

Summary

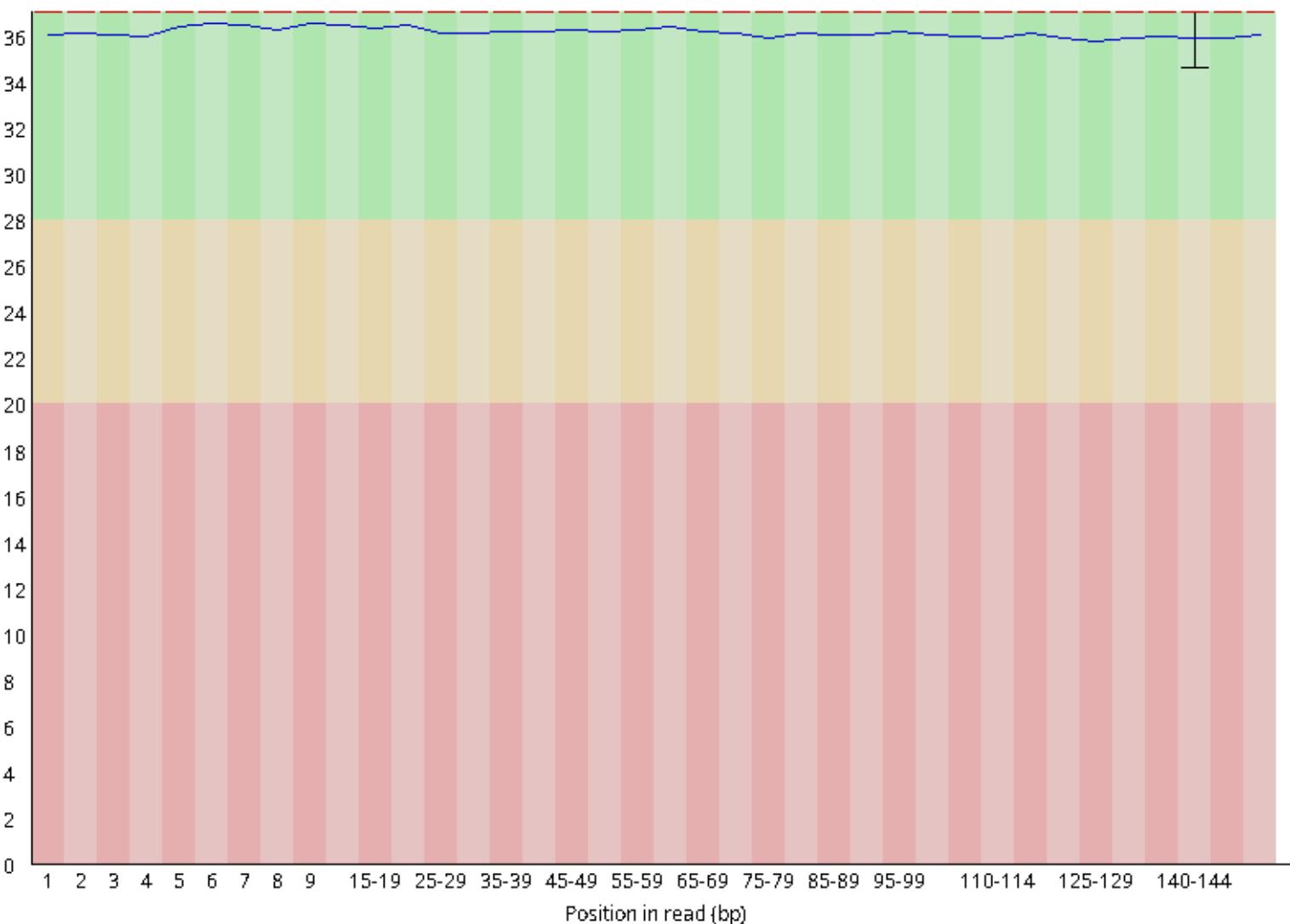
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Basic Statistics

