

Wed 5 Nov 2025
SRR396786_1_trim.fastq.gz

FastQC Report

Summary

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Basic Statistics

Measure	Value
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Filename	SRR396786_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	10268186
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Total Bases	362.3 Mbp
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Sequences flagged as poor quality	0
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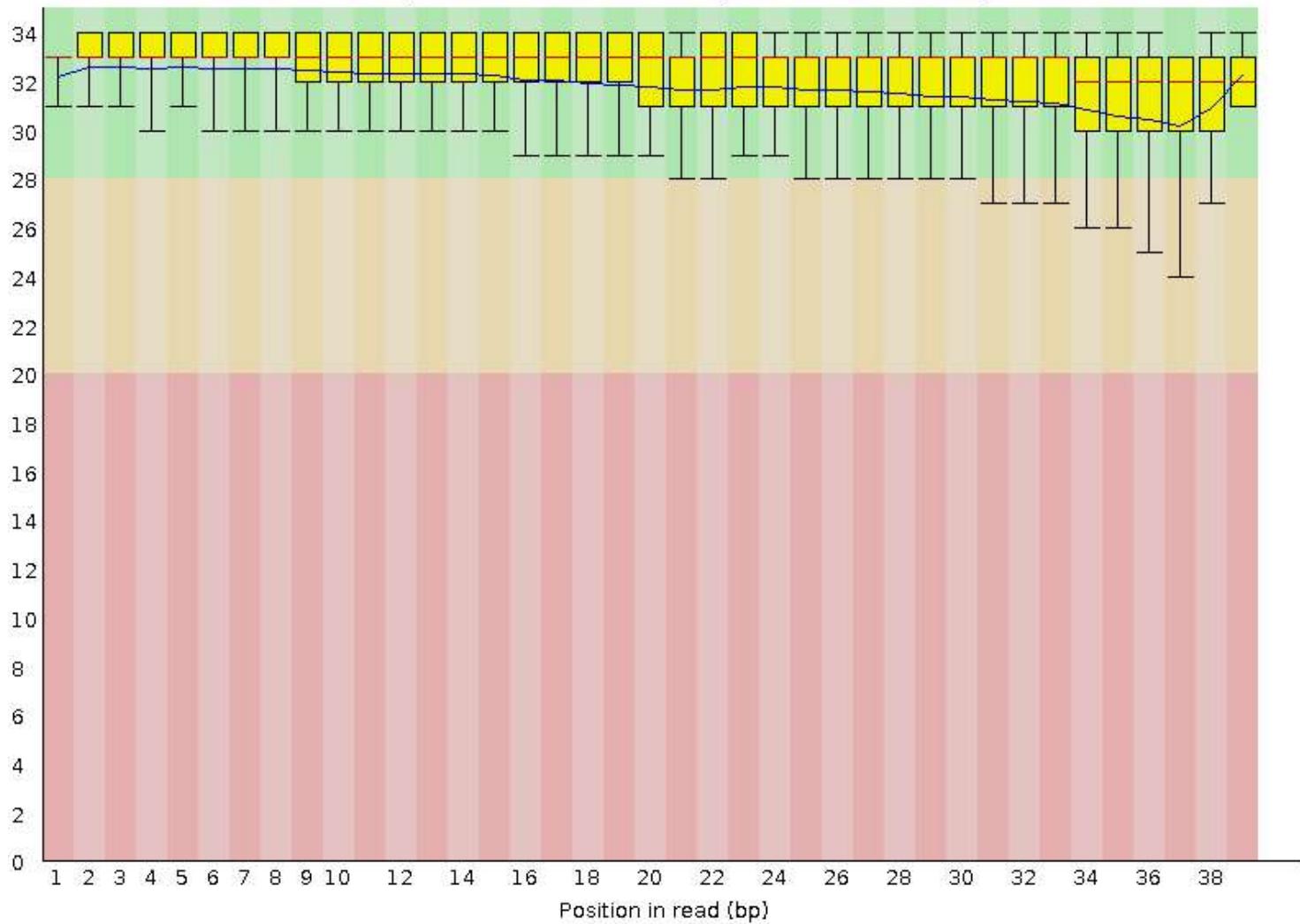
Sequence length	20-39
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%GC	48
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Per base sequence quality

