



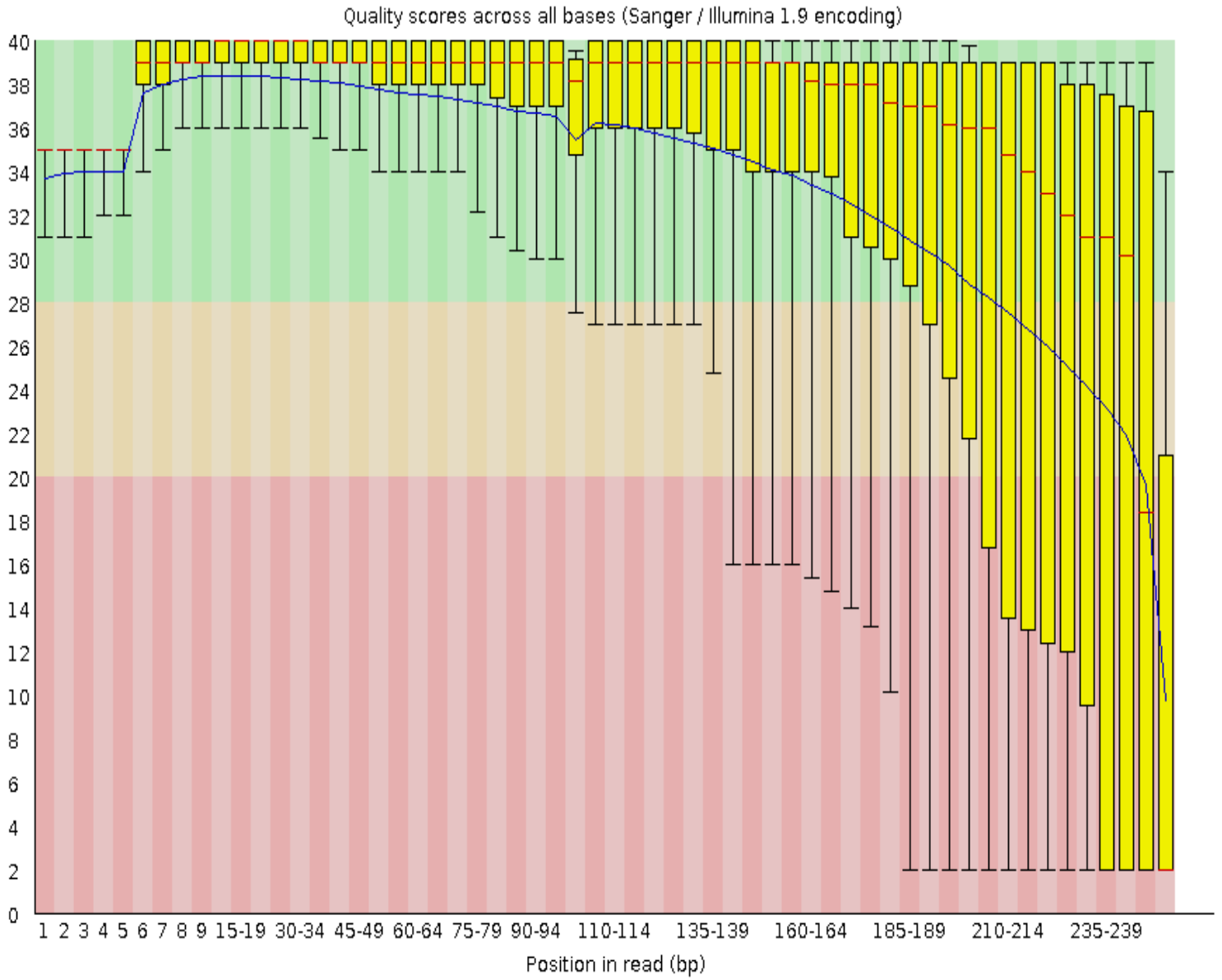
## Summary

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## Basic Statistics

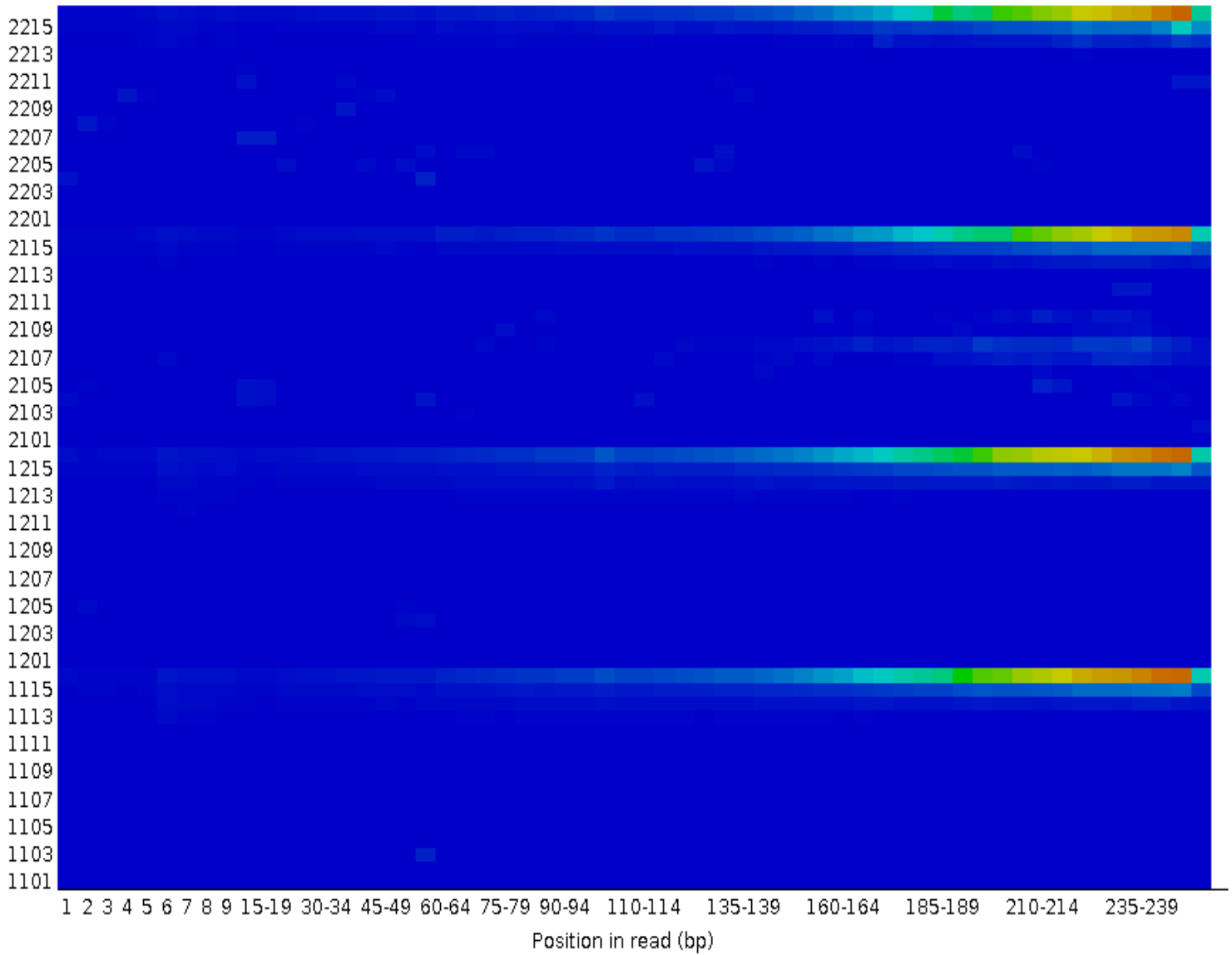
Measure	Value
Filename	BS-MK_CATCCGG_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	158447750
Sequences flagged as poor quality	0
Sequence length	250
%GC	41

