













# FastQC Report

## Summary

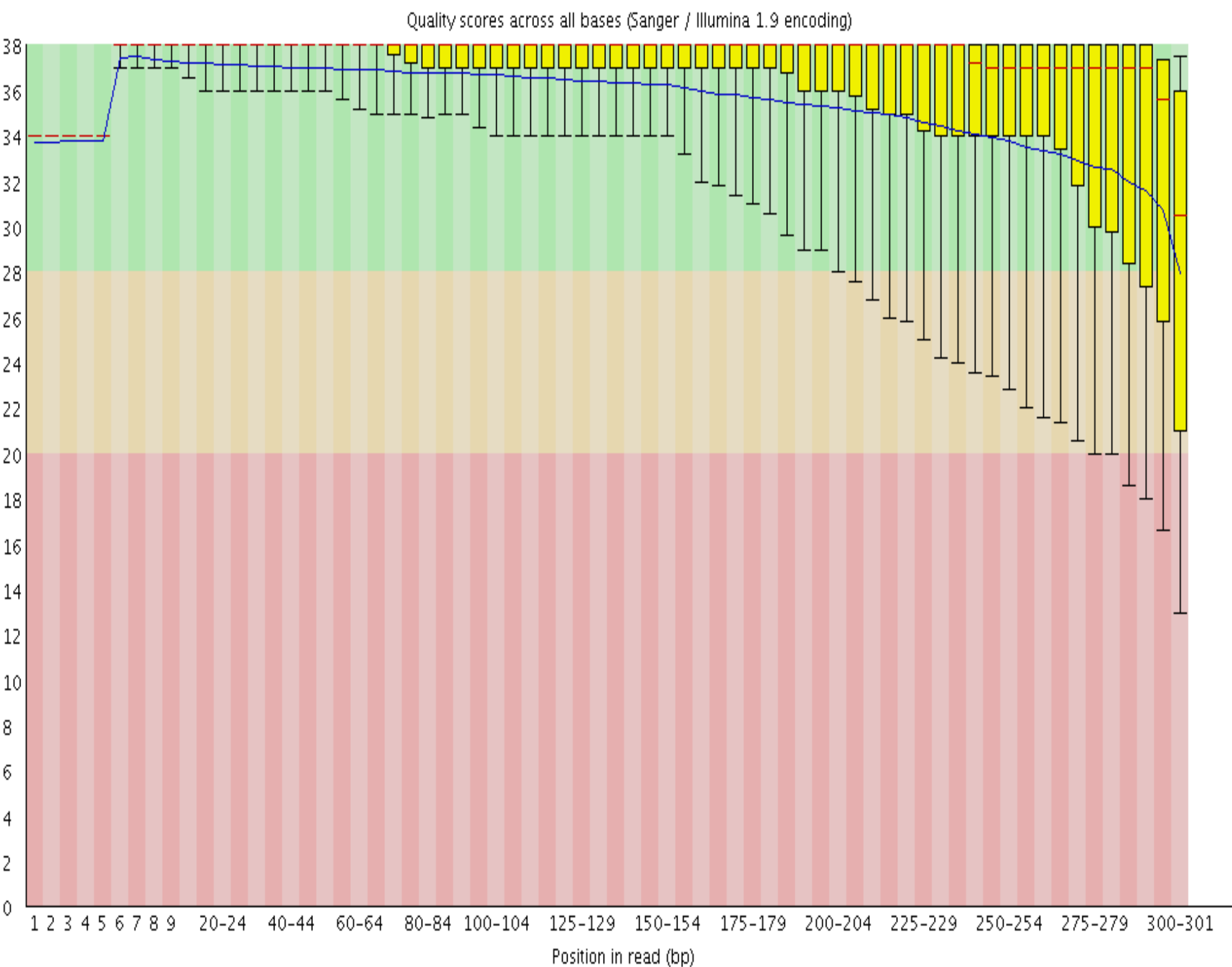
Wed 24 Apr 2019  
BJ1\_S5\_L001\_R1\_001.fastq.gz

