PE500

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:	146bp, 146bp
duplication rate:	3.224185%
Insert size peak:	151

Before filtering

total reads:	626.930540 M
total bases:	94.666512 G
Q20 bases:	88.200403 G (93.169592%)
Q30 bases:	81.377053 G (85.961817%)
GC content:	46.100595%

After filtering

total reads:	478.955820 M
total bases:	70.144072 G
Q20 bases:	68.463901 G (97.604686%)
Q30 bases:	64.829581 G (92.423464%)
GC content:	44.865838%

Filtering result

reads passed filters:	478.955820 M (76.396951%)
reads with low quality:	118.694782 M (18.932685%)
reads with too many N:	4.750000 K (0.000758%)
reads too short:	29.240170 M (4.664021%)
reads with low complexity:	35.018000 K (0.005586%)

Adapters

Adapter or bad ligation of read1

Sequence	Occurrences
A	900457
AG	805683
AGA	916776
AGAT	772406
AGATC	902546

AGATCG	975134
AGATCGG	967119
AGATCGGA	1114232
AGATCGGAA	1148214
AGATCGGAAG	1093704
AGATCGGAAGA	1056252
AGATCGGAAGAG	925835
AGATCGGAAGAGC	789494
AGATCGGAAGAGCA	779653
AGATCGGAAGAGCAC	861368
AGATCGGAAGAGCACA	746933
AGATCGGAAGAGCACAC	860300
AGATCGGAAGAGCACACG	932693
AGATCGGAAGAGCACACGT	883622
AGATCGGAAGAGCACACGTC	899782
AGATCGGAAGAGCACACGTCT	788636
AGATCGGAAGAGCACACGTCTG	674080
AGATCGGAAGAGCACACGTCTGA	613186
AGATCGGAAGAGCACACGTCTGAA	576974
AGATCGGAAGAGCACACGTCTGAAC	565570
AGATCGGAAGAGCACACGTCTGAACT	566691
AGATCGGAAGAGCACACGTCTGAACTC	682278
AGATCGGAAGAGCACACGTCTGAACTCC	690214
AGATCGGAAGAGCACACGTCTGAACTCCA	812752
AGATCGGAAGAGCACACGTCTGAACTCCAG	839218
AGATCGGAAGAGCACACGTCTGAACTCCAGT	711492
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	697356
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	547339
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAA	571316
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAAC	621651
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACC	710881
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCT	678196
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTT	579666
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTC	526496
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCG	758607
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCGA	600124
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCGATC	601838
other adapter sequences	19178204

Adapter or bad ligation of read2

Sequence	Occurrences
A	903889

AG	792176
AGA	878941
AGAT	811324
AGATC	1007860
AGATCG	988131
AGATCGG	1044726
AGATCGGA	1110518
AGATCGGAA	1078763
AGATCGGAAG	1089410
AGATCGGAAGA	1079489
AGATCGGAAGAG	950838
AGATCGGAAGAGC	838829
AGATCGGAAGAGCG	888774
AGATCGGAAGAGCGT	668378
AGATCGGAAGAGCGTC	936682
AGATCGGAAGAGCGTCG	899017
AGATCGGAAGAGCGTCGT	823140
AGATCGGAAGAGCGTCGTG	908011
AGATCGGAAGAGCGTCGTGT	792237
AGATCGGAAGAGCGTCGTGTA	601684
AGATCGGAAGAGCGTCGTGTAG	699214
AGATCGGAAGAGCGTCGTGTAGG	674364
AGATCGGAAGAGCGTCGTGTAGGG	564195
AGATCGGAAGAGCGTCGTGTAGGGA	586247
AGATCGGAAGAGCGTCGTGTAGGGAA	545824
AGATCGGAAGAGCGTCGTGTAGGGAAAG	595503
AGATCGGAAGAGCGTCGTGTAGGGAAAGA	654133
AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	744614
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGT	715275
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTG	647621
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTT	535769
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAAT	604544
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	761706
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGG	578834
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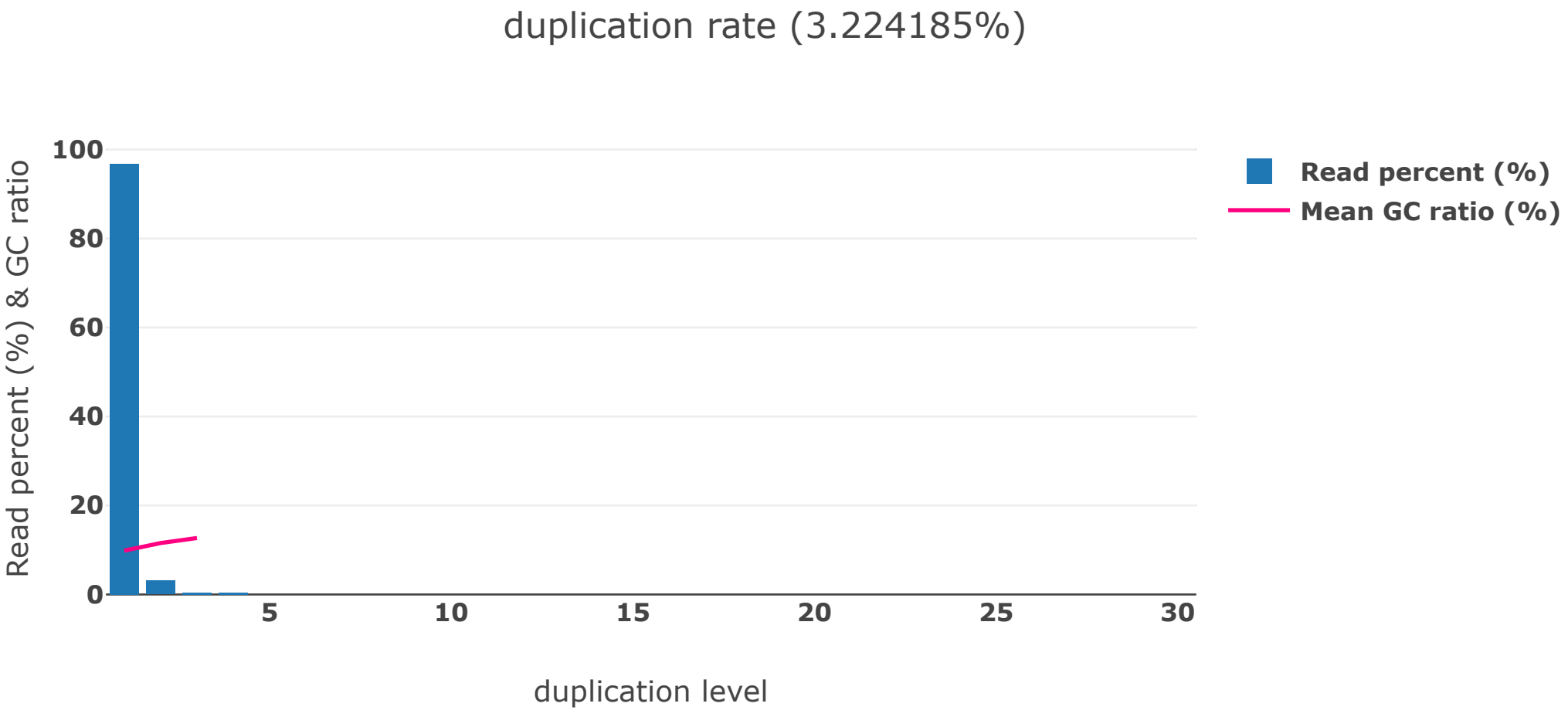
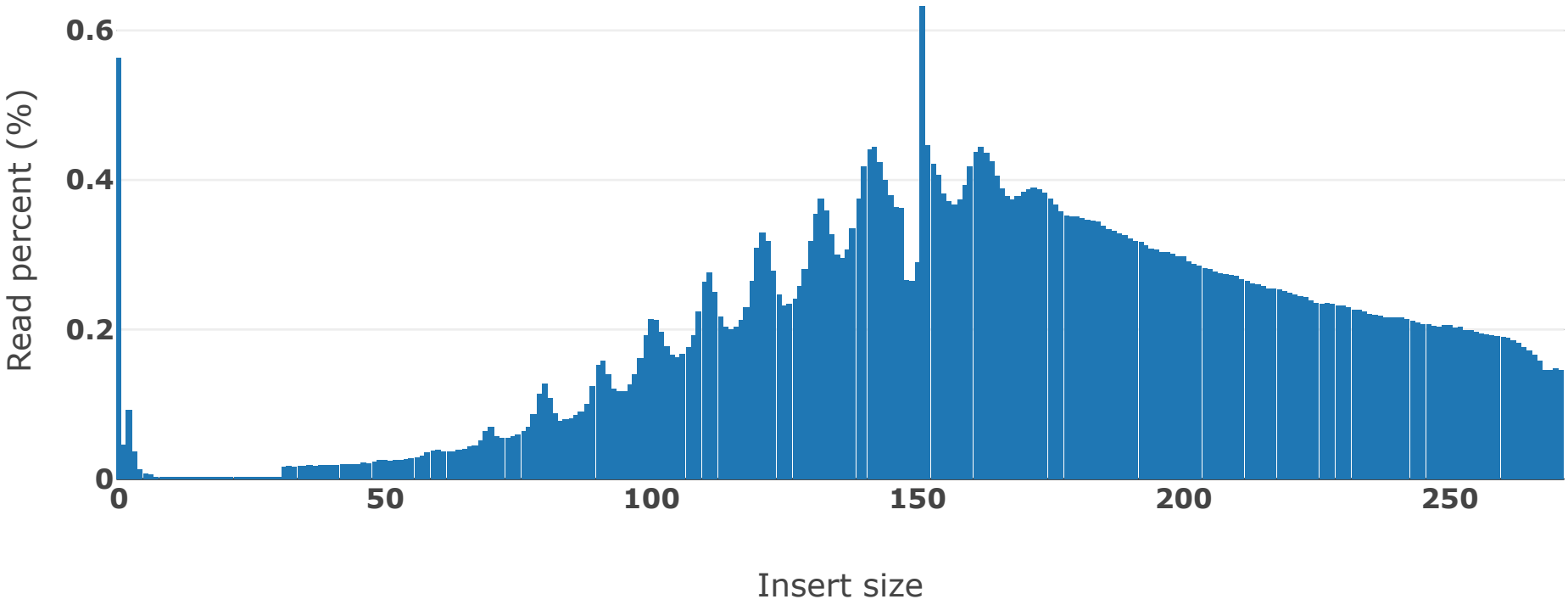
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCA	639699
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAG	1250450
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGG	1106741
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTG	885744
other adapter sequences	20461951

