











# FastQC Report

## Summary

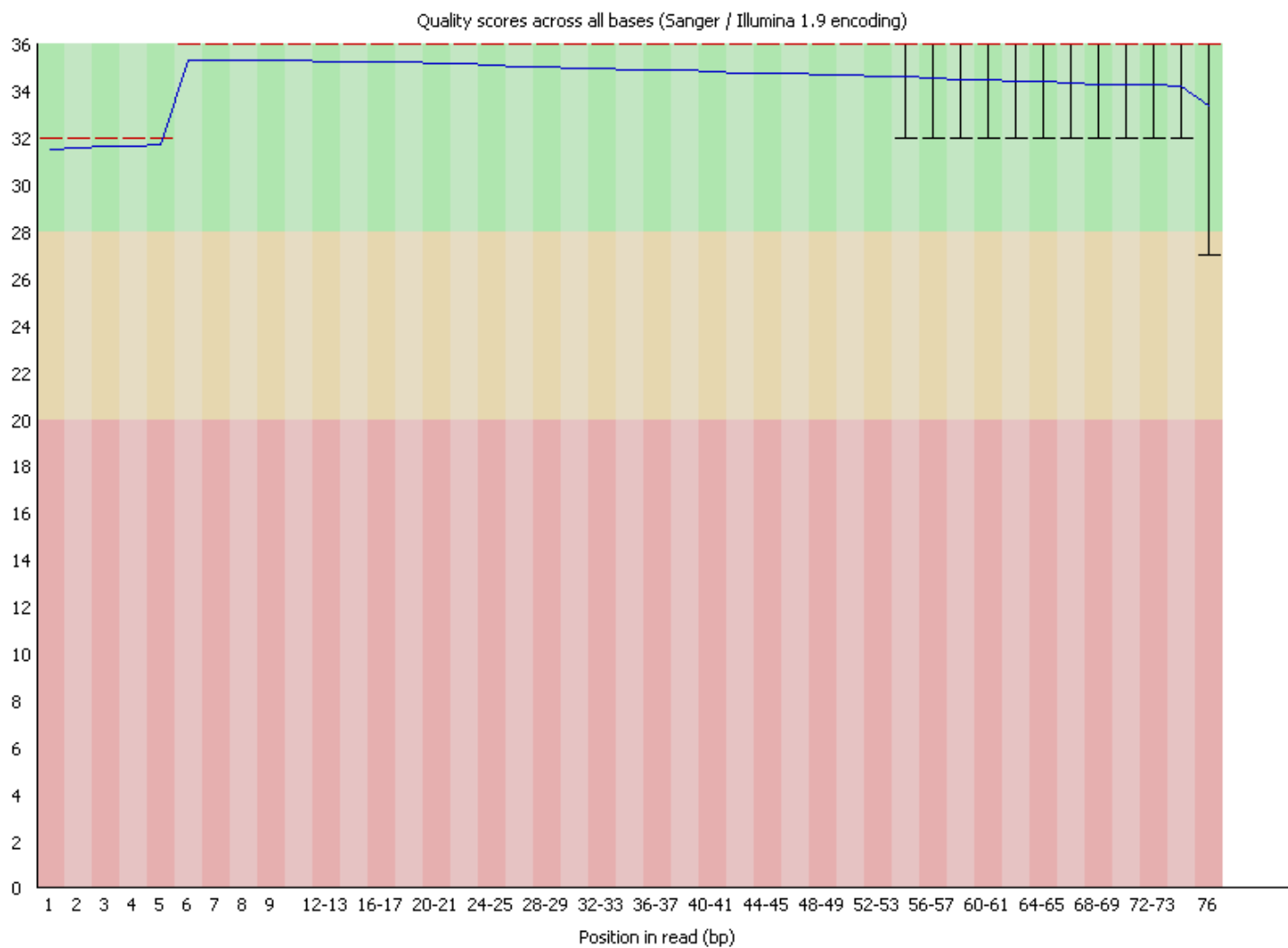
sab 10 giu 2023  
SRR12951228.fastq

