













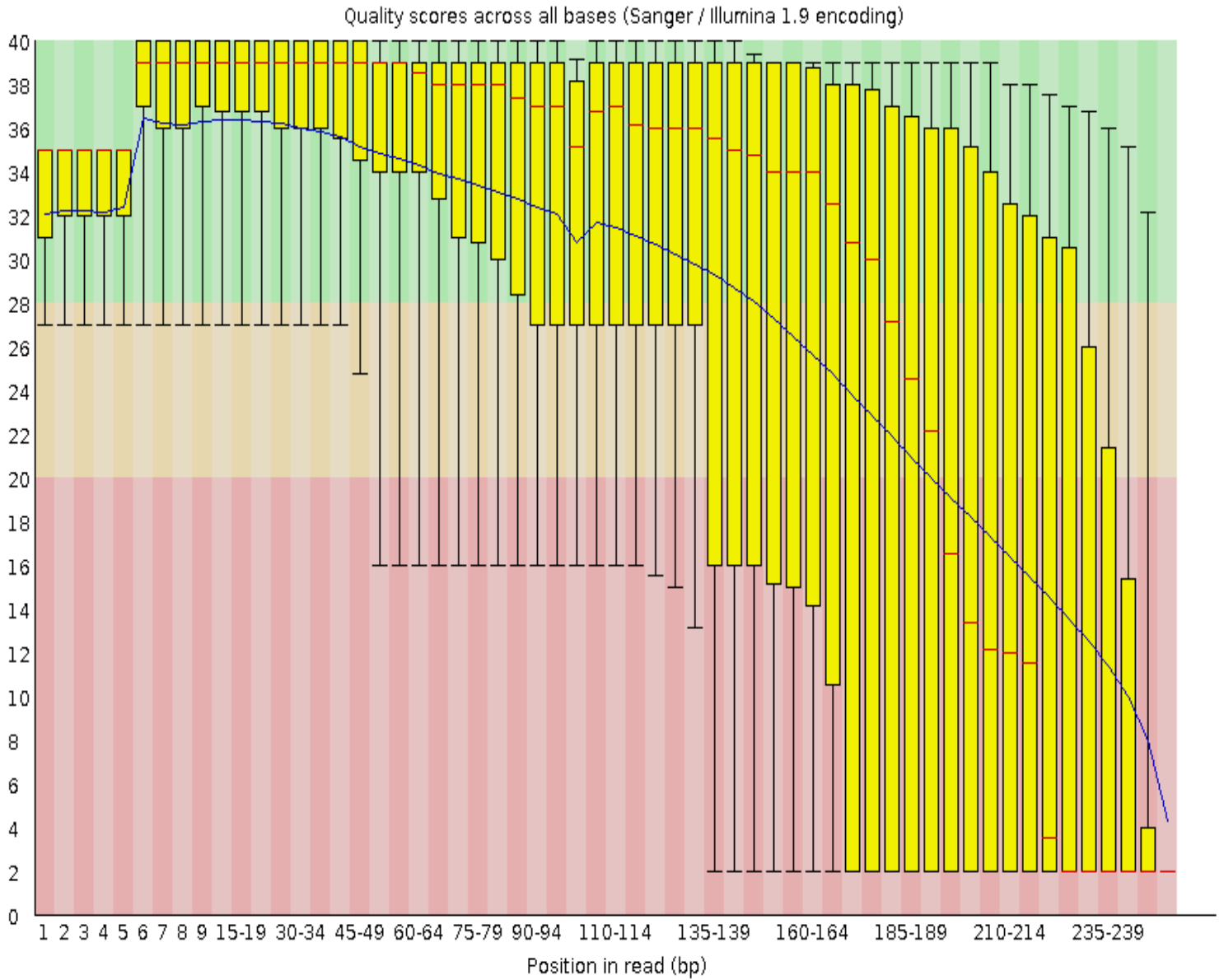
Summary

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Basic Statistics

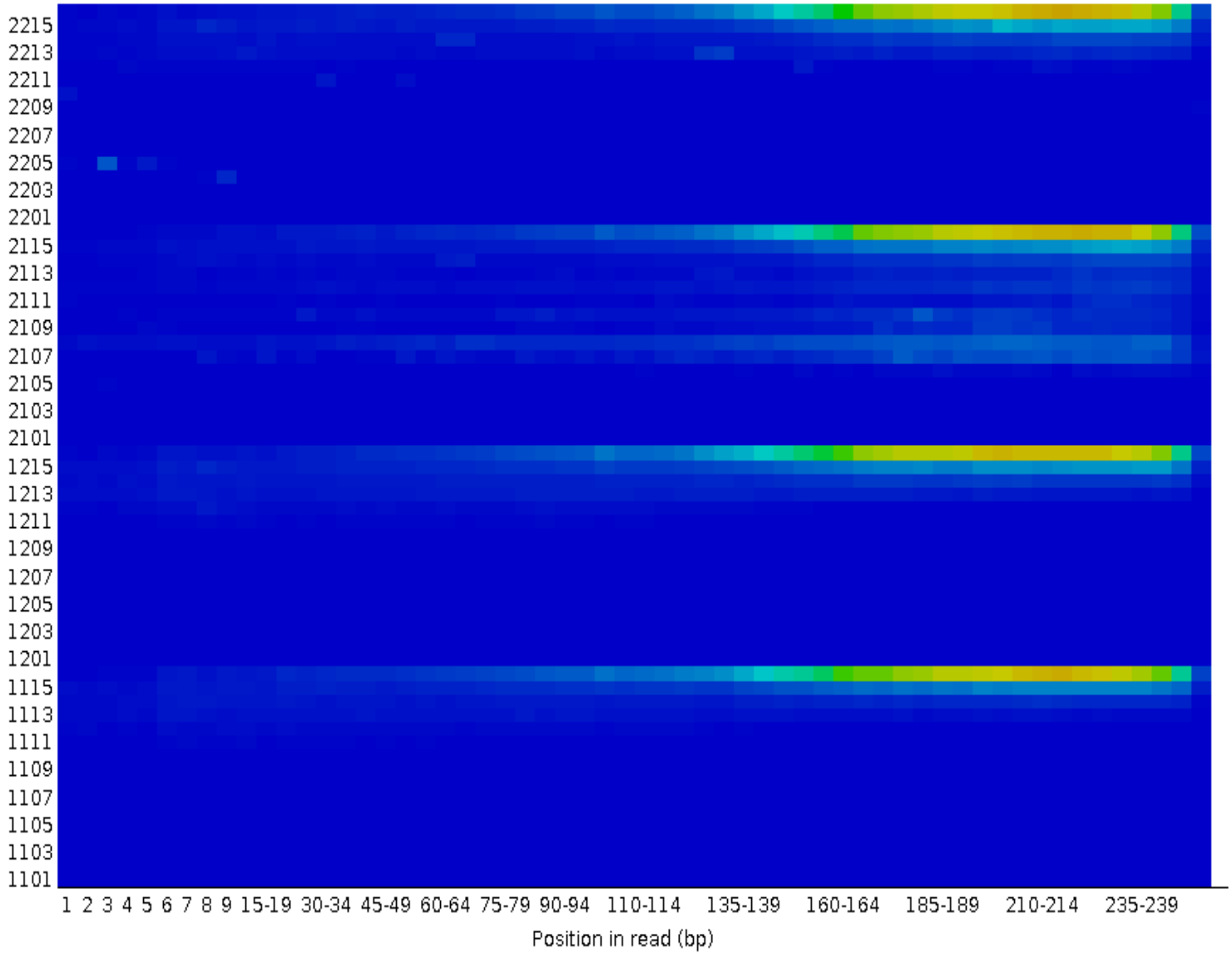
Measure	Value
Filename	BS-MK_seqprep_dupRemoved_ec_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	124784959
Sequences flagged as poor quality	0
Sequence length	250
%GC	42

