











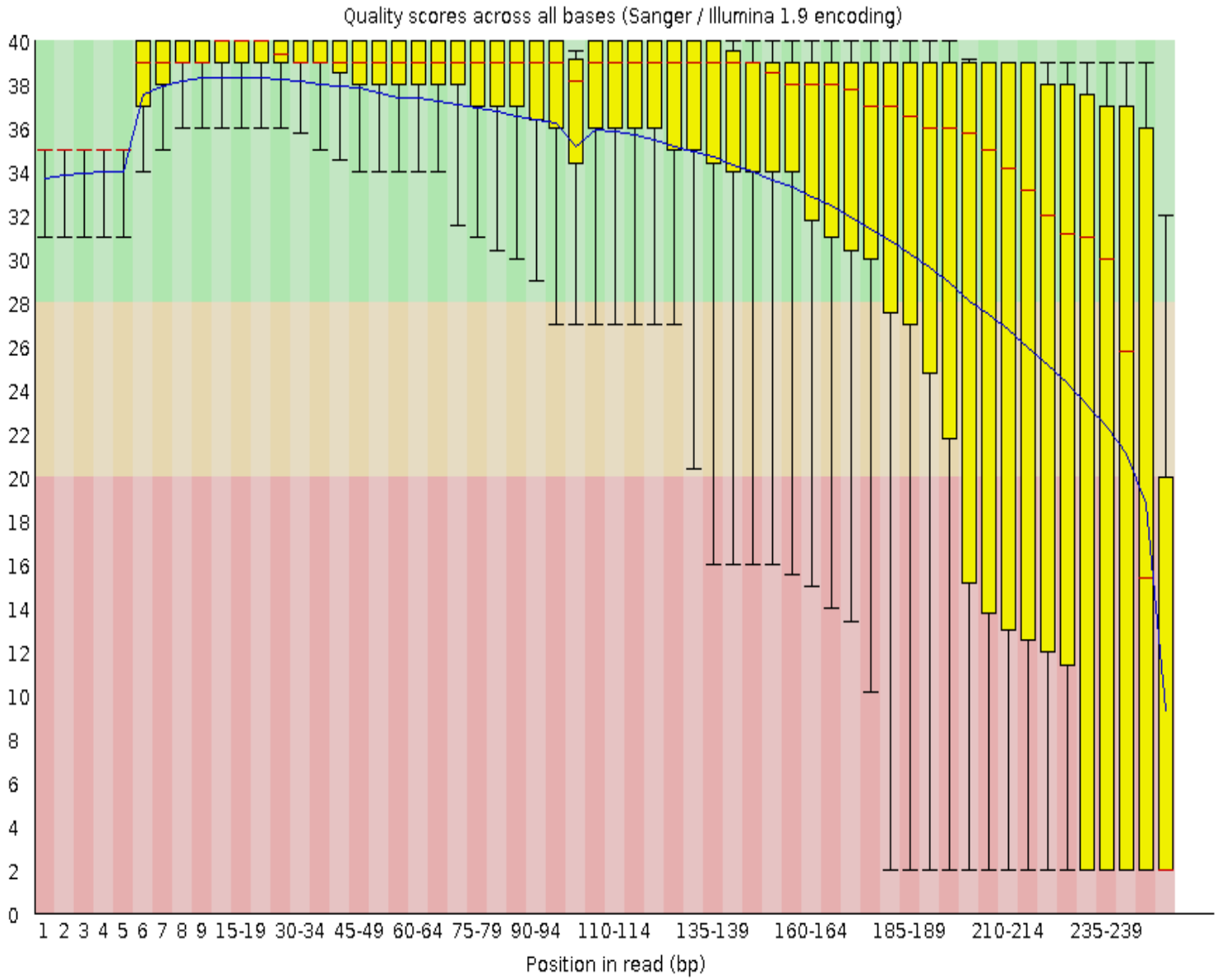
Summary

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Basic Statistics

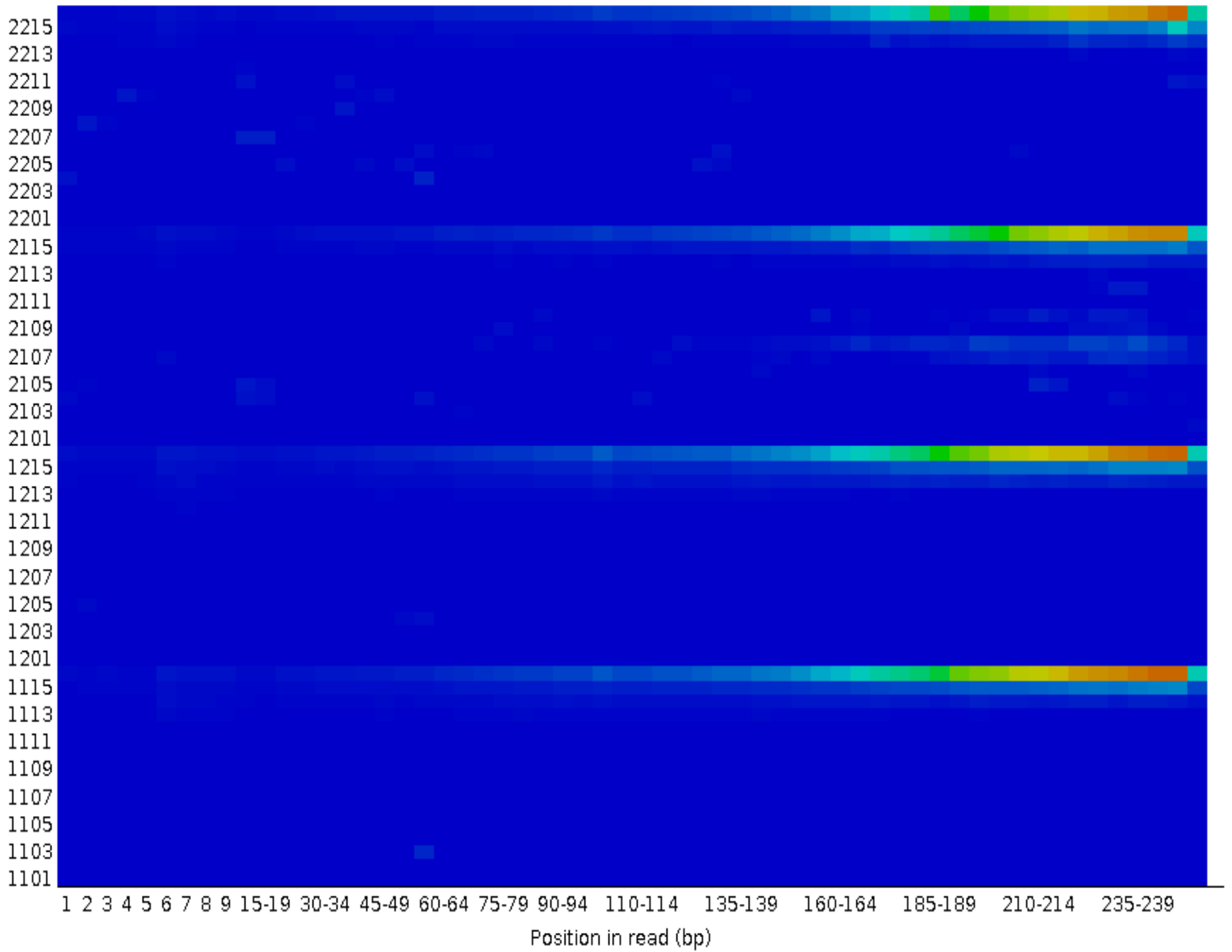
Measure	Value
Filename	BS-MK_seqprep_dupRemoved_ec_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	124784959
Sequences flagged as poor quality	0
Sequence length	250
%GC	42

