













Summary

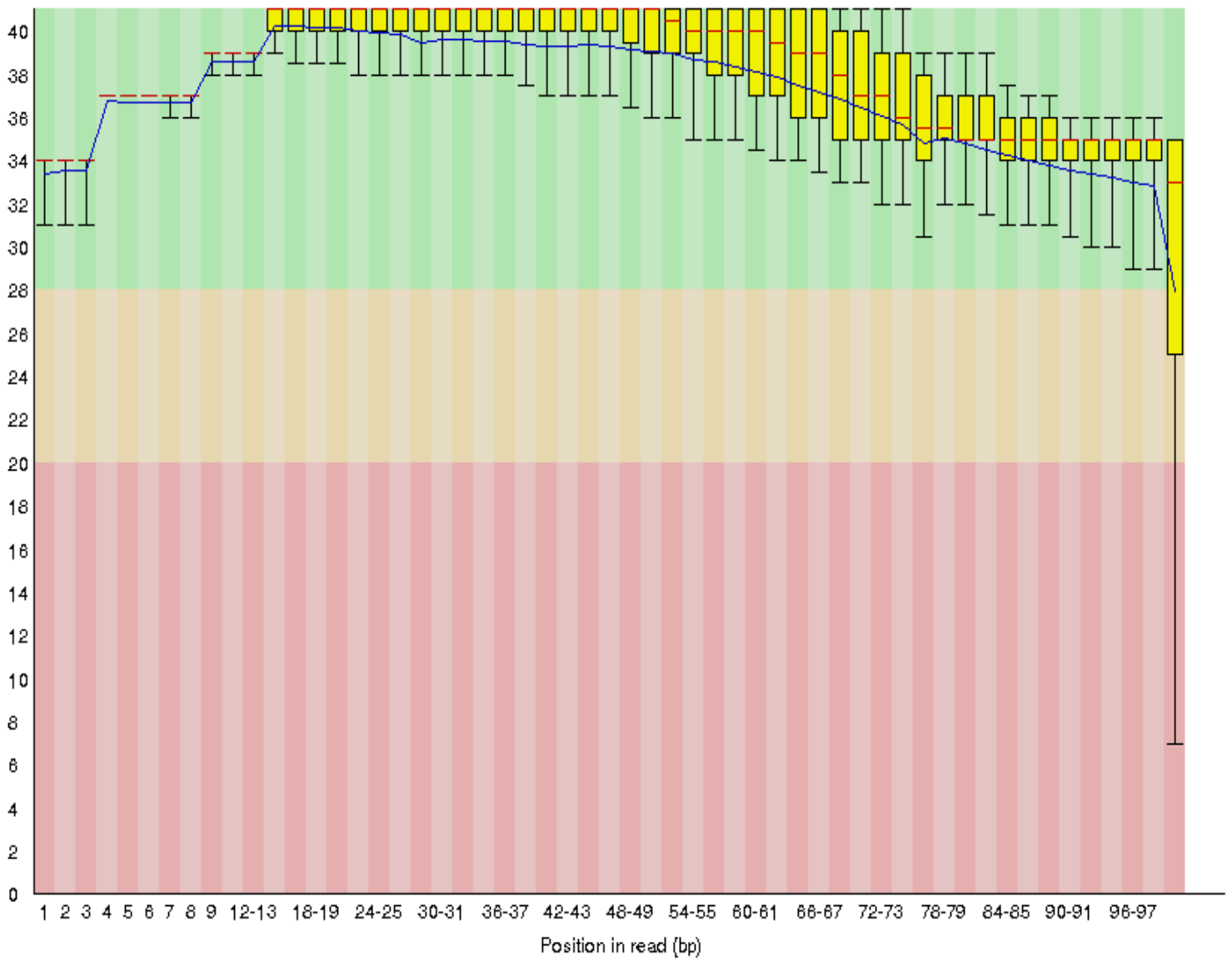
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Basic Statistics

Measure	Value
Filename	Undetermined_S0_L008_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1793423
Sequences flagged as poor quality	0
Sequence length	100
%GC	41

