












FastQC Report

Summary

Thu 16 May 2024
M3_S3_L001_R1_001.fastq.gz

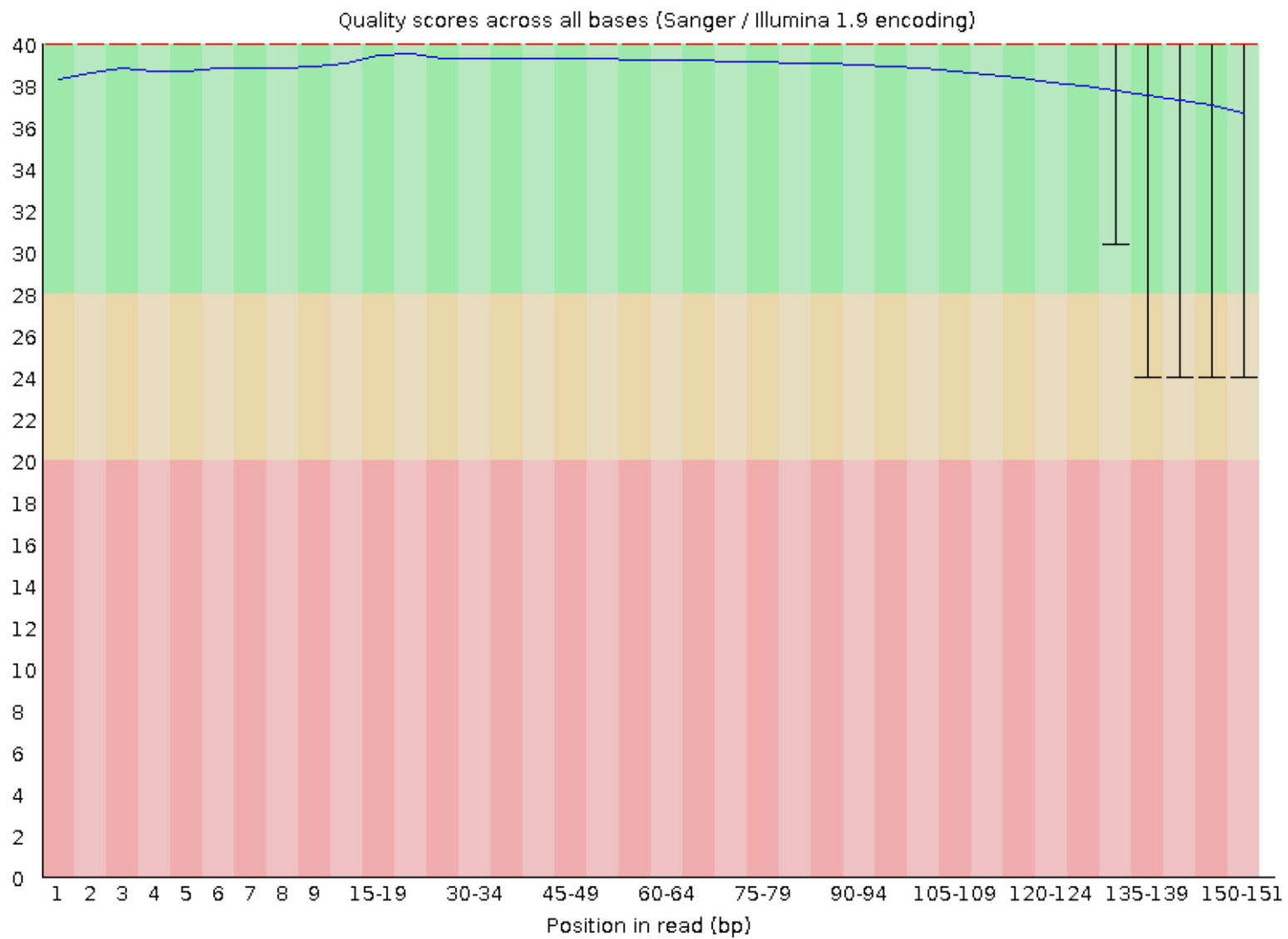
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-  [Per base sequence content](#)
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Basic Statistics

