

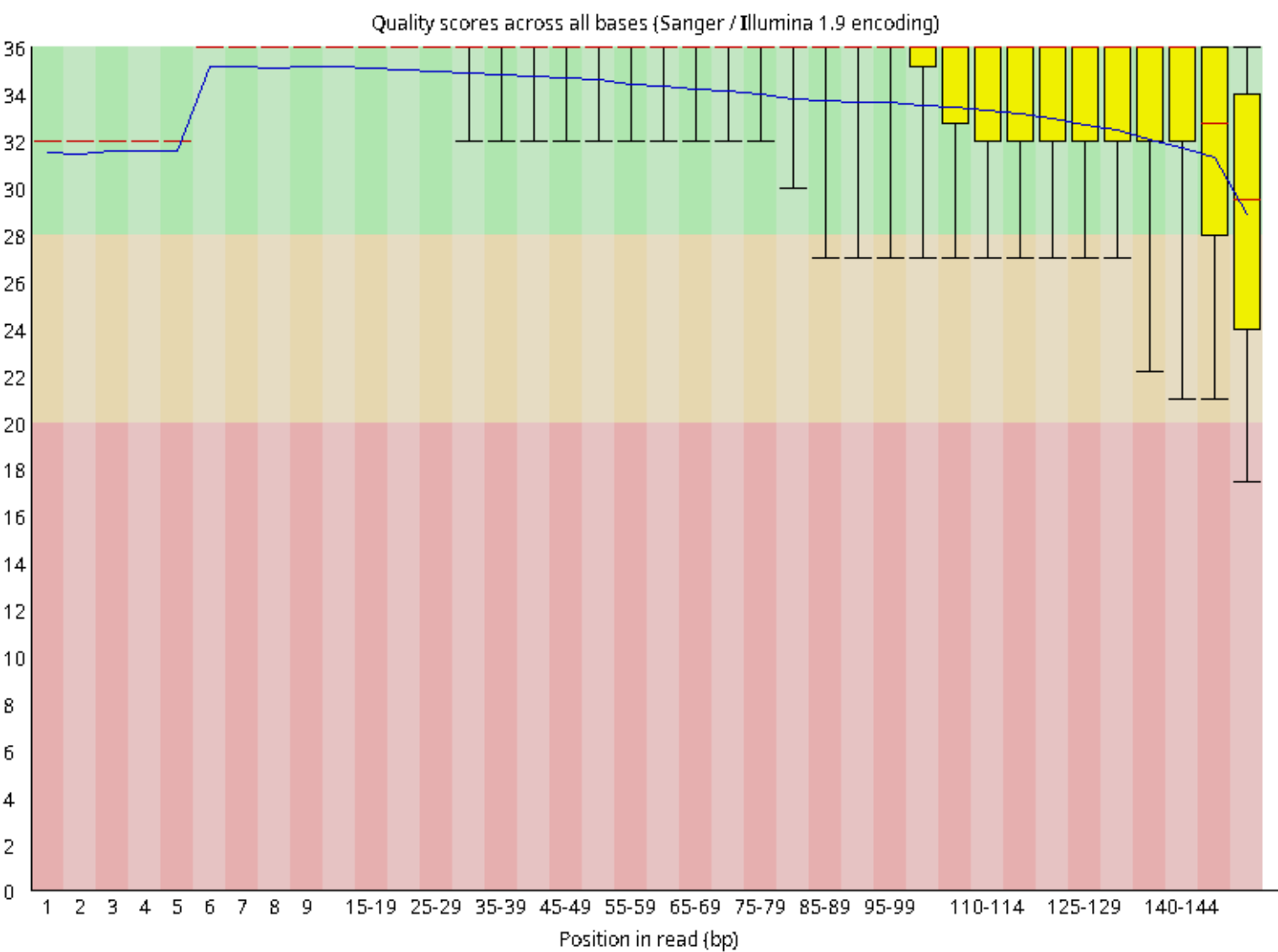
Summary

- ✓ [Basic Statistics](#)
- ✓ [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](#)
- ✓ [Adapter Content](#)

