













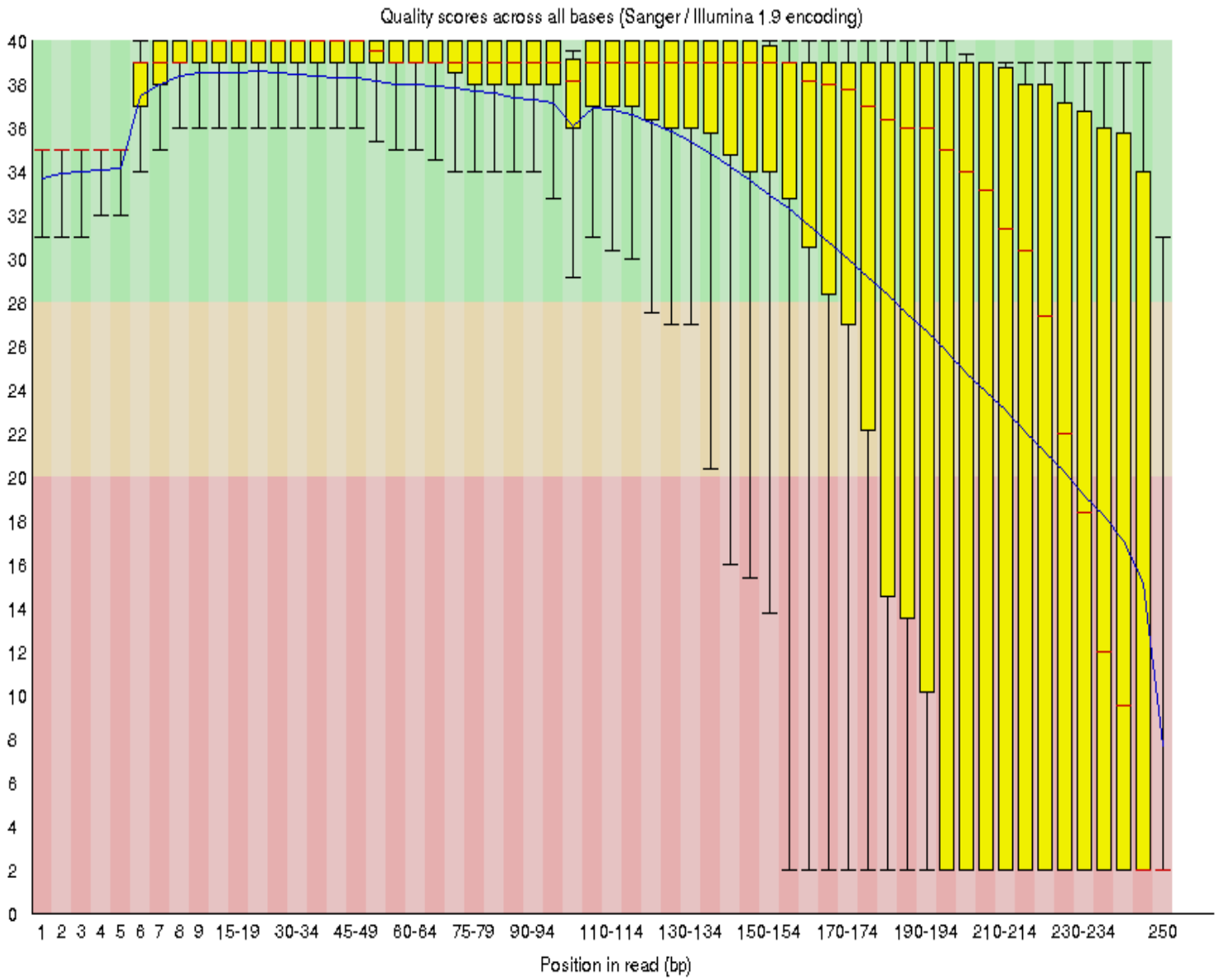
Summary

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Basic Statistics

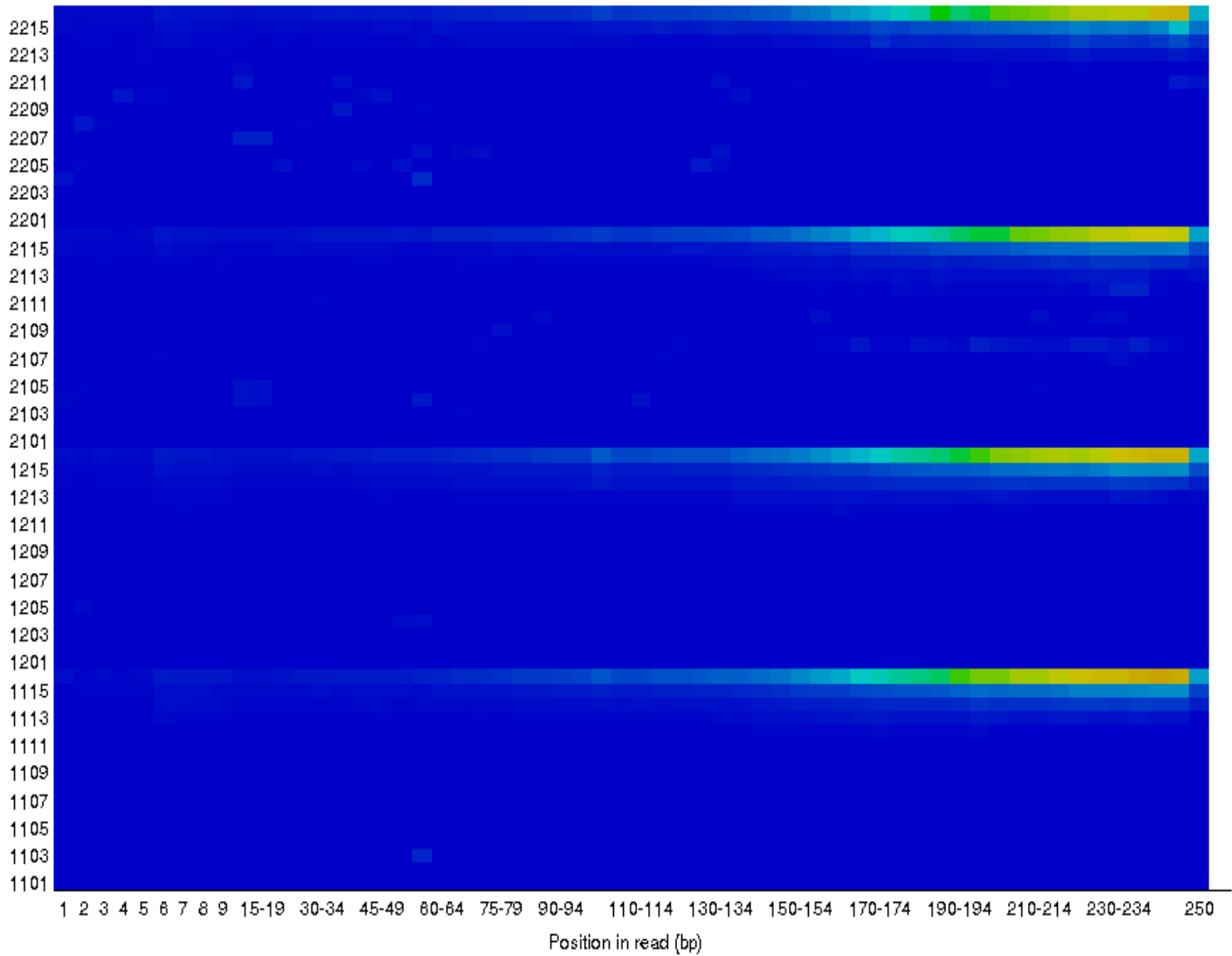
Measure	Value
Filename	BS-tag_GTAGAGG_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	67916291
Sequences flagged as poor quality	0
Sequence length	250
%GC	42

