

# MP5k\_unk

## Summary

### General

fastp version:	0.19.6 ( <a href="https://github.com/OpenGene/fastp">https://github.com/OpenGene/fastp</a> )
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	150bp, 150bp
mean length after filtering:	150bp, 150bp
duplication rate:	63.168306%
Insert size peak:	0

### Before filtering

total reads:	120.869114 M
total bases:	18.208906 G
Q20 bases:	16.417683 G (90.162933%)
Q30 bases:	14.774755 G (81.140268%)
GC content:	43.322278%

### After filtering

total reads:	101.028768 M
total bases:	15.183734 G
Q20 bases:	14.313465 G (94.268413%)
Q30 bases:	13.111521 G (86.352413%)
GC content:	42.588647%

### Filtering result

reads passed filters:	101.028768 M (83.585264%)
reads with low quality:	19.123774 M (15.821886%)
reads with too many N:	1.782000 K (0.001474%)
reads too short:	624.196000 K (0.516423%)
reads with low complexity:	90.594000 K (0.074952%)

## Adapters

### Adapter or bad ligation of read1

The input has little adapter percentage (~0.021208%), probably it's trimmed before.

Sequence	Occurrences
all adapter sequences	28362

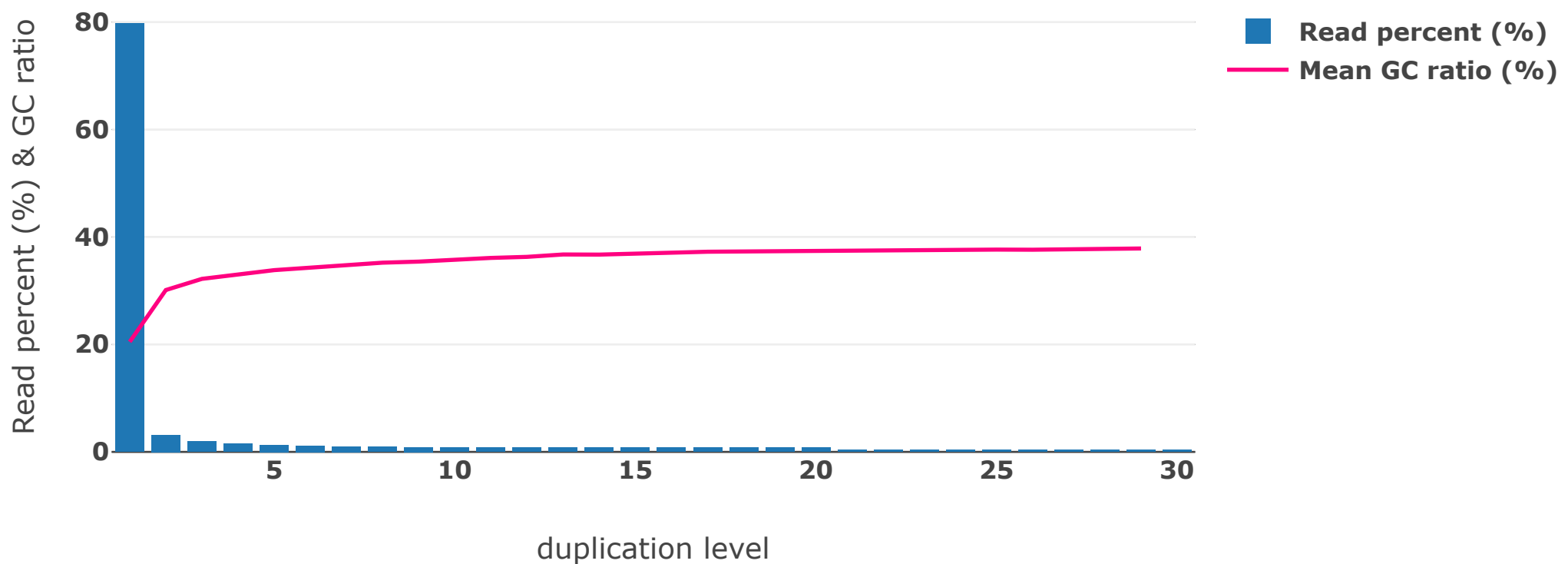
### Adapter or bad ligation of read2

The input has little adapter percentage (~0.019327%), probably it's trimmed before.

