












FastQC Report

Summary

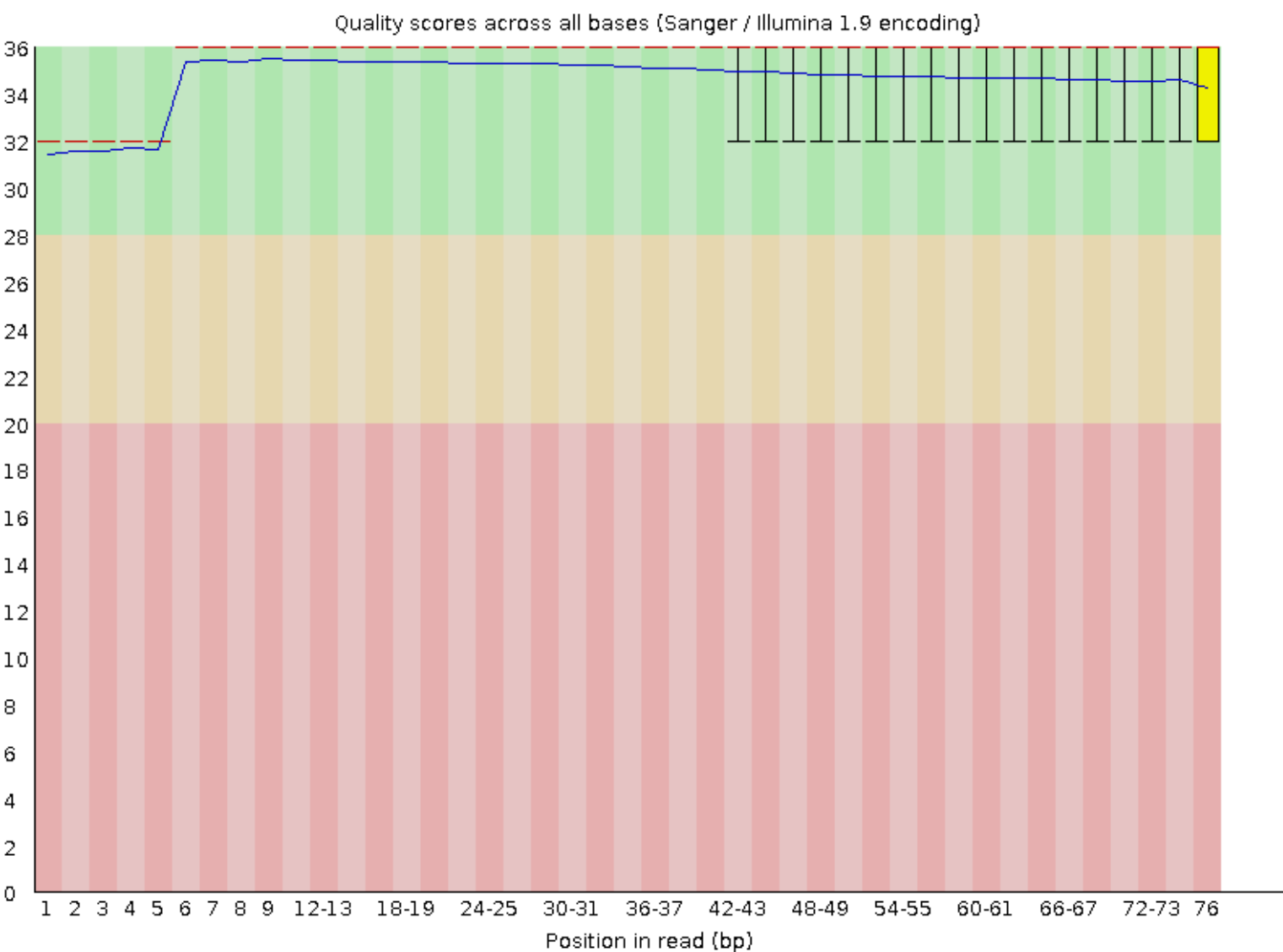
Mon 3 Mar 2025
ERR13985875_2_paired.fastq

