

Wed 12 Apr 2023 SAMN26643022\_forward.gz

#### **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



Measure Value

Filename SAMN26643022\_forward.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

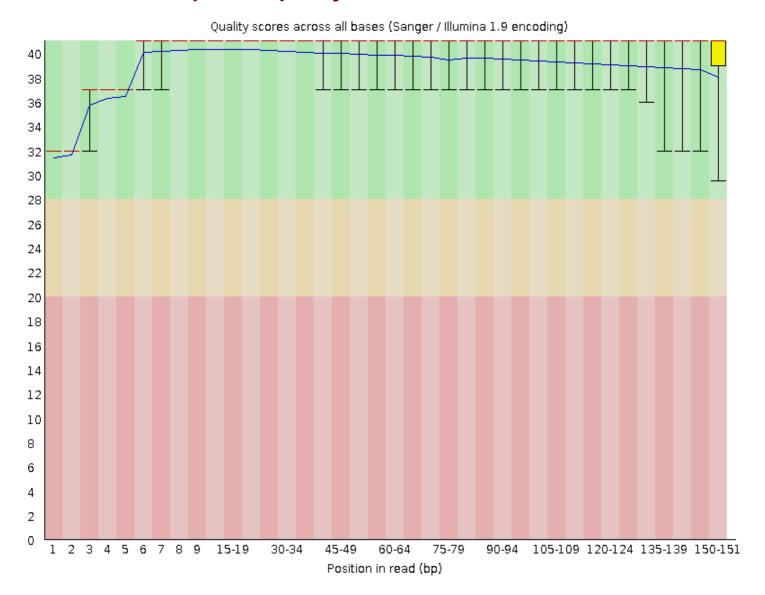
Total Sequences 72393372

Sequences flagged as poor quality 0

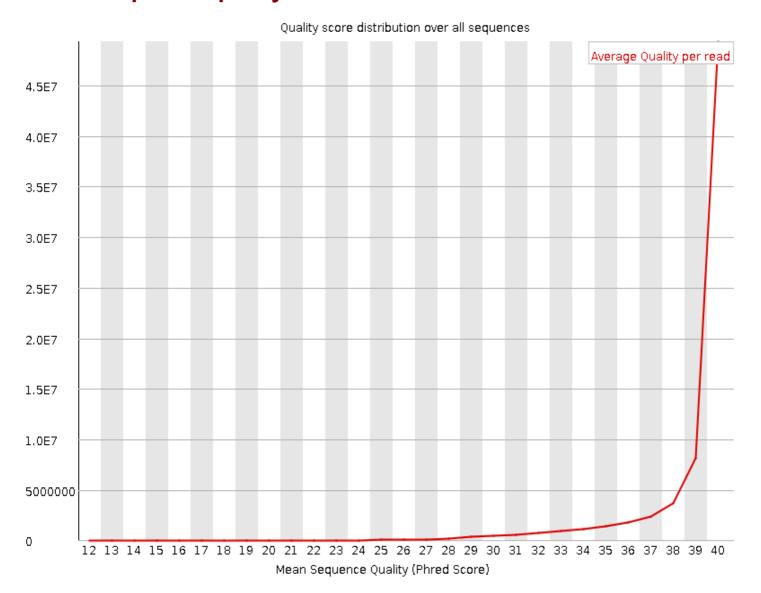
Sequence length 151

%GC 39

