

MP10k

Summary

General

fastp version:	0.19.4 (https://github.com/OpenGene/fastp)
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	151bp, 151bp
mean length after filtering:	150bp, 150bp
duplication rate:	70.067729%
Insert size peak:	0

Before filtering

total reads:	446.717352 M
total bases:	67.454320 G
Q20 bases:	62.581933 G (92.776761%)
Q30 bases:	57.303928 G (84.952198%)
GC content:	44.969723%

After filtering

total reads:	388.457622 M
total bases:	58.364281 G
Q20 bases:	55.595814 G (95.256573%)
Q30 bases:	51.419543 G (88.101047%)
GC content:	42.682058%

Filtering result

reads passed filters:	388.457622 M (86.958257%)
reads with low quality:	43.425834 M (9.721099%)
reads with too many N:	4.586000 K (0.001027%)
reads too short:	14.685600 M (3.287448%)
reads with low complexity:	143.710000 K (0.032170%)

Adapters

Adapter or bad ligation of read1

The input has little adapter percentage (~0.396219%), probably it's trimmed before.

Sequence	Occurrences
A	73927
AG	69294
AGA	70800
AGAT	68279
AGATC	

	68658
AGATCG	66726
AGATCGG	63439
AGATCGGA	60059
AGATCGGAA	60570
AGATCGGAAG	59743
AGATCGGAAGA	59369
AGATCGGAAGAG	58055
AGATCGGAAGAGC	56139
AGATCGGAAGAGCA	56413
AGATCGGAAGAGCAC	53685
AGATCGGAAGAGCACA	53857
AGATCGGAAGAGCACAC	50866
AGATCGGAAGAGCACACG	50719
AGATCGGAAGAGCACACGT	48312
AGATCGGAAGAGCACACGTC	48210
AGATCGGAAGAGCACACGTCT	46842
AGATCGGAAGAGCACACGTCTG	45625
AGATCGGAAGAGCACACGTCTGA	45280
AGATCGGAAGAGCACACGTCTGAA	44556
AGATCGGAAGAGCACACGTCTGAAC	43315
AGATCGGAAGAGCACACGTCTGAACT	41029
AGATCGGAAGAGCACACGTCTGAACTC	41219
AGATCGGAAGAGCACACGTCTGAACTCC	40438
AGATCGGAAGAGCACACGTCTGAACTCCA	40394
AGATCGGAAGAGCACACGTCTGAACTCCAG	38577
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGCCGTCTTCTGCTT	45958
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGCCGTCTTCTGCTTGAAAA	50994
other adapter sequences	2029764

Adapter or bad ligation of read2

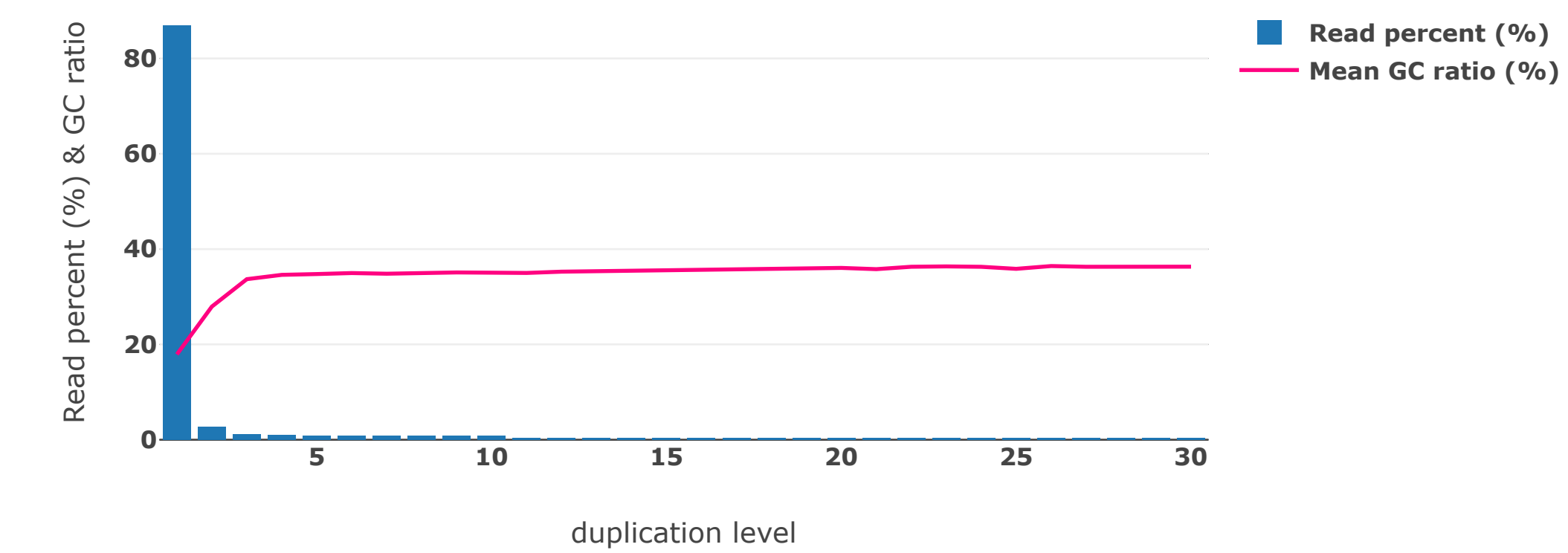
The input has little adapter percentage (~0.347312%), probably it's trimmed before.

Sequence	Occurrences
A	73924
AG	69319
AGA	70763
AGAT	68718
AGATC	68941
AGATCG	67205
AGATCGG	64632
AGATCGGA	60215
AGATCGGAA	60367

AGATCGGAAG	60334
AGATCGGAAGA	59304
AGATCGGAAGAG	58668
AGATCGGAAGAGC	56676
AGATCGGAAGAGCG	56616
AGATCGGAAGAGCGT	51222
AGATCGGAAGAGCGTC	54225
AGATCGGAAGAGCGTCG	51137
AGATCGGAAGAGCGTCGT	48558
AGATCGGAAGAGCGTCGTG	49770
AGATCGGAAGAGCGTCGTGT	46900
AGATCGGAAGAGCGTCGTGTA	47455
AGATCGGAAGAGCGTCGTGTAG	44764
AGATCGGAAGAGCGTCGTGTAGG	55309
AGATCGGAAGAGCGTCGTGTAGGG	45414
AGATCGGAAGAGCGTCGTGTAGGGA	45315
AGATCGGAAGAGCGTCGTGTAGGGAA	39710
AGATCGGAAGAGCGTCGTGTAGGGAAA	60619
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGT	51962
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTG	63656
other adapter sequences	2106054

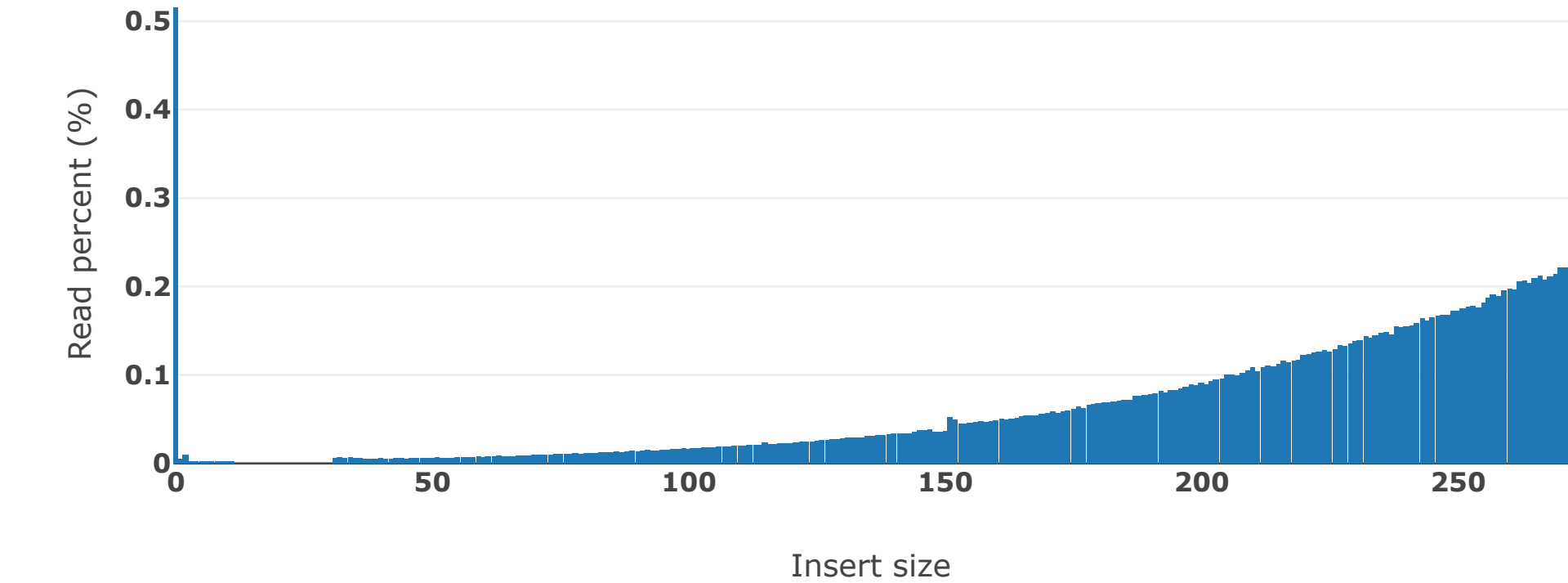
Duplication

duplication rate (70.067729%)



