

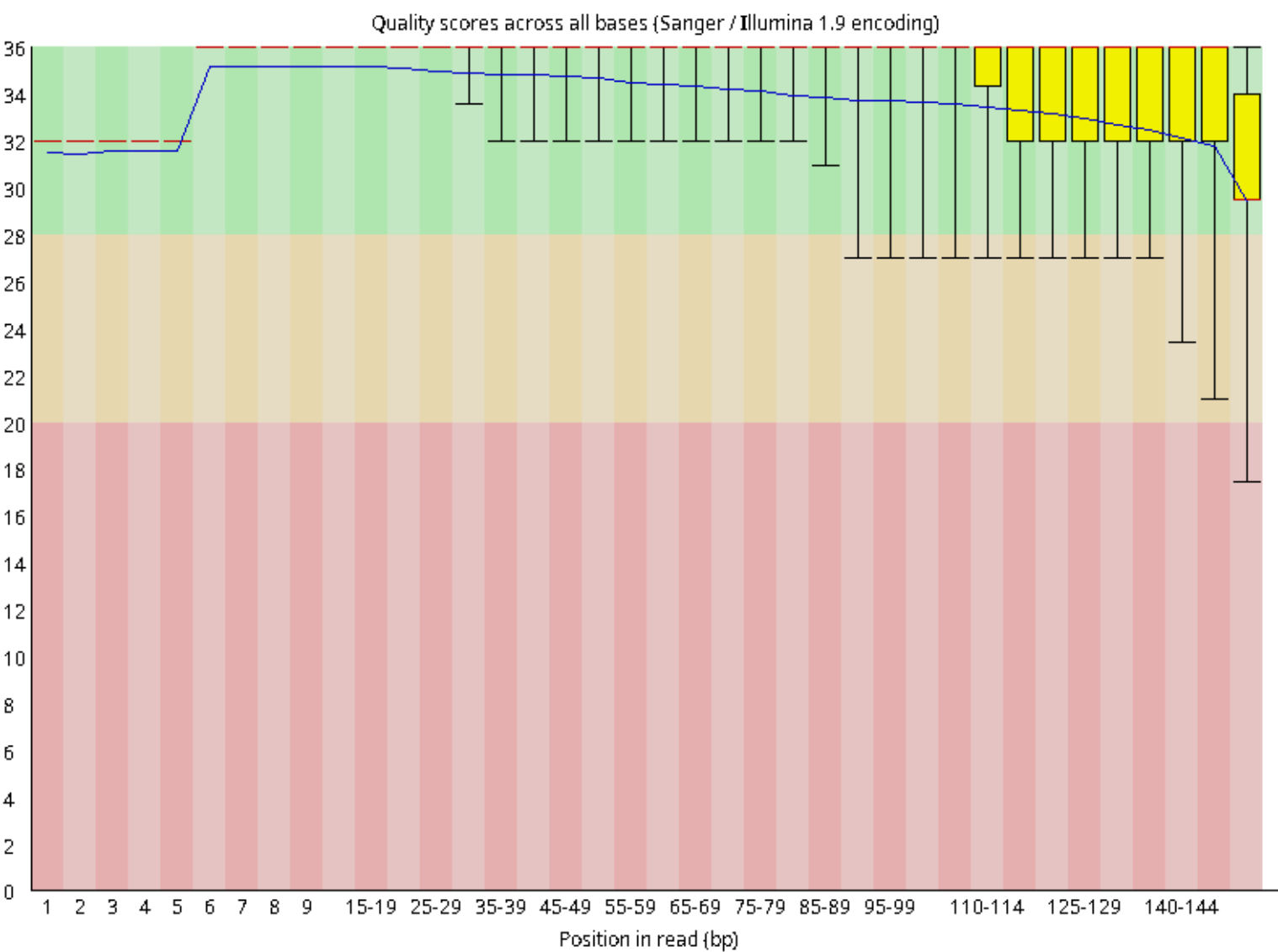
Summary

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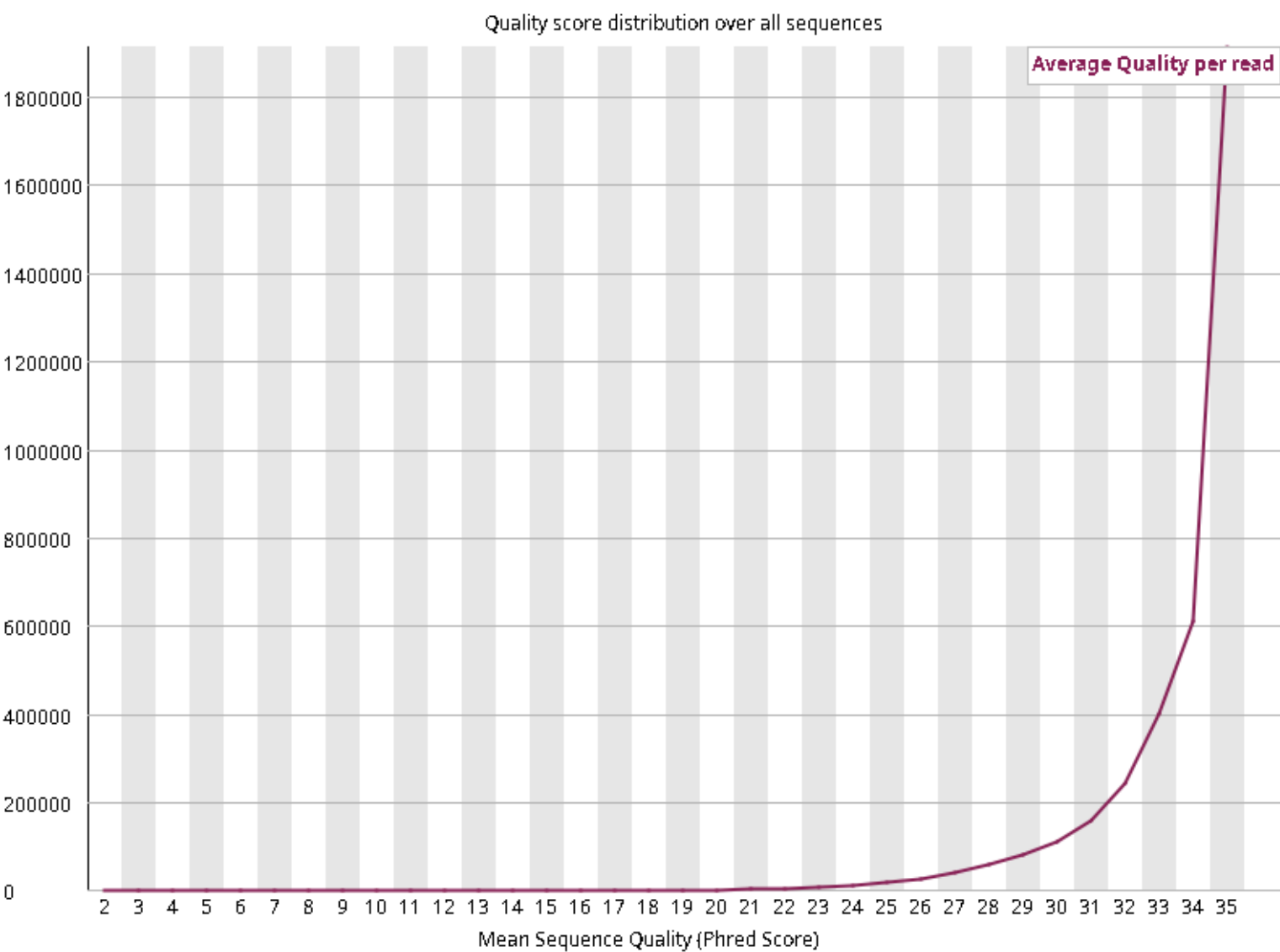
✓ Basic Statistics

Measure	Value
