













FastQC Report

Summary

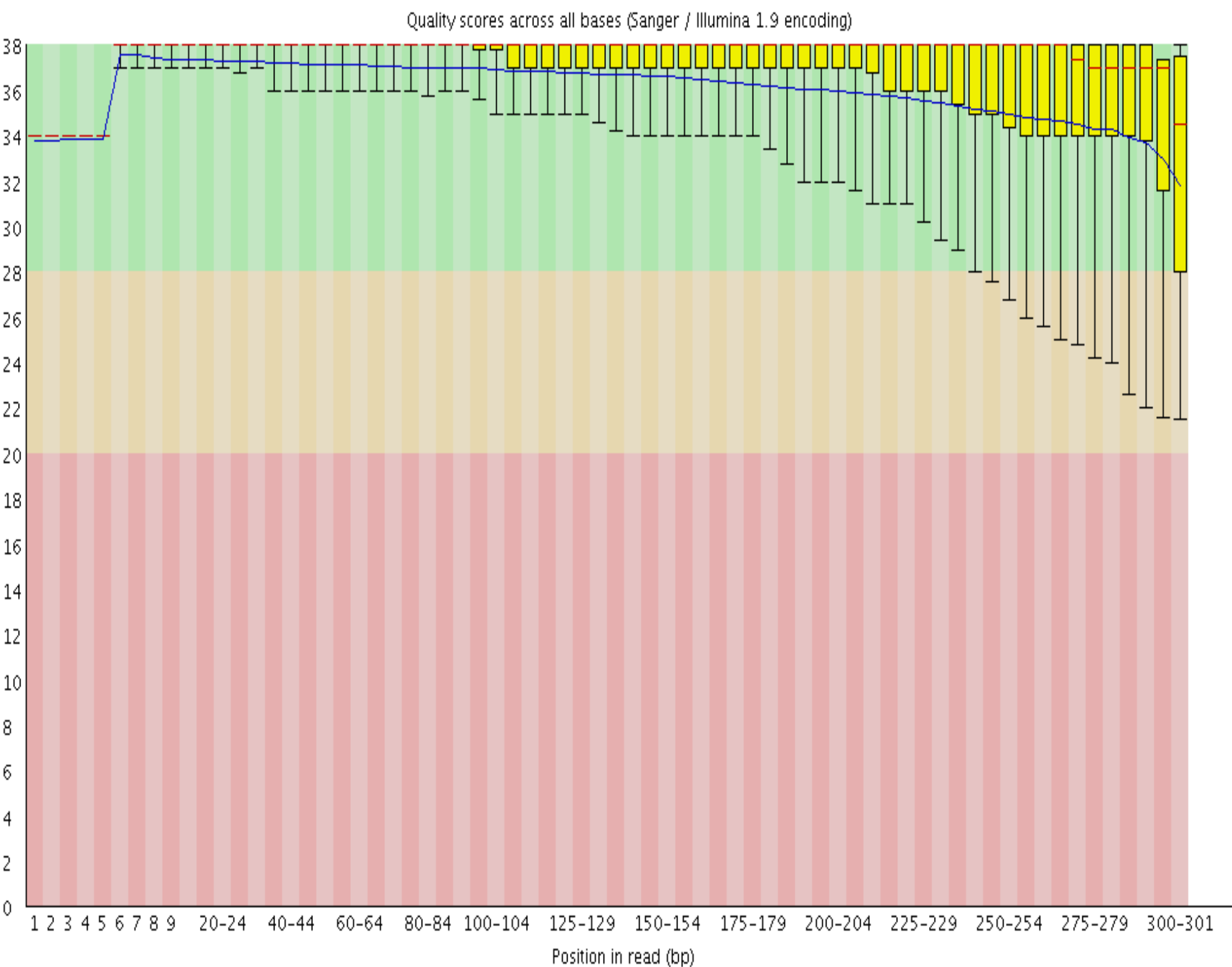
Fri 26 Apr 2019
output_R1_paired.fq.gz

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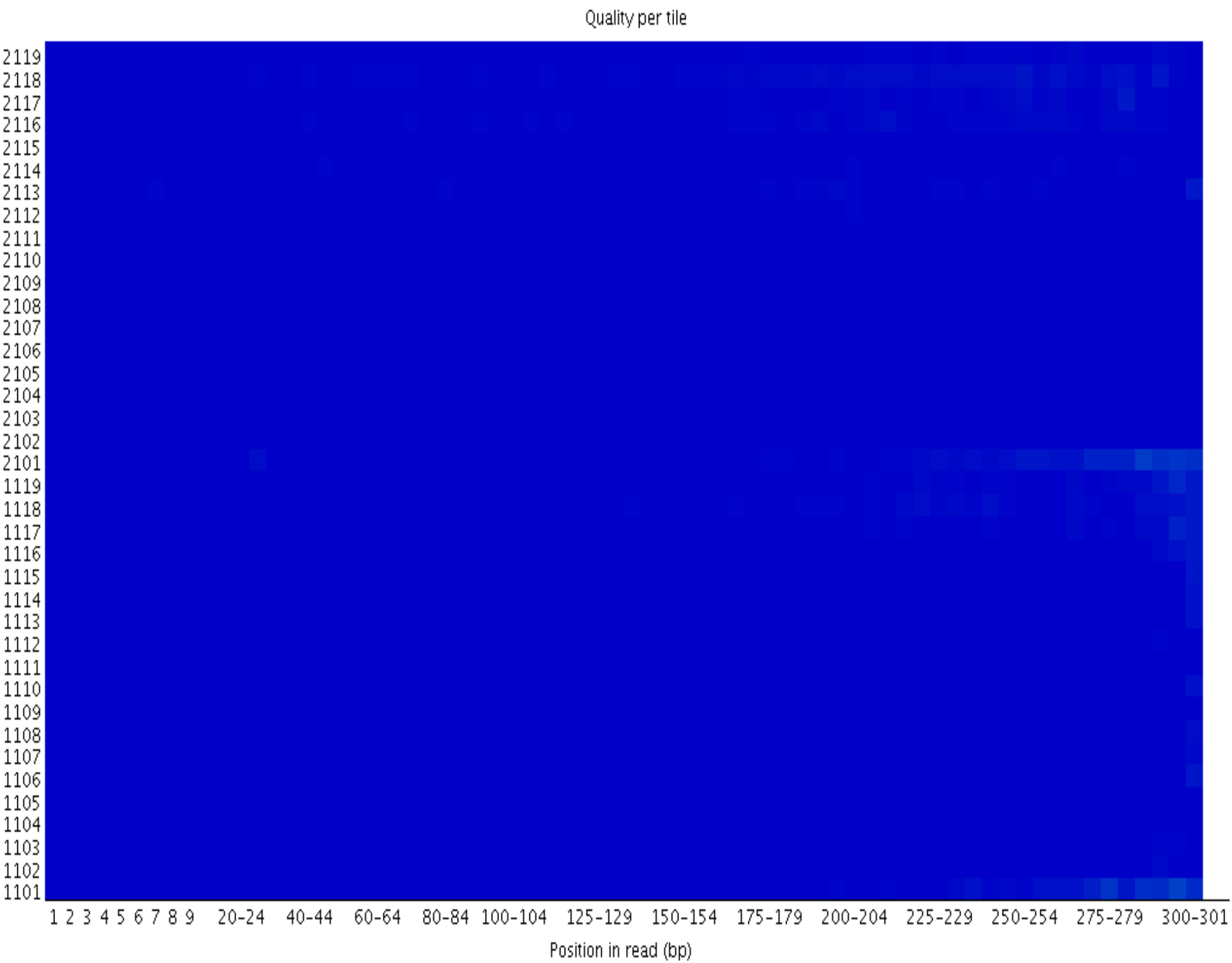
Basic Statistics

Measure	Value
Filename	output_R1_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2503029
Sequences flagged as poor quality	0
Sequence length	36–301
%GC	36

