











FastQC Report

Summary

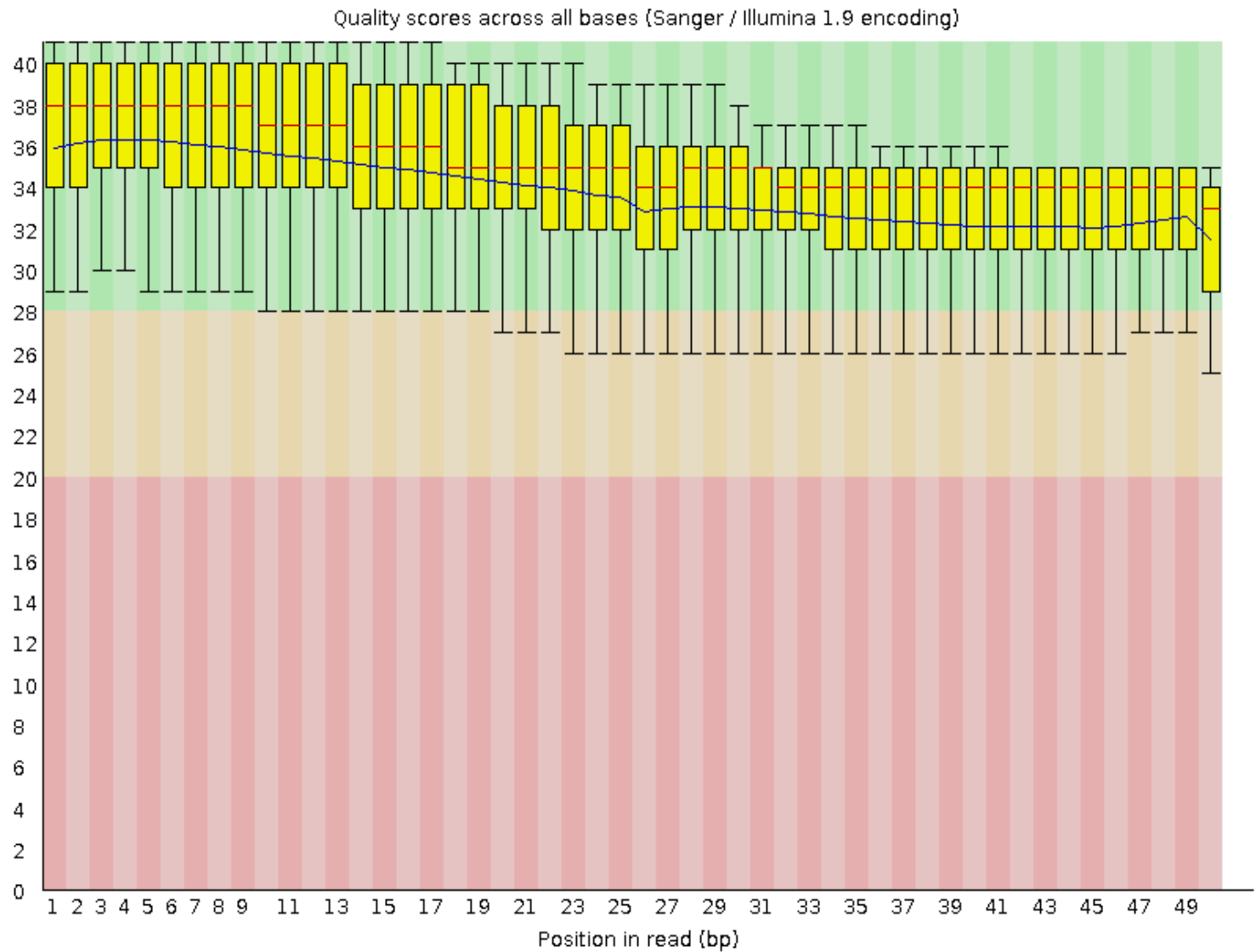
Mon 19 Jul 2021
SRR1554556_2_adapt_fastq_gz.gz