Filename	SRR11412228_pass.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3718540
Total Bases	502.2 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	50

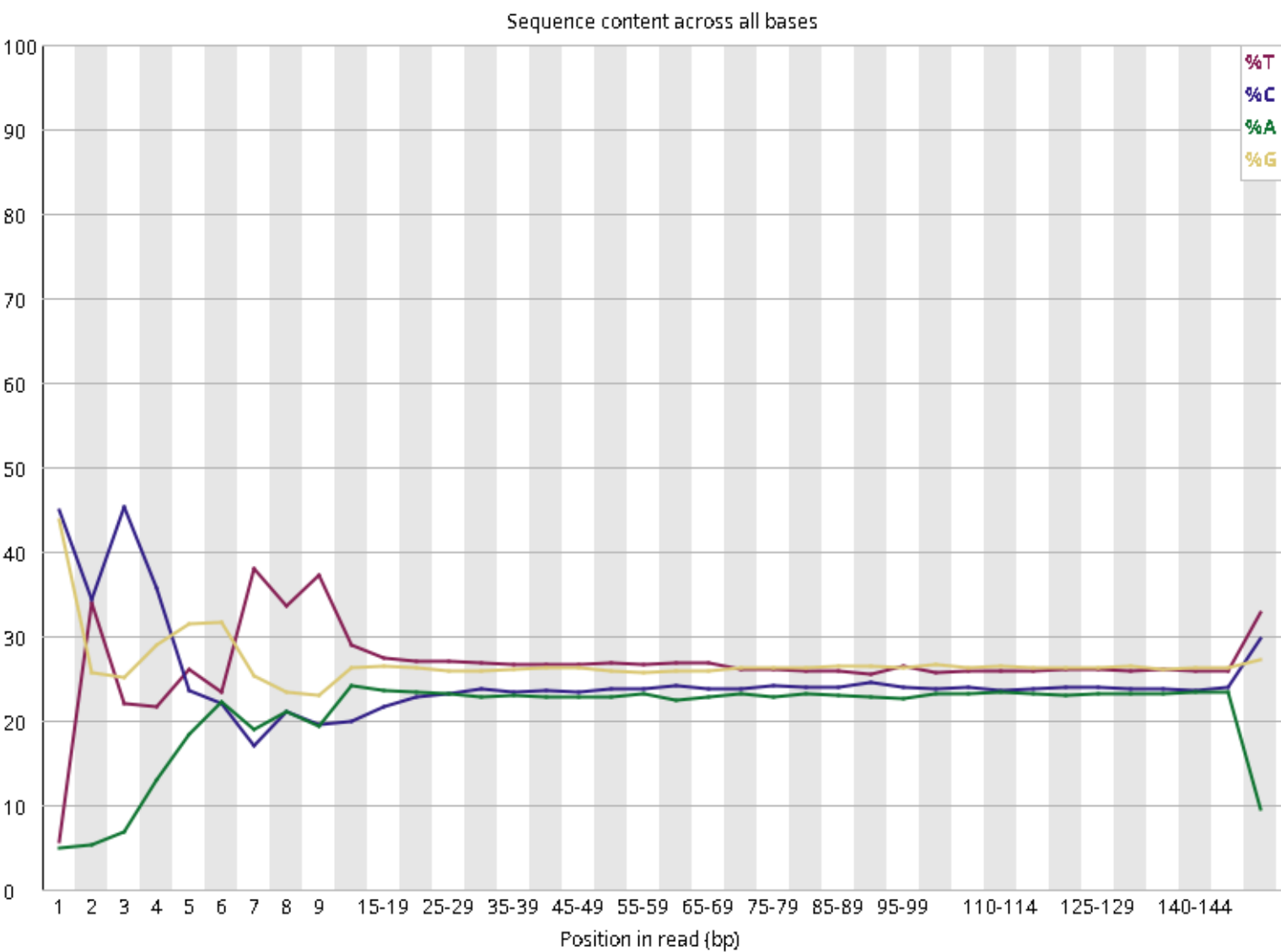
✔ Per base sequence quality



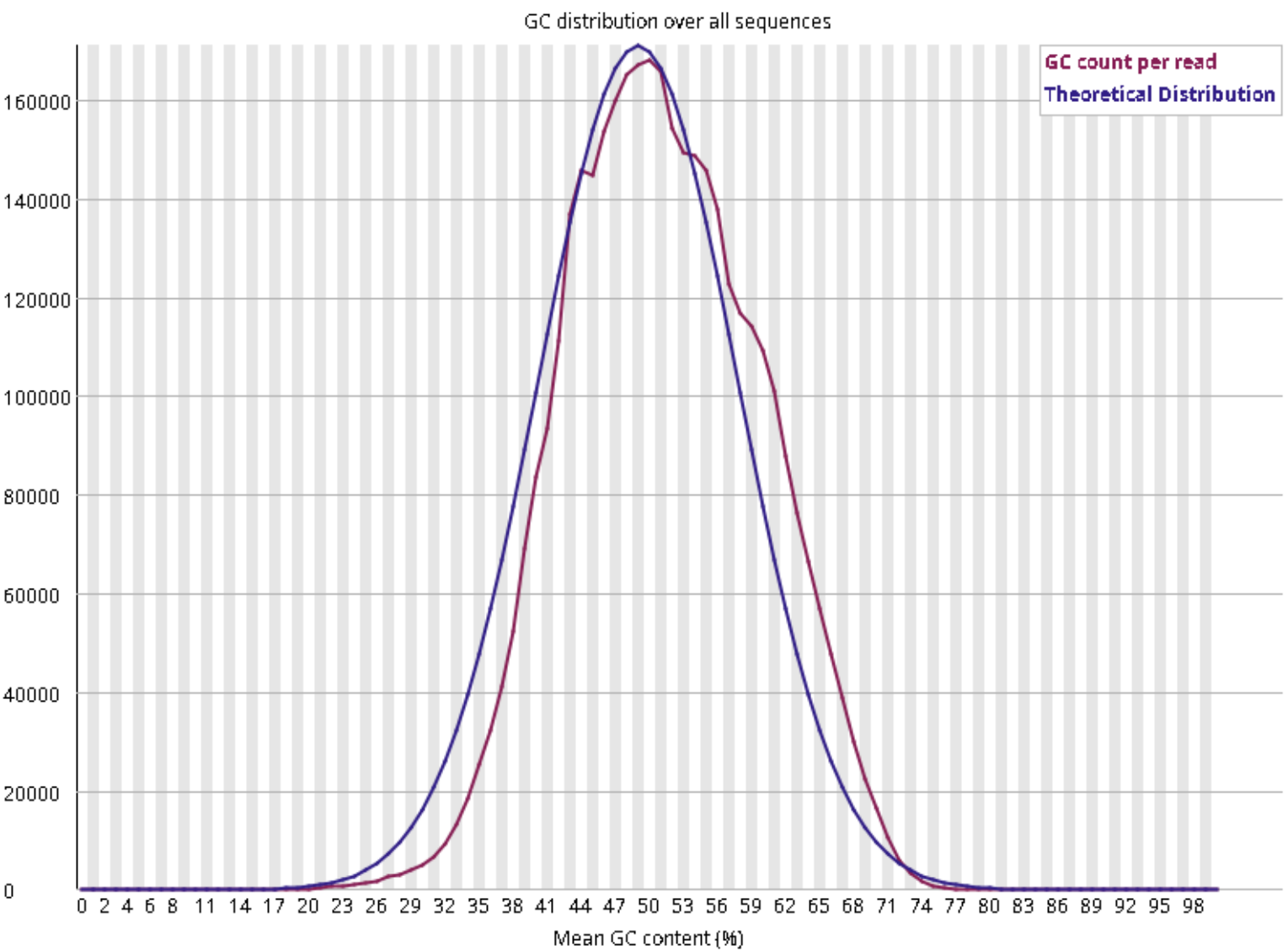
✔ Per sequence quality scores



❌ Per base sequence content

