

MP5k_se

Summary

General

fastp version:	0.19.6 (https://github.com/OpenGene/fastp)
sequencing:	single end (138 cycles)
mean length before filtering:	66bp
mean length after filtering:	66bp
duplication rate:	69.197527% (may be overestimated since this is SE data)

Before filtering

total reads:	17.345347 M
total bases:	1.152136 G
Q20 bases:	1.103155 G (95.748665%)
Q30 bases:	1.030206 G (89.417010%)
GC content:	43.834162%

After filtering

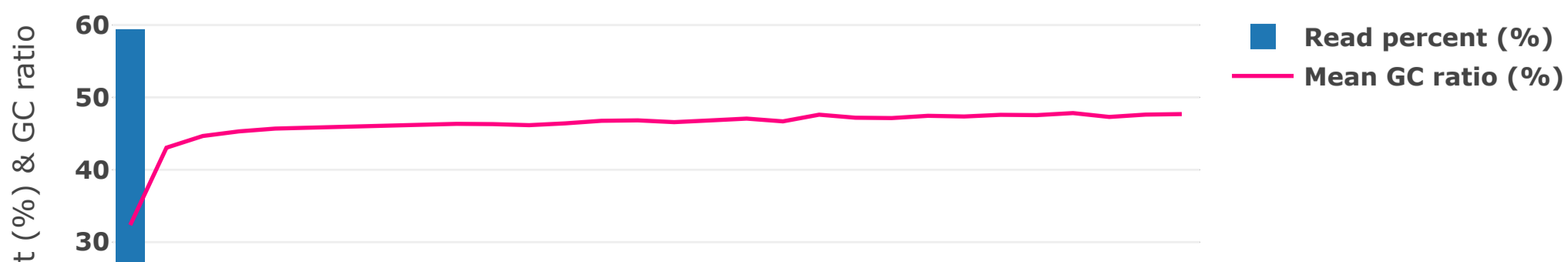
total reads:	16.861797 M
total bases:	1.124360 G
Q20 bases:	1.085462 G (96.540405%)
Q30 bases:	1.017086 G (90.459142%)
GC content:	43.811910%

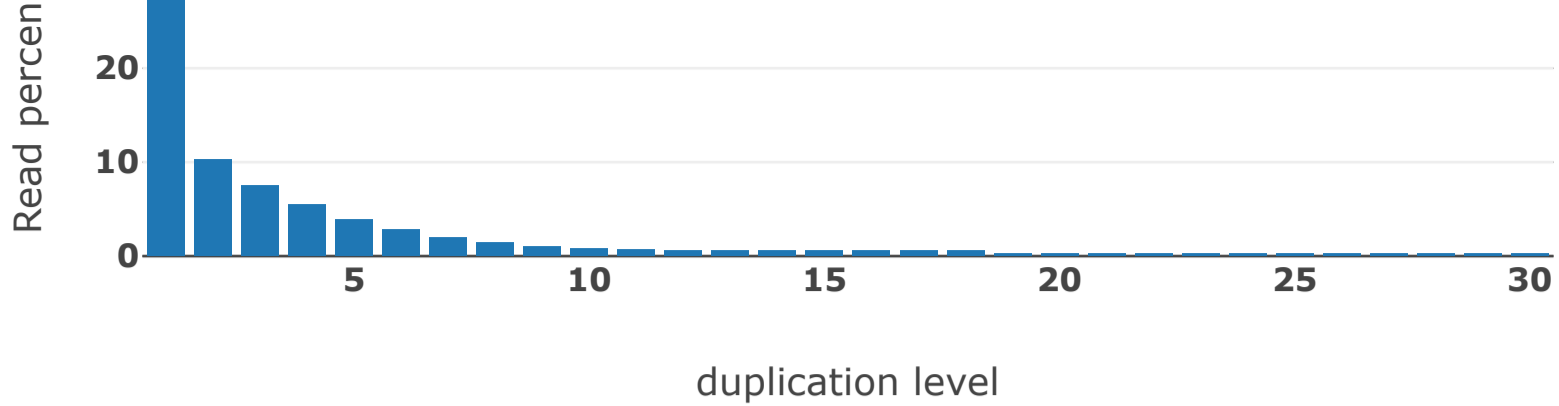
Filtering result

reads passed filters:	16.861797 M (97.212221%)
reads with low quality:	351.338000 K (2.025546%)
reads with too many N:	55 (0.000317%)
reads too short:	131.753000 K (0.759587%)
reads with low complexity:	404 (0.002329%)

