












# FastQC Report

## Summary

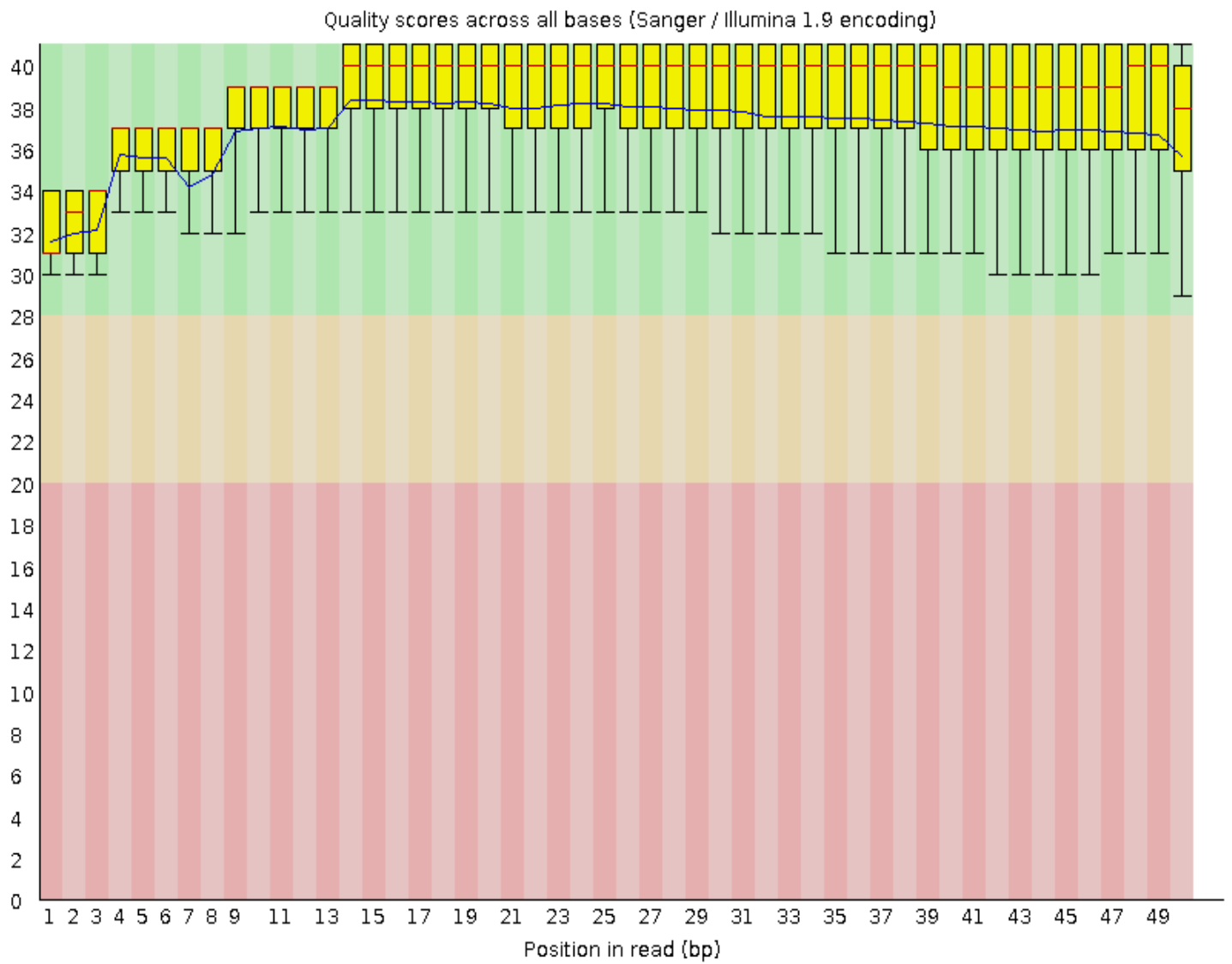
Tue 17 Sep 2019  
SRR10085026.fastq

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### Basic Statistics

