













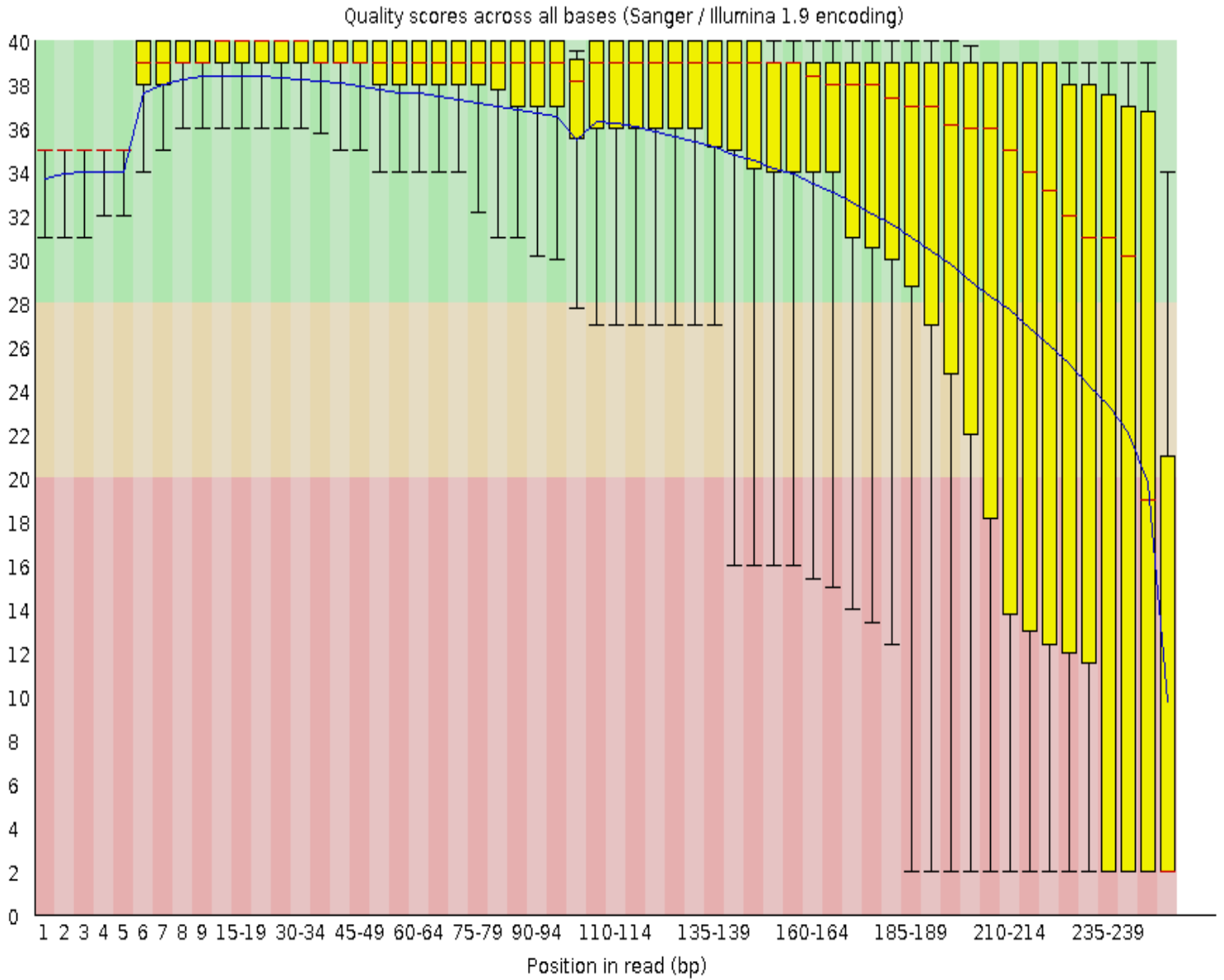
## Summary

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## Basic Statistics

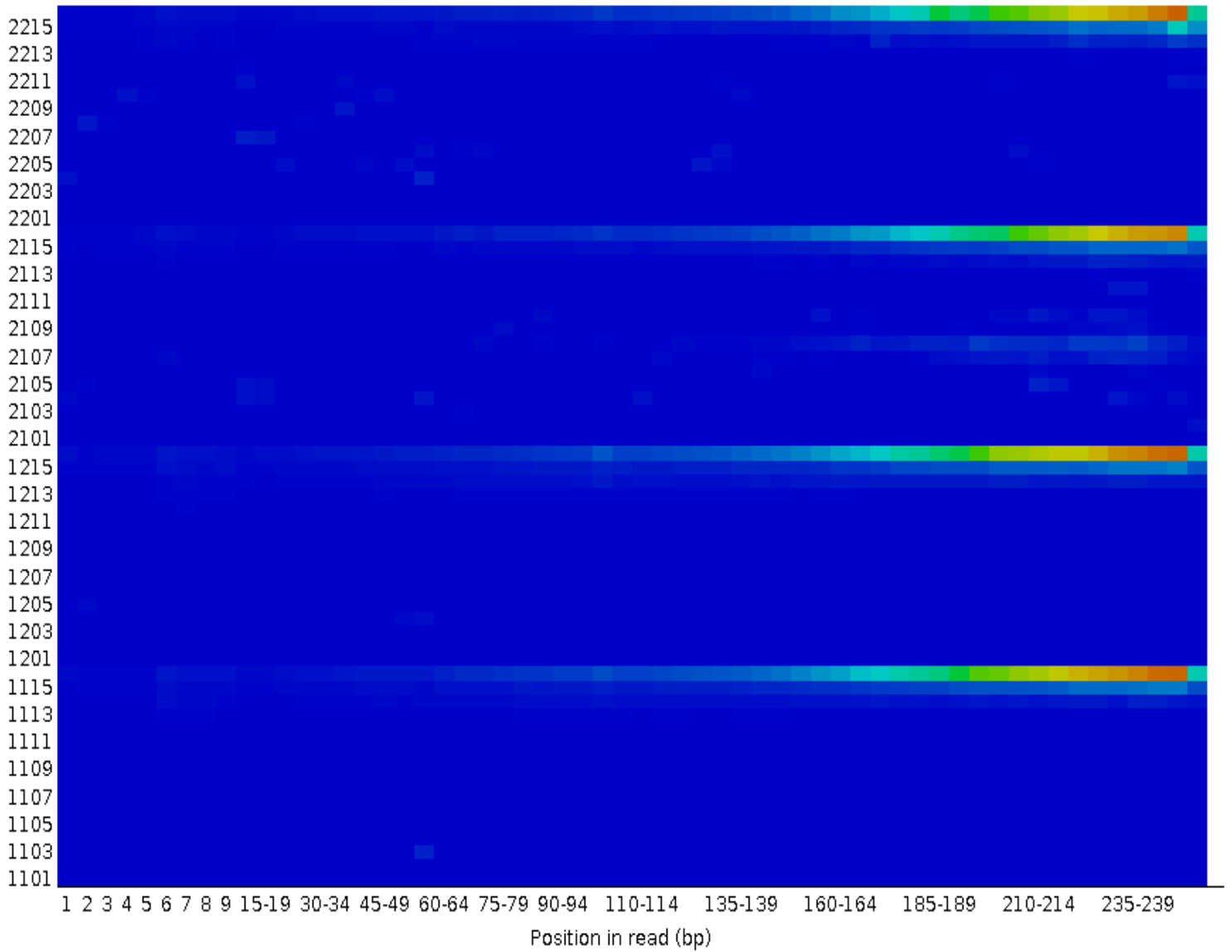
Measure	Value
Filename	UCSF_BS-MK_CATCCGG_R1_trimmed.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	157363331
Sequences flagged as poor quality	0
Sequence length	30-250
%GC	41

