

# FastQC Report

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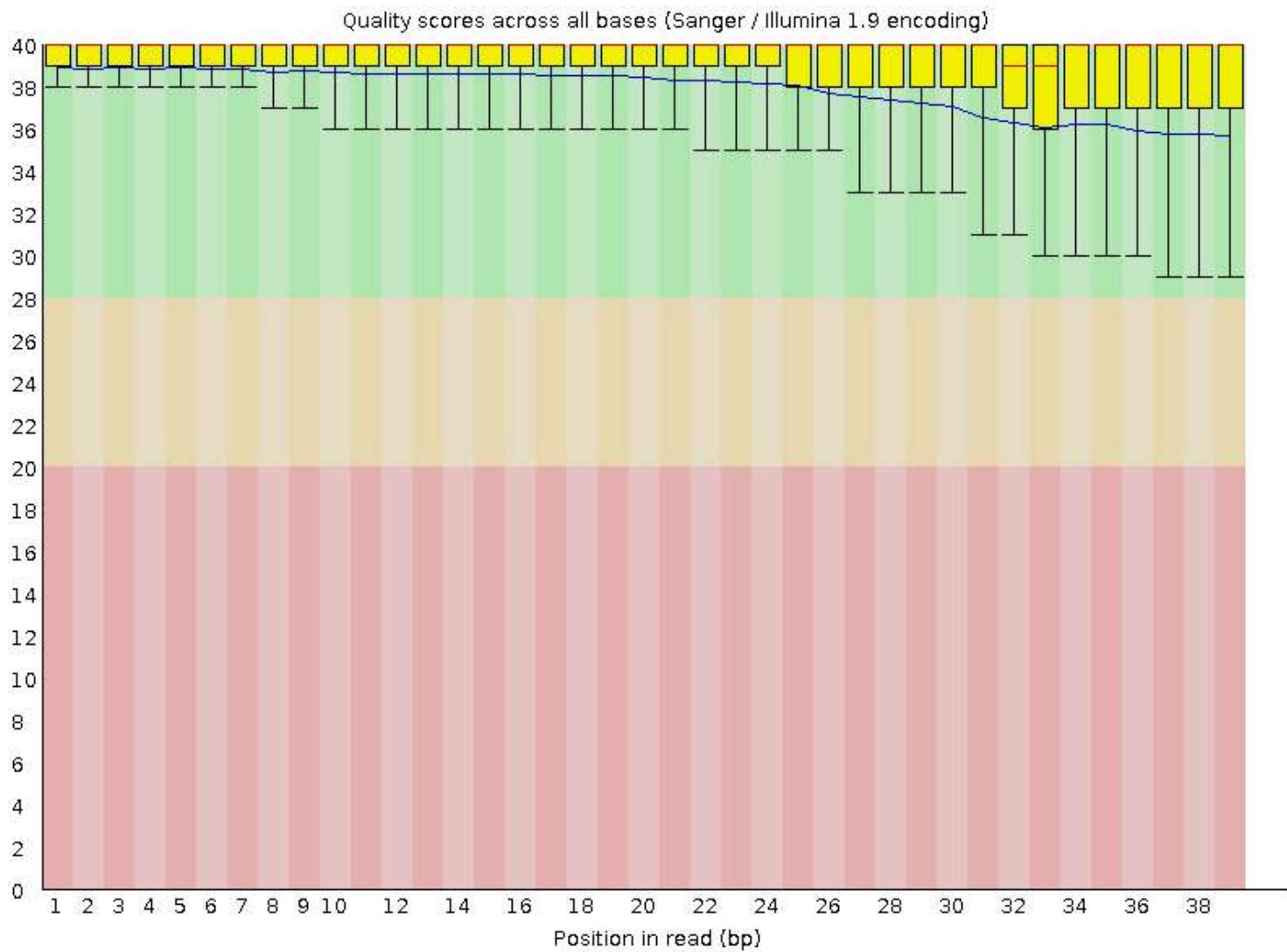
 [Adapter Content](#)

## Basic Statistics

Measure	Value
Filename	SRR398262_1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	19448688
Total Bases	758.4 Mbp
Sequences flagged as poor quality	0
Sequence length	39
%GC	46

