

## QC stats

### Before Trimming

**Reads #: 100,000**

**Total bases: 25,100,000**

**Reads Length: 251.00**

### After Trimming

**Reads #: 82,172 (82.17 %)**

**Total bases: 16,005,103 (63.77 %)**

**Mean Reads Length: 194.78**

**Paired Reads #: 69,984 (85.17 %)**

**Paired total bases: 13,581,564 (84.86 %)**

**Unpaired Reads: 12,188 (14.83 %)**

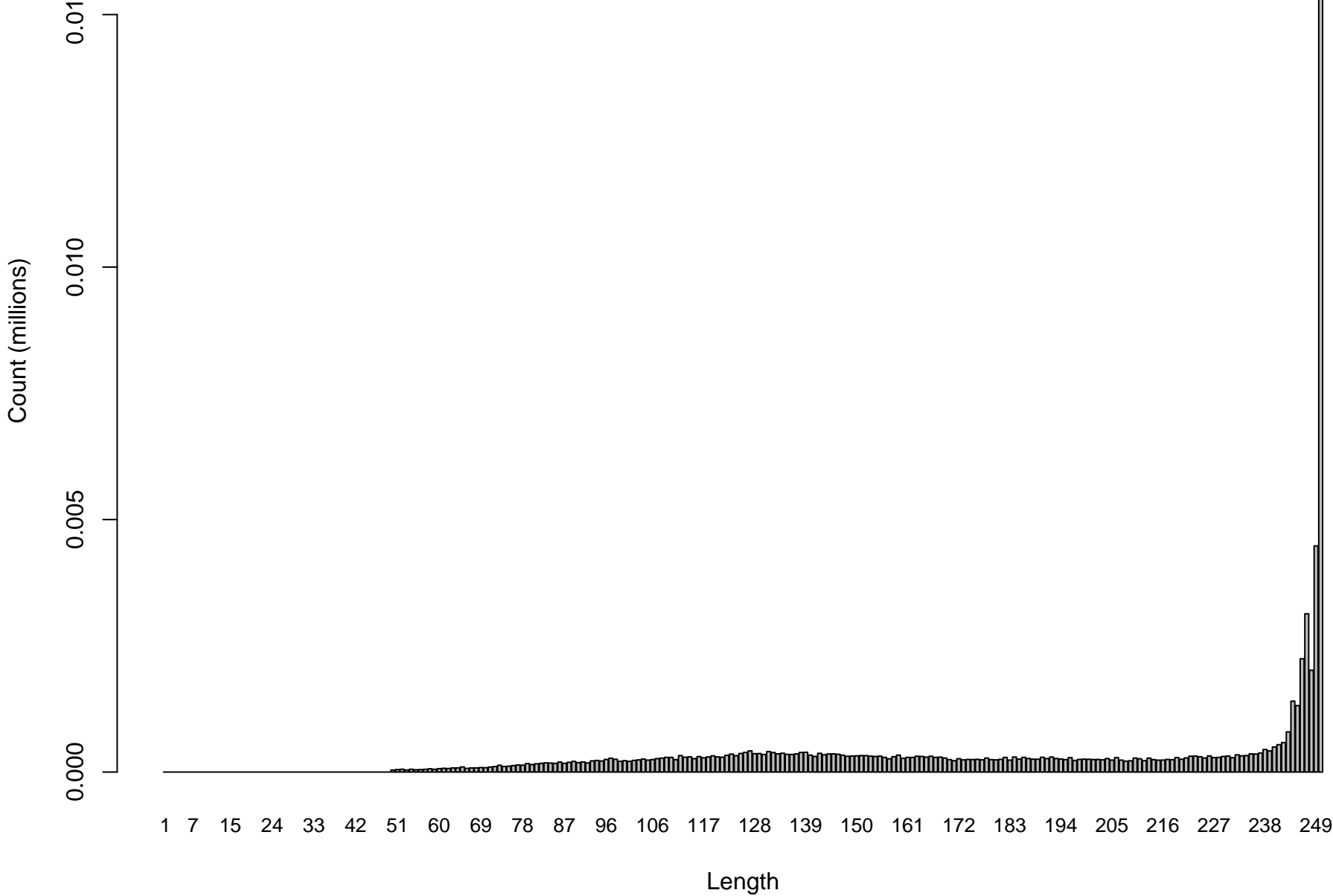
**Unpaired total bases: 2,423,539 (15.14 %)**

