











# FastQC Report

## Summary

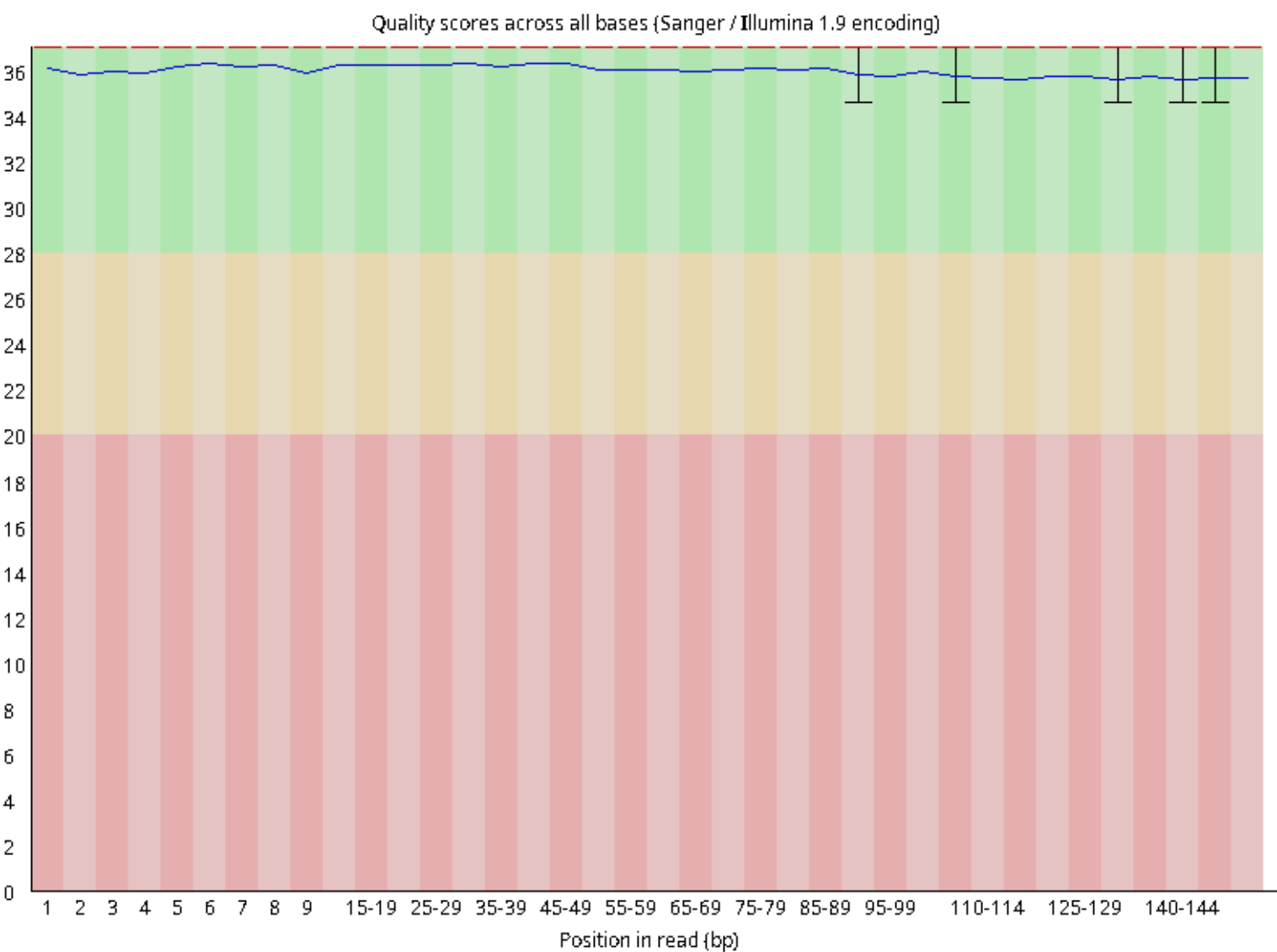
sáb 20 dic 2025  
MargeSimpson\_R2.fastq

-  [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](#)