## Per base sequence quality



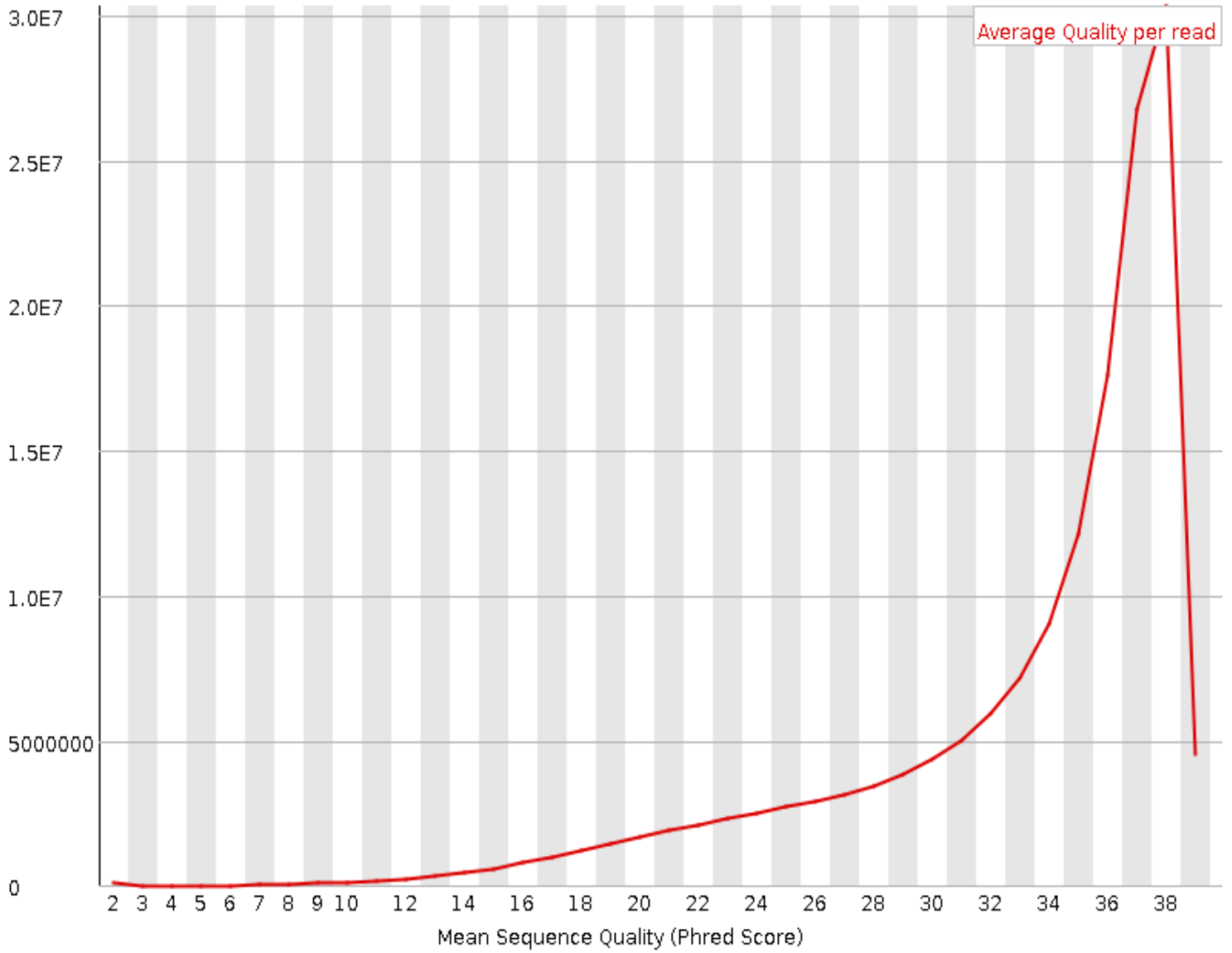
**! Per tile sequence quality**

Quality per tile



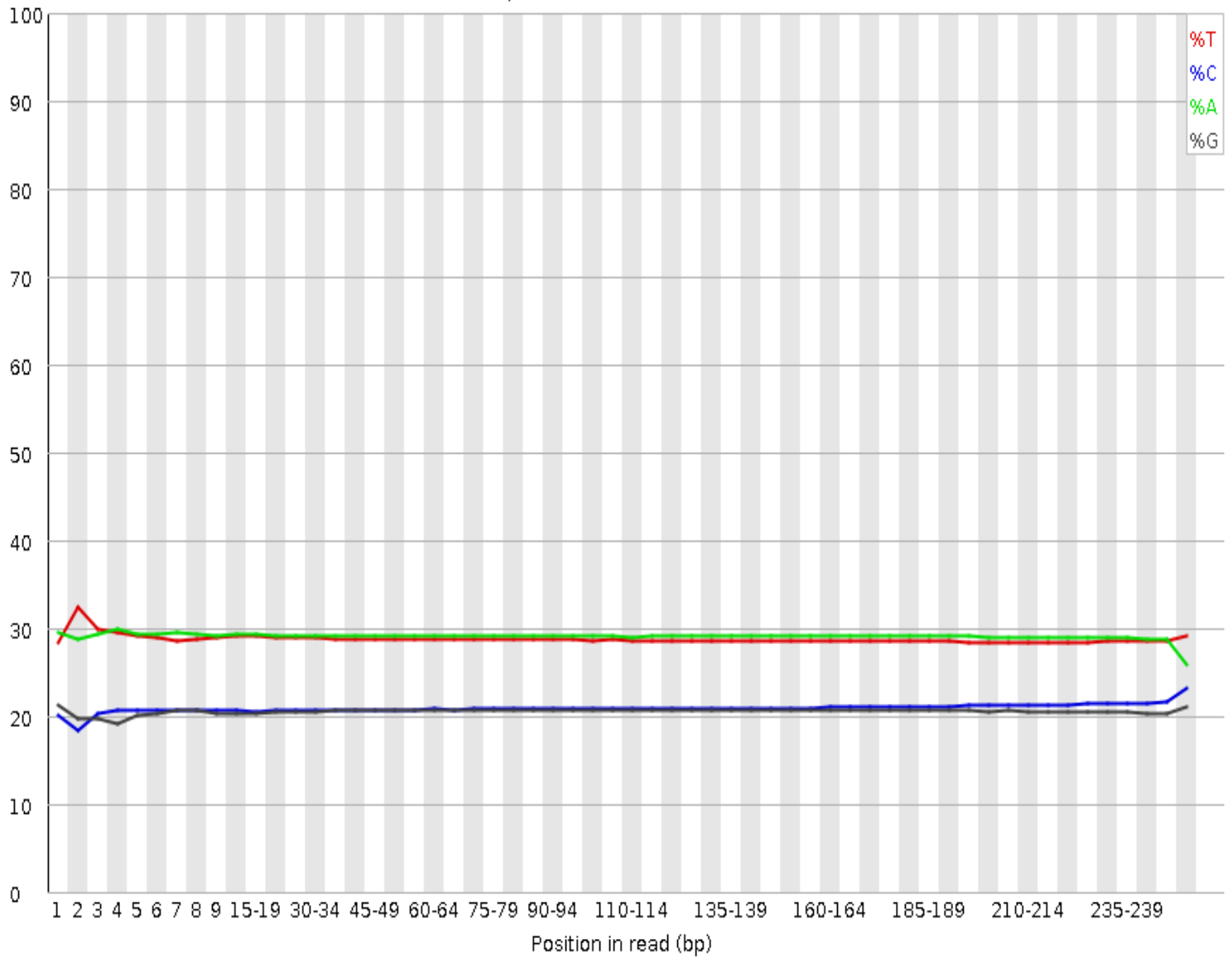
