












FastQC Report

Summary

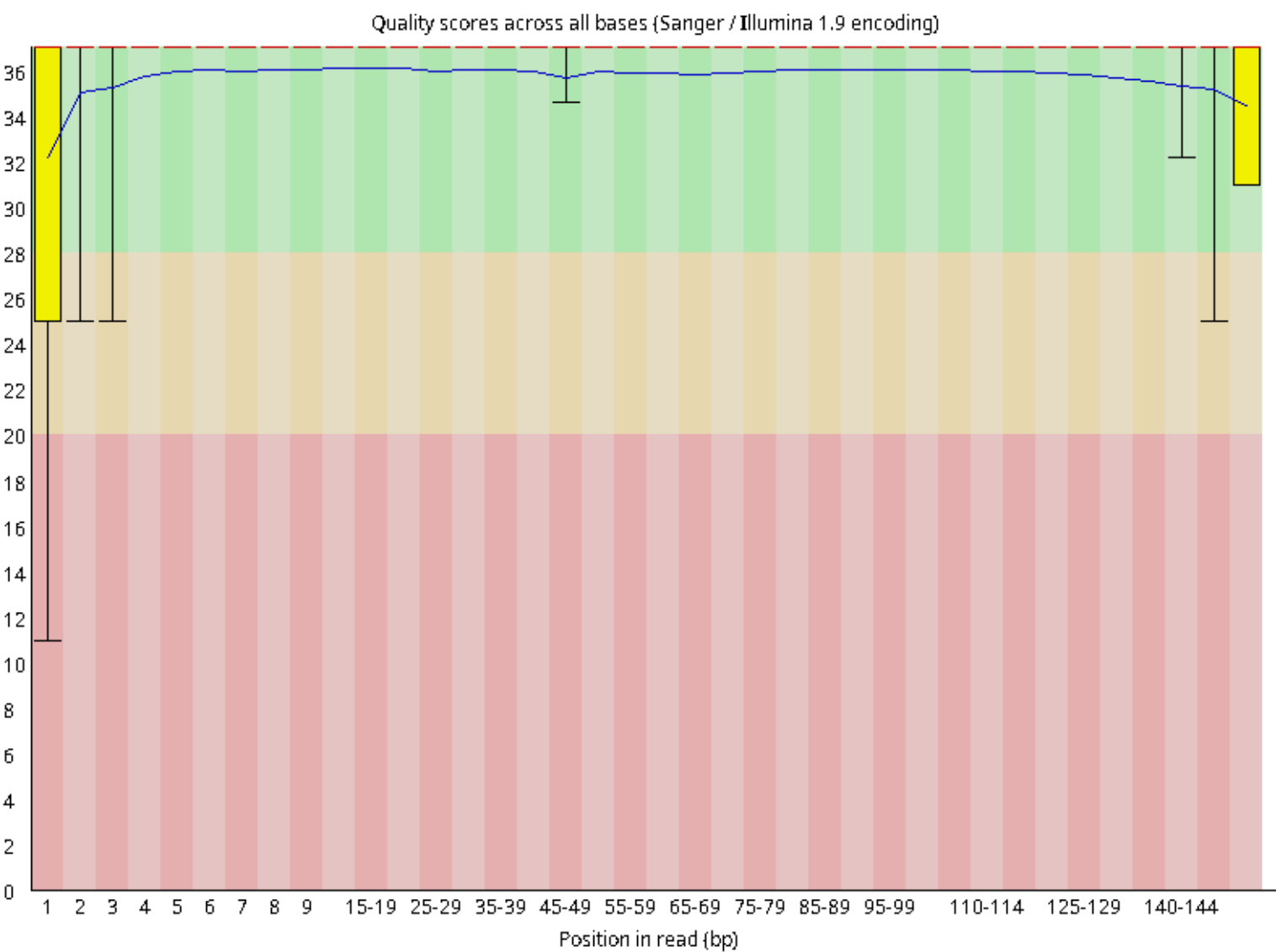
Mon 9 Jun 2025
SRR33784444_1_unpaired.fastq

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