











# FastQC Report

## Summary

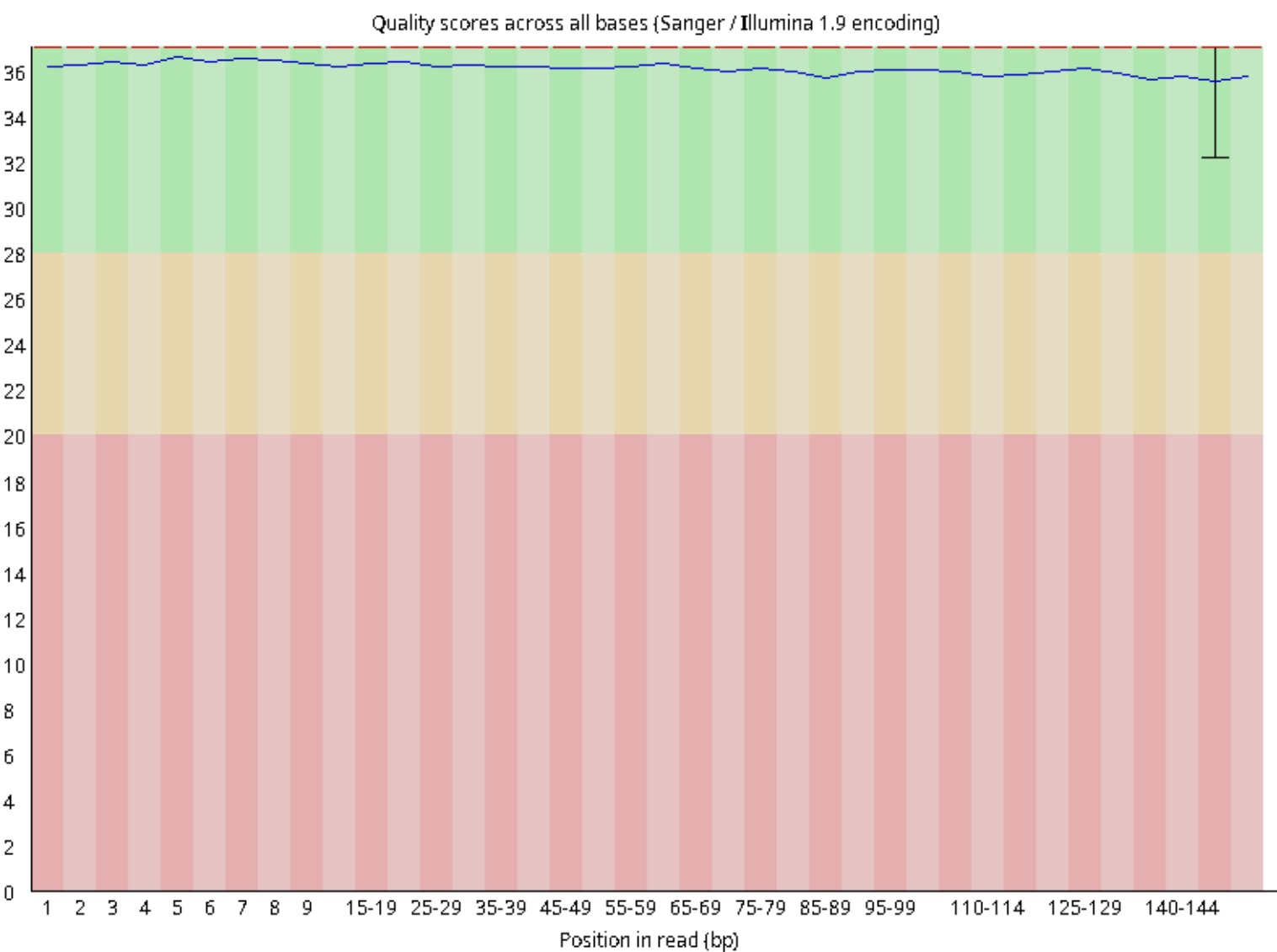
sáb 20 dic 2025  
PattyBouvier\_R2.fastq

