












FastQC Report

Summary

Thu 31 Oct 2024
SRR491287_1.fastq.gz

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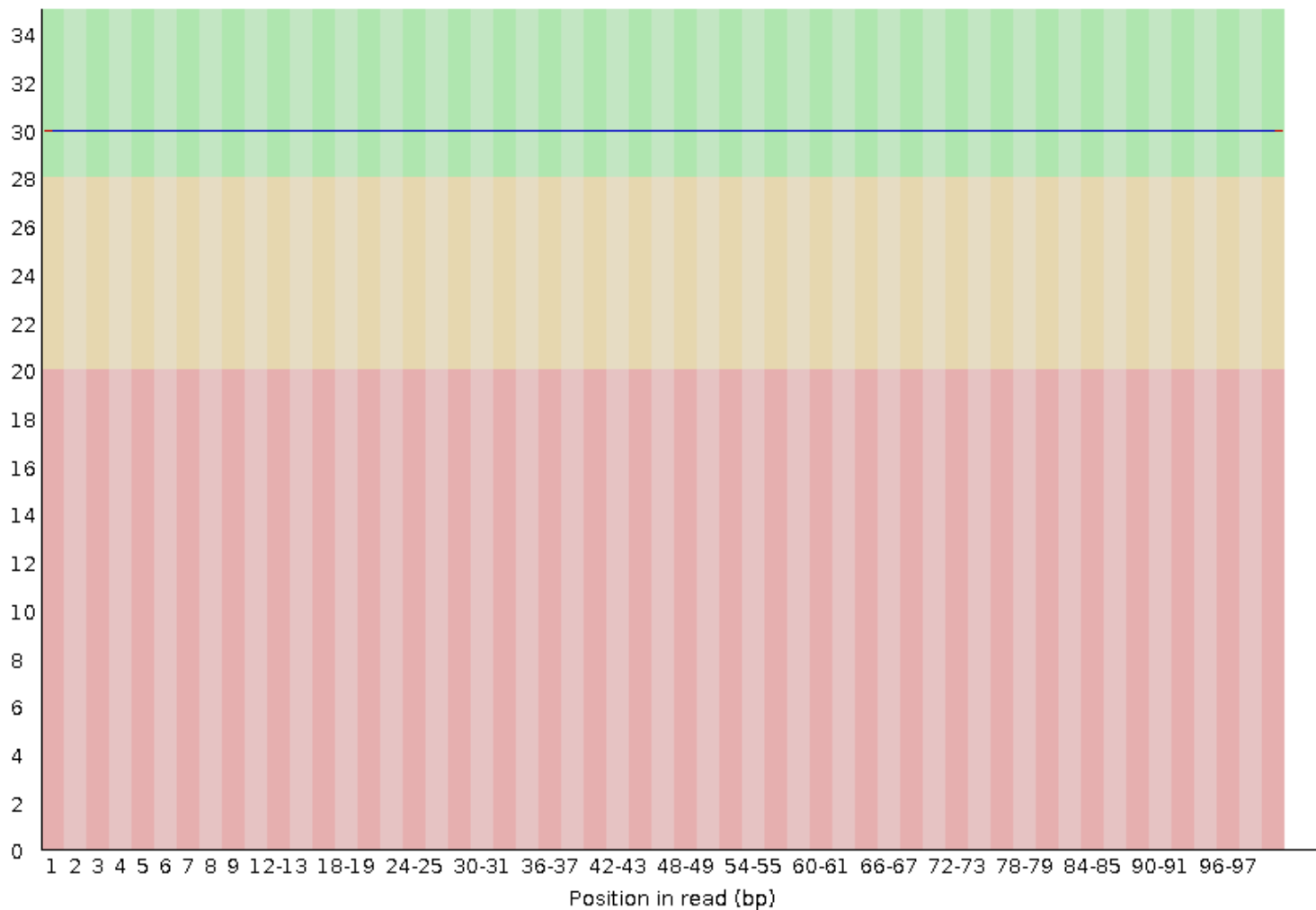
Basic Statistics

