












FastQC Report

Summary

Mon 4 Jun 2012
gli3amyc.bam

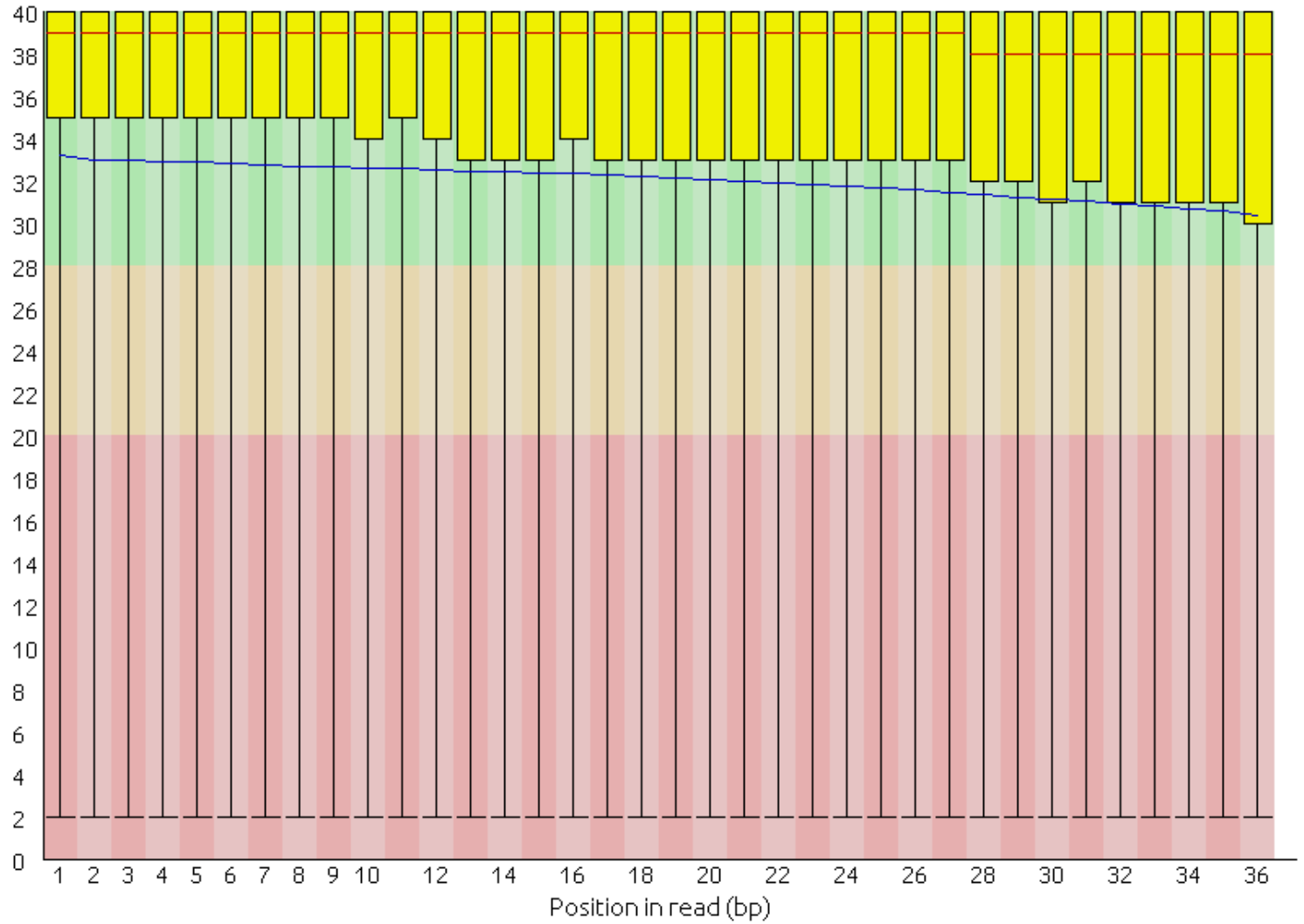
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Basic Statistics

