











FastQC Report

Summary

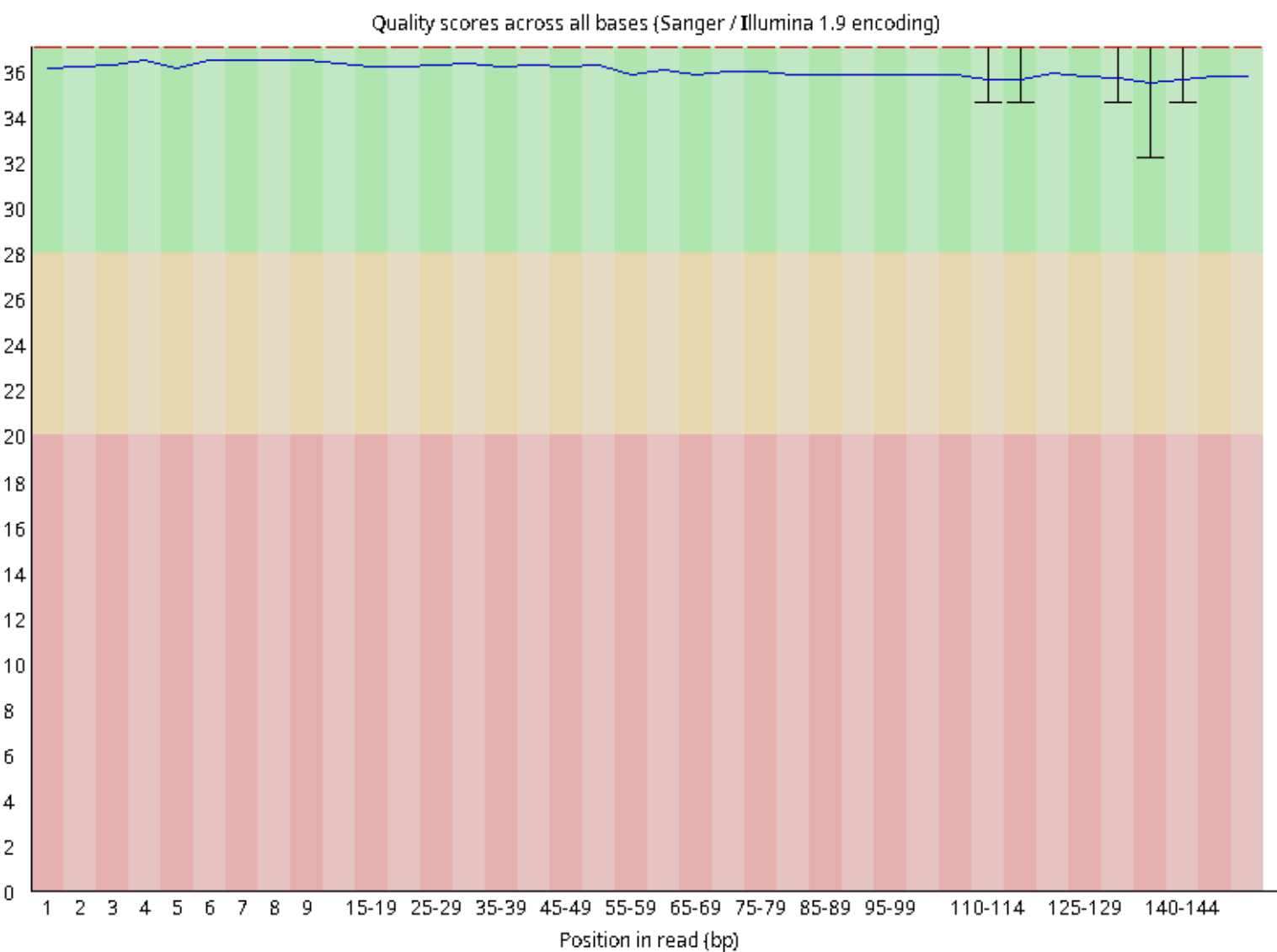
sáb 20 dic 2025
HomerSimpson_R2.fastq

-  [Basic Statistics](#)
-  [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](#)
-  [Adapter Content](#)