-  [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](#)

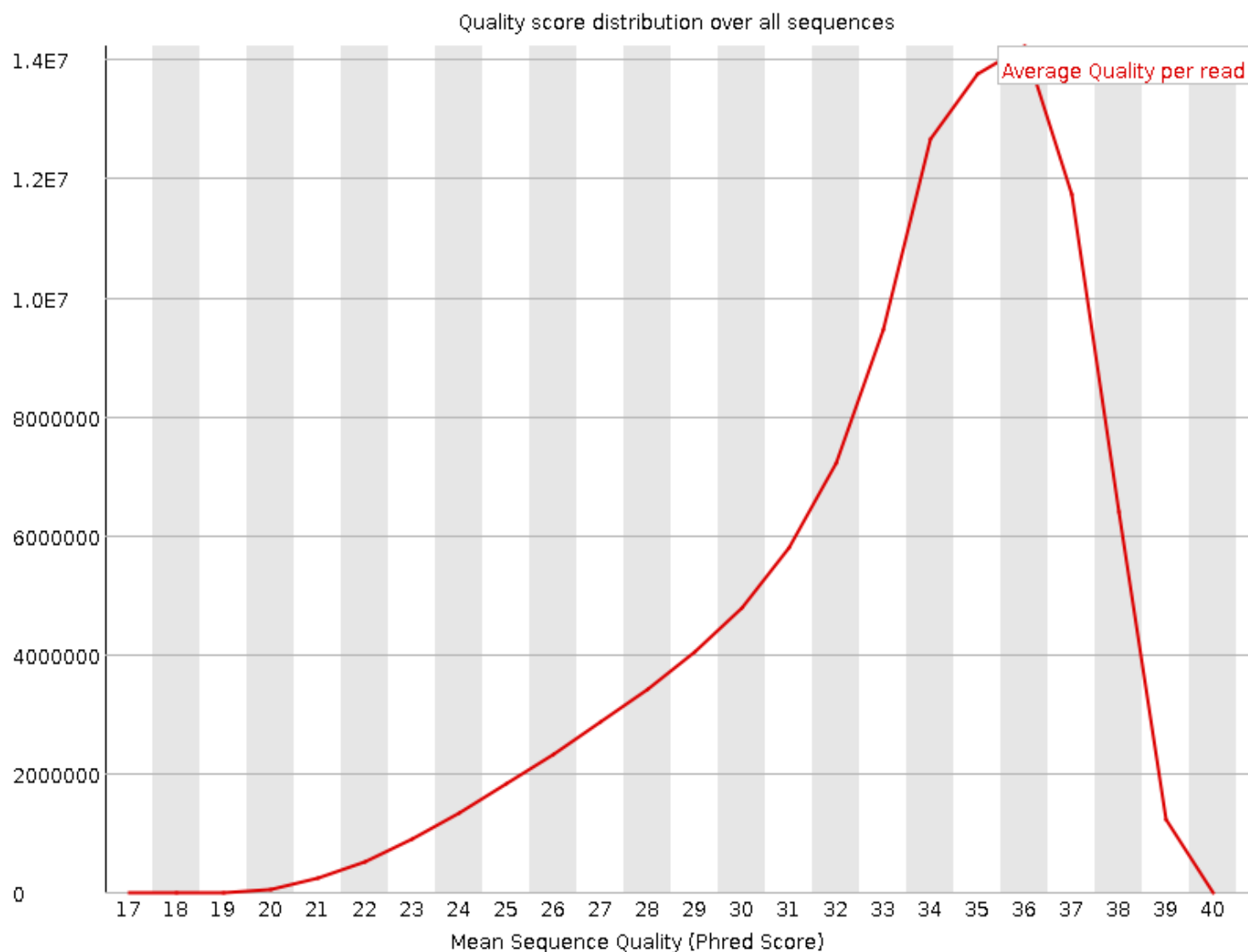
Basic Statistics

Measure	Value
Filename	SRR1554556_2_adapt_fastq_gz.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	105054168
Sequences flagged as poor quality	0
Sequence length	20-50
%GC	47

