

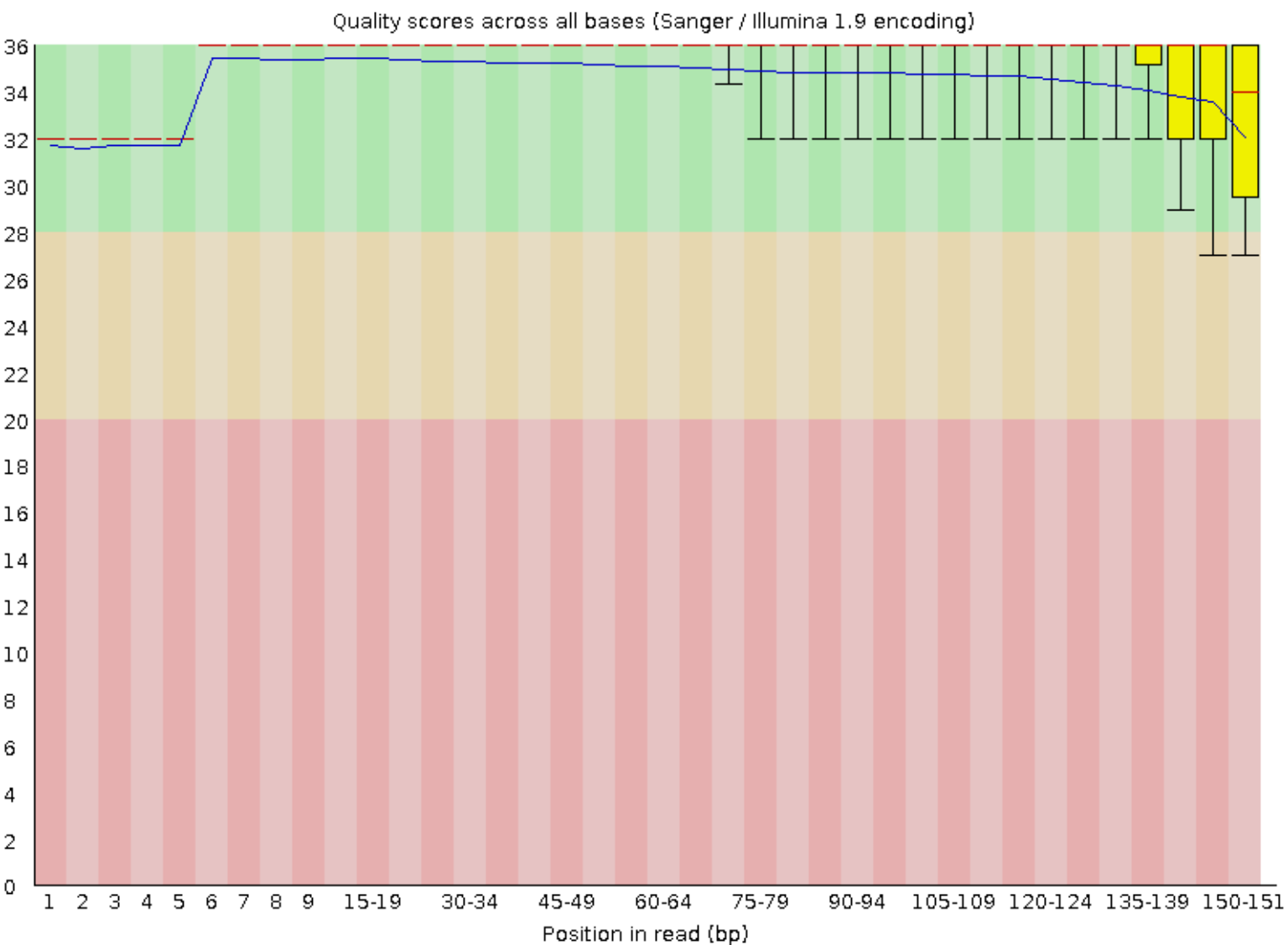
Summary

- ✓ [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](#)

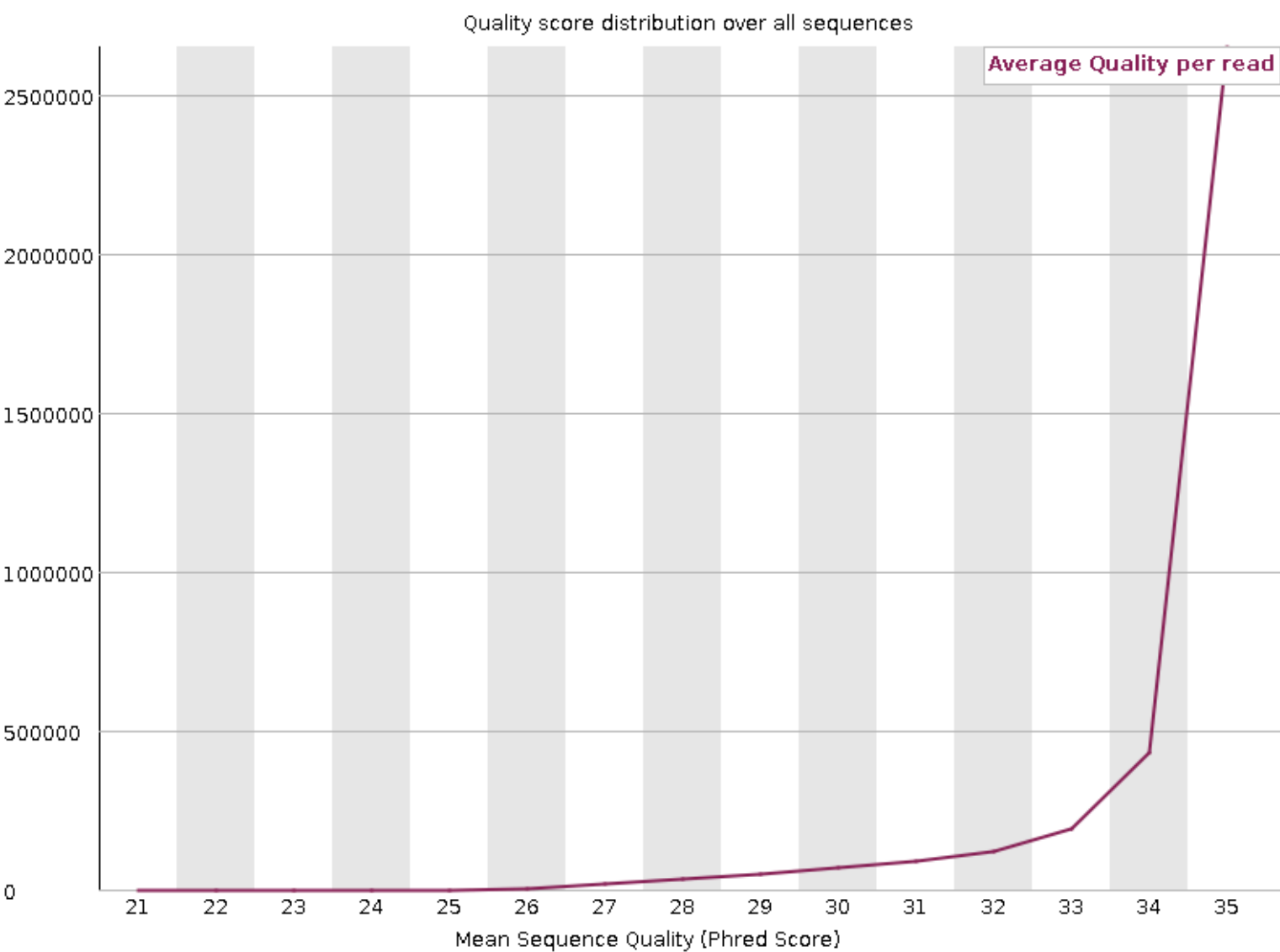
✓ Basic Statistics

