

FastQC Report

Summary

Mon 7 Oct 2013
Galaxy160-[8990.bam].bam

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Basic Statistics

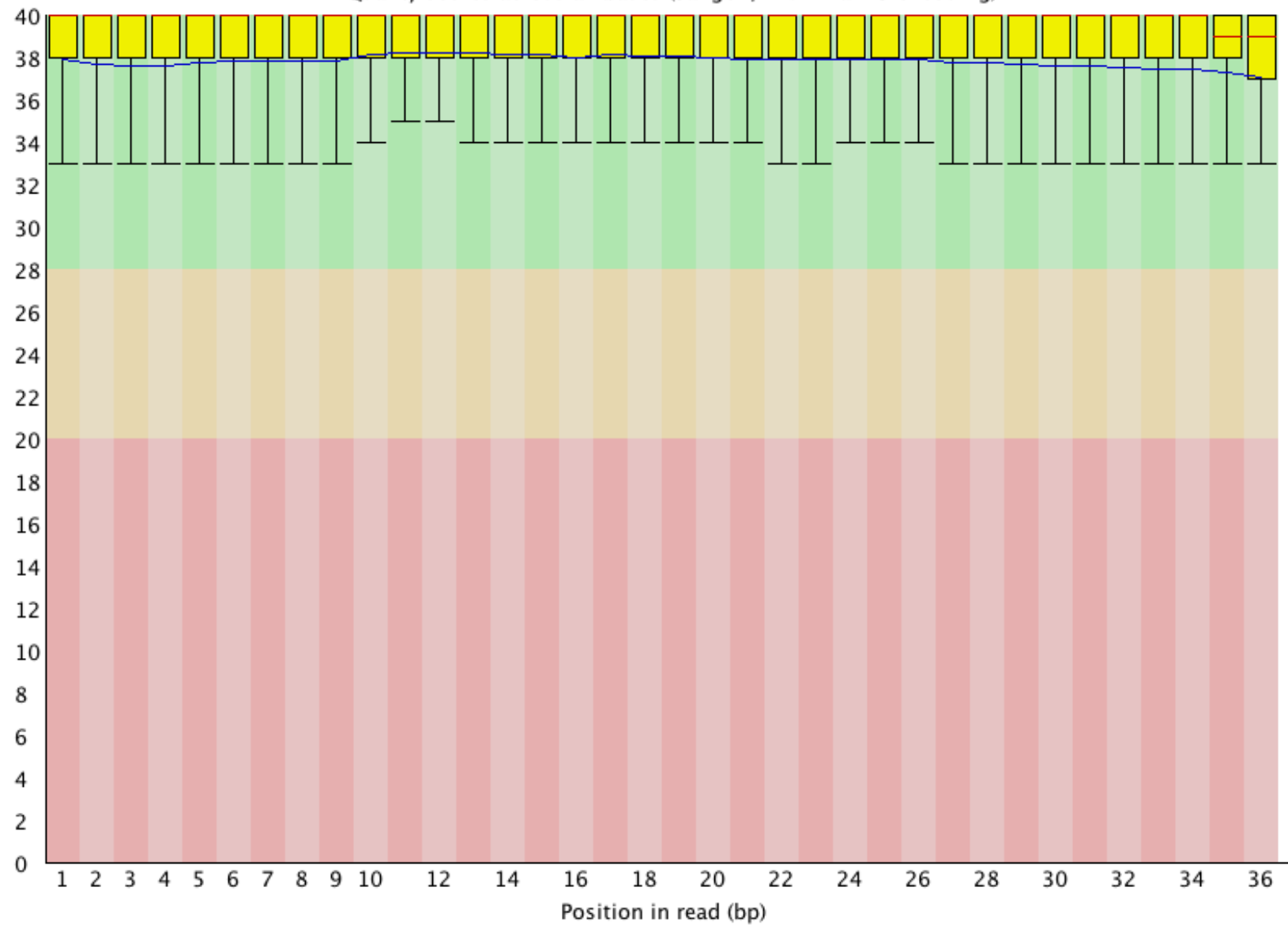
Measure	Value
Filename	Galaxy160-[8990.bam].bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9

