FastQC Report

Mon 10 Mar 2025
infected1_trimmed.fastq

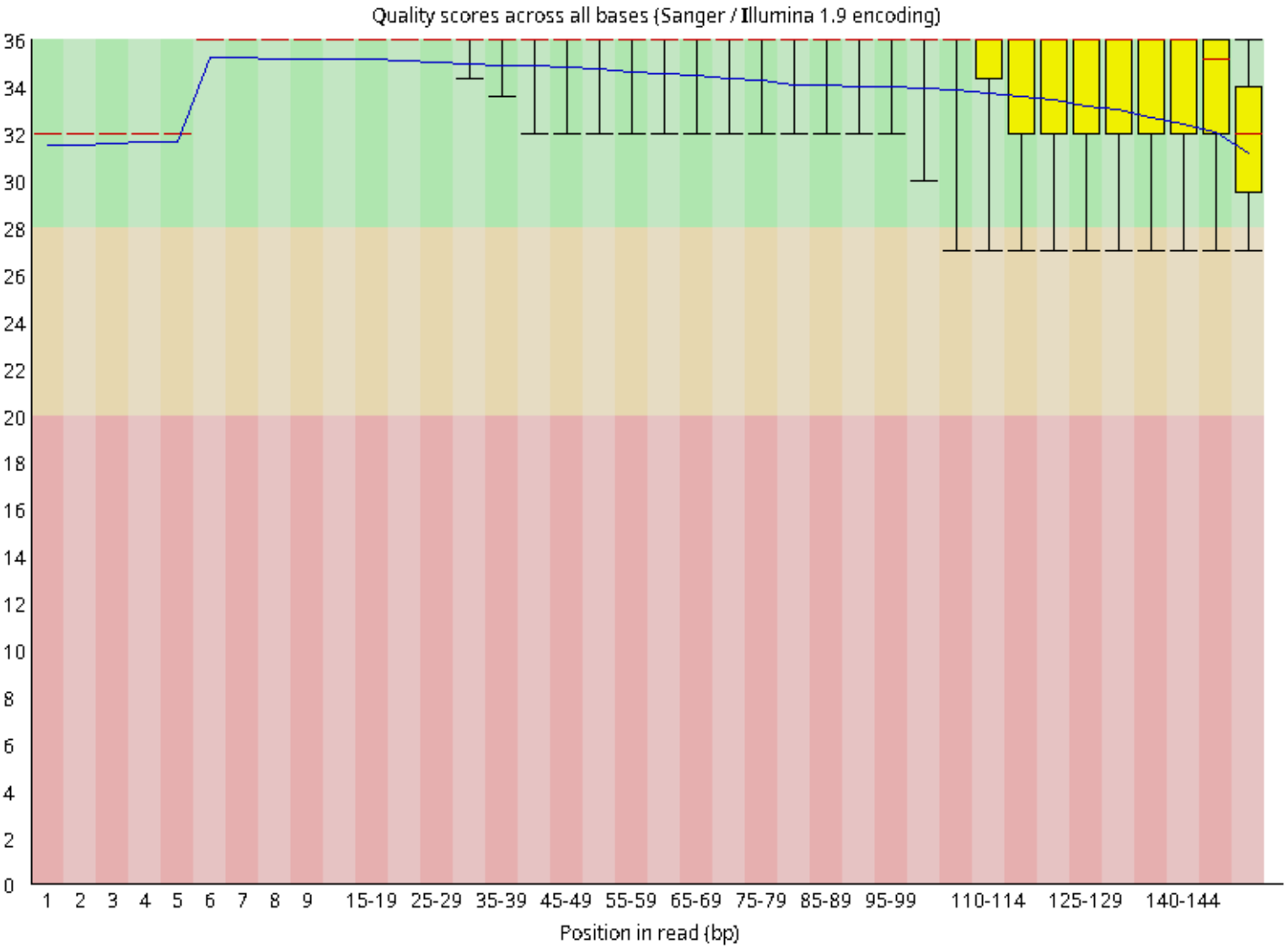
Summary

- Basic Statistics
- 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
