QC stats

Before Trimming
Reads #: 4589774
Total bases: 165231864
Reads Length: 36.00

After Trimming
Reads #: 4363656 (95.07 %)
Total bases: 156398472 (94.65 %)
Mean Reads Length: 35.84

Discarded reads #: 226118 (4.93 %)
Trimmed bases: 8833392 (5.35 %)
  Reads Filtered by length cutoff (20 bp): 68065 (1.48 %)
  Bases Filtered by length cutoff: 626136 (0.38 %)
  Reads Filtered by continuous base "N" (2): 104727 (2.28 %)
  Bases Filtered by continuous base "N": 3686831 (2.23 %)
  Reads Filtered by low complexity ratio (0.8): 53326 (1.16 %)
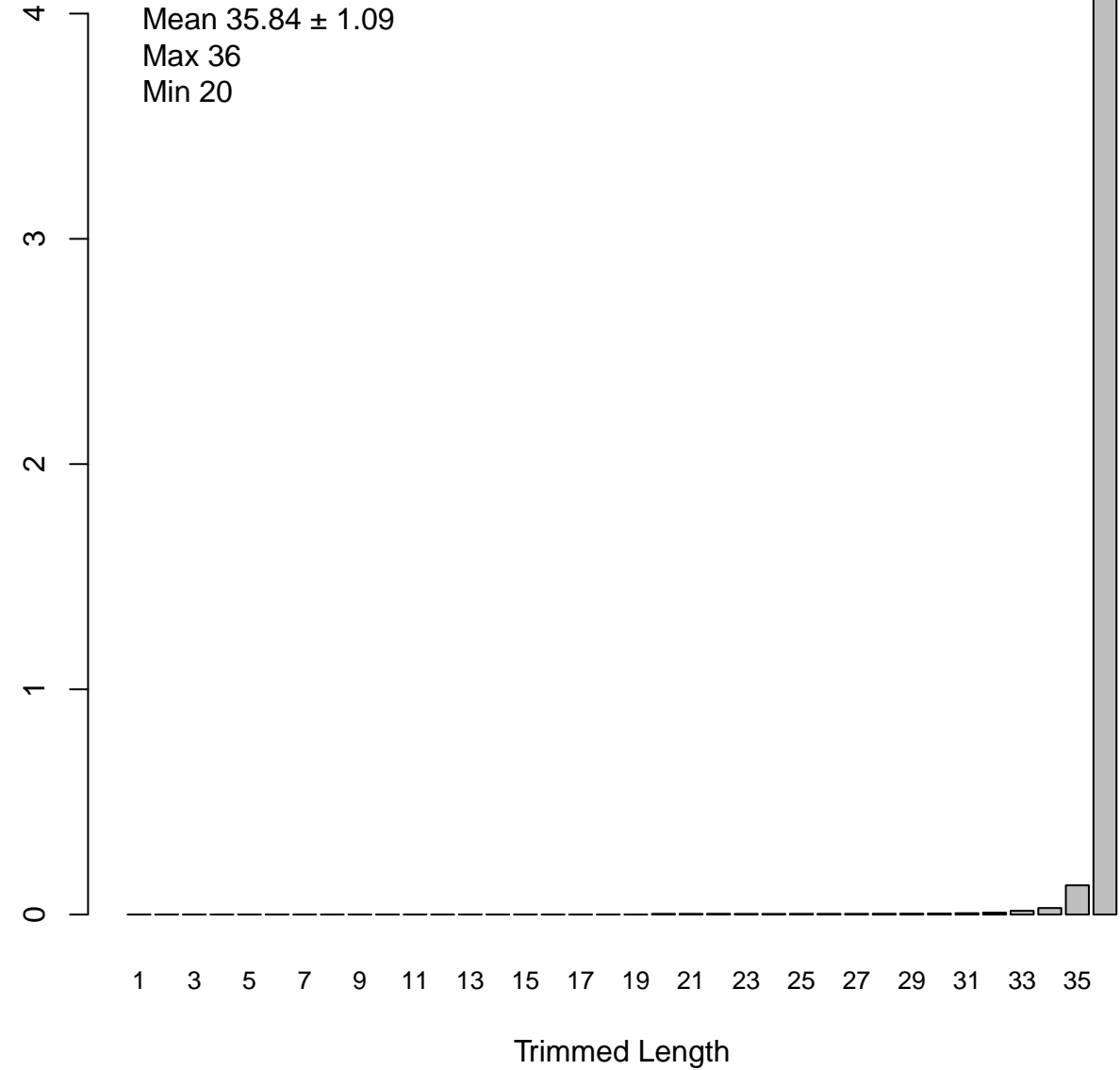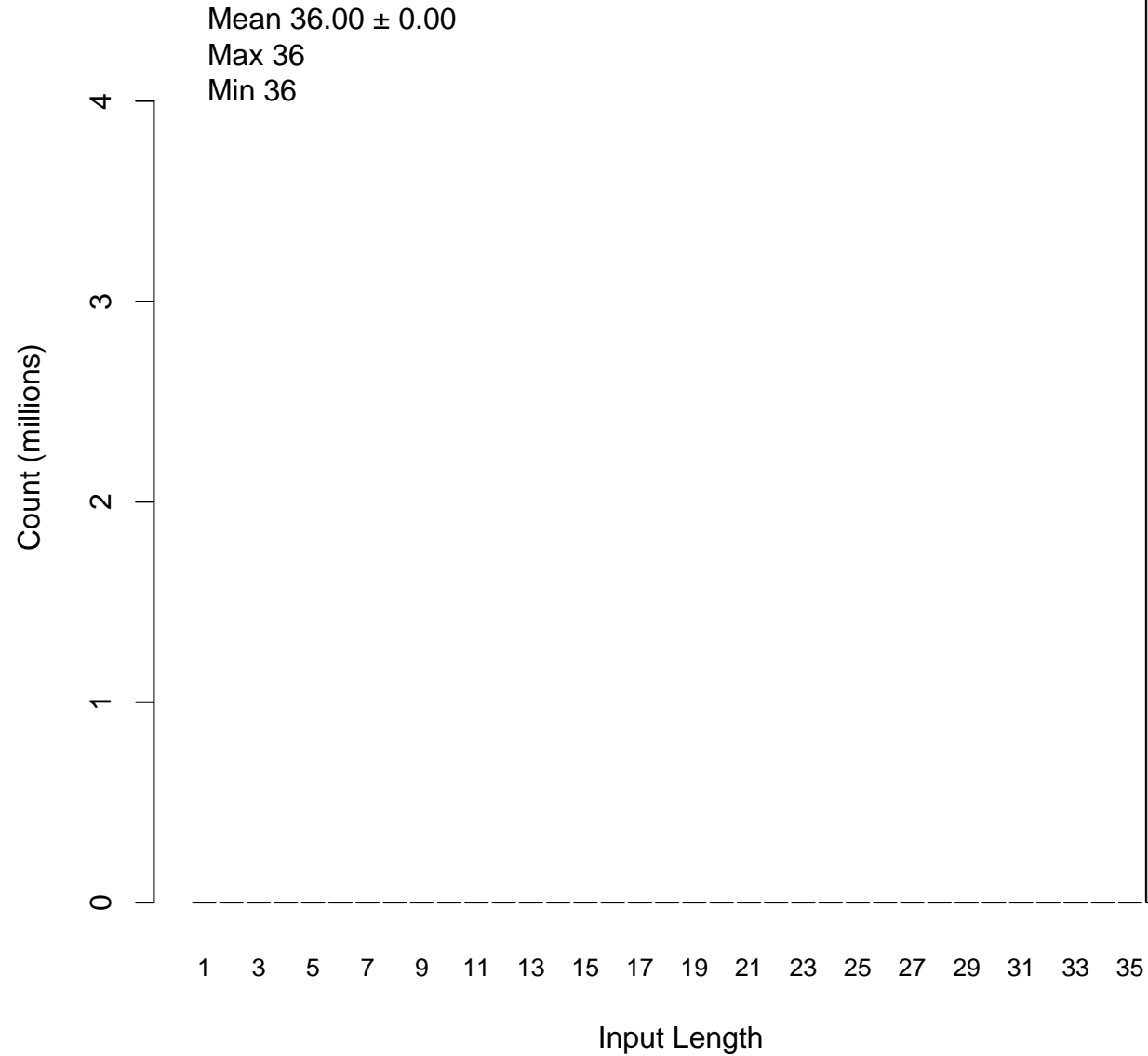 Bases Filtered by low complexity ratio: 1903712 (1.15 %)
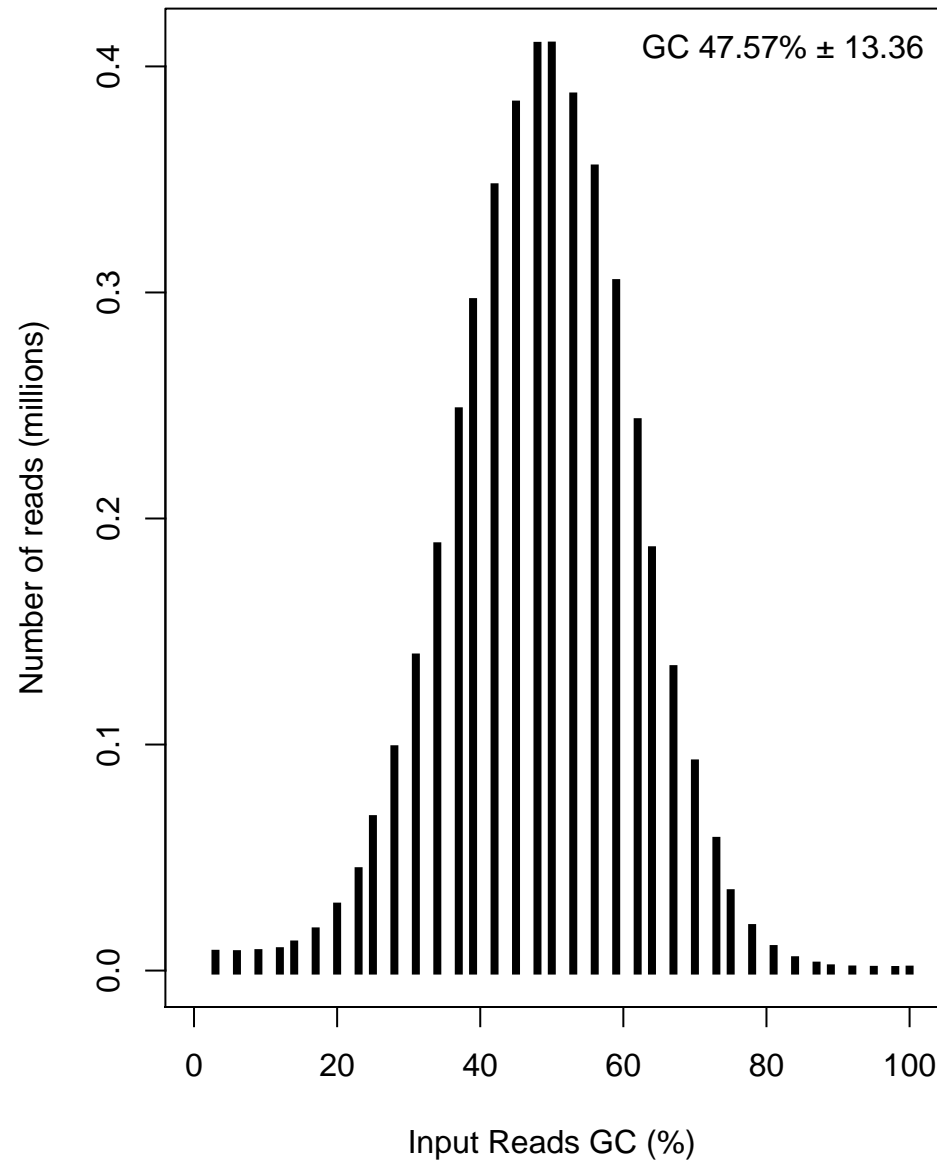 Reads Trimmed by quality (5.0): 327035 (7.13 %)
  Bases Trimmed by quality: 2616713 (1.58 %)
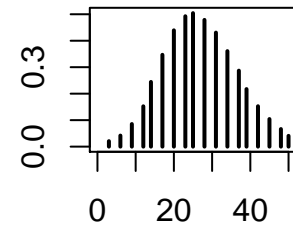 Reads Trimmed with Adapters/Primers: 0 (0.00 %)
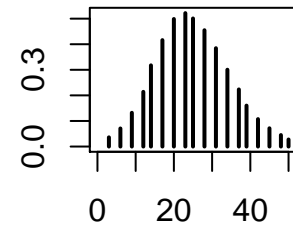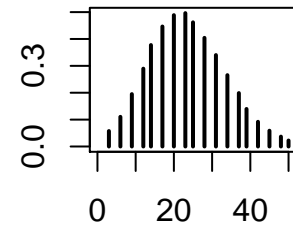 Bases Trimmed with Adapters/Primers: 0 (0.00 %)

