












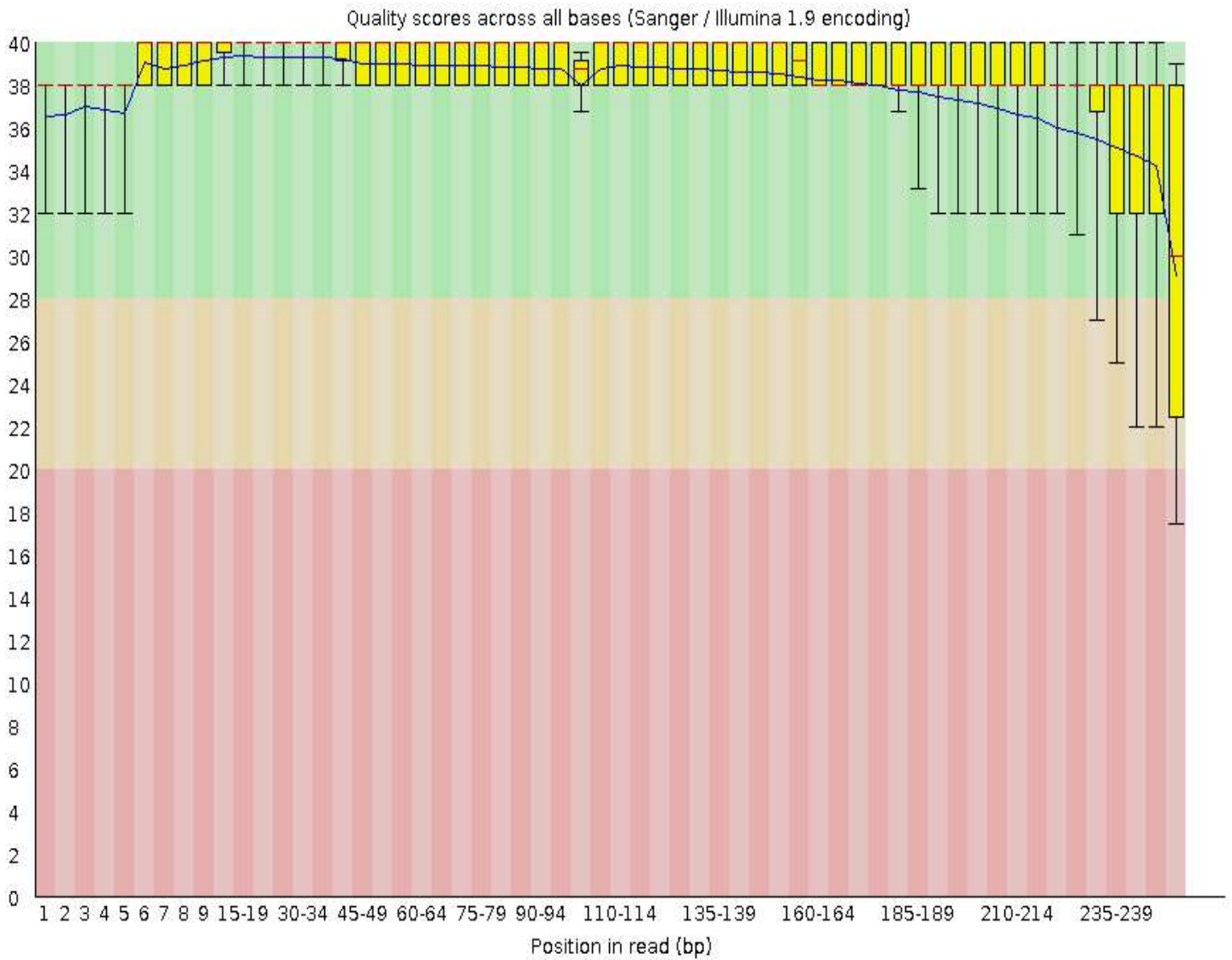
## Summary

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## Basic Statistics

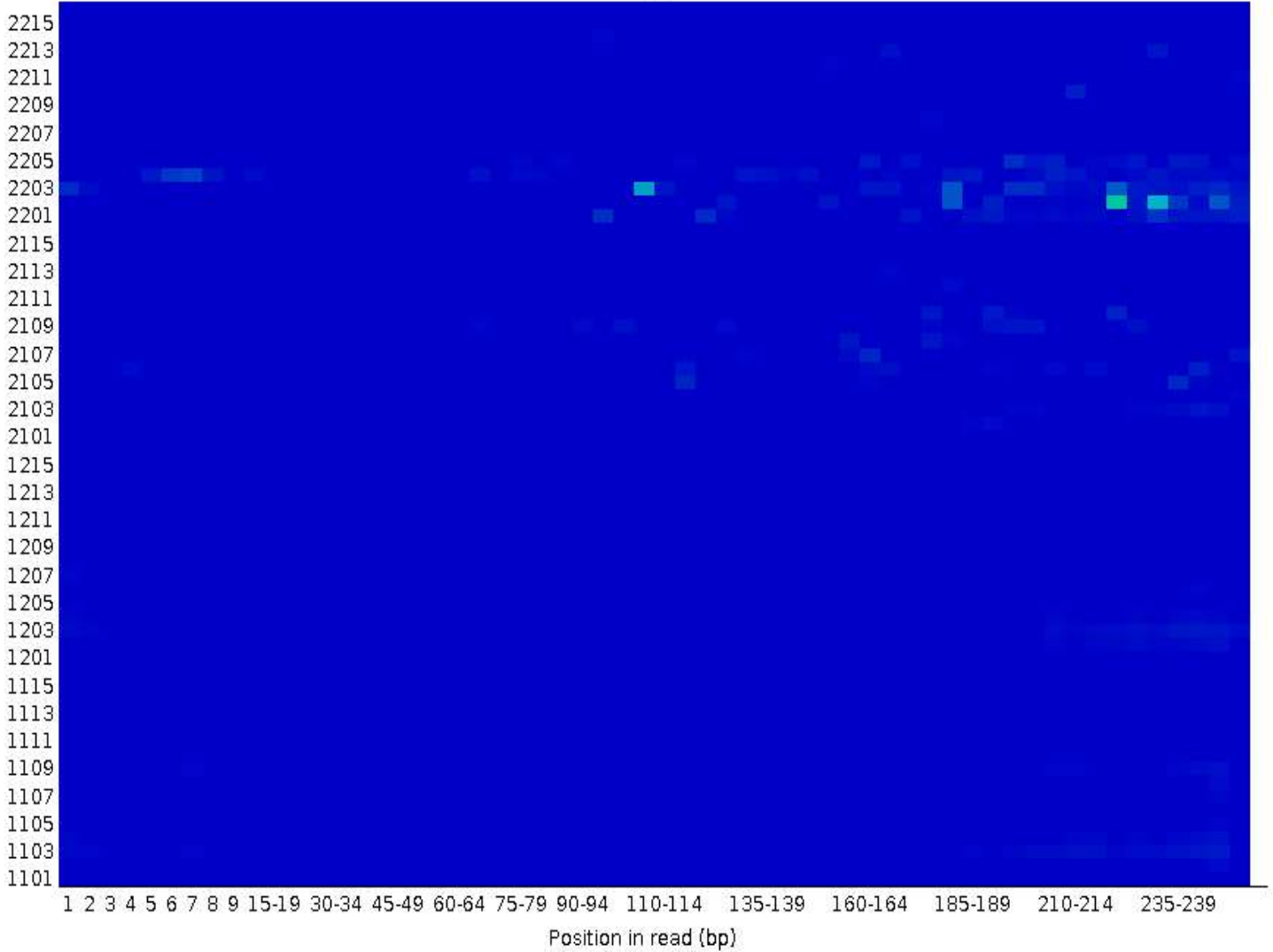
Measure	Value
Filename	10_EC092_R2_PE_fastpCleaned.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	12347656
Sequences flagged as poor quality	0
Sequence length	31-251
%GC	51