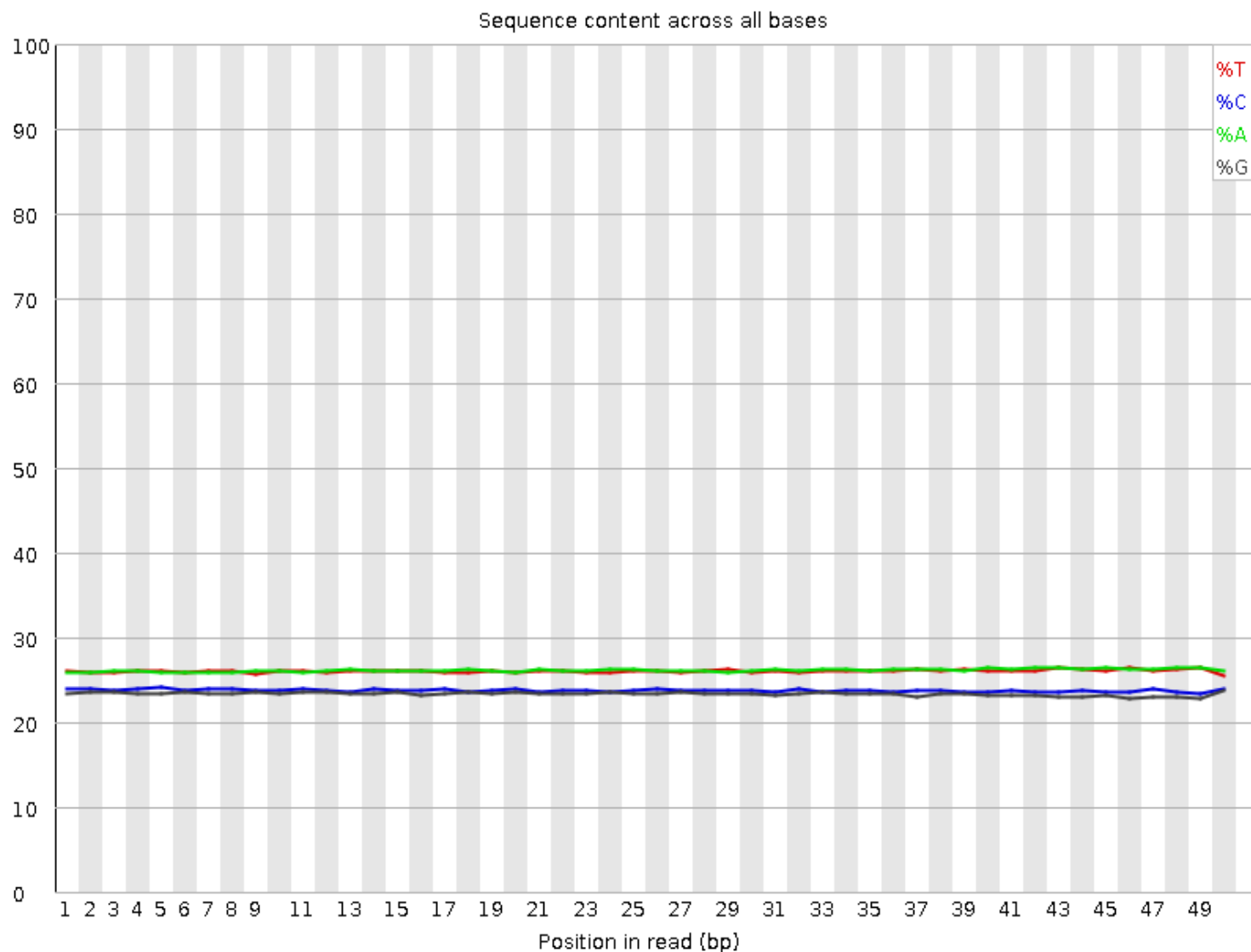
Per base sequence quality



Per sequence quality scores

