

Wed 5 Nov 2025
SRR398262_1_trim.fastq.gz

FastQC Report

Summary

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Basic Statistics

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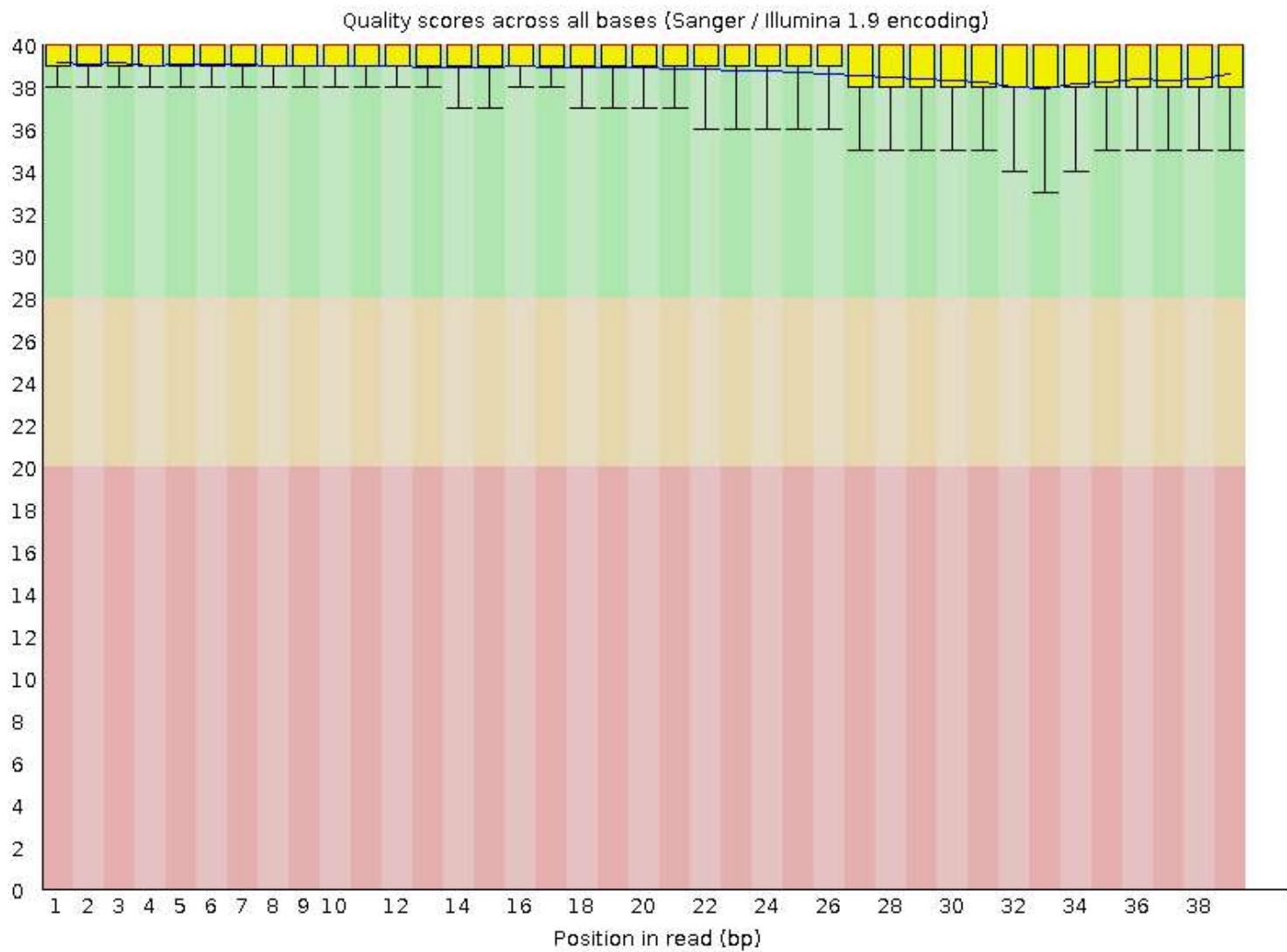
