











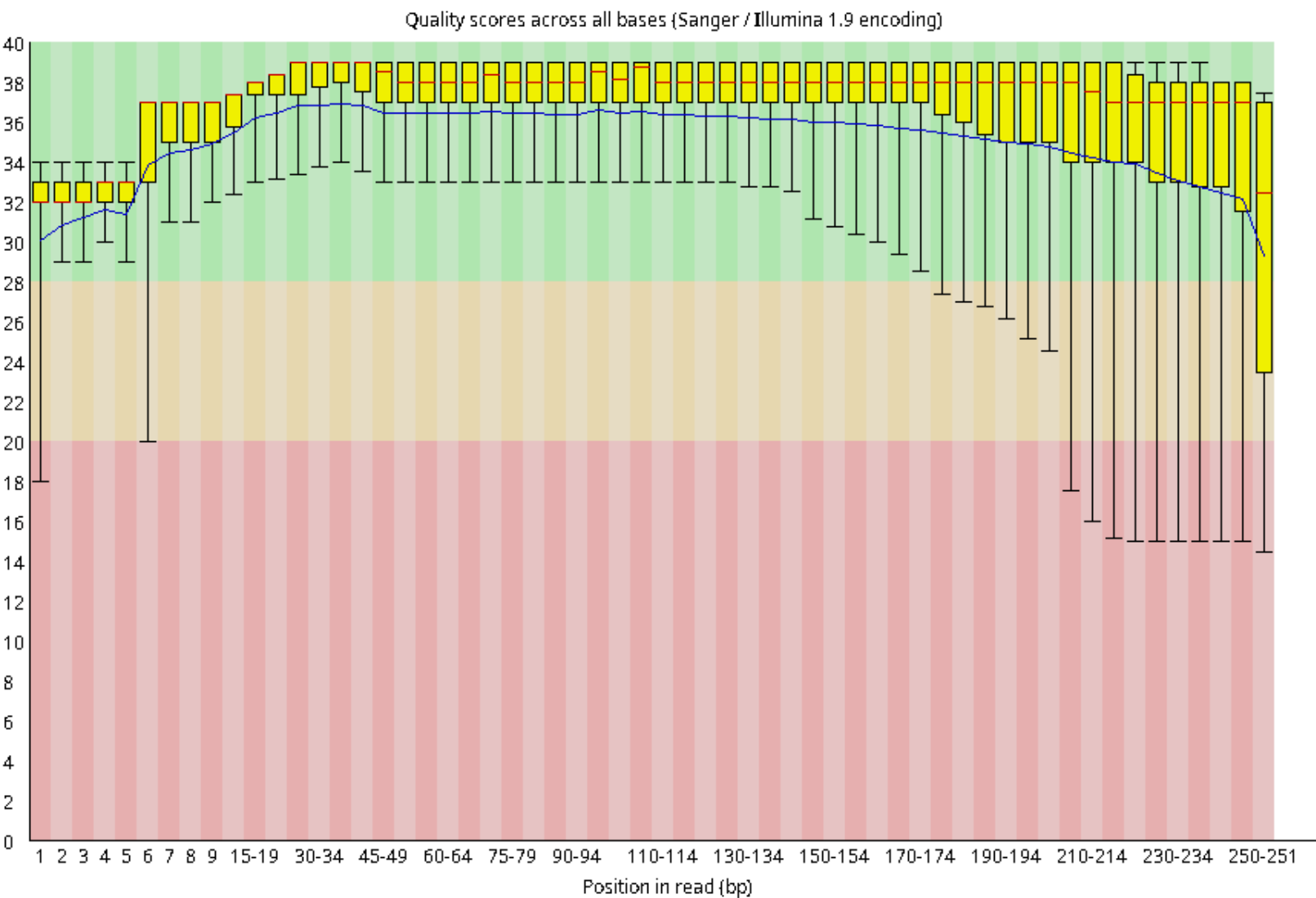
## Summary

