












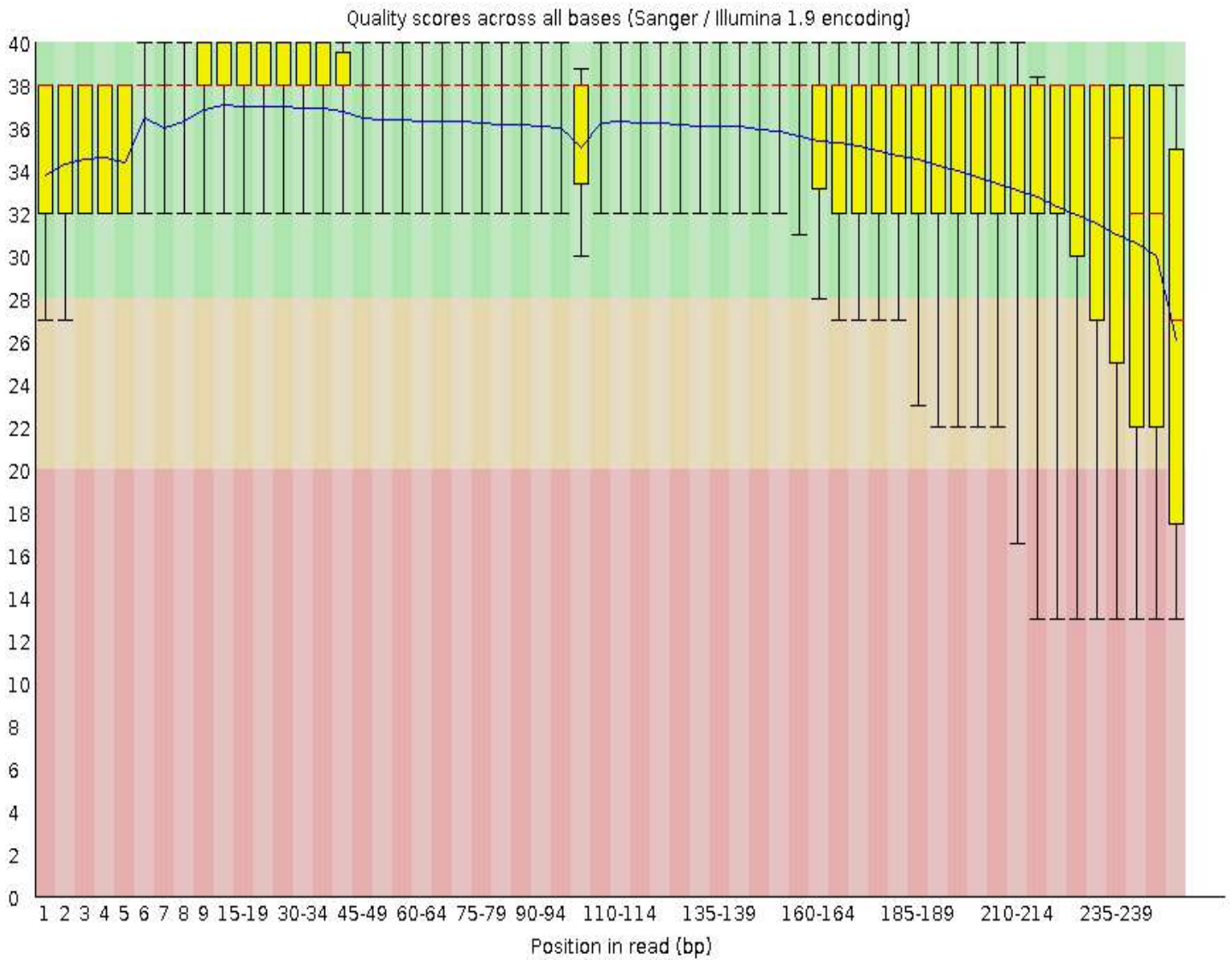
Summary

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Basic Statistics

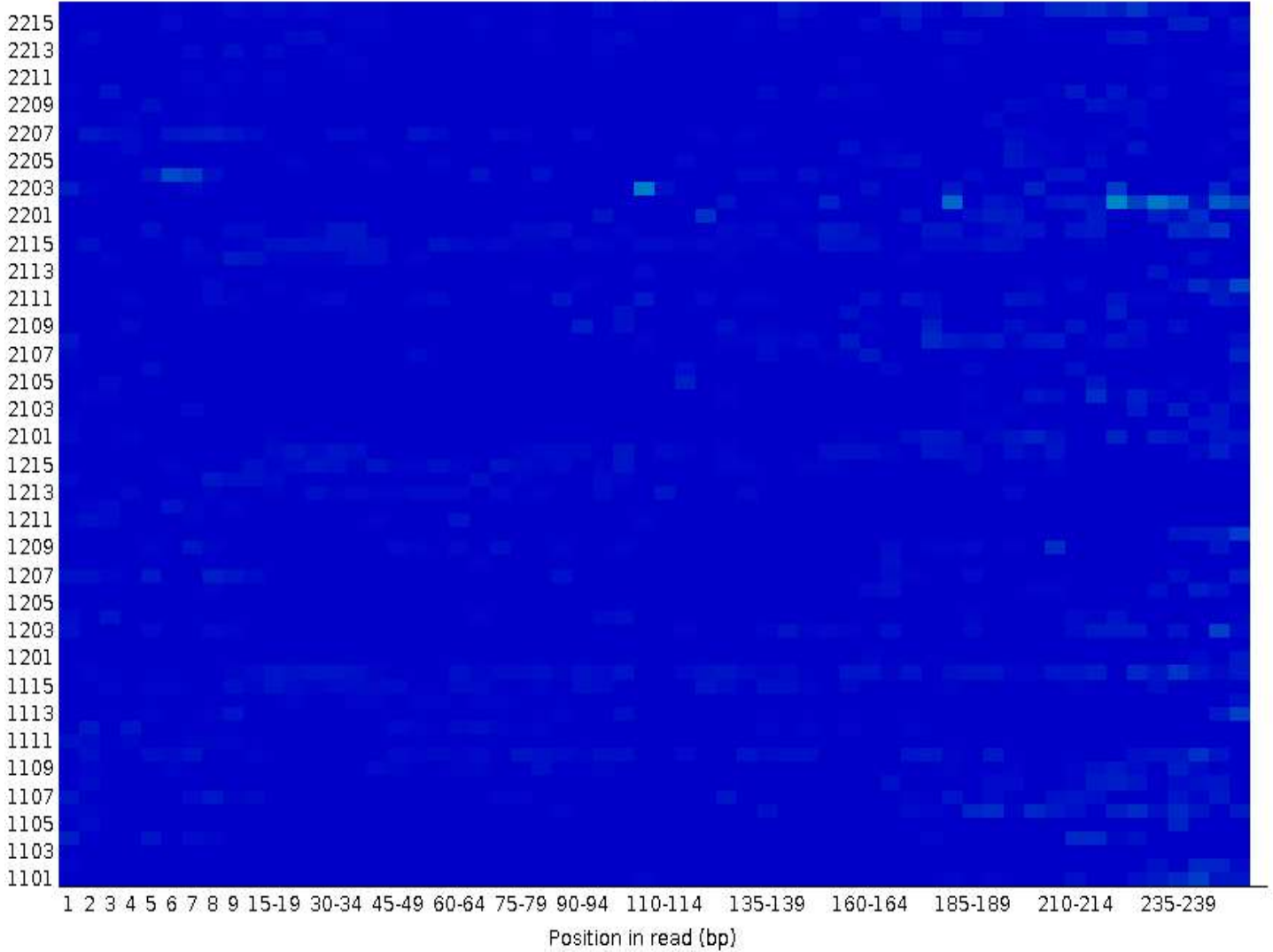
Measure	Value
Filename	10_EC092_R2_SingleEnd_fastpCleaned.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	222245
Sequences flagged as poor quality	0
Sequence length	31-251
%GC	51

