













# FastQC Report

## Summary

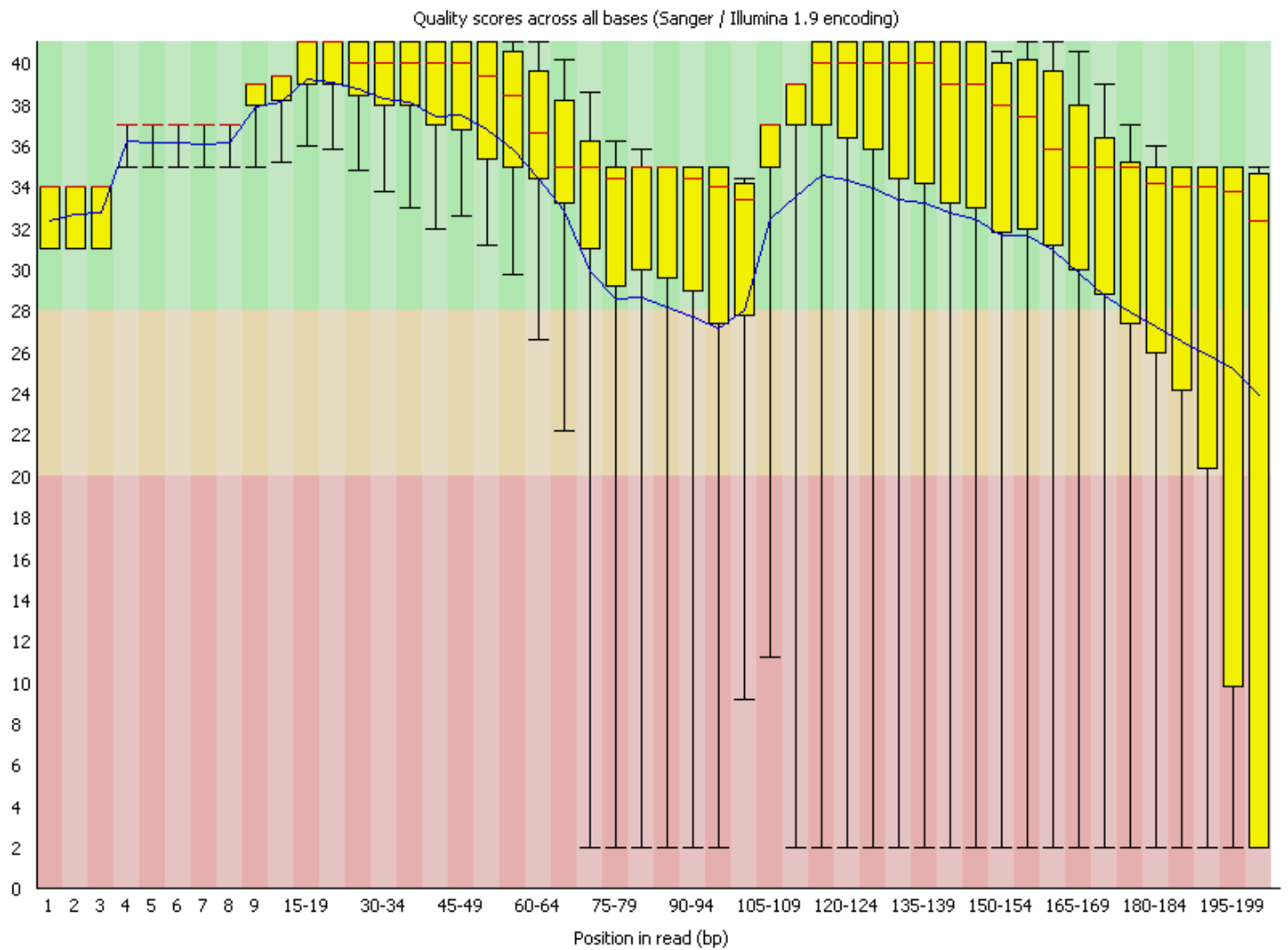
Sun 21 Sep 2014  
SRR1033794.fastq

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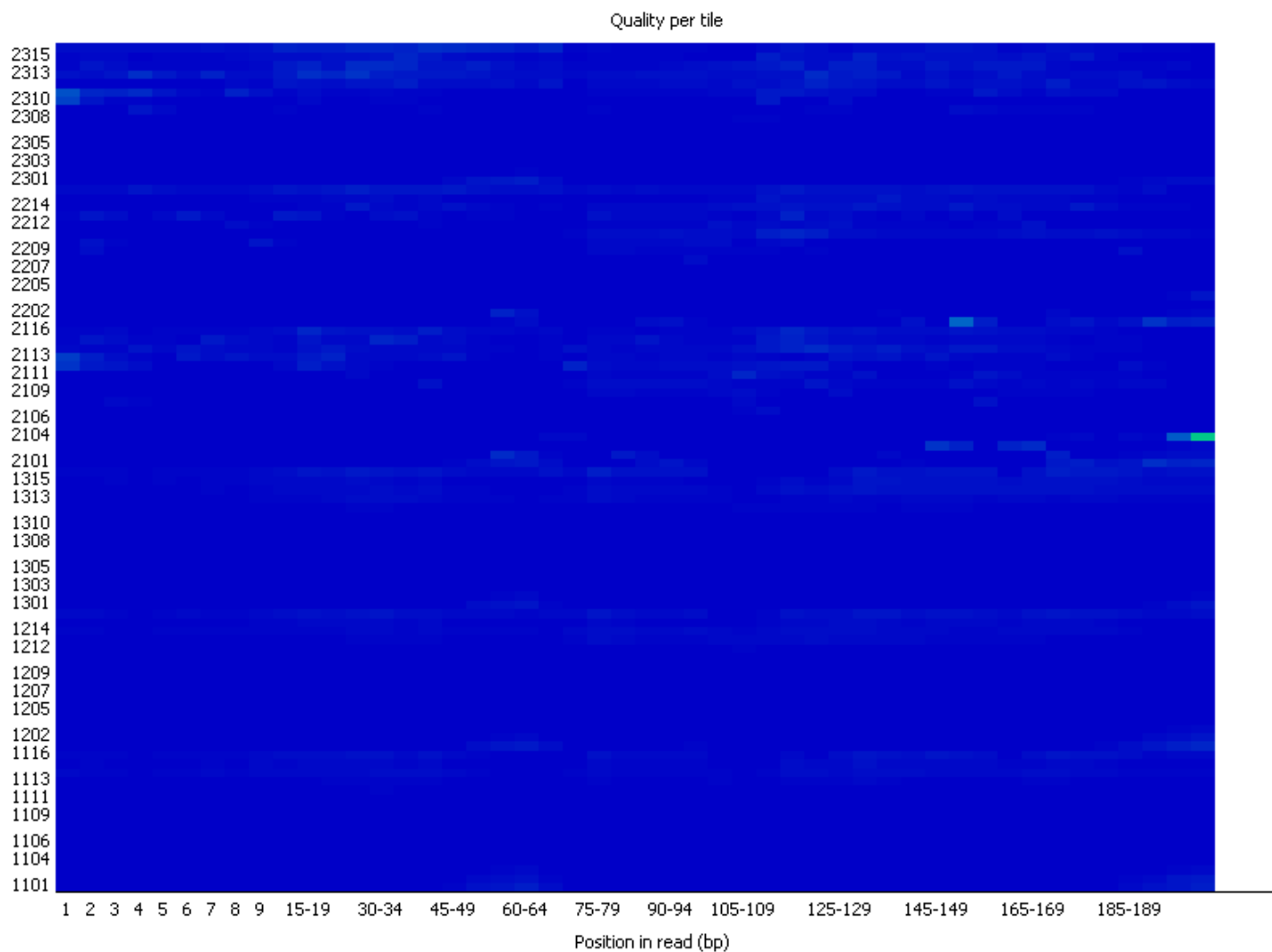
## Basic Statistics

Measure	Value
Filename	SRR1033794.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	30007340
Sequences flagged as poor quality	0
Sequence length	202
%GC	53

