

# Rfastp Report

## Summary

General	
fastp version:	0.21.0 ( <a href="https://github.com/OpenGene/fastp">https://github.com/OpenGene/fastp</a> )
sequencing:	single end (148 cycles)
mean length before filtering:	148bp
mean length after filtering:	103bp
duplication rate:	7.818643% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

## Before filtering

total reads:	55.298915 M
total bases:	8.184106 G
Q20 bases:	7.180657 G (87.739654%)
Q30 bases:	6.752060 G (82.502103%)
GC content:	58.774653%

## After filtering

total reads:	47.263923 M
total bases:	4.871268 G
Q20 bases:	4.556968 G (93.547888%)
Q30 bases:	4.387680 G (90.072659%)
GC content:	56.527932%

## Filtering result

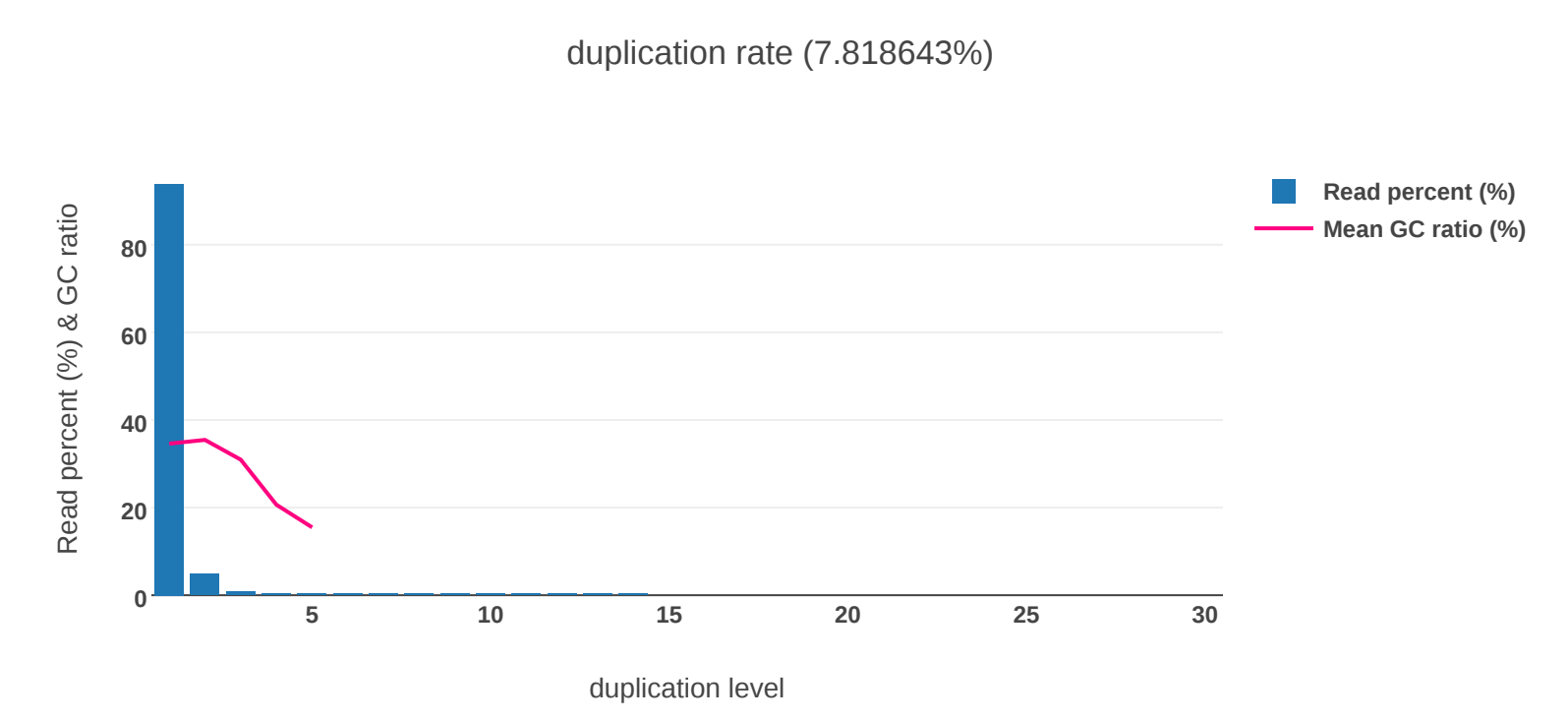
reads passed filters:	47.263923 M (85.46956%)
reads with low quality:	6.148562 M (11.118956%)
reads with too many N:	9.201090 K (0.016639%)
reads too short:	1.877229 M (3.394749%)

