












# FastQC Report

## Summary

Thu 31 Oct 2024  
SRR491287\_2.fastq.gz

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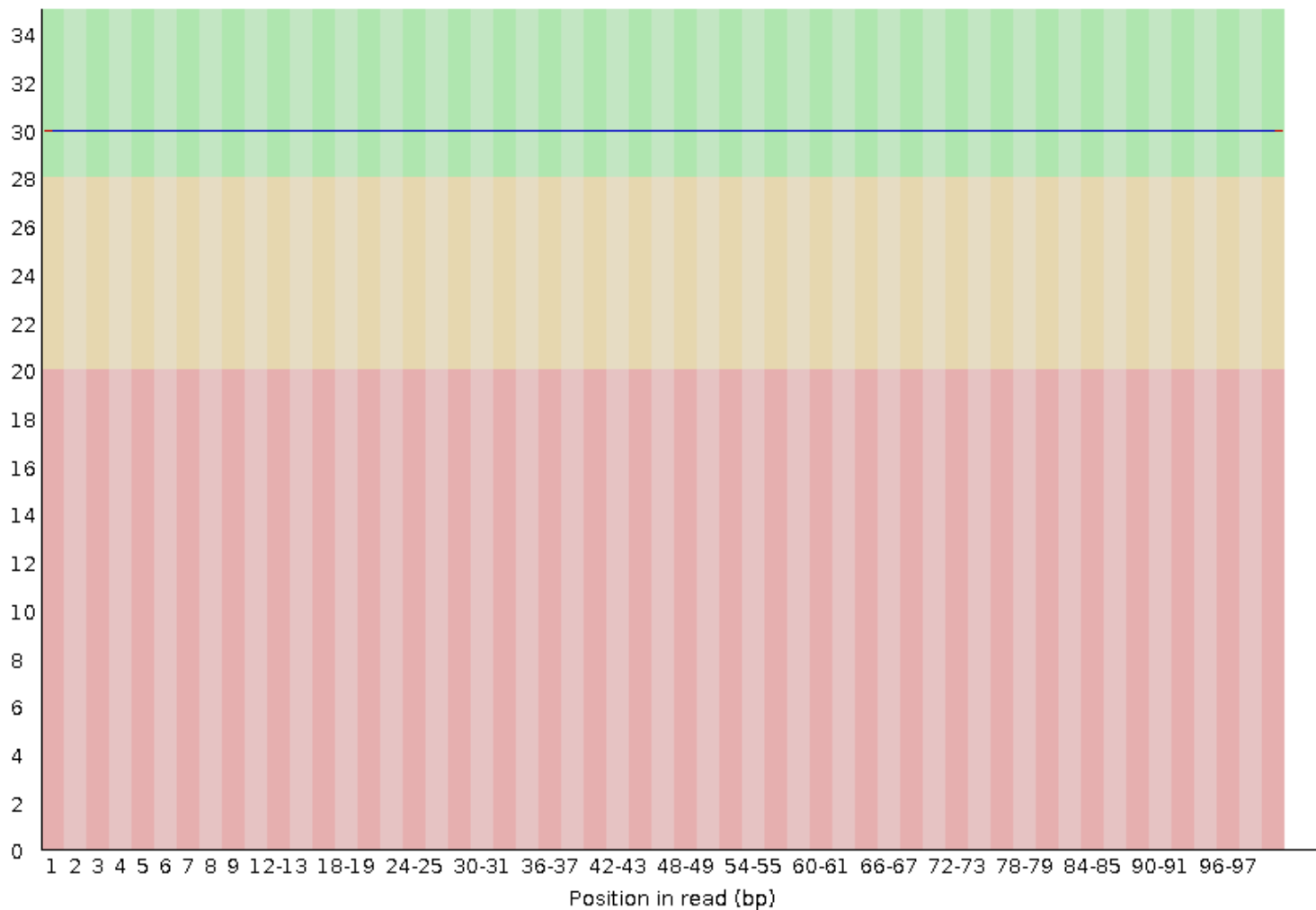
## Basic Statistics

Measure	Value
Filename	SRR491287_2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	20004674
Total Bases	2 Gbp
Sequences flagged as poor quality	0
Sequence length	101
%GC	59