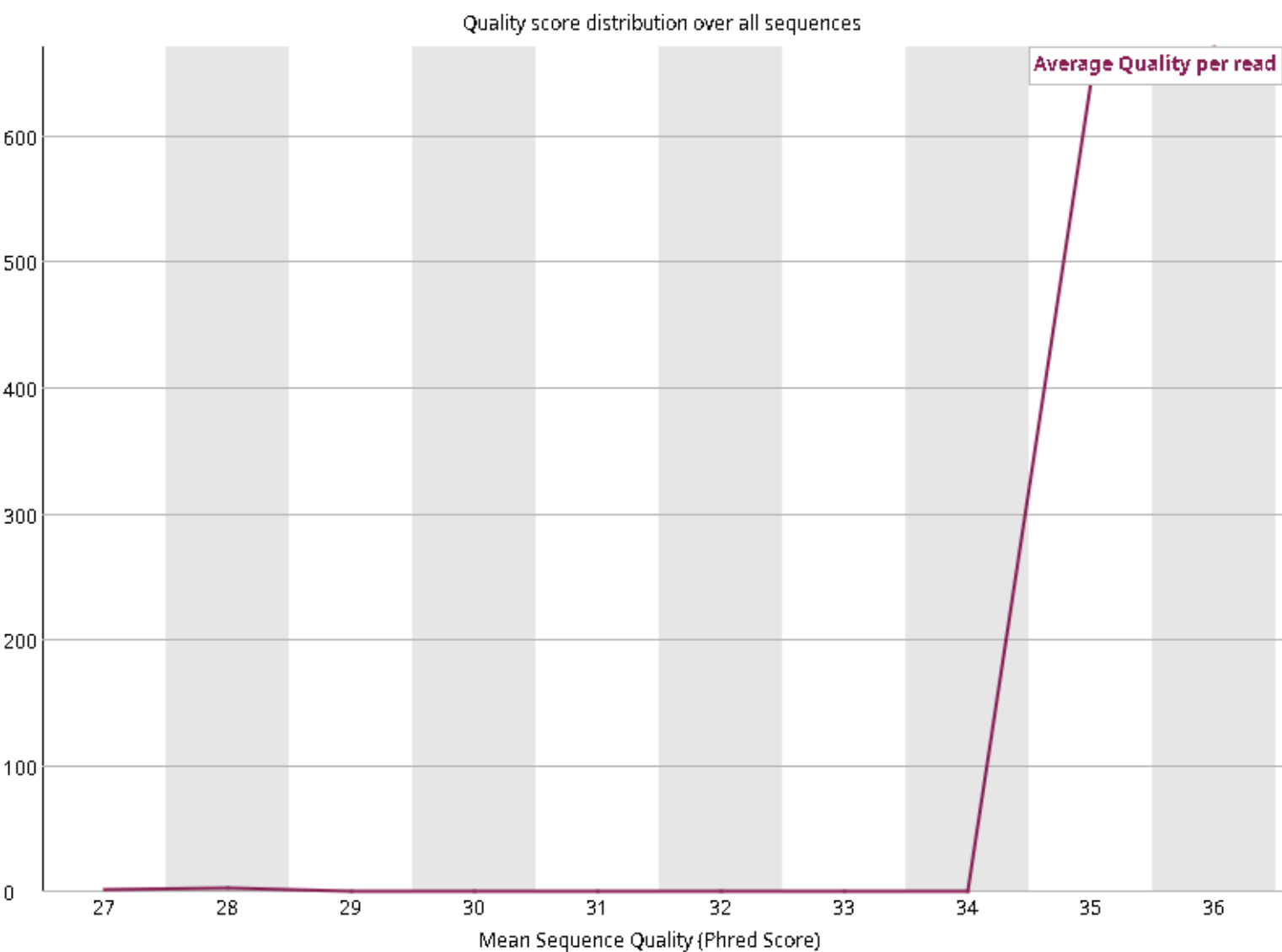
Basic Statistics

Measure	Value
Filename	HomerSimpson_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

