











FastQC Report

Summary

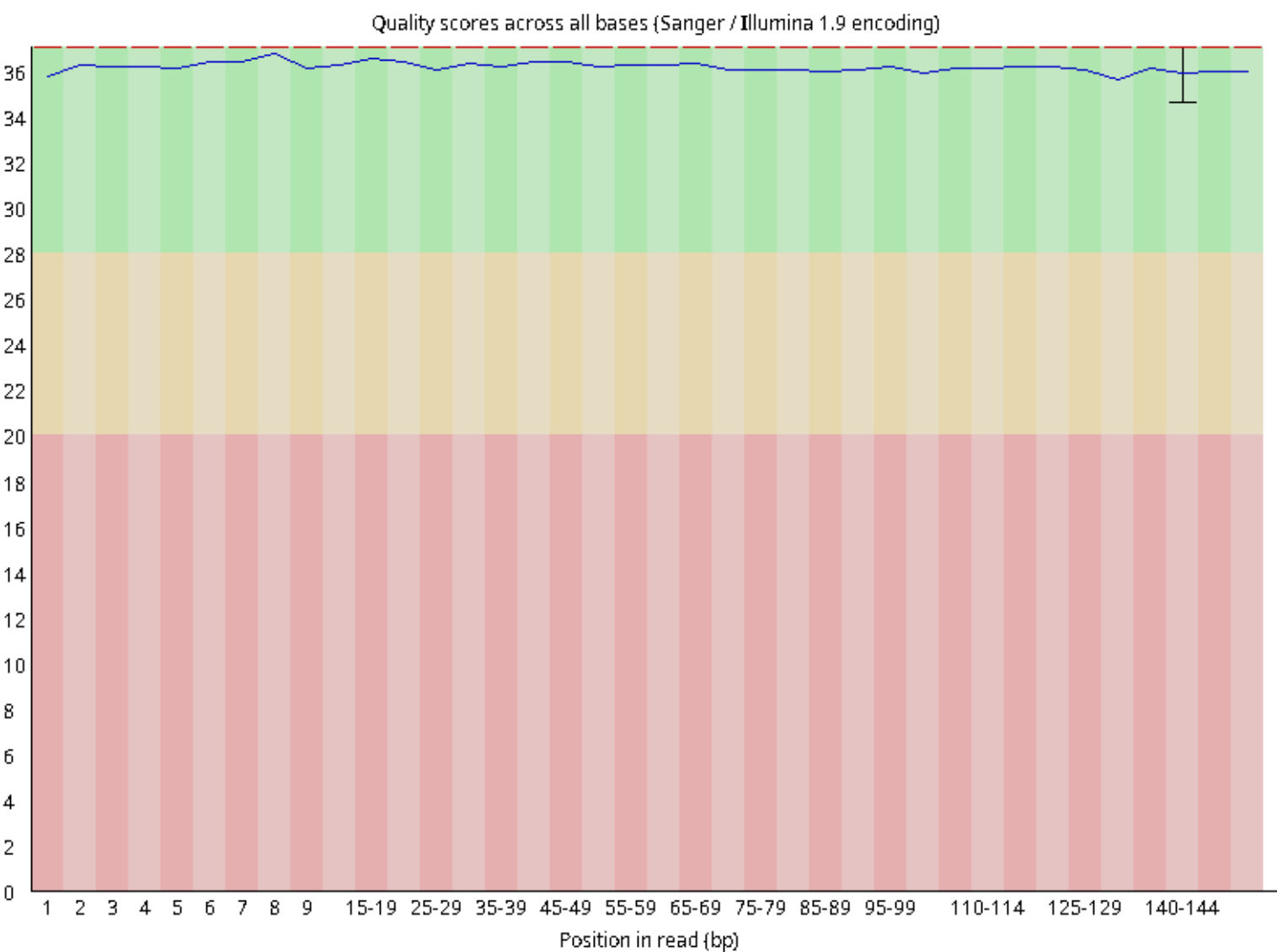
sáb 20 dic 2025
AbrahamSimpson_R1.fastq

-  [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](#)

