

FastQC Report

Thu 21 Dec 2017
good_sequence_short.txt

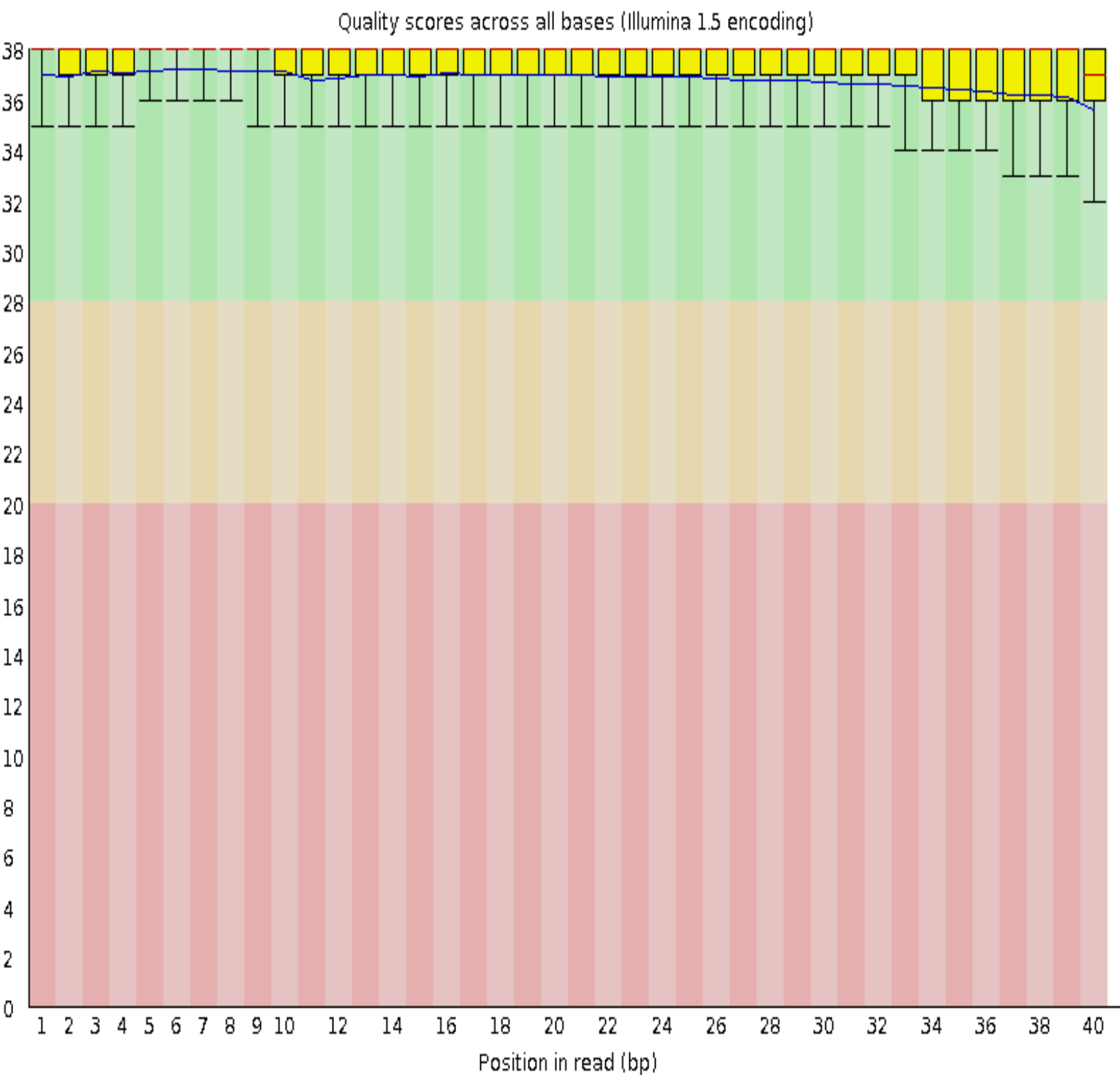
Summary