Duplication

duplication rate (69.197527%)

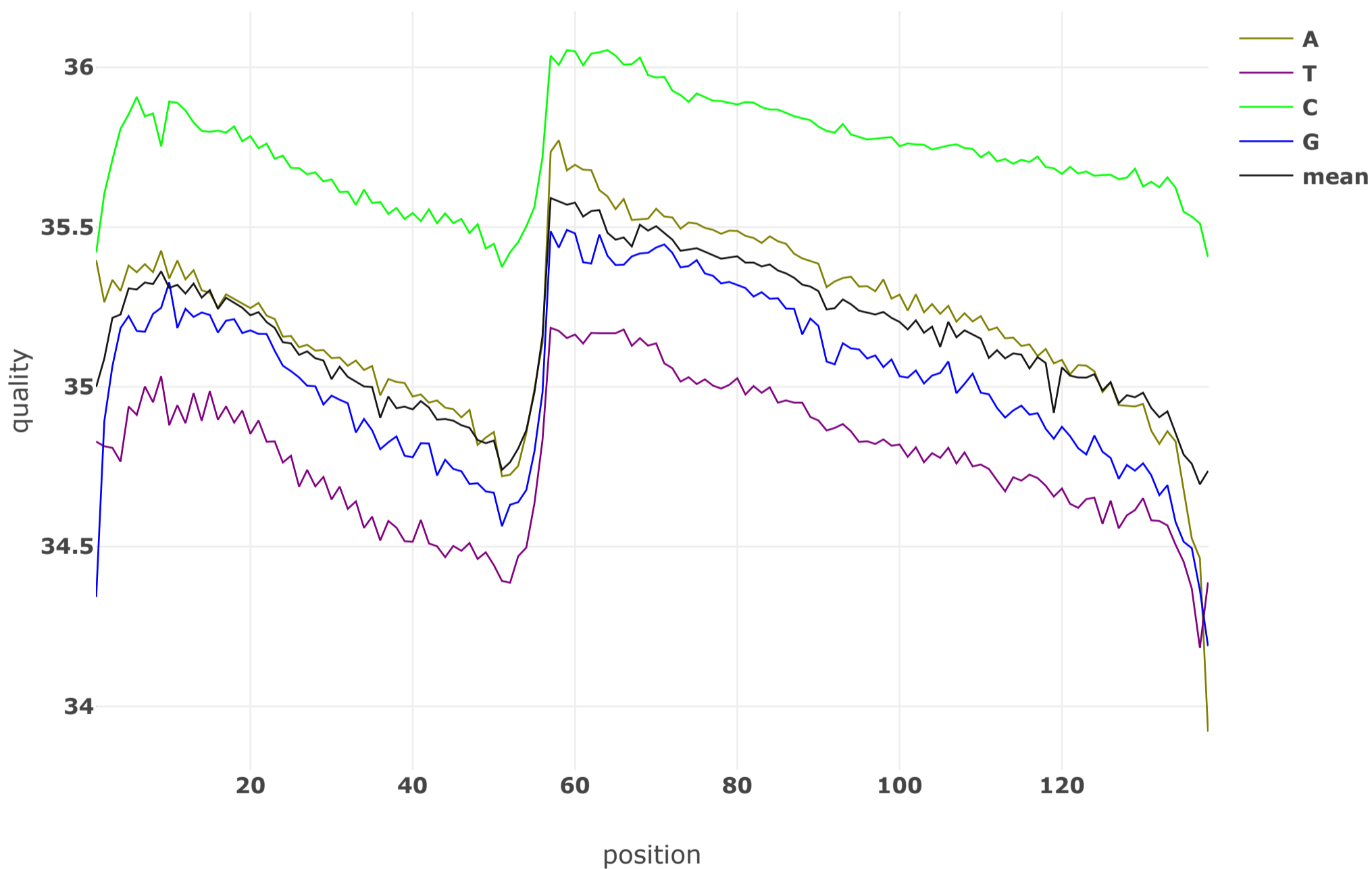




Before filtering

Before filtering: read1: quality

Value of each position will be shown on mouse over.

