FastQC Report

sáb 20 dic 2025
SelmaBouvier_R2.fastq

Summary

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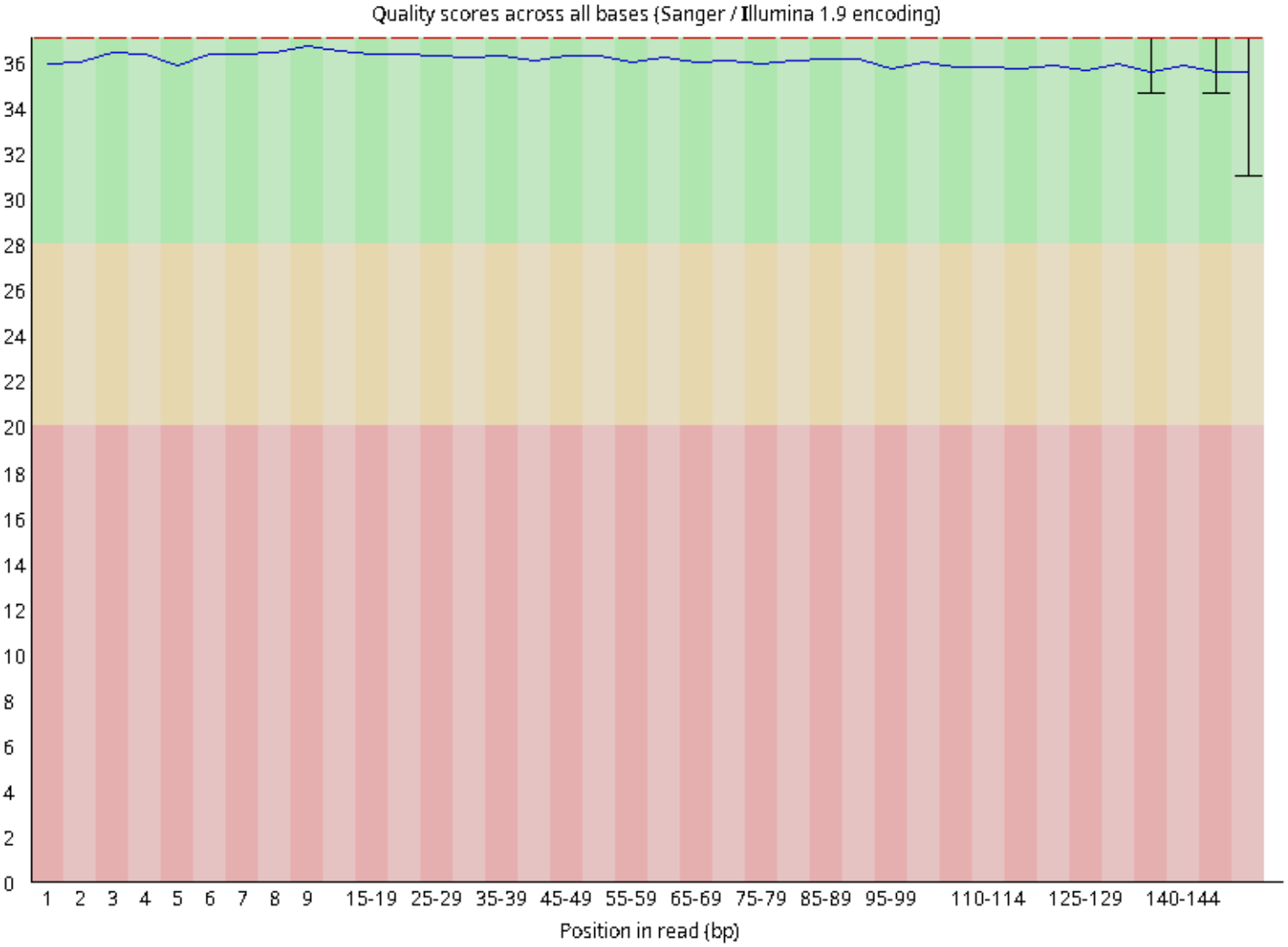
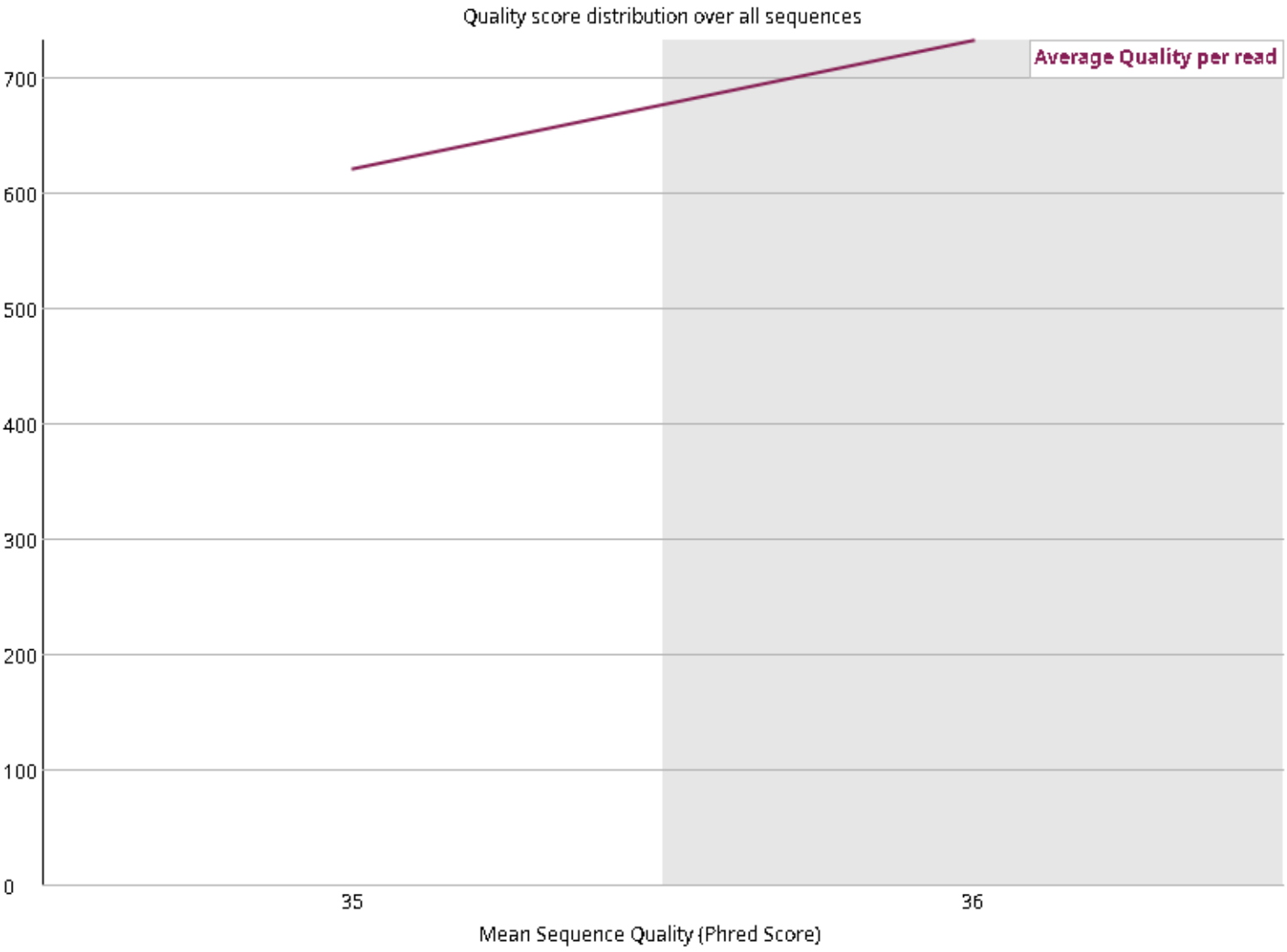
