











FastQC Report

Summary

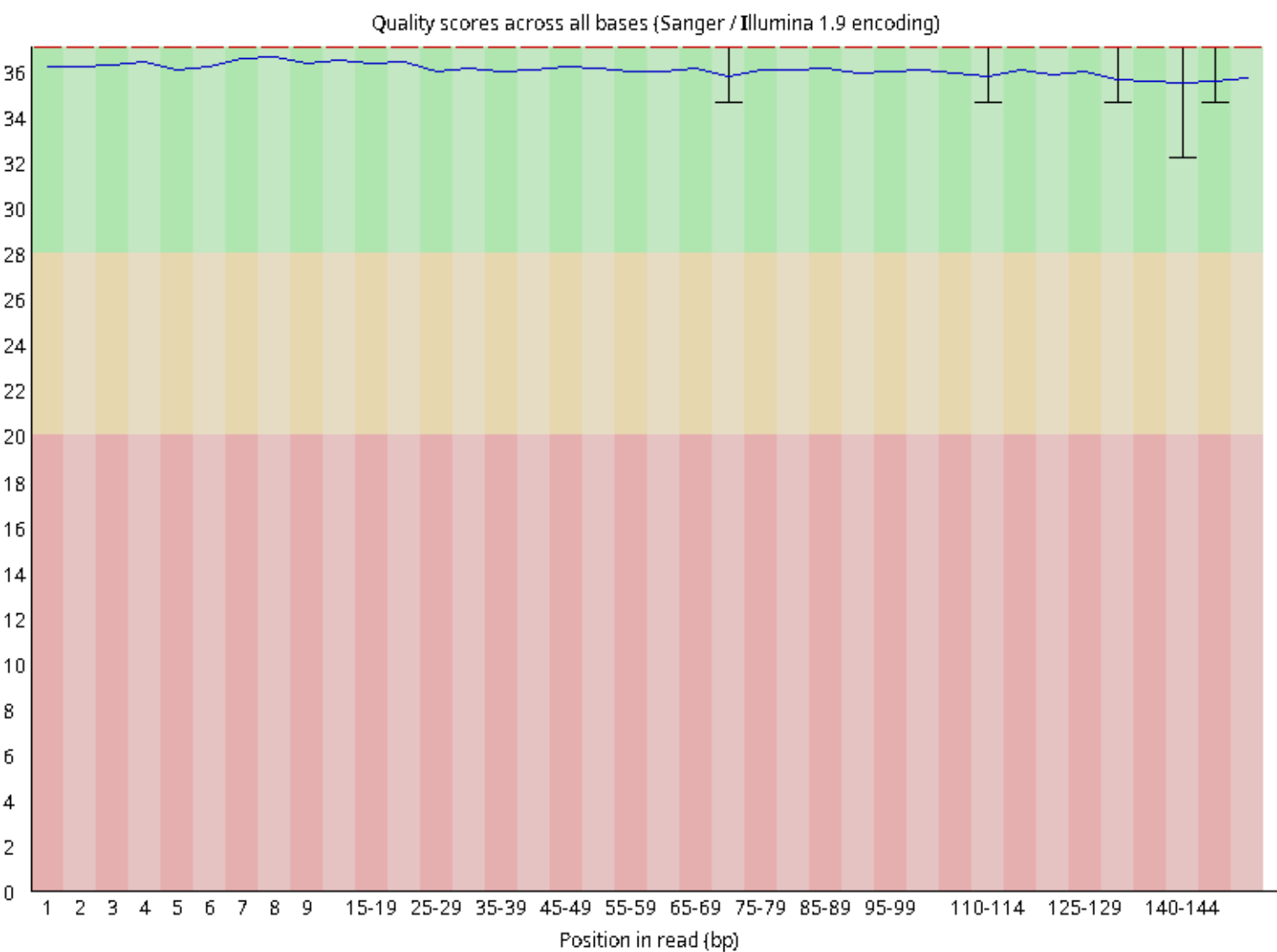
sáb 20 dic 2025
AbrahamSimpson_R2.fastq

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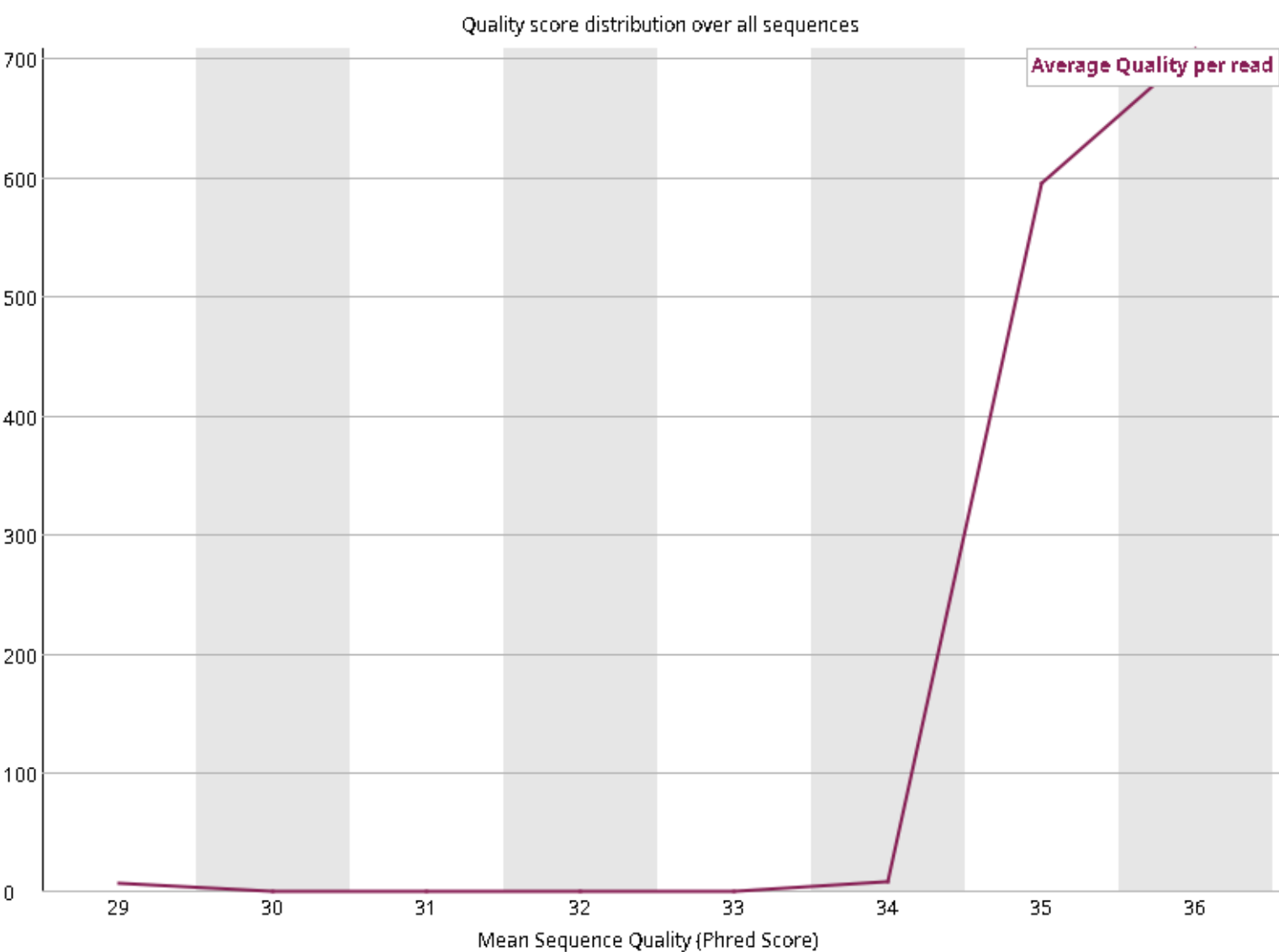
Basic Statistics

Measure	Value
Filename	AbrahamSimpson_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1320
Total Bases	199.3 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

