

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:	90bp
duplication rate:	65.802840% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Before filtering

total reads:	25.273334 M
total bases:	3.184440 G
Q20 bases:	3.078720 G (96.680100%)
Q30 bases:	2.952858 G (92.727700%)
GC content:	54.638086%

After filtering

total reads:	24.832458 M
total bases:	2.258322 G
Q20 bases:	2.222147 G (98.398163%)
Q30 bases:	2.152971 G (95.335627%)
GC content:	58.519620%

Filtering result

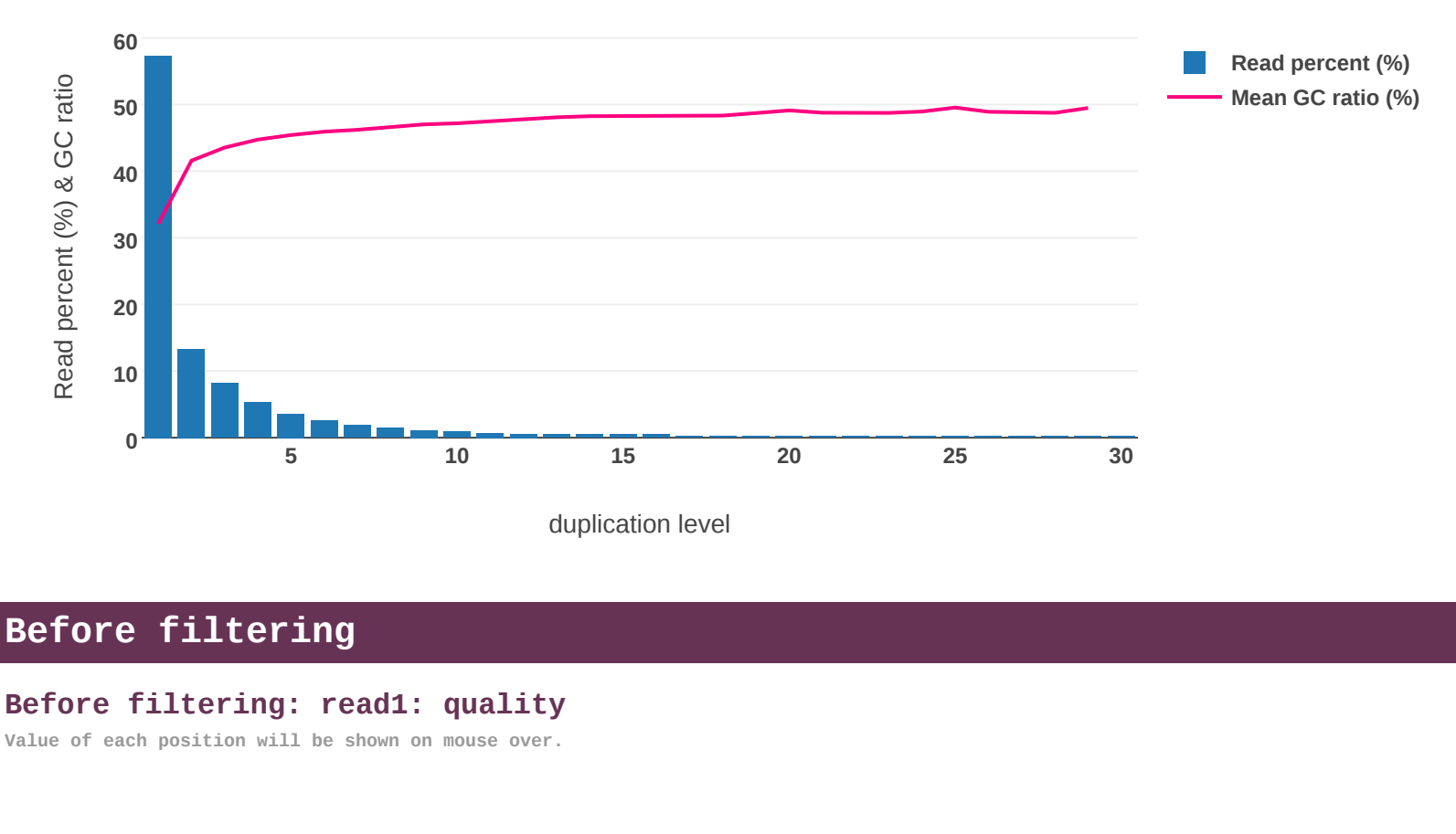
reads passed filters:	24.832458 M (98.25568%)
reads with low quality:	35.551000 K (0.148666%)
reads with too many N:	9.165090 K (0.03624%)
reads too short:	396.168000 K (1.567502%)

