











FastQC Report

Summary

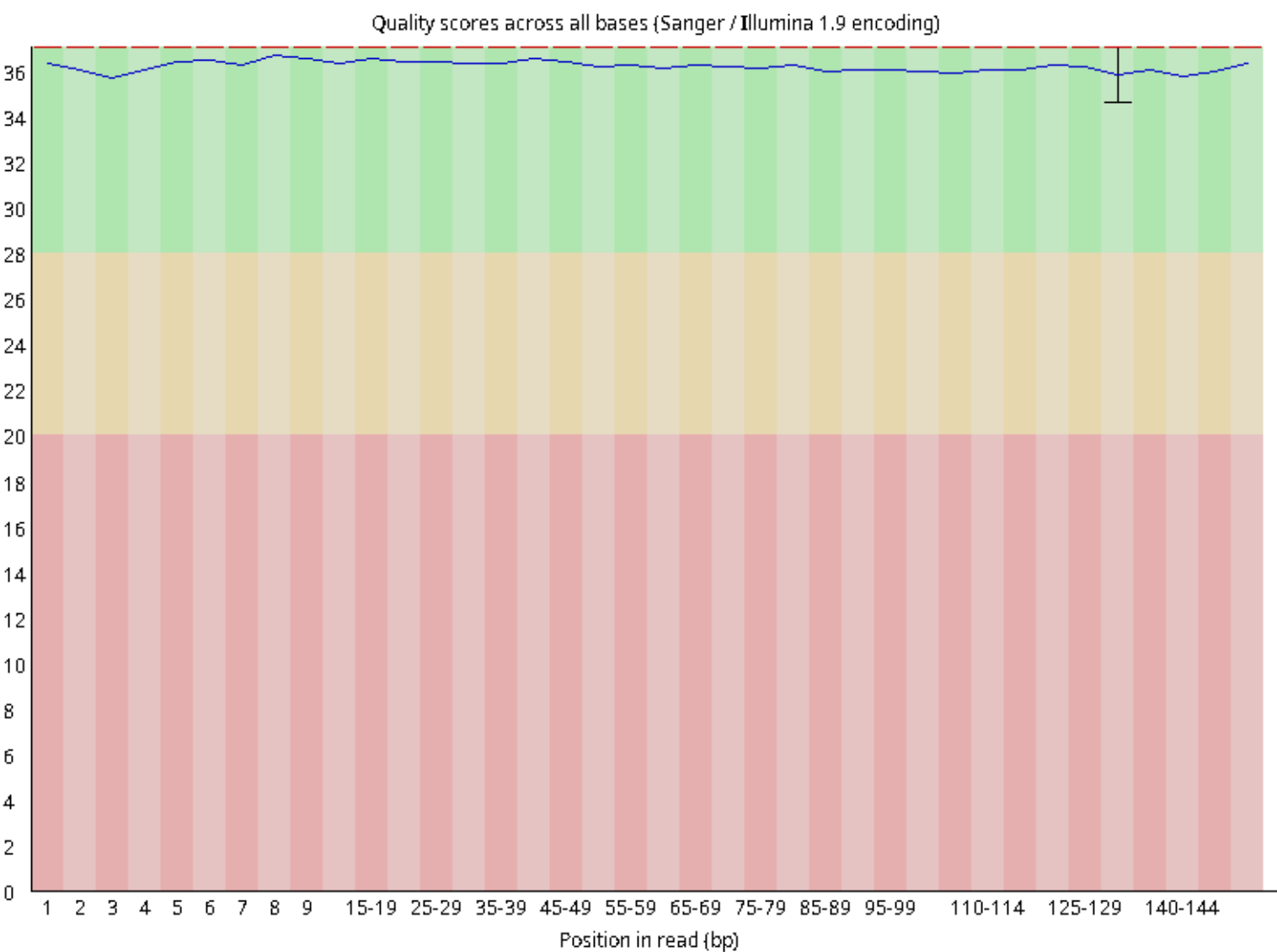
sáb 20 dic 2025
SelmaBouvier_R1.fastq

-  [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](#)