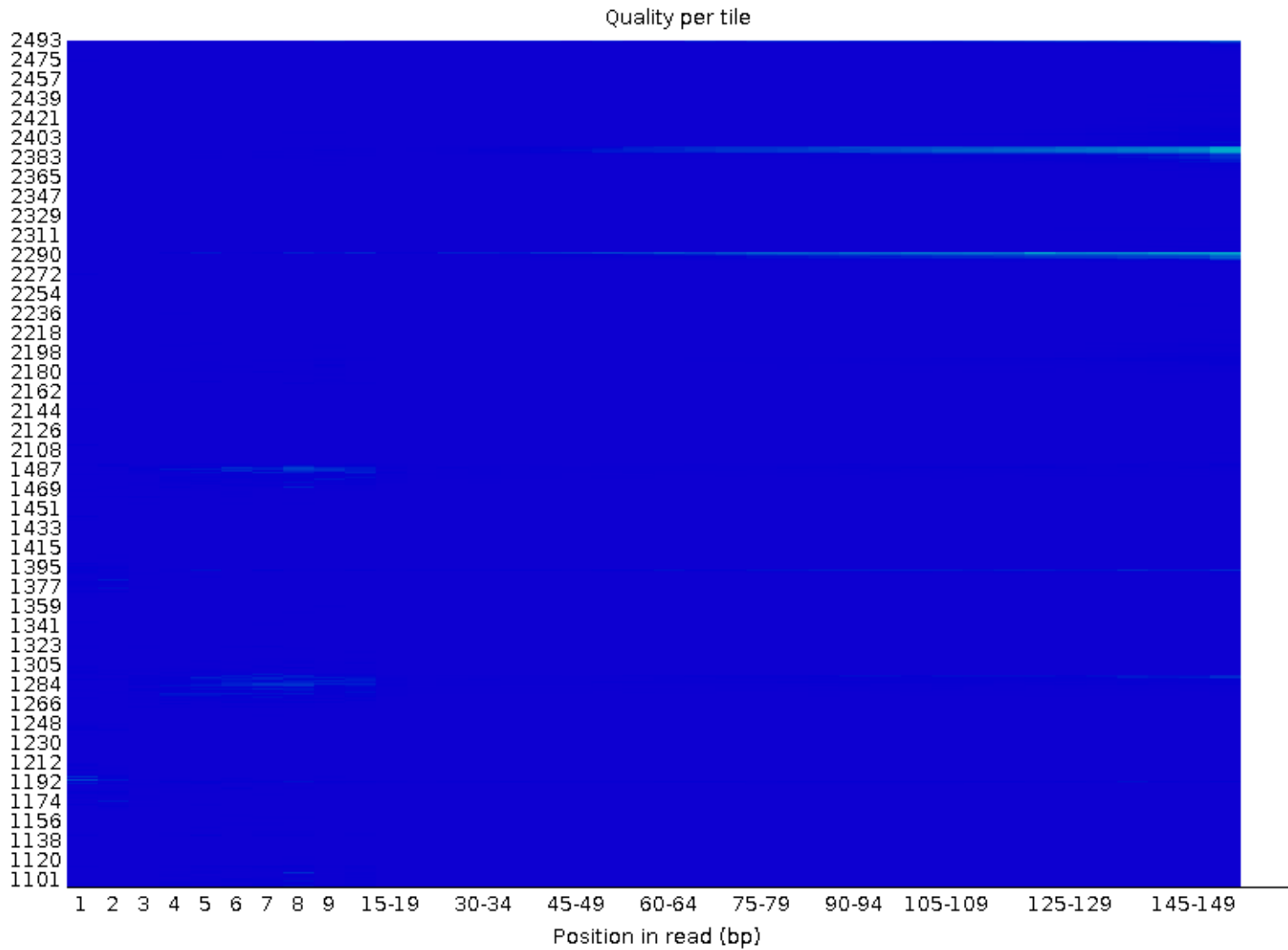
Measure	Value
Filename	M3_S3_L001_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	142846739

