












# FastQC Report

## Summary

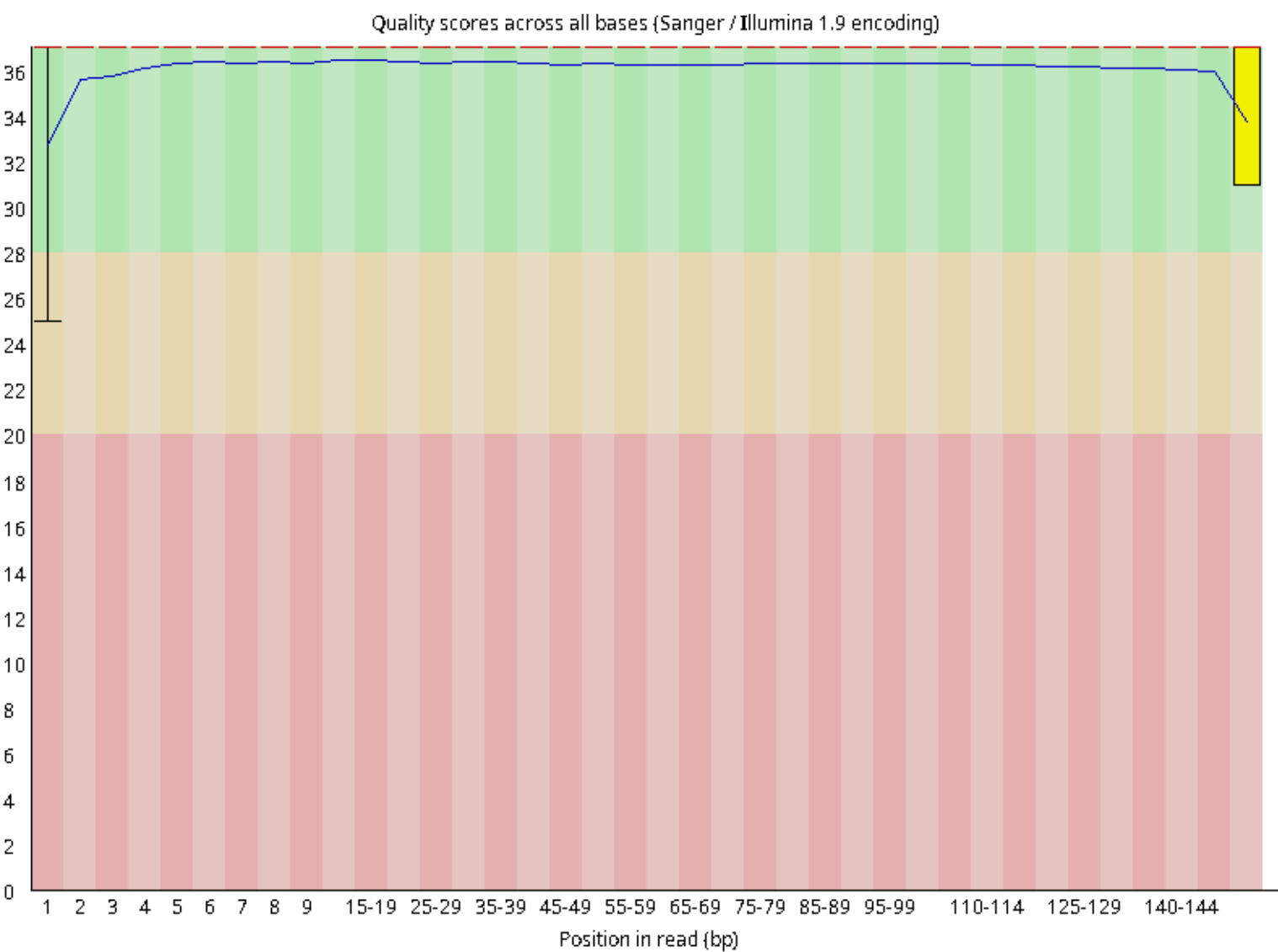
Mon 9 Jun 2025  
SRR33784444\_1\_paird.fastq

