











FastQC Report

Summary

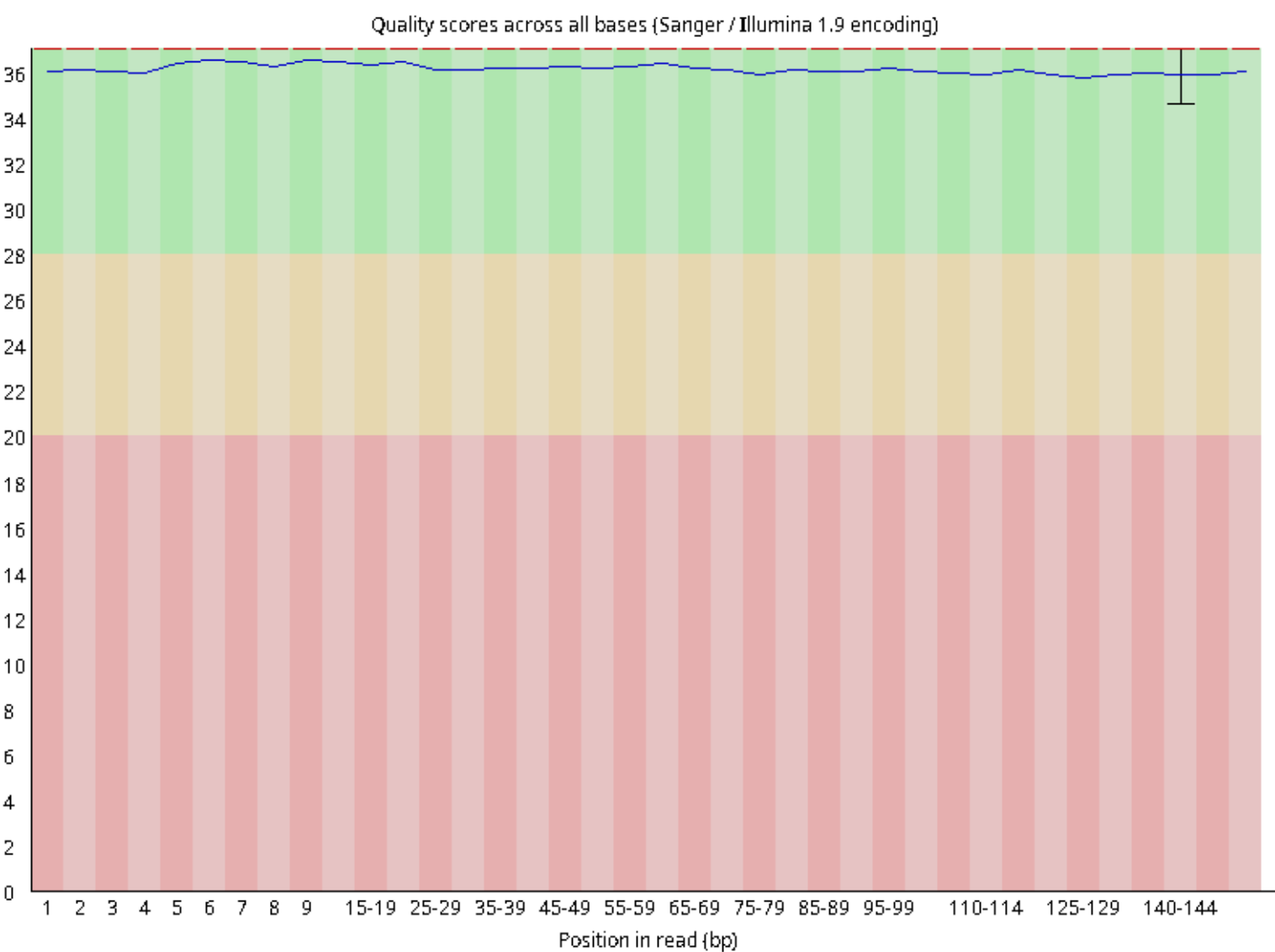
sáb 20 dic 2025
MargeSimpson_R1.fastq

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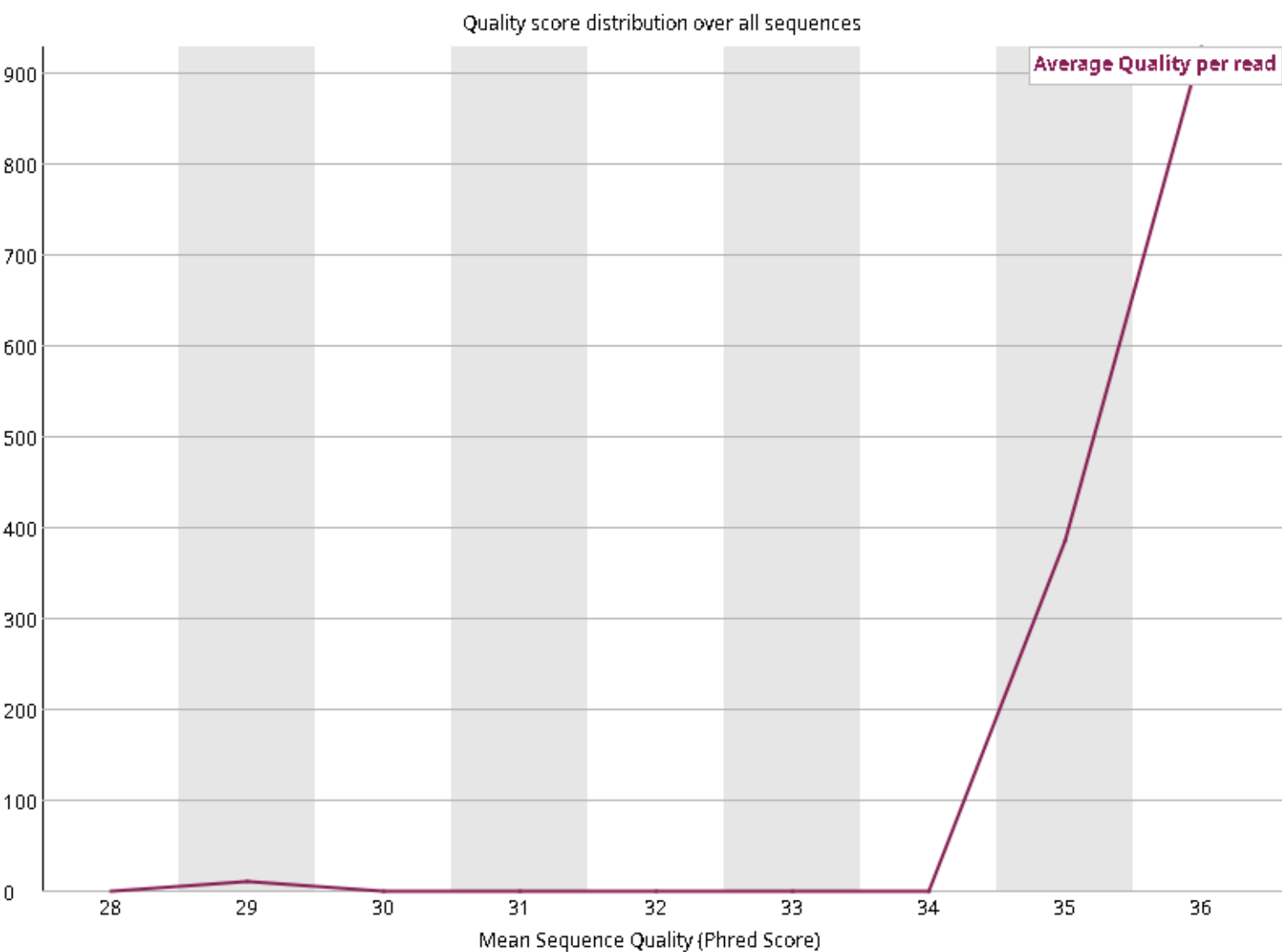
Basic Statistics

Measure	Value
Filename	MargeSimpson_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1328
Total Bases	200.5 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