Sequence	Occurrences
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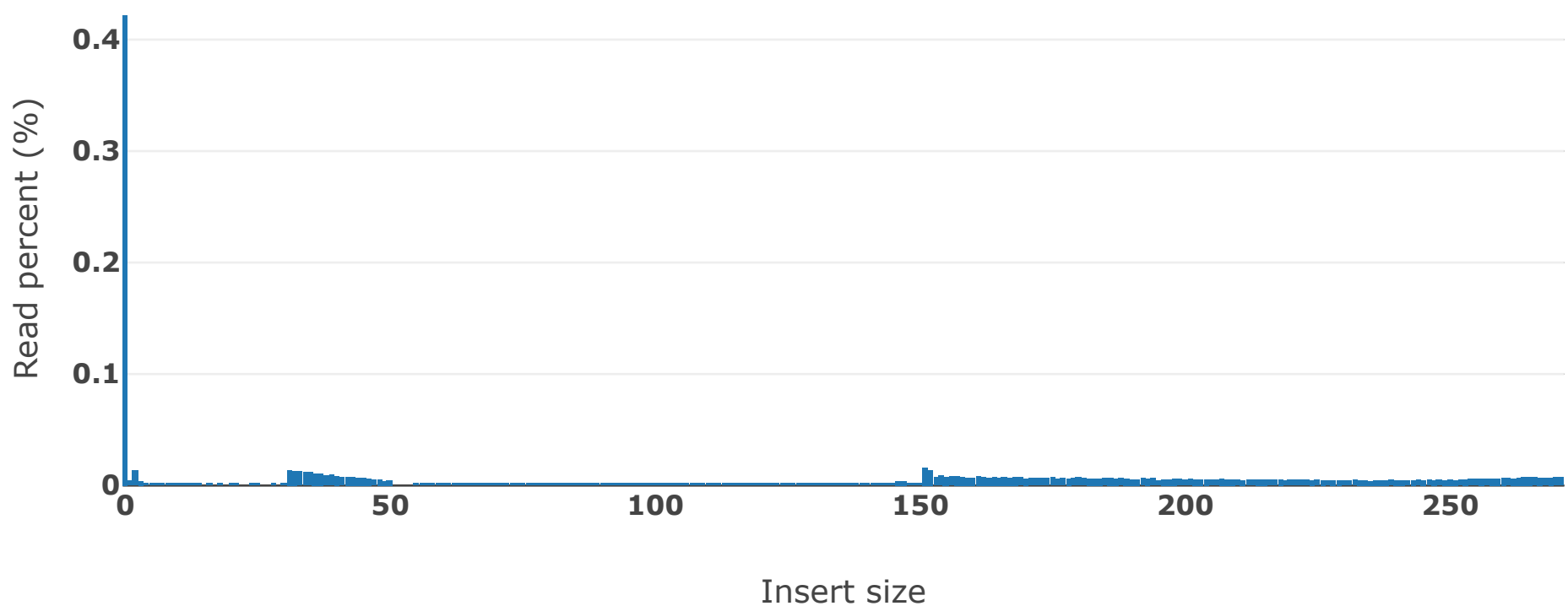
## Duplication

duplication rate (63.168306%)



## Insert size estimation

Insert size distribution (98.530240% reads are with unknown length)

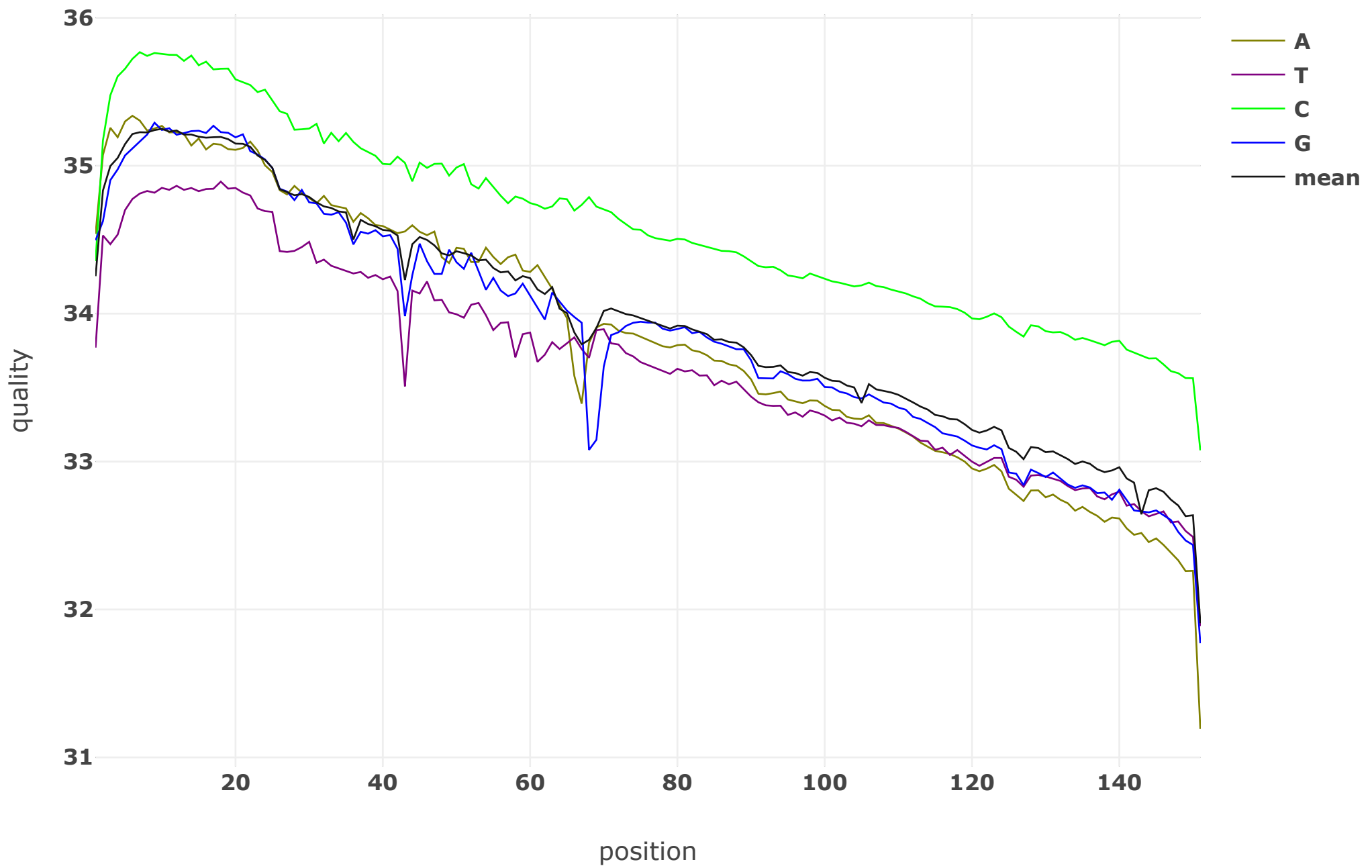


This estimation is based on paired-end overlap analysis, and there are 98.530240% reads found not overlapped. The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

