

fastp report

Summary

General

fastp version:	0.19.10 (https://github.com/OpenGene/fastp)
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	151bp, 151bp
mean length after filtering:	128bp, 128bp
duplication rate:	33.377162%
Insert size peak:	145
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Detected read2 adapter:	AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

Before filtering

total reads:	58.421052 M
total bases:	8.821579 G
Q20 bases:	8.611655 G (97.620337%)
Q30 bases:	8.280739 G (93.869130%)
GC content:	50.181722%

After filtering

total reads:	57.280906 M
total bases:	7.366429 G
Q20 bases:	7.228813 G (98.131852%)
Q30 bases:	6.968340 G (94.595903%)
GC content:	50.041684%

Filtering result

reads passed filters:	57.280906 M (98.048399%)
reads with low quality:	838.284000 K (1.434901%)
reads with too many N:	273.594000 K (0.468314%)
reads too short:	5.178000 K (0.008863%)
reads with low complexity:	23.090000 K (0.039523%)

Adapters

Adapter or bad ligation of read1

Sequence	Occurrences
A	256107
AG	258777
AGA	267890
AGAT	271243
AGATC	293348
AGATCG	285563
AGATCGG	278316

AGATCGGA	271228
AGATCGGAA	261425
AGATCGGAAG	253478
AGATCGGAAGA	252508
AGATCGGAAGAG	249862
AGATCGGAAGAGC	253030
AGATCGGAAGAGCA	257765
AGATCGGAAGAGCAC	258771
AGATCGGAAGAGCACA	260035
AGATCGGAAGAGCACAC	254107
AGATCGGAAGAGCACACG	246150
AGATCGGAAGAGCACACGT	232679
AGATCGGAAGAGCACACGTC	223996
AGATCGGAAGAGCACACGTCT	216712
AGATCGGAAGAGCACACGTCTG	211267
AGATCGGAAGAGCACACGTCTGA	209425
AGATCGGAAGAGCACACGTCTGAA	210353
AGATCGGAAGAGCACACGTCTGAAC	207942
AGATCGGAAGAGCACACGTCTGAACT	204778
AGATCGGAAGAGCACACGTCTGAACTC	201454
AGATCGGAAGAGCACACGTCTGAACTCC	189581
AGATCGGAAGAGCACACGTCTGAACTCCA	179495
AGATCGGAAGAGCACACGTCTGAACTCCAG	166953
AGATCGGAAGAGCACACGTCTGAACTCCAGT	155209
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	149211
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	143457
AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC	141264
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACG	138103
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGT	132337
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTG	125746
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGA	118608
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAA	107707
other adapter sequences	1621107

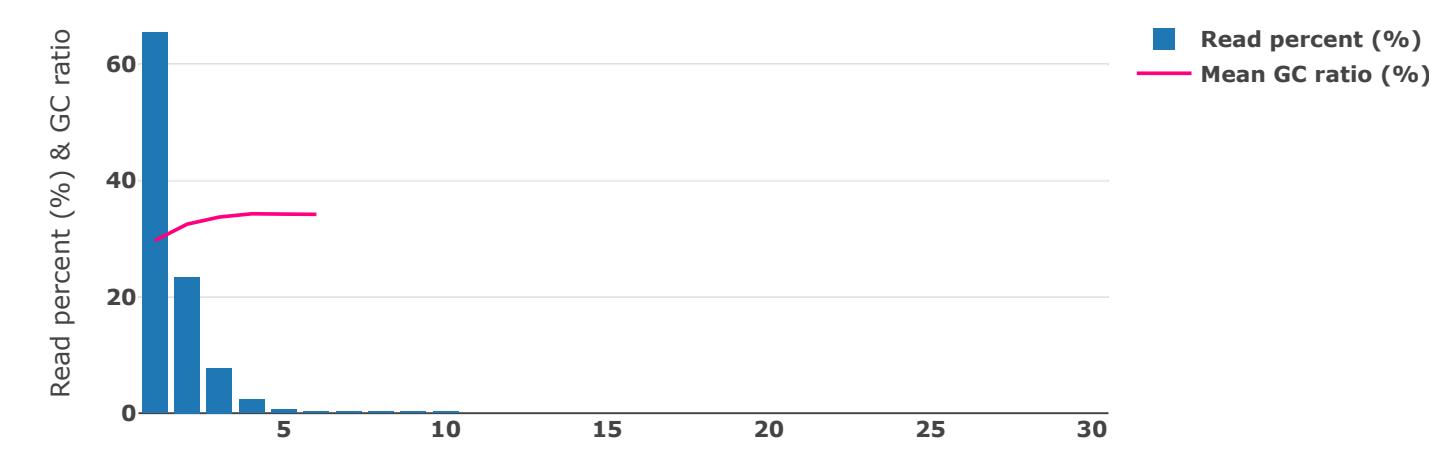
Adapter or bad ligation of read2

Sequence	Occurrences
A	254522
AG	259342
AGA	268178
AGAT	270216
AGATC	294164
AGATCG	284076
AGATCGG	278102
AGATCGGA	270241
AGATCGGAA	261291
AGATCGGAAG	254231