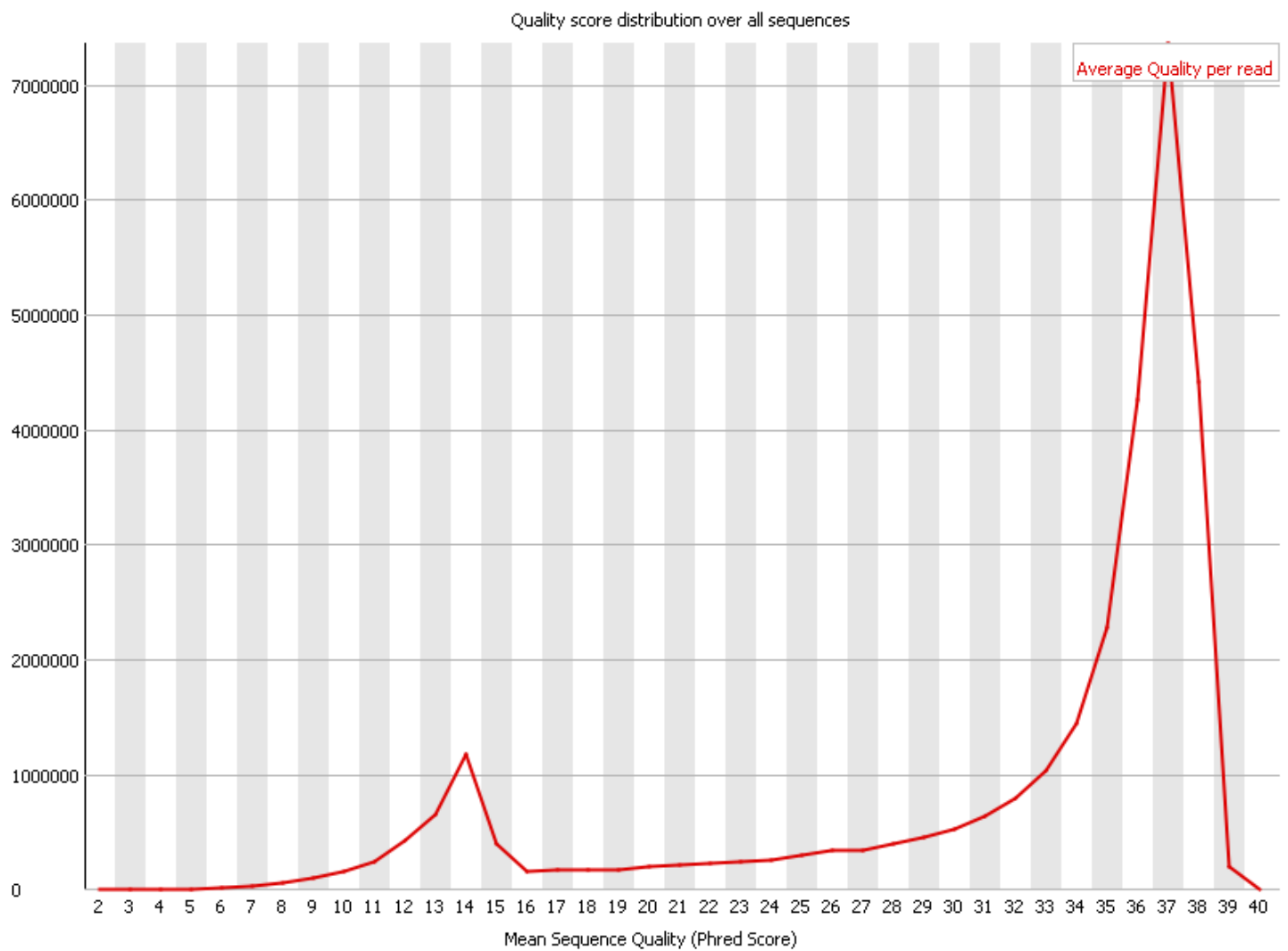
## Per base sequence quality



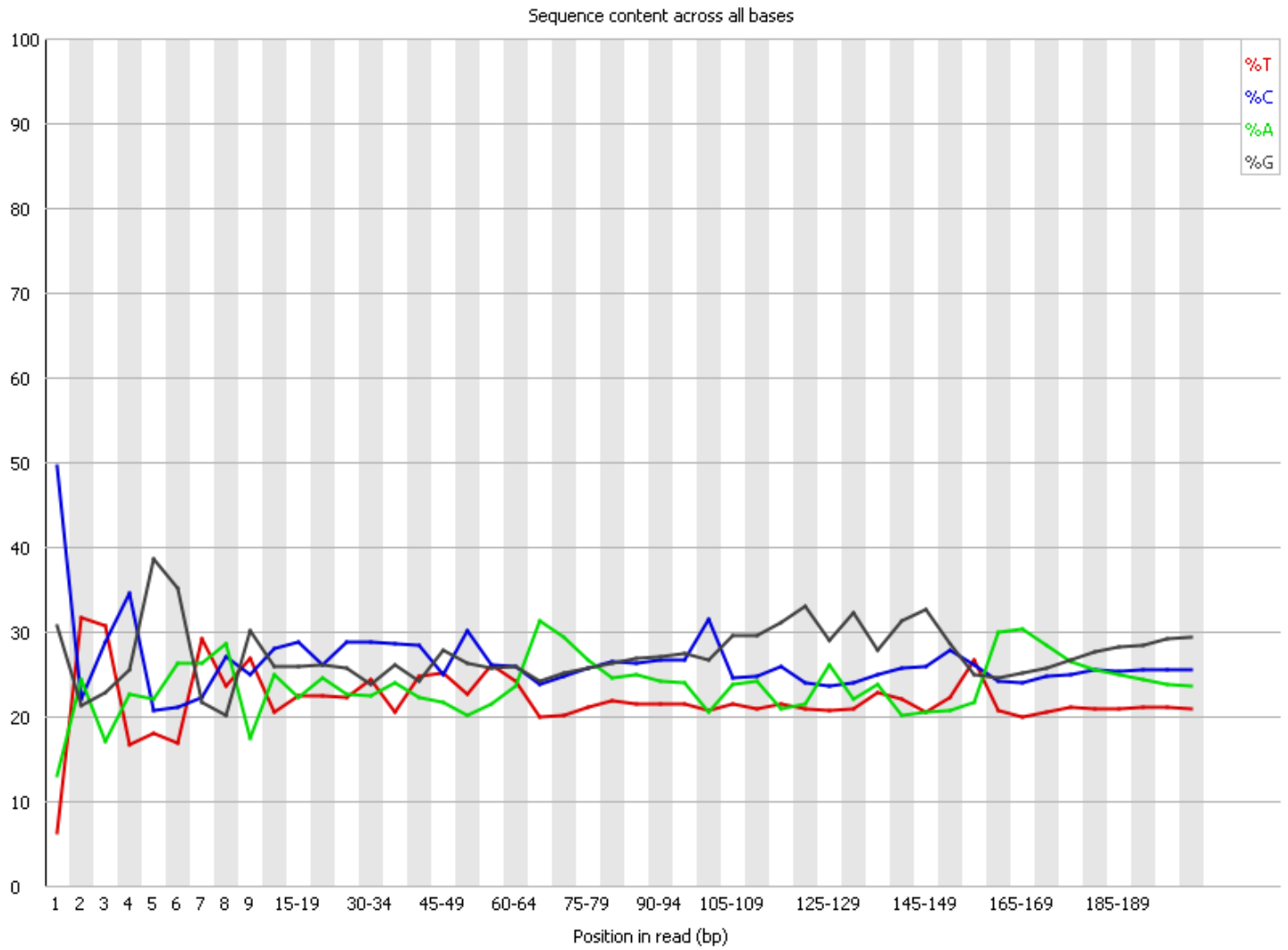
**Per tile sequence quality**



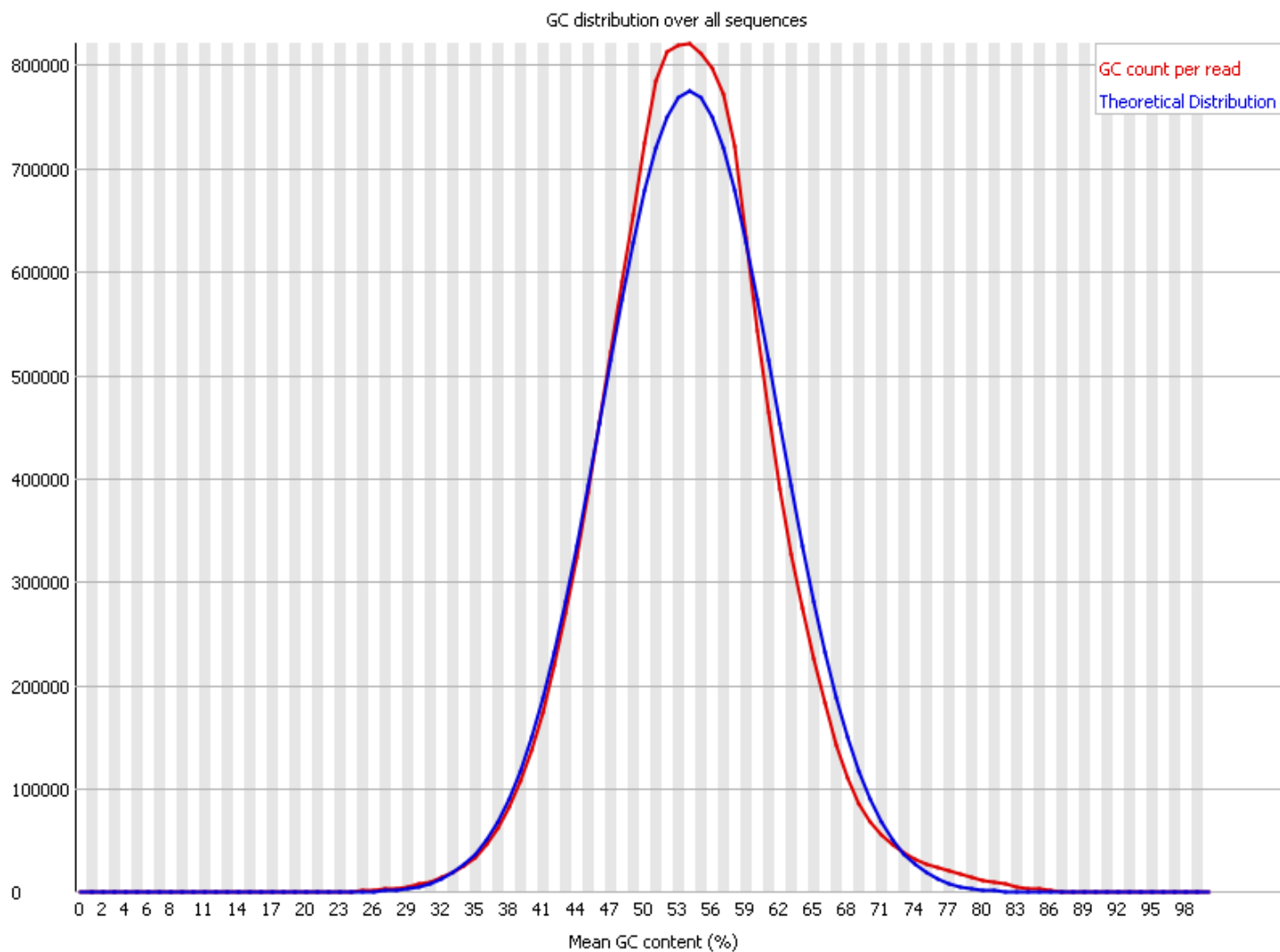