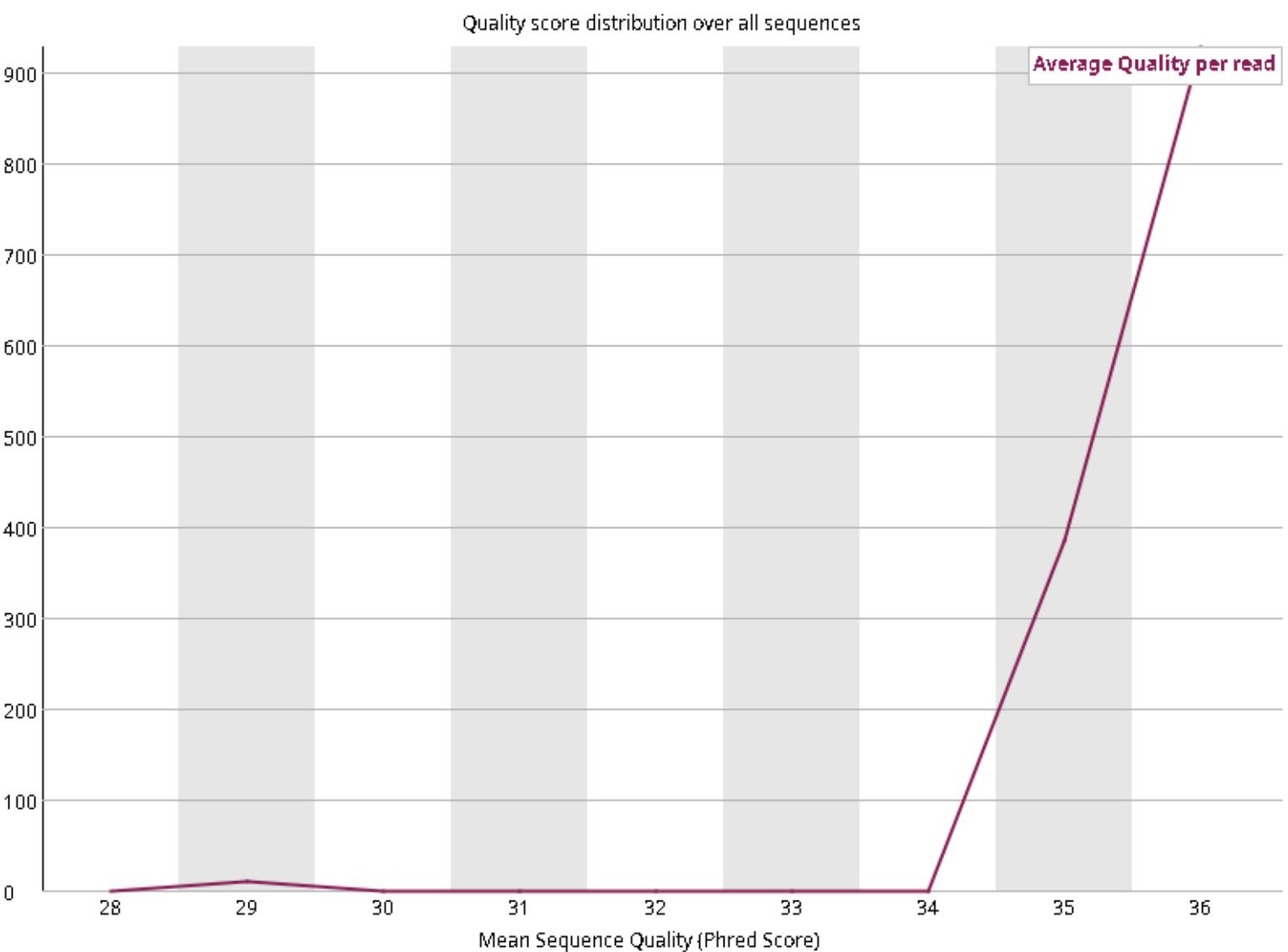
Measure	Value
Filename	MargeSimpson_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1328
Total Bases	200.5 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