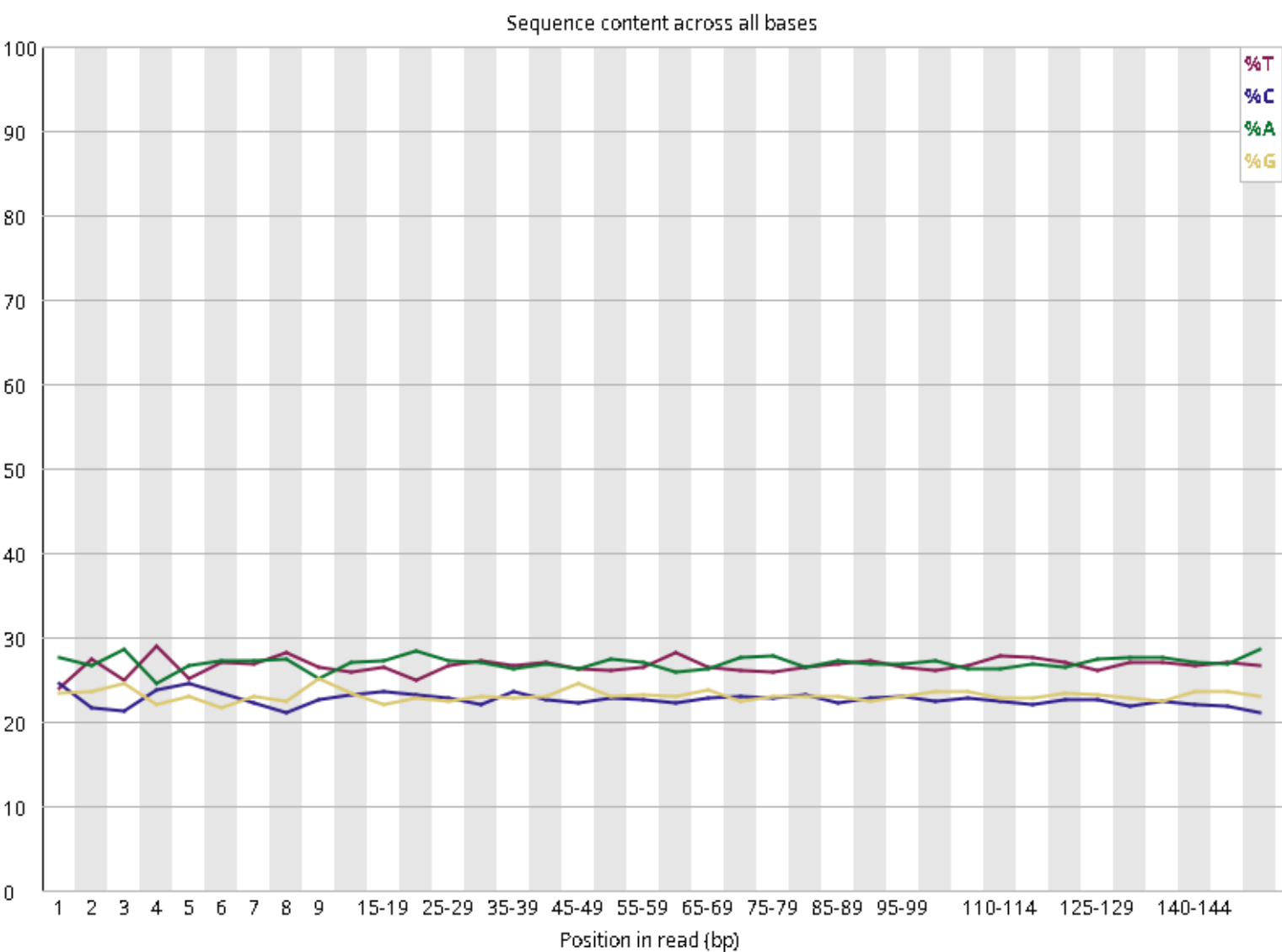
✔ Per base sequence quality



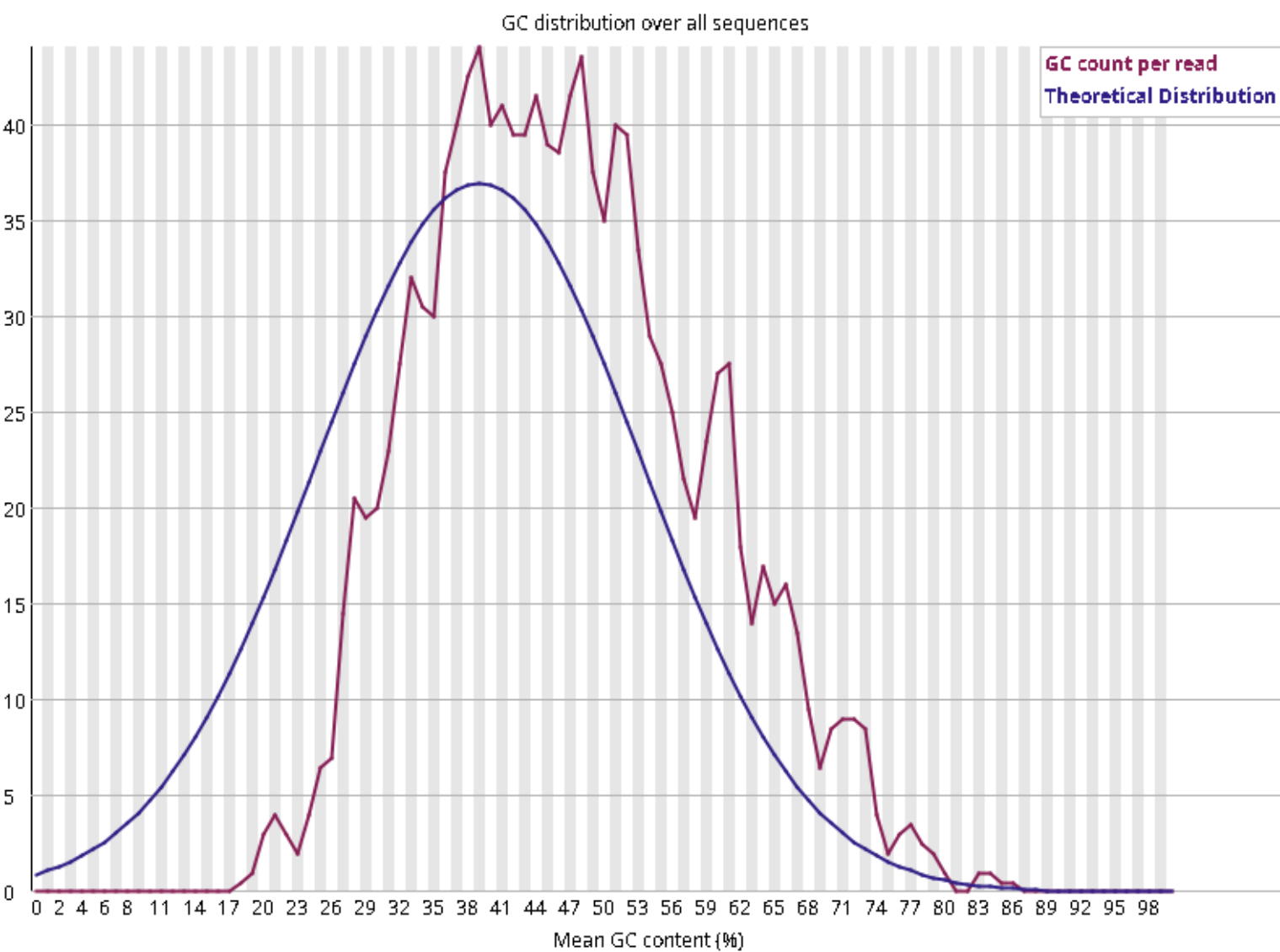
✔ Per sequence quality scores



✔ Per base sequence content