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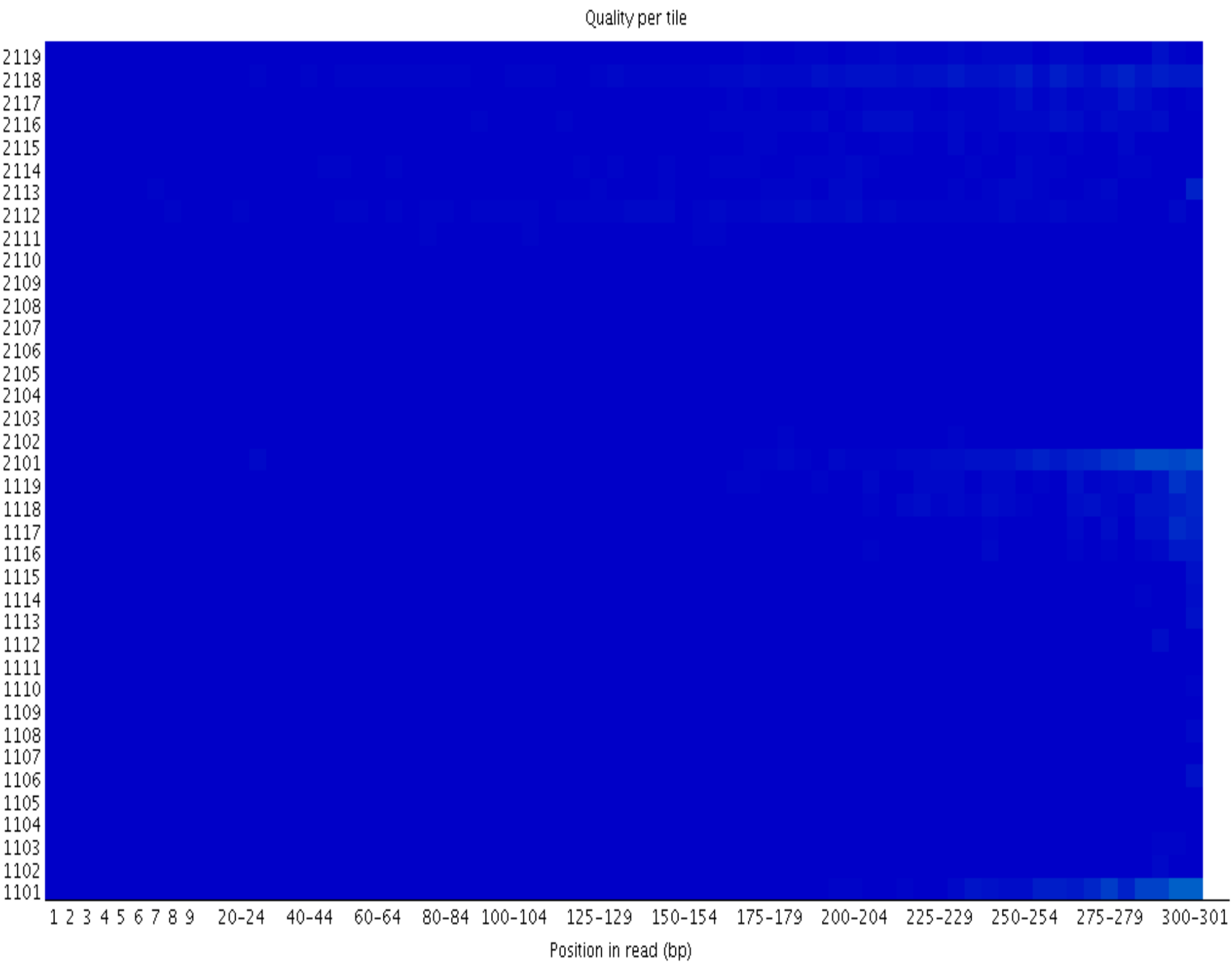
## Basic Statistics

Measure	Value
Filename	BJ1_S5_L001_R1_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	36

