

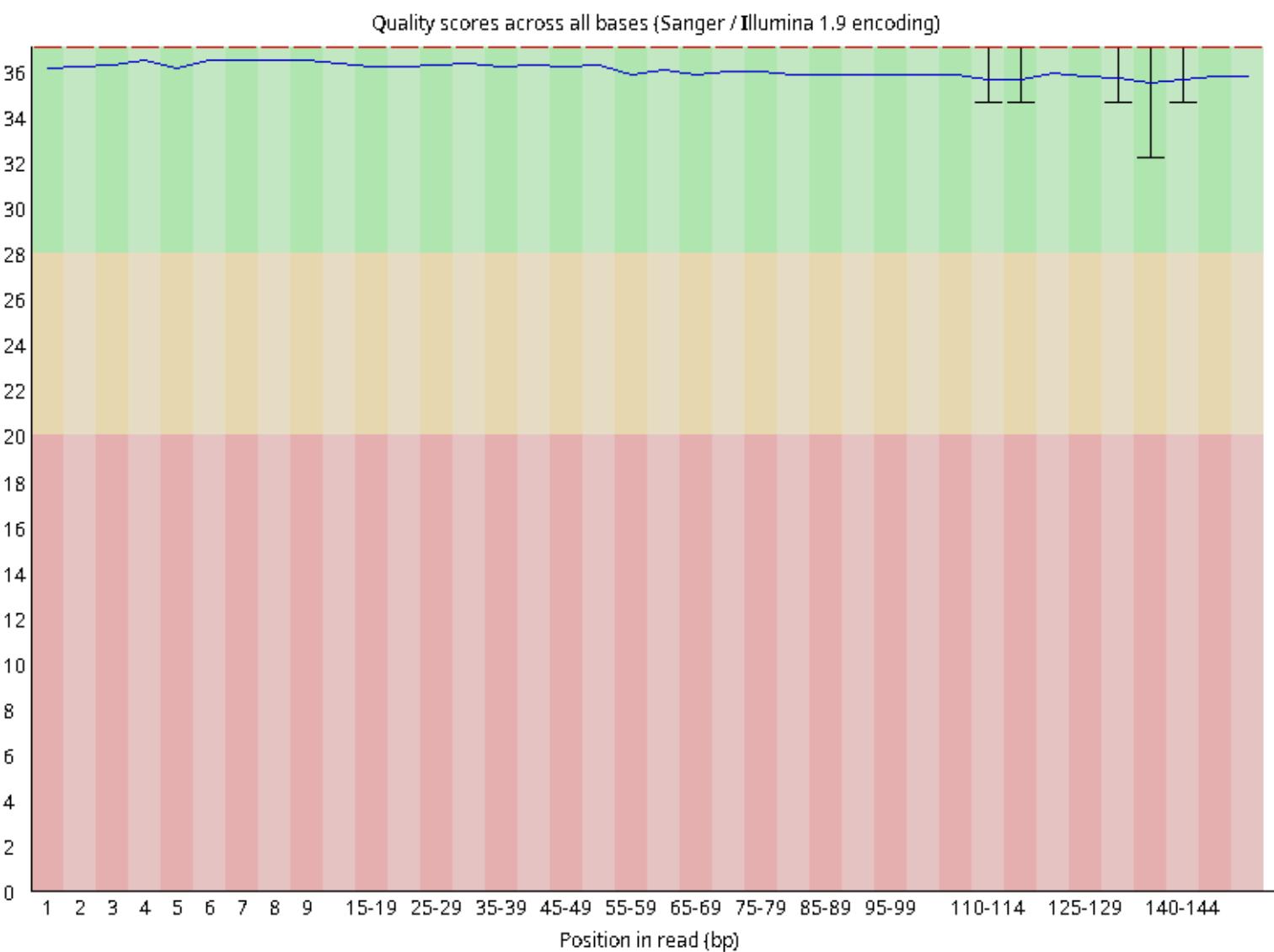
Summary

-  [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](#)

