












FastQC Report

Mon 29 Jan 2024
241155E_R2.fastq.gz

Summary

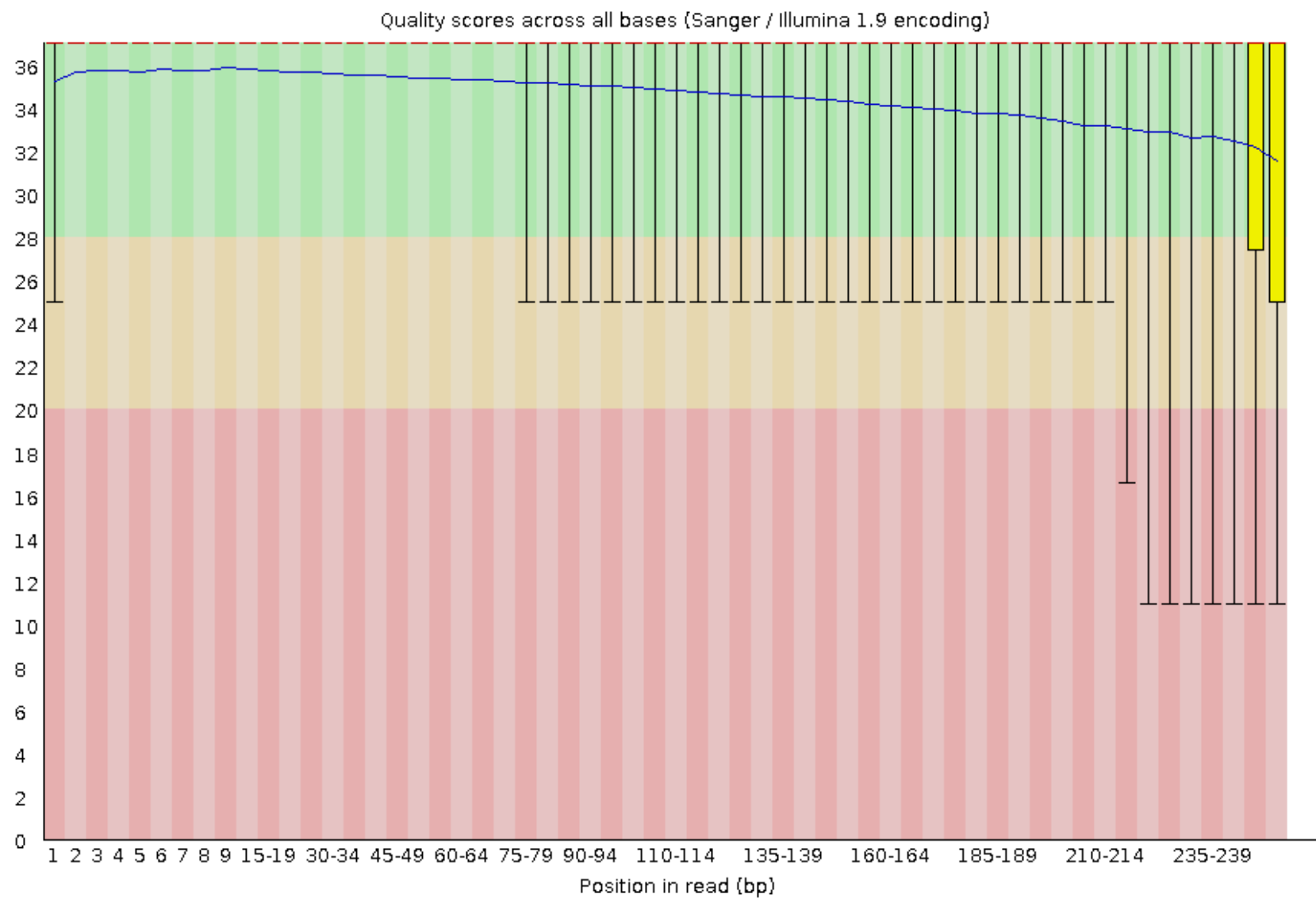
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Basic Statistics

Measure	Value
Filename	241155E_R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9

Measure	Value
Total Sequences	1639549
Total Bases	411.5 Mbp
Sequences flagged as poor quality	0
Sequence length	251
%GC	45