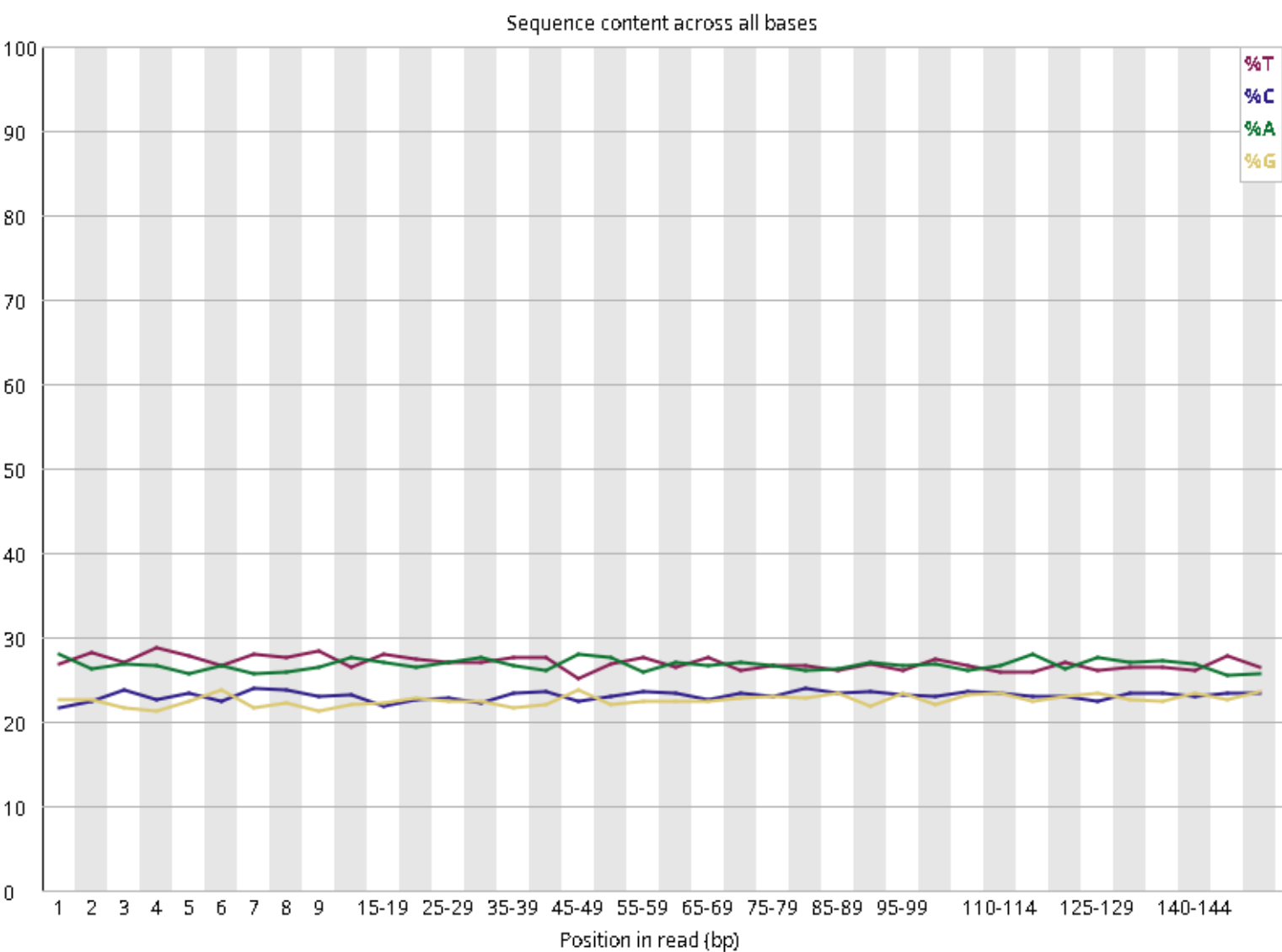
✔ Per base sequence quality



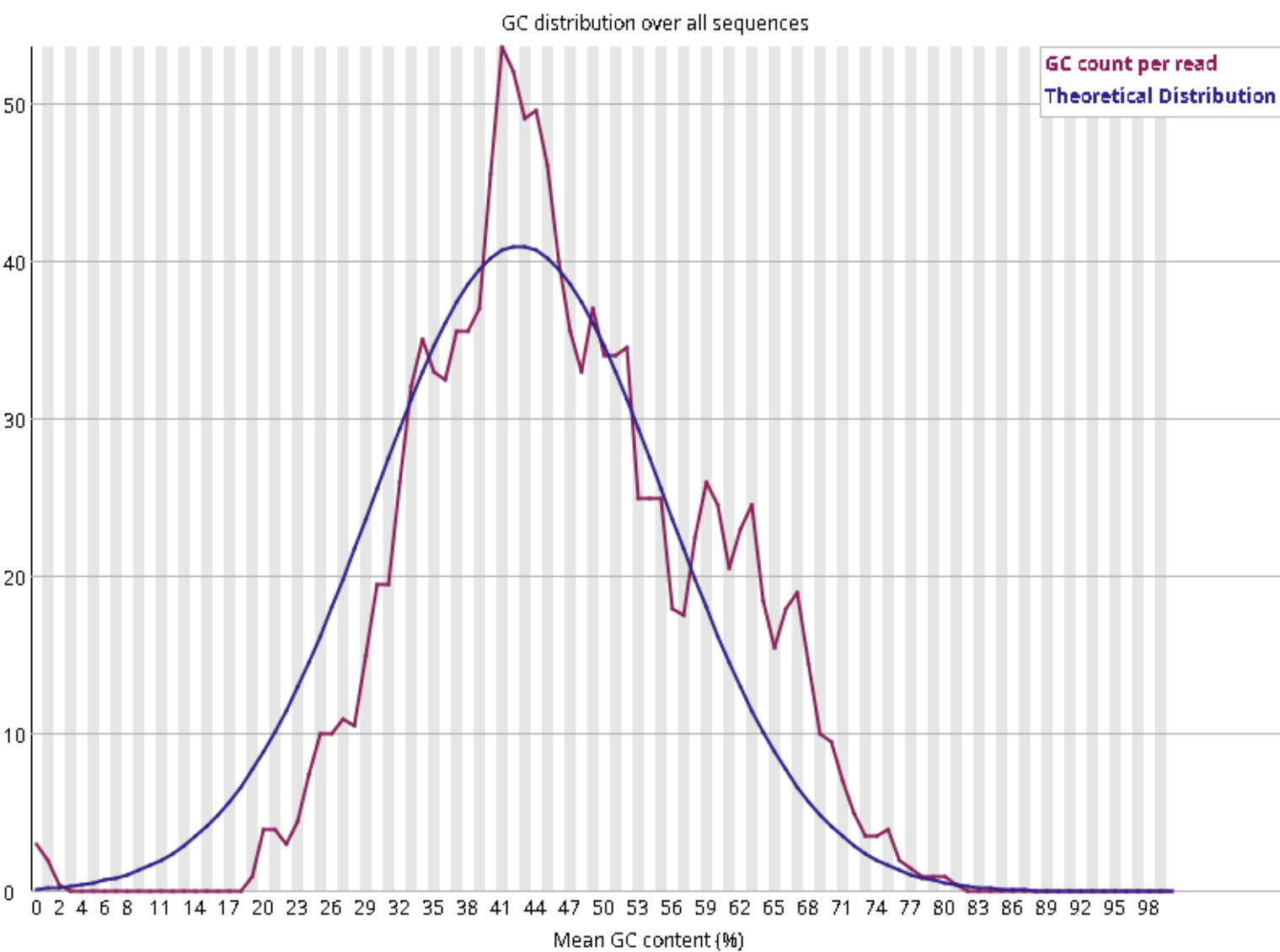
✔ Per sequence quality scores



✔ Per base sequence content