**Per sequence quality scores**



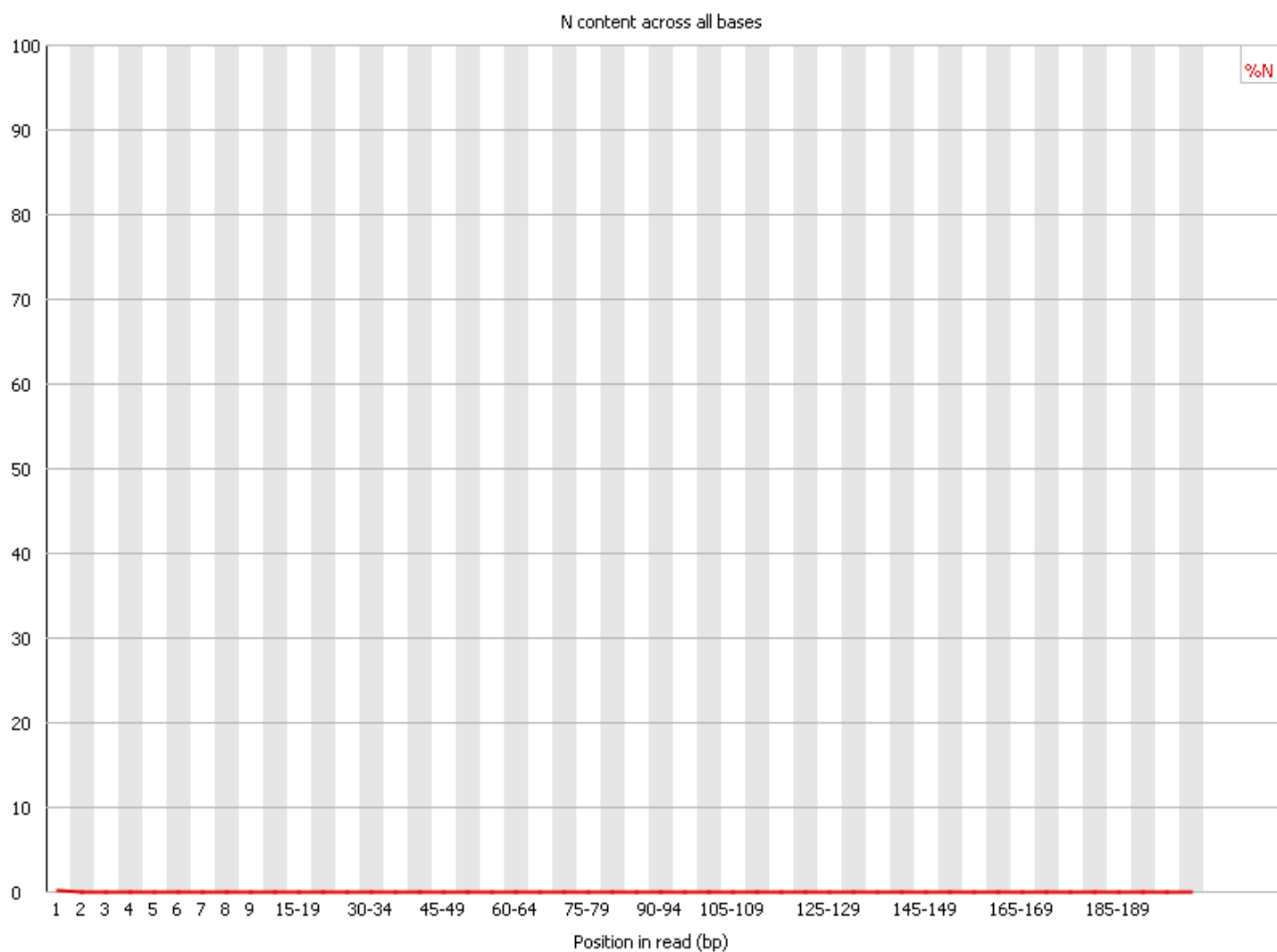
## ✖ Per base sequence content



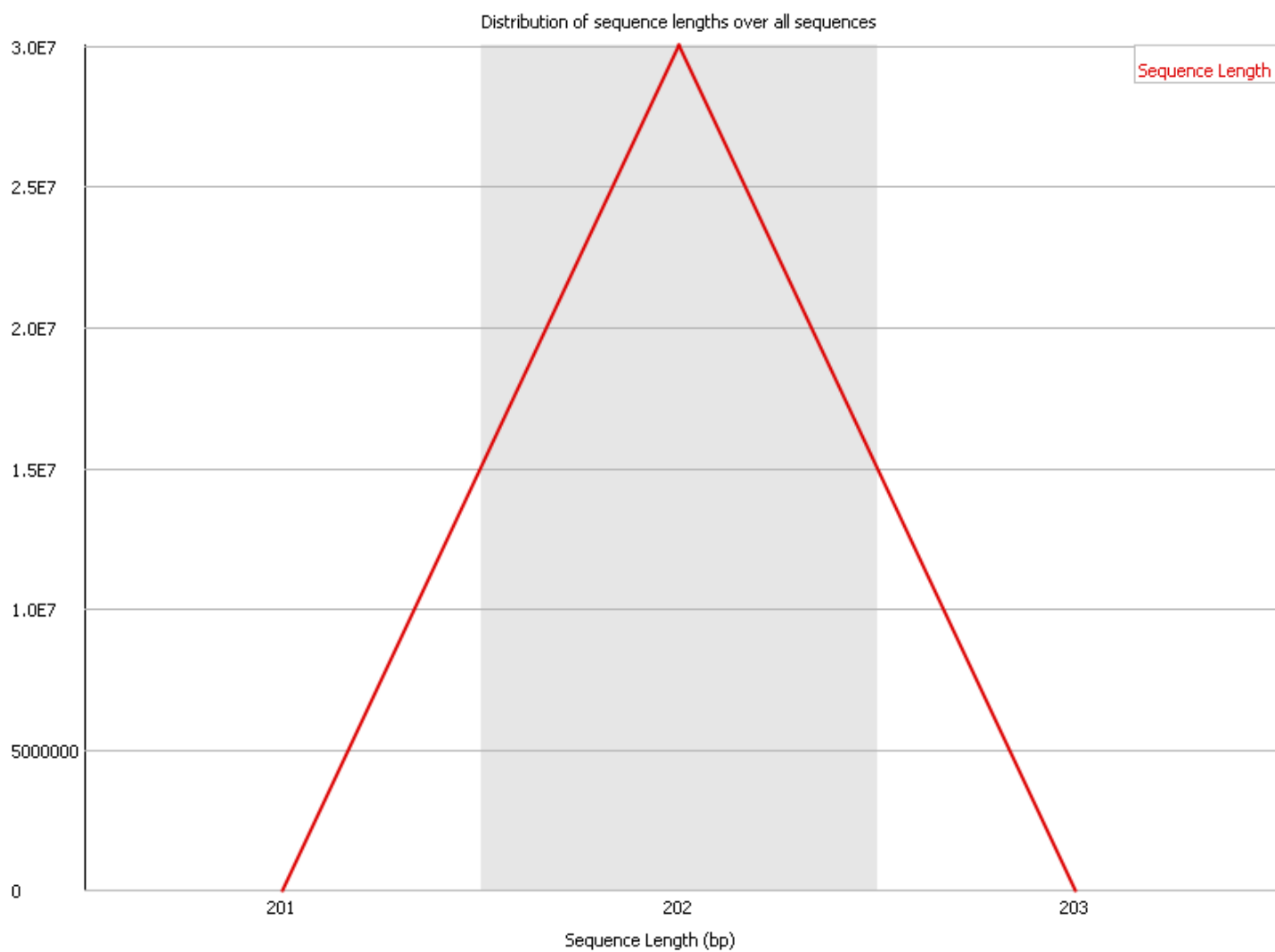
**Per sequence GC content**



