

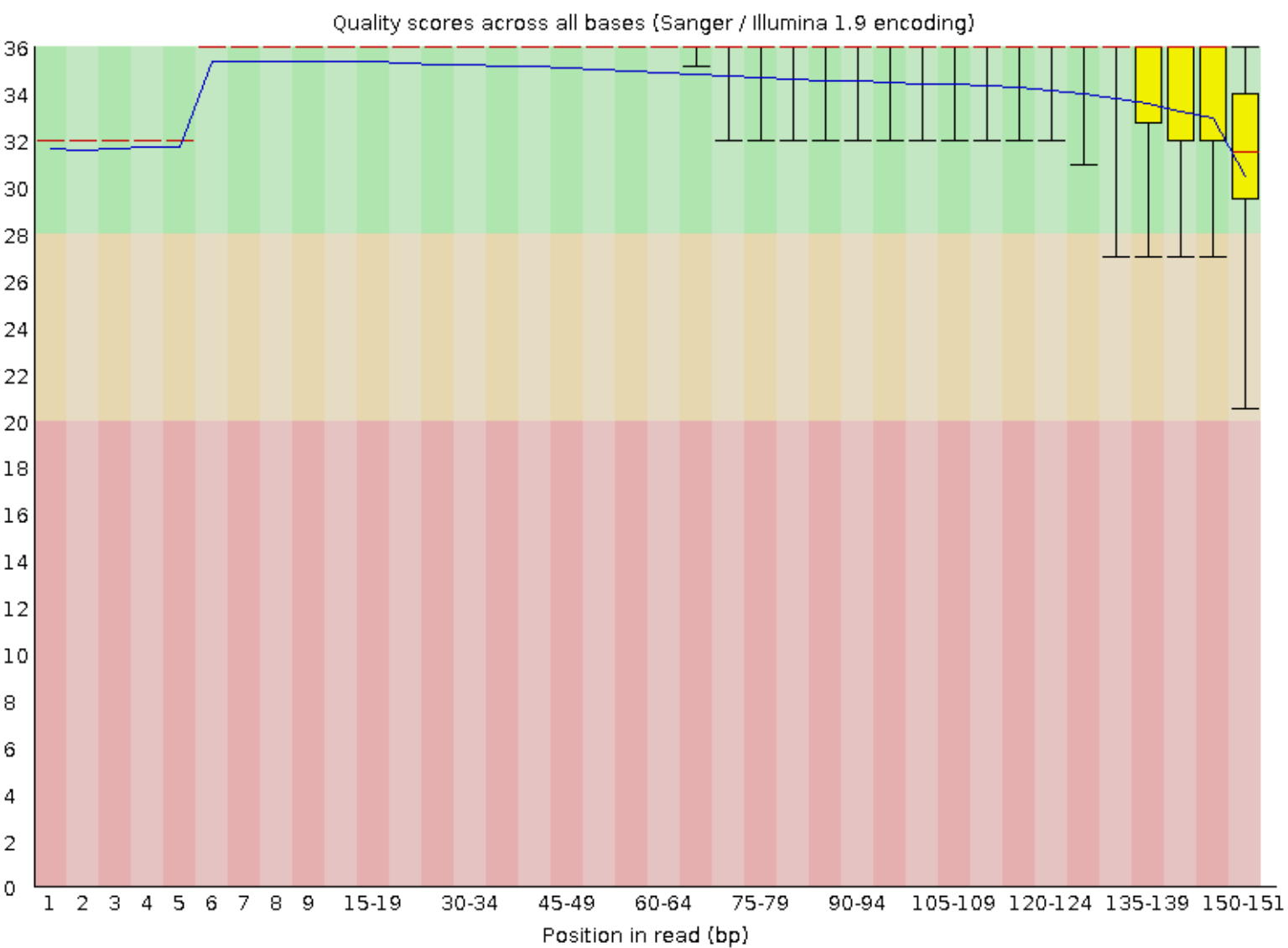
Summary

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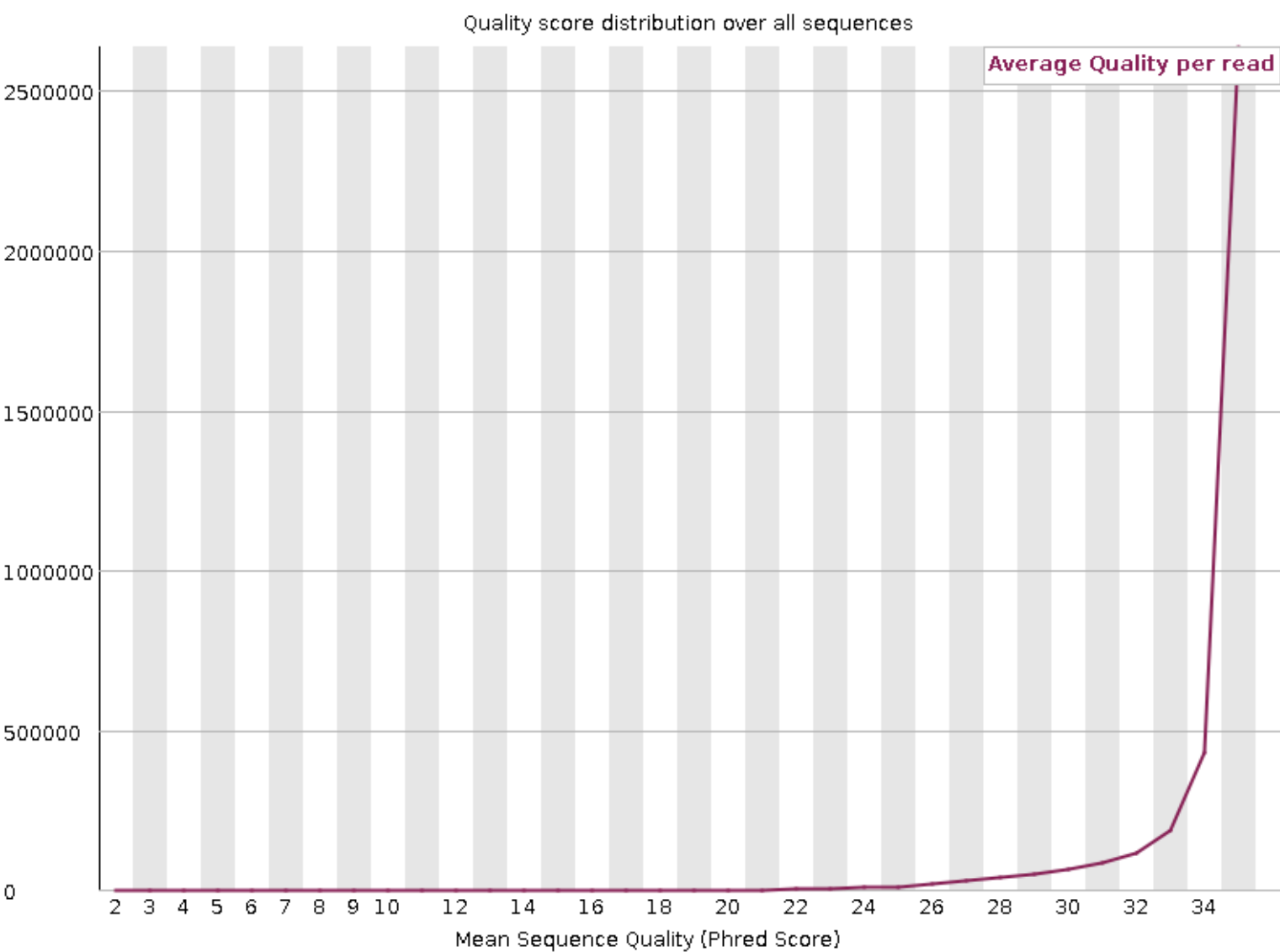
✓ Basic Statistics

Measure	Value
