SRR7973880

Summary

General

fastp version:	0.20.0 (https://github.com/OpenGene/fastp)
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	138bp, 138bp
mean length after filtering:	130bp, 130bp
duplication rate:	54.422938%
Insert size peak:	151

Before filtering

total reads:	451.413450 M
total bases:	62.563999 G
Q20 bases:	45.854462 G (73.292088%)
Q30 bases:	42.008316 G (67.144550%)
GC content:	33.910754%

After filtering

total reads:	251.128204 M
total bases:	32.741591 G
Q20 bases:	31.164613 G (95.183562%)
Q30 bases:	28.810100 G (87.992364%)
GC content:	42.730511%

Filtering result

reads passed filters:	251.128204 M (55.631529%)
reads with low quality:	30.868710 M (6.838234%)
reads with too many N:	3.136000 K (0.000695%)
reads too short:	167.485482 M (37.102457%)
reads with low complexity:	1.927918 M (0.427085%)

Adapters

Adapter or bad ligation of read1

The input has little adapter percentage (~0.307789%), probably it's trimmed before.

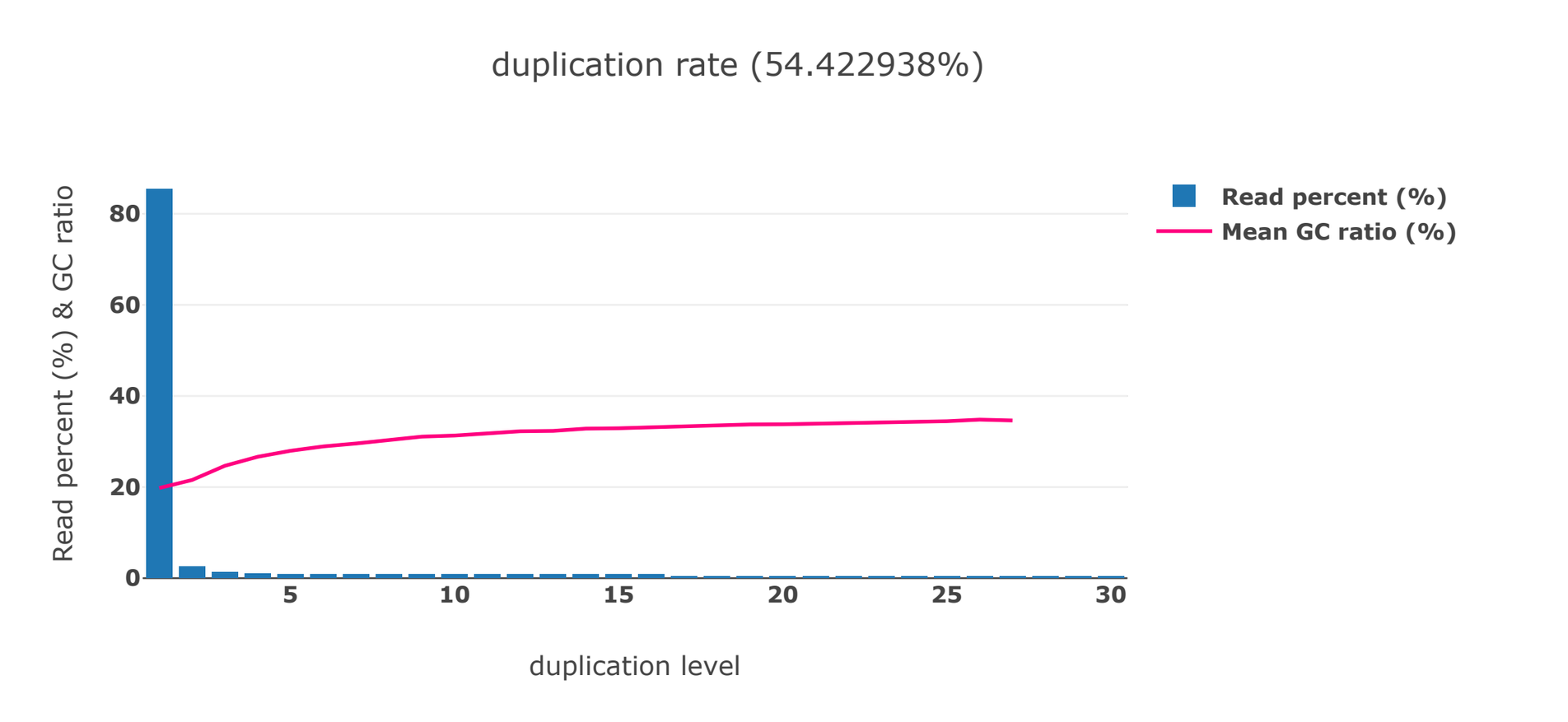
Sequence	Occurrences
AAAAAA	88206
AATGAT	47954
CAAGCA	47884
CTGTCT	82388
TACACT	47300
TTTTTT	82656
CTCTCTCT	173865
CTCTCTCTCTCTCTCT	171175
GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC	749438
other adapter sequences	3060387

Adapter or bad ligation of read2

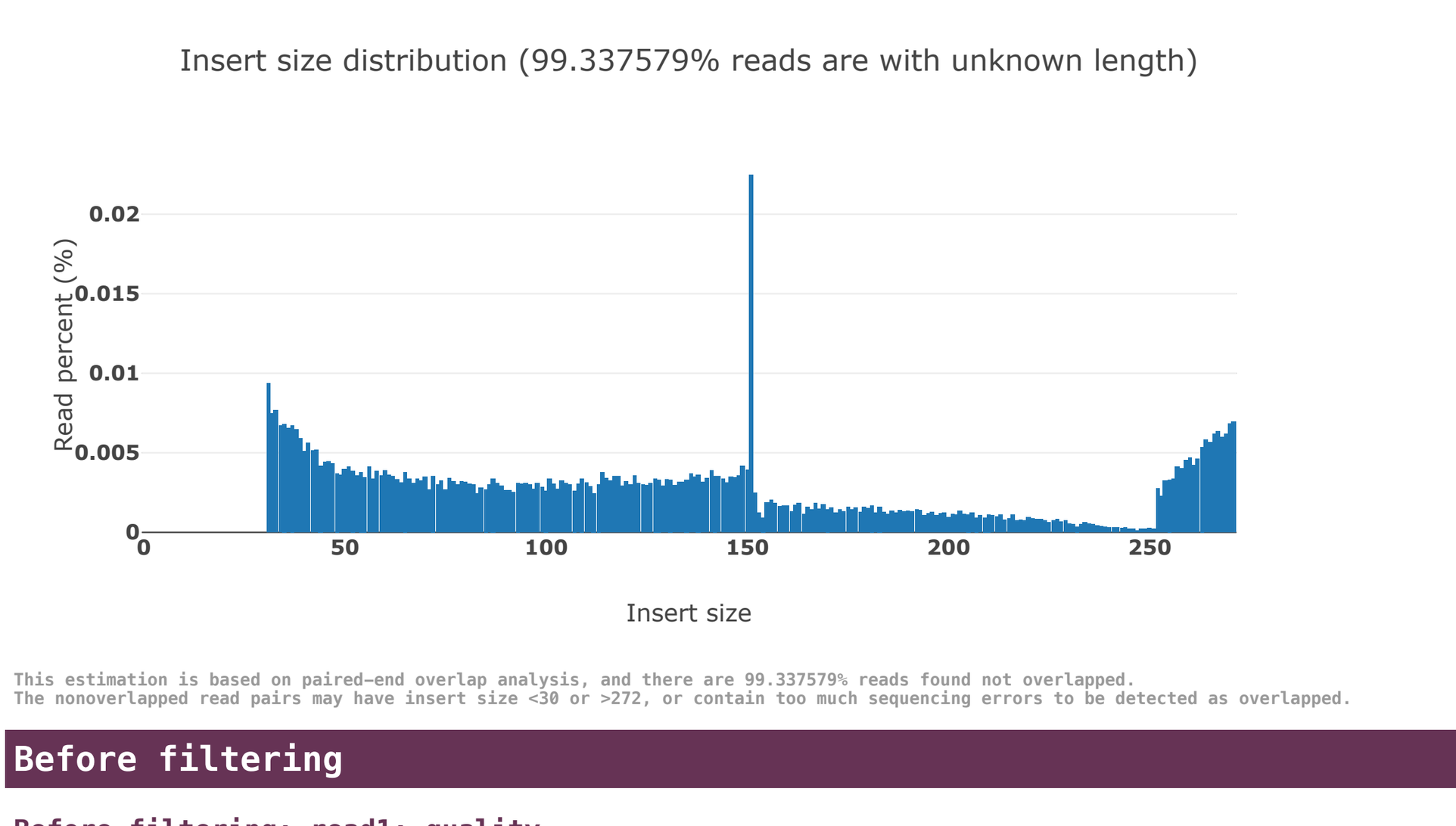
The input has little adapter percentage (~0.240199%), probably it's trimmed before.