Duplication



Insert size estimation

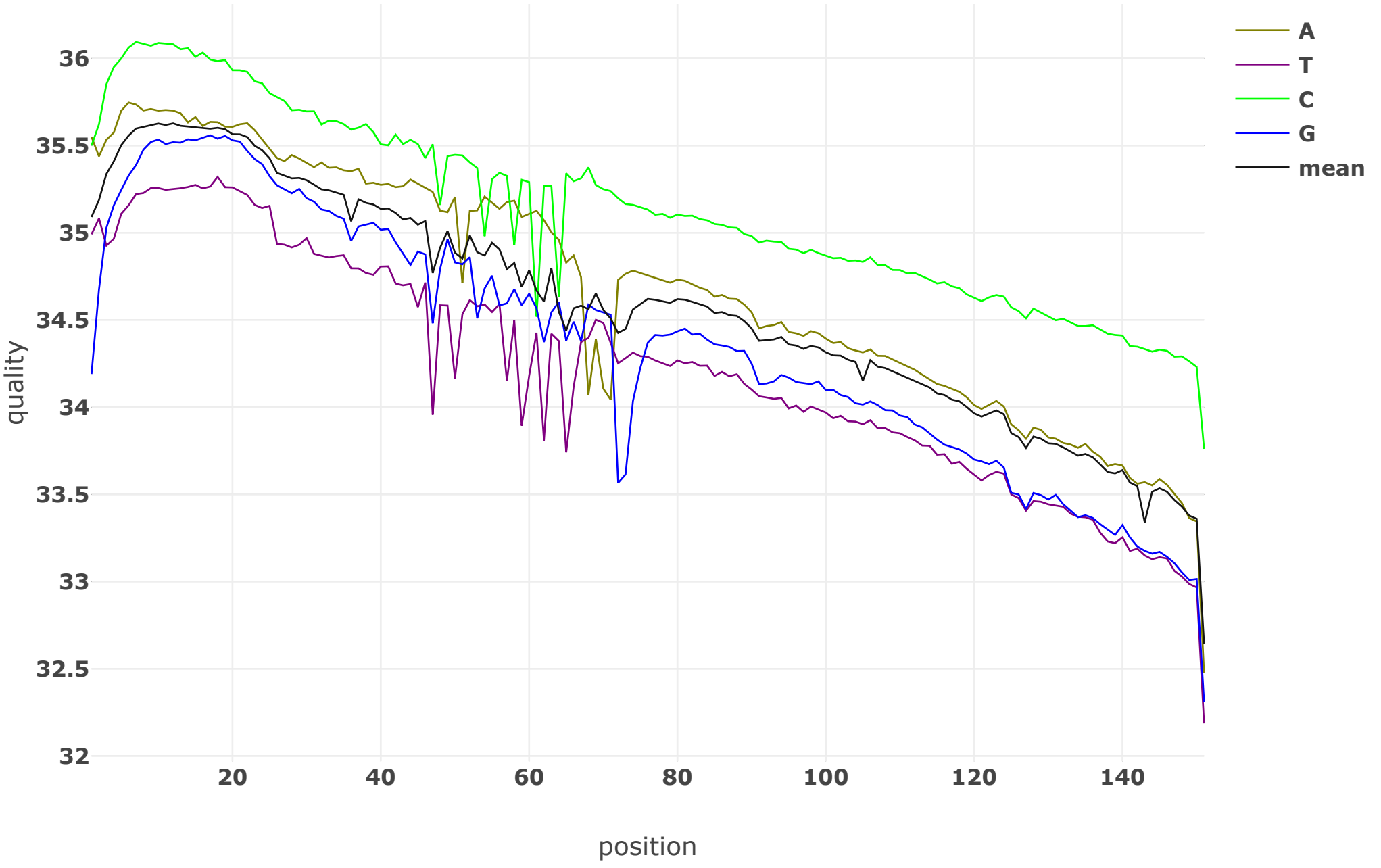


This estimation is based on paired-end overlap analysis, and there are 46.461314% reads found not overlapped.
The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