AGATCGGAAGA	252508
AGATCGGAAGAG	250597
AGATCGGAAGAGC	251865
AGATCGGAAGAGCG	257777
AGATCGGAAGAGCGT	244827
AGATCGGAAGAGCGTC	257746
AGATCGGAAGAGCGTCG	251697
AGATCGGAAGAGCGTCGT	223072
AGATCGGAAGAGCGTCGTG	228952
AGATCGGAAGAGCGTCGTGT	214287
AGATCGGAAGAGCGTCGTGTA	210694
AGATCGGAAGAGCGTCGTGTAG	207957
AGATCGGAAGAGCGTCGTGTAGG	205450
AGATCGGAAGAGCGTCGTGTAGGG	205254
AGATCGGAAGAGCGTCGTGTAGGGA	200018
AGATCGGAAGAGCGTCGTGTAGGGAA	200648
AGATCGGAAGAGCGTCGTGTAGGGAAA	196483
AGATCGGAAGAGCGTCGTGTAGGGAAAG	184344
AGATCGGAAGAGCGTCGTGTAGGGAAAGA	174606
AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	163801
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGT	139573
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTG	146002
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT	140484
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTA	137547
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAG	135040
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGA	130012
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGAT	123198
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATC	115514
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCT	105379
other adapter sequences	1761231

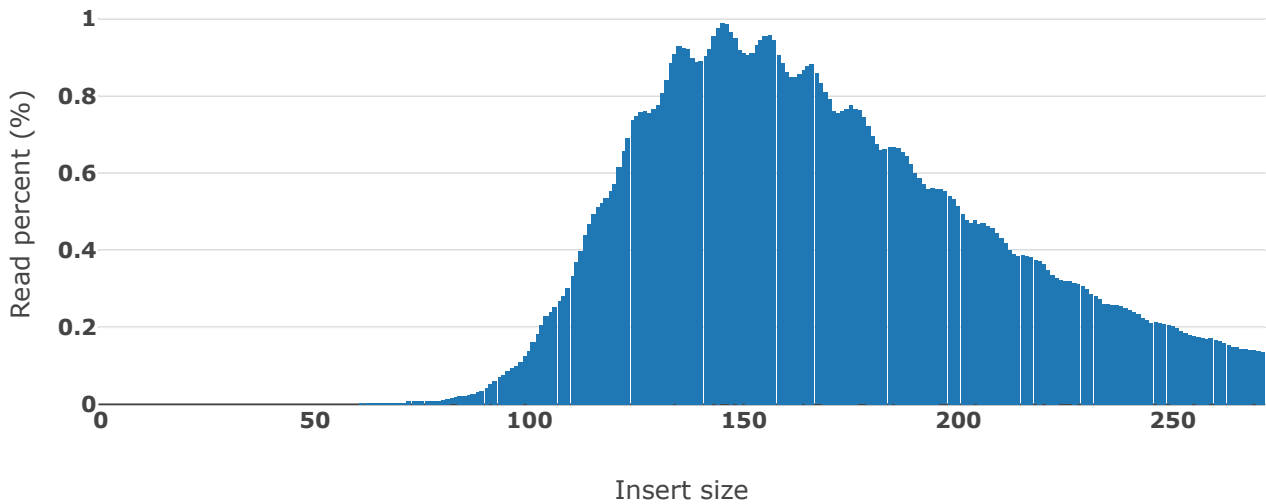
Duplication

duplication rate (33.377162%)



Insert size estimation

Insert size distribution (8.630549% reads are with unknown length)

