

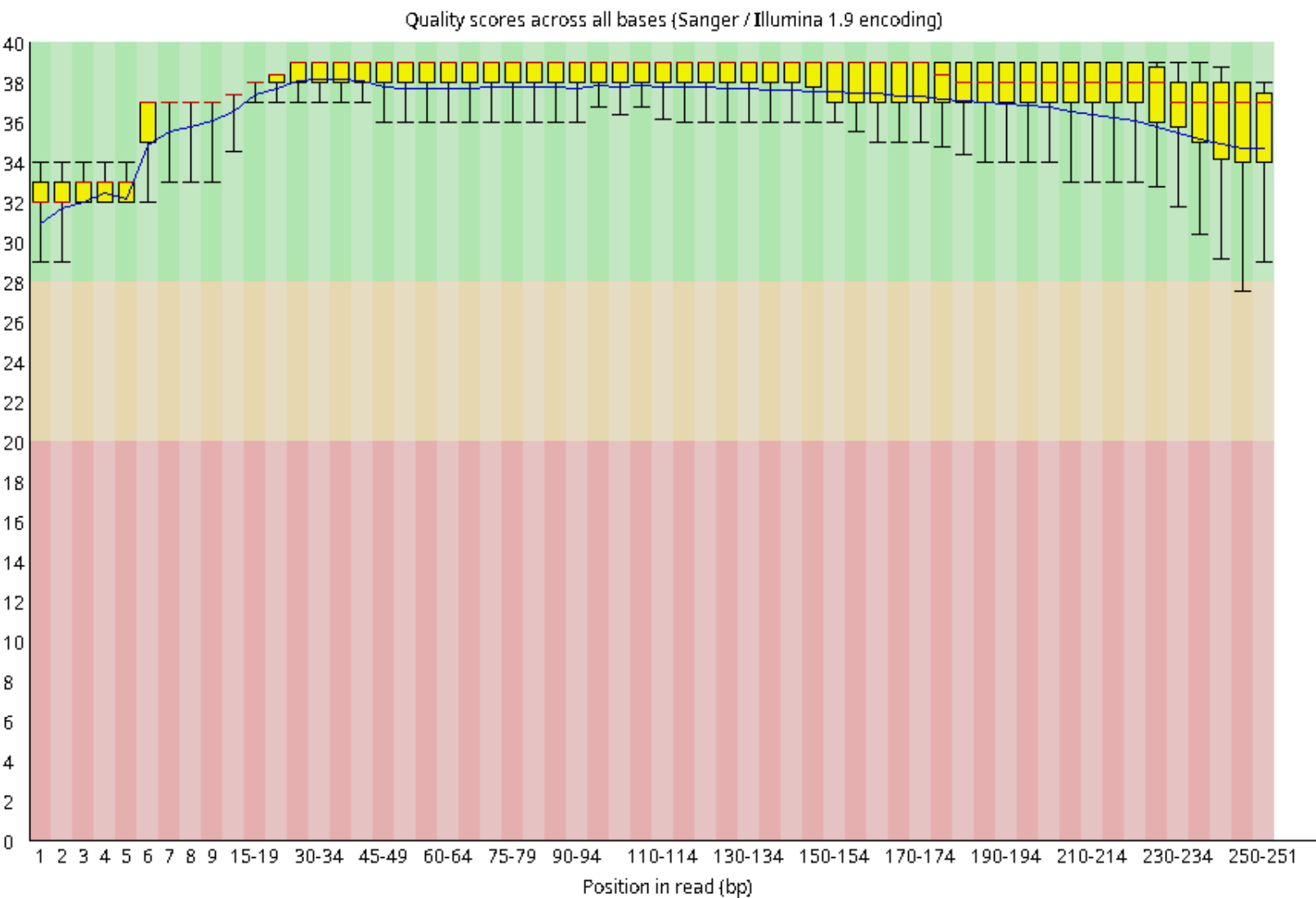
Summary

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