











FastQC Report

Summary

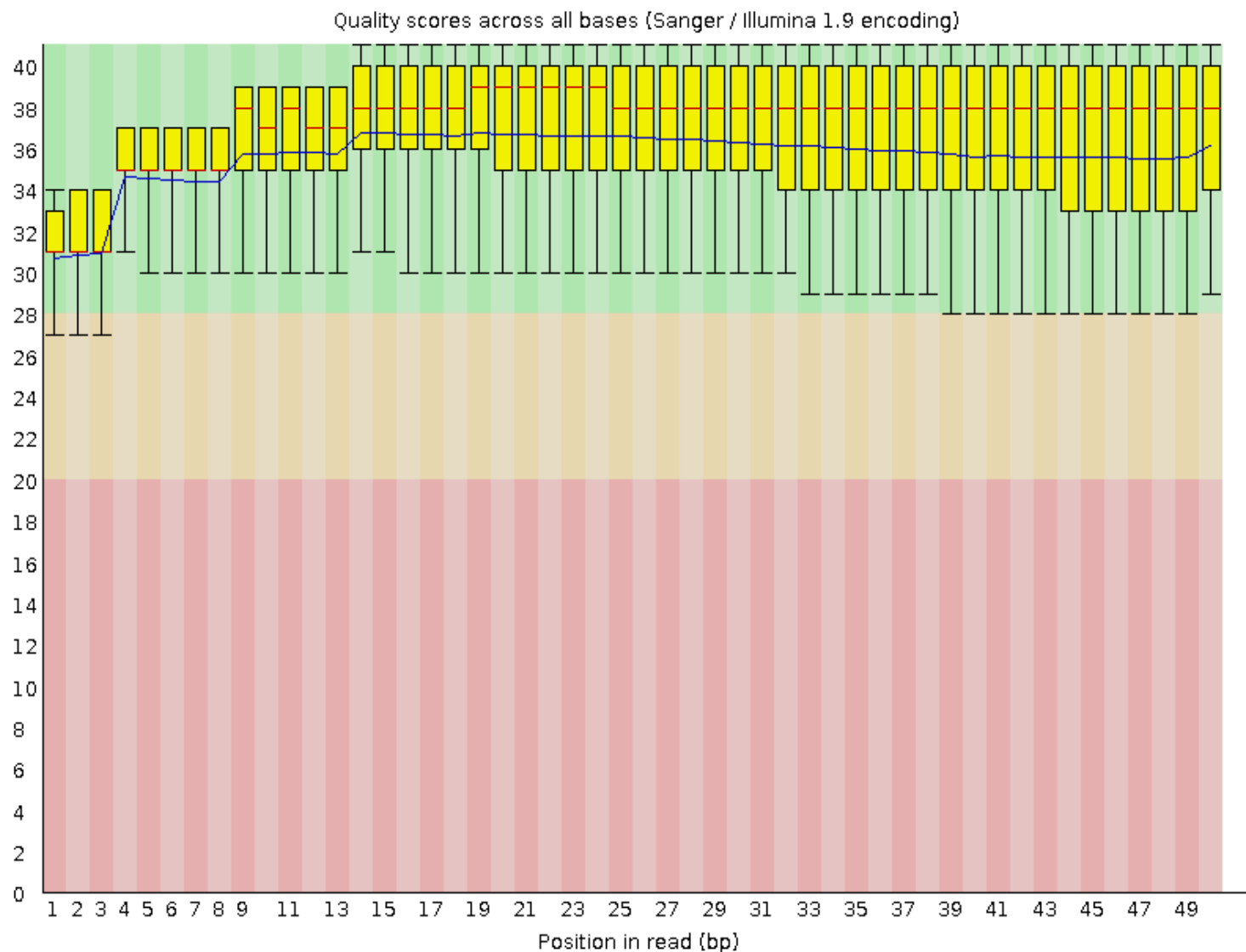
Wed 30 Jun 2021
SRR1554535_1_adapt_fastq_gz.gz