✔ Per base sequence quality

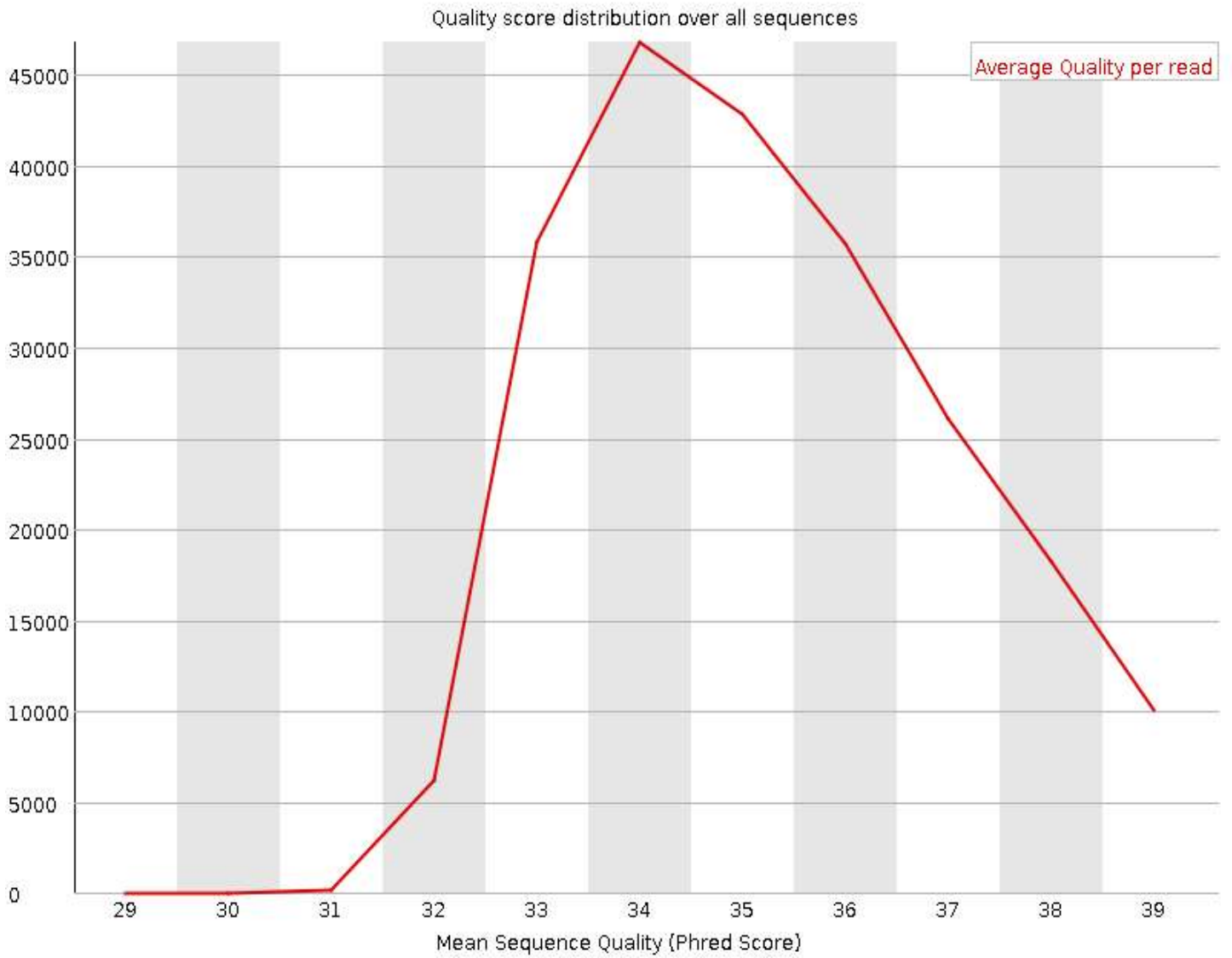


✔ Per tile sequence quality