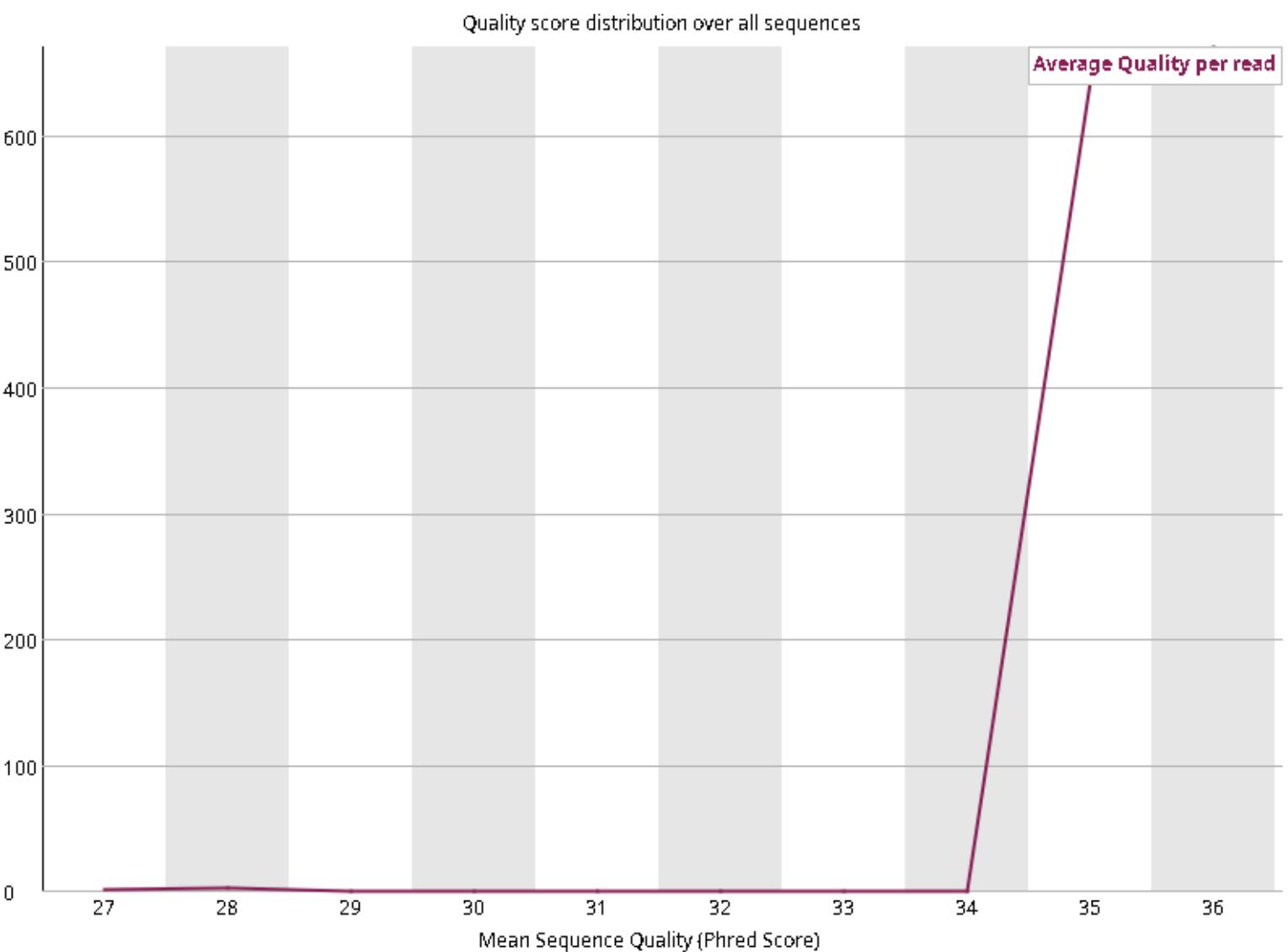
Basic Statistics

Measure	Value
Filename	HomerSimpson_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1320
Total Bases	199.3 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