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

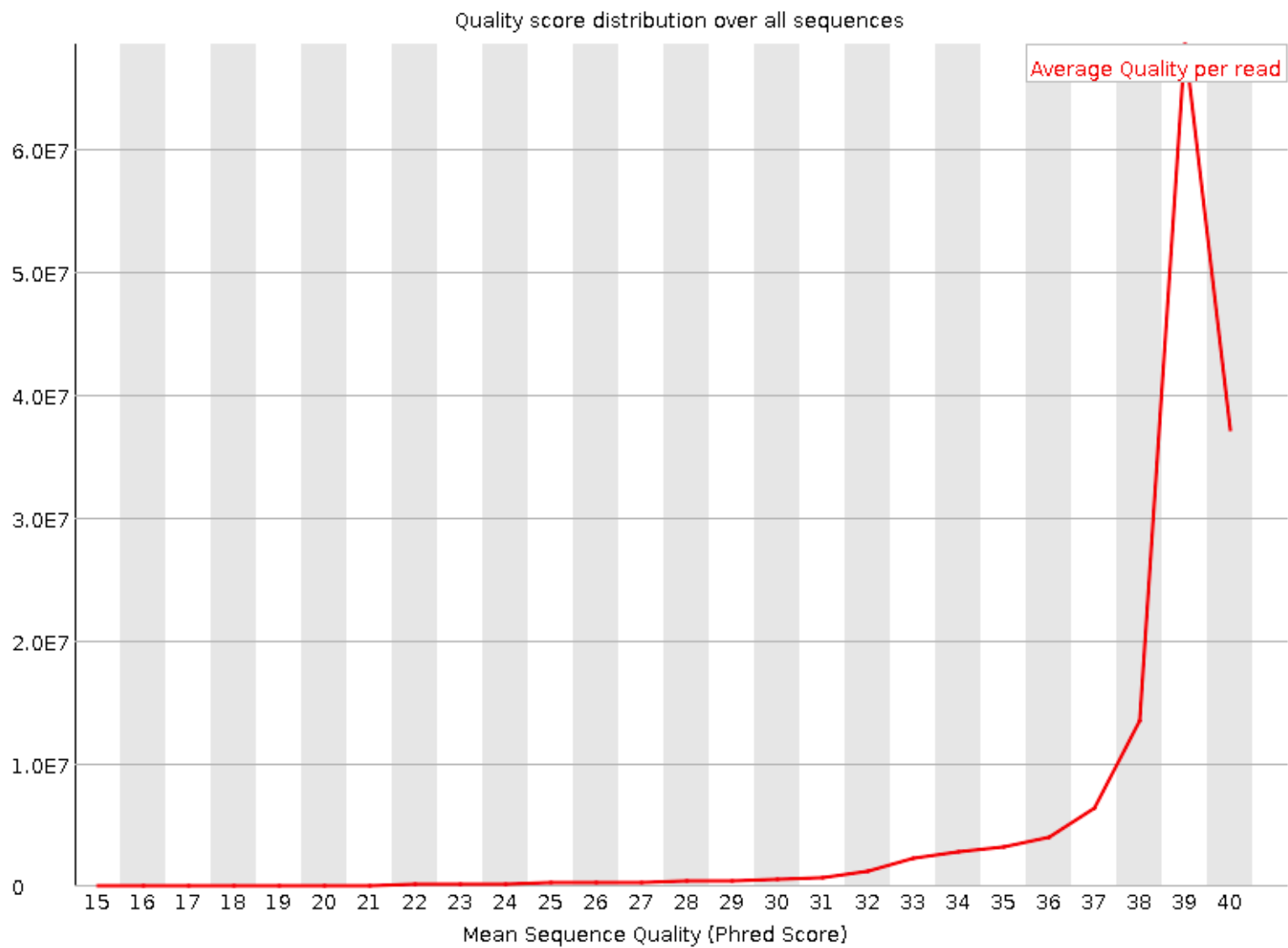
Per base sequence quality