## Before filtering

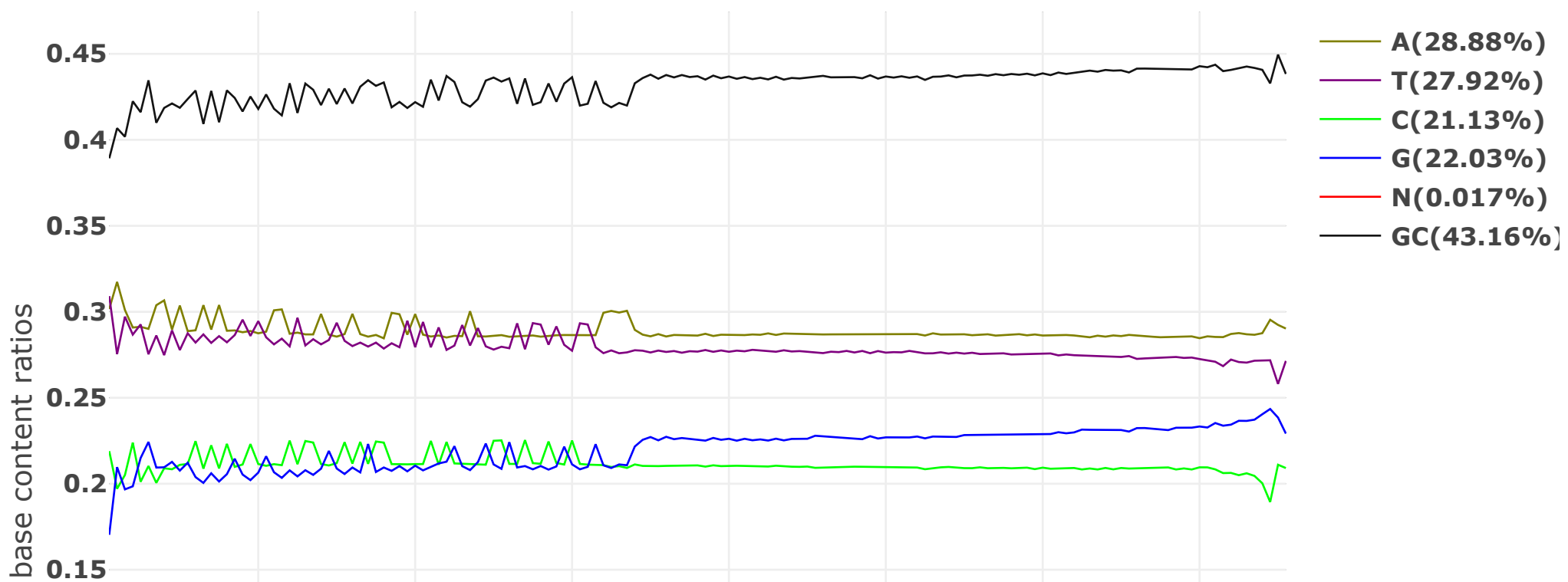
### Before filtering: read1: quality

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.