 **Per sequence quality scores**

Quality score distribution over all sequences



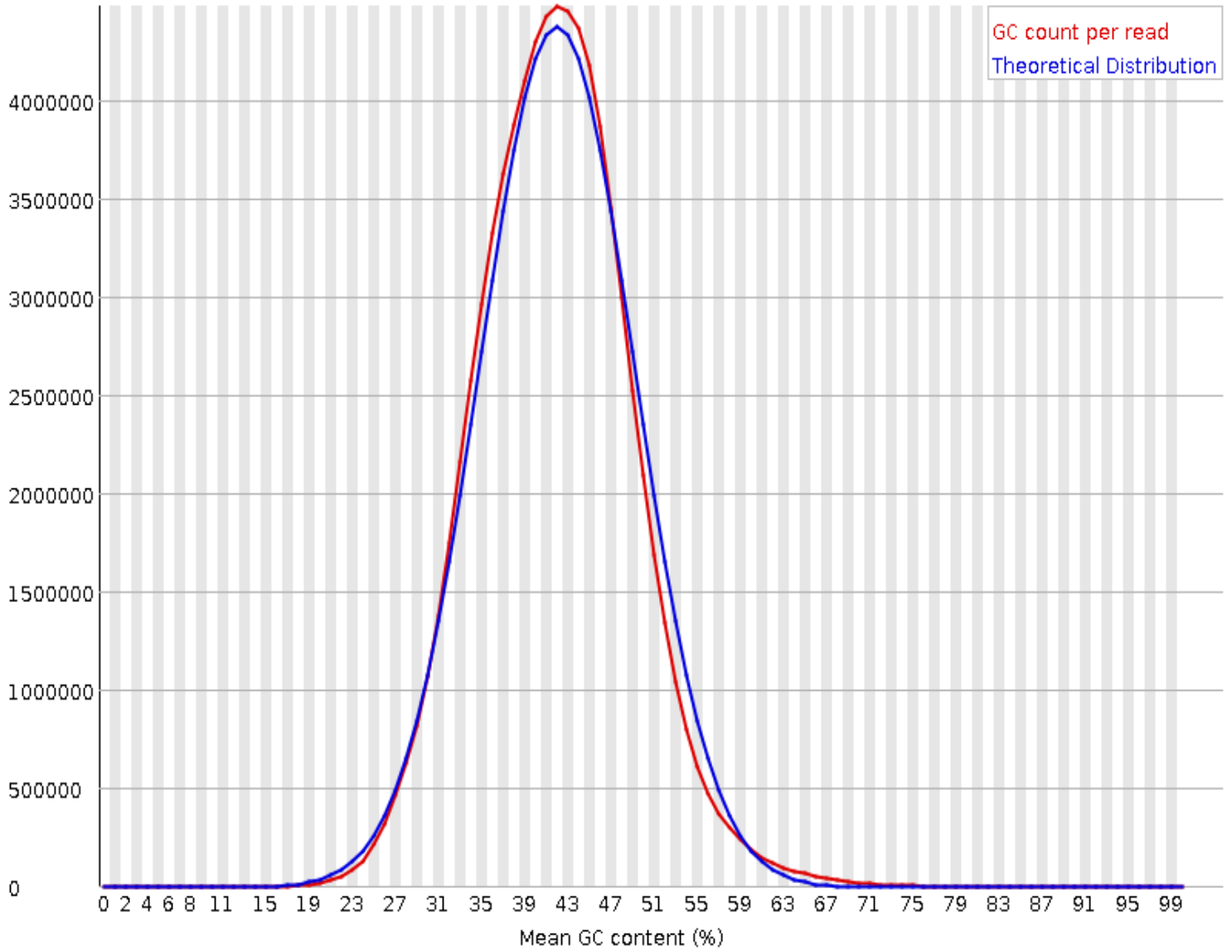
 **Per base sequence content**