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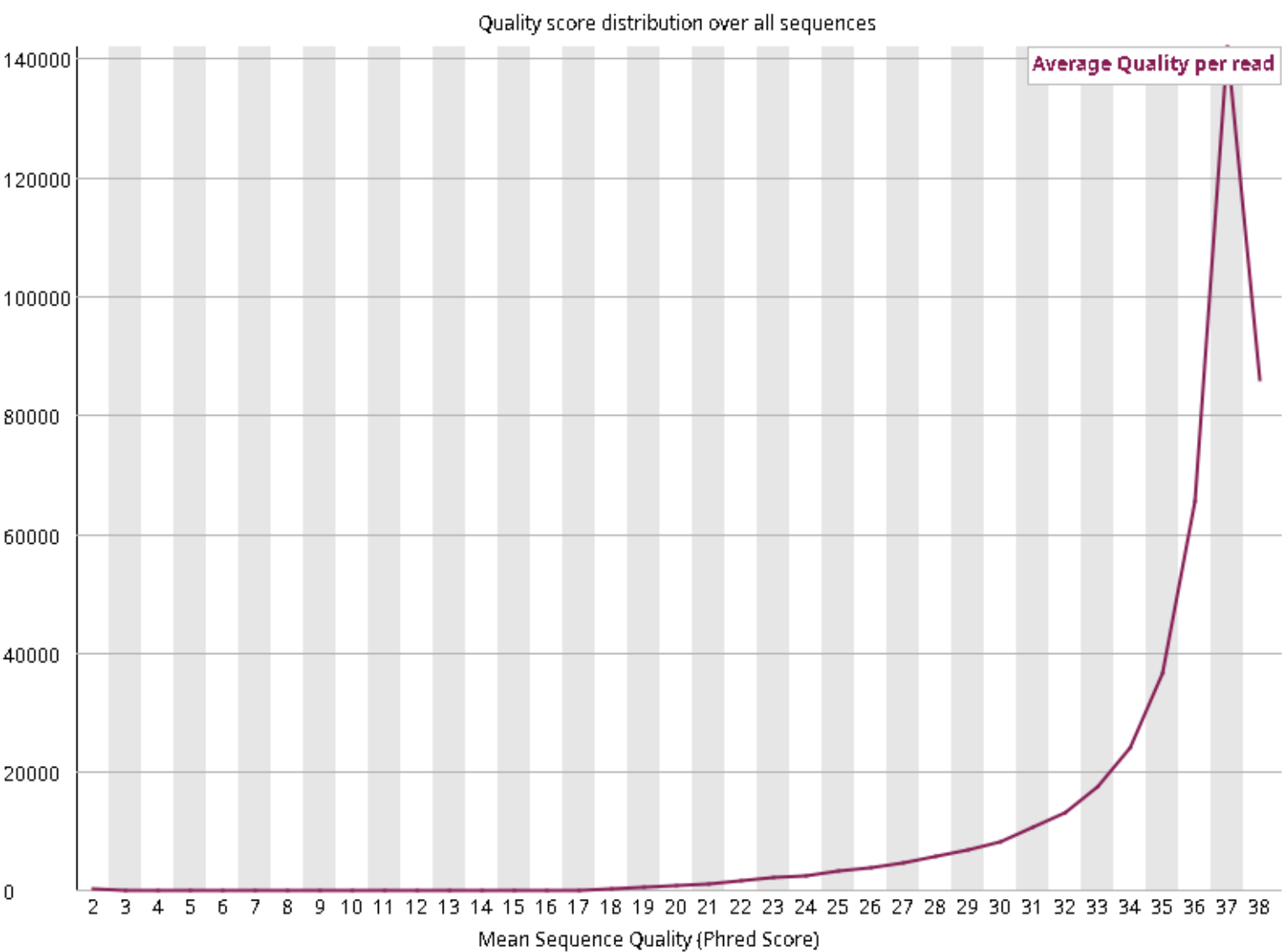
## Basic Statistics