Measure	Value
Filename	SRR491287_1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	20004674
Total Bases	2 Gbp
Sequences flagged as poor quality	0
Sequence length	101
%GC	59



Per base sequence quality

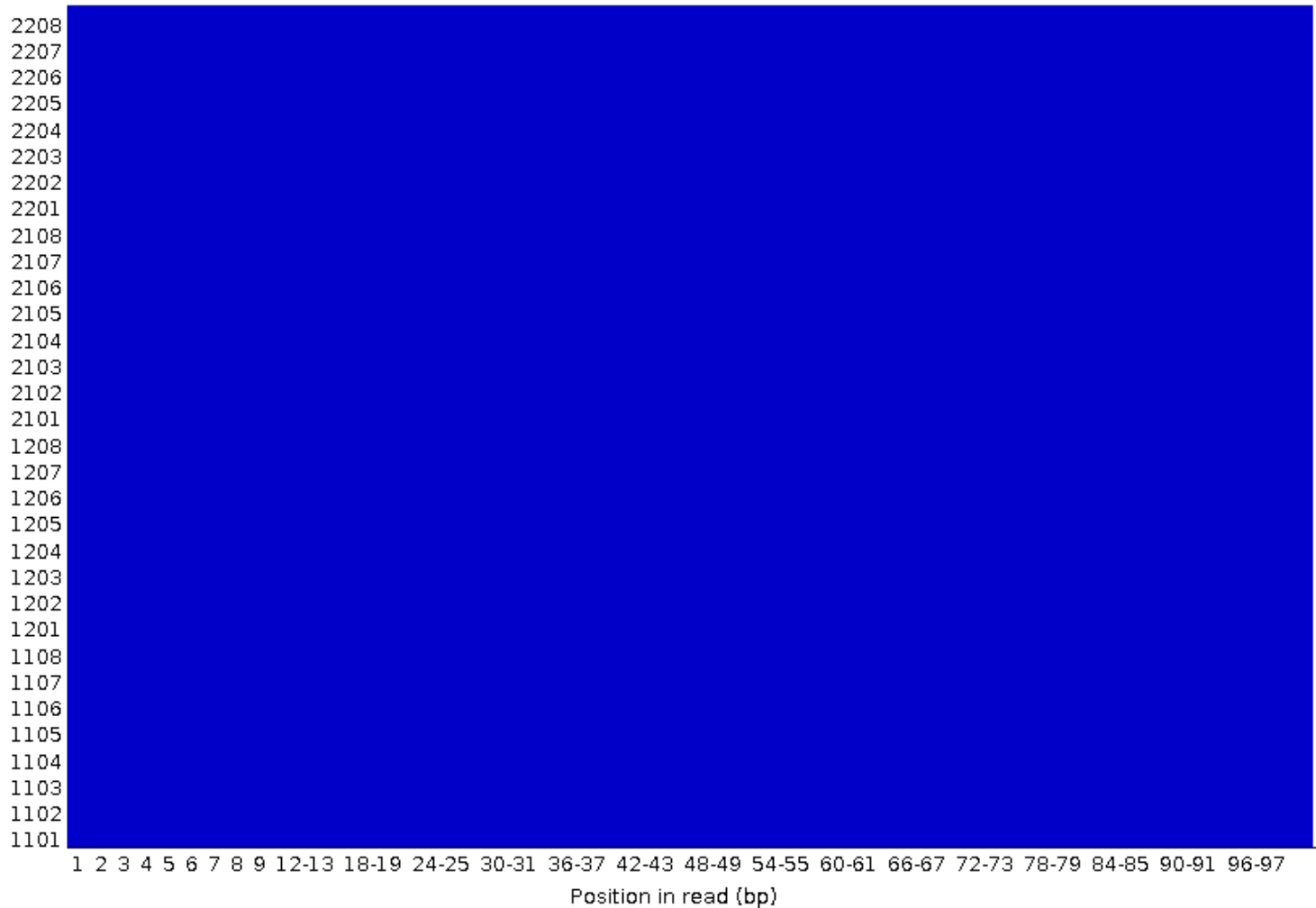
Quality scores across all bases (Sanger / Illumina 1.9 encoding)





