











FastQC Report

Summary

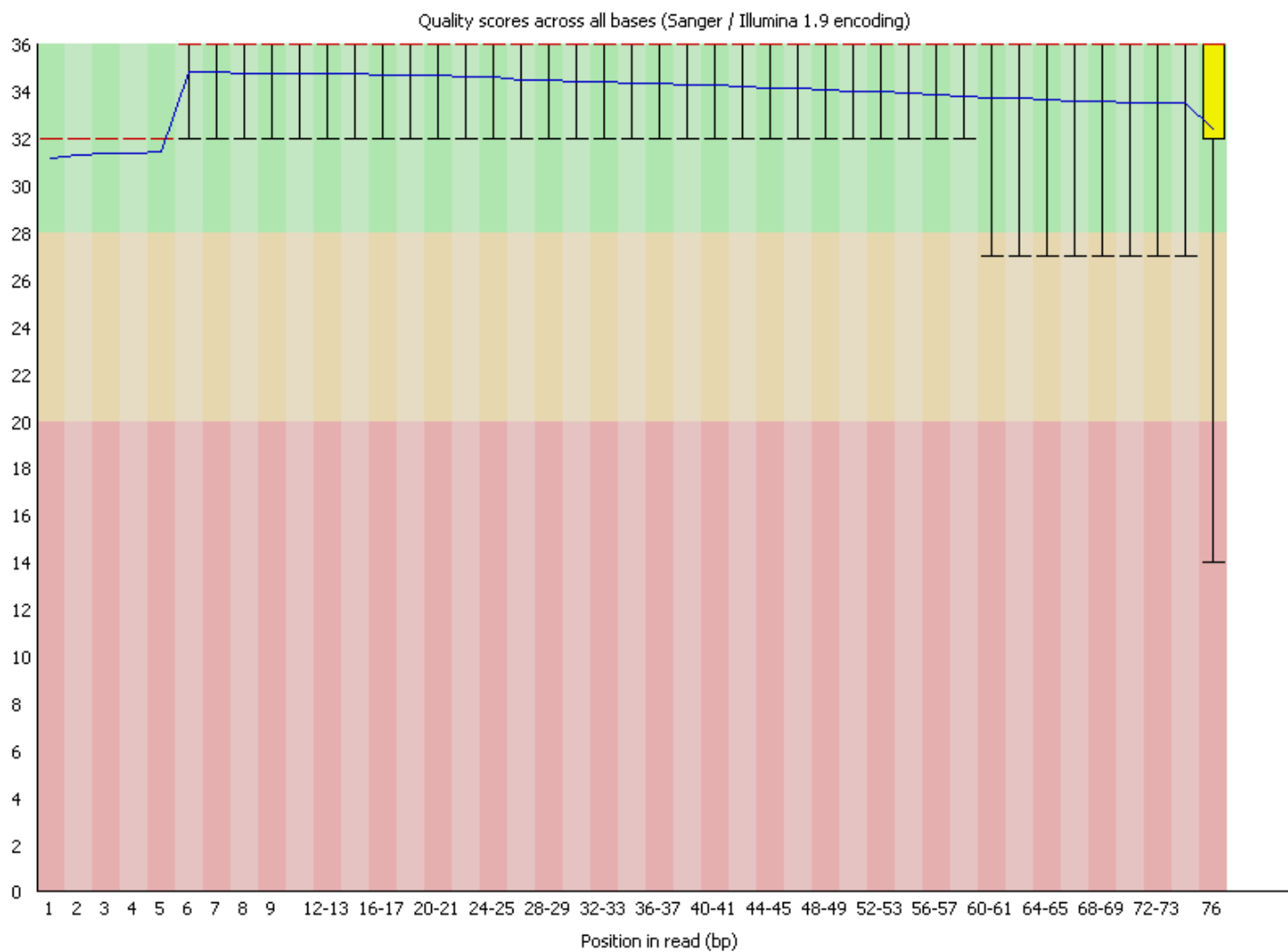
mar 6 giu 2023
SRR12816729.fastq

-  [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](#)