Measure	Value
Filename	SRR9620862_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	439576
Total Bases	100.7 Mbp
Sequences flagged as poor quality	0
Sequence length	35-251
%GC	33

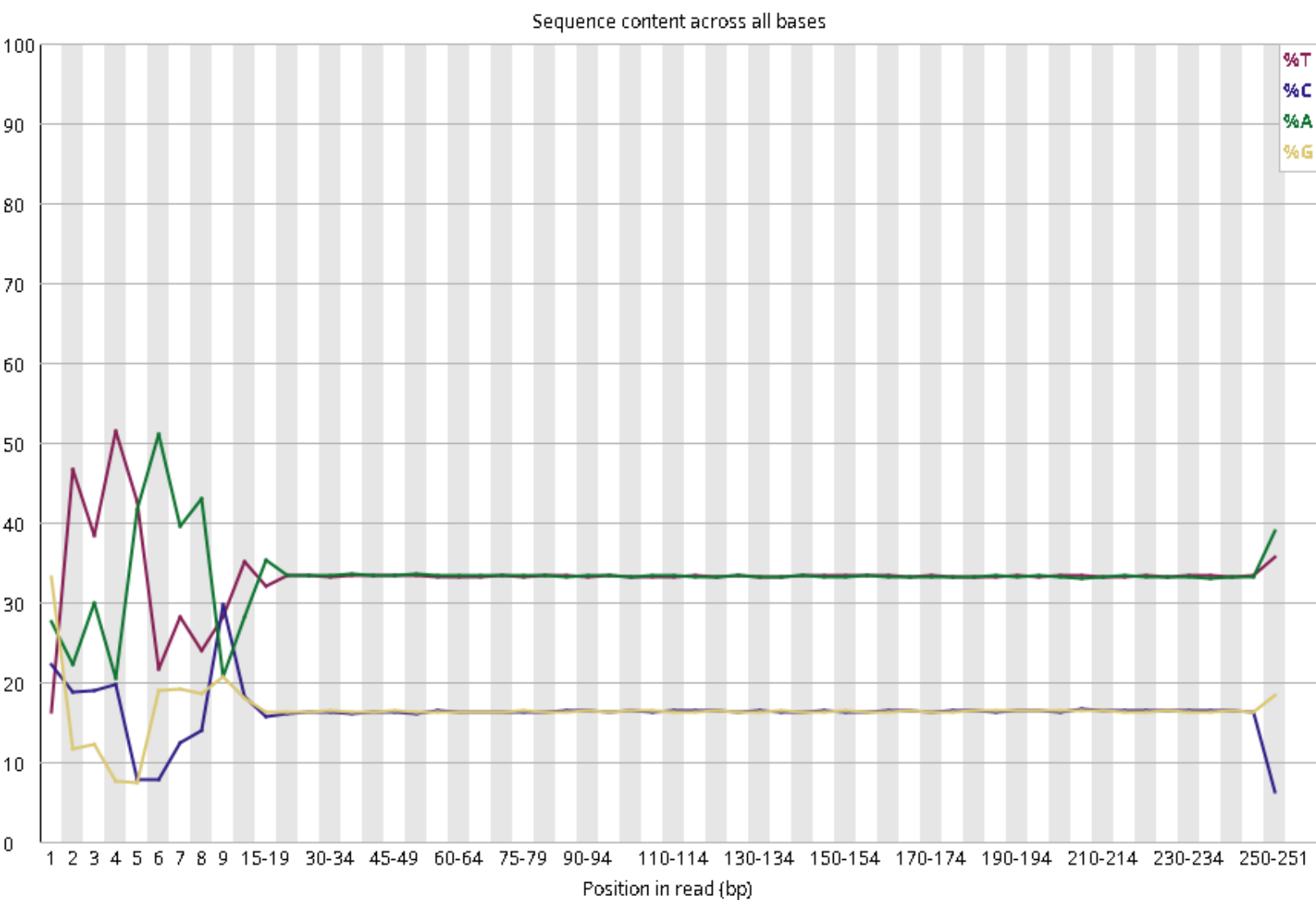
## ✔ Per base sequence quality



