

FastQC Report

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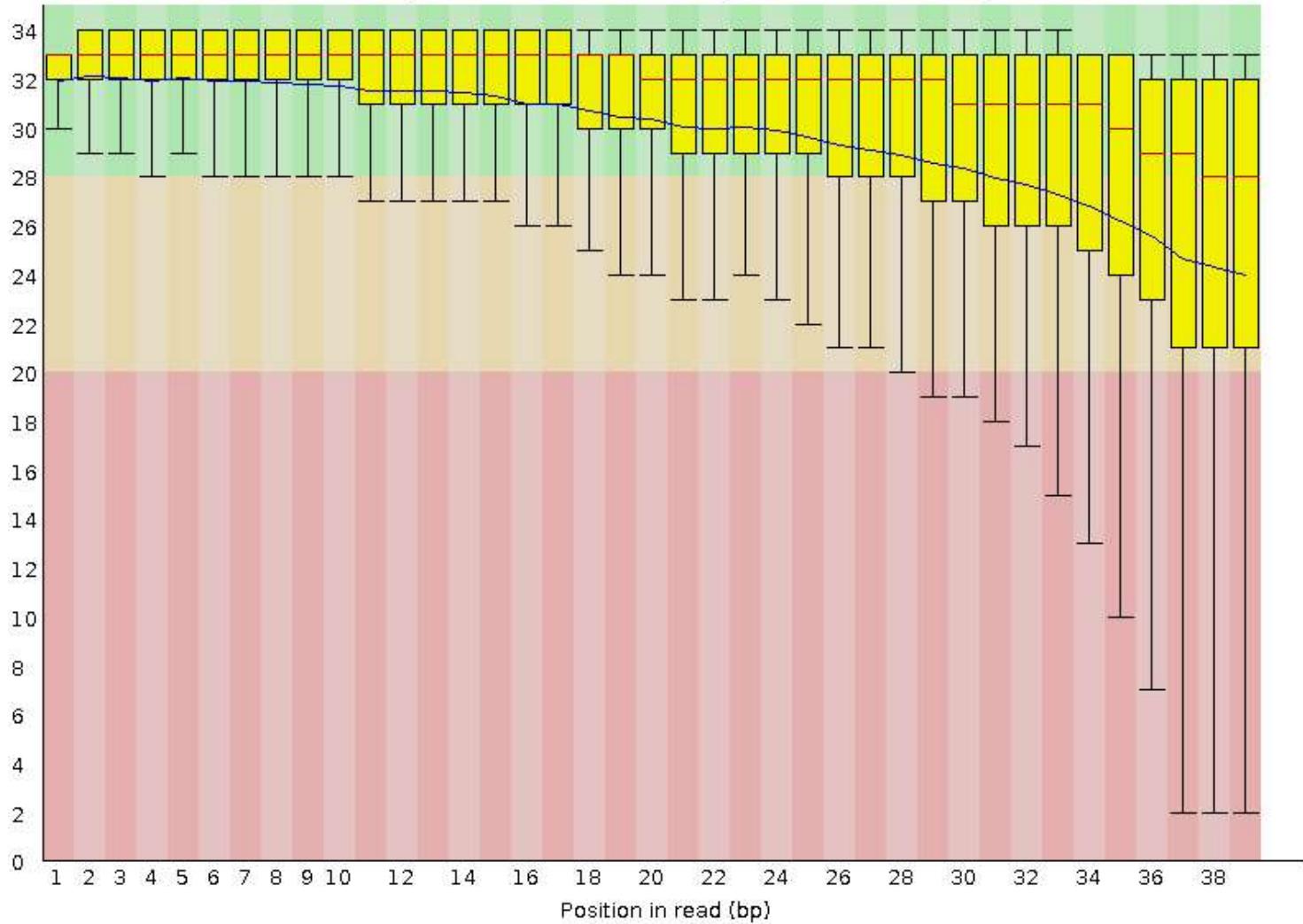
Basic Statistics

Measure	Value
Filename	SRR396786_1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	13549670
Total Bases	528.4 Mbp
Sequences flagged as poor quality	0
Sequence length	39
%GC	51



