











# FastQC Report

## Summary

Fri 1 Nov 2024  
SRR14866425\_low1\_1.fastq

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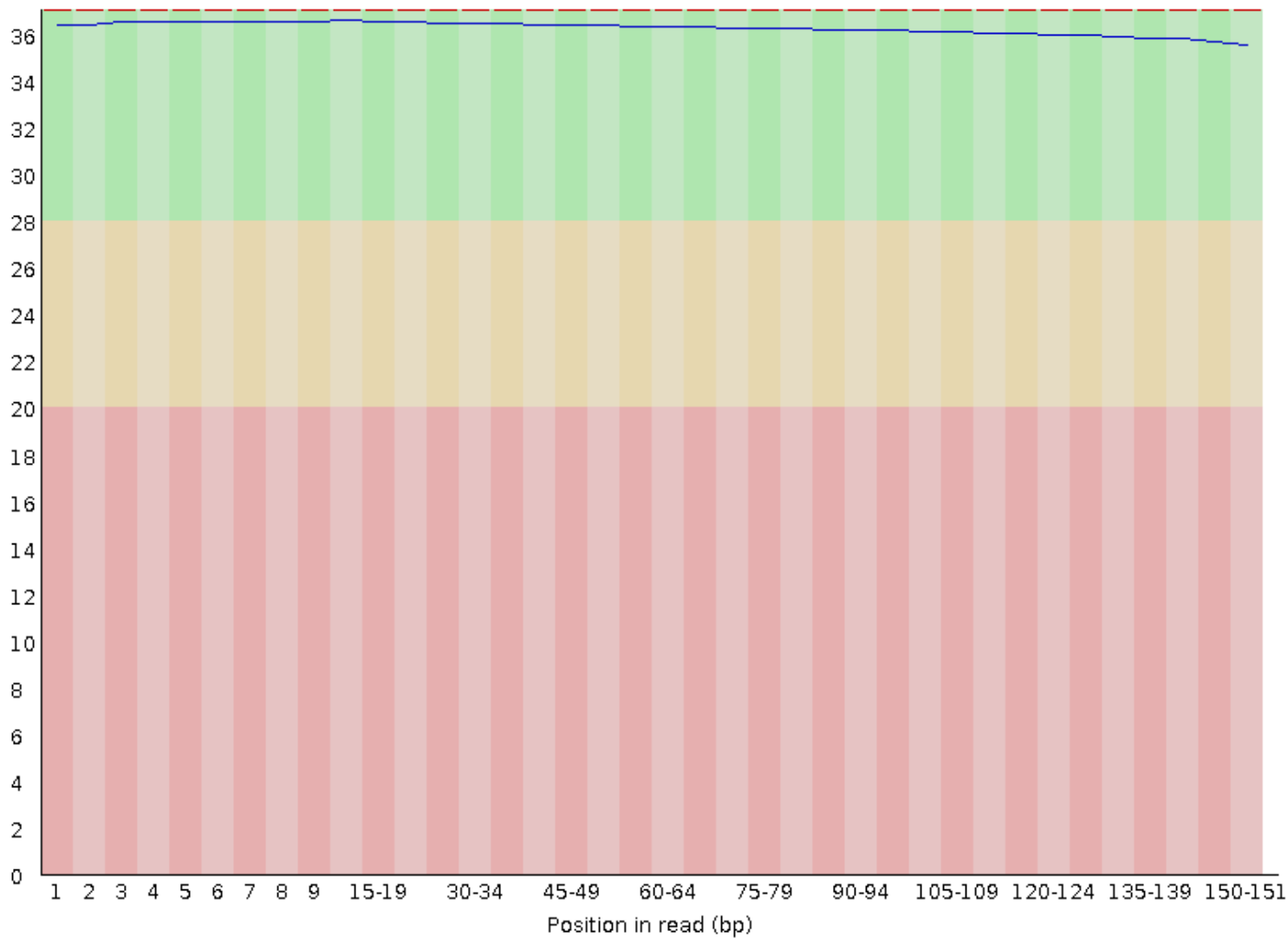
## Basic Statistics