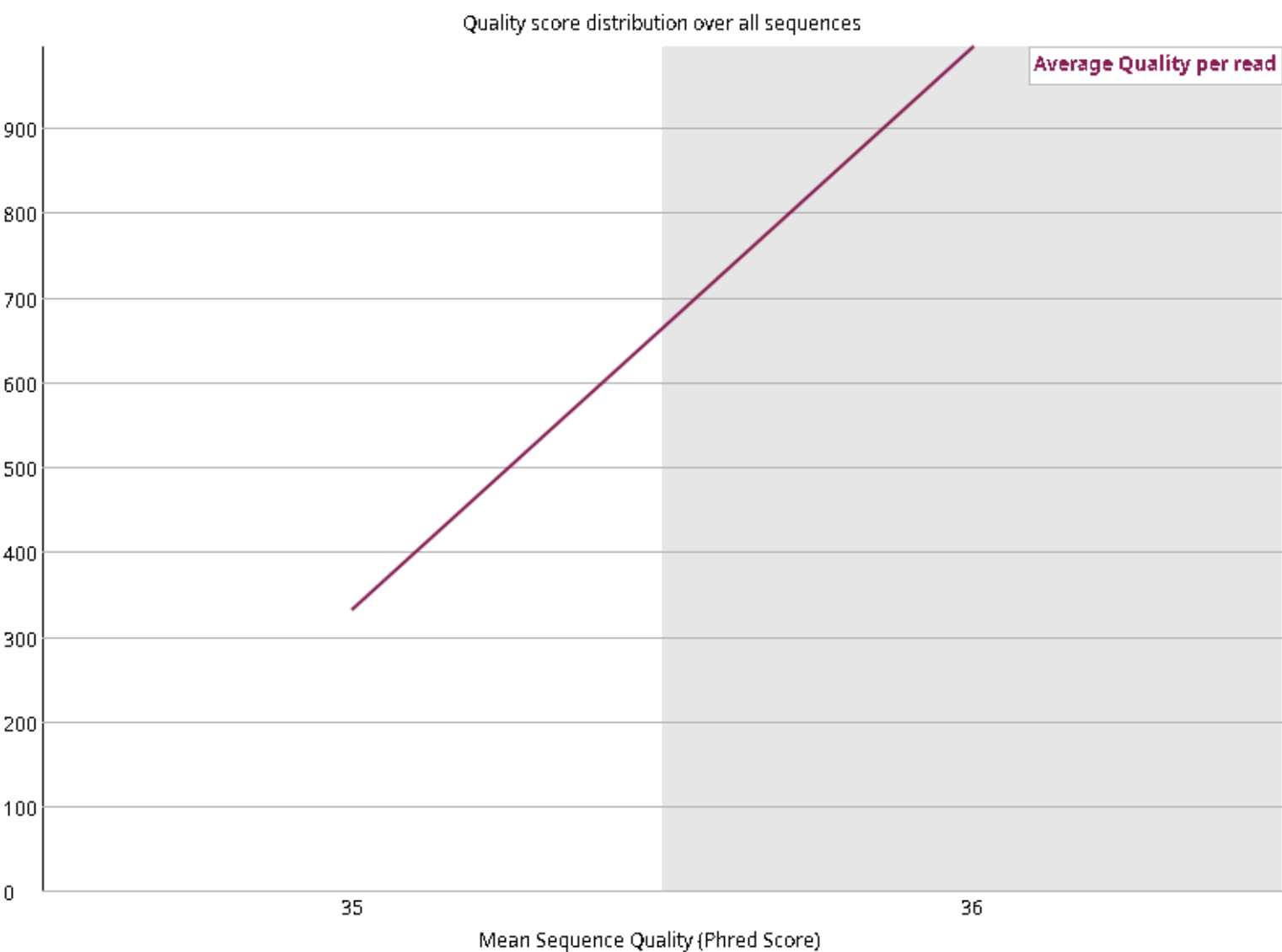
Basic Statistics

Measure	Value
Filename	SelmaBouvier_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	45

