











FastQC Report

Summary

seg. 4 jul. 2022
SRR2154343_1.fastq

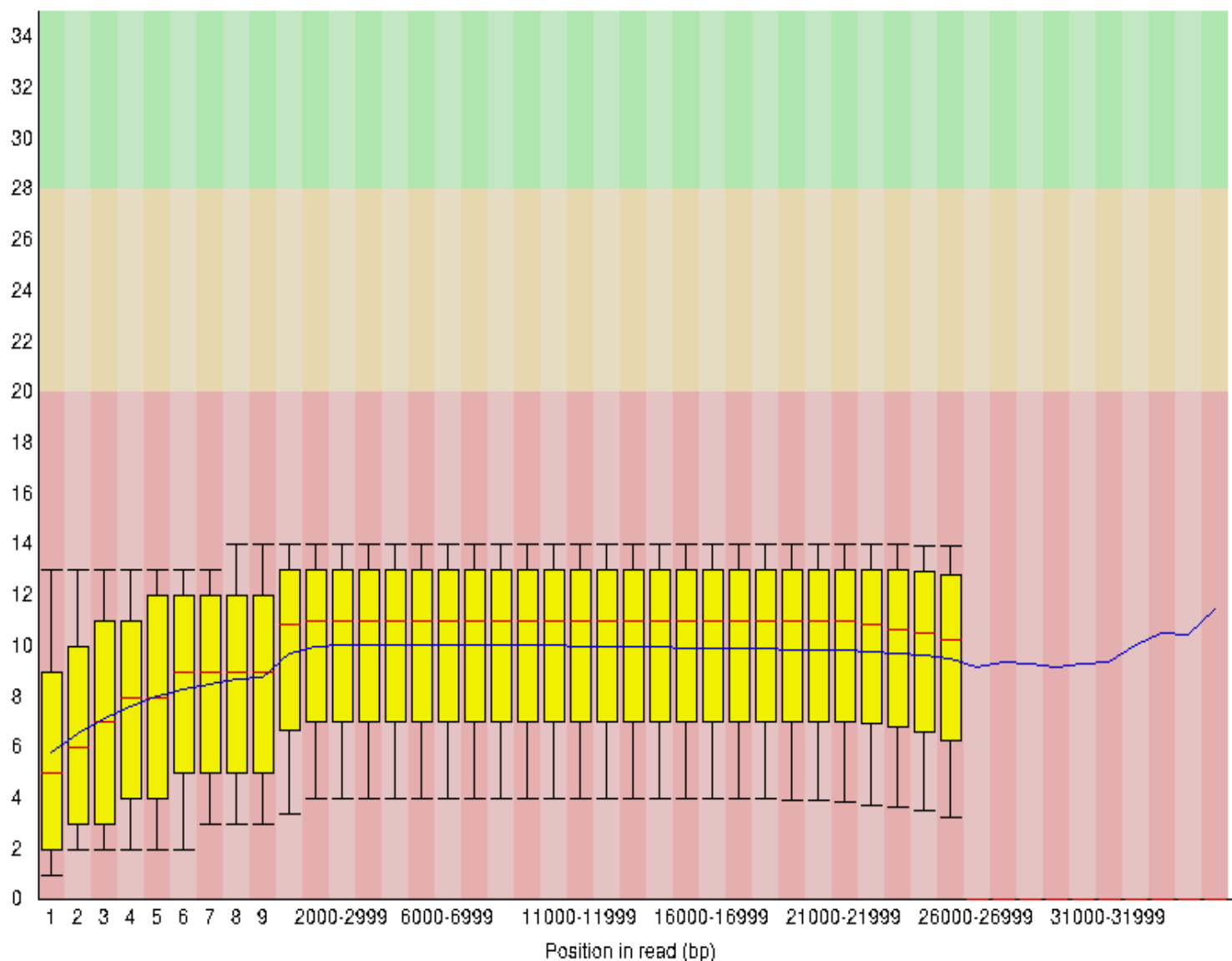