Reads Length Histogram
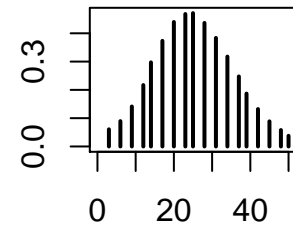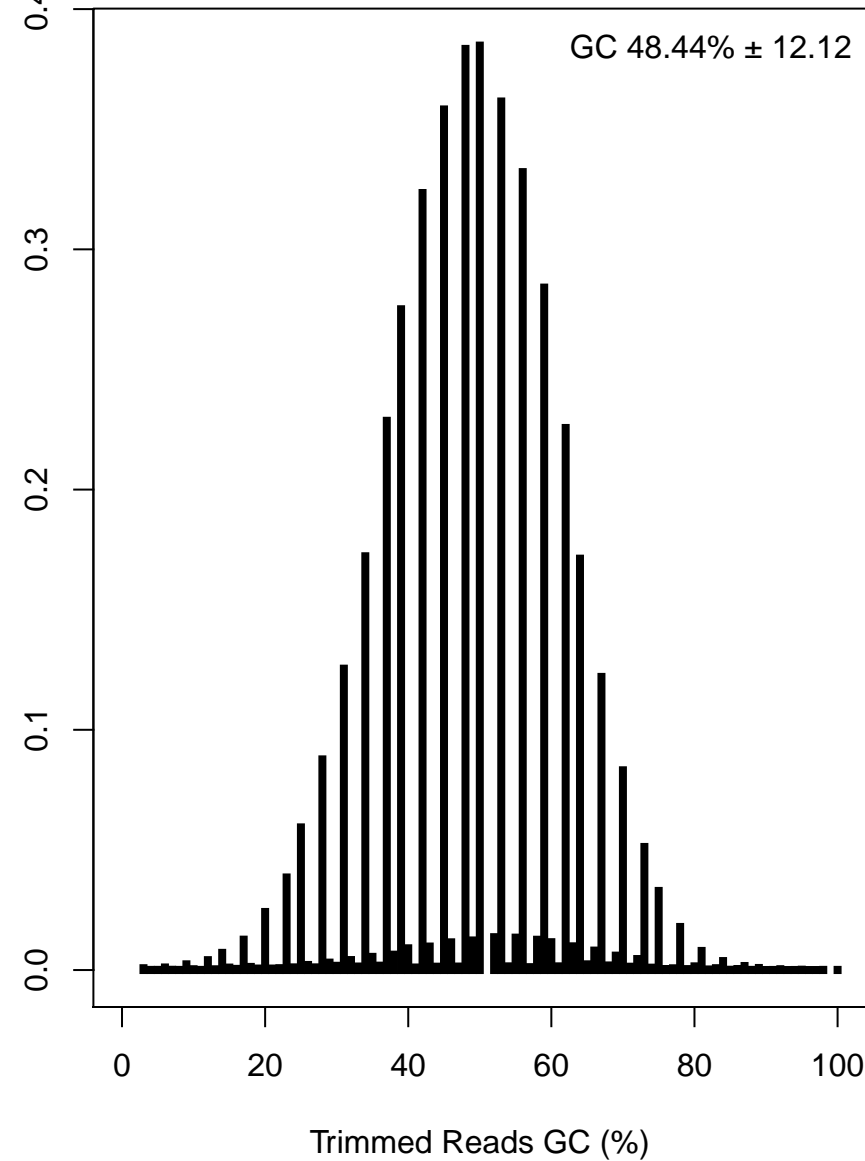
Mean 36.00 ± 0.00
Max 36
Min 36