Sequences flagged as poor quality	0
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Sequence length	20-39
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%GC	46
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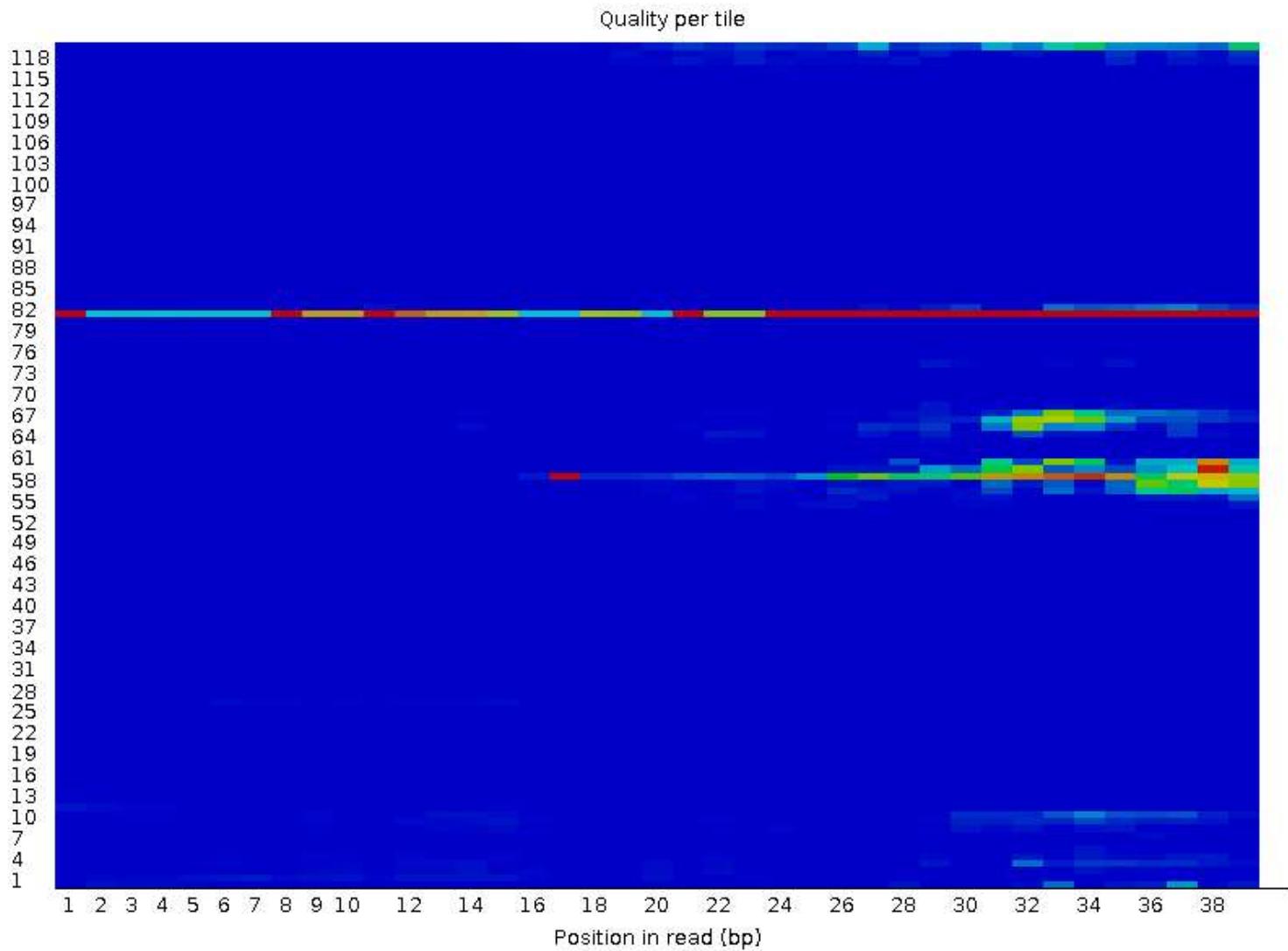


