












FastQC Report

Summary

Mon 4 Jun 2012
trps1myc.bam

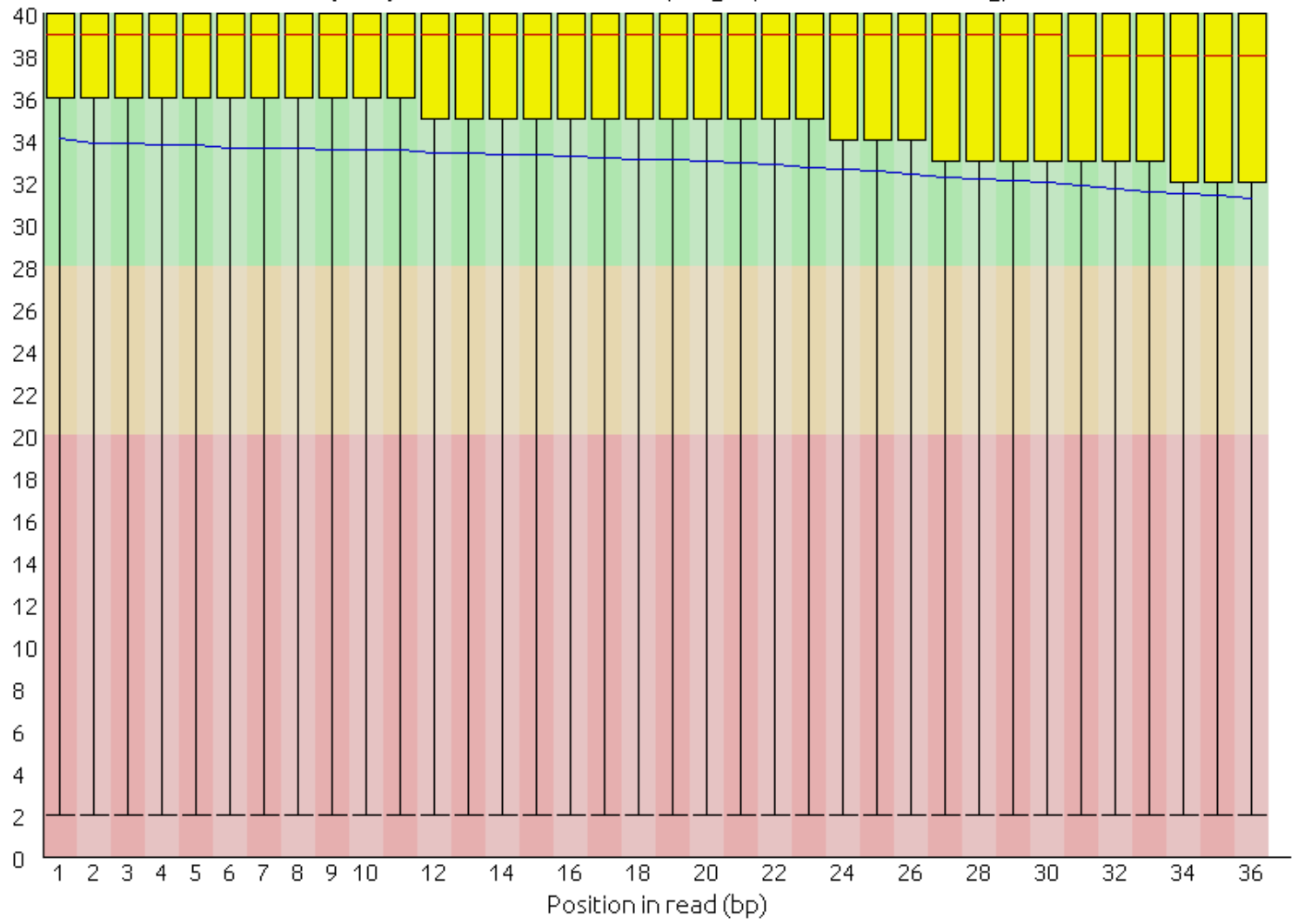
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per base GC content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented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

