FastQC Report

Thu 27 Mar 2025
SRR9620862_1_unpaired.fastq

Summary

- Basic Statistics
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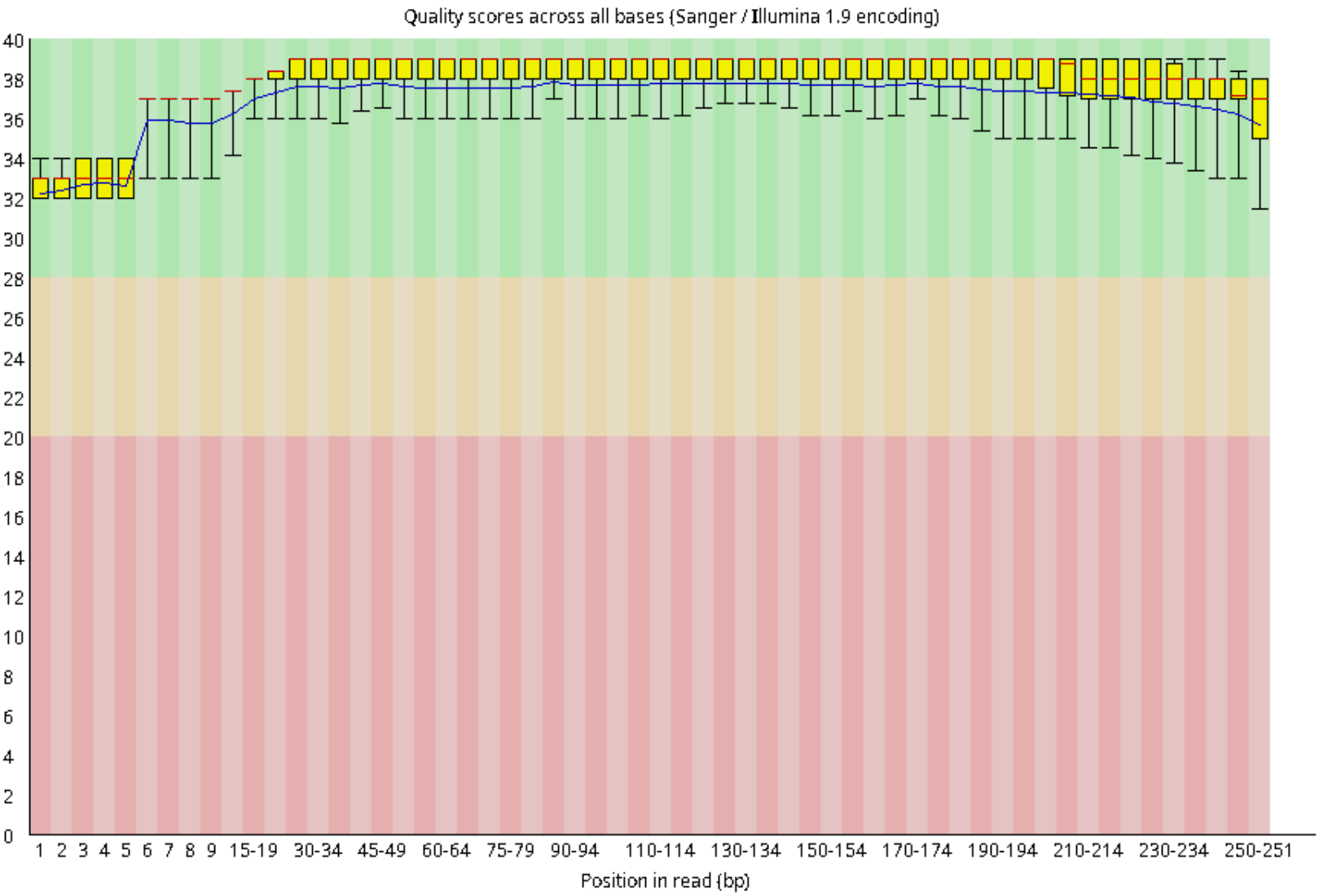
- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Adapter