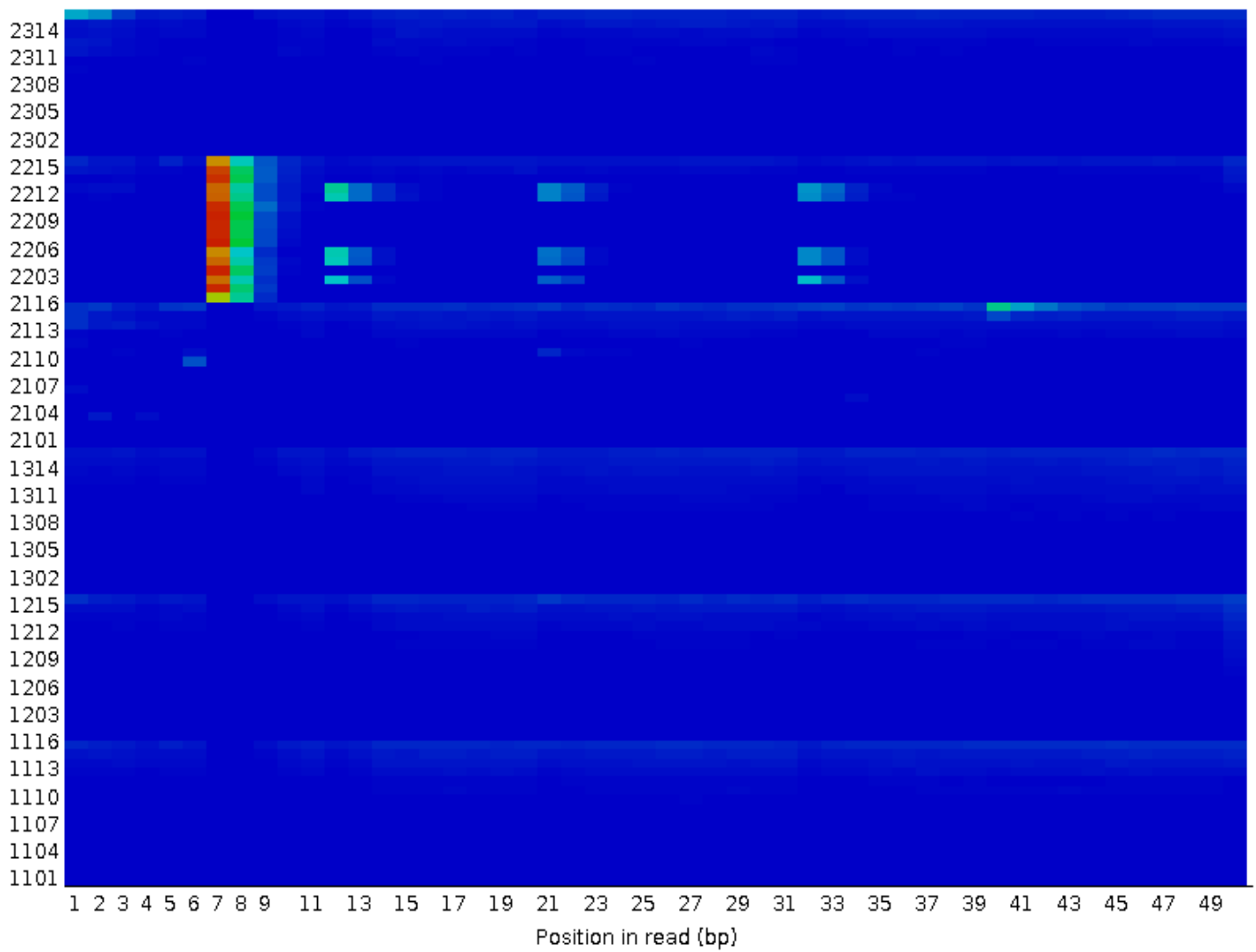
Measure	Value
Filename	SRR10085026.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	67582396
Sequences flagged as poor quality	0
Sequence length	50
%GC	41

