

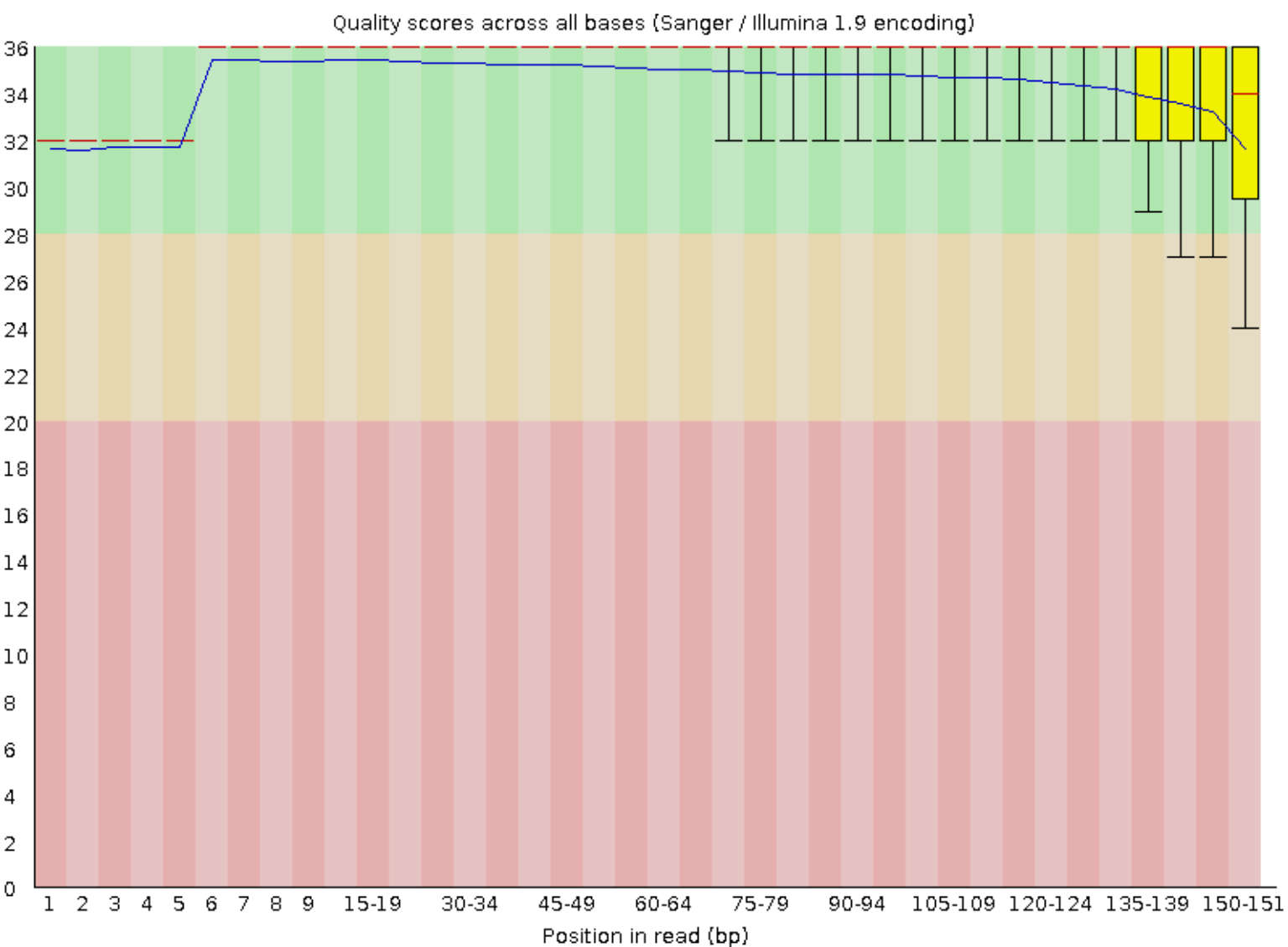
## Summary

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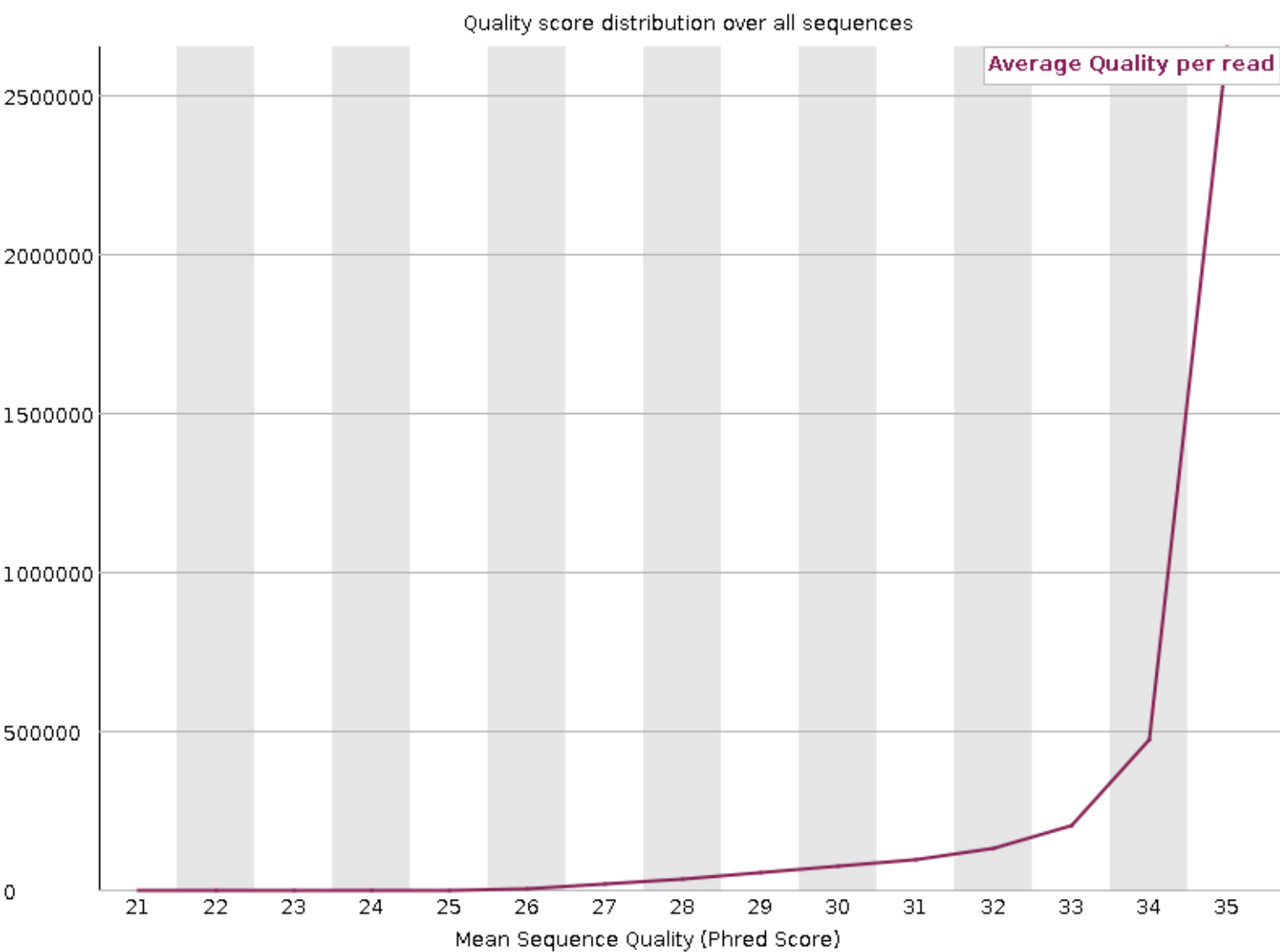
## ✓ Basic Statistics

Measure	Value
