FastQC Report

Mon 1 Mar 2021
P0_1_2.fastq

Summary

- Basic Statistics
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- Per tile sequence quality
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- Per base sequence content
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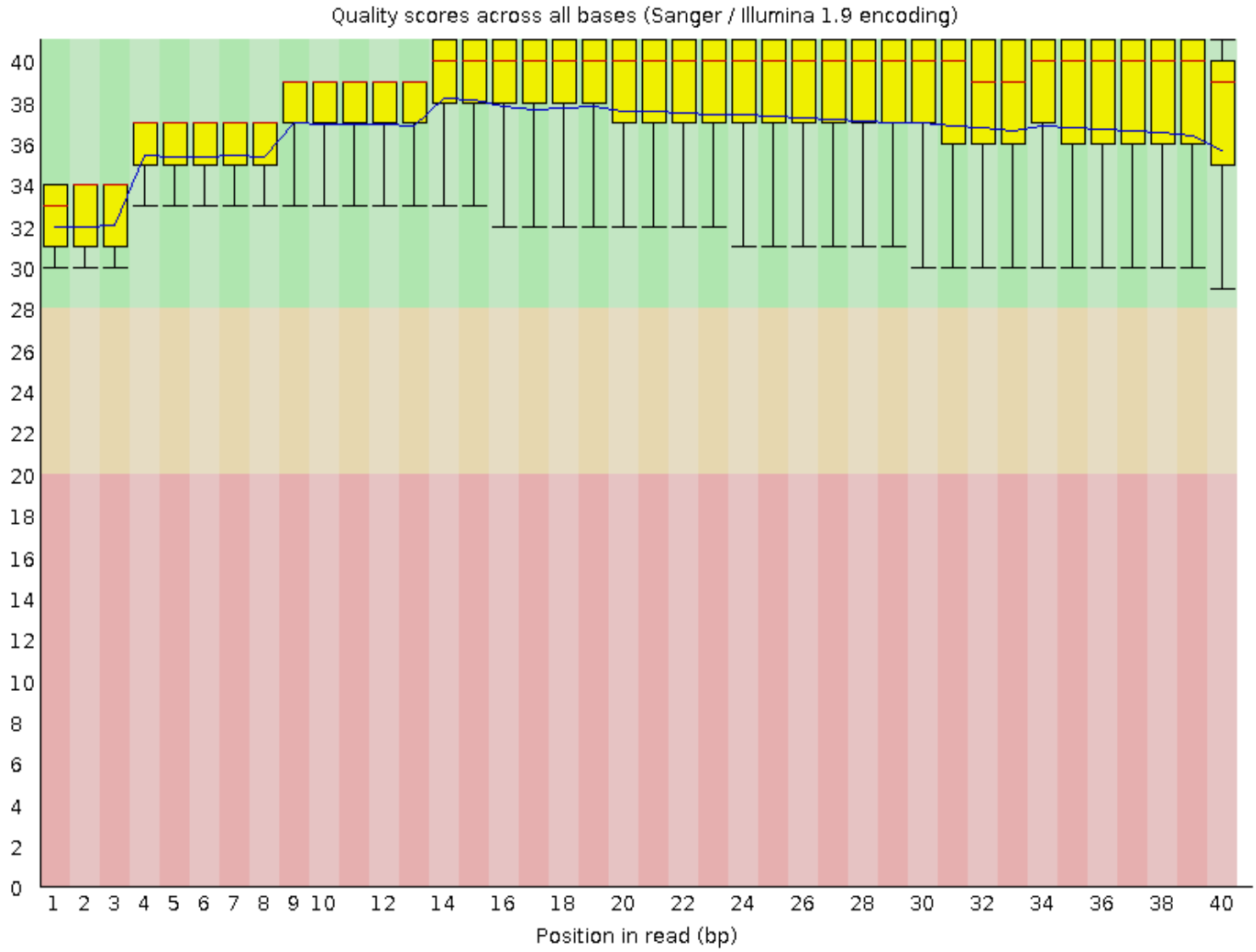
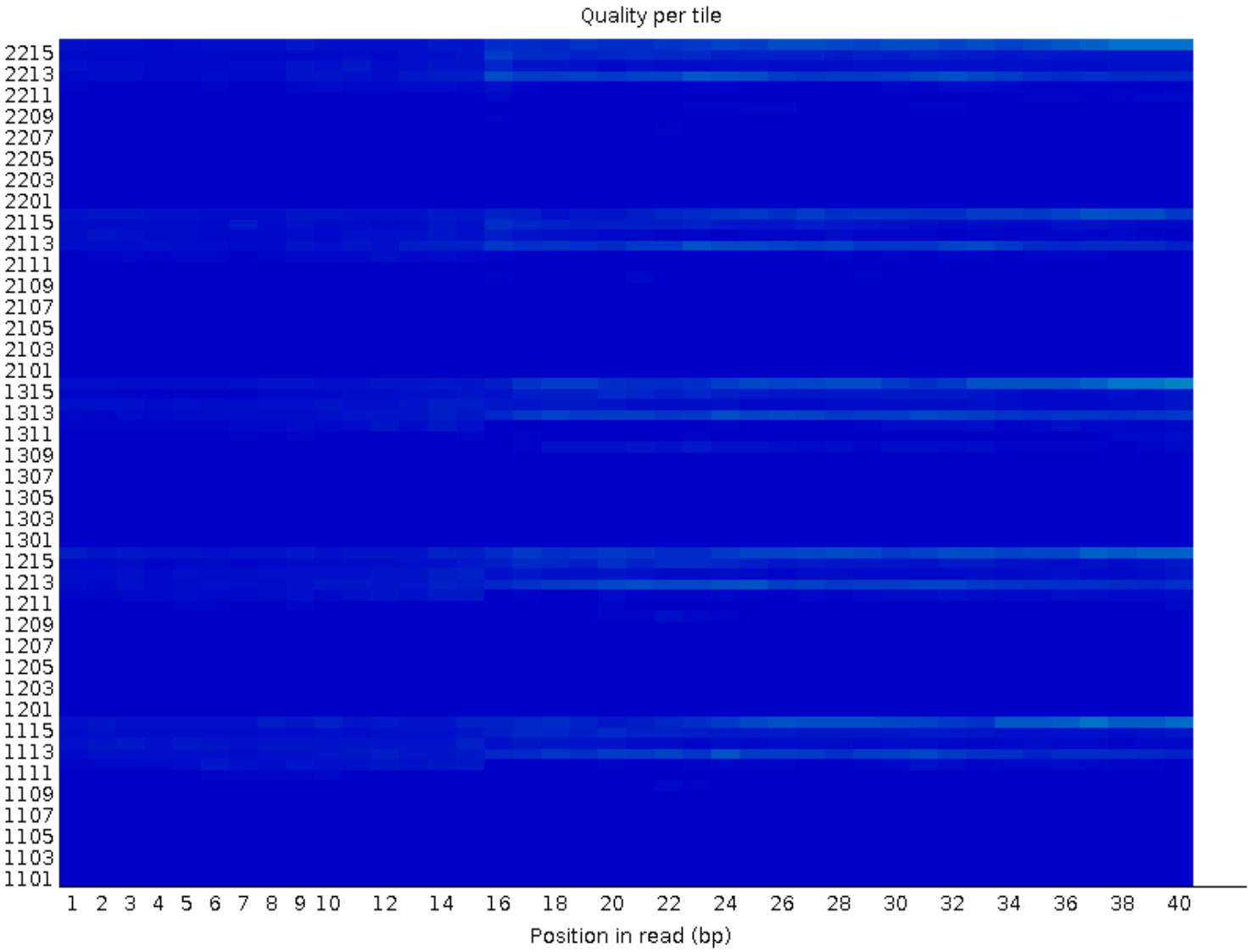
Basic Statistics

Measure	Value