Content

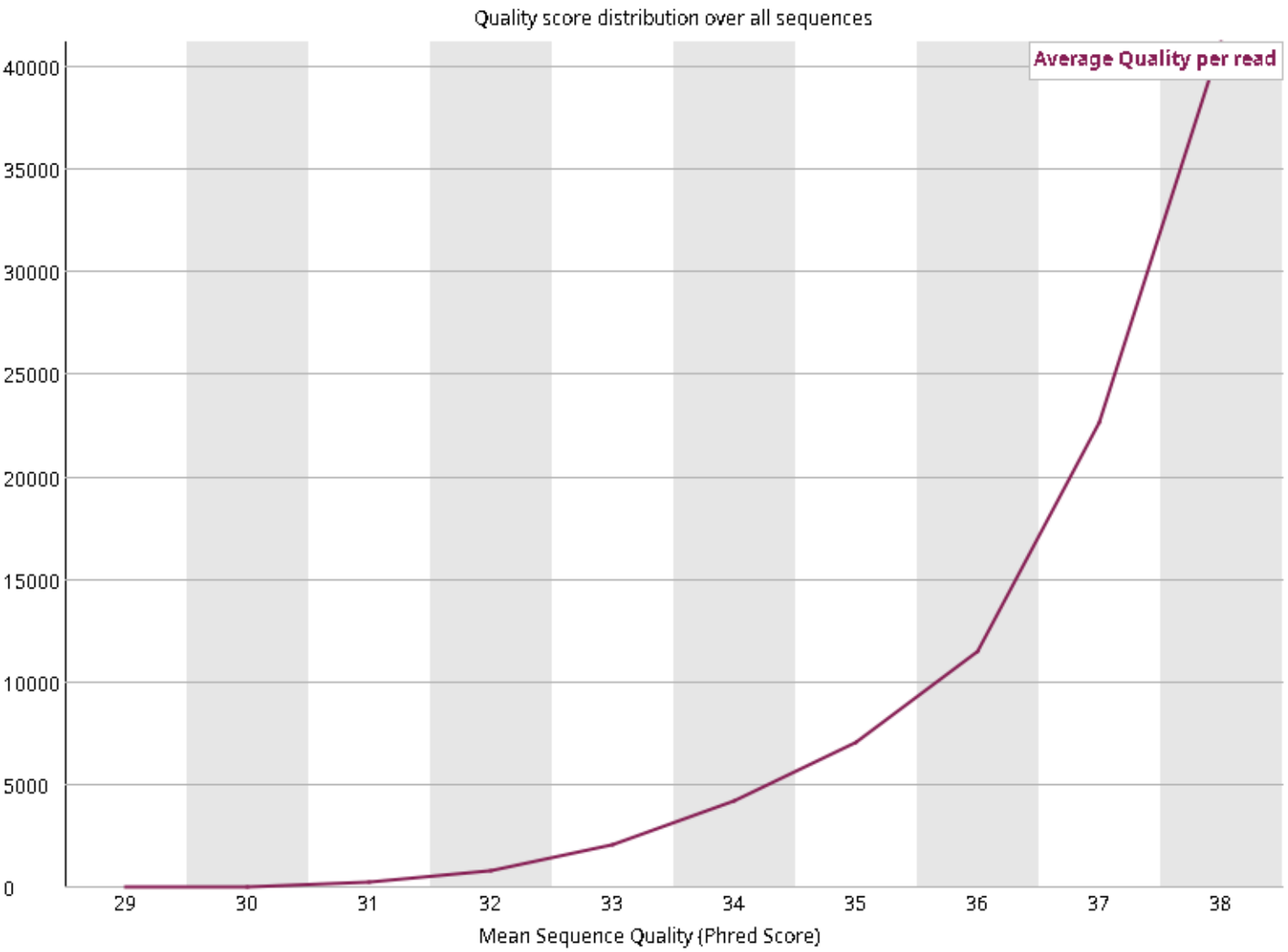
Basic Statistics

Measure	Value
Filename	SRR9620862_1_