

Rfastp Report

Summary

General

fastp version:	0.21.0 (https://github.com/OpenGene/fastp)
sequencing:	single end (148 cycles)
mean length before filtering:	148bp
mean length after filtering:	121bp
duplication rate:	14.361106% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Before filtering

total reads:	41.128399 M
total bases:	6.086990 G
Q20 bases:	5.524668 G (90.761908%)
Q30 bases:	5.222853 G (85.803553%)
GC content:	57.126367%

After filtering

total reads:	36.080651 M
total bases:	4.377634 G
Q20 bases:	4.108131 G (93.843628%)
Q30 bases:	3.930947 G (89.796145%)
GC content:	56.199247%

Filtering result

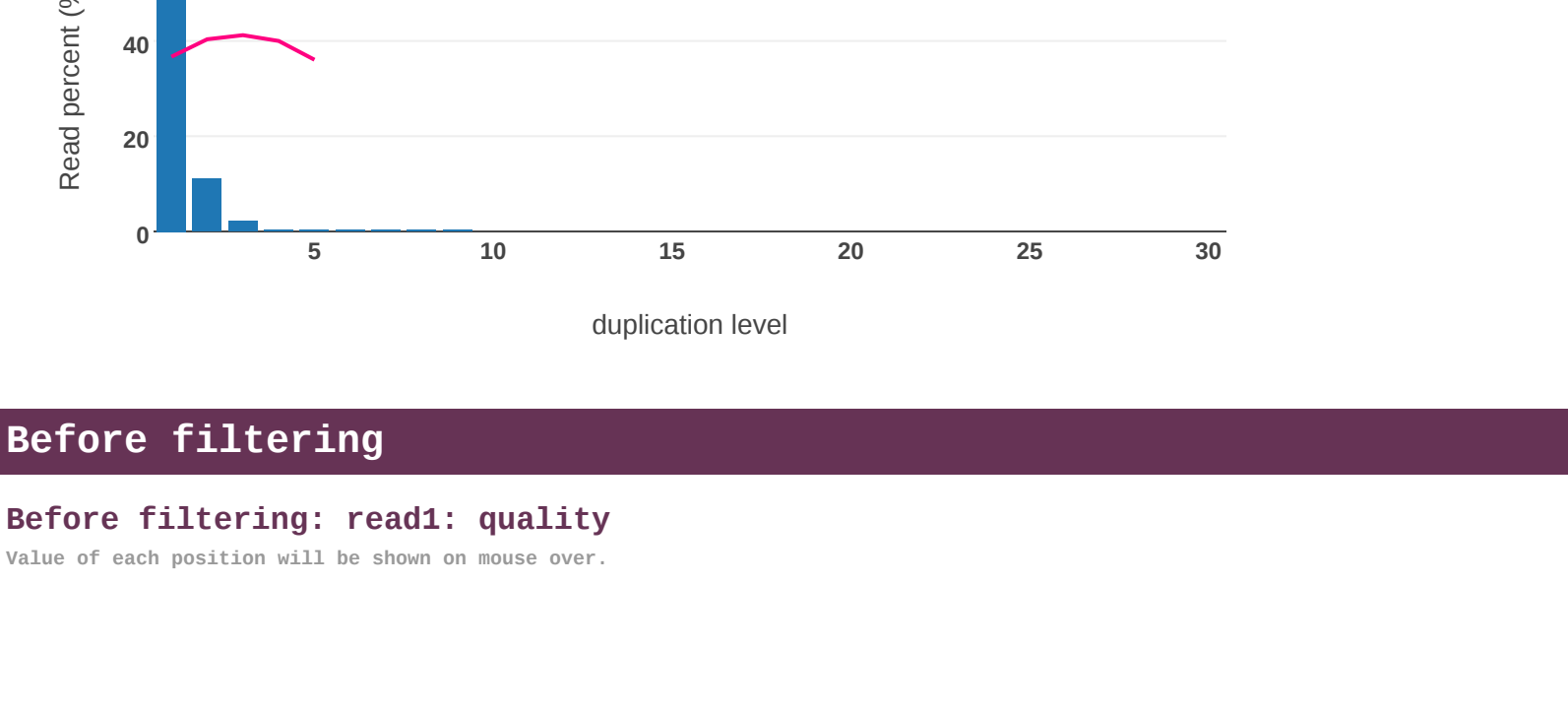
reads passed filters:	36.080651 M (87.727047%)
reads with low quality:	2.233788 M (5.431266%)
reads with too many N:	7.999000 K (0.019449%)
reads too short:	2.805871 M (6.822238%)