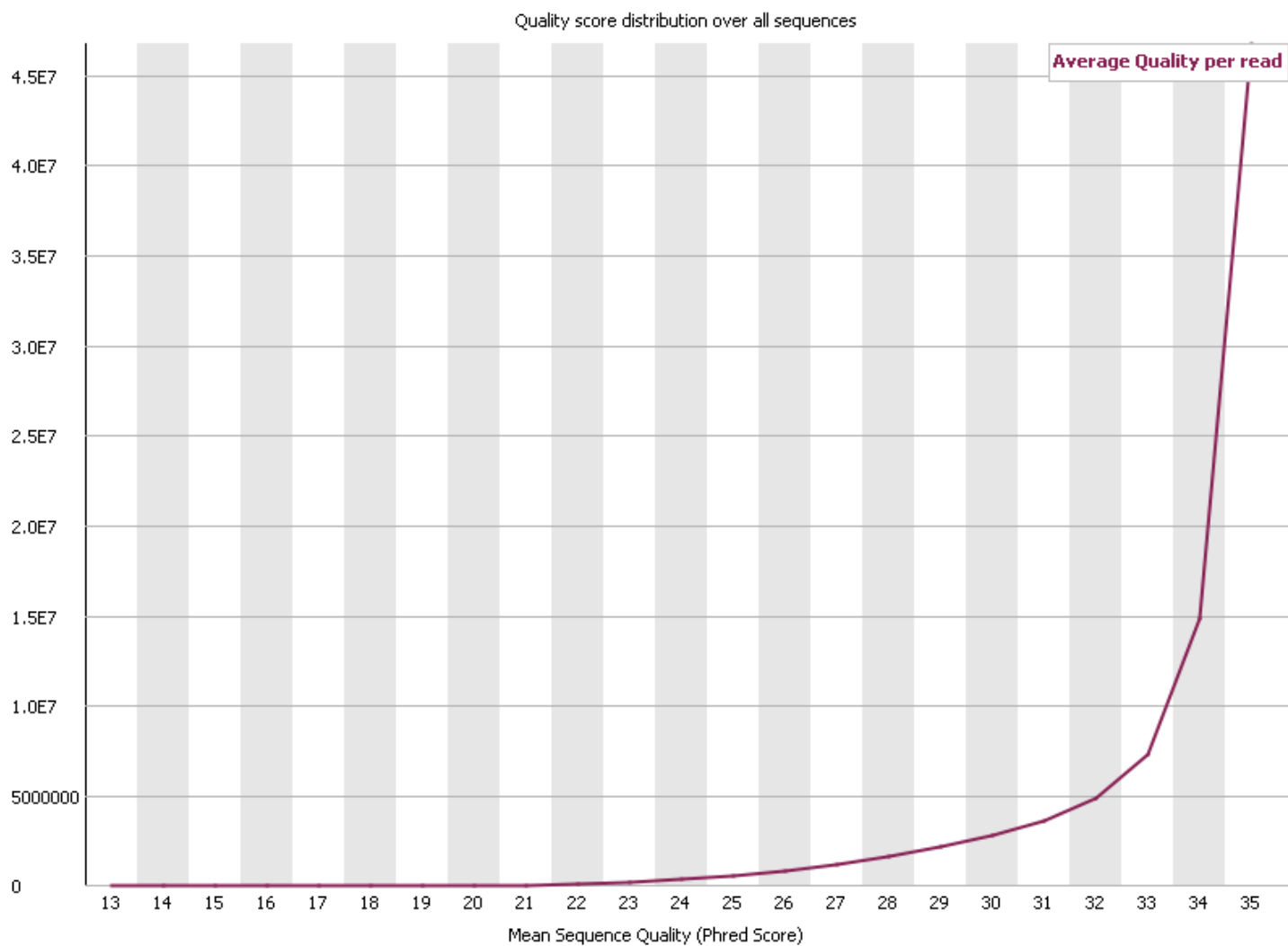
Basic Statistics

Measure	Value
Filename	SRR12816729.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	87671699
Total Bases	6.6 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	40