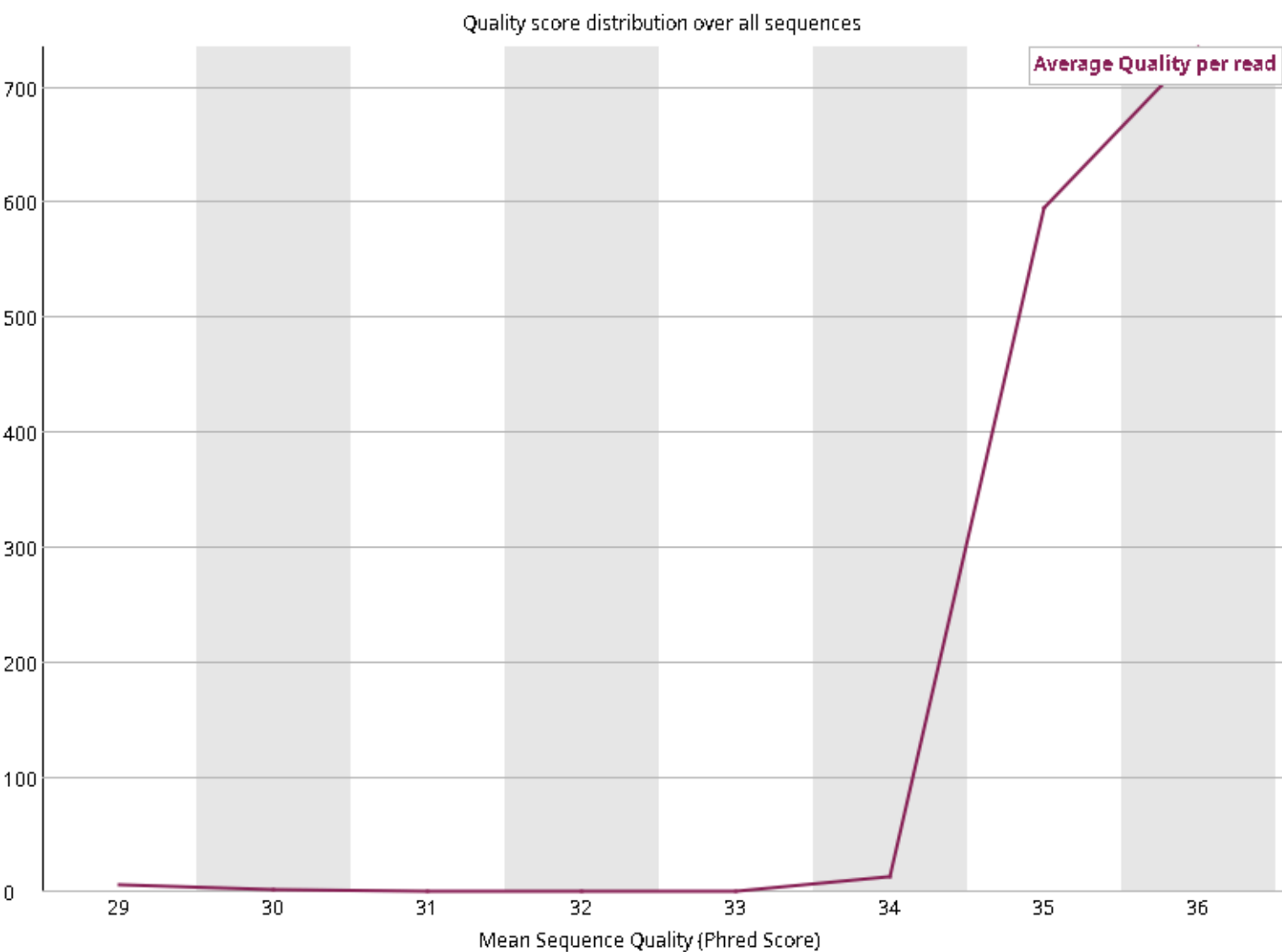
## Basic Statistics

Measure	Value
Filename	MargeSimpson_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