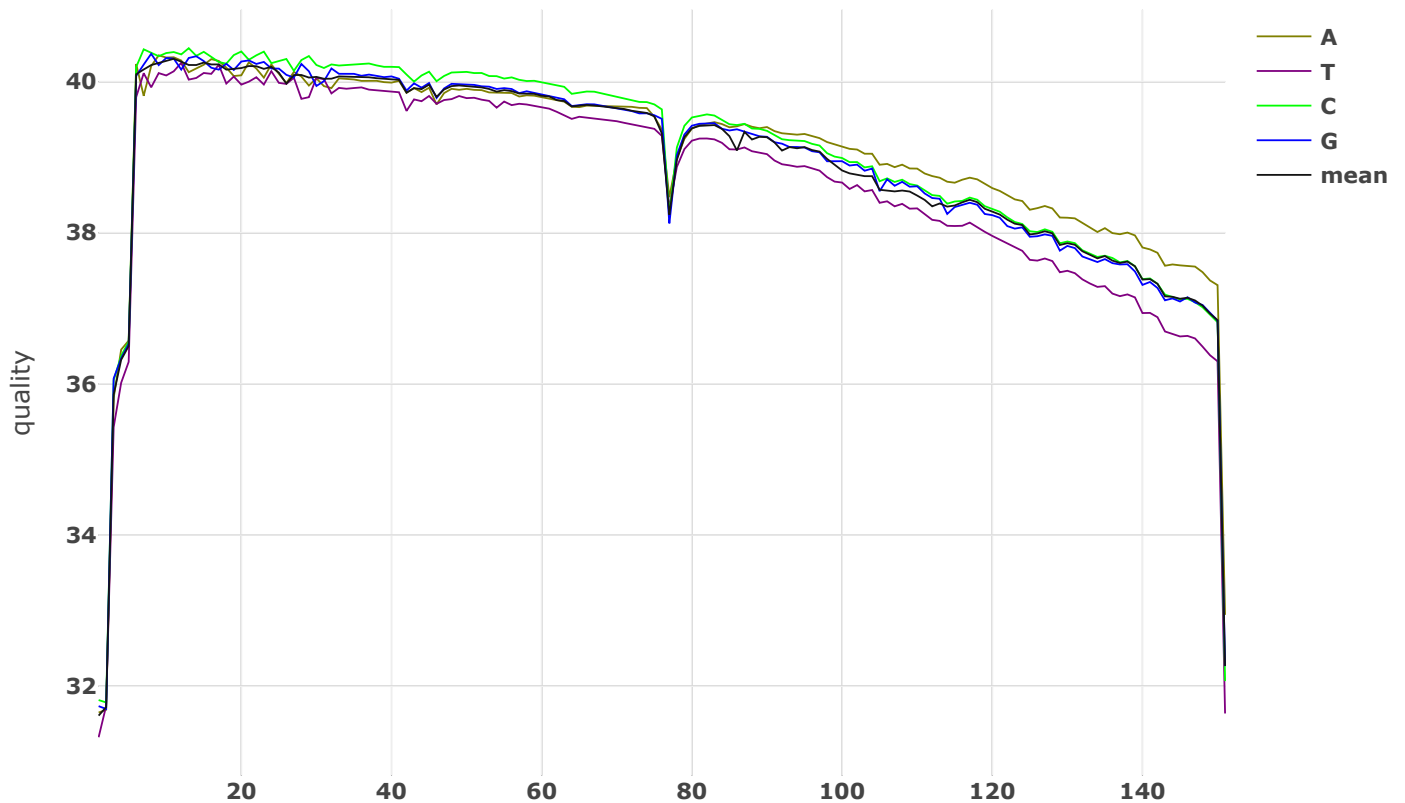


This estimation is based on paired-end overlap analysis, and there are 8.630549% reads found not overlapped. The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