Measure	Value
Filename	SRR14866425_low1_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23240071
Sequences flagged as poor quality	0
Sequence length	151
%GC	51



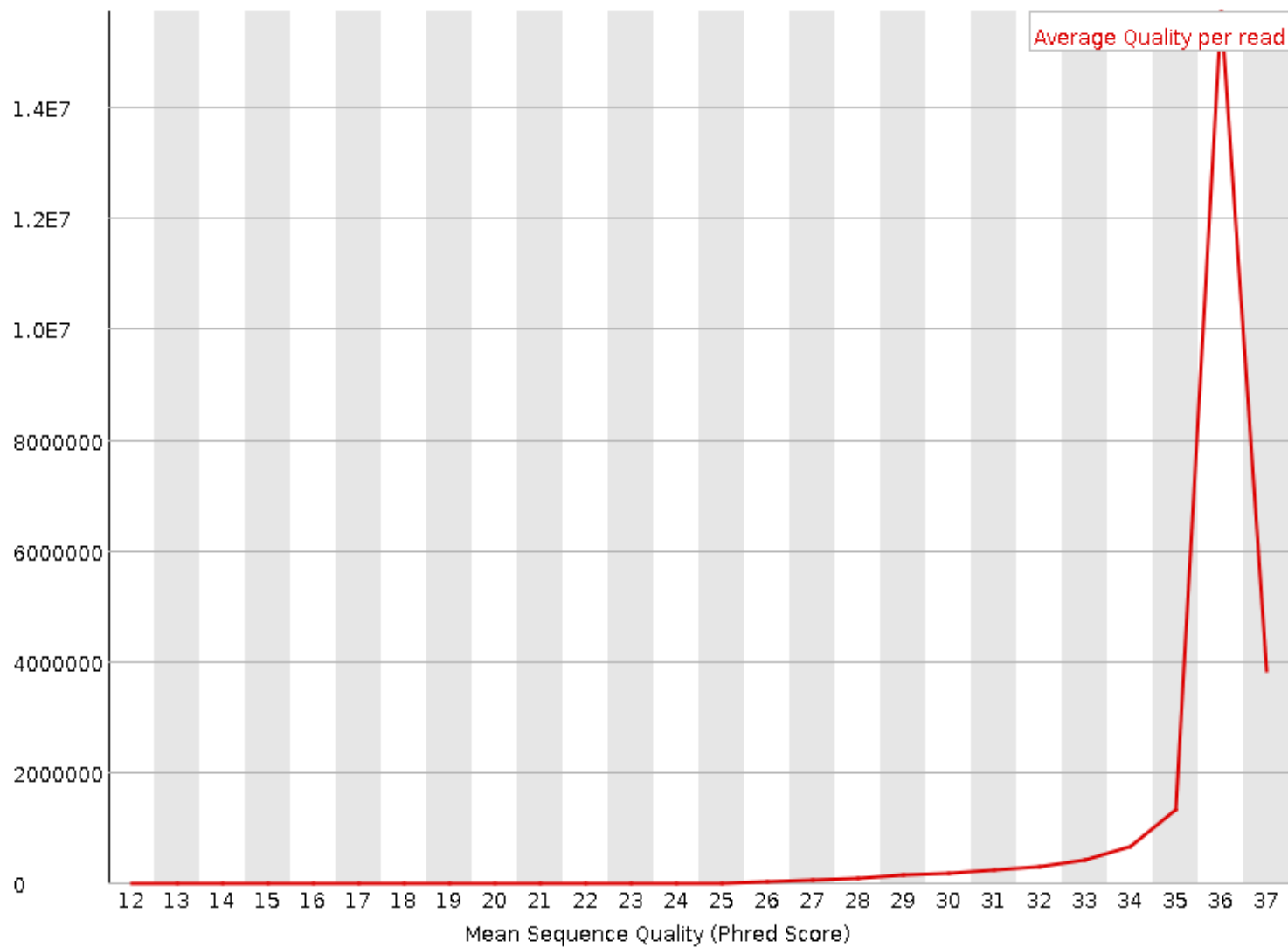
## Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)