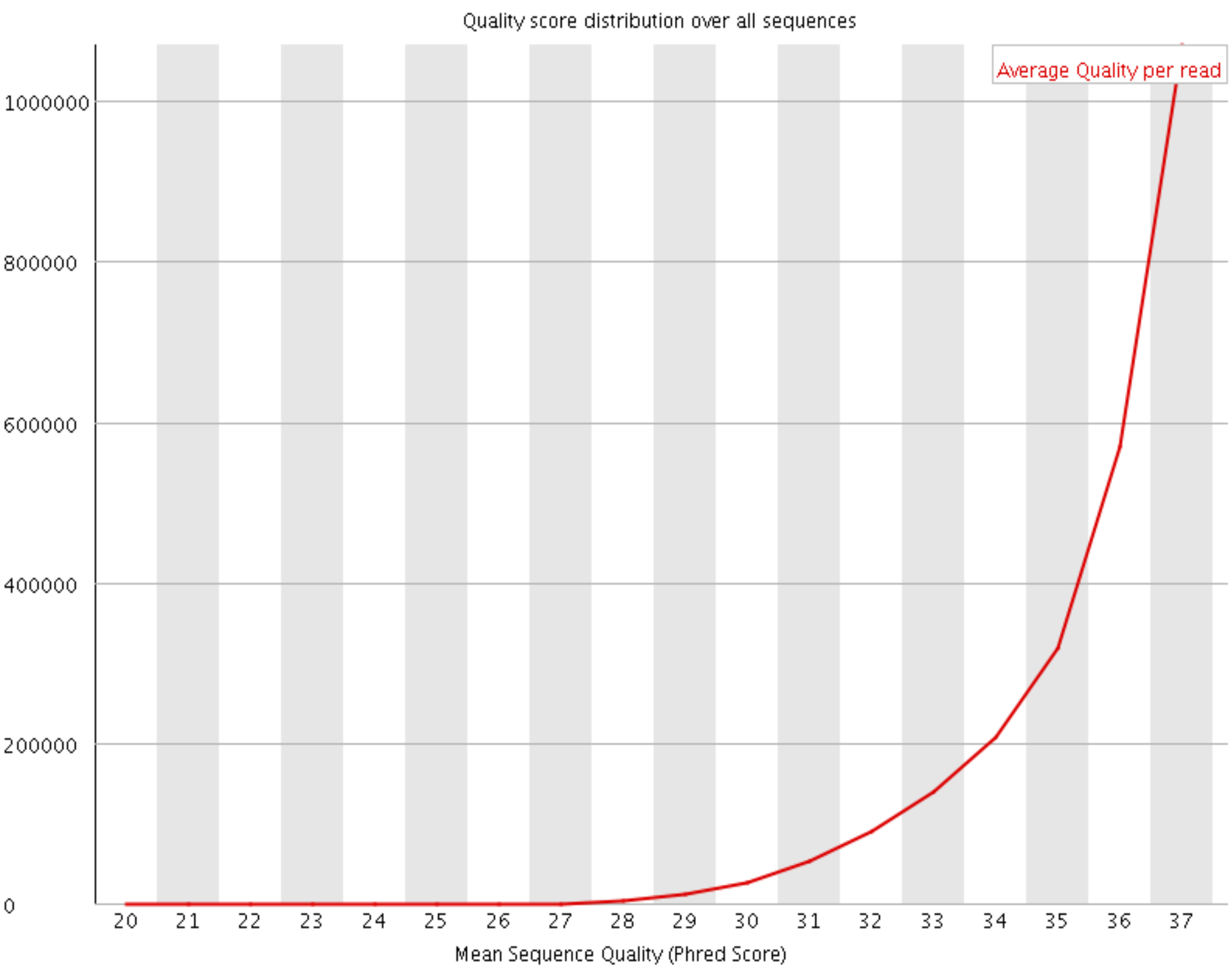
✔ Per base sequence quality



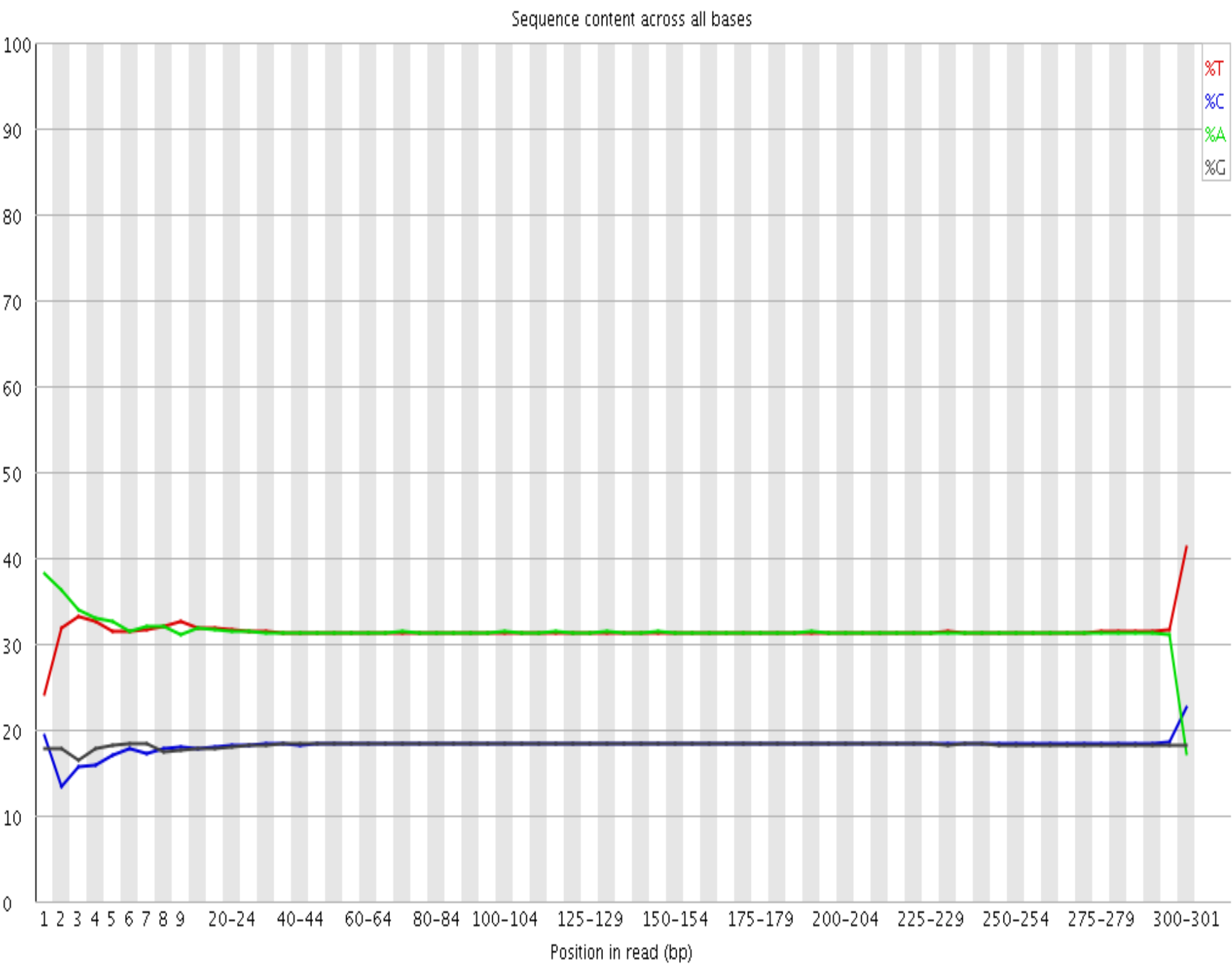