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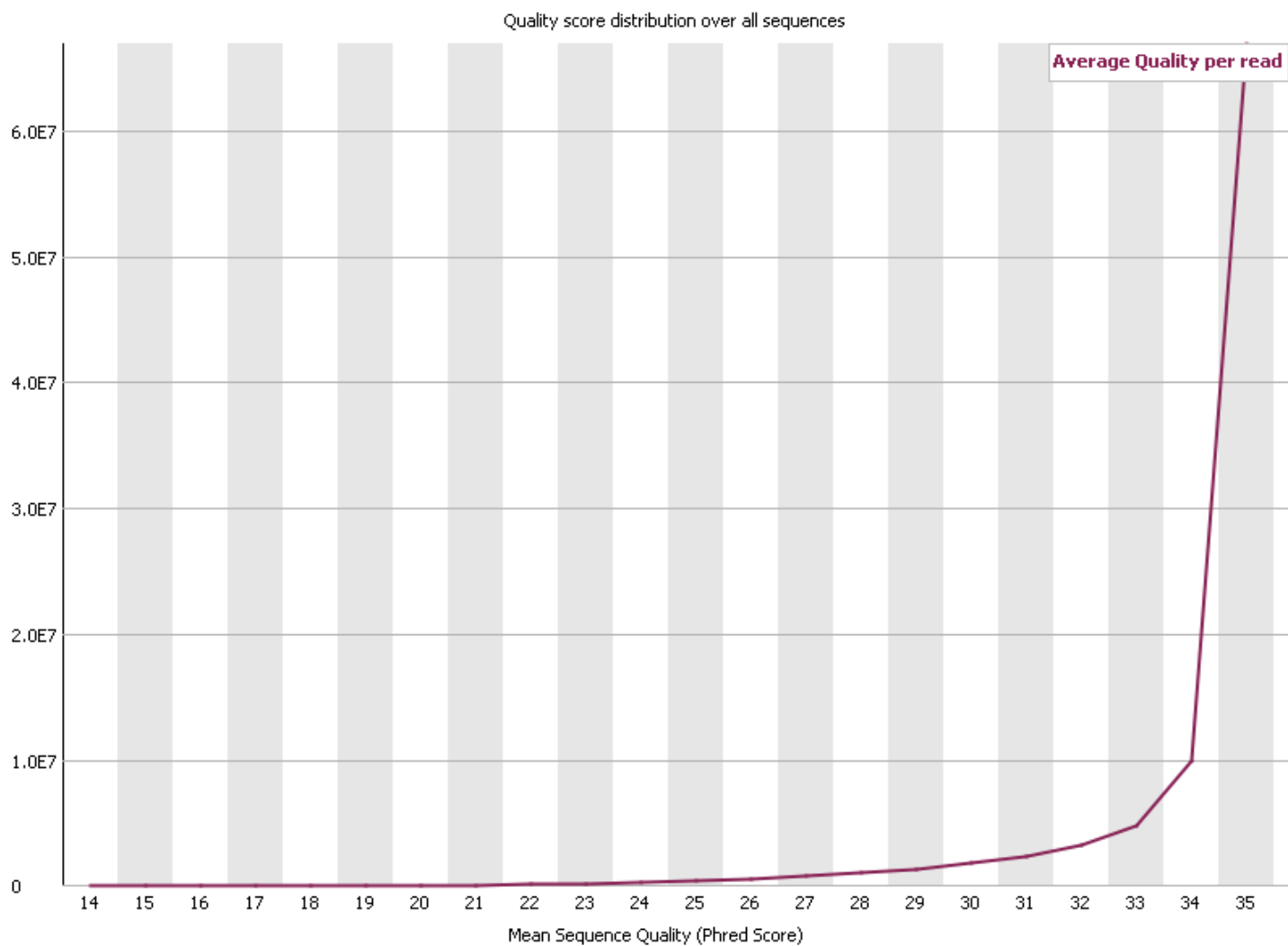
## Basic Statistics

