













FastQC Report

Summary

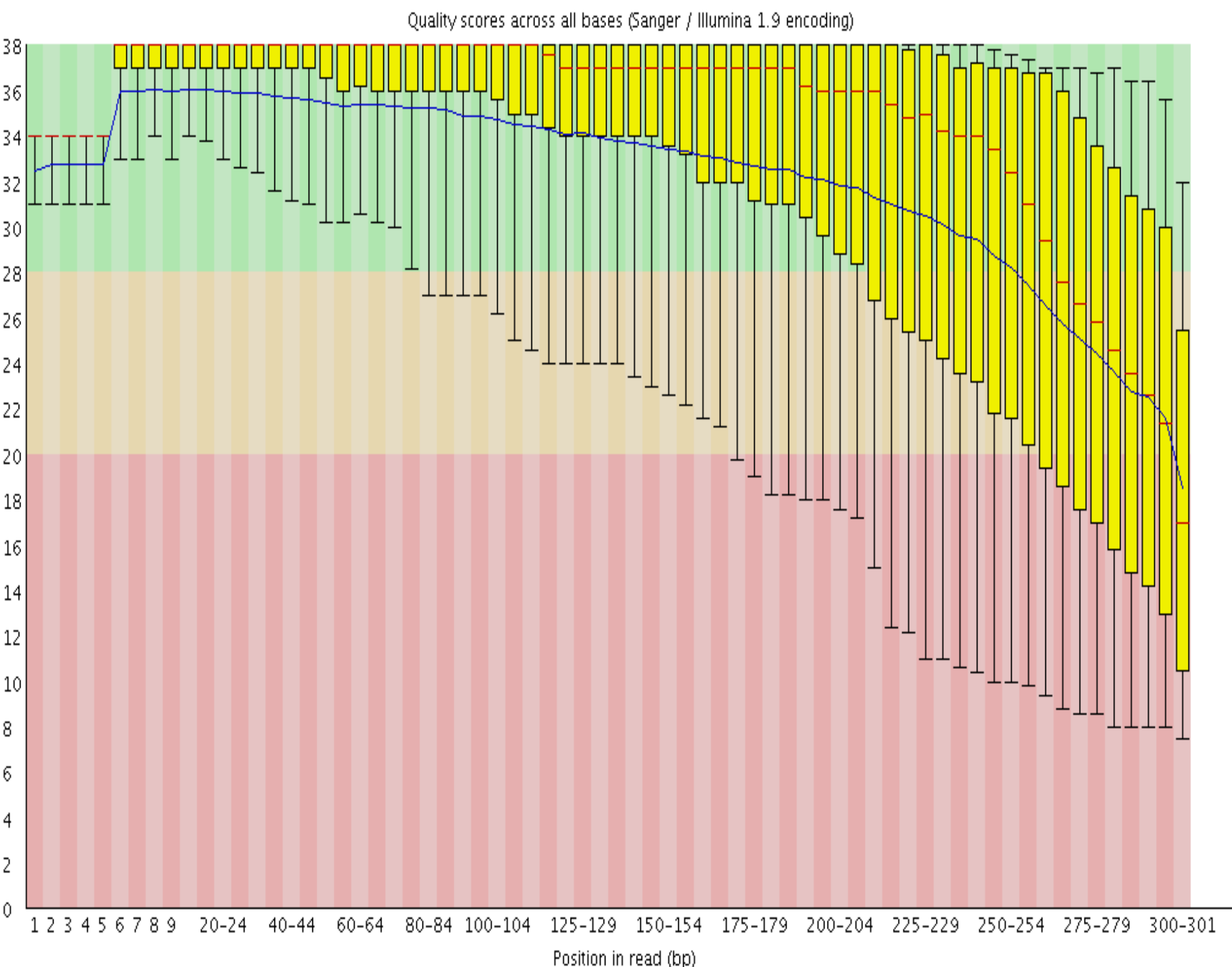
Wed 24 Apr 2019
BJ1_S5_L001_R2_001.fastq.gz

