












FastQC Report

Summary

Mon 4 Jun 2012
myc.bam

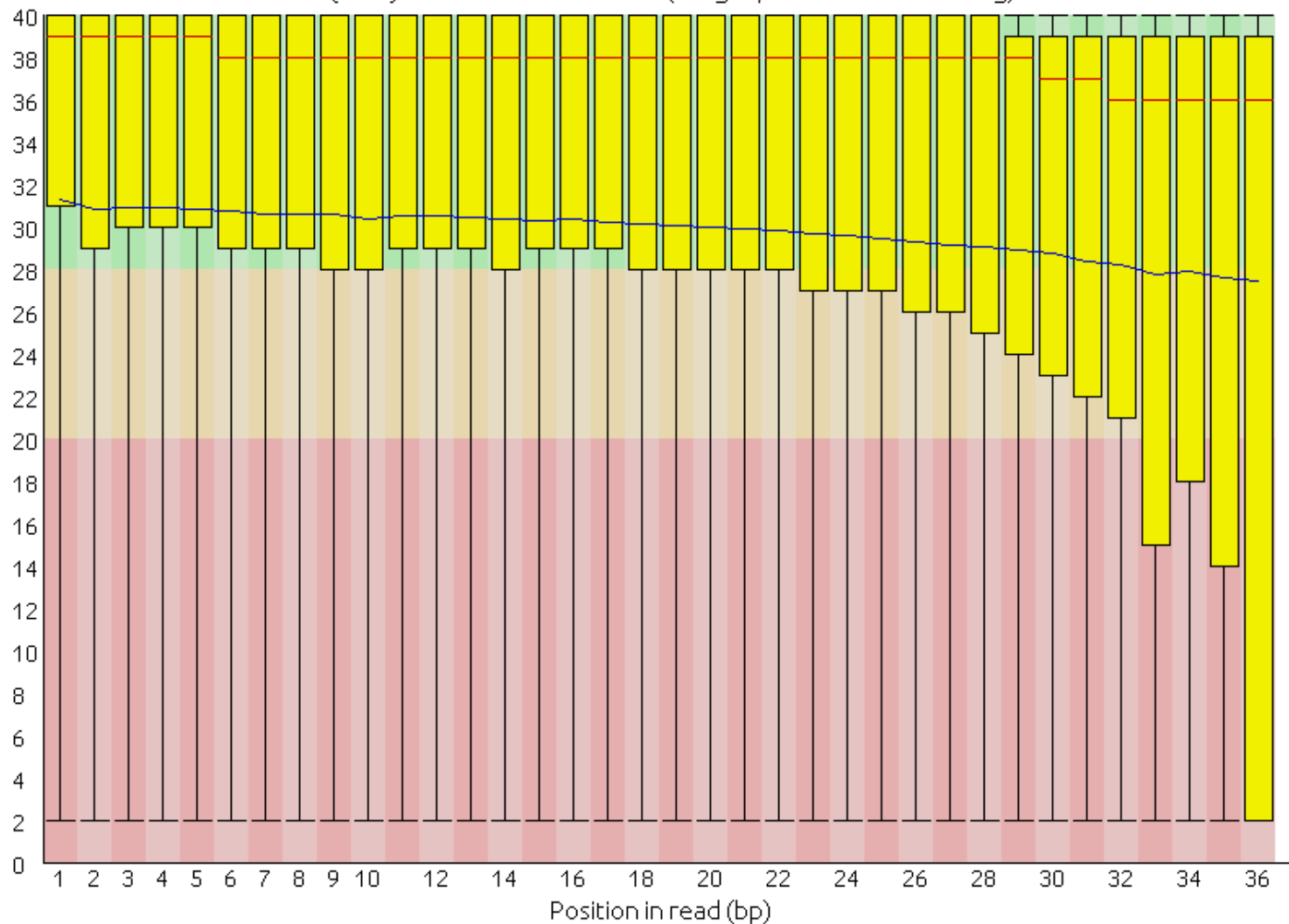
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Basic Statistics