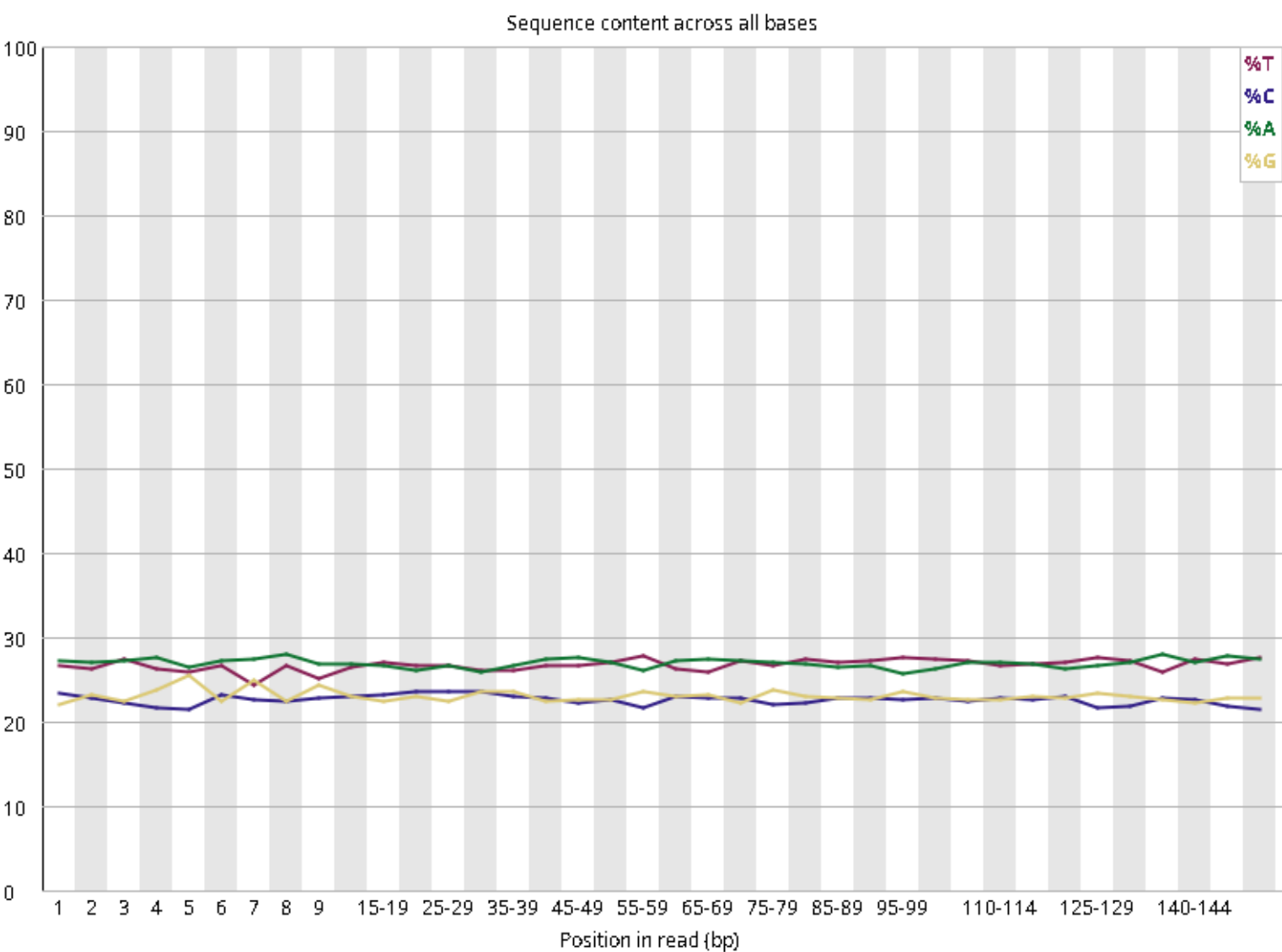
✔ Per base sequence quality



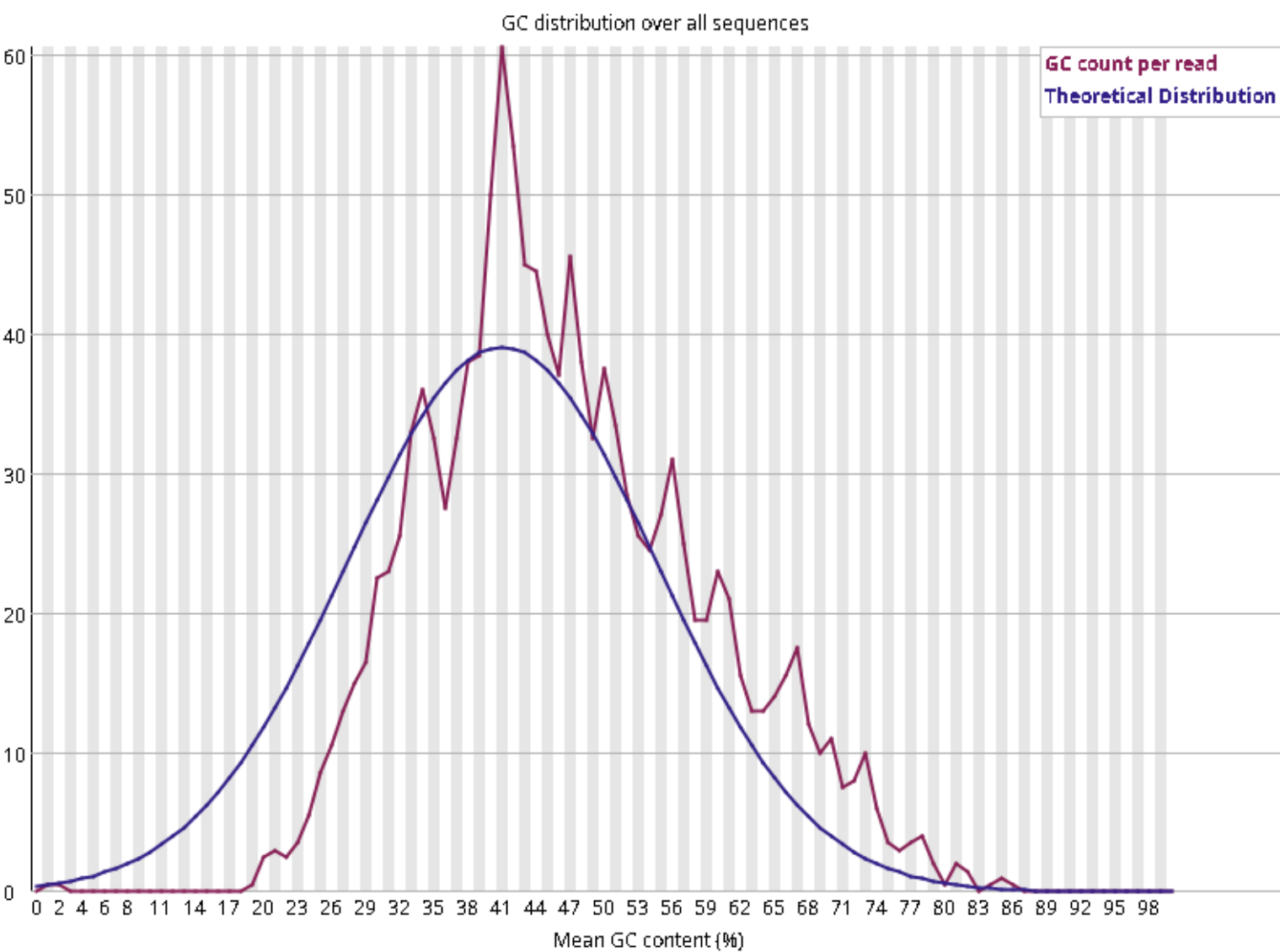
✔ Per sequence quality scores