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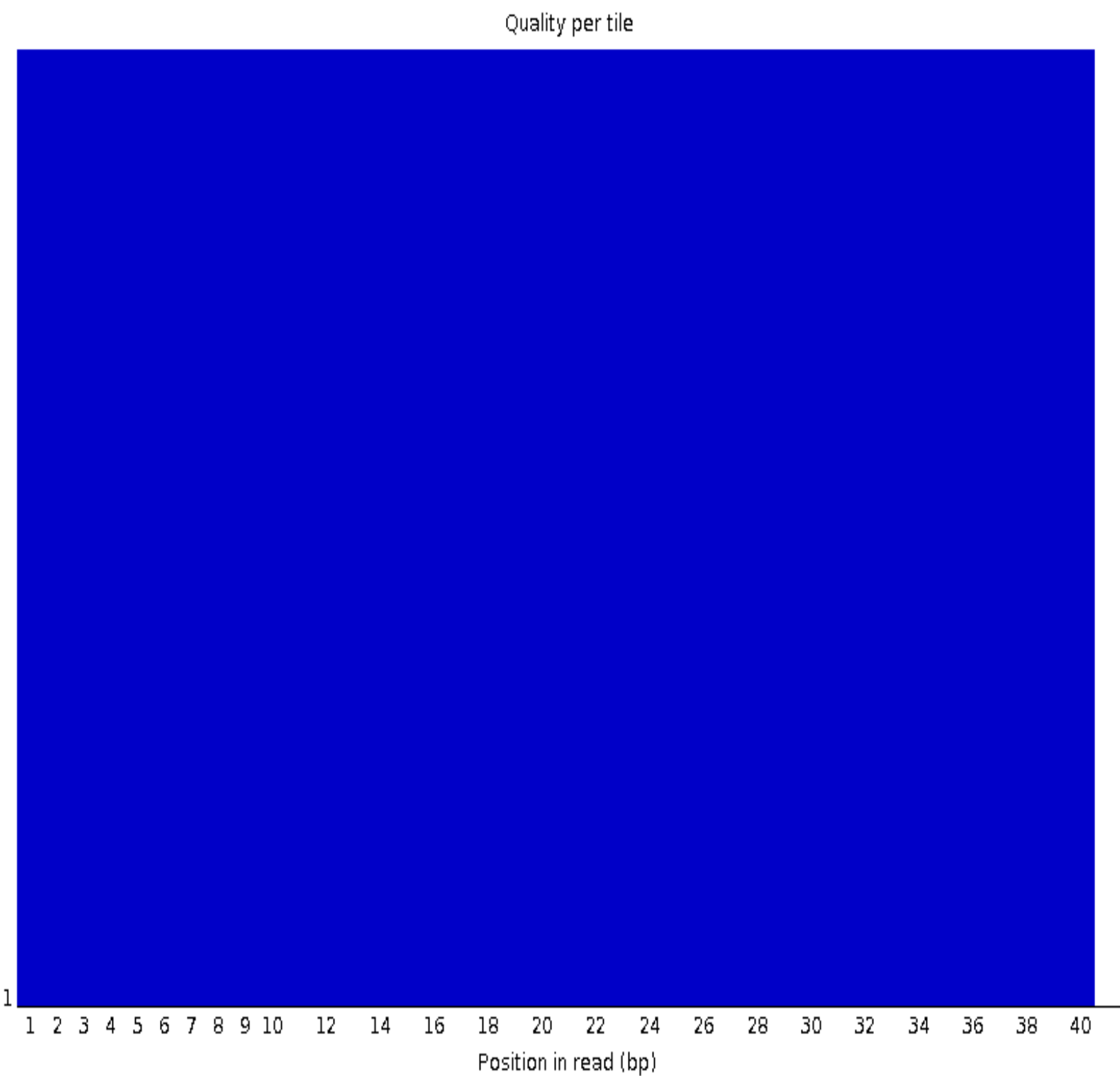
✓ Basic Statistics

