

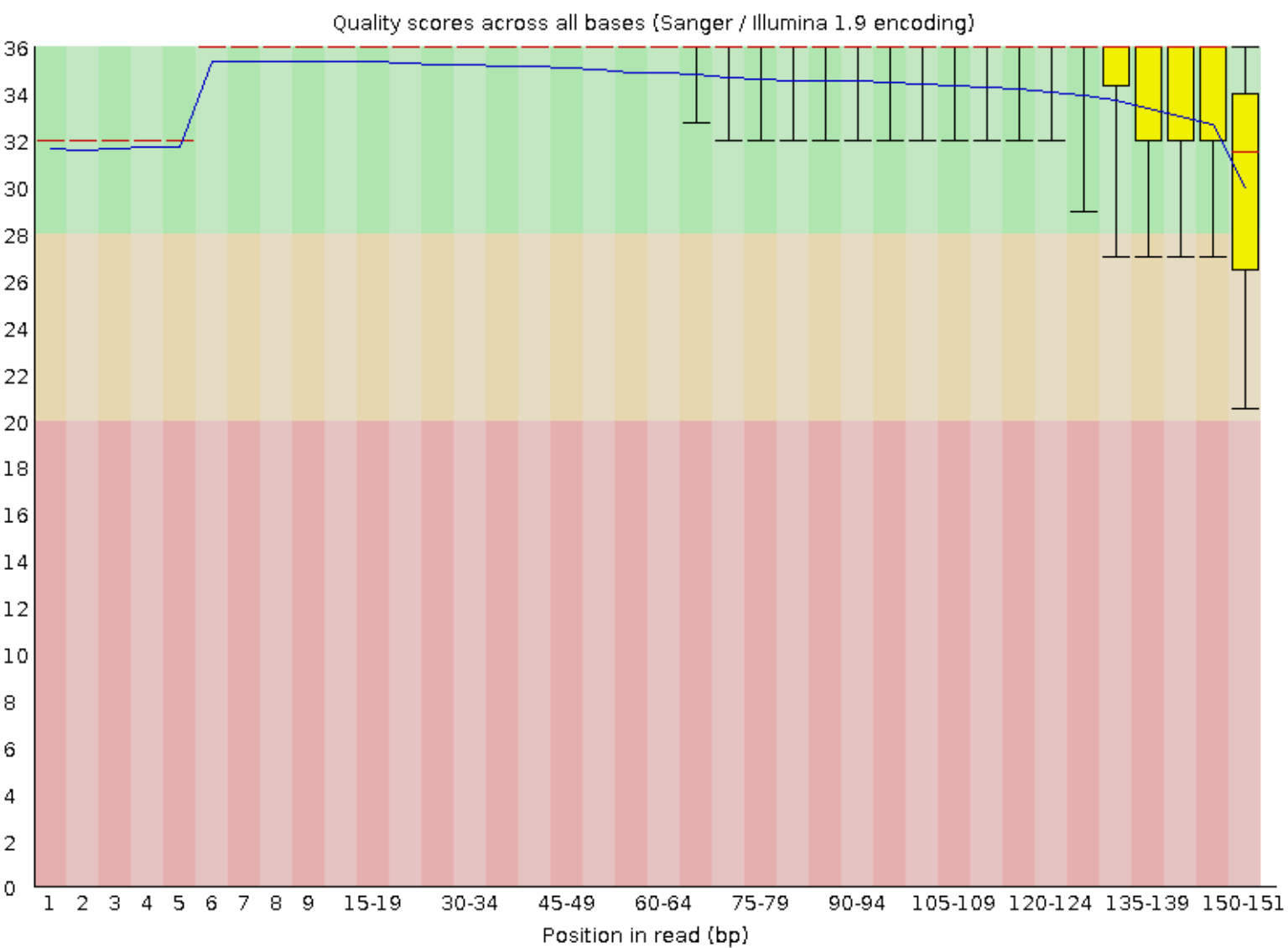
## Summary

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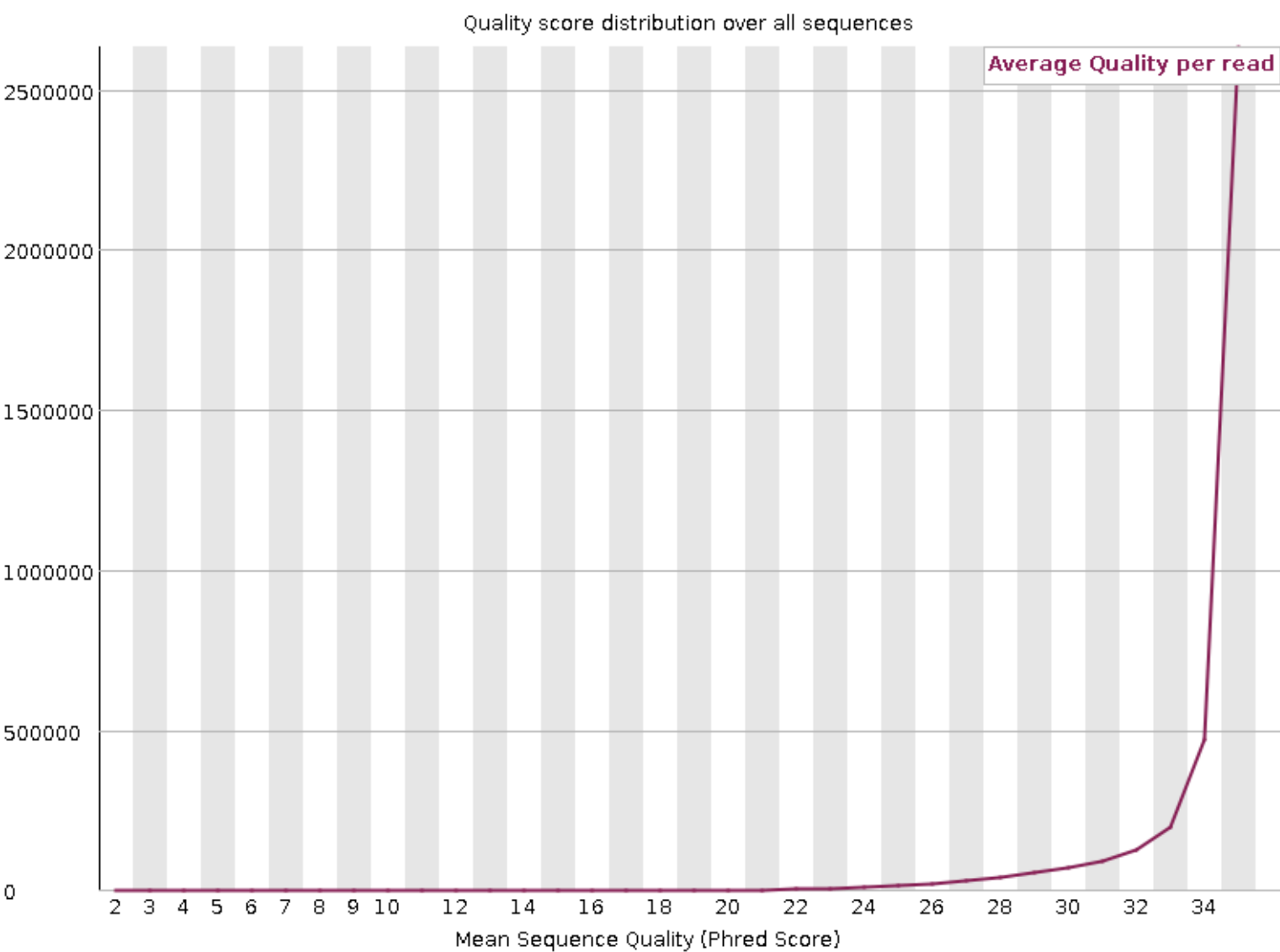
## ✓ Basic Statistics

Measure	Value