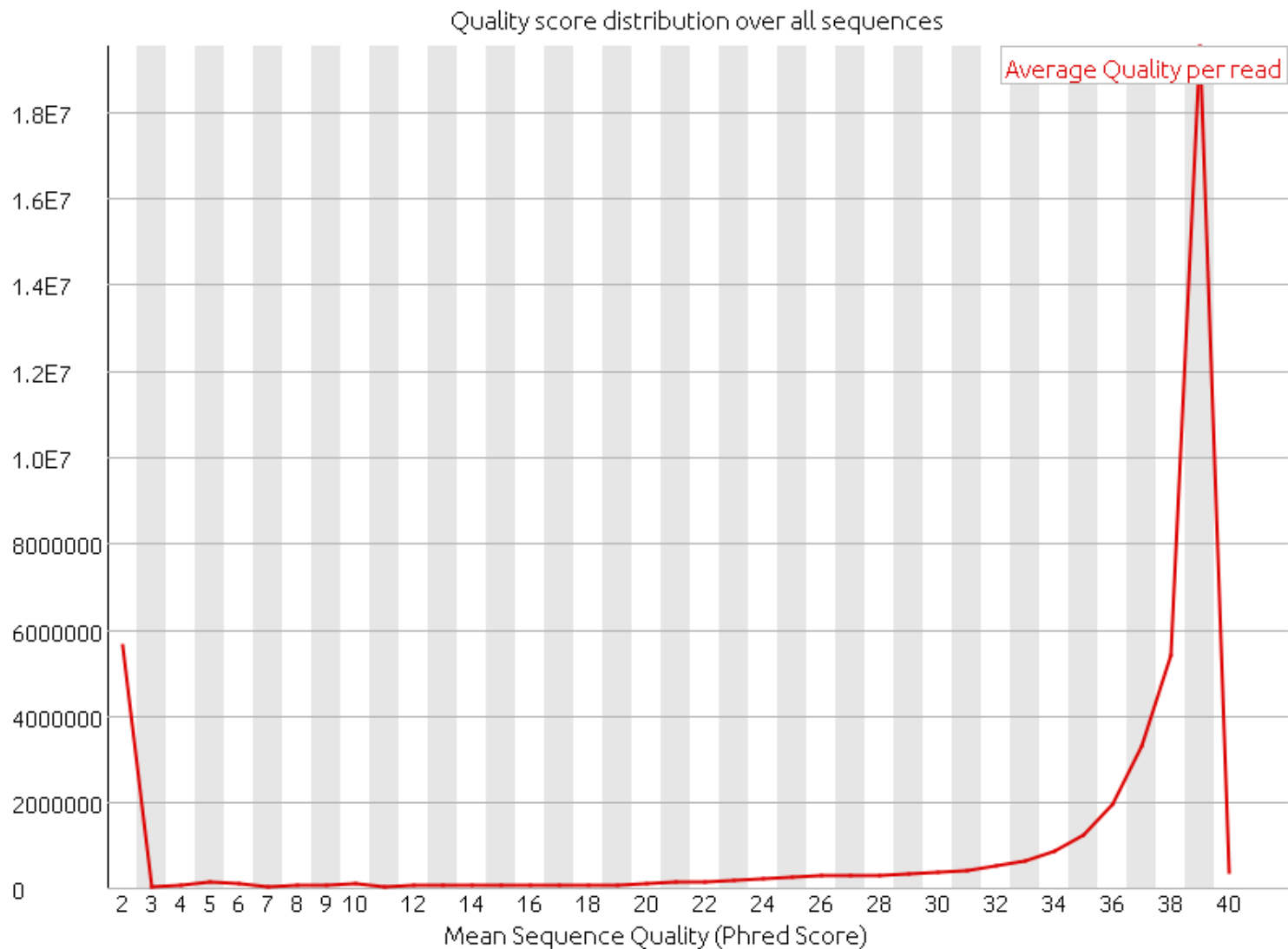
Measure	Value
Filename	gli3amyc.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	44583670
Filtered Sequences	0
Sequence length	36
%GC	43