Per base sequence quality



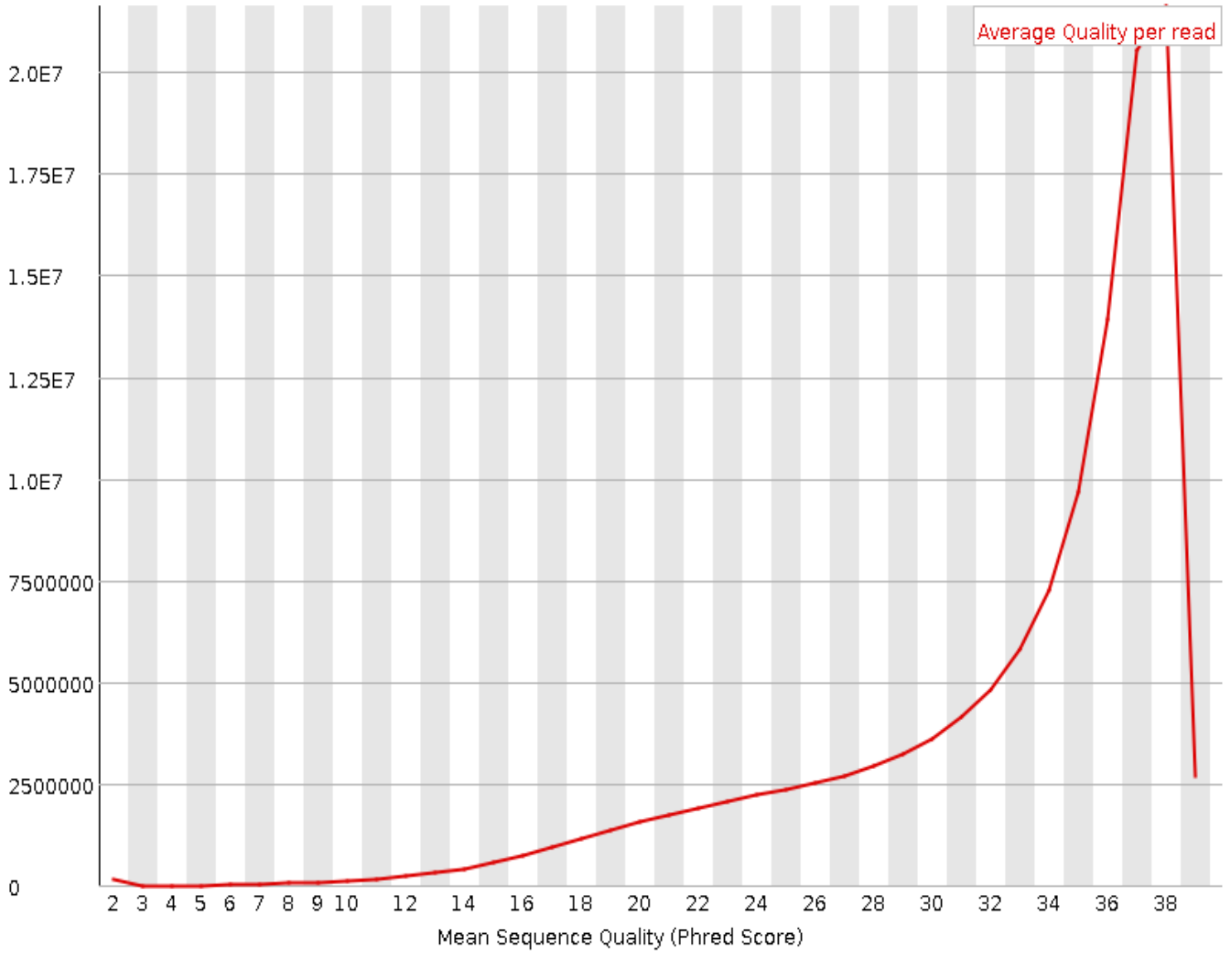
! Per tile sequence quality

Quality per tile



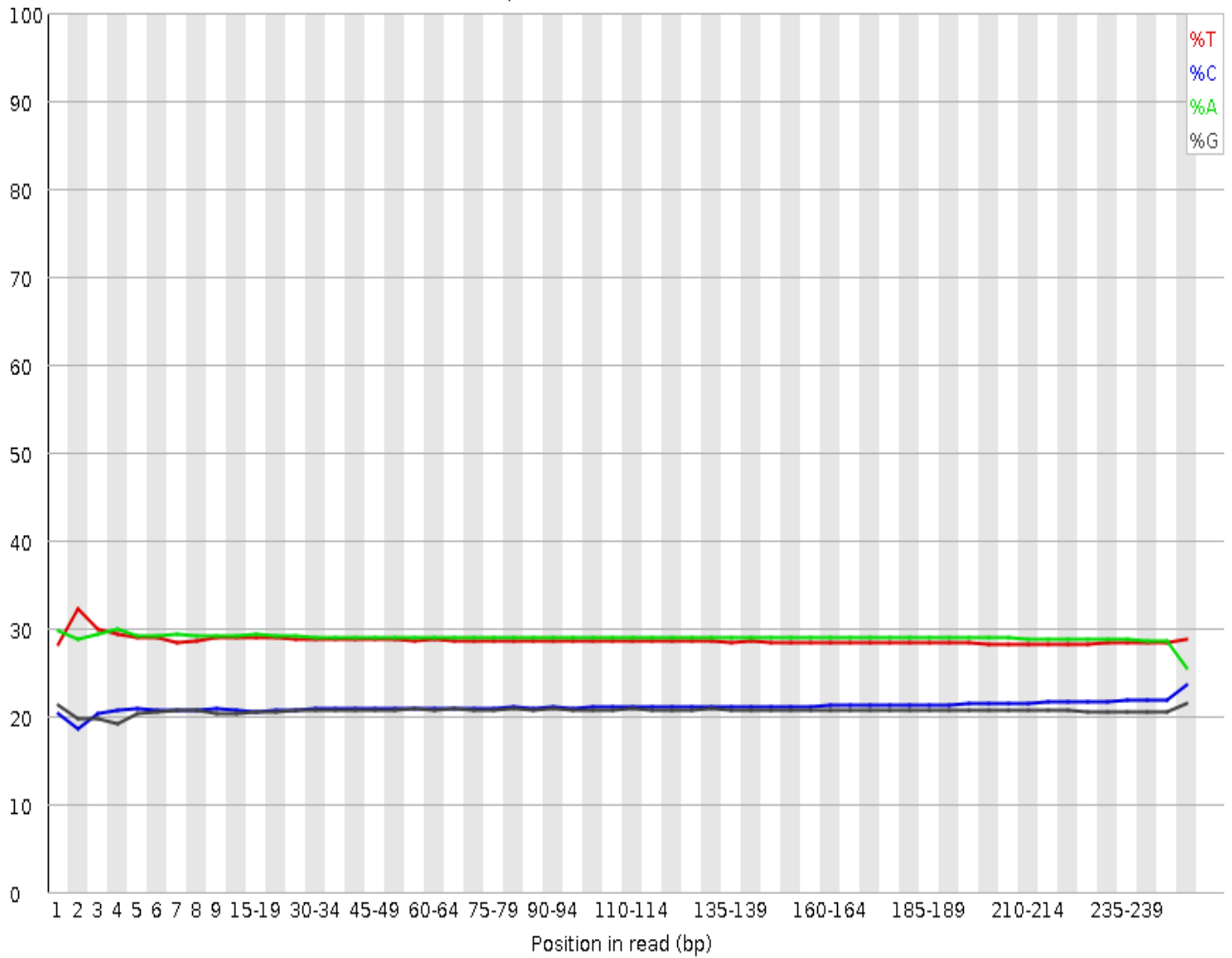
 **Per sequence quality scores**

Quality score distribution over all sequences



