












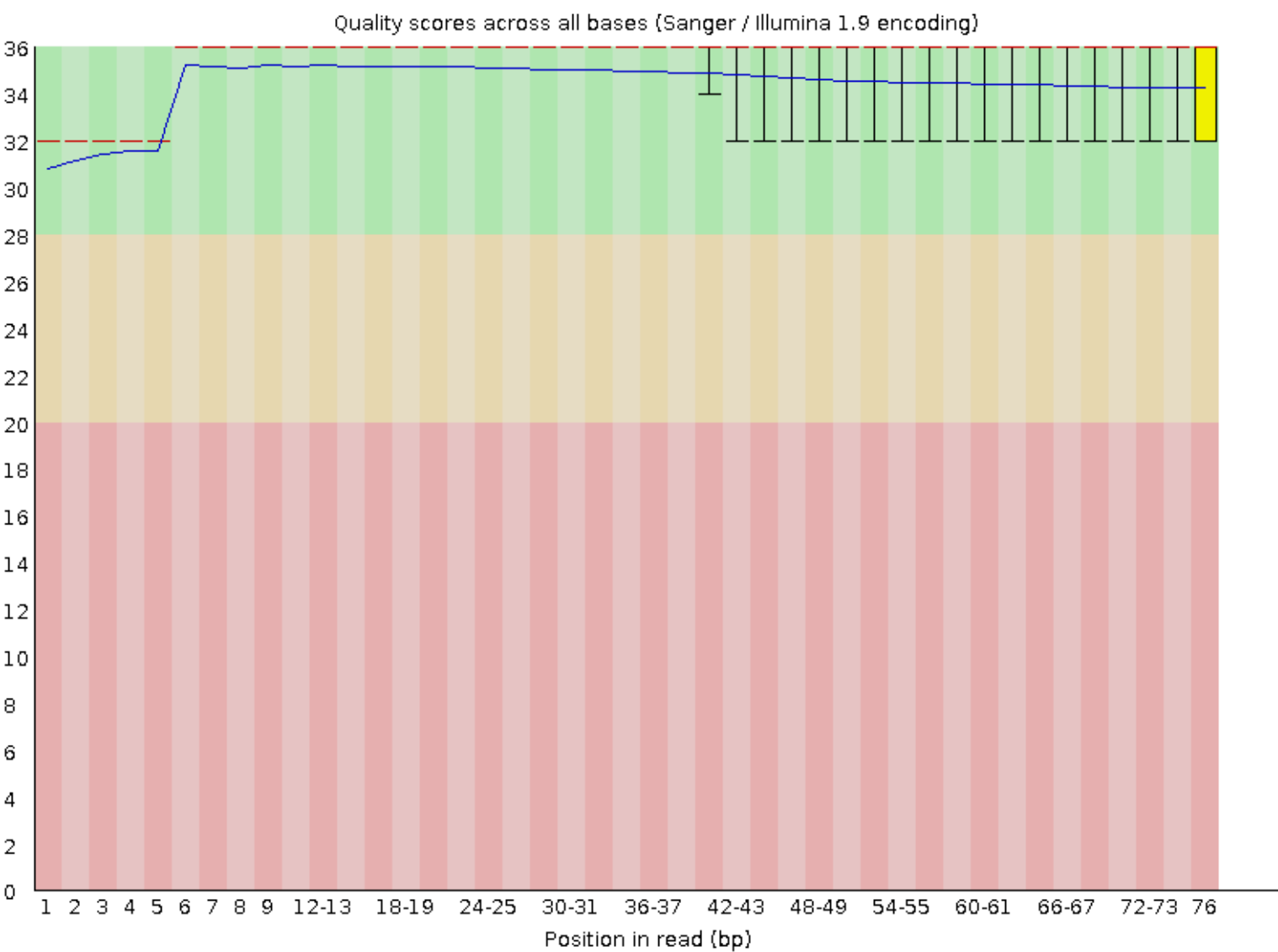
## Summary

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## Basic Statistics

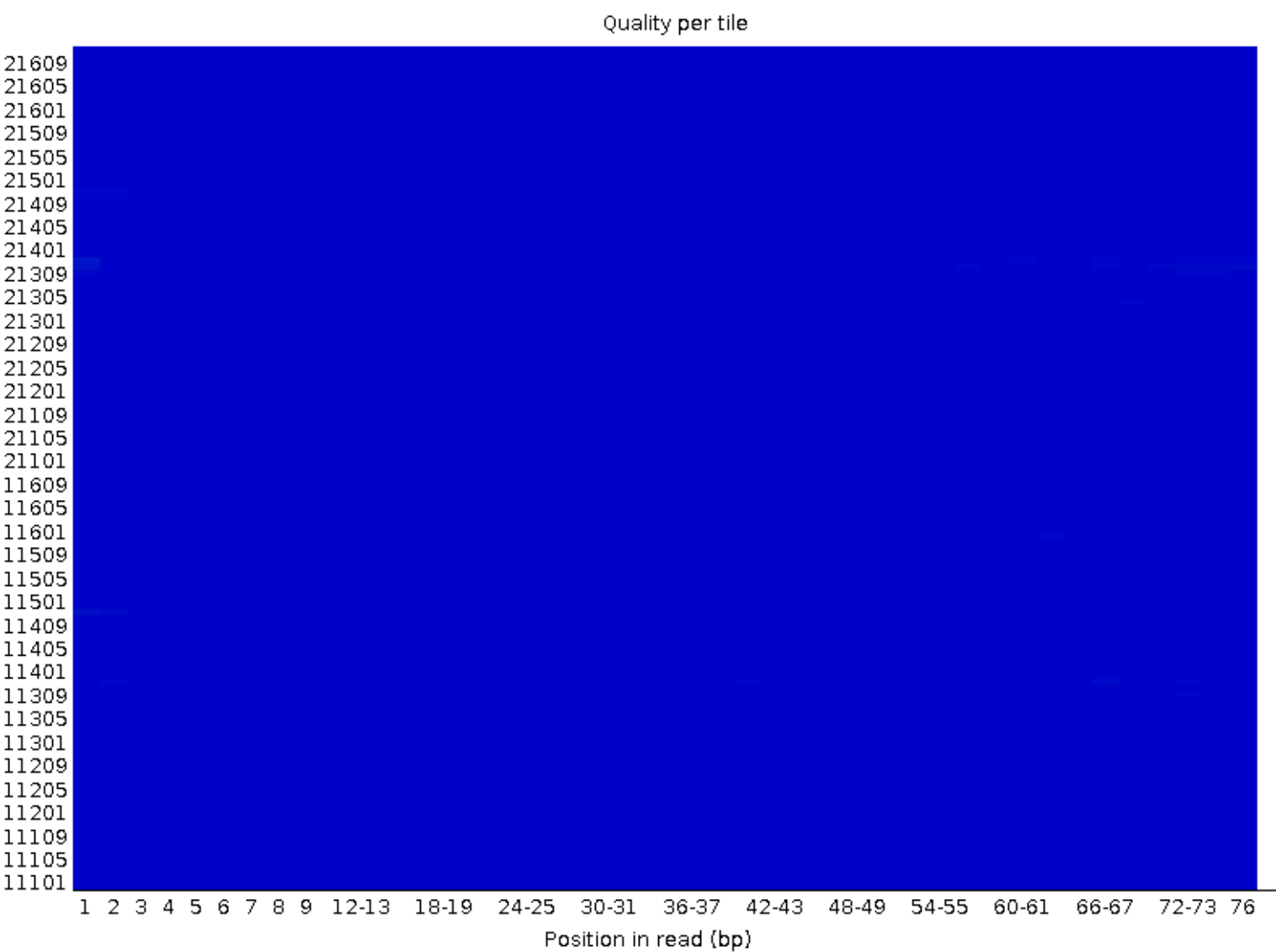
Measure	Value
Filename	ERR13985875_1_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	8902949
Sequences flagged as poor quality	0
Sequence length	50-76
%GC	46