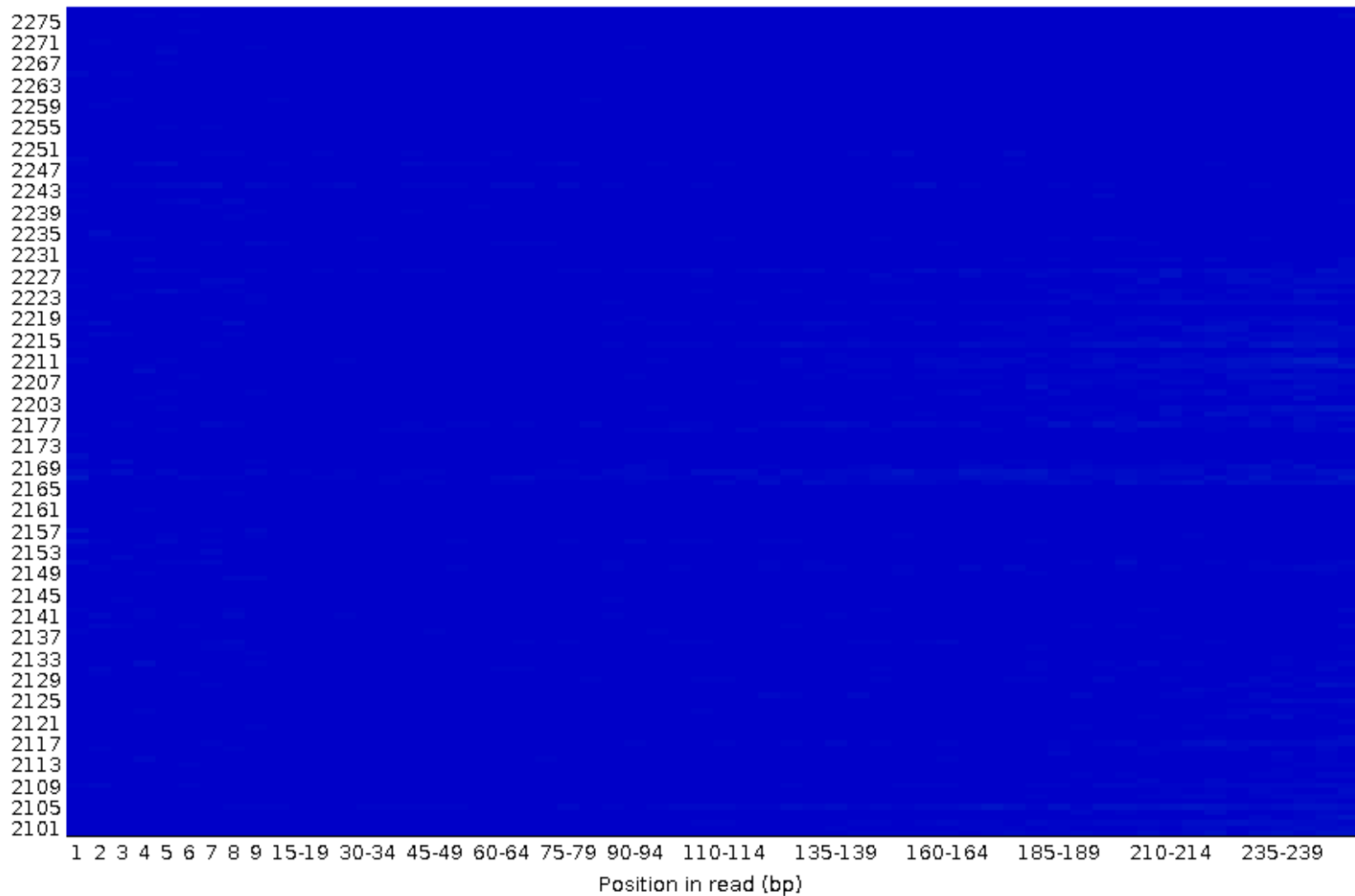
Per base sequence quality





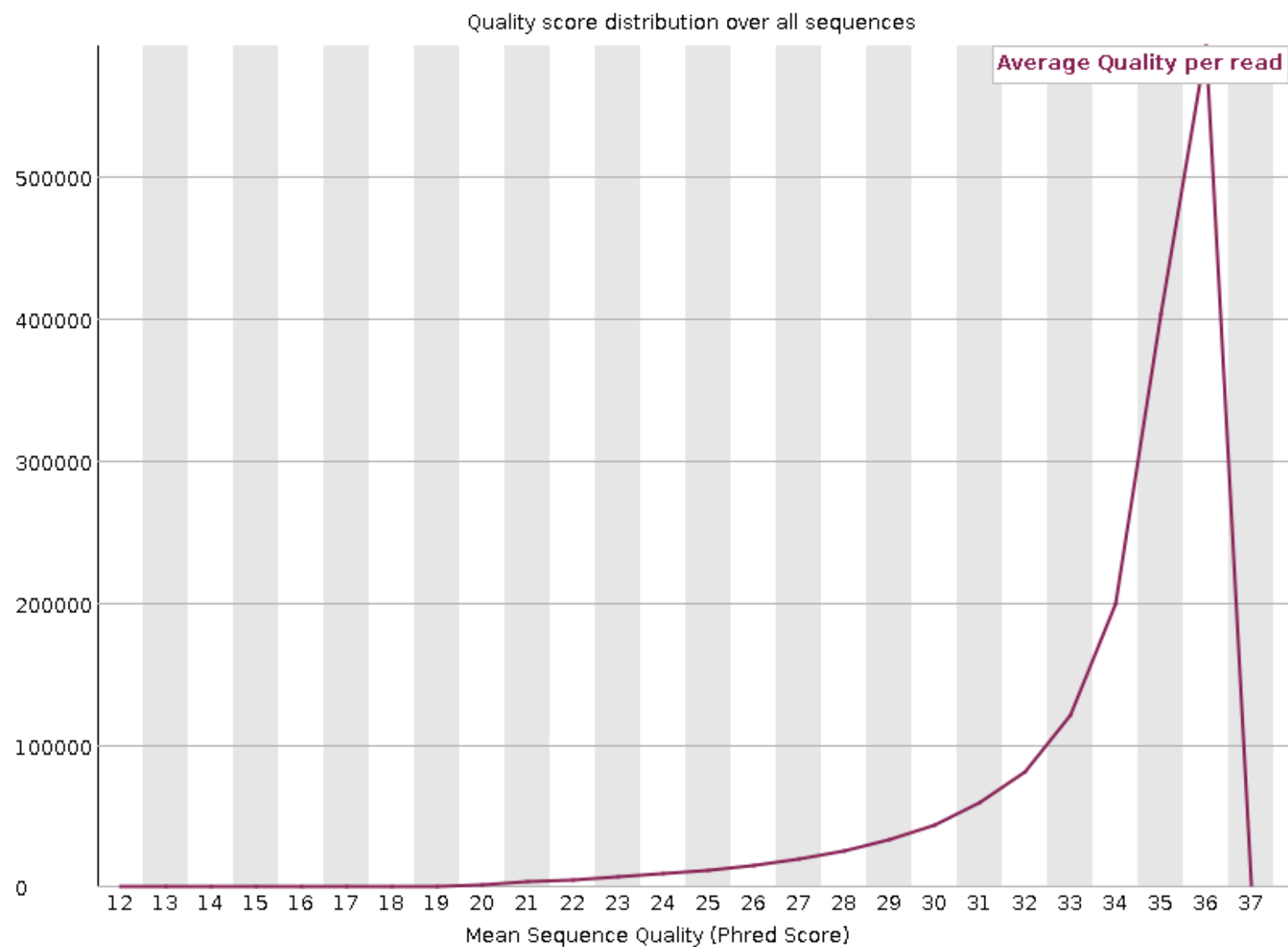