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## Basic Statistics

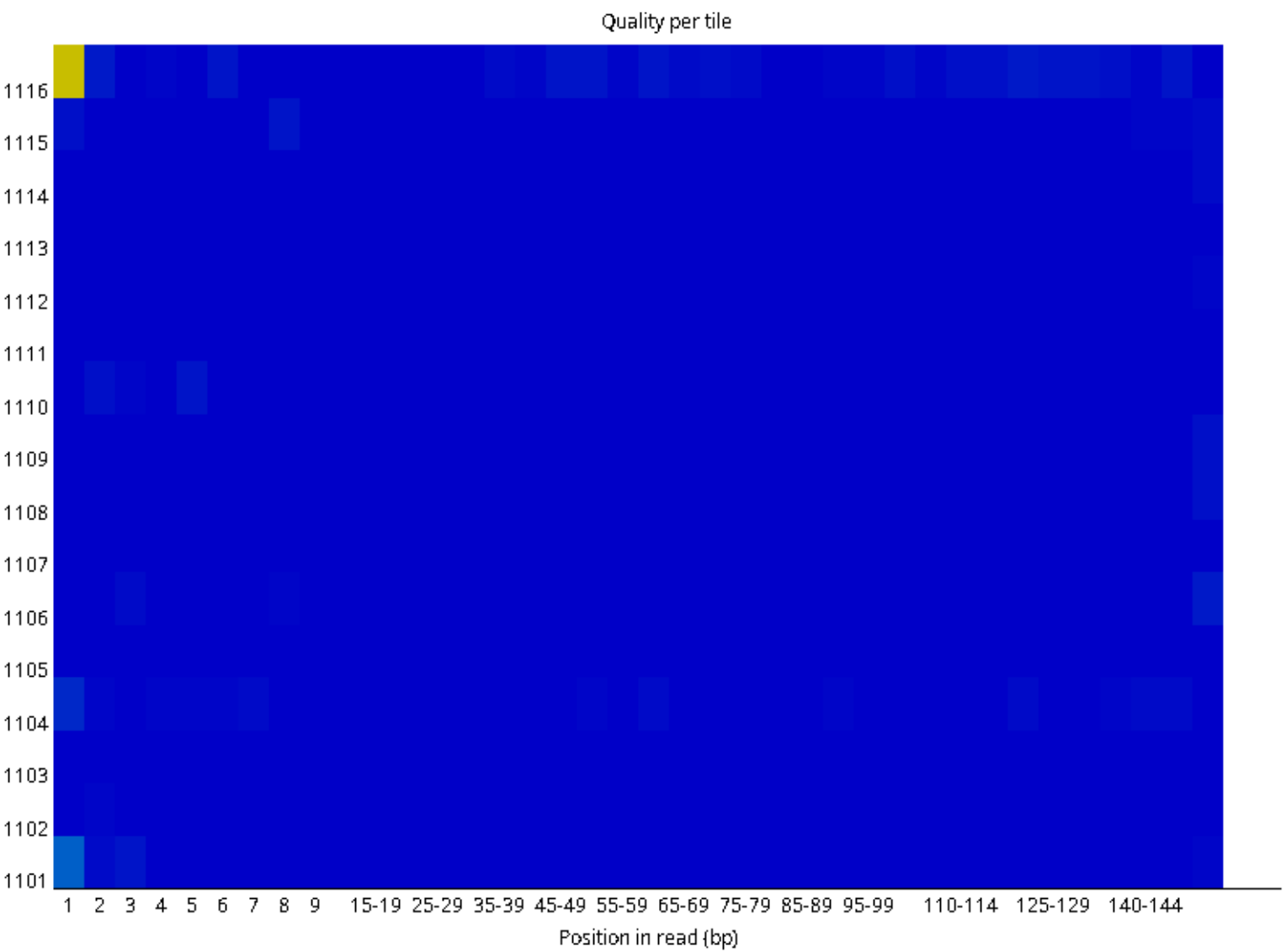
Measure	Value
Filename	SRR33784444_1_paird.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	49186
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	44