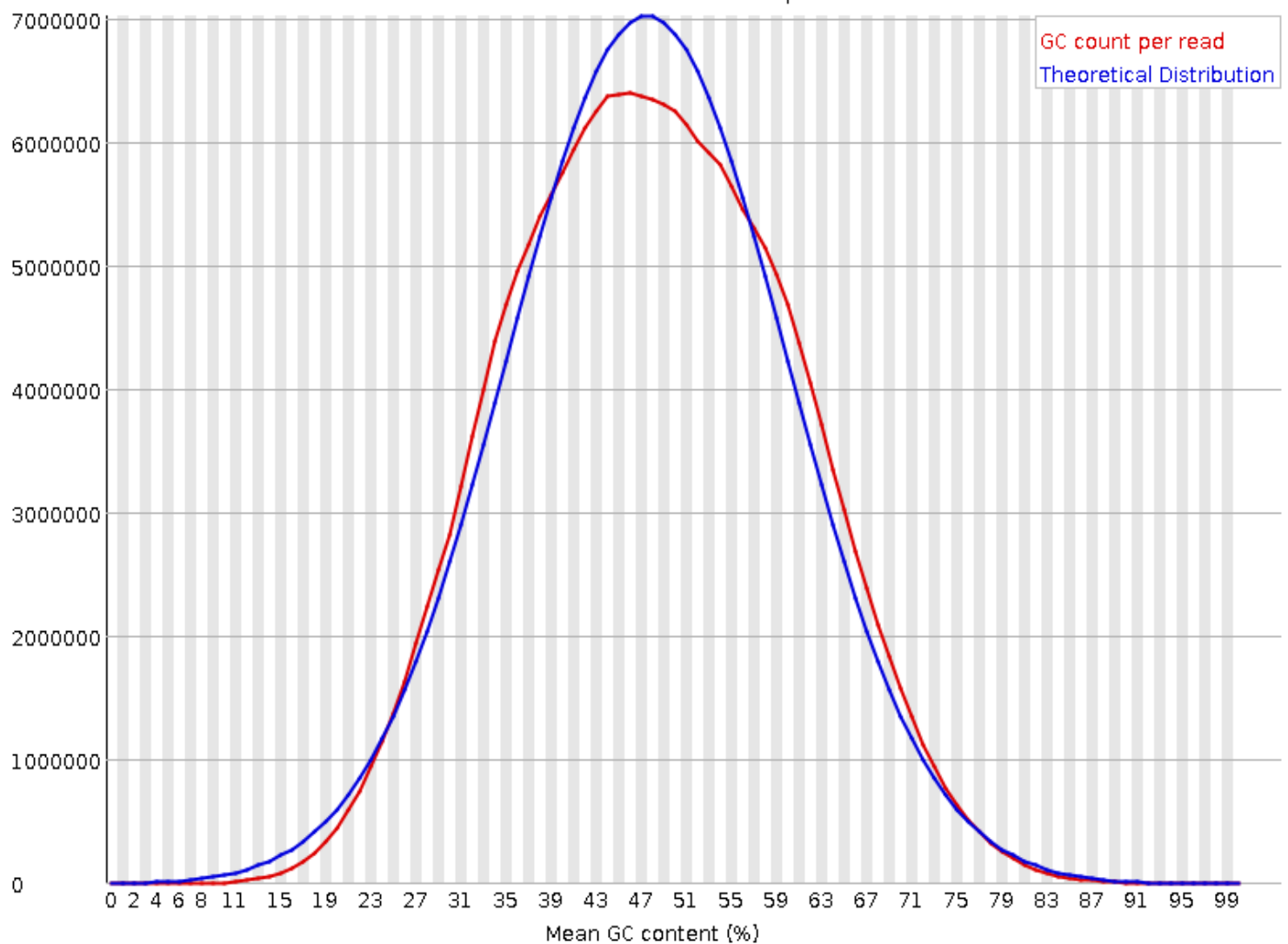


Per base sequence content

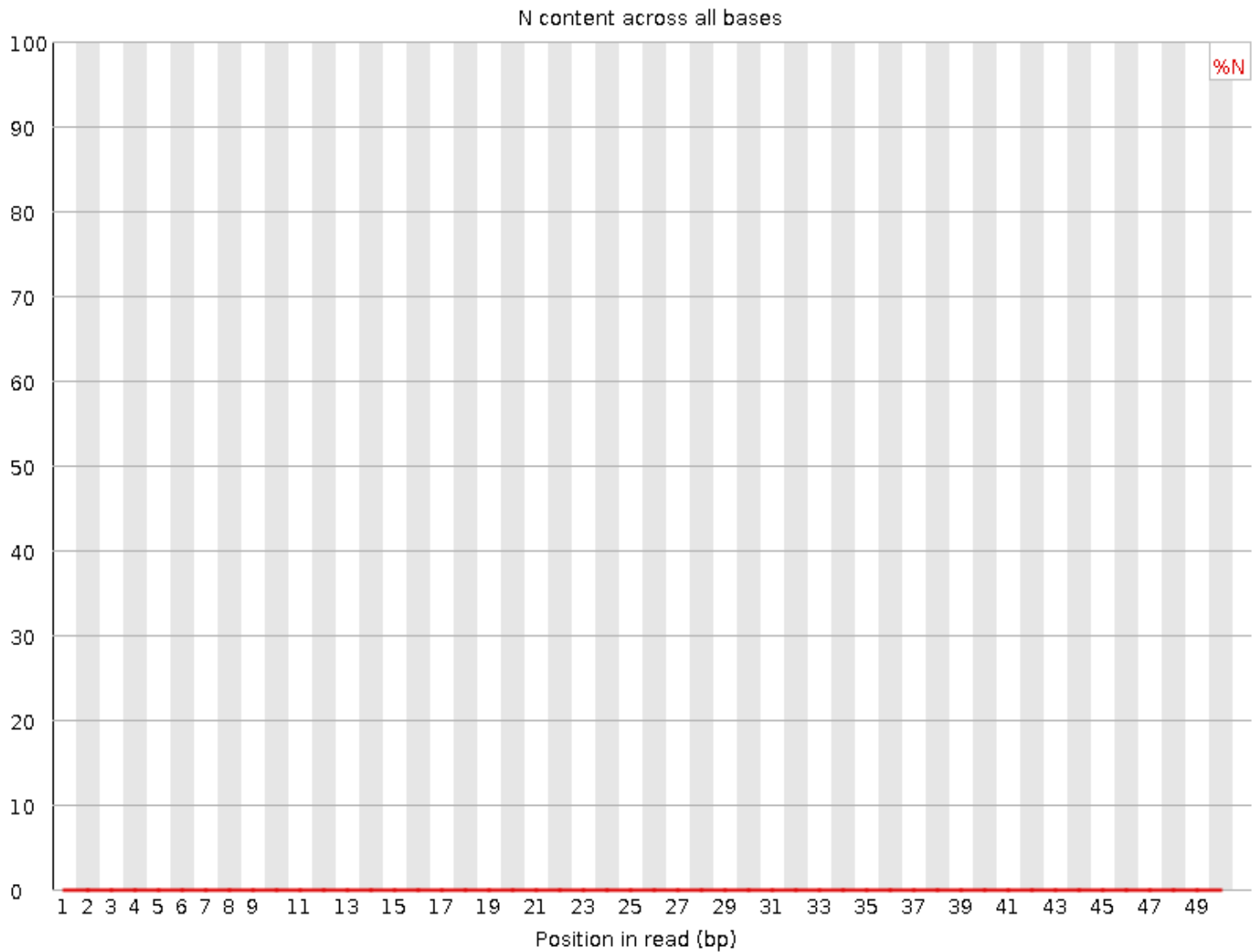


