

# fastp report

## Summary

### General

fastp version:	0.24.0 ( <a href="https://github.com/OpenGene/fastp">https://github.com/OpenGene/fastp</a> )
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	151bp, 151bp
mean length after filtering:	146bp, 146bp
duplication rate:	14.709138%
Insert size peak:	175

### Before filtering

total reads:	53.502904 M
total bases:	8.078939 G
Q20 bases:	7.769507 G (96.169897%)
Q30 bases:	7.324285 G (90.659007%)
GC content:	49.228071%

### After filtering

total reads:	52.770468 M
total bases:	7.745854 G
Q20 bases:	7.484912 G (96.631204%)
Q30 bases:	7.071122 G (91.289125%)
GC content:	49.101083%

### Filtering result

reads passed filters:	52.770468 M (98.631035%)
reads with low quality:	718.224000 K (1.342402%)
reads with too many N:	3.180000 K (0.005944%)
reads too short:	11.032000 K (0.020619%)

## Adapters

### Adapter or bad ligation of read1

Sequence	Occurrences
A	97354
AG	96302
AGA	96305
AGAT	92726
AGATC	92694
AGATCG	91628
AGATCGG	89485

AGATCGGA	89965
AGATCGGAA	89132
AGATCGGAAG	87675
AGATCGGAAGA	86913
AGATCGGAAGAG	89834
AGATCGGAAGAGC	85613
AGATCGGAAGAGCA	85524
AGATCGGAAGAGCAC	84022
AGATCGGAAGAGCACA	80997
AGATCGGAAGAGCACAC	80287
AGATCGGAAGAGCACACG	83618
AGATCGGAAGAGCACACGT	77680
AGATCGGAAGAGCACACGTC	79801
AGATCGGAAGAGCACACGTCT	76426
AGATCGGAAGAGCACACGTCTG	75262
AGATCGGAAGAGCACACGTCTGA	73109
AGATCGGAAGAGCACACGTCTGAA	72695
AGATCGGAAGAGCACACGTCTGAAC	70371
AGATCGGAAGAGCACACGTCTGAACT	69080
AGATCGGAAGAGCACACGTCTGAACTC	67723
AGATCGGAAGAGCACACGTCTGAACTCC	67465
AGATCGGAAGAGCACACGTCTGAACTCCA	65109
AGATCGGAAGAGCACACGTCTGAACTCCAG	64481
AGATCGGAAGAGCACACGTCTGAACTCCAGT	61464
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	61368
AGATCGGAAGAGCACACGTCTGAACTCCAGTCA	59862
AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC	57722
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACA	56225
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACAC	55853
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACA	52302
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAG	51005
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGG	49349
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGGC	47439
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGGCA	46087
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGGCAT	44375
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGGCATA	42396
other adapter sequences	999070

