#### Sat 15 Apr 2023 SAMN26643021.gz

# **№**FastQC Report

#### **Summary**



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 SAMN26643021.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 5132493

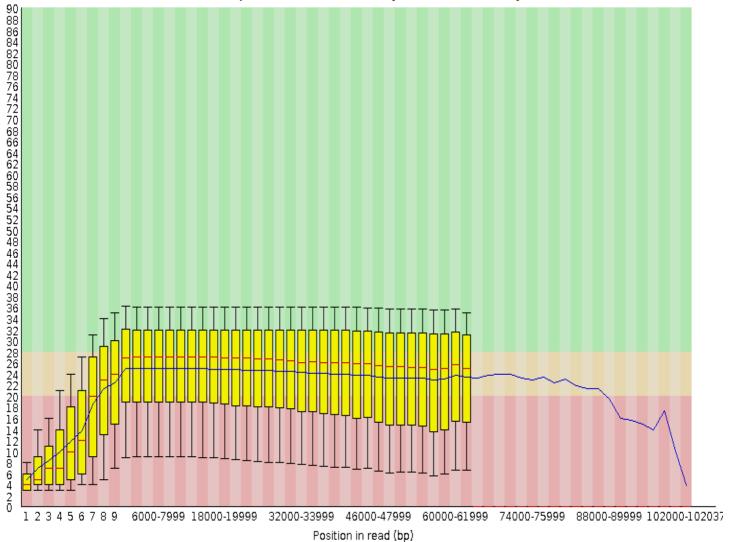
Sequences flagged as poor quality 0

Sequence length 1000-102037

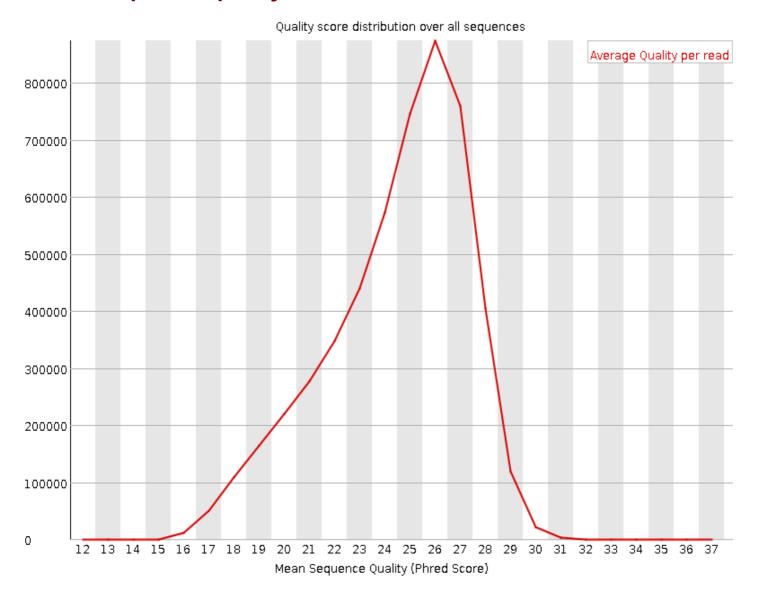
%GC 35

# Per base sequence quality

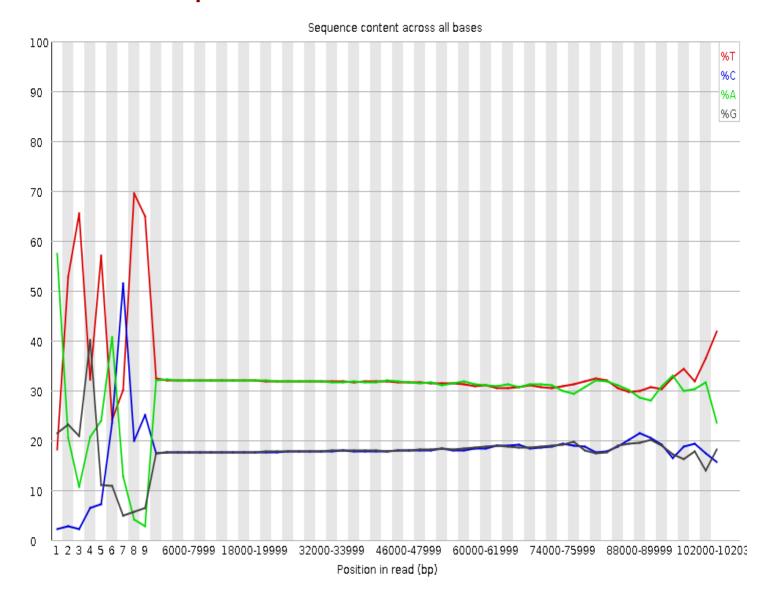
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