Total Sequences	11127208
Filtered Sequences	0
Sequence length	35-36
%GC	42



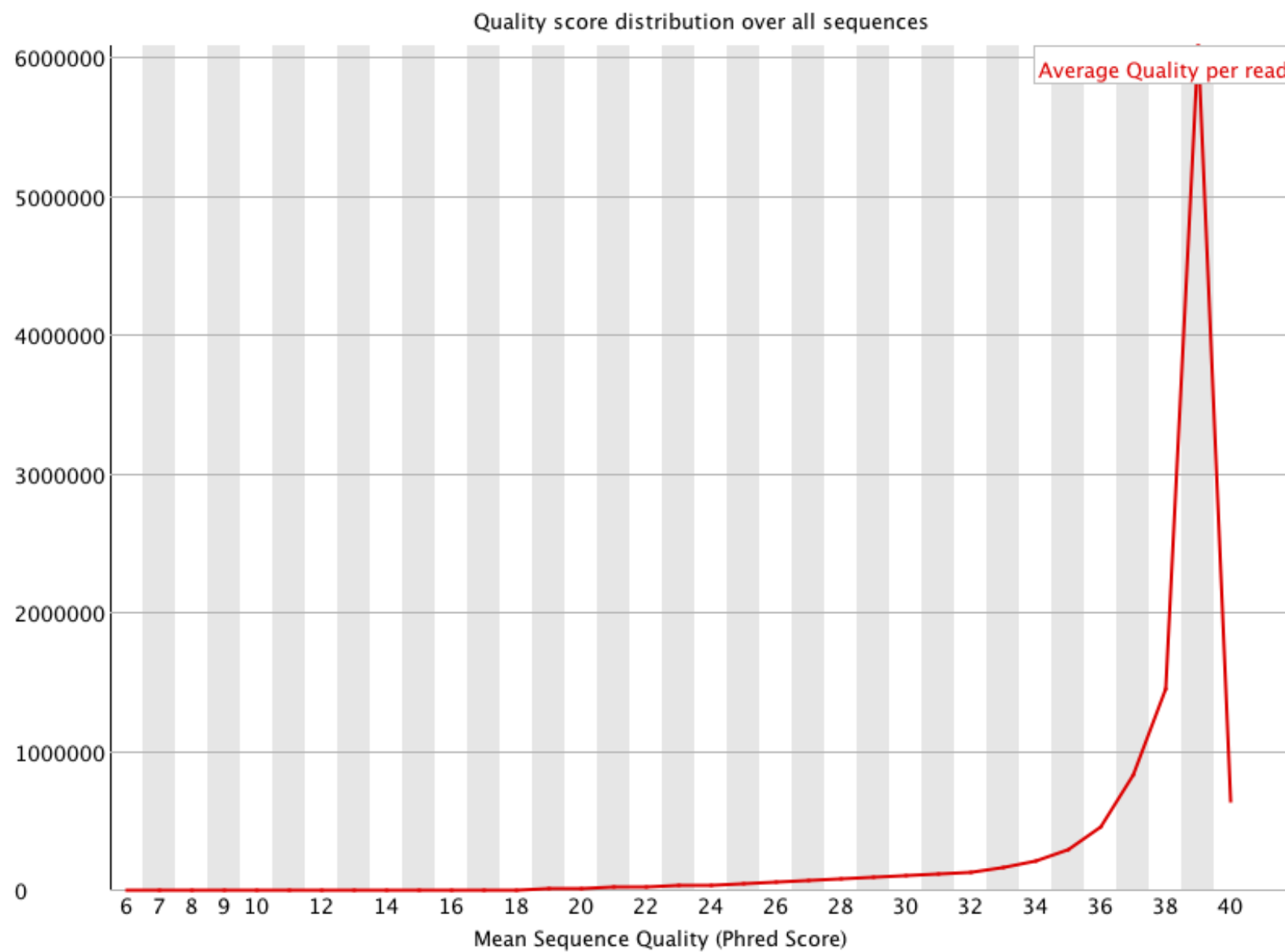
