






Summary

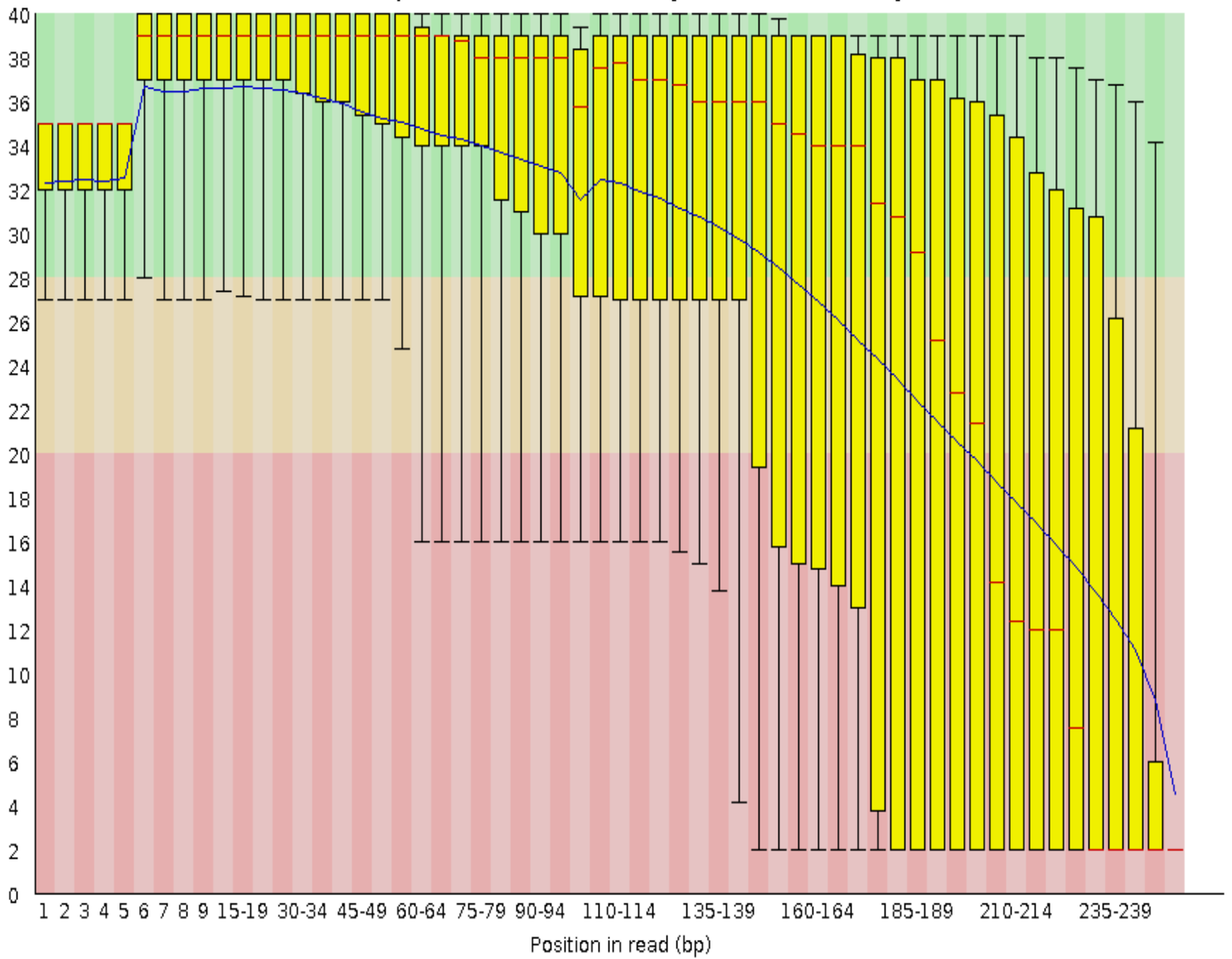
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Basic Statistics

Measure	Value
Filename	UCSF_BS-MK_CATCCGG_R2_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	42

