

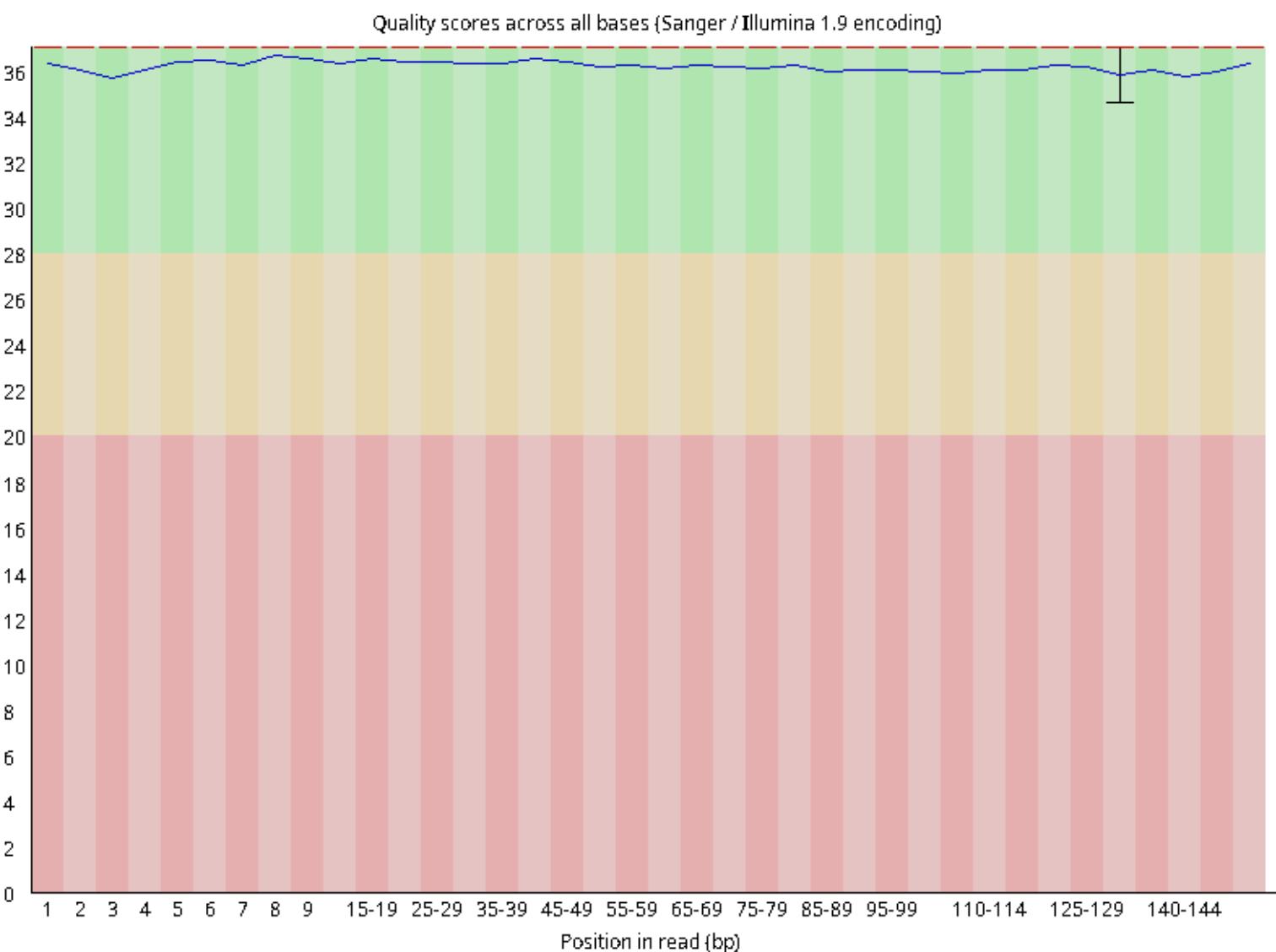
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Basic Statistics

