












FastQC Report

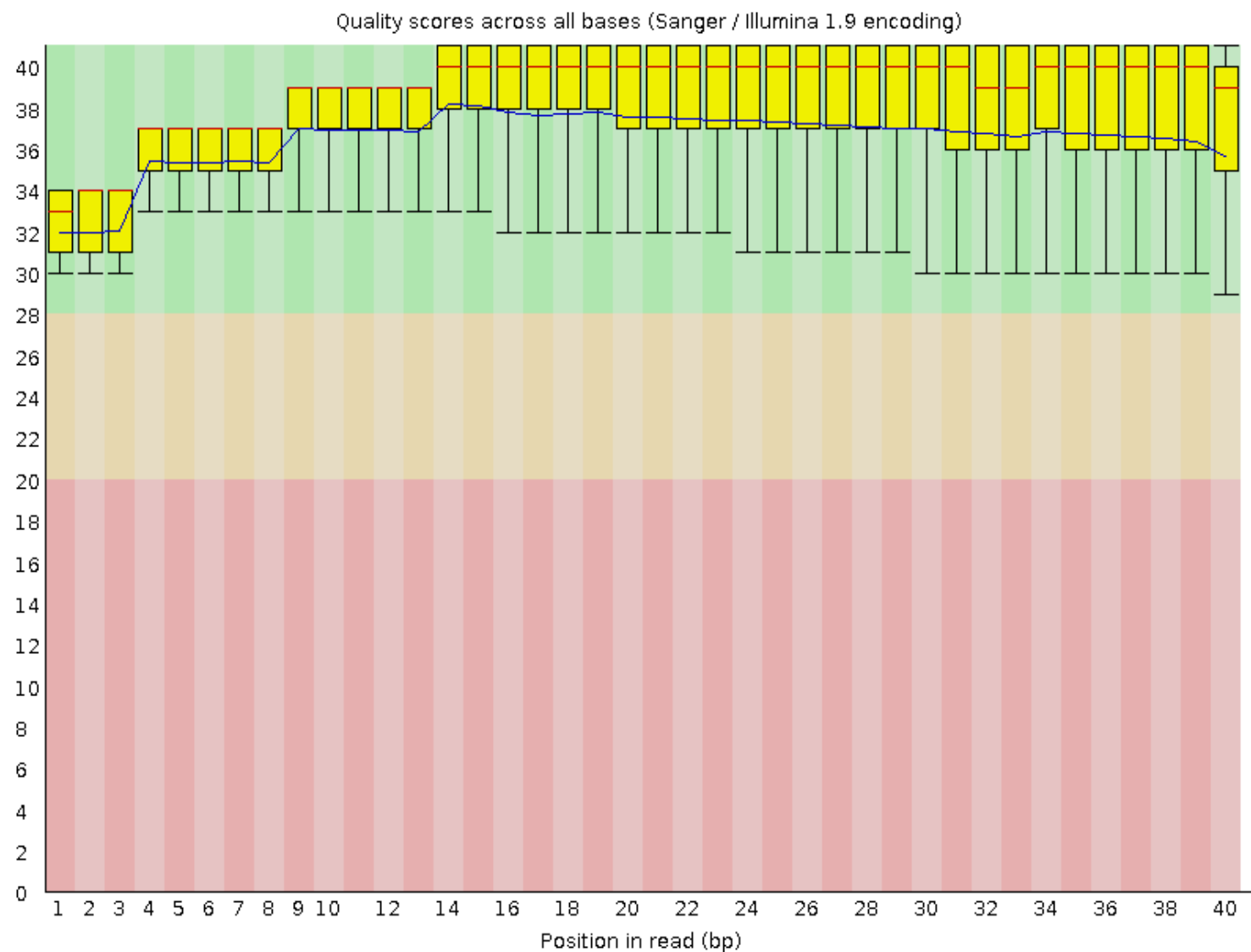
Summary

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Basic Statistics

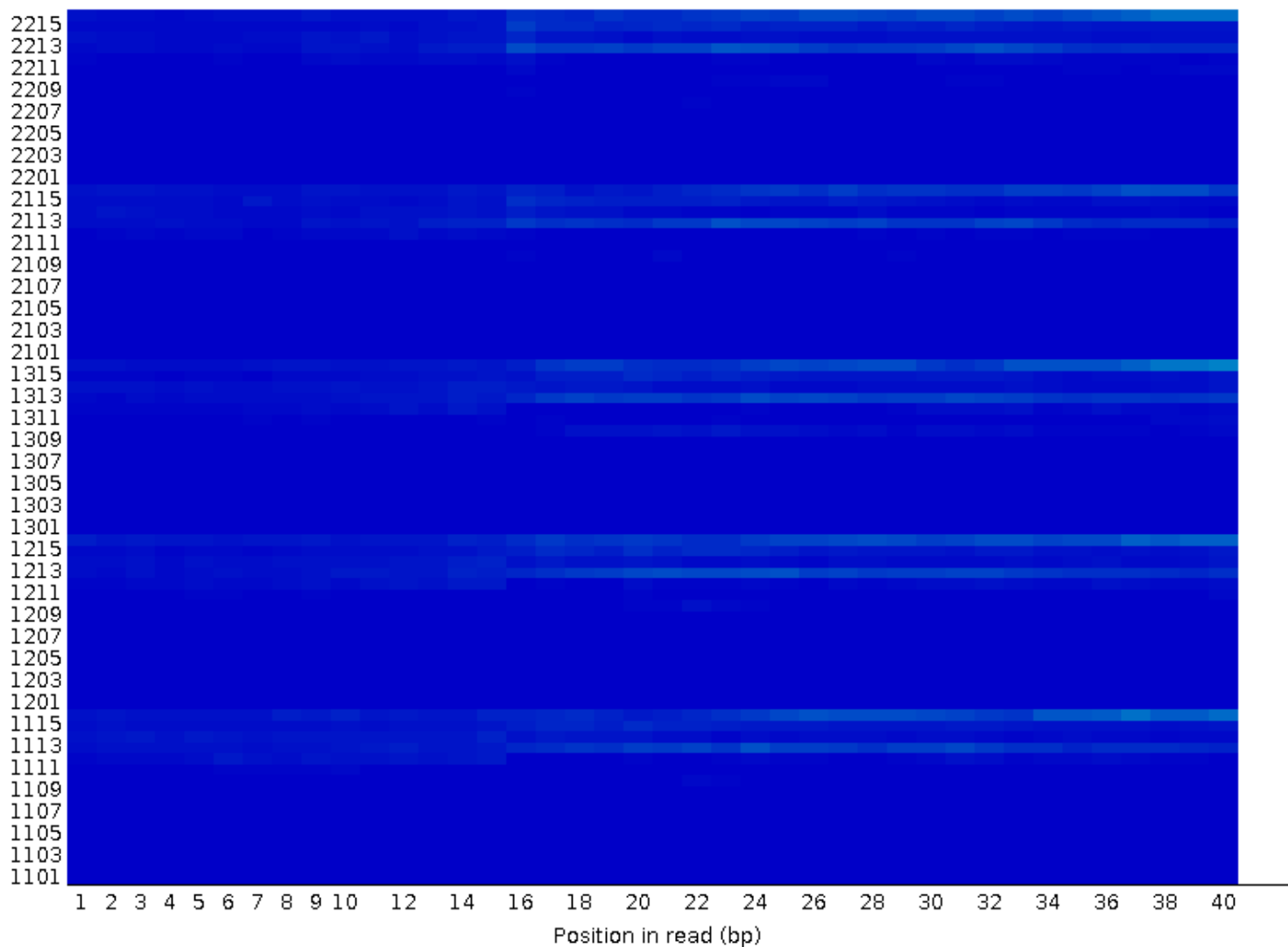
Measure	Value
Filename	P0_1_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	21577562
Sequences flagged as poor quality	0
Sequence length	40
%GC	49

