












FastQC FastQC Report

Tue 5 May 2015

SW019_TGGCAAT_L001_R2_001.fastq.gz

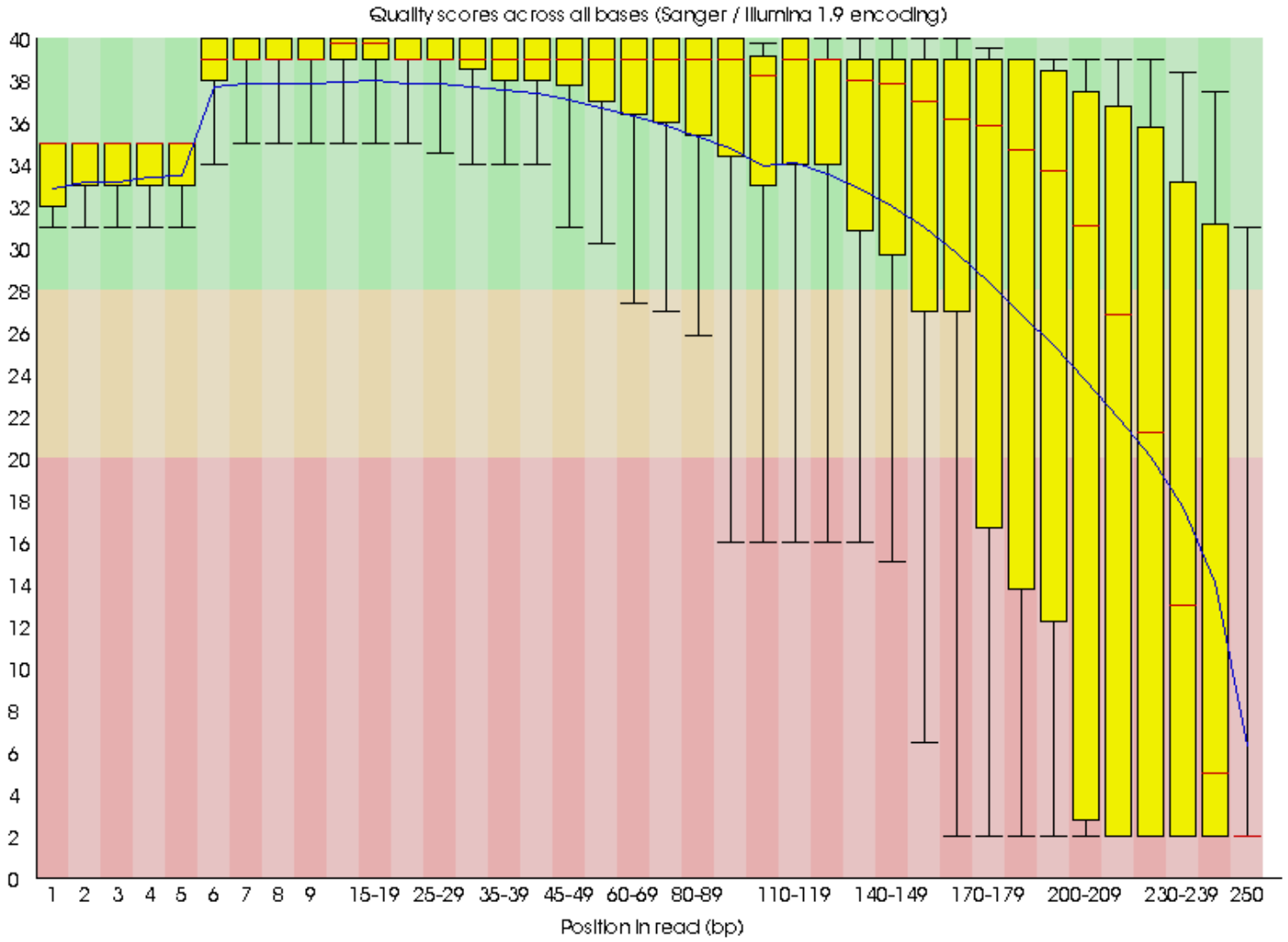
Summary

-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per base GC content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented sequences](#)
-  [Kmer Content](#)