Per base sequence quality



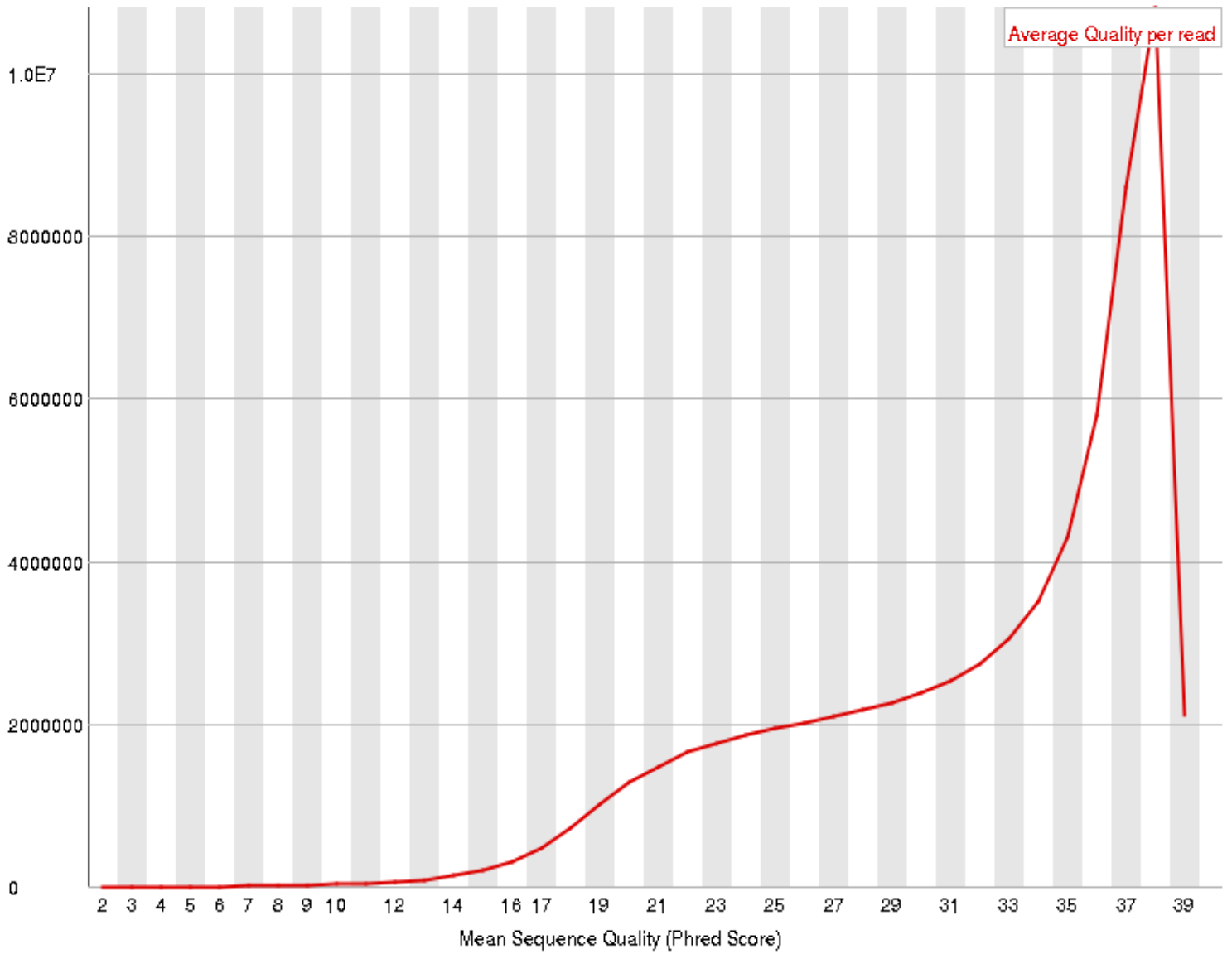
! Per tile sequence quality

Quality per tile



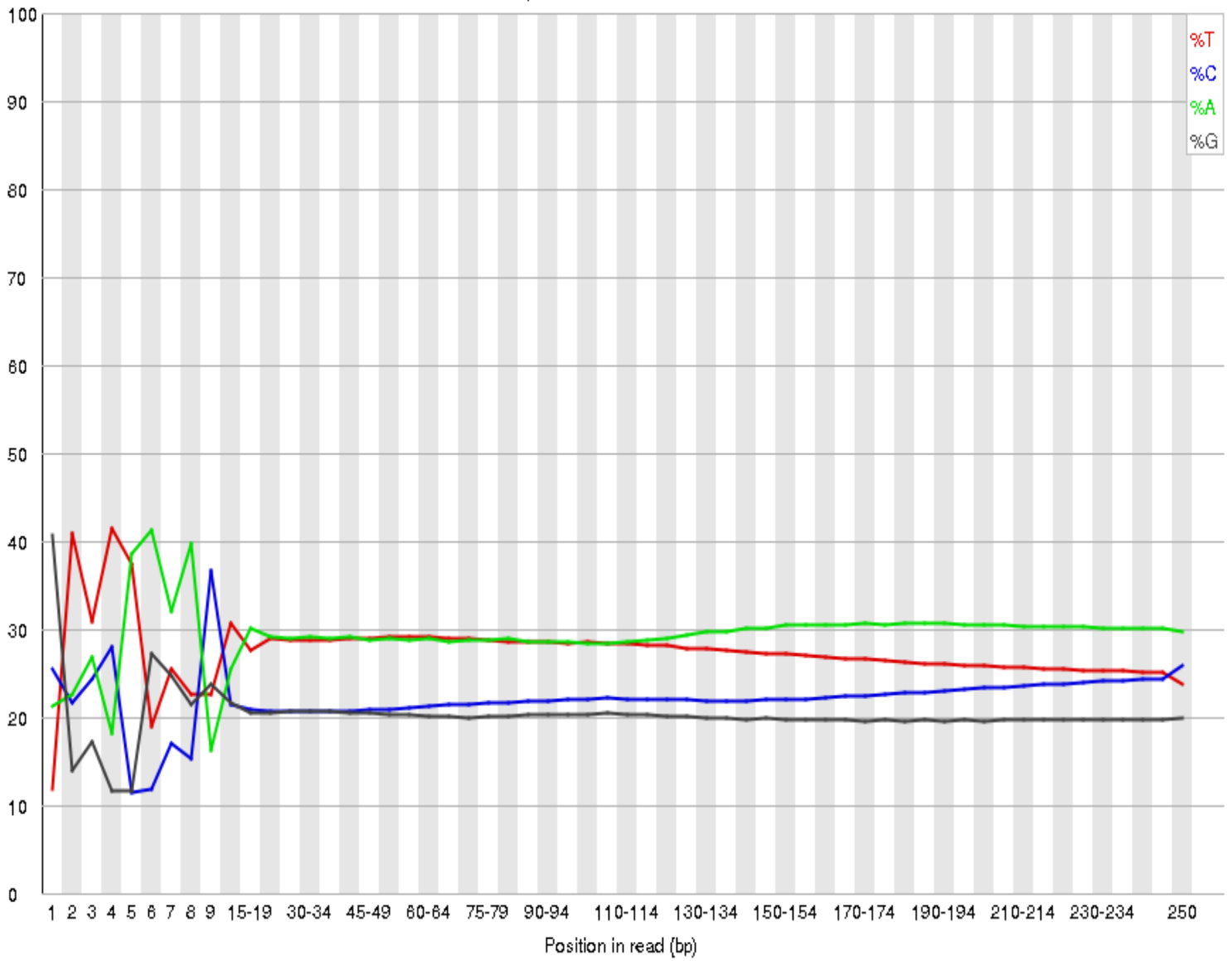
 **Per sequence quality scores**

Quality score distribution over all sequences