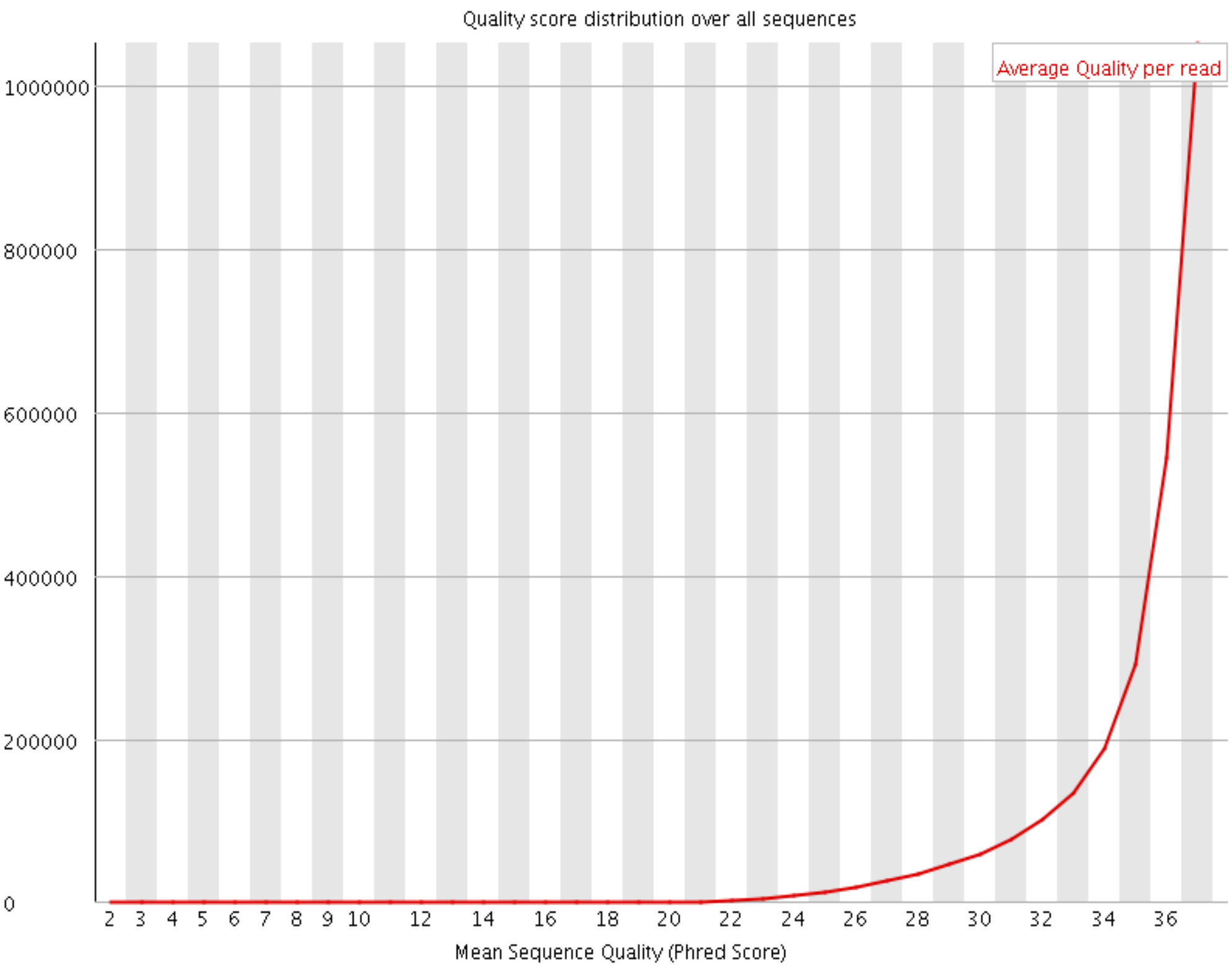
## ✔ Per base sequence quality



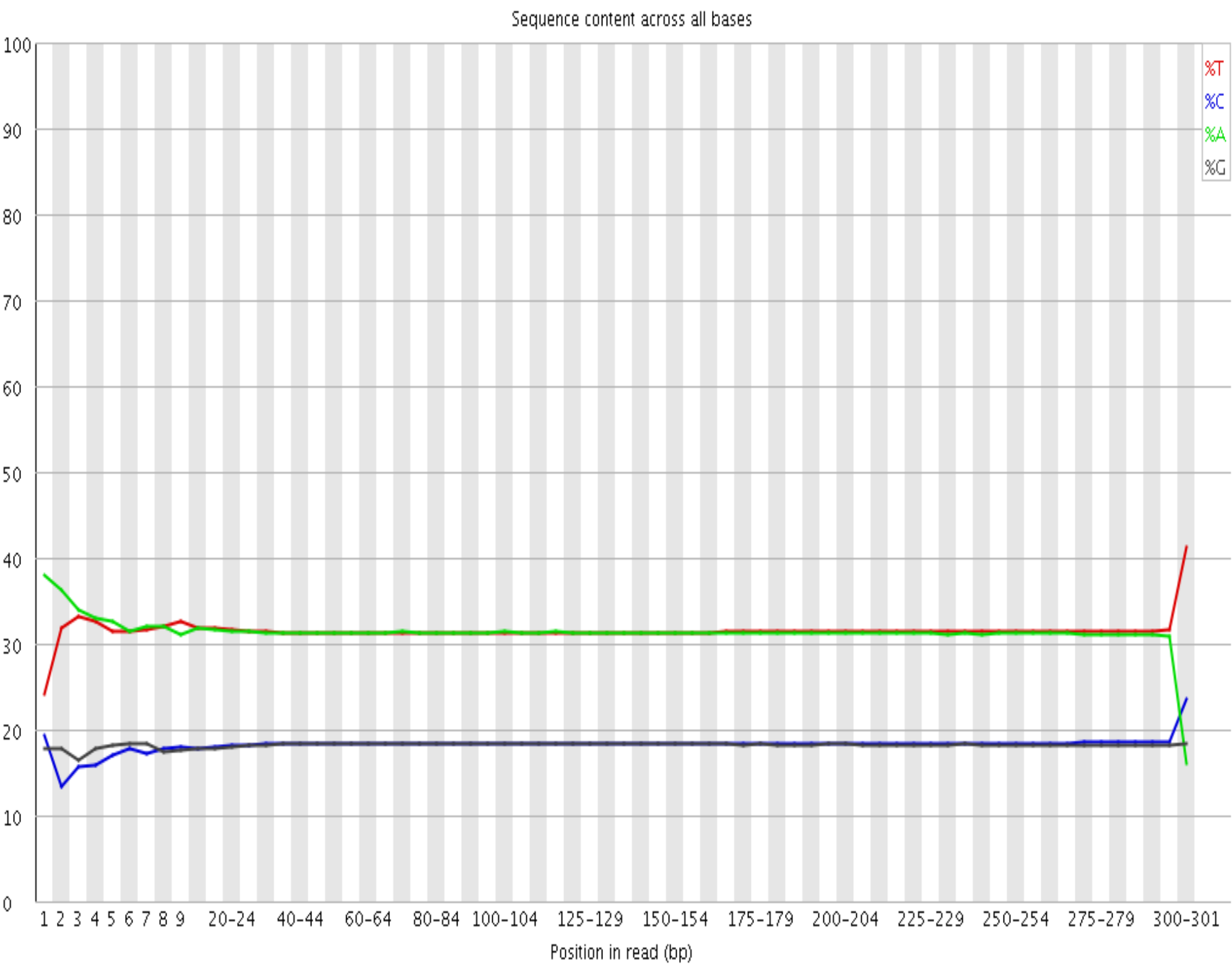
## ✔ Per tile sequence quality