Sequence content across all bases



 **Per sequence GC content**

GC distribution over all sequences



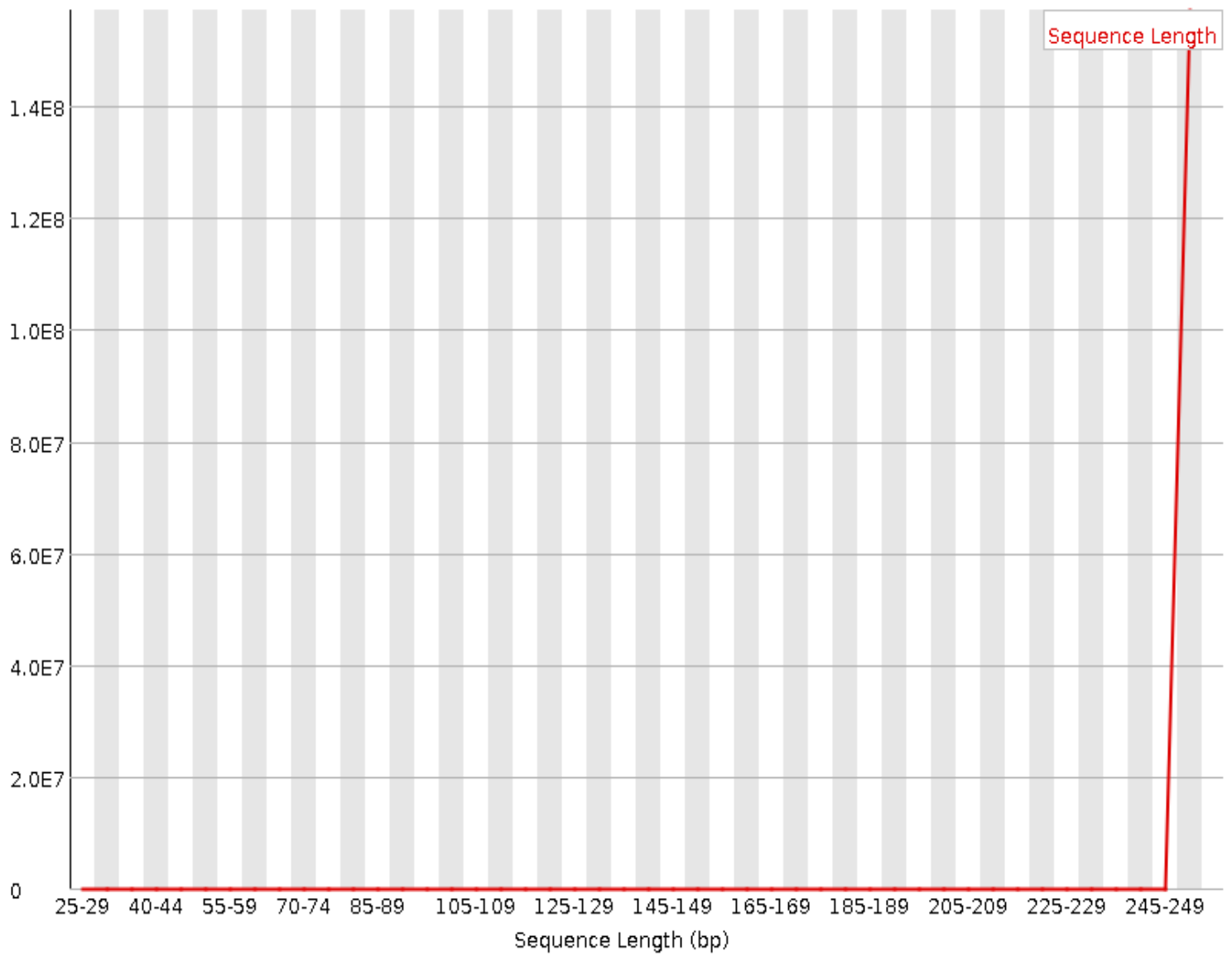