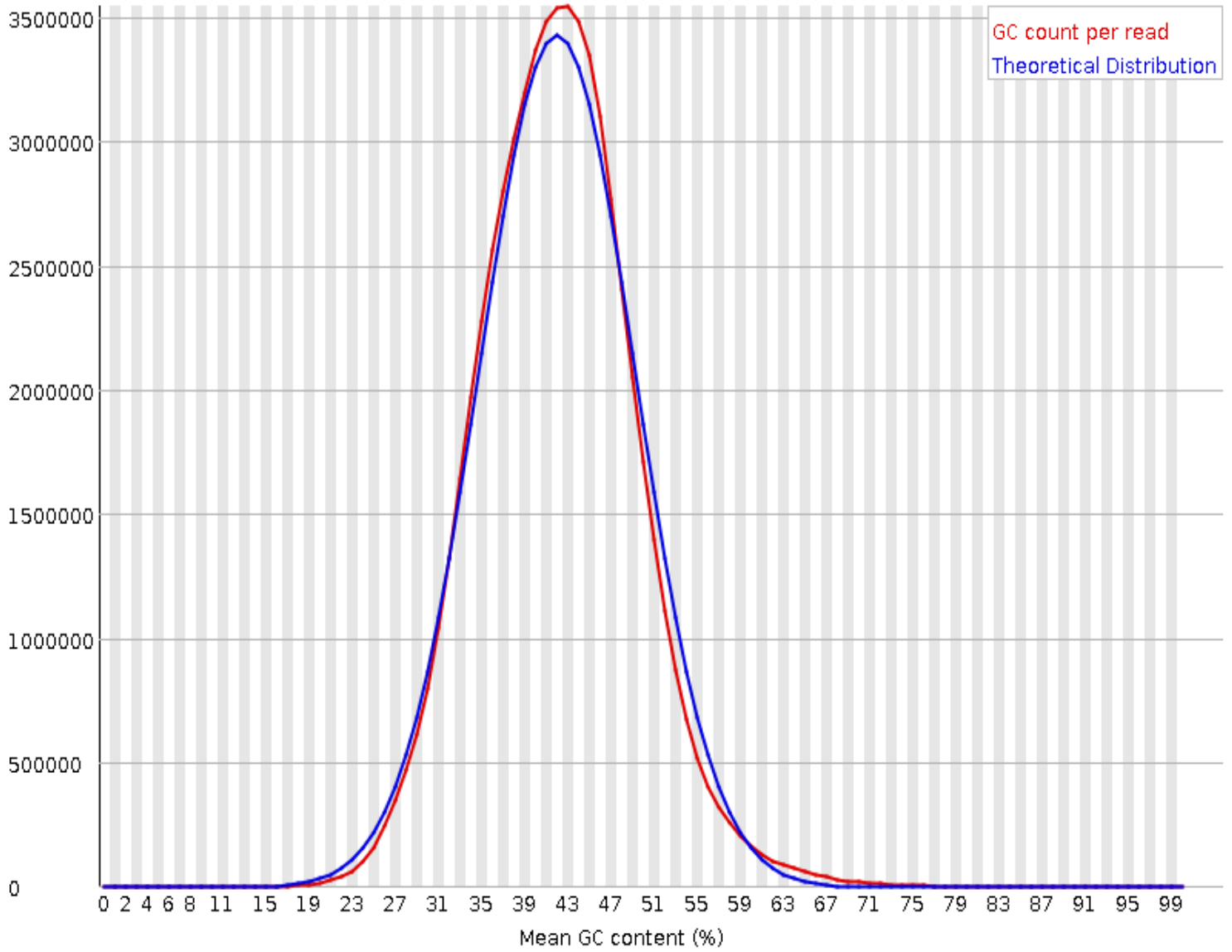
 **Per base sequence content**

Sequence content across all bases



 **Per sequence GC content**

GC distribution over all sequences



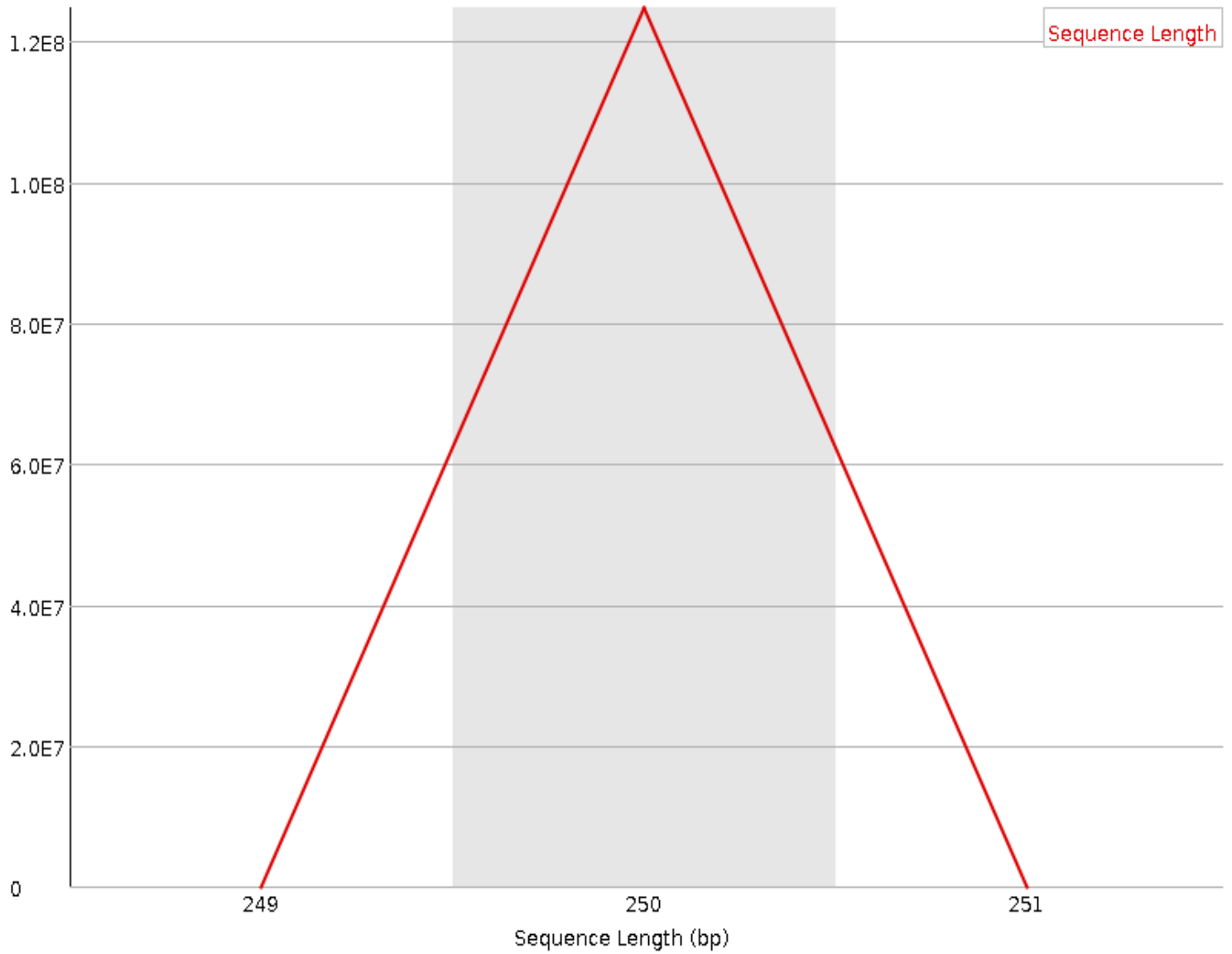
 **Per base N content**

N content across all bases