Filename	SRR11412229_pass.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3803175
Total Bases	513.5 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	50

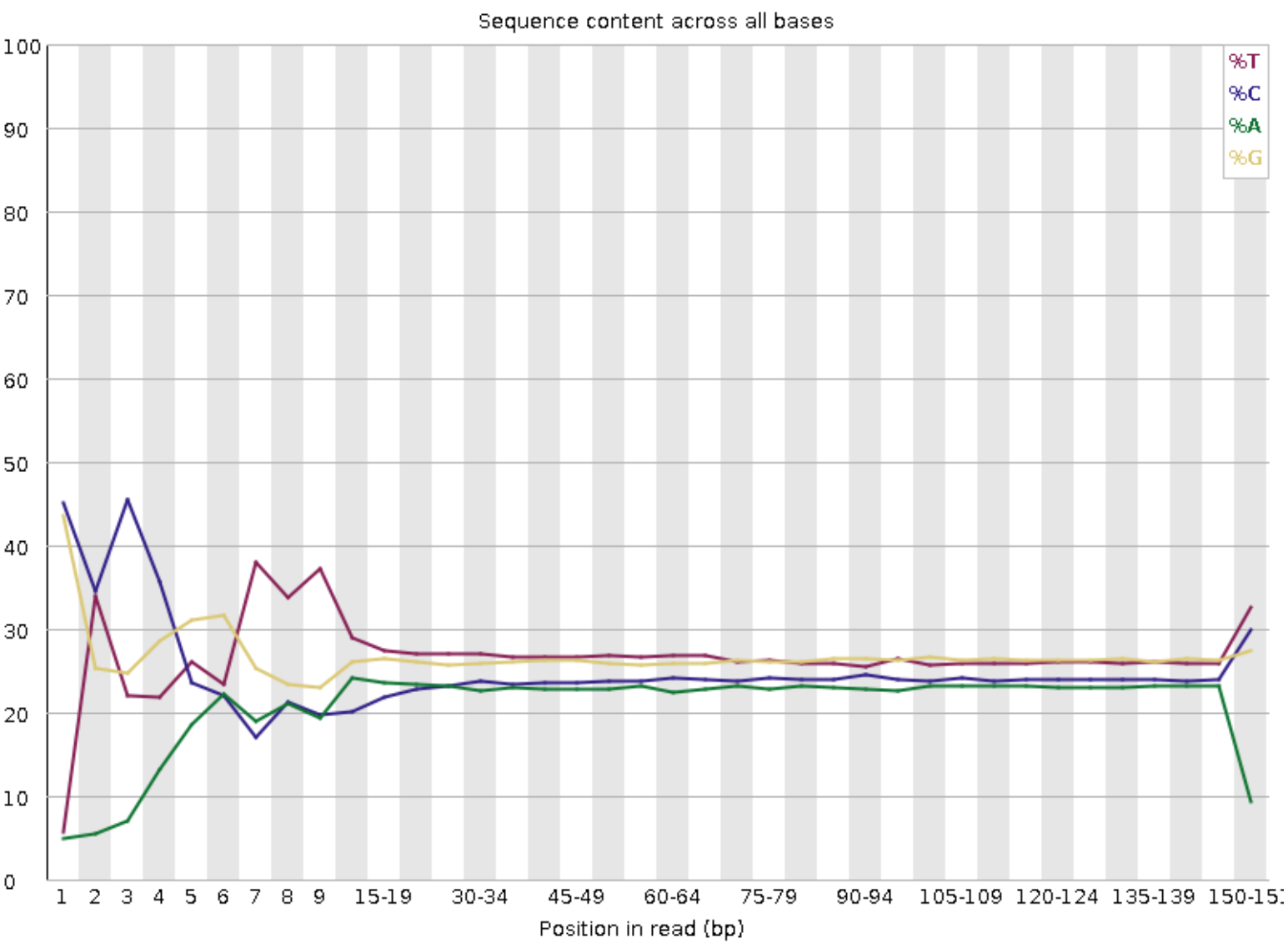