Insert size estimation

Insert size distribution (83.584125% reads are with unknown length)

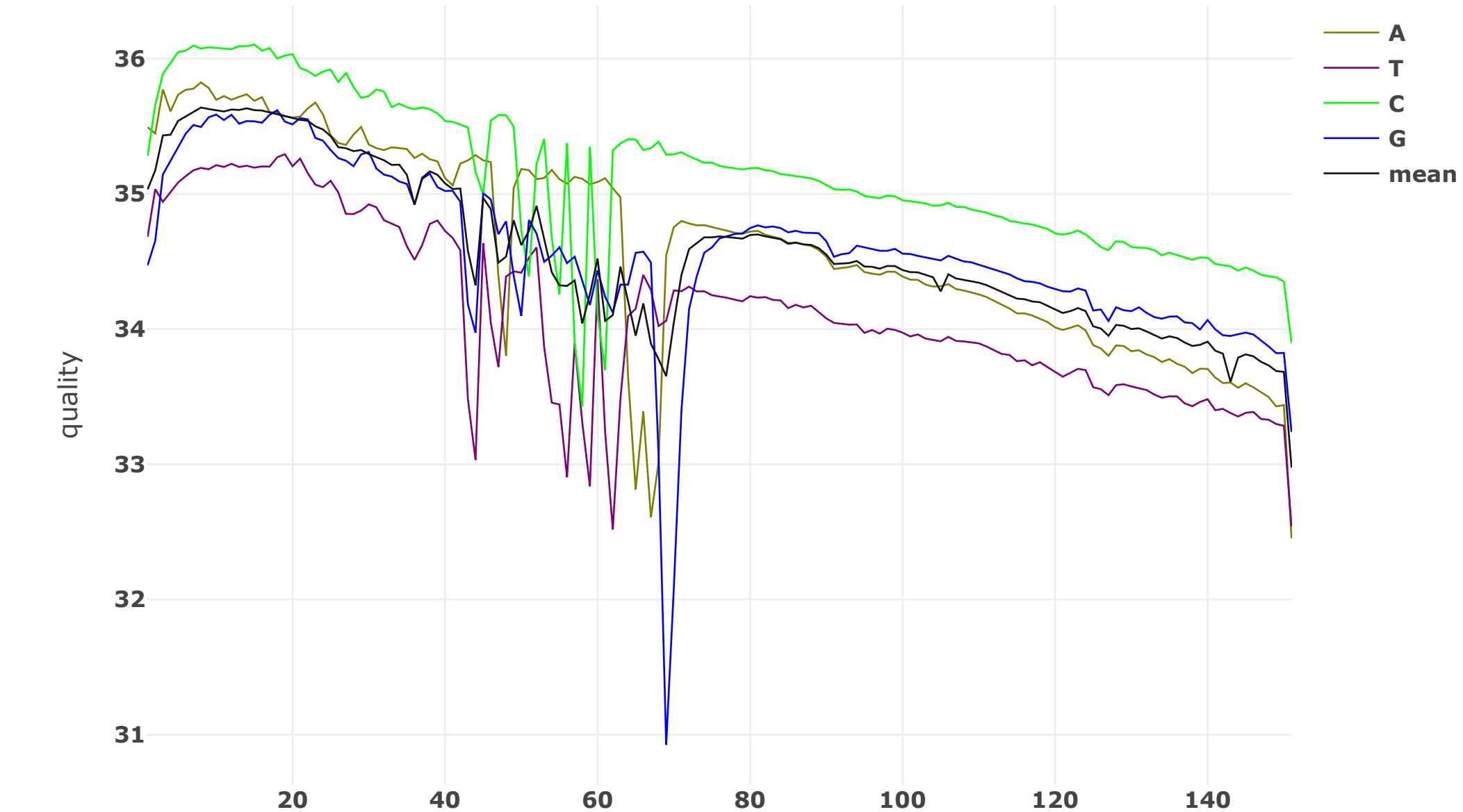


This estimation is based on paired-end overlap analysis, and there are 83.584125% reads found not overlapped. The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

Before filtering

Before filtering: read1: quality

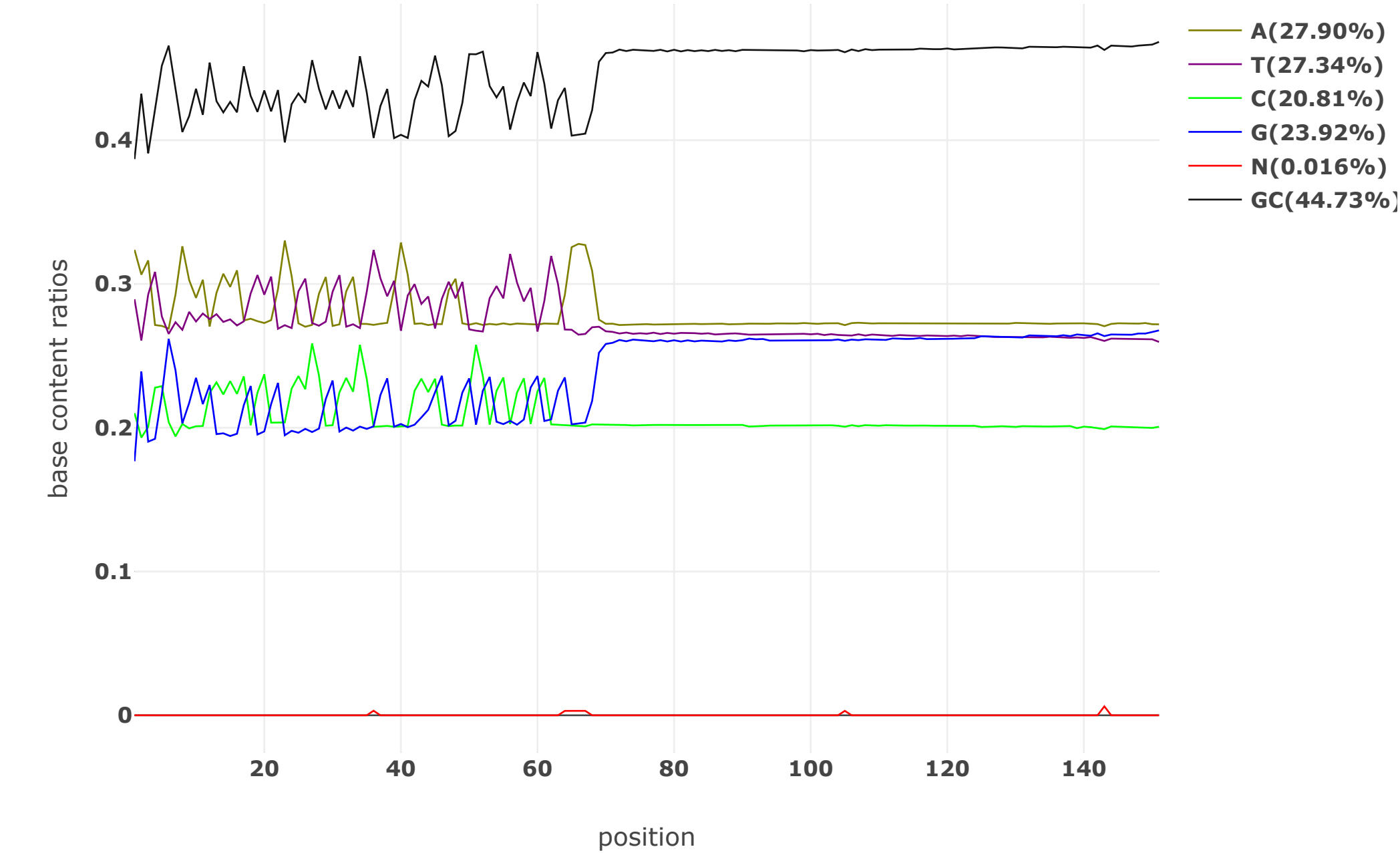
Value of each position will be shown on mouse over.



position

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.