Before filtering

Before filtering: read1: quality

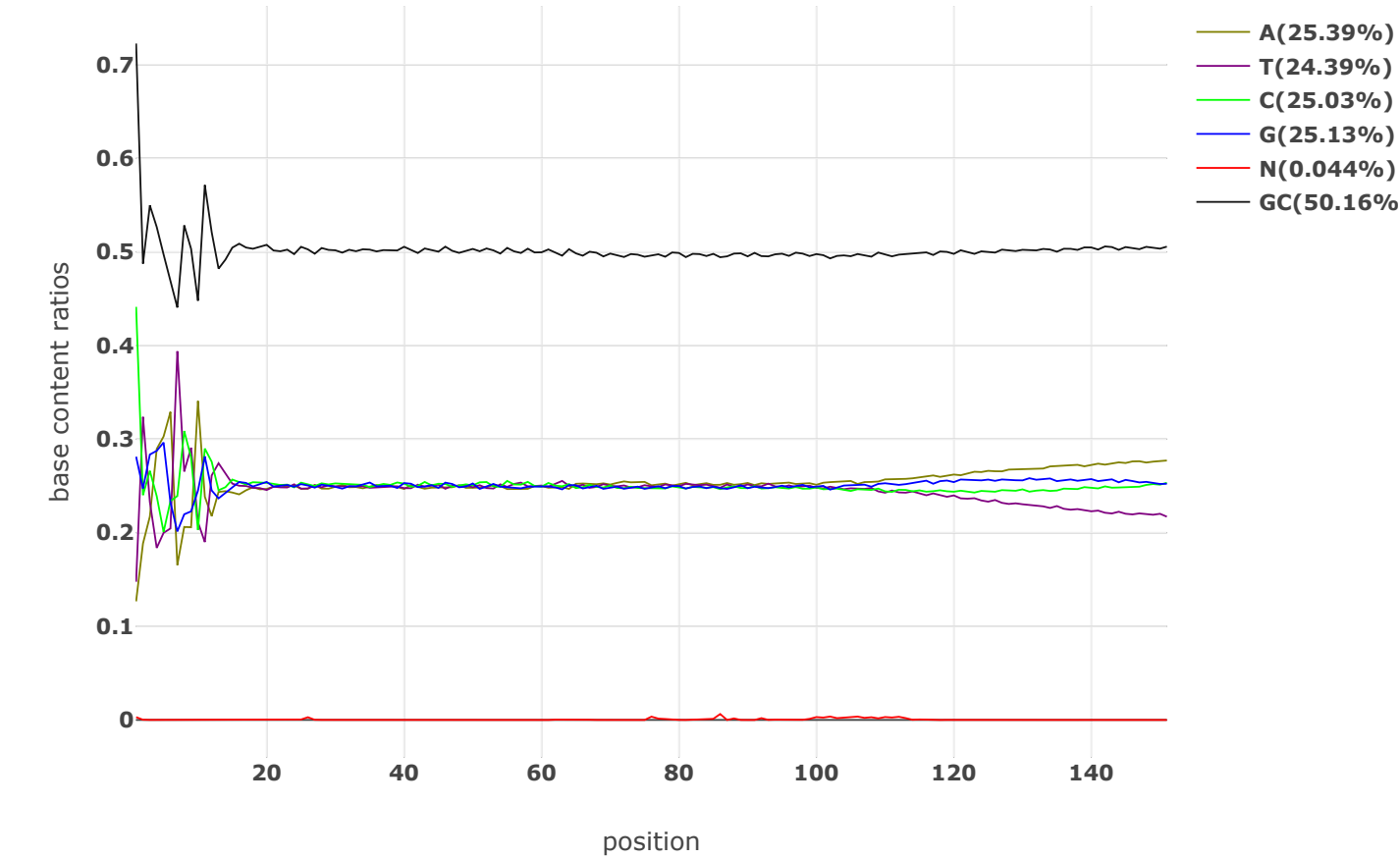
Value of each position will be shown on mouse over.



position

Before filtering: read1: base contents

Value of each position will be shown on mouse over.



Before filtering: read1: KMER counting

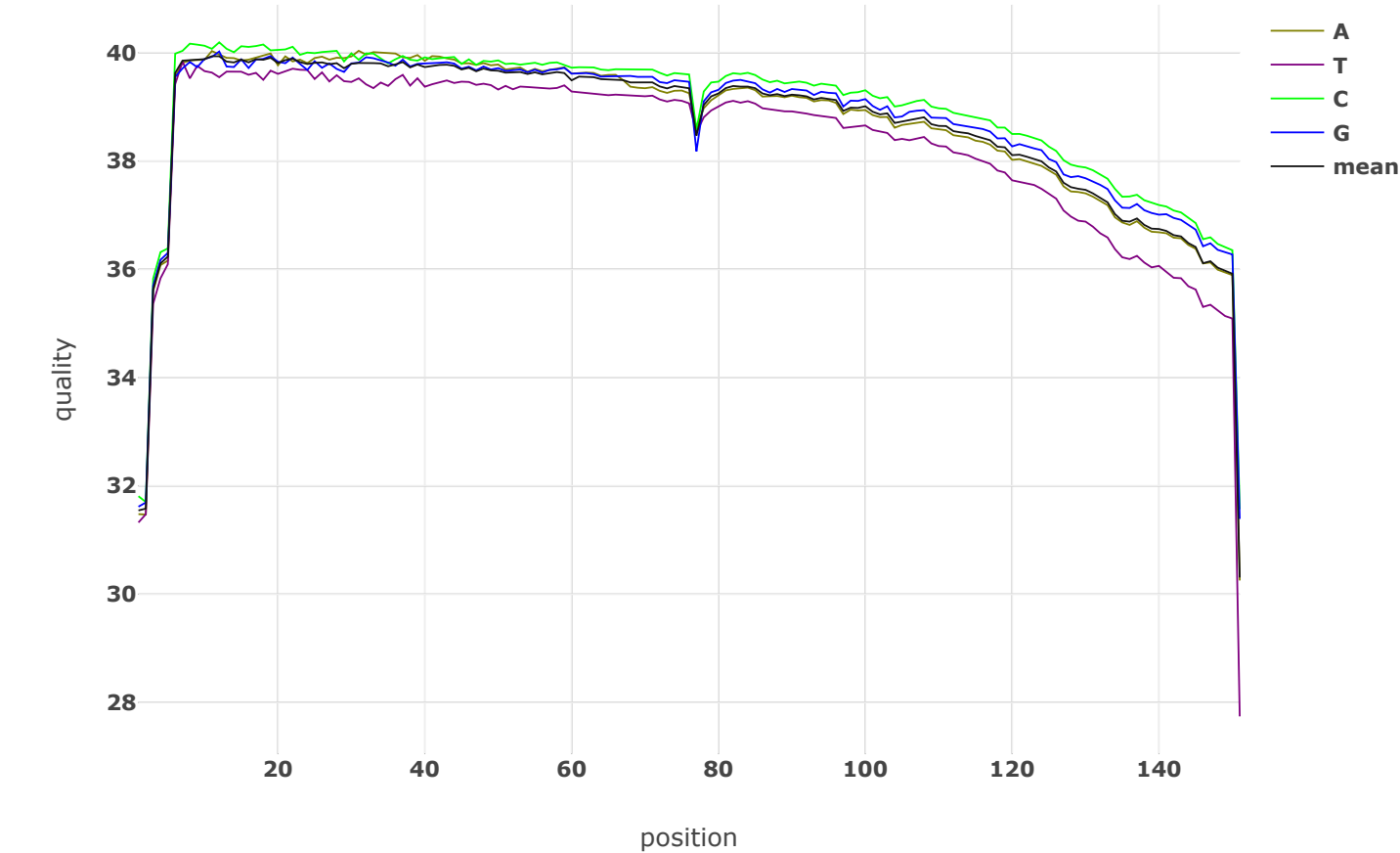
Darker background means larger counts. The count will be shown on mouse over.

