FastQC Report

Thu 16 May 2024
M5_S5_L002_R1_001.fastq.gz

Summary

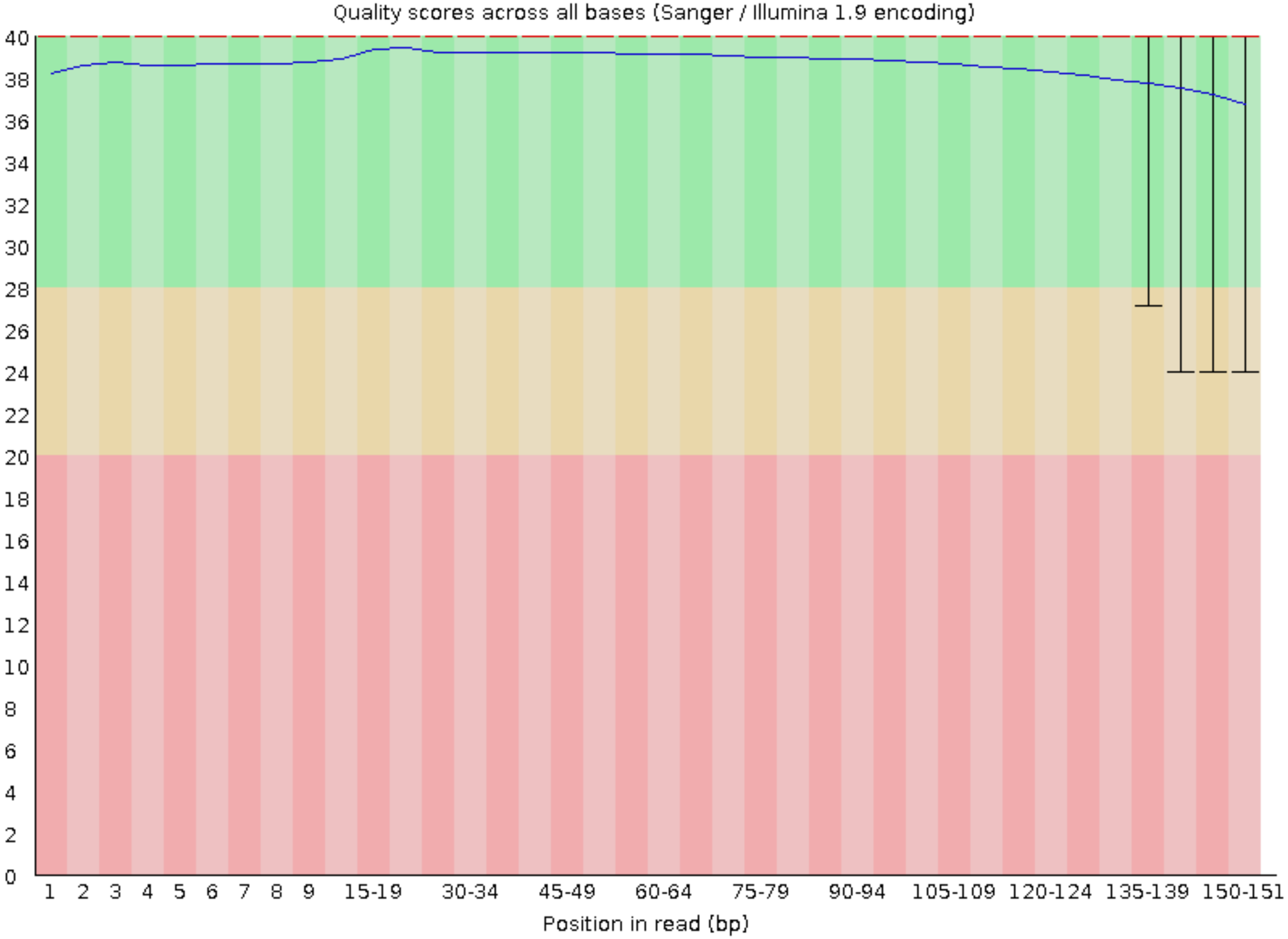
- ✓ Basic Statistics
- ✓ Per base sequence quality
- ✗ Per tile sequence quality
- ✓ Per sequence quality scores
- ✗ Per base sequence content
- ✓ Per sequence GC content
- ✓ Per base N content
- ✓ Sequence Length Distribution
- ✓ Sequence Duplication Levels
- ✓ Overrepresented sequences
- ✗ Adapter Content