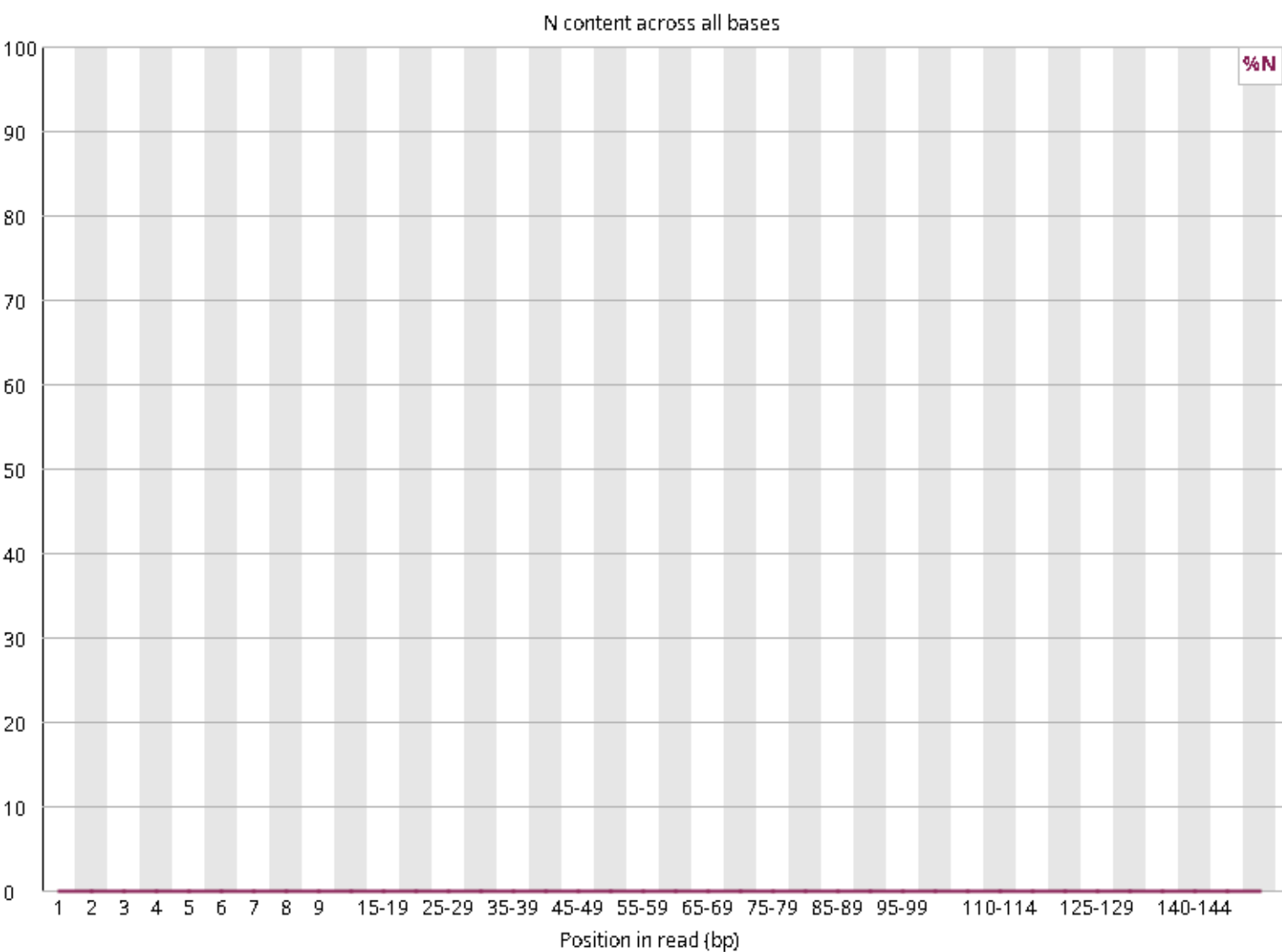


✖ Per sequence GC content

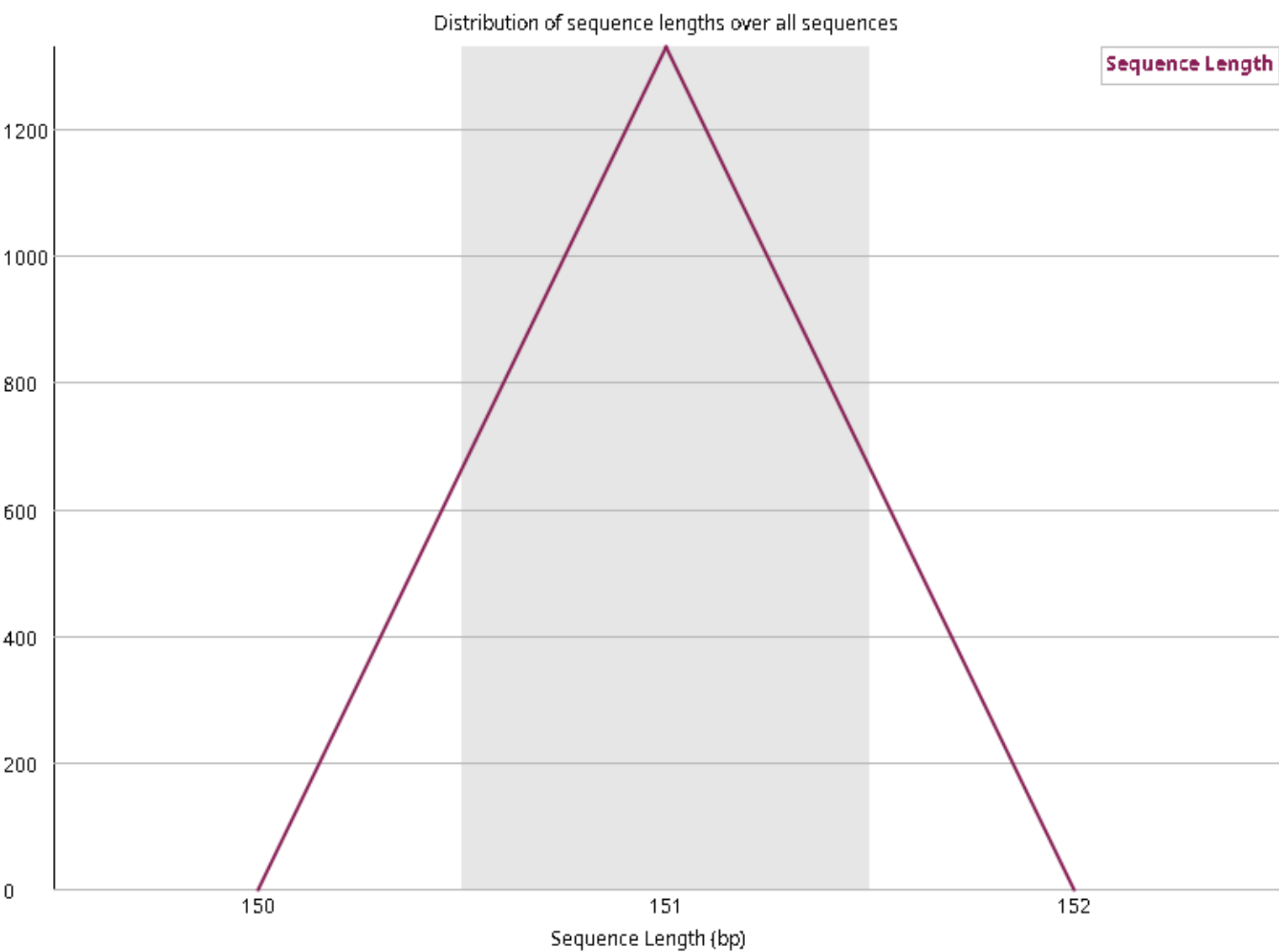




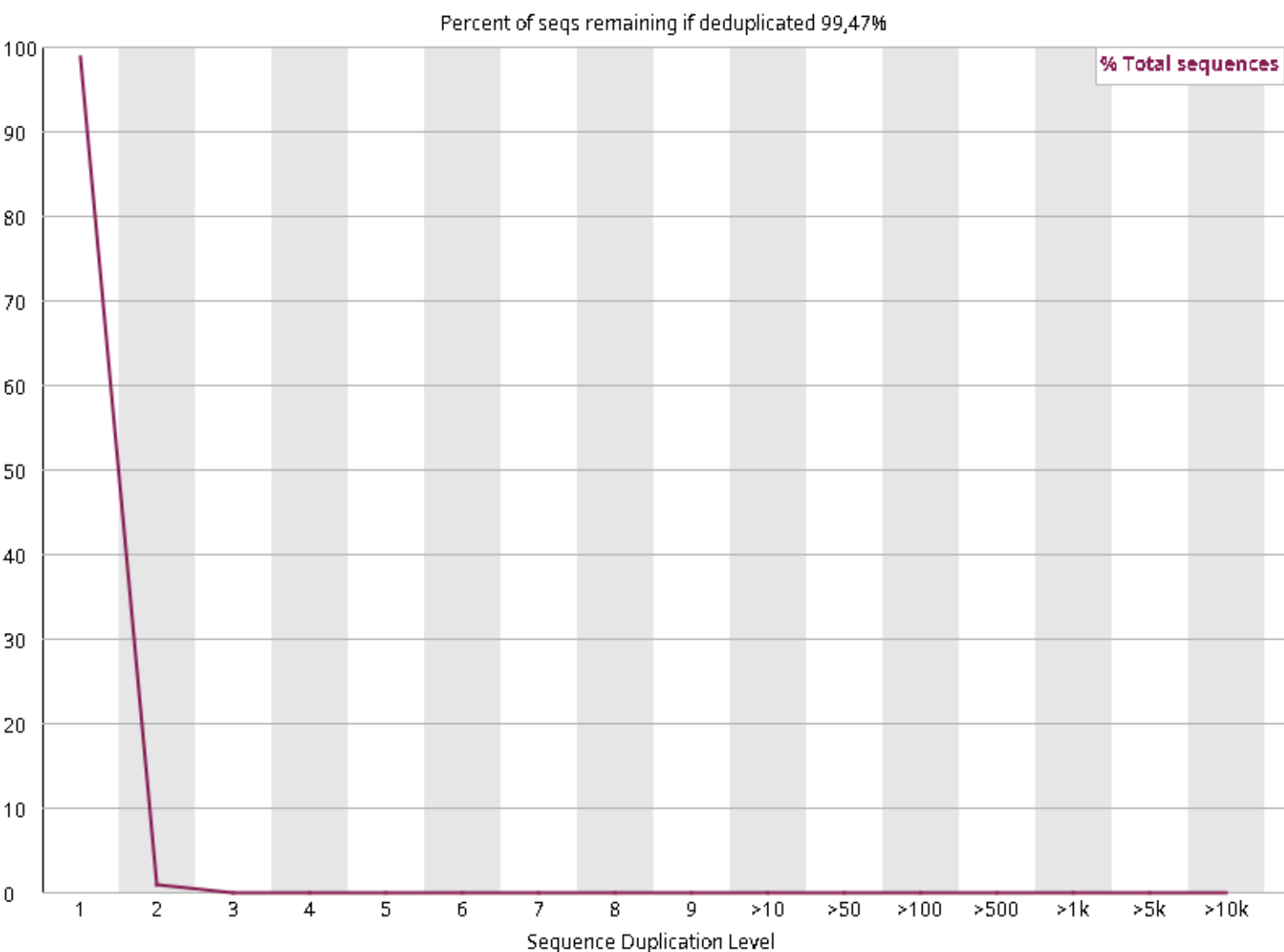
Per base N content



✔ Sequence Length Distribution