Per base sequence quality

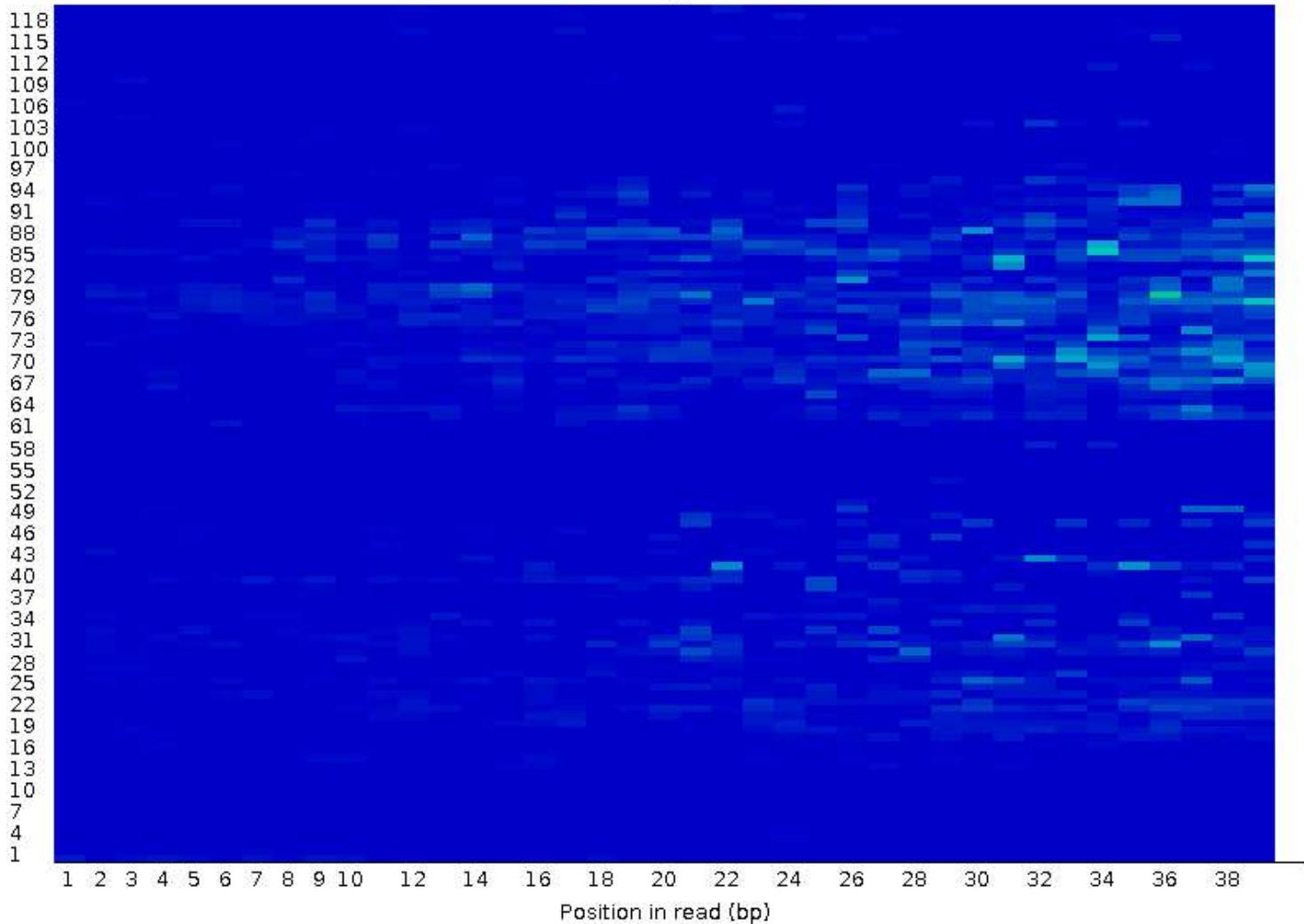
Quality scores across all bases (Sanger / Illumina 1.9 encoding)





