

## QC stats

### Before Trimming

Reads #: 2000000  
Total bases: 200000000  
Reads Length: 100.00

### After Trimming

Reads #: 1972635 (98.63 %)  
Total bases: 195946714 (97.97 %)  
Mean Reads Length: 99.33  
Paired Reads #: 1954404 (99.08 %)  
Paired total bases: 194059653 (99.04 %)  
Unpaired Reads #: 18231 (0.92 %)  
Unpaired total bases: 1887061 (0.96 %)

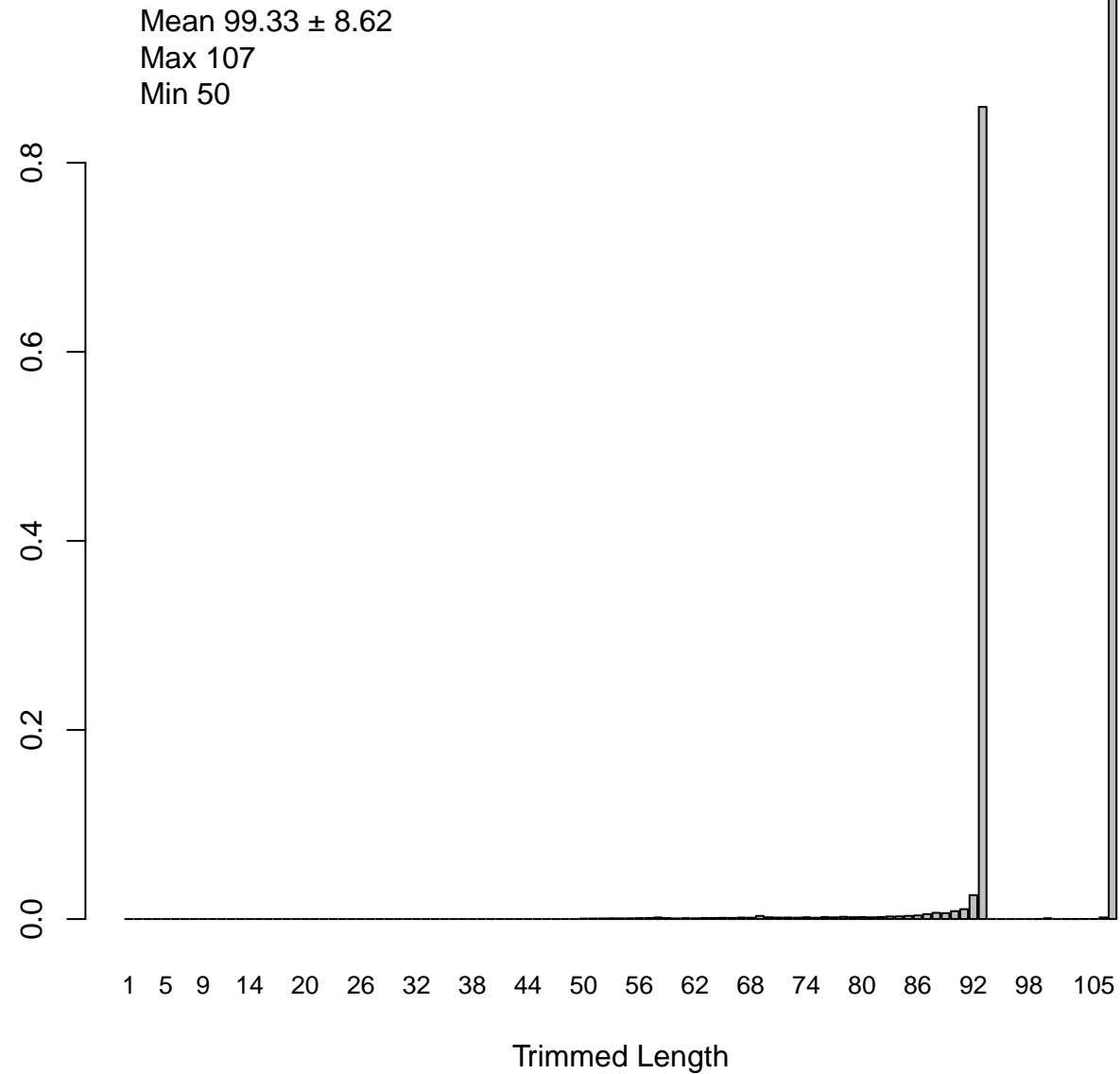
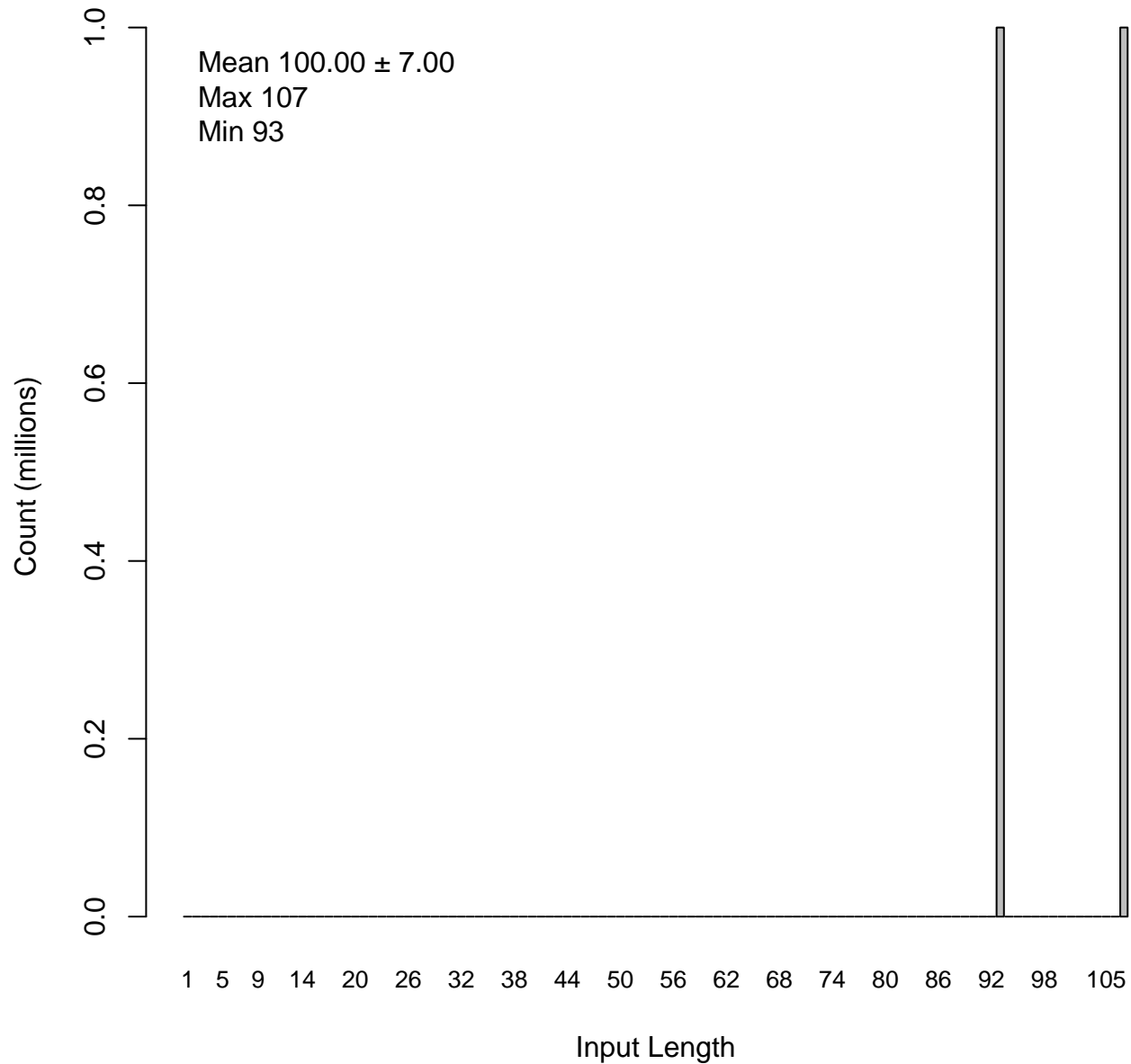
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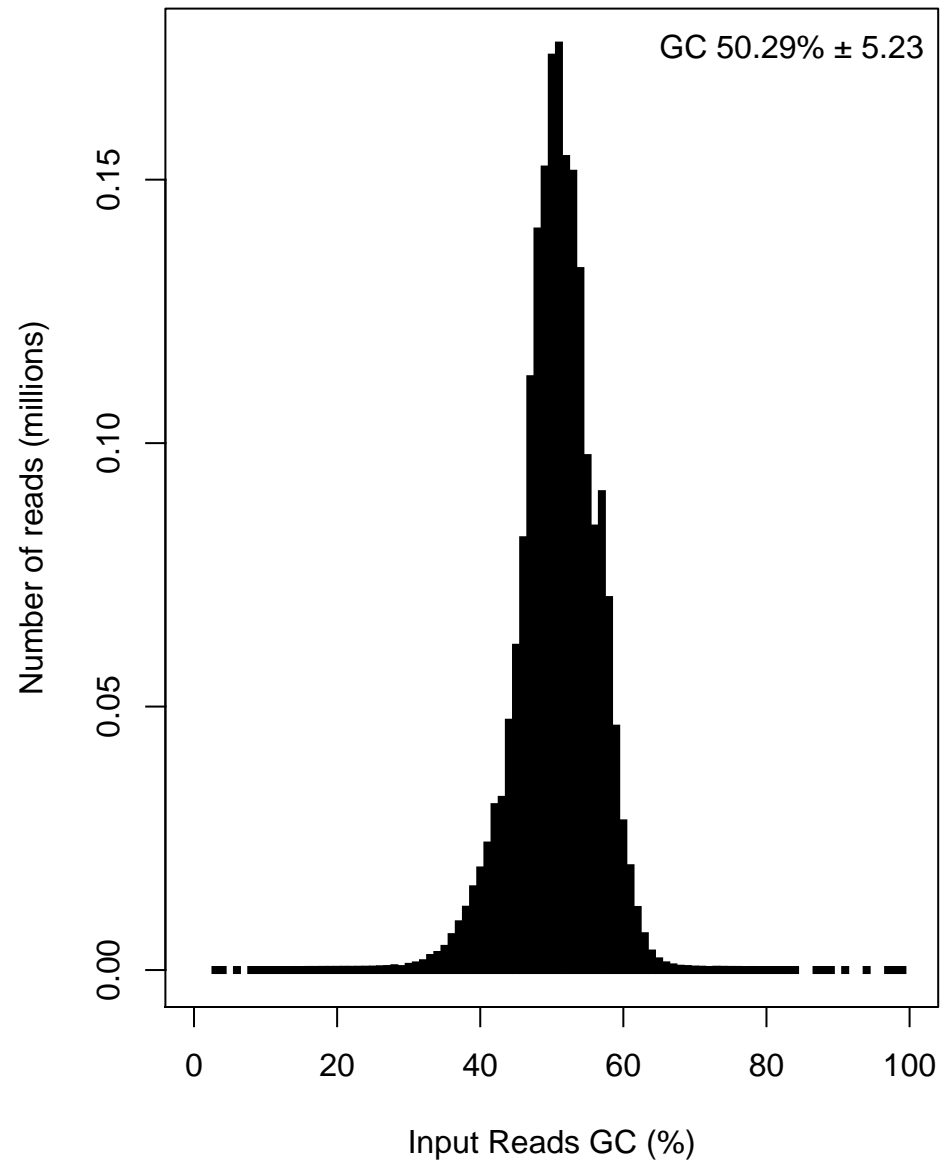
Discarded reads #: 27365 (1.37 %)