Before filtering

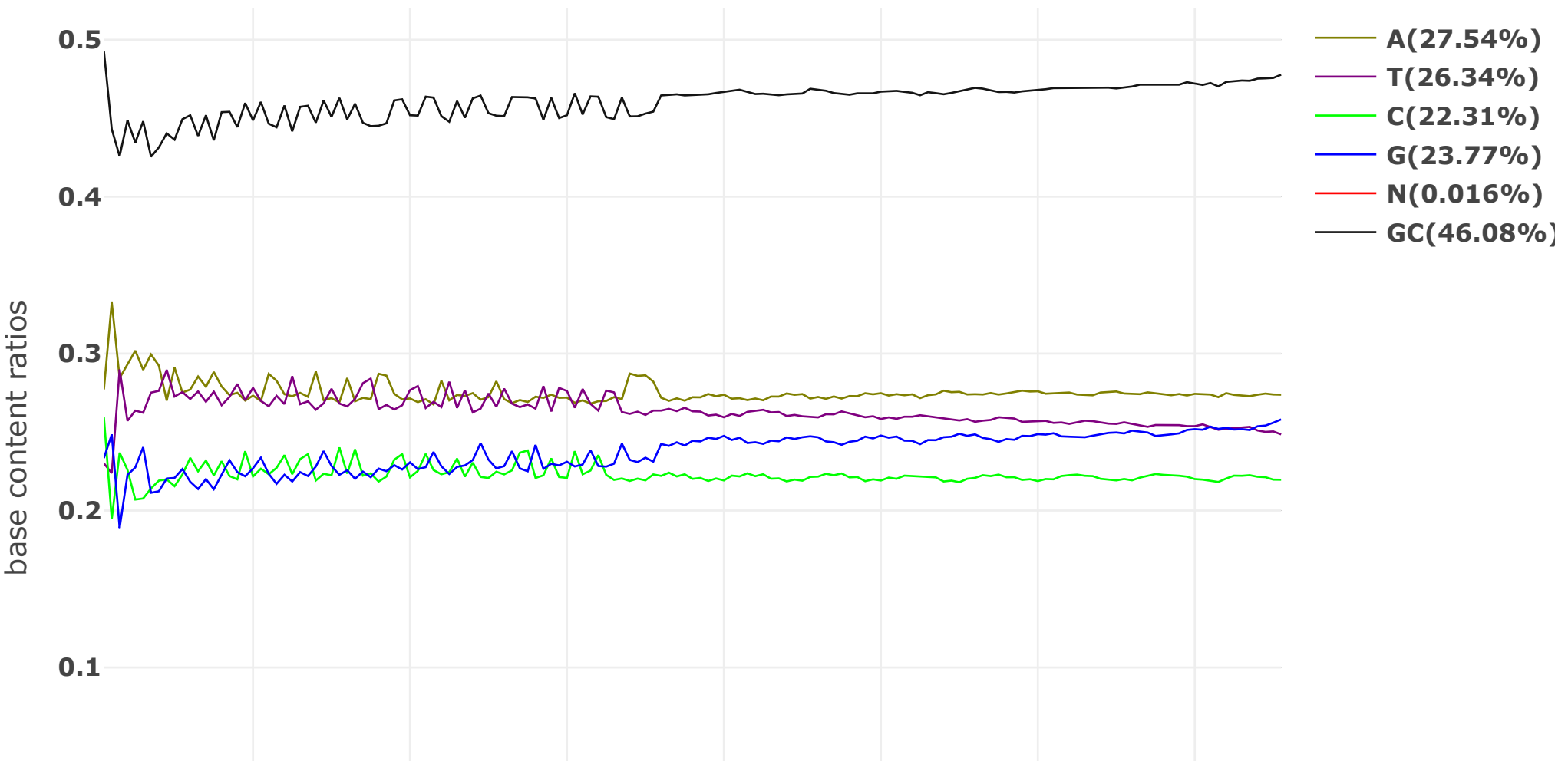
Before filtering: read1: quality

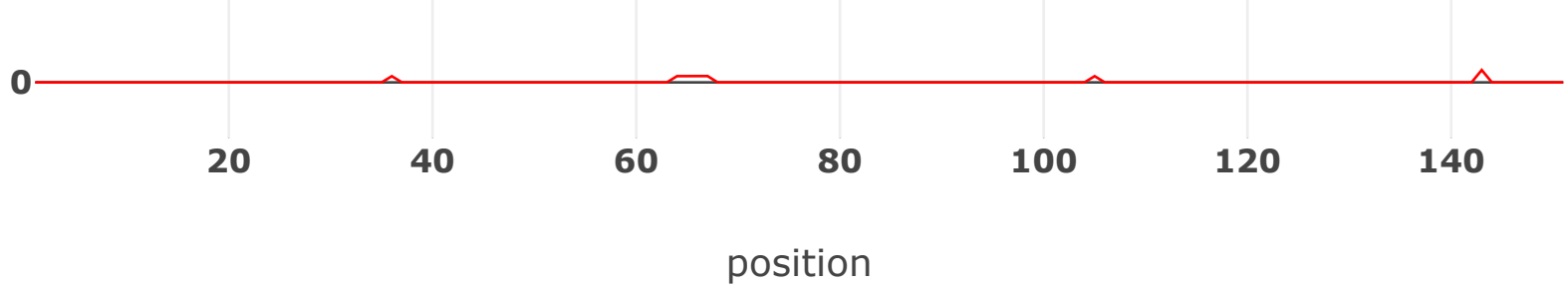
Value of each position will be shown on mouse over.



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.

