

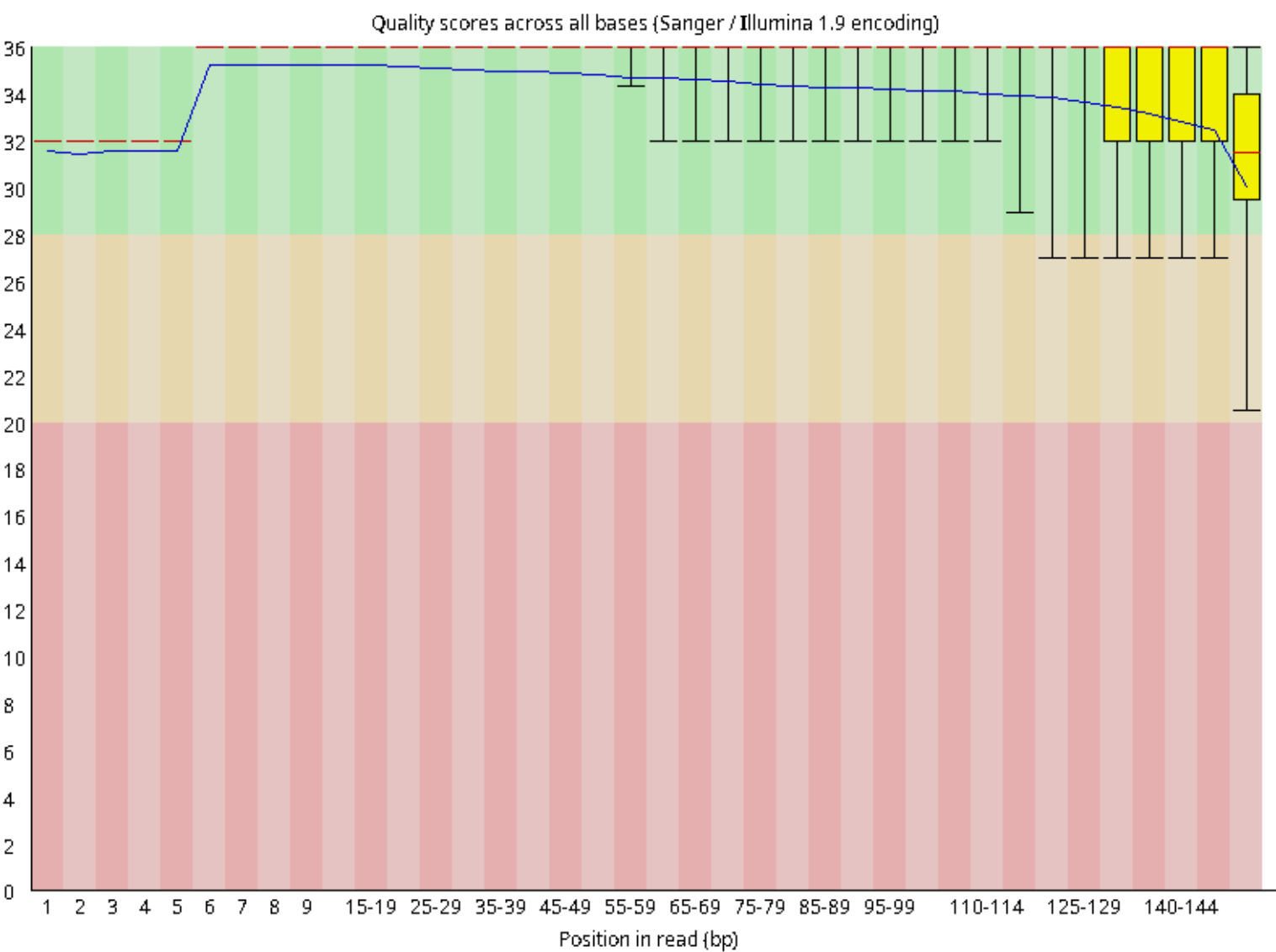
## Summary

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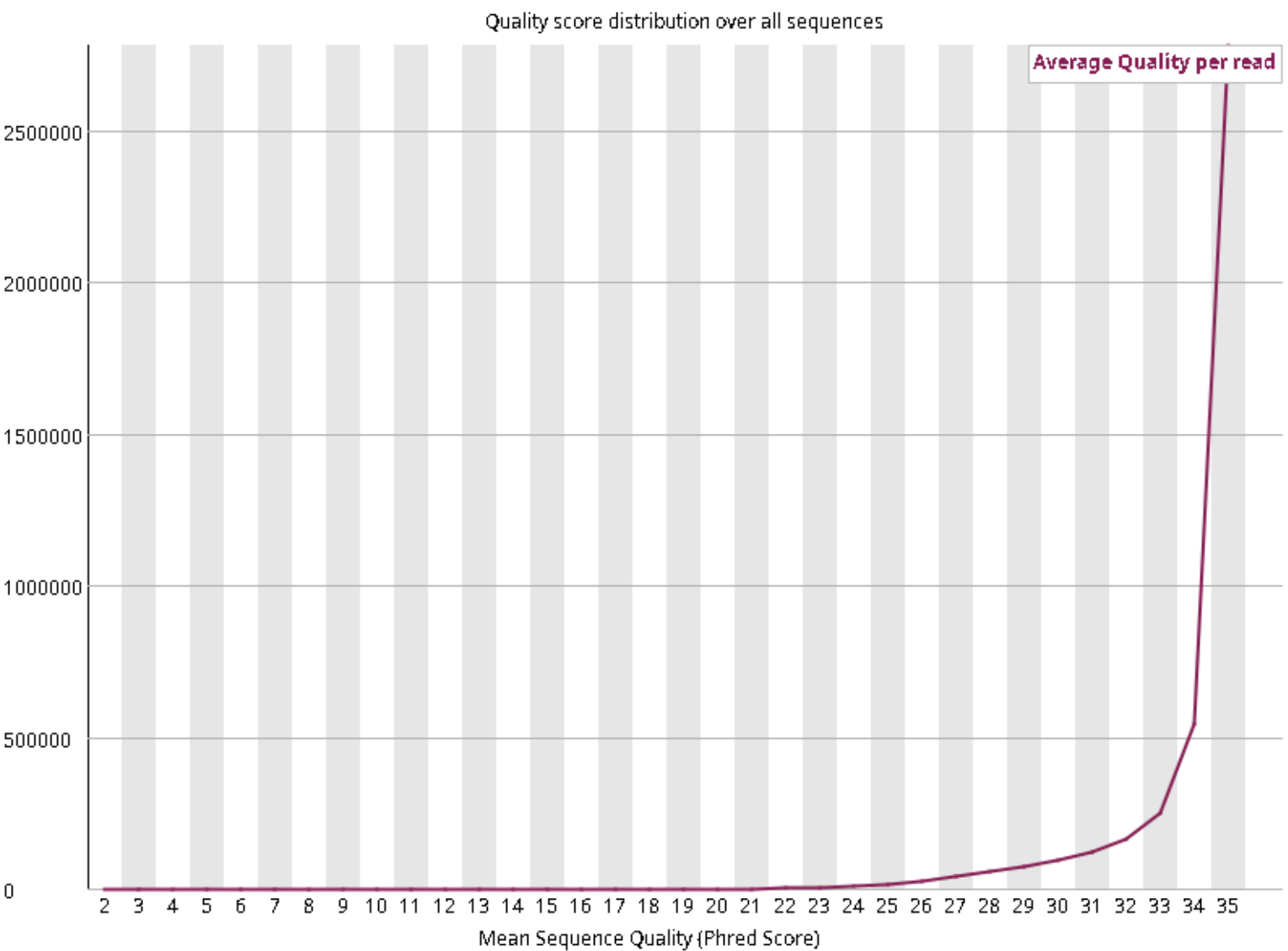
## ✓ Basic Statistics

Measure	Value
Filename	SRR11412218_pass.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4245291
Total Bases	555.6 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	49