### Per base sequence quality

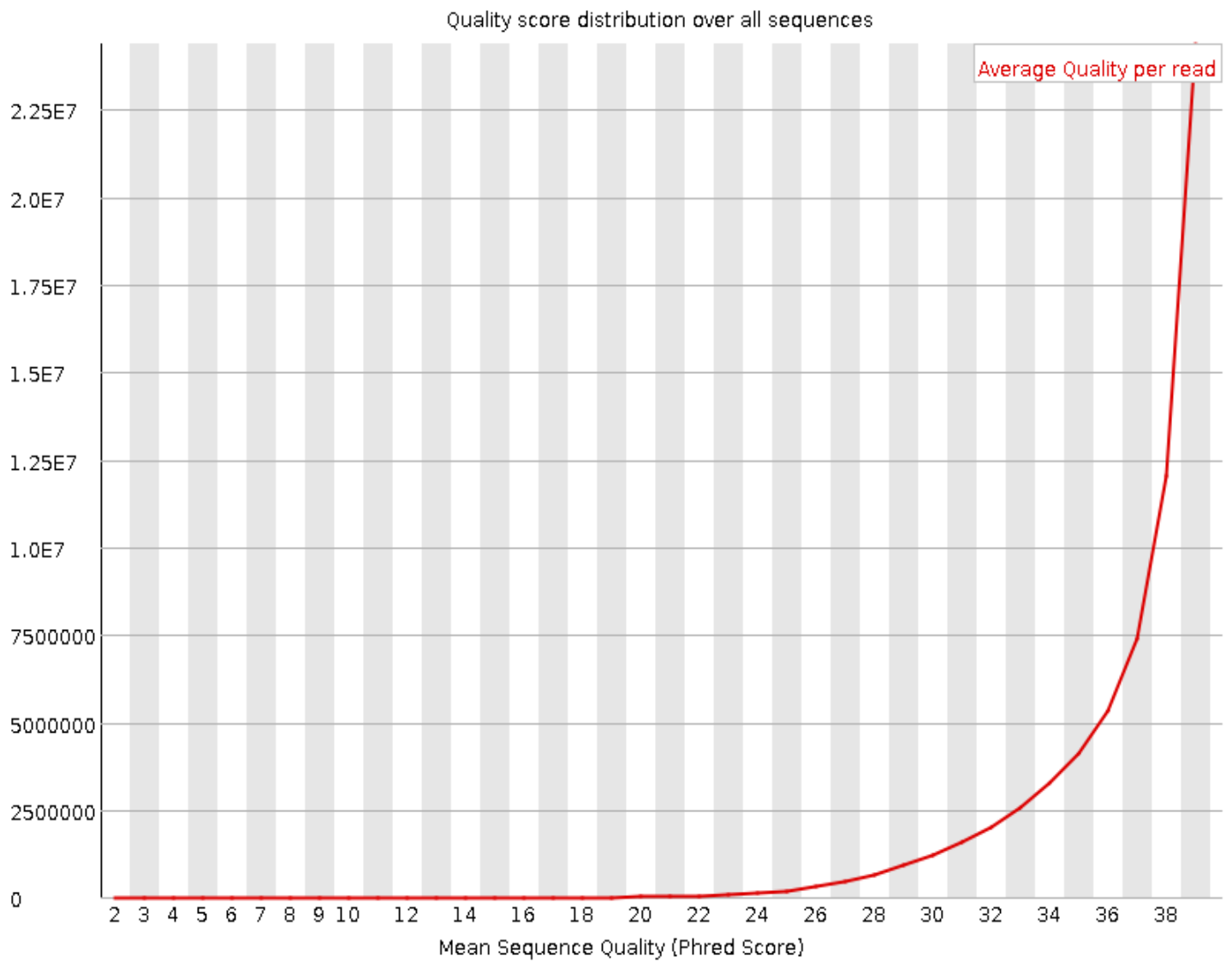


! Per tile sequence quality

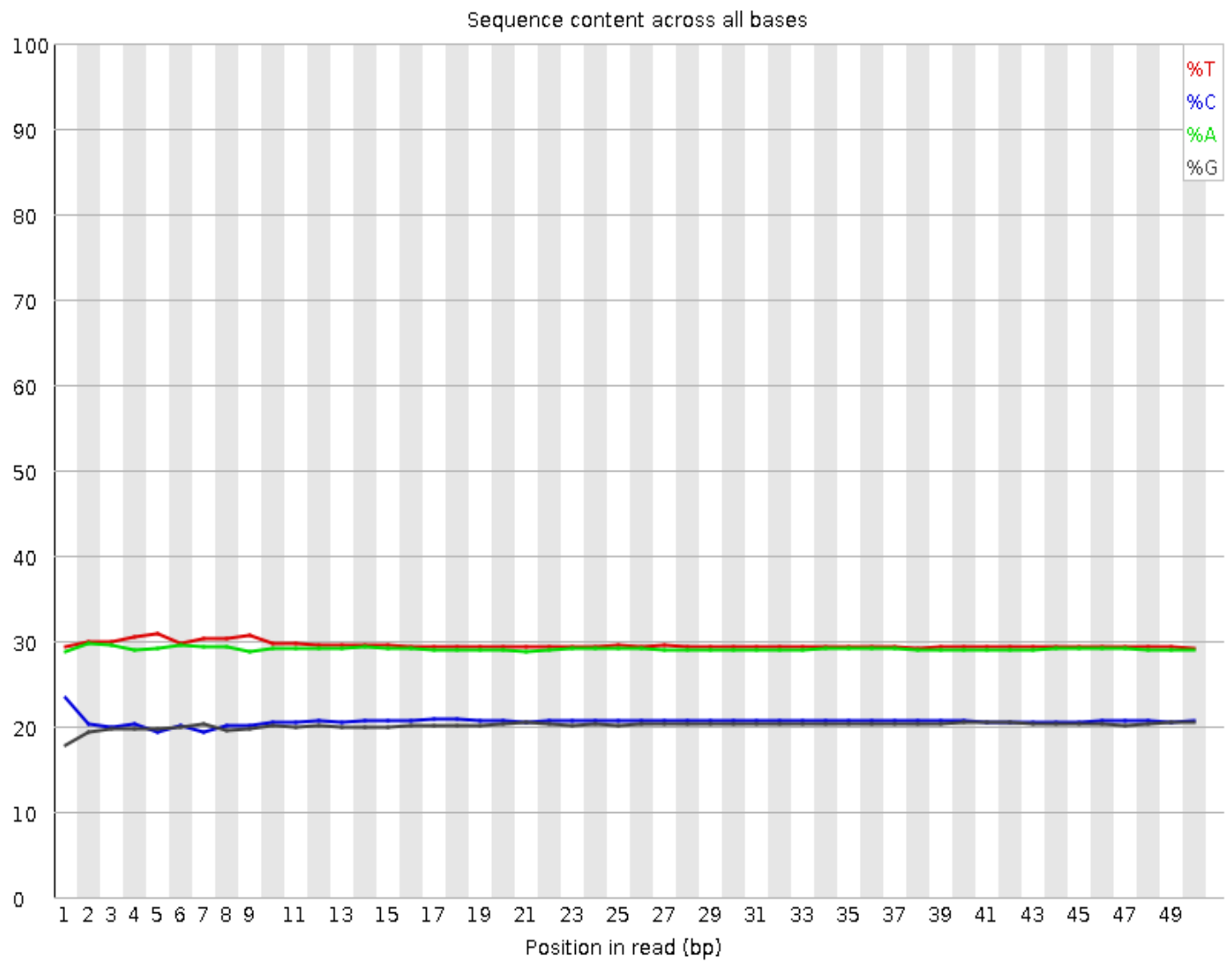
