

## QC stats

### Before Trimming

Reads #: 432520  
Total bases: 43684520  
Reads Length: 101.00

### After Trimming

Reads #: 372971 (86.23 %)  
Total bases: 36912363 (84.50 %)  
Mean Reads Length: 98.97  
Paired Reads #: 344388 (92.34 %)  
Paired total bases: 34190884 (92.63 %)  
Unpaired Reads #: 28583 (7.66 %)  
Unpaired total bases: 2721479 (7.37 %)

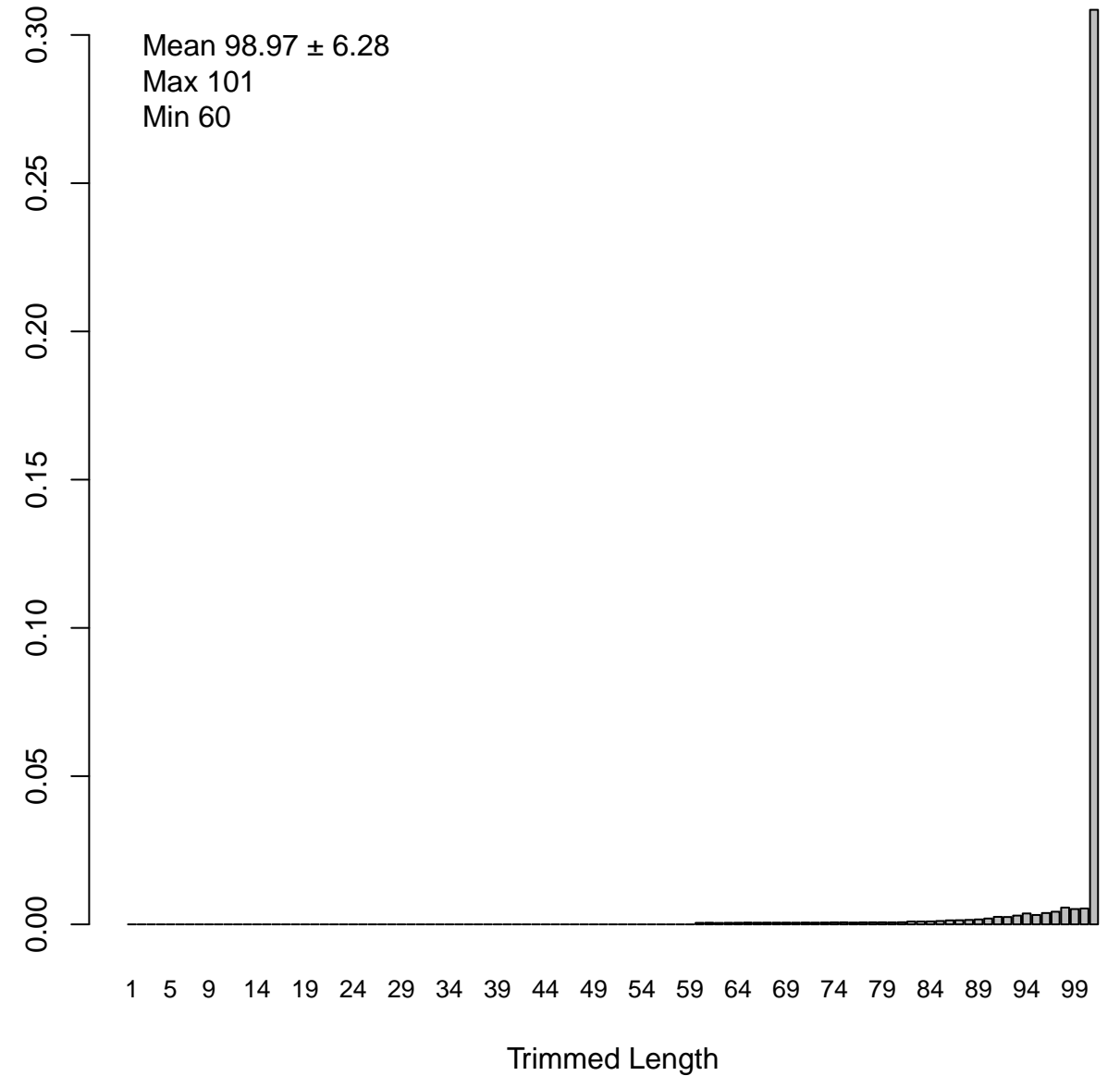
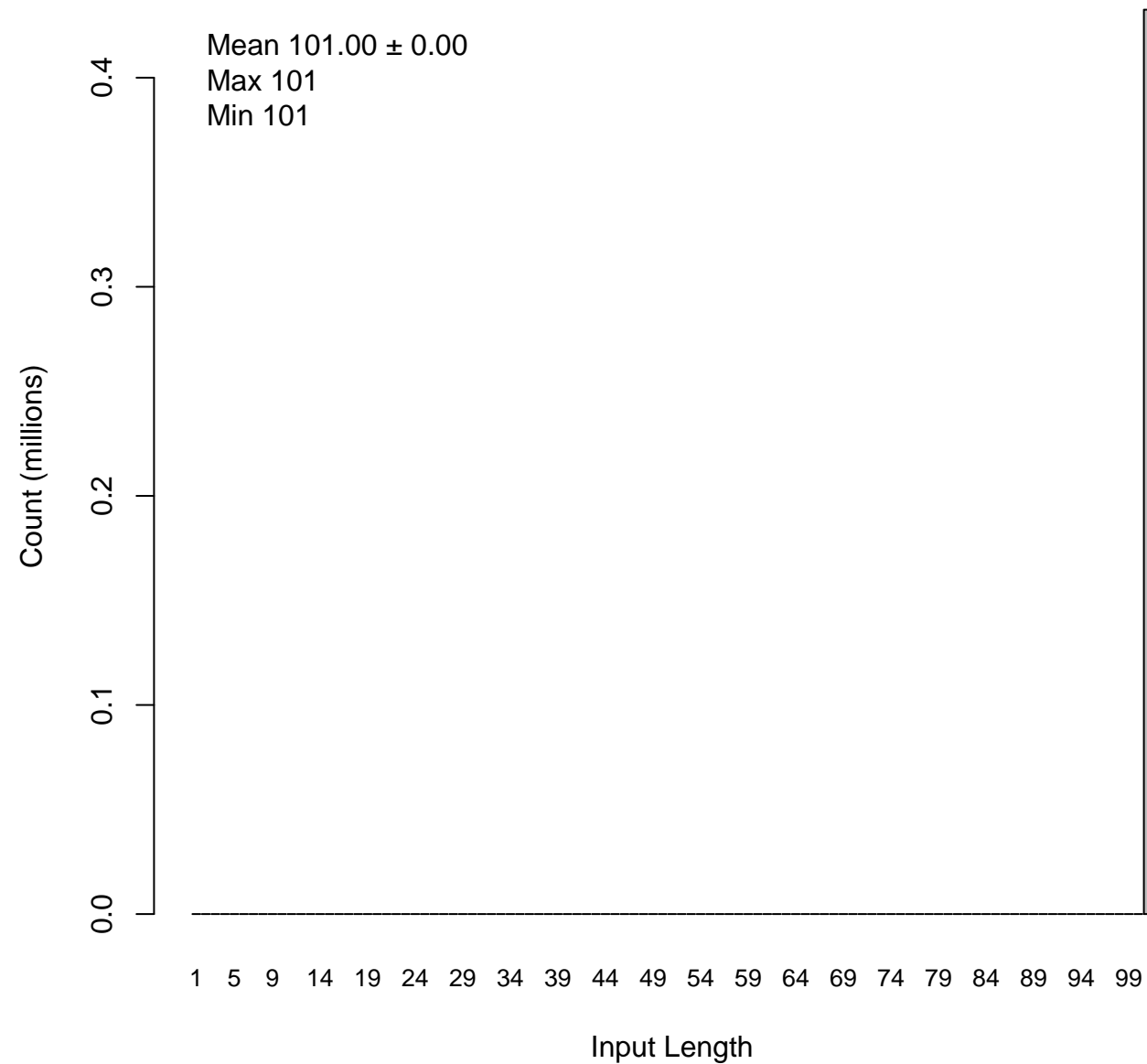