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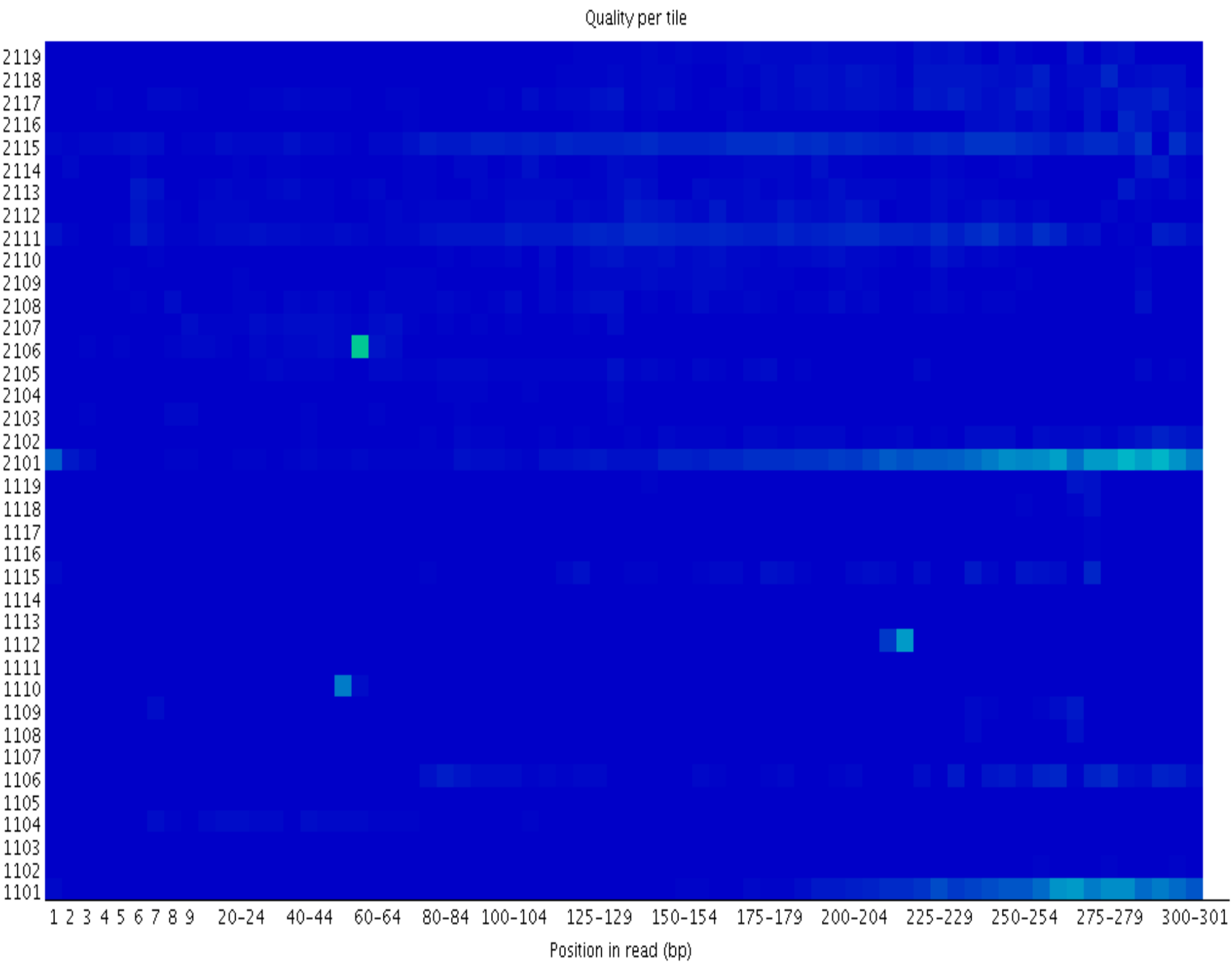
Basic Statistics

Measure	Value
Filename	BJ1_S5_L001_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2614628
Sequences flagged as poor quality	0
Sequence length	35–301
%GC	37