Adapters

Adapter or bad ligation of read1

Sequence	Occurrences
AGATC	271180
AGATCGGAAGAGC	263471
AGATCGGAAGAGCAC	264727
AGATCGGAAGAGCACAC	297301
AGATCGGAAGAGCACACG	294841
AGATCGGAAGAGCACACAGT	311429
AGATCGGAAGAGCACACAGCT	309484
AGATCGGAAGAGCACACAGCTCT	328836
AGATCGGAAGAGCACACAGCTCTG	314893
AGATCGGAAGAGCACACAGCTCTGA	323661
AGATCGGAAGAGCACACAGCTCTGAAG	339926
AGATCGGAAGAGCACACAGCTCTGAAC	301436
AGATCGGAAGAGCACACAGCTCTGAACCT	298550
AGATCGGAAGAGCACACAGCTCTGAACCTC	348459
AGATCGGAAGAGCACACAGCTCTGAACCTCC	336929
AGATCGGAAGAGCACACAGCTCTGAACCTCCA	337318
AGATCGGAAGAGCACACAGCTCTGAACCTCCAG	344396
AGATCGGAAGAGCACACAGCTCTGAACCTCCAAT	348426
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCC	3122011
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCA	293000
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCAC	320643
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACC	337966
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCT	304046
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTT	321862
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTG	317845
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGT	317493
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTA	308972
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAAG	331636
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAAT	315610
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCT	267704
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTC	270917
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTCG	261999
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTCGAT	269571
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTCGATG	263739
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTCGATGAC	267466
AGATCGGAAGAGCACACAGCTCTGAACCTCCAGTCCACCTTGTAATCTCGATGACCG	262468
other adapter sequences	12386283

