












FastQC Report

Summary

Wed 5 Nov 2025
SRR398262_1_trim.fastq.gz

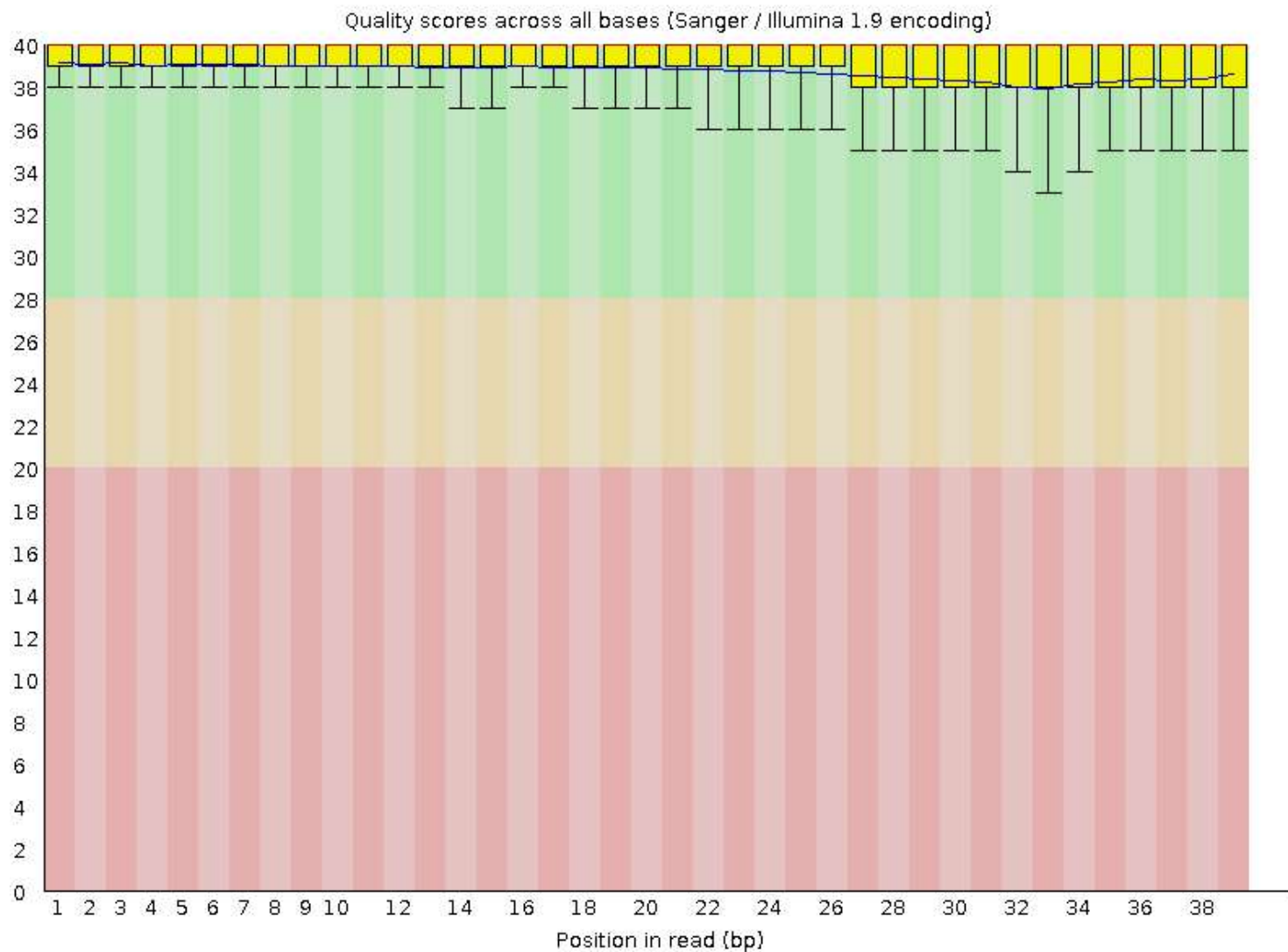
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Basic Statistics

Measure	Value
Filename	SRR398262_1_trim.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	19018965
Total Bases	728.3 Mbp
Sequences flagged as poor quality	0
Sequence length	20-39
%GC	46