## ✔ Per base sequence quality

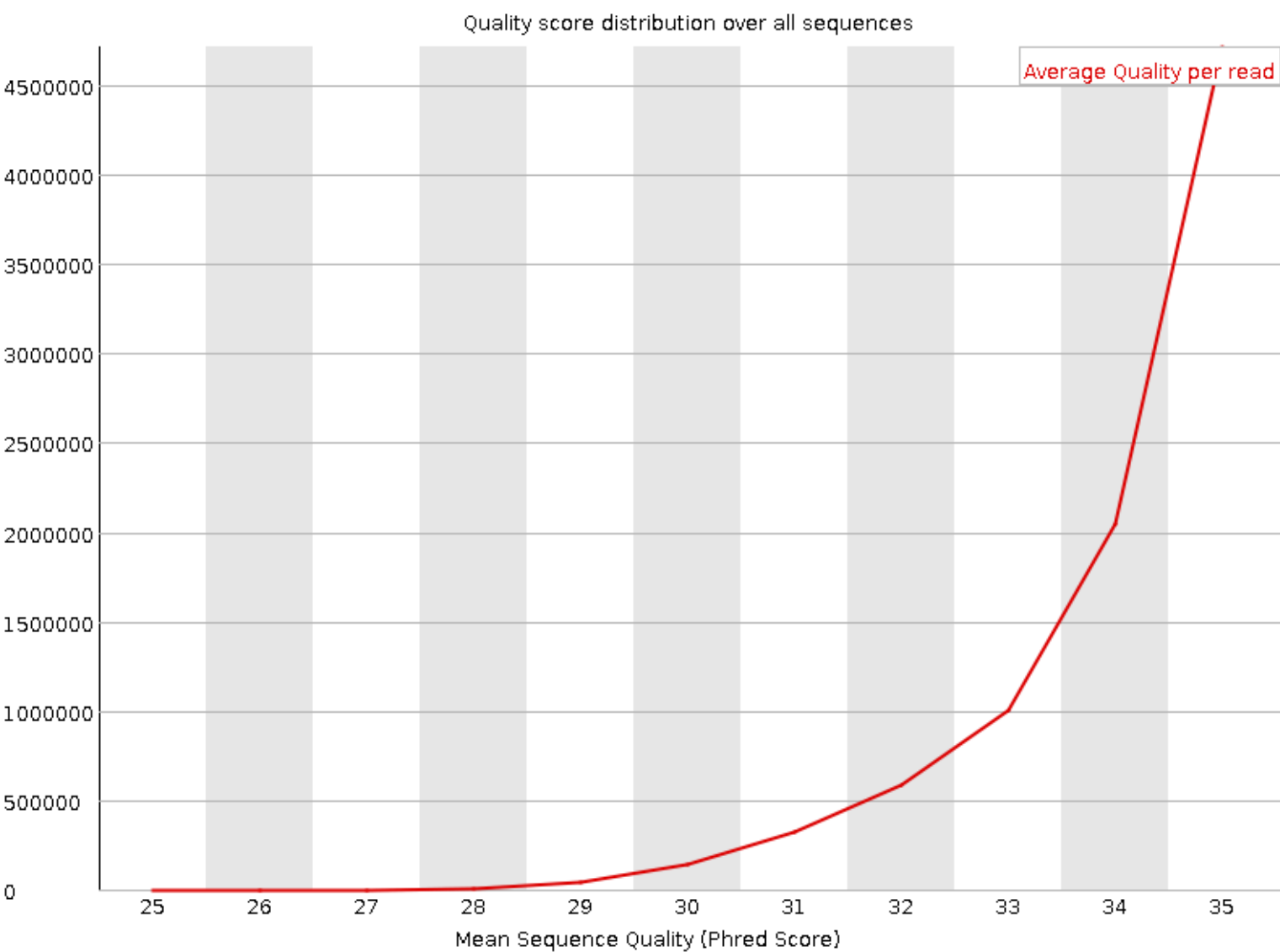




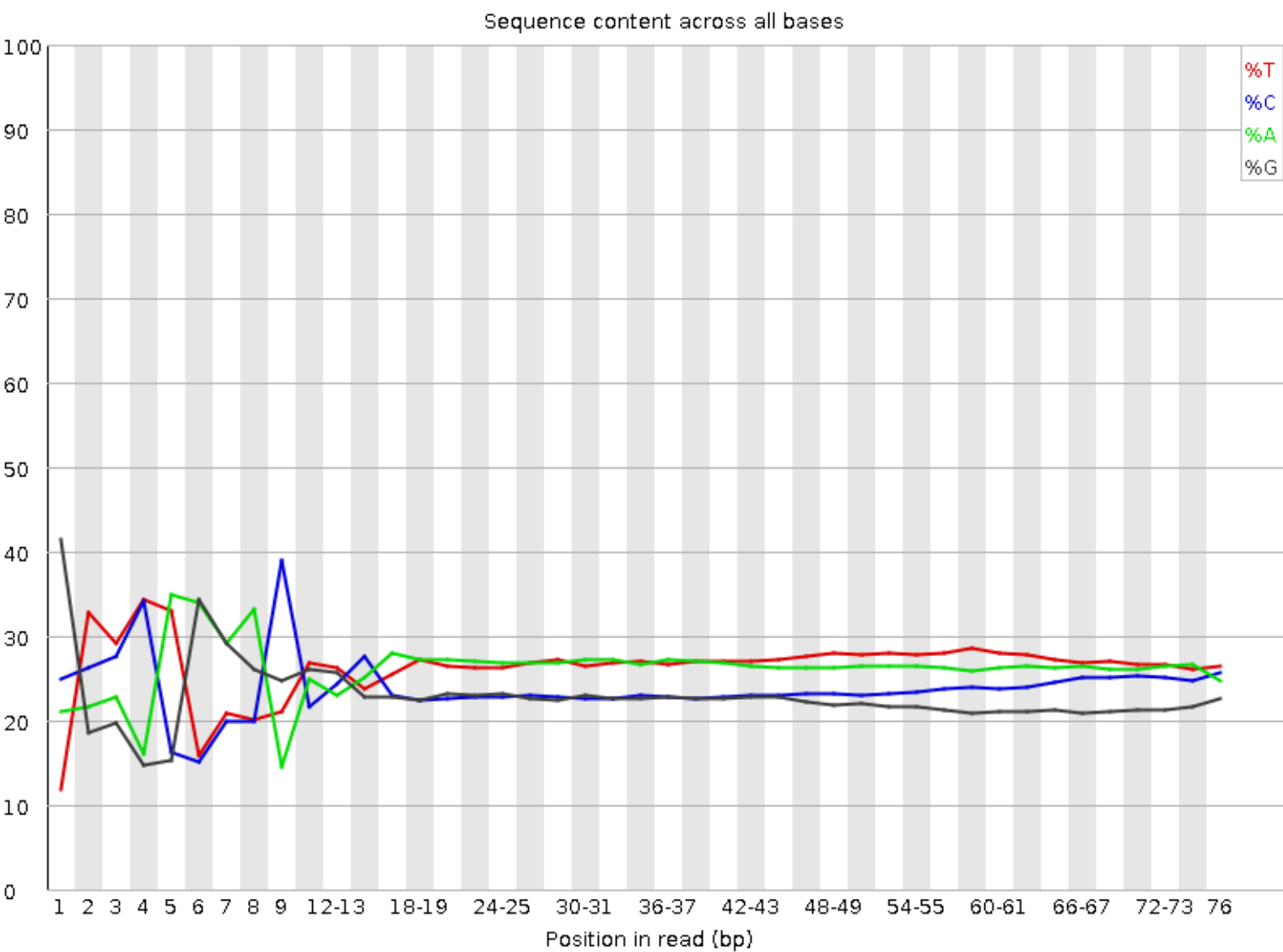