Filename	P0_1_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	21577562
Sequences flagged as poor quality	0
Sequence length	40
%GC	49

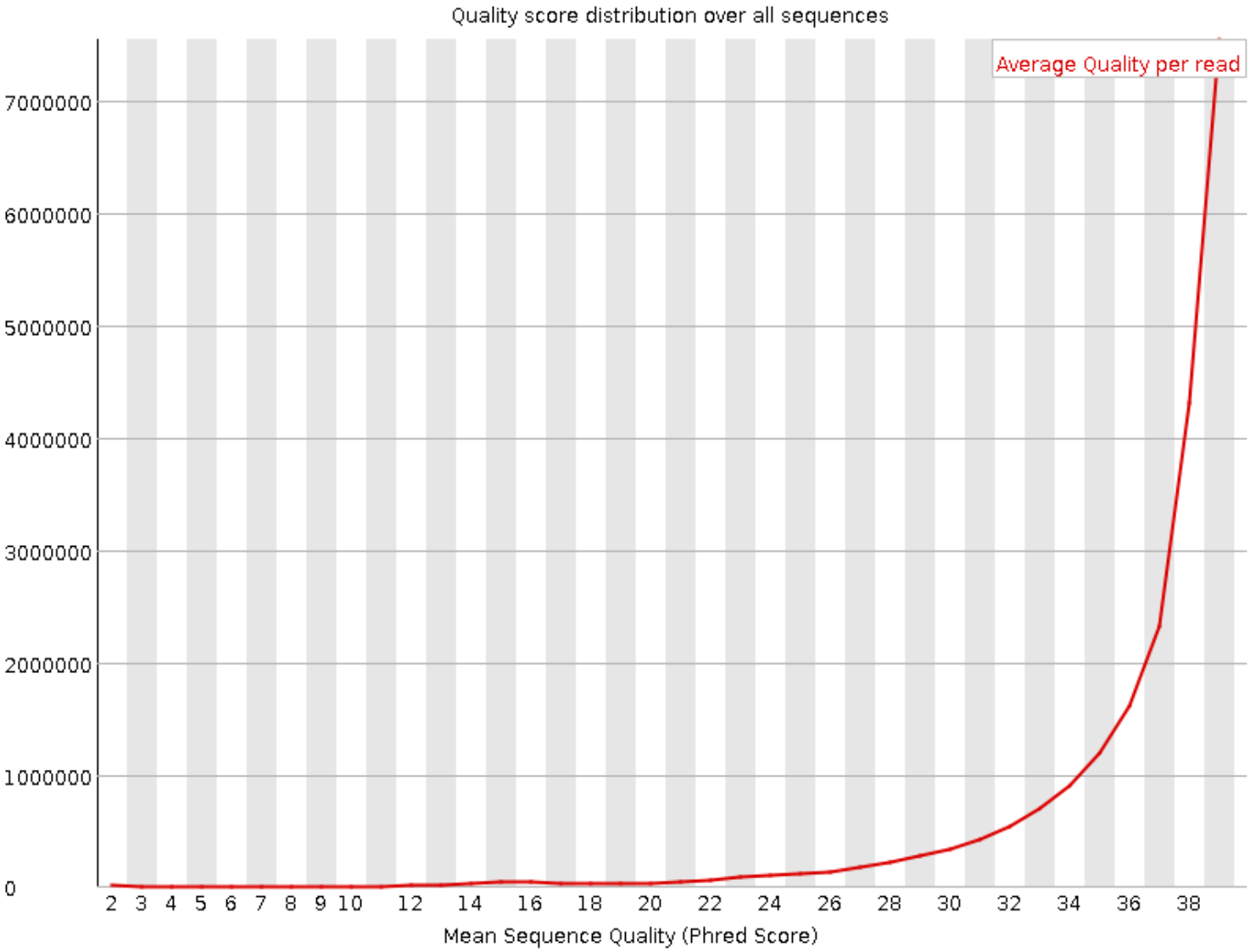
Per base sequence quality



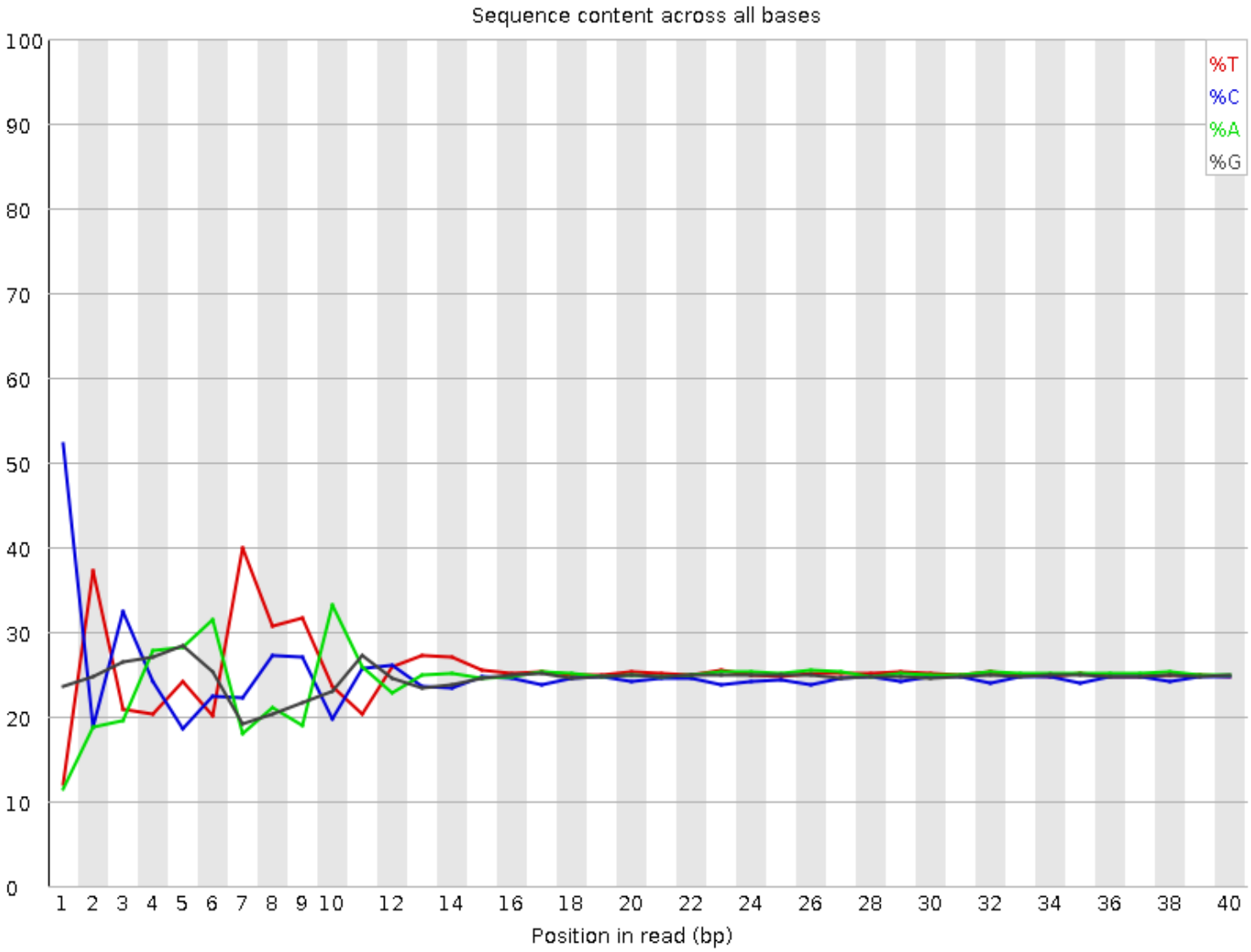
Per tile sequence quality