Per tile sequence quality

Quality per tile



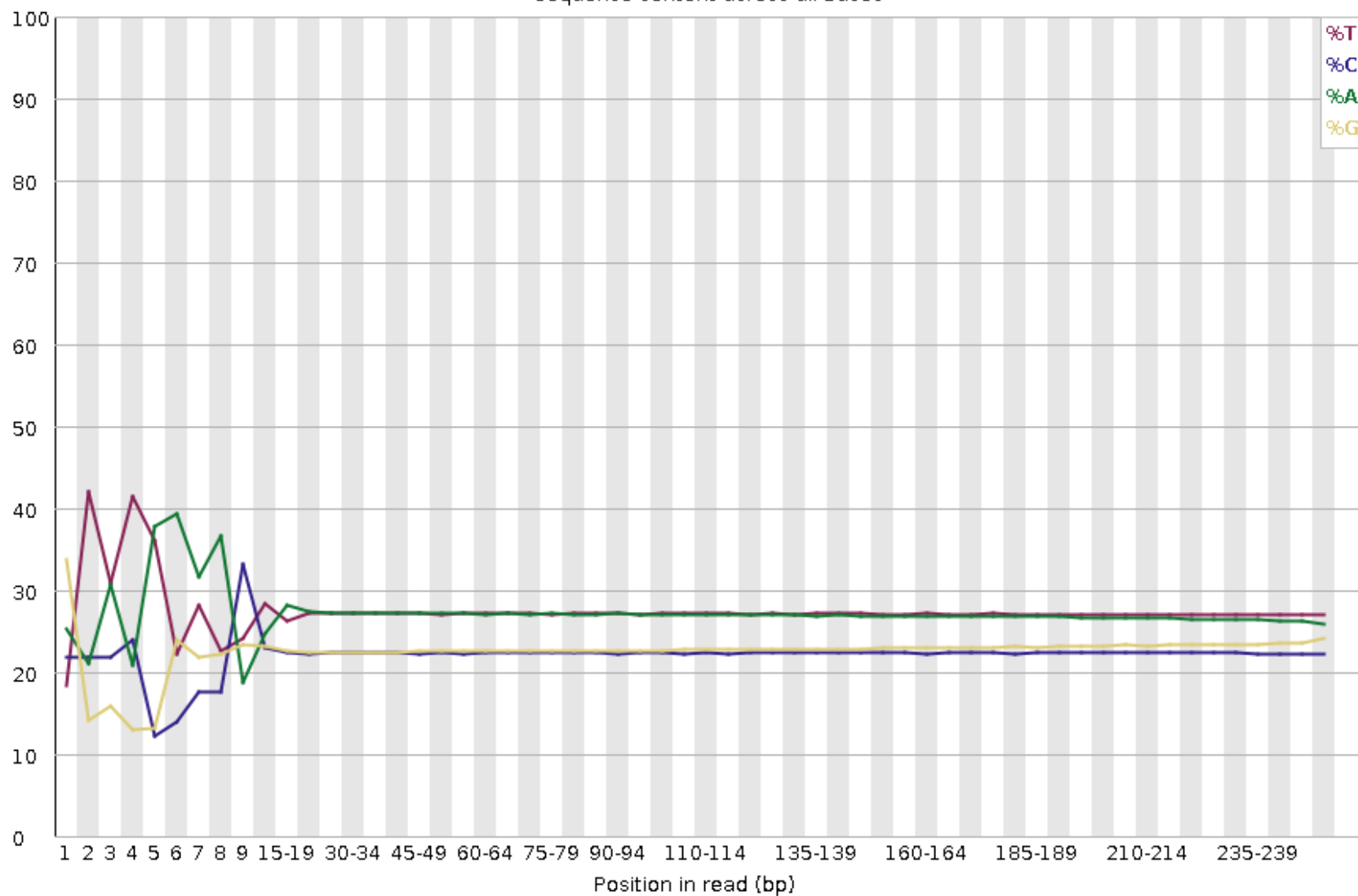


Per sequence quality scores