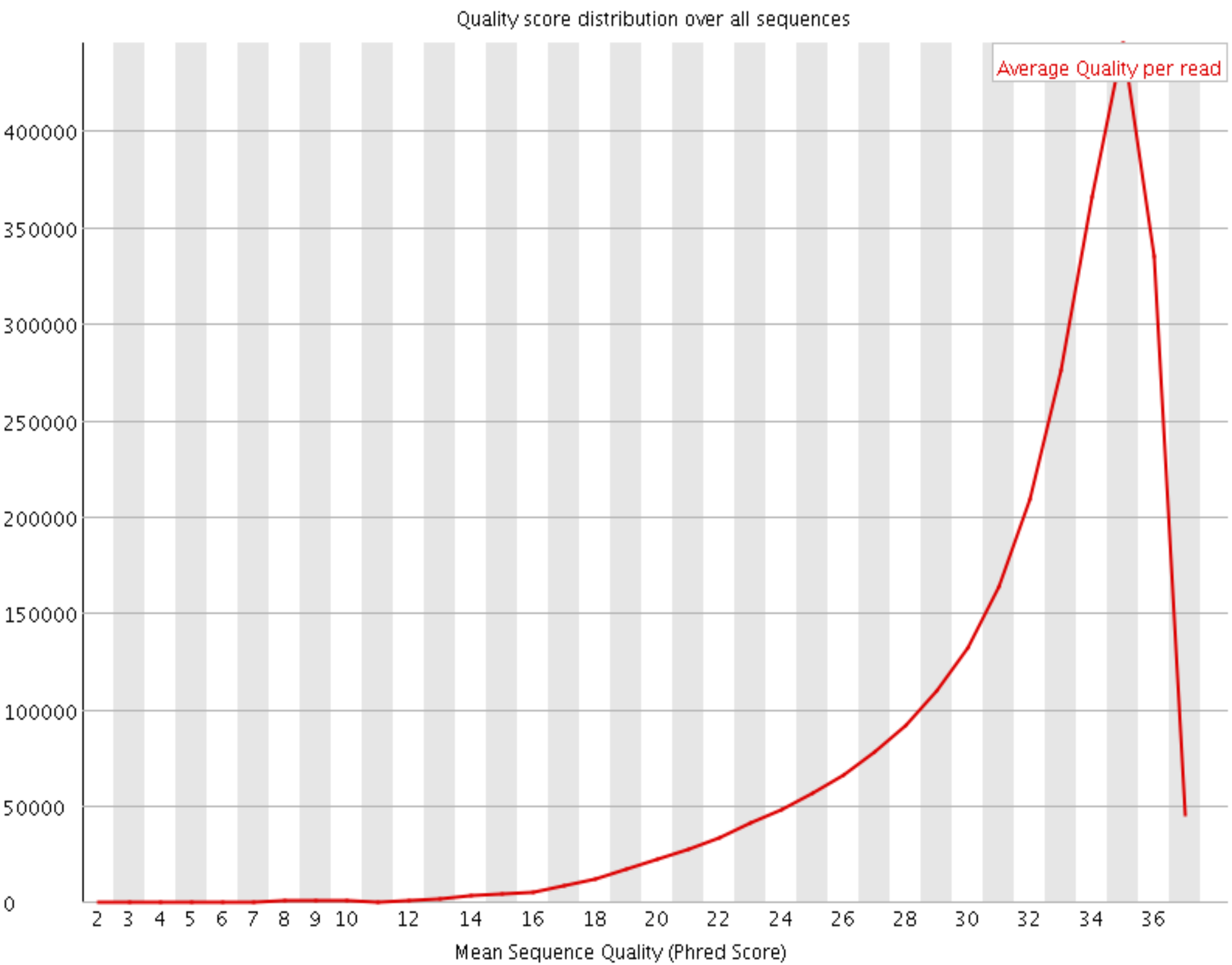
❌ Per base sequence quality



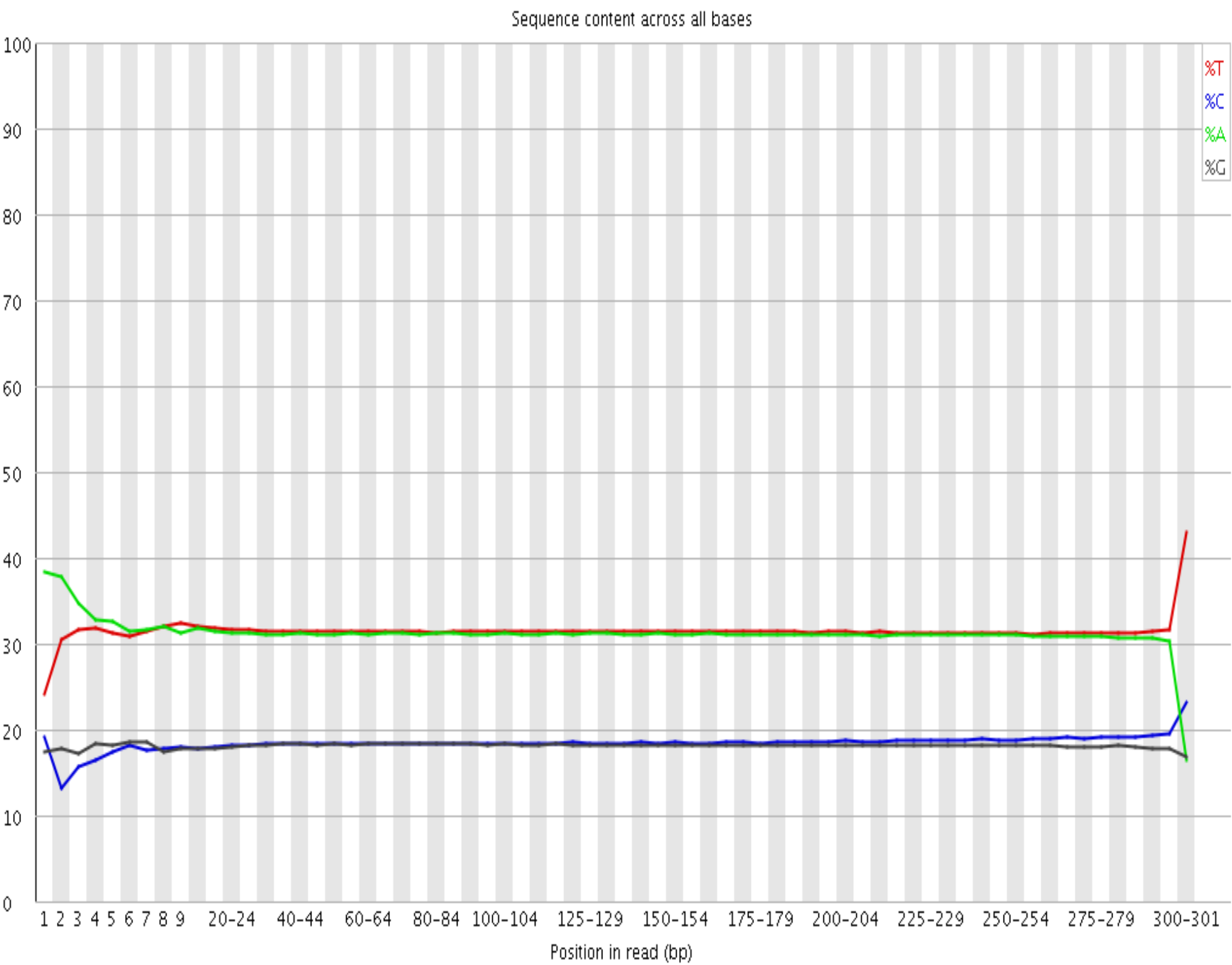
✅ Per tile sequence quality



