

## Summary

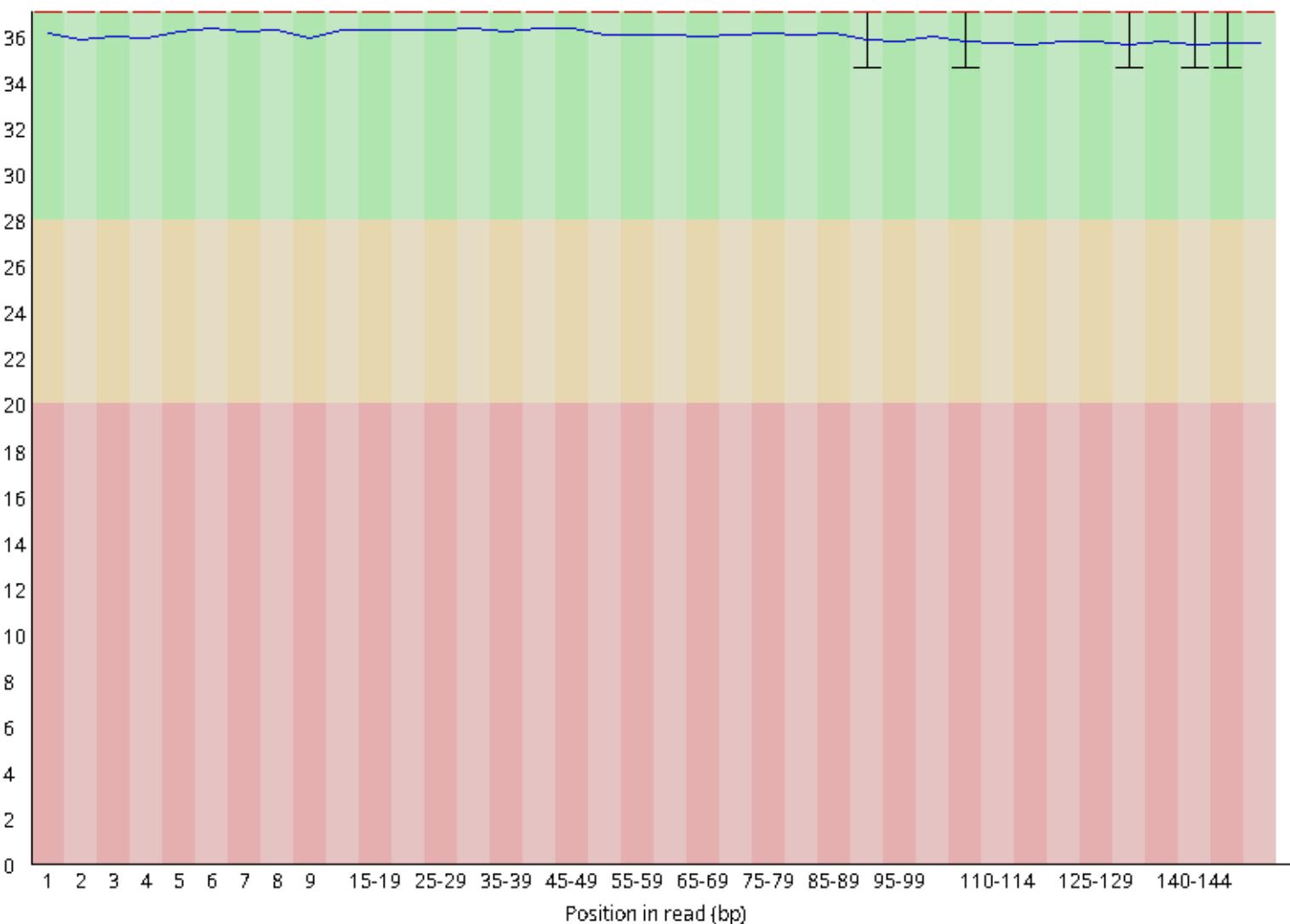
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## Basic Statistics