Per base sequence quality

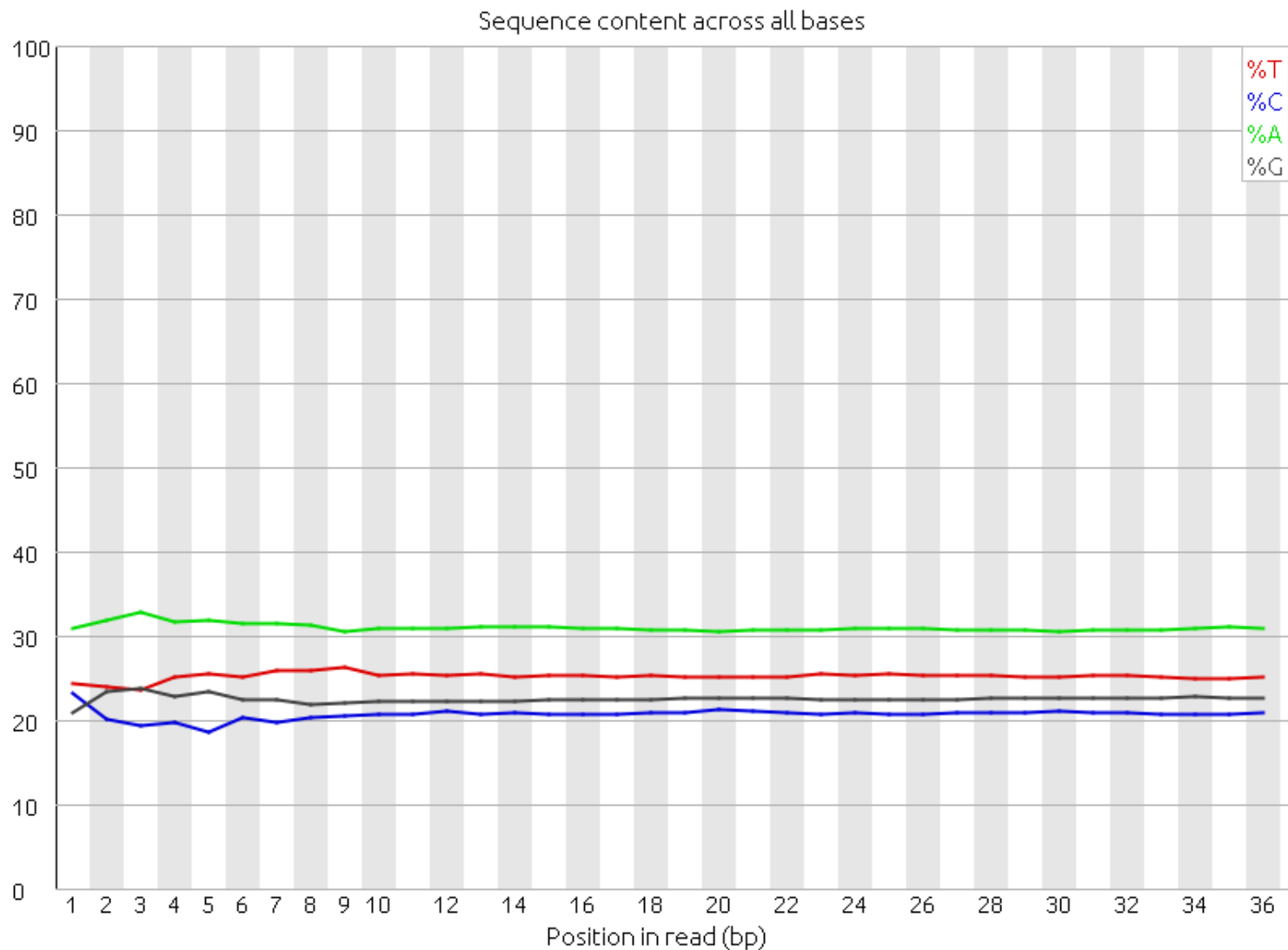
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