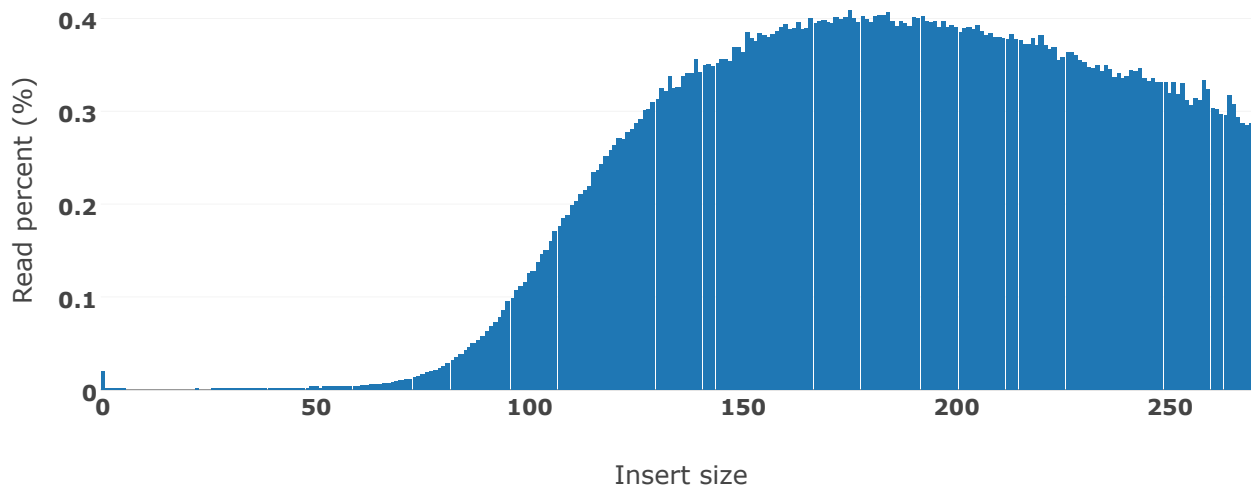
Adapter or bad ligation of read2

Sequence	Occurrences
A	97369
AG	96901
AGA	96671

AGAT	92826
AGATC	93262
AGATCG	92103
AGATCGG	90211
AGATCGGA	90518
AGATCGGAA	87588
AGATCGGAAG	87242
AGATCGGAAGA	86162
AGATCGGAAGAG	89555
AGATCGGAAGAGC	85235
AGATCGGAAGAGCG	84713
AGATCGGAAGAGCGT	81405
AGATCGGAAGAGCGTC	79762
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AGATCGGAAGAGCGTCGT	77683
AGATCGGAAGAGCGTCGTG	76527
AGATCGGAAGAGCGTCGTGT	75047
AGATCGGAAGAGCGTCGTGTA	70862
AGATCGGAAGAGCGTCGTGTAG	70408
AGATCGGAAGAGCGTCGTGTAGG	68266
AGATCGGAAGAGCGTCGTGTAGGG	67977
AGATCGGAAGAGCGTCGTGTAGGGA	66015
AGATCGGAAGAGCGTCGTGTAGGGAA	64219
AGATCGGAAGAGCGTCGTGTAGGGAAA	61254
AGATCGGAAGAGCGTCGTGTAGGGAAAG	61428
AGATCGGAAGAGCGTCGTGTAGGGAAAGA	59222
AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	58663
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGT	56204
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTG	55682
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT	53143
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTG	52325
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGA	50184
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGAT	48604
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGATG	46421
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGATGG	44932
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGATGGA	43971
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGATGGAG	42510
other adapter sequences	1262336

## Insert size estimation

Insert size distribution (40.284940% reads are with unknown length)

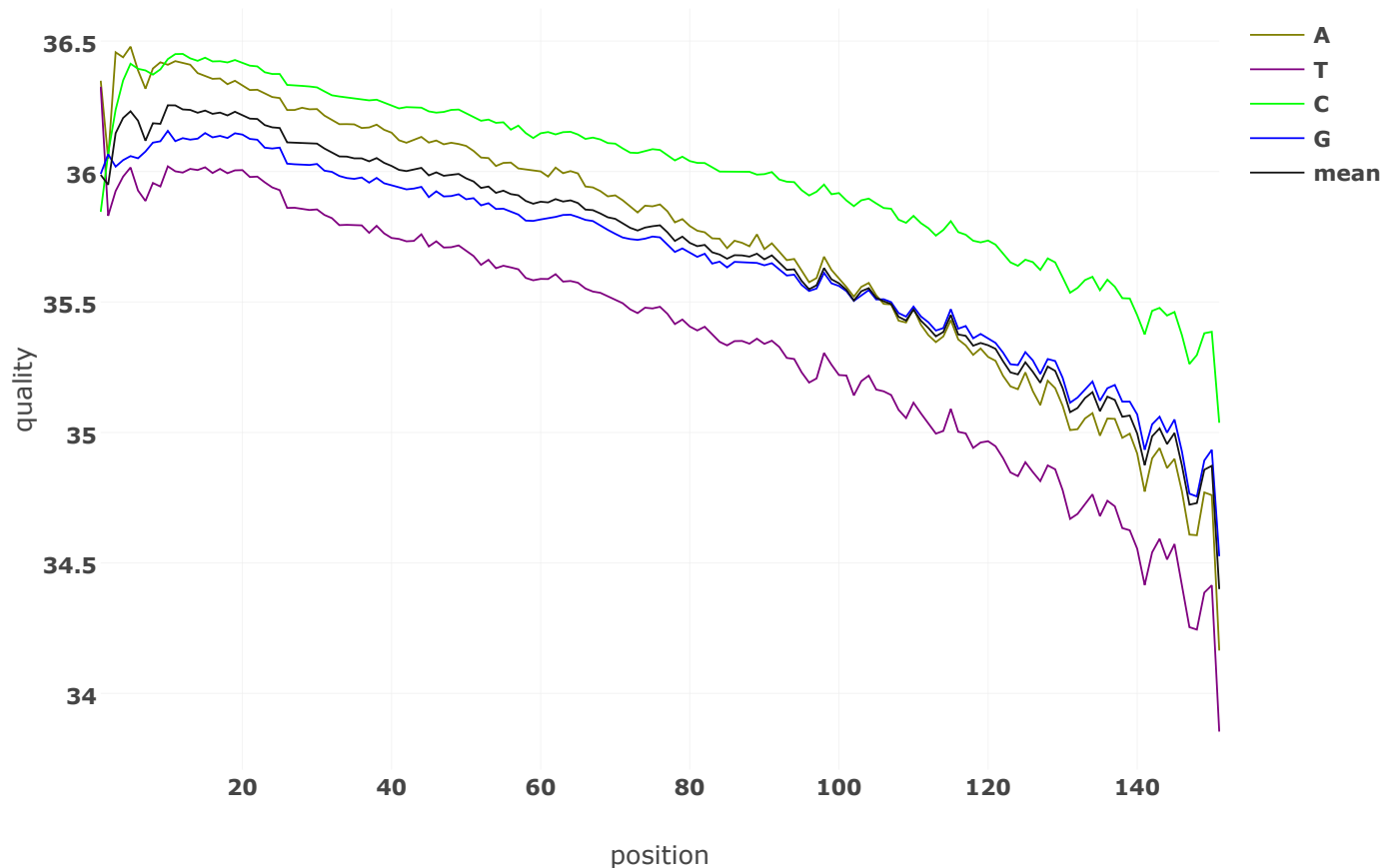


This estimation is based on paired-end overlap analysis, and there are 40.284940% reads found not overlapped. The nonoverlapped read pairs may have insert size <30 or >272, or contain too much sequencing errors to be detected as overlapped.