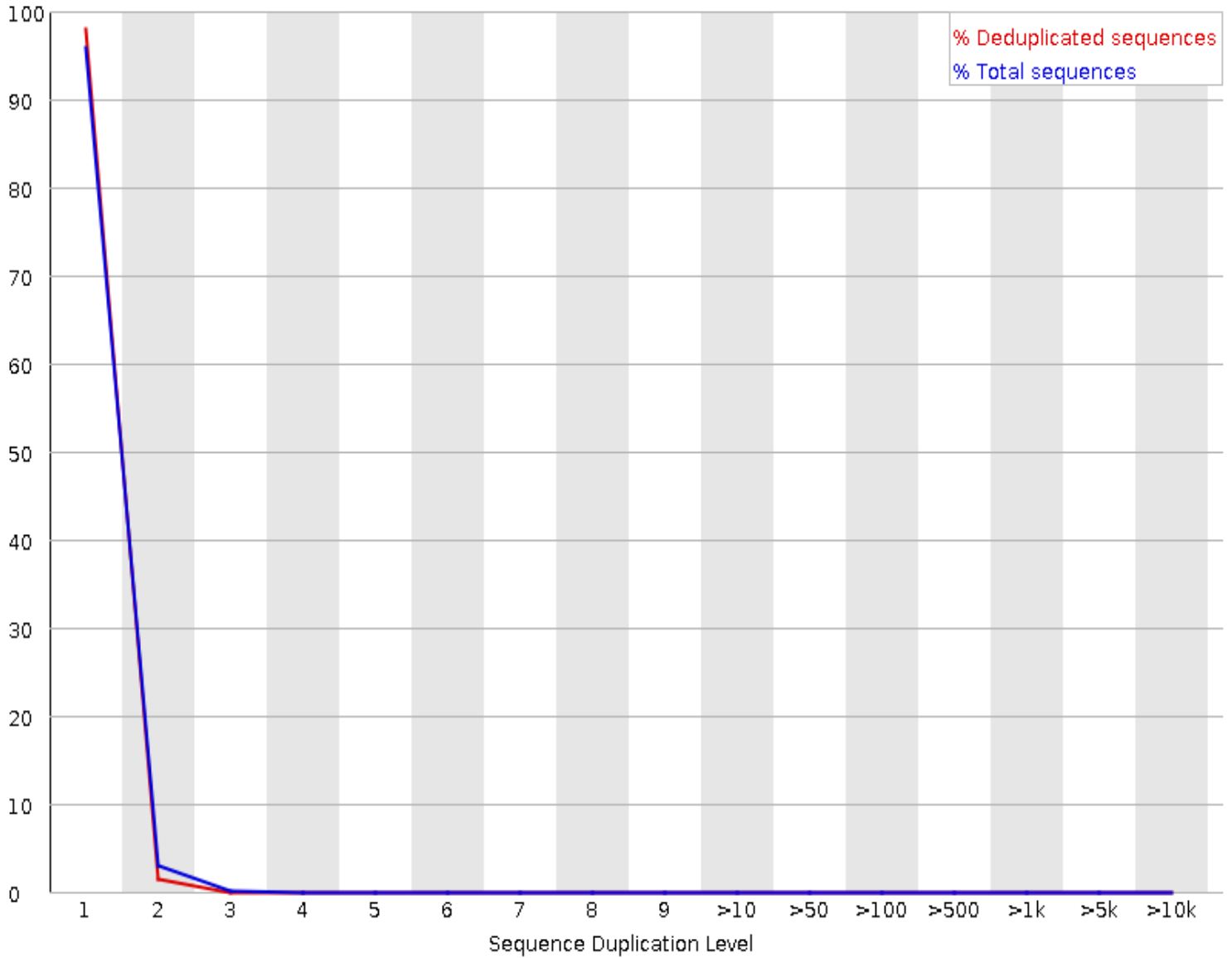
 **Sequence Length Distribution**

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 97.78%

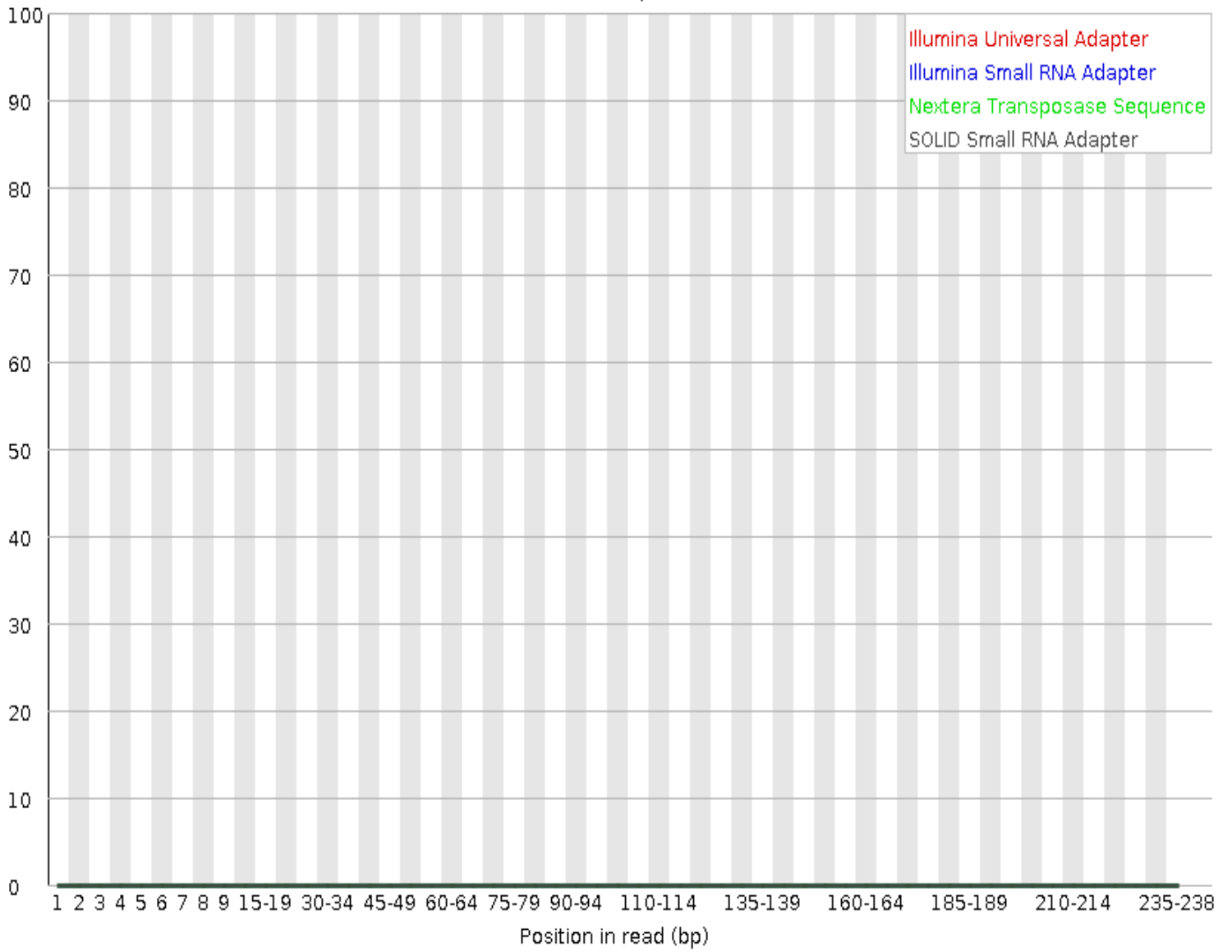


 **Overrepresented sequences**

No overrepresented sequences