✓ Basic Statistics

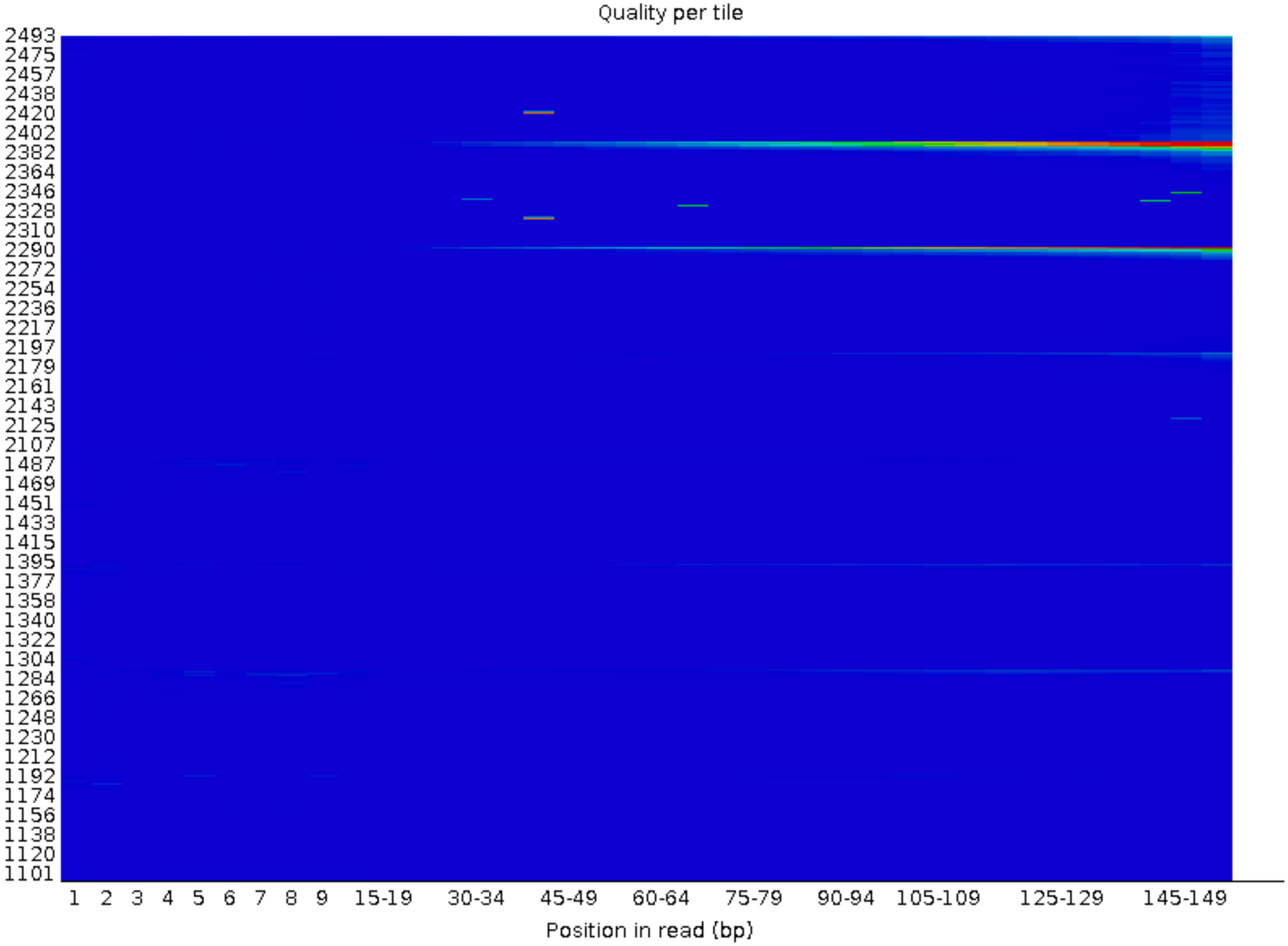
Measure	Value
Filename	M5_S5_L002_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	103949860

