

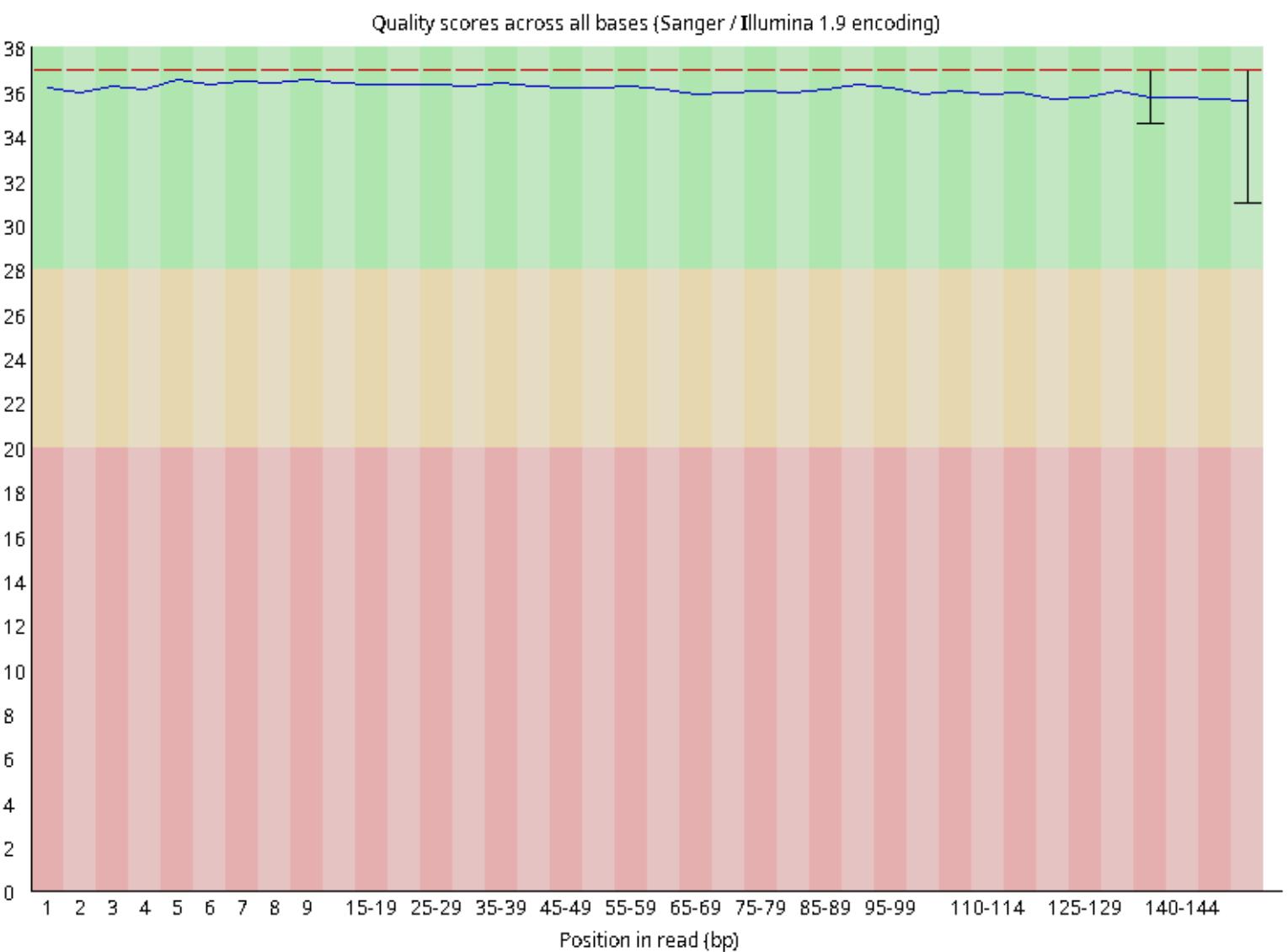
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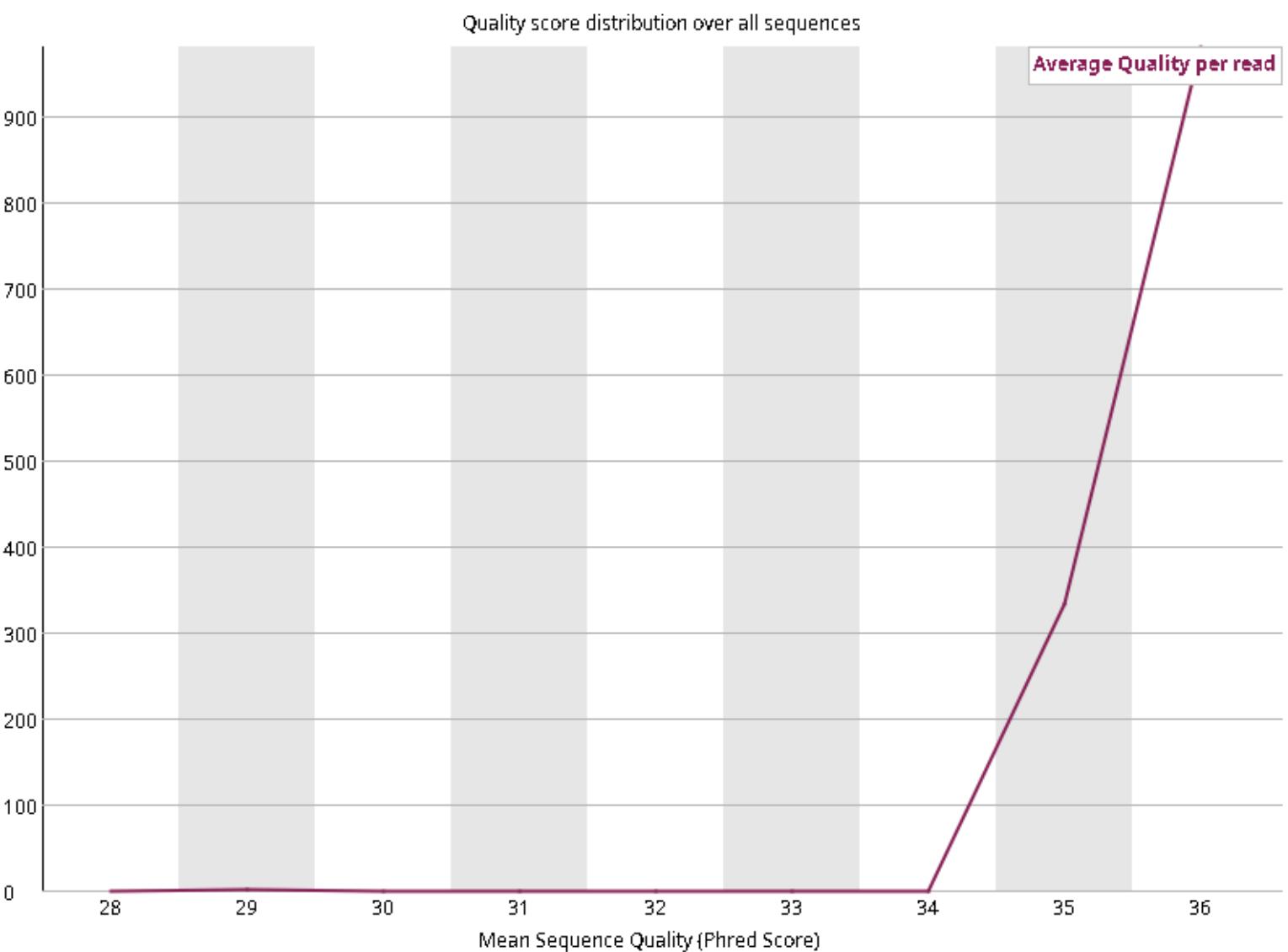
Basic Statistics

Measure	Value
