











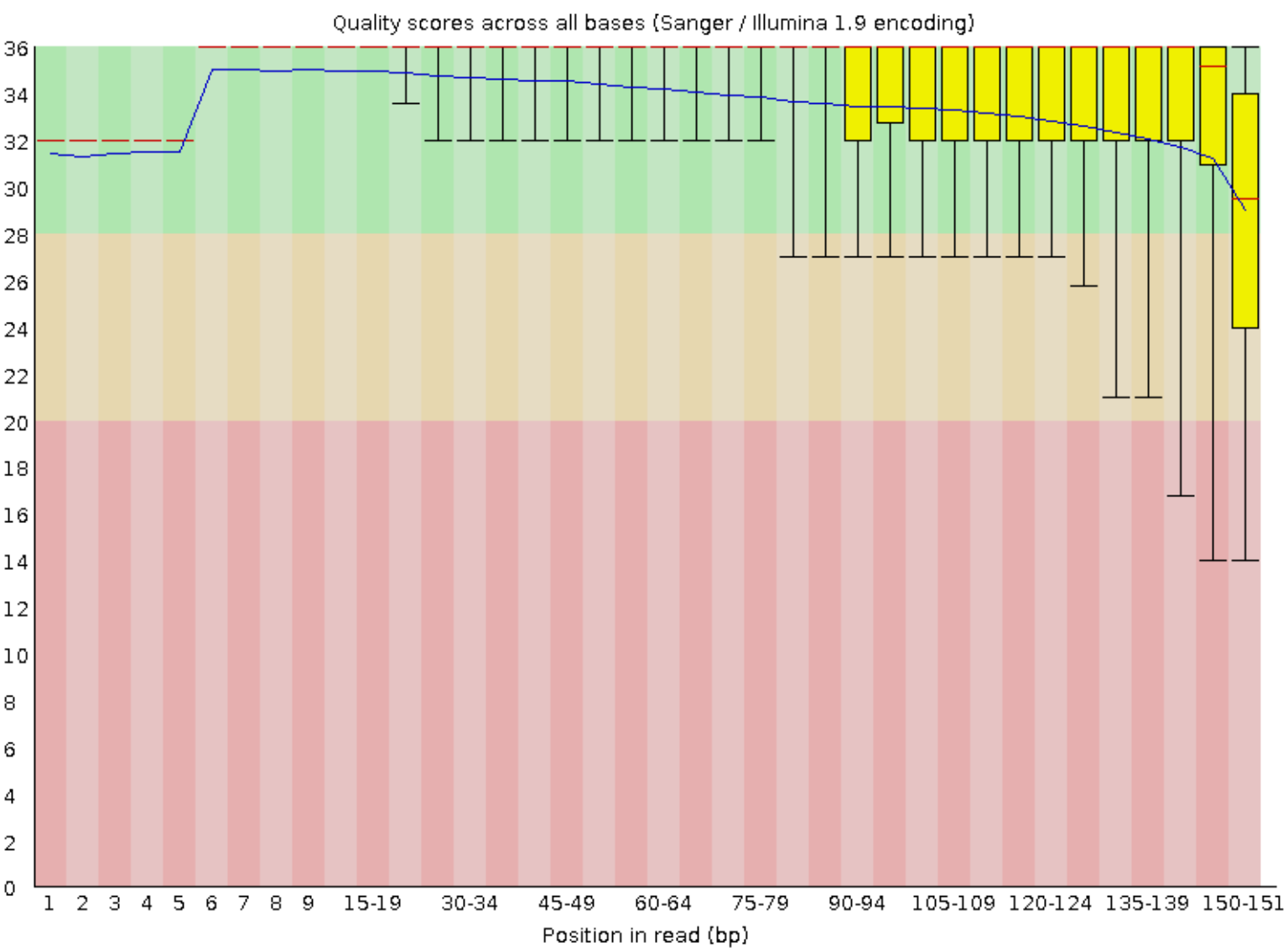
Summary

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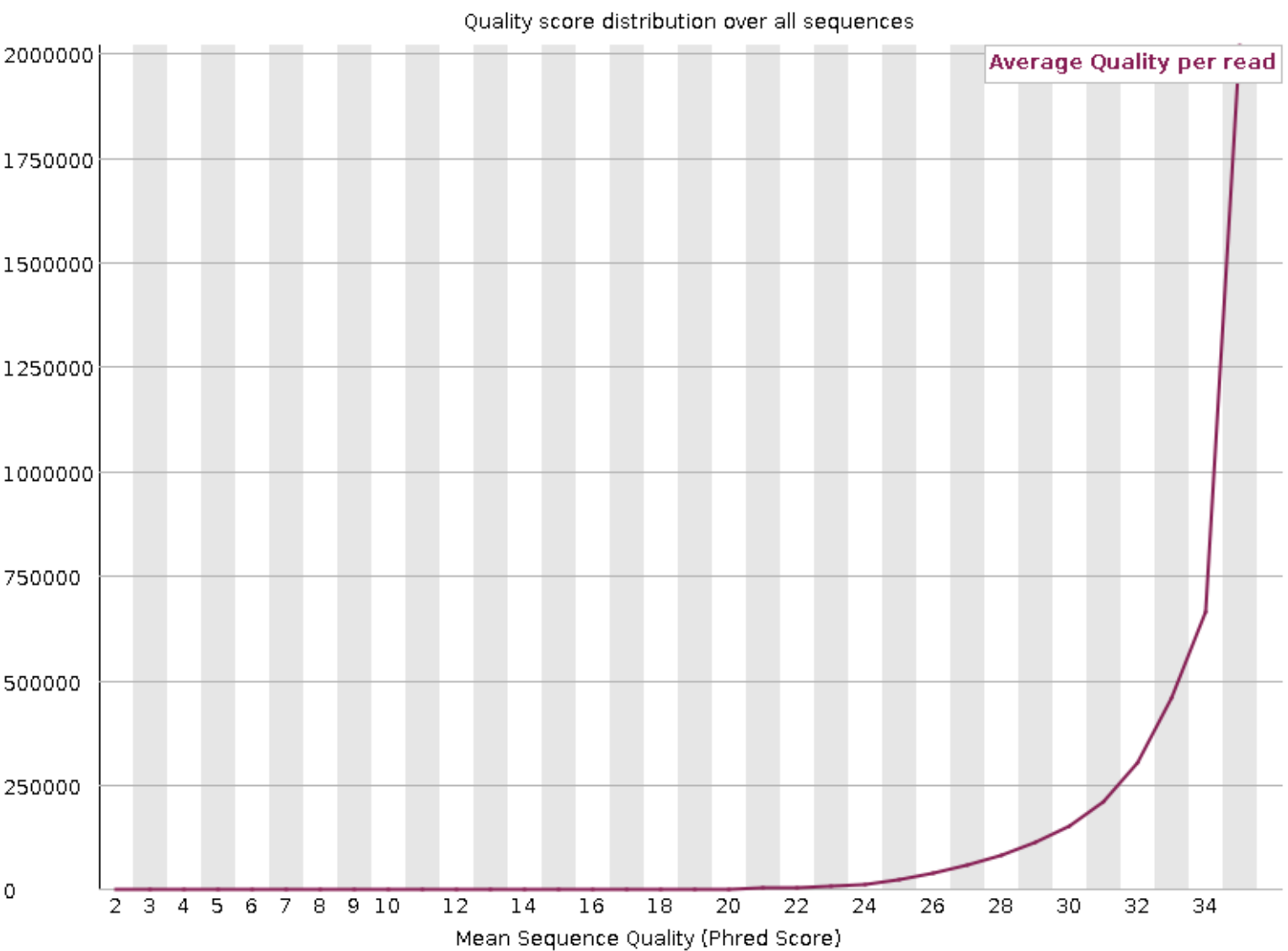
Basic Statistics

Measure	Value