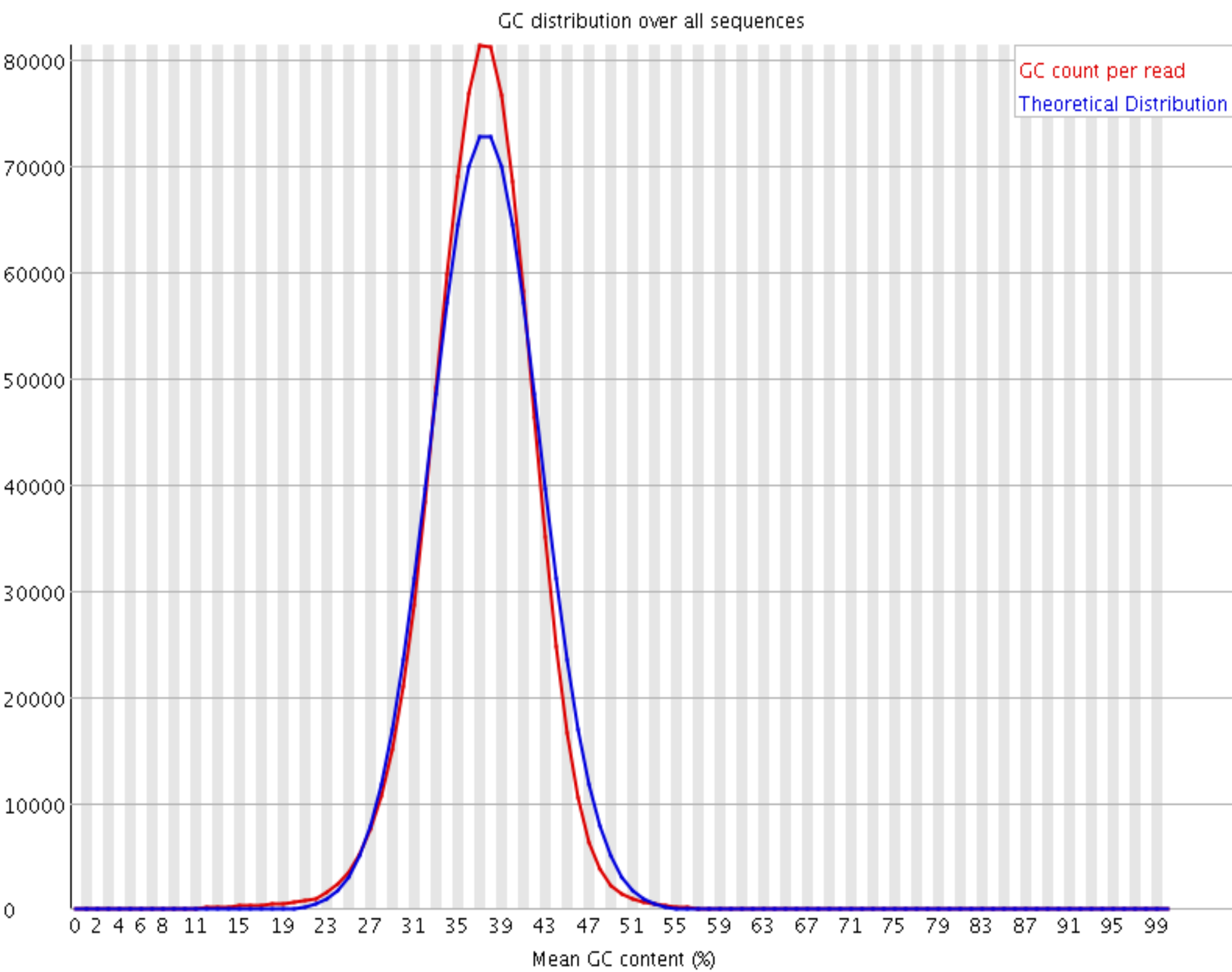
✅ **Per sequence quality scores**



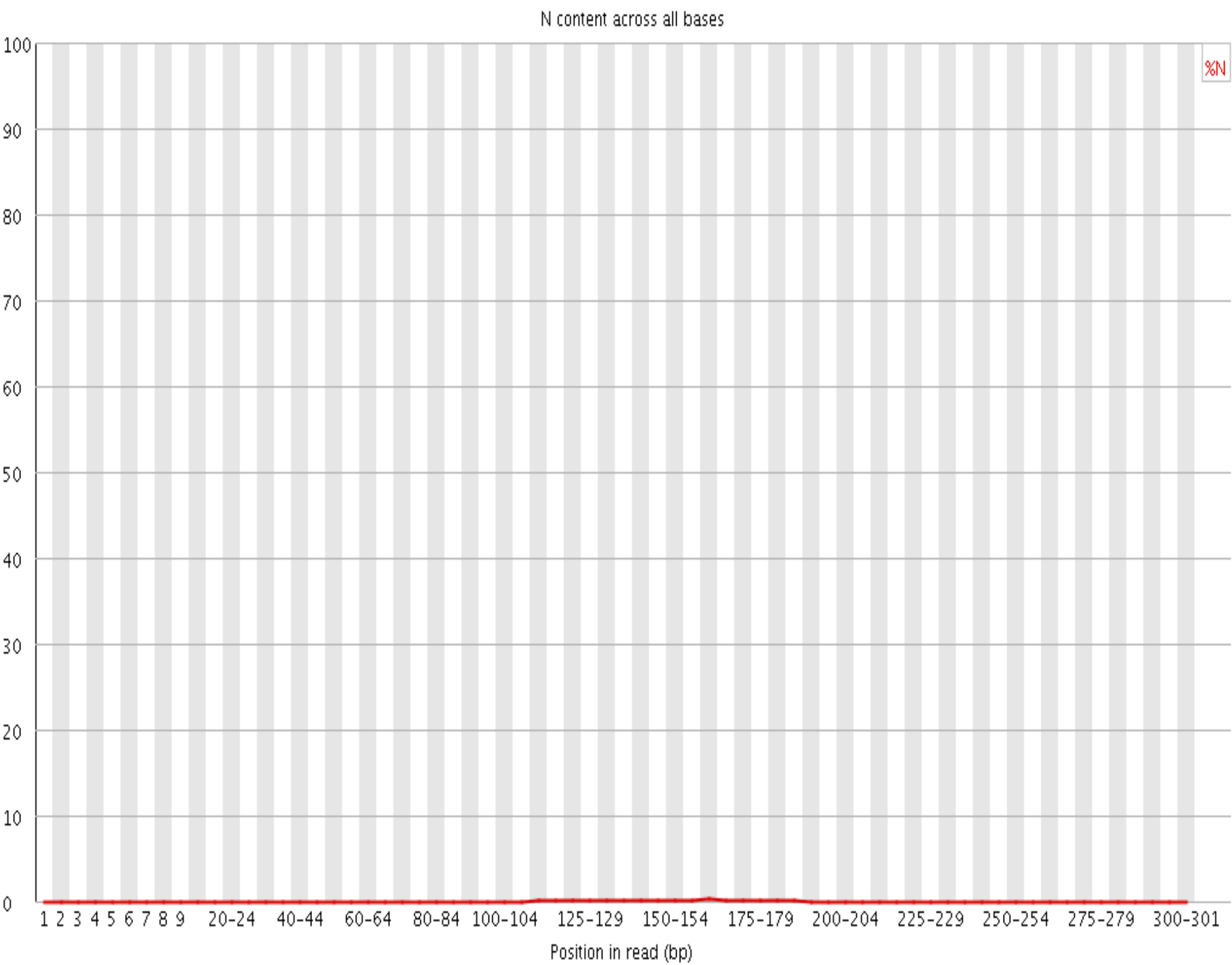
❌ Per base sequence content