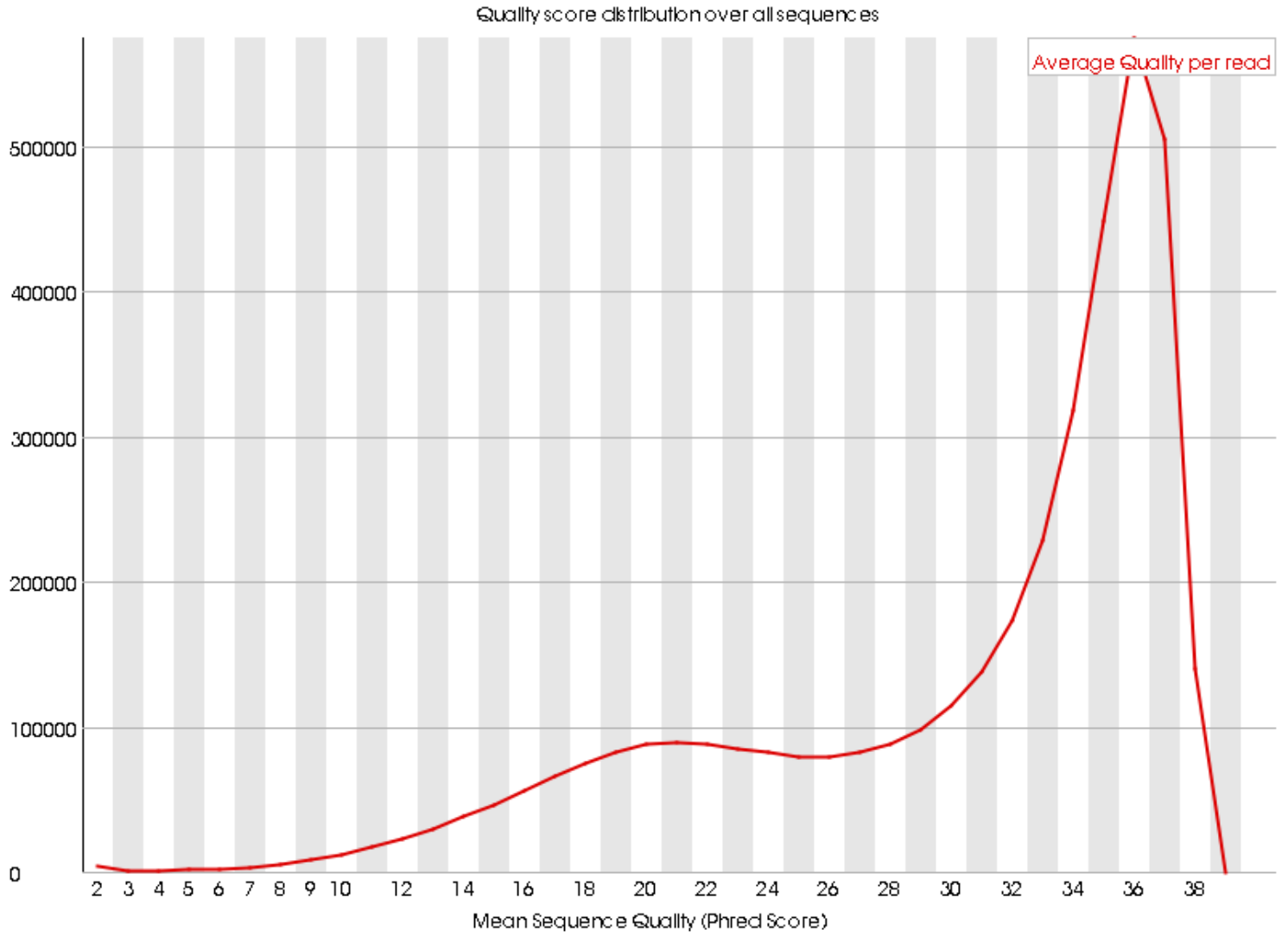
Basic Statistics

Measure	Value
Filename	SW019_TGGCAAT_L001_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4000000
Filtered Sequences	0
Sequence length	250
%GC	41