## Adapters

### Adapter or bad ligation of read1

Sequence	Occurrences
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	2128885
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCAGTCACGTGAACGATCTCGTATGCCGCTCTTCTGCTTGA AAAA	384928
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAACGATCTCGTATGCCGCTCTTCTGCTTGA AAAA	377537
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAACGATCTCGTATGCCGCTCTTCTGCTTGA AAAA	375373
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAACGATCTCGTATGCCGCTCTTCTGCTTGA AAAA	379867
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAACGATCTCGTATGCCGCTCTTCTGCTTGA AAAA	394396
other adapter sequences	33399893

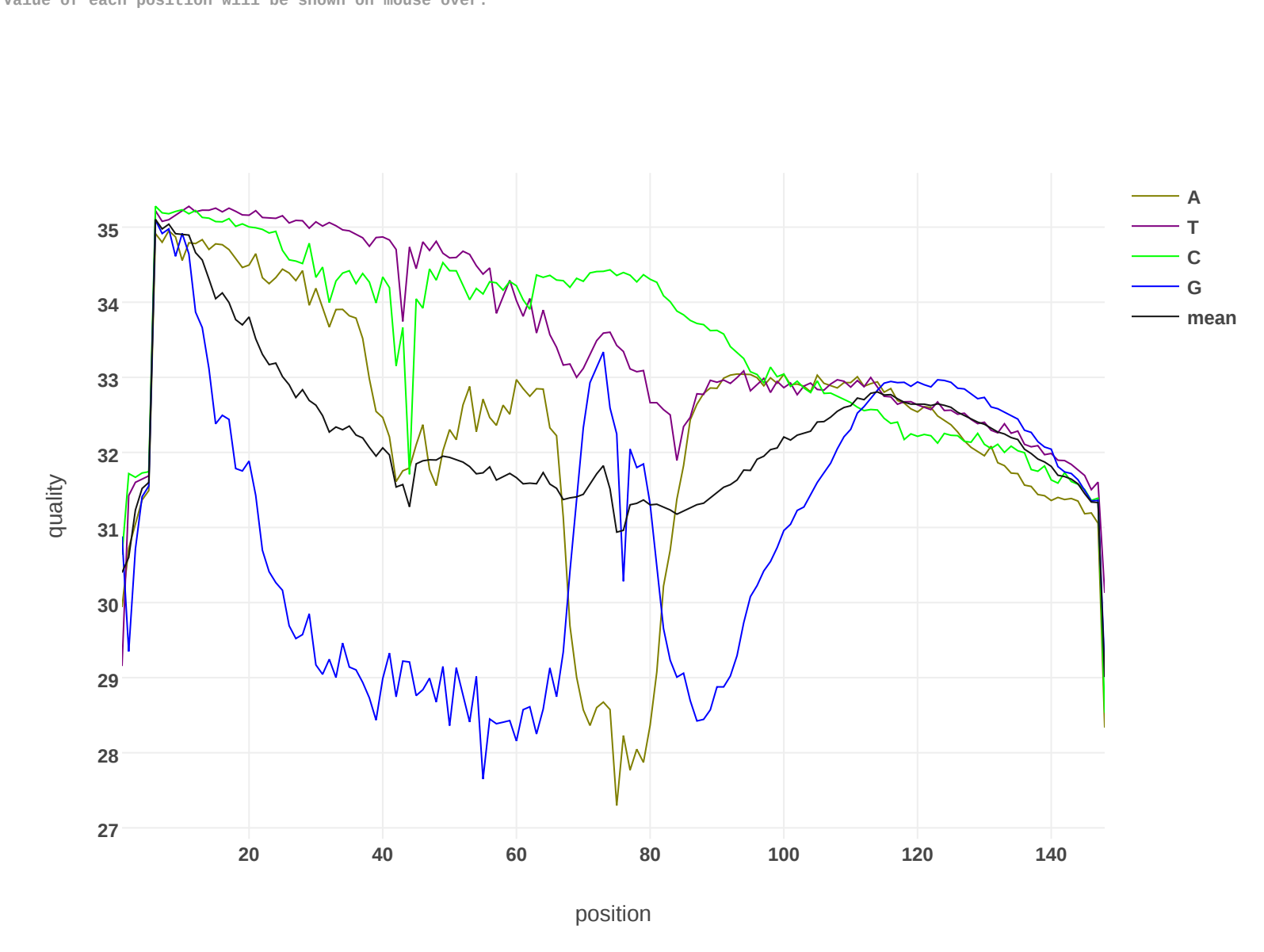
## Duplication



## Before filtering

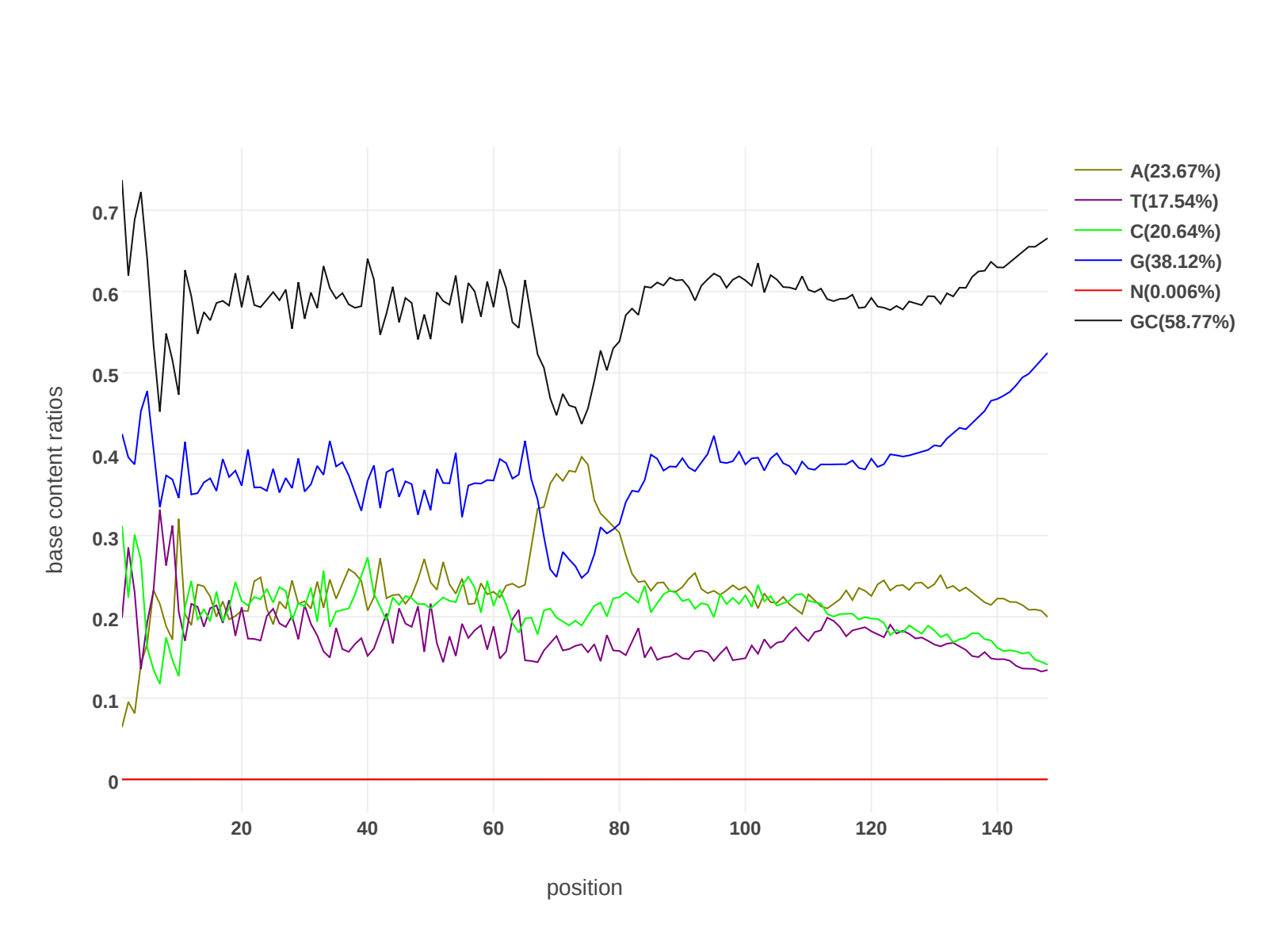
### Before filtering: read1: quality

Value of each position will be shown on mouse over.



