













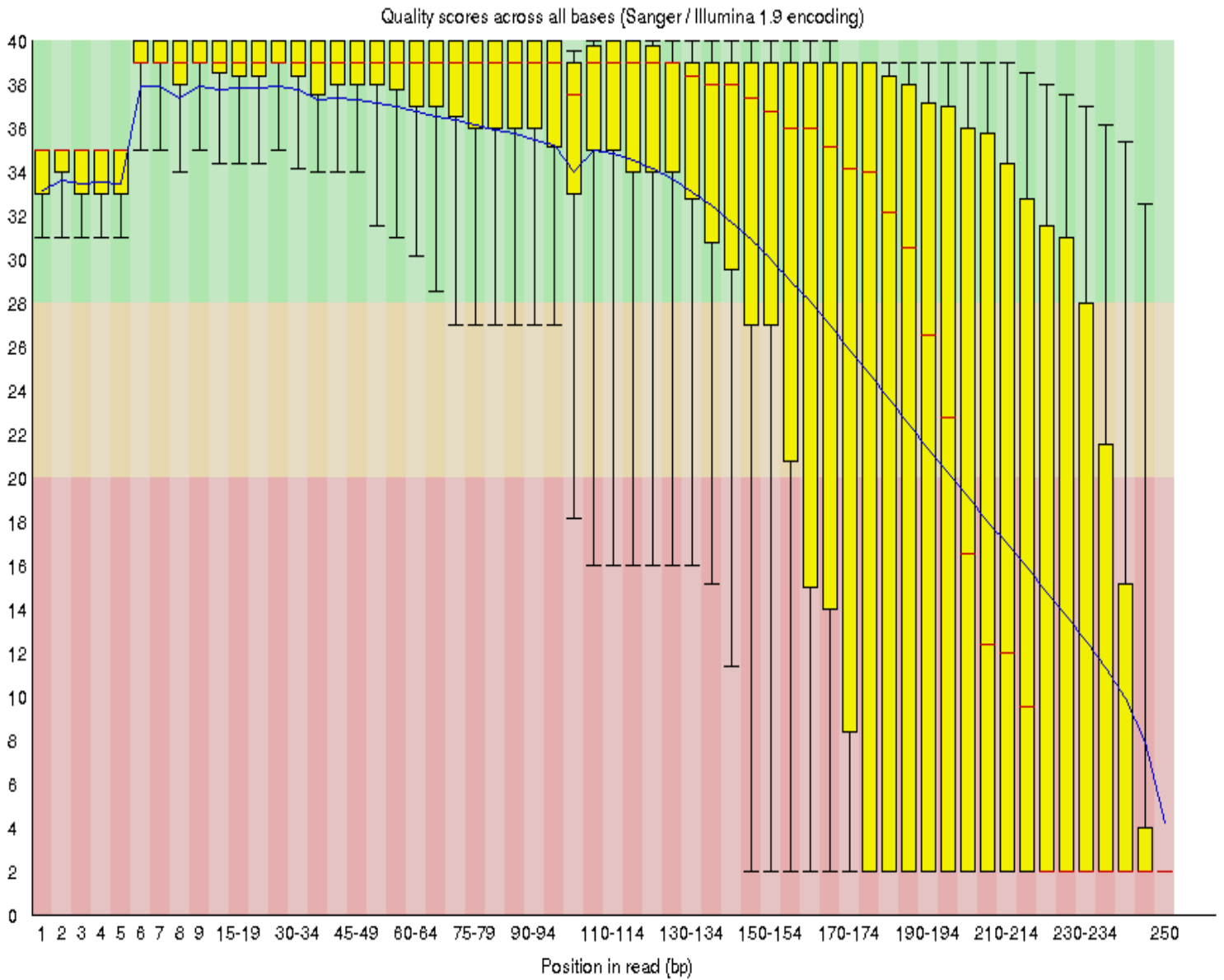
Summary

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Basic Statistics

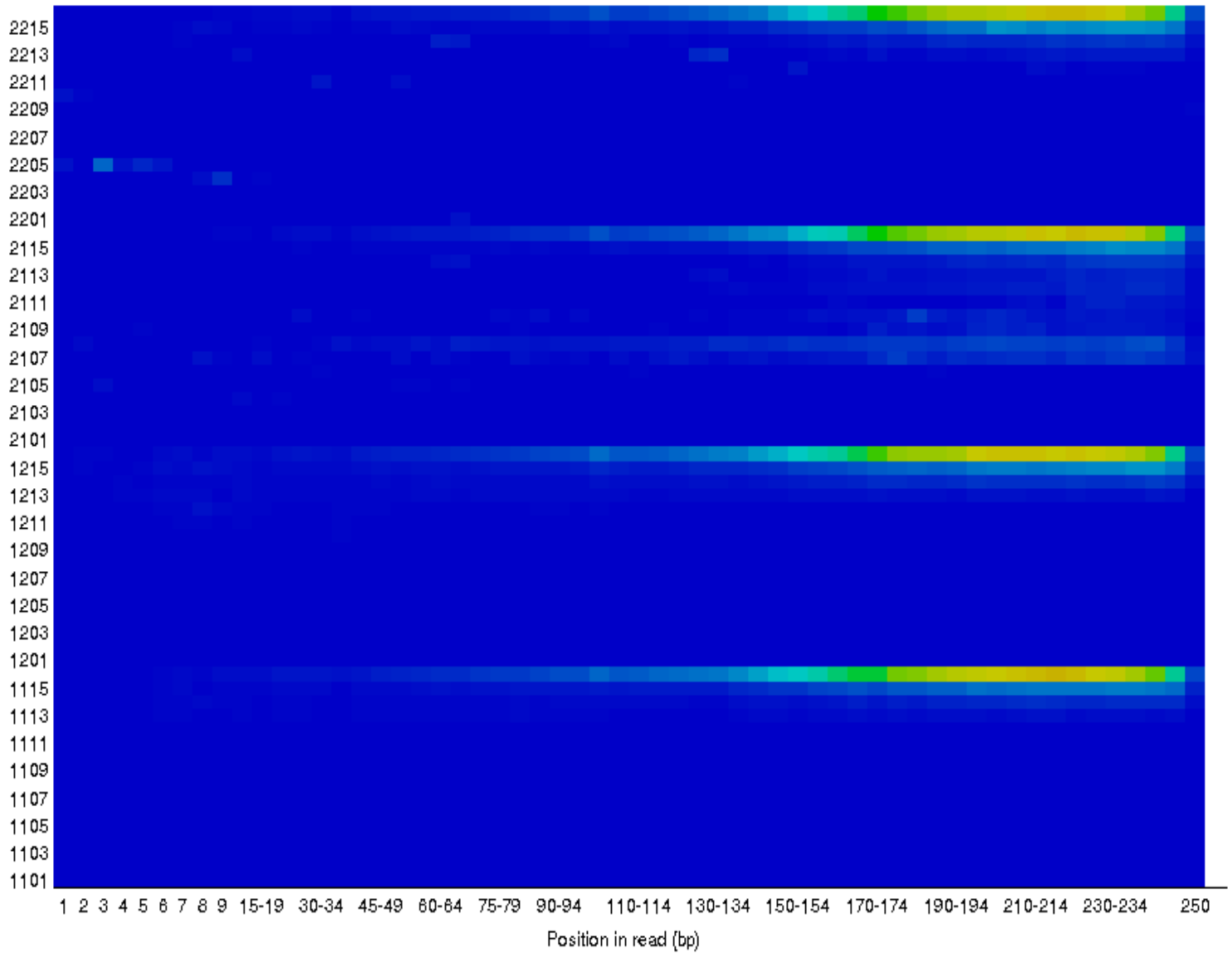
Measure	Value
Filename	BS-tag_GTAGAGG_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	67916291
Sequences flagged as poor quality	0
Sequence length	250
%GC	43