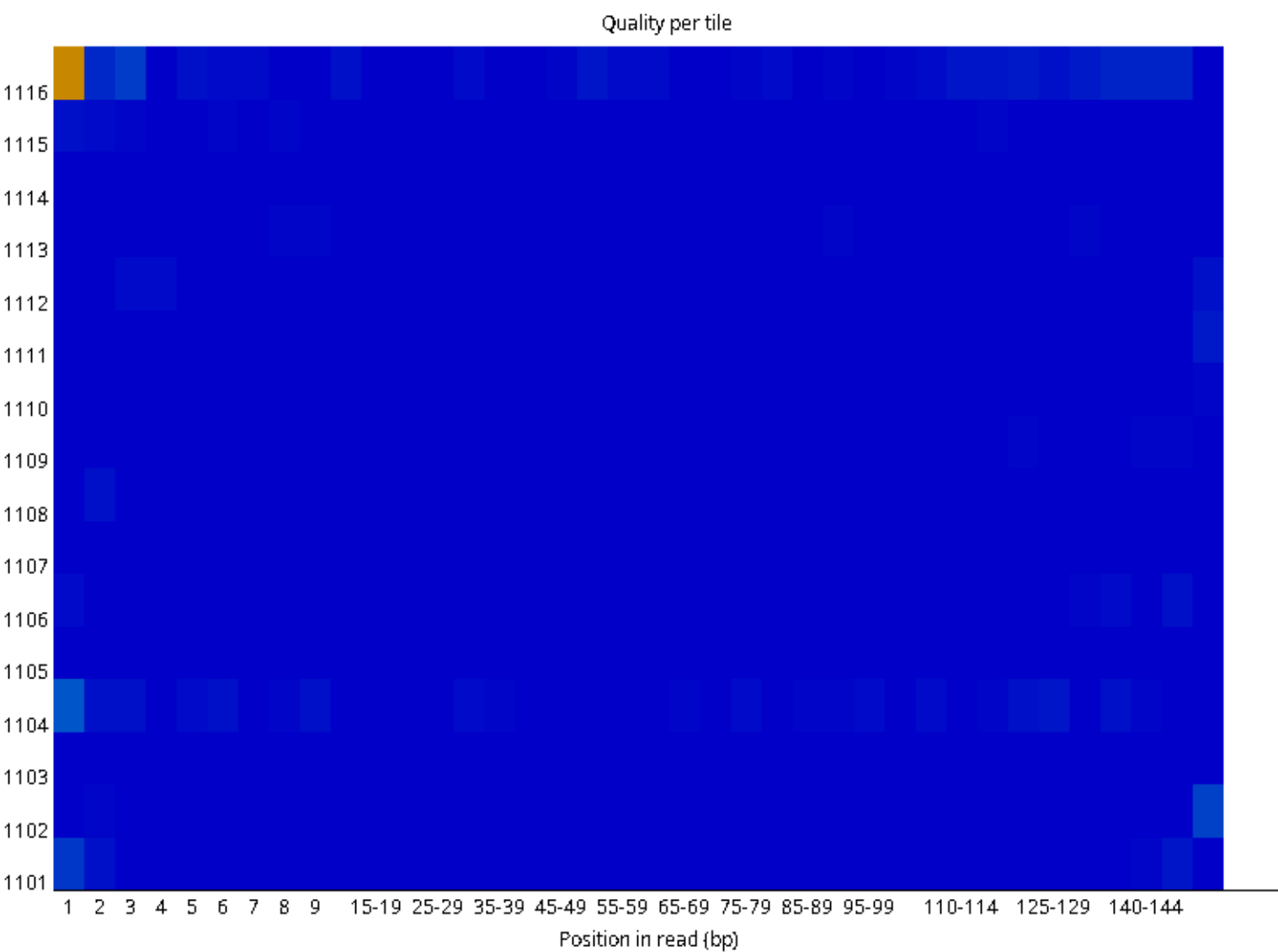
Basic Statistics

Measure	Value
Filename	SRR33784444_1_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	63122
