












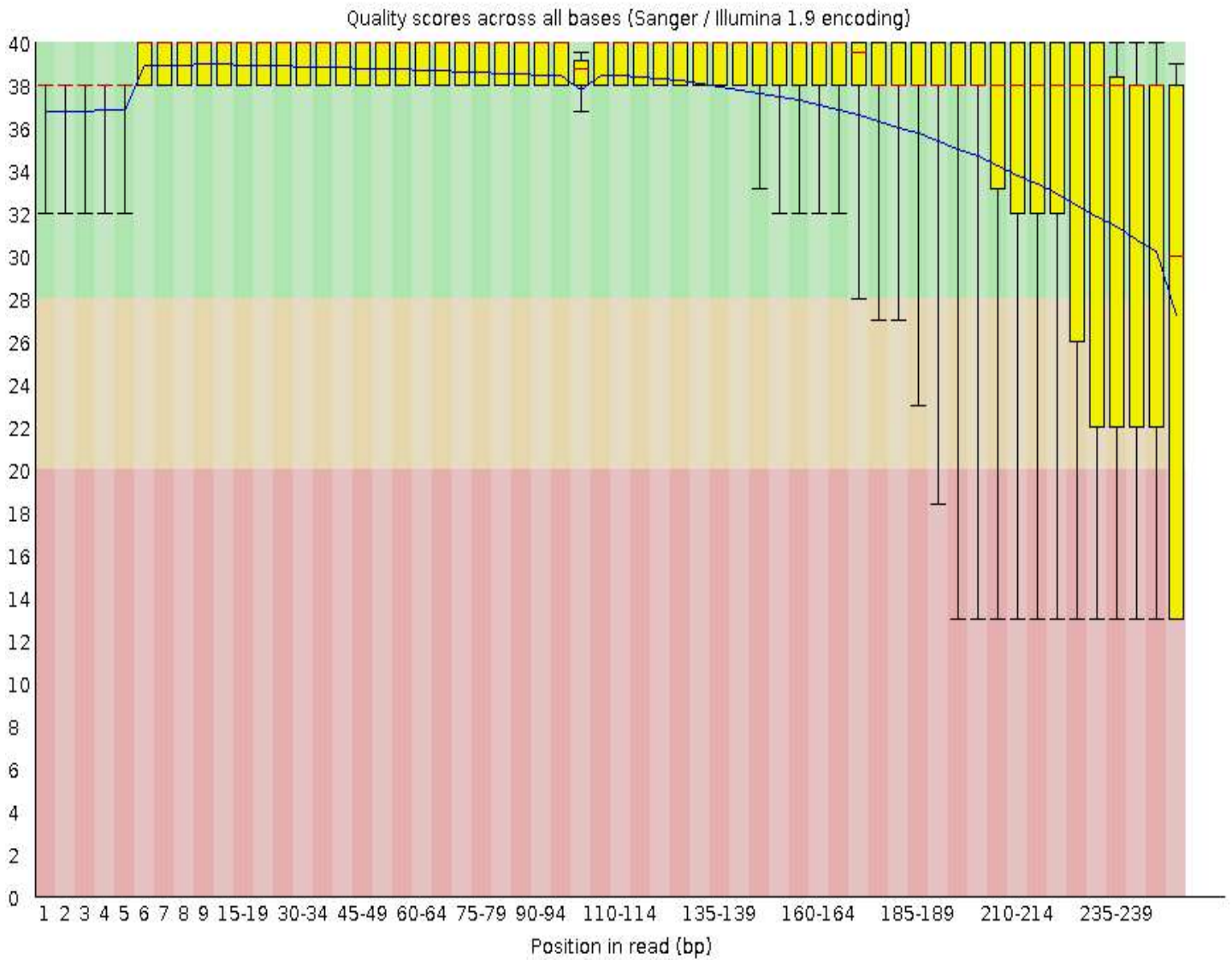
Summary

-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per tile 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](#)
-  [Adapter Content](#)