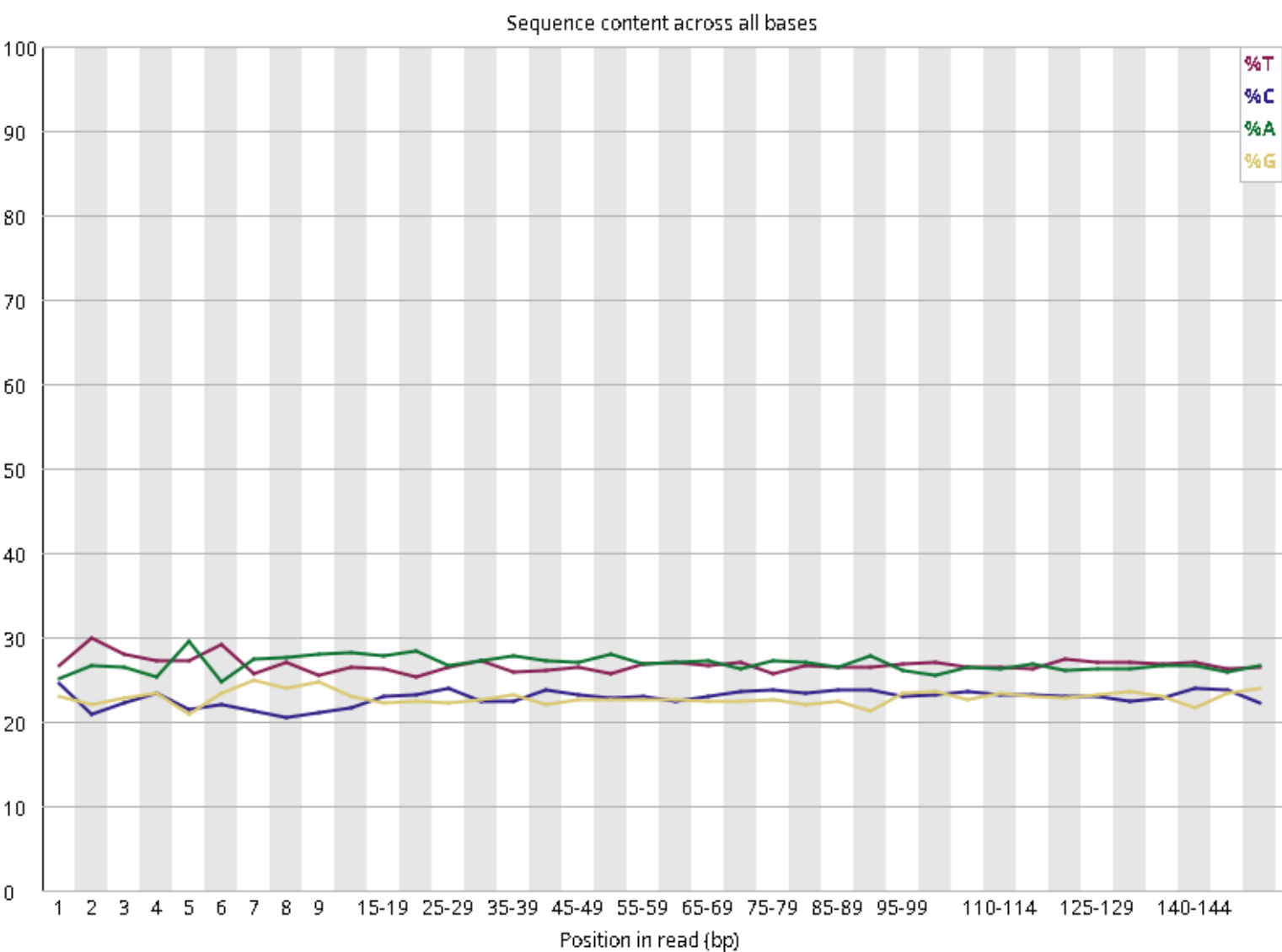
✔ Per base sequence quality



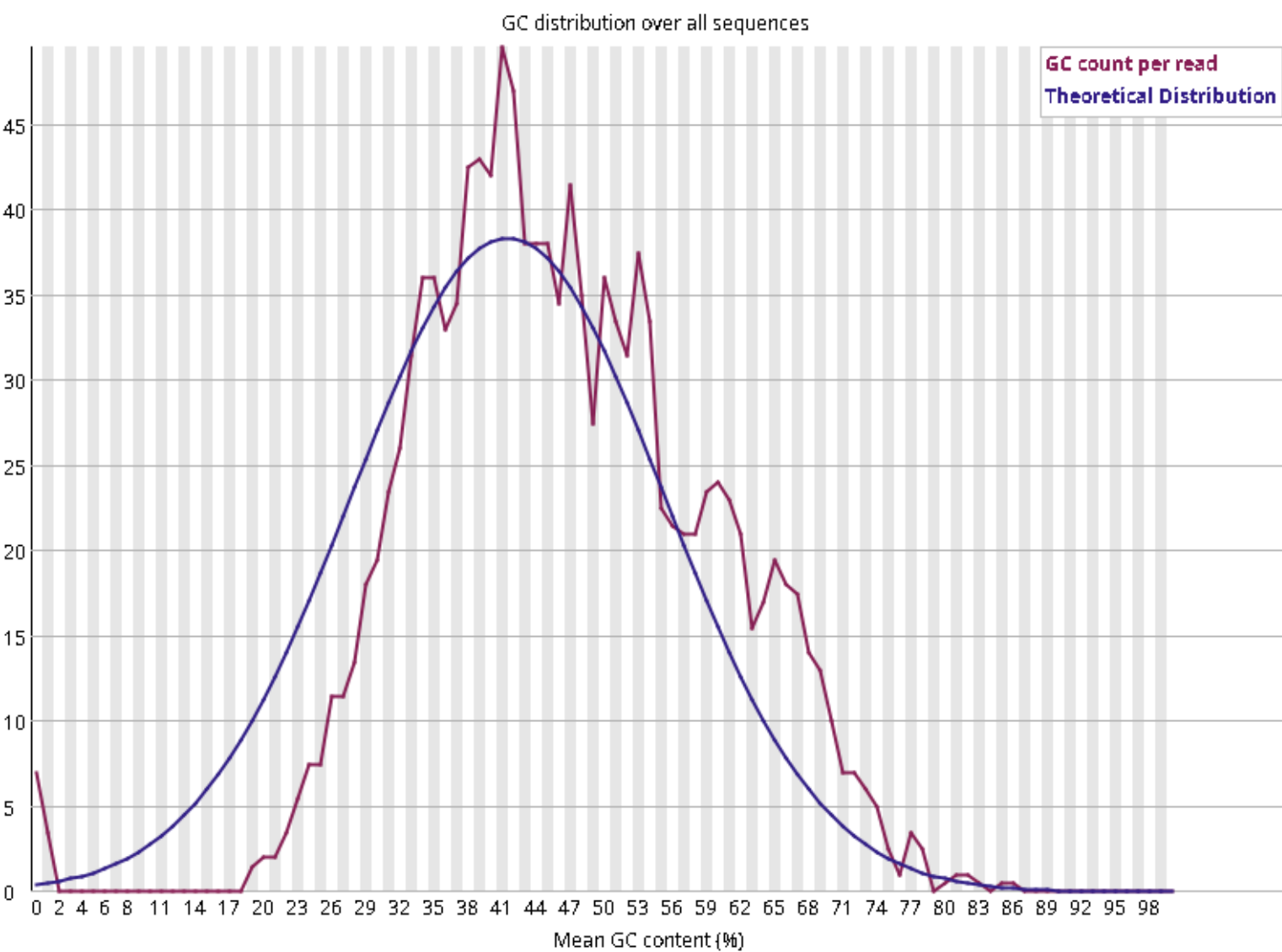
✔ Per sequence quality scores