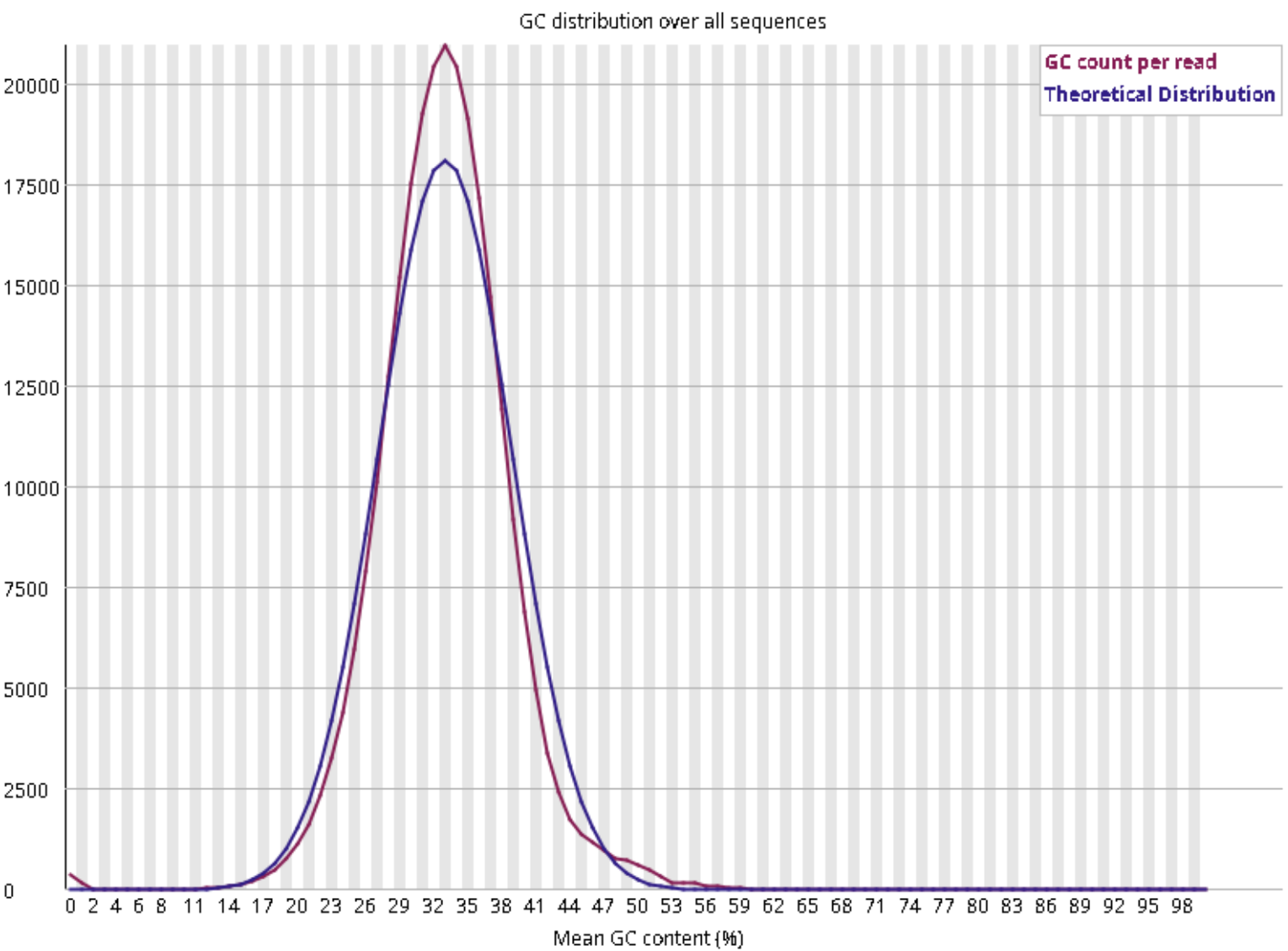
## ✔ Per sequence quality scores



# ✖ Per base sequence content

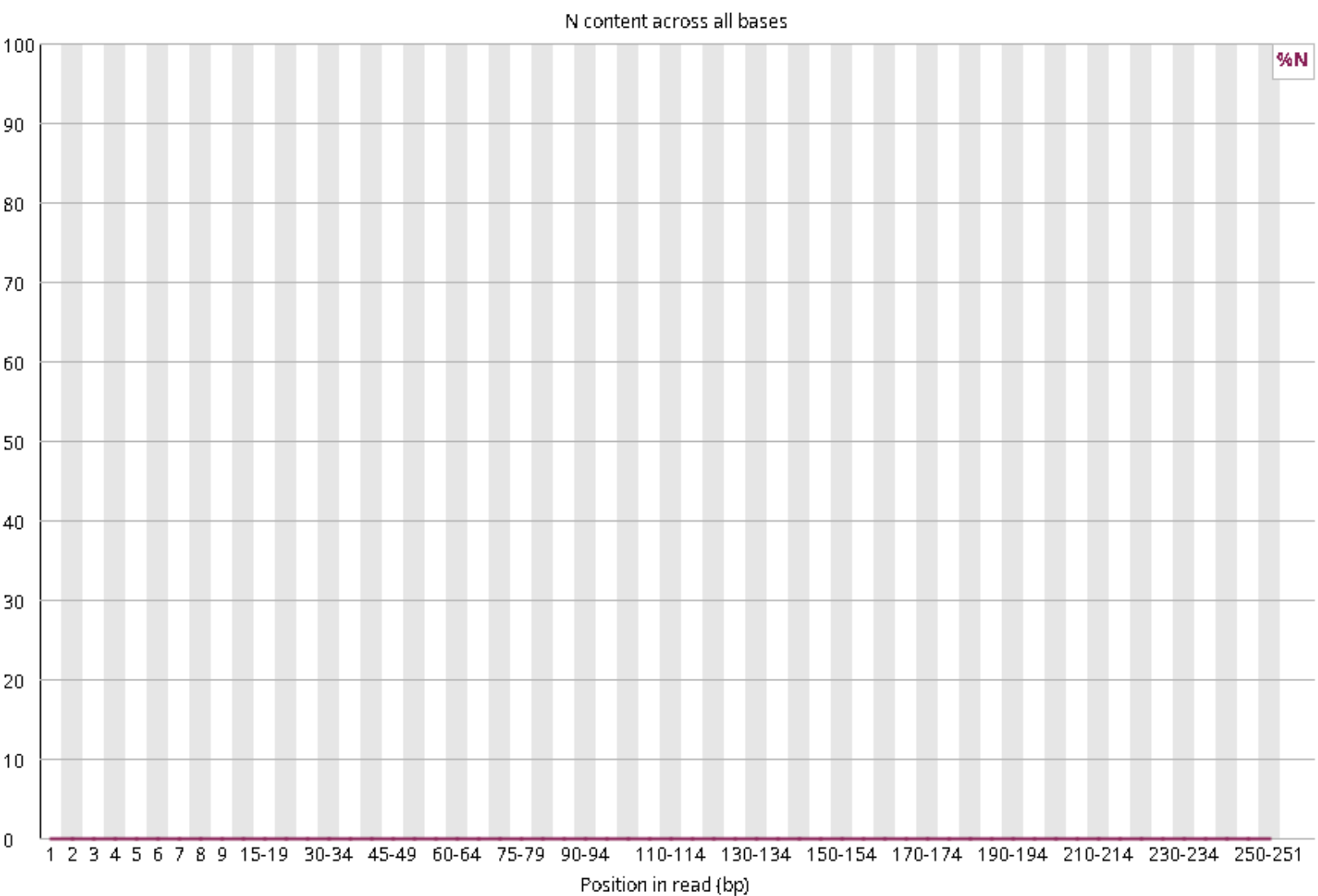