**Discarded reads #: 17,828 (17.83 %)**

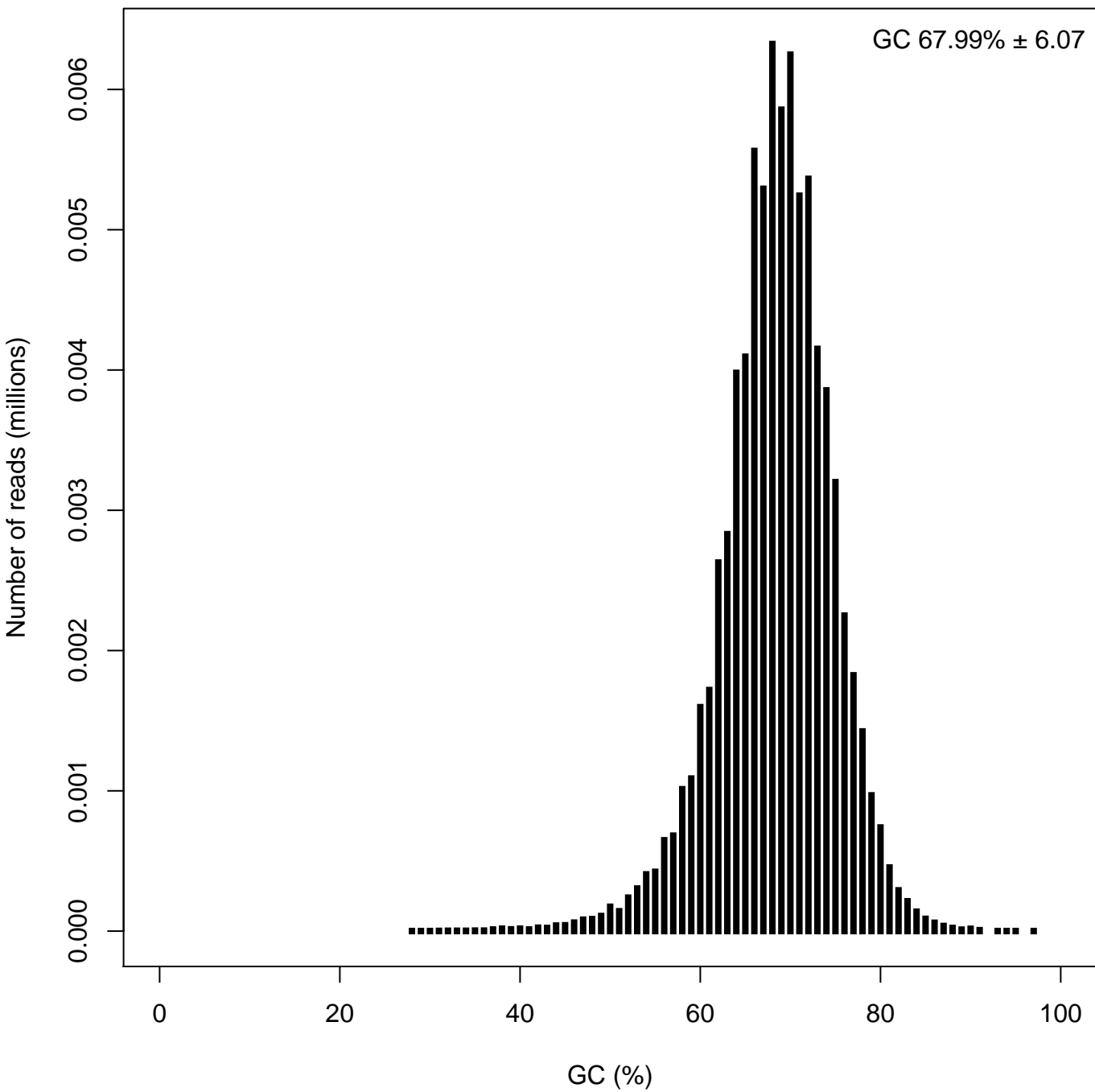
**Discarded bases: 9,094,897 (36.23 %)**

Reads Length Histogram

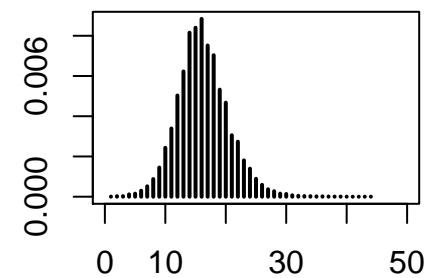
Mean  $194.78 \pm 58.41$   
Max 250  
Min 50



