FastQC Report

Tue 5 May 2015
SW019_TGGCAAT_L001_R1_001.fastq.gz

Summary

[PASS] Basic Statistics

[FAIL] Per base sequence quality

[PASS] Per sequence quality scores

[WARNING] Per base sequence content

[PASS] Per base GC content

[PASS] Per sequence GC content

[PASS] Per base N content

[PASS] Sequence Length Distribution

[PASS] Sequence Duplication Levels

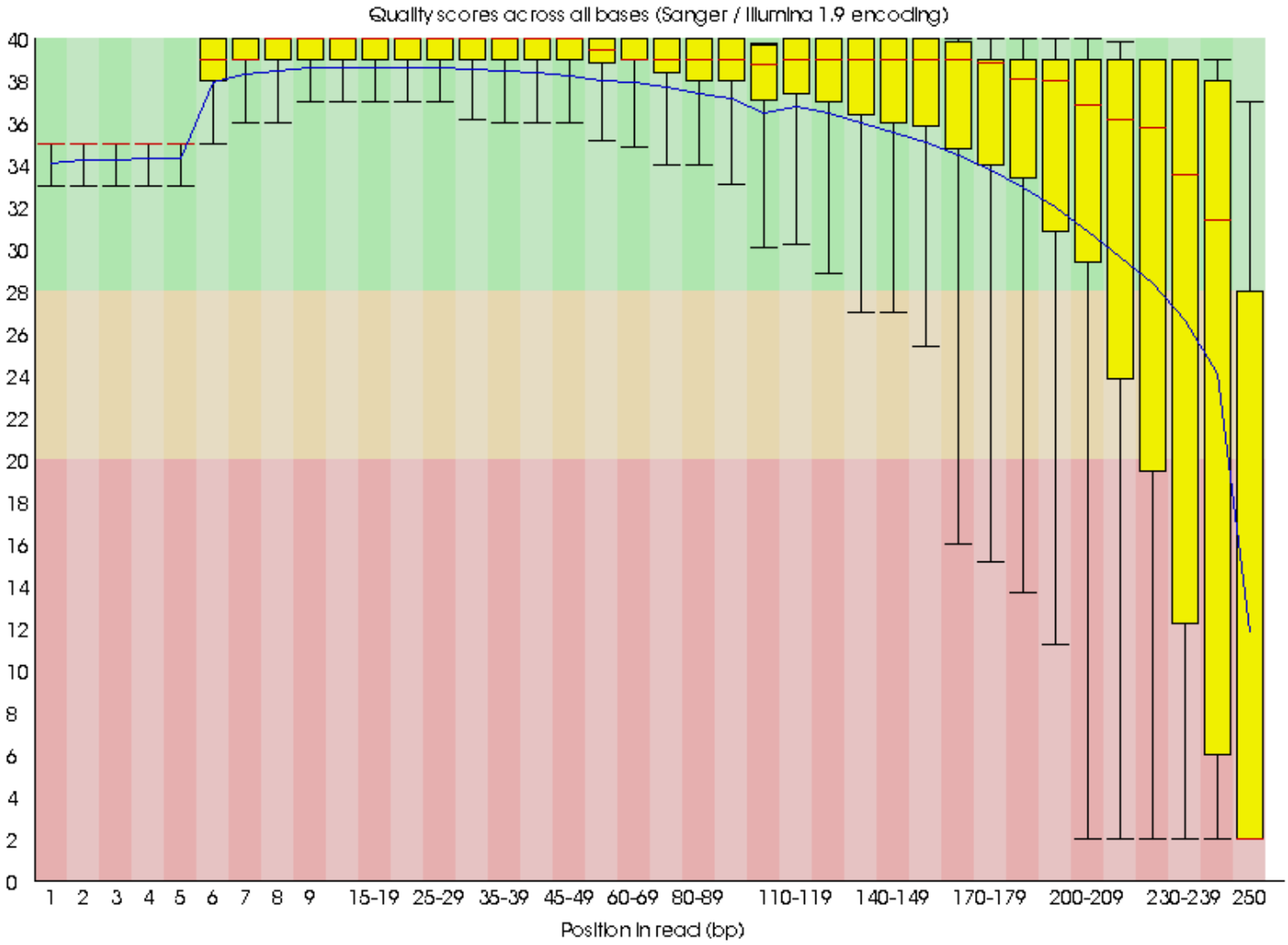
[PASS] Overrepresented sequences

[WARNING] Kmer Content

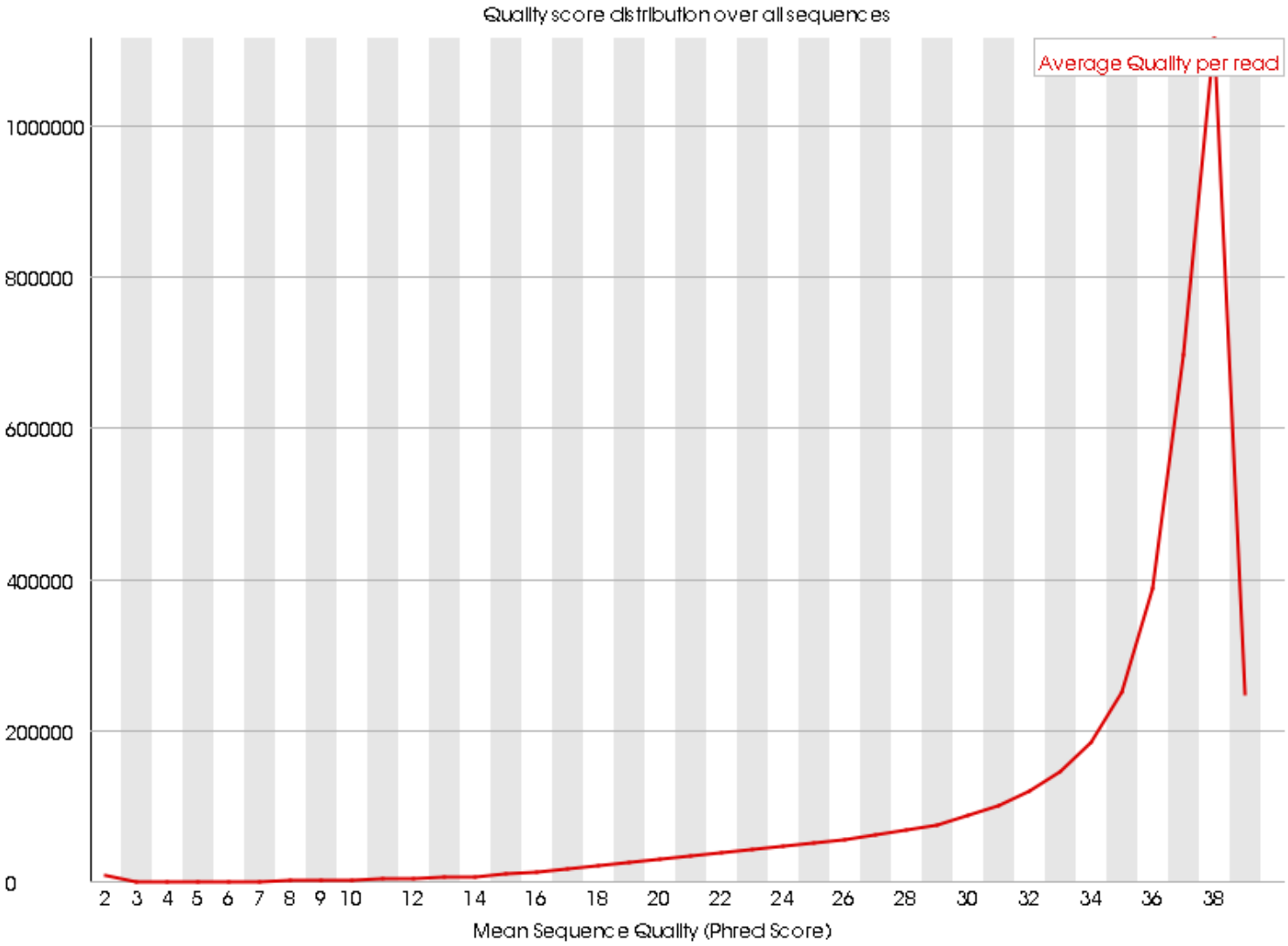
[OK] Basic Statistics

Measure	Value
Filename	SW019_TGGCAAT_L001_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4000000
Filtered Sequences	0
Sequence length	250
%GC	41