Basic Statistics

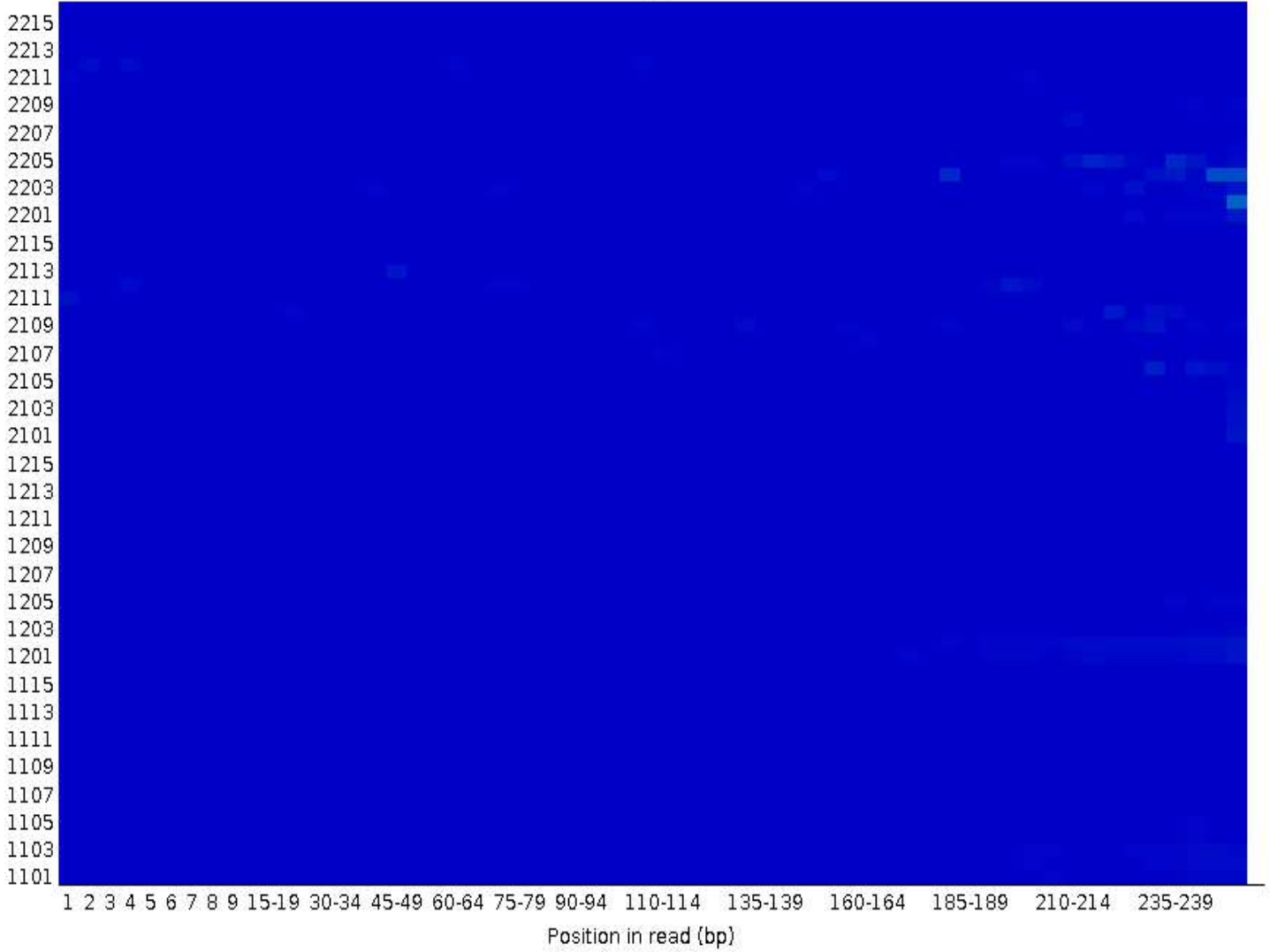
Measure	Value
Filename	10_EC092_r1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	13808011
Sequences flagged as poor quality	0
Sequence length	251
%GC	50