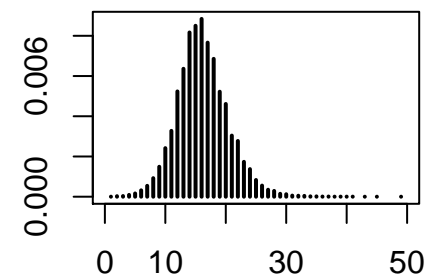
## Reads GC content



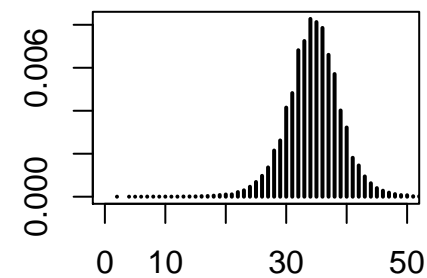
**A 15.74%  $\pm$  4.20**



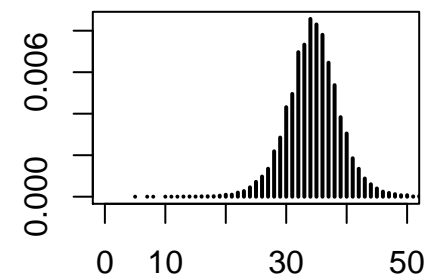