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	46

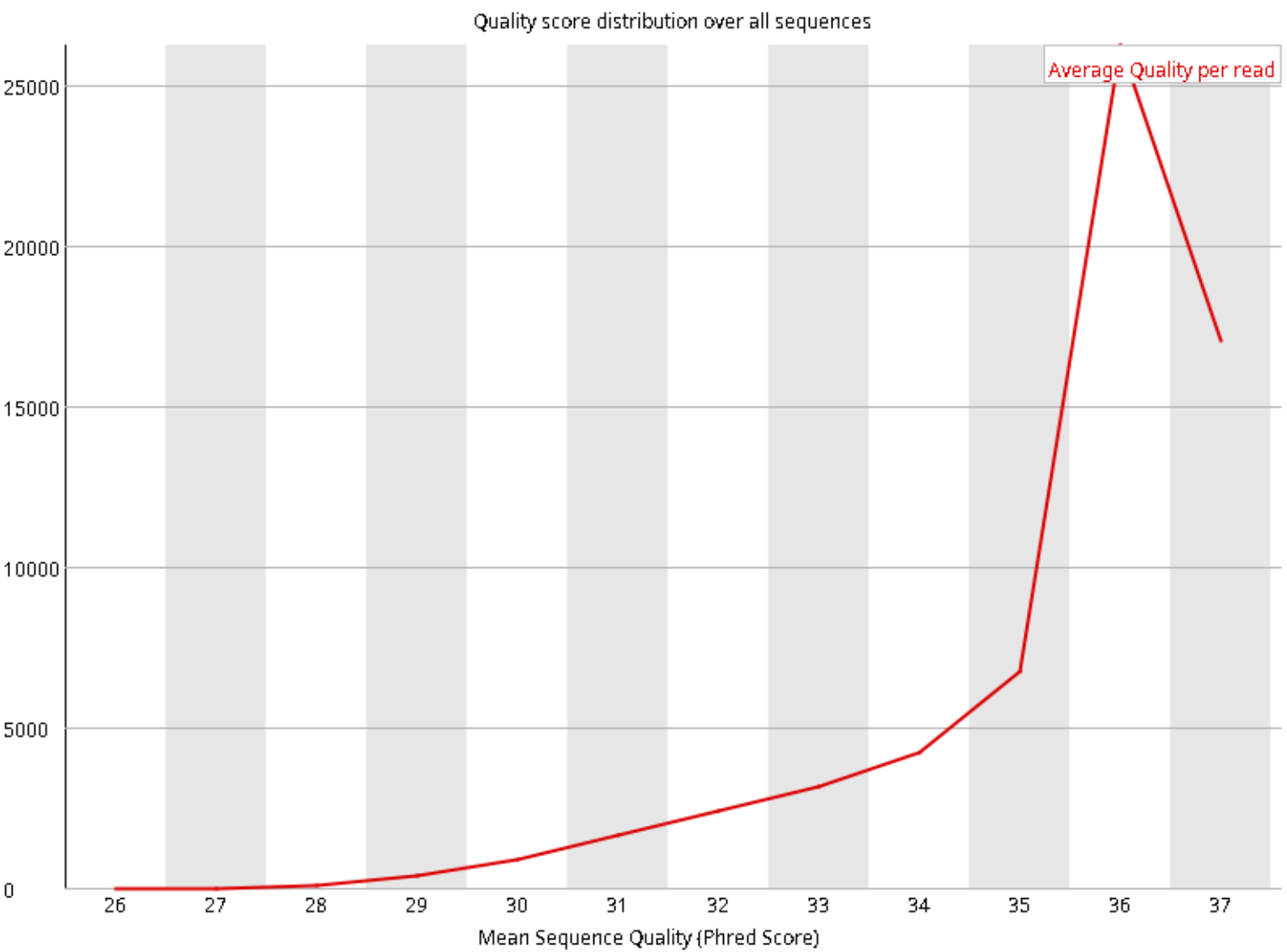
✔ Per base sequence quality