 **Per base N content**

N content across all bases



## Sequence Length Distribution

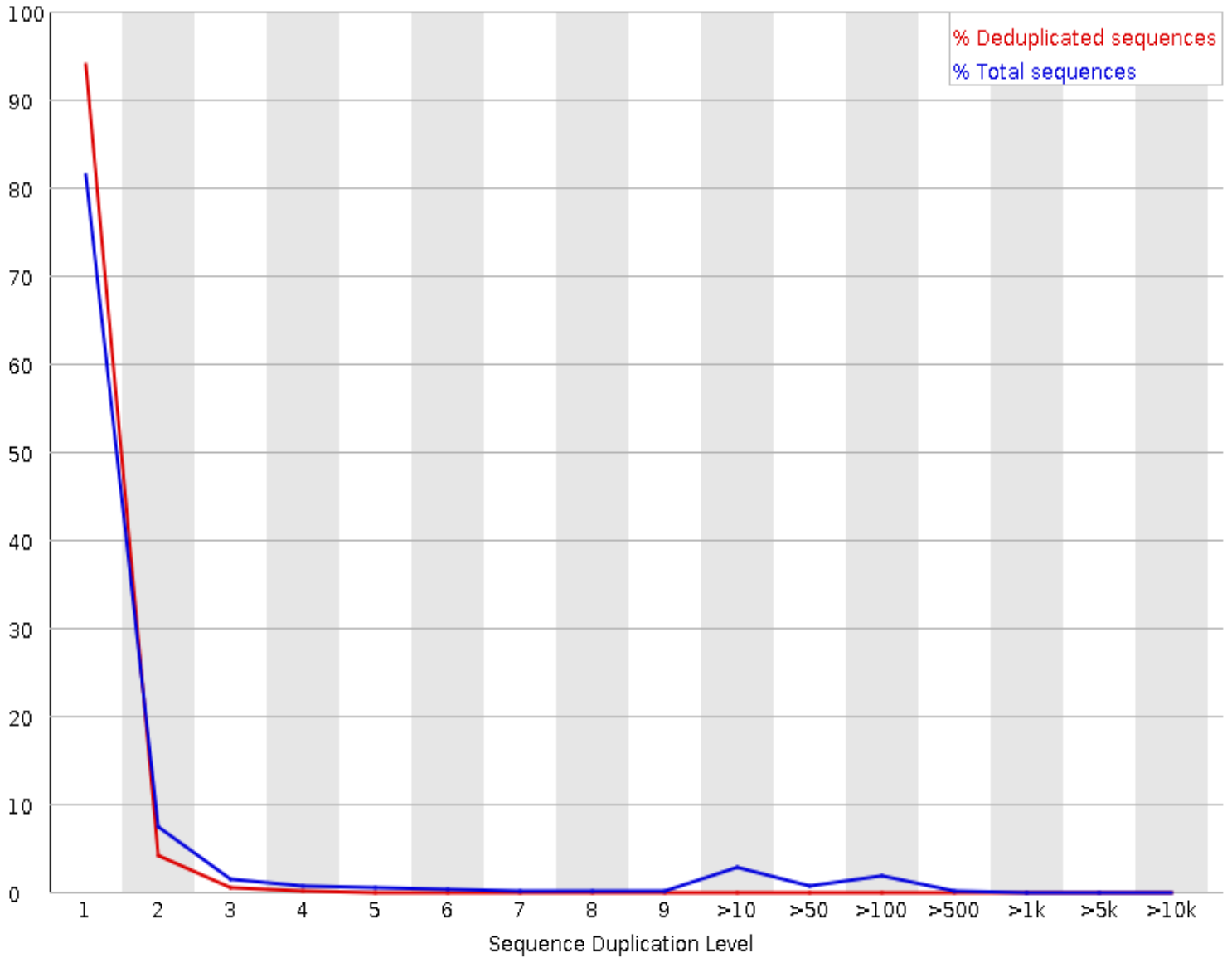
Distribution of sequence lengths over all sequences