	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	ATTTC	ATTTG	ATTCA	ATTCT	ATTCC	ATTCG	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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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
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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
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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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CTT	CTTAA	CTTAT	CTTAC	CTTAG	CTTTA	CTTTT	CTTTC	CTTTG	CTTCA	CTTCT	CTTCC	CTTCG	CTTGA	CTTGT	CTTGC	CTTGG
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GAA	GAAAA	GAAAT	GAAAC	GAAAG	GAATA	GAATT	GAATC	GAATG	GAACA	GAACT	GAACC	GAACG	GAAGA	GAAGT	GAAGC	GAAGG
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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	GCCCT	GCCCC	GCCCG	GCCGA	GCCGT	GCCGC	GCCGG
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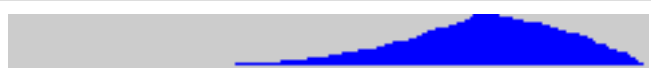
GGT	GGTAA	GGTAT	GGTAC	GGTAG	GGTTA	GGTTT	GGTTC	GGTTG	GGTCA	GGTCT	GGTCC	GGTCG	GGTGA	GGTGT	GGTGC	GGTGG
GGC	GGCAA	GGCAT	GGCAC	GGCAG	GGCTA	GGCTT	GGCTC	GGCTG	GGCCA	GGCCT	GGCCC	GGCCG	GGCGA	GGCGT	GGCGC	GGCGG
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

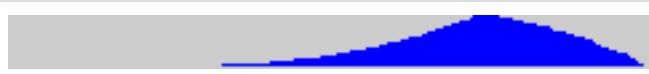
Before filtering: read1: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAAAAAAAA	196364 (0.082971%)	
AACACACACACACACACACACACACACACACACACACACA	39015 (0.065941%)	
AAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAAC	30455 (0.051473%)	
ACAAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTA	32048 (0.054166%)	

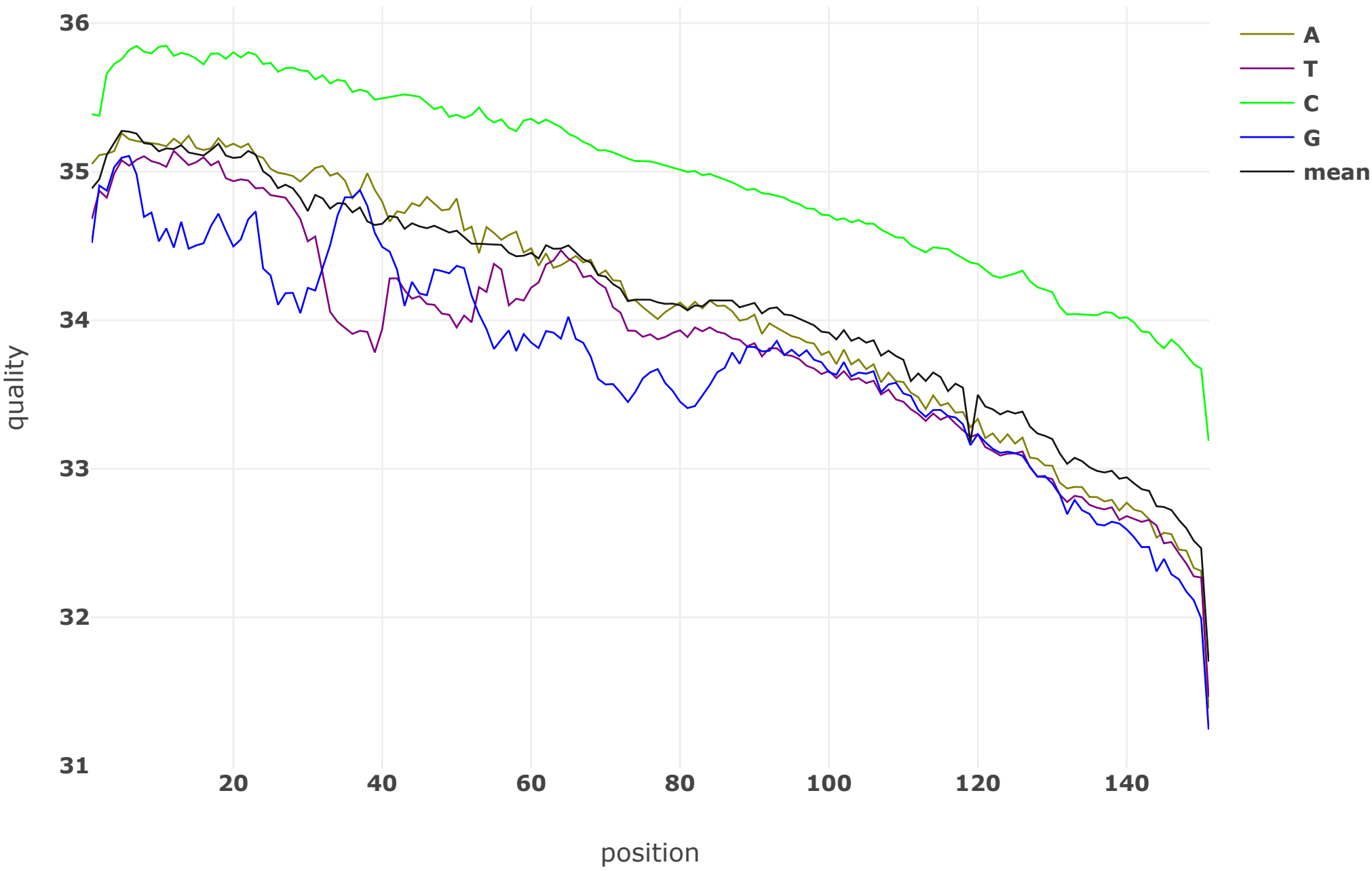
ACACACACACACACACACACACACACACACACACAA	1432 (0.002420%)	
ACACACACACACACACACACACACACACACACACAC	35817 (0.060536%)	
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	837 (0.003537%)	
ACACACACACACACACACACACACACACACACACAG	1006 (0.001700%)	
ACAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAA	49438 (0.083557%)	
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15042 (0.025423%)	
AGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAA	47750 (0.080704%)	
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACC	297 (0.000502%)	
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCGATCTCGTATGCCGTCTTCTGCTTGAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6492 (0.027431%)	
AGGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTA	26694 (0.045117%)	
ATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAA	43281 (0.073151%)	
ATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCGATCGCGTATGCCGTCTTCTGCTTGAAAAGGGGGGGGGGGGGGGGGGG

GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCT	200478 (0.338837%)	
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAACCTTCGATCGCGTATGCCGTCTTCTGCTTGAAAAGGG

TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTT	1135 (0.001918%)	
TTAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAA	41148 (0.069546%)	
TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	29671 (0.050148%)	
TTTAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTA	24687 (0.041725%)	