Per sequence GC content

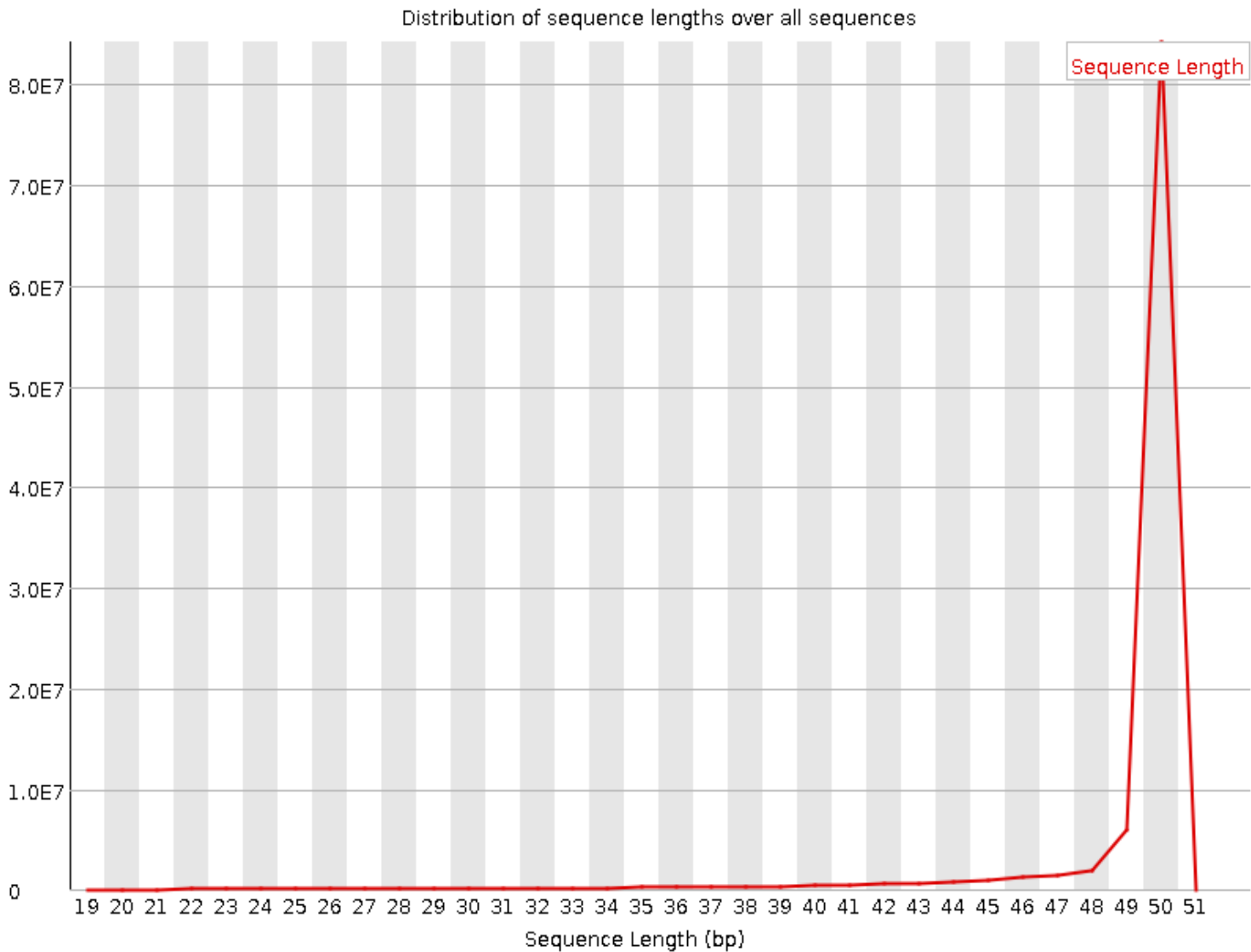
GC distribution over all sequences