✔ Per base sequence content

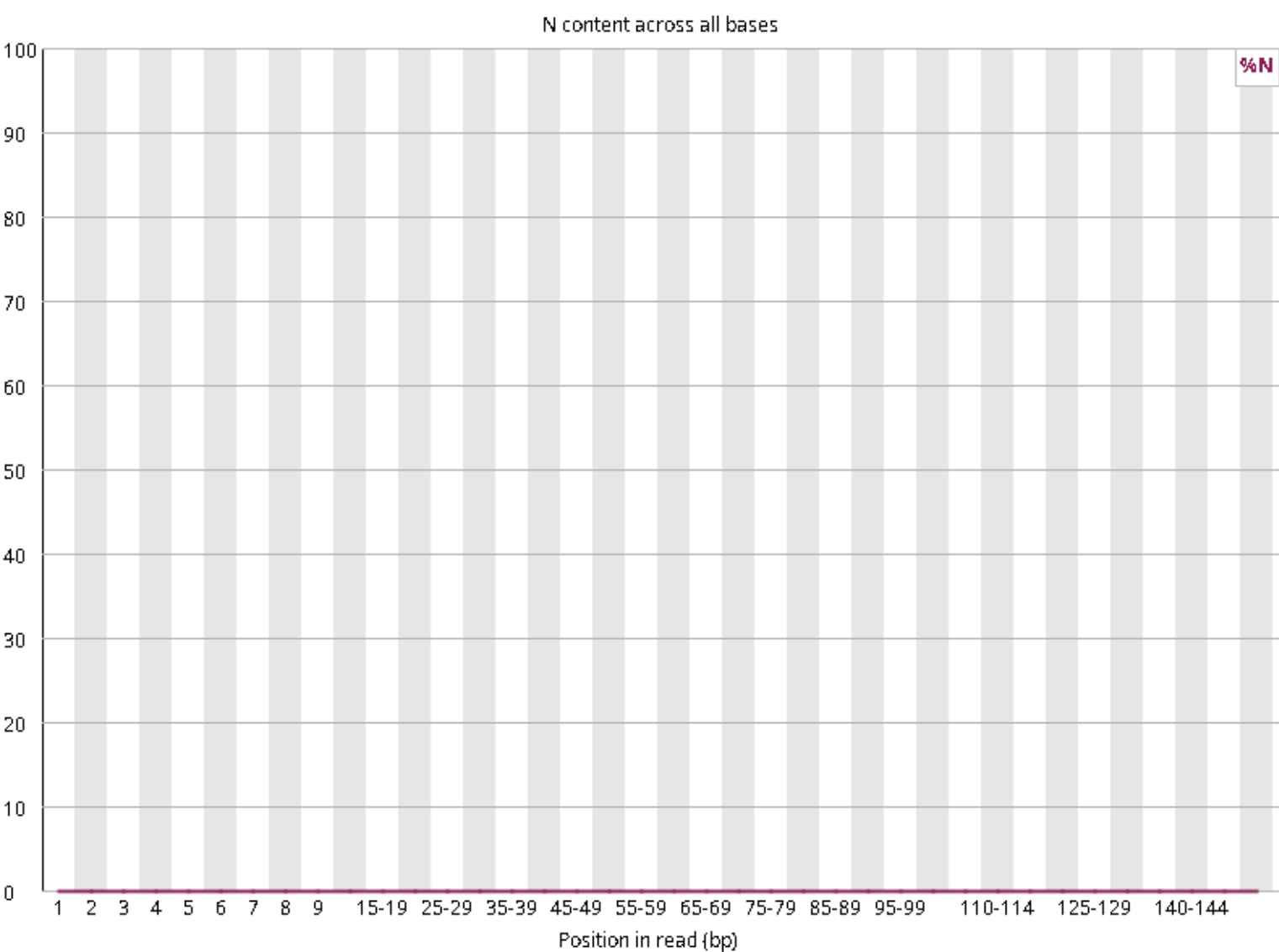


❌ Per sequence GC content

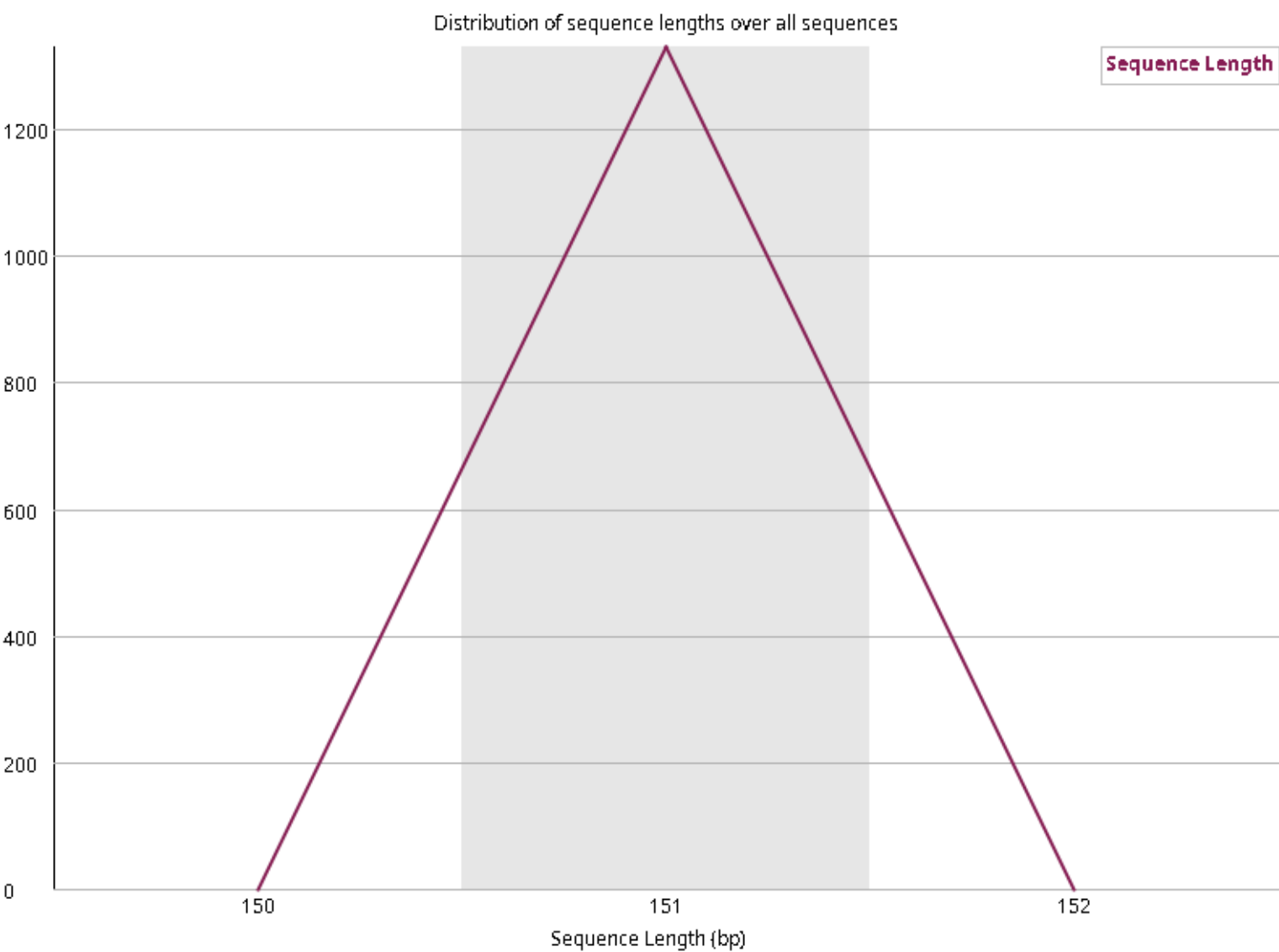