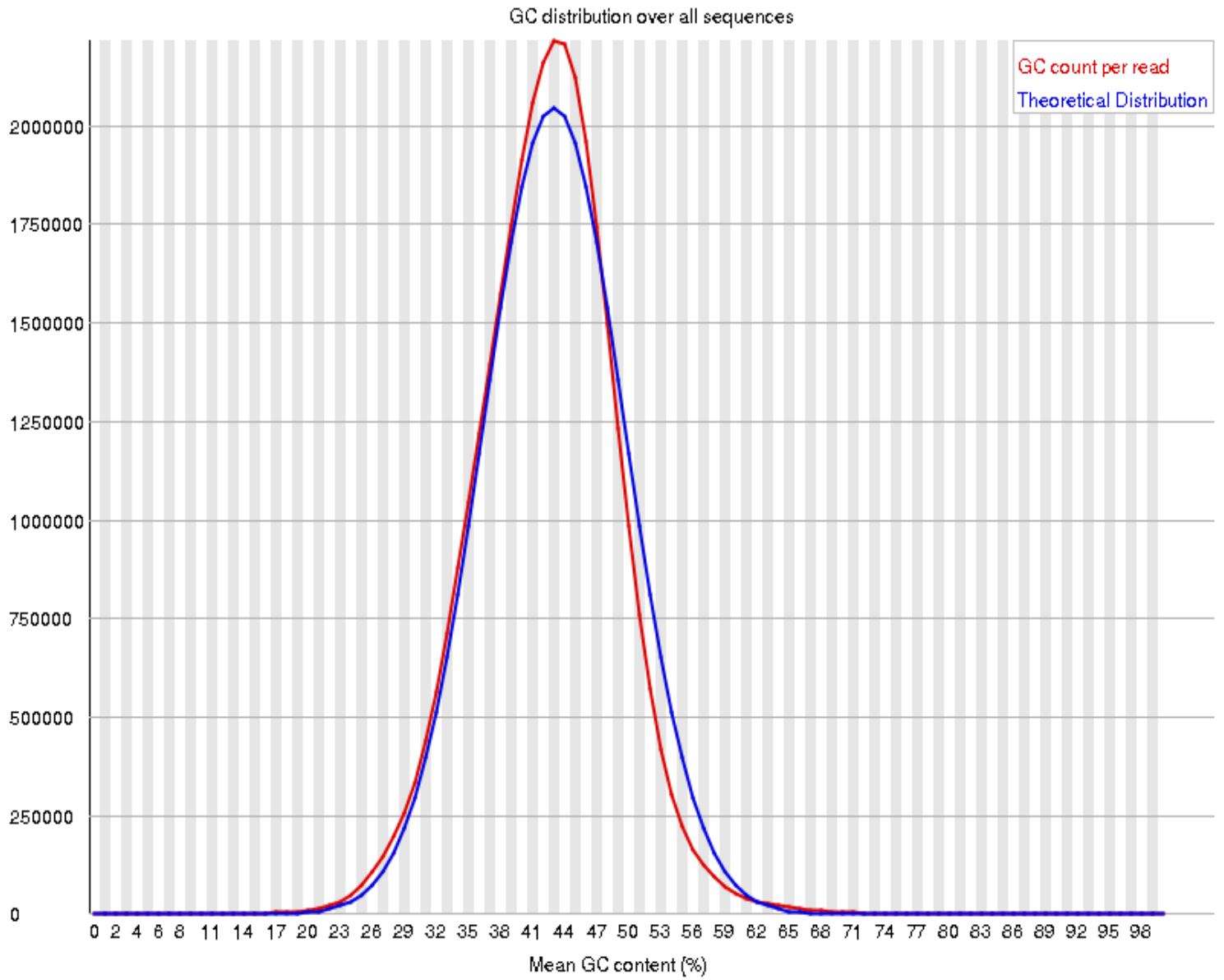


Per base sequence content

Sequence content across all bases

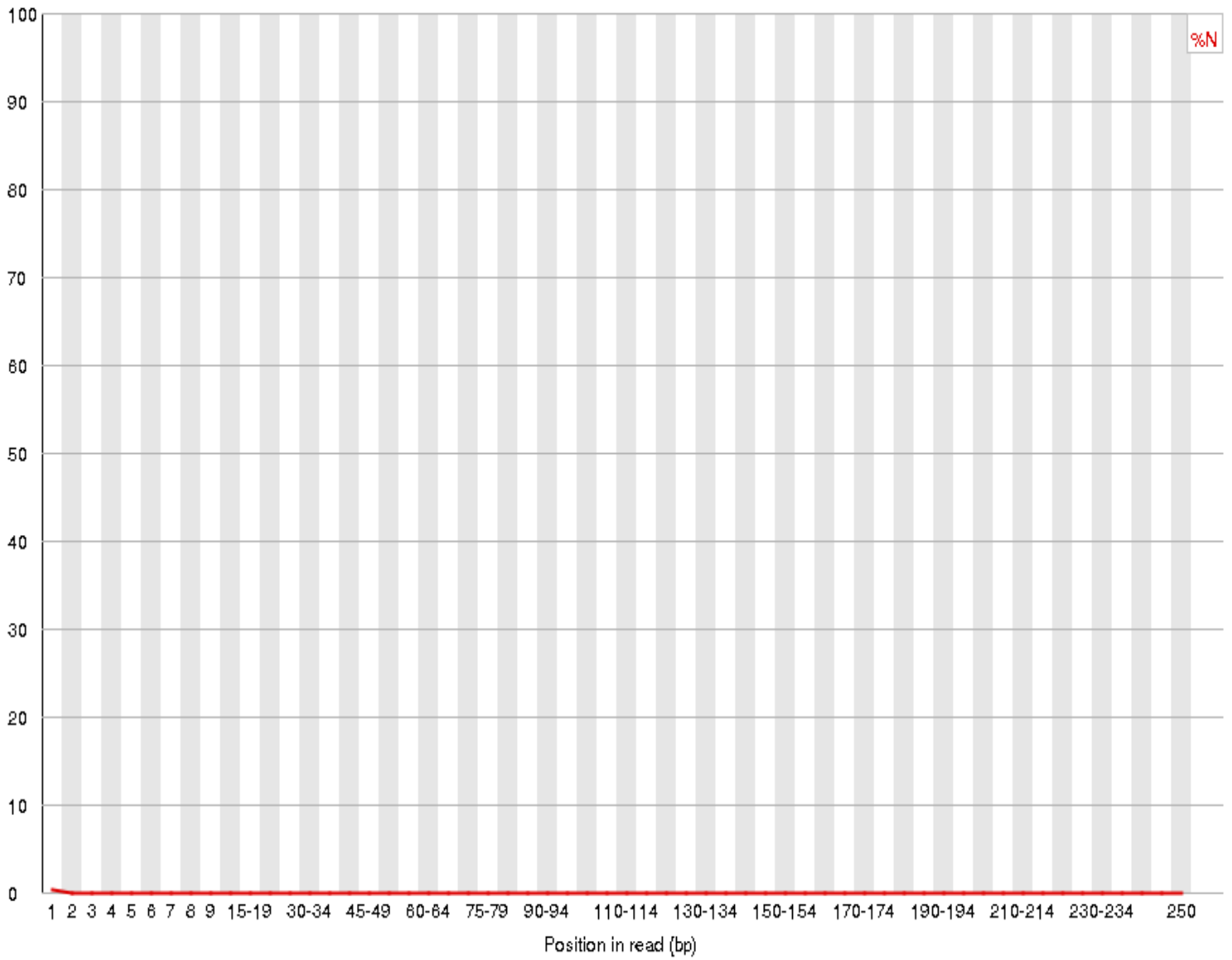


 **Per sequence GC content**



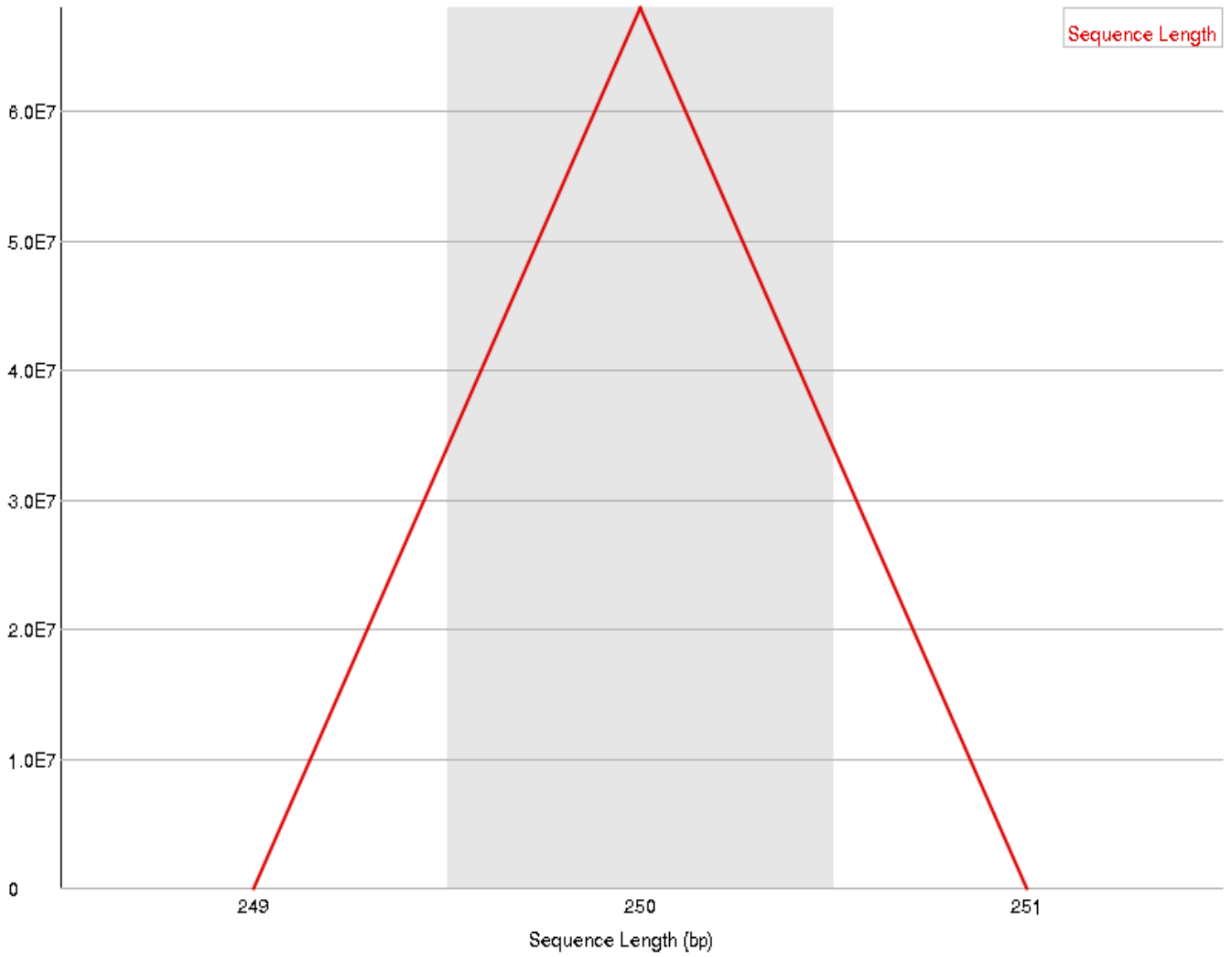
 **Per base N content**

N content across all bases