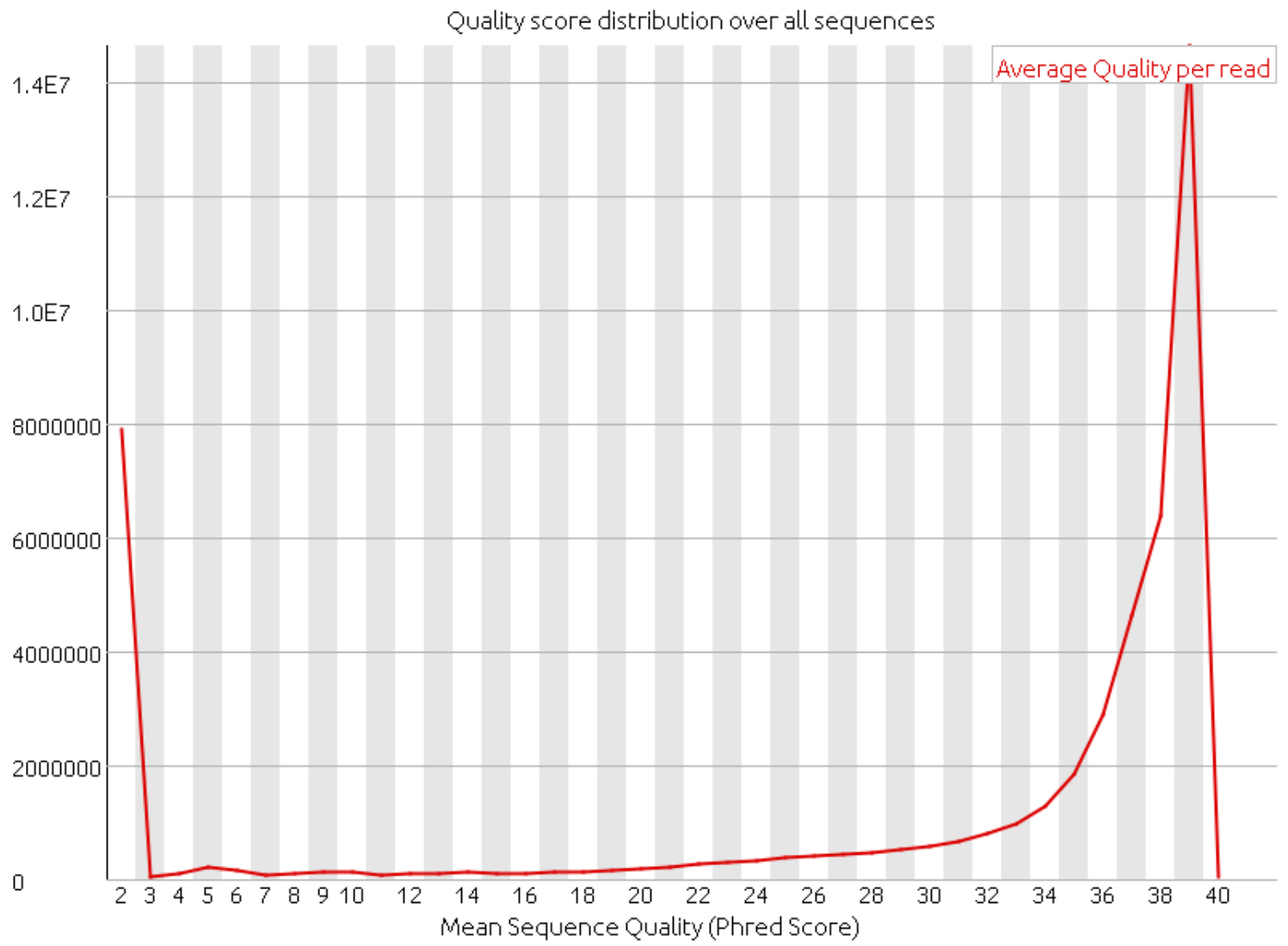
Measure	Value
Filename	myc.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	48998693
Filtered Sequences	0
Sequence length	36
%GC	43