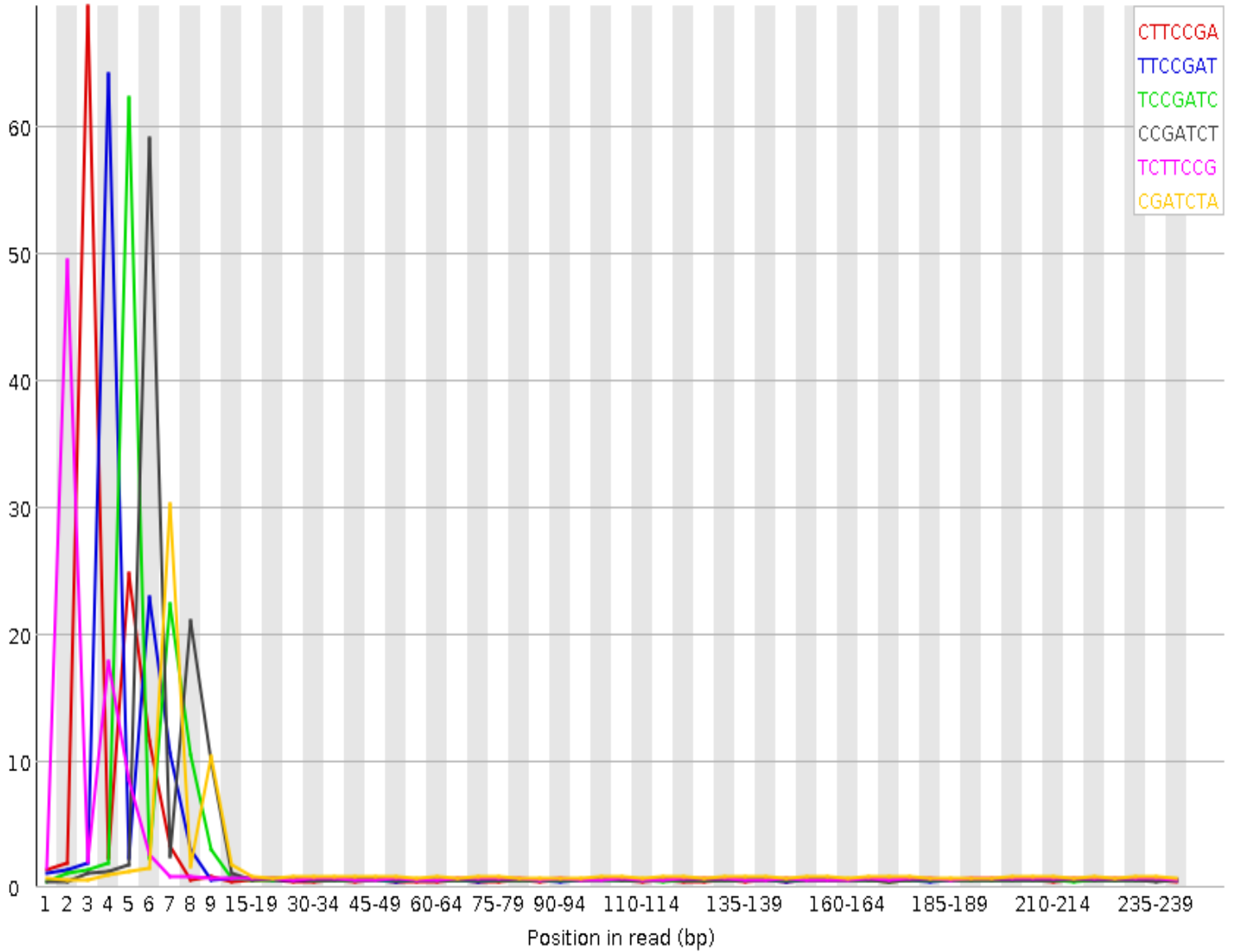
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCGGA	117525	0.0	69.355576	3
TTCCGAT	127095	0.0	64.0469	4
TCCGATC	130860	0.0	62.278736	5
CCGATCT	137730	0.0	58.986347	6
TCTTCCG	165950	0.0	49.42588	2
CGATCTA	82755	0.0	30.145443	7
CGATCTT	104770	0.0	22.391253	7
CTCTTCC	392790	0.0	21.407354	1
TCGGAAG	68895	0.0	20.848164	4
ATCGGAA	78540	0.0	18.318983	3
GATCGGA	83705	0.0	17.217749	2

ACGCTCT	79370	0.0	16.84384	1
AGATCGG	90875	0.0	15.965407	1
GCTCTTC	204150	0.0	14.78807	2
CGATCTC	120500	0.0	14.439334	7
CGATCTG	133640	0.0	13.612648	7
CGCTCTT	105250	0.0	12.859117	2
CGGAAGA	116555	0.0	12.584761	5
GAAGAGC	192725	0.0	8.041142	7
TGCTCTT	320230	0.0	8.001377	1

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