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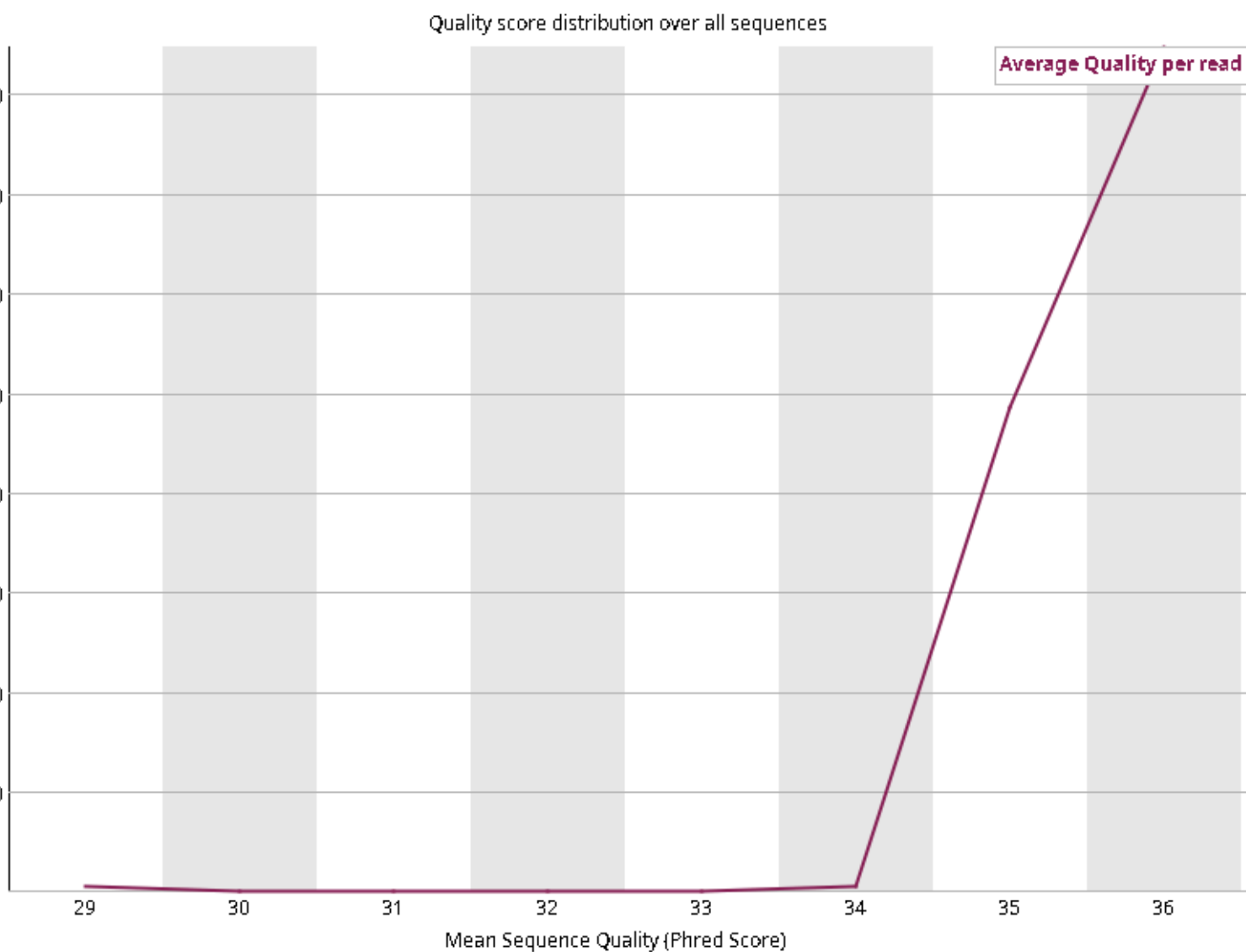
## Basic Statistics

Measure	Value
Filename	PattyBouvier_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1344
Total Bases	202.9 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