0.1

0.05

0

20

40

60

80

100

120

140

position

### Before 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
AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACTT	AACTC	AACTG	AACCA	AACCT	AACCC	AACCG	AACGA	AACGT	AACGC	AACGG
AAG	AAGAA	AAGAT	AAGAC	AAGAG	AAGTA	AAGTT	AAGTC	AAGTG	AAGCA	AAGCT	AAGCC	AAGCG	AAGGA	AAGGT	AAGGC	AAGGG
ATA	ATAAA	ATAAT	ATAAC	ATAAG	ATATA	ATATT	ATATC	ATATG	ATACA	ATACT	ATACC	ATACG	ATAGA	ATAGT	ATAGC	ATAGG
ATT	ATTAA	ATTAT	ATTAC	ATTAG	ATTTA	ATTTT	ATTTT	ATTTG	ATTCA	ATTCT	ATTCC	ATTCTG	ATTGA	ATTGT	ATTGC	ATTGG
ATC	ATCAA	ATCAT	ATCAC	ATCAG	ATCTA	ATCTT	ATCTC	ATCTG	ATCCA	ATCCT	ATCCC	ATCCG	ATCGA	ATCGT	ATCGC	ATCGG
ATG	ATGAA	ATGAT	ATGAC	ATGAG	ATGTA	ATGTT	ATGTC	ATGTG	ATGCA	ATGCT	ATGCC	ATGCG	ATGGA	ATGGT	ATGGC	ATGGG
ACA	ACAAA	ACAAT	ACAAC	ACAAG	ACATA	ACATT	ACATC	ACATG	ACACA	ACACT	ACACC	ACACG	ACAGA	ACAGT	ACAGC	ACAGG
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CAT	CATAA	CATAT	CATAC	CATAG	CATTA	CATTT	CATTC	CATTG	CATCA	CATCT	CATCC	CATCG	CATGA	CATGT	CATGC	CATGG
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GGC	GGCAA	GGCAT	GGCAC	GGCAG	GGCTA	GGCTT	GGCTC	GGCTG	GGCCA	GG CCT	GGCCC	GGCCG	GGCGA	GGCGT	GGCGC	GGCGG
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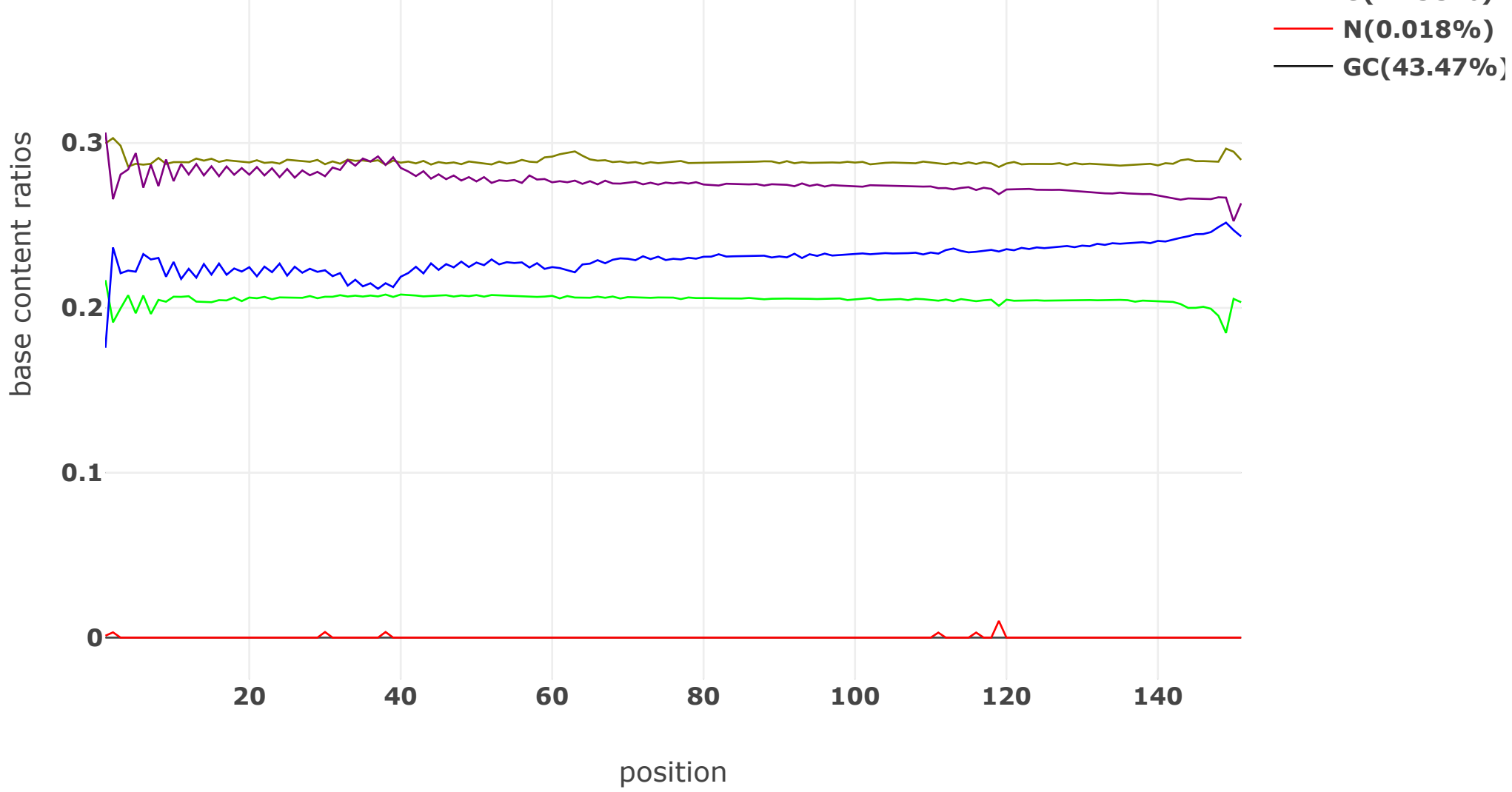
### Before filtering: read1: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAAAAAAAA	51619 (0.113399%)	
AACACACACACACACACACACACACACACACACACA	7620 (0.066960%)	







