












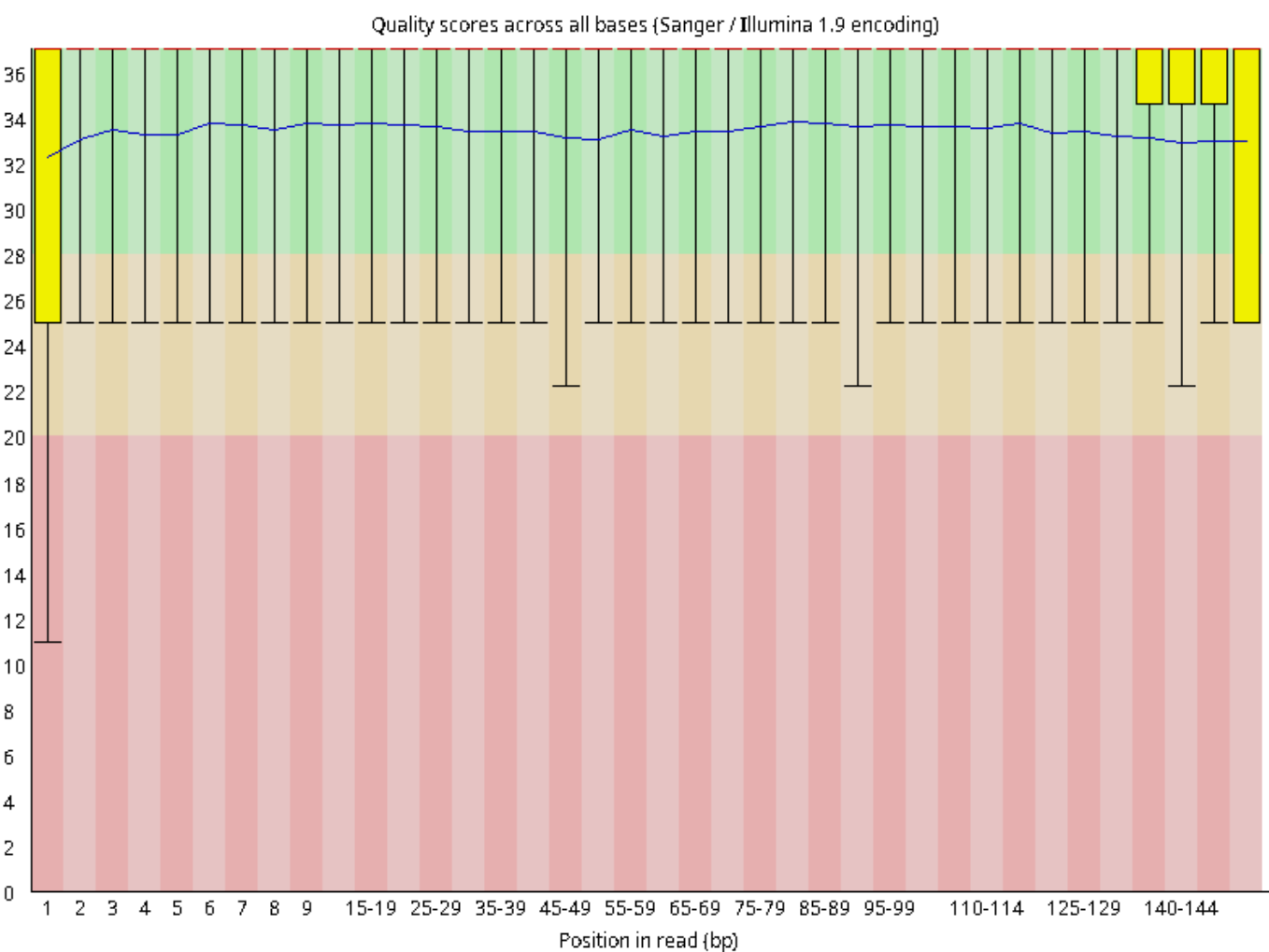
Summary

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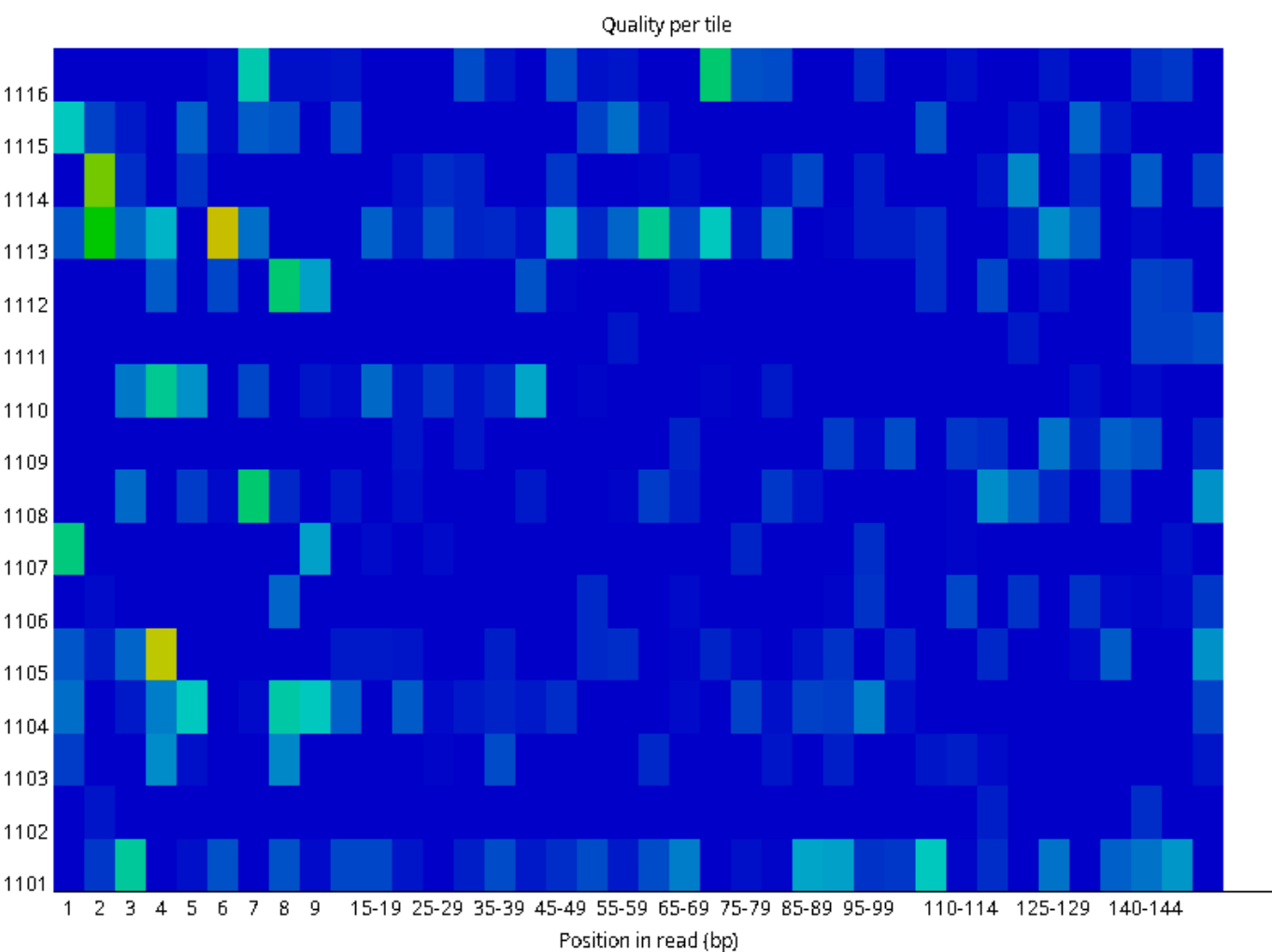
Basic Statistics

Measure	Value
Filename	SRR33784444_2_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1511
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	48