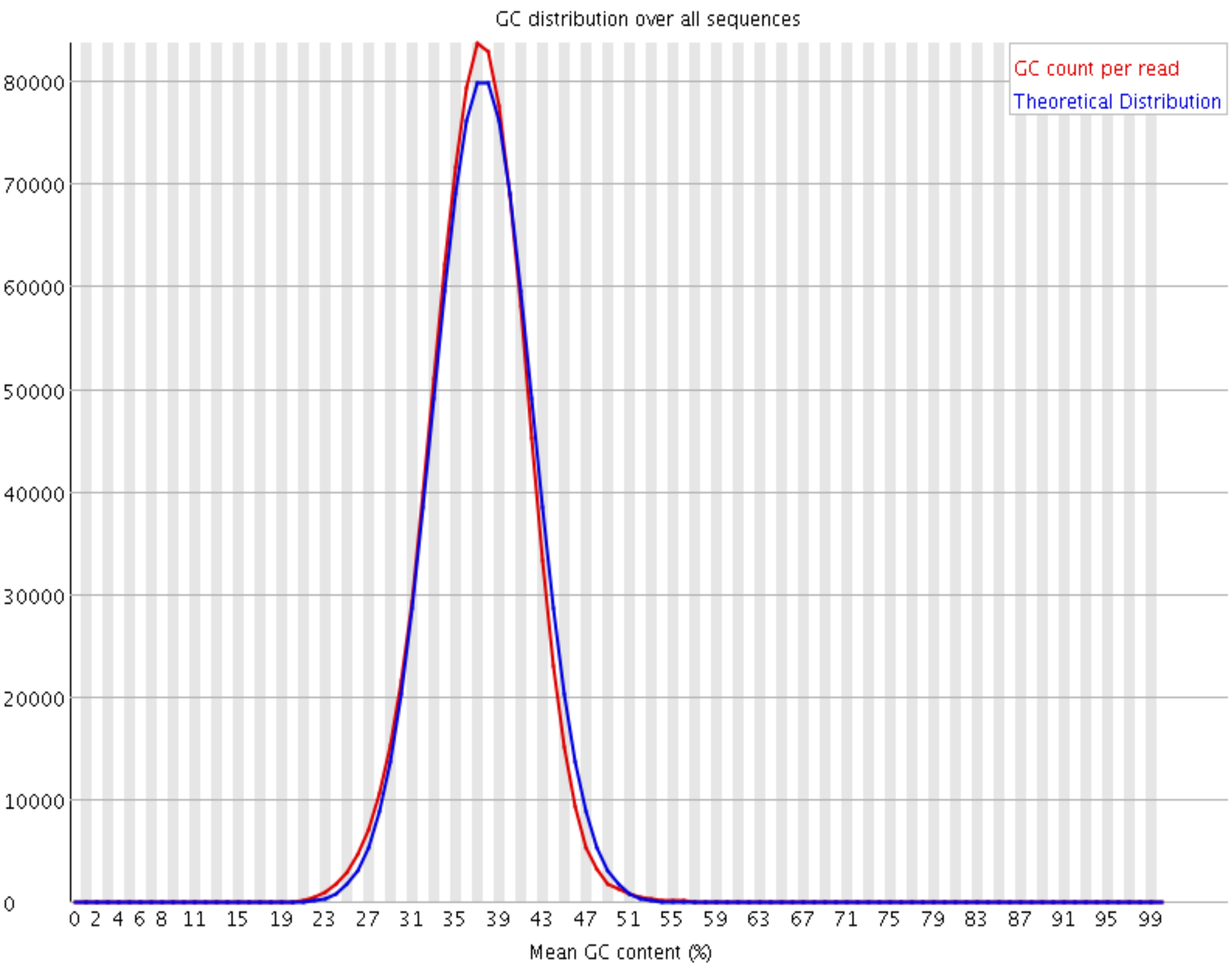
✔ **Per sequence quality scores**



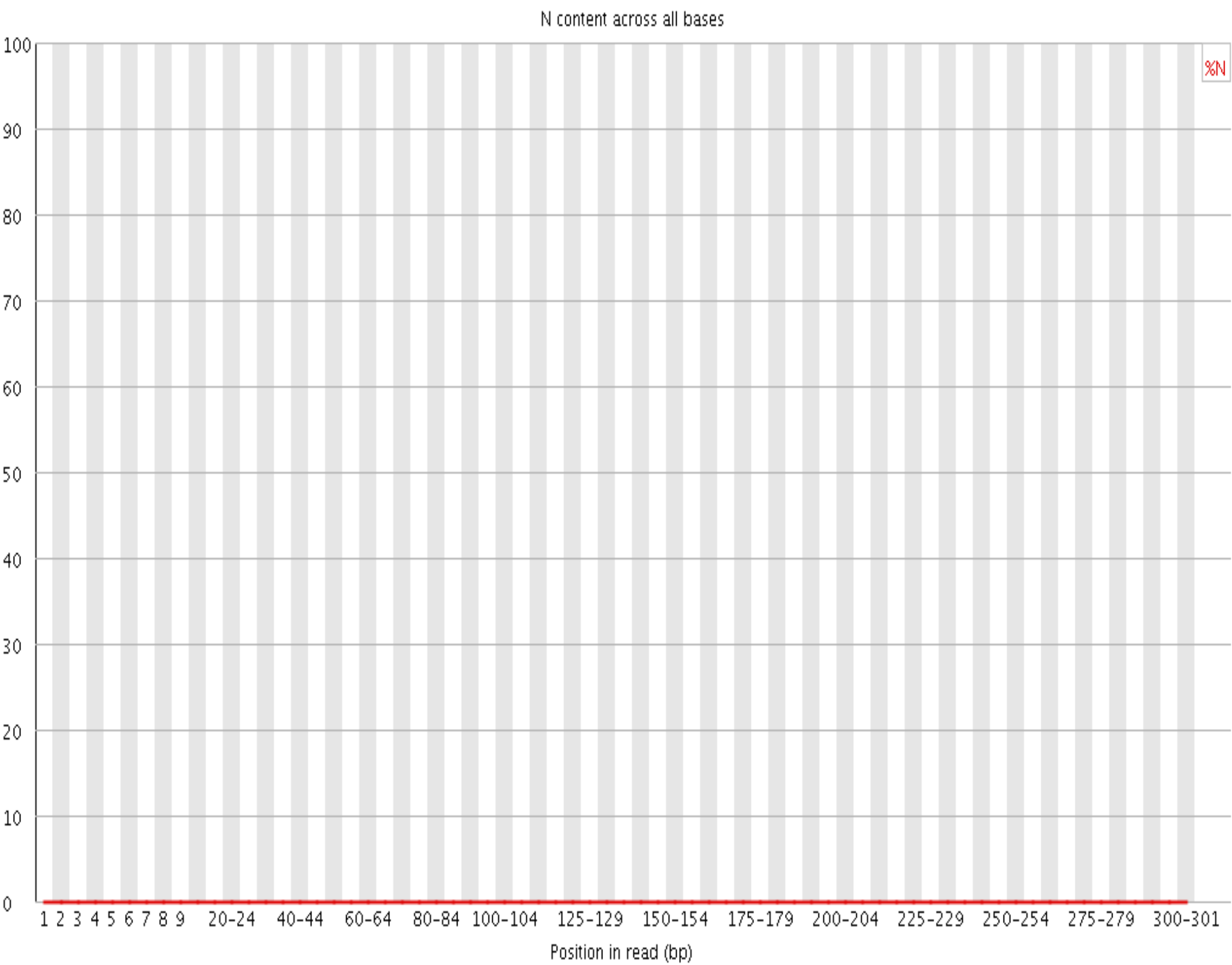
❌ Per base sequence content



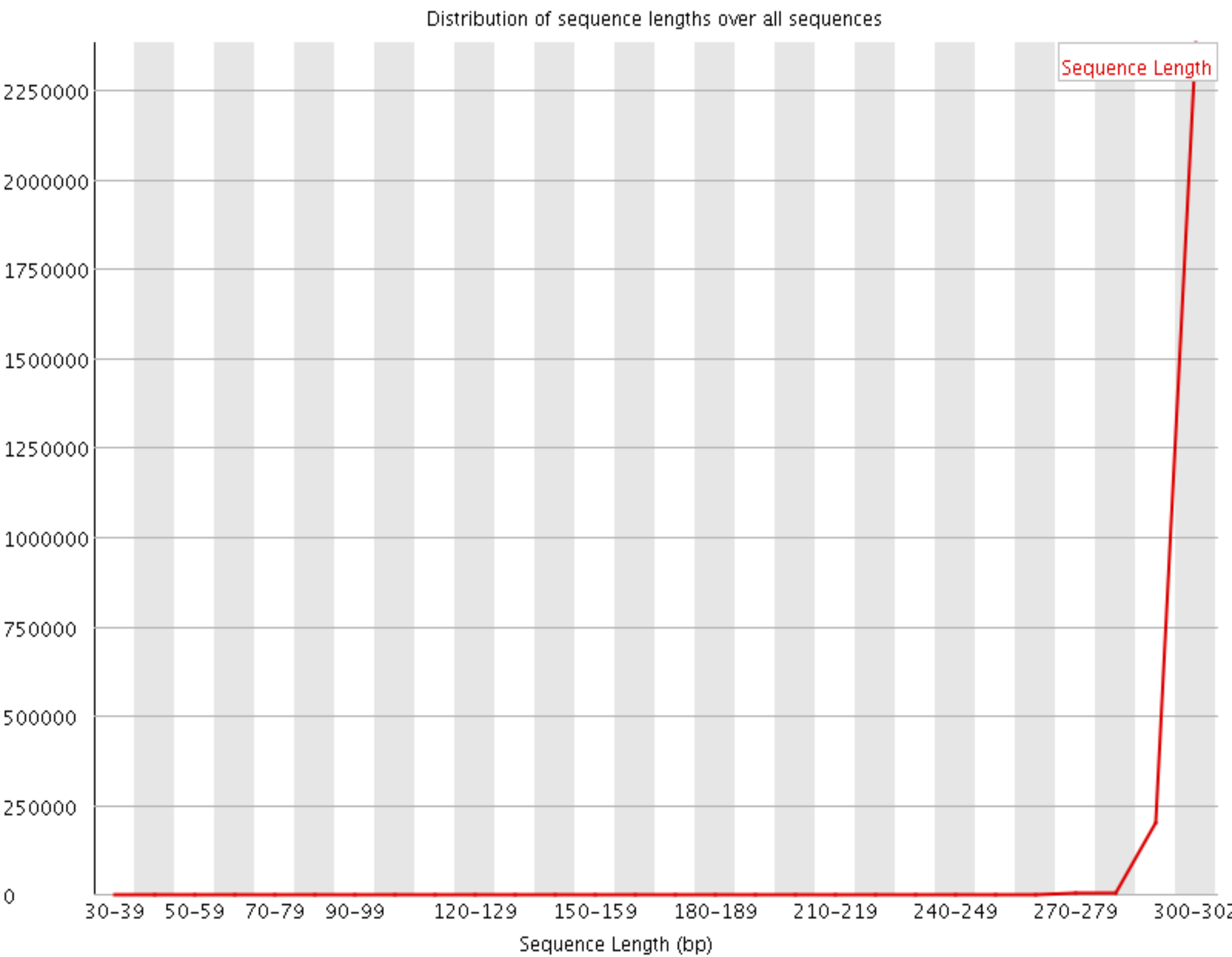