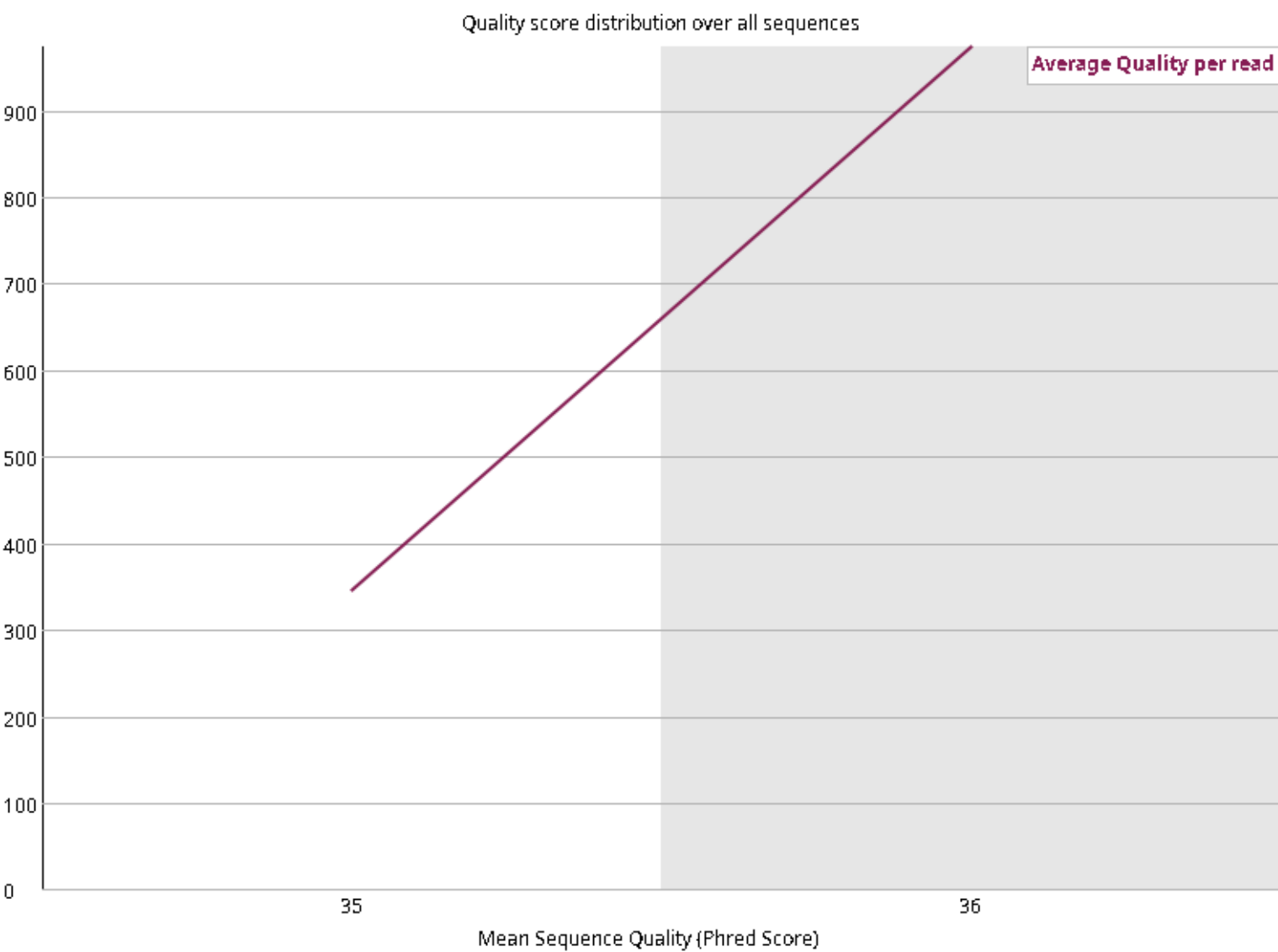
Basic Statistics

Measure	Value
Filename	AbrahamSimpson_R1.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

