












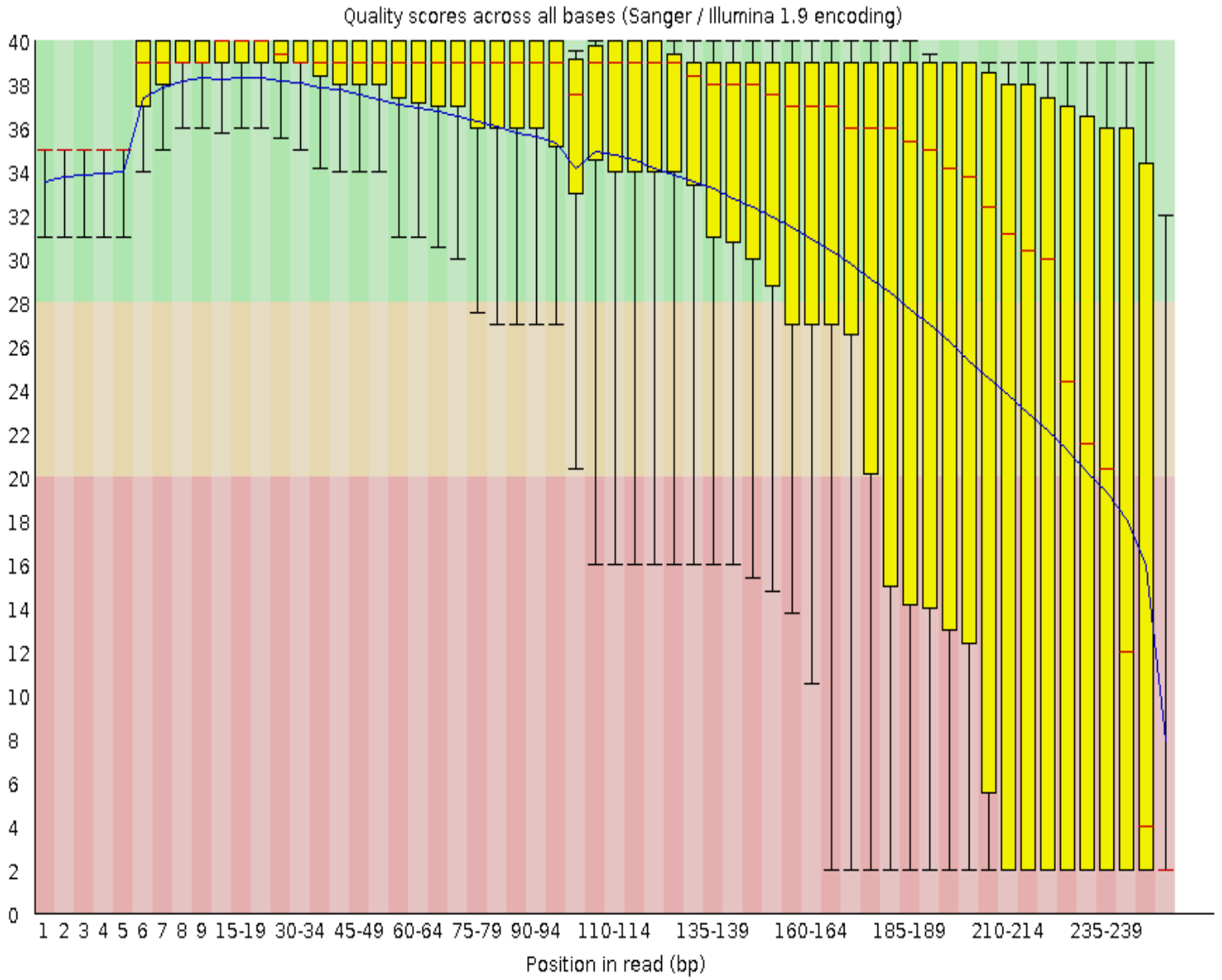
Summary

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Basic Statistics

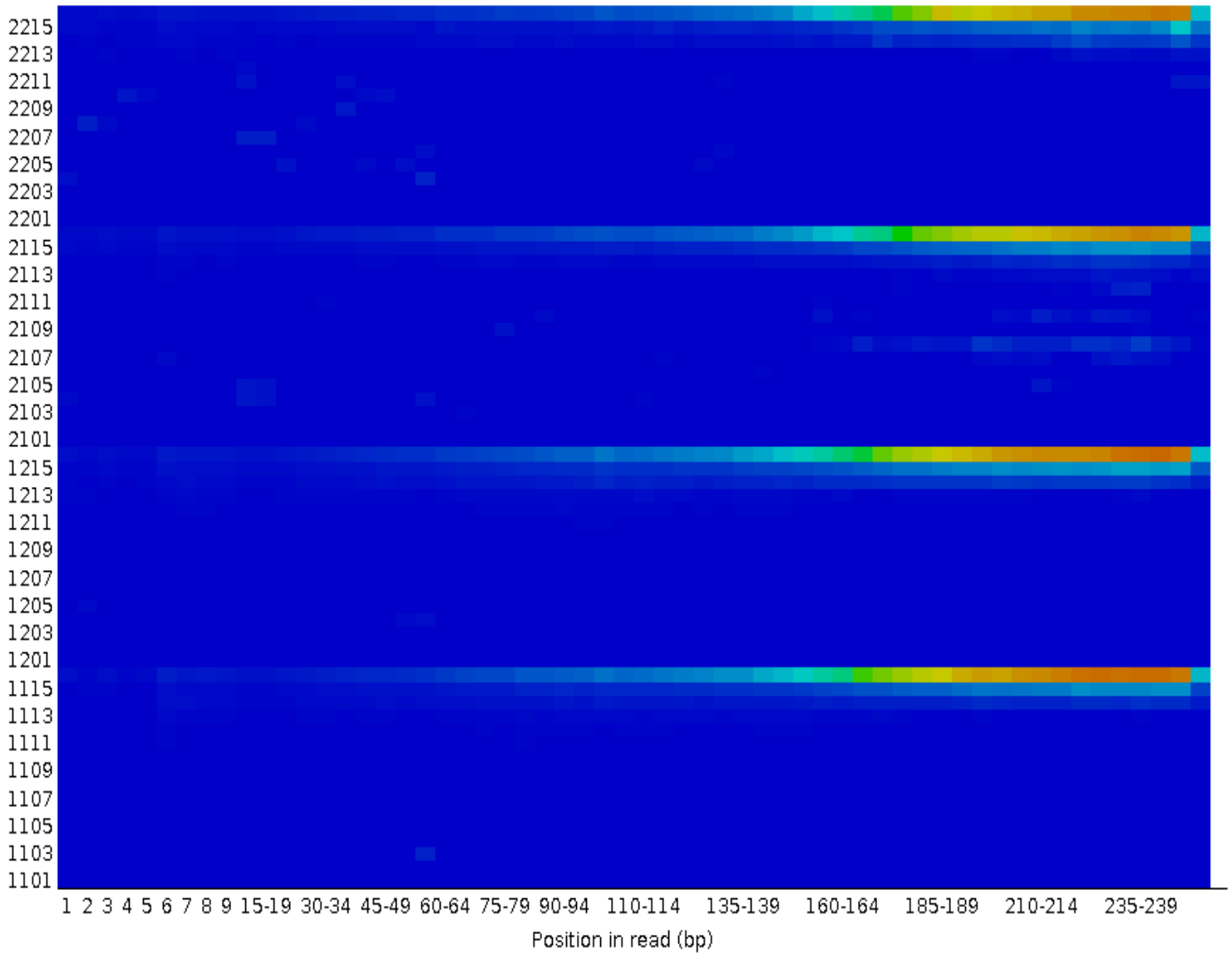
Measure	Value
Filename	BS-tag_seqprep_dupRemoved_ec_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	17663182
Sequences flagged as poor quality	0
Sequence length	250
%GC	42