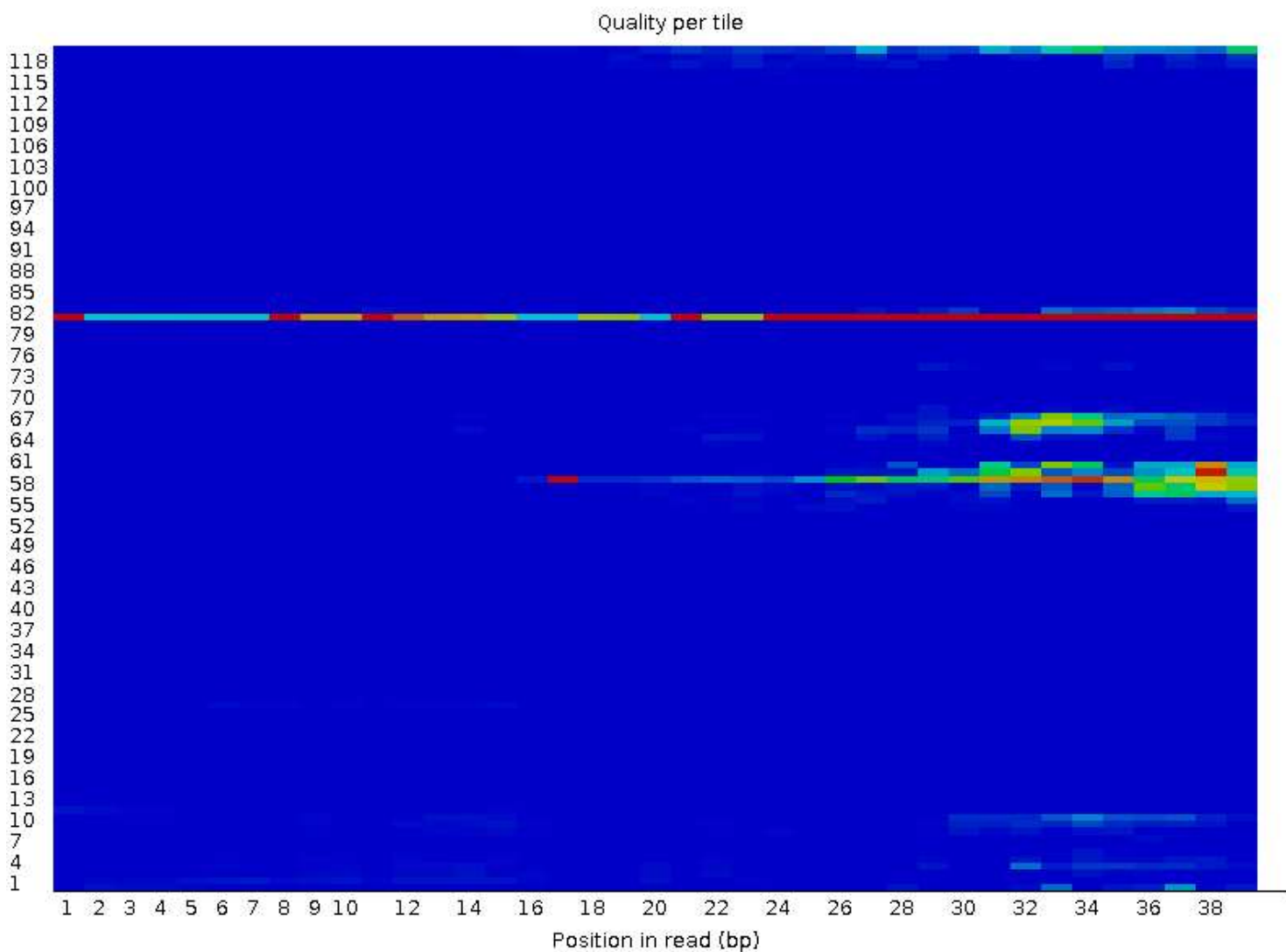


Per base sequence quality



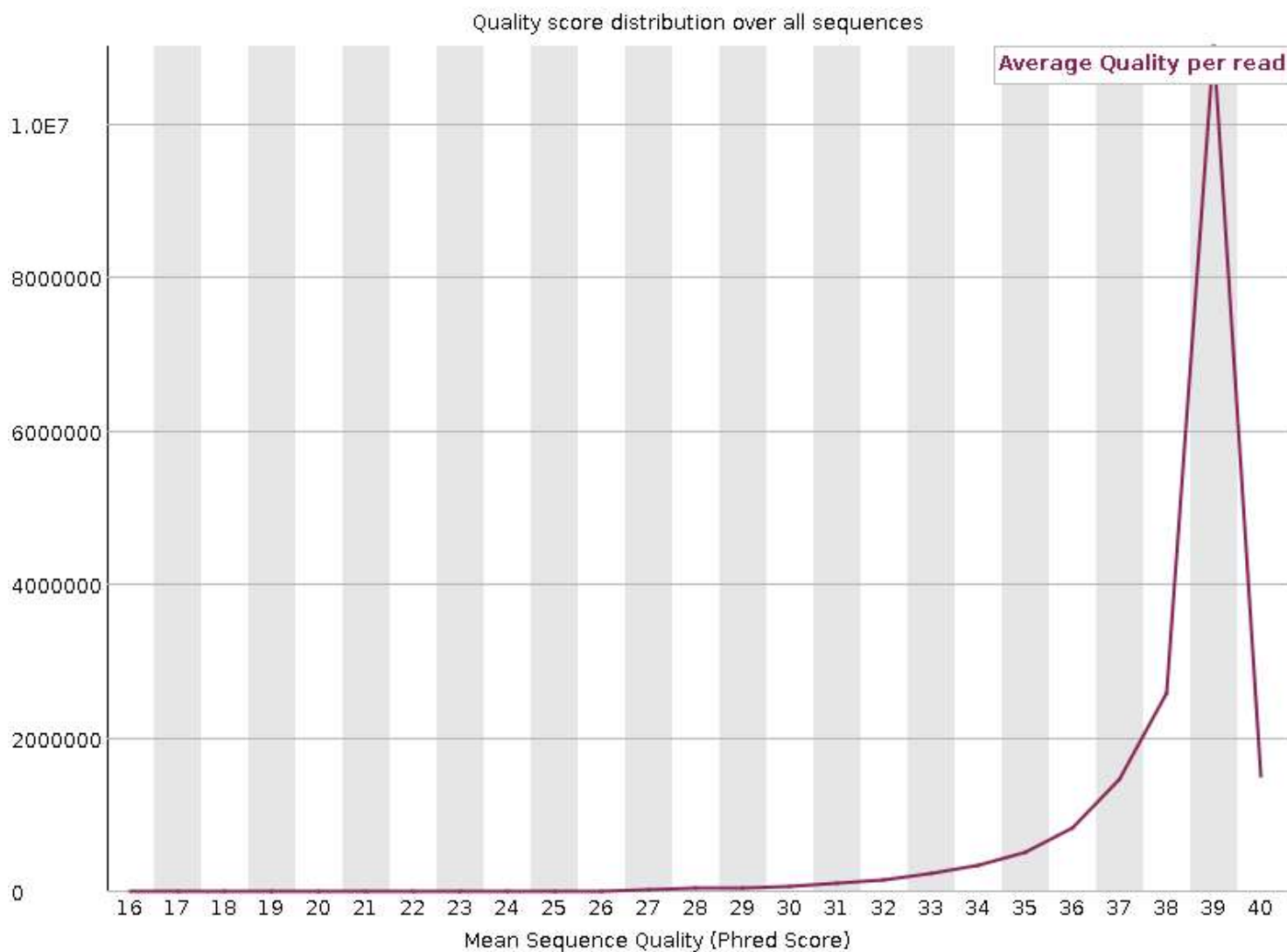