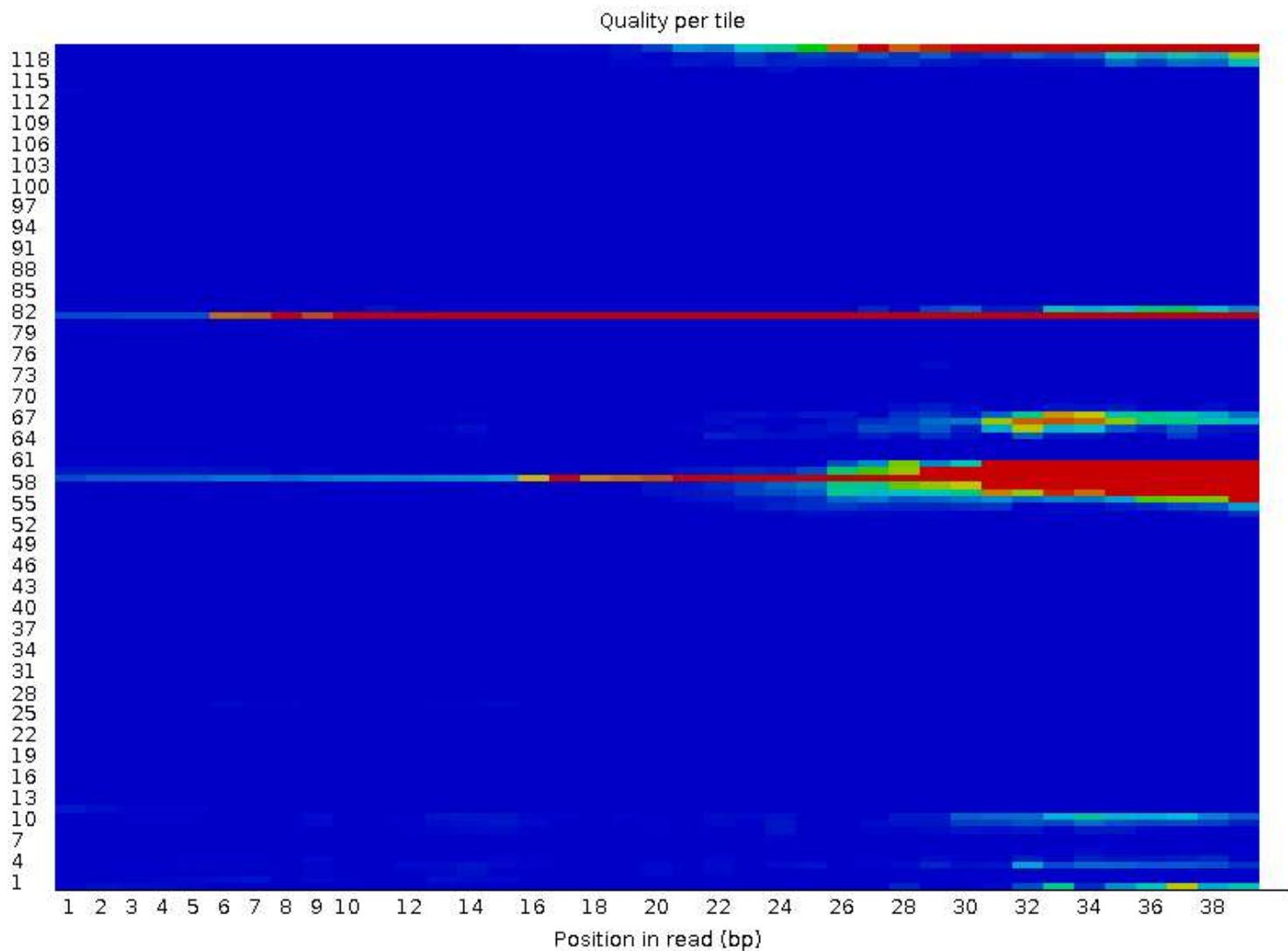


## Per base sequence quality



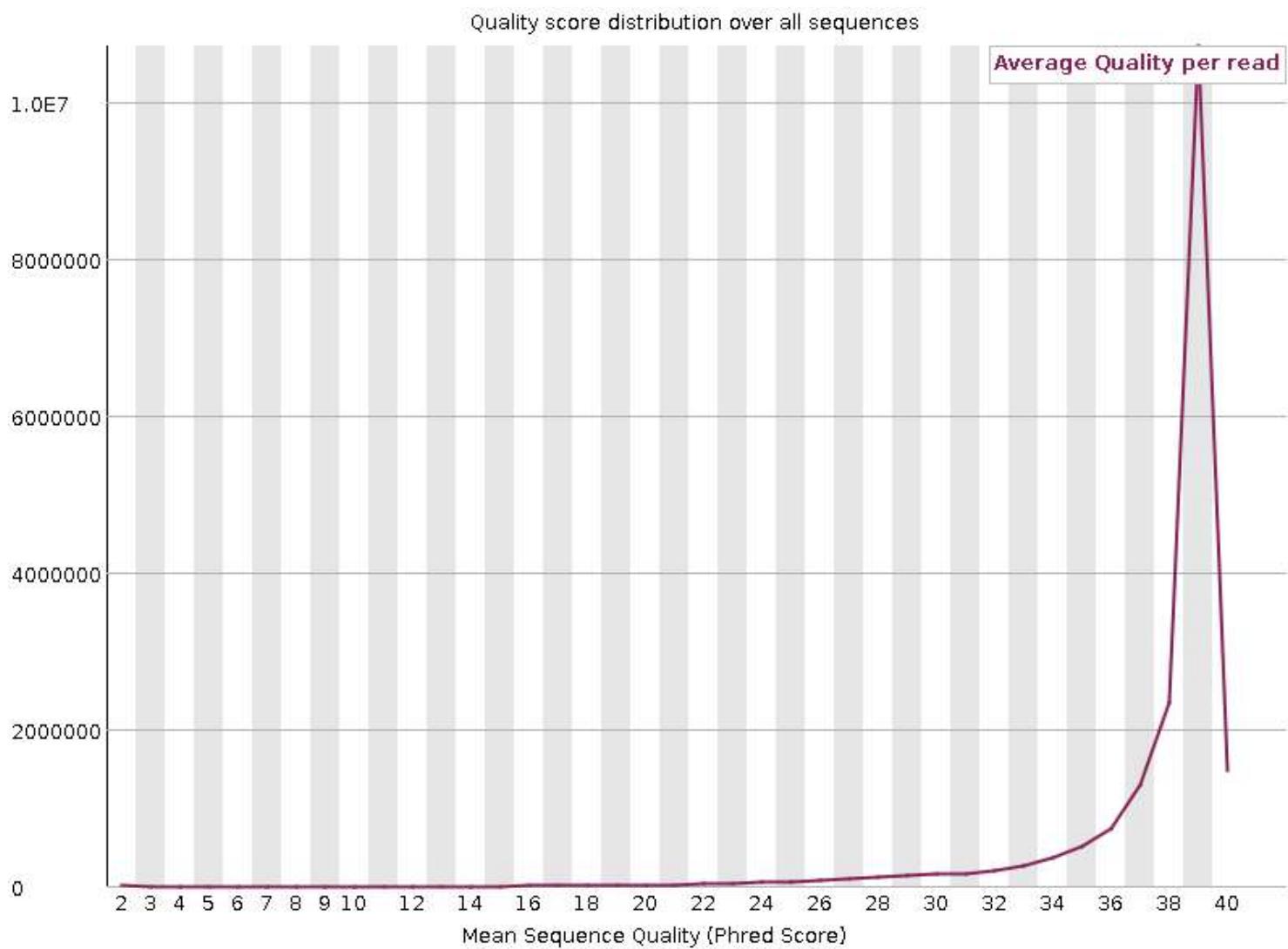


