

RTastp Report

Summary

fastp ver:

sequencing:	single end (126 cycles)
mean length before filtering:	126bp
mean length after filtering:	88bp
duplication rate:	61.958343% (may be overestimated since this is SE data)
Detected read adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Before filtering

total reads:	25,289,141
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total bases:

Q20 bases:	3.279958 G (96.337365%)
Q30 bases:	3.130849 G (92.070099%)
GC content:	58.470097%
After filtering	
total reads:	26.643859 M
total bases:	2.346268 G

220 hours:

GC content:	64.532993%
Filtering result	
reads passed filters:	26.643859 M (98.724321%)
reads with low quality:	64.381000 K (0.238256%)
reads with too many N:	9.273800 K (0.034360%)

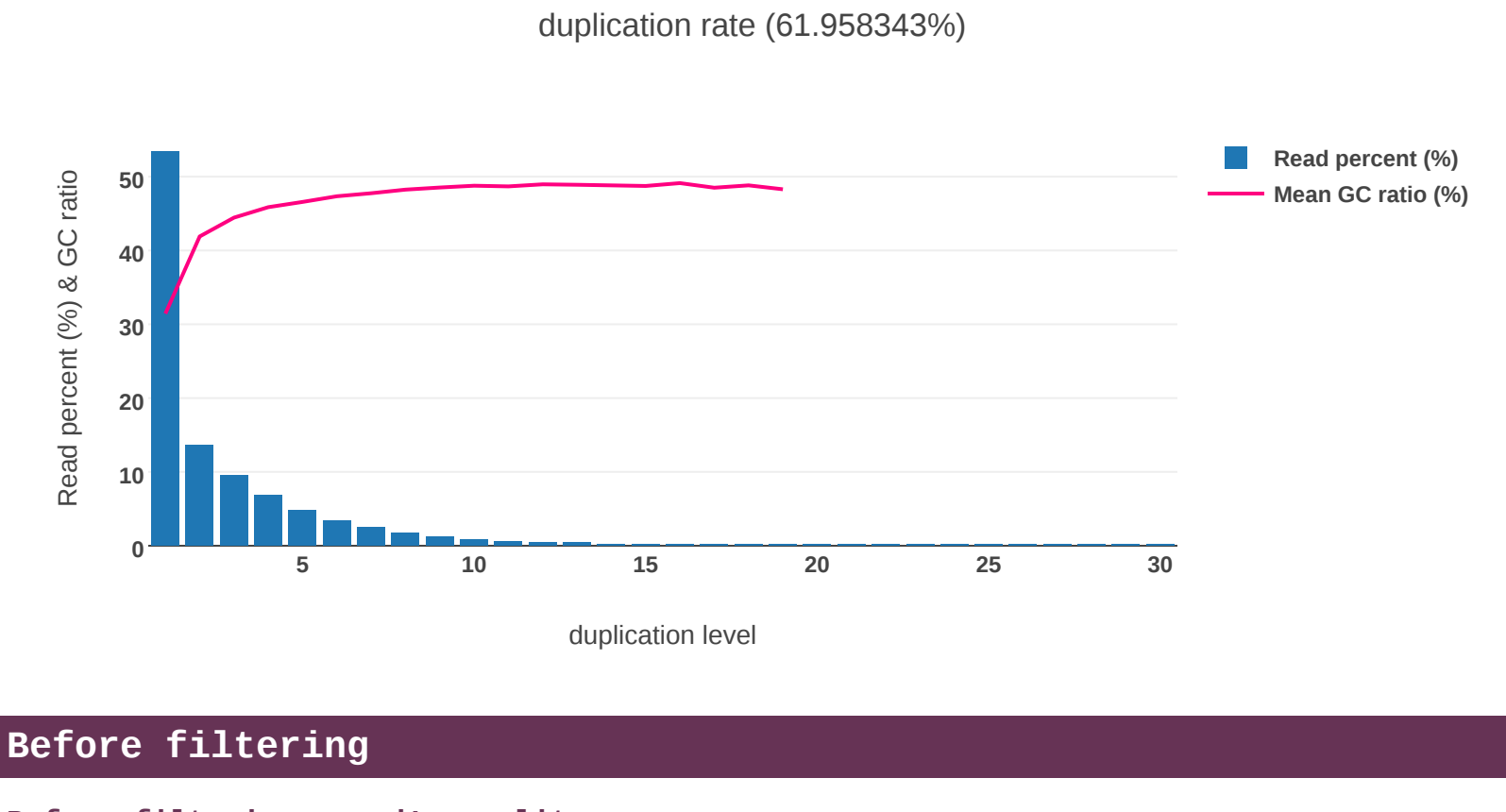
Advantages

Sequence	Occurrences
AGATCGGAAGAGCACACG	218130
AGATCGGAAGAGCACACGTCTGAACTC	198661

