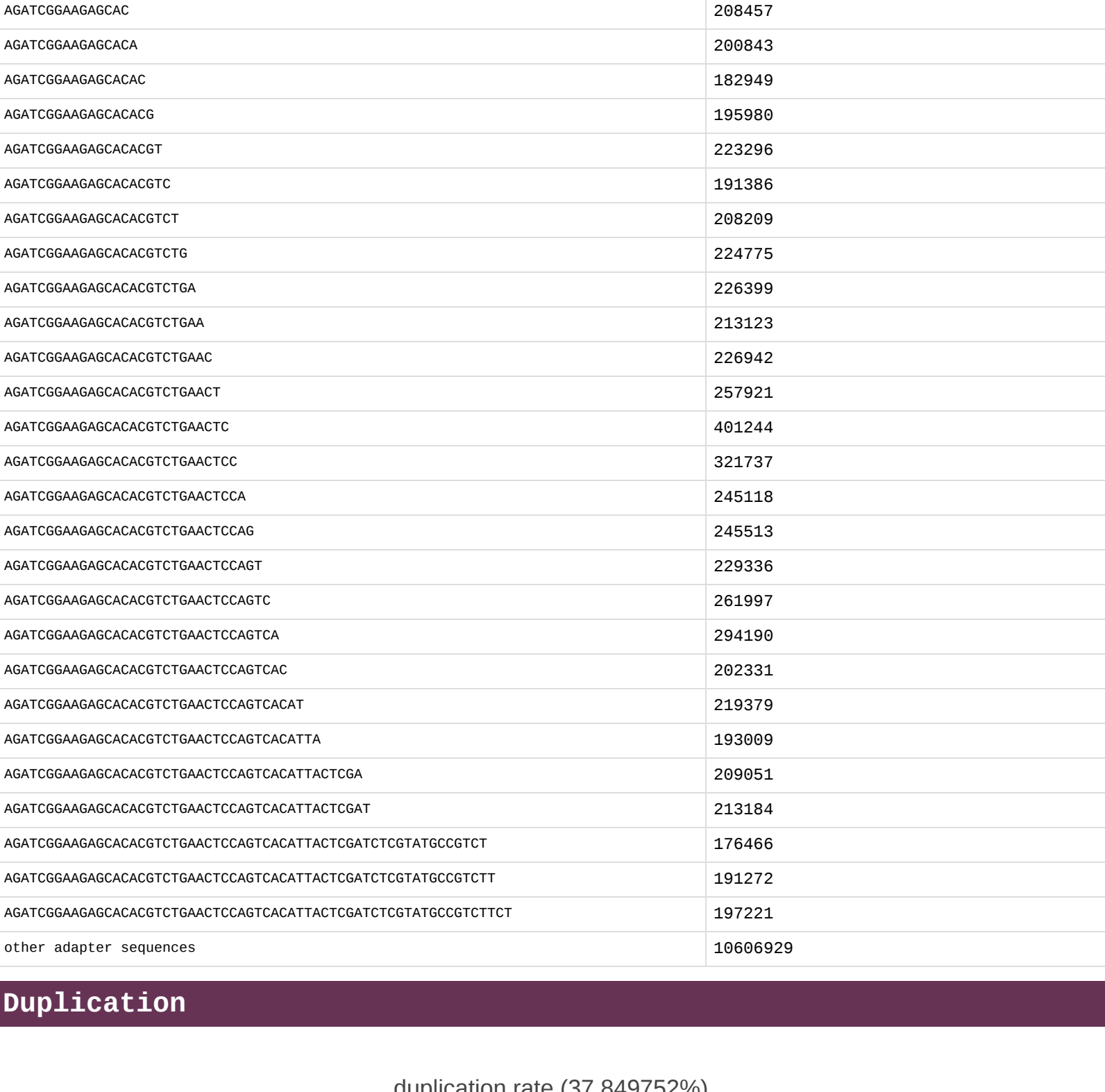


Rfastp Report

Summary	
General	
fastp version:	0.21.0 (https://github.com/OpenGene/fastp)
sequencing:	single end (126 cycles)
mean length before filtering:	126bp
mean length after filtering:	102bp
duplication rate:	37.849752% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Before filtering	
total reads:	34.921201 M
total bases:	4.400071 G
Q20 bases:	4.237703 G (96.309872%)
Q30 bases:	4.029685 G (91.582269%)
GC content:	65.865252%
After filtering	
total reads:	34.547425 M
total bases:	3.526023 G
Q20 bases:	3.435119 G (97.421888%)
Q30 bases:	3.285569 G (93.180566%)
GC content:	70.682598%
Filtering result	
reads passed filters:	34.547425 M (98.929659%)
reads with low quality:	205.309000 K (0.587921%)
reads with too many N:	13.066000 K (0.037416%)
reads too short:	155.401000 K (0.445005%)
Adapters	
Adapter or bad ligation of read1	
Sequence	Occurrences
AGATC	204146
AGATCG	216065
AGATCGG	232133
AGATCGGA	199154
AGATCGGAAGAGCAC	208457
AGATCGGAAGAGCACCA	200843
AGATCGGAAGAGCACAC	182949
AGATCGGAAGAGCACACG	105900
AGATCGGAAGAGCACACGT	223296
AGATCGGAAGAGCACACGTCT	191386
AGATCGGAAGAGCACACGTCTCT	208209
AGATCGGAAGAGCACACGTCTG	224775
AGATCGGAAGAGCACACGTCTGA	226399
AGATCGGAAGAGCACACGTCTGAA	213123
AGATCGGAAGAGCACACGTCTGAACT	226942
AGATCGGAAGAGCACACGTCTGAACT	257921
AGATCGGAAGAGCACACGTCTGAACTC	401244
AGATCGGAAGAGCACACGTCTGAACTCC	321737
AGATCGGAAGAGCACACGTCTGAACTCCA	245118
AGATCGGAAGAGCACACGTCTGAACTCCAG	245513
AGATCGGAAGAGCACACGTCTGAACTCCAGT	229336
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	261997
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	294190
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACT	202331
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTAT	219379
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTA	193009
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTCGA	299051
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTCGAT	213184
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTCGATCGATGCGCTCT	176466
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTCGATCGATGCGCTCTT	191272
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTATTCGATCGATGCGCTCTCTT	197221
other adapter sequences	10606929