## Per tile sequence quality



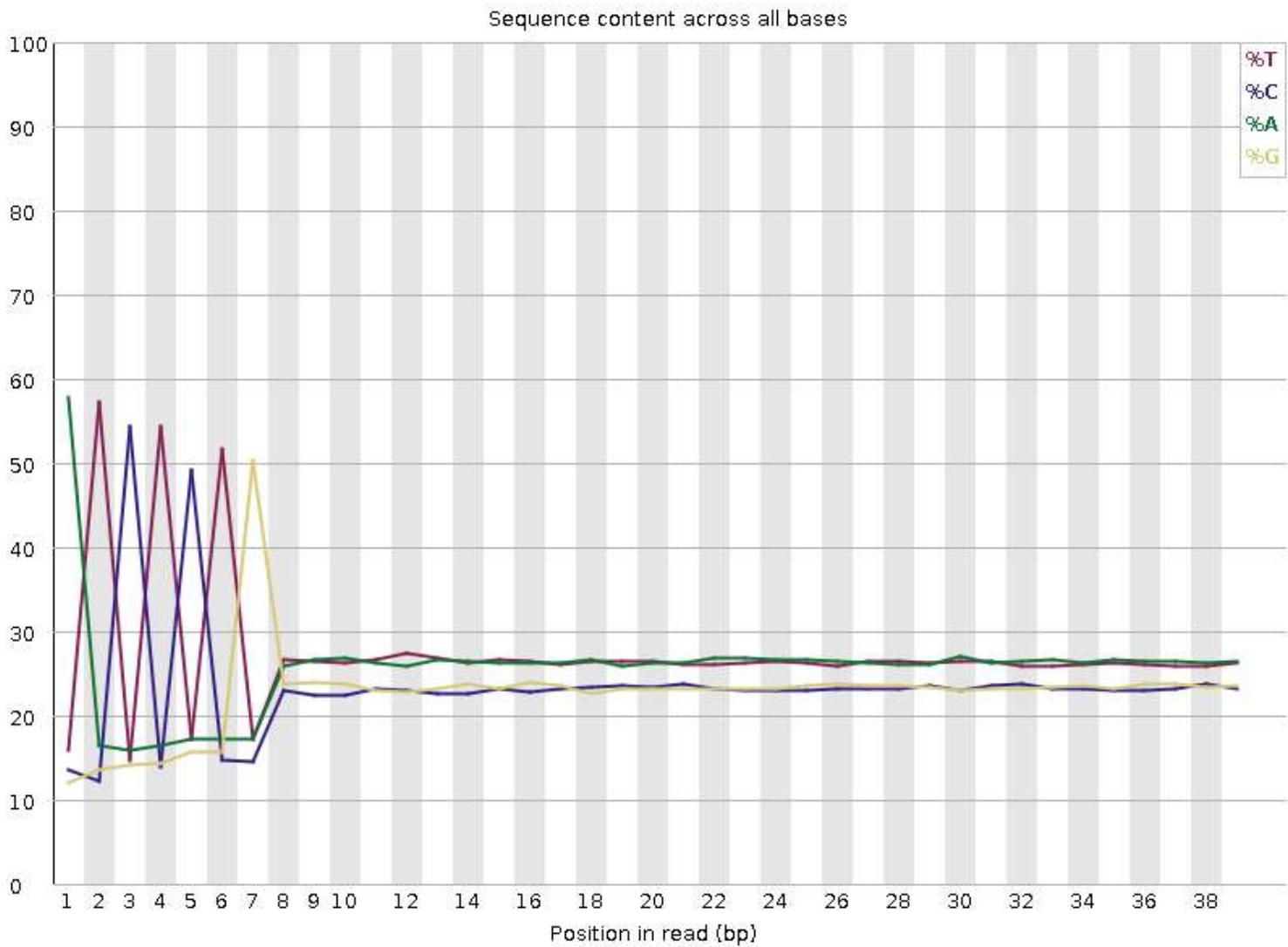