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Basic Statistics

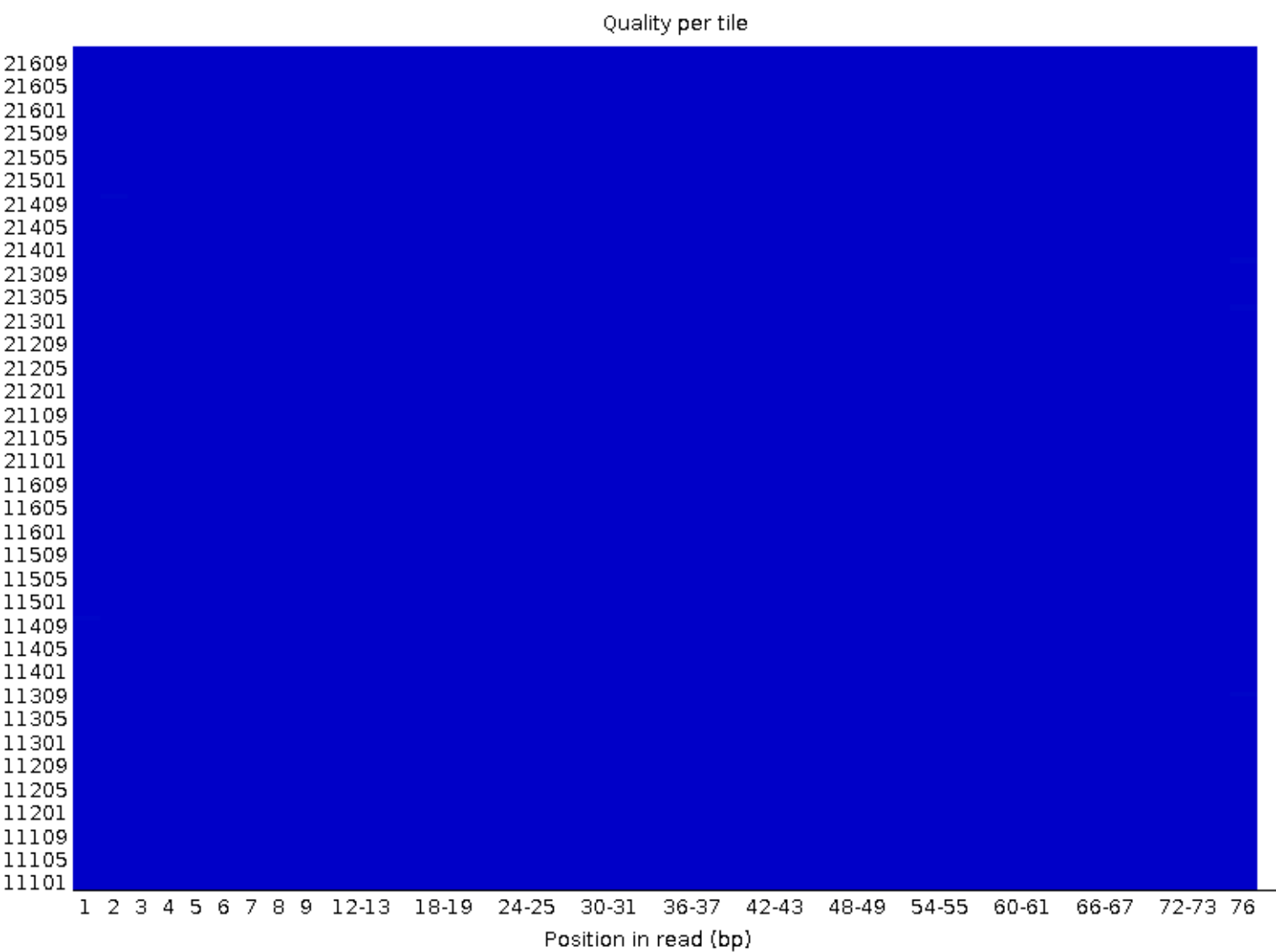