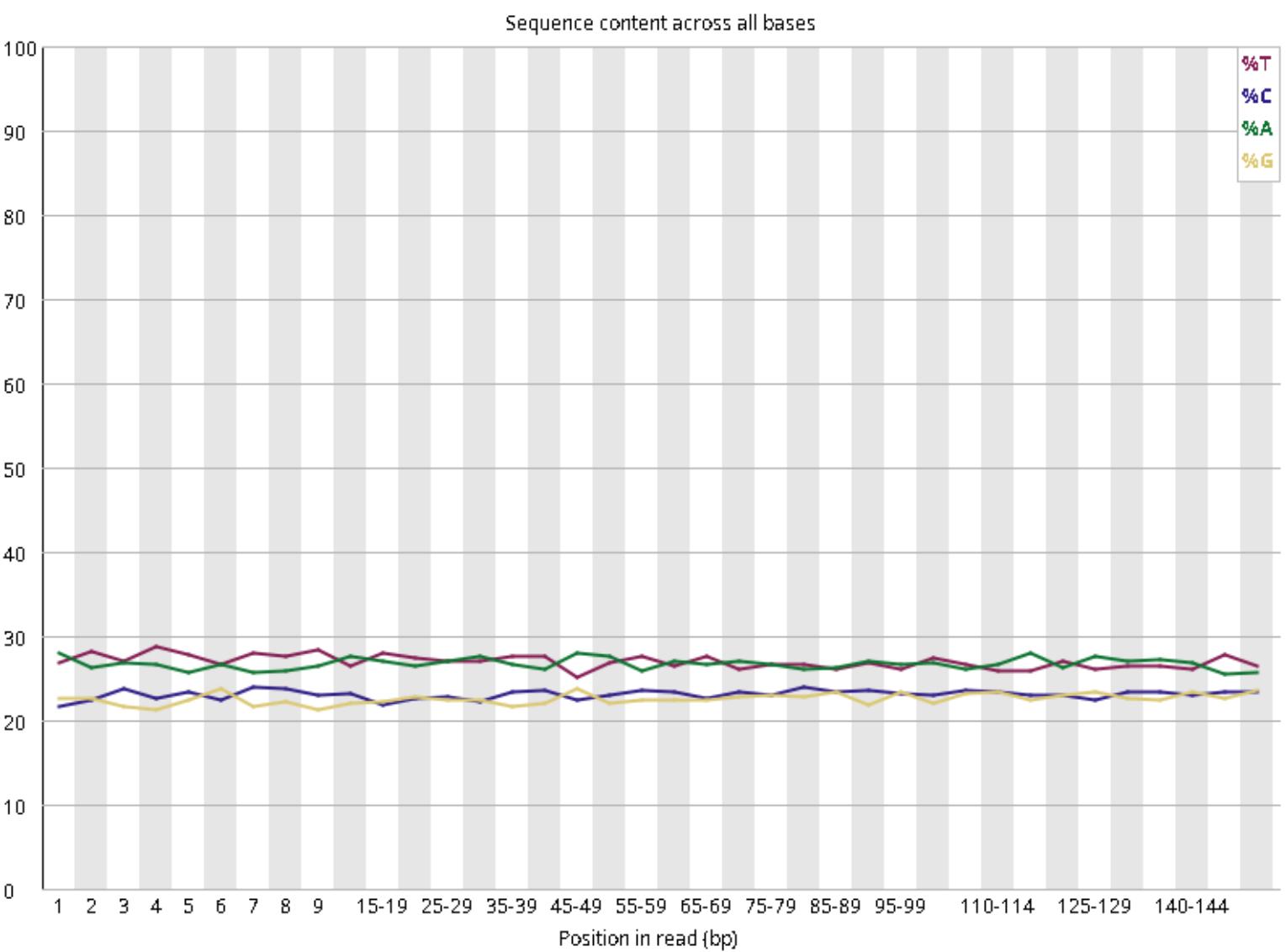
Per base sequence quality



Per sequence