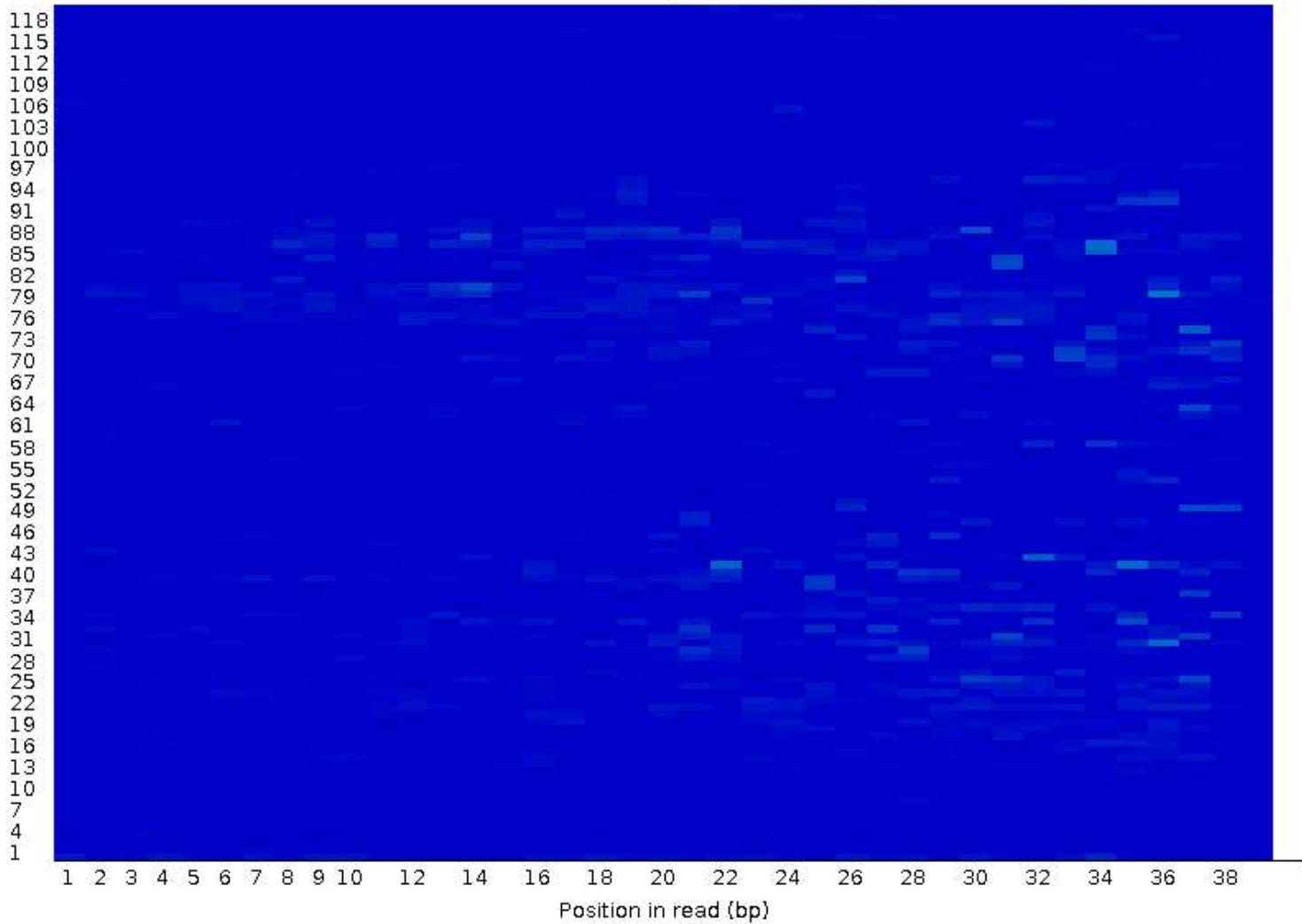
Quality scores across all bases (Sanger / Illumina 1.9 encoding)