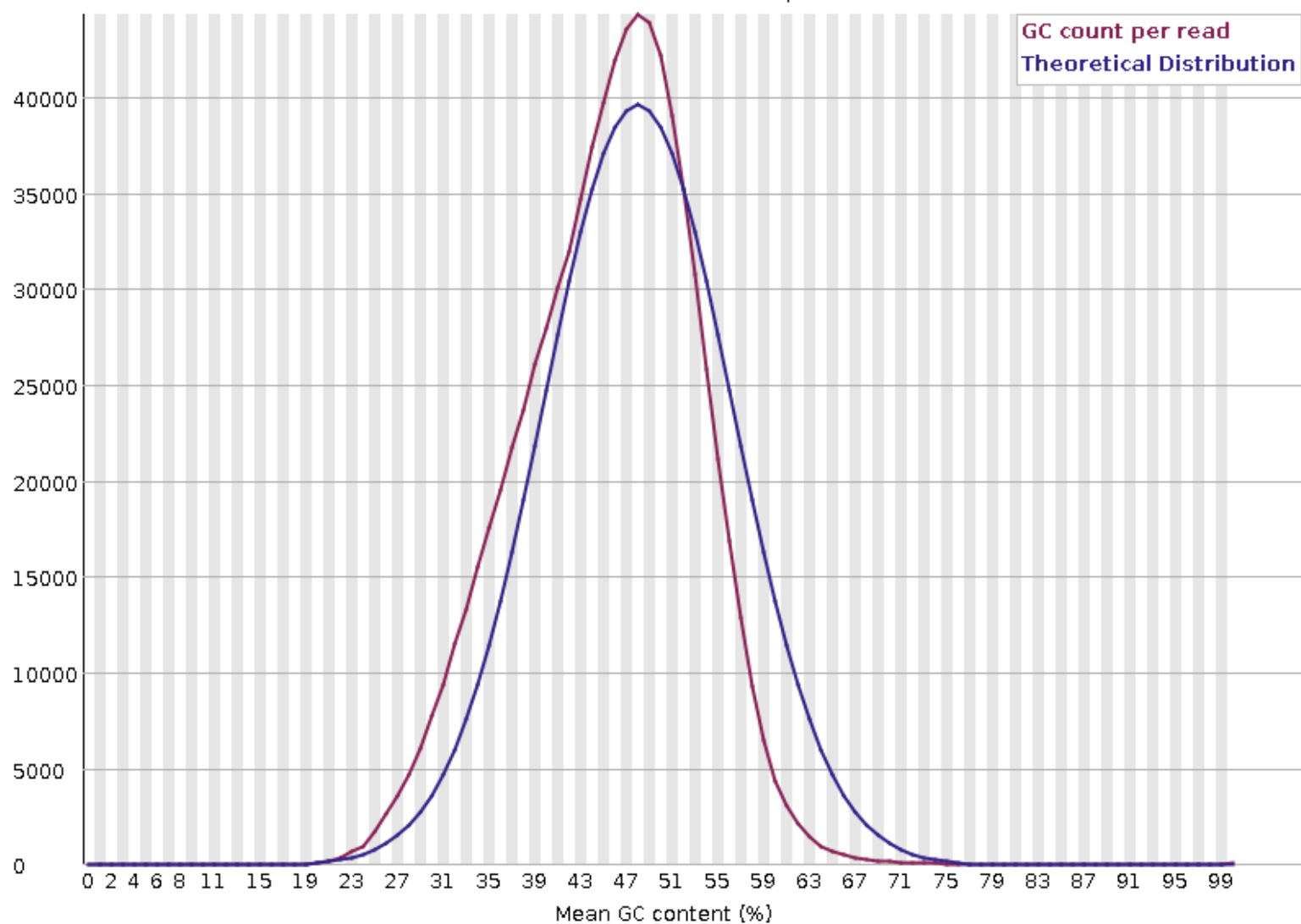
✖ Per base sequence content

Sequence content across all bases