Per base sequence quality



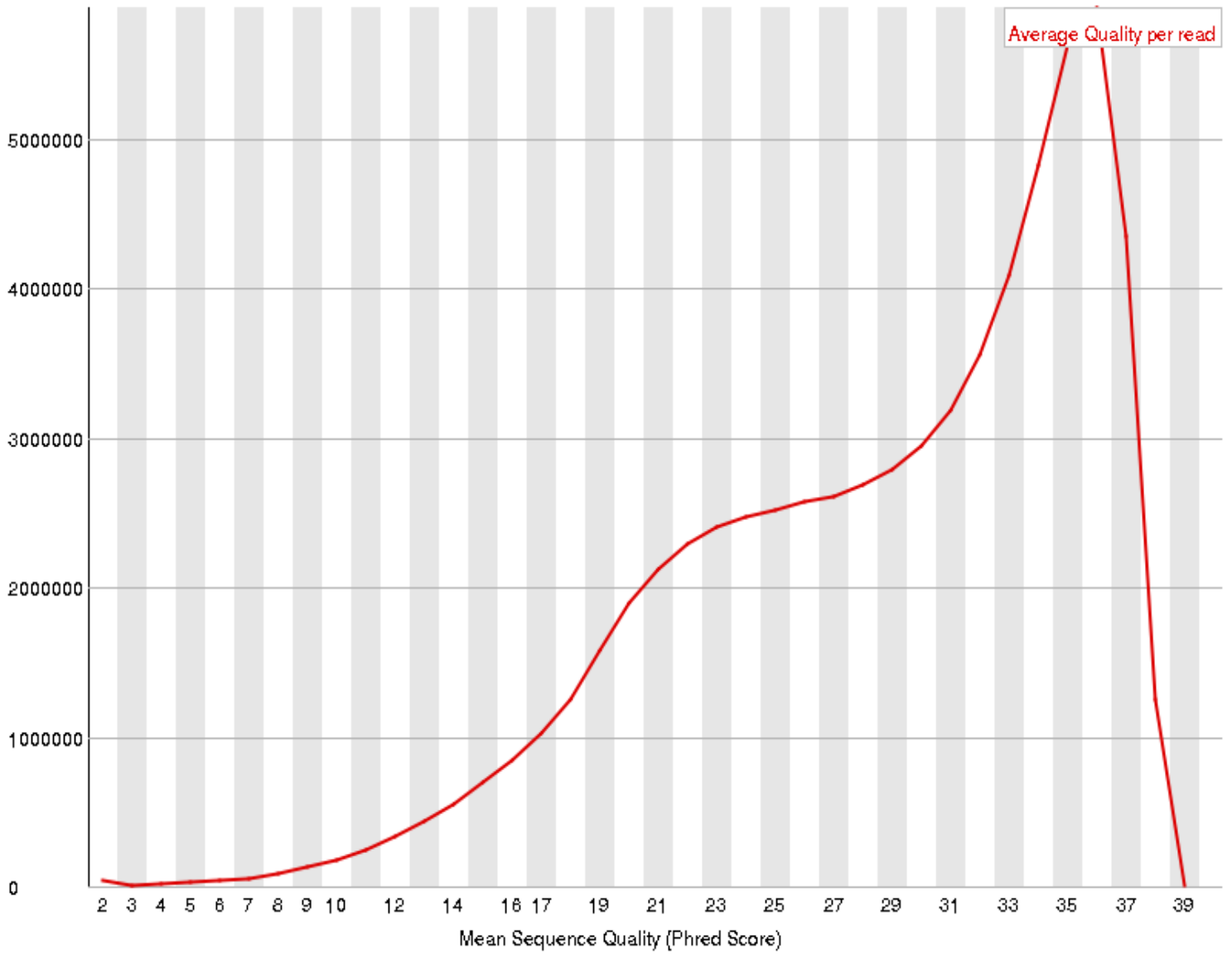
! Per tile sequence quality

Quality per tile



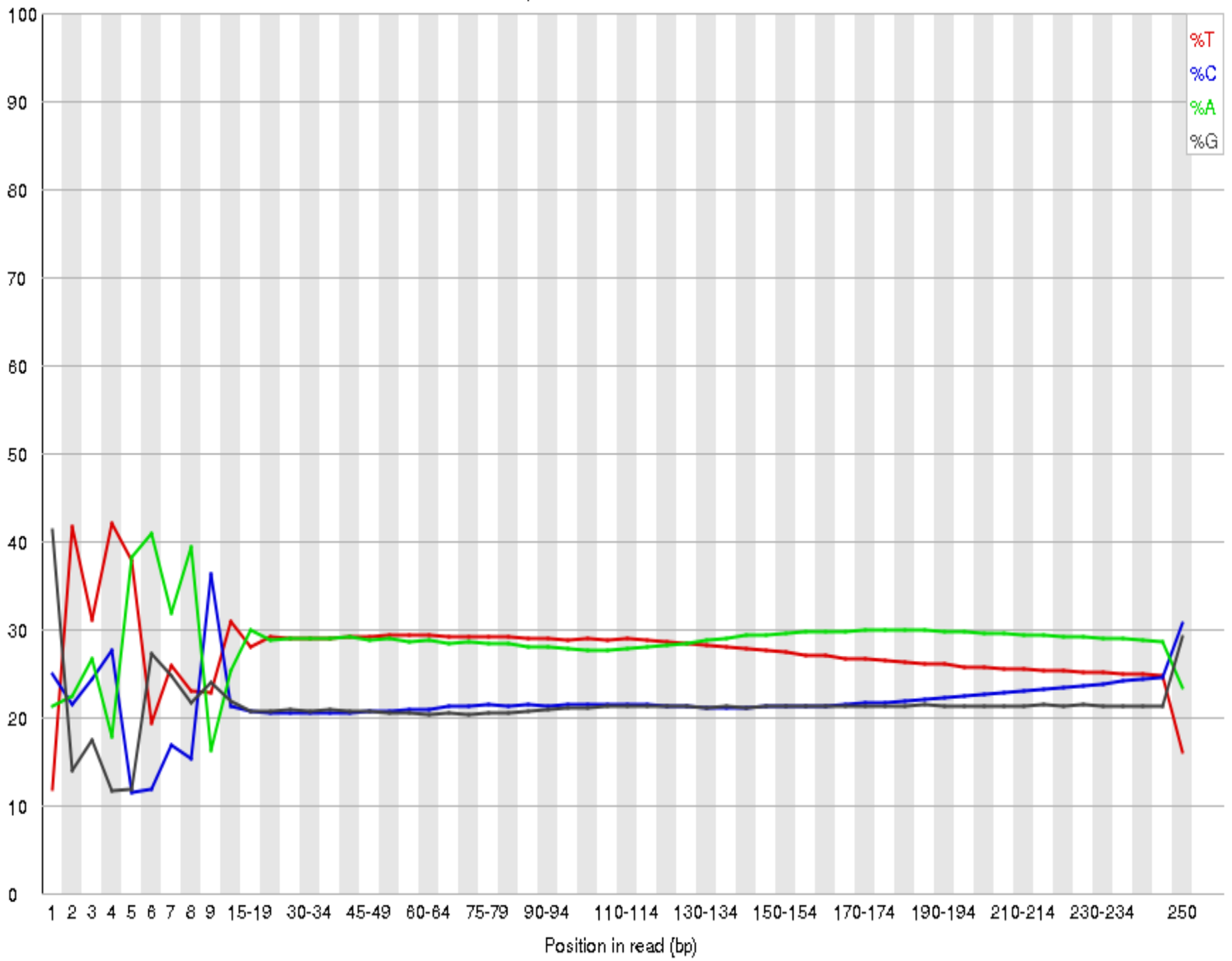
 **Per sequence quality scores**

Quality score distribution over all sequences

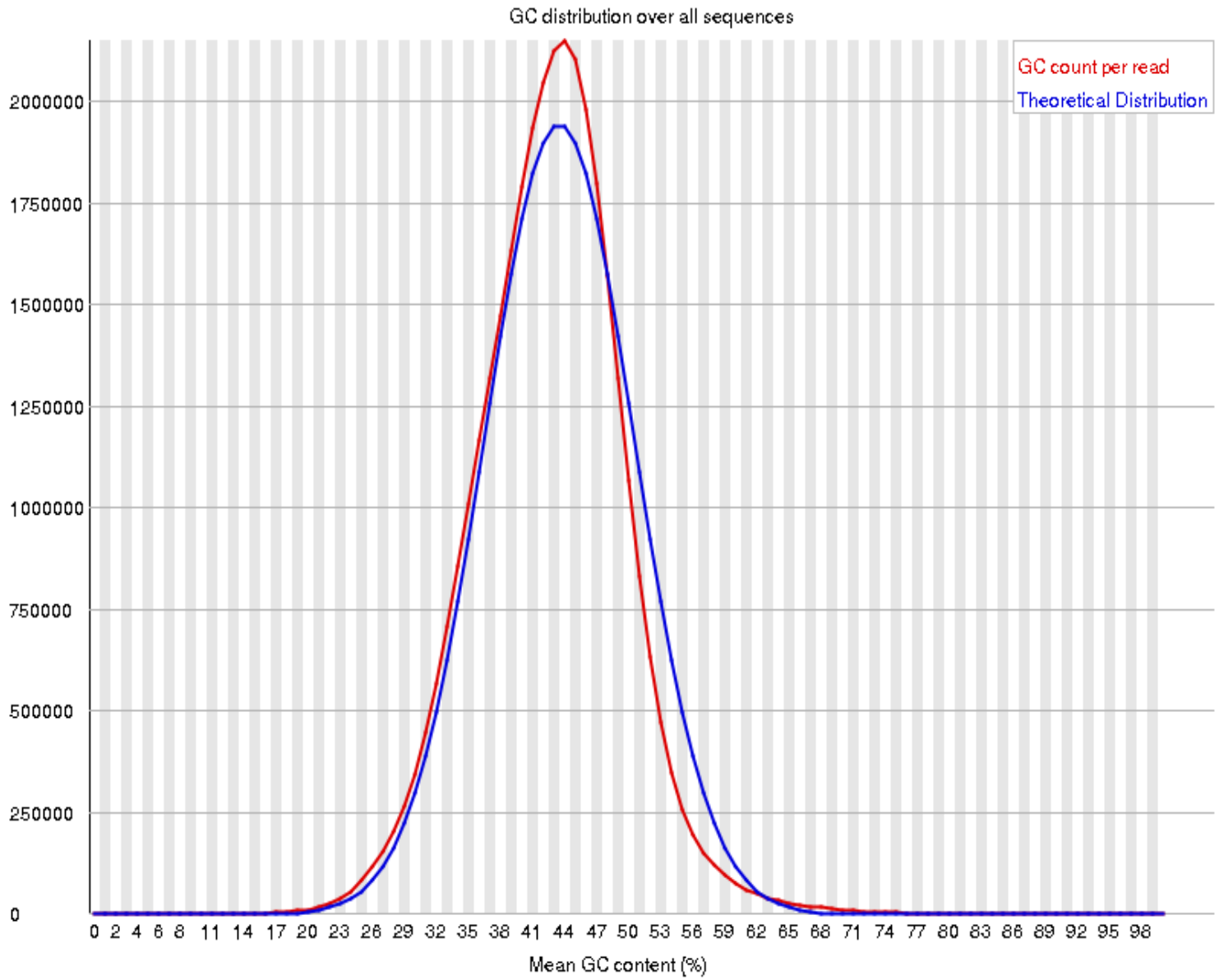


✖ Per base sequence content

Sequence content across all bases