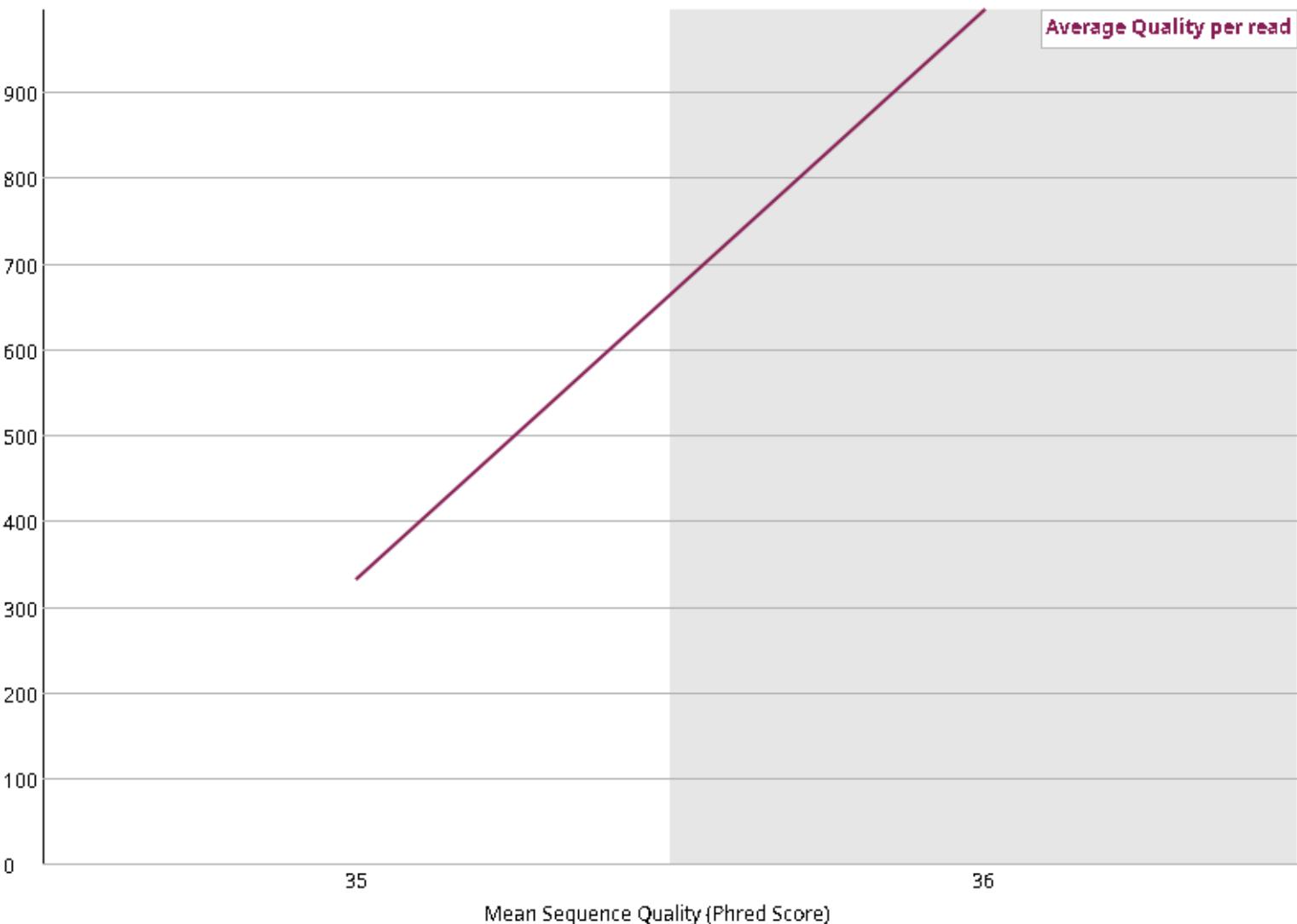
Measure	Value
Filename	SelmaBouvier_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1328
Total Bases	200.5 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	45

