FastQC Report

sáb 20 dic 2025
HomerSimpson_R1.fastq

Summary

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- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
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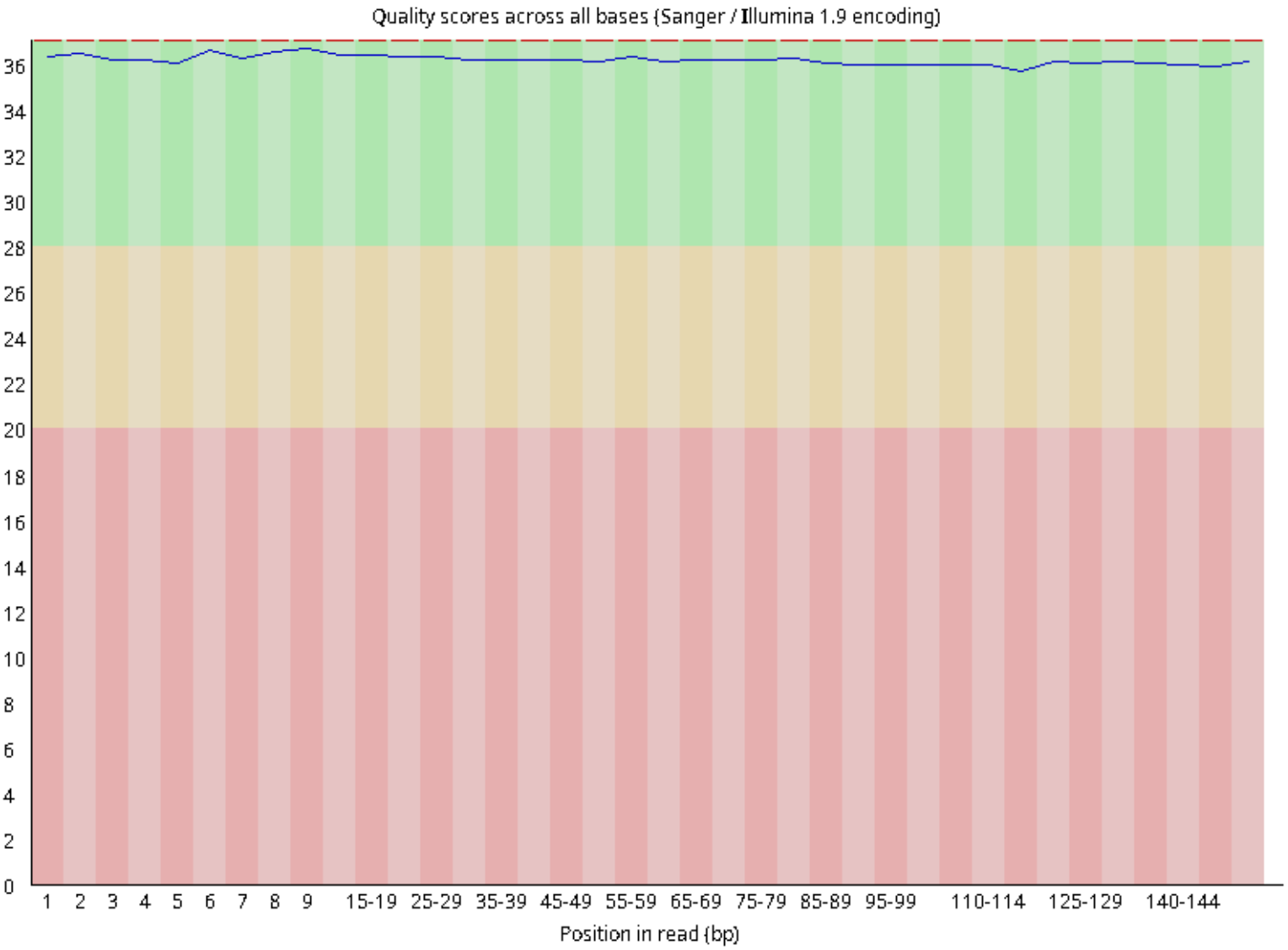
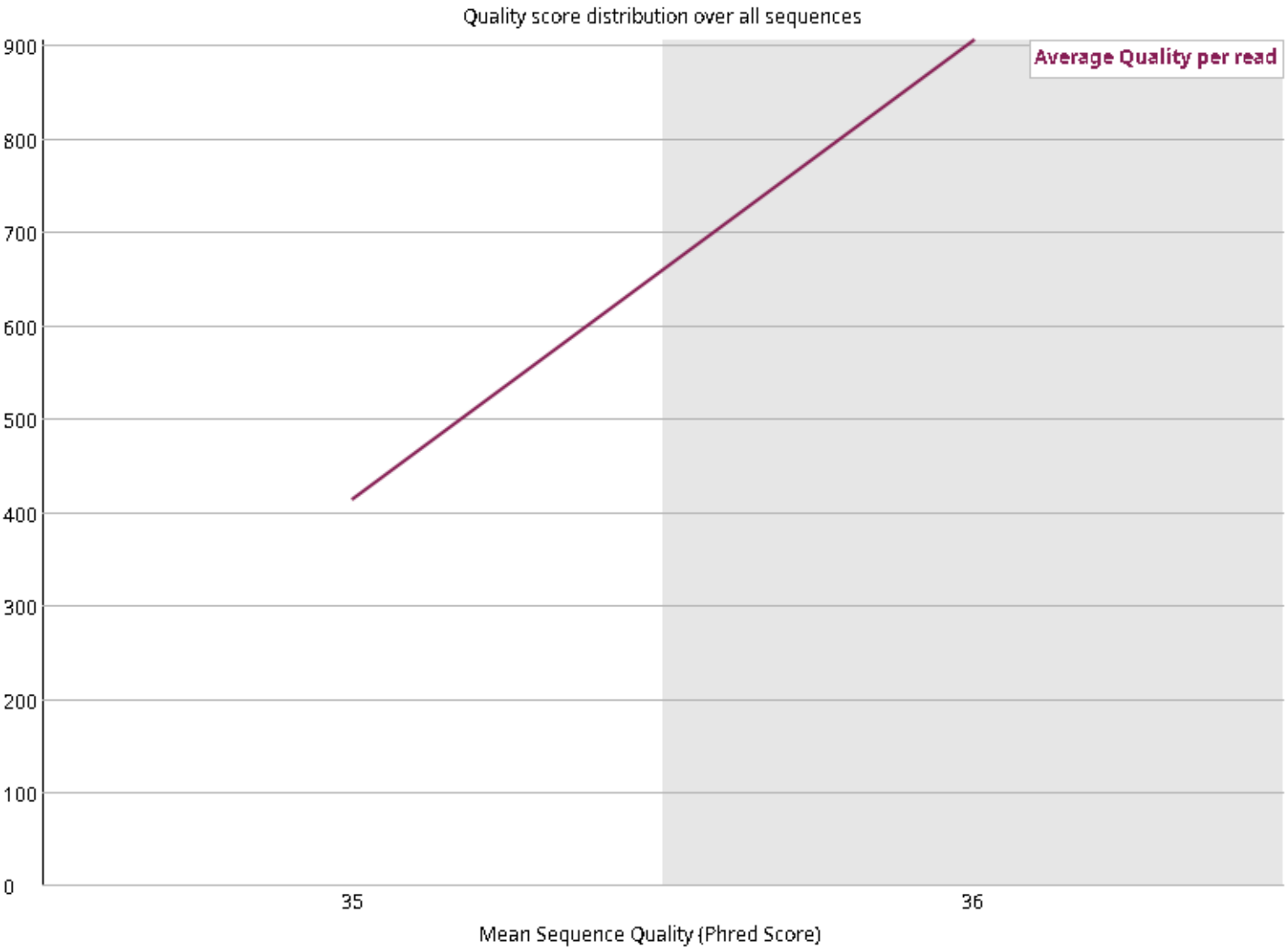
Basic Statistics

Measure	Value
Filename	HomerSimpson_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	45