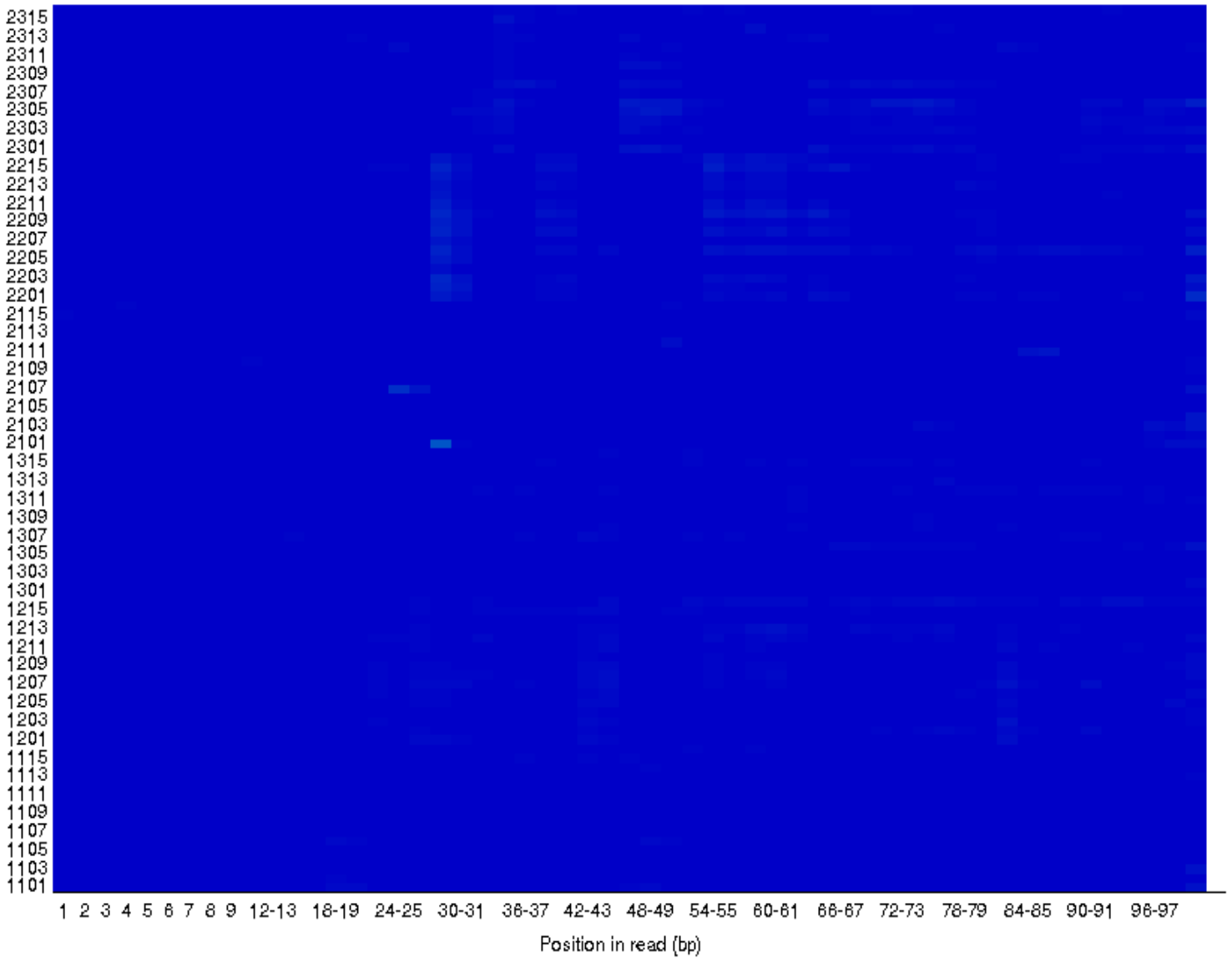
Per base sequence quality

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