Per base sequence quality



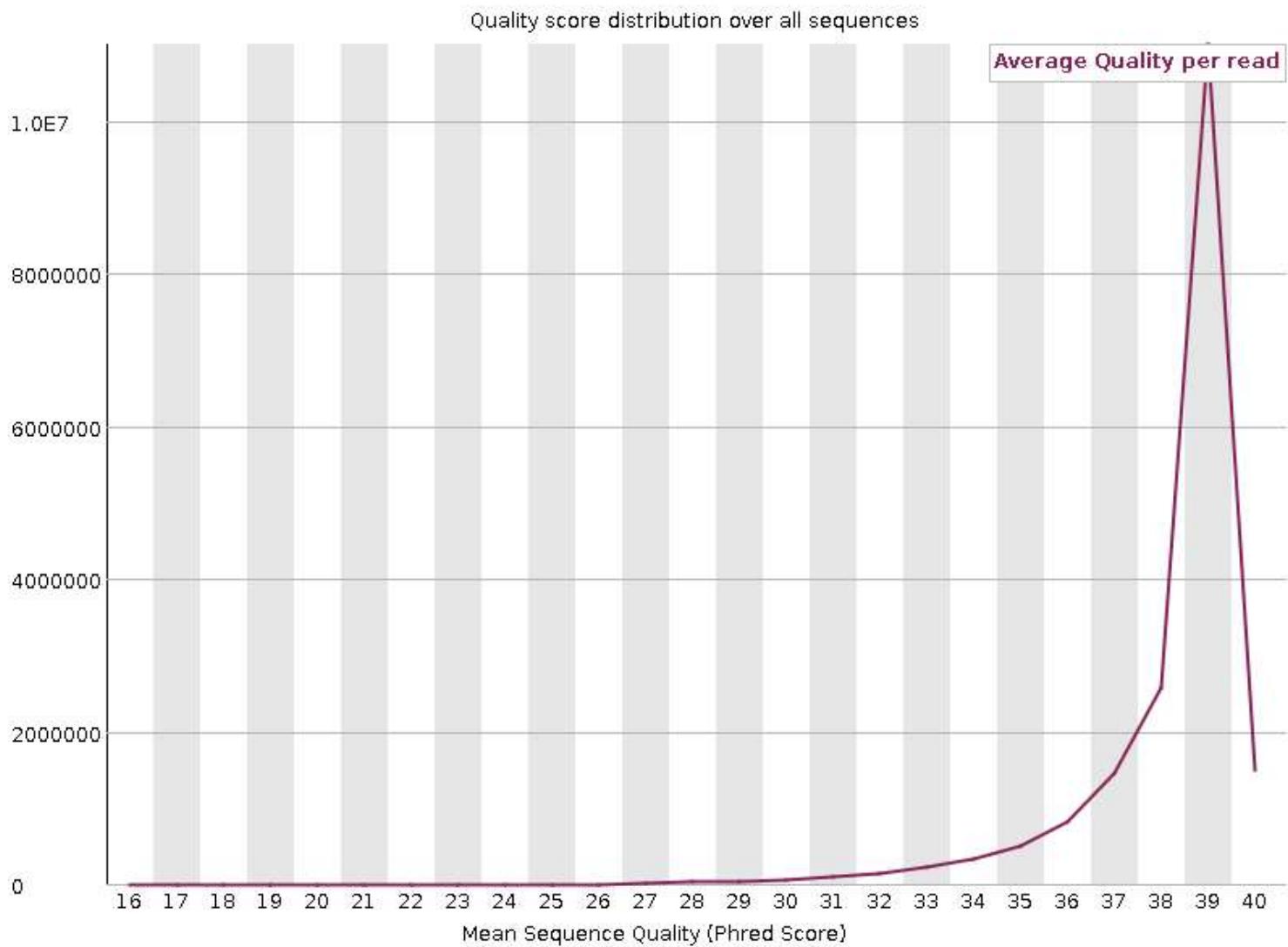


Per tile sequence quality