✔ Per tile sequence quality



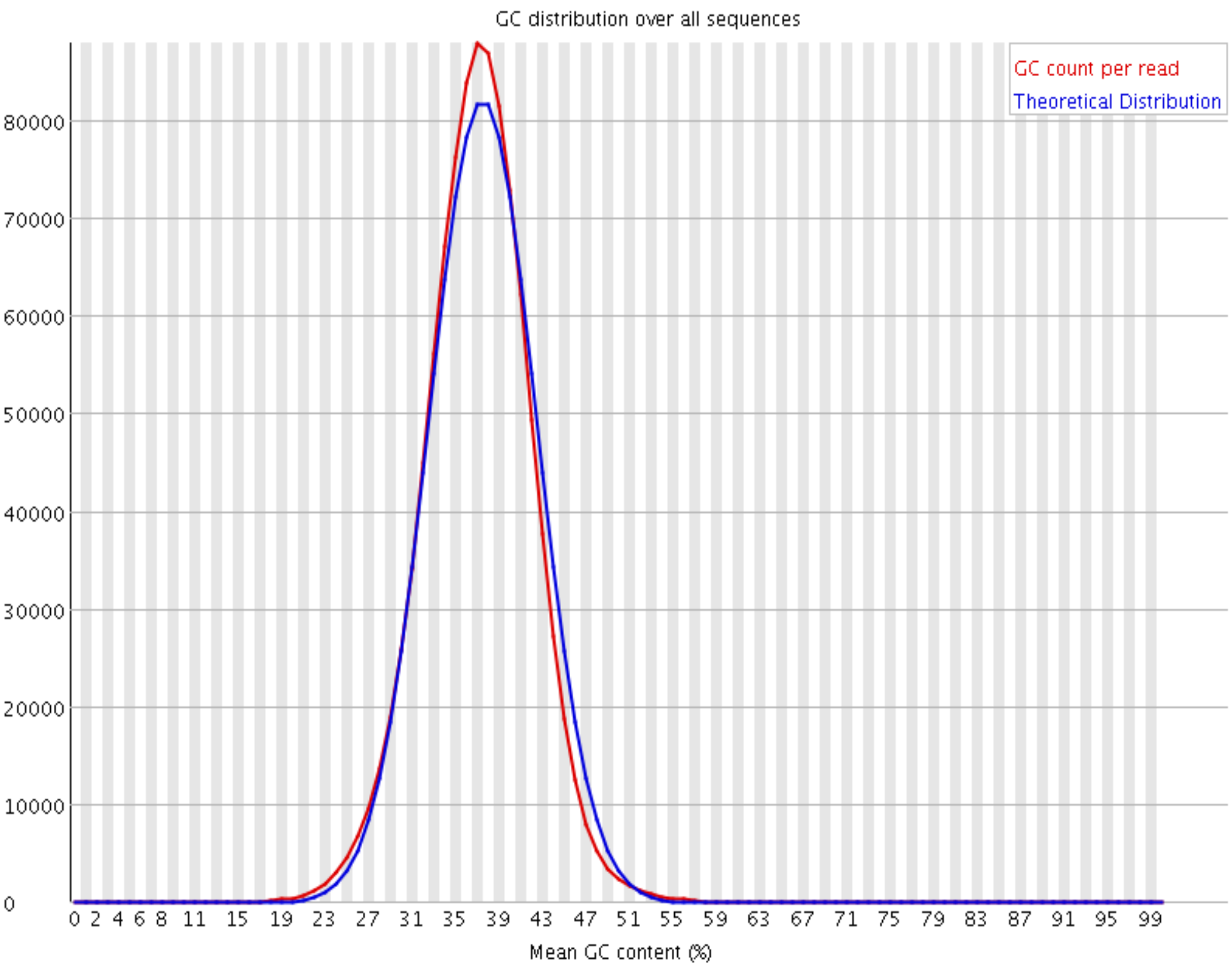
✔ **Per sequence quality scores**