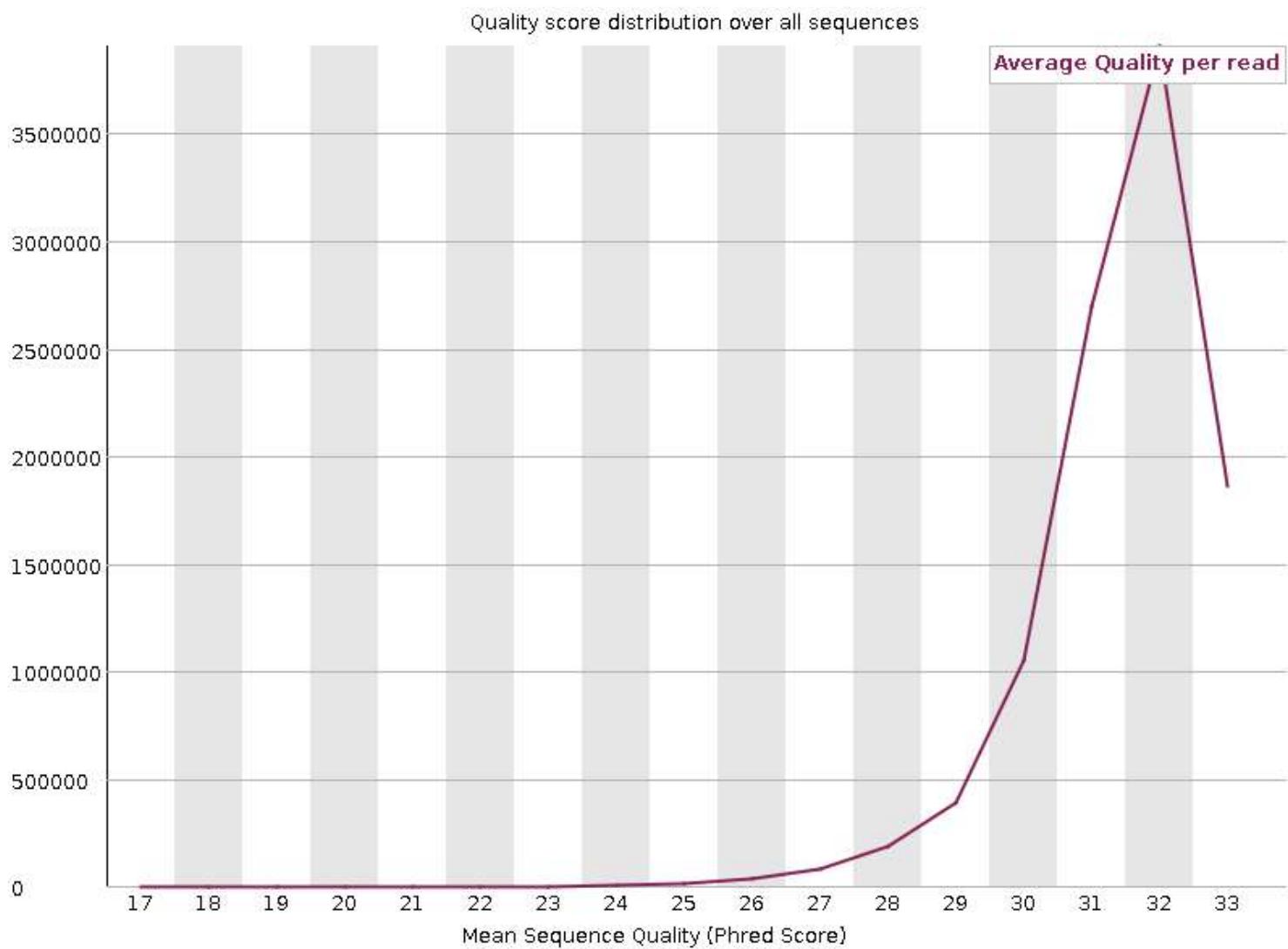
Per tile sequence quality

Quality per tile



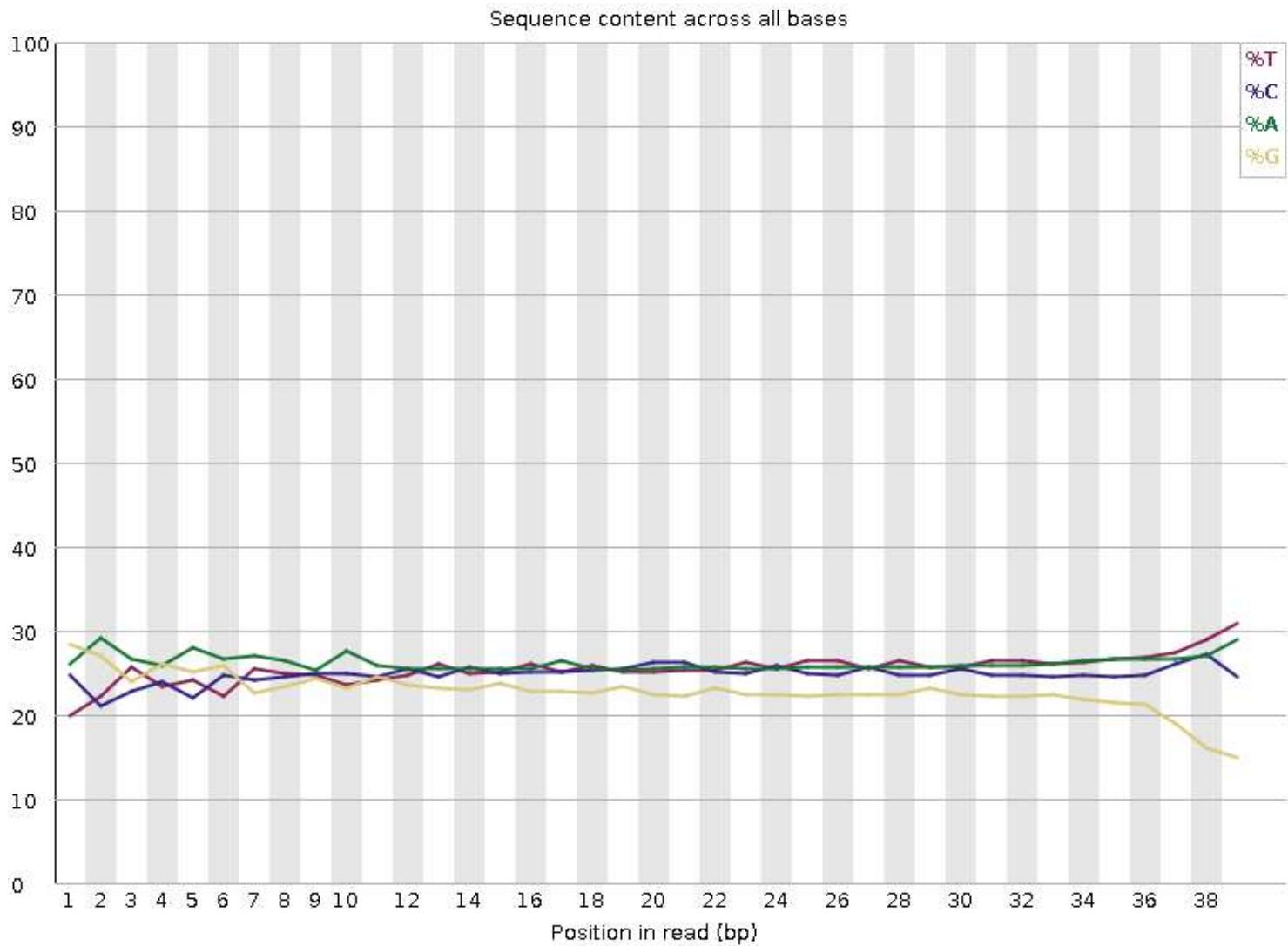


Per sequence quality scores



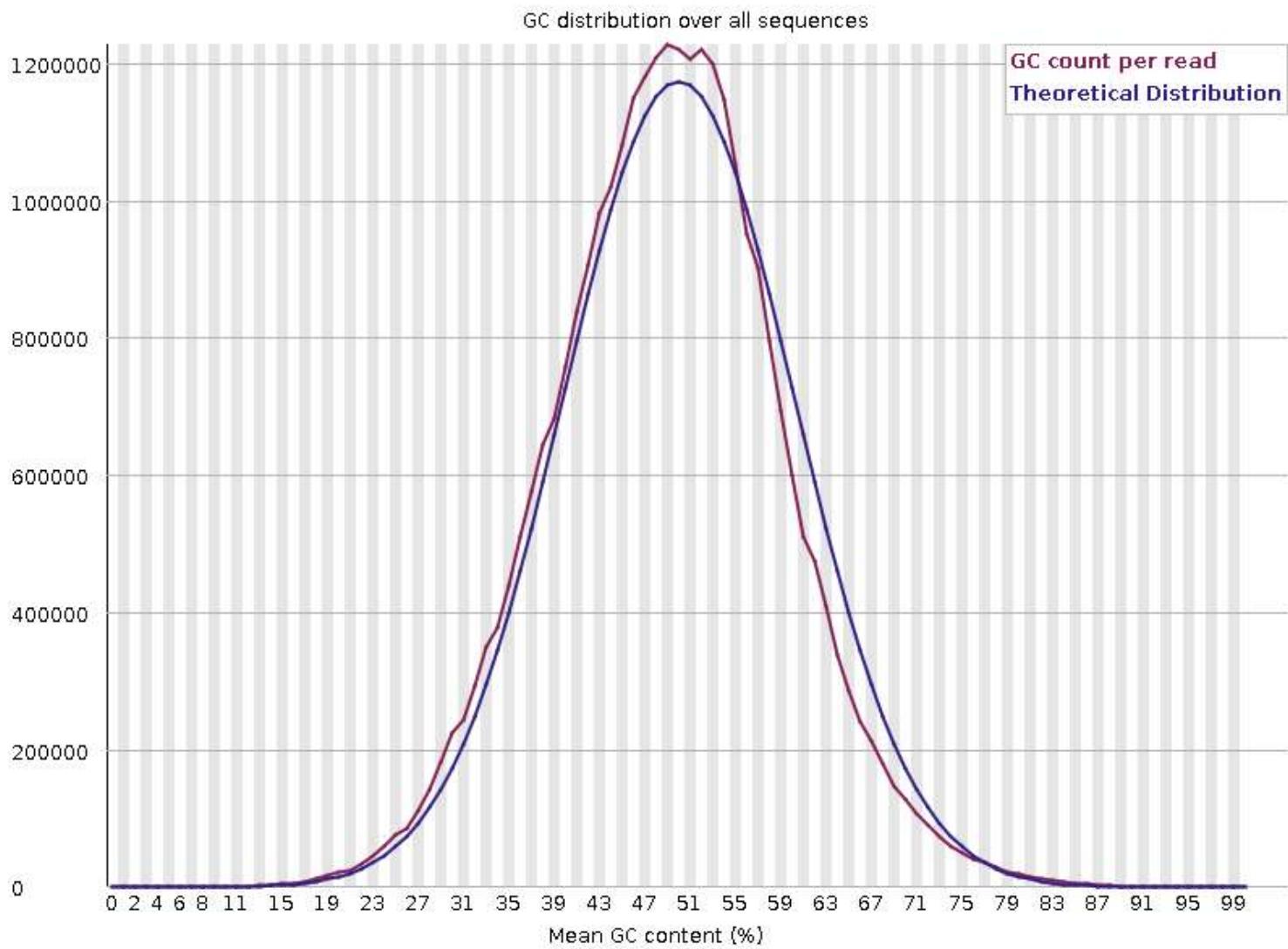