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	89860
Total Bases	22.5 Mbp
Sequences flagged as poor quality	0
Sequence length	250-251
%GC	33

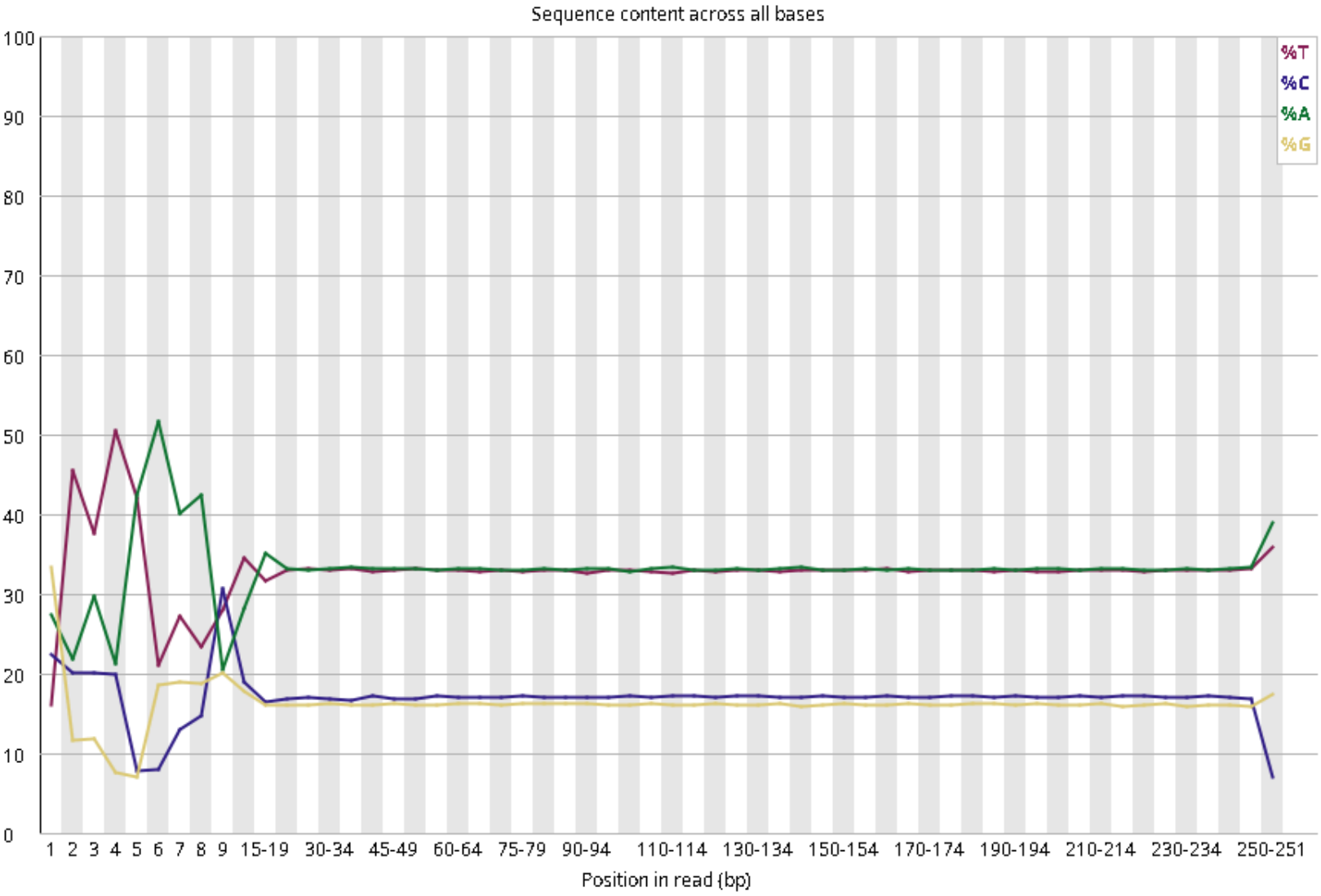
Per base sequence quality



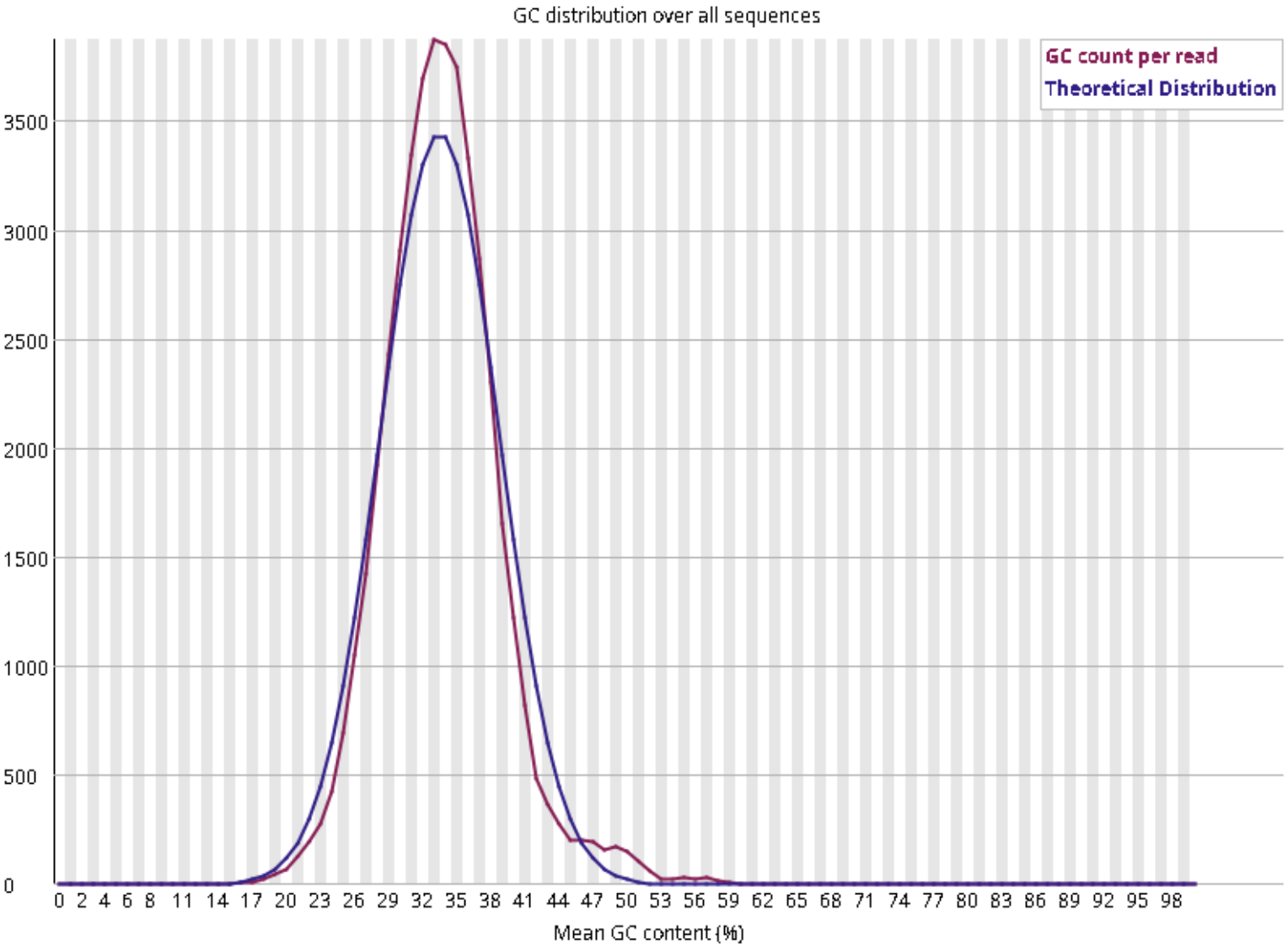