Per base sequence quality



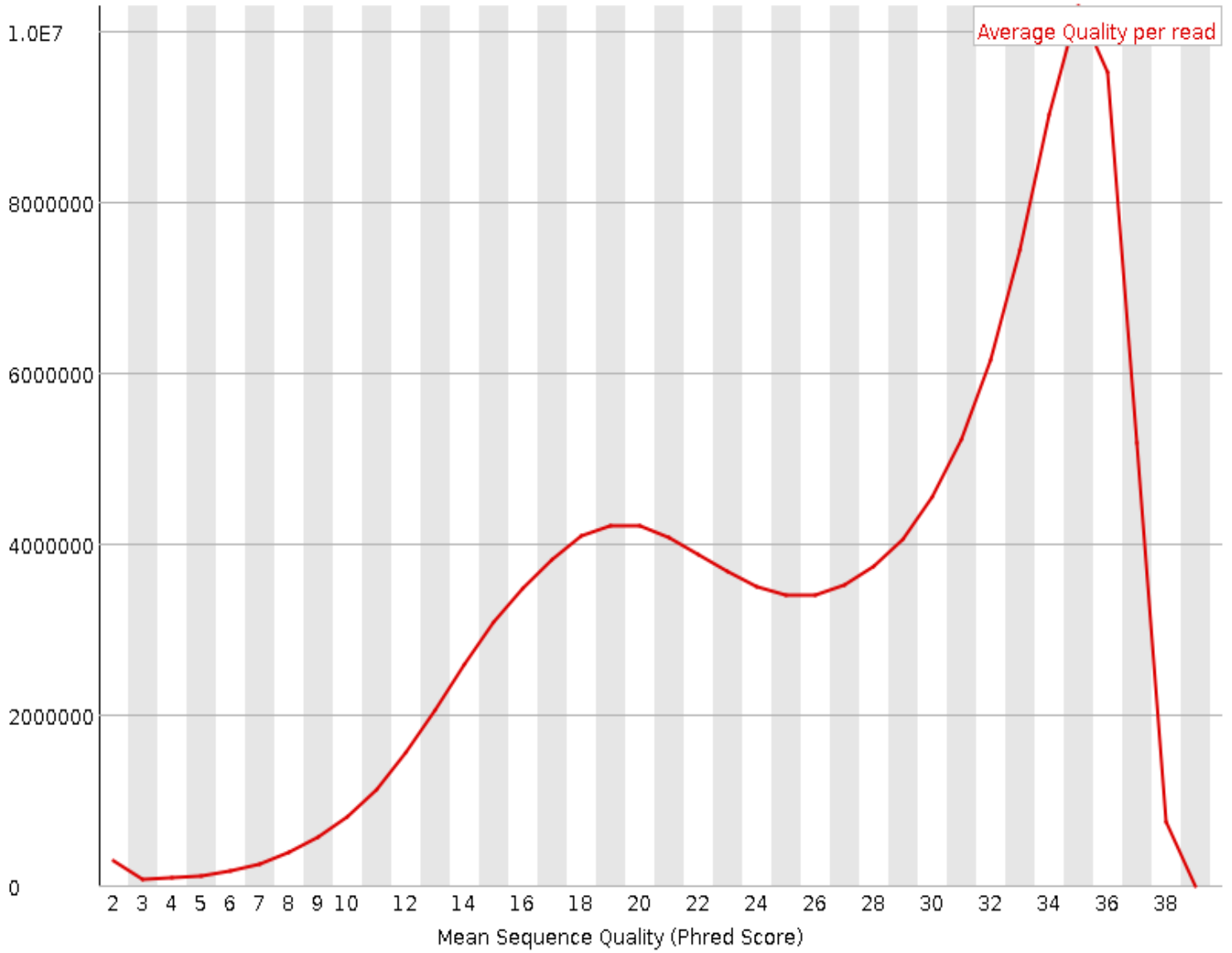
! Per tile sequence quality

Quality per tile



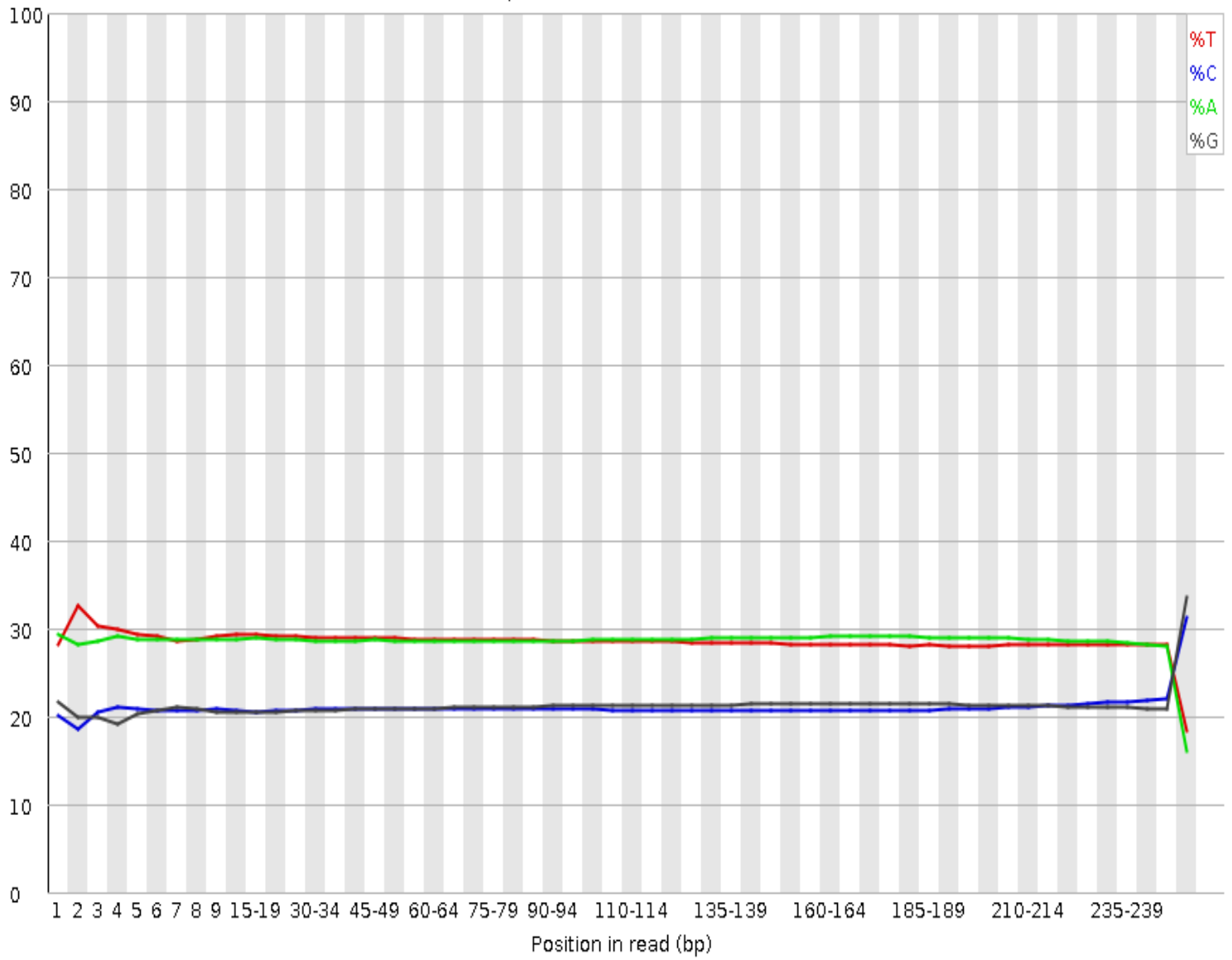
 **Per sequence quality scores**

Quality score distribution over all sequences



