











FastQC Report

Summary

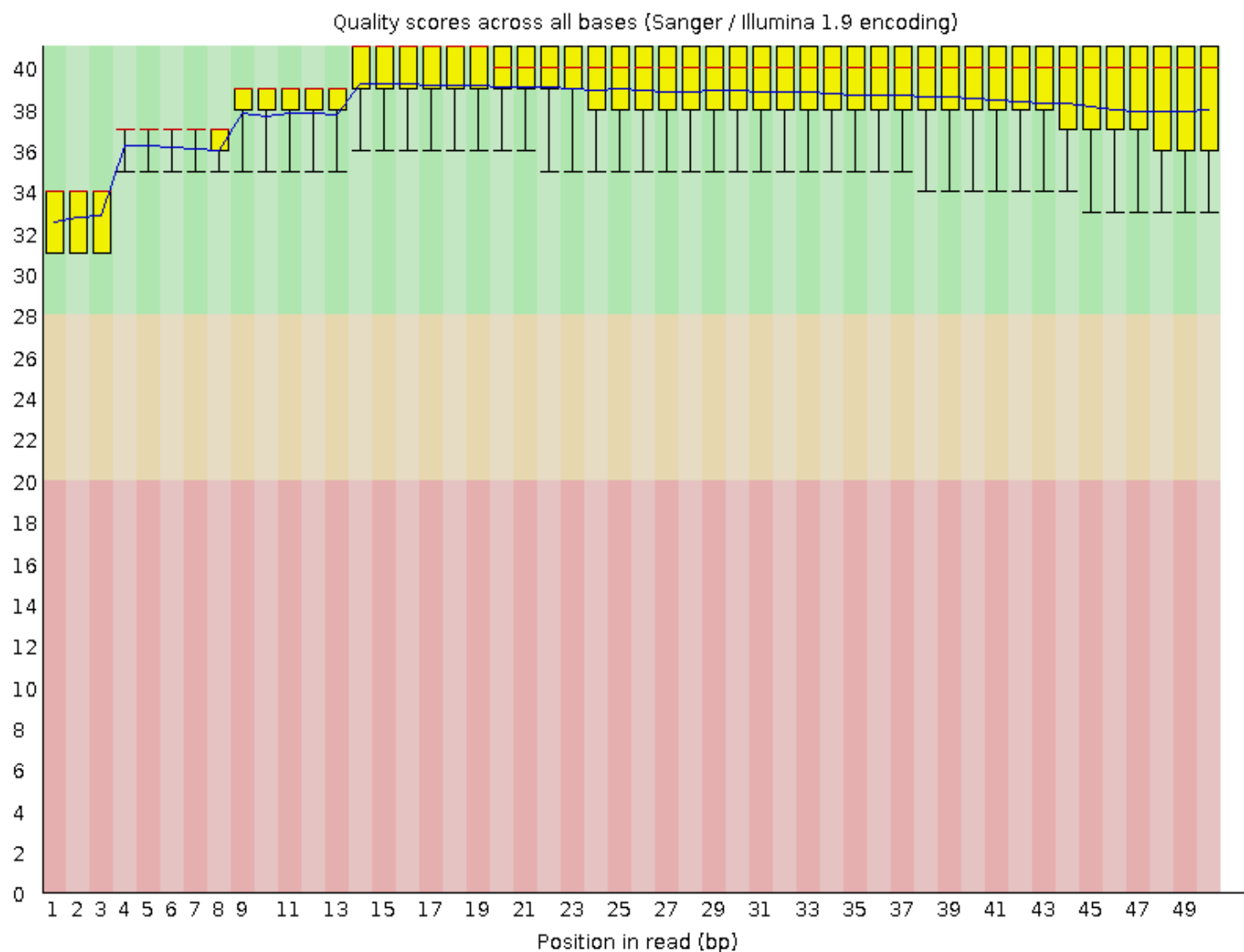
Wed 30 Jun 2021
SRR1554534_1_adapt_fastq_gz.gz