## ✔ Per sequence GC content

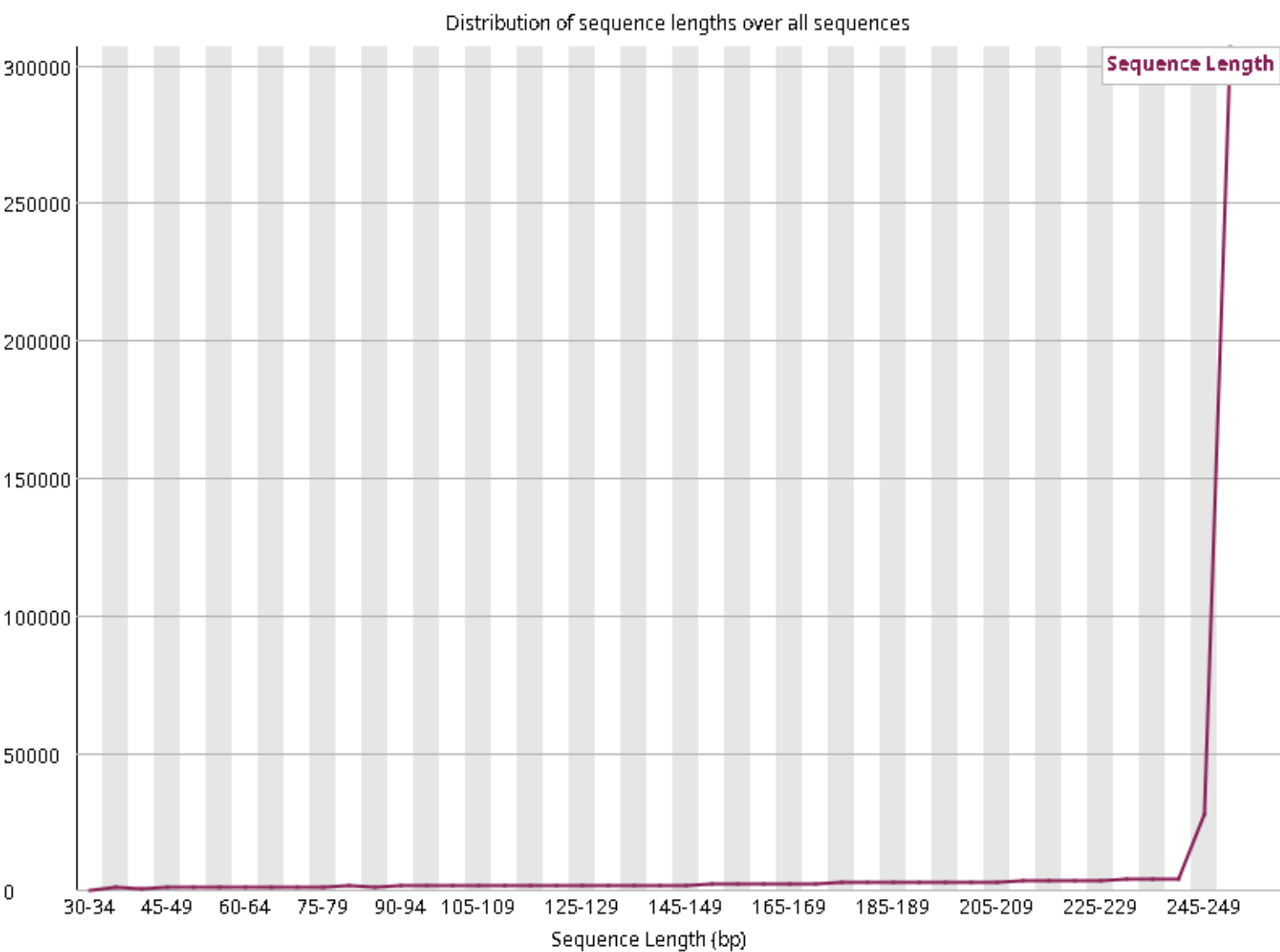




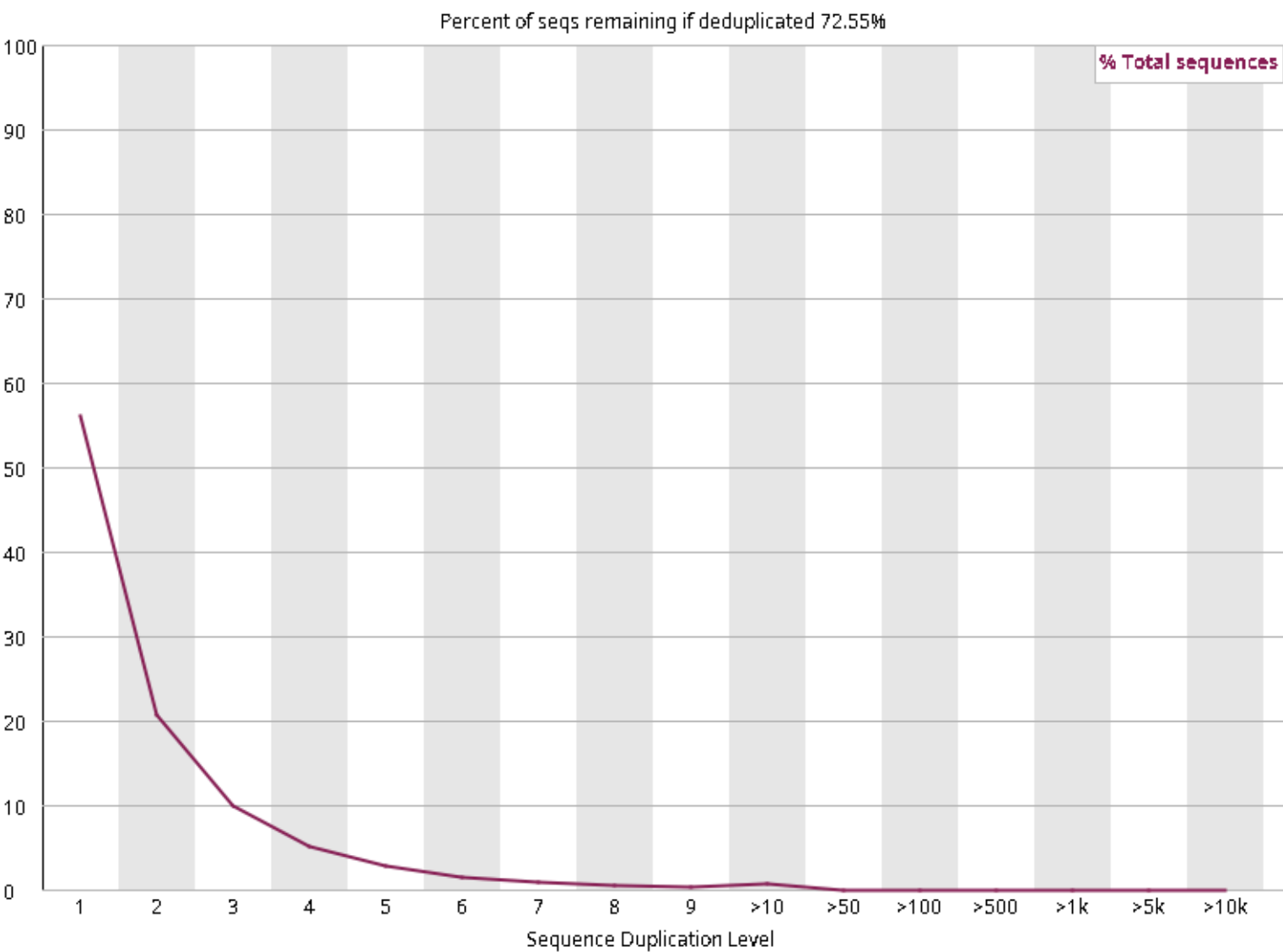
## Per base N content



# 🚨 Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

No overrepresented sequences





## Adapter Content