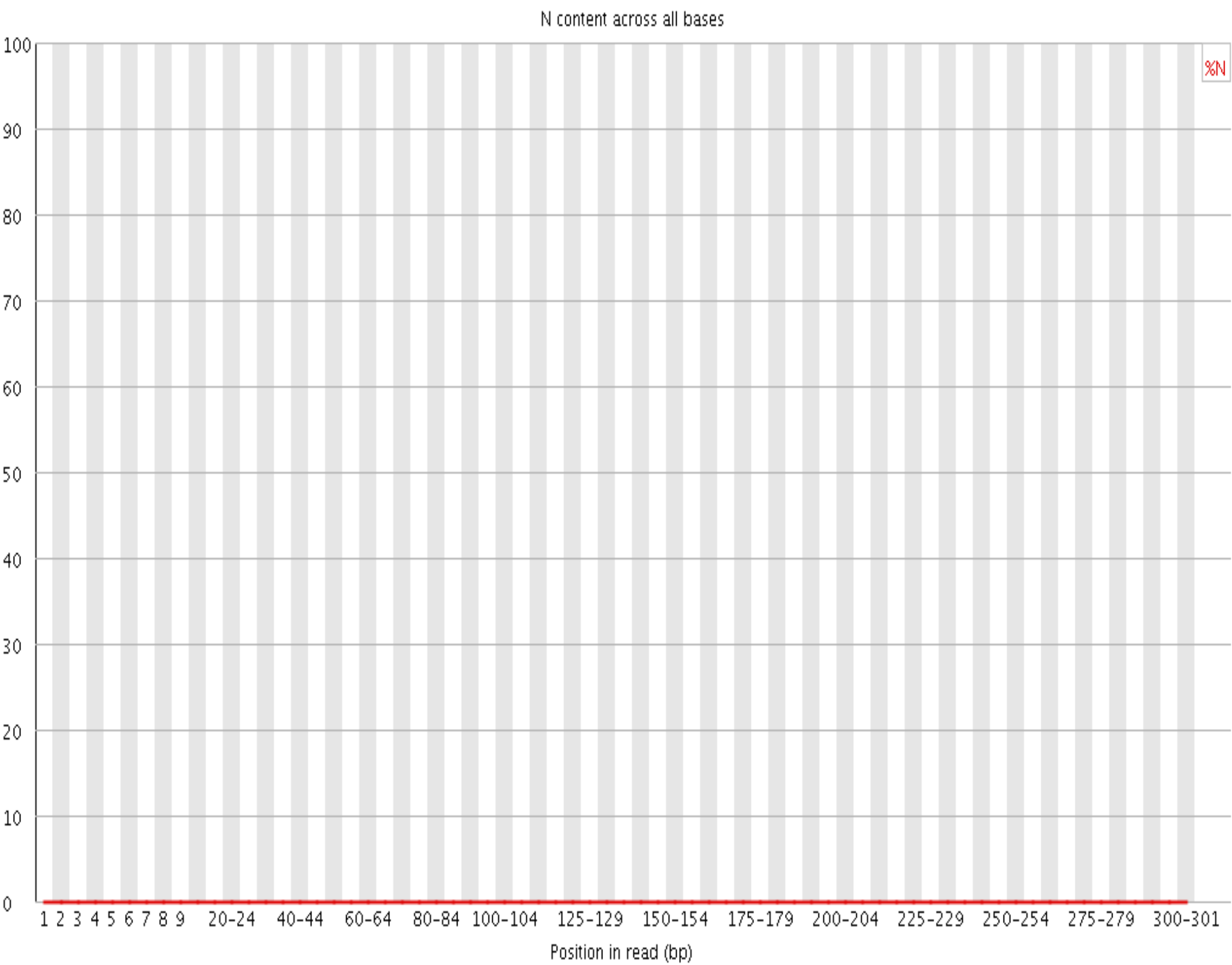
❌ Per base sequence content



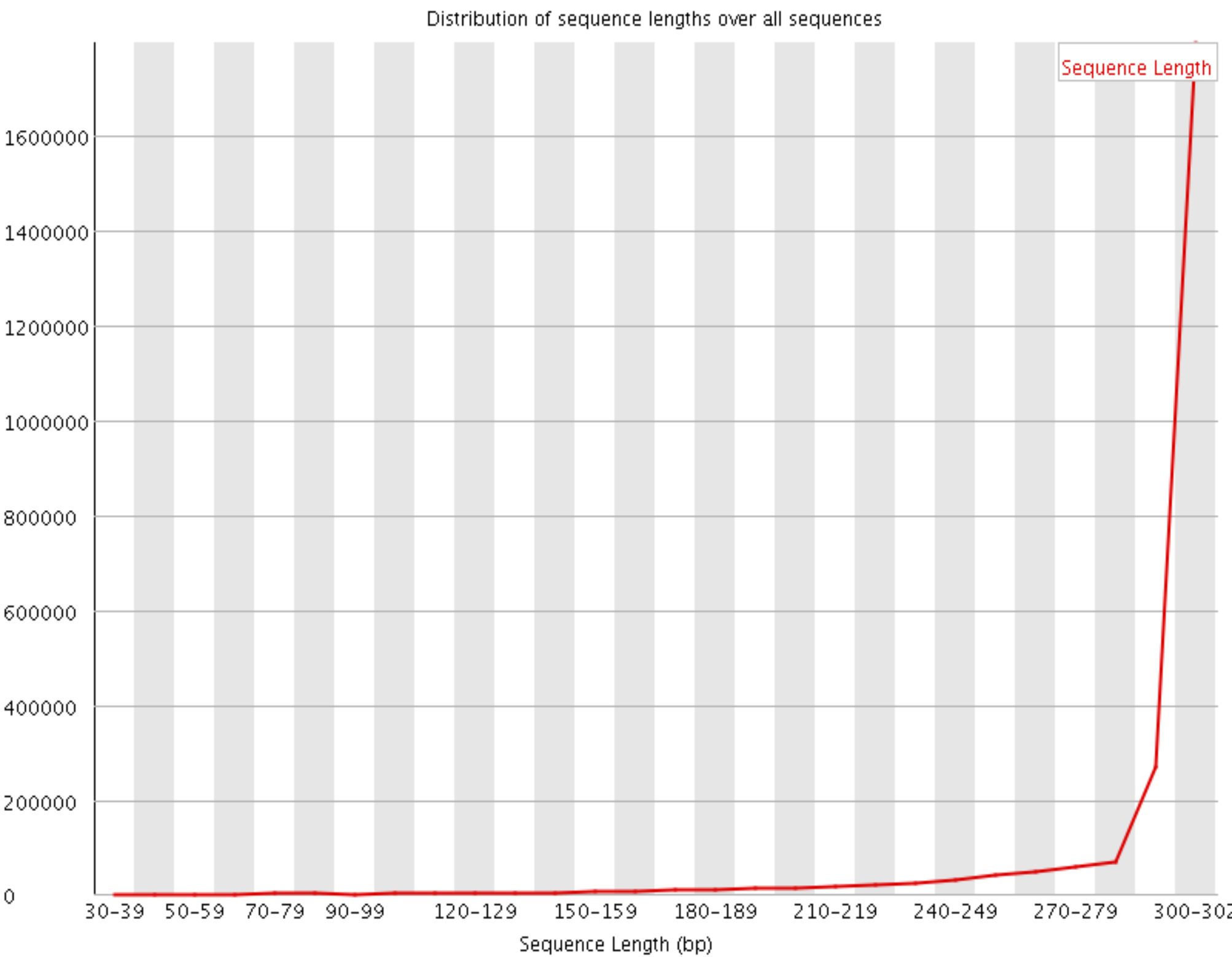