Per base sequence quality

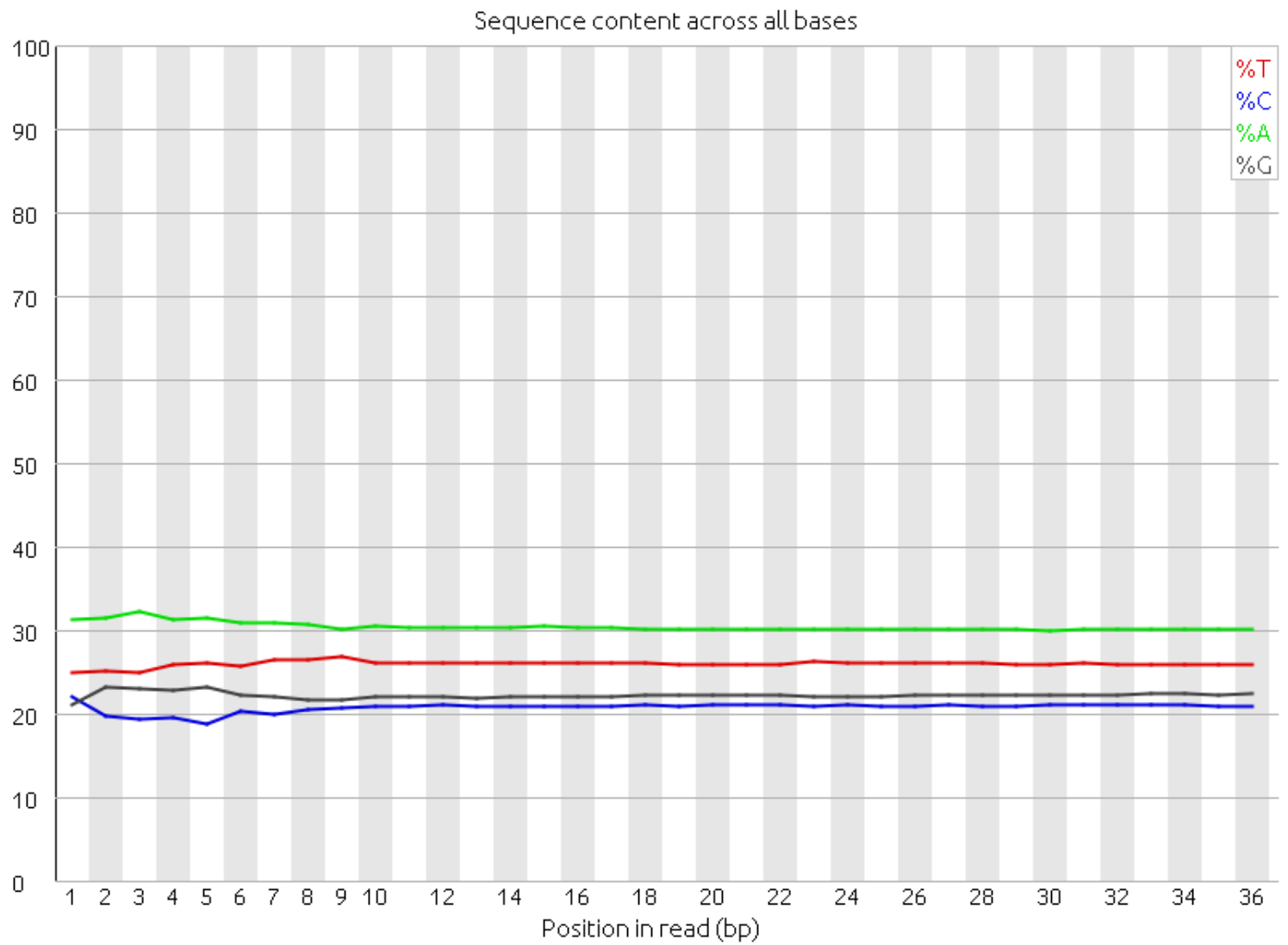
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