Trimmed bases: 4053286 (2.03 %)

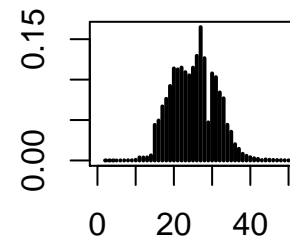
Reads Filtered by length cutoff (50 bp): 26089 (1.30 %)  
Bases Filtered by length cutoff: 602583 (0.30 %)  
Reads Filtered by continuous base "N" (2): 1270 (0.06 %)  
Bases Filtered by continuous base "N": 125675 (0.06 %)  
Reads Filtered by low complexity ratio (0.8): 6 (0.00 %)  
Bases Filtered by low complexity ratio: 600 (0.00 %)  
Reads Trimmed by quality (5.0): 148776 (7.44 %)  
Bases Trimmed by quality: 3044709 (1.52 %)  
Reads Trimmed with Adapters/Primers: 7418 (0.37 %)  
Bases Trimmed with Adapters/Primers: 279719 (0.14 %)  
Nextera-primer-adaptor-1 7270 reads (0.36 %) 272839 bases (0.14 %)  
Nextera-primer-adaptor-2 148 reads (0.01 %) 6880 bases (0.00 %)

# Reads Length Histogram



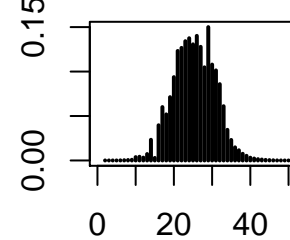


**A 24.79% ± 5.64**



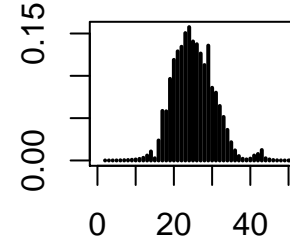
0 20 40

**T 24.90% ± 5.41**



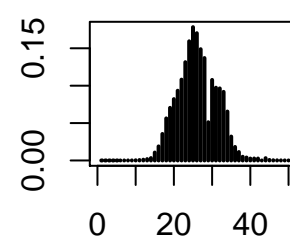
0 20 40

**C 24.70% ± 5.38**

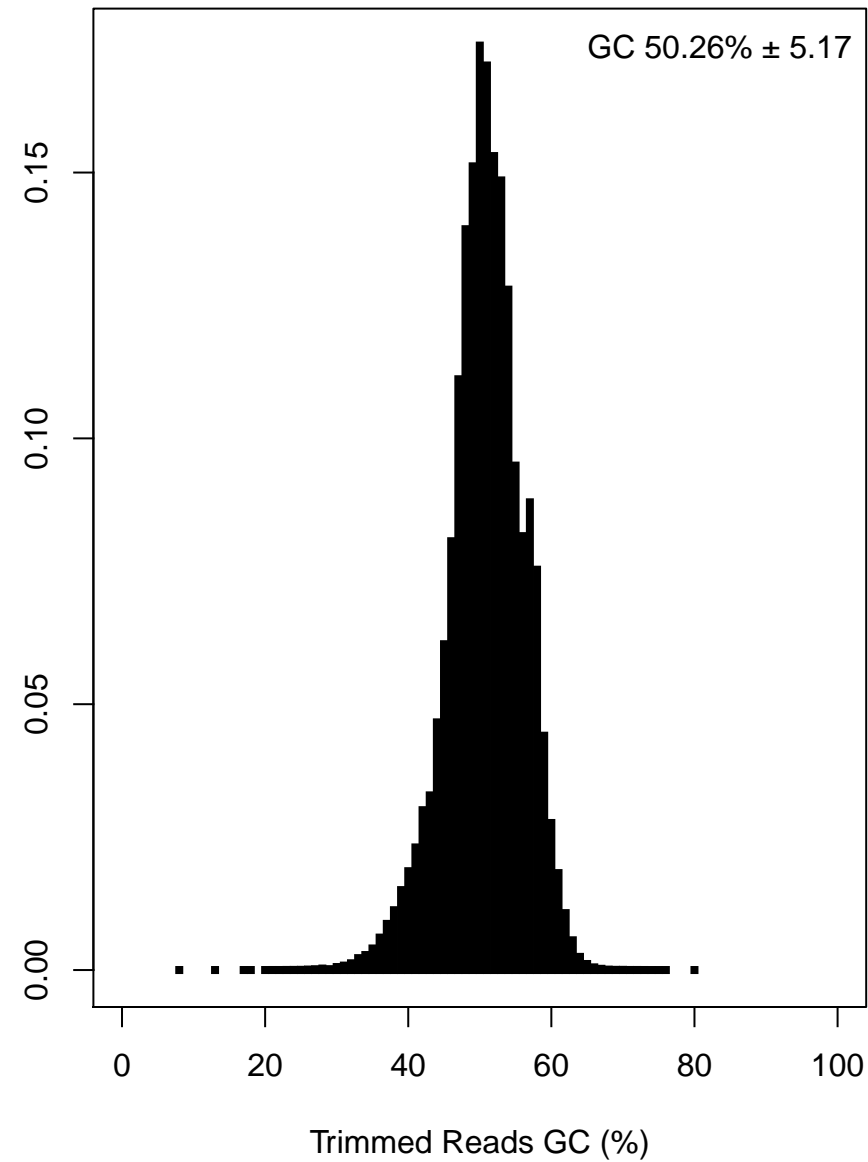


0 20 40

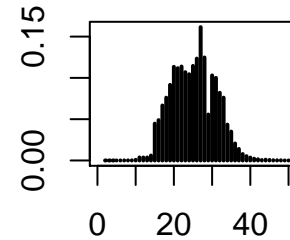
**G 25.59% ± 5.01**



0 20 40

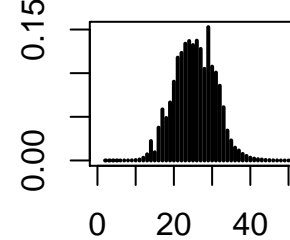


**A 24.74% ± 5.58**



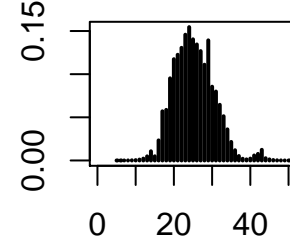
0 20 40

**T 25.00% ± 5.33**



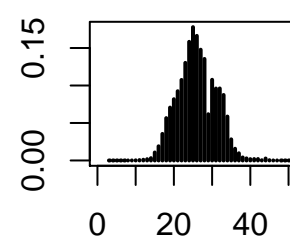
0 20 40

**C 24.77% ± 5.34**



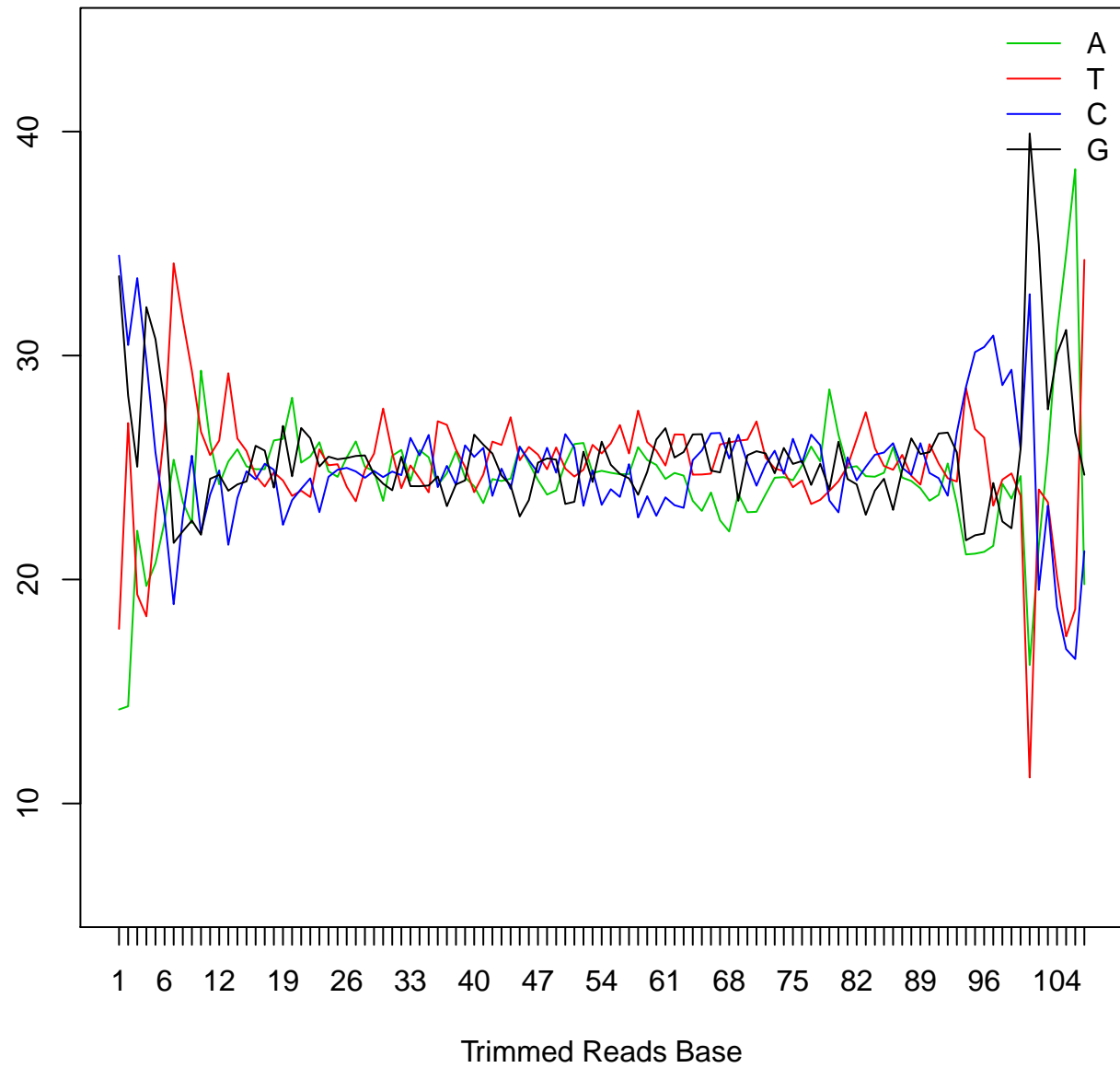
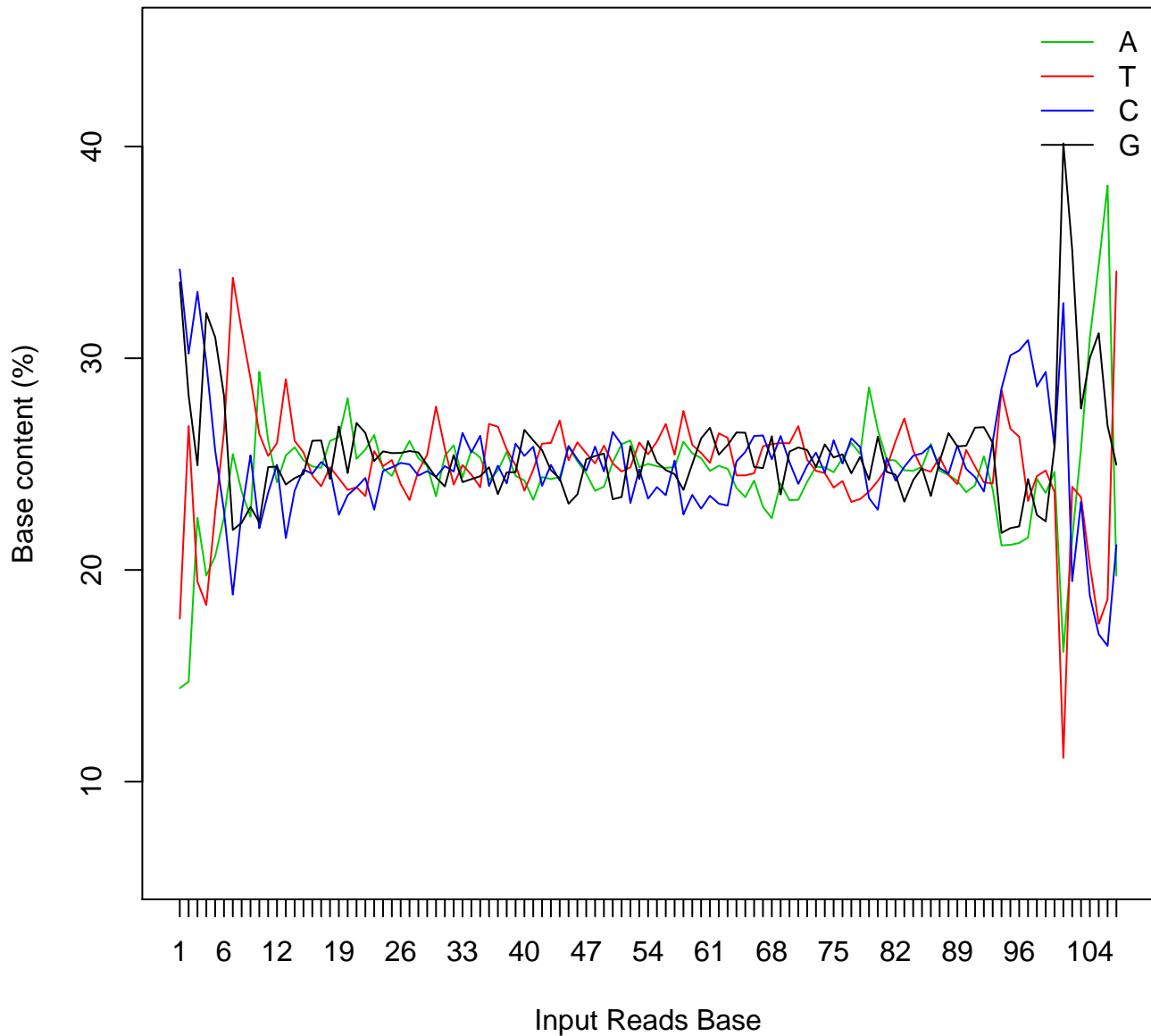
0 20 40