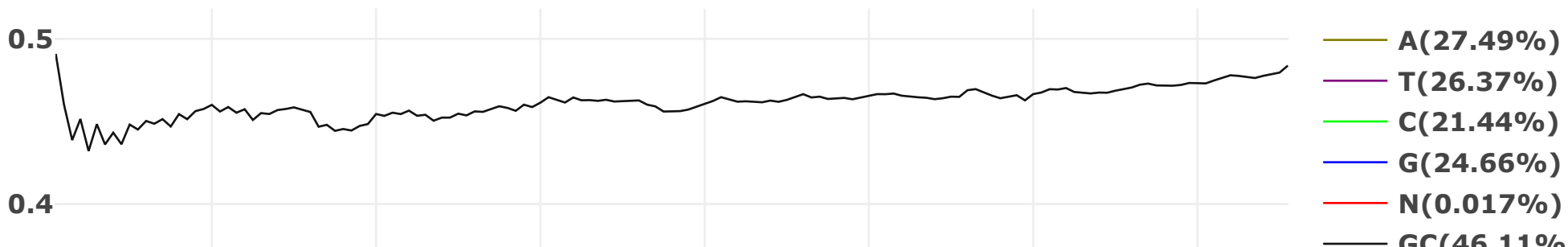
Before filtering: read2: quality

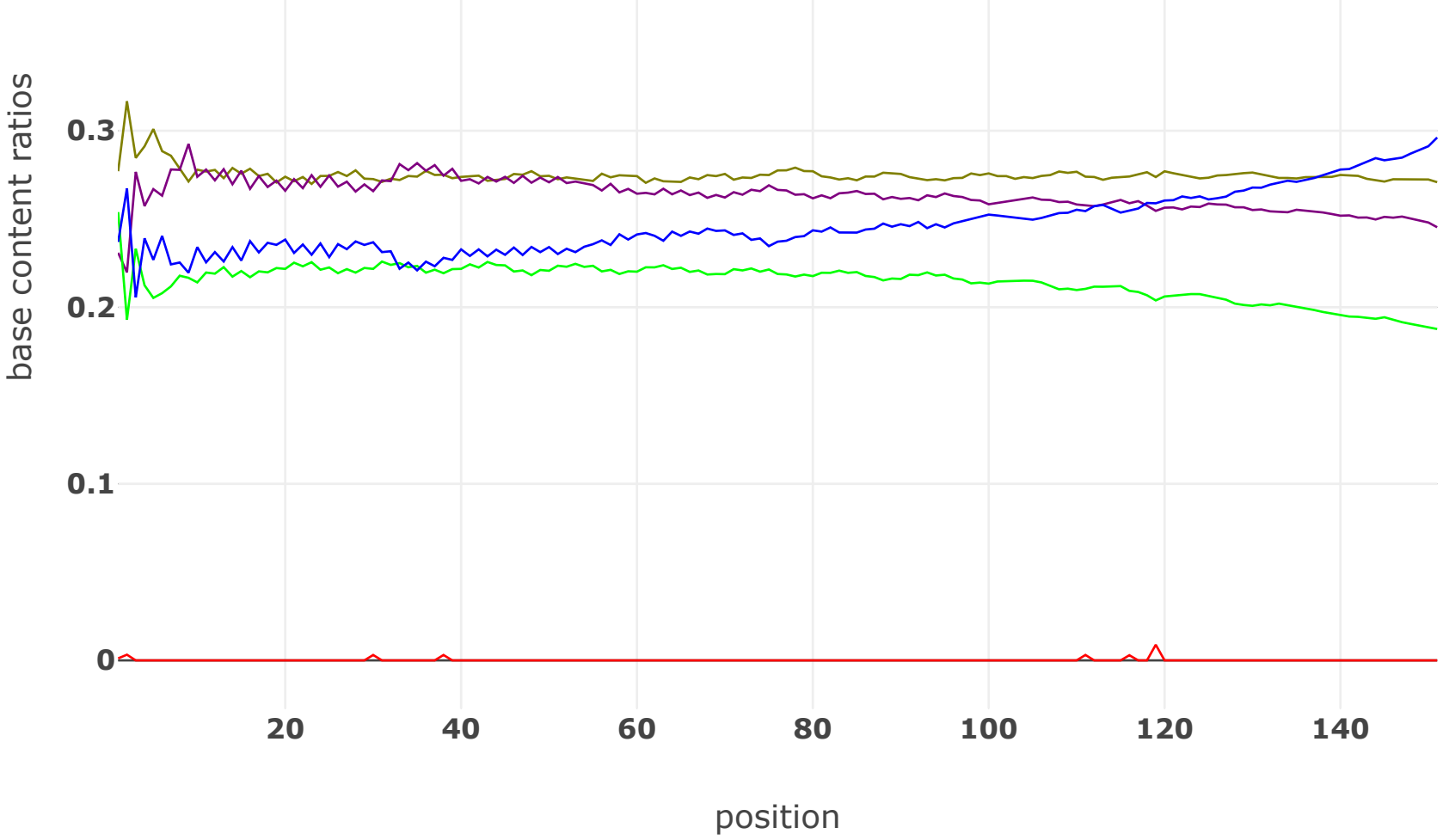
Value of each position will be shown on mouse over.



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
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CCT	CCTAA	CCTAT	CCTAC	CCTAG	CCTTA	CCTTT	CCTTC	CCTTG	CCTCA	CCTCT	CCTCC	CCTCG	CCTGA	CCTGT	CCTGC	CCTGG
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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	GCCCT	GCCCC	GCCCG	GCCGA	GCCGT	GCCGC	GCCGG
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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
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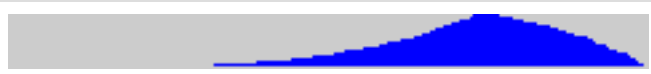
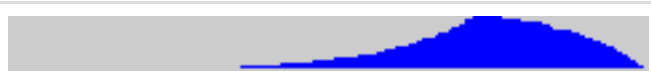
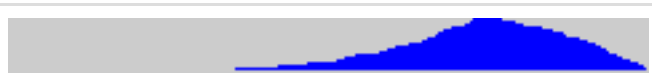
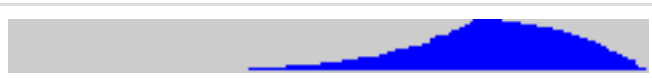
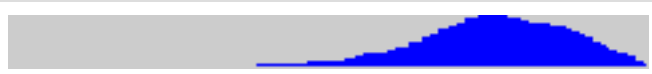
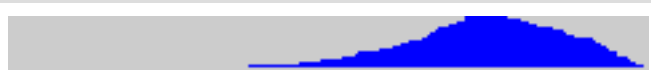
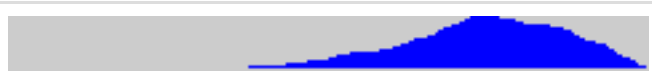
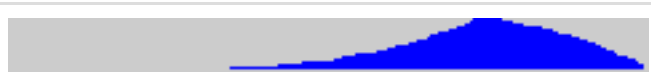
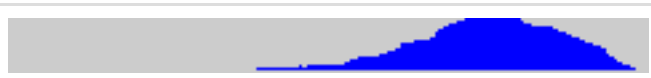
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