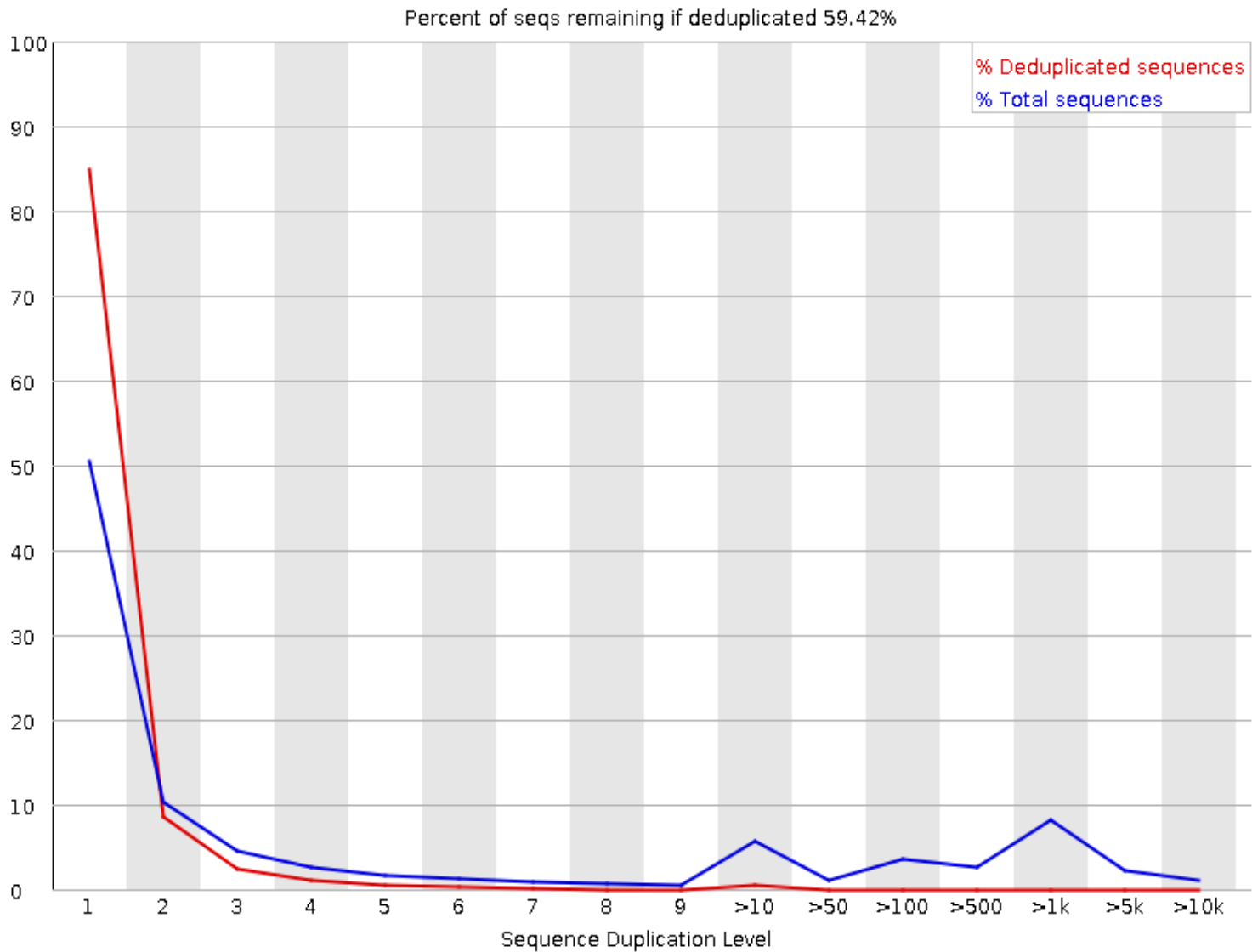
Per base N content



! Sequence Length Distribution