Per base sequence quality



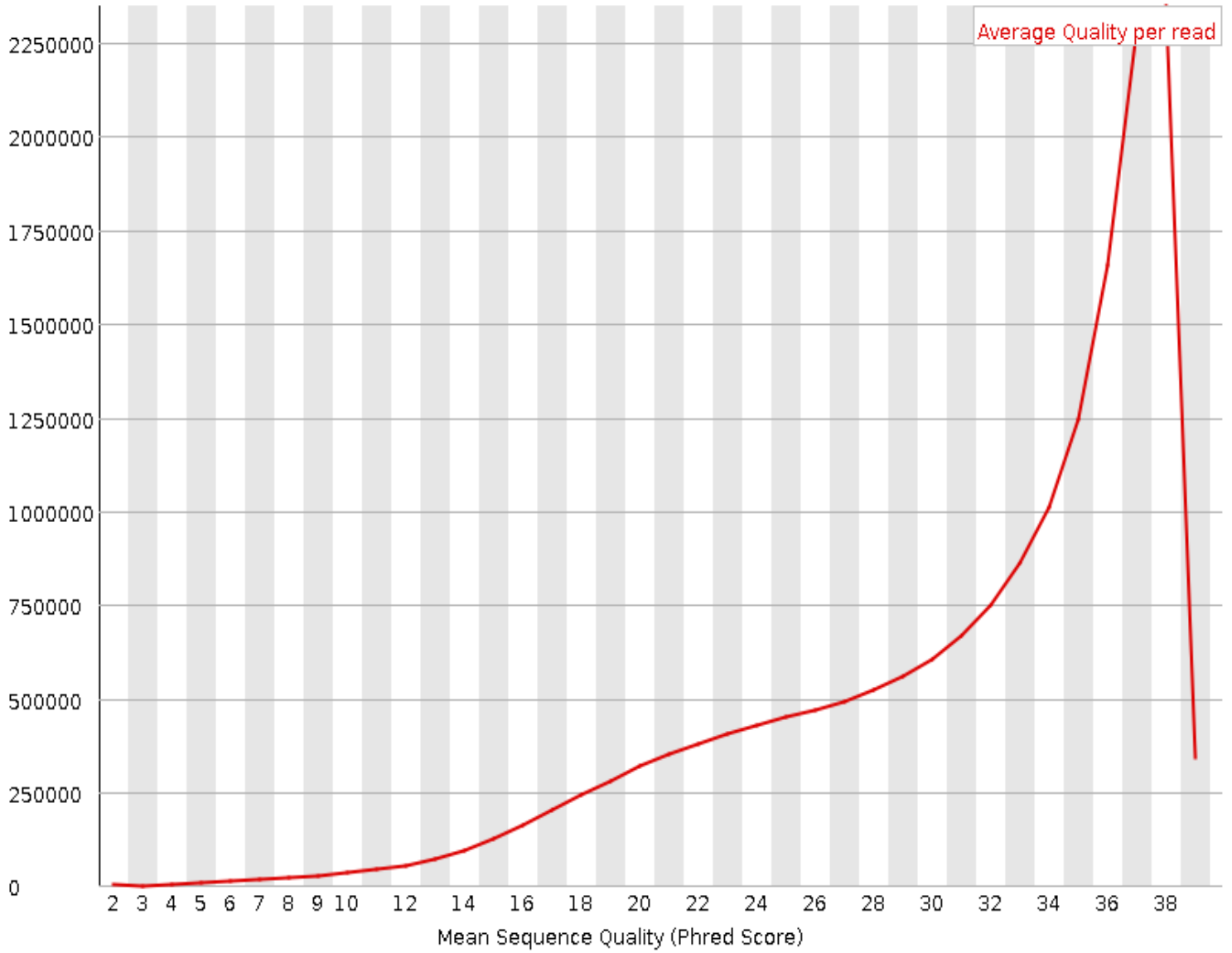
! Per tile sequence quality

Quality per tile