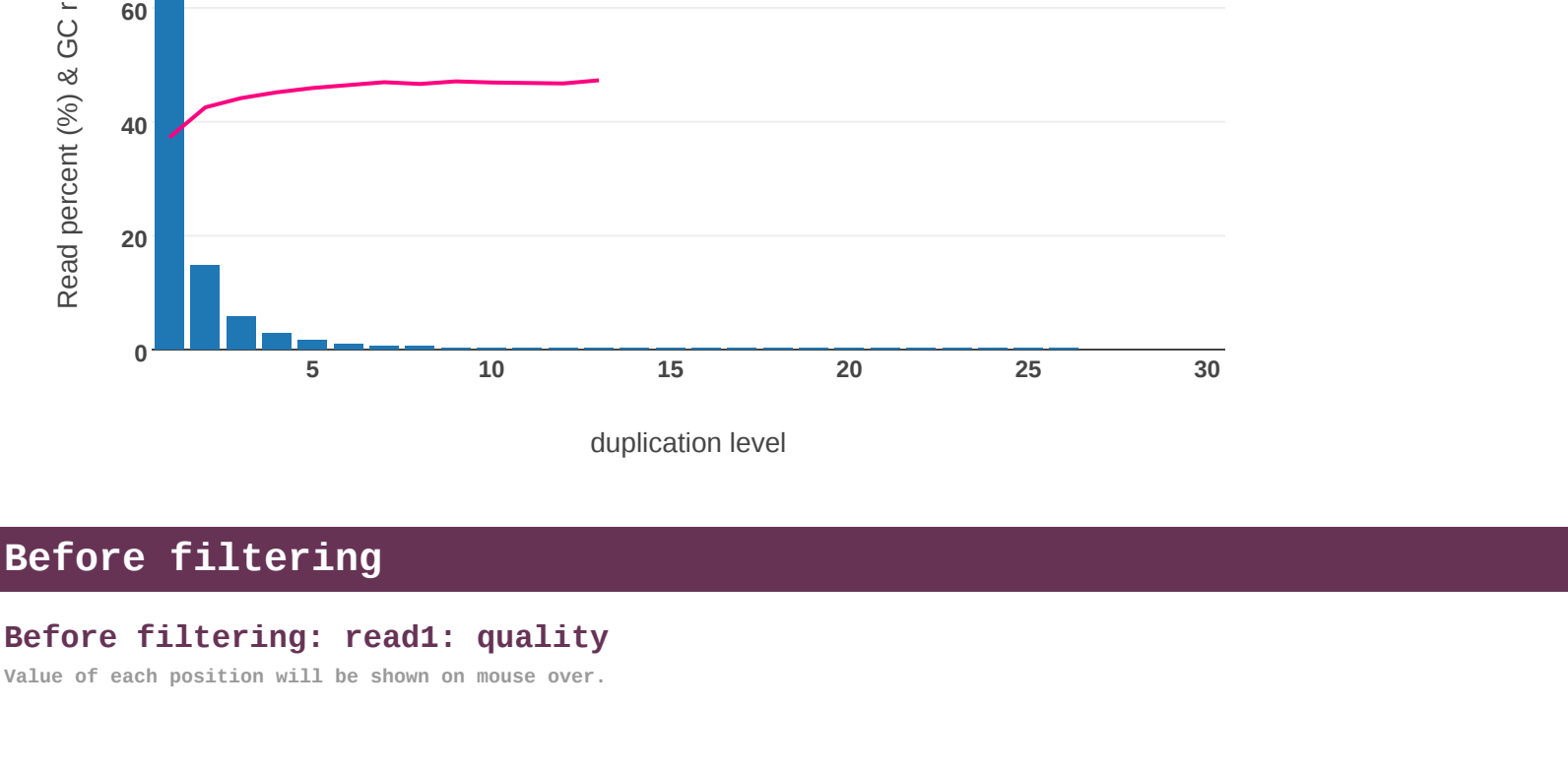
Duplication



Before filtering

Before filtering: read1: quality