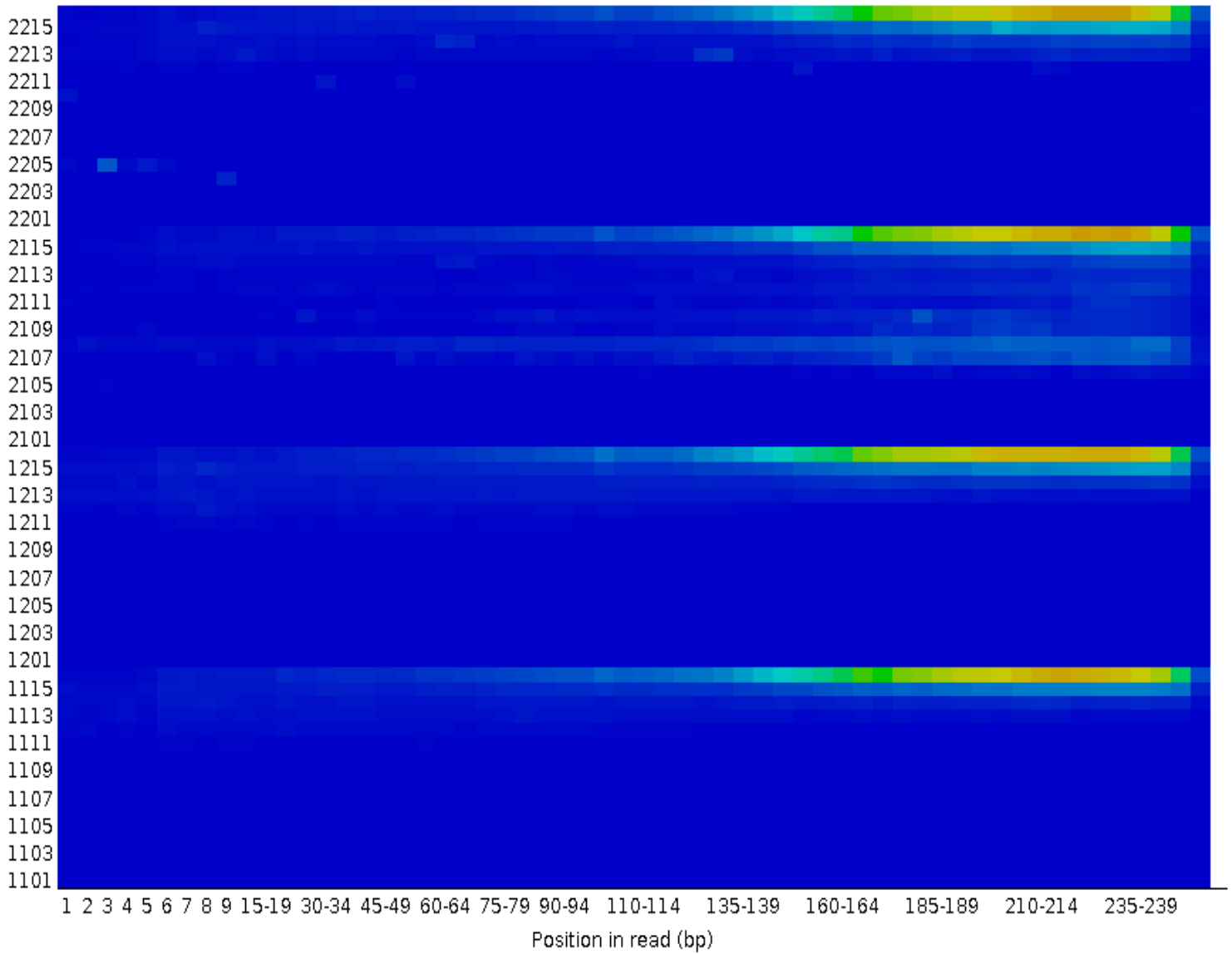
Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)