Per base sequence quality

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



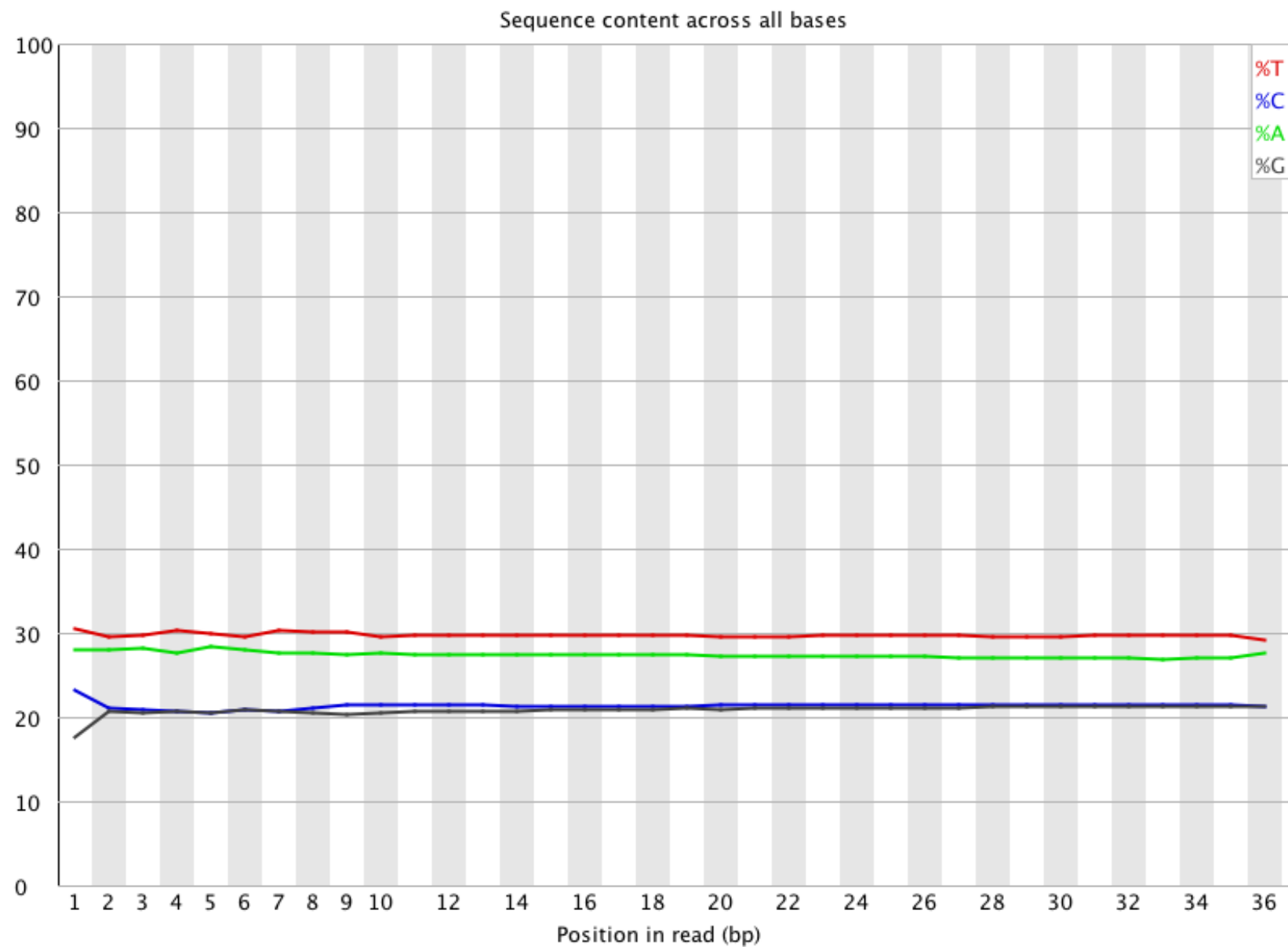