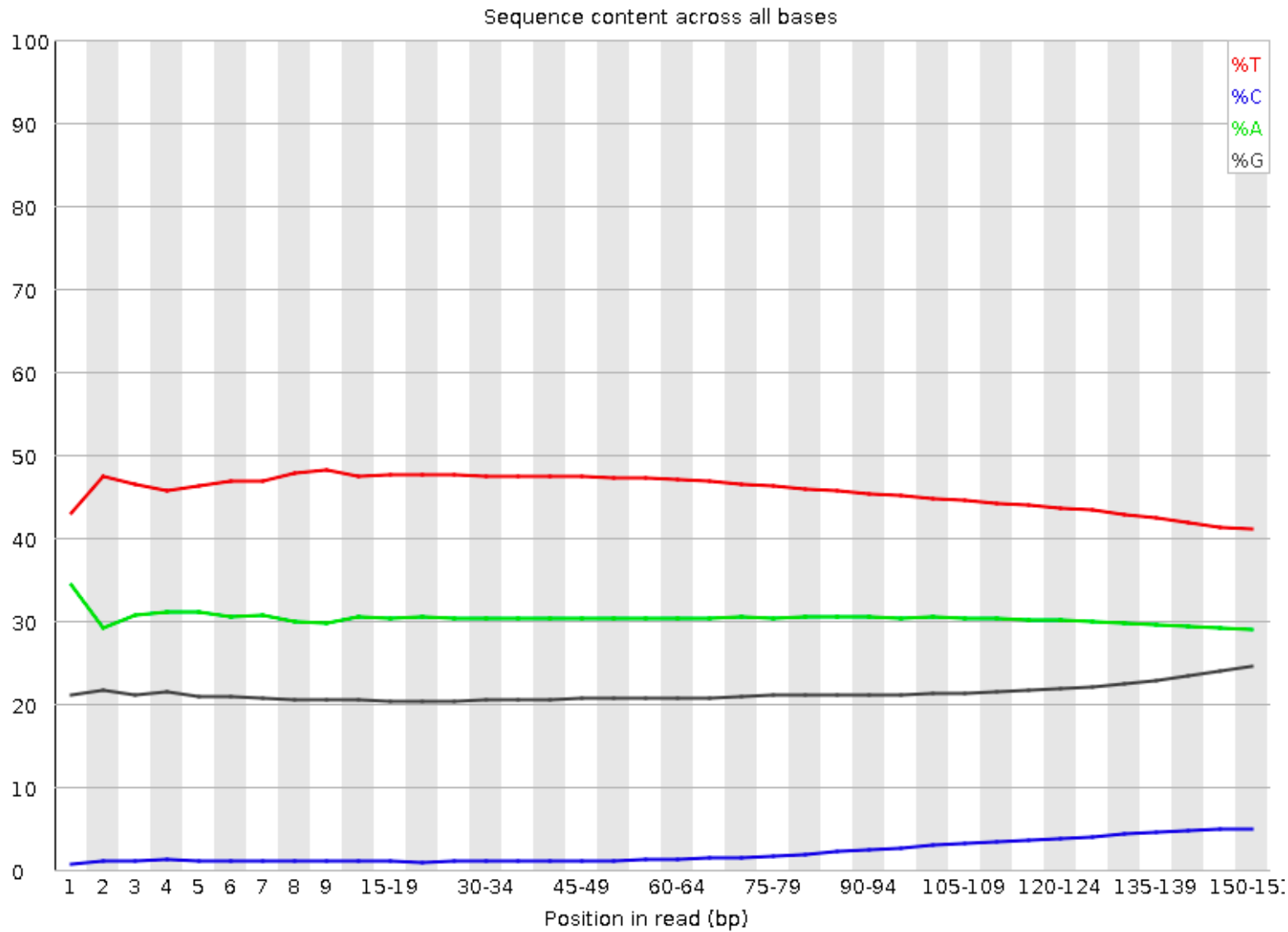
Per tile sequence quality



Per sequence quality scores

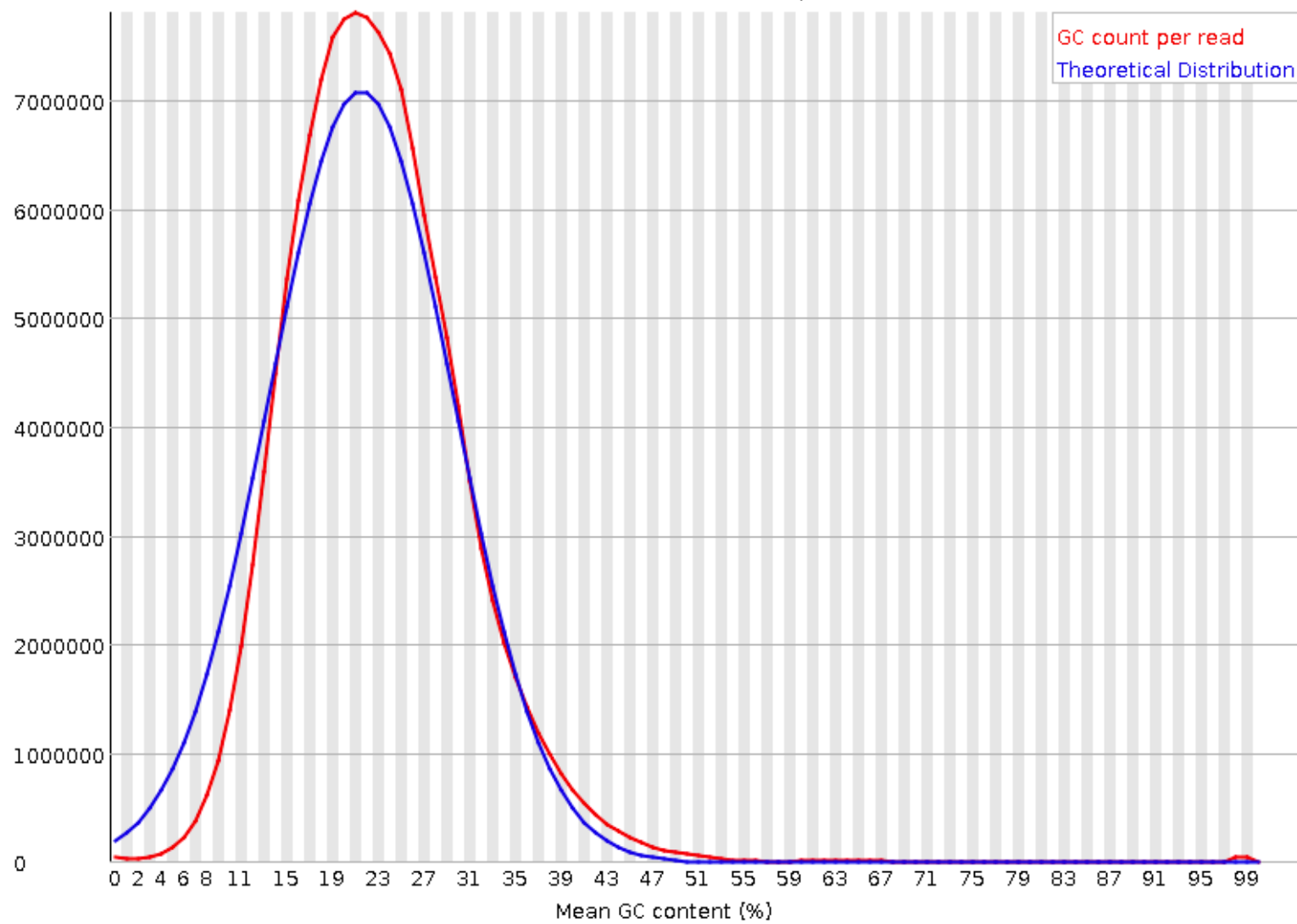