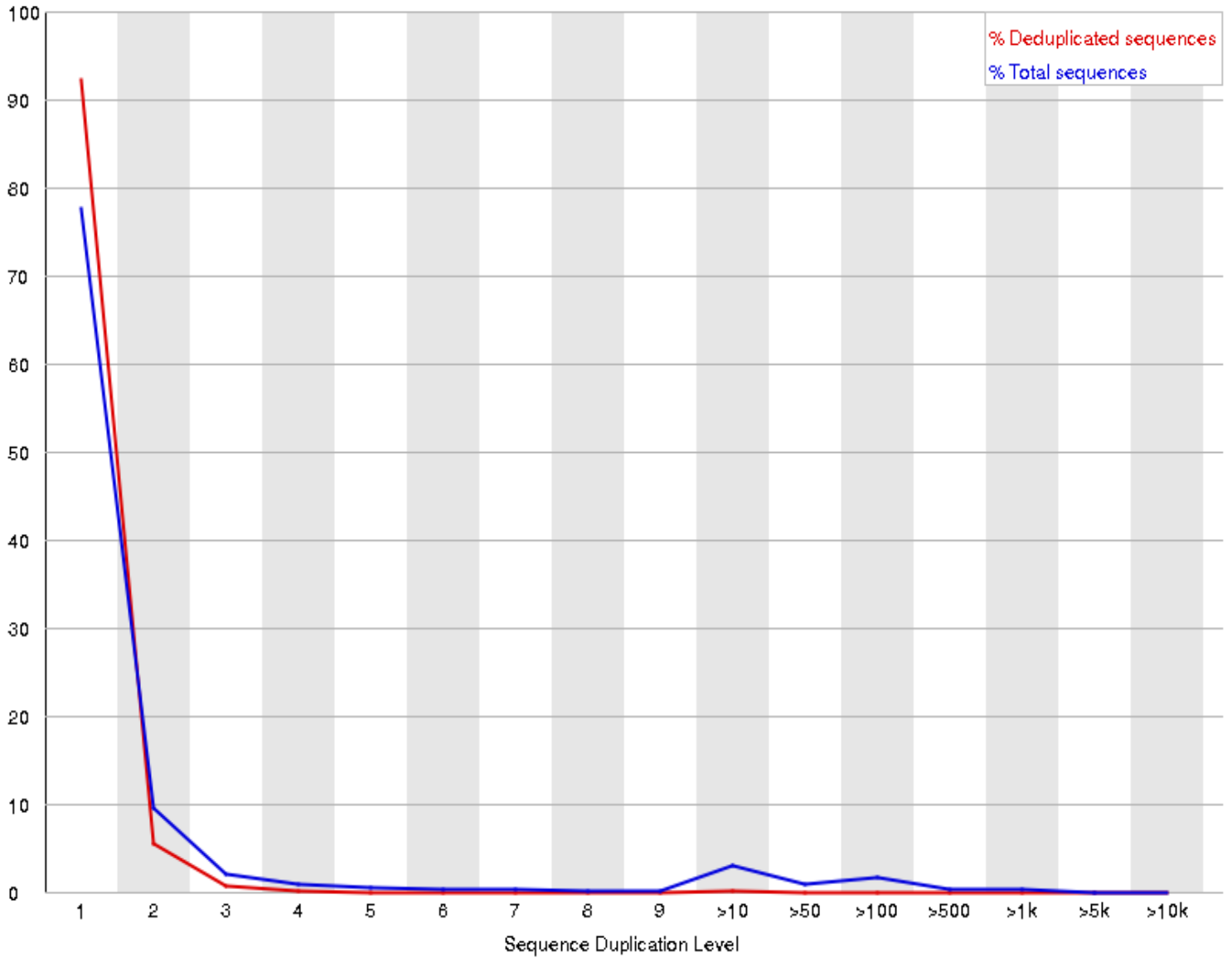
 **Sequence Length Distribution**

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 84.2%

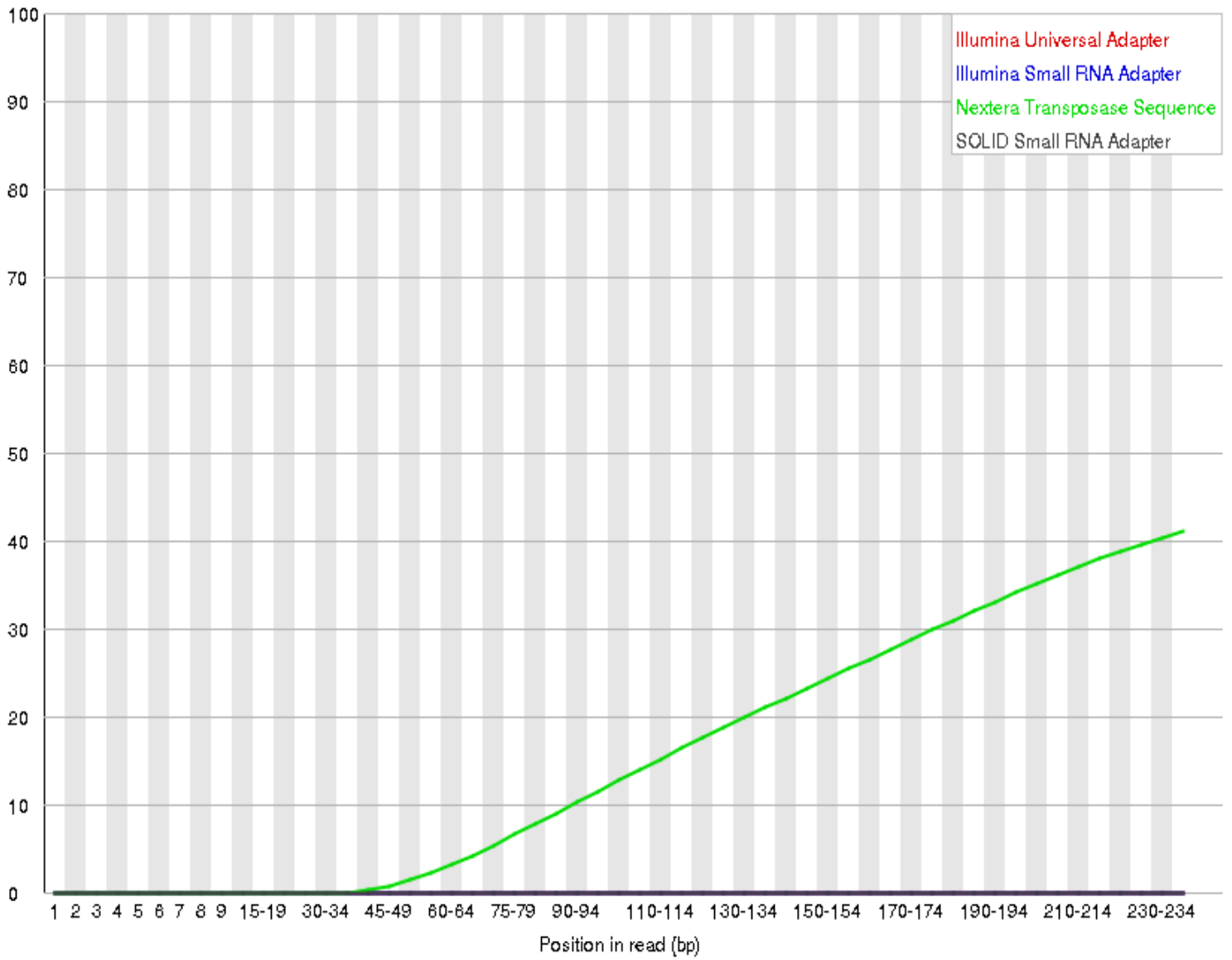


 **Overrepresented sequences**

No overrepresented sequences

