












FastQC Report

Summary

Mon 4 Jun 2012
gli3rmvc.bam

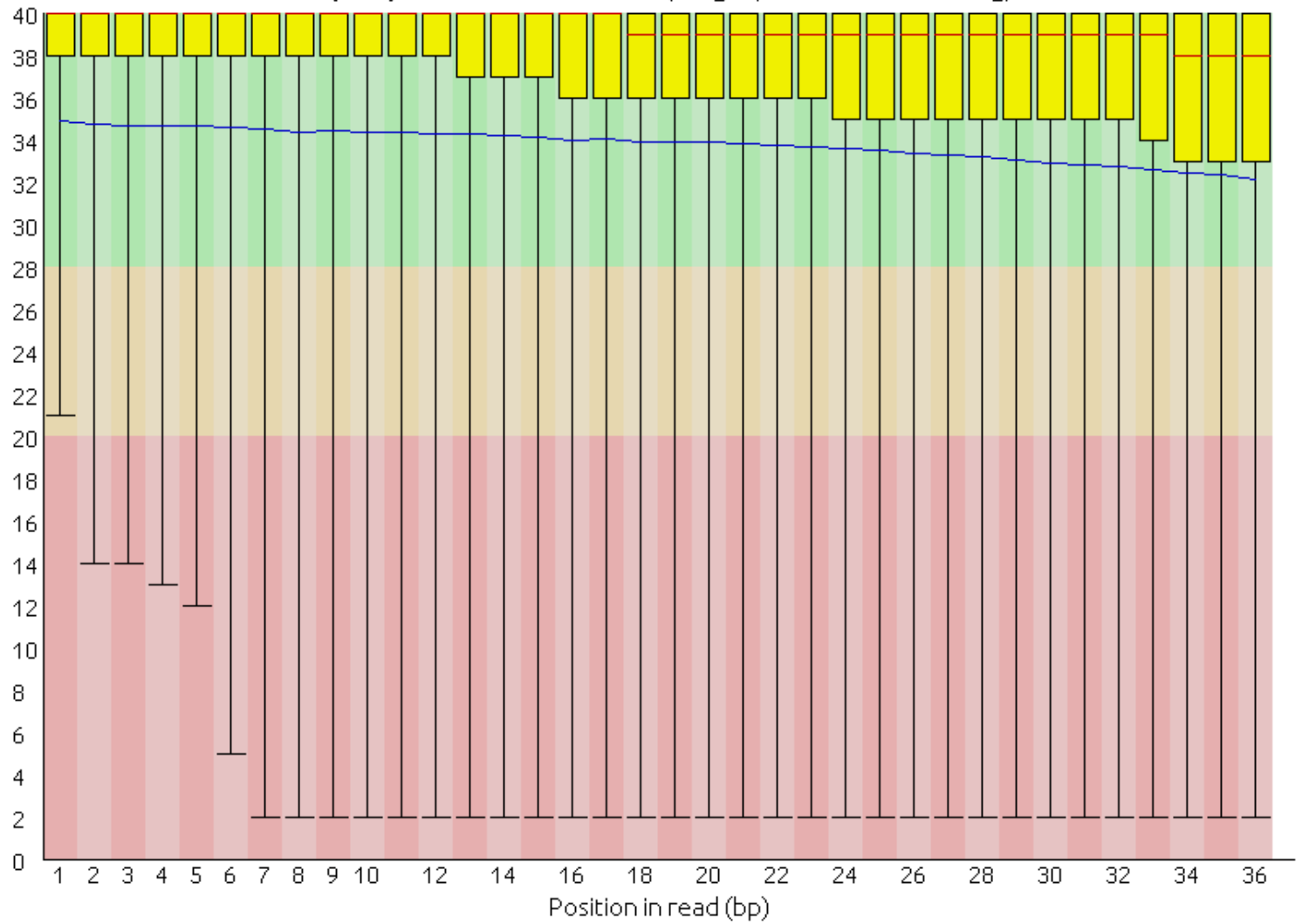
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Basic Statistics