✖ Per base sequence content

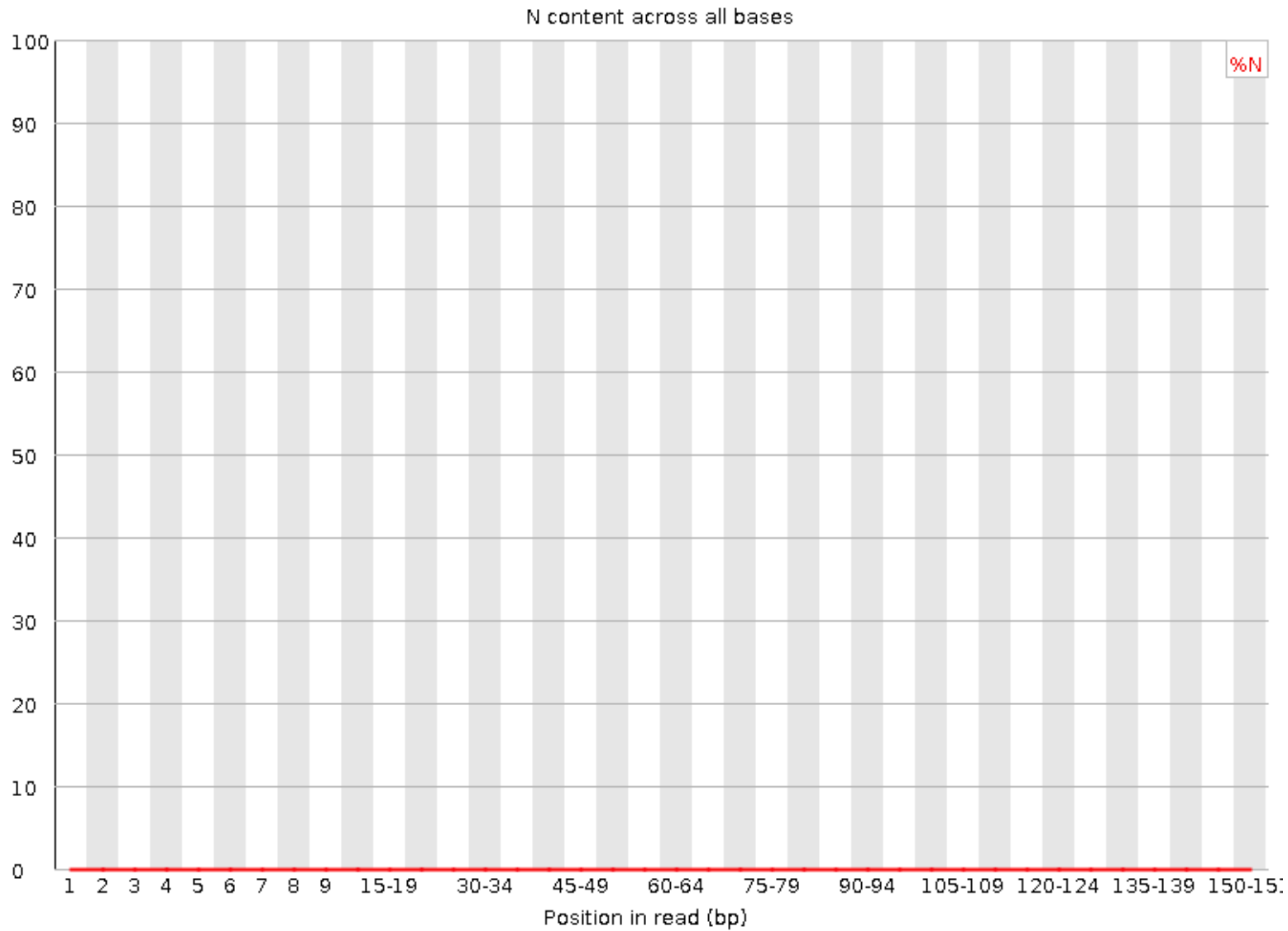


Per sequence GC content