Per base sequence quality



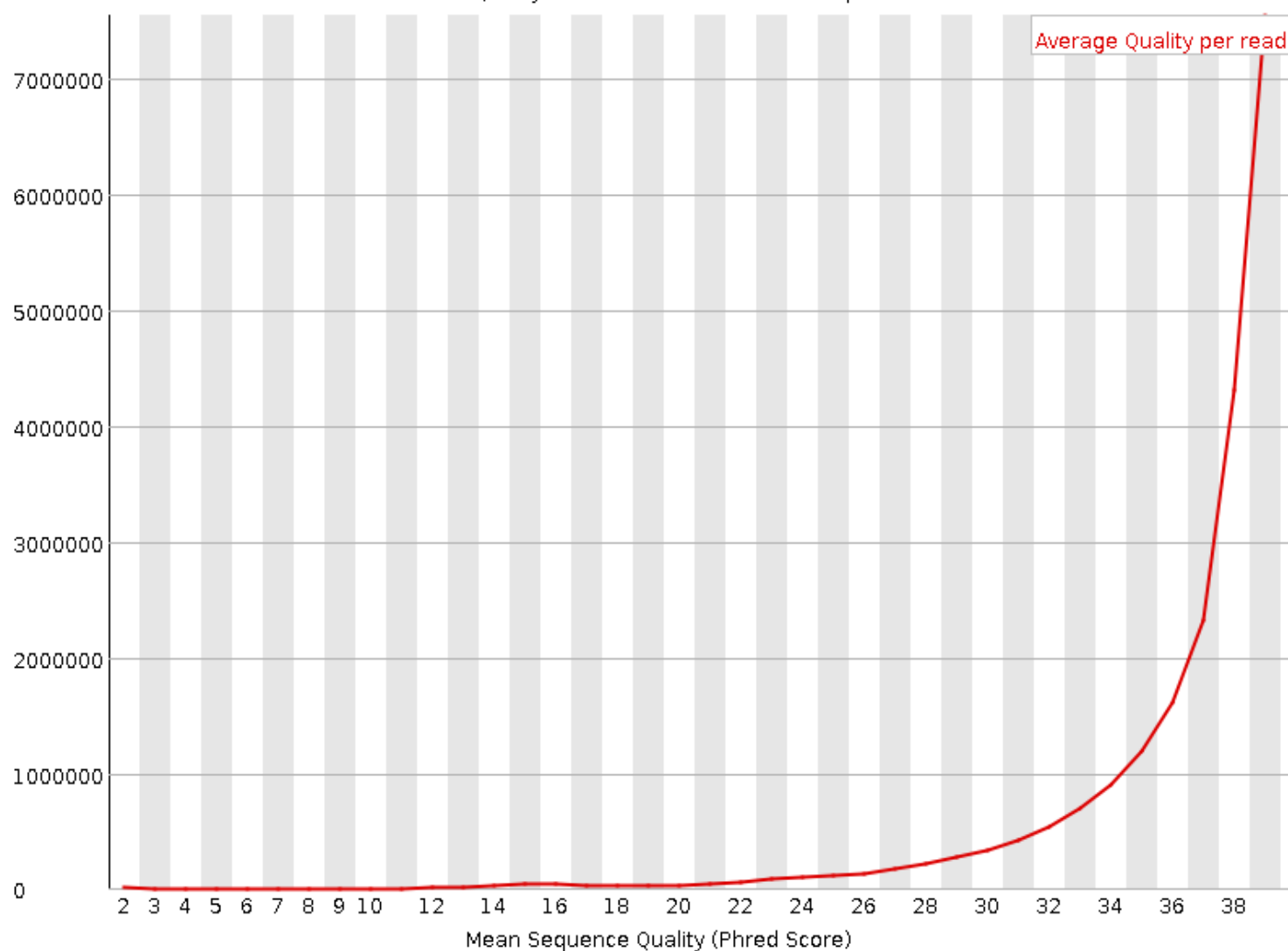
Per tile sequence quality

Quality per tile