- Adapter Content

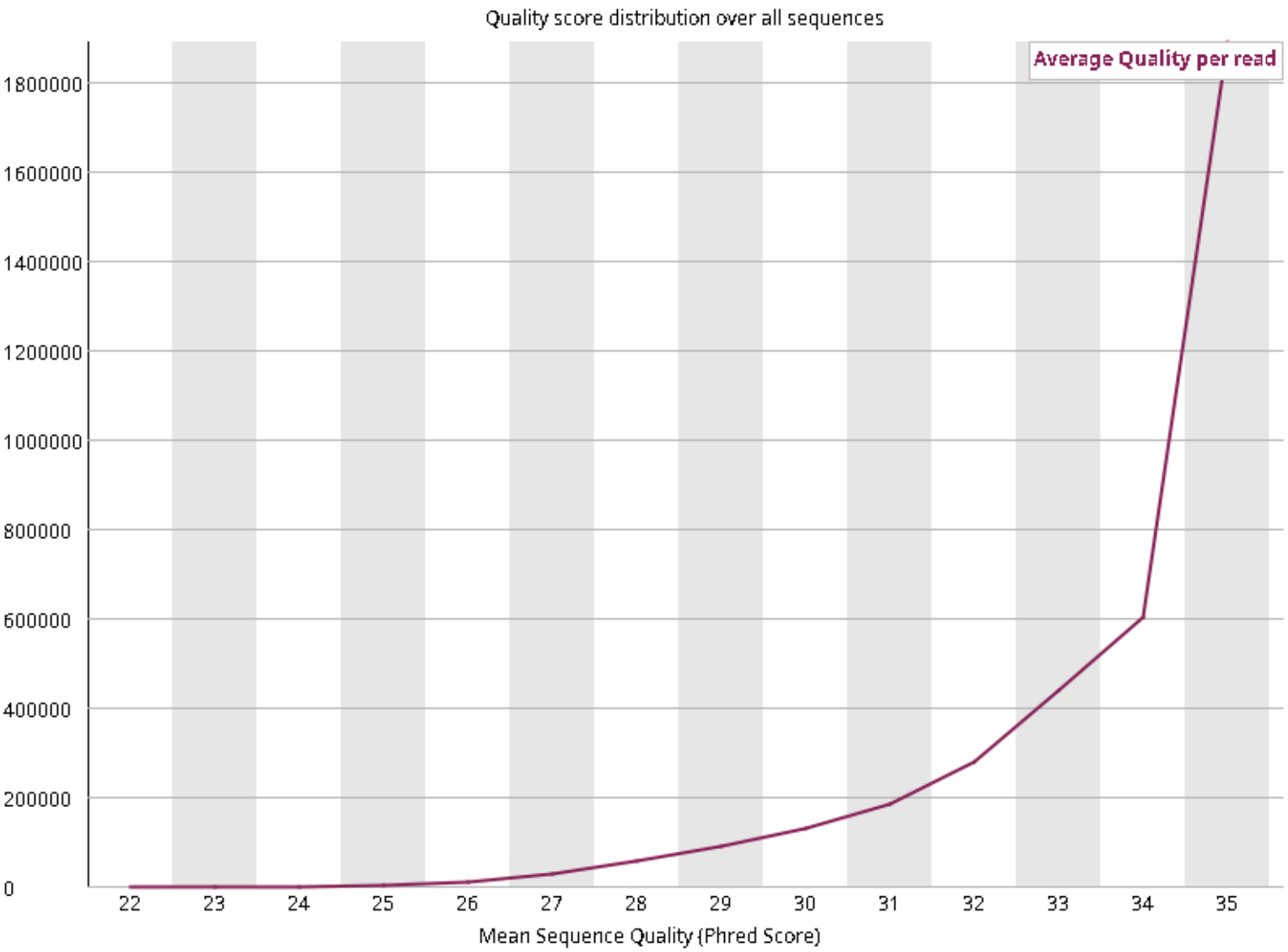
Basic Statistics

Measure	Value
Filename	infected1_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3743171