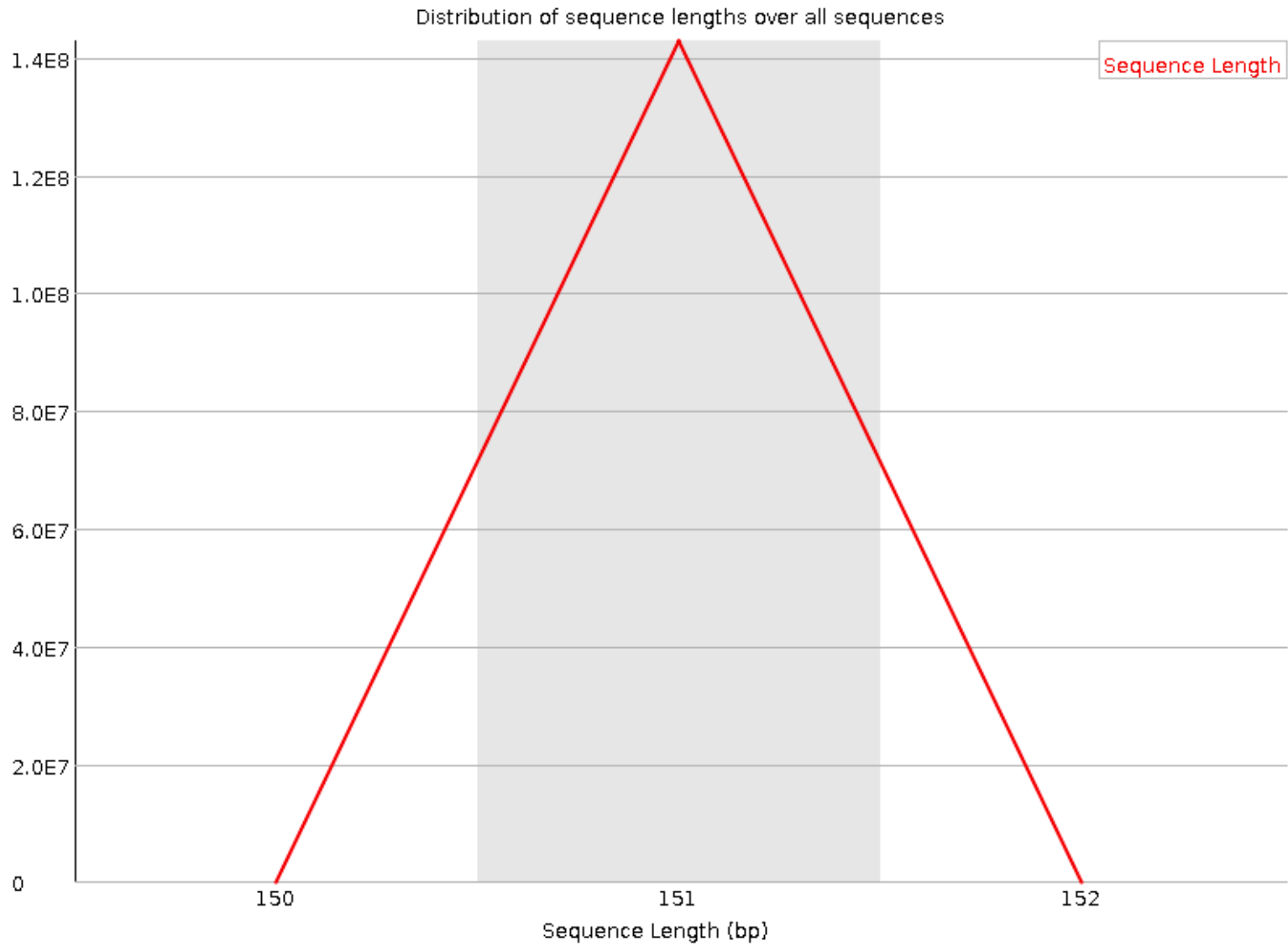
GC distribution over all sequences



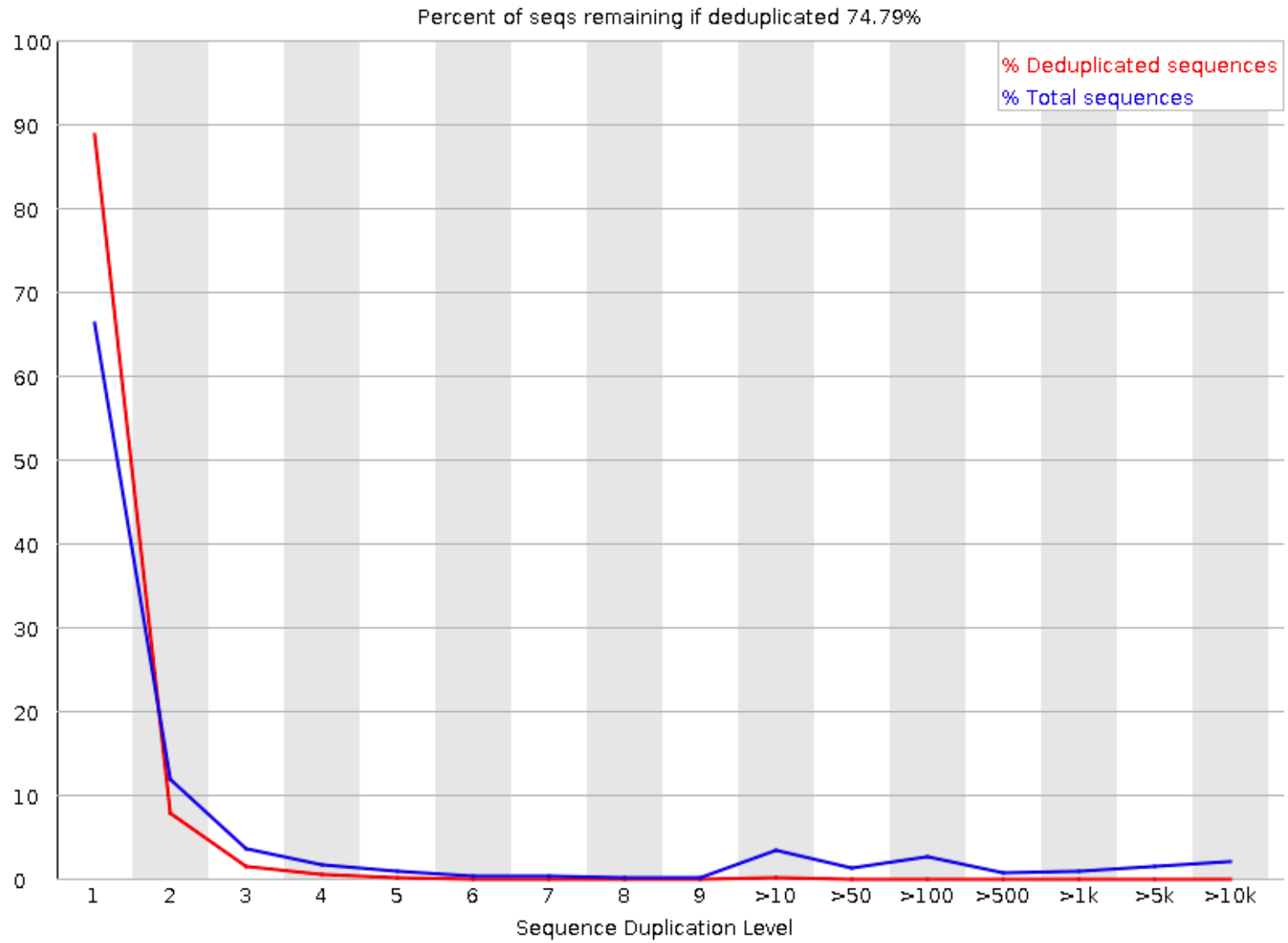