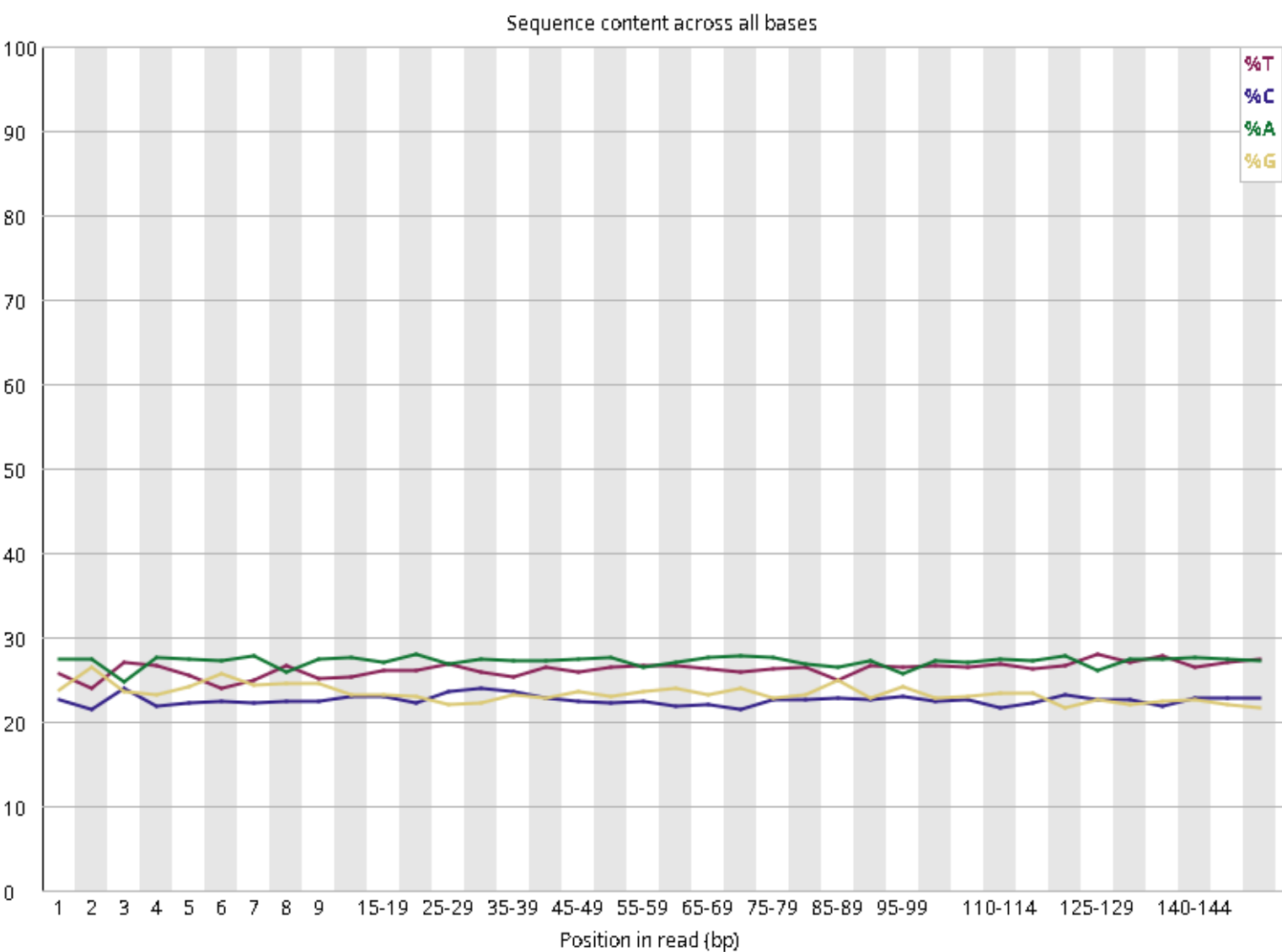
✔ Per base sequence quality



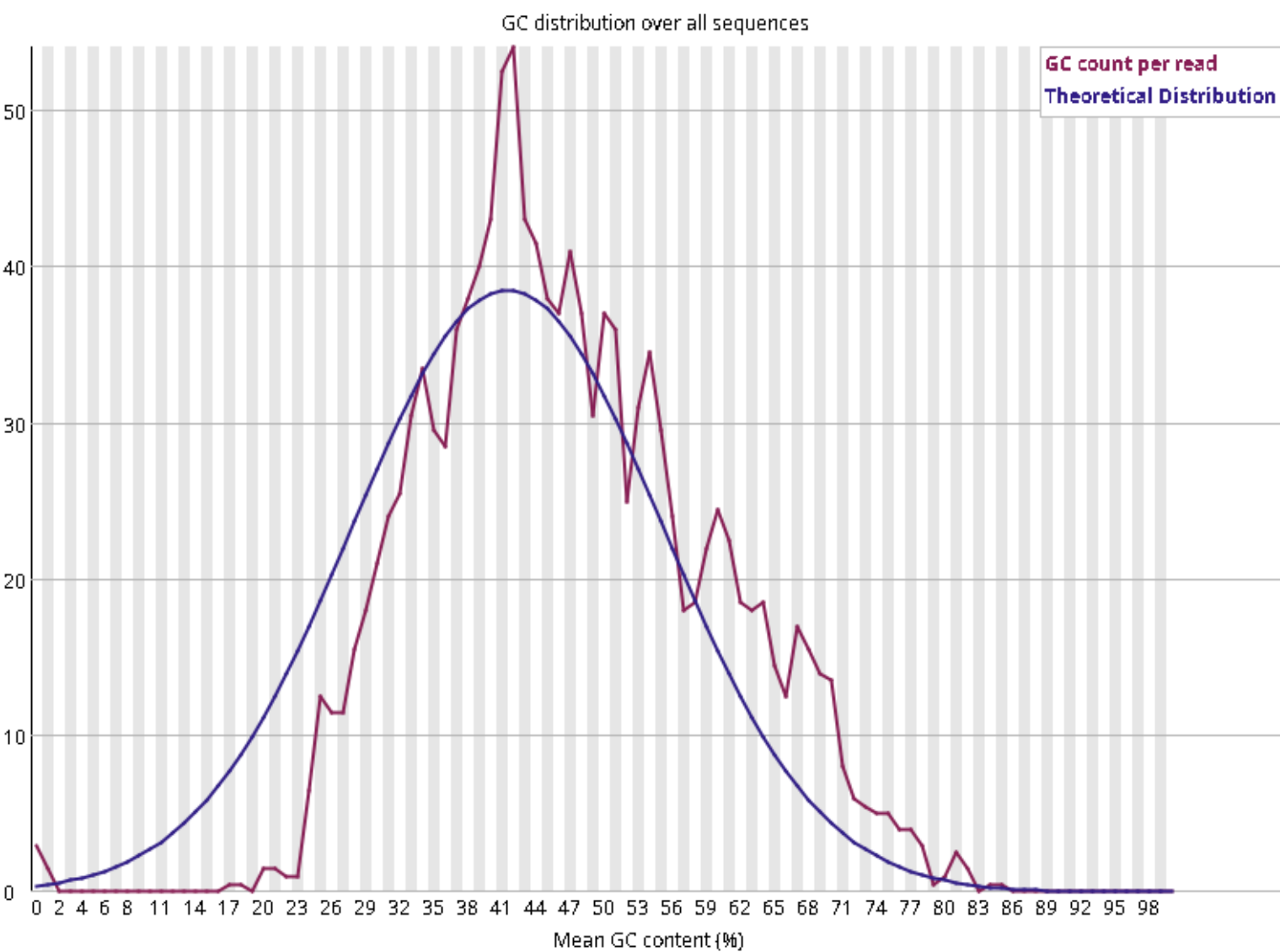
✔ Per sequence quality scores



✔ Per base sequence content

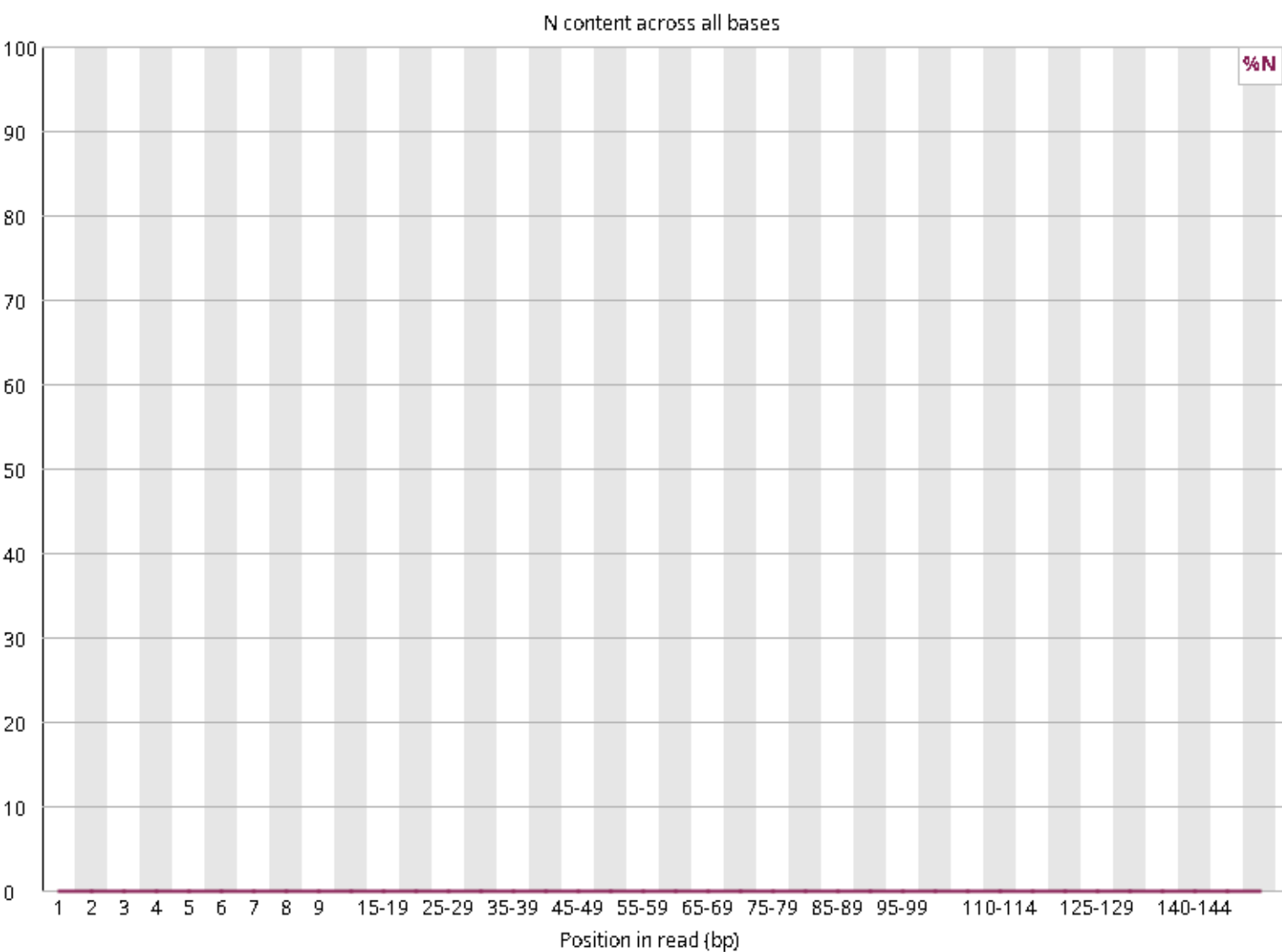


✖ Per sequence GC content