## Before filtering

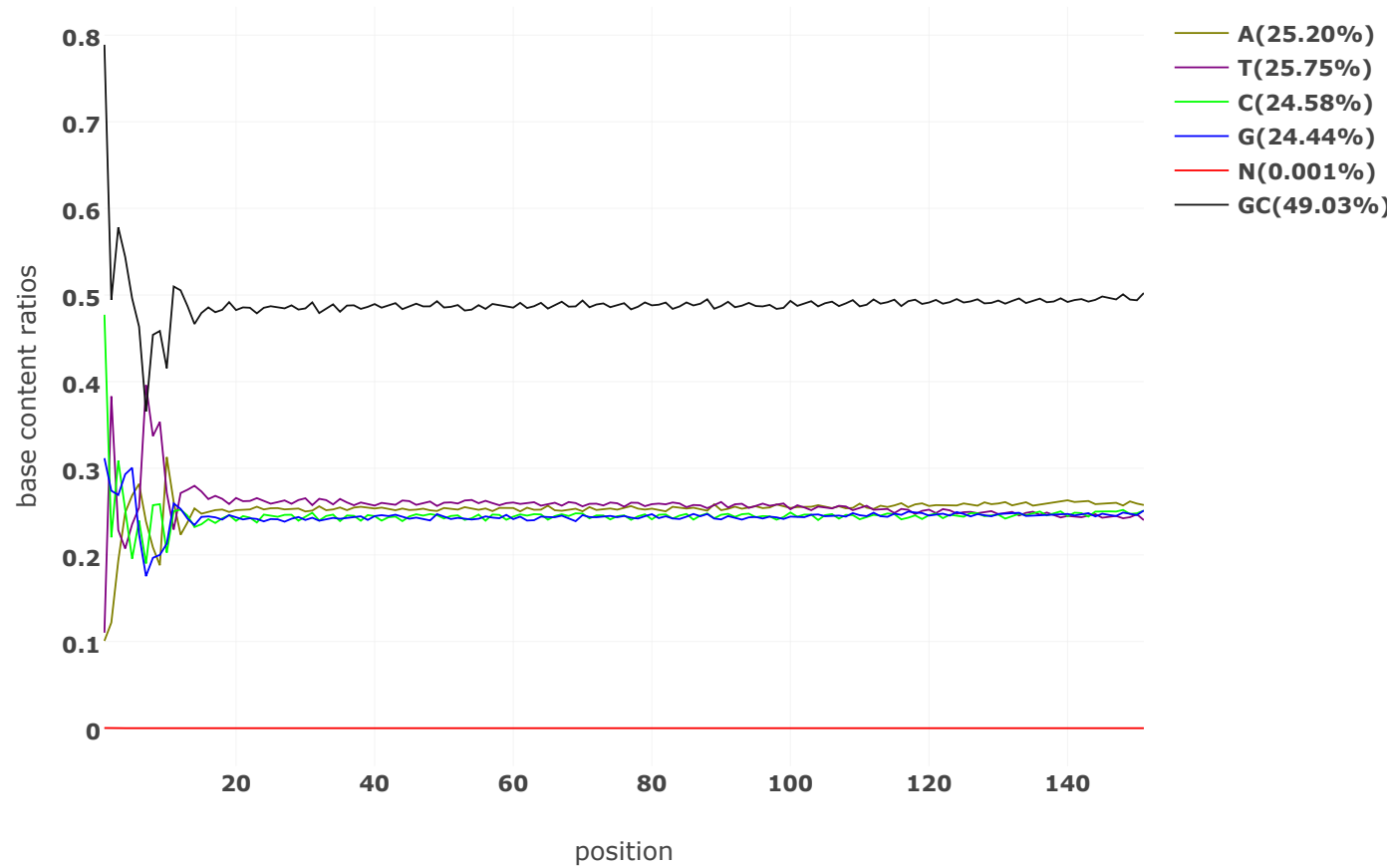
### Before filtering: read1: quality

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

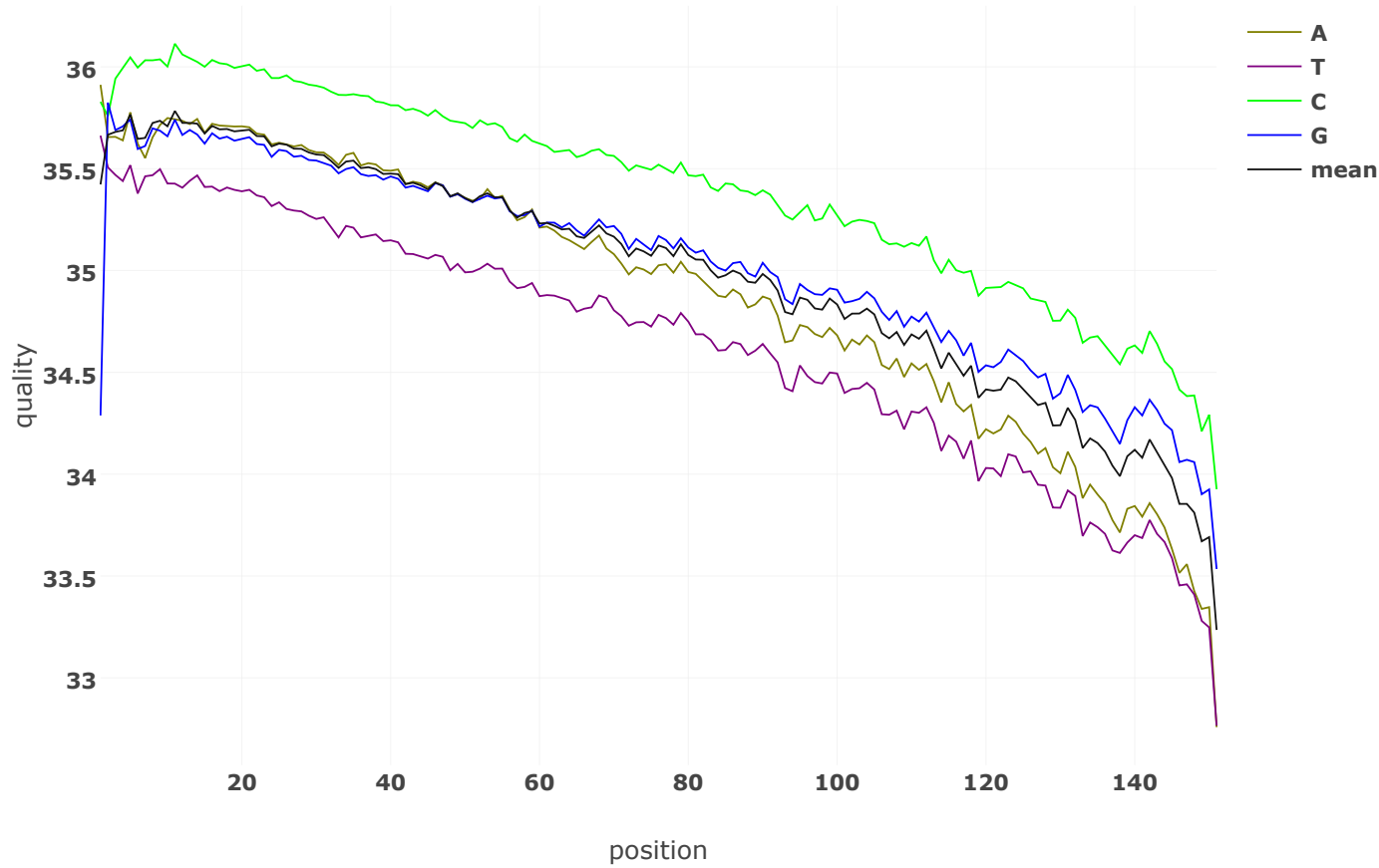
Darker background means larger counts. The count will be shown on mouse over.

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AAT	AATAA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
AAC	AACAA	AACAT	AACAC	AACAG	AACTA	AACCT	AACTC	AACGT	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
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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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CAA	CAAAA	CAAAAT	CAAAAC	CAAAAG	CAATA	CAATT	CAATC	CAATG	CAACA	CAACT	CAACC	CAACG	CAAGA	CAAGT	CAAGC	CAAGG
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CCA	CCAAA	CCAAT	CCAAC	CCAAG	CCATA	CCATT	CCATC	CCATG	CCACA	CCACT	CCACC	CCACG	CCAGA	CCAGT	CCAGC	CCAGG
CCT	CCTAA	CCTAT	CCTAC	CCTAG	CCTTA	CCTTT	CCTTC	CCTTG	CCTCA	CCTCT	CCTCC	CCTCG	CCTGA	CCTGT	CCTGC	CCTGG
CCC	CCCAA	CCCAT	CCCAC	CCCAG	CCCTA	CCCTT	CCCTC	CCCTG	CCCCA	CCCCT	CCCCC	CCCCG	CCCCA	CCCGT	CCCGC	CCCGG
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CGA	CGAAA	CGAAT	CGAAC	CGAAG	CGATA	CGATT	CGATC	CGATG	CGACA	CGACT	CGACC	CGACG	CGAGA	CGAGT	CGAGC	CGAGG
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Before filtering: read2: quality