	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	ACCCT	ACCCC	ACCCG	ACCGA	ACCGT	ACCGC	ACCGG
ACG	ACGAA	ACGAT	ACGAC	ACGAG	ACGTA	ACGTT	ACGTC	ACGTG	ACGCA	ACGCT	ACGCC	ACGCG	ACGGA	ACGGT	ACGGC	ACGGG
AGA	AGAAA	AGAAT	AGAAC	AGAAG	AGATA	AGATT	AGATC	AGATG	AGACA	AGACT	AGACC	AGACG	AGAGA	AGAGT	AGAGC	AGAGG
AGT	AGTAA	AGTAT	AGTAC	AGTAG	AGTTA	AGTTT	AGTTC	AGTTG	AGTCA	AGTCT	AGTCC	AGTCG	AGTGA	AGTGT	AGTGC	AGTGG
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
TTA	TTAAA	TTAAT	TTAAC	TTAAG	TTATA	TTATT	TTATC	TTATG	TTACA	TTACT	TTACC	TTACG	TTAGA	TTAGT	TTAGC	TTAGG
TTT	TTTAA	TTTAT	TTTAC	TTTAG	TTTTA	TTTTT	TTTTT	TTTTG	TTTCA	TTTCT	TTTCC	TTTCG	TTTGA	TTTGT	TTTGC	TTTGG
TTC	TTCAA	TTCAT	TTCAC	TTCAG	TTCTA	TTCTT	TTCTC	TTCTG	TTCCA	TTCCT	TTCCC	TTCCG	TTCGA	TTCGT	TTCGC	TTCGG
TTG	TTGAA	TTGAT	TTGAC	TTGAG	TTGTA	TTGTT	TTGTC	TTGTG	TTGCA	TTGCT	TTGCC	TTGCG	TTGGA	TTGGT	TTGGC	TTGGG
TCA	TCAAA	TCAAT	TCAAC	TCAAG	TCATA	TCATT	TCATC	TCATG	TCACA	TCACT	TCACC	TCACG	TCAGA	TCAGT	TCAGC	TCAGG
TCT	TCTAA	TCTAT	TCTAC	TCTAG	TCTTA	TCTTT	TCTTC	TCTTG	TCTCA	TCTCT	TCTCC	TCTCG	TCTGA	TCTGT	TCTGC	TCTGG
TCC	TCCAA	TCCAT	TCCAC	TCCAG	TCCTA	TCCTT	TCCTC	TCCTG	TCCCA	TCCCT	TCCCC	TCCCG	TCCGA	TCCGT	TCCGC	TCCGG

TGG	TCGAA	TCGAT	TCGAC	TCGAG	TCGTA	TCGTT	TCGTC	TCGTG	TCGCA	TCGCT	TCGCC	TCGCG	TCGGA	TCGGT	TCGGC	TCGGG
TGA	TGAAA	TGAAT	TGAAC	TGAAG	TGATA	TGATT	TGATC	TGATG	TGACA	TGACT	TGACC	TGACG	TGAGA	TGAGT	TGAGC	TGAGG
TGT	TGTAA	TGTAT	TGTAC	TGTAG	TGTTA	TGTTT	TGTTT	TGTTG	TGTCA	TGTCT	TGTCC	TGTCT	TGTGA	TGTGT	TGTGC	TGTGG
TGC	TGCAA	TGCAT	TGCAC	TGCAG	TGCTA	TGCTT	TGCTC	TGCTG	TGCCA	TGCCT	TGCCC	TGCCG	TGCCA	TGCGT	TGCGC	TGCGG
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
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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CTC	CTCAA	CTCAT	CTCAC	CTCAG	CTCTA	CTCTT	CTCTC	CTCTG	CTCCA	CTCCT	CTCCC	CTCCG	CTCGA	CTCGT	CTCGC	CTCGG
CTG	CTGAA	CTGAT	CTGAC	CTGAG	CTGTA	CTGTT	CTGTC	CTGTG	CTGCA	CTGCT	CTGCC	CTGCG	CTGGA	CTGGT	CTGGC	CTGGG
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
CCG	CCGAA	CCGAT	CCGAC	CCGAG	CCGTA	CCGTT	CCGTC	CCGTG	CCGCA	CCGCT	CCGCC	CCGCG	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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CGC	CGCAA	CGCAT	CGCAC	CGCAG	CGCTA	CGCTT	CGCTC	CGCTG	CGCCA	CGCCT	CGCCC	CGCCG	CGCGA	CGCGT	CGCGC	CGCGG
CGG	CGGAA	CGGAT	CGGAC	CGGAG	CGGTA	CGGTT	CGGTC	CGGTG	CGGCA	CGGCT	CGGCC	CGGCG	CGGGA	CGGGT	CGGGC	CGGGG
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	GTAAA	GTAAT	GTAAC	GTAAG	GTATA	GTATT	GTATC	GATG	GTACA	GTA	GTA	GTA	GTA	GTA	GTA	GTA
GTT	GTTAA	GTTAT	GTTAC	GTTAG	GTTTA	GTTTT	GTTTC	GTTTG	GTTCA	GTTCT	GTTCC	GTTCT	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCAC	GTCAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GTCTT	GTCCC	GTCCG	GTCTGA	GTCTGT	GTCTGC	GTCTGG
GTG	GTGAA	GTGAT	GTGAC	GTGAG	GTGTA	GTGTT	GTGTC	GTGTG	GTGCA	GTGCT	GTGCC	GTGCG	GTGGA	GTGGT	GTGGC	GTGGG
GCA	GCAAA	GCAAT	GCAAC	GCAAG	GCATA	GCATT	GCATC	GCATG	GCACA	GCA	GCA	GCA	GCA	GCA	GCA	GCA
GCT	GCTAA	GCTAT	GCTAC	GCTAG	GCTTA	GCTTT	GCTTC	GCTTG	GCTCA	GCTCT	GCTCC	GCTCG	GCTGA	GCTGT	GCTGC	GCTGG
GCC	GCCAA	GCCAT	GCCAC	GCCAG	GCCTA	GCCTT	GCCTC	GCCTG	GCCCA	GCCTT	GCCCC	GCCCG	GCCGA	GCCGT	GCCGC	GCCGG
GCG	GCGAA	GCGAT	GCGAC	GCGAG	GCGTA	GCGTT	GCGTC	GCGTG	GCGCA	GCGCT	GCGCC	GCGCG	GCGGA	GCGGT	GCGGC	GCGGG
GGA	GGAAA	GGAAT	GGAAC	GGAAG	GGATA	GGATT	GGATC	GGATG	GGACA	GGA	GGA	GGA	GGA	GGA	GGA	GGA
GGT	GGTAA	GGTAT	GGTAC	GGTAG	GGTTA	GGTTT	GGTTC	GGTTG	GGTCA	GGTCT	GGTCC	GGTCG	GGTGA	GGTGT	GGTGC	GGTGG
GGC	GGCAA	GGCAT	GGCAC	GGCAG	GGCTA	GGCTT	GGCTC	GGCTG	GGCCA	GGCCT	GGCCC	GGCCG	GGCGA	GGCGT	GGCGC	GGCGG
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

Before filtering: read1: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAGATGTGTATAAGAGACA	86282 (0.102329%)	
AAGATGTGTATAAGAGACAG	149980 (0.177874%)	
AAGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	17427 (0.041336%)	
ACACACACACACACACACACACACACACACACACAA	2326 (0.005517%)	
ACACACACACACACACACACACACACACACACACACAC	58007 (0.137591%)	
ACACACACACACACACACACACACACACACACACACAG	1568 (0.003719%)	
ACACACACACACACACACACACACCTGTCTCTTATACACATC	15516 (0.036804%)	
ACACACACACACCTGTCTCTTATACACATCTAGATGTGTATA	11379 (0.026991%)	
ACACACACACCTGTCTCTTATACACATCTAGATGTGTATA	1309 (0.003105%)	
ACACACACCTGTCTCTTATACACATCTAGATGTGTATAAG	1667 (0.003954%)	
ACACACCTGTCTCTTATACACATCTAGATGTGTATAAGAG	3488 (0.008273%)	
ACACATCTAGATGTGTATAAGAGACAGCACACACACACAC	157 (0.000372%)	
ACACATCTAGATGTGTATAAGAGACAGGTGTGTGTGTGTG	157 (0.000372%)	
ACACCTGTCTCTTATACACATCTAGATGTGTATAAGAGAC	21275 (0.050464%)	
ACAGATGTGTATAAGAGACA	98384 (0.116682%)	
ACATCTAGATGTGTATAAGAGACAGGTGTGTGTGTGTG	199 (0.000472%)	
ACCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	27626 (0.065528%)	
ACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	31832 (0.075505%)	
ACTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGC	15738 (0.037330%)	


























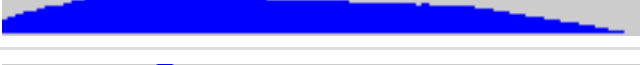



[illegible]

[illegible]

[illegible]