Basic Statistics

Measure	Value
Filename	SelmaBouvier_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1352
Total Bases	204.1 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

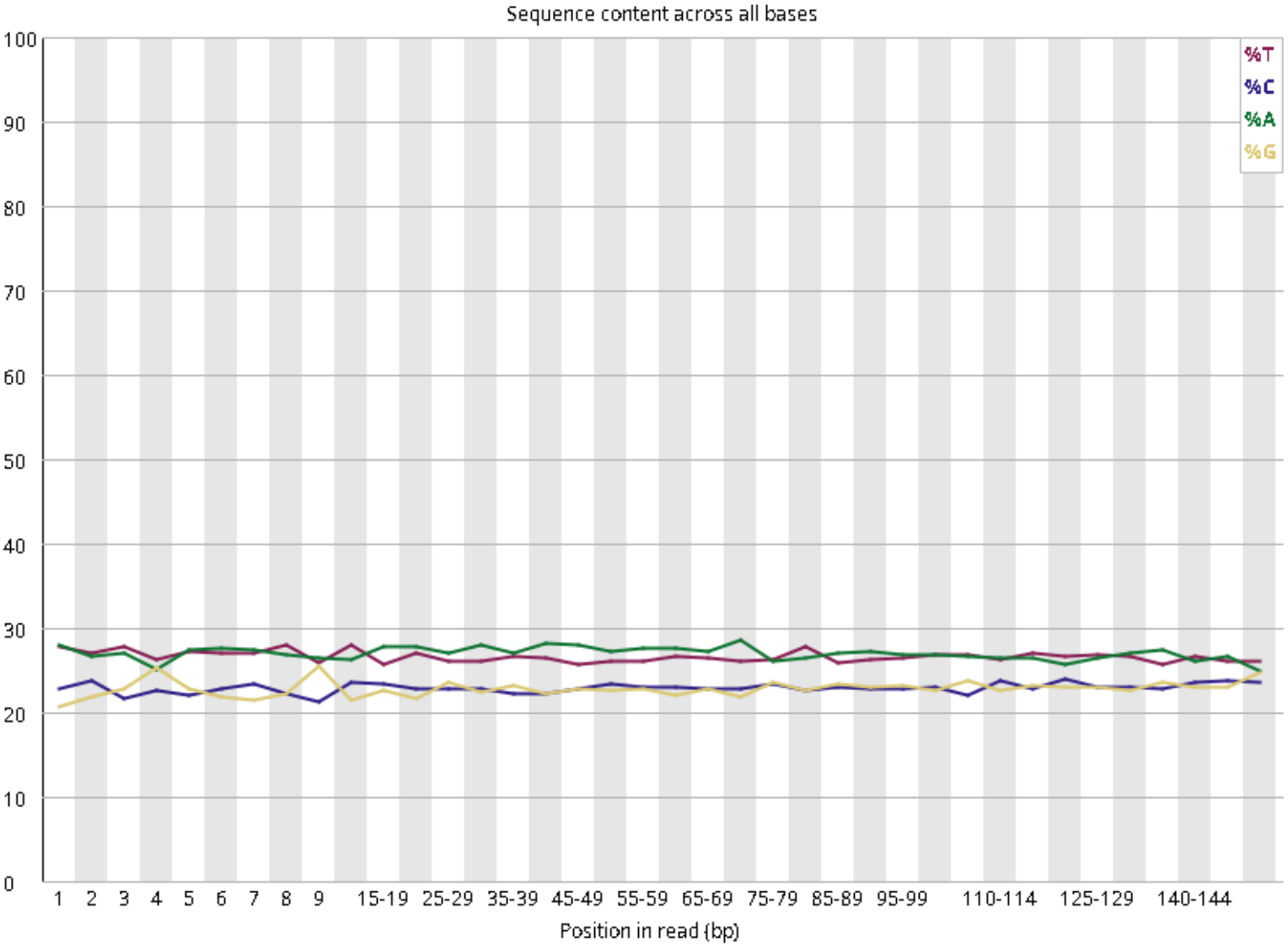
Per base sequence quality



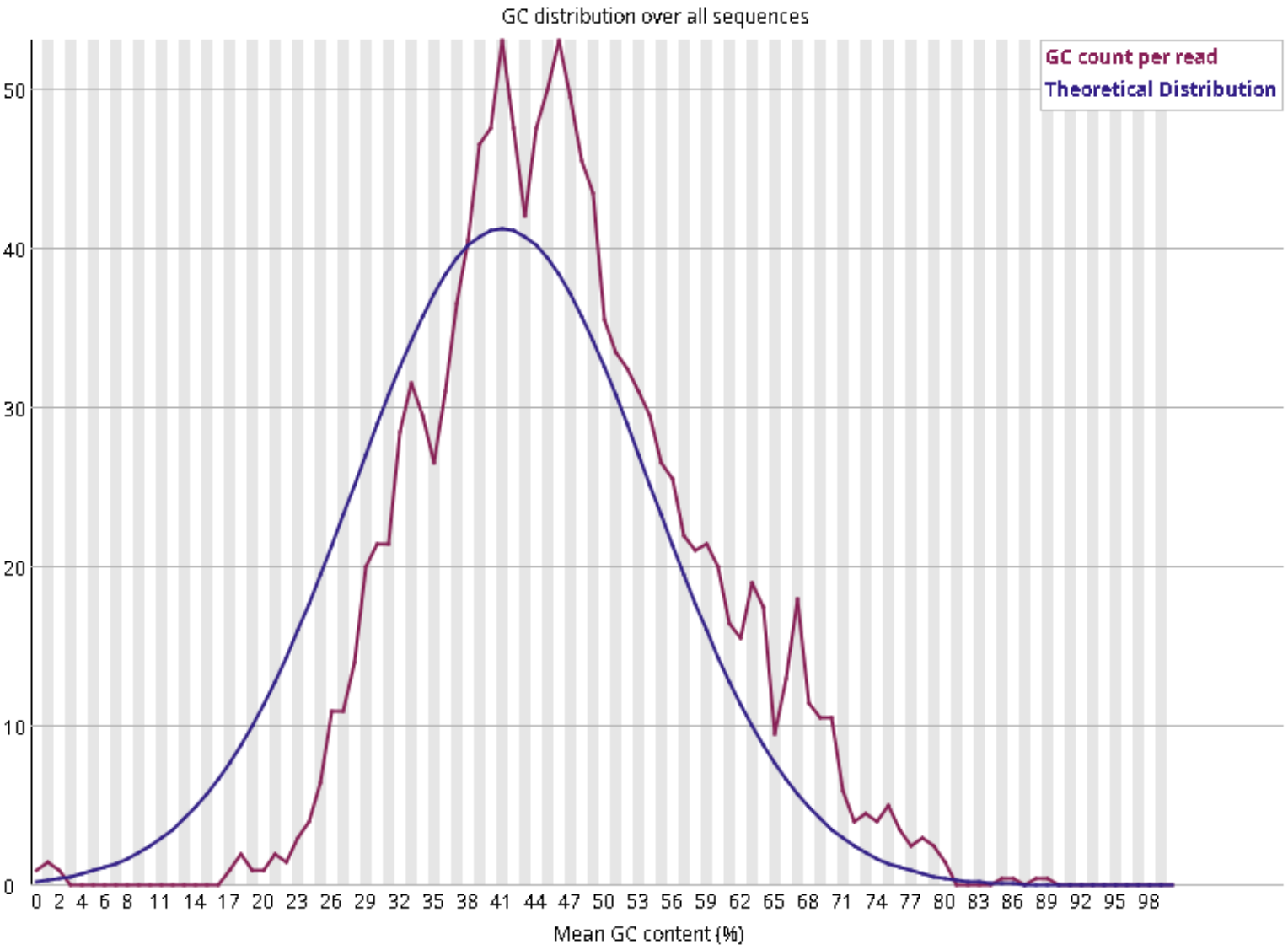
Per sequence quality scores



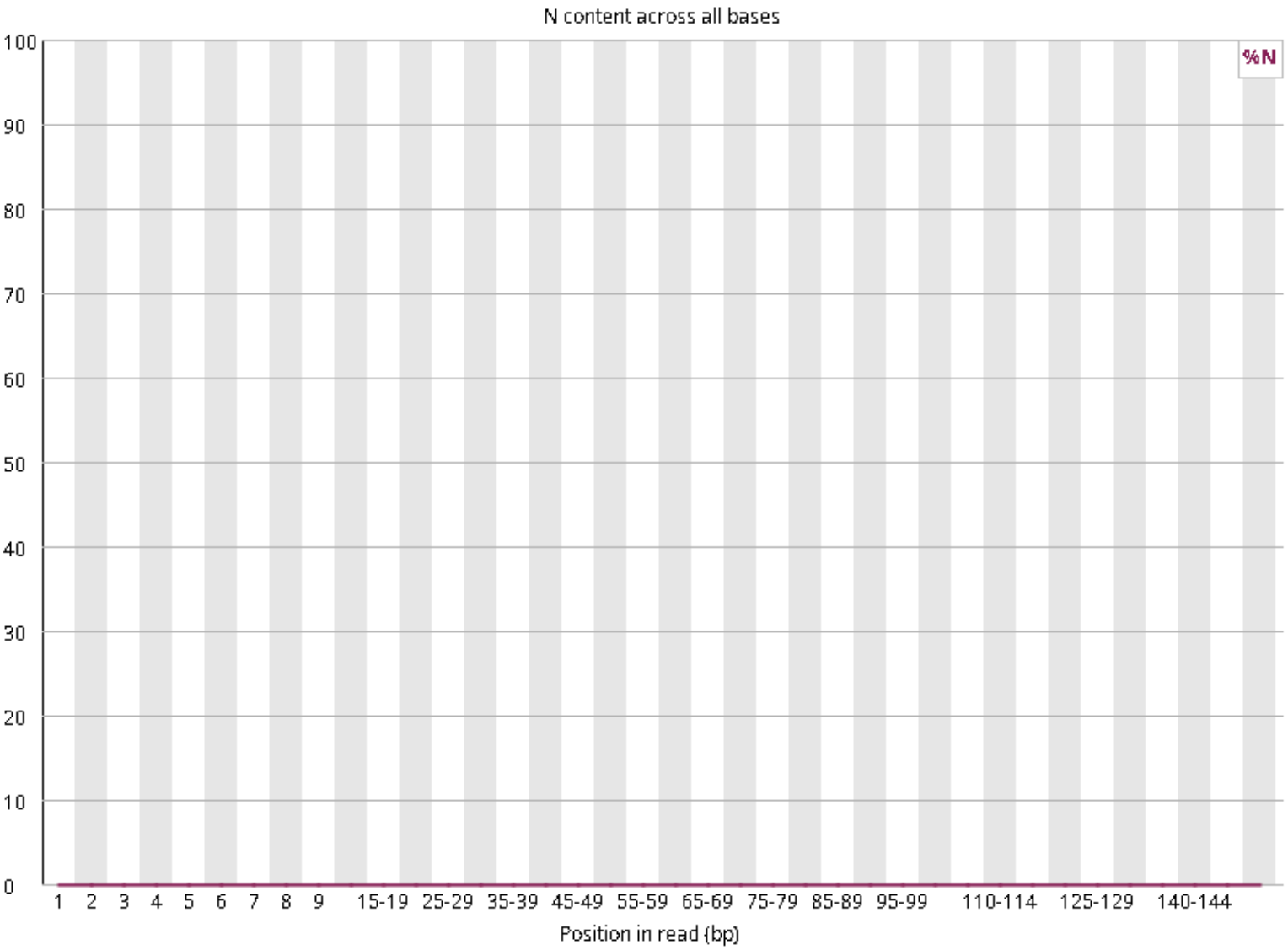
Per base sequence content