Per tile sequence quality

Quality per tile





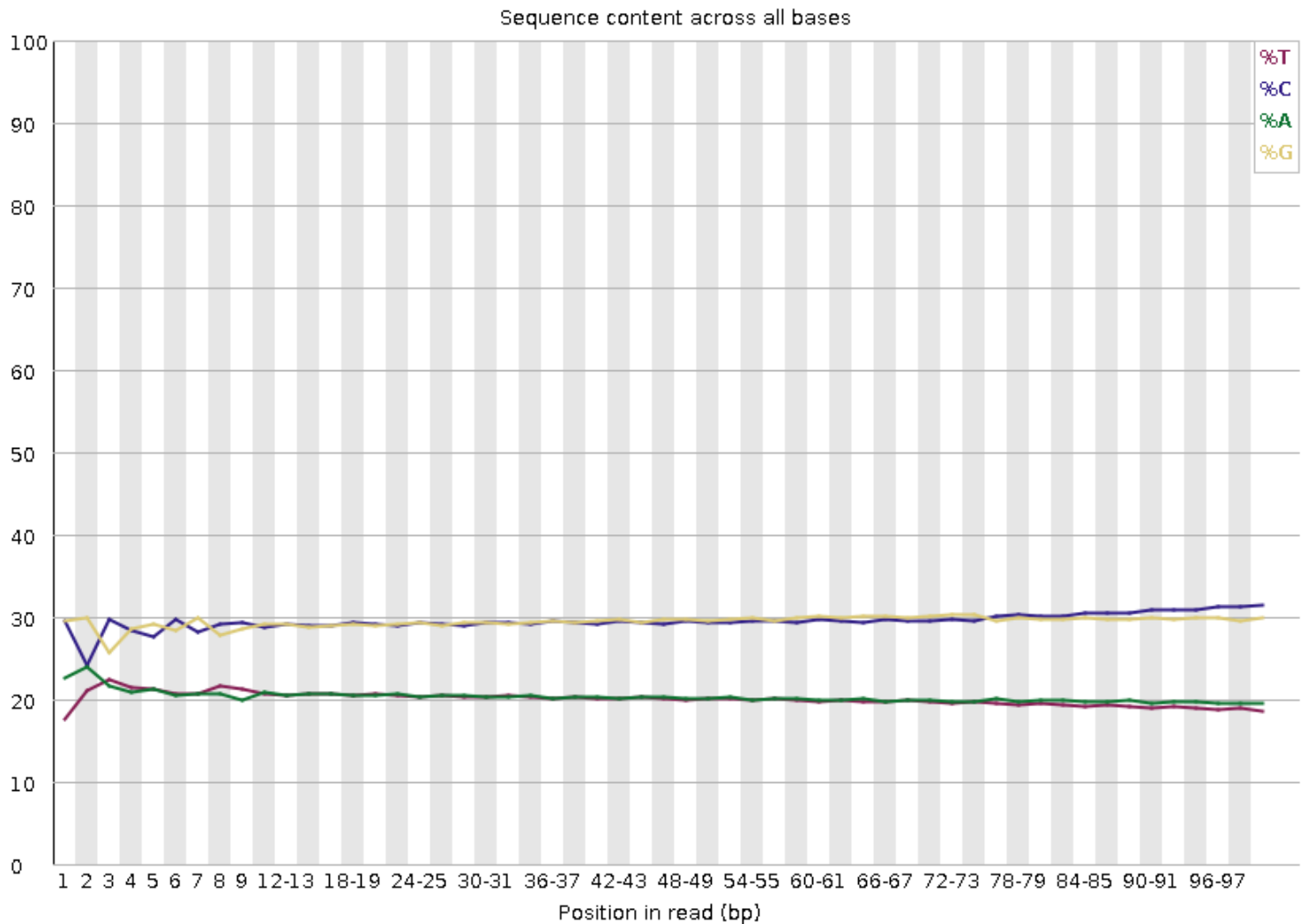
