

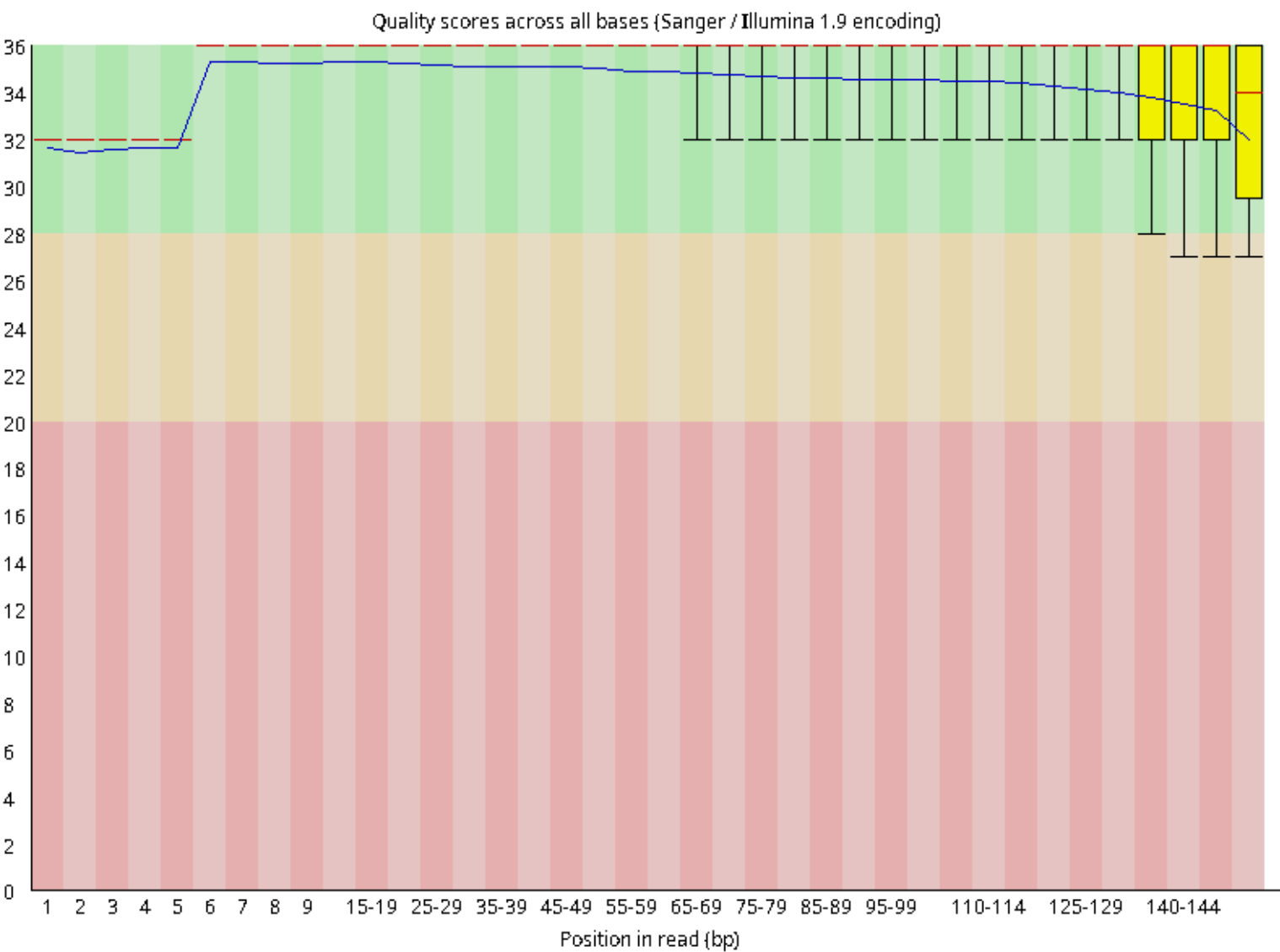
Summary

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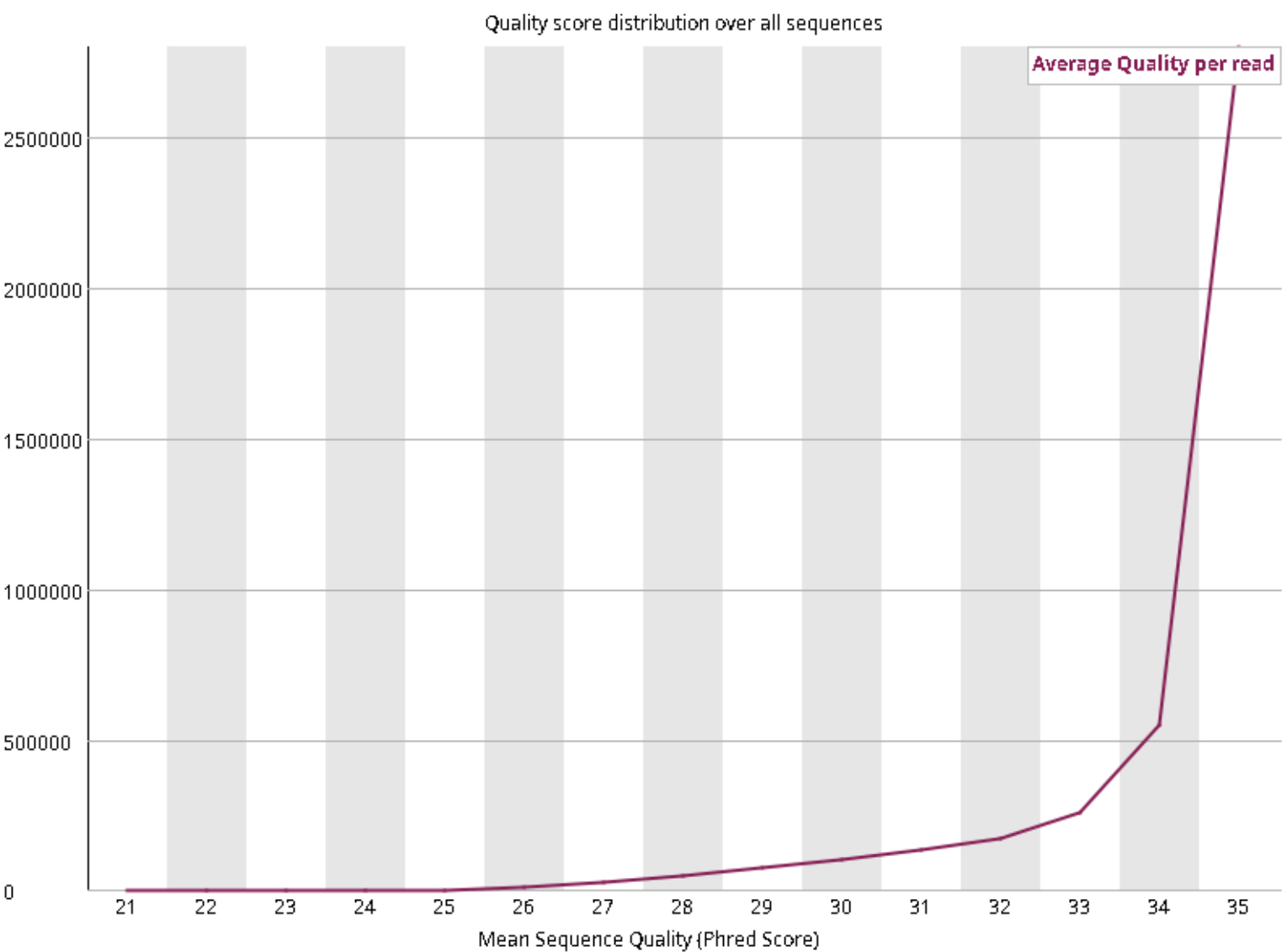
✓ Basic Statistics

Measure	Value
Filename	controlled1_trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4205678
Total Bases	541.8 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	49

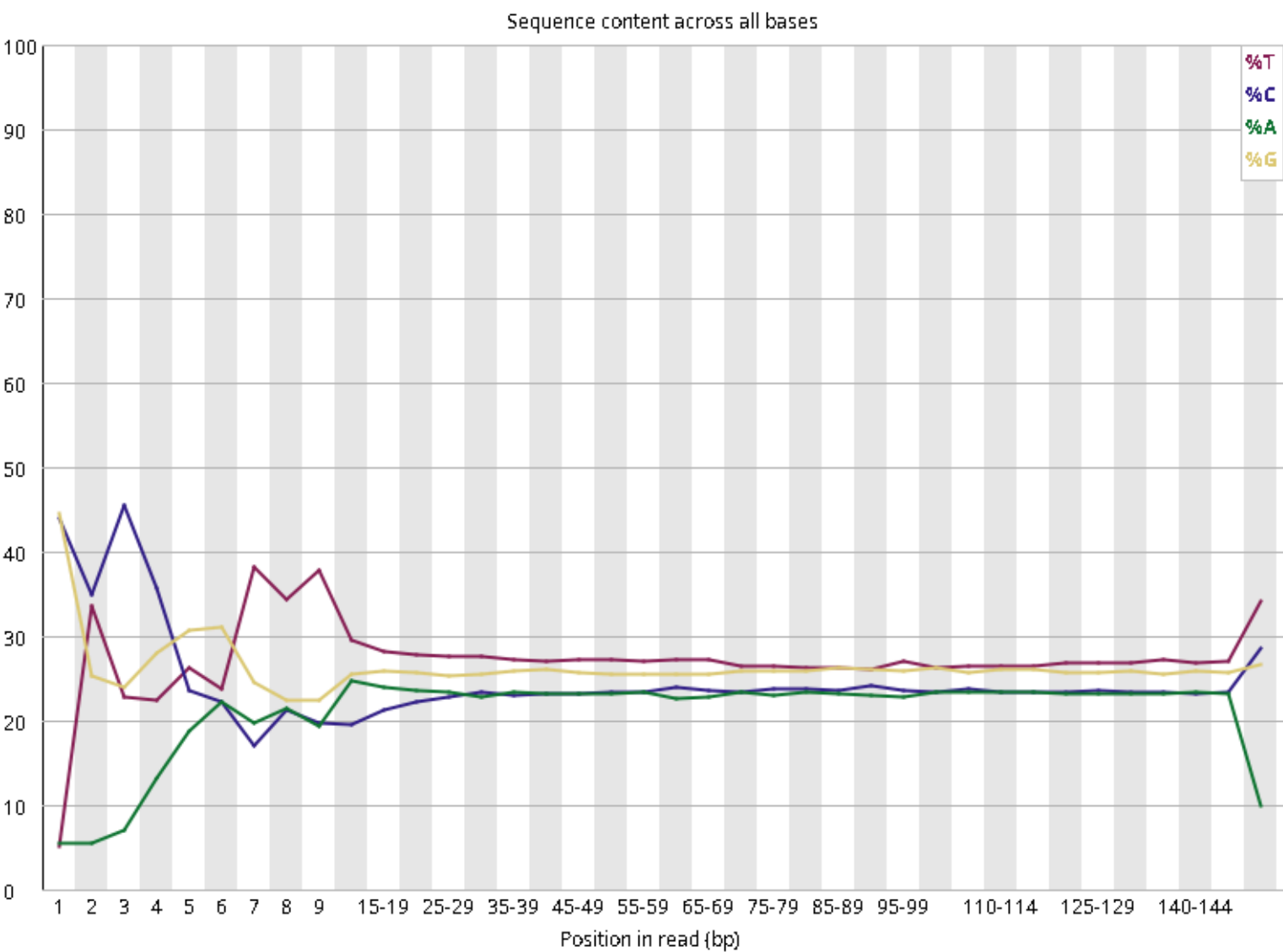
✔ Per base sequence quality



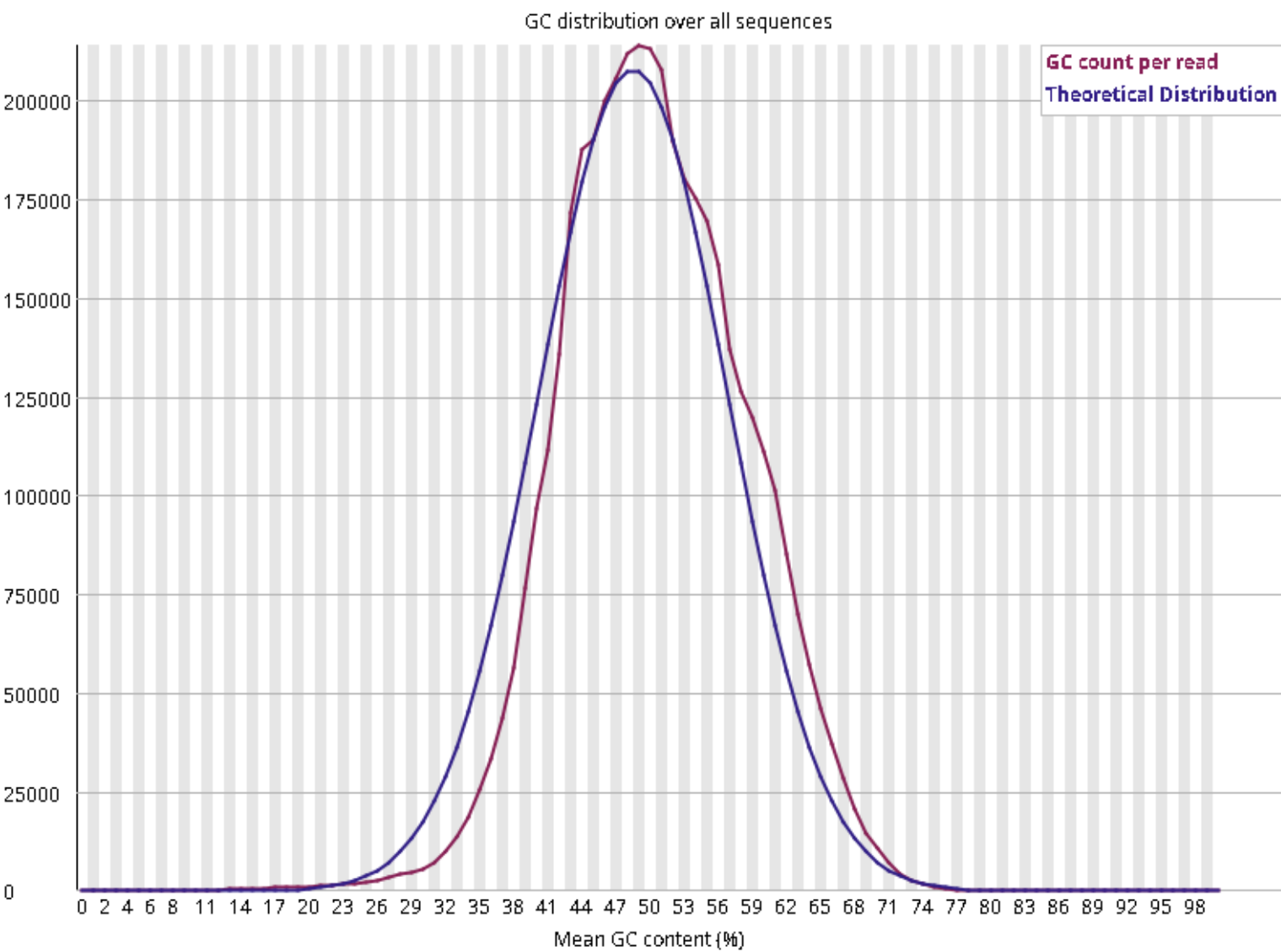