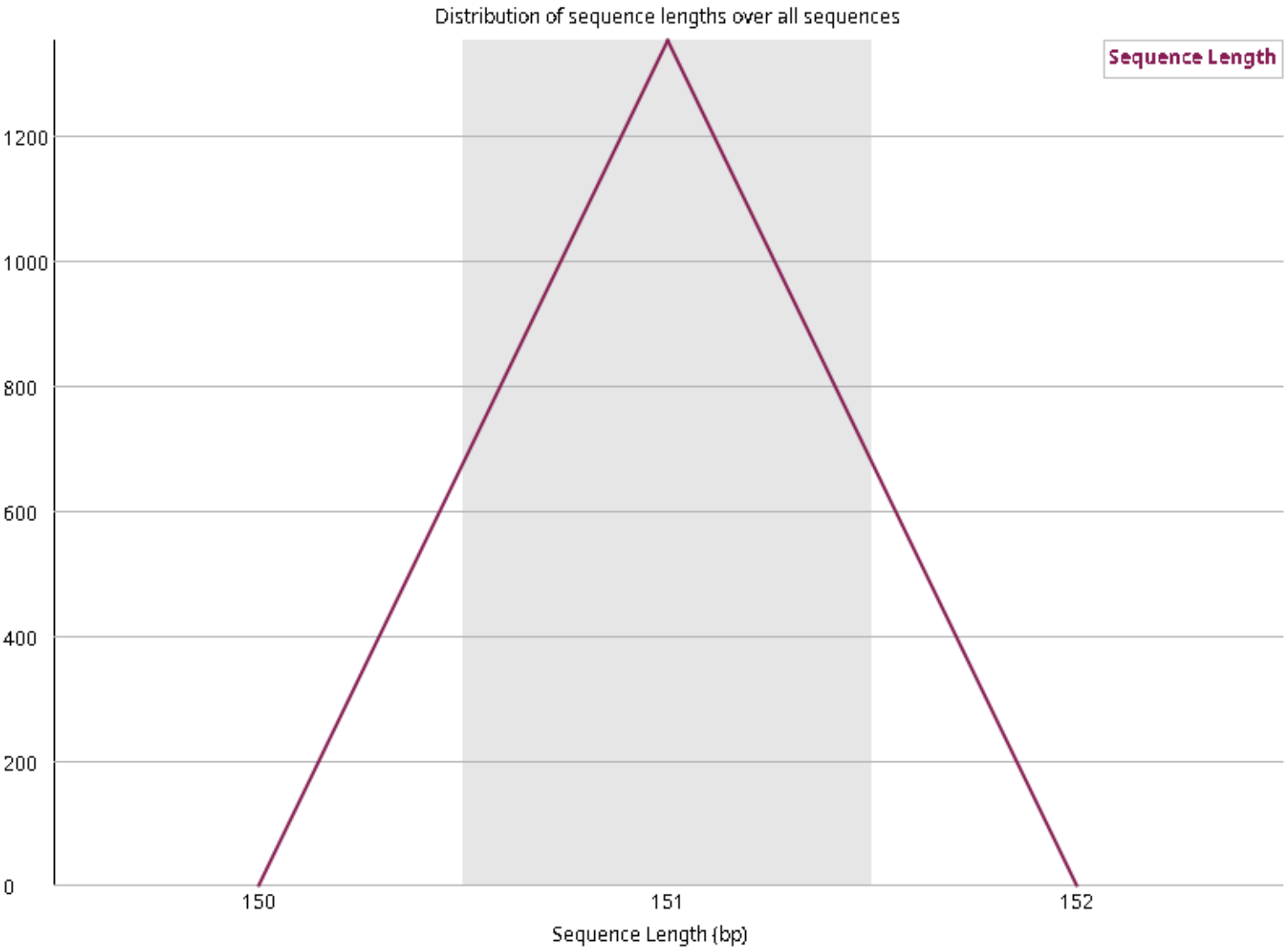
Per sequence GC content



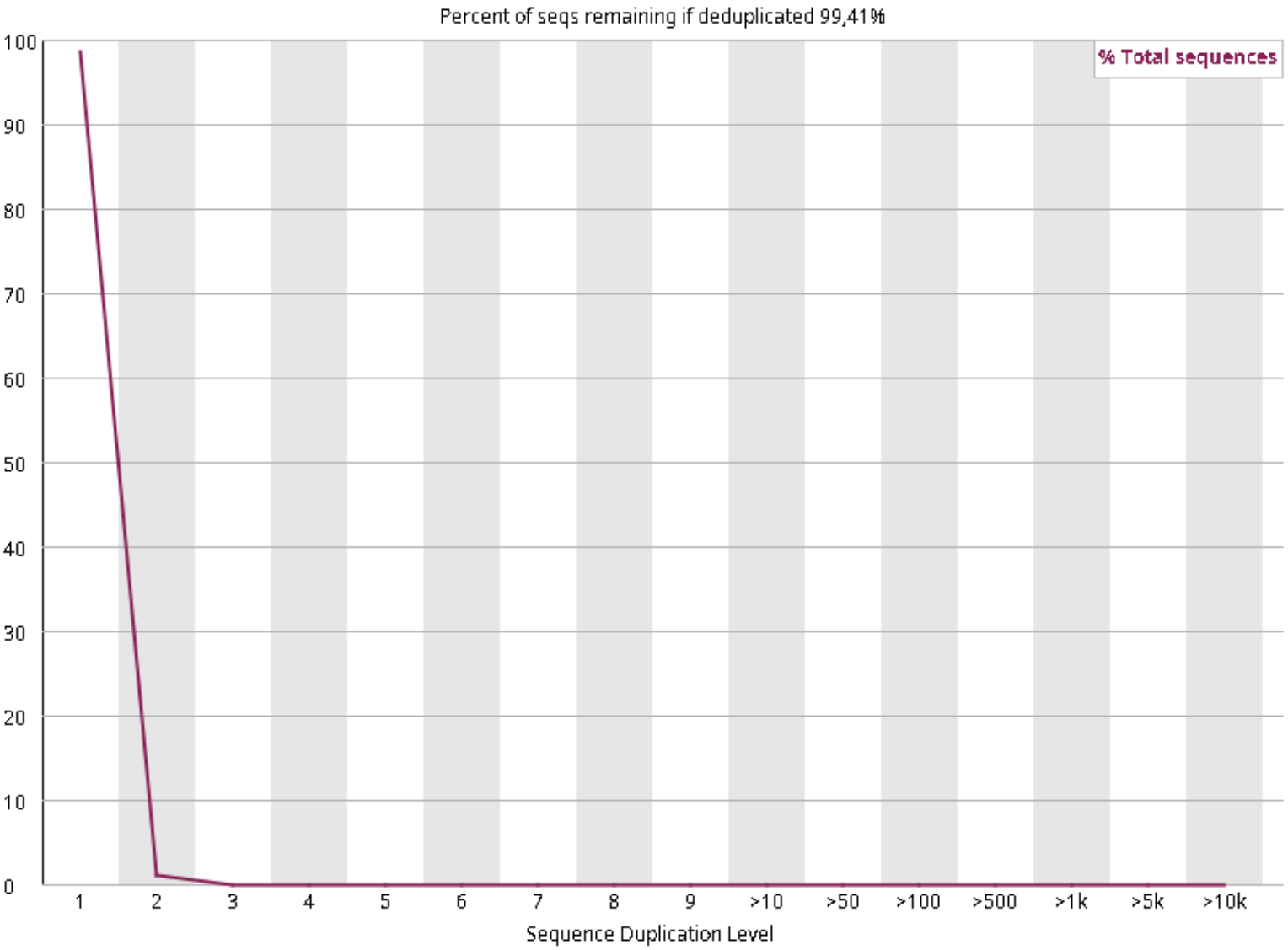
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

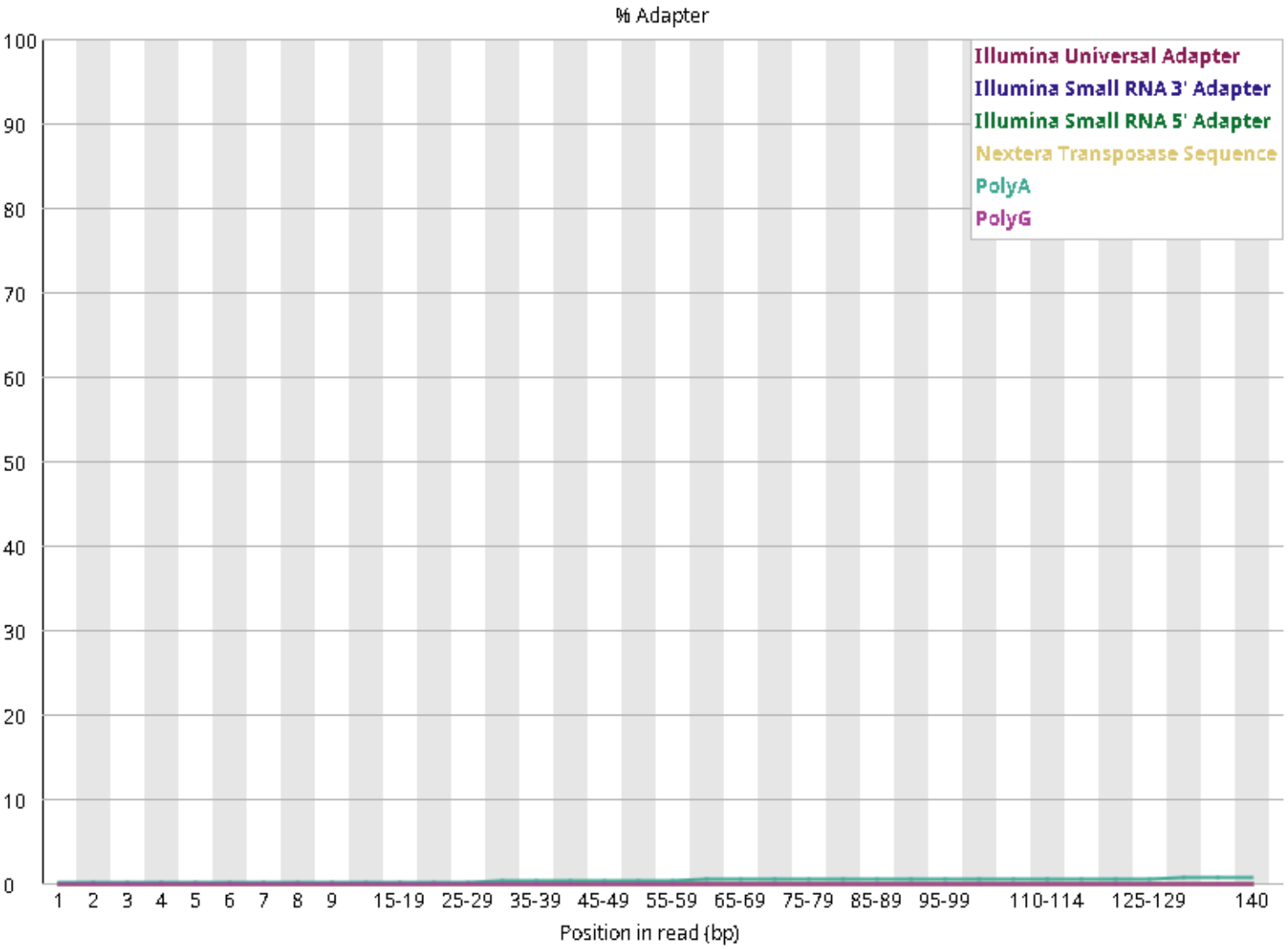


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CAGGCAGGACTCATGCAGCCTTACGCAGCGACGTGAGGAGCGGGGCTCGC	2	0.14792899408284024	No Hit
TGGATGGATTTGAAGCAAAGCATCAGCTTCTCCAGGCTCTTTGGGGTCAG	2	0.14792899408284024	No Hit
GTCATAATGTTATGGTACTGGAGAGCATAGAAGATAGTAAAGTACCTGTC	2	0.14792899408284024	No Hit
TCCTCGGCGCCGTTAGGGTACACCTTCACTGGGCGCCGCTTCTTGCCCAC	2	0.14792899408284024	No Hit
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2	0.14792899408284024	No Hit
GAGGAGCGGGGCTCGCGGTCCTGCAGGTCTAGTACCTCTGCCAAGGCCTG	2	0.14792899408284024	No Hit
GCTAGGTGCGGCTGCAGGGATTCATGGCAGTACCCAGCTTGCGGCAGTAG	2	0.14792899408284024	No Hit

Sequence	Count	Percentage	Possible Source
AATTCTCAGAGGGAACCTTGTTCTGGTCATCCAAAGGCTCTGCCTACCCC	2	0.14792899408284024	No Hit

Adapter Content



Produced by FastQC (version 0.12.1)