## Per base sequence quality



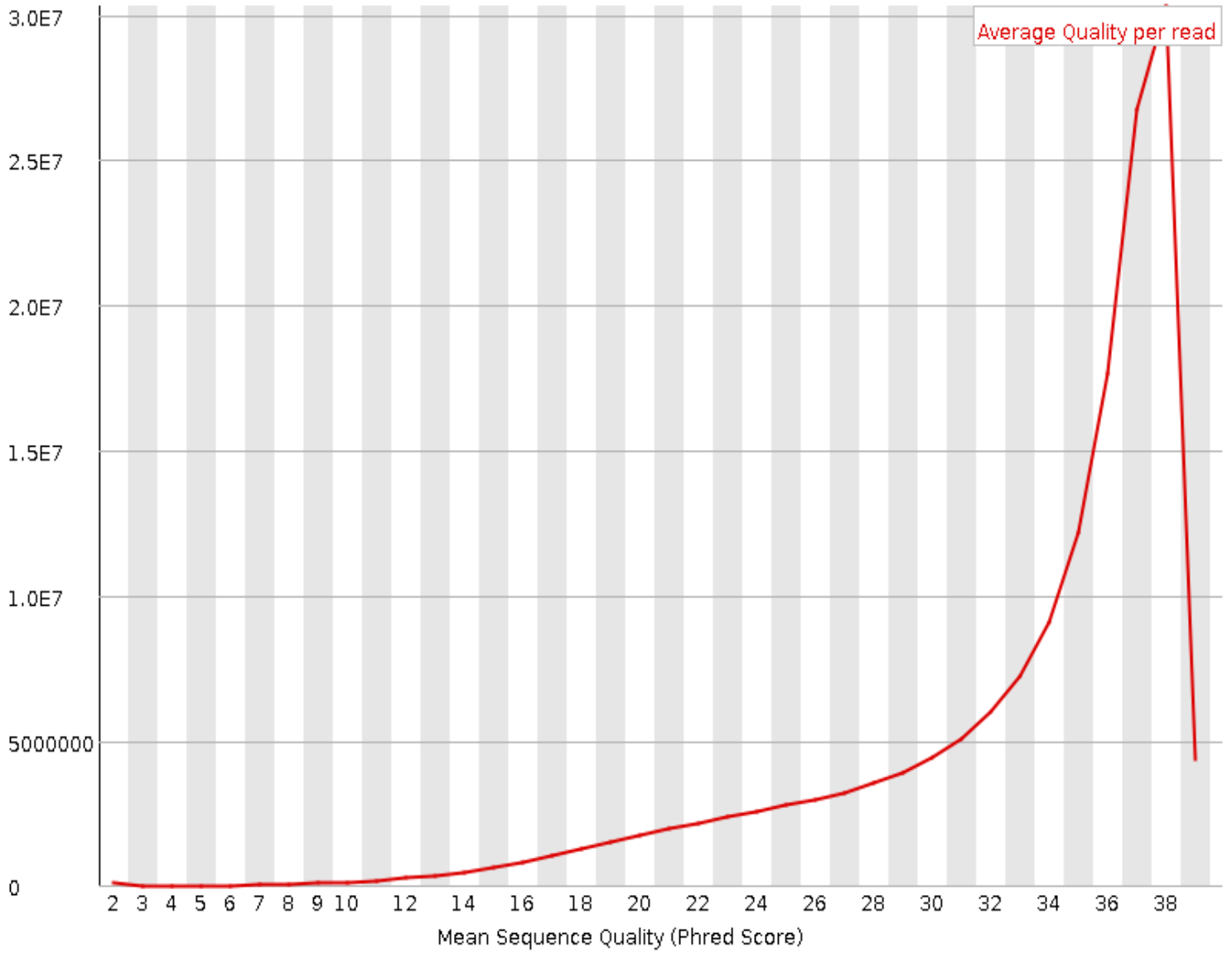
**! Per tile sequence quality**

Quality per tile