Measure	Value
Filename	infected_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3708490
Total Bases	493.7 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	50

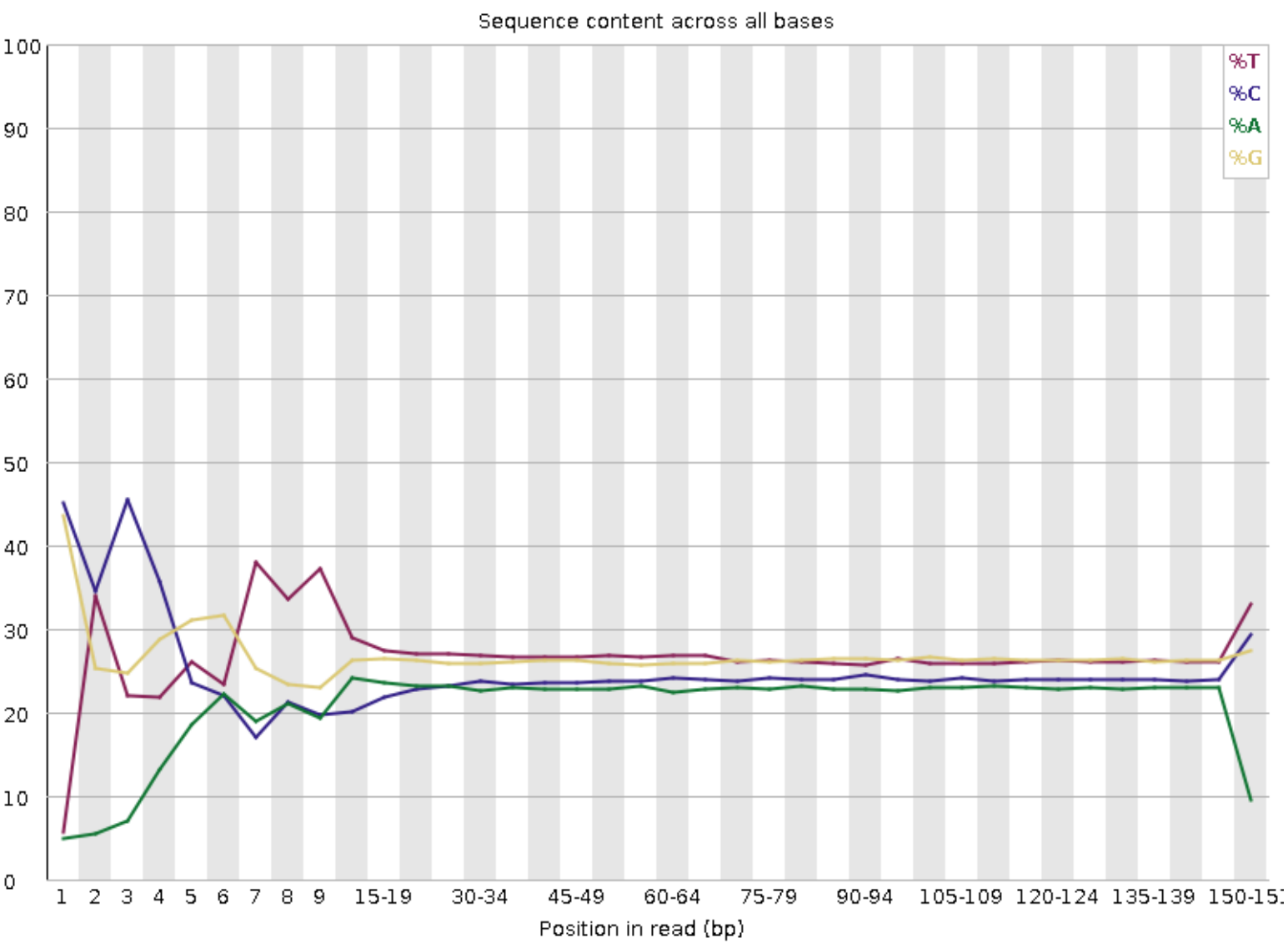
✔ Per base sequence quality



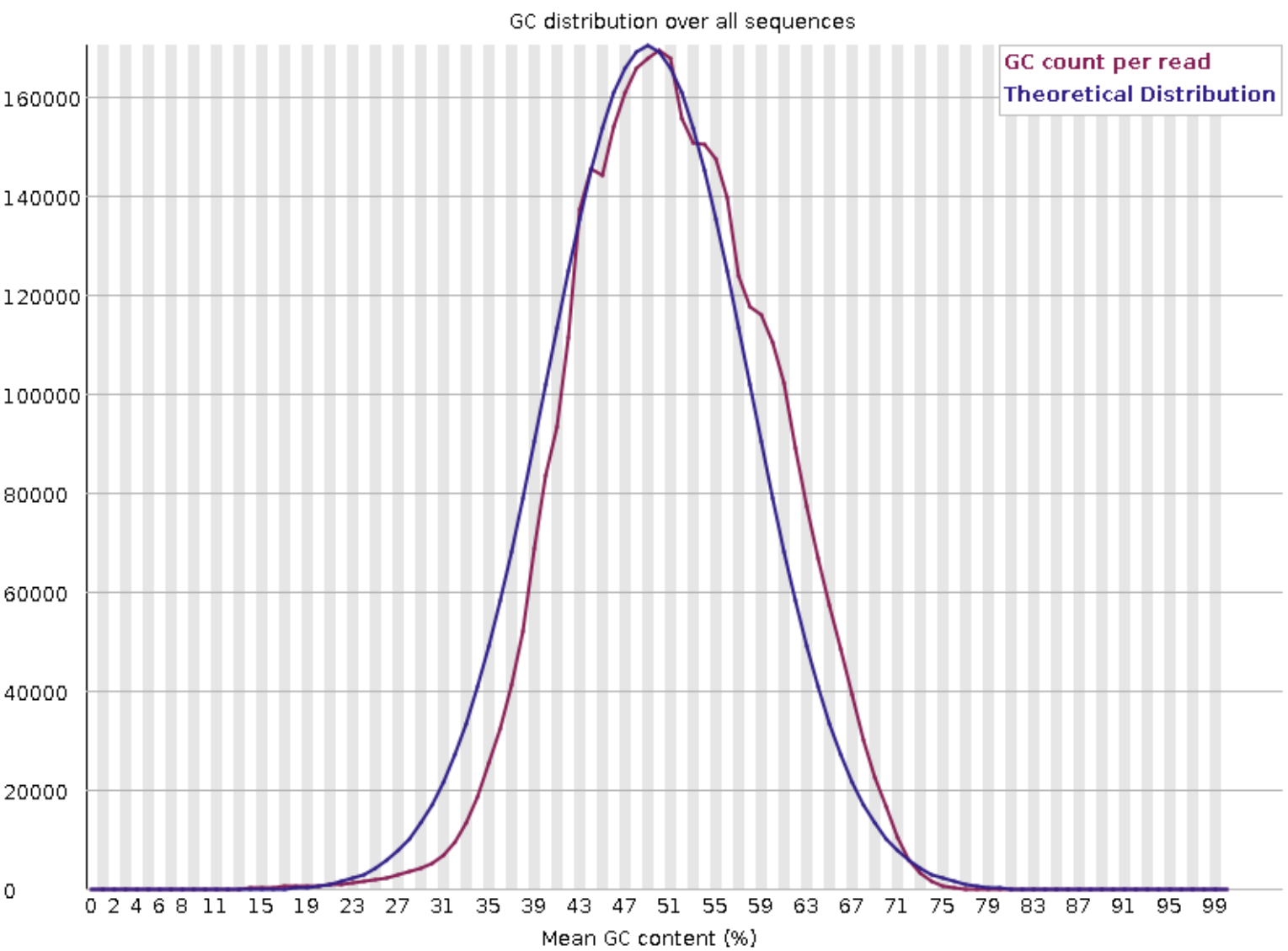
✔ Per sequence quality scores



✖ Per base sequence content

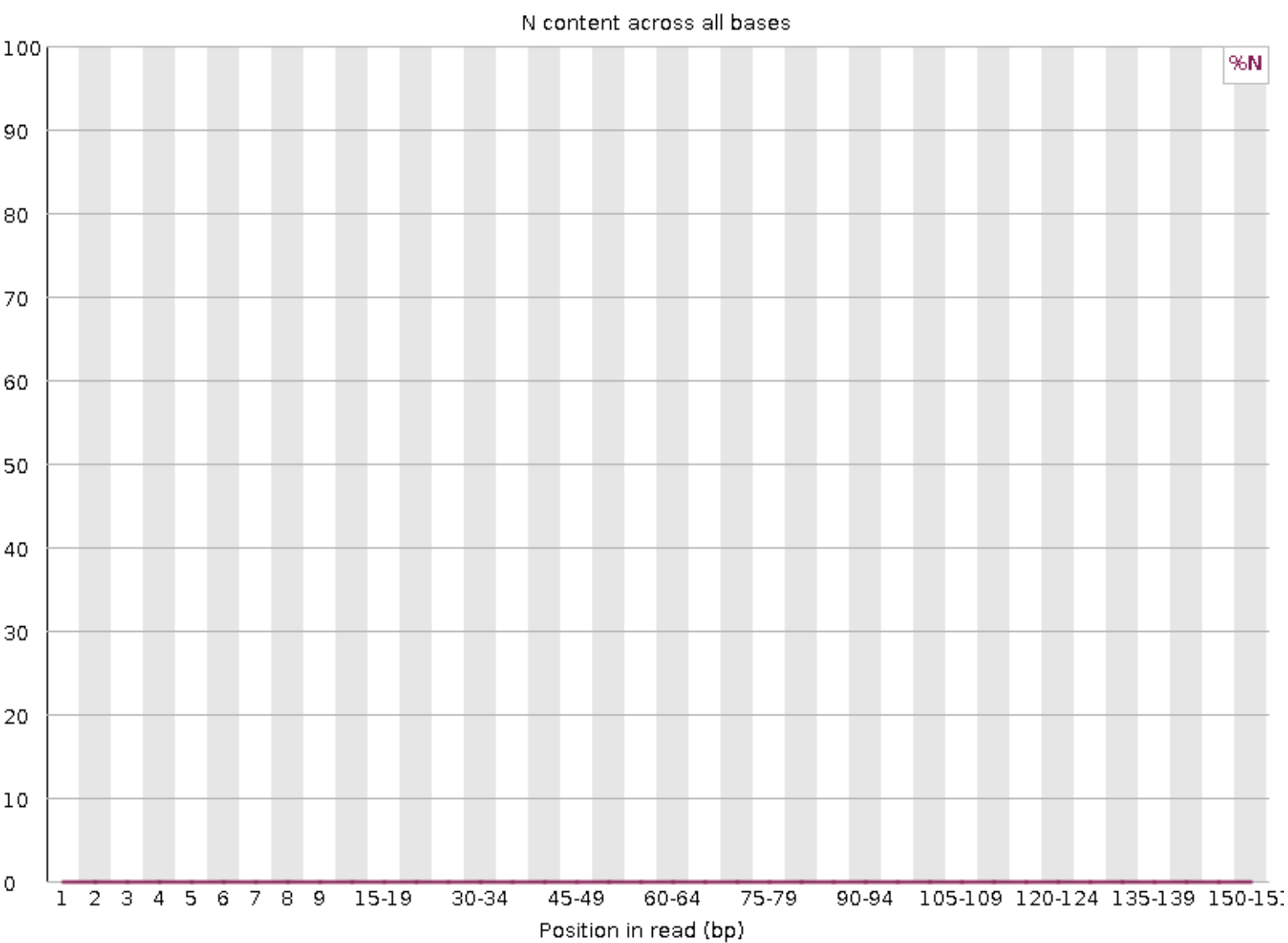