Per base sequence quality

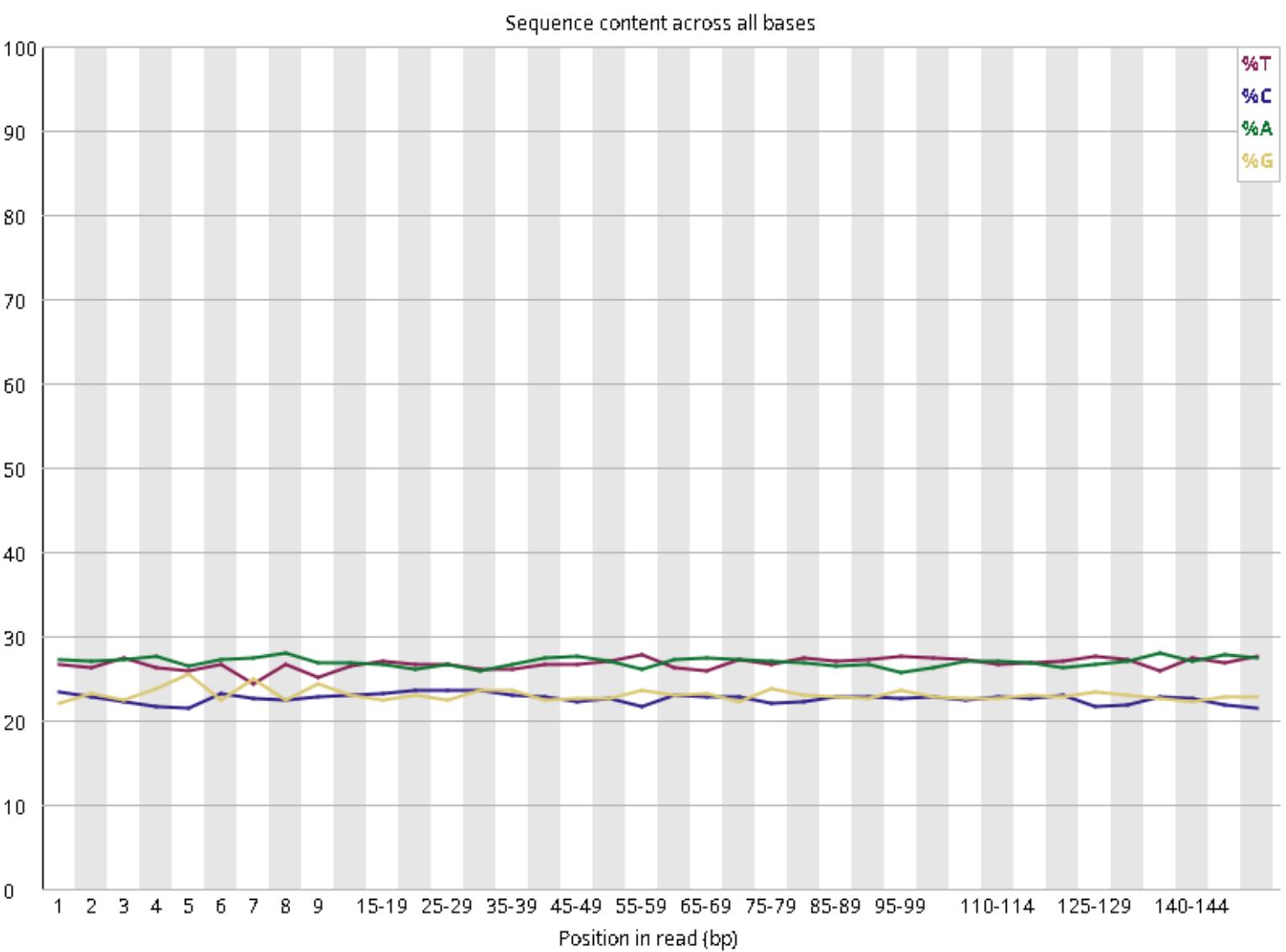


Per sequence quality scores

