

## 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 %)

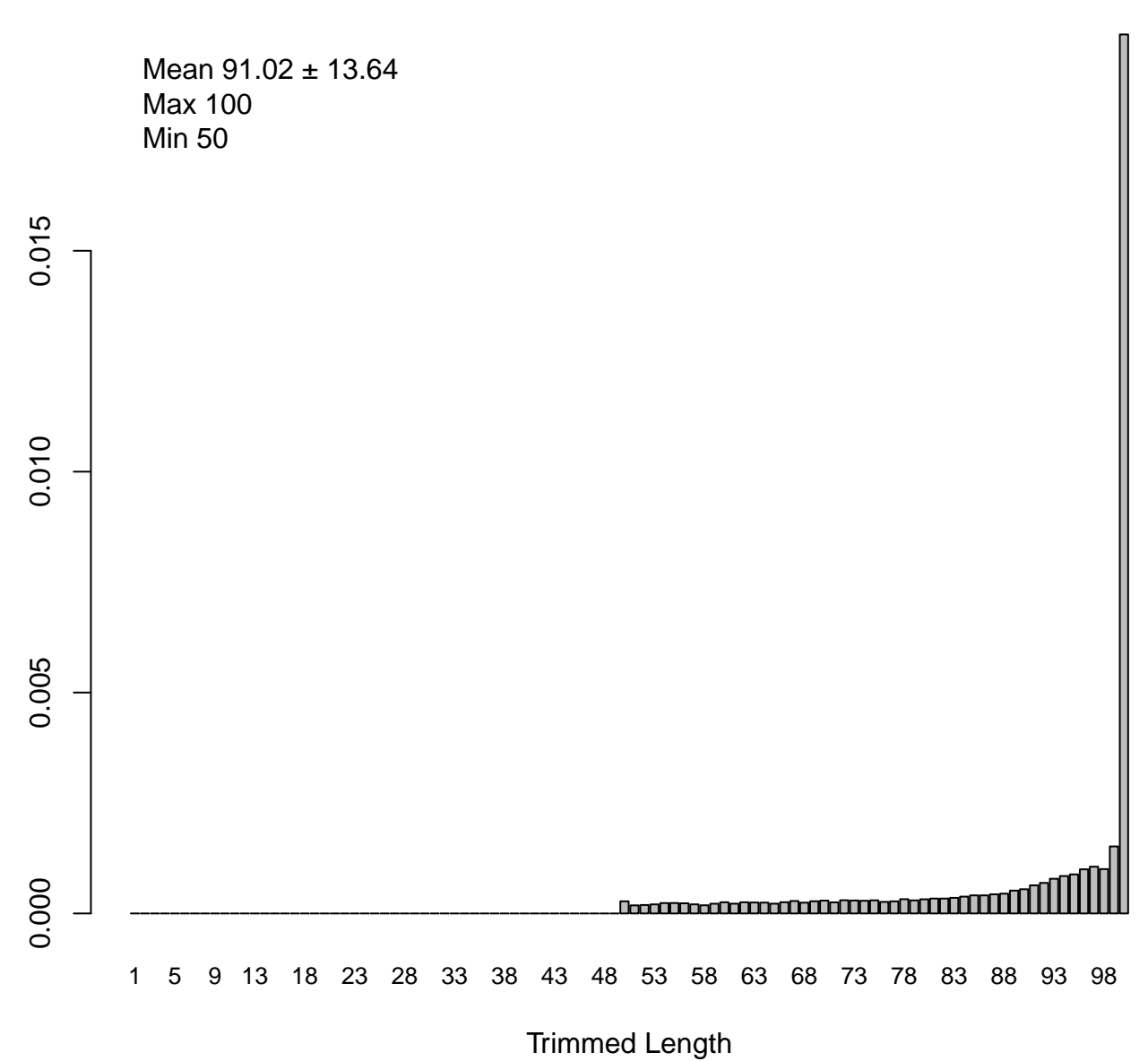
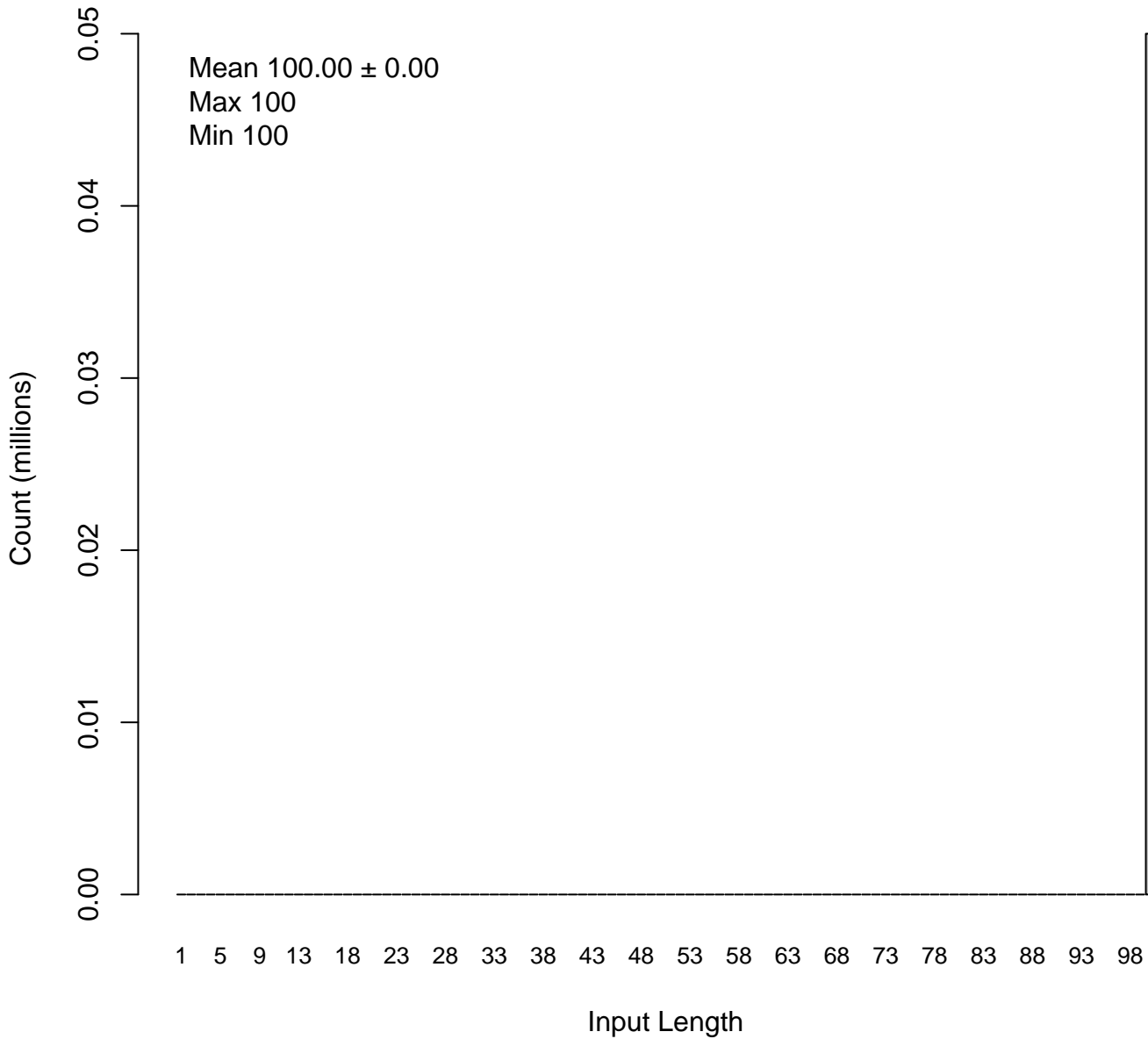