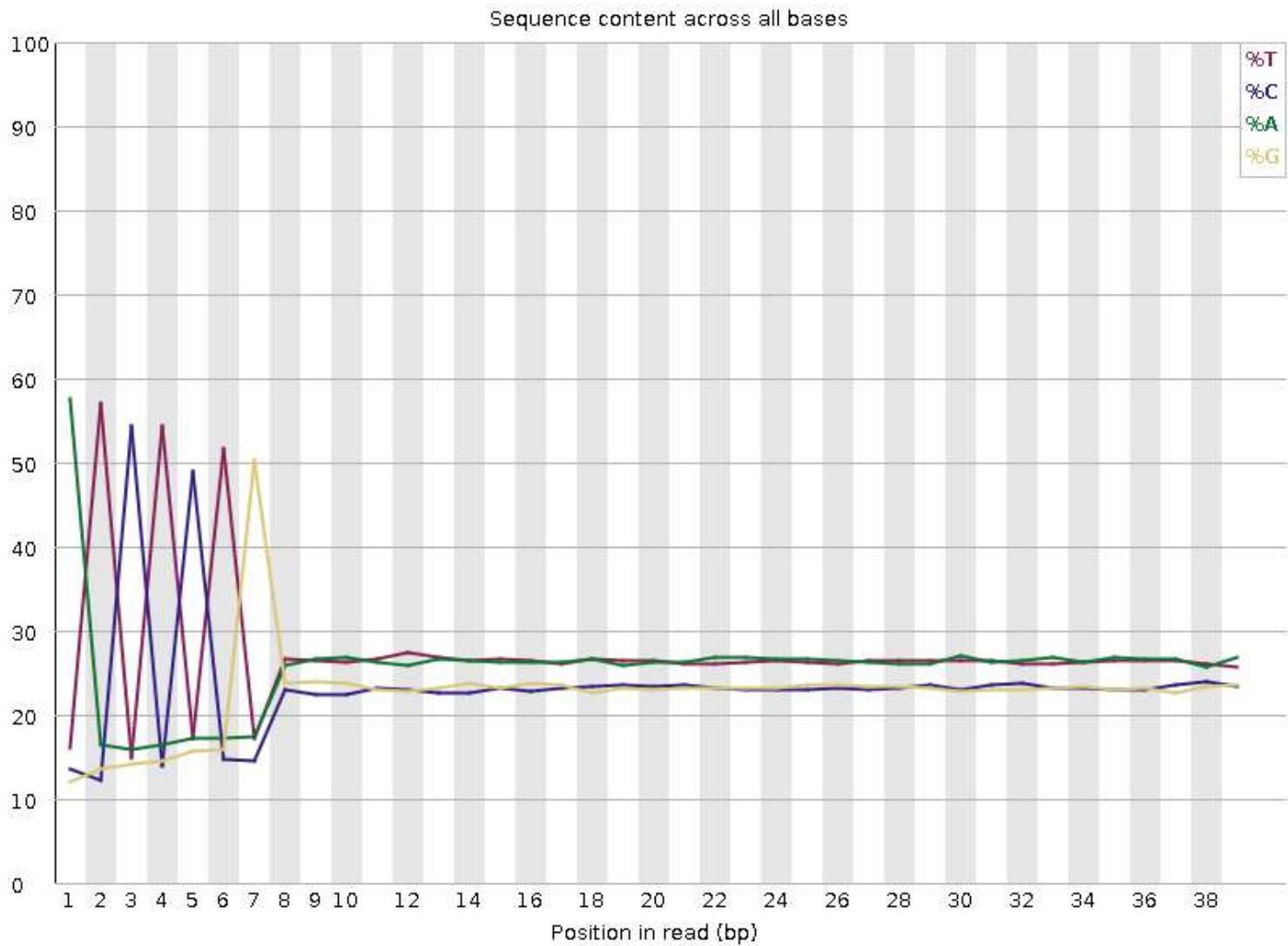


Per sequence quality scores



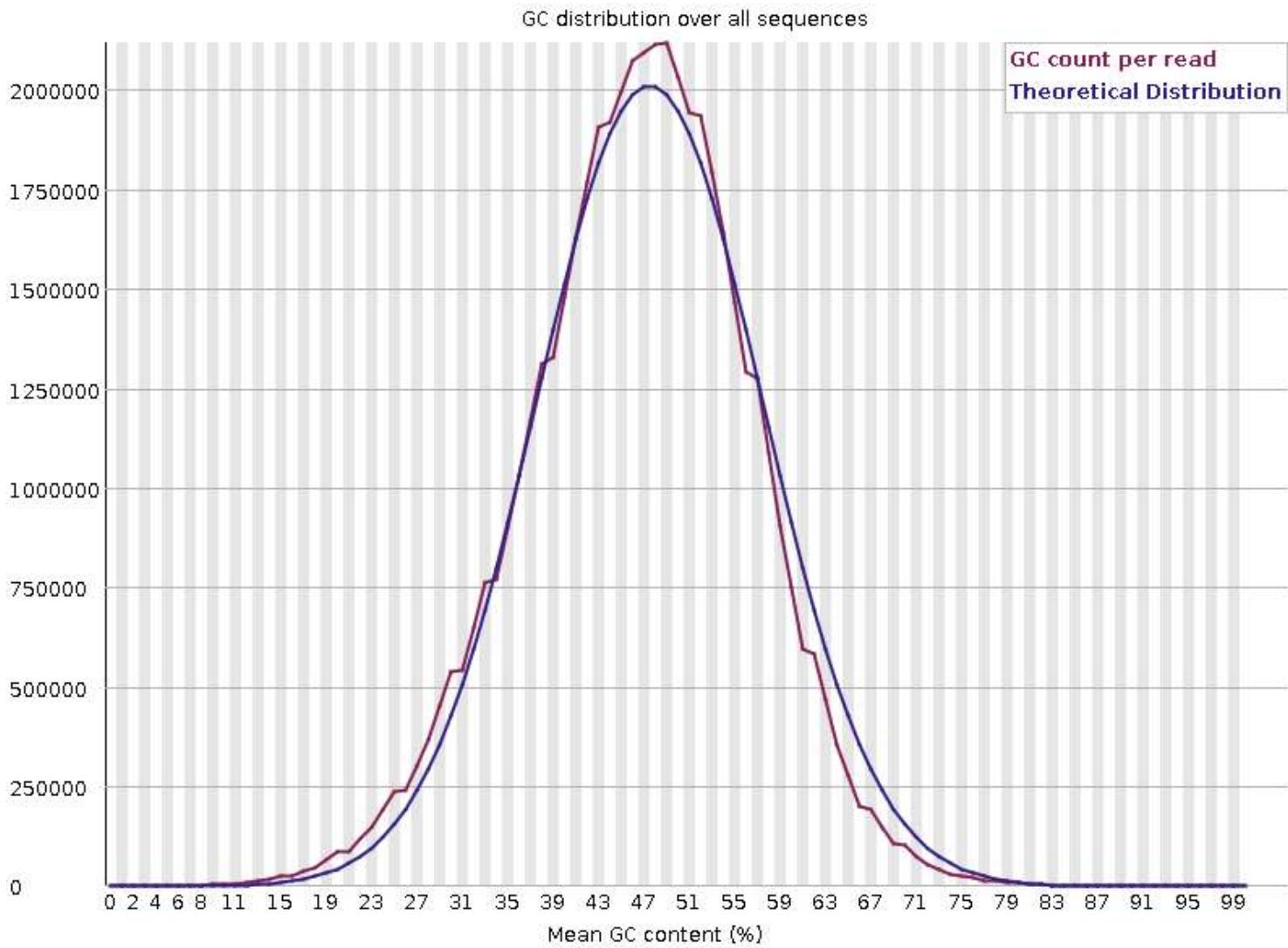


Per base sequence content