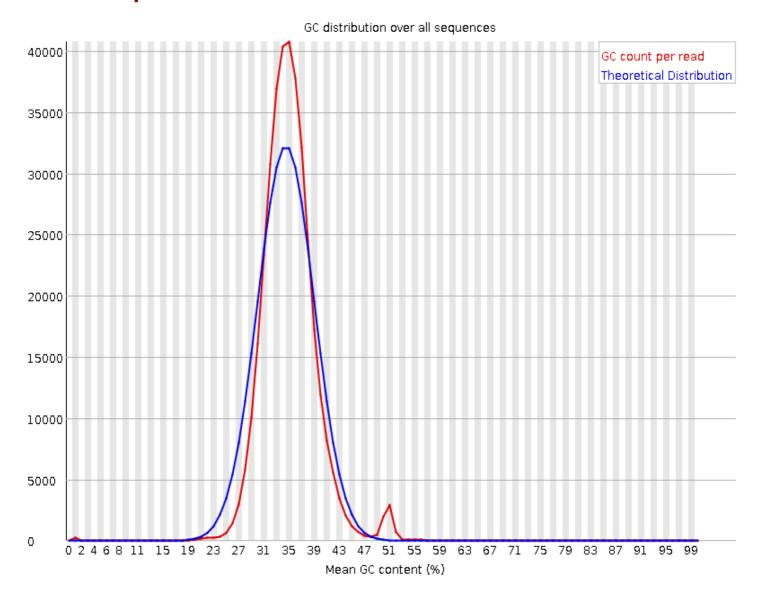
## Per sequence quality scores



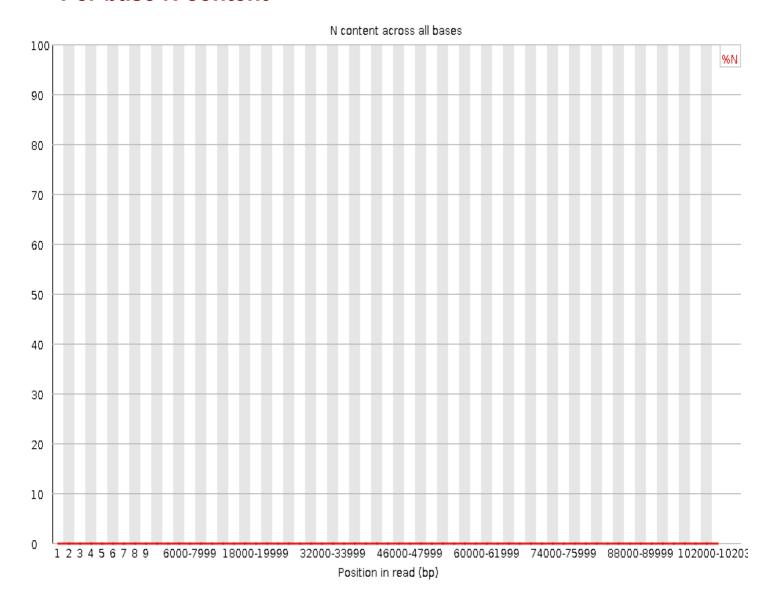
# Per base sequence content



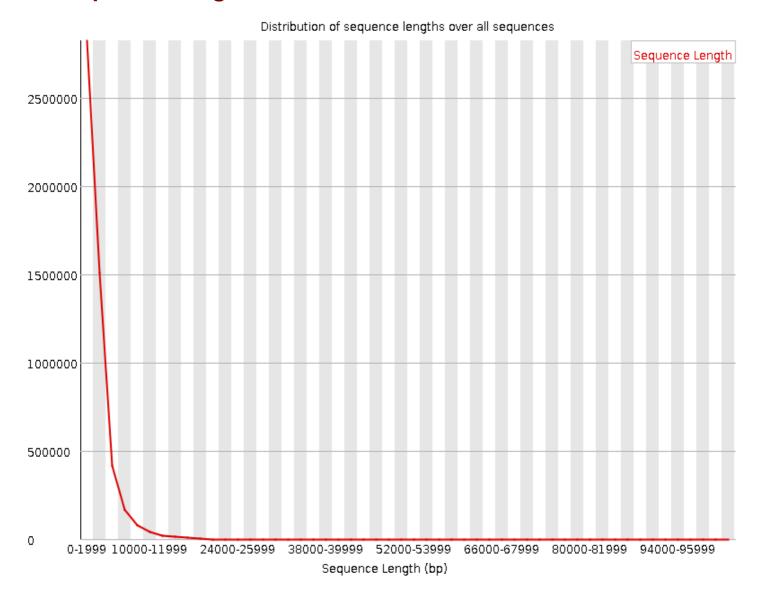
### Per sequence GC content



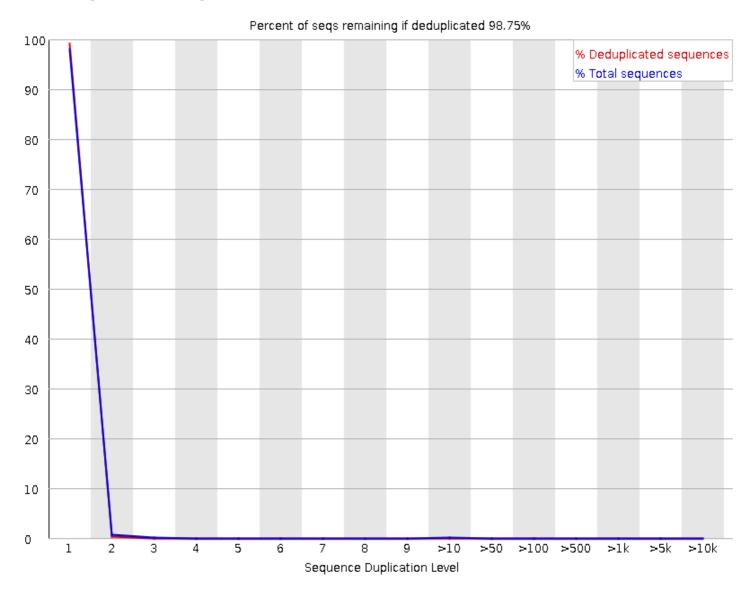