Basic Statistics

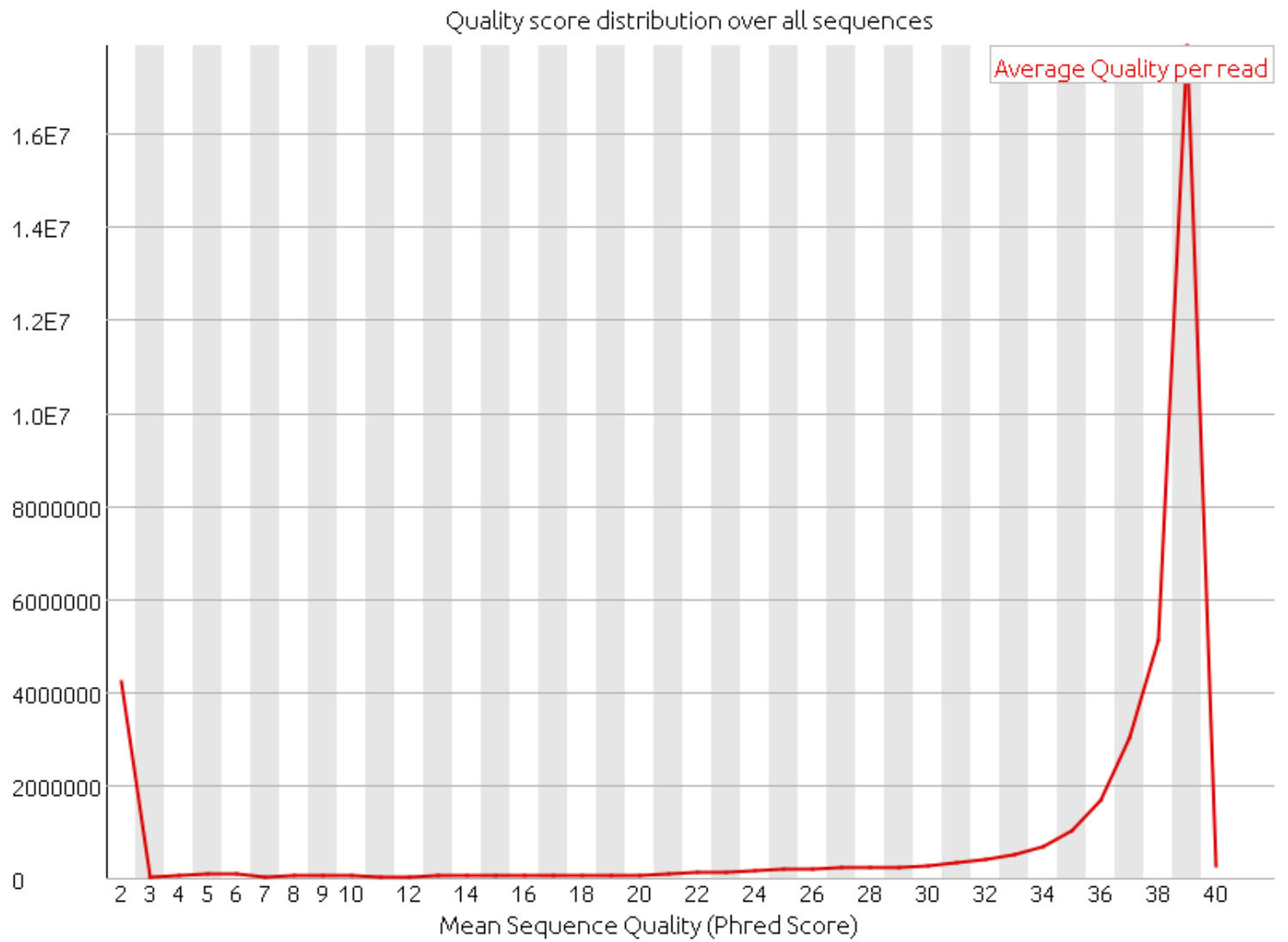
| Measure | Value |
|--------------------|-------------------------|
| Filename | trps1myc.bam |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 38947351 |
| Filtered Sequences | 0 |
| Sequence length | 36 |
| %GC | 43 |

