

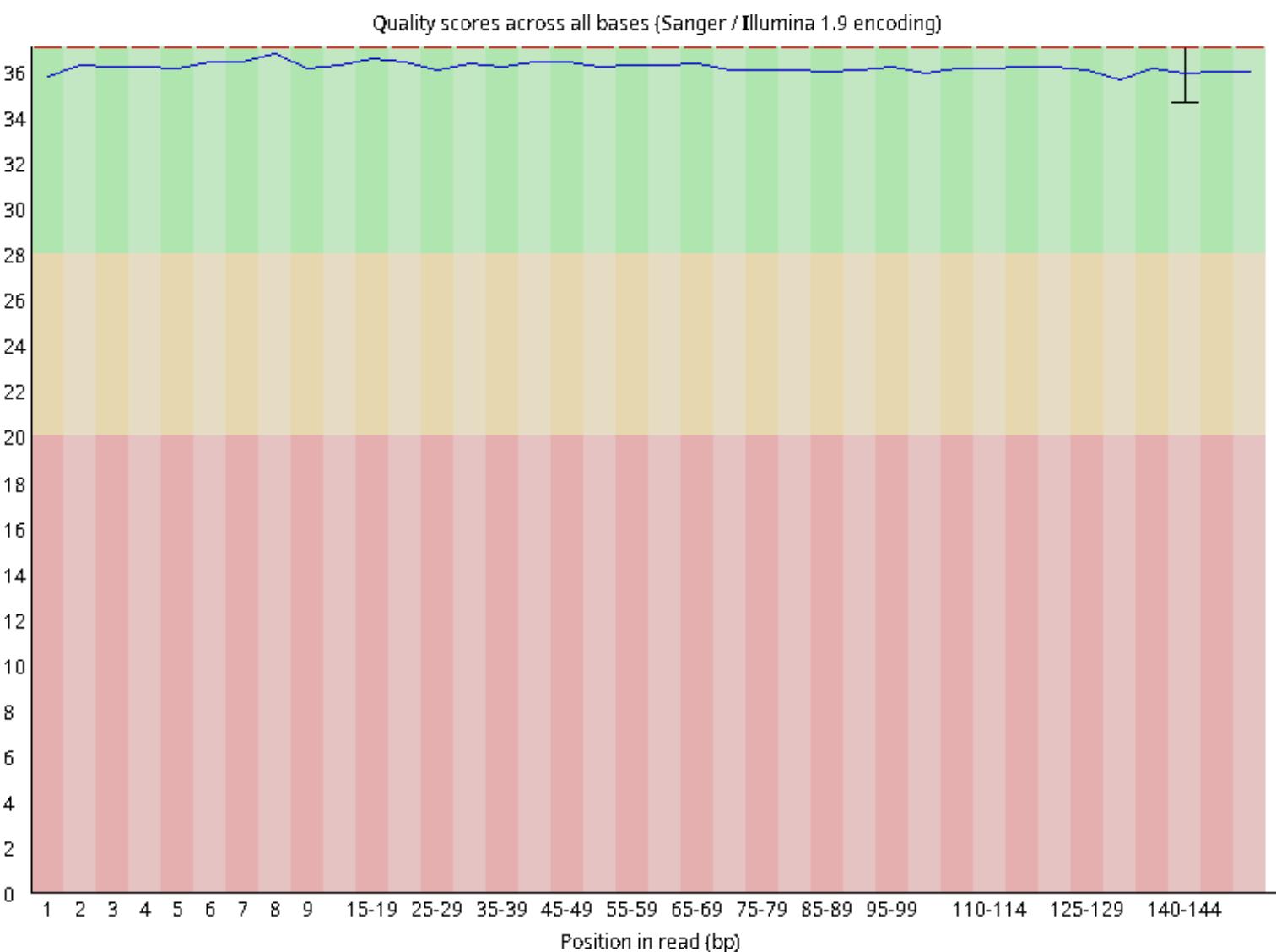
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Basic Statistics

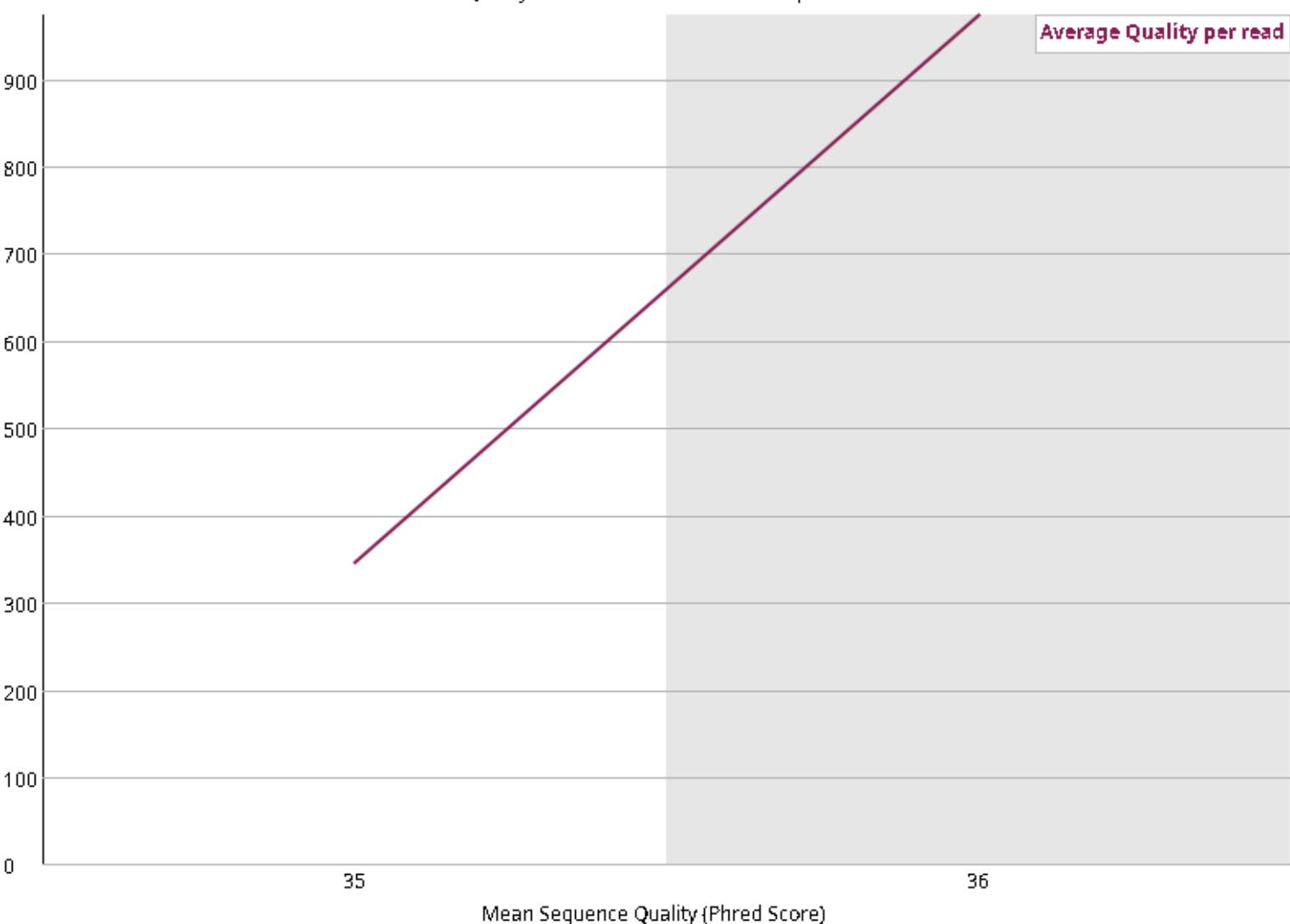
Measure	Value
Filename	AbrahamSimpson_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1320
Total Bases	199.3 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

Per base sequence quality

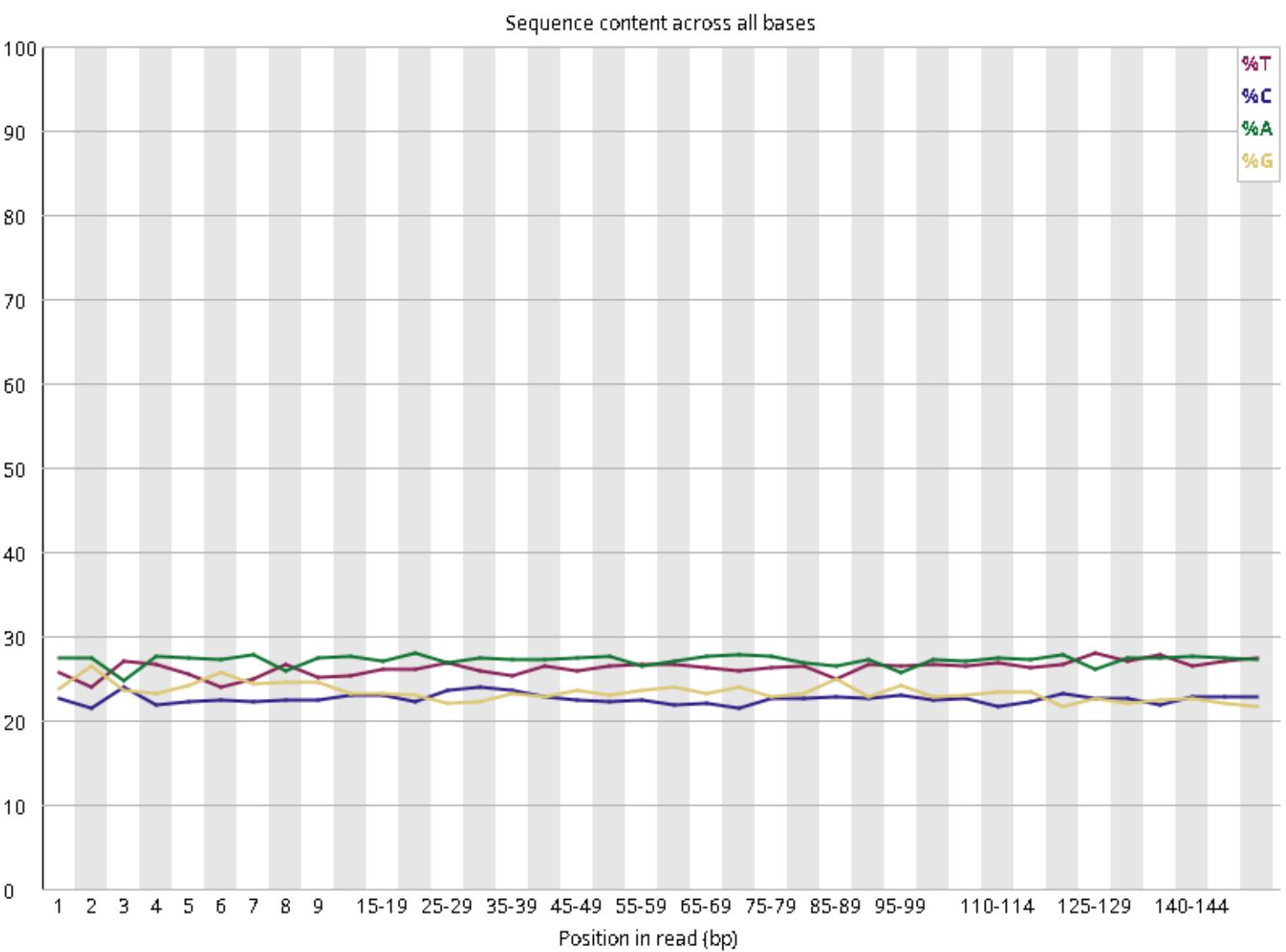


✓ Per sequence quality scores

Quality score distribution over all sequences

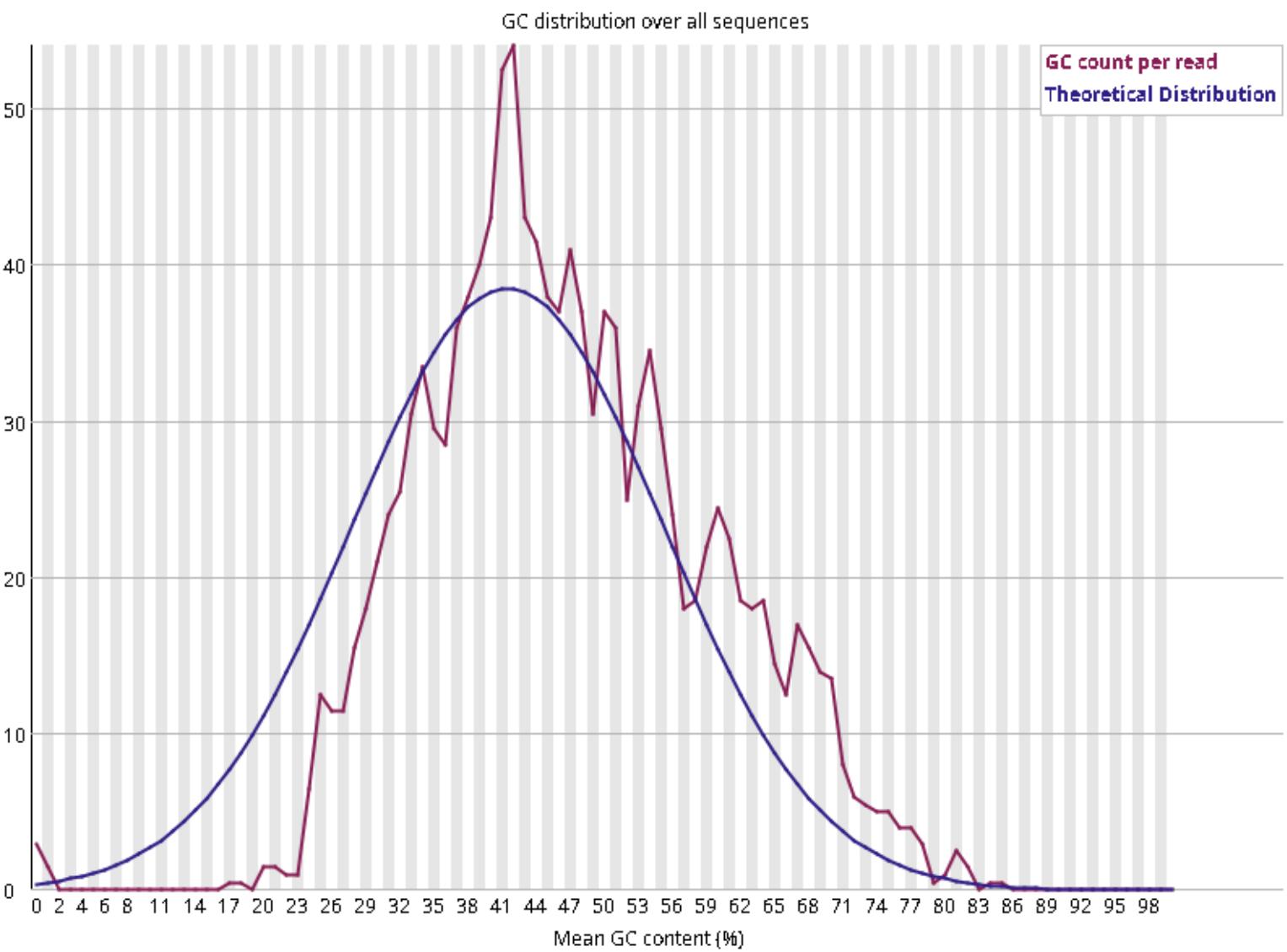


Per base sequence content





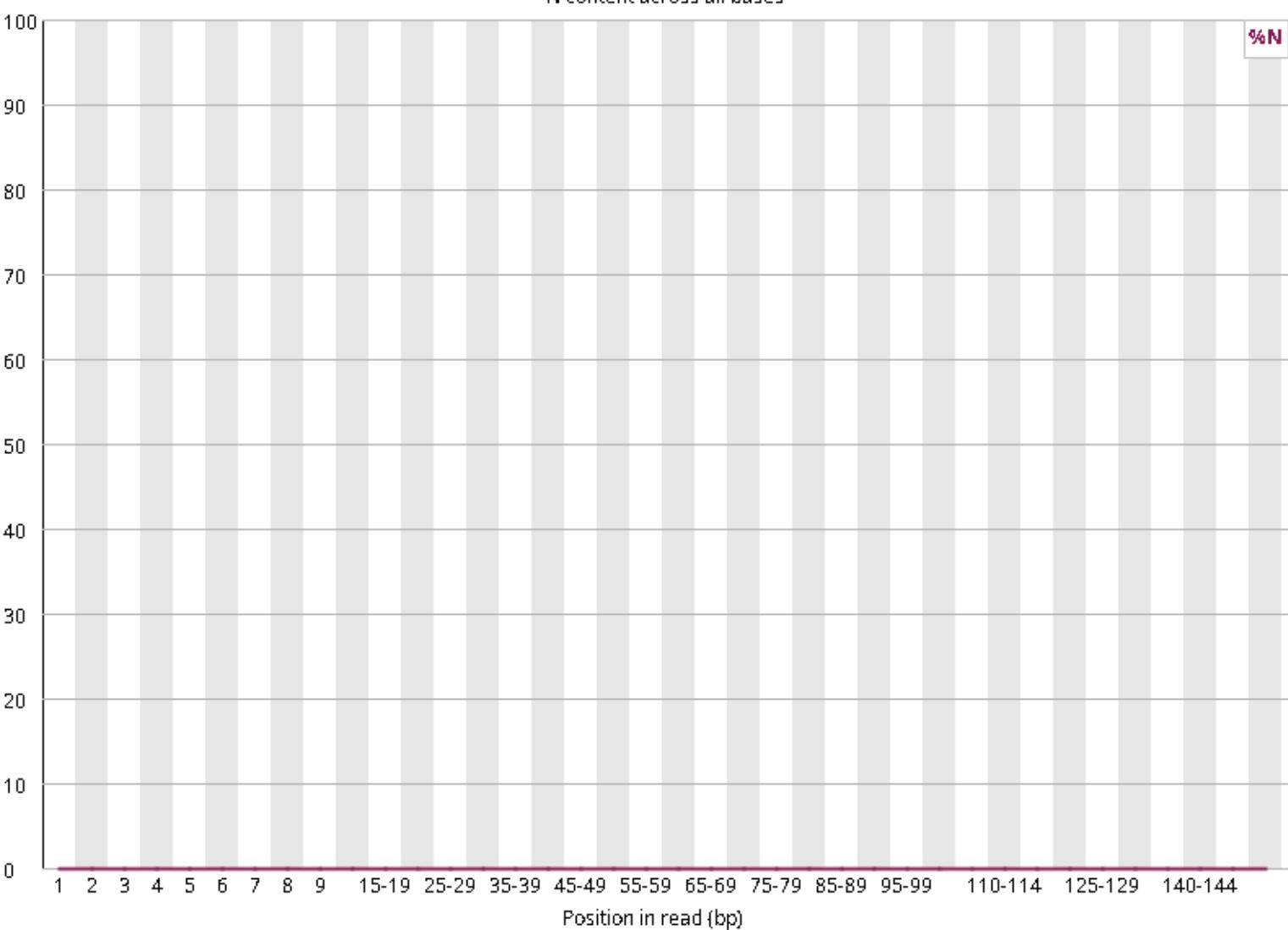
Per sequence GC content





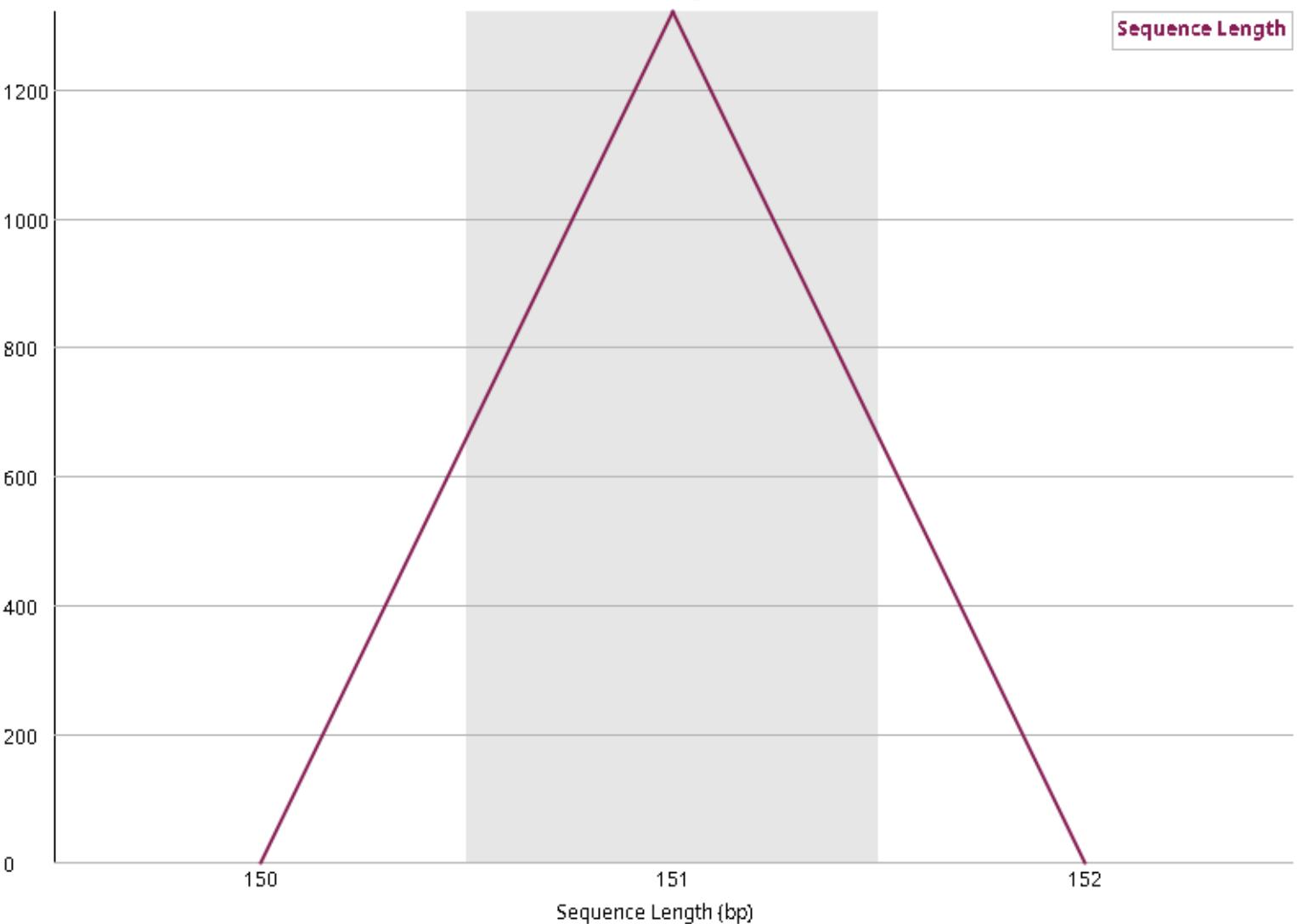
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

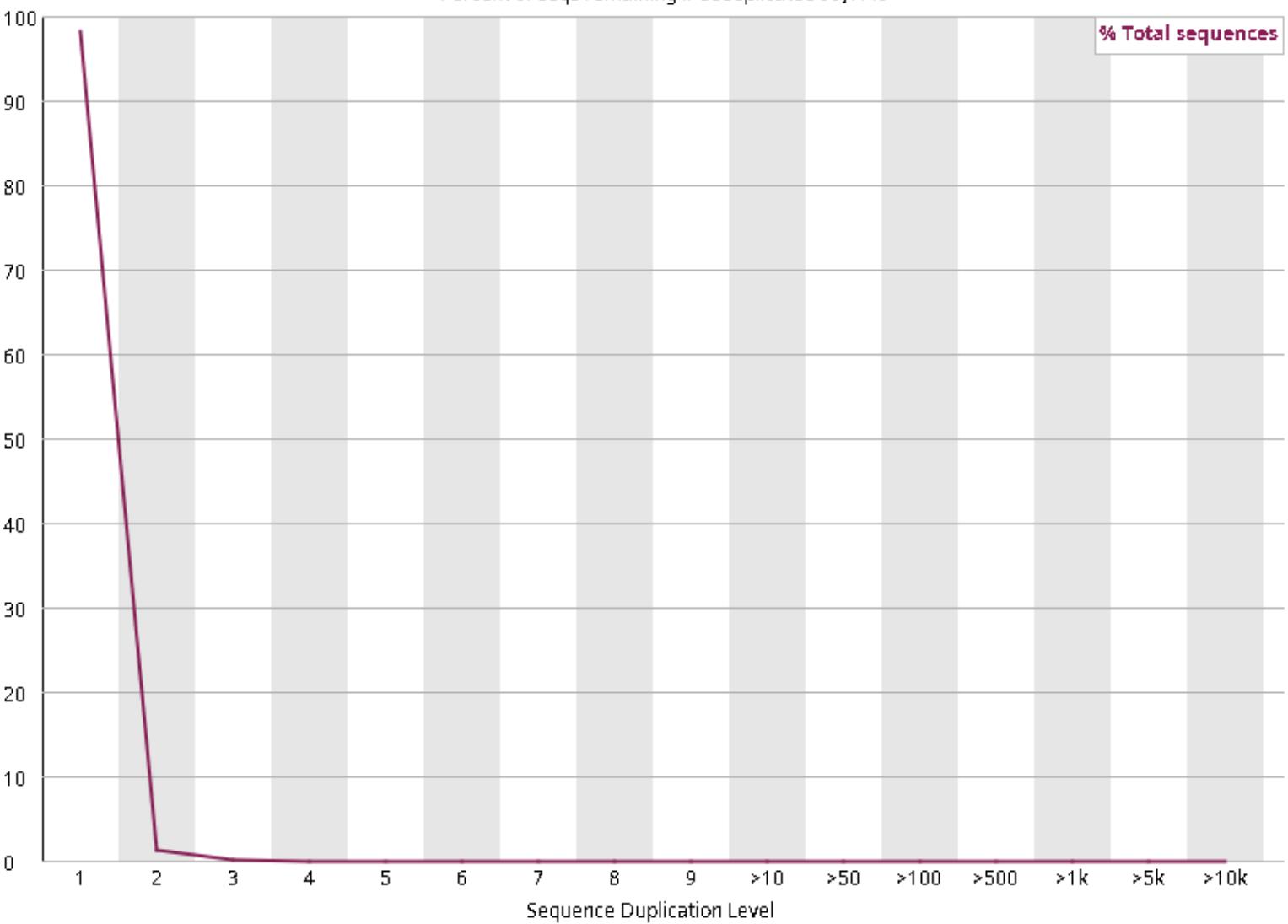


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,17%



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3	0.227272727272727	No Hit
TCCCCCTCACTGAATGCCCTAACATGTGACCAGGGGTATTTCAGAGAGGGC	2	0.15151515151515152	No Hit
ATTCGAATTCTGACTTGAGAACCGATCTGAGCCTGAATCTGATGGCA	2	0.15151515151515152	No Hit
GCACTTGAAGCCGAGGTGGCCGGGCCTCTGGCTCCCTGTCGCCACCCA	2	0.15151515151515152	No Hit
CTGAAGAACAACTGCAGAACAGGCAGAACAGGGATCTGTTGCAGGAGGC	2	0.15151515151515152	No Hit
CATTGAAGCAATCCTGCTACGGATCTAAAAAGCATTGATTTCTCG	2	0.15151515151515152	No Hit
AGATCCCCACAGCCTGGGCAGAACAGGGCGTCAGGGCGCCAGAAGTGG	2	0.15151515151515152	No Hit

Sequence	Count	Percentage	Possible Source
CGCCGAGGACGAGTCGGCCGAGGCCTCCCCCTGGAGTTCAAGAGGGAGC	2	0.15151515151515152	No Hit
GAGTGAGGGCACAGCGGGGCCAGGGCTACCCCTCCCCAGGAGGTCGAC	2	0.15151515151515152	No Hit
AGTGATCCTCAAACACACAAACTATTACTTACAAACTGCGGTATACATT	2	0.15151515151515152	No Hit



Adapter Content