Total Bases	496.2 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	50

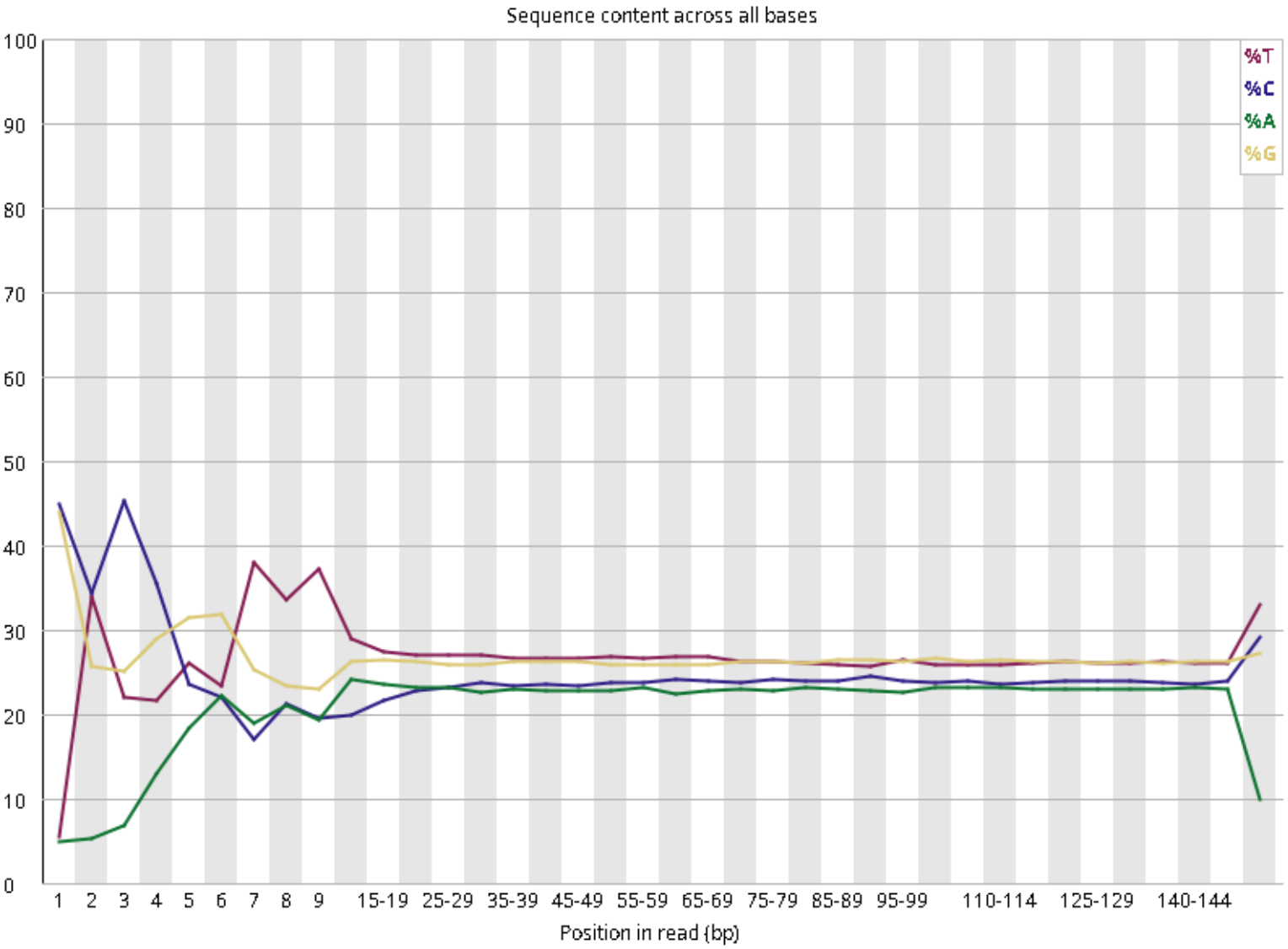
Per base sequence quality



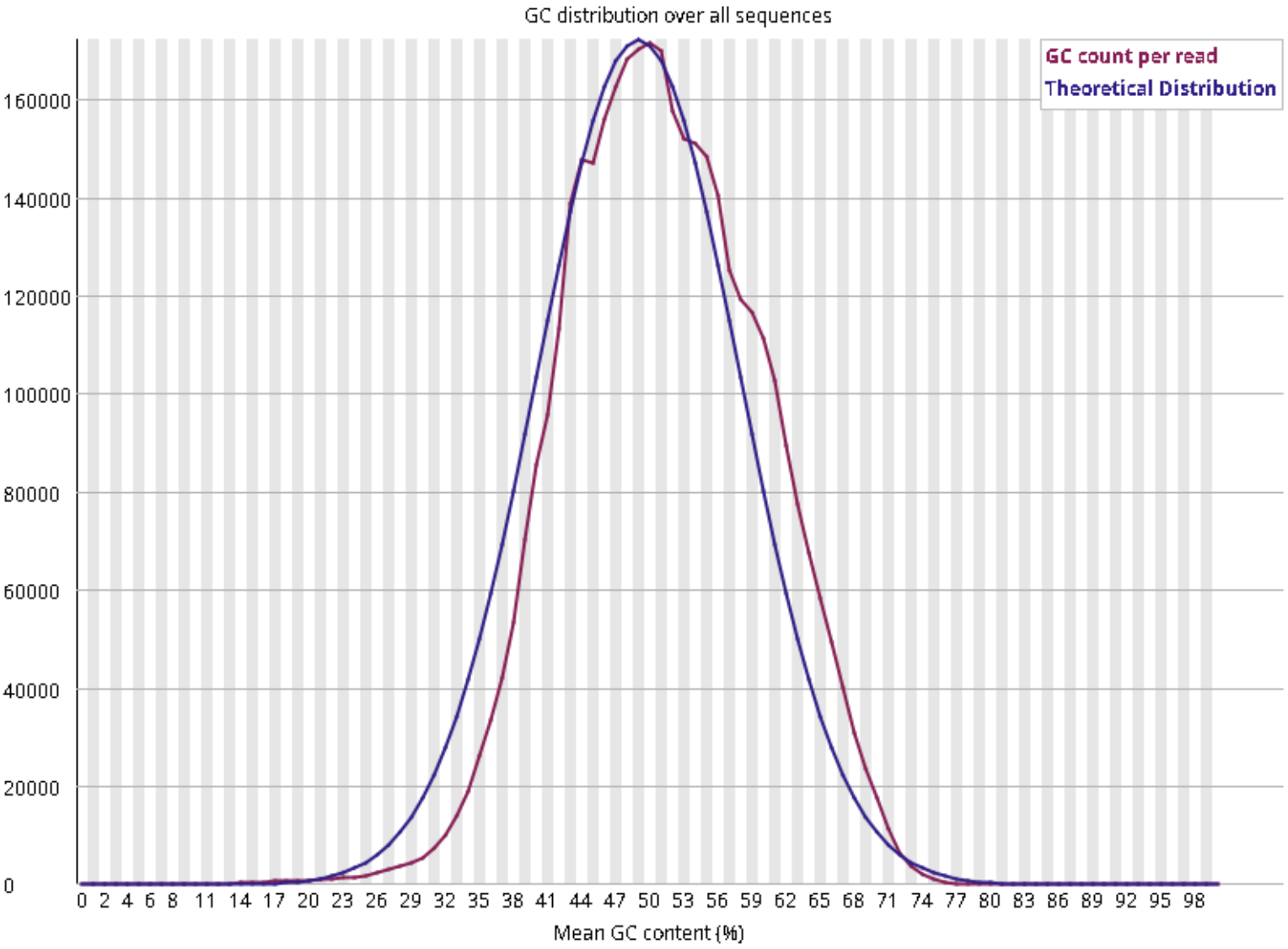