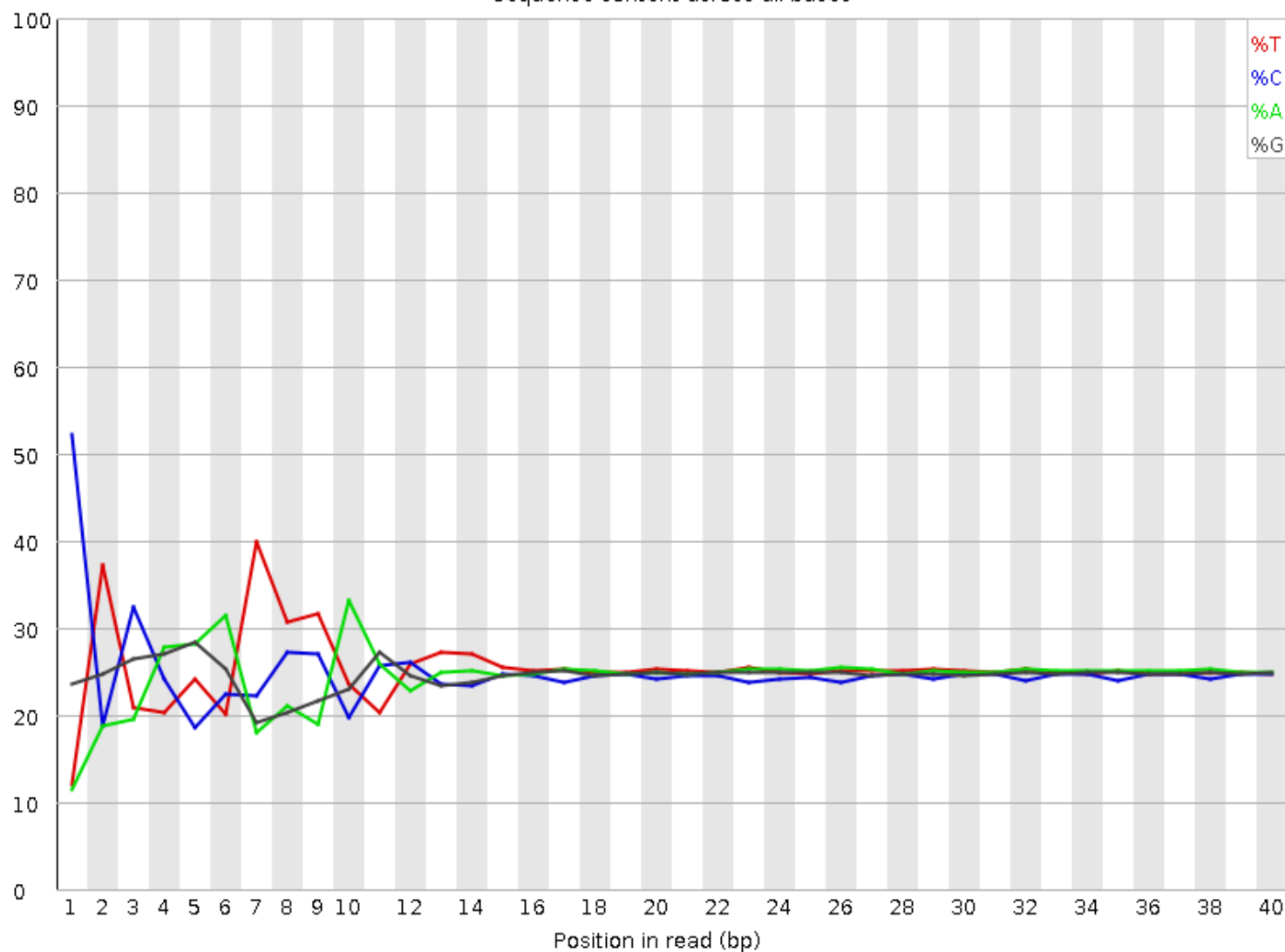
Per sequence quality scores

Quality score distribution over all sequences

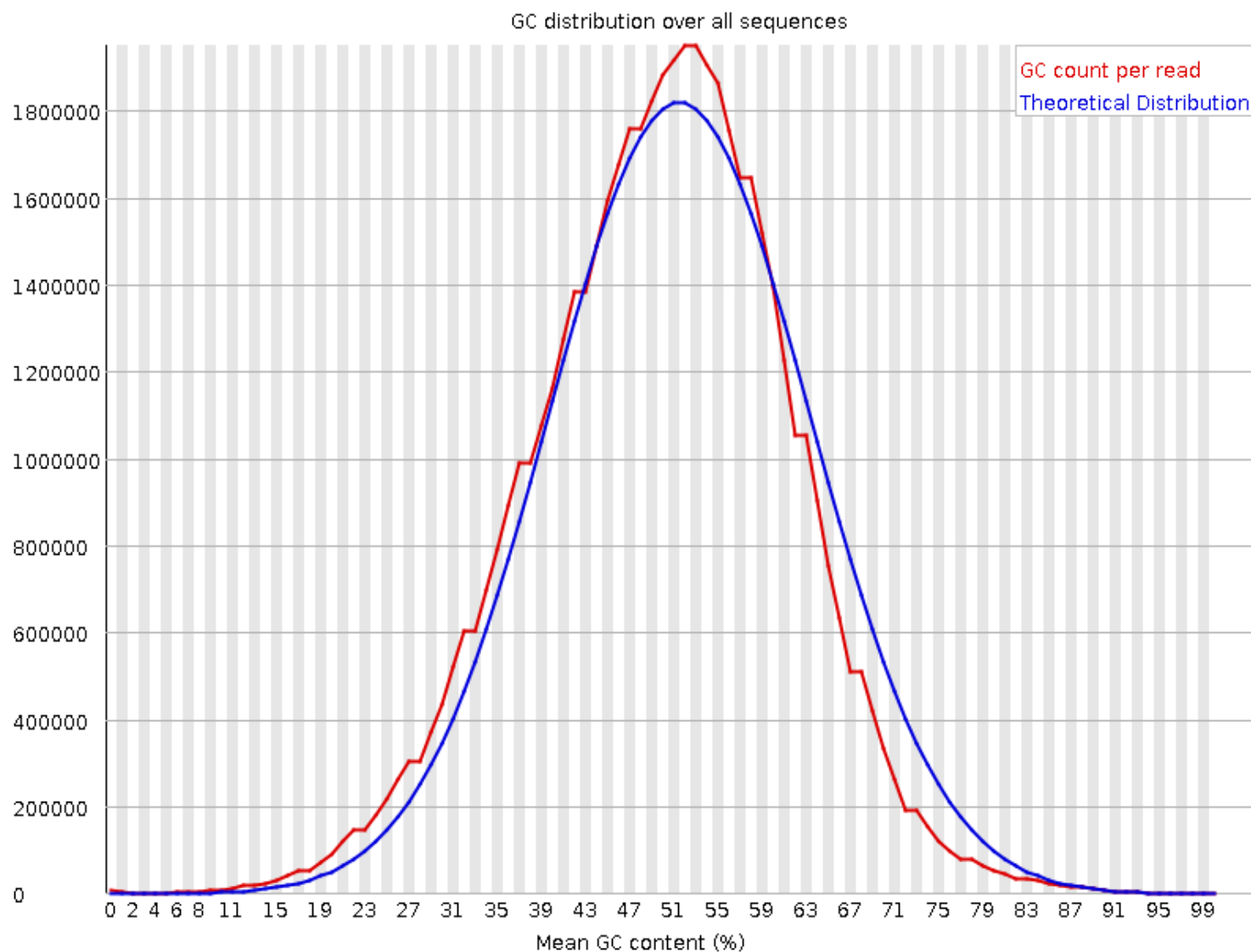