Sequence	Occurrences
AAAAAA	87514
AATGAT	50135
AGATGT	42853
CAAGCA	46976
CTGTCT	85010
TACACT	47672
TTTTTT	88002
CTCTCTCT	177231
CTCTCTCTCTCTCTCT	167833
other adapter sequences	3067920

Duplication



Insert size estimation

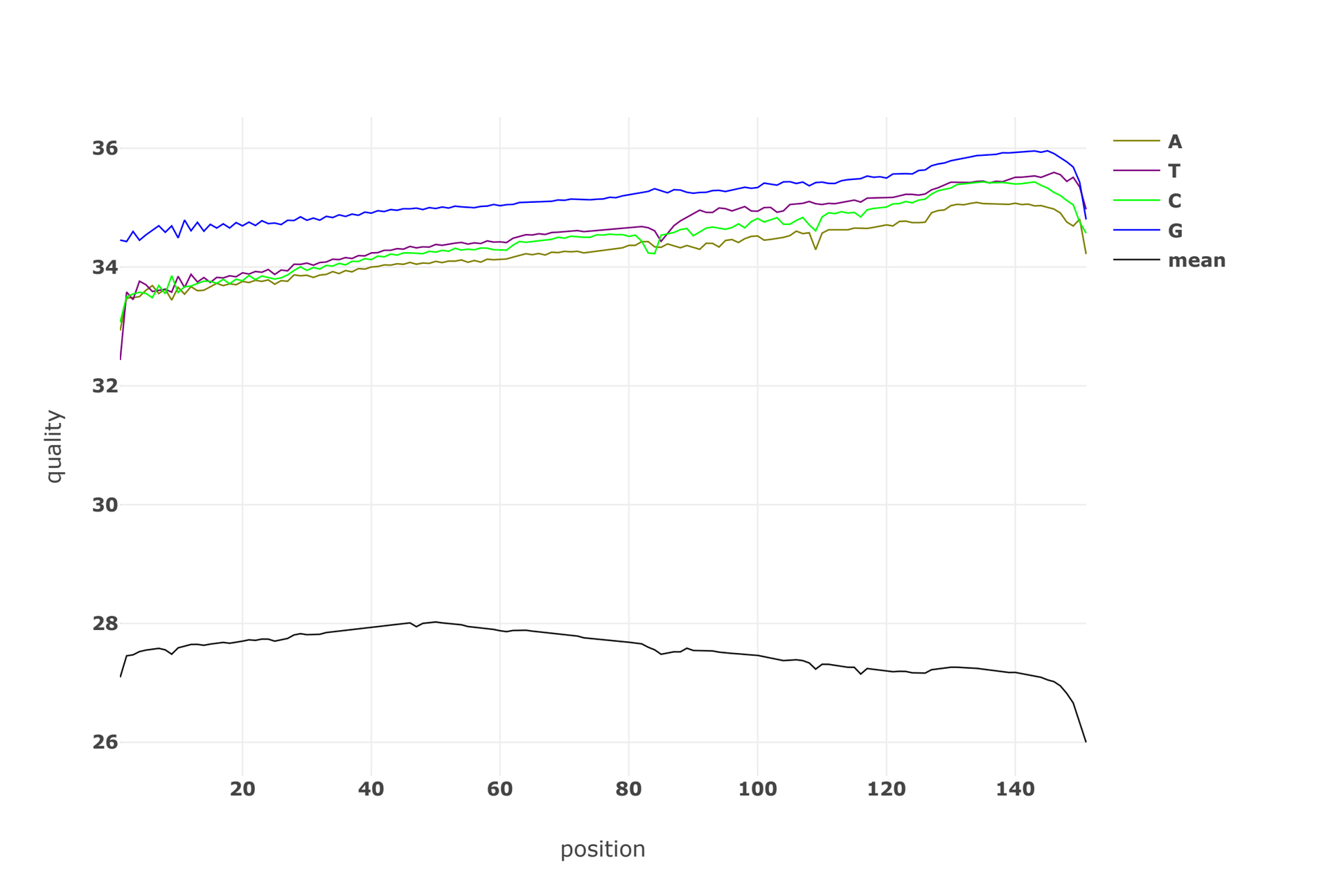


This estimation is based on paired-end overlap analysis, and there are 99.337579% reads found not overlapped.
The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