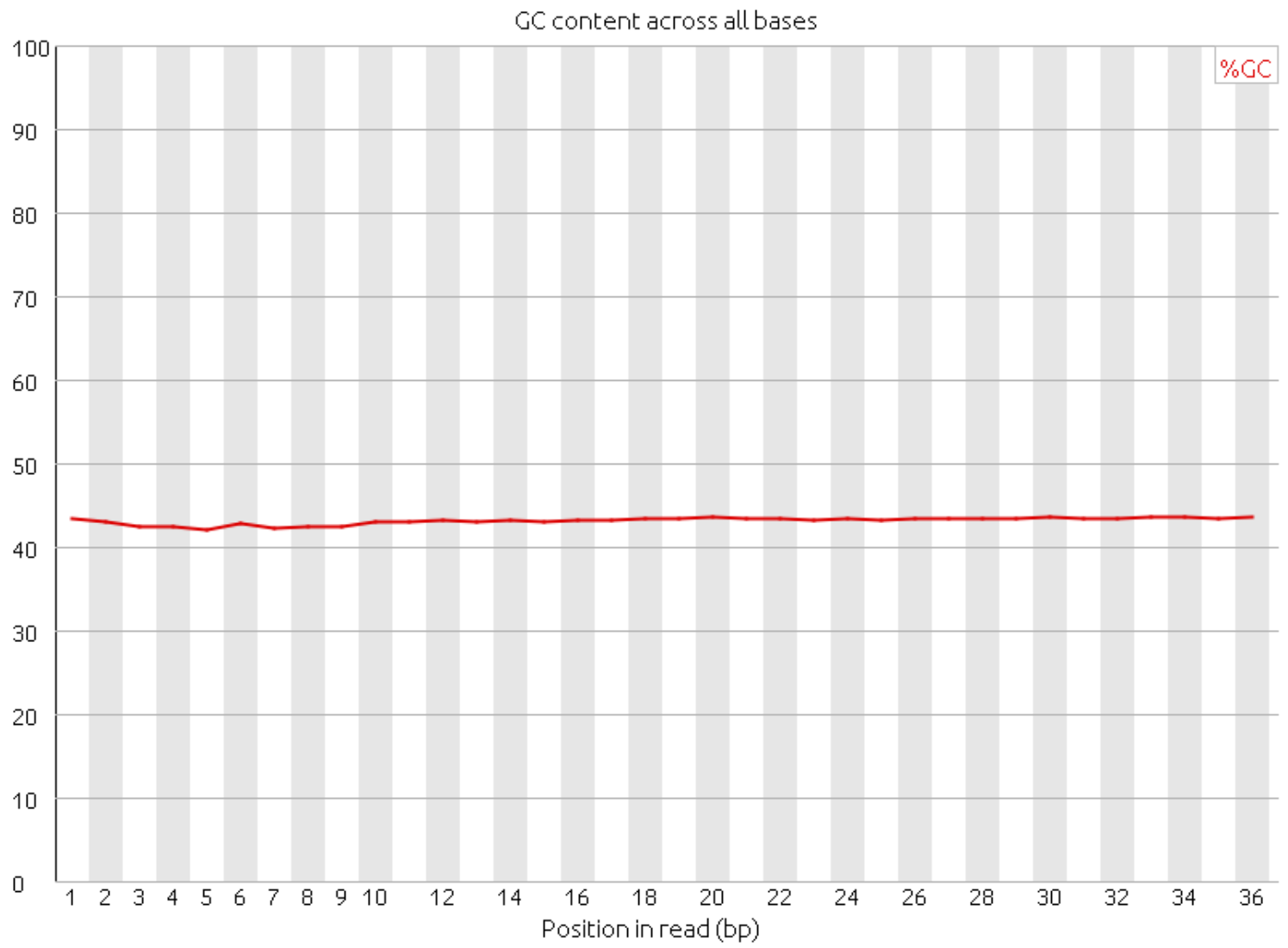
Per sequence quality scores



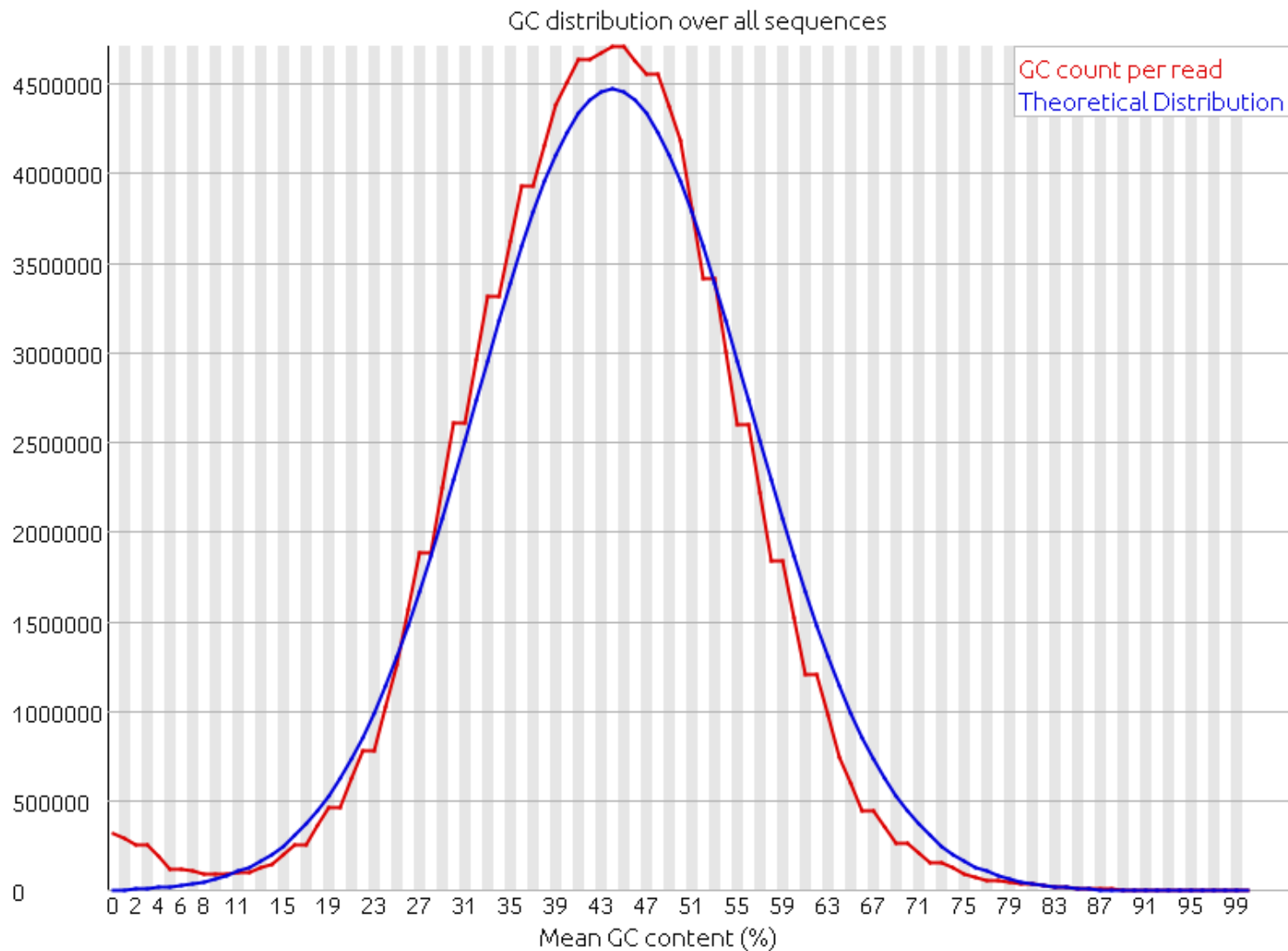
Per base sequence content