✖ Per base sequence content

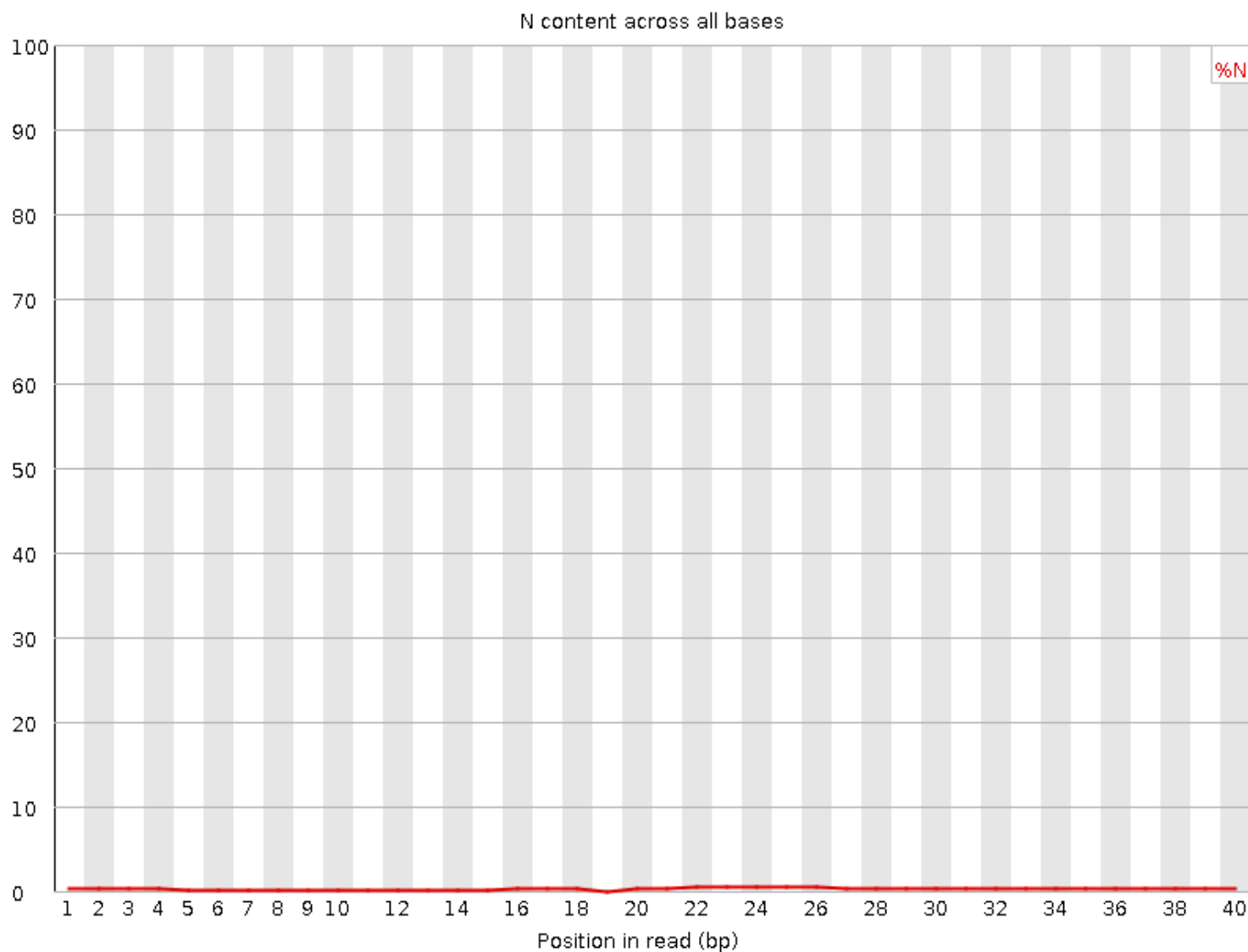
Sequence content across all bases