-  [Basic Statistics](#)
-  [Per base 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](#)
-  [Adapter Content](#)

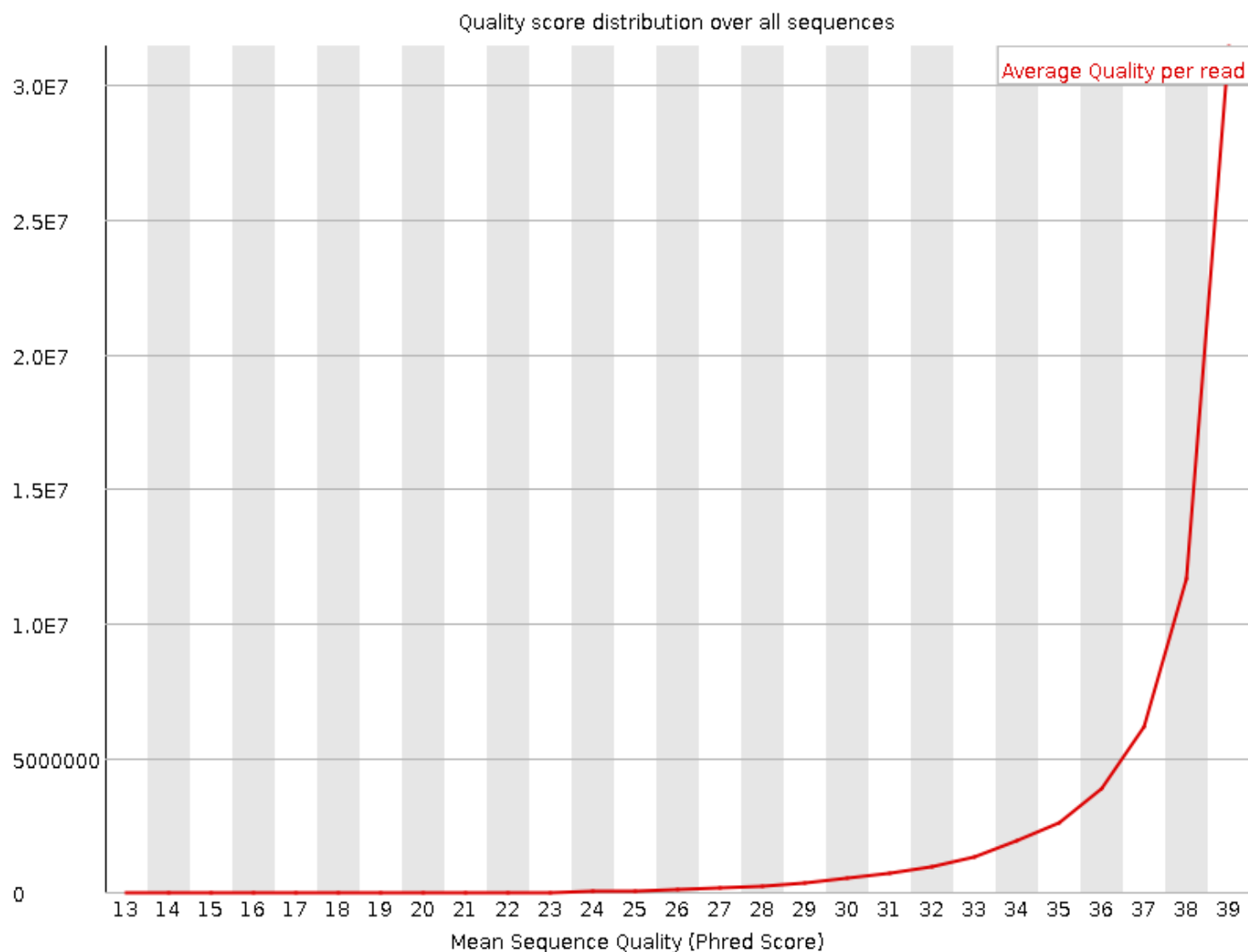
Basic Statistics

Measure	Value
Filename	SRR1554534_1_adapt_fastq_gz.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	62707044
Sequences flagged as poor quality	0
Sequence length	20-50
%GC	52