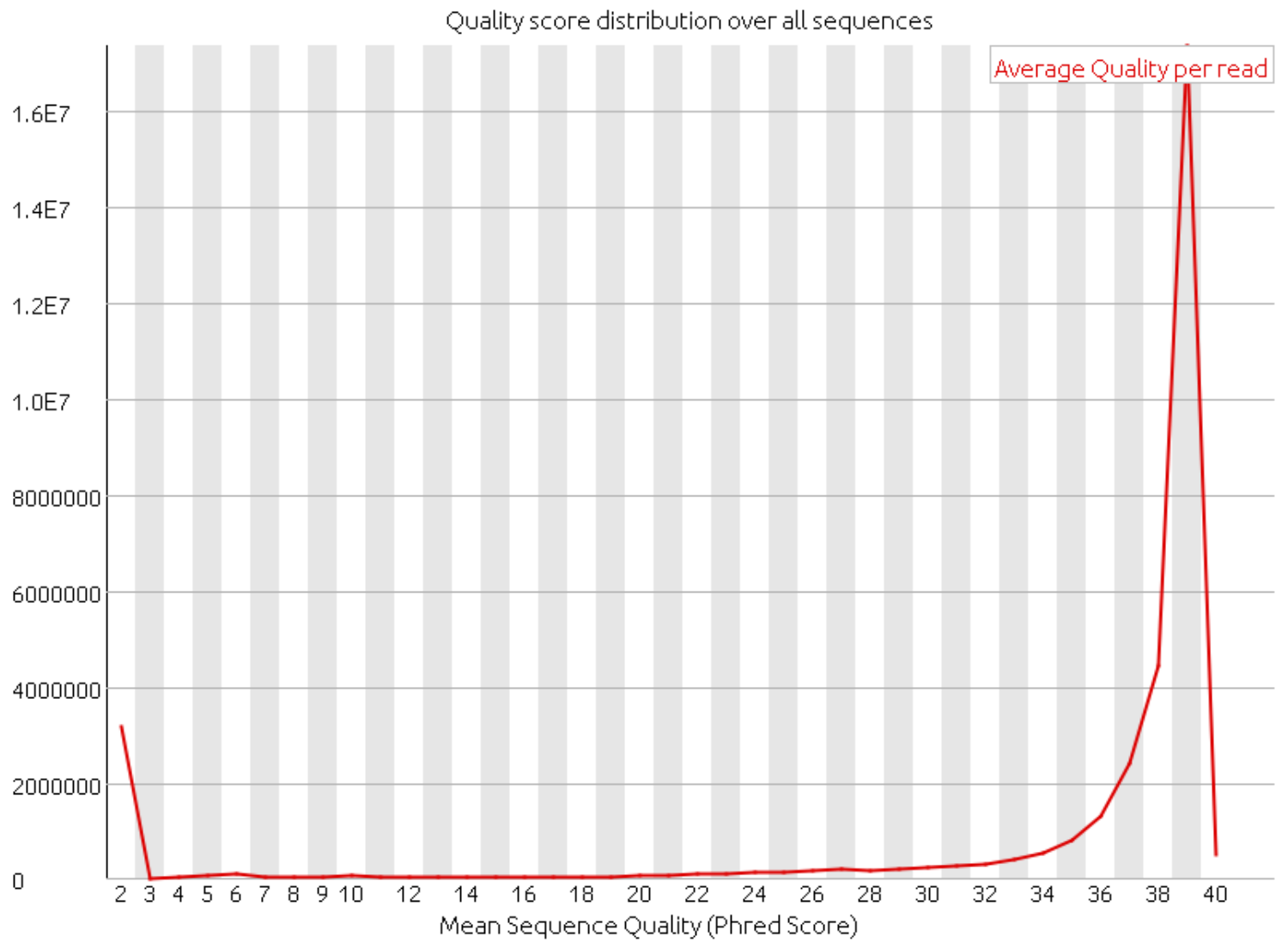
Measure	Value
Filename	gli3rmvc.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	34421313
Filtered Sequences	0
Sequence length	36
%GC	44