Before filtering

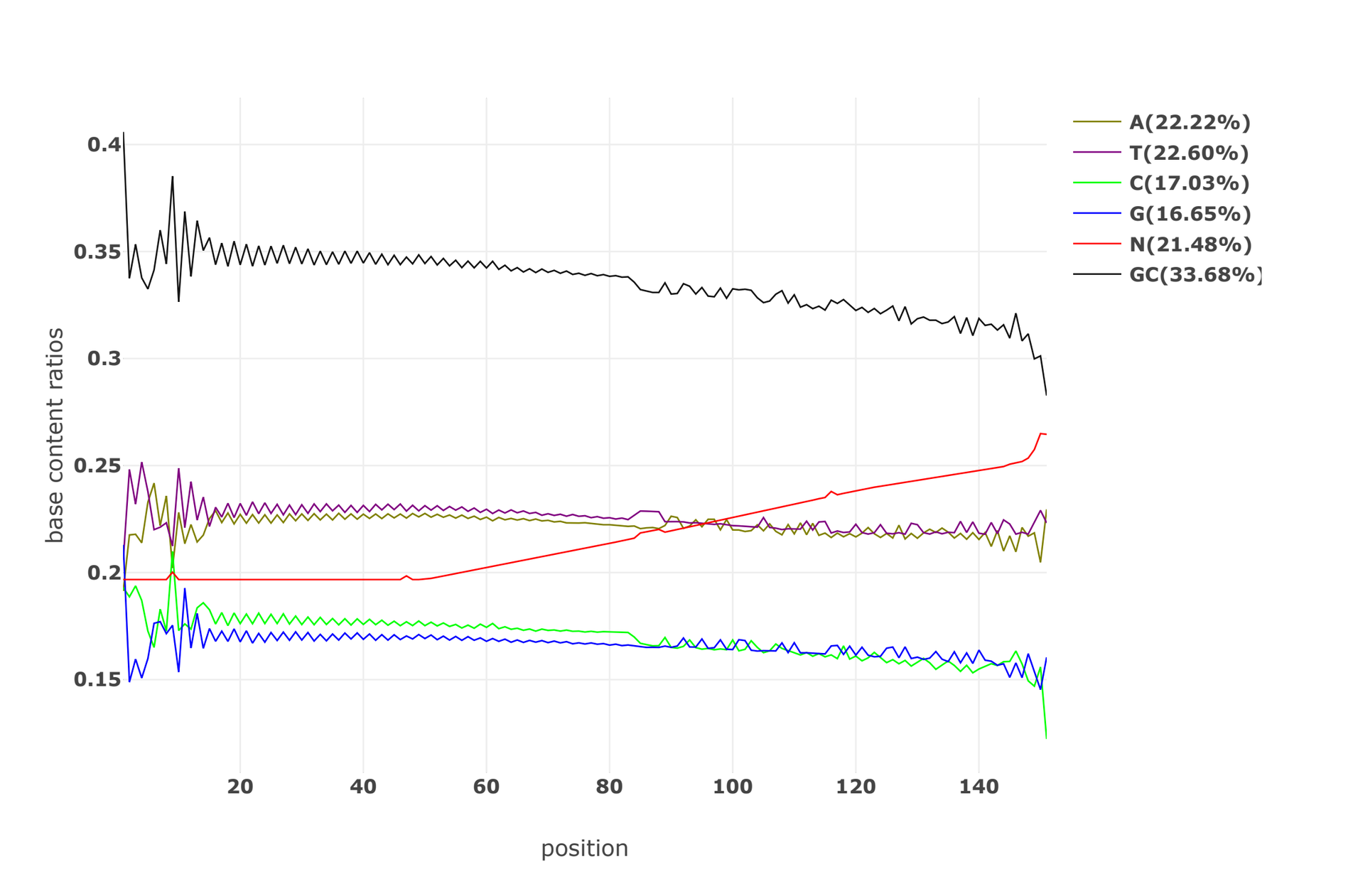
Before filtering: read1: quality

Value of each position will be shown on mouse over.



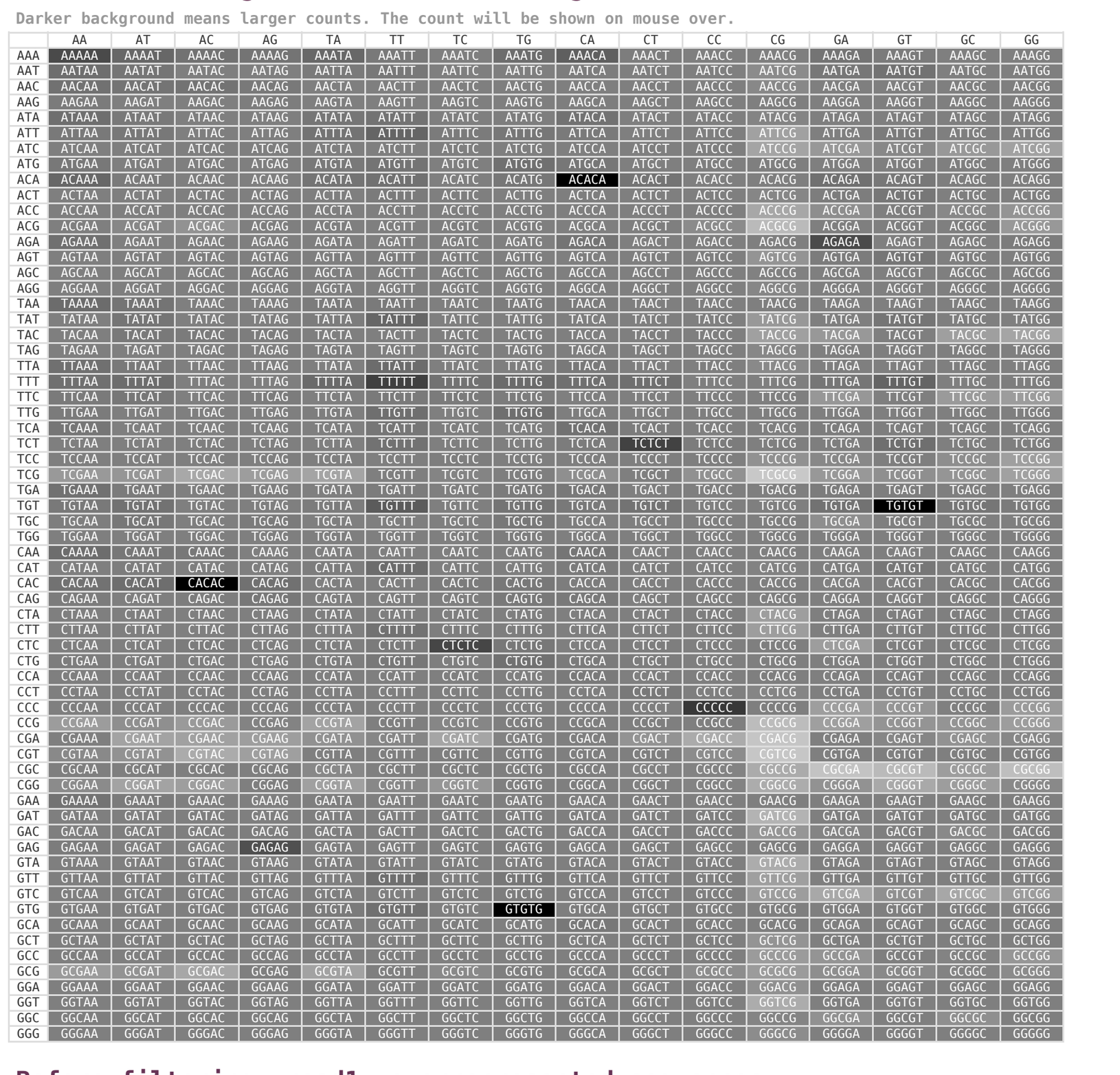
Before filtering: read1: base contents

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.