Quality per tile



**Per sequence quality scores**

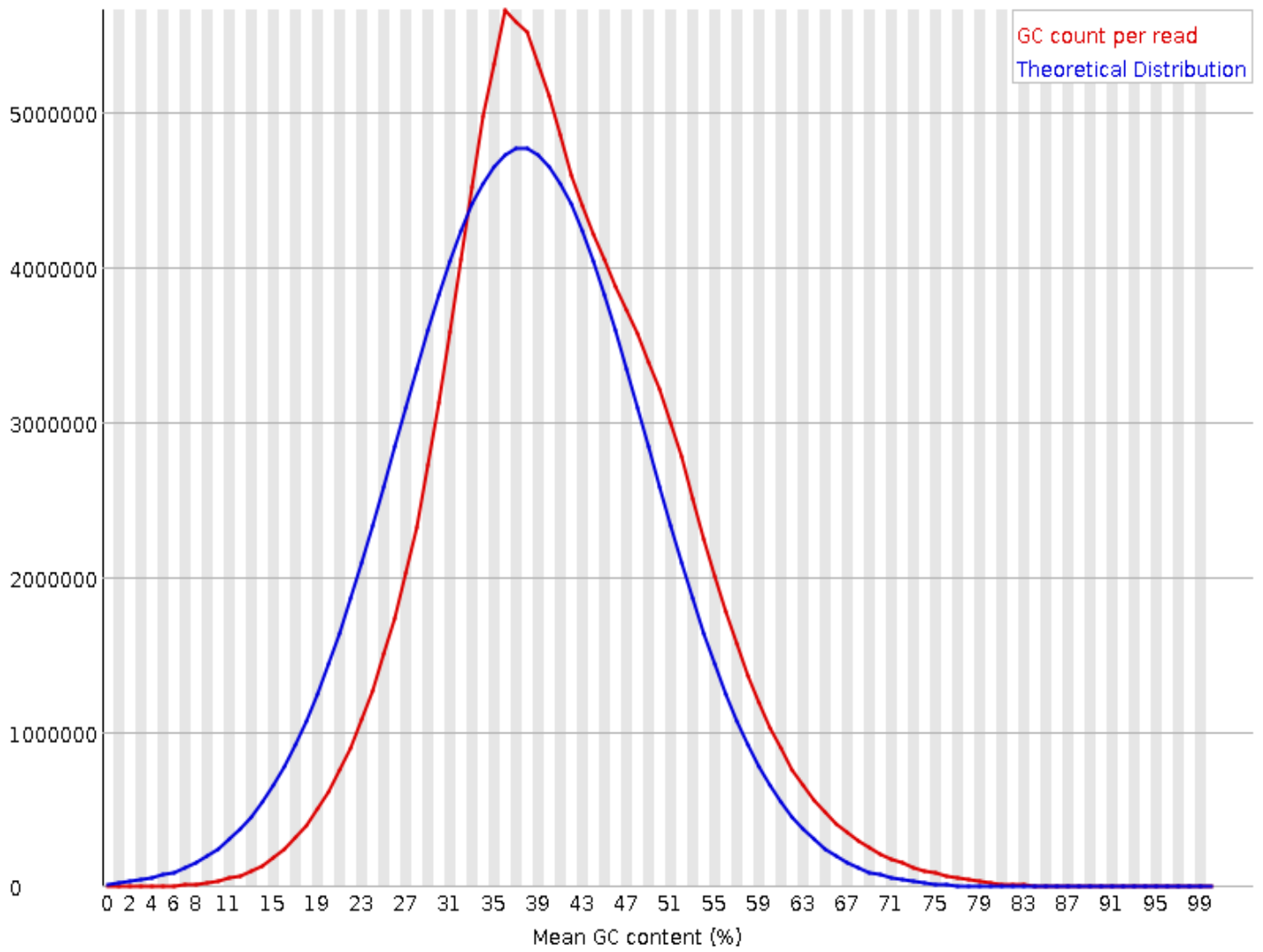


