FastQC Report

Mon 10 Mar 2025
infected_trimmed.fastq

Summary

- Basic Statistics
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- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
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- Sequence Length Distribution
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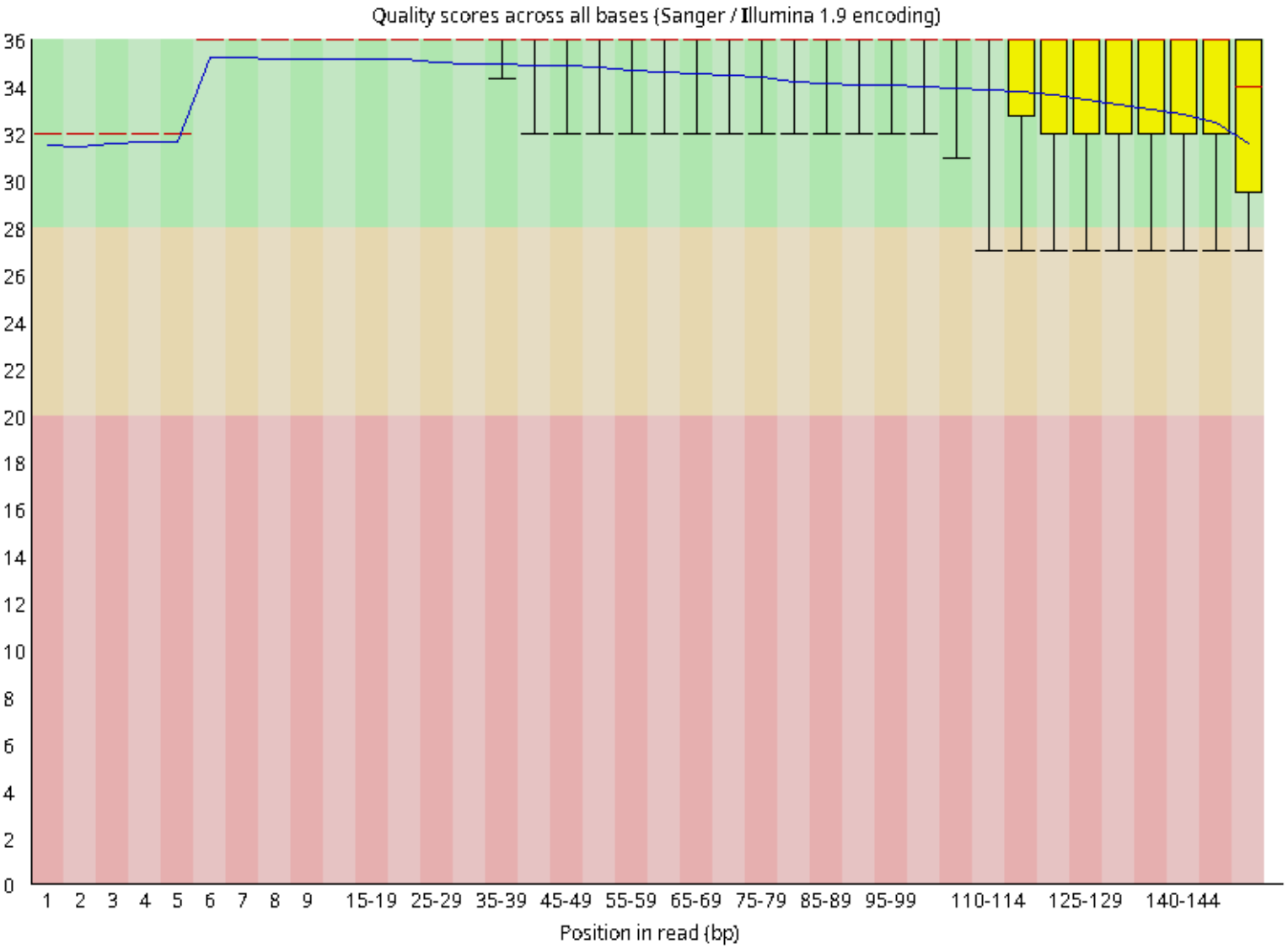
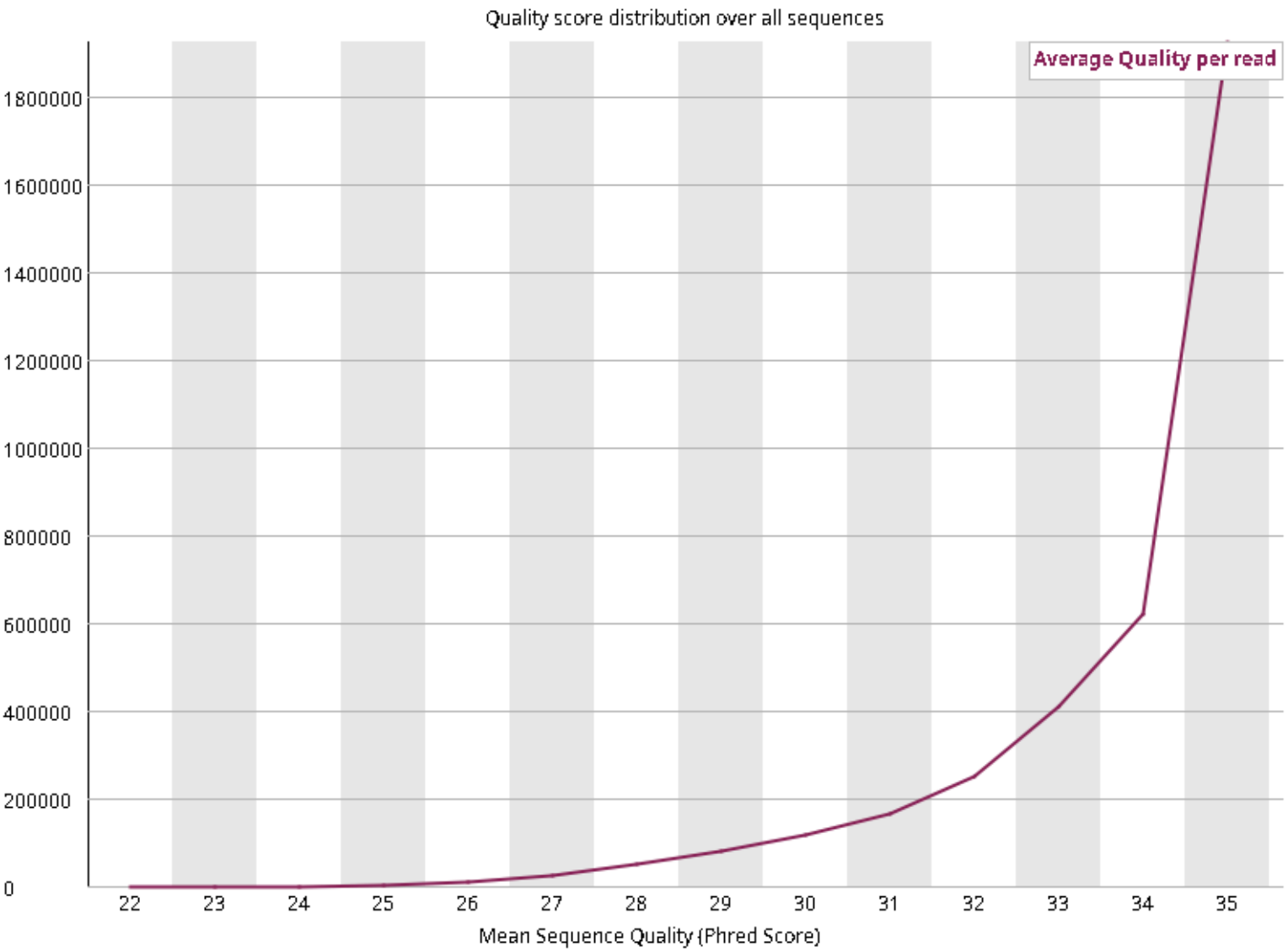