Measure	Value
Sequences flagged as poor quality	0
Sequence length	151
%GC	23

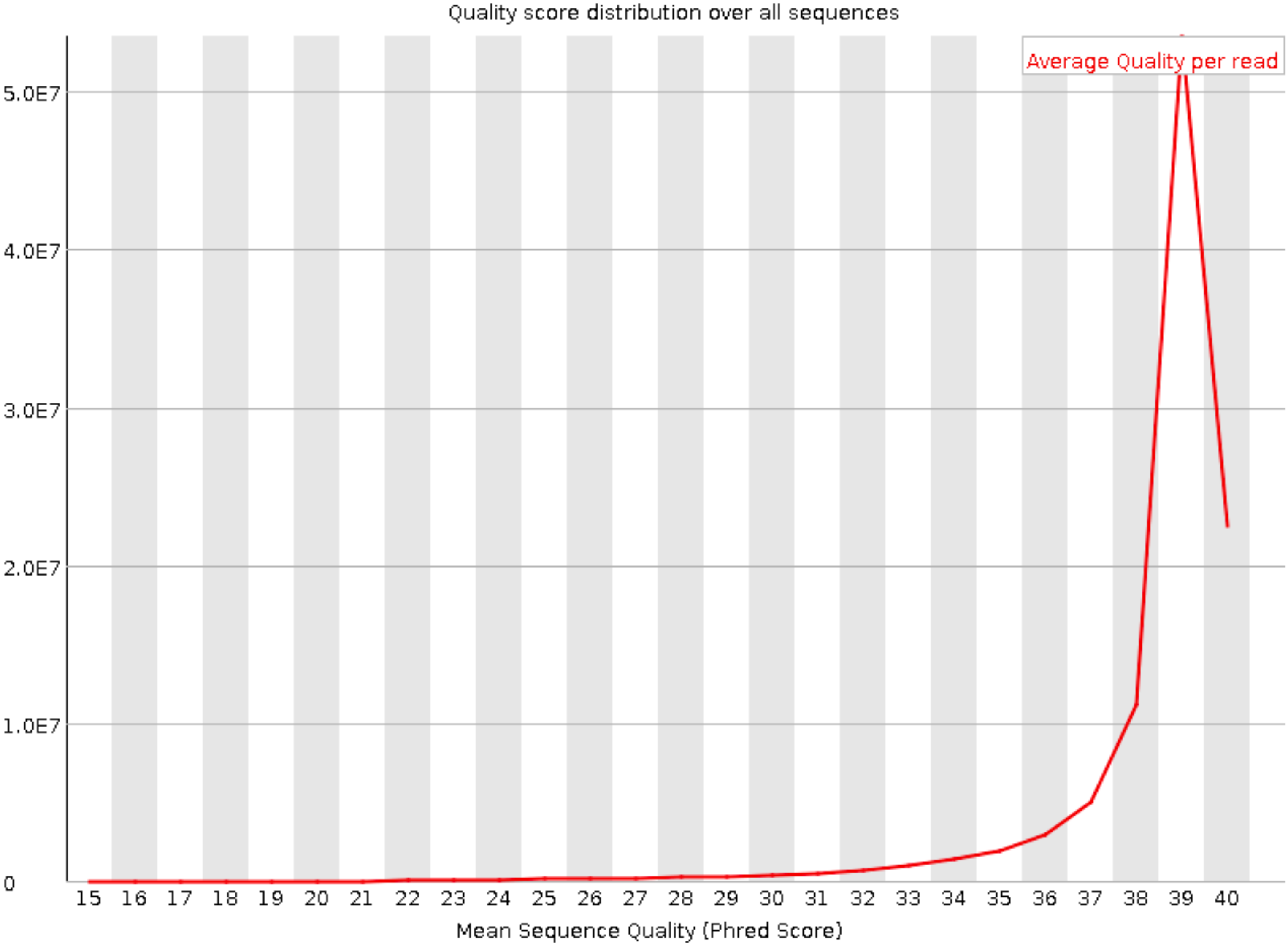