Per sequence quality scores

Quality score distribution over all sequences



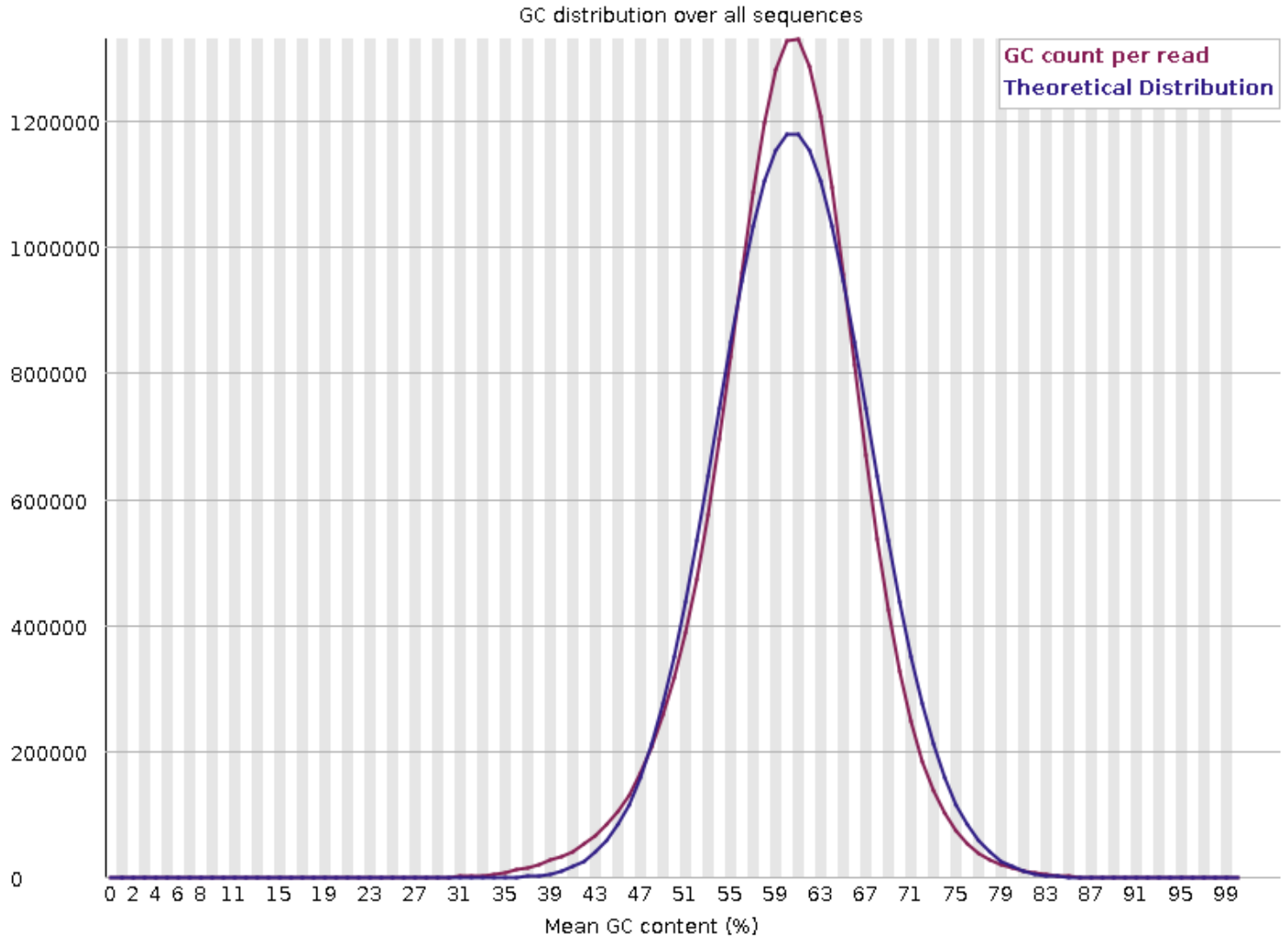