Basic Statistics

Measure	Value
Filename	infected_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3689303
Total Bases	489.6 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	50

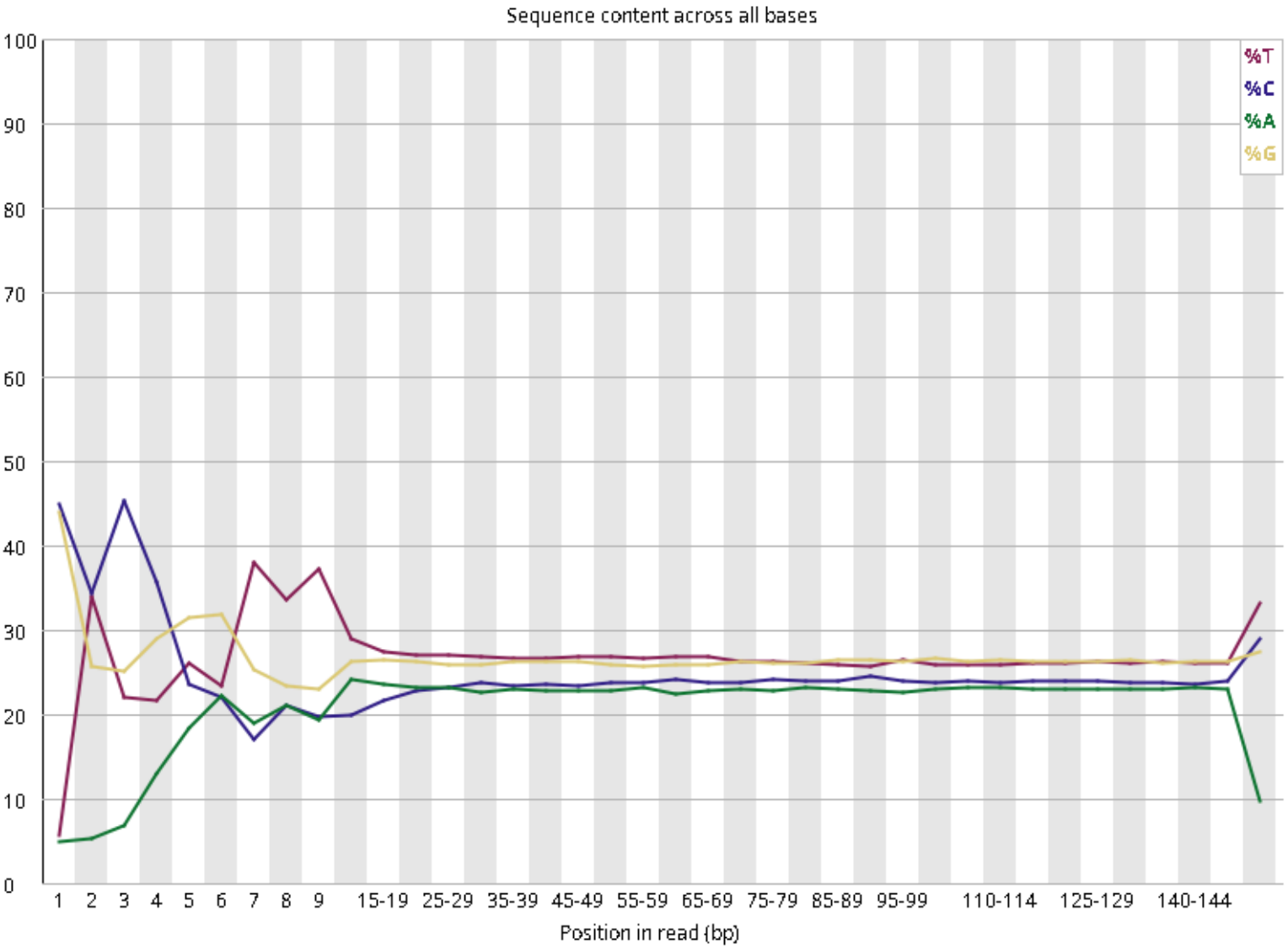
Per base sequence quality



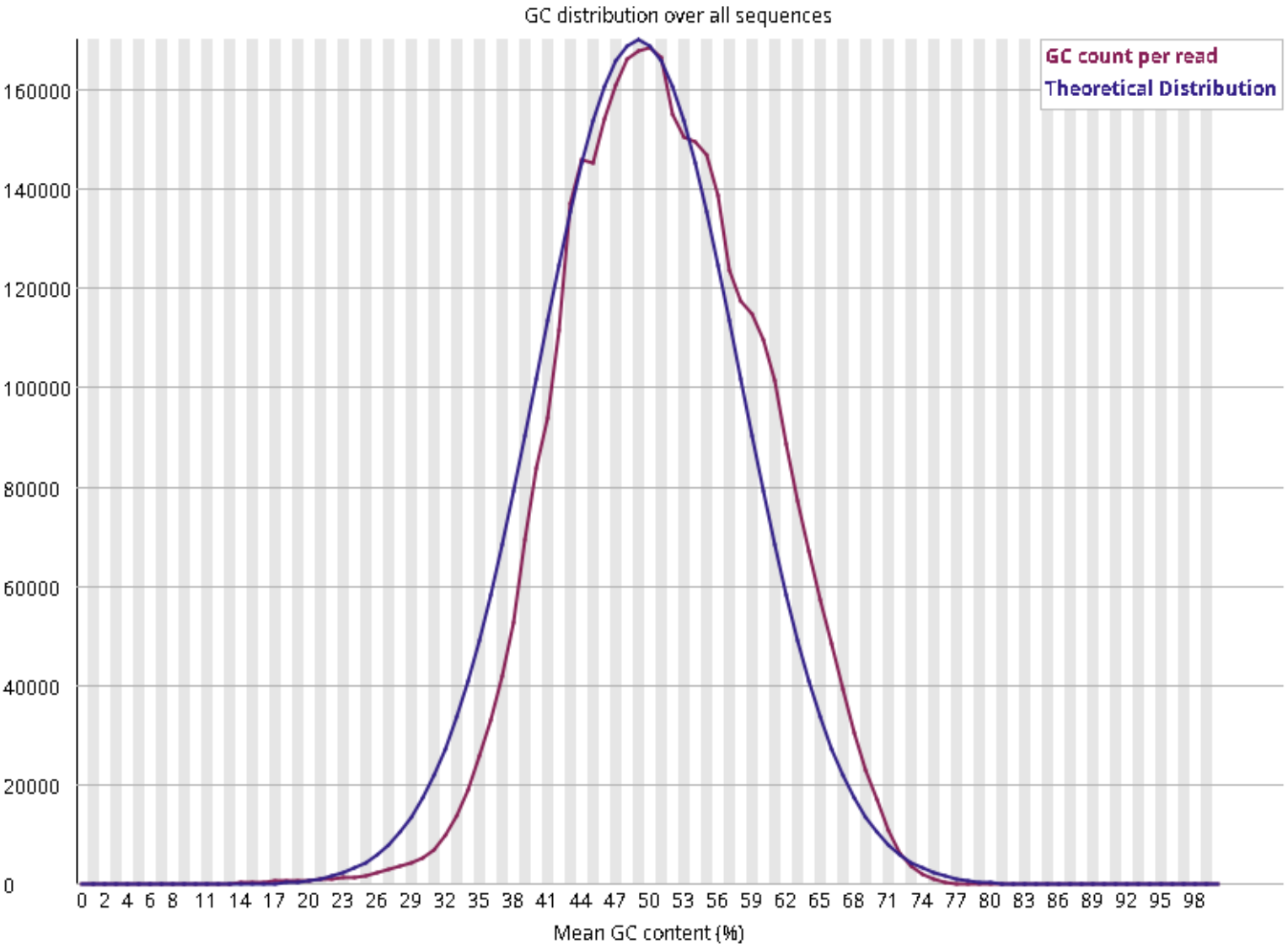
Per sequence quality scores



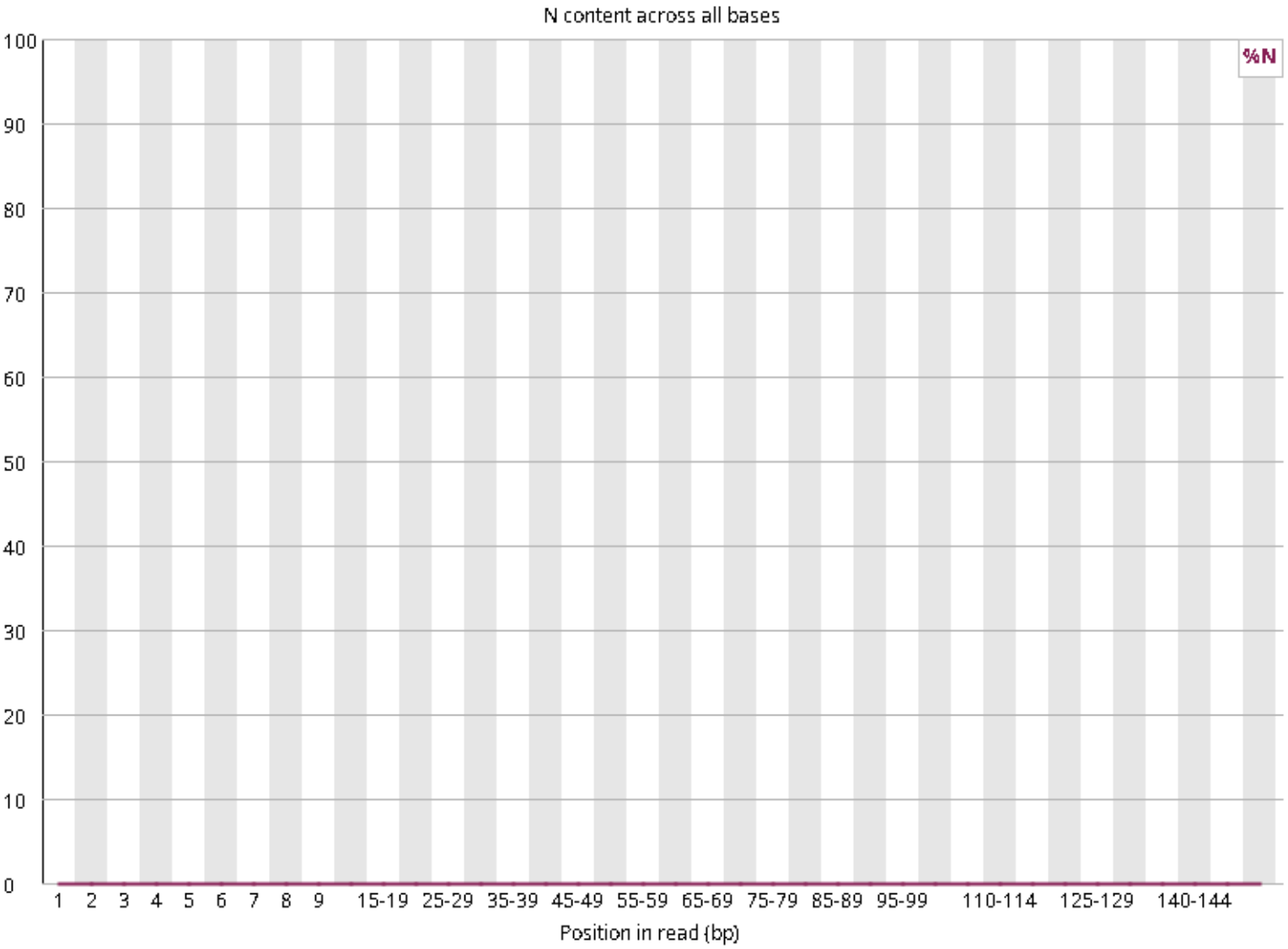