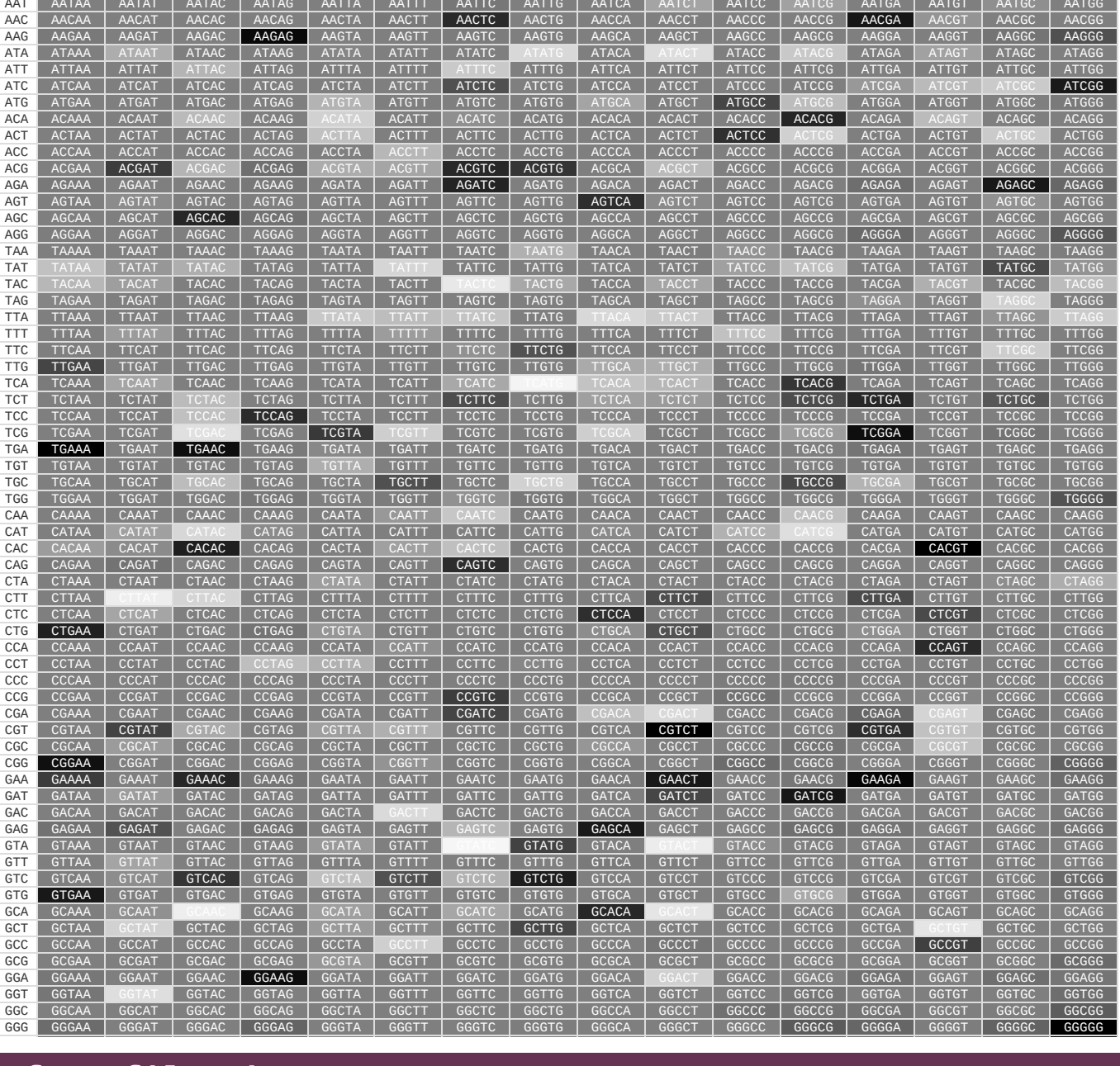
### Before filtering: read1: base contents

Value of each position will be shown on mouse over.