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Discarded reads #: 9657 (19.31 %)

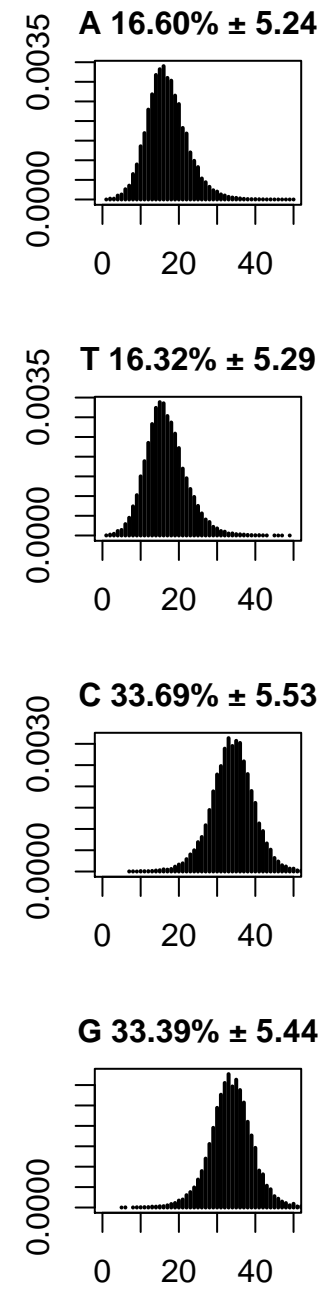
