FastQC Report

Thu 16 May 2024
M4_S4_L001_R1_001.fastq.gz

Summary

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- Per base sequence content
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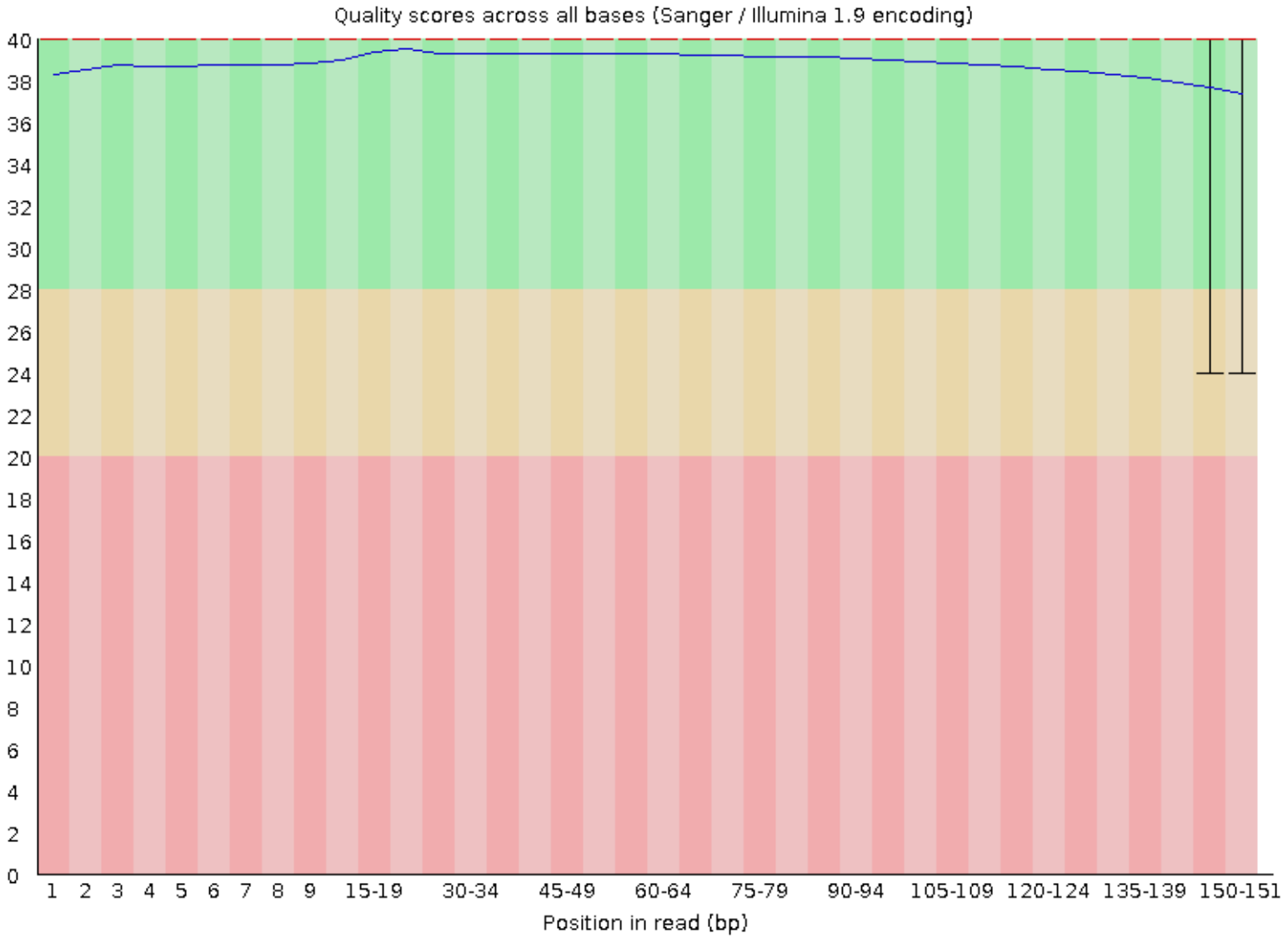
Basic Statistics