Per sequence quality scores



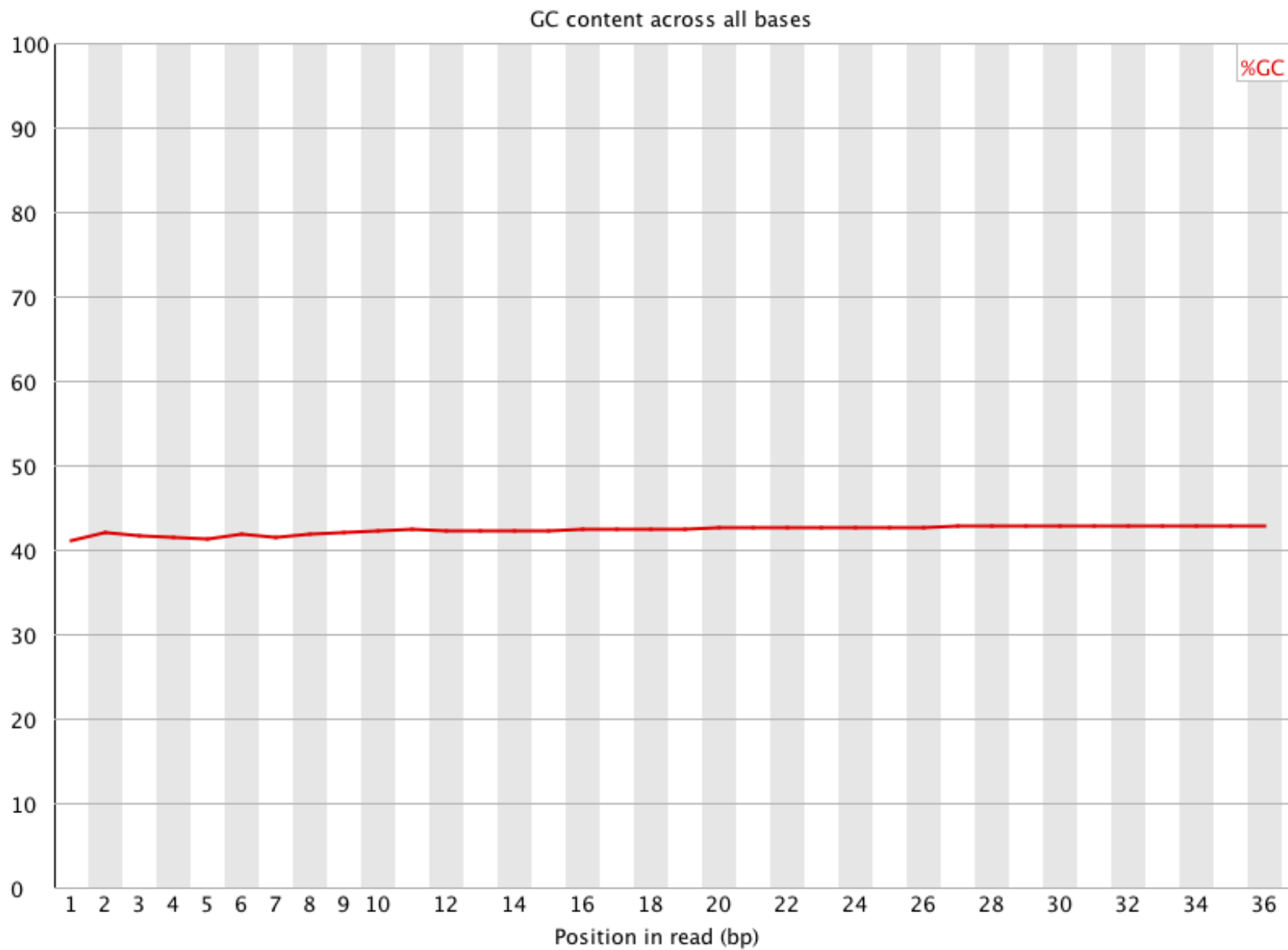


Per base sequence content



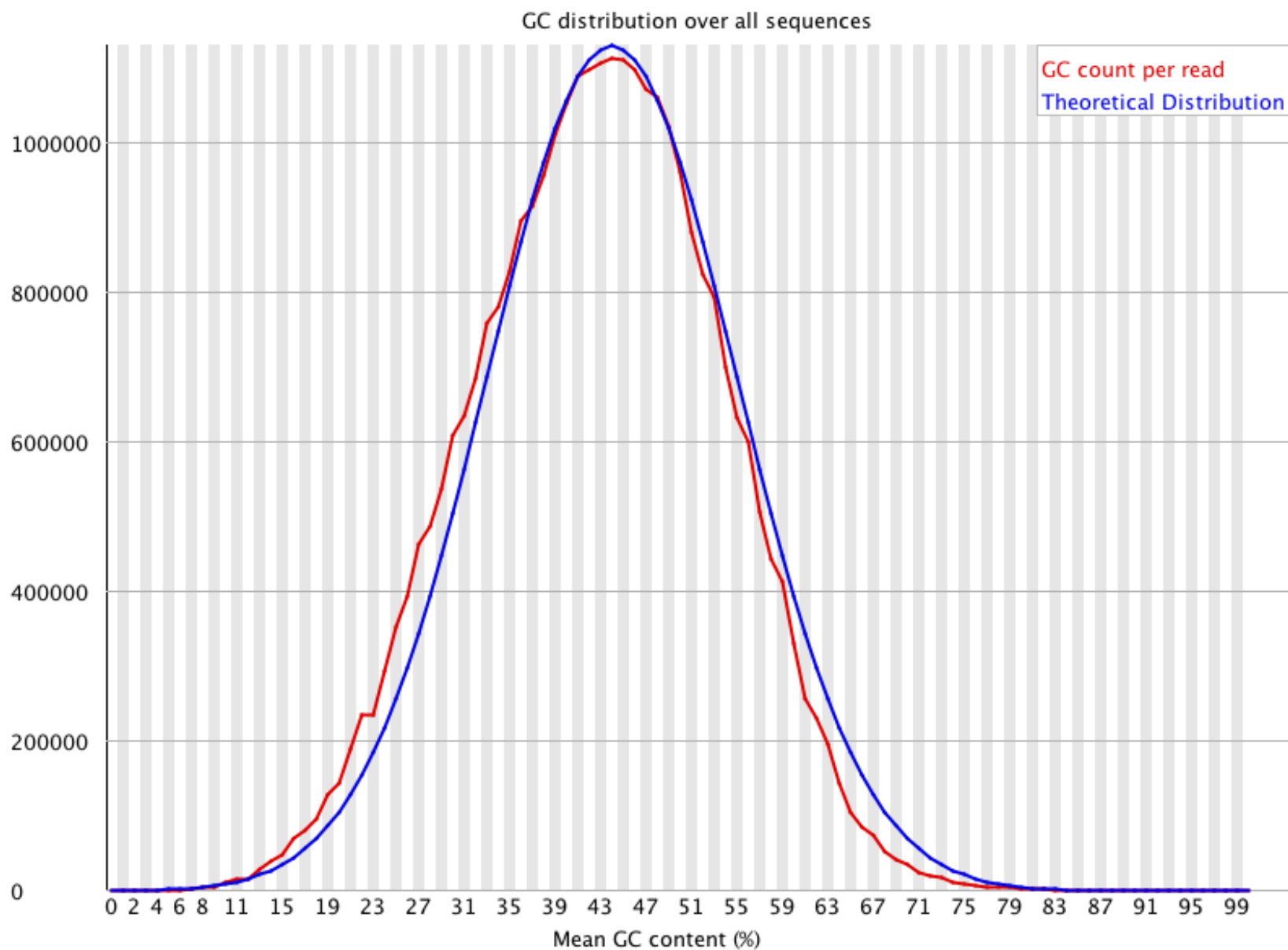