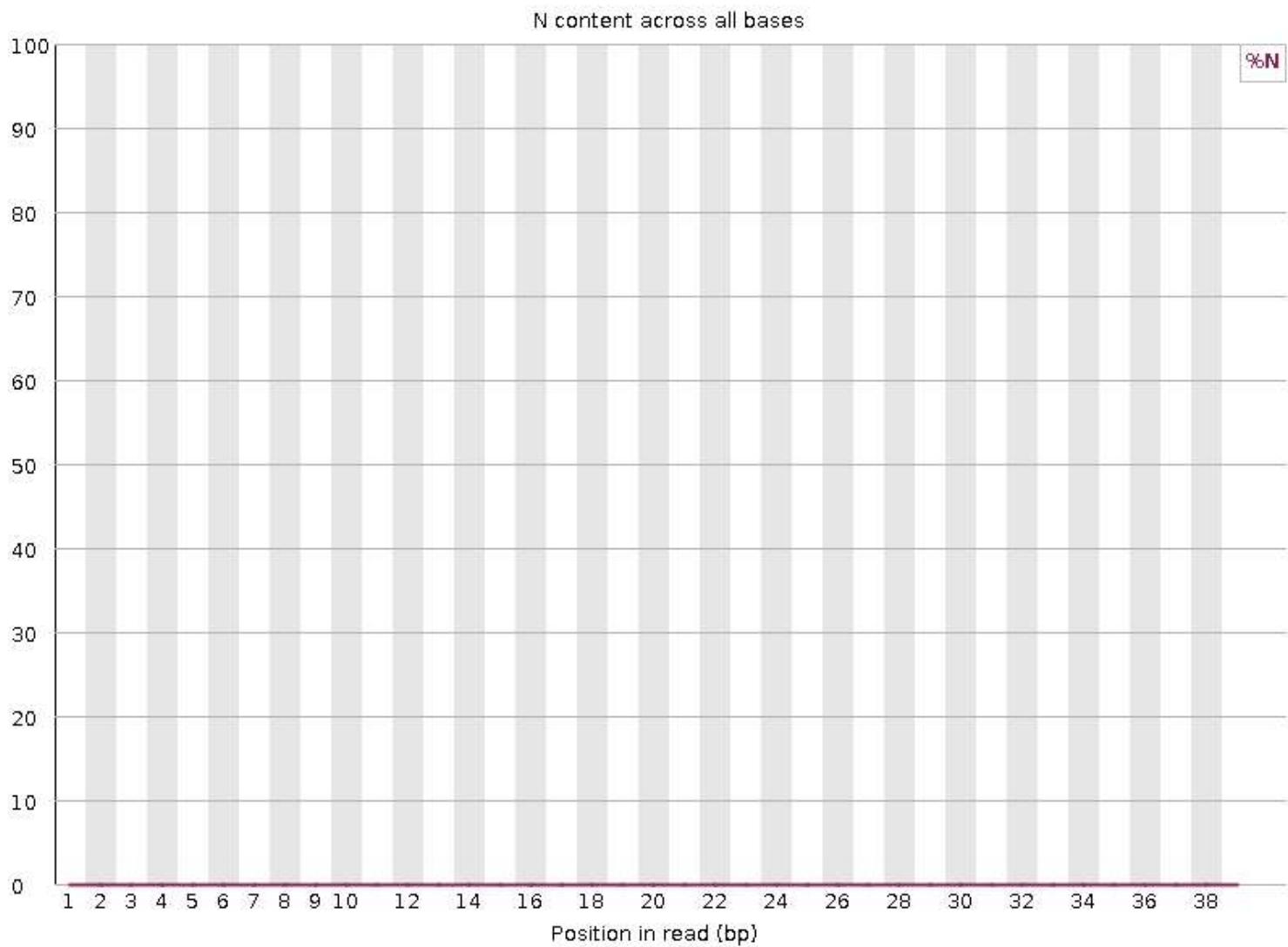


Per sequence GC content



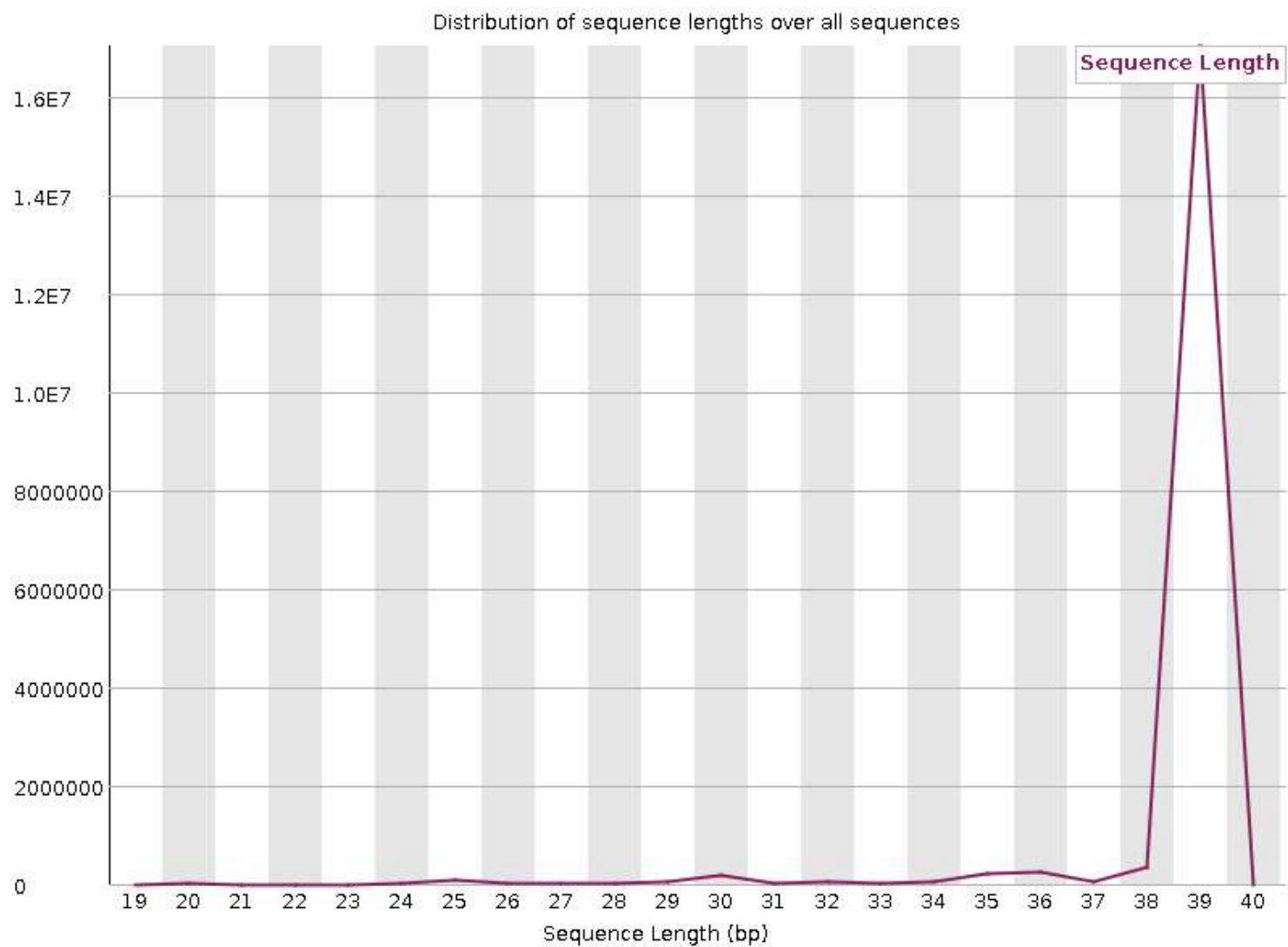