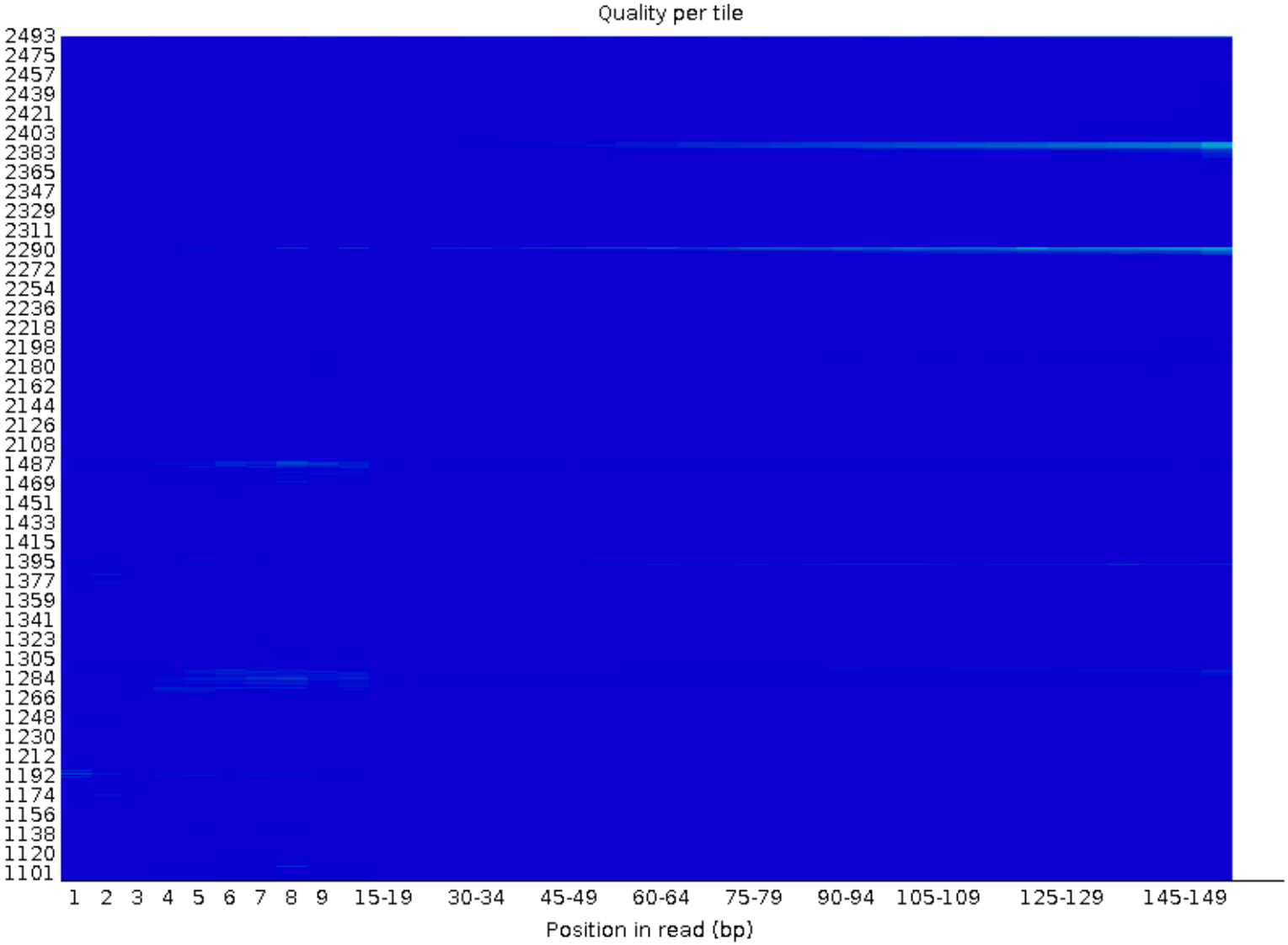
Measure	Value
Filename	M4_S4_L001_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	118155020