Filename	PattyBouvier_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1320
Total Bases	199.3 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

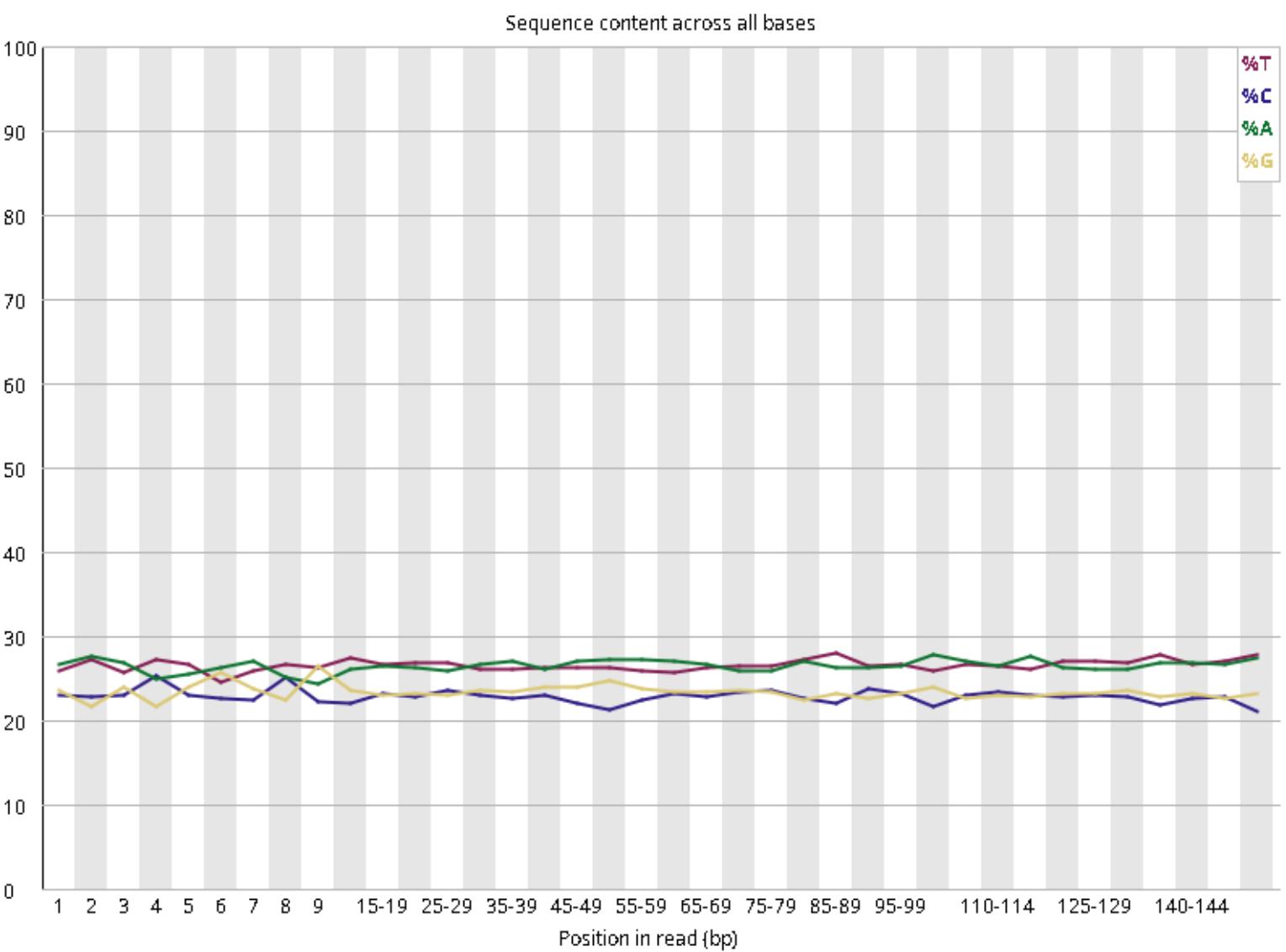