Per base sequence quality

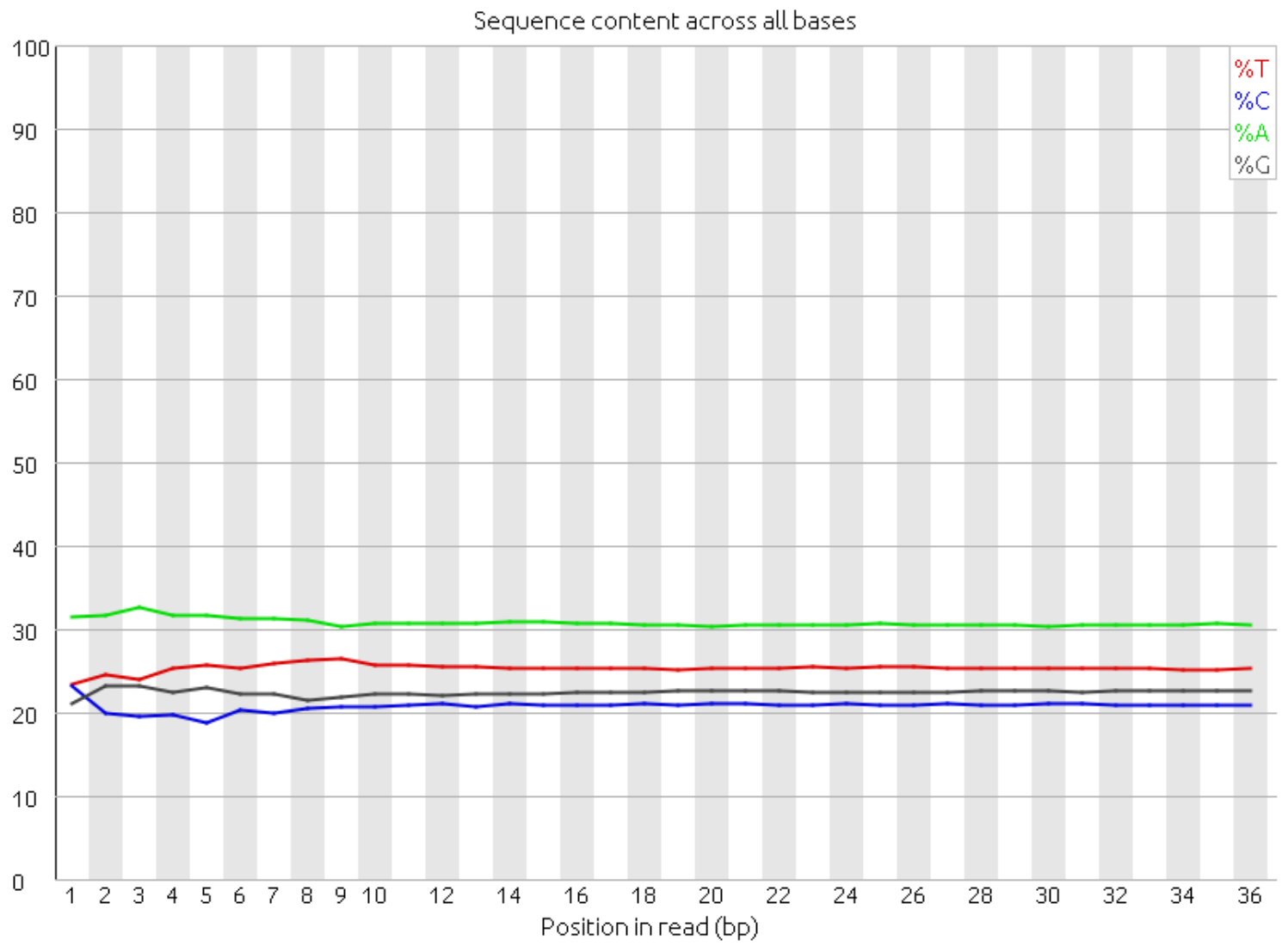
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