**T 15.68%  $\pm$  4.18**



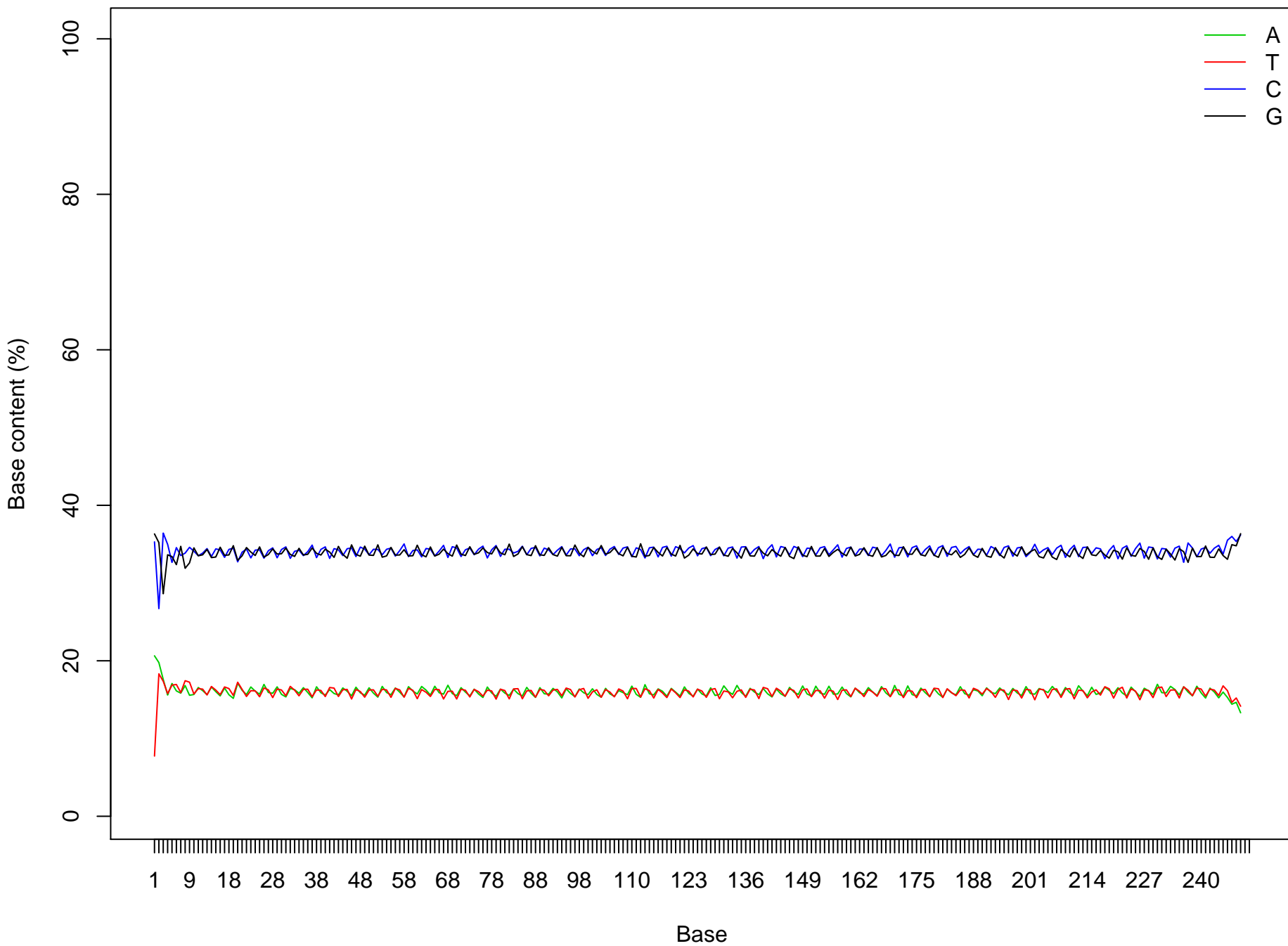
**C 34.03%  $\pm$  4.47**



**G 33.96%  $\pm$  4.36**

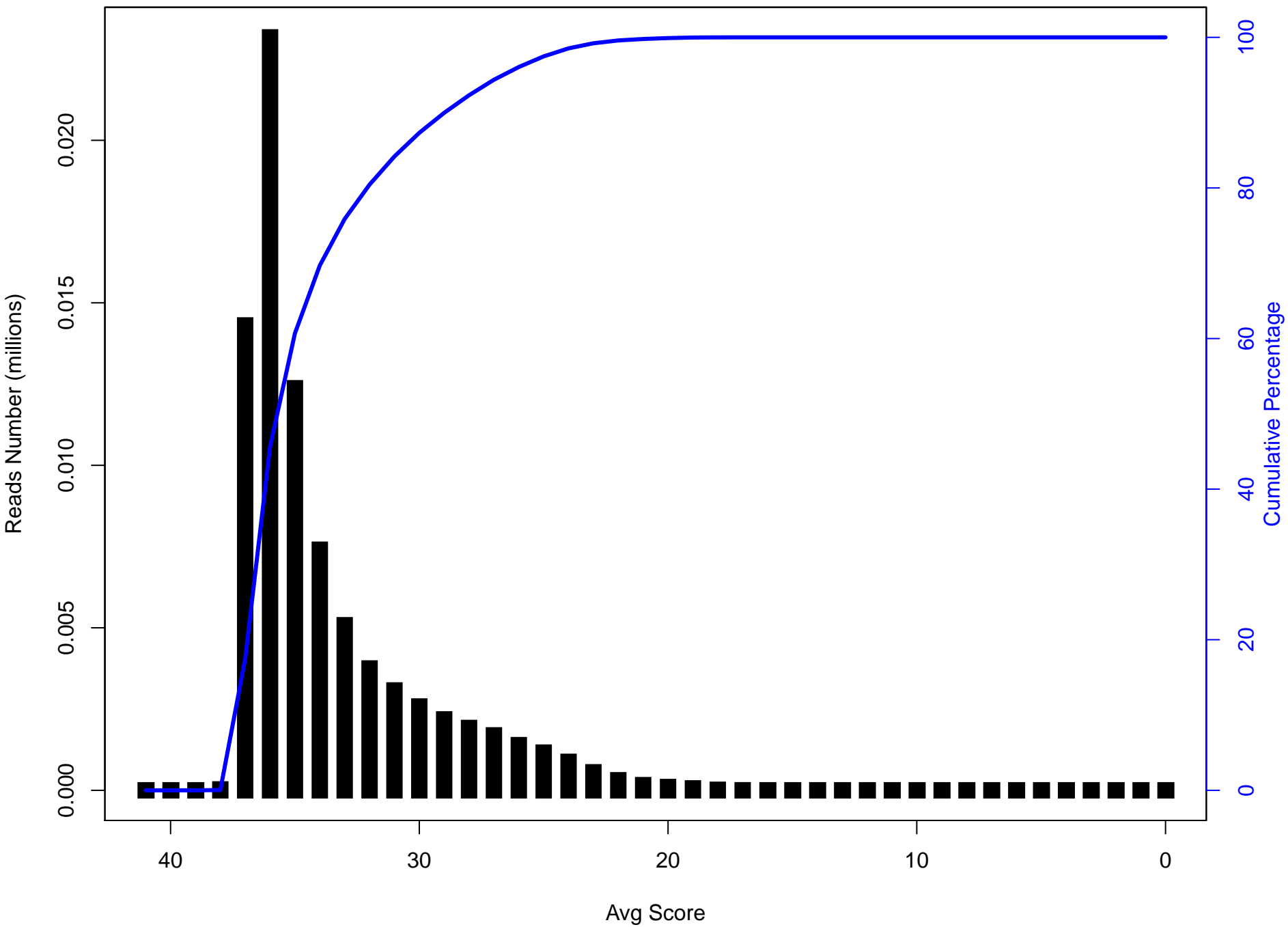


# Nucleotide Content Per Cycle

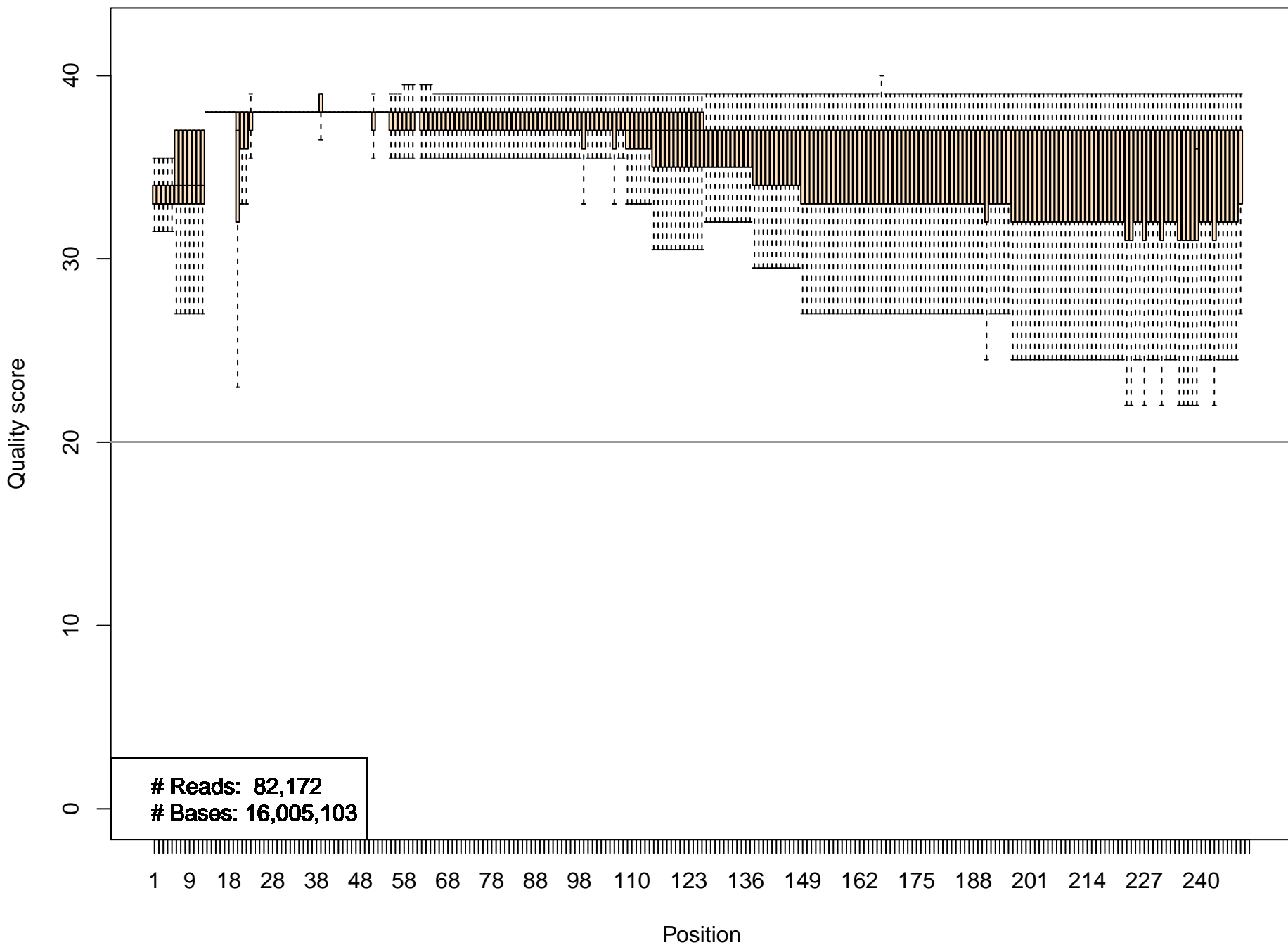


# Reads Average Quality Histogram

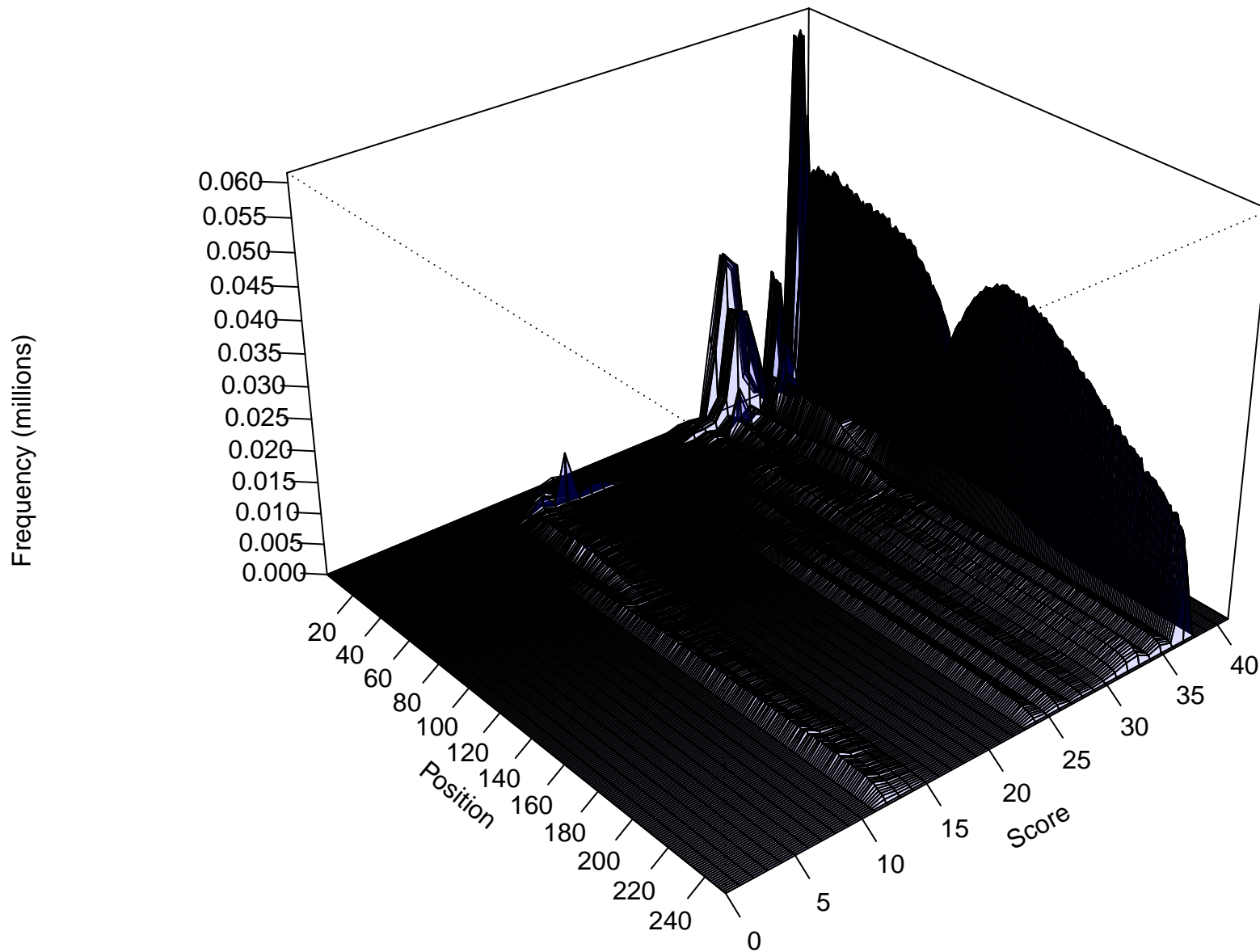
Number of Q>=20 reads: 82,095 ( 99.91% ) , mean Length: 194.87



# Quality Boxplot Per Cycle



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



# Quality report