## Sequence Duplication Levels



Percent of seqs remaining if deduplicated 86.59%

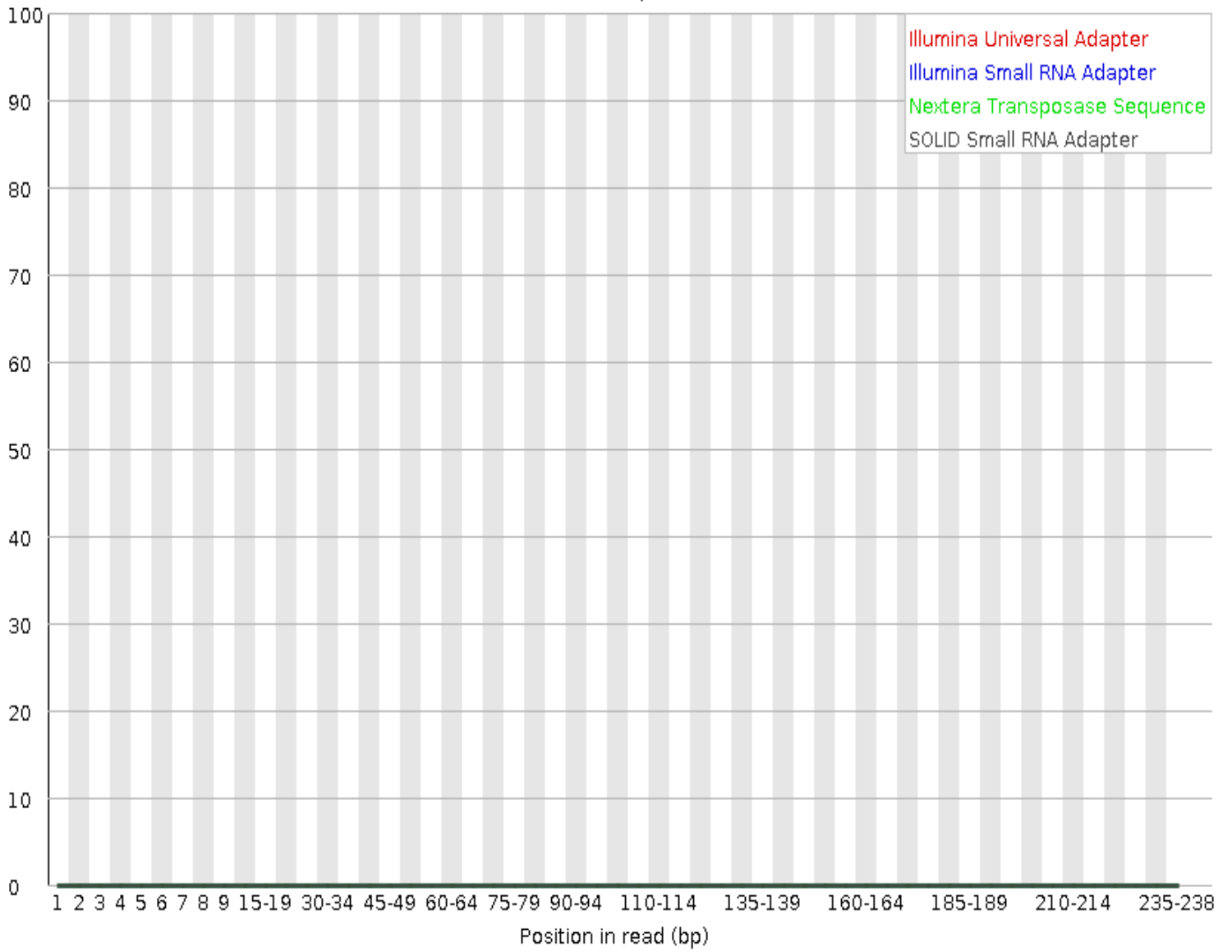


 **Overrepresented sequences**

No overrepresented sequences

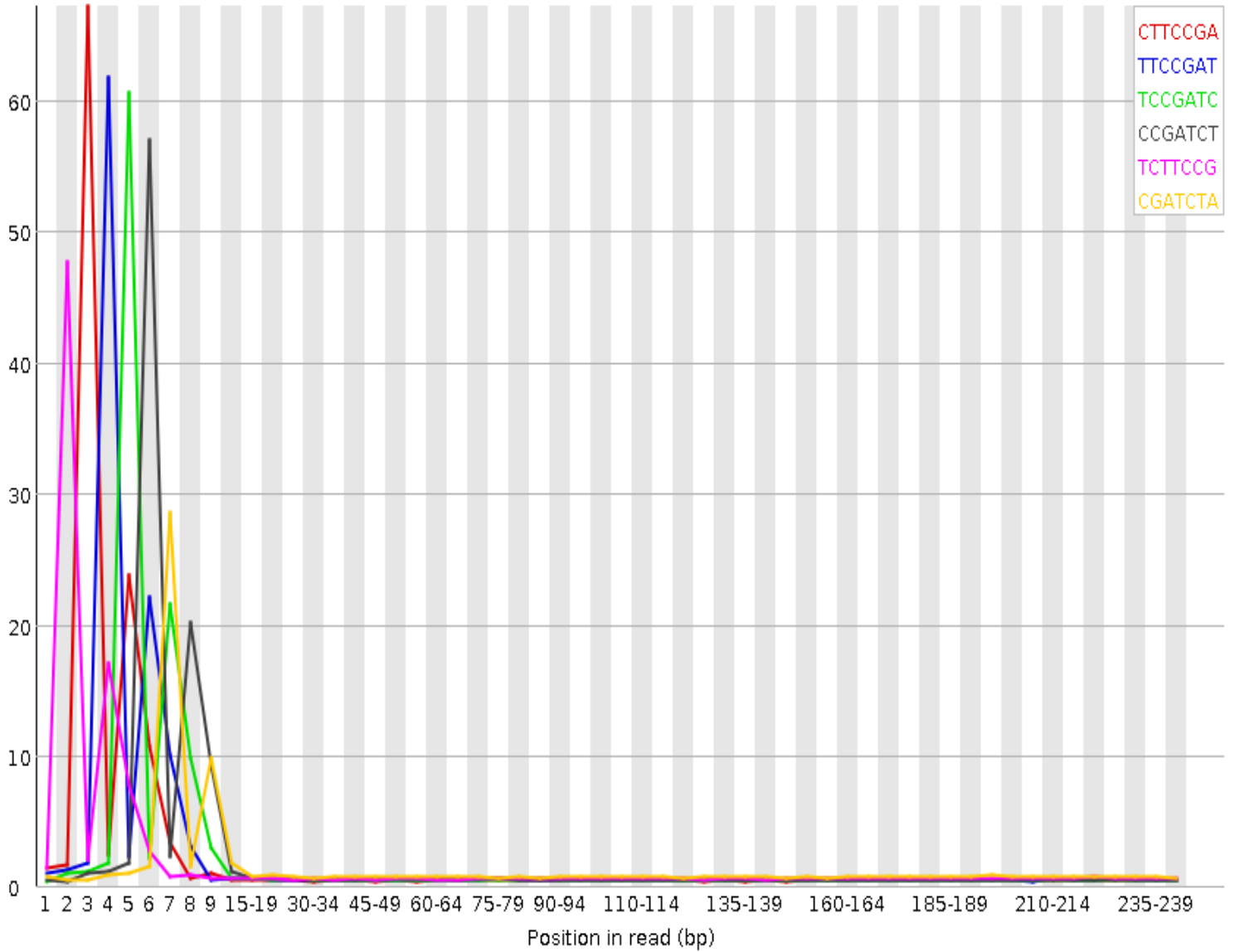
 **Adapter Content**

% Adapter



## Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCGGA	143335	0.0	67.14851	3
TTCCGAT	155890	0.0	61.73272	4
TCCGATC	159055	0.0	60.634537	5
CCGATCT	168920	0.0	57.035748	6
TCTTCCG	203520	0.0	47.668472	2
CGATCTA	102625	0.0	28.574884	7
CGATCTT	131365	0.0	21.340202	7
CTCTTCC	478450	0.0	20.850239	1
TCGGAAG	87075	0.0	19.672222	4
ATCGGAA	100820	0.0	17.23195	3
GATCGGA	104015	0.0	16.690928	2

ACGCTCT	97285	0.0	15.55497	1
AGATCGG	113180	0.0	15.209403	1
GCTCTTC	250850	0.0	14.138055	2
CGATCTC	151250	0.0	13.669355	7
CAAGTCG	106330	0.0	12.844328	5
CGATCTG	171085	0.0	12.604421	7
CGGAAGA	146760	0.0	12.0371	5
CGCTCTT	130435	0.0	11.993127	2
AAGTCGT	133315	0.0	10.482044	6

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