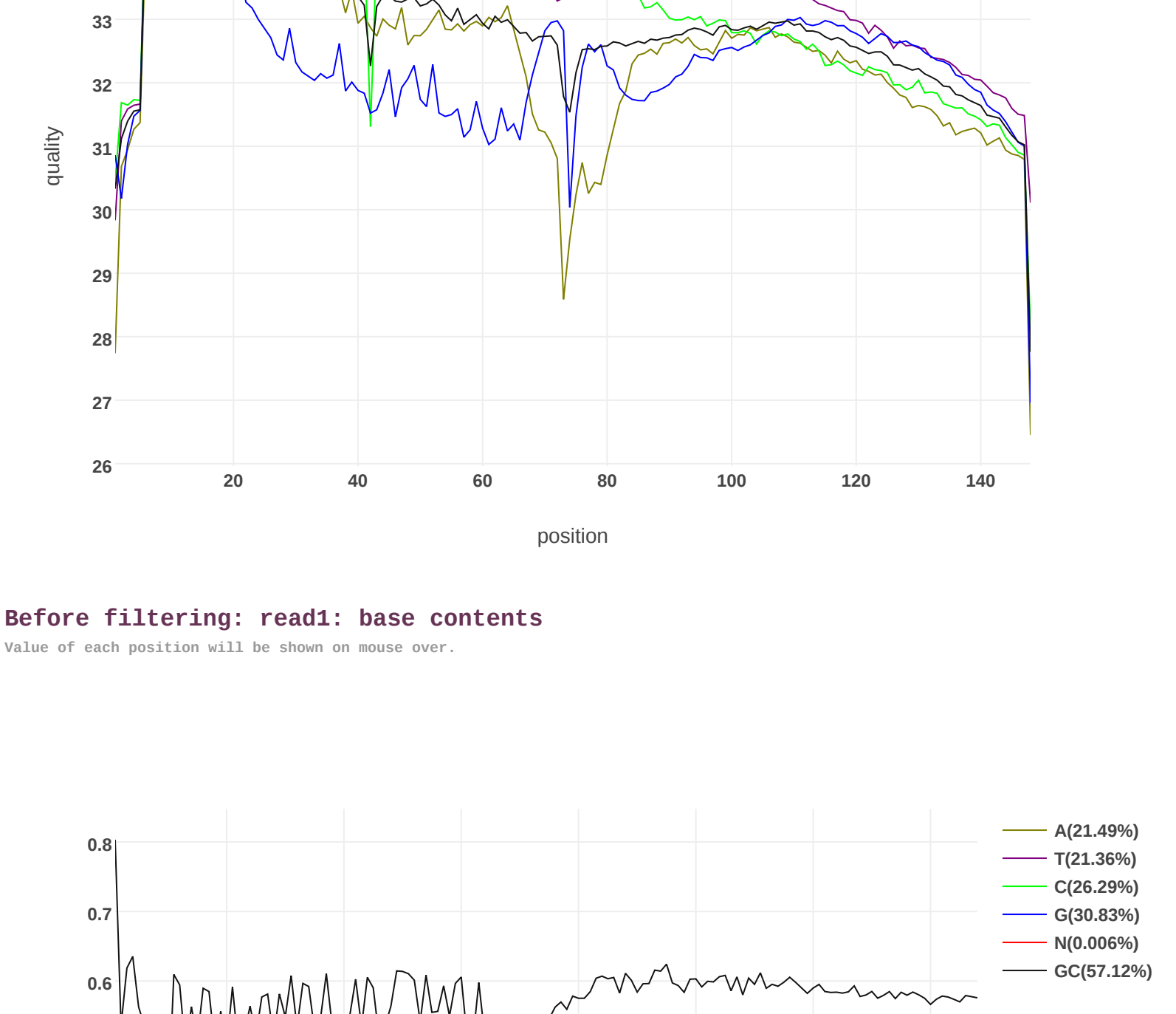
Duplication



Before filtering

Before filtering: read1: quality

Value of each position will be shown on mouse over .