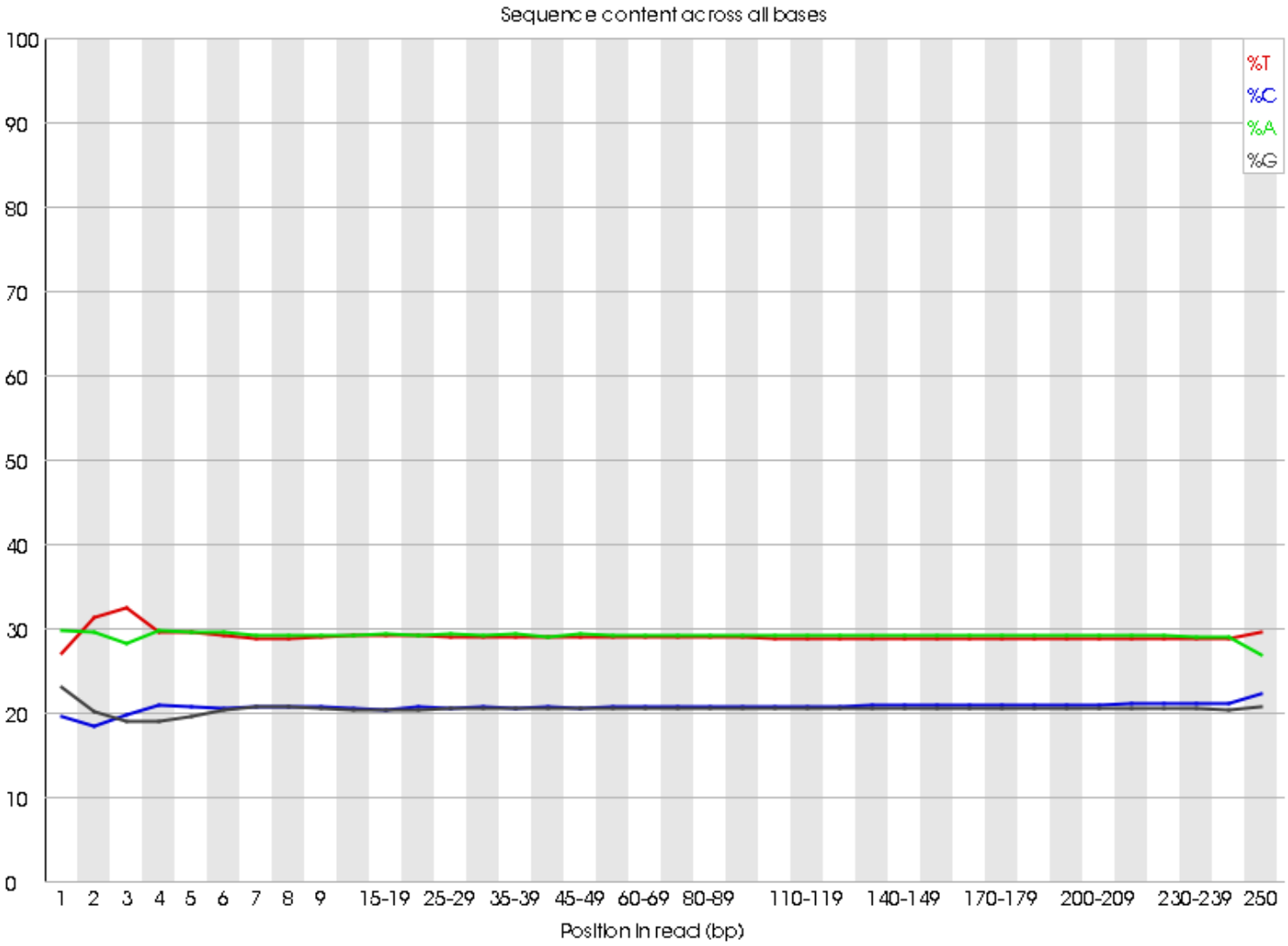
[FAIL] Per base sequence quality



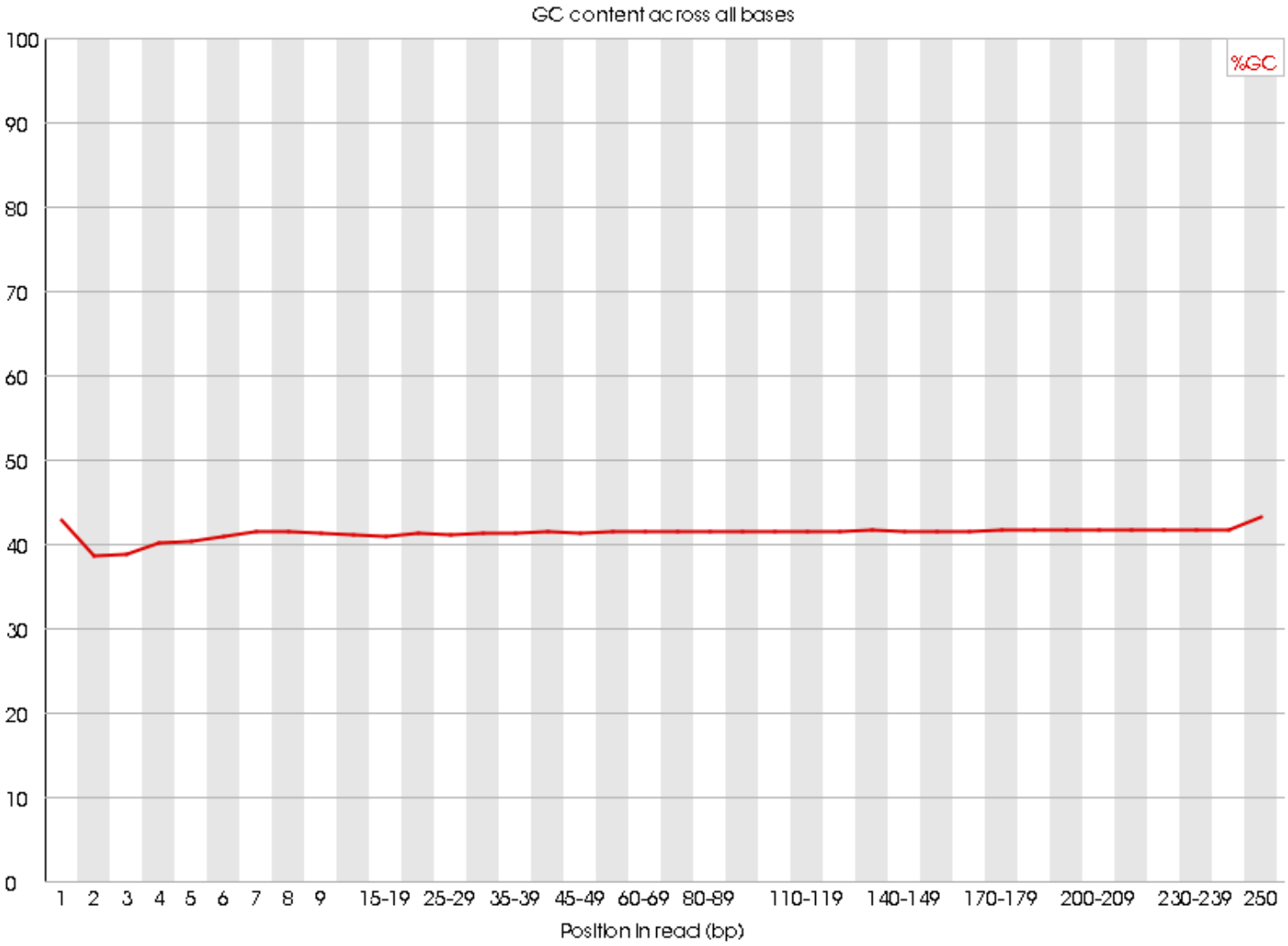