Per base N content





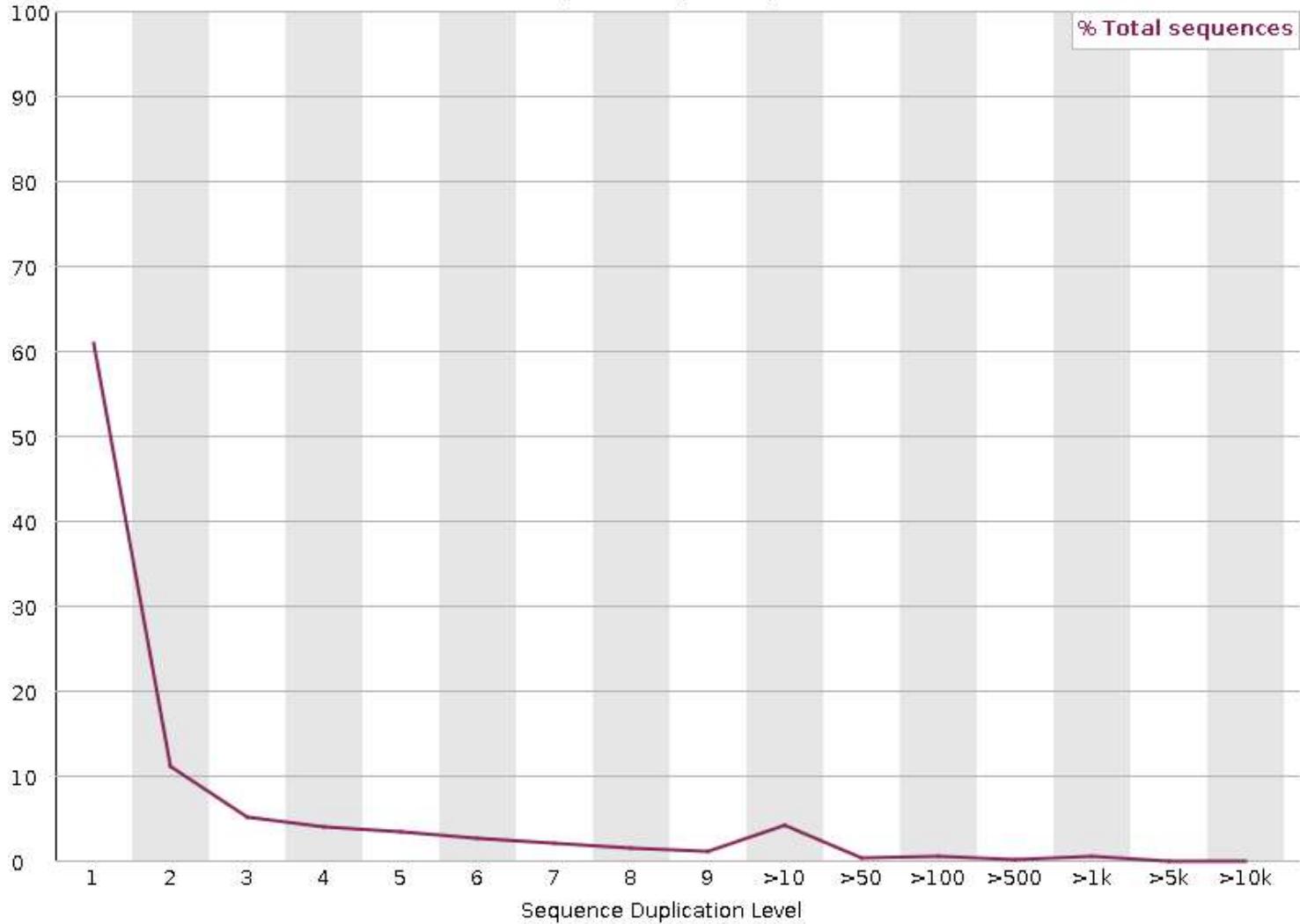
Sequence Length Distribution