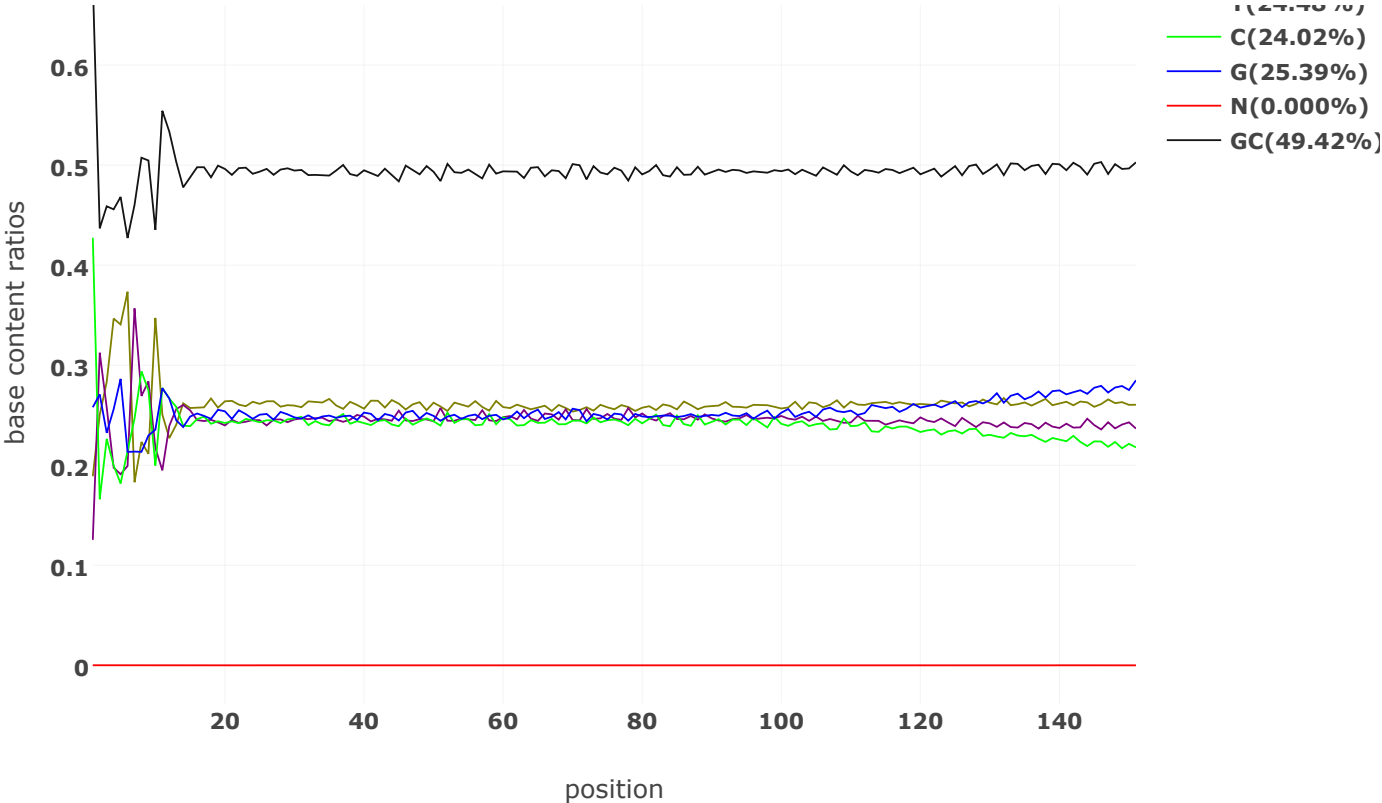
Value of each position will be shown on mouse over.



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.

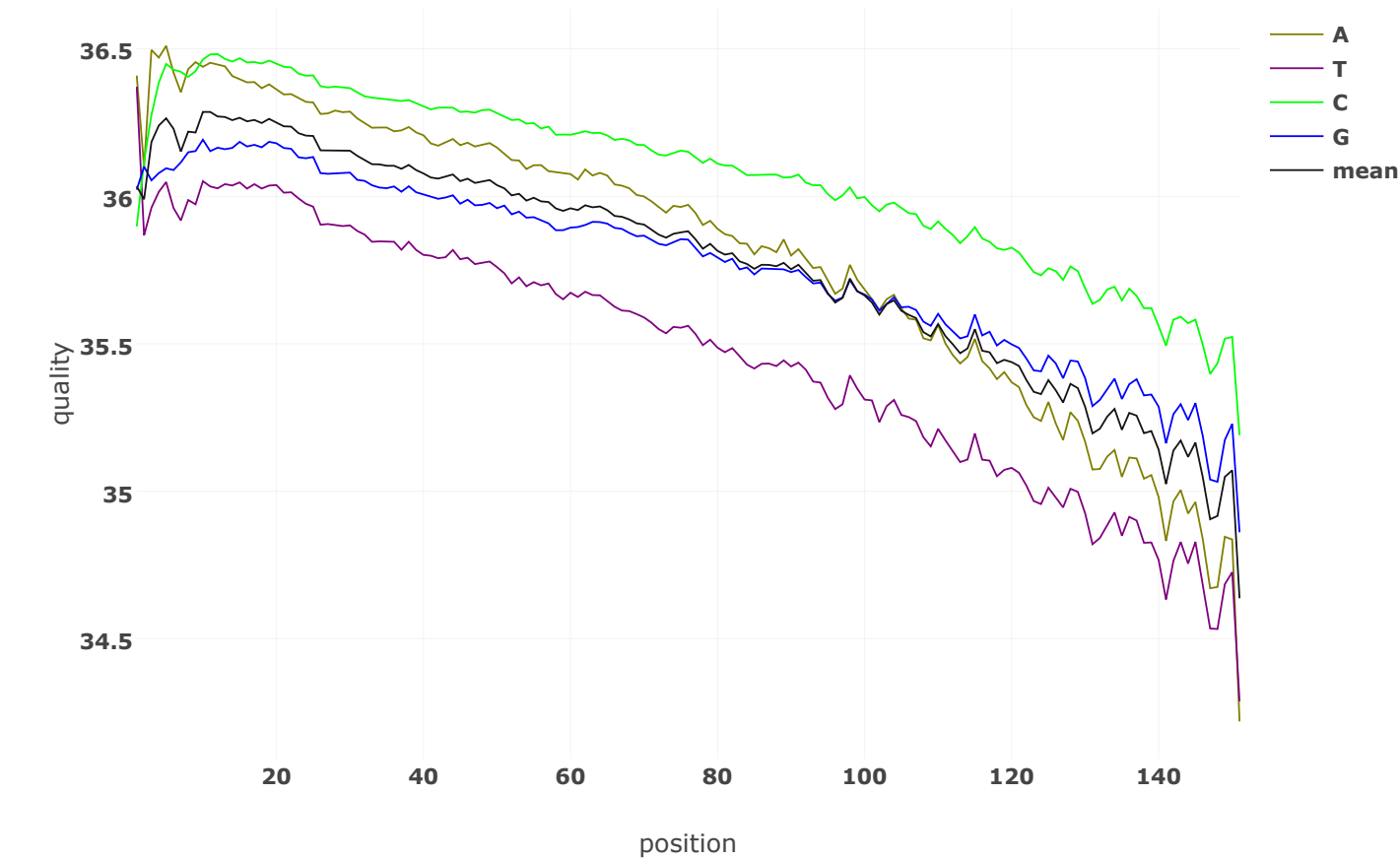
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TCC	TCCAA	TCCAT	TCCAC	TCCAG	TCCTA	TCCTT	TCCTTC	TCCTTG	TCCCA	TC CCT	TCCCC	TCCCG	TCCGA	TCCGT	TCCGC	TCCGG
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CAT	CATAA	CATAT	CATAC	CATAG	CATTA	CATTT	CATTC	CATTG	CATCA	CATCT	CATCC	CATCG	CATGA	CATGT	CATGC	CATGG
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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	CTCTTC	CTCTTG	CTCCA	CTCCT	CTCCC	CTCCG	CTCGA	CTCGT	CTCGC	CTCGG
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CCC	CCCAA	CCCAT	CCCAC	CCCAG	CCCTA	CCCTT	CCCTTC	CCCTTG	CCCCA	CC CCT	CCCCC	CCCCG	CCCCGA	CCCCGT	CCCCC	CCCCG
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CGG	CGGAA	CGGAT	CGGAC	CGGAG	CGGTA	CGGTT	CGGTC	CGGTG	CGGCA	CGGCT	CGGCC	CGGCG	CGGGA	CGGGT	CGGGC	CGGGG
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GAG	GAGAA	GAGAT	GAGAC	GAGAG	GAGTA	GAGTT	GAGTC	GAGTG	GAGCA	GAGCT	GAGCC	GAGCG	GAGGA	GAGGT	GAGGC	GAGGG
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GTC	GTC AA	GTCAT	GTCAC	GTCAG	GTCTA	GTCTT	GTCTTC	GTCTTG	GTCCA	GT CCT	GTCCC	GTCCG	GTCGA	GTCGT	GTCGC	GTCGG