## Per base sequence quality

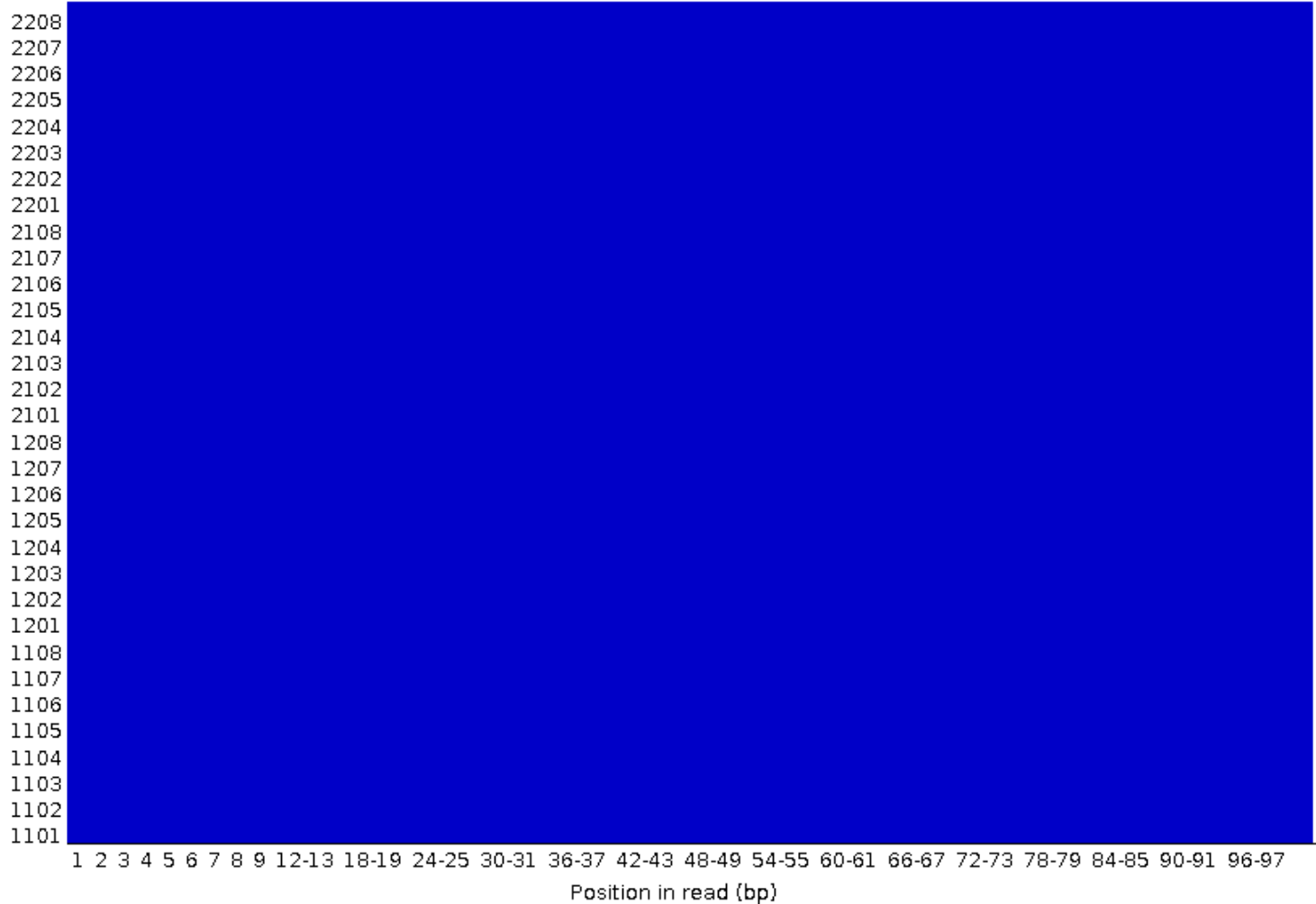
Quality scores across all bases (Sanger / Illumina 1.9 encoding)