Measure	Value
Filename	ERR13985875_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	8902949
Sequences flagged as poor quality	0
Sequence length	50-76
%GC	46

Per base sequence quality

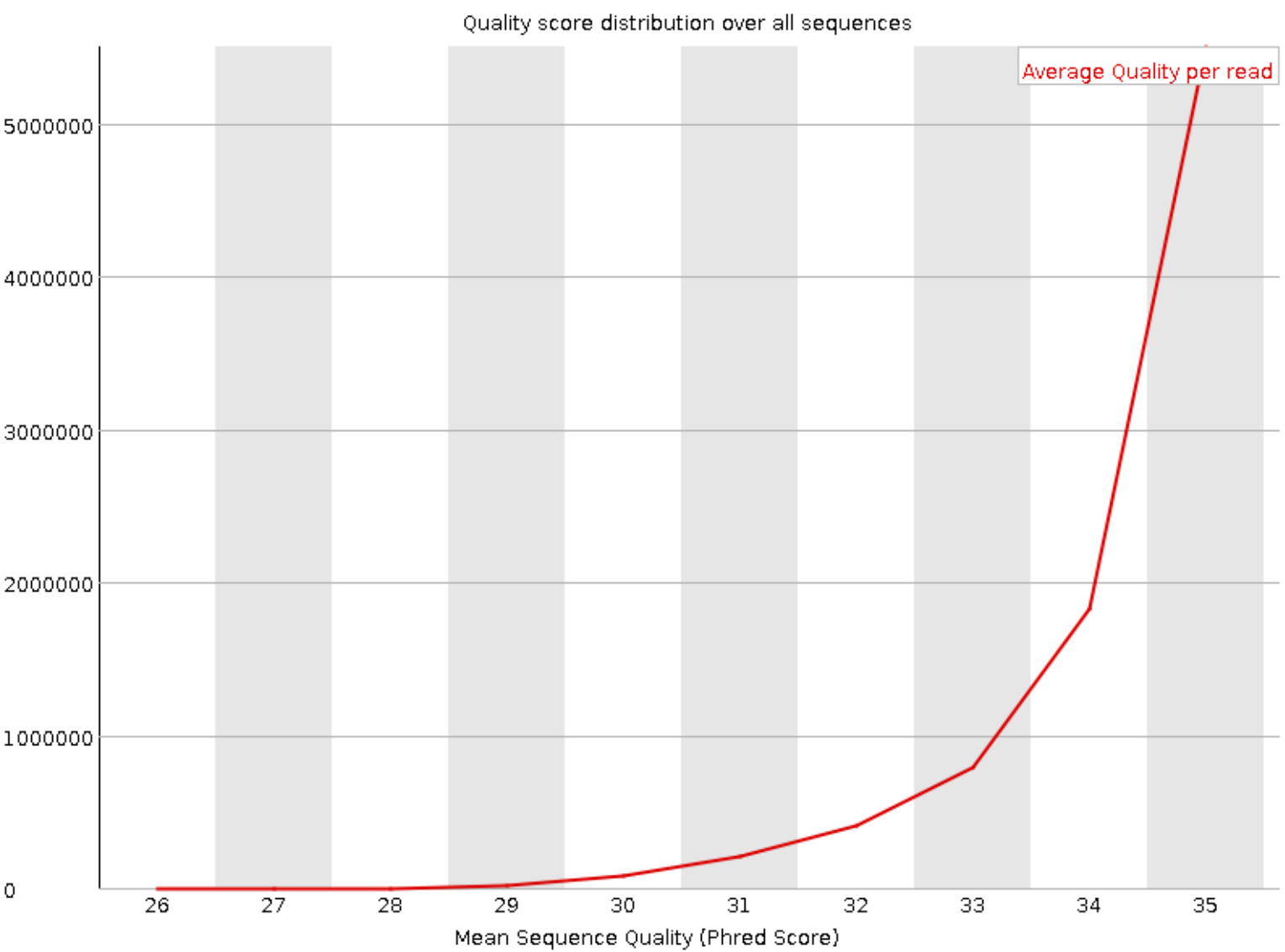




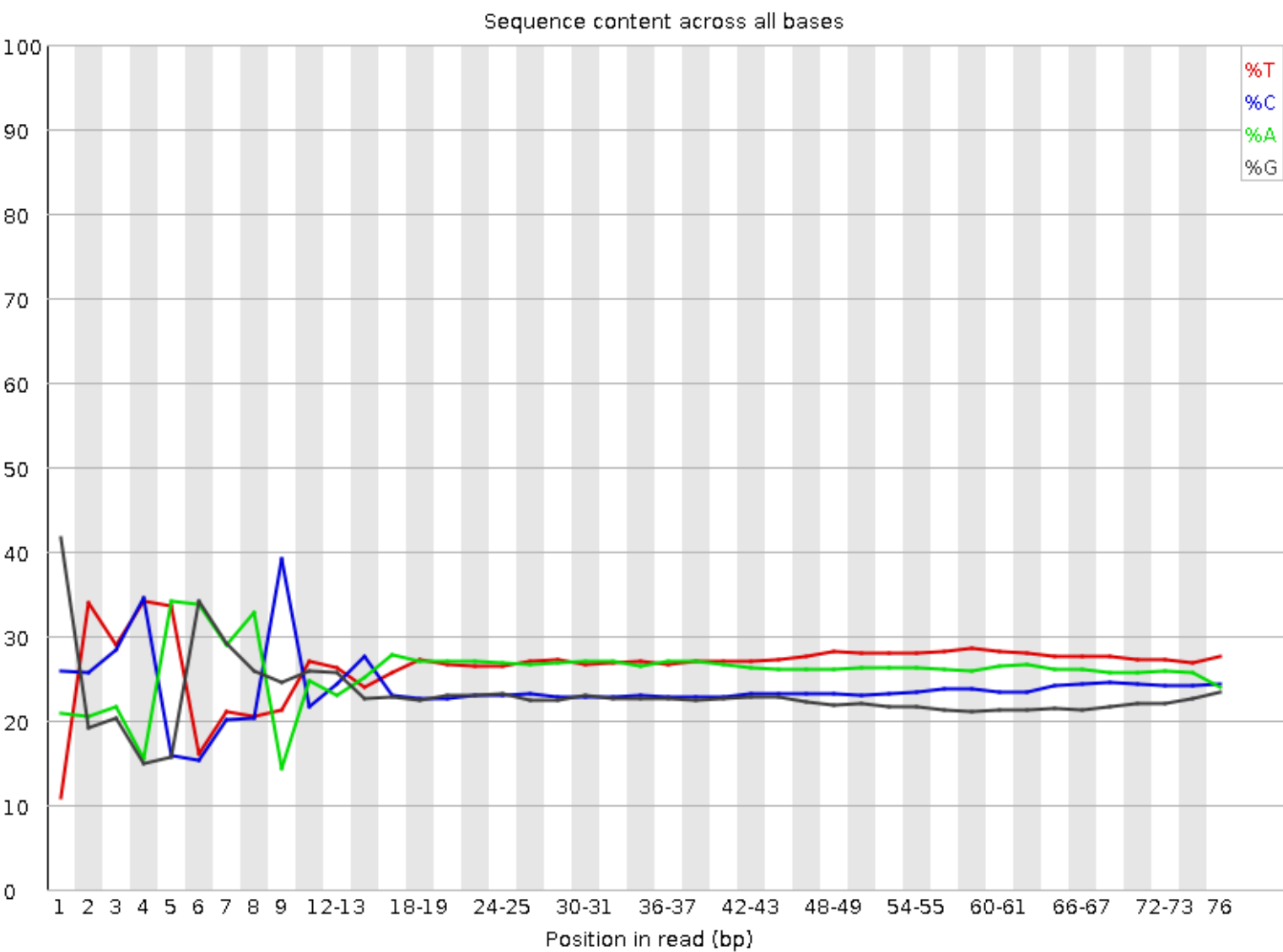
✓ Per tile sequence quality