✔ Per base sequence quality

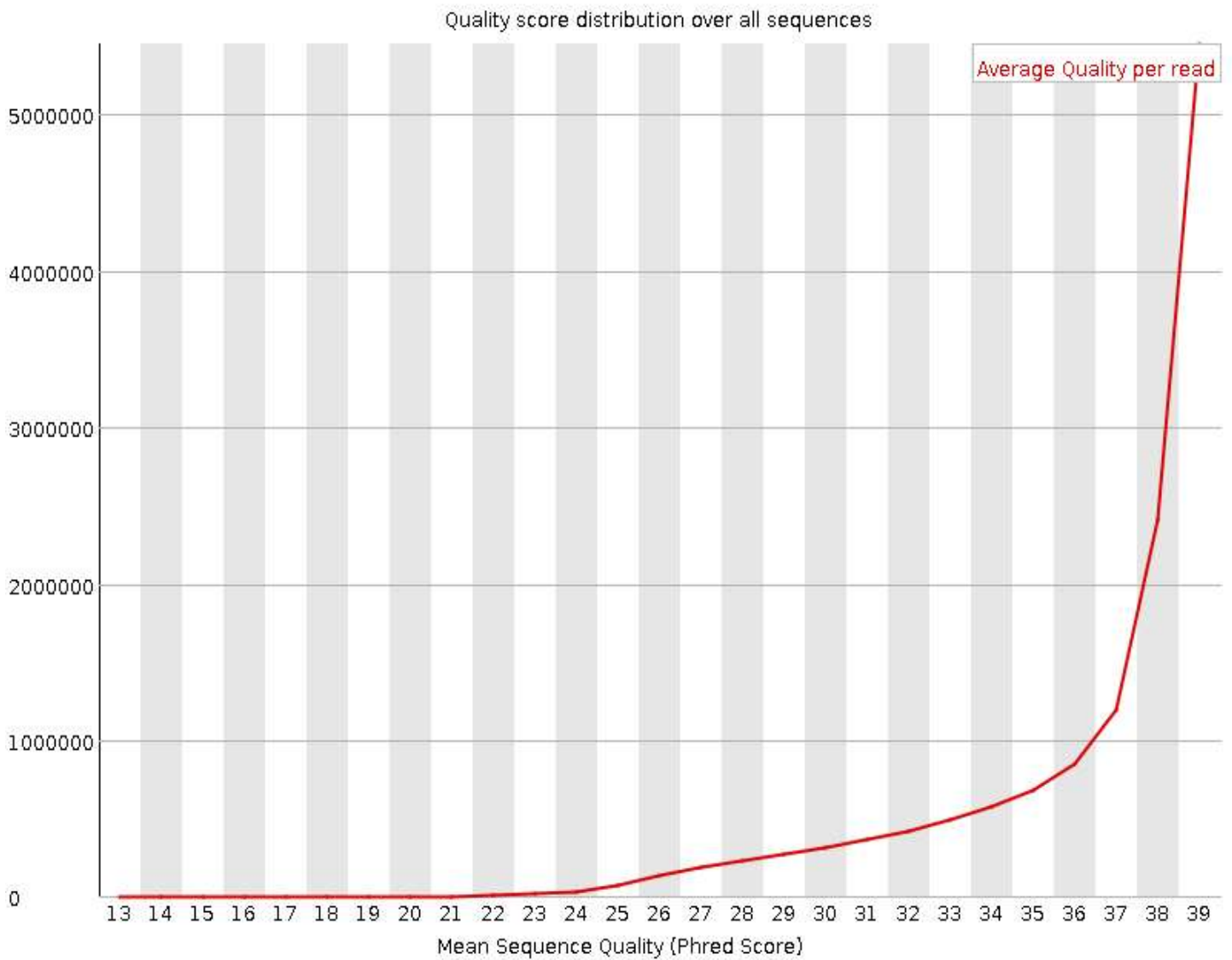


✔ Per tile sequence quality