Per base sequence quality



Per sequence quality scores

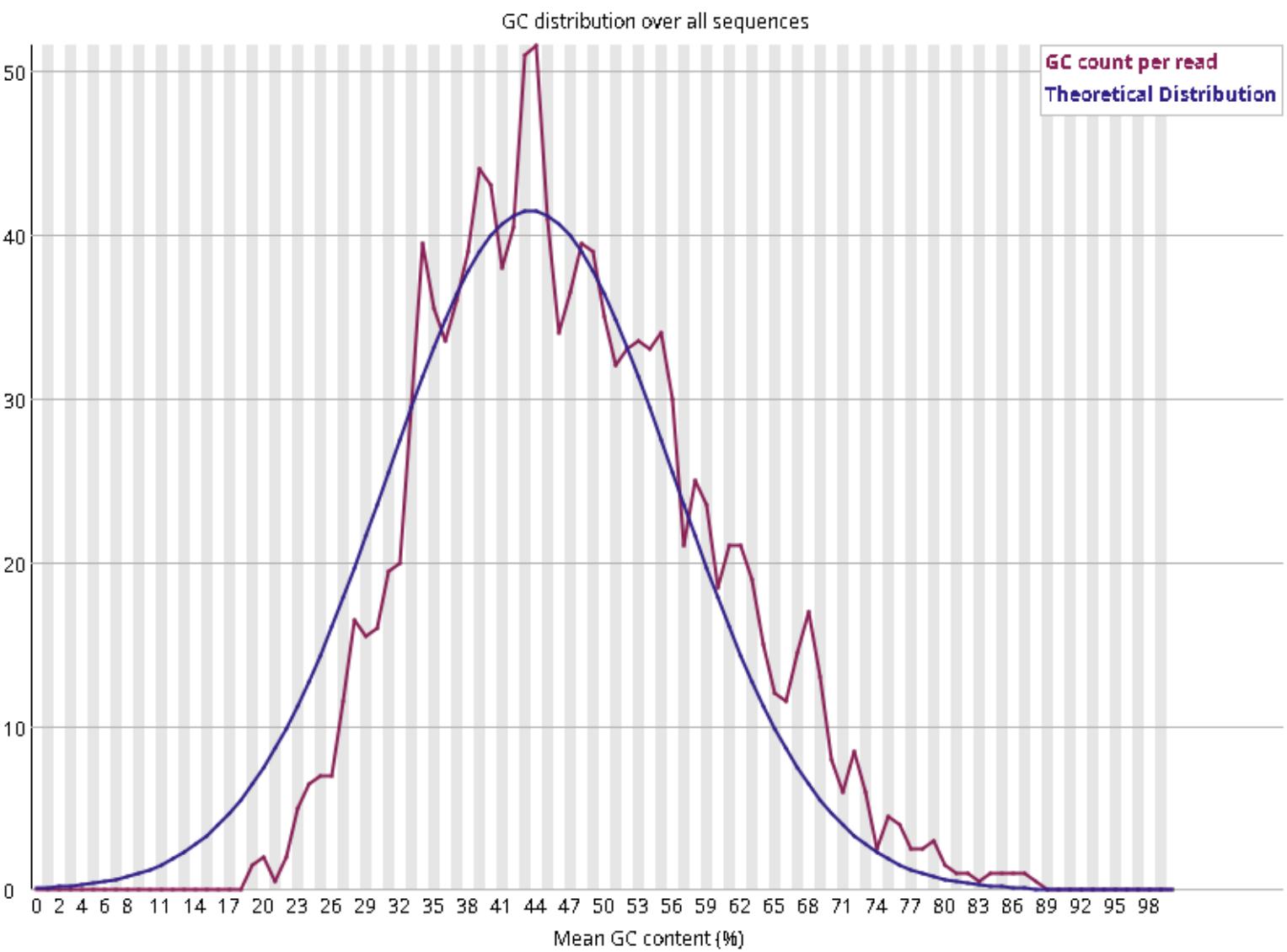


Per base sequence content





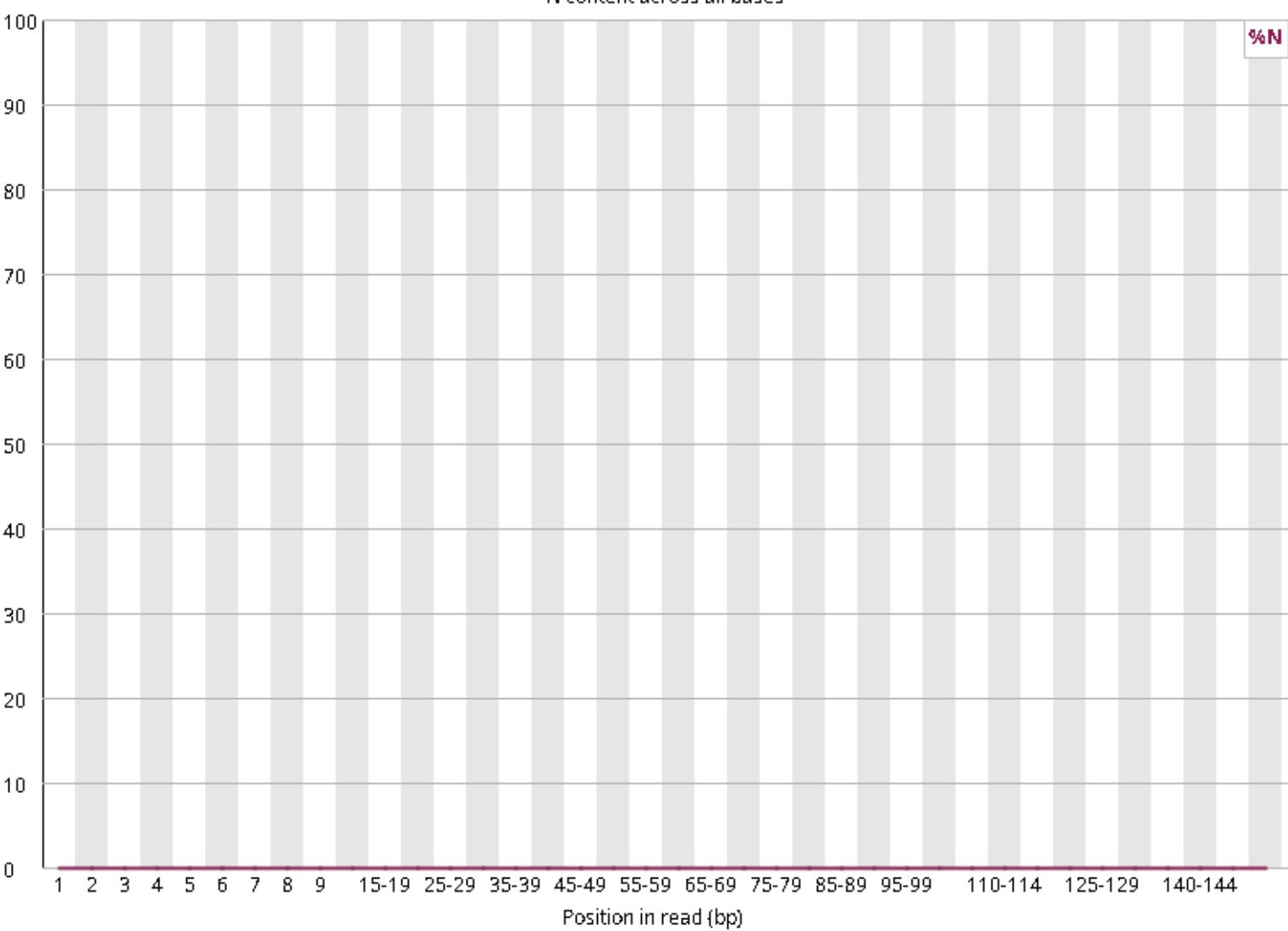