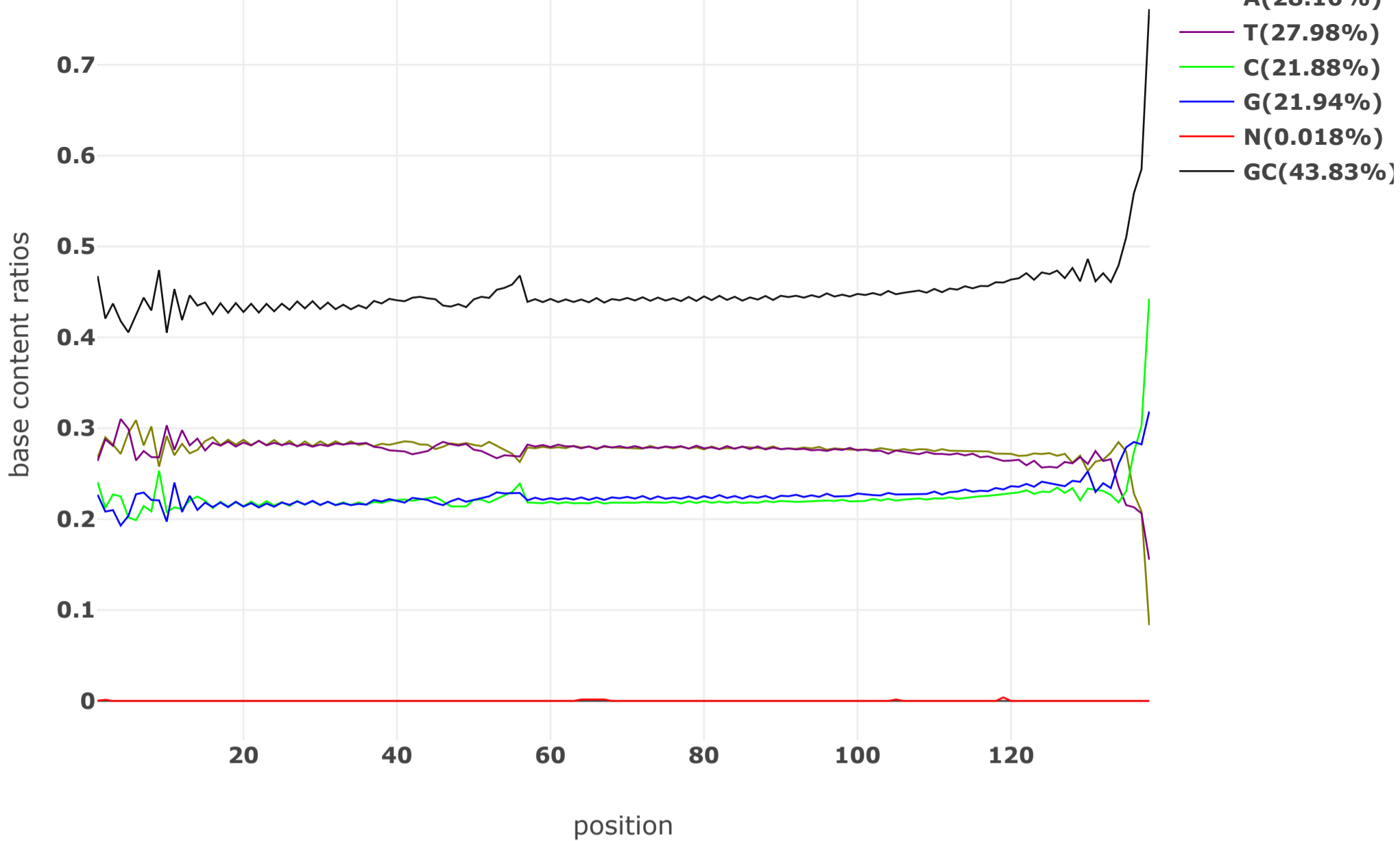


Before filtering: read1: base contents

Value of each position will be shown on mouse over.