### ✓ Per tile sequence quality



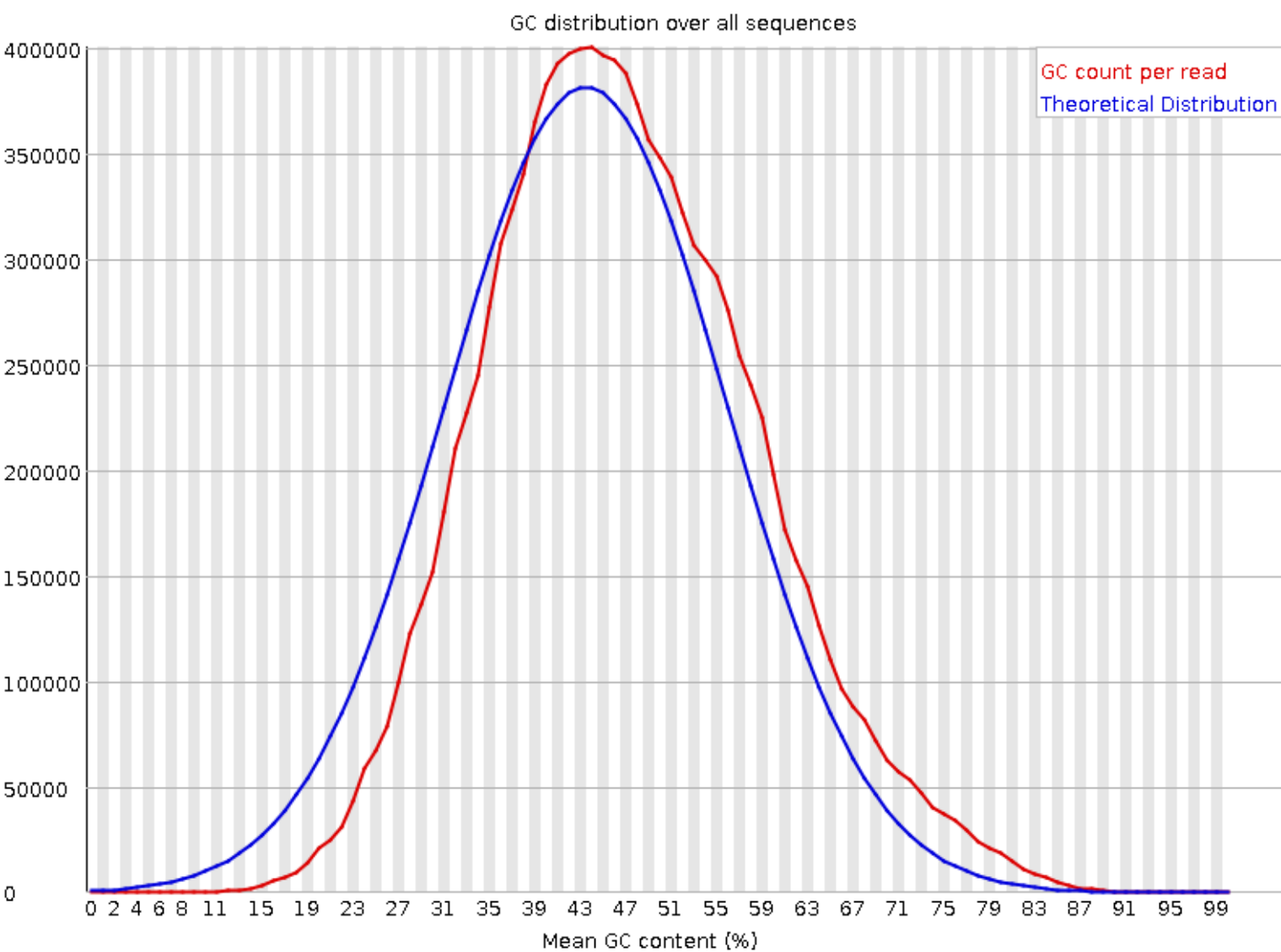