Adapters

Adapter or bad ligation of read1

Sequence	Occurrences
AGATCGGAAGAGCACCA	178012
AGATCGGAAGAGCACACGTCTG	176997
AGATCGGAAGAGCACACGTCTGA	182100
AGATCGGAAGAGCACACGTCTGAA	177908
AGATCGGAAGAGCACACGTCTGAAC	195046
AGATCGGAAGAGCACACGTCTGAACTC	256252
AGATCGGAAGAGCACACGTCTGAACTCC	191234
AGATCGGAAGAGCACACGTCTGAACTCCA	191238
AGATCGGAAGAGCACACGTCTGAACTCCAG	185513
AGATCGGAAGAGCACACGTCTGAACTCCAGT	175961
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	190211
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	185218
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACAT	194951
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATT	176589
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTAA	218075
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTAC	201805
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACT	187059
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTC	185388
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCG	200857
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGA	211452
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGATT	213168
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGATCTC	199533
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGATCTCGTGGTGGTCTT	184091
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGATCTCGTATGCCGTCTCT	195434
other adapter sequences	12715473

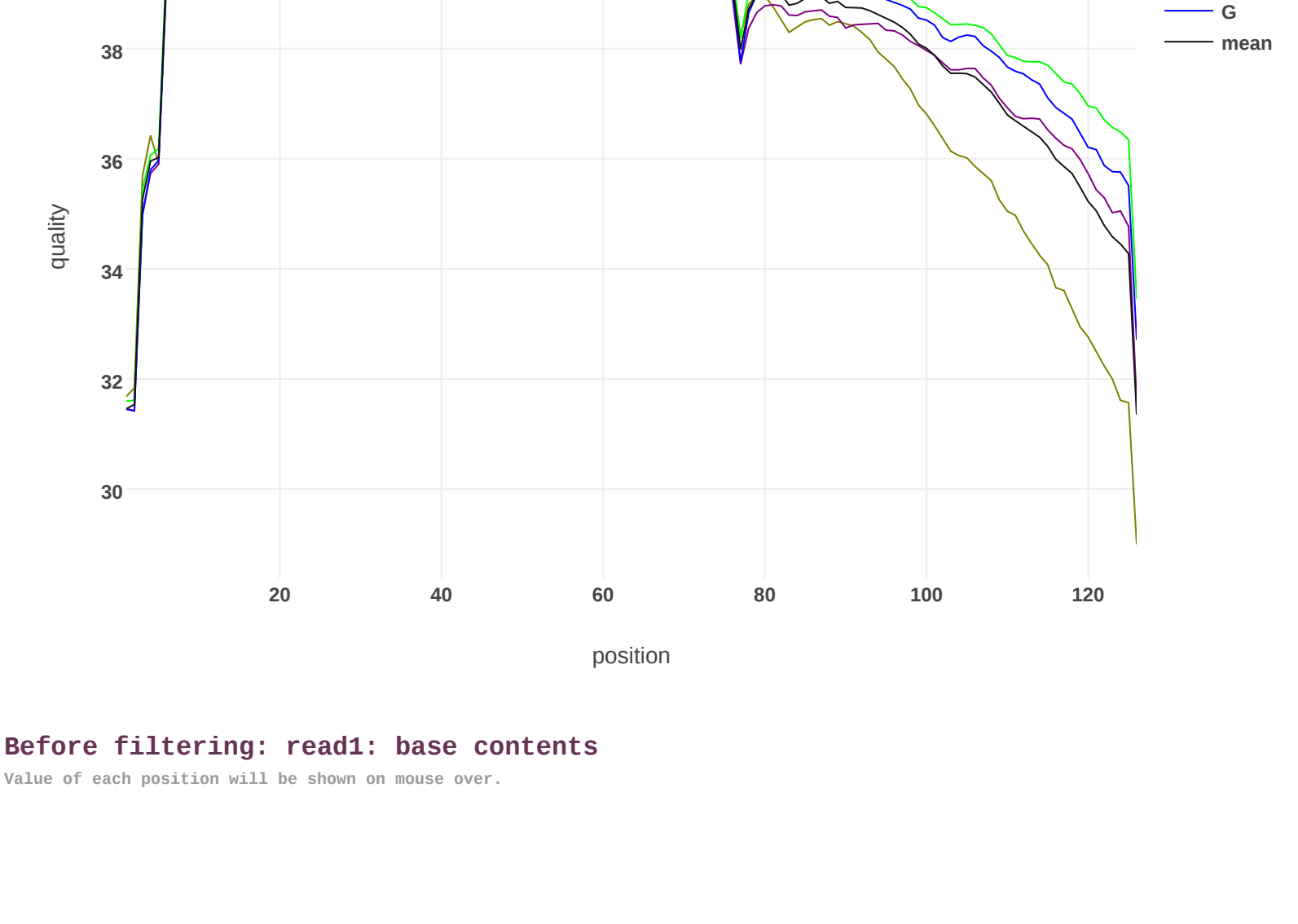
Duplication



Before filtering

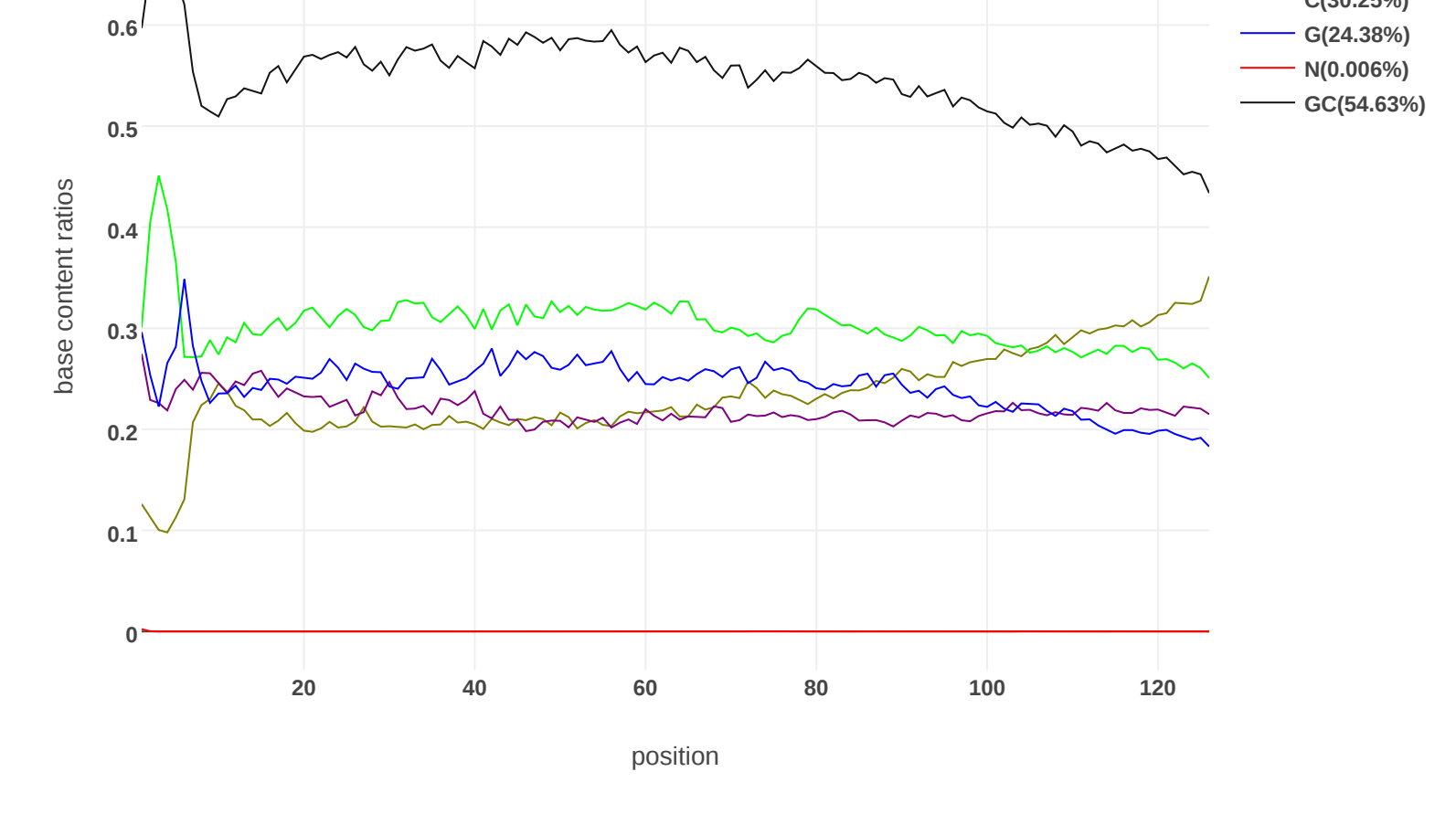
Before filtering: read1: quality

Value of each position will be shown on mouse over.



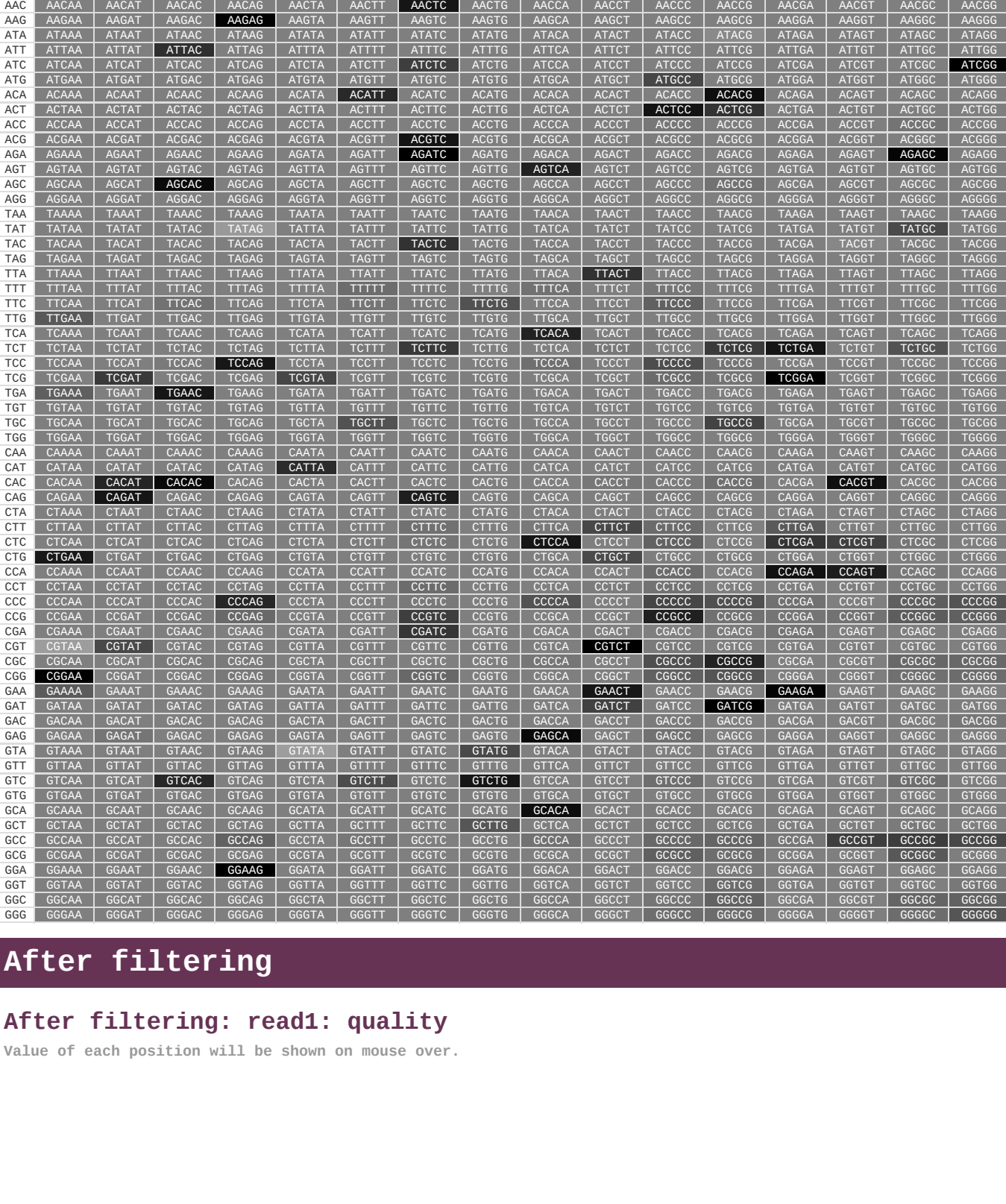
Before filtering: read1: base contents

Value of each position will be shown on mouse over.