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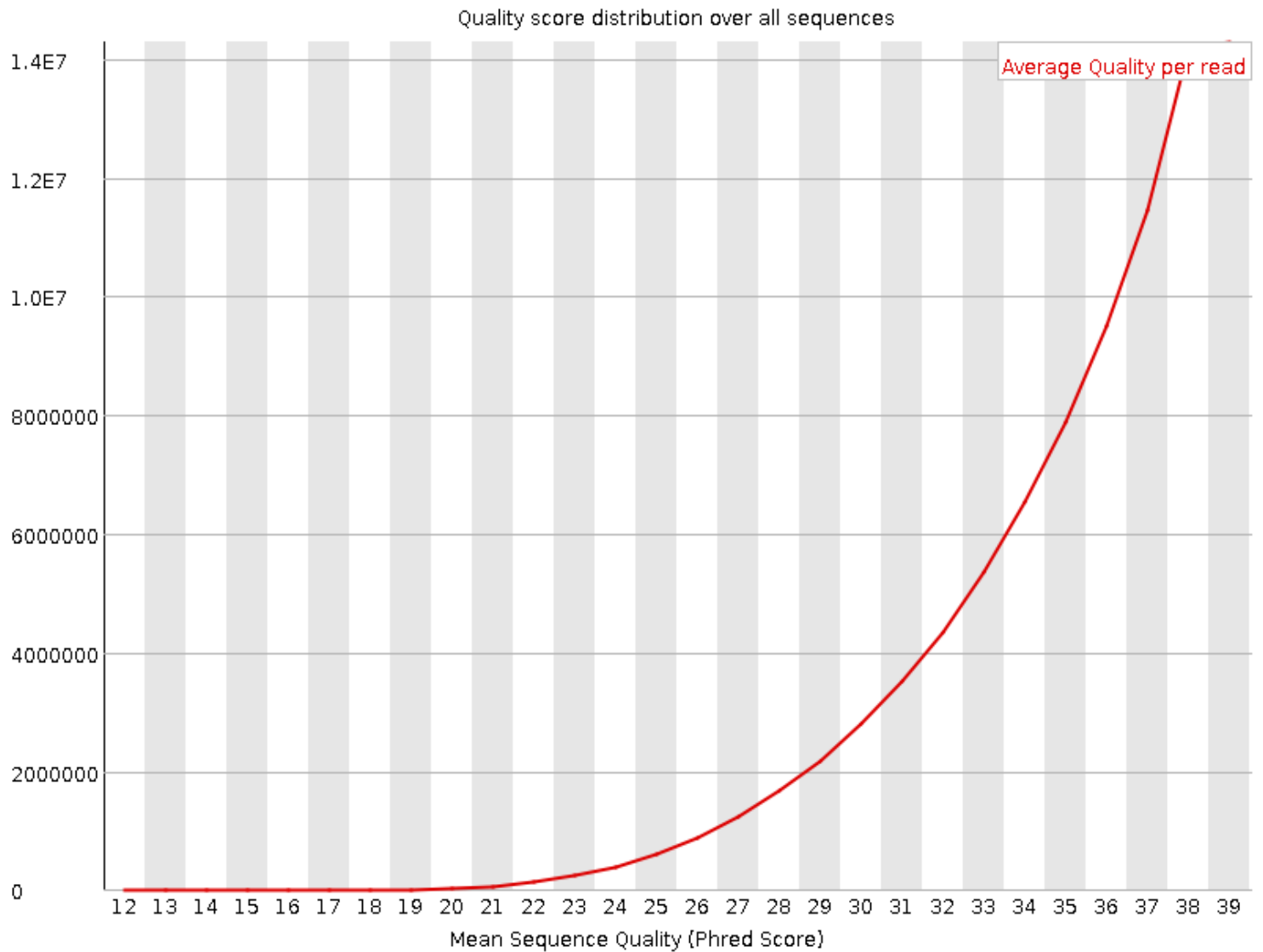
Basic Statistics