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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	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	ATTTT	ATT TG	ATTCA	AT TCT	AT TCC	AT TCG	ATTGA	ATTGT	ATTGC	ATTGG
ATC	ATCAA	ATCAT	ATCAC	ATCAG	ATCTA	ATCTT	ATCTC	ATCTG	ATCCA	AT CCT	AT CCC	AT CCG	ATCGA	ATCGT	ATCGC	ATCGG
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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	AC CCT	AC CCC	AC CCG	ACCGA	ACCGT	ACCGC	ACCGG
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AGC	AGCAA	AGCAT	AGCAC	AGCAG	AGCTA	AGCTT	AGCTC	AGCTG	AGCCA	AG CCT	AG CCC	AG CCG	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	TAA GG
TAT	TATAA	TATAT	TATAC	TATAG	TATTA	TATTT	TATTC	TATTG	TATCA	TATCT	TATCC	TATCG	TATGA	TATGT	TATGC	TATGG
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GAA	GA AAA	GA AAT	GA AAC	GA AAG	GA ATA	GA ATT	GA ATC	GA ATG	GA ACA	GA ACT	GA ACC	GA ACG	GA AGA	GA AGT	GA AGC	GA AGG
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GTA	GTA AA	GTA AT	GTA AC	GTA AG	GT ATA	GT ATT	GT ATC	GT ATG	GT ACA	GT ACT	GT ACC	GT ACG	GT AGA	GT AGT	GT AGC	GT AGG
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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: read2: quality

Value of each position will be shown on mouse over.