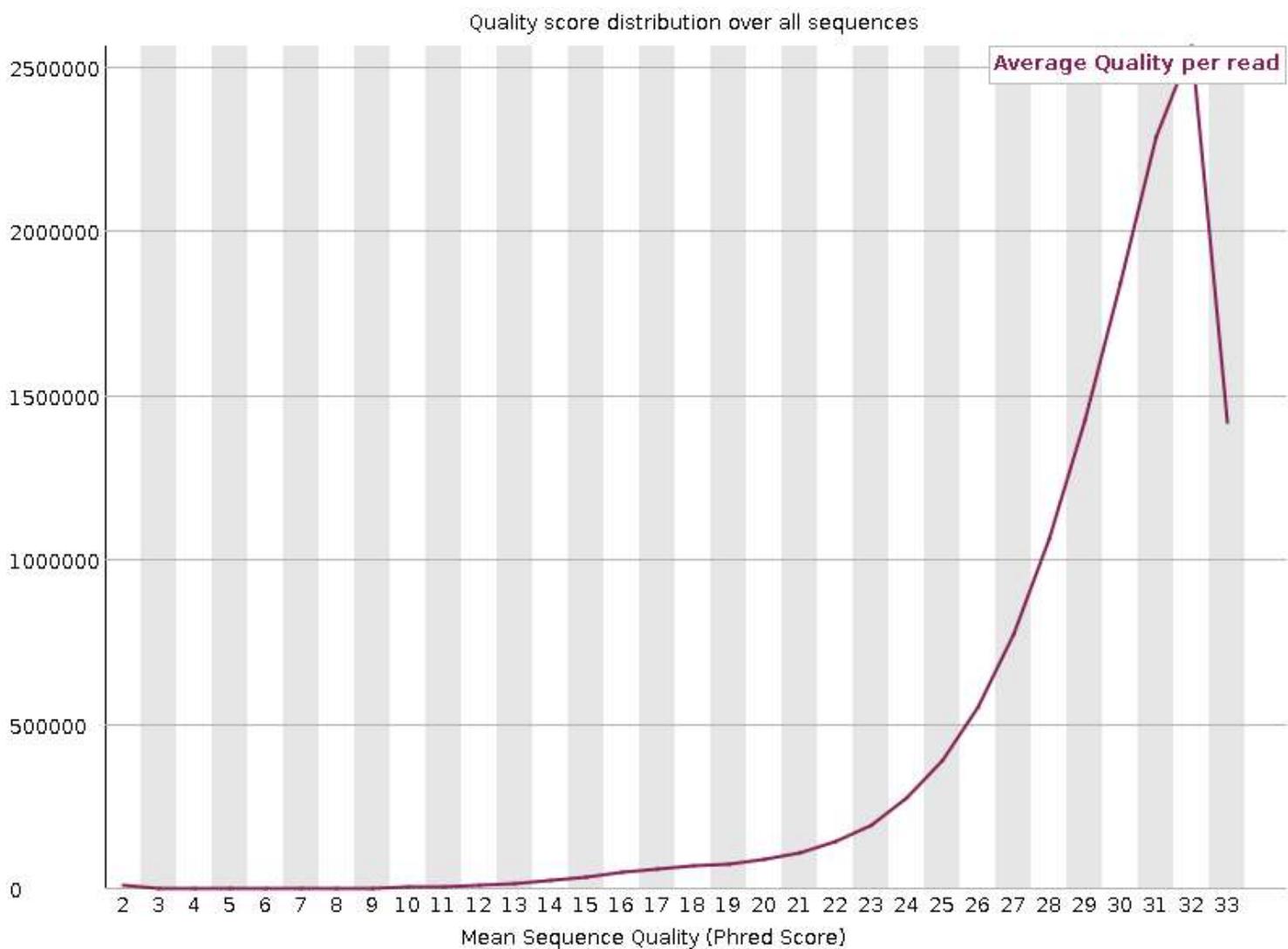
Per tile sequence quality

Quality per tile



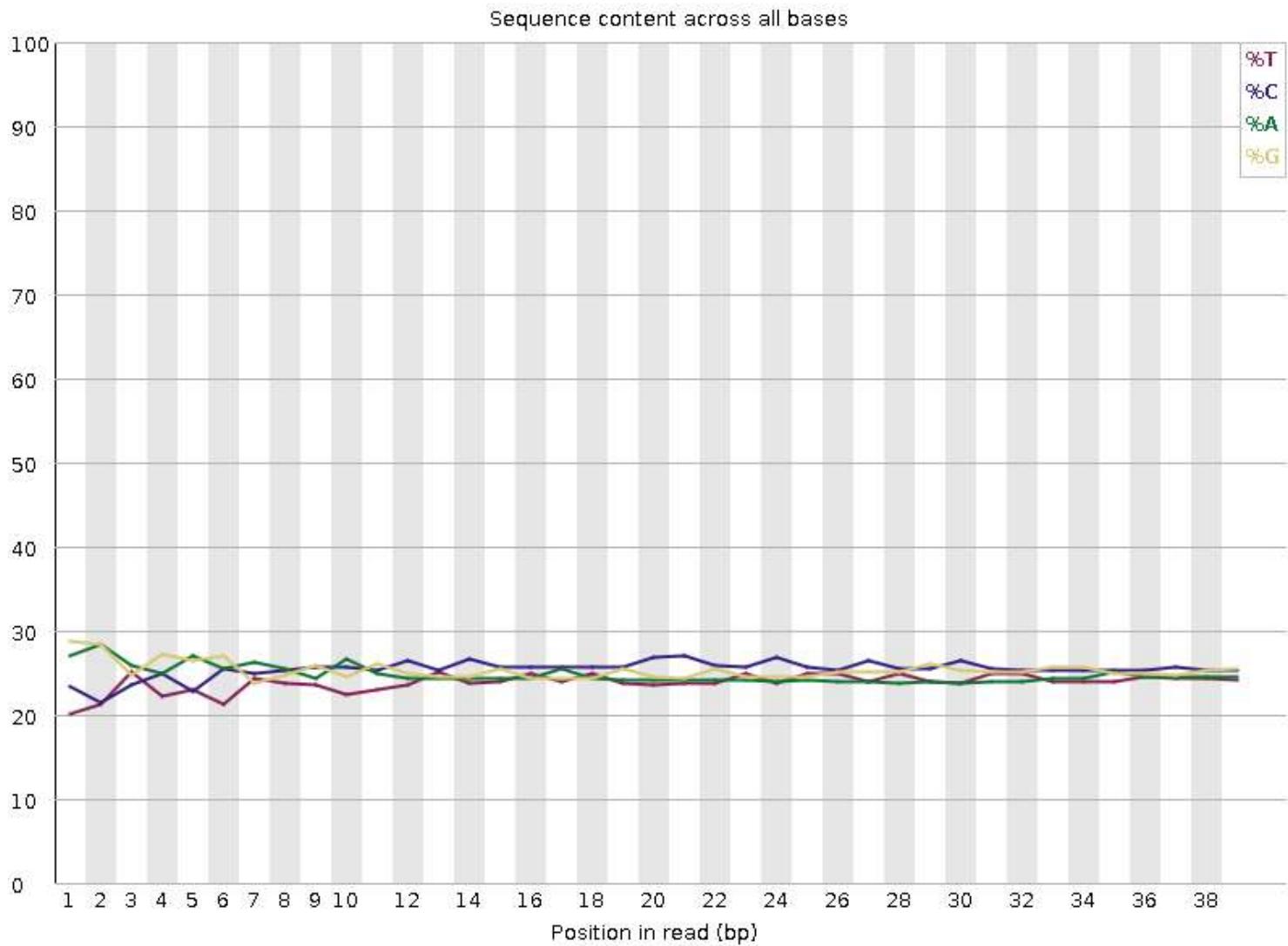


Per sequence quality scores