## Per sequence quality scores



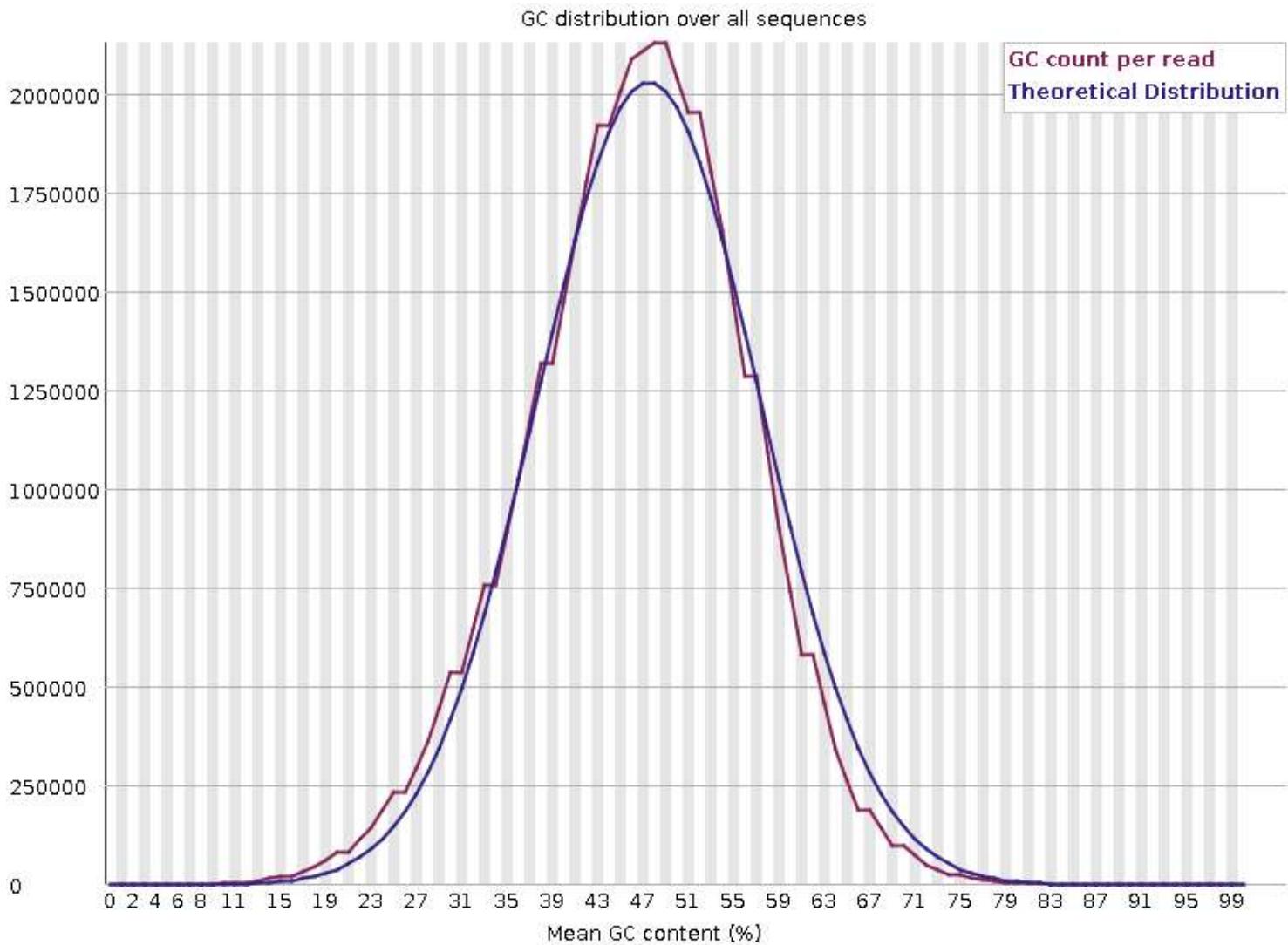


## Per base sequence