Mean 35.84 ± 1.09
Max 36
Min 20

Count (millions)

Input Length

Trimmed Length

A 27.42% ± 12.59

T 24.39% ± 10.55

C 22.87% ± 10.53

G 24.70% ± 11.08

A 26.78% ± 10.06

T 24.77% ± 9.94

C 23.07% ± 10.03

G 25.37% ± 10.61

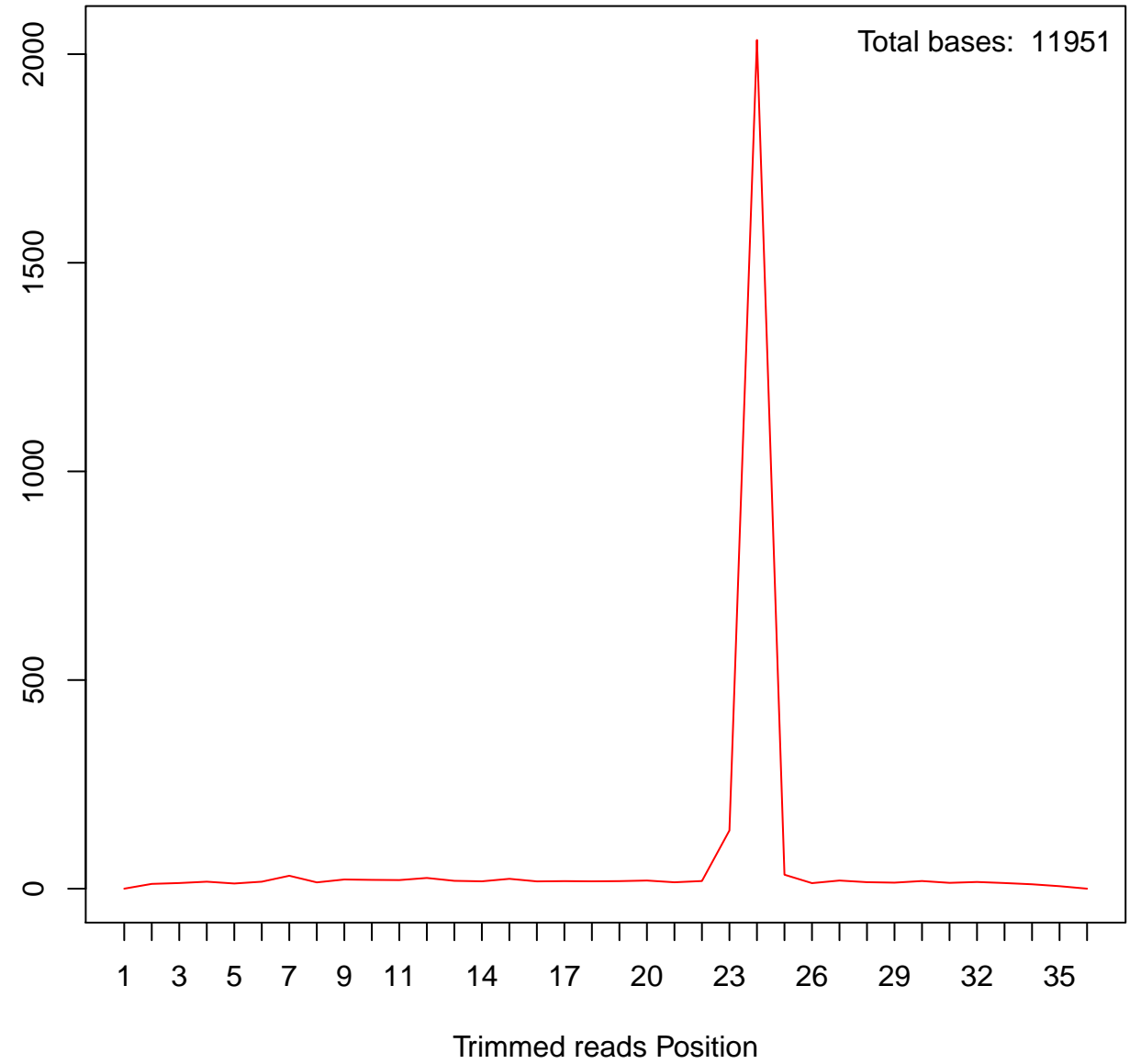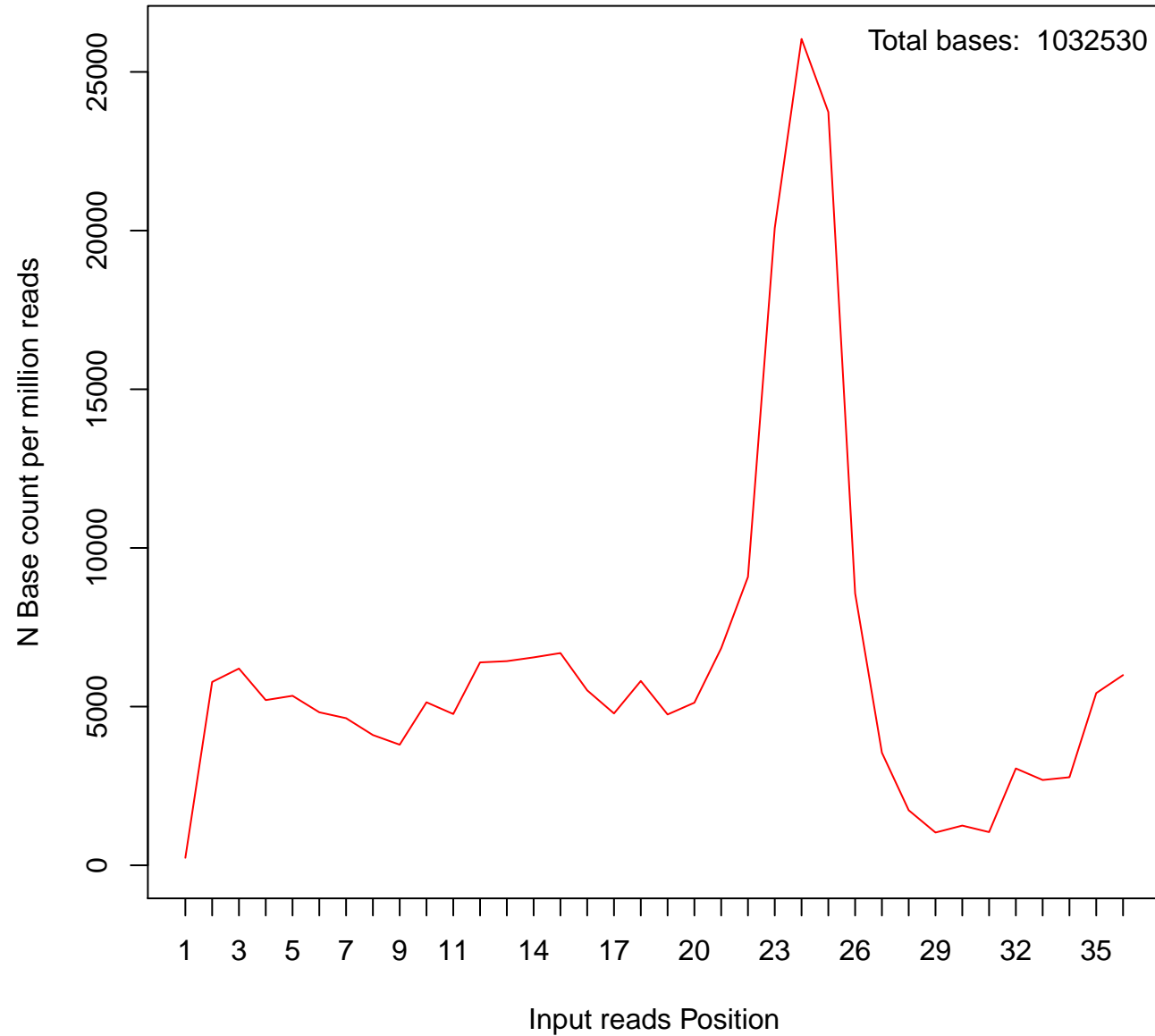GC 47.57% ± 13.36