## ✔ Per base sequence quality

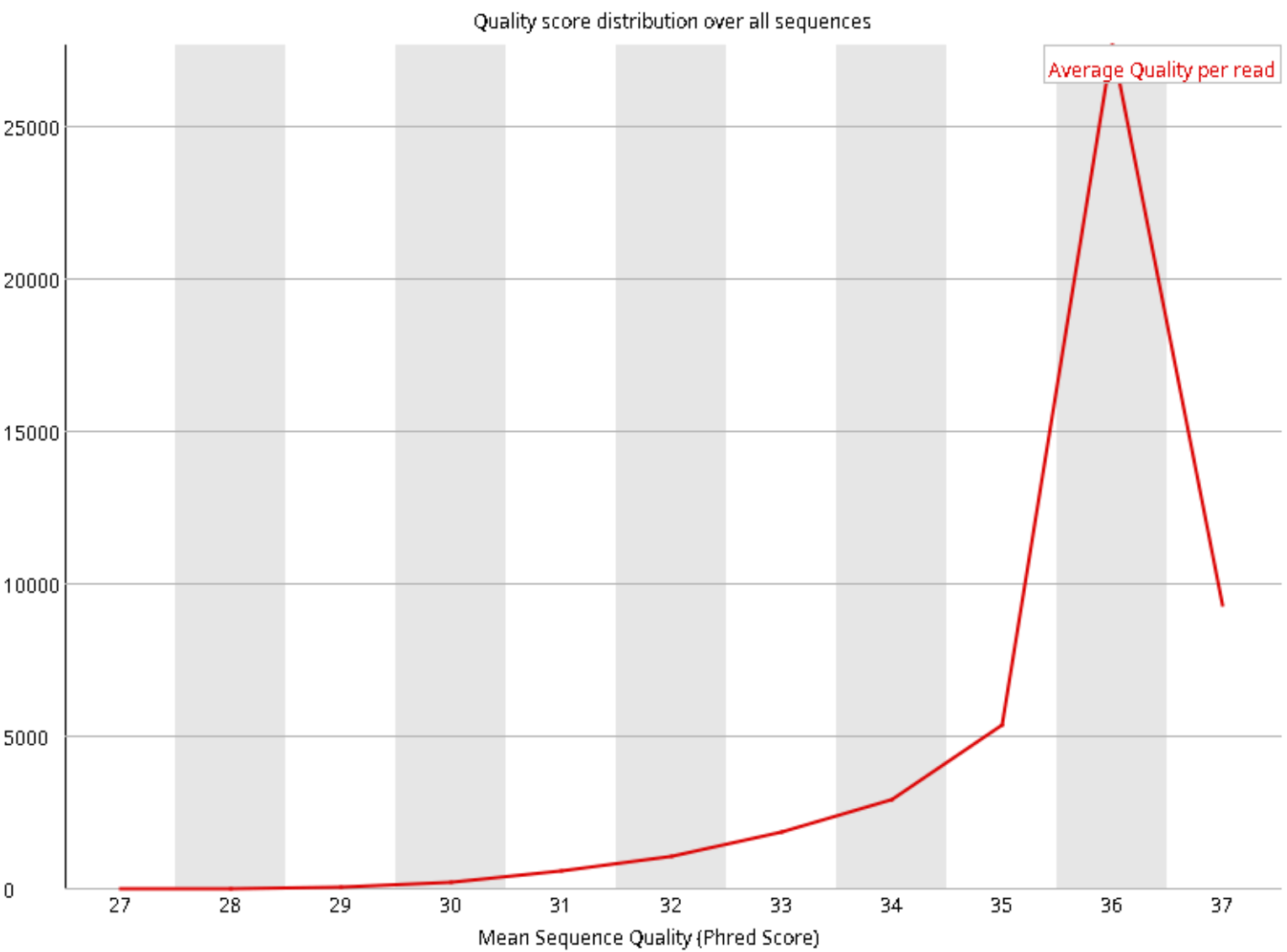




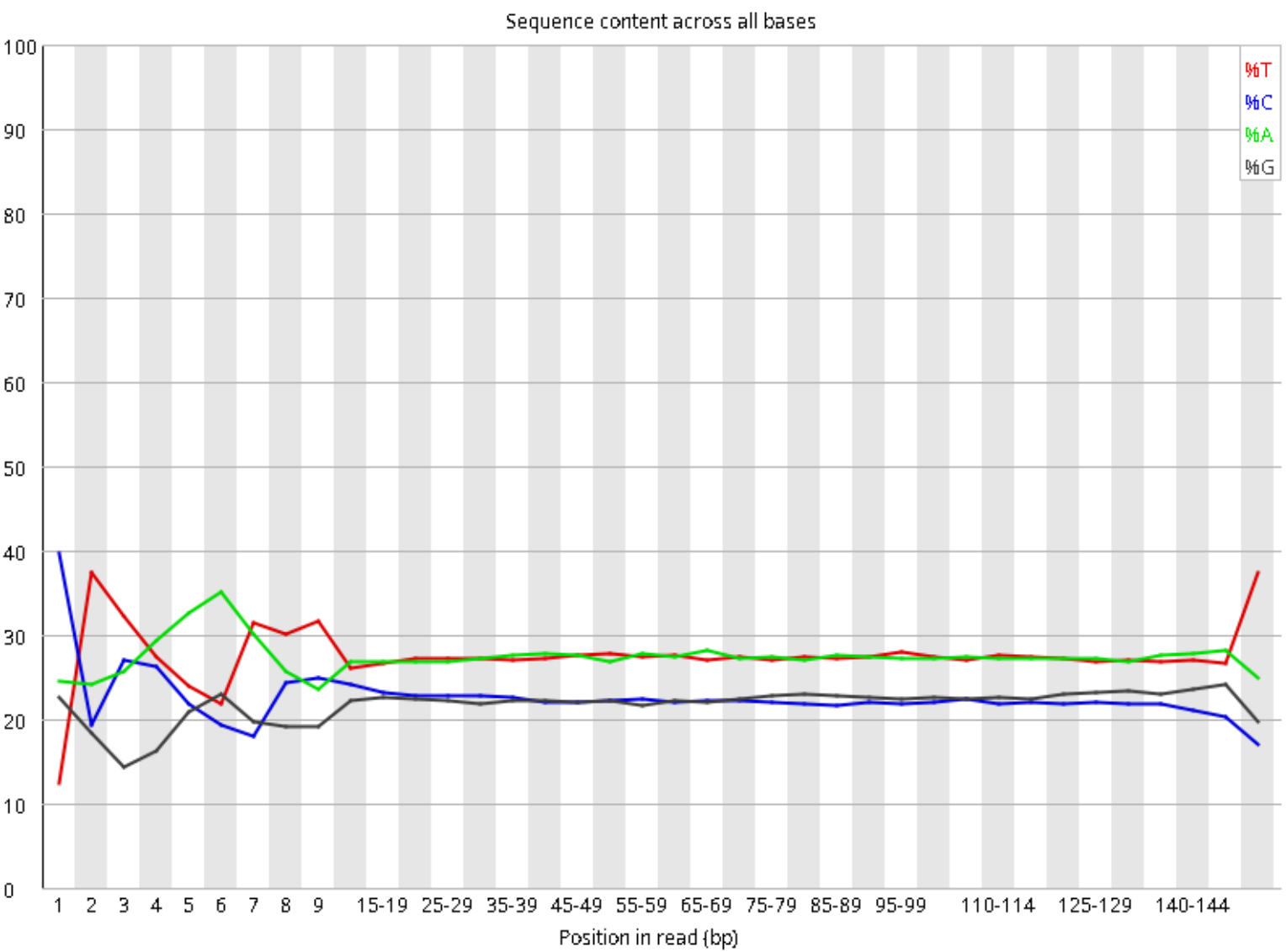
## ! Per tile sequence quality