Per base sequence content



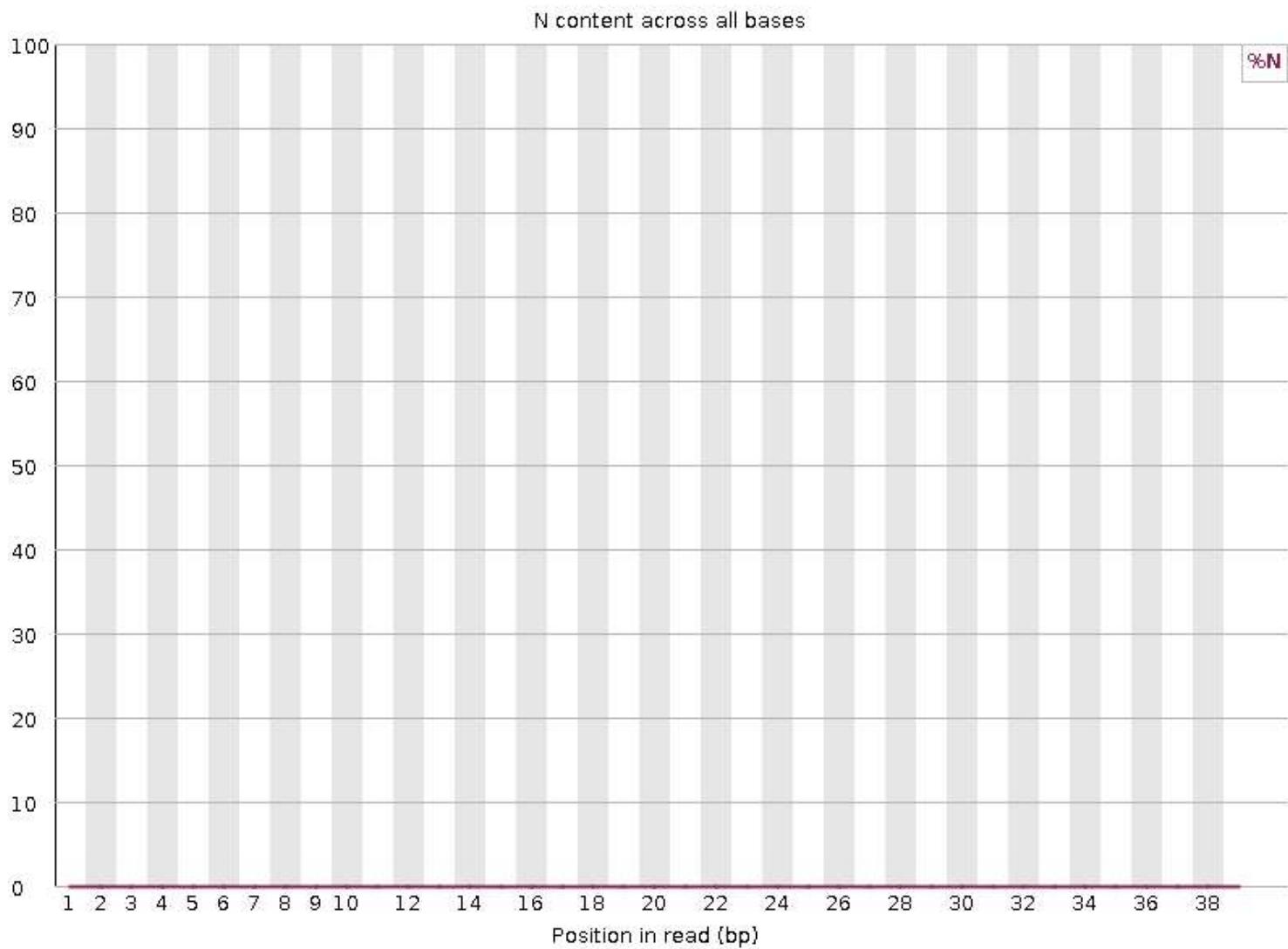


Per sequence GC content



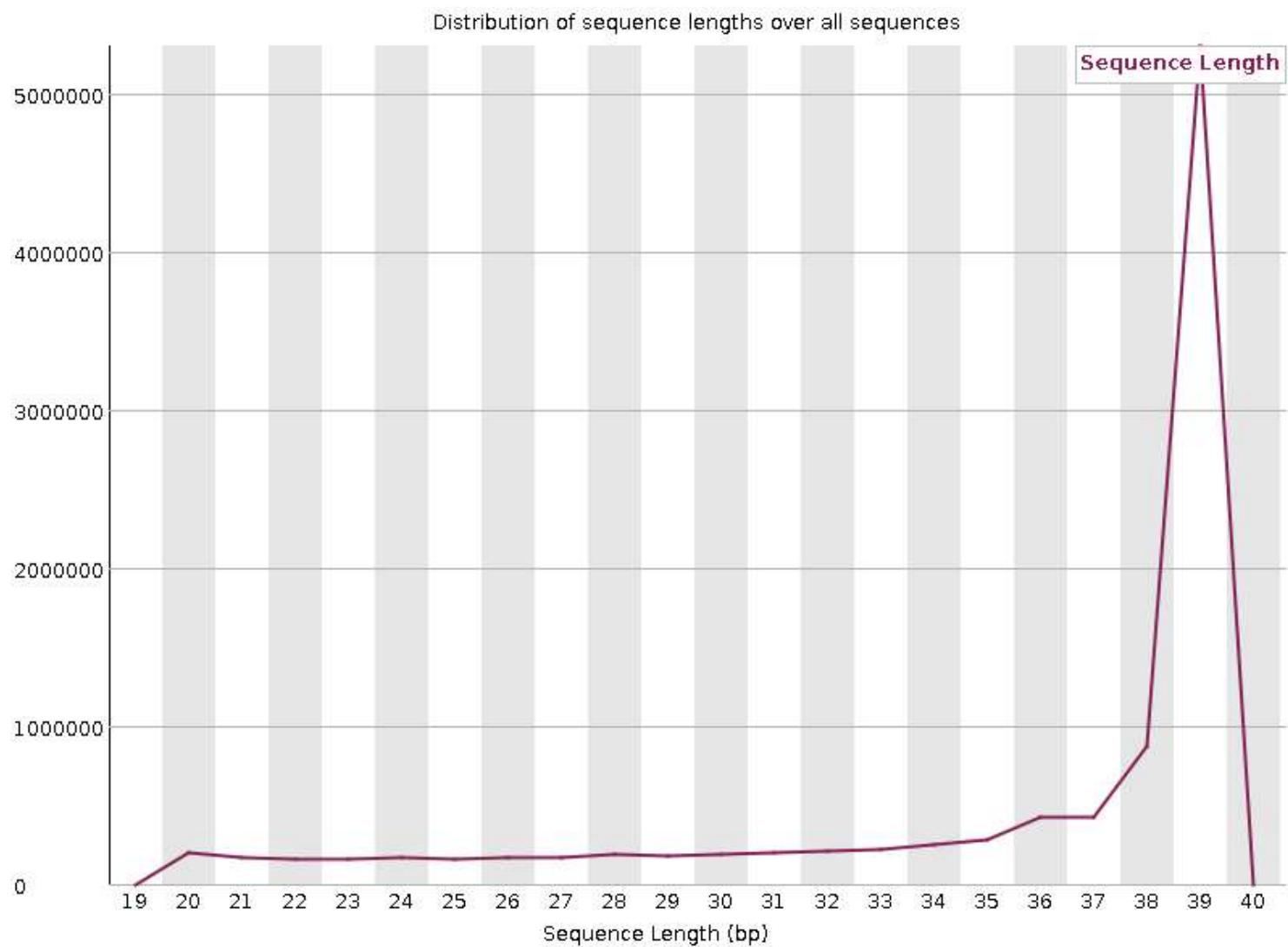


Per base N content