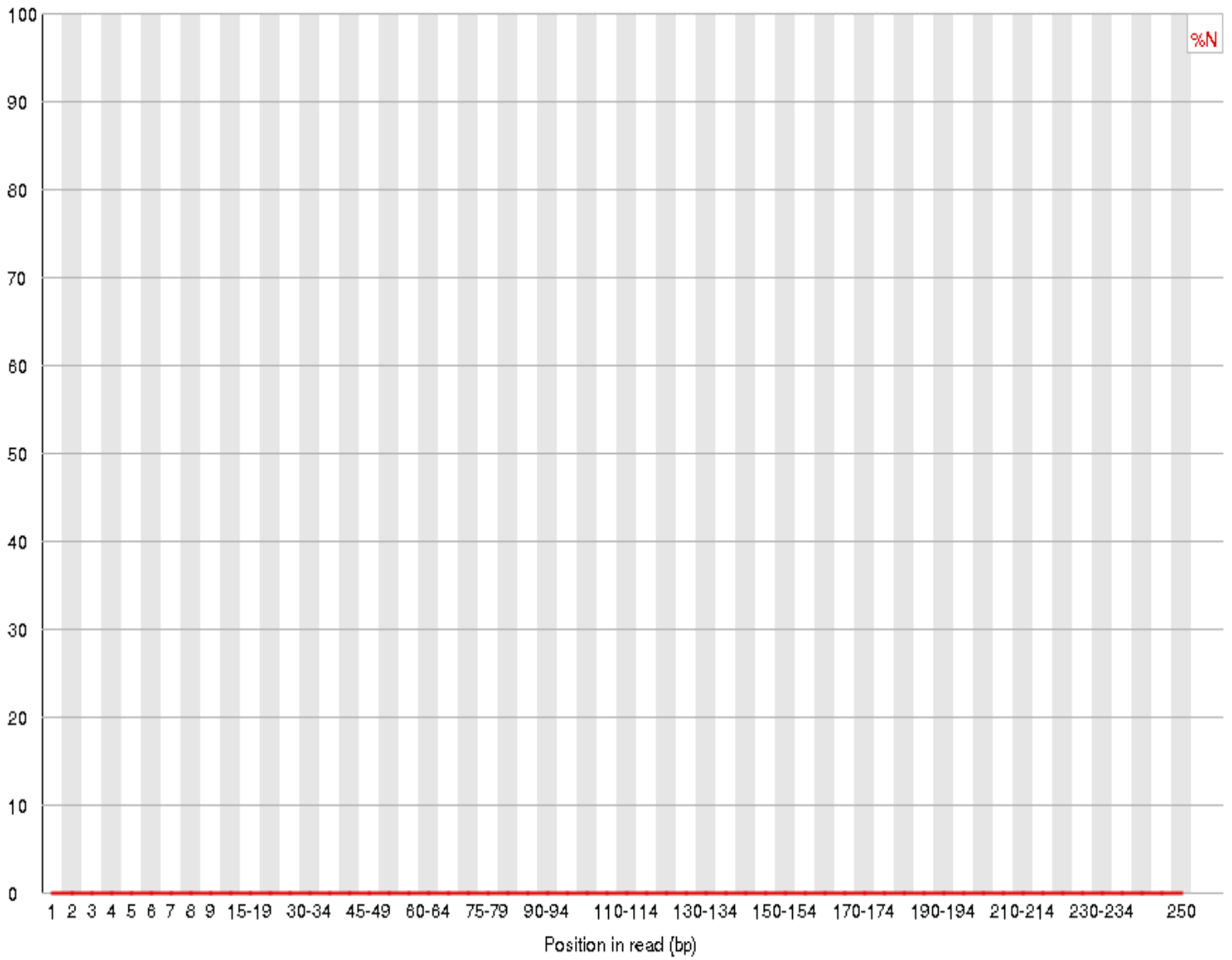


 **Per sequence GC content**



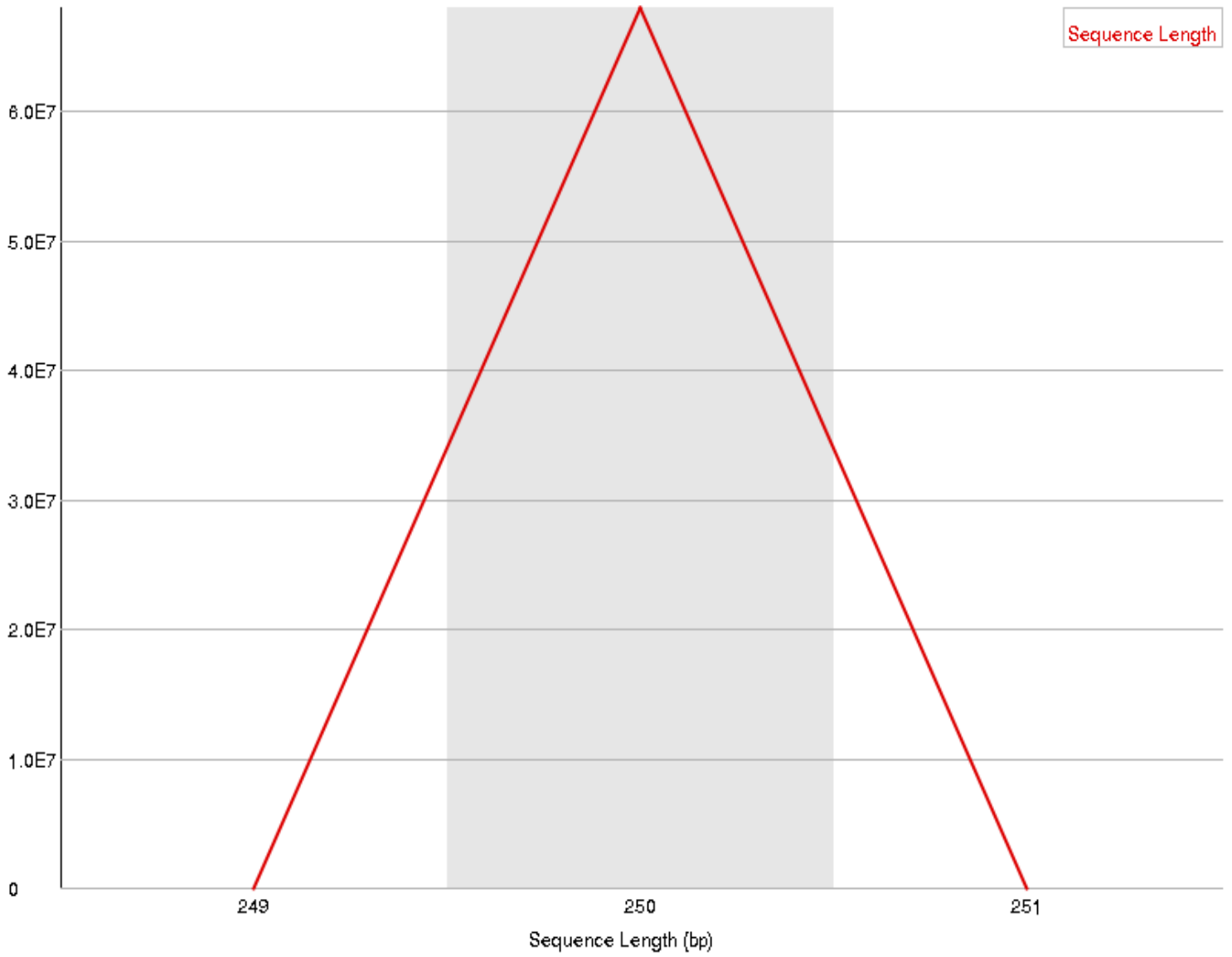
 **Per base N content**

N content across all bases



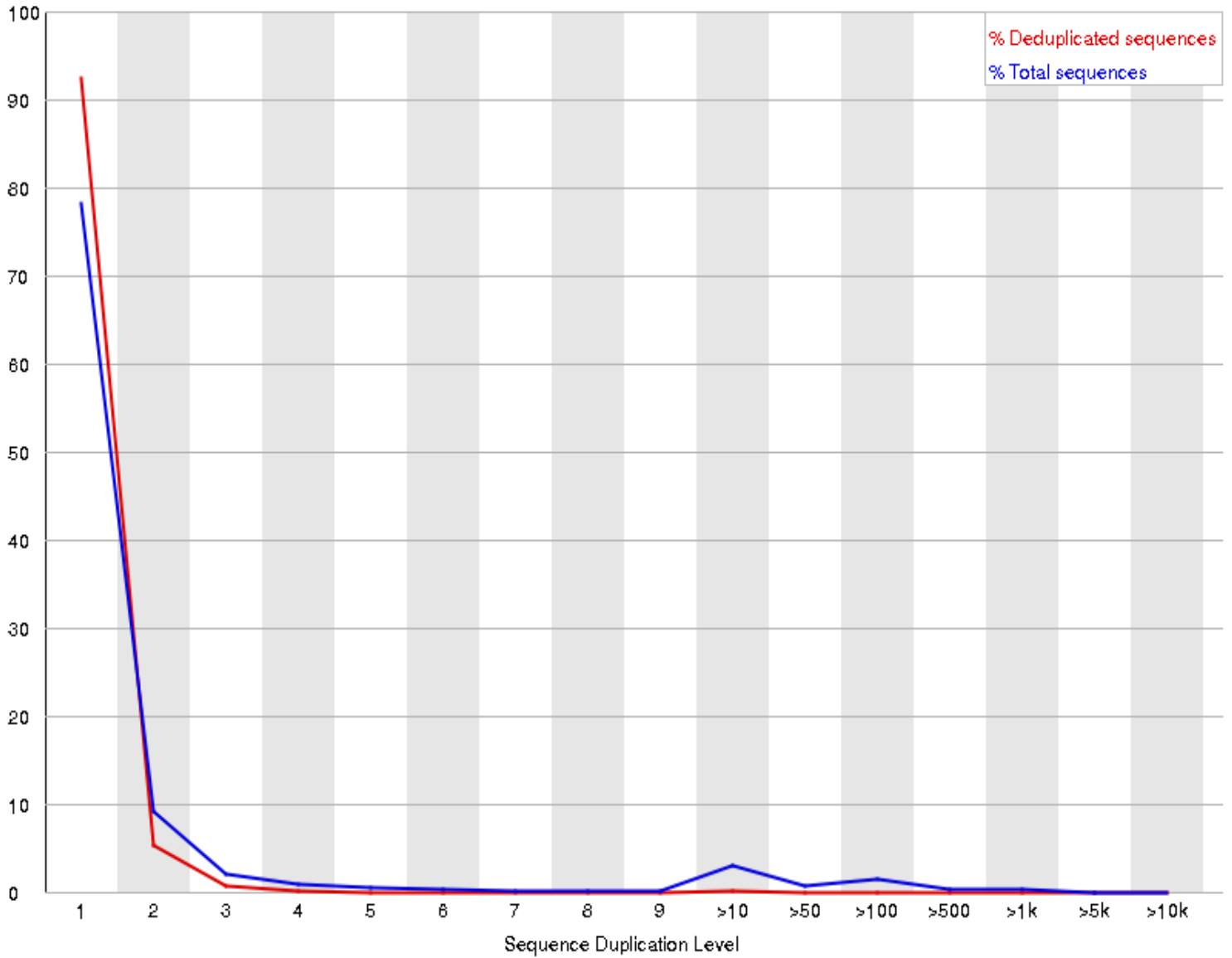
 **Sequence Length Distribution**

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 84.64%



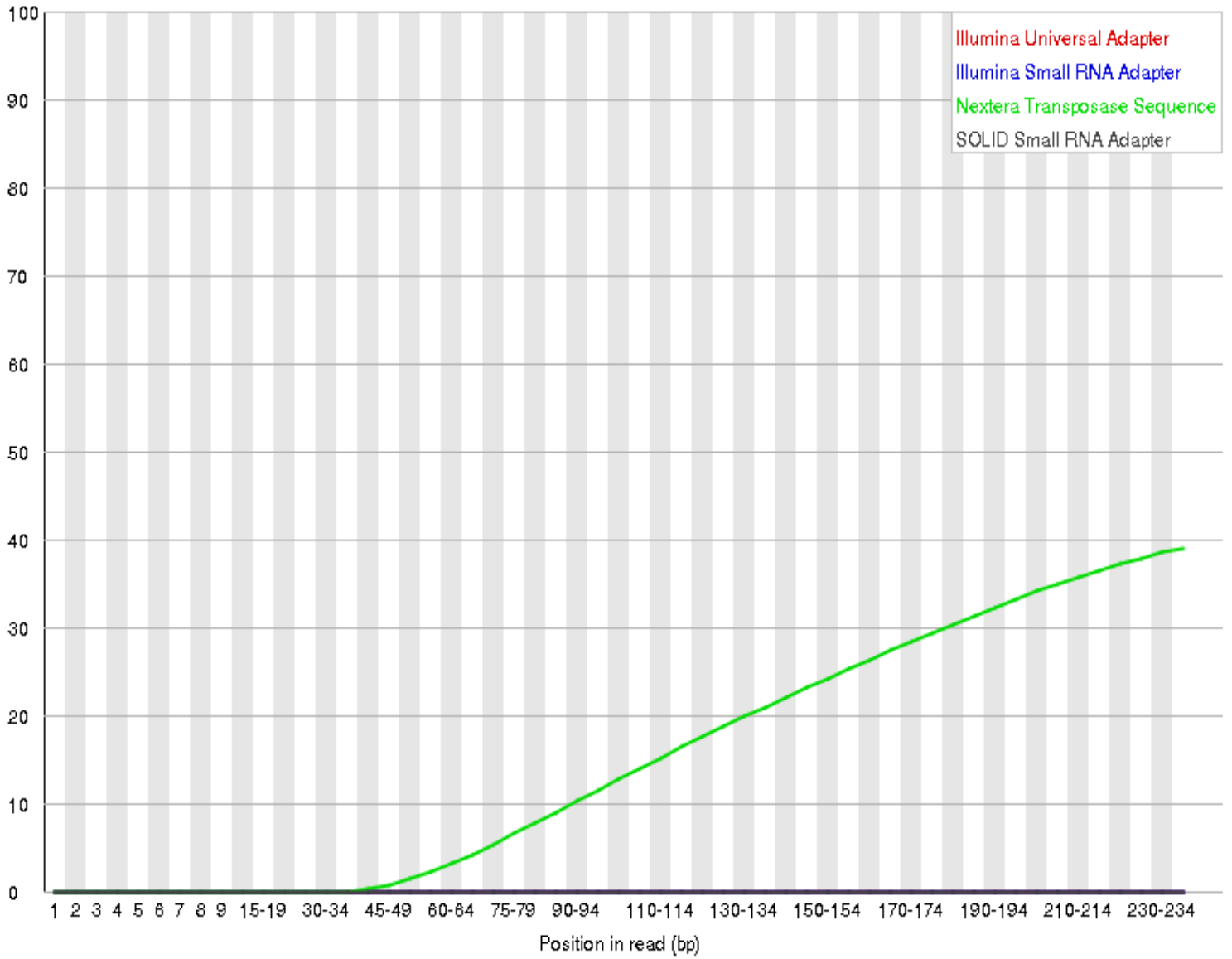
Overrepresented sequences