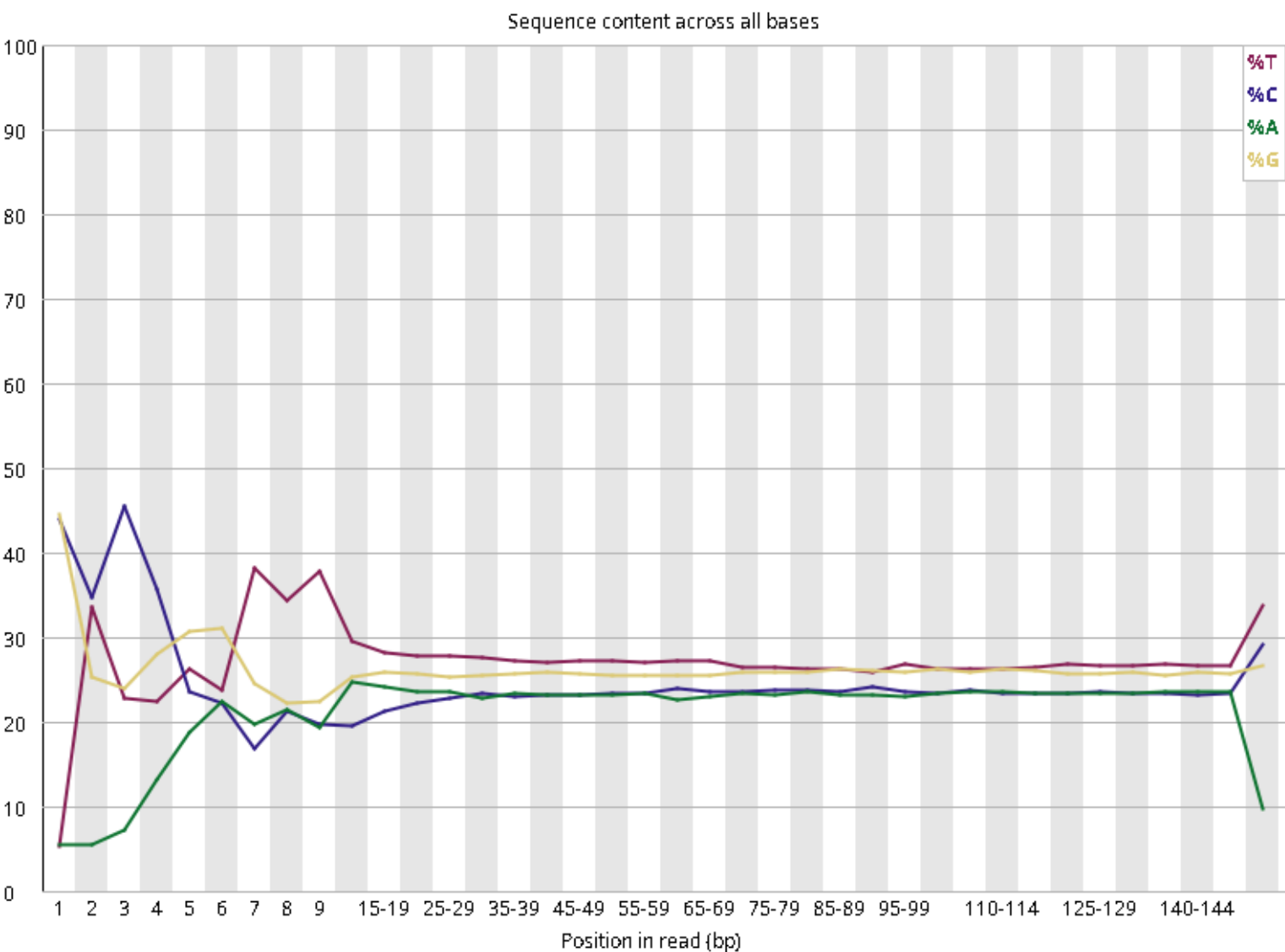
## ✔ Per base sequence quality



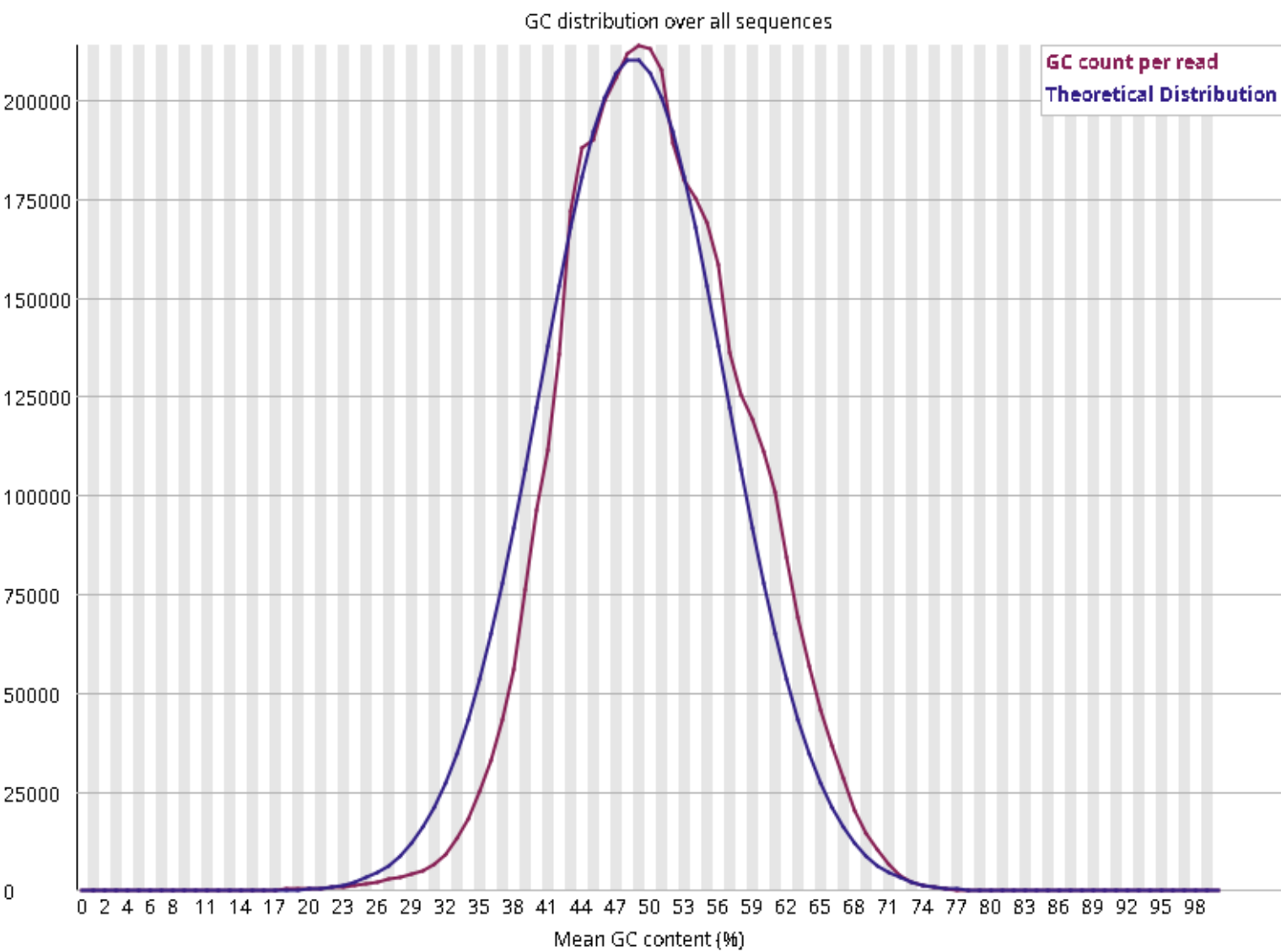
## ✔ Per sequence quality scores



# ✖ Per base sequence content

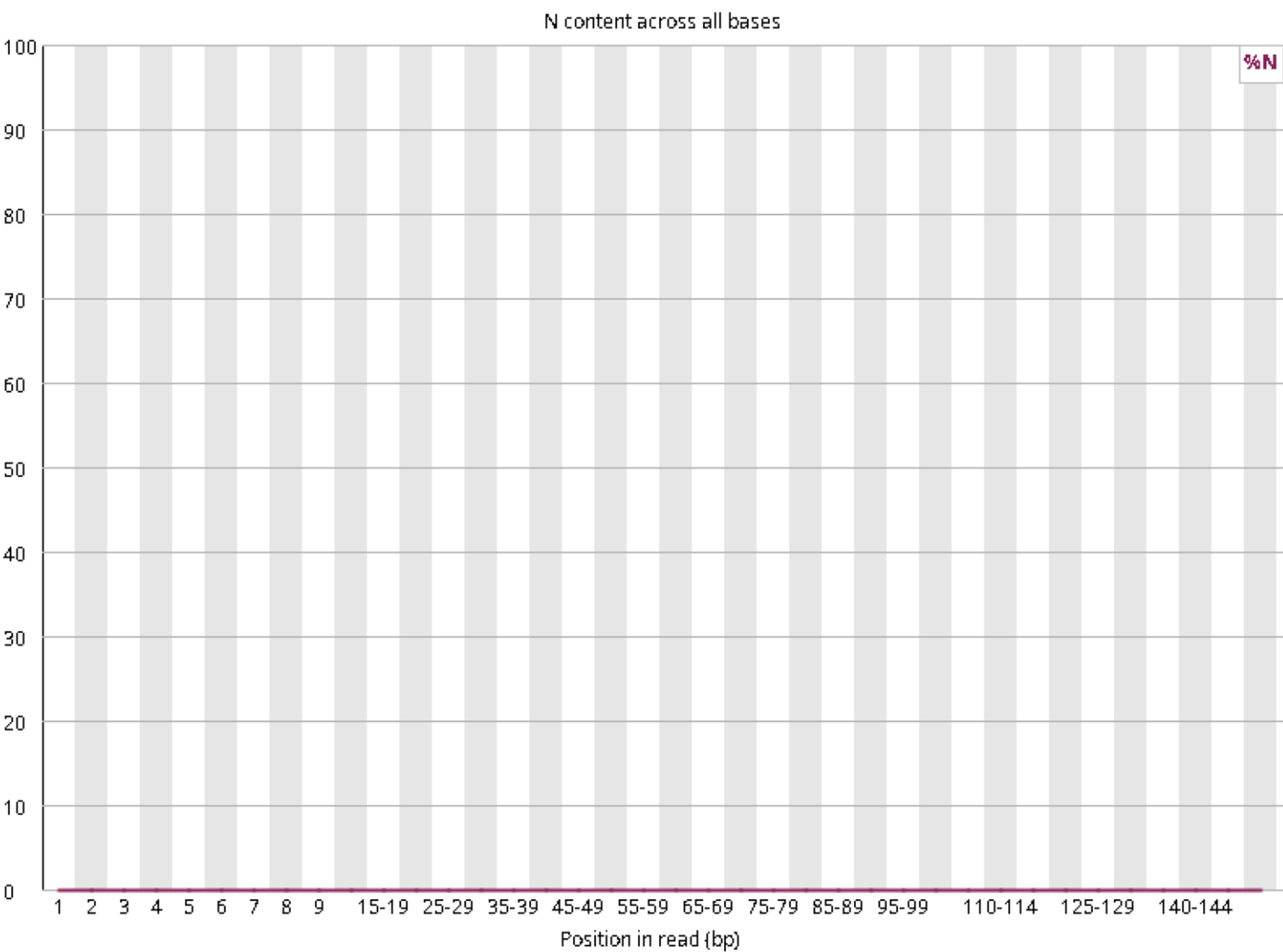