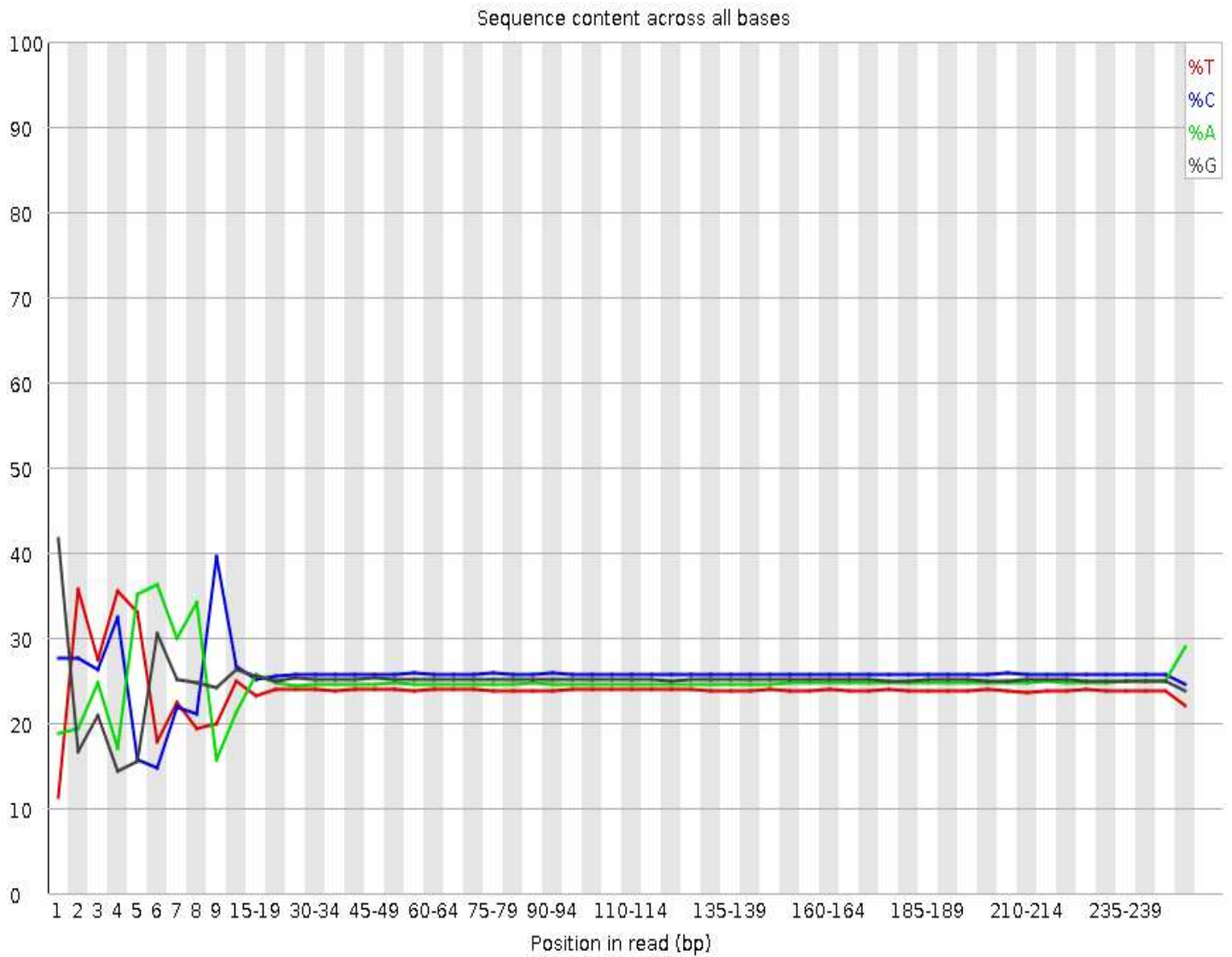
Quality per tile



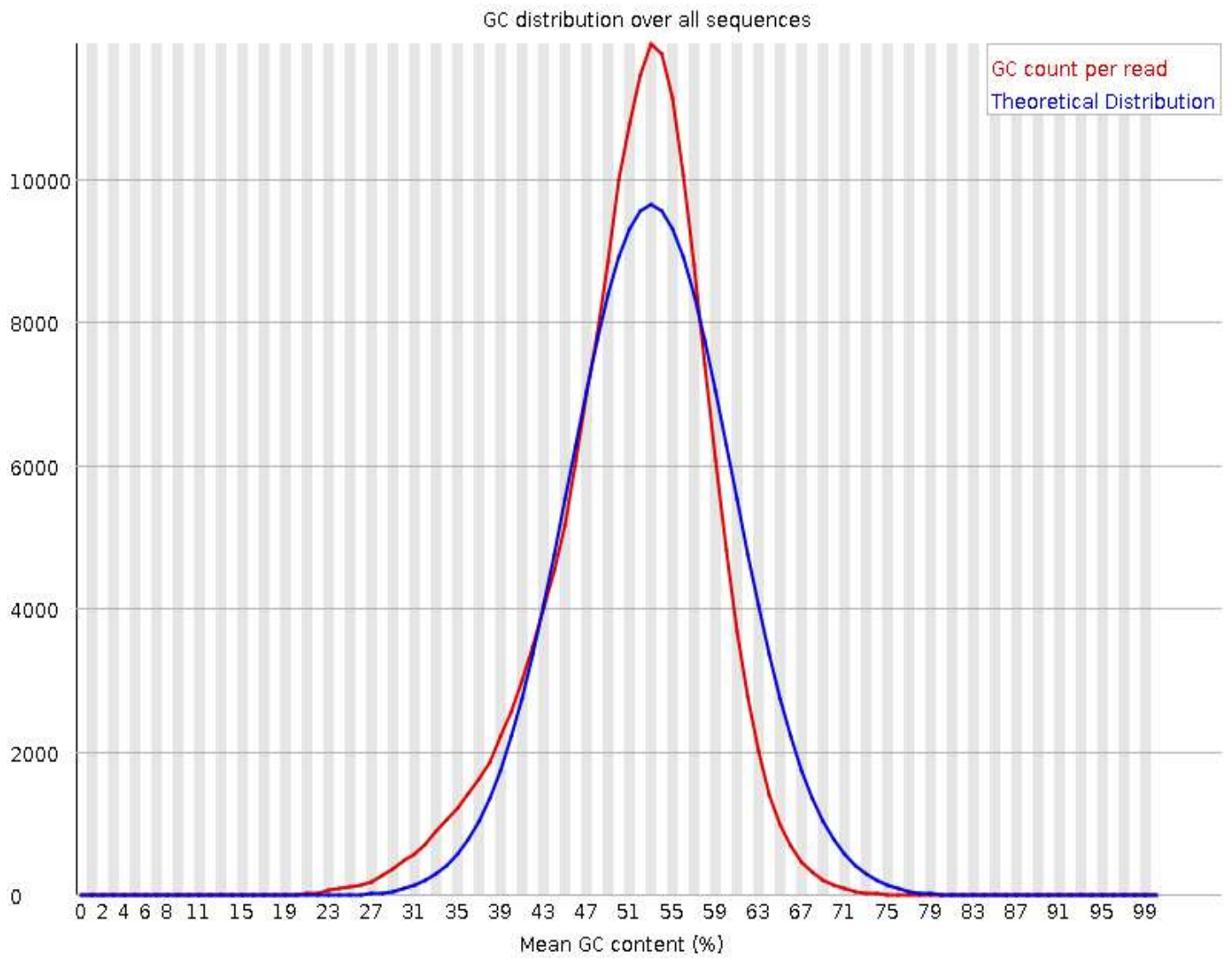
✔ Per sequence quality scores