Sequence Duplication Levels

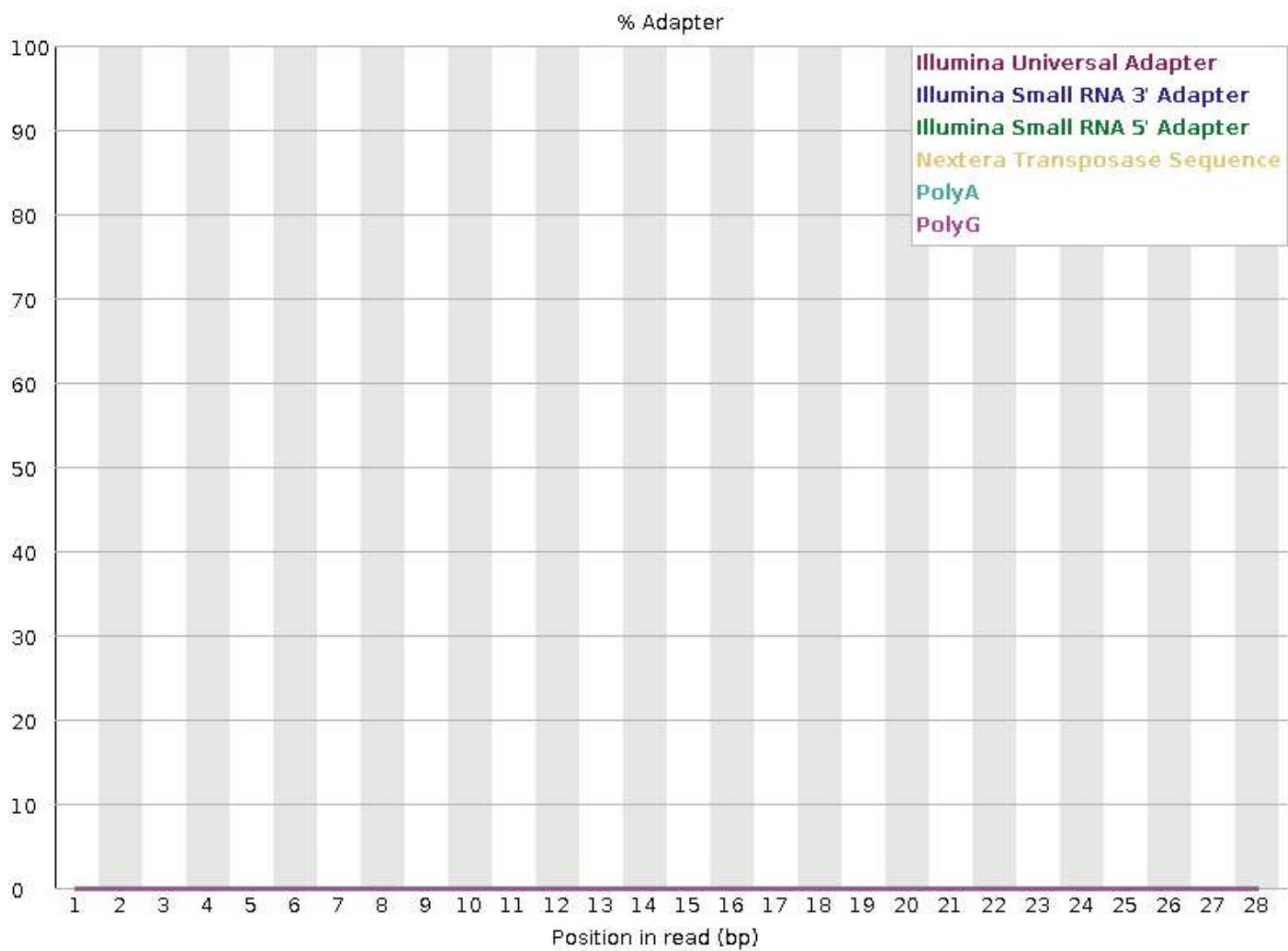
Percent of seqs remaining if deduplicated 71.72%



Overrepresented sequences

No overrepresented sequences

Adapter Content



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