Per base sequence content



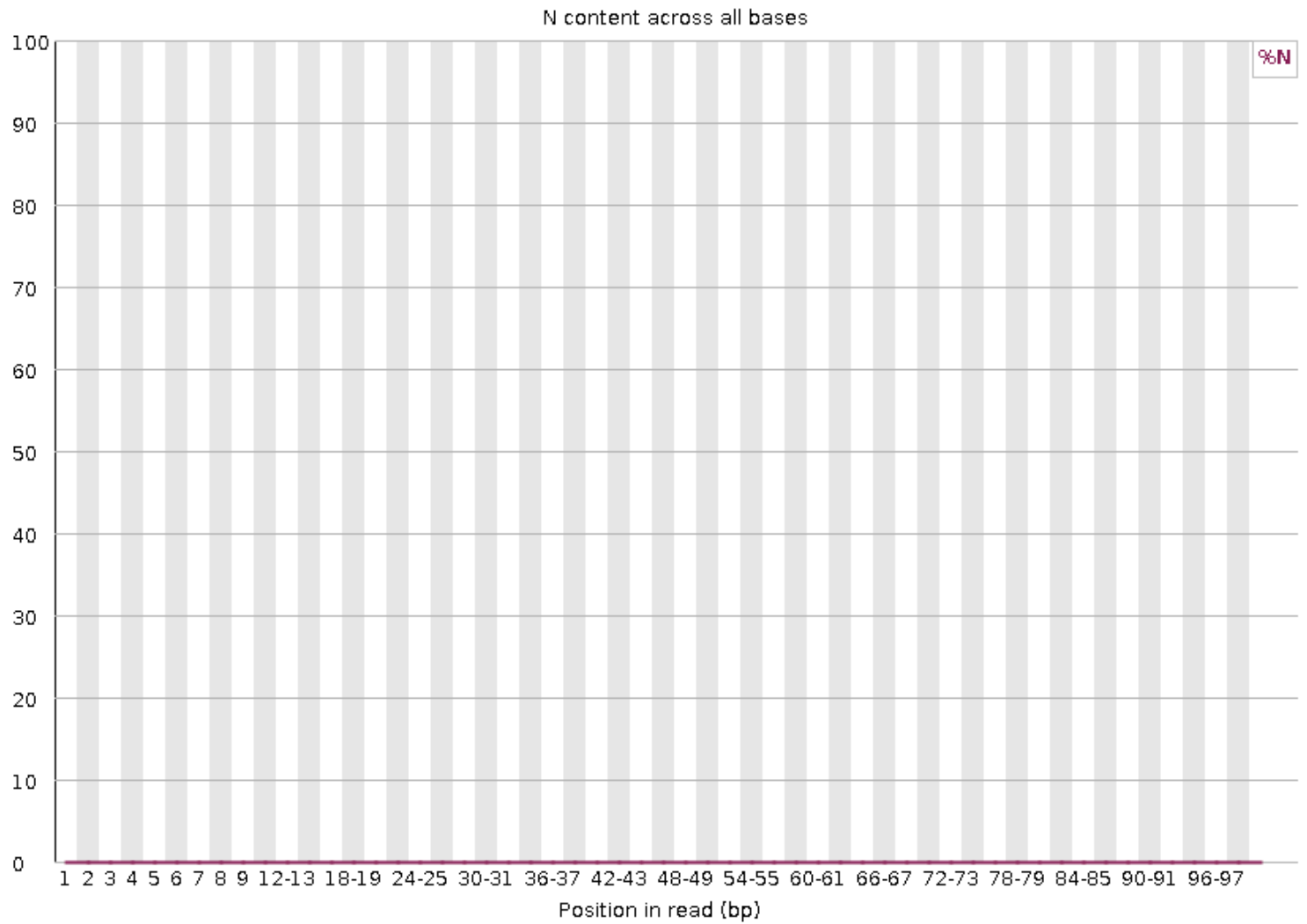