[OK] Per sequence quality scores



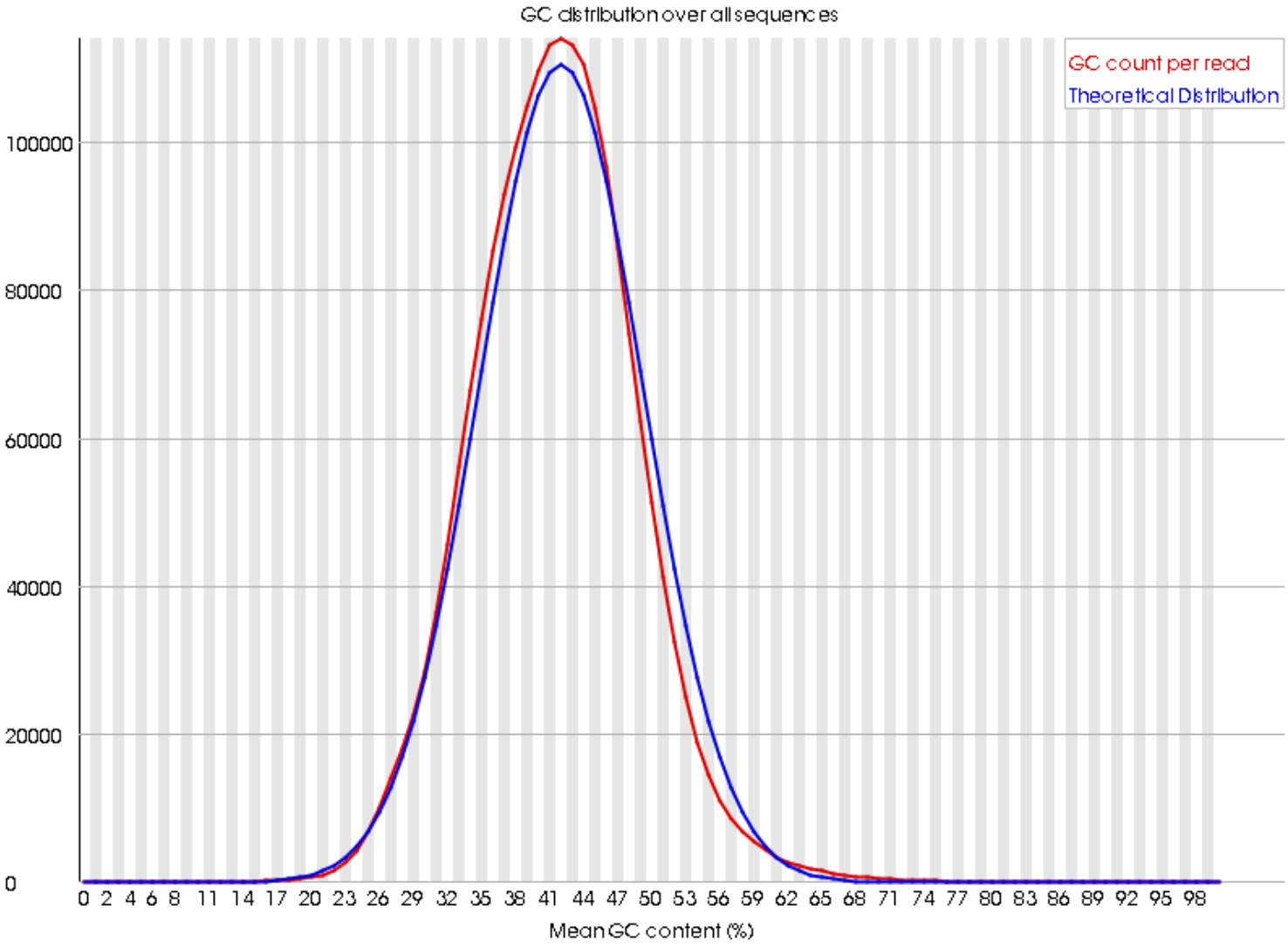
[WARN] Per base sequence content