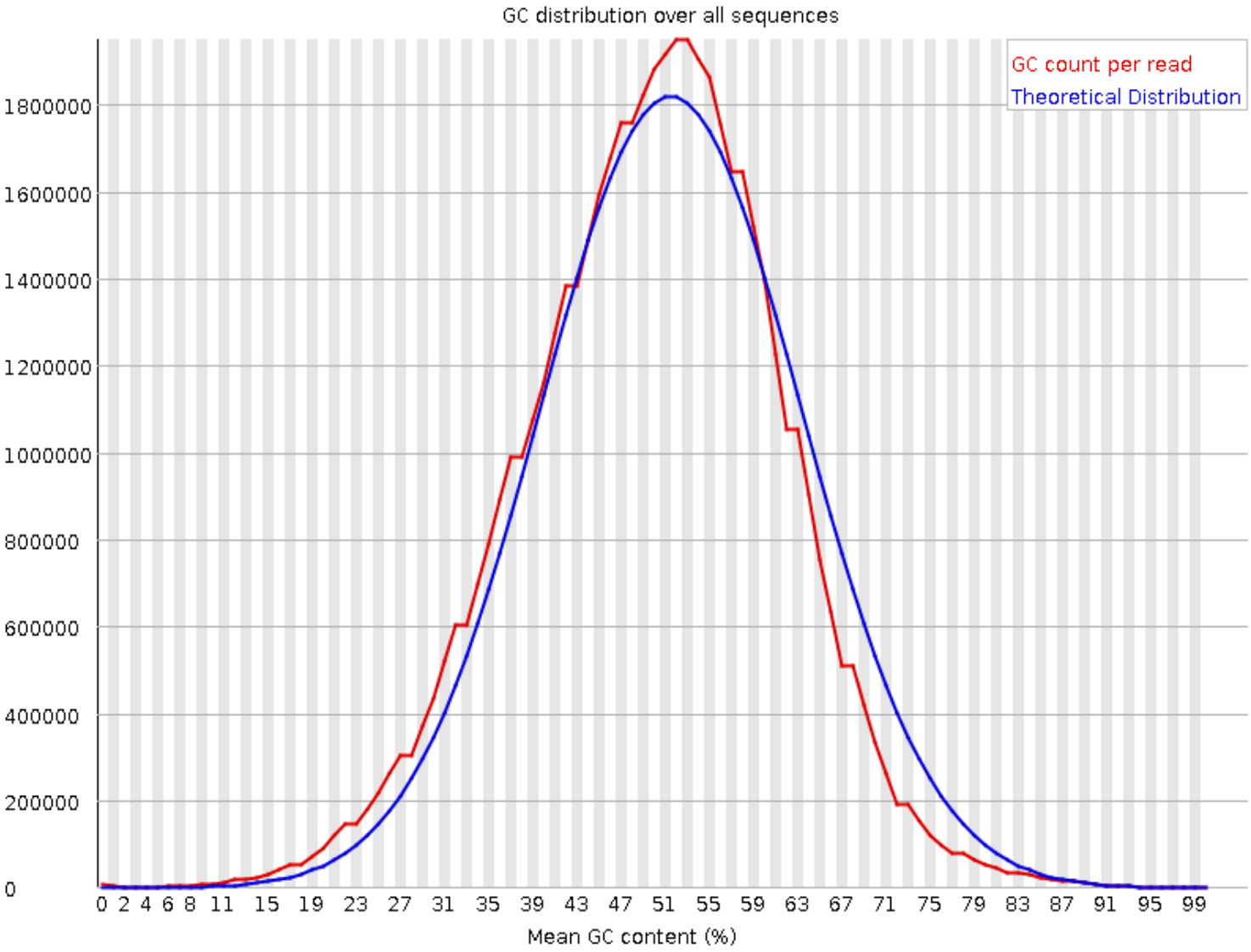
Per sequence quality scores



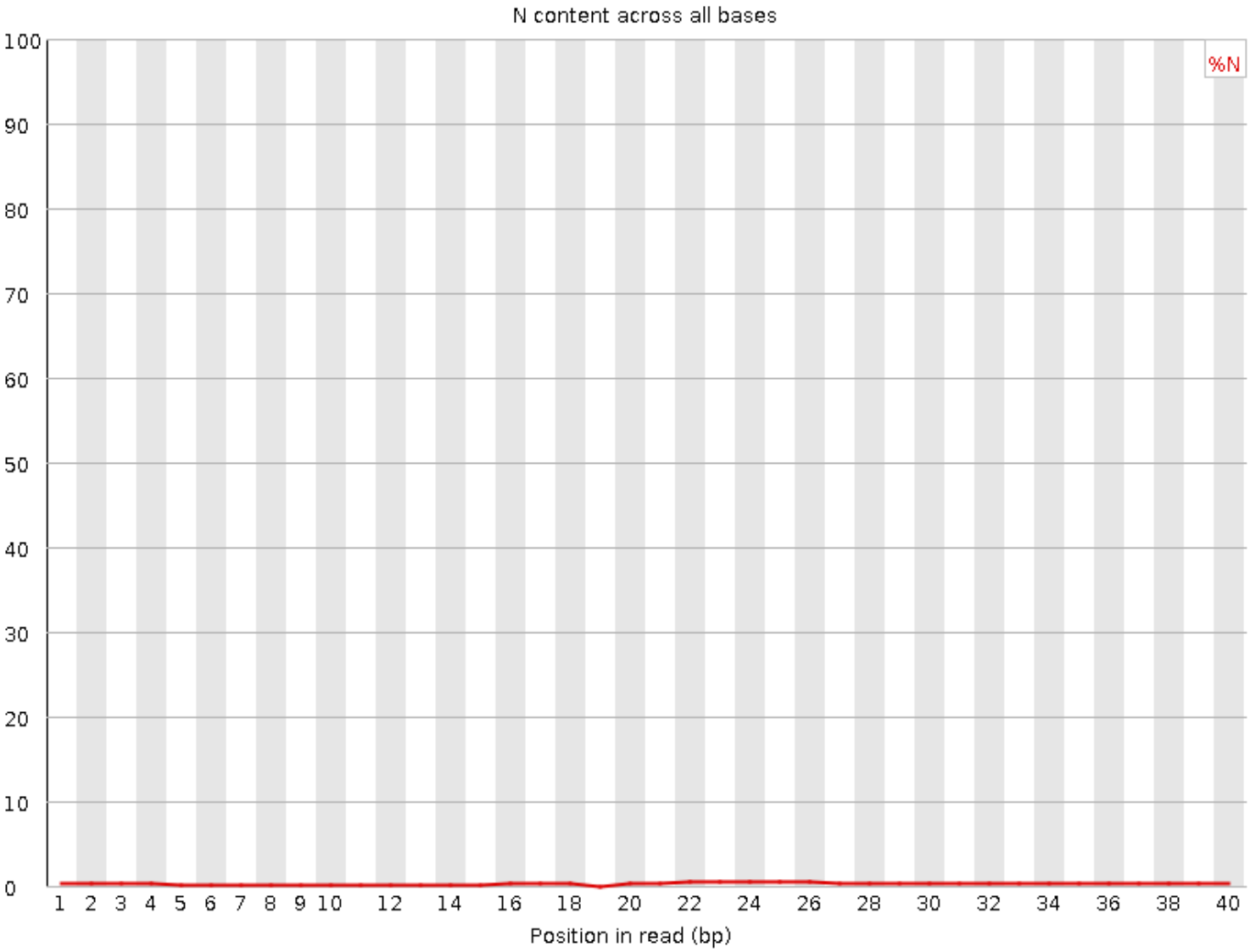
Per base sequence content