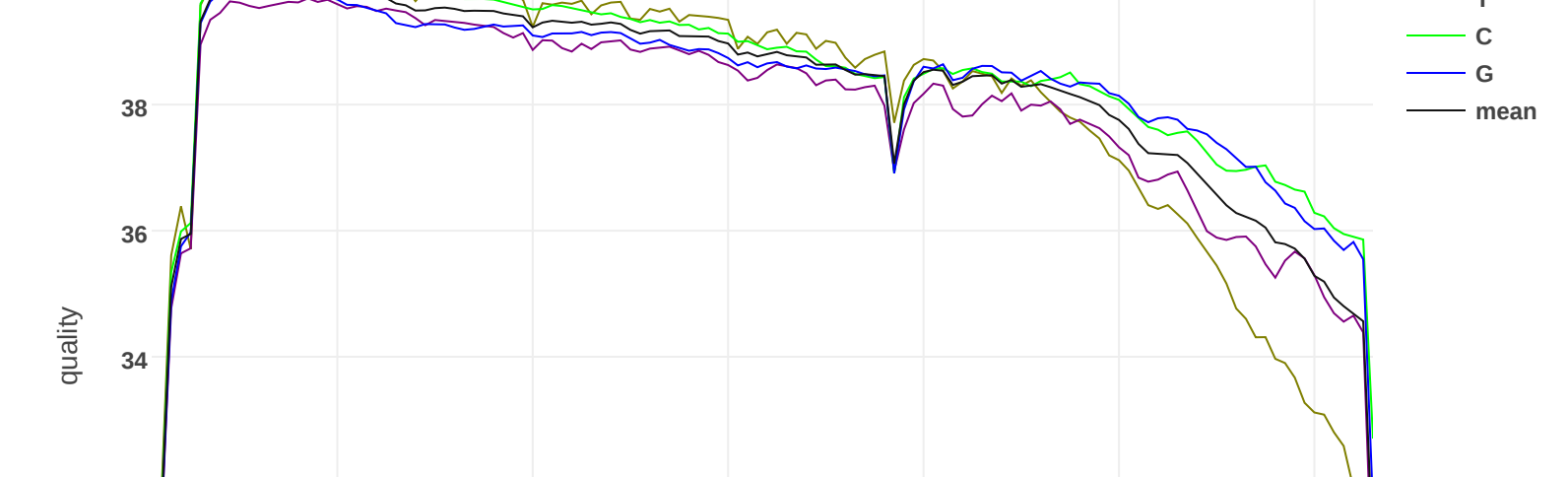
Value of each position will be shown on mouse over .