## Before filtering: read2: KMER counting

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

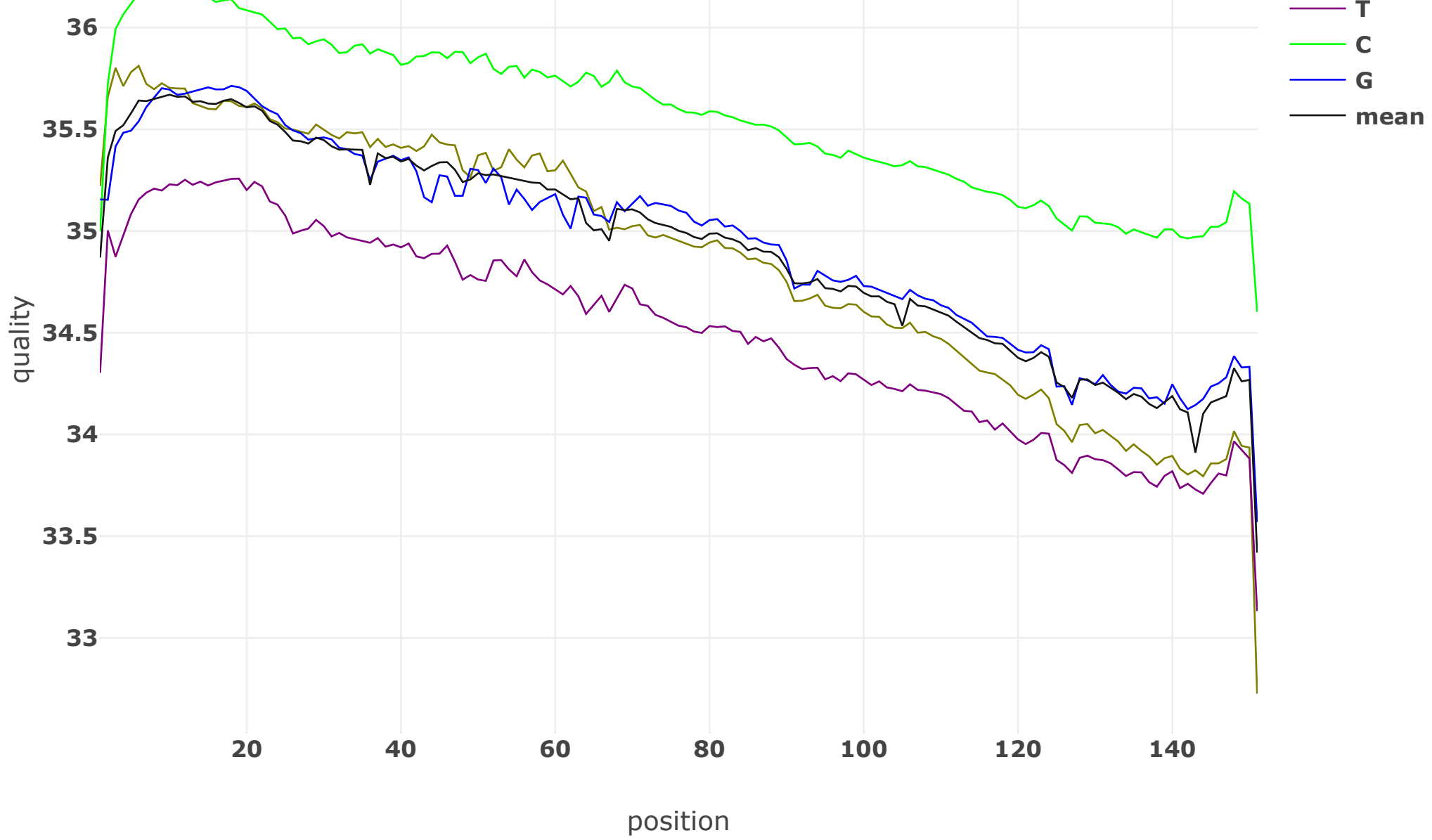
	AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC	CG	GA	GT	GC	GG
AAA	AAAAA	AAAAT	AAAAC	AAAAG	AAATA	AAATT	AAATC	AAATG	AAACA	AAACT	AAACC	AAACG	AAAGA	AAAGT	AAAGC	AAAGG
AAT	AATAA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACCT	AACCTC	AACCTG	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
ATA	ATAAA	ATAAT	ATAAC	ATAAG	ATATA	ATATT	ATATC	ATATG	ATACA	ATACT	ATACC	ATACG	ATAGA	ATAGT	ATAGC	ATAGG
ATT	ATTAA	ATTAT	ATTAC	ATTAG	ATTTA	ATTTT	ATTTT	ATTTG	ATTCA	ATTCT	ATTCC	ATTCTG	ATTGA	ATTGT	ATTGC	ATTGG
ATC	ATCAA	ATCAT	ATCAC	ATCAG	ATCTA	ATCTT	ATCTC	ATCTG	ATCCA	ATCCT	ATCCC	ATCCG	ATCGA	ATCGT	ATCGC	ATCGG
ATG	ATGAA	ATGAT	ATGAC	ATGAG	ATGTA	ATGTT	ATGTC	ATGTG	ATGCA	ATGCT	ATGCC	ATGCG	ATGGA	ATGGT	ATGGC	ATGGG
ACA	ACAAA	ACAAT	ACAAC	ACAAG	ACATA	ACATT	ACATC	ACATG	ACACA	ACACT	ACACC	ACACG	ACAGA	ACAGT	ACAGC	ACAGG
ACT	ACTAA	ACTAT	ACTAC	ACTAG	ACTTA	ACTTT	ACTTC	ACTTG	ACTCA	ACTCT	ACTCC	ACTCG	ACTGA	ACTGT	ACTGC	ACTGG
ACC	ACCAA	ACCAT	ACCAC	ACCAG	ACCTA	ACCTT	ACCTC	ACCTG	ACCCA	ACCTT	ACCCC	ACCCG	ACCGA	ACCGT	ACCGC	ACCGG
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AGC	AGCAA	AGCAT	AGCAC	AGCAG	AGCTA	AGCTT	AGCTC	AGCTG	AGCCA	AGCCT	AGCCC	AGCCG	AGCGA	AGCGT	AGCGC	AGCGG
AGG	AGGAA	AGGAT	AGGAC	AGGAG	AGGTA	AGGTT	AGGTC	AGGTG	AGGCA	AGGCT	AGGCC	AGGCG	AGGGA	AGGGT	AGGGC	AGGGG
TAA	TAAAA	TAAAT	TAAAC	TAAAG	TAATA	TAATT	TAATC	TAATG	TAACA	TAACT	TAACC	TAACG	TAAGA	TAAGT	TAAGC	TAAGG
TAT	TATAA	TATAT	TATAC	TATAG	TATTA	TATTT	TATTC	TATTG	TATCA	TATCT	TATCC	TATCG	TATGA	TATGT	TATGC	TATGG
TAC	TACAA	TACAT	TACAC	TACAG	TACTA	TACTT	TACTC	TACTG	TACCA	TACCT	TACCC	TACCG	TACGA	TACGT	TACGC	TACGG
TAG	TAGAA	TAGAT	TAGAC	TAGAG	TAGTA	TAGTT	TAGTC	TAGTG	TAGCA	TAGCT	TAGCC	TAGCG	TAGGA	TAGGT	TAGGC	TAGGG
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CAT	CATAA	CATAT	CATAC	CATAG	CATTA	CATTT	CATTC	CATTG	CATCA	CATCT	CATCC	CATCG	CATGA	CATGT	CATGC	CATGG
CAC	CACAA	CACAT	CACAC	CACAG	CACTA	CACTT	CACTC	CACTG	CACCA	CACCT	CACCC	CACCG	CACGA	CACGT	CACGC	CACGG
CAG	CAGAA	CAGAT	CAGAC	CAGAG	CAGTA	CAGTT	CAGTC	CAGTG	CAGCA	CAGCT	CAGCC	CAGCG	CAGGA	CAGGT	CAGGC	CAGGG
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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
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CCG	CCGAA	CCGAT	CCGAC	CCGAG	CCGTA	CCGTT	CCGTC	CCGTG	CCGCA	CCGCT	CCGCC	CCCG	CCGGA	CCGGT	CCGGC	CCGGG
CGA	CGAAA	CGAAT	CGAAC	CGAAG	CGATA	CGATT	CGATC	CGATG	CGACA	CGACT	CGACC	CGACG	CGAGA	CGAGT	CGAGC	CGAGG
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GAA	GAAAA	GAAAT	GAAAC	GAAAG	GAATA	GAATT	GAATC	GAATG	GAACA	GAACT	GAACC	GAACG	GAAGA	GAAGT	GAAGC	GAAGG
GAT	GATAA	GATAT	GATAC	GATAG	GATTA	GATTT	GATTC	GATTG	GATCA	GATCT	GATCC	GATCG	GATGA	GATGT	GATGC	GATGG
GAC	GACAA	GACAT	GACAC	GACAG	GACTA	GACTT	GACTC	GACTG	GACCA	GACCT	GACCC	GACCG	GACGA	GACGT	GACGC	GACGG
GAG	GAGAA	GAGAT	GAGAC	GAGAG	GAGTA	GAGTT	GAGTC	GAGTG	GAGCA	GAGCT	GAGCC	GAGCG	GAGGA	GAGGT	GAGGC	GAGGG
GTA	GTAATA	GTAAT	GTAAC	GTAAG	GTATA	GTATT	GTATC	GTATG	GTACA	GTACT	GTACC	GTACG	GTAGA	GTAGT	GTAGC	GTAGG
GTT	GTTAA	GTTAT	GTTAC	GTTAG	GTTTA	GTTTT	GTTTC	GTTTG	GTTCA	GTTCT	GTTCC	GTTCTG	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCAC	GTCAG	GTCATA	GTCCT	GTCCT	GTCCTG	GTCCTA	GTCCT	GTCCT	GTCCTG	GTCCTA	GTCCT	GTCCT	GTCCTG