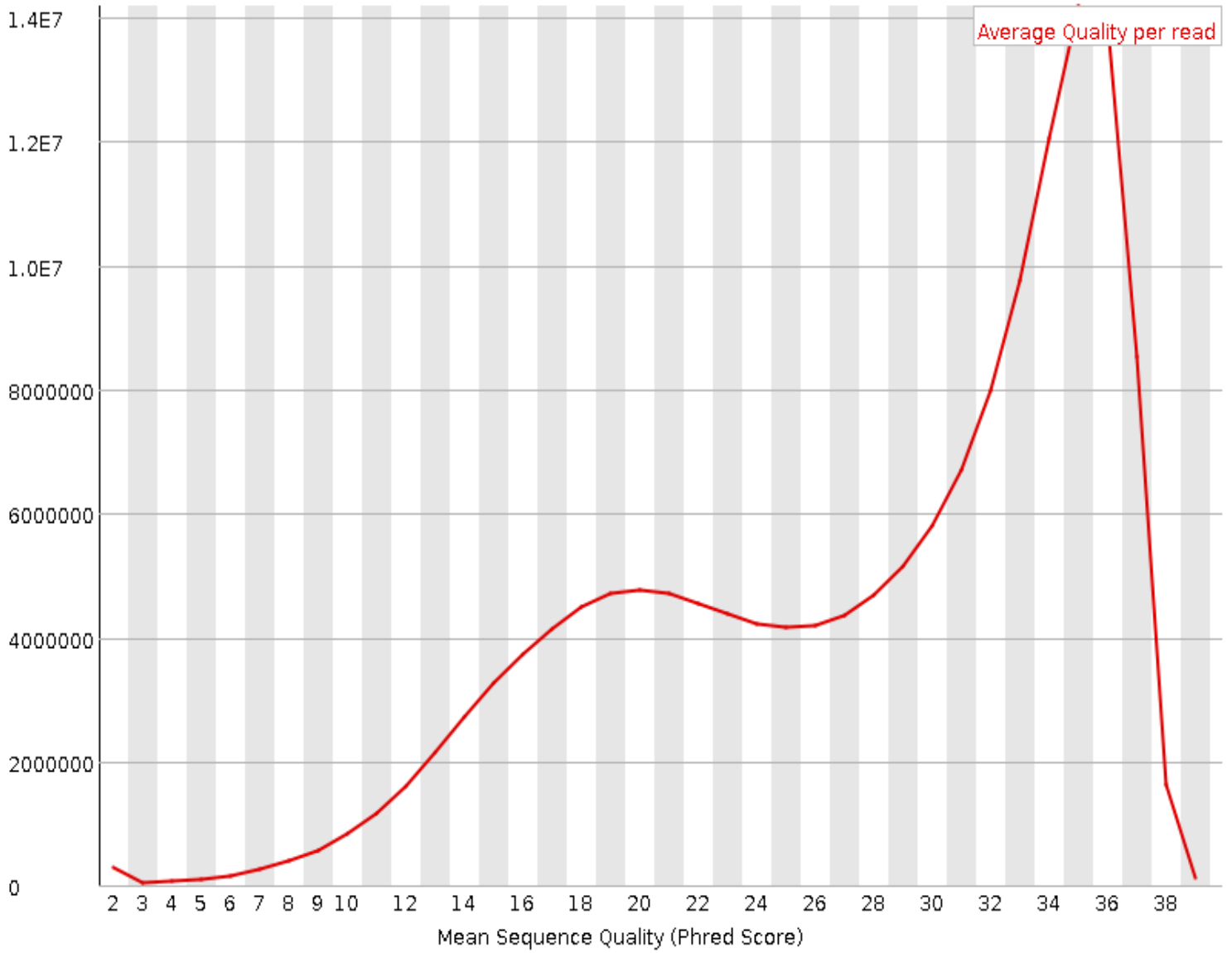
! Per tile sequence quality

Quality per tile



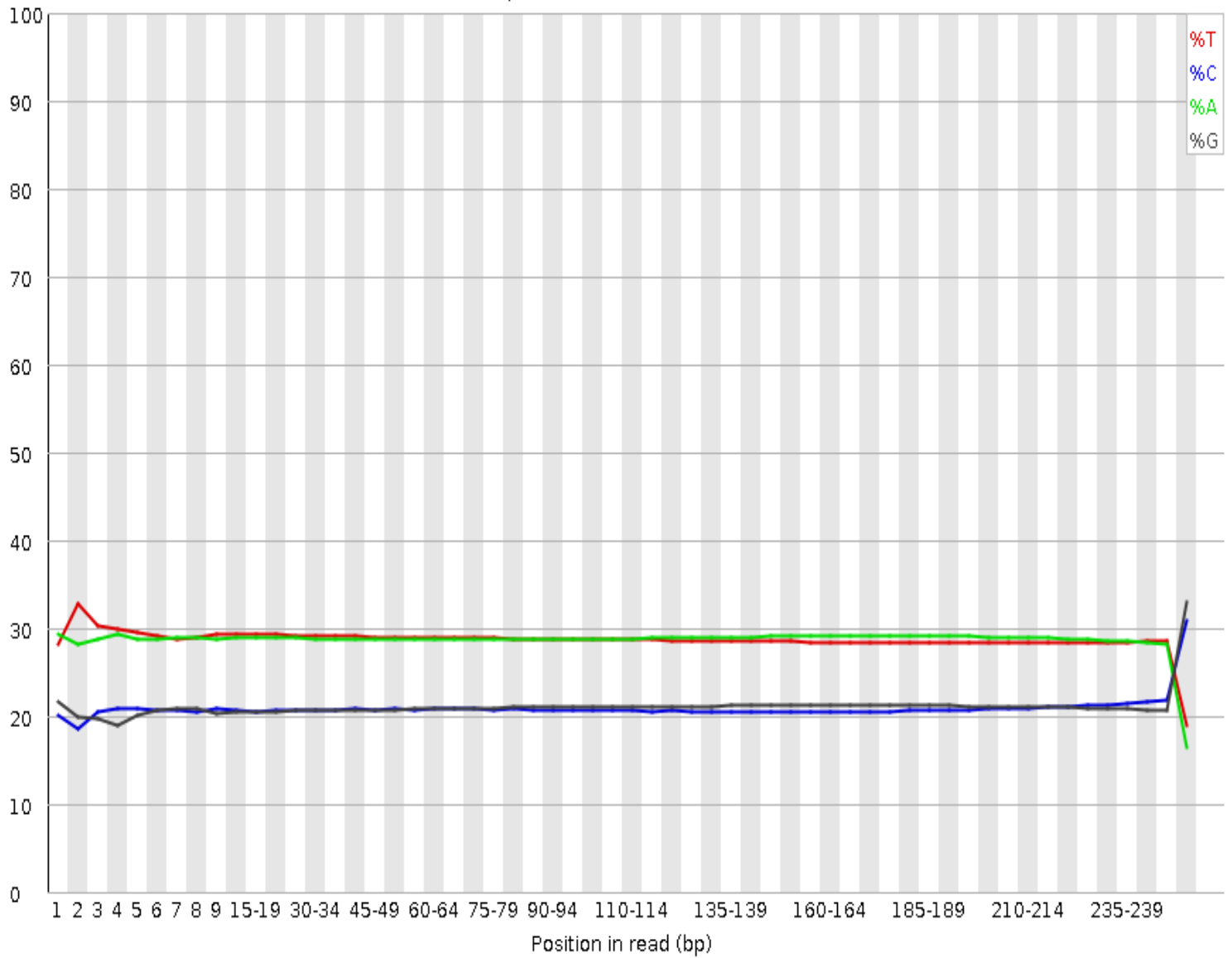
 **Per sequence quality