

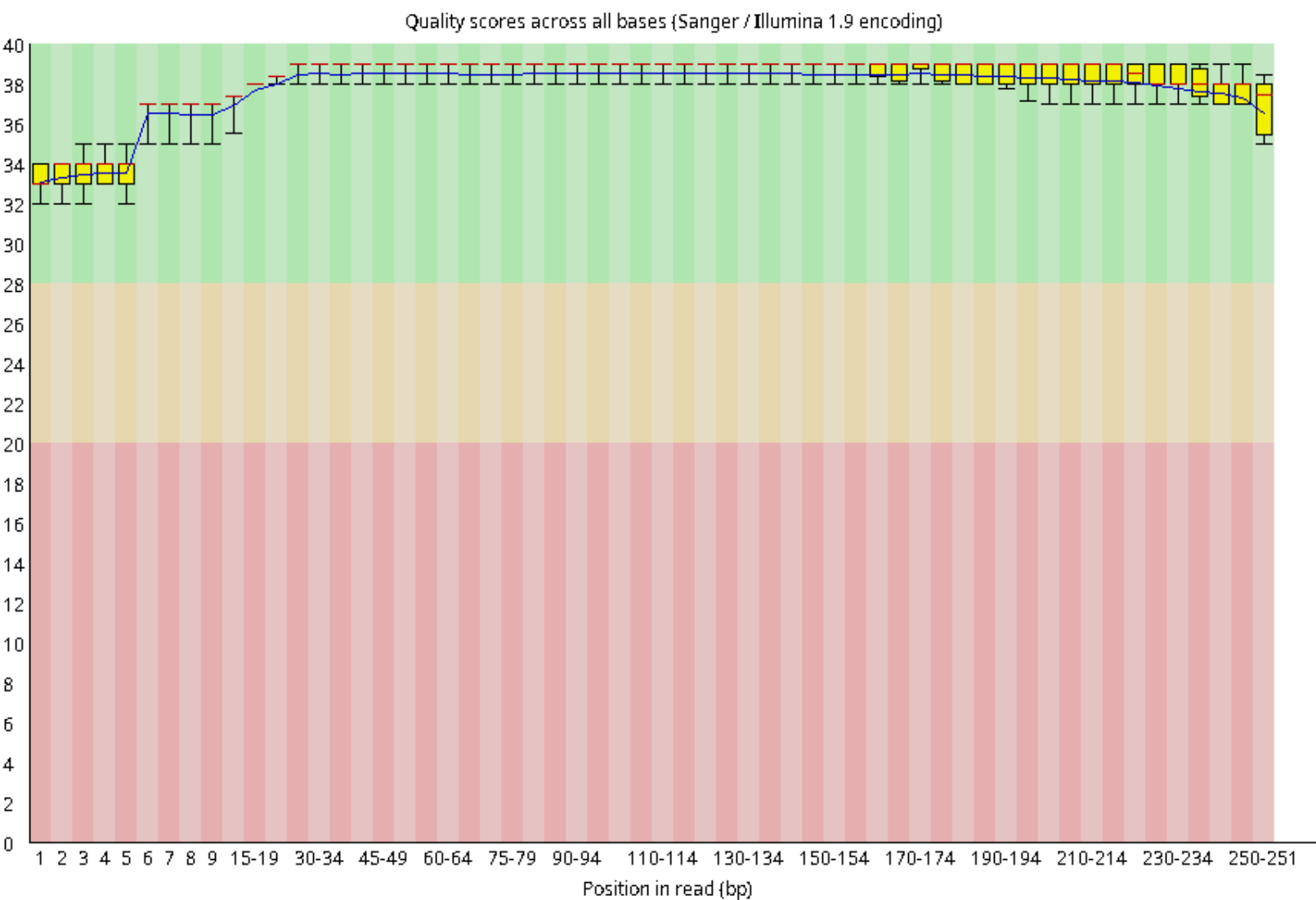
## Summary

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