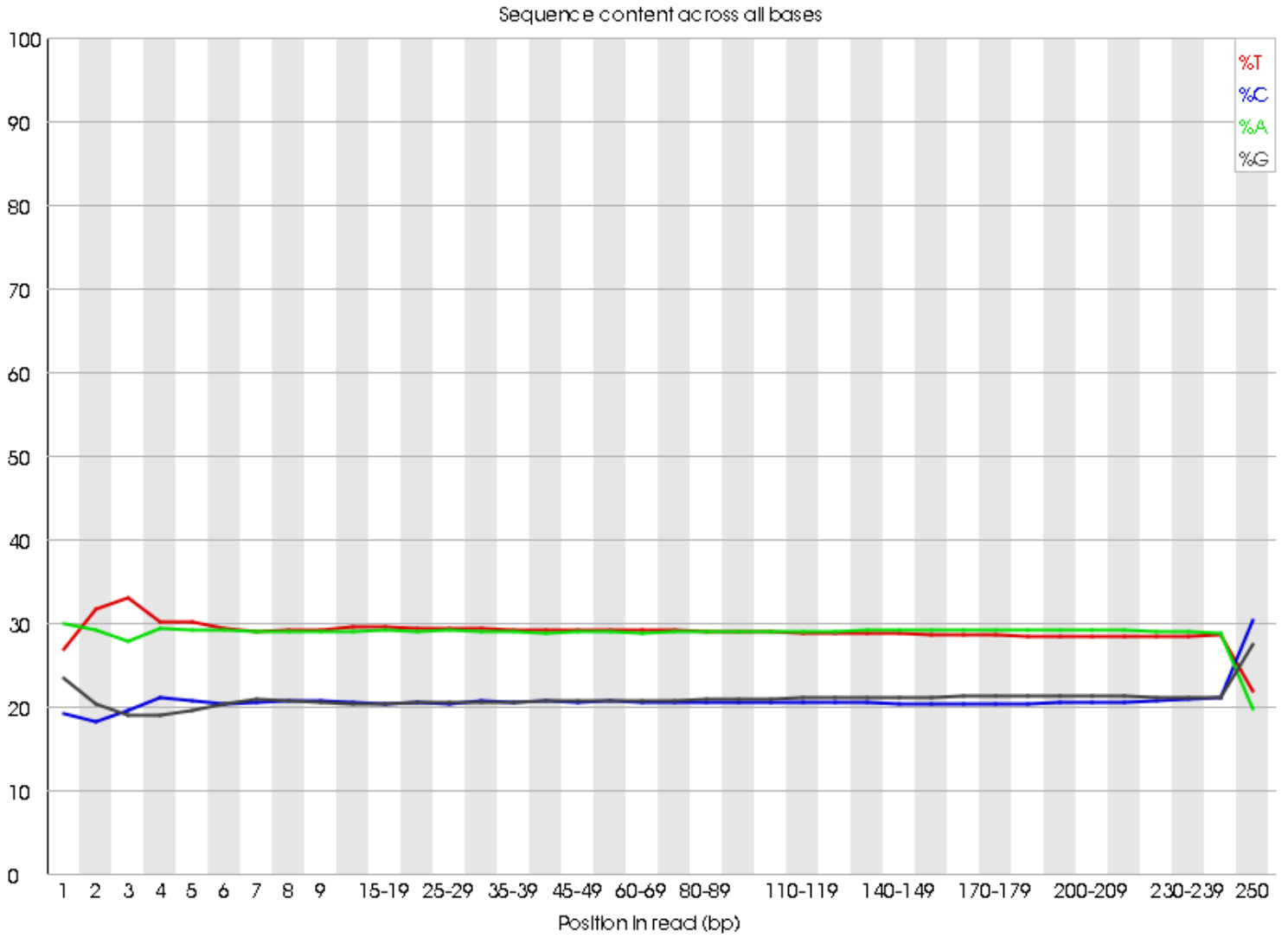
Per base sequence quality



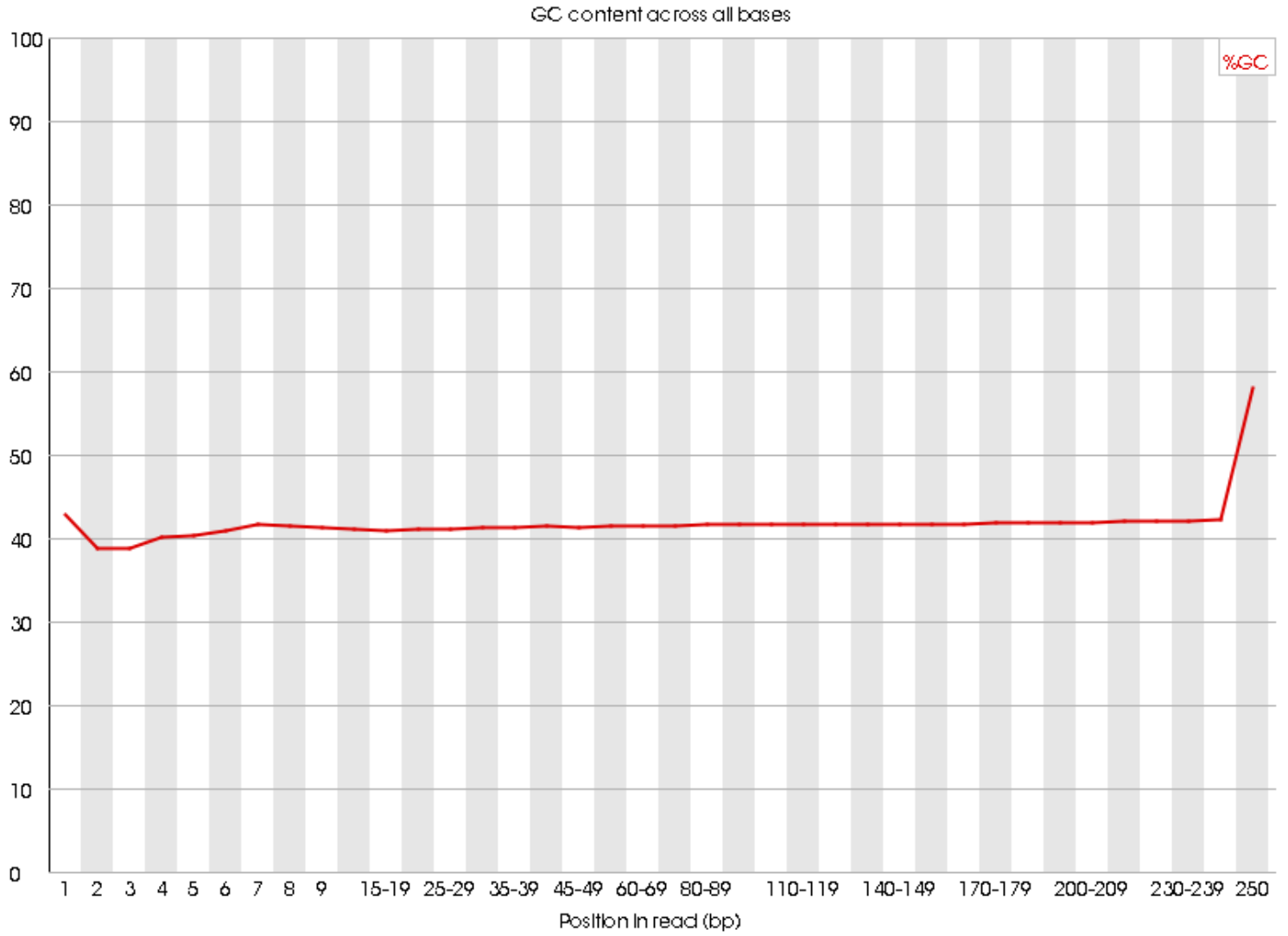
 **Per sequence quality scores**



 **[WARN]** Per base sequence content

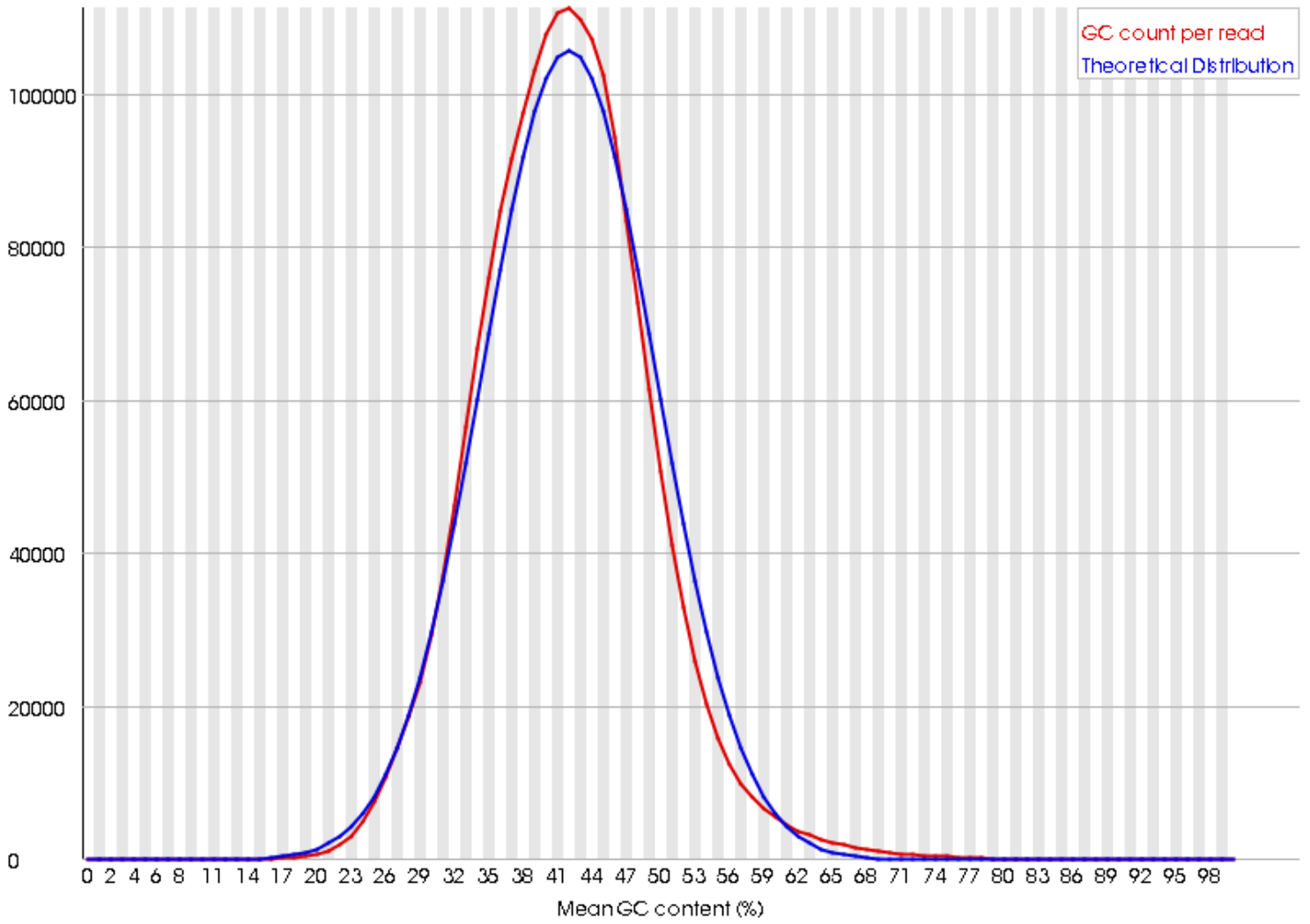


 **[FAIL] Per base GC content**



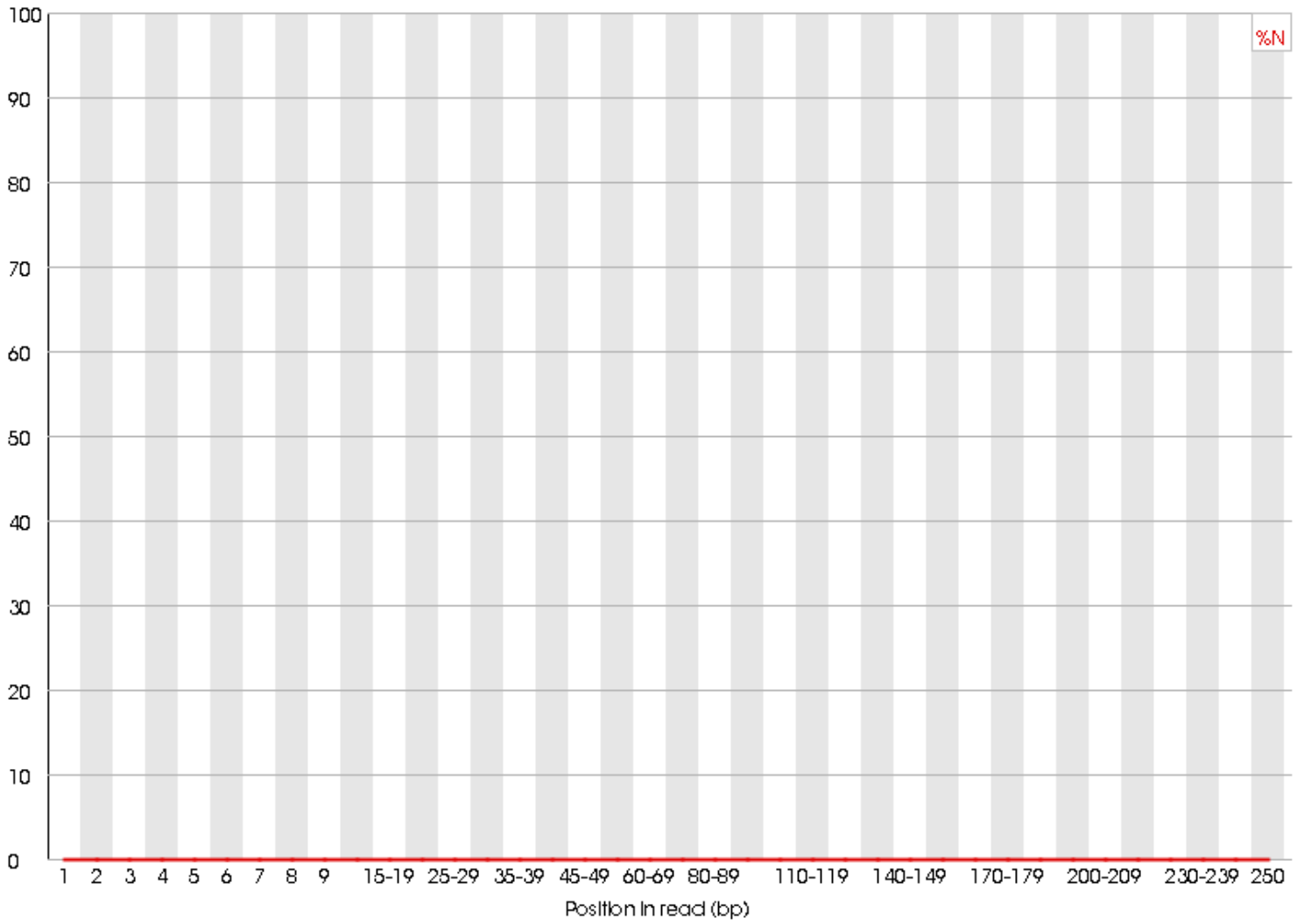