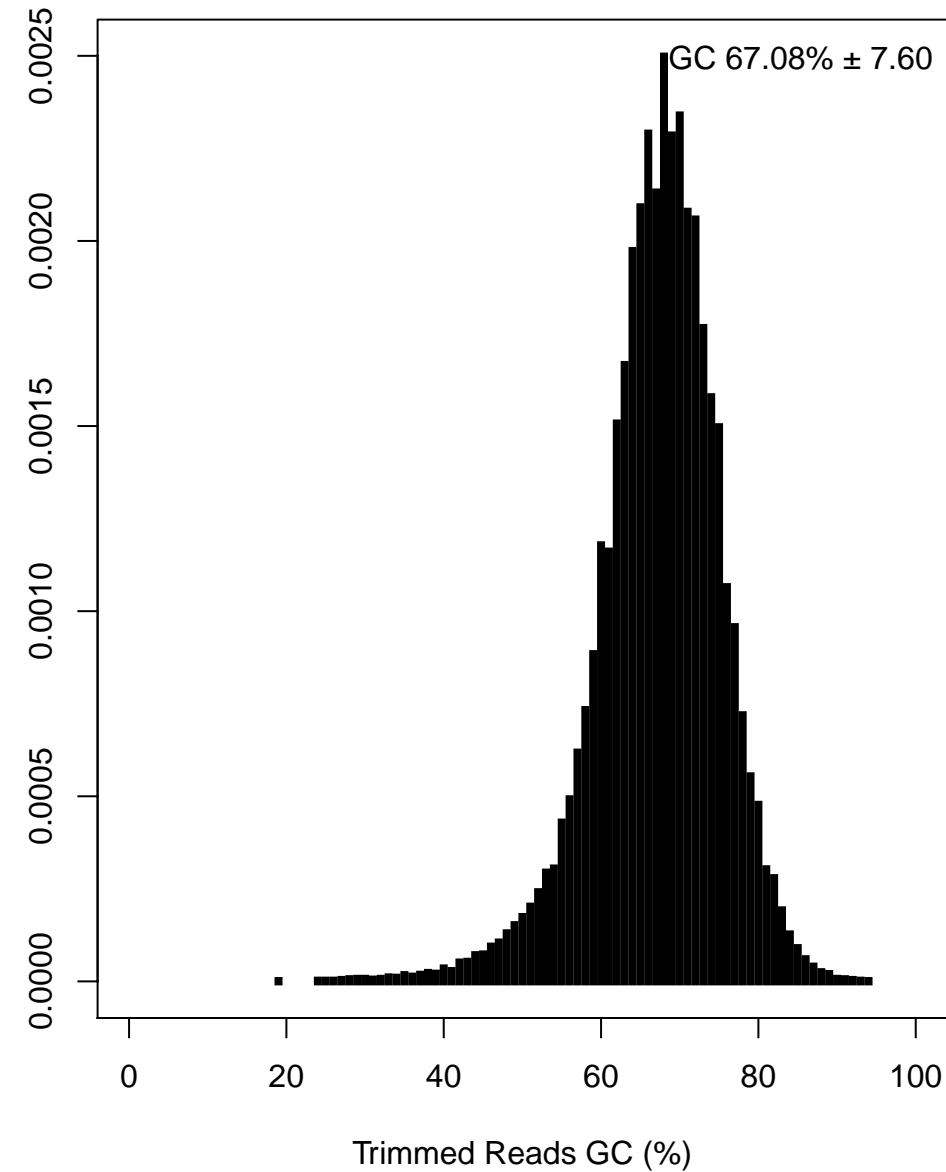
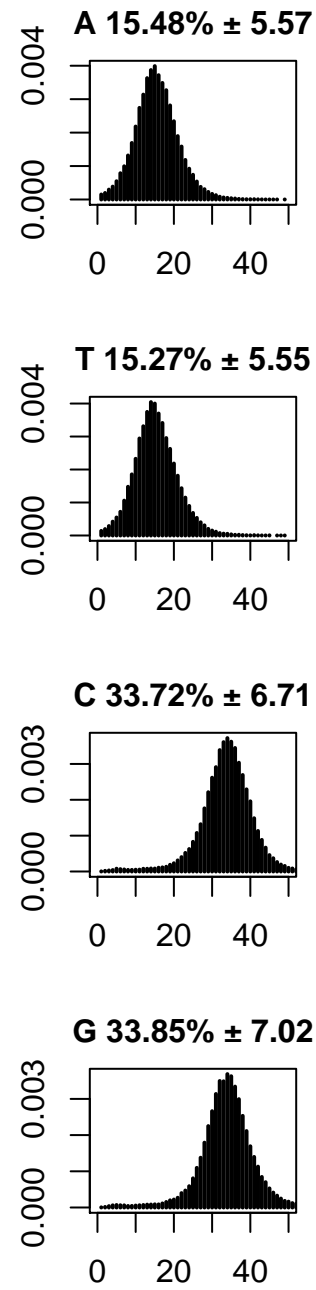
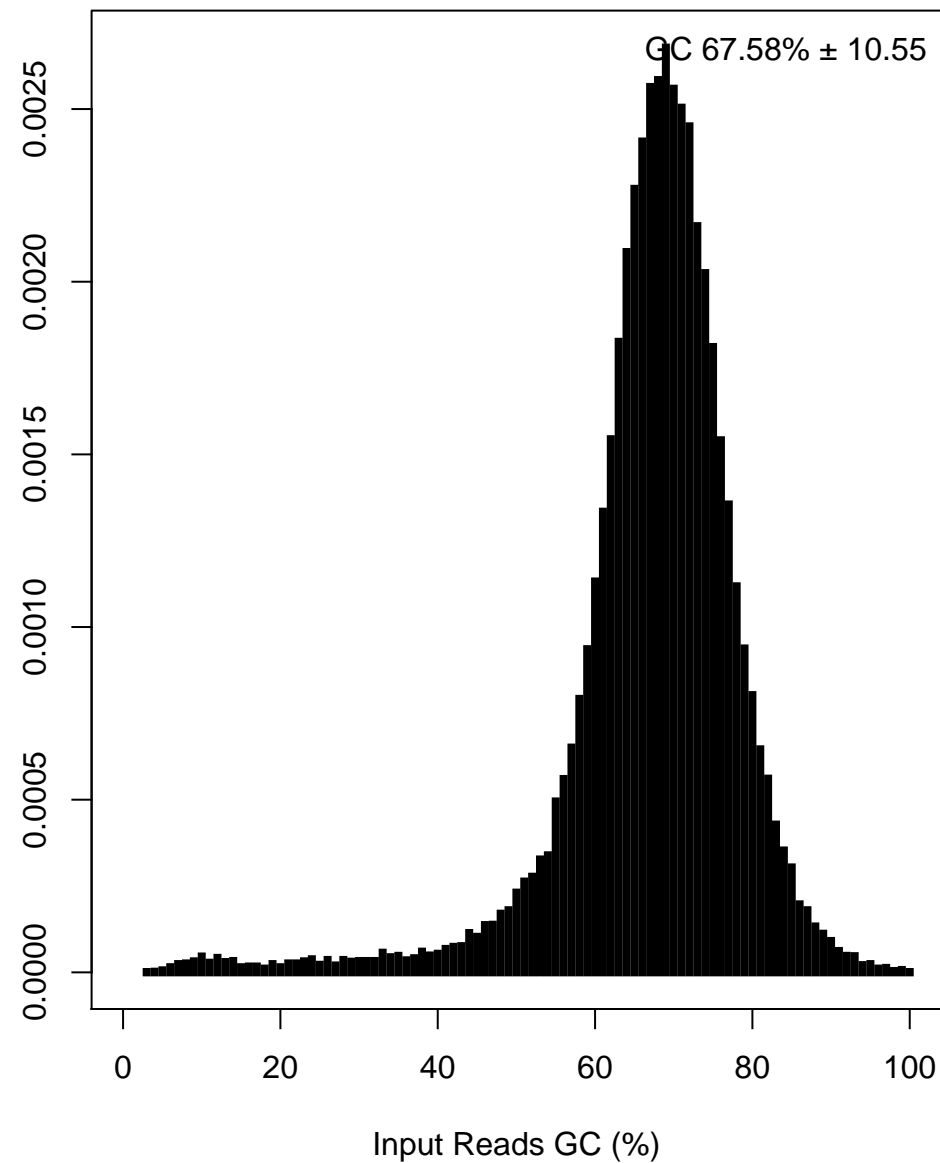
Trimmed bases: 1327781 (26.56 %)