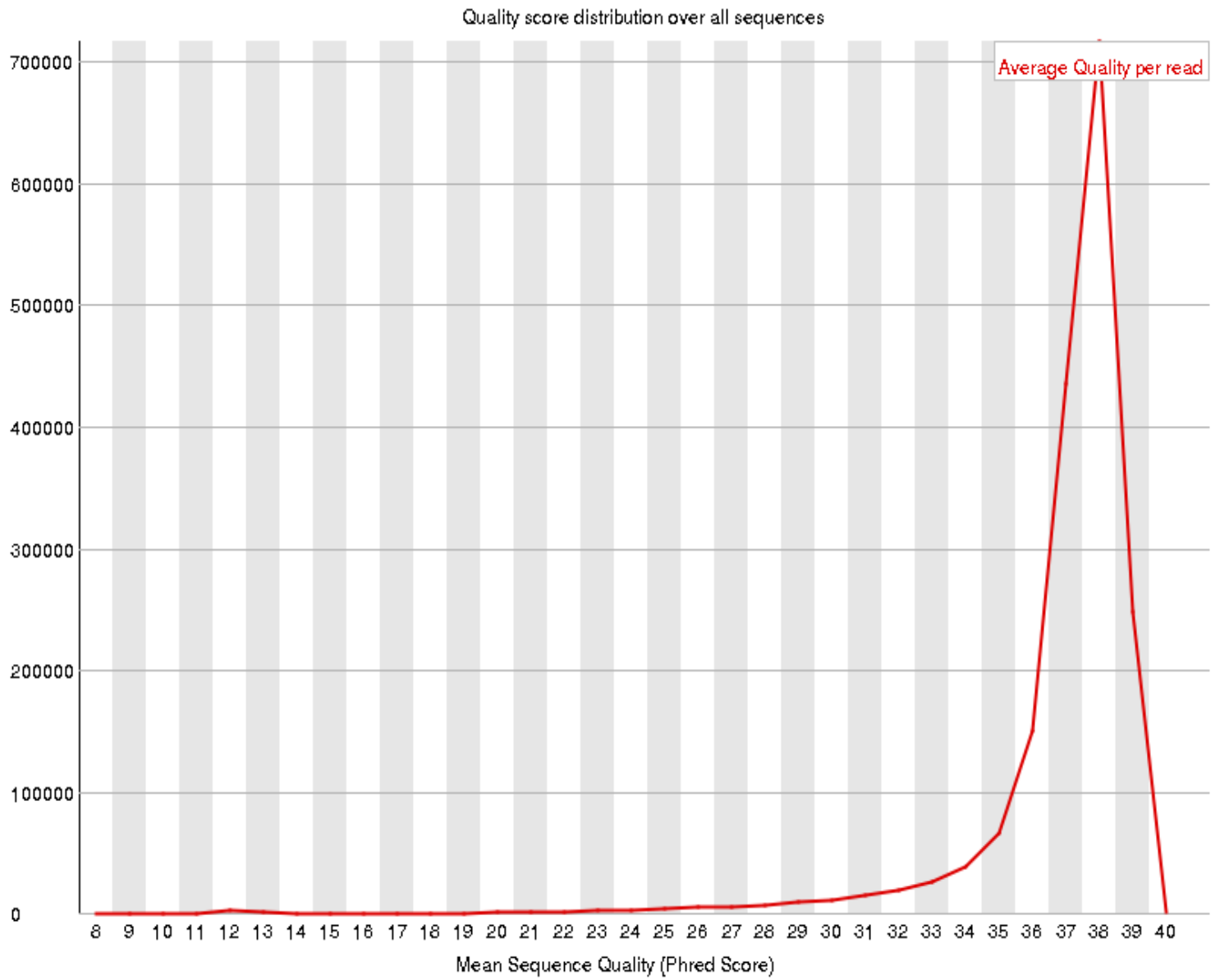


Per tile sequence quality

Quality per tile

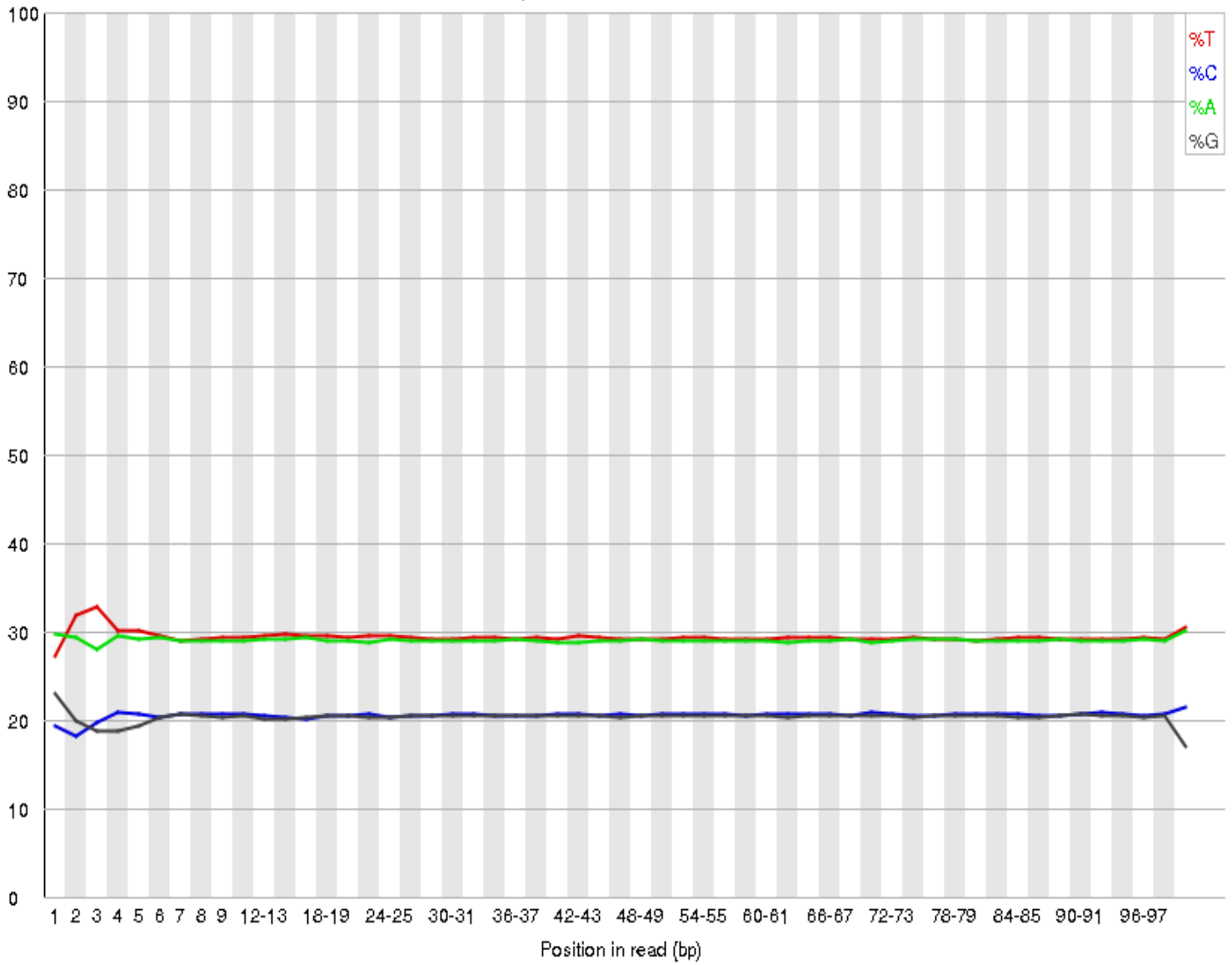


 **Per sequence quality