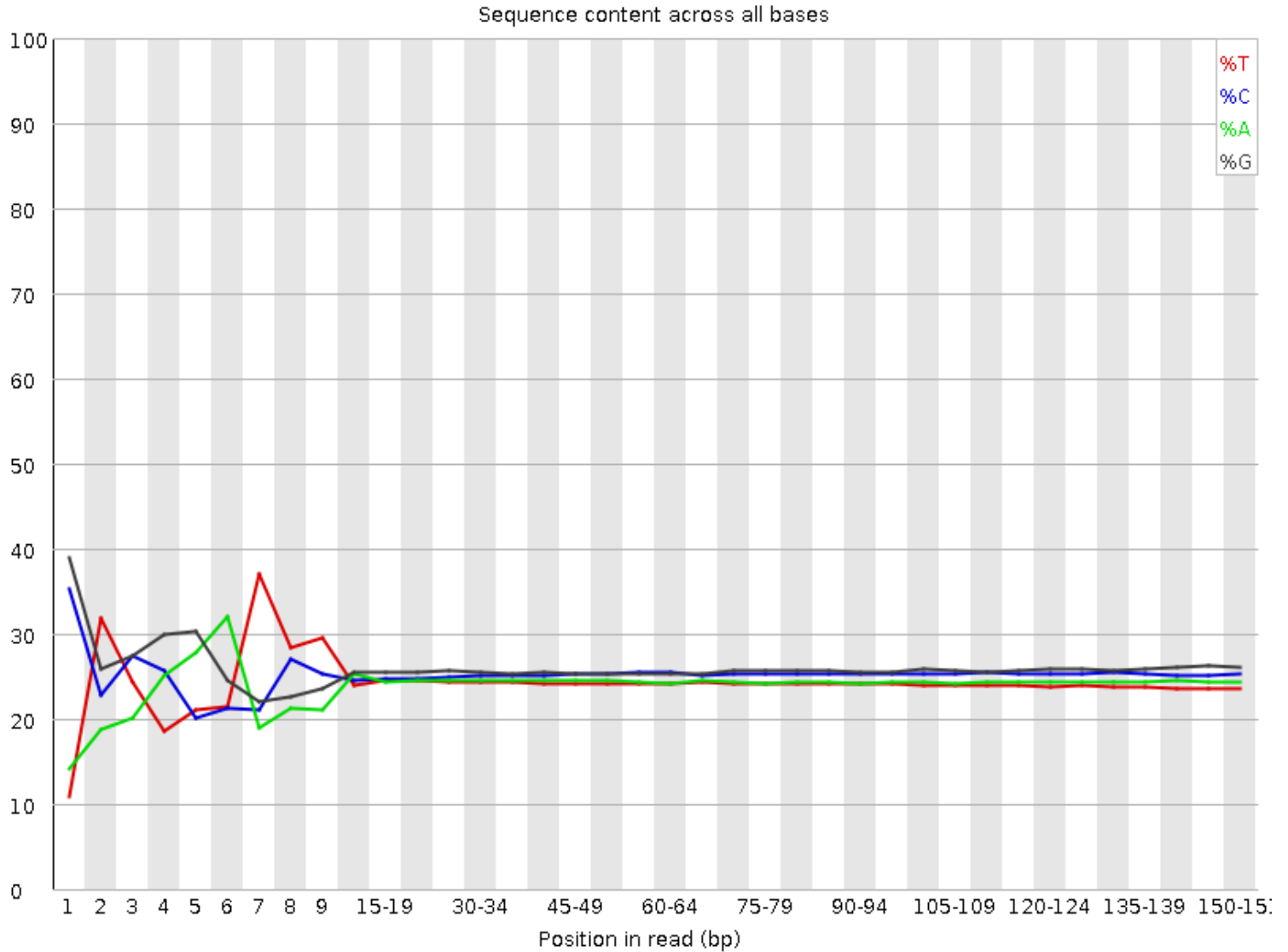
## ✓ Per sequence quality scores

Quality score distribution over all sequences