Measure	Value
Filename	SRR12951228.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	94315400
Total Bases	7.1 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	42

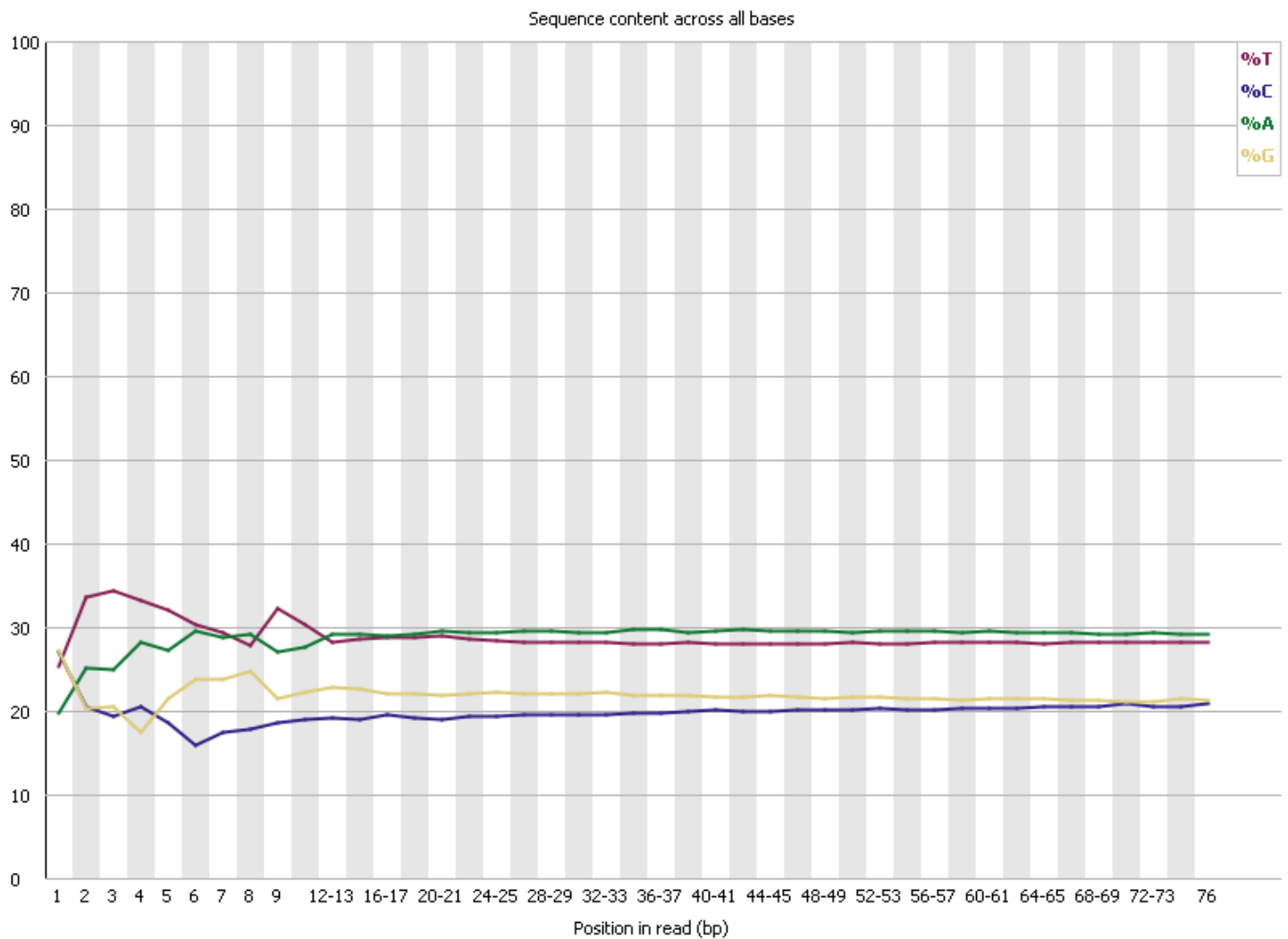
## Per base sequence quality