Measure	Value
Filename	good_sequence_short.txt
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	250000
Sequences flagged as poor quality	0
Sequence length	40

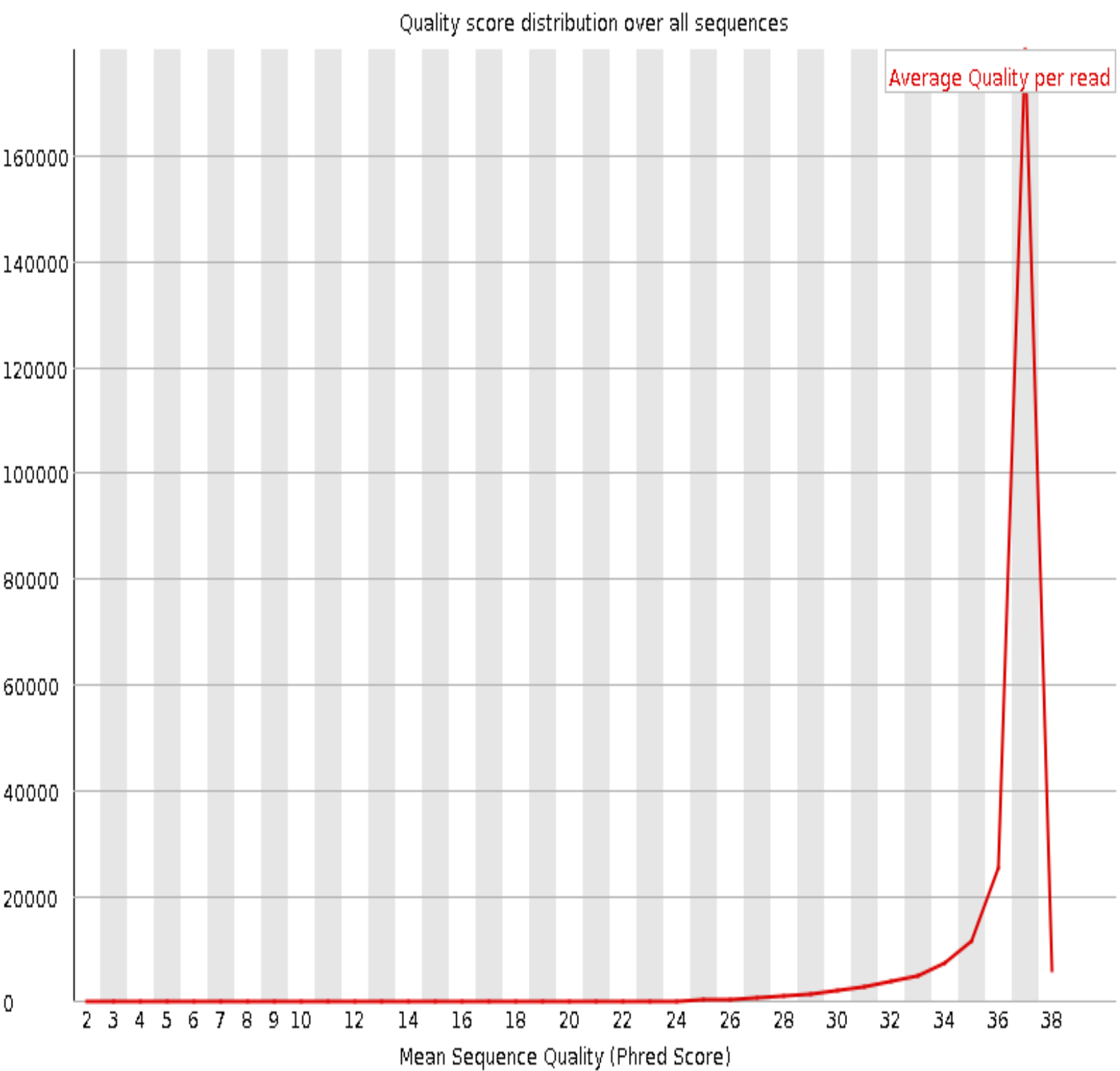
Per base sequence quality