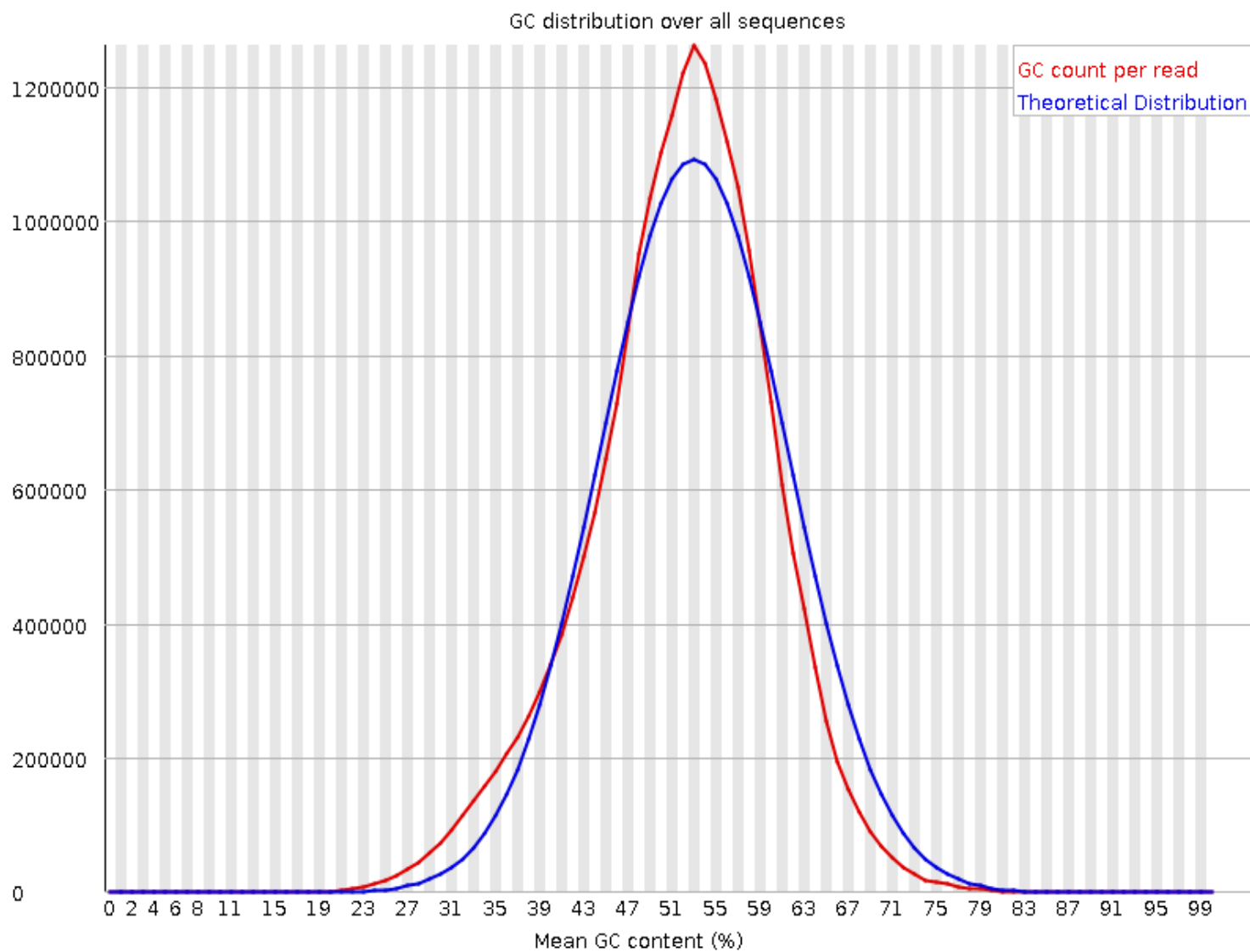




## Per base sequence content



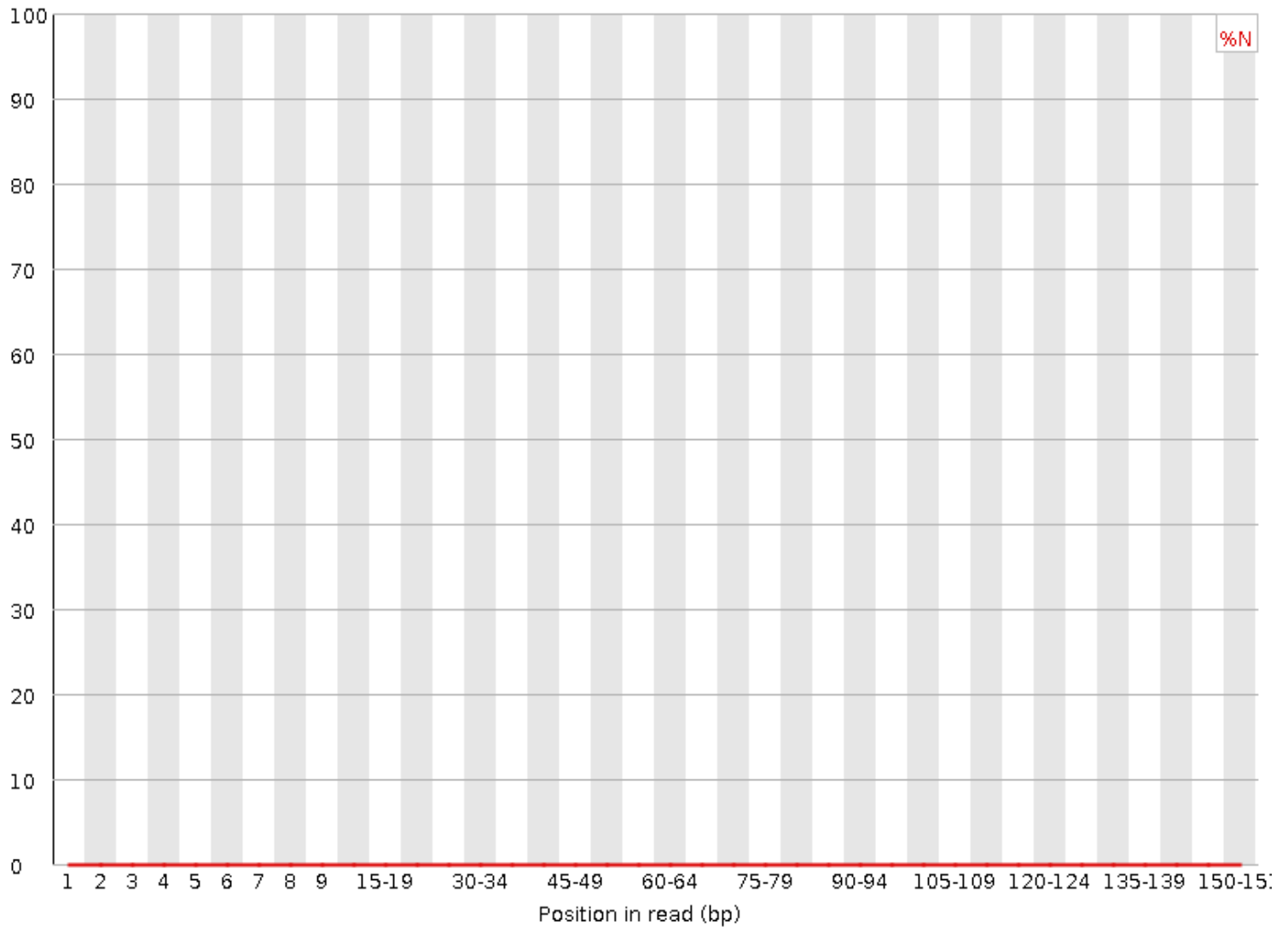