Filename	SRR11412230_pass.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3735882
Total Bases	504.1 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	50

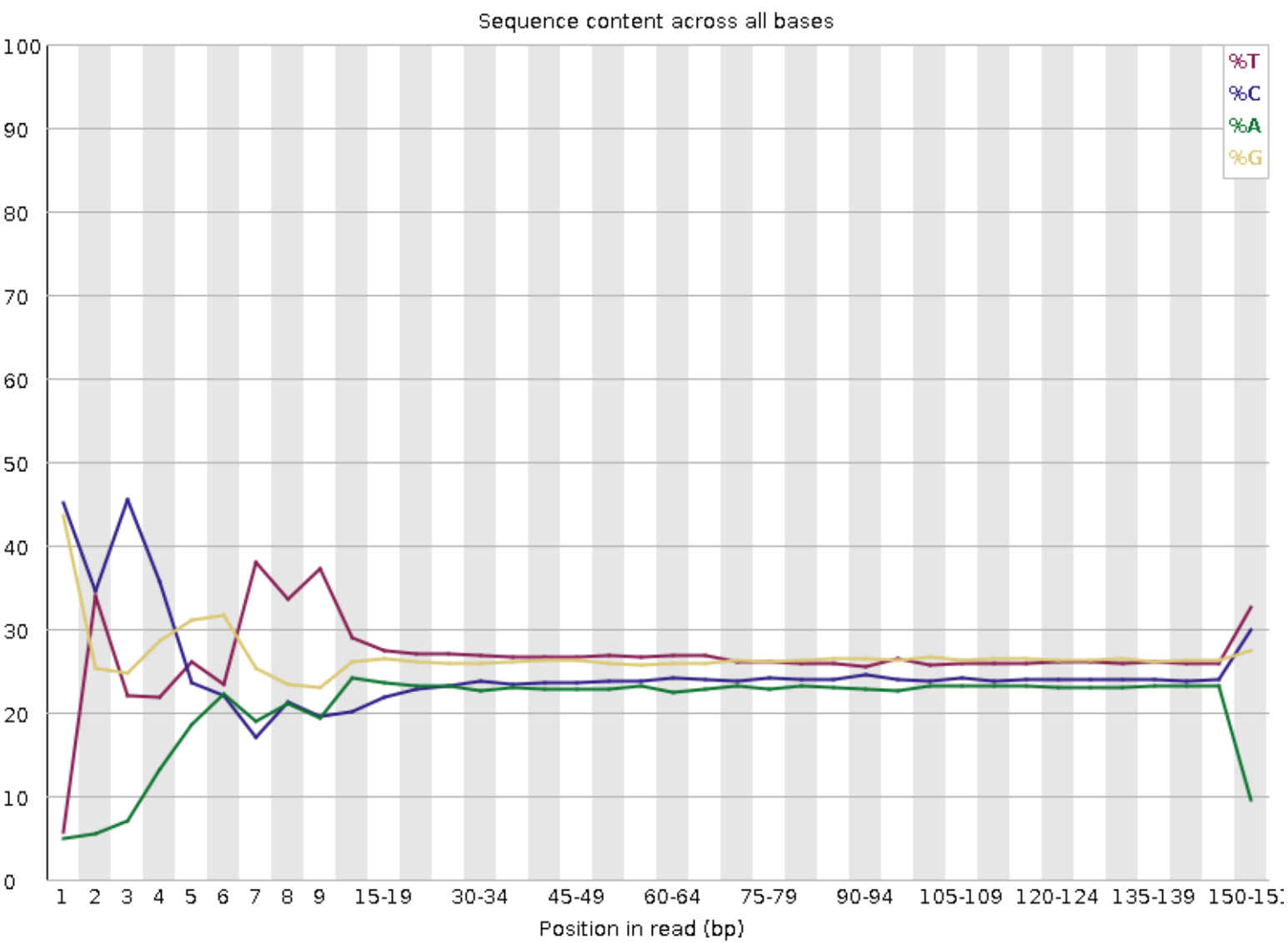
✔ Per base sequence quality



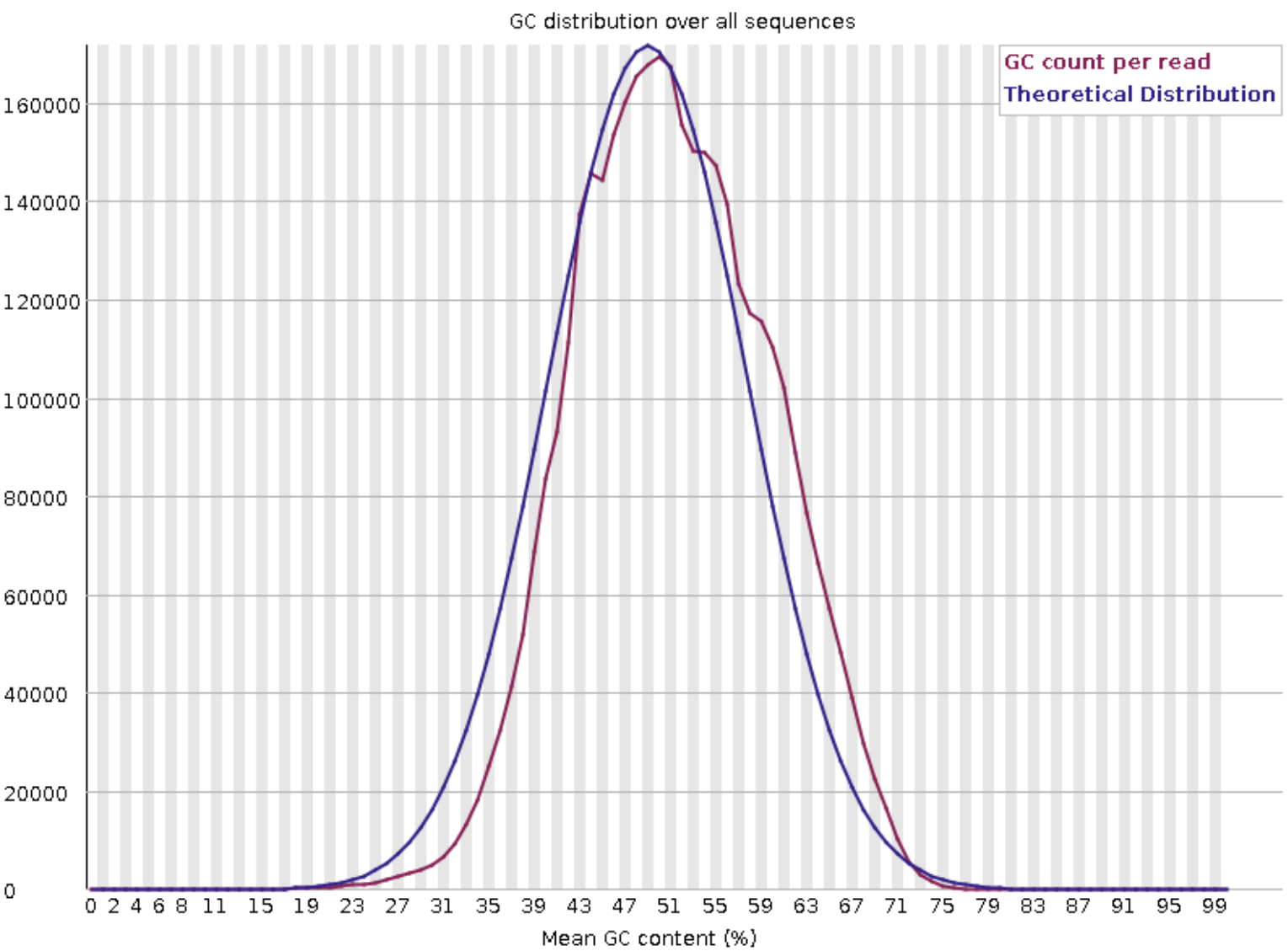
✔ Per sequence quality scores



✖ Per base sequence content