No overrepresented sequences



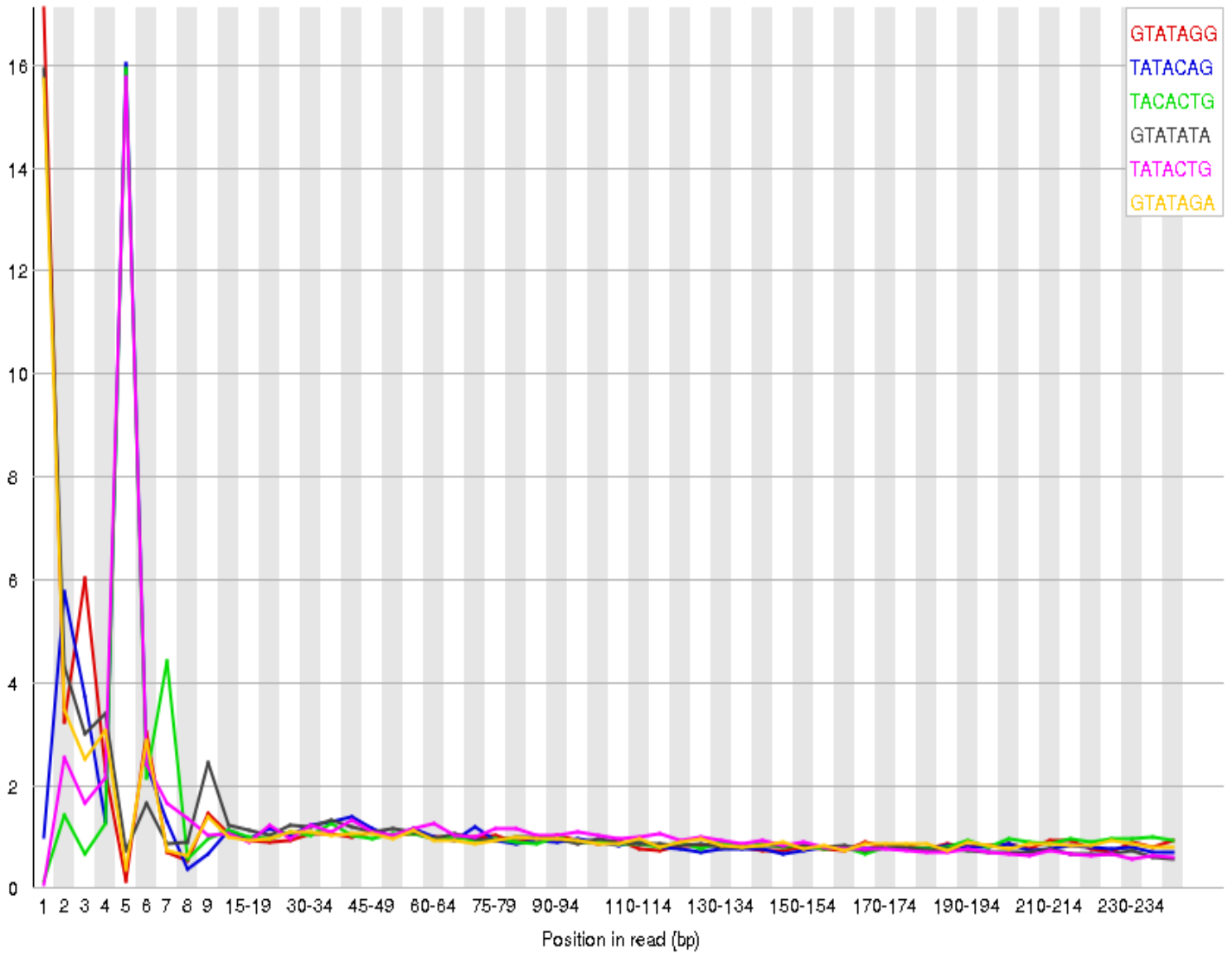
Adapter Content

% Adapter



 **Kmer Content**

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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GTATAGG	52530	0.0	17.09431	1
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TATACAG	147615	0.0	16.02623	5
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TACTACTG	125020	0.0	15.9169	5
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GTATATA	155070	0.0	15.916562	1
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TATACTG	170460	0.0	15.760823	5
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GTATAGA	91875	0.0	15.736282	1
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CTATACT	83915	0.0	15.731557	4
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GTCCTAG	53535	0.0	15.519955	1
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GTCCTAA	52755	0.0	14.8706	1
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TCTATAC	89735	0.0	14.819689	3
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GTATAAG	65990	0.0	14.716891	1
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GTCTTAG	79020	0.0	14.359096	1
GTATAAA	141155	0.0	14.123323	1
TATACCG	31170	0.0	13.973831	5
GTCTAGG	57235	0.0	13.941105	1
TTATACT	126525	0.0	13.66399	4
GTATTAA	92800	0.0	13.581056	1
GTATTAG	89615	0.0	13.573618	1
TATAGTG	96075	0.0	13.410271	5
GTCCTAT	69055	0.0	13.339298	1

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