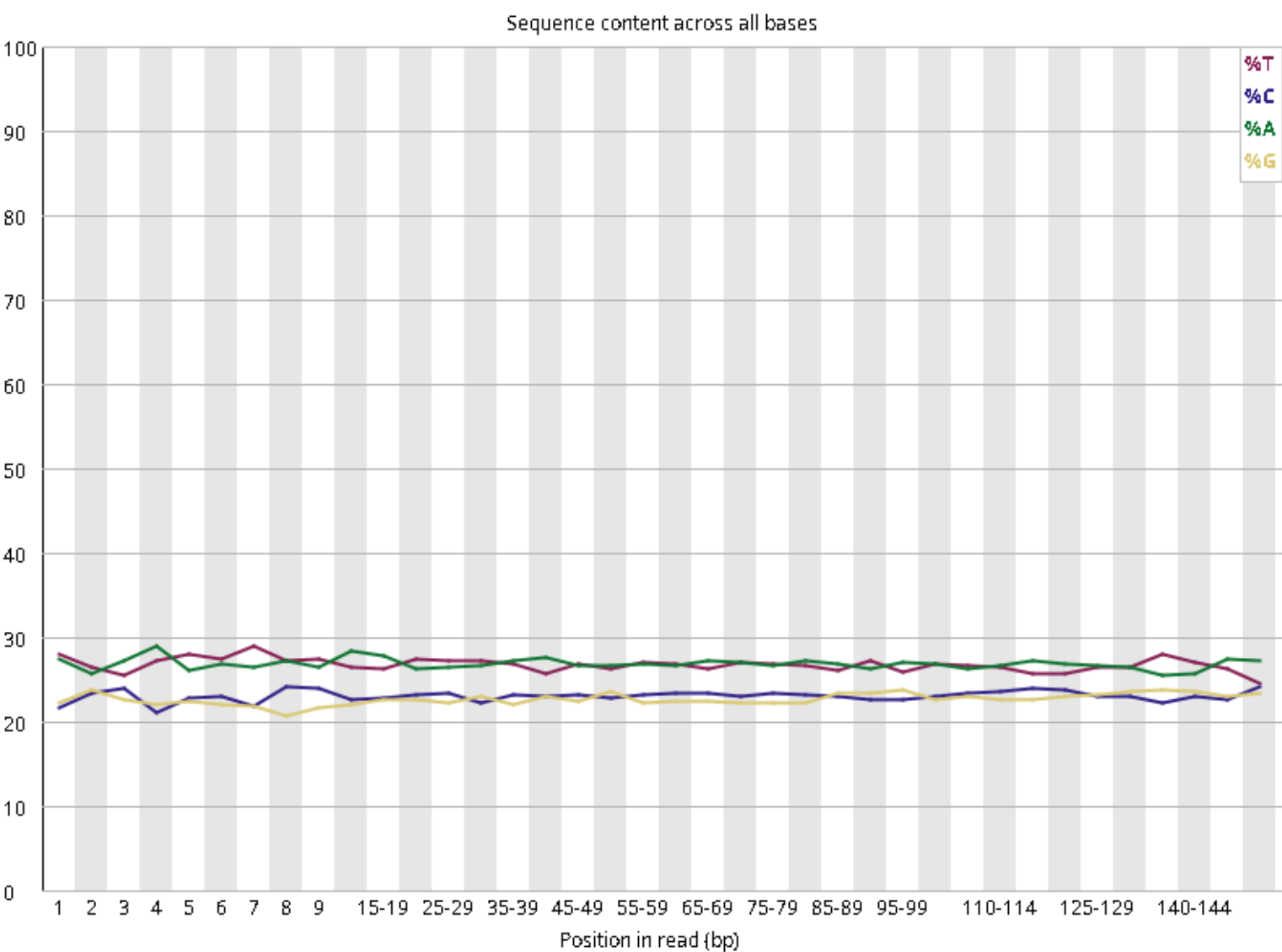
## ✔ Per base sequence quality



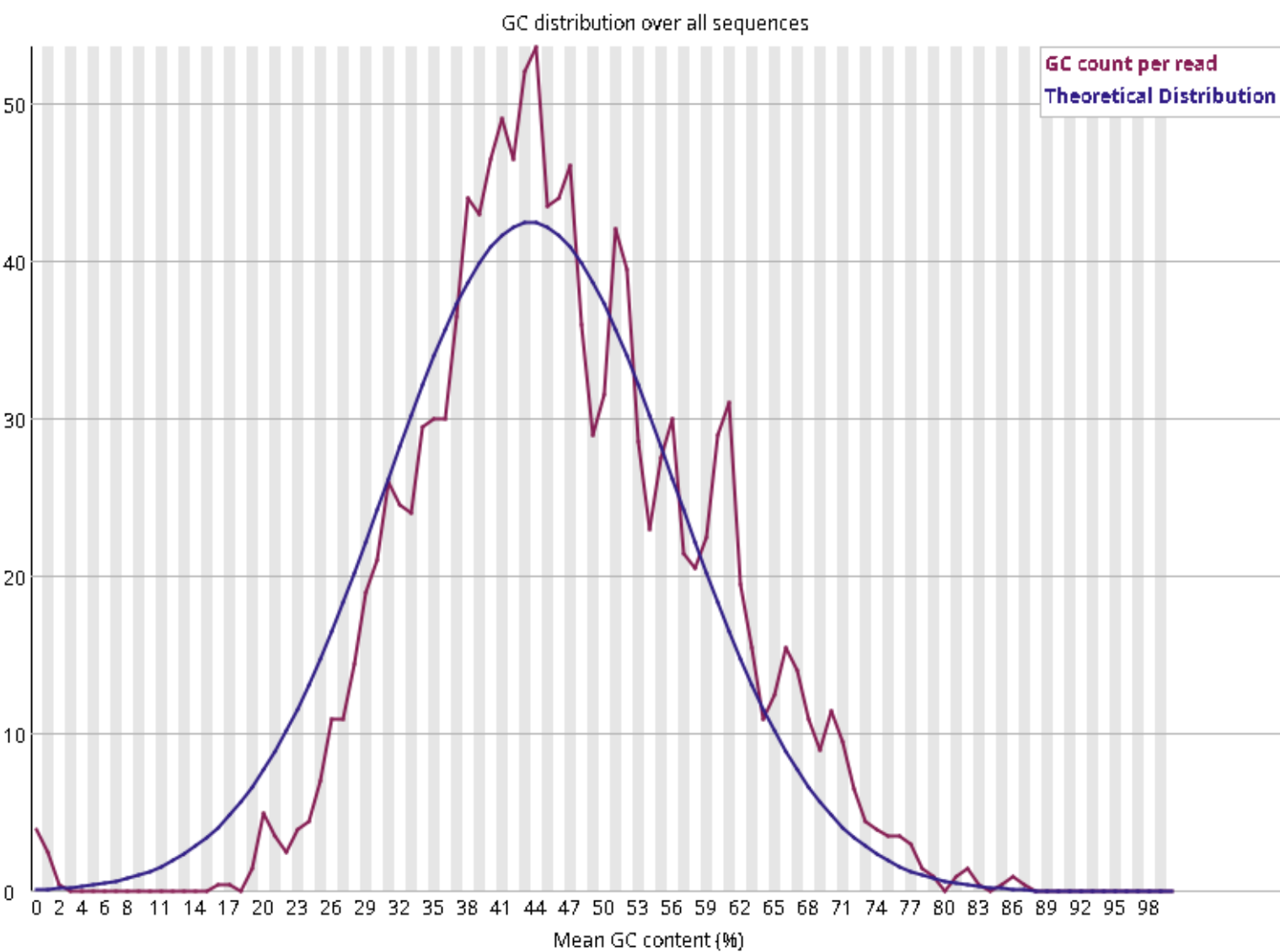
## ✔ Per sequence quality scores



## ✔ Per base sequence content

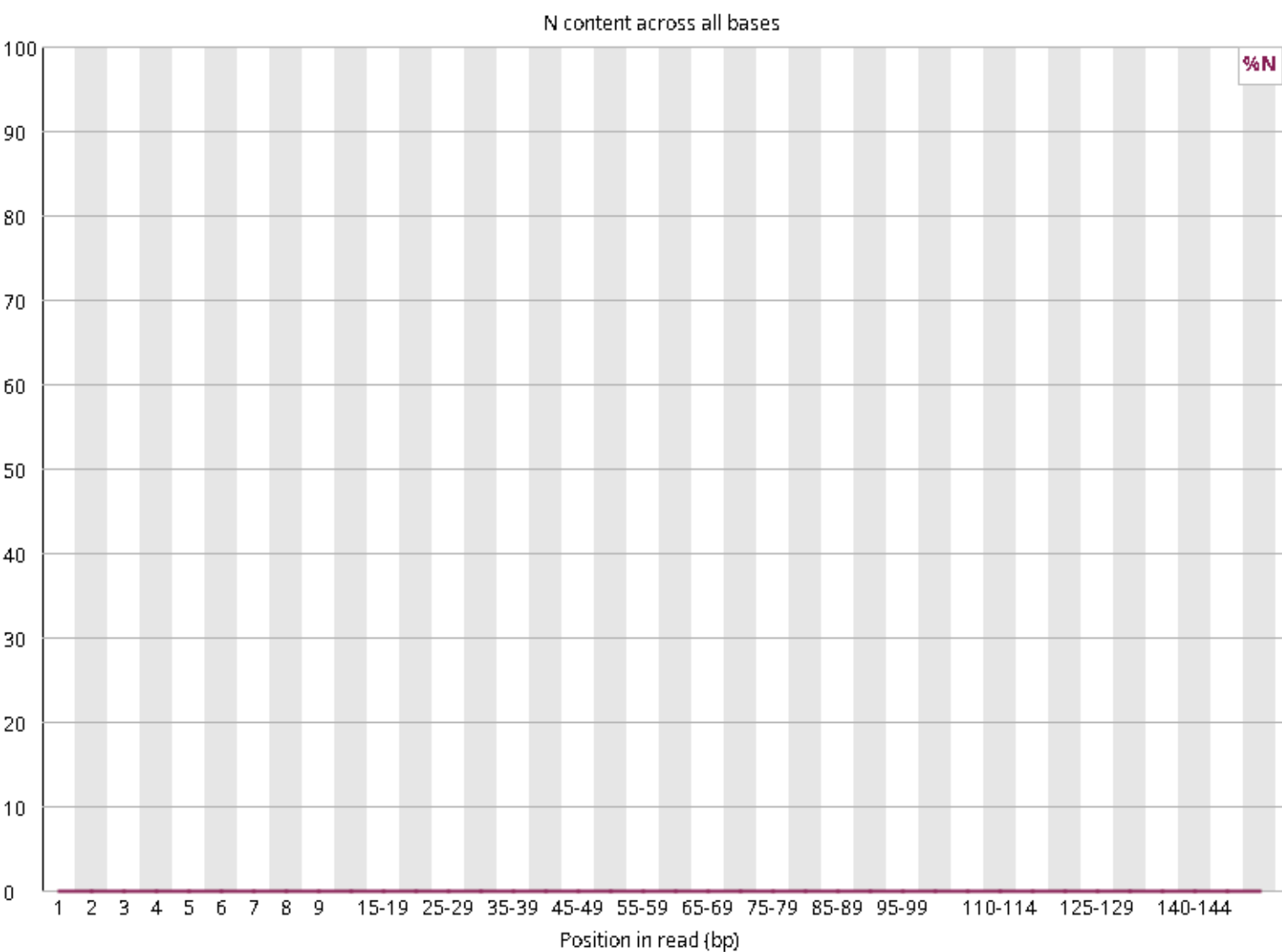