Per sequence GC content





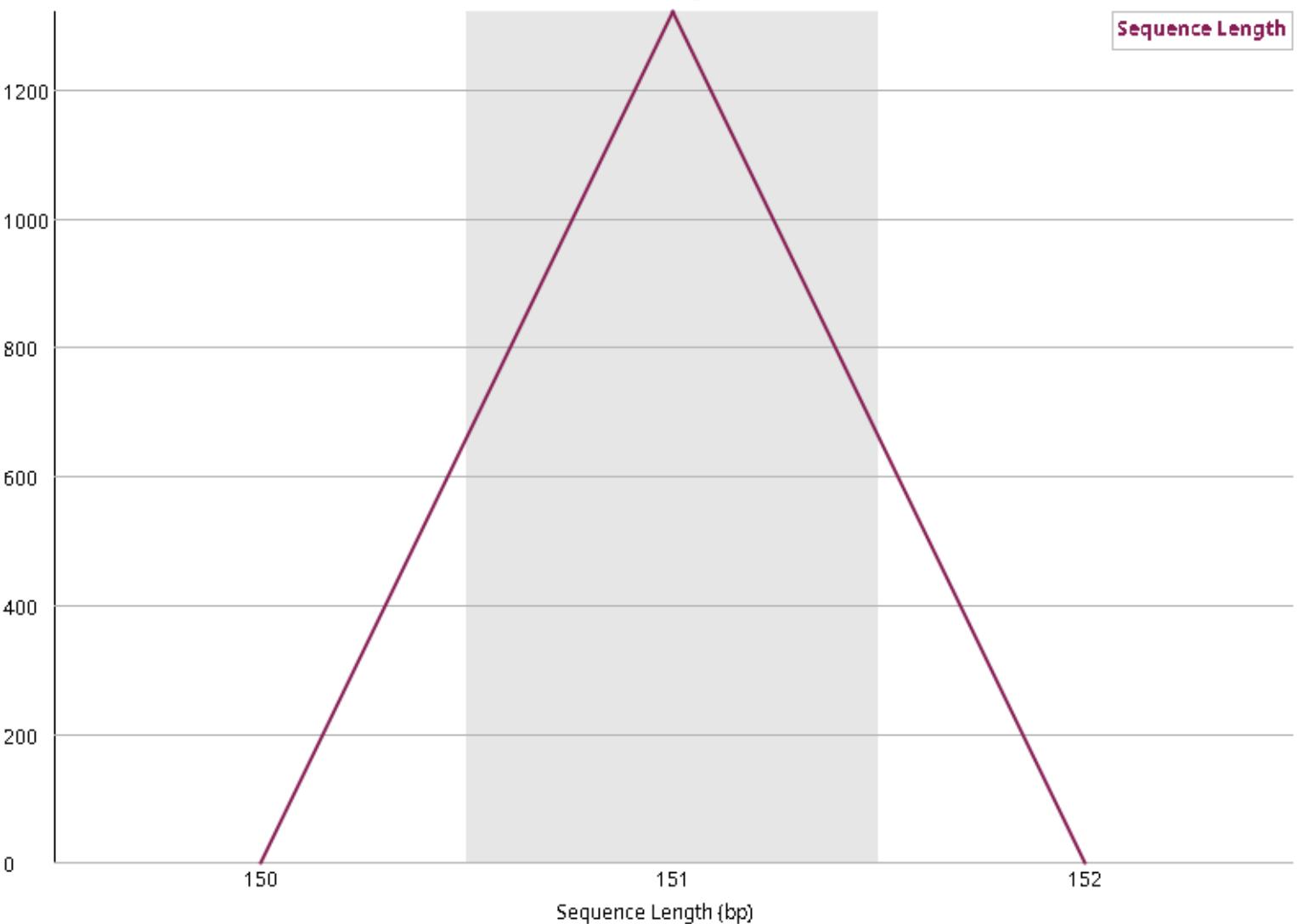
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

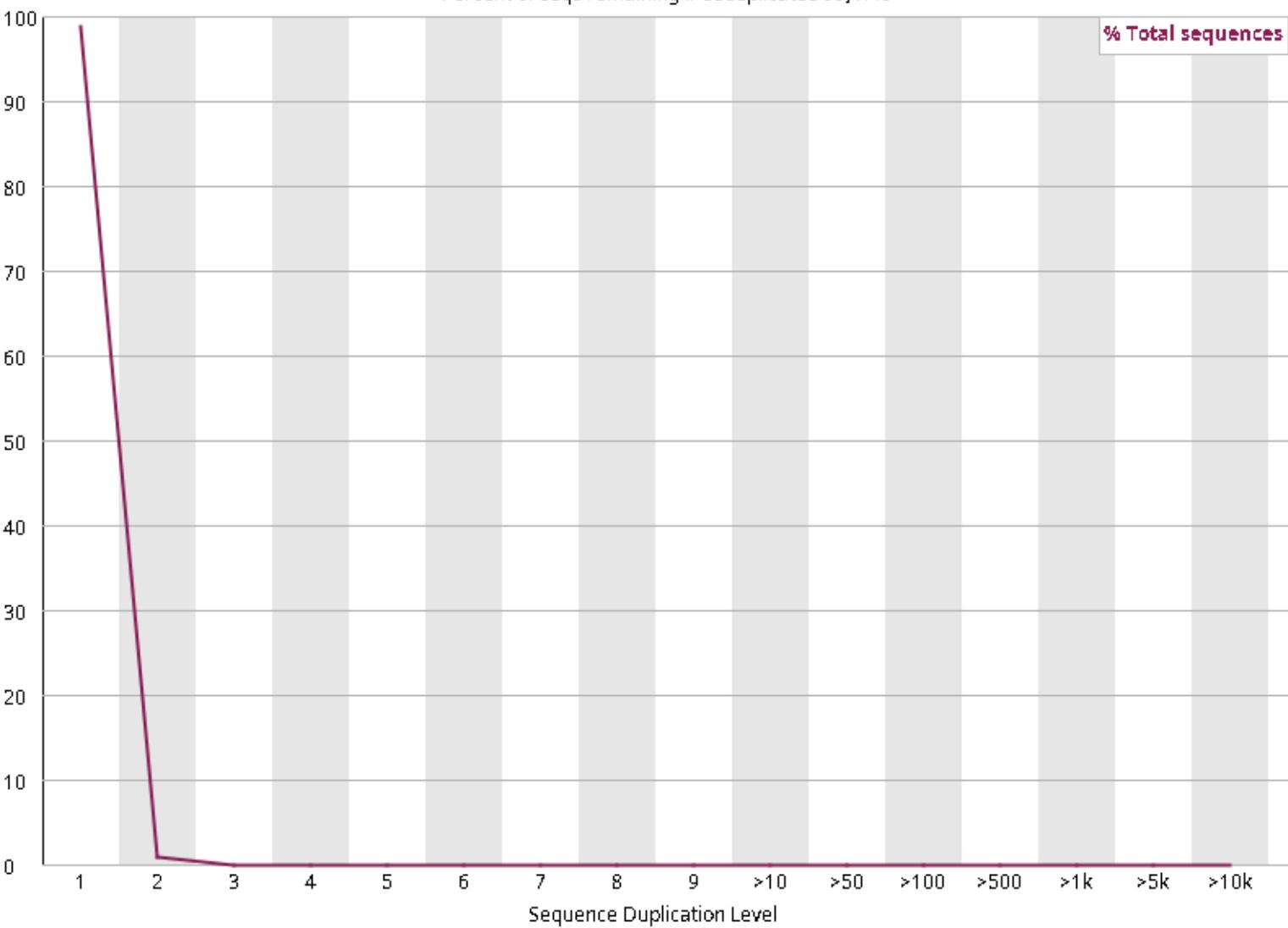


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