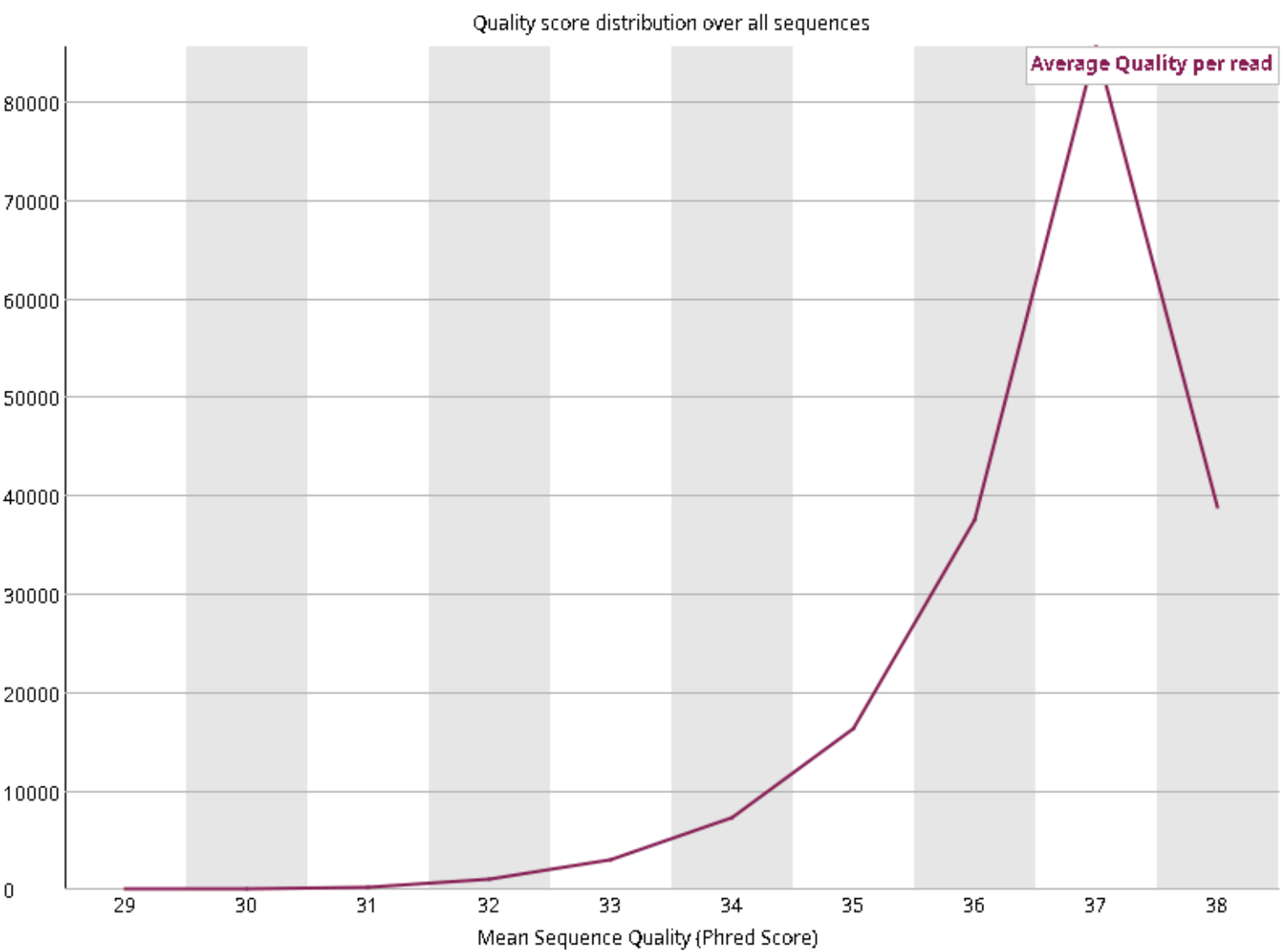
✓ Basic Statistics

Measure	Value
Filename	SRR9620862_