Before filtering

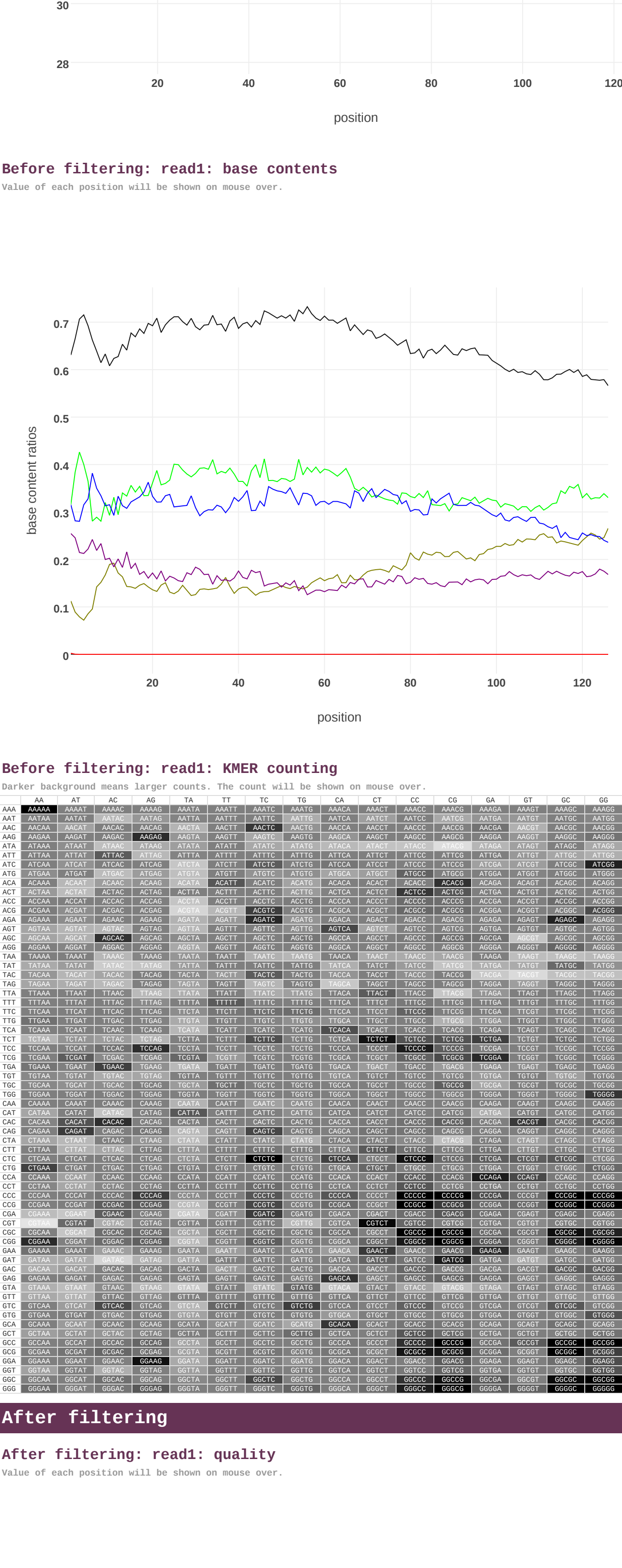
Before filtering: read1: base contents

Value of each position will be shown on mouse over .