scores**



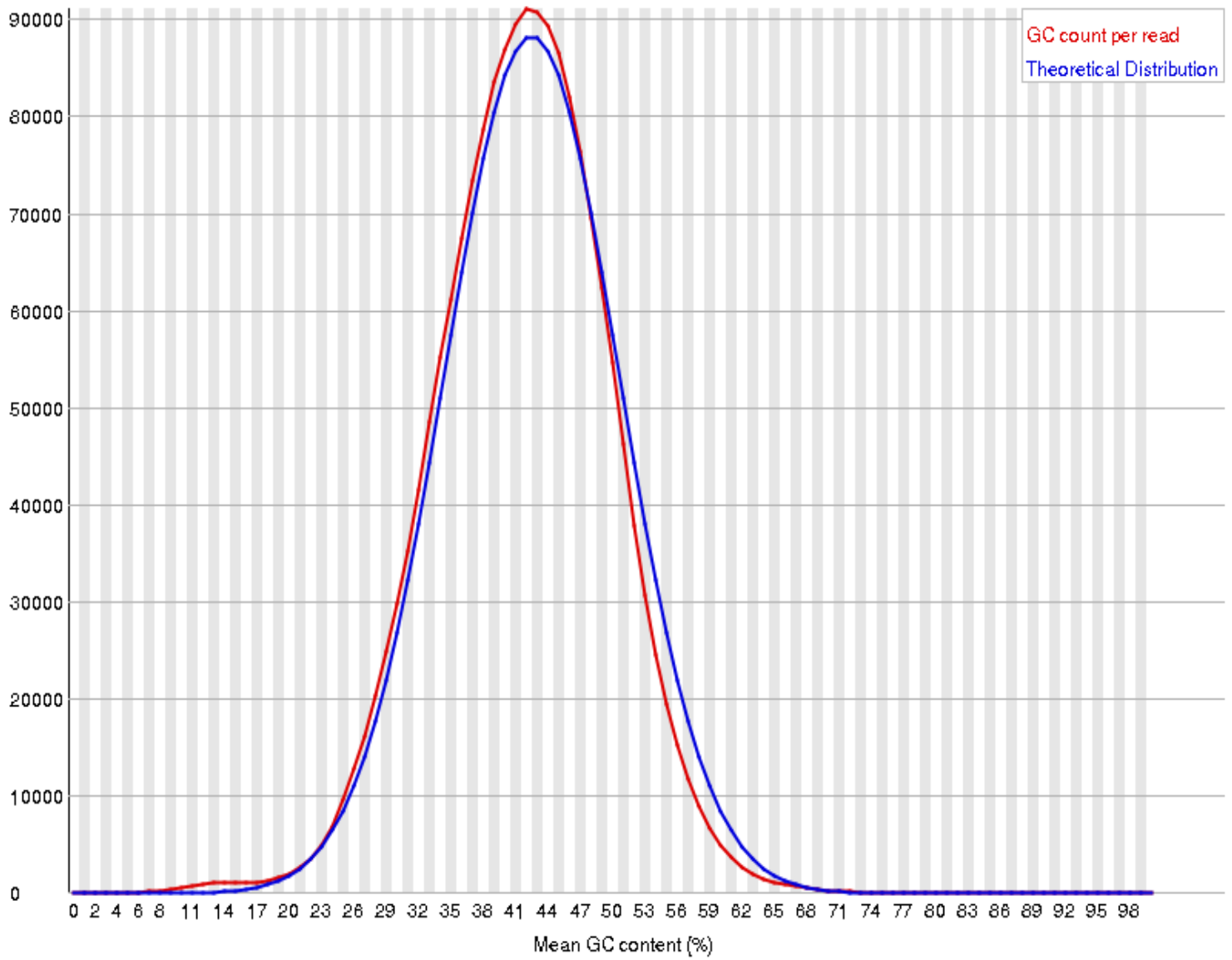
! Per base sequence content

Sequence content across all bases



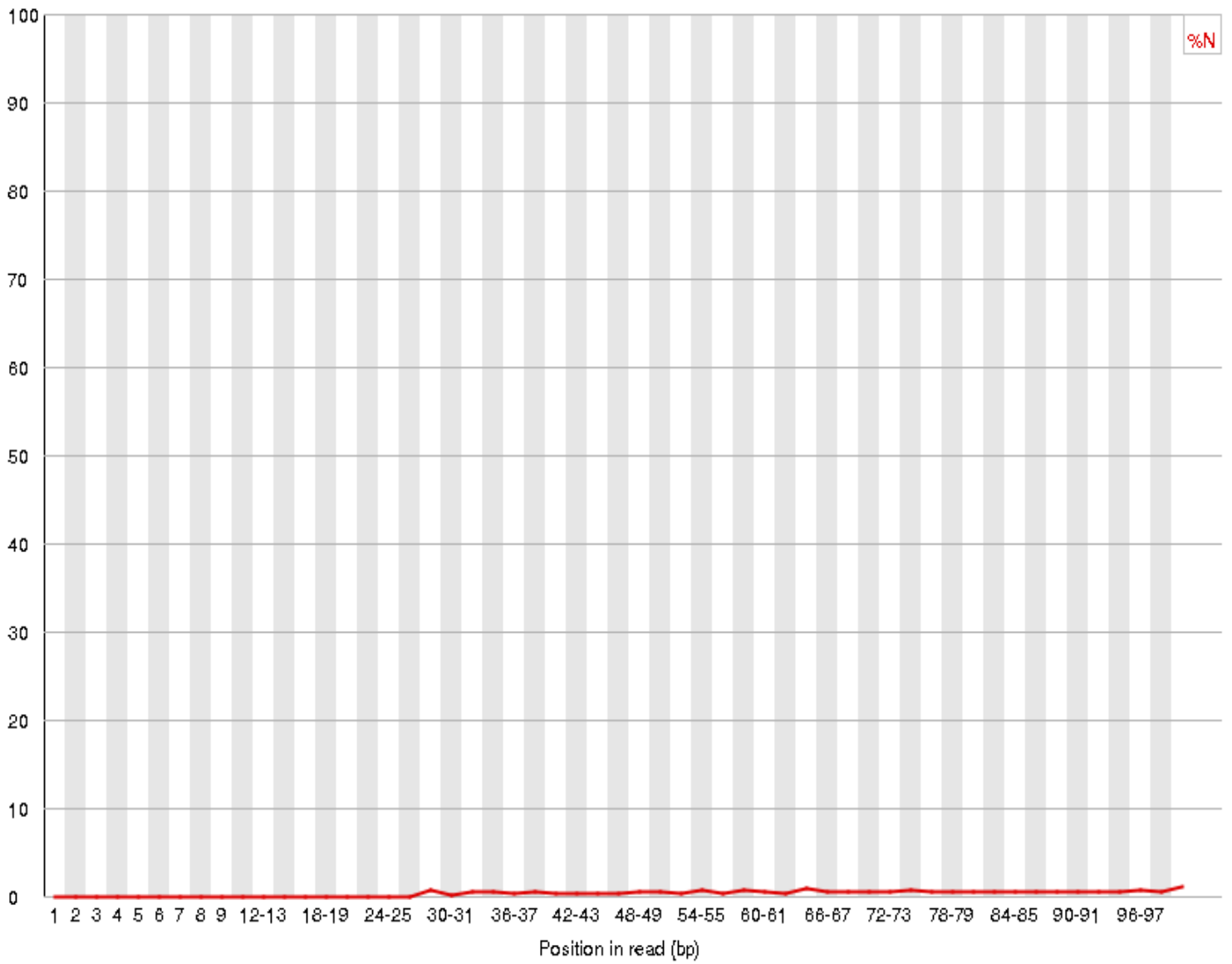