Measure	Value
Filename	SRR1554535_1_adapt_fastq_gz.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	87566336
Sequences flagged as poor quality	0
Sequence length	20-50
%GC	48

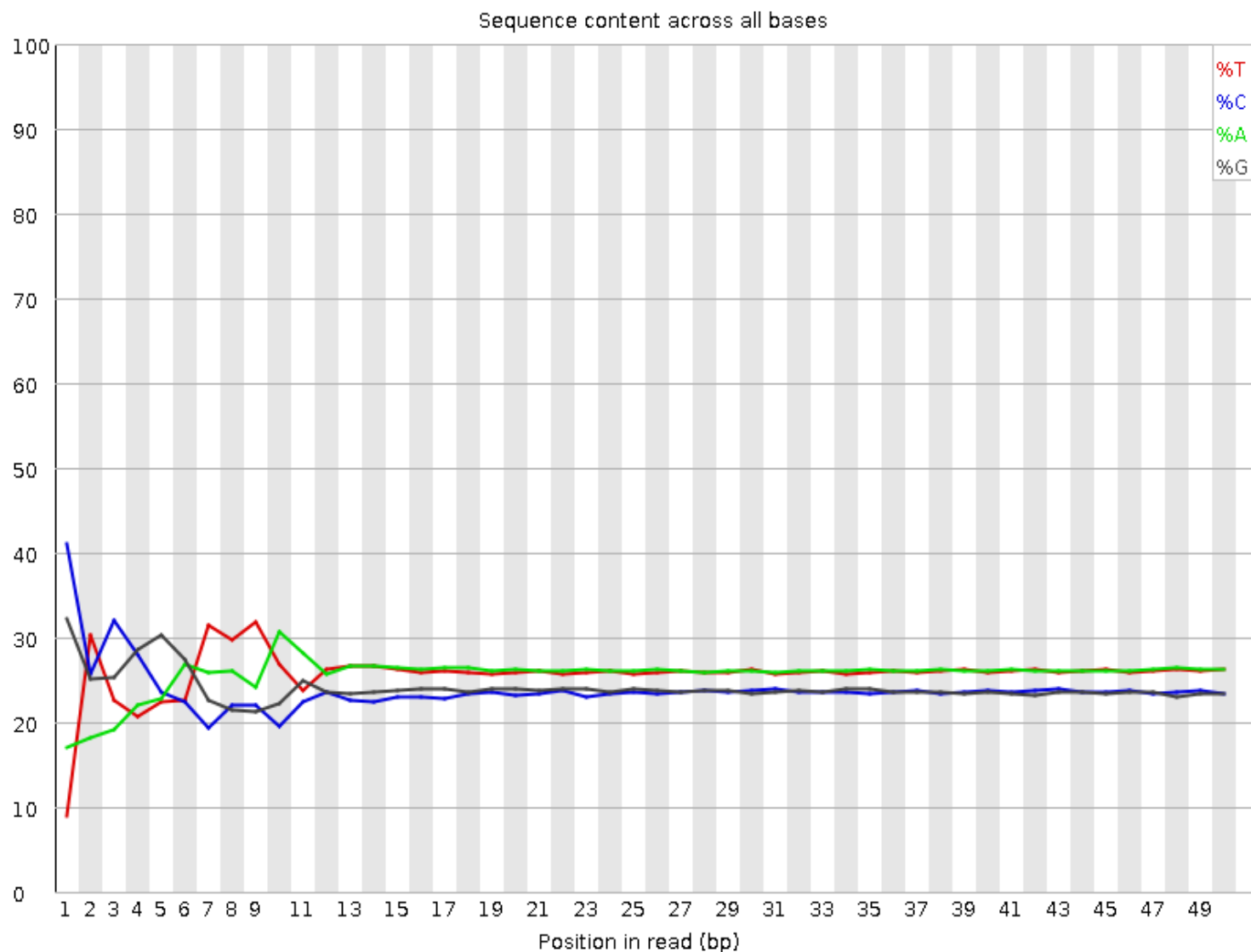
Per base sequence quality