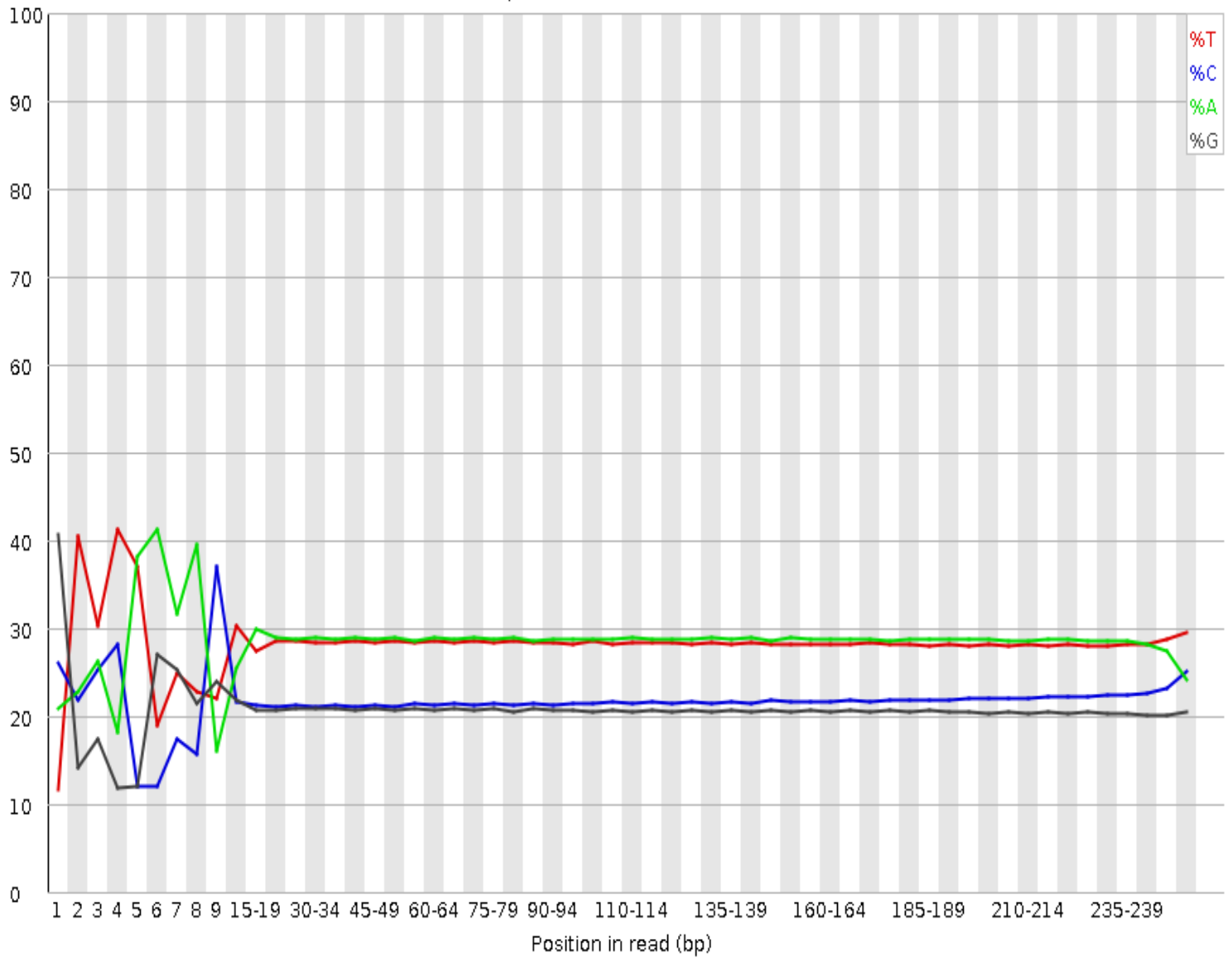
 **Per sequence quality scores**

Quality score distribution over all sequences



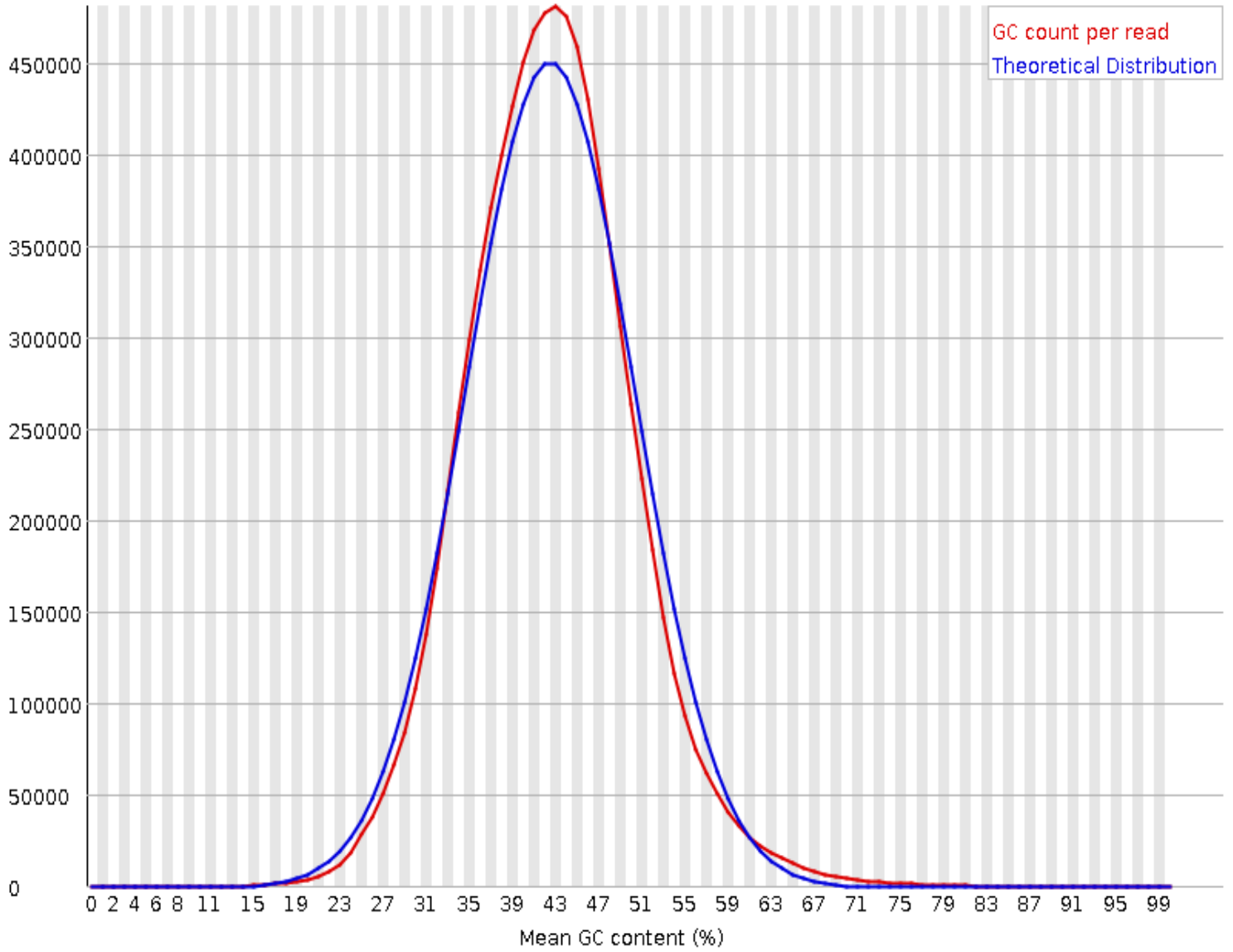