## ✔ Per sequence quality scores



## ! Per base sequence content

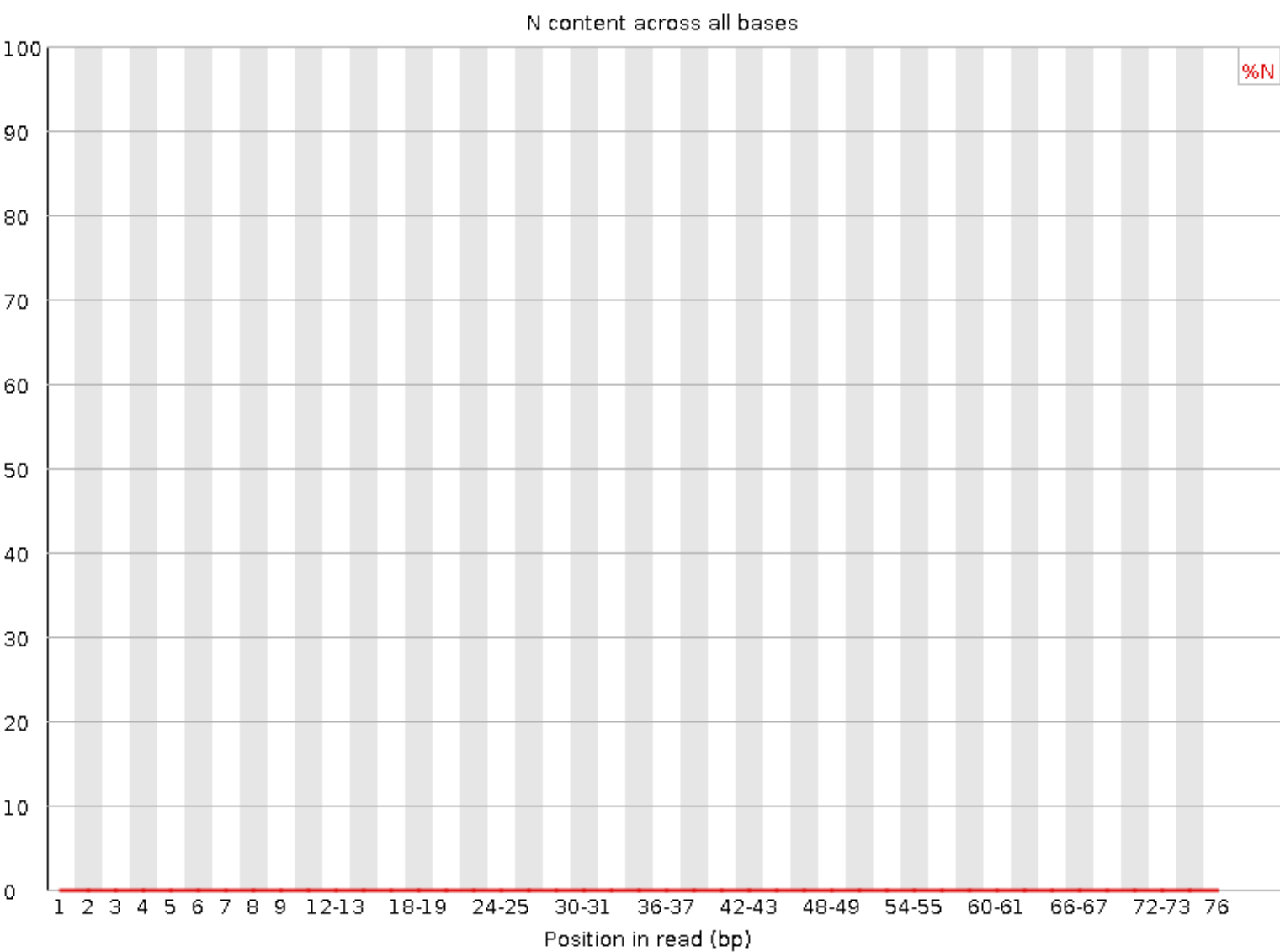