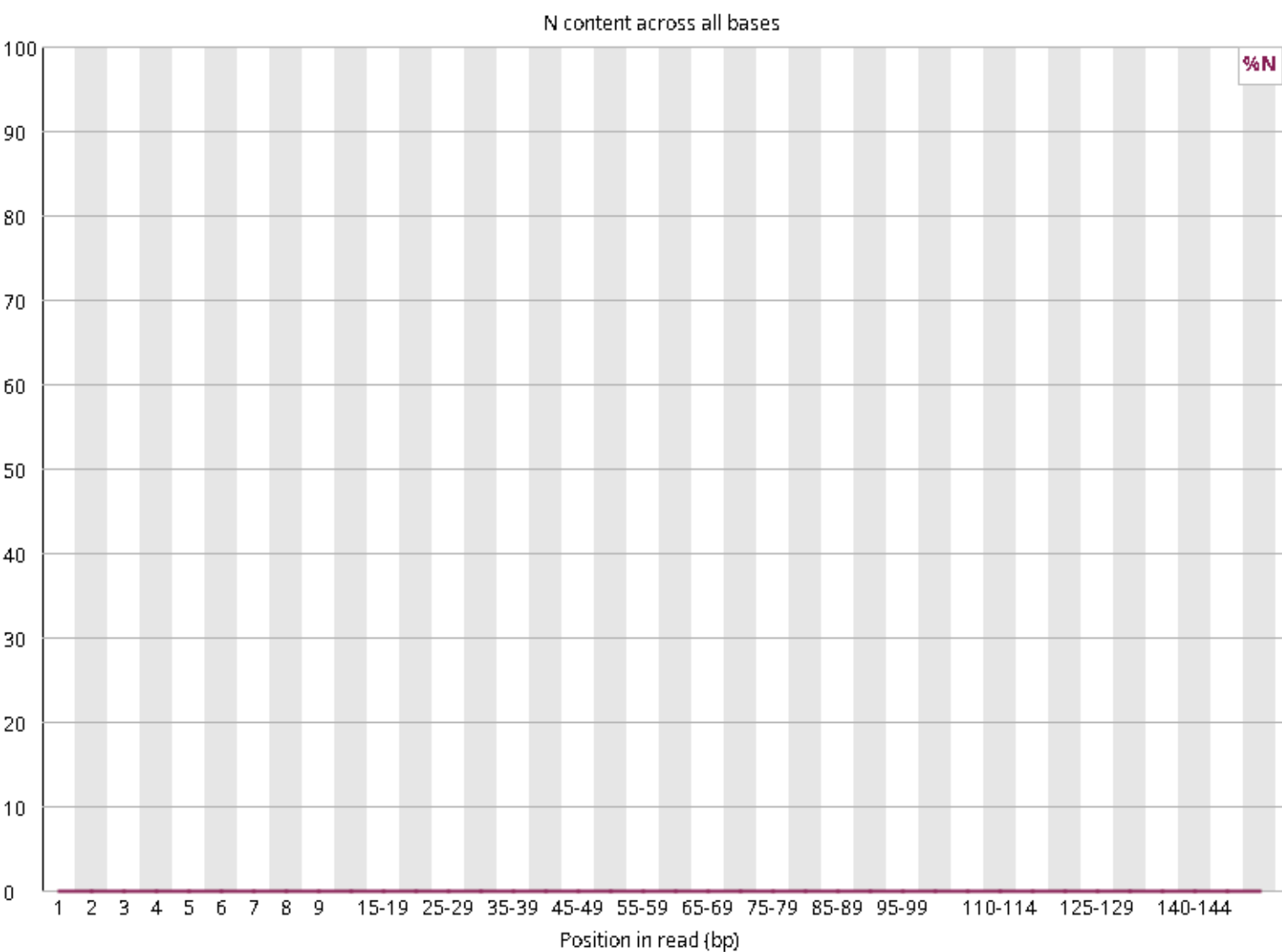


🚨 Per sequence GC content

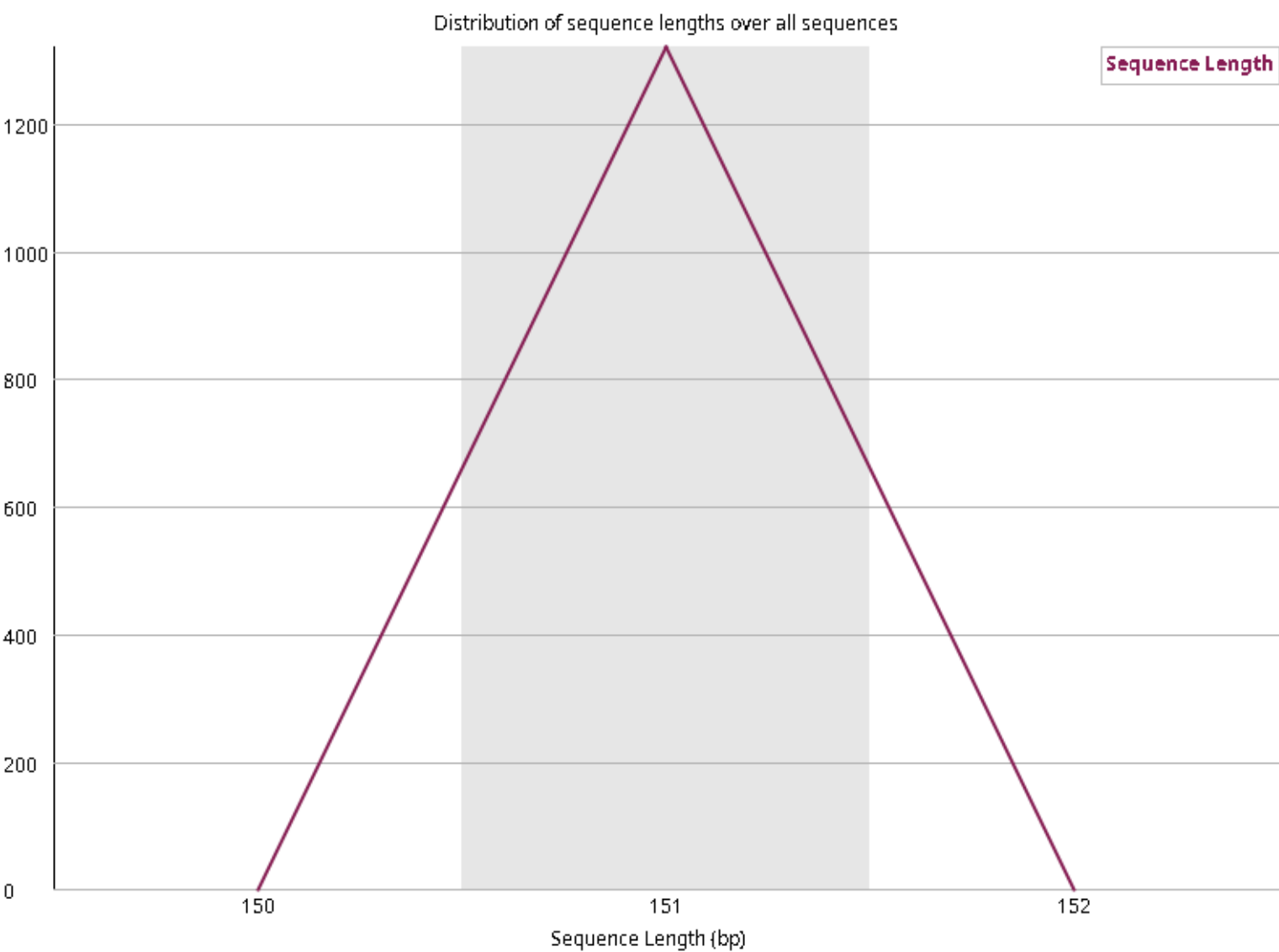




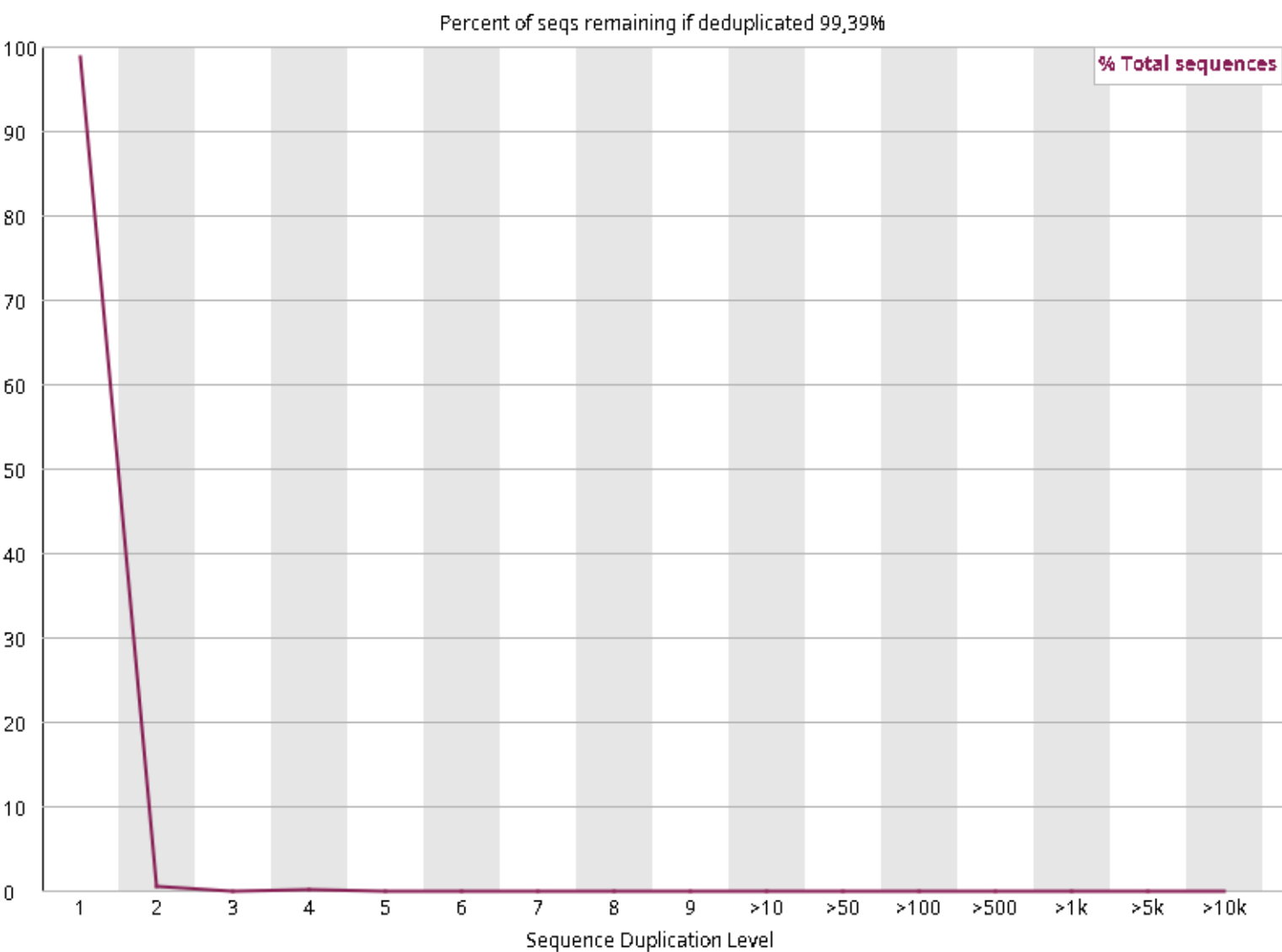