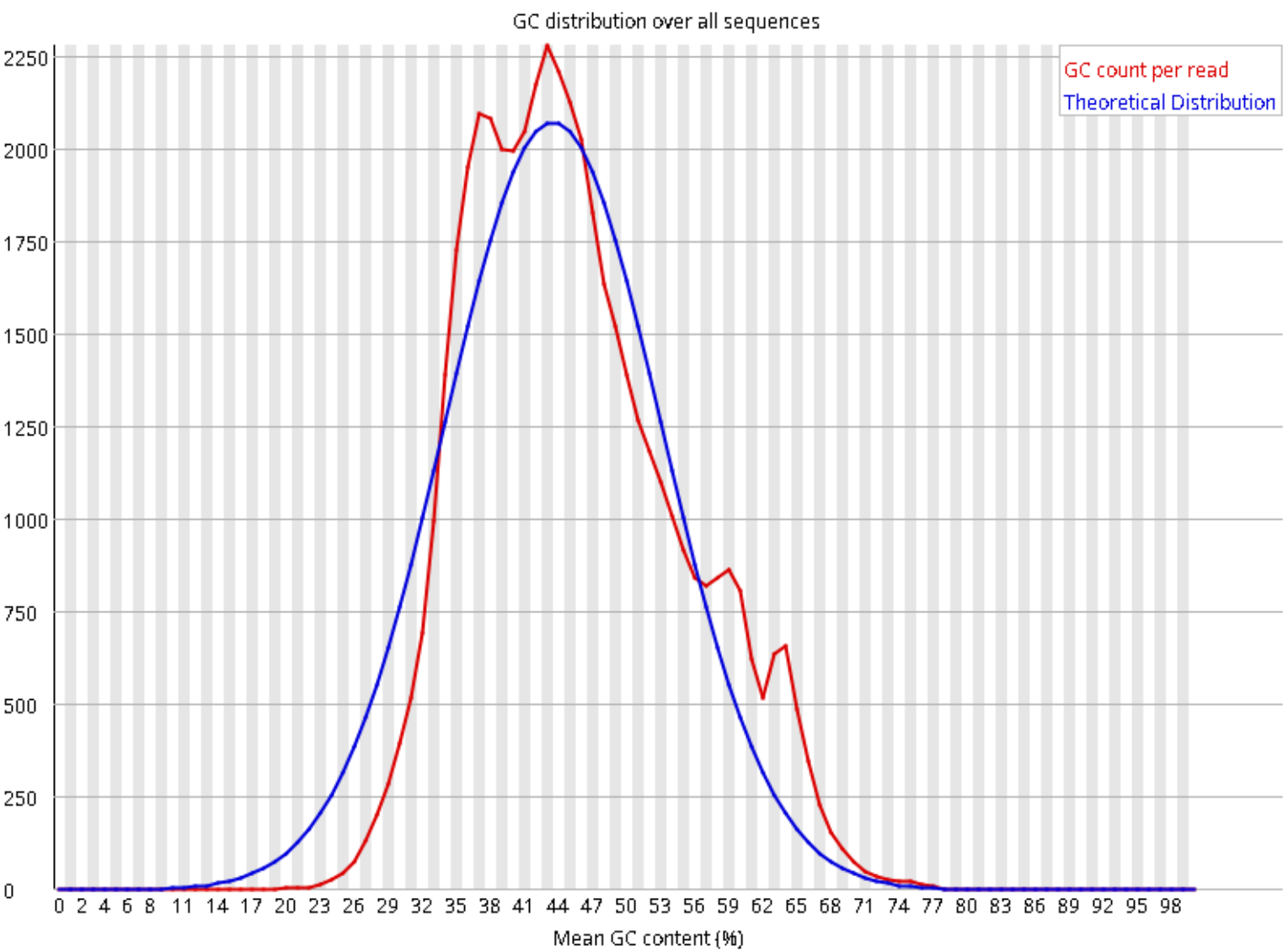
## Per sequence quality scores



## ! Per base sequence content

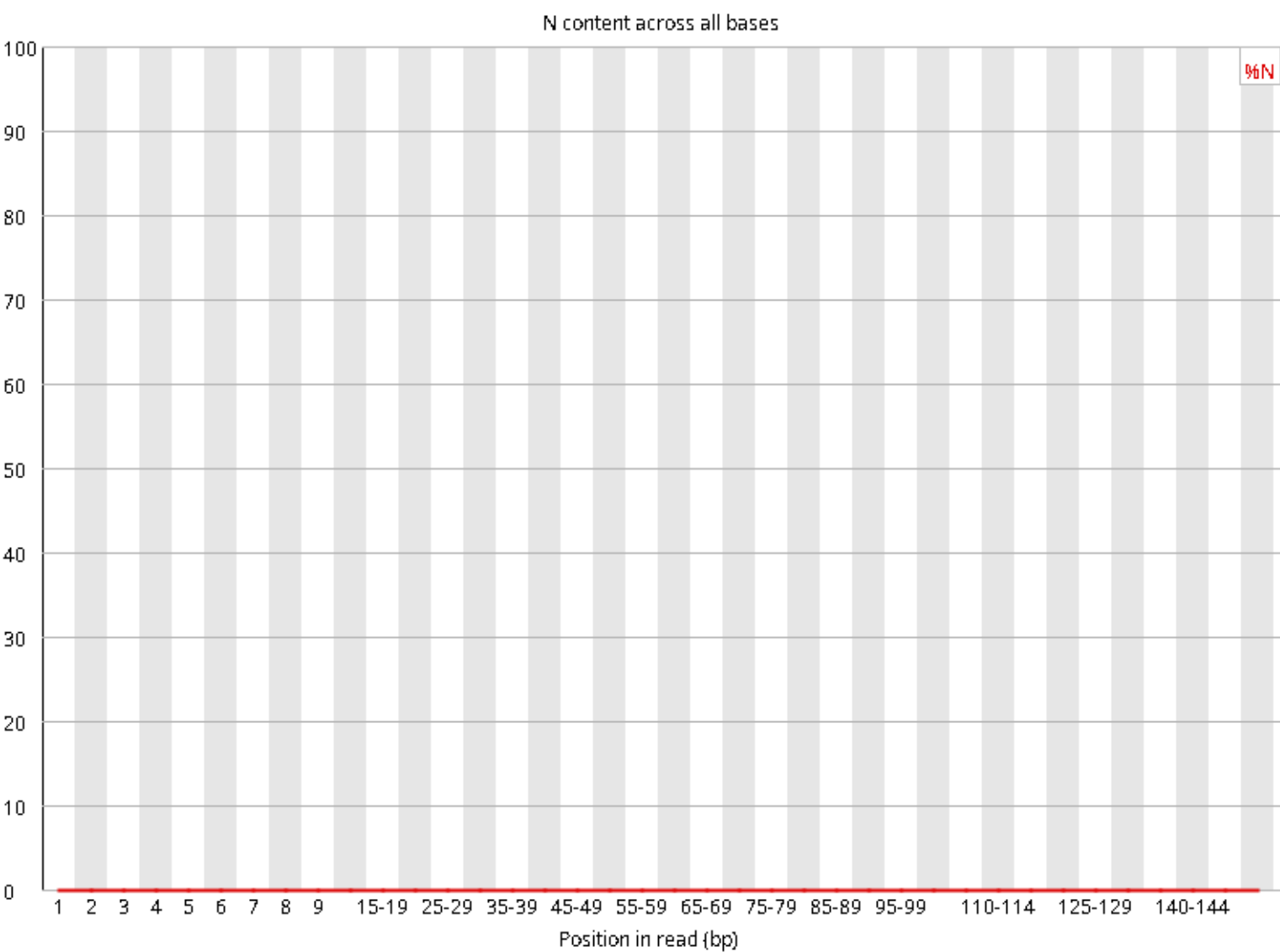


## ! Per sequence GC content