 **Per base sequence content**

Sequence content across all bases



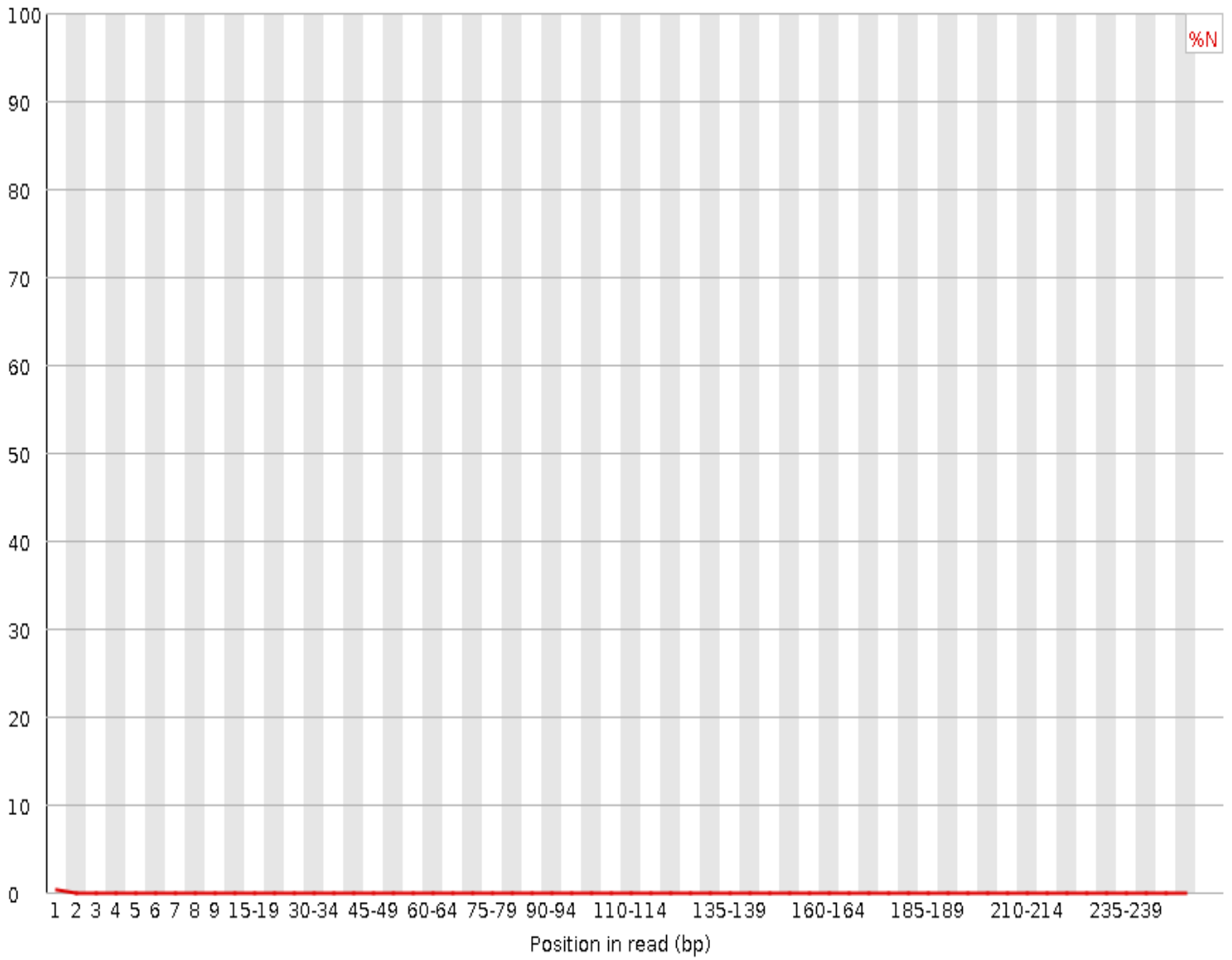