## Per tile sequence quality

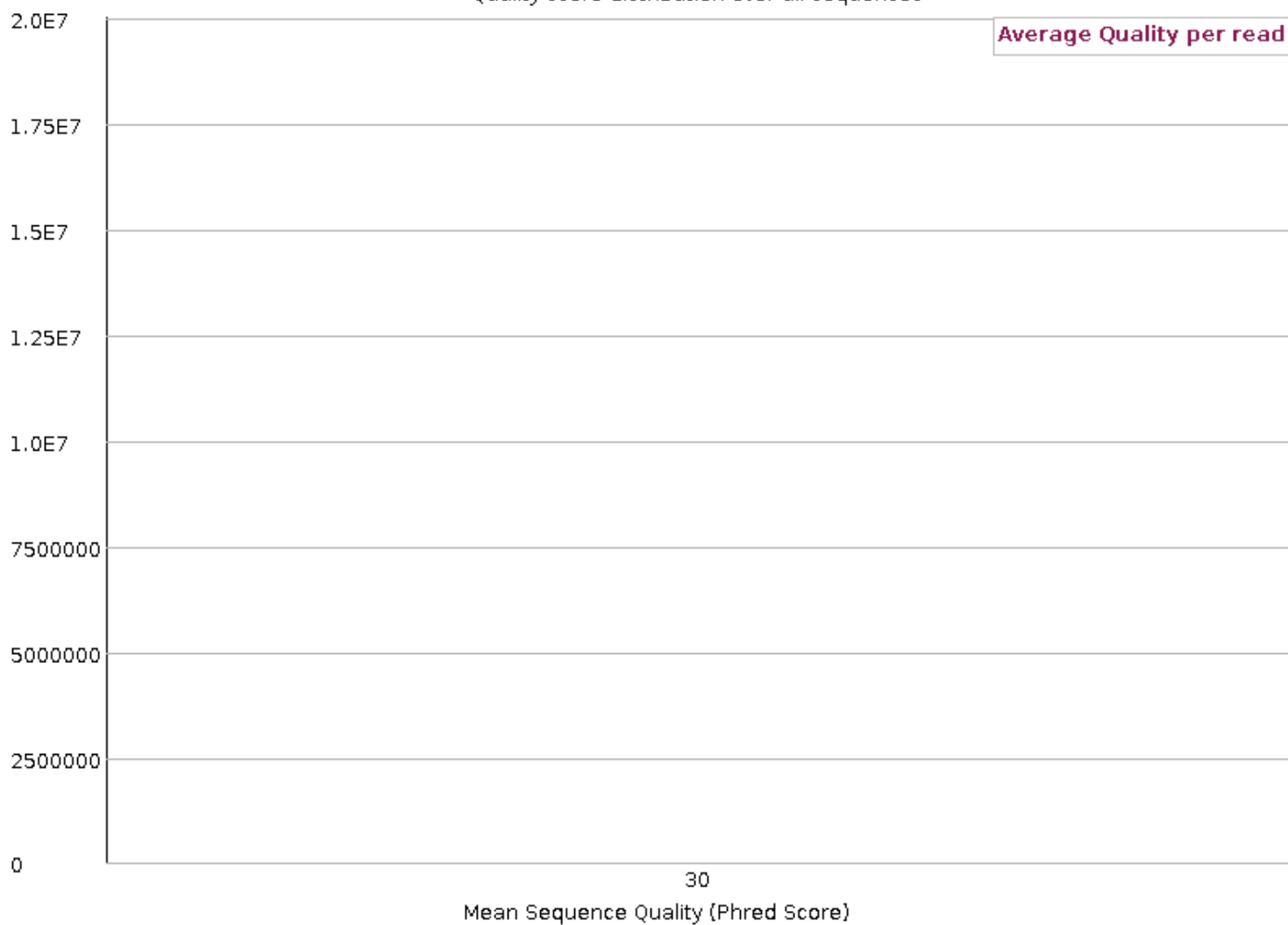
Quality per tile





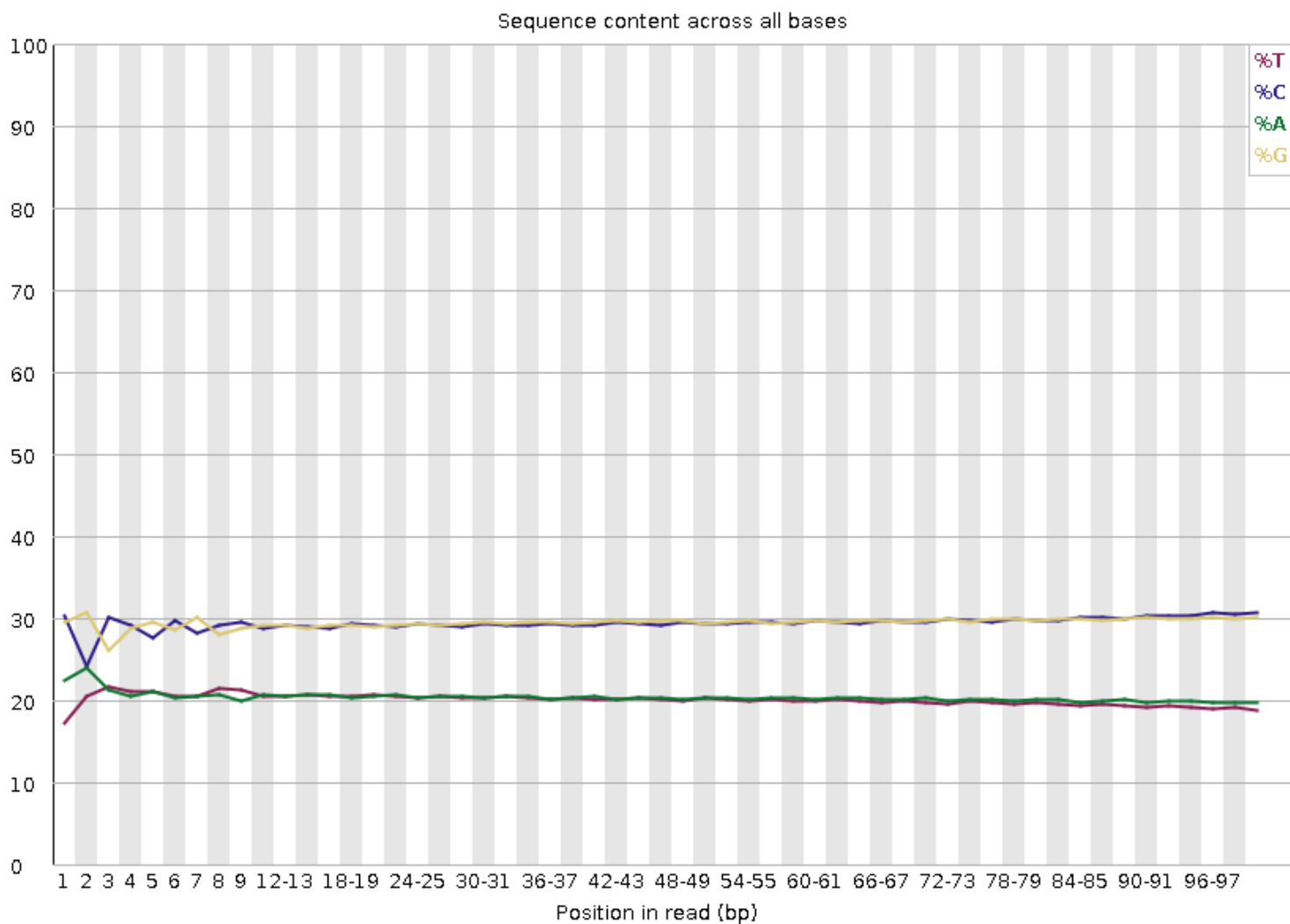