Per base GC content



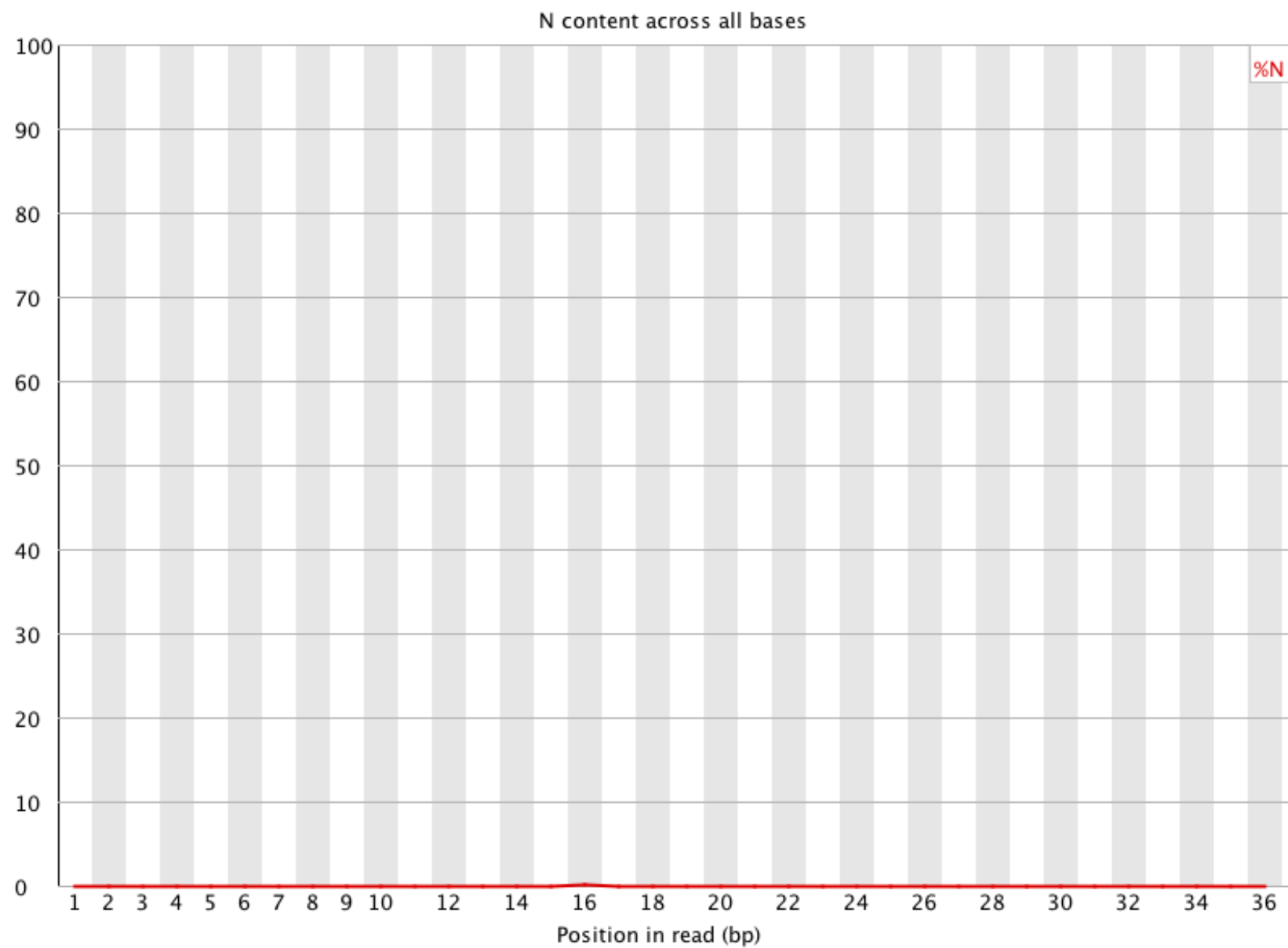


Per sequence GC content