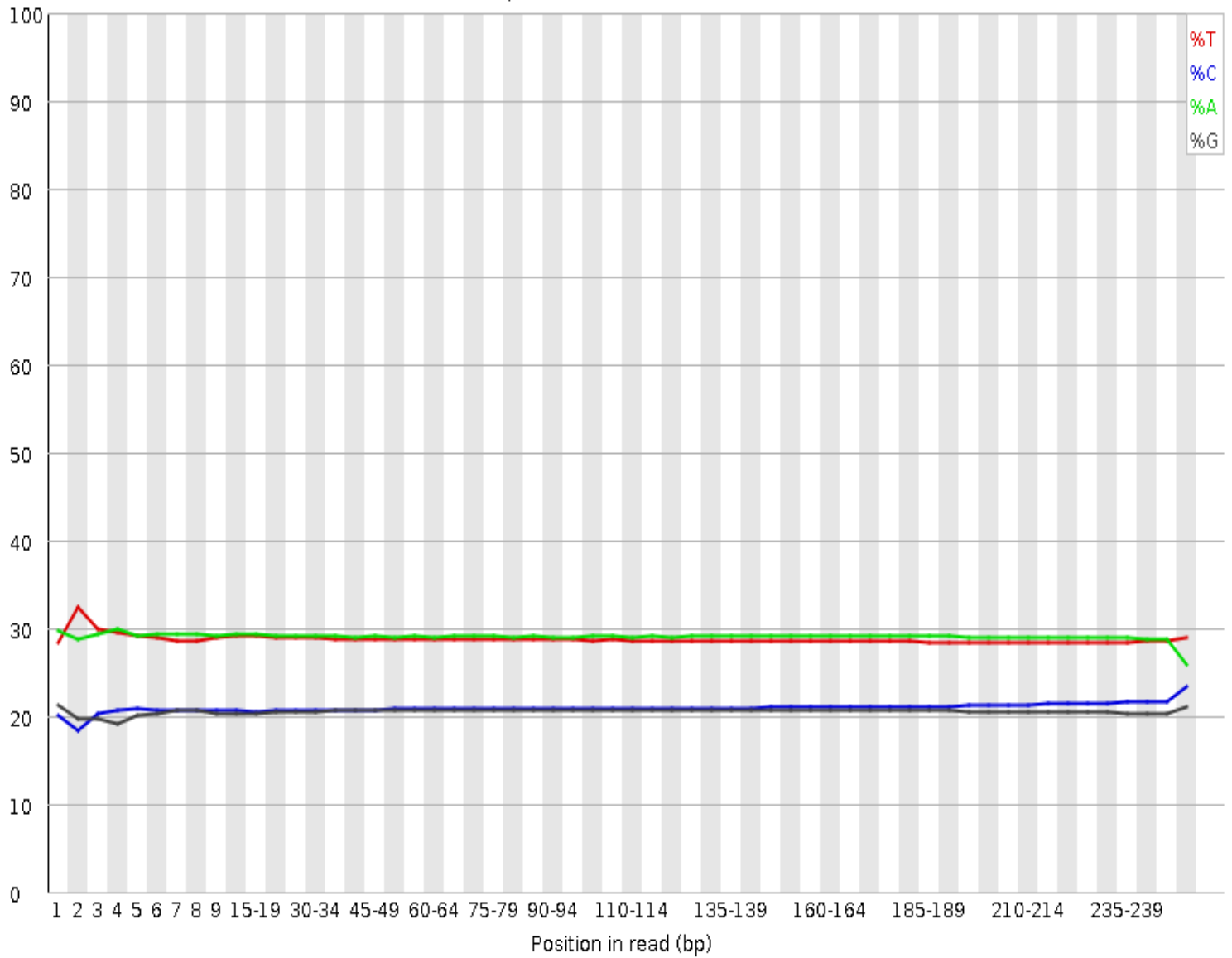
 **Per sequence quality scores**

Quality score distribution over all sequences