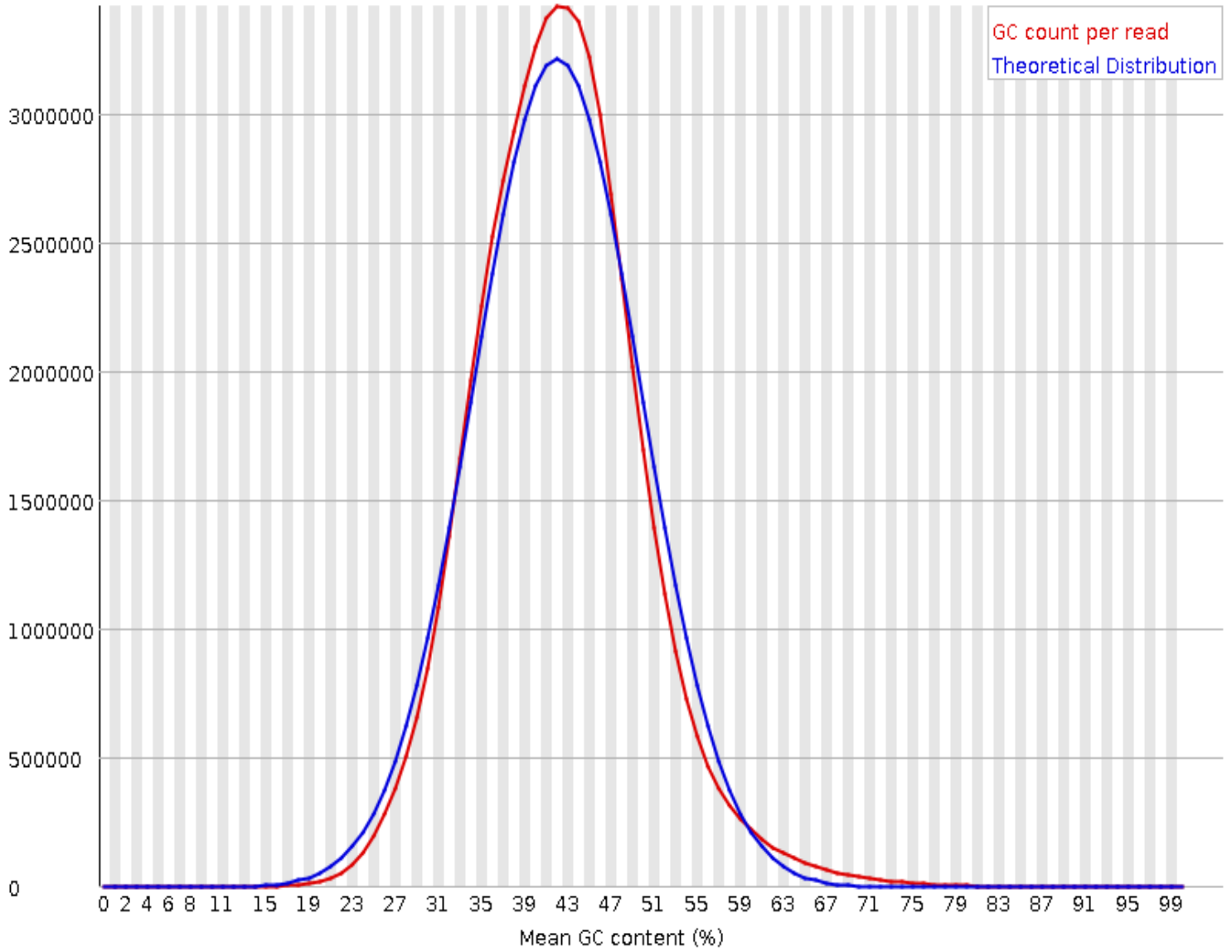
 **Per base sequence content**

Sequence content across all bases



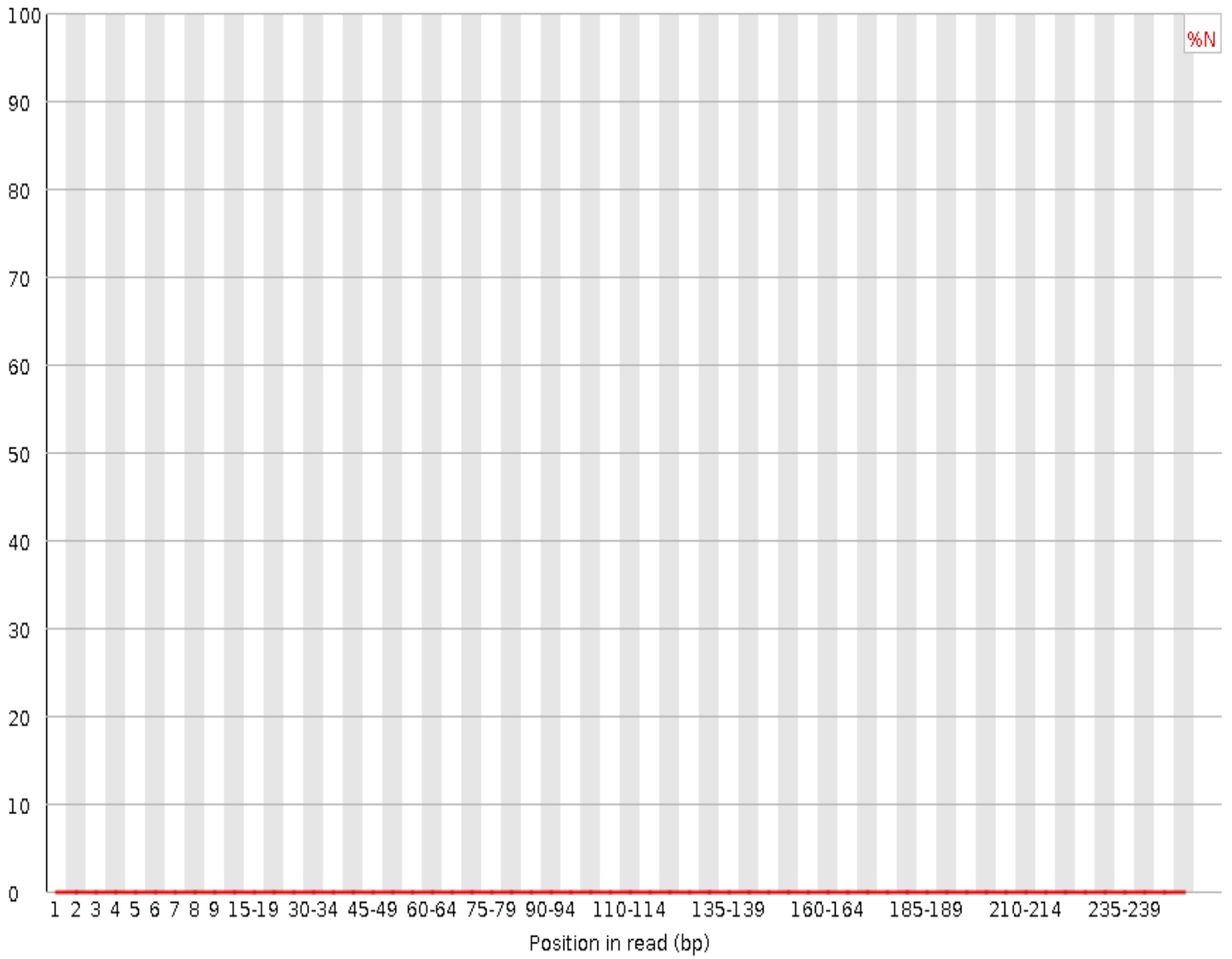
 **Per sequence GC content**

GC distribution over all sequences



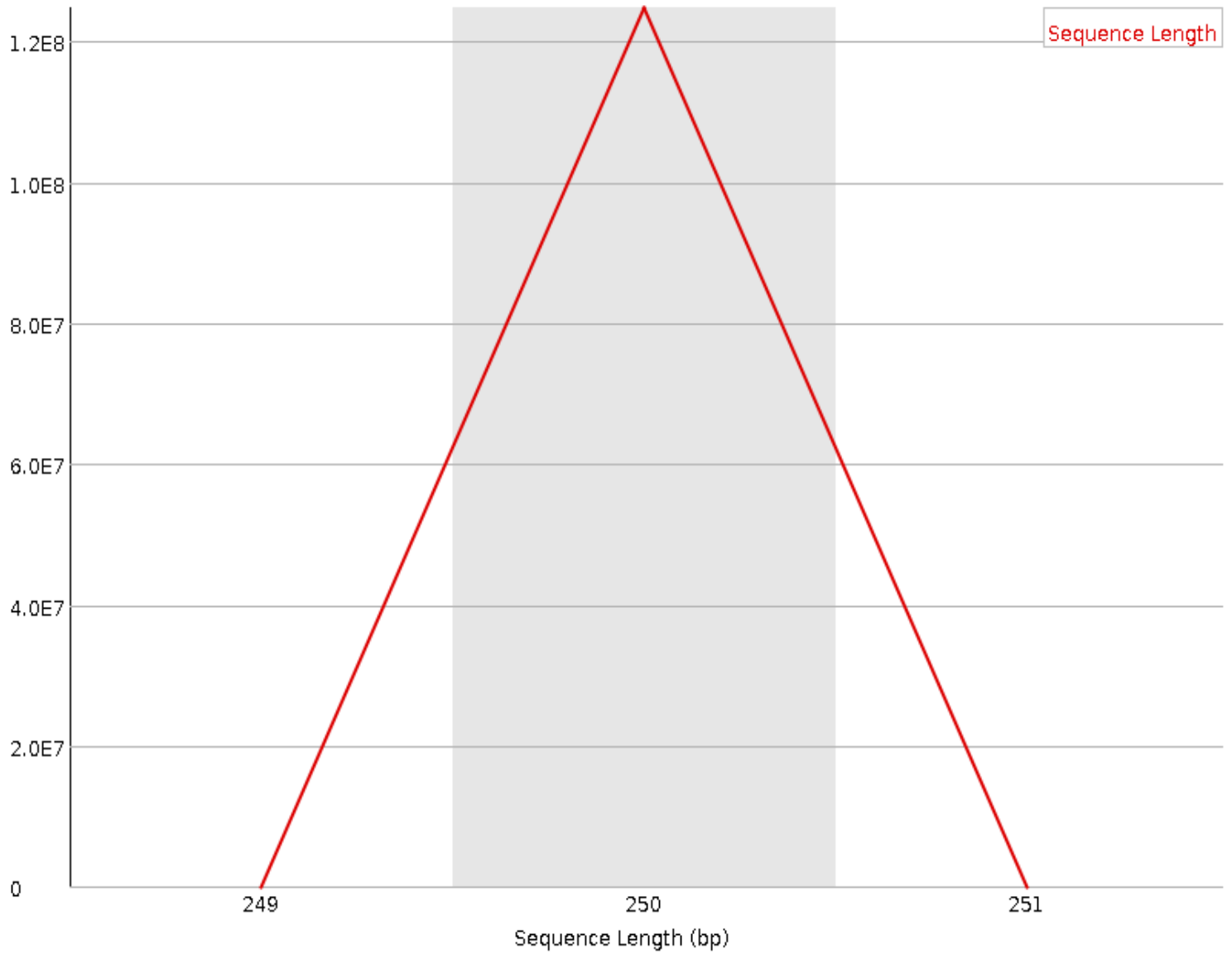