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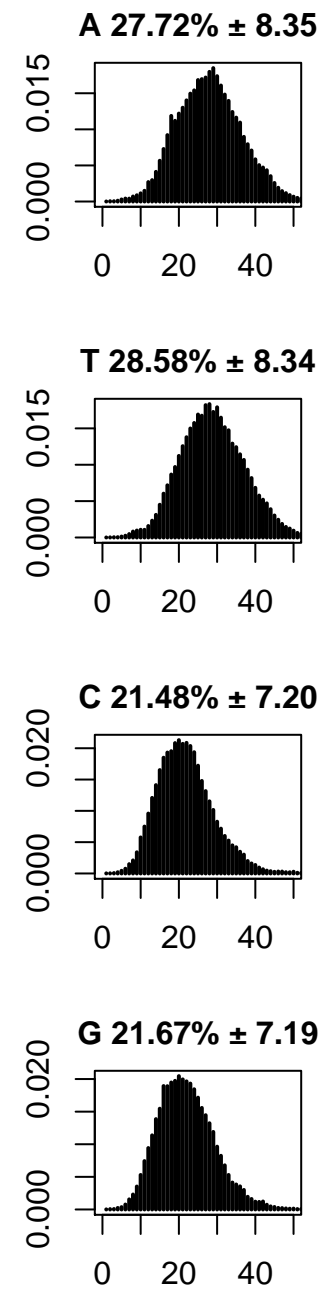
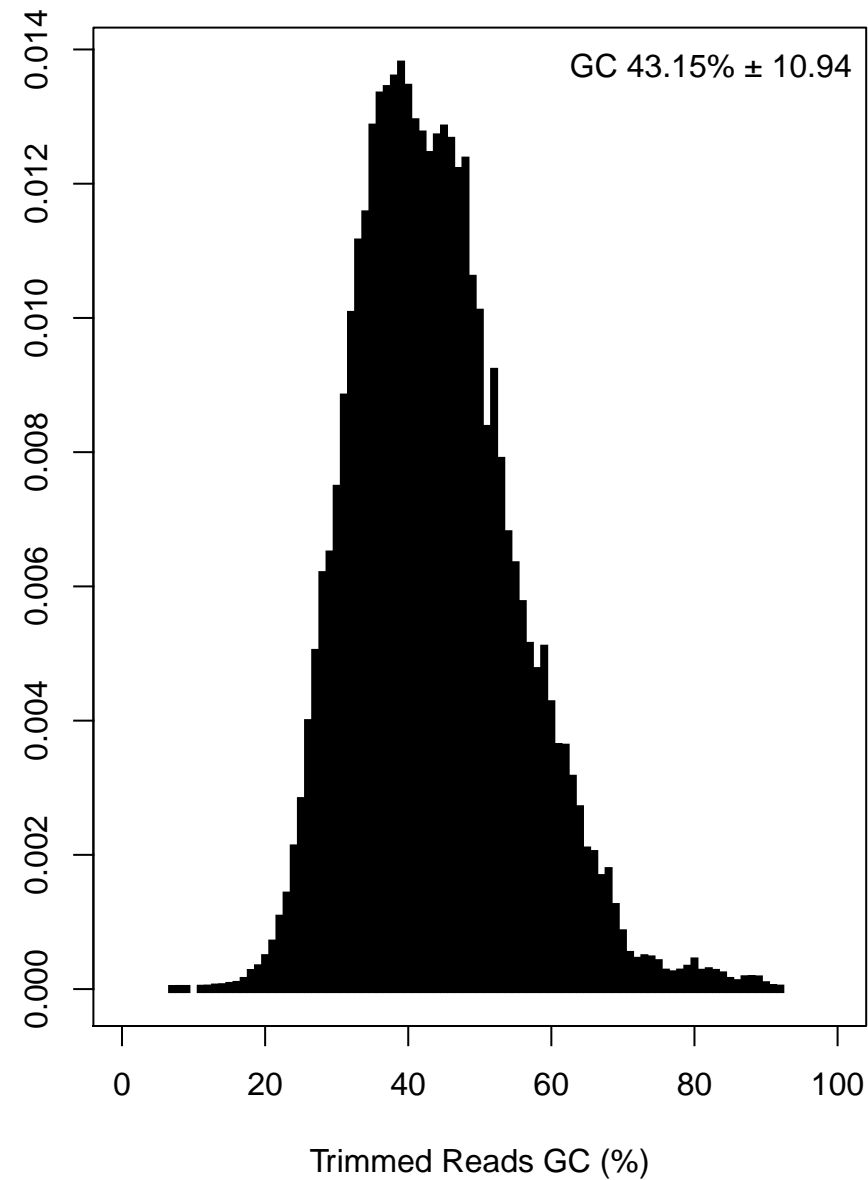
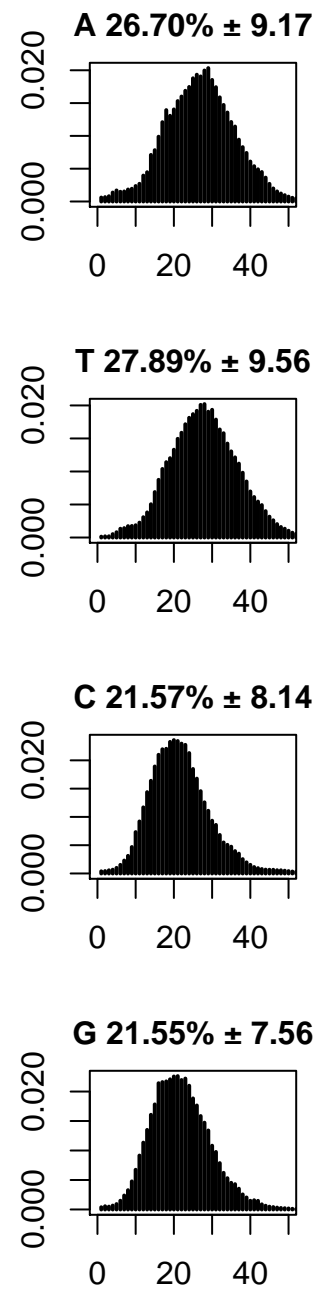
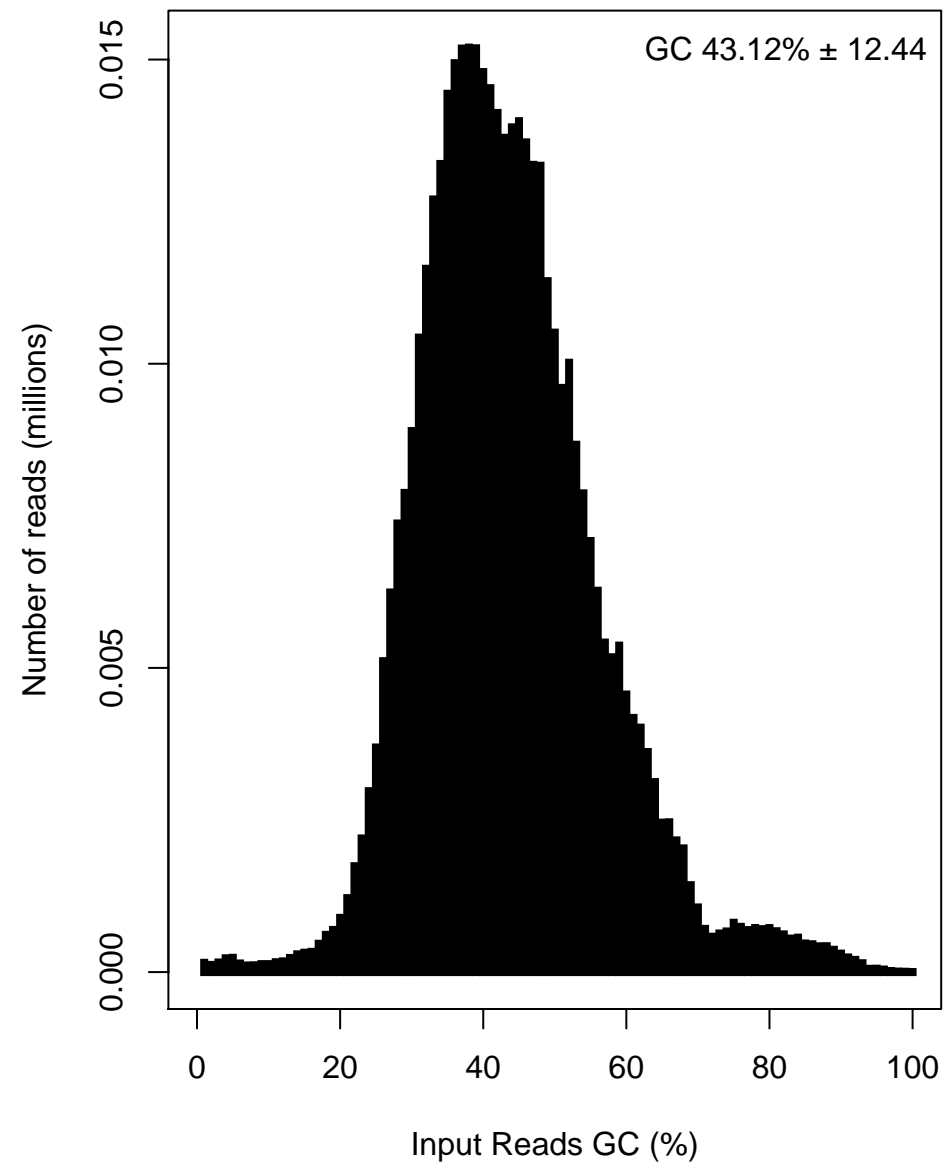
Discarded reads #: 59549 (13.77 %)