Per base N content



✔ Sequence Length Distribution



Sequence Duplication Levels

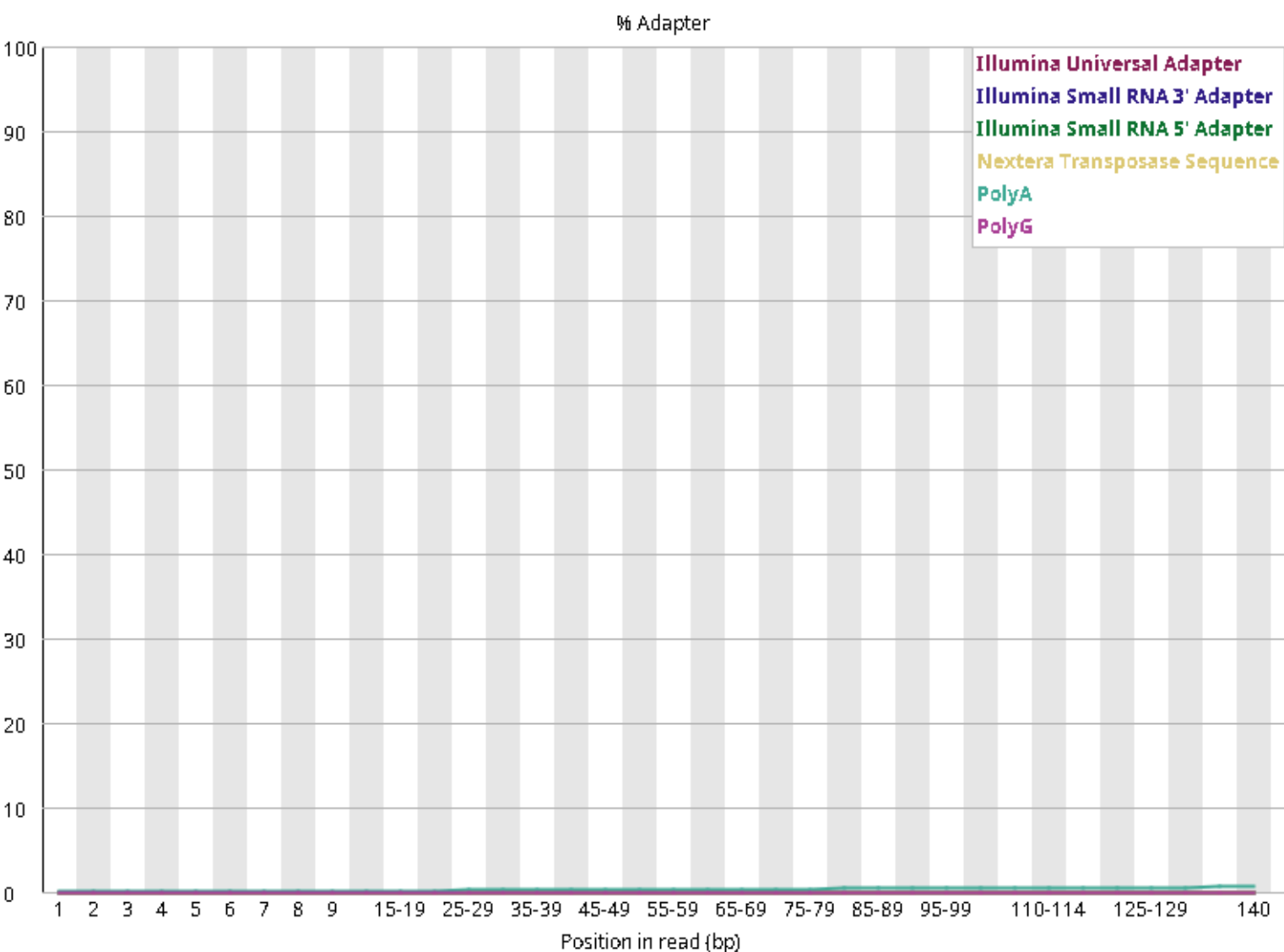


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AA	4	0.30303030303030304	No Hit
CTCTCTCTTTTCGATTCTCTTCTCTCTTATACACACATATACACAC	2	0.15151515151515152	No Hit
AGTACCTCTGCCAAGGCCTGAGCCTCCTGCAACAGATCCTCTTCTGCCTG	2	0.15151515151515152	No Hit
GATAGCATCCTTGACTTGAAATGCCAAATCTTGGTGAGGTCTTTTGCCA	2	0.15151515151515152	No Hit
TGCCATGCCTGCTGTGAGTAAATGTCACAAGTCCAGAGCTTGACATGGAG	2	0.15151515151515152	No Hit
TAGTACTGGAGACAGCTGAGCATGTCCACGACATTTGCCATCACCAGGAT	2	0.15151515151515152	No Hit



Adapter Content



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