

# FastQC Report

## Summary

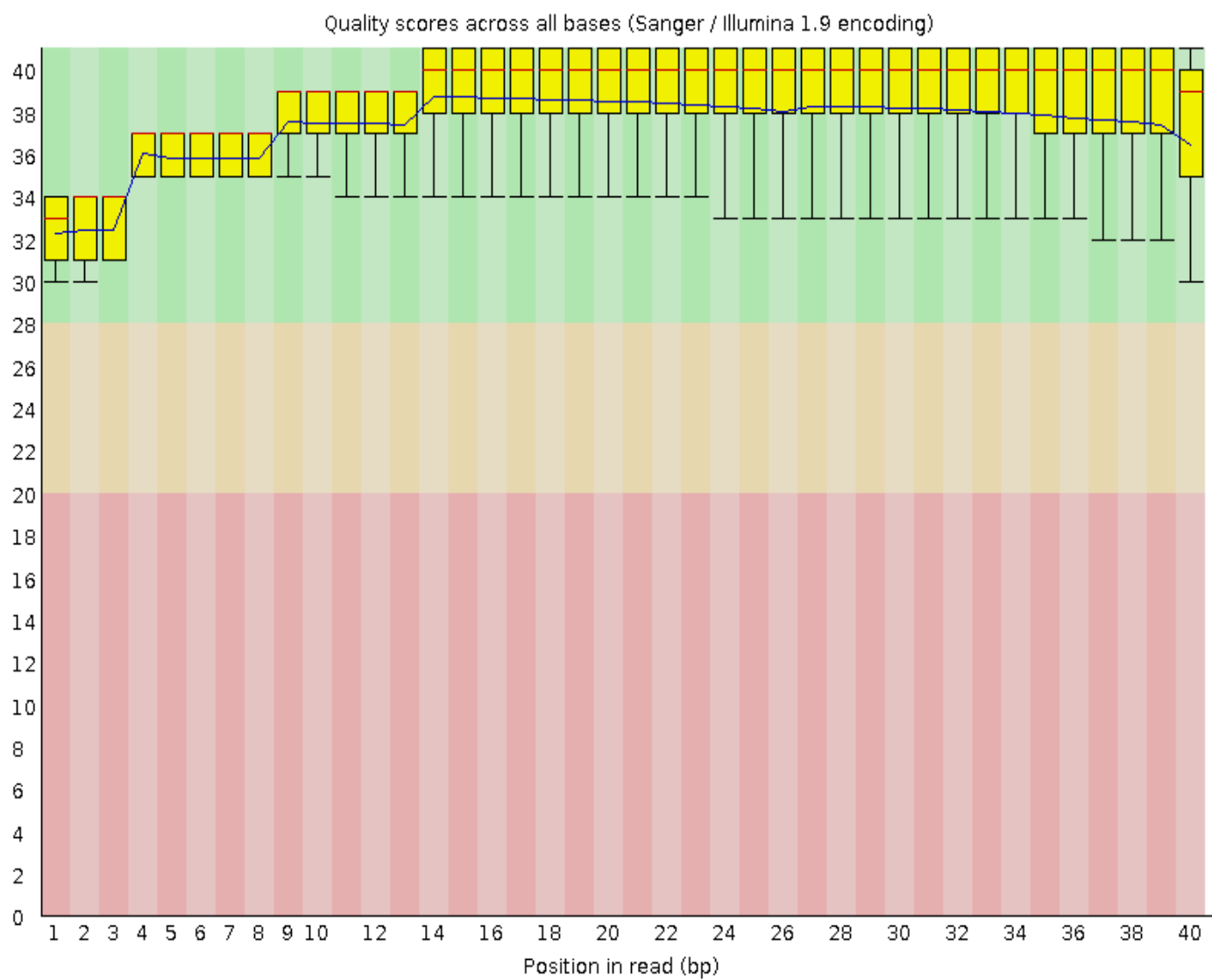
Tue 1 Mar 2022  
P0\_1\_1.fastq

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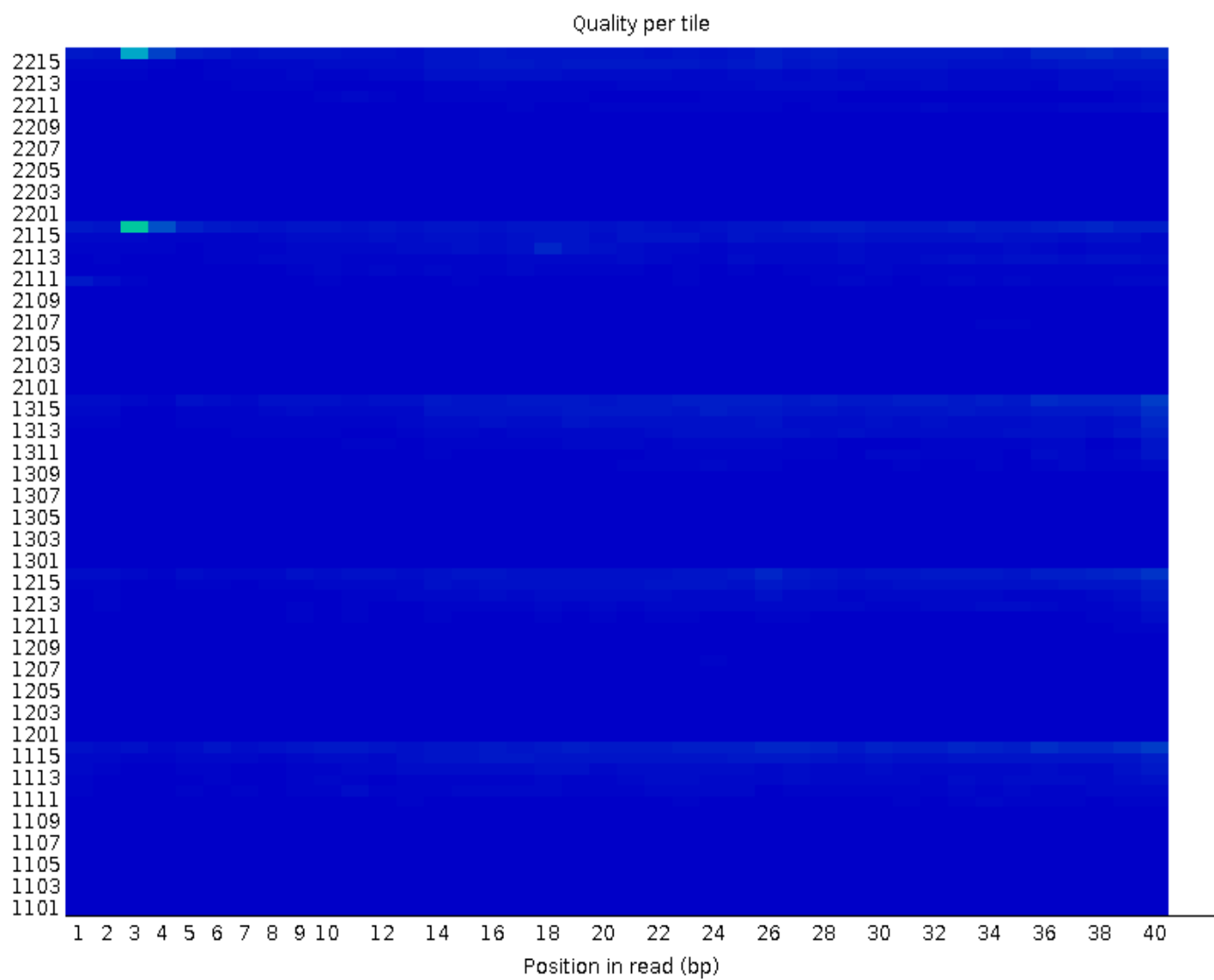
## ✓ Basic Statistics

Measure	Value
Filename	P0_1_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	21577562
Sequences flagged as poor quality	0
Sequence length	40
%GC	49