GC 48.44% ± 12.12
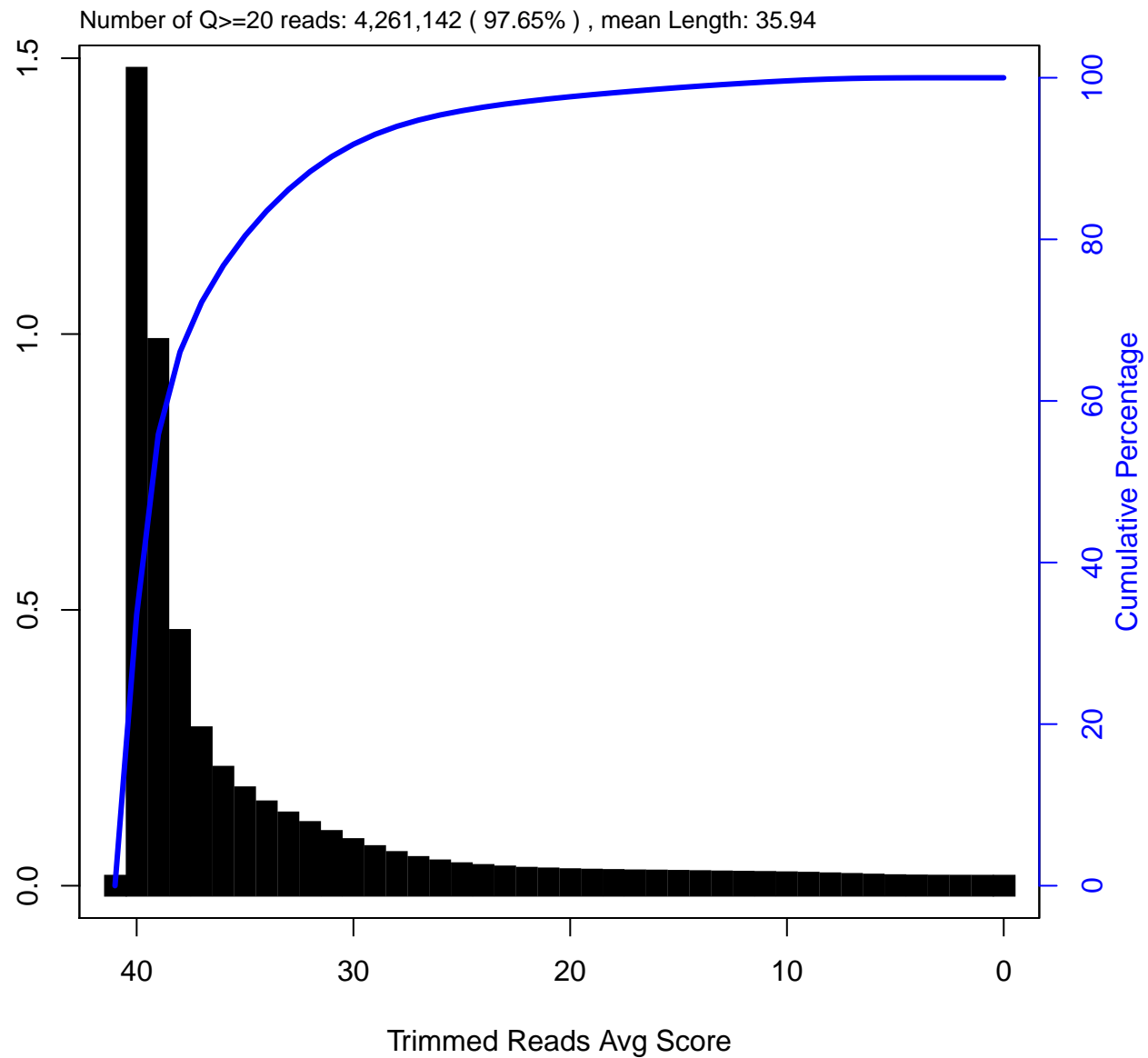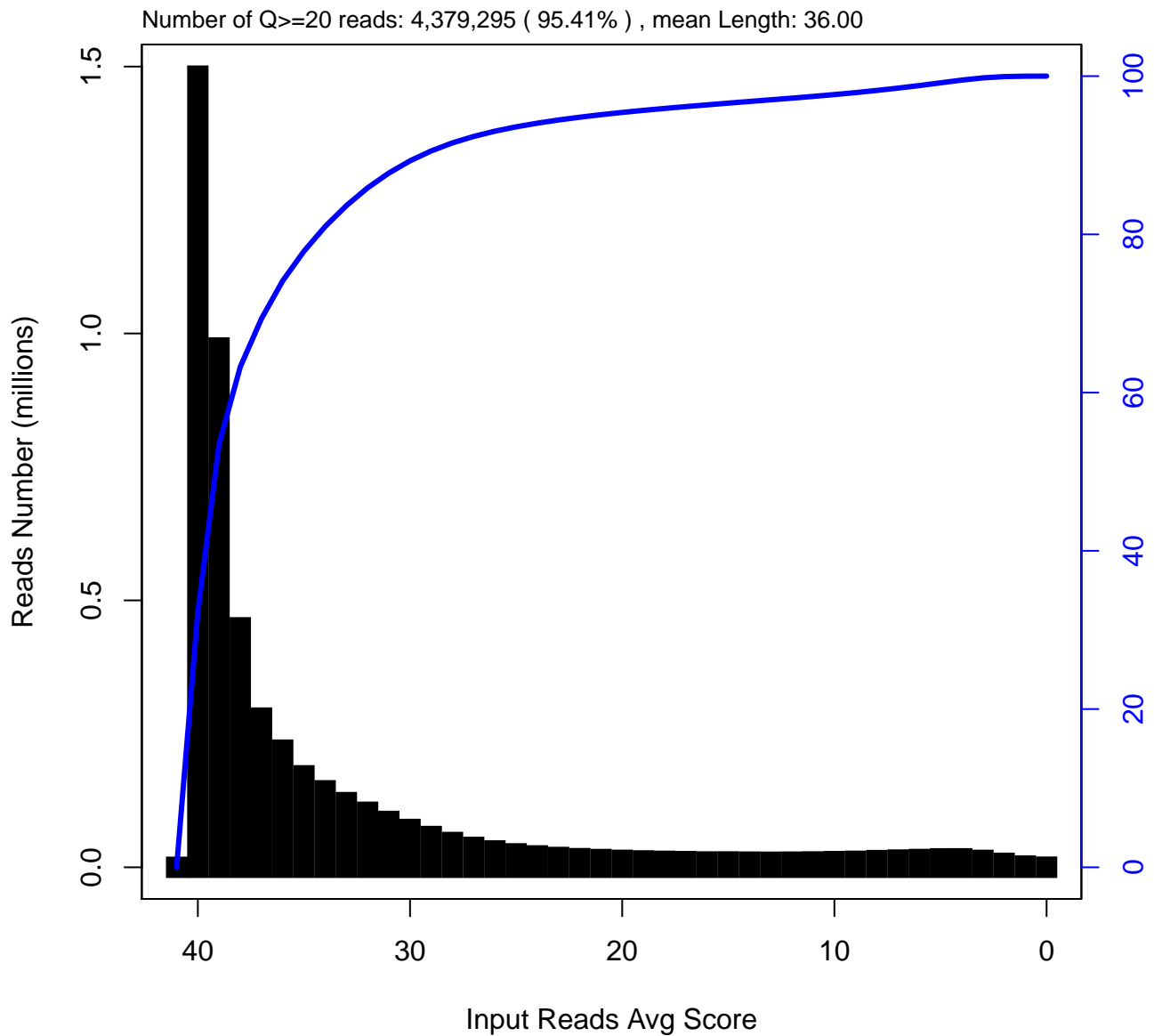
Number of reads (millions)