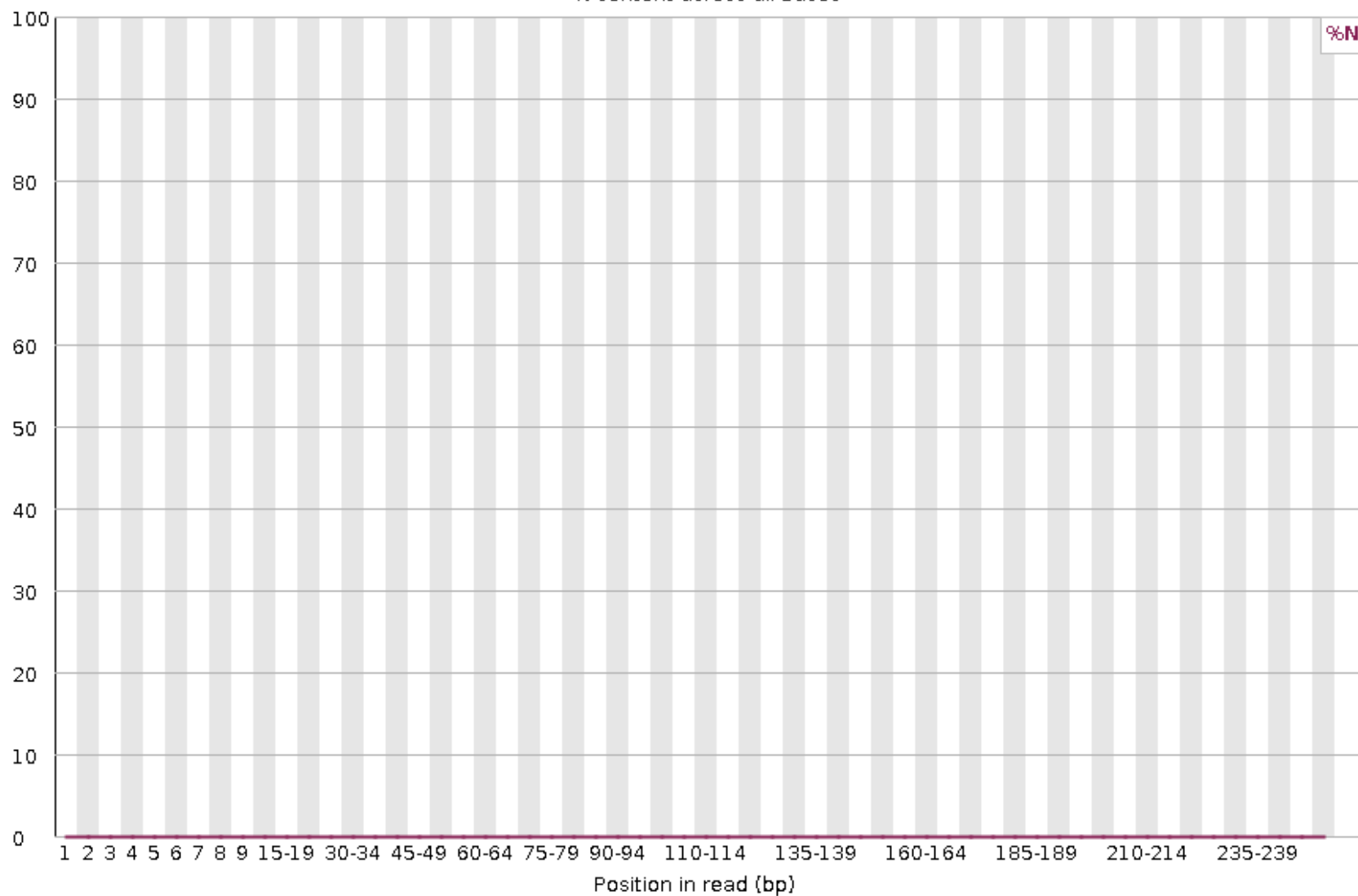
🚨 Per sequence GC content

GC distribution over all sequences