! Per base sequence content

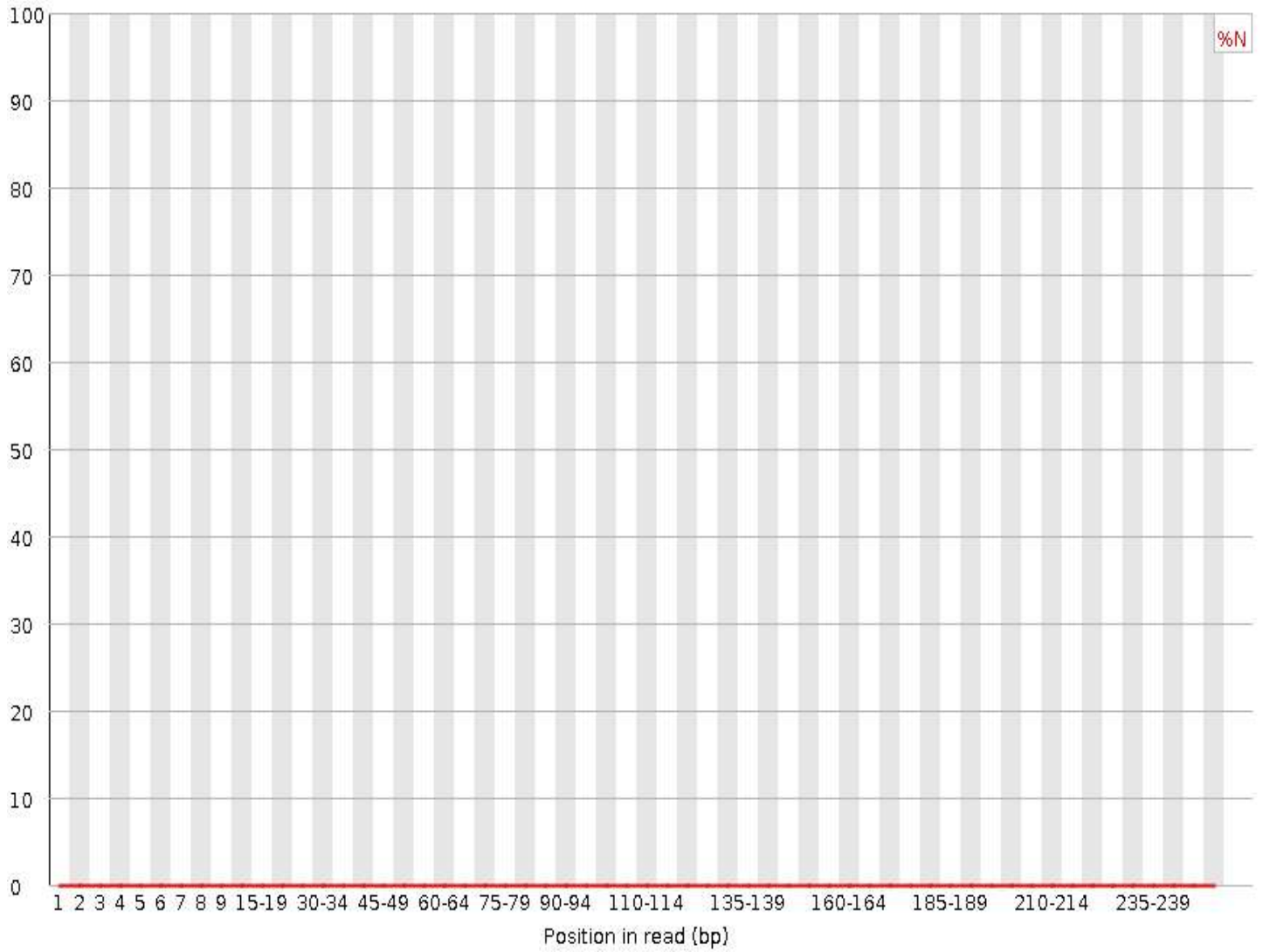


! Per sequence GC content