**Per base N content**

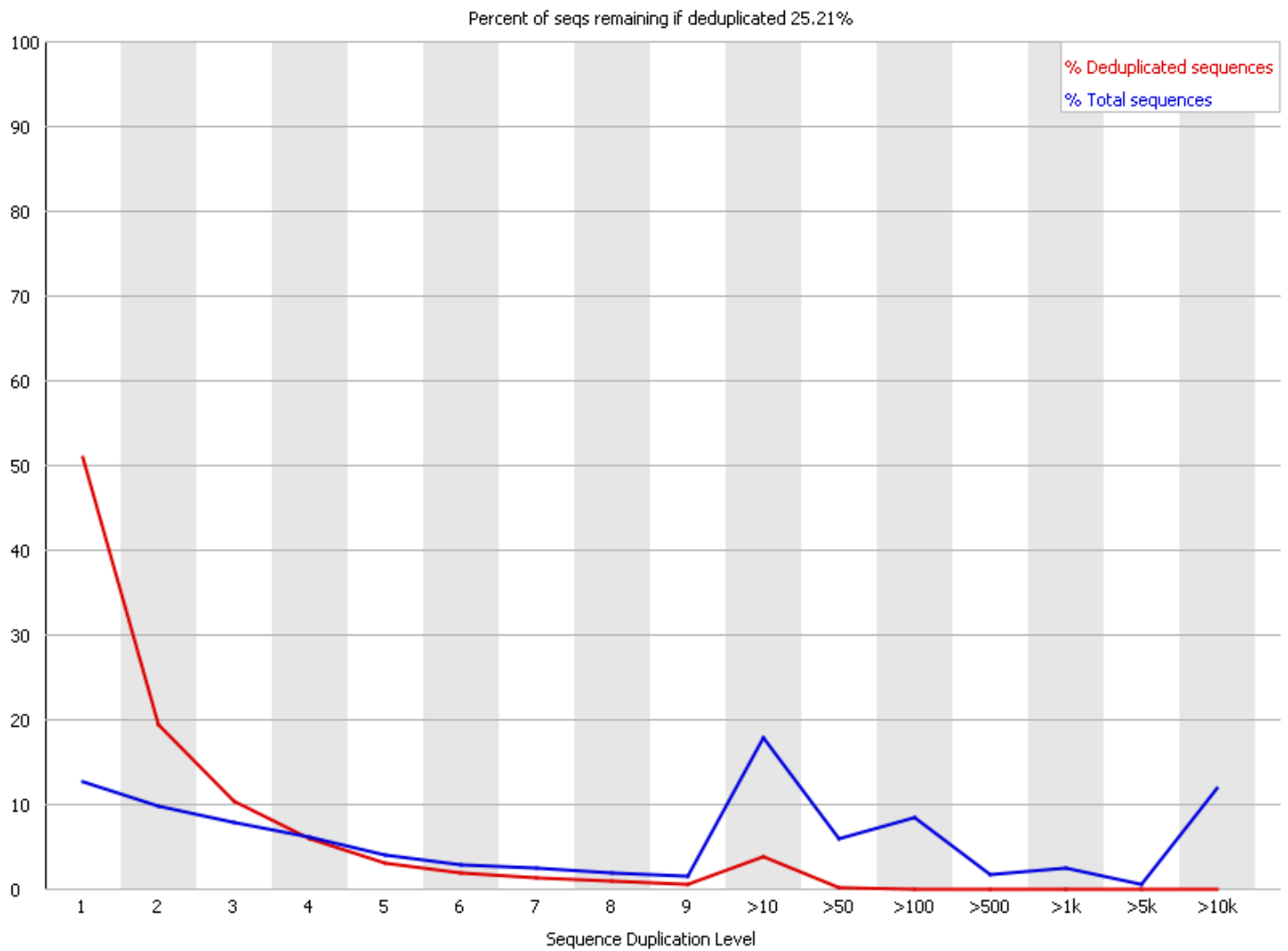


## Sequence Length Distribution



## Sequence Duplication Levels





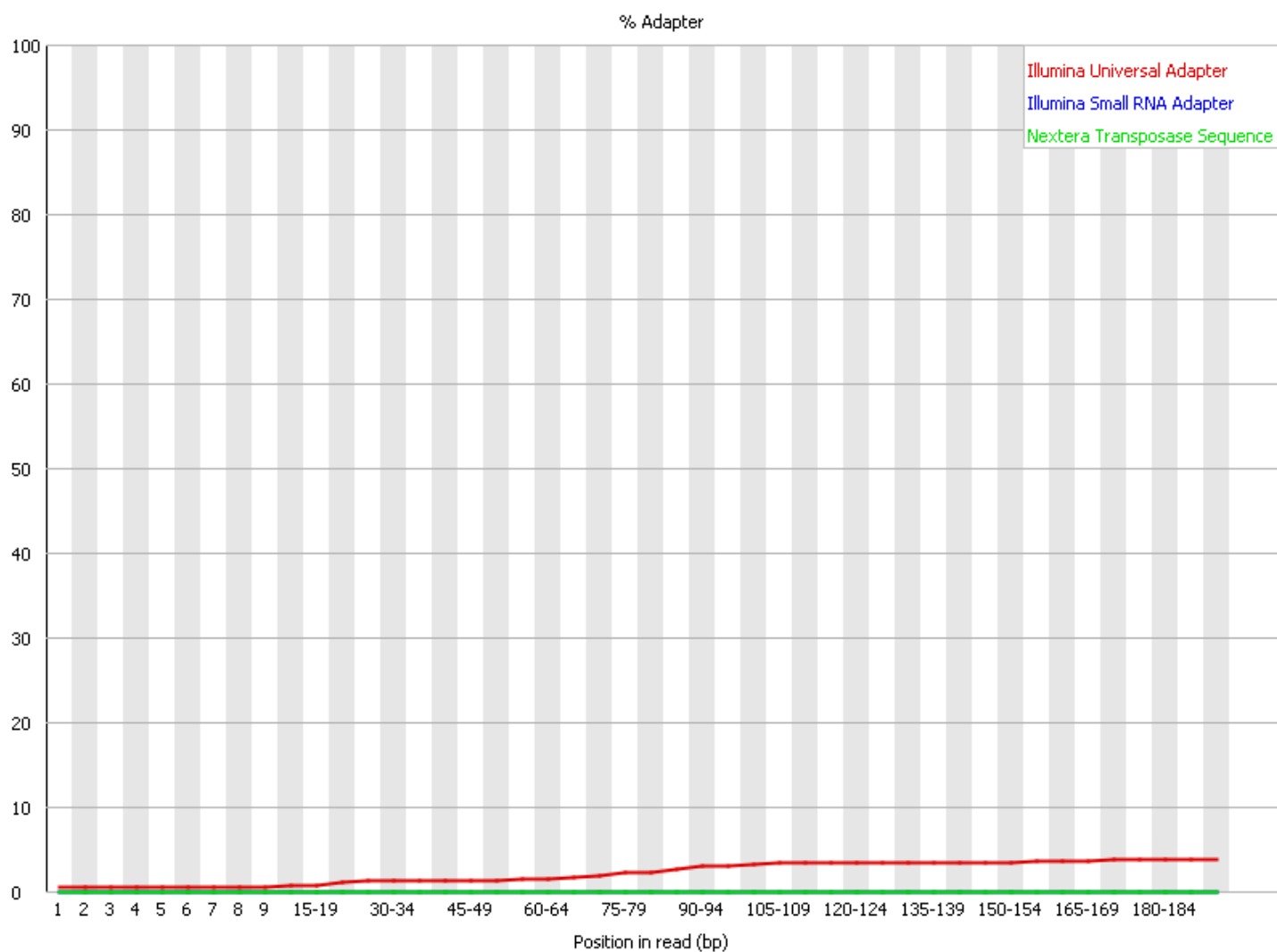
## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGC	2444375	8.145923630685026	TruSeq Adapter, Index 4 (100% over 50bp)
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATG	187522	0.6249204361332927	TruSeq Adapter, Index 4 (100% over 49bp)
CACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTGCT	183465	0.6114004106995155	TruSeq Adapter, Index 4 (100% over 50bp)