 **Per base N content**

N content across all bases



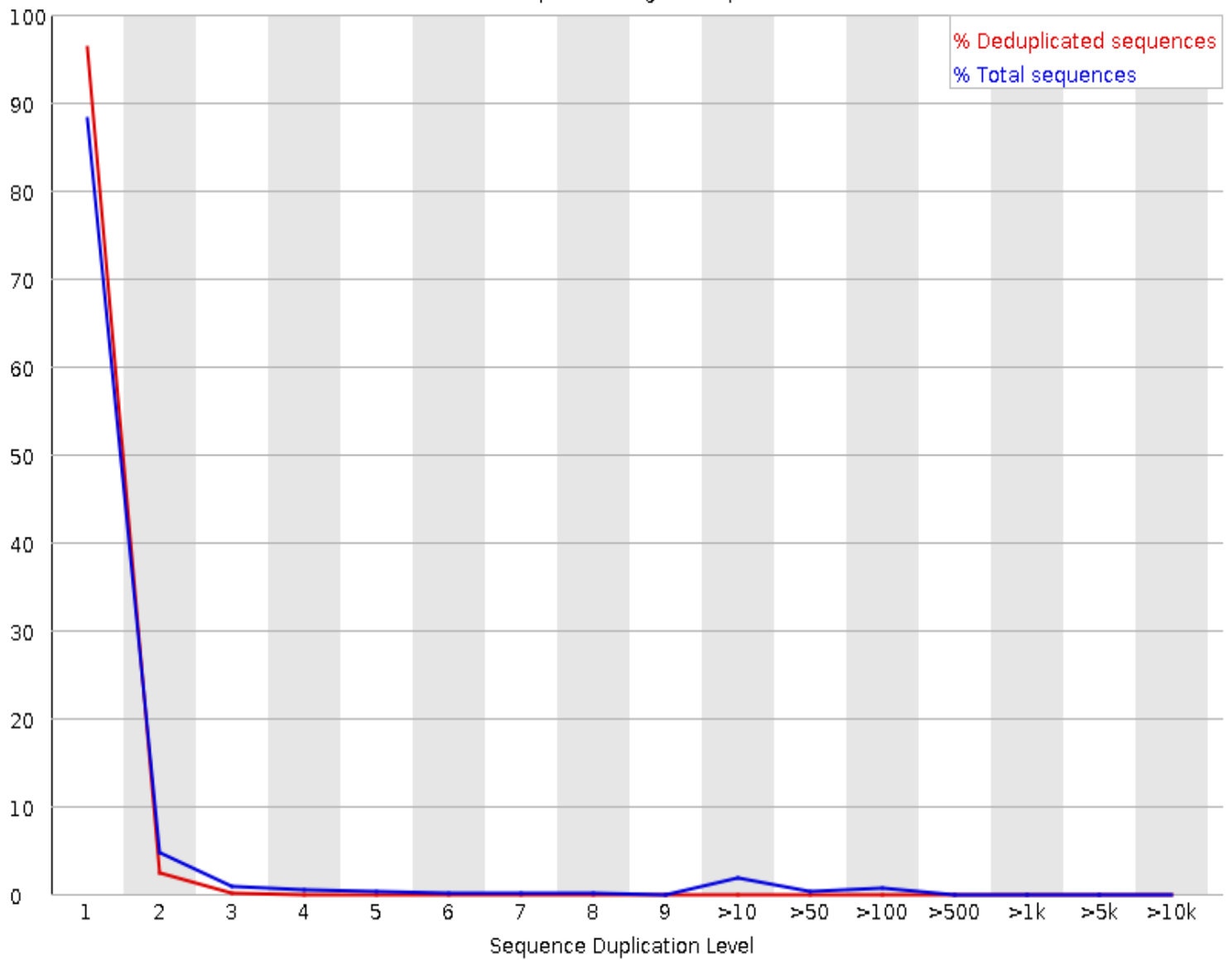
 **Sequence Length Distribution**

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 91.7%

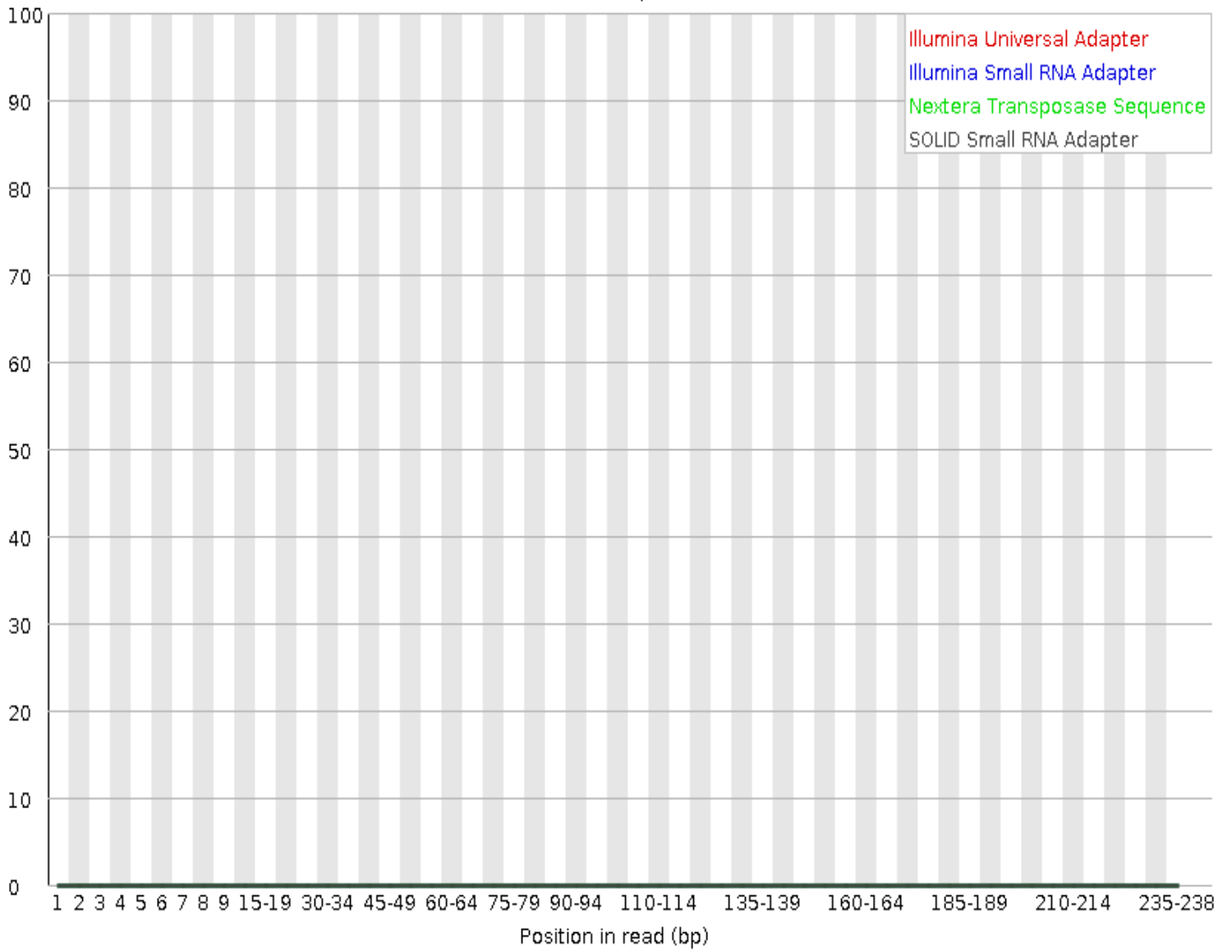


 **Overrepresented sequences**

No overrepresented sequences