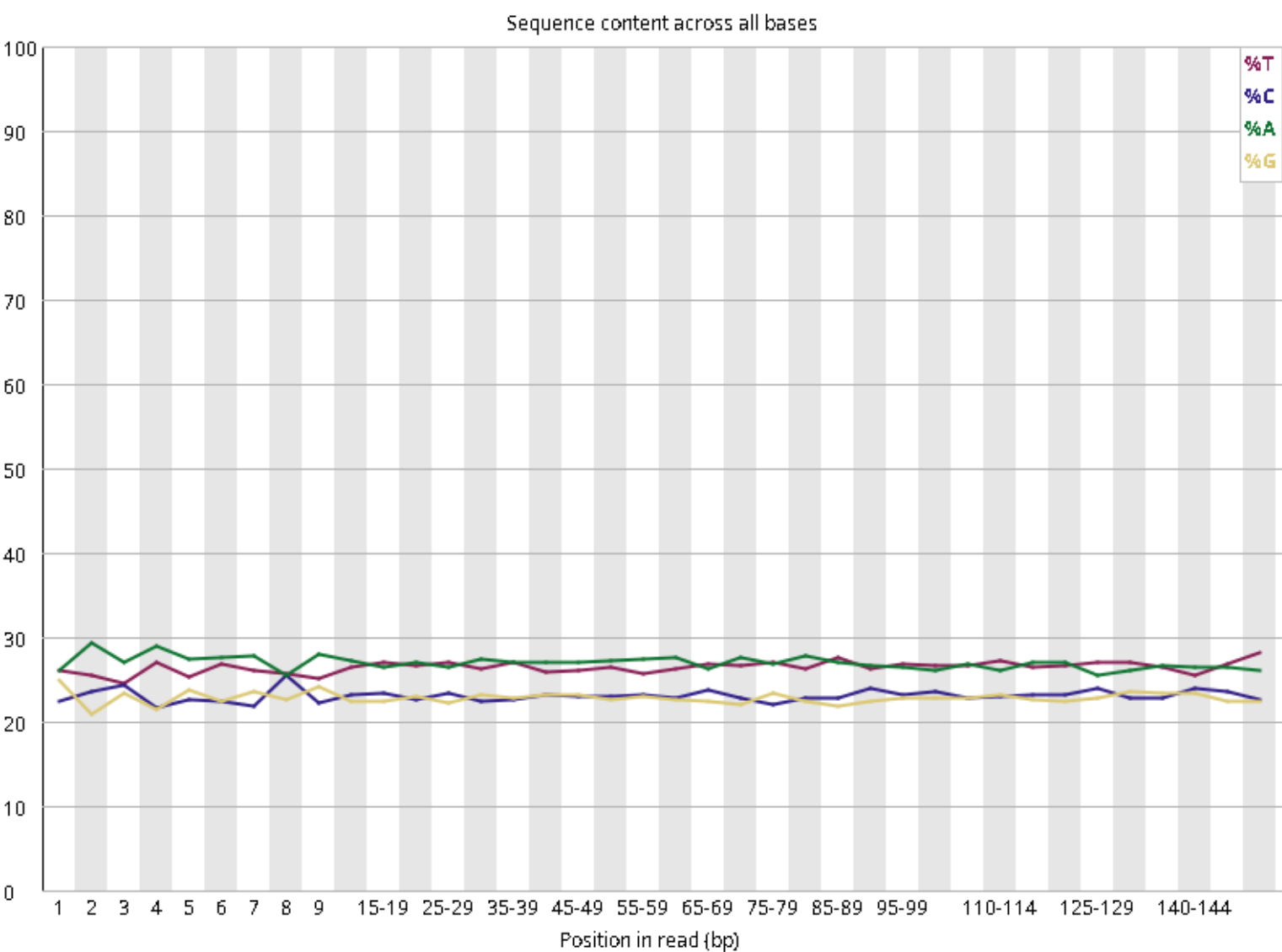
## ✔ Per base sequence quality



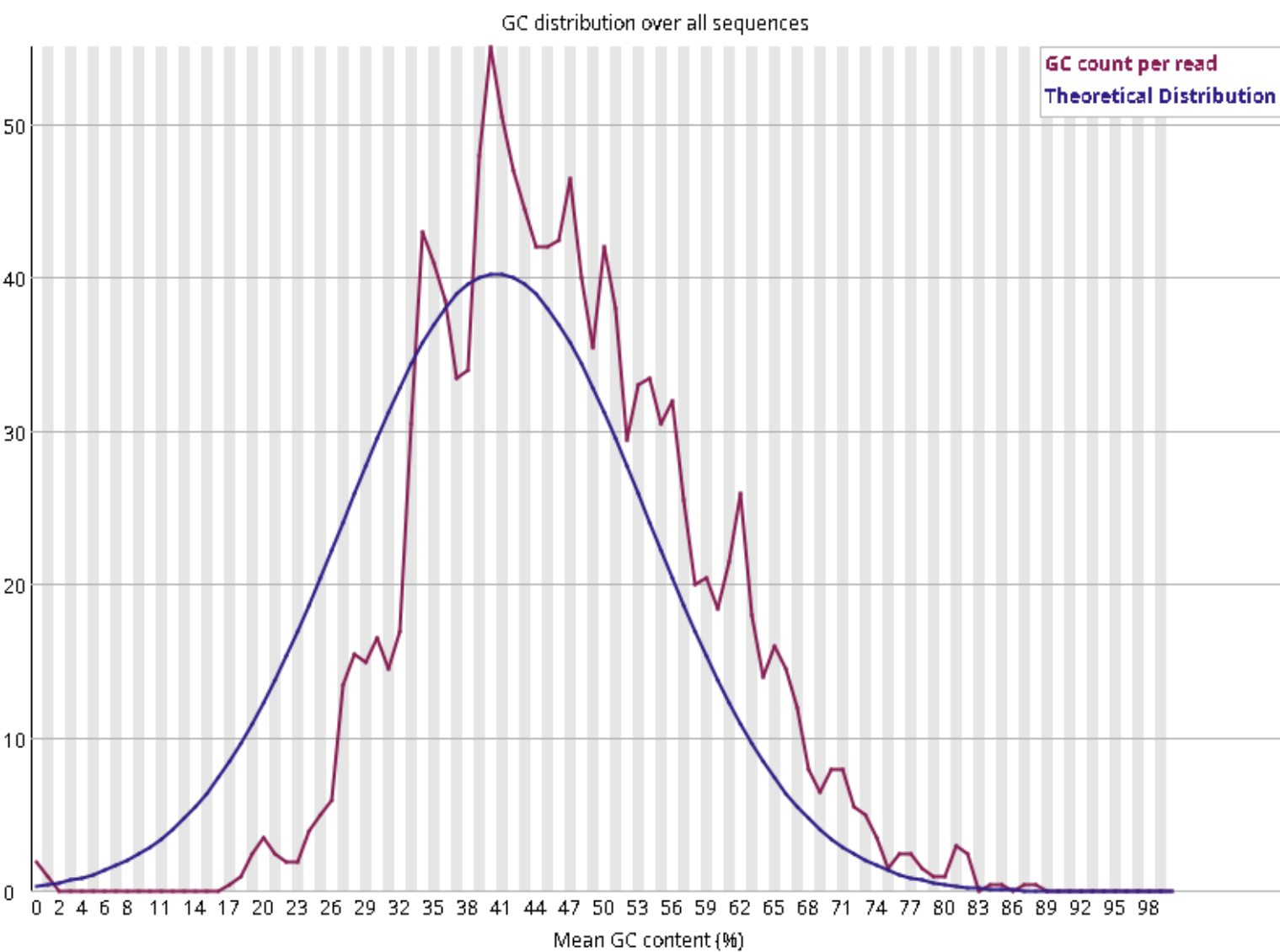
## ✔ Per sequence quality scores



## ✔ Per base sequence content