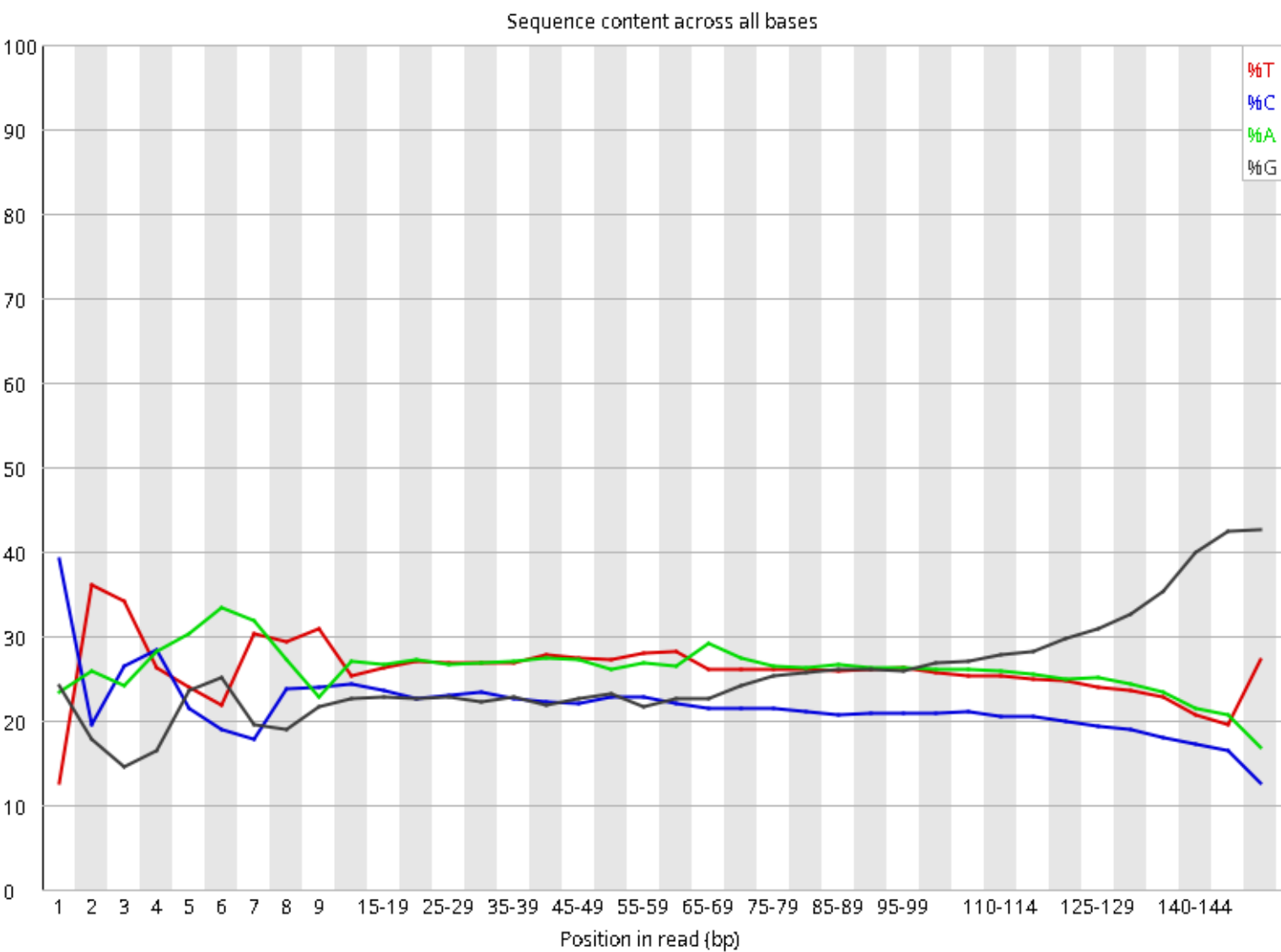
! Per tile sequence quality



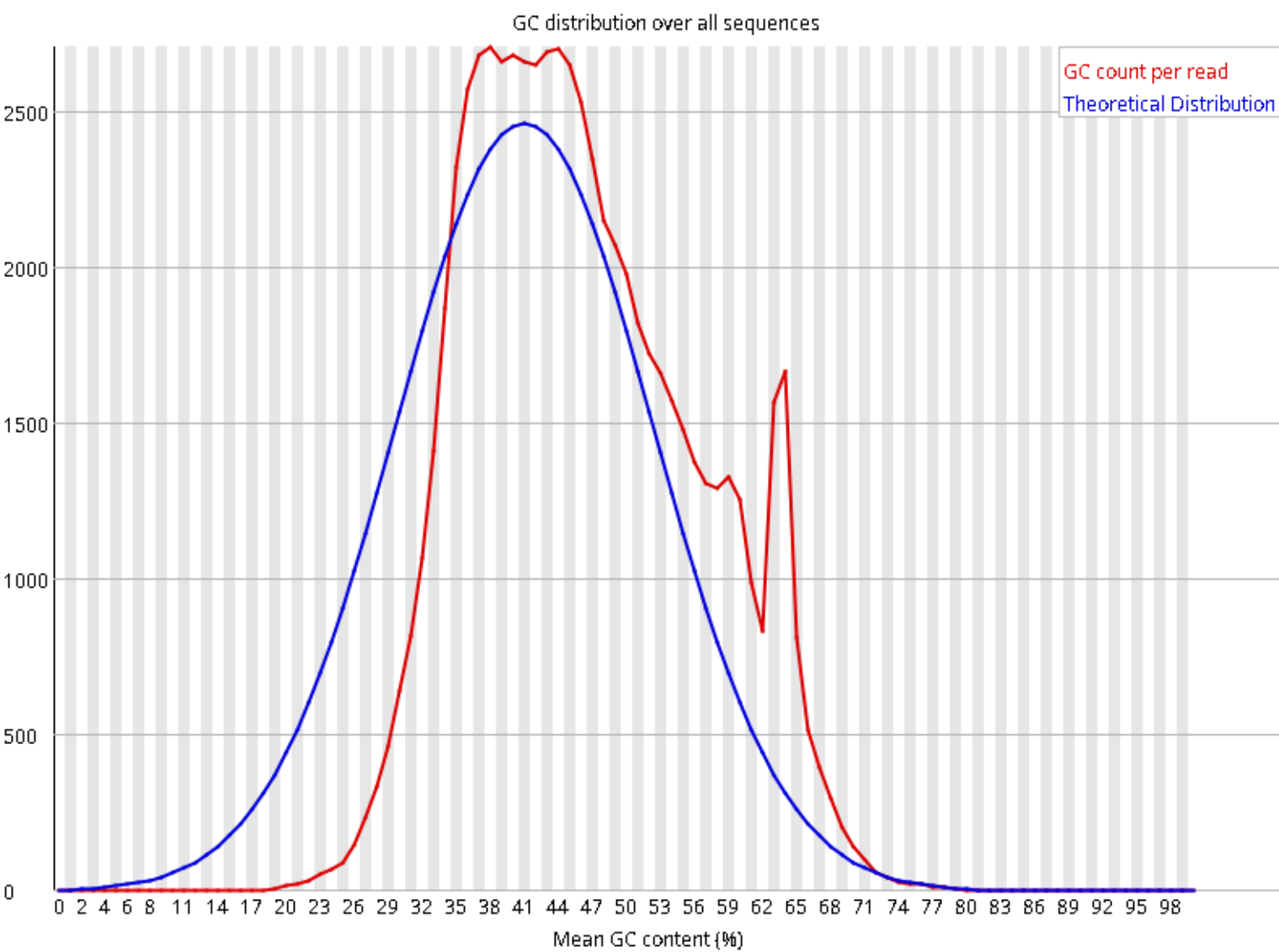
Per sequence quality scores



✖ Per base sequence content