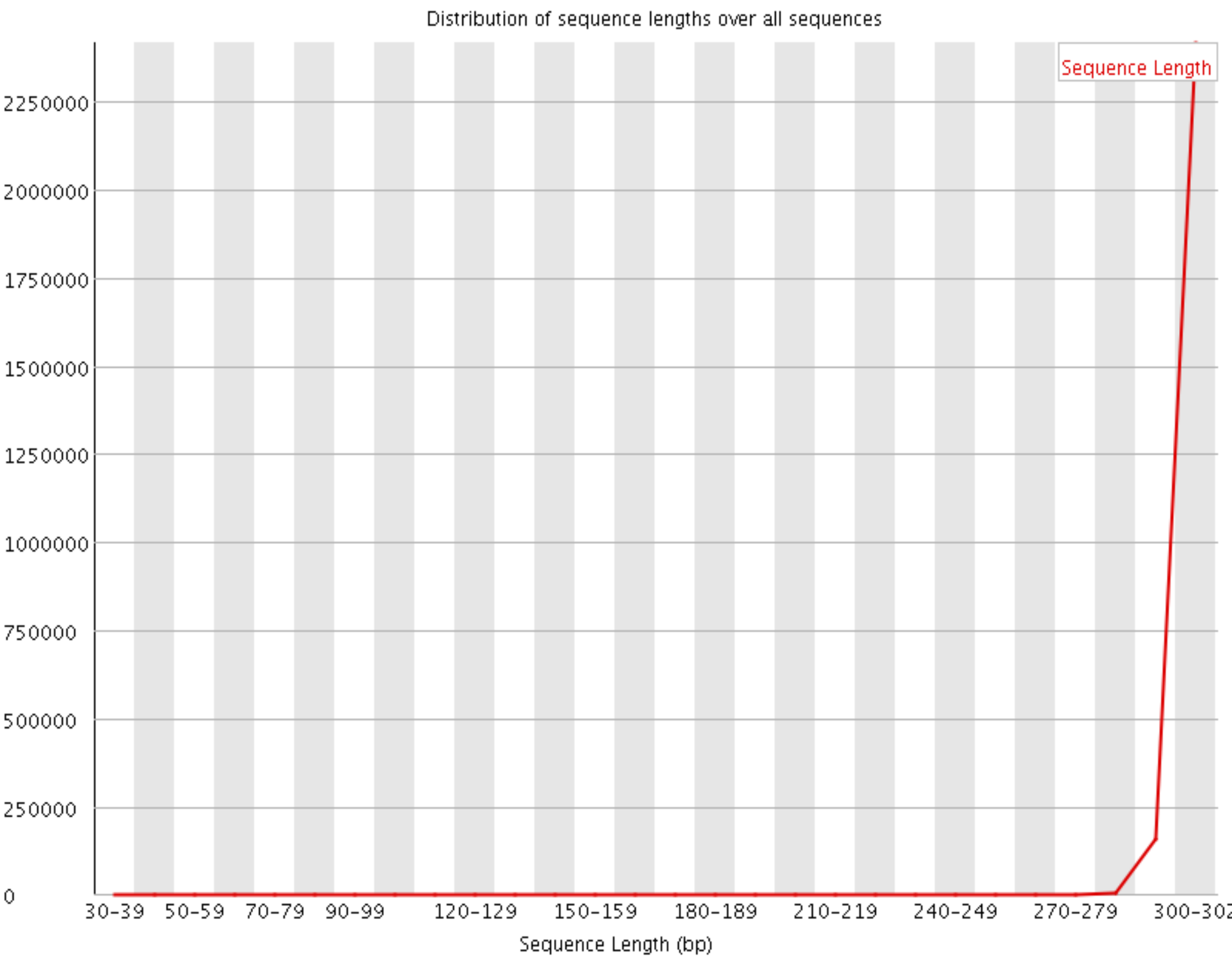
✔ Per sequence GC content



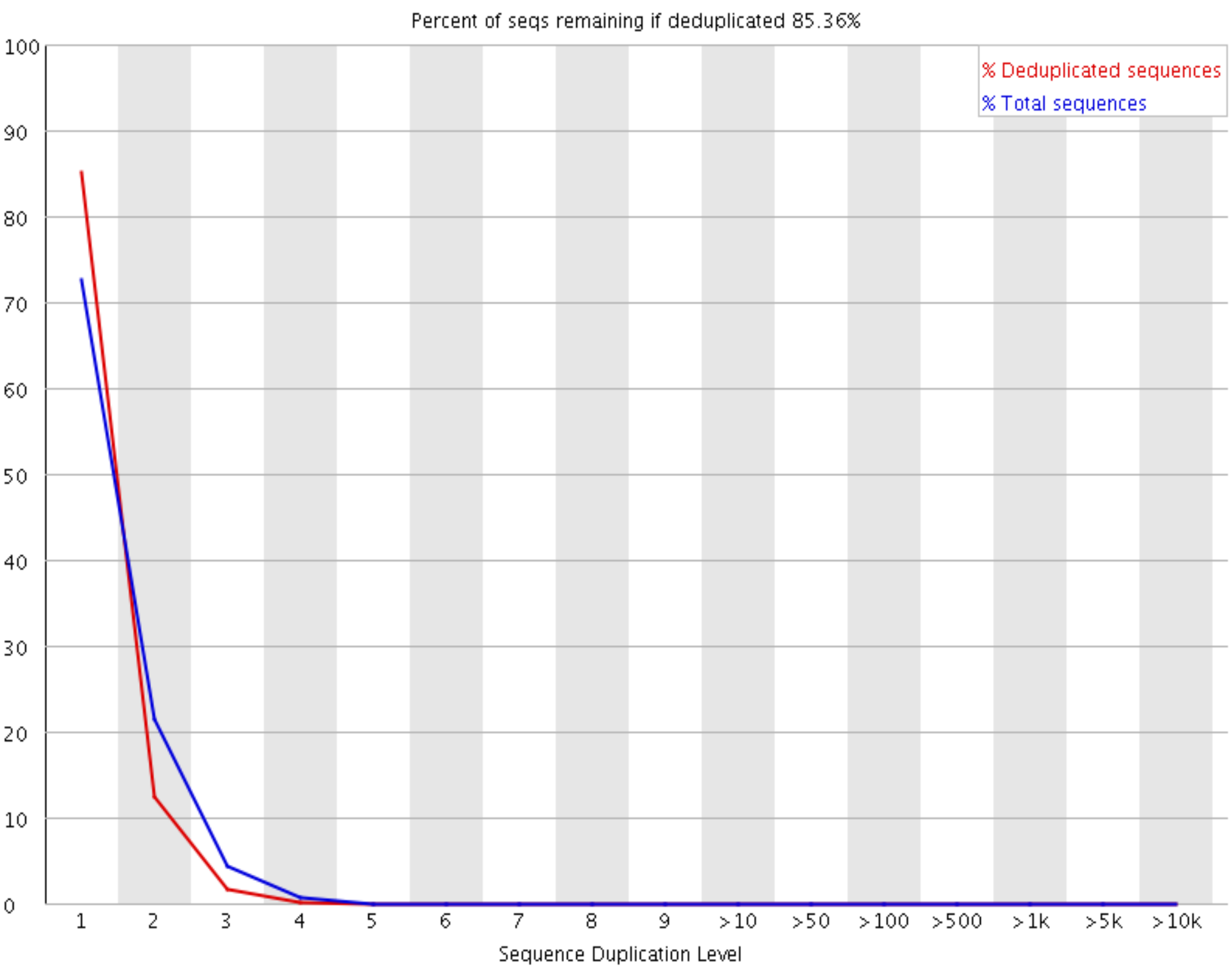
Per base N content