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 %)

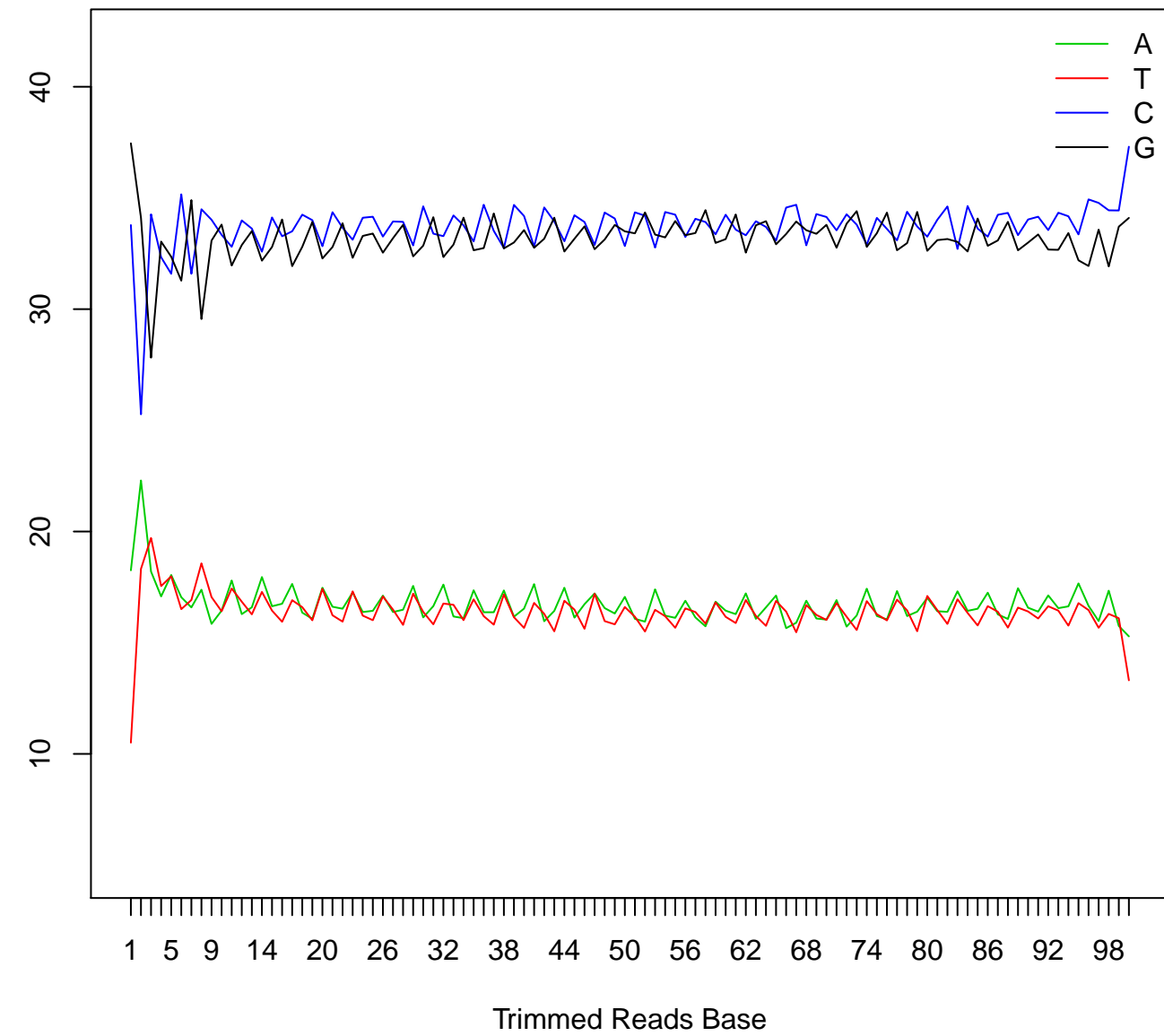
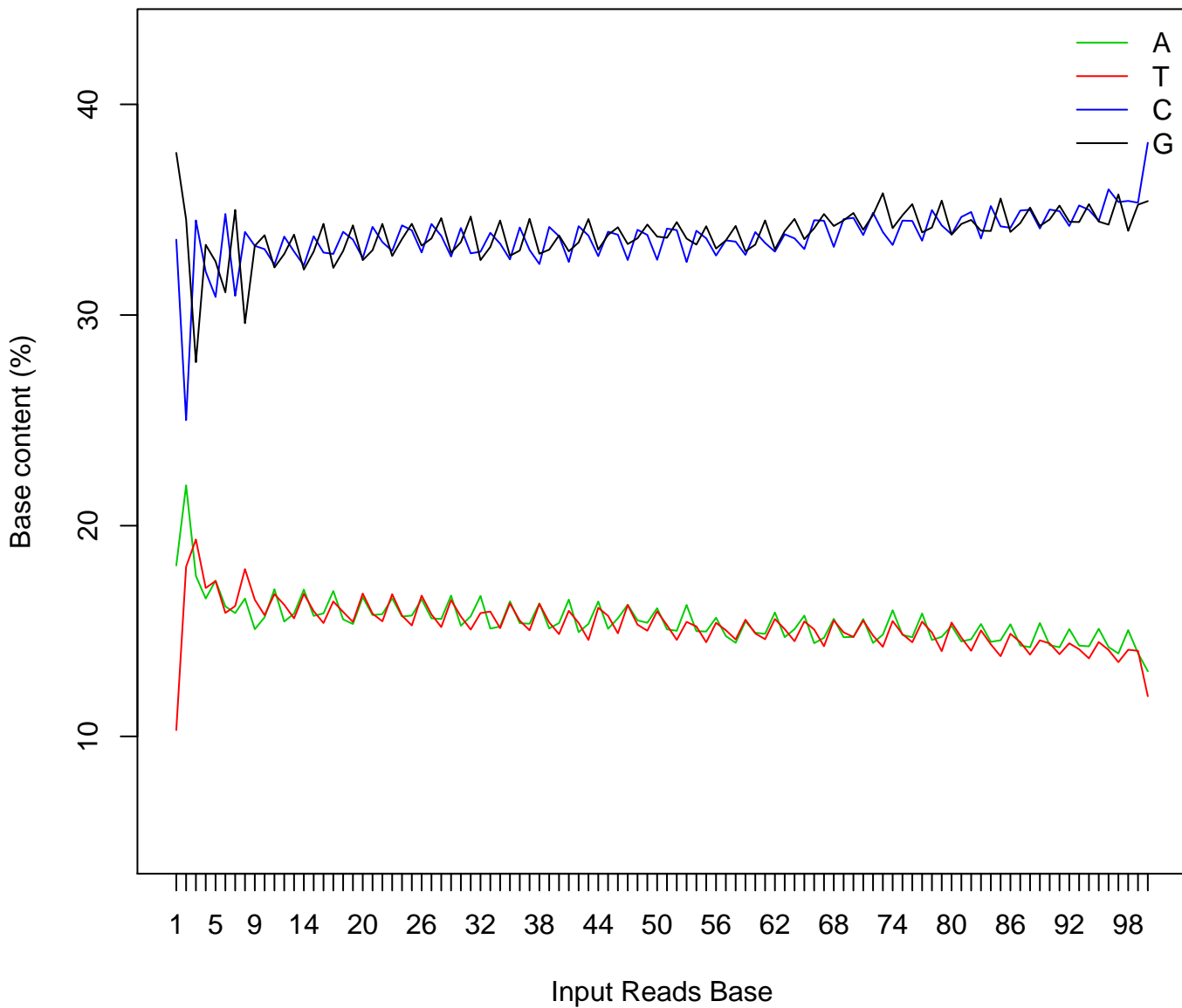
Reads Length Histogram