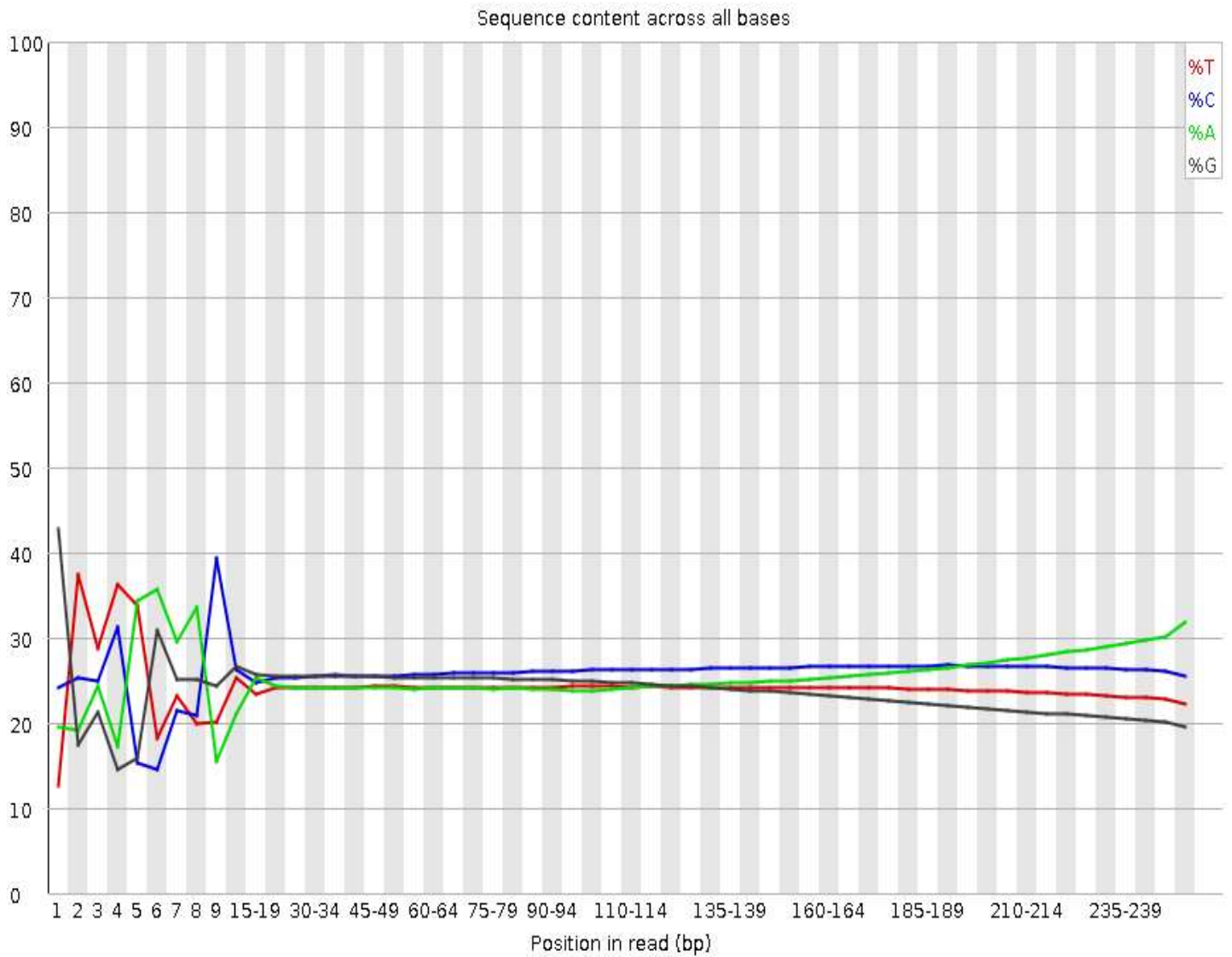
Quality per tile



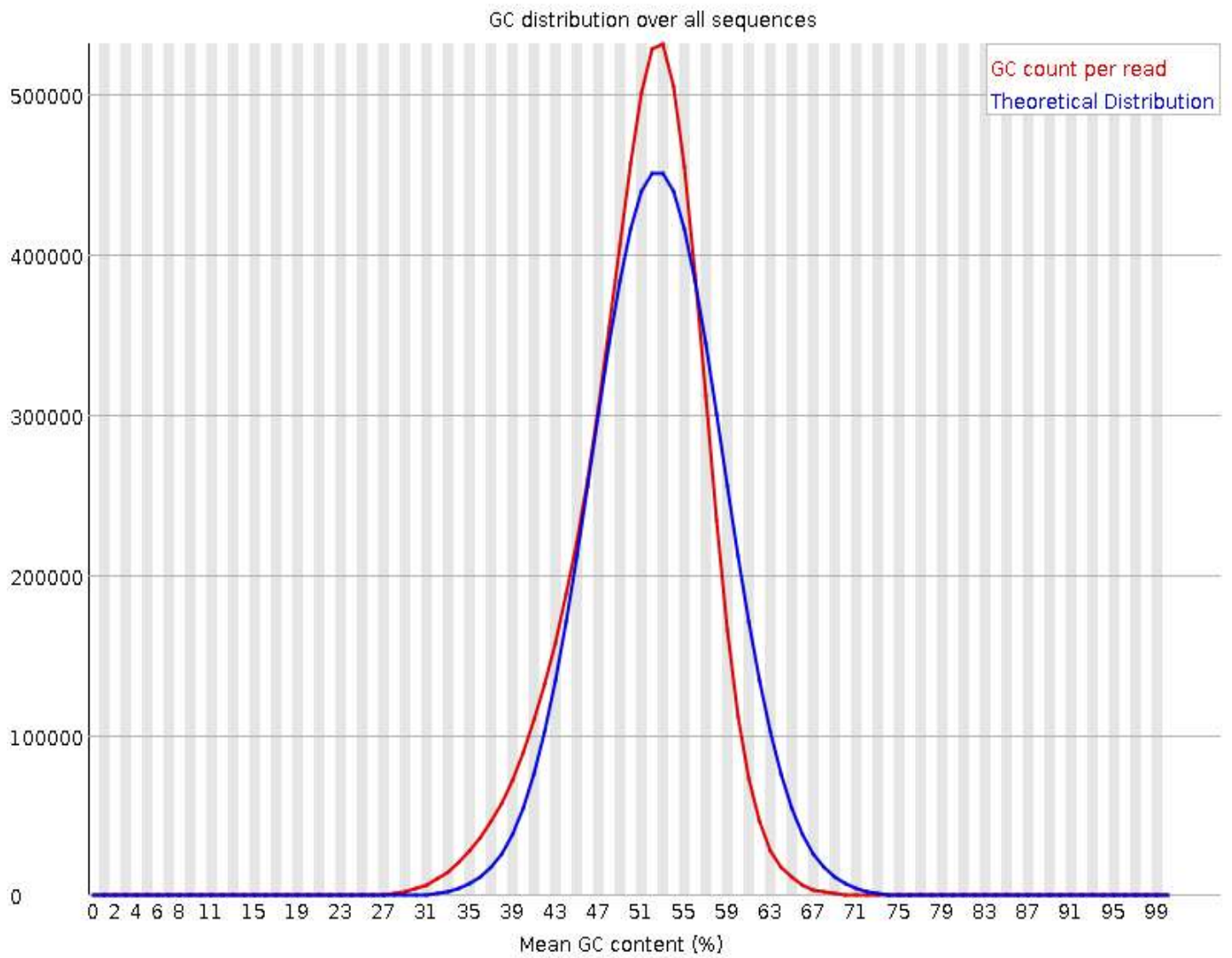
✔ Per sequence quality scores