0.8

A(28.16%)



Before filtering: read1: KMER counting

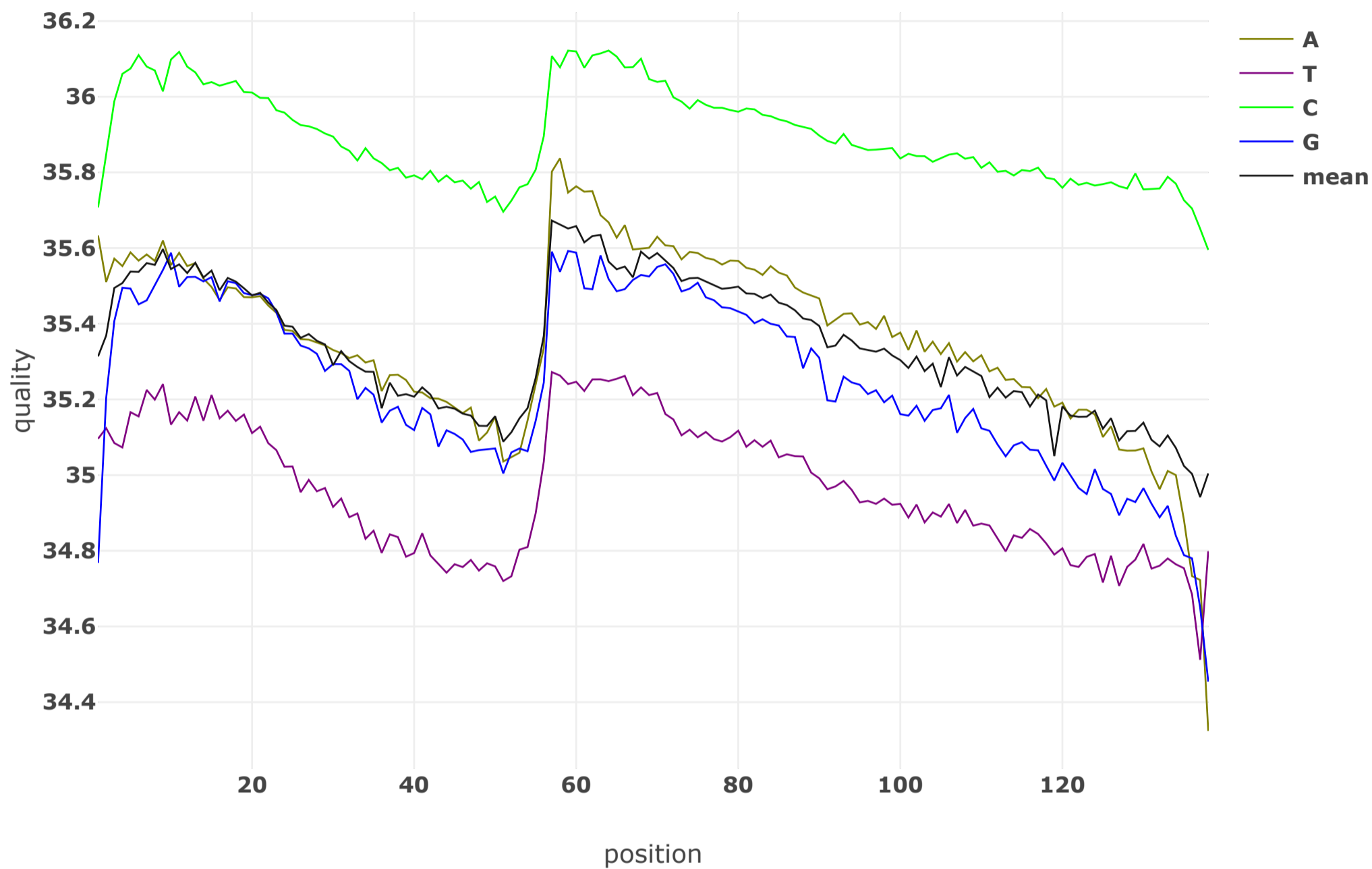
Darker background means larger counts. The count will be shown on mouse over.