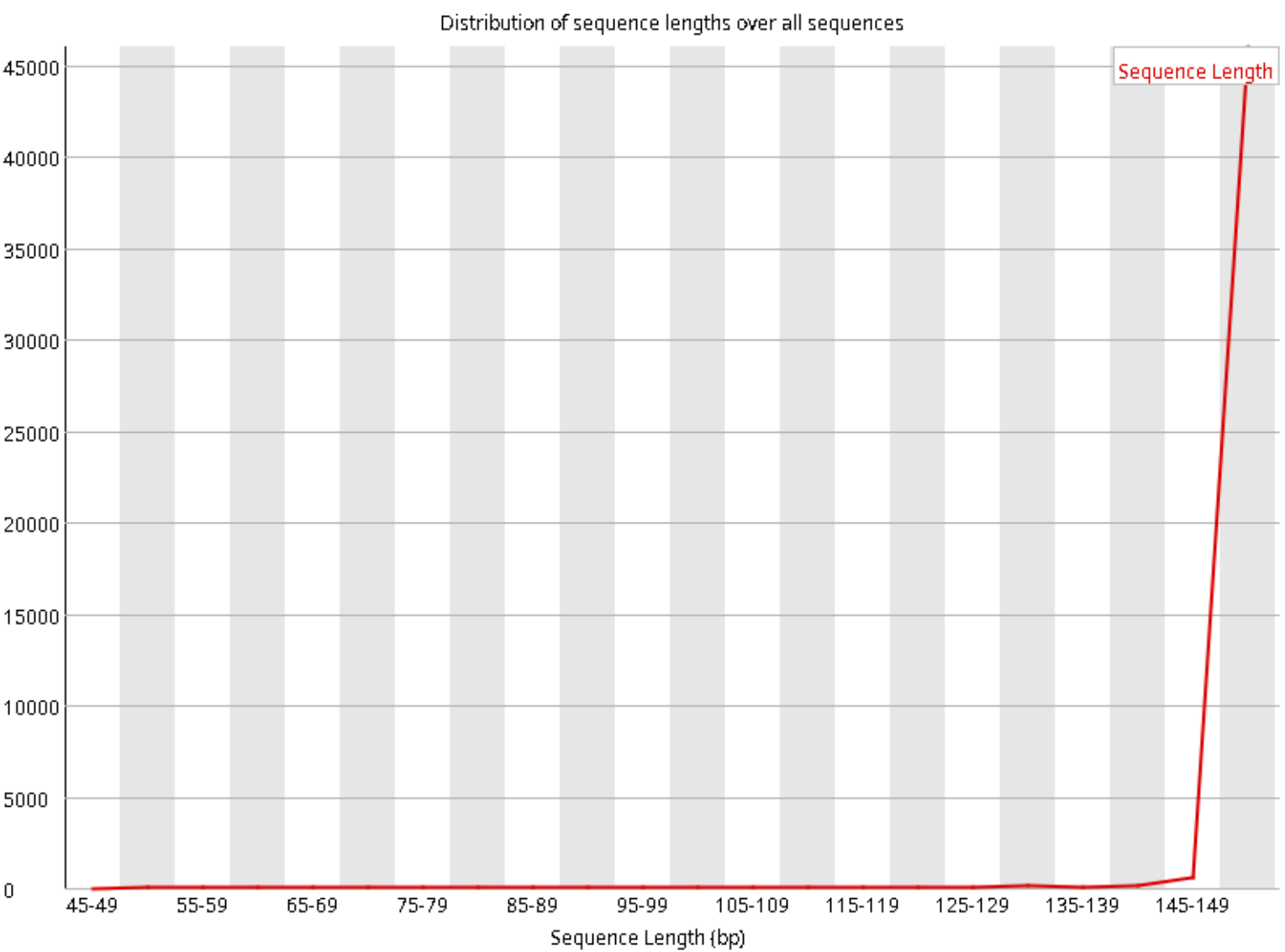




## Per base N content

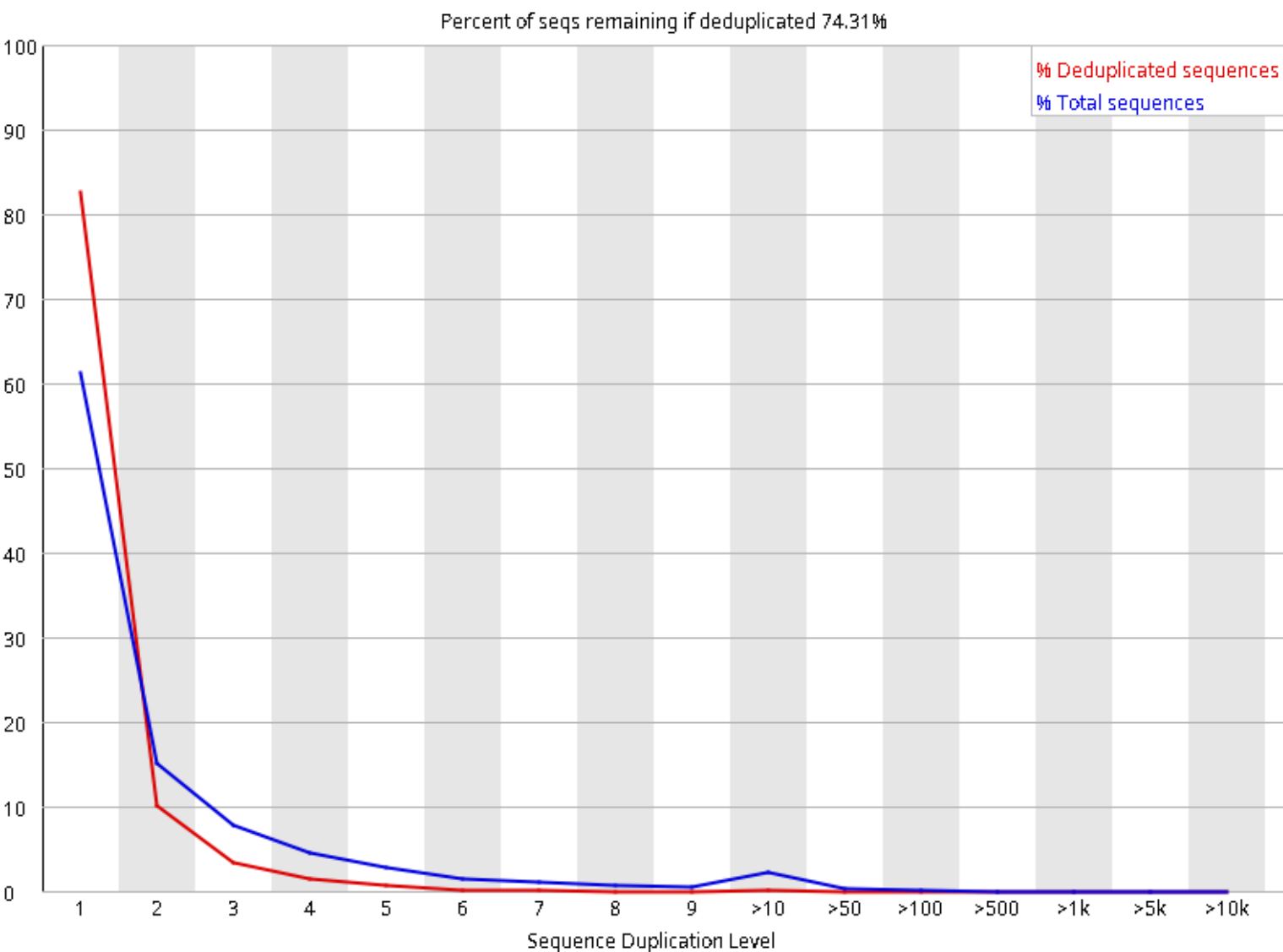


# Sequence Length Distribution





## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCGGTATTATCTCGTAT	182	0.3700239905664213	TruSeq Adapter, Index 20 (97% over 37bp)
CCTCCAATTCTCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	76	0.1545155125442199	No Hit
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	67	0.13621762290082542	No Hit
CTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTATT	51	0.10368804131256862	No Hit
CTCCAATTCTCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTATT	50	0.10165494246330256	No Hit



## Adapter Content