## Per sequence quality scores

Quality score distribution over all sequences



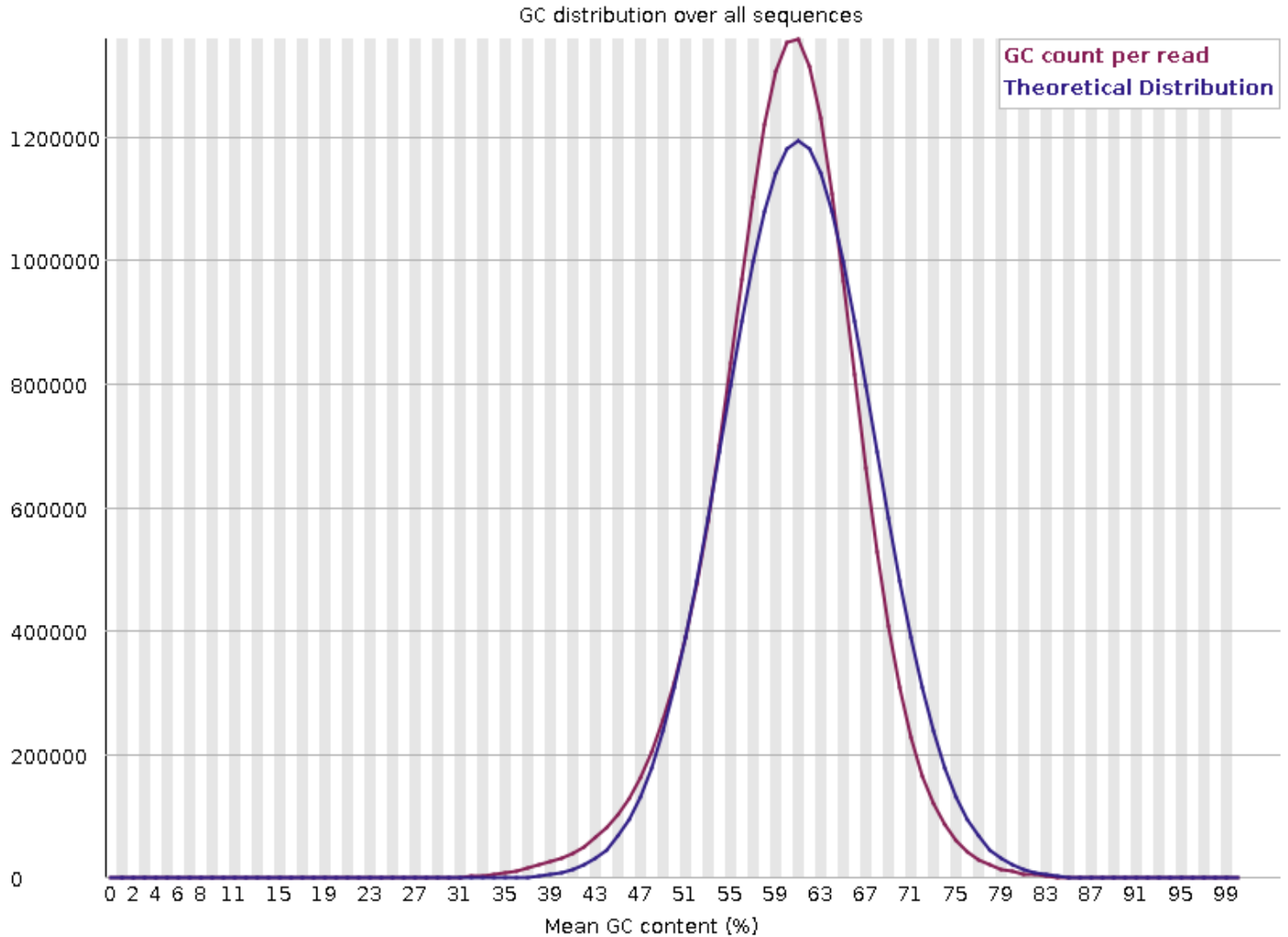