Before filtering: read2: base contents

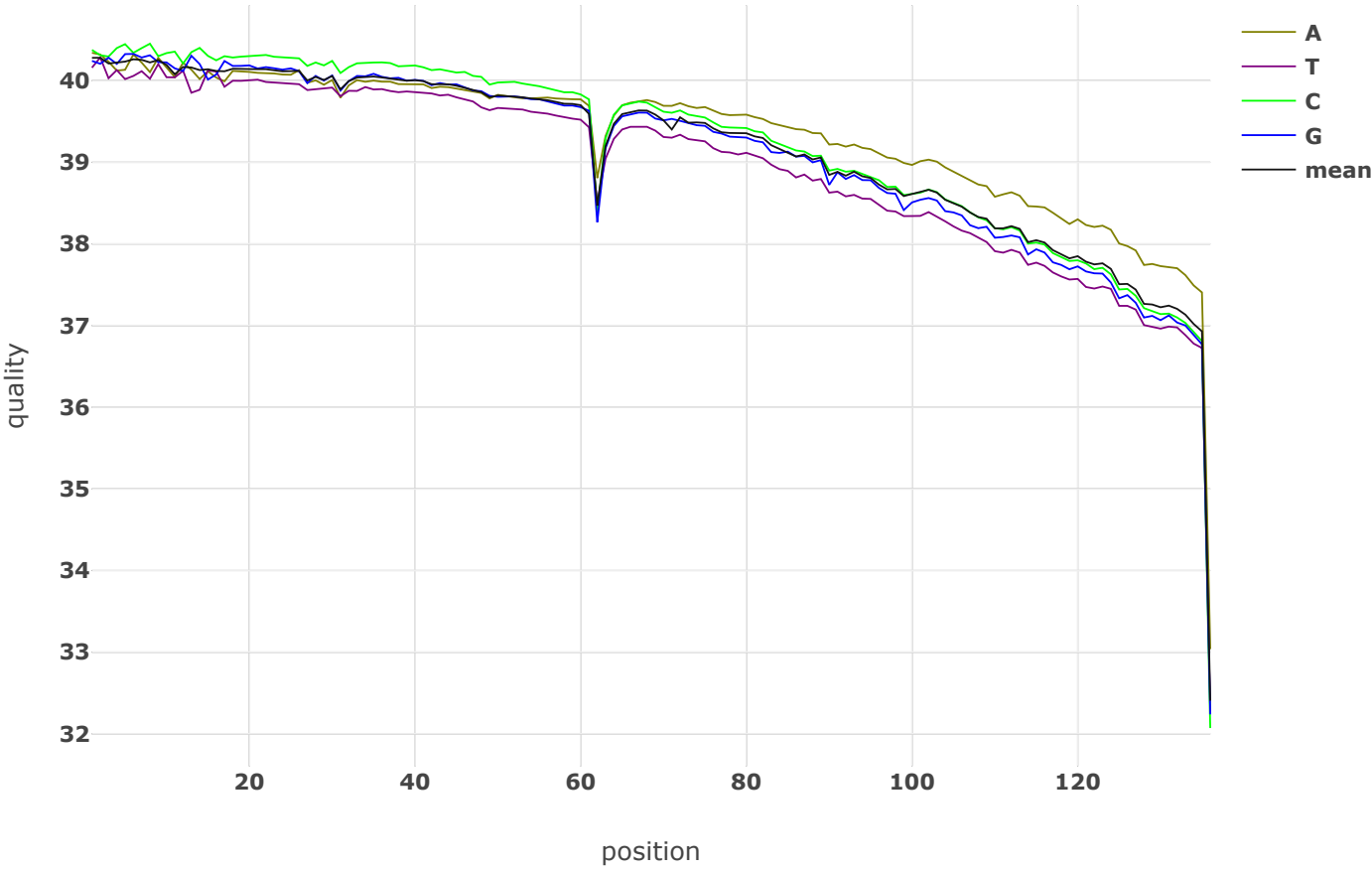
Value of each position will be shown on mouse over.



After filtering

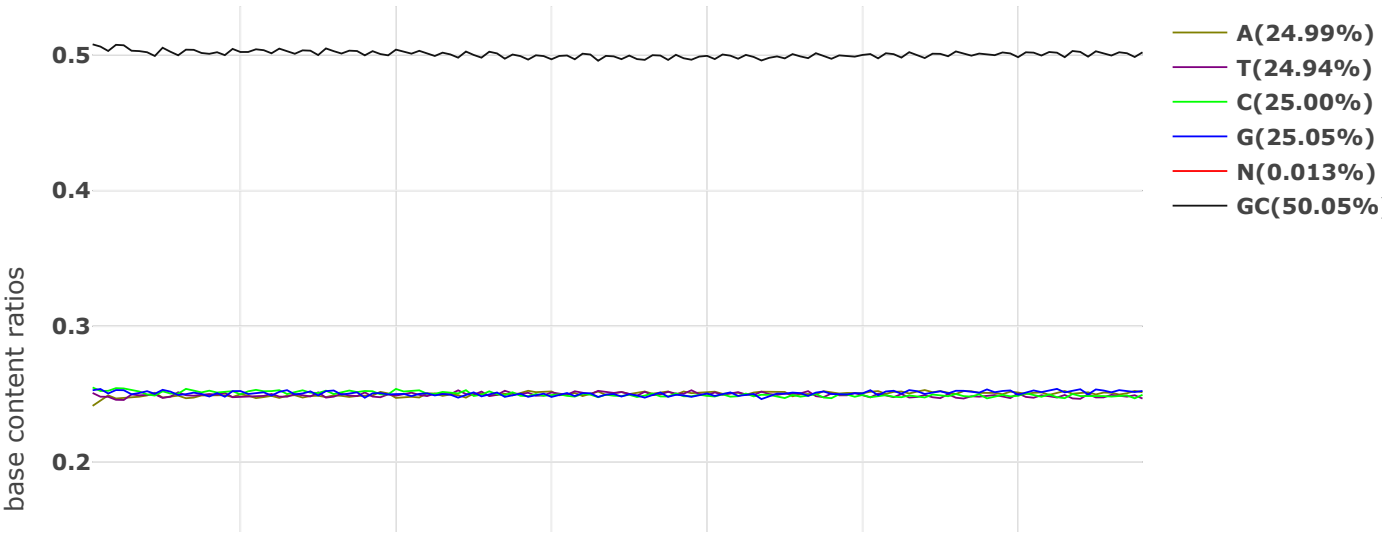
After filtering: read1: quality

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.