scores**

Quality score distribution over all sequences



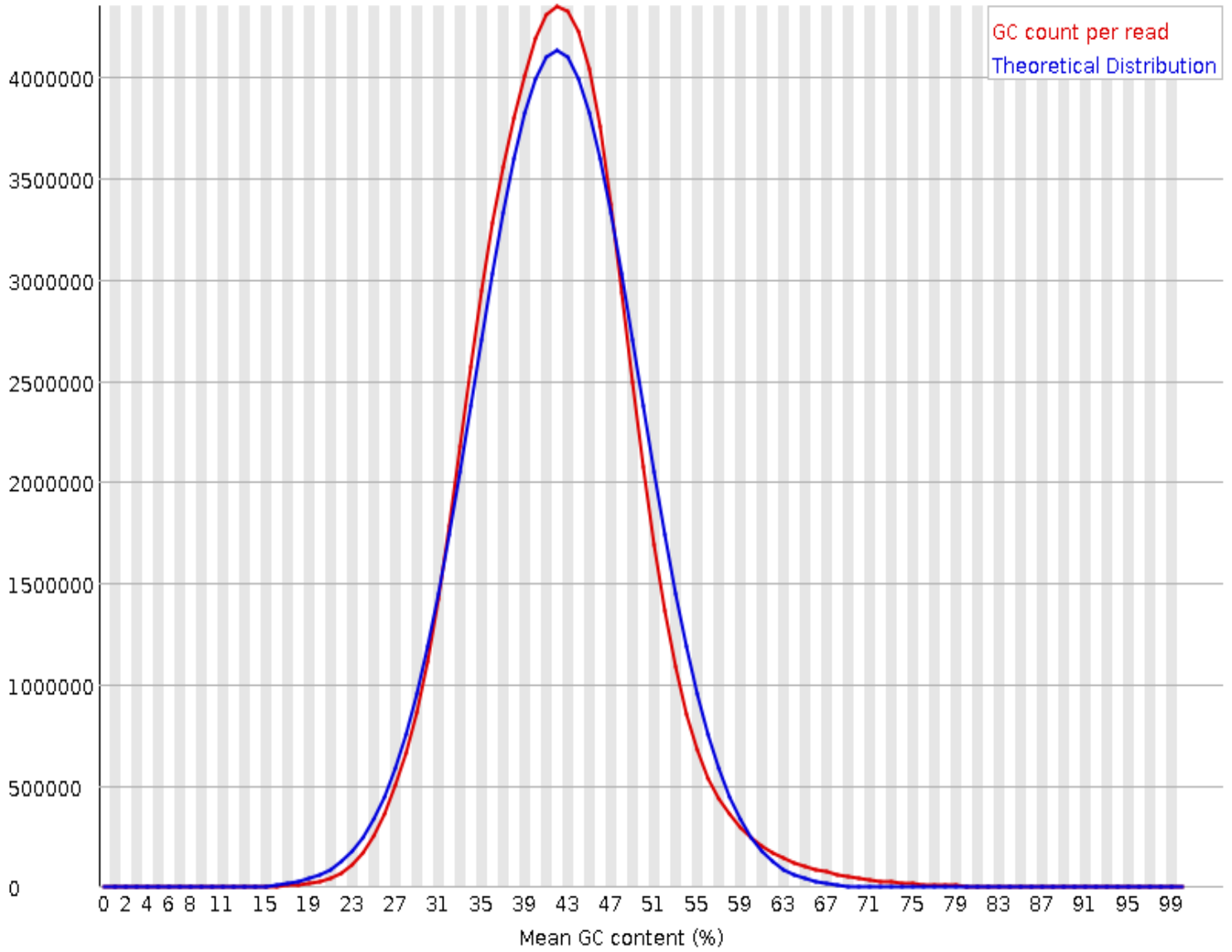
 **Per base sequence content**

Sequence content across all bases