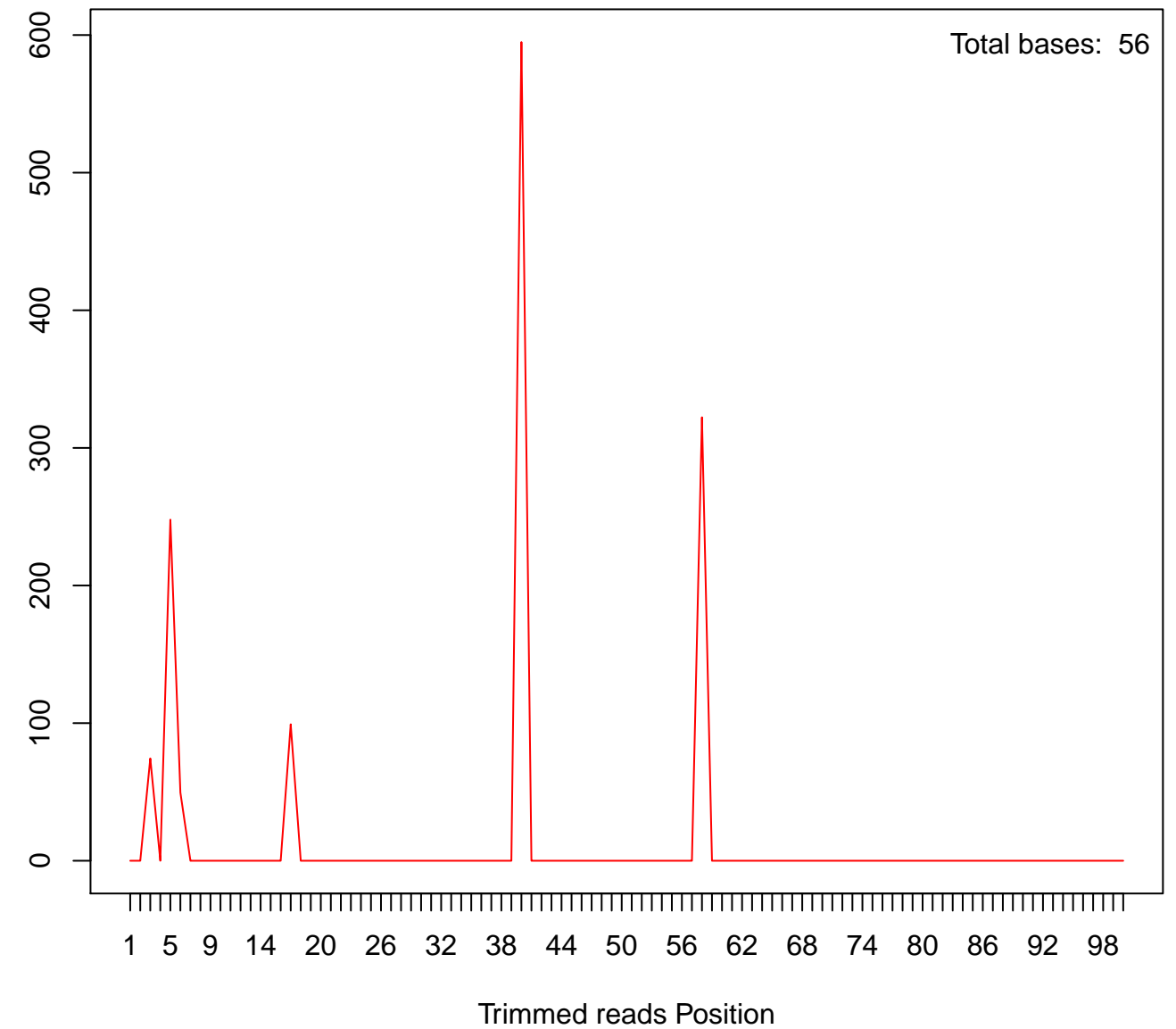
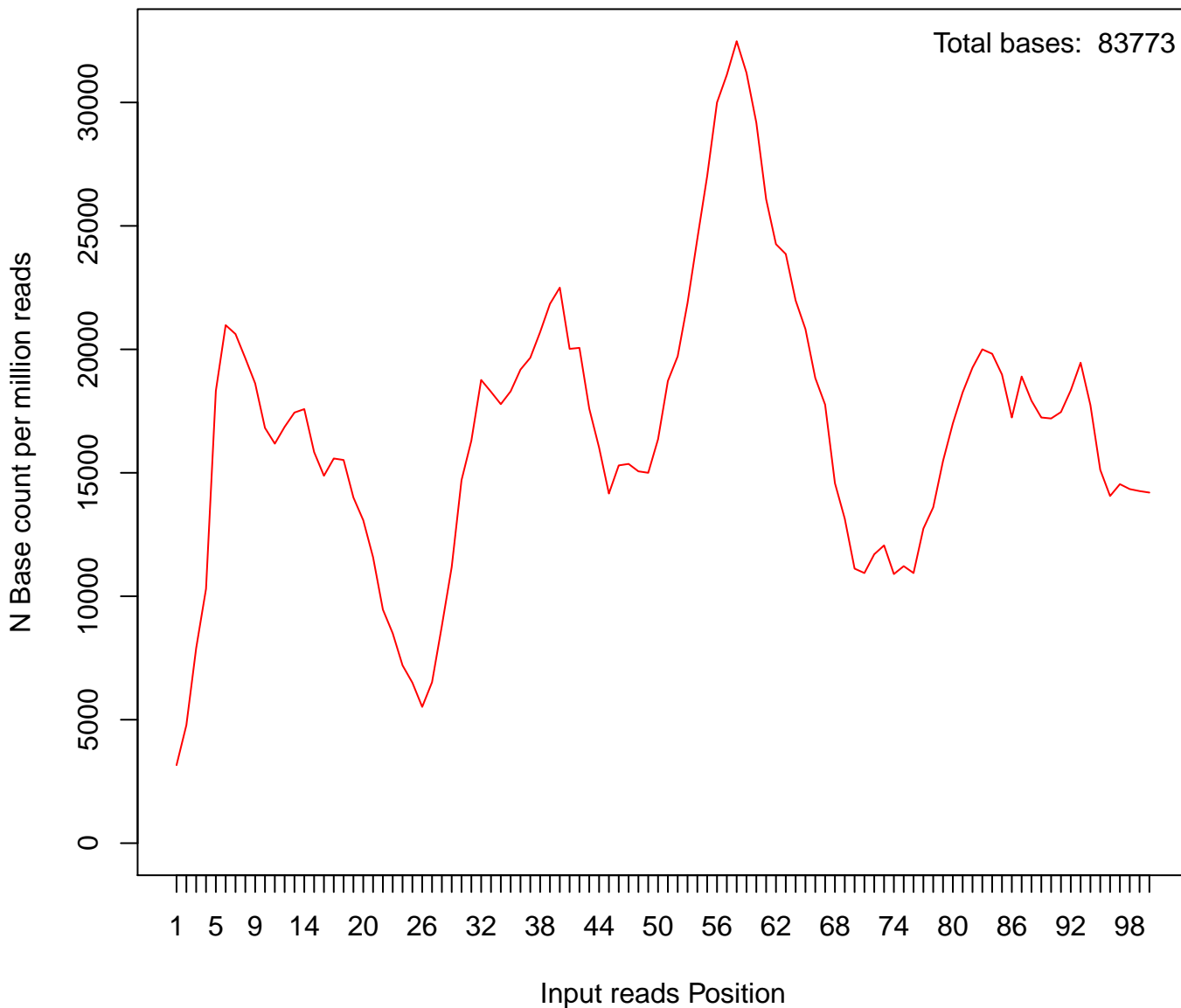
Number of reads (millions)



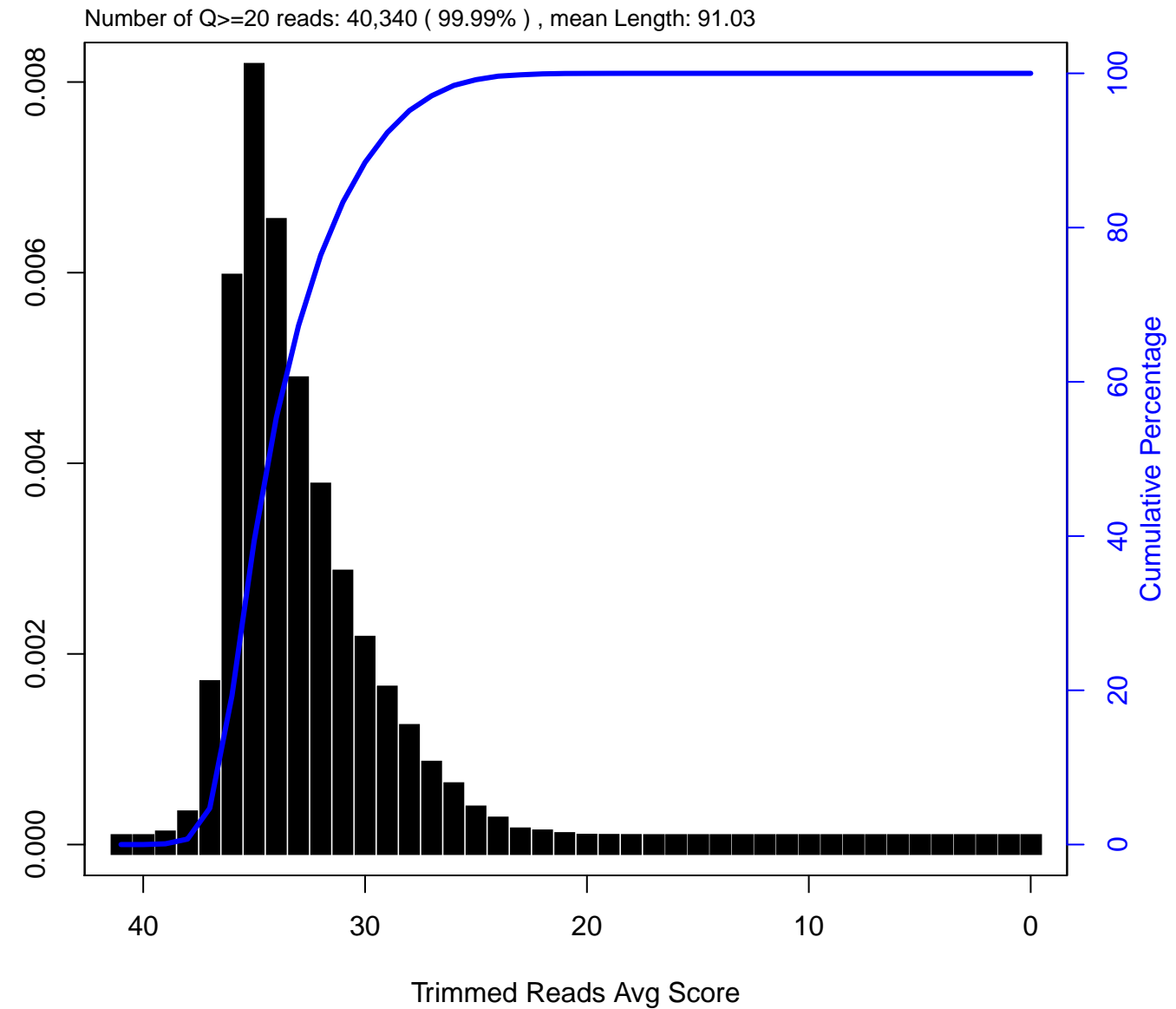