 **Per sequence GC content**

GC distribution over all sequences

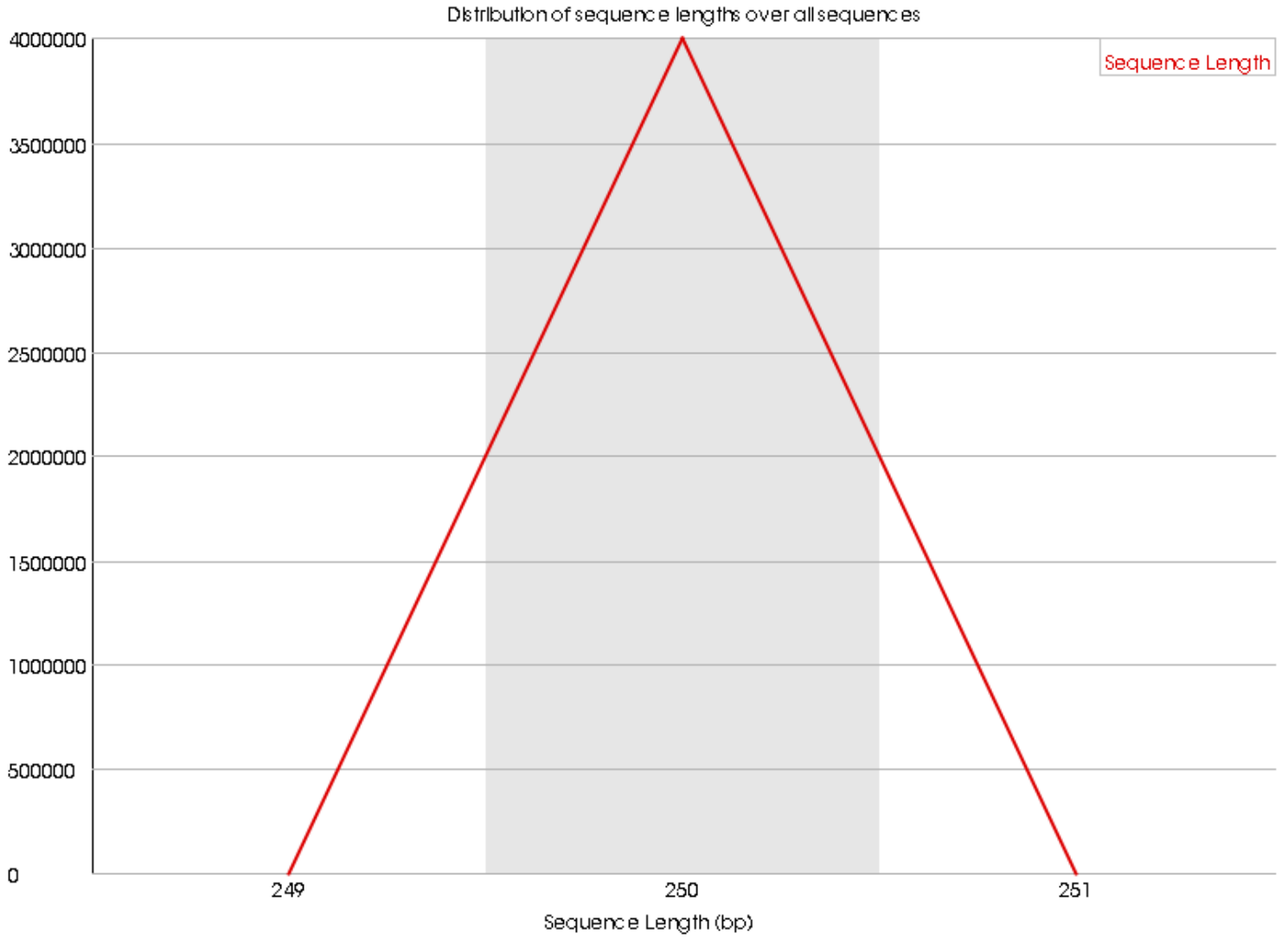


 **Per base N content**