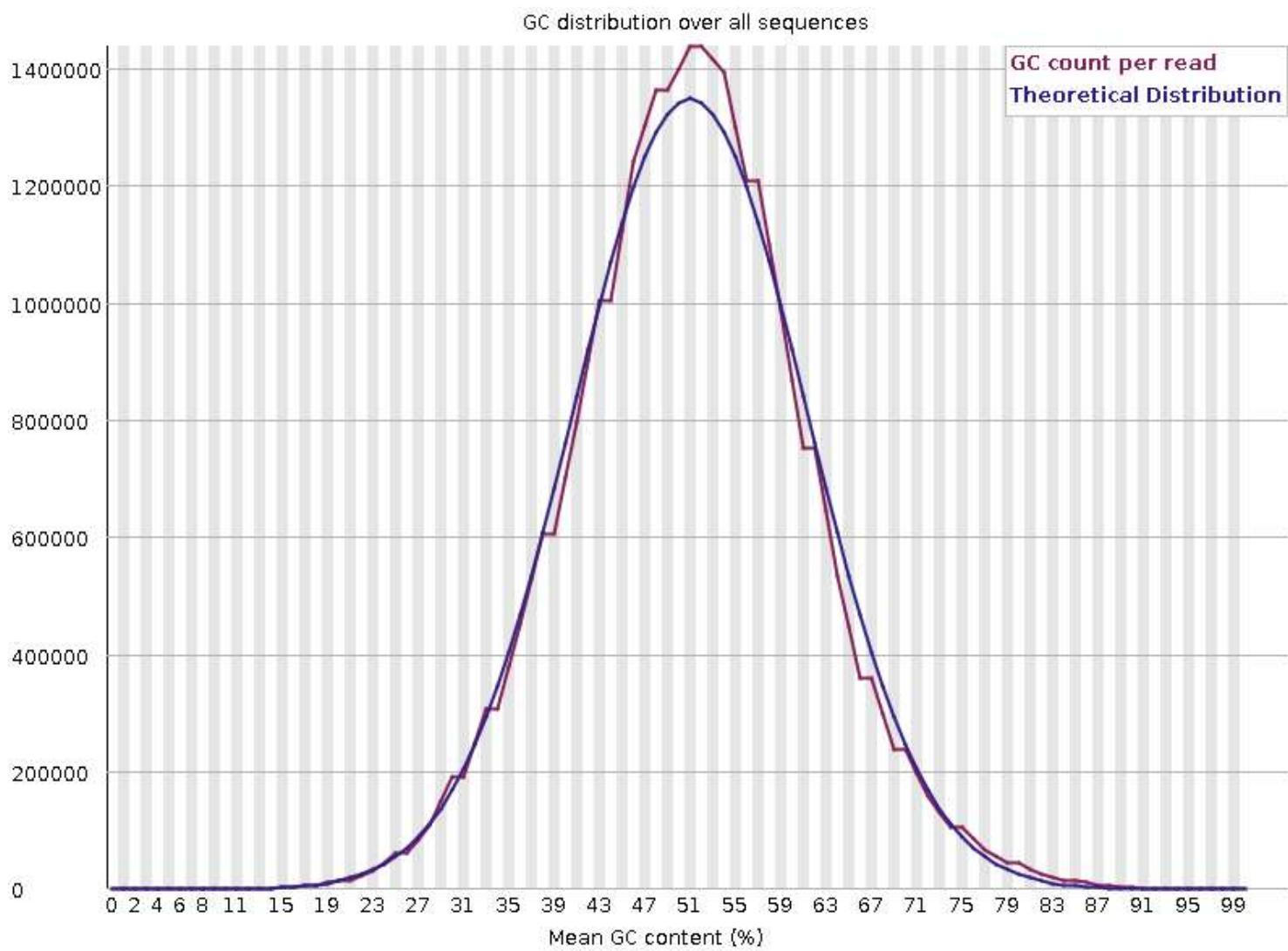


Per base sequence content



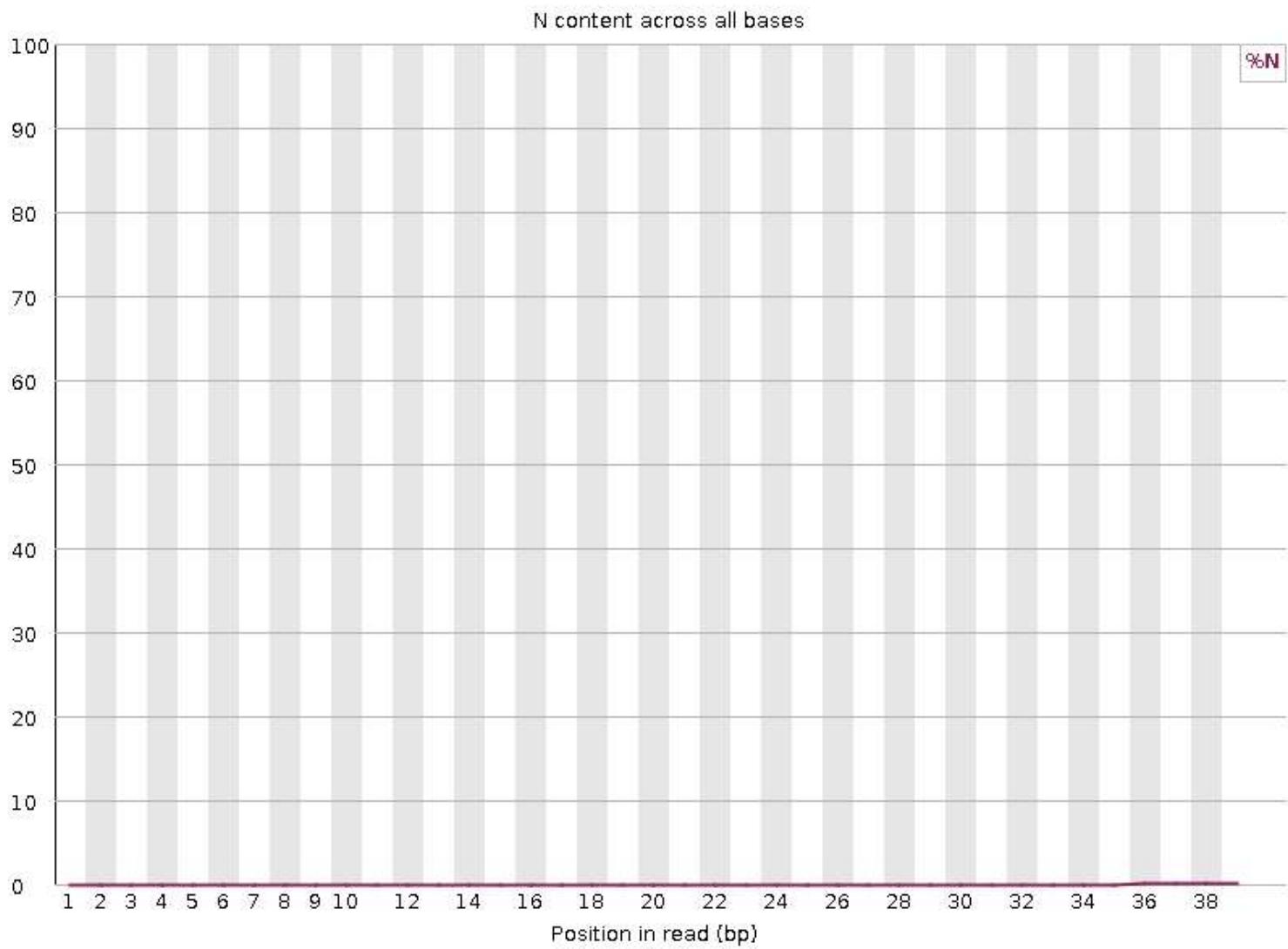


Per sequence GC content