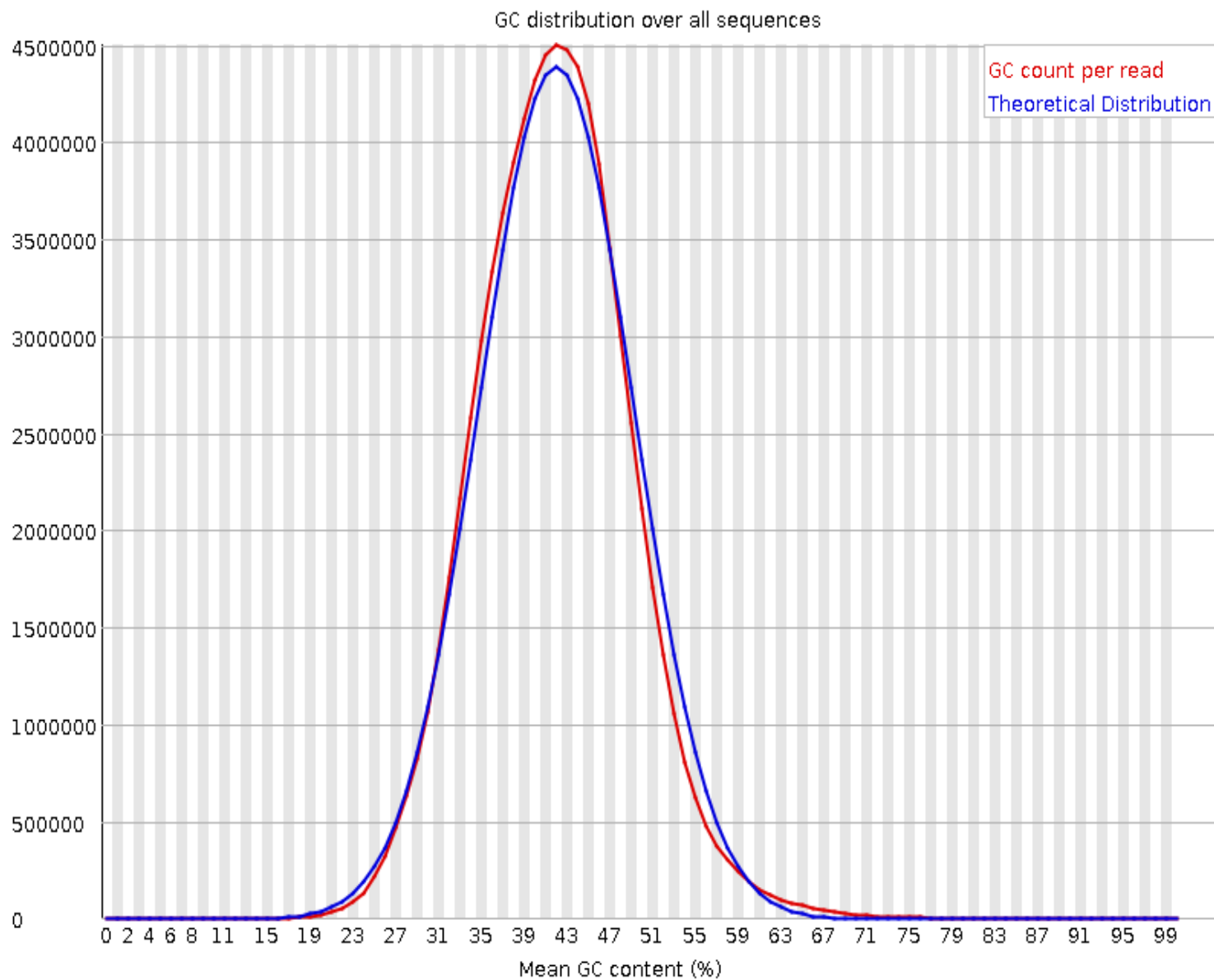


**! Per base sequence content**

Sequence content across all bases

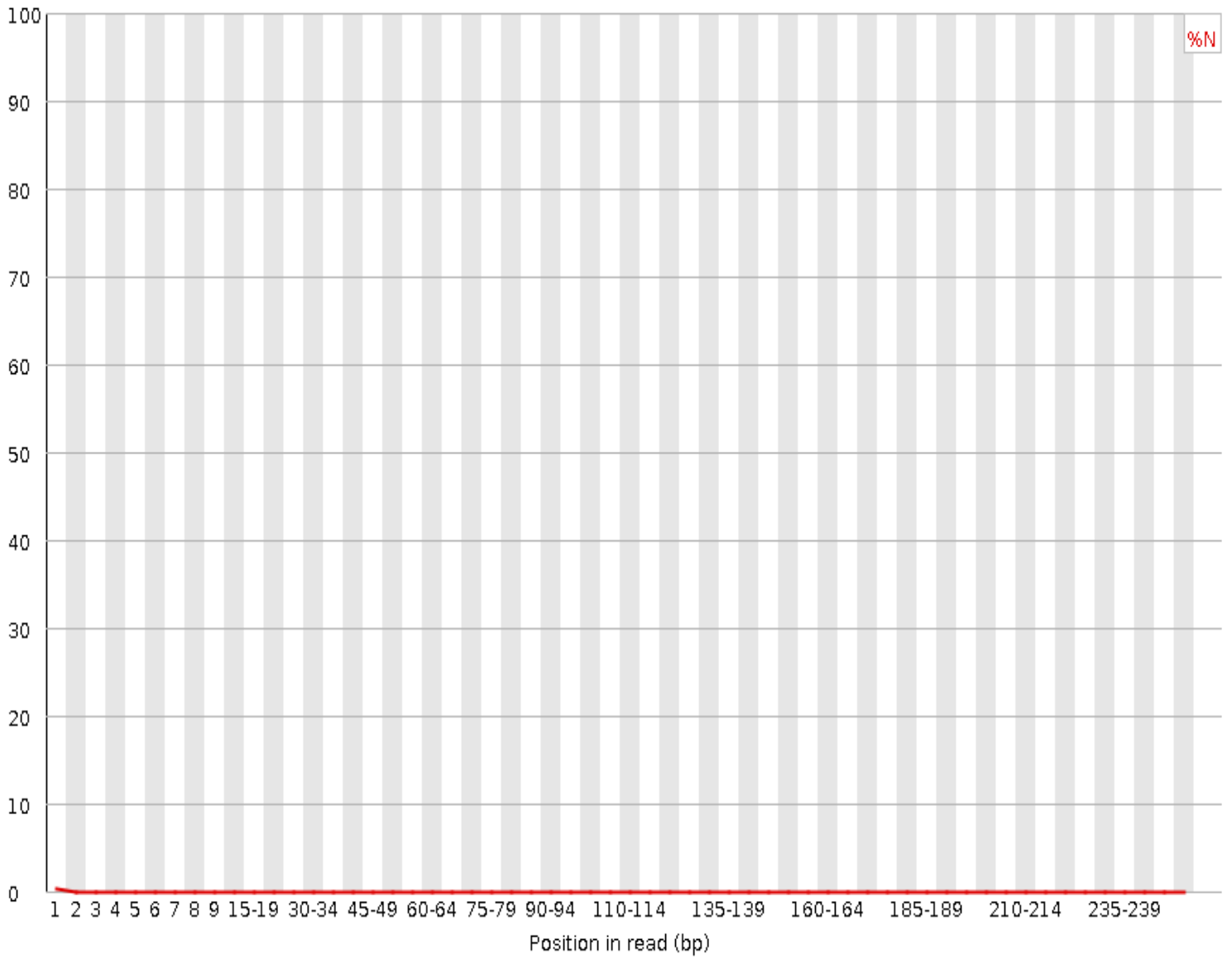