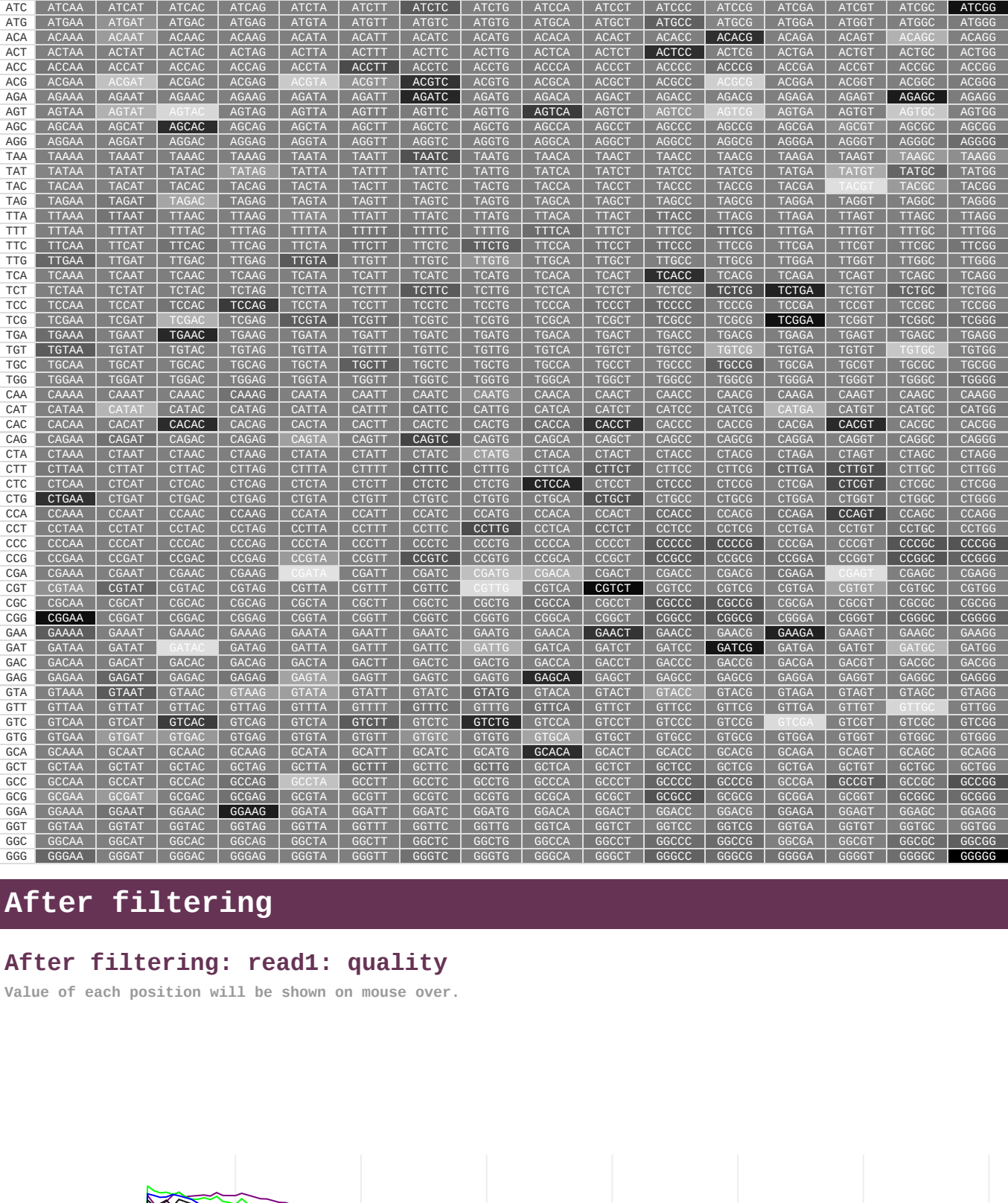
Before filtering: read1: base contents

Value of each position will be shown on mouse over .



Before filtering: read1: KMER counting

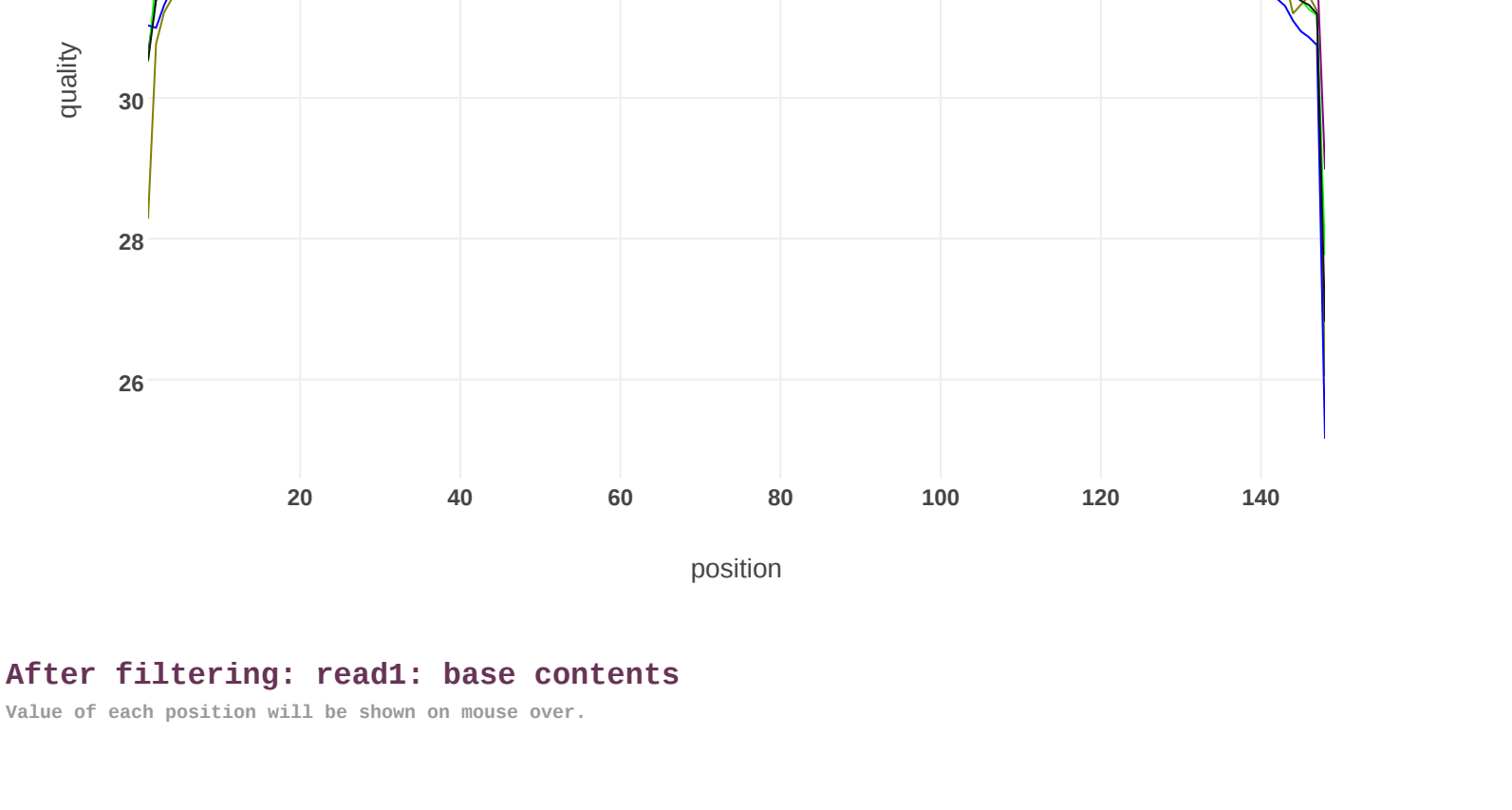
Darkar background means larger counts. The count will be shown on mouse over.