Per base N content



Sequence Length Distribution

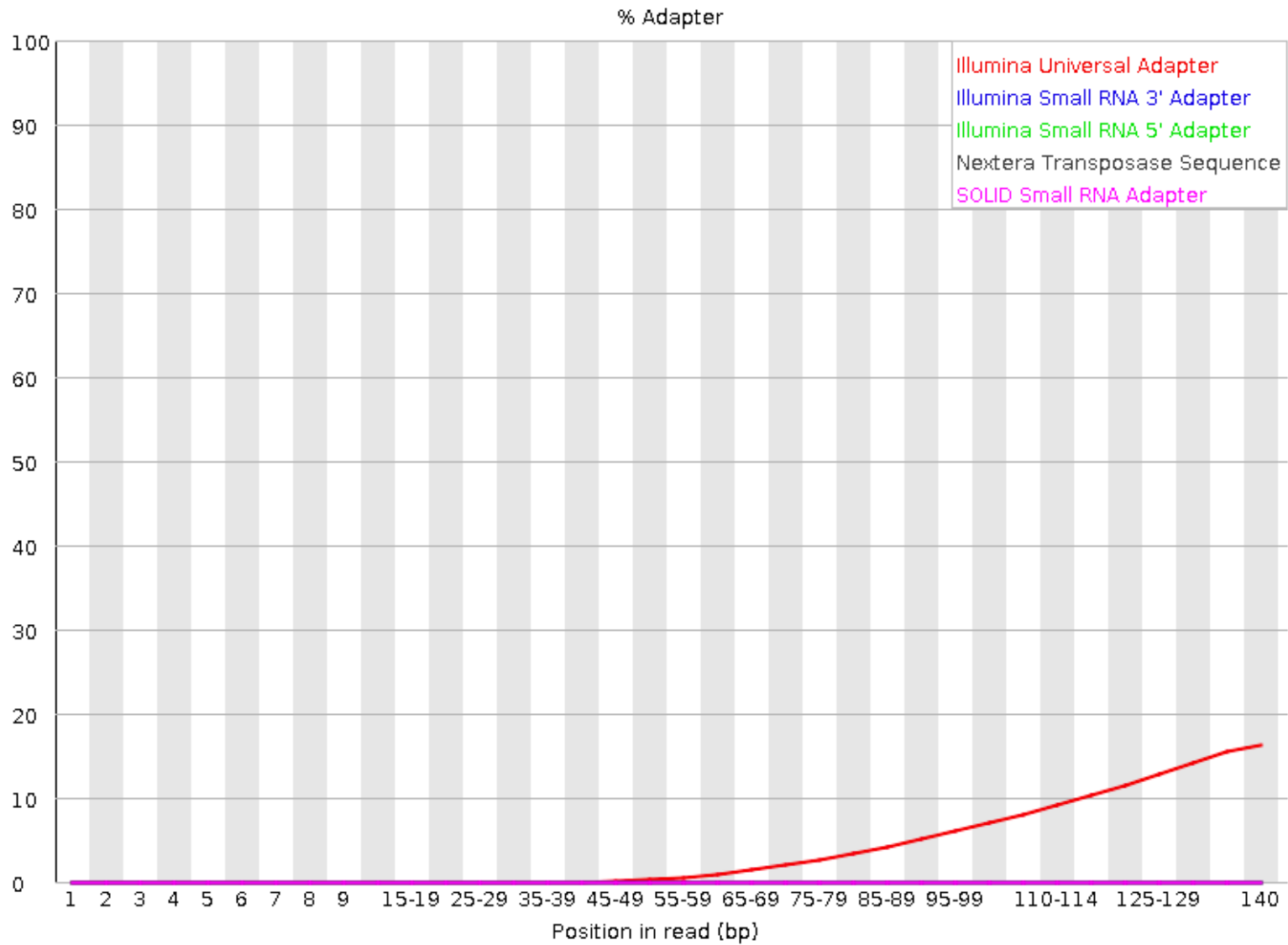


Sequence Duplication Levels



 **Overrepresented sequences**
No overrepresented sequences

 **Adapter Content**



Produced by [FastQC](#) (version 0.11.7)