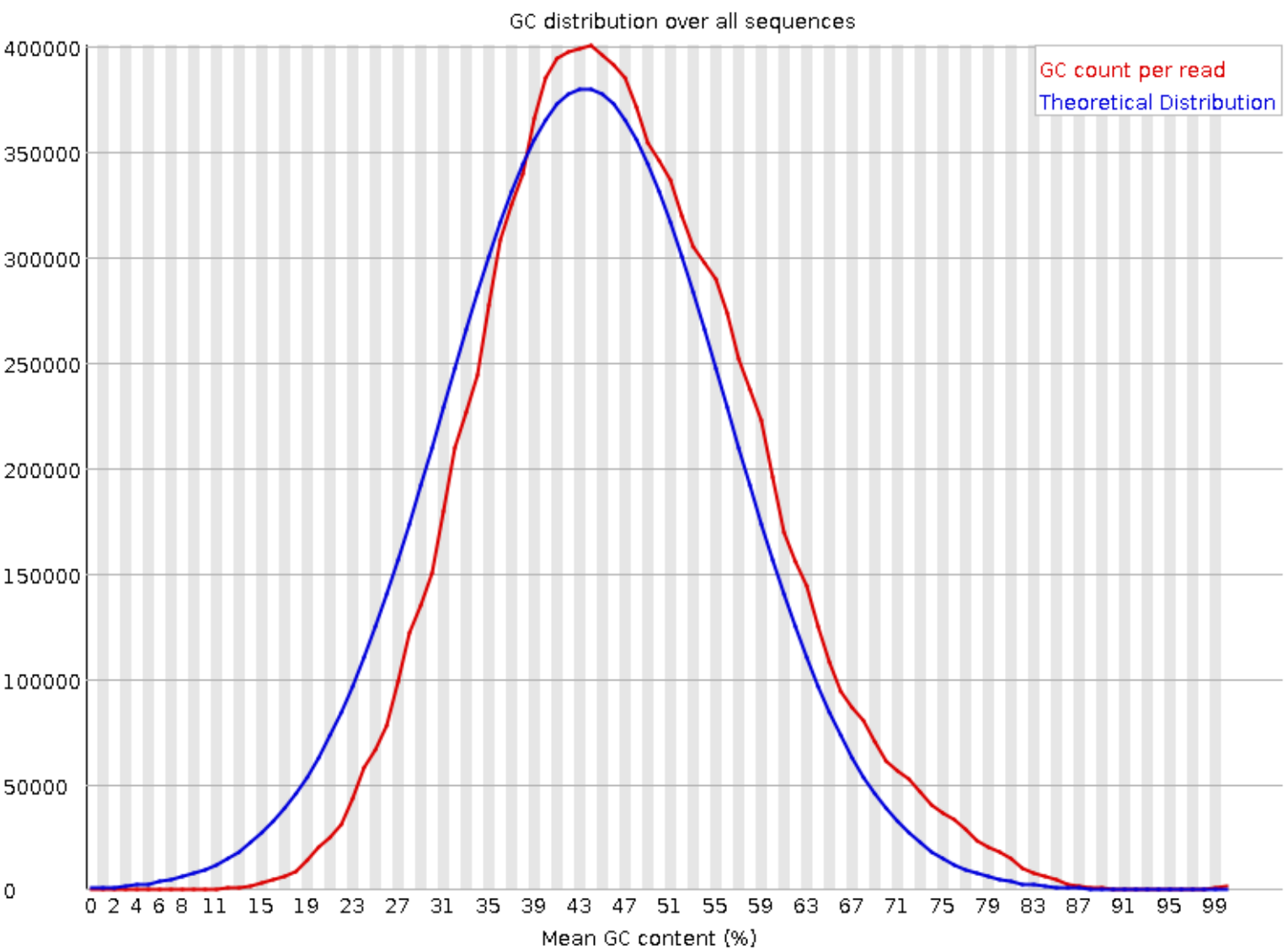
✔ Per sequence quality scores



! Per base sequence content