## ✔ Per base sequence quality



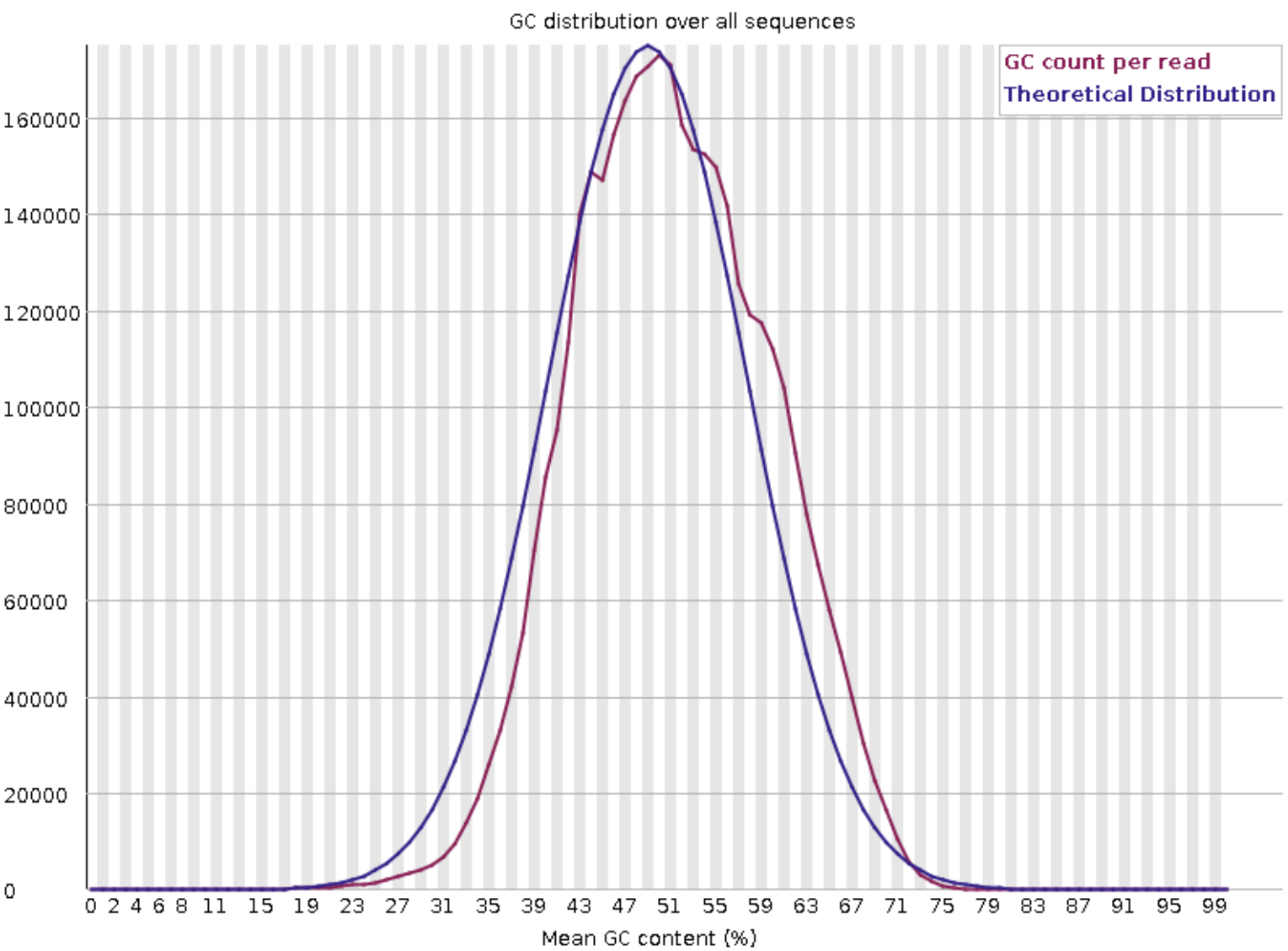
## ✔ Per sequence quality scores



## ✖ Per base sequence content

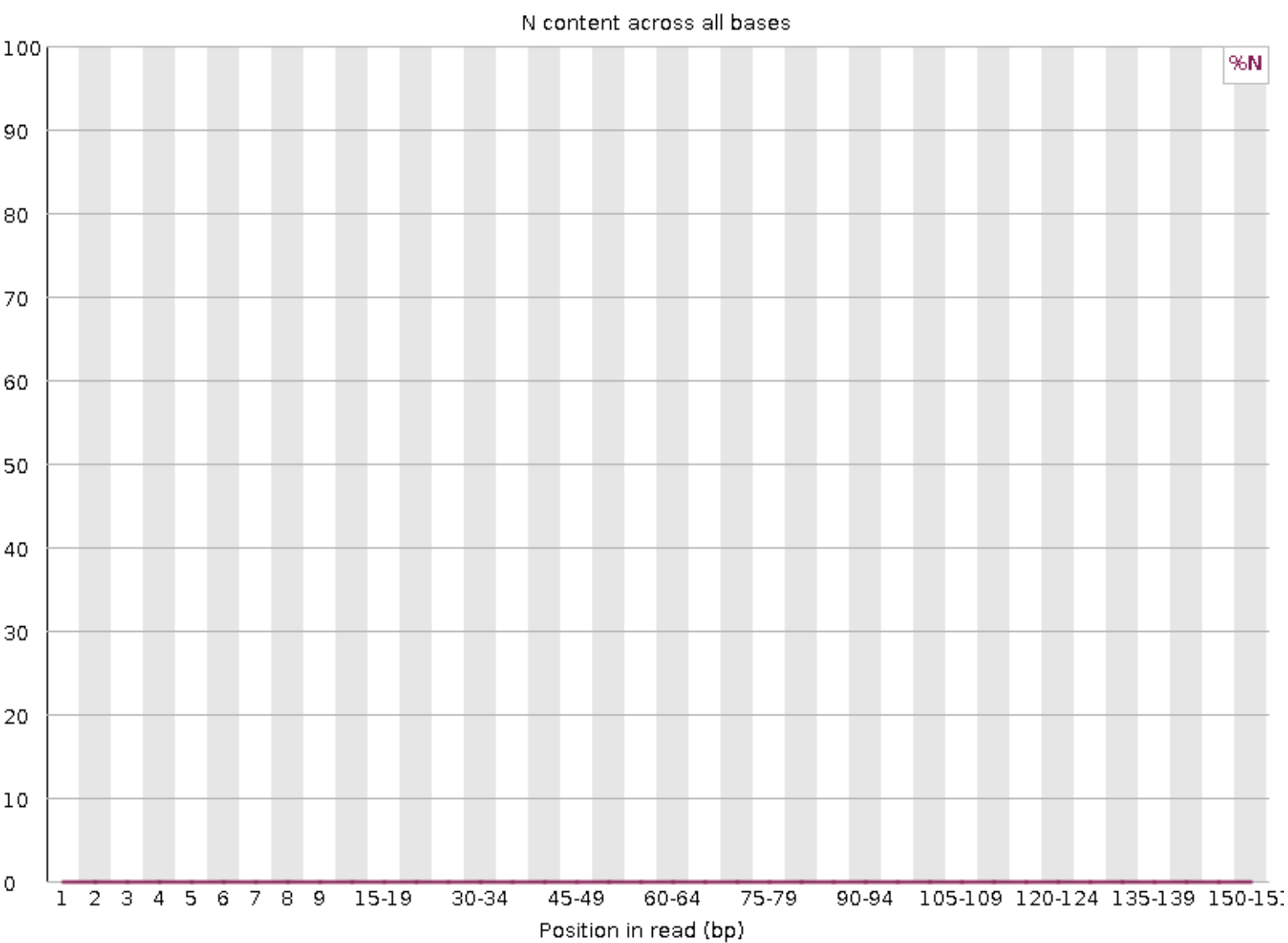