Per sequence GC content

GC distribution over all sequences



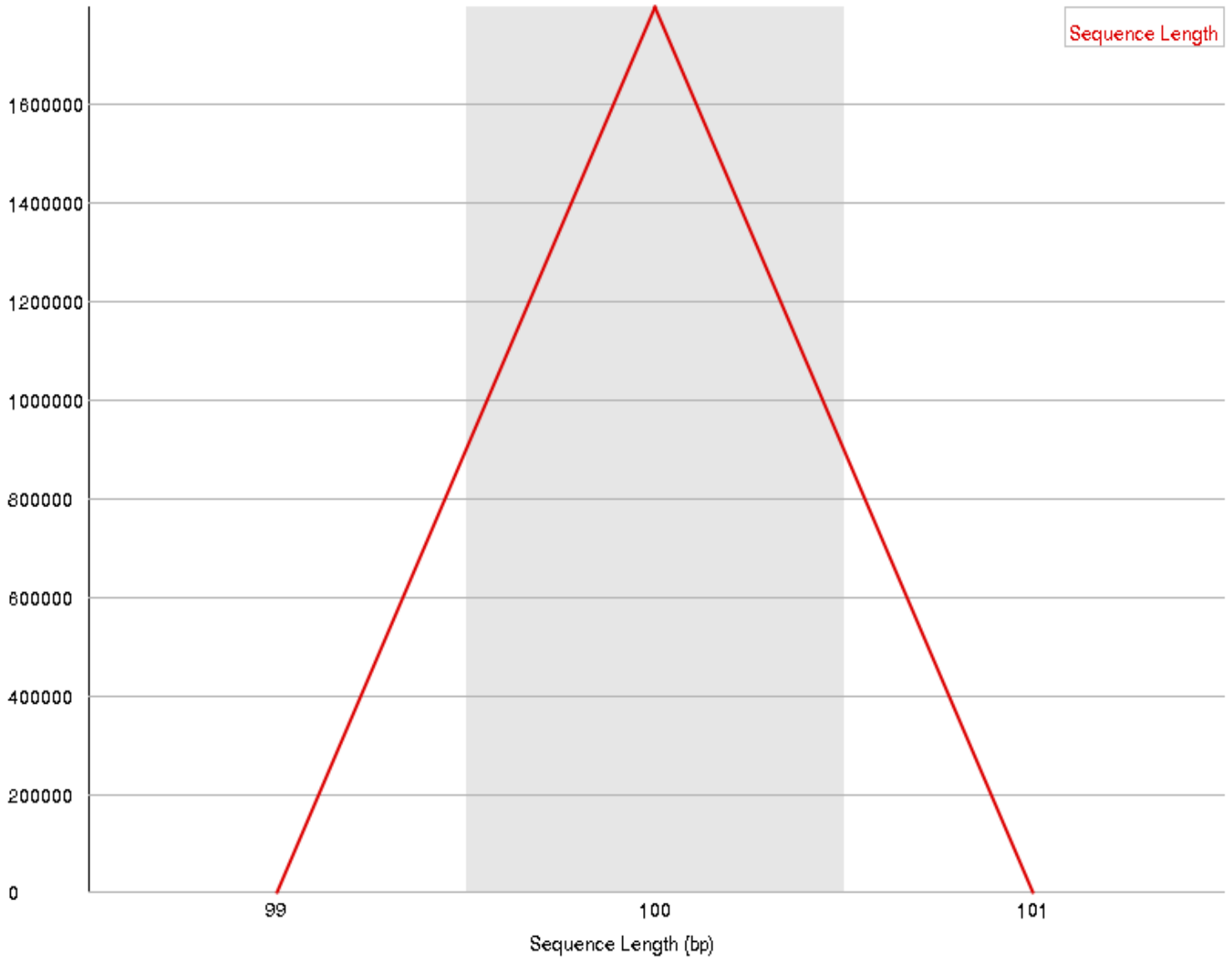
Per base N content