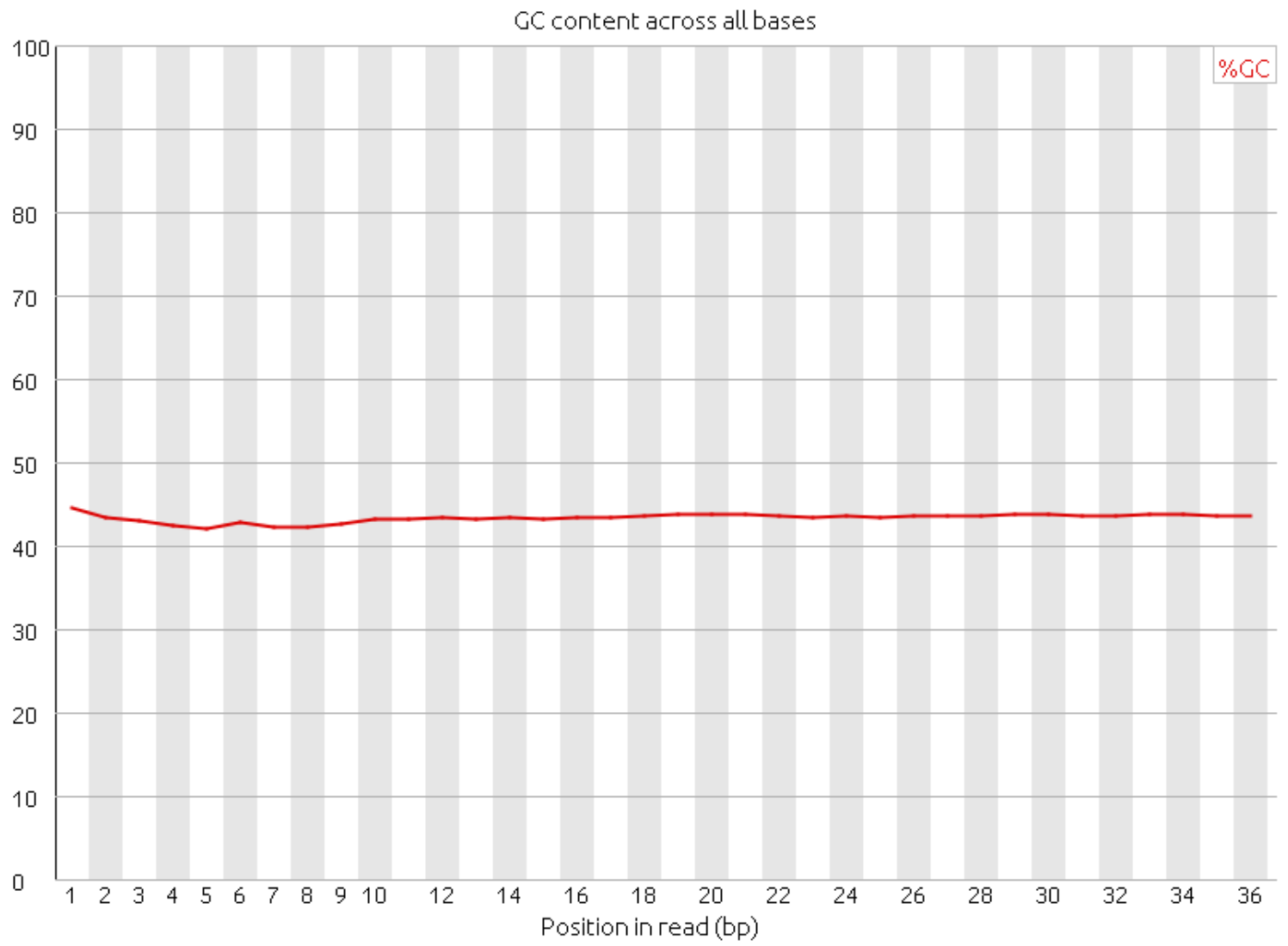
Per sequence quality scores



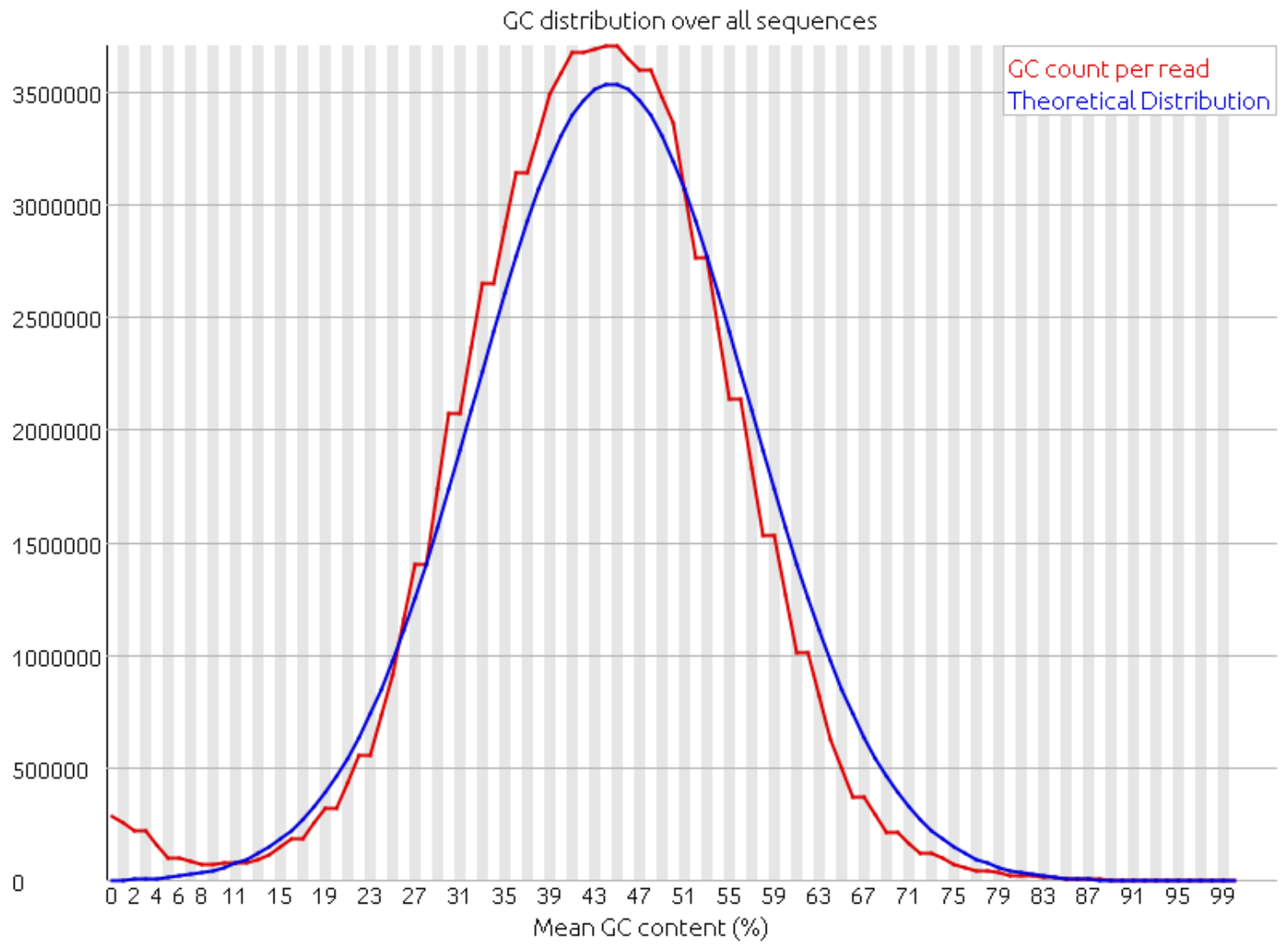
⚠ Per base sequence content



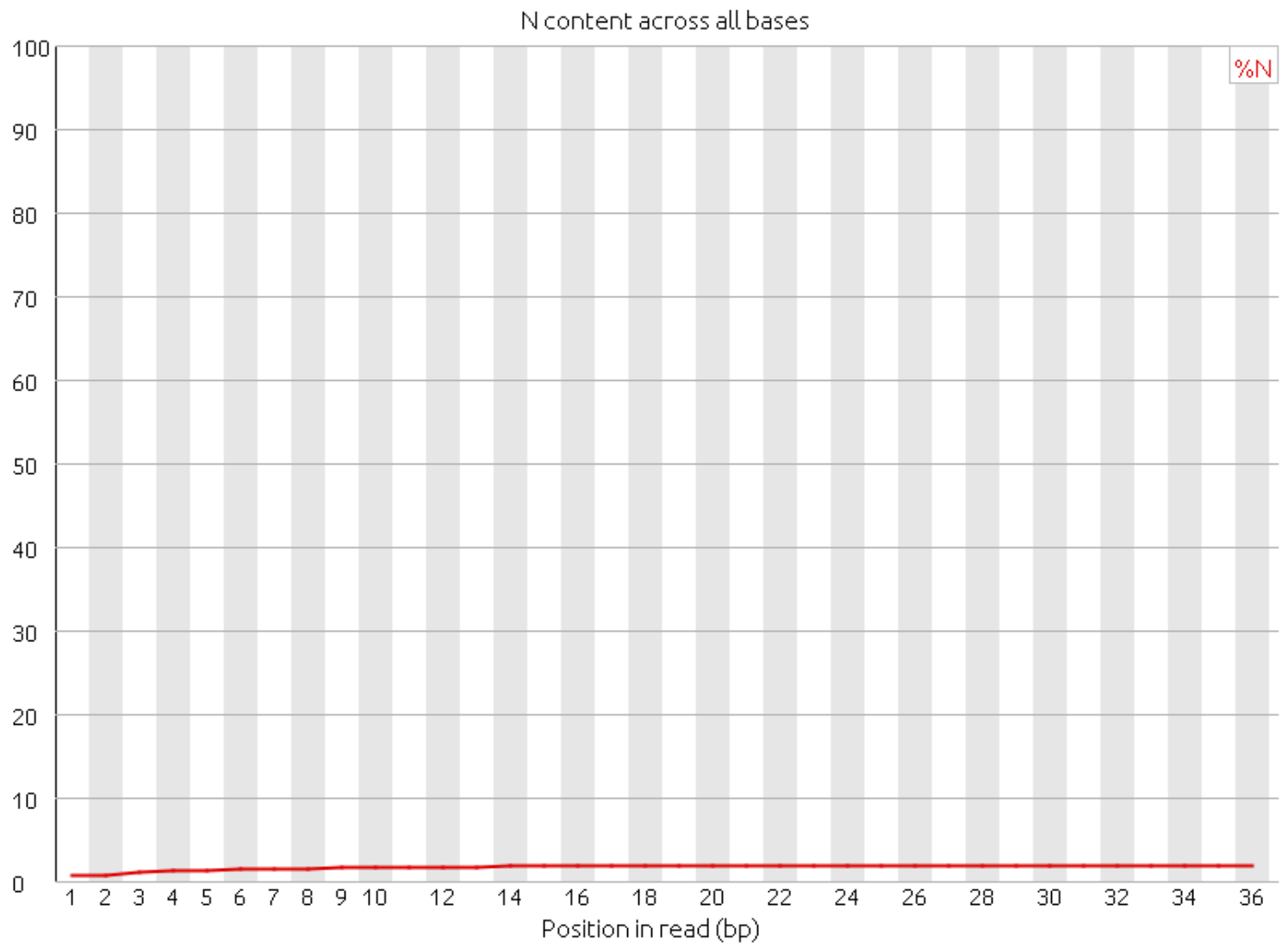