0.1

0

20

40

60

80

100

120

position

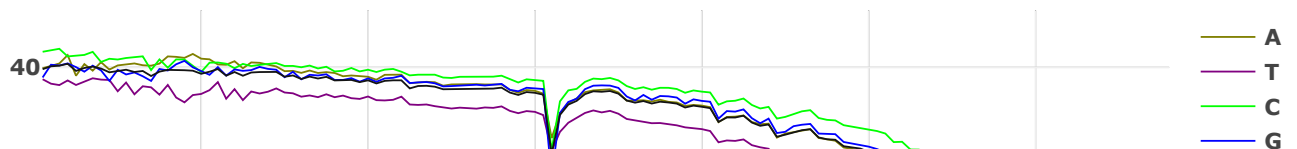
After filtering: read1: KMER counting

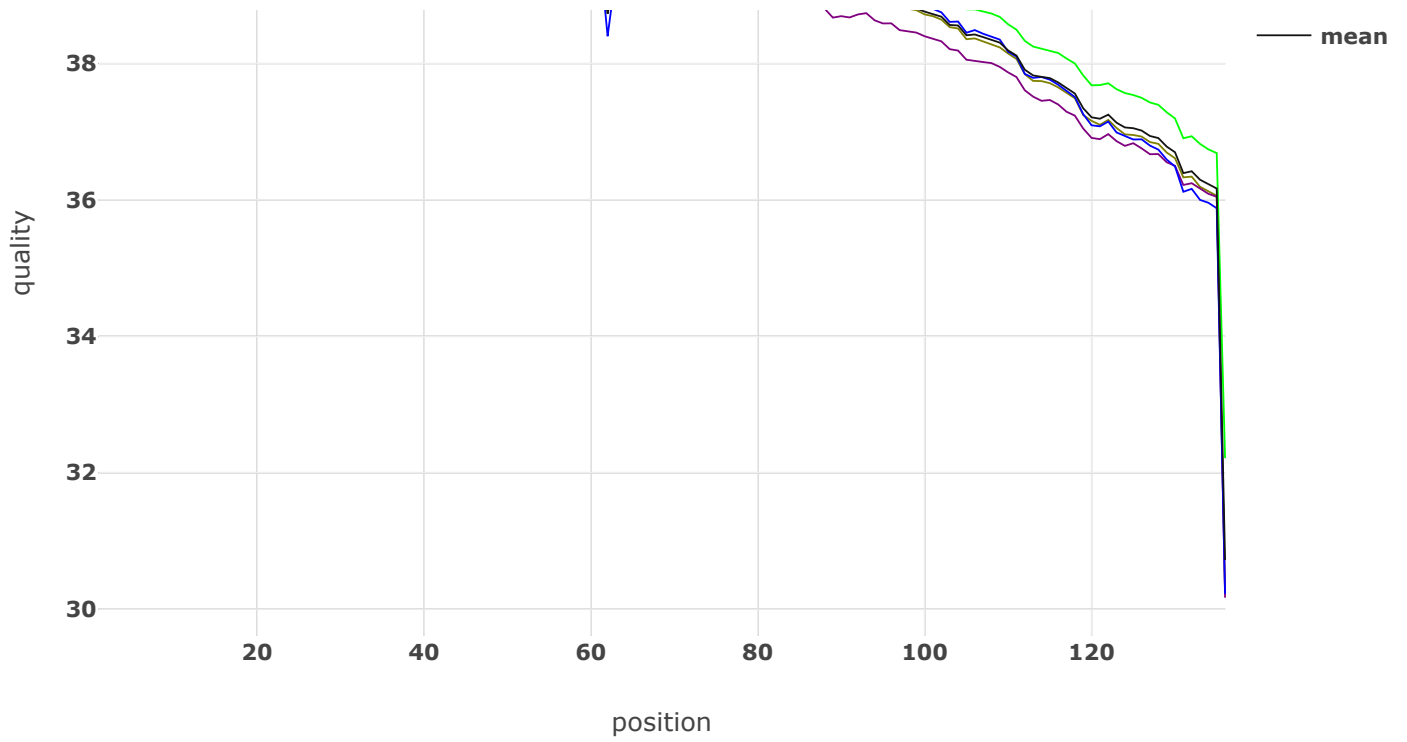
Darker background means larger counts. The count will be shown on mouse over.