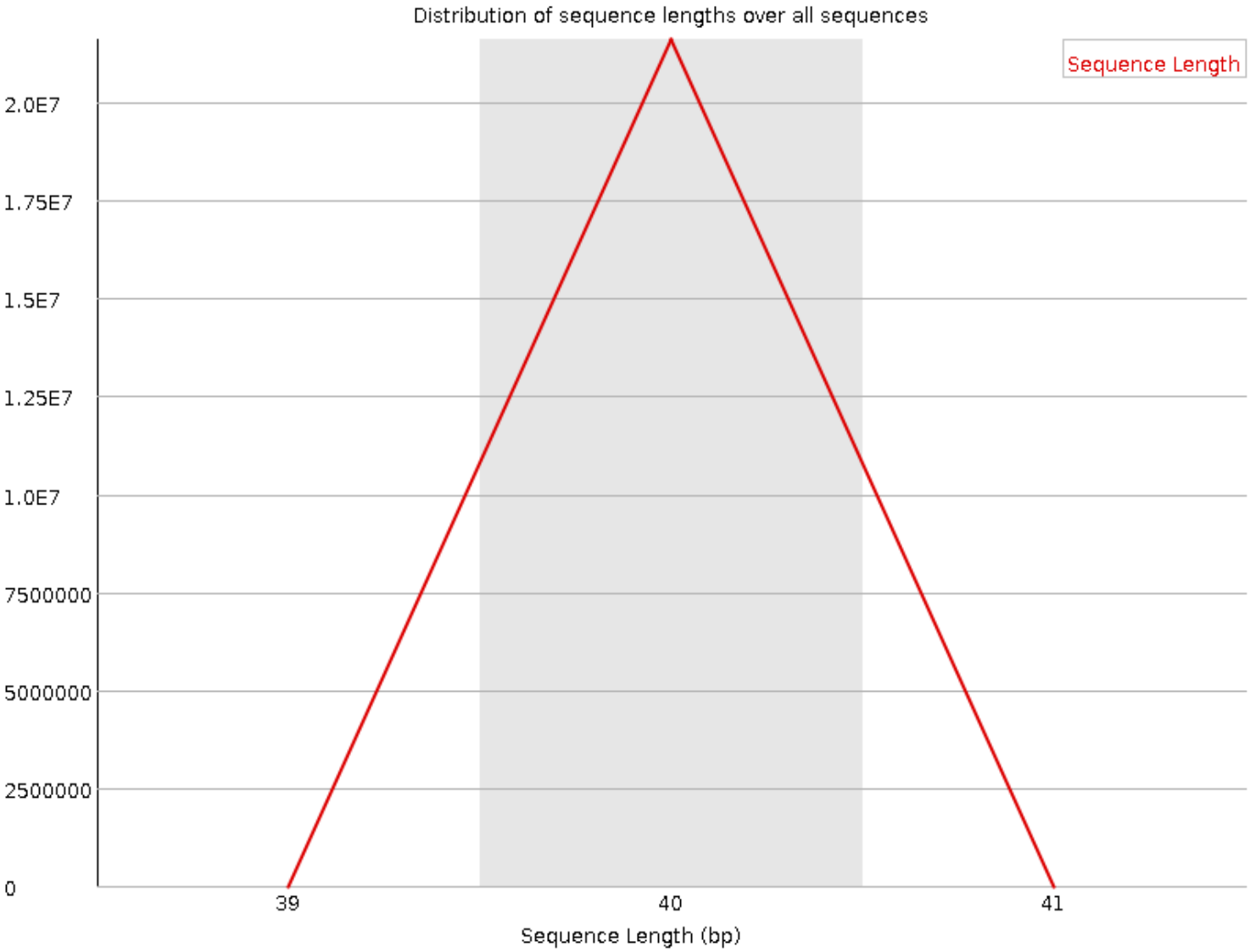
Per sequence GC content



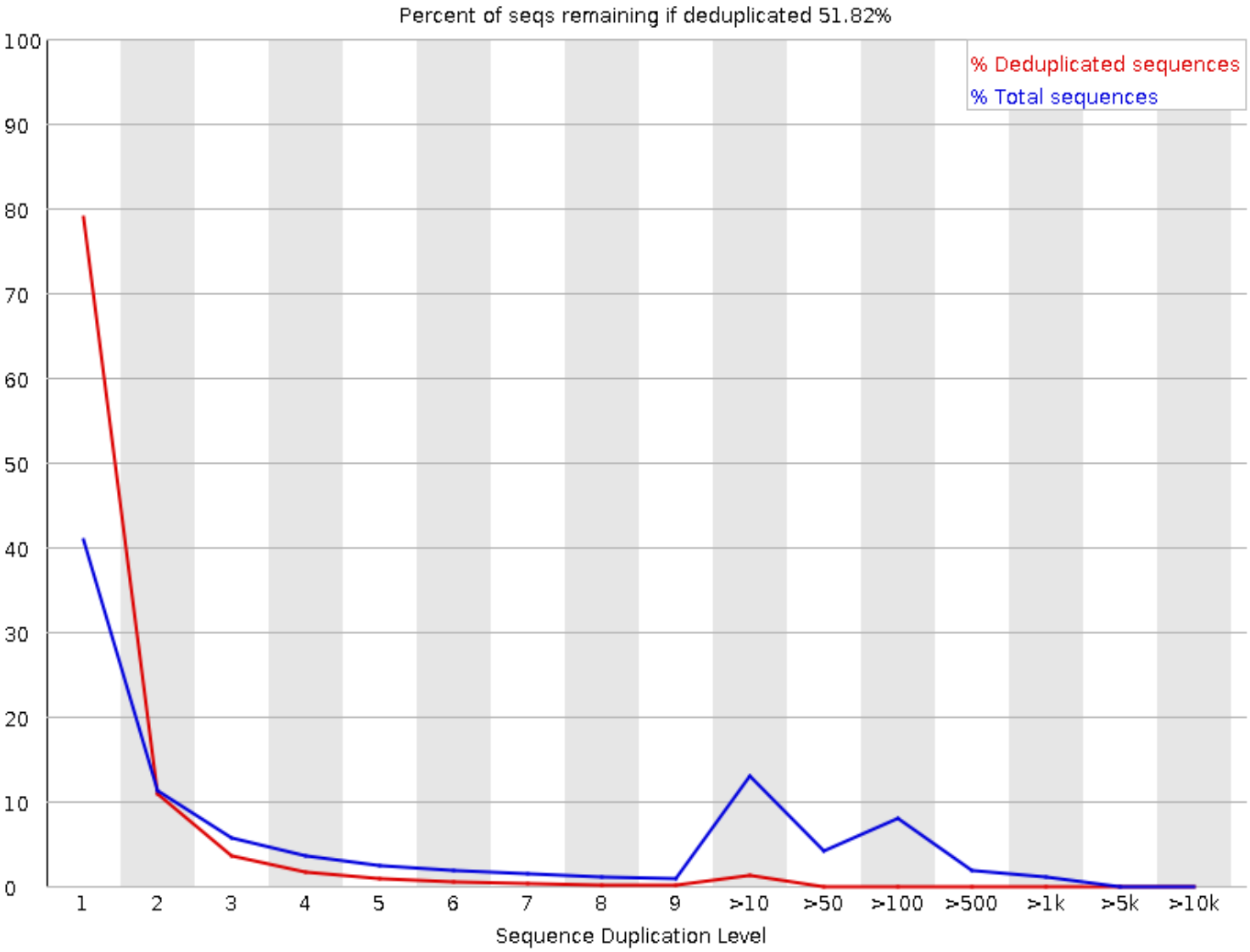
Per base N content