Quality score distribution over all sequences

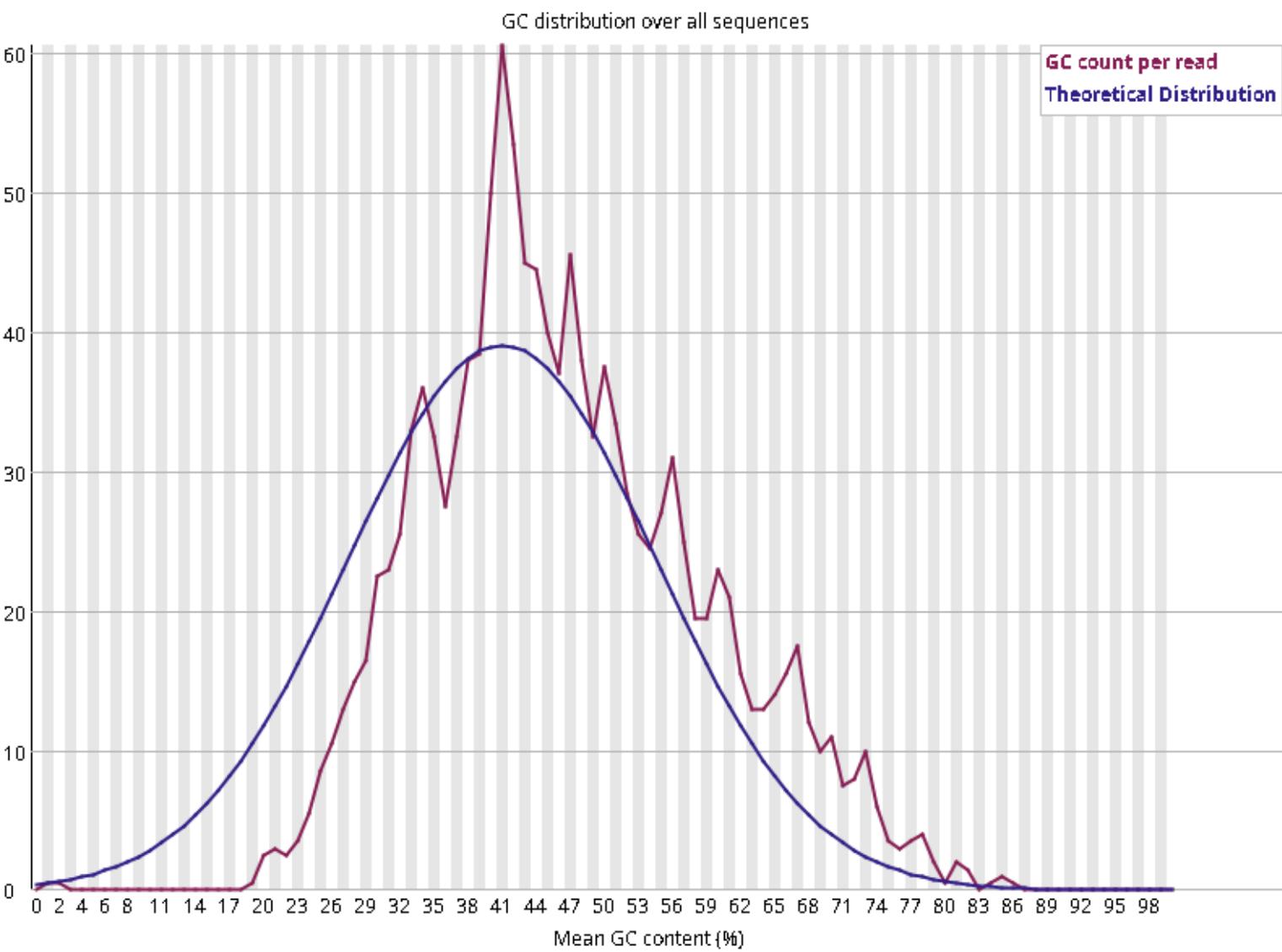