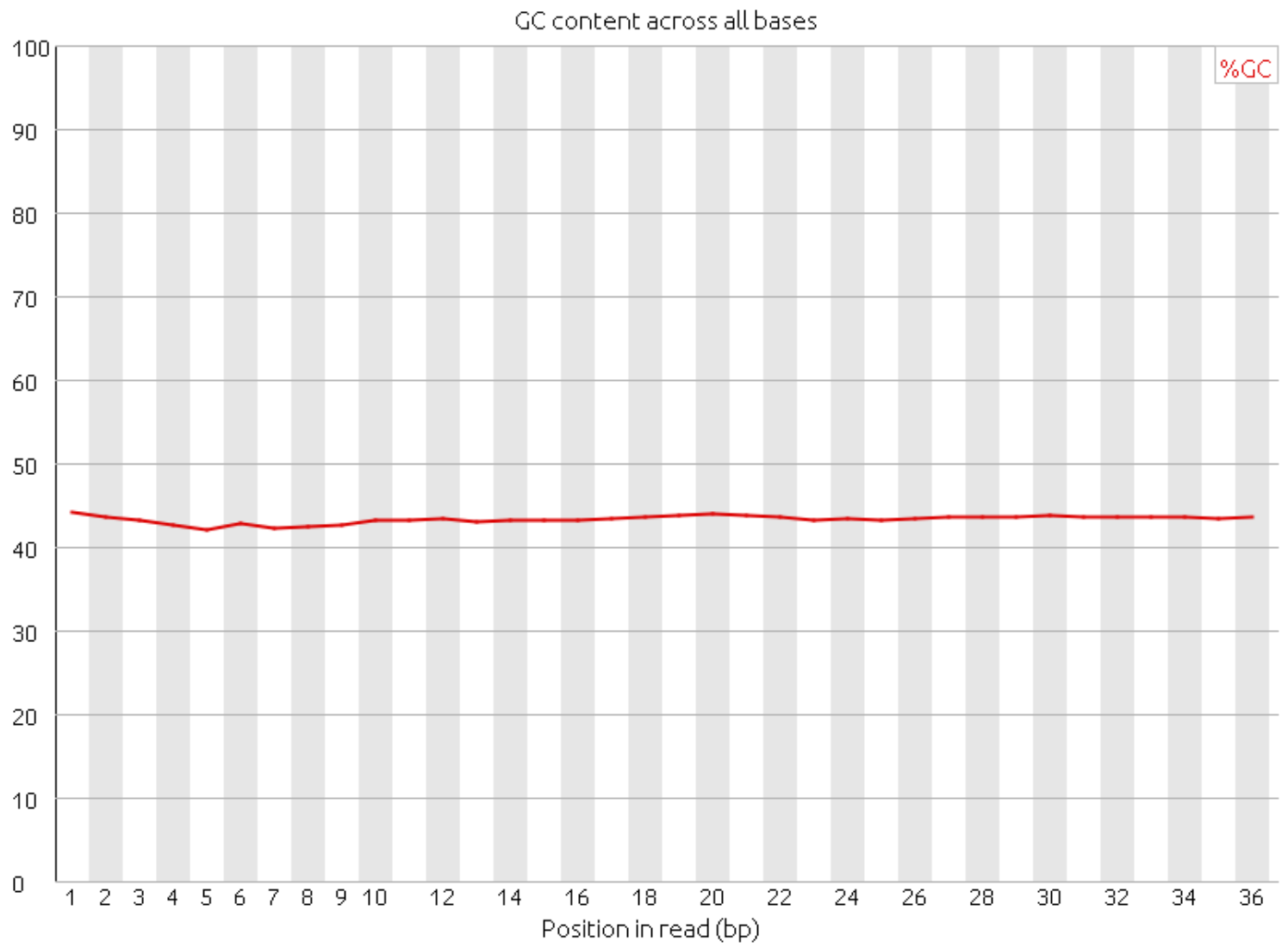
Per sequence quality scores



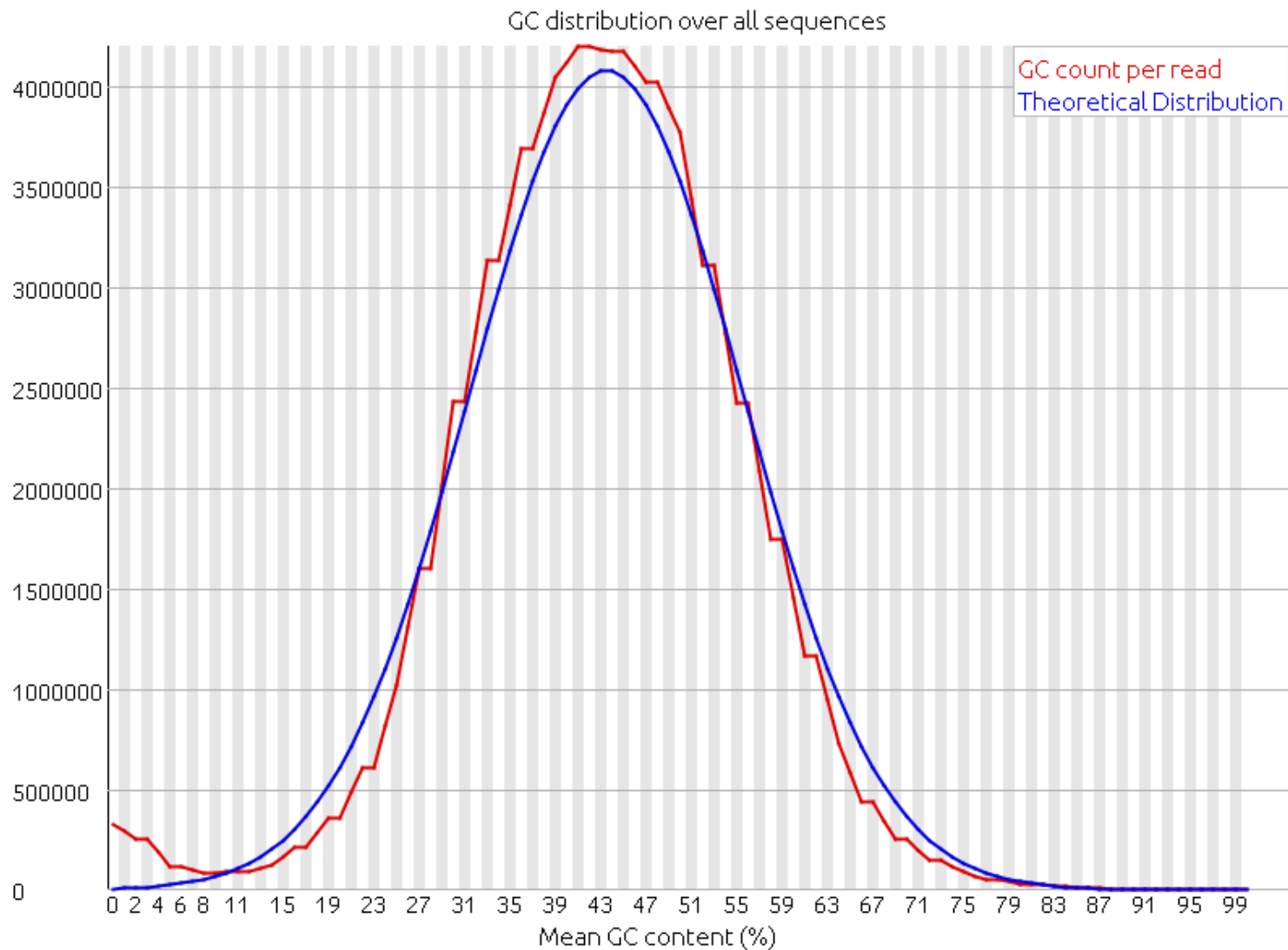
Per base sequence content