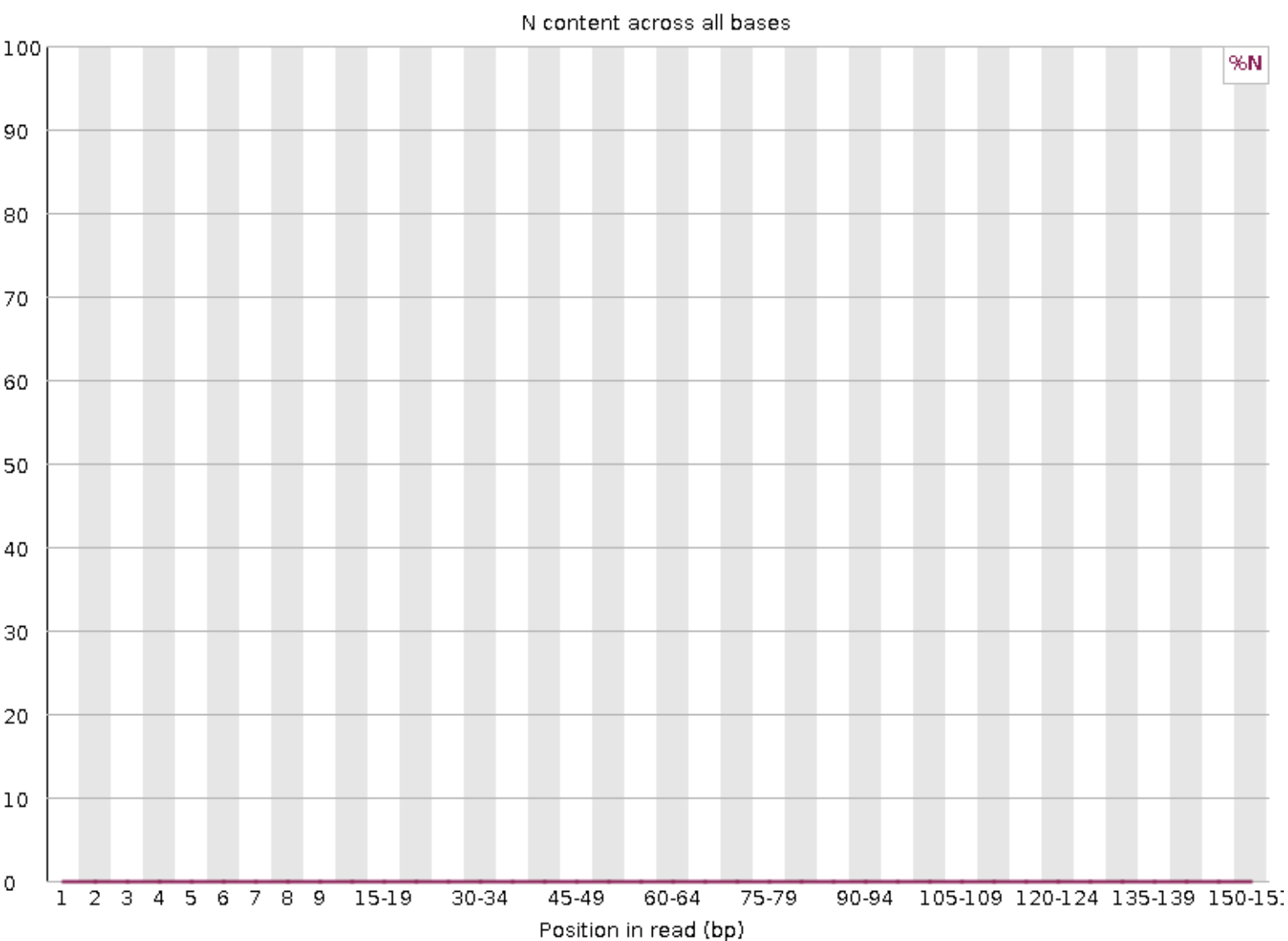


! Per sequence GC content

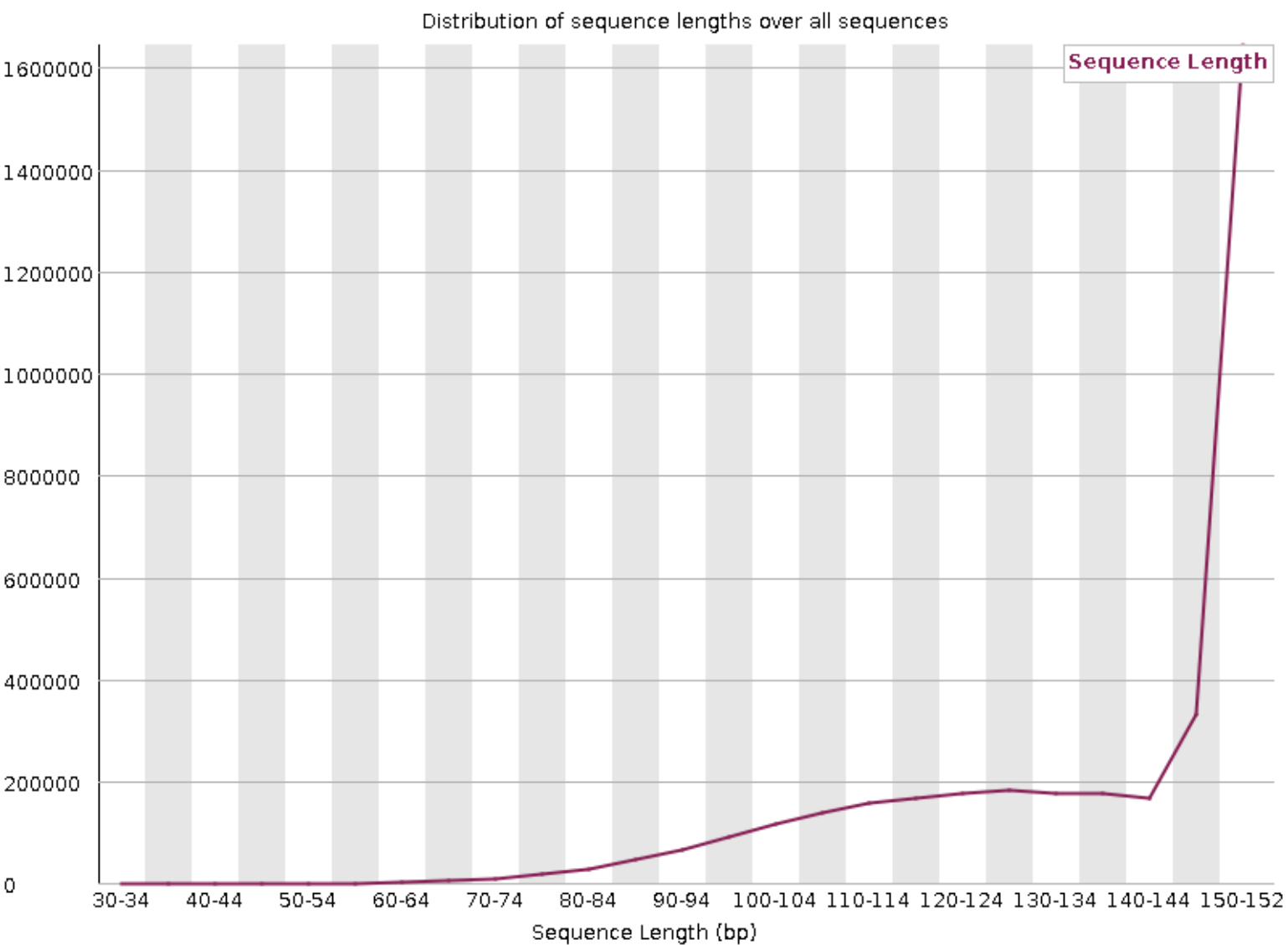




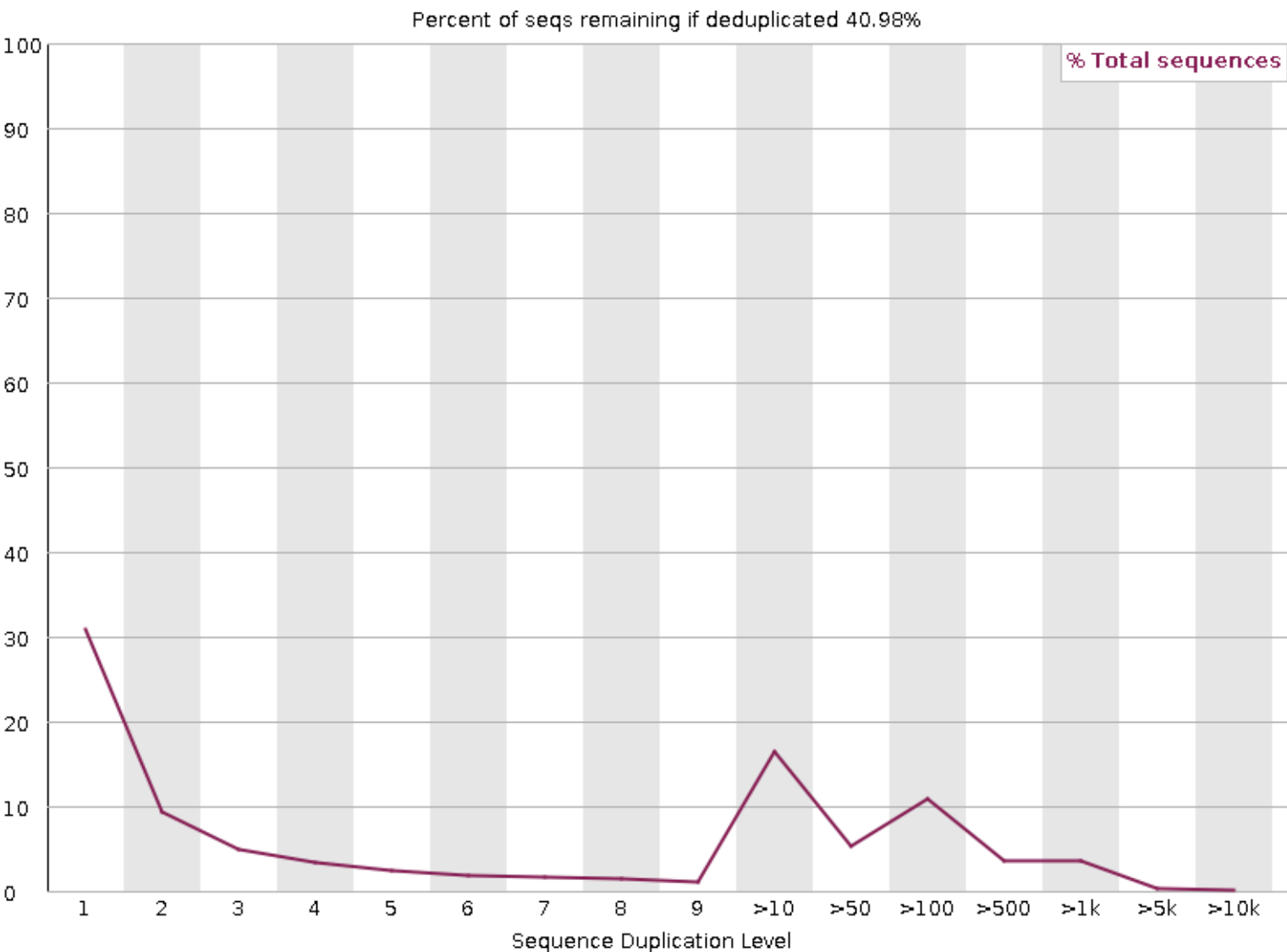
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	11246	0.3010266384216632	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6734	0.1802519458591037	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5512	0.14754213329007715	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5215	0.1395922033940044	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4281	0.11459141375450295	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	4204	0.11253032081848409	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3758	0.10059204225401122	No Hit



Adapter Content