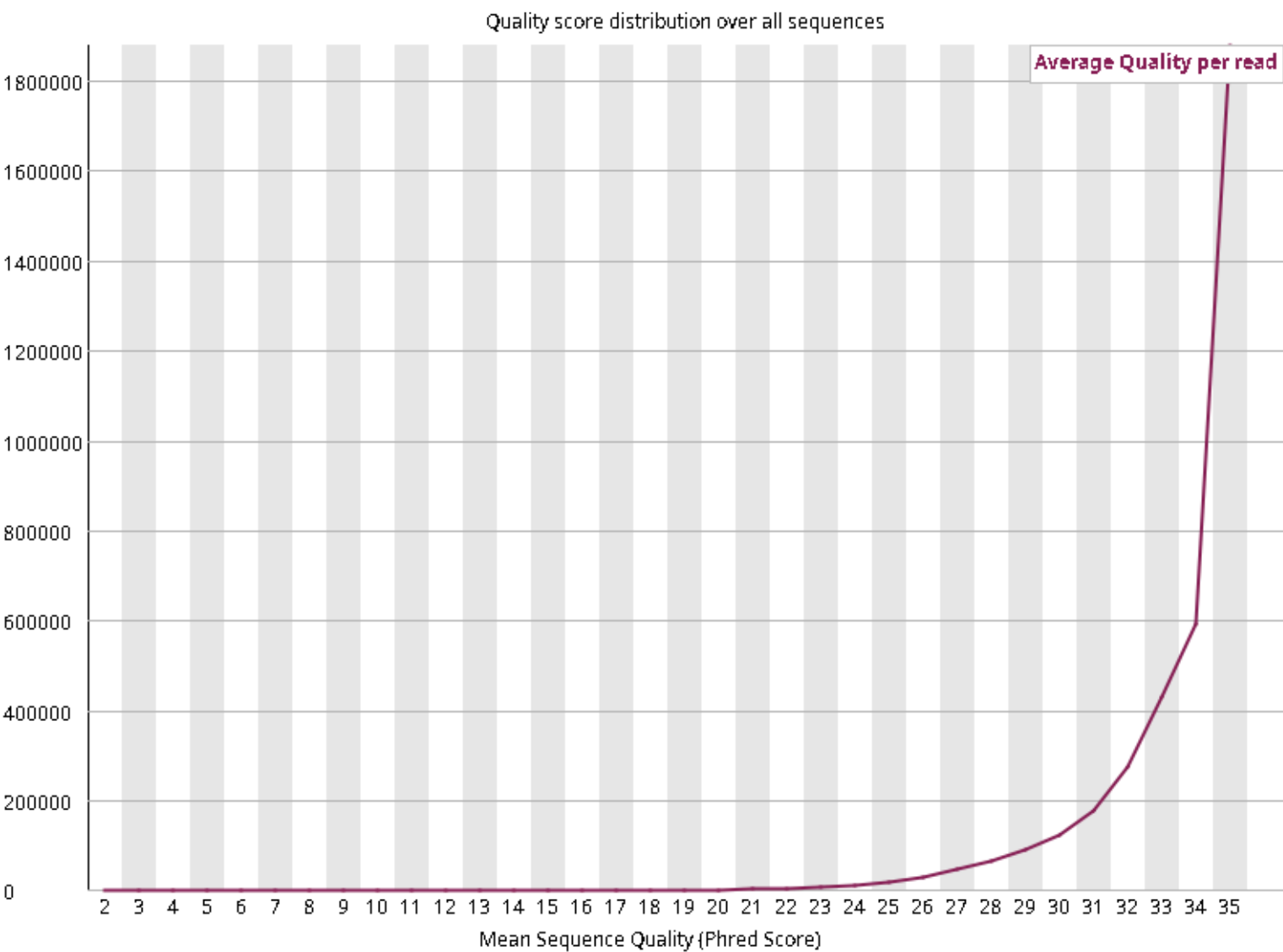
✓ Basic Statistics

Measure	Value
Filename	SRR11412227_pass.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3774499
Total Bases	509.6 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	