✔ Per base sequence content

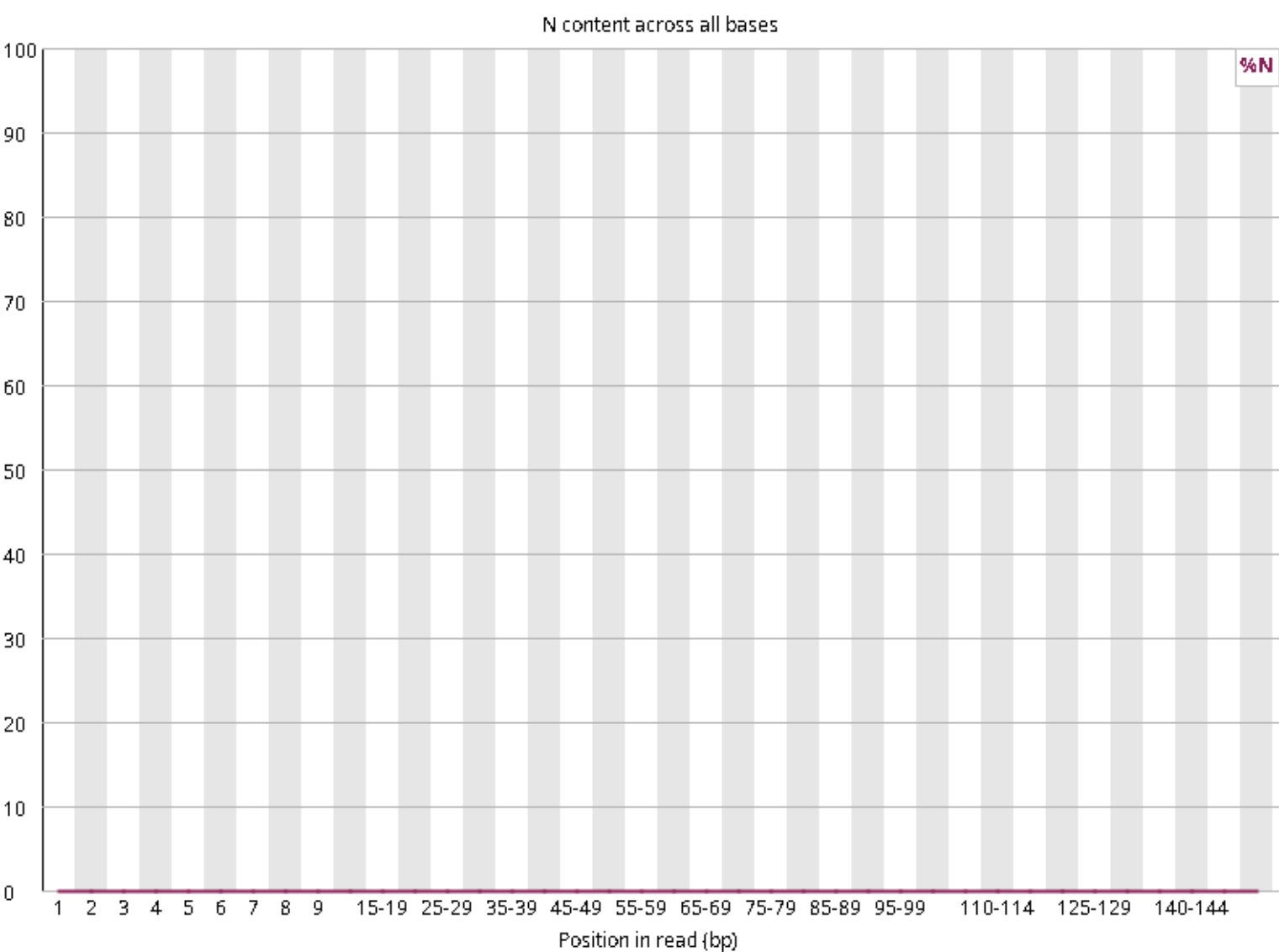


✖ Per sequence GC content

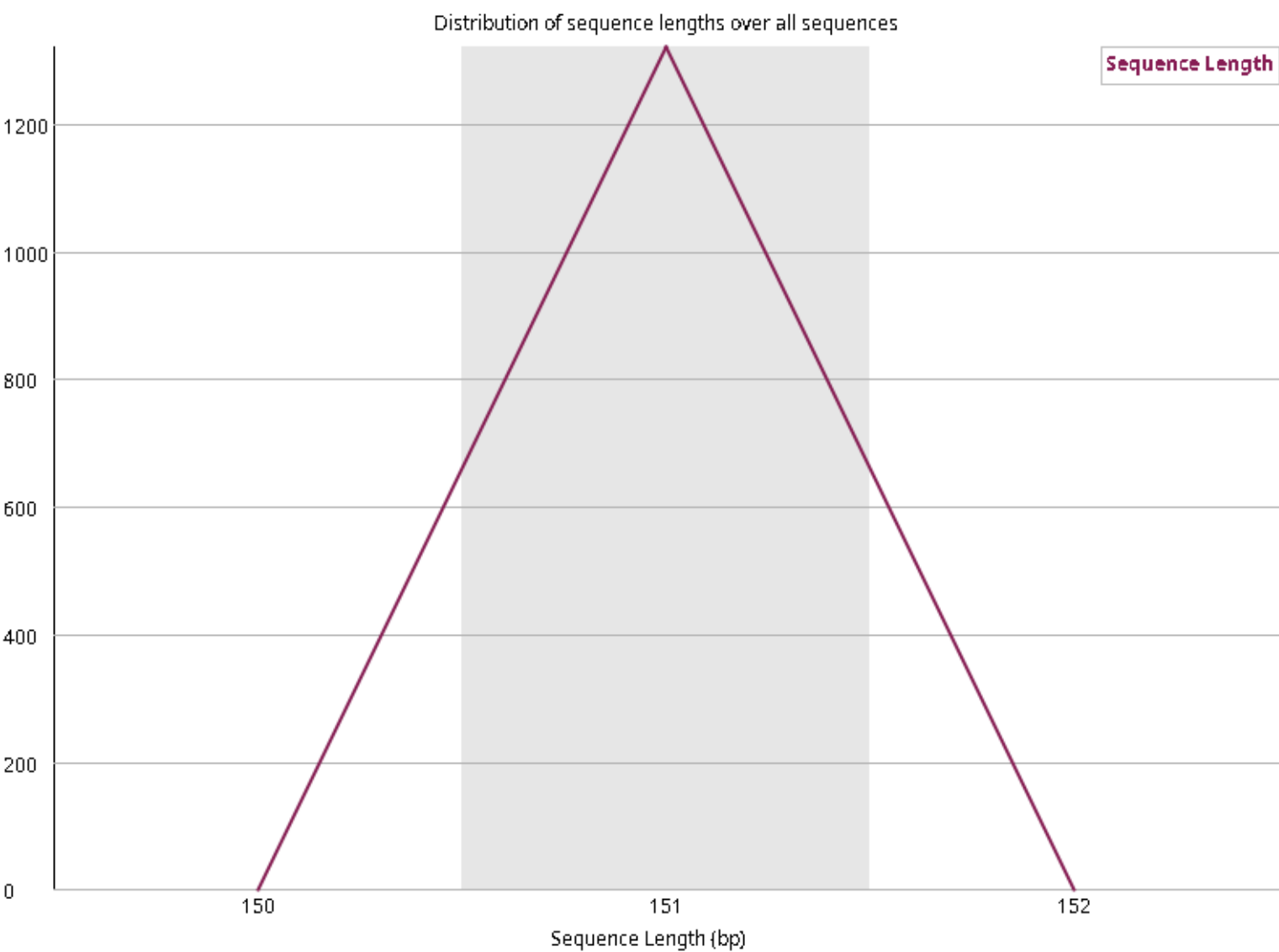