Per sequence quality scores



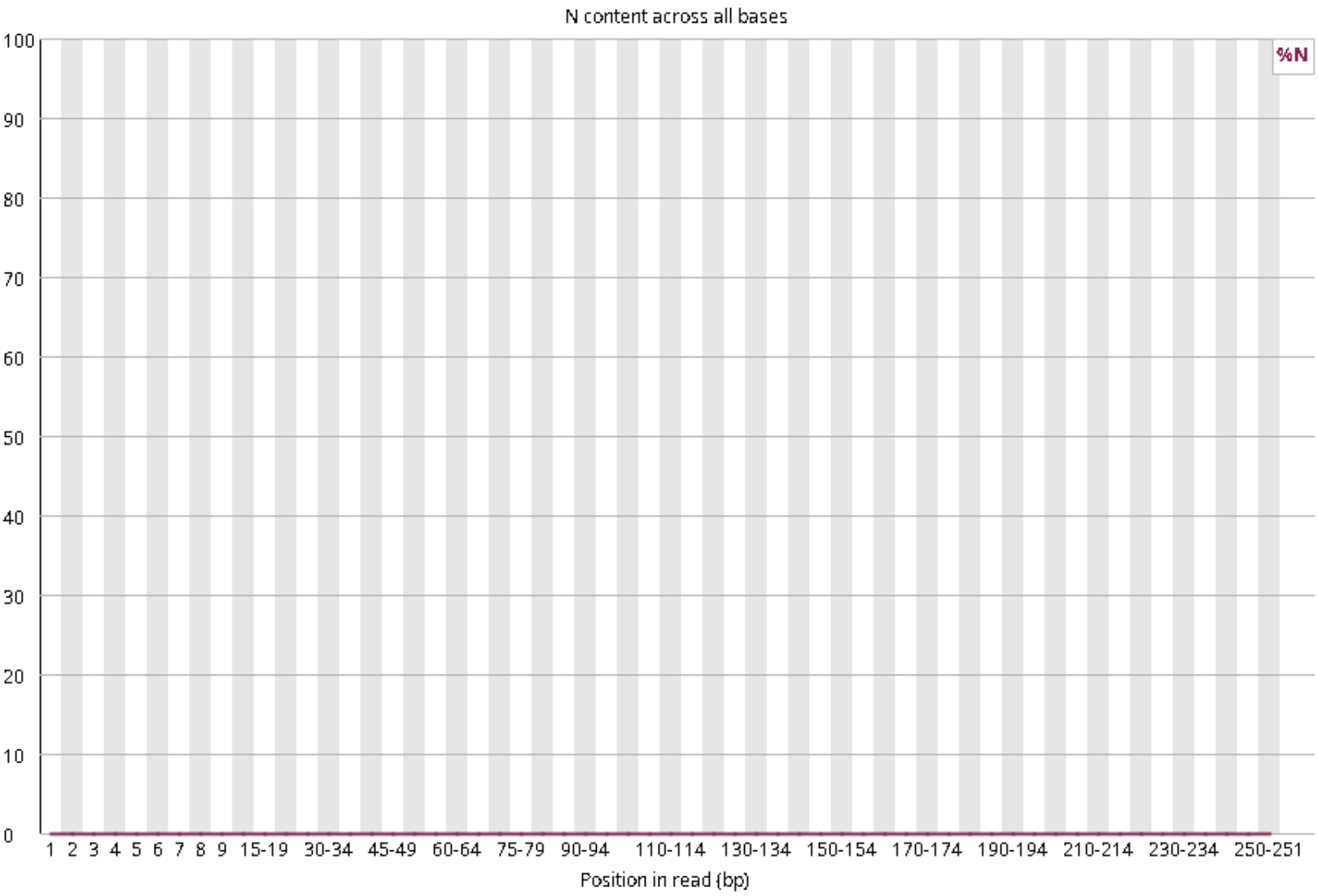
Per base sequence content