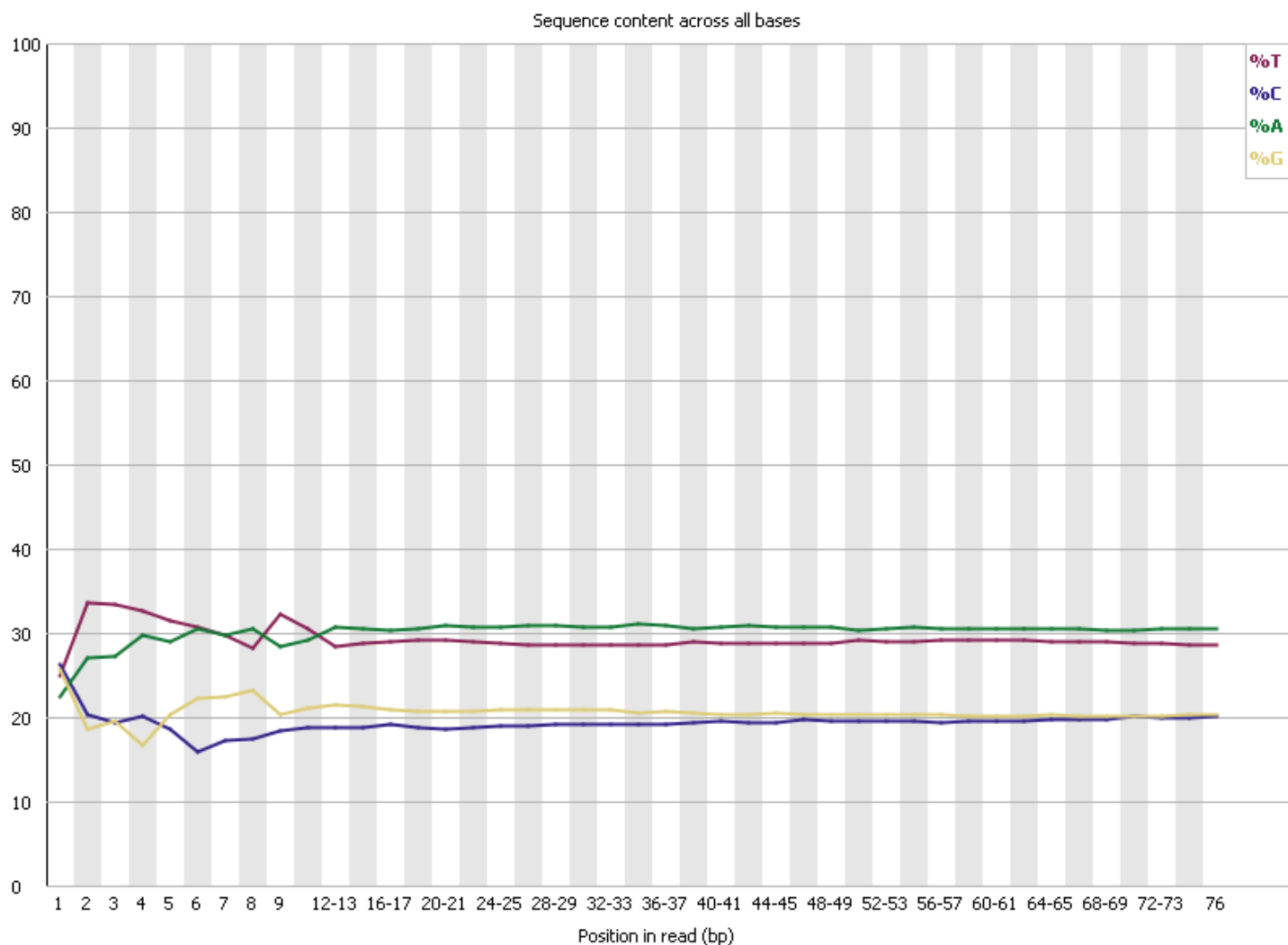
Per base sequence quality