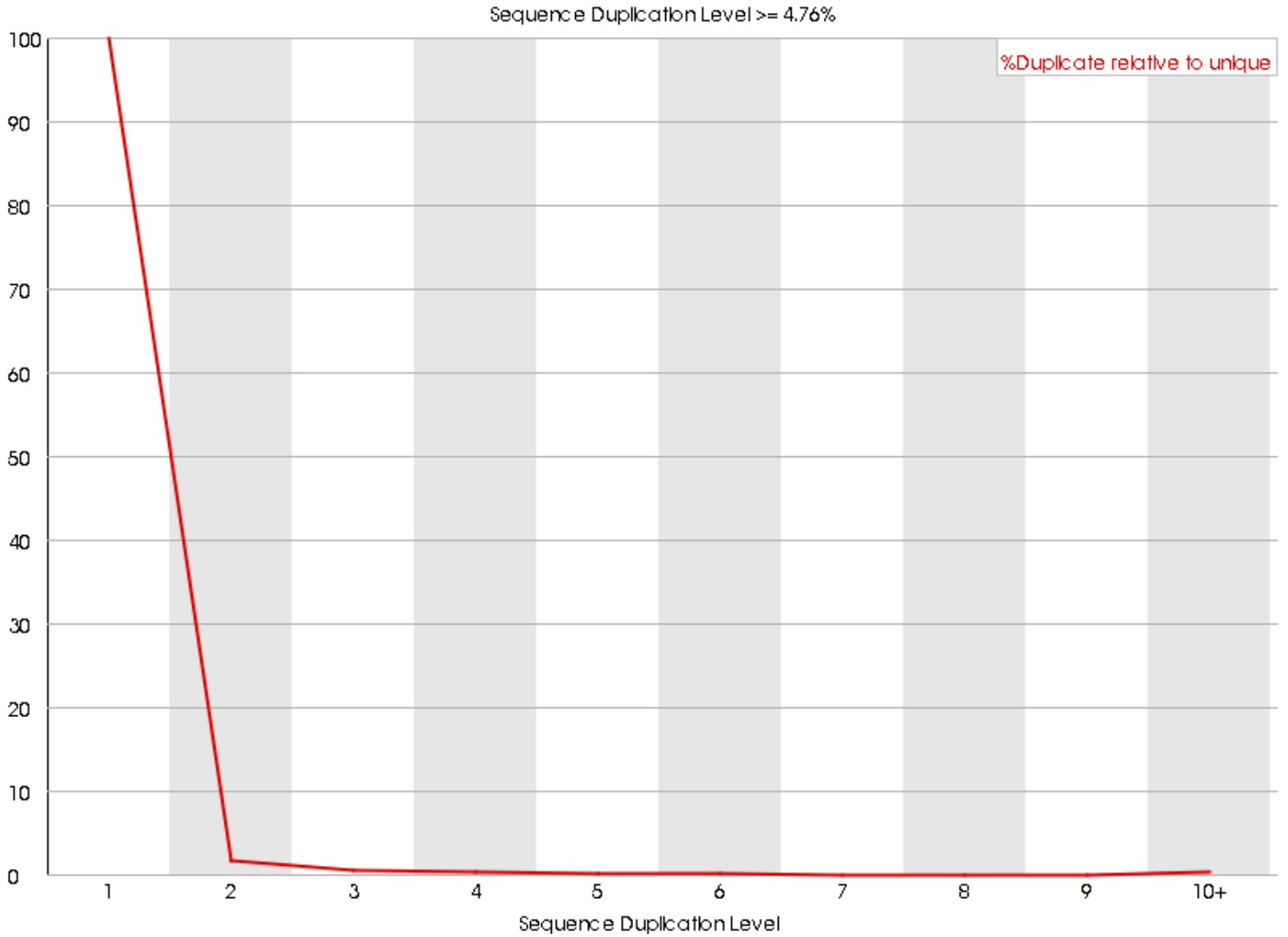
N content across all bases



 **Sequence Length Distribution**



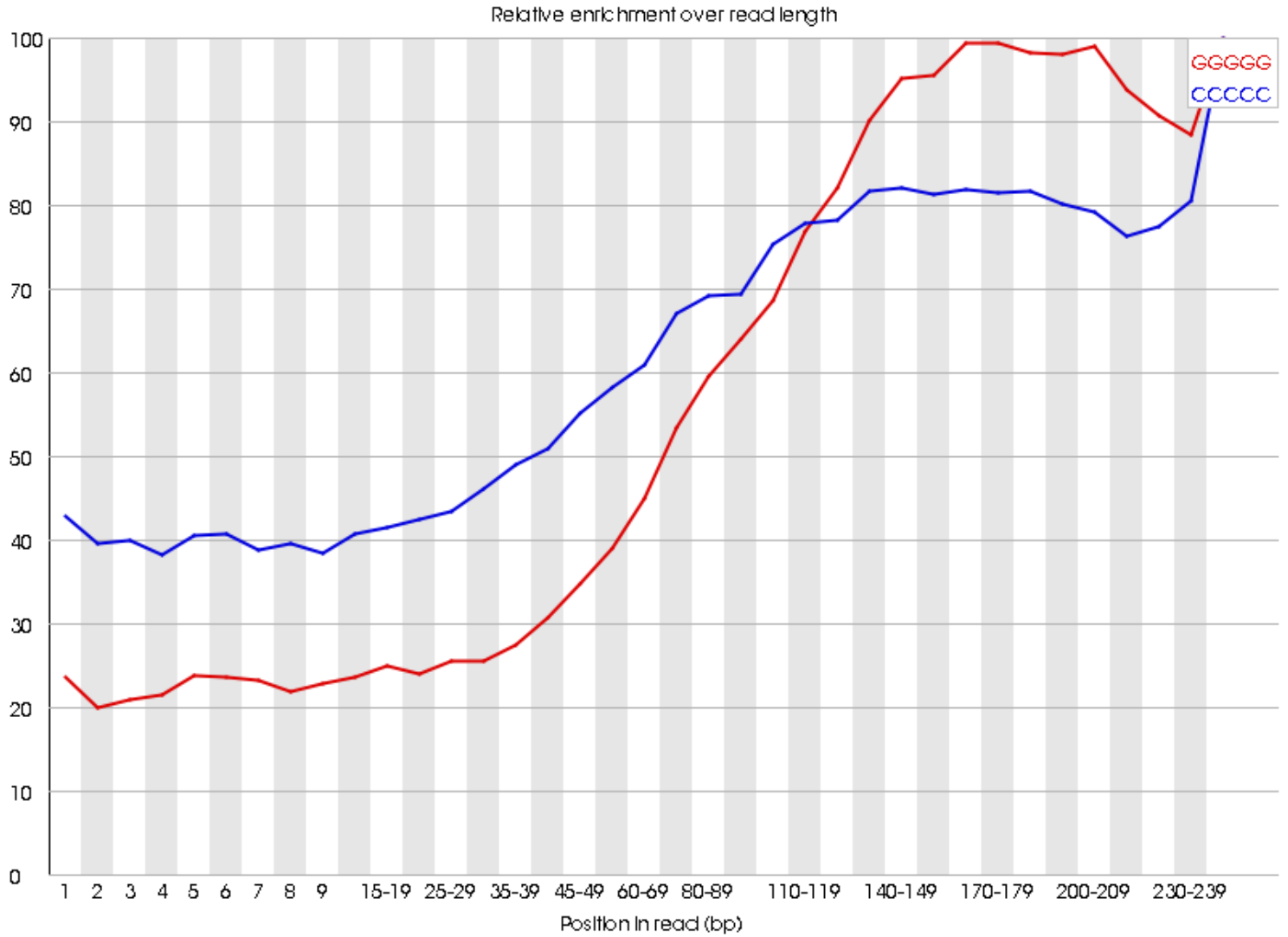
 **Sequence Duplication Levels**



 **[OK] Overrepresented sequences**

No overrepresented sequences

 **[WARN] Kmer Content**



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
GGGGG	1730880	4.1686106	5.9015985	240-246
CCCCC	1139060	3.0332878	4.3039985	240-246

Produced by [FastQC](#) (version 0.10.1)