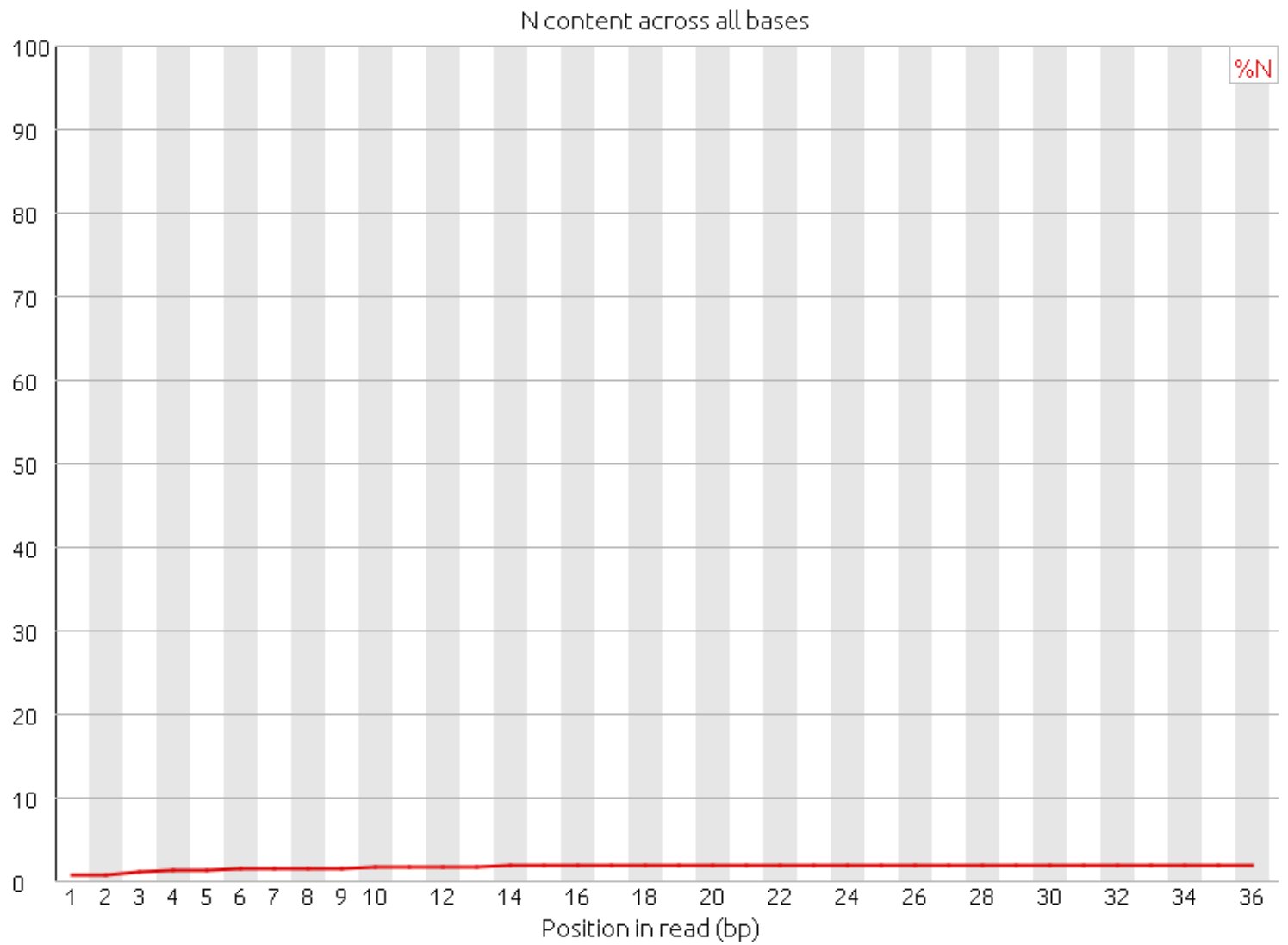
 **Per base GC content**



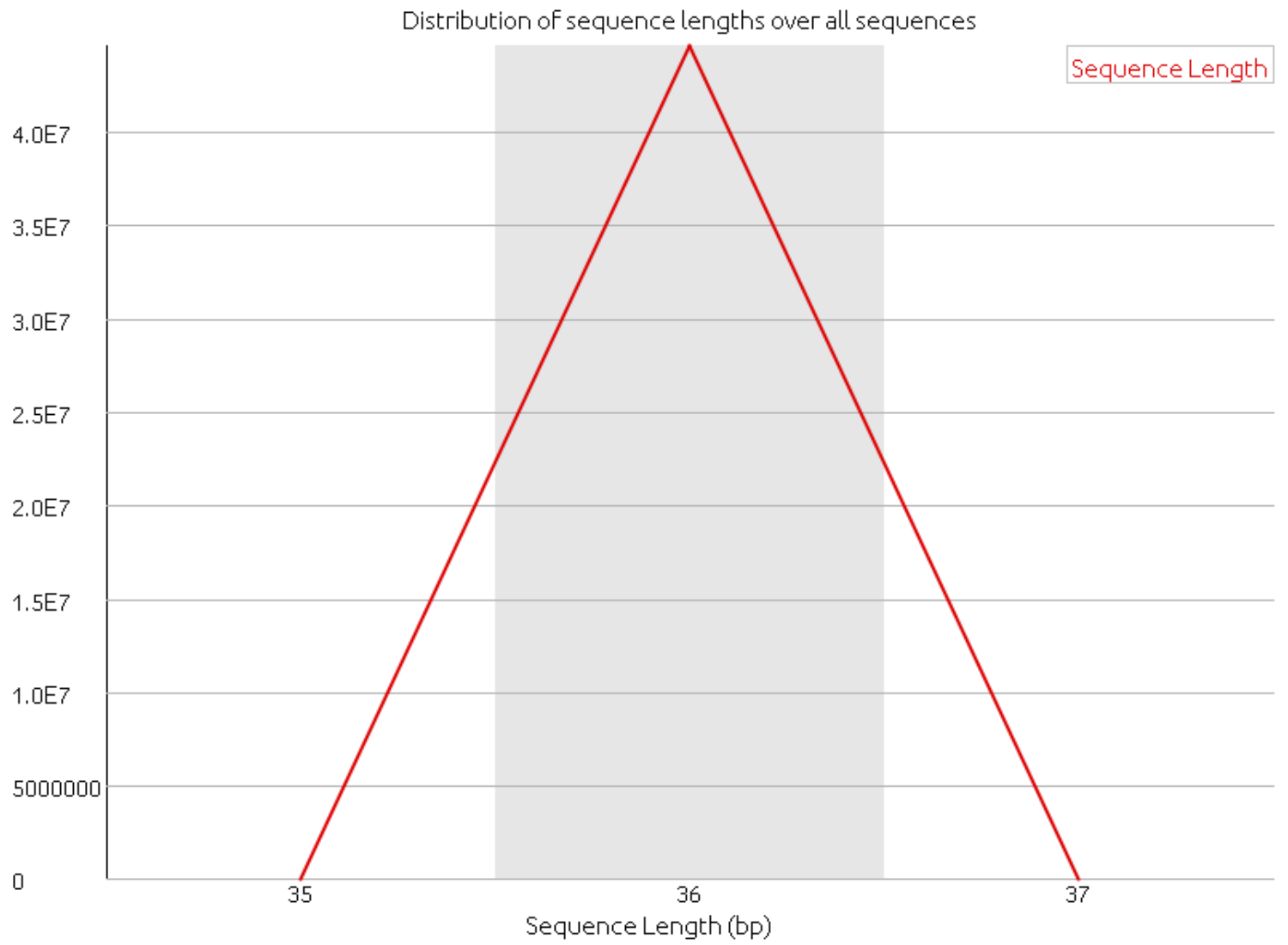
Per sequence GC content



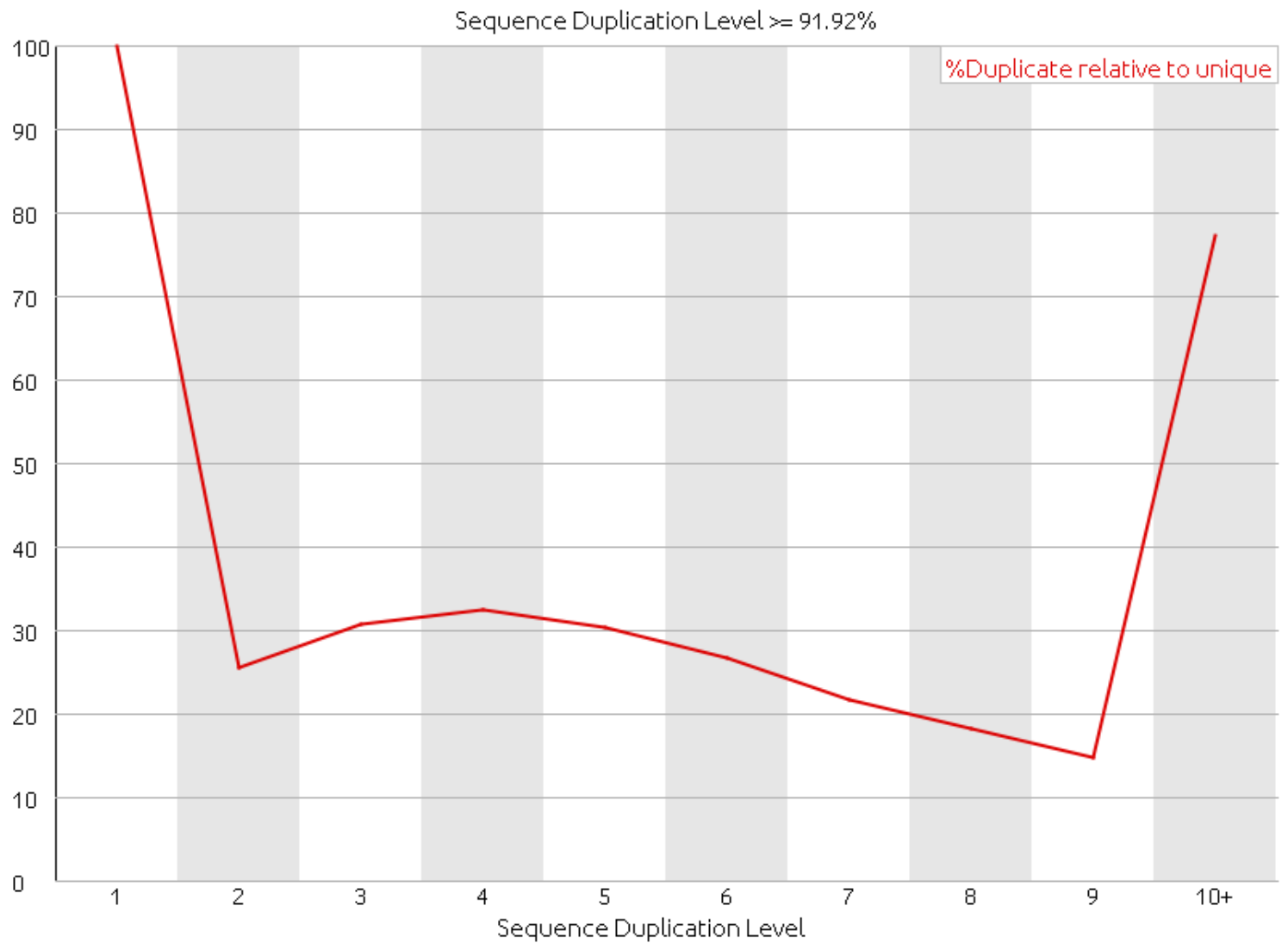