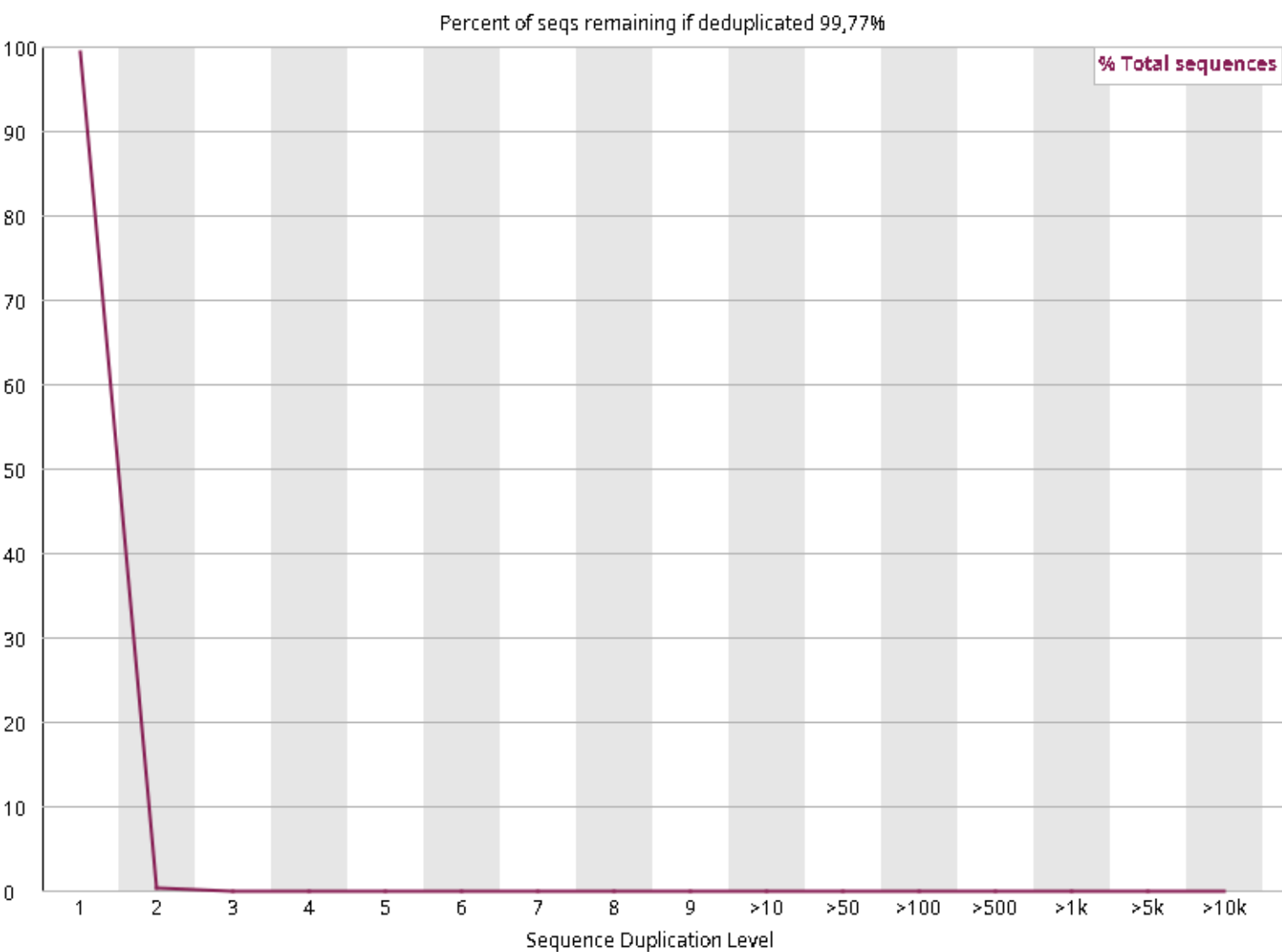
Per base N content



✔ Sequence Length Distribution



Sequence Duplication Levels

