











FastQC Report

Summary

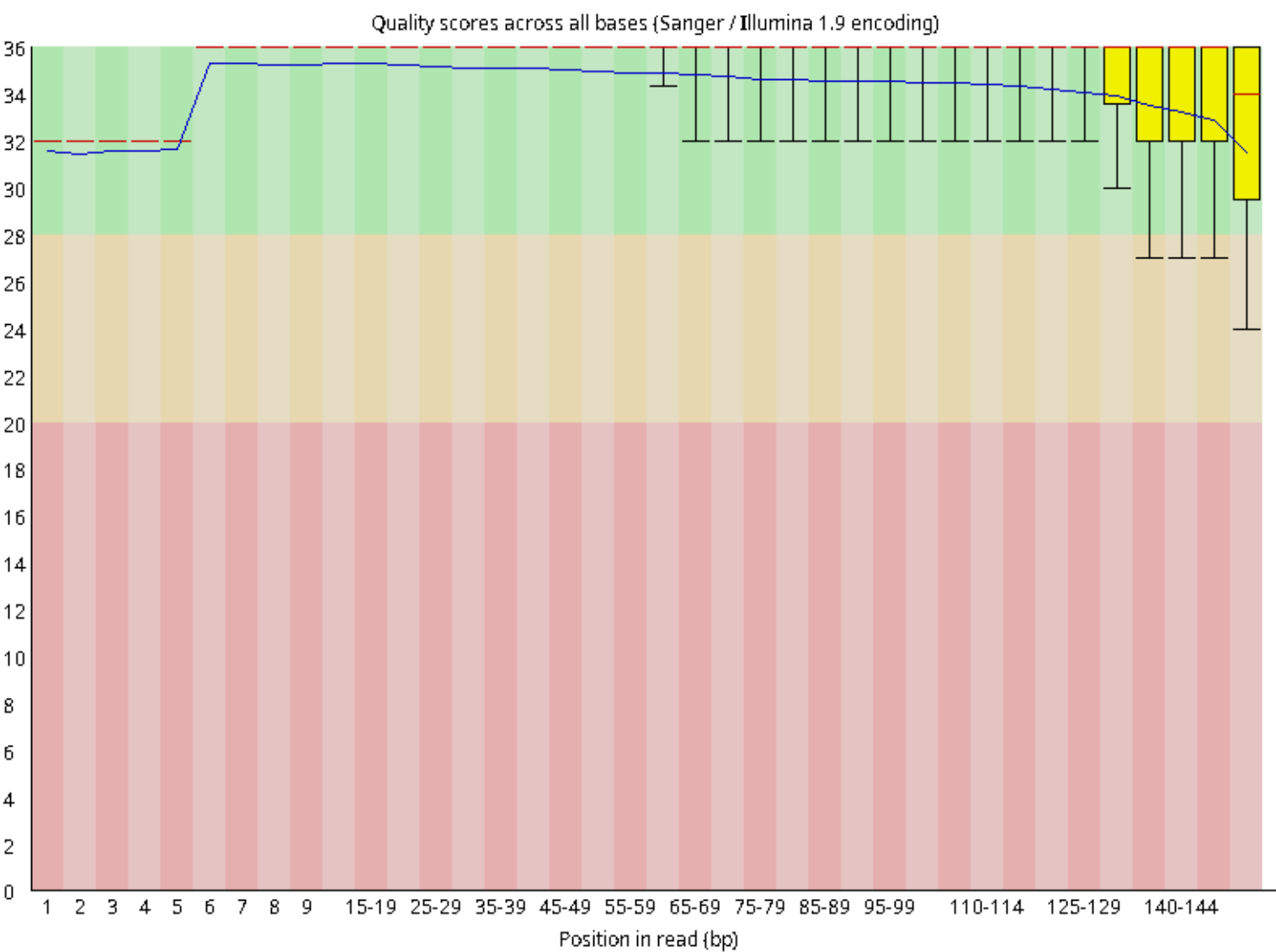
Mon 10 Mar 2025
controlled_trimmed.fastq