## ✅ Per base sequence content



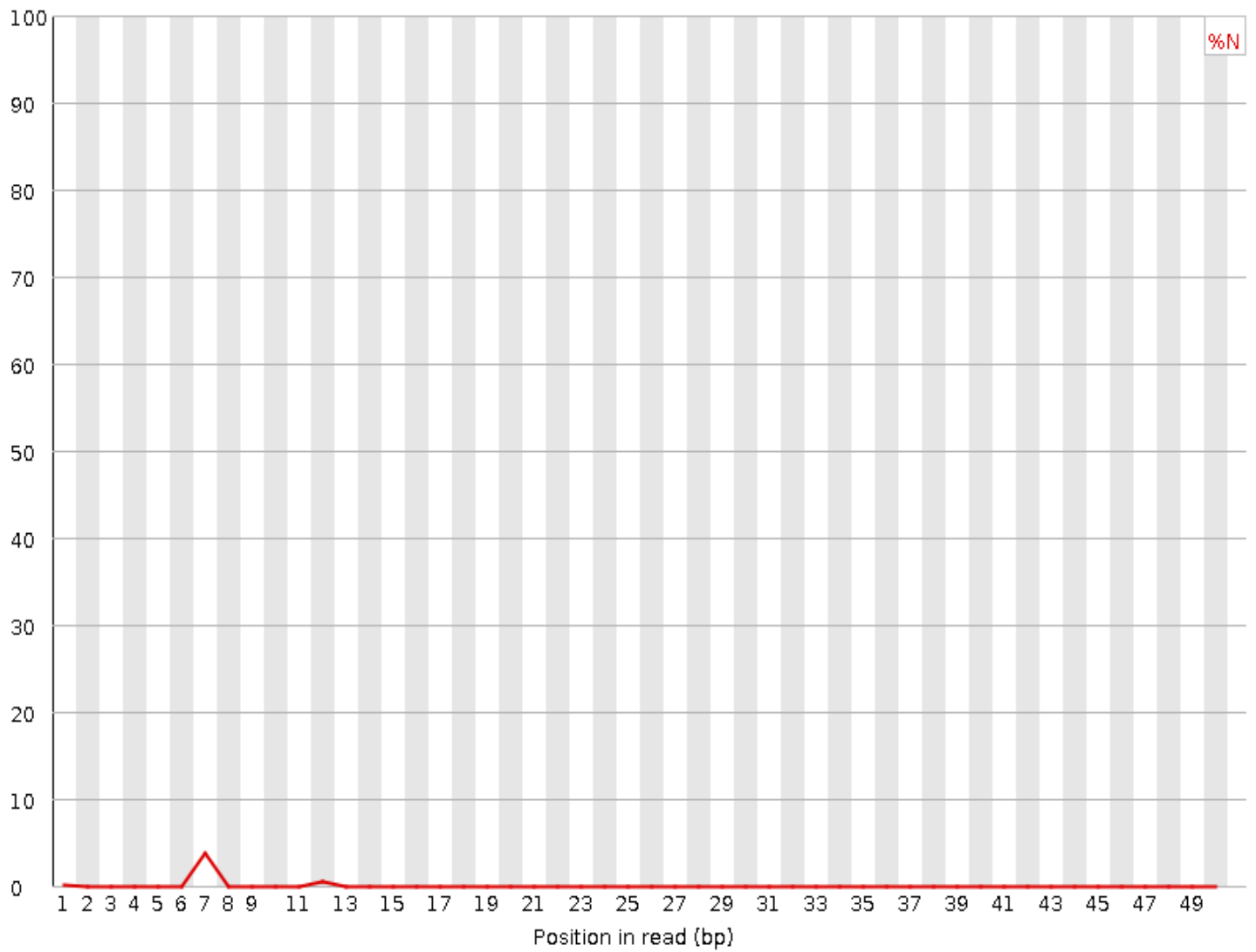
! Per sequence GC content

GC distribution over all sequences