## ✓ Per sequence GC content





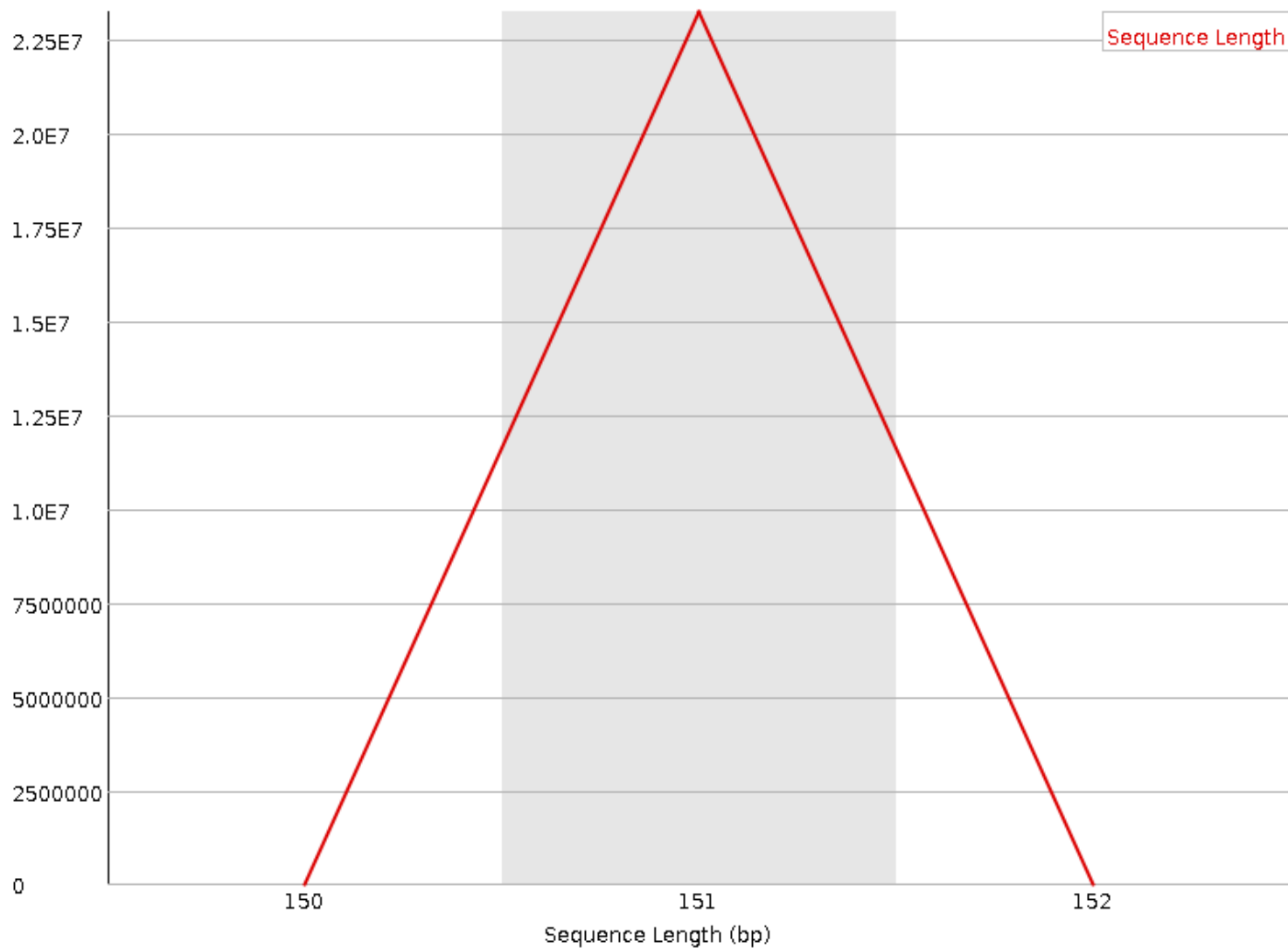
## Per base N content

N content across all bases

