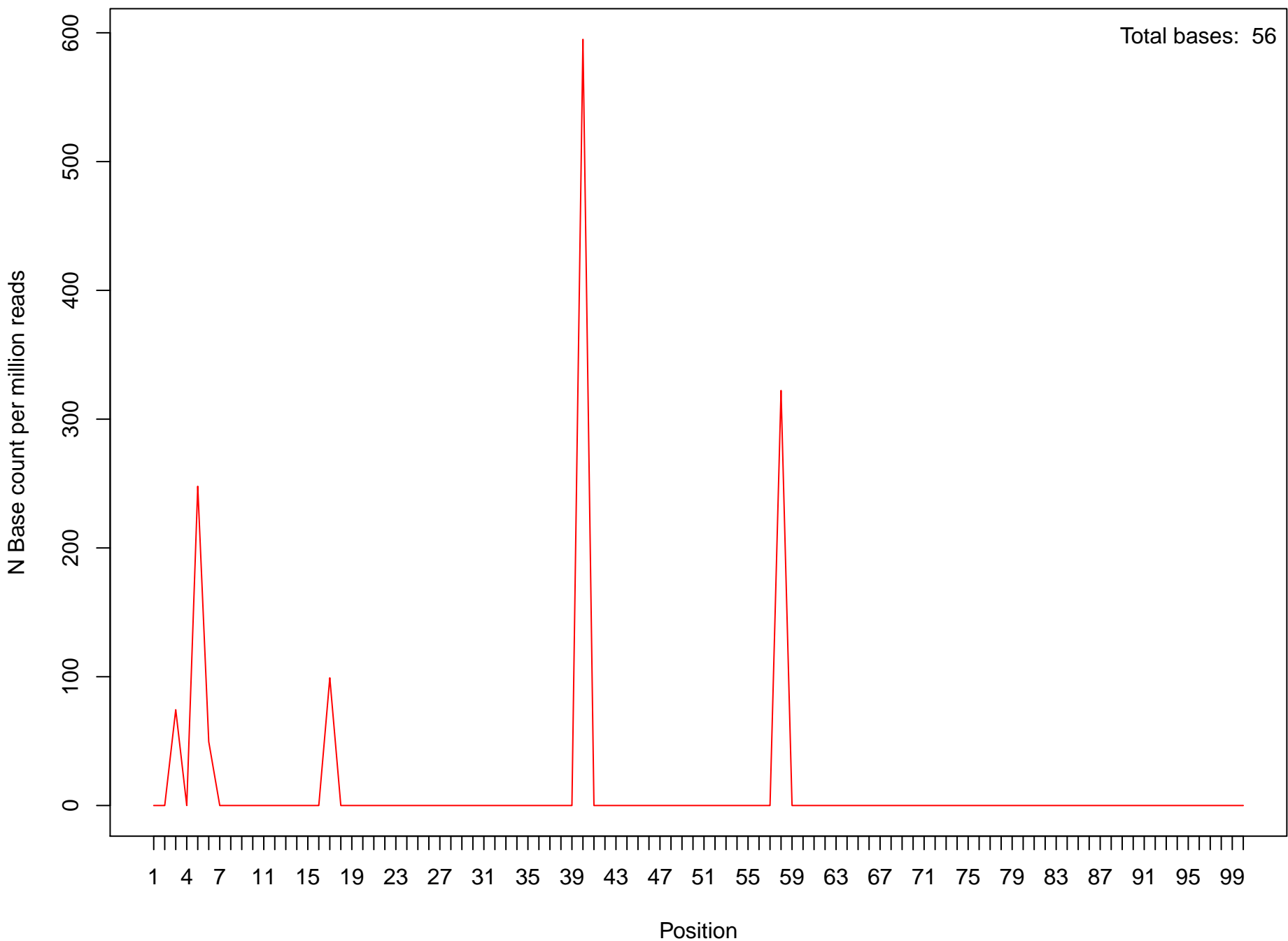
G 33.39% \pm 5.44



Nucleotide Content Per Cycle