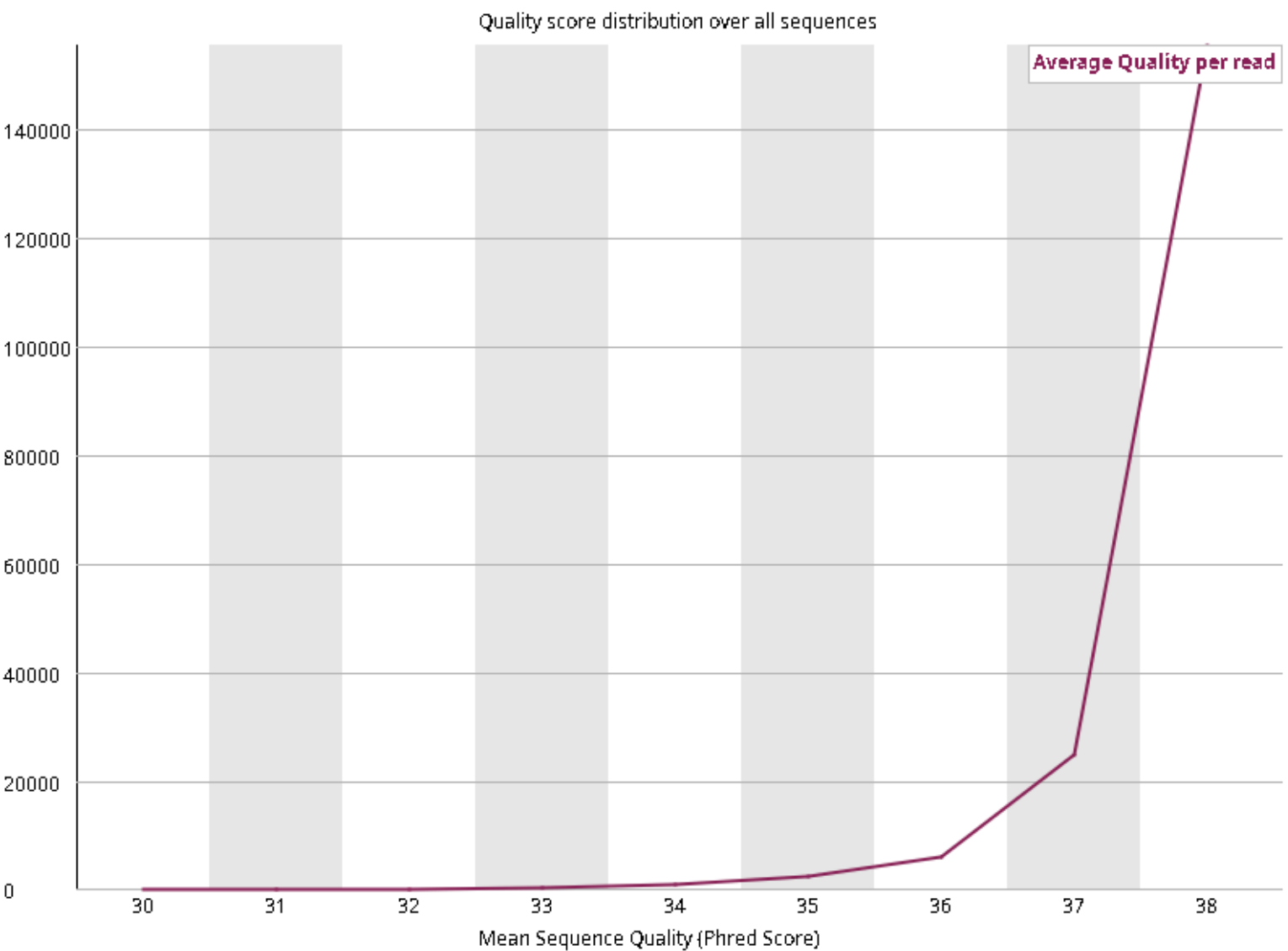
## ✓ Basic Statistics