## ✔ Per base sequence quality

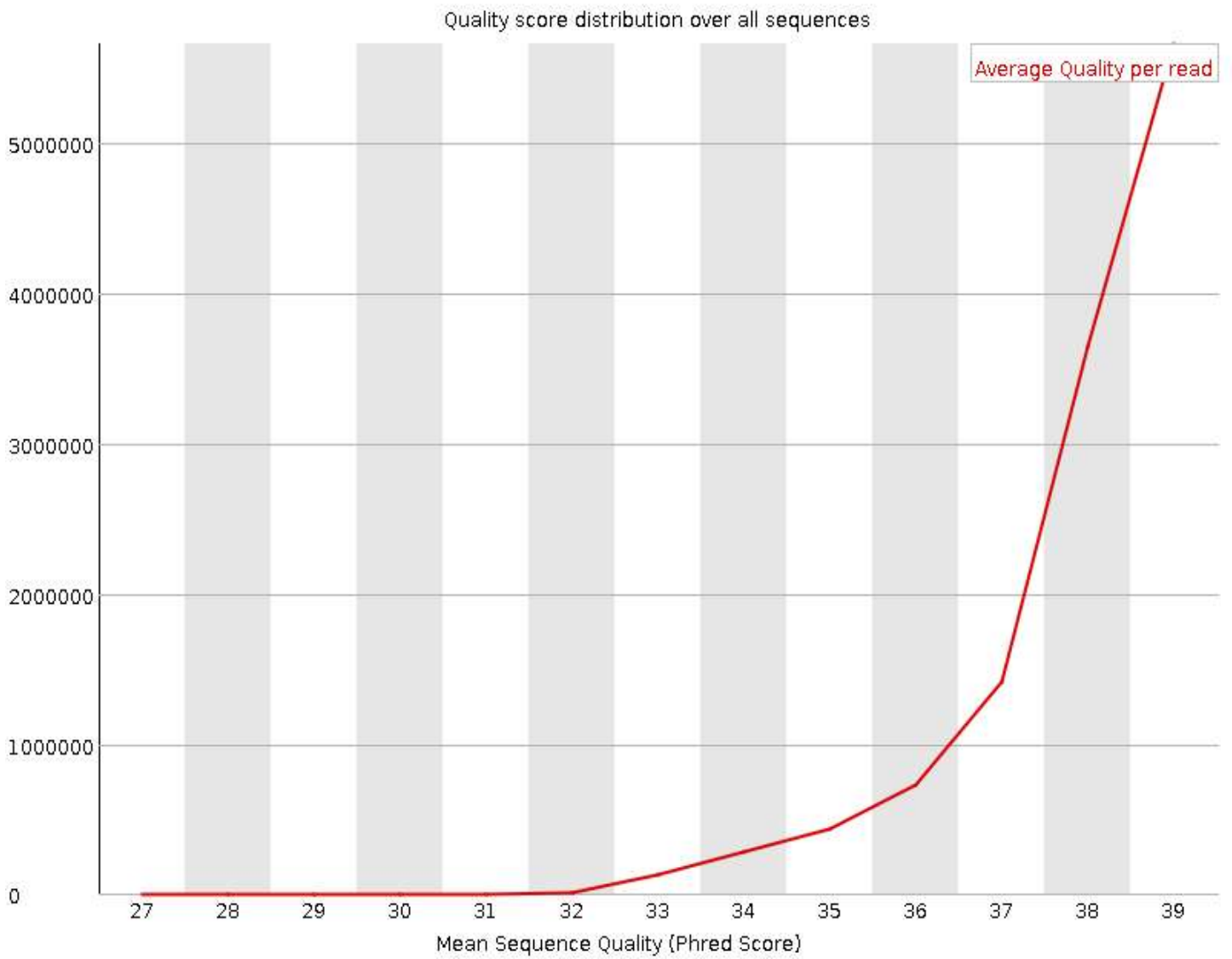


## ✔ Per tile sequence quality