Per base sequence quality

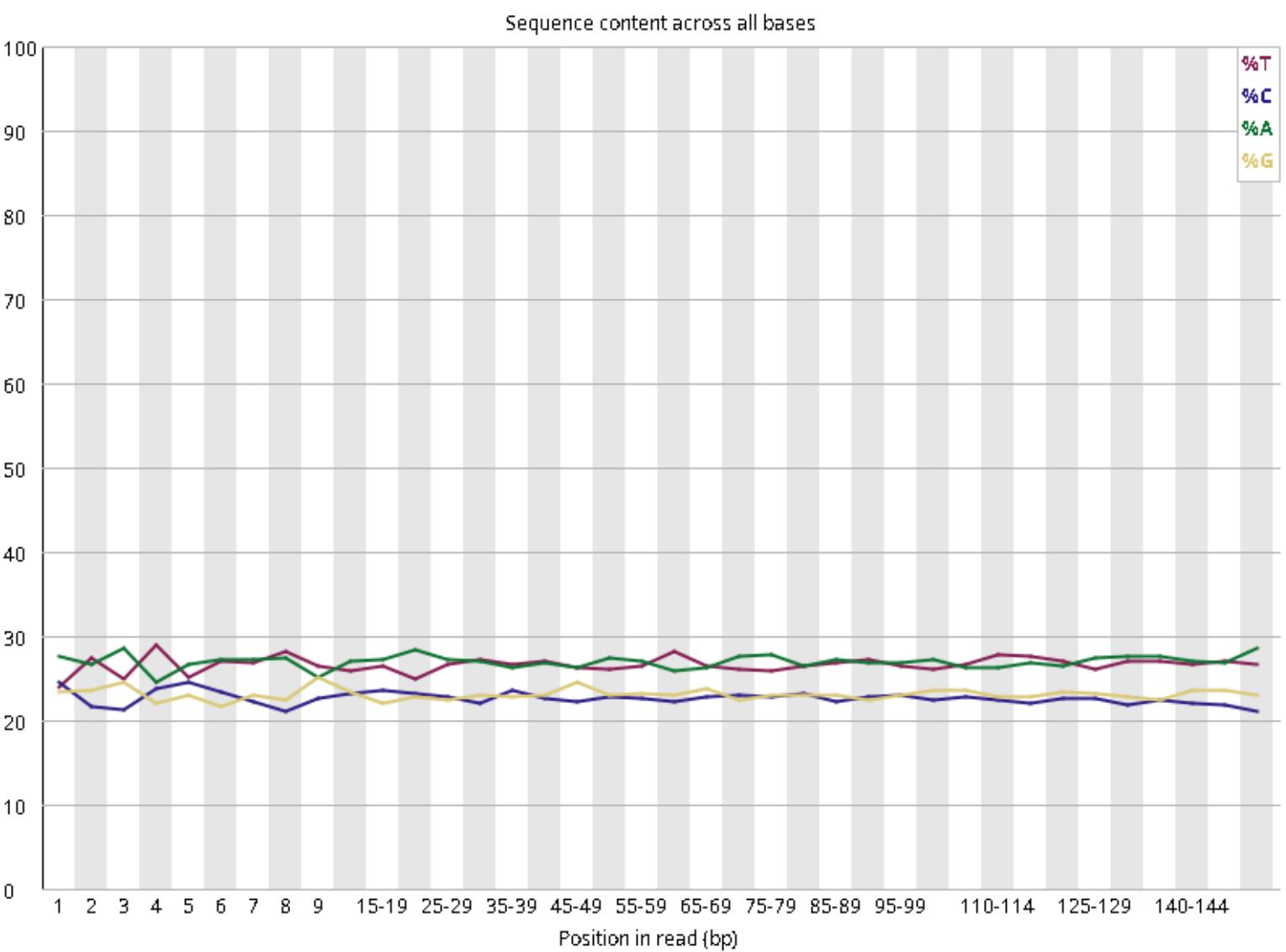
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