,47%

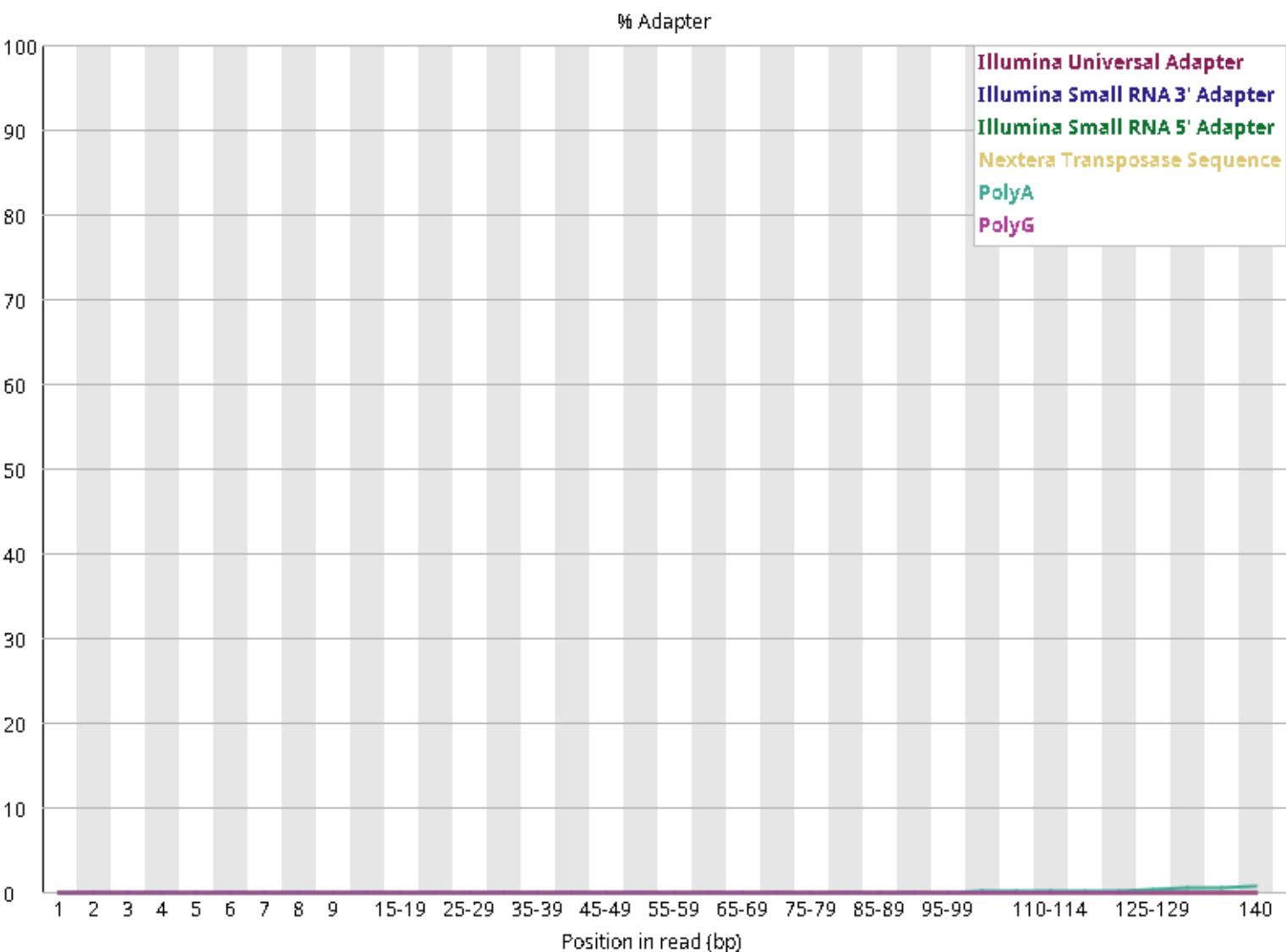


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
ACGCTGACGCTGGTGCCCTGCTGGGTGCCACGAGGTGGTGGTCTCC	2	0.15151515151515152	No Hit
ATCCTGACCCTGCTCCCTGGCTGCCATCTTCCCCGGGCCTTCCTAA	2	0.15151515151515152	No Hit
TATTGTGTGCTTCATGTCTCACTTAACTTGATCTCATACTGATCAT	2	0.15151515151515152	No Hit
GCACTAAACTGGTGCTTATTGATATTCTAAGAAATATCTGTGAAATATC	2	0.15151515151515152	No Hit
AAAGTGAATCTAACTAGTTAACCTTTAAATGAAGGTTGTATAACA	2	0.15151515151515152	No Hit
ACCGTCGTTGCCTTGATTCCAGAGAACAGATGATTCTTGGGATTGGG	2	0.15151515151515152	No Hit
AAATGAACCTAACAGGCCACCTTCAGGATGCCACCTCGCTC	2	0.15151515151515152	No Hit



Adapter Content



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