Per sequence quality scores

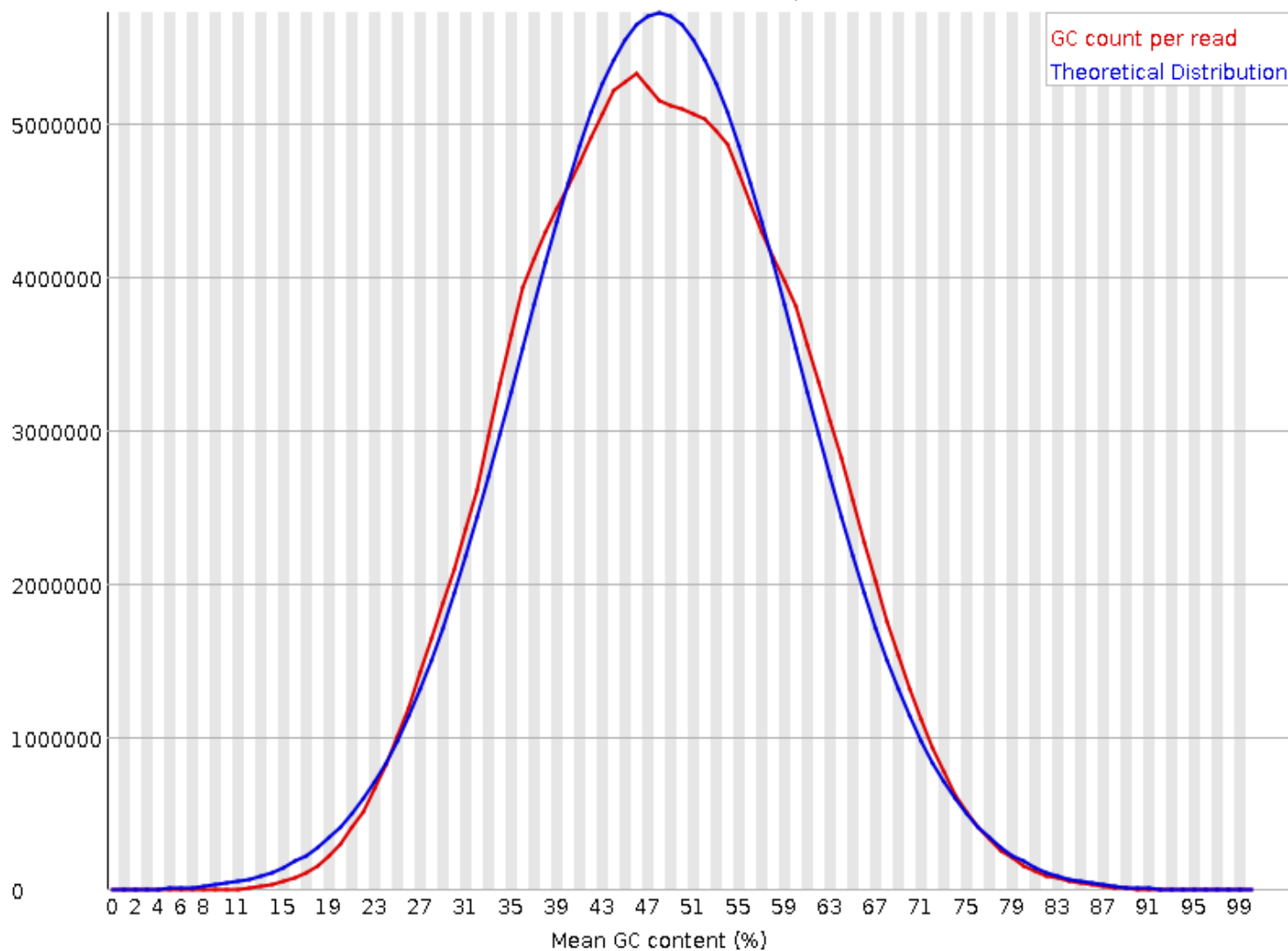


! Per base sequence content

