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:	120bp
duplication rate:	62.739158% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Defens filtoning	

Before filtering total reads: 45.461404 M

total bases: 5.728137 G

5.397462 G (94.227176%) Q20 bases: Q30 bases: 4.961569 G (86.617504%) GC content: 52.468200%

After filtering total reads: 44.863915 M total bases: 5.410145 G

5.138826 G (94.984980%) Q20 bases: Q30 bases: 4.747385 G (87.749673%) GC content: 52.807475% Filtering result

reads passed filters: 44.863915 M (98.685723%) 571.190000 K (1.256428%) reads with low quality: reads with too many N: 4.723000 K (0.010389%) reads too short: 21.576000 K (0.047460%)

Adapters Adapter or bad ligation of read1

Sequence	Occurrences
AGATC	203183
AGATCG	169220
AGATCGG	164508
GATCGGA	157253
GATCGGAA	153985
GATCGGAAG	148867
GATCGGAAGA	141674
GATCGGAAGAG	139447
GATCGGAAGAGC	140061
GATCGGAAGAGCA	138941
GATCGGAAGAGCAC	134892
AGATCGGAAGAGCACA	130481
GATCGGAAGAGCACAC	123487
GATCGGAAGAGCACACG	122511
GATCGGAAGAGCACACGT	116445
GATCGGAAGAGCACACGTC	110768
GATCGGAAGAGCACACGTCT	108341
GATCGGAAGAGCACACGTCTG	105854
GATCGGAAGAGCACACGTCTGA	110039
GATCGGAAGAGCACACGTCTGAA	109972
SATCGGAAGAGCACACGTCTGAAC	99094
GATCGGAAGAGCACACGTCTGAACT	96174
GATCGGAAGAGCACACGTCTGAACTC	93389
GATCGGAAGAGCACACGTCTGAACTCC	91730
GATCGGAAGAGCACACGTCTGAACTCCA	89553
GATCGGAAGAGCACACGTCTGAACTCCAG	85878
GATCGGAAGAGCACACGTCTGAACTCCAGT	82280
GATCGGAAGAGCACACGTCTGAACTCCAGTC	80232
GATCGGAAGAGCACACGTCTGAACTCCAGTCA	79994
GATCGGAAGAGCACACGTCTGAACTCCAGTCAC	82355
GATCGGAAGAGCACACGTCTGAACTCCAGTCACA	90075
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAT	135463
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATT	83040
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATTA	89297
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATTAC	71944
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACT	77365
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTC	78338

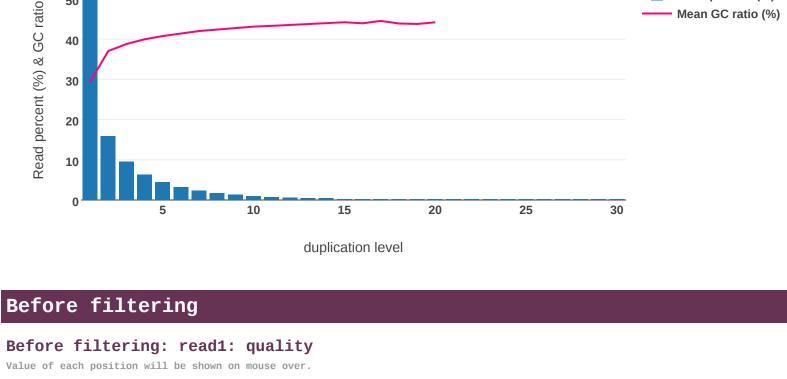
50

other adapter sequences

Duplication

AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCG

AGATCGGAAGACCACACTCTGAACTCCAGTCACATTACTCGA



duplication rate (62.739158%)