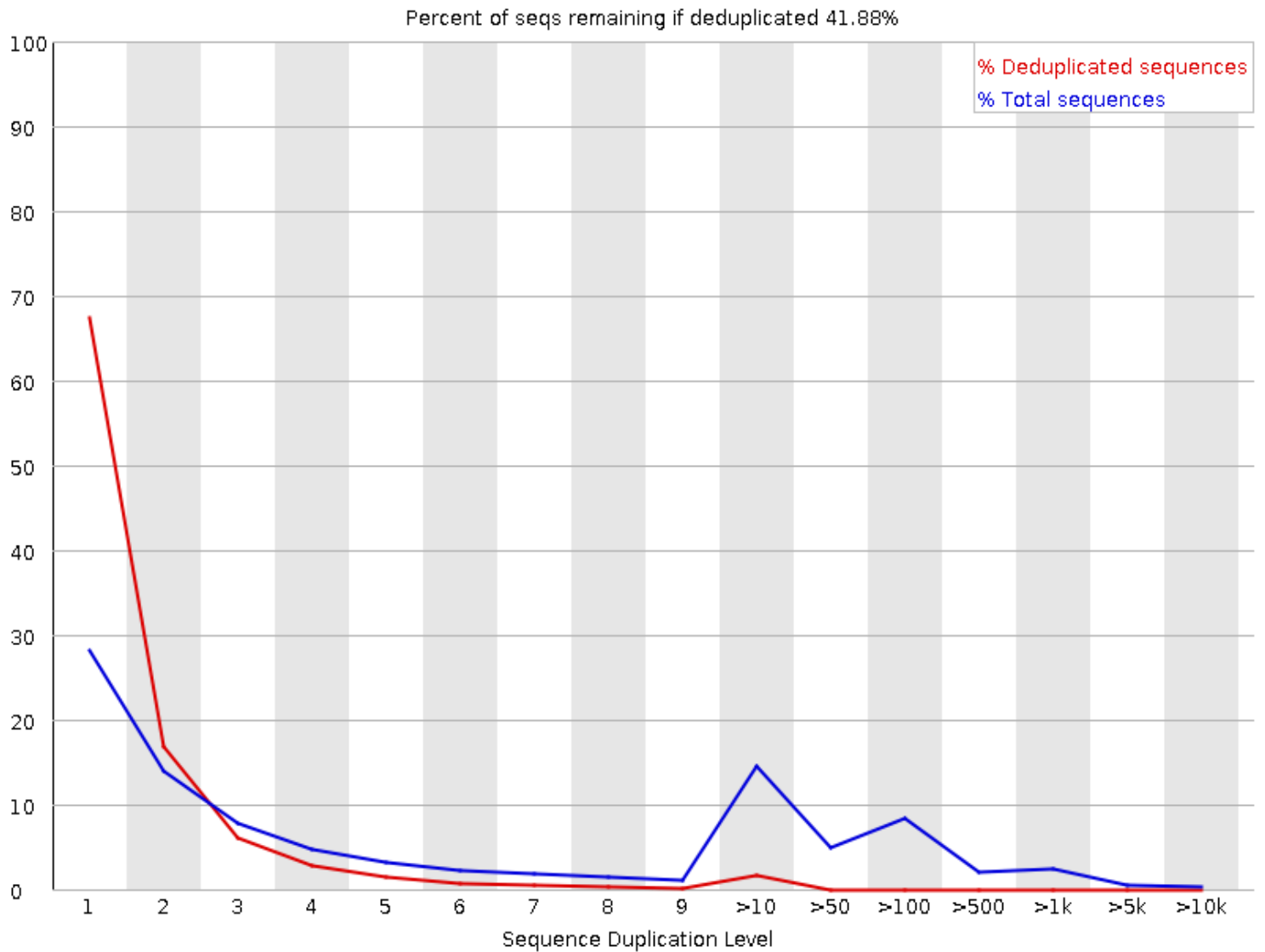


## Sequence Length Distribution

Distribution of sequence lengths