Per sequence GC content



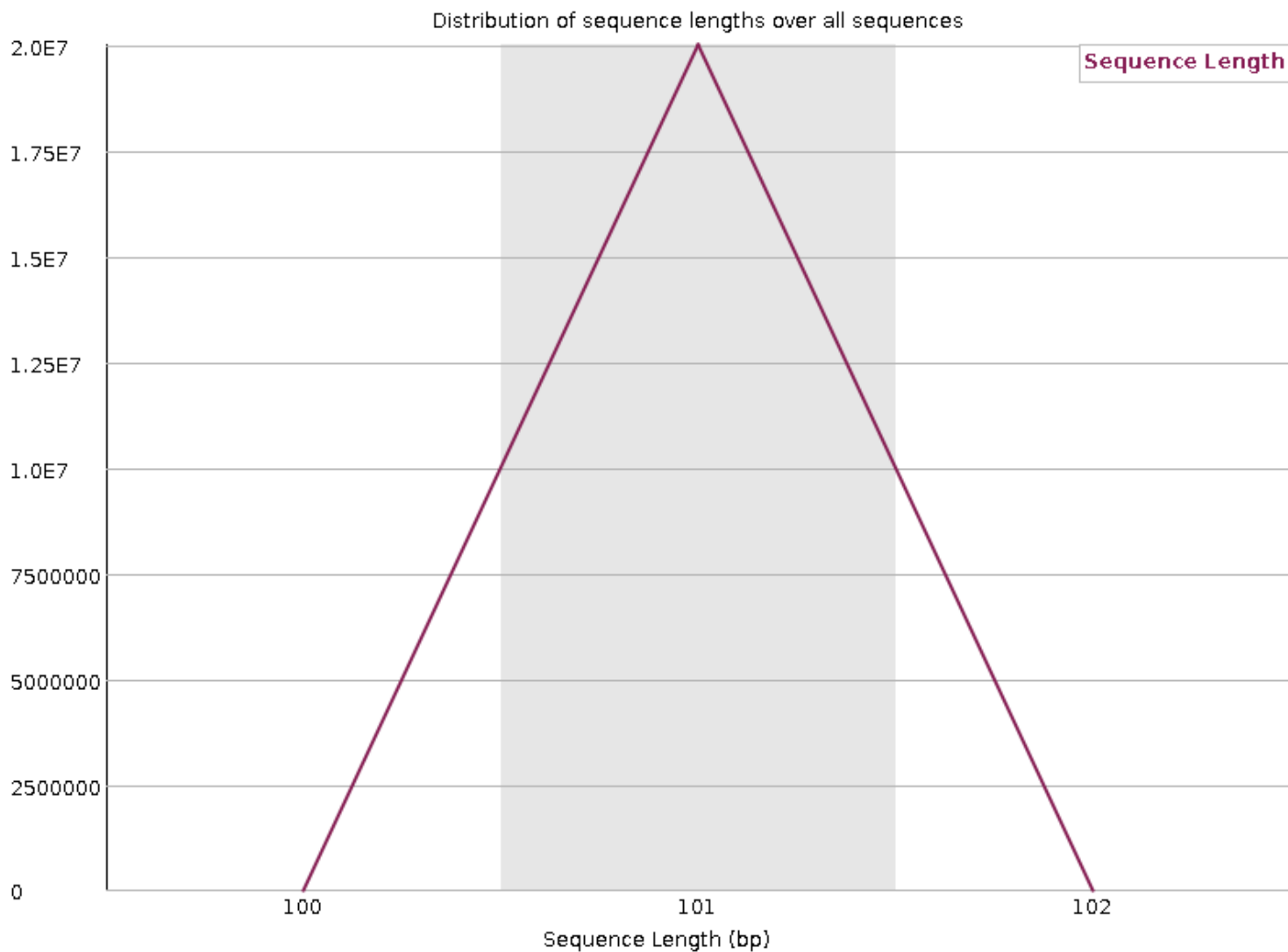


Per base N content