**G 25.49% ± 4.89**

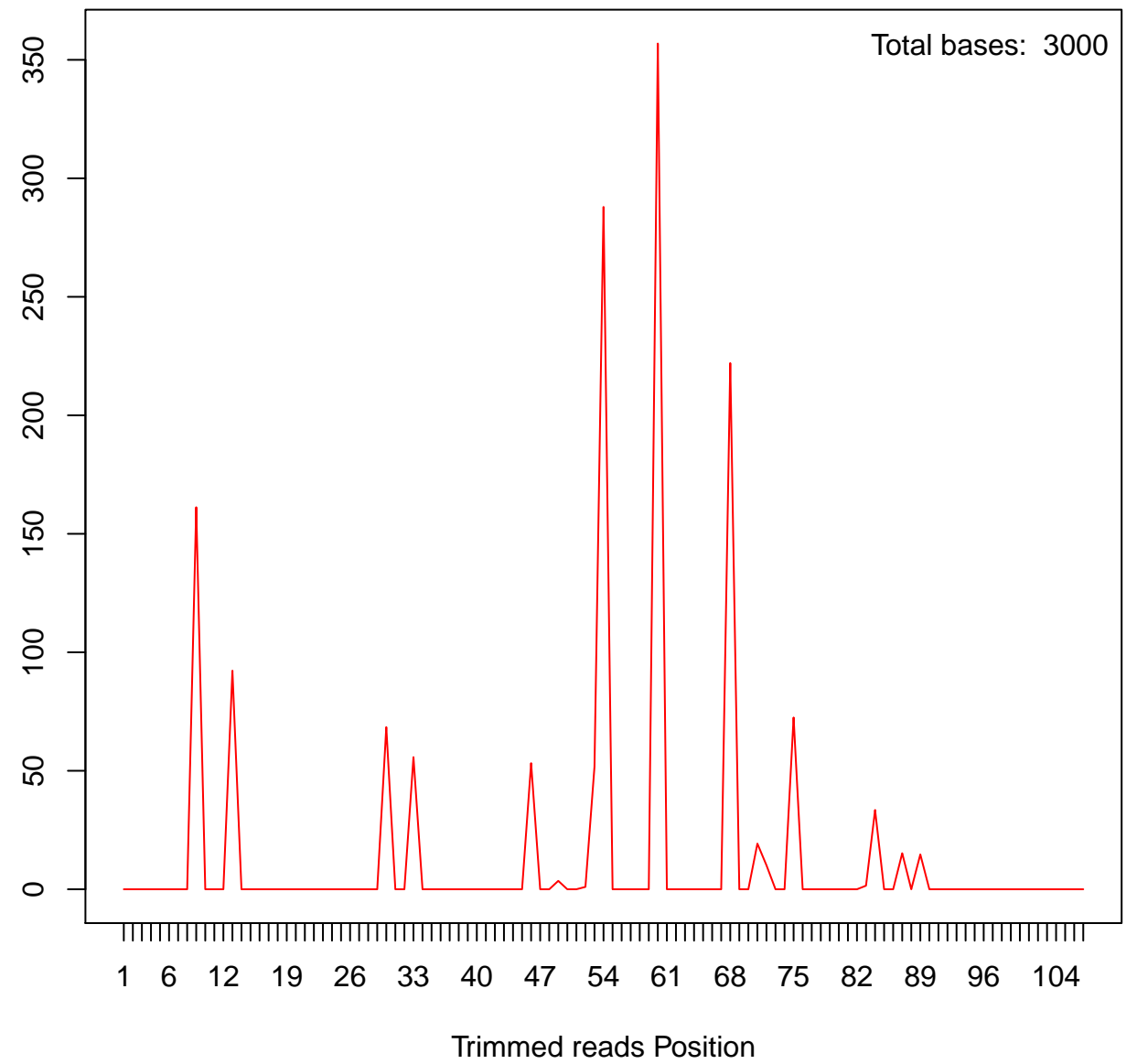
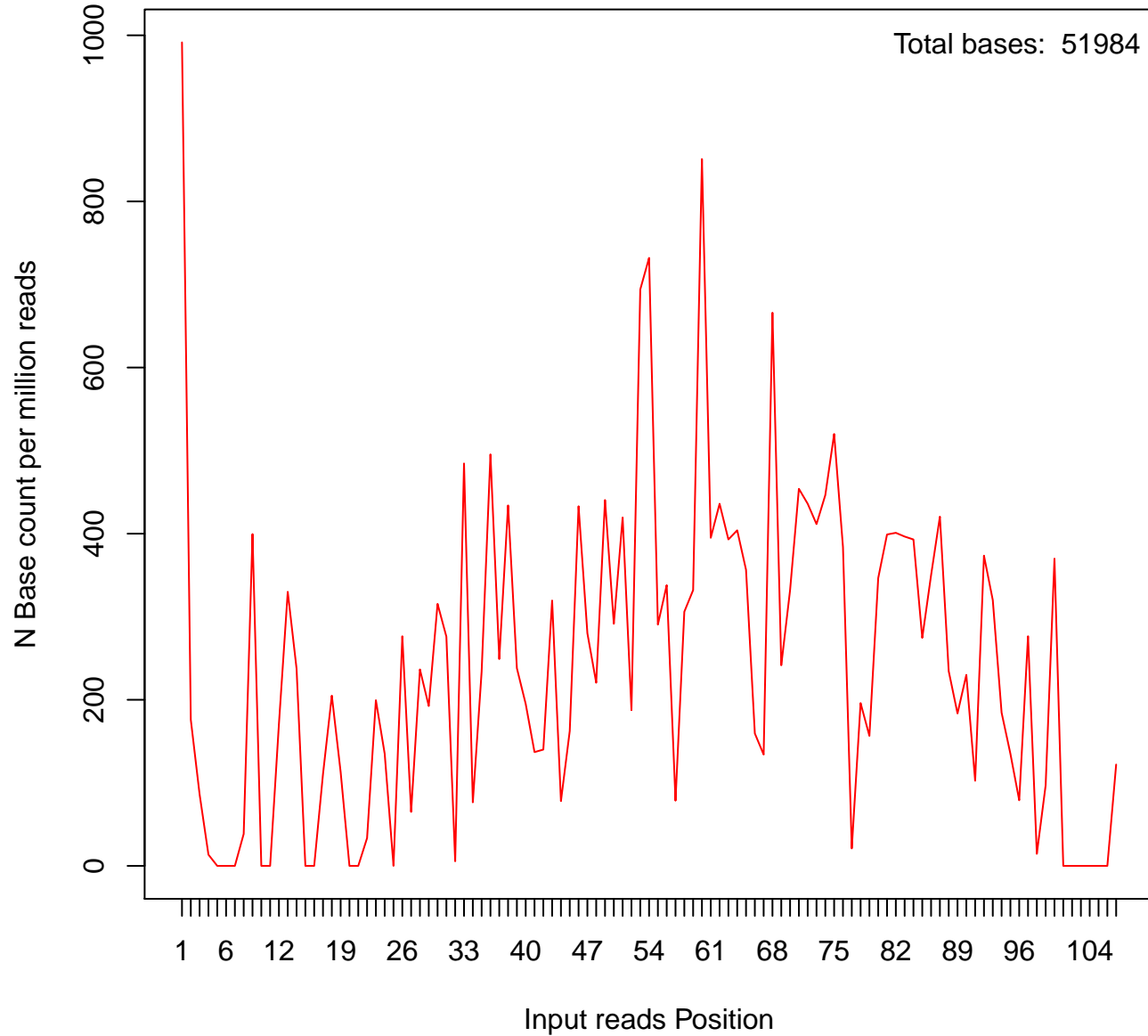