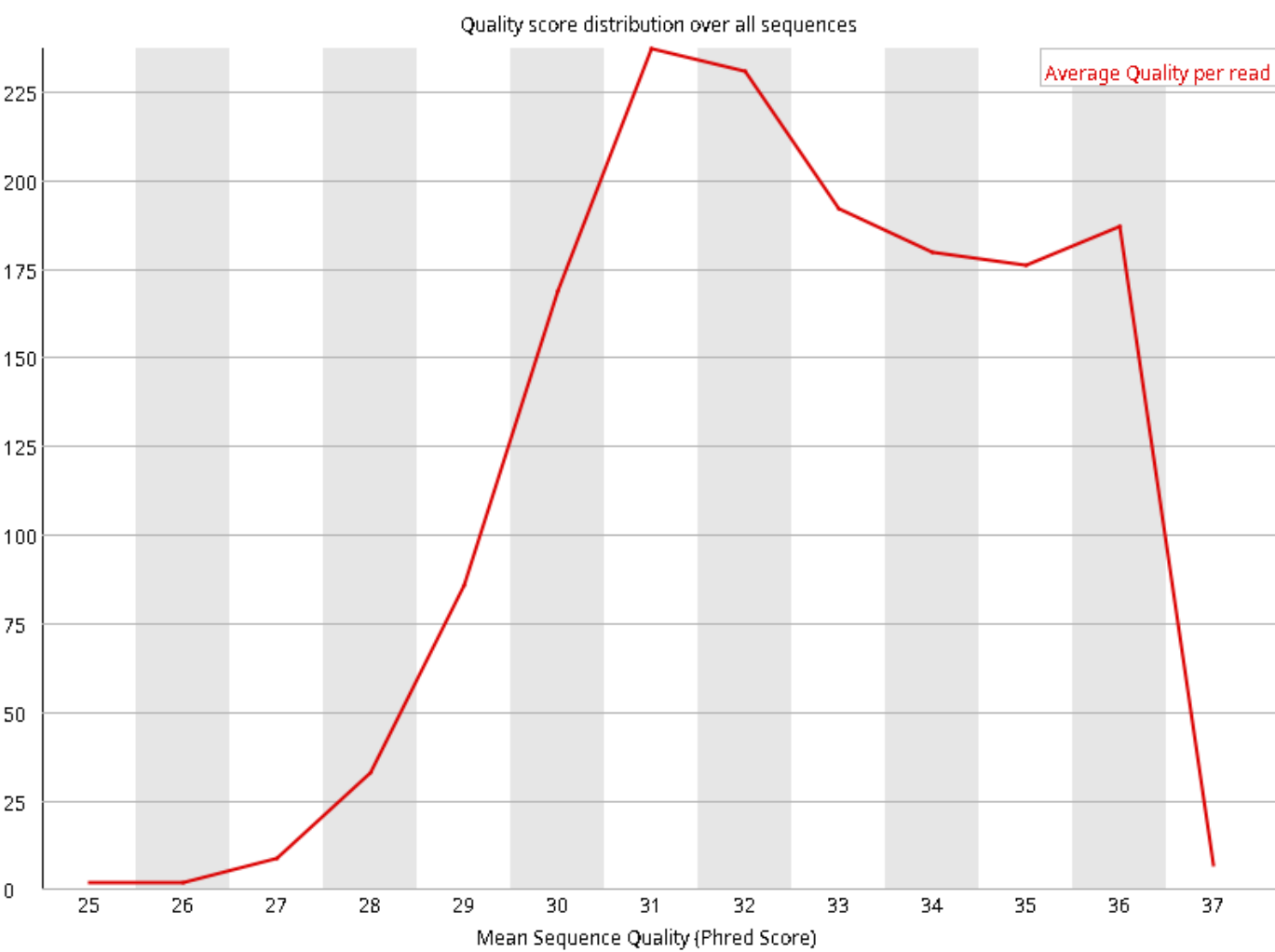
✔ Per base sequence quality



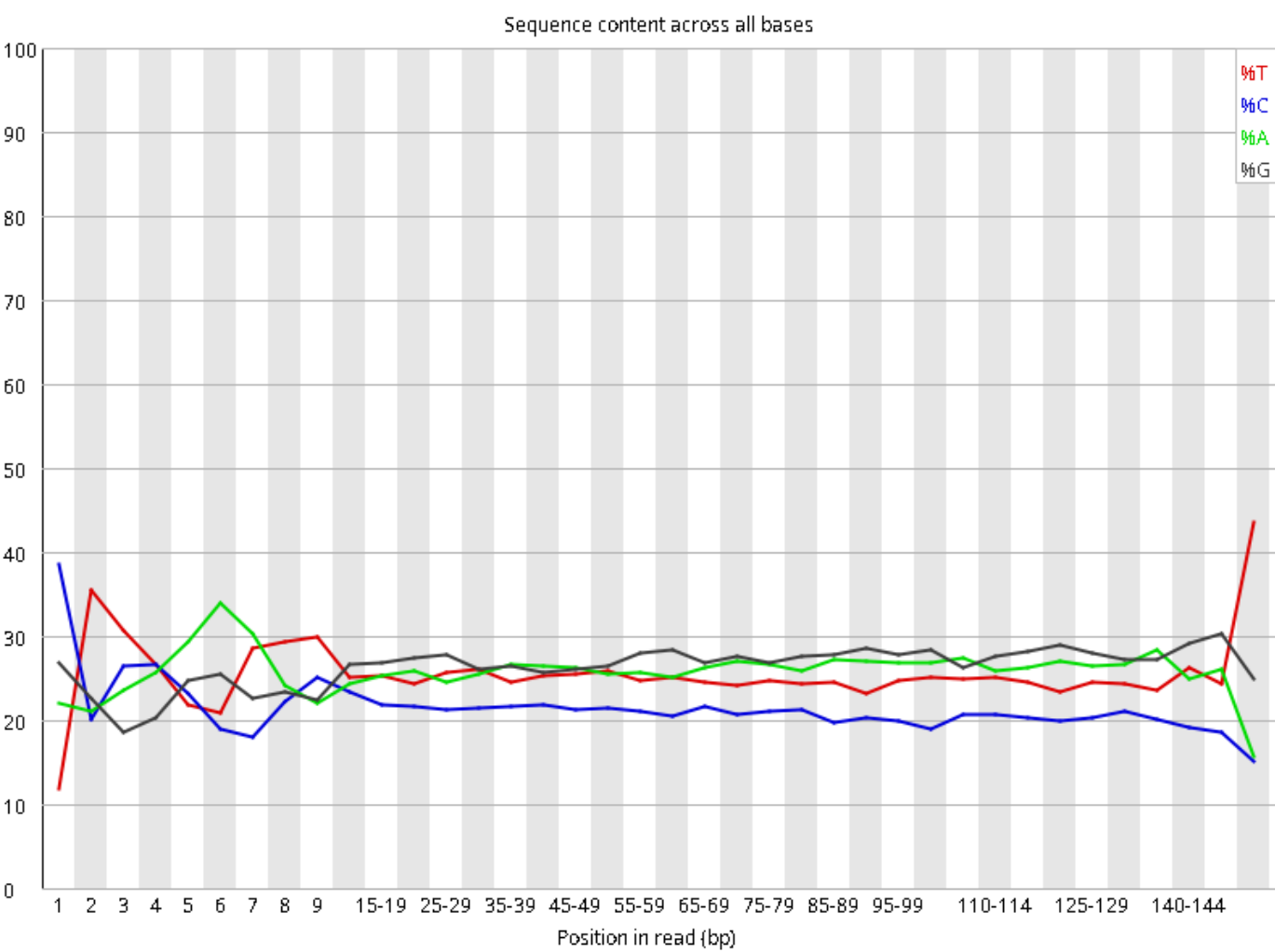
! Per tile sequence quality



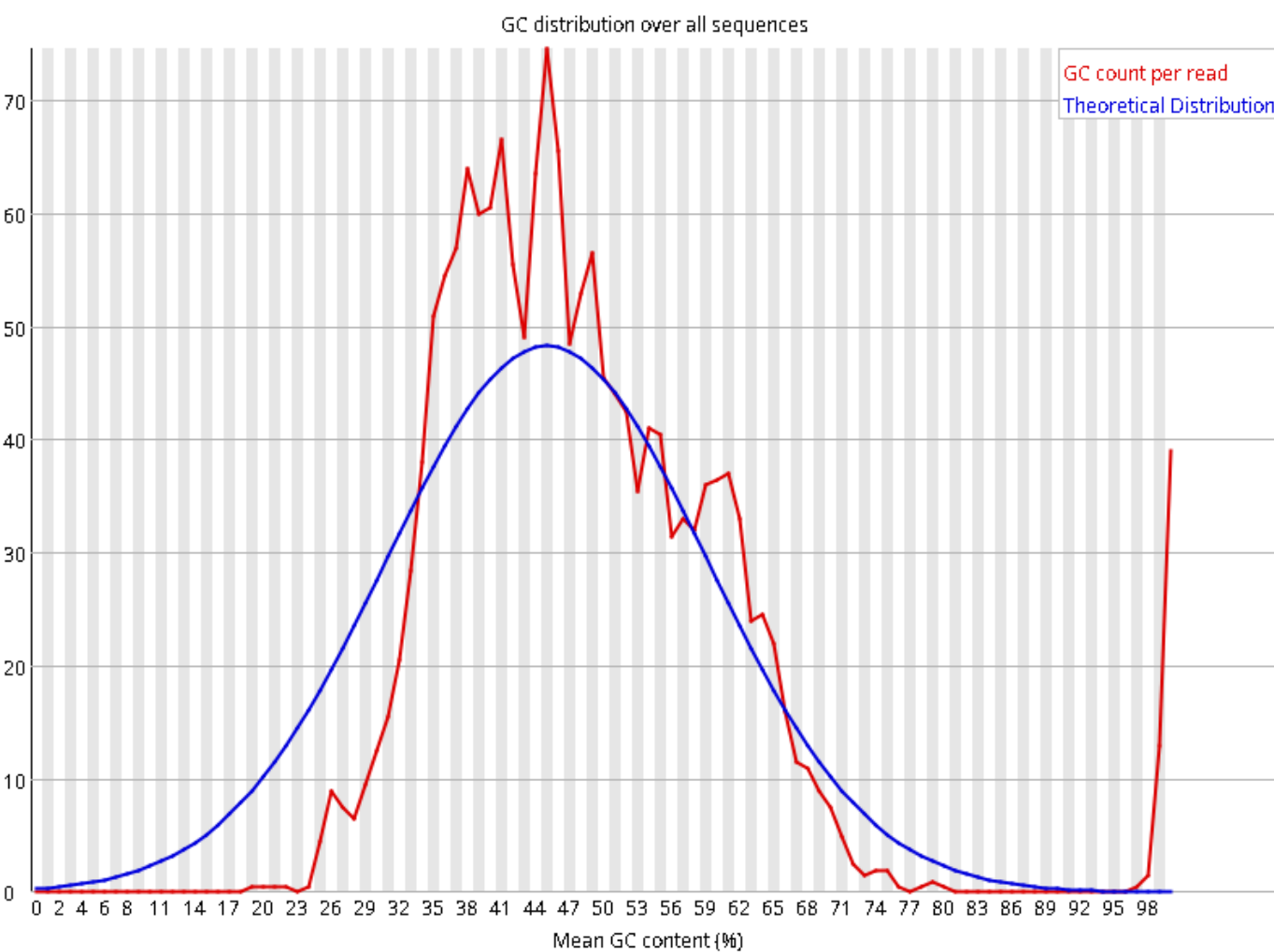
Per sequence quality scores



✖ Per base sequence content

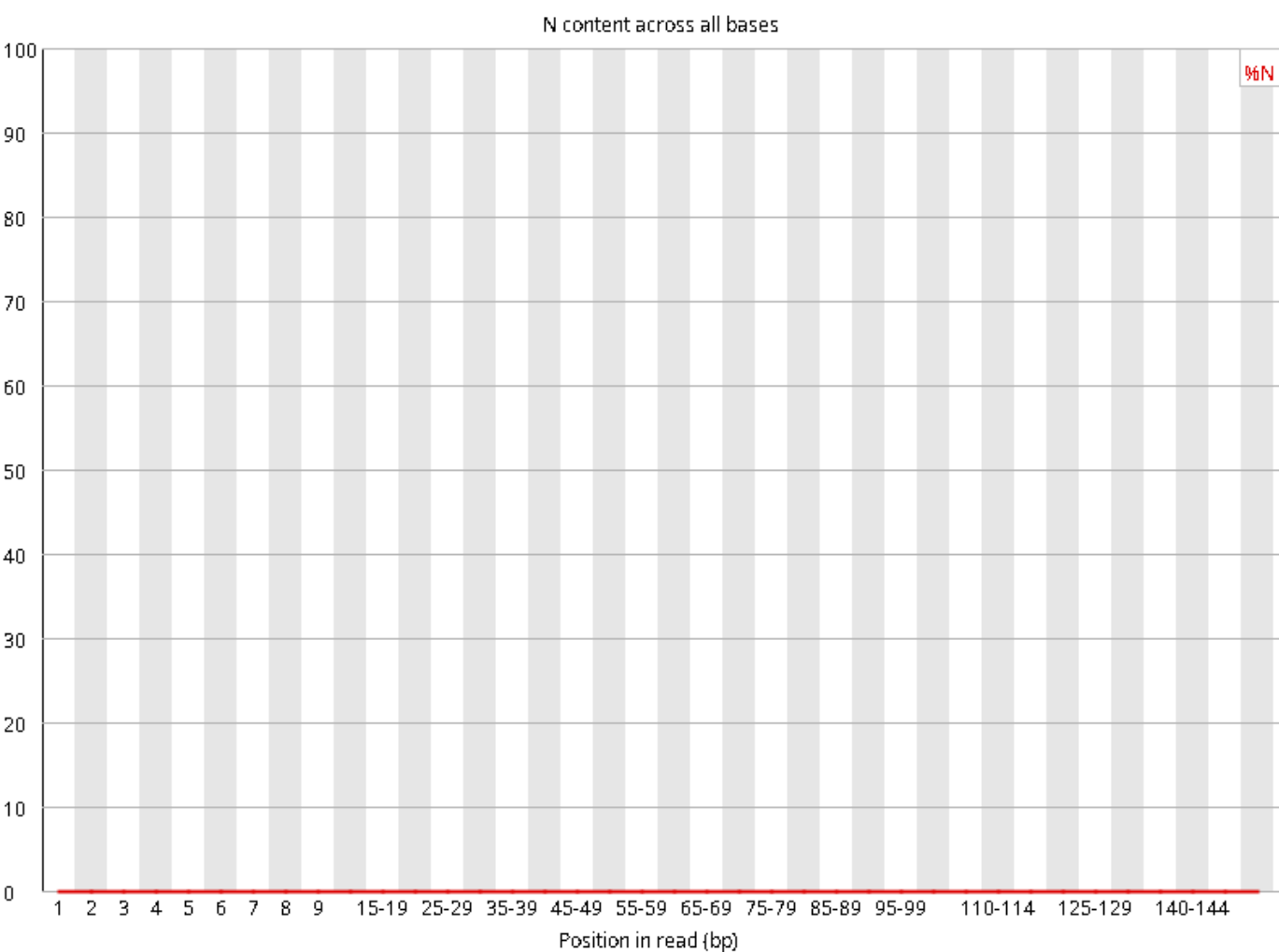