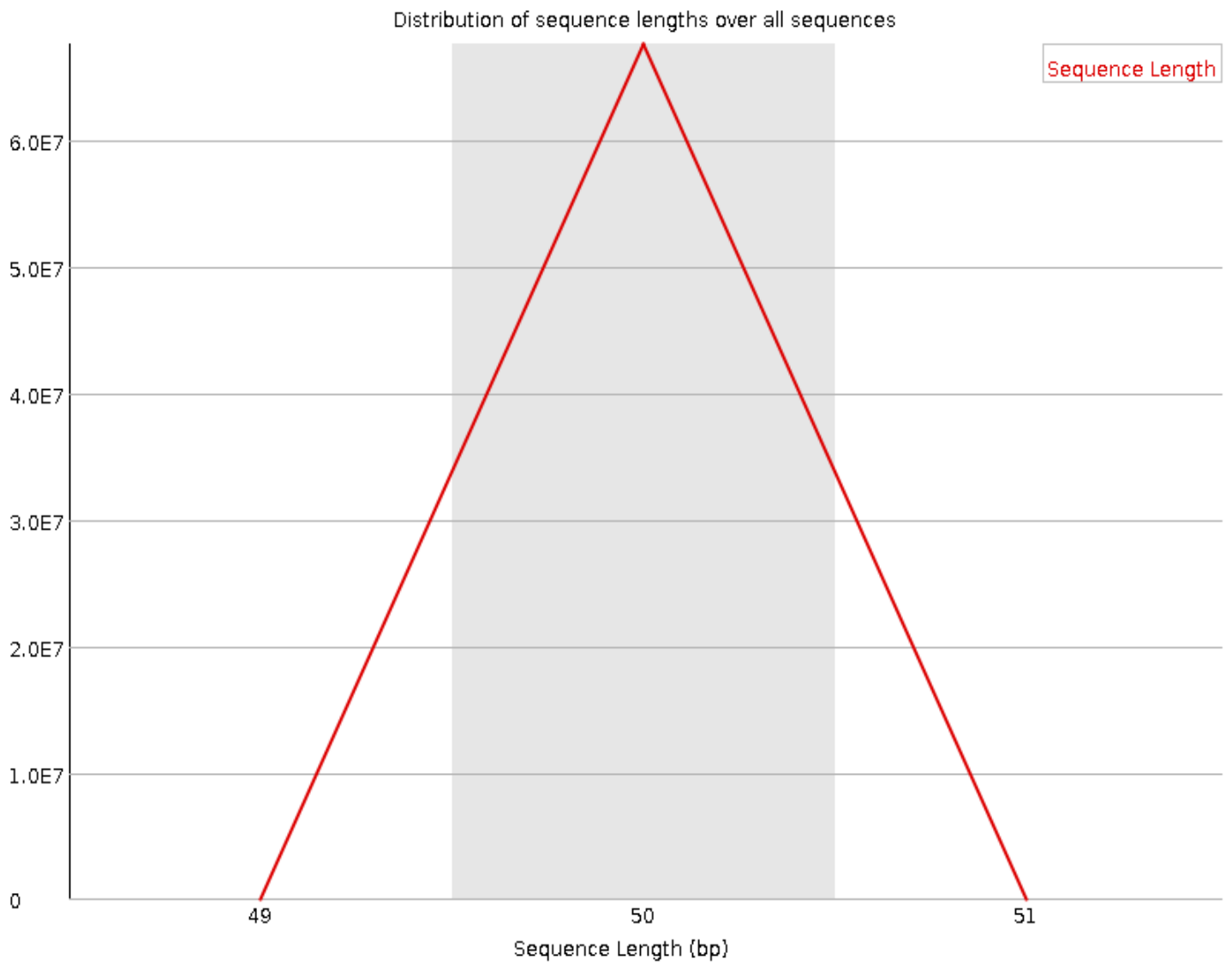


**Per base N content**

N content across all bases

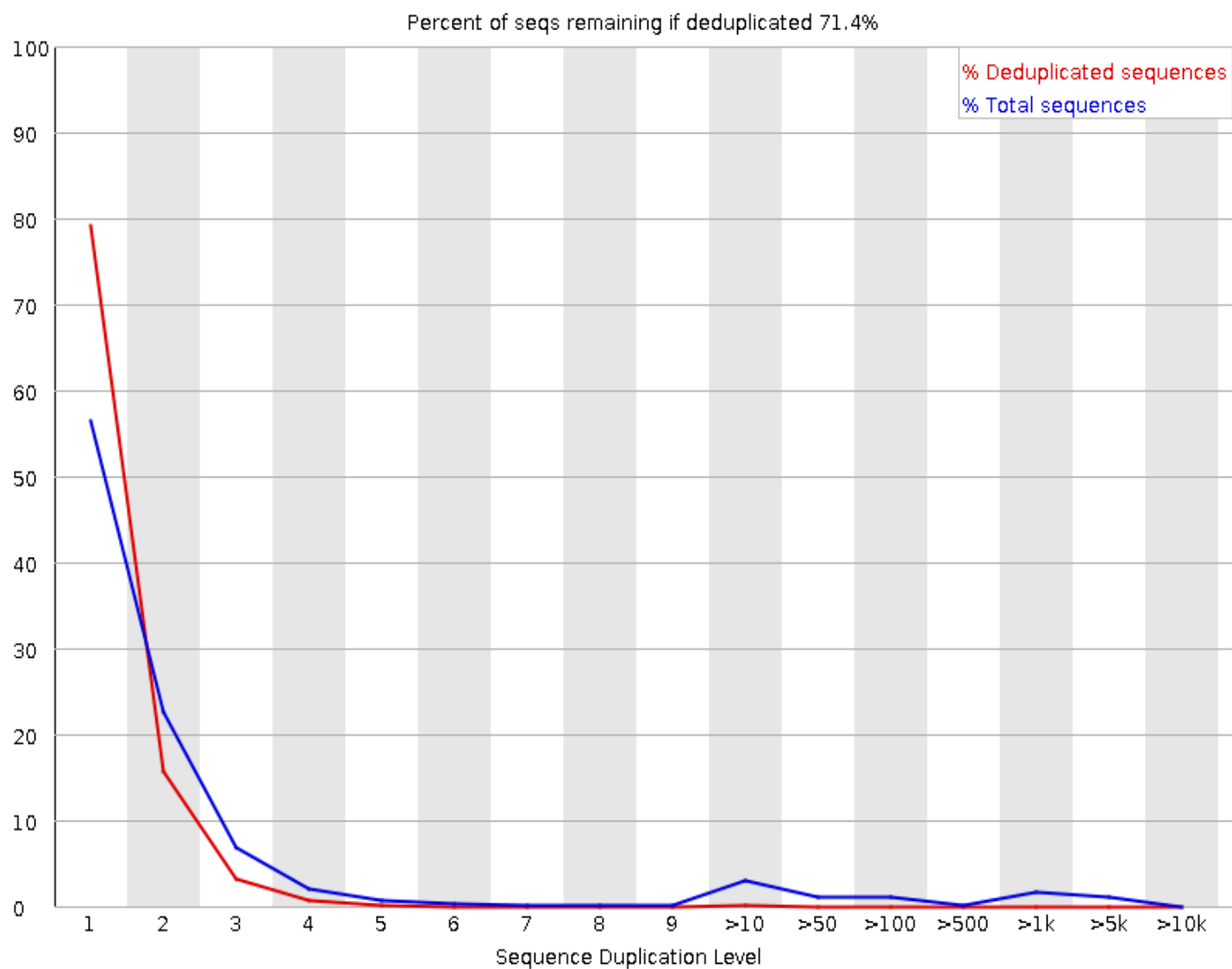