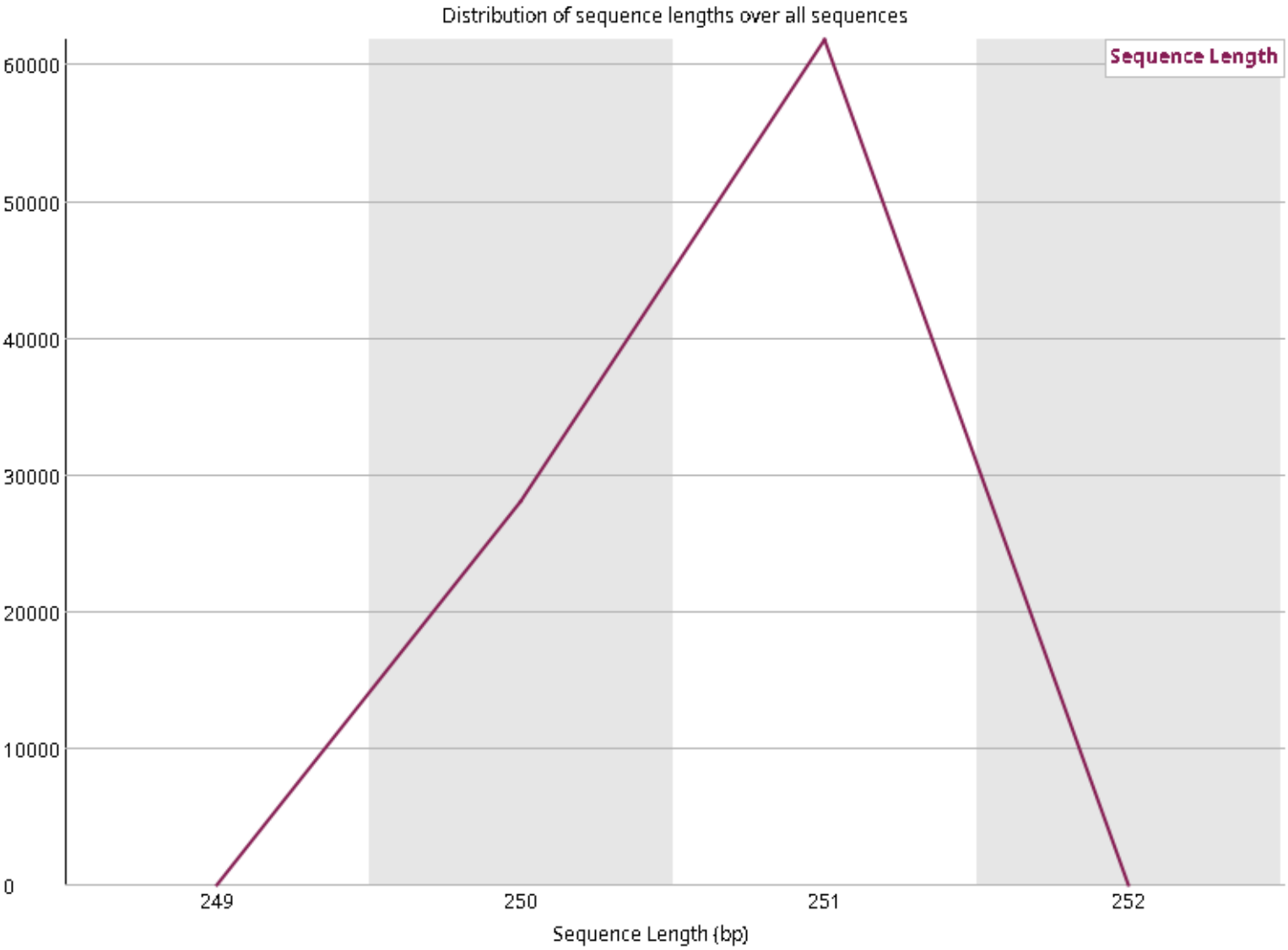
Per sequence GC content



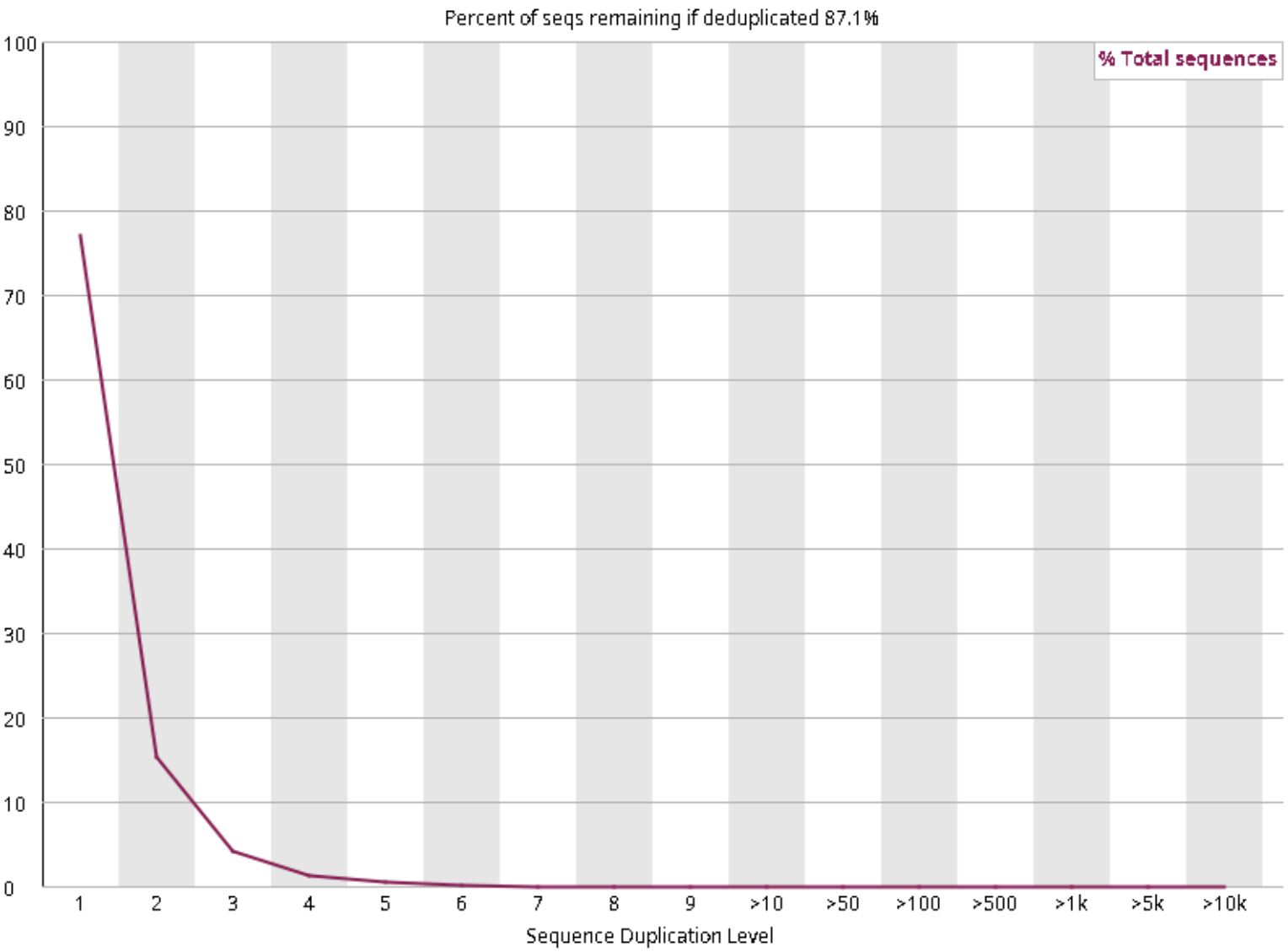
