

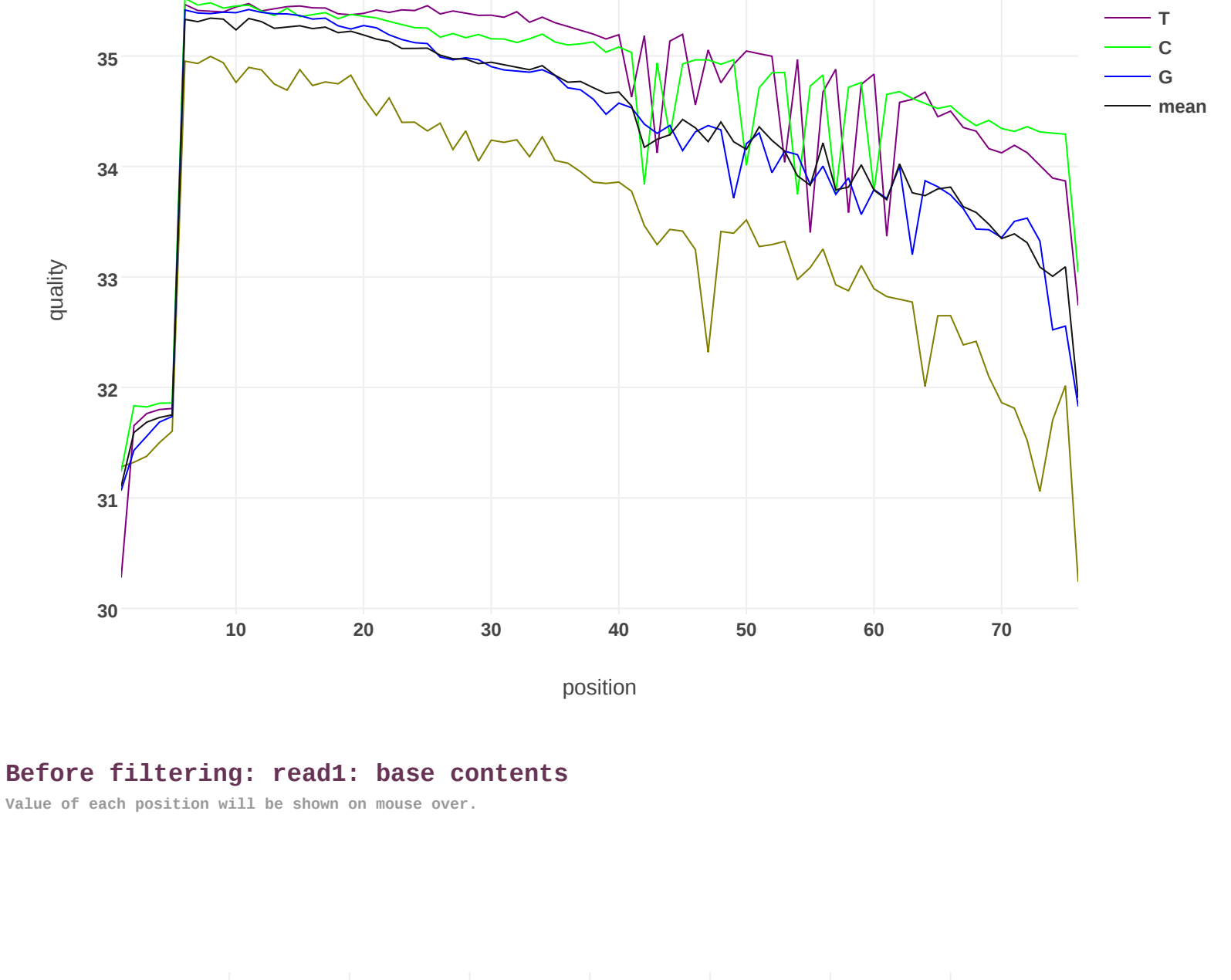
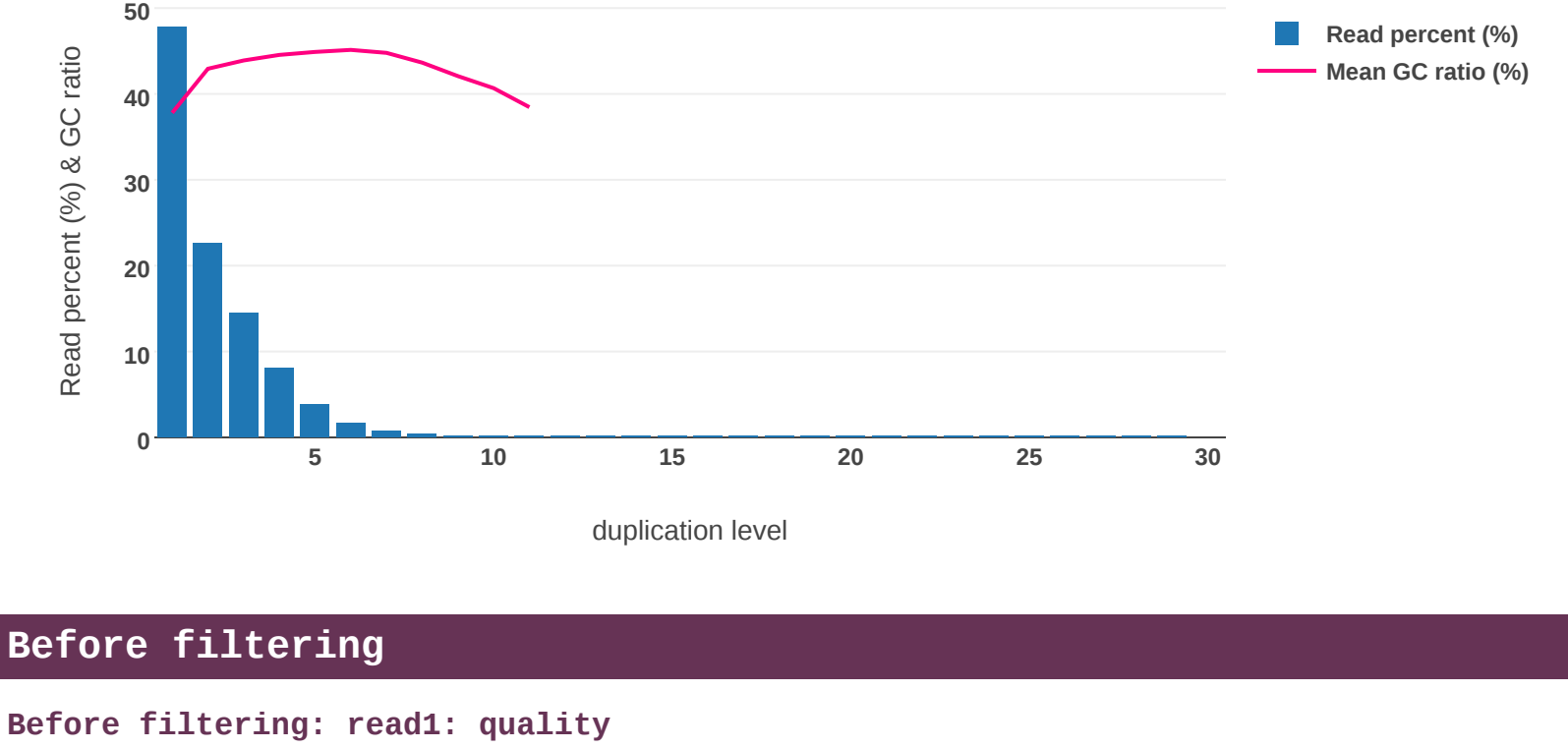
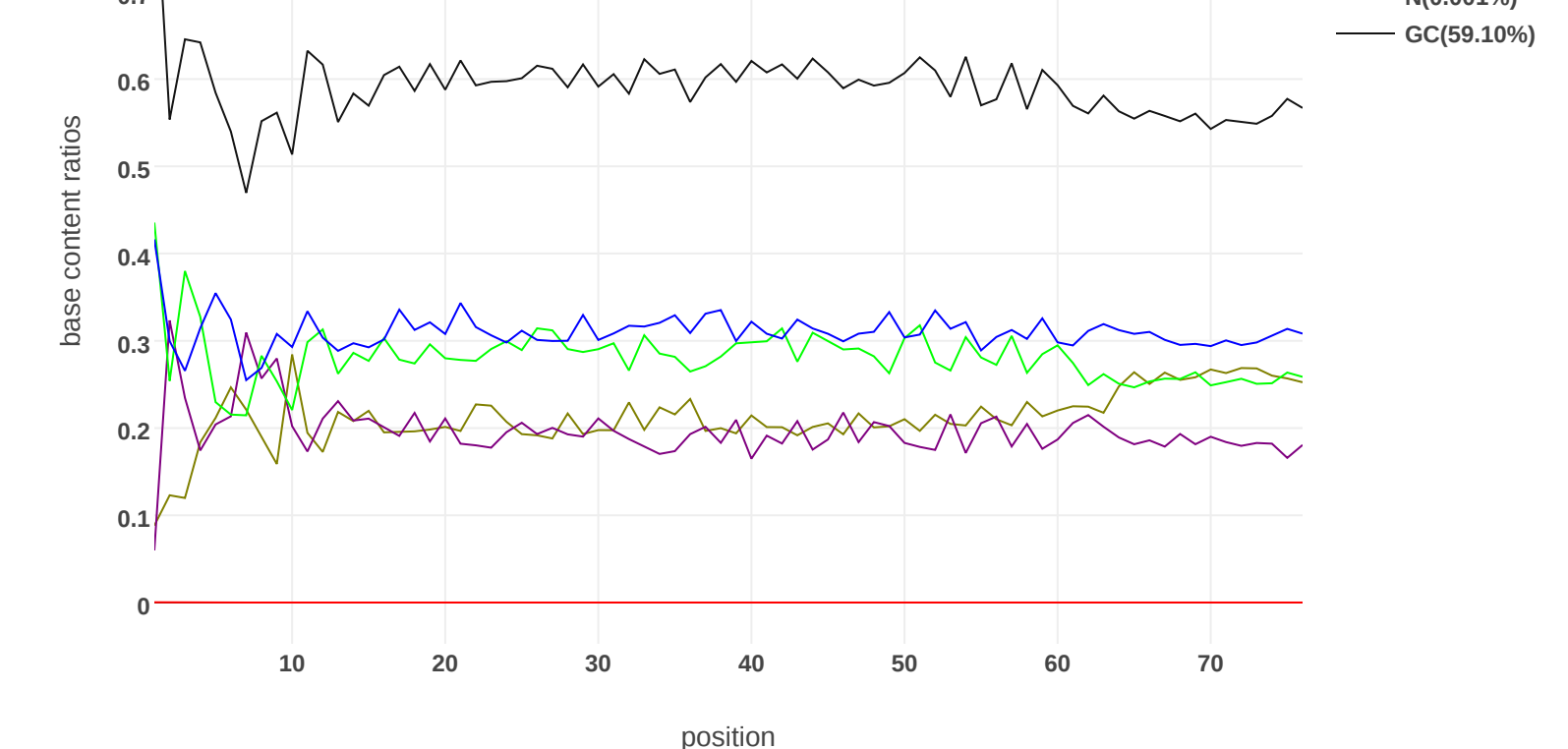
sequencing:	single end (76 cycles)
mean length before filtering:	76bp
mean length after filtering:	70bp
duplication rate:	52.874903% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Before filtering	