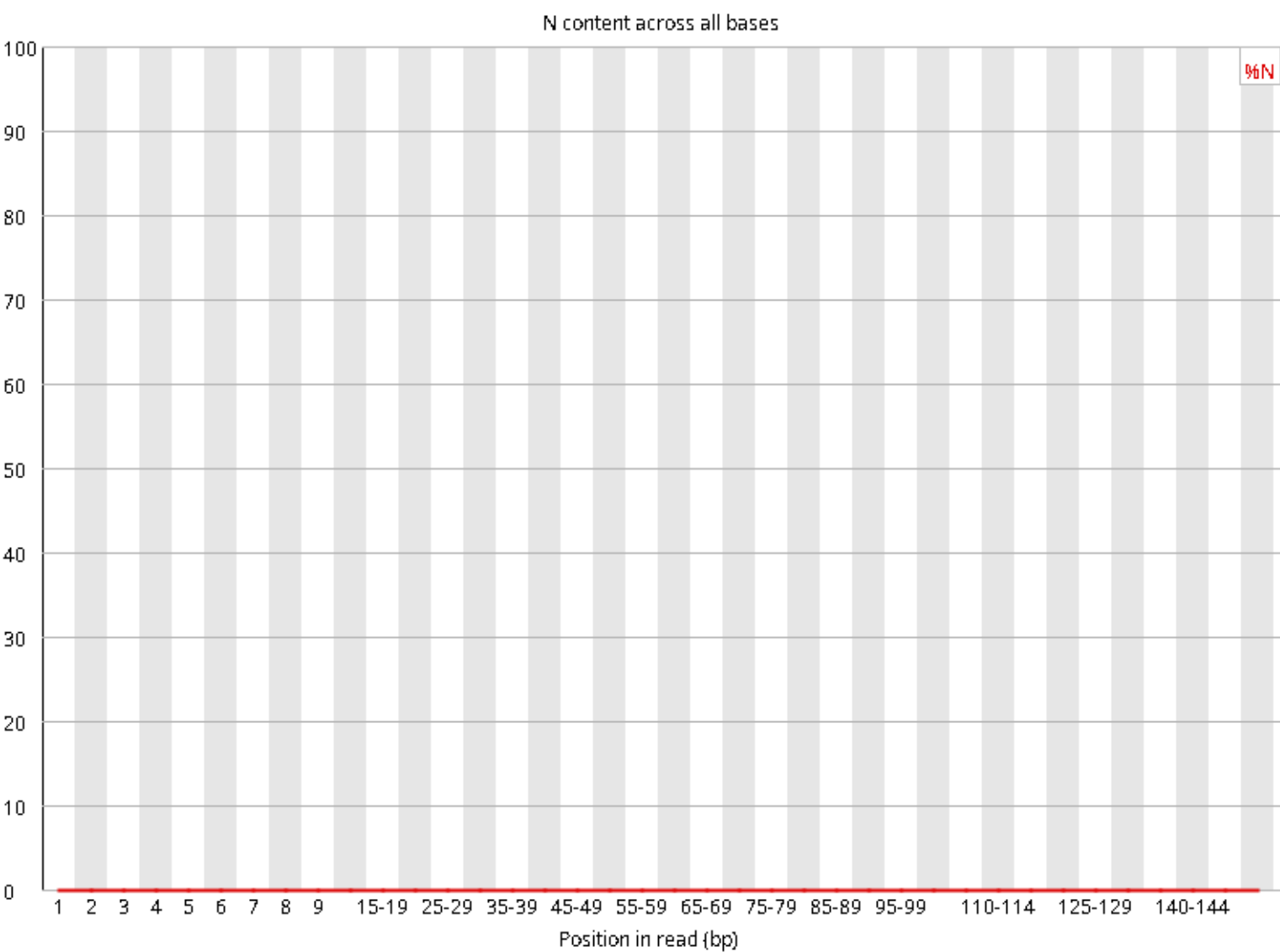


✖ Per sequence GC content

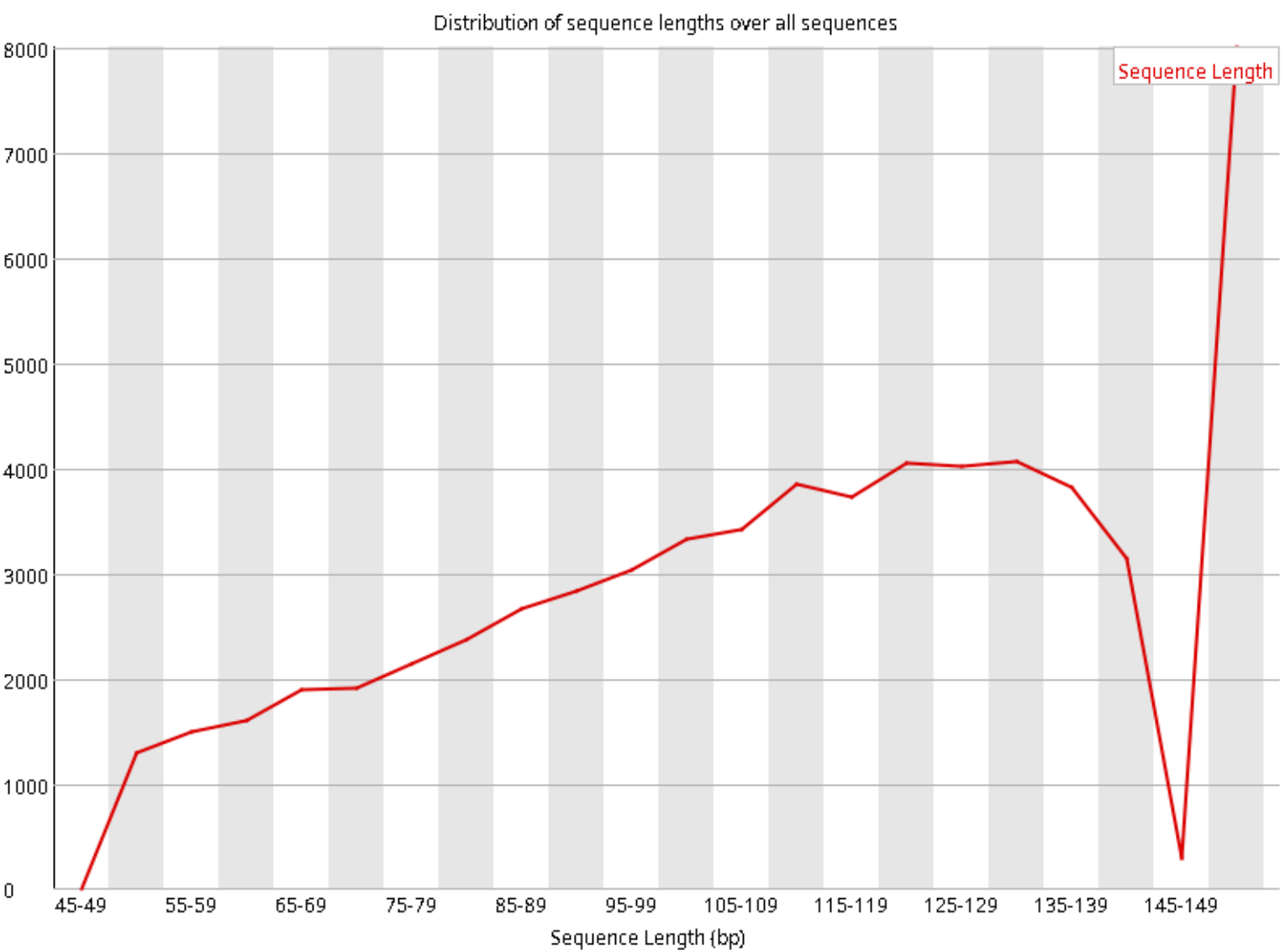




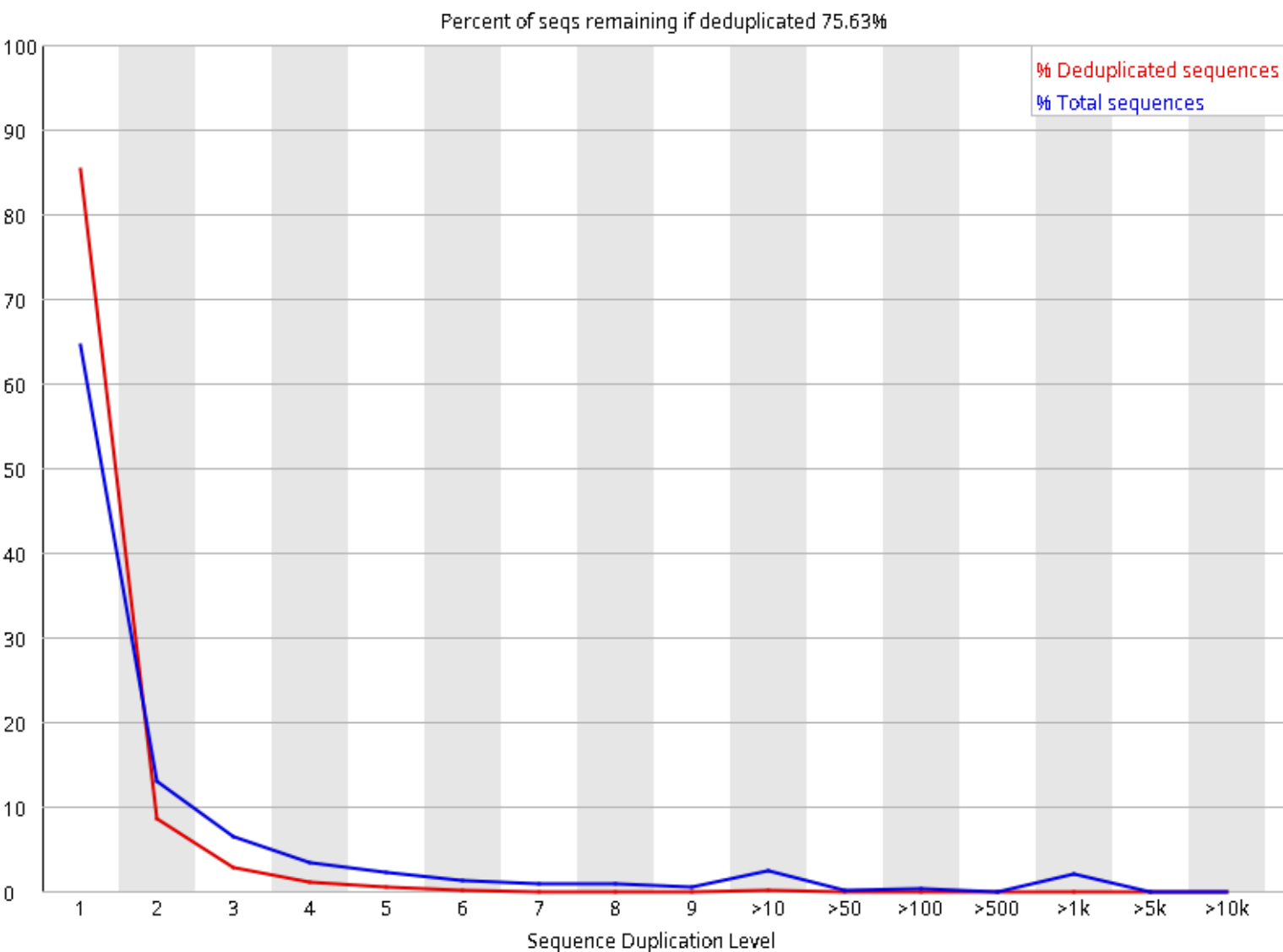
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCGGTATTATCTCGTAT	1359	2.152973606666455	TruSeq Adapter, Index 20 (97% over 37bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCGGTATTATCGCGTAT	177	0.2804093659896708	TruSeq Adapter, Index 20 (97% over 37bp)
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	108	0.17109724026488388	No Hit
CCTCCAATTCCTCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	68	0.10772789201863059	No Hit



Adapter Content