## ✔ Sequence Length Distribution



## ✔ Sequence Duplication Levels

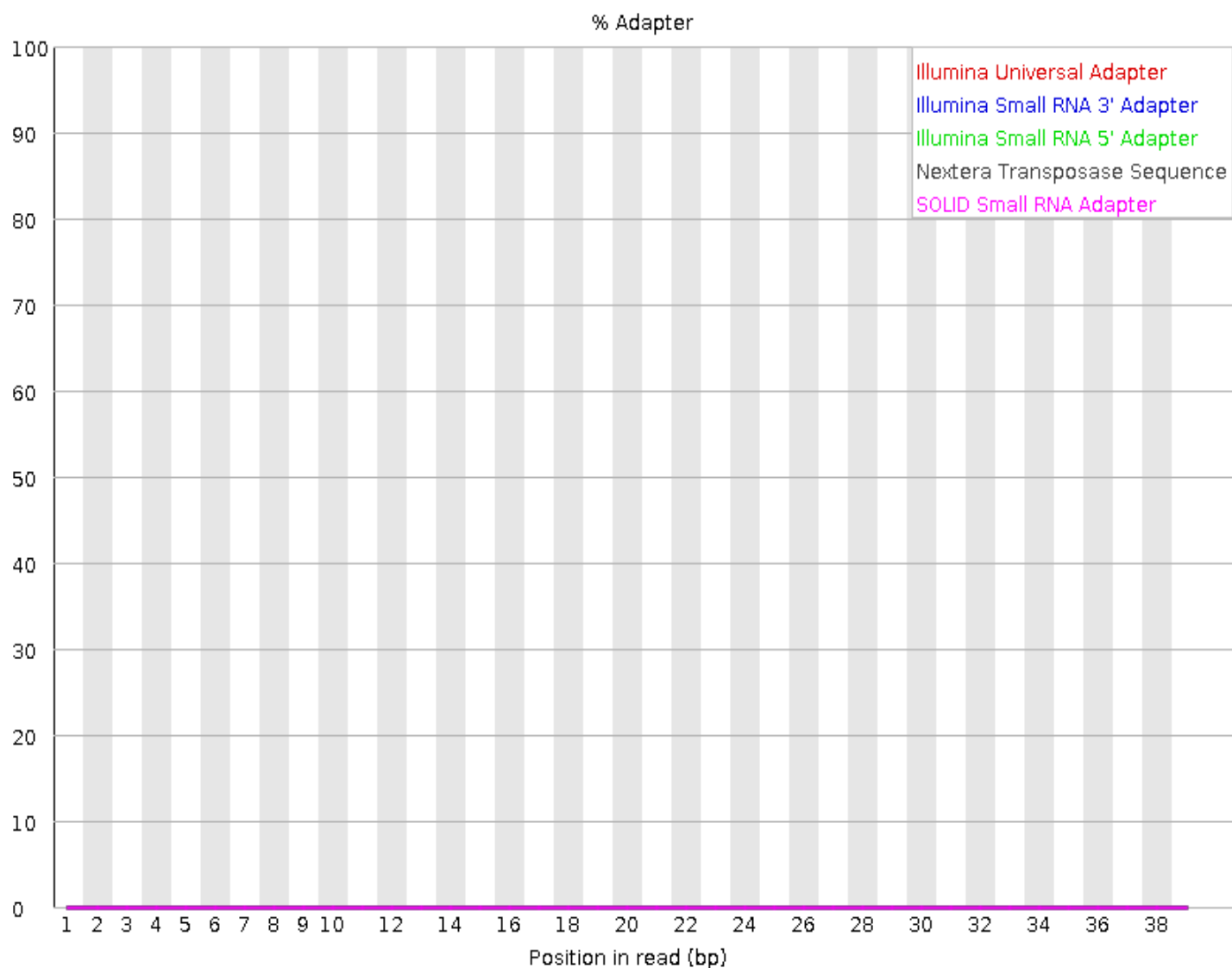




## ✔ Overrepresented sequences

No overrepresented sequences

## ✔ Adapter Content



Produced by [FastQC](#) (version 0.11.8)