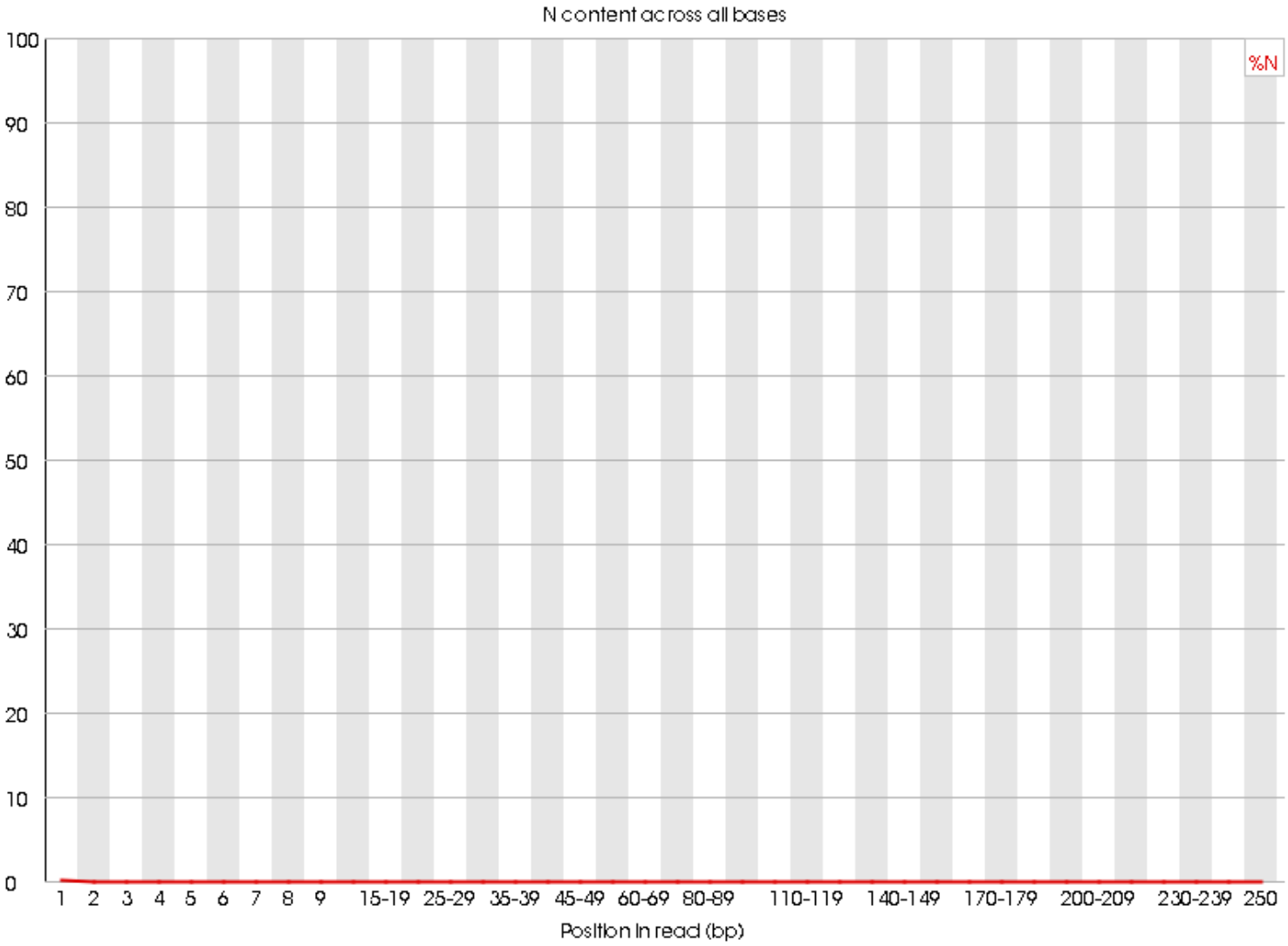
[OK] Per base GC content



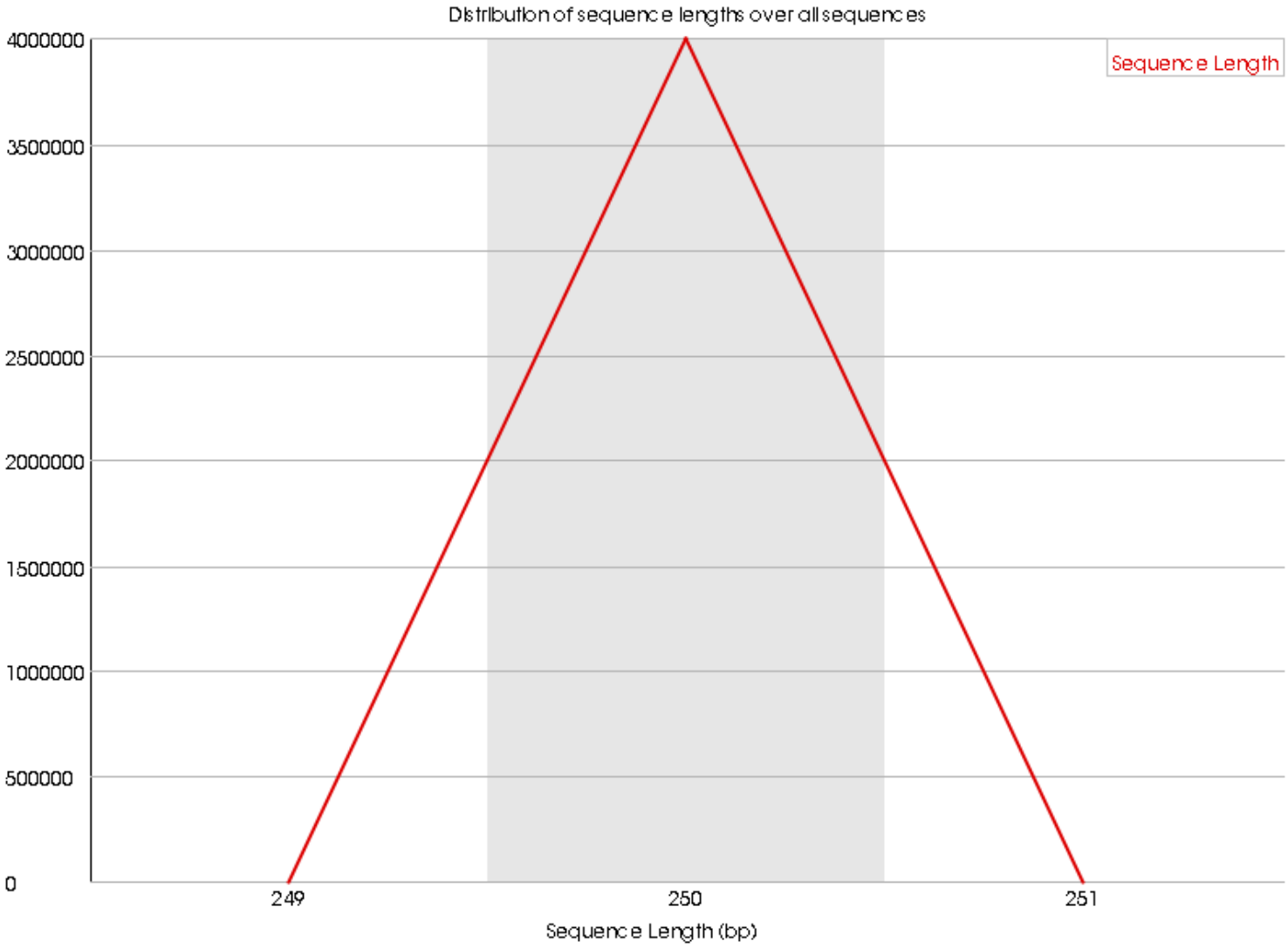
[OK] Per sequence GC content