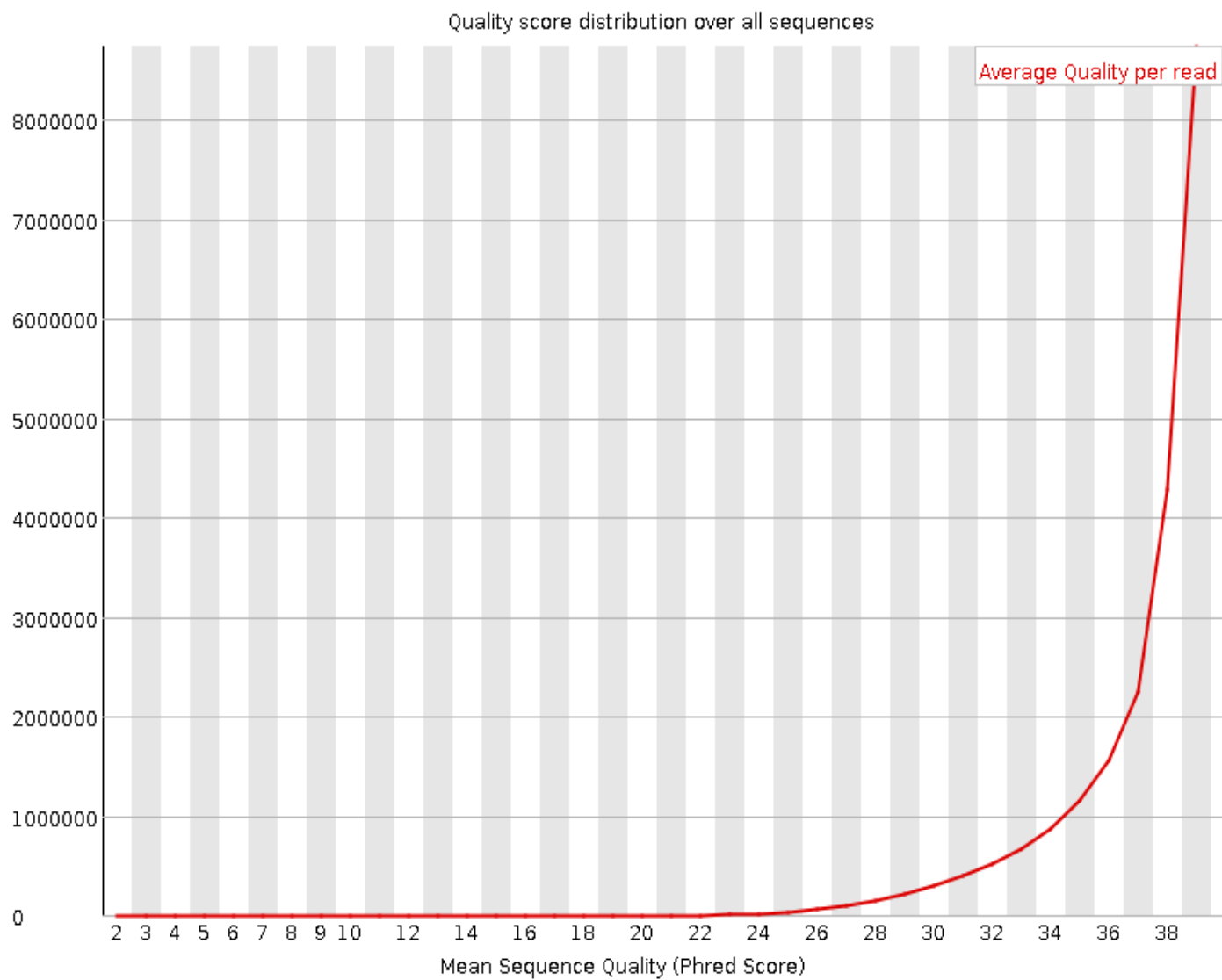
## ✓ Per base sequence quality



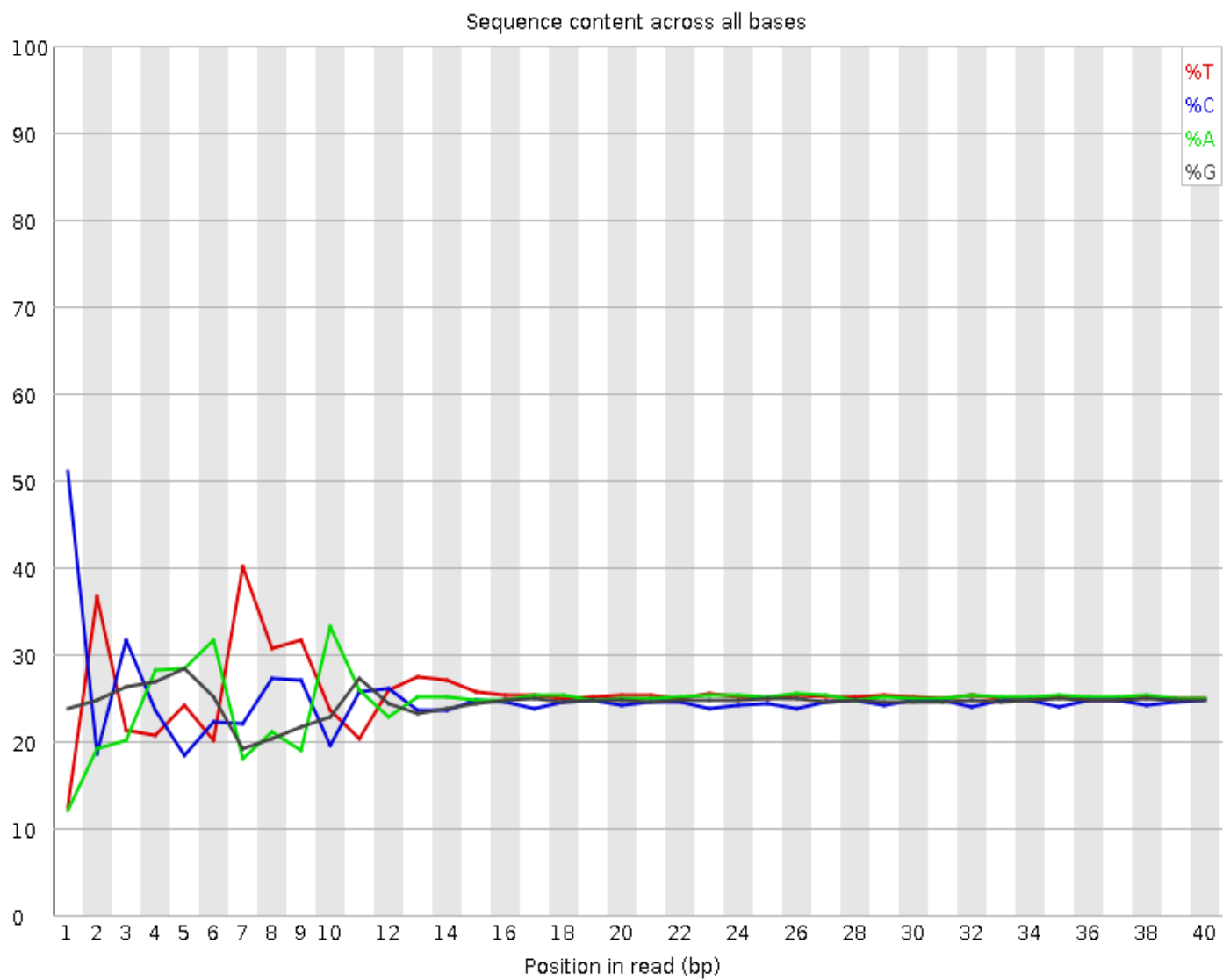