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AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACCT	AACCT	AACGT	AACCA	AACCT	AACCC	AACCG	AACGA	AACGT	AACGC	AACGG
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ATA	ATAAA	ATAAT	ATAAC	ATAAG	ATATA	ATATT	ATATC	ATATG	ATACA	ATACT	ATACC	ATACG	ATAGA	ATAGT	ATAGC	ATAGG
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ACT	ACTAA	ACTAT	ACTAC	ACTAG	ACTTA	ACTTT	ACTTC	ACTTG	ACTCA	ACTCT	ACTCC	ACTCG	ACTGA	ACTGT	ACTGC	ACTGG
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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	TC CCT	TCCCC	TCCCG	TCCGA	TCCGT	TCCGC	TCCGG
TCG	TCGAA	TCGAT	TCGAC	TCGAG	TCGTA	TCGTT	TCGTC	TCGTG	TGCGA	TGCGT	TGCGC	TGCGG	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	TGTGC	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	CAAAAT	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	CACCT	CACCT	CACGT	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	CCAAAT	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	CCCCC	CCCCG
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	CGGT	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	CGGCC	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	GTAAB	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	GT CAT	GT CAC	GT CAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GT CCT	GTCCC	GTCCG	GT CGA	GT CGT	GT CGC	GT CGG
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	GC ACT	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	GG AAT	GG AAC	GG AAG	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	GGGT	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	GGGCC	GGGGA	GGGGT	GGGGC	GGGGG

After filtering: read2: quality

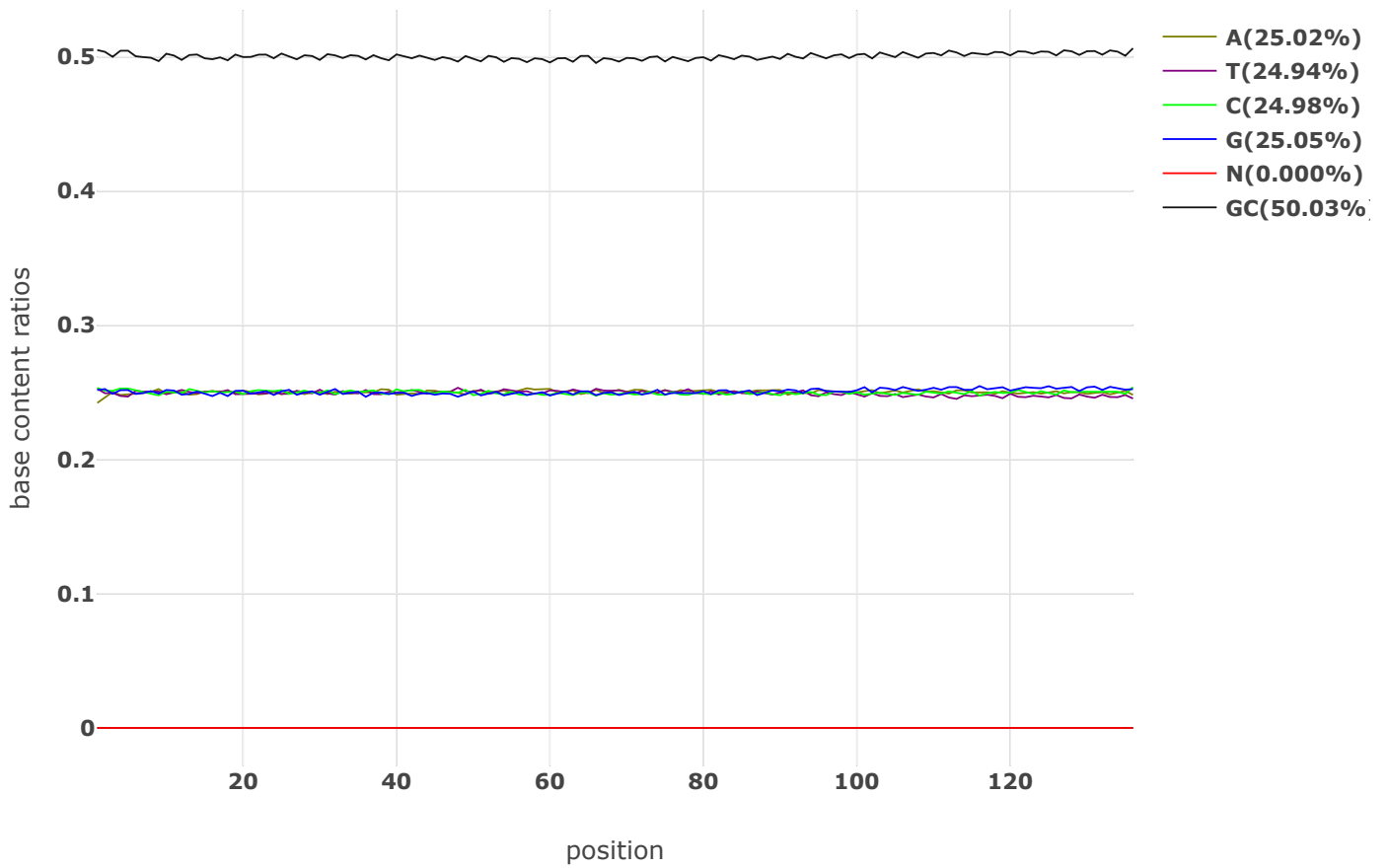
Value of each position will be shown on mouse over.





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
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