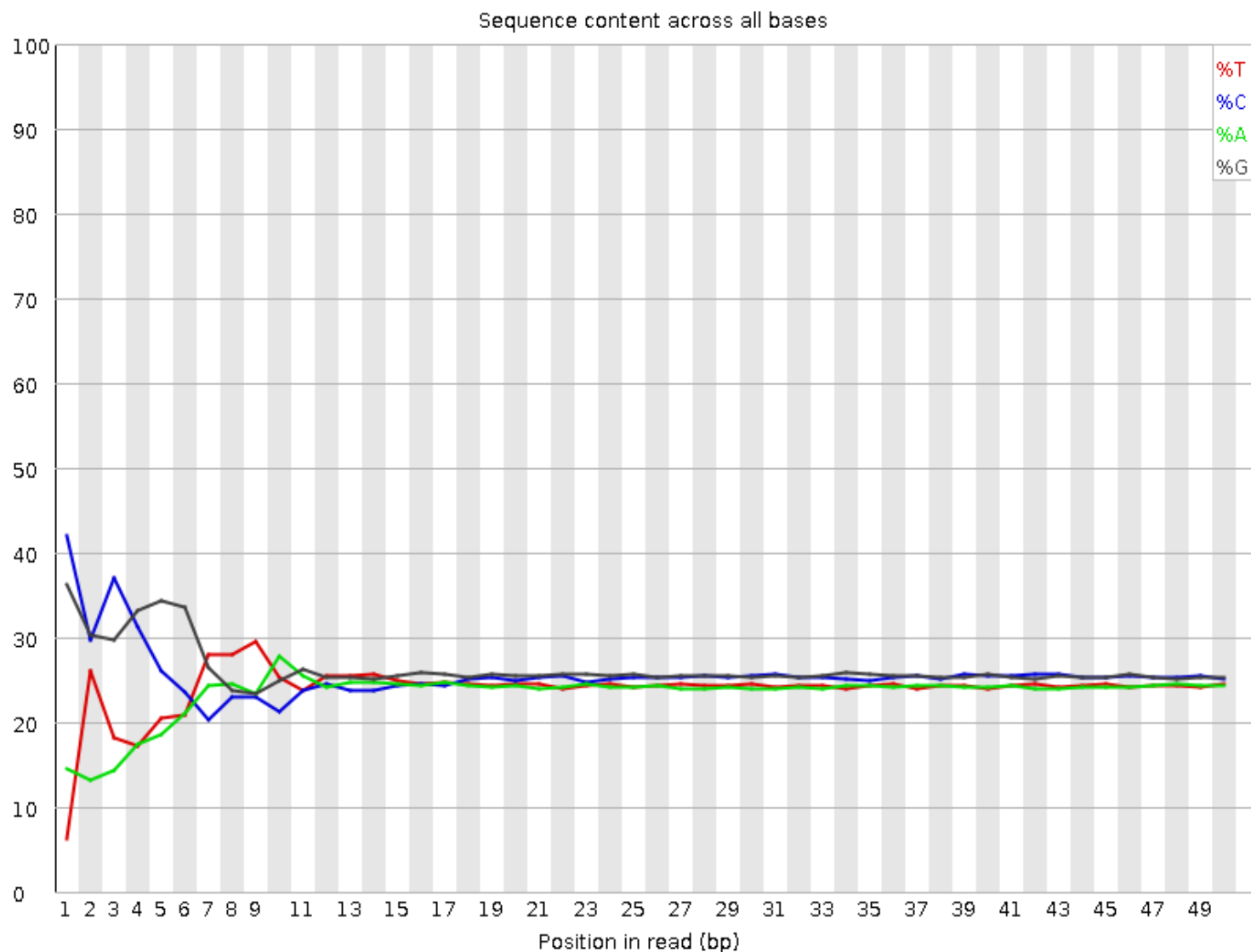
Per base sequence quality



Per sequence quality scores