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Basic Statistics

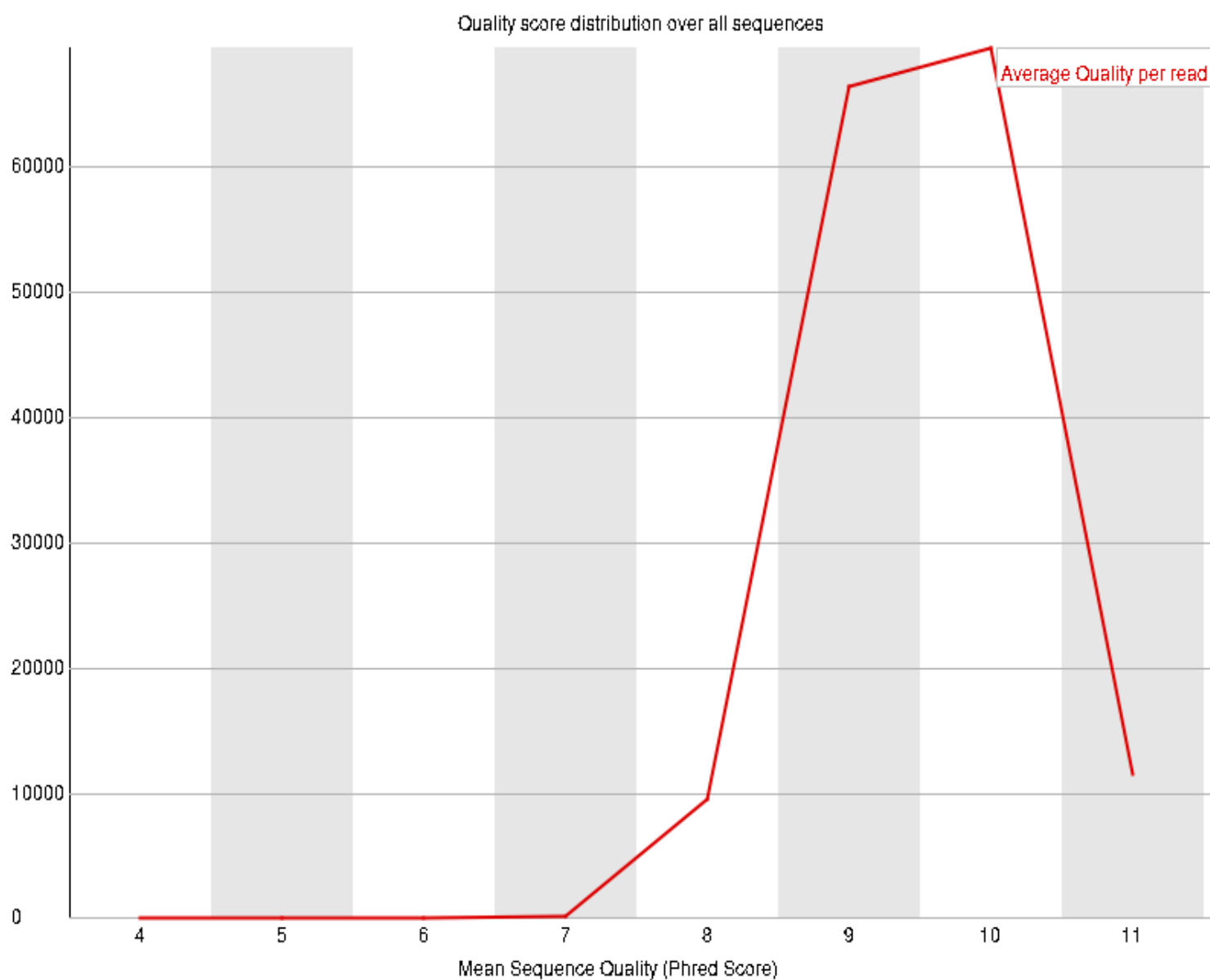