50

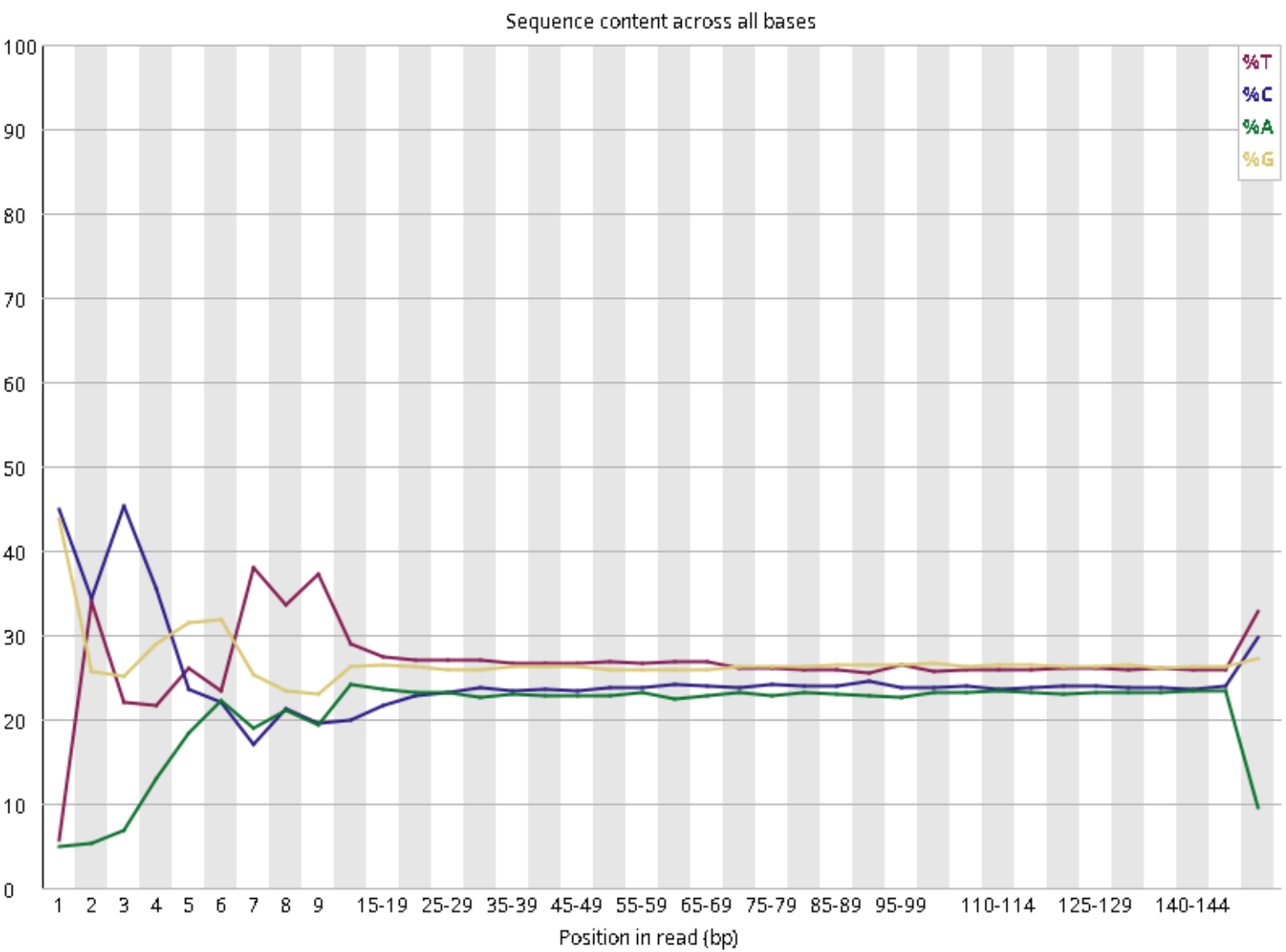
✔ Per base sequence quality



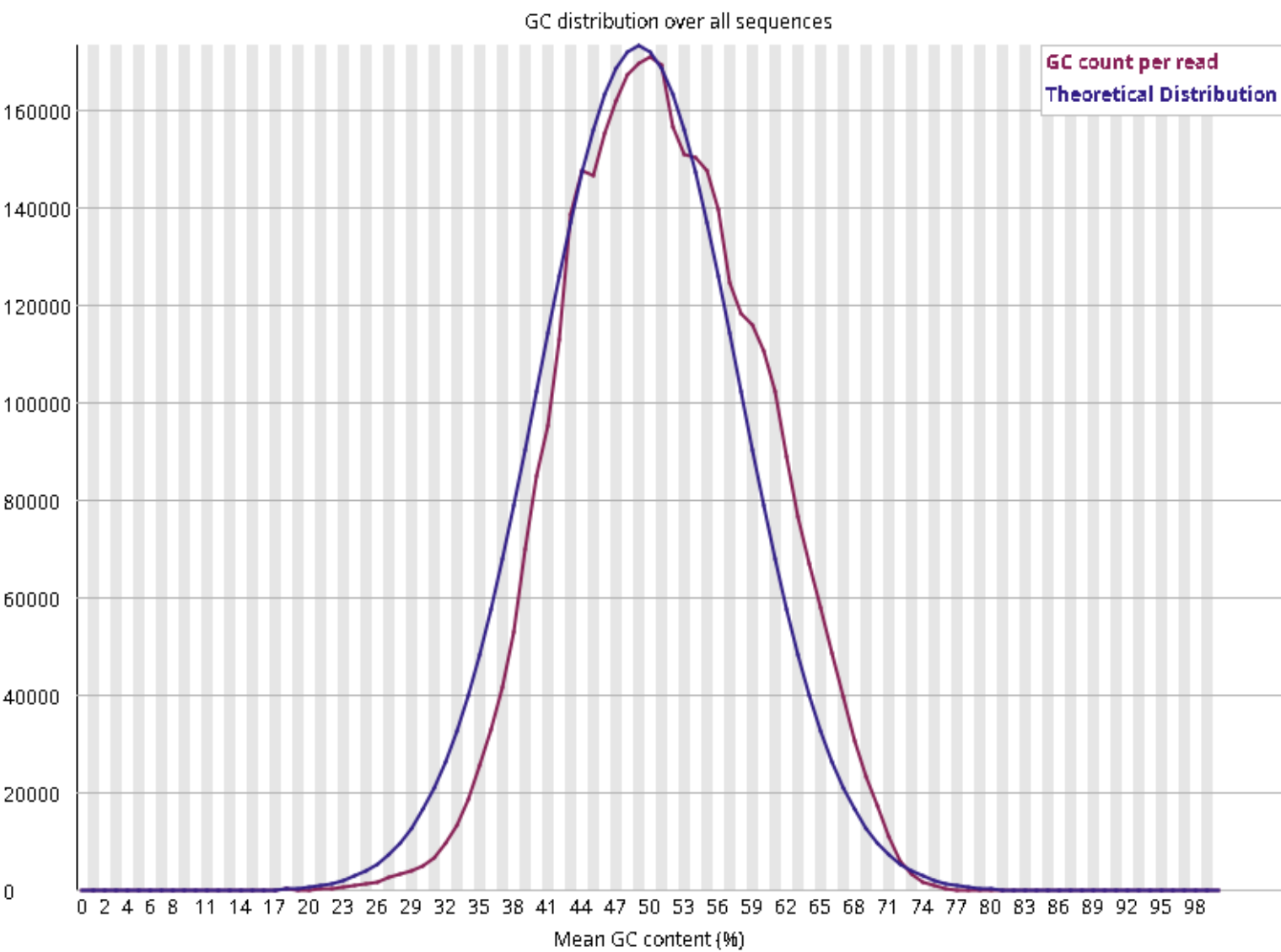
✔ Per sequence quality scores