Measure	Value
Sequences flagged as poor quality	0
Sequence length	151
%GC	22

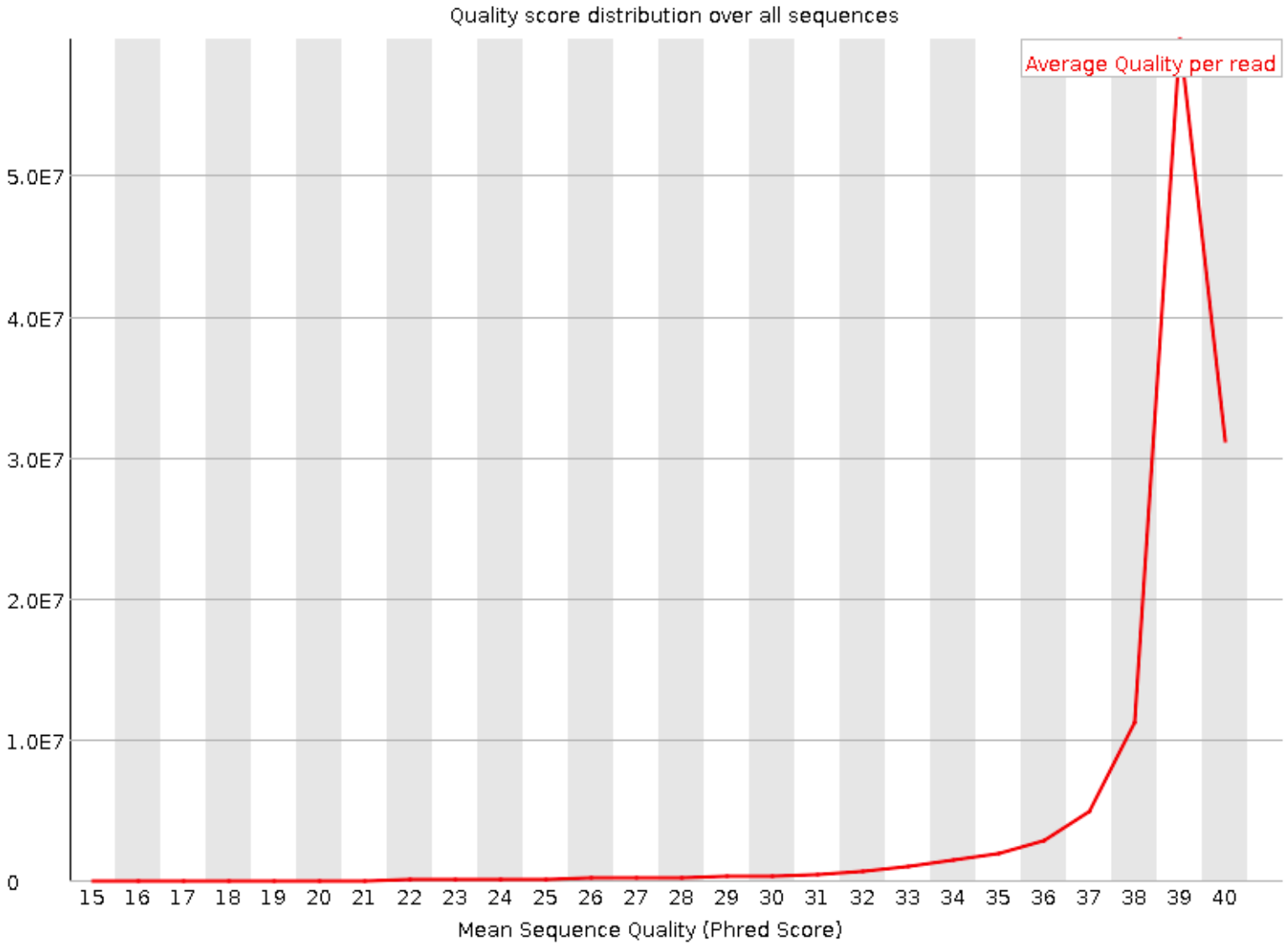
Per base sequence quality