 **Per sequence GC content**



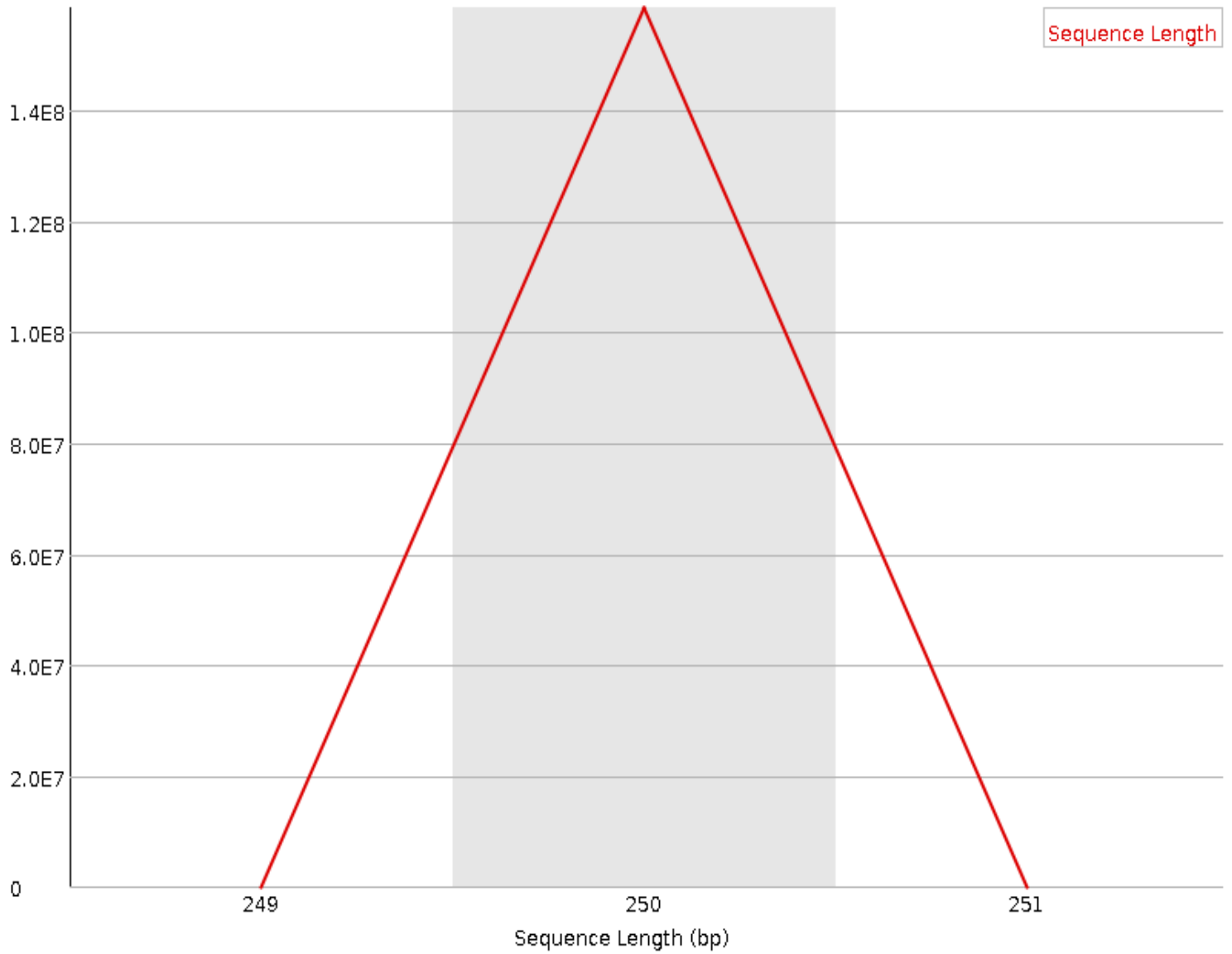
 **Per base N content**

N content across all bases