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AAT	AATAA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACCT	AACCTC	AACCTG	AACCA	AACCTT	AACCC	AACCG	AACGA	AACGT	AACGC	AACGG
AAG	AAGAA	AAGAT	AAGAC	AAGAG	AAGTA	AAGTT	AAGTC	AAGTG	AAGCA	AAGCT	AAGCC	AAGCG	AAGGA	AAGGT	AAGGC	AAGGG
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TAC	TACAA	TACAT	TACAC	TACAG	TACTA	TACTT	TACTC	TACTG	TACCA	TACCT	TACCC	TACCG	TACGA	TACGT	TACGC	TACGG
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TGG	TGGAA	TGGAT	TGGAC	TGGAG	TGGTA	TGGTT	TGGTC	TGGTG	TGGCA	TGGCT	TGGCC	TGGCG	TGGGA	TGGGT	TGGGC	TGGGG
CAA	CAAAA	CAAAT	CAAAC	CAAAG	CAATA	CAATT	CAATC	CAATG	CAACA	CAACT	CAACC	CAACG	CAAGA	CAAGT	CAAGC	CAAGG
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CCA	CCAAA	CCAAT	CCAAC	CCAAG	CCATA	CCATT	CCATC	CCATG	CCACA	CCACT	CCACC	CCACG	CCAGA	CCAGT	CCAGC	CCAGG
CCT	CCTAA	CCTAT	CCTAC	CCTAG	CCTTA	CCTTT	CCTTC	CCTTG	CCTCA	CCTCT	CCTCC	CCTCG	CCTGA	CCTGT	CCTGC	CCTGG
CCC	CCCAA	CCCAT	CCCAC	CCCAG	CCCTA	CCCTT	CCCTC	CCCTG	CCCCA	CCCCT	CCCCC	CCCCG	CCCGA	CCCGT	CCCGC	CCCGG
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After filtering