over all sequences



## ✖ Sequence Duplication Levels

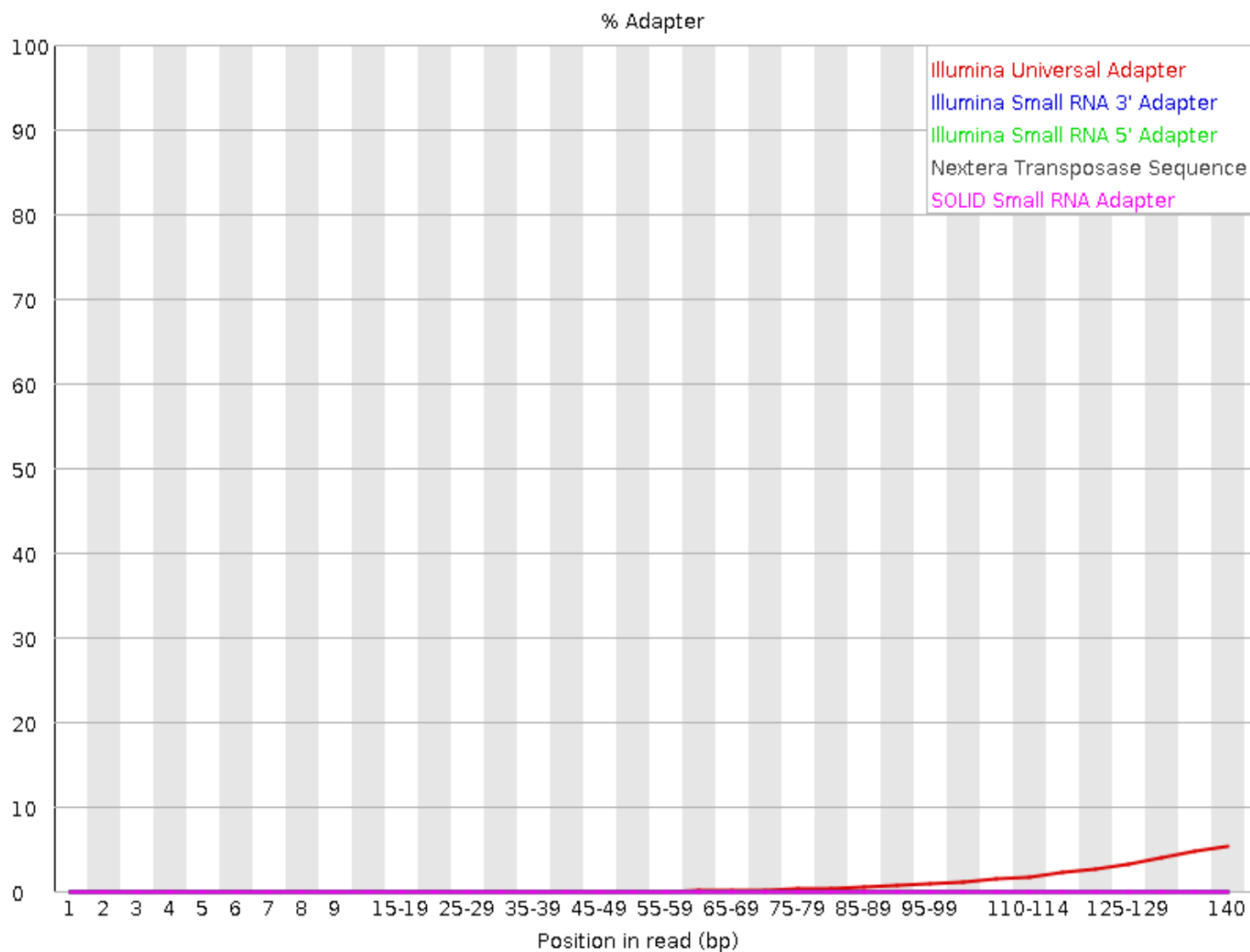


## ✔ Overrepresented sequences

No overrepresented sequences



## Adapter Content



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