Before filtering: read2: overrepresented sequences

Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAA

CAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGG	8 (0.000014%)	
CCAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	51751 (0.087467%)	
CCCCCCCCCCCCCCCCCCC	25483 (0.021535%)	
CGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGG	769 (0.001300%)	
CGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGATC	84 (0.000142%)	
CGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGTTC	30 (0.000051%)	
CGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGTTG	11 (0.000019%)	
CGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGATCTCG	216 (0.000365%)	
CGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGTTCTCG	80 (0.000135%)	
CTAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	48763 (0.082416%)	
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	9687 (0.016372%)	
GAAAGAGTGTTAATGGCAAGGTGTAGATCTCGGTGGTCGC	38 (0.000064%)	
GAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTG	1112 (0.001879%)	
GAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	28432 (0.048054%)	
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	13860 (0.023425%)	
GAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGG	29137 (0.049246%)	
GAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAG	1317 (0.002226%)	
GAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTTG	328 (0.000554%)	
GATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCA	848 (0.001433%)	
GCACACACACACACACACACACACACACACACACACACAC	43014 (0.072700%)	
GCAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	37725 (0.063761%)	
GCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGAT	177 (0.000299%)	
GCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGGT	97 (0.000164%)	
GCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGTT	162 (0.000274%)	
GGAAAGAGTGTTAATGGCAAGGTGTAGATCTCGGTGGTCG	131 (0.000221%)	
GGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAGGT	721 (0.001219%)	
GGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	51754 (0.087472%)	
GGGAAAGAGTGTTAATGGCAAGGTGTAGATCTCGGTGGTC	70 (0.000118%)	
GGGG

GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	2354 (0.003979%)	
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GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	2009 (0.003395%)	
GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	2449 (0.004139%)	
GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	1713 (0.002895%)	
GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	2223 (0.003757%)	
GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGG	1600 (0.002704%)	
GGGGGGGGGGGGGGGGGGGGTGGGGGGGGGGGGGGGGGGG

TCAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	46839 (0.079165%)	
TCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAG	639 (0.001080%)	
TCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGATCTC	140 (0.000237%)	
TCGTGTAGGGAAAGAGTGTTAATGGCAAGGTGTAGTTCTC	68 (0.000115%)	
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	12449 (0.021041%)	
TGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	86880 (0.146840%)	
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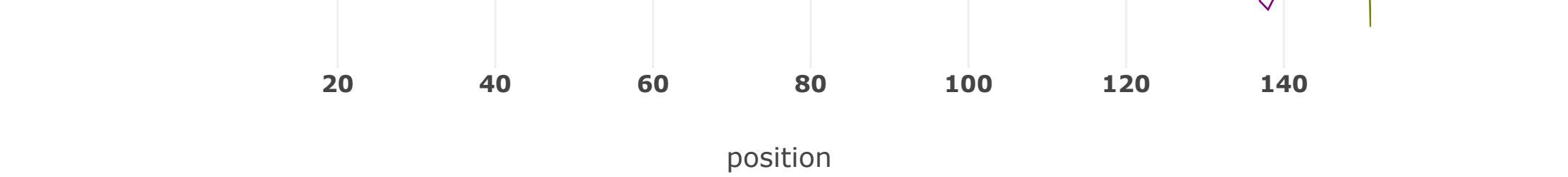
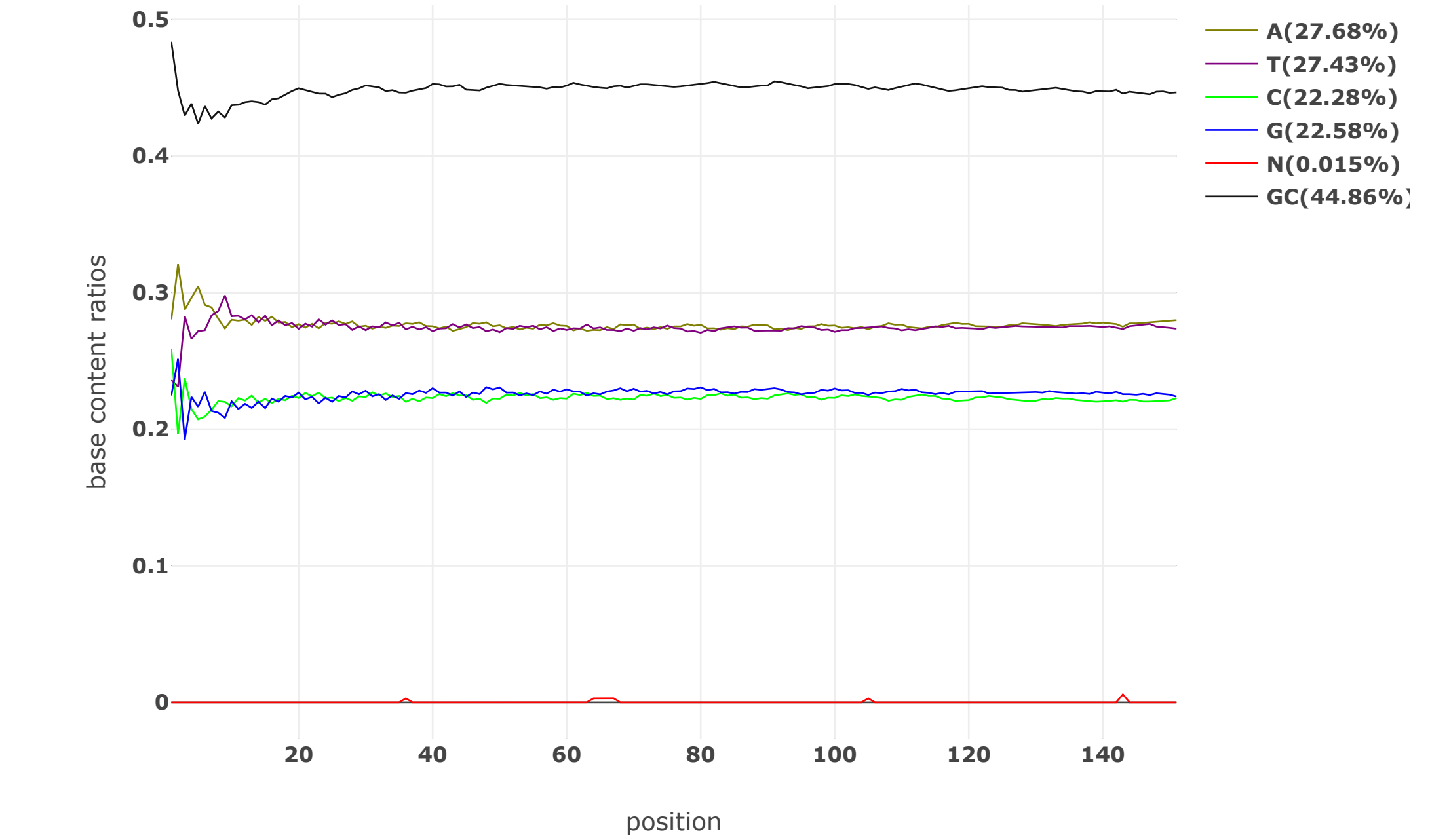