Per base sequence quality

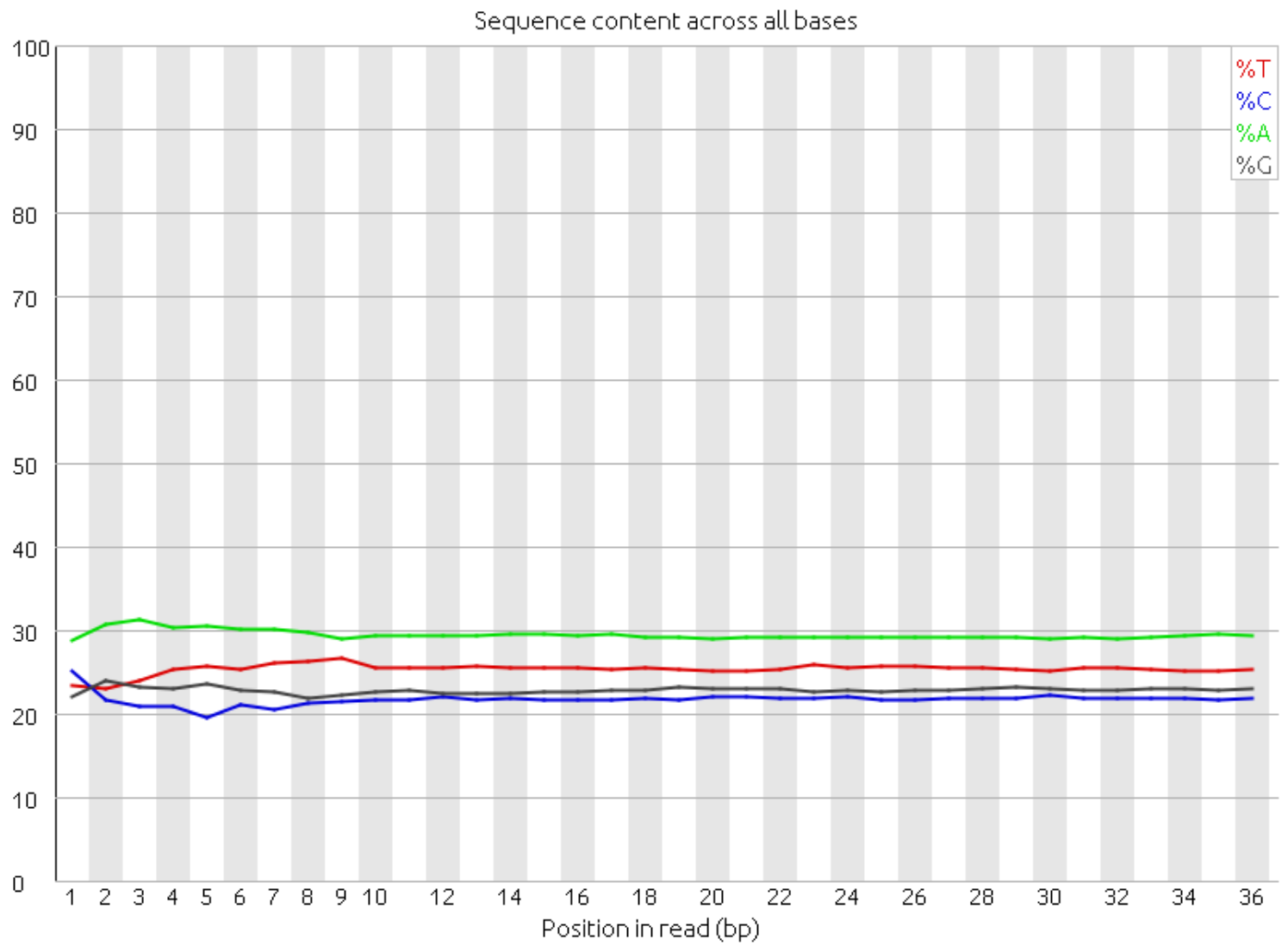
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