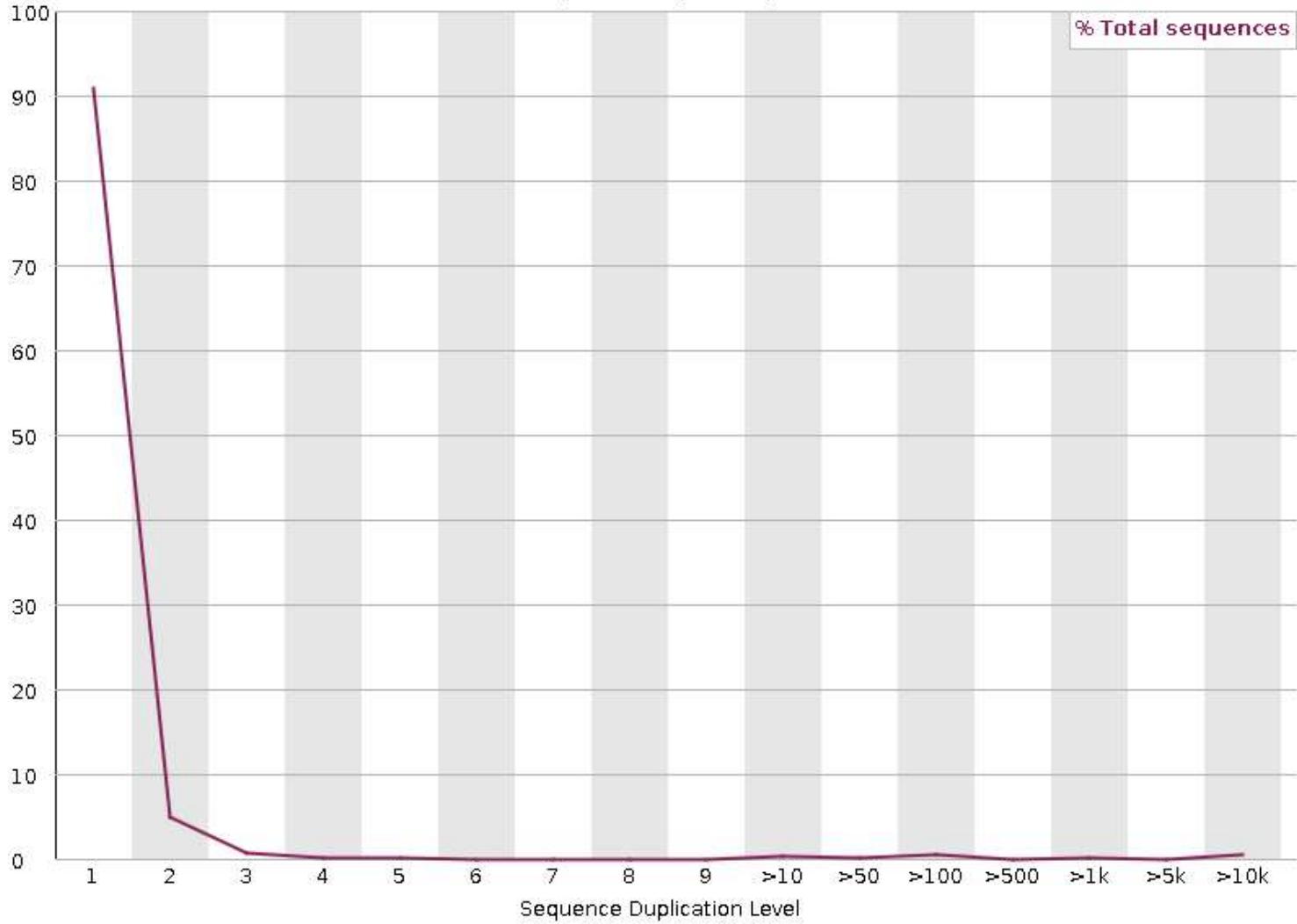
Sequence Length Distribution





Sequence Duplication Levels

Percent of seqs remaining if deduplicated 93.98%

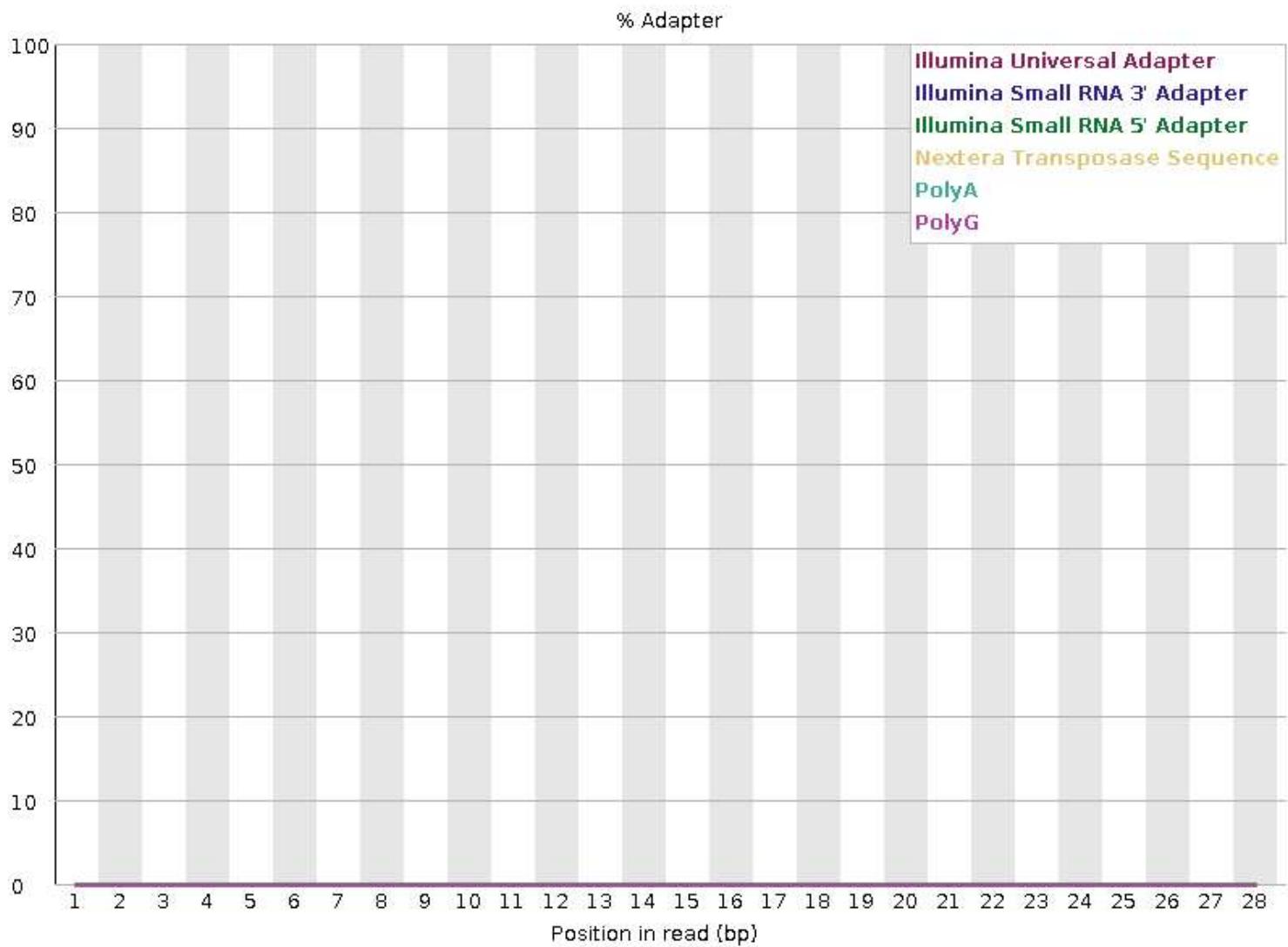


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCTGTATGCCGTCTTCTGCTT	18481	0.17998310509762874	Illumina Single End Adapter 1 (100% over 32bp)
GATCGGAAGAGCTGTATGCCGTCTTCT	17524	0.1706630557724607	Illumina Single End Adapter 1 (100% over 28bp)
GATCGGAAGAGCTGTATGCCGTCTTCTGCTTGAAAAAA	16627	0.16192733555858843	Illumina Single End Adapter 1 (100% over 33bp)
GATCGGAAGAGCTGTATGCCGTCTTCTGCT	13322	0.12974054034471133	Illumina Single End Adapter 1 (100% over 31bp)



Adapter Content



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