 **Sequence Length Distribution**

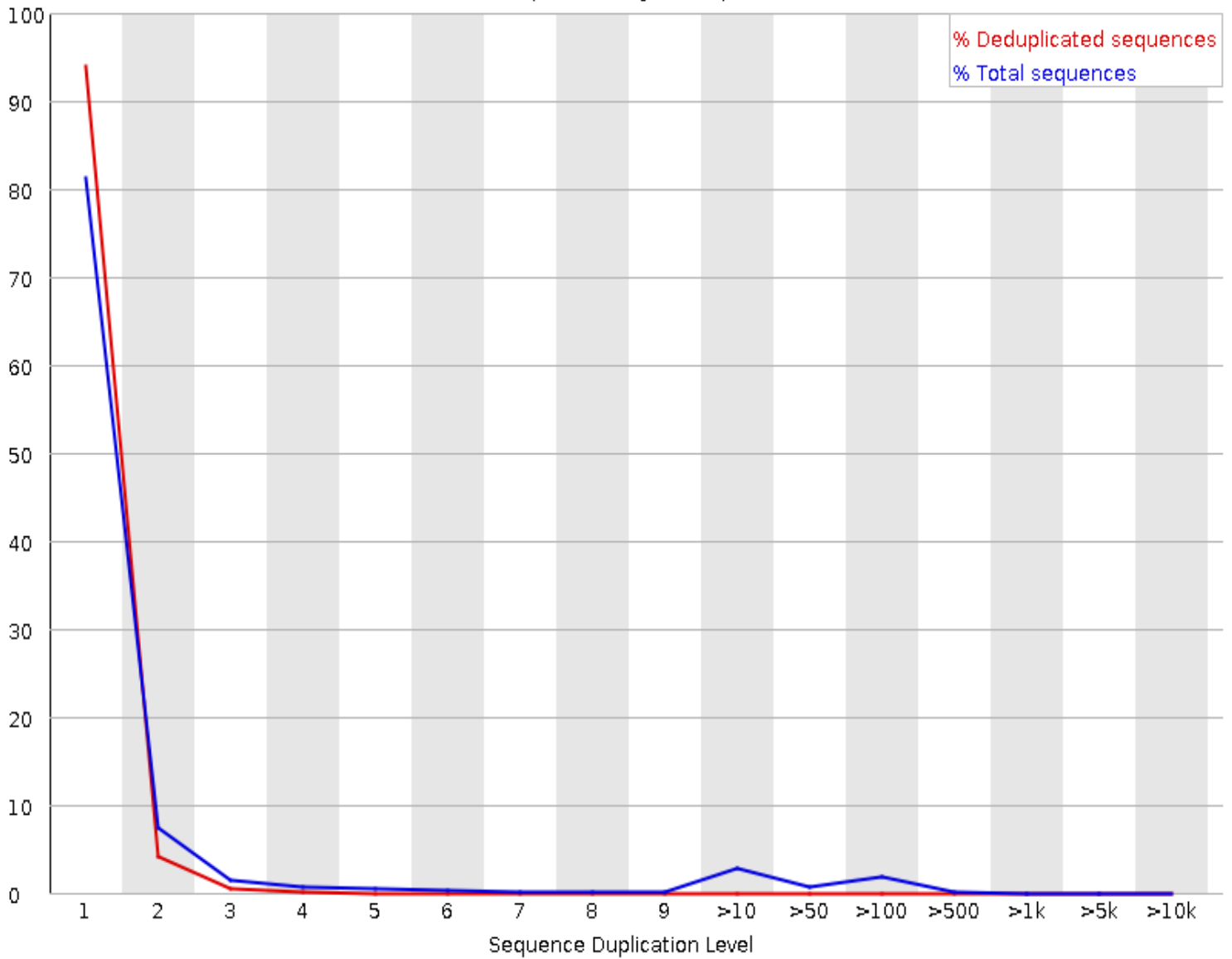
Distribution of sequence lengths over all sequences



