











Sat 2 Nov 2024
SRR14866428_1.fastq

FastQC Report

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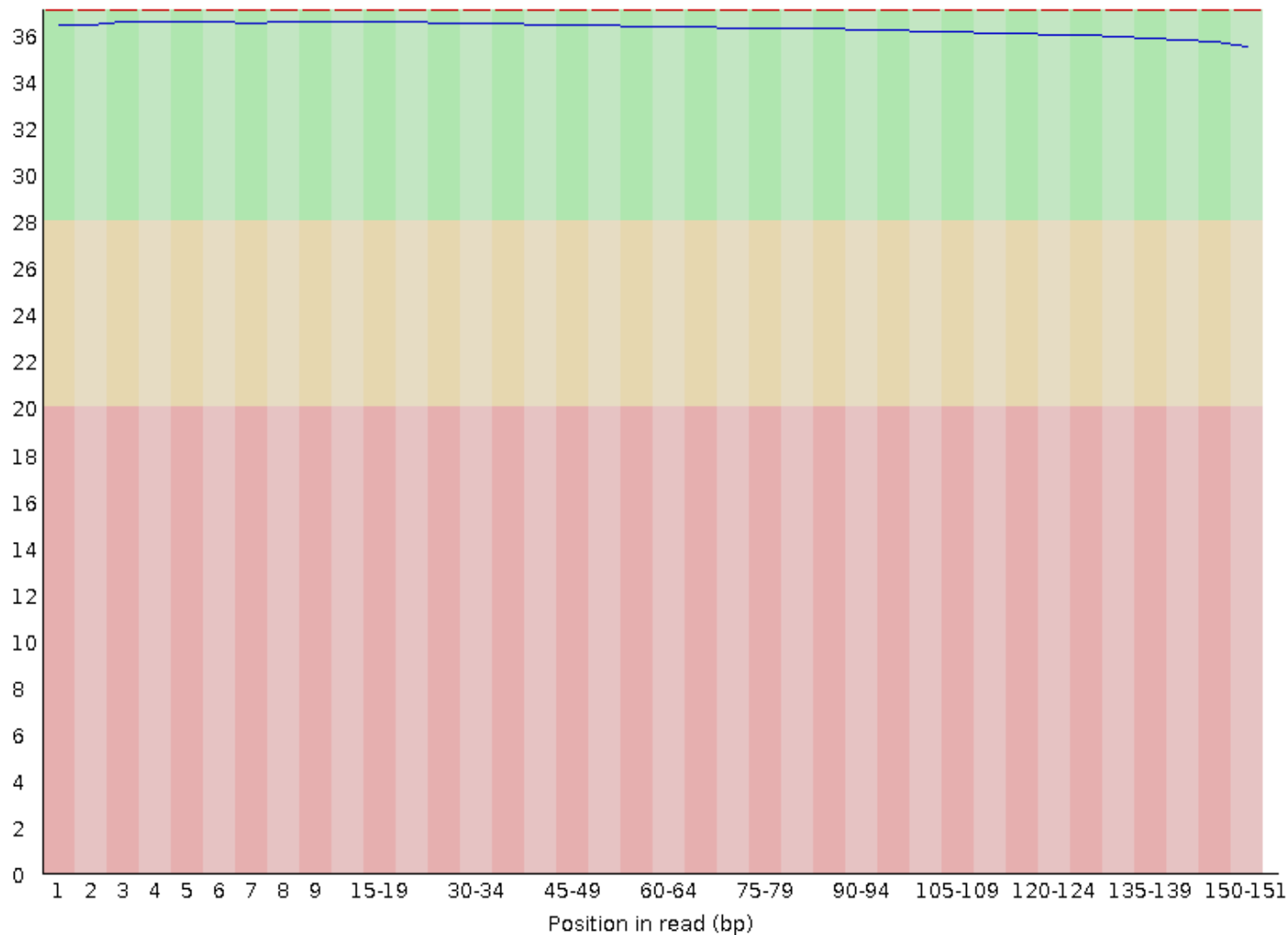
Basic Statistics