Per tile sequence quality



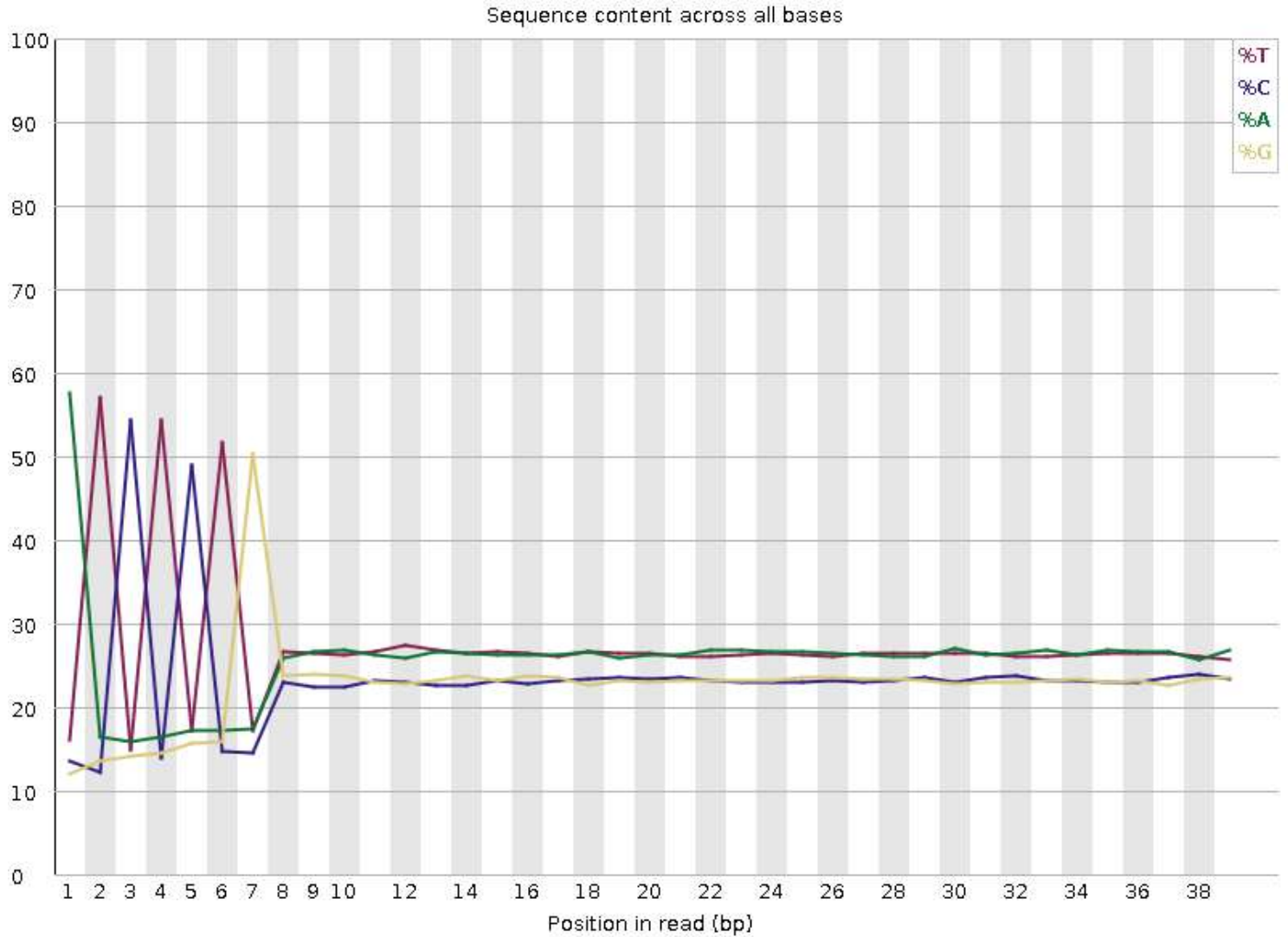