❌ Per base sequence content

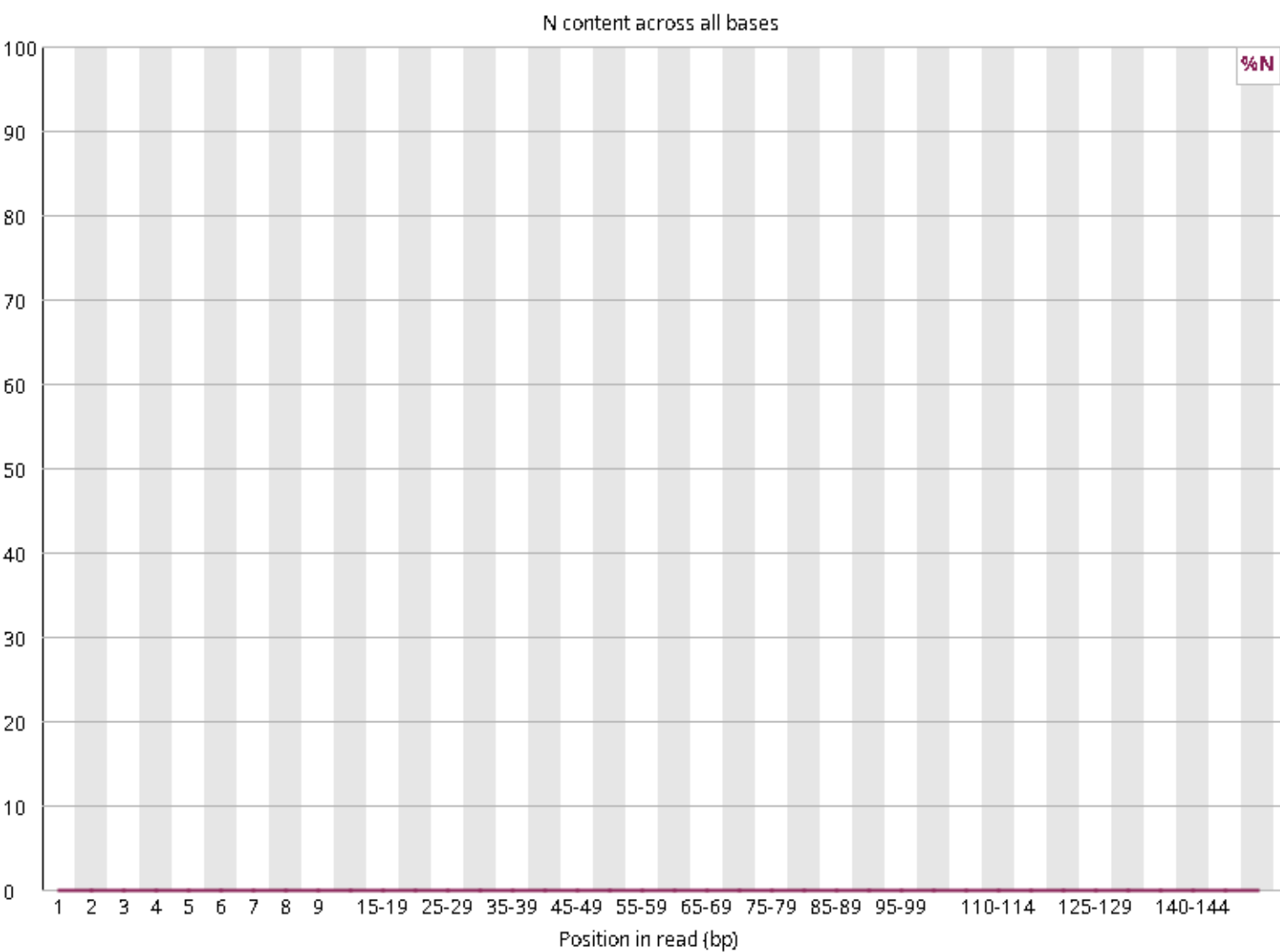


! Per sequence GC content

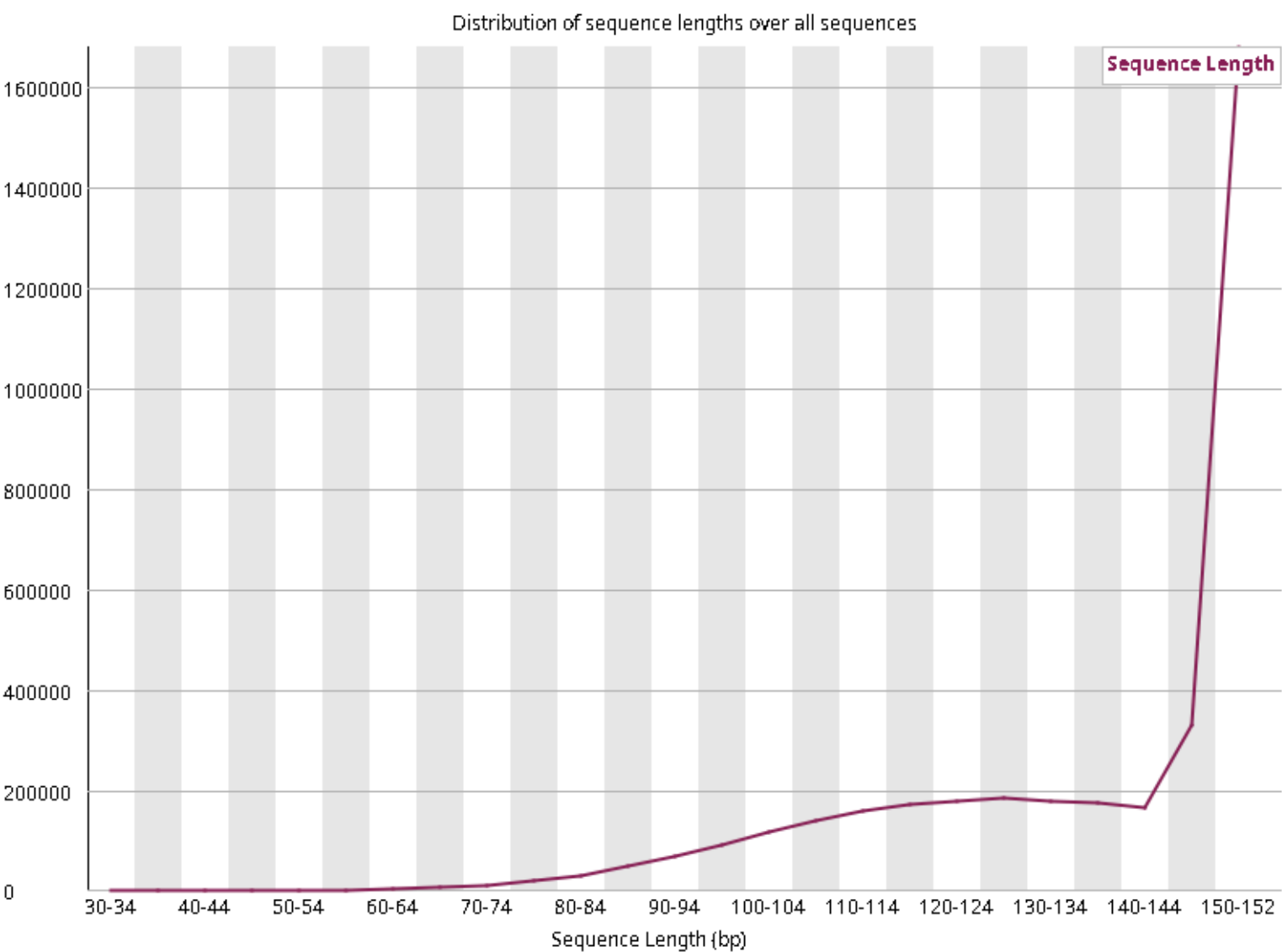




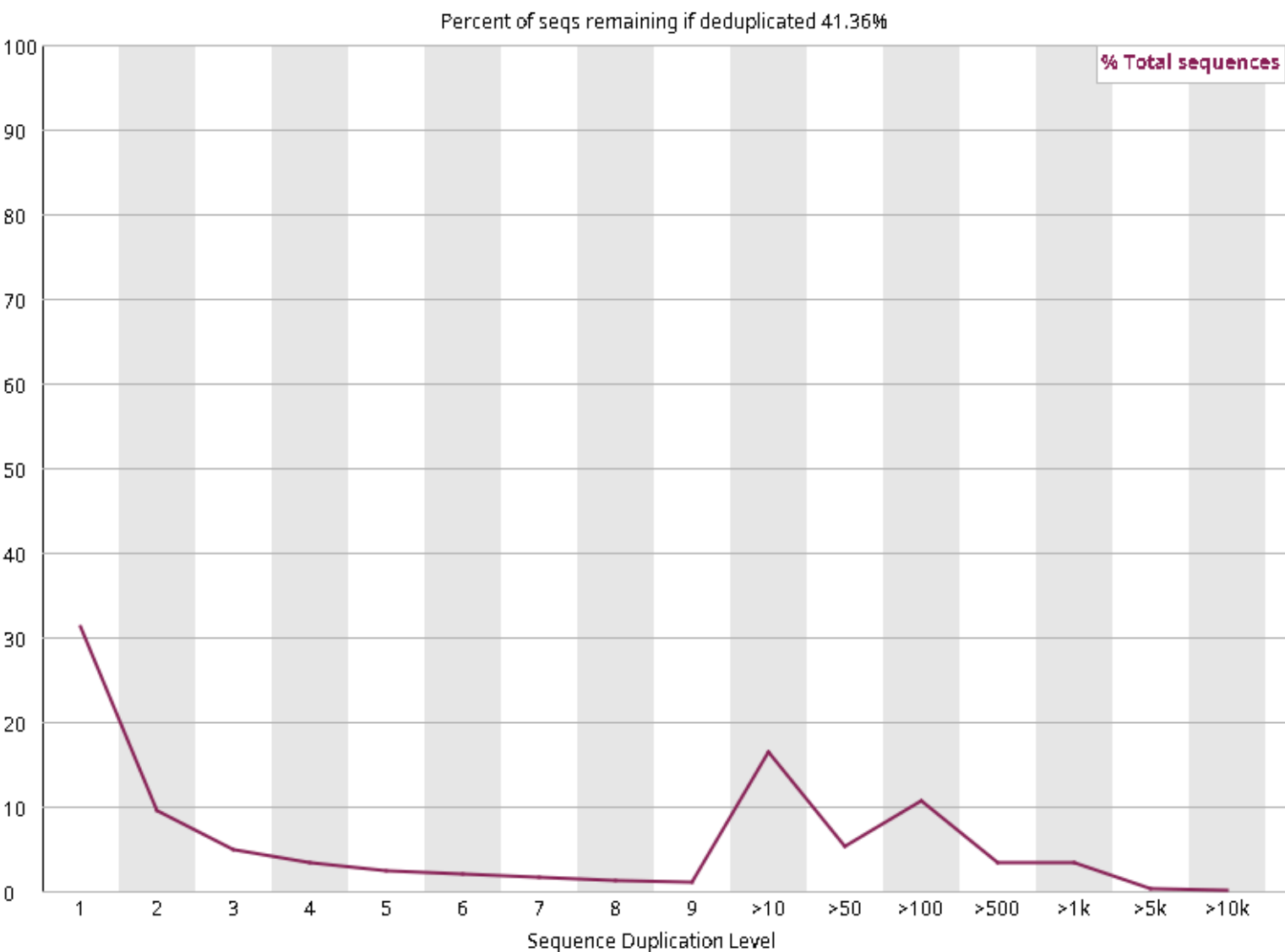
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	10926	0.2894688805057307	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6665	0.17657972621002152	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5418	0.14354222904814654	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5140	0.1361770131612169	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4155	0.11008083456903817	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	4040	0.10703407260142339	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3856	0.10215925345323976	No Hit



Adapter Content