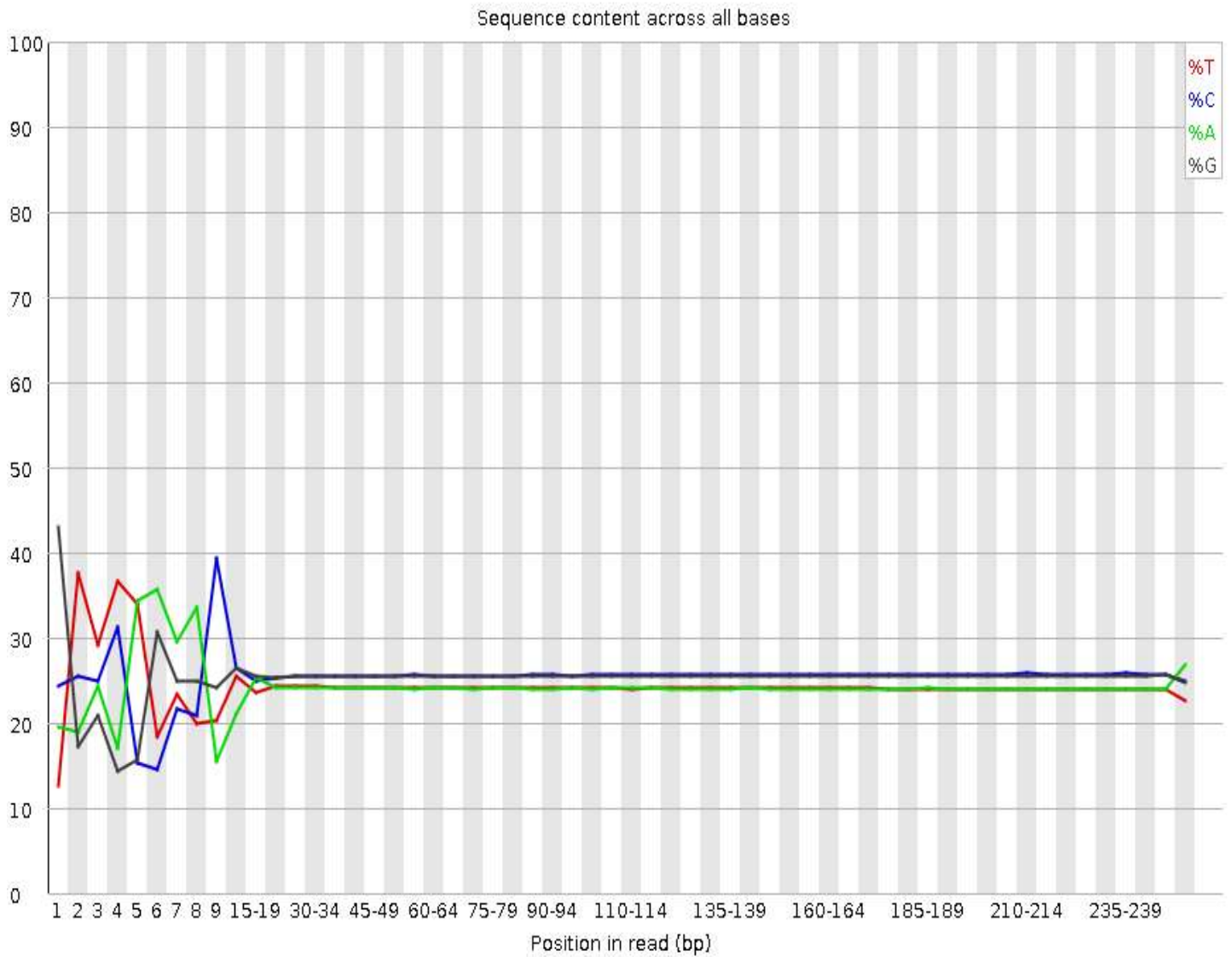
Quality per tile



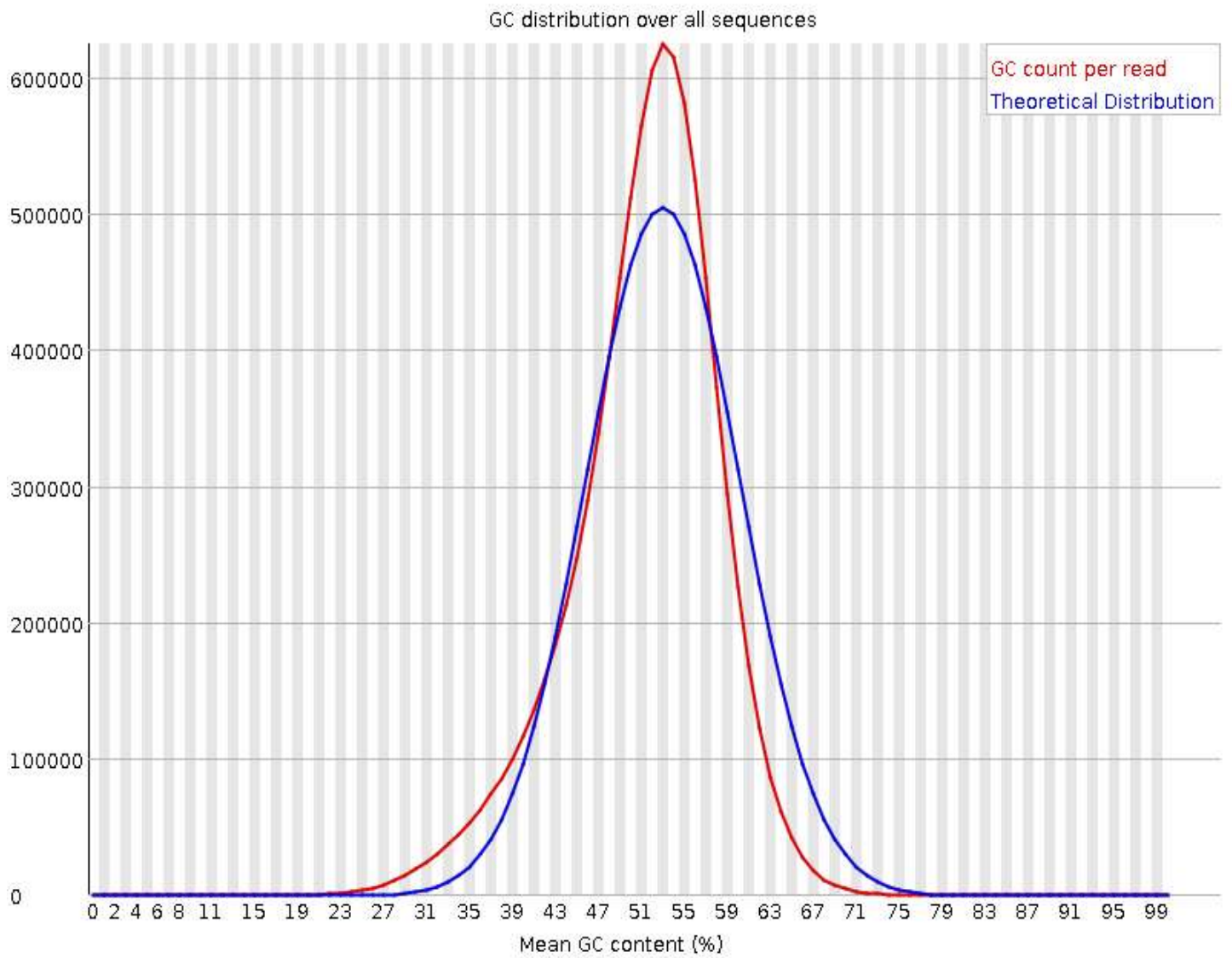
## ✔ Per sequence quality scores