Per sequence quality scores



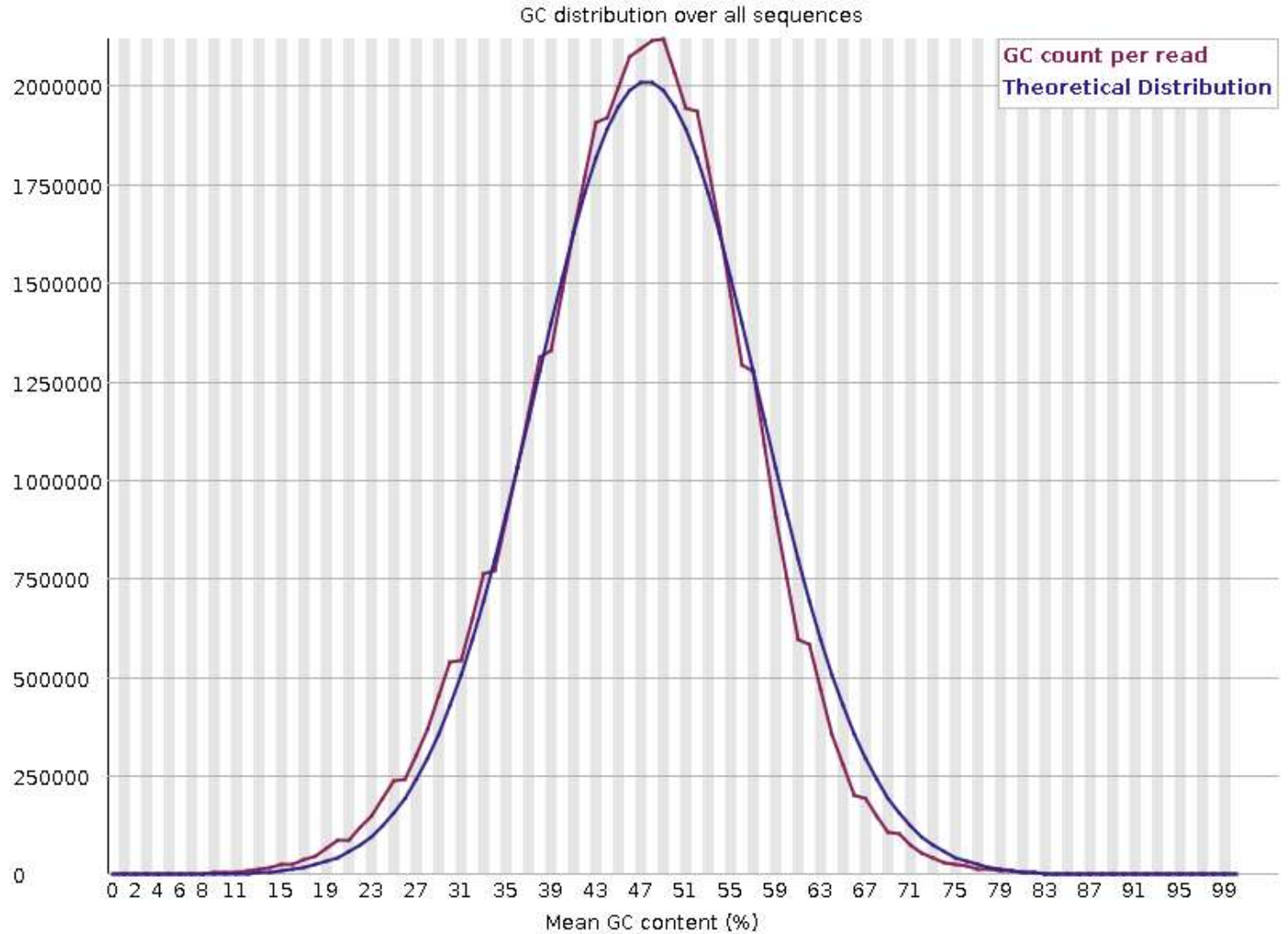


Per base sequence content