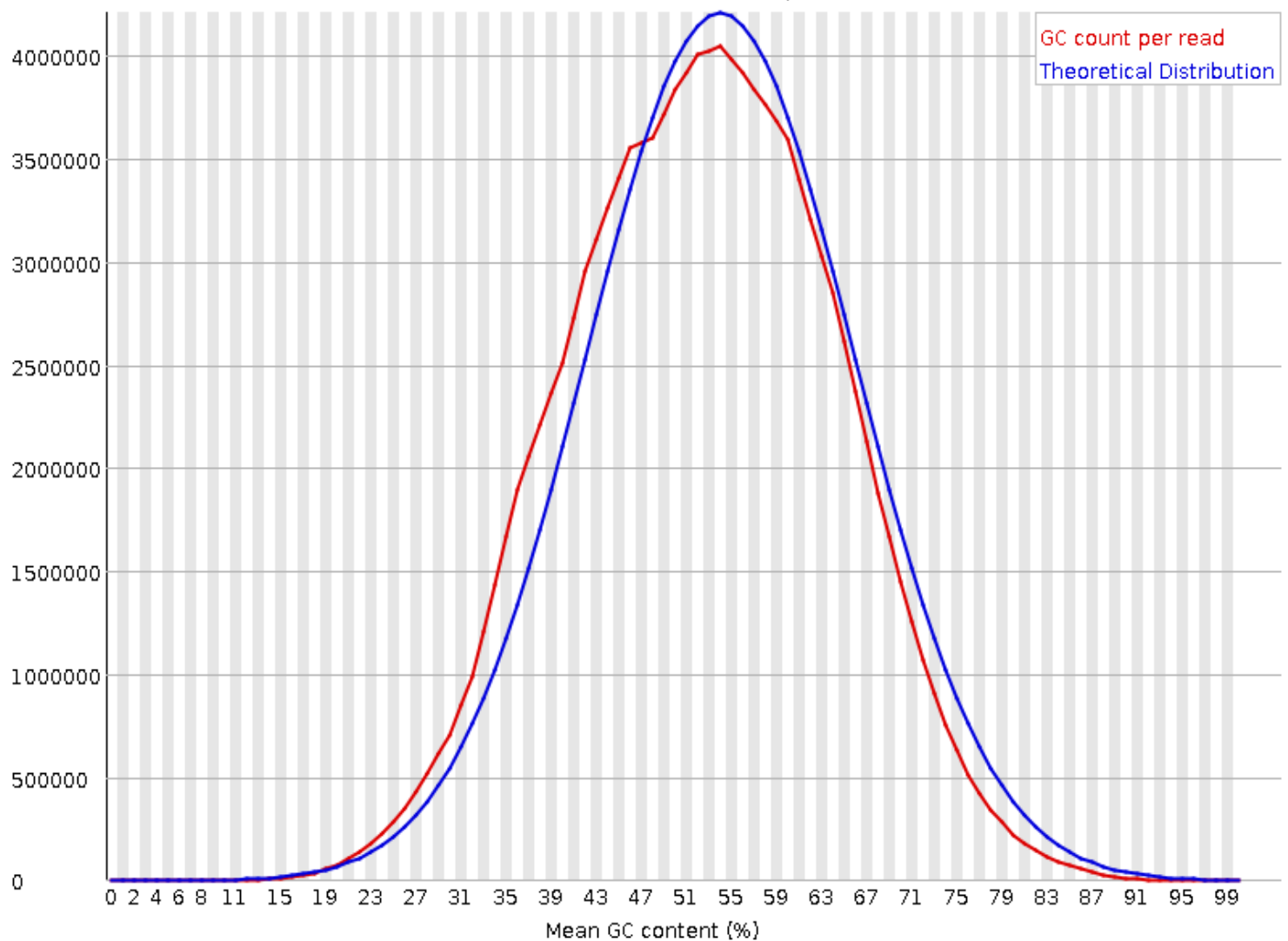


! Per base sequence content