Before filtering: read1: KMER counting

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



After filtering

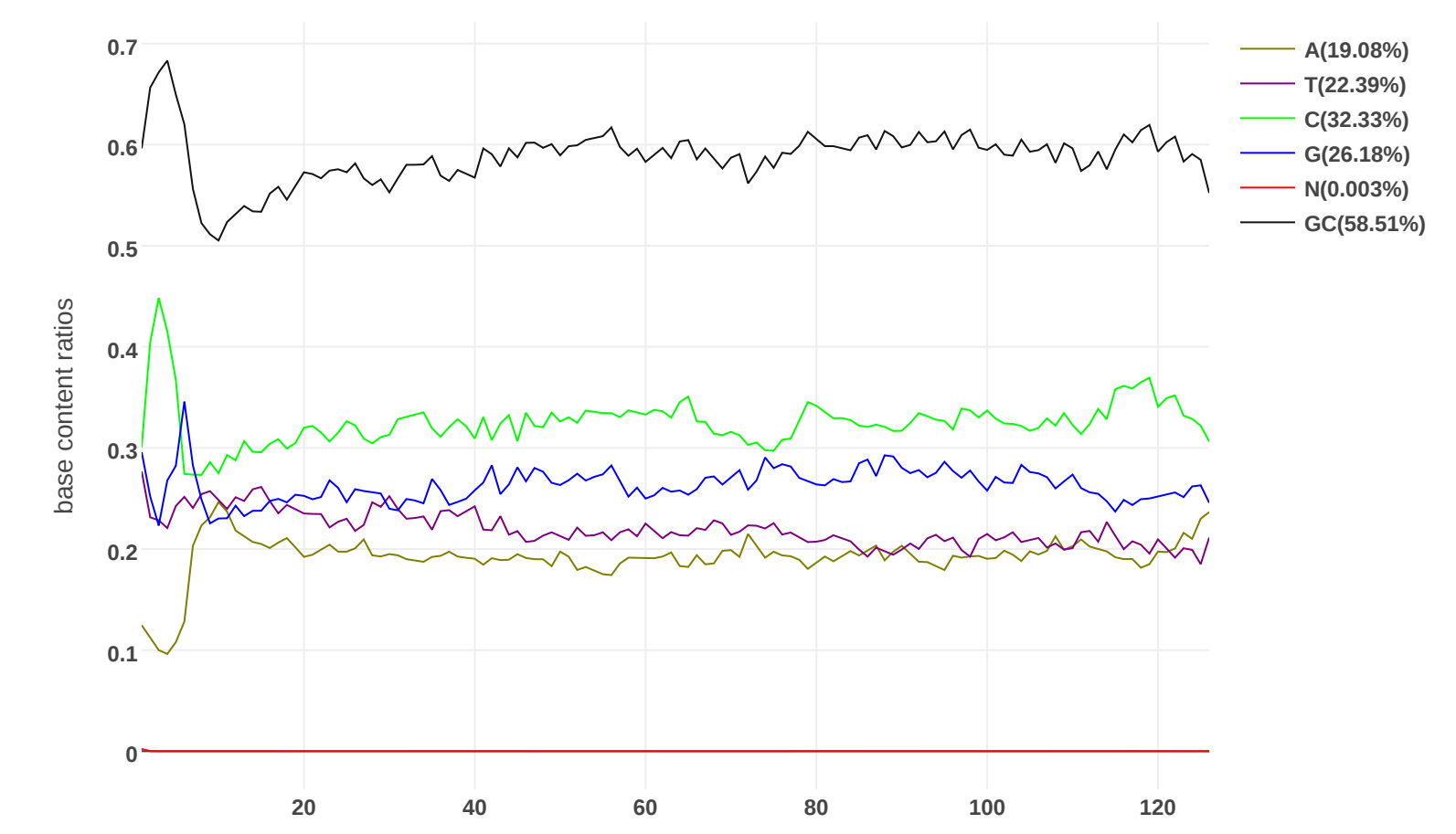
After filtering: read1: quality

Value of each position will be shown on mouse over.