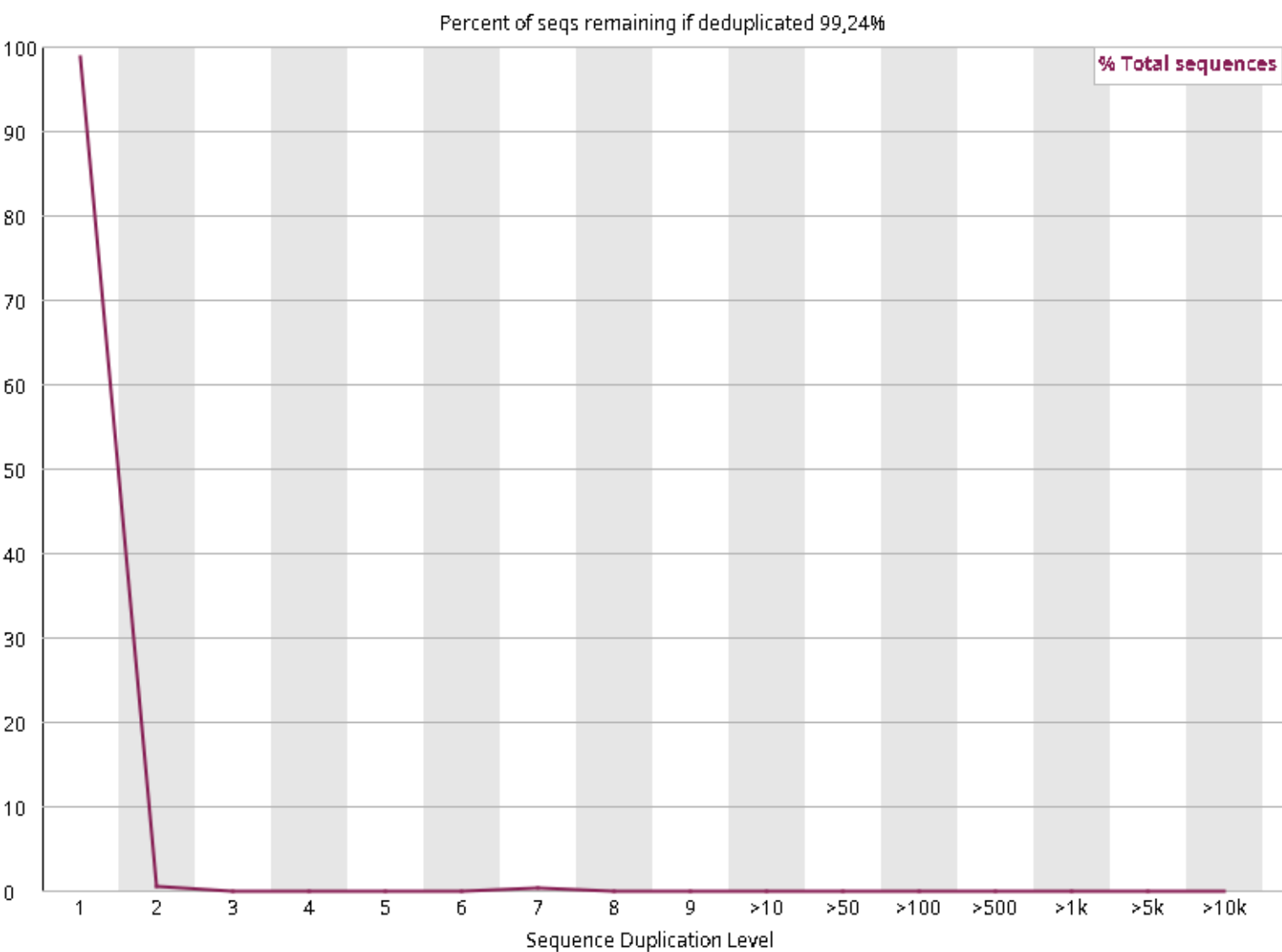
Per base N content



✔ Sequence Length Distribution



Sequence Duplication Levels

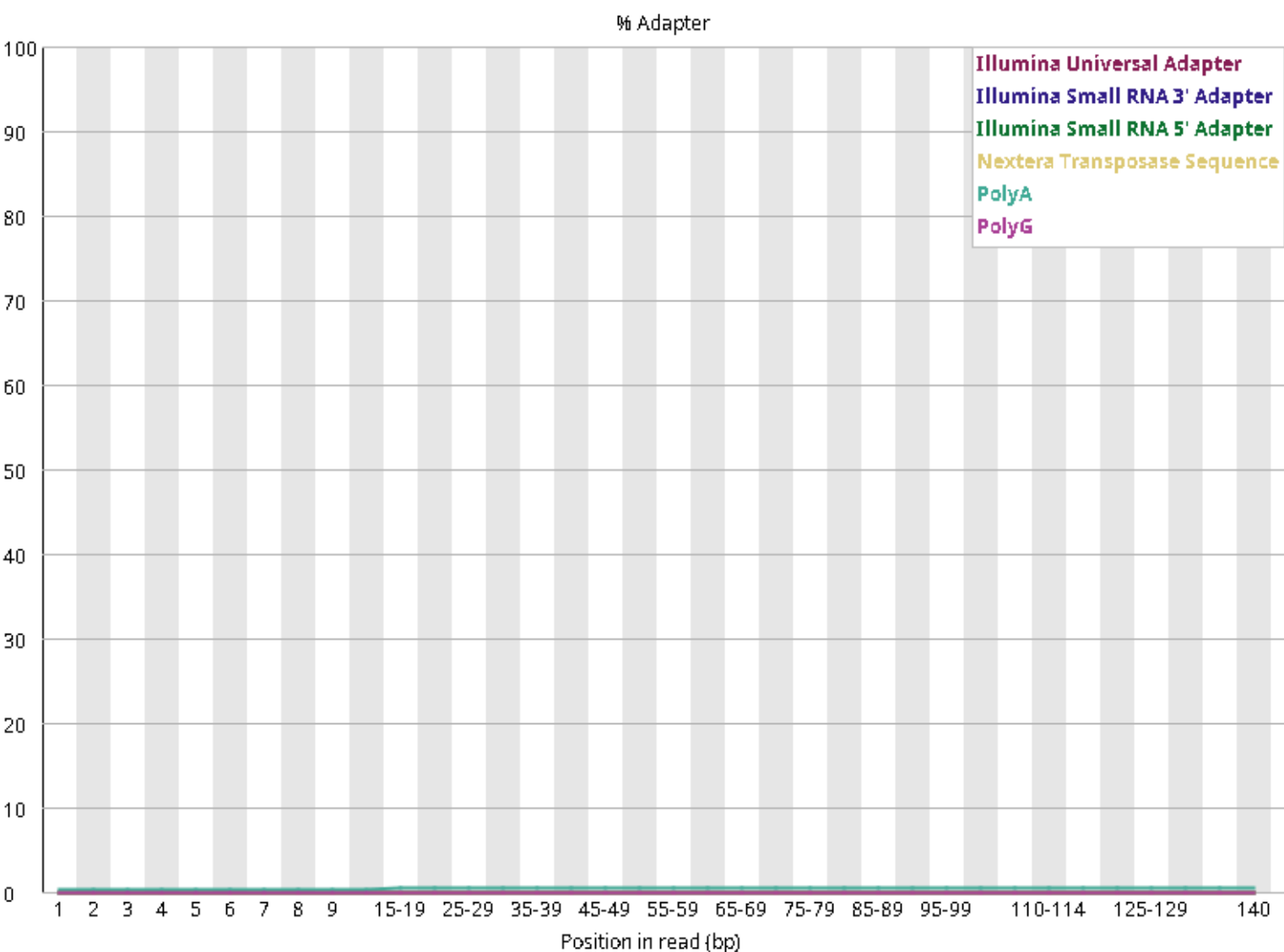


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AA	7	0.5303030303030304	No Hit
CTGTGCCCTCACTCGCCCTTCTTGTAGGCGTTCTTGATGATGGCGTTTTT	2	0.15151515151515152	No Hit
CGGGTCTGAACGTGCTGCAGTTTGTGTAACTCTGGTTCCTATACAGAGC	2	0.15151515151515152	No Hit
GCAGGACTCATGCAGCCTTACGCAGCGACGTGAGGAGCGGGGCTCGCGGT	2	0.15151515151515152	No Hit
GGAGAGCAAGGGGCTTTGGGGTCGACCTCCTGGGGGAGGGTAGCCCTGGG	2	0.15151515151515152	No Hit



Adapter Content



Produced by [FastQC](#) (version 0.12.1)