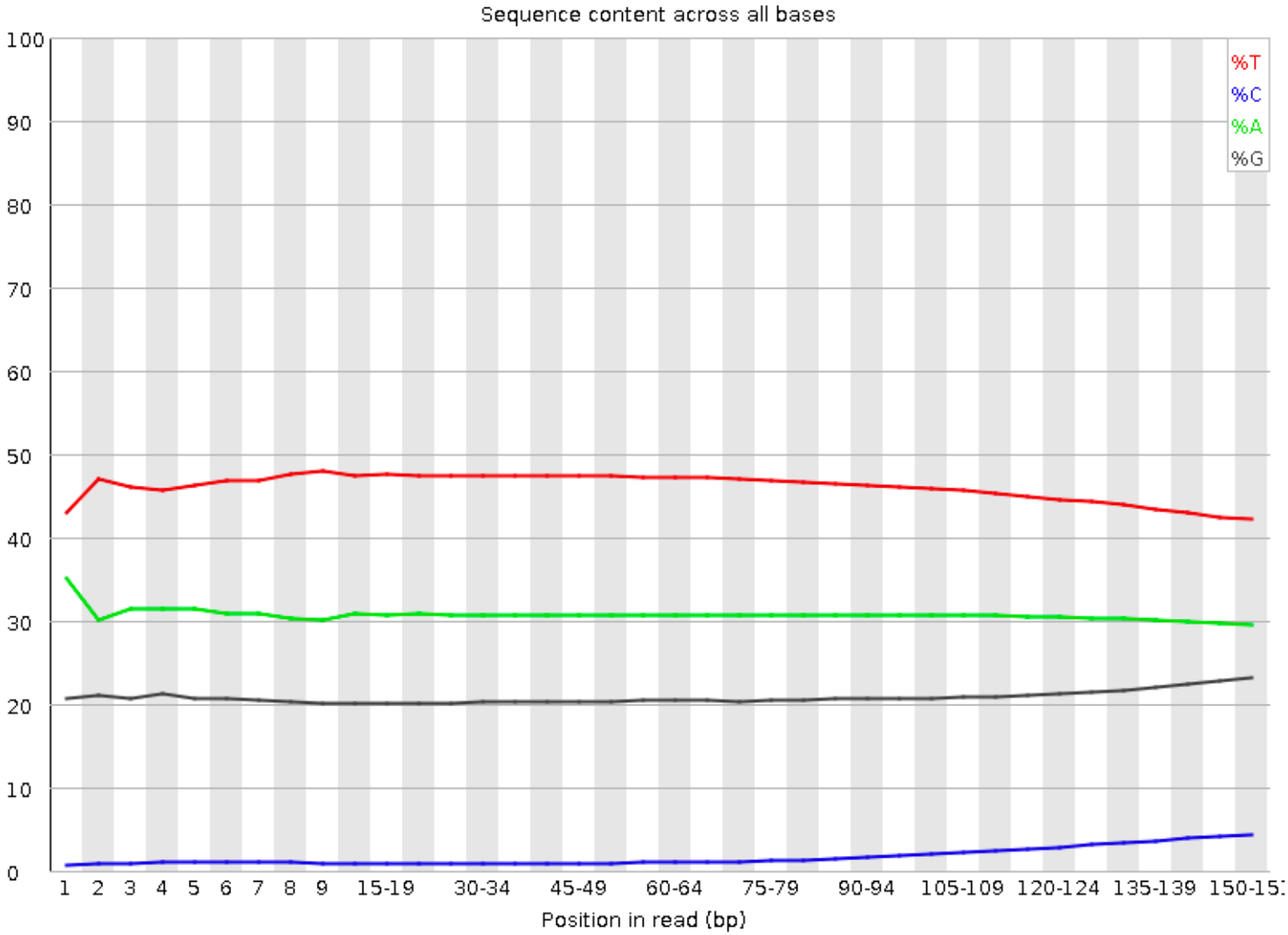
Per tile sequence quality



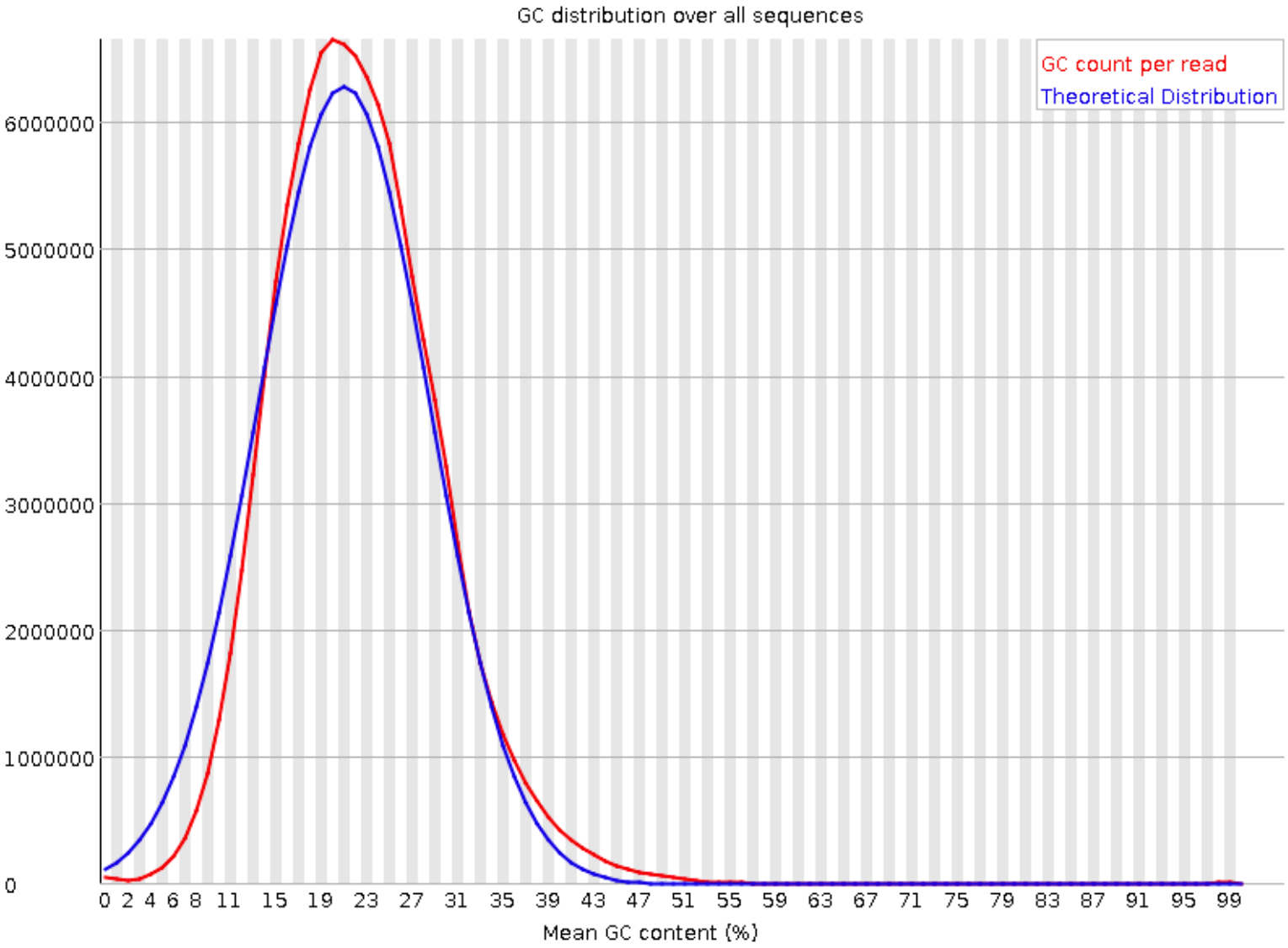
Per sequence quality scores