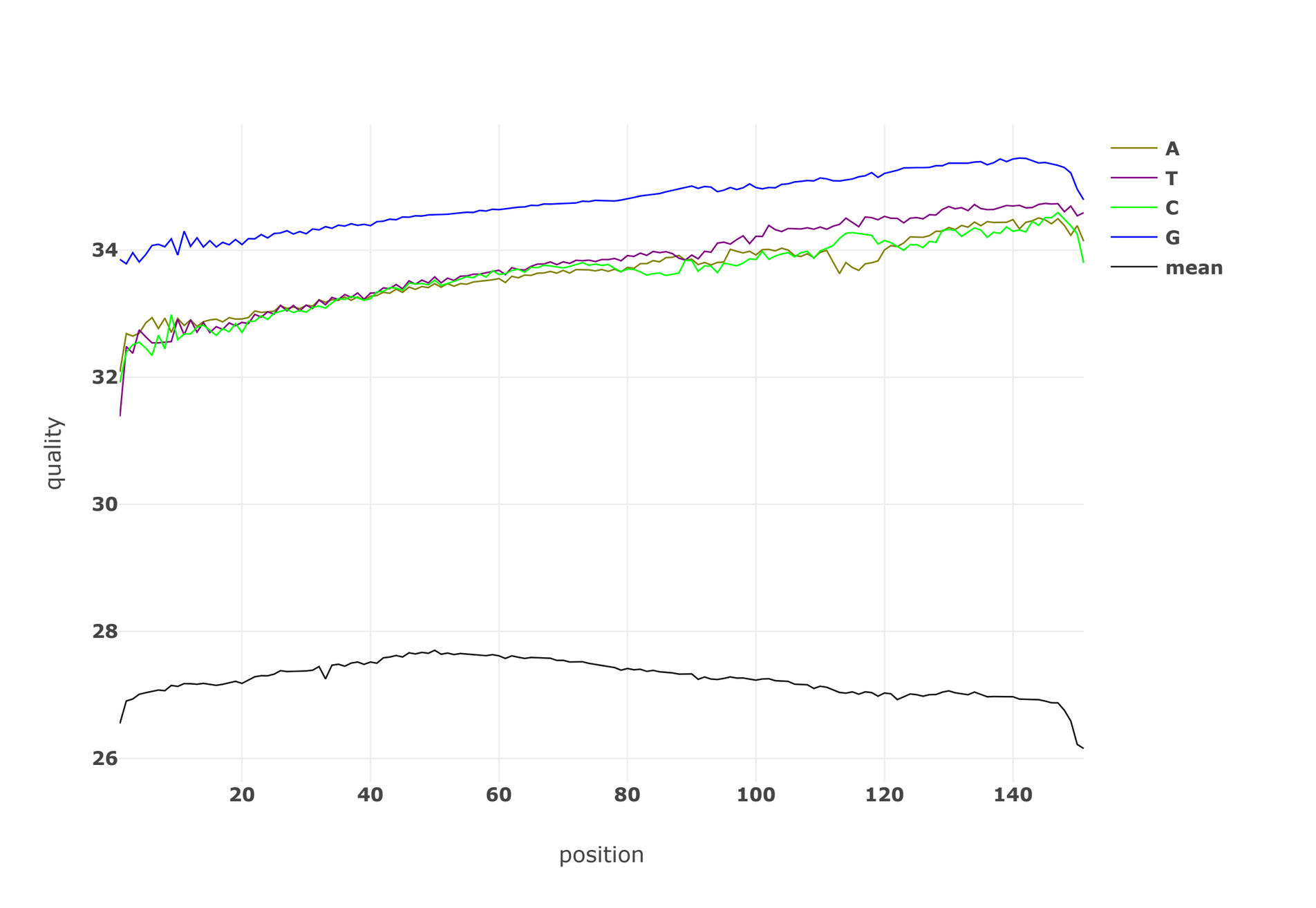
Before filtering: read1: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
not found		

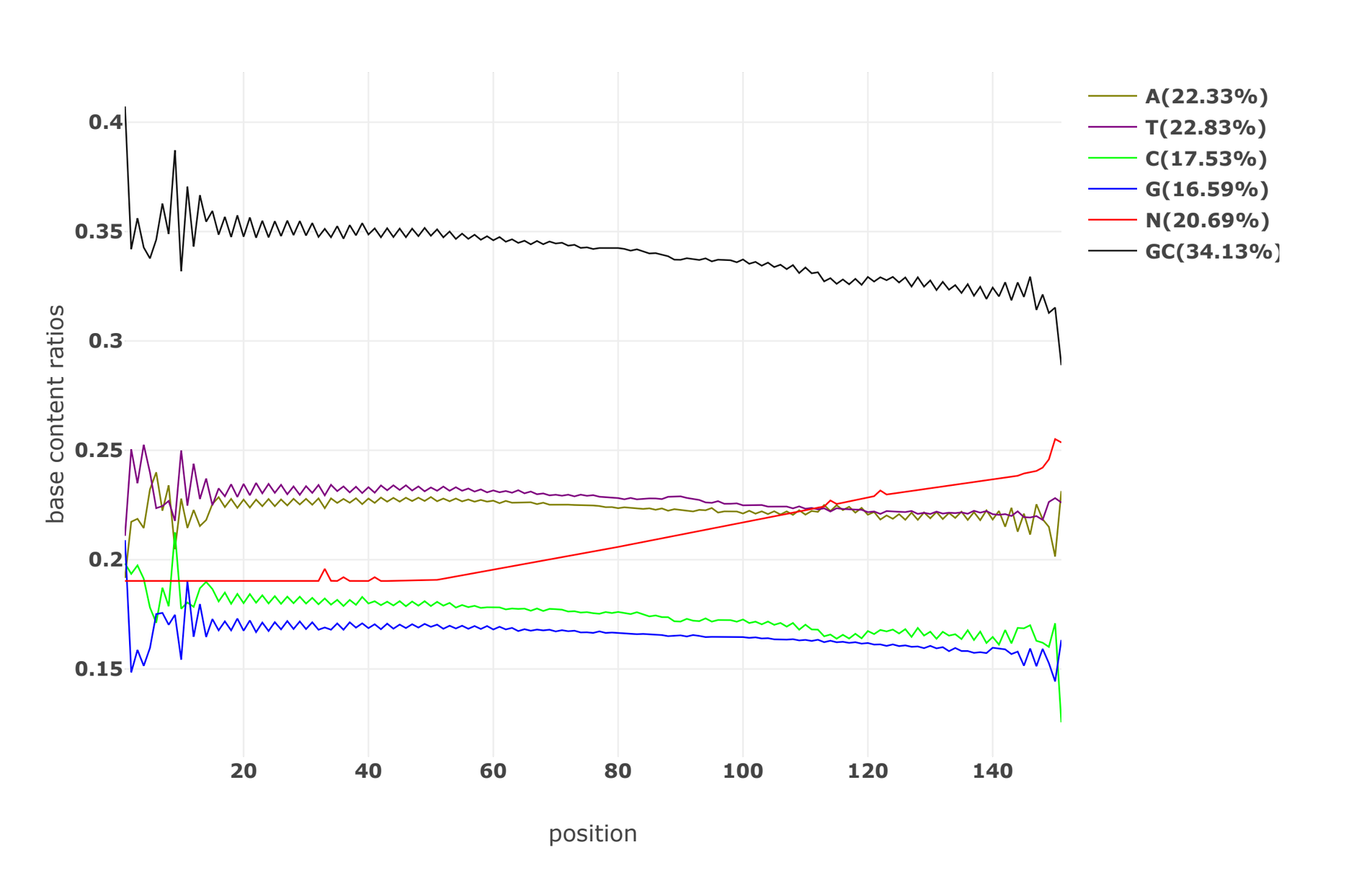
Before filtering: read2: quality

Value of each position will be shown on mouse over.