! Per base sequence content

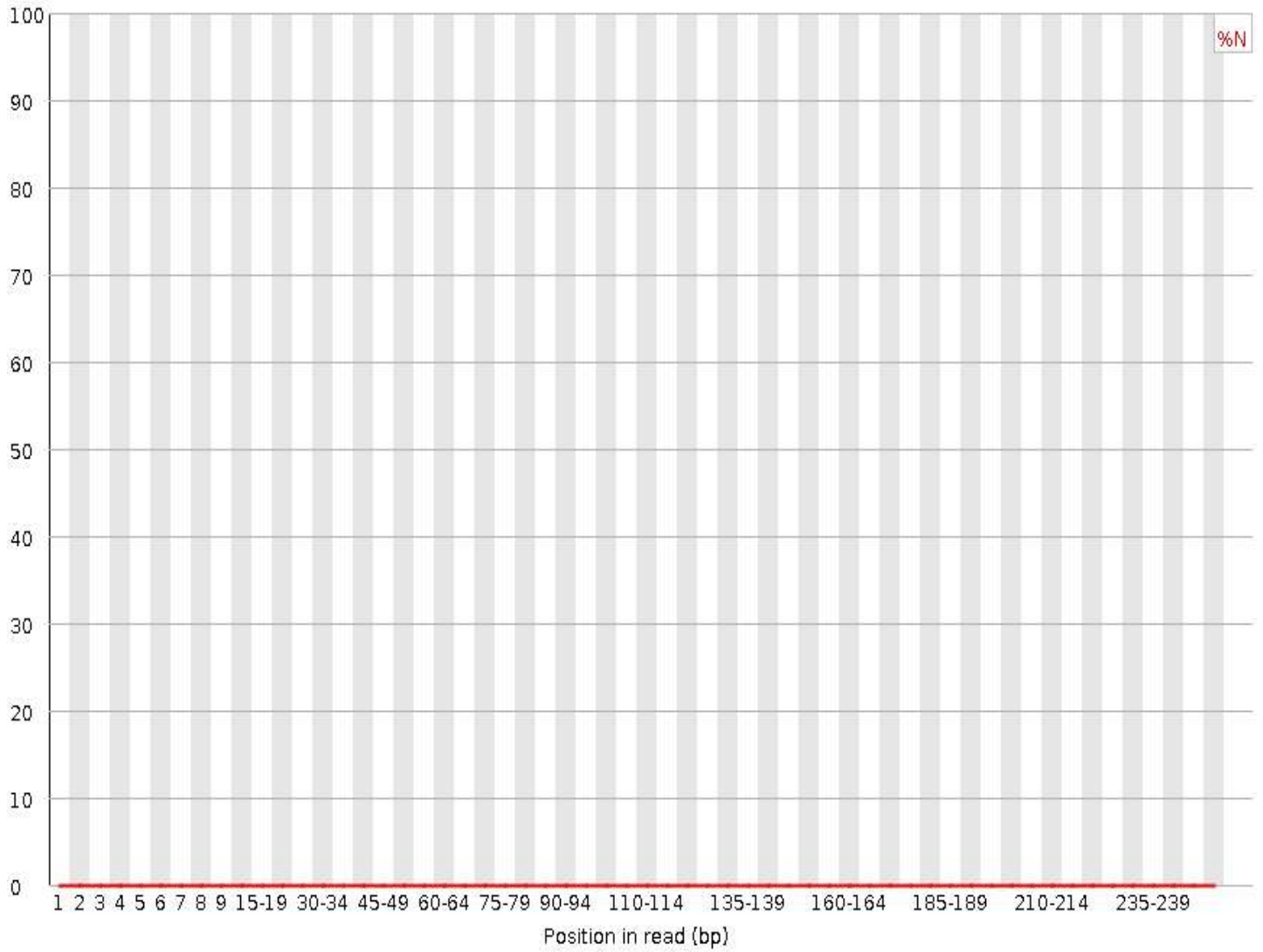


! Per sequence GC content