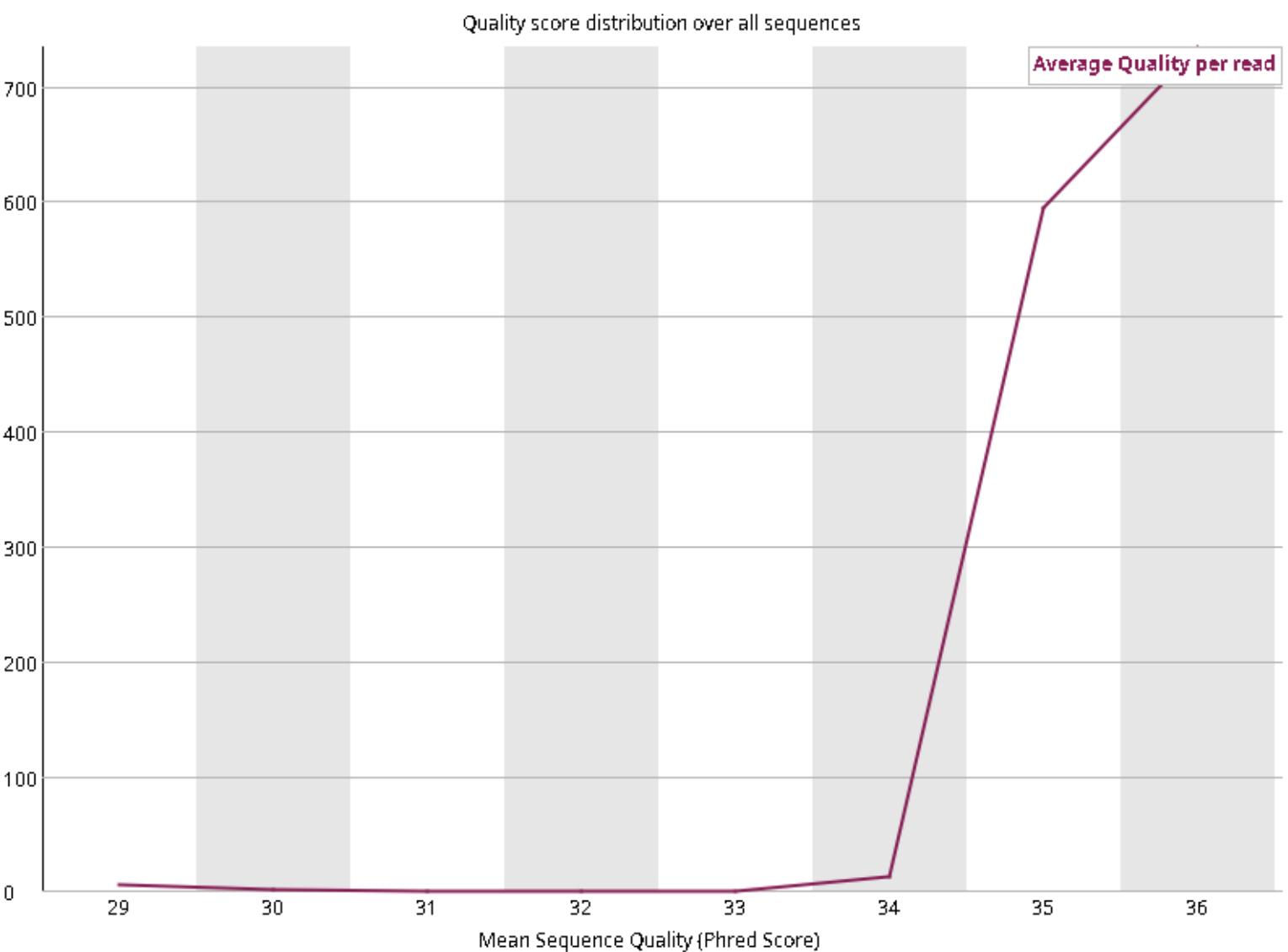
Measure	Value
Filename	MargeSimpson_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1352
Total Bases	204.1 kbp
Sequences flagged as poor quality	0
Sequence length	151
%GC	46