Per sequence quality scores



Per base sequence content

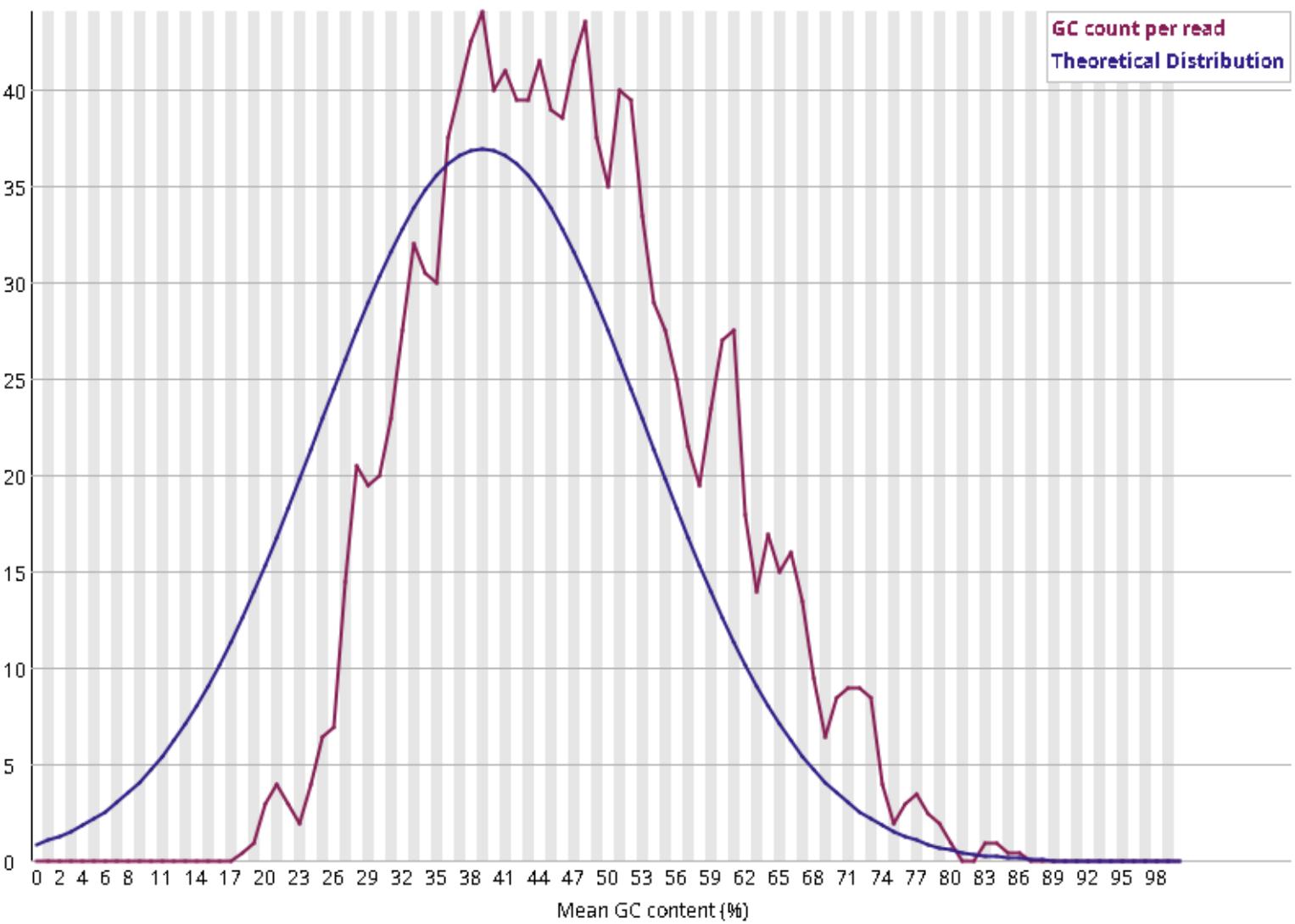




Per sequence GC content