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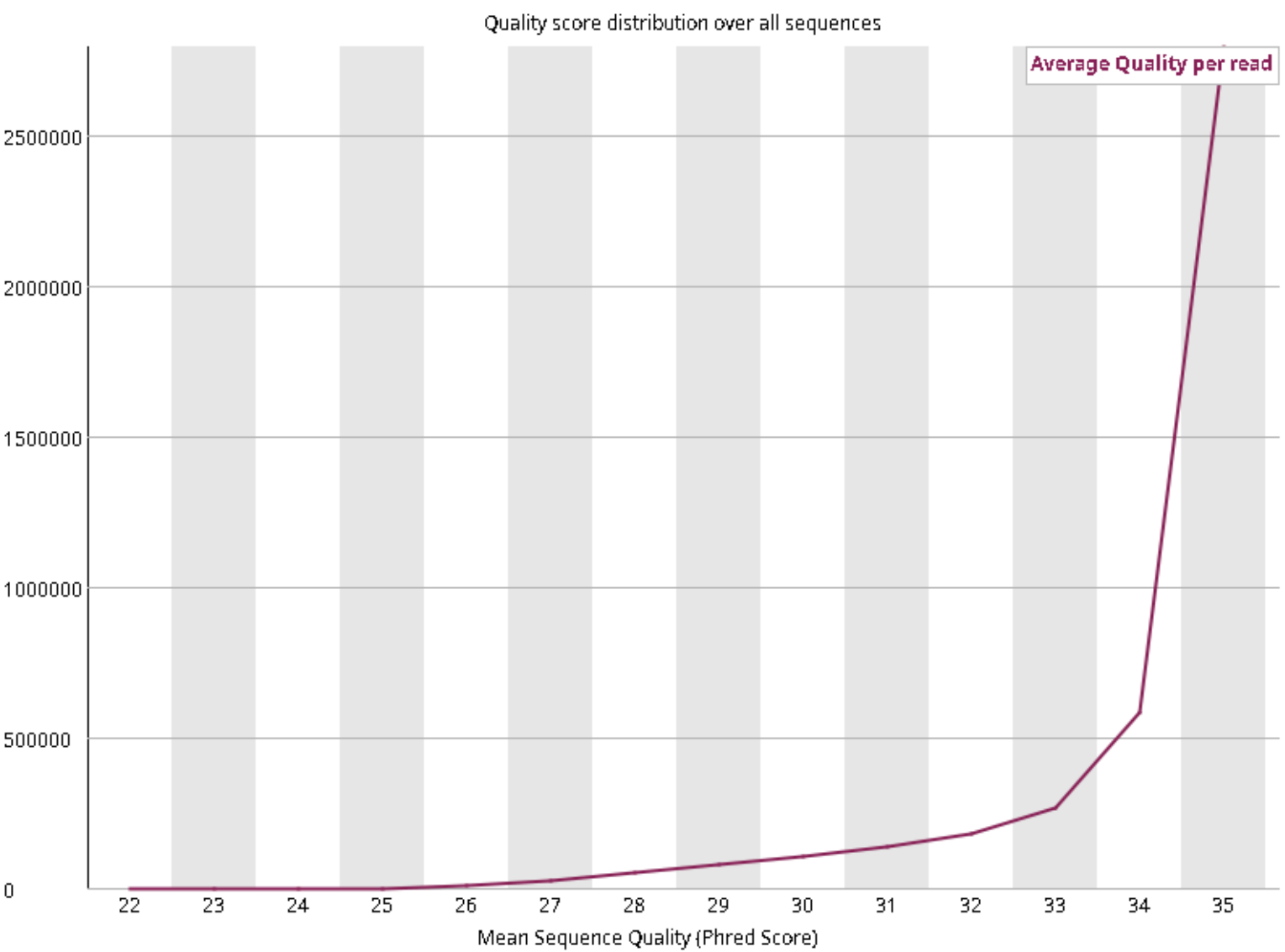
Basic Statistics

Measure	Value
Filename	controlled_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4281392
Total Bases	551.7 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	49