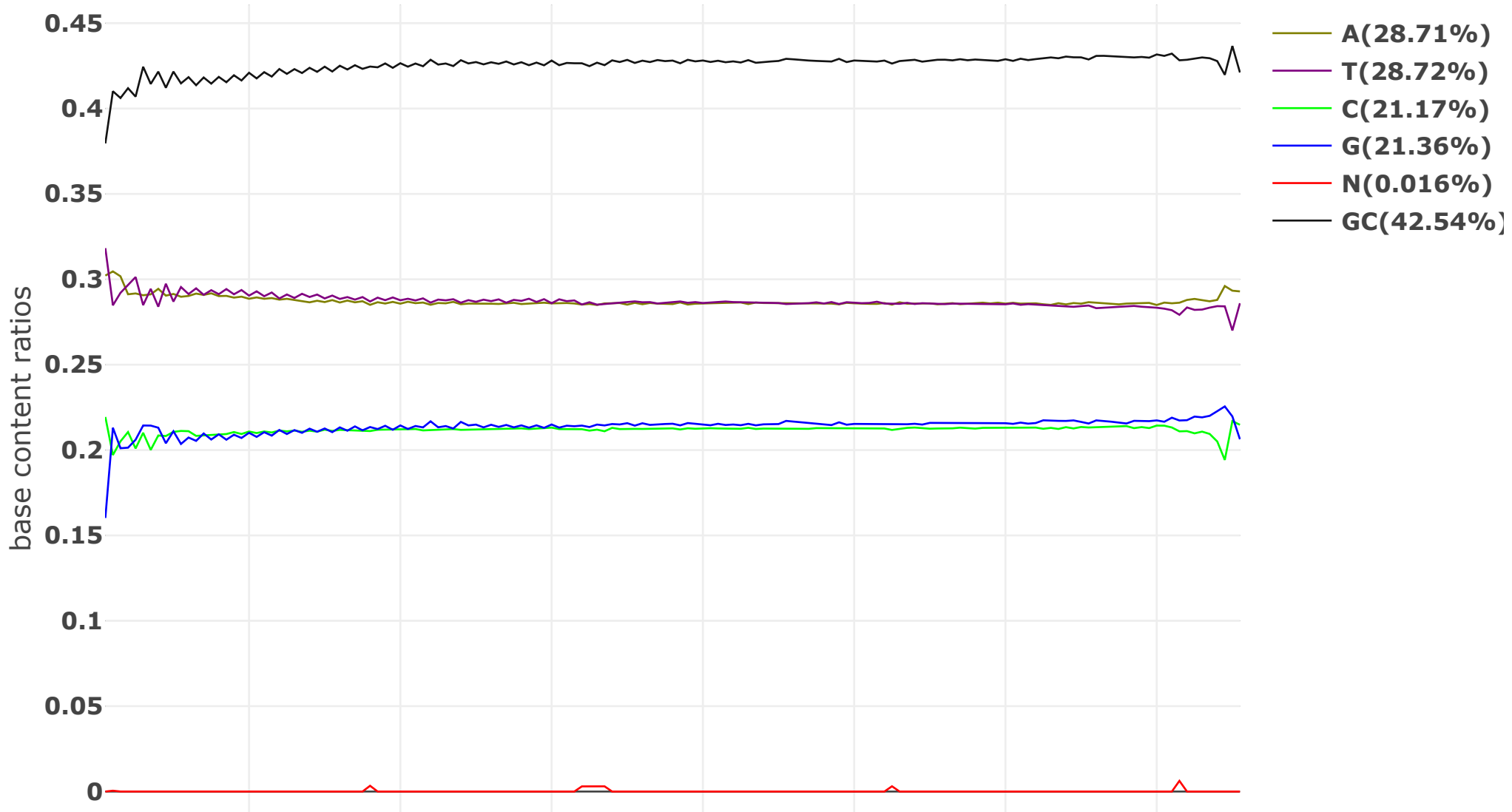

























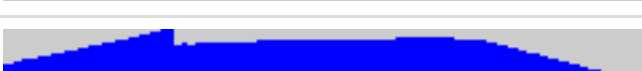


### After filtering: read1: base contents

Value of each position will be shown on mouse over.