GC distribution over all sequences

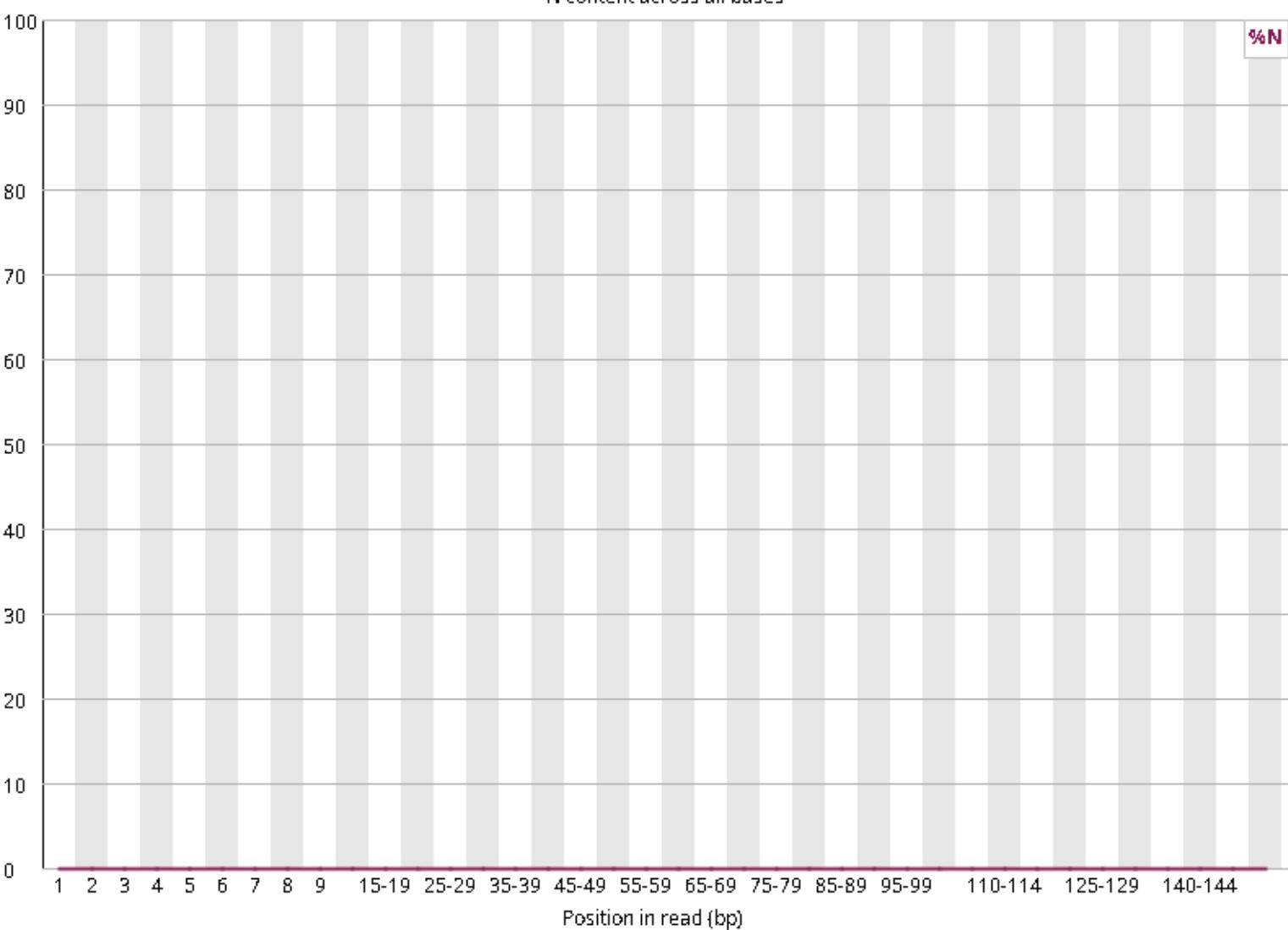
GC count per read
Theoretical Distribution