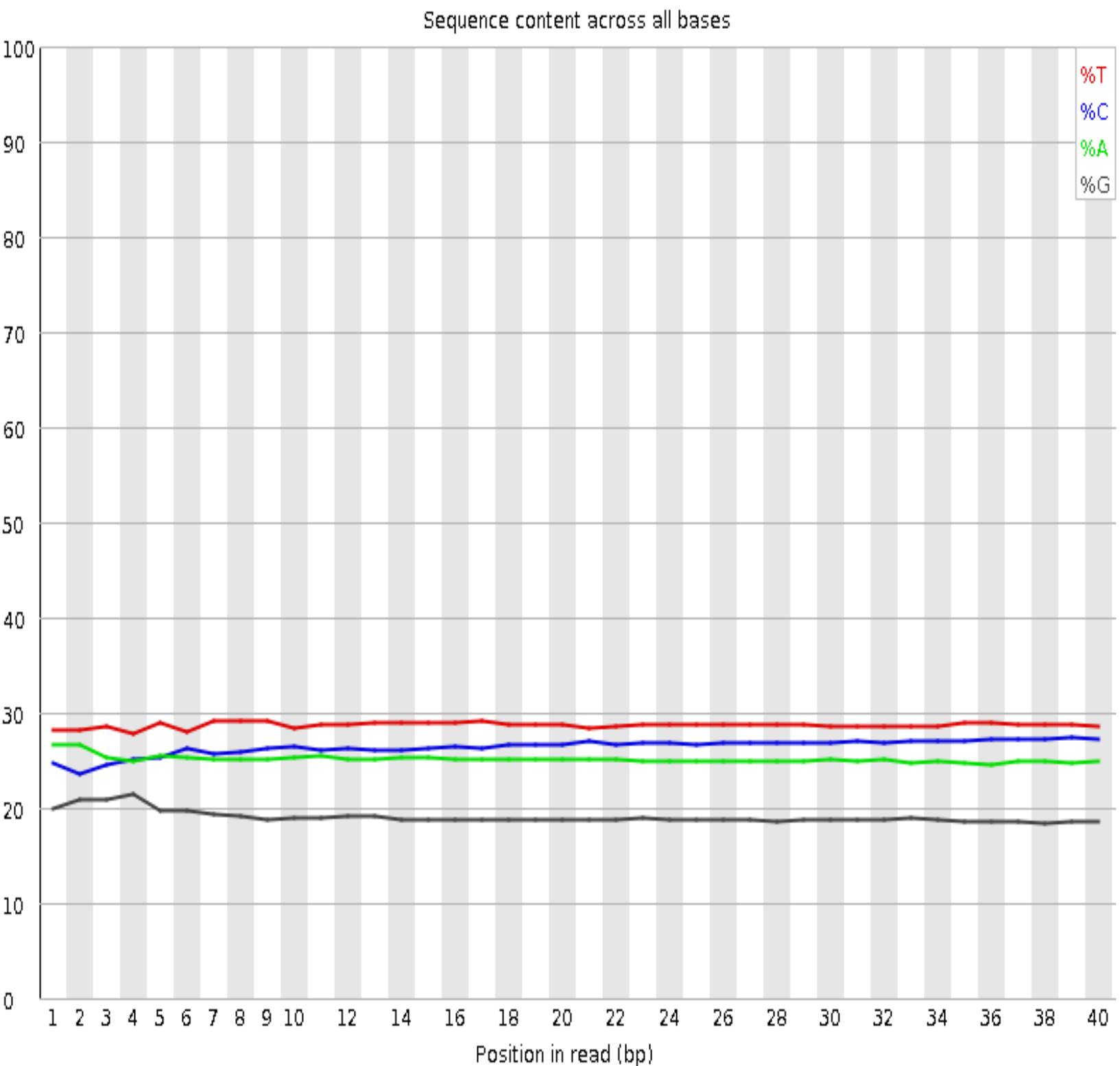
✔ Per tile sequence quality



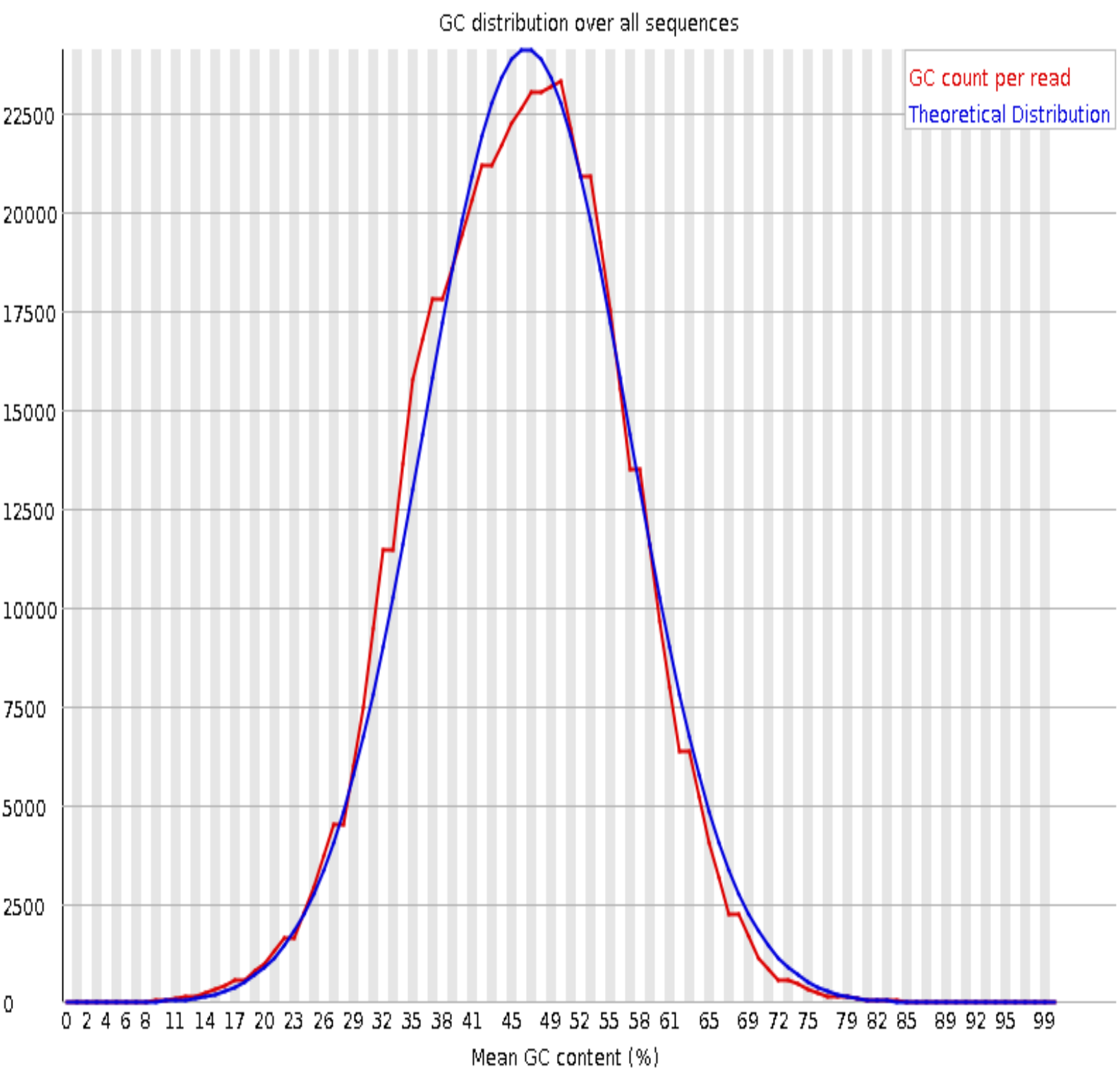
✔ Per sequence quality scores