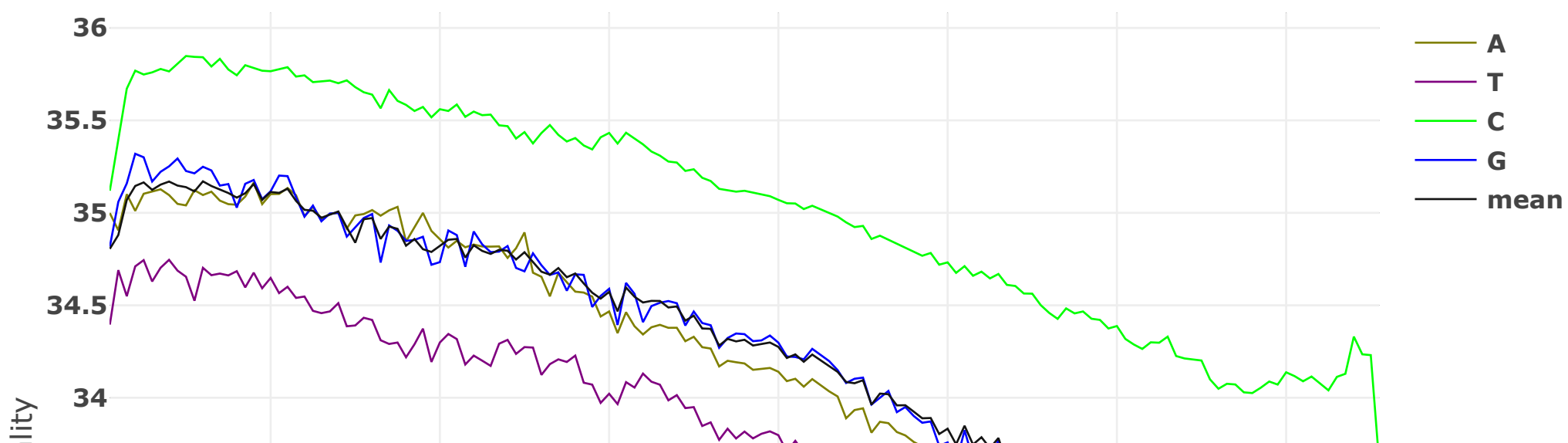


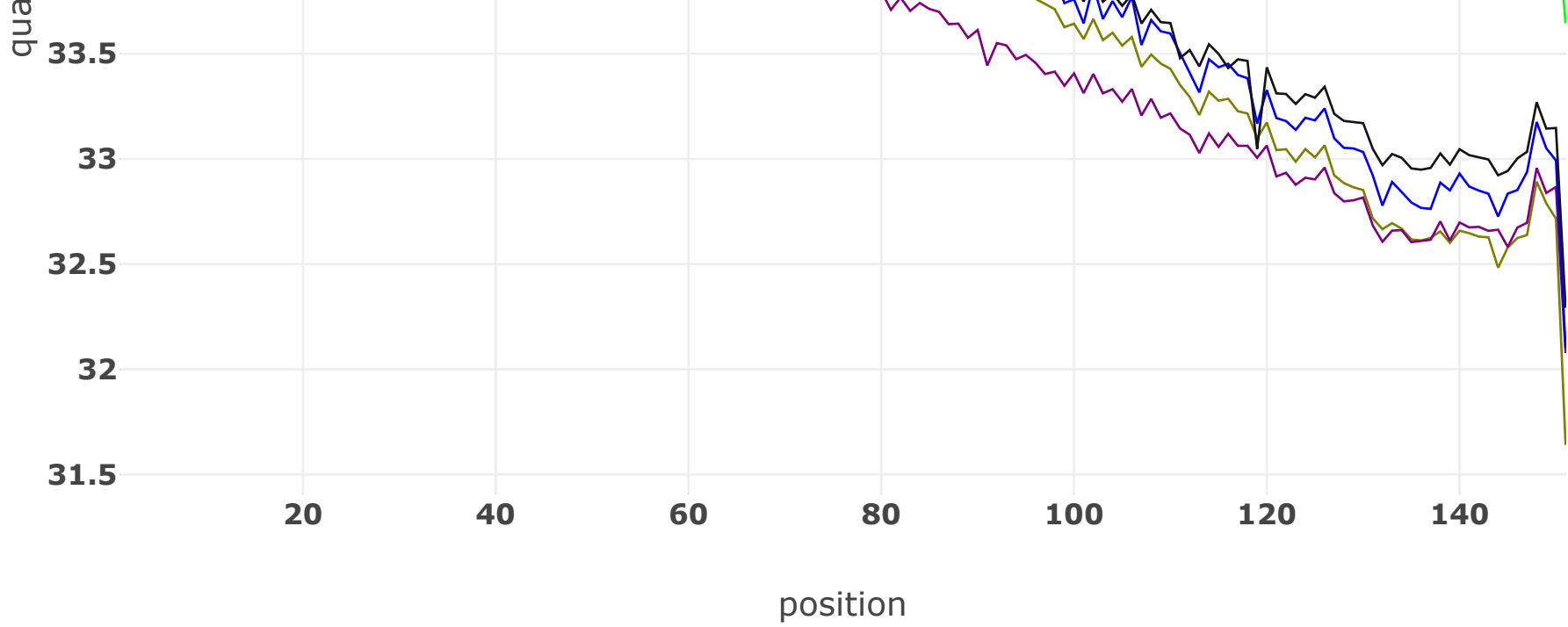


ACACACACACACACACACACACACACACACACACACAG	144 (0.001517%)	
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4365 (0.045988%)	
AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	4142 (0.043639%)	
ATAGATAGATAGATAGATAGATAGATAGATAGATAG	157 (0.001654%)	
ATGTGTGTGTGTGTGTGTGT	22475 (0.118394%)	
CACACACACACACACACACACACACACACACACAAACA	185 (0.001949%)	
CACACACACACACACACACACACACACACACACACAAA	316 (0.003329%)	
CACACACACACACACACACACACACACACACACACACA	8488 (0.089426%)	
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1744 (0.018374%)	
CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4674 (0.049243%)	
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	3841 (0.040467%)	
GATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	492 (0.005184%)	
GCACACACACACACACACACACACACACACACACACAC	5883 (0.061981%)	