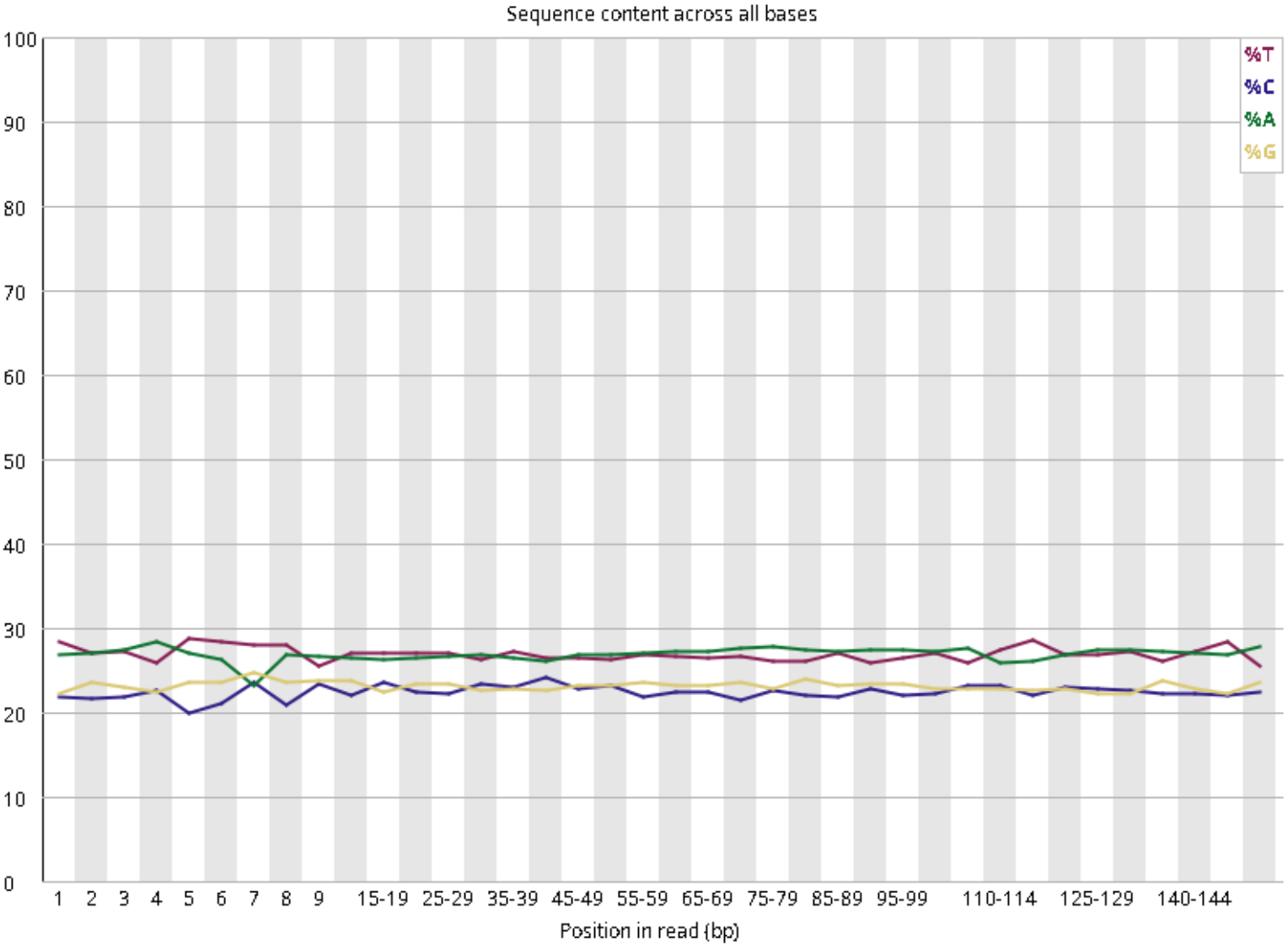
Per base sequence quality



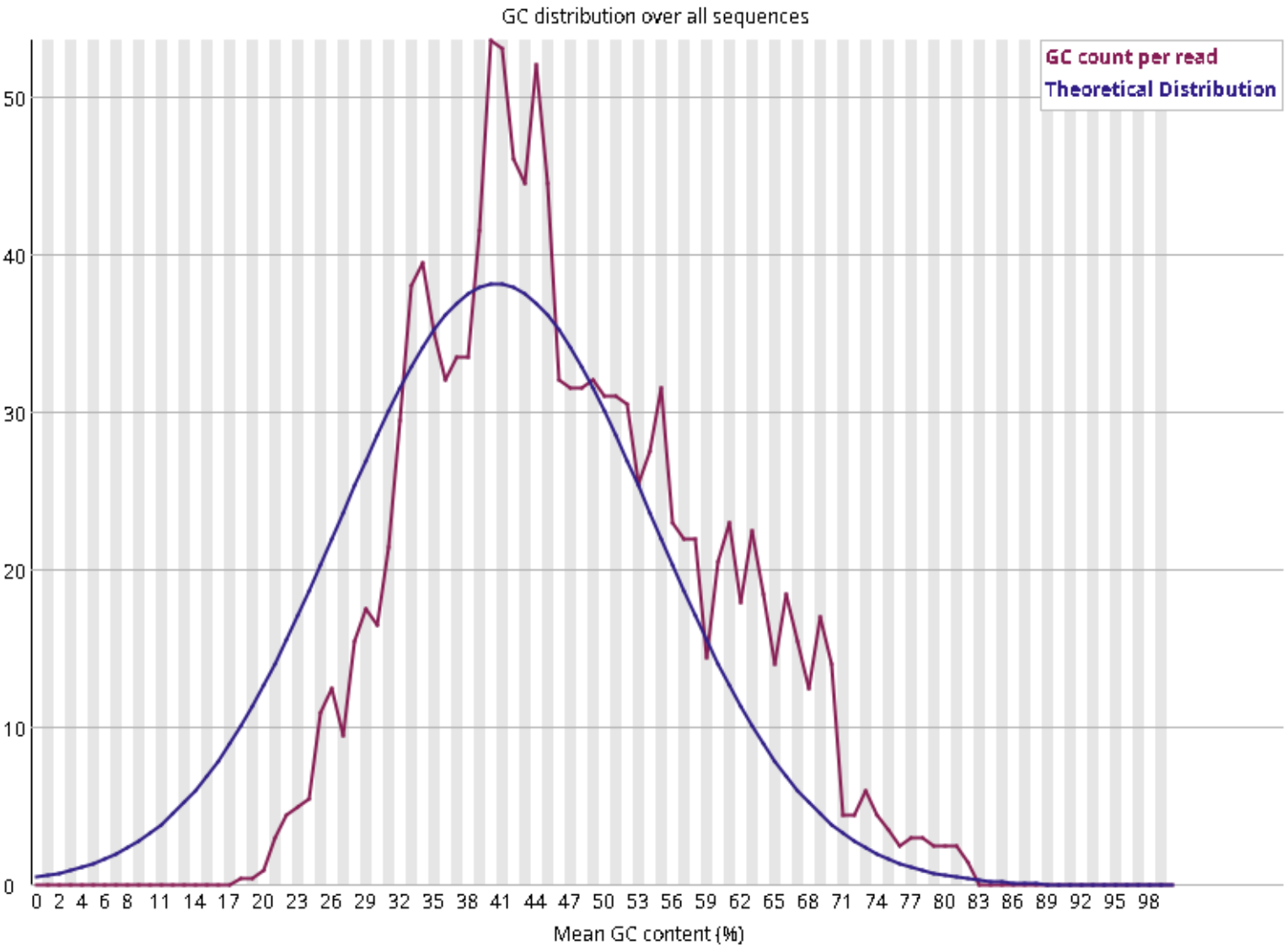
Per sequence quality scores



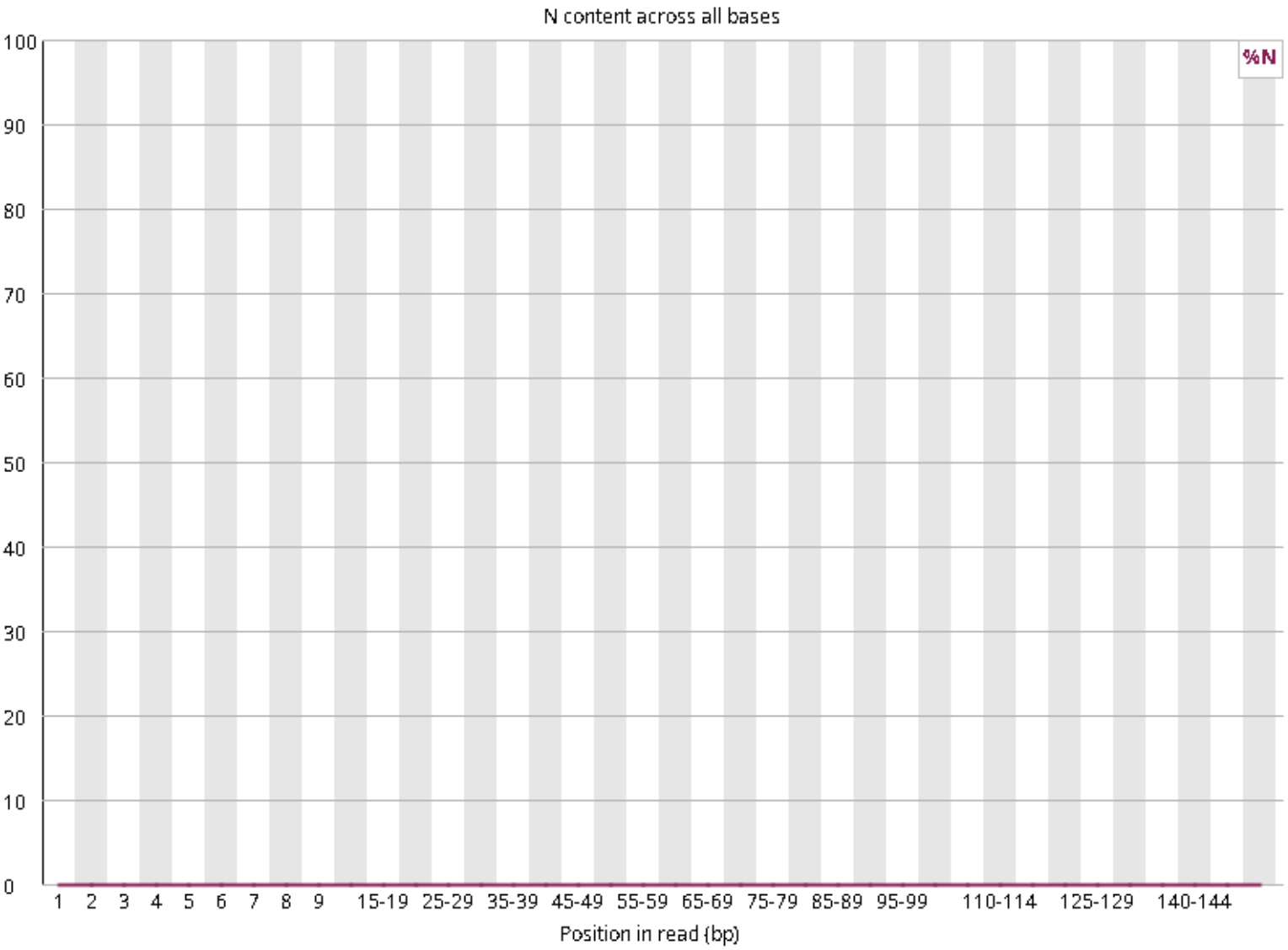