94208

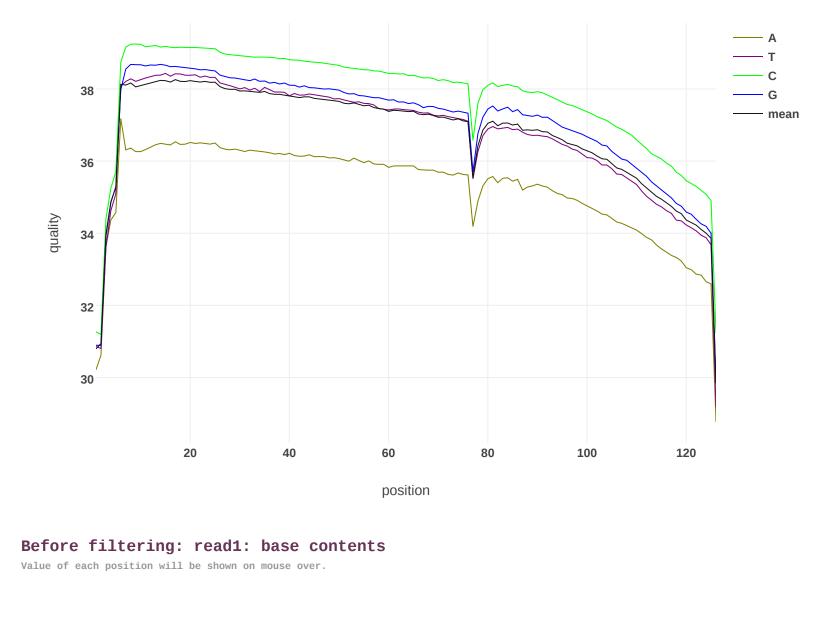
114521 2533816

Read percent (%)

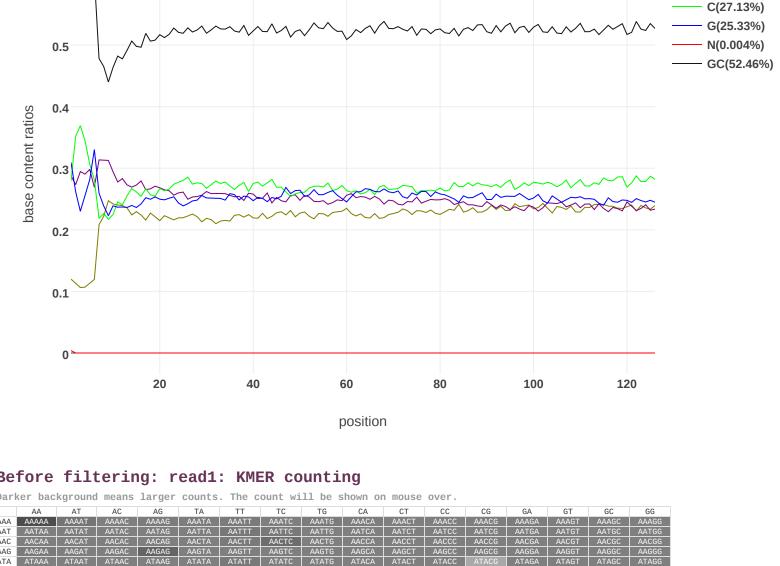
Mean GC ratio (%)

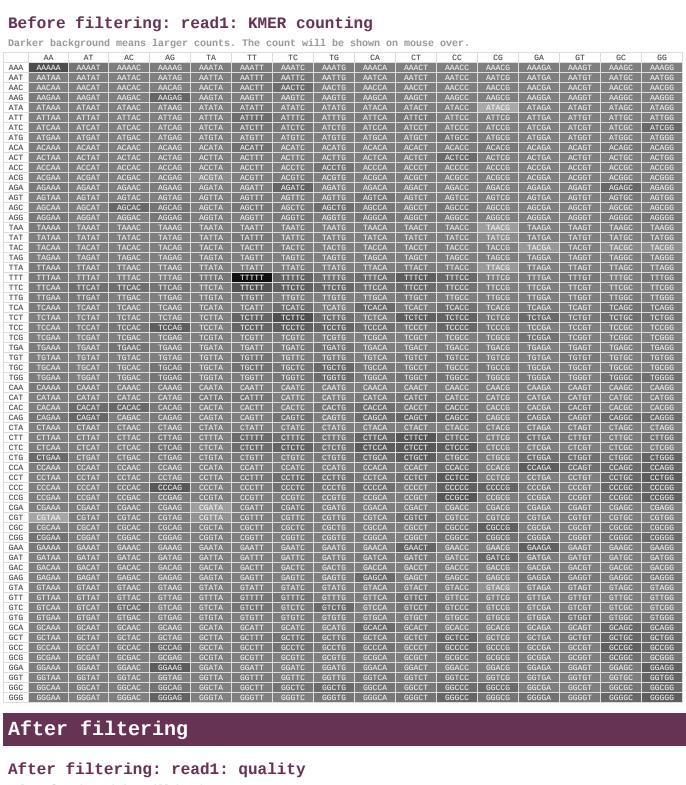
- A(22.31%)