total reads:	29.767372 M

Q20 bases:	2.152990 G (95.16/344%)
Q30 bases:	2.115502 G (93.510285%)
GC content:	59.108956%
After filtering	
total reads:	28.740027 M
total bases:	2.013900 G

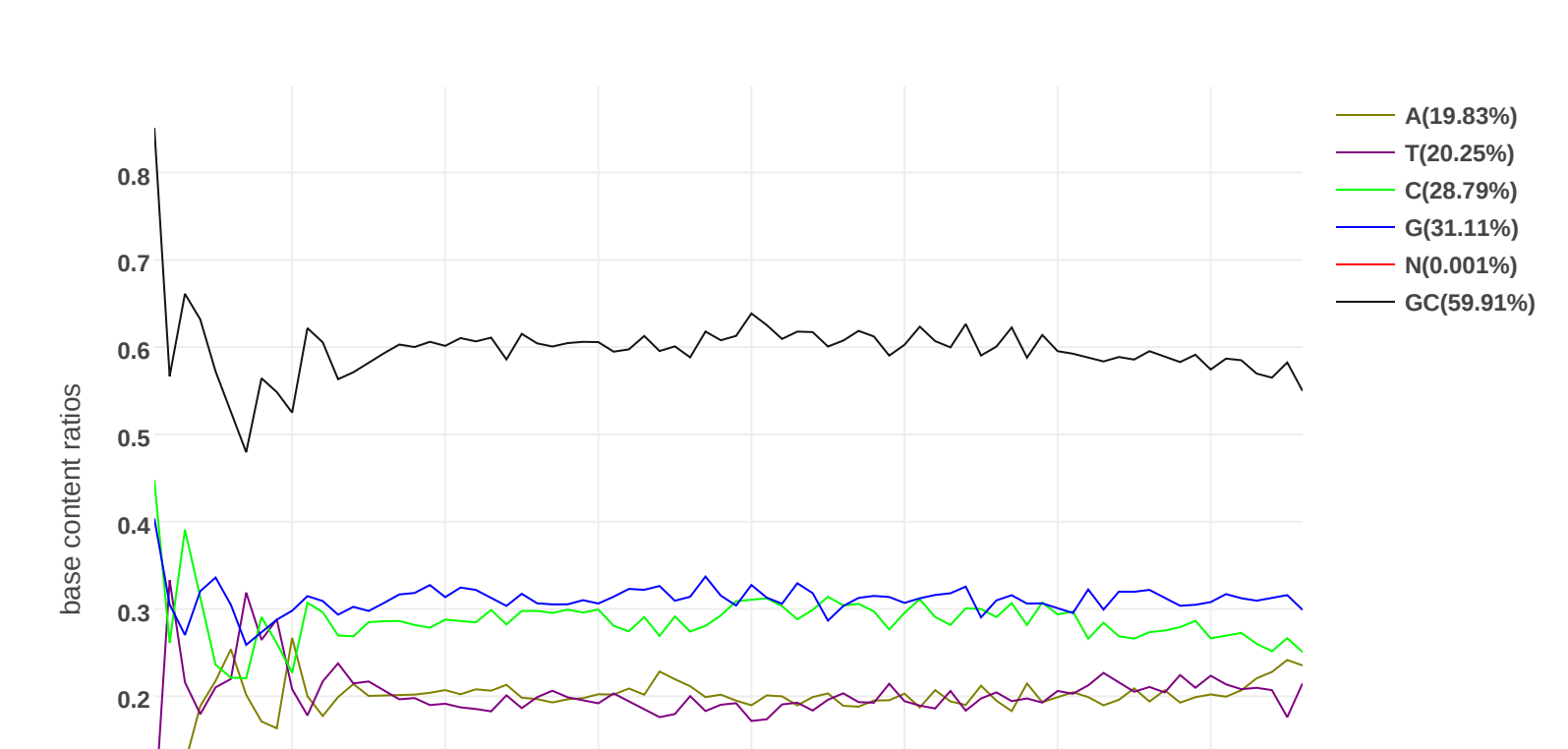
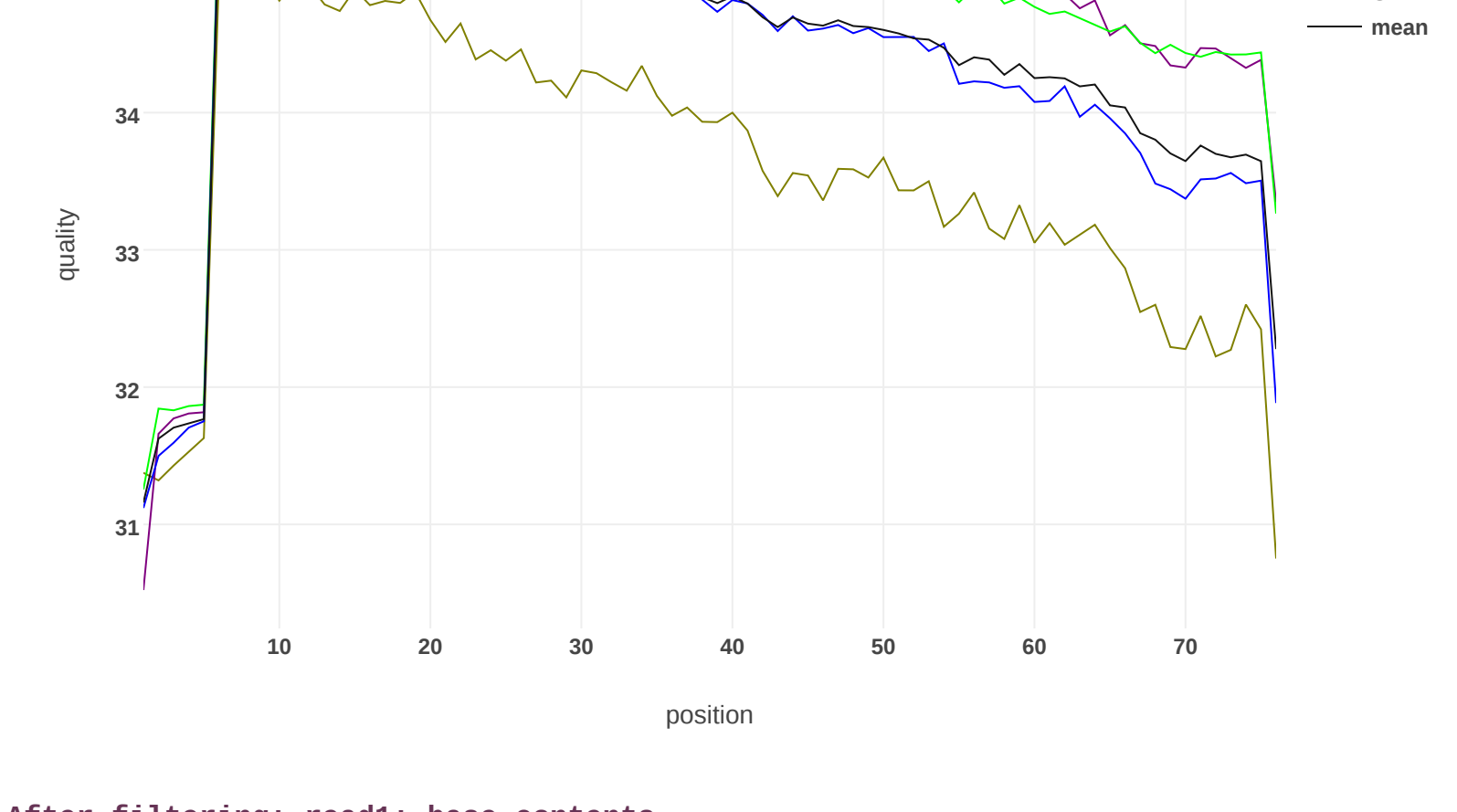