Measure	Value
Filename	SRR14866428_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	22794073
Sequences flagged as poor quality	0
Sequence length	151
%GC	51



Per base sequence quality

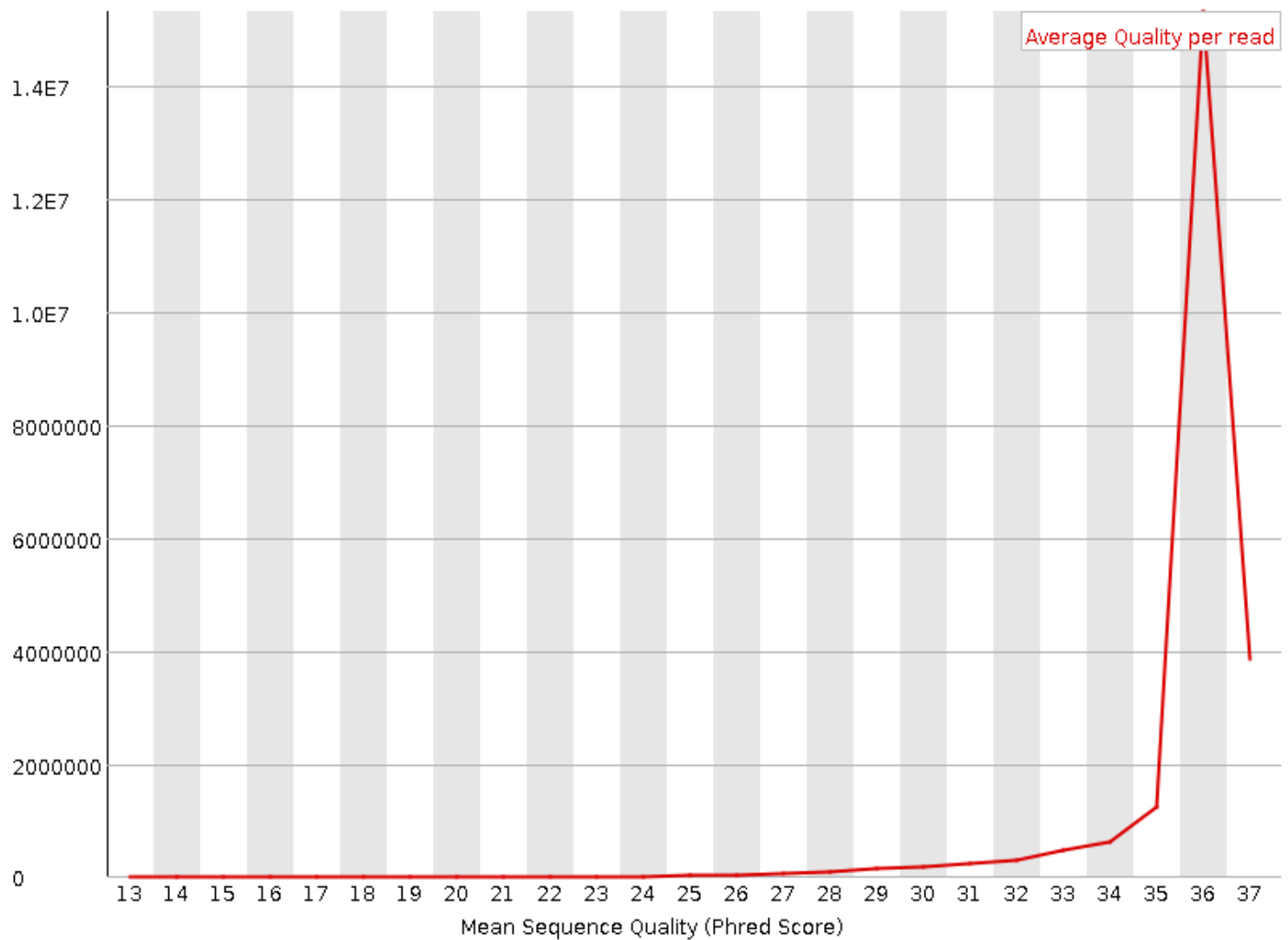
Quality scores across all bases (Sanger / Illumina 1.9 encoding)