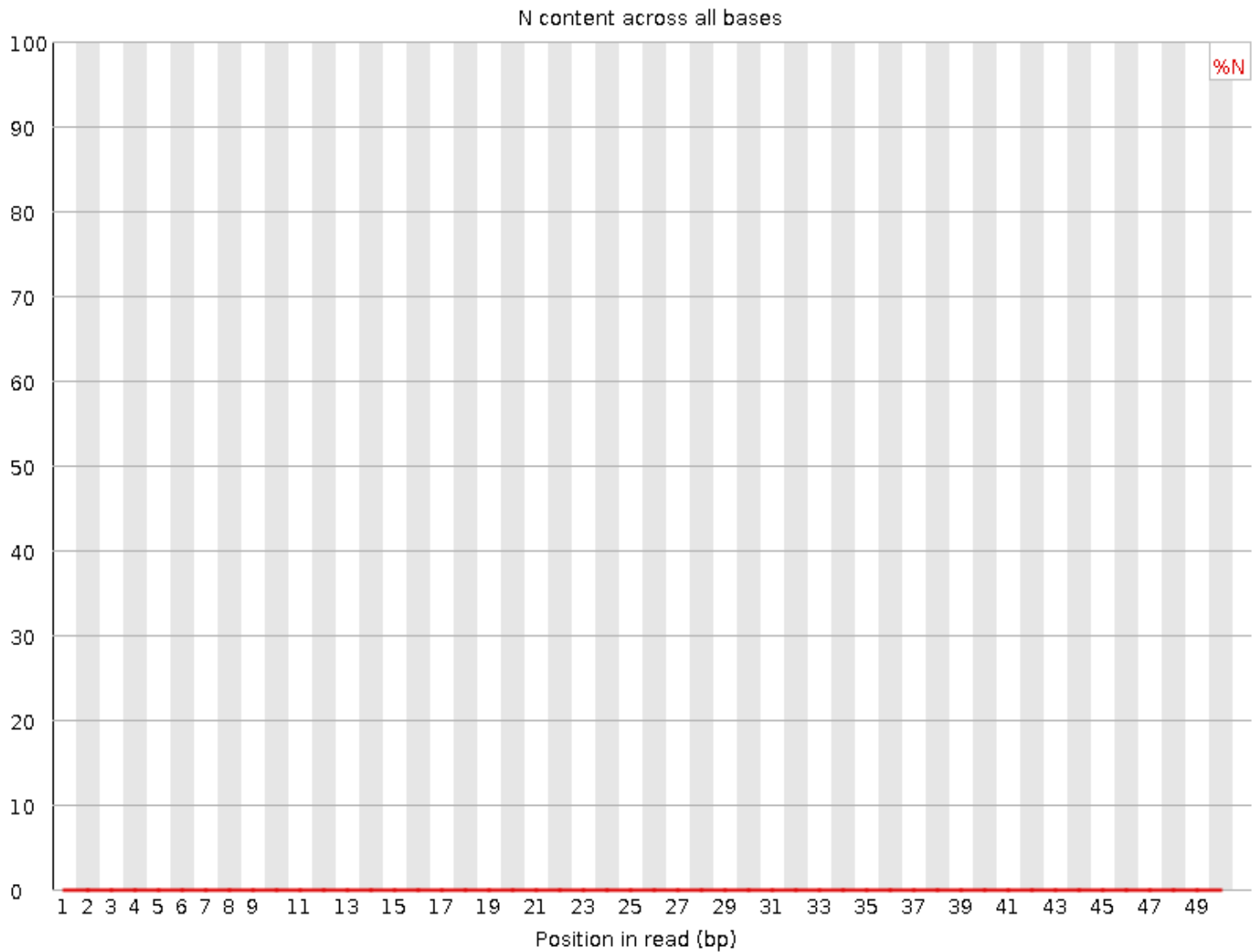


Per sequence GC content

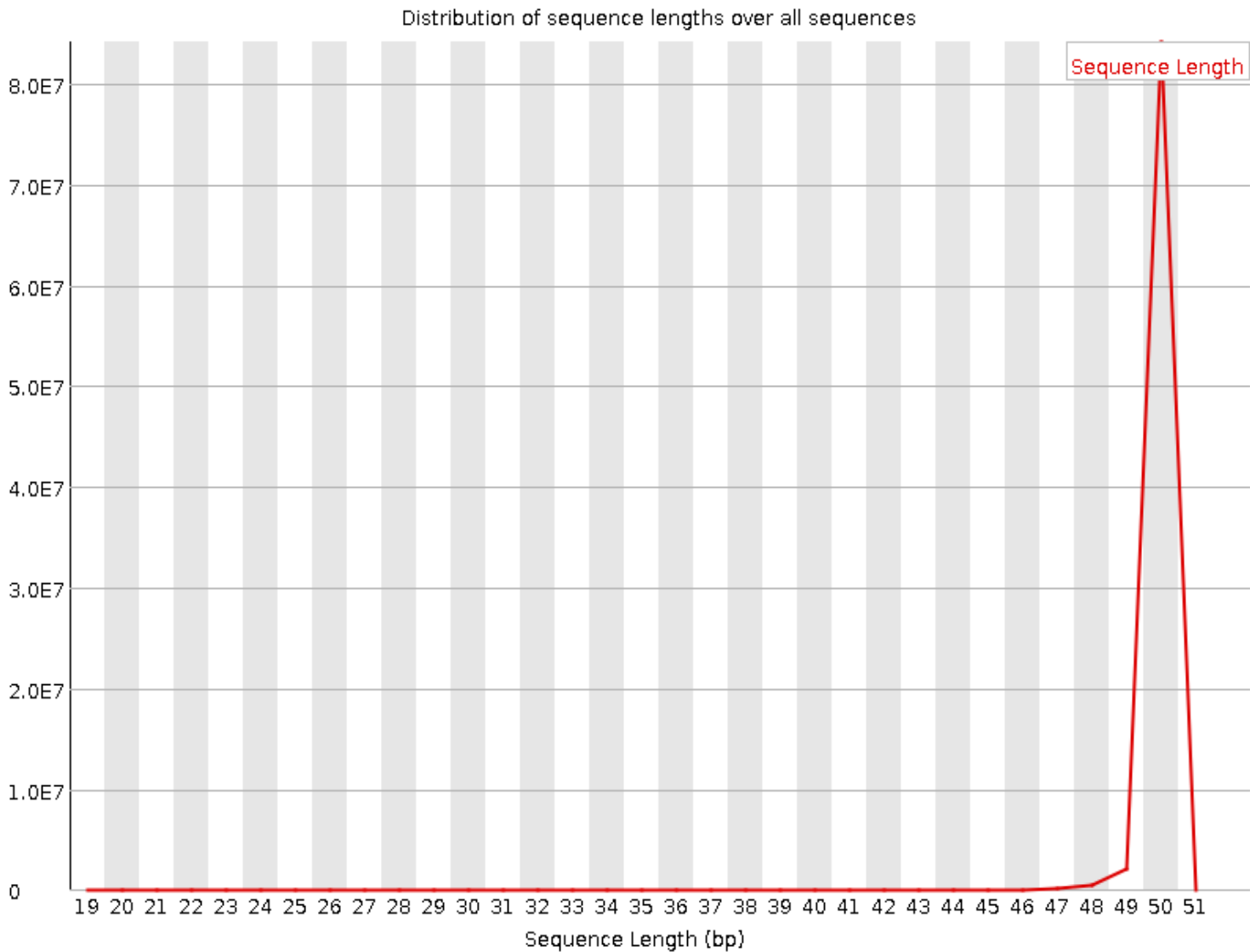
GC distribution over all sequences