N content across all bases



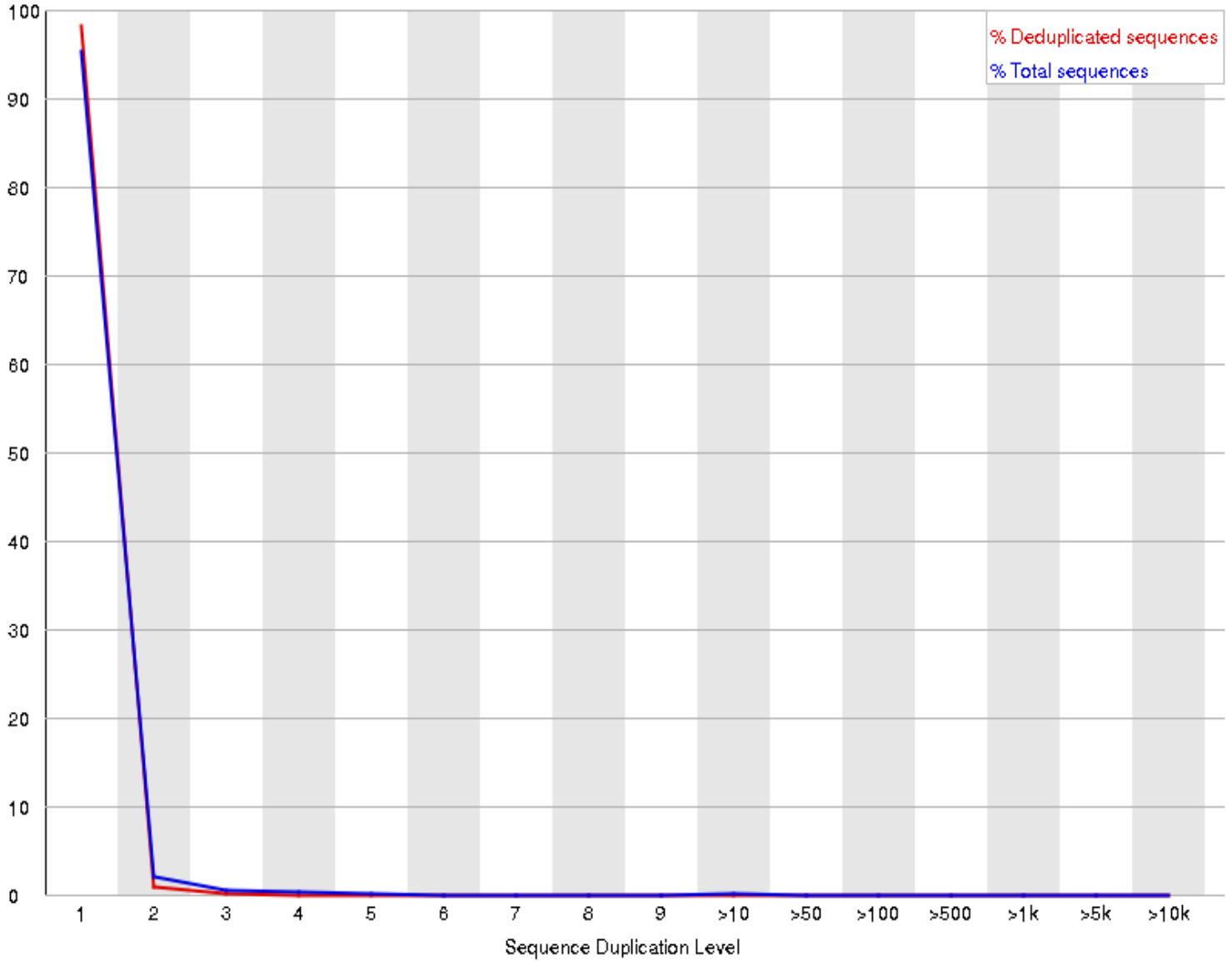
Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 97.07%