Measure	Value
Filename	SRR2154343_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	157129
Sequences flagged as poor quality	0
Sequence length	500–35005
%GC	57

Per base sequence quality

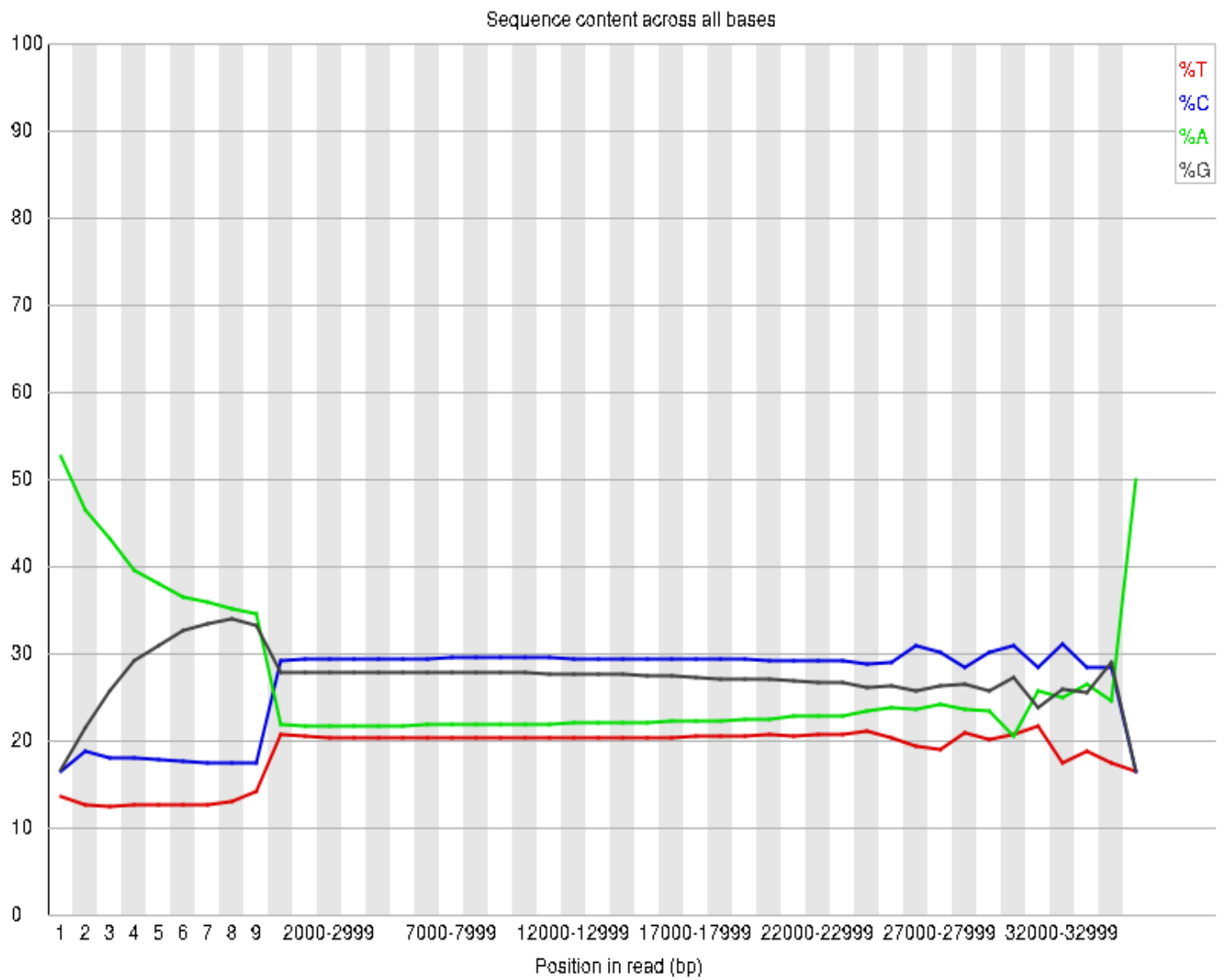