Trimmed bases: 6772157 (15.50 %)

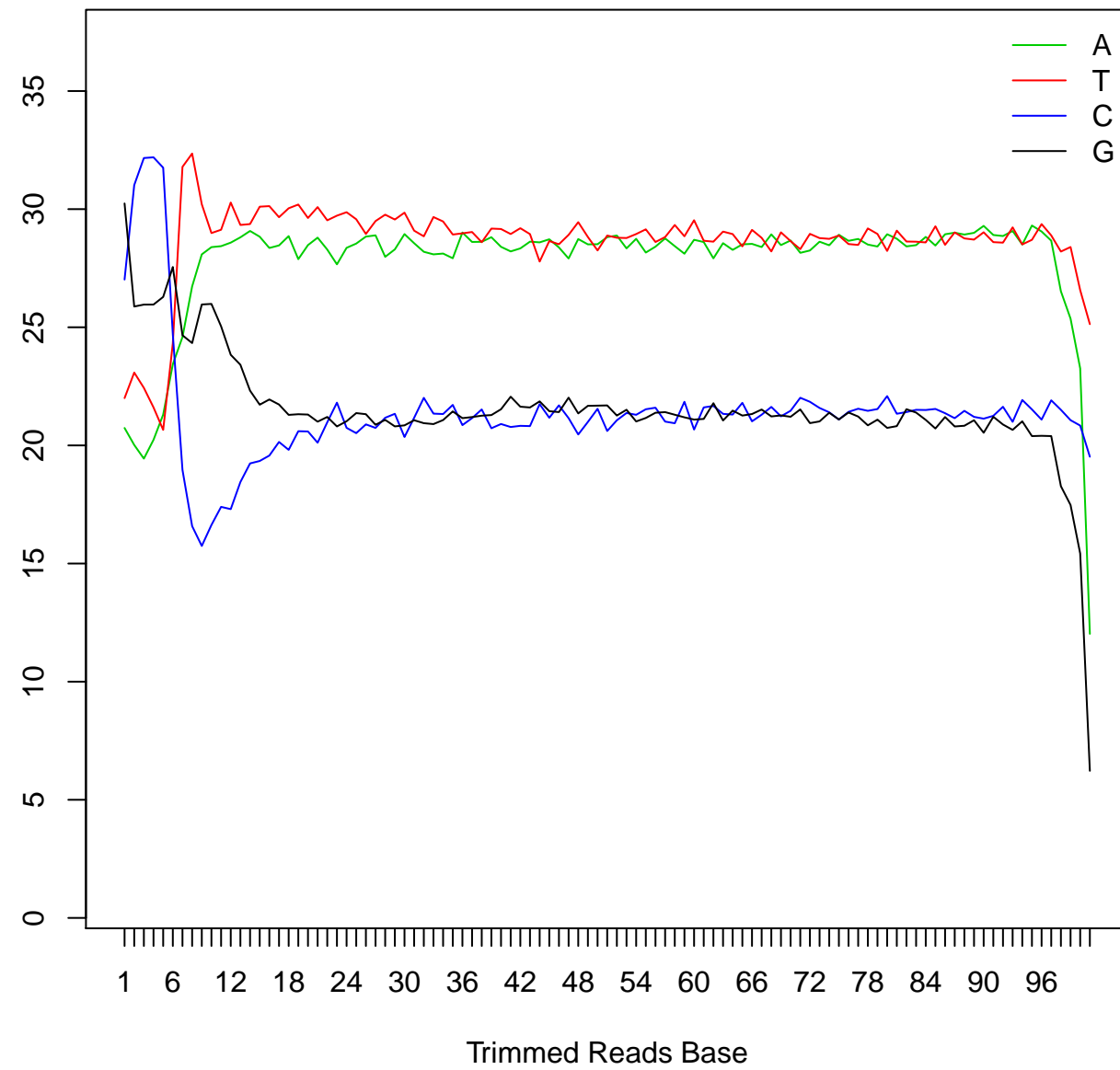
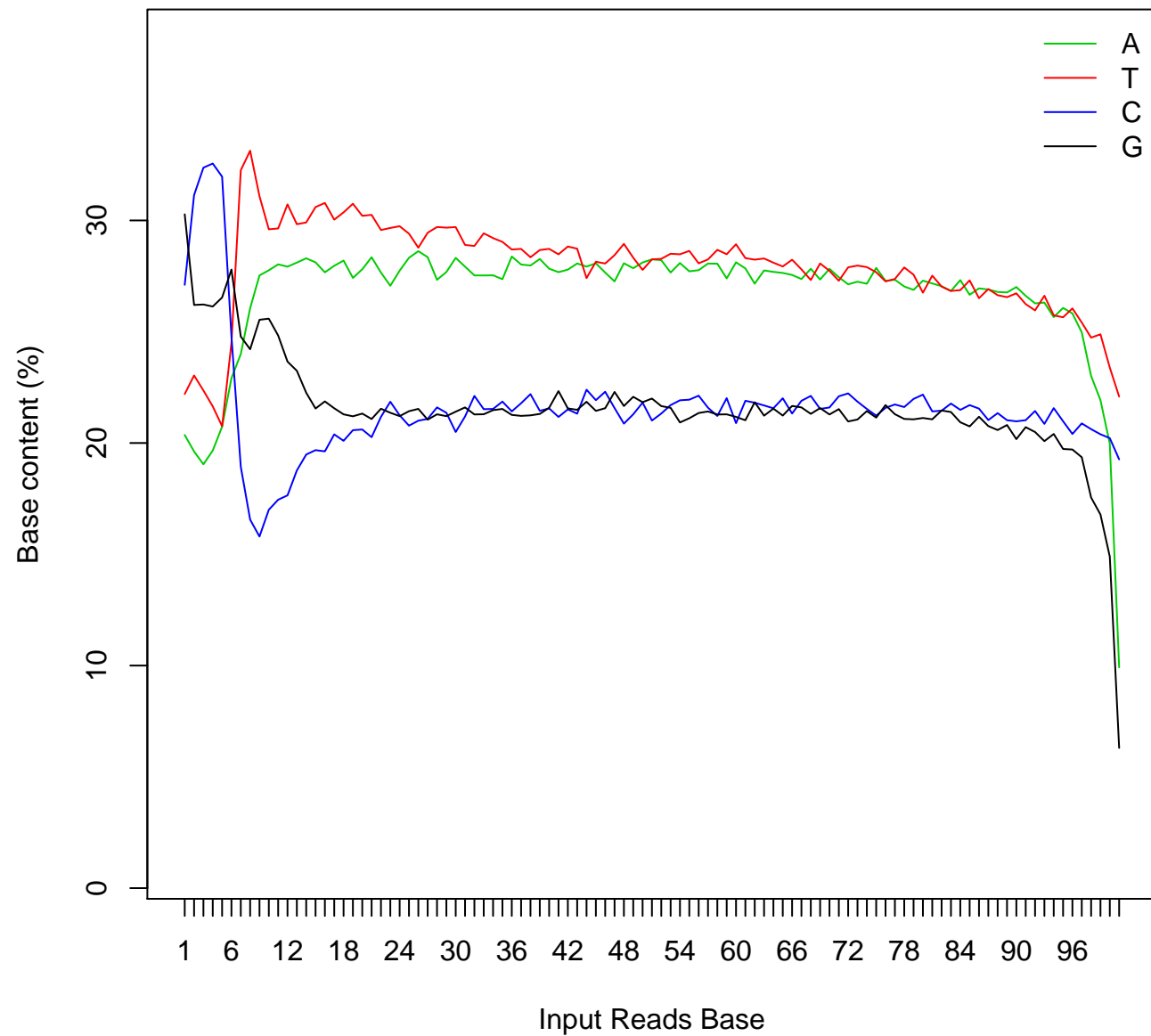
Reads Filtered by length cutoff (60 bp): 22794 (5.27 %)  
Bases Filtered by length cutoff: 838831 (1.92 %)  
Reads Filtered by continuous base "N" (5): 35052 (8.10 %)  
Bases Filtered by continuous base "N": 3488759 (7.99 %)  
Reads Filtered by low complexity ratio (0.7): 1703 (0.39 %)  
Bases Filtered by low complexity ratio: 156376 (0.36 %)  
Reads Trimmed by quality (15.0): 94205 (21.78 %)  
Bases Trimmed by quality: 2288191 (5.24 %)