GTG	GTGA	GTGAT	GTGAC	GTGAG	GTGTA	GTGTT	GTGTC	GTGTG	GTGCA	GTGCT	GTGCC	GTGCG	GTGGA	GTGGT	GTGGC	GTGGG
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GCT	GCTAA	GCTAT	GCTAC	GCTAG	GCTTA	GCTTT	GCTTC	GCTTG	GCTCA	GCTCT	GCTCC	GCTCG	GCTGA	GCTGT	GCTGC	GCTGG
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GGT	GGTAA	GGTAT	GGTAC	GGTAG	GGTTA	GGTTT	GGTTC	GGTTG	GGTCA	GGTCT	GGTCC	GGTCG	GGTGA	GGTGT	GGTGC	GGTGG
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After filtering

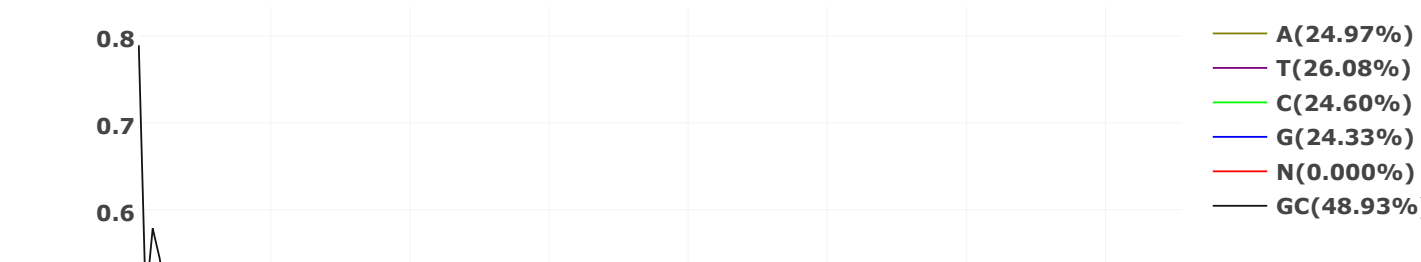
After filtering: read1: quality

Value of each position will be shown on mouse over.