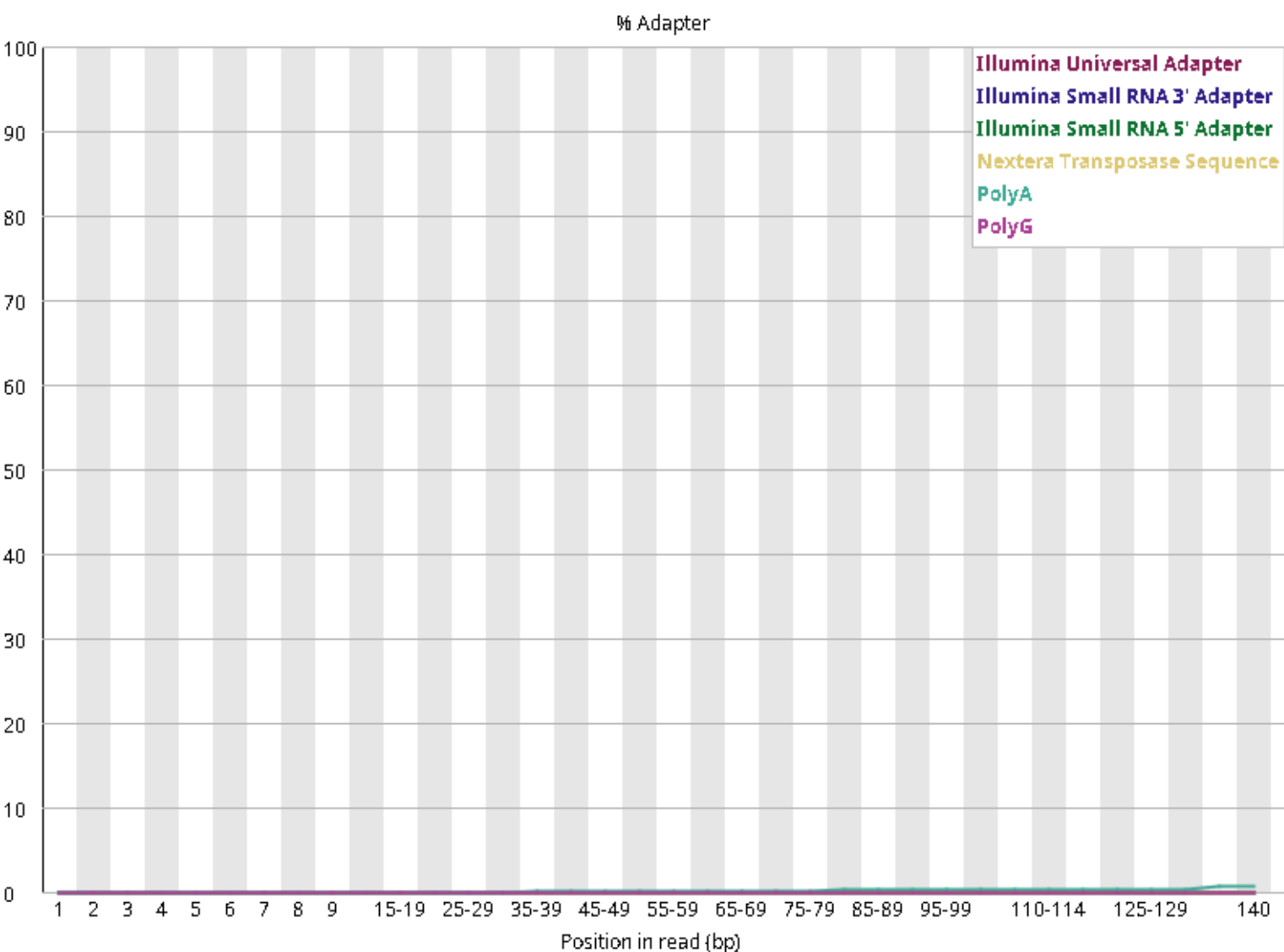


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CACTGAGTTGTGAATTTTTCTTAAAGCAGTACTGTAGTACTGAATATTC	2	0.15060240963855423	No Hit
TCCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATATGAAGGGAGCGATT	2	0.15060240963855423	No Hit
AGGAACTAAGACTCAAAATCTTAGAAACCAGATACGCTCAAAGCAAGTCA	2	0.15060240963855423	No Hit



Adapter Content



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