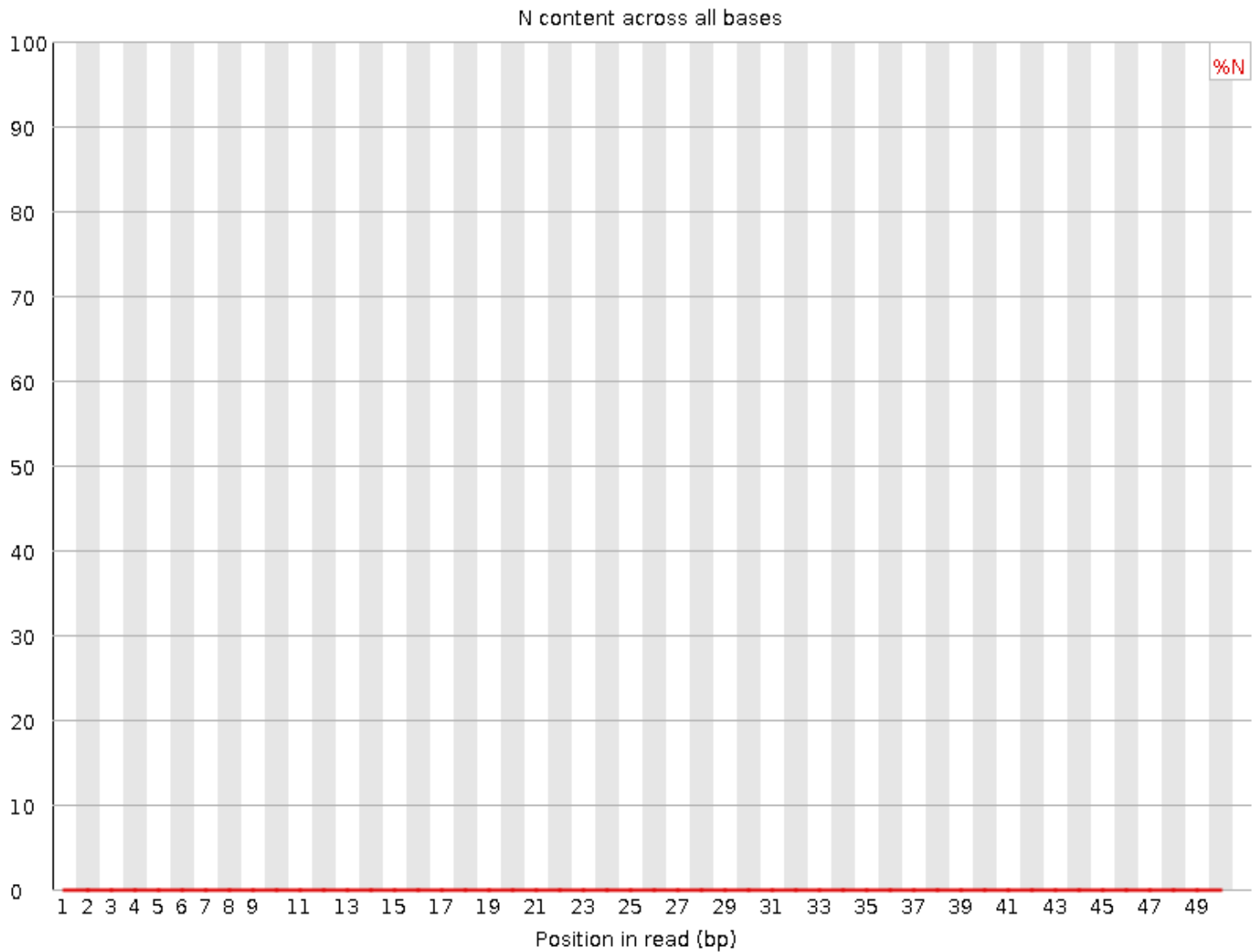


Per sequence GC content

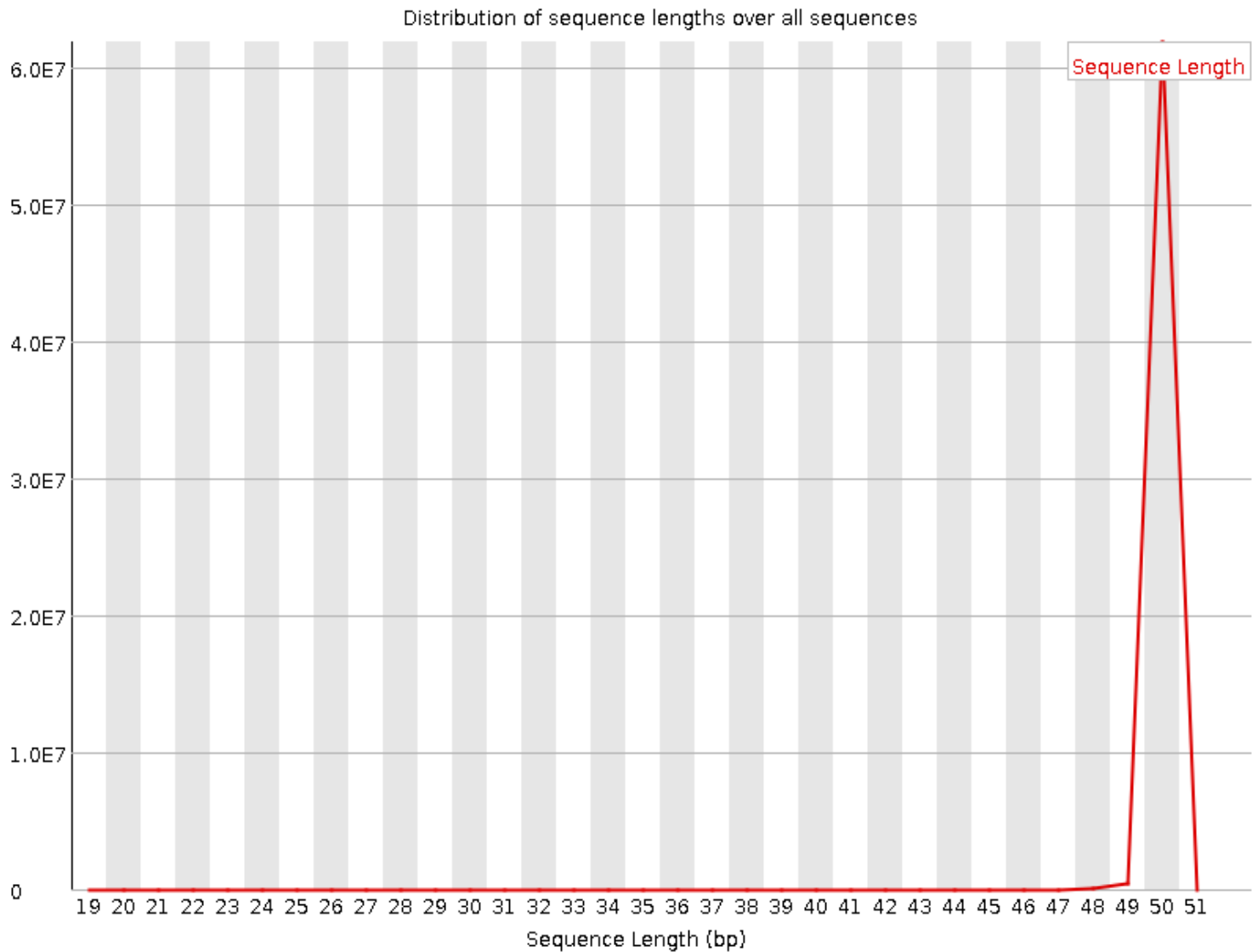