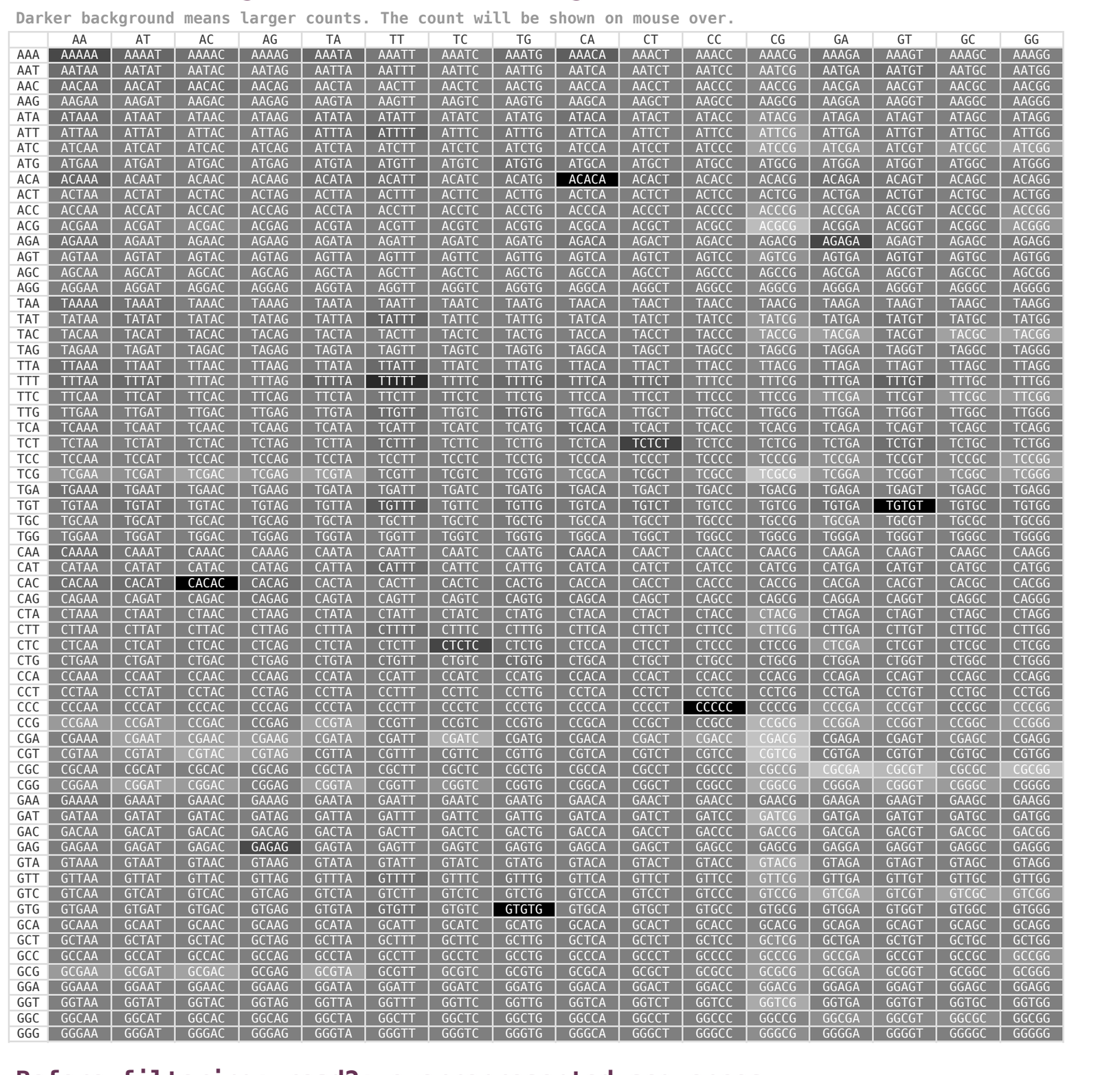
Before filtering: read2: base contents

Value of each position will be shown on mouse over.



Before filtering: read2: KMER counting

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



Before filtering: read2: overrepresented sequences

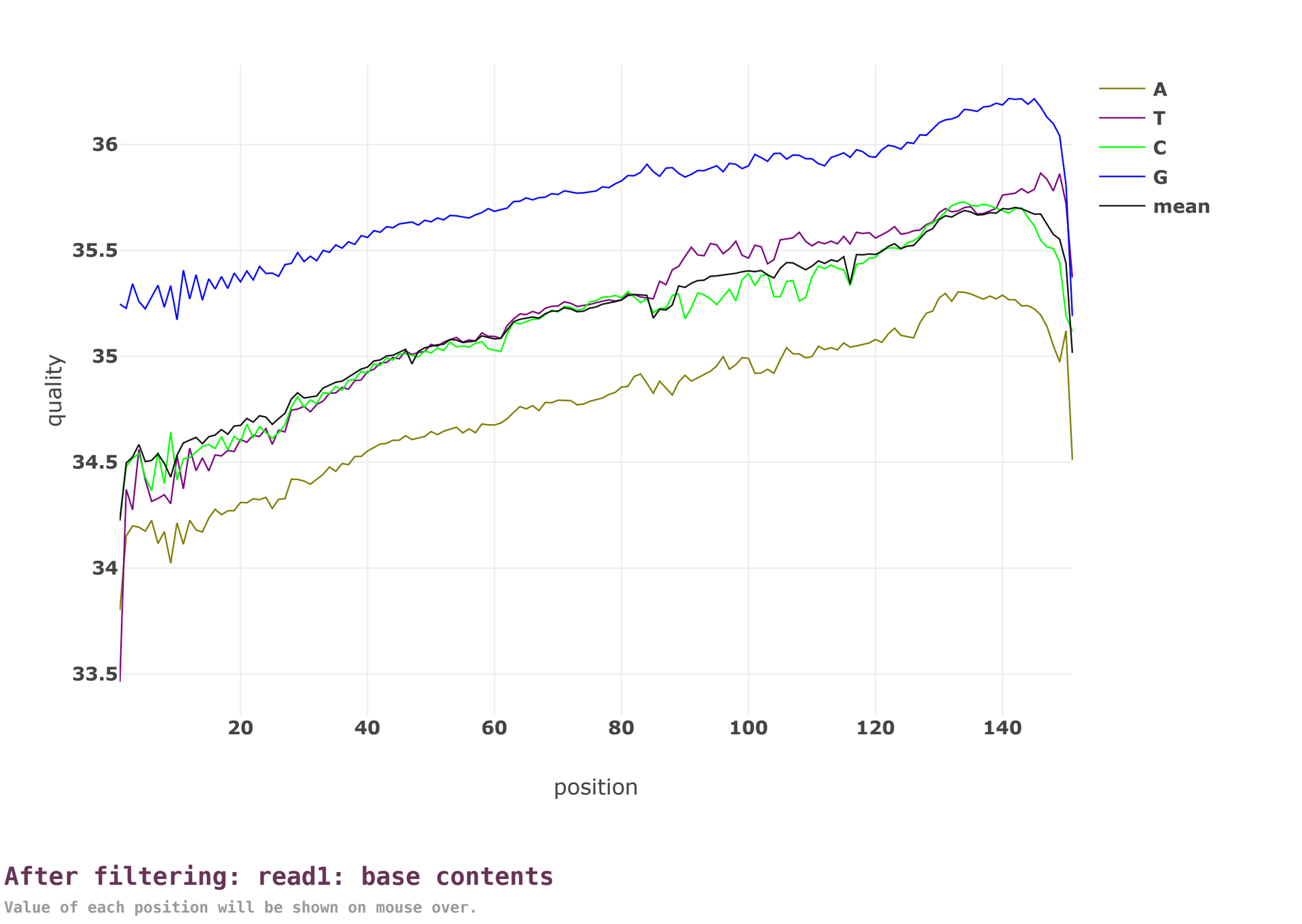
Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
not found		