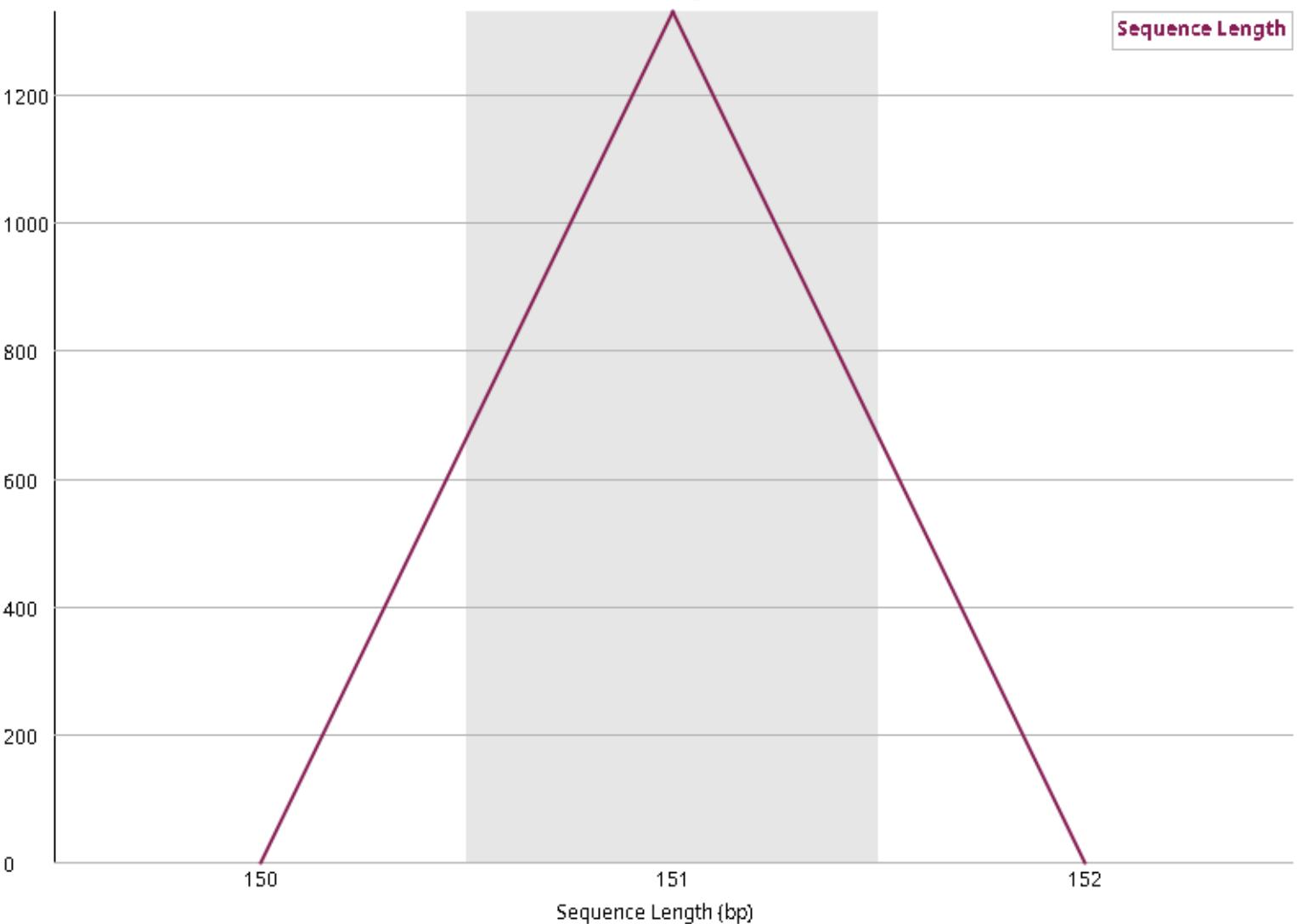
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