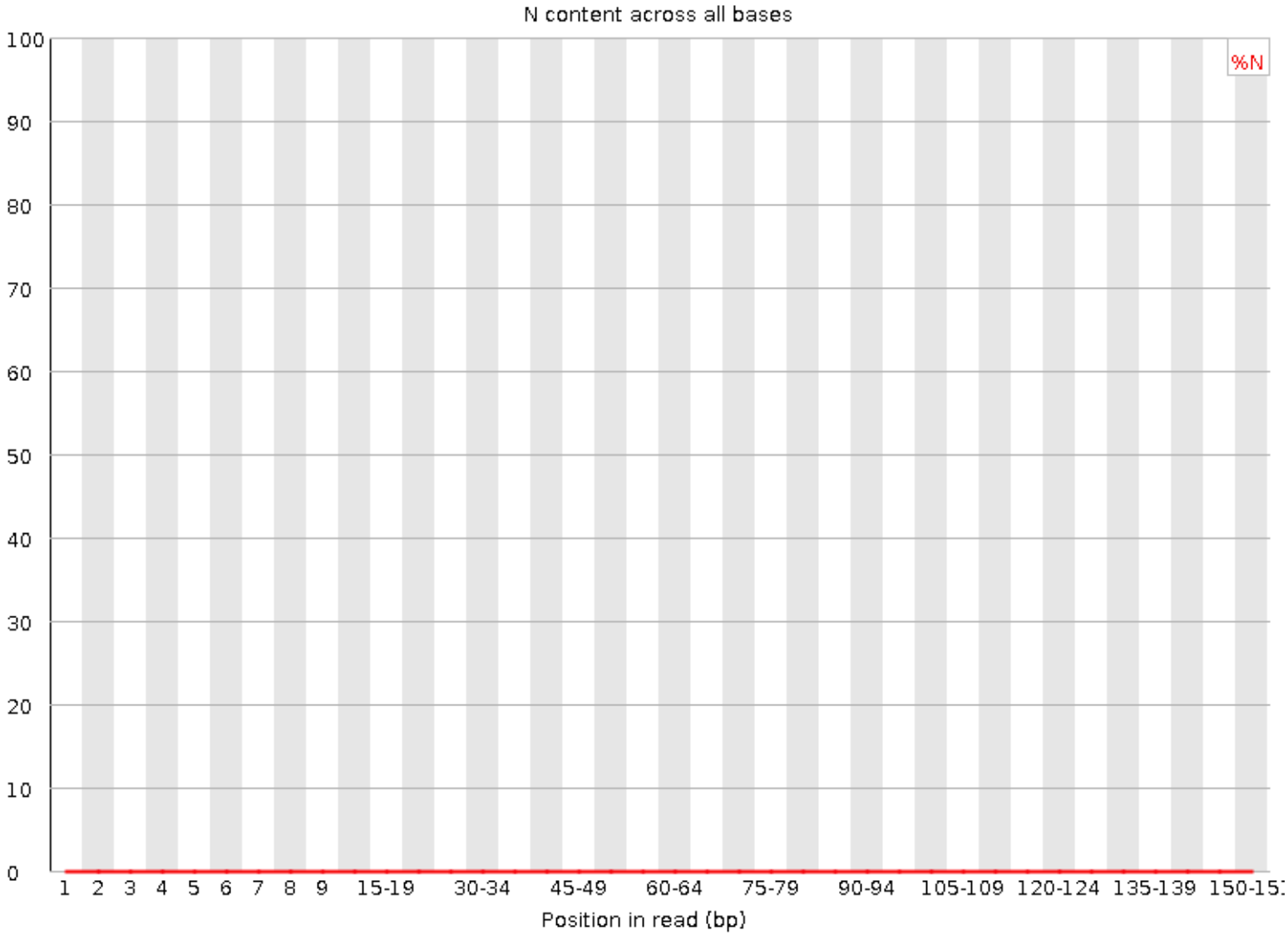
Per base sequence content



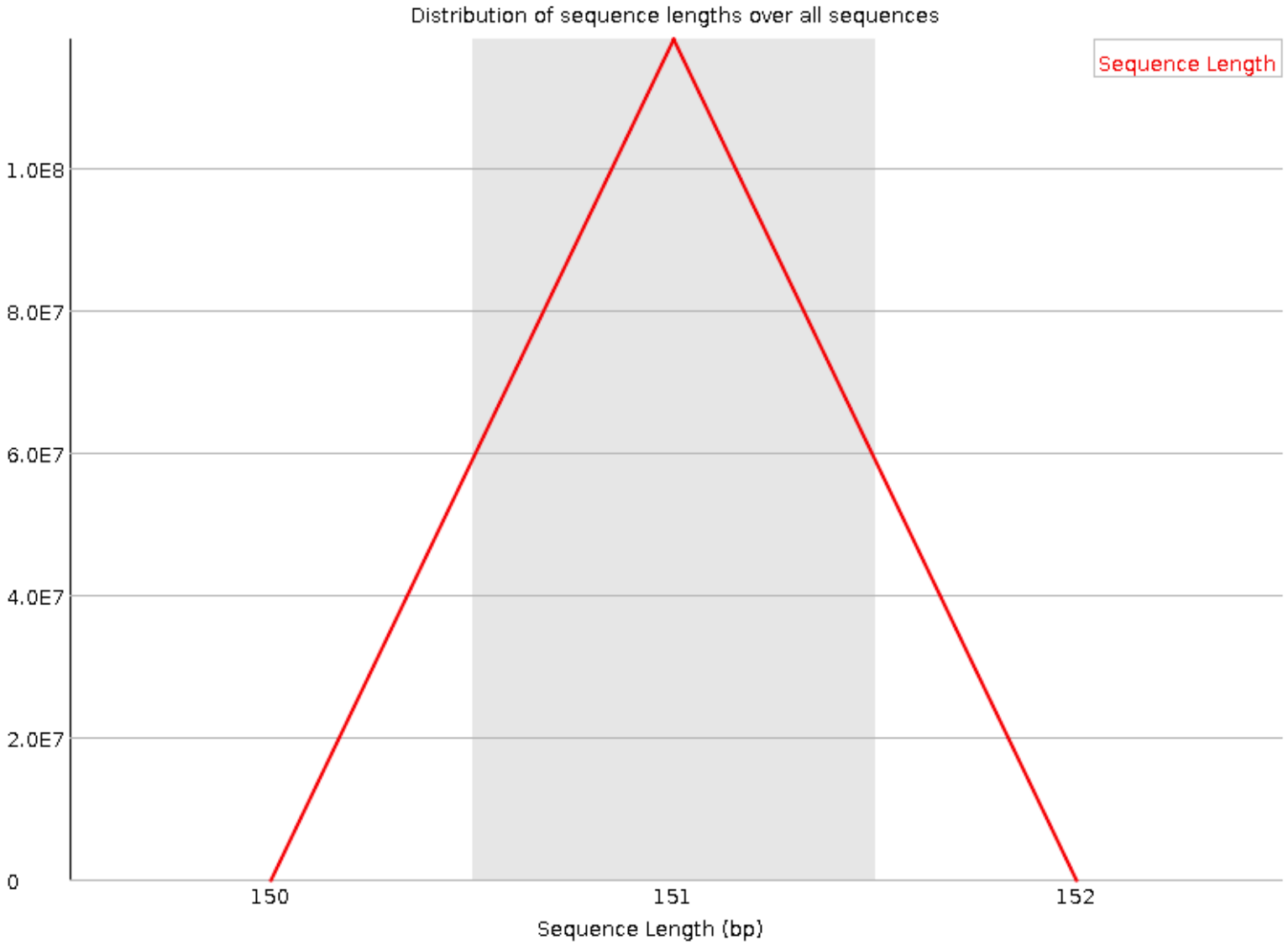
Per sequence GC content