content



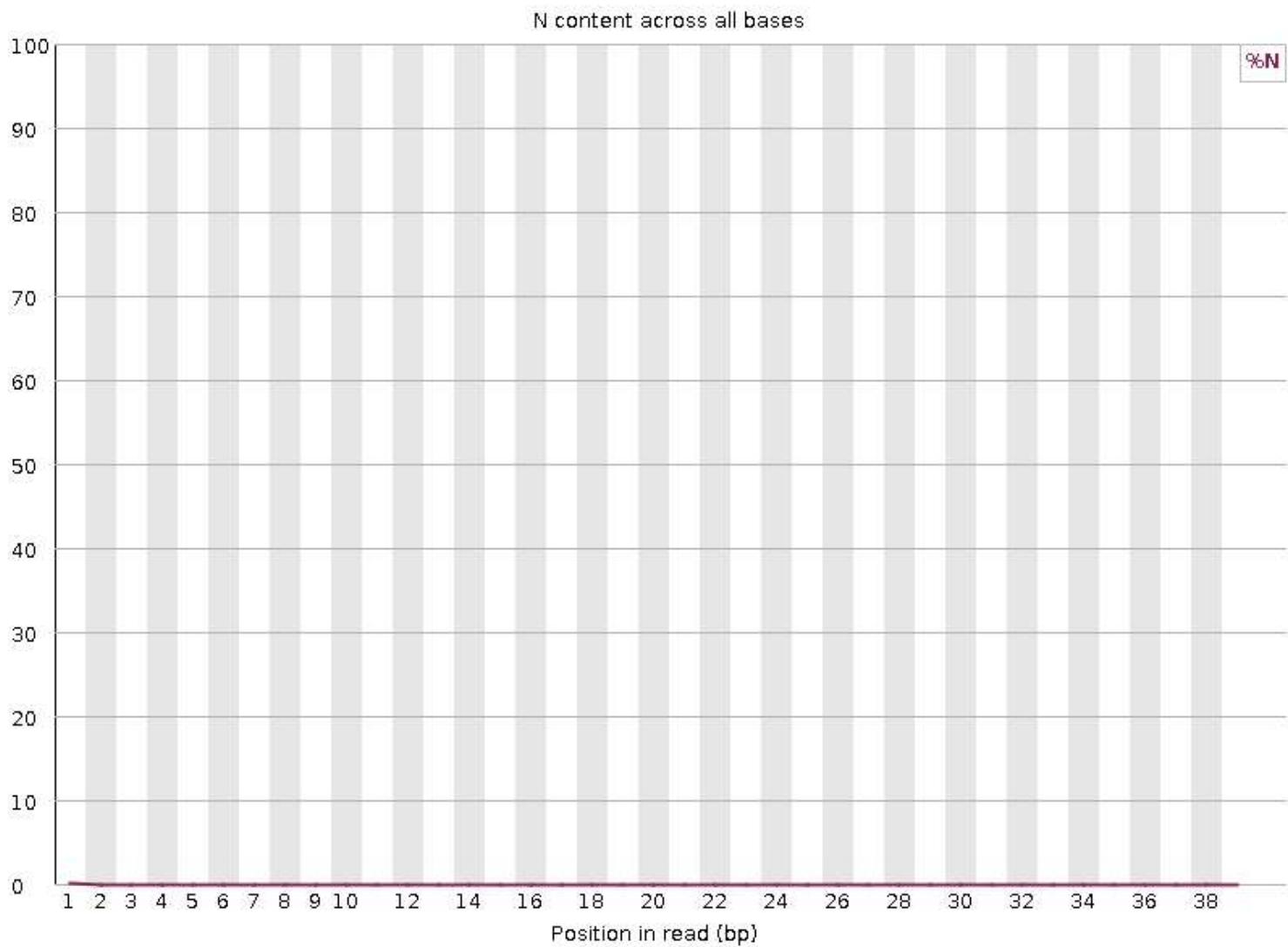


## Per sequence GC content