## ! Per sequence GC content

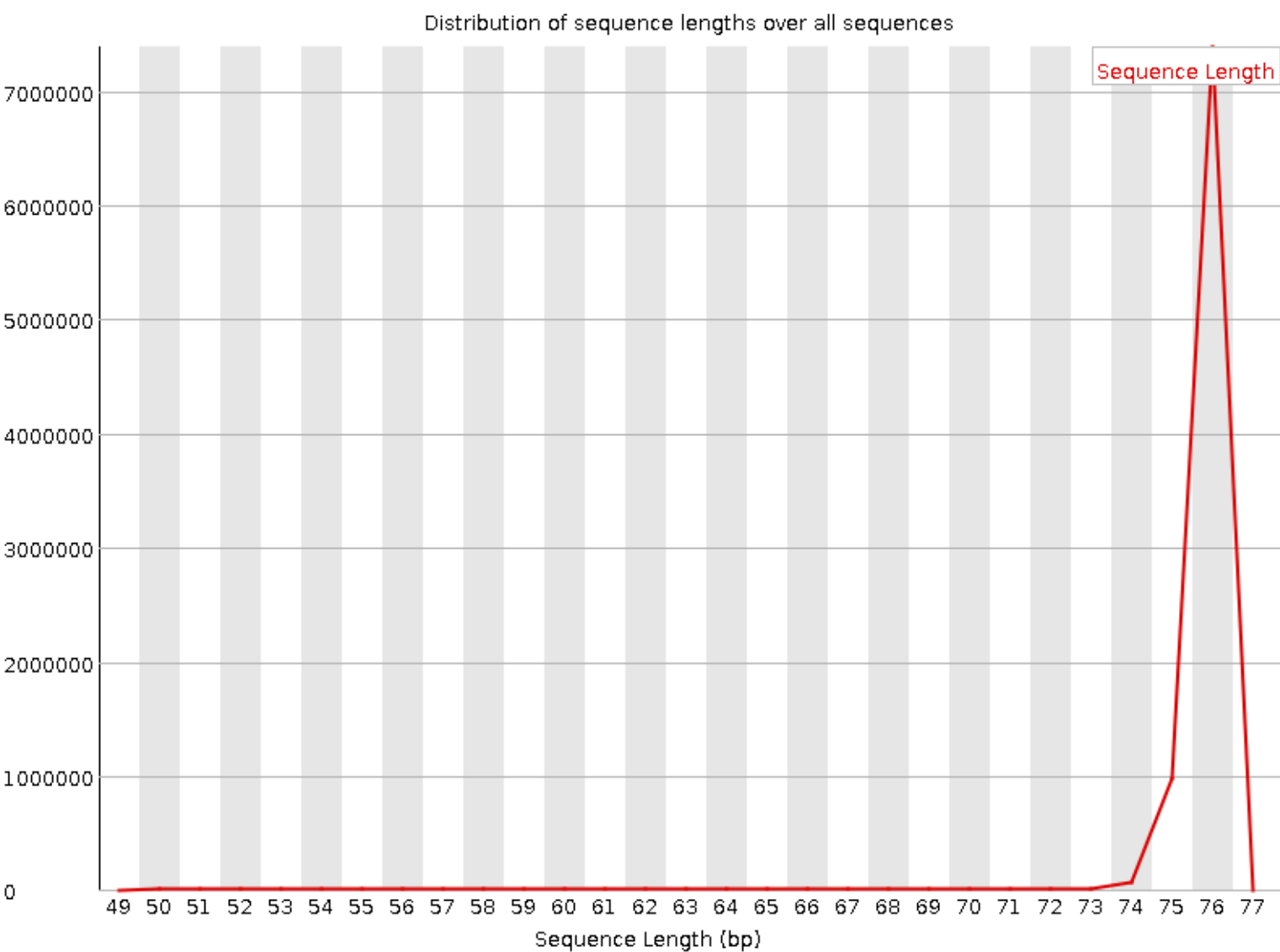




## Per base N