Before filtering: read1: KMER counting

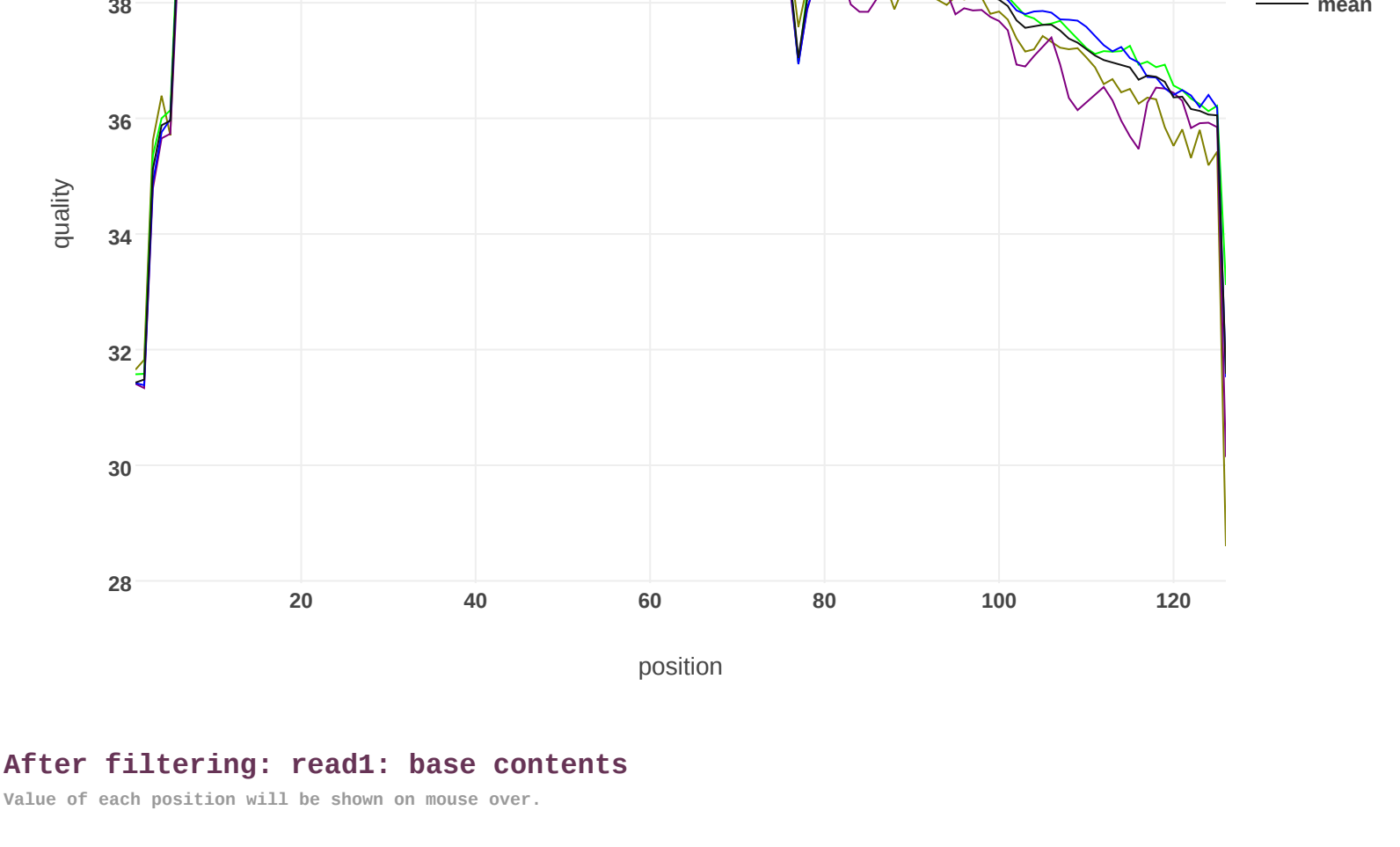
Darkner background means larger counts. The count will be shown on mouse over .



After filtering

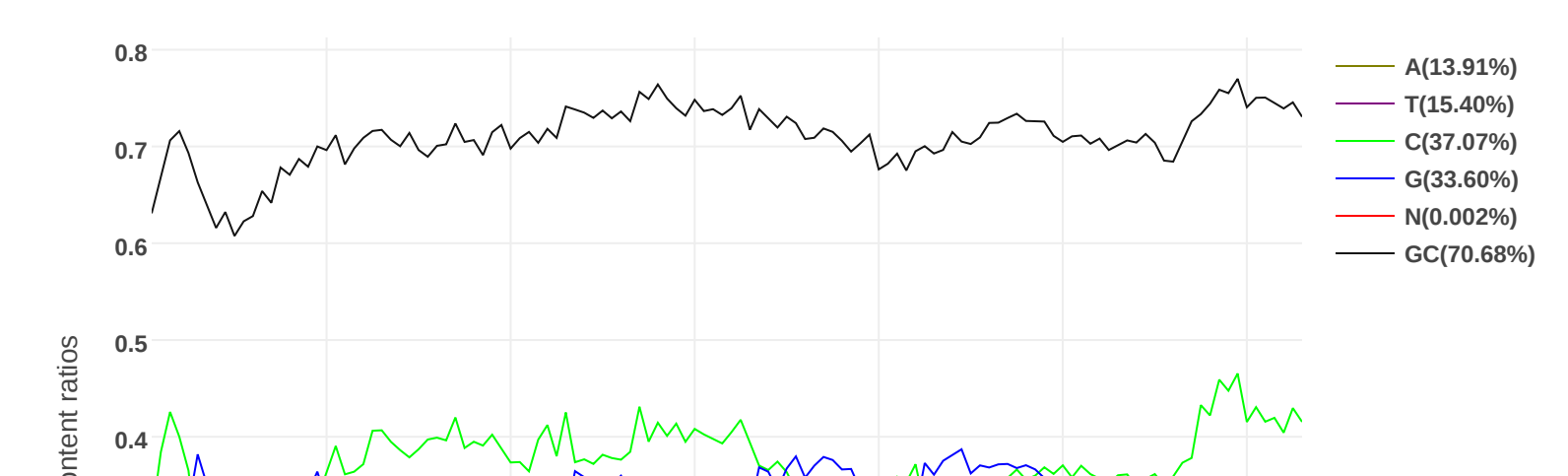
After filtering: read1: quality

Value of each position will be shown on mouse over .



