











FastQC Report

Summary

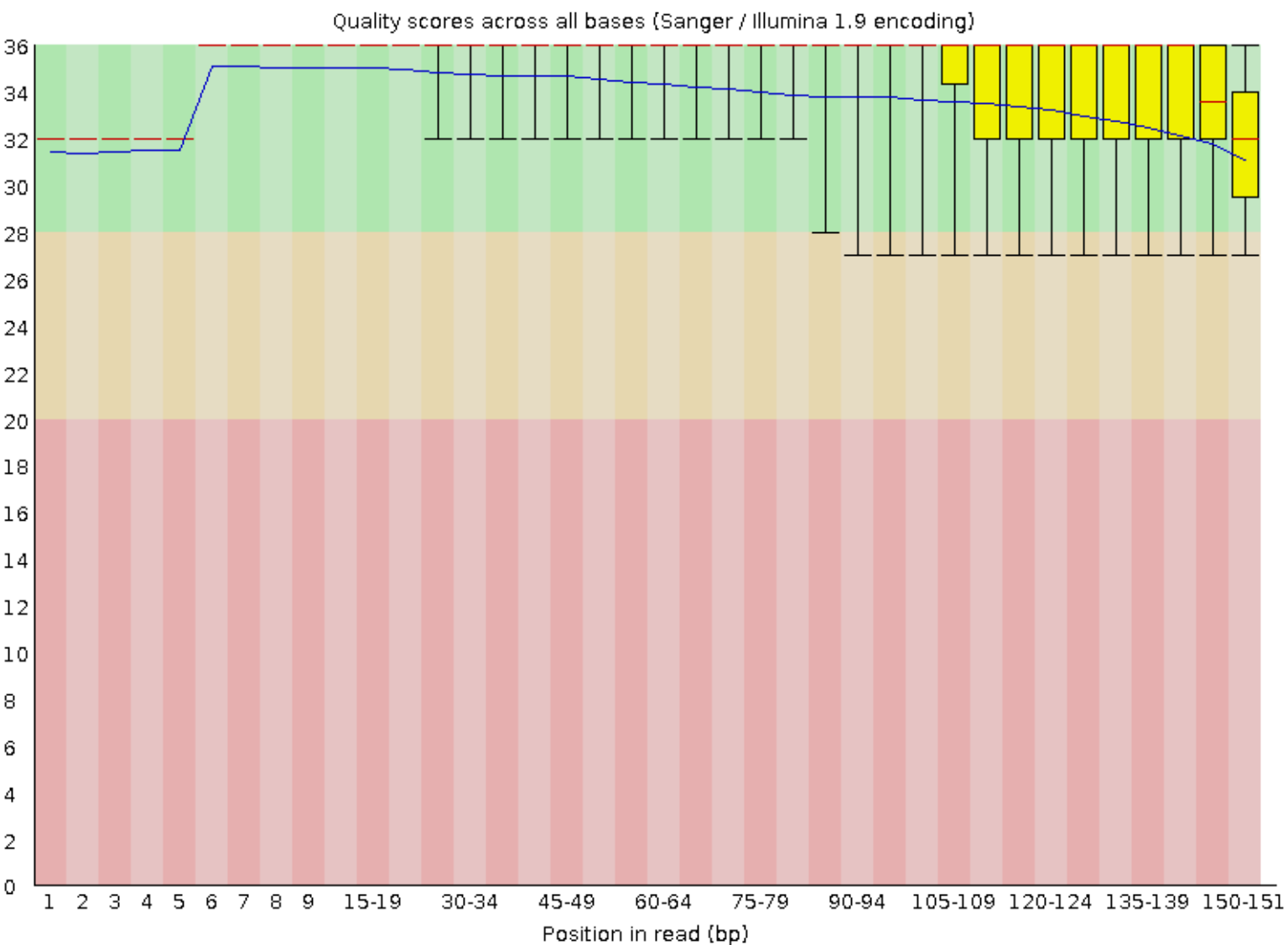
Wed 5 Mar 2025
controlled_trimmed.fastq

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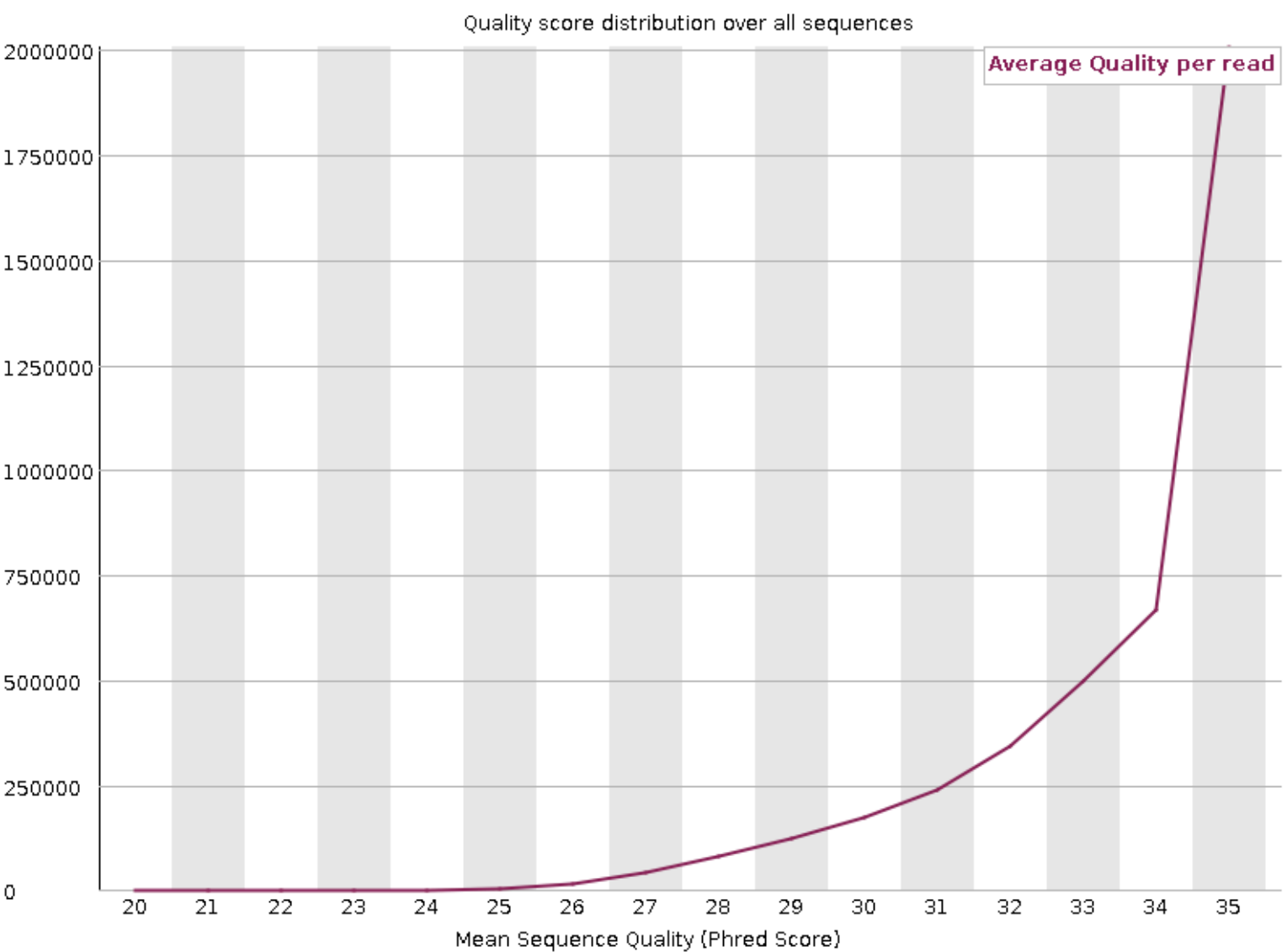
Basic Statistics

Measure	Value
Filename	controlled_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4216854
Total Bases	540.7 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	49

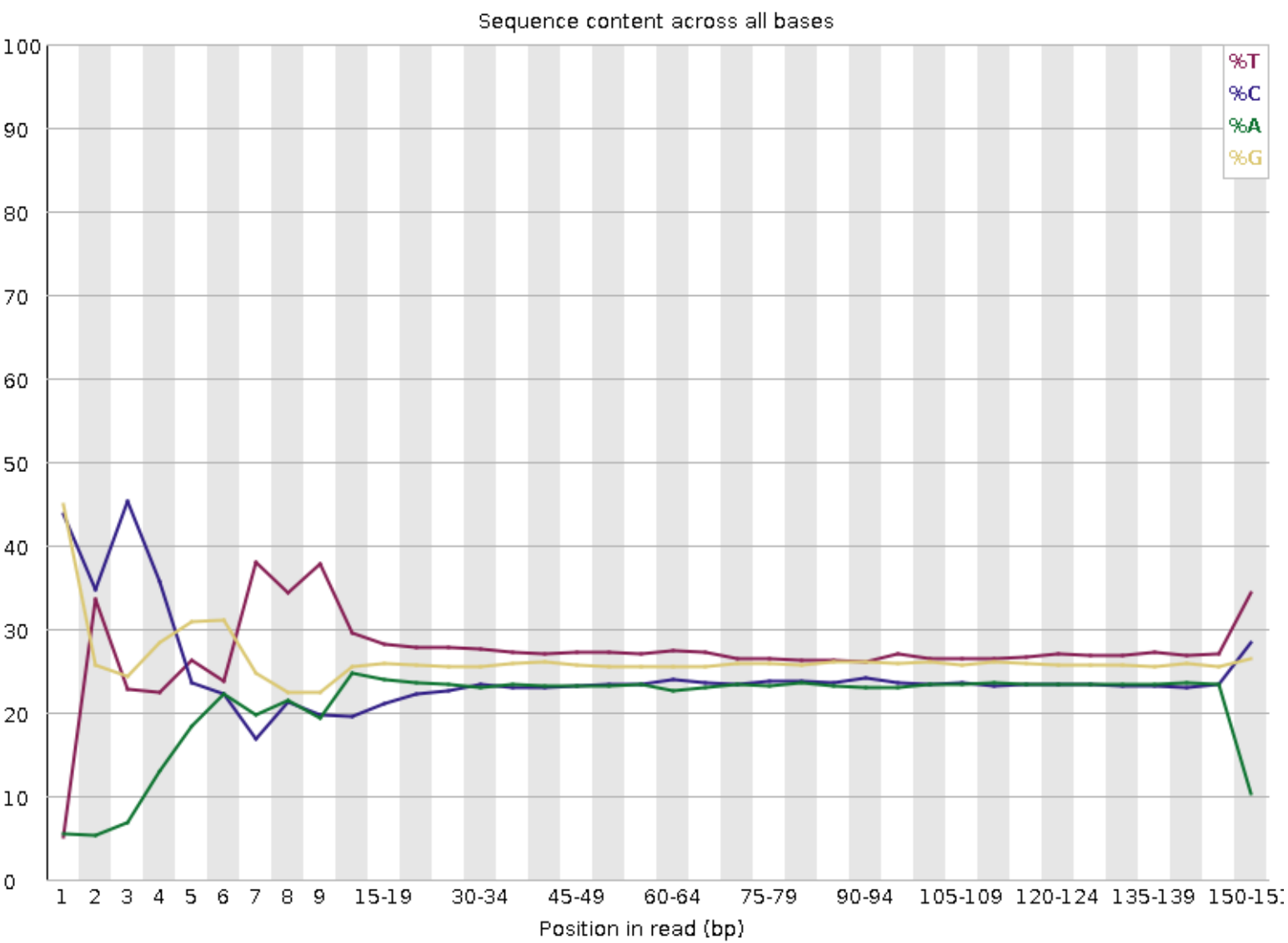
✔ Per base sequence quality



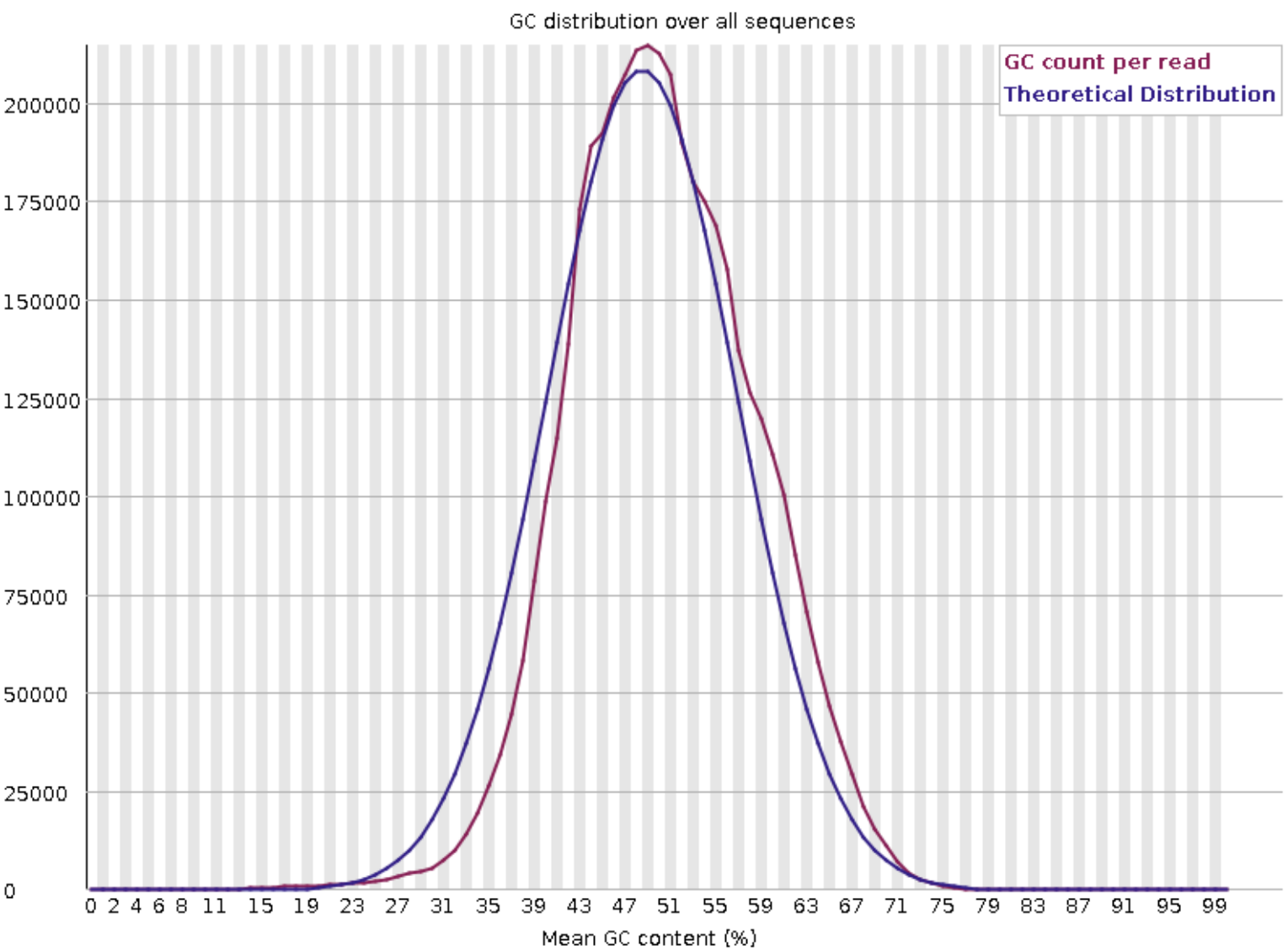
✅ Per sequence quality scores



❌ Per base sequence content

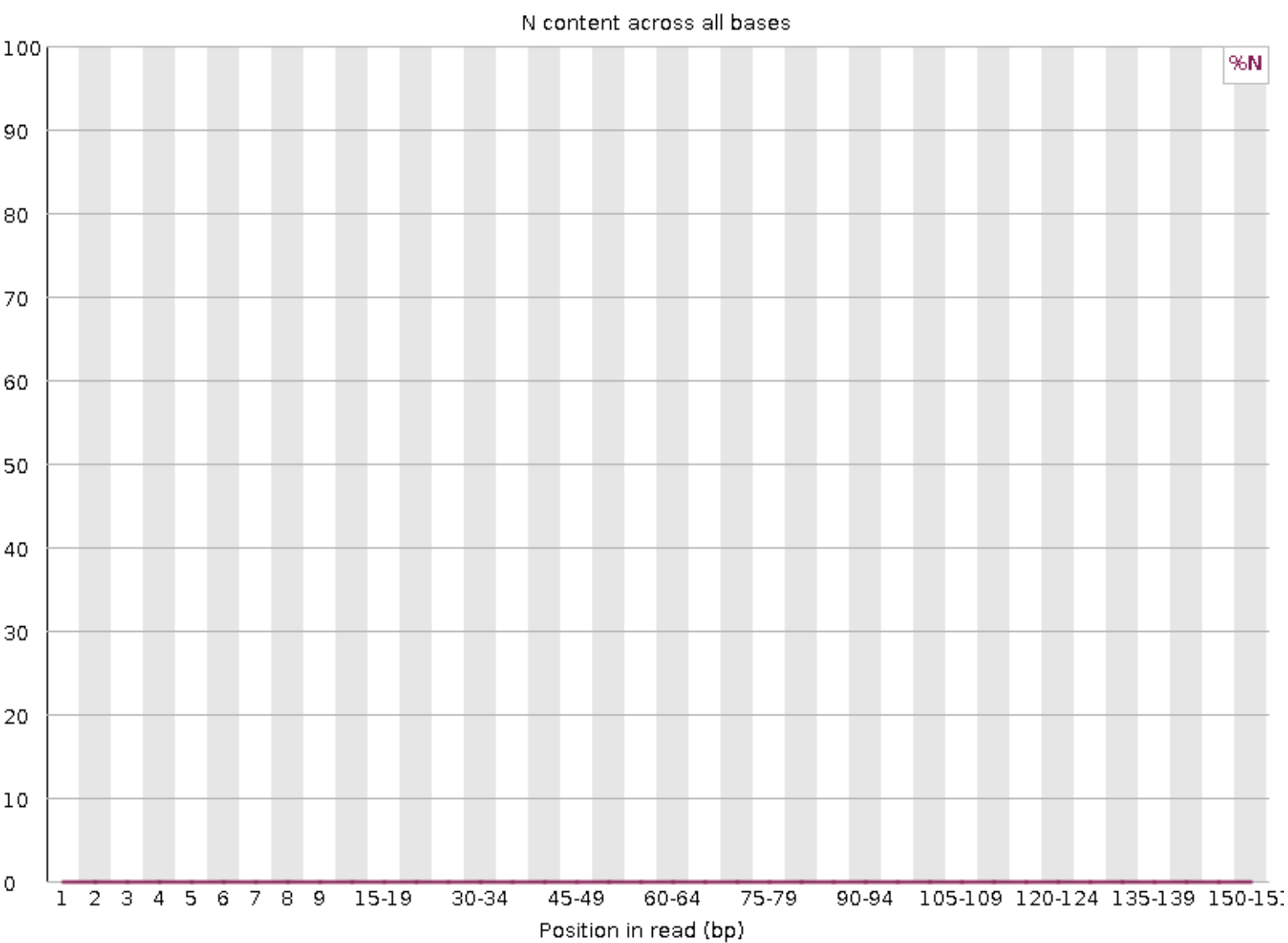


! Per sequence GC content

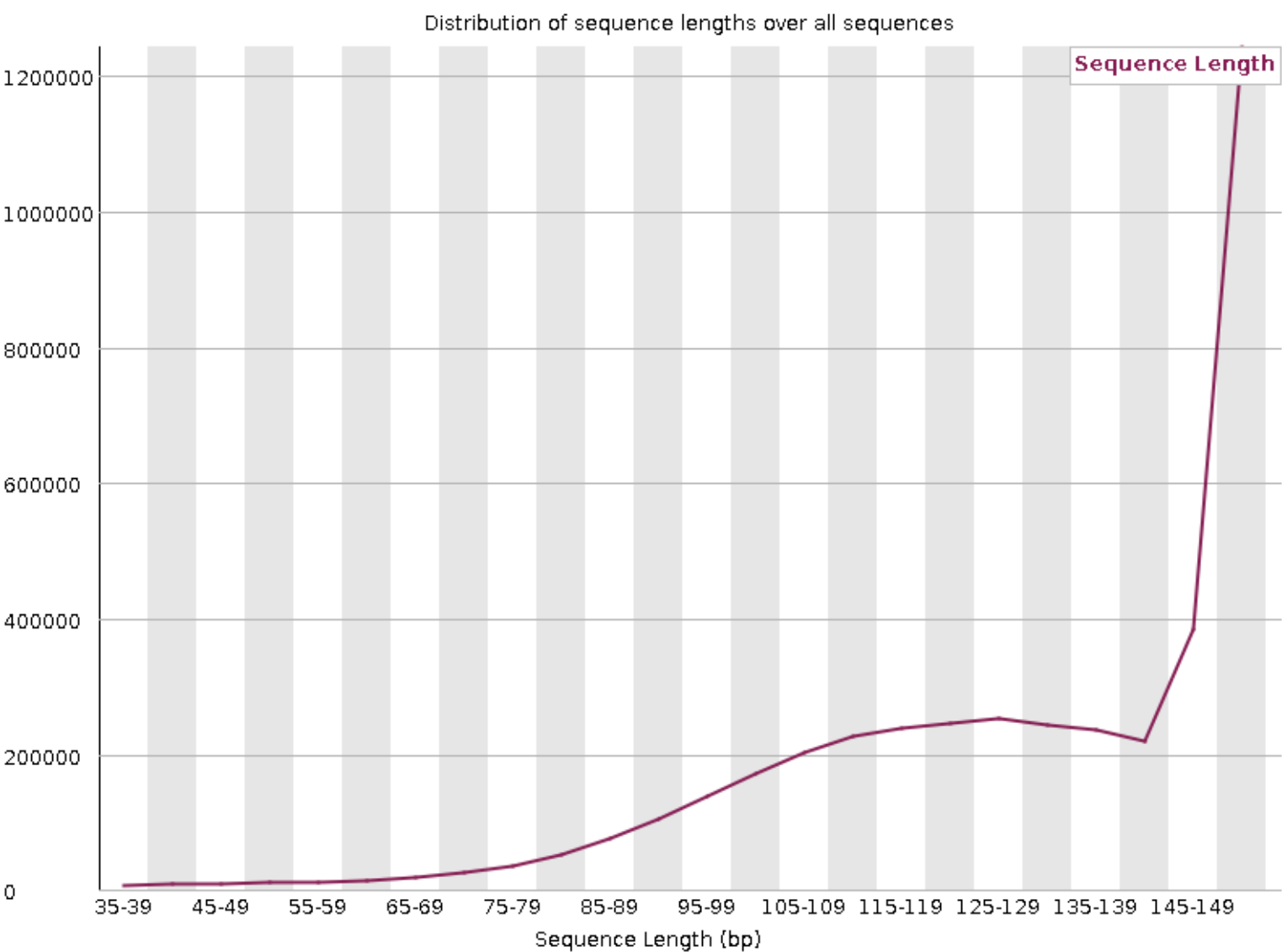




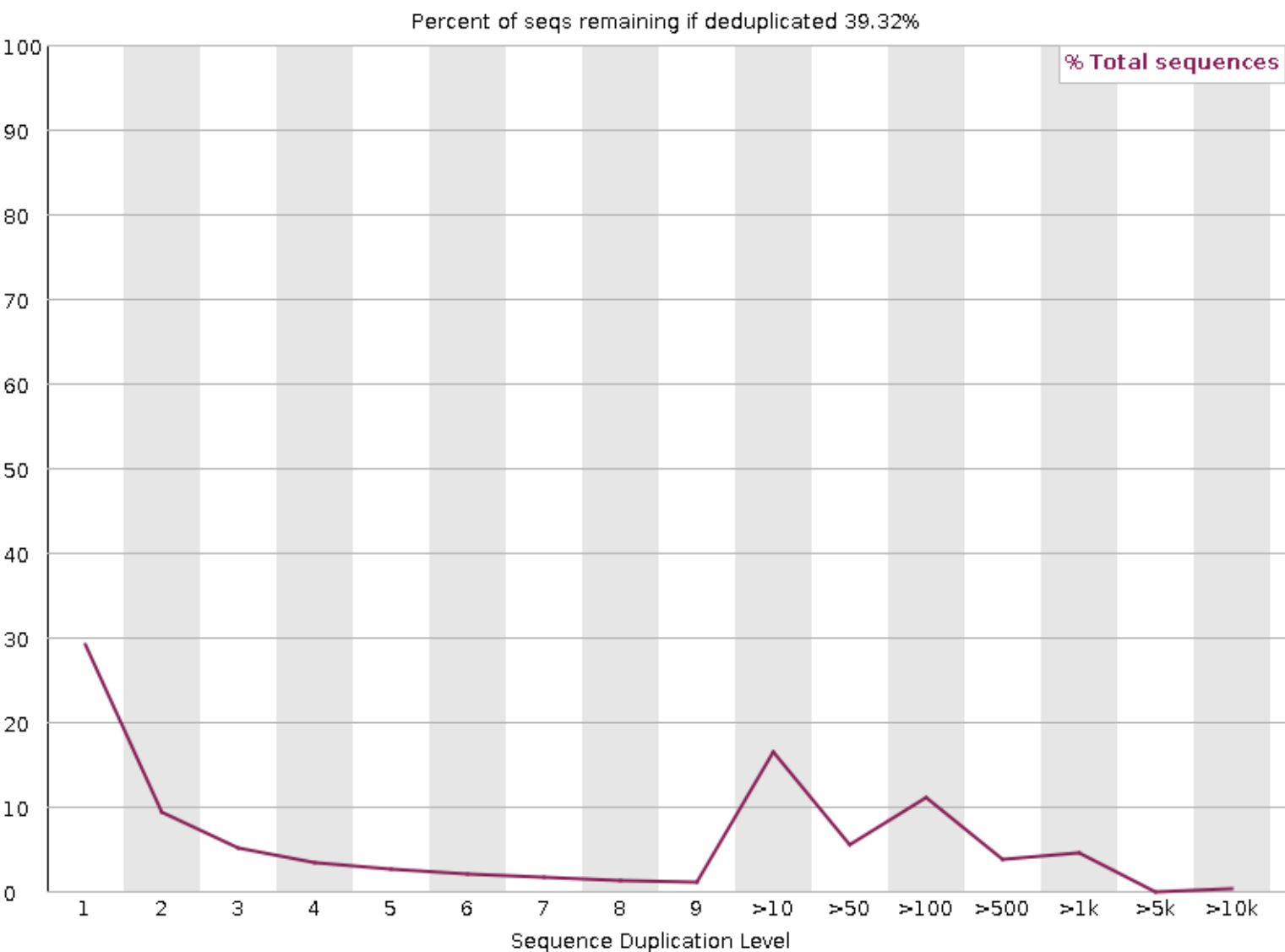
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	12637	0.29967838582981526	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	10261	0.24333306298961263	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA	5063	0.12006581209593693	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	4799	0.11380522066924774	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4726	0.11207407228232232	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4632	0.10984492230463752	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	4573	0.10844577497821836	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCTTTGGTTCTCAGGGT	4450	0.10552890851805637	No Hit

Sequence	Count	Percentage	Possible Source
CCCCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGG	4283	0.10156861015344615	No Hit



Adapter Content