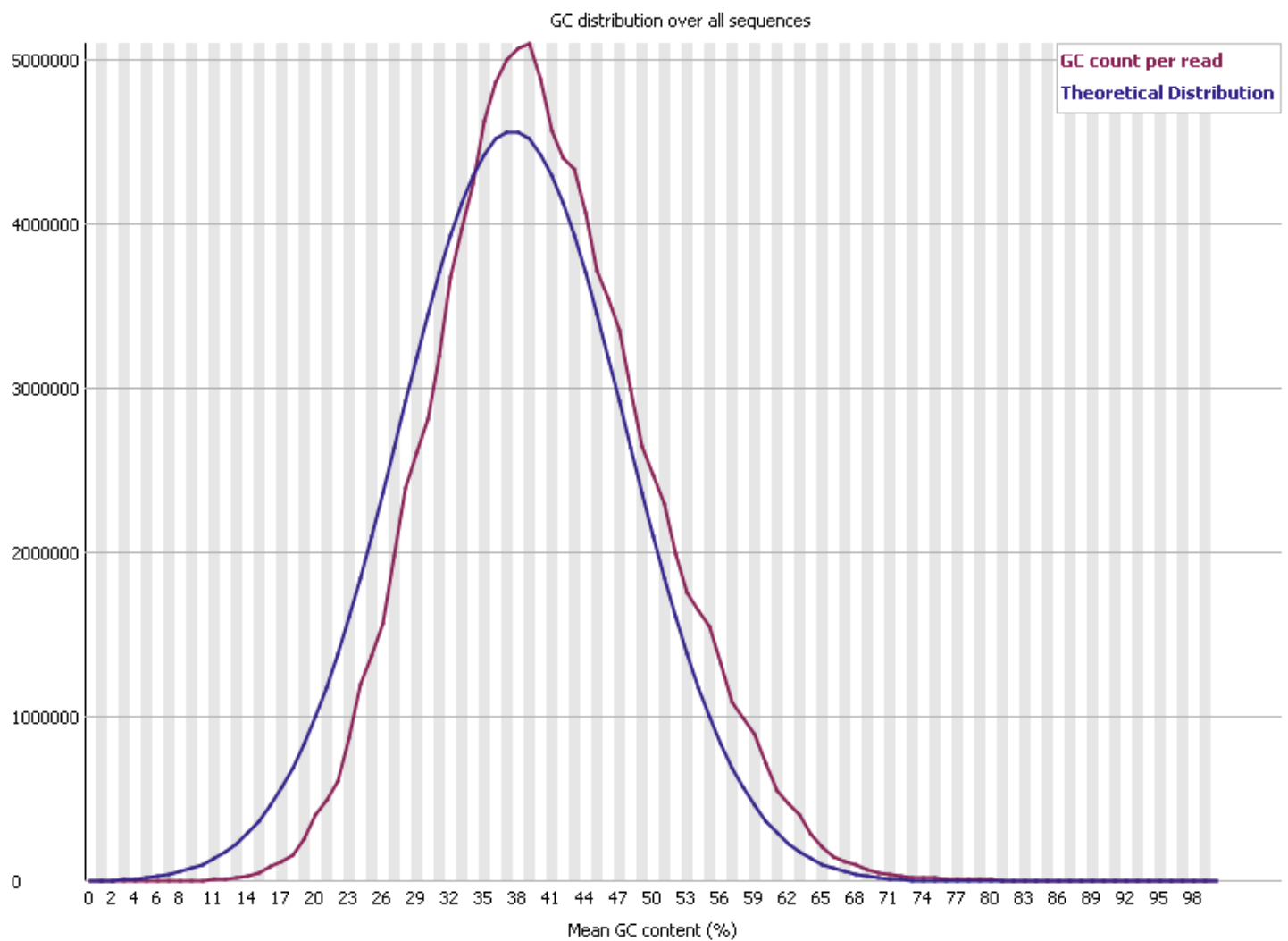
Per sequence quality scores



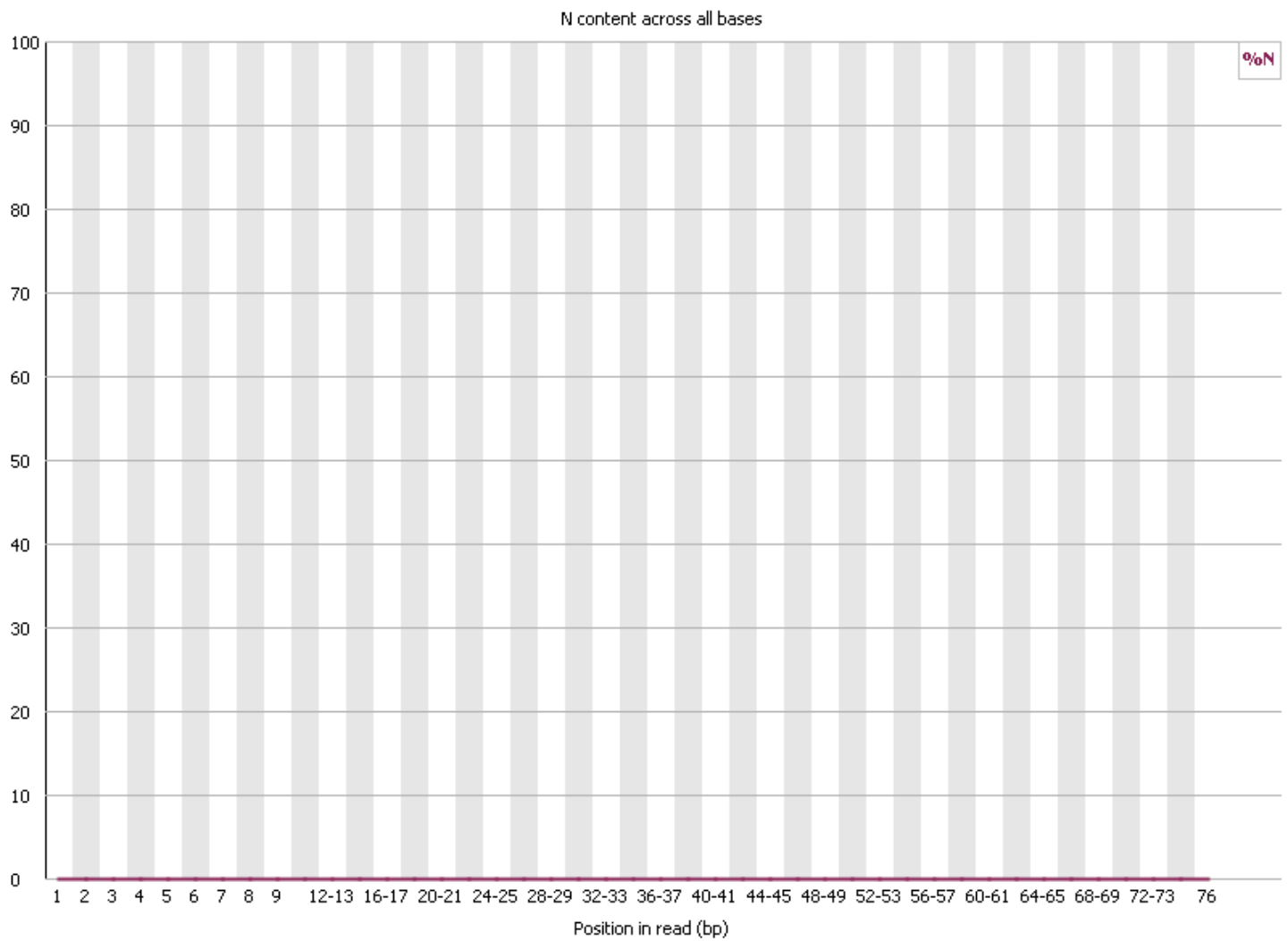