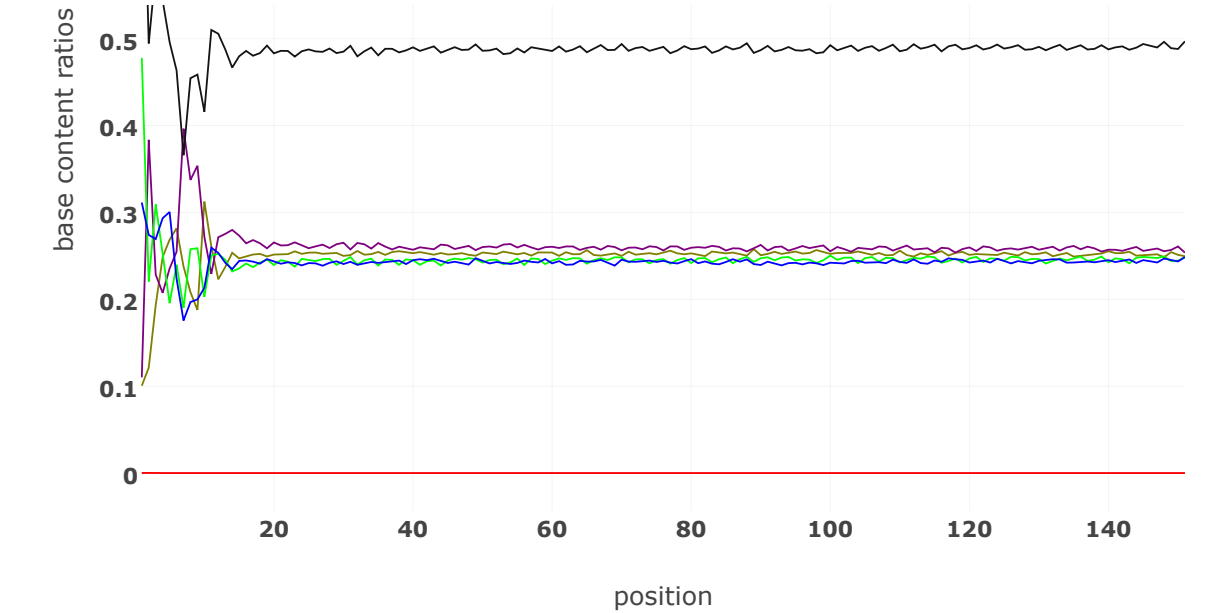


After filtering: read1: base contents

Value of each position will be shown on mouse over.