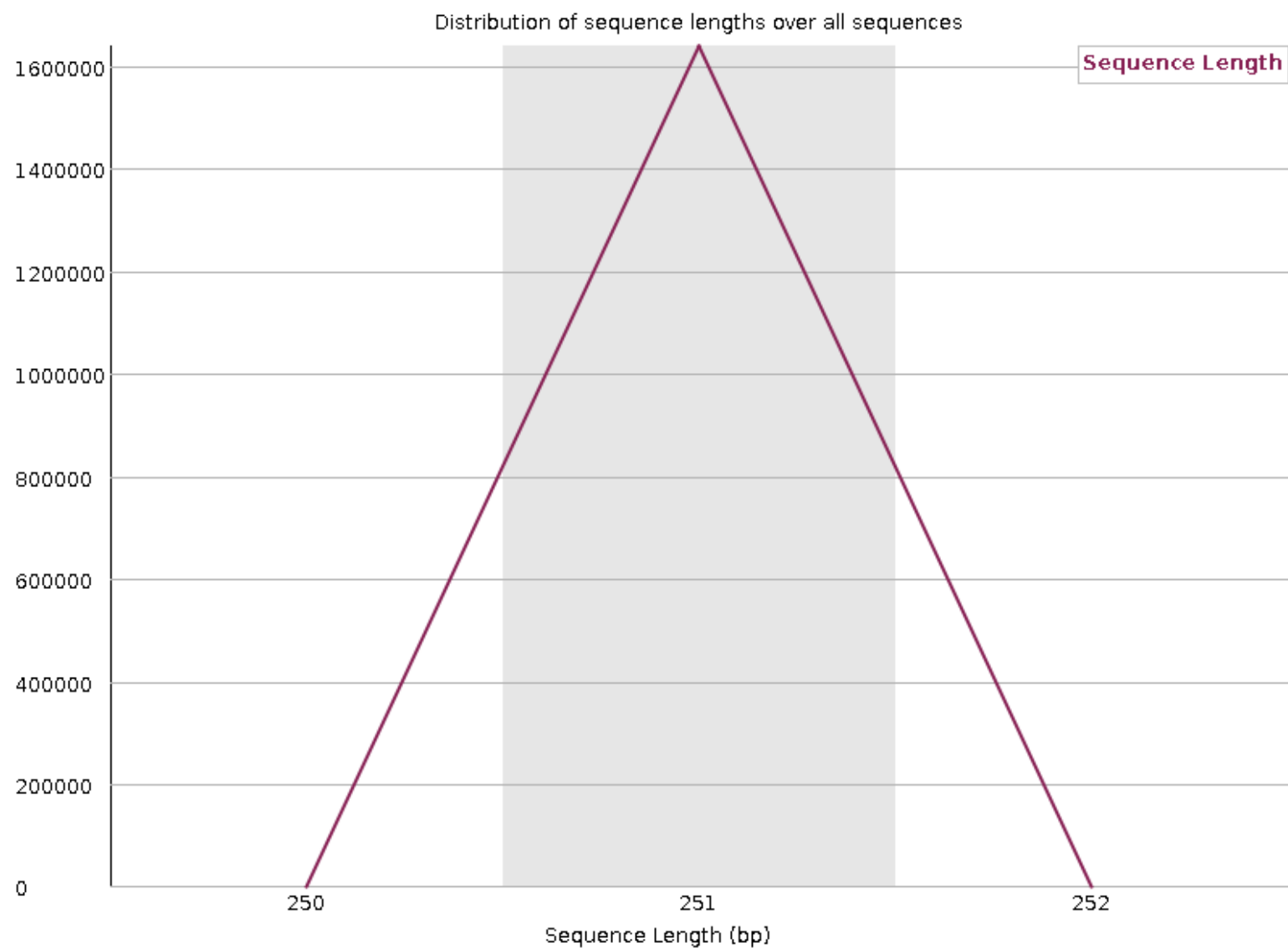


✔ Per base N content

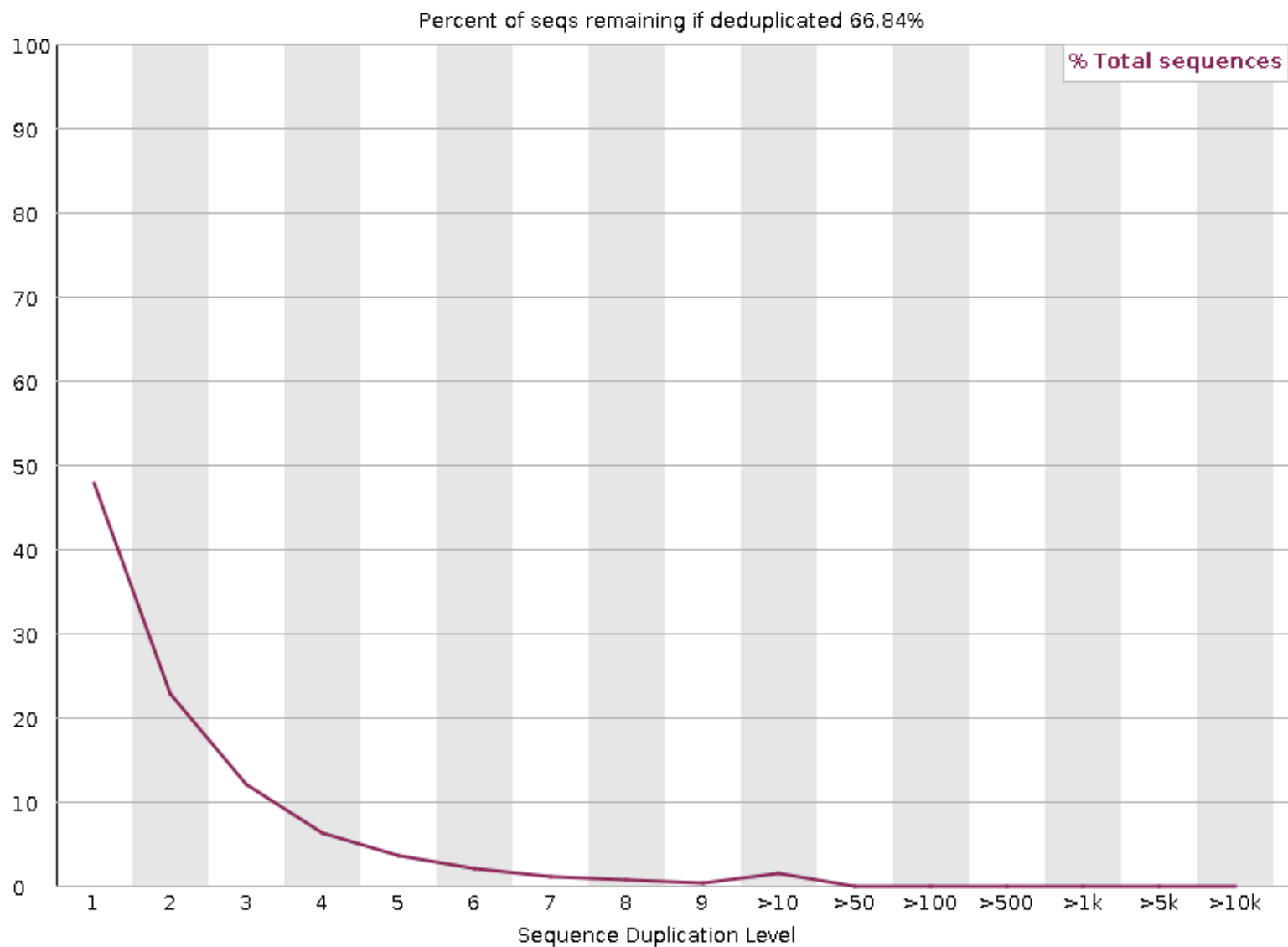