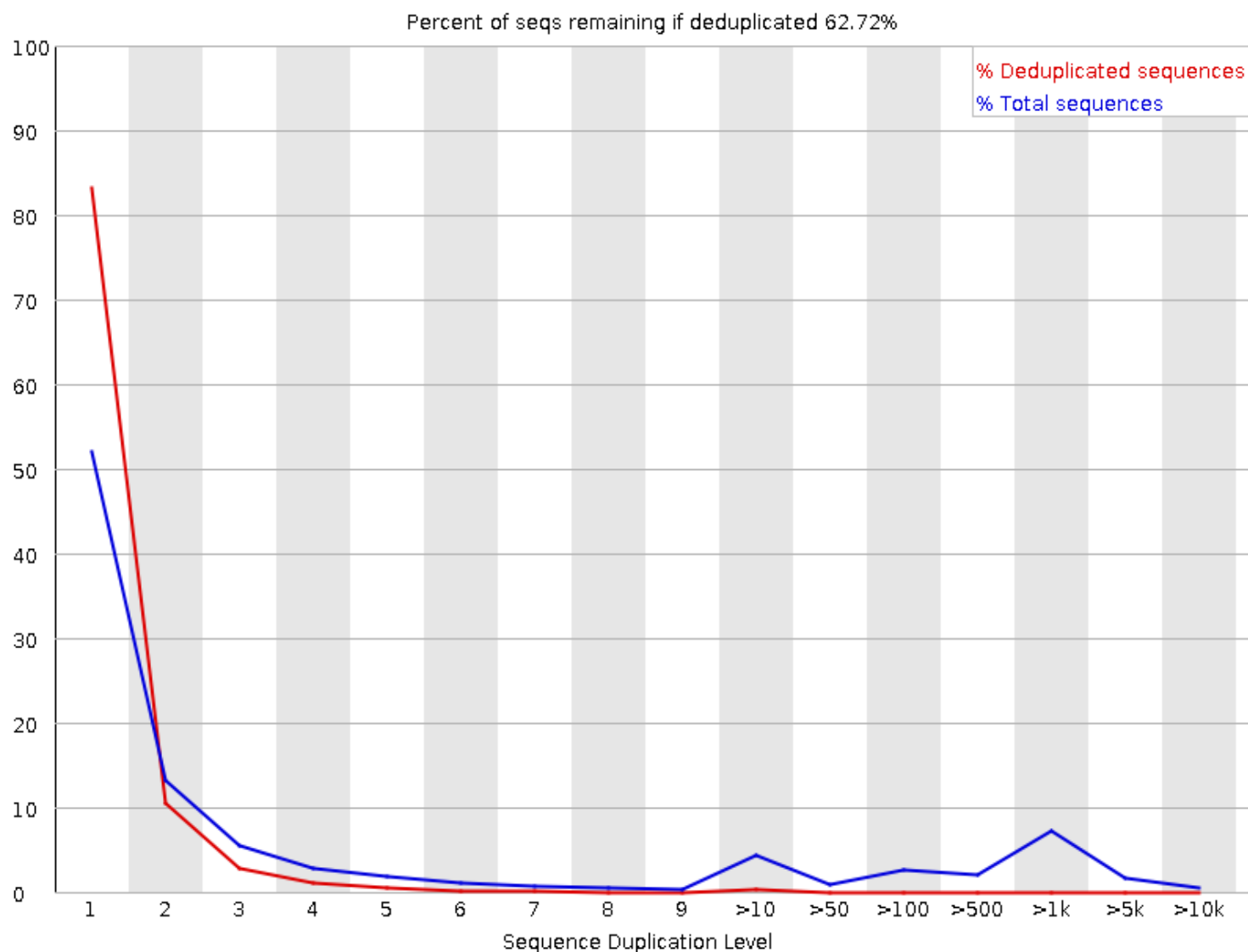
Per base N content



Sequence Length Distribution