Filename	infected1_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3774724
Total Bases	502.6 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	50

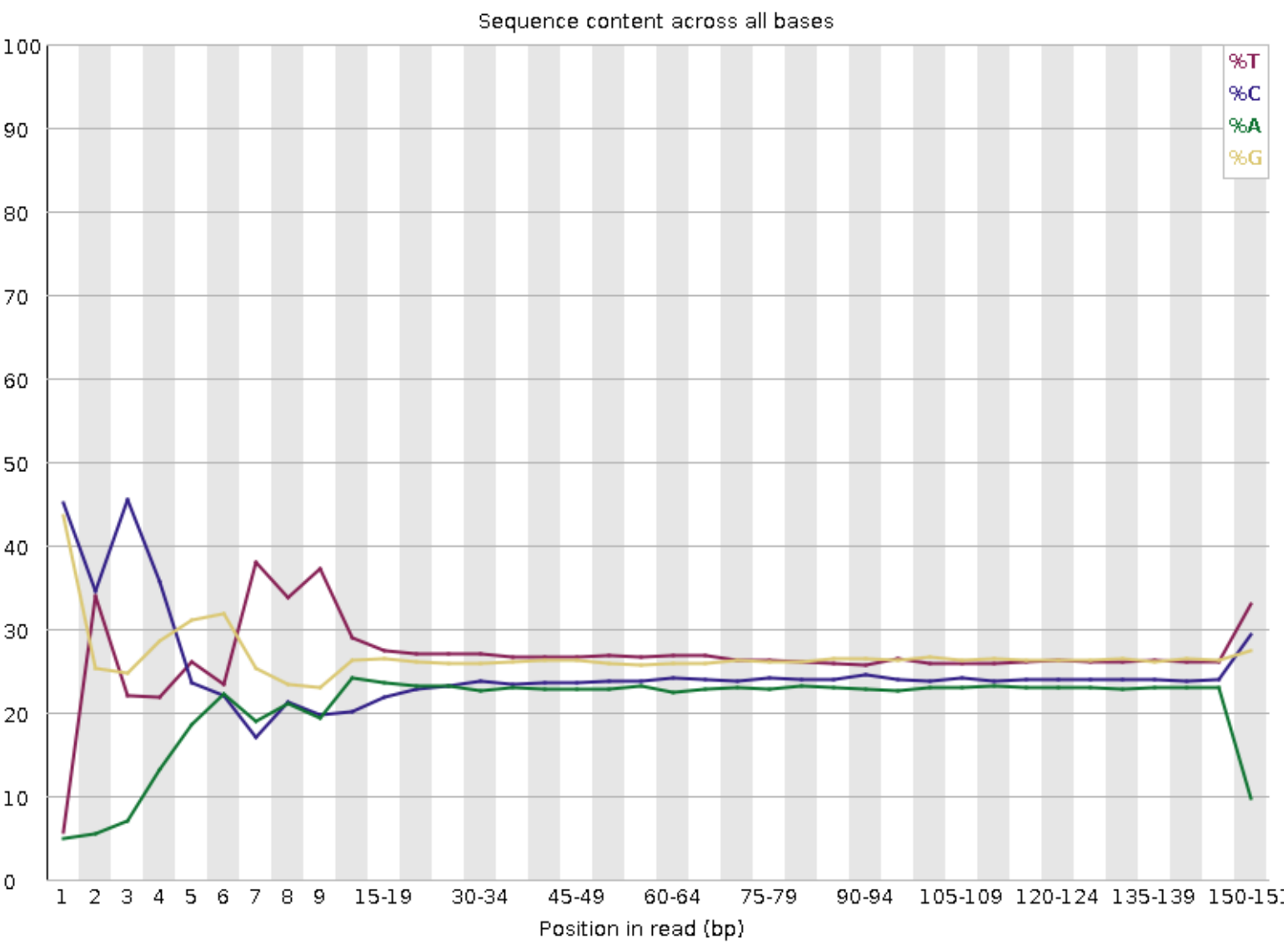