✔ Per sequence GC content



**Per base N content**

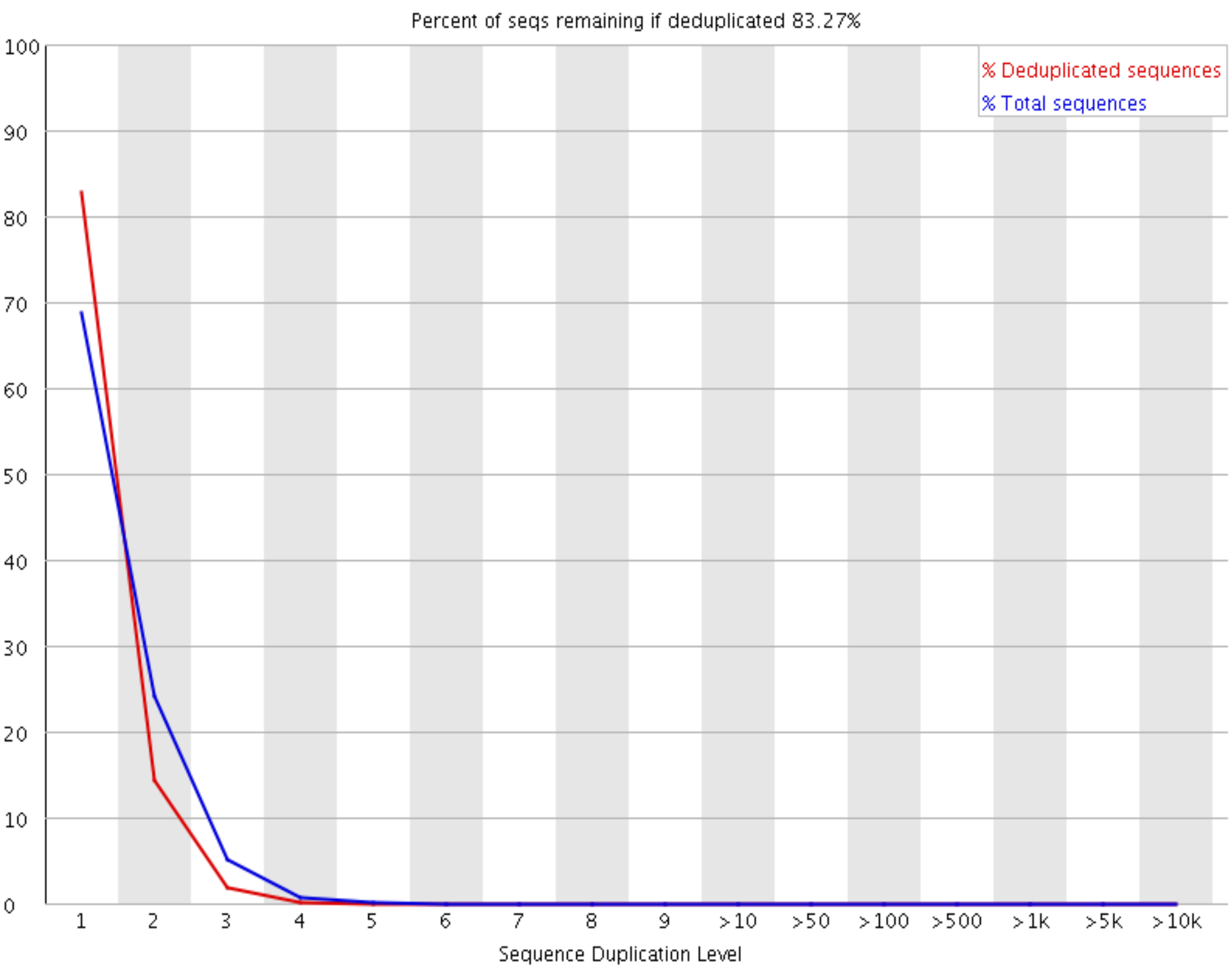


## ! Sequence Length Distribution



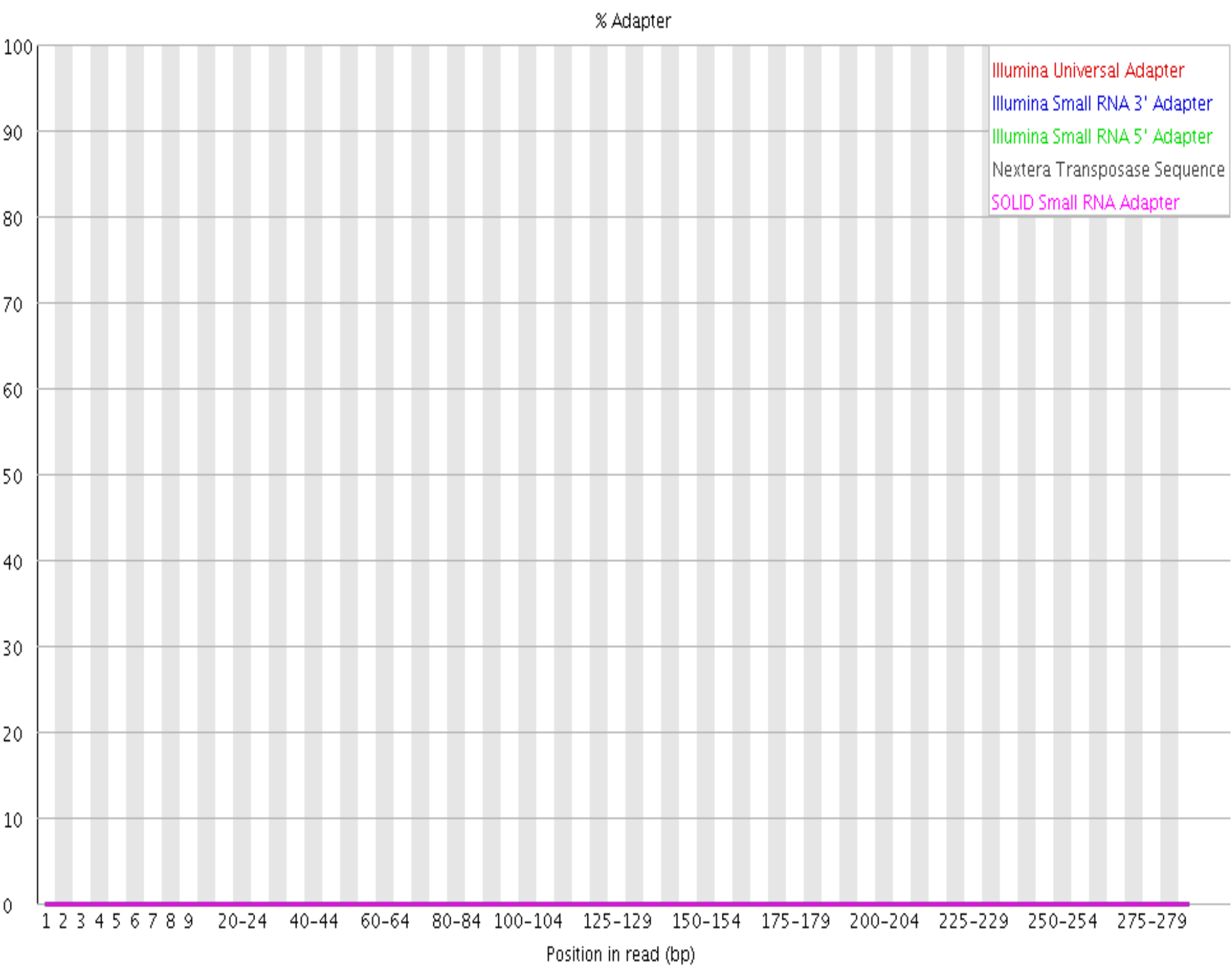