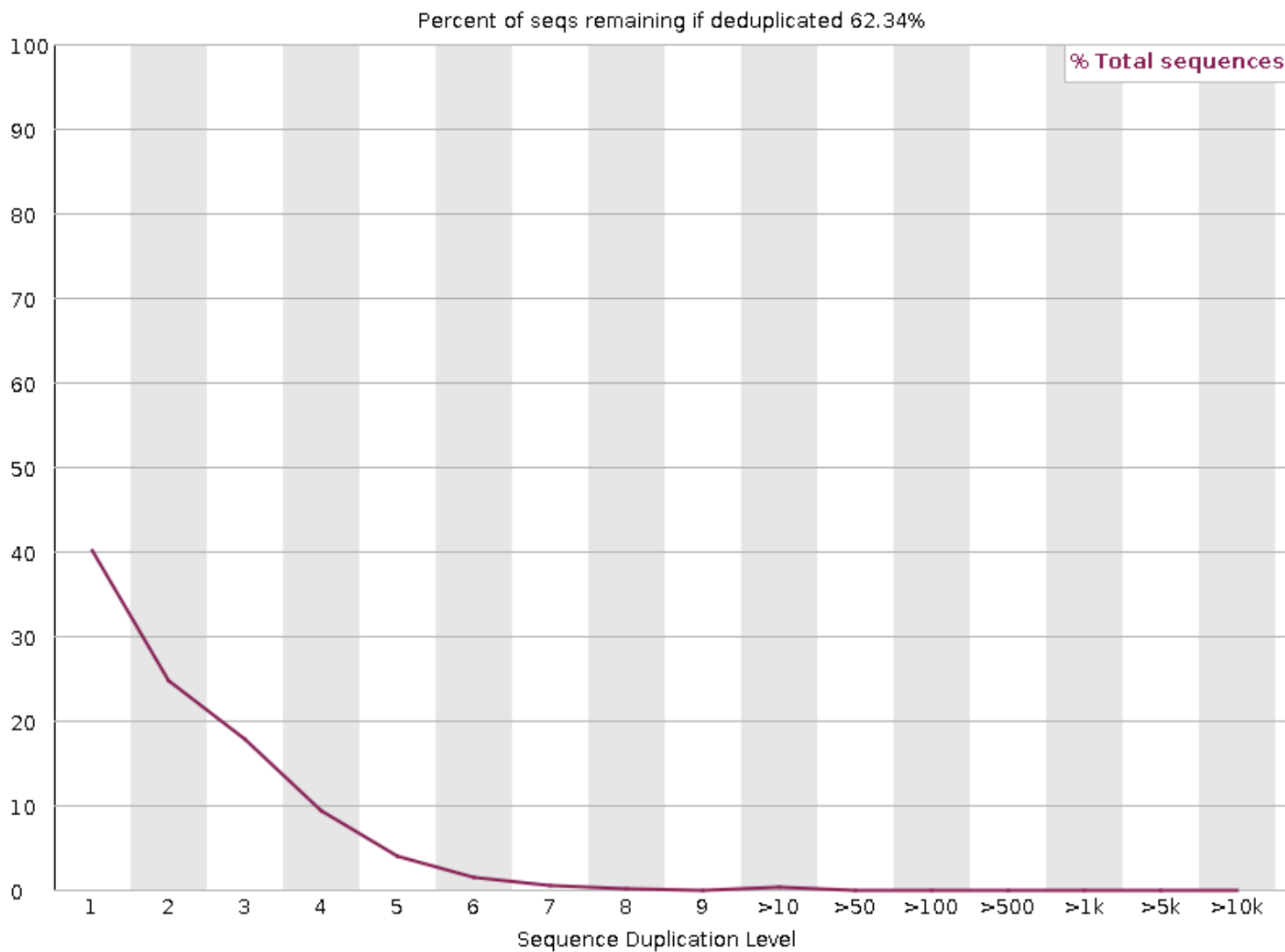




Sequence Length Distribution



! Sequence Duplication Levels