## ! Per sequence GC content

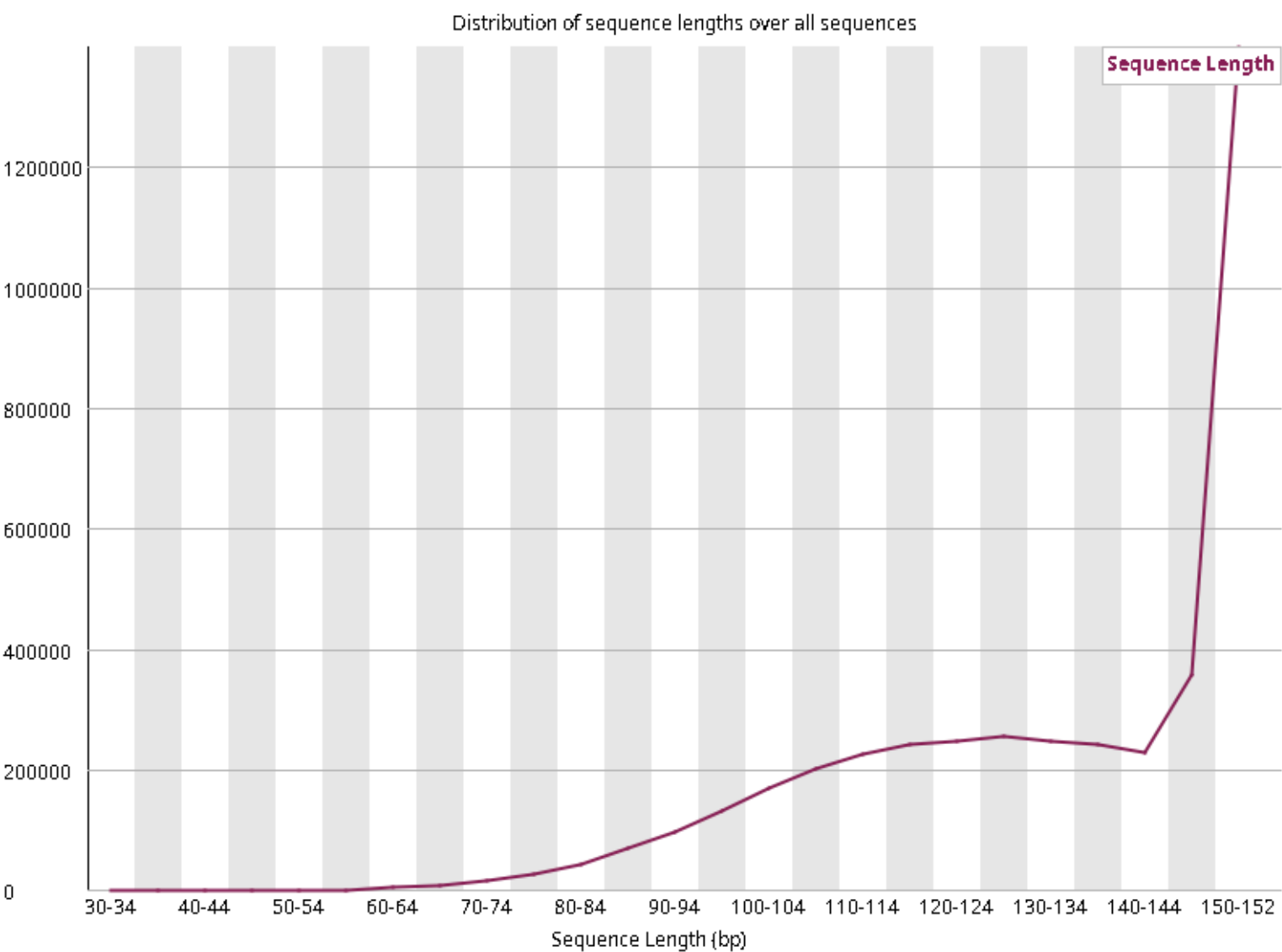




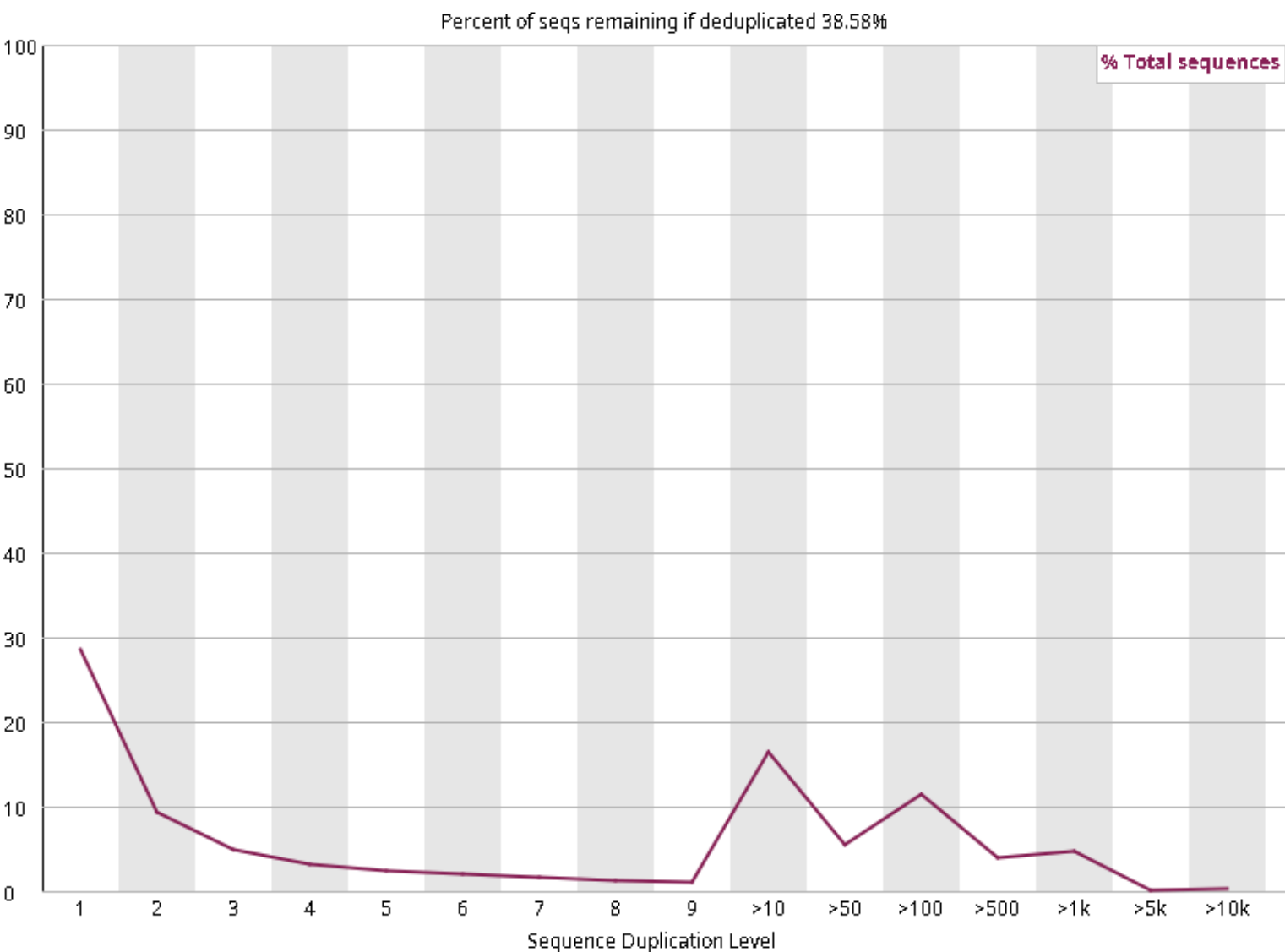
## Per base N content



# Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	13264	0.31244030150112206	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	10694	0.25190263753415254	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA	5310	0.12507976485004207	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5055	0.11907310947588752	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4990	0.11754200124325989	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4921	0.11591667096554747	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	4831	0.11379667495113999	No Hit
CCCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGG	4605	0.10847312940385007	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCTTTGGTTCTCAGGGT	4544	0.10703624321630718	No Hit



Sequence	Count	Percentage	Possible Source
CCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGGAA	4347	0.10239580749588191	No Hit



# Adapter Content