✔ Per sequence GC content



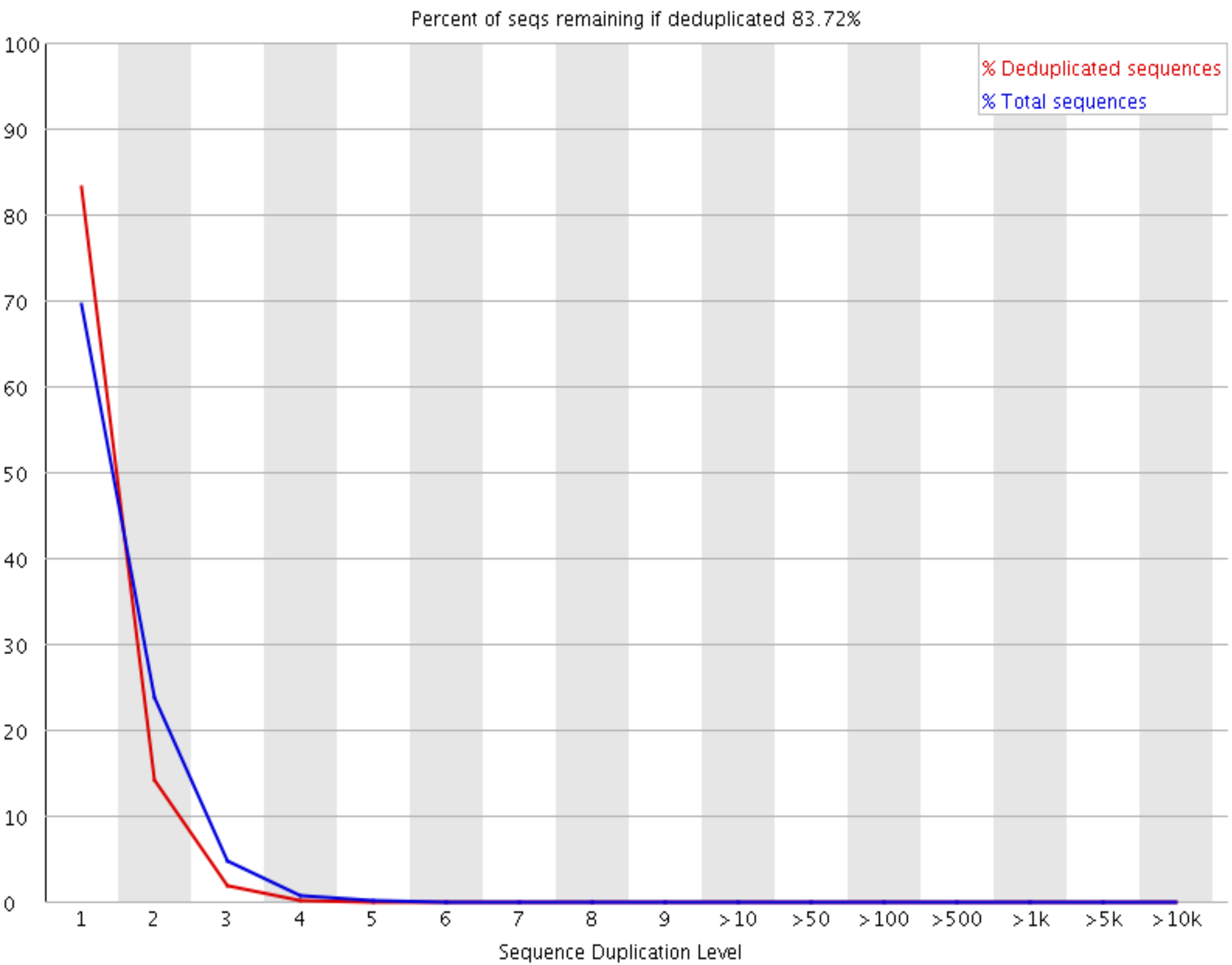
Per base N content