### Before filtering: read1: KMER counting

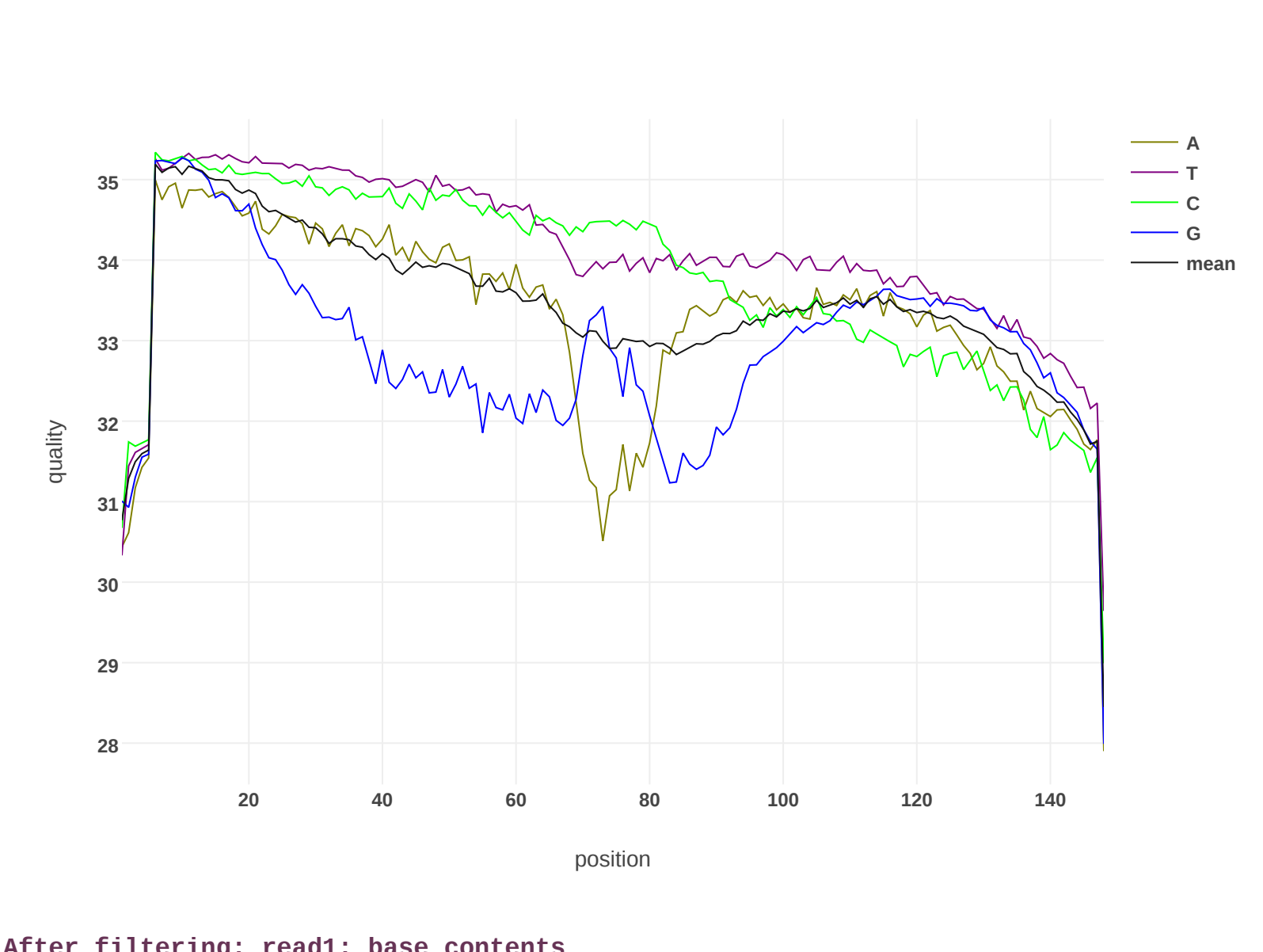
Darker background means larger counts. The count will be shown on mouse over.