Per sequence GC content

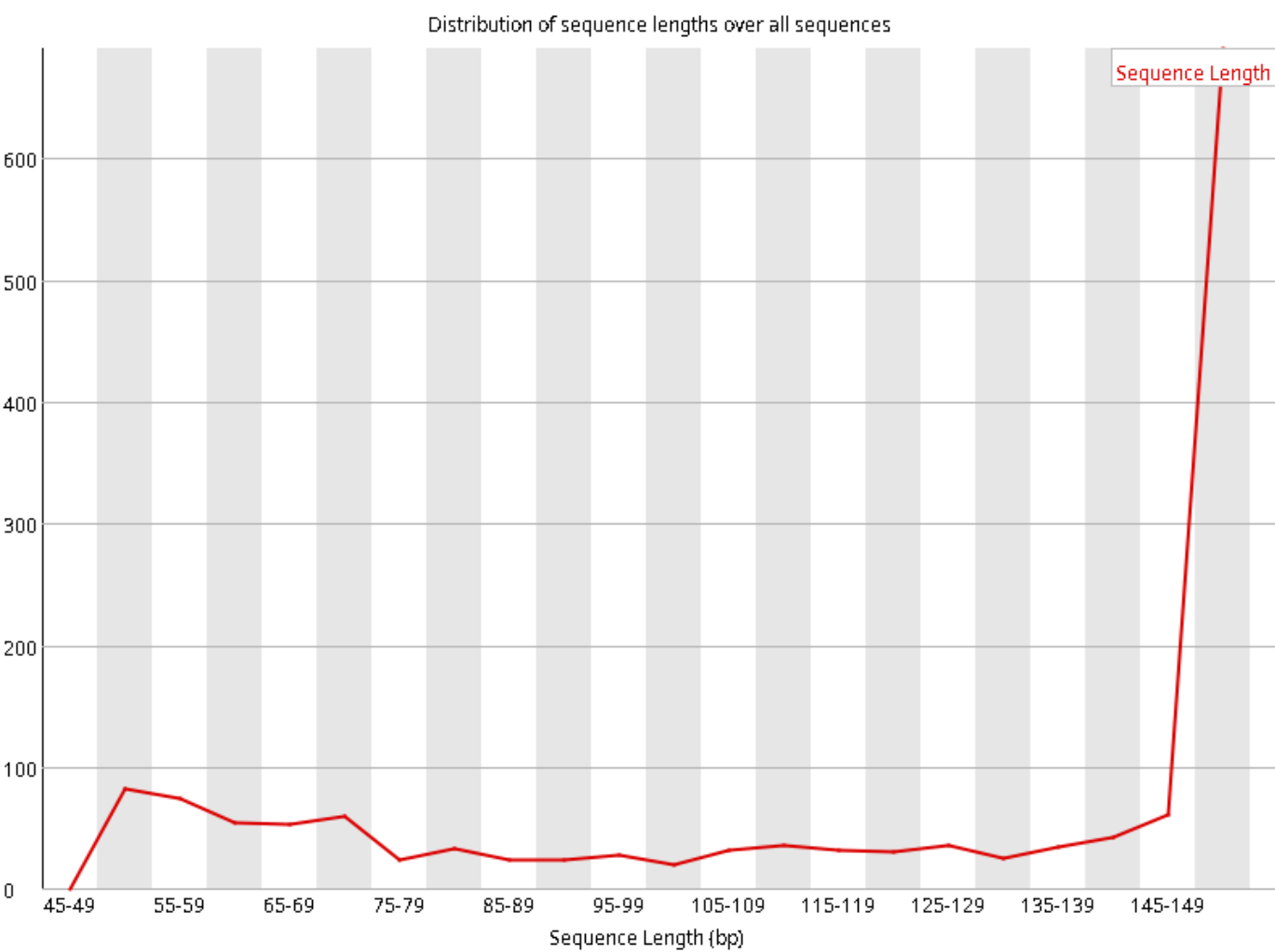




Per base N content



Sequence Length Distribution



[illegible]

Sequence	Count	Percentage	Possible Source
CTCCCATTCCTGCTCTTTTTTCTCTCTGCACCACTCTTCTCCTTGCC	2	0.13236267372600927	No Hit