quality scores

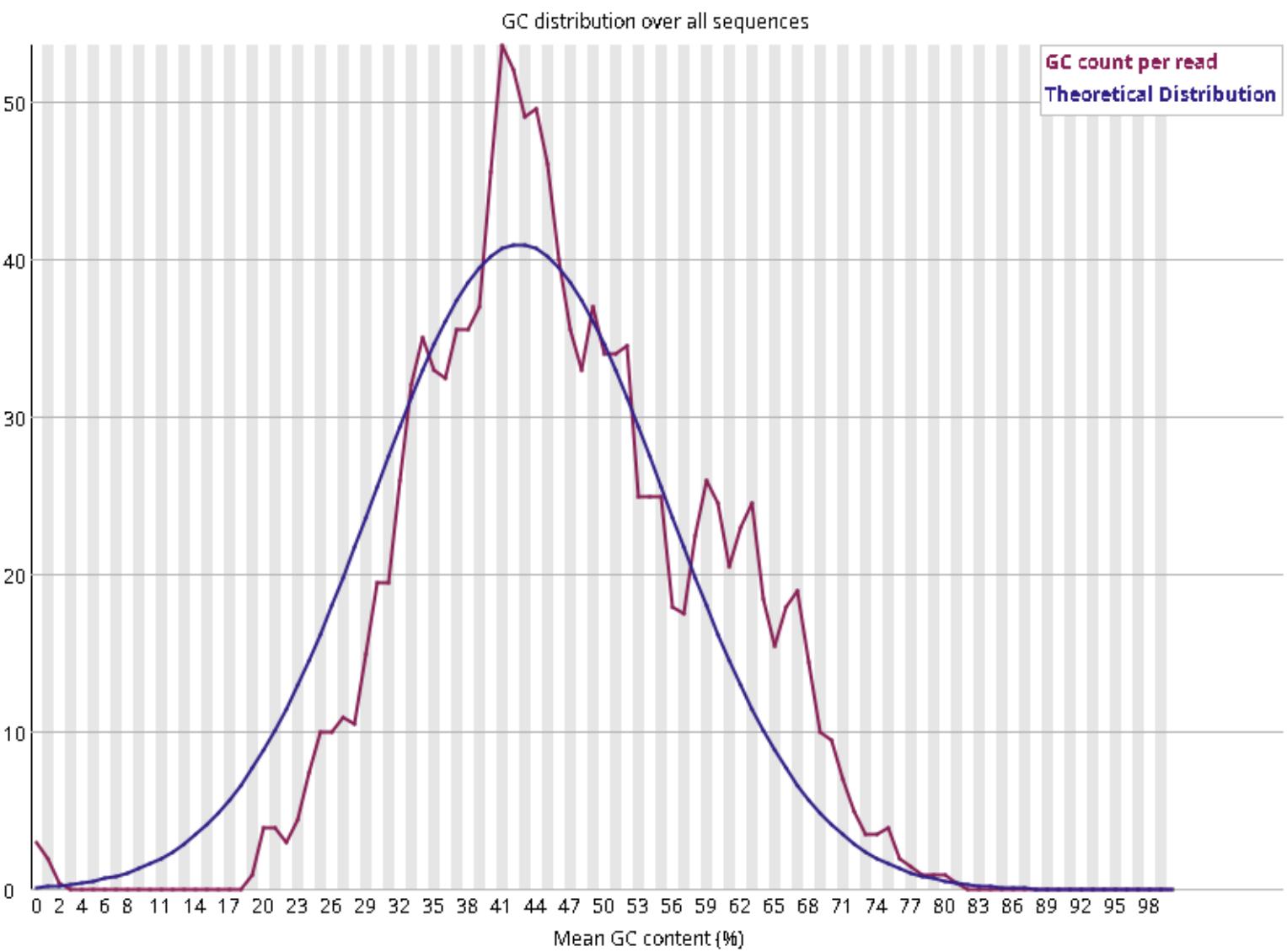


Per base sequence content