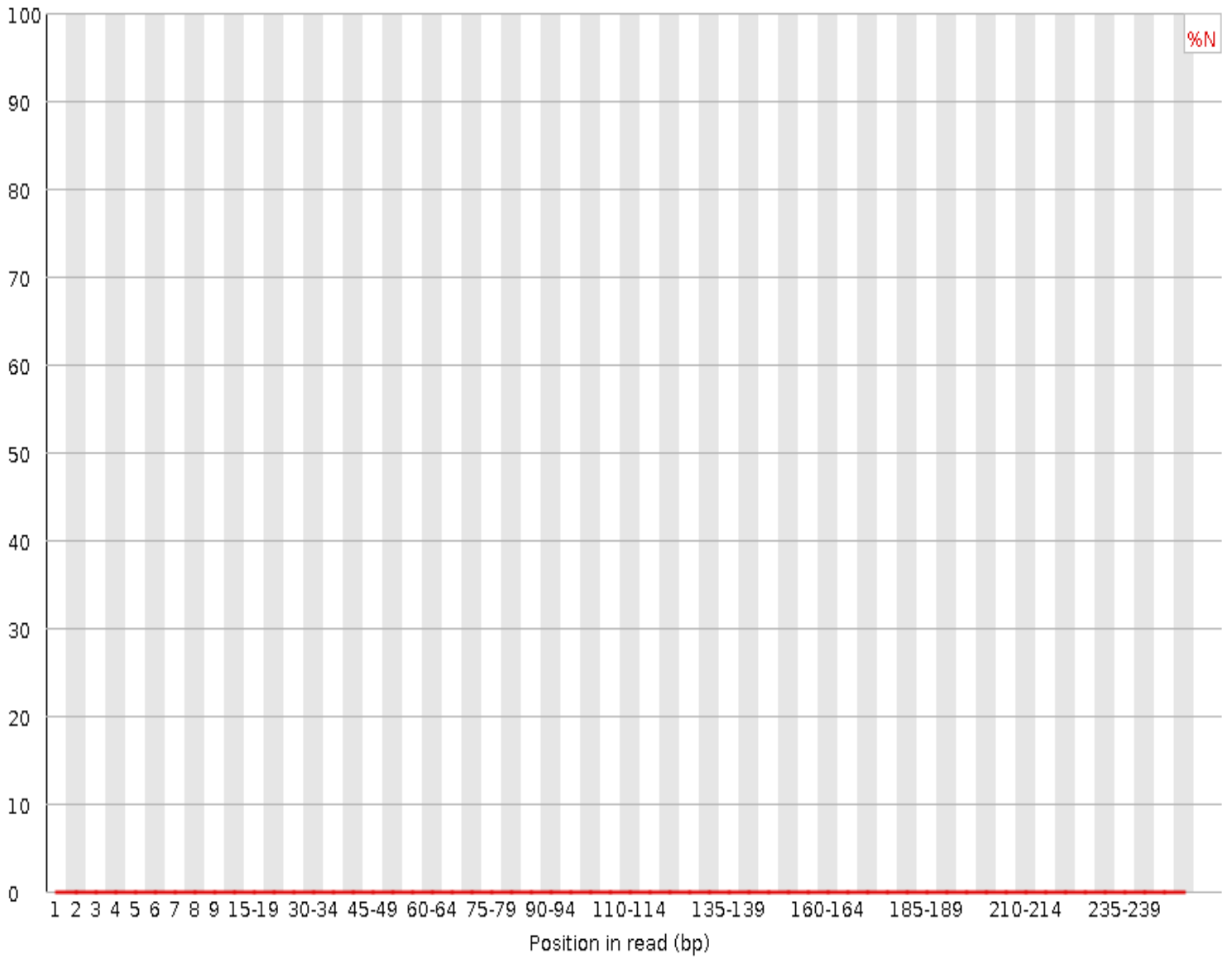
 **Per sequence GC content**

GC distribution over all sequences



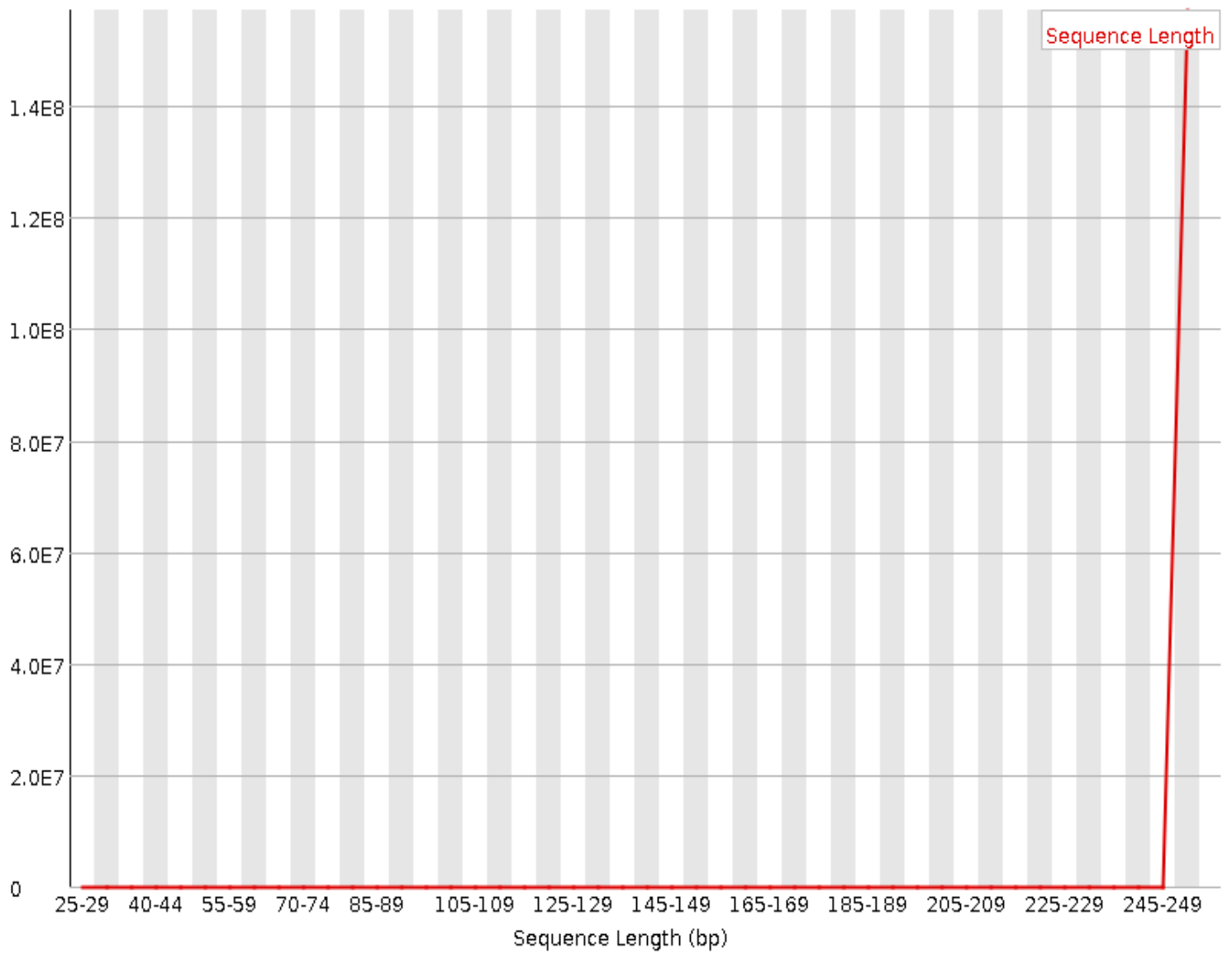