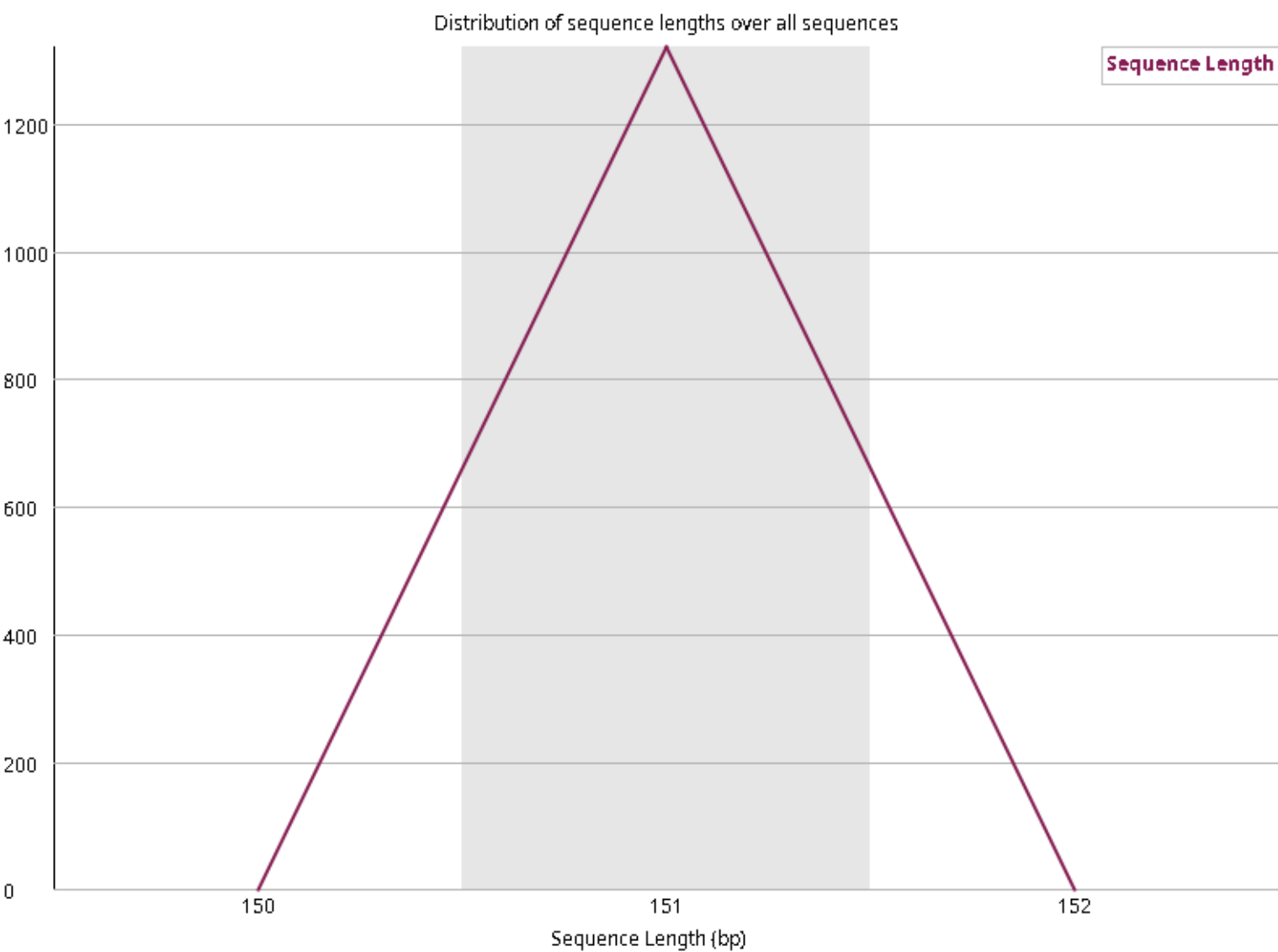




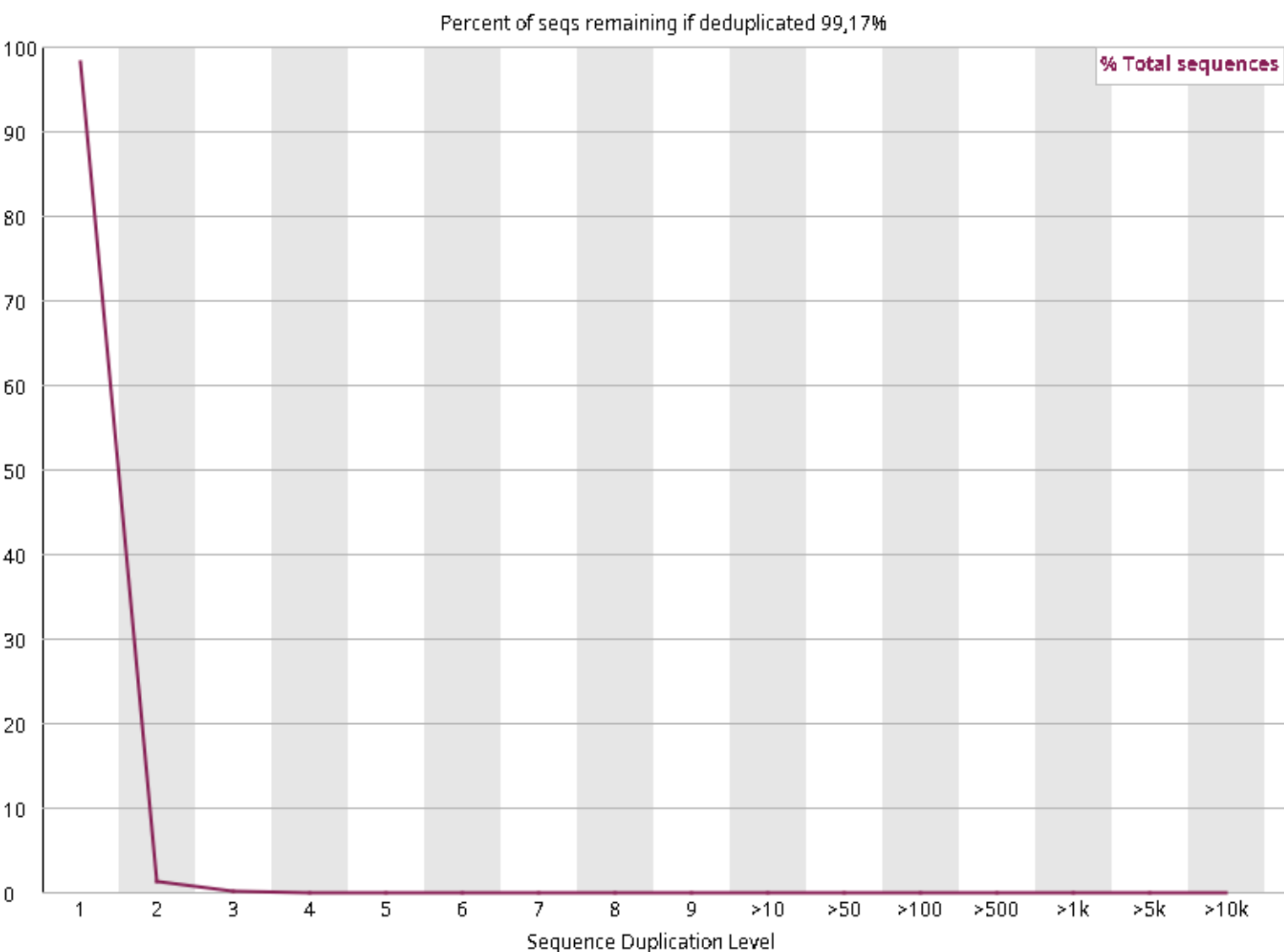
Per base N content



✔ Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AA	3	0.22727272727272727	No Hit
TCCCCCTCACTGAATGCCTCAATGTGACCAGGGGTGATTCAGAGAGGGC	2	0.15151515151515152	No Hit