Per base sequence content



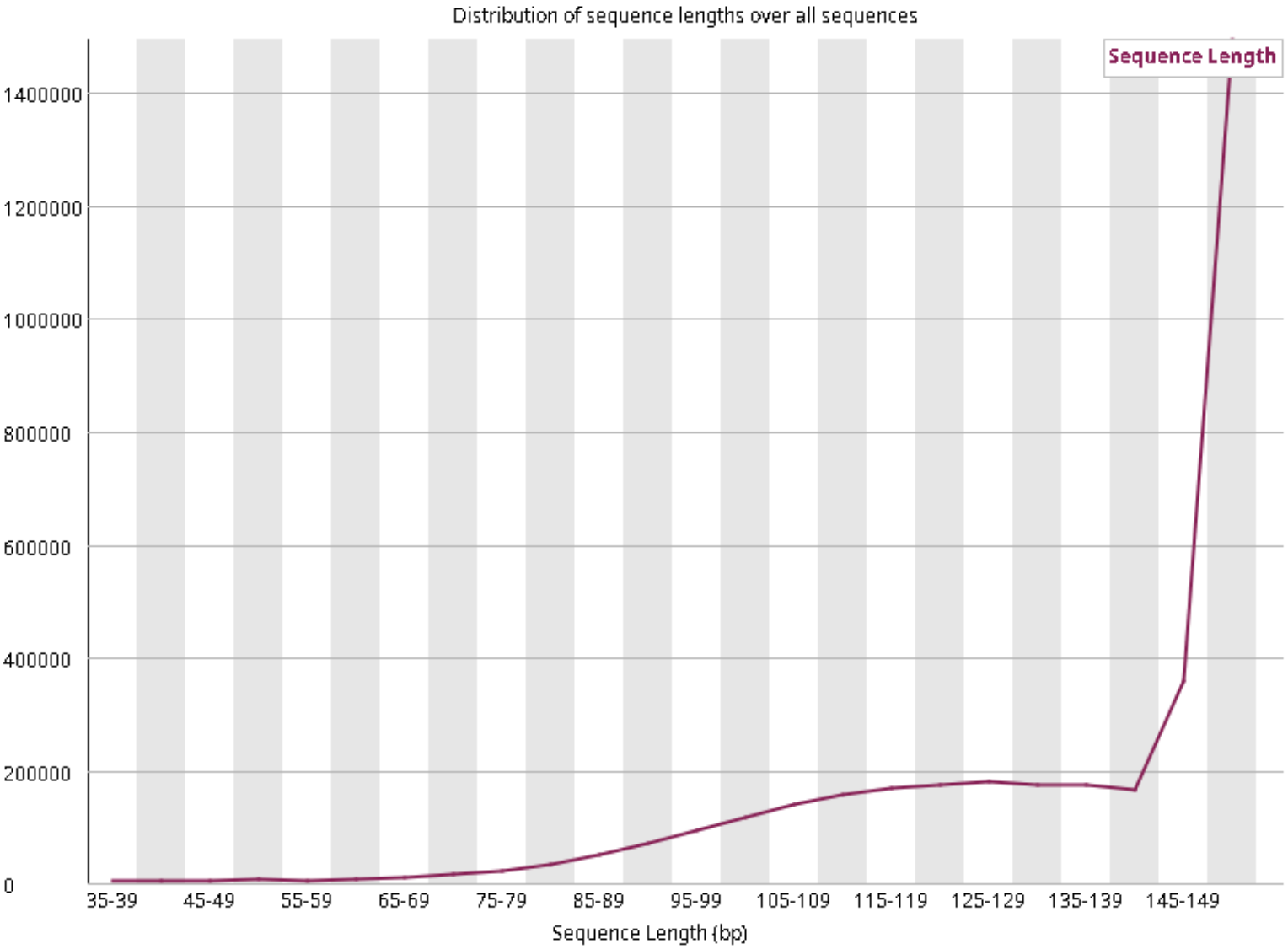
Per sequence GC content



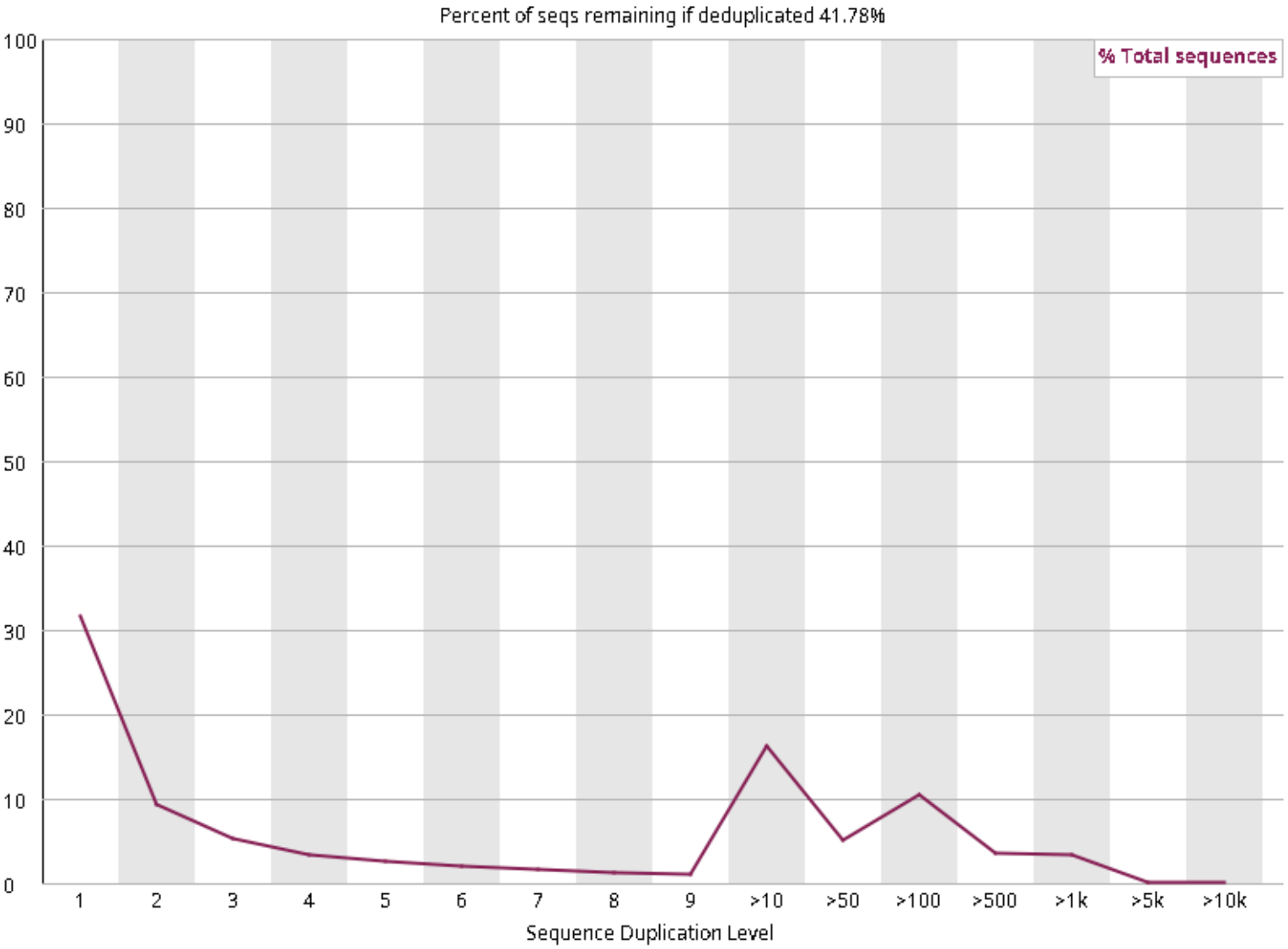
Per base N content



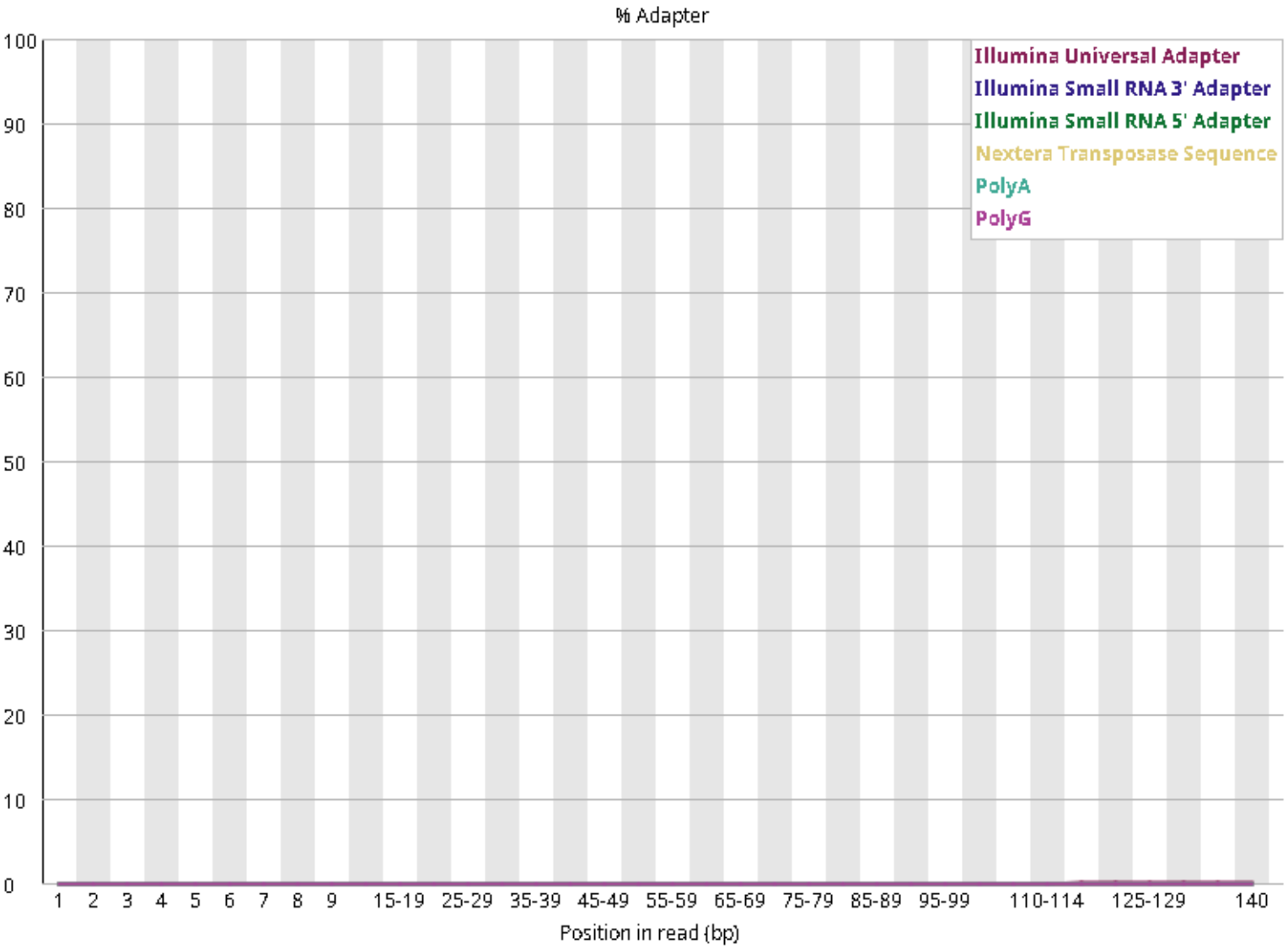
Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCCTGAGCGTCTGAGATGTTAG	10739	0.29108479298122164	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6636	0.17987137407797624	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5292	0.143441728695095	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	4966	0.13460537125847347	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4171	0.11305658548511738	No Hit
CCCCTTACTCAGCTTGAACTTGTCGCCCTCTTGGCAGGAGTACTTGTGGA	3847	0.10427443883031565	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3739	0.1013470566120484	No Hit

Adapter Content