Sequence Duplication Levels

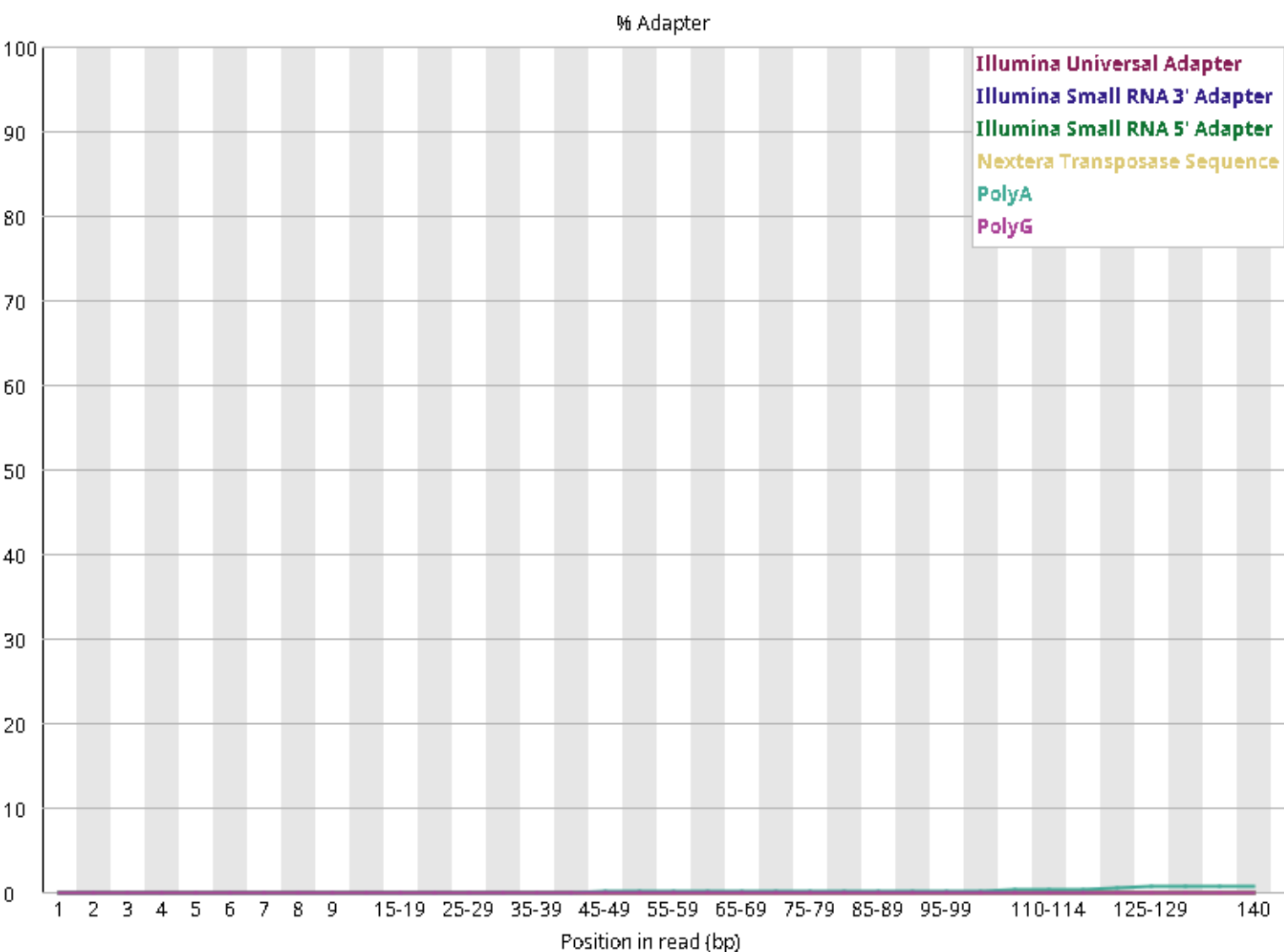


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGATCGTCATTTACCGGGTGGTGACTGTCAGCACTTTCGCTGCCTTTAAG	2	0.15060240963855423	No Hit
TGGTGTTGTTCTTATTATCTTGAGGGATTTCAGTACTGTATAGTAGAGGG	2	0.15060240963855423	No Hit
GCGACGAGCAGCCTCTGACCGAGAACCCCCGGAAGTACGTCATGGGCCAC	2	0.15060240963855423	No Hit
CTCAGGTTGGGCAGGGACTCCTCCTCTCTGTGGGGTCTCTATCTGGGCAC	2	0.15060240963855423	No Hit
TAATGGCAAAAGACCTCACCAAGAATTTGGCATTTCAGTCAAGGATGCT	2	0.15060240963855423	No Hit
TAAGAAAATACATAAGACCATAACAGCCAACAGGTGGCAGGACCAGGACT	2	0.15060240963855423	No Hit
AGCTTCTACTACTTCTCCCGCCACGTAGAAAACTGGCACGGGACACTTTT	2	0.15060240963855423	No Hit



Adapter Content



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