Filename	SRR11412216_pass.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4175640
Total Bases	547.1 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	49

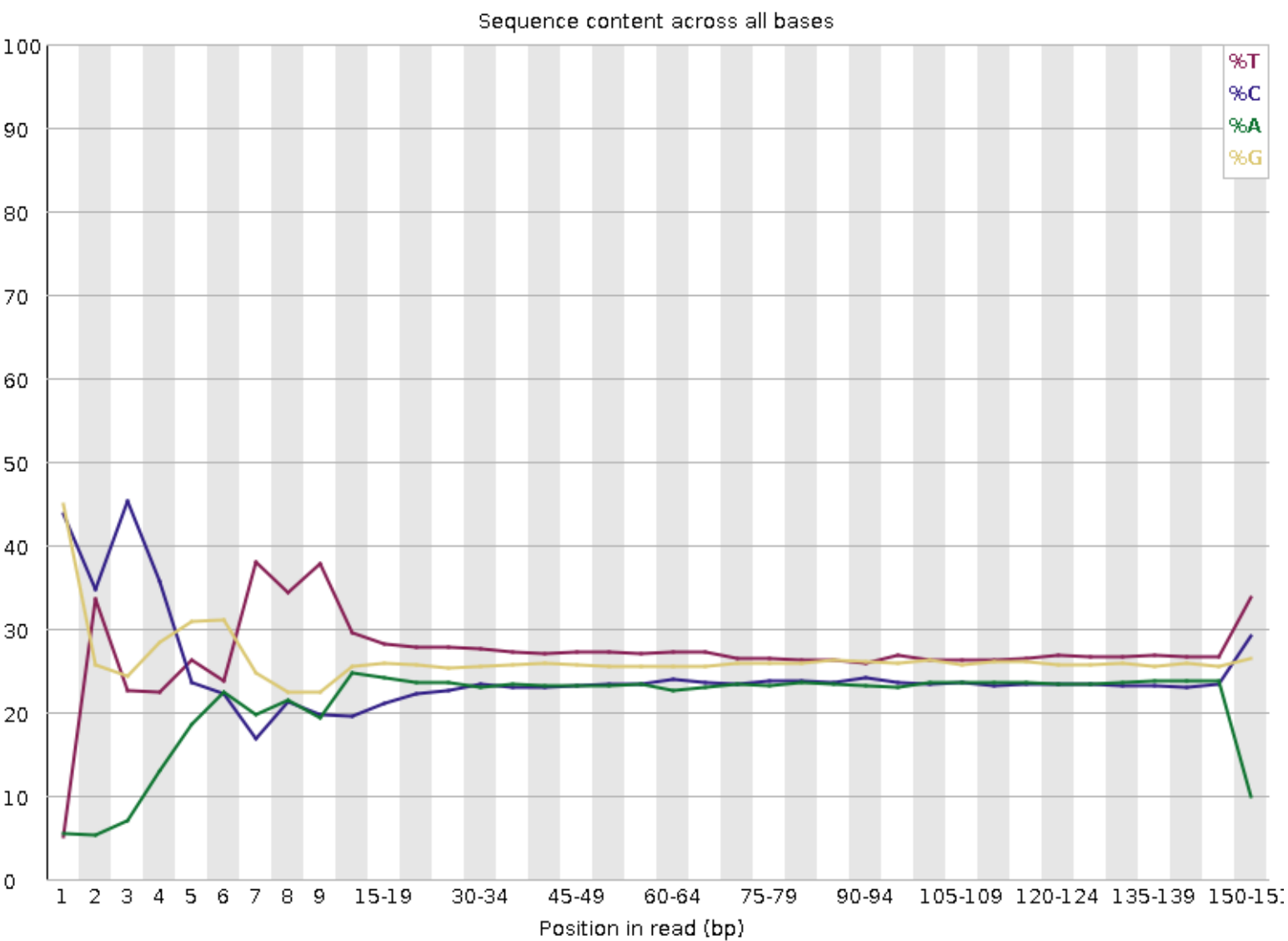
✔ Per base sequence quality