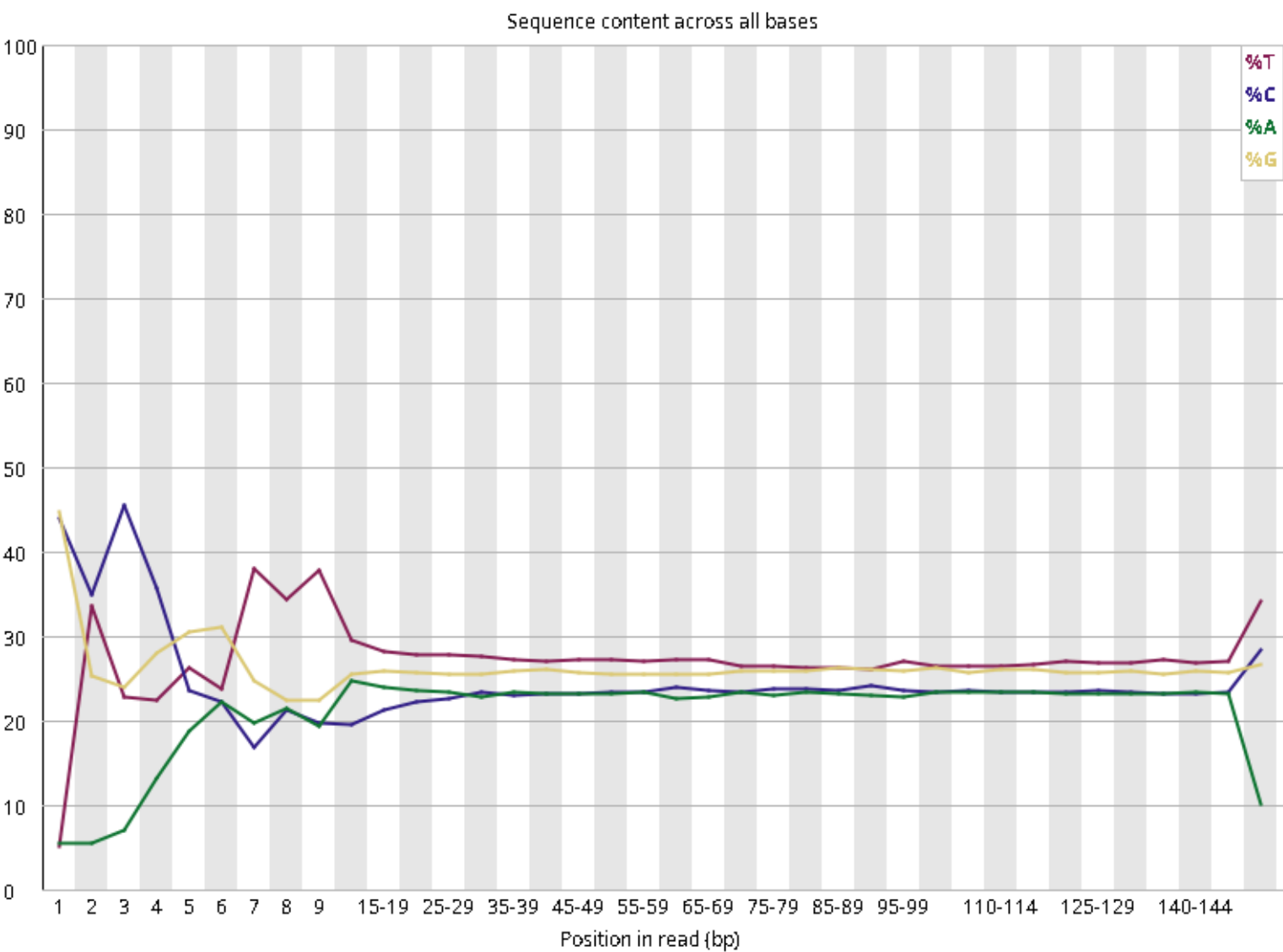
✔ Per base sequence quality



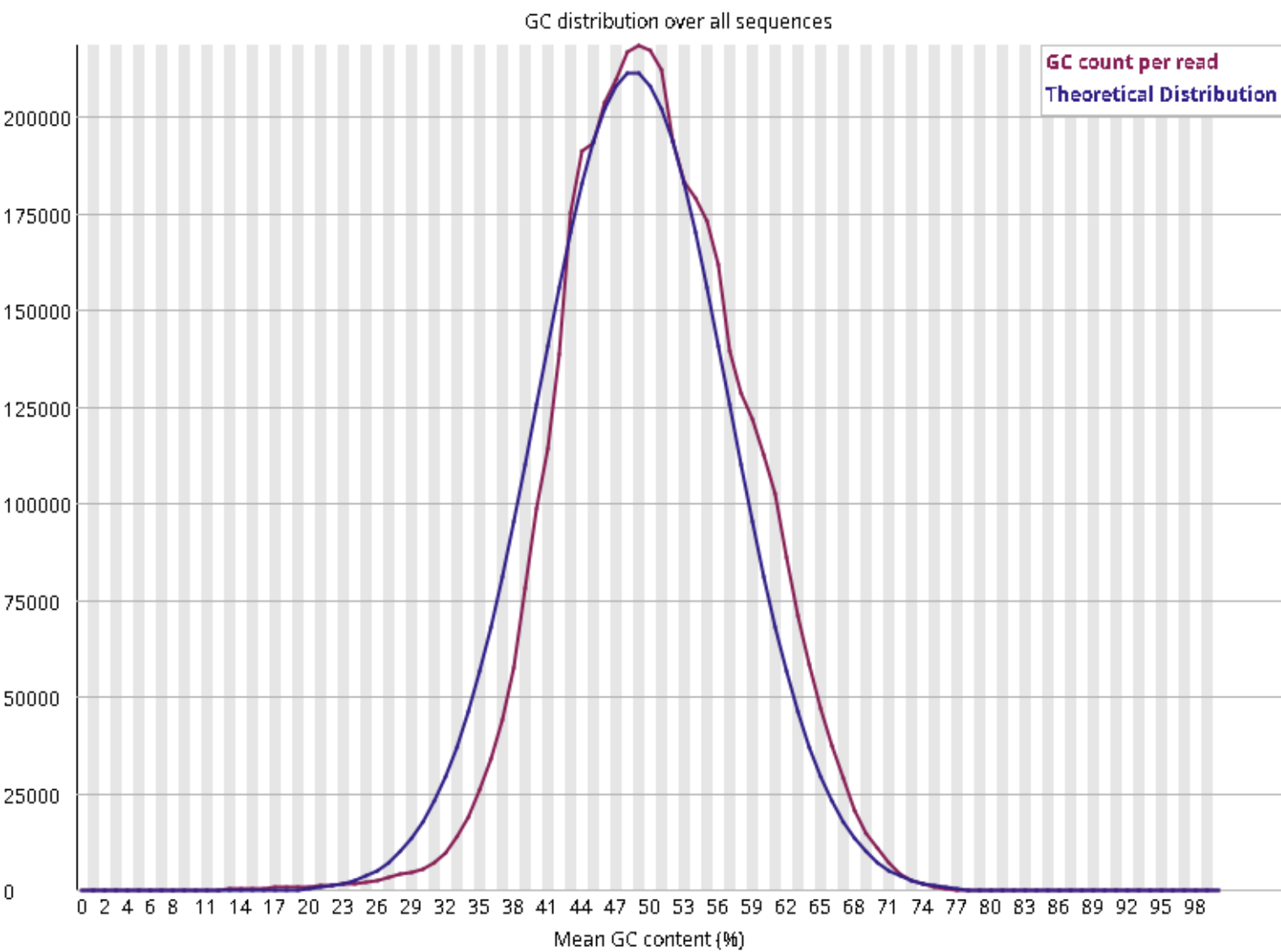
✔ Per sequence quality scores



✖ Per base sequence content

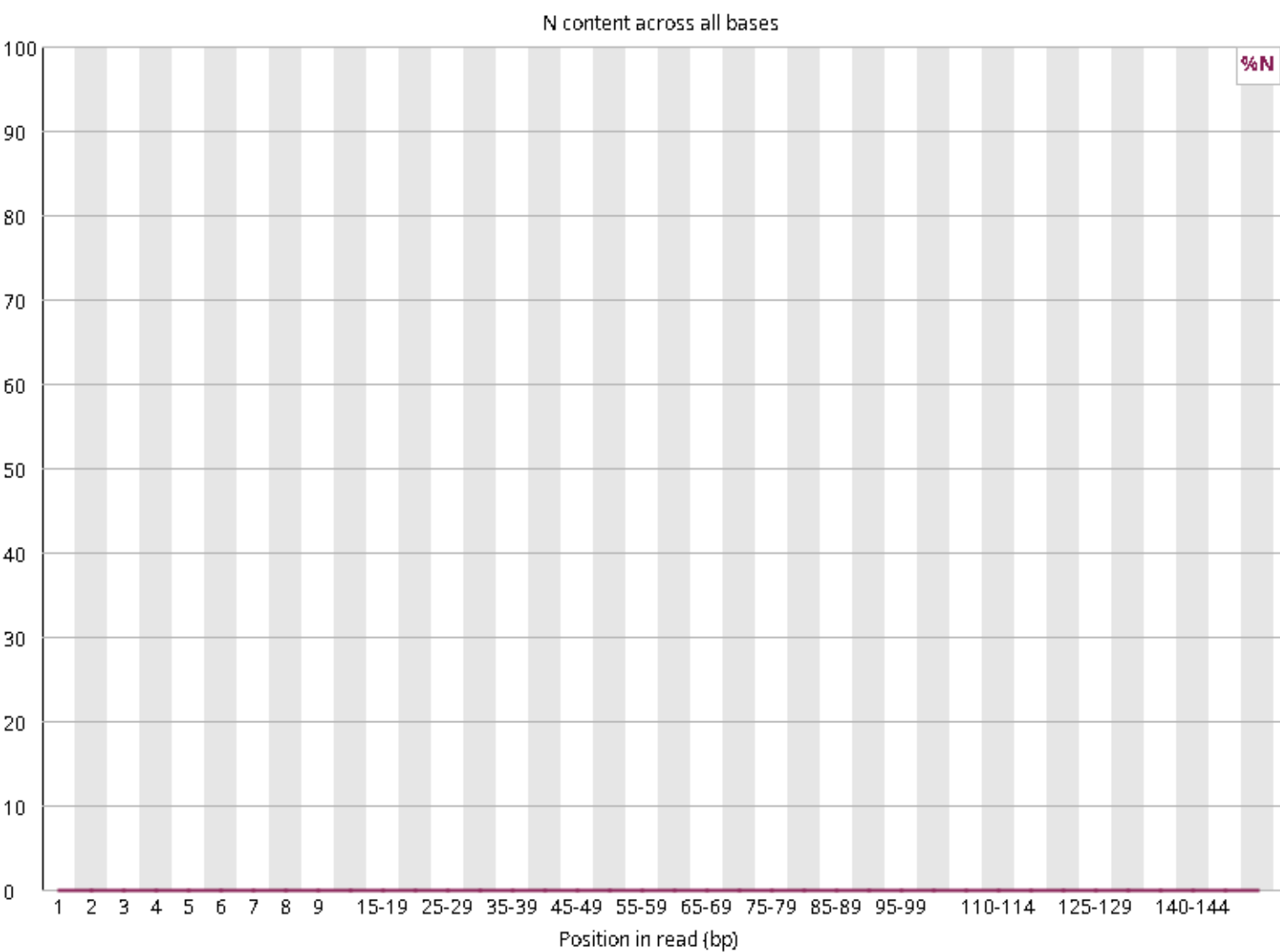


! Per sequence GC content