✅ **Per tile sequence quality**



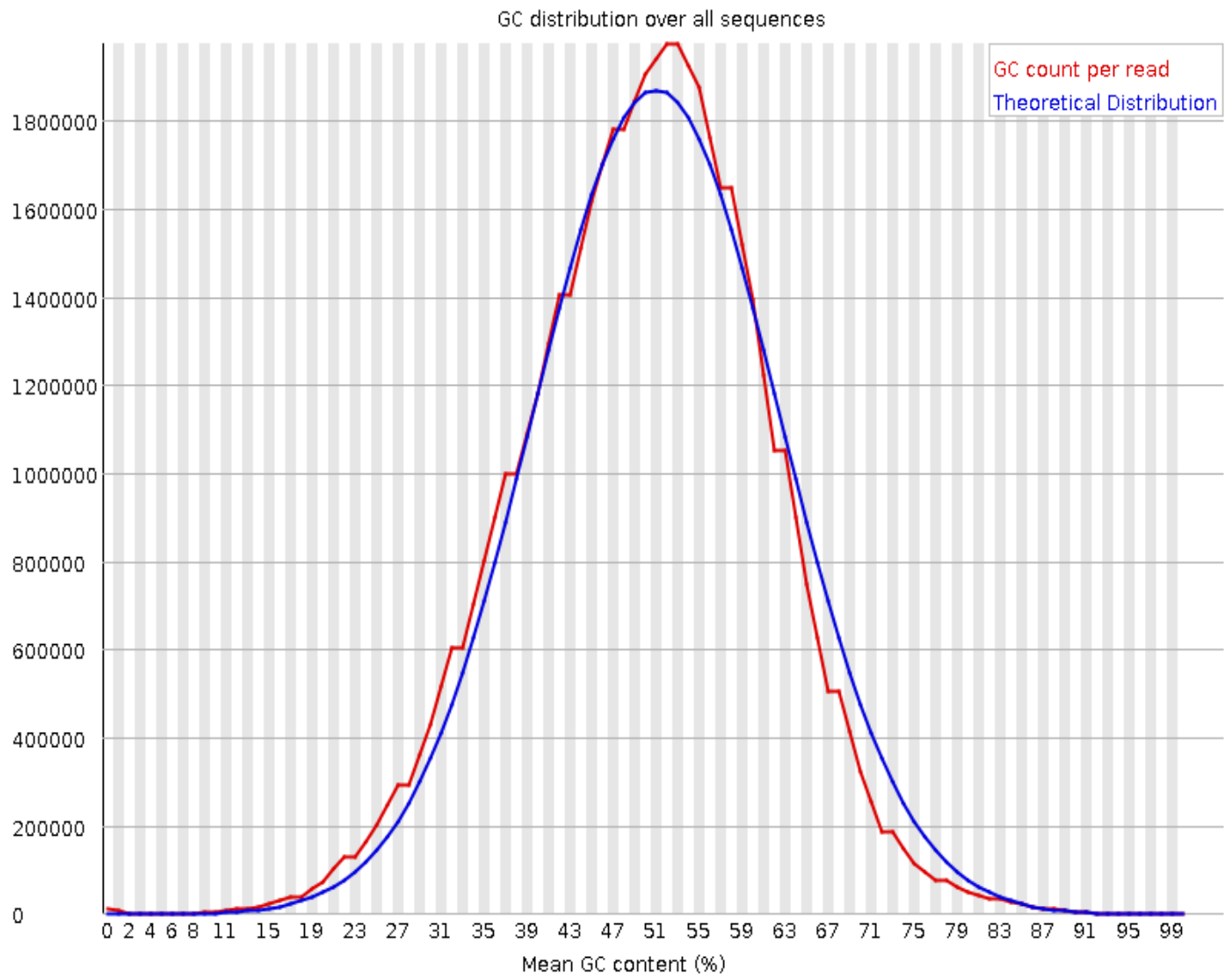
## Per sequence quality scores