## ✔ Per base sequence quality



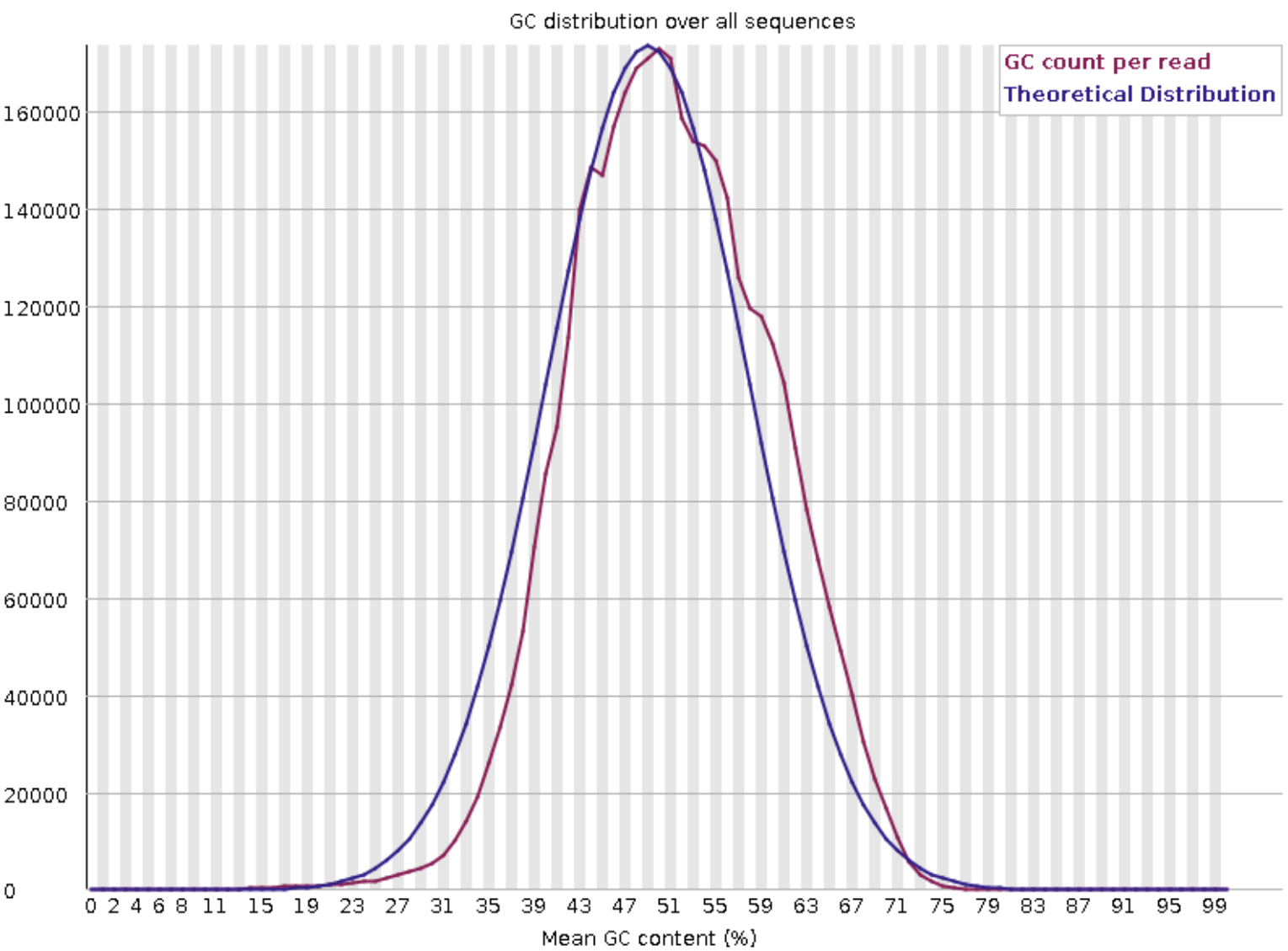
## ✔ Per sequence quality scores



## ✖ Per base sequence content

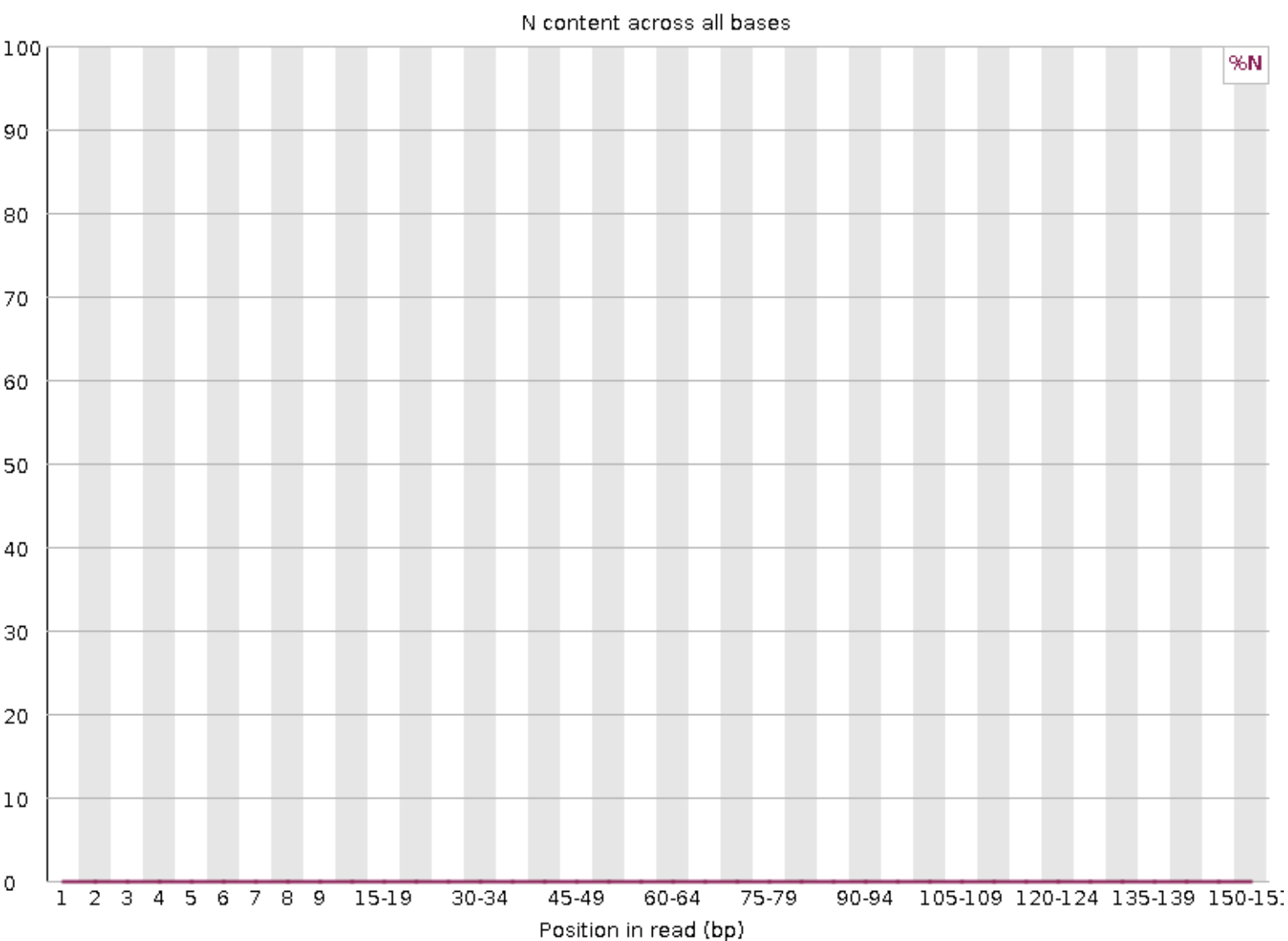