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	190313
Total Bases	47.6 Mbp
Sequences flagged as poor quality	0
Sequence length	250-251
%GC	32

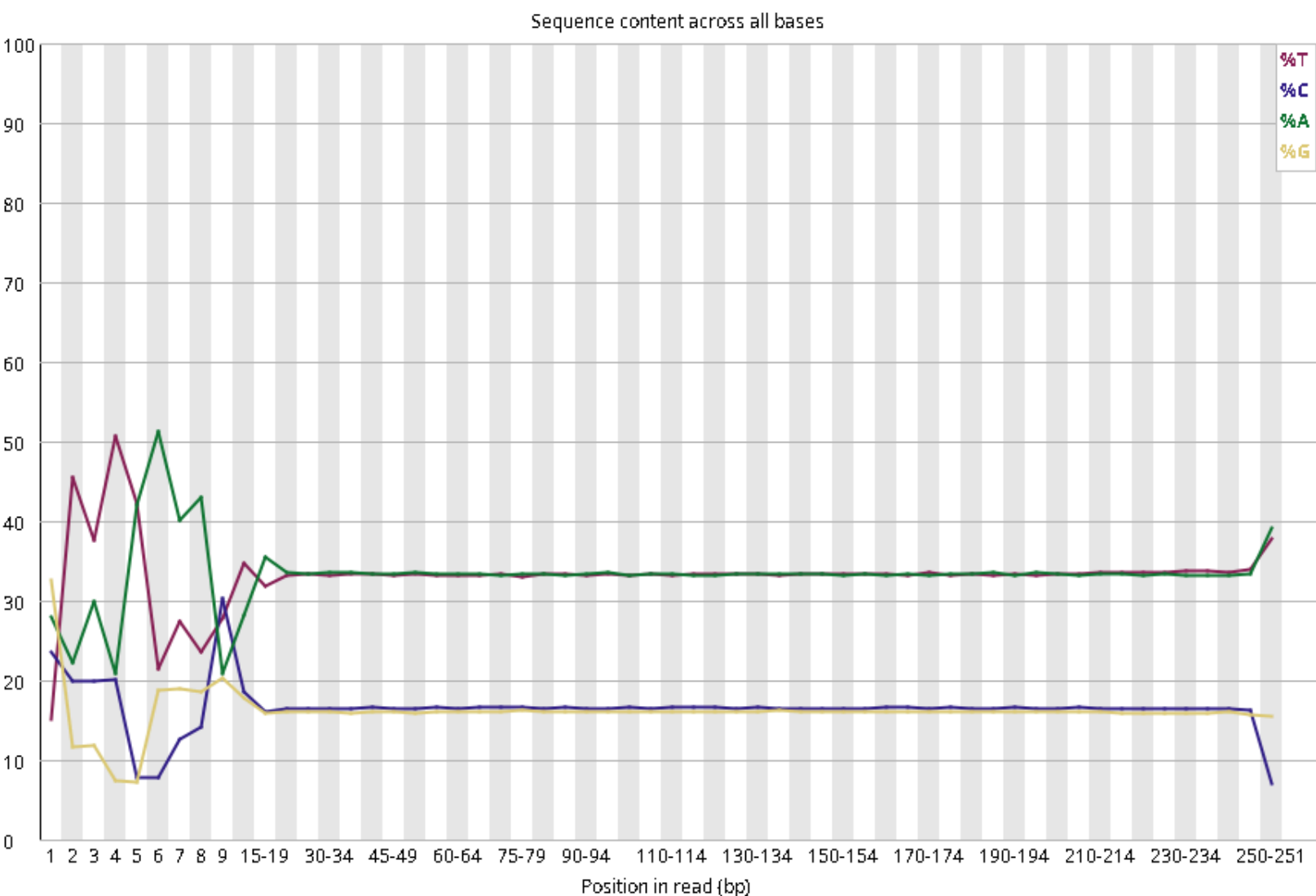
✔ Per base sequence quality