# ! Per base sequence content

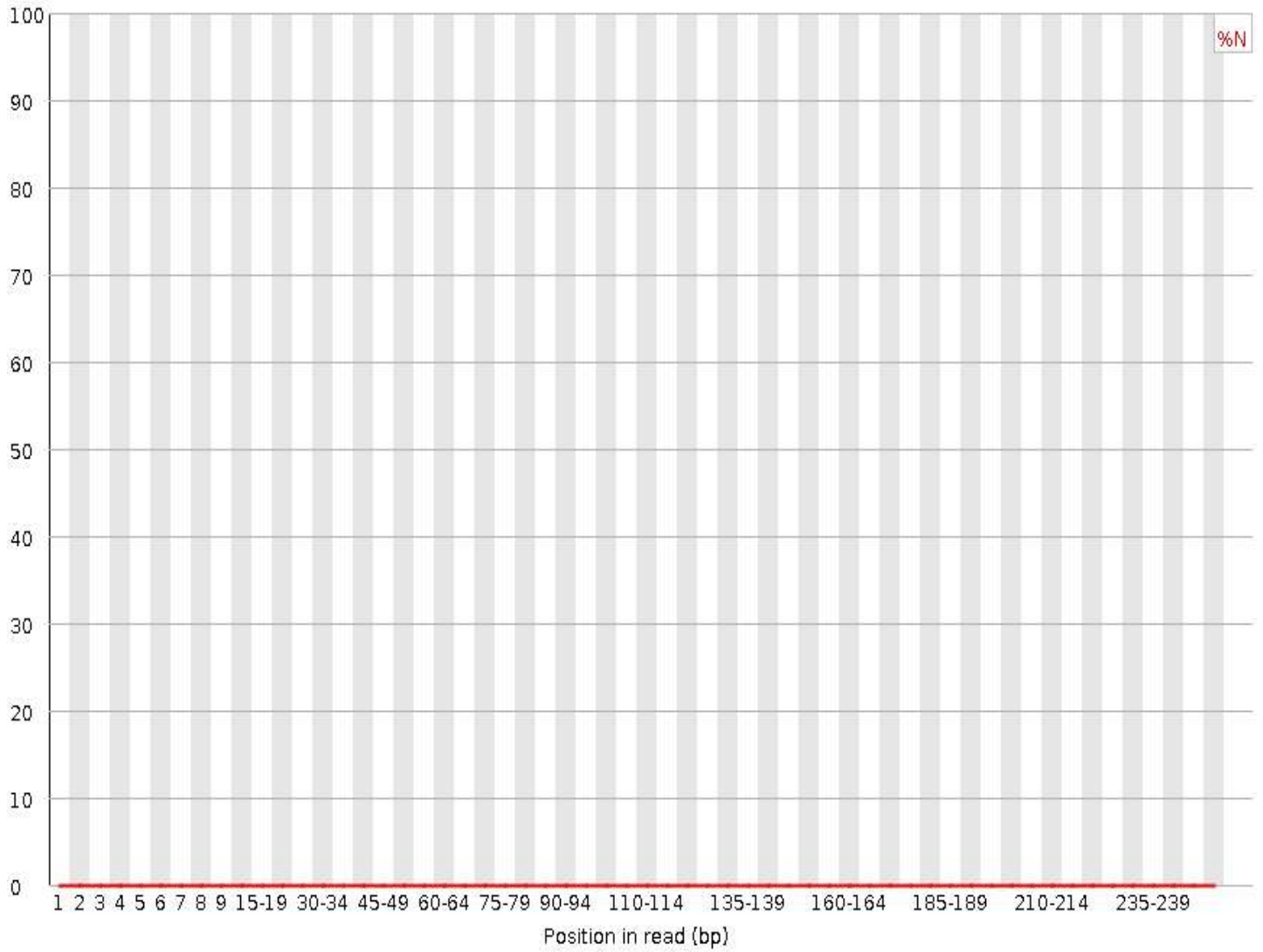


## ! Per sequence GC content