! Sequence Duplication Levels

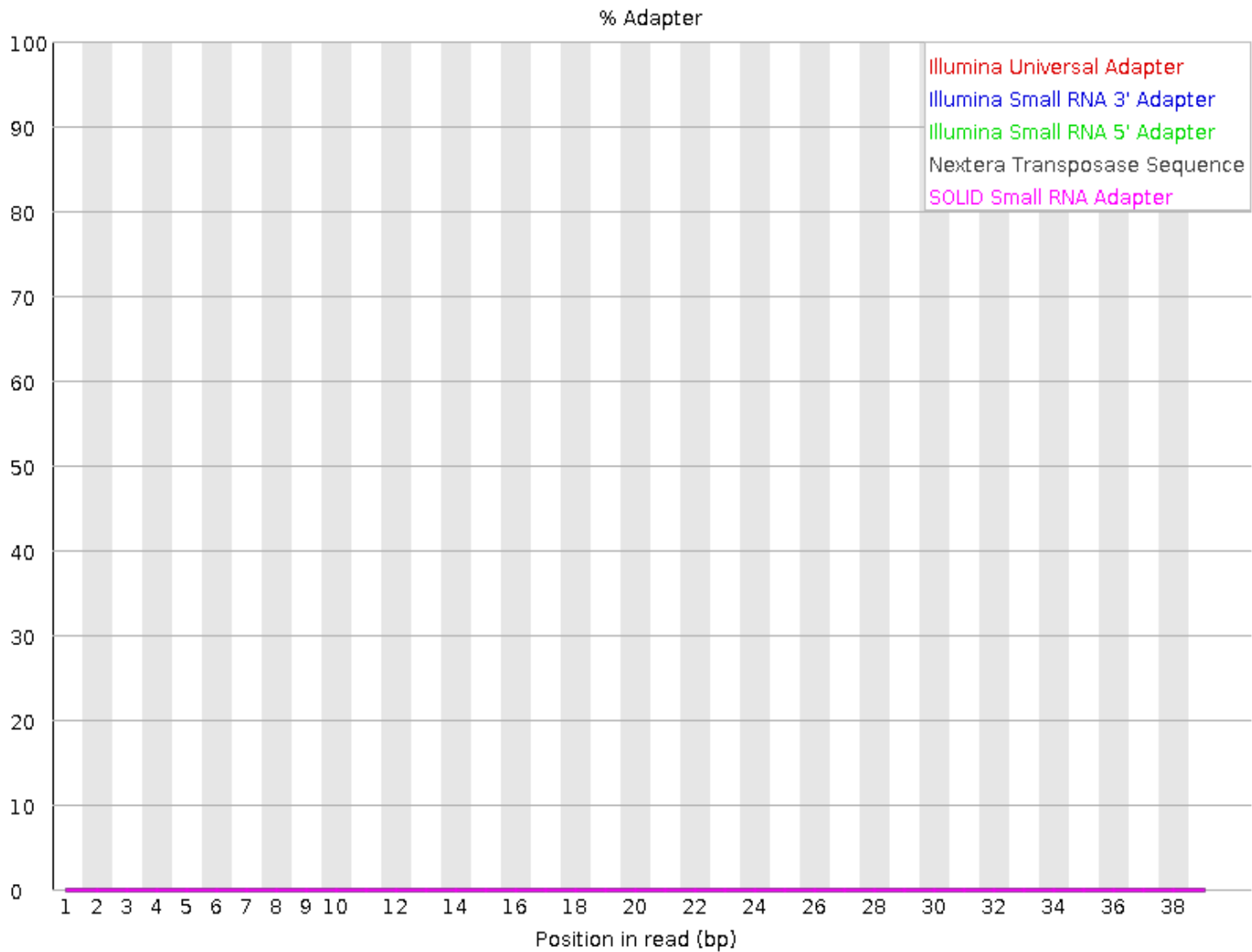


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.11.8)