## ! Per sequence GC content

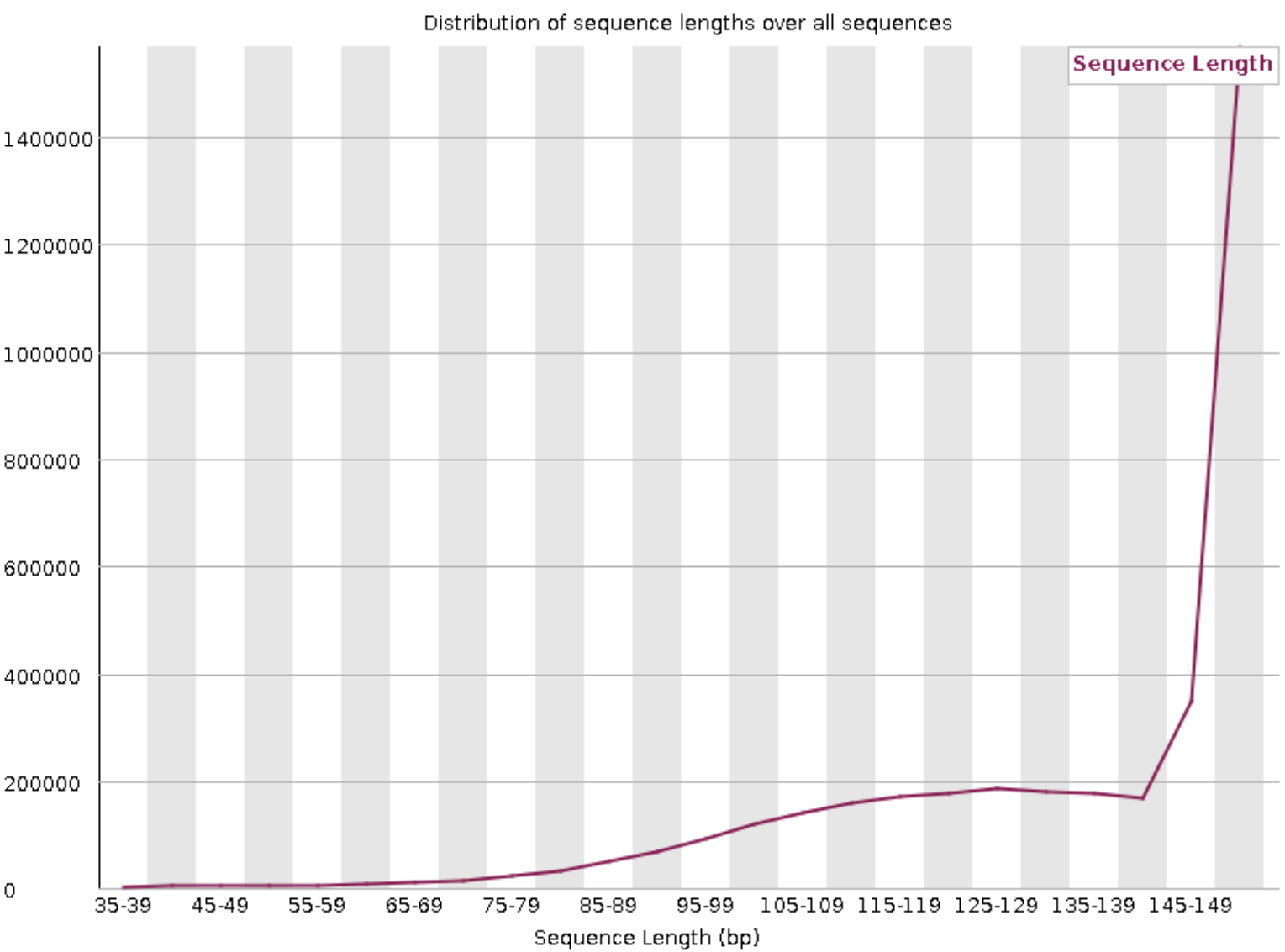




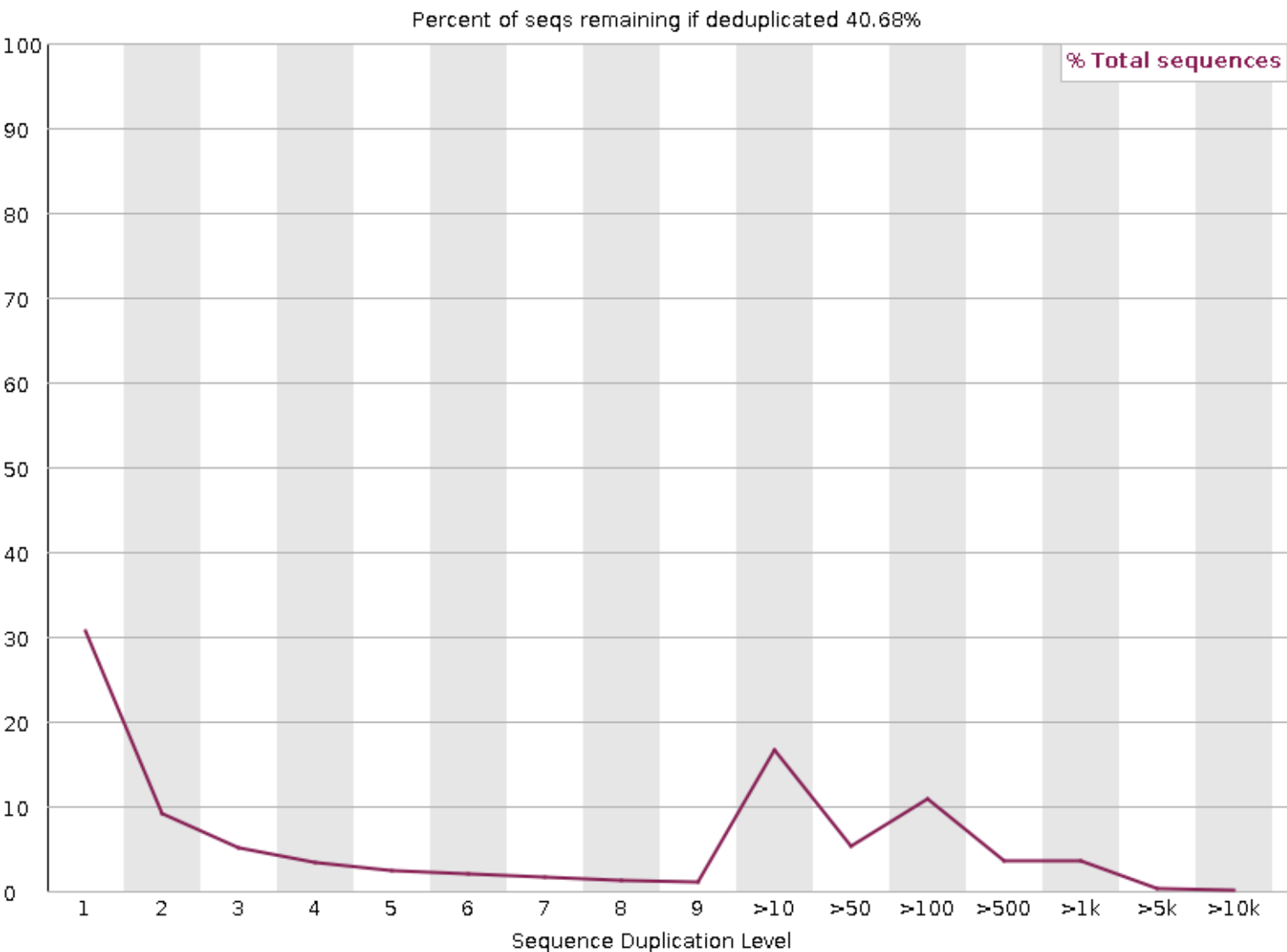
## Per base N content



# Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	11404	0.3021148036253776	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6686	0.17712553288664284	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5706	0.15116336982518458	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5144	0.13627486406953196	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4248	0.11253802927048441	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	3996	0.10586204448325229	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3866	0.10241808407714047	No Hit





## Adapter Content