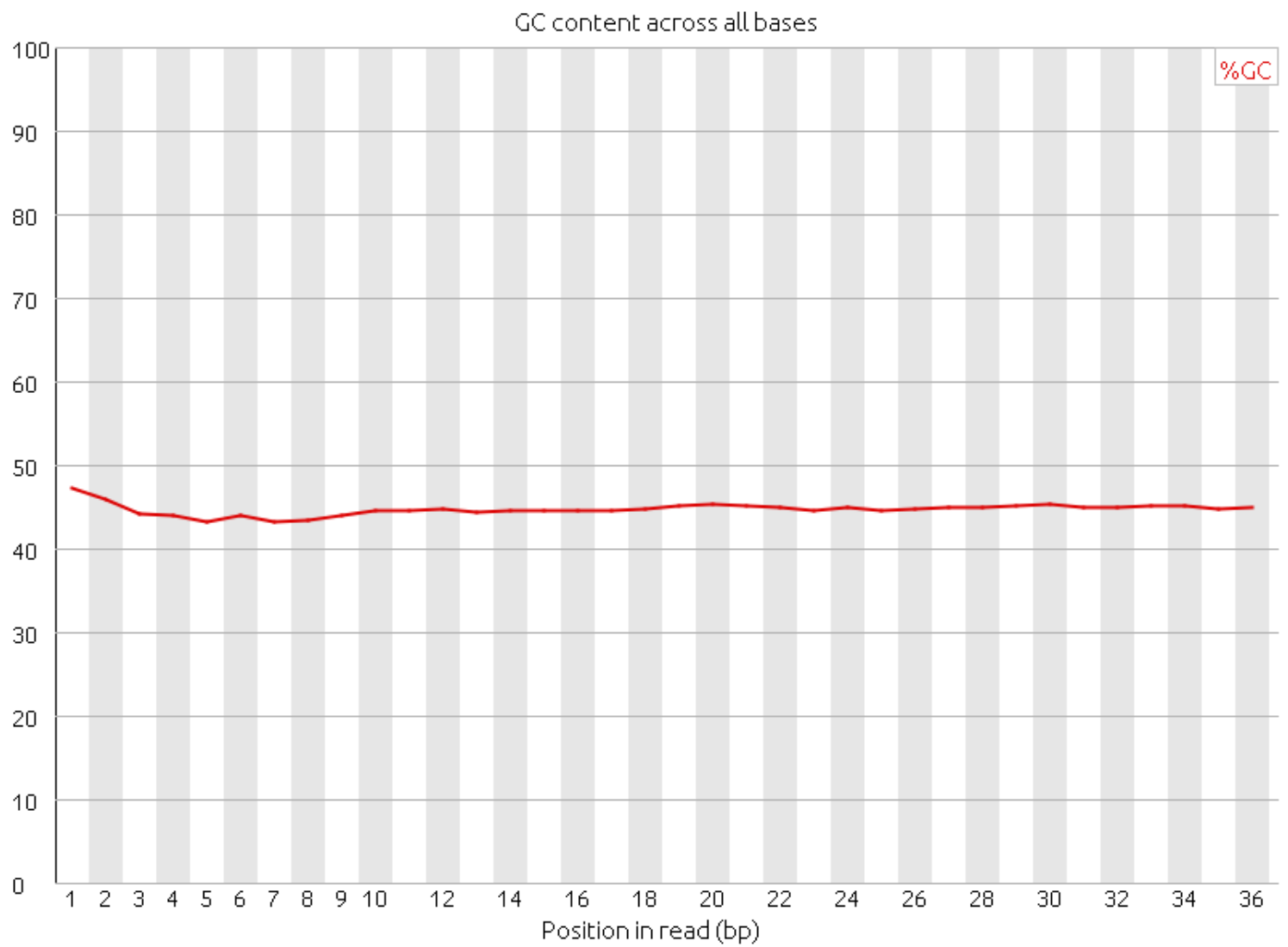
Per sequence quality scores



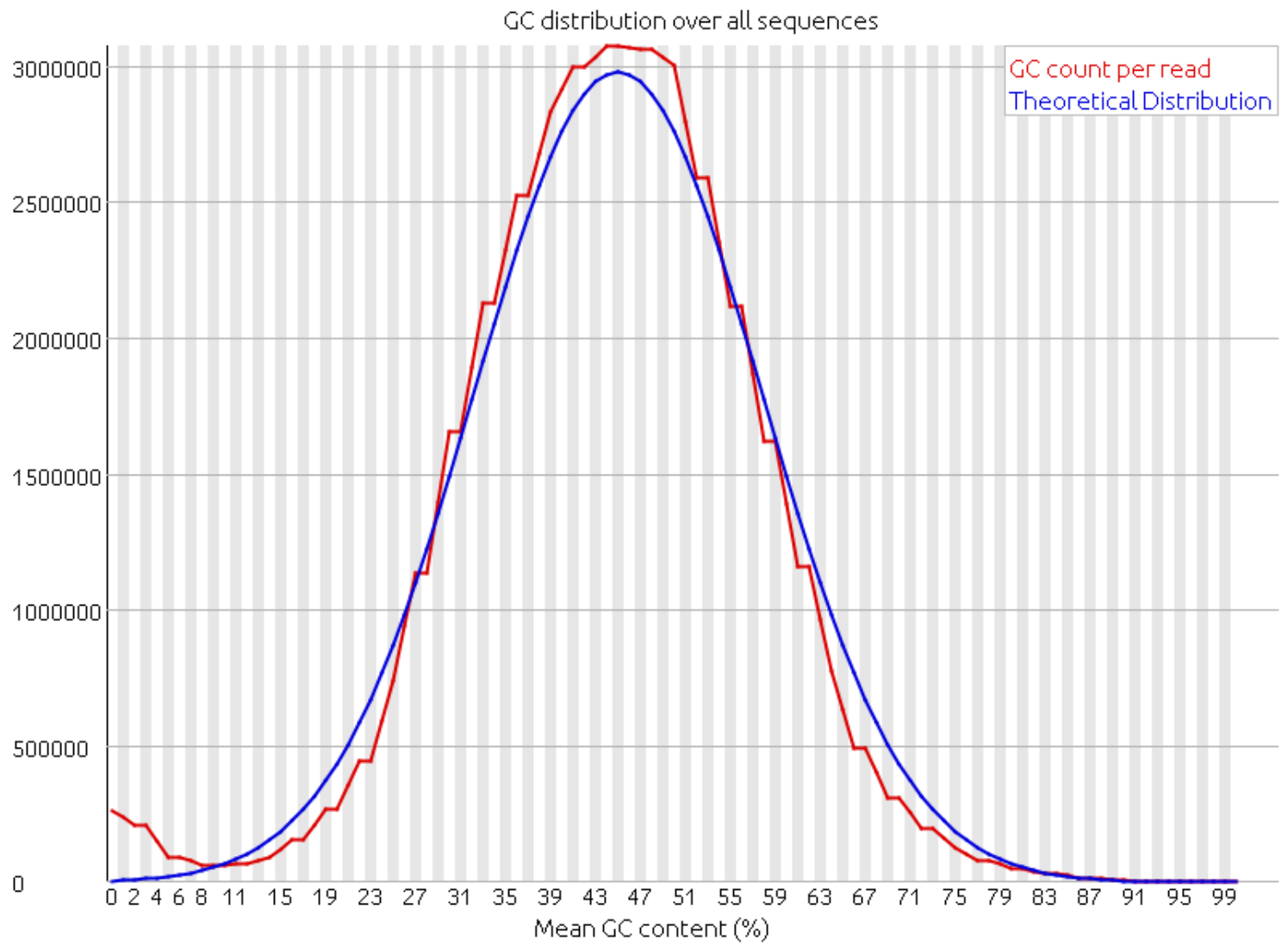