## Per base sequence content





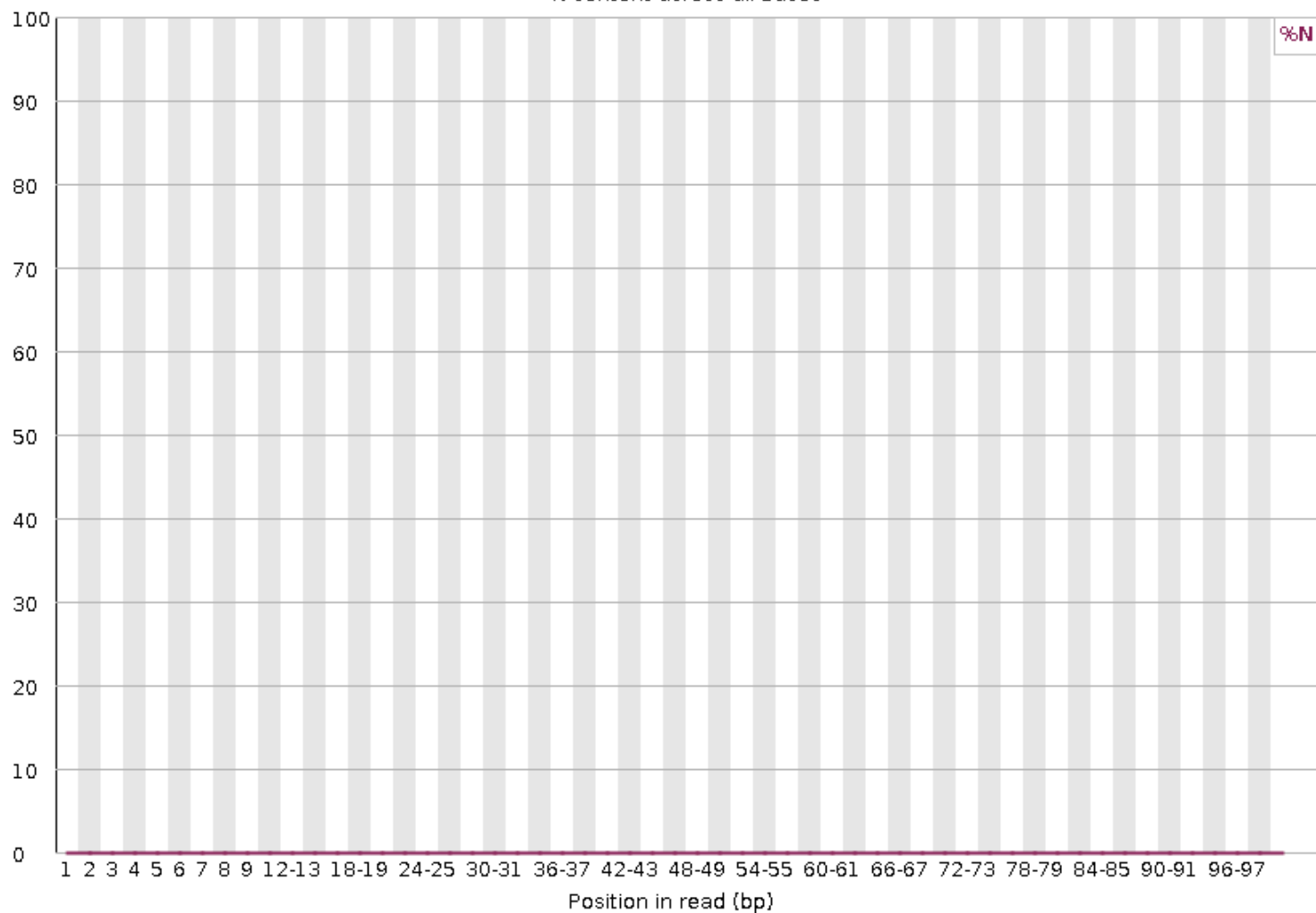
## Per sequence GC content