 **Per base GC content**



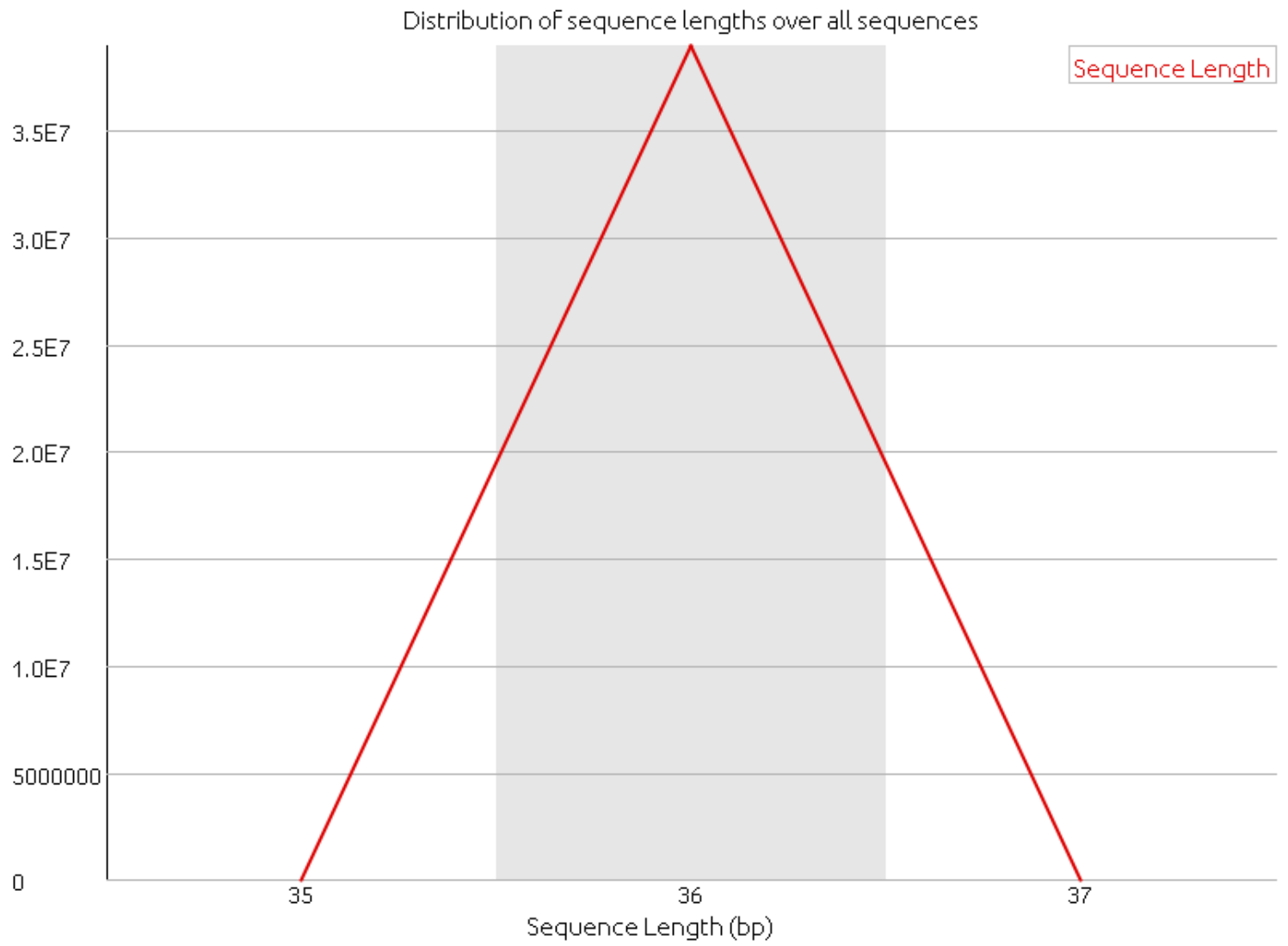
 **Per sequence GC content**



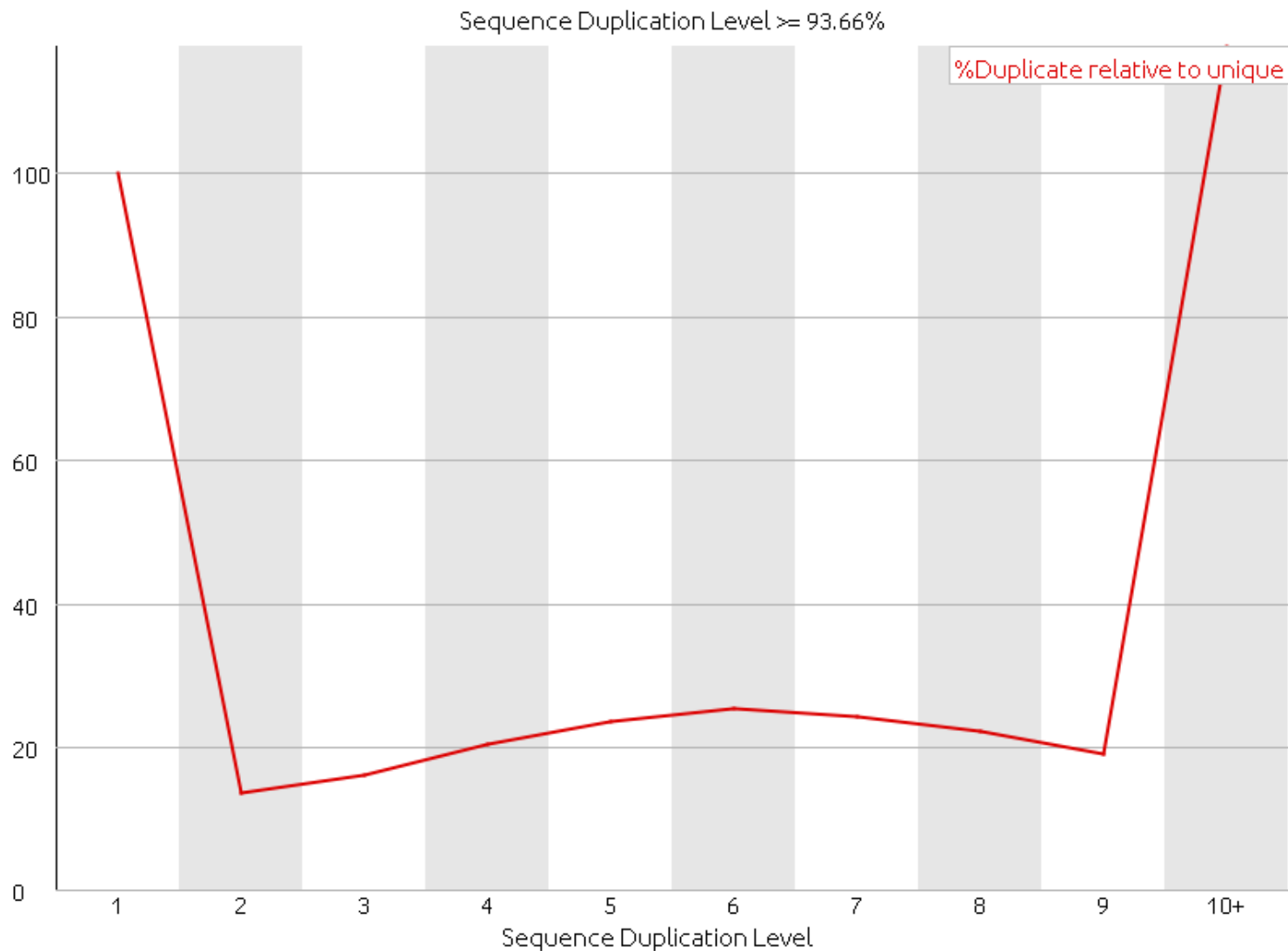
 **Per base N content**



Sequence Length Distribution