Per base sequence content



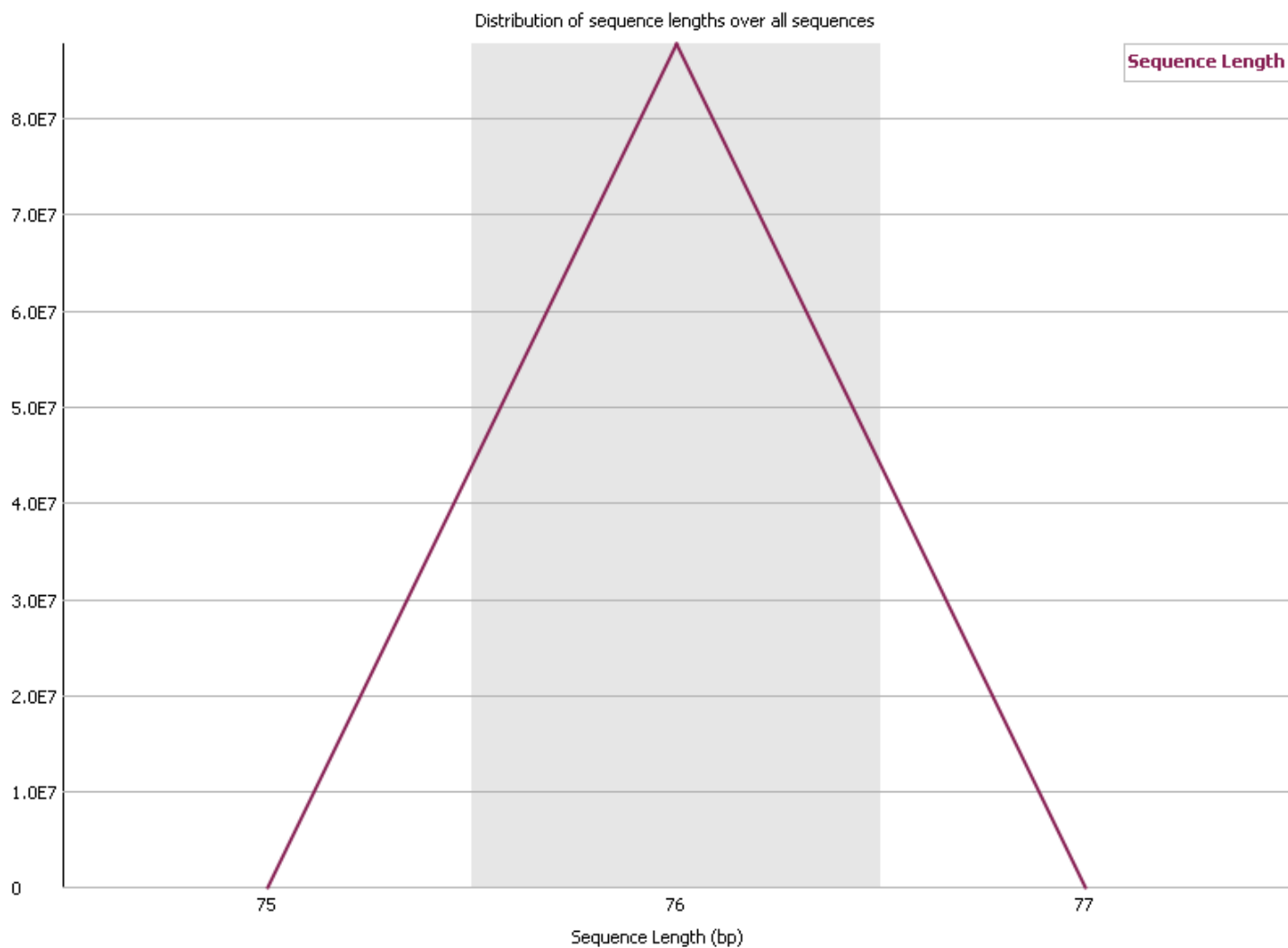