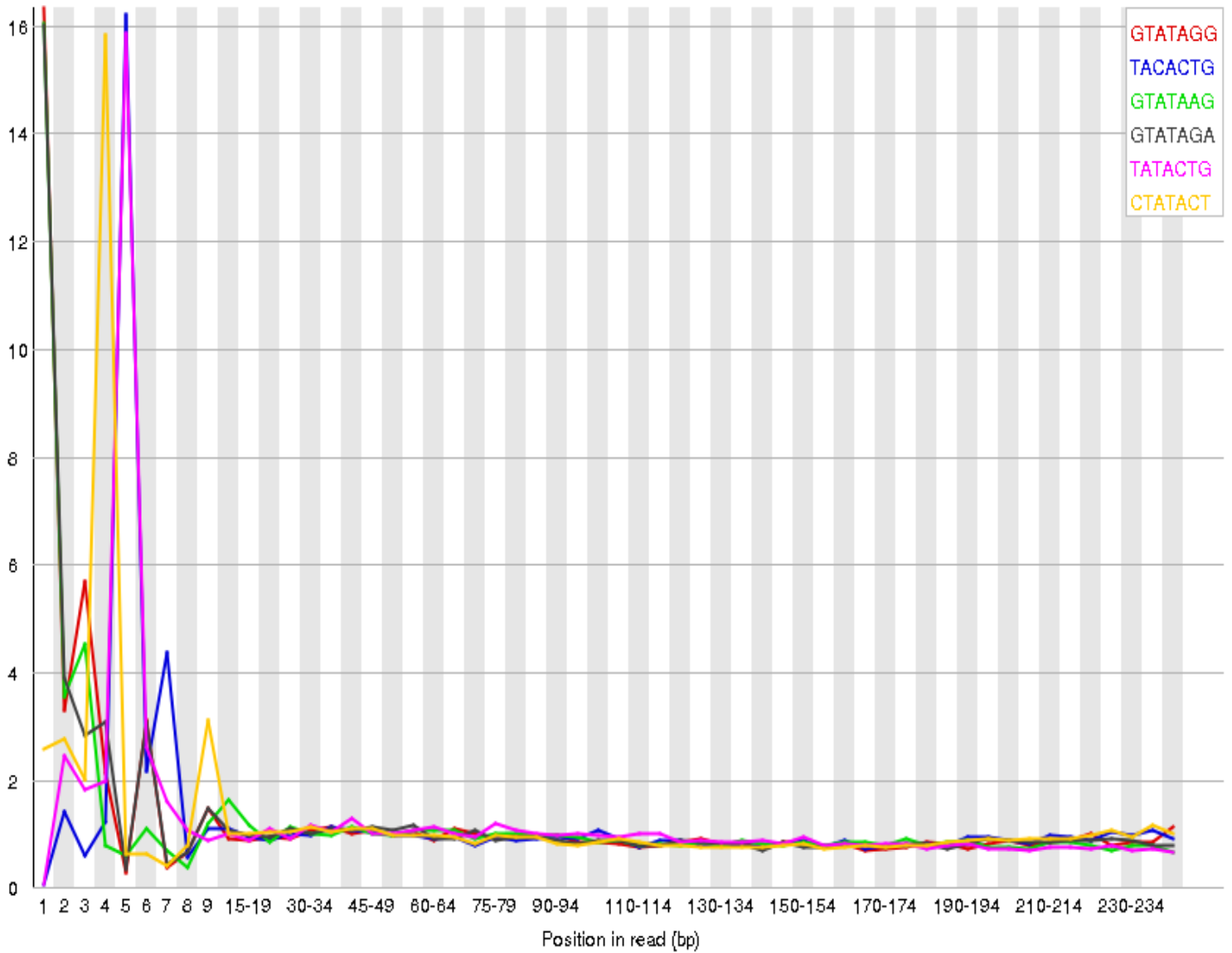
 **Adapter Content**

% Adapter



 **Kmer Content**

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTATAGG	51070	0.0	16.317749	1
TACTACTG	130275	0.0	16.22118	5
GTATAAG	62870	0.0	16.062048	1
GTATAGA	88245	0.0	16.0124	1
TATACTG	178030	0.0	15.876882	5
CTATACT	86820	0.0	15.82884	4
TATACAG	150360	0.0	15.733103	5
GTATATA	155320	0.0	15.480637	1
GTCCTAG	56550	0.0	15.213239	1
TTATACT	124185	0.0	14.679693	4
TATACCG	33620	0.0	14.43545	5

TAGACAG	147810	0.0	14.107083	5
GTGTAGG	80700	0.0	14.077431	1
TCTATAC	92825	0.0	13.898428	3
GTCTAGG	56535	0.0	13.786592	1
GTATAAA	140755	0.0	13.713045	1
CTAGGAC	58520	0.0	13.690082	3
GTGTATA	128300	0.0	13.487306	1
GTCCTAA	55630	0.0	13.4821615	1
GTCTTAG	78725	0.0	13.449875	1

Produced by [FastQC](#) (version 0.11.3)