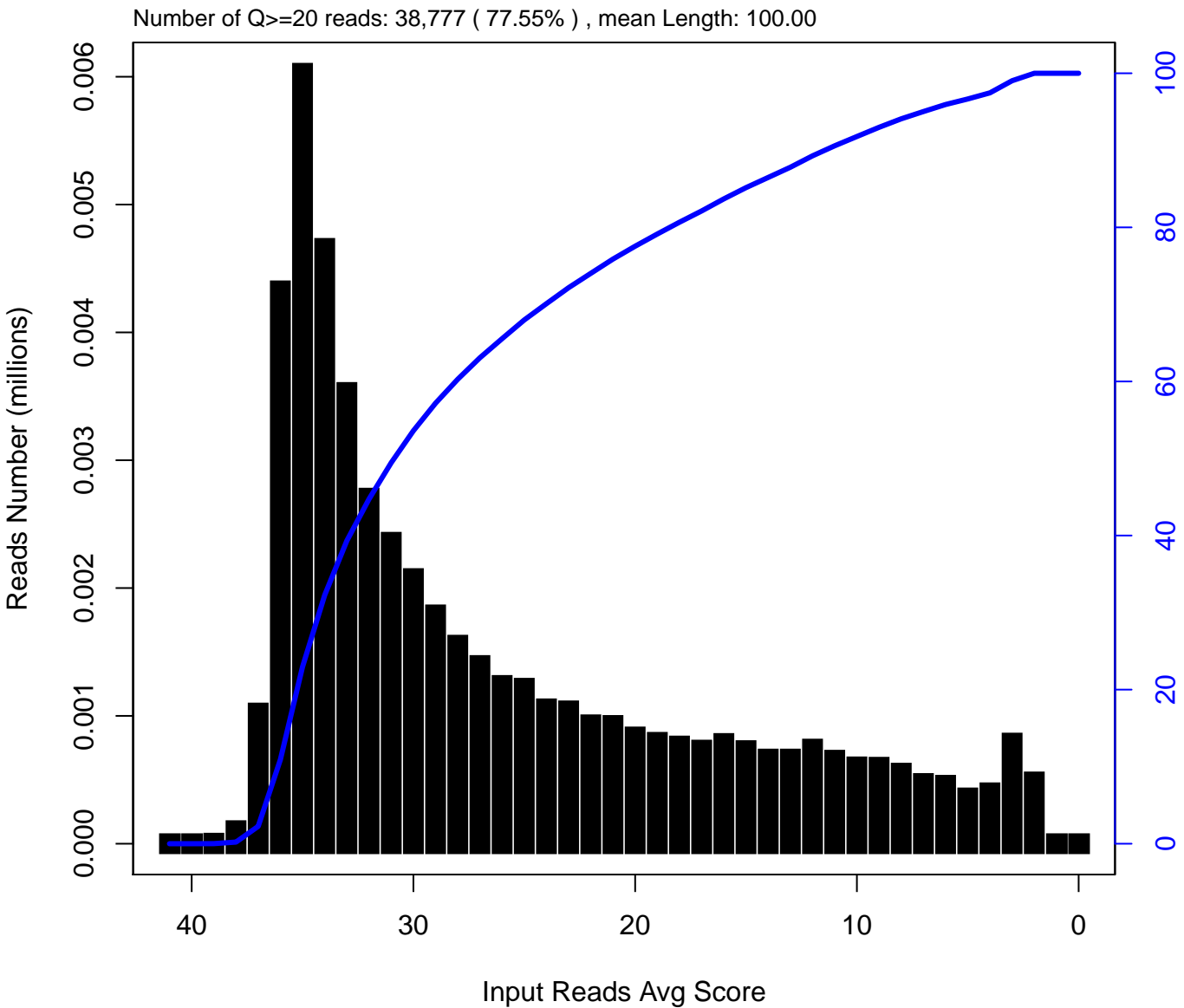
Nucleotide Content Per Cycle



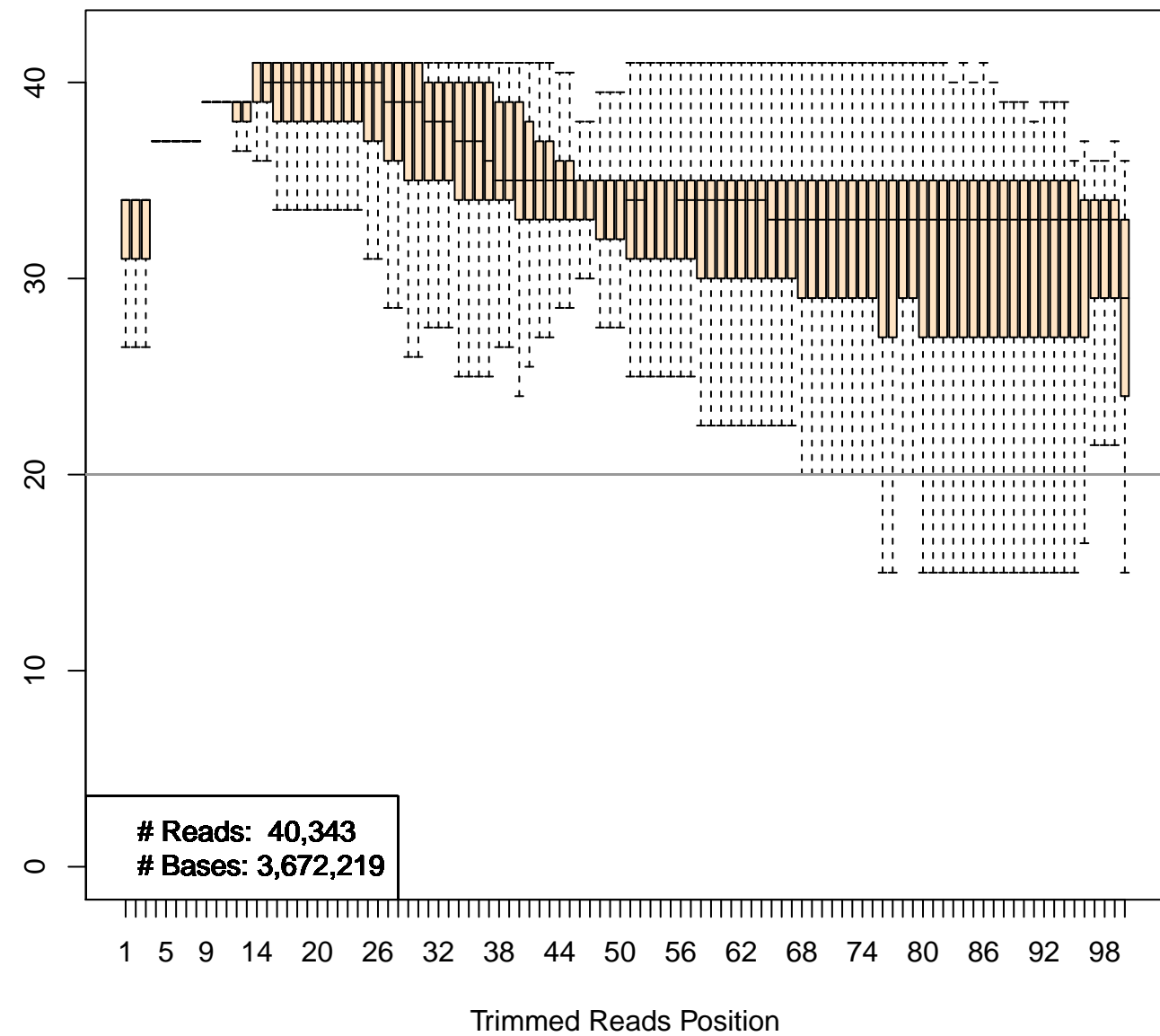