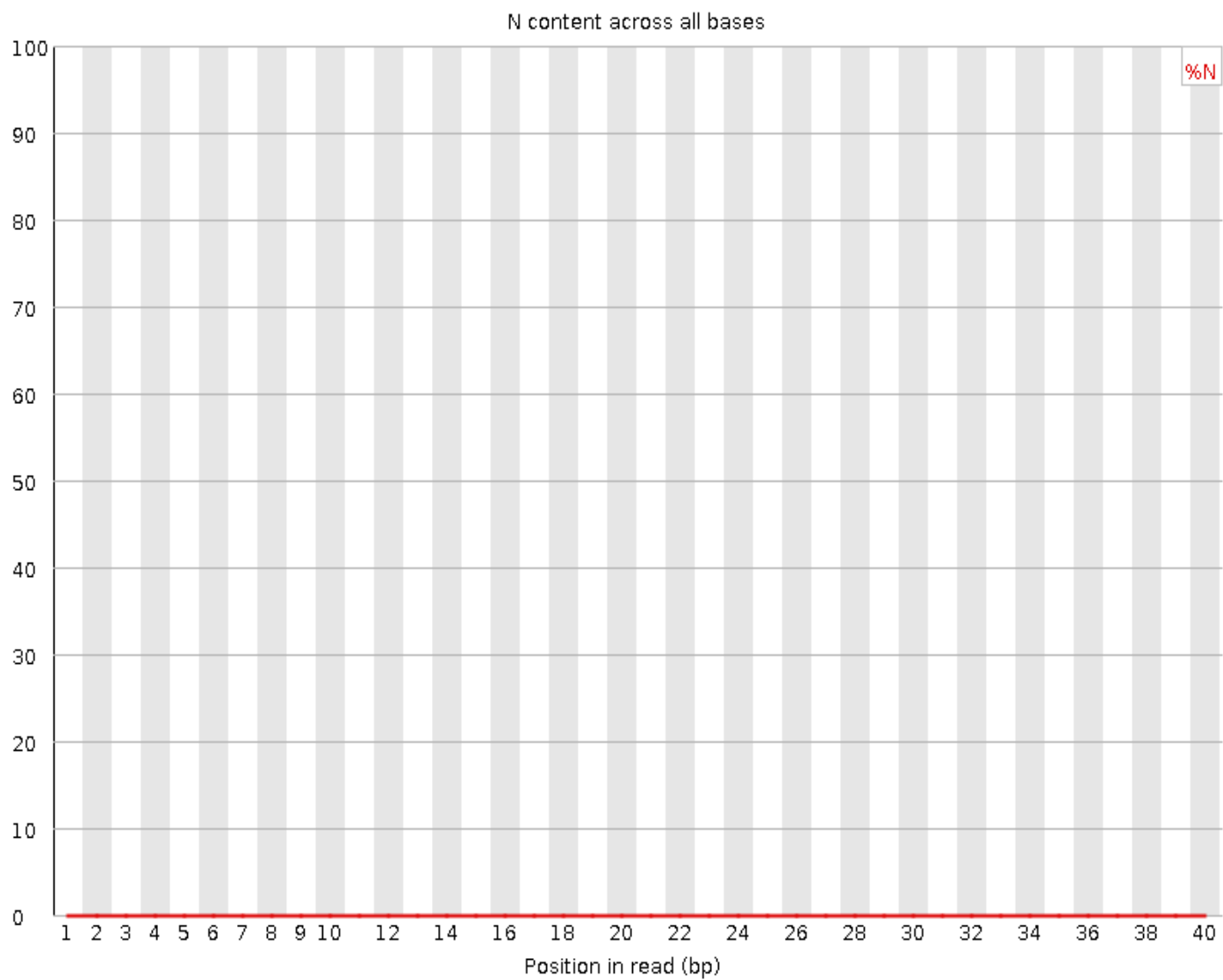
## ❌ Per base sequence content



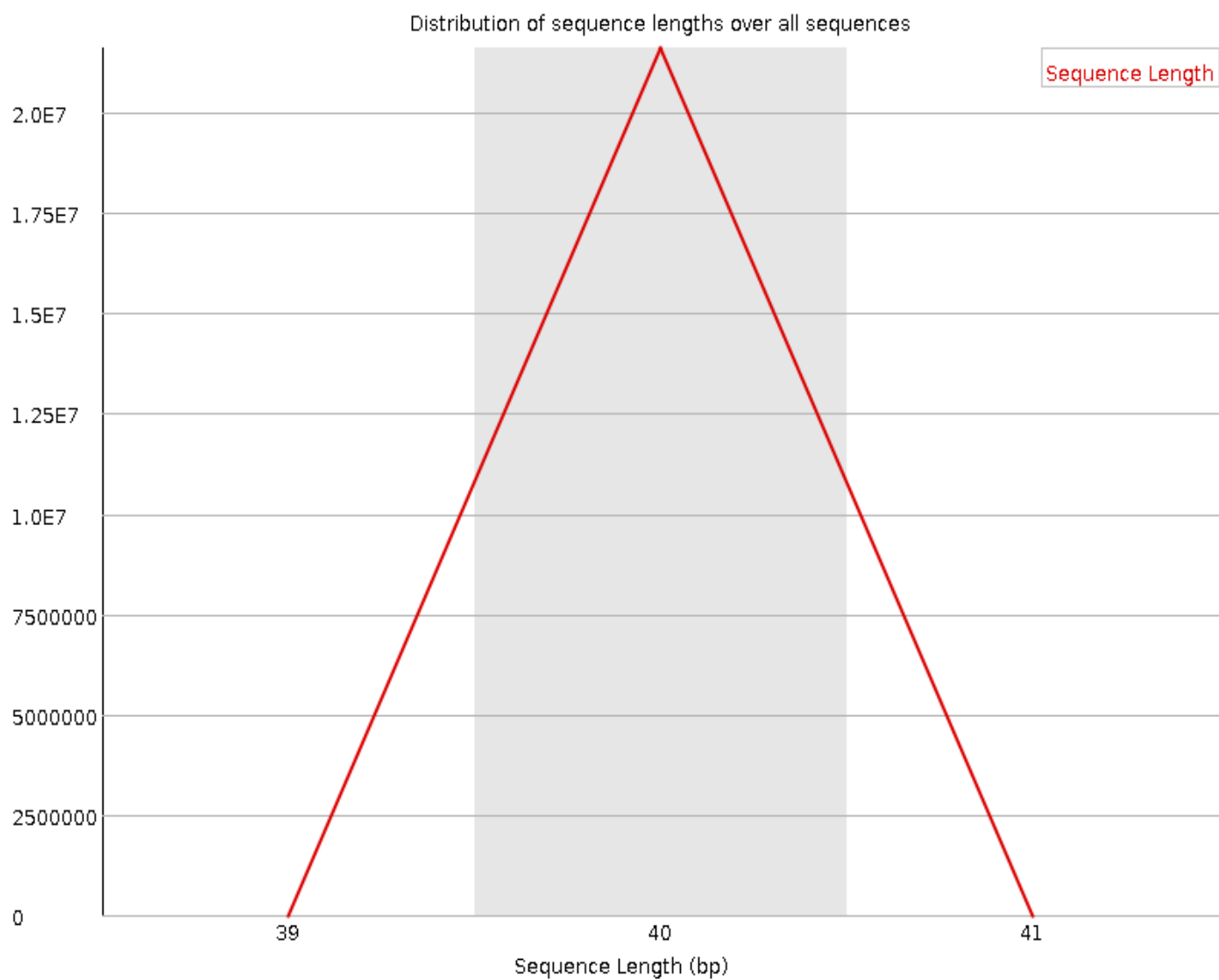