## Per base sequence quality

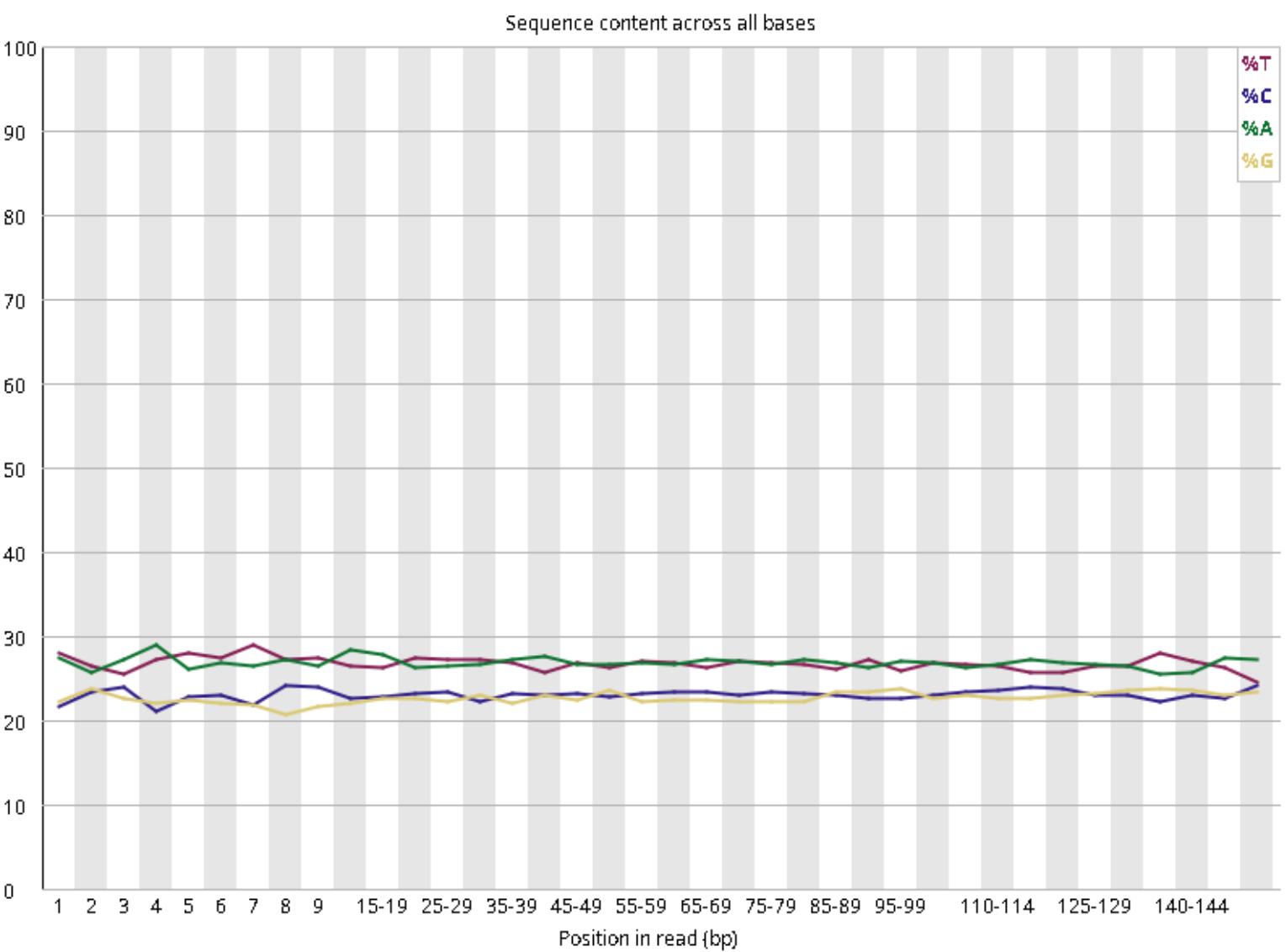
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