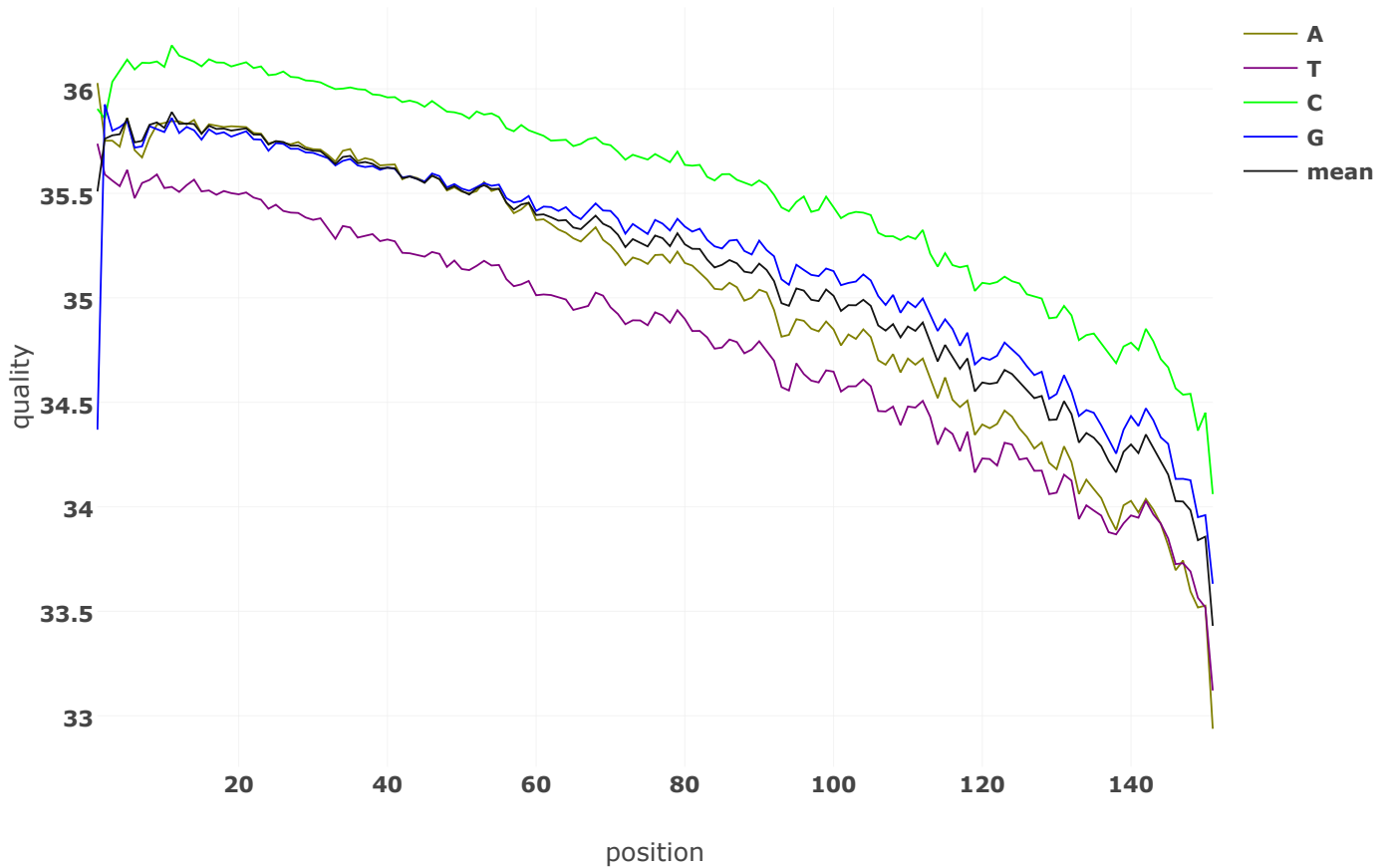
After filtering: read1: KMER counting

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

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AAG	AAGAA	AAGAT	AAGAC	AAGAG	AAGTA	AAGTT	AAGTC	AAGTG	AAGCA	AAGCT	AAGCC	AAGCG	AAGGA	AAGGT	AAGGC	AAGGG
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GAT	GATAA	GATAT	GATAC	GATAG	GATTA	GATTT	GATTC	GATTG	GATCA	GATCT	GATCC	GATCG	GATGA	GATGT	GATGC	GATGG
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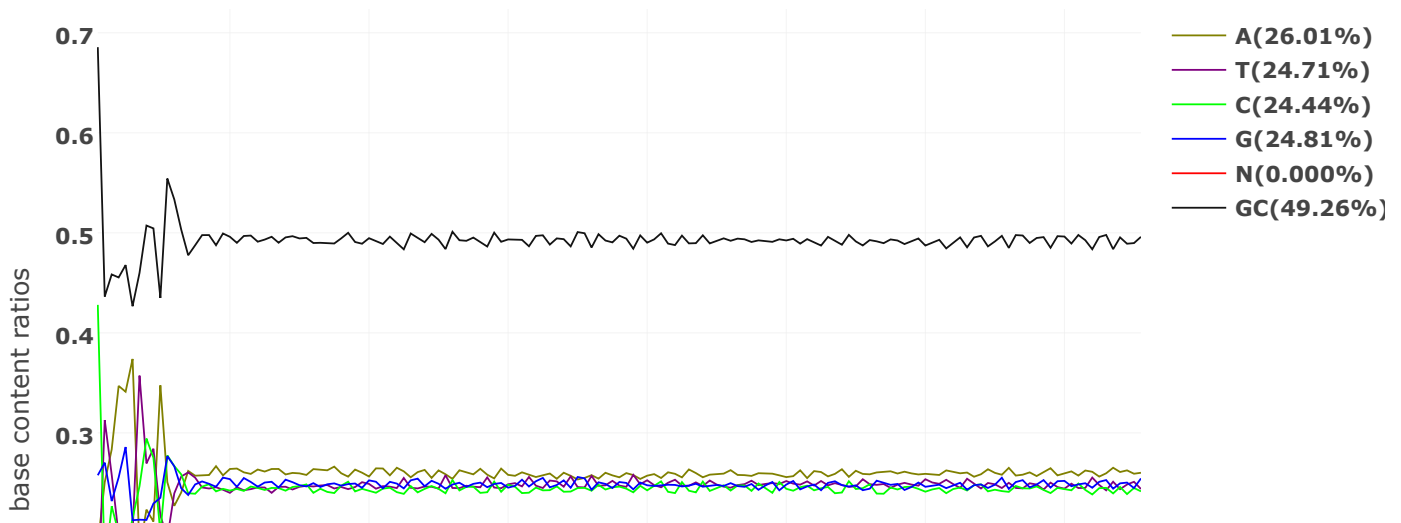
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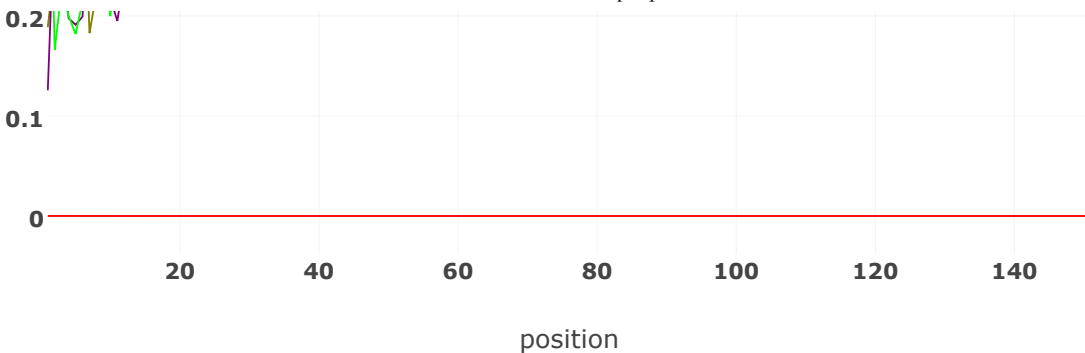
Value of each position will be shown on mouse over.



## 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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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	