Per base sequence content





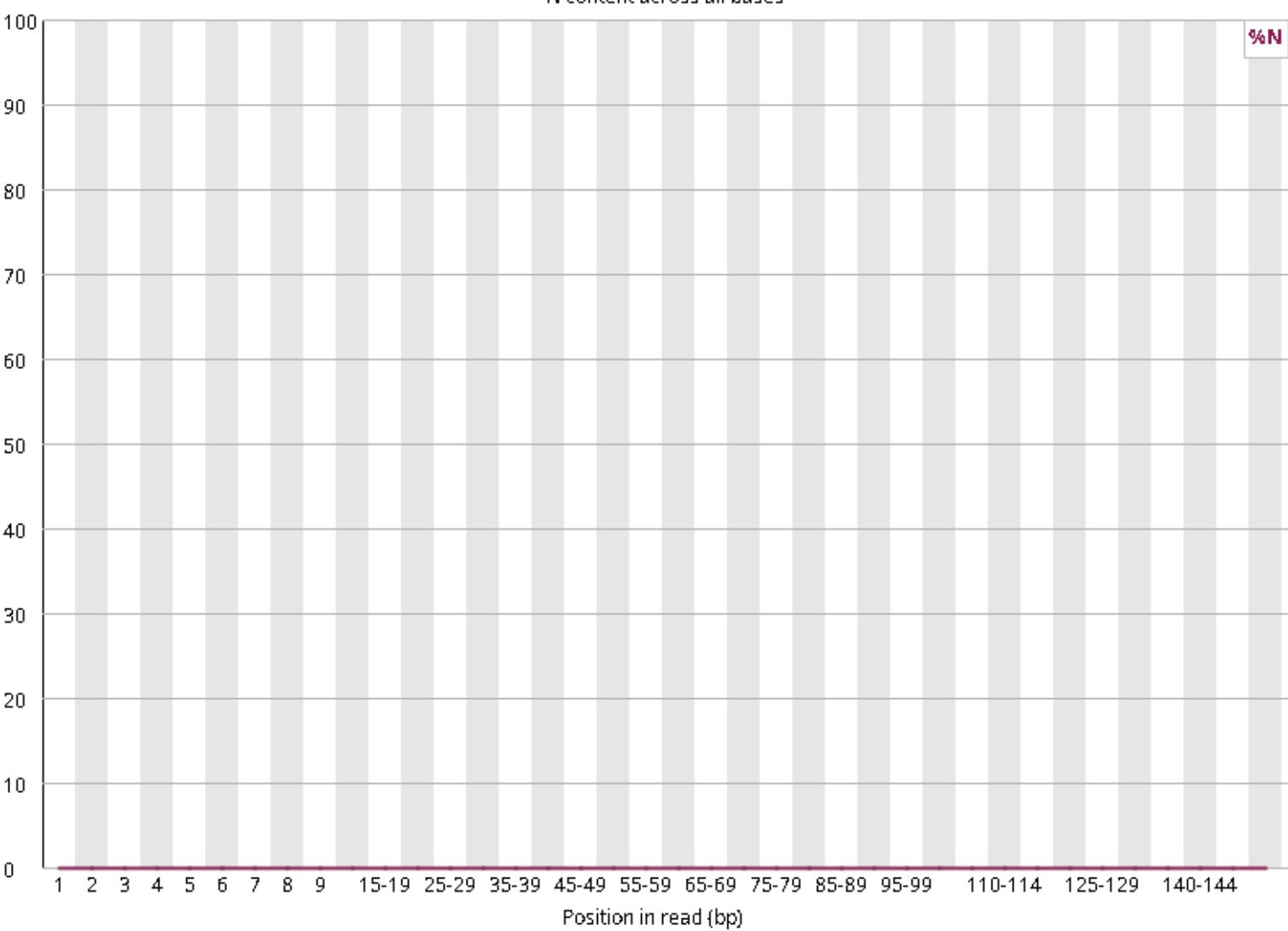
Per sequence GC content