CTAAACACTGTGGGGGACATCAAGCAGCTATGCAAATGCTAAAGGATAC	2	0.13236267372600927	No Hit
AAGAAGTGAACCCCAATTACATTGCCACGTGTATACCCAGATCTGCGG	2	0.13236267372600927	No Hit
CTACCACCGATTGAGAGACTTCATATTGATTGCAGCGAGGACAATACAAC	2	0.13236267372600927	No Hit
CTCACAATTTGTTTTATCCTACATGGGAGTGTGACAGTGTCTATTCTTGAA	2	0.13236267372600927	No Hit
CAAACATTCTATGCAACAGGTGACATAATAGGAGATATAAGACAAGCACA	2	0.13236267372600927	No Hit
TGGCCTGTACCGTCAGCGCCCGAGCTTCGCTGCTAATTGAATGCAAGC	2	0.13236267372600927	No Hit
CCTCCAATTCCCCTATCATTTTTTGTTTTCCATTTTCCTGGTAAATTTAT	2	0.13236267372600927	No Hit
CTCCAGAGAGCAGTAAGGACATAAGACTCCTGGTTTTAACTGGGGATAAA	2	0.13236267372600927	No Hit
CTCTCACCTTCTCTGTAGCACATGGGCACAGCCCTGGTCTGATGGGTCA	2	0.13236267372600927	No Hit
CATCACACCTCACCTACCAAGCACAAATTCAAGGAAAGAAATAGTTAAGA	2	0.13236267372600927	No Hit
CTCCAATTCCCCTATCATTTTTTGTTTTCCACTTCCTGGTAAATTTATT	2	0.13236267372600927	No Hit



Adapter Content