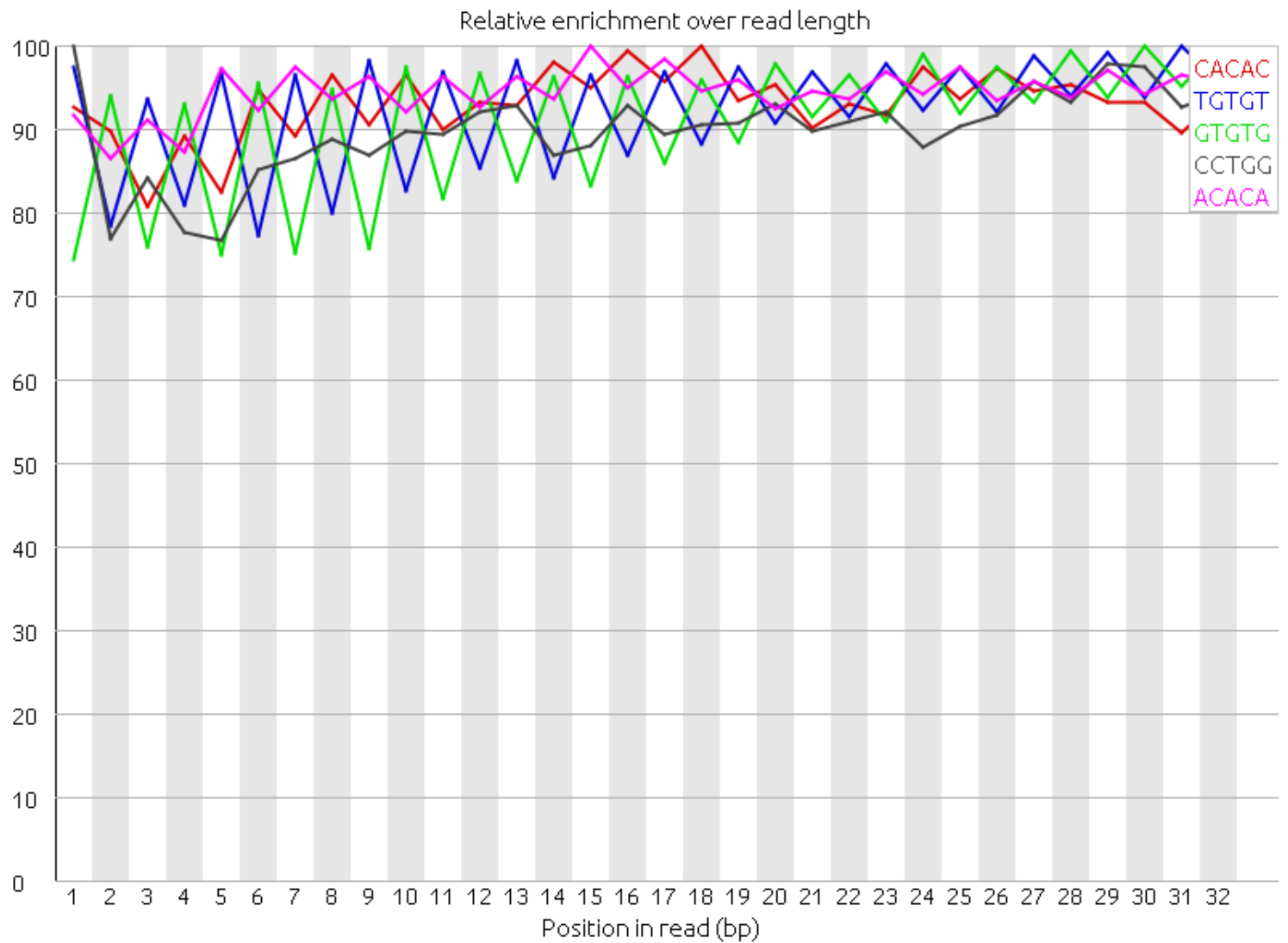
Sequence Duplication Levels



 **Overrepresented sequences**

No overrepresented sequences

 **Kmer Content**



| Sequence | Count | Obs/Exp Overall | Obs/Exp Max | Max Obs/Exp Position |
|----------|---------|-----------------|-------------|----------------------|
| CACAC | 4181625 | 3.8788815 | 4.1621475 | 18 |
| TGTGT | 3596700 | 3.4858143 | 3.773373 | 31 |
| GTGTG | 3016100 | 3.3008983 | 3.6306105 | 30 |
| CCTGG | 2161945 | 3.101977 | 3.4514375 | 1 |
| ACACA | 4937525 | 3.0984564 | 3.2751606 | 15 |

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