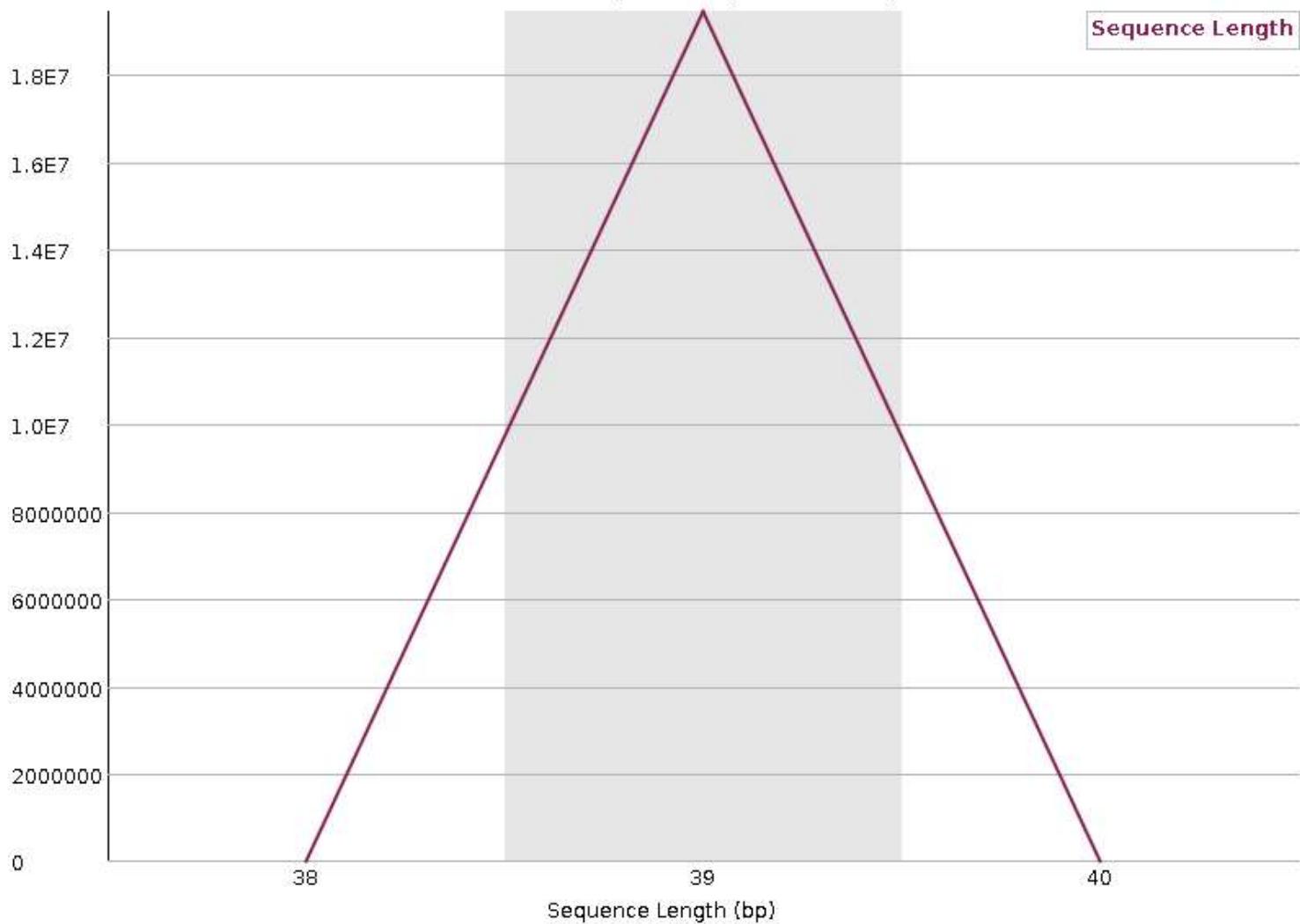
## Per base N content





## Sequence Length Distribution