Per sequence GC content

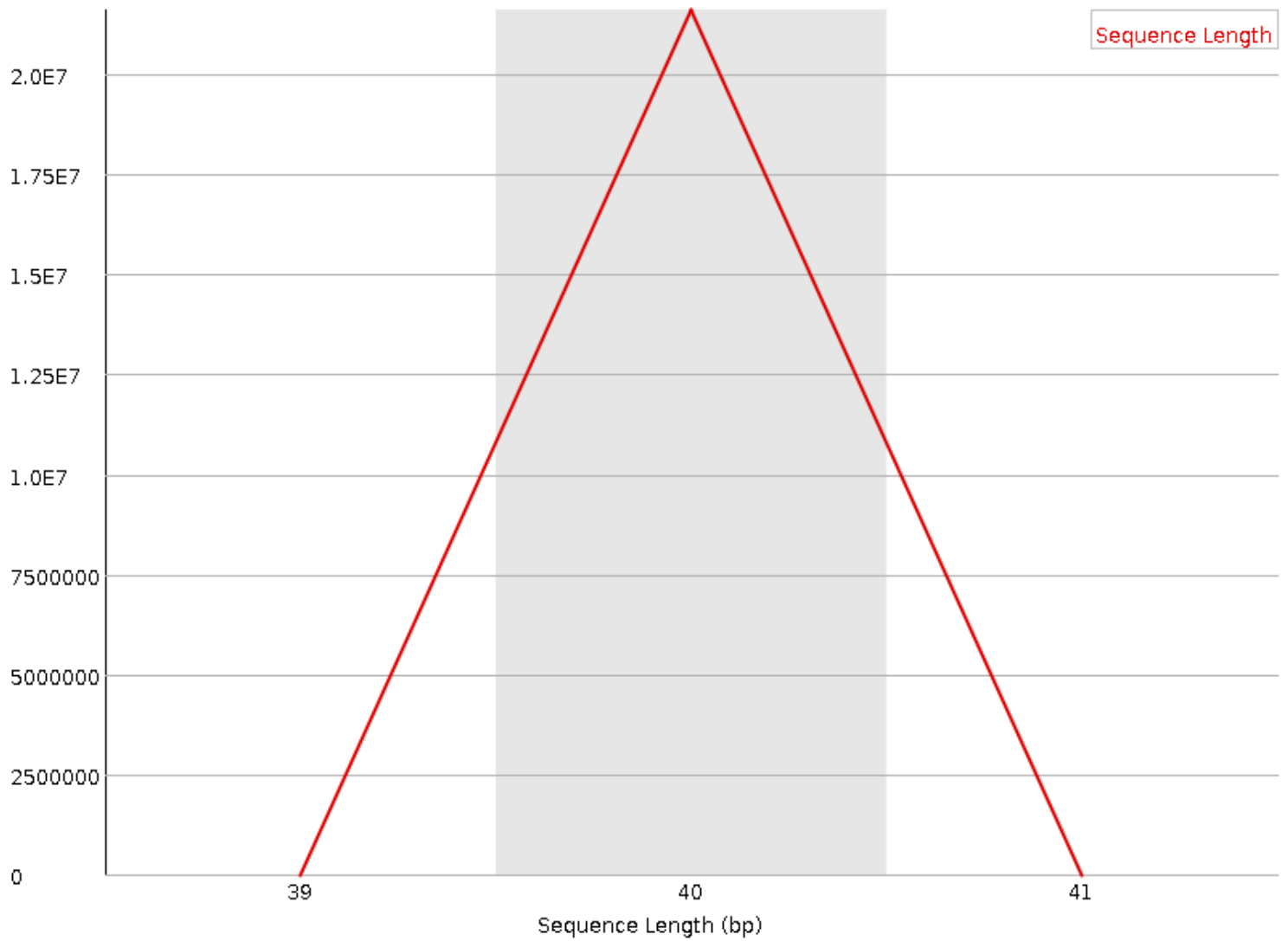


Per base N content



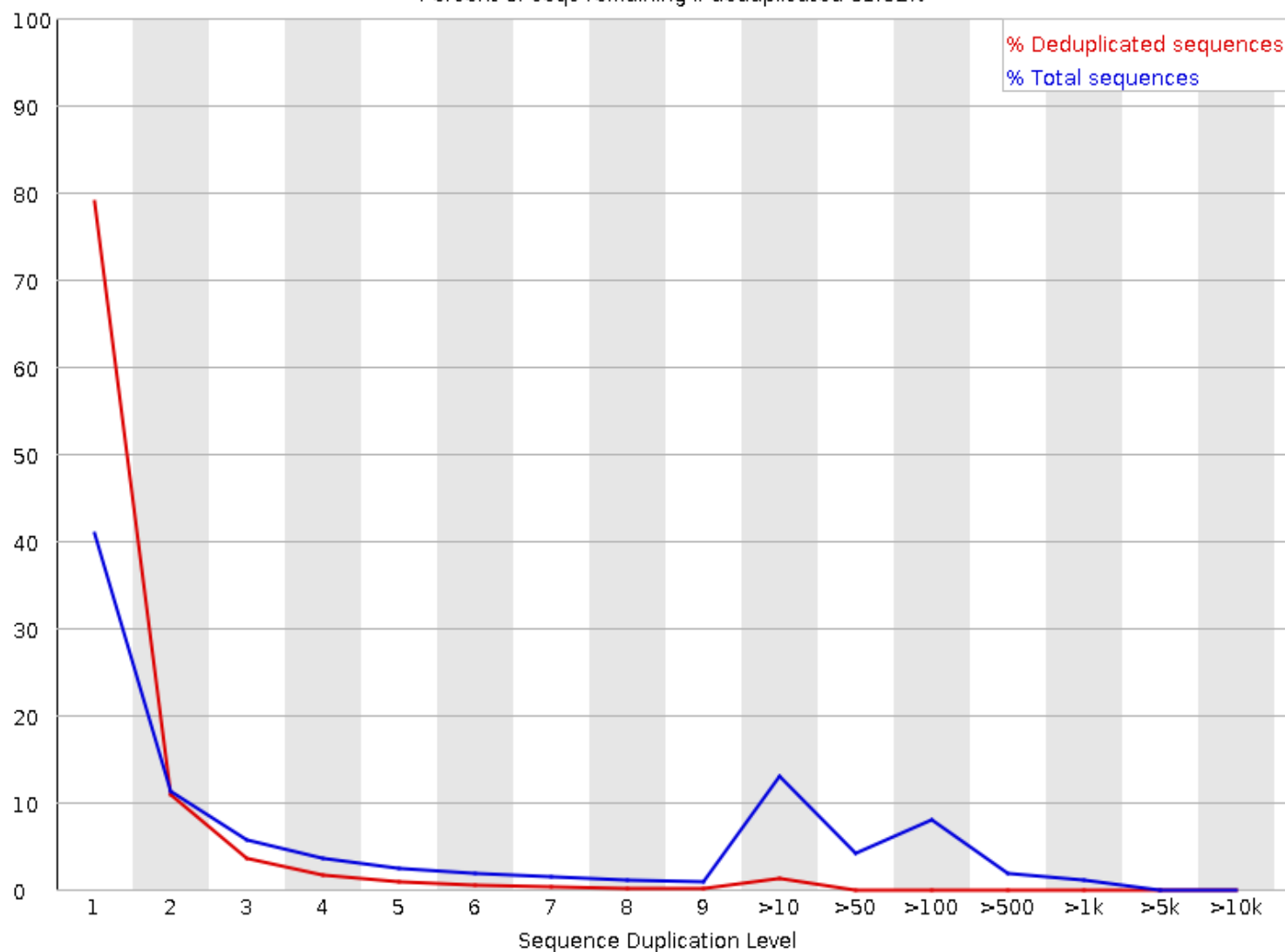