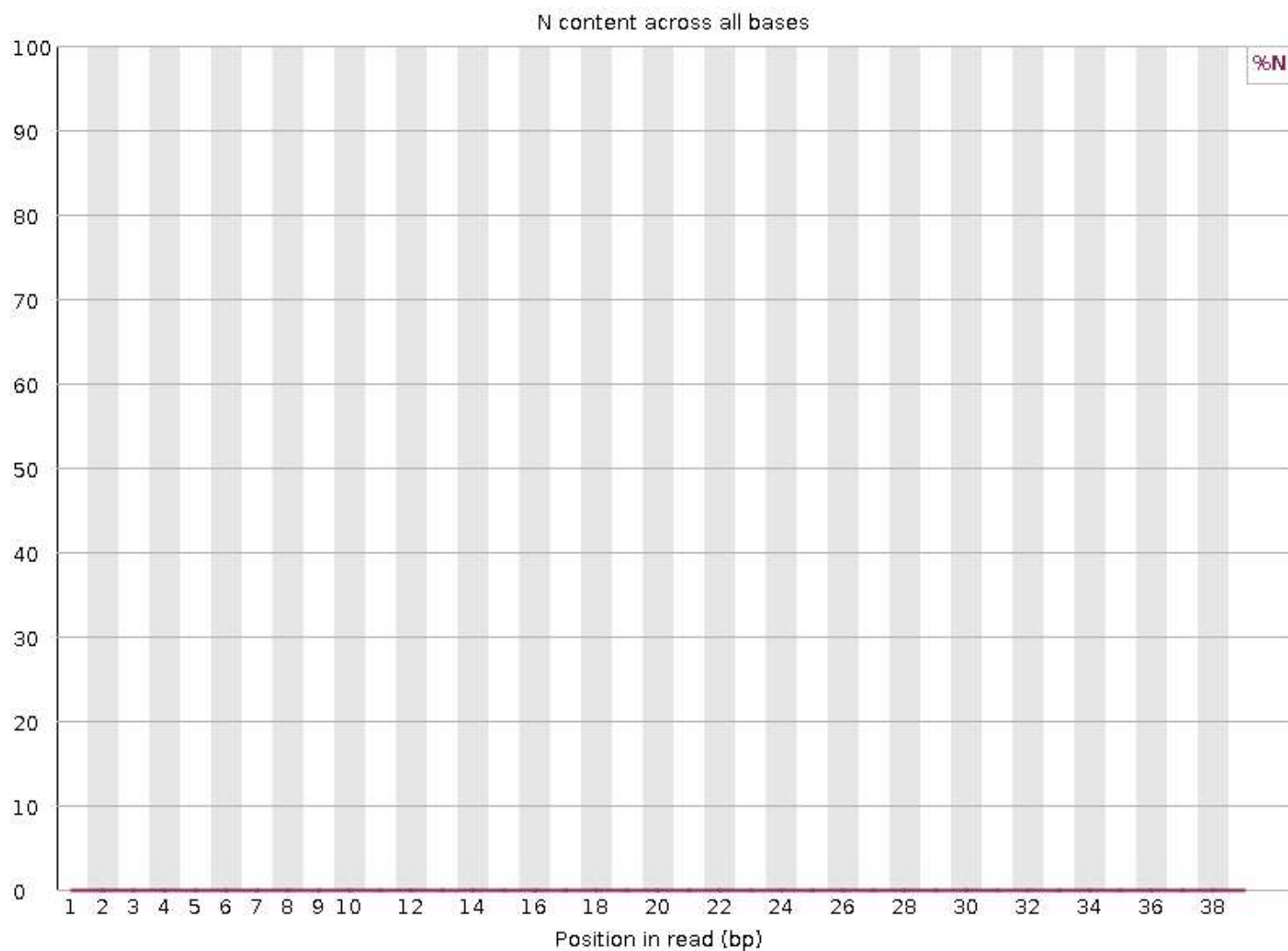


Per sequence GC content

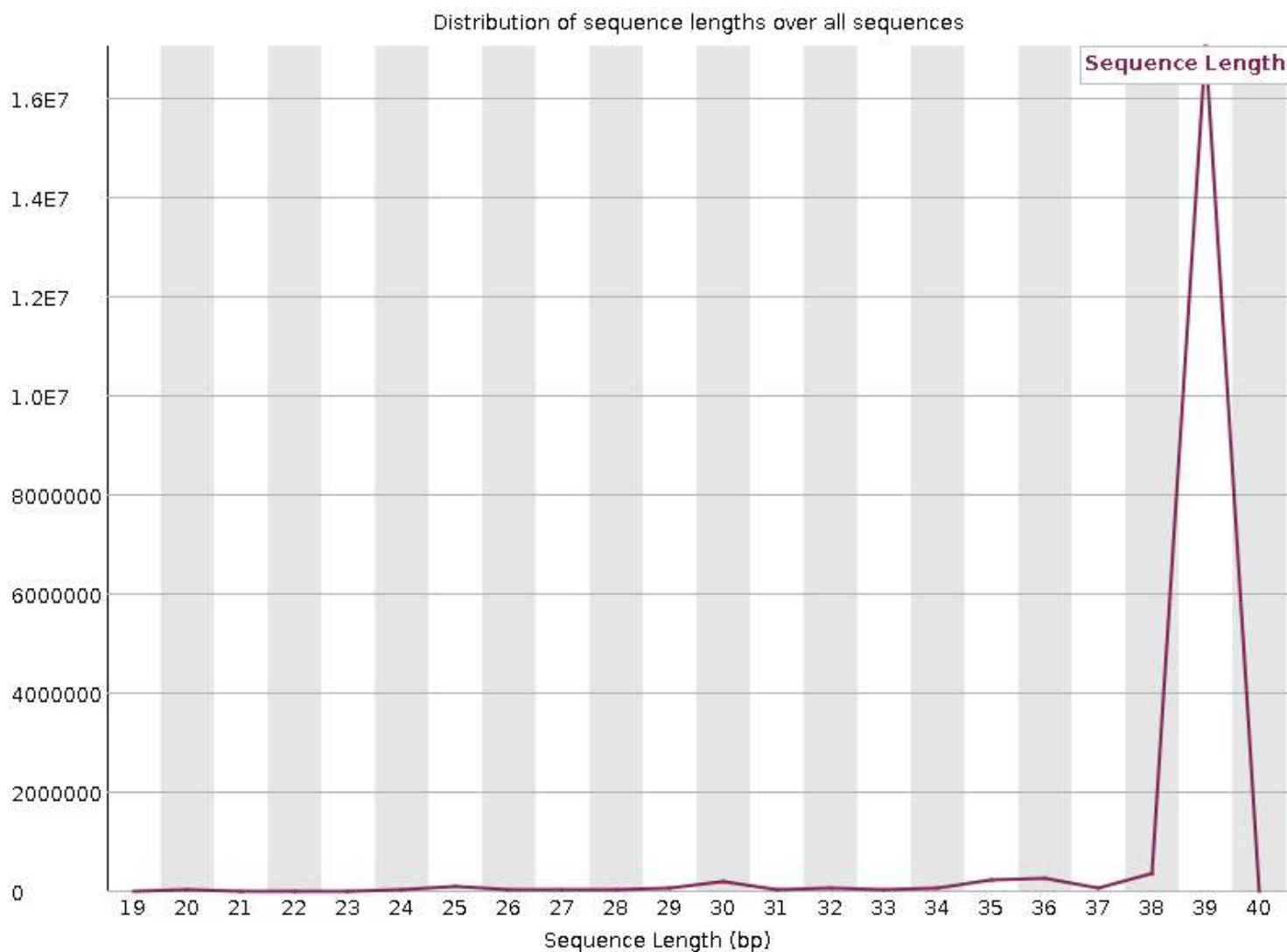