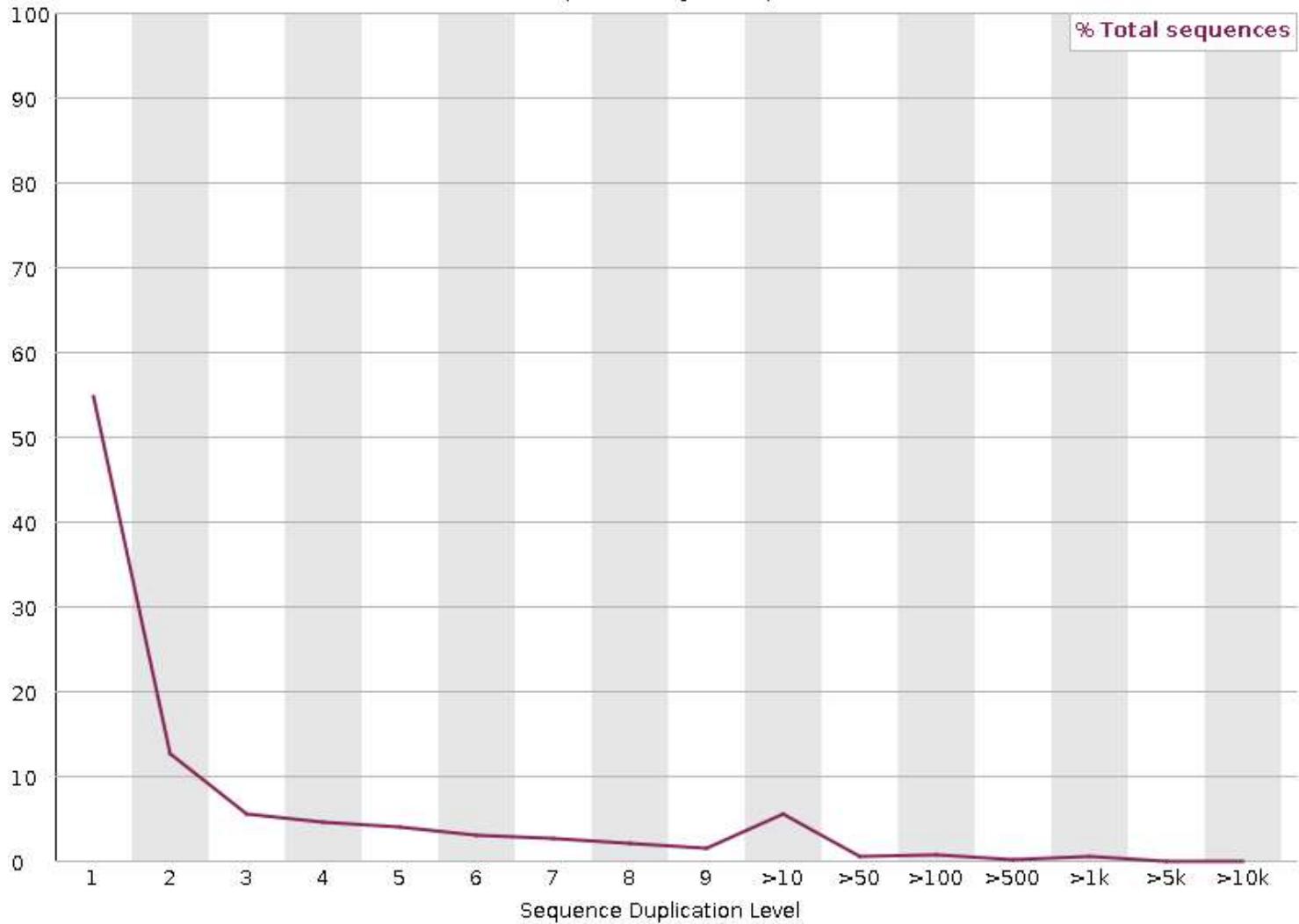
Distribution of sequence lengths over all sequences