⚠ Per base sequence content



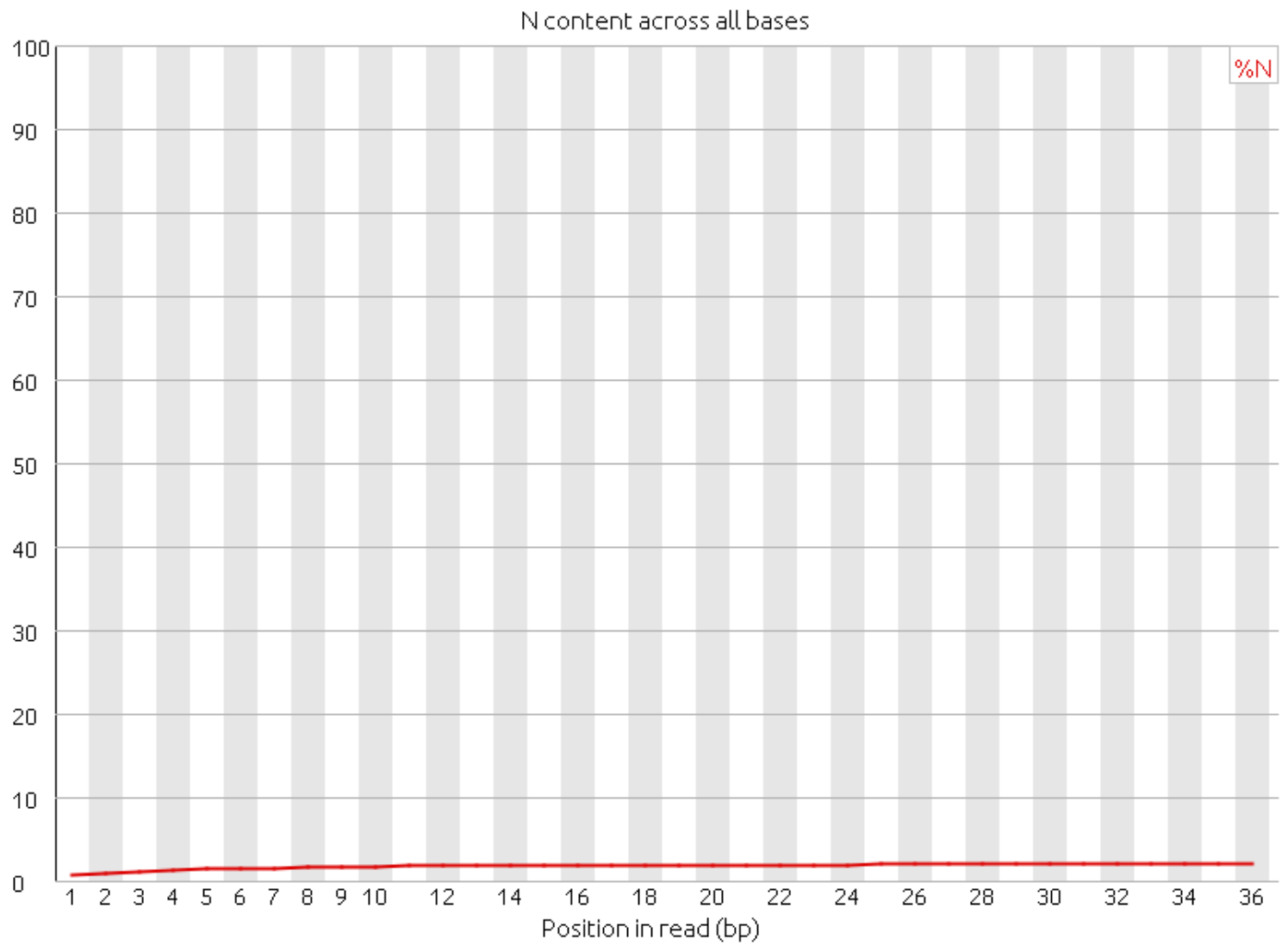