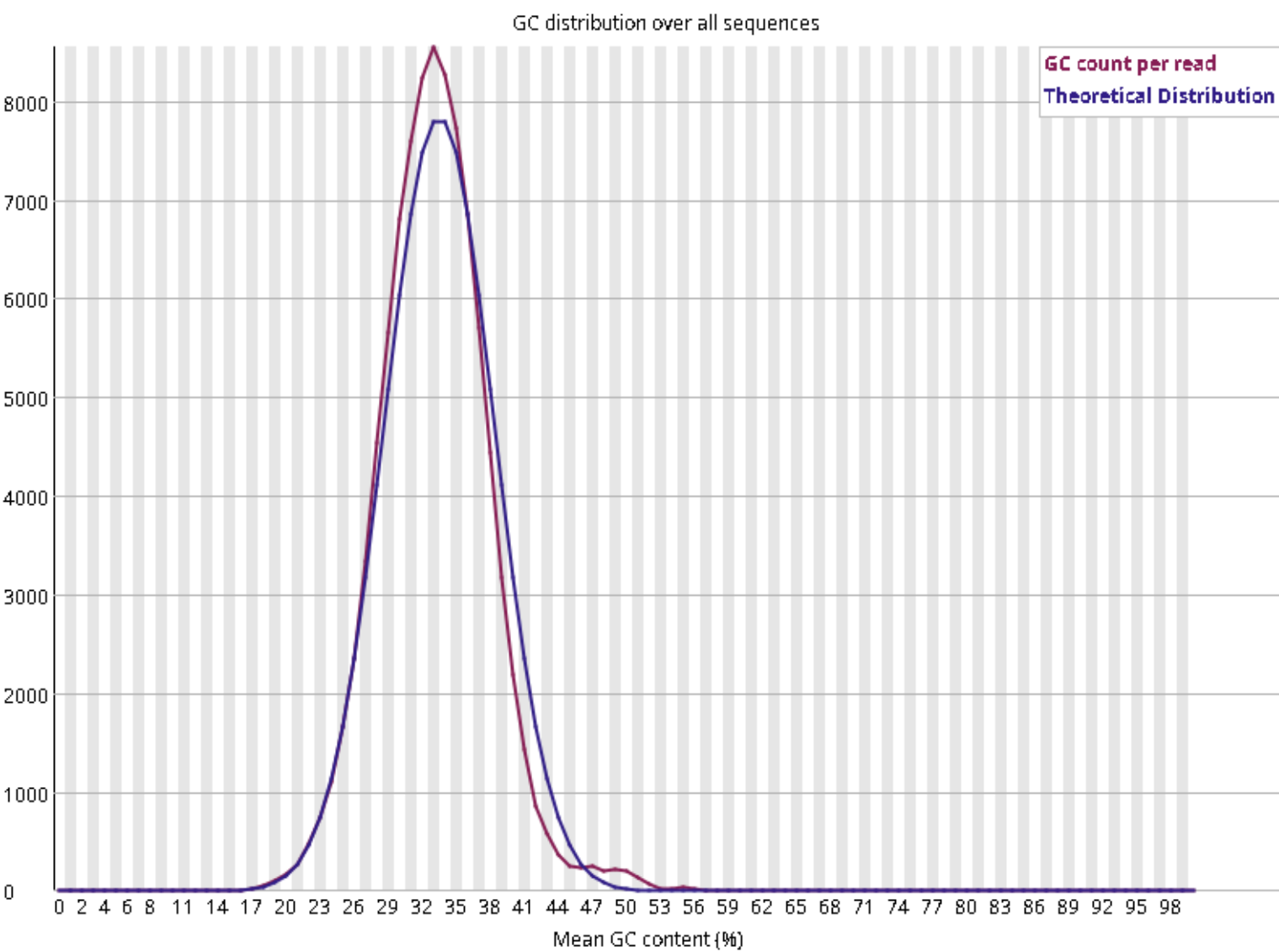
Per sequence quality scores



✖ Per base sequence content