! Per sequence GC content

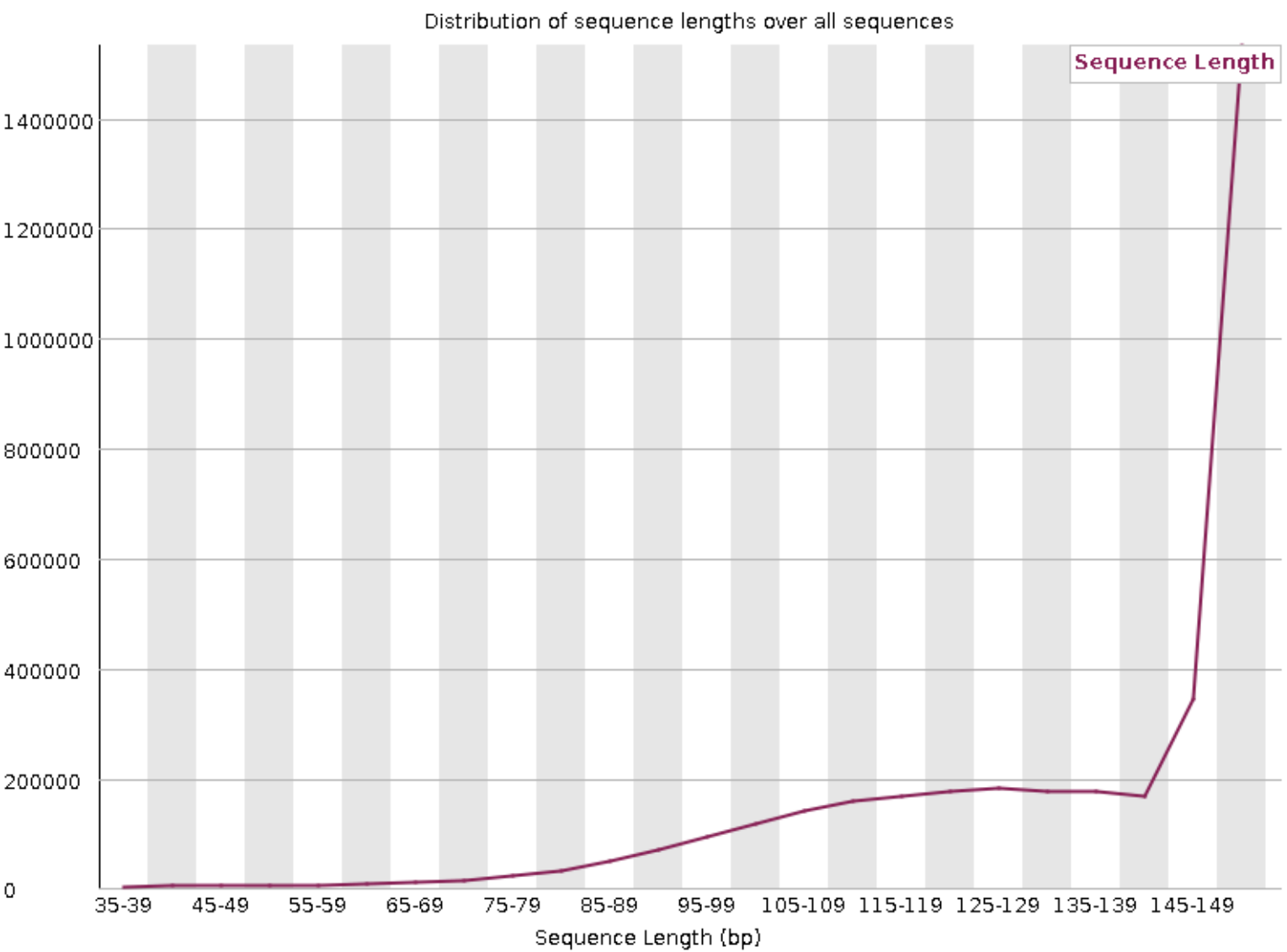




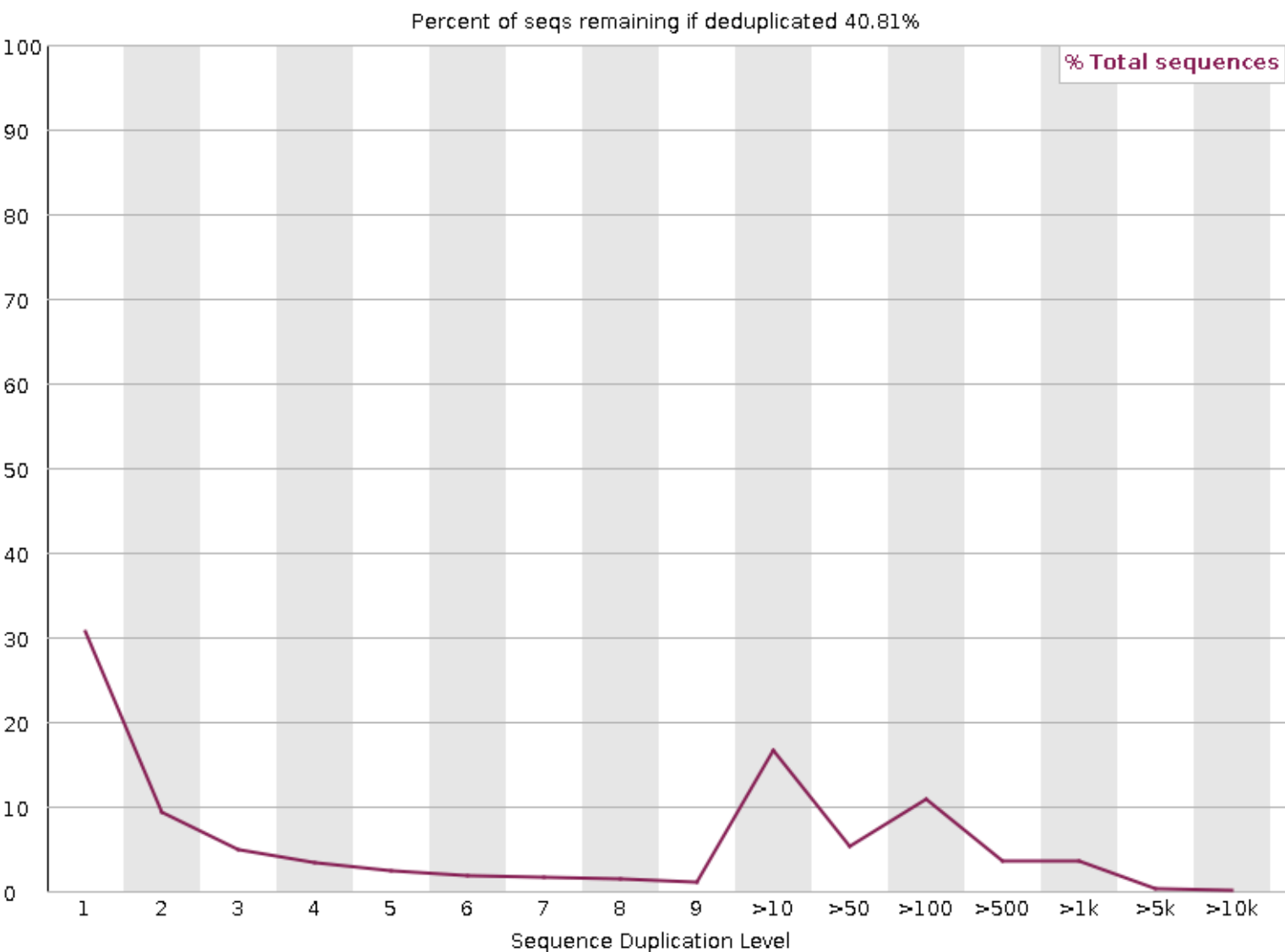
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	11203	0.302090608306885	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	6713	0.18101707163832179	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	5475	0.14763421230743512	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5194	0.14005700433330007	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4237	0.1142513529765484	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTGGCAGGAGTACTTGTGGA	4186	0.1128761301769723	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	3732	0.10063395074545166	No Hit



Adapter Content