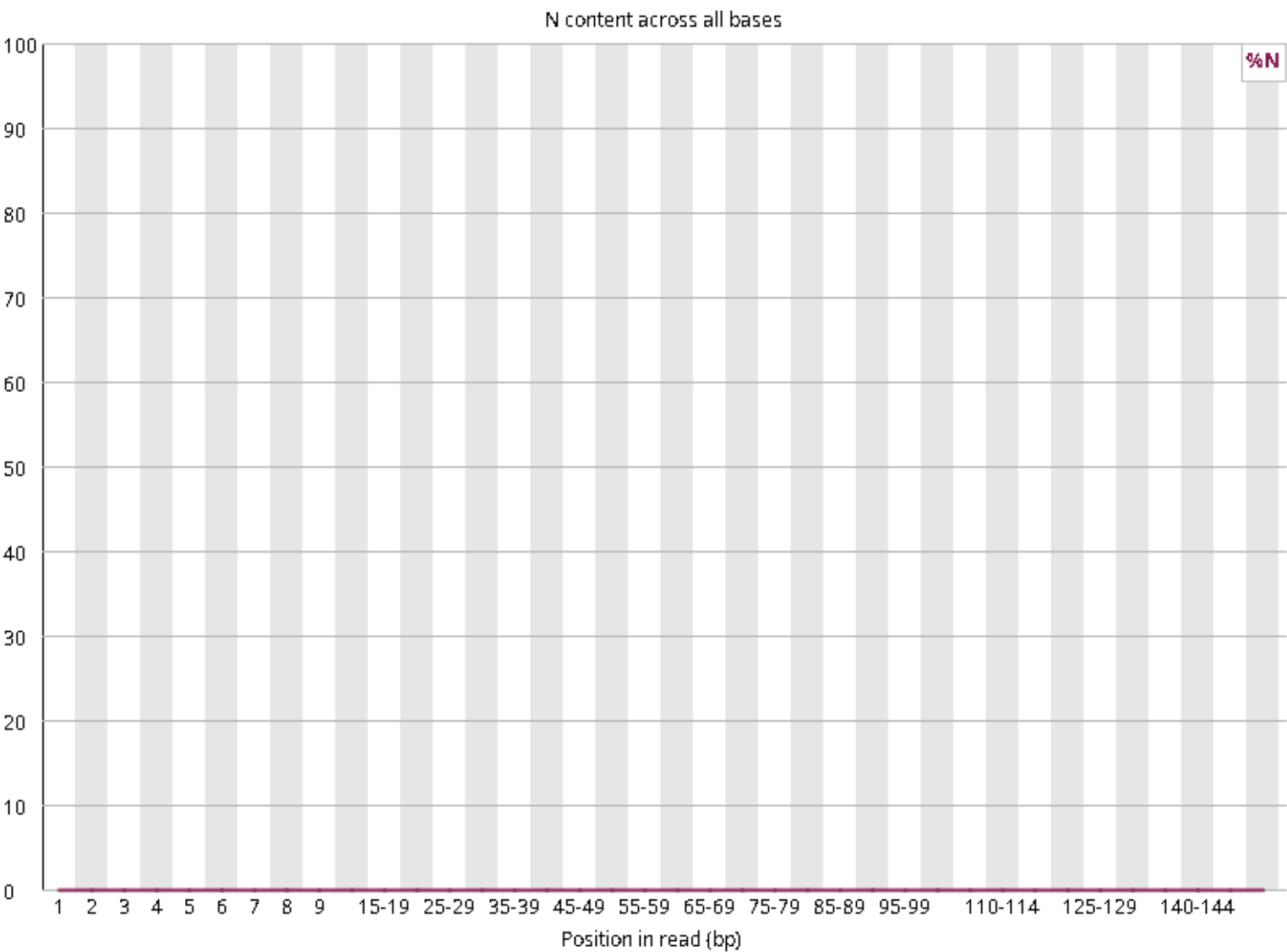


! Per sequence GC content

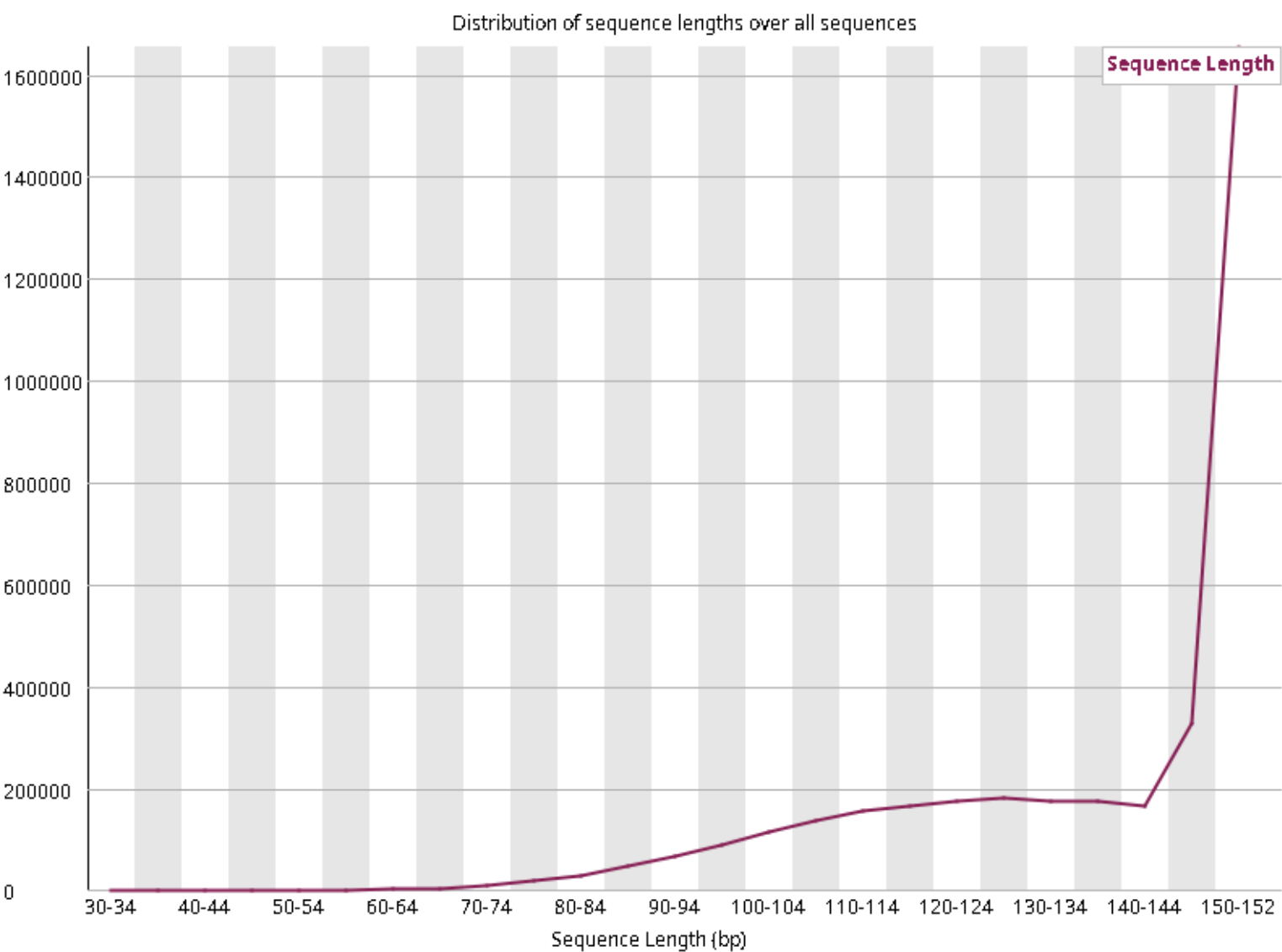




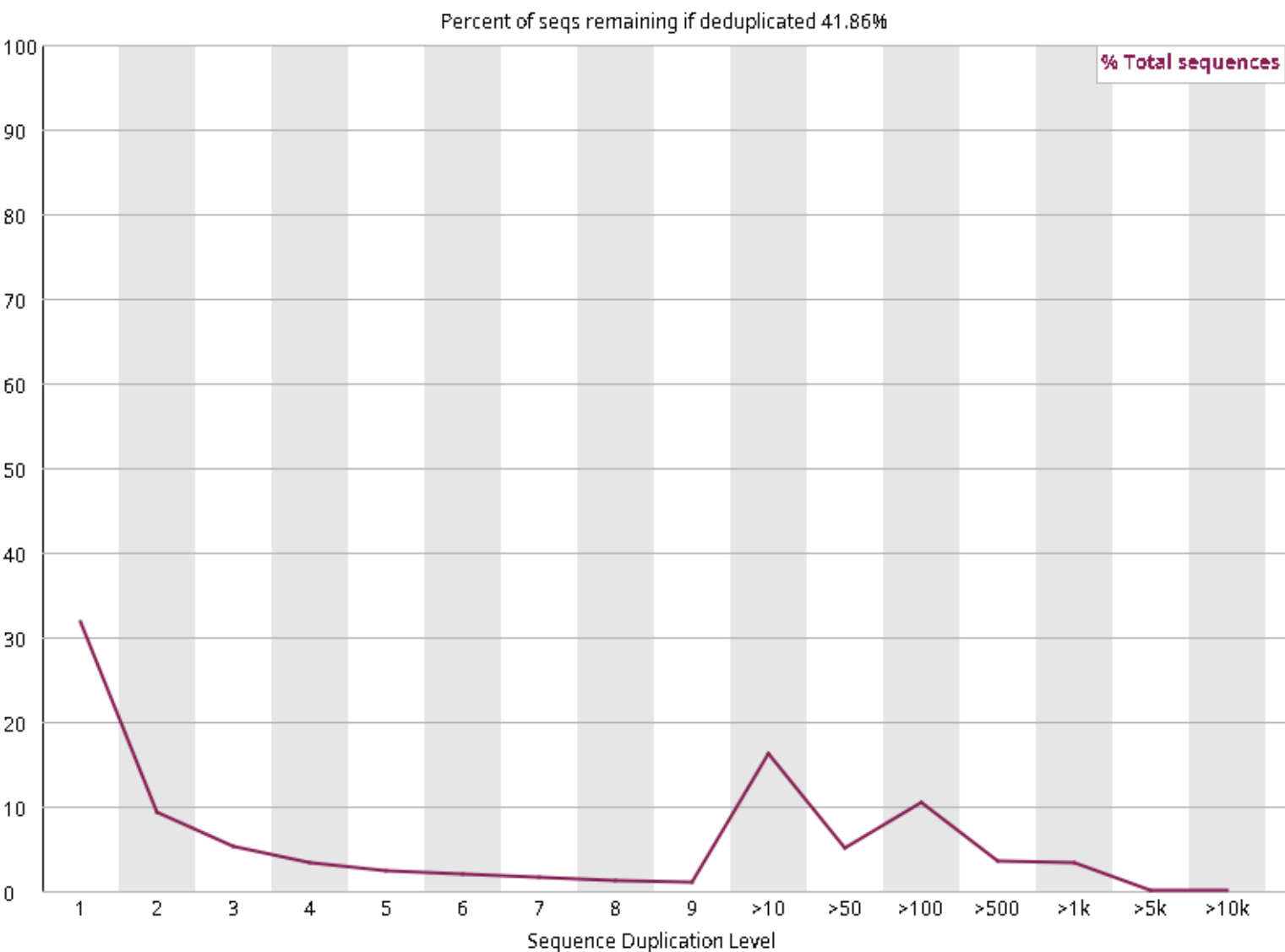
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	10784	0.2900062927923325	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6657	0.1790218741764241	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5340	0.14360474810006077	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	4983	0.1340042059517983	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4221	0.11351229245886826	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	3866	0.103965534860456	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3760	0.10111495371839486	No Hit



Adapter Content