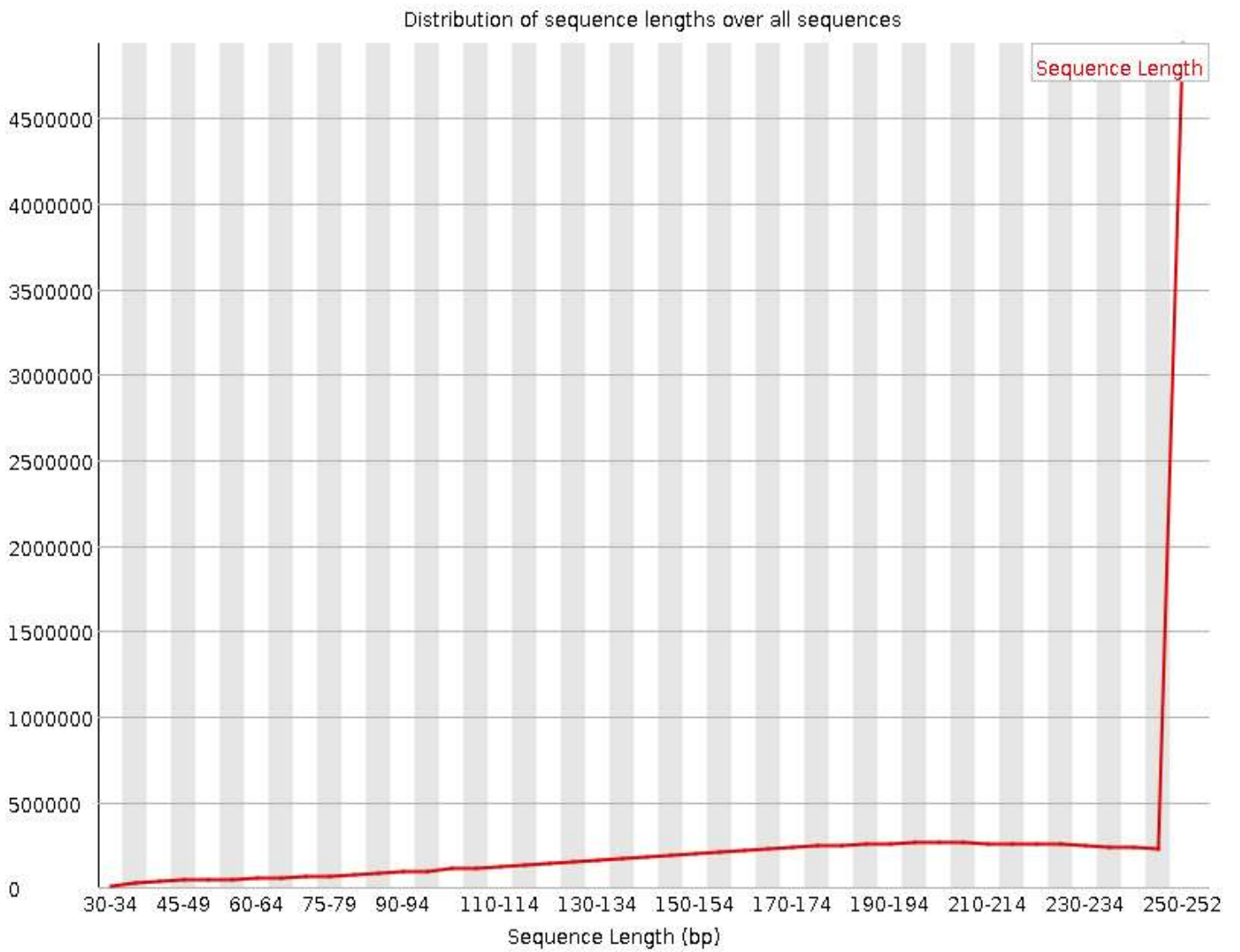


# ✔ Per base N content

N content across all bases

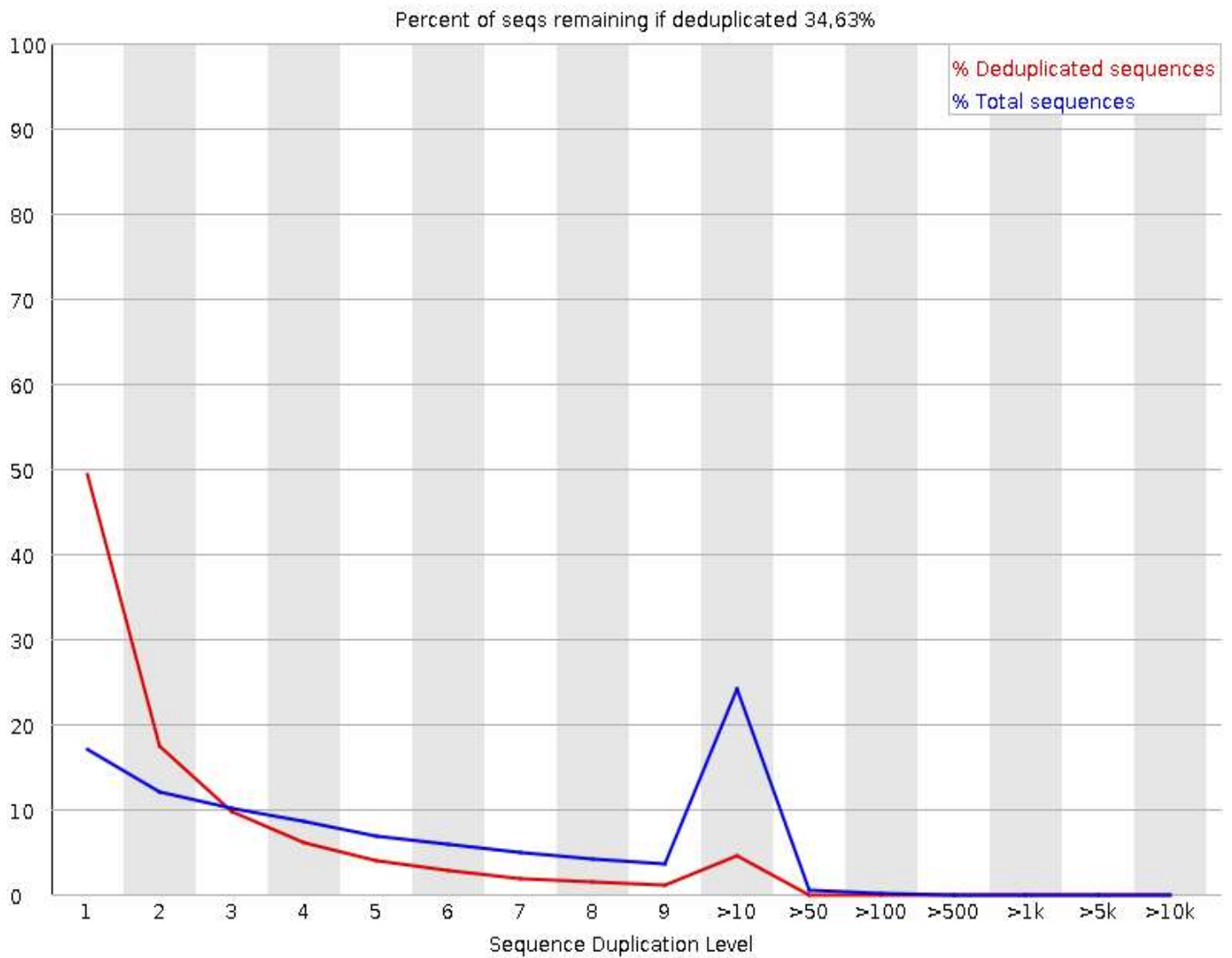