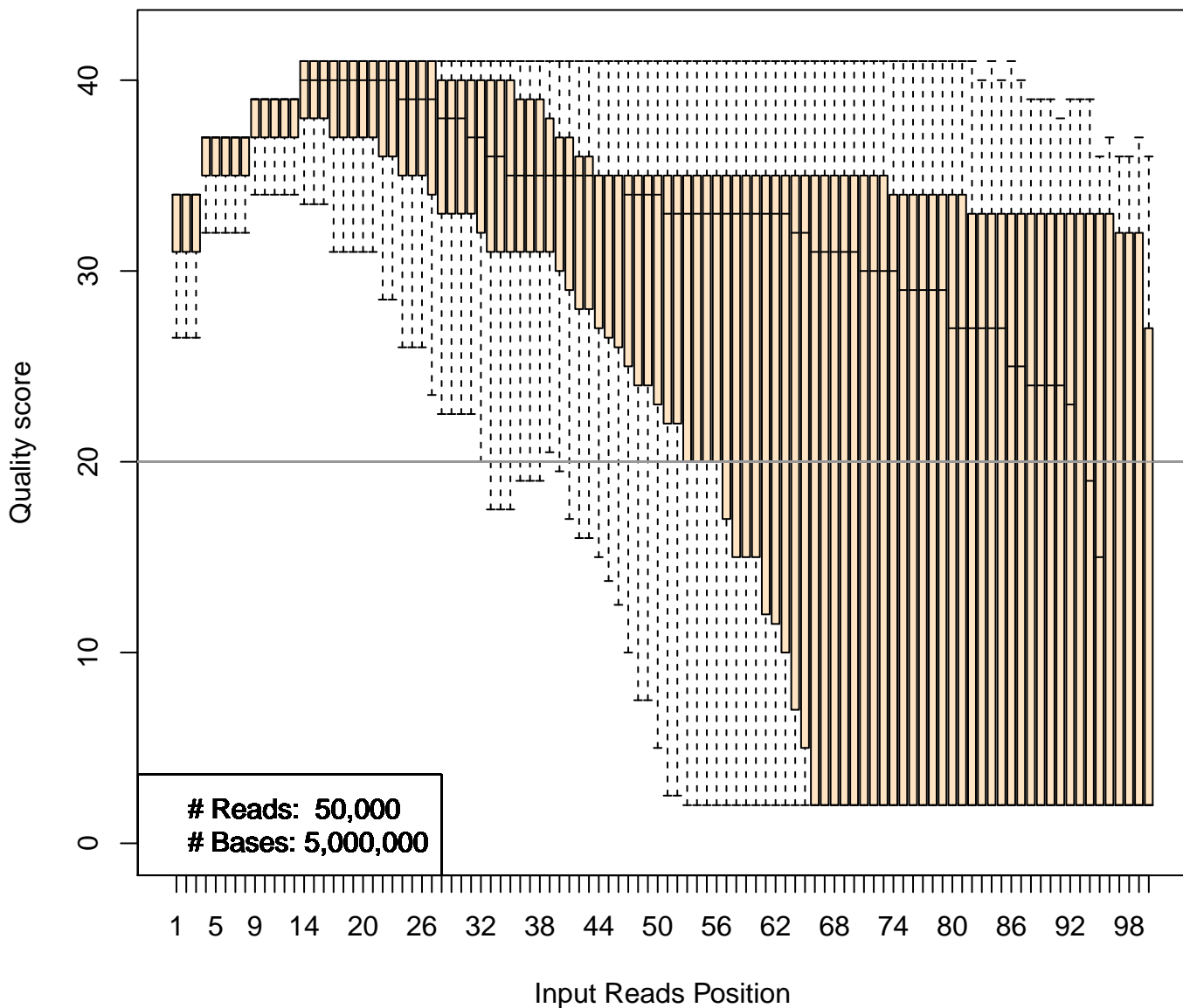
## N Nucleotide Content Per Cycle



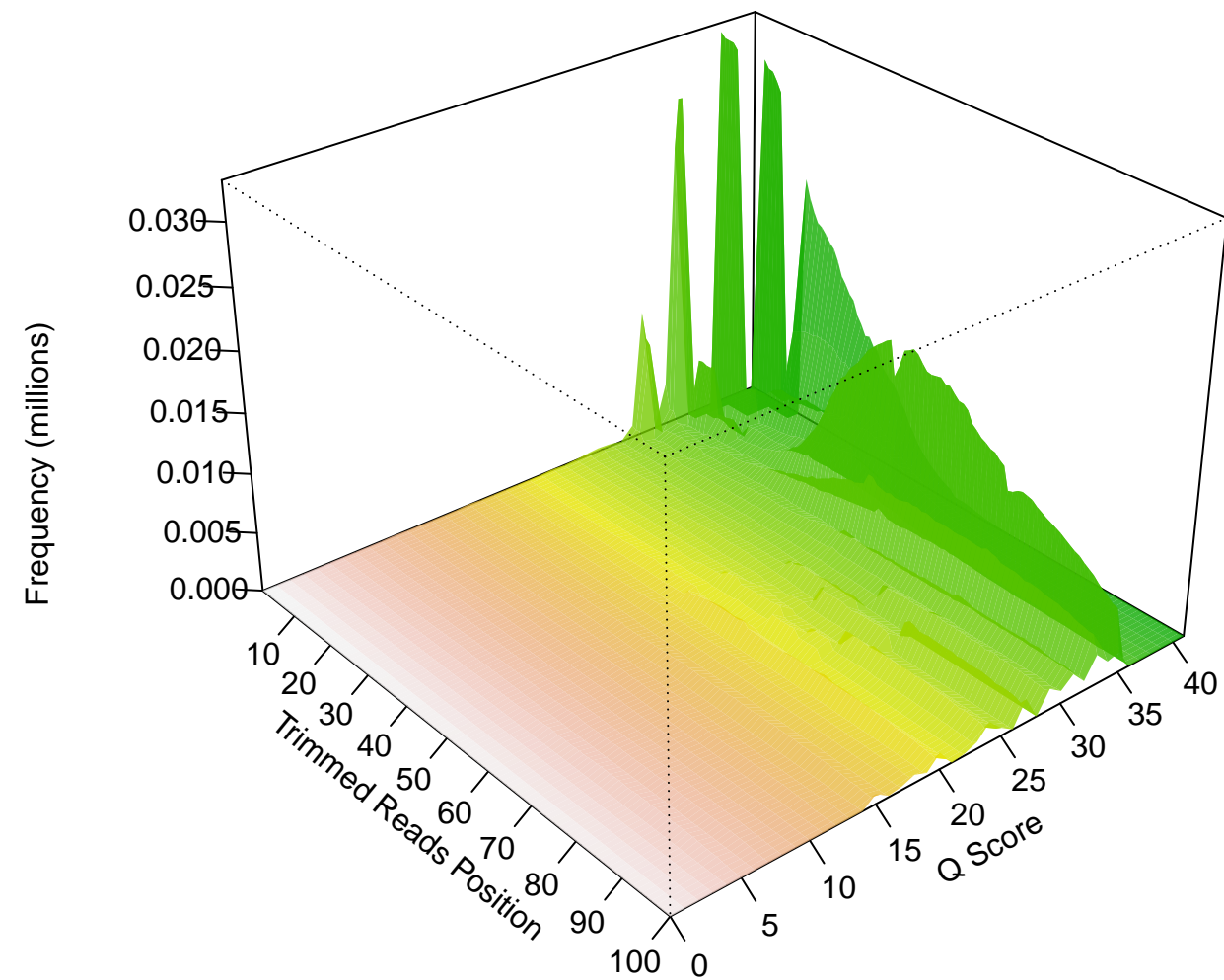
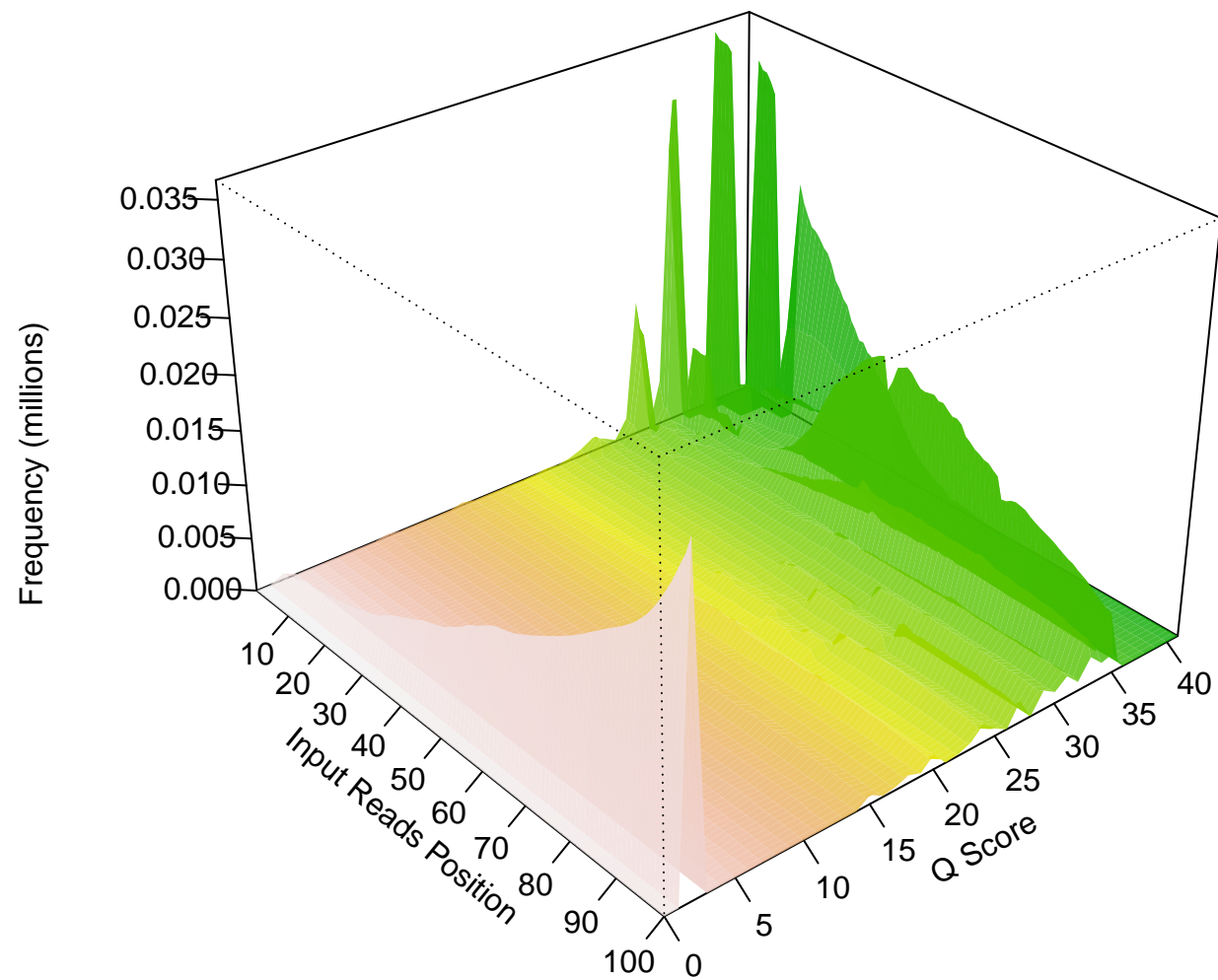
## Reads Average Quality Histogram



Quality Boxplot Per Cycle



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





## Quality report