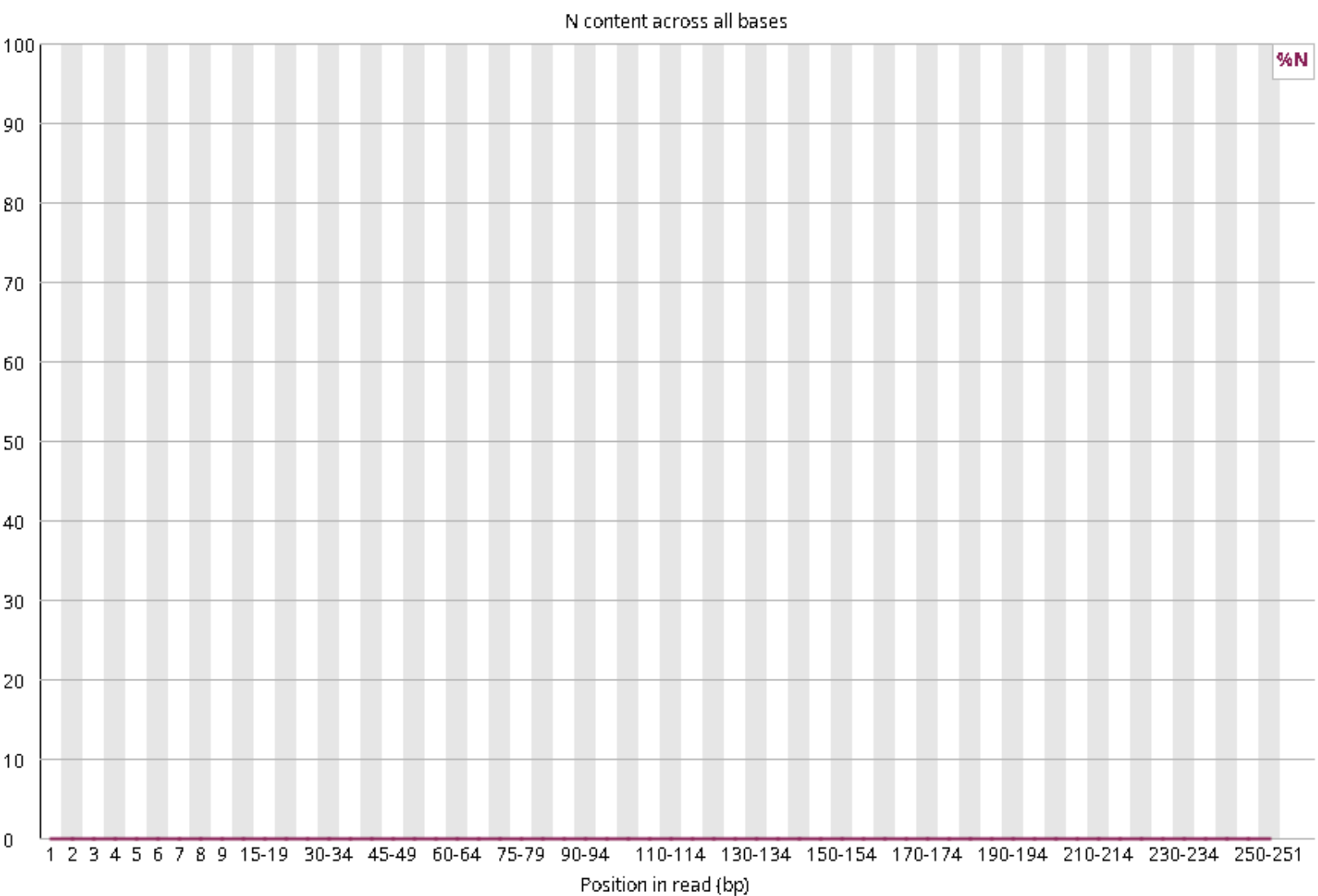


Per sequence GC content

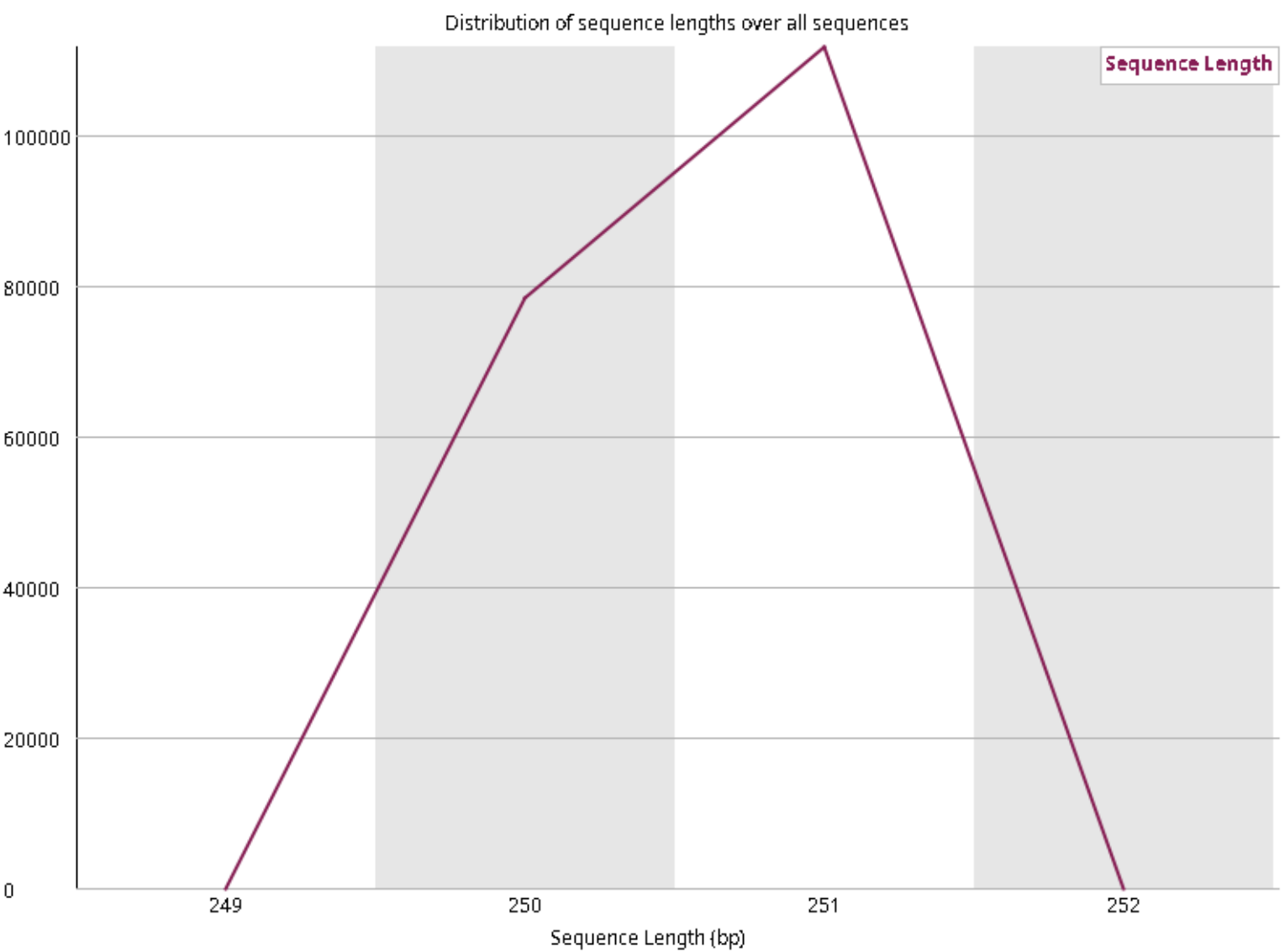