## Sequence Duplication Levels



Percent of seqs remaining if deduplicated 86.49%

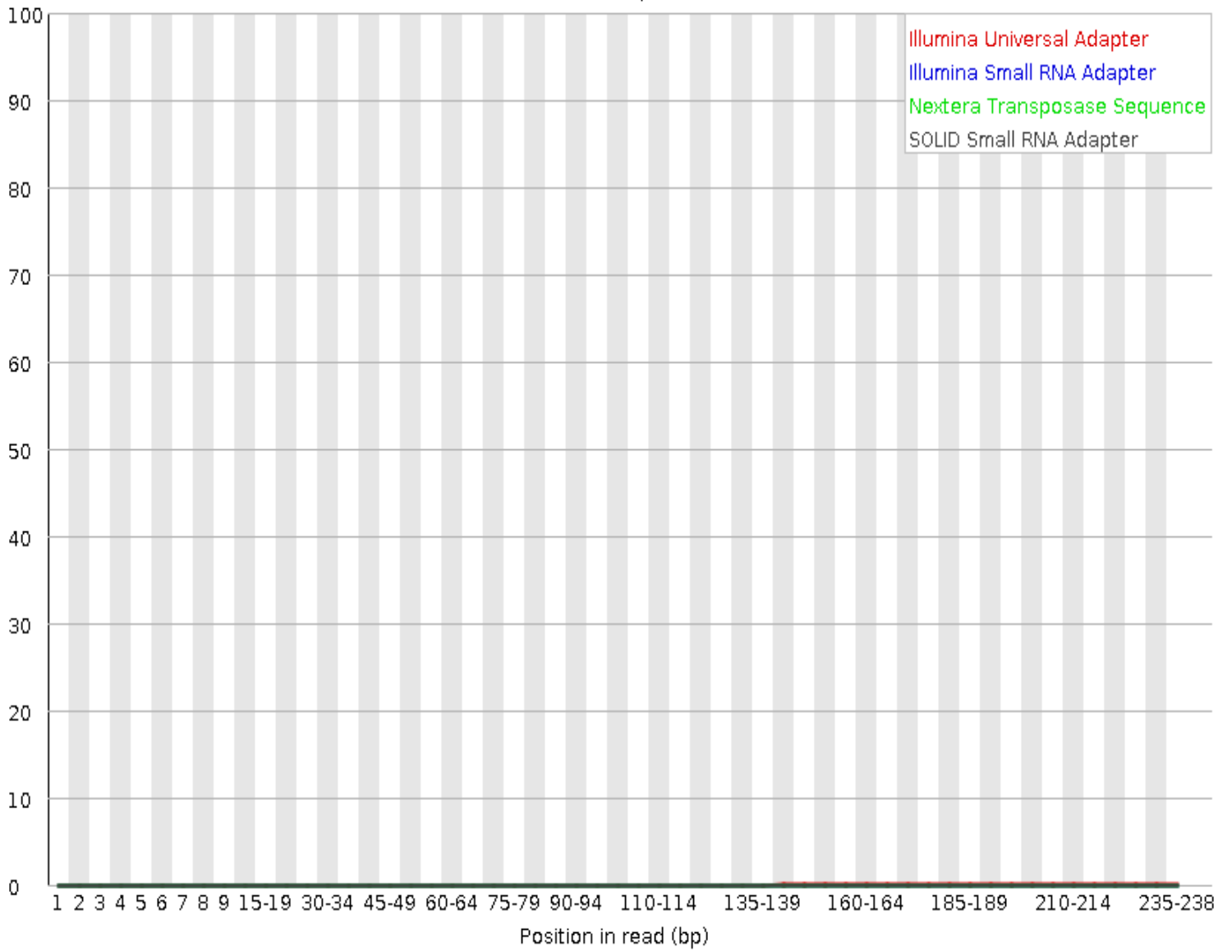


 **Overrepresented sequences**

No overrepresented sequences

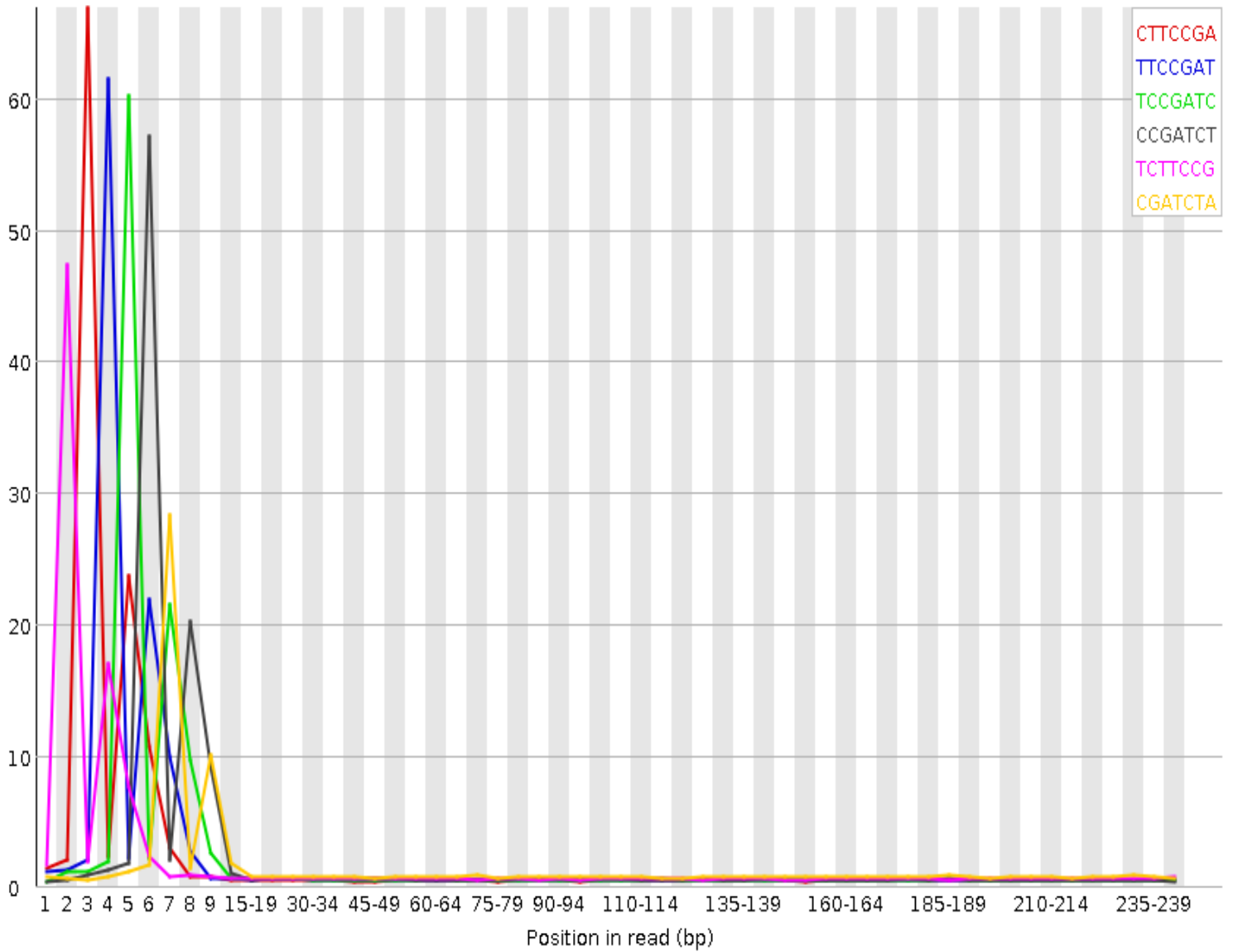
 **Adapter Content**

% Adapter



## Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCGA	144305	0.0	66.864975	3
TTCCGAT	156690	0.0	61.587643	4
TCCGATC	160100	0.0	60.283497	5
CCGATCT	168640	0.0	57.136715	6
TCTCCG	204560	0.0	47.443493	2
CGATCTA	103710	0.0	28.300514	7
TCGGAAG	133620	0.0	24.76722	4
ATCGGAA	146830	0.0	22.538961	3
GATCGGA	149545	0.0	22.203152	2
CGATCTT	131790	0.0	21.530432	7
AGATCGG	160140	0.0	20.752117	1

CTCTTCC	483950	0.0	20.583025	1
CGGAAGA	192485	0.0	17.383053	5
ACGCTCT	97715	0.0	15.550094	1
CAAGTCG	111095	0.0	14.488328	5
GCTCTTC	252895	0.0	14.151637	2
CGATCTC	152420	0.0	13.568216	7
CGATCTG	174220	0.0	12.703326	7
GTCGTCA	134145	0.0	12.135163	8
GAAGAGC	287310	0.0	12.015116	7

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