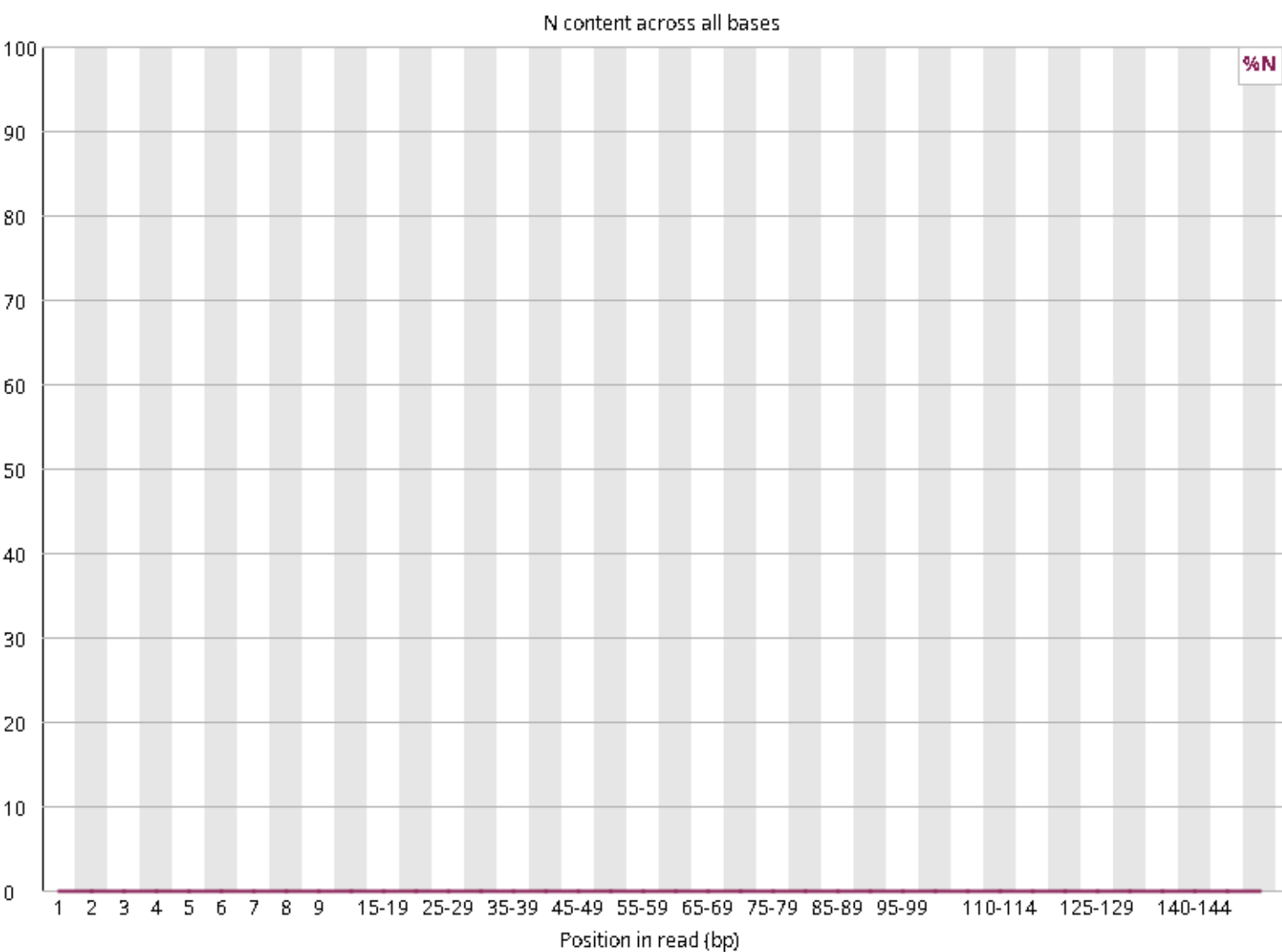


## ✖ Per sequence GC content

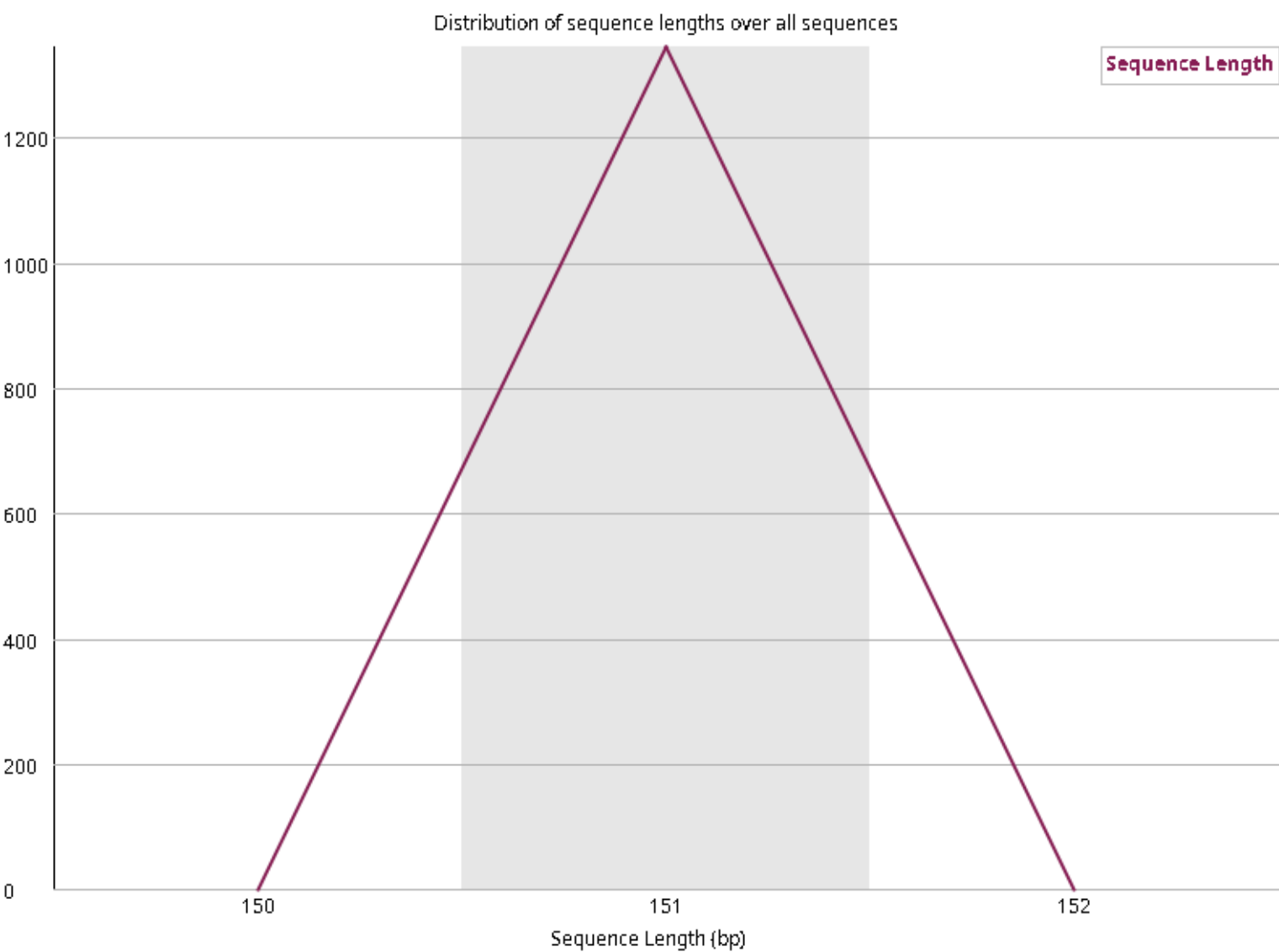




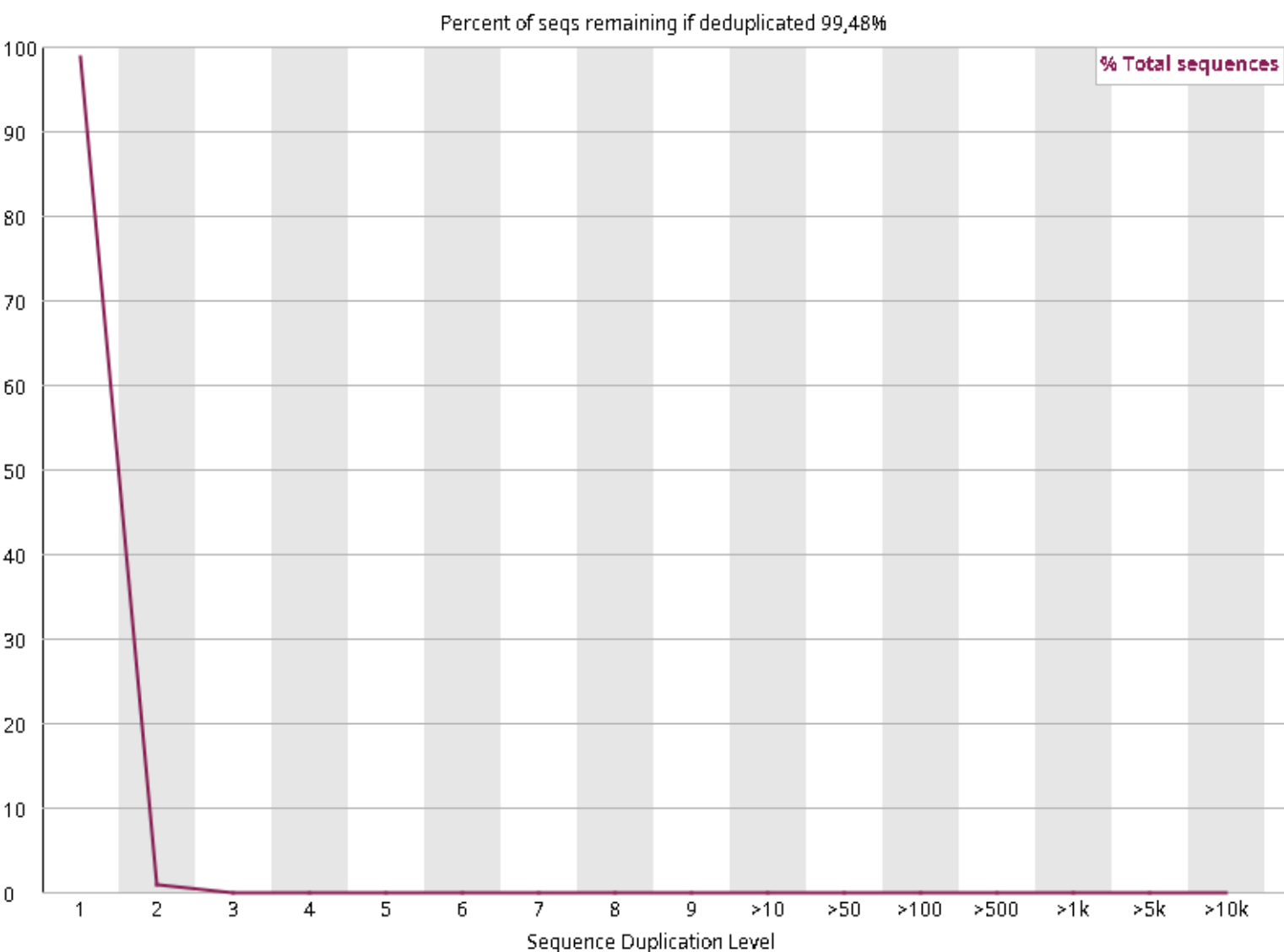
## Per base N content



## ✔ Sequence Length Distribution



## Sequence Duplication Levels



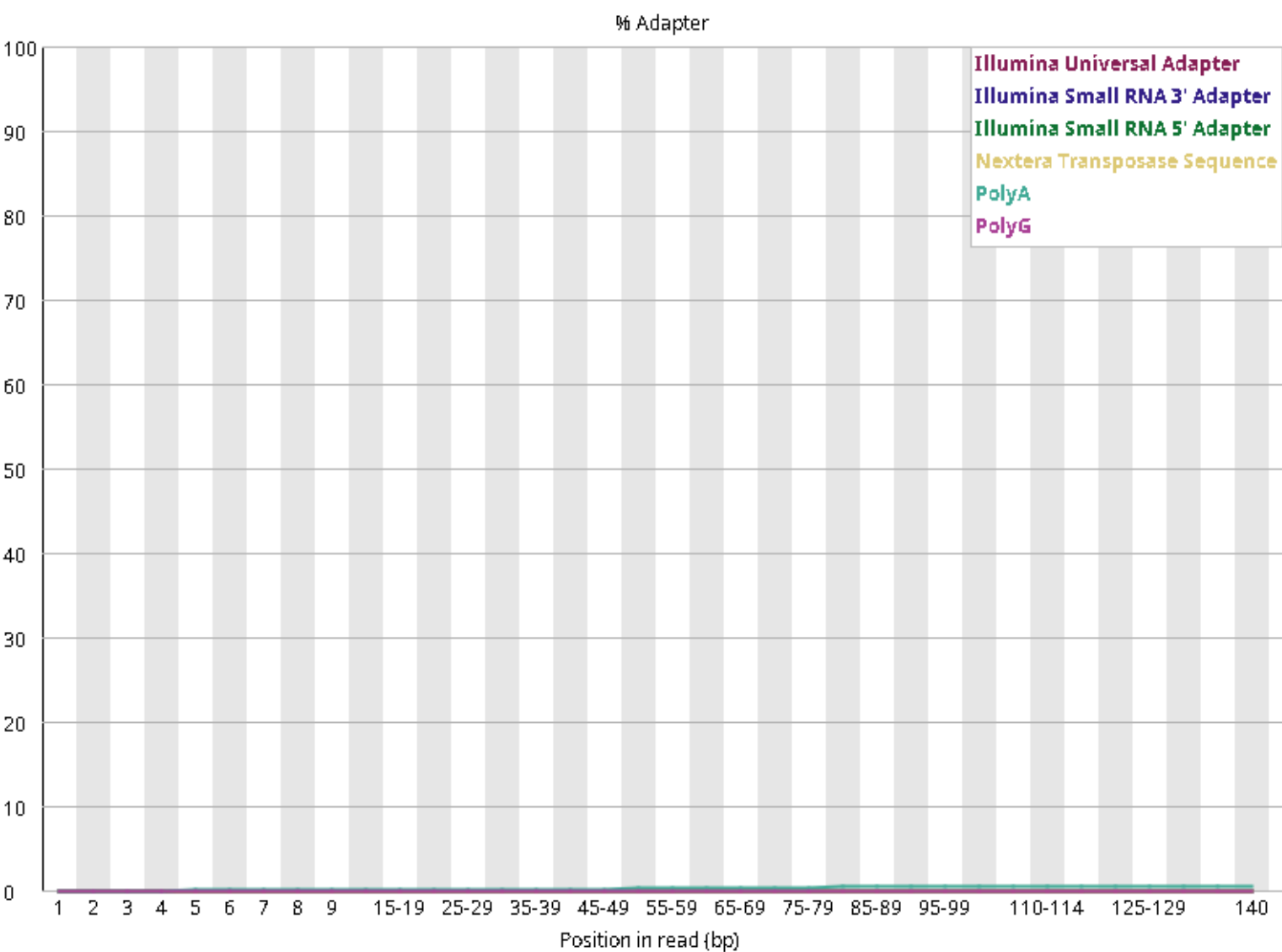
## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AATGCAGGATAAACAGTATTAGAAGATGCAATCGTAACATTGCTGACTTC	2	0.1488095238095238	No Hit
TTCTCACAGTCATCGCAGAAGCAGAGAGGGTGACACATCTTTTGACGGT	2	0.1488095238095238	No Hit
TTGTAGACGTGCACGCAGGGCGGCGTGCTCACGCTGCTGTAGTGCGTGAC	2	0.1488095238095238	No Hit
AAAGTGAATCTAACTAGTTTTAAACCTTTTTAAATGAAGGTTGTATAACA	2	0.1488095238095238	No Hit
GAGCAAACCCCTATTTGGCAATGACCACACTCTCACTTTTTGAGTTAAGC	2	0.1488095238095238	No Hit
AAACCCAGAAAATTTTGACTTTTATACTATCATATGTGACTCAATCTAA	2	0.1488095238095238	No Hit
AA	2	0.1488095238095238	No Hit





## Adapter Content



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