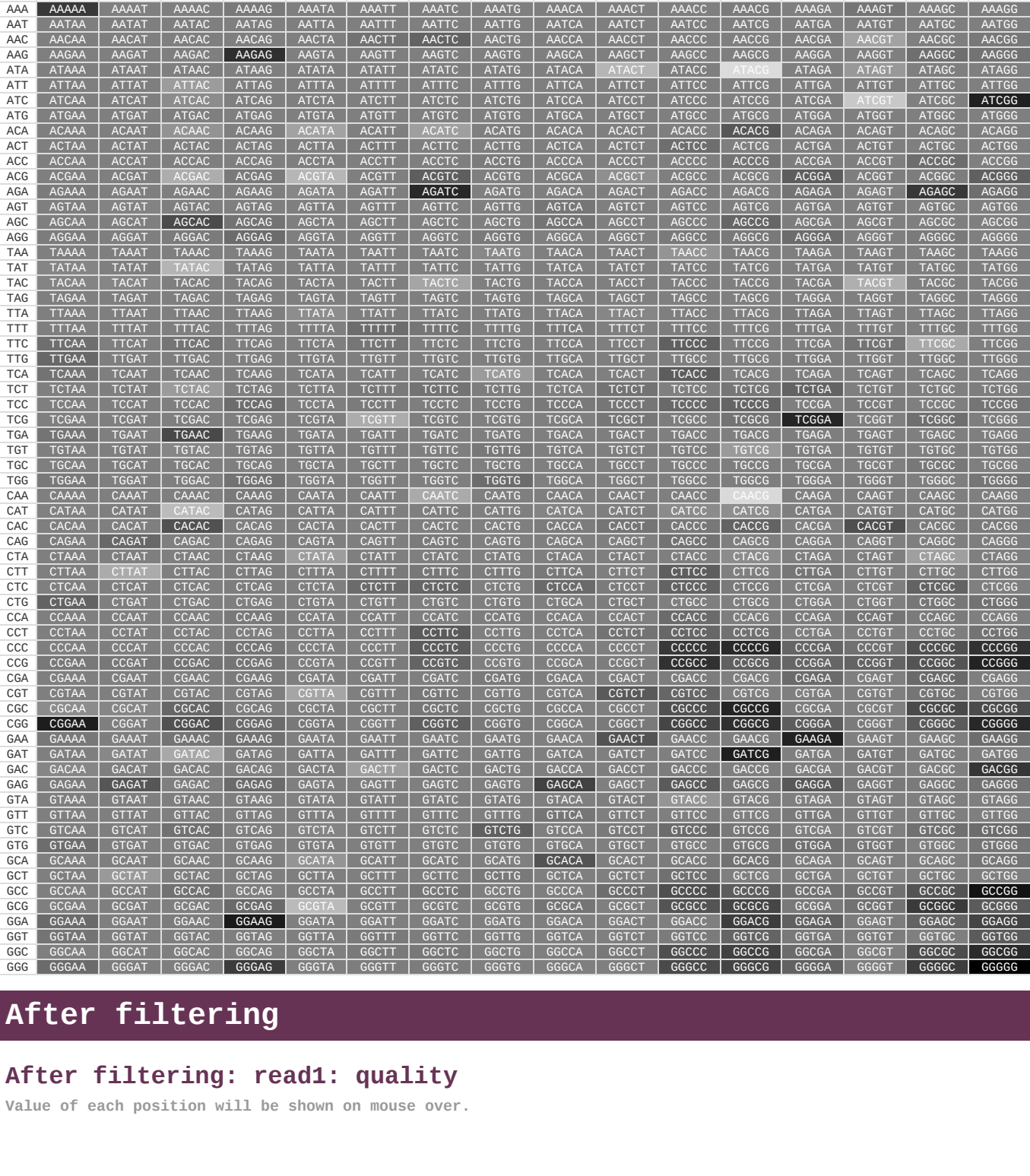
GC content:	59.912326%
Filtering result	
reads passed filters:	28.740027 M (96.548755%)
reads with low quality:	276.674000 K (0.929454%)
reads with too many N:	822 (0.002761%)
reads too short:	749.849000 K (2.519830%)

Sequence	Occurrences
AGATC	362011
AGATCG	352692

AGATCGGAAG	309322