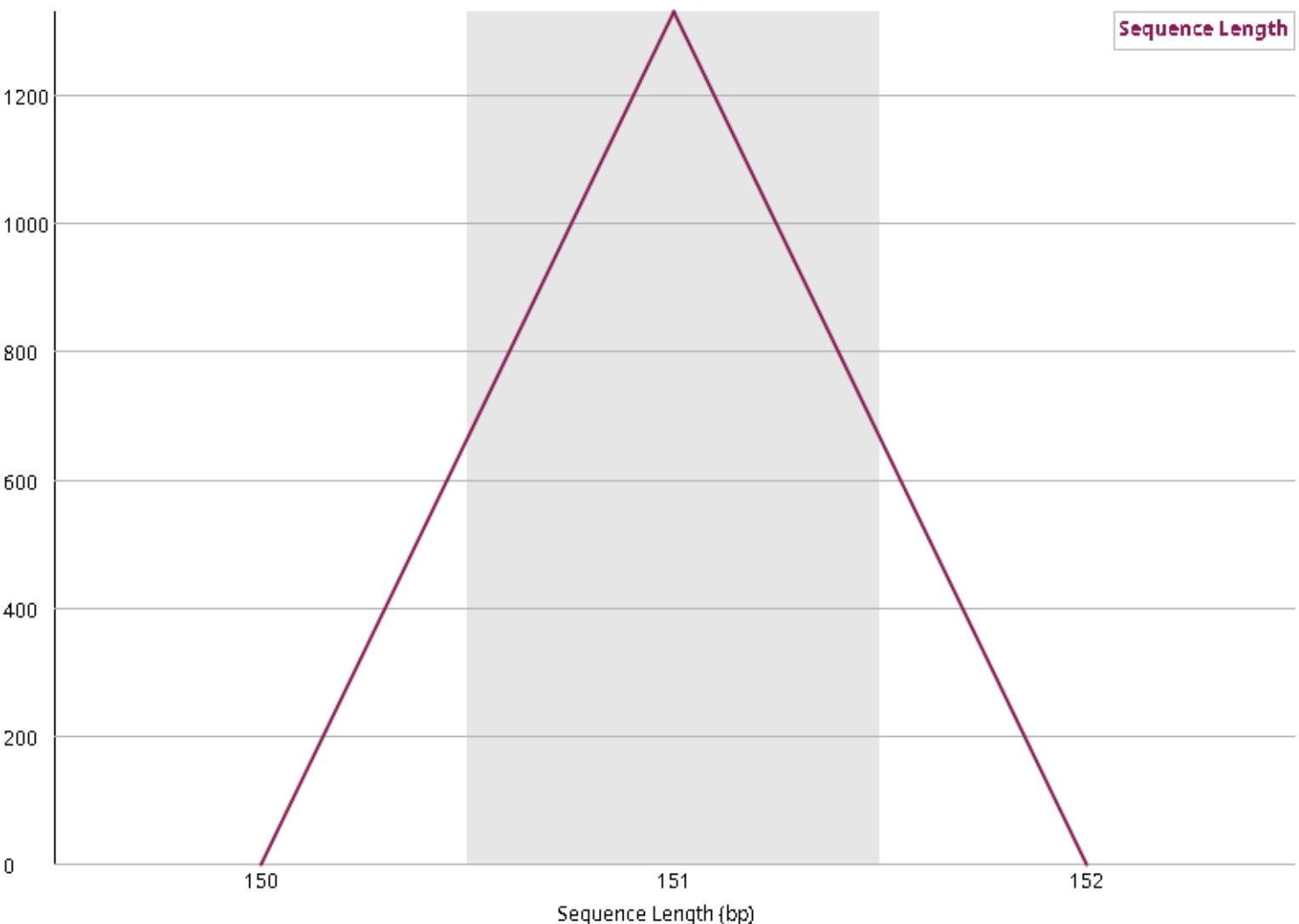
Per base N content

N content across all bases



Sequence Length Distribution