After filtering

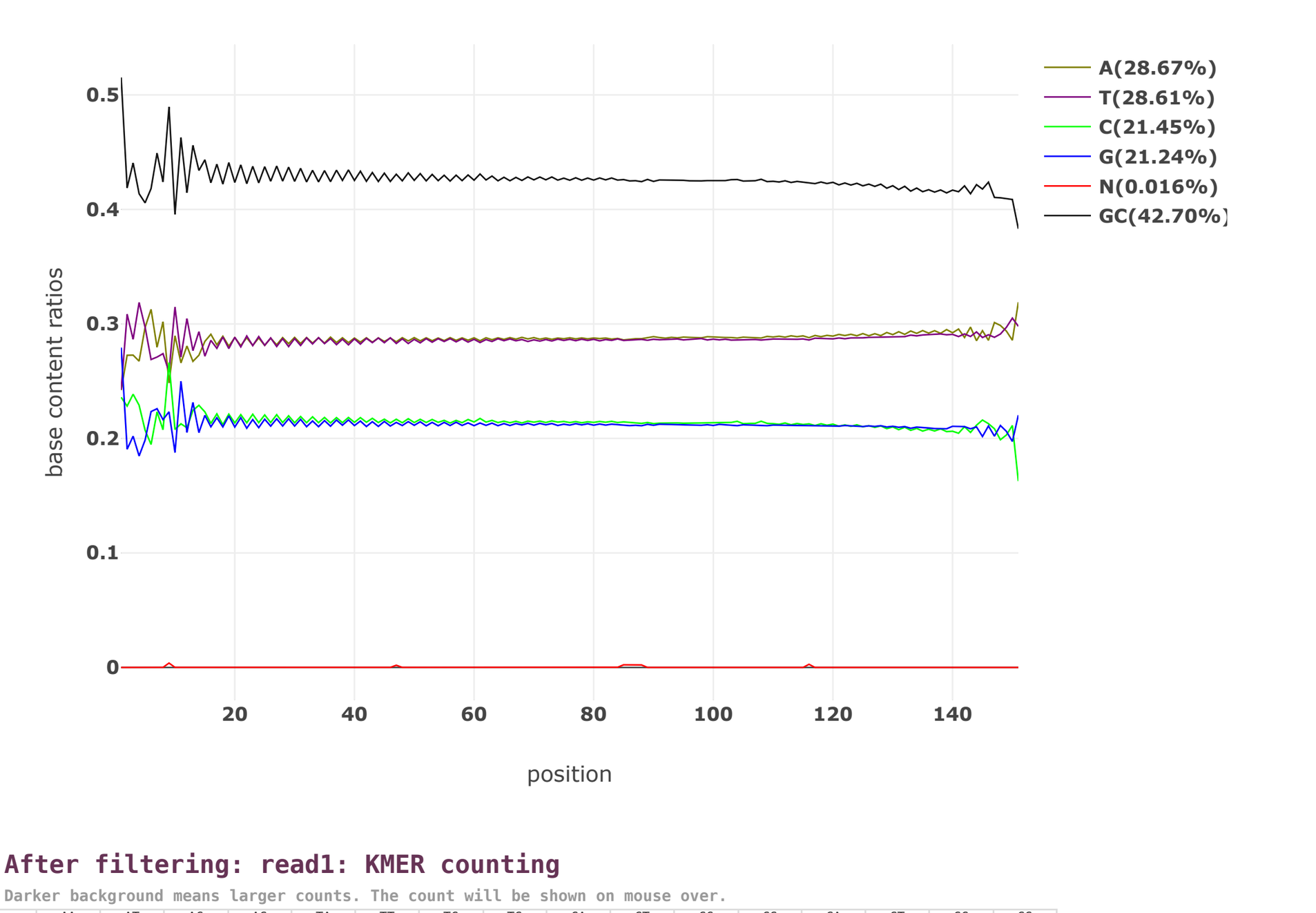
After filtering: read1: quality

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

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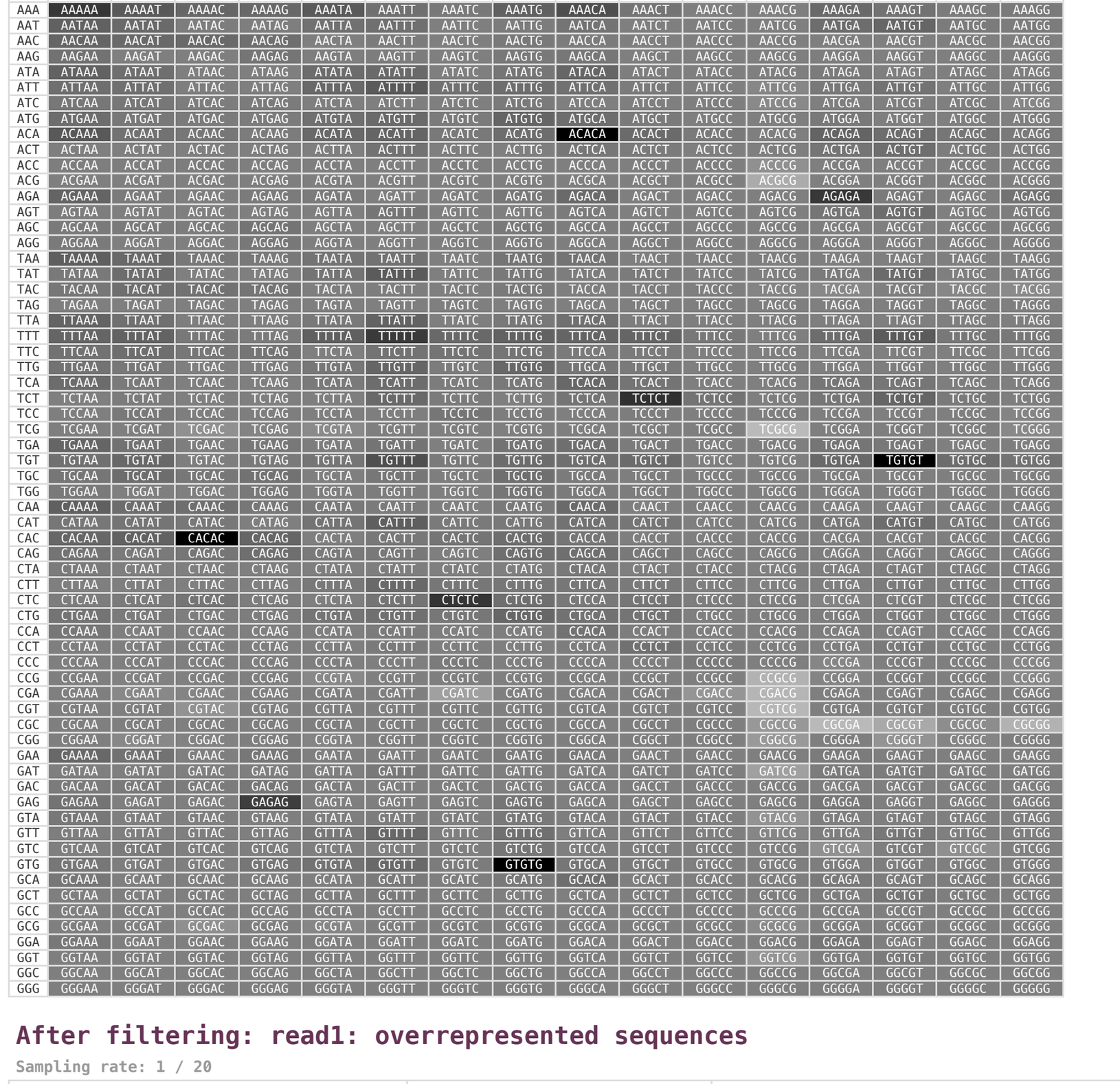