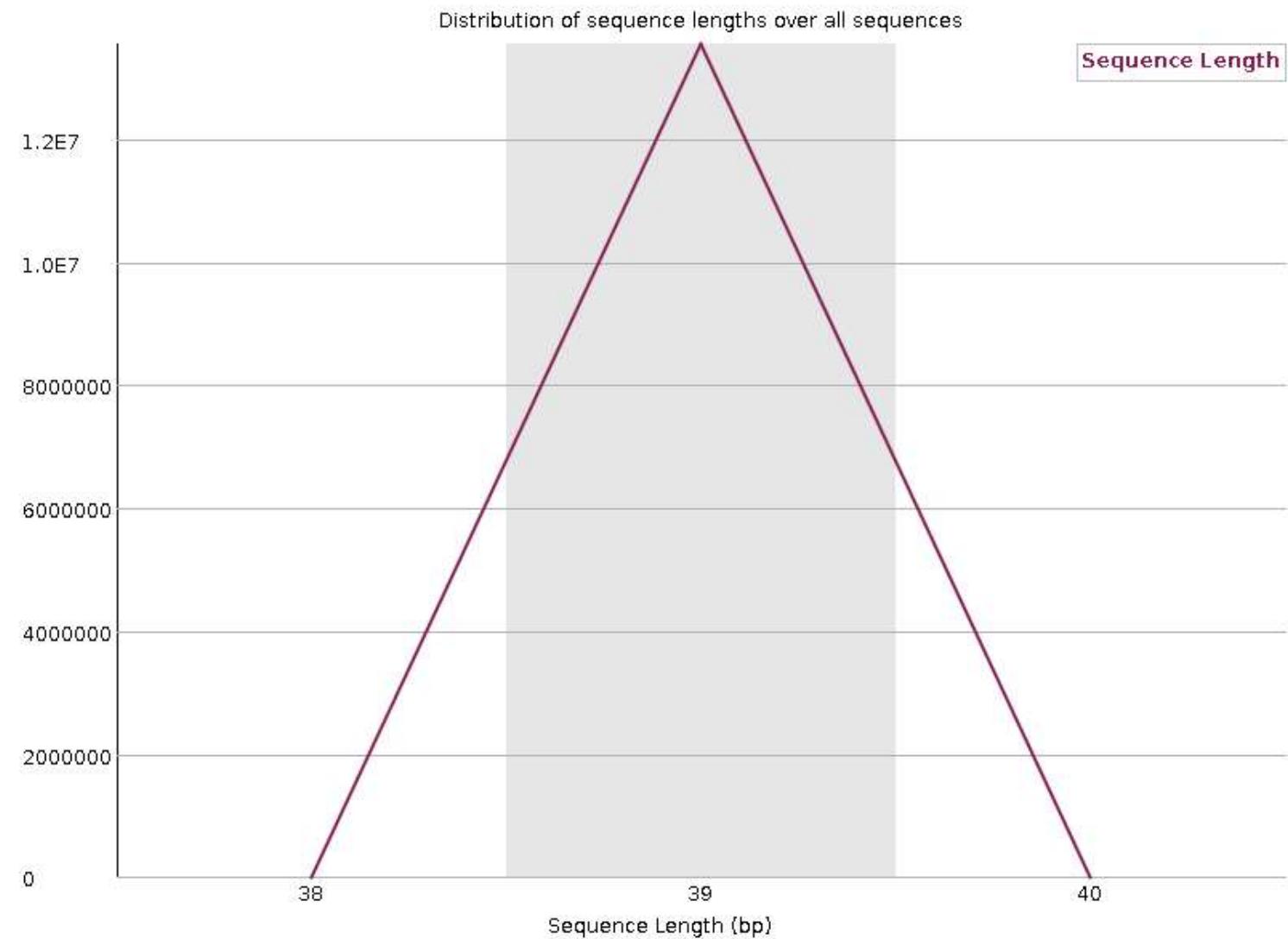


Per base N content





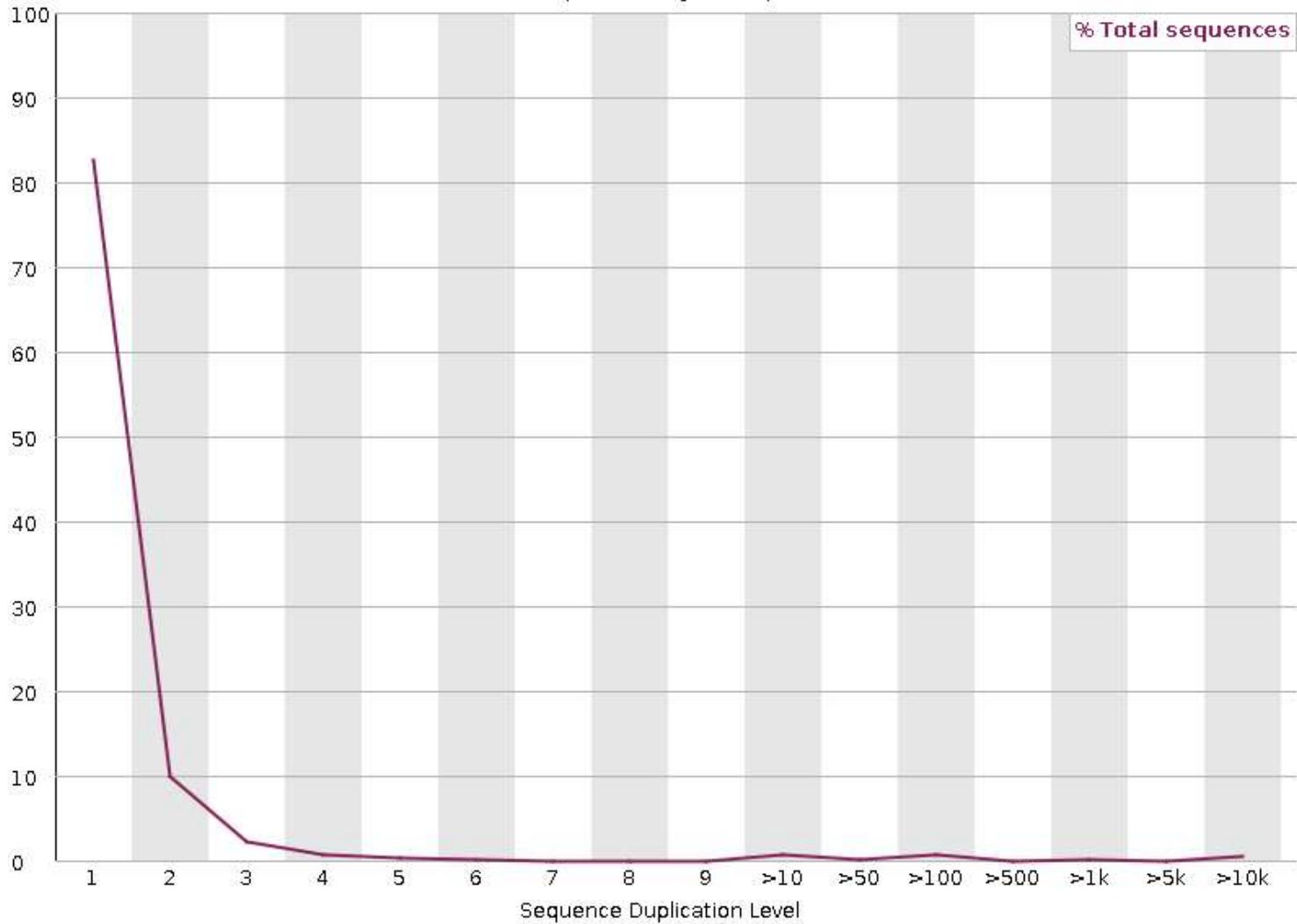
Sequence Length Distribution