## 🚨 Per sequence GC content

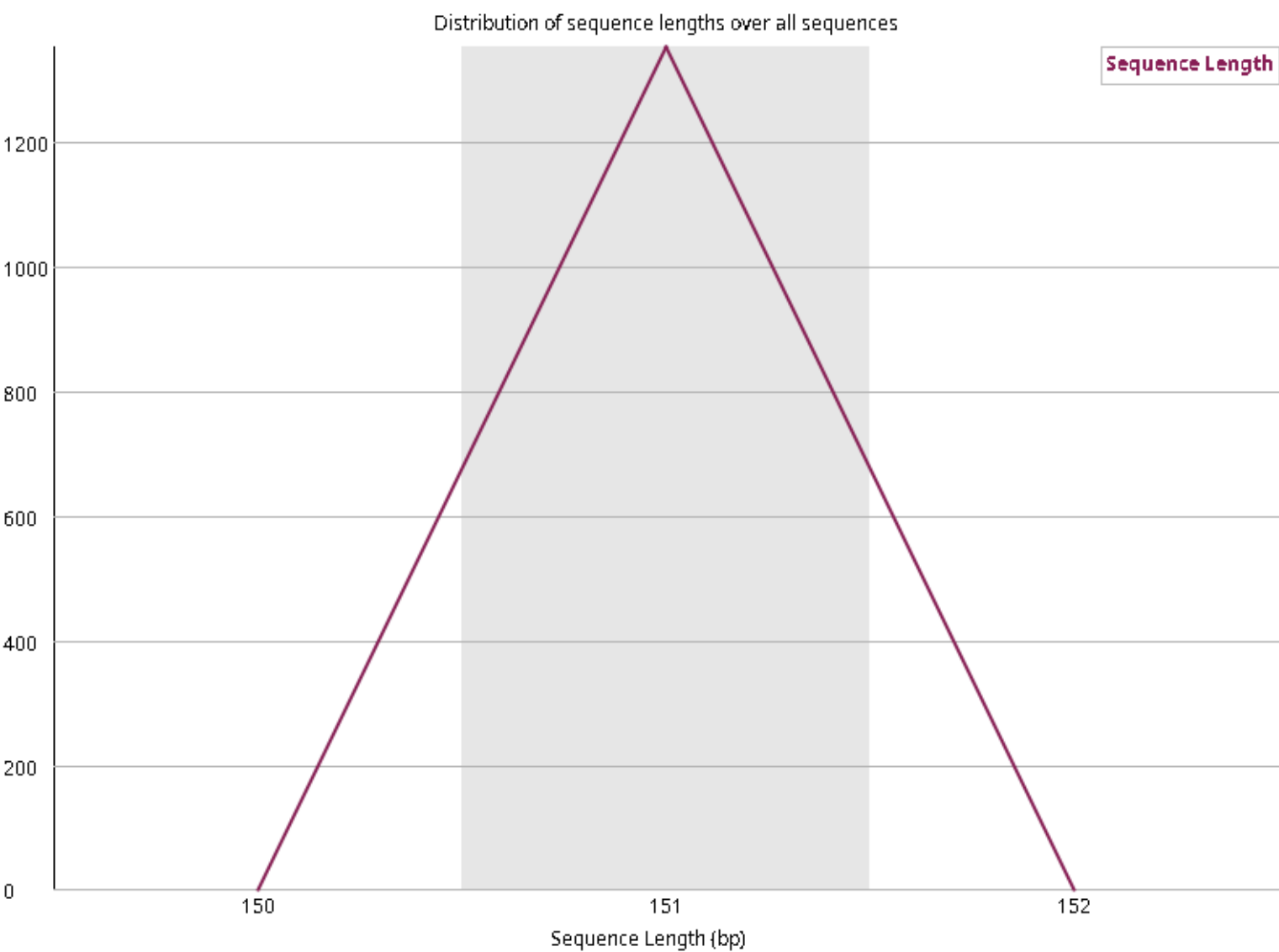




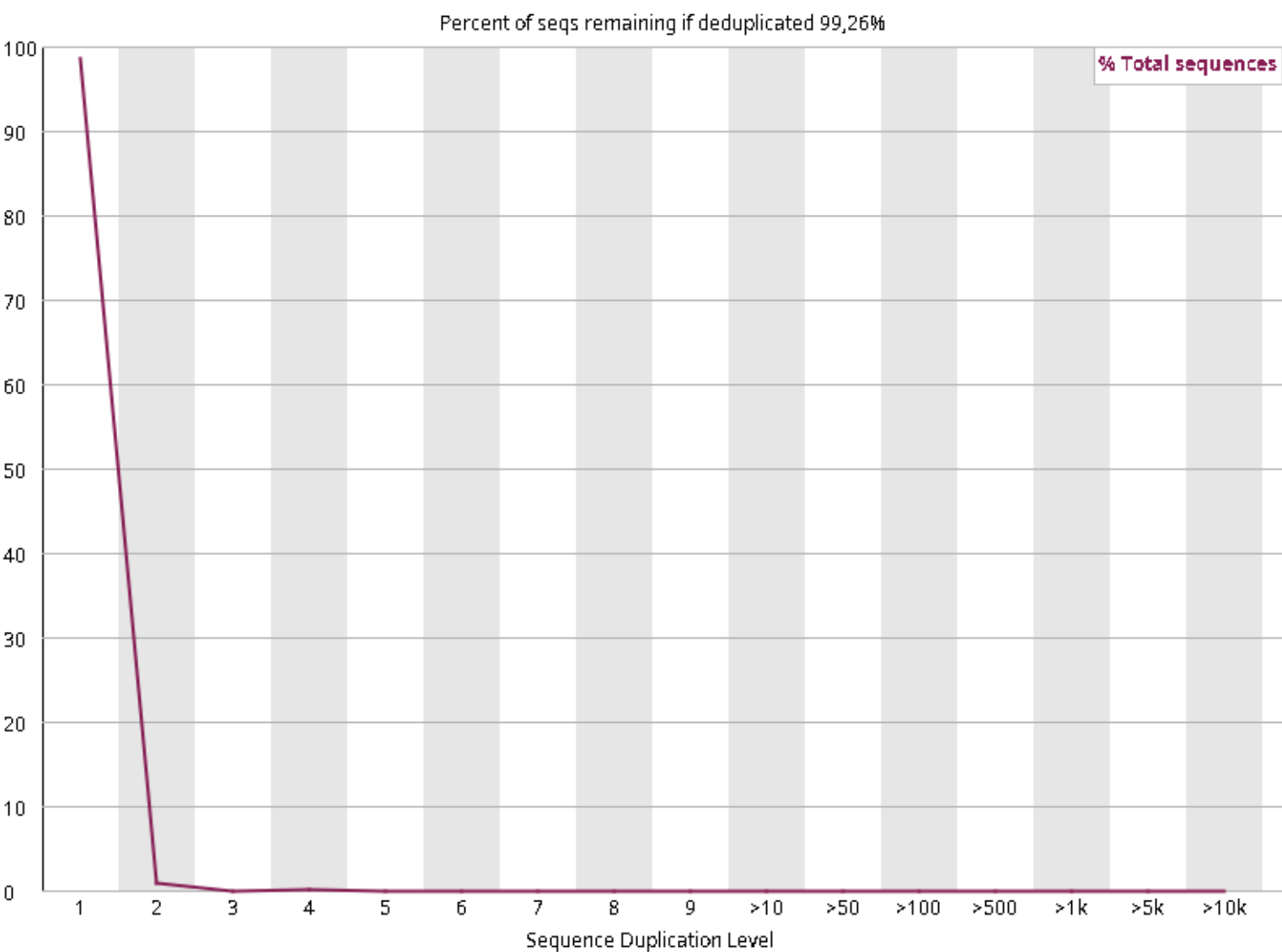
## Per base N content



## ✔ Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AA	4	0.2958579881656805	No Hit
TCGTCAGAAGCAGGGCAACTTTTTCATAGAGCACATTCAGCAACATAATG	2	0.14792899408284024	No Hit
TGAAGTATTTGCACCAAGAACAGTGTATTGATGGCAGTAAAAGACCAGCG	2	0.14792899408284024	No Hit
TGATTAATAAAAAGGATATAGCTGCTCAGTCTGGTGCTGATAATGGTGGTA	2	0.14792899408284024	No Hit
TGCAGAGAAGTGTGCATCCACGGTGGGTGGAGTTACCATGCTGGCAGG	2	0.14792899408284024	No Hit
TAAATAATTATTTCTCTATTTATATTGAAGTATCATAGCCCATGTTAAA	2	0.14792899408284024	No Hit
AGGCAGTGCCAGCAGCAGGGCACAGCTCAGCACCGCTGCGGTCAGCATGG	2	0.14792899408284024	No Hit



Sequence	Count	Percentage	Possible Source
ATATTTGAGGAGAGTTACTTGGTCGTTCAAGTCAAGATTTACAAAACCAG	2	0.14792899408284024	No Hit



# Adapter Content