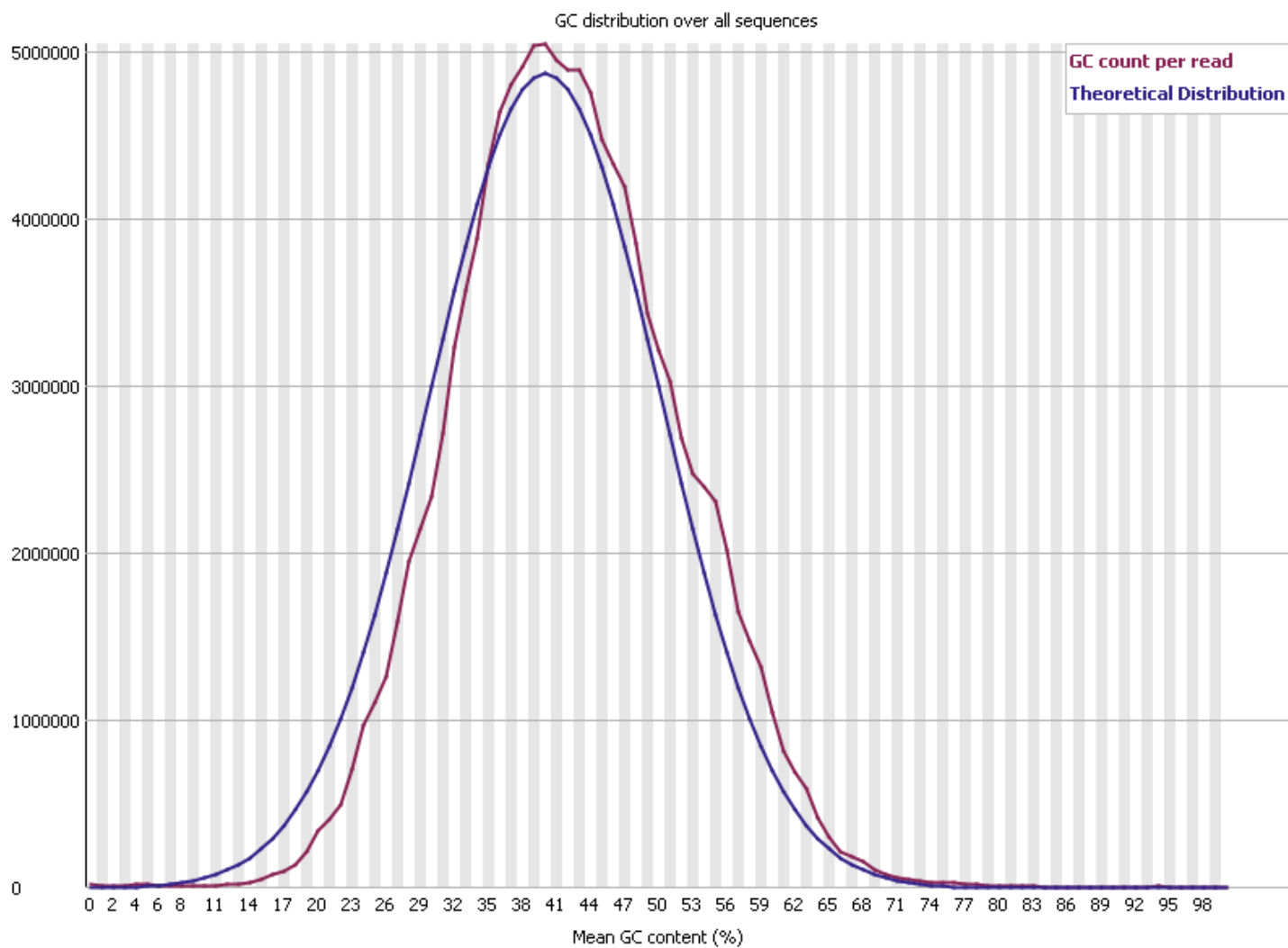
## Per sequence quality scores



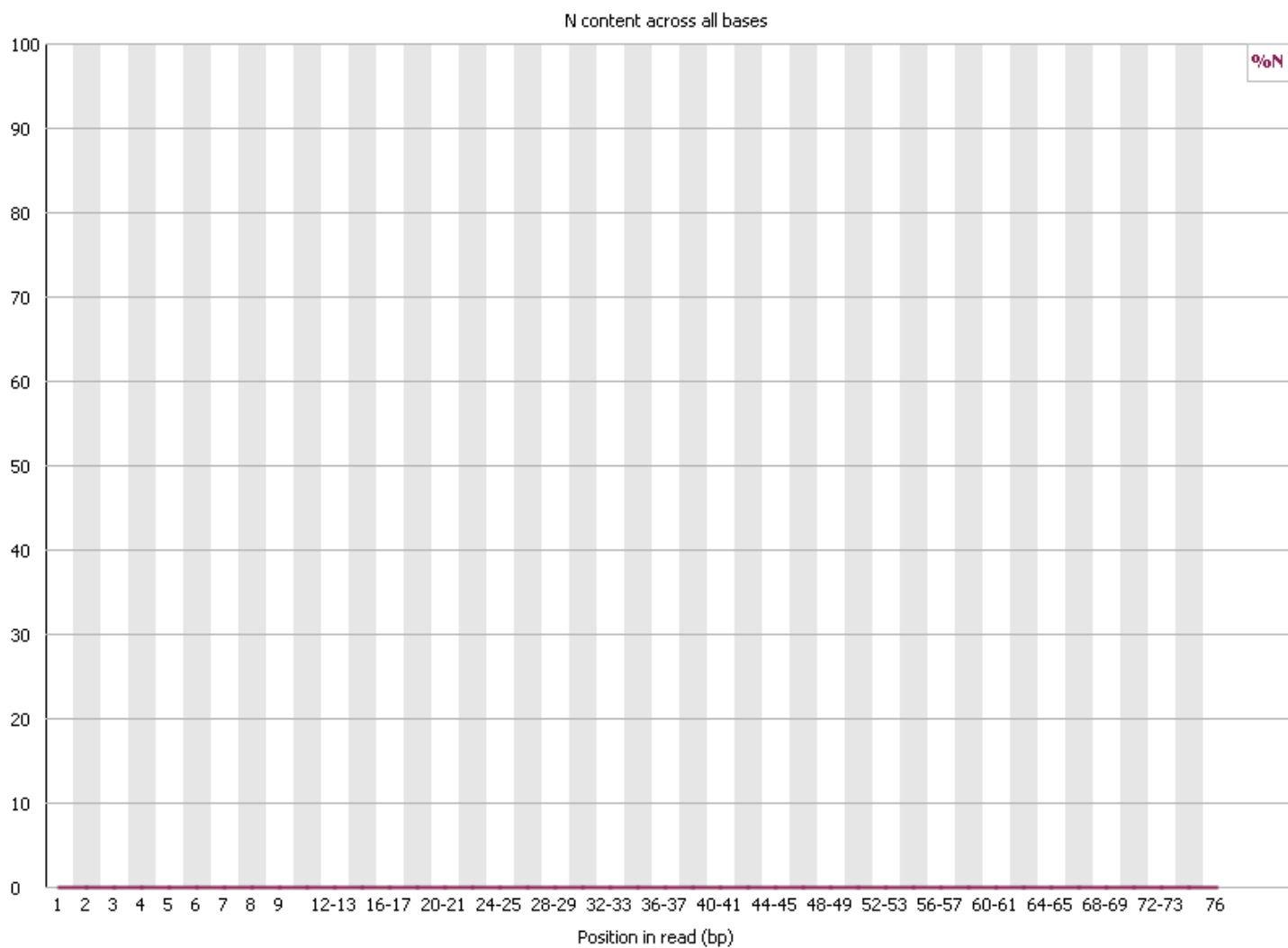
## Per base sequence