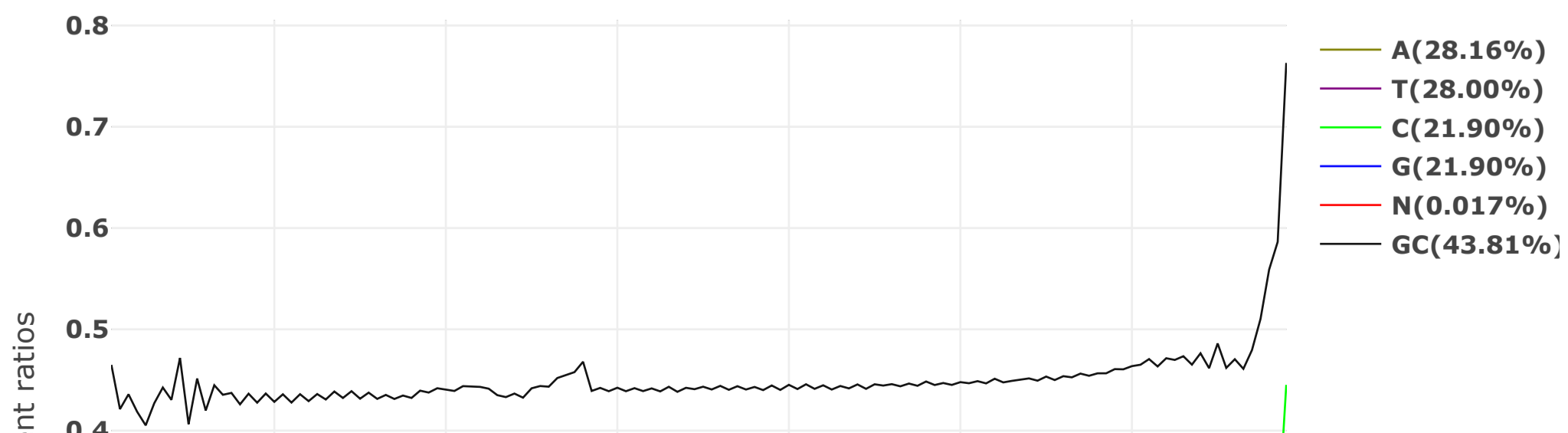
After filtering: read1: quality

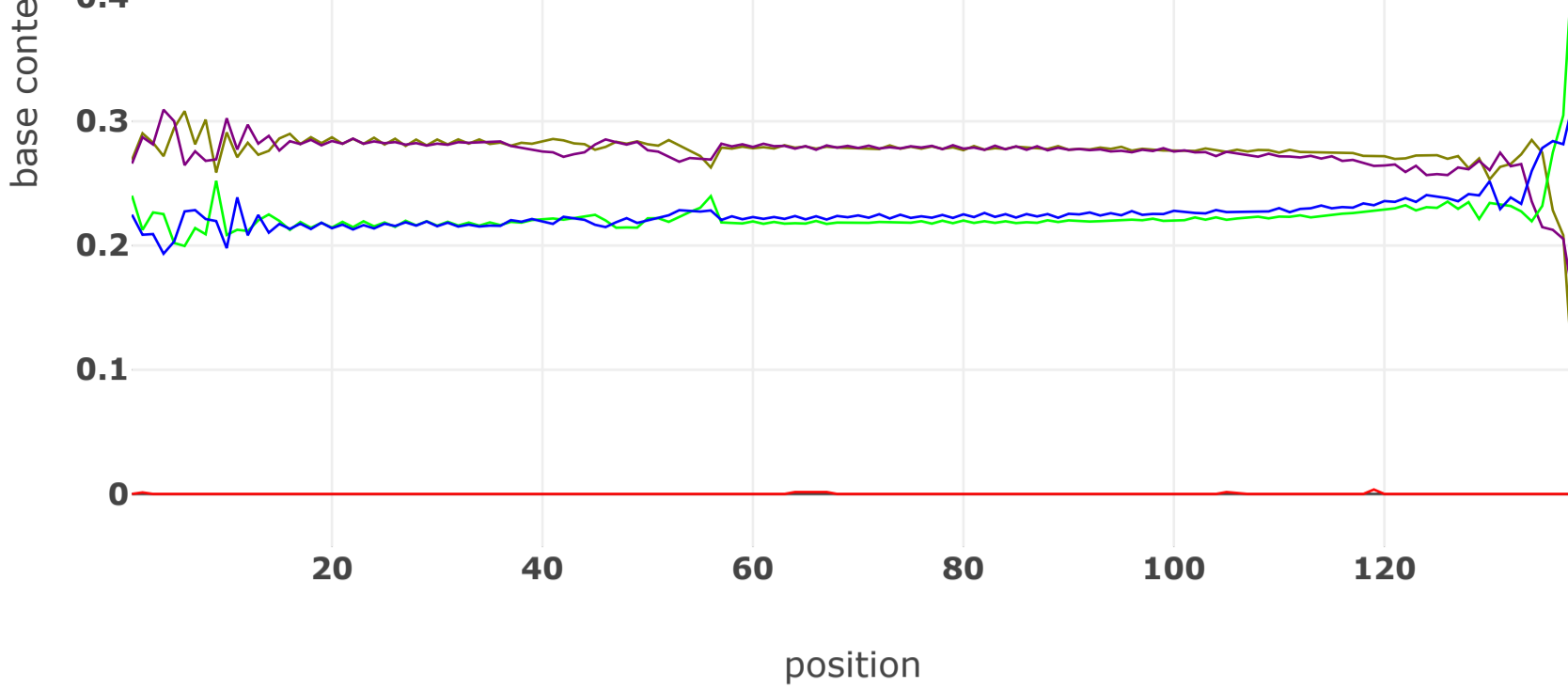
Value of each position will be shown on mouse over.



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.

	AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC	CG	GA	GT	GC	GG
AAA	AAAAA	AAAAT	AAAAC	AAAAG	AAATA	AAATT	AAATC	AAATG	AAACA	AAACT	AAACC	AAACG	AAAGA	AAAGT	AAAGC	AAAGG
AAT	AATAA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
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GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

After filtering: read1: overrepresented sequences