Measure	Value
Filename	SRR9620862_1_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	190313
Total Bases	47.7 Mbp
Sequences flagged as poor quality	0
Sequence length	250-251
%GC	32

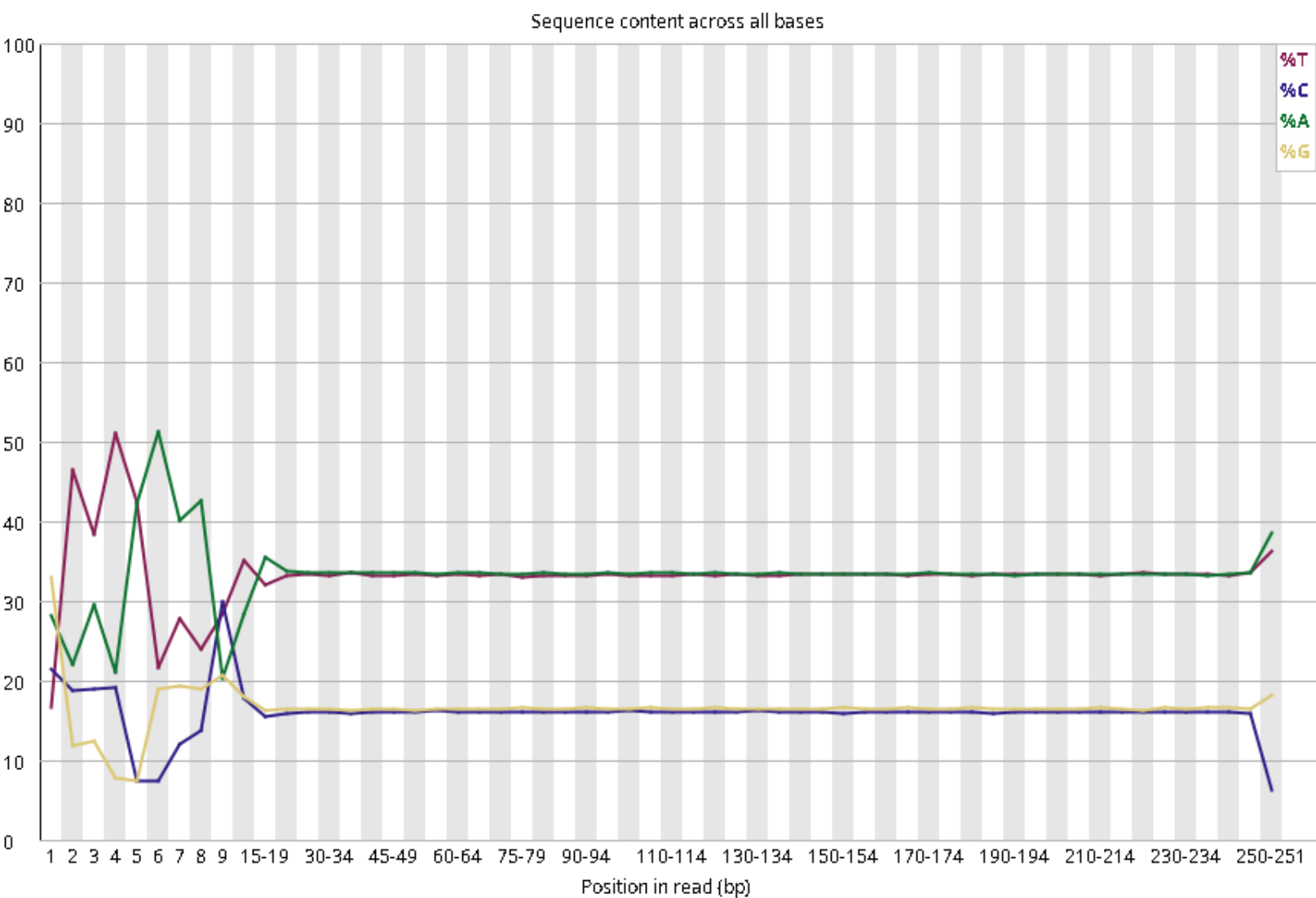
## ✔ Per base sequence quality