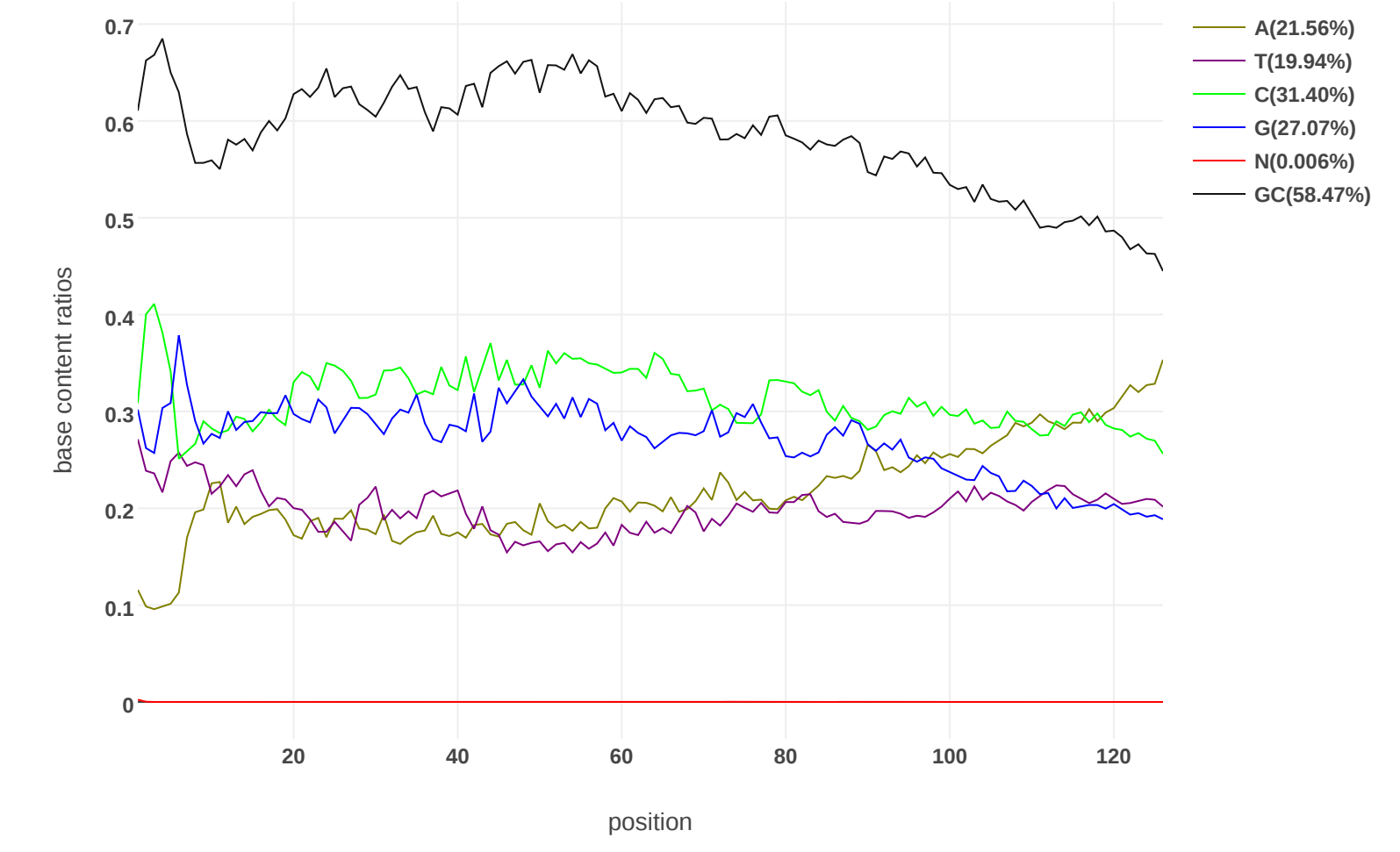