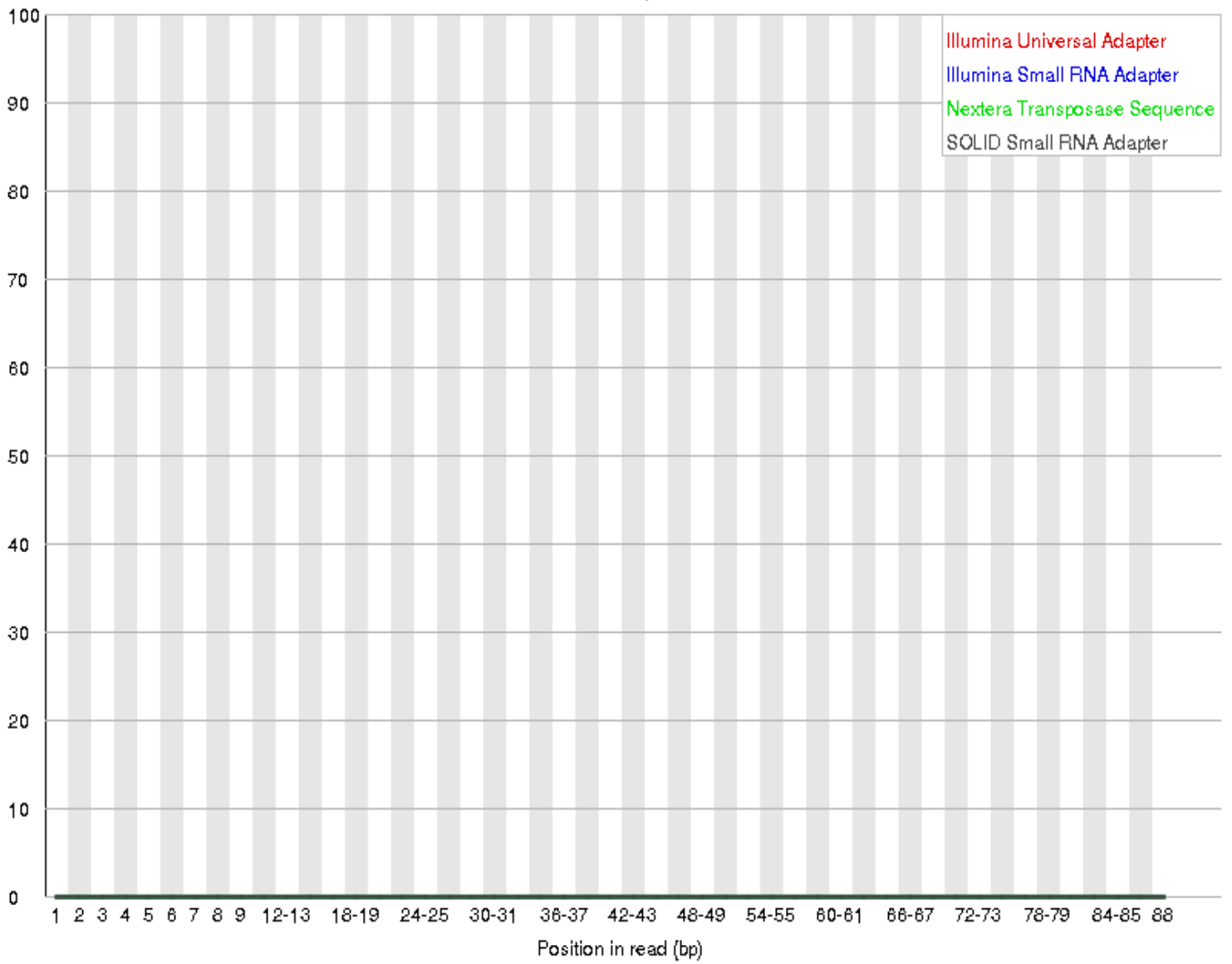
Overrepresented sequences

No overrepresented sequences

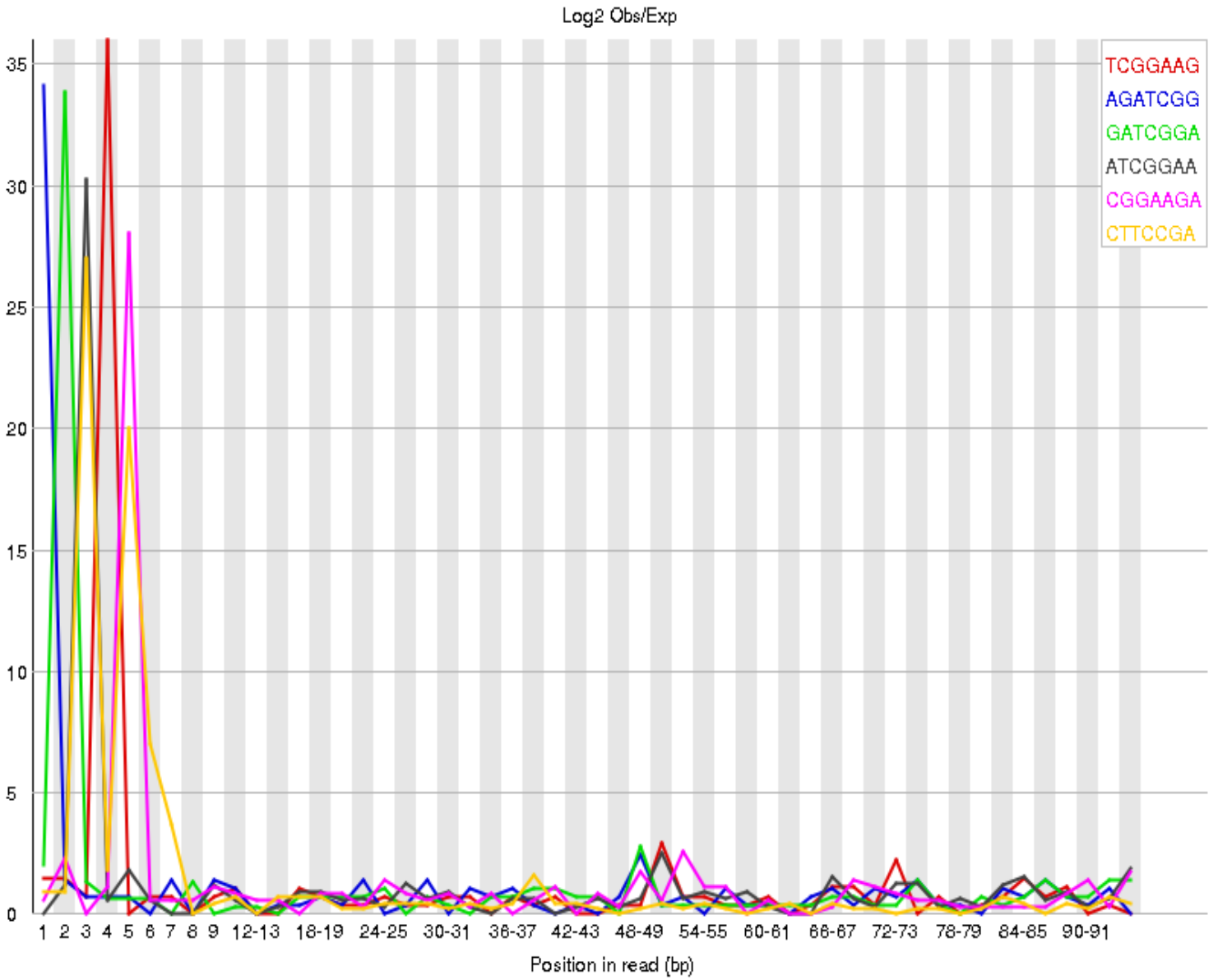


Adapter Content

% Adapter



 **Kmer Content**



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	635	0.0	35.966366	4
AGATCGG	670	0.0	34.099888	1
GATCGGA	675	0.0	33.835026	2
ATCGGAA	755	0.0	30.249857	3
CGGAAGA	815	0.0	28.018187	5
CTTCCGA	1000	0.0	27.033495	3
TTCCGAT	1035	0.0	25.668985	4
TCCGATC	1090	0.0	23.942146	5
CCGATCT	1180	0.0	22.116049	6
TCTCCG	1210	0.0	21.956528	2
GAAGAGC	1170	0.0	20.313553	7

GCTCTTC	1460	0.0	14.046691	2
ACGCTCT	475	6.364644E-9	13.742511	1
GGAAGAG	1765	0.0	13.201607	6
CGCTCTT	560	4.7621143E-9	12.48468	2
CGATCTT	635	1.8371793E-10	12.476039	7
CGATCTA	545	4.3819455E-8	11.971073	9
CTCTTCC	2670	0.0	11.874882	1
AGAGCAC	1015	5.456968E-12	10.100857	9
TGCTCTT	1865	0.0	9.250274	1

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