Per sequence quality scores

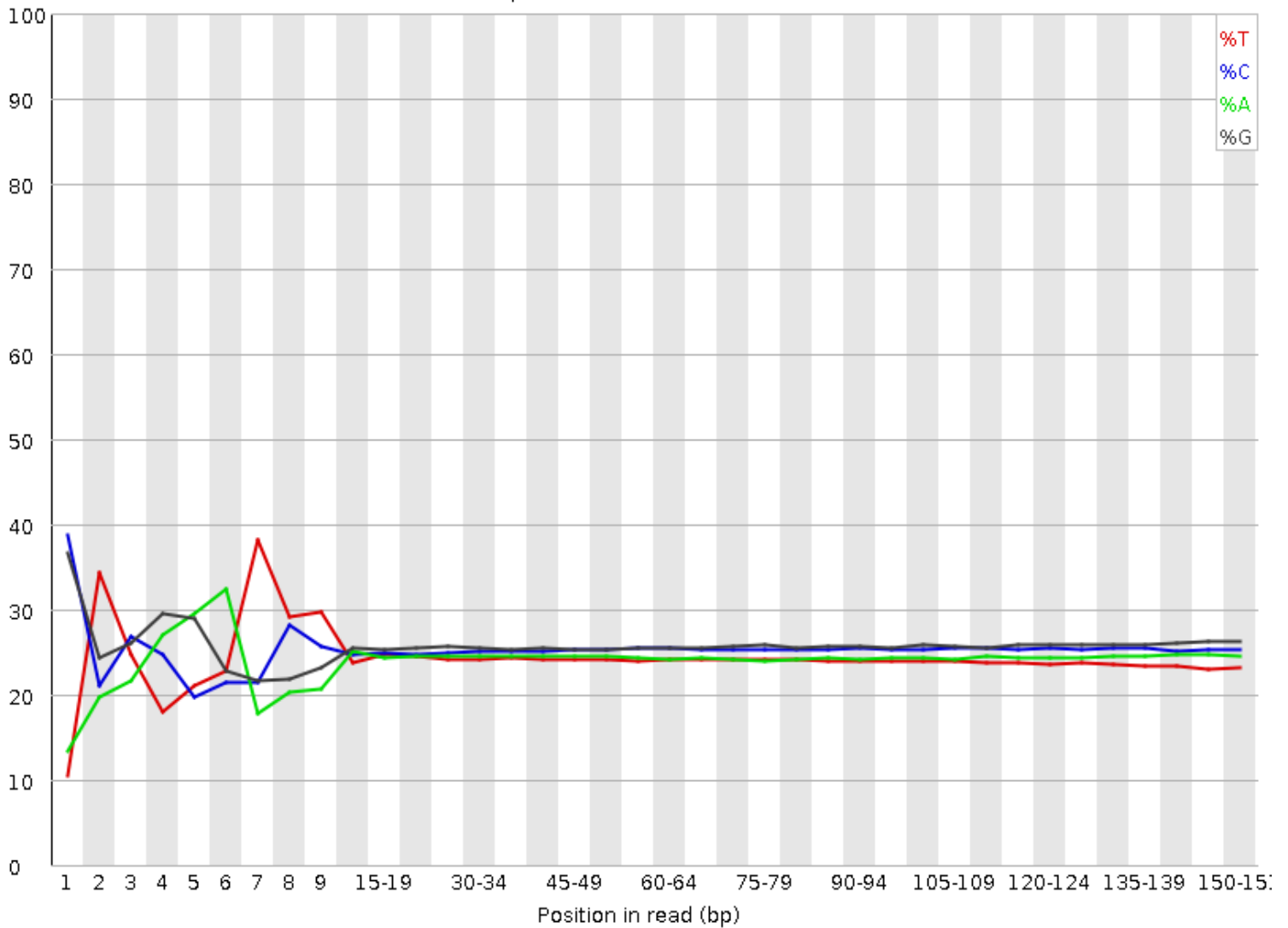
Quality score distribution over all sequences