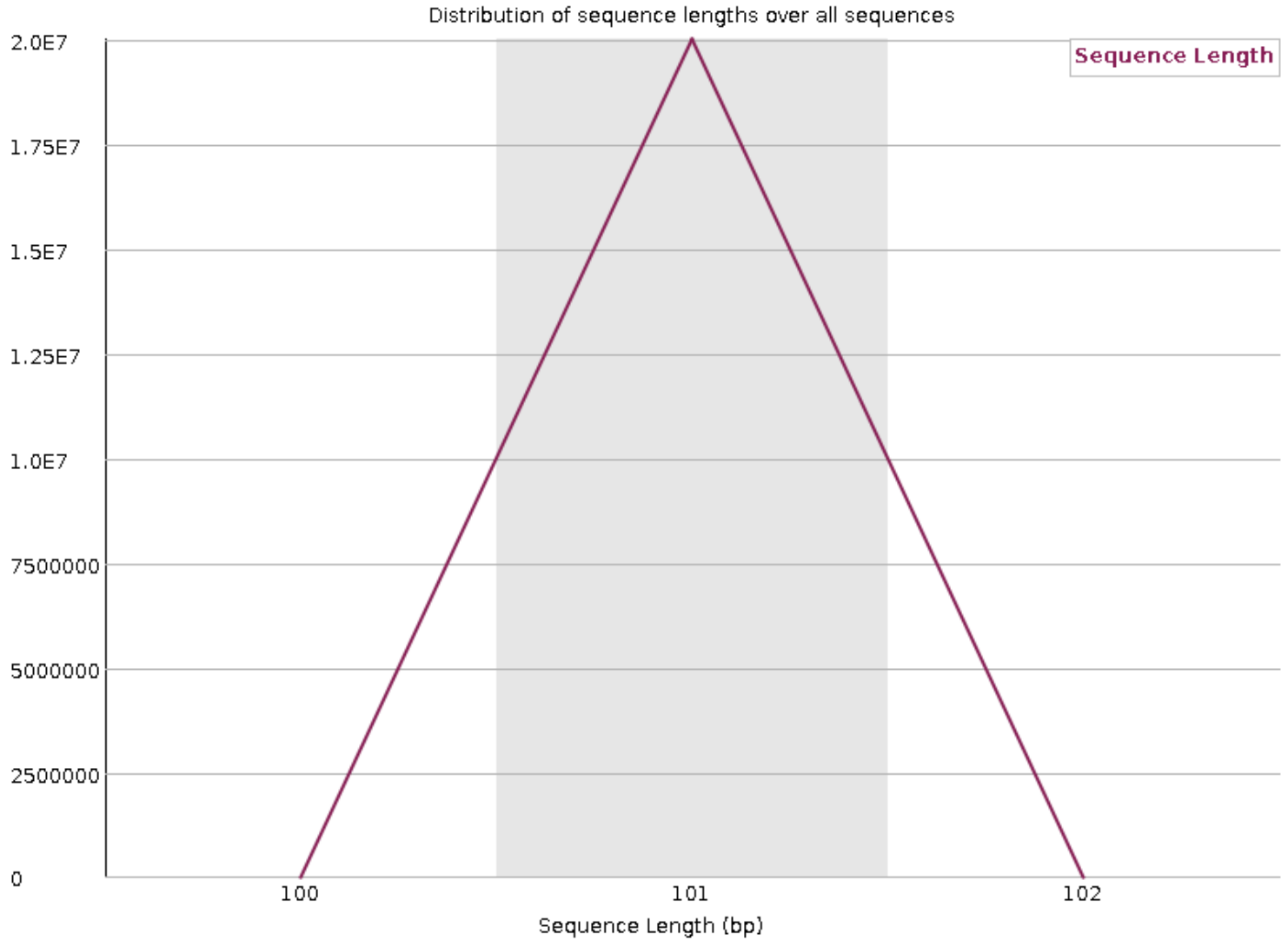
## Per base N content

N content across all bases



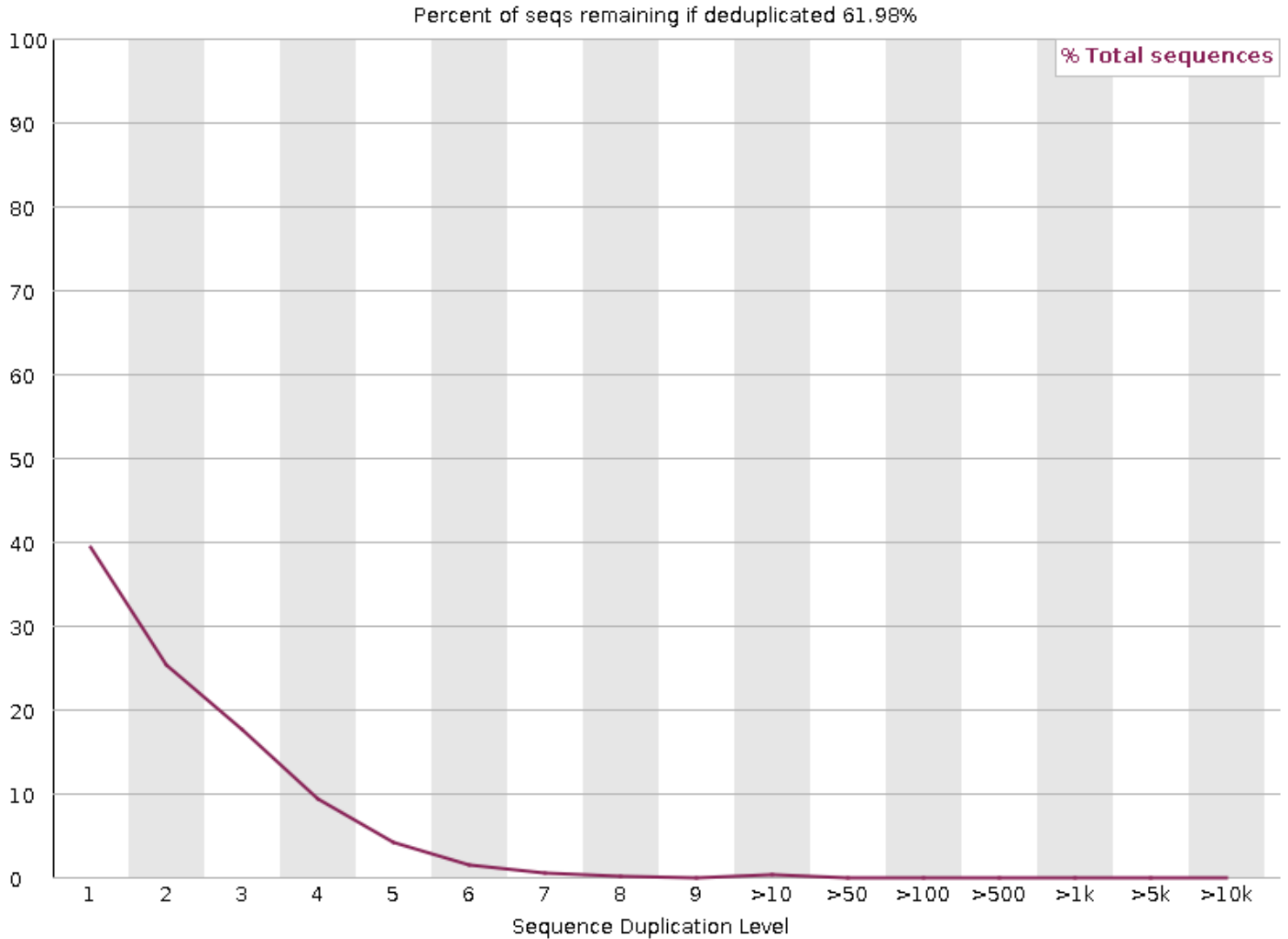