## ! Per sequence GC content

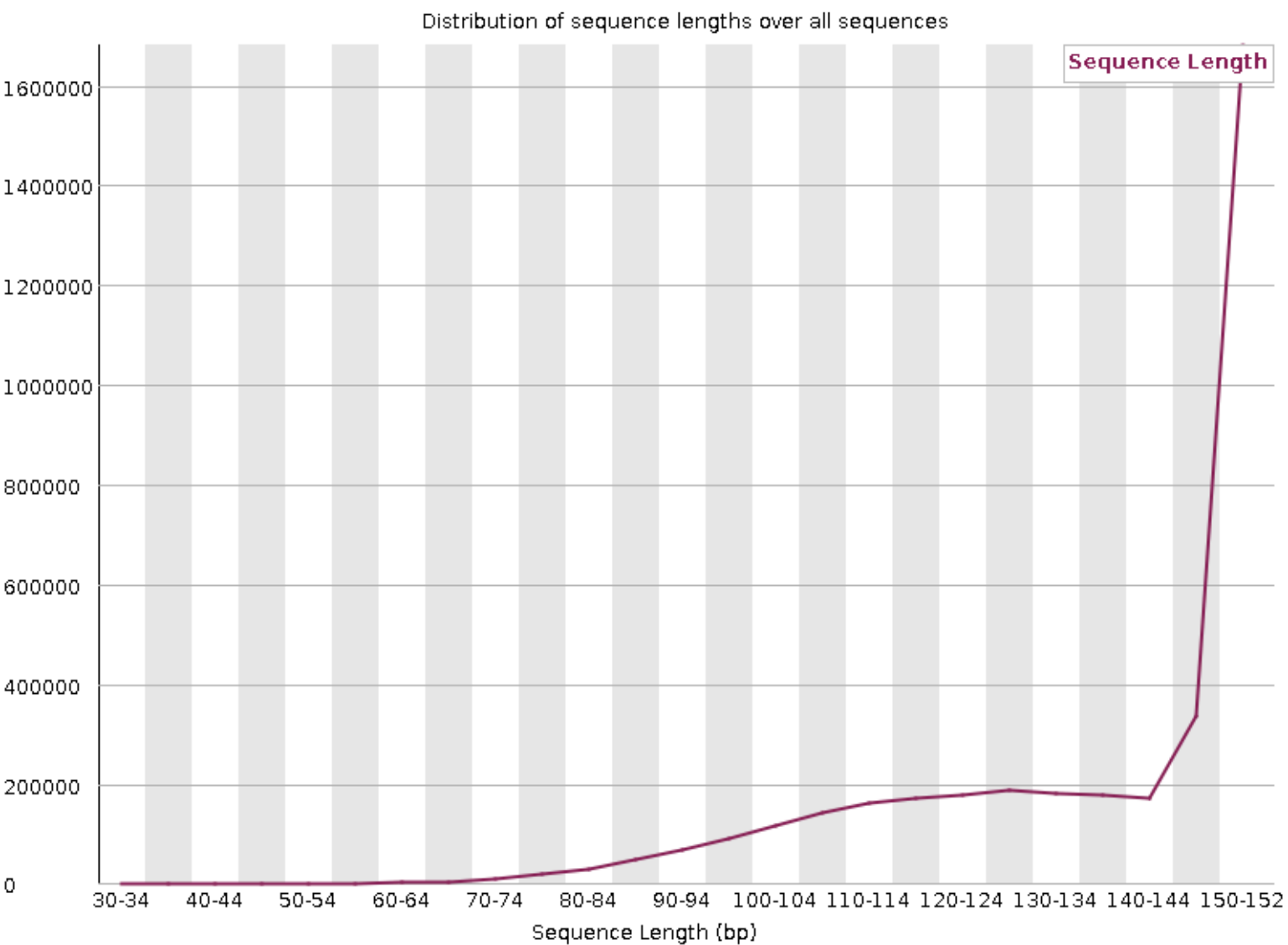




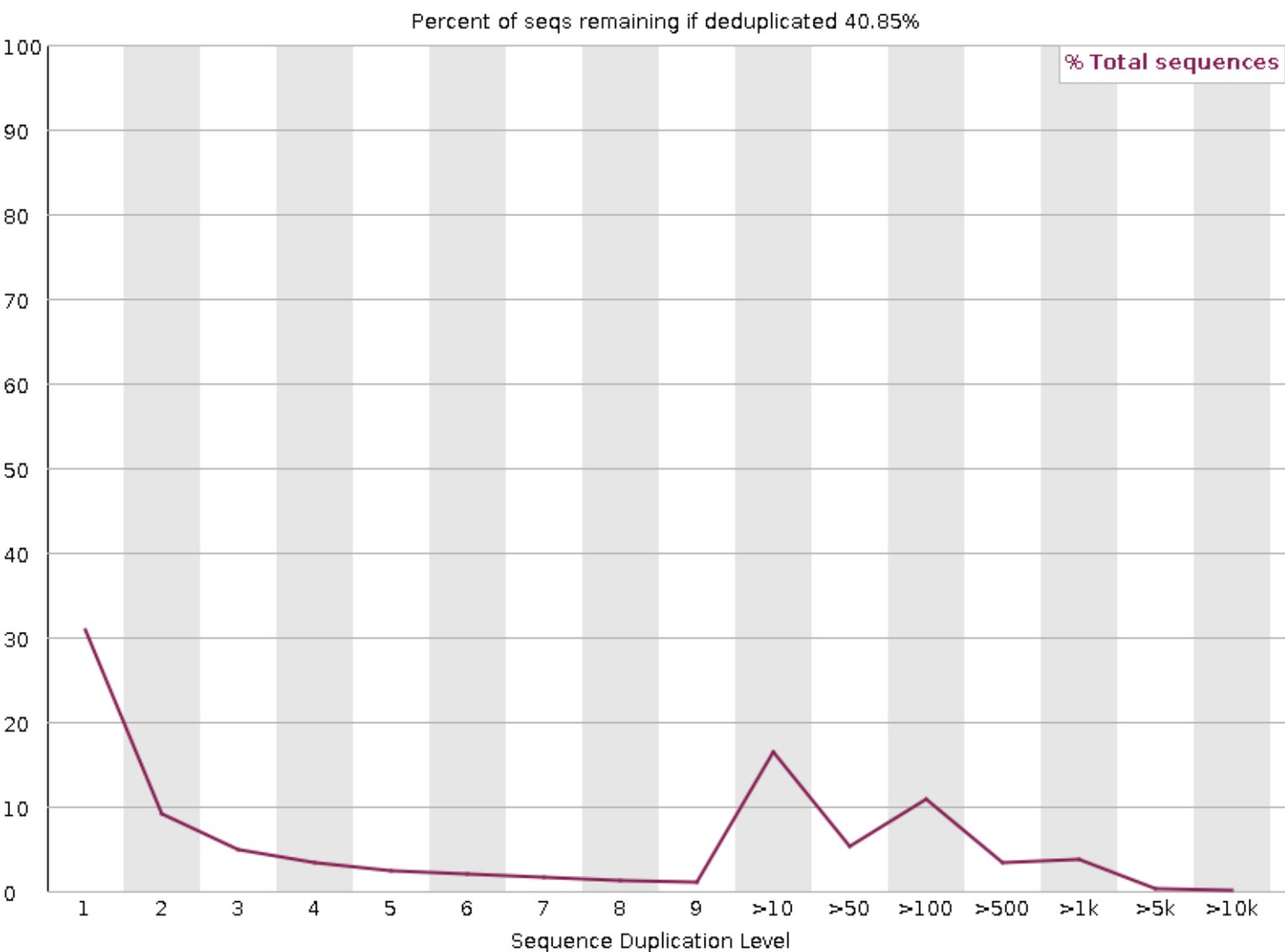
## Per base N content



# Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	11451	0.3010905361967304	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6701	0.17619488979602568	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5748	0.1511368790550001	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5171	0.13596534474485136	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4282	0.11259013850269839	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	4015	0.10556968848396406	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3881	0.10204631656444943	No Hit





## Adapter Content