! Sequence Length Distribution

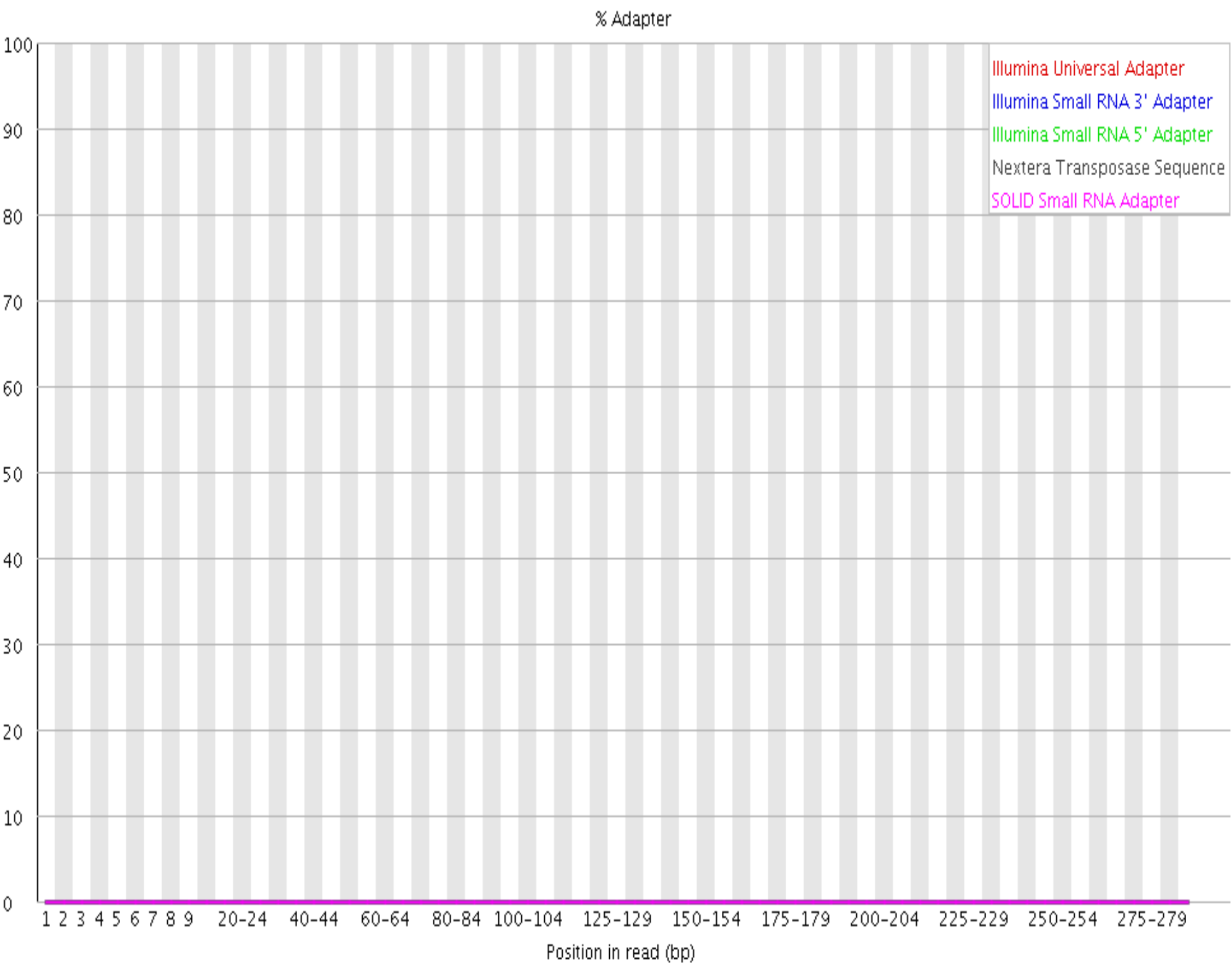


✔ Sequence Duplication Levels



✔ **Overrepresented sequences**
No overrepresented sequences

✔ **Adapter Content**



Kmer Content

No overrepresented Kmers