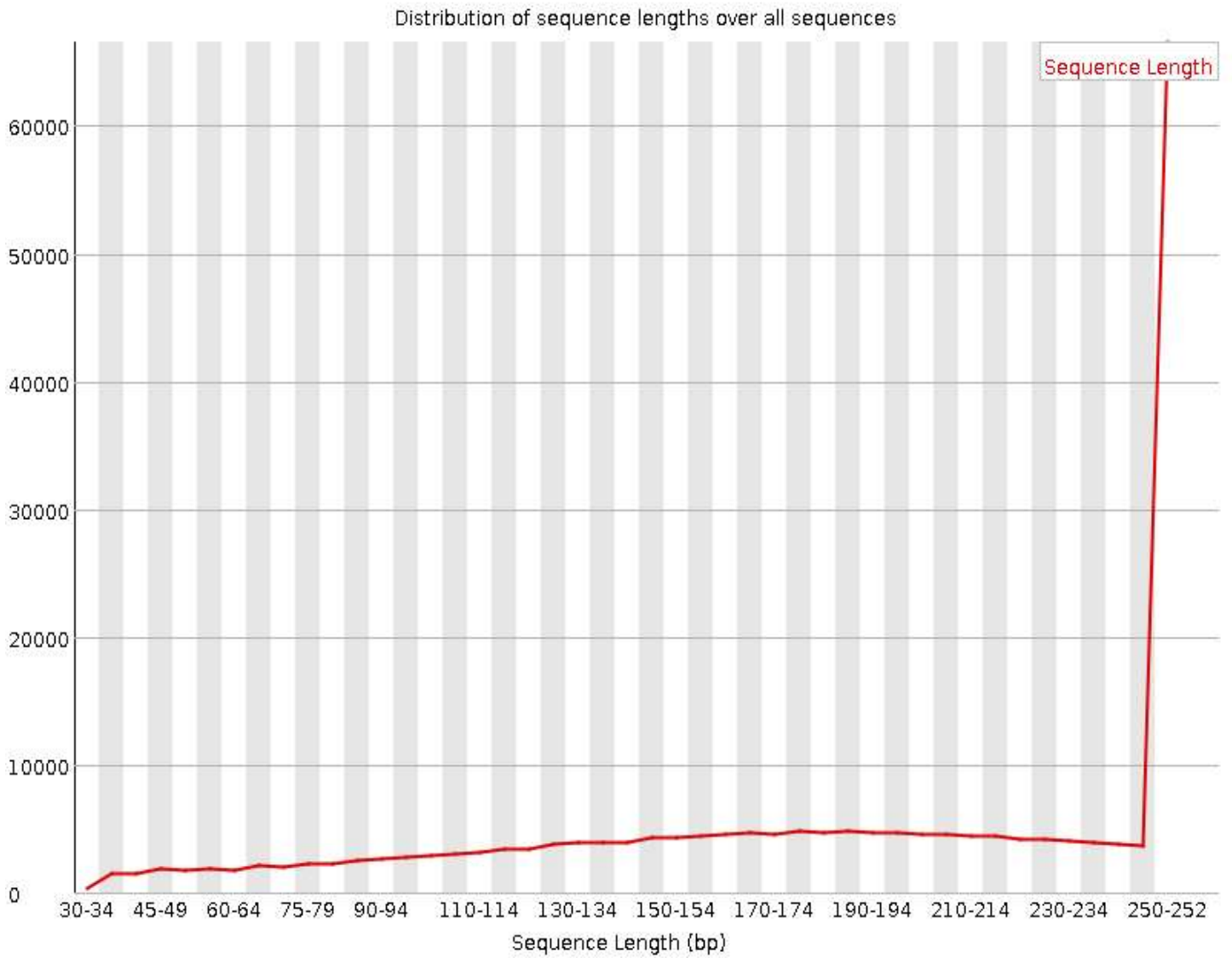


✔ Per base N content

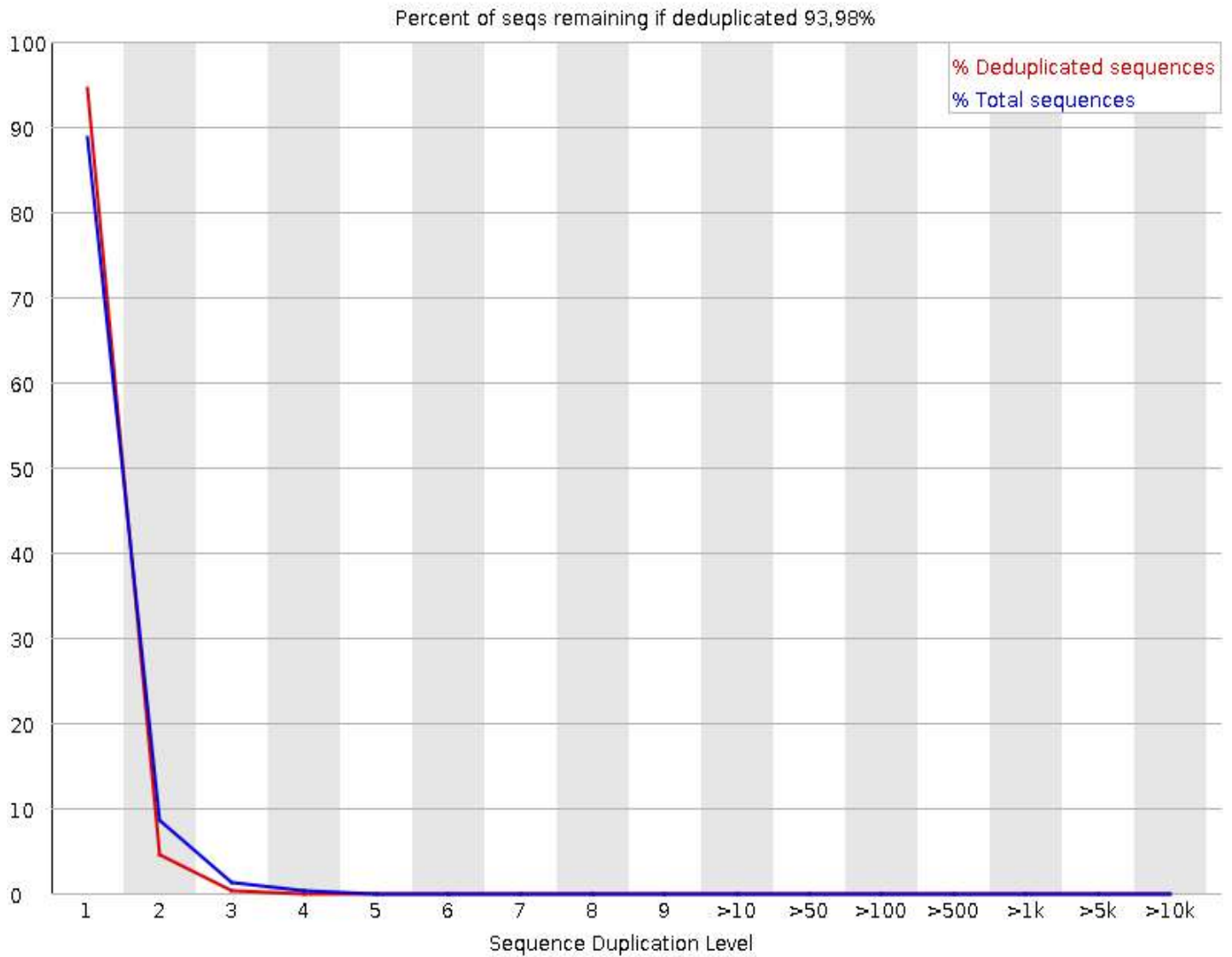