 **Per sequence GC content**

GC distribution over all sequences



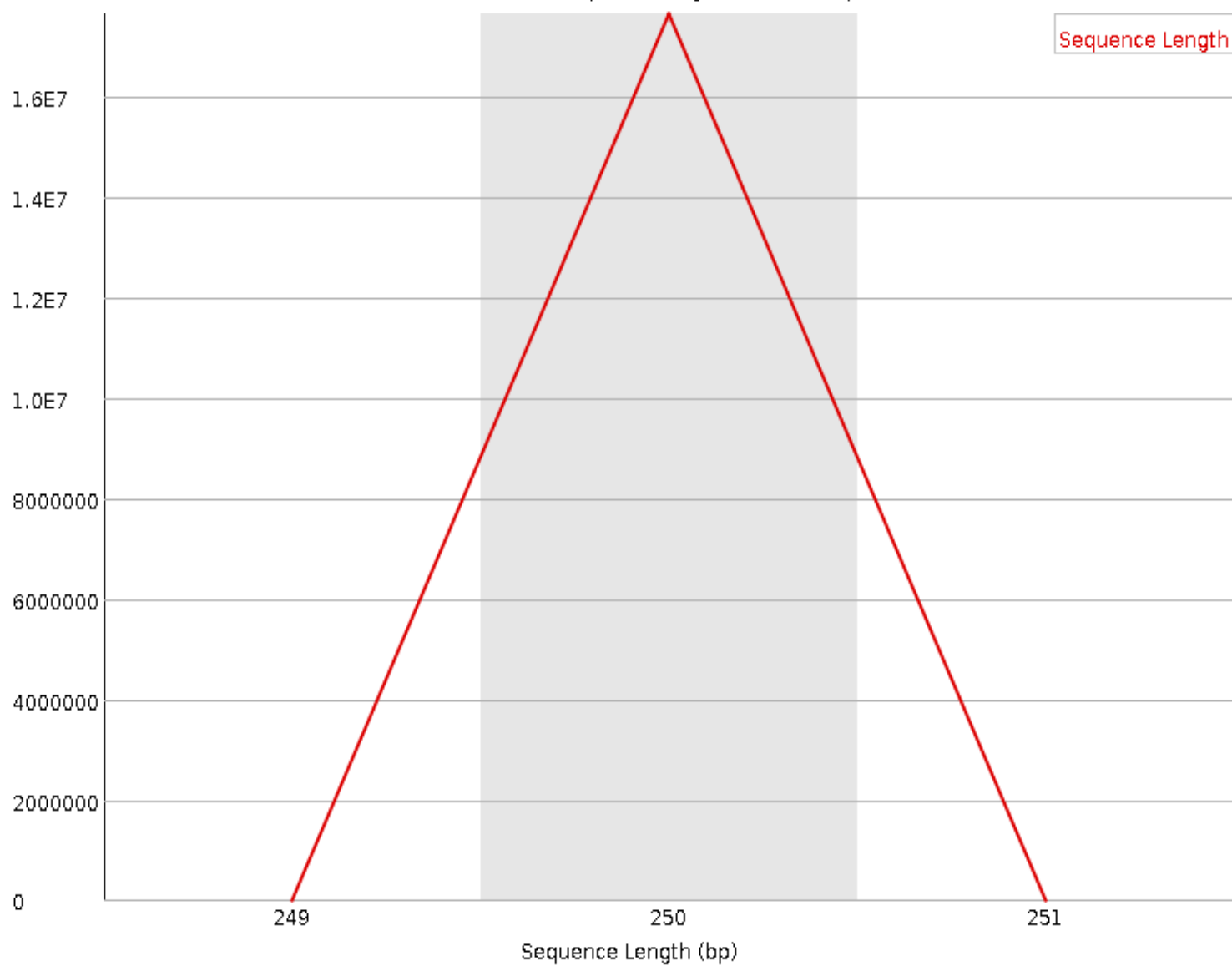
 **Per base N content**