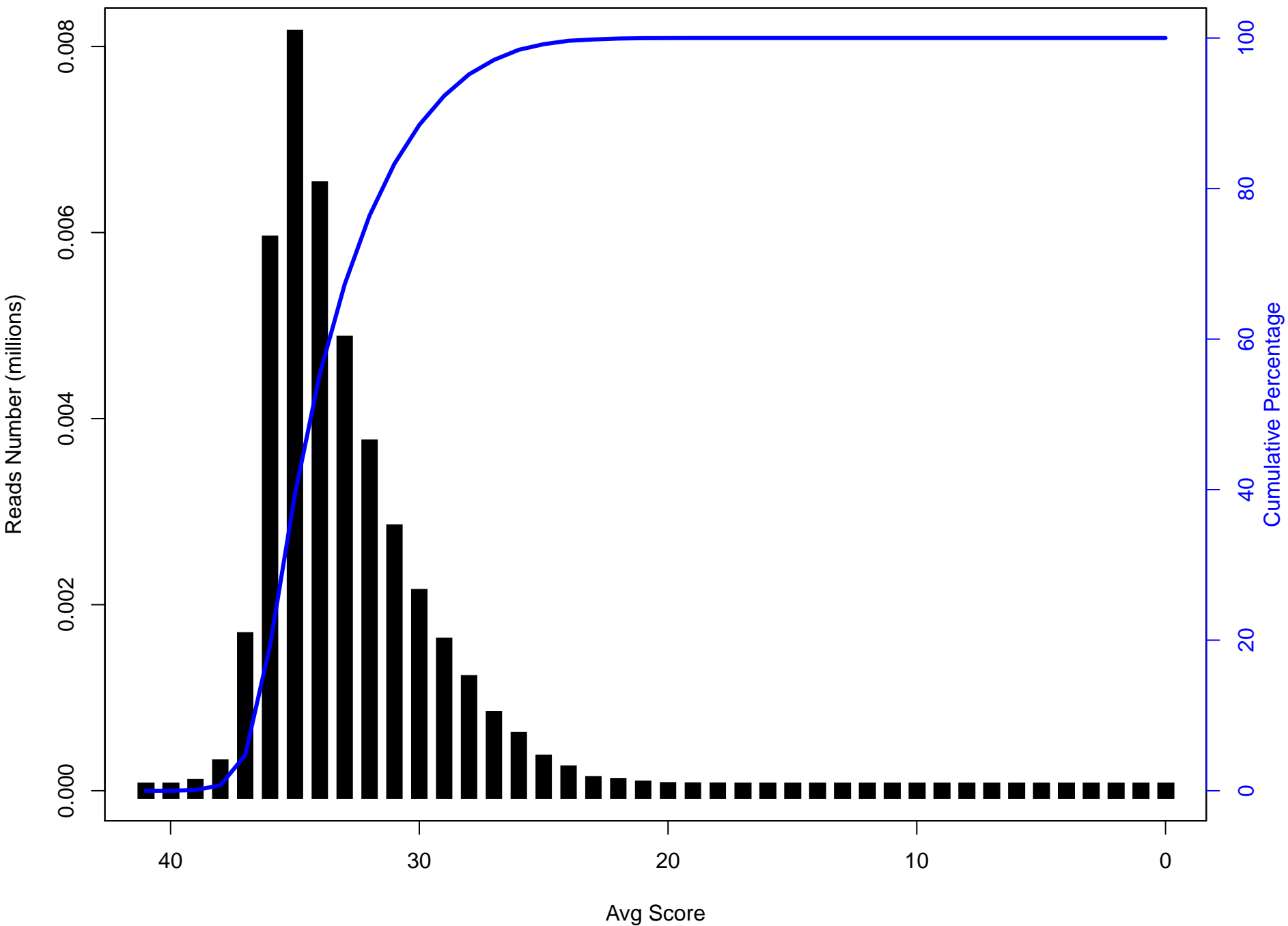


N Nucleotide Content Per Cycle

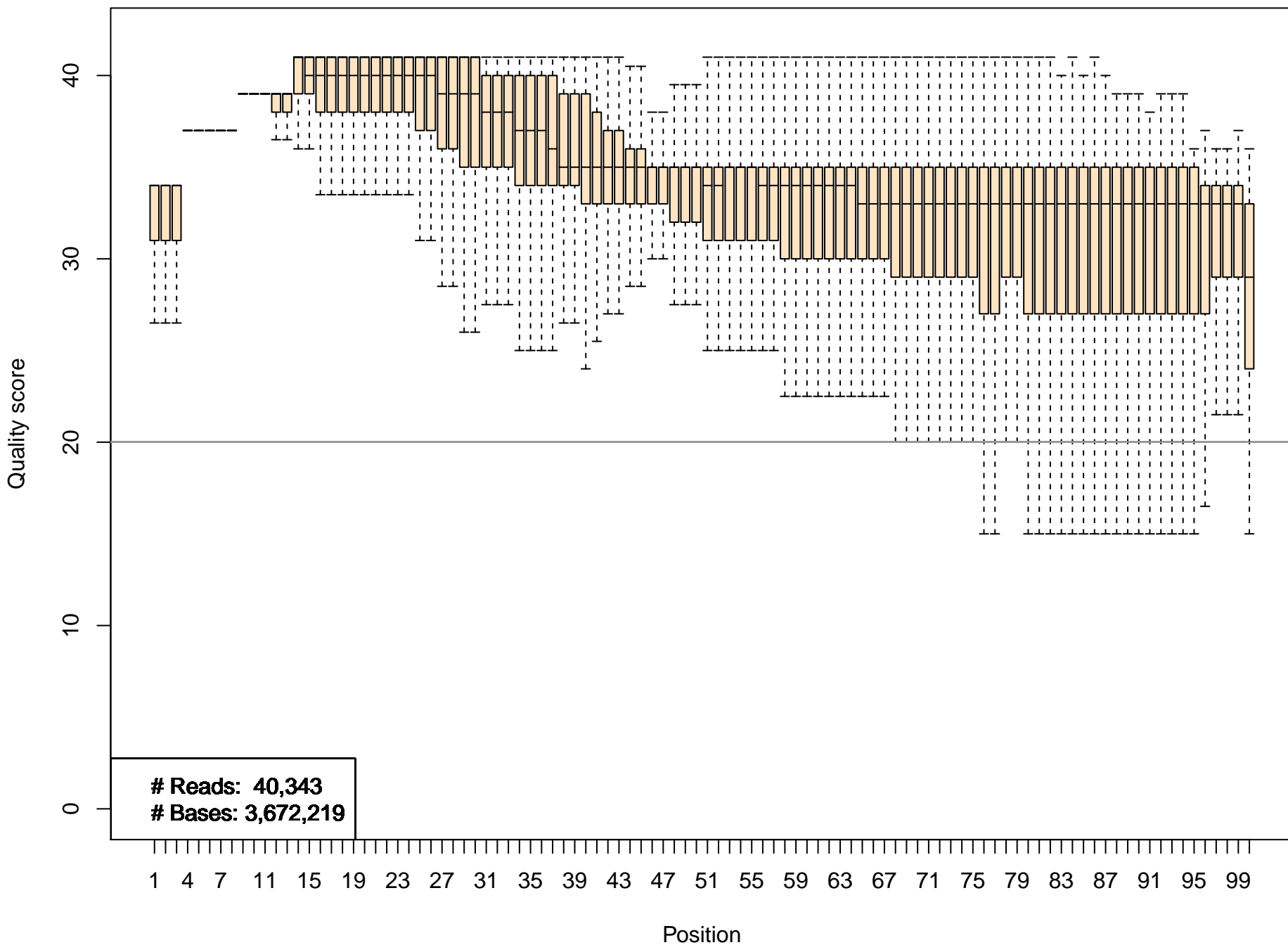