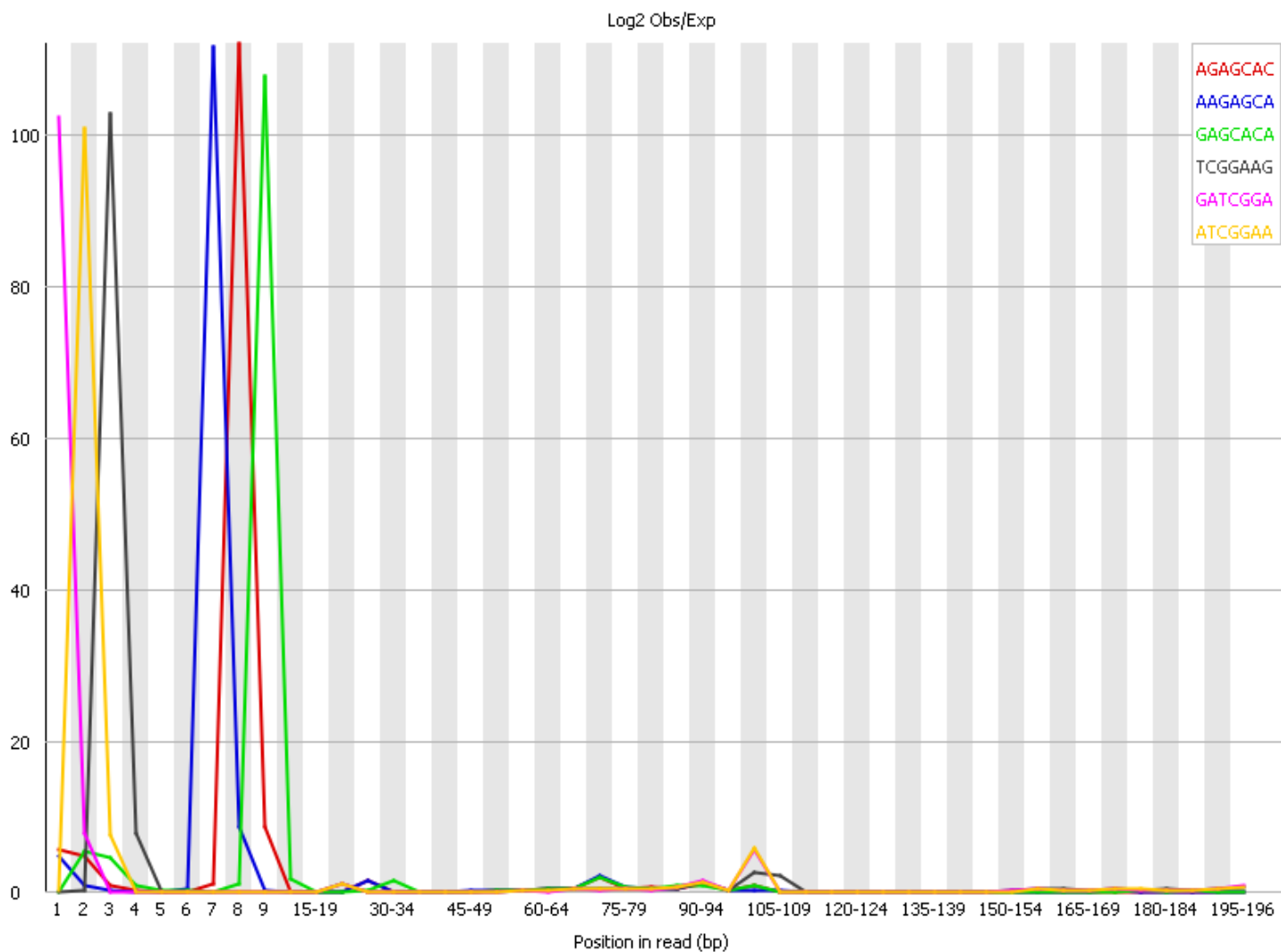
Sequence	Count	Percentage	Possible Source
AGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTG	133833	0.4460008784517388	TruSeq Adapter, Index 4 (100% over 50bp)
AGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTC	130683	0.43550344682334385	TruSeq Adapter, Index 4 (100% over 50bp)
CGTATGCCGTCTTCTGCTTGAGATCGGAAGAGCACACGTCTGAACTCCAG	109077	0.3635010634064865	Illumina Multiplexing PCR Primer 2.01 (100% over 30bp)
AAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTT	104426	0.348001522294212	TruSeq Adapter, Index 4 (100% over 50bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATATCGTATGC	66035	0.22006282462890747	TruSeq Adapter, Index 4 (98% over 50bp)
ACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTGCTT	37127	0.12372639494203752	TruSeq Adapter, Index 4 (100% over 50bp)
GCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTGC	33879	0.11290237655187031	TruSeq Adapter, Index 4 (100% over 50bp)
GATTGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGC	30163	0.10051873974834158	TruSeq Adapter, Index 4 (98% over 50bp)



## Adapter Content



## Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGAGCAC	508635	0.0	111.91078	8
AAGAGCA	512140	0.0	111.523865	7
GAGCACA	528620	0.0	107.668755	9
TCGGAAG	550430	0.0	102.692345	3
GATCGGA	557120	0.0	102.343124	1
ATCGGAA	561350	0.0	100.89536	2
CGGAAGA	566580	0.0	99.74074	4
GAAGAGC	625780	0.0	91.27612	6
GGAAGAG	704780	0.0	81.403046	5
ATTTTCGG	42790	0.0	32.469765	135-139
TTAAAAA	347085	0.0	29.828262	155-159
TTTAAAA	210200	0.0	29.676819	155-159
AATTTTCG	25155	0.0	29.054312	135-139
TTTCGGG	53725	0.0	28.623331	135-139

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGTATG	444400	0.0	27.818113	40-44
TTGAAAA	410715	0.0	27.602919	60-64
CTCGTAT	434190	0.0	27.587223	40-44
TGAAAAA	409595	0.0	27.41861	60-64
TCTCGTA	436475	0.0	27.187796	40-44
CTTGAAA	409255	0.0	27.100466	60-64

Produced by [FastQC](#) (version 0.11.2)