## Per sequence quality scores

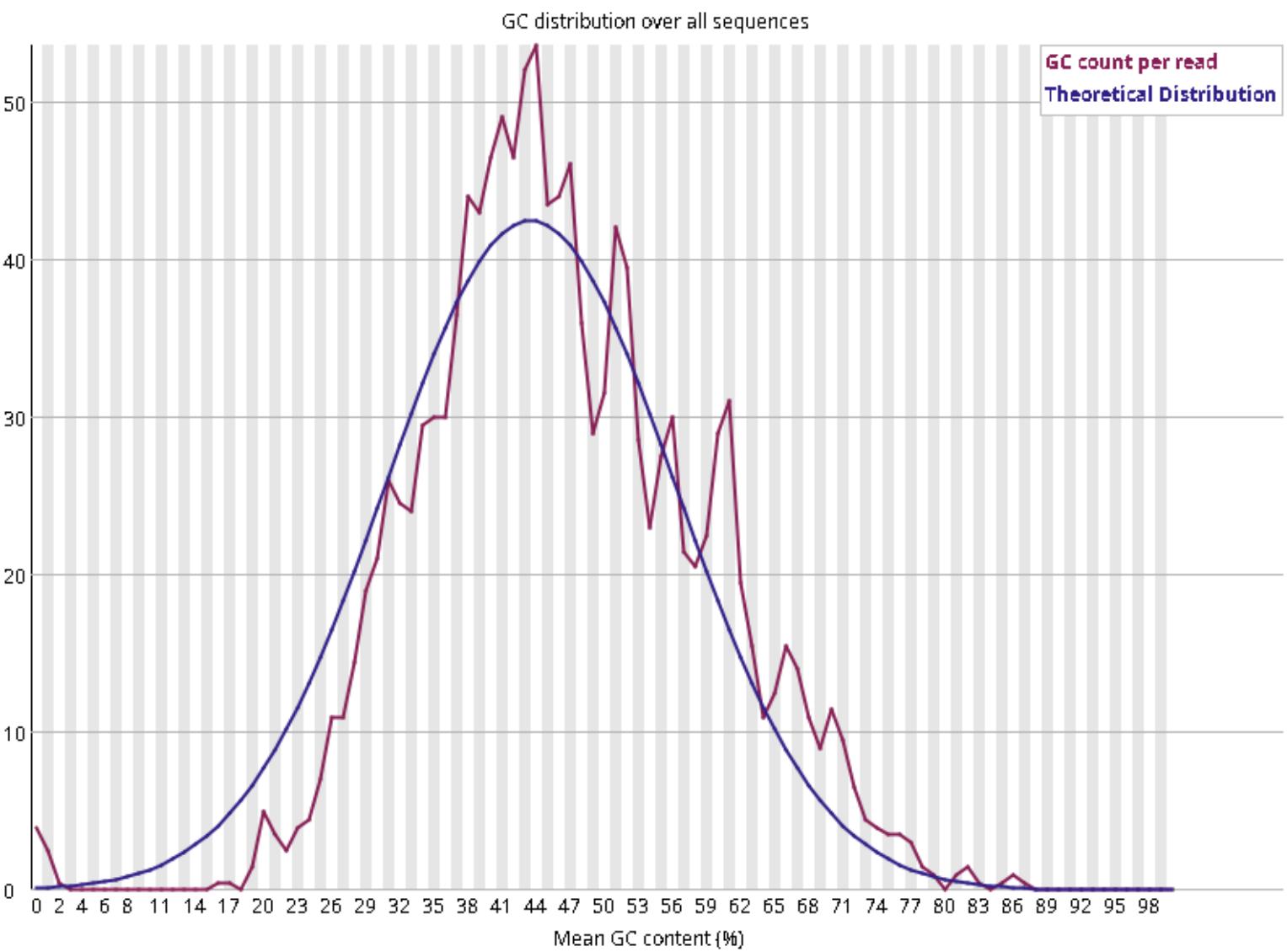


## Per base sequence content





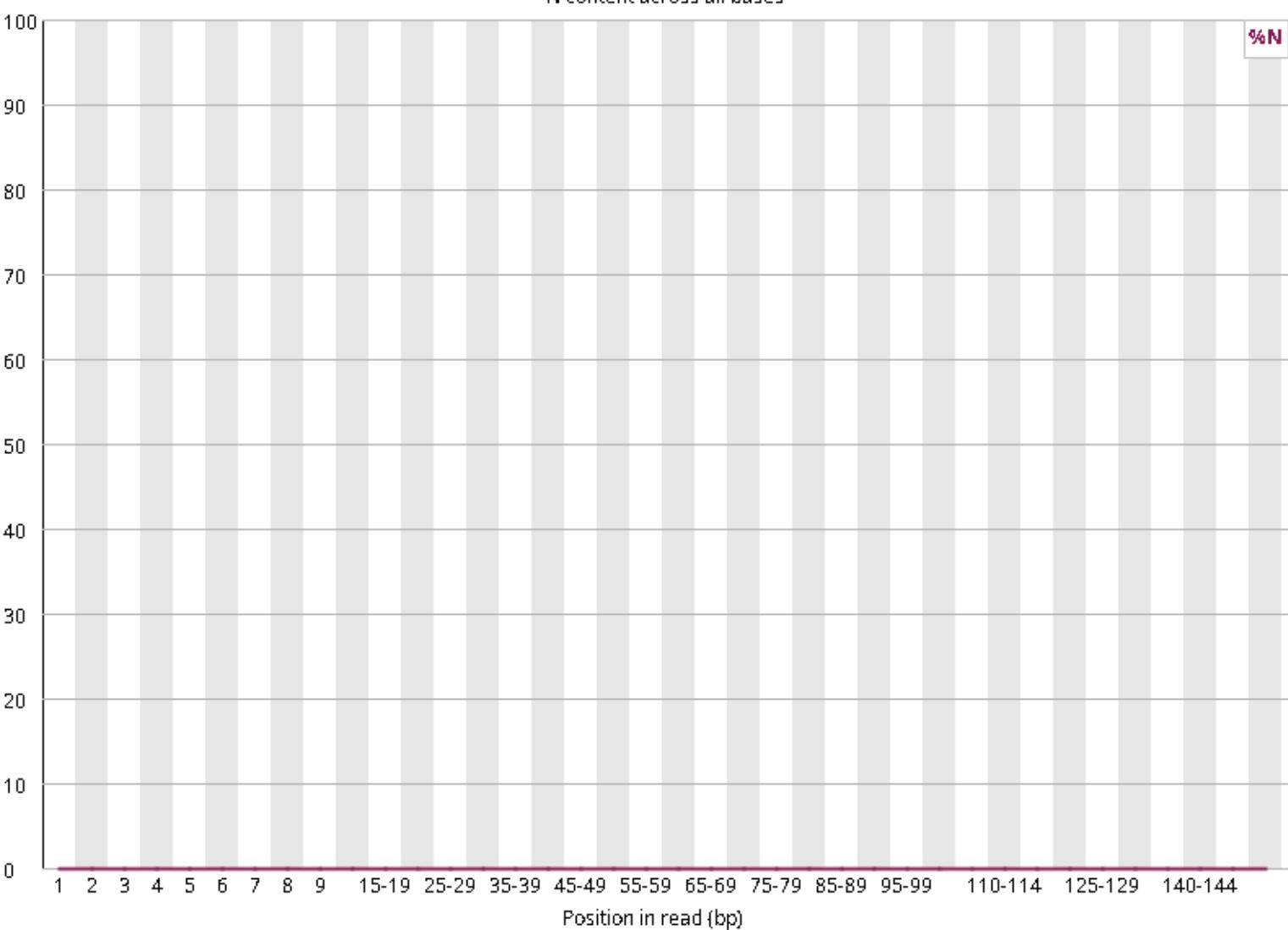
## Per sequence GC content





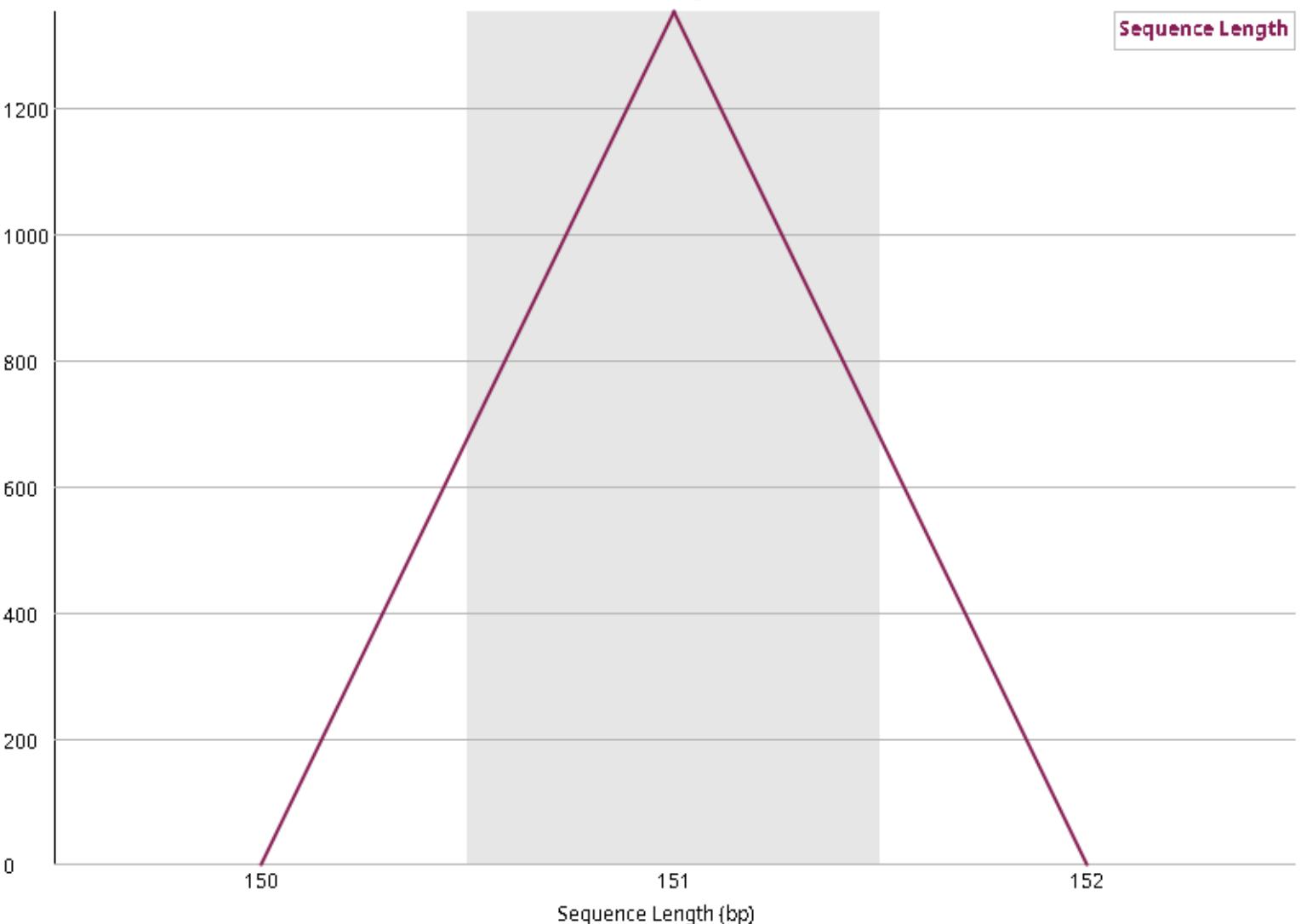
## Per base N content

N content across all bases