Per base sequence content



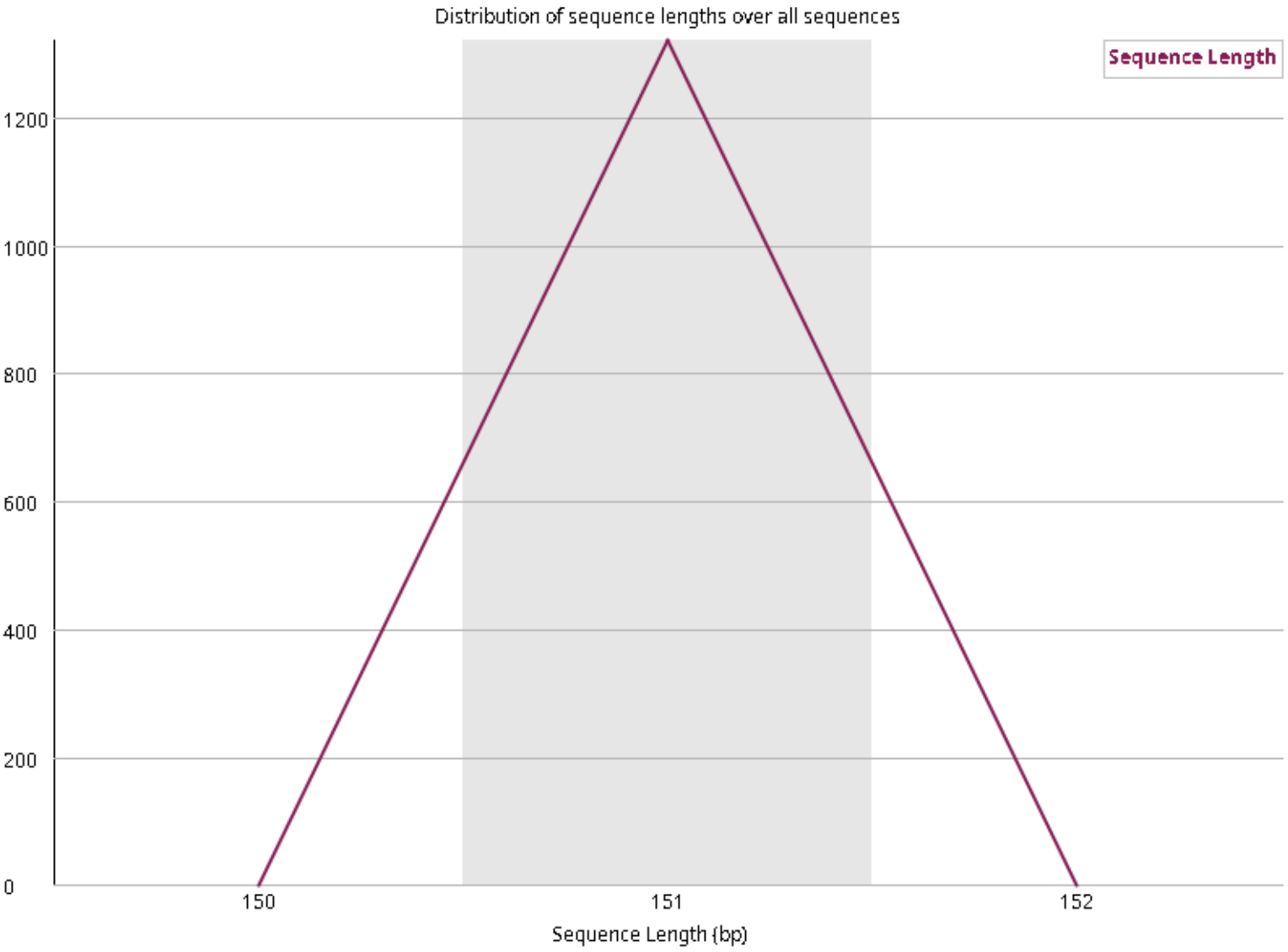
Per sequence GC content



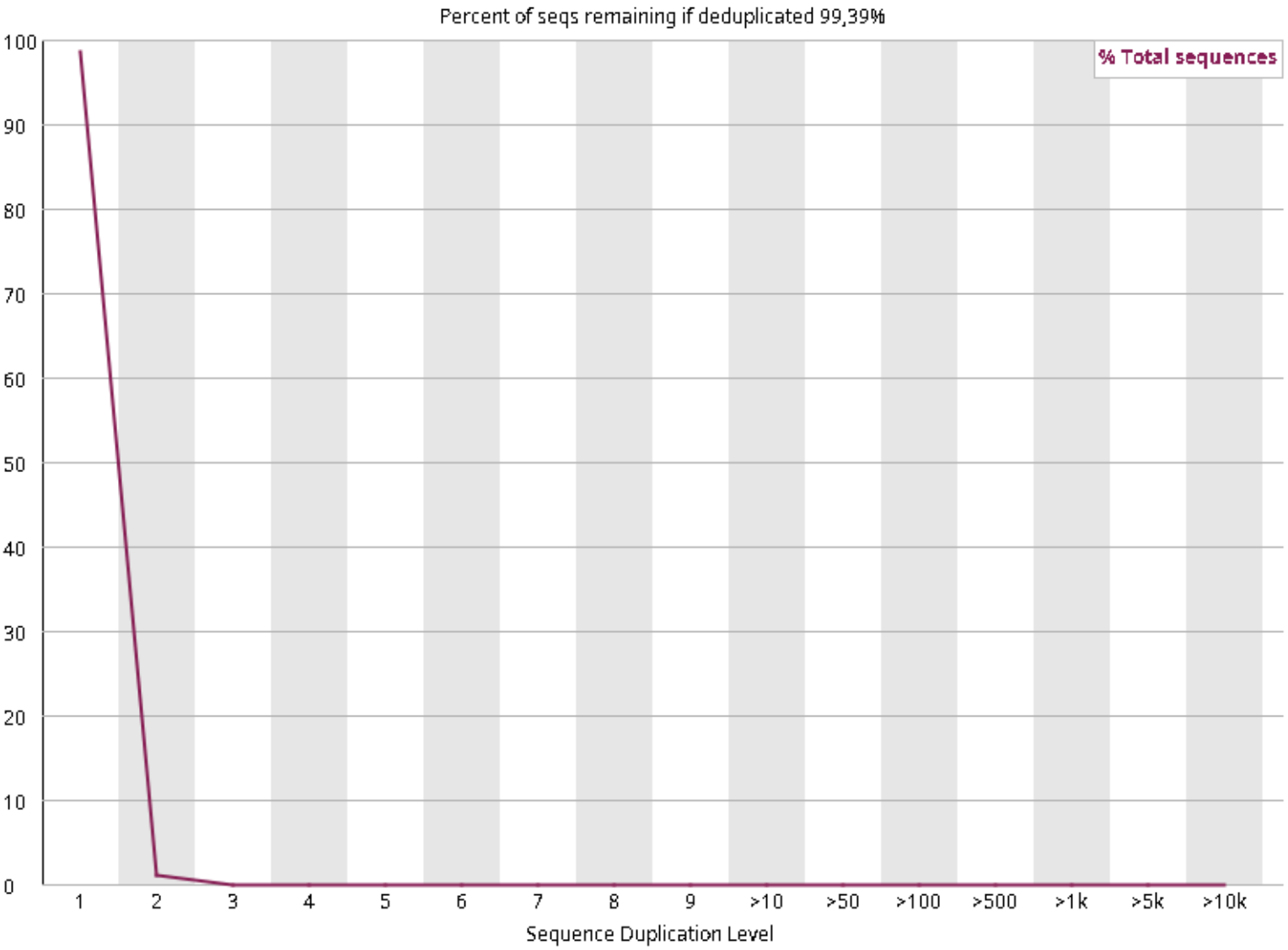
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