## Sequence Length Distribution





## ! Sequence Duplication Levels

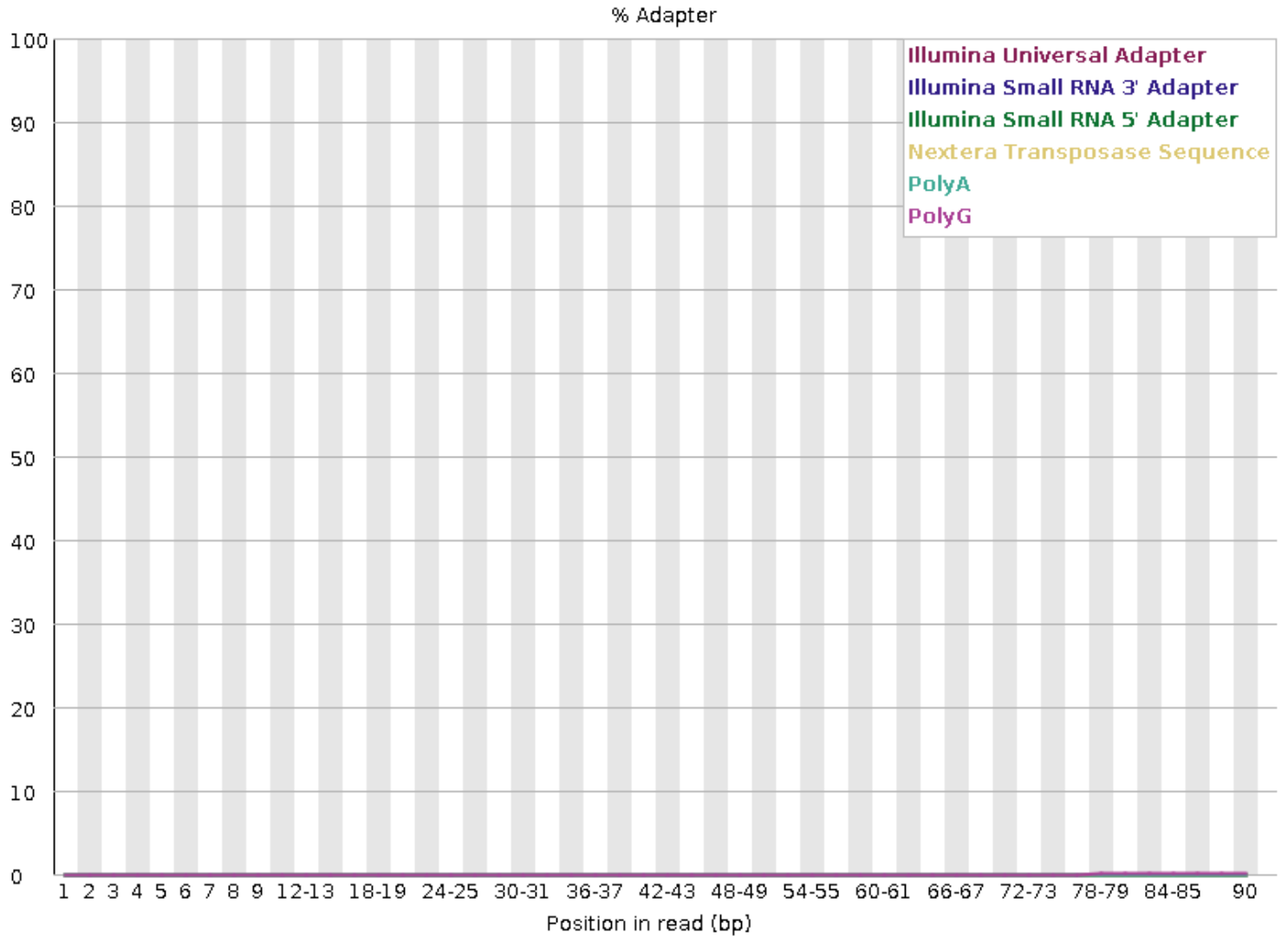


## ✓ Overrepresented sequences

No overrepresented sequences



## Adapter Content



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