✓ Per base sequence quality



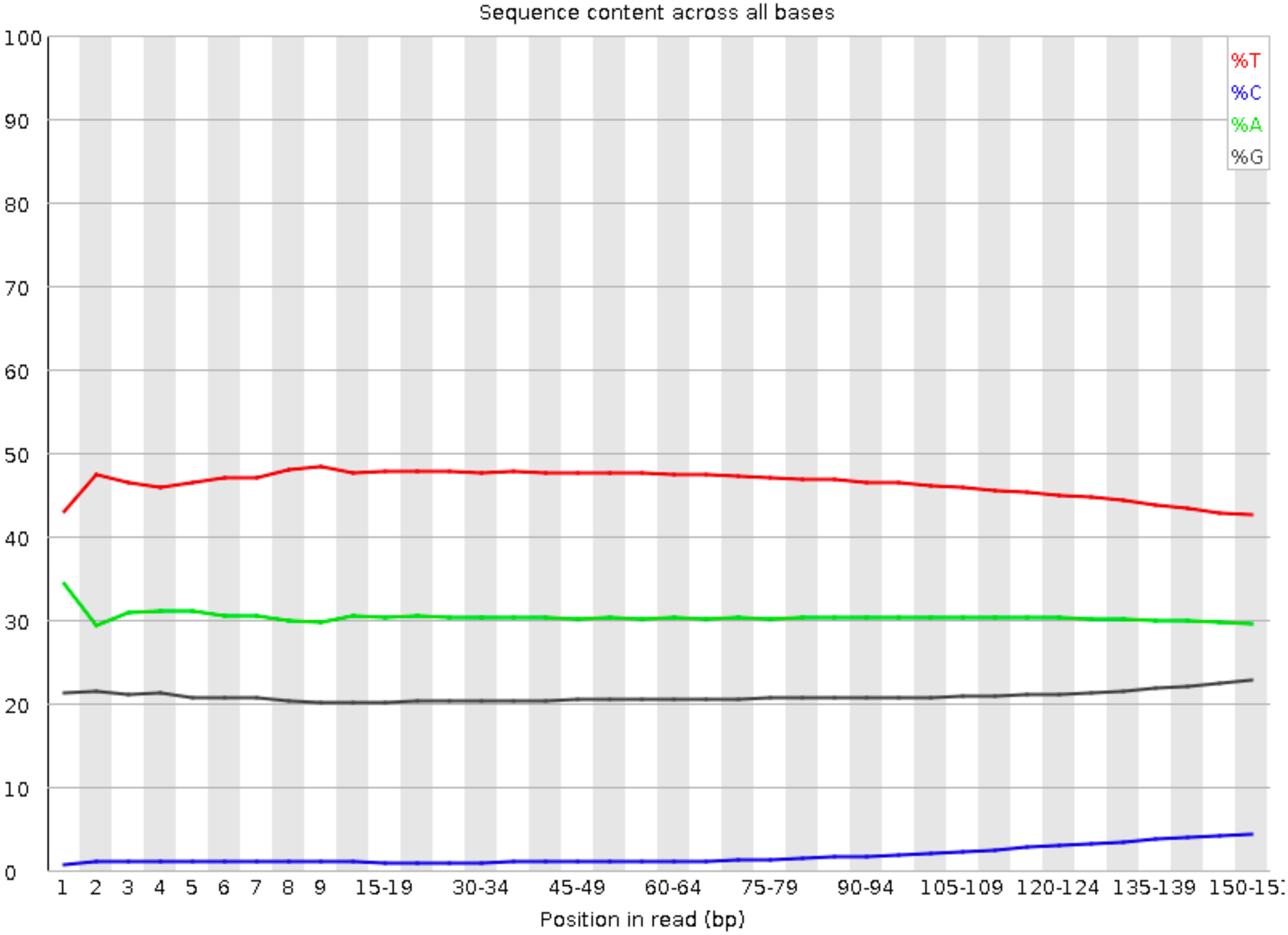
✖ Per tile sequence quality