GC distribution over all sequences



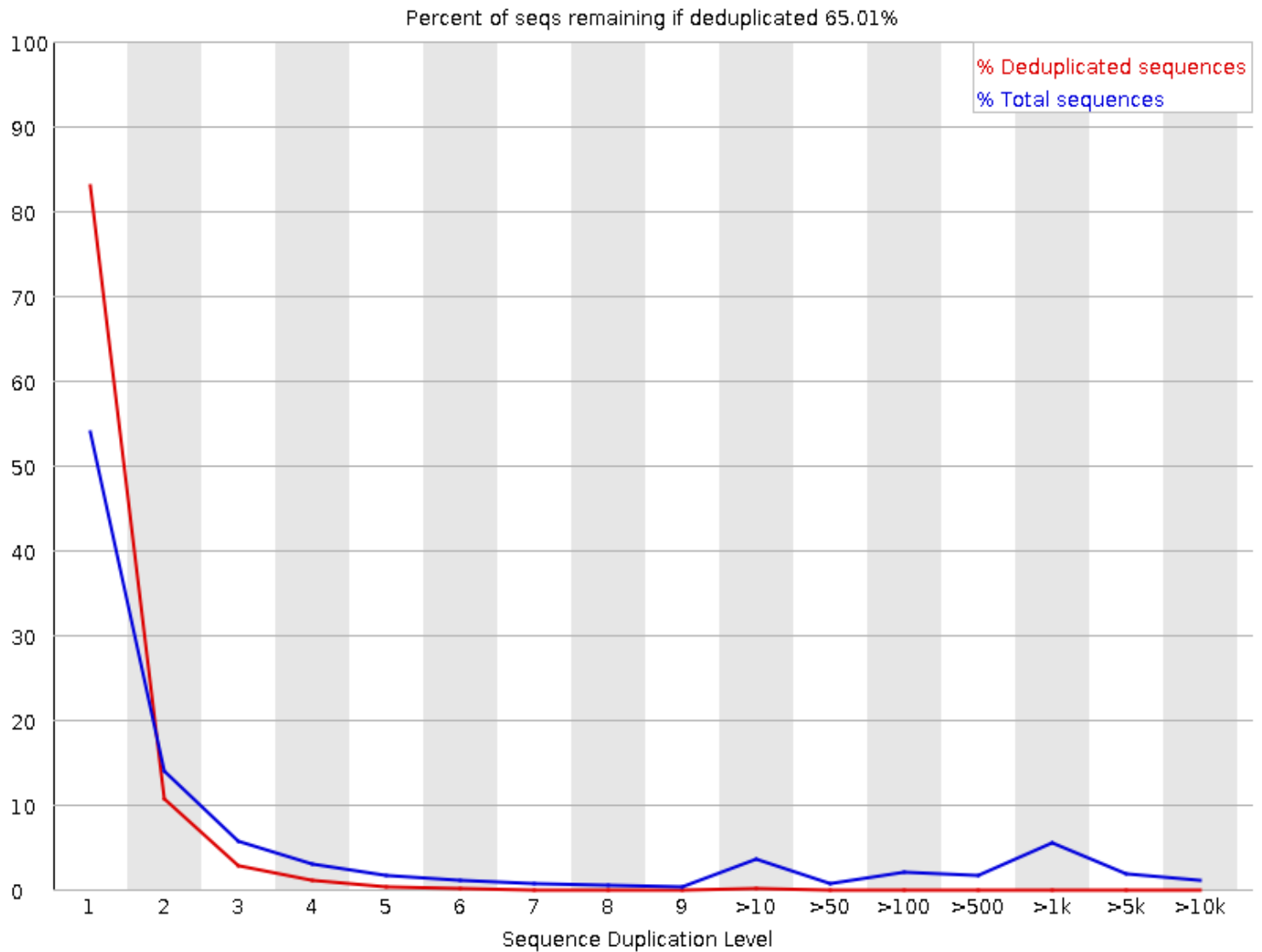