Reads Average Quality Histogram

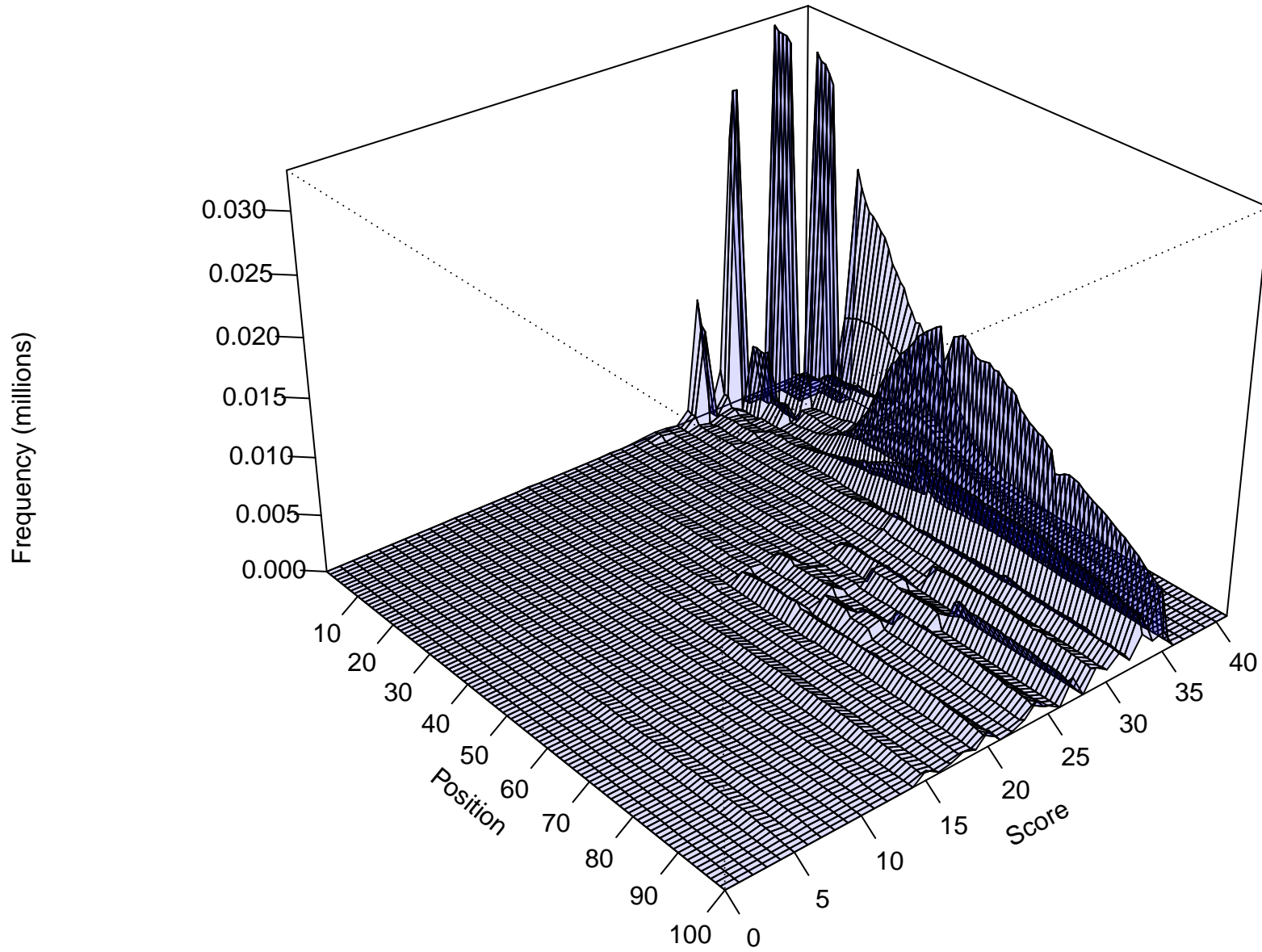
Number of Q>=20 reads: 40,340 (99.99%) , mean Length: 91.03



Quality Boxplot Per Cycle



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



Quality report