N content across all bases



! Sequence Length Distribution



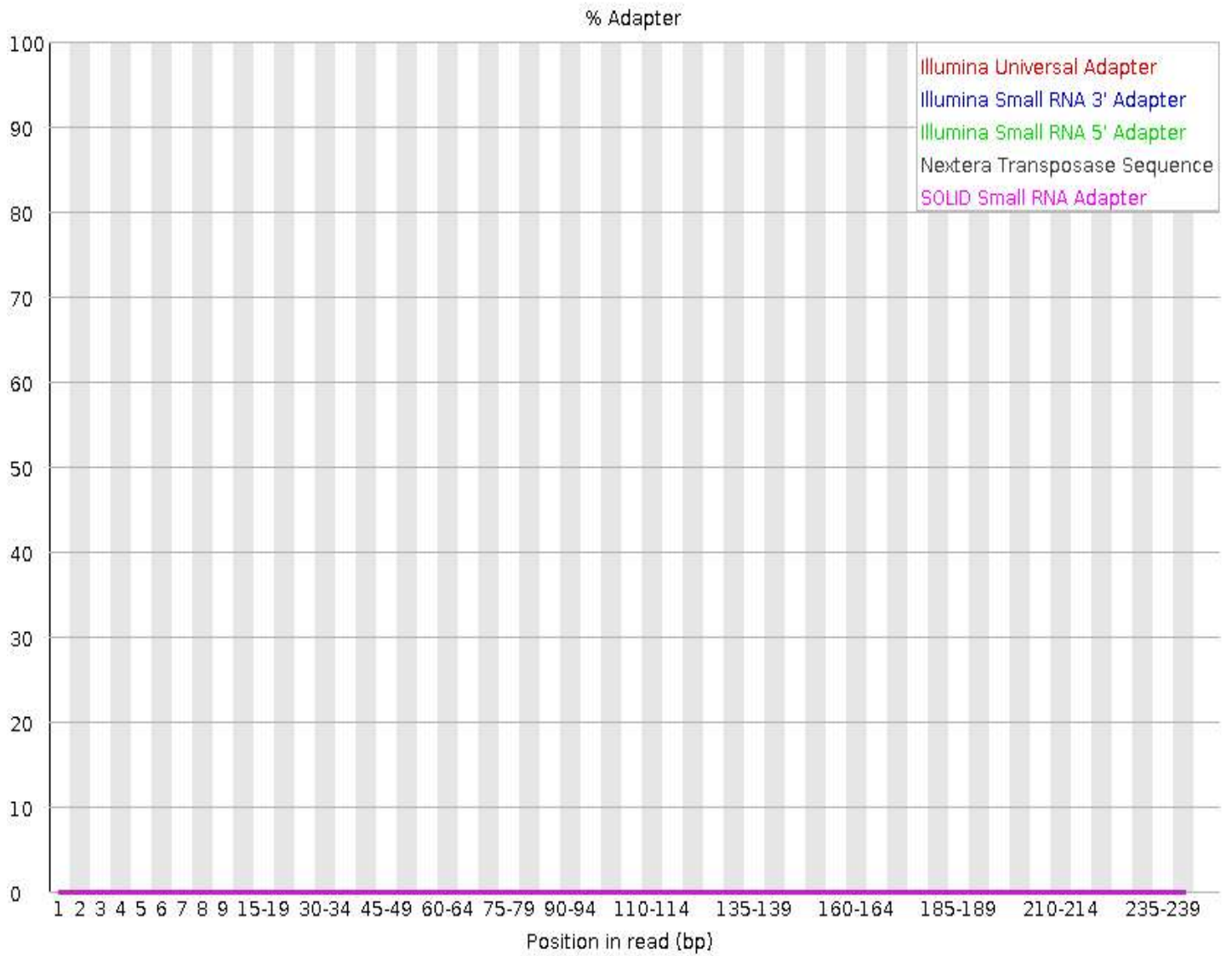
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

Adapter Content



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