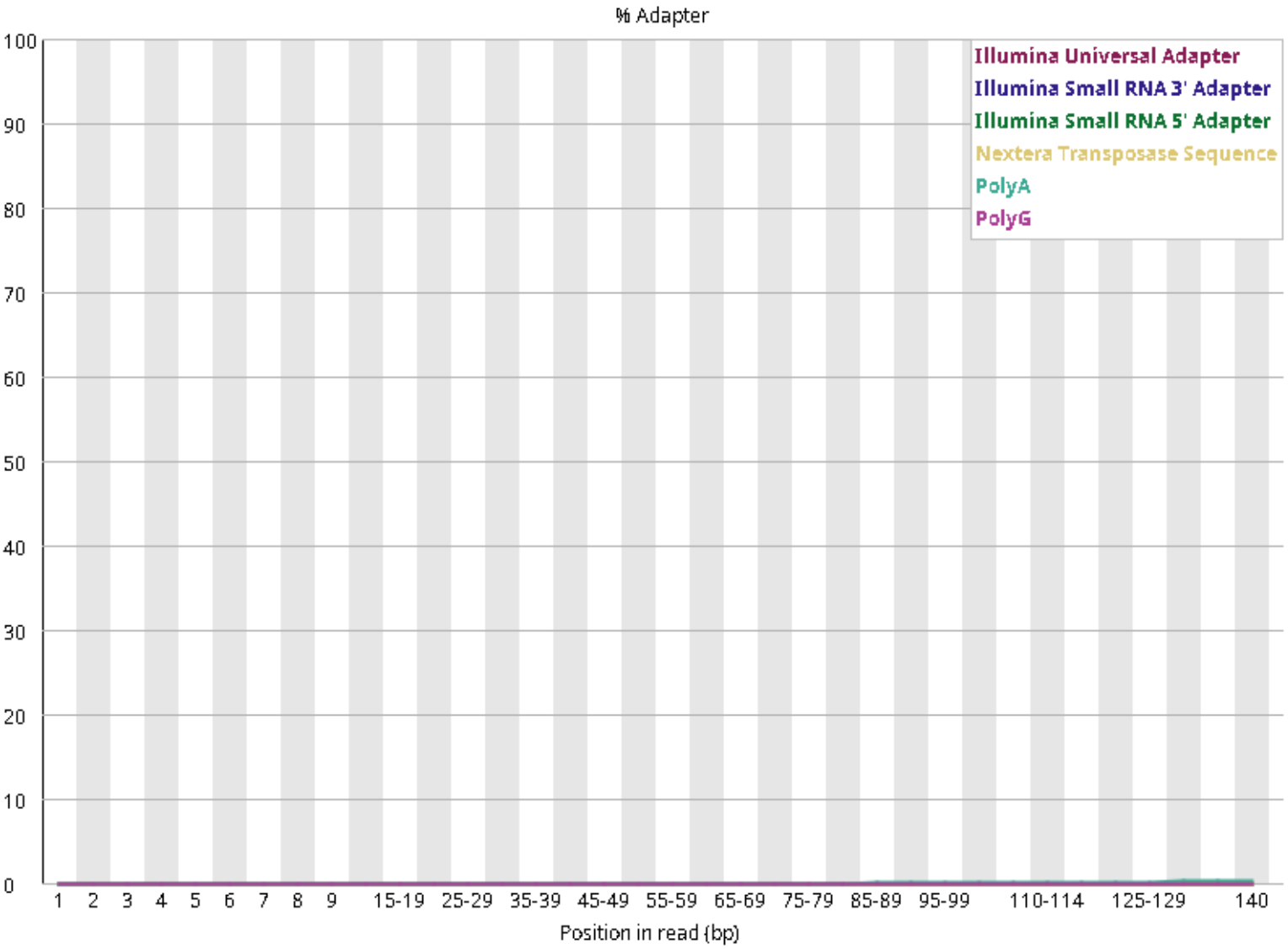


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CTGCAGAACAGGCAGAAGAGGATCTGTTGCAGGAGGCTCAGGCCTTGGCA	2	0.15151515151515152	No Hit
AAGCCCAAGATTTTAAAGTGATGATGATTAGAGTCGTACCTAAAAGAGAC	2	0.15151515151515152	No Hit
GTATACTTCCTGGGTCTTCGTATGAGGTTCAGGTGAGGGGCAAGAGACTG	2	0.15151515151515152	No Hit
CGAGGAACTAAGACTCAAAATCTTAGAAACCAGATACGCTCAAAGCAAGT	2	0.15151515151515152	No Hit
CCATGCTGACCGCAGCGGTGCTGAGCTGTGCCCTGCTGCTGGCACTGCCT	2	0.15151515151515152	No Hit
TAGGAGTCGCAGGGTCAGCGGGCCTGAAGGGGGCTGGGTCTGTCTGCGGT	2	0.15151515151515152	No Hit
ACAAATTTTAAACTTTATTAAAACATGAGTTTTGTTTTTTTTTTTGCTAT	2	0.15151515151515152	No Hit

Sequence	Count	Percentage	Possible Source
TCCACTGCGTGCTCCCCTCATCCCCATGGAGCATTGCACCACCCGCTTTT	2	0.15151515151515152	No Hit

Adapter Content



Produced by FastQC (version 0.12.1)