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



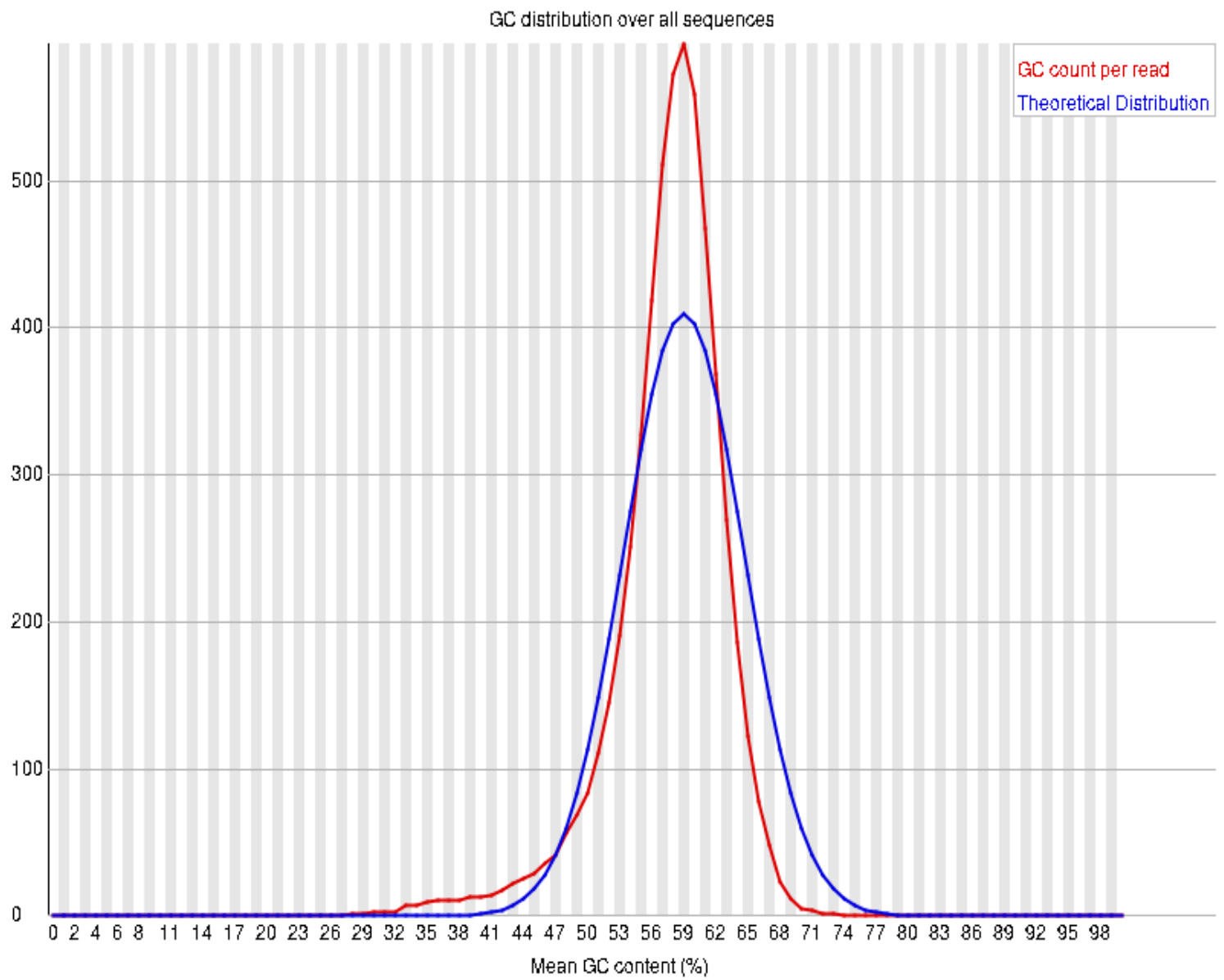
Per sequence quality scores