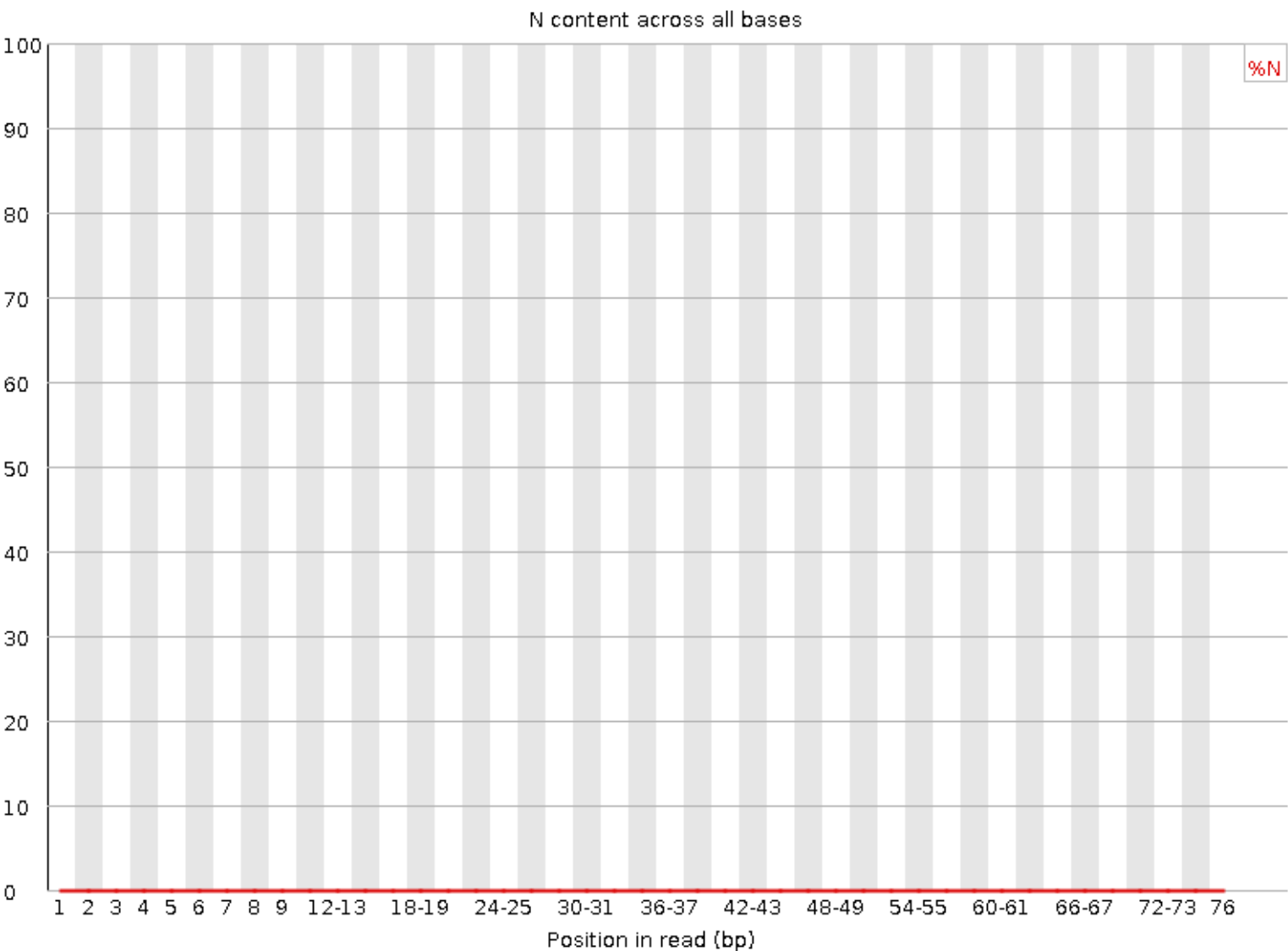


🚨 Per sequence GC content

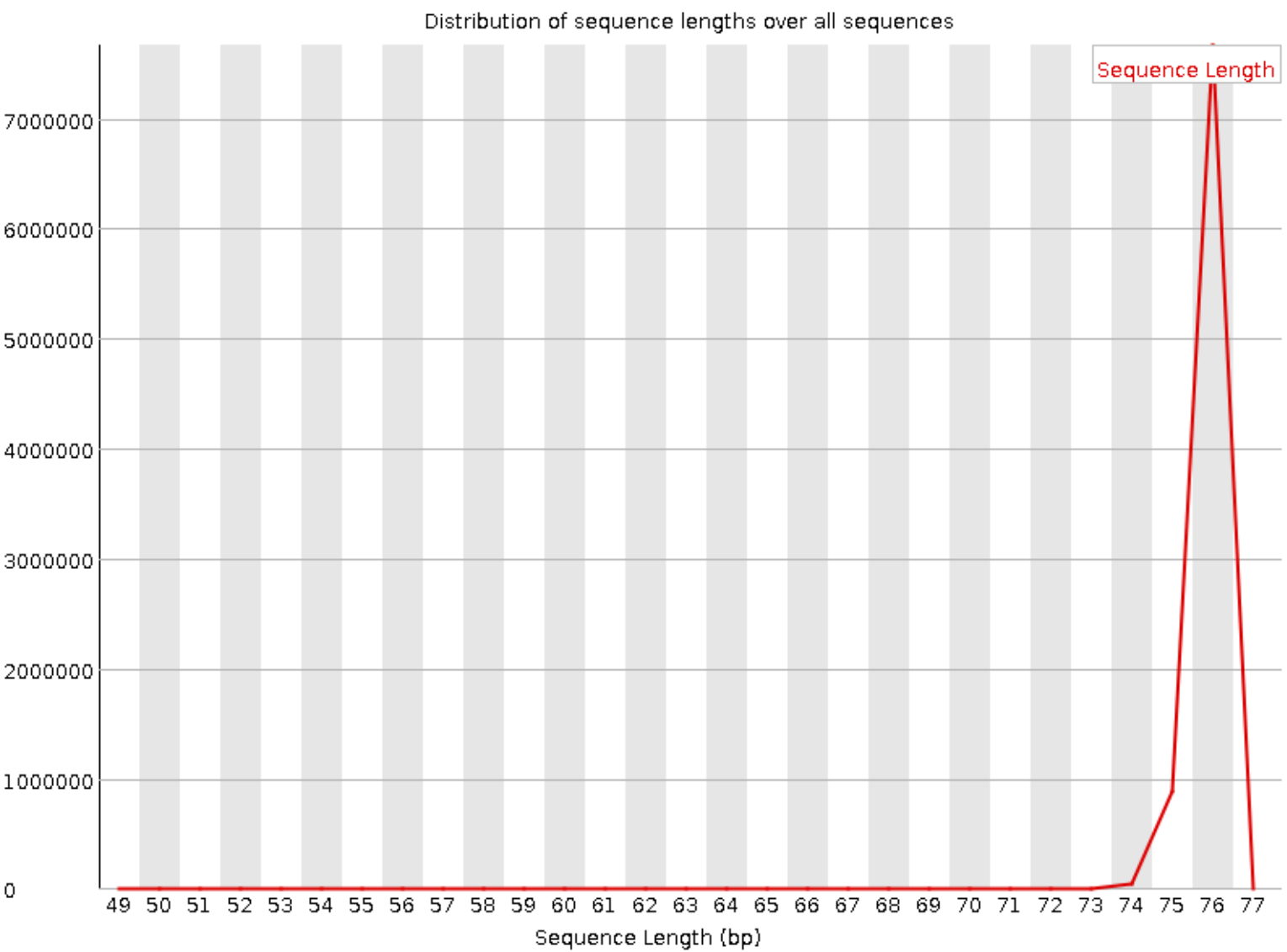