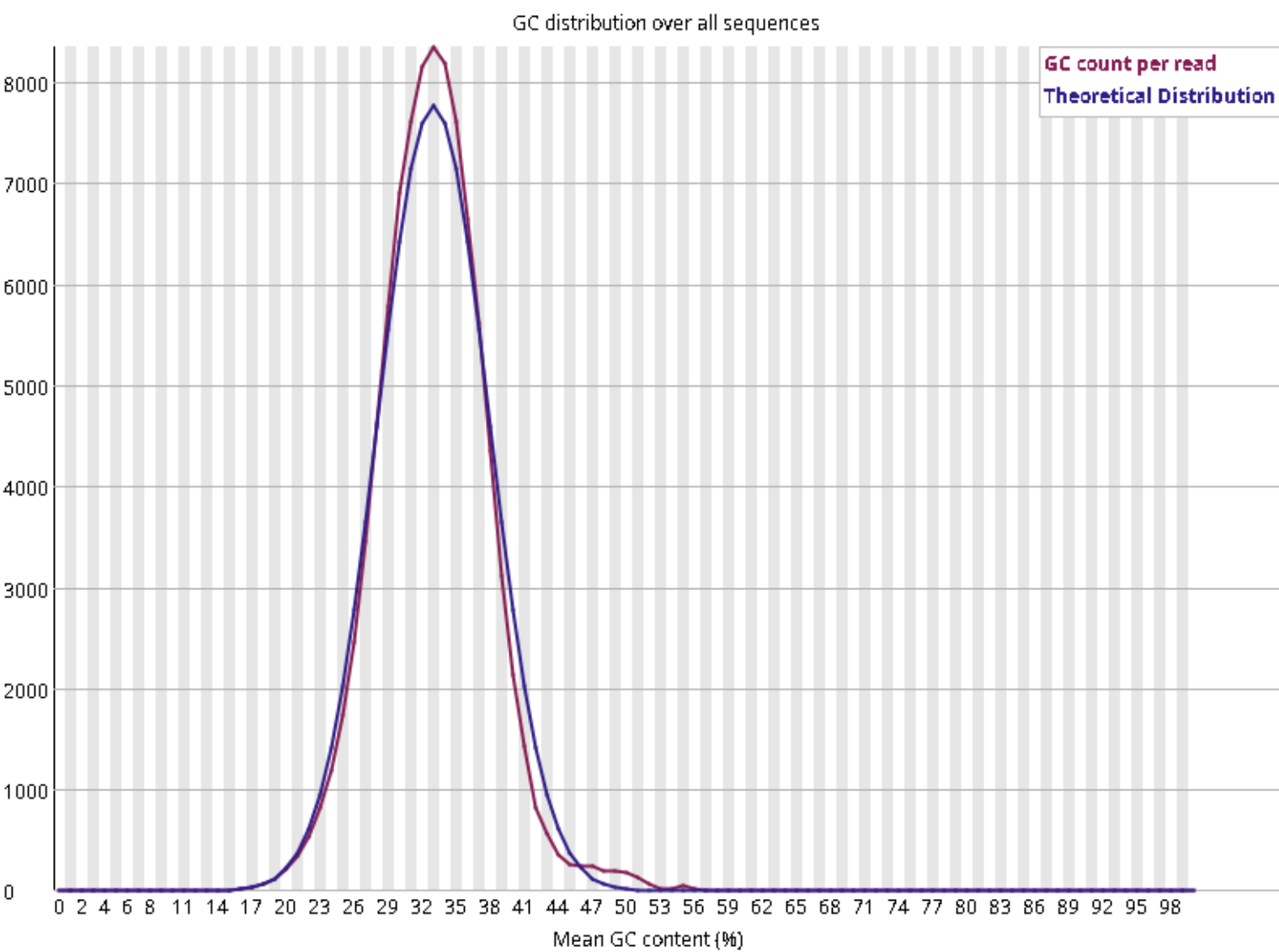
## ✔ Per sequence quality scores



# ❌ Per base sequence content

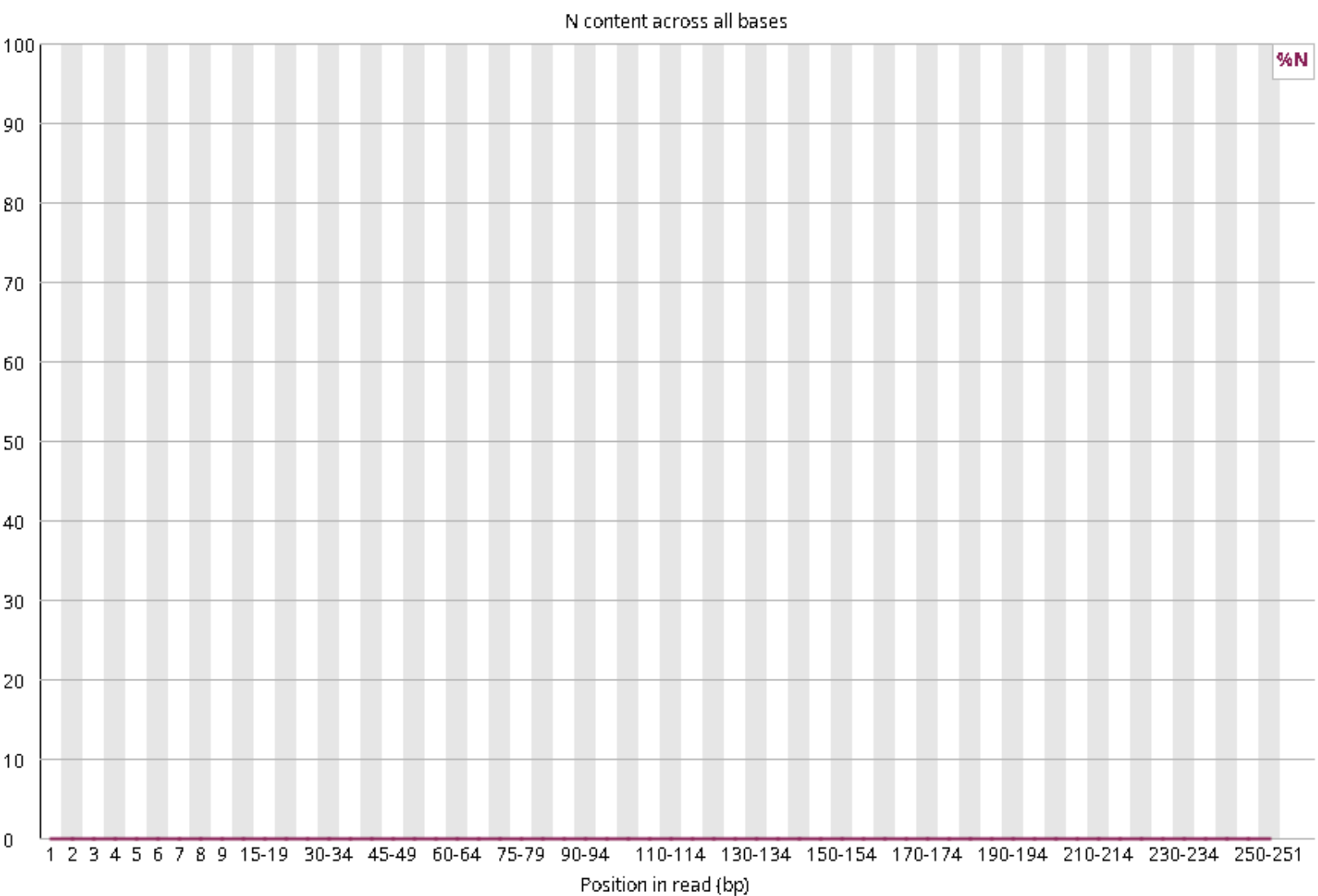