# Per base N content



### Sequence Length Distribution



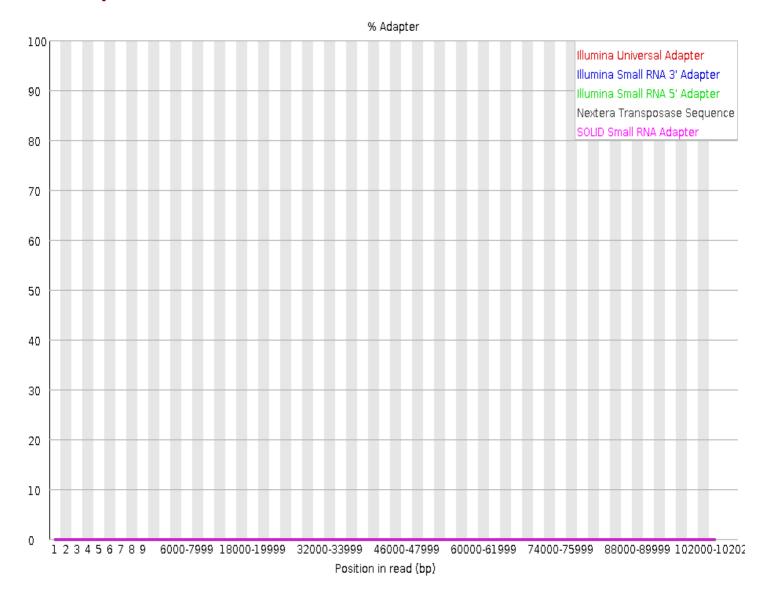
## Sequence Duplication Levels





 $file: /\!//C: /Users/usuario/Downloads/Annex\_3\_FASTQC\_Nanopore.html$ 

# Adapter Content



Produced by FastQC (version 0.11.9)