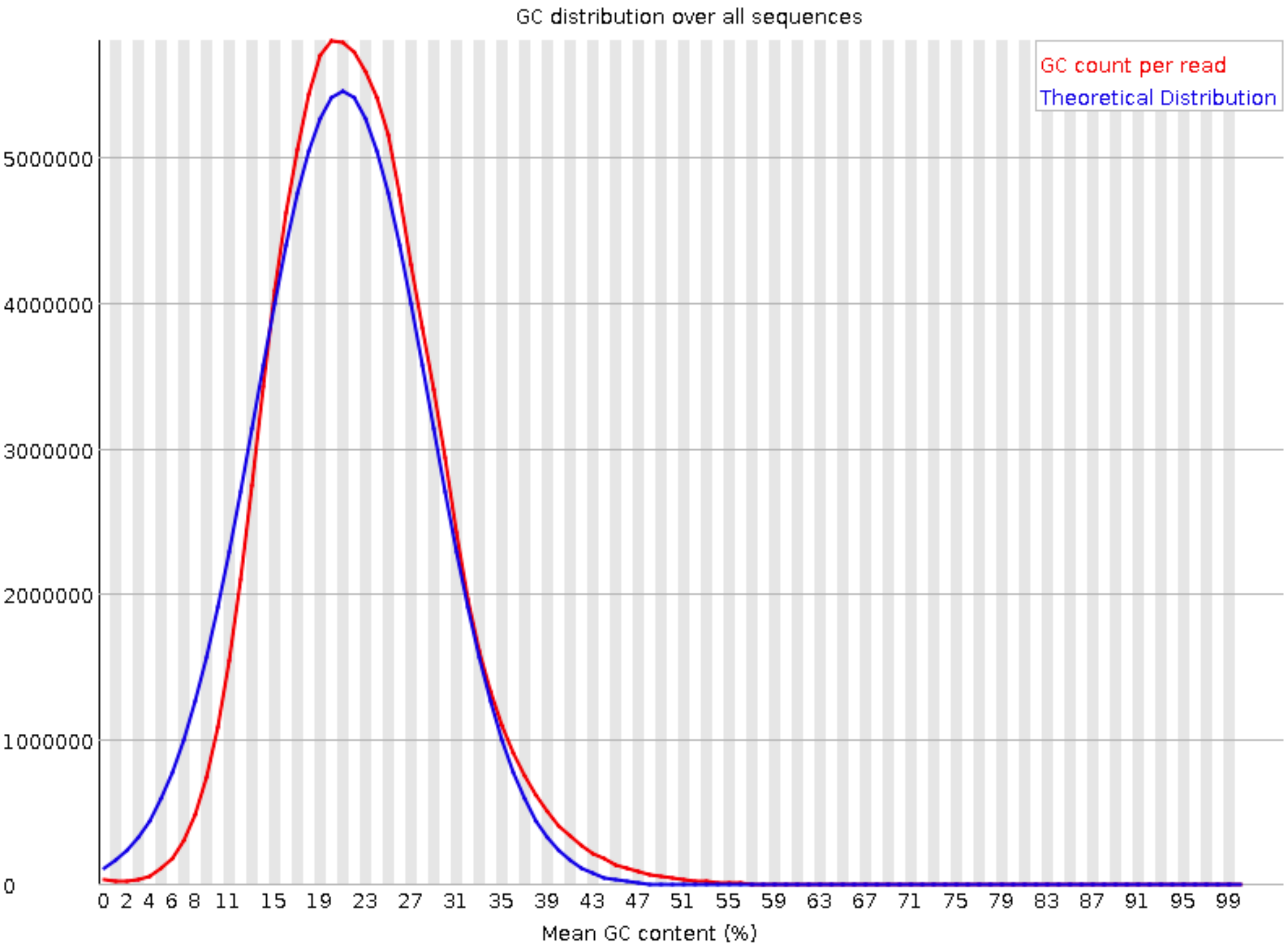
✓ Per sequence quality scores



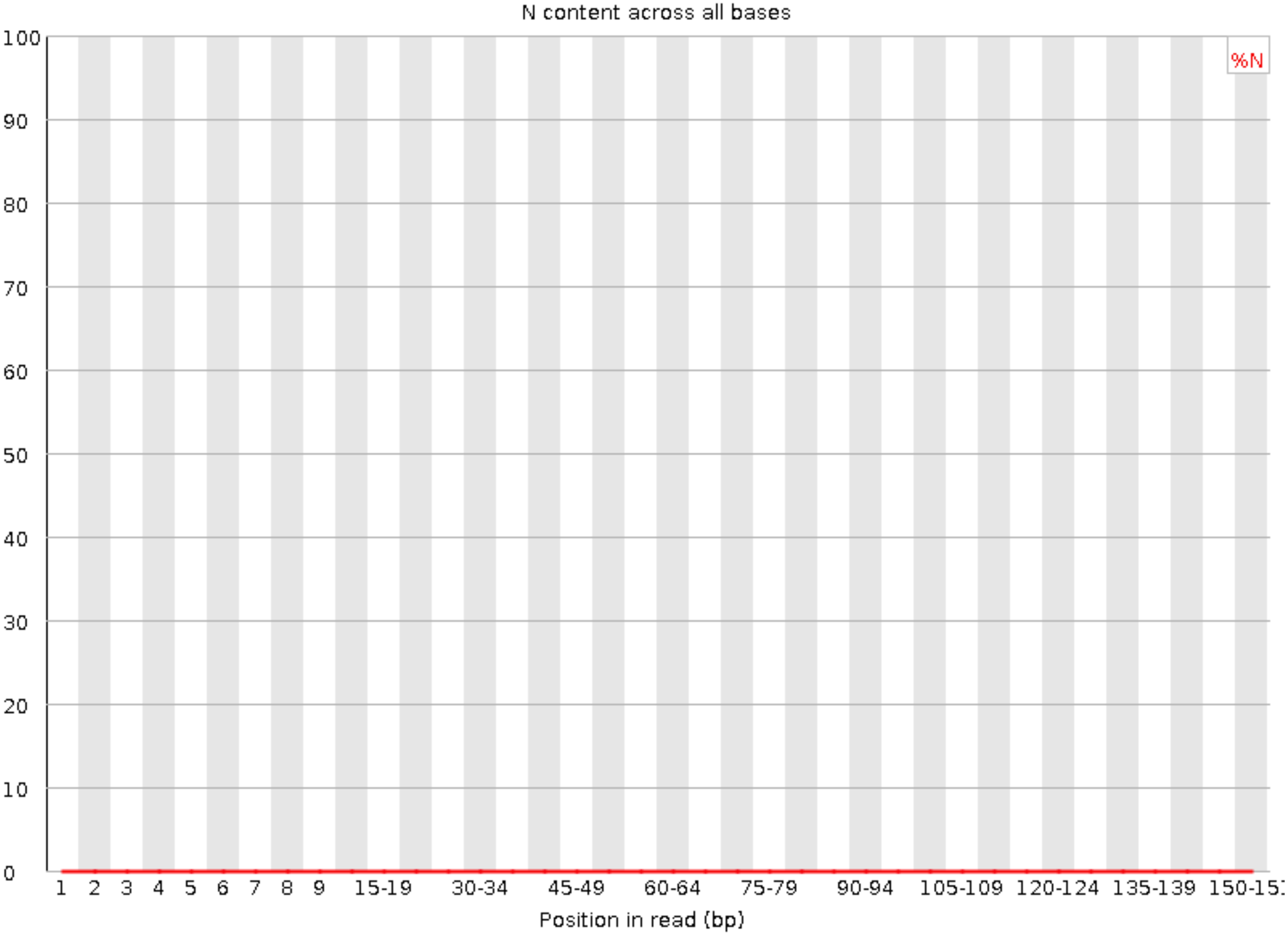
❌ Per base sequence content