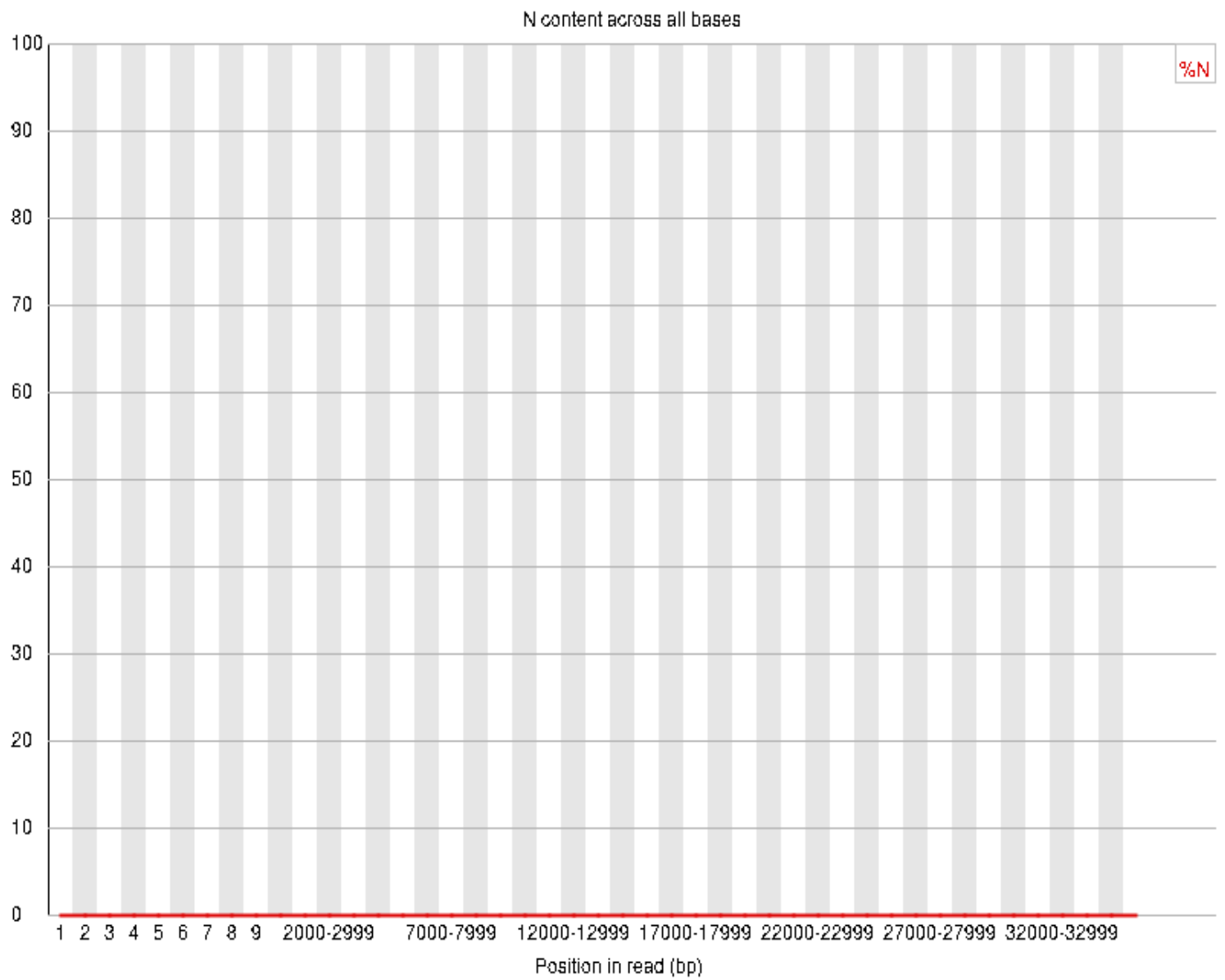
✖ Per base sequence content



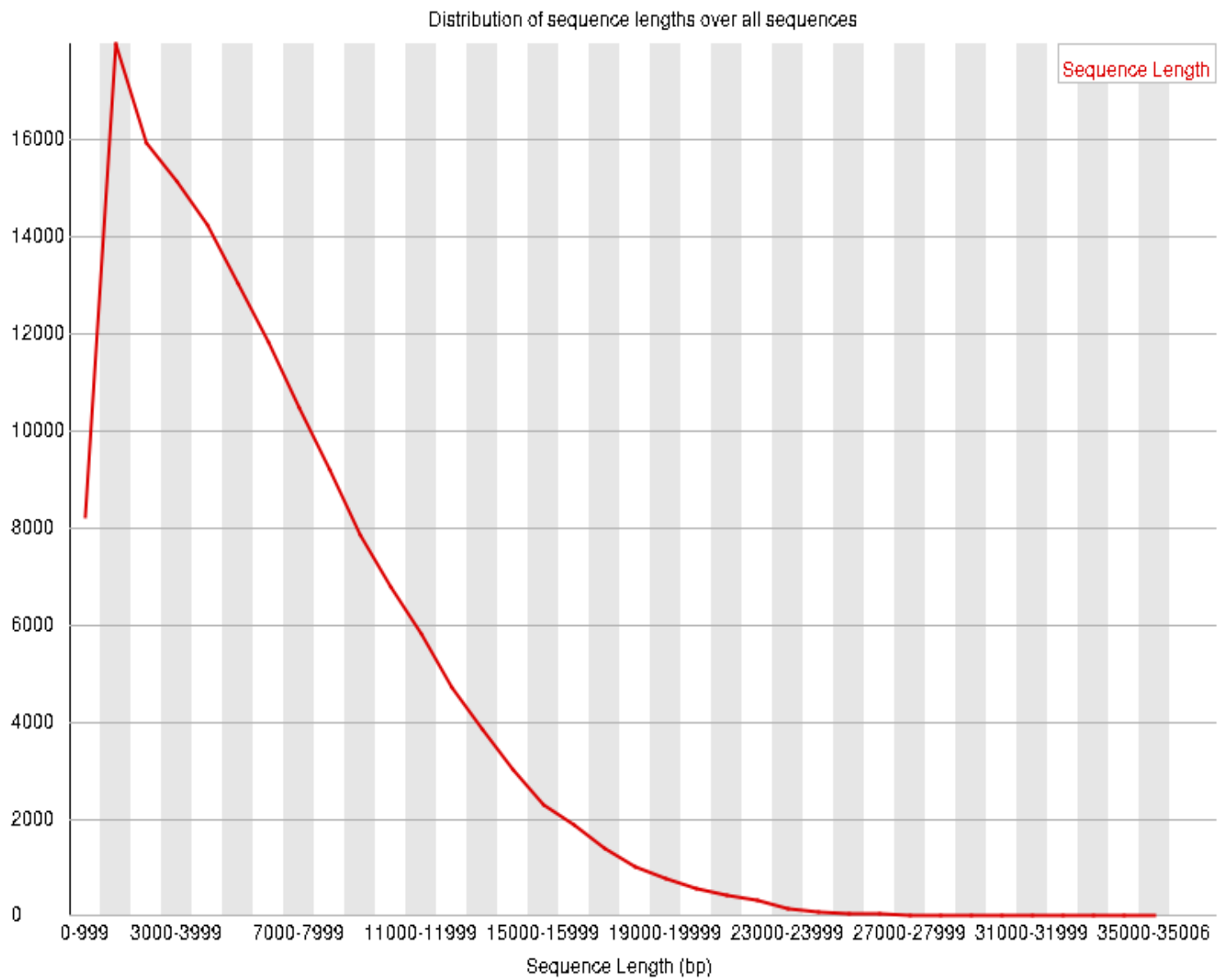