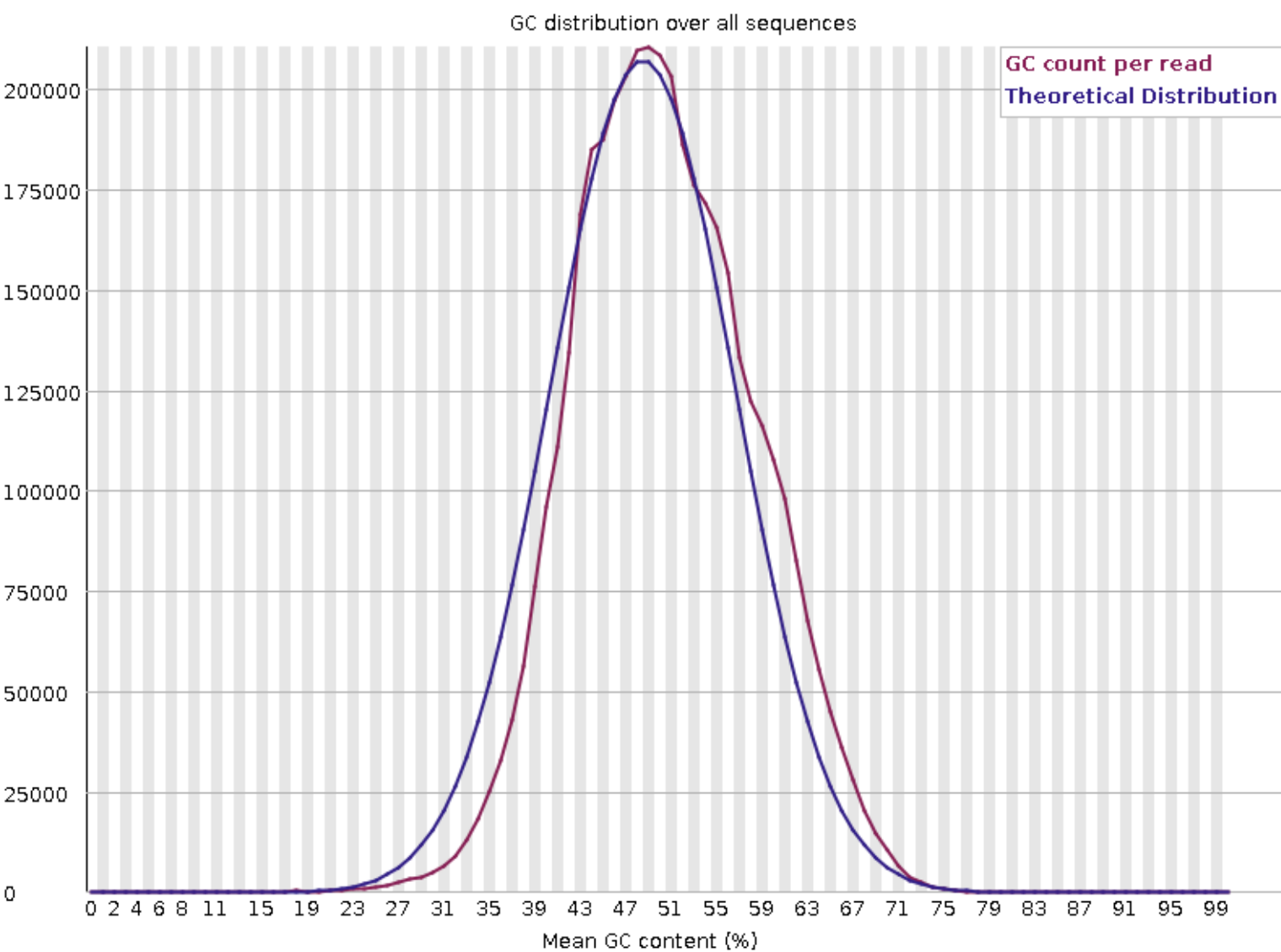
✔ Per sequence quality scores



✖ Per base sequence content

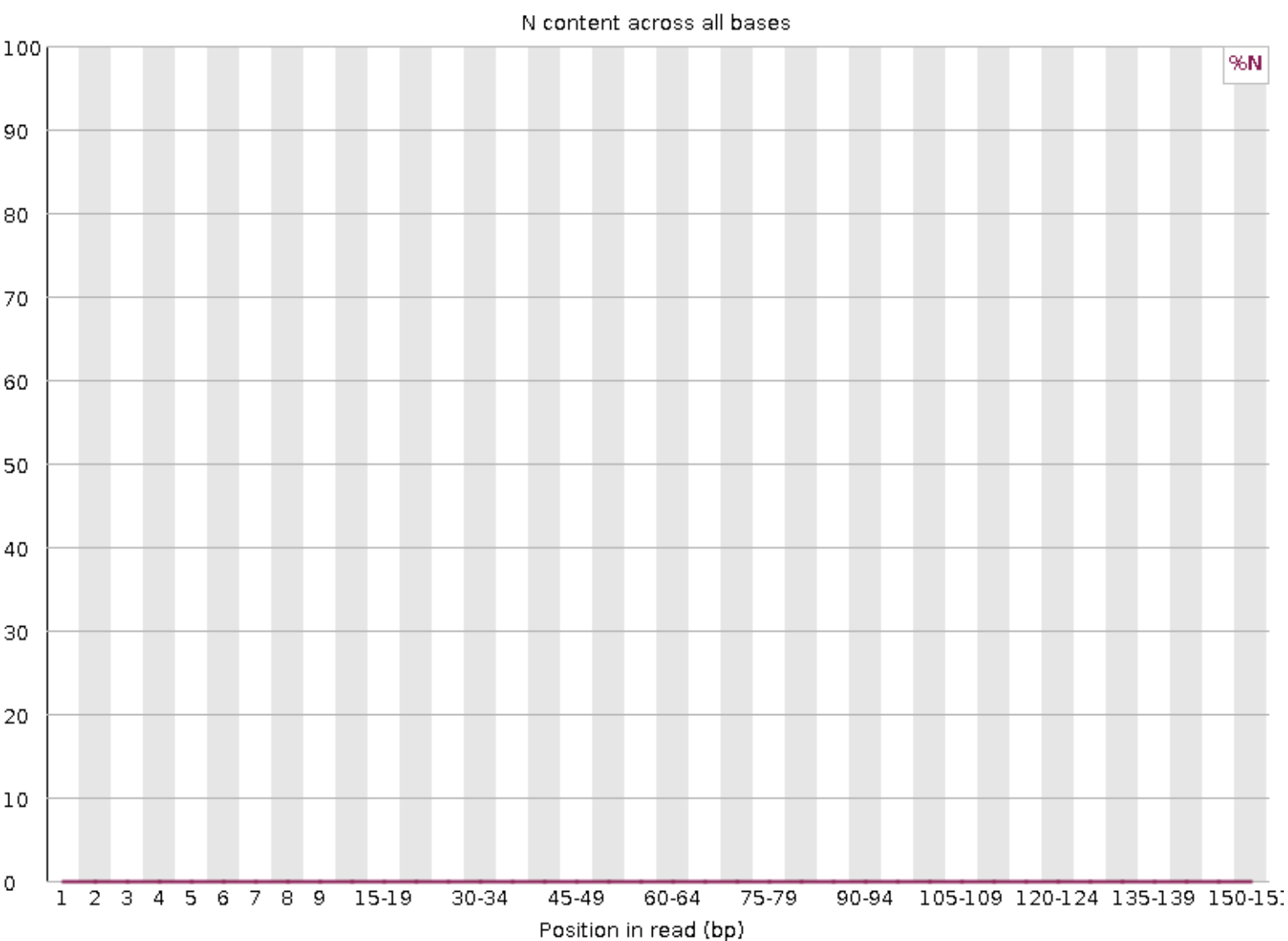


🚨 Per sequence GC content

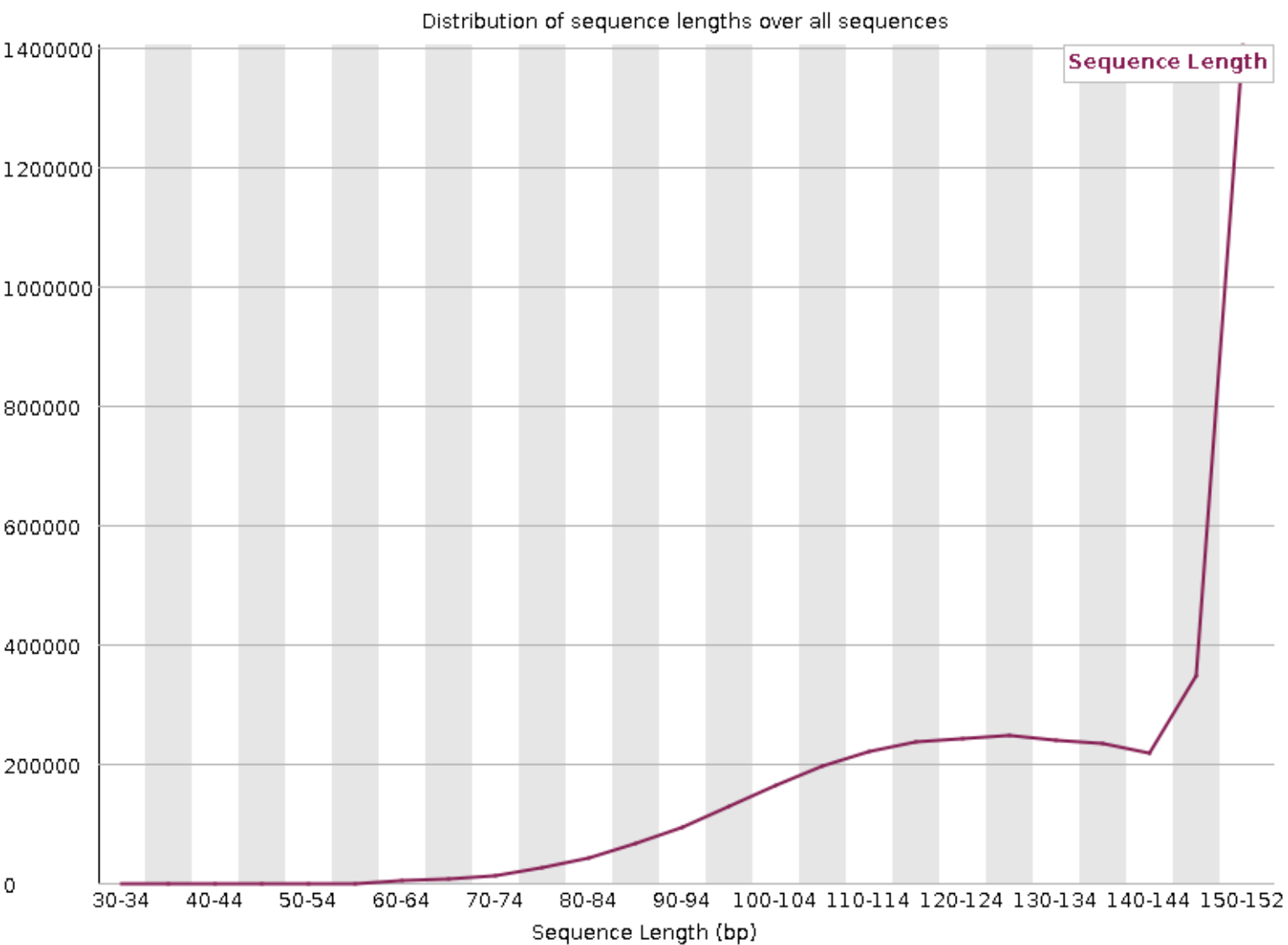