- T(25.20%)

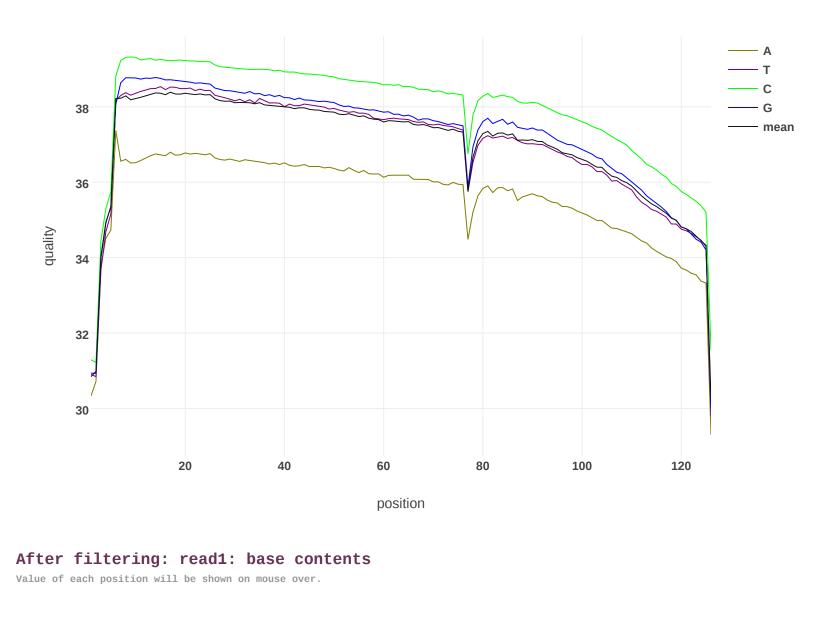


0.6

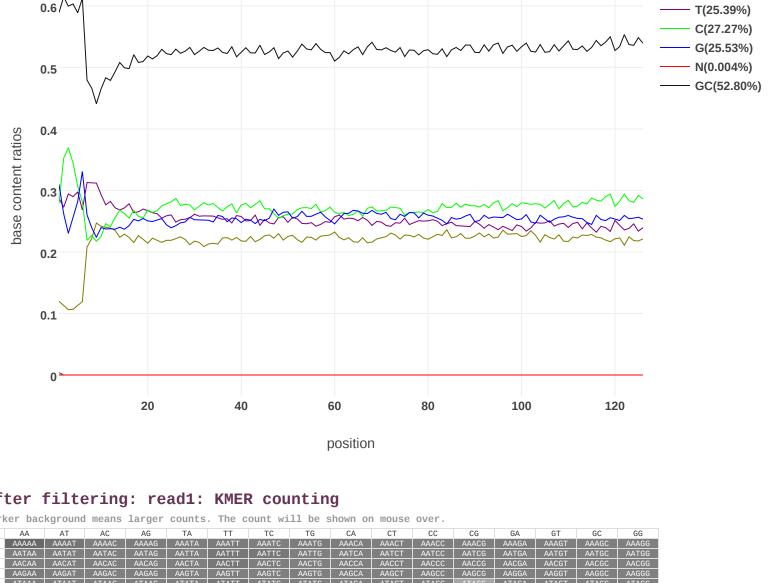




Value of each position will be shown on mouse over.



0.6



- A(21.78%)