## ✔ Sequence Duplication Levels



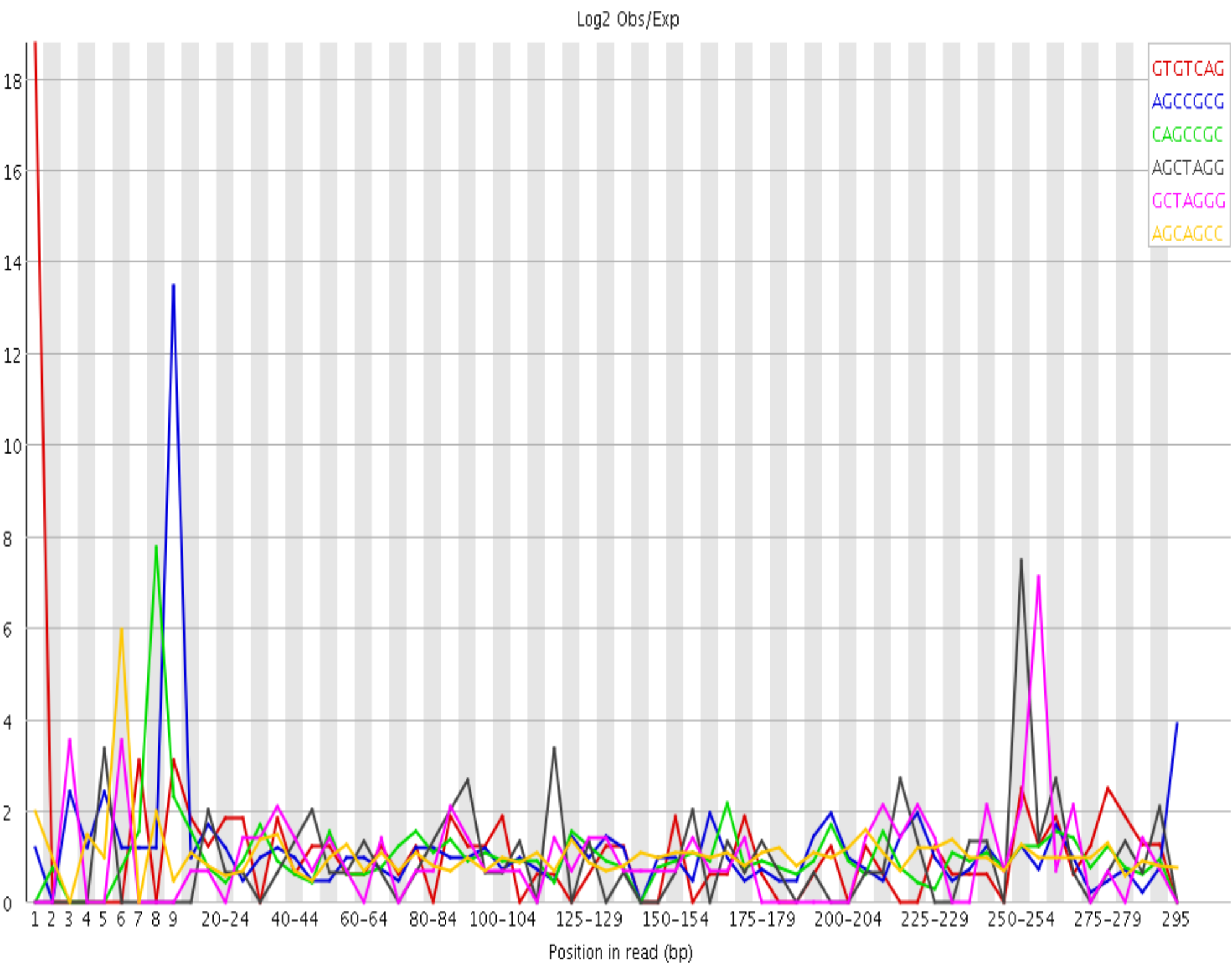


✔ **Overrepresented sequences**  
No overrepresented sequences

✔ **Adapter Content**



**Kmer Content**



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTGTCAG	470	8.4147655E-4	18.759708	1
AGCCGCG	1200	1.4161342E-6	13.470511	9
CAGCCGC	1890	0.0020197395	7.775187	8
AGCTAGG	435	9.180801E-4	7.4702926	250-254
GCTAGGG	415	0.0047486895	7.1248426	255-259
AGCAGCC	2960	0.003673816	5.957474	6