## Sequence Duplication Levels

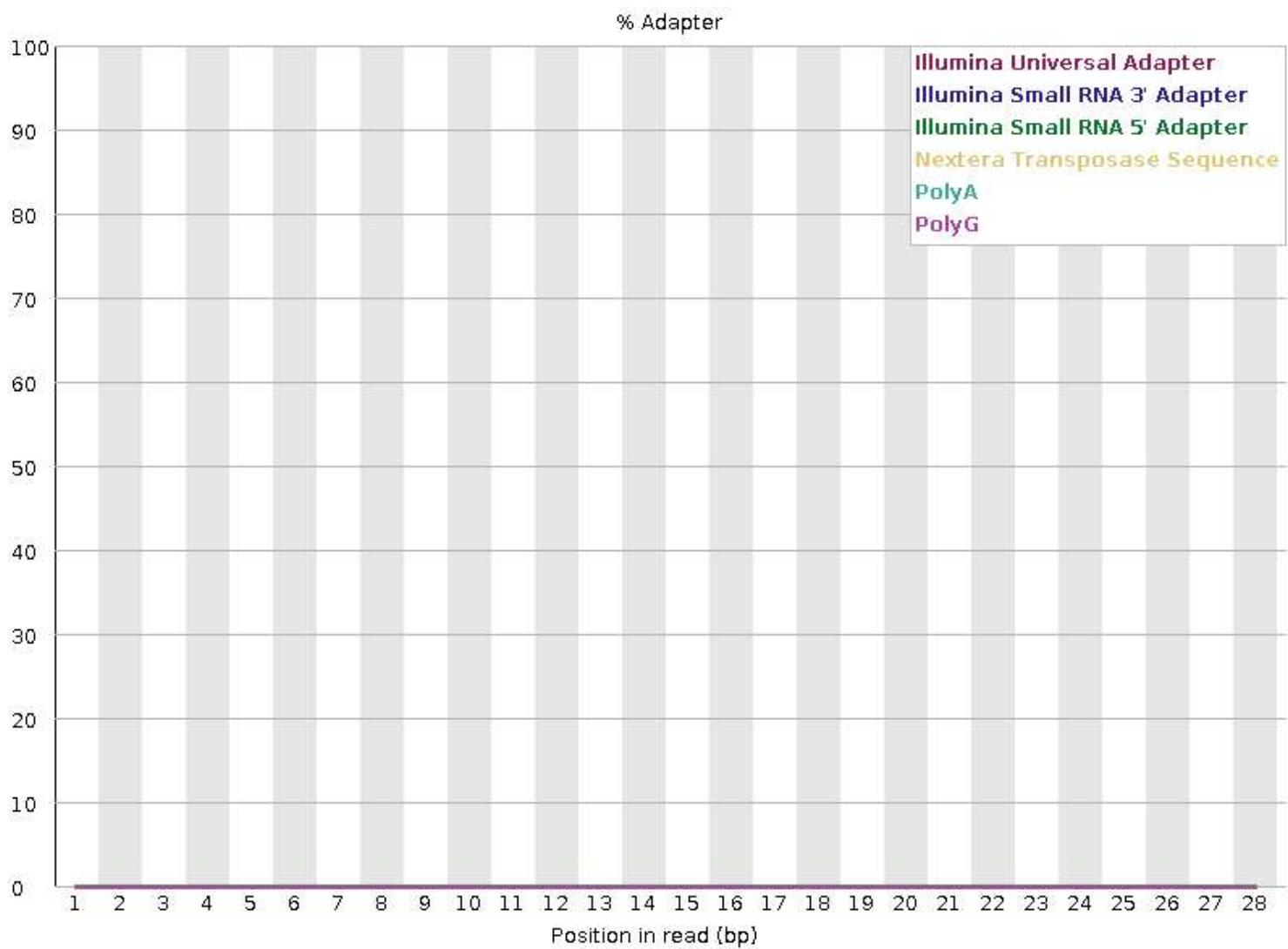
Percent of seqs remaining if deduplicated 66.93%



## Overrepresented sequences

No overrepresented sequences

## Adapter Content



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