Per sequence quality scores



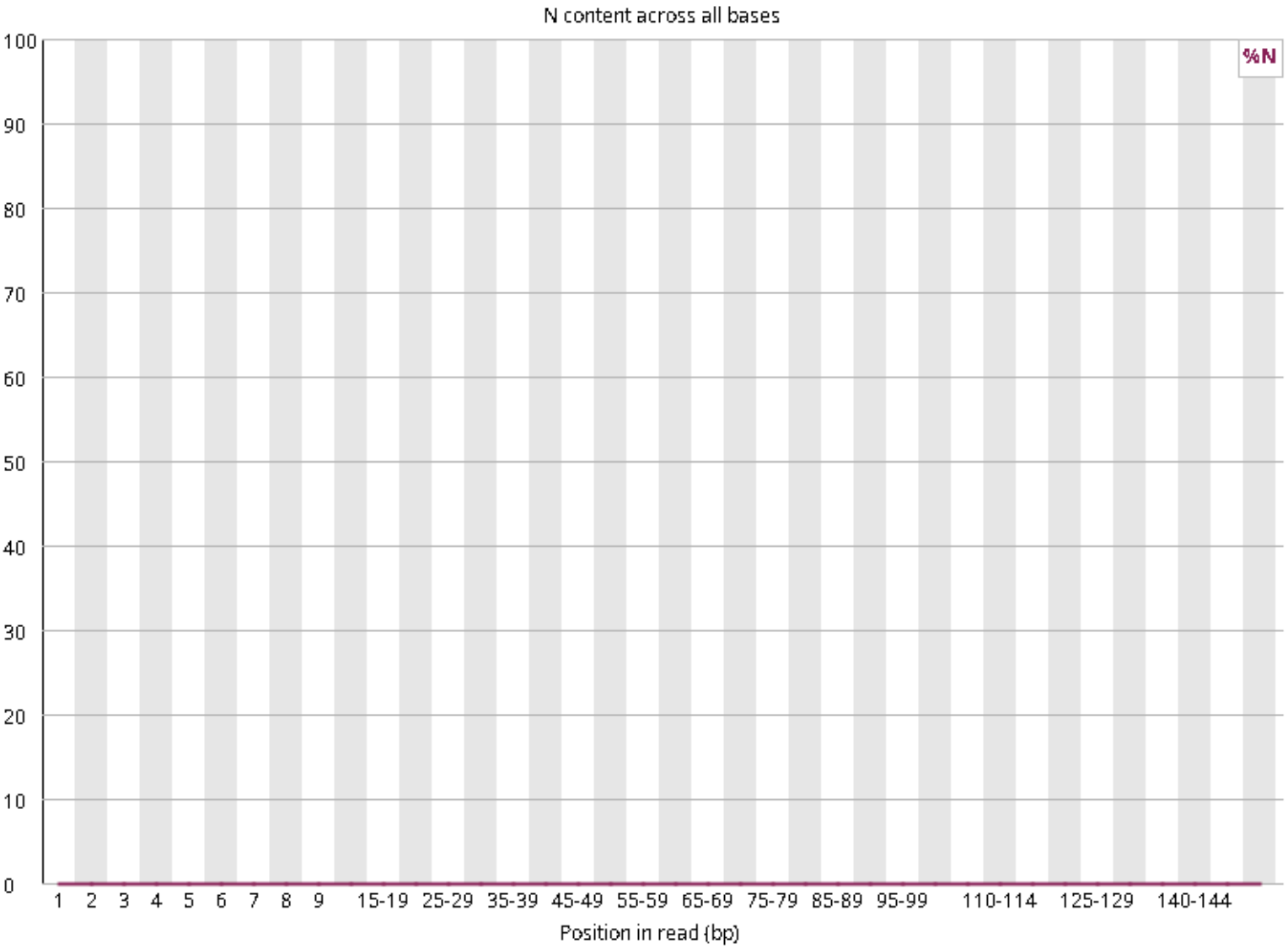
Per base sequence content



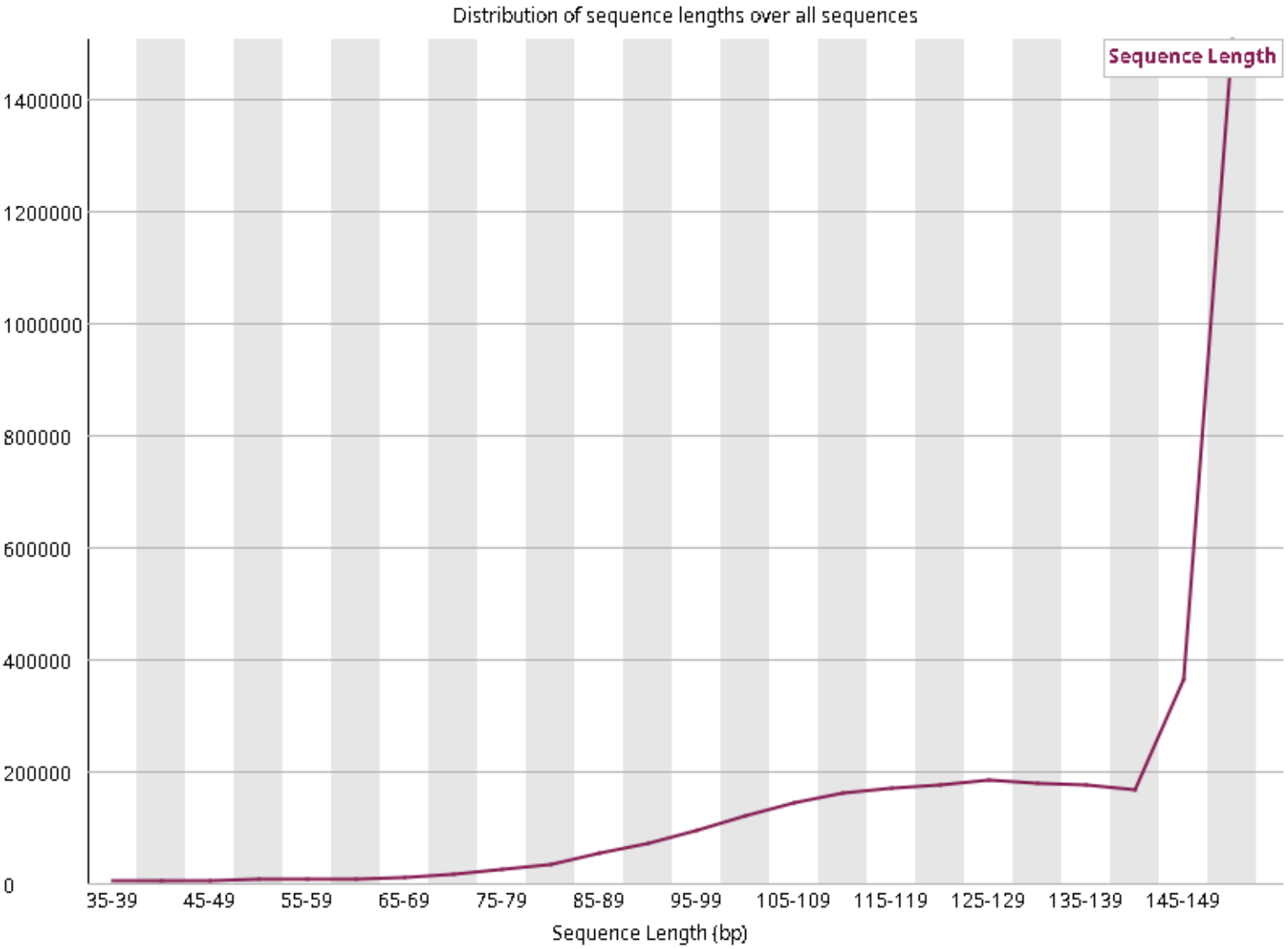
Per sequence GC content