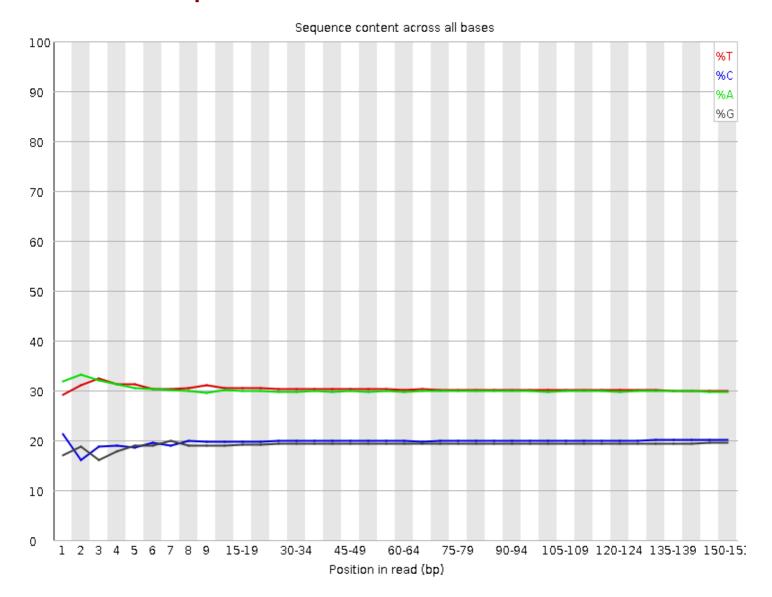
#### Per base sequence quality



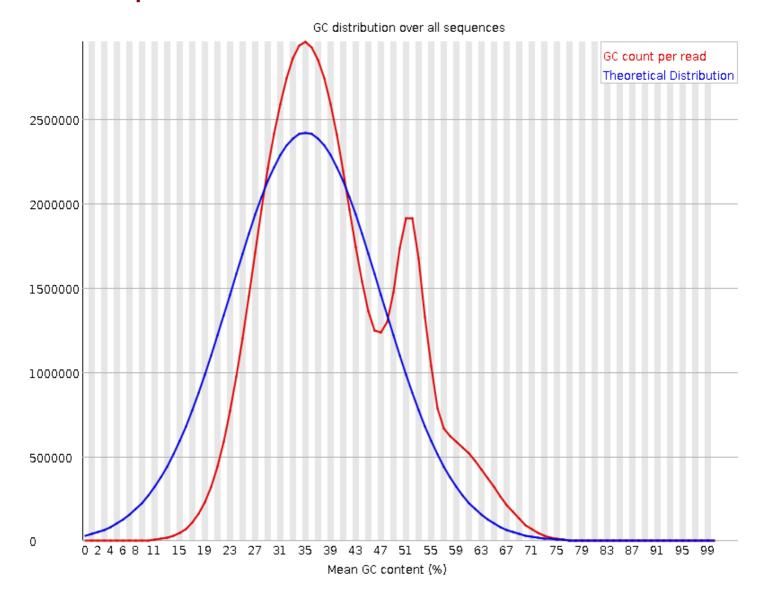
# Per sequence quality scores



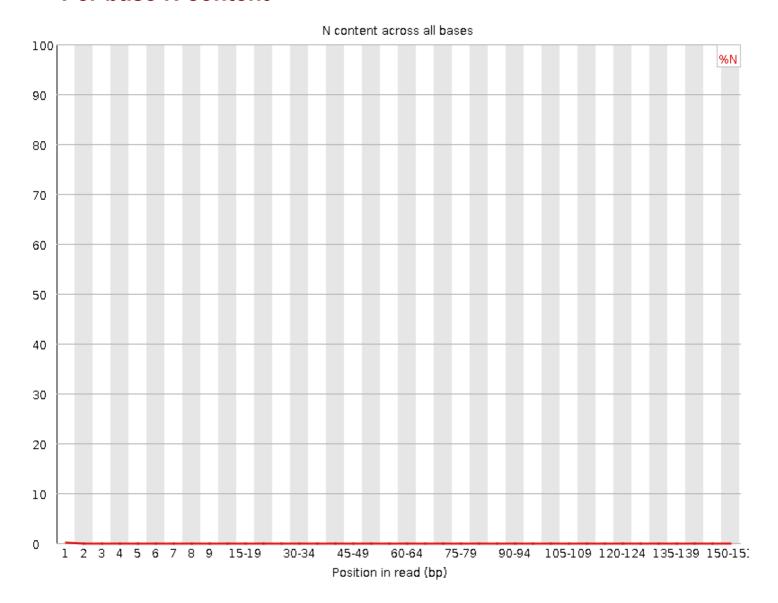
# Per base sequence content



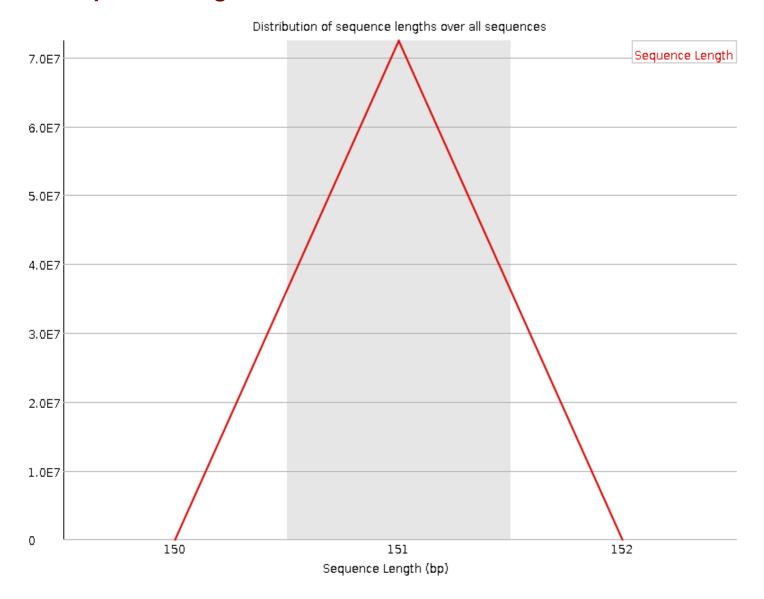
### Per sequence GC content



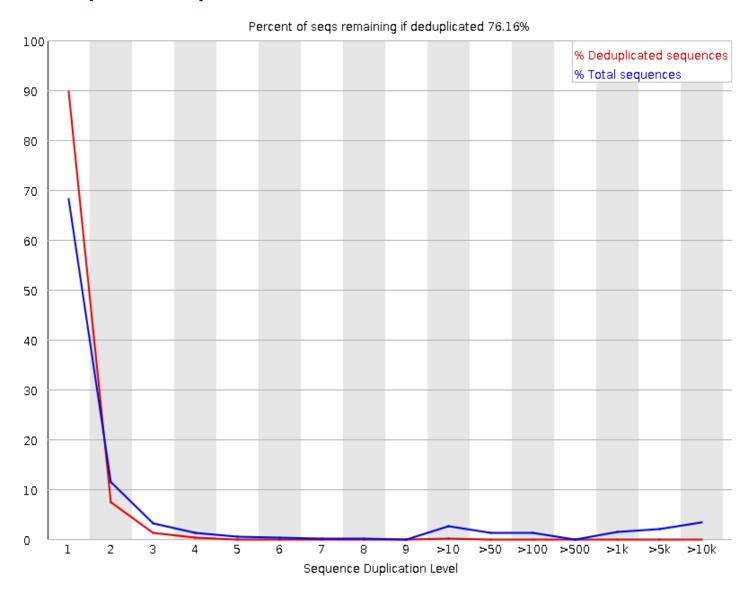
### Per base N content



#### Sequence Length Distribution