Input Reads GC (%)

Trimmed Reads GC (%)
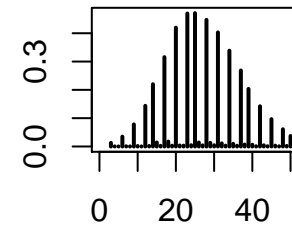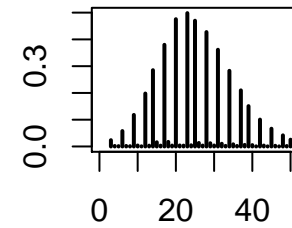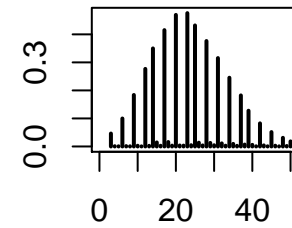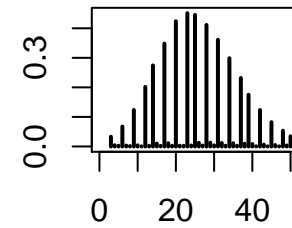
Nucleotide Content Per Cycle
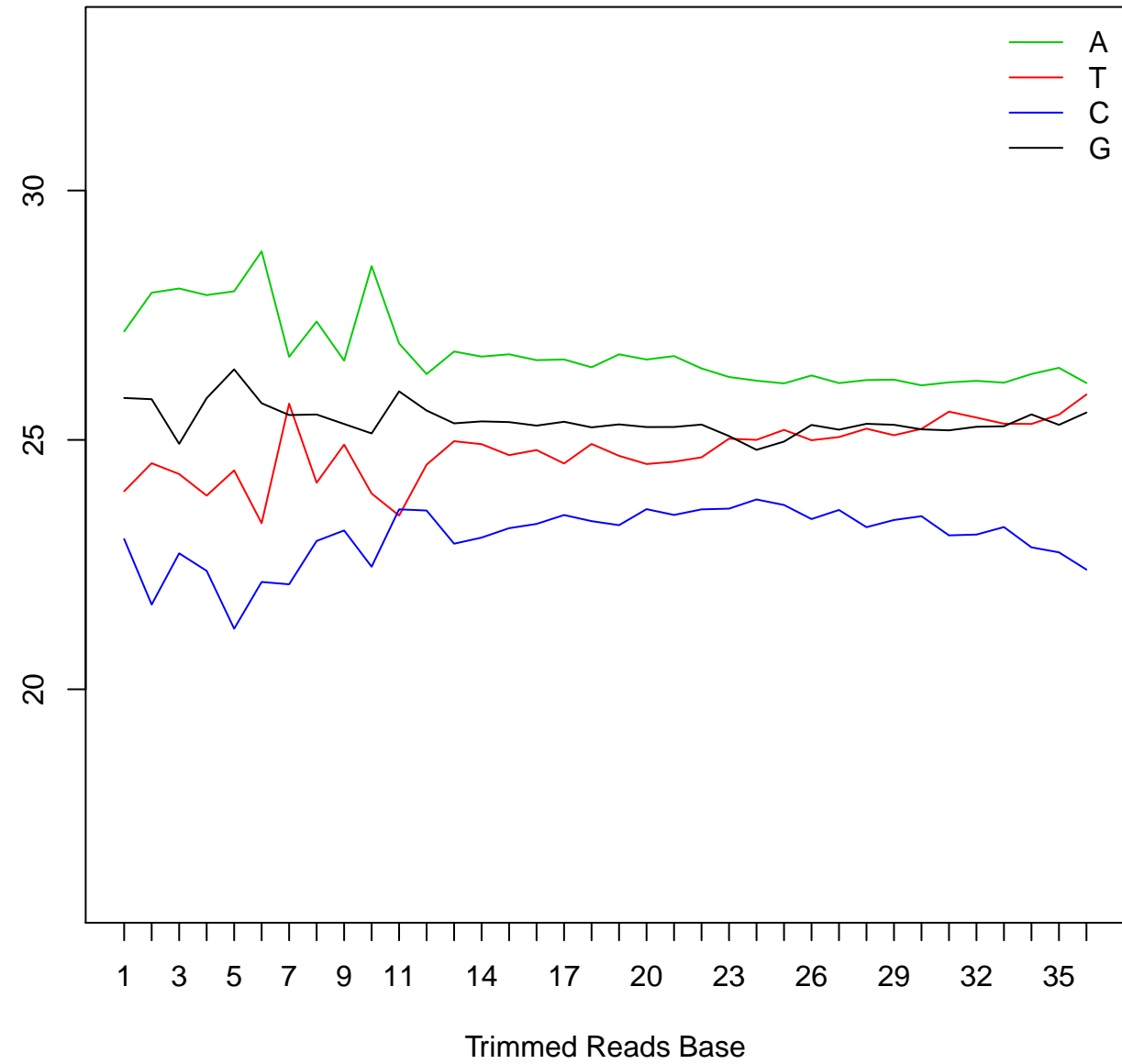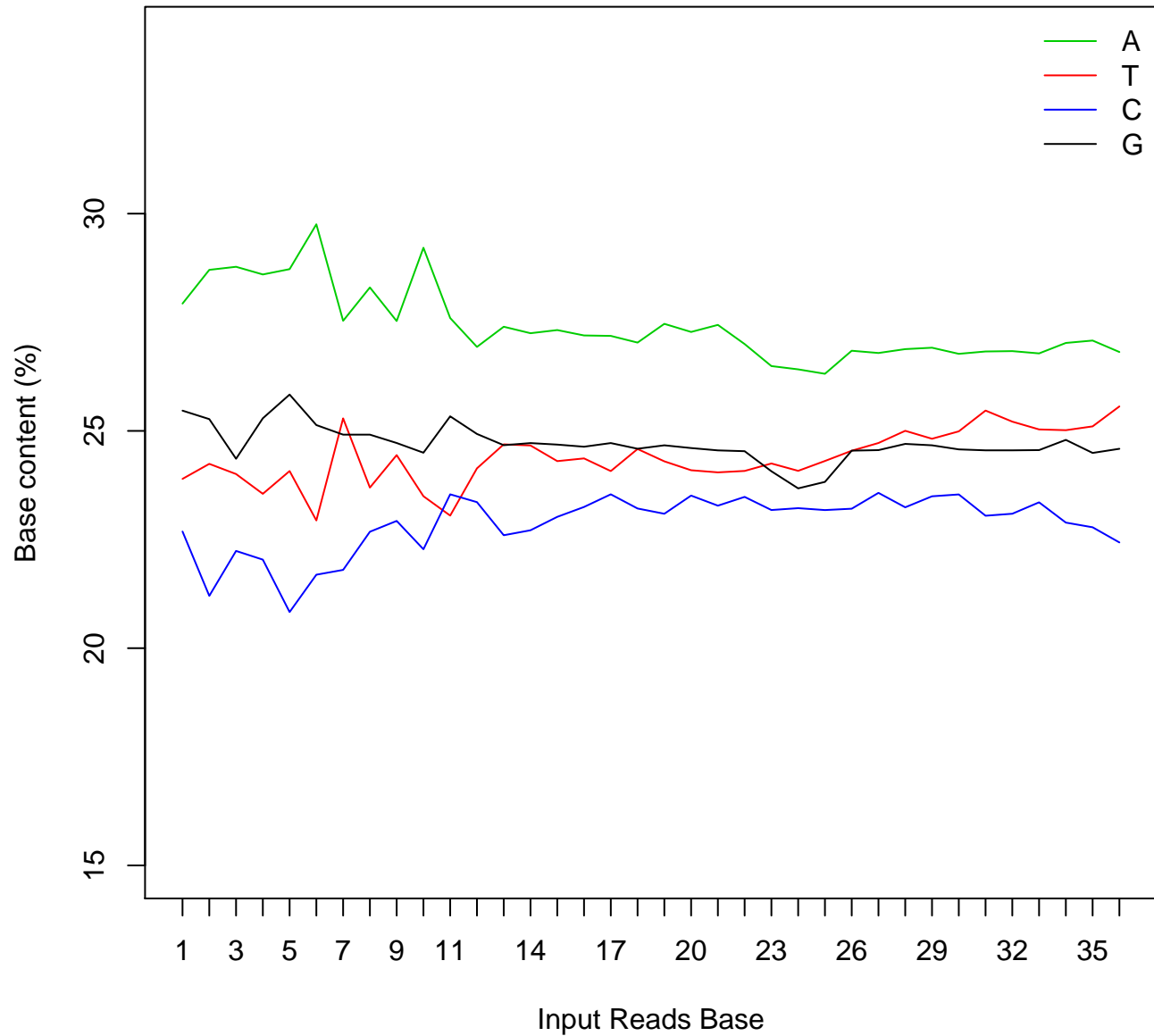
N Nucleotide Content Per Cycle