# ! Sequence Length Distribution





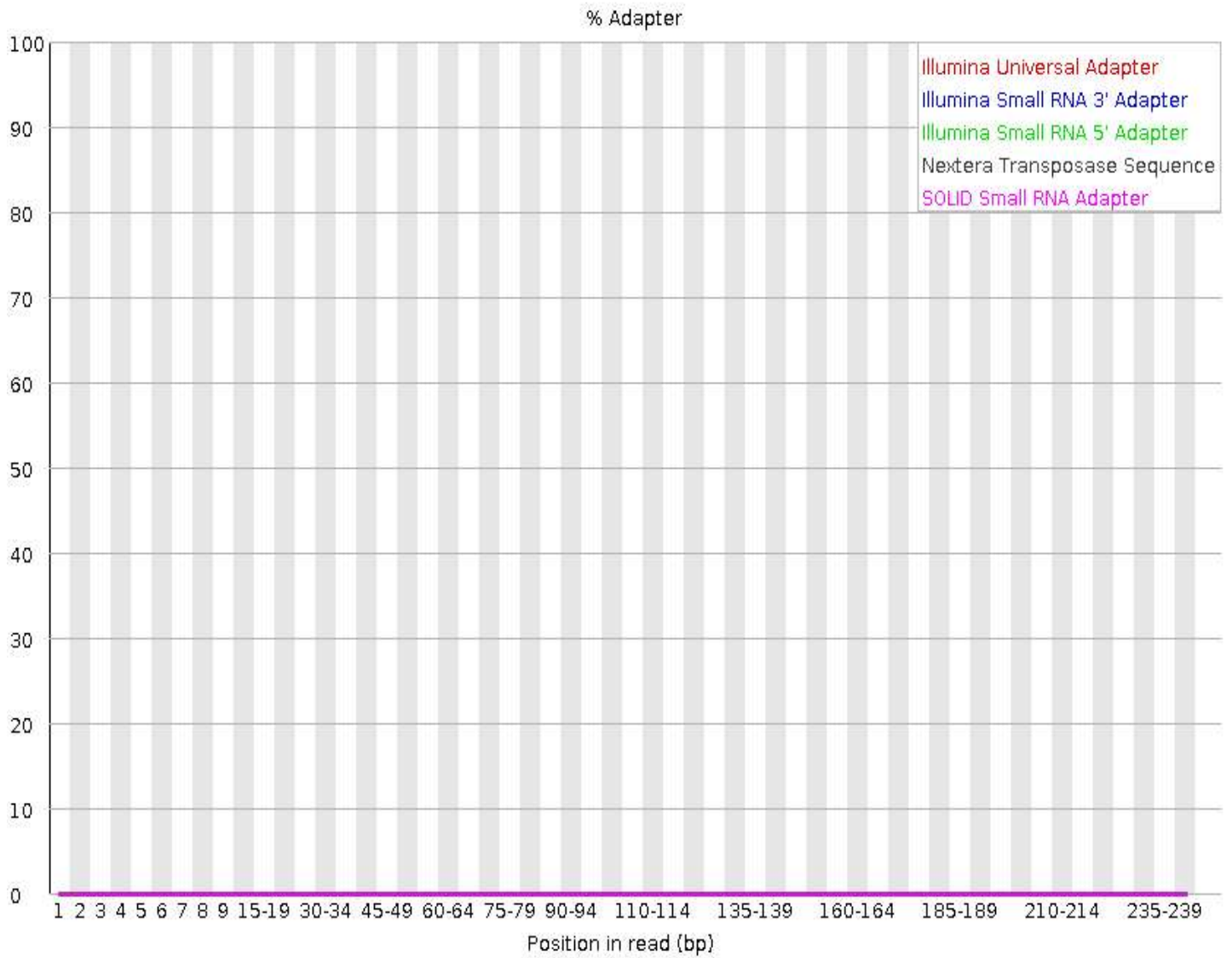
## ✘ Sequence Duplication Levels



## ✔ Overrepresented sequences

No overrepresented sequences

# Adapter Content



Produced by [FastQC](#) (version 0.11.9)