Reads Length Histogram

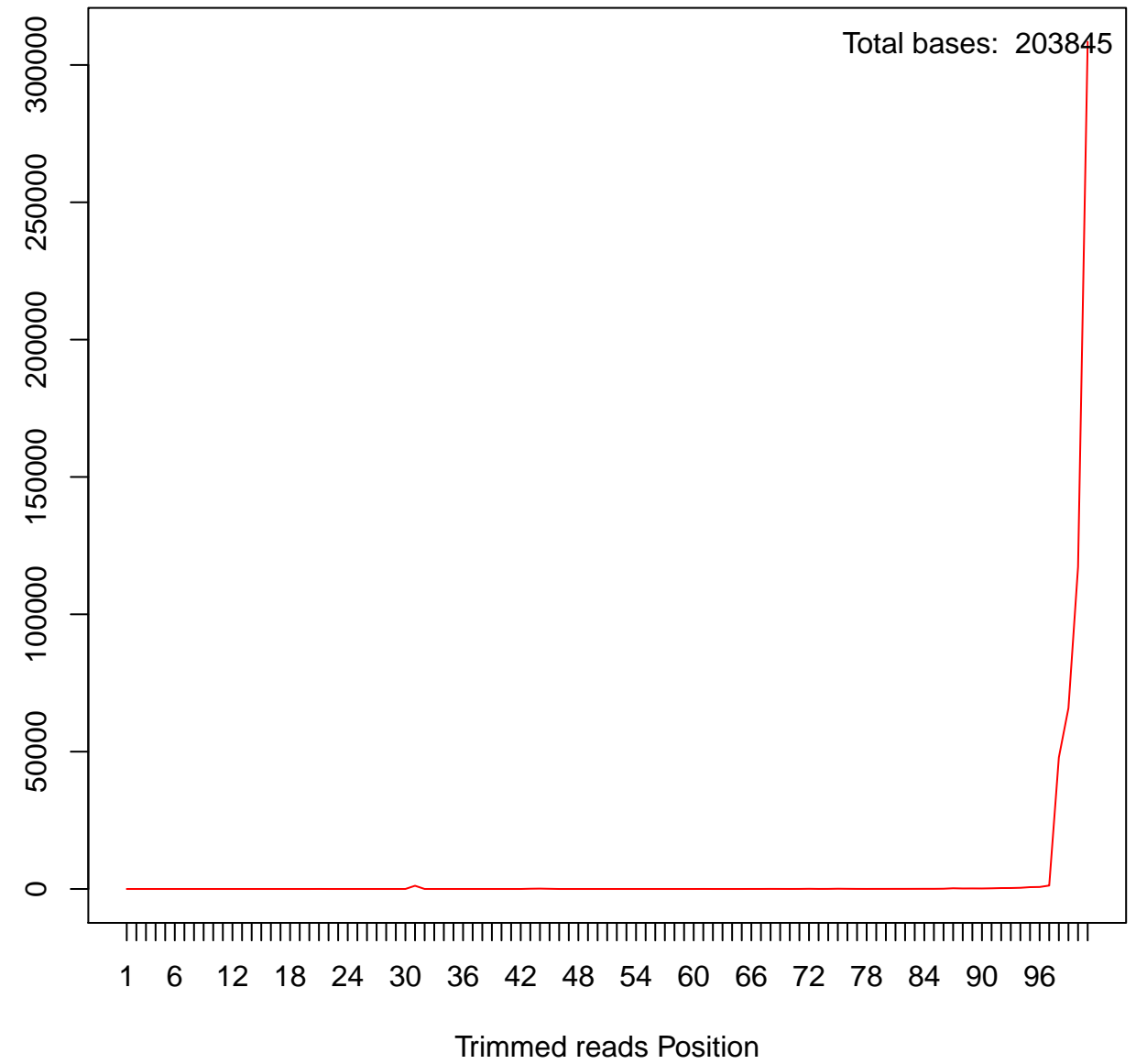
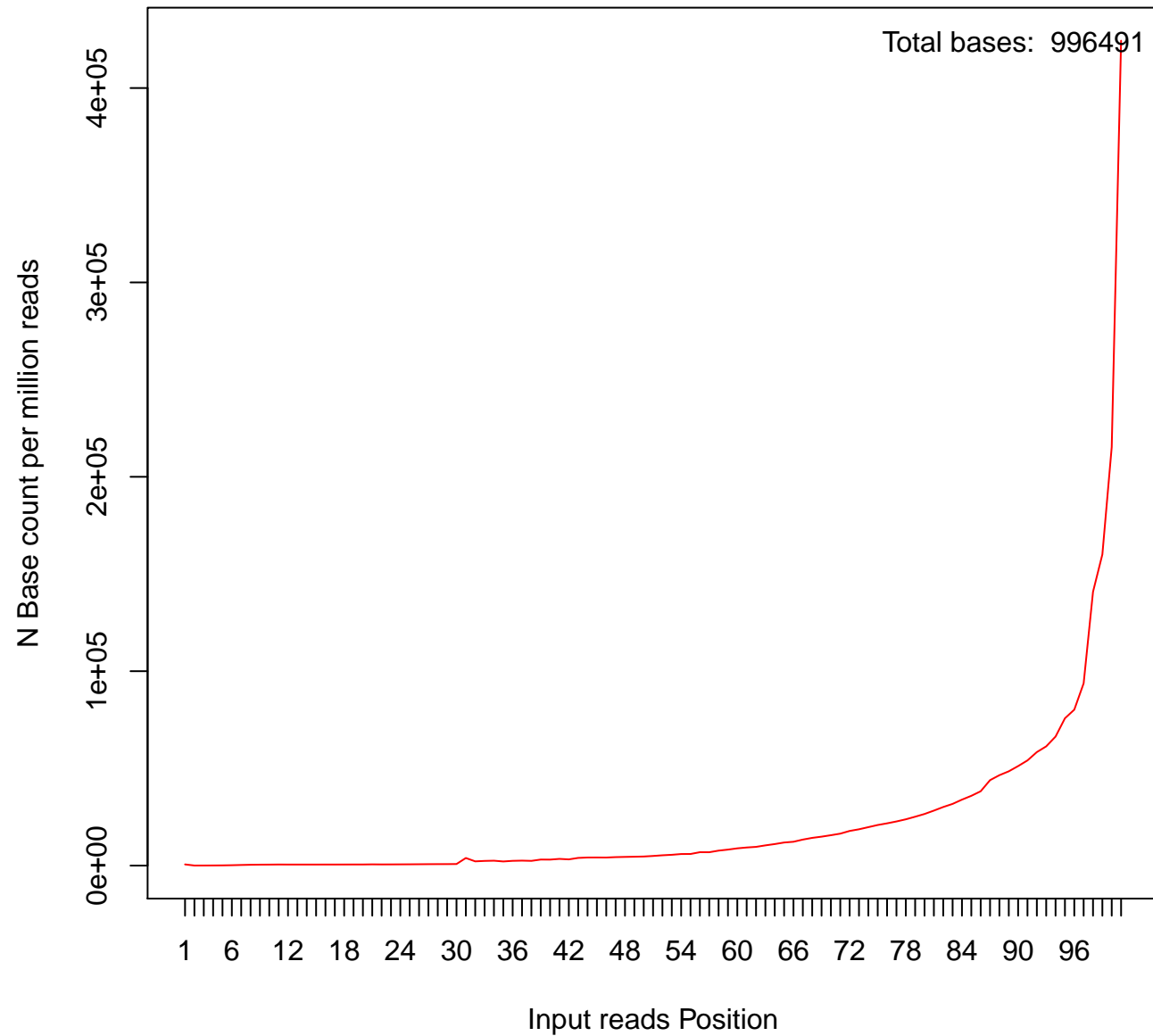