Per base N content



! Sequence Length Distribution



! Sequence Duplication Levels

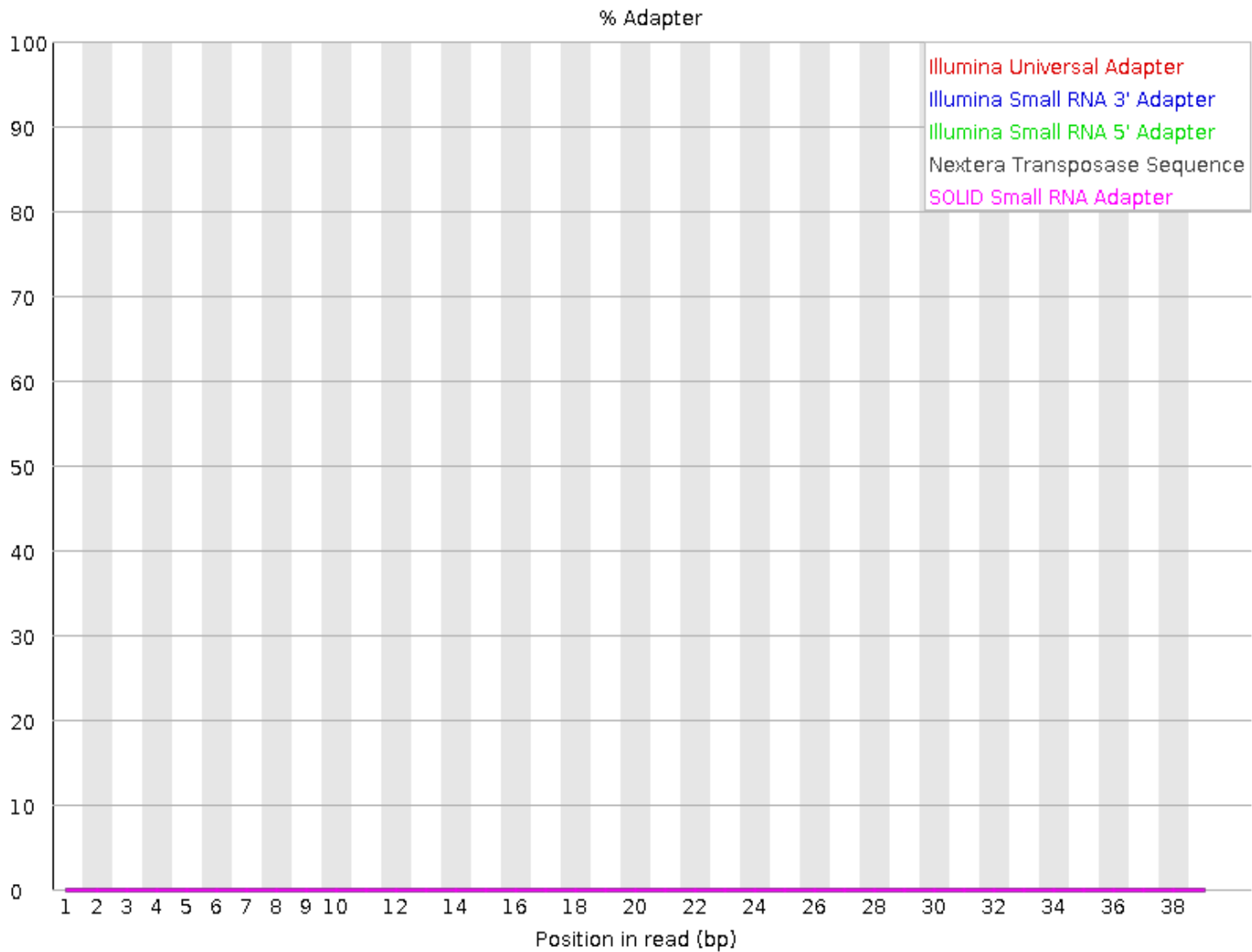


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.11.8)