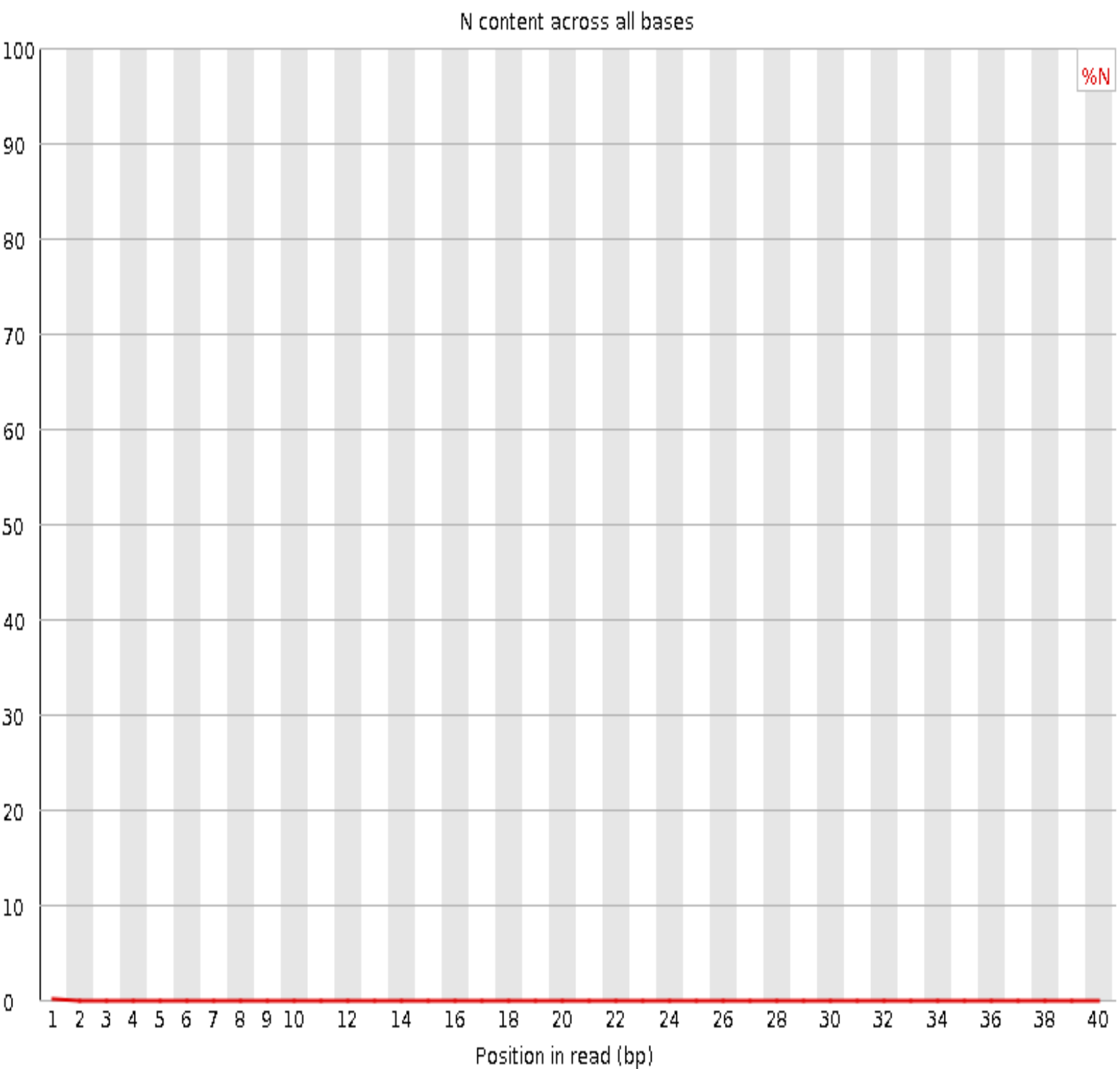
✅ Per base sequence content



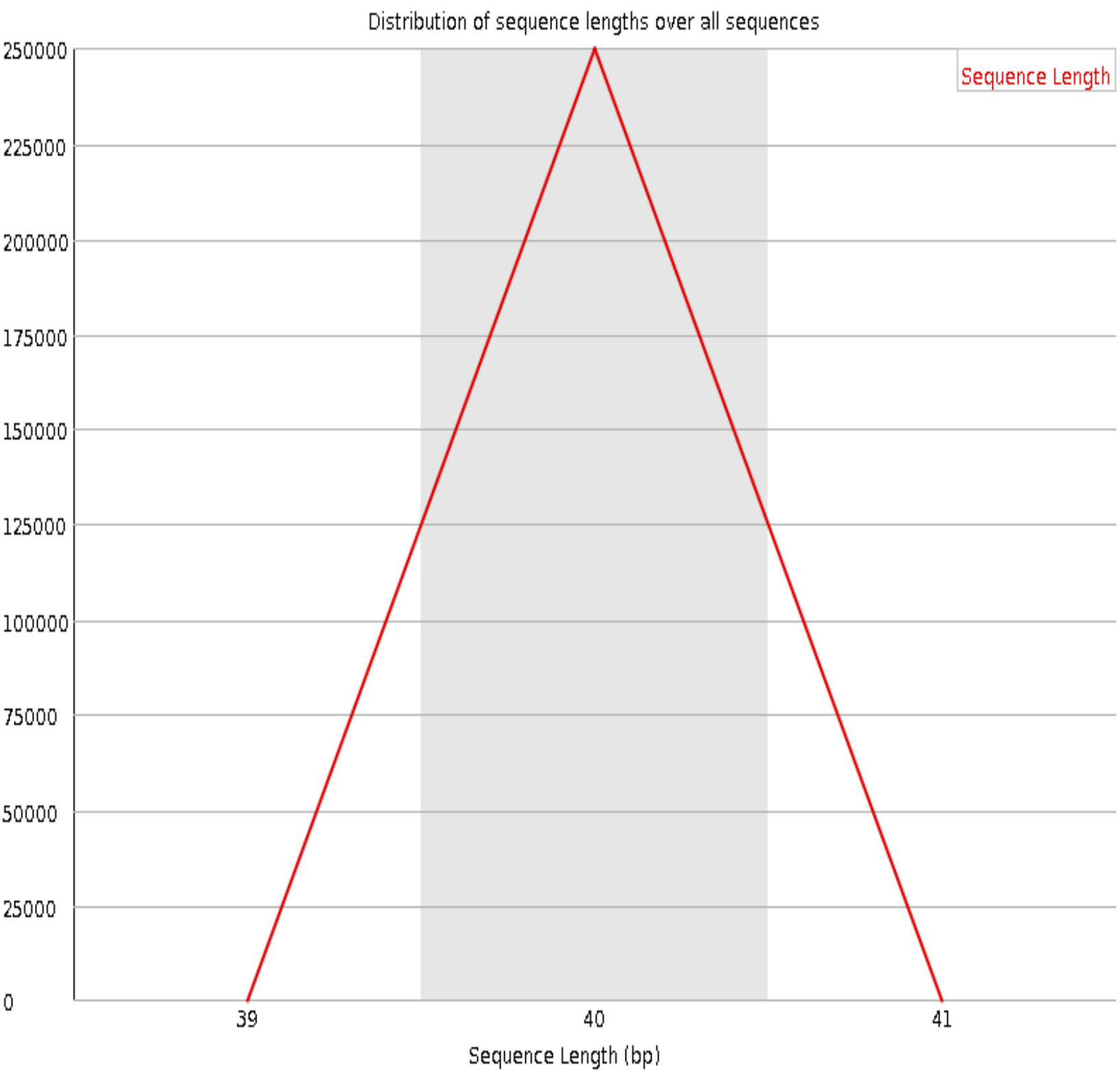