0 20 40

### Nucleotide Content Per Cycle

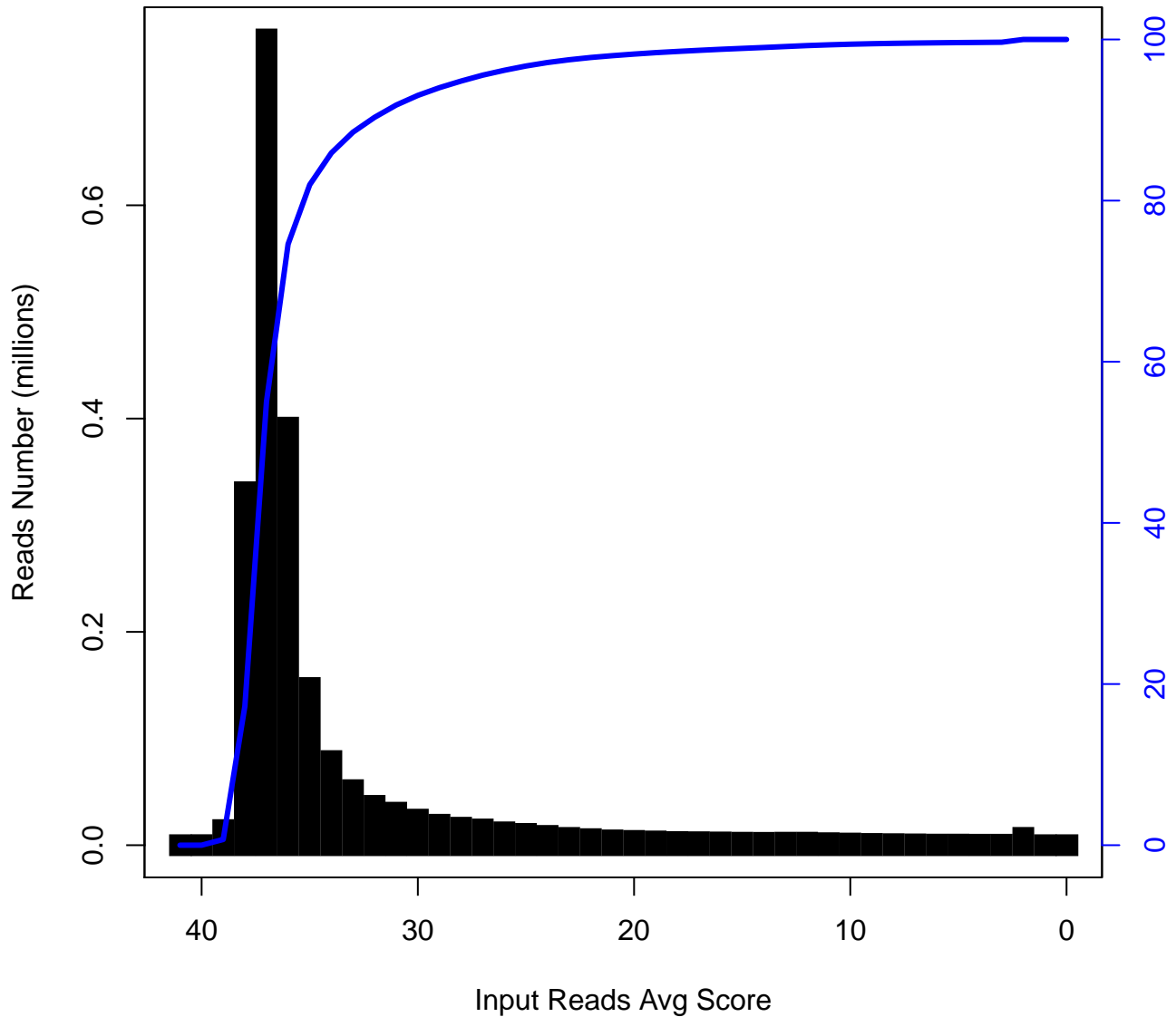


# N Nucleotide Content Per Cycle

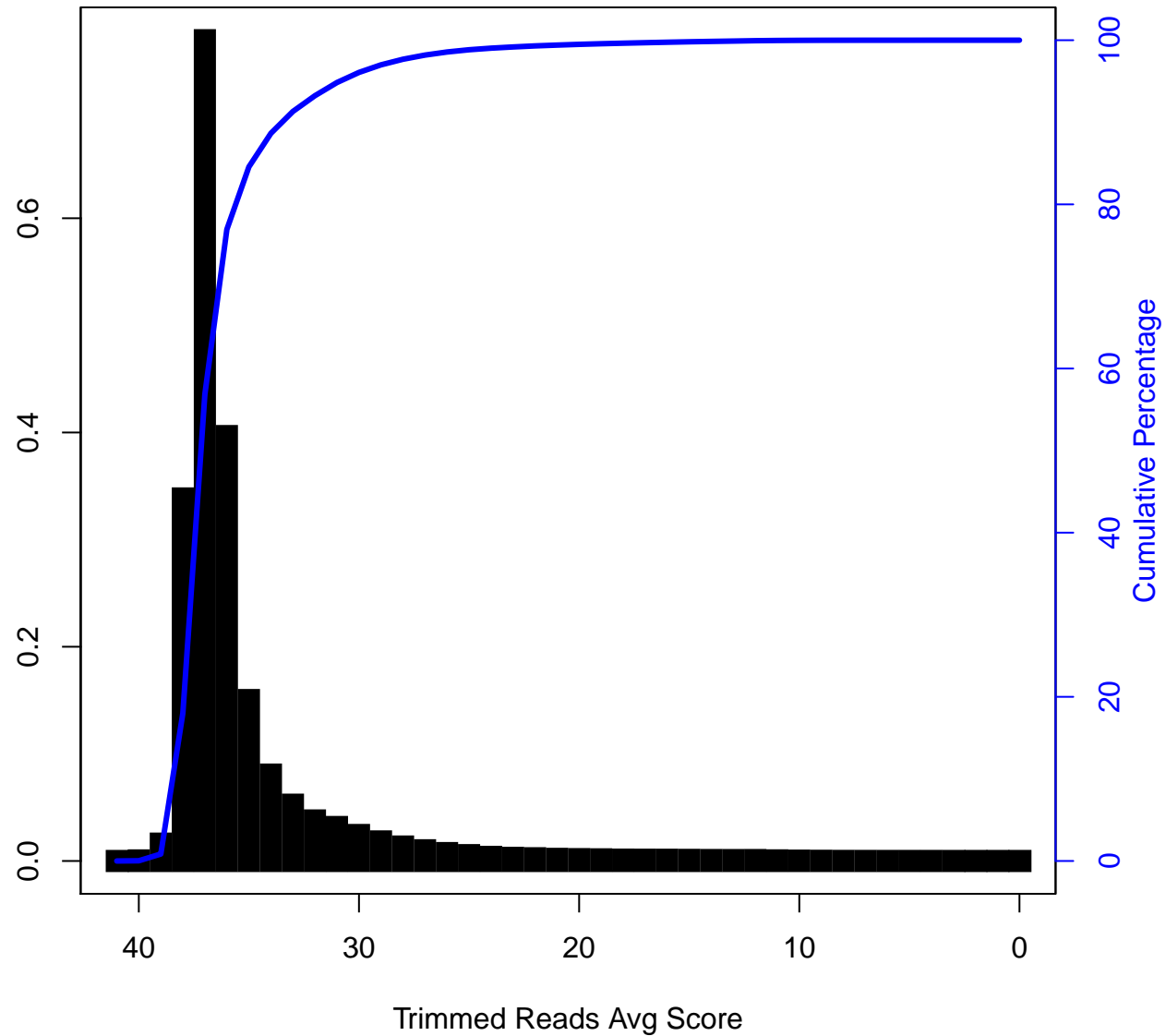