After filtering: read1: base contents

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
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ATT	ATTAA	ATTAT	ATTAC	ATTAG	ATTTA	ATTTT	ATTTC	ATTTG	ATTCA	ATTCT	ATTCC	ATTCG	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
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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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AGC	AGCAA	AGCAT	AGCAC	AGCAG	AGCTA	AGCTT	AGCTC	AGCTG	AGCCA	AGCCT	AGCCC	AGCCG	AGCGA	AGCGT	AGCGC	AGCGG
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TTT	TTTAA	TTTAT	TTTAC	TTTAG	TTTTA	TTTTT	TTTTC	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	TGTTT	TGTTC	TGTTG	TGTCA	TGTCT	TGTCC	TGTCG	TGTGA	TGTGT	TGTGC	TGTGG
TGC	TGCAA	TGCAT	TGCAC	TGCAG	TGCTA	TGCTT	TGCTC	TGCTG	TGCCA	TGCCT	TGCCC	TGCCG	TGCGA	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	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
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	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	GTATG	GTACA	GTACT	GTACC	GTACG	GTAGA	GTAGT	GTAGC	GTAGG
GTT	GTTAA	GTTAT	GTTAC	GTTAG	GTTTA	GTTTT	GTTTC	GTTTG	GTTCA	GTTCT	GTTCC	GTTCG	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCAC	GTCAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GTCCT	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	GCCCT	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	GGCCT	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: read1: overrepresented sequences

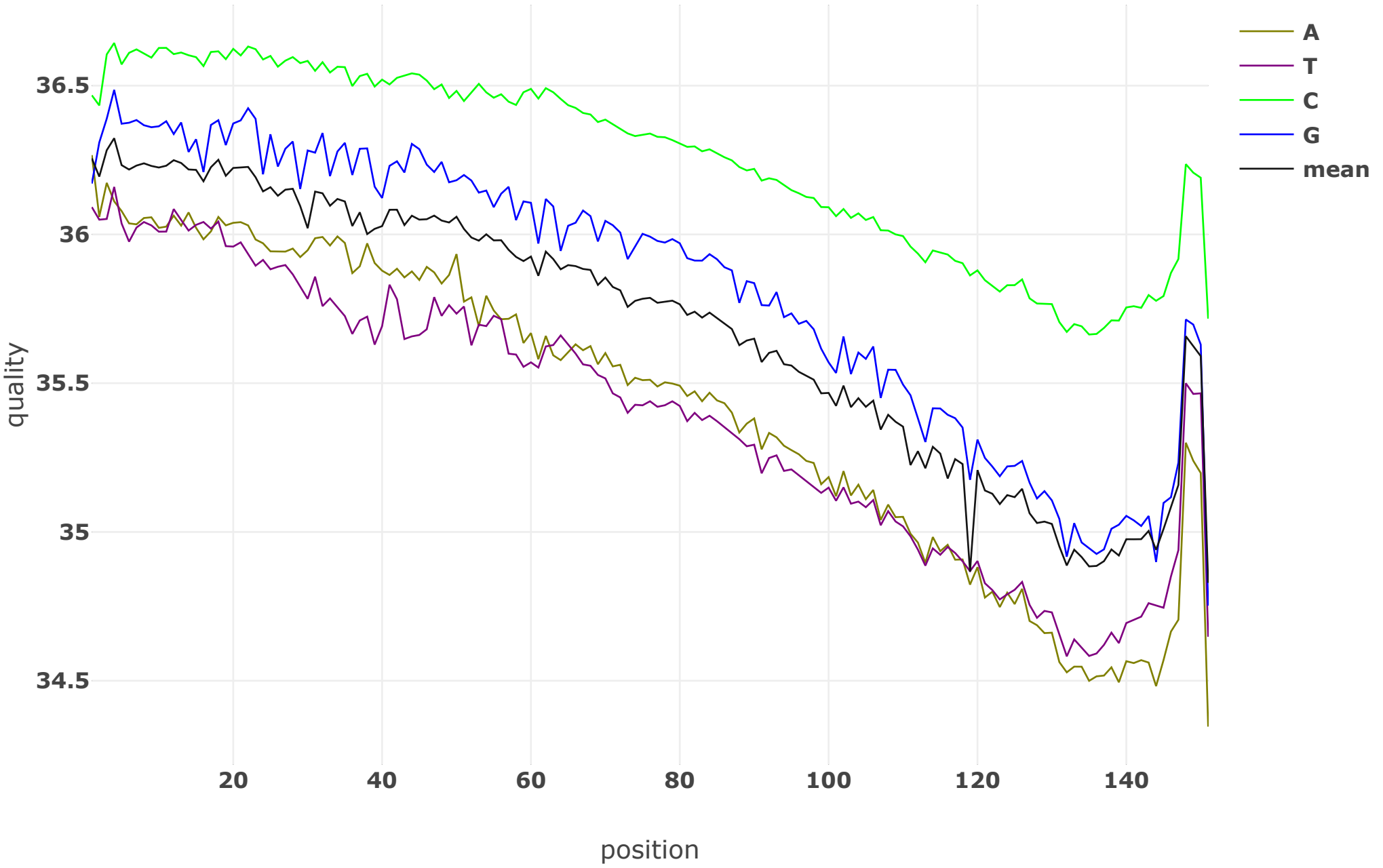
Sampling rate: 1 / 20

overrepresented sequence	count (% of bases)	distribution: cycle 1 ~ cycle 151
AAAAAAAAAA	101615 (0.057908%)	
AACACACACACACACACACACACACACACACACACACA	22451 (0.051178%)	
AAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAAC	93 (0.000212%)	
ACAAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTTA	204 (0.000465%)	
ACACACACACACACACACACACACACACACACACACAA	599 (0.001365%)	
ACACACACACACACACACACACACACACACACACACAC	20432 (0.046575%)	
ACACACACACACACACACACACACACACACACACAC