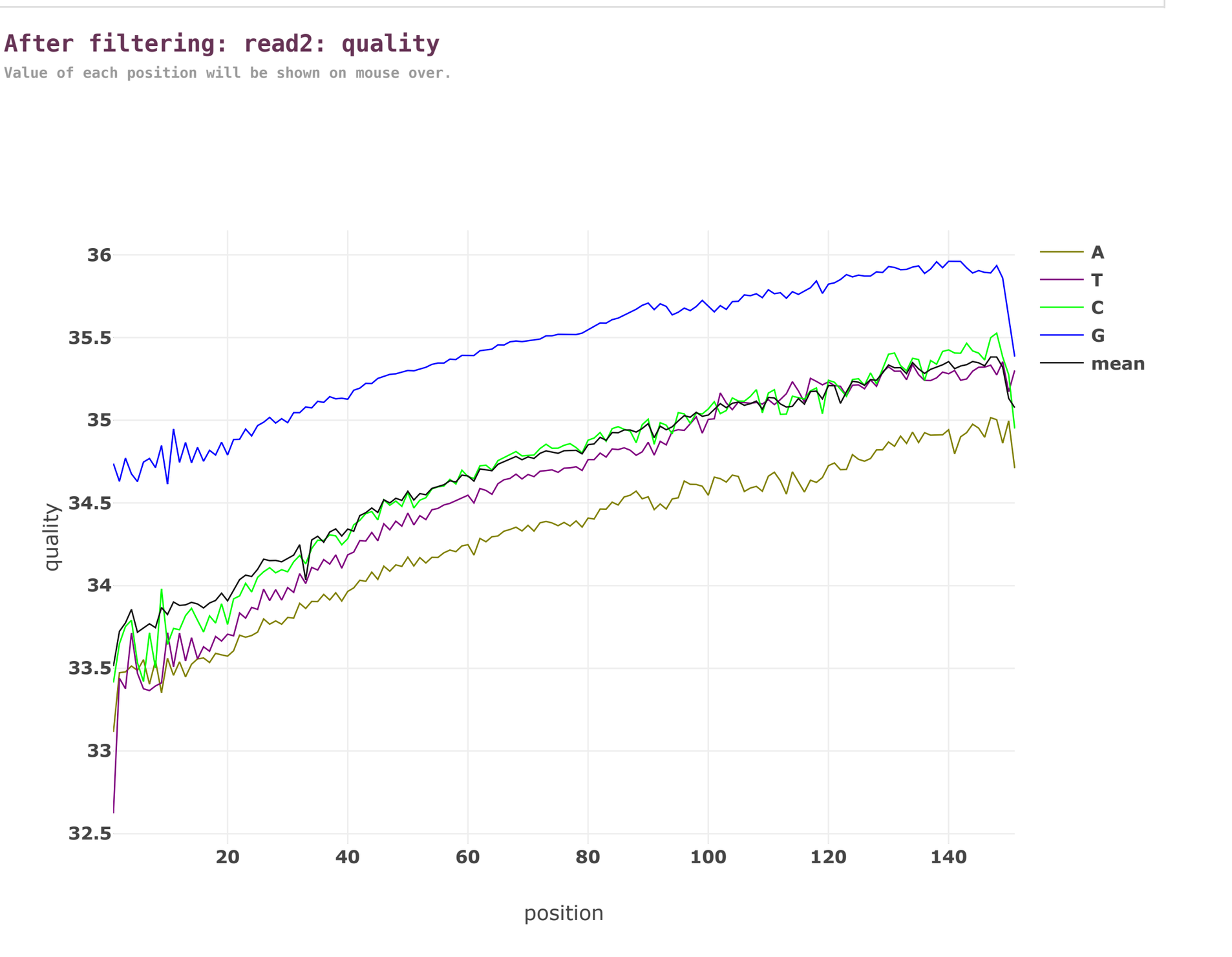
After filtering: read1: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
not found		