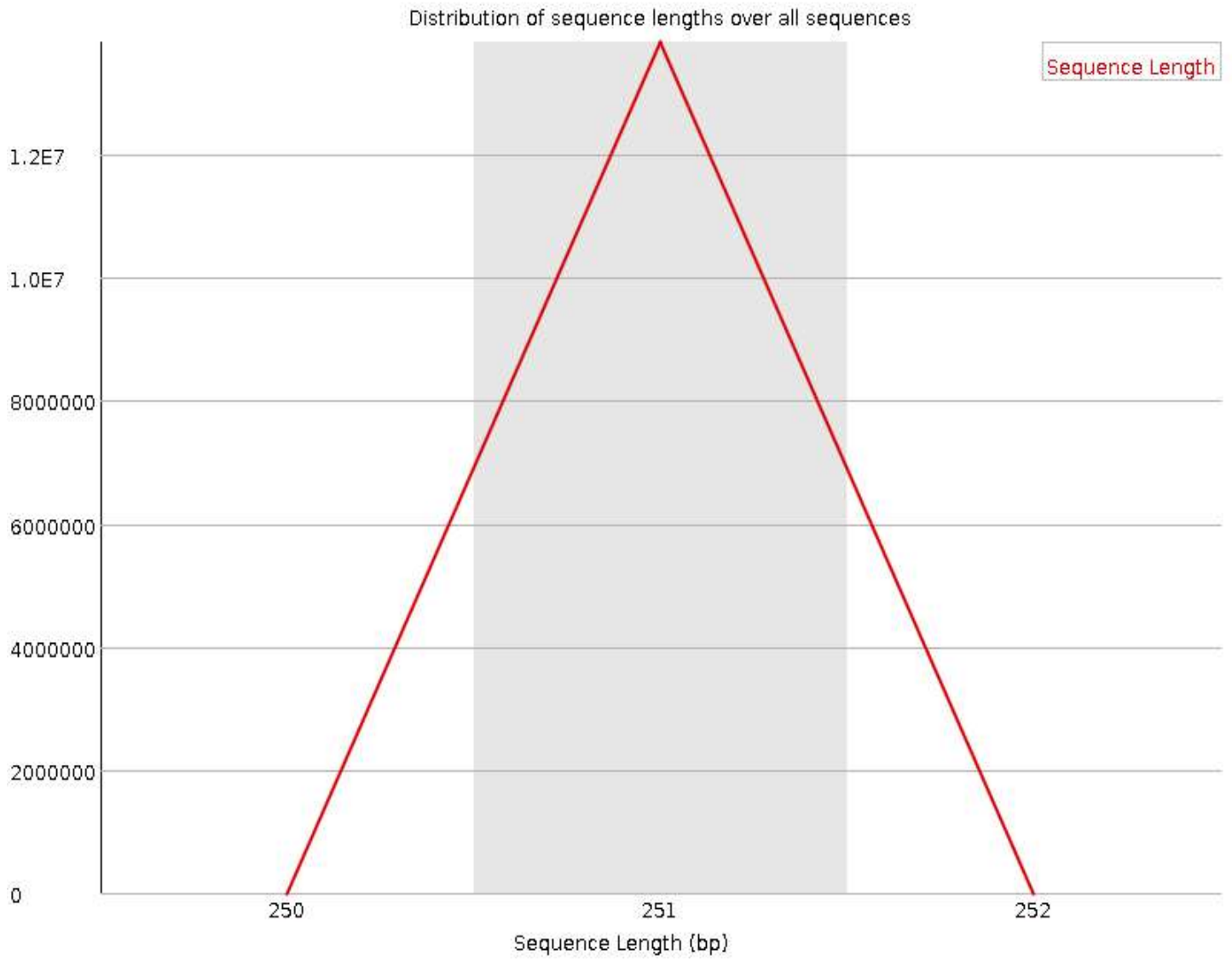


✔ Per base N content

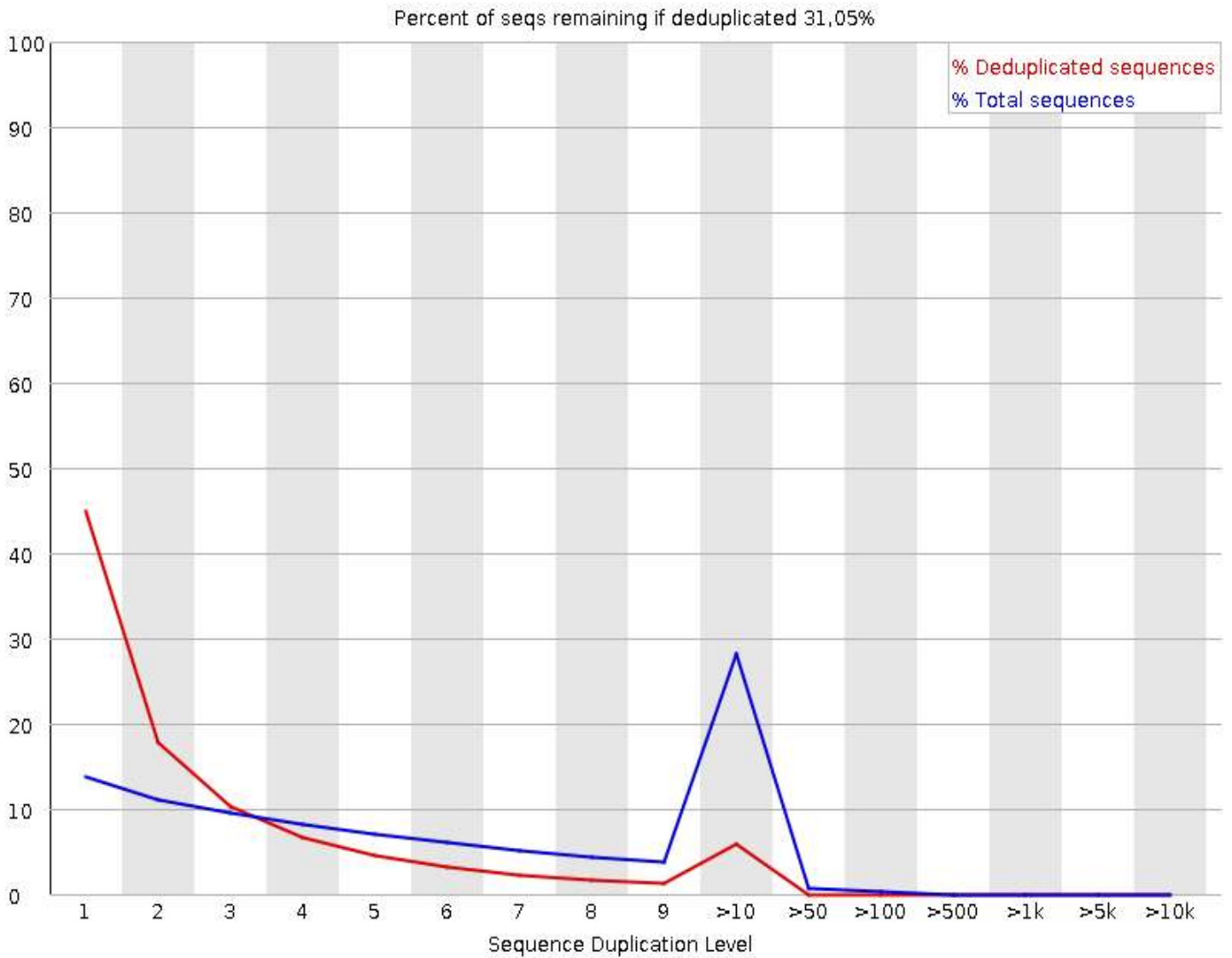