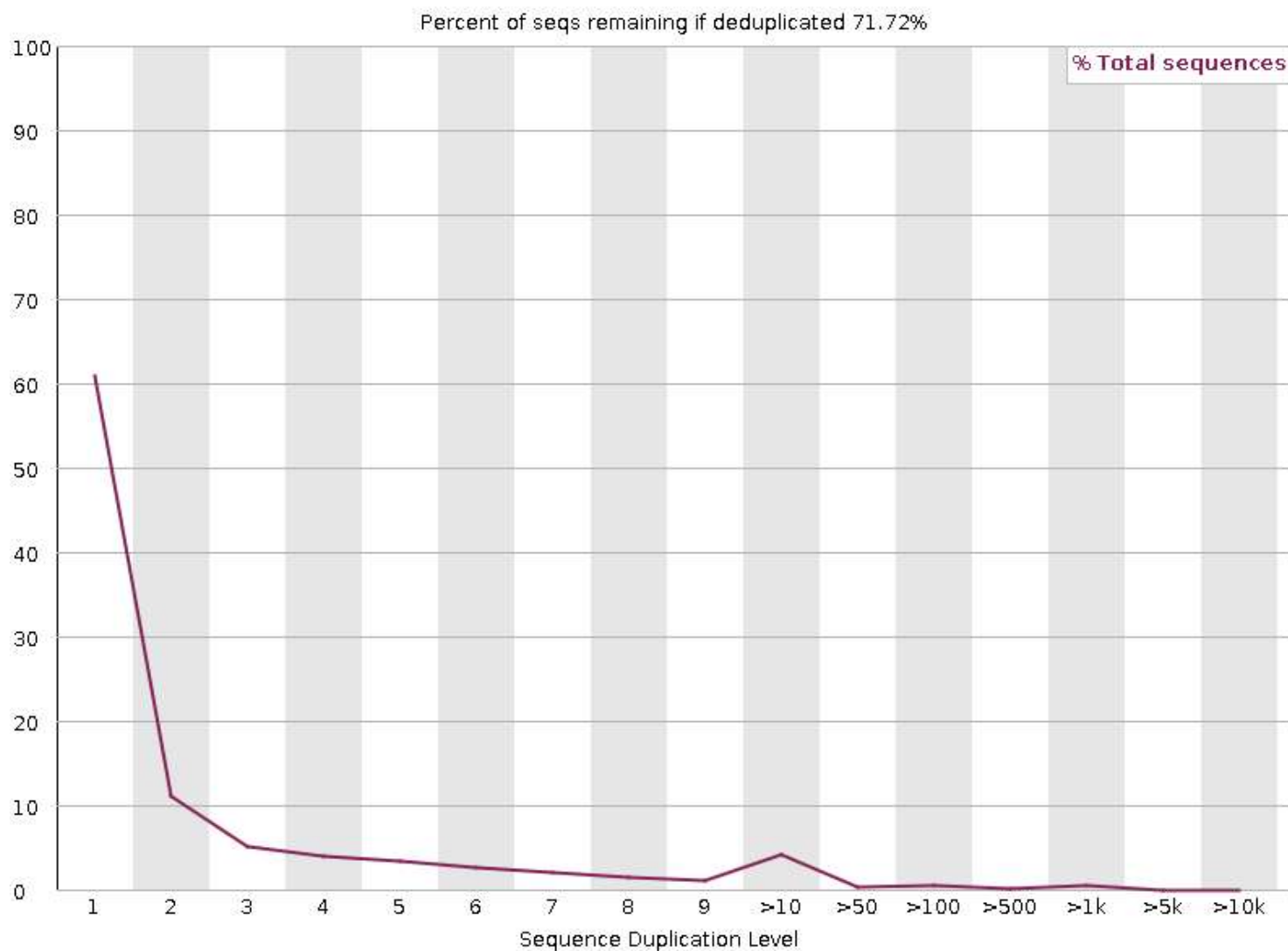
Per base N content



! Sequence Length Distribution