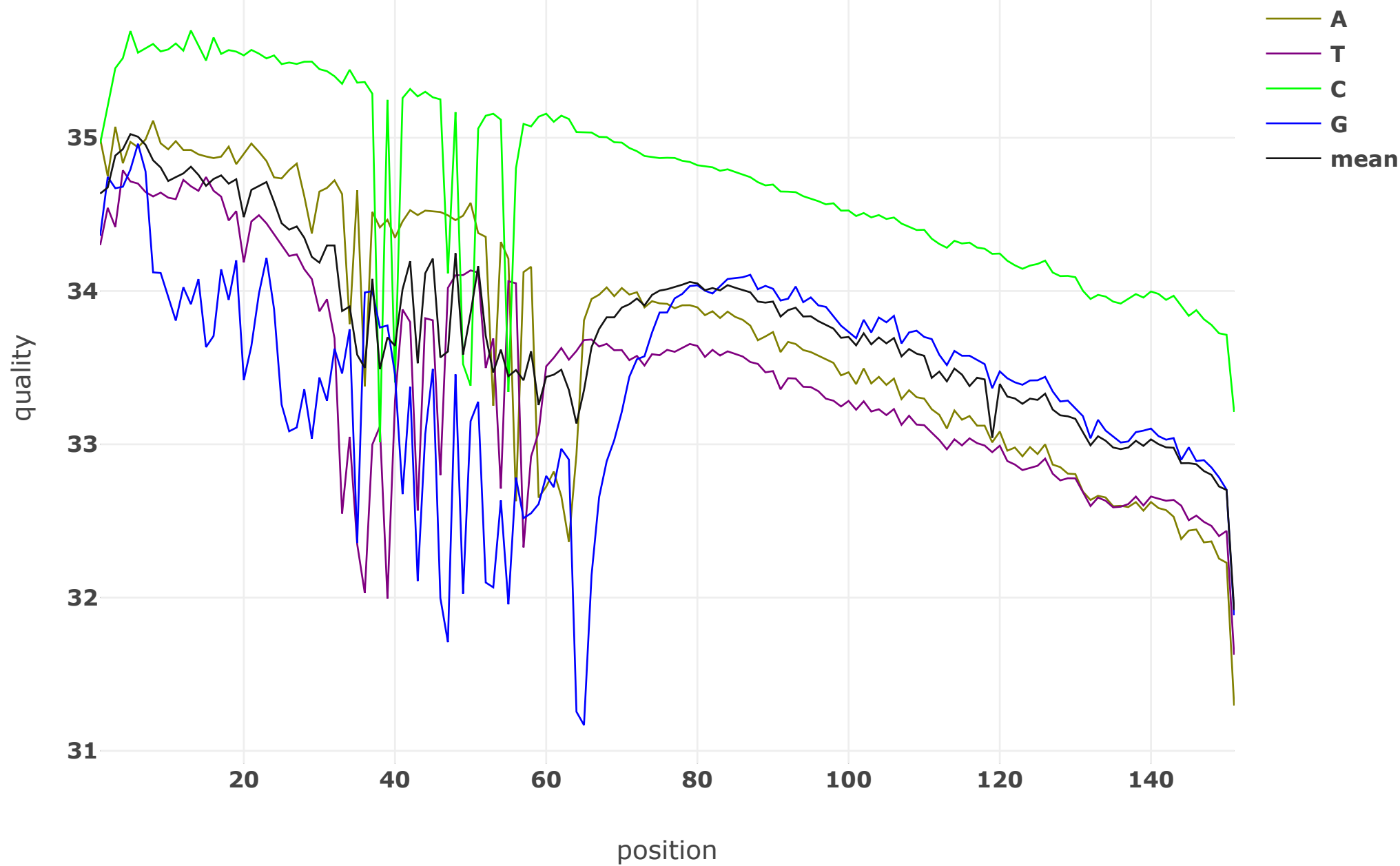
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[illegible]

TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCTT	56 (0.000133%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAA	68 (0.000161%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAG	86 (0.000204%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAT	79 (0.000187%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGCA	62 (0.000147%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGCT	95 (0.000225%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGG	101 (0.000240%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGT	88 (0.000209%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTA	137 (0.000325%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTC	78 (0.000185%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTG	261 (0.000619%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTT	99 (0.000235%)	
TGTCTCTTATACACATCTCA	891 (0.001057%)	
TGTCTCTTATACACATCTCT	623 (0.000739%)	
TGTCTCTTATACACATCTTG	655 (0.000777%)	
TGTCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	17648 (0.041861%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGAC	11772 (0.027923%)	
TGTGTATAAGAGACAGCACACACACACACACACACACA	36 (0.000085%)	
TGTGTATAAGAGACAGGTGTGTGTGTGTGTGTGTGTGT	49 (0.000116%)	
TGTGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAG	4414 (0.010470%)	
TGTGTGTGCTGTCTCTTATACACATCTAGATGTGTATAAG	2093 (0.004965%)	
TGTGTGTGTGCTGTCTCTTATACACATCTAGATGTGTATA	3993 (0.009471%)	
TGTGTGTGTGTGCTGTCTCTTATACACATCTAGATGTGTA	13161 (0.031218%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTCTTATACACATC	16029 (0.038020%)	
TG	39916 (0.094680%)	
TGTT	1082 (0.002566%)	
TTATACACATCTAGATGTGTATAAGAGACAGCACACACAC	70 (0.000166%)	
TTATACACATCTAGATGTGTATAAGAGACAGGTGTGTGTG	36 (0.000085%)	
TTCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	20890 (0.049551%)	

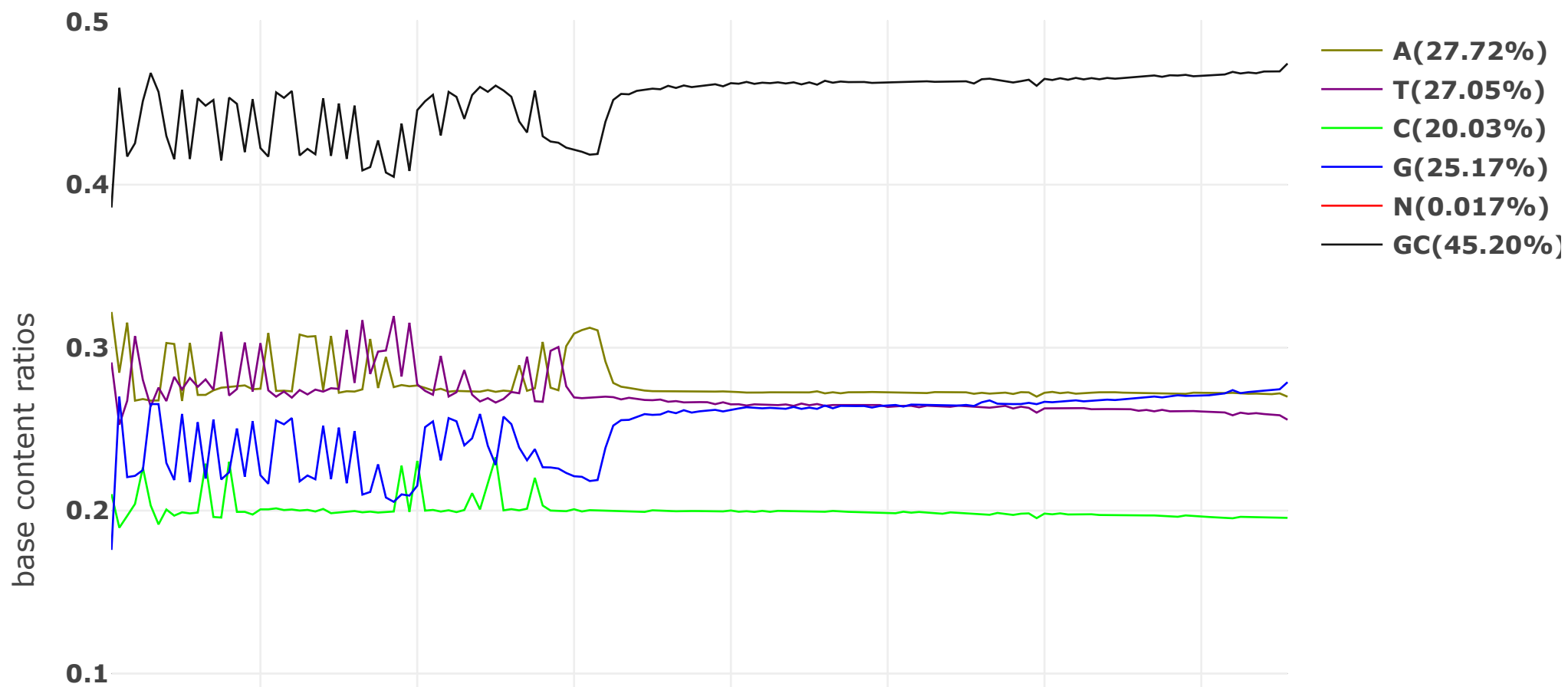
Before filtering: read2: quality

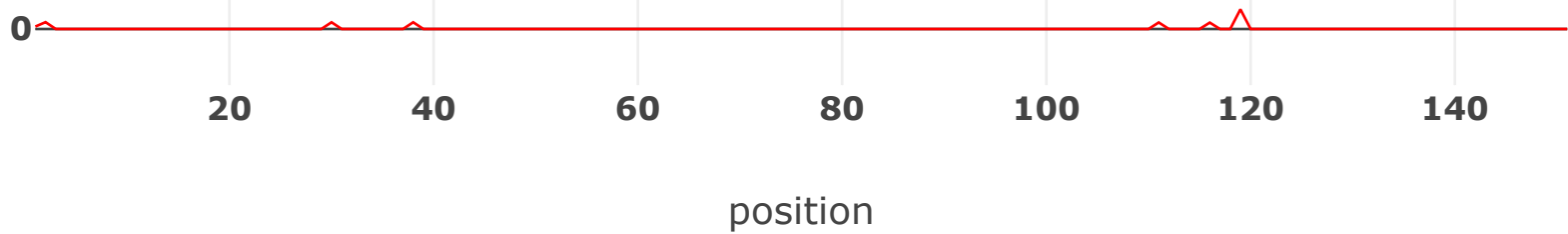
Value of each position will be shown on mouse over.