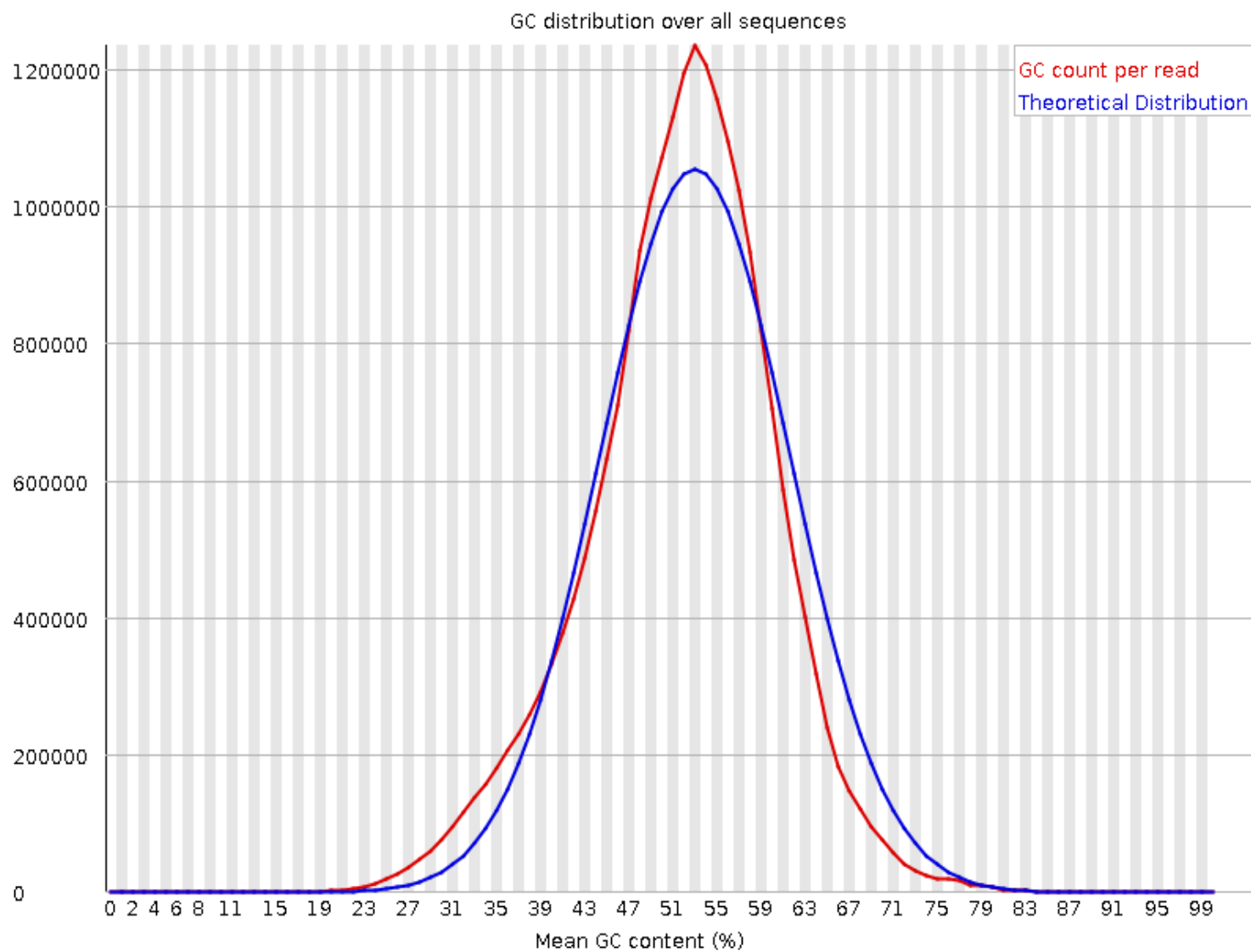


Per base sequence content

Sequence content across all bases

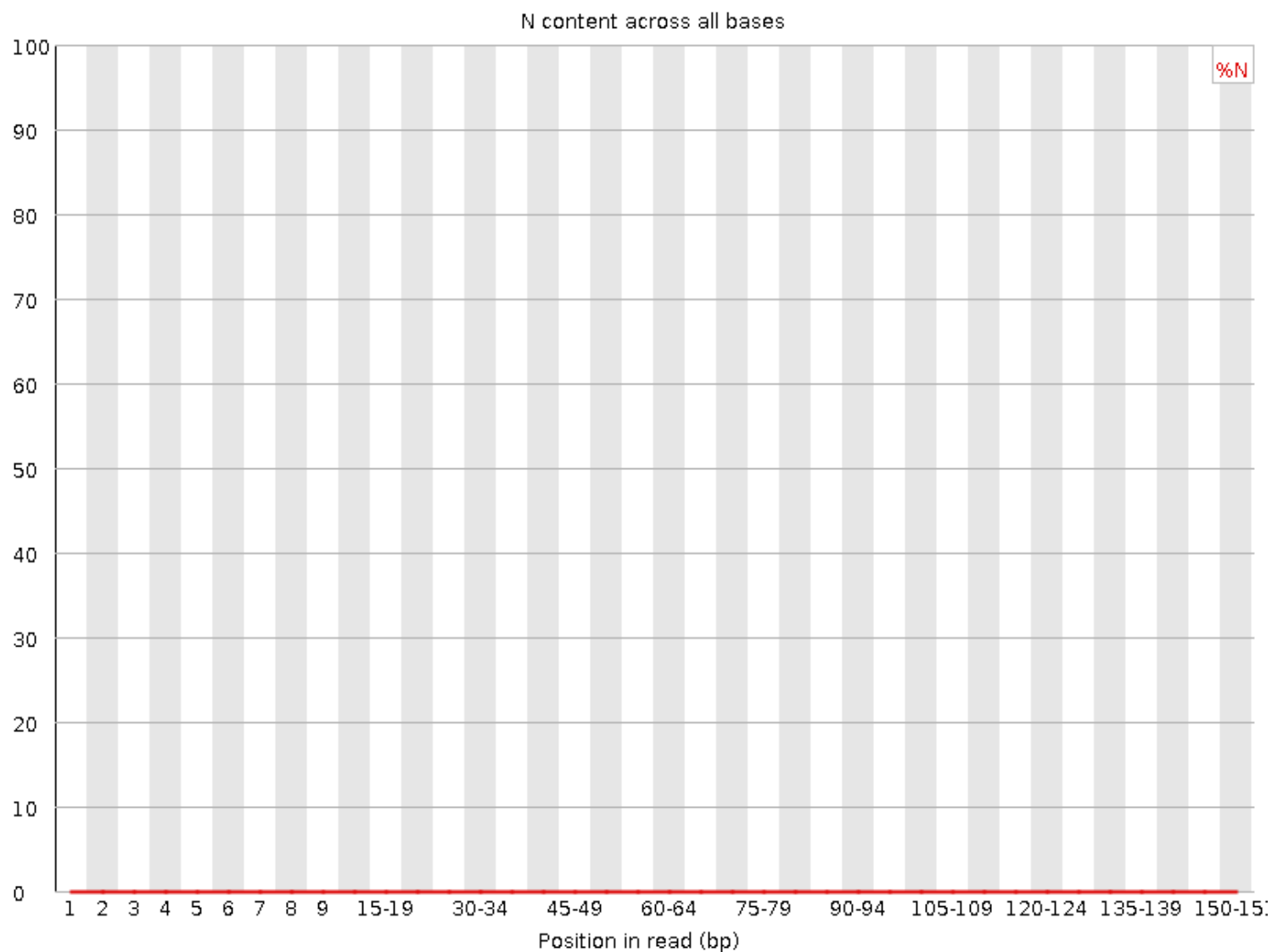