Sequence Length Distribution

Distribution of sequence lengths over all sequences



! Sequence Duplication Levels

Percent of seqs remaining if deduplicated 51.82%

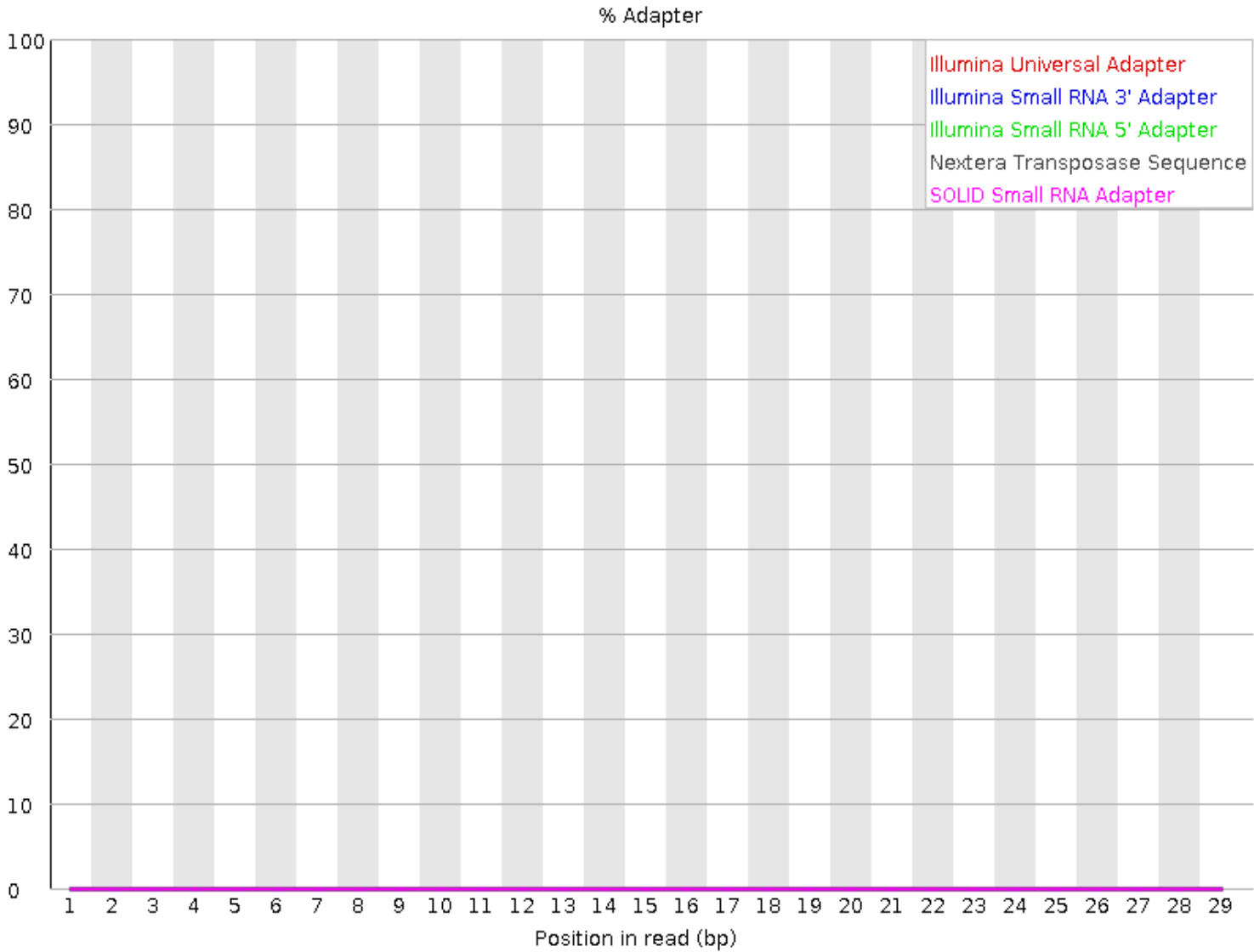


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.11.7)