Reads Average Quality Histogram

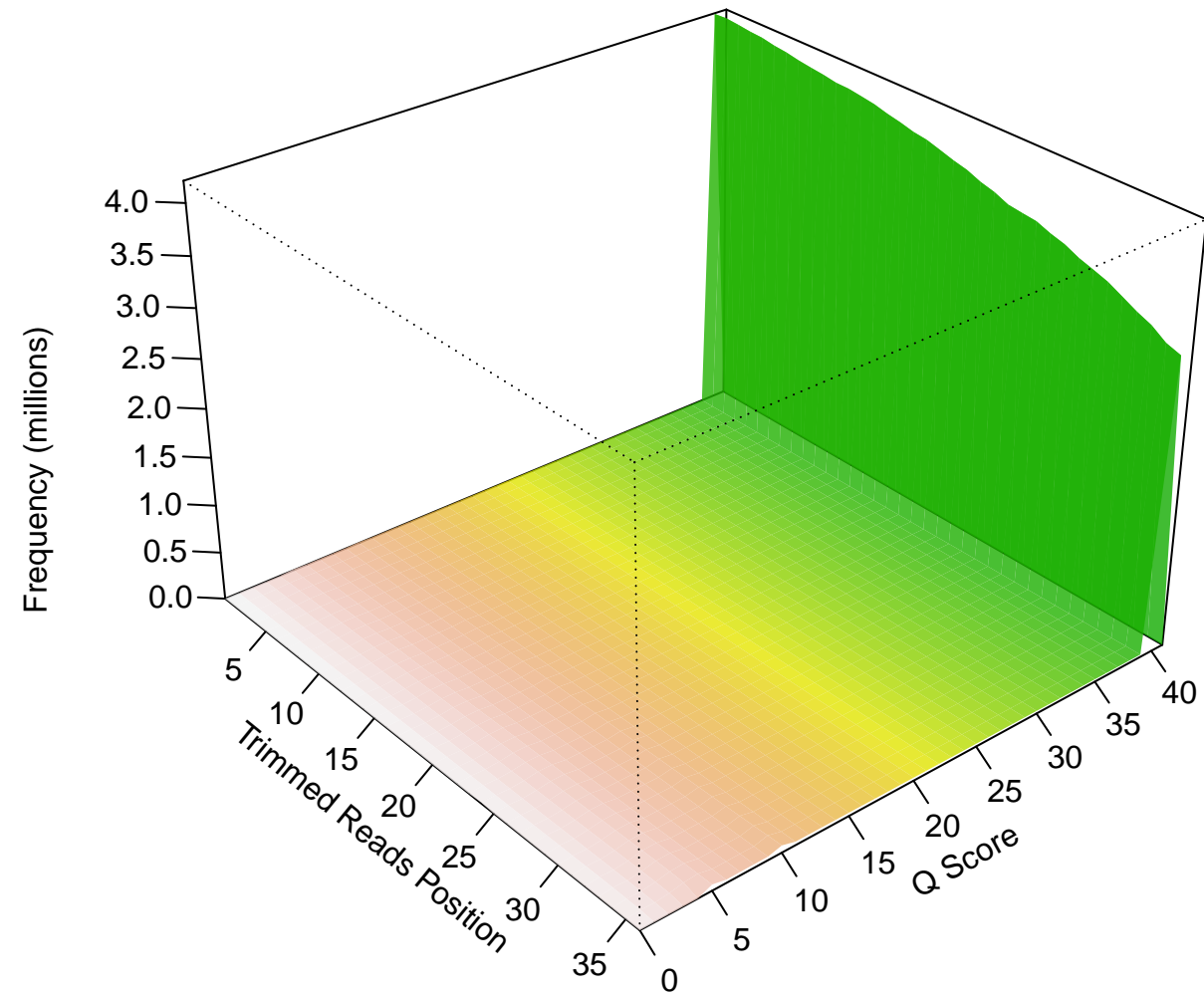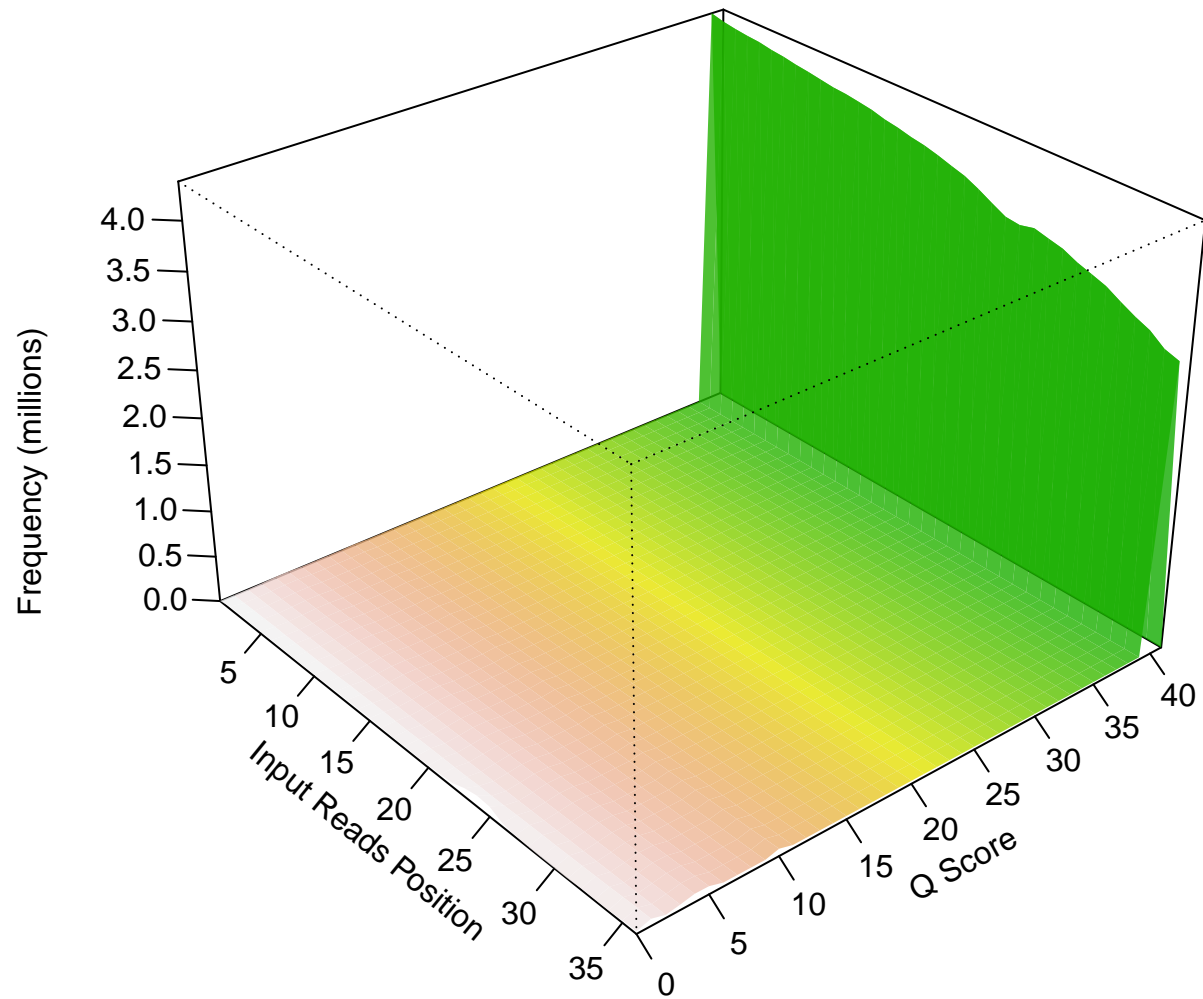Number of Q>=20 reads: 4,379,295 (95.41%) , mean Length: 36.00