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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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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TTA	TTAAA	TTAAT	TTAAC	TTAAG	TTATA	TTATT	TTATC	TTATG	TTACA	TTACT	TTACC	TTACG	TTAGA	TTAGT	TTAGC	TTAGG
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CAA	CAAAA	CAAAAT	CAAAAC	CAAAAG	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
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CAG	CAGAA	CAGAT	CAGAC	CAGAG	CAGTA	CAGTT	CAGTC	CAGTG	CAGCA	CAGCT	CAGCC	CAGCG	CAGGA	CAGGT	CAGGC	CAGGG
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CCA	CCAAA	CCAAAT	CCAAAC	CCAAAG	CCATA	CCATT	CCATC	CCATG	CCACA	CCACT	CCACC	CCACG	CCAGA	CCAGT	CCAGC	CCAGG
CCT	CCTAA	CCTAT	CCTAC	CCTAG	CCTTA	CCTTT	CCTTC	CCTTG	CCTCA	CCTCT	CCTCC	CCTCG	CCTGA	CCTGT	CCTGC	CCTGG
CCC	CCCAA	CCCAT	CCCAC	CCCAG	CCCTA	CCCTT	CCCTC	CCCTG	CCCCA	CCCCT	CCCCC	CCCCG	CCCGA	CCCGT	CCCGC	CCCGG
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