 **Per base N content**



Sequence Length Distribution



Sequence Duplication Levels

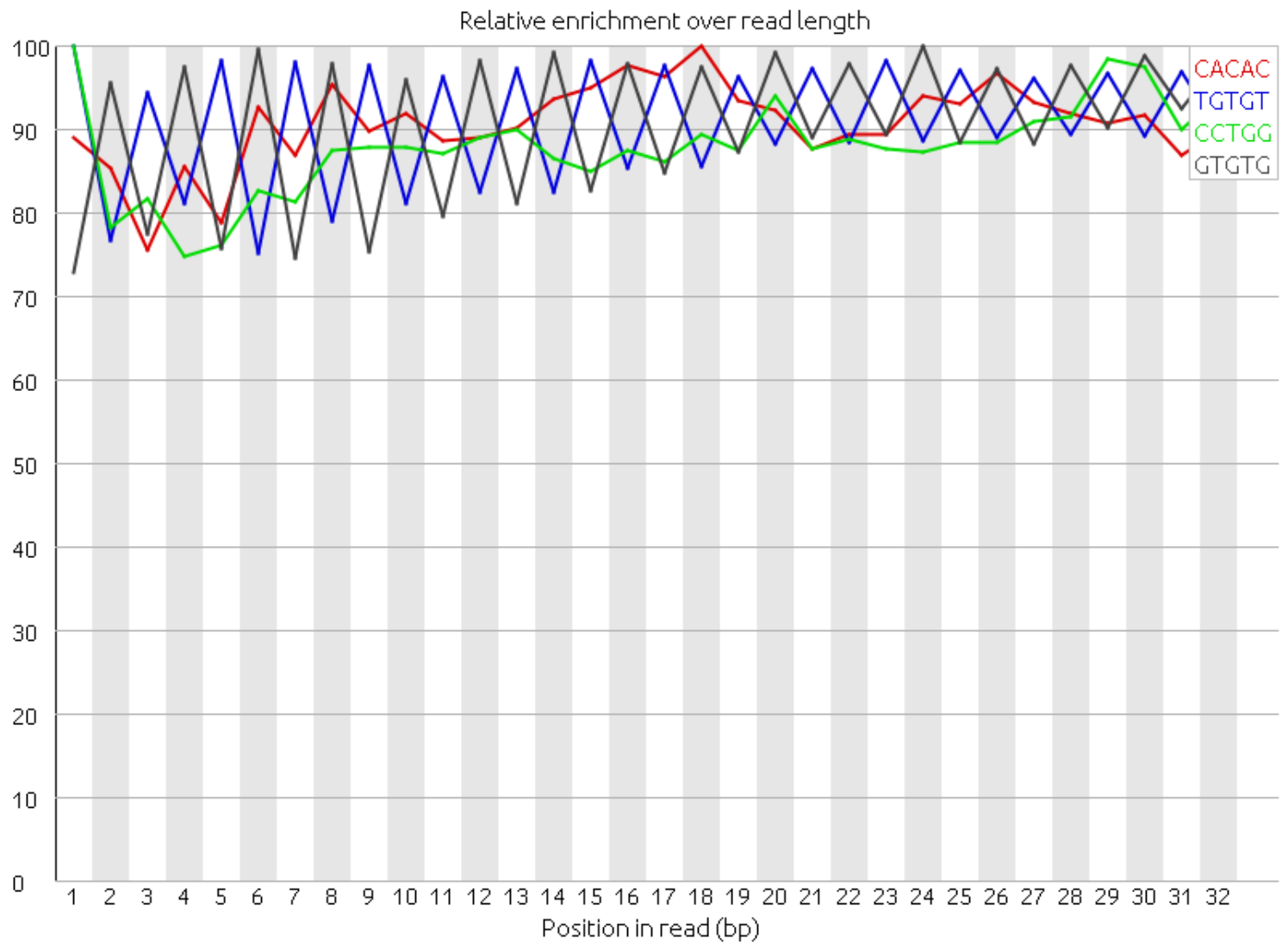


Overrepresented sequences

No overrepresented sequences



Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CACAC	4601305	3.747464	4.1270356	18
TGTGT	3856245	3.2961237	3.6223402	1
CCTGG	2510665	3.1787033	3.6143844	1
GTGTG	3237345	3.0985126	3.4176283	24

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