✅ **Per sequence GC content**



✅ **Per base N content**

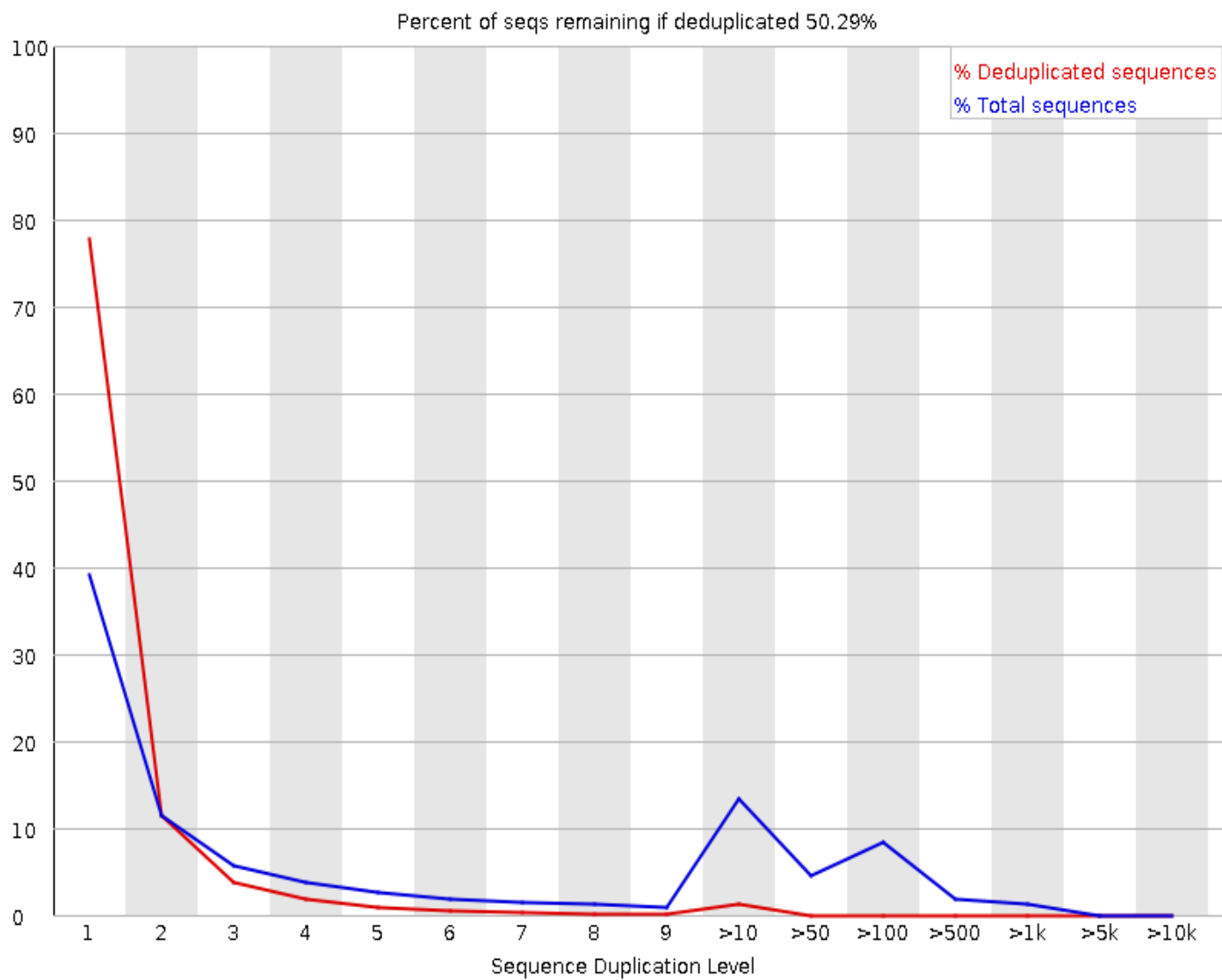


## Sequence Length