## After filtering

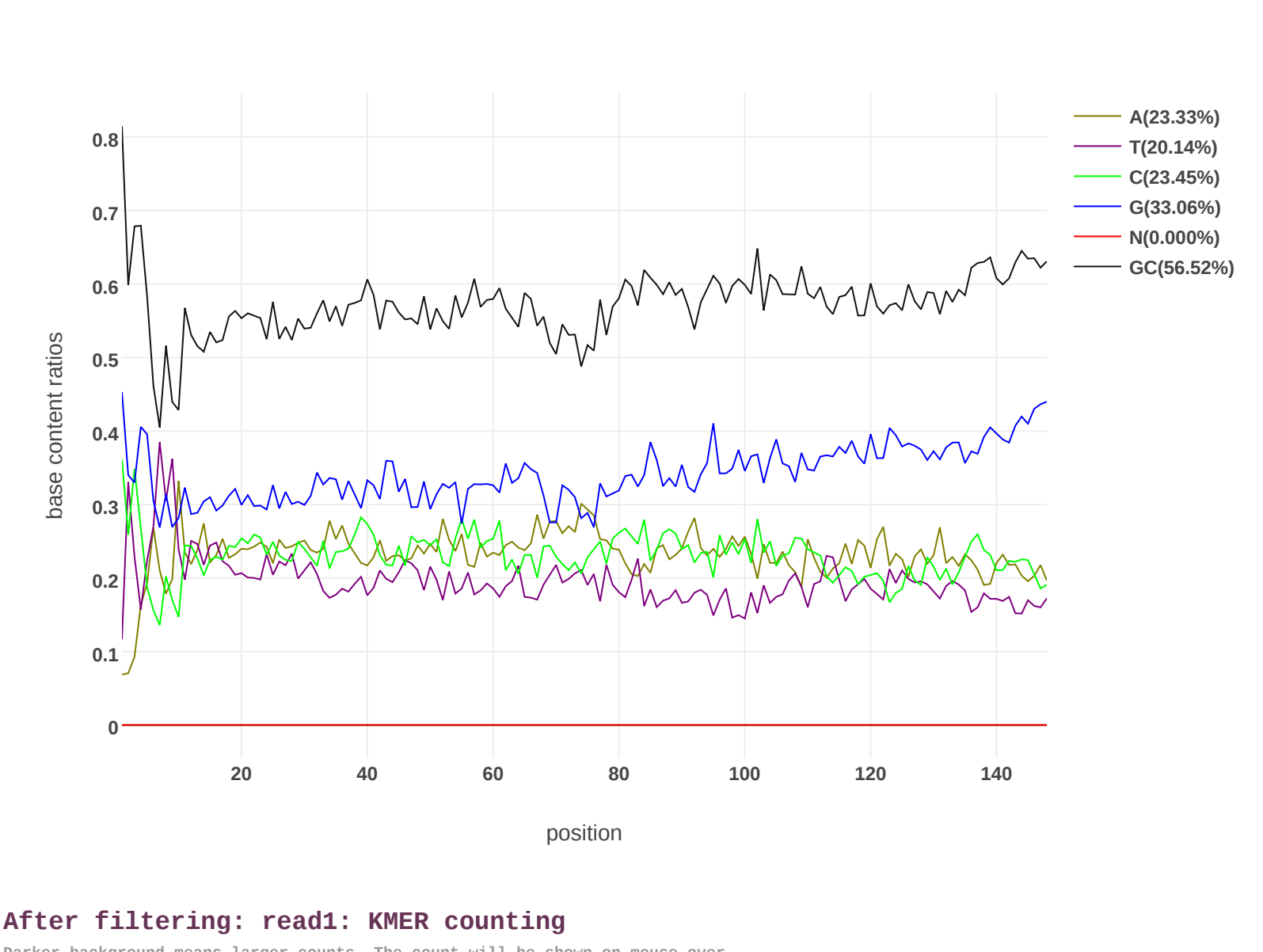
### After filtering: read1: quality

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.