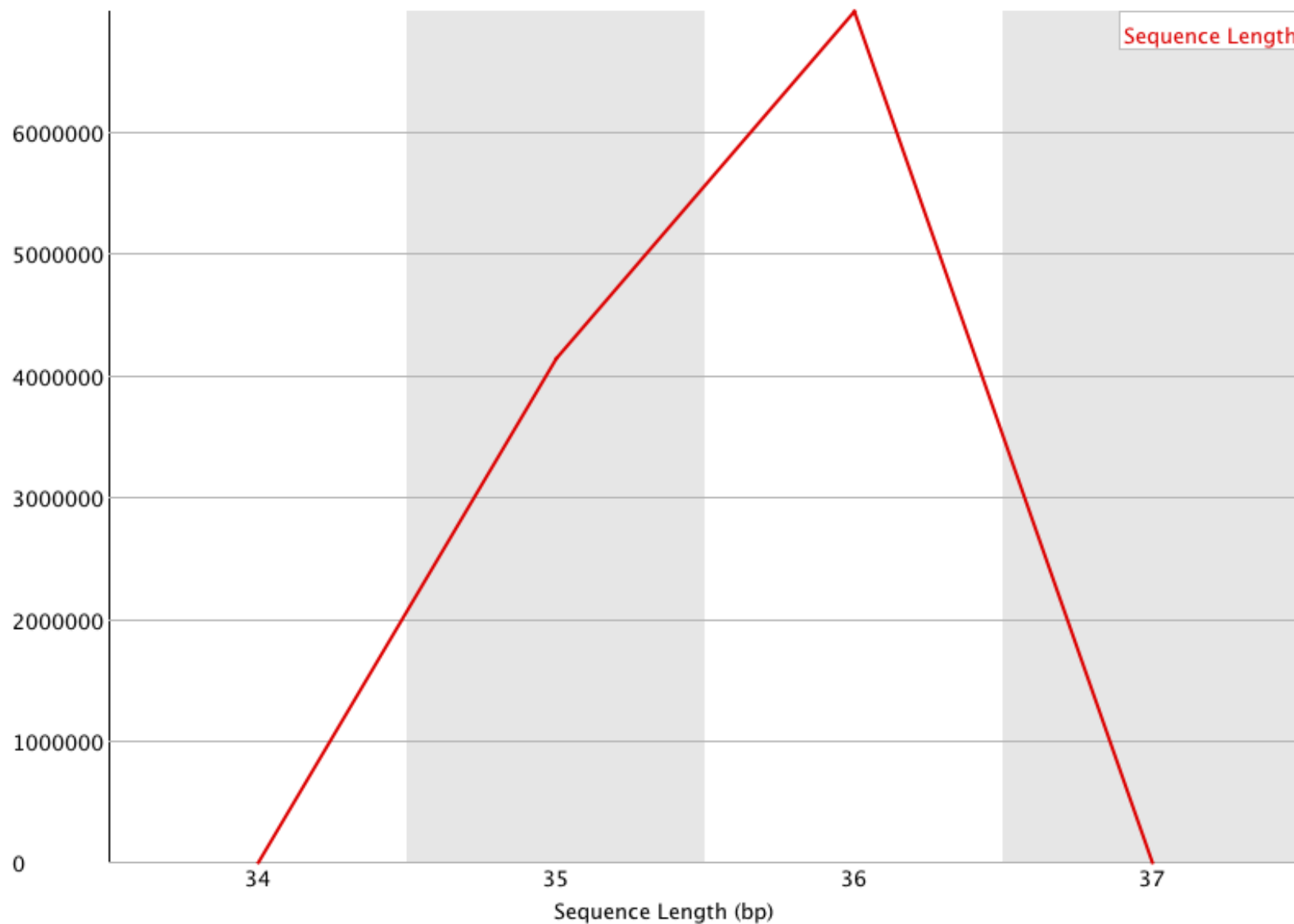
Per base N content





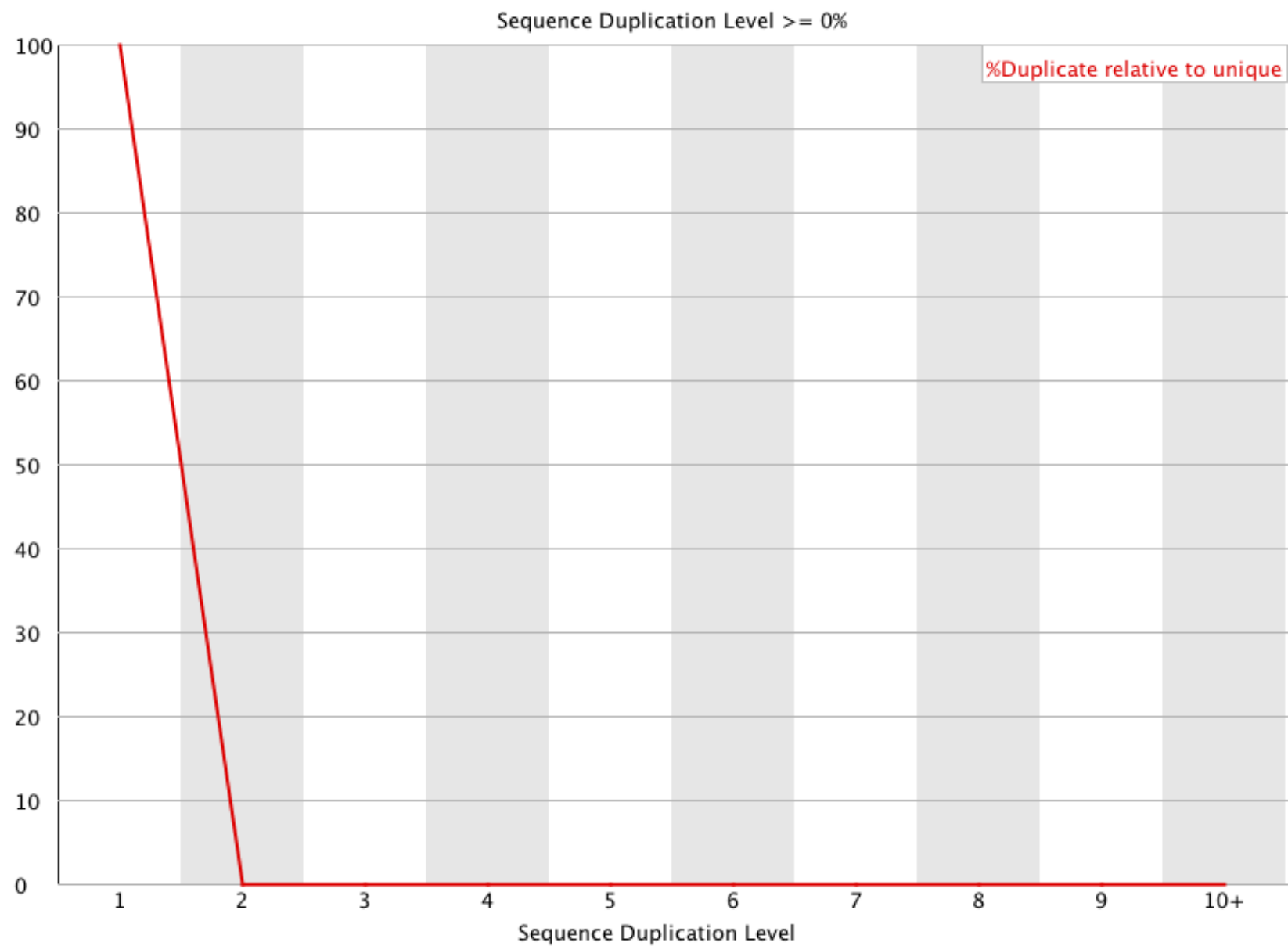
Sequence Length Distribution

Distribution of sequence lengths over all sequences





Sequence Duplication Levels





Overrepresented sequences

No overrepresented sequences



Kmer Content

No overrepresented Kmers

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