AGATCGGAAGAG	378834
AGATCGGAAGAG	381166
AGATCGGAAGAGC	348023
AGATCGGAAGAGCA	390907
AGATCGGAAGAGCAC	355756
AGATCGGAAGAGCACACA	386742
AGATCGGAAGAGCACAC	343578
AGATCGGAAGAGCACACG	396078
AGATCGGAAGAGCACACGT	298903
AGATCGGAAGAGCACACGTC	278349
AGATCGGAAGAGCACACGCTCT	324294
AGATCGGAAGAGCACACGCTG	258074
AGATCGGAAGAGCACACGCTGGA	214643
AGATCGGAAGAGCACACGCTGGA	203275
AGATCGGAAGAGCACACGCTGGAAC	194583
AGATCGGAAGAGCACACGCTGGAAGT	171856
AGATCGGAAGAGCACACGCTGGAAGTC	161960
AGATCGGAAGAGCACACGCTGGAAGTCC	155093
AGATCGGAAGAGCACACGCTGGAAGTCCA	150753
AGATCGGAAGAGCACACGCTGGAAGTCCAG	131317
AGATCGGAAGAGCACACGCTGGAAGTCCAGT	119499
AGATCGGAAGAGCACACGCTGGAAGTCCAGTC	854718
AGATCGGAAGAGCACACGCTGGAAGTCCAGTCA	102540
AGATCGGAAGAGCACACGCTGGAAGTCCAGTCAC	106109
AGATCGGAAGAGCACACGCTGGAAGTCCAGTCCAC	99318
other adapter sequences	1074269

[illegible]

Before filtering: read1: KMER counting



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