After filtering

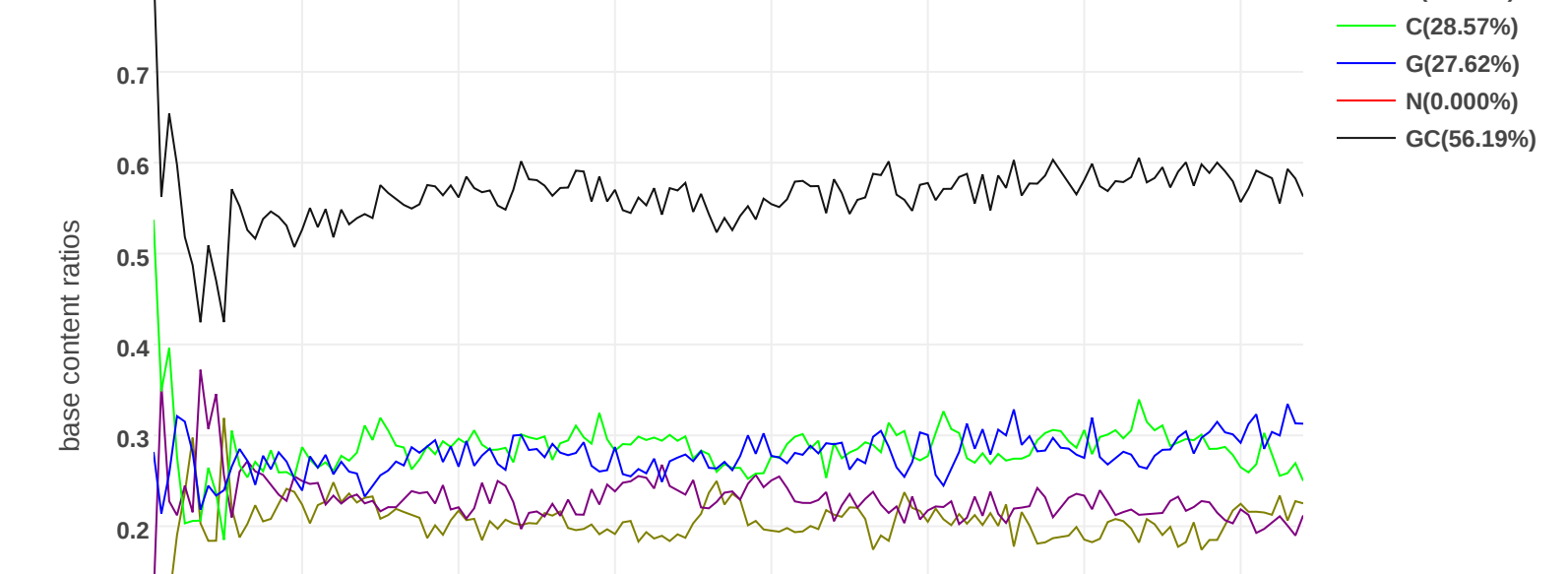
After filtering: read1: quality

Value of each position will be shown on mouse over .