content



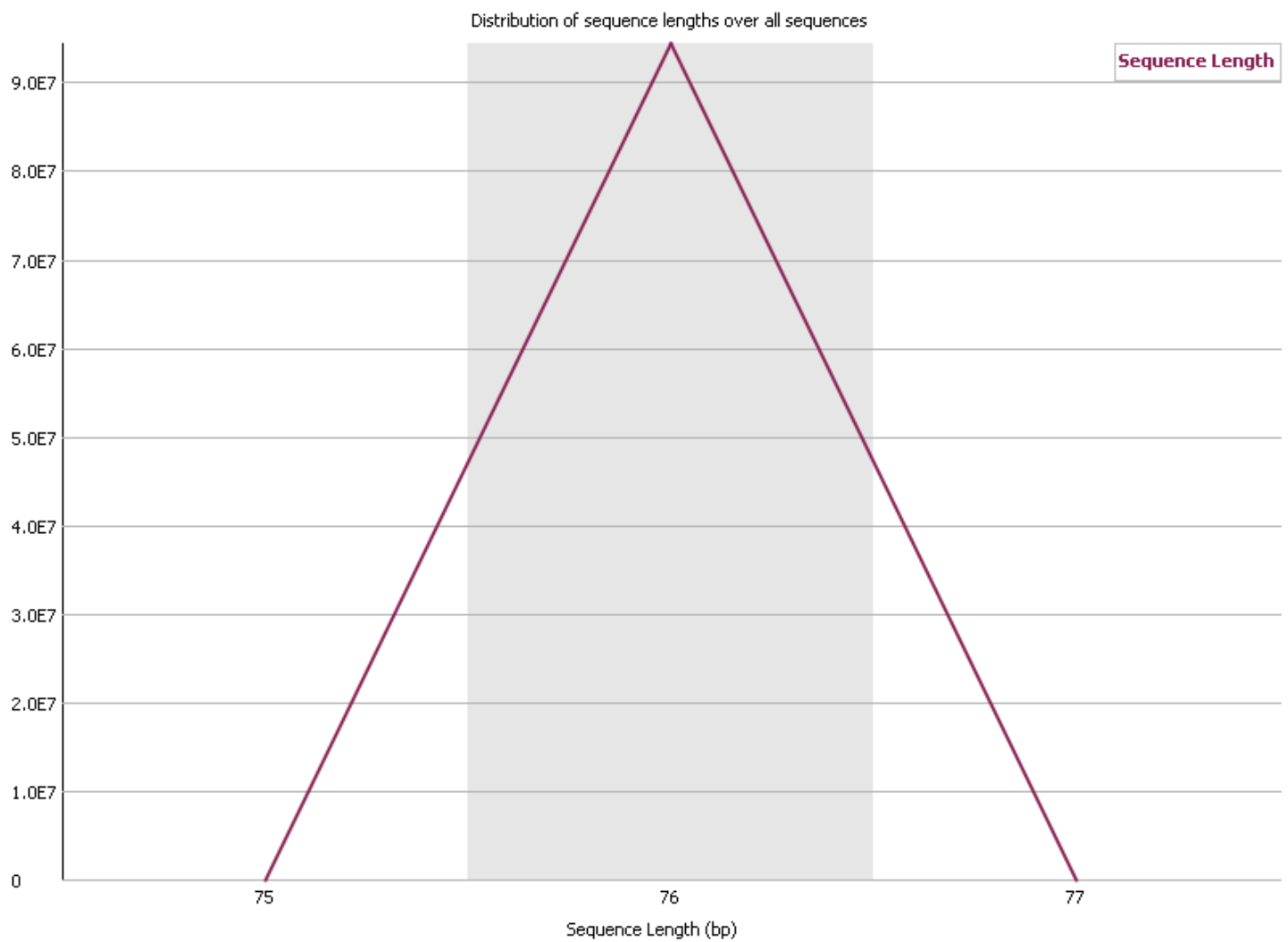
**Per sequence GC content**



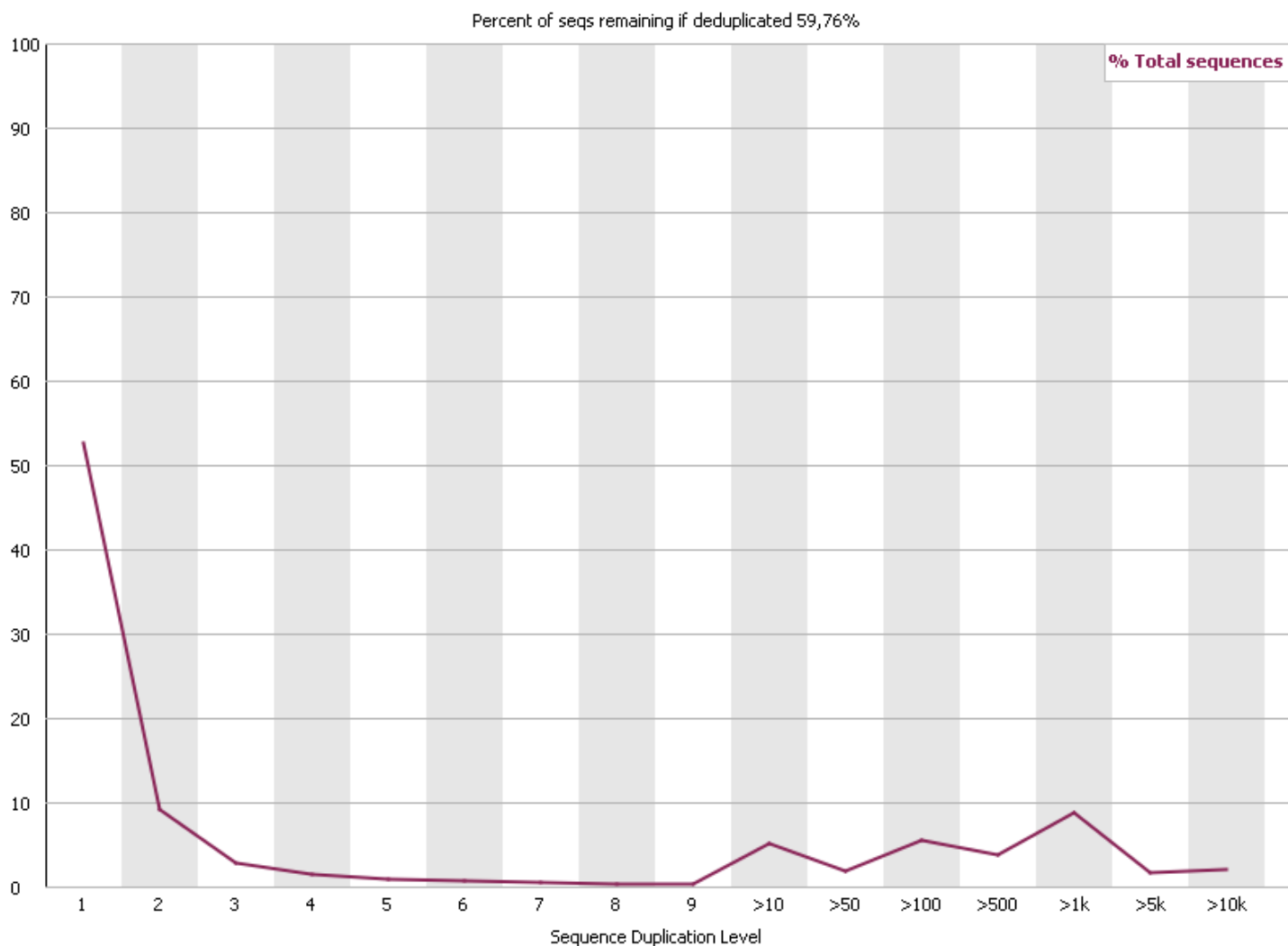