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.

	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	AAC TT	AAC TC	AAC TG	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	ATTT C	ATTT G	ATTCA	ATTCT	ATTCC	ATT CG	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	ACCCT	ACCCC	ACCCG	ACCGA	ACCGT	ACCGC	ACCGG
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TAT	TATAA	TATAT	TATAC	TATAG	TATTA	TATTT	TATTC	TATTG	TATCA	TATCT	TATCC	TATCG	TATGA	TATGT	TATGC	TATGG
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Before filtering: read2: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	10218 (0.024237%)	
AAAATGGGGGGGGGGGGGGGGGGGGG	26622 (0.063147%)	
AAATGGGGGGGGGGGGGGGGGGGGGG	5980 (0.014184%)	
AACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	25390 (0.060224%)	

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[illegible]

[illegible]

[illegible]

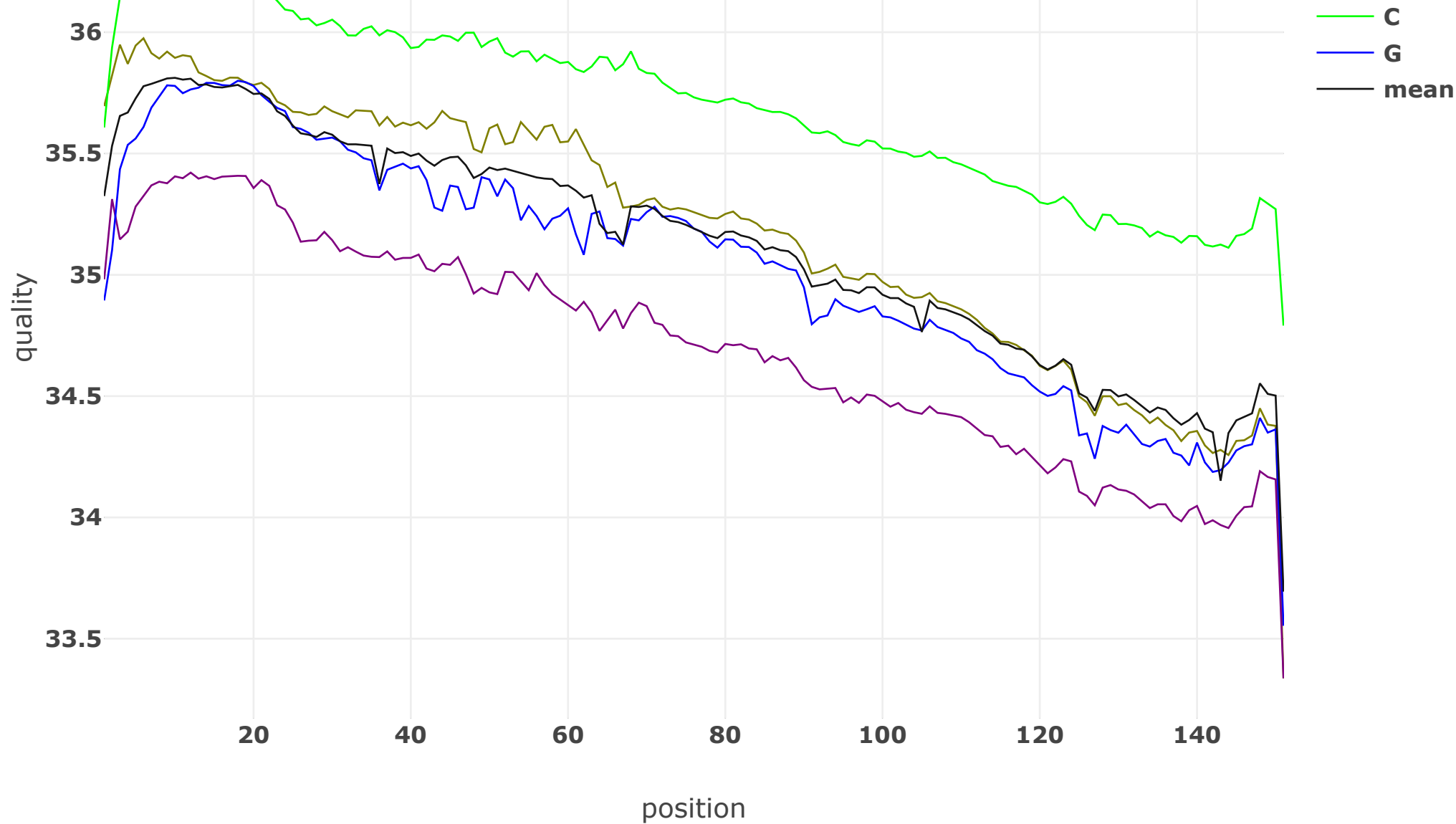
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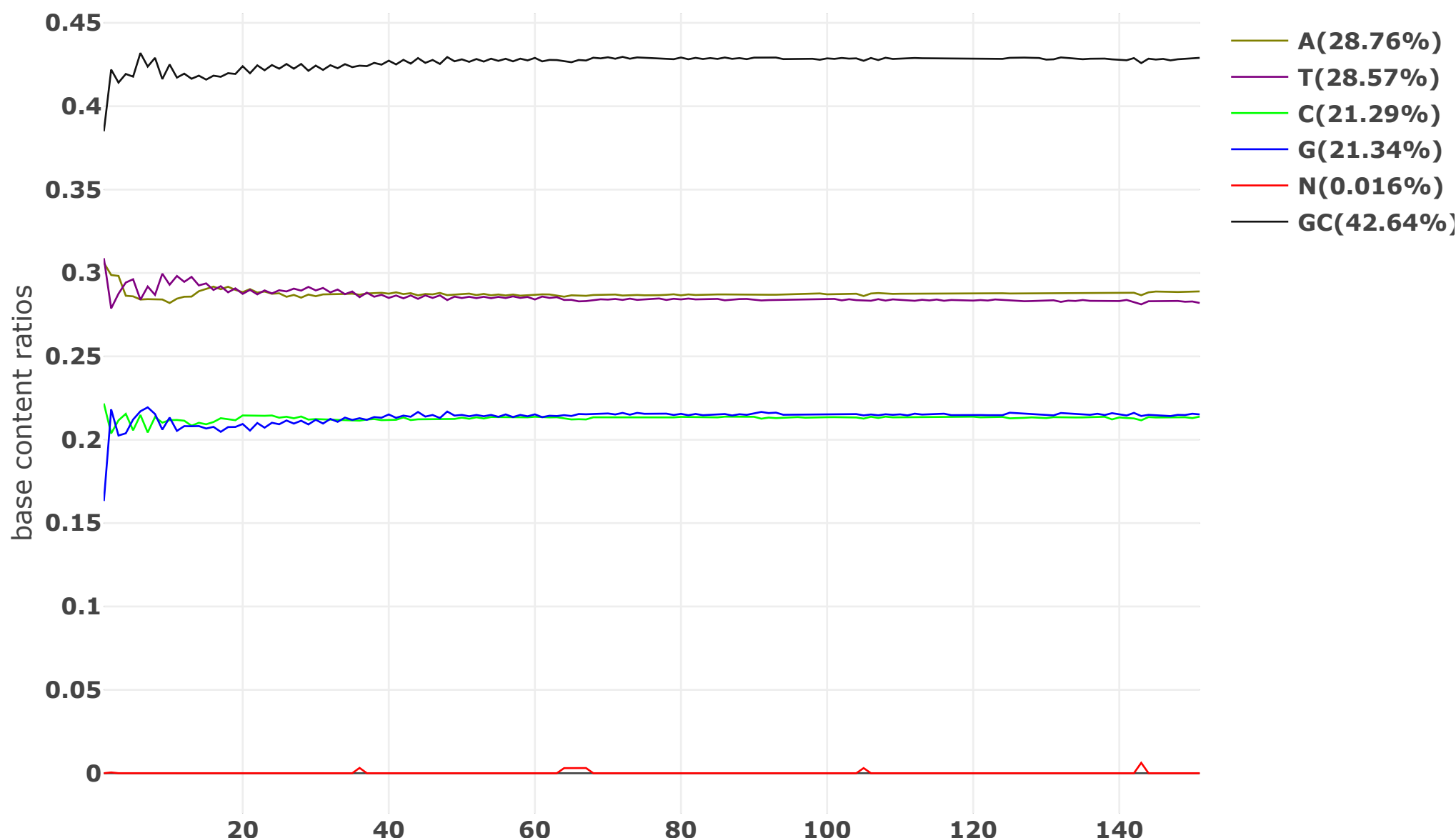
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[illegible]



After filtering: read1: base contents

Value of each position will be shown on mouse over.