Per sequence GC content



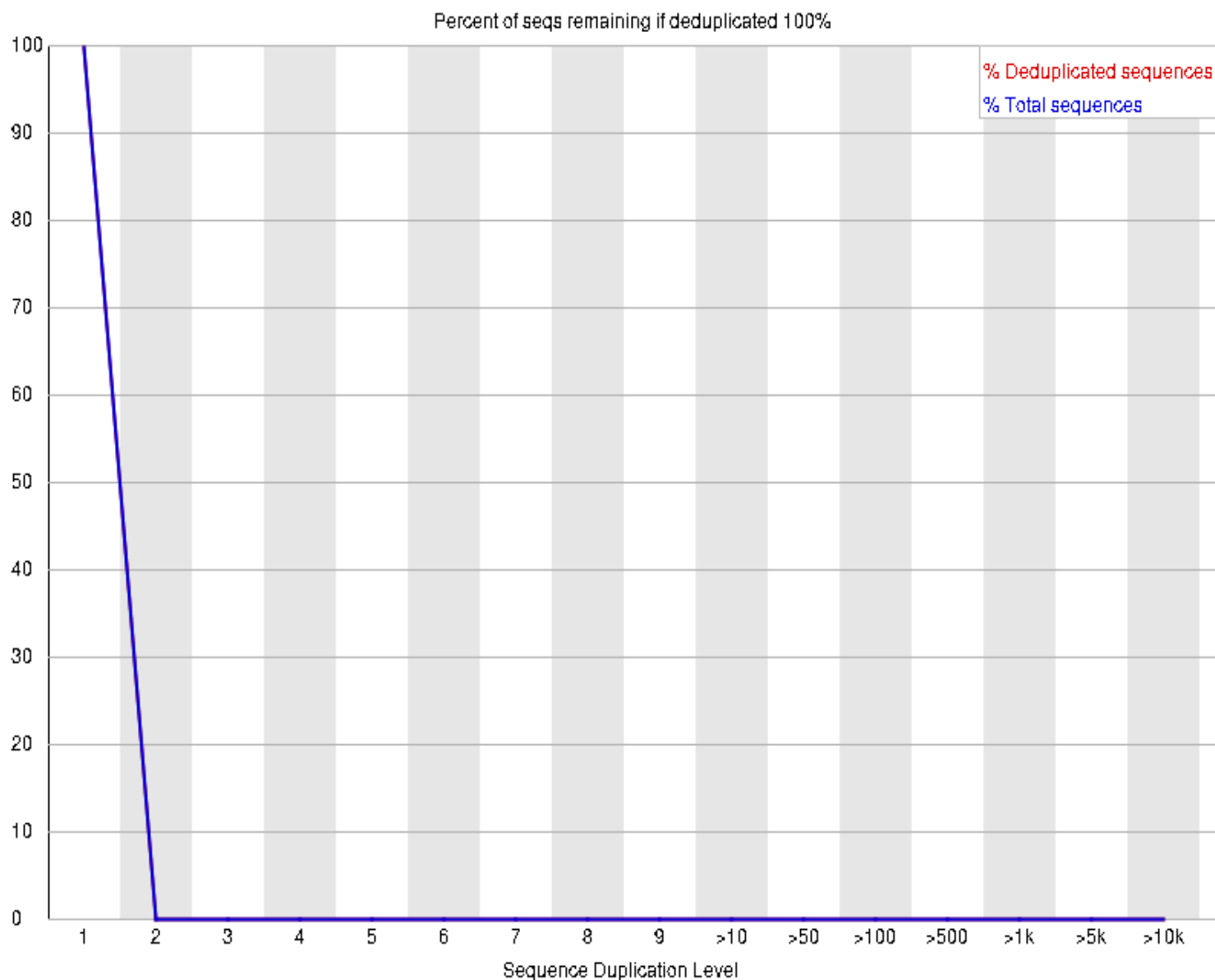
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