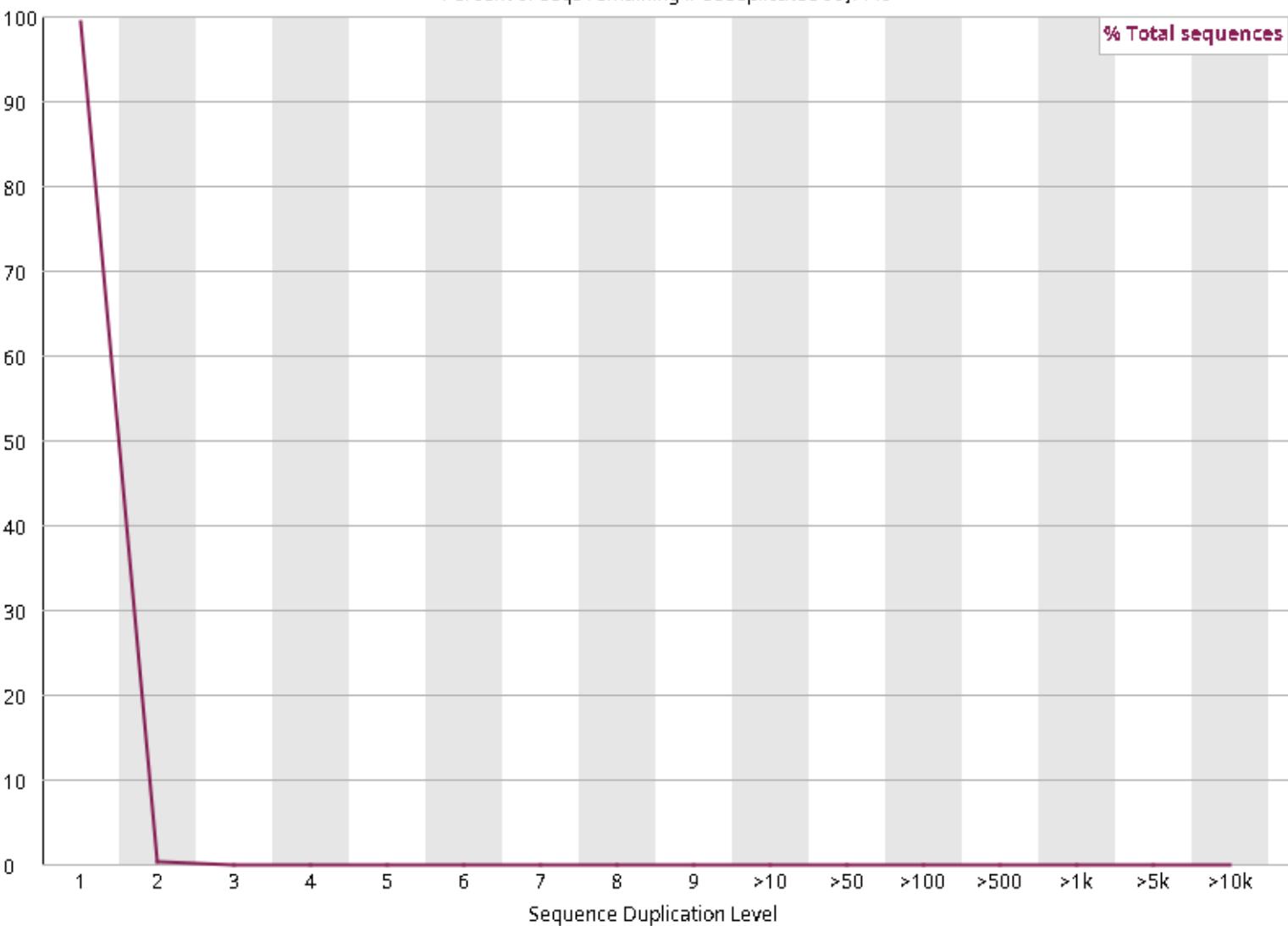
Distribution of sequence lengths over all sequences





Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,77%

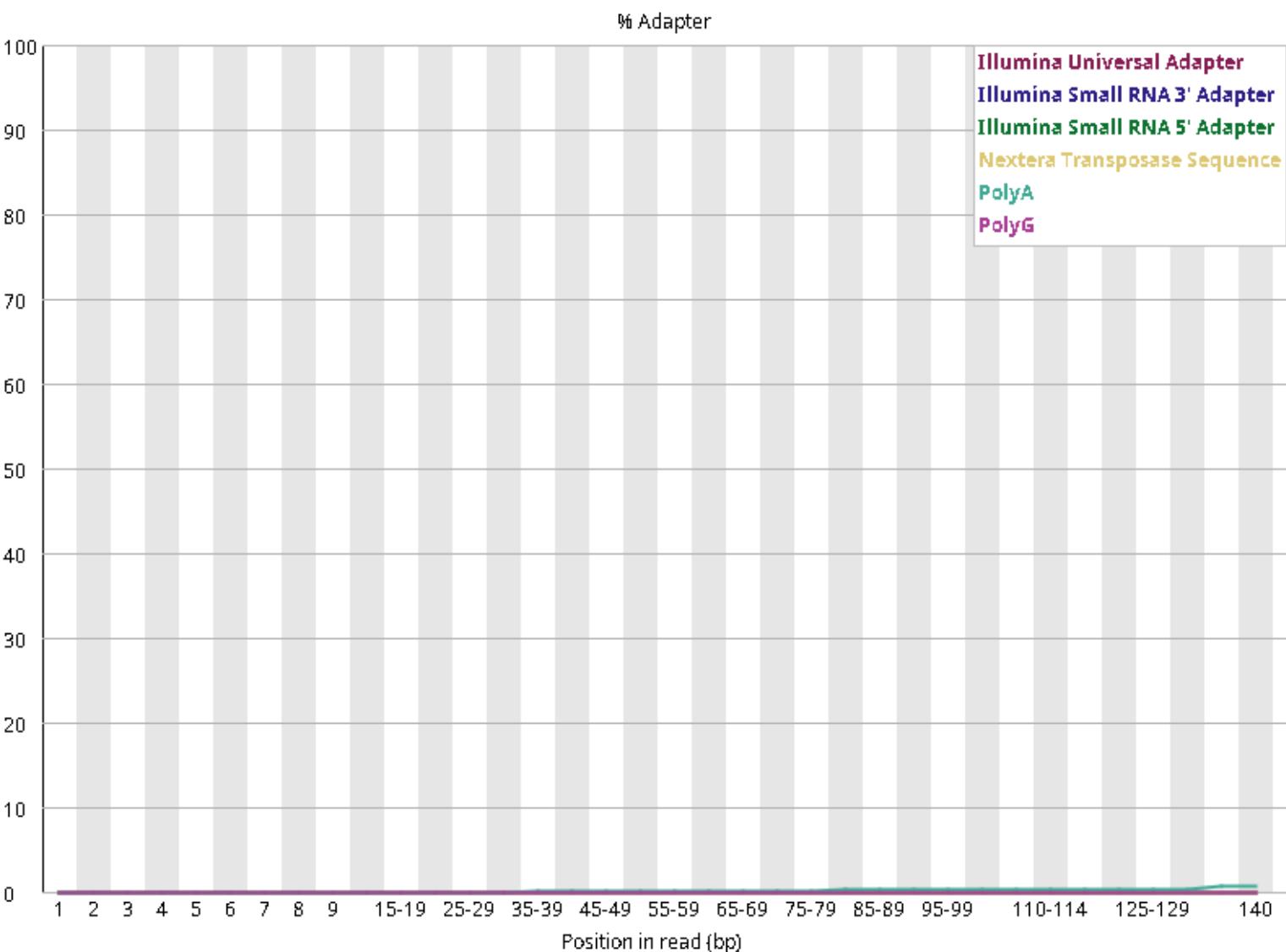


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CACTGAGTTGTGAATTTTTCTTAAAGCAGTACTGTAGTACTGAATATT	2	0.15060240963855423	No Hit
TCCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATATGAAGGGAGCGATT	2	0.15060240963855423	No Hit
AGGAACATAAGACTCAAATCTTAGAAACCAGATACGCTCAAAGCAAGTCA	2	0.15060240963855423	No Hit



Adapter Content



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