N content across all bases



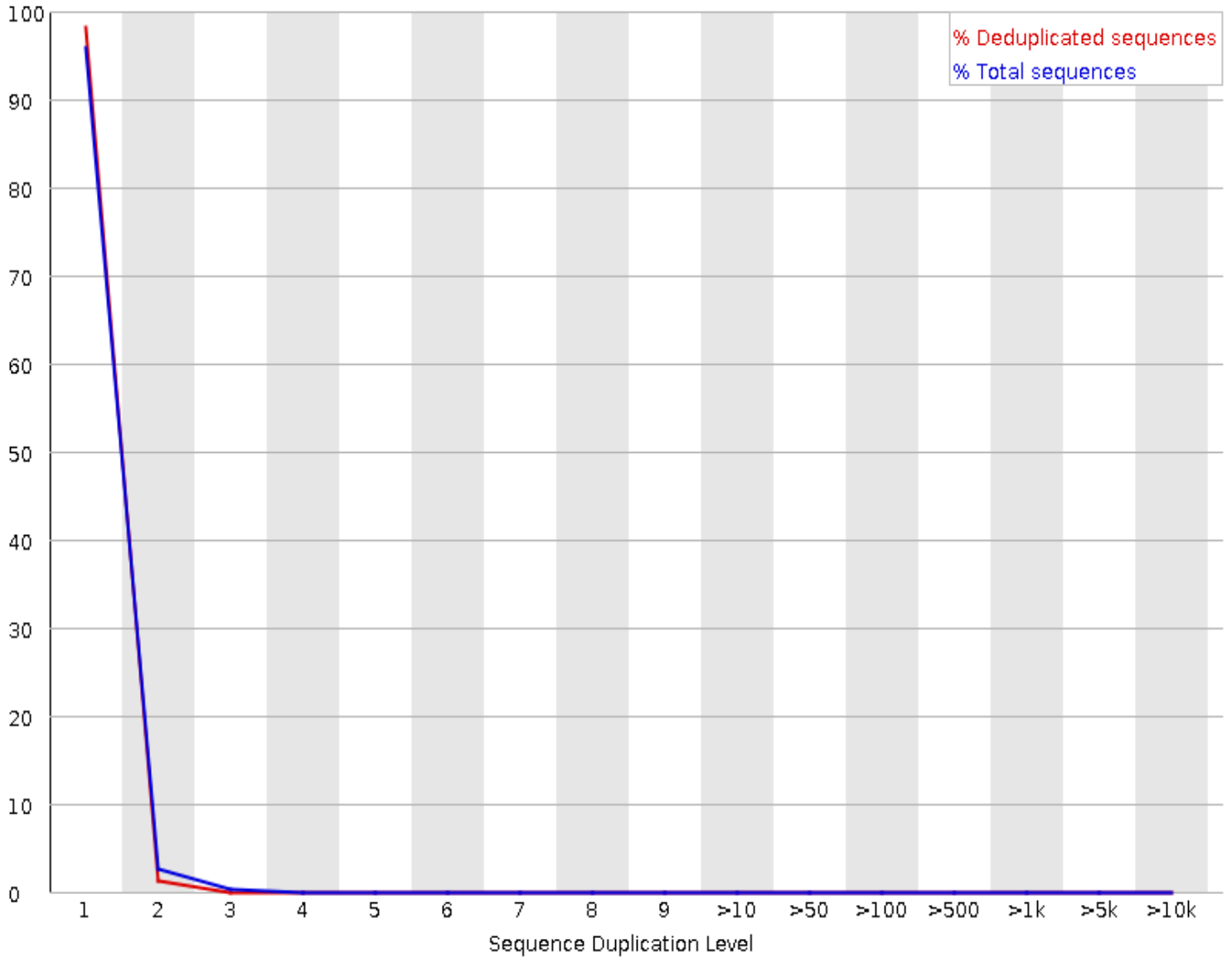
Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 97.75%