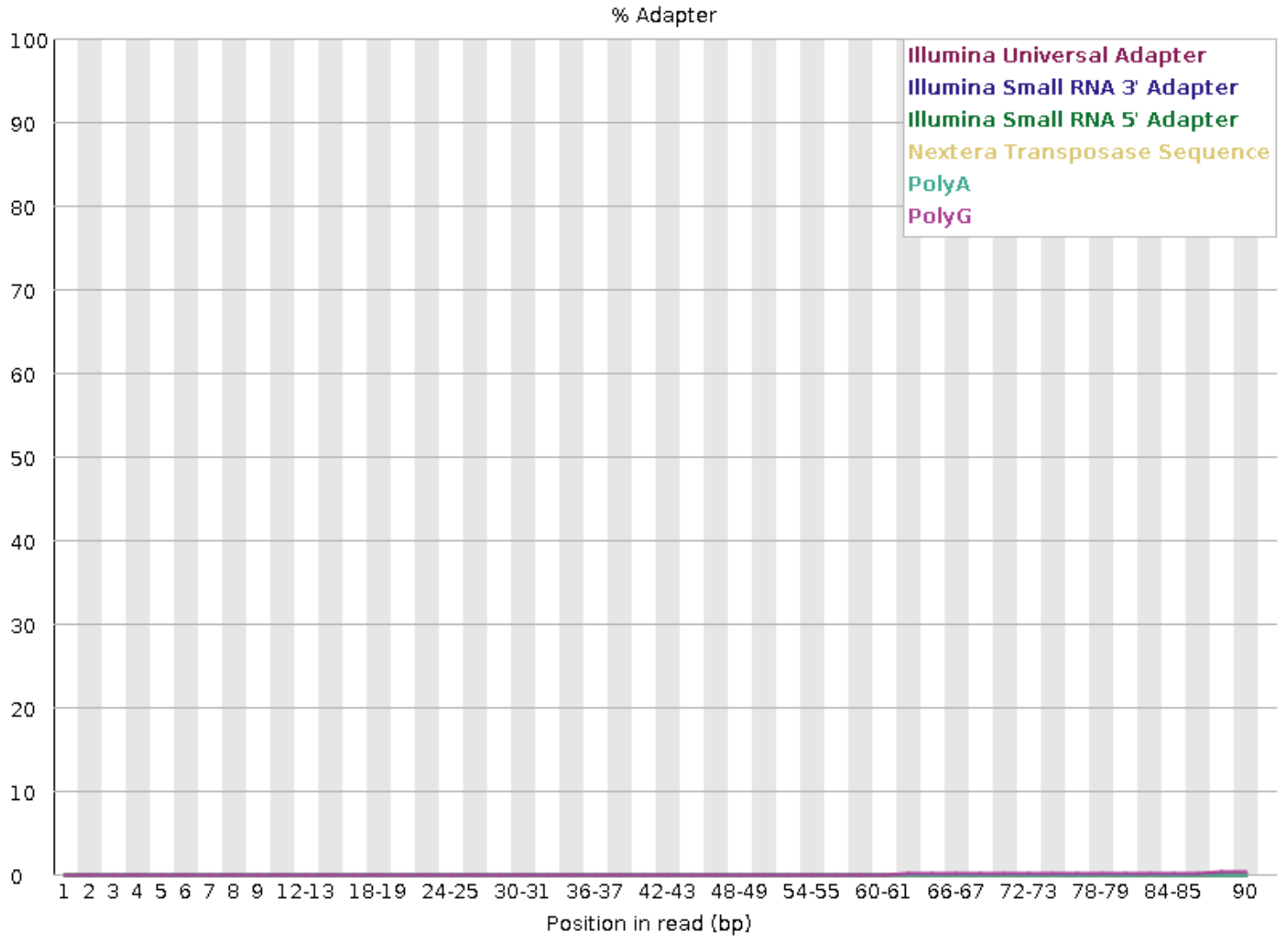


✓ Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.12.1)