N content across all bases



✔ Sequence Length Distribution



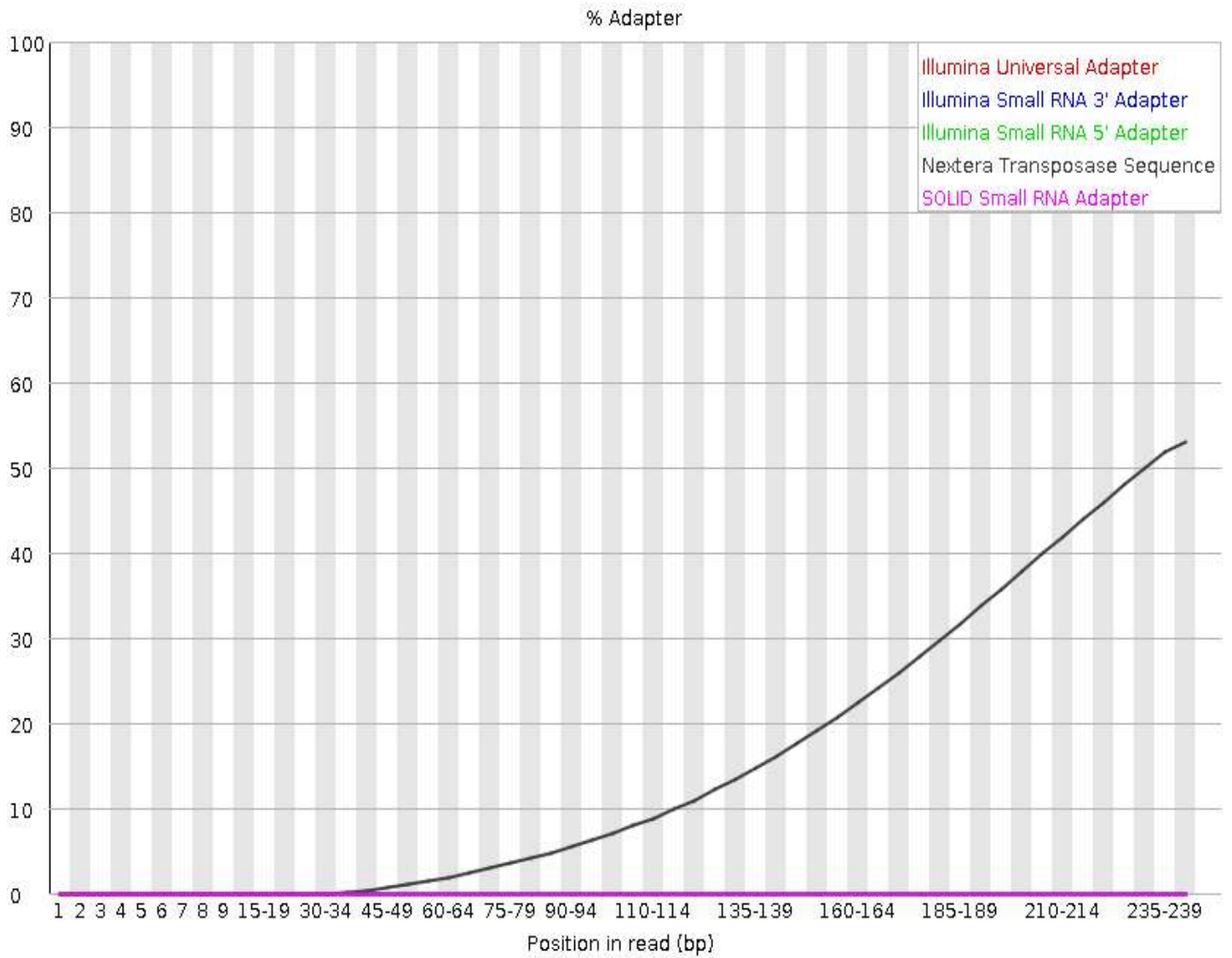
✘ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

Adapter Content



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