 **Per base N content**

N content across all bases



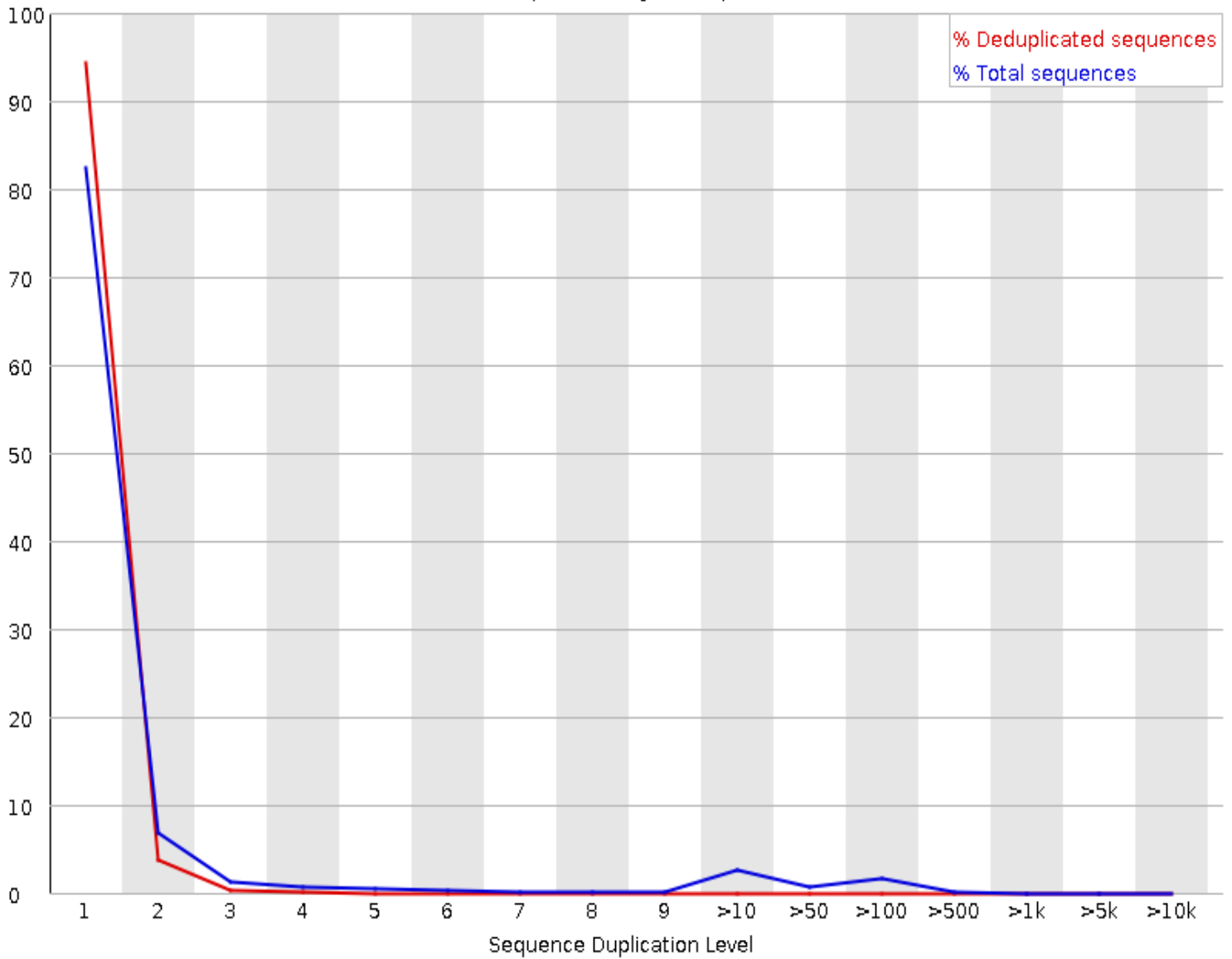
Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 87.37%