✔ Per sequence GC content



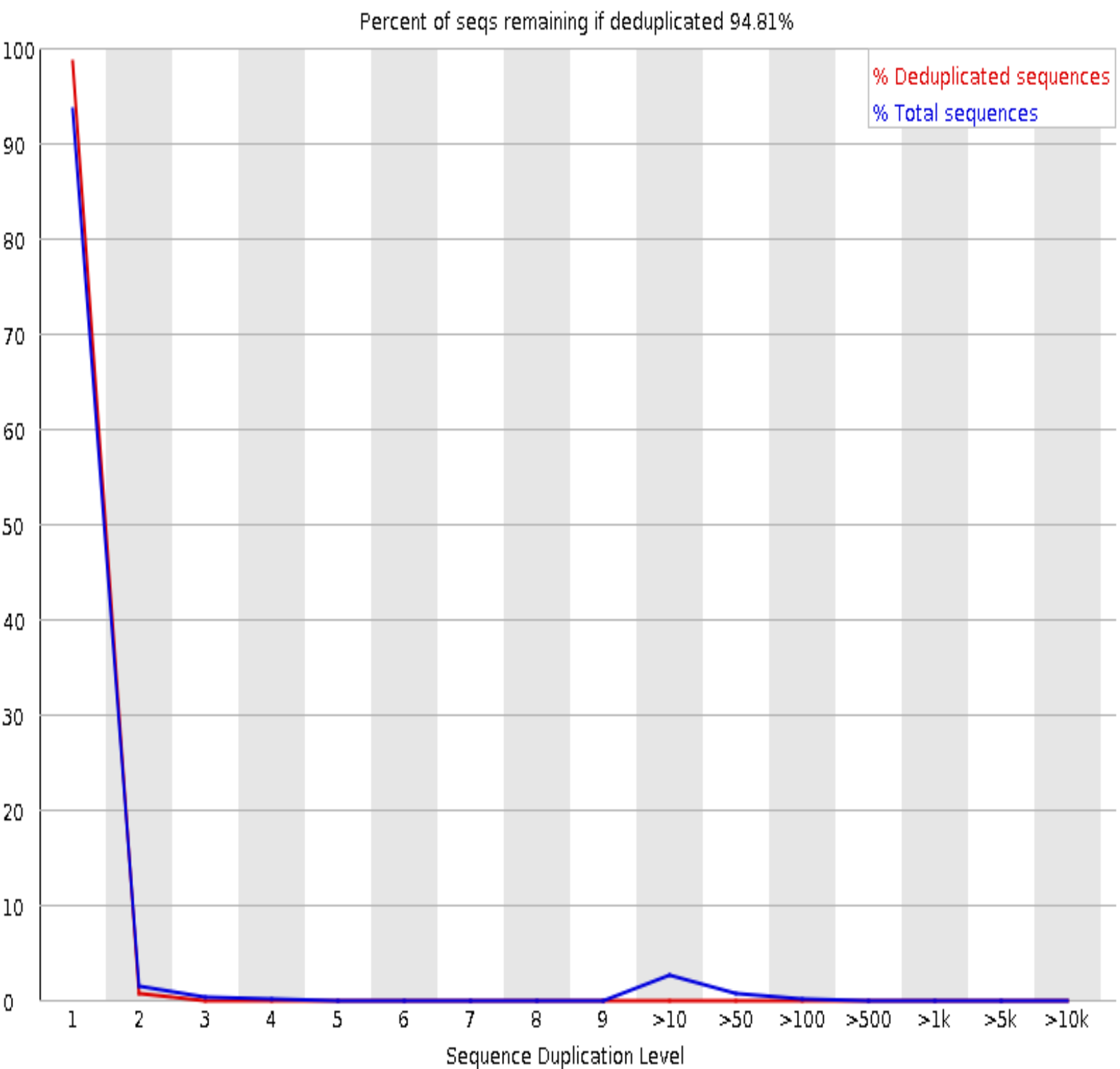
Per base N content



✔ Sequence Length Distribution



✔ Sequence Duplication Levels



 **Overrepresented sequences**
No overrepresented sequences



Adapter Content