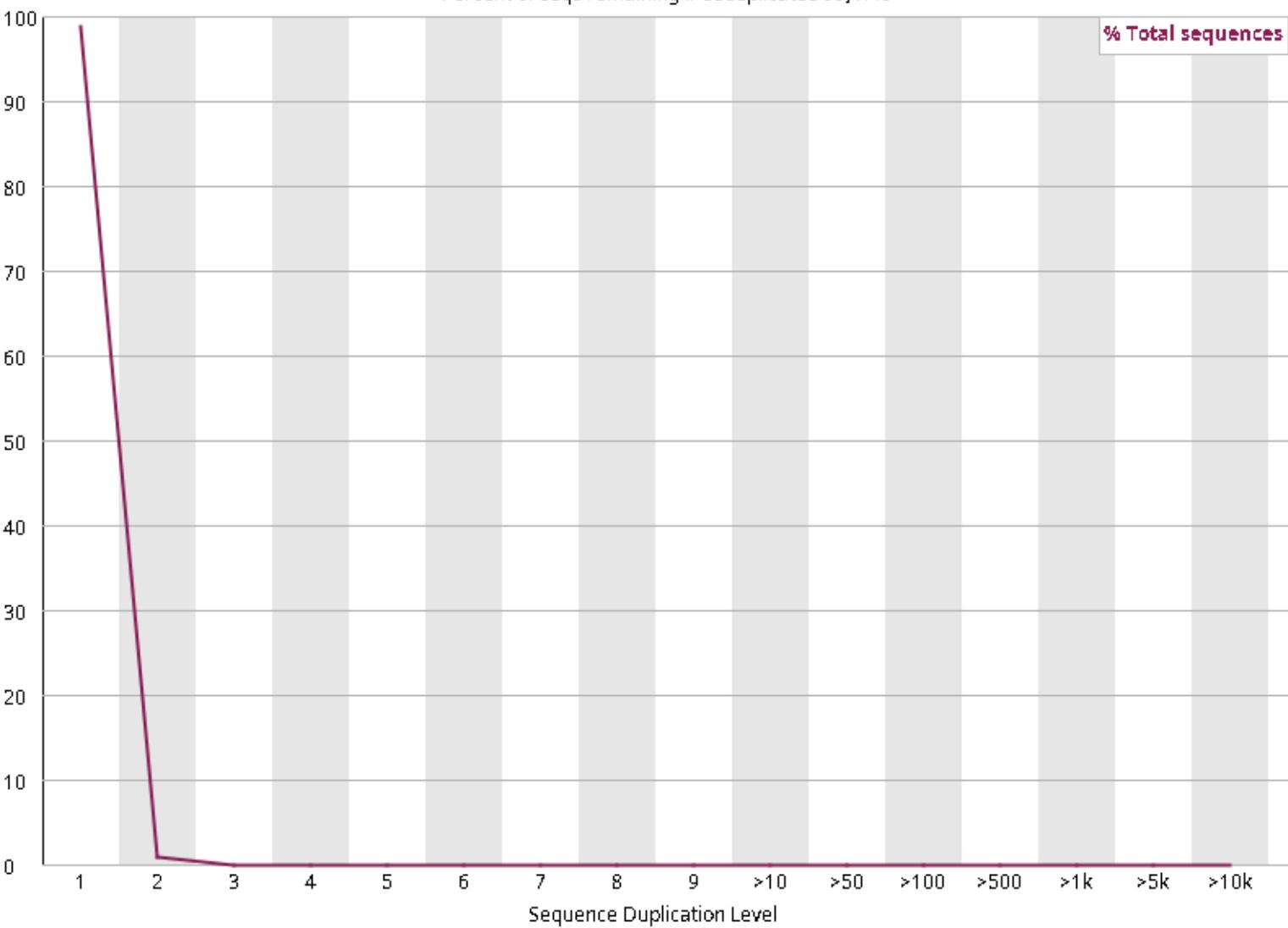


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,47%

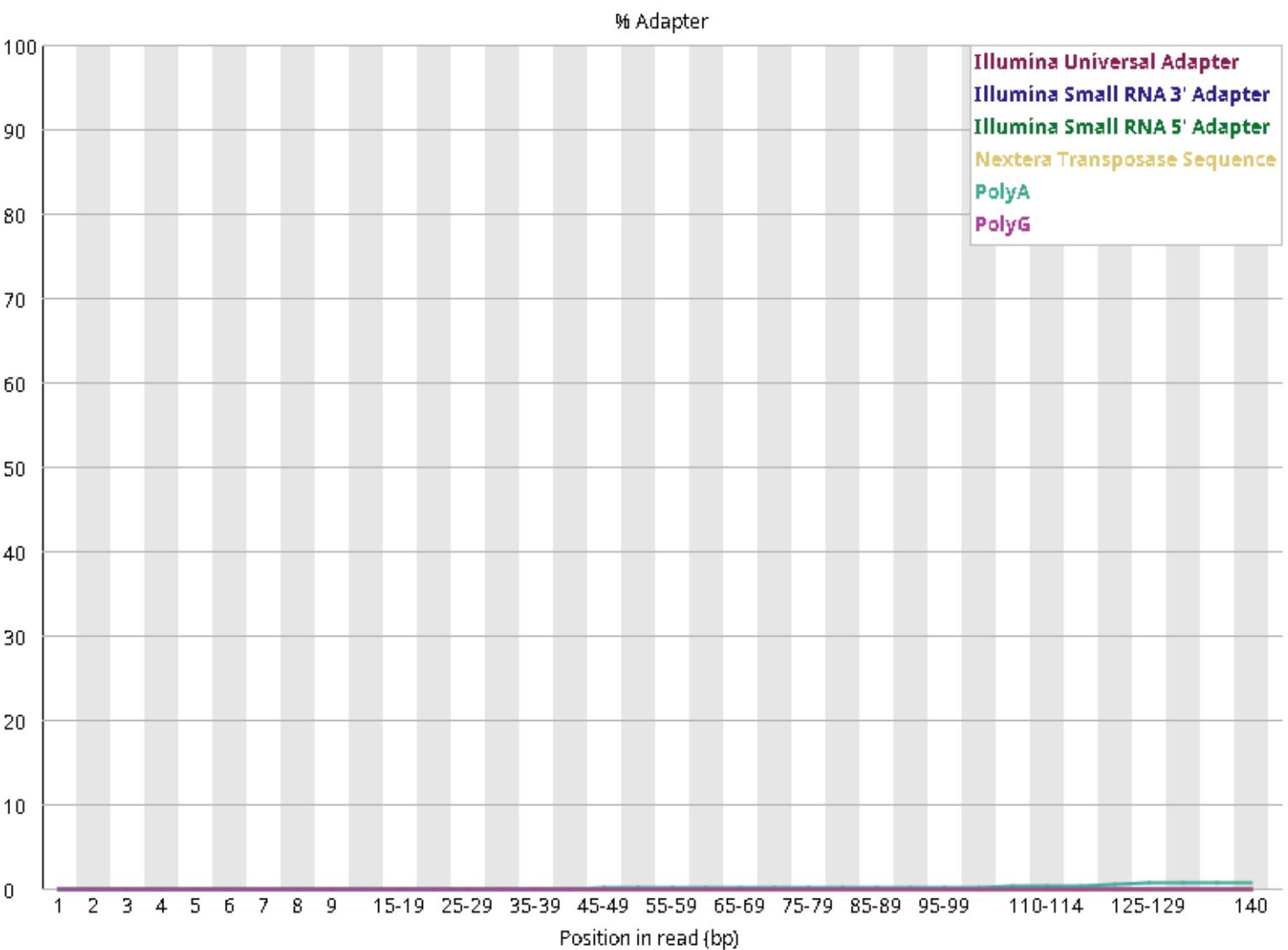


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGATCGTCATTACCGGGTGGTACTGTCAGCACTTCGCTGCCCTTAAG	2	0.15060240963855423	No Hit
TGGTGTGTTCTTATTATCTTGAGGGATTTCAGTACTGTATAGTAGAGGG	2	0.15060240963855423	No Hit
GCGACGAGCAGCCTCTGACCGAGAACCCCCGGAAGTACGTATGGGCAC	2	0.15060240963855423	No Hit
CTCAGGTTGGGCAGGGACTCCTCTCTGTGGGTCTATCTGGGCAC	2	0.15060240963855423	No Hit
TAATGGCAAAAGACCTACCAAGAATTGGCATTCAGTCAGGATGCT	2	0.15060240963855423	No Hit
TAAGAAAATACATAAGACCATAACAGCCAACAGGTGGCAGGACCAGGACT	2	0.15060240963855423	No Hit
AGCTTCTACTACTTCTCCGCCACGTAGAAAAACTGGCACGGACACTTT	2	0.15060240963855423	No Hit



Adapter Content



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