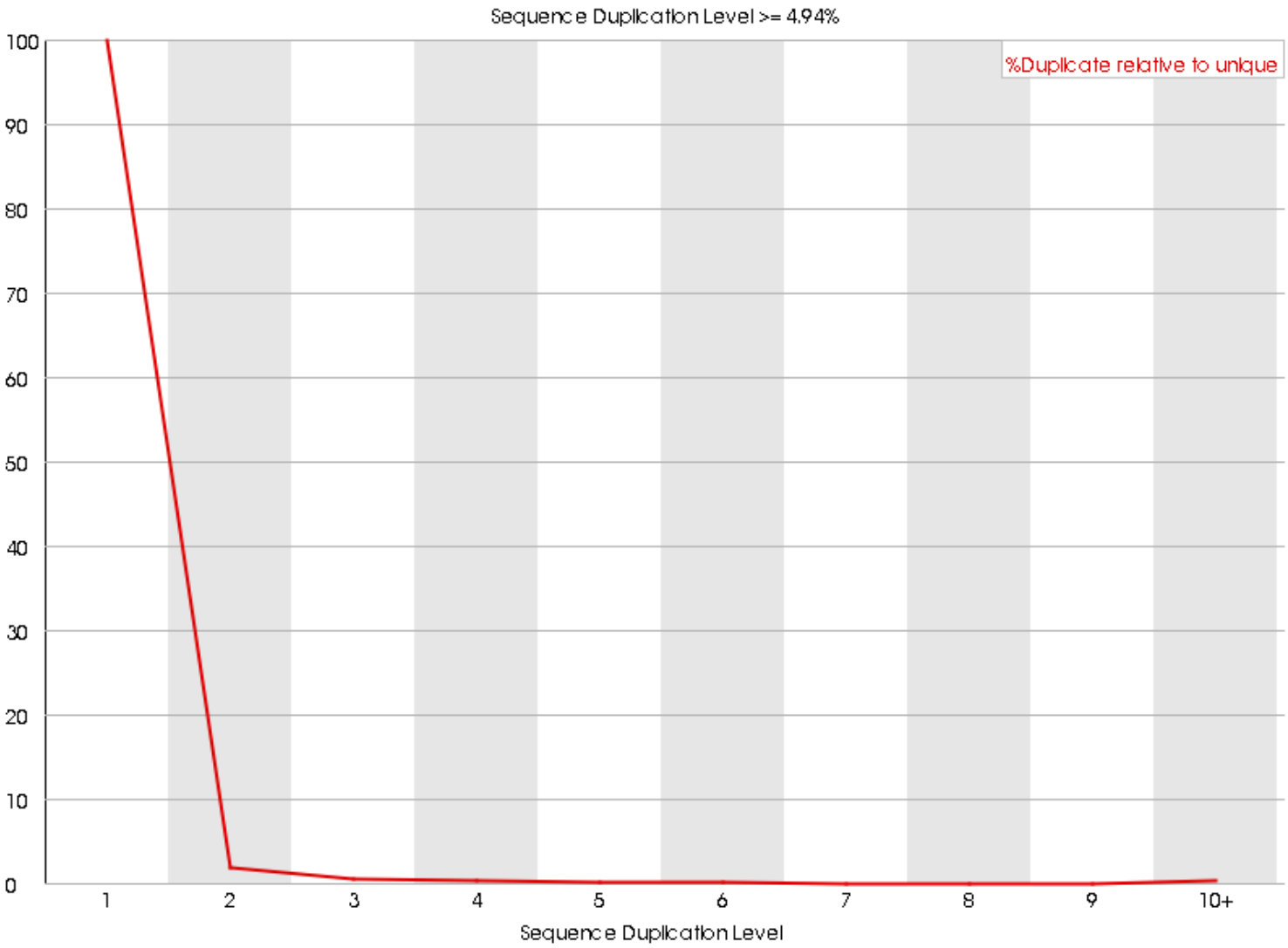
[OK] Per base N content



[OK] Sequence Length Distribution



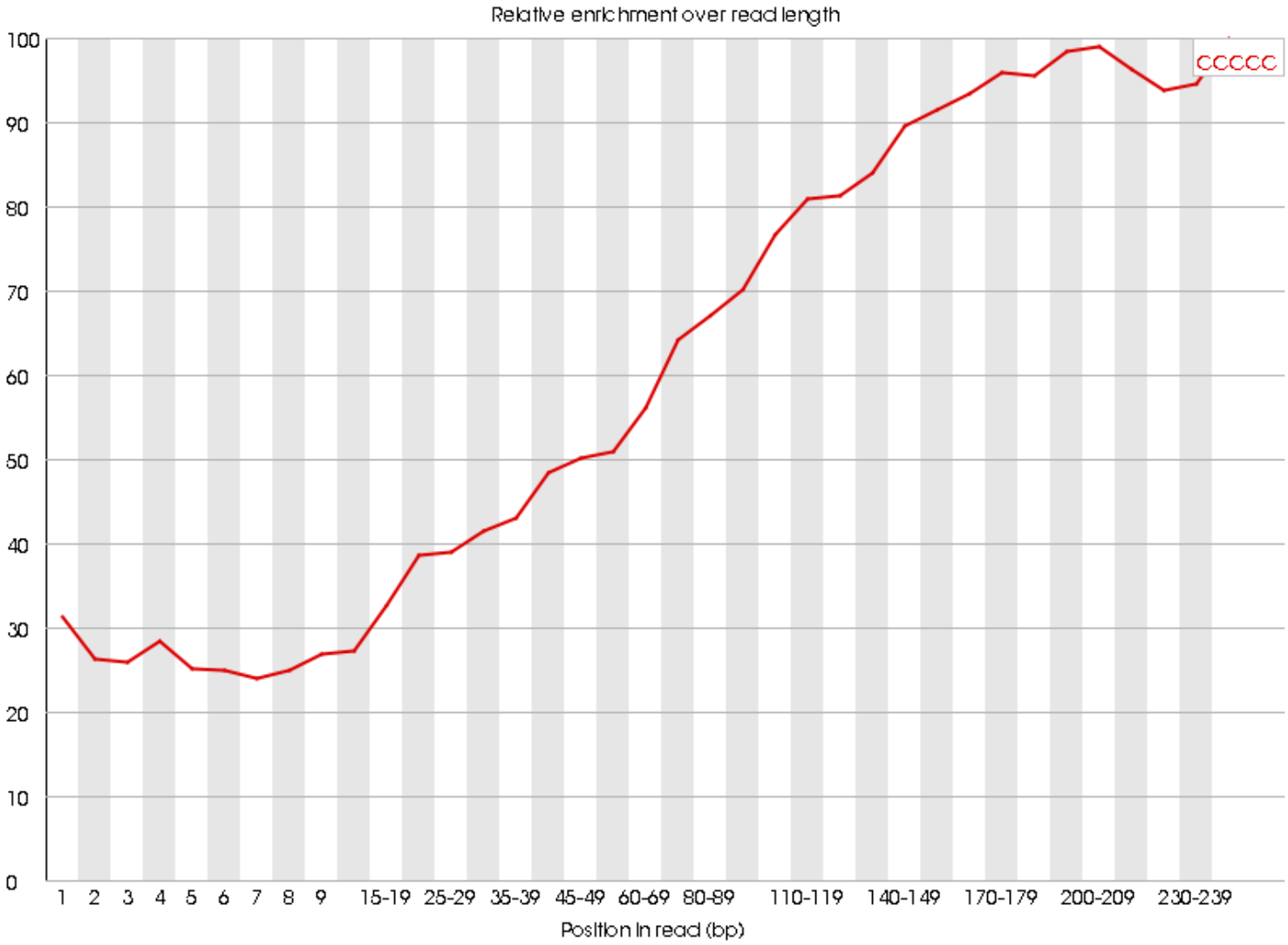
[OK] Sequence Duplication Levels



[OK] Overrepresented sequences

No overrepresented sequences

[WARN] Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CCCCC	1383140	3.4691947	4.647249	240-246

Produced by FastQC (version 0.10.1)