ATTTCGAATTTCTGACTTTGAGAACCGATCTGAGCCTGAATCTGATGGCA	2	0.15151515151515152	No Hit
GCACTTTGAAGCCGAGGTGGCCCGGGCCTCTGGCTCCCTGTCGCCACCCA	2	0.15151515151515152	No Hit
CTGAAGAAGACAACCTGCAGAACAGGCAGAAGAGGATCTGTTGCAGGAGGC	2	0.15151515151515152	No Hit
CATTGAAGCAATCCTTGCTACGGATCTTAAAAAGCATTTTGATTTTCTCG	2	0.15151515151515152	No Hit
AGATCCCCCACAGCCTGGGGCAGAAGAGGCGTCGAGGGGCCAGAAGTGG	2	0.15151515151515152	No Hit

Sequence	Count	Percentage	Possible Source
CGCCGAGGACGAGTCGGCCGAGGCCTTCCCCCTGGAGTTCAAGAGGGAGC	2	0.151515151515152	No Hit
GAGTGAGGGCACAGCGGGGCCCCAGGGCTACCCTCCCCAGGAGGTCGAC	2	0.151515151515152	No Hit
AGTGATCCTCAAACACACAACTATTACTTACAACTGCGGTATACATT	2	0.151515151515152	No Hit



Adapter Content