N content across all bases



✔ Sequence Length Distribution



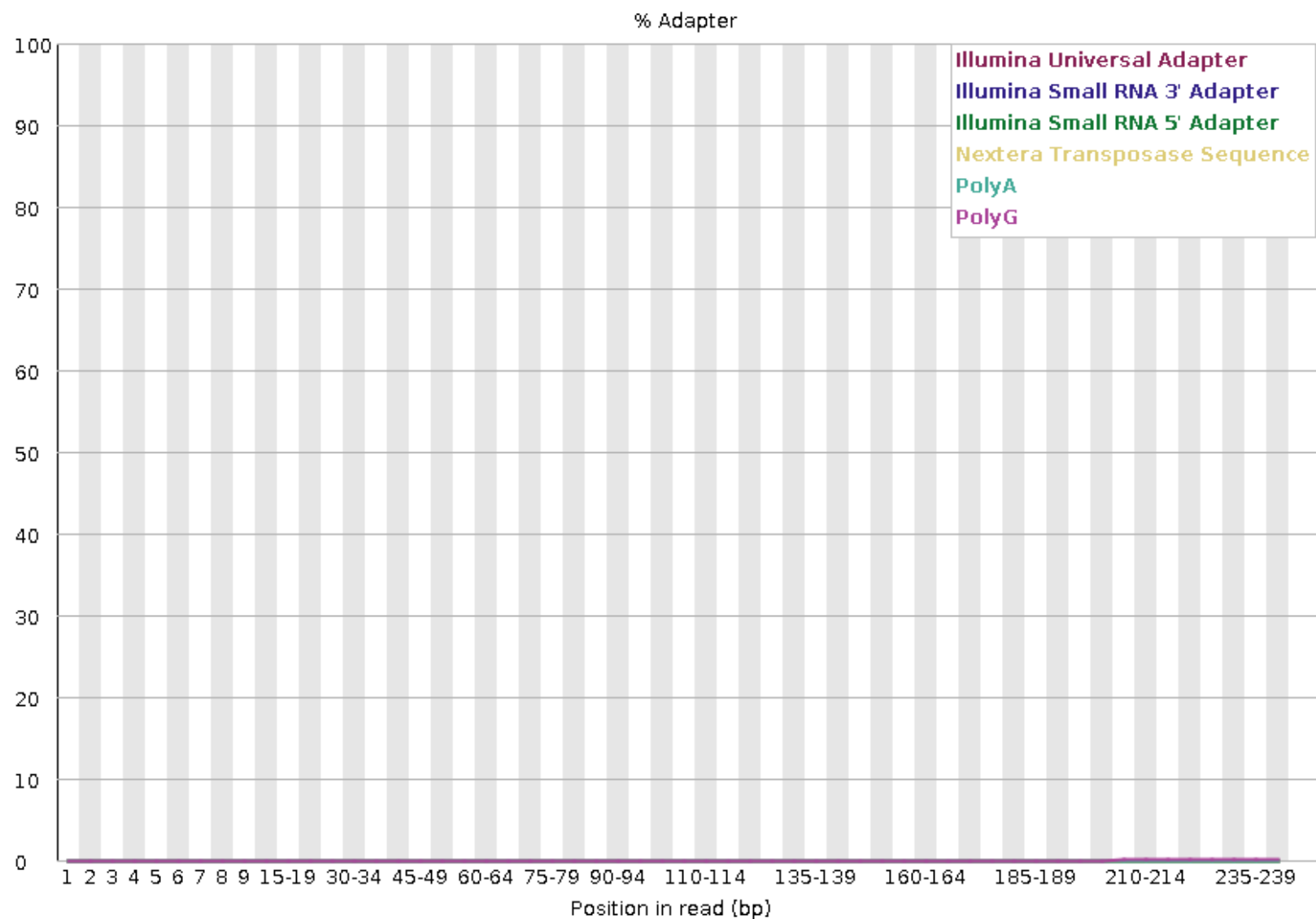
! Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content



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