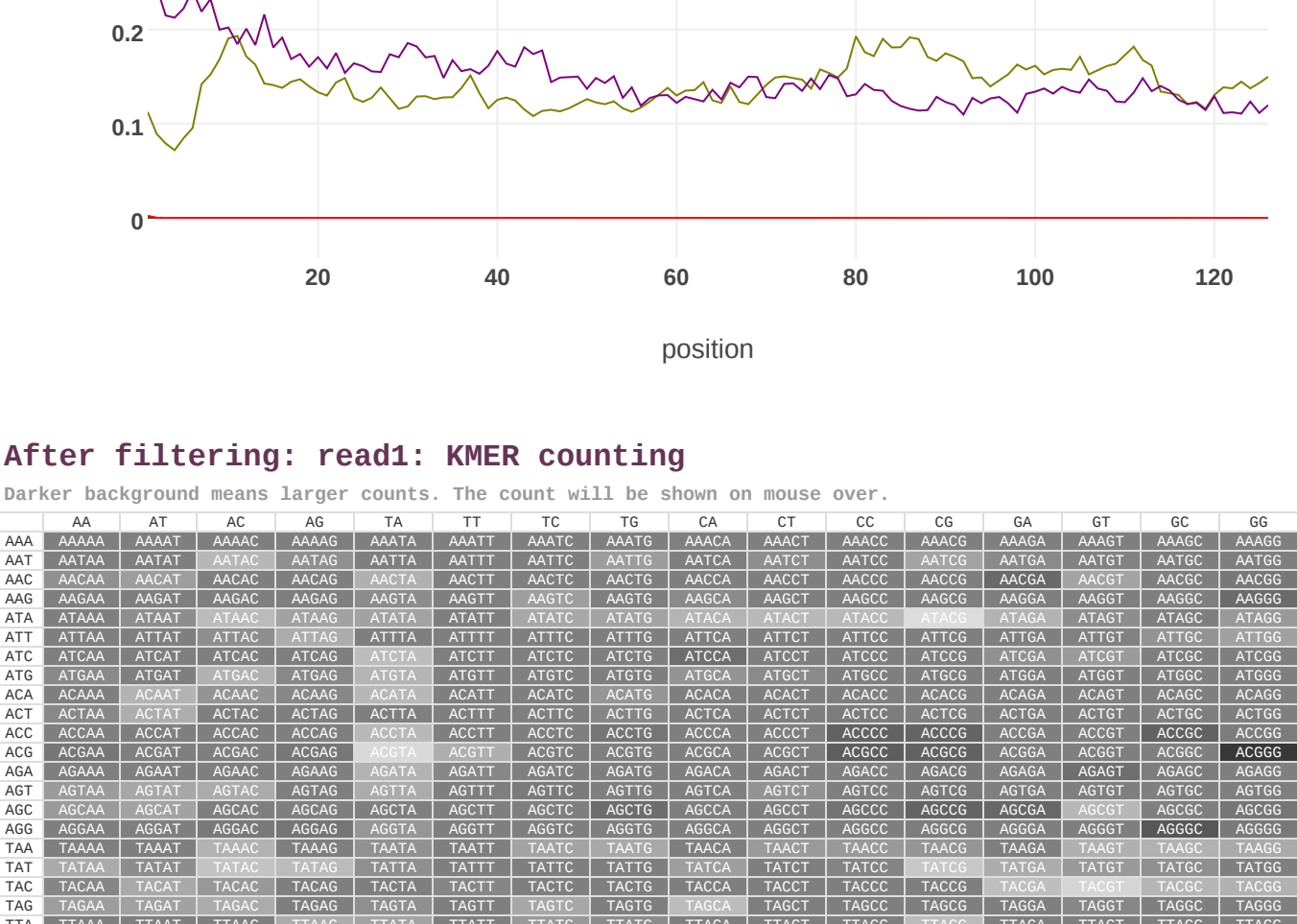
After filtering: read1: base contents

Value of each position will be shown on mouse over .



After filtering: read1: KMER counting

Darkner background means larger counts. The count will be shown on mouse over .



testcommand

fastp 0.21.0, at 2022-10-03 21:36:42