! Per sequence GC content



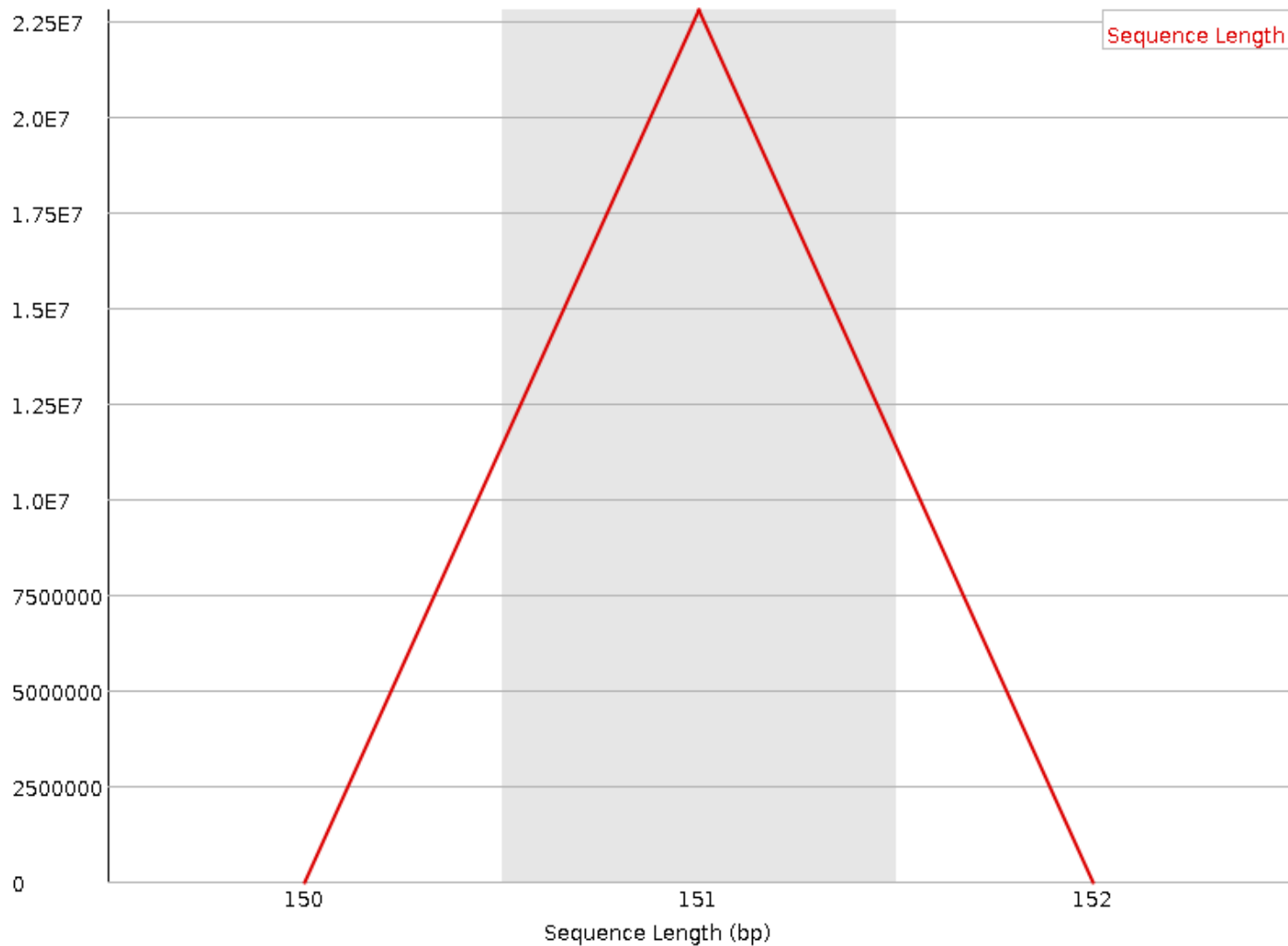


Per base N content