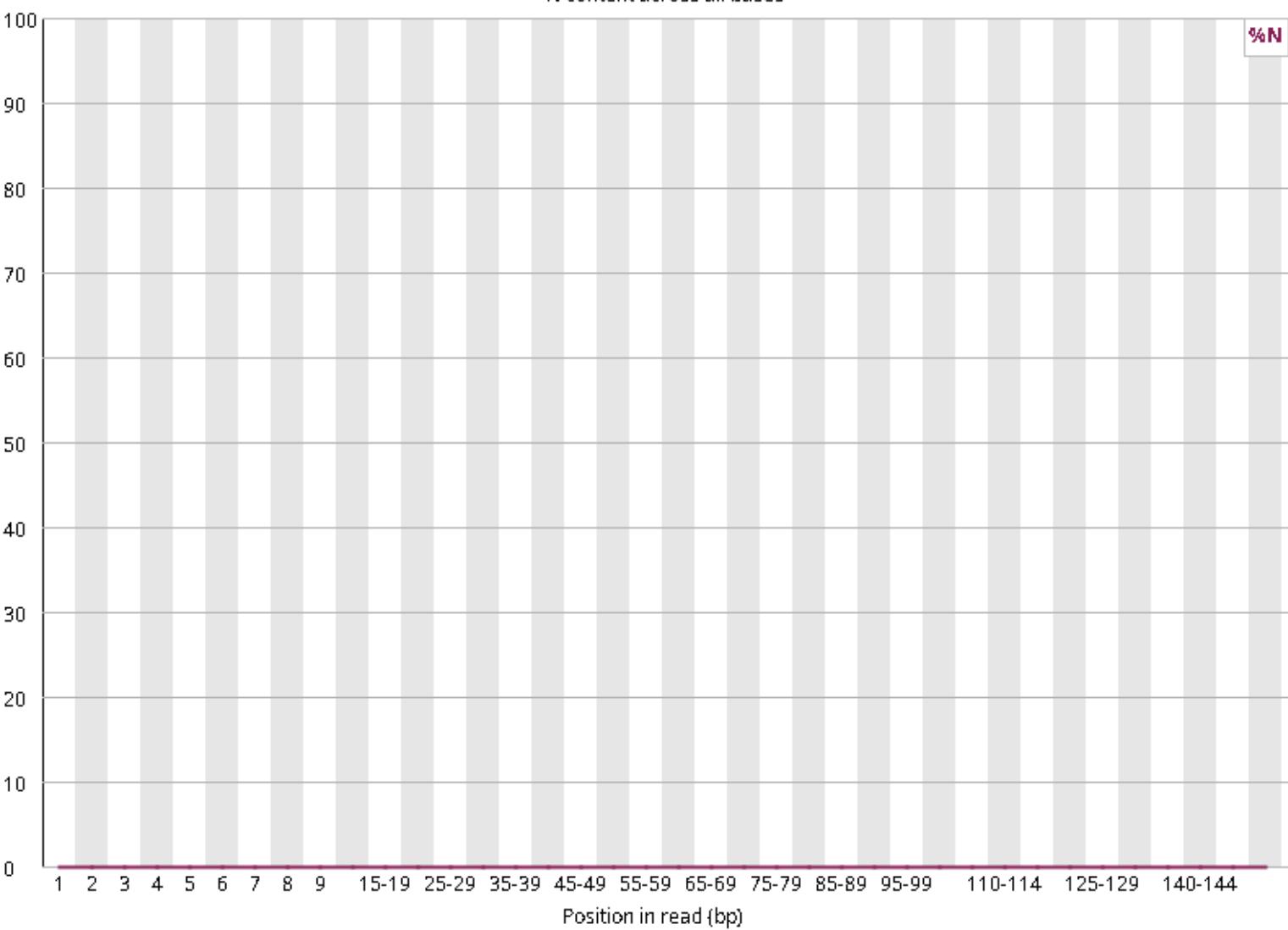
Per sequence GC content