! Per sequence GC content



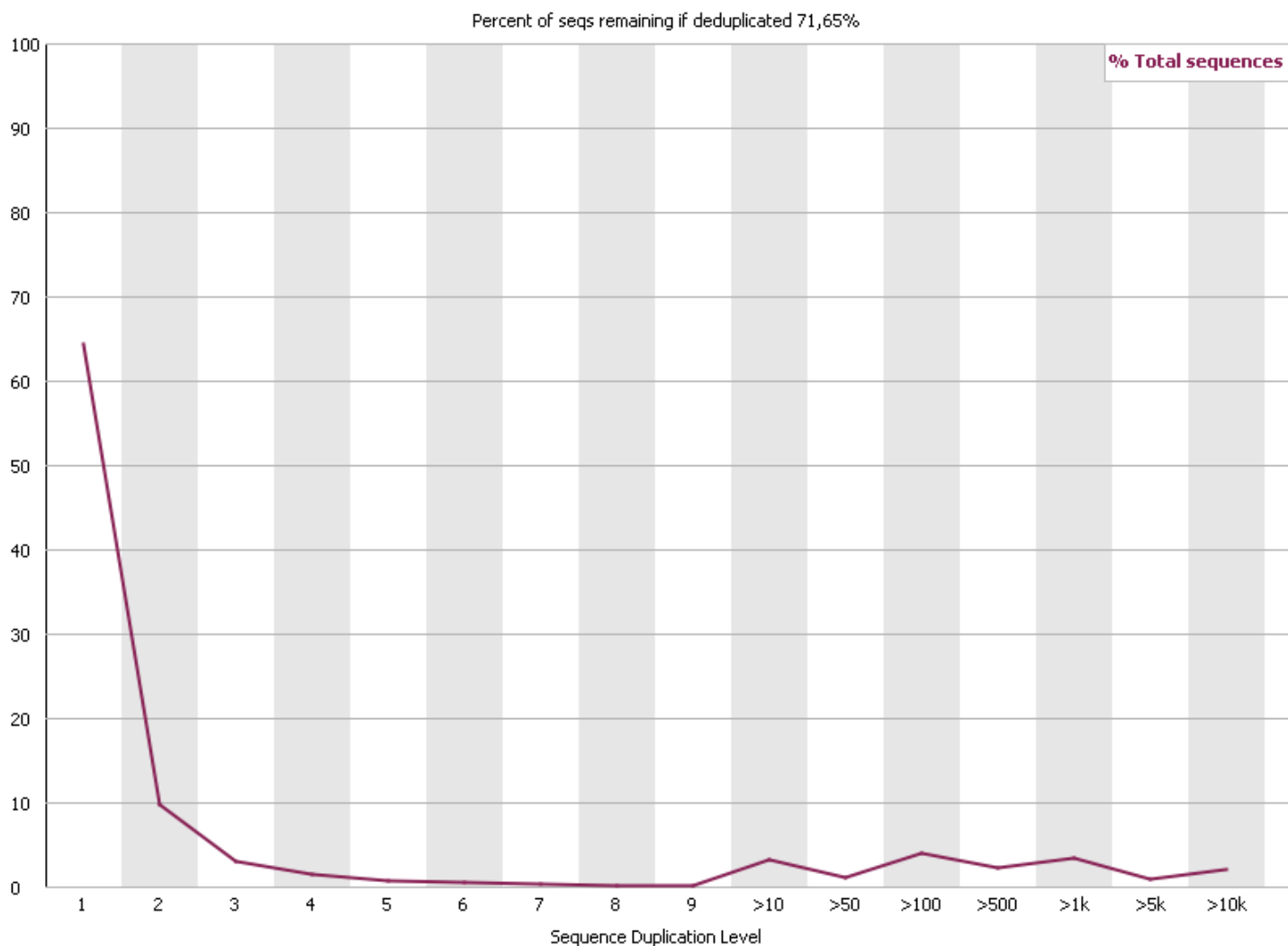
✅ Per base N content