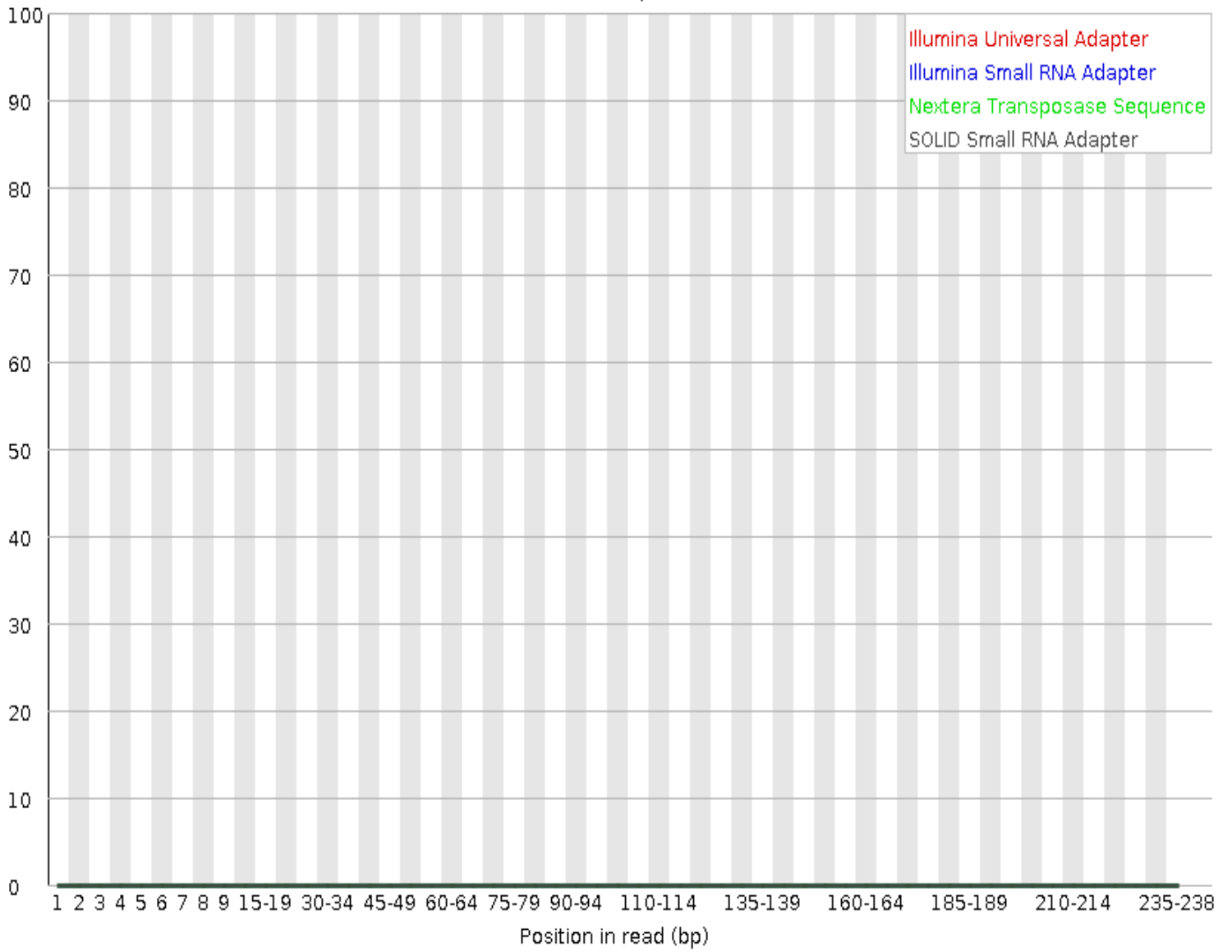


 **Overrepresented sequences**

No overrepresented sequences

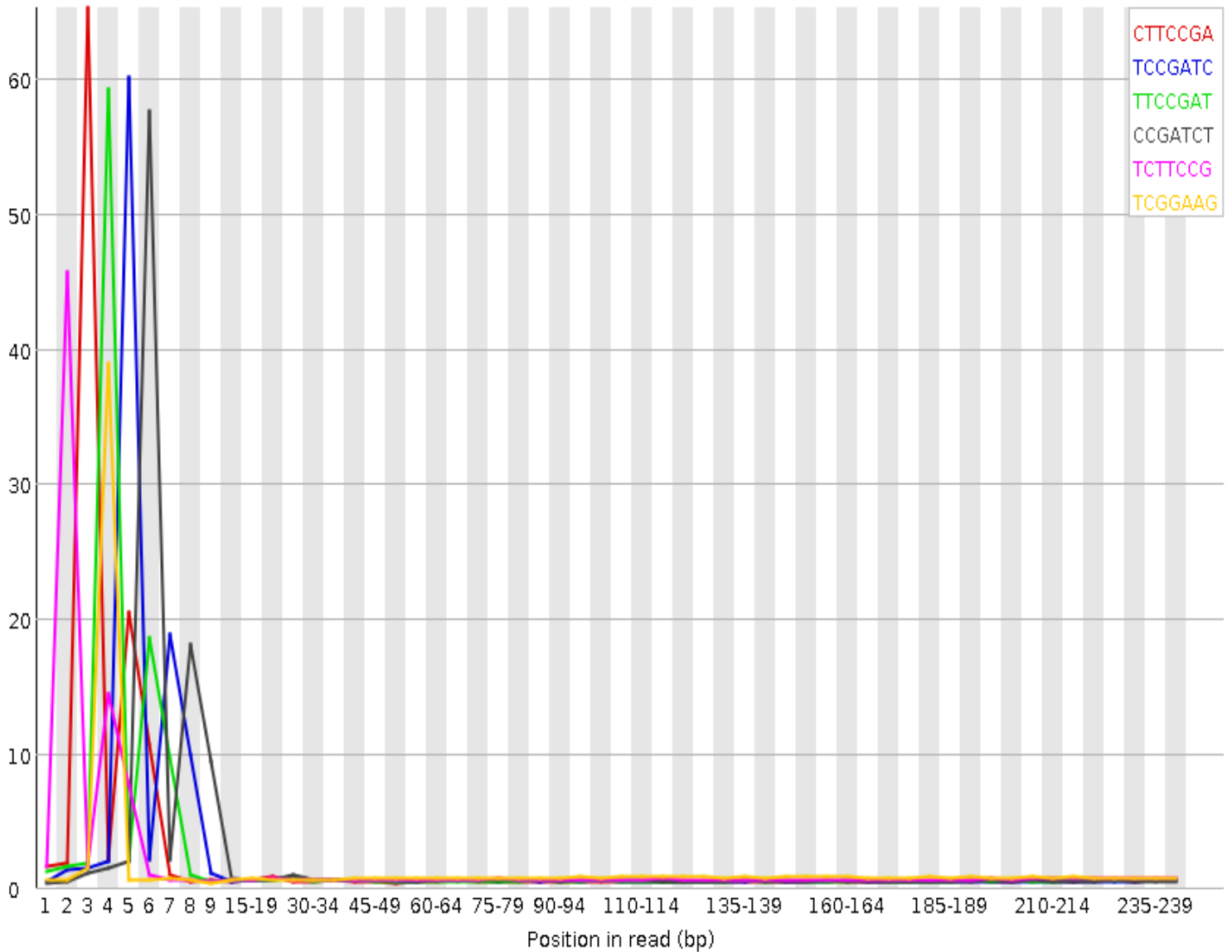
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	144430	0.0	65.26576	3
TCCGATC	155205	0.0	60.225315	5
TTCCGAT	157855	0.0	59.330116	4
CCGATCT	161885	0.0	57.634758	6
TCTTCCG	208255	0.0	45.715096	2
TCGGAAG	108480	0.0	38.992626	4
ATCGGAA	119080	0.0	35.572205	3
GATCGGA	119925	0.0	35.21616	2
AGATCGG	131970	0.0	32.153973	1
CGATCTA	102435	0.0	28.540365	7
CGGAAGA	174835	0.0	24.605146	5

CTCTTCC	481065	0.0	20.40102	1
CGATCTT	134665	0.0	20.05223	7
GAAGAGC	262125	0.0	16.532045	7
ACGCTCT	99625	0.0	15.245987	1
CGATCTC	149365	0.0	13.514157	7
CGATCTG	166920	0.0	12.794332	7
CAAGTCG	109905	0.0	12.522157	5
GCTCTTC	252150	0.0	12.205367	2
CGCTCTT	135130	0.0	11.301803	2

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