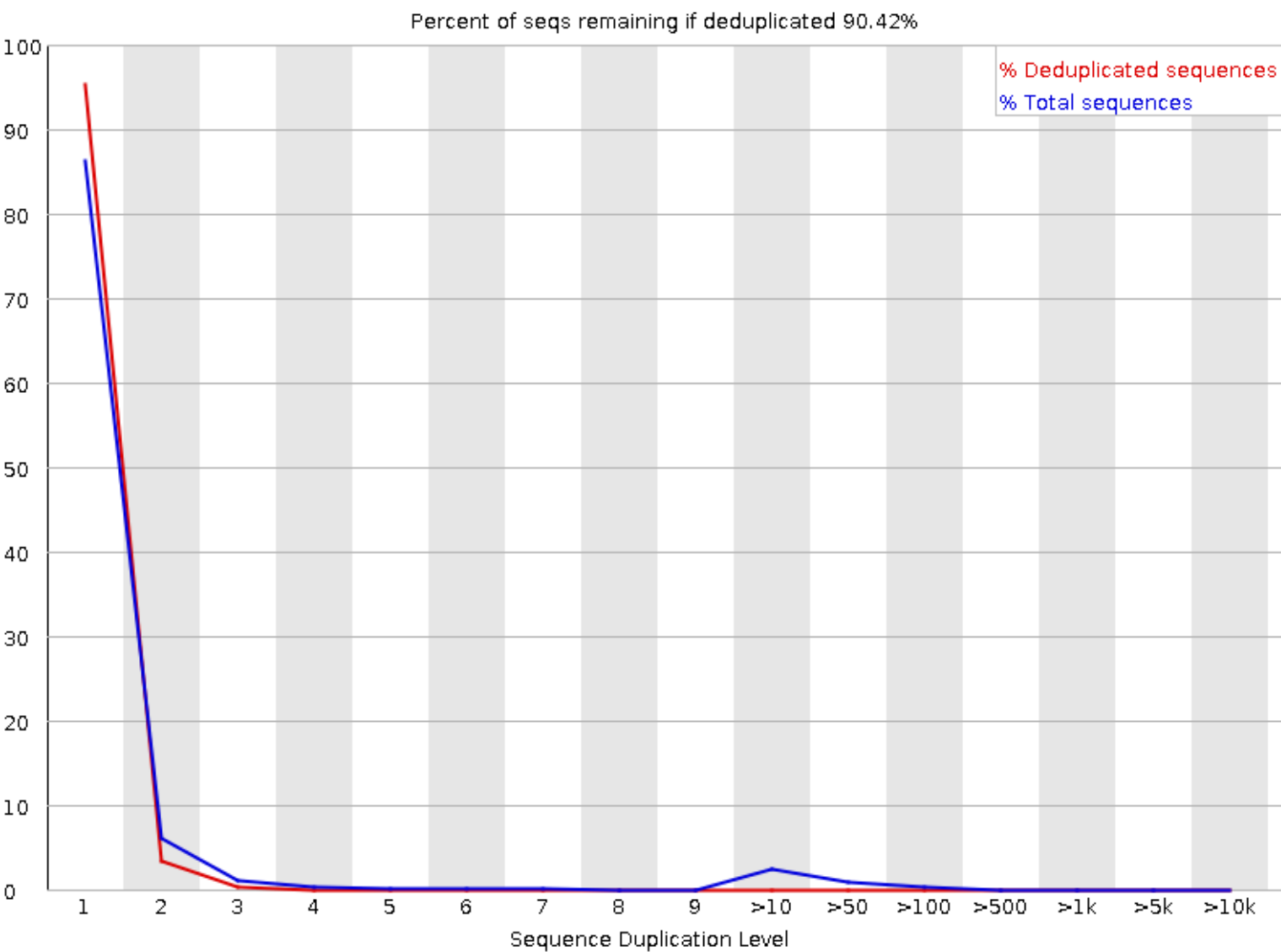
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content