Per base GC content



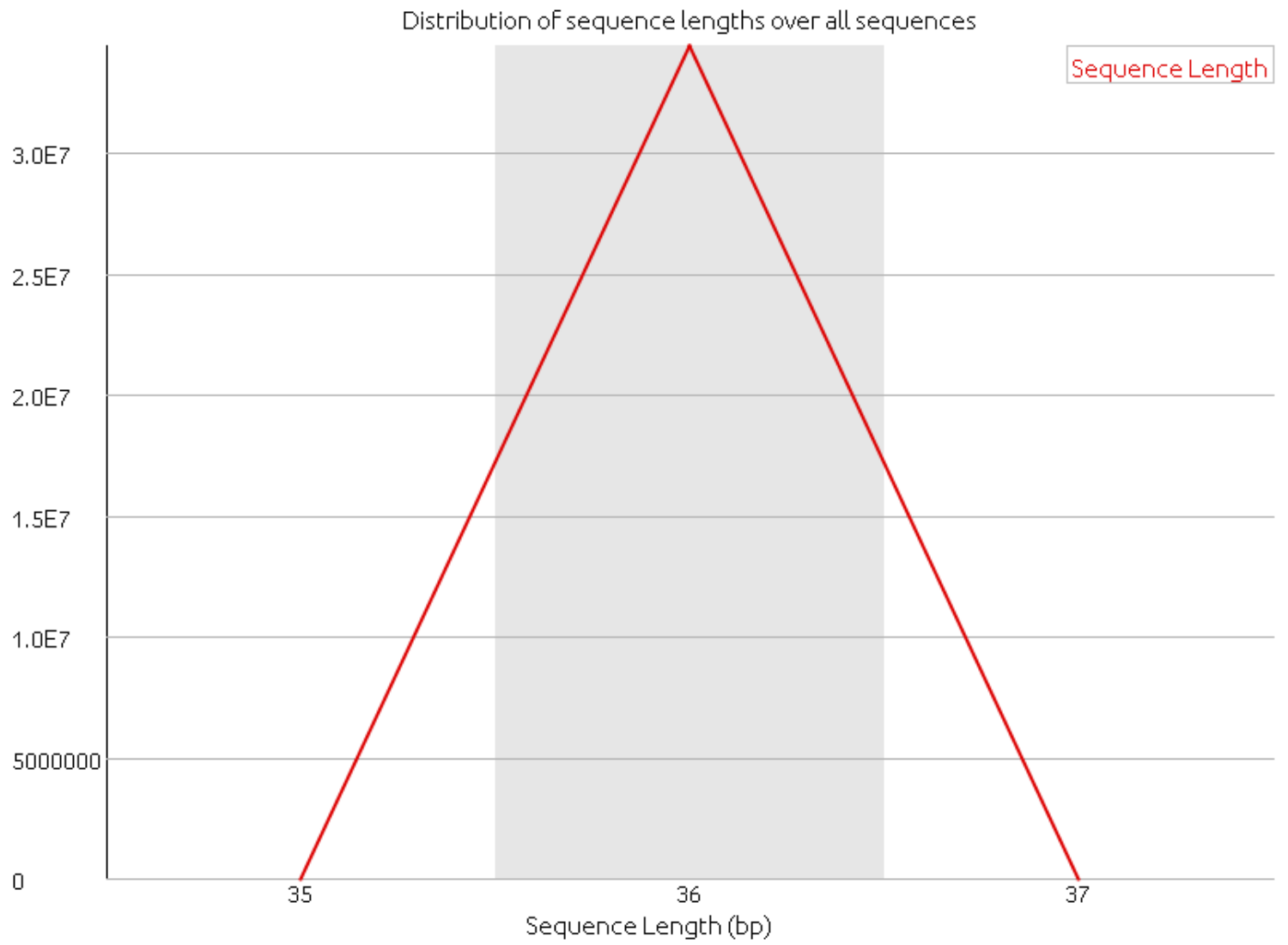
Per sequence GC content