Per base N content



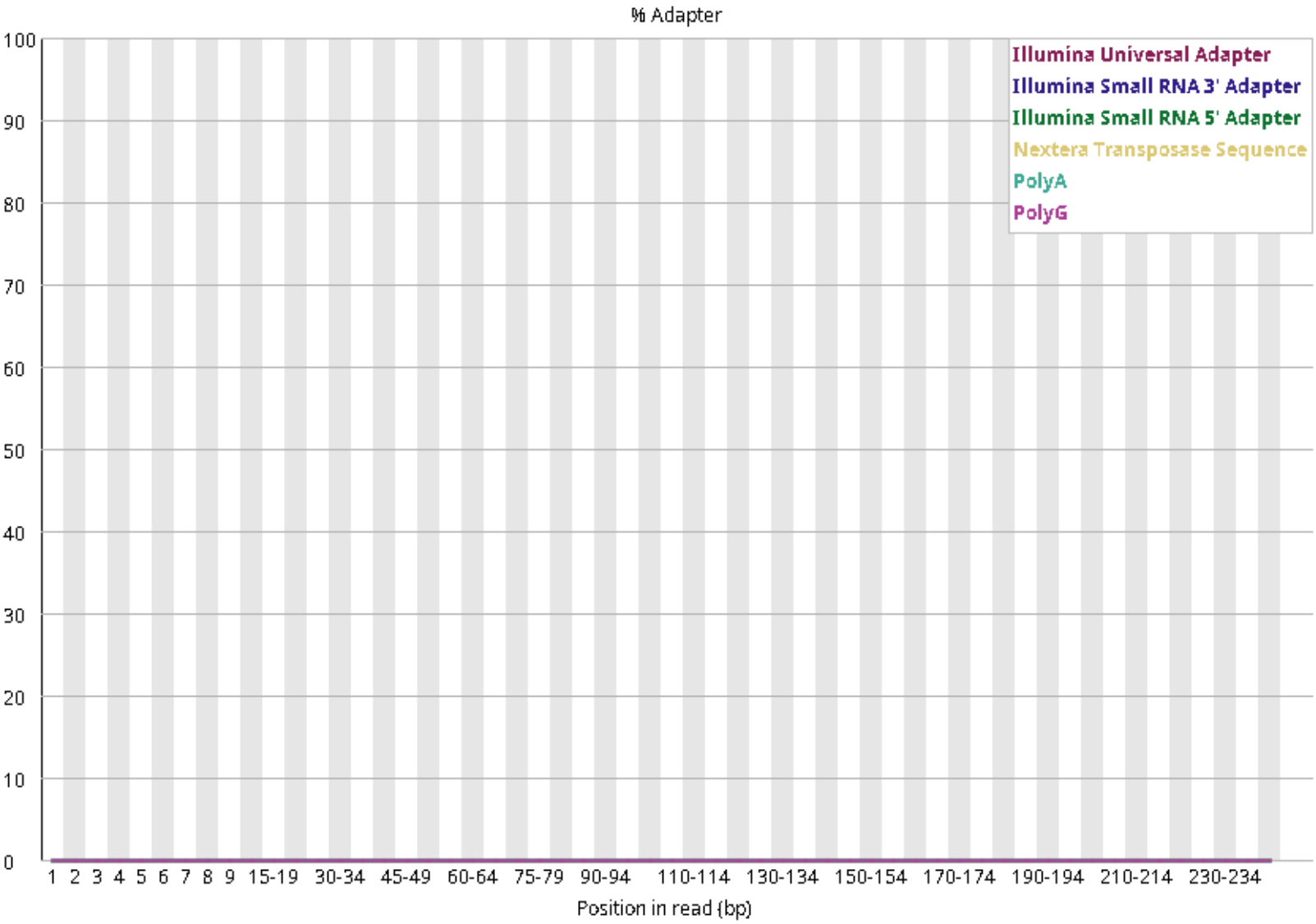
Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content