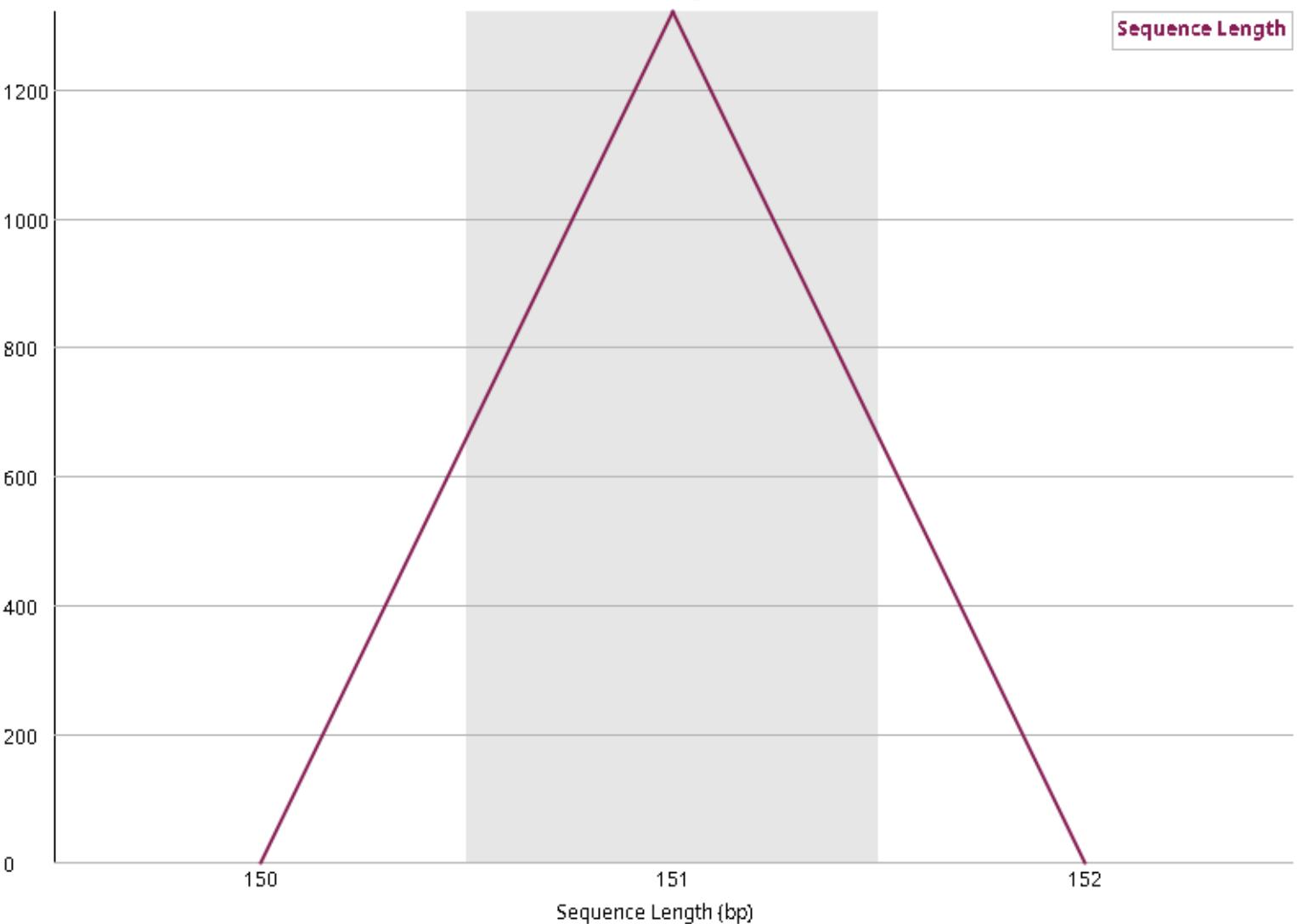
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