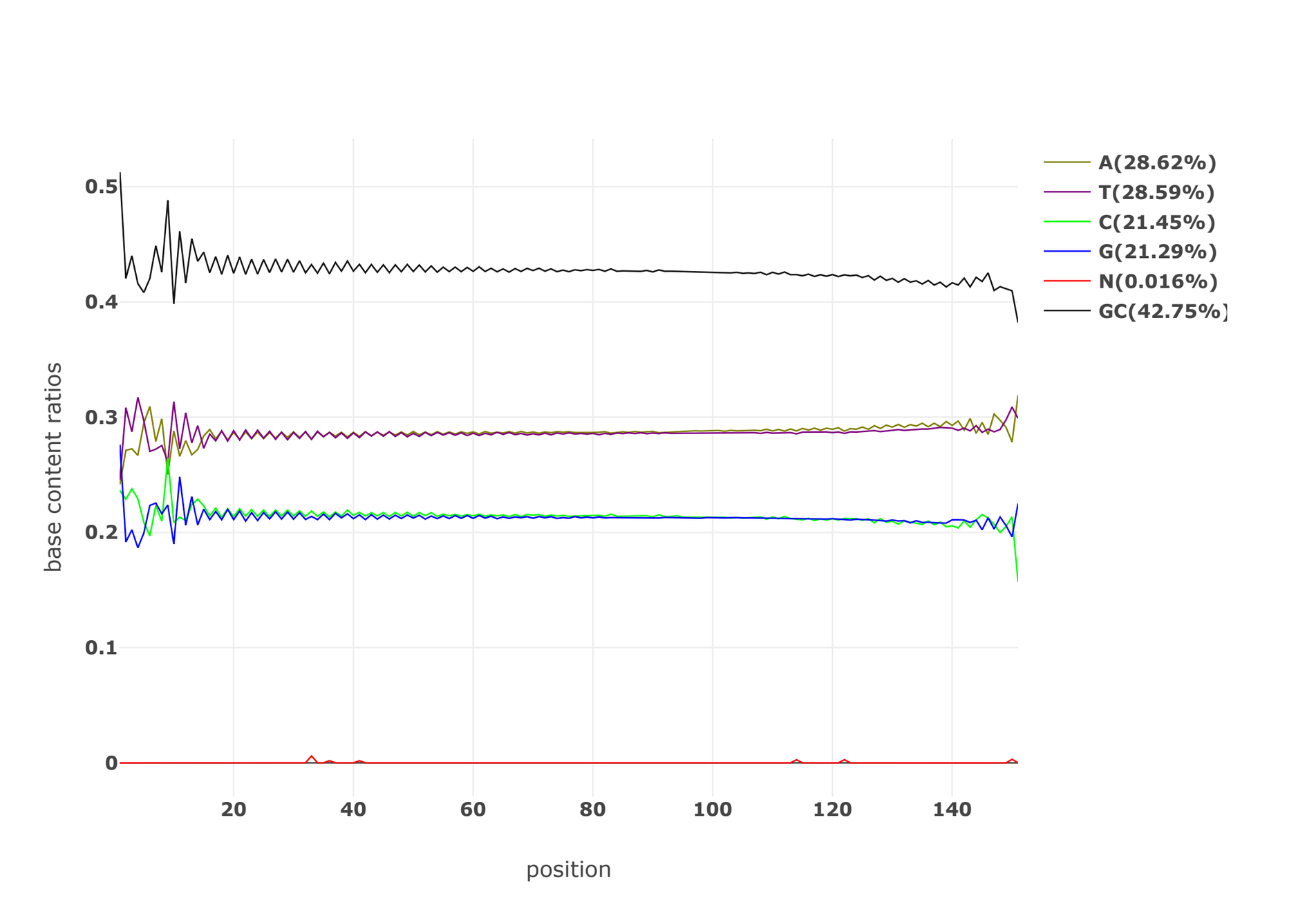
After filtering: read2: quality

Value of each position will be shown on mouse over.



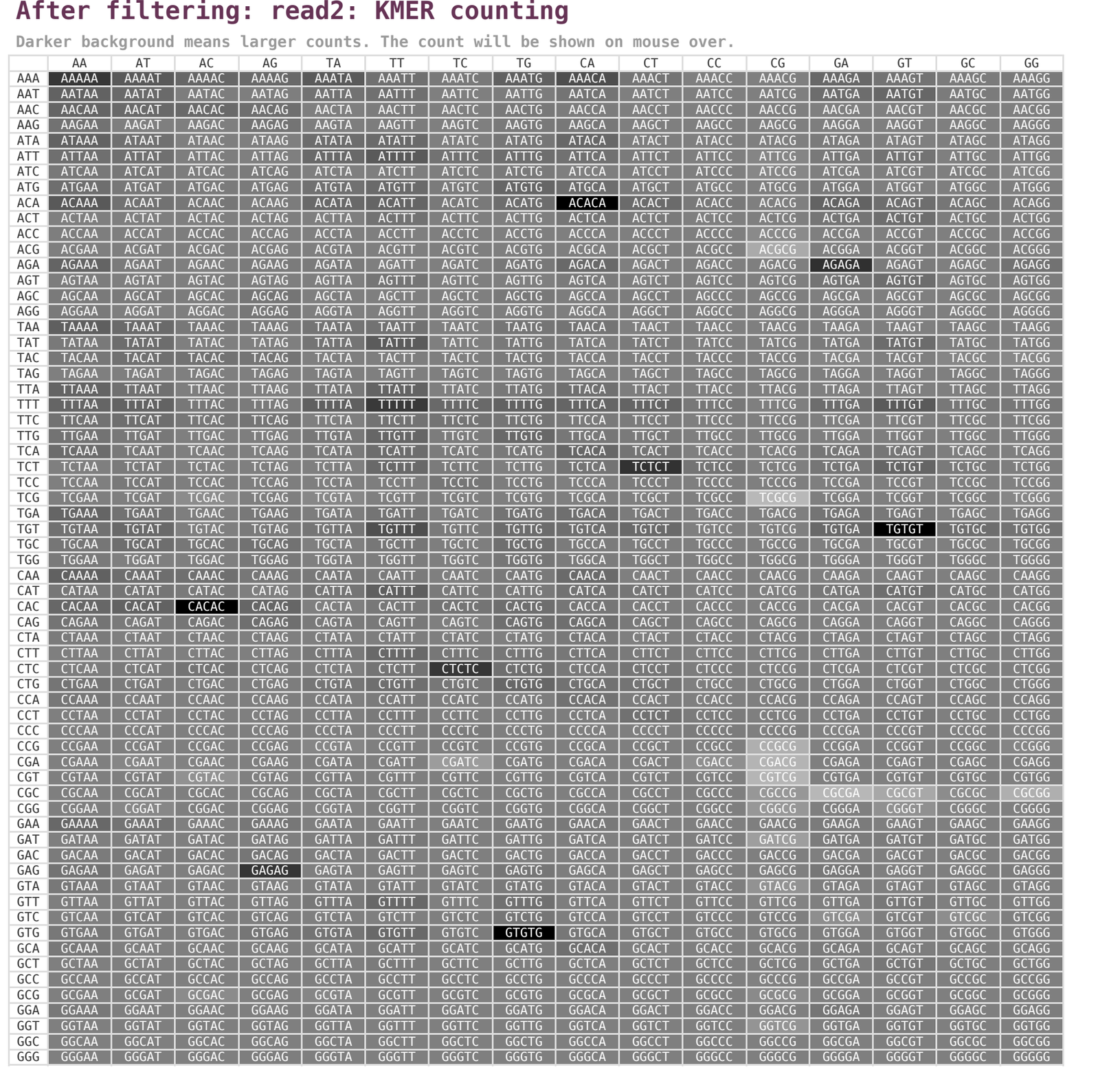
After filtering: read2: base contents

Value of each position will be shown on mouse over.



After filtering: read2: KMER counting

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



After filtering: read2: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
not found		

```
fastp --stdin --stdout --interleaved_in --adapter_fasta=/home/rfitak/.bin/adapters.fa --cut_front --cut_tail --cut_window_size=4 --cut_mean_quality=20 --qualified_quality_phred=20 --average_qual=20 --unqualified_percent_limit=30 --n_base_limit=5 --length_required=50 --low_complexity_filter --complexity_threshold=30 --overrepresentation_analysis --trim_poly_x --poly_x_min_len=10 --html=SRR7973880.html --report_title=SRR7973880 --thread=24
```

fastp 0.20.0, at 2024-11-19 05:18:22