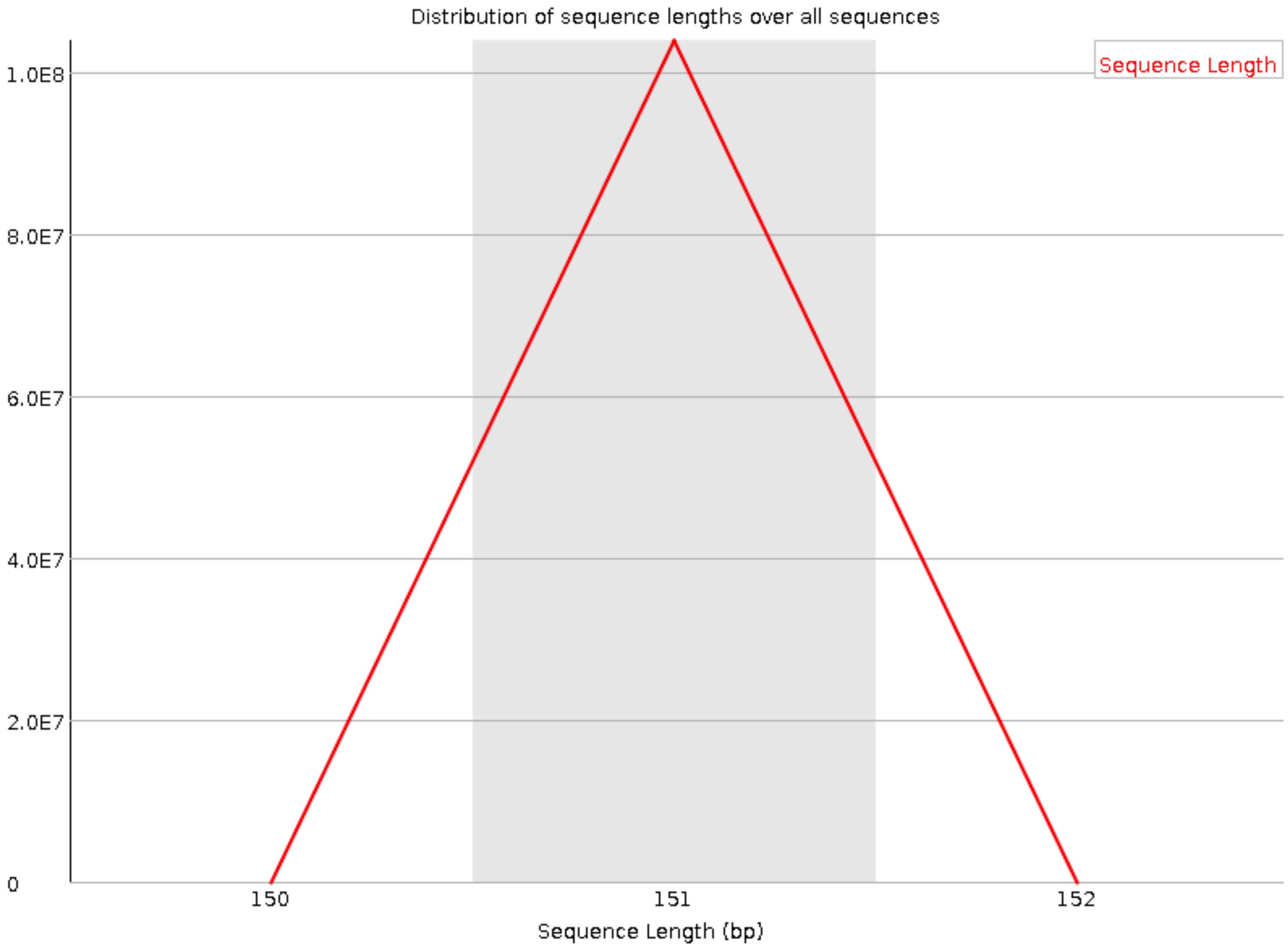
✓ Per sequence GC content



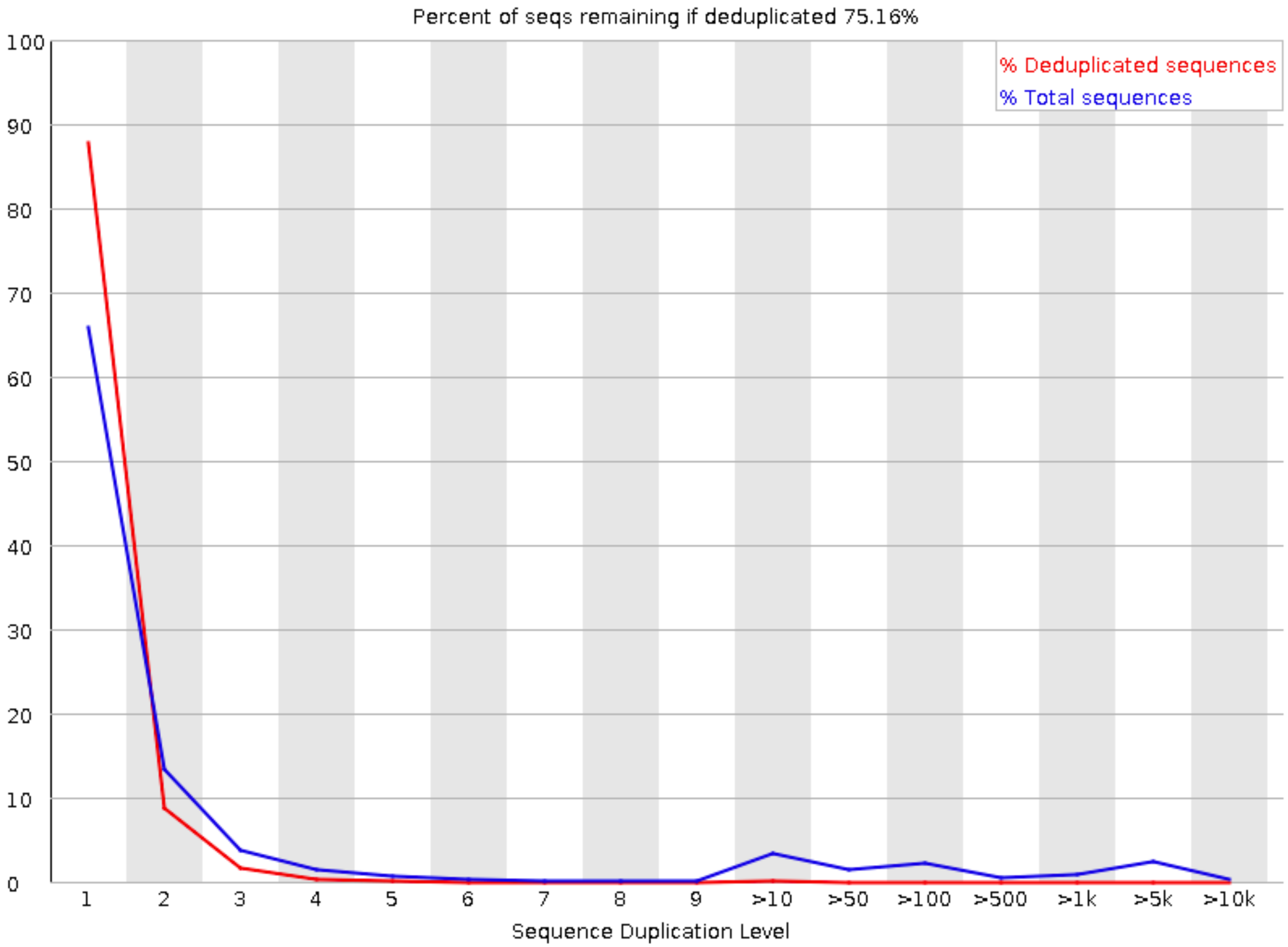