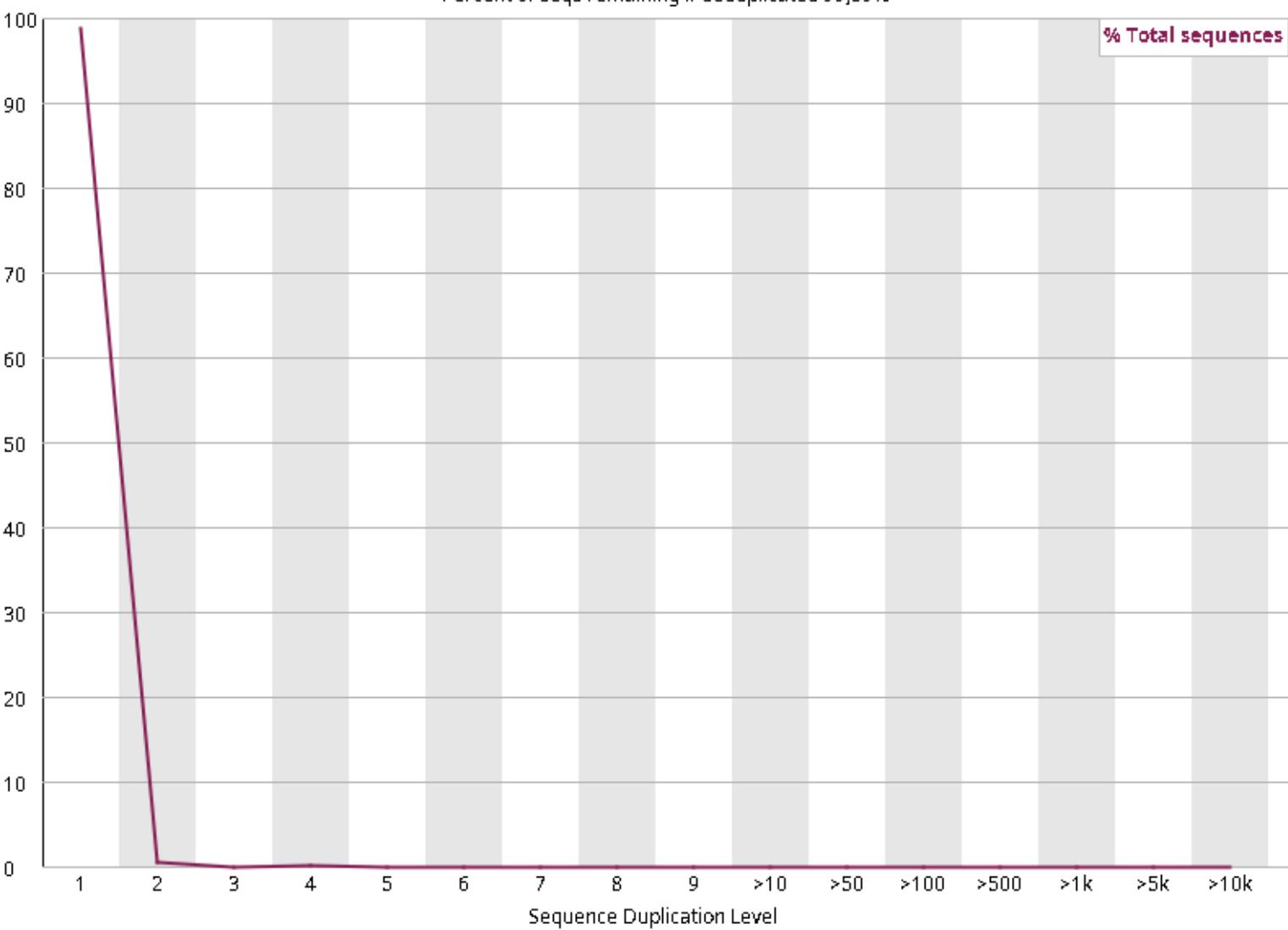


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,39%

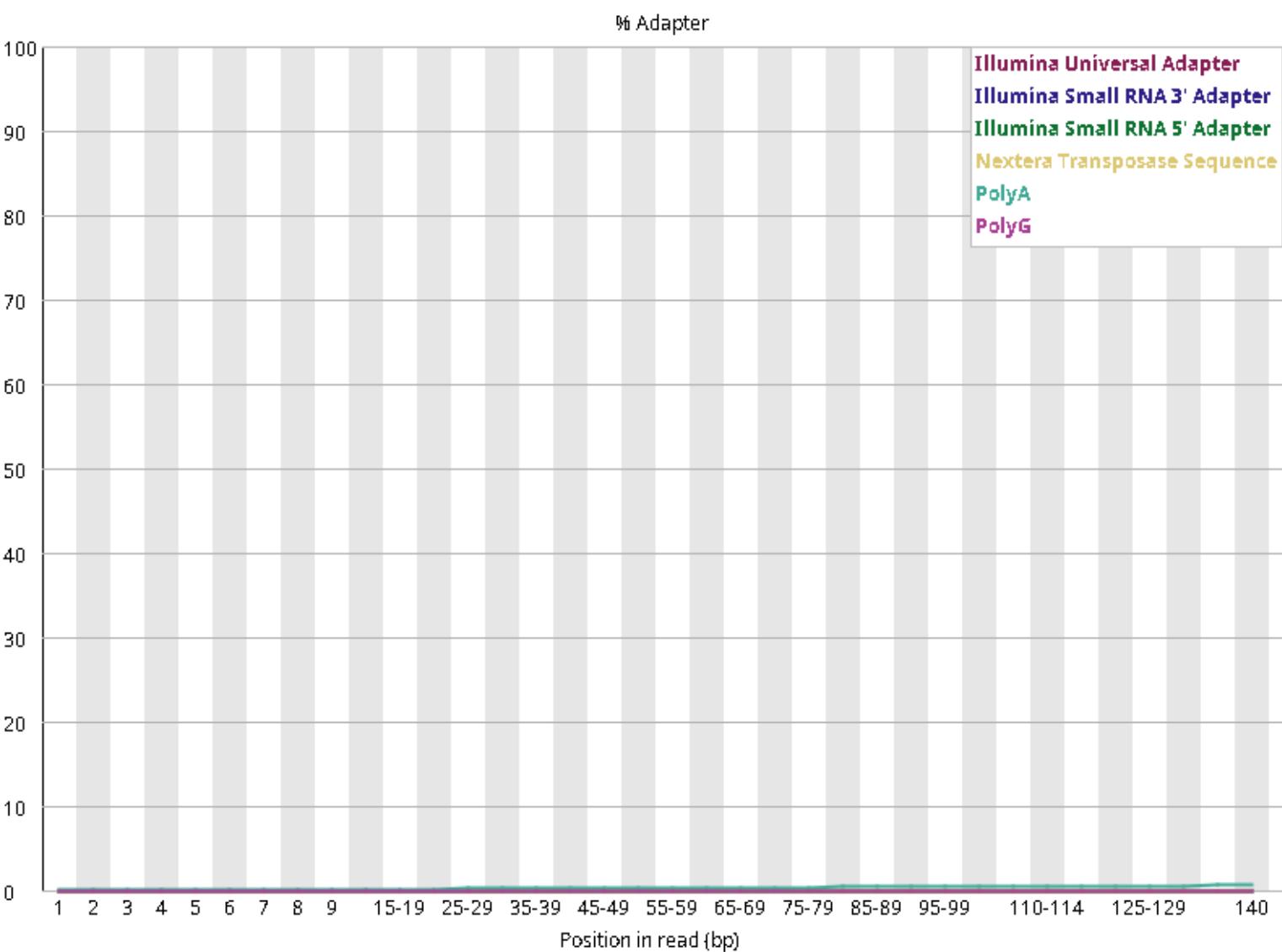


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAA	4	0.303030303030304	No Hit
CTCTCTTTCTGATTTCTCTT	2	0.151515151515152	No Hit
AGTACCTCTGCCAAGGCCTGAGCCTCTGCAACAGATCCTCTGCCTG	2	0.151515151515152	No Hit
GATAGCATCCTGACTTGAAATGCCAATTCTGGTGAGGTCTTGCCA	2	0.151515151515152	No Hit
TGCCATGCCTGCTGTGAGTAATGTCACAAGTCCAGAGCTGACATGGAG	2	0.151515151515152	No Hit
TAGTACTGGAGACAGCTGAGCATGCCACGACATTGCCATCACCAGGAT	2	0.151515151515152	No Hit



Adapter Content



Produced by [FastQC](#) (version 0.12.1)