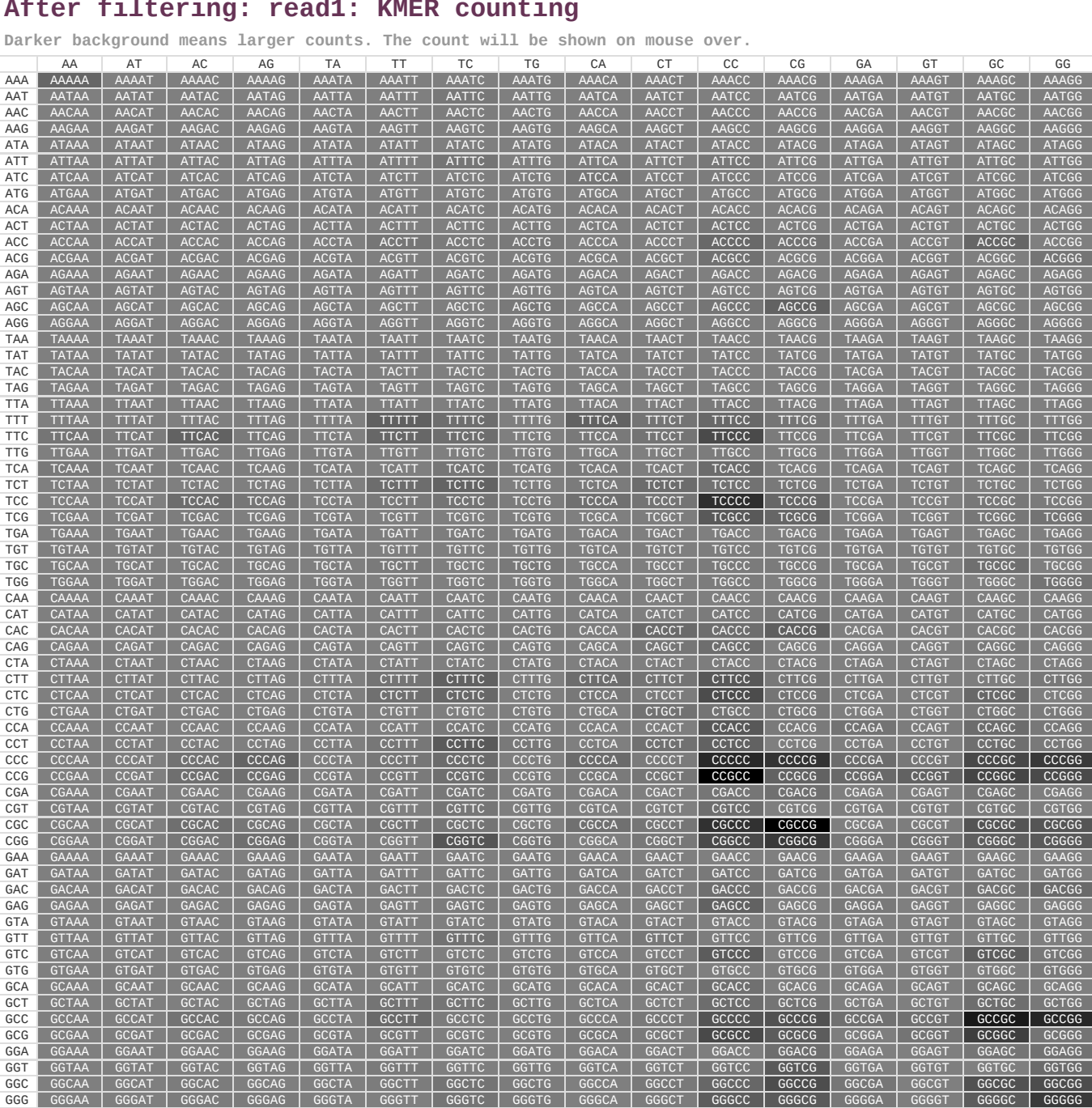
After filtering: read1: base contents

Value of each position will be shown on mouse over.



After filtering: read1: KMER counting

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



test command

fastp 0.21.0, at 2022-10-01 21:55:49