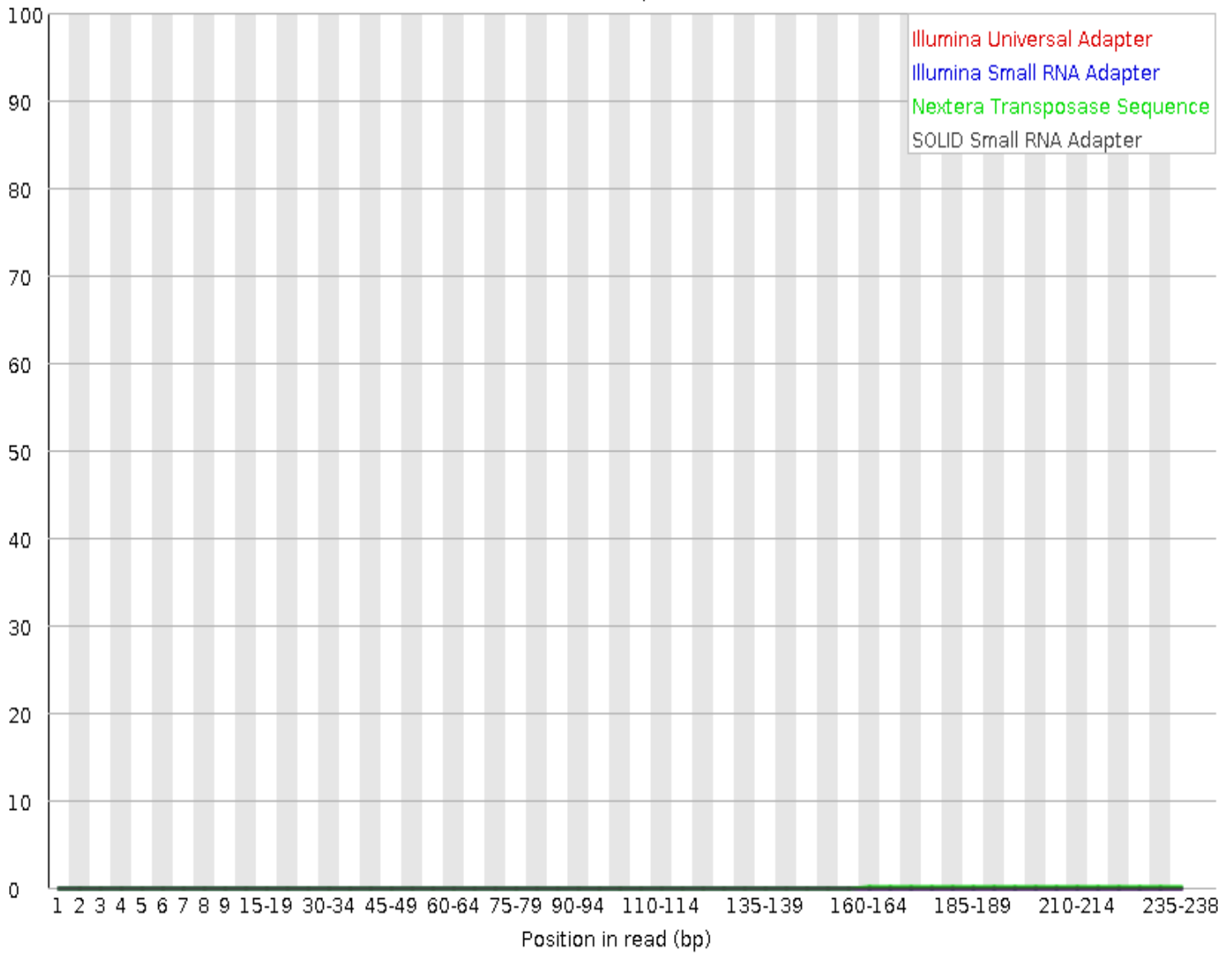


 **Overrepresented sequences**

No overrepresented sequences

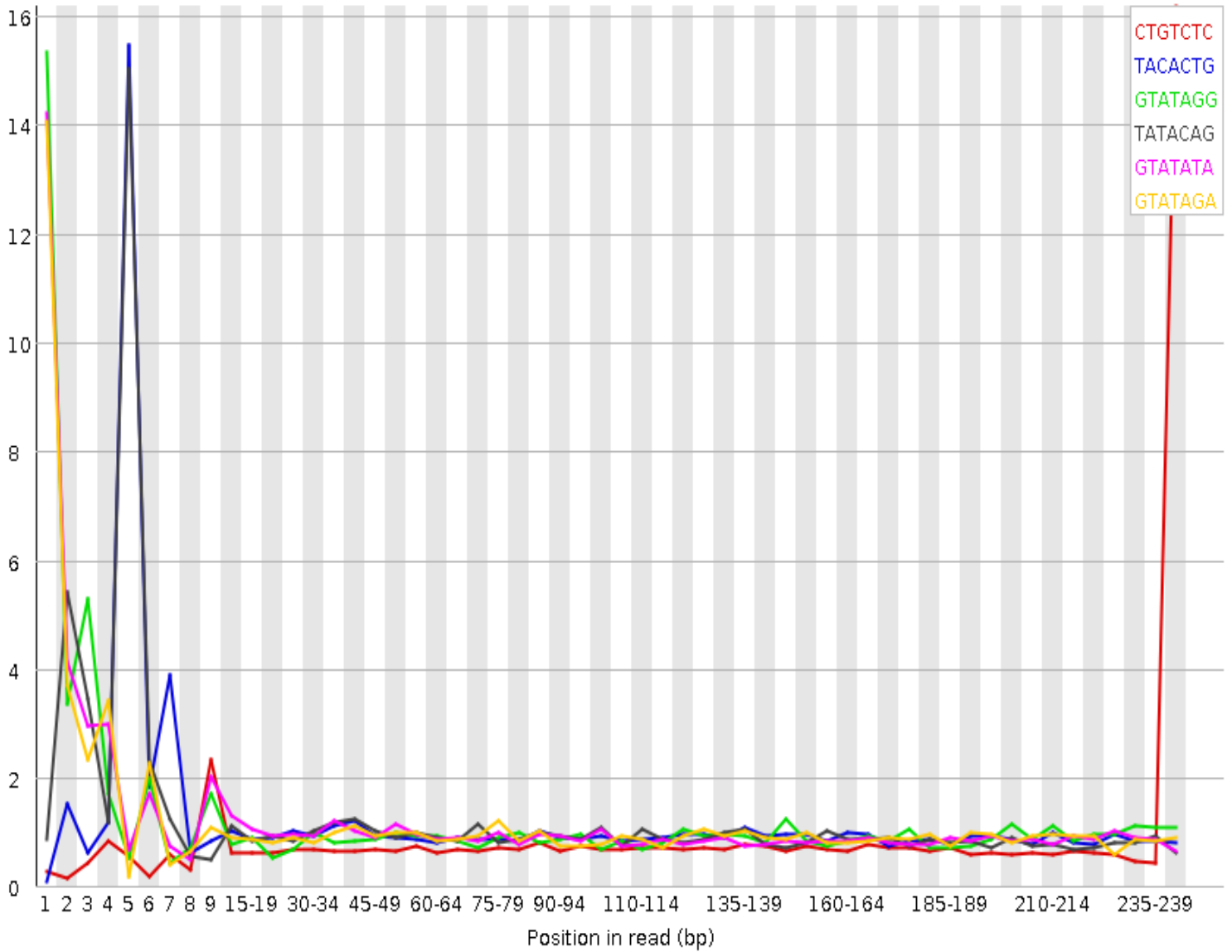
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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CTGTCTC	108930	0.0	16.170988	240-244
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TACTACTG	32285	0.0	15.480981	5
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GTATAGG	13320	0.0	15.361157	1
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TATACAG	38580	0.0	15.040425	5
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GTATATA	38175	0.0	14.217931	1
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GTATAGA	23335	0.0	14.0714445	1
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GTATAAG	17610	0.0	13.706247	1
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CTATACT	23755	0.0	13.7016115	4
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CCTGTCT	64700	0.0	13.618528	240-244
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TACACAG	39115	0.0	13.556931	5
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TACACCG	10530	0.0	13.54481	5
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TATACTG	49565	0.0	13.477857	5
TATACCG	8570	0.0	13.086467	5
GTCCTAG	18070	0.0	12.950512	1
TTATACT	32250	0.0	12.927418	4
CCTATAC	16045	0.0	12.763947	3
TCTATAC	24480	0.0	12.648461	3
GTCTCTT	74415	0.0	12.601344	240-244
CTAGGAC	18415	0.0	12.378992	3
ACTGTGC	20600	0.0	12.367858	8

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