Sequence Length Distribution



Sequence Duplication Levels

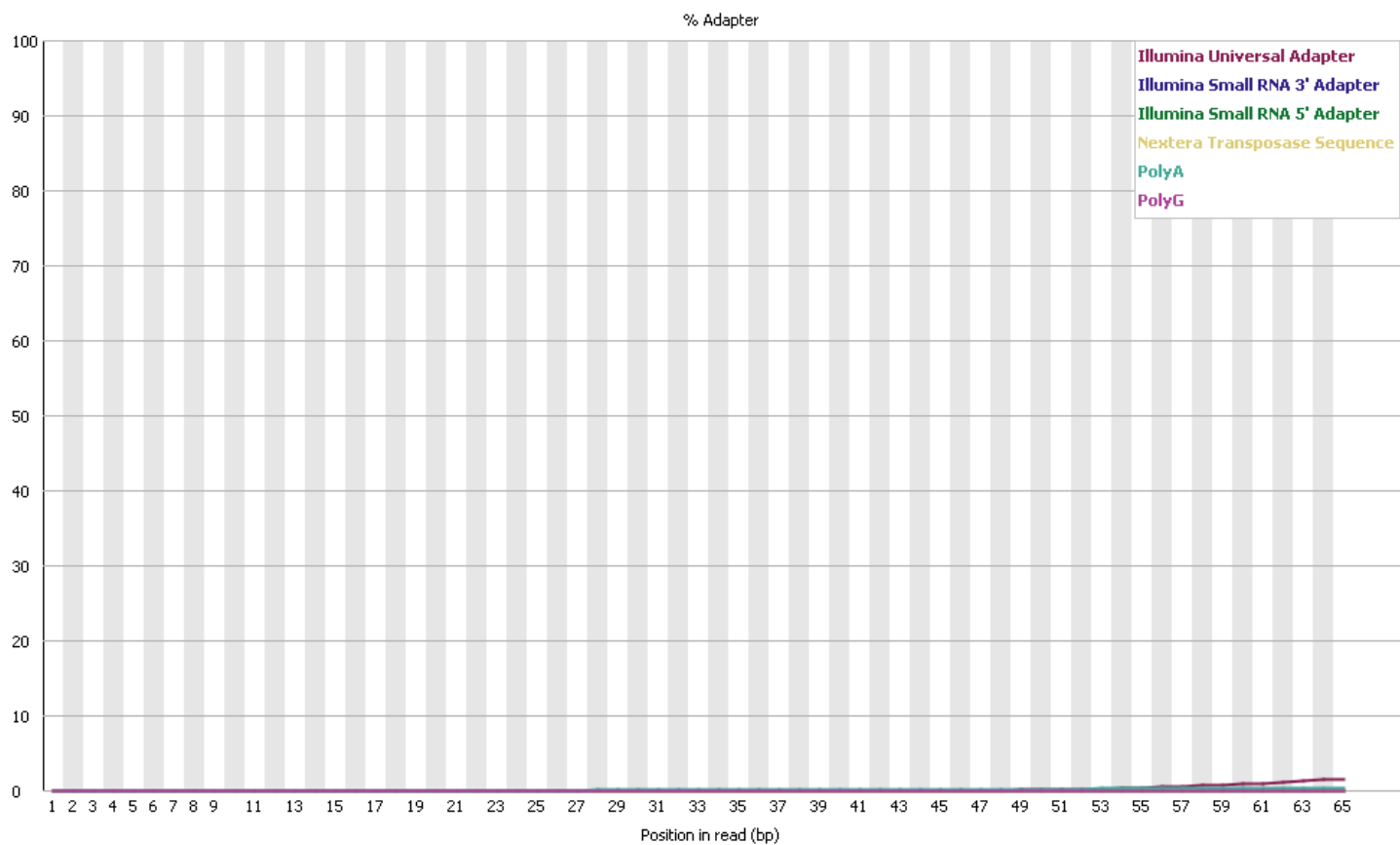


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.12.1)