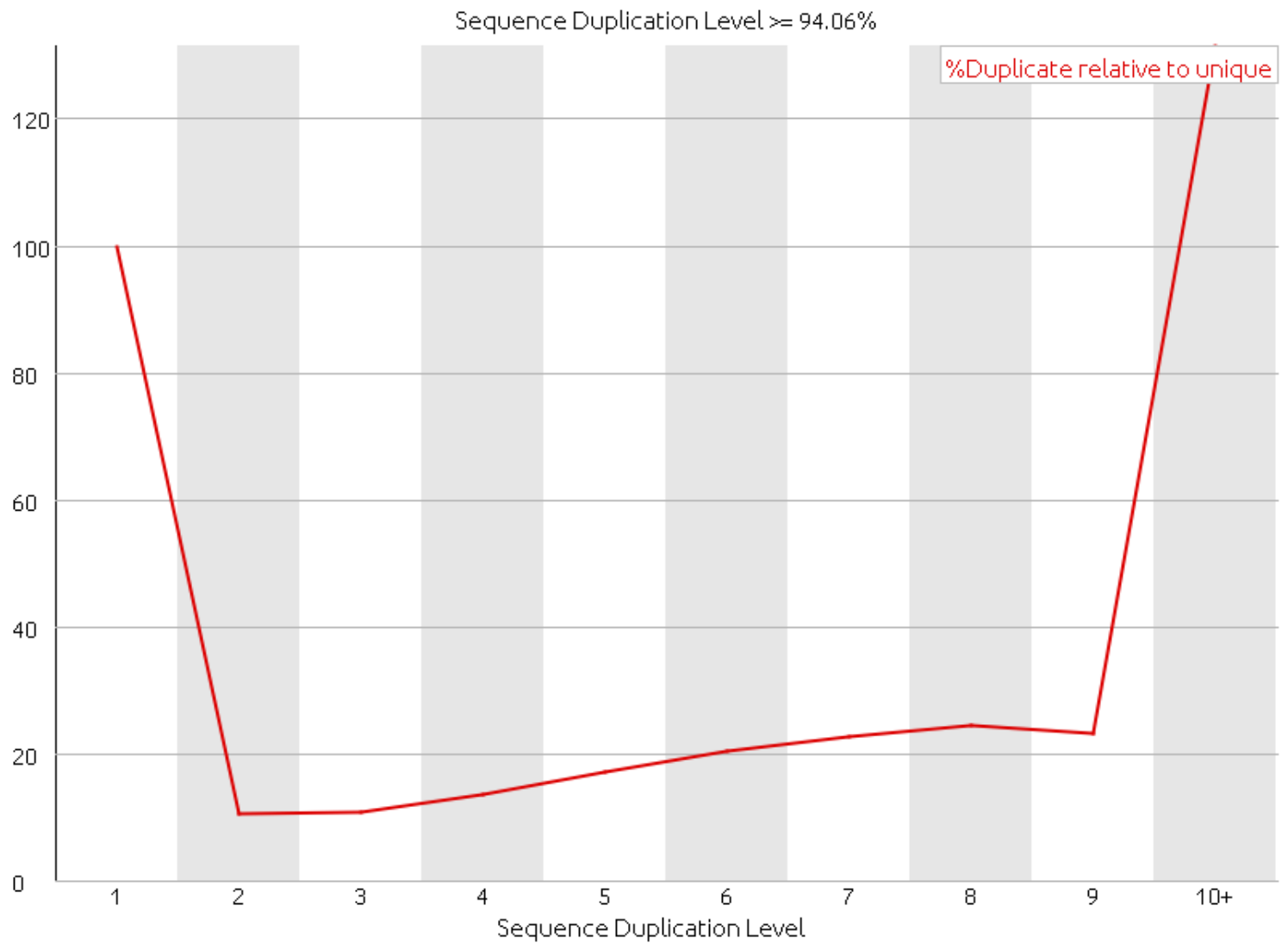
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