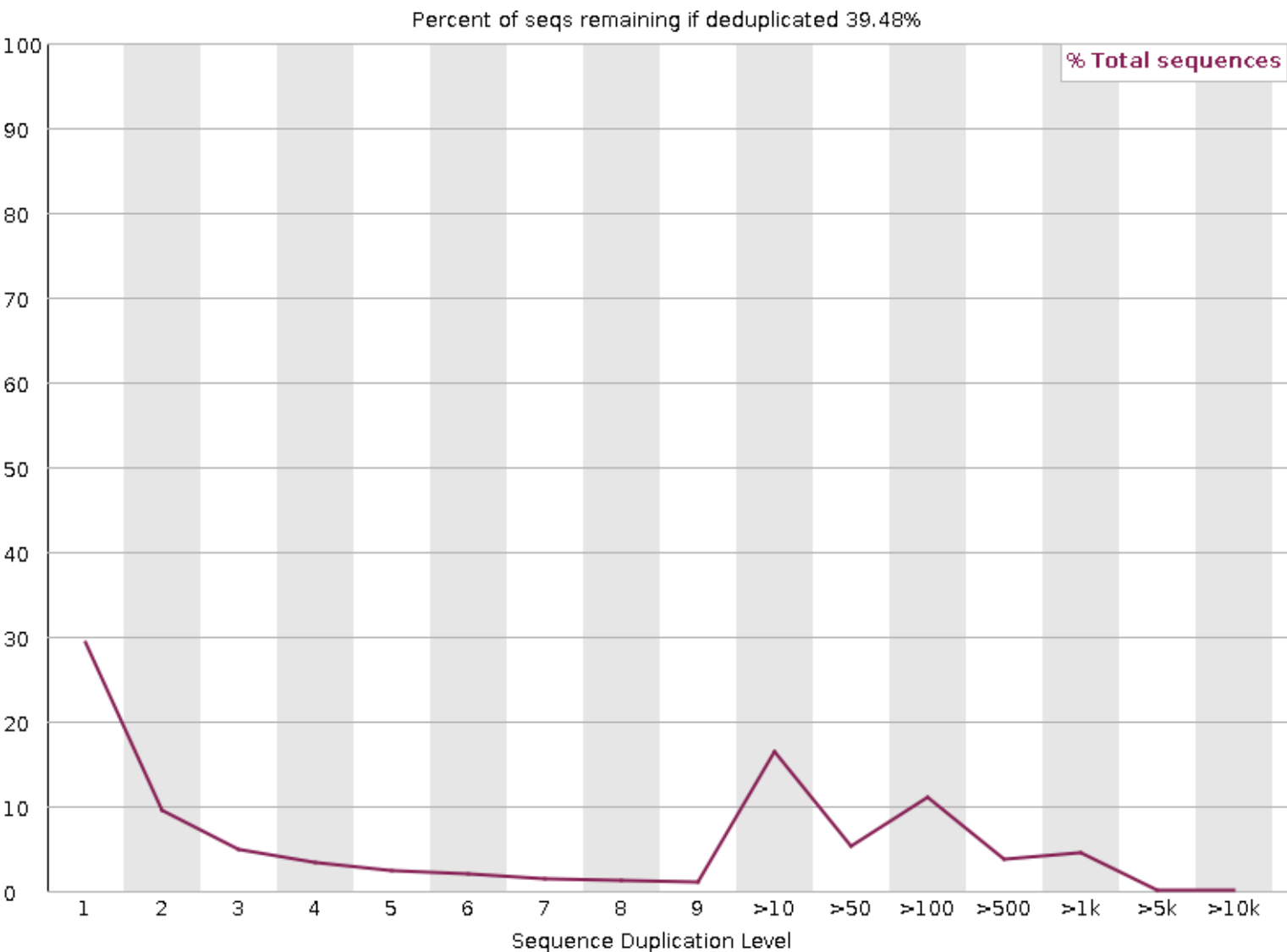
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	12454	0.2982536808728722	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	9951	0.23831077391729172	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA	4882	0.11691620925175543	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	4799	0.11492849000392755	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4699	0.11253364753666503	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	4480	0.10728894253336015	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4473	0.10712130356065179	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCTTTGGTTCTCAGGGT	4454	0.10666628349187192	No Hit

Sequence	Count	Percentage	Possible Source
CCCCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGG	4244	0.10163711431062064	No Hit



Adapter Content