Sequence Length Distribution



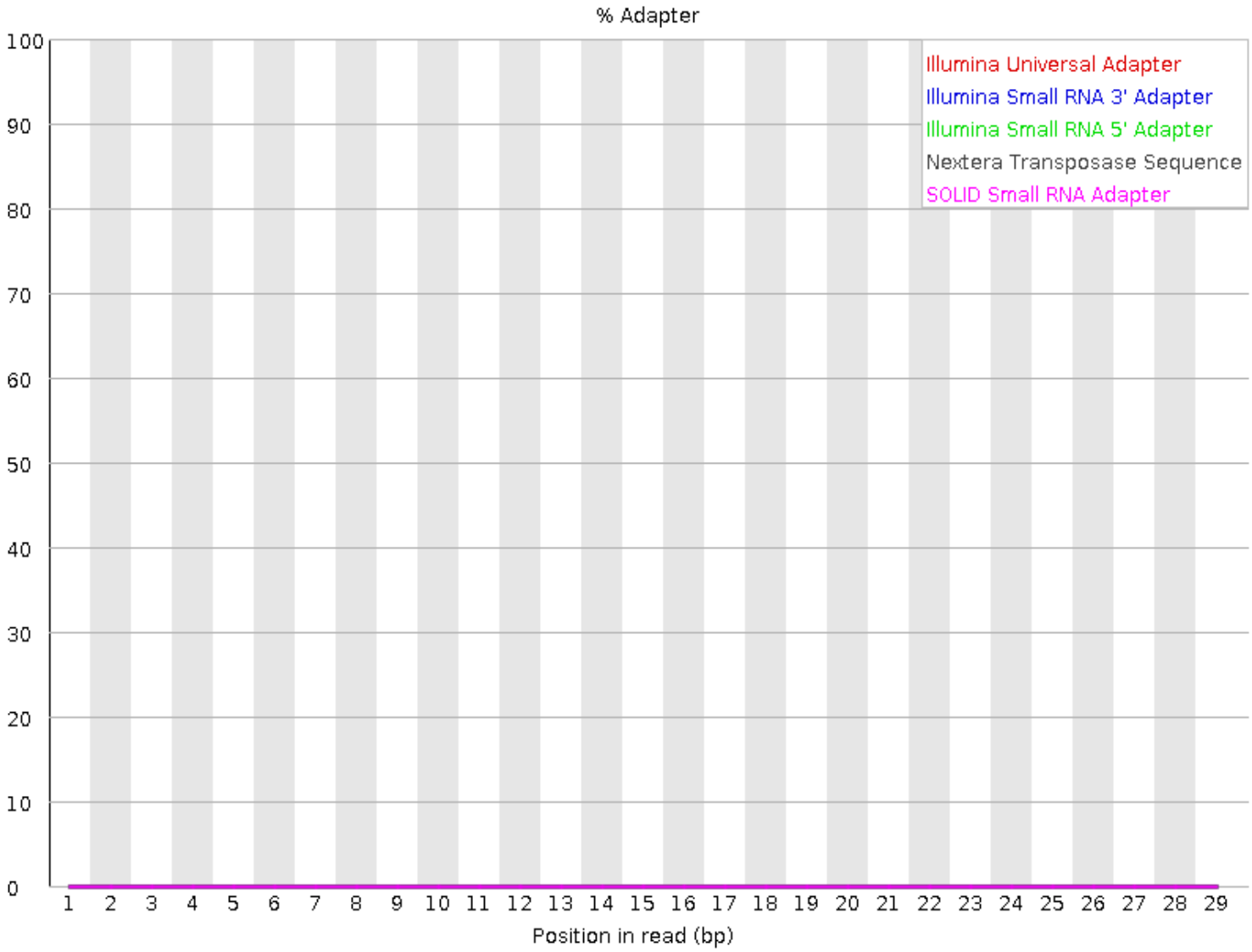
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.11.7)