# Reads Average Quality Histogram

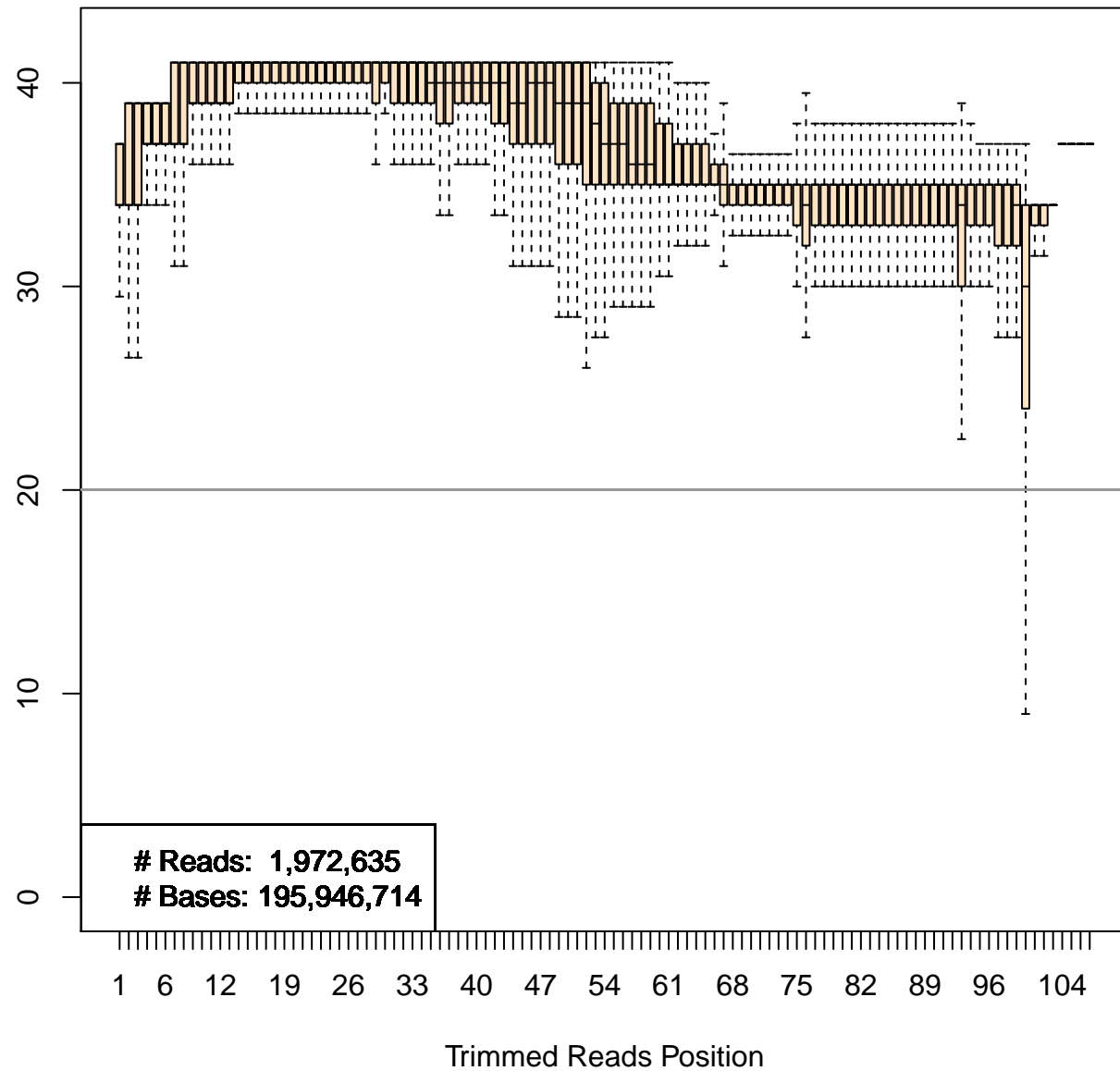
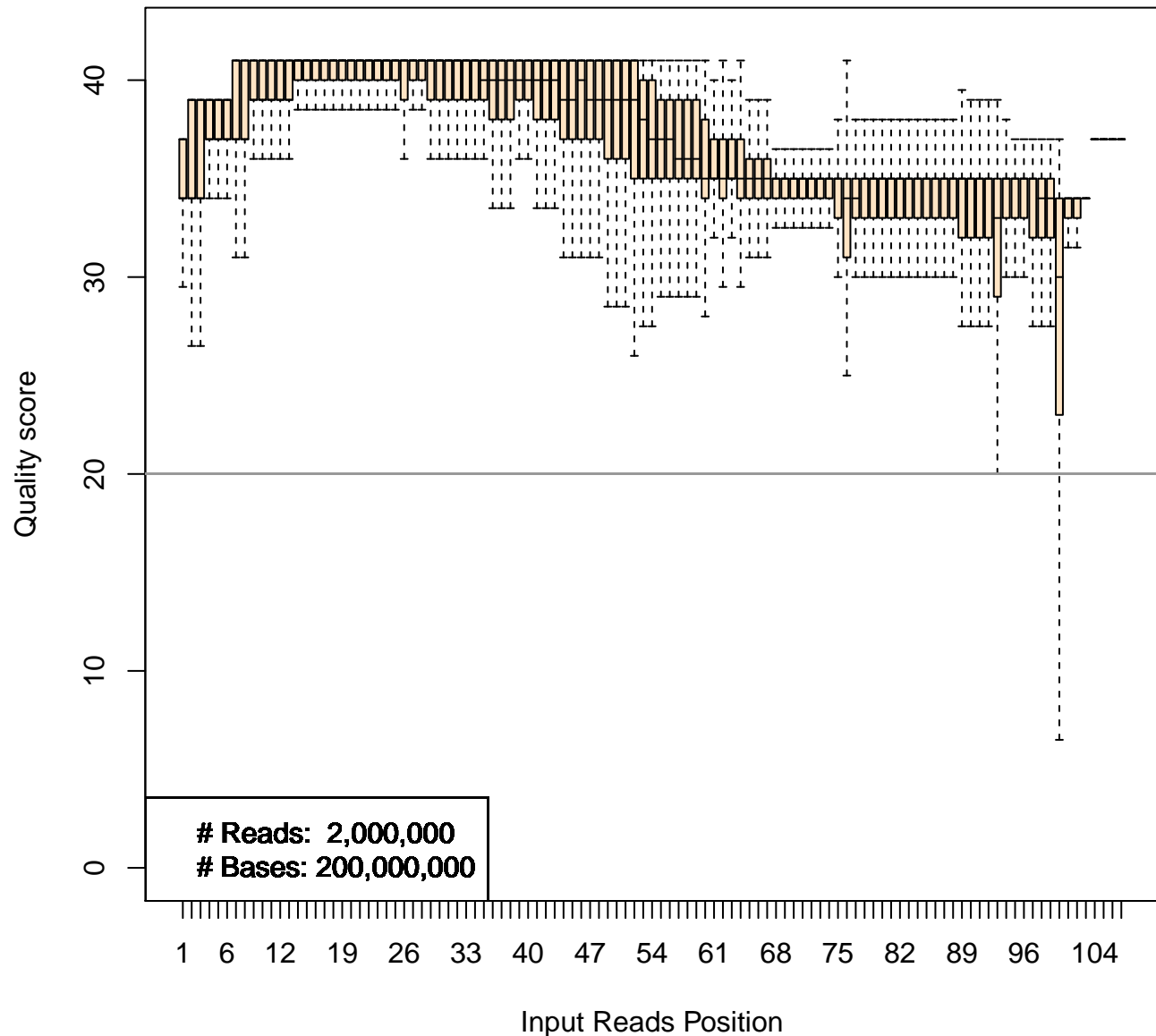
Number of Q>=20 reads: 1,963,799 ( 98.19% ) , mean Length: 100.06