✔ Per sequence quality scores



❌ Per base sequence content

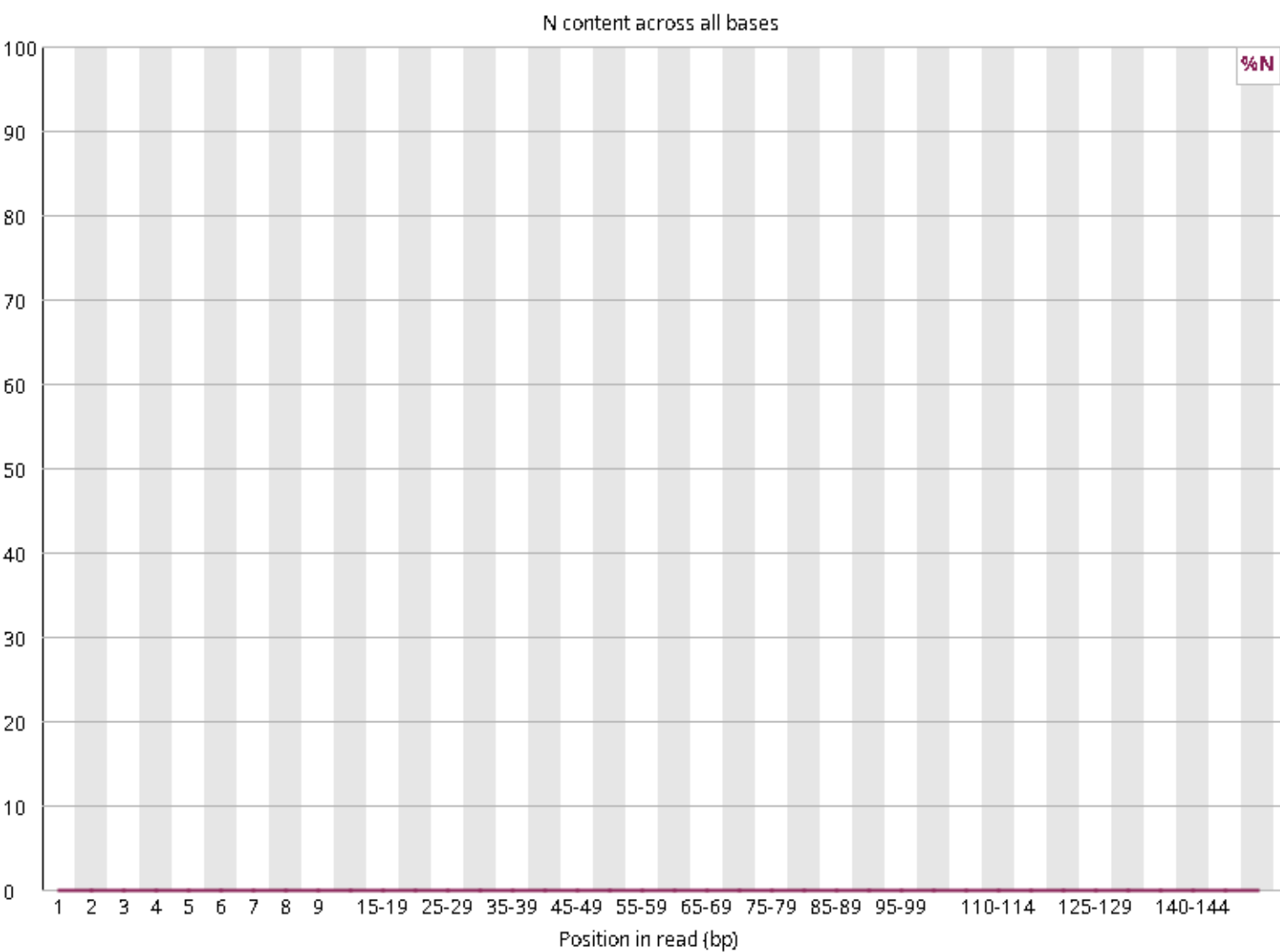


! Per sequence GC content

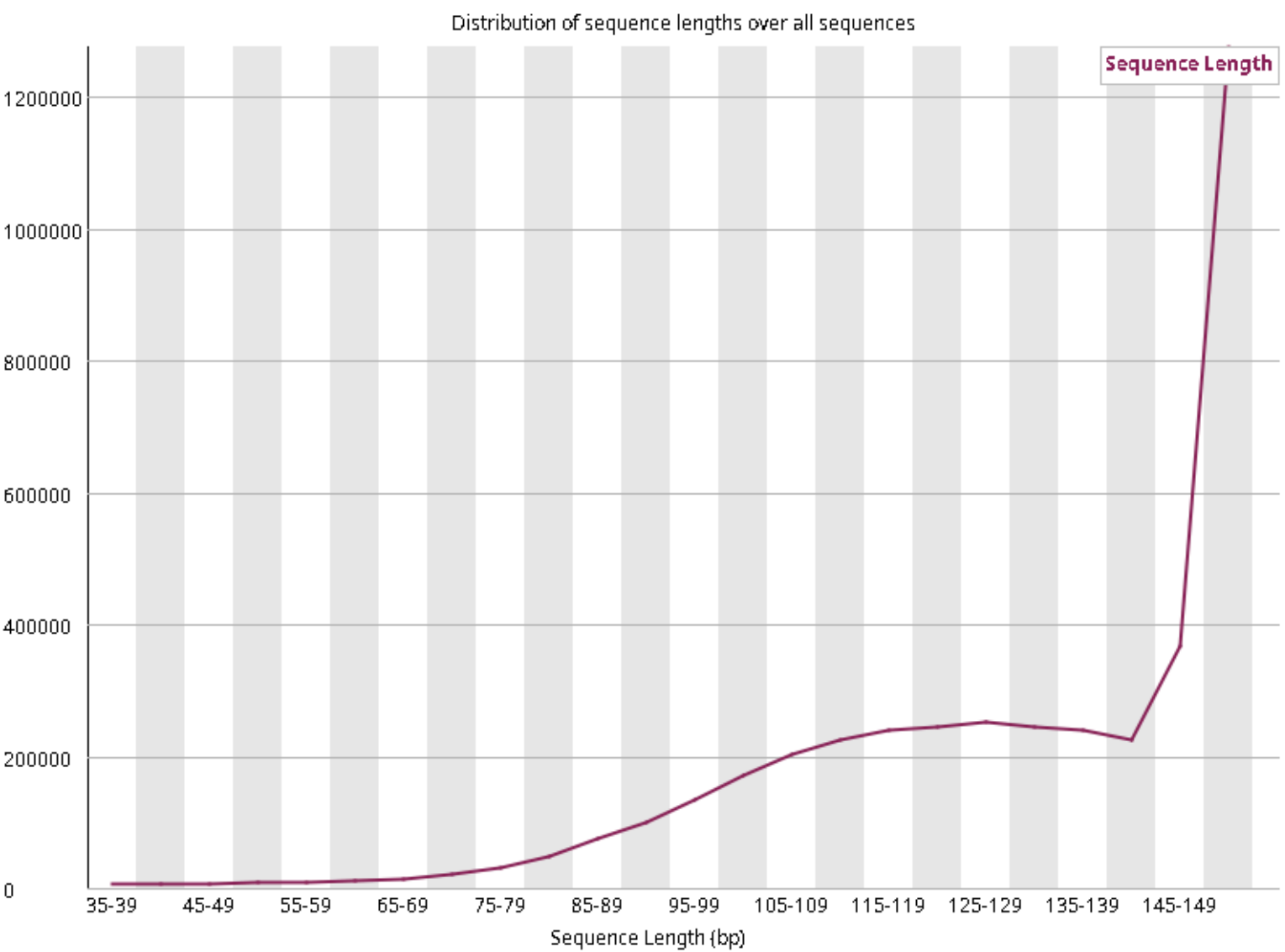




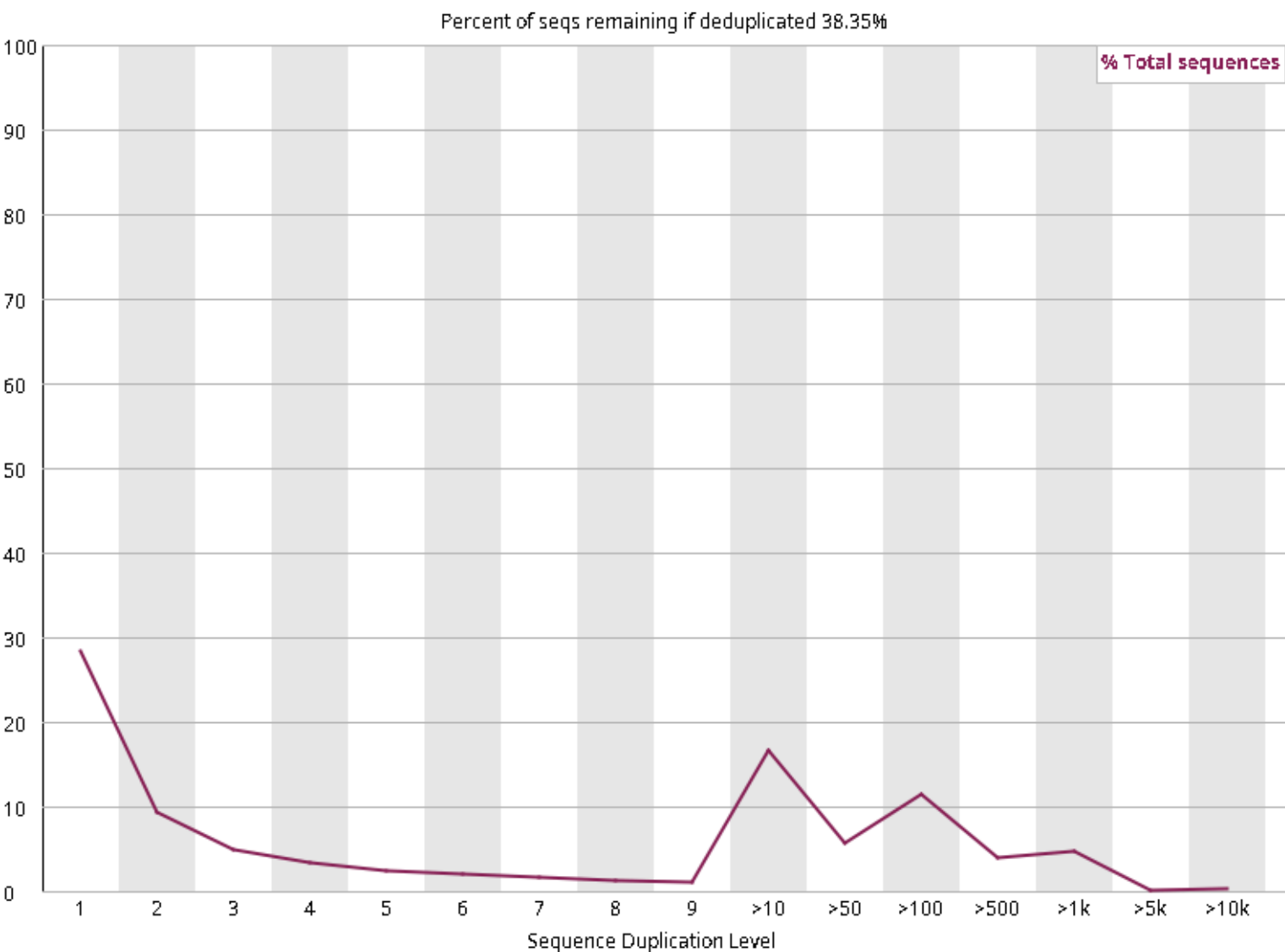
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG	13186	0.31352852025285816	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	10659	0.25344308337442856	No Hit
CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA	5280	0.12554456142386552	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	5022	0.11940999762701757	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4931	0.1172462561327805	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4897	0.11643782524482378	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	4795	0.11401253258095366	No Hit
CCCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGG	4572	0.10871017705111993	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCTTTGGTTCTCAGGGT	4483	0.10659399031499796	No Hit

Sequence	Count	Percentage	Possible Source
CCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGGAA	4331	0.10297982869825033	No Hit



Adapter Content