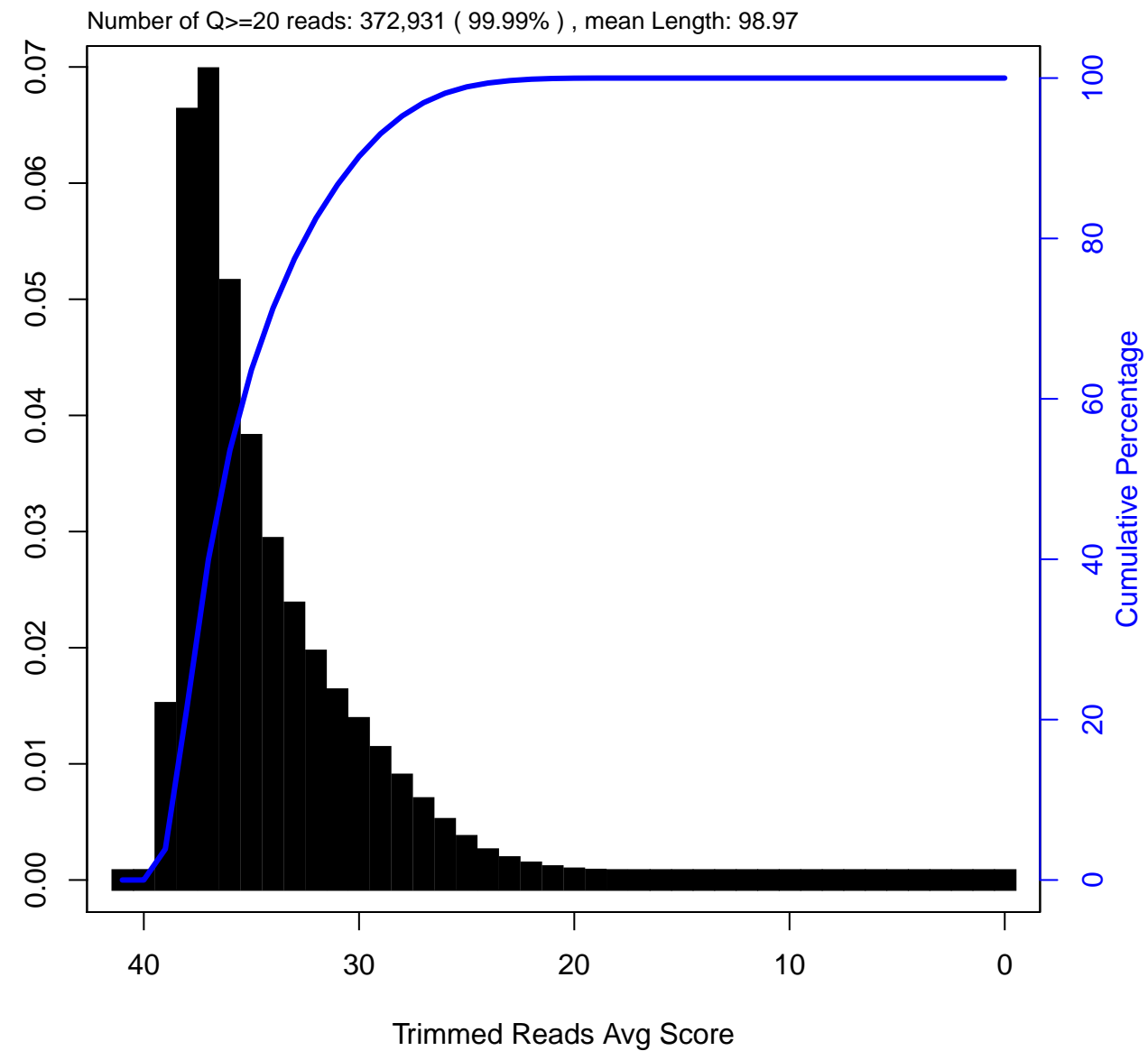
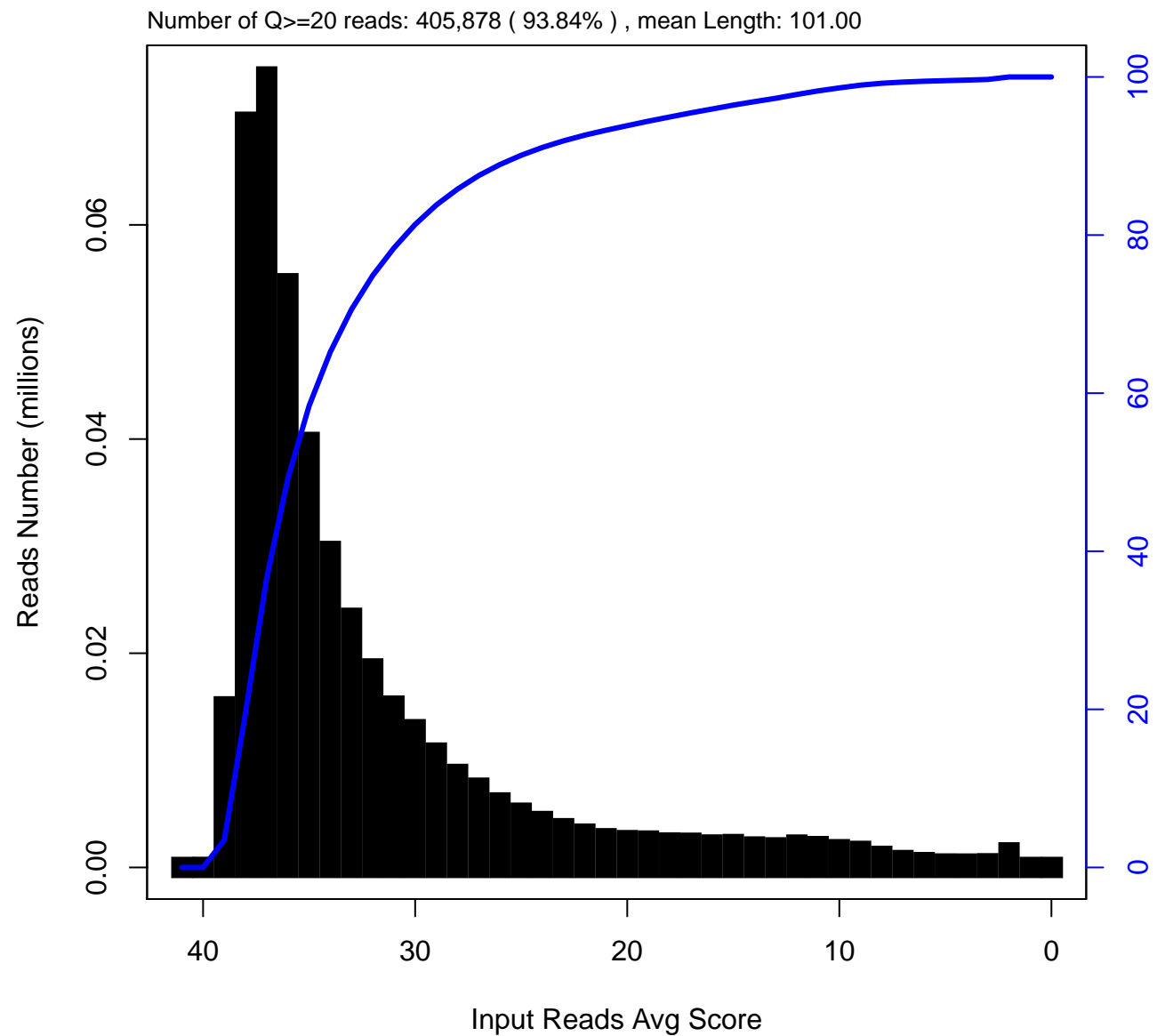
# Nucleotide Content Per Cycle