position

After filtering: read1: KMER counting

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






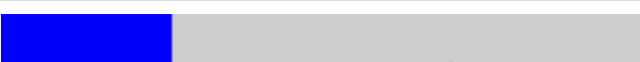




















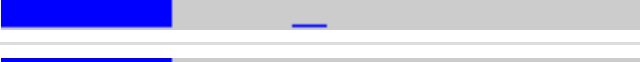
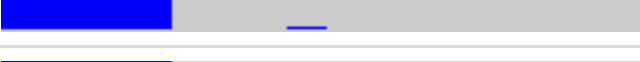





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After filtering: read1: overrepresented sequences


















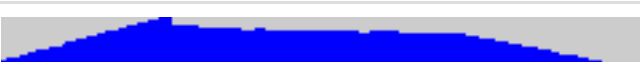















Sampling rate: 1 / 20












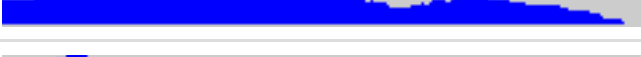
















overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
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AAGATGTGTATAAGAGACAG	142516 (0.195314%)	
AAGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	17095 (0.046856%)	
ACACACACACACACACACACACACACACACACACAA	1655 (0.004536%)	
ACACACACACACACACACACACACACACACACACAC	47647 (0.130598%)	
ACACACACACACACACACACACACACACACACACAG	1316 (0.003607%)	

[illegible]

		
CACACACACACCTGTCTCTTATACACATCTAGATGTGTAT	1514 (0.004150%)	
CACACACACCTGTCTCTTATACACATCTAGATGTGTATAA	1226 (0.003360%)	
CACACACCTGTCTCTTATACACATCTAGATGTGTATAAGA	2568 (0.007039%)	
CACACCTGTCTCTTATACACATCTAGATGTGTATAAGAGA	5941 (0.016284%)	
CACATCTAGATGTGTATAAGAGACAGGTGTGTGTGTGT	133 (0.000365%)	
CACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	21127 (0.057908%)	
CAGATGTGTATAAGAGACAG	113028 (0.154902%)	
CATCTAGATGTGTATAAGAGACAGGTGTGTGTGTGTGT	151 (0.000414%)	
CCAGATGTGTATAAGAGACA	103373 (0.141670%)	
CCCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	21814 (0.059791%)	
CCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	42989 (0.117831%)	
CCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGA	774 (0.002121%)	
CCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGC	1760 (0.004824%)	
CCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGG	2430 (0.006661%)	
CCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGT	398 (0.001091%)	
CTCACACACACACACACACACACACACACACACACACA	11921 (0.032675%)	
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4865 (0.013335%)	
CTCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	22256 (0.061003%)	
CTCTTATACACATCTAGATGTGTATAAGAGACAGCACACA	96 (0.000263%)	
CTCTTATACACATCTAGATGTGTATAAGAGACAGGTGTGT	49 (0.000134%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGAC	2718 (0.007450%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGAT	3101 (0.008500%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCA	584 (0.001601%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCC	345 (0.000946%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCT	319 (0.000874%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGA	319 (0.000874%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGC	343 (0.000940%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGG	444 (0.001217%)	
CTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGT	814 (0.002231%)	
CTGTCTCTTATACACATCTC	370290 (0.507473%)	
CTGTCTCTTATACACATCTG	318051 (0.435881%)	
CTGTCTCTTATACACATCTT	331418 (0.454200%)	
CTTATACACATCTAGATGTGTATAAGAGACAGCACACACA	58 (0.000159%)	

[illegible]

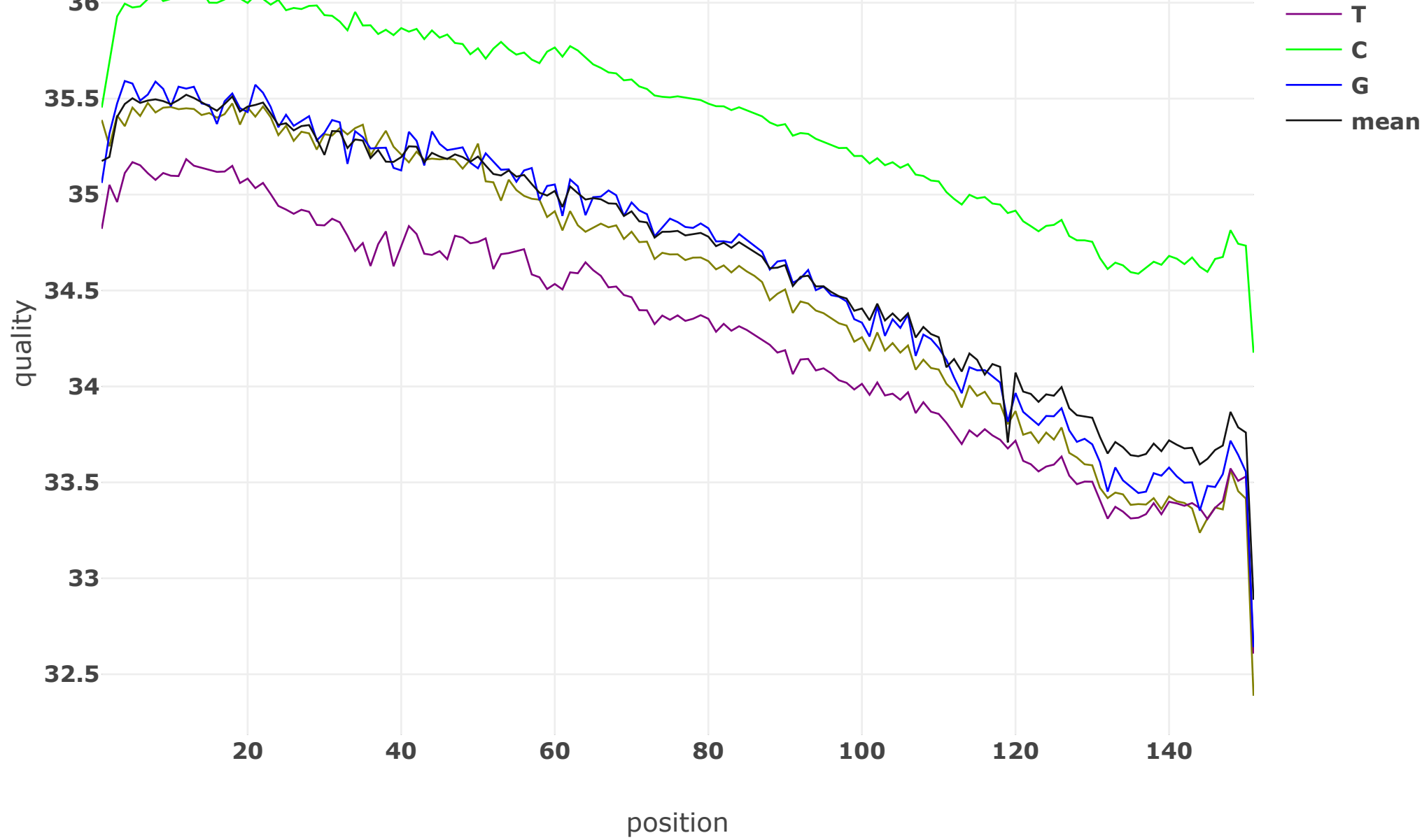
		
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GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA	828 (0.002270%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	23346 (0.063990%)	
TACACACACACACACACA	87313 (0.119660%)	
TACACATCTAGATGTGTATAAGAGACAGCACACACACA	147 (0.000403%)	
TACACATCTAGATGTGTATAAGAGACAGGTGTGTGTGTGT	108 (0.000296%)	
TACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	36917 (0.101188%)	
TATAAGAGACAGGTGTGTGTGTGTGTGTGTGTGTGTGT	28 (0.000077%)	
TATACACATCTAGATGTGTATAAGAGACAGCACACACACA	98 (0.000269%)	
TATACACATCTAGATGTGTATAAGAGACAGGTGTGTGTGT	79 (0.000217%)	
TATCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	17904 (0.049074%)	
TCACACACACACACACACACACACACACACACACACAC	5414 (0.014839%)	
TCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	41050 (0.112516%)	
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	6341 (0.017380%)	
TCTCTTATACACATCTAGATGTGTATAAGAGACAGCACAC	75 (0.000206%)	
TCTCTTATACACATCTAGATGTGTATAAGAGACAGGTGTG	50 (0.000137%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGA	2830 (0.007757%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGC	5698 (0.015618%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGG	8667 (0.023756%)	
TCTTATACACATCTAGATGTGTATAAGAGACAGCACACAC	43 (0.000118%)	
TCTTATACACATCTAGATGTGTATAAGAGACAGGTGTGTG	16 (0.000044%)	
TGAGATGTGTATAAGAGACA	136004 (0.186390%)	
TGCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	24963 (0.068422%)	
TGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	30250 (0.082914%)	
TGTATAAGAGACAGGTGTGTGTGTGTGTGTGTGTGTGT	43 (0.000118%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCAC	218 (0.000598%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCAT	132 (0.000362%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCCC	79 (0.000217%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCCT	96 (0.000263%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCTC	102 (0.000280%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCTG	56 (0.000153%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCTT	54 (0.000148%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAA	62 (0.000170%)	