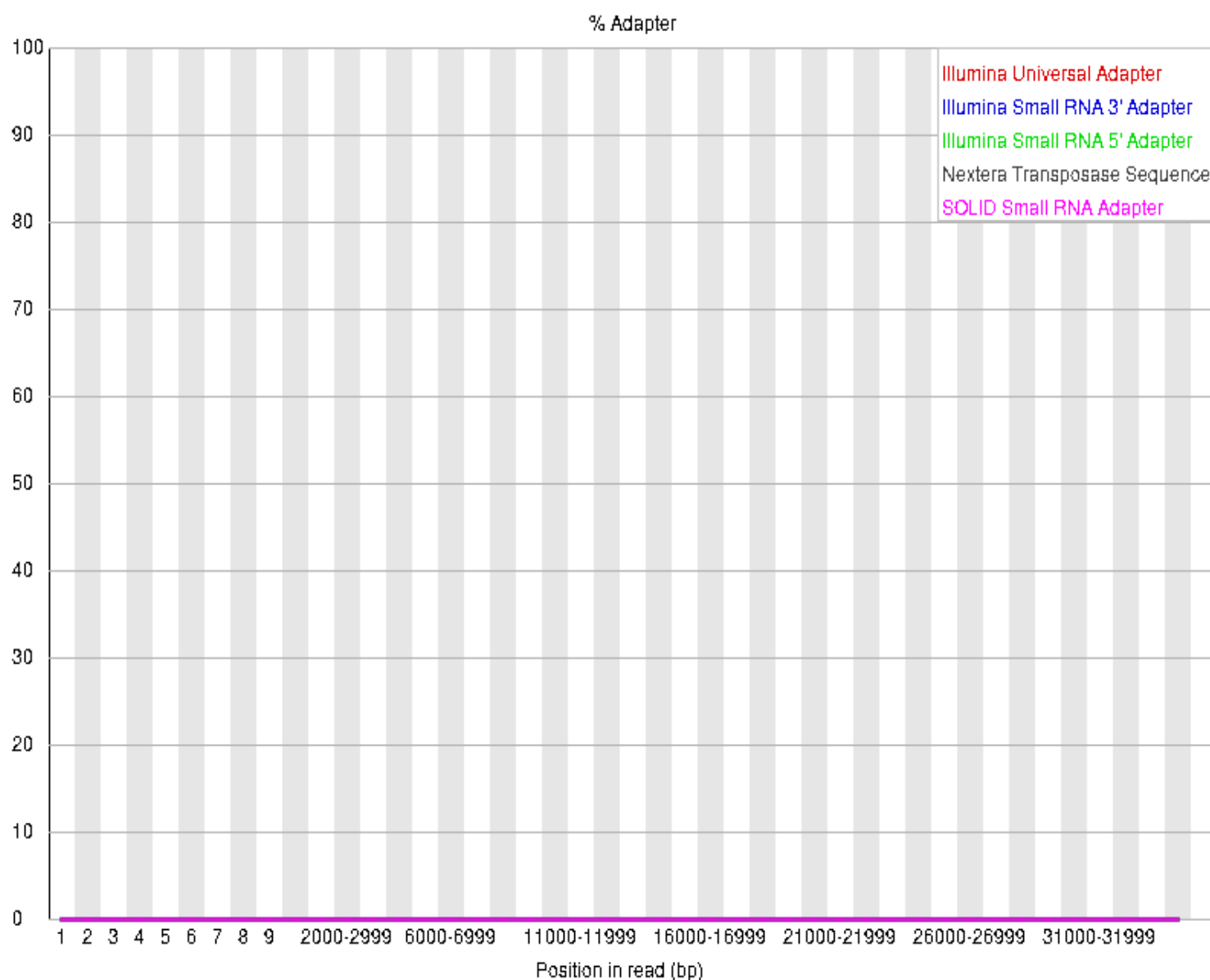


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.11.9)