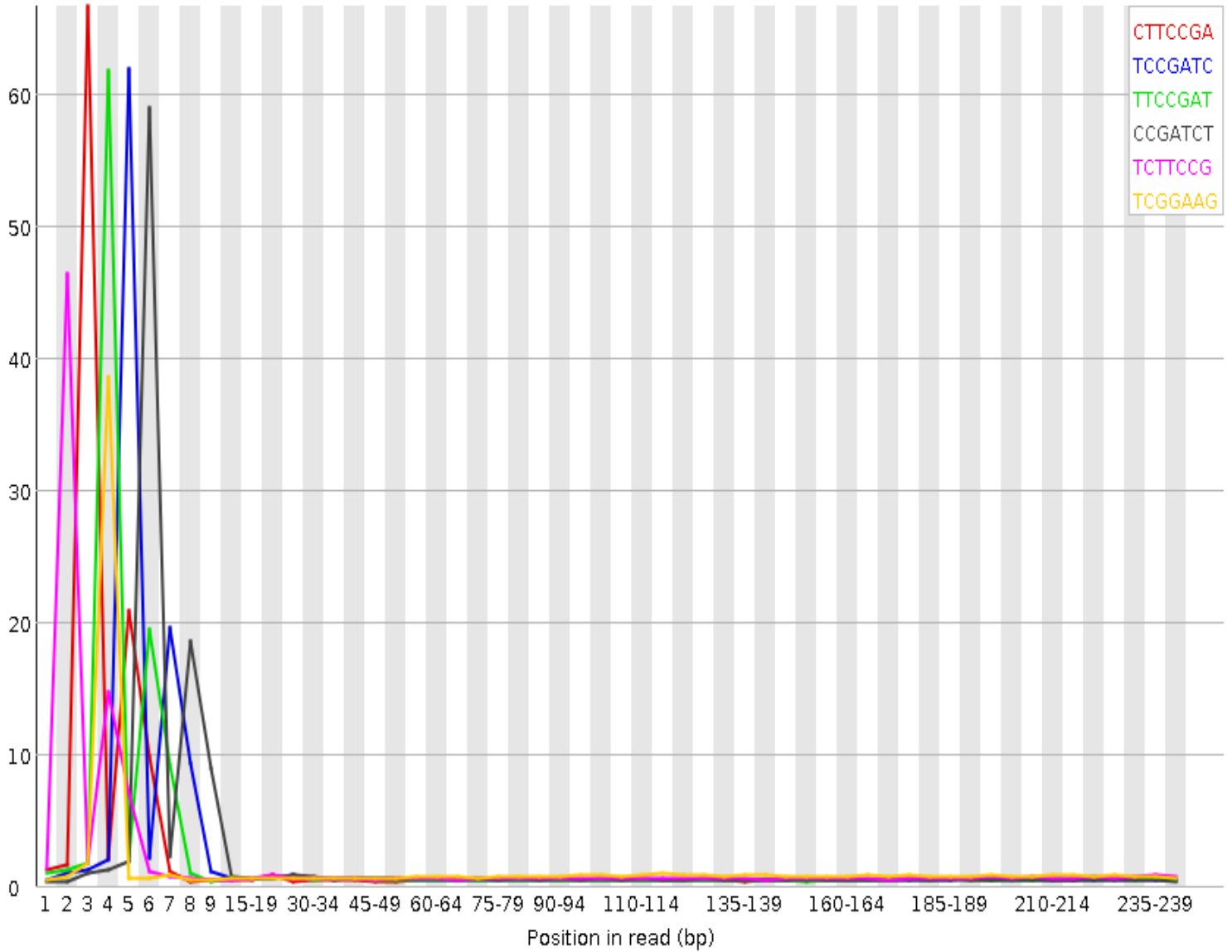
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	116345	0.0	66.58939	3
TCCGATC	124735	0.0	61.906082	5
TTCCGAT	125110	0.0	61.740032	4
CCGATCT	130770	0.0	58.946507	6
TCTTCCG	168810	0.0	46.45909	2
TCGGAAG	88285	0.0	38.58469	4
ATCGGAA	94685	0.0	36.169315	3
GATCGGA	97065	0.0	35.479187	2
AGATCGG	107905	0.0	31.91979	1
CGATCTA	82835	0.0	29.106043	7
CGGAAGA	143050	0.0	24.341797	5

CGATCTT	106805	0.0	20.790792	7
CTCTTCC	390370	0.0	20.67806	1
GAAGAGC	213745	0.0	16.608423	7
ACGCTCT	80165	0.0	13.941241	1
CGATCTC	120125	0.0	13.7700615	7
CGATCTG	128135	0.0	13.633327	7
GCTCTTC	200500	0.0	12.764875	2
CGCTCTT	110185	0.0	10.418198	2
GGAAGAG	394445	0.0	9.316548	6

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