Sequence Duplication Levels

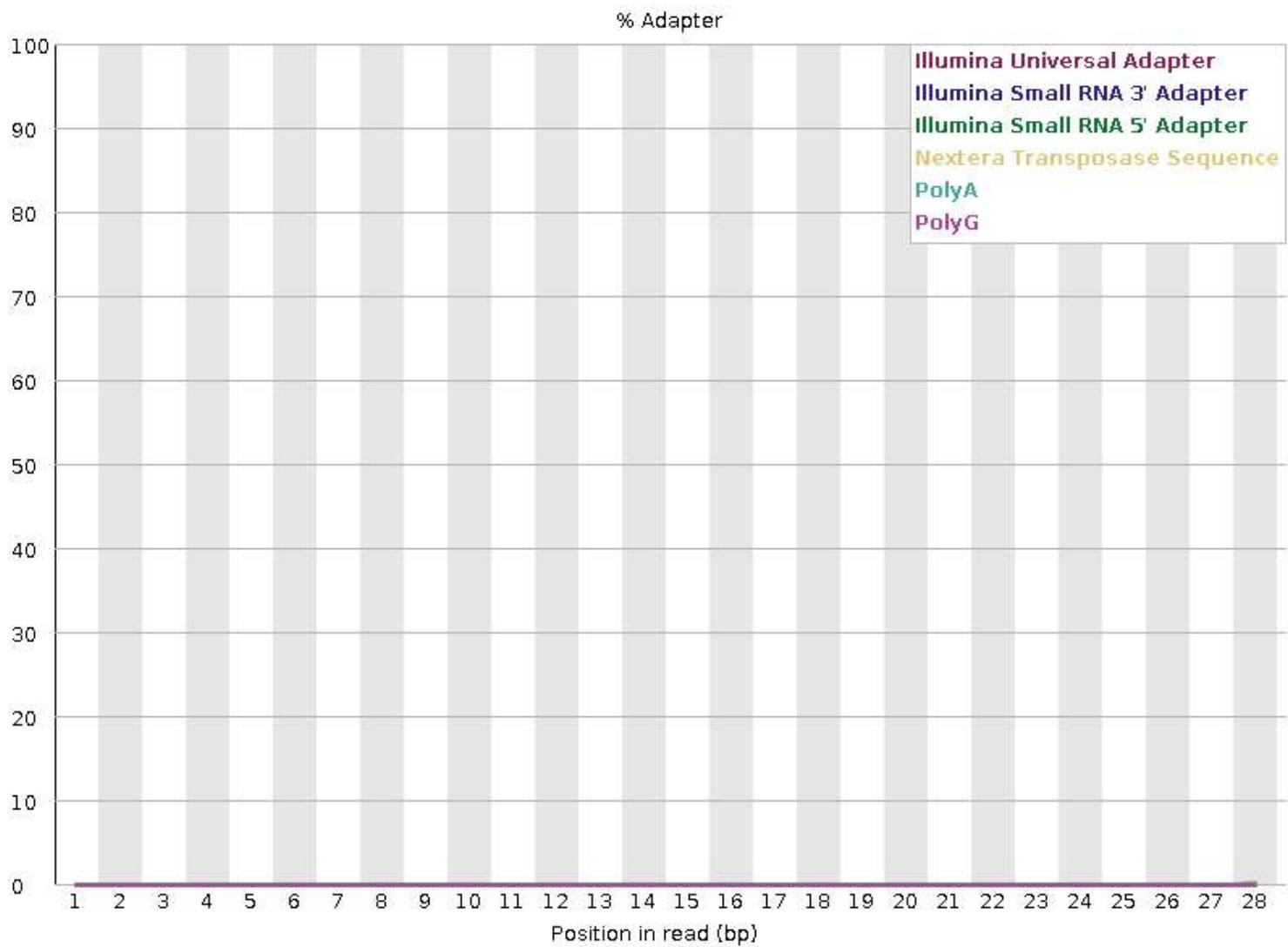
Percent of seqs remaining if deduplicated 89.11%



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCTGTATGCCGTCTTCTGCTTGAAAAAA	39681	0.2928558407695538	Illumina Single End Adapter 1 (100% over 33bp)
GATCGGAAGAGCTGTATGCCGTCTTCTGCTTAGATCGG	29017	0.2141528170058754	Illumina Single End Adapter 1 (96% over 32bp)

Adapter Content



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