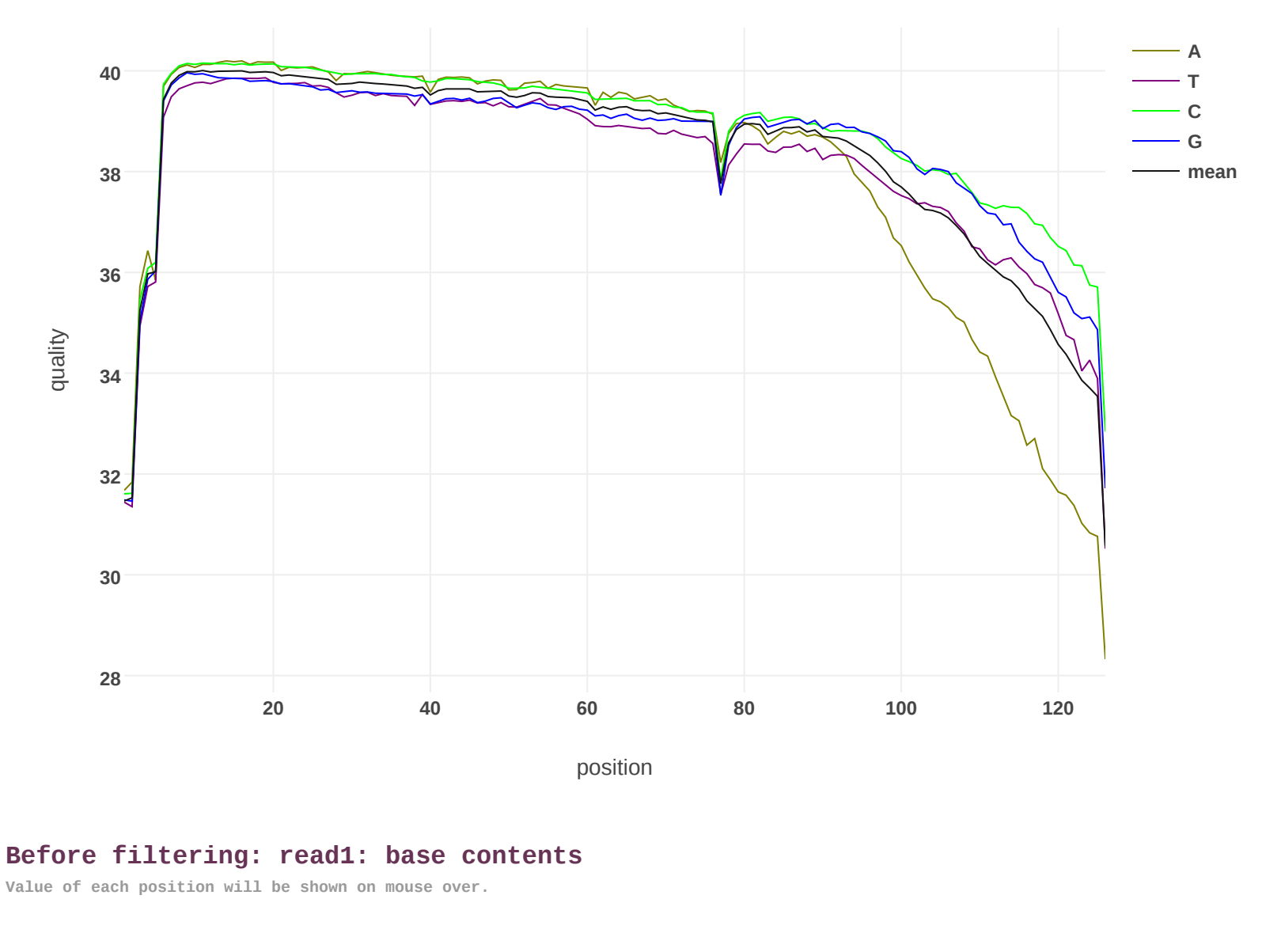
AGATCGGAAGAGCAC

AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTAC

Sequence	Count
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCT	227,106
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCT	219,714
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTG	284,064
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGA	255,489
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGAT	299,855
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCT	204,786
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTC	272,540
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCT	192,006
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTC	191,982
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCT	226,615
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTG	213,849
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTT	201,713
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAA	228,520
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAAA	225,686
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAAAA	243,382
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAAAAA	230,623
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAAAAAA	213,167
AGATCGGAAGAGCACACGTCTGAACTCCAGTCCACATTCATCTGGATCTCGTATGCCGCTCTTCTGCTTGAAAAAAA	190,820
other adapter sequences	135,59908

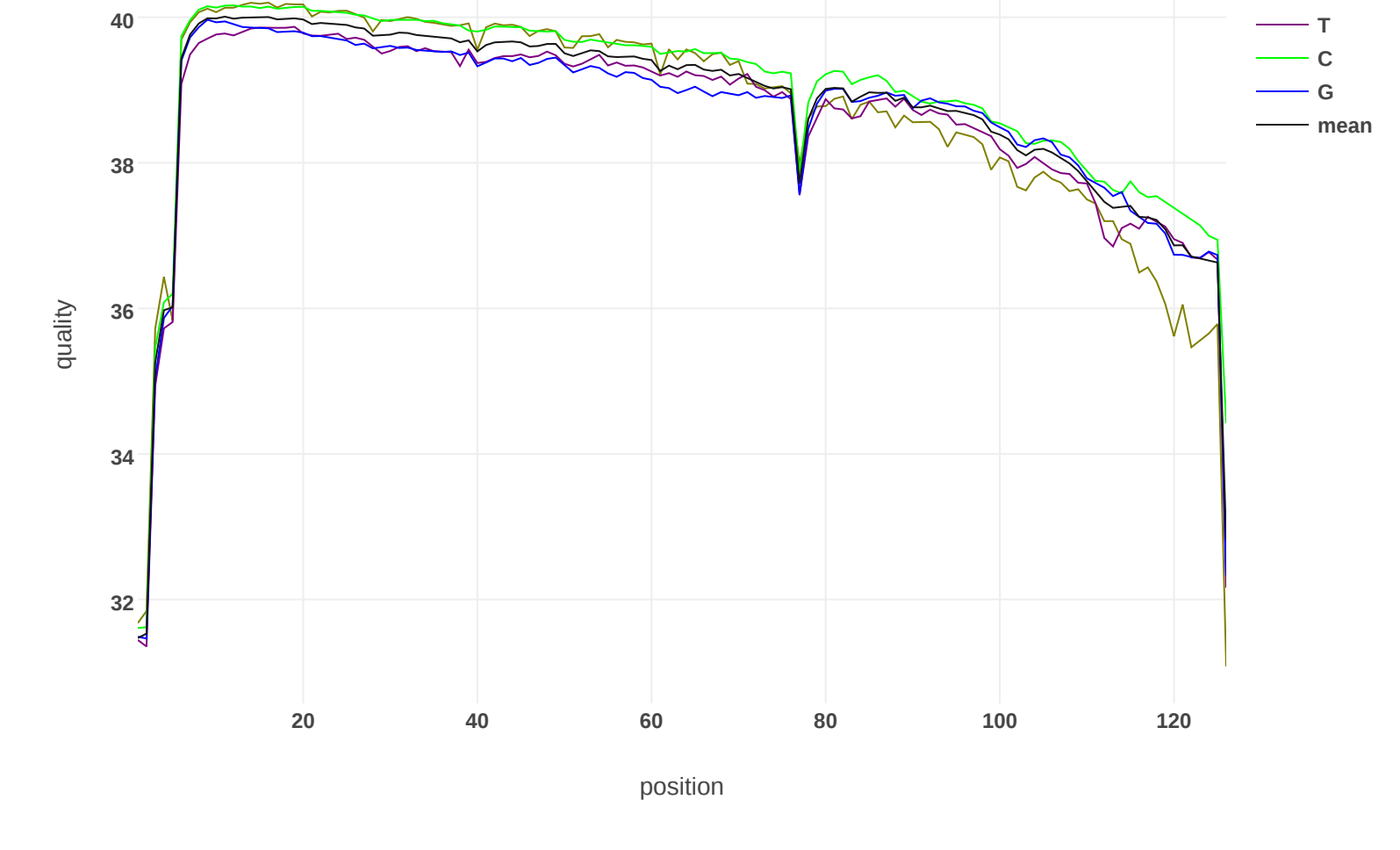
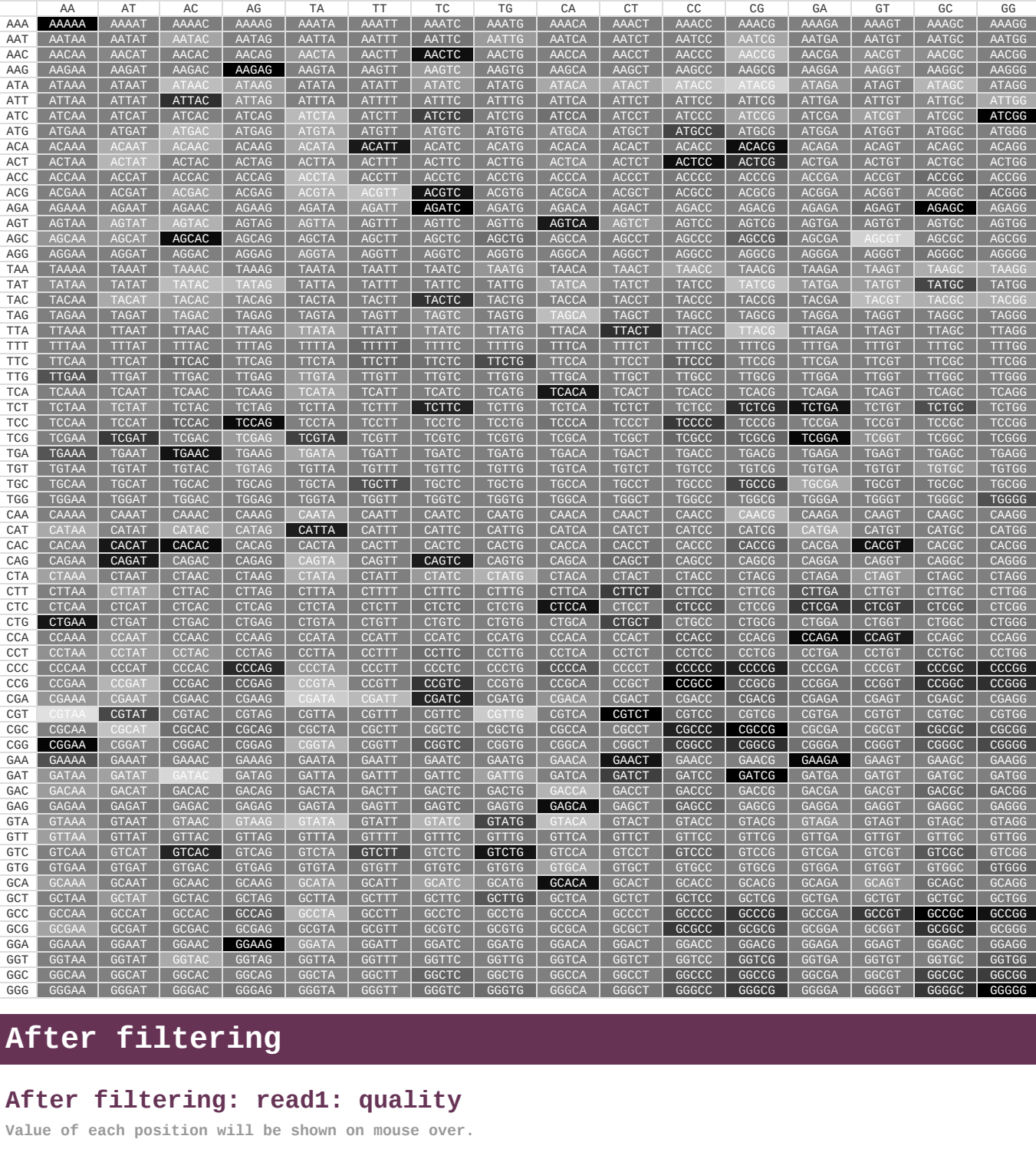