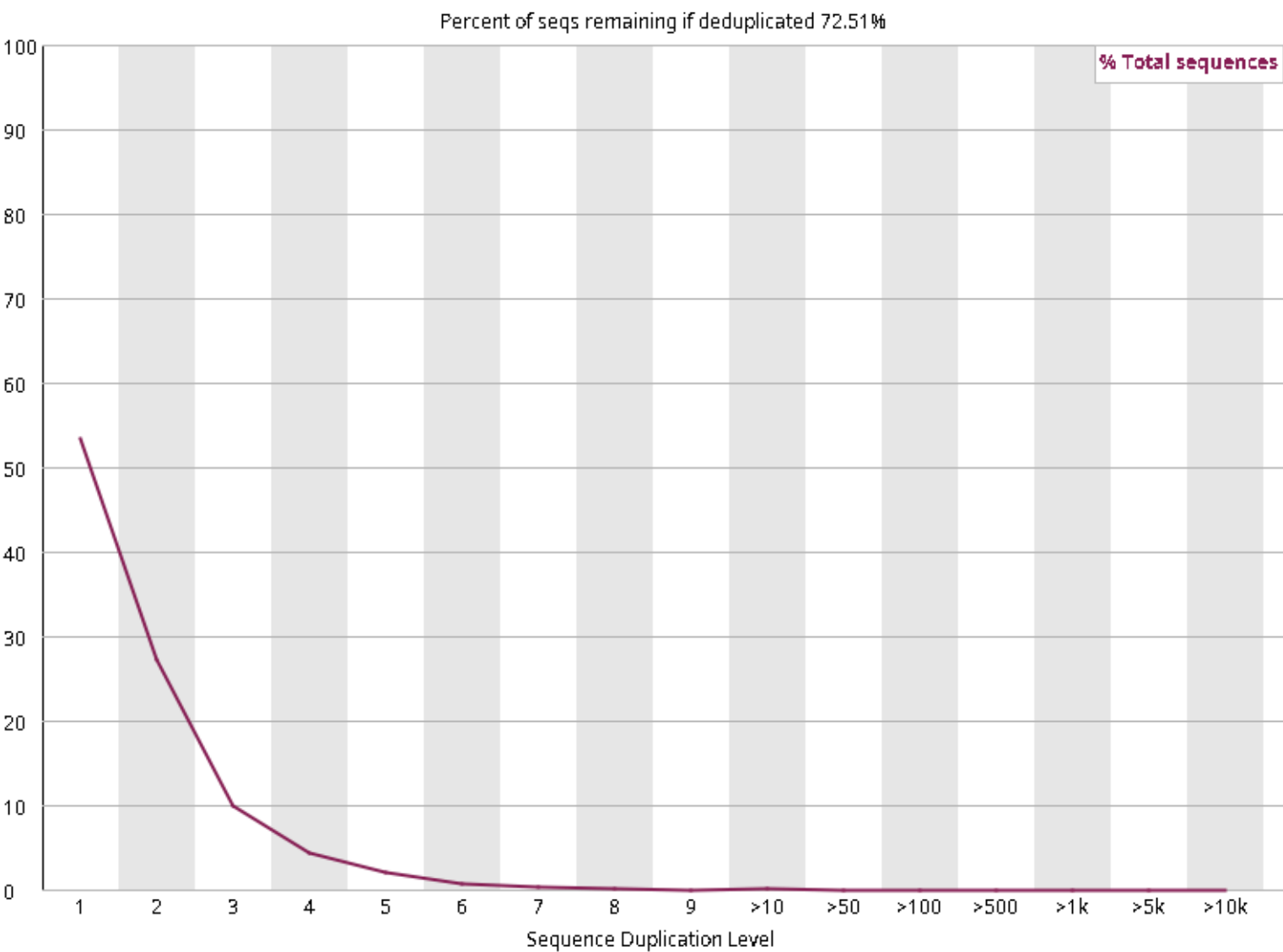
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences



Adapter Content