		
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAG	80 (0.000219%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAT	91 (0.000249%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGCA	56 (0.000153%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGCT	104 (0.000285%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGG	89 (0.000244%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGT	98 (0.000269%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTA	114 (0.000312%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTC	72 (0.000197%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTG	243 (0.000666%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTT	88 (0.000241%)	
TGTCTCTTATACACATCTCA	749 (0.001026%)	
TGTCTCTTATACACATCTCT	566 (0.000776%)	
TGTCTCTTATACACATCTTG	559 (0.000766%)	
TGTCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	17239 (0.047251%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGAC	11371 (0.031167%)	
TGTGTATAAGAGACAGCACACACACACACACACACACA	29 (0.000079%)	
TGTGTATAAGAGACAGGTGTGTGTGTGTGTGTGTGTGT	37 (0.000101%)	
TGTGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAG	4228 (0.011589%)	
TGTGTGTGCTGTCTCTTATACACATCTAGATGTGTATAAG	1933 (0.005298%)	
TGTGTGTGTGCTGTCTCTTATACACATCTAGATGTGTATA	3942 (0.010805%)	
TGTGTGTGTGTGCTGTCTCTTATACACATCTAGATGTGTA	12604 (0.034547%)	
TGTGTGTGTGTGTGTGTGTGTGTGCTGTCTCTTATACACATC	15567 (0.042668%)	
TG	34347 (0.094143%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTT	870 (0.002385%)	
TTATACACATCTAGATGTGTATAAGAGACAGCACACACAC	58 (0.000159%)	
TTATACACATCTAGATGTGTATAAGAGACAGGTGTGTGTG	36 (0.000099%)	
TTCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	20104 (0.055104%)	

After filtering: read2: quality

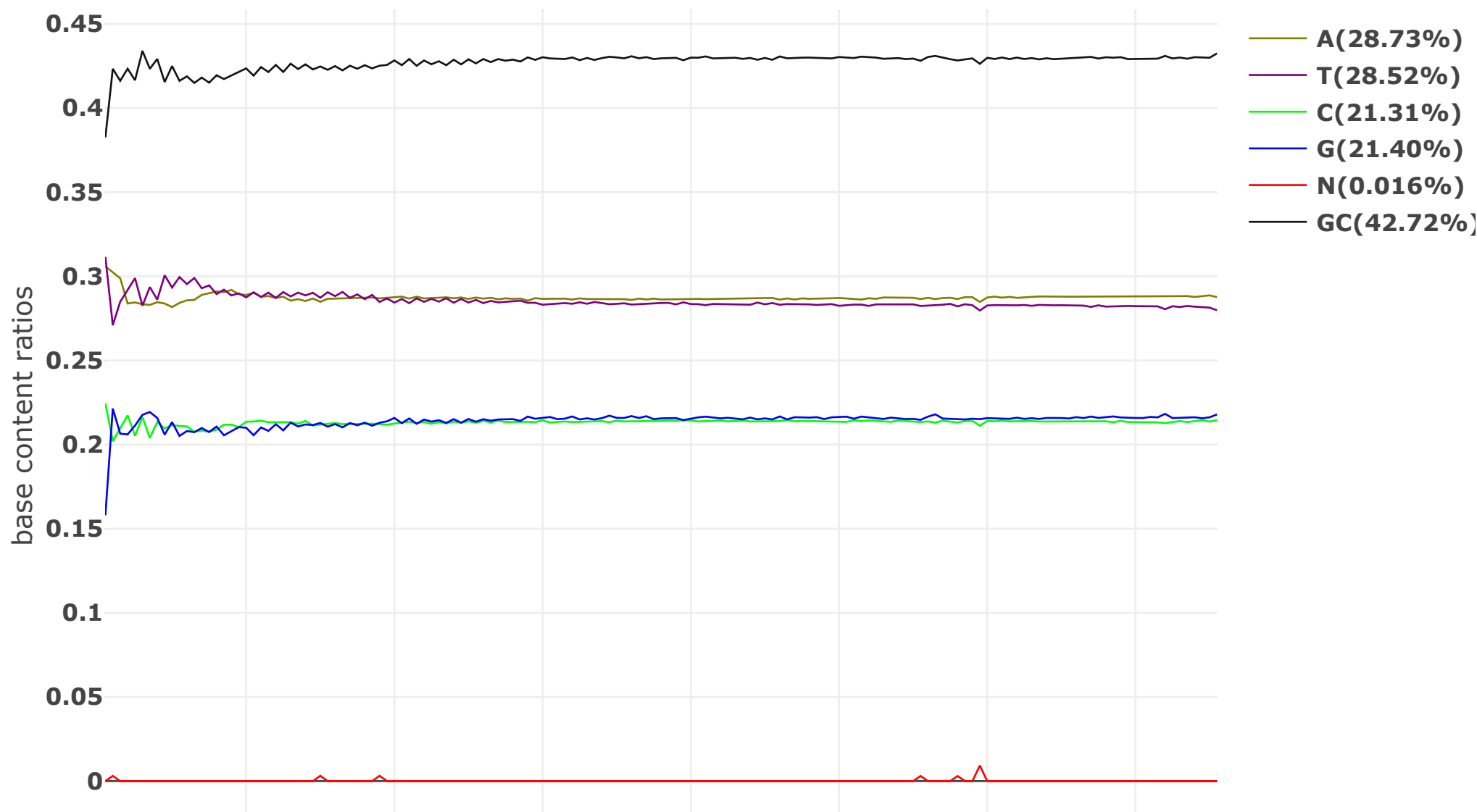
Value of each position will be shown on mouse over.