content

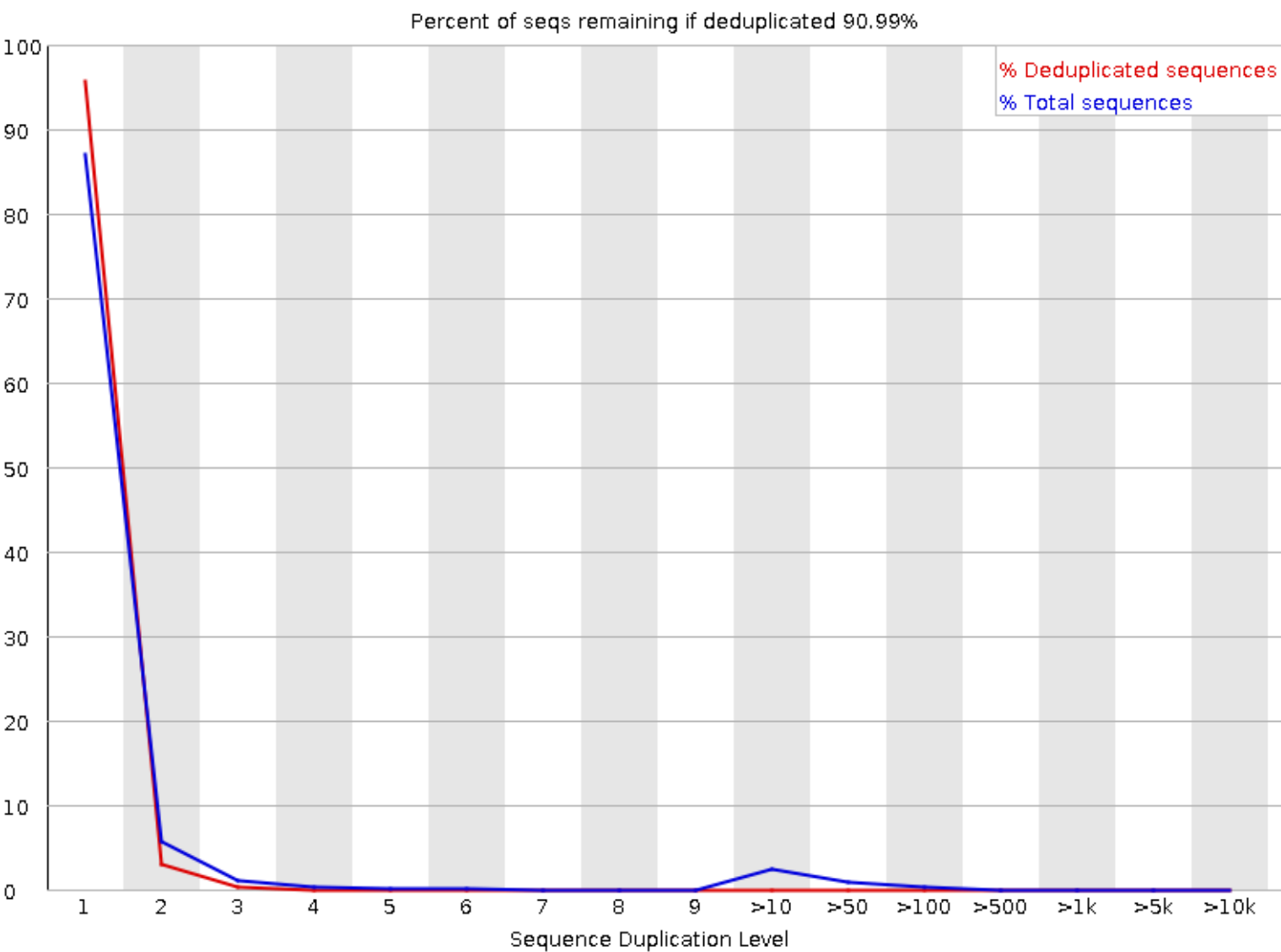


# Sequence Length Distribution





## Sequence Duplication Levels



## Overrepresented sequences

No overrepresented sequences

# Adapter Content