✓ Per base N content



✓ Sequence Length Distribution



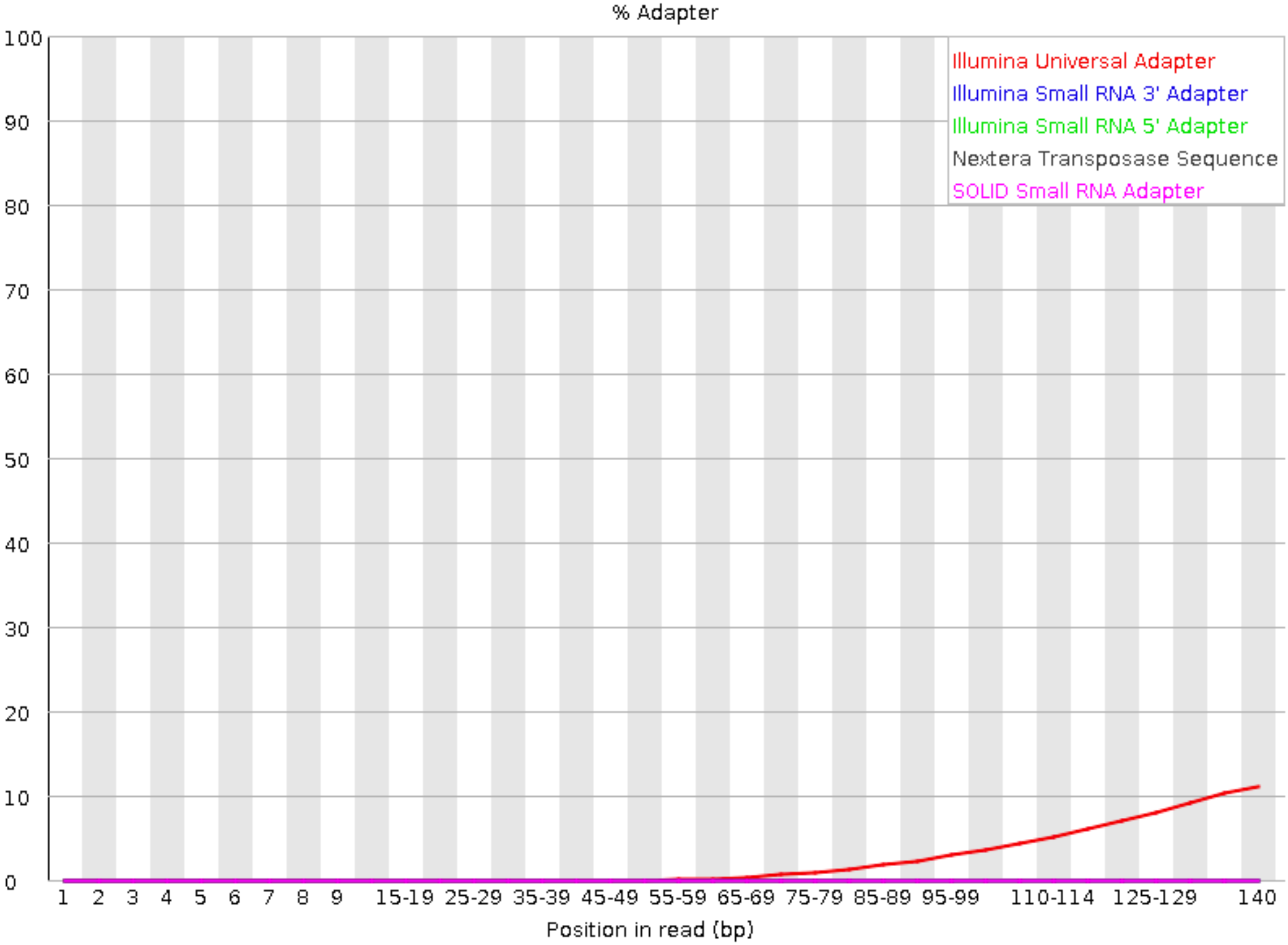
✓ Sequence Duplication Levels


Percent of seqs remaining if deduplicated 75.16%
% 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)