## Sequence Length Distribution

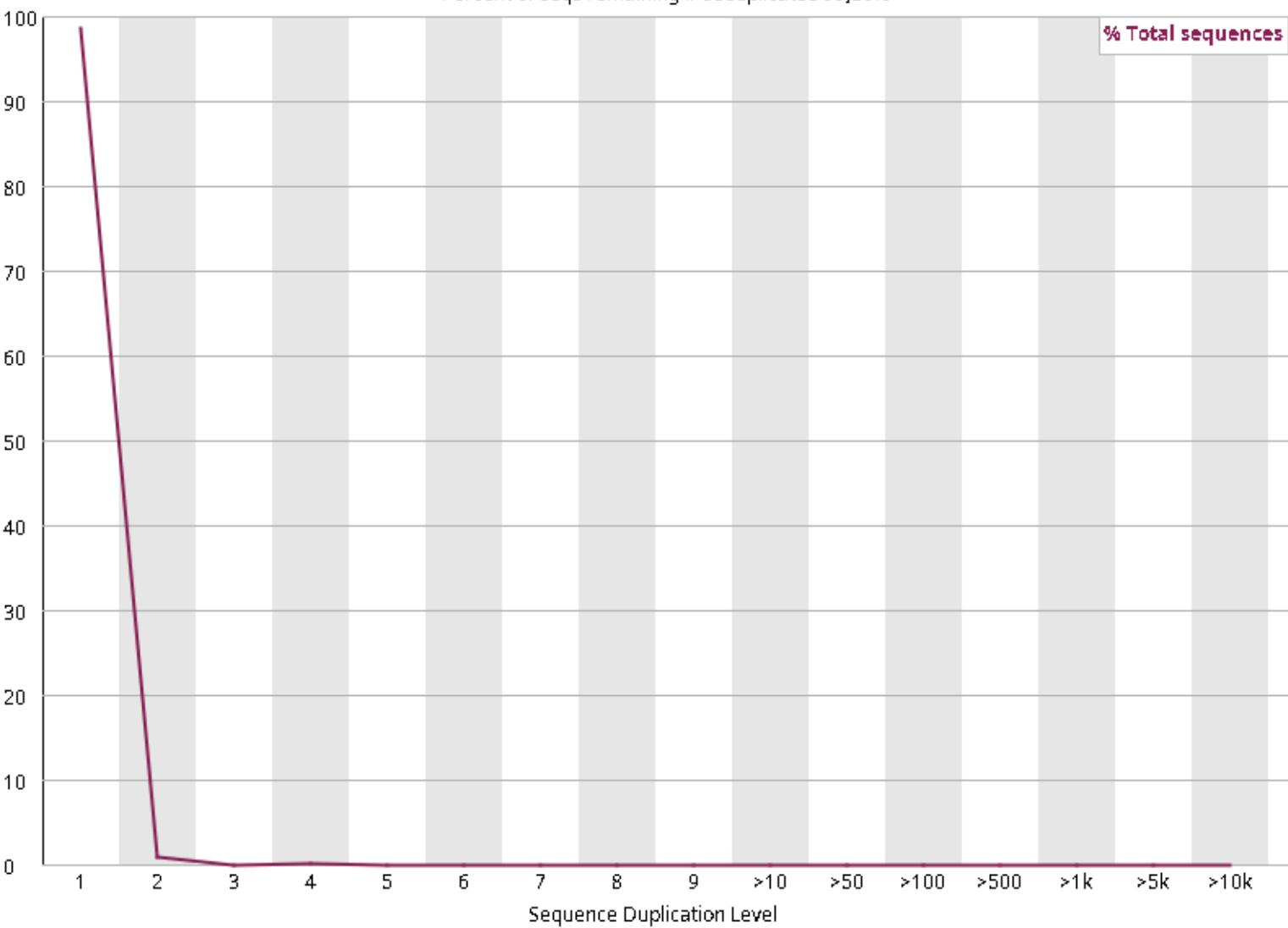
Distribution of sequence lengths over all sequences





## Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,26%



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	4	0.2958579881656805	No Hit
TCGTCAGAACGGCAACTTTTCTAGAGCACATTCA	2	0.14792899408284024	No Hit
TGAAGTATTGCACCAAGAACAGTGTATTGATGGC	2	0.14792899408284024	No Hit
TGATTAATAAAAGGATATAGCTGCTCAGTCTGGTG	2	0.14792899408284024	No Hit
TGCAGAGAAGTGTGCATCCCACGGTGGTGGAGTT	2	0.14792899408284024	No Hit
TAAATAATTATTCCTATTATTAAGTATCATGCCAT	2	0.14792899408284024	No Hit
AGGCAGTGCCAGCAGCAGGGCACAGCTCAGCACCG	2	0.14792899408284024	No Hit

Sequence	Count	Percentage	Possible Source
ATATTTGAGGAGAGTTACTTGGTCGTTCAAGTCAAGATTACAAAACCAG	2	0.14792899408284024	No Hit



## Adapter Content