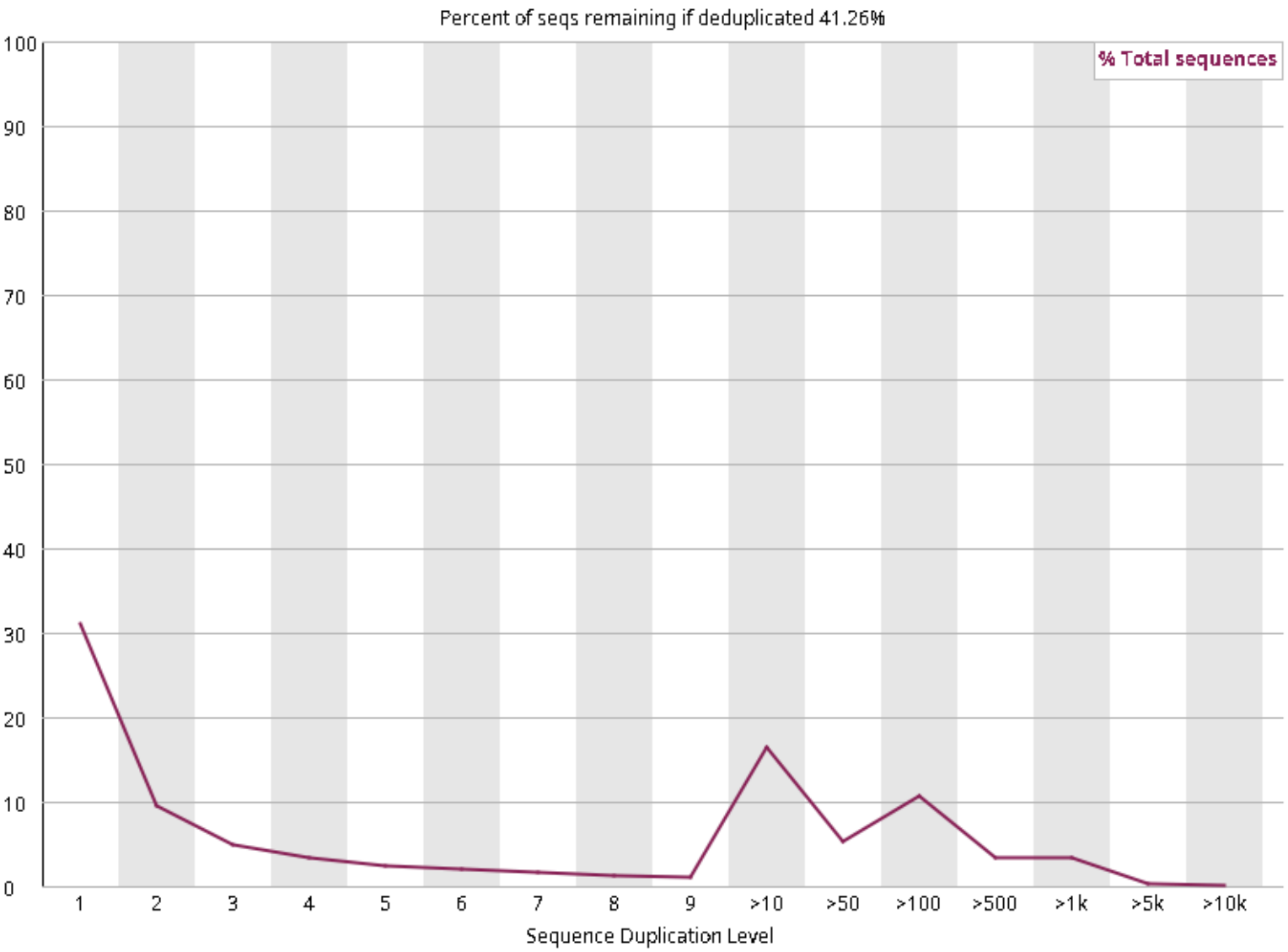
Per base N content



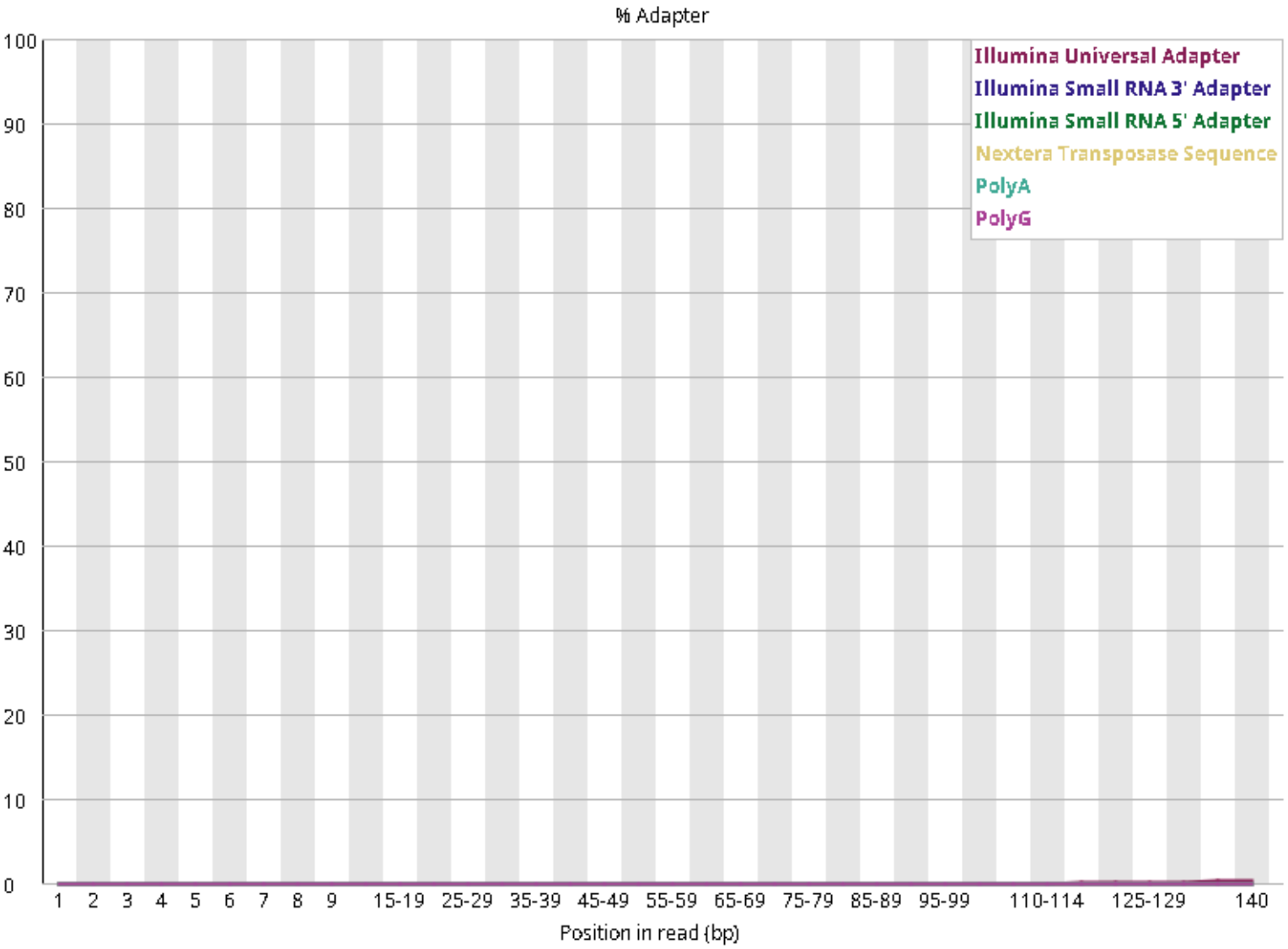
Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCCTGAGCGTCTGAGATGTTAG	10886	0.2908229412976324	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6649	0.17763014299907753	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5373	0.14354139845601496	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5121	0.1368091385619305	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4125	0.1102006827900729	No Hit
CCCCTTACTCAGCTTGAACTTGTCGCCCTCTTGGCAGGAGTACTTGTGGA	4022	0.10744900513495108	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3838	0.10253338679958783	No Hit

Adapter Content