Number of Q>=20 reads: 4,261,142 (97.65%) , mean Length: 35.94

Quality Boxplot Per Cycle
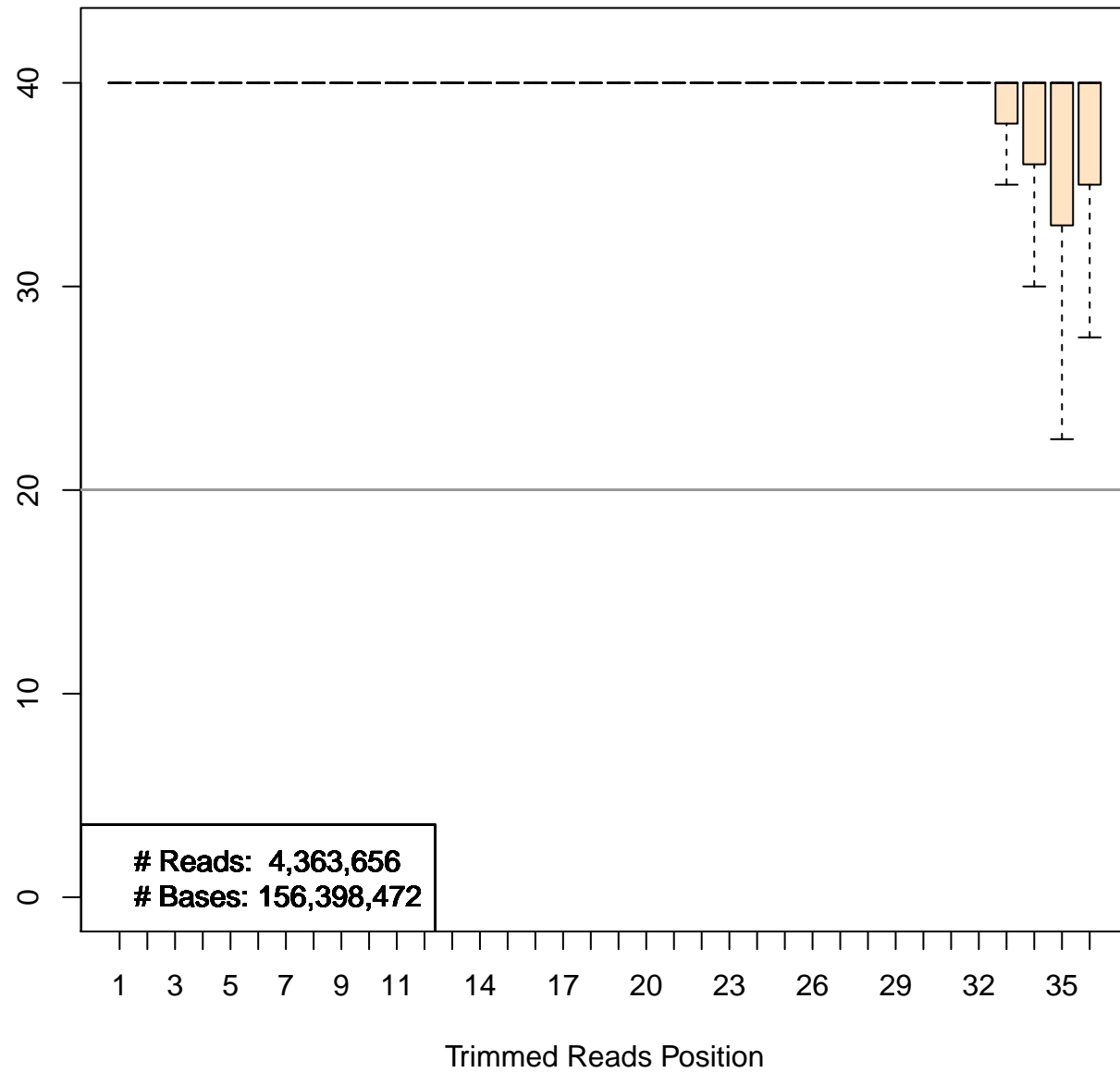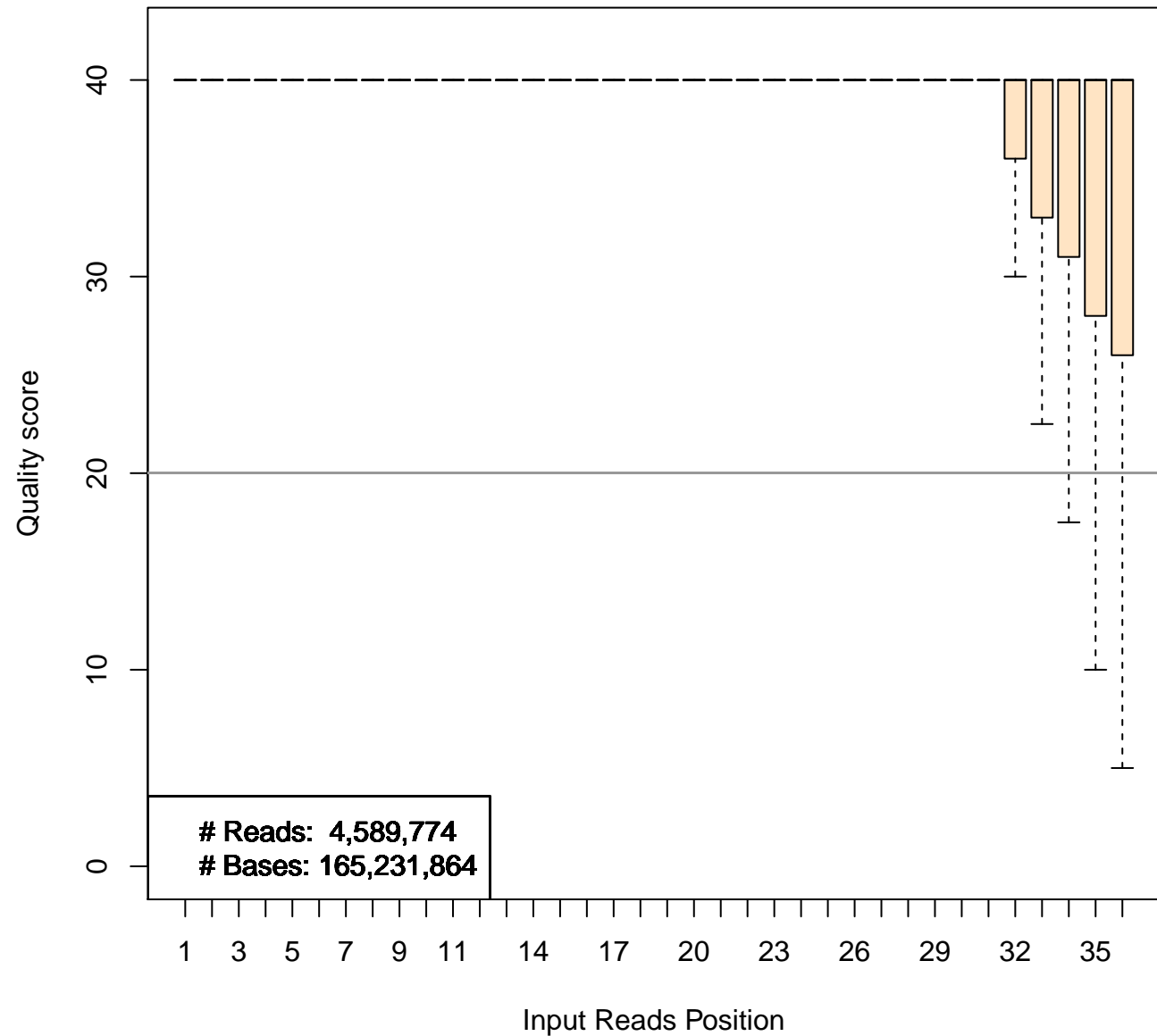
Quality 3D plot. (Position vs. Score vs. Frequency)

Quality report