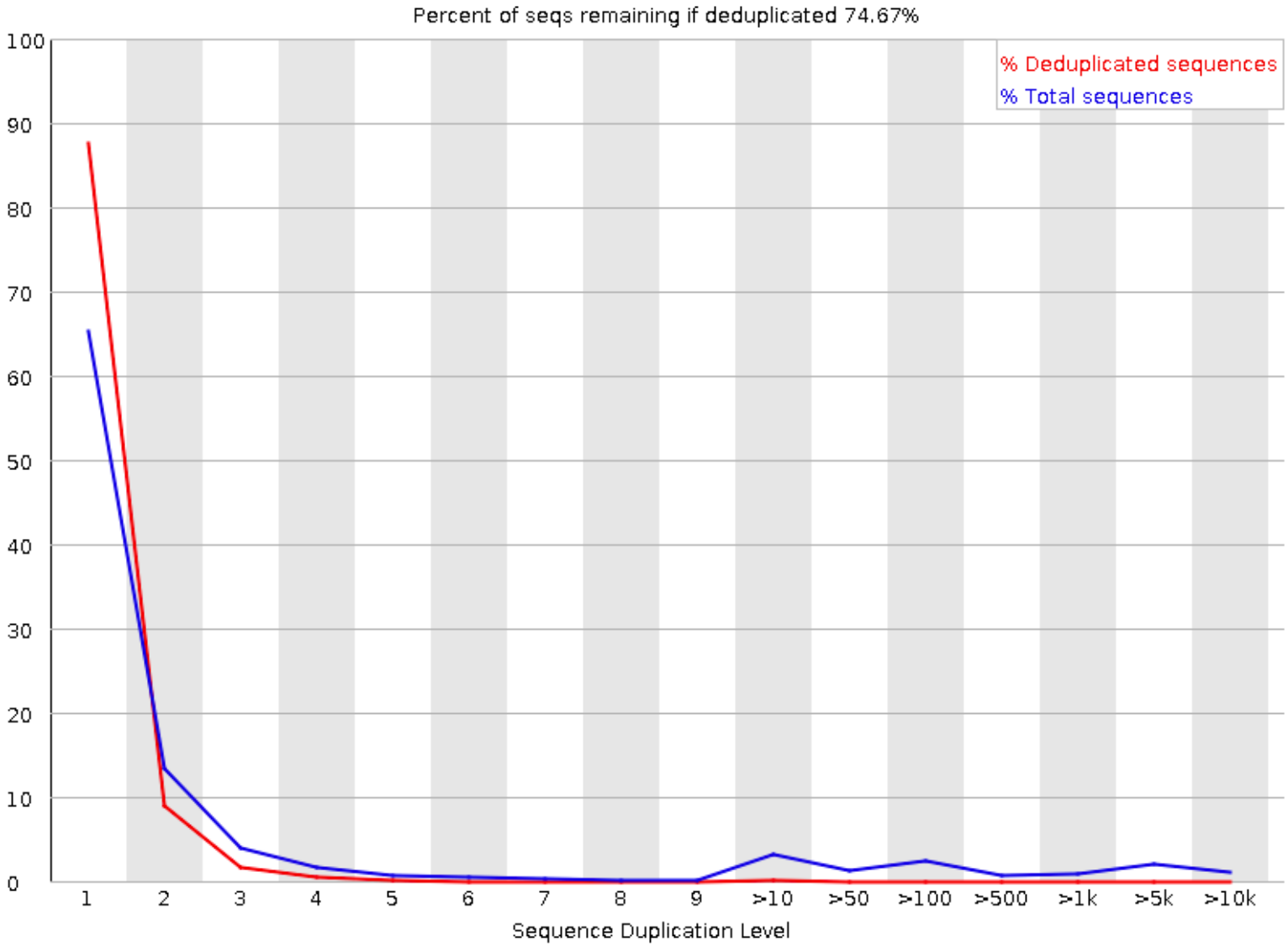
Per base N content



Sequence Length Distribution



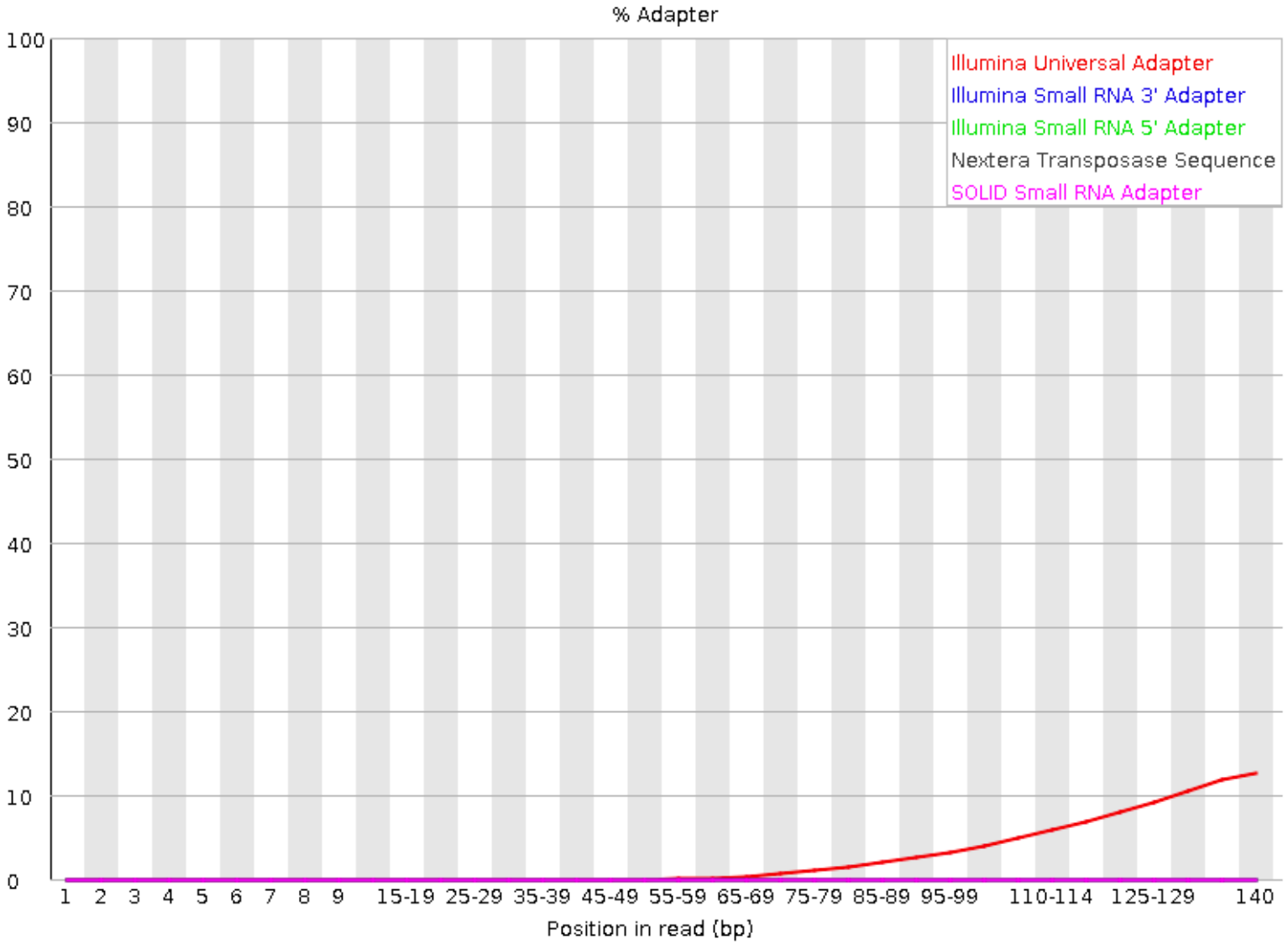
Sequence Duplication Levels


Percent of seqs remaining if deduplicated 74.67%
% Deduplicated sequences
% Total sequences
100
90
80
70
60
50
40
30
20
10
0
1
2
3
4
5
6
7
8
9
>10
>50
>100
>500
>1k
>5k
>10k
Sequence Duplication Level

Overrepresented sequences

No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.11.7)