Value of each position will be s

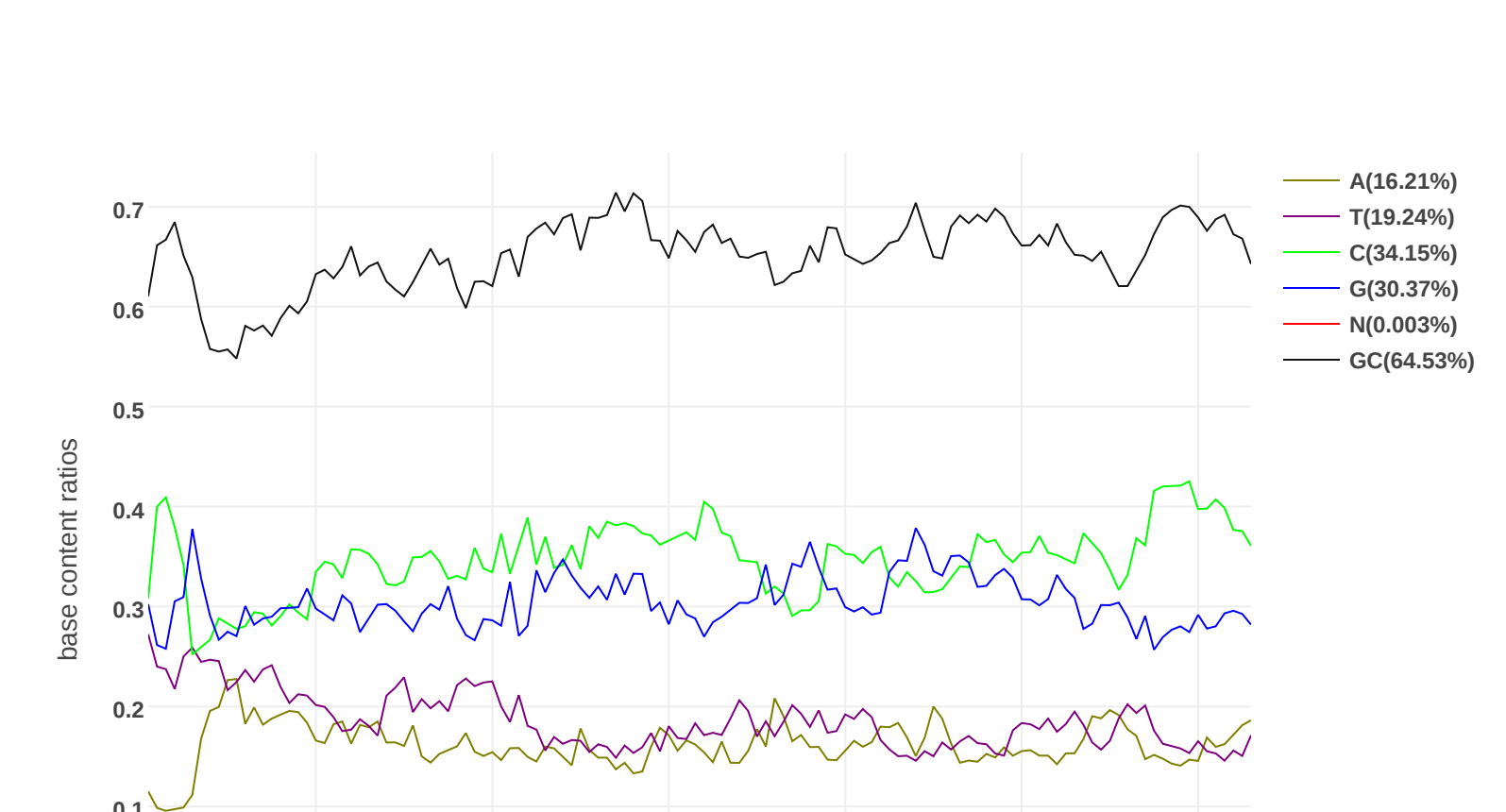


Before filtering: read1: KMER counting

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



Value of each position will be shown on mouse over.



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