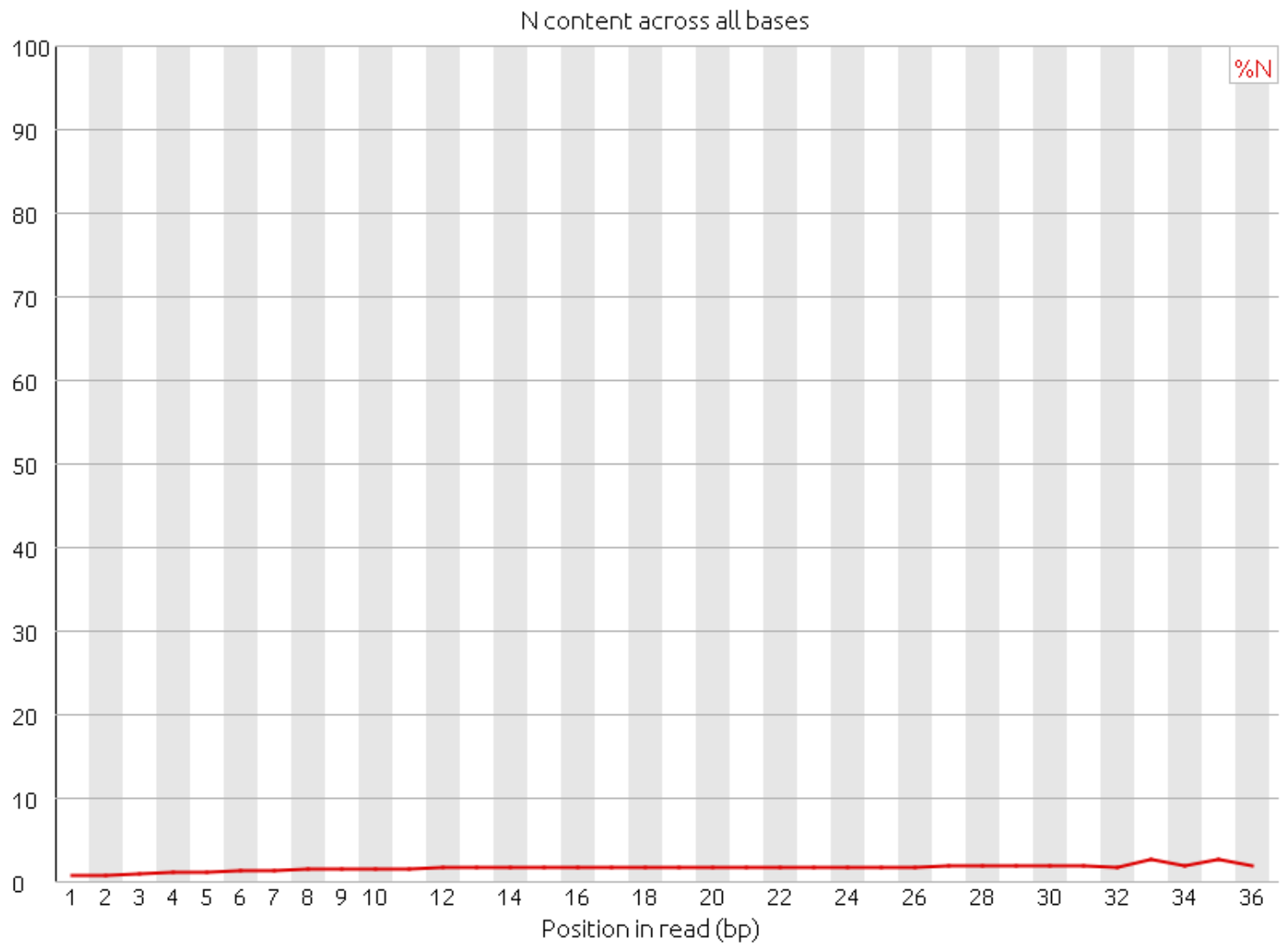
Per base GC content



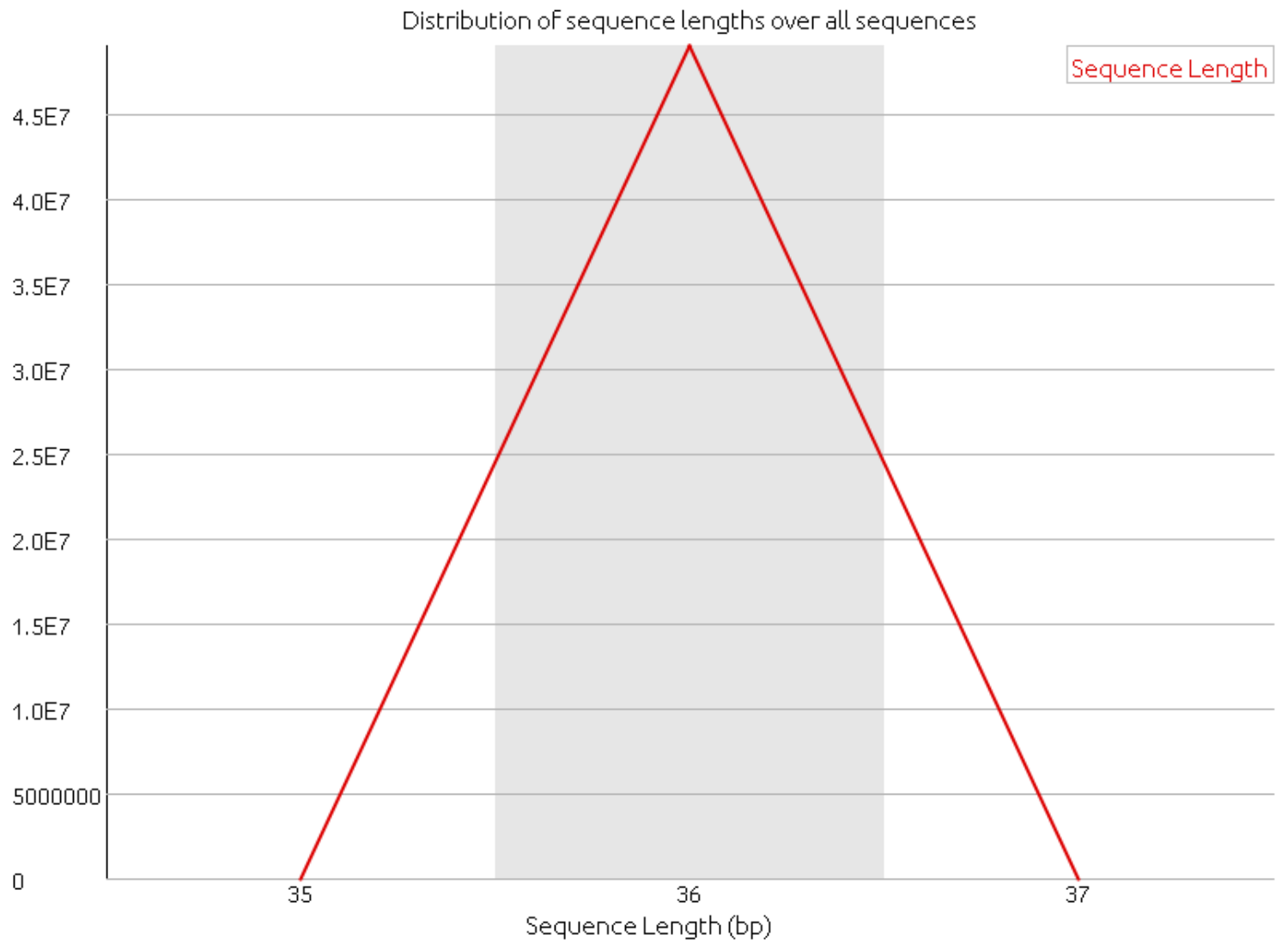
Per sequence GC content



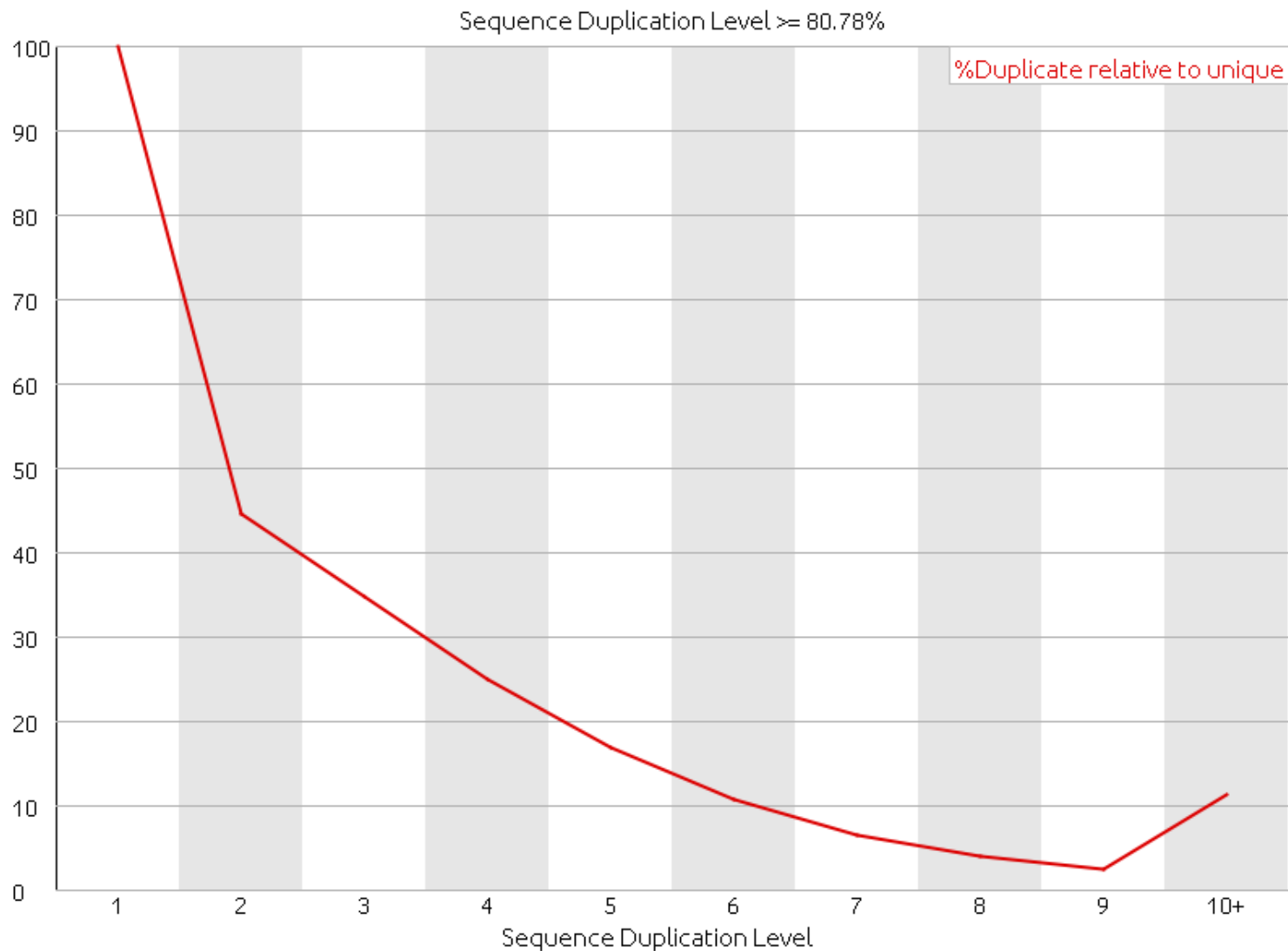