Distribution



## ! Sequence Duplication Levels



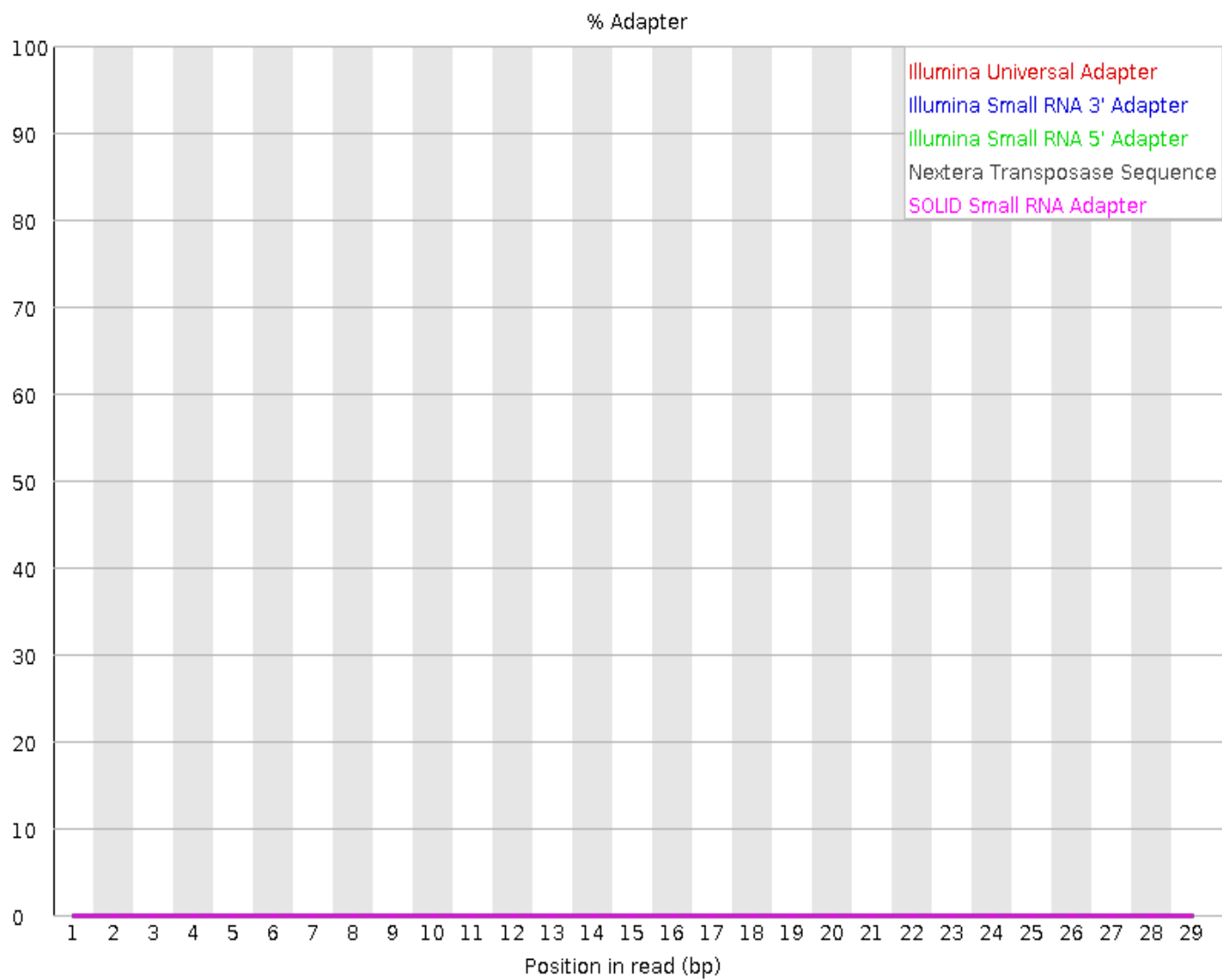


## Overrepresented sequences

No overrepresented sequences



## Adapter Content



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