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	27 (0.000284%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA	205 (0.002160%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5193 (0.054711%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTT	166 (0.001749%)	
TACACACACACACACACACACACACACACACACACACA	5055 (0.053258%)	
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	2469 (0.026012%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAG	308 (0.003245%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	9598 (0.101121%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTT	277 (0.002918%)	

## After filtering: read2: quality

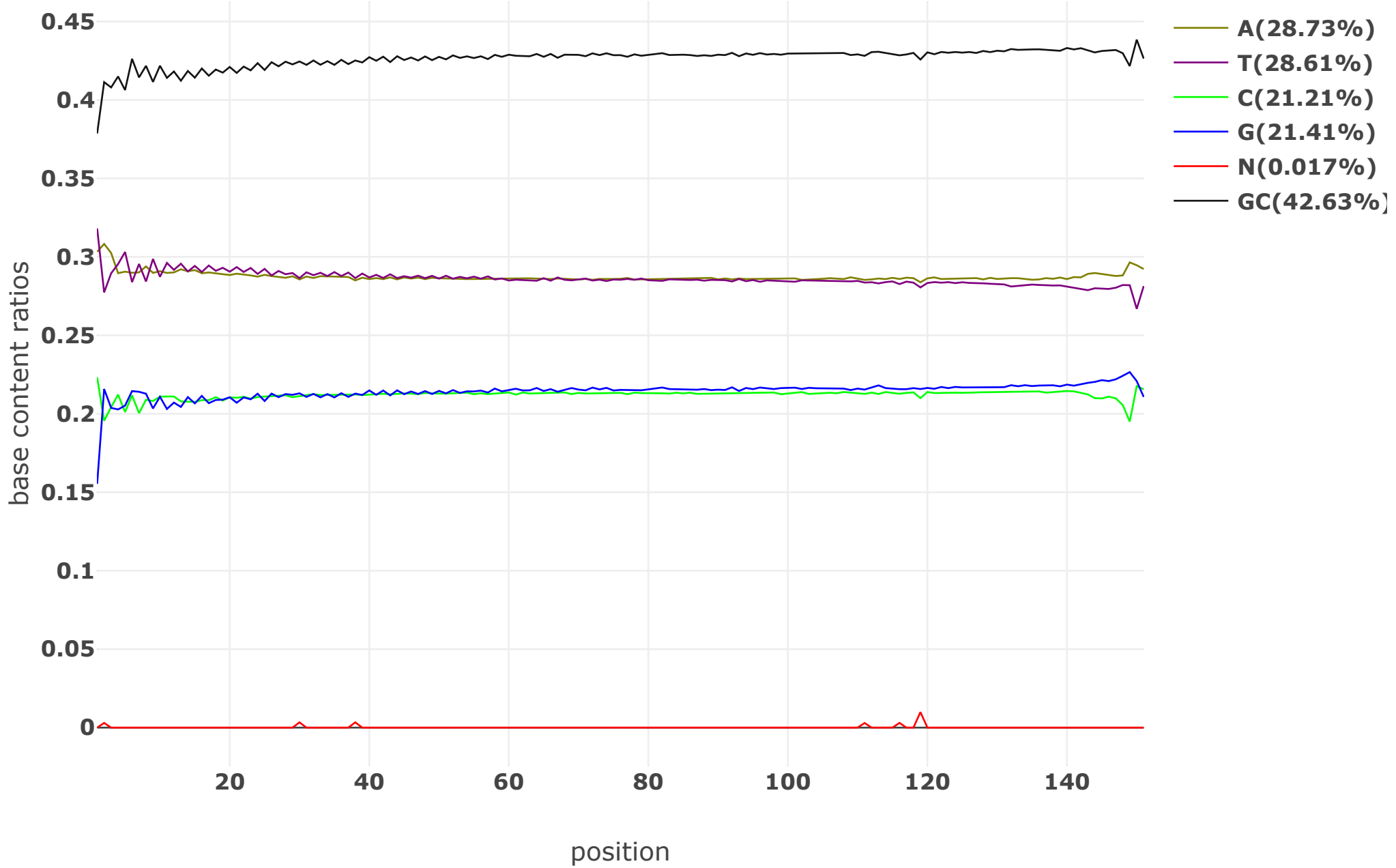
Value of each position will be shown on mouse over.





### 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.

	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
AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACTT	AACTC	AACTG	AACCA	AACCT	AACCC	AACCG	AACGA	AACGT	AACGC	AACGG