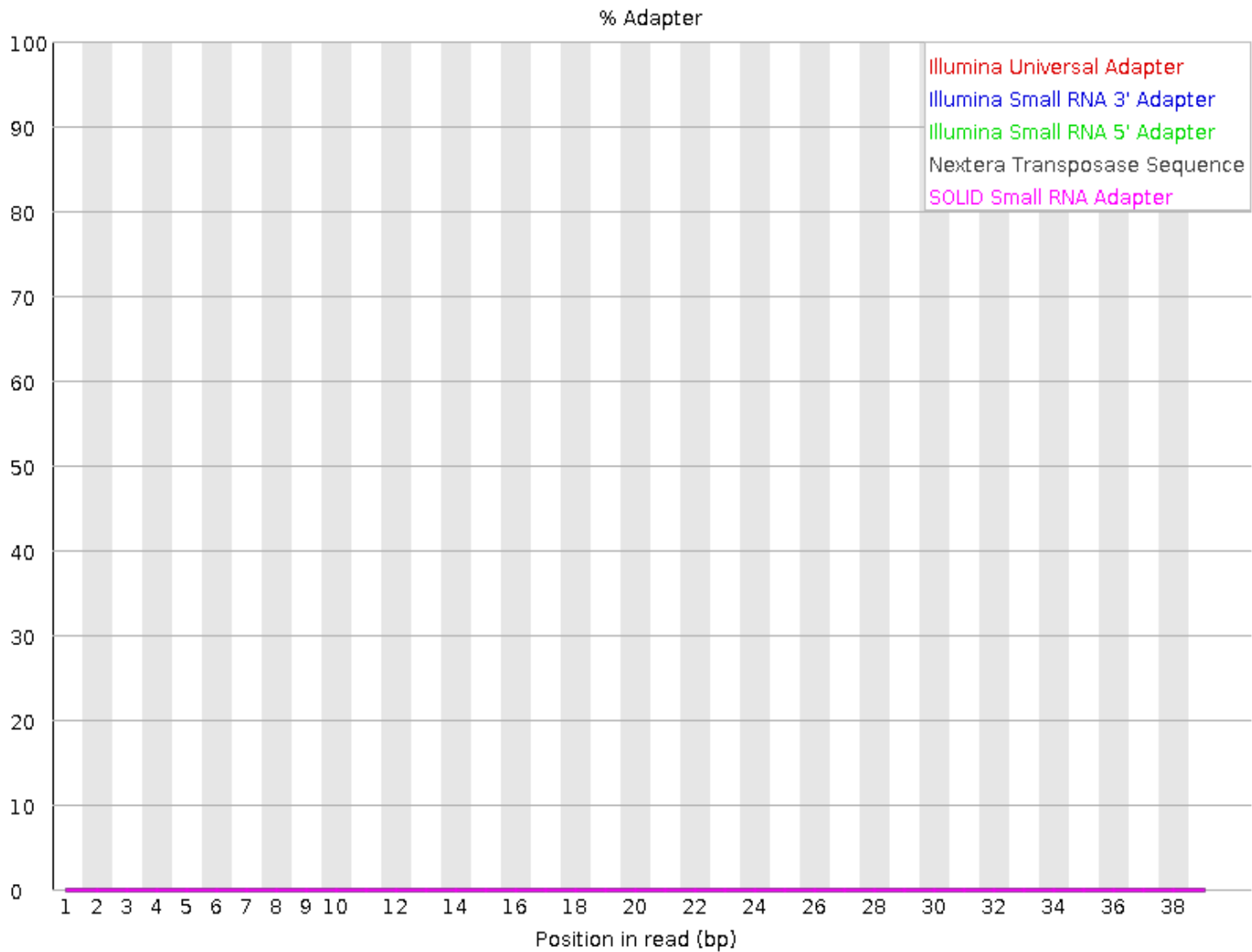


! Sequence Duplication Levels



 **Overrepresented sequences**
No overrepresented sequences

 **Adapter Content**



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