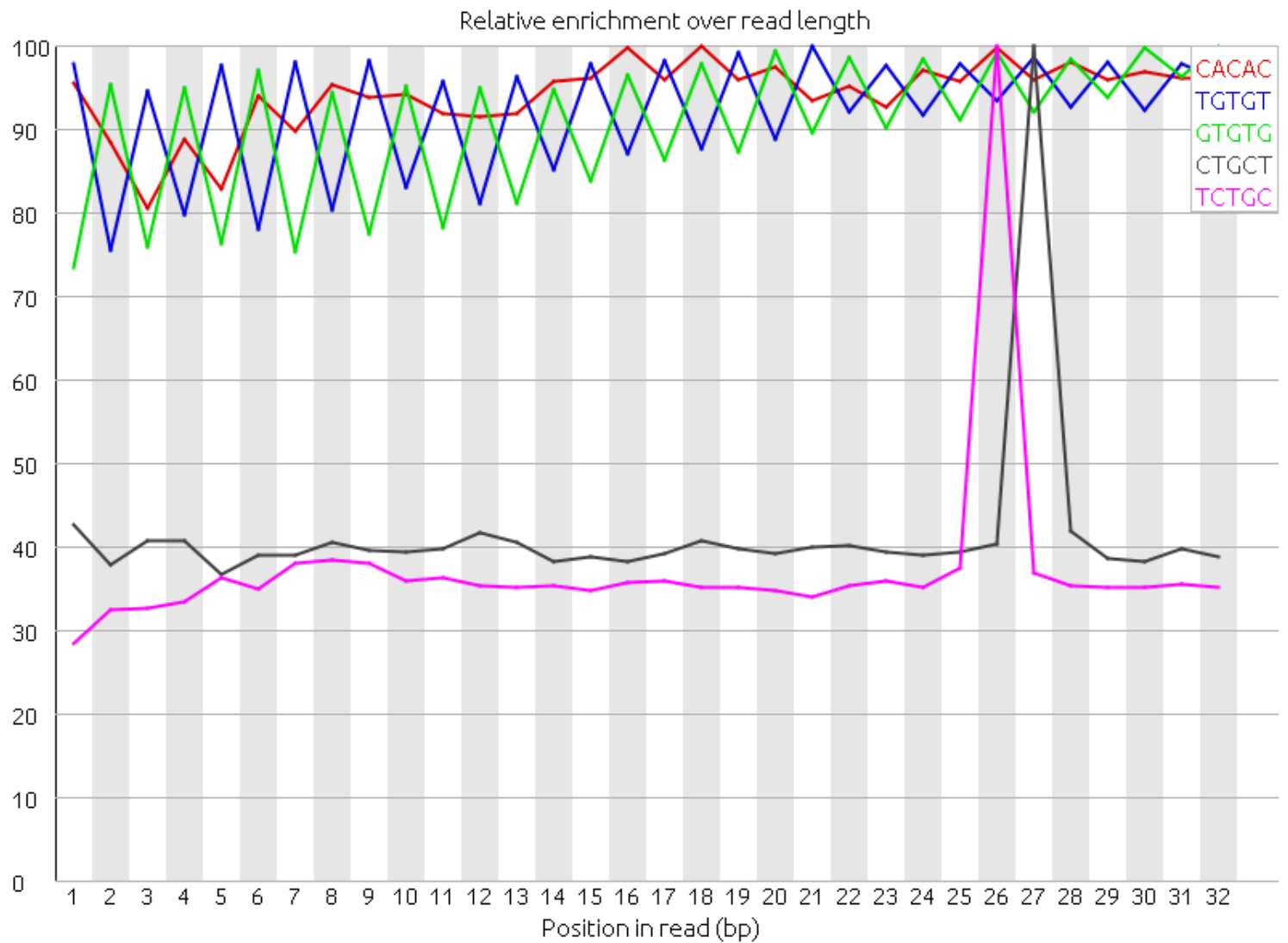


Overrepresented sequences

No overrepresented sequences



Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CACAC	3415185	3.4420815	3.6520646	18
TGTGT	3006040	3.1786807	3.4448757	21
GTGTG	2585565	3.0321624	3.3380108	32
CTGCT	1691190	2.188253	5.259263	27
TCTGC	1471435	1.903909	5.0891814	26

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