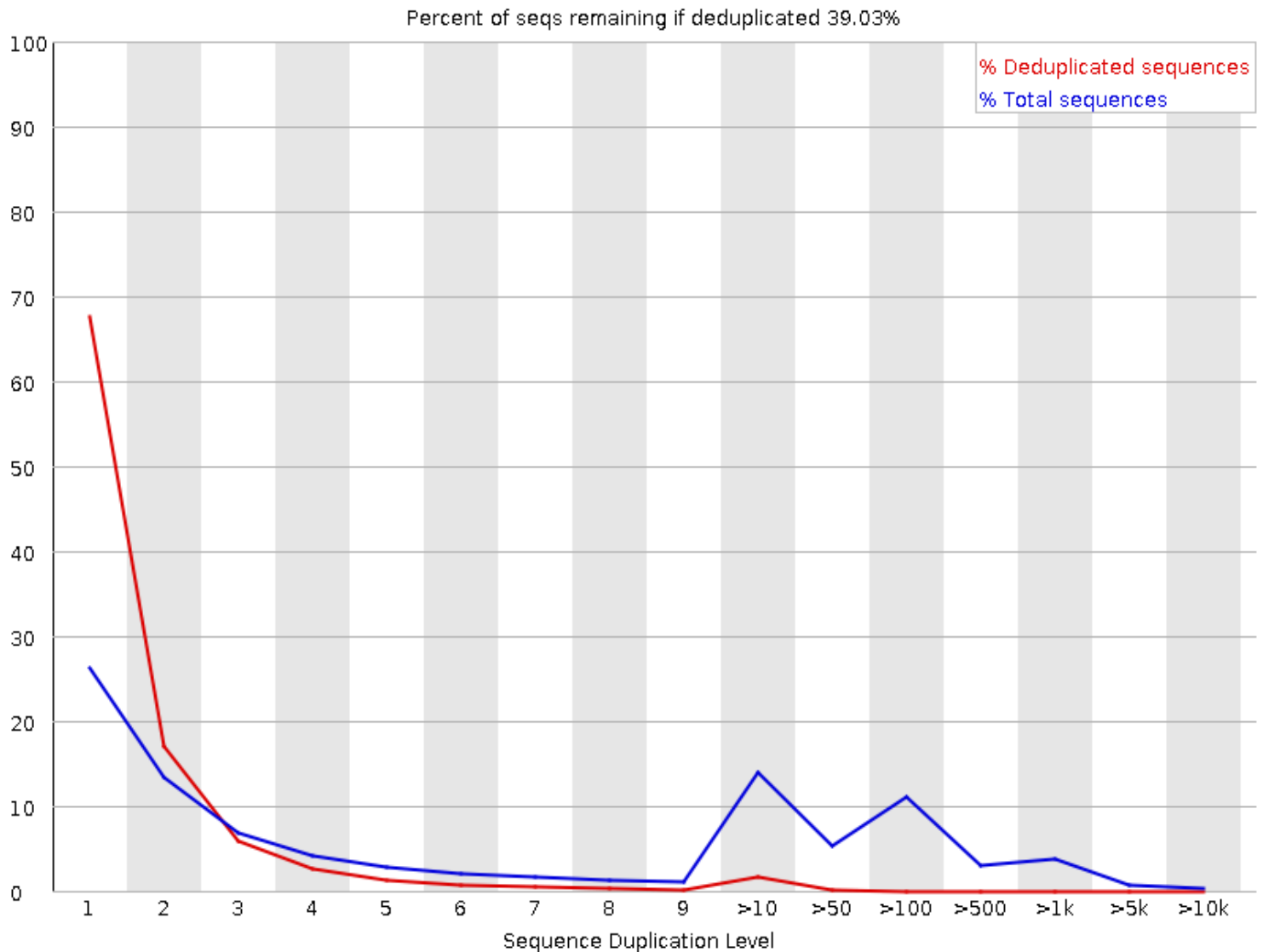


Sequence Length Distribution

Distribution of sequence lengths over all sequences



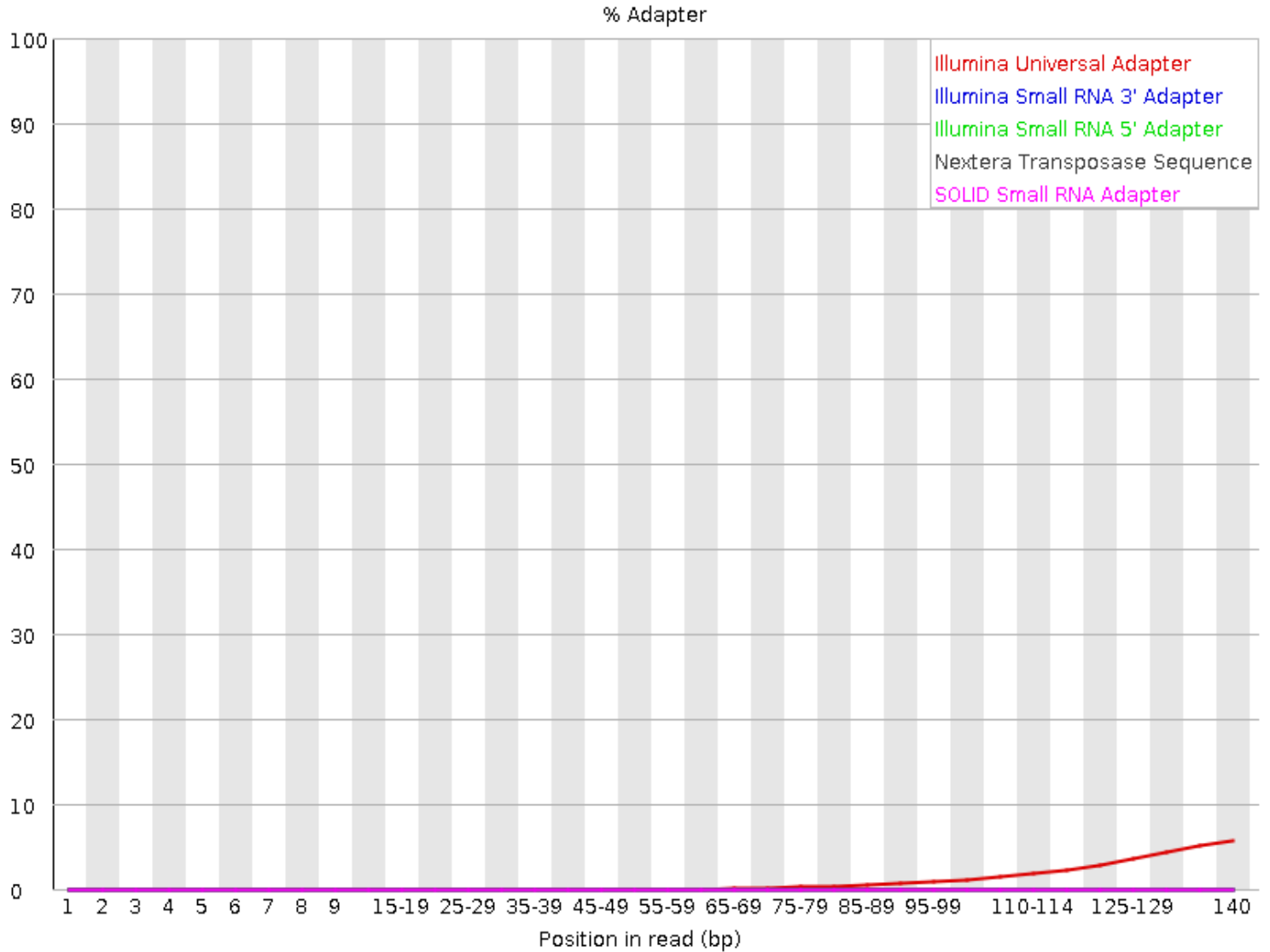
✖ Sequence Duplication Levels



⚠ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CGCAAACAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	26056	0.11431041744930798	No Hit

Adapter Content



Produced by [FastQC](#) (version 0.11.7)