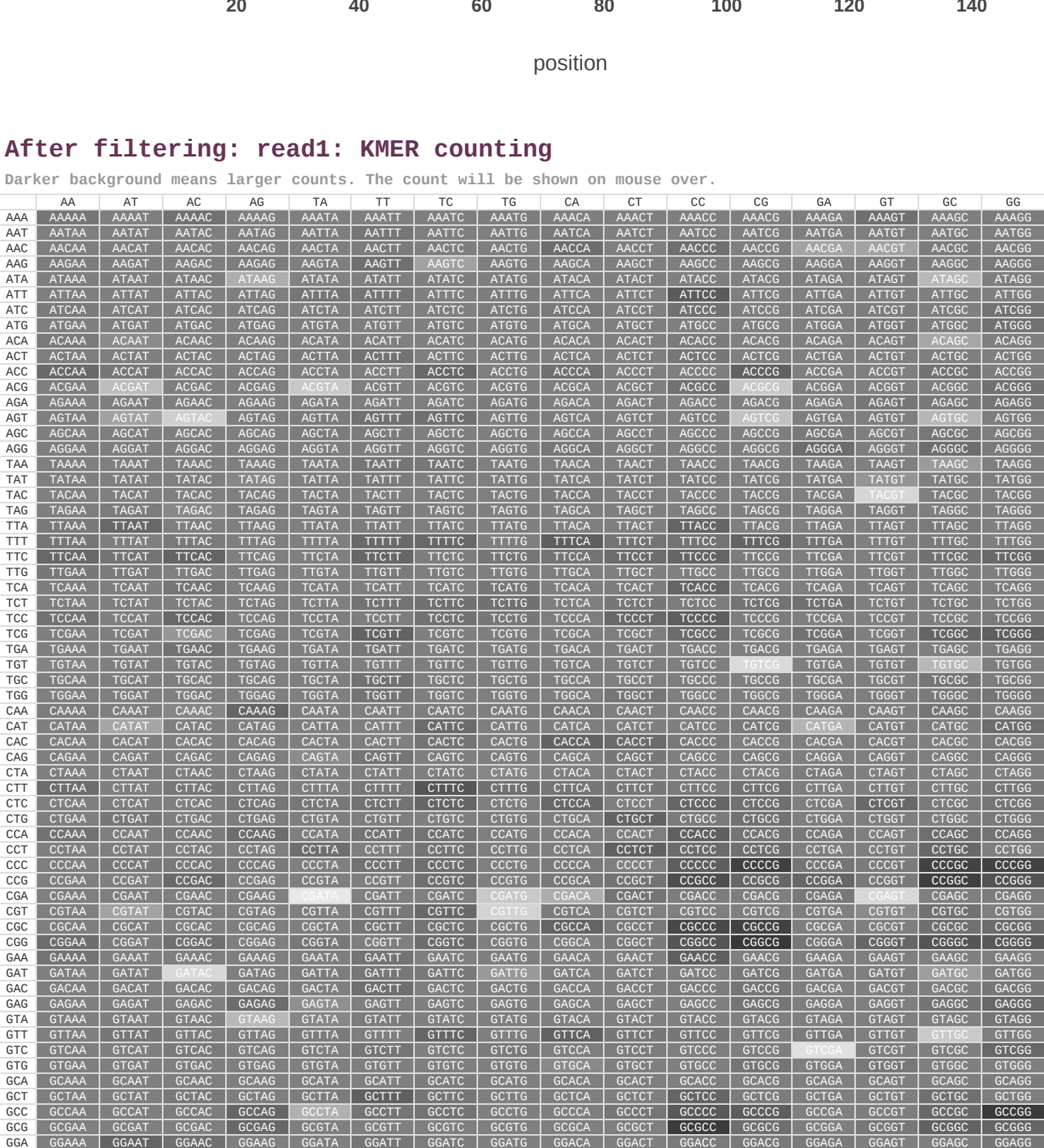
After filtering: read1: base contents

Value of each position will be shown on mouse over .



After filtering: read1: KMER counting

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



Test command

fastp 0.21.0, at 2023-02-26 16:19:49