CACACAC

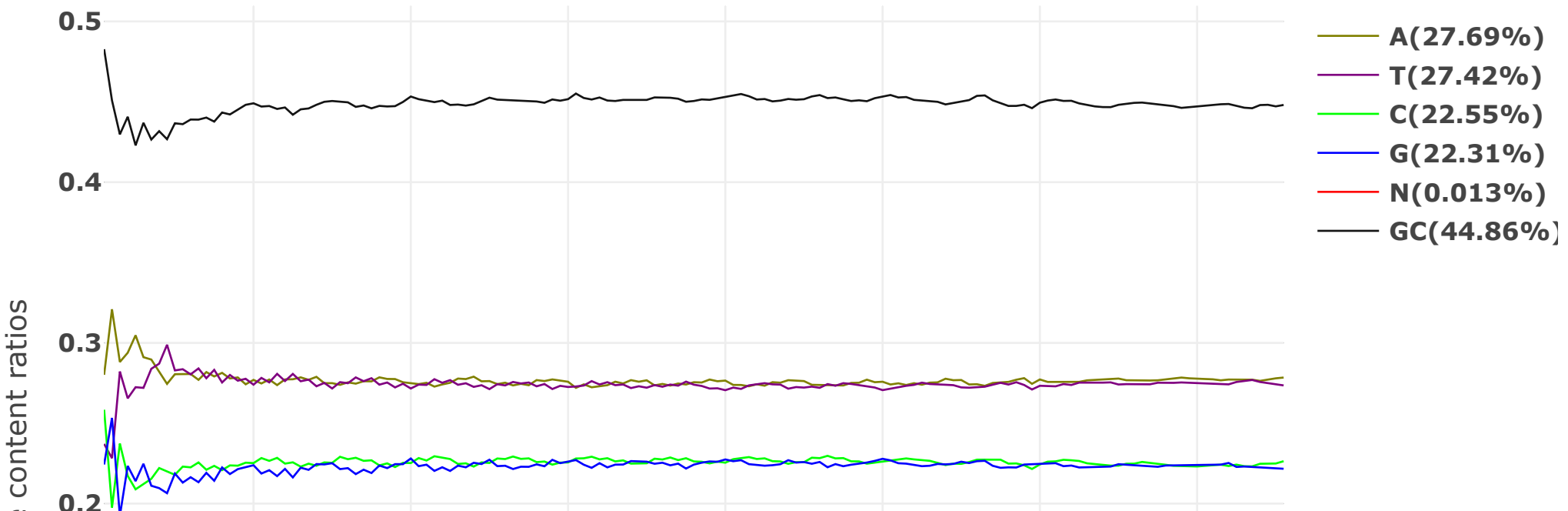
After filtering: read2: quality

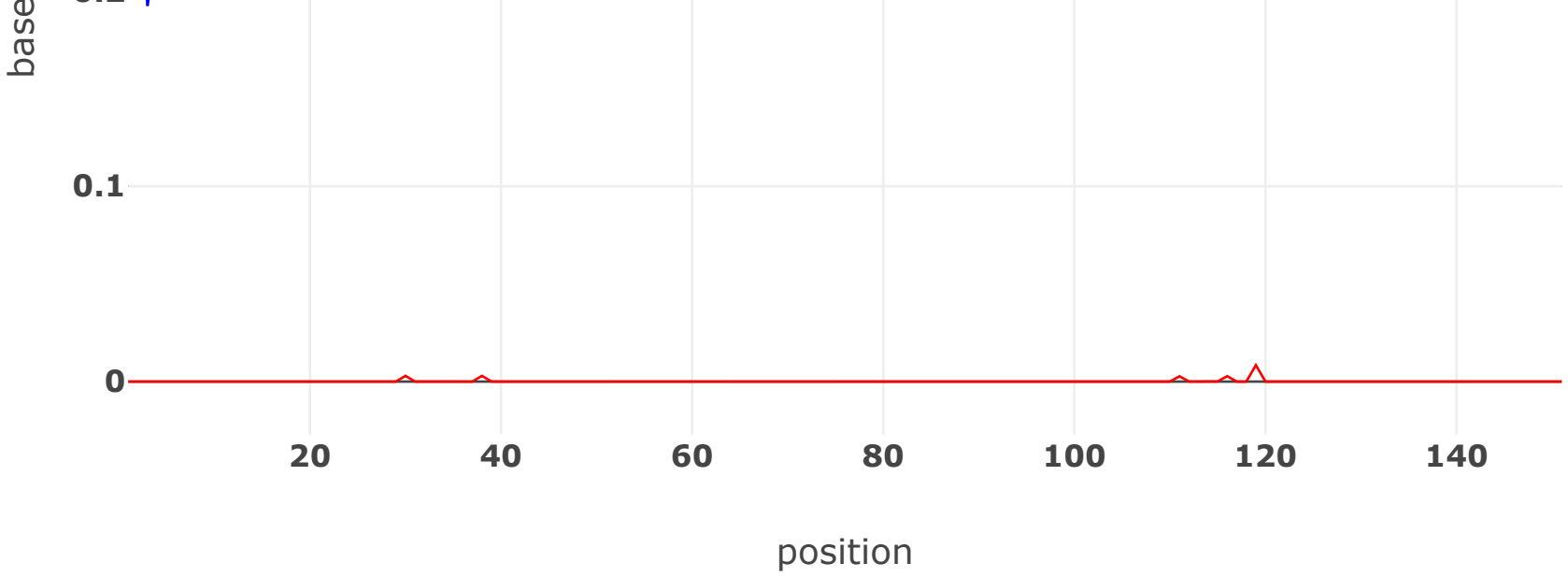
Value of each position will be shown on mouse over.



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	ATTTC	ATTTG	ATTCA	ATTCT	ATTCC	ATTCG	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	TTTTC	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	TGTTT	TGTTC	TGTTG	TGTCA	TGTCT	TGTCC	TGTCG	TGTGA	TGTGT	TGTGC	TGTGG
TGC	TGCAA	TGCAT	TGCAC	TGCAG	TGCTA	TGCTT	TGCTC	TGCTG	TGCCA	TGCCT	TGCCC	TGCCG	TGCGA	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	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
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	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	GTATG	GTACA	GTACT	GTACC	GTACG	GTAGA	GTAGT	GTAGC	GTAGG
GTT	GTTAA	GTTAT	GTTAC	GTTAG	GTTTA	GTTTT	GTTTC	GTTTG	GTTCA	GTTCT	GTTCC	GTTCG	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCAC	GTCAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GTCCT	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	GCCCT	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	GGCCT	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

AAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	83 (0.000189%)	
ACAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAAT	157 (0.000358%)	
ACACACACACACACACACACACACACACACACACACAA	1815 (0.004143%)	
ACACACACACACACACACACACACACACACACACAC	64015 (0.146116%)	
ACACACACACACACACACACACACACACACACACAC

GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	263 (0.001501%)	
TAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	81 (0.000185%)	
TCAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	100 (0.000228%)	
TCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATGGCAAG	10 (0.000023%)	
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	7759 (0.017710%)	
TGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	327 (0.000746%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAG	1141 (0.002604%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	41790 (0.095387%)	
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	555 (0.003167%)	
TTAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTAATG	123 (0.000281%)	

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fastp -i gDNA_S18_L002_R1_001.fastq.gz -I gDNA_S18_L002_R2_001.fastq.gz -o PE500_F.trimmed.fq.gz -O PE500_R.trimmed.fq.gz -n 5 -q 30 -u 30 --length_required=100 --low_complexity_filter --complexity_threshold=20 --cut_by_quality3 --cut_by_quality5 --cut_window_size=4 --cut_mean_quality=30 --trim_poly_g --poly_g_min_len=10 --overrepresentation_analysis --json=PE500.json --html=PE500.html --report_title=PE500 --thread=8

fastp 0.19.4, at 2018-10-07 00:13:24
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