## ✔ Per sequence GC content

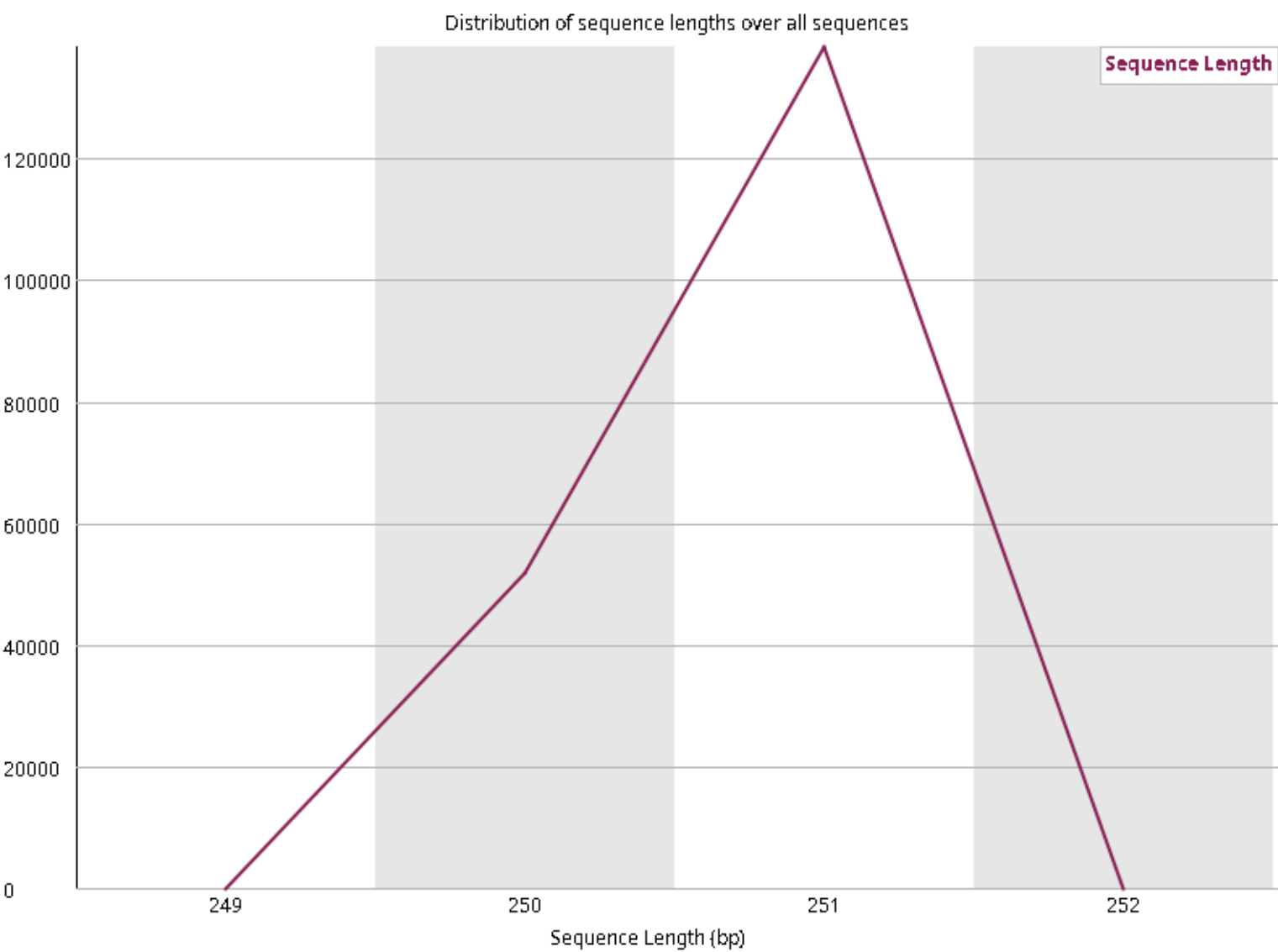




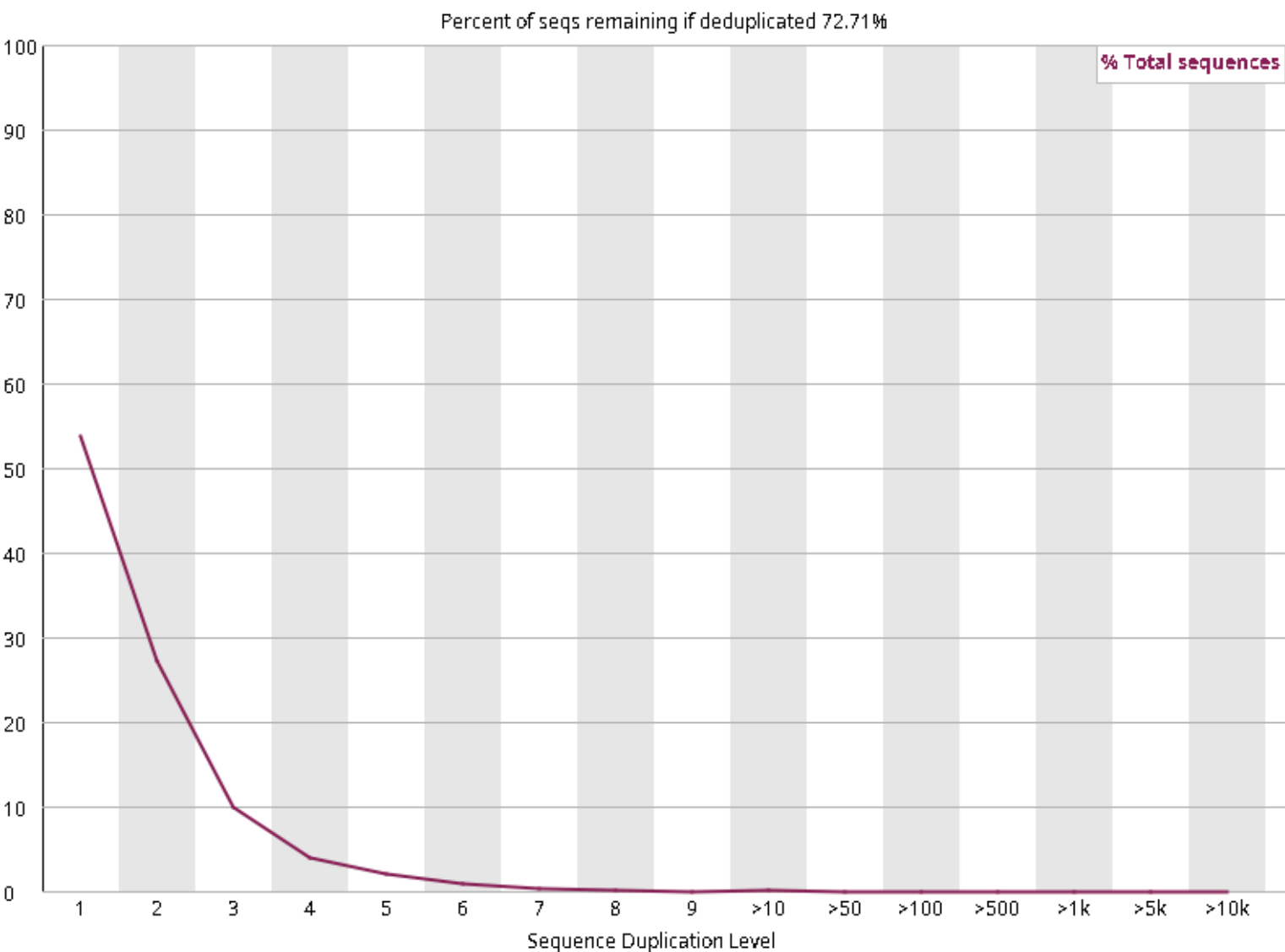
## Per base N content



# Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

No overrepresented sequences





# Adapter Content