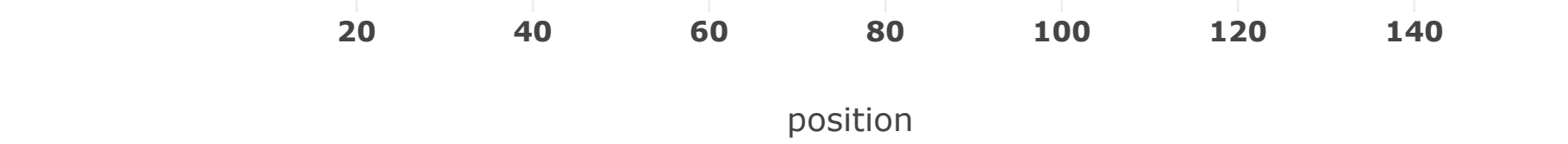




After filtering: read2: base contents

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
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	ATTCC	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	AC CCT	ACCCC	ACCCG	ACCGA	ACCGT	ACCGC	ACCGG
ACG	ACGAA	ACGAT	ACGAC	ACGAG	ACGTA	ACGTT	ACGTC	ACGTG	ACGCA	ACGCT	ACGCC	ACGCG	ACGGA	ACGGT	ACGGC	ACGGG
AGA	AGAAA	AGAAT	AGAAC	AGAAG	AGATA	AGATT	AGATC	AGATG	AGACA	AGACT	AGACC	AGACG	AGAGA	AGAGT	AGAGC	AGAGG
AGT	AGTAA	AGTAT	AGTAC	AGTAG	AGTTA	AGTTT	AGTTC	AGTTG	AGTCA	AGTCT	AGTCC	AGTCG	AGTGA	AGTGT	AGTGC	AGTGG
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
TTA	TTAAA	TTAAT	TTAAC	TTAAG	TTATA	TTATT	TTATC	TTATG	TTACA	TTACT	TTACC	TTACG	TTAGA	TTAGT	TTAGC	TTAGG
TTT	TTTAA	TTTAT	TTTAC	TTTAG	TTTTA	TTTTT	TTTTT	TTTTG	TTTCA	TTTCT	TTTCC	TTTCG	TTTGA	TTTGT	TTTGC	TTTGG
TTC	TTCAA	TTCAT	TTCAC	TTCAG	TTCTA	TTCTT	TTCTC	TTCTG	TTCCA	TTCCT	TTCCC	TTCCG	TTCGA	TTCGT	TTCGC	TTCGG
TTG	TTGAA	TTGAT	TTGAC	TTGAG	TTGTA	TTGTT	TTGTC	TTGTG	TTGCA	TTGCT	TTGCC	TTGCG	TTGGA	TTGGT	TTGGC	TTGGG
TCA	TCAAA	TCAAT	TCAAC	TCAAG	TCATA	TCATT	TCATC	TCATG	TCACA	TCACT	TCACC	TCACG	TCAGA	TCAGT	TCAGC	TCAGG
TCT	TCTAA	TCTAT	TCTAC	TCTAG	TCTTA	TCTTT	TCTTC	TCTTG	TCTCA	TCTCT	TCTCC	TCTCG	TCTGA	TCTGT	TCTGC	TCTGG
TCC	TCCAA	TCCAT	TCCAC	TCCAG	TCCTA	TCCTT	TCCTC	TCCTG	TCCCA	TCCCT	TCCCC	TCCCG	TCCGA	TCCGT	TCCGC	TCCGG
TCG	TCGAA	TCGAT	TCGAC	TCGAG	TCGTA	TCGTT	TCGTC	TCGTG	TCGCA	TCGCT	TCGCC	TCGCG	TCGGA	TCGGT	TCGGC	TCGGG
TGA	TGAAA	TGAAT	TGAAC	TGAAG	TGATA	TGATT	TGATC	TGATG	TGACA	TGACT	TGACC	TGACG	TGAGA	TGAGT	TGAGC	TGAGG
TGT	TGTAA	TGTAT	TGTAC	TGTAG	TGTTA	TGT TT	TGTTC	TGT TG	TGTCA	TGTCT	TGTCC	TGT CG	TGTGA	TGTGT	TGTGC	TGTGG
TGC	TGCAA	TGCAT	TGCAC	TGCAG	TGCTA	TGCTT	TGCTC	TGCTG	TGCCA	TG CCT	TGCCC	TGCCG	TGCCA	TGCGT	TGCGC	TGCGG
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
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
CTA	CTAAA	CTAAT	CTAAC	CTAAG	CTATA	CTATT	CTATC	CTATG	CTACA	CTACT	CTACC	CTACG	CTAGA	CTAGT	CTAGC	CTAGG
CTT	CTTAA	CTTAT	CTTAC	CTTAG	CTTTA	CTTTT	CTTTC	CTTTG	CTTCA	CTTCT	CTTCC	CTTCG	CTTGA	CTTGT	CTTGC	CTTGG
CTC	CTCAA	CTCAT	CTCAC	CTCAG	CTCTA	CTCTT	CTCTC	CTCTG	CTCCA	CTCCT	CTCCC	CTCCG	CTCGA	CTCGT	CTCGC	CTCGG
CTG	CTGAA	CTGAT	CTGAC	CTGAG	CTGTA	CTGTT	CTGTC	CTGTG	CTGCA	CTGCT	CTGCC	CTGCG	CTGGA	CTGGT	CTGGC	CTGGG
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	CC CCT	CCCCC	CCCCG	CCCCA	CCCGT	CCCGC	CCCGG
CCG	CCGAA	CCGAT	CCGAC	CCGAG	CCGTA	CCGTT	CCGTC	CCGTG	CCGCA	CCGCT	CCGCC	CCGCG	CCGGA	CCGGT	CCGGC	CCGGG
CGA	CGAAA	CGAAT	CGAAC	CGAAG	CGATA	CGATT	CGATC	CGATG	CGACA	CGACT	CGACC	CGACG	CGAGA	CGAGT	CGAGC	CGAGG
CGT	CGTAA	CGTAT	CGTAC	CGTAG	CGTTA	CGTTT	CGTTC	CGTTG	CGTCA	CGTCT	CGTCC	CGTCG	CGTGA	CGTGT	CGTGC	CGTGG
CGC	CGCAA	CGCAT	CGCAC	CGCAG	CGCTA	CGCTT	CGCTC	CGCTG	CGCCA	CG CCT	CGCCC	CGCCG	CGCCA	CGCGT	CGCGC	CGCGG
CGG	CGGAA	CGGAT	CGGAC	CGGAG	CGGTA	CGGTT	CGGTC	CGGTG	CGGCA	CGGCT	CGGCC	CGGCG	CGGGA	CGGGT	CGGGC	CGGGG
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	GTAAA	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	GTT CG	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCAC	GTCAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GT CCT	GTCCC	GTCCG	GTCGA	GTCGT	GTCGC	GTCGG
GTG	GTGAA	GTGAT	GTGAC	GTGAG	GTGTA	GTGTT	GTGTC	GTGTG	GTGCA	GTGCT	GTGCC	GTGCG	GTGGA	GTGGT	GTGGC	GTGGG
GCA	GCAAA	GCAAT	GCAAC	GCAAG	GCATA	GCATT	GCATC	GCATG	GCACA	GCACT	GCACC	GCACG	GCAGA	GCAGT	GCAGC	GCAGG
GCT	GCTAA	GCTAT	GCTAC	GCTAG	GCTTA	GCTTT	GCTTC	GCTTG	GCTCA	GCTCT	GCTCC	GCTCG	GCTGA	GCTGT	GCTGC	GCTGG
GCC	GCCAA	GCCAT	GCCAC	GCCAG	GCCTA	GCCTT	GCCTC	GCCTG	GCCCA	GC CCT	GCCCC	GCCCG	GCCGA	GCCGT	GCCGC	GCCGG
GCG	GCGAA	GCGAT	GCGAC	GCGAG	GCGTA	GCGTT	GCGTC	GCGTG	GCGCA	GCGCT	GCGCC	GCGCG	GCGGA	GCGGT	GCGGC	GCGGG
GGA	GGAAA	GGAAT	GGAAC	GGAAG	GGATA	GGATT	GGATC	GGATG	GGACA	GGACT	GGACC	GGACG	GGAGA	GGAGT	GGAGC	GGAGG
GGT	GGTAA	GGTAT	GGTAC	GGTAG	GGTTA	GGTTT	GGTTC	GGTTG	GGTCA	GGTCT	GGTCC	GGTCG	GGTGA	GGTGT	GGTGC	GGTGG
GGC	GGCAA	GGCAT	GGCAC	GGCAG	GGCTA	GGCTT	GGCTC	GGCTG	GGCCA	GG CCT	GGCCC	GGCCG	GGCGA	GGCGT	GGCGC	GGCGG
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG



































After filtering: read2: overrepresented sequences
















Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	182 (0.000499%)	
AACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	24838 (0.068102%)	
AAGATGTGTATAAGAGACAG	335251 (0.459605%)	
ACACACACACACACACACACACACACACACACACAA	1578 (0.004327%)	
ACACACACACACACACACACACACACACACACACAC	44138 (0.121020%)	

[illegible]

[illegible]

		
GTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTGT	117 (0.000321%)	
GTCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	38180 (0.104684%)	
GTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	14173 (0.038860%)	
GTGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGA	2274 (0.006235%)	
GTGTGTGCTGTCTCTTATACACATCTAGATGTGTATAAGA	1811 (0.004966%)	
GTGTGTGTGCTGTCTCTTATACACATCTAGATGTGTATAA	2913 (0.007987%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA	1215 (0.003331%)	
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	31155 (0.085423%)	
TACCTGTCTCTTATACACATCTAGATGTGTATAAGAGACA	15668 (0.042959%)	
TATACACATCTAGATGTGTATAAGAGACAGCACACACACA	85 (0.000233%)	
TCACACACACACACACACACACACACACACACACACAC	15346 (0.042077%)	
TCCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	30209 (0.082829%)	
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	8746 (0.023980%)	
TCTCTTATACACATCTAGATGTGTATAAGAGACAGCACAC	76 (0.000208%)	
TCTCTTATACACATCTAGATGTGTATAAGAGACAGGTGTG	45 (0.000123%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGA	183 (0.000502%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGC	357 (0.000979%)	
TCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGG	553 (0.001516%)	
TCTTATACACATCTAGATGTGTATAAGAGACAGCACACAC	48 (0.000132%)	
TGAGATGTGTATAAGAGACA	138851 (0.190355%)	
TGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	26751 (0.073347%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCAC	295 (0.000809%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCAT	105 (0.000288%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCCC	108 (0.000296%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCCT	91 (0.000250%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCTC	124 (0.000340%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGAG	91 (0.000250%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGCA	68 (0.000186%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGA	98 (0.000269%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGC	109 (0.000299%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGG	107 (0.000293%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGGT	106 (0.000291%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTA	124 (0.000340%)	

		
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTC	134 (0.000367%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTG	358 (0.000982%)	
TGTCTCTTATACACATCTAGATGTGTATAAGAGACAGGTT	135 (0.000370%)	
TGTCTCTTATACACATCTCA	951 (0.001304%)	
TGTCTCTTATACACATCTCT	791 (0.001084%)	
TGTCTCTTATACACATCTGG	663 (0.000909%)	
TGTCTCTTATACACATCTGT	752 (0.001031%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGAC	9797 (0.026862%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAG	3702 (0.010150%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAG	1671 (0.004582%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATA	20876 (0.057239%)	
TGTGCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAGCACACACAC	42541 (0.116641%)	
TTATACACATCTAGATGTGTATAAGAGACAGCACACACAC	56 (0.000154%)	
TTCTGTCTCTTATACACATCTAGATGTGTATAAGAGACAG	15670 (0.042965%)	

```
fastp -i ../RAW_READS/10-12kb_S17_L002_R1_001.fastq.gz -I ../RAW_READS/10-12kb_S17_L002_R2_001.fastq.gz -o MP10k_F.trimmed.fq.gz
-o MP10k_R.trimmed.fq.gz -n 5 -q 20 -u 30 --length_required=70 --low_complexity_filter --complexity_threshold=20 --
cut_by_quality3 --cut_by_quality5 --cut_window_size=4 --cut_mean_quality=20 --trim_poly_g --poly_g_min_len=10 --
overrepresentation_analysis --json=MP10k.json --html=MP10k.html --report_title=MP10k --thread=8

fastp 0.19.4, at 2018-12-19 16:16:28
```