✓ Per base N content



## Sequence Length Distribution



## ! Sequence Duplication Levels



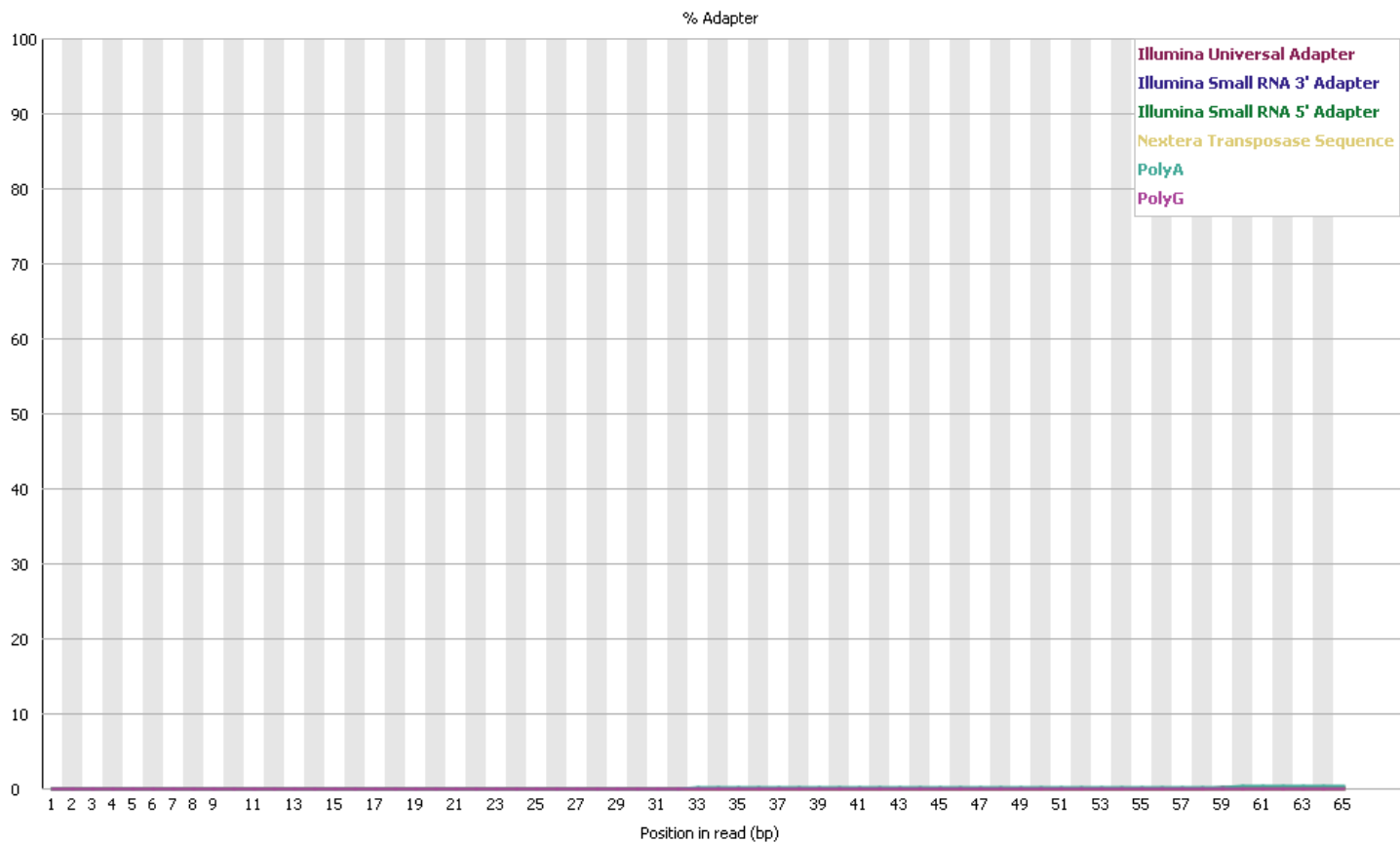
## Overrepresented sequences

No overrepresented sequences



## Adapter Content





Produced by [FastQC](#) (version 0.12.1)