! Sequence Length Distribution

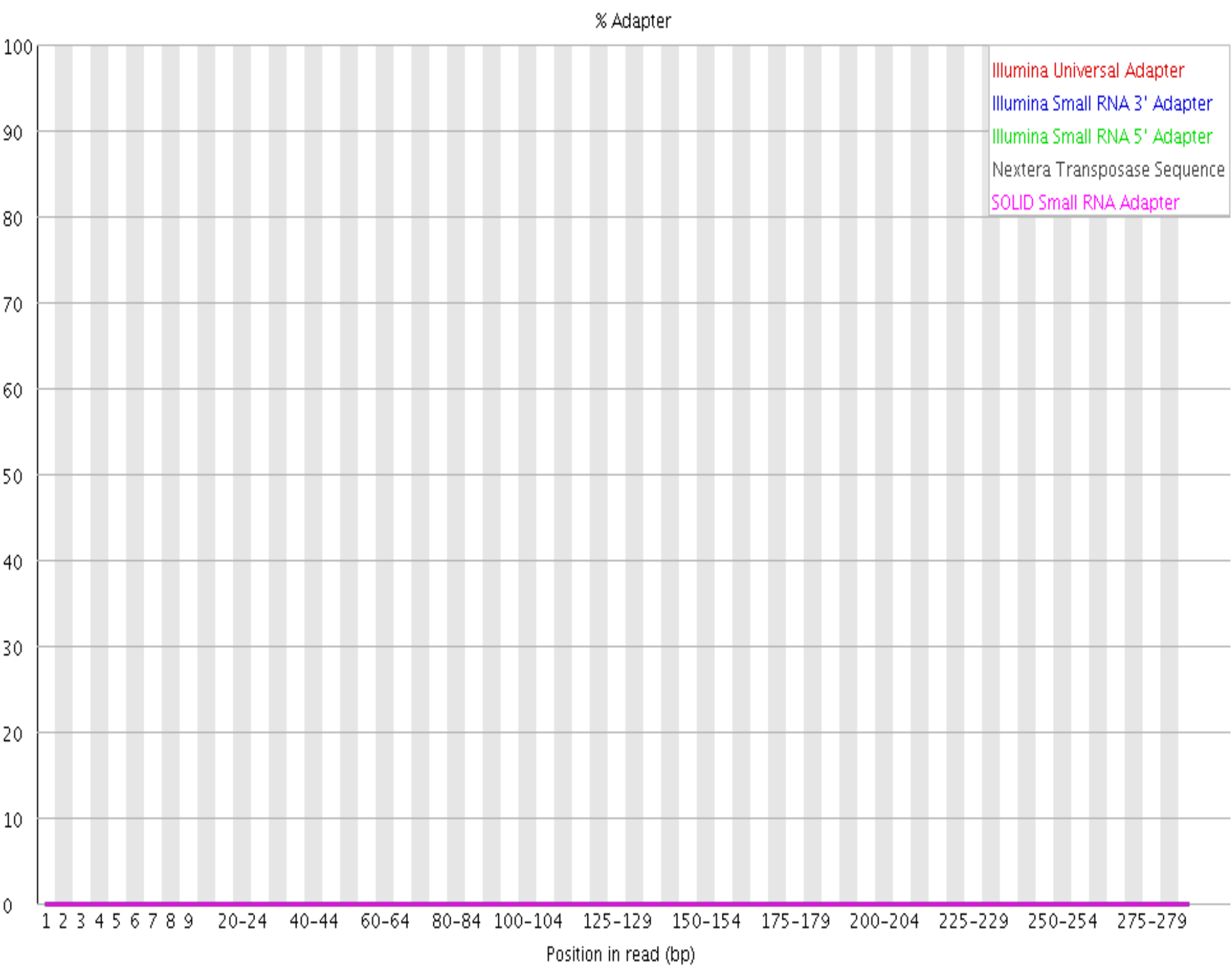


✔ Sequence Duplication Levels

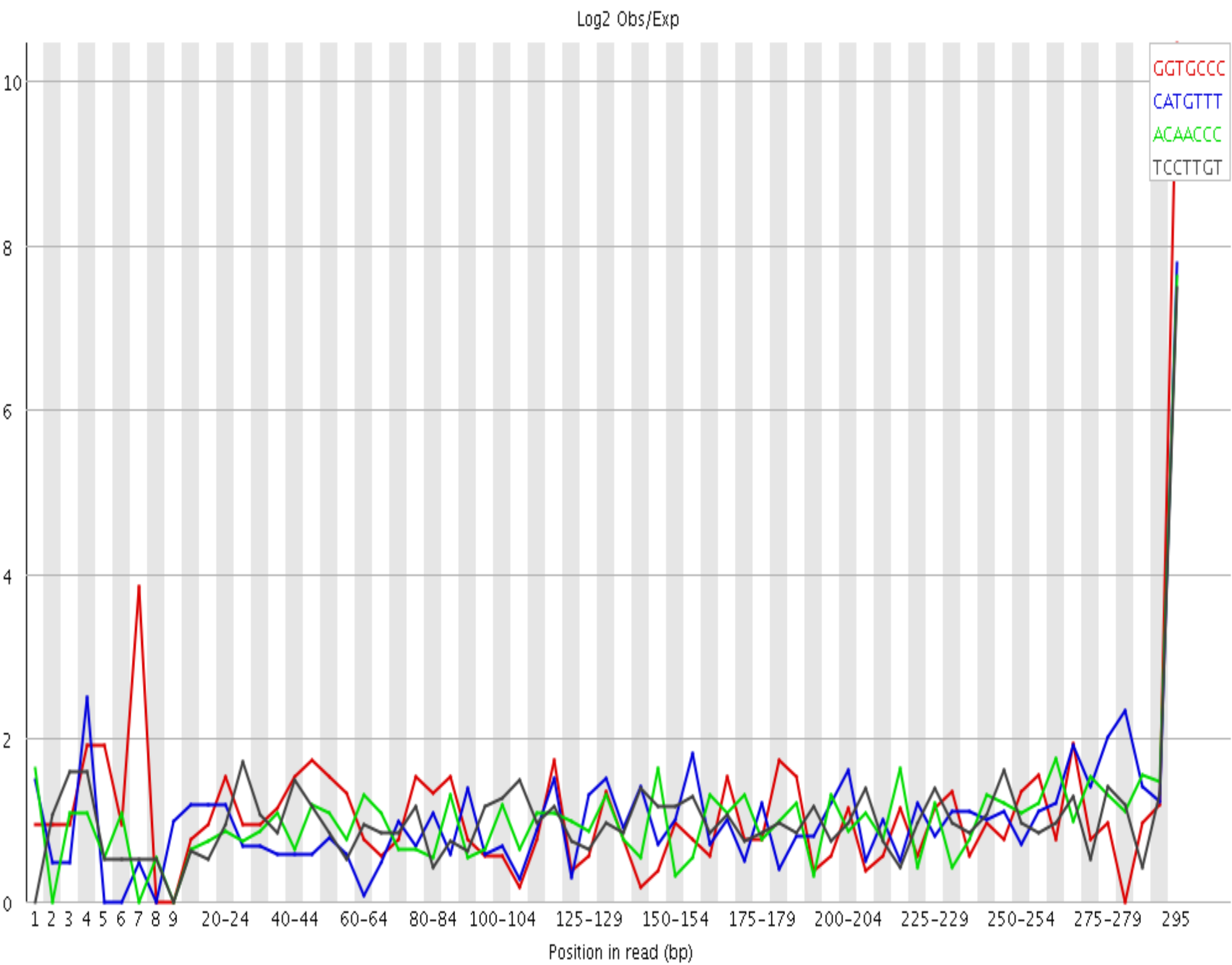


✔ **Overrepresented sequences**
No overrepresented sequences

✔ **Adapter Content**



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGTGCCC	1525	0.009050021	10.457158	295
CATGTTT	2925	0.001984884	7.788604	295
ACAACCC	2685	0.0080289645	7.6363125	295
TCCTTGT	2740	0.009622457	7.4830294	295