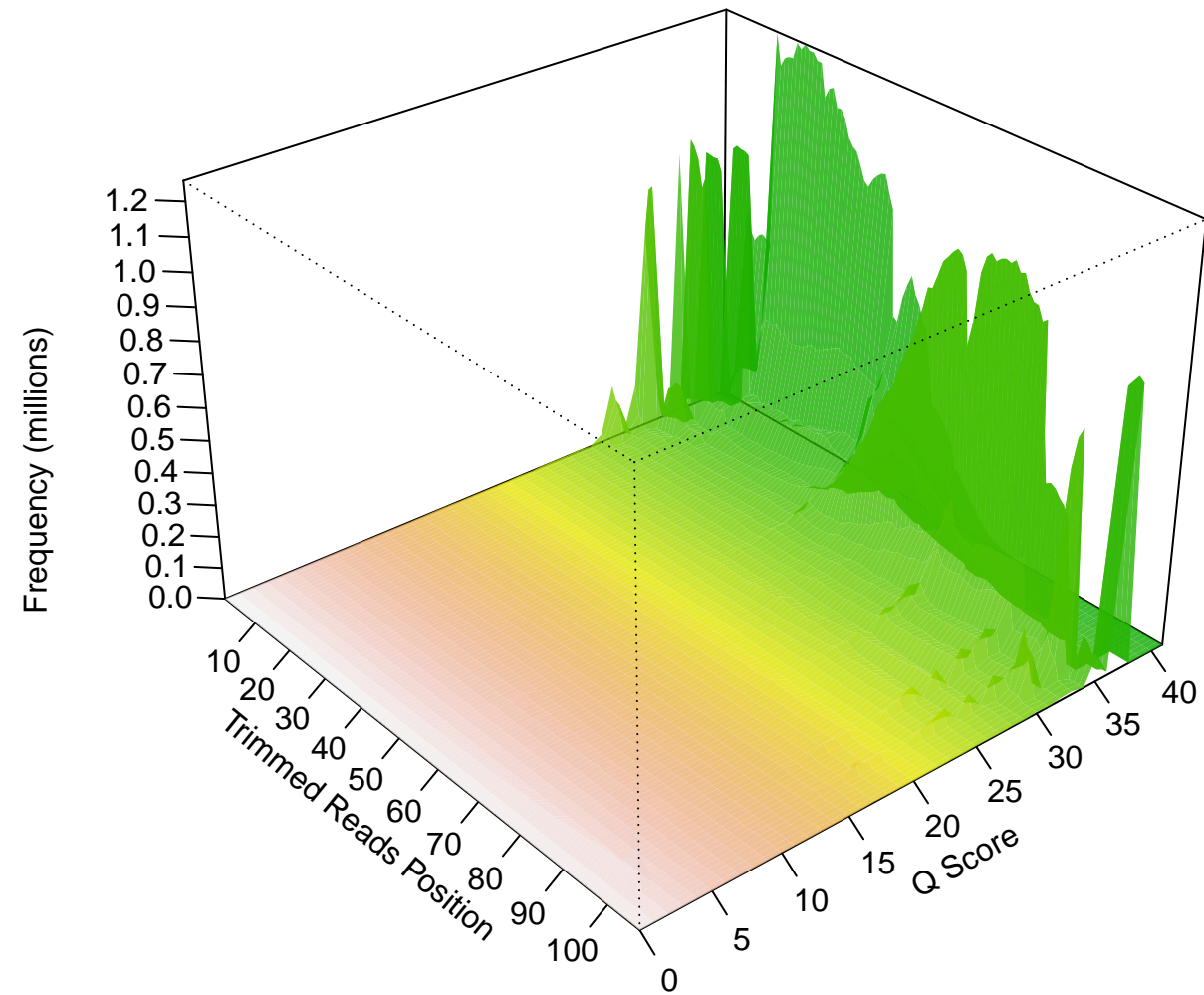
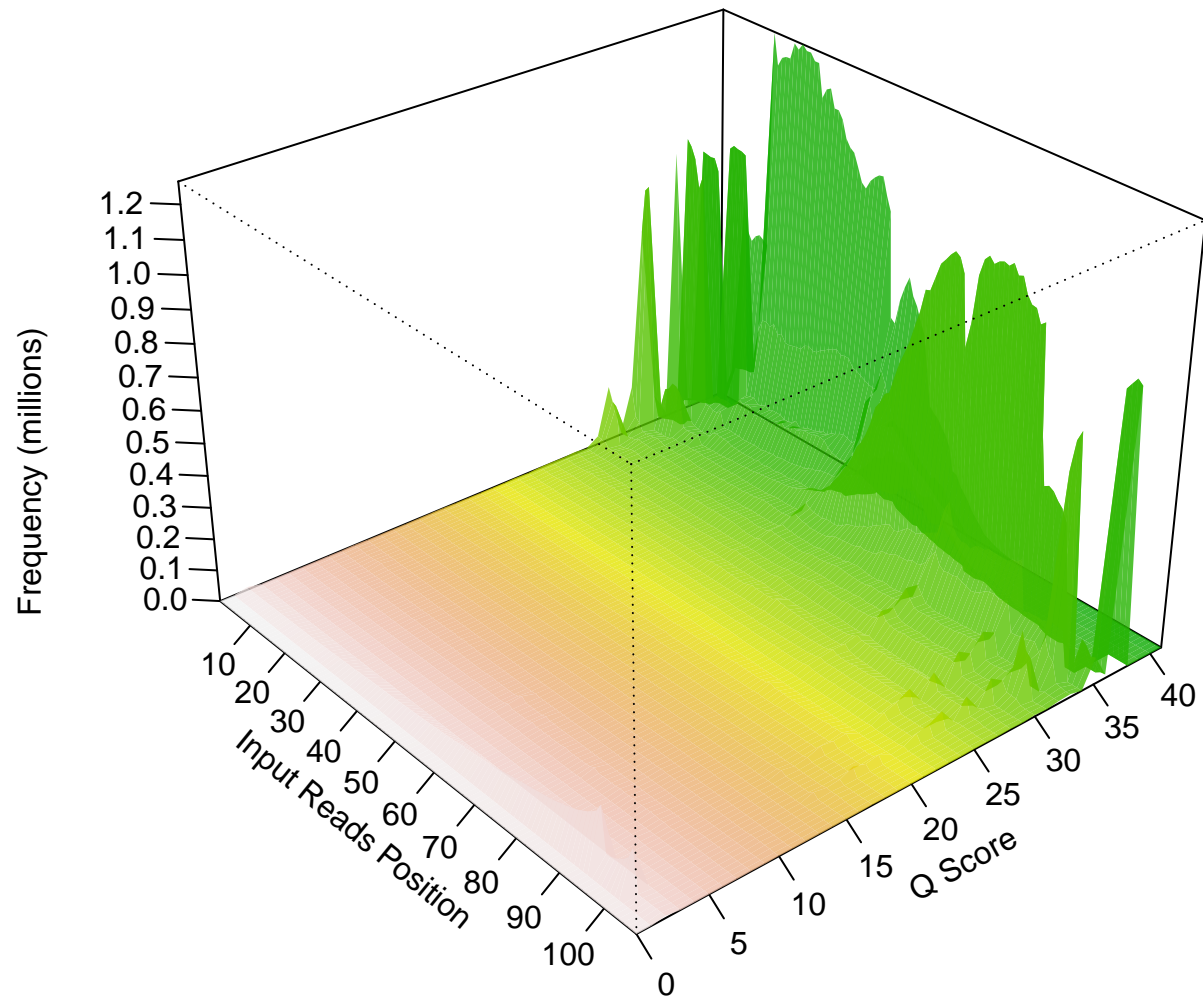
Number of Q>=20 reads: 1,962,686 ( 99.50% ) , mean Length: 99.32