Sequence Duplication Levels

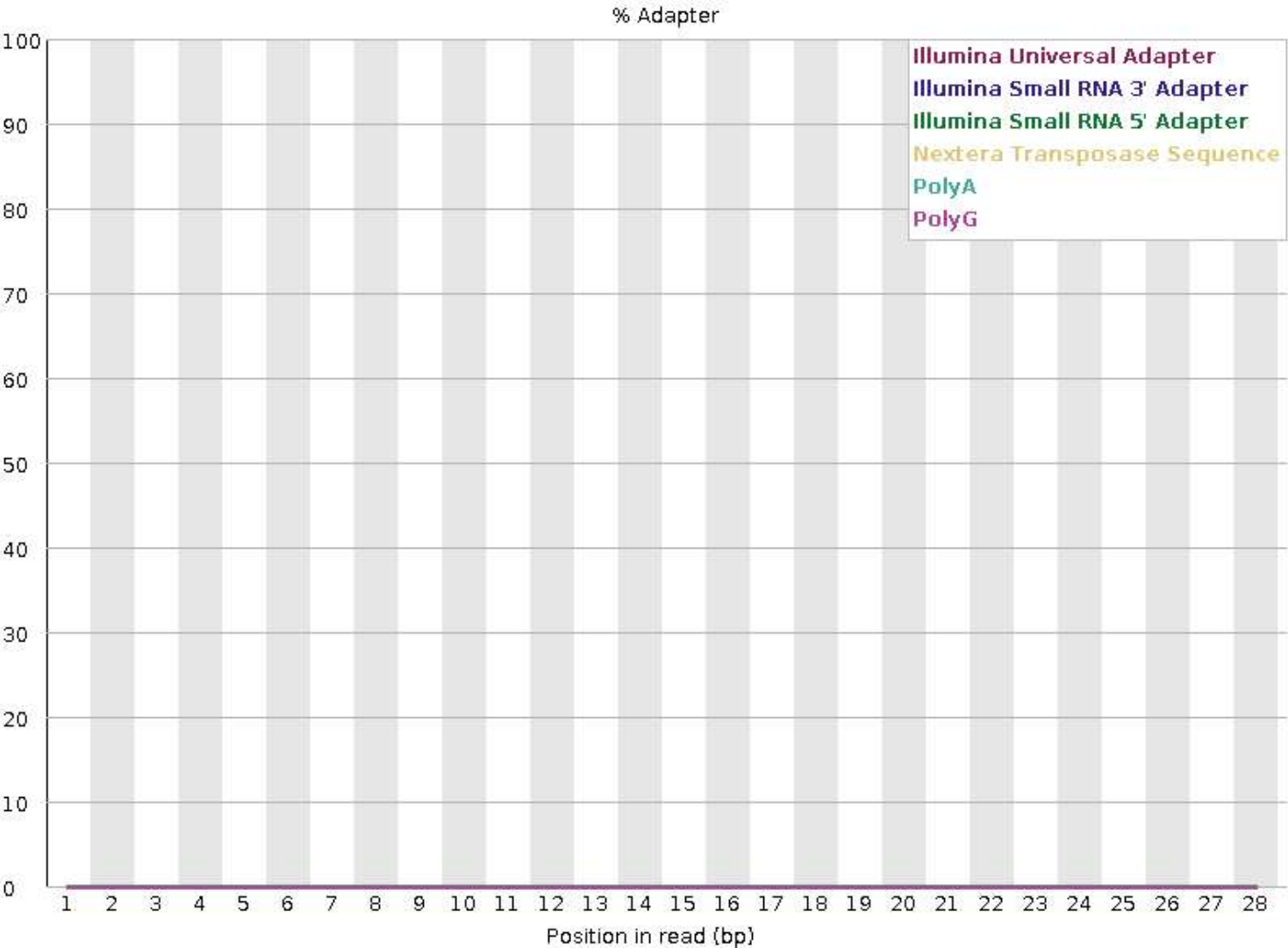


Overrepresented sequences

No overrepresented sequences



Adapter Content



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