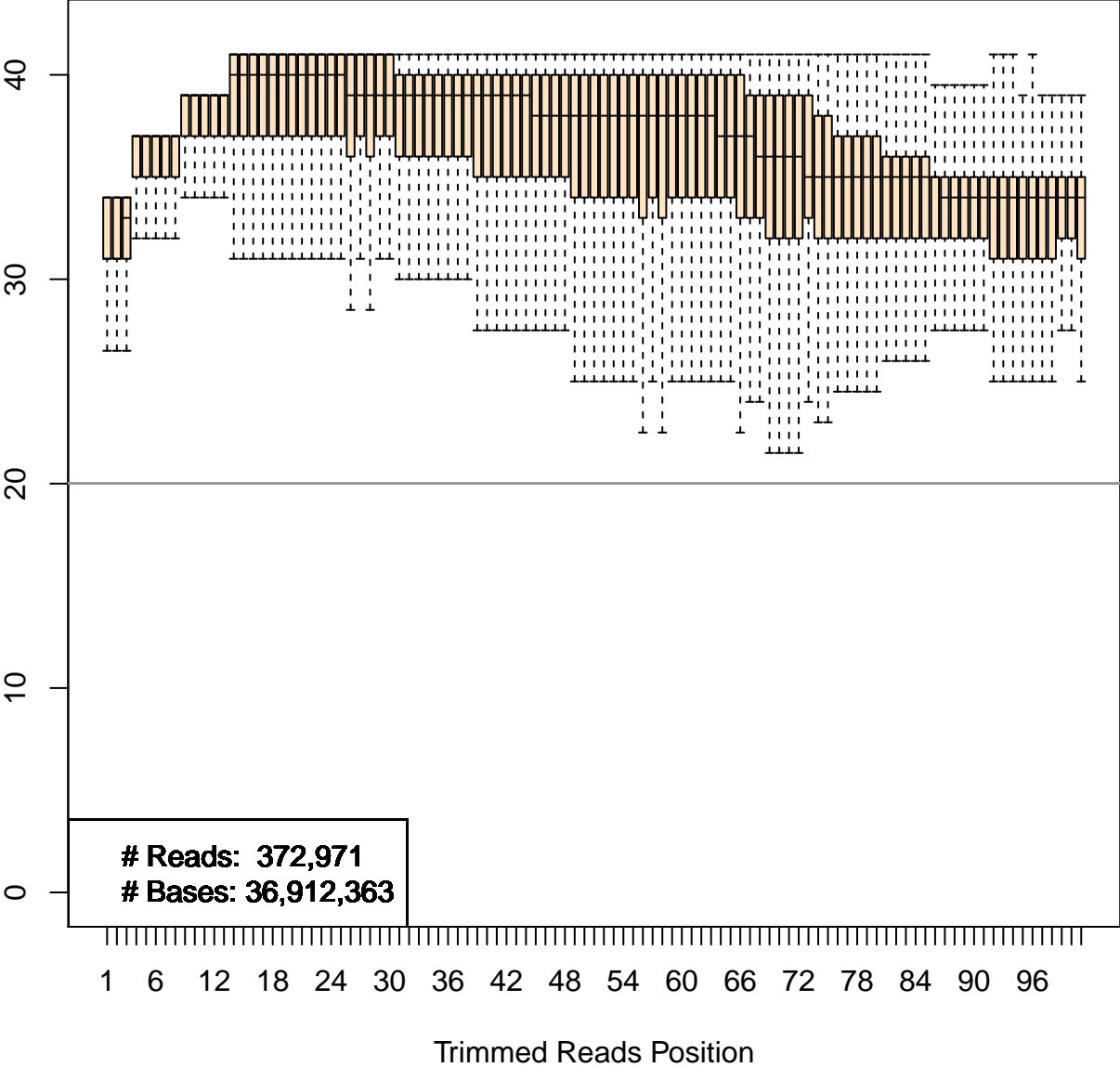
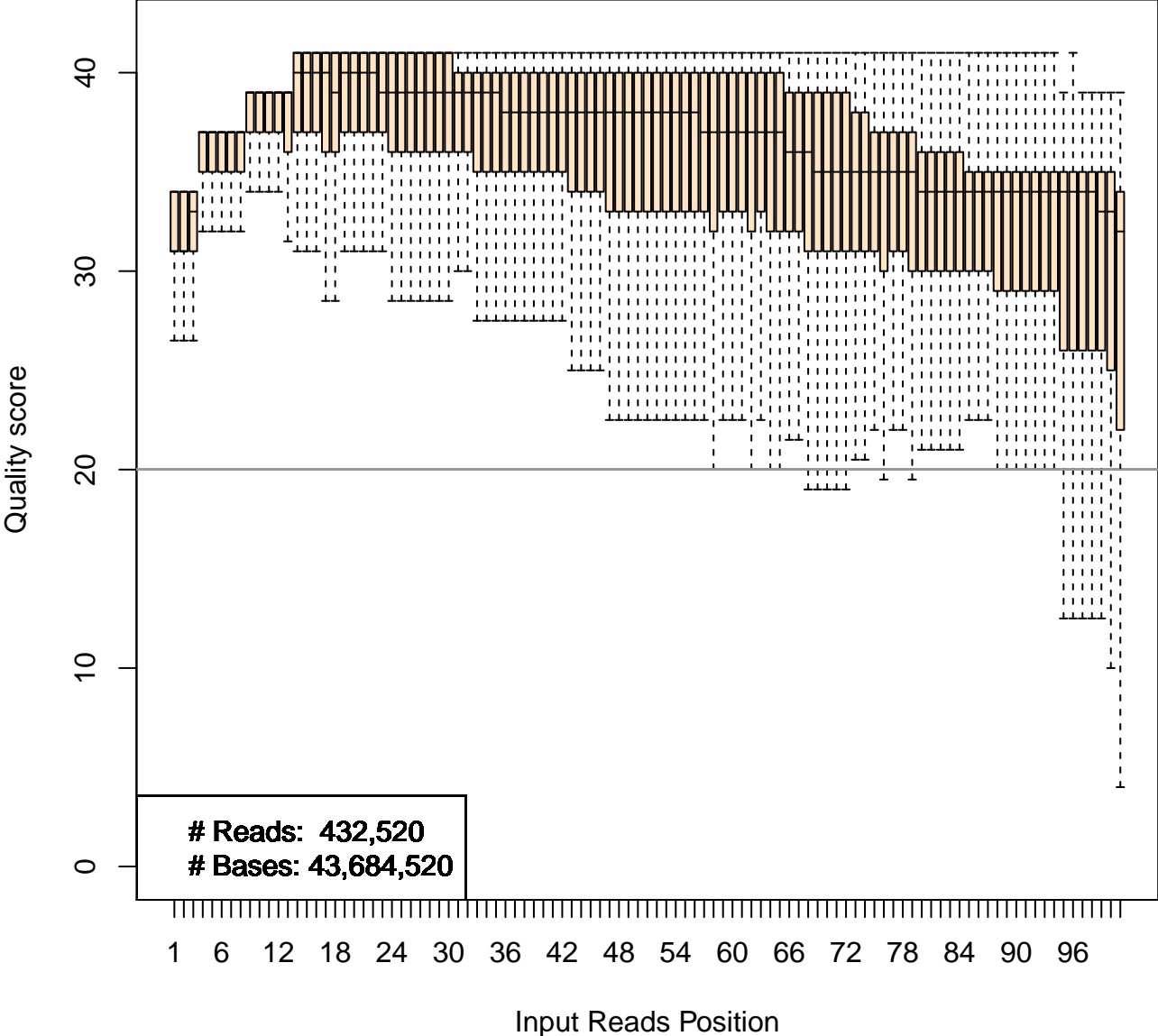
## N Nucleotide Content Per Cycle



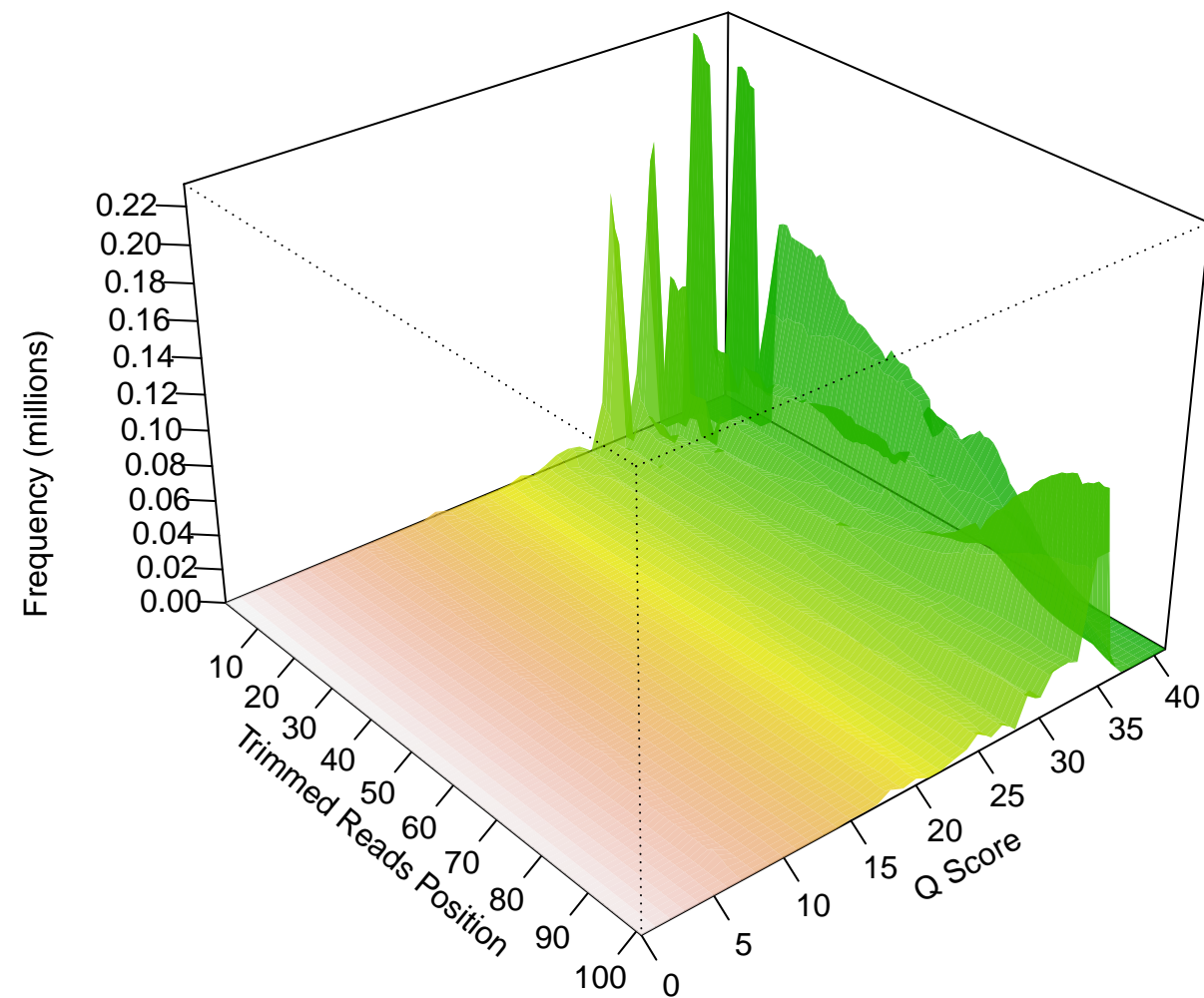
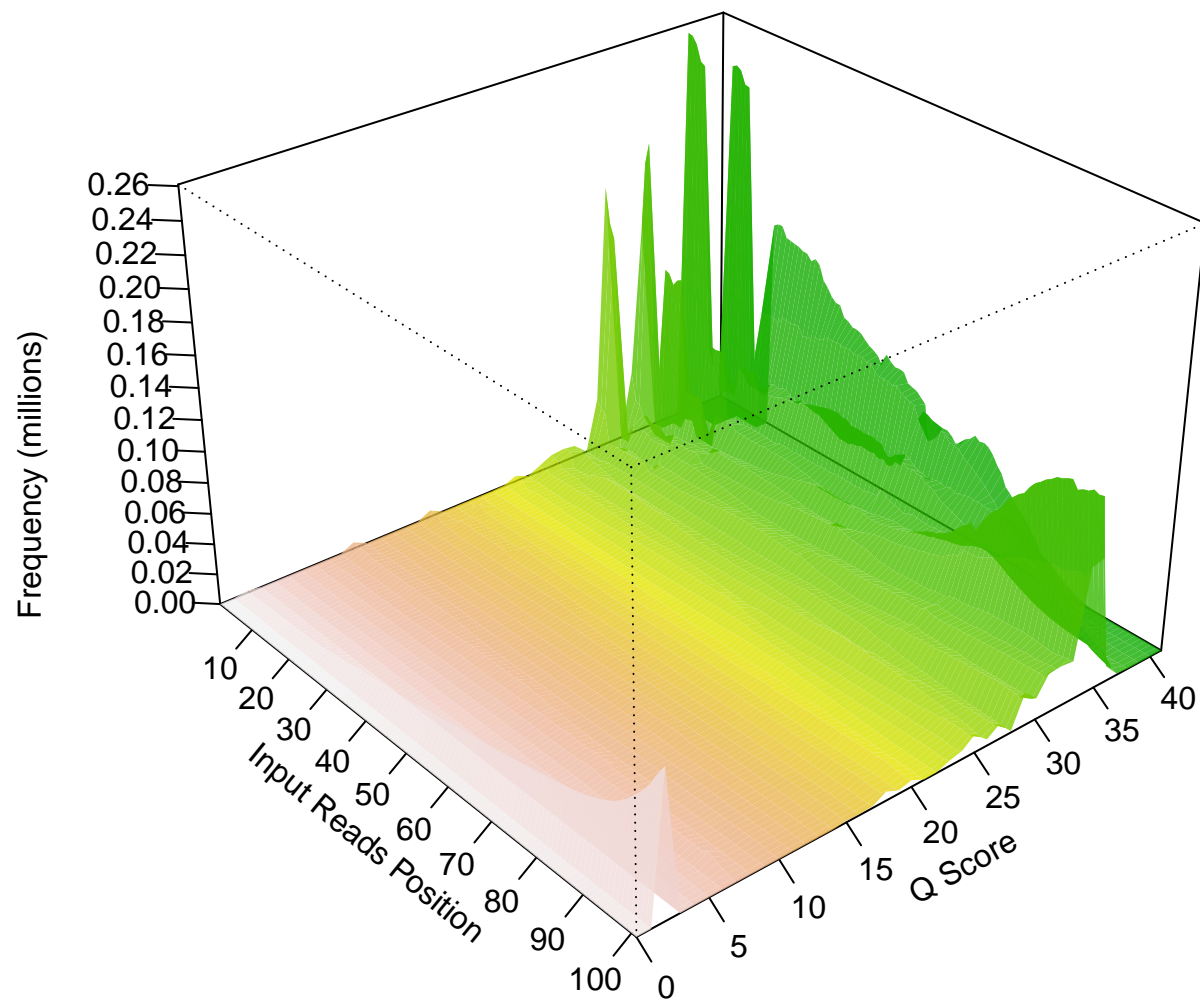
## Reads Average Quality Histogram



Quality Boxplot Per Cycle



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





## Quality report