### Quality Boxplot Per Cycle



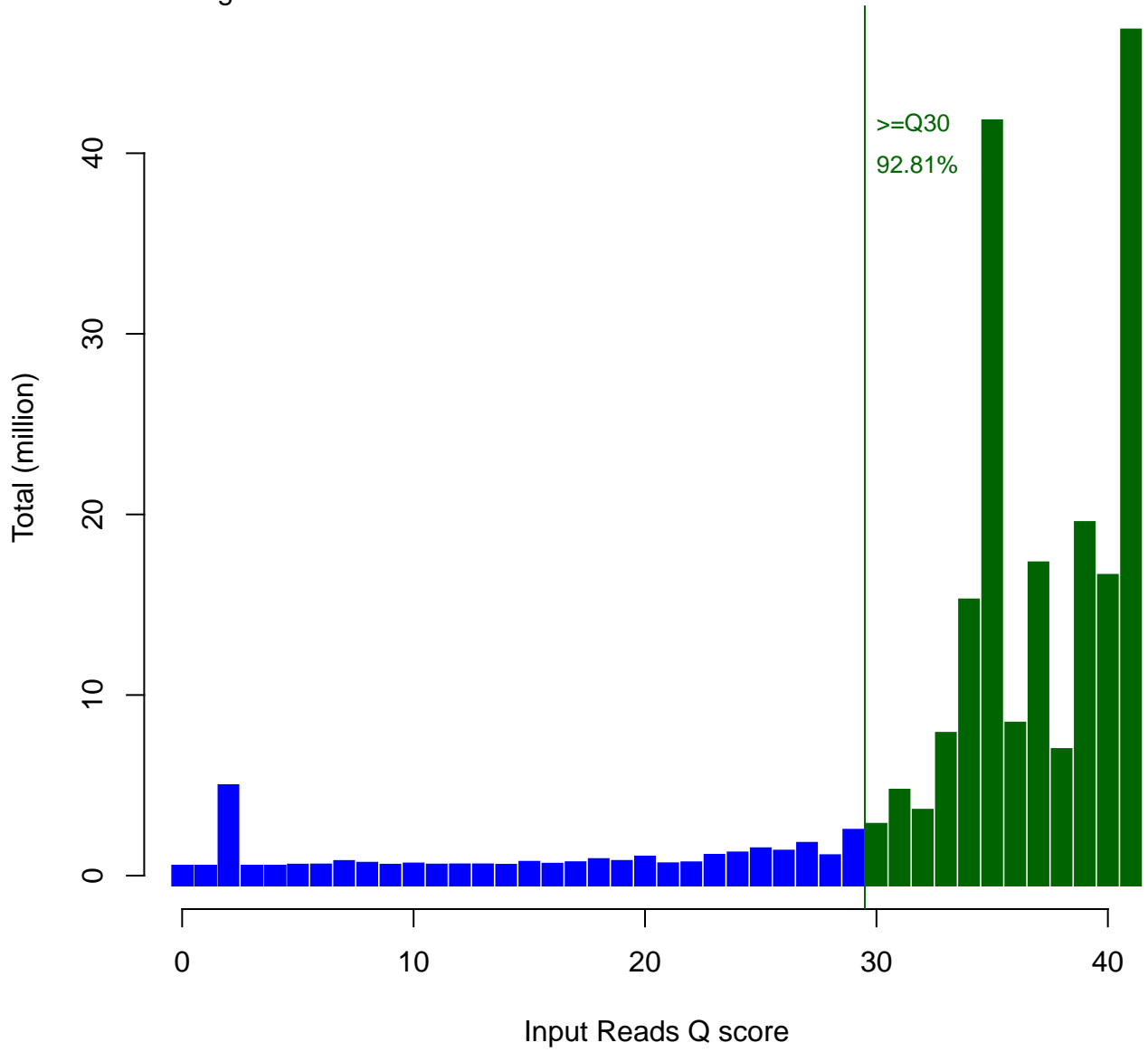
Quality 3D plot. (Position vs. Score vs. Frequency)





# Quality report

Average: 35.82



Average: 36.37