 **Per base N content**



Sequence Length Distribution



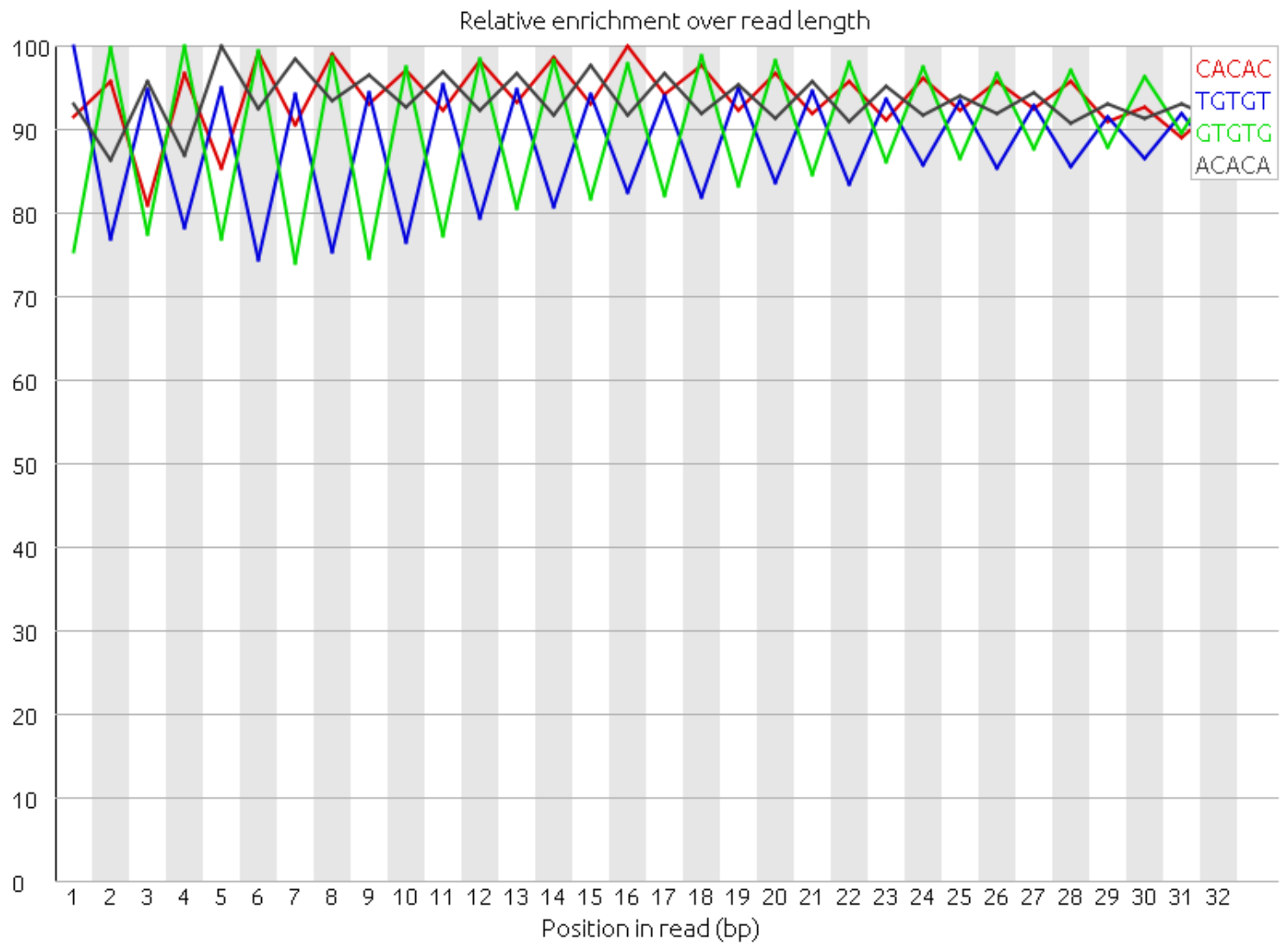
Sequence Duplication Levels



 **Overrepresented sequences**

No overrepresented sequences

 **Kmer Content**



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CACAC	4676650	3.5502748	3.7794206	16
TGTGT	4402830	3.2164383	3.6550167	1
GTGTG	3600600	3.0706112	3.4139528	4
ACACA	5844455	3.0337605	3.241231	5

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