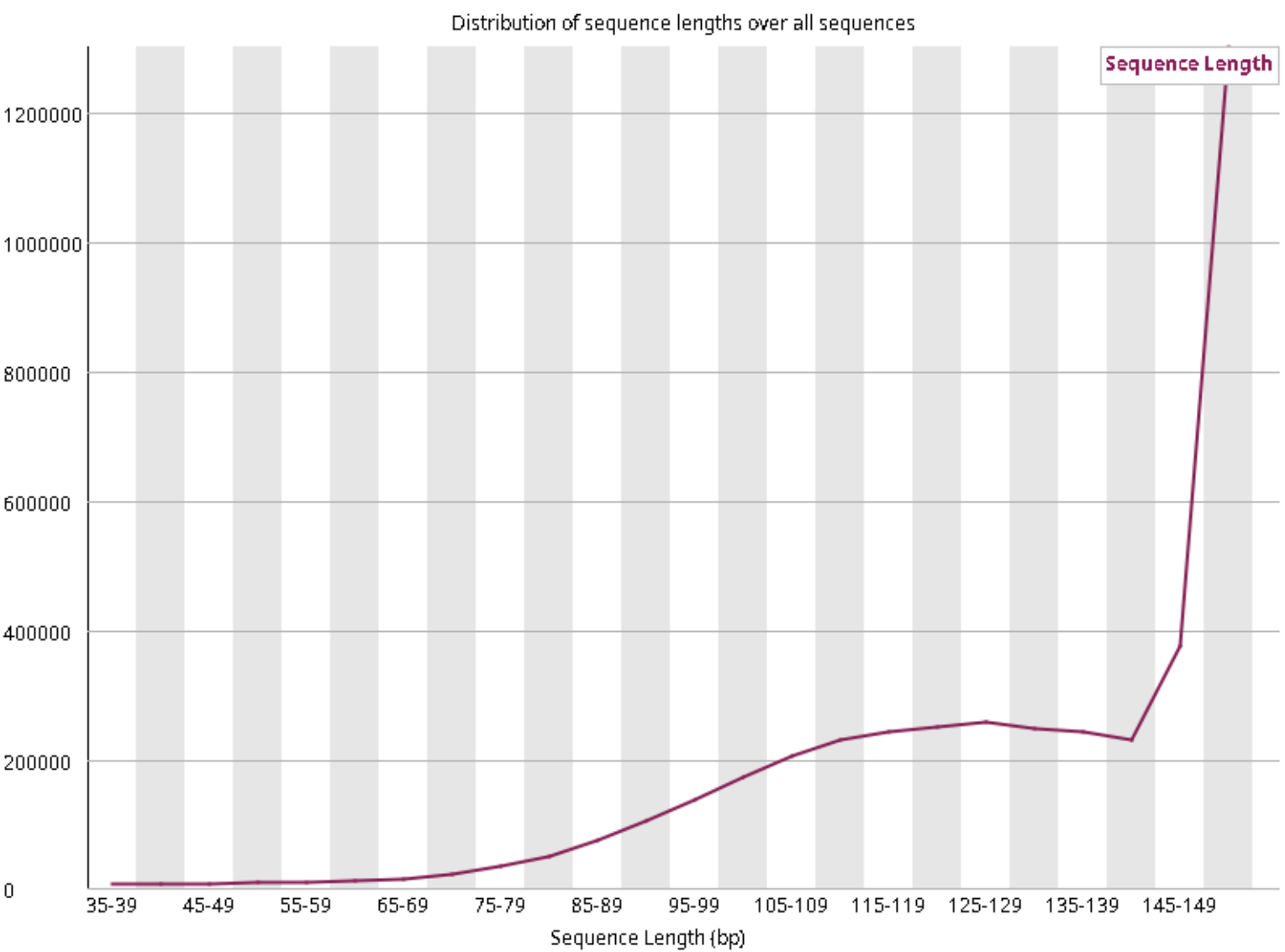




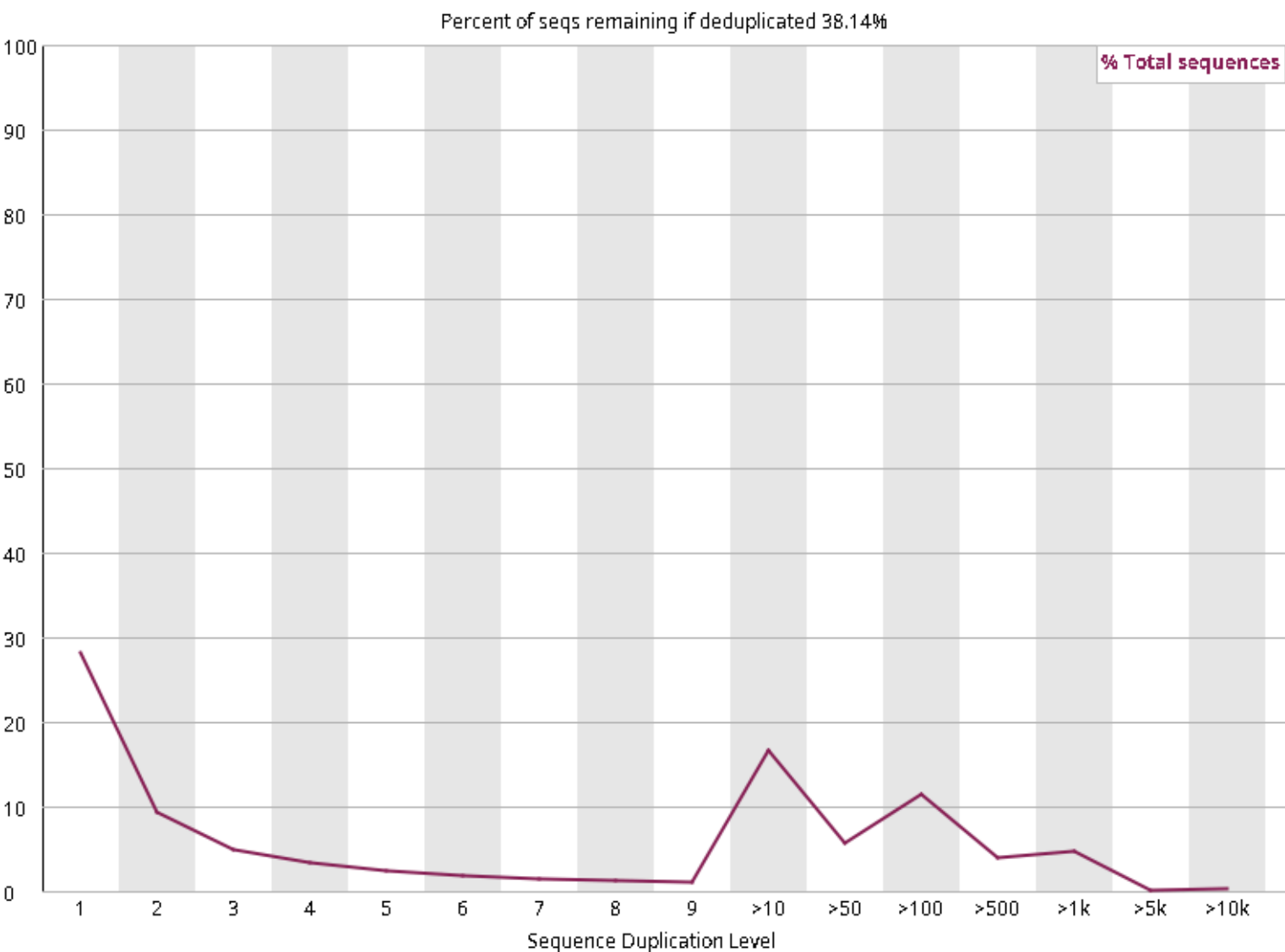
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	13203	0.3083810125305041	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	10689	0.24966179223953333	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA	5322	0.12430536610522933	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	5249	0.12260031316917488	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5009	0.11699465968077671	No Hit
GTGGTGATTAGTCGTTTGTGATGAGATATTTGGAGGTGGGGATCAATAG	4967	0.11601367032030704	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCATTTGGTTCTCAGGGT	4776	0.11155250441912348	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4758	0.11113208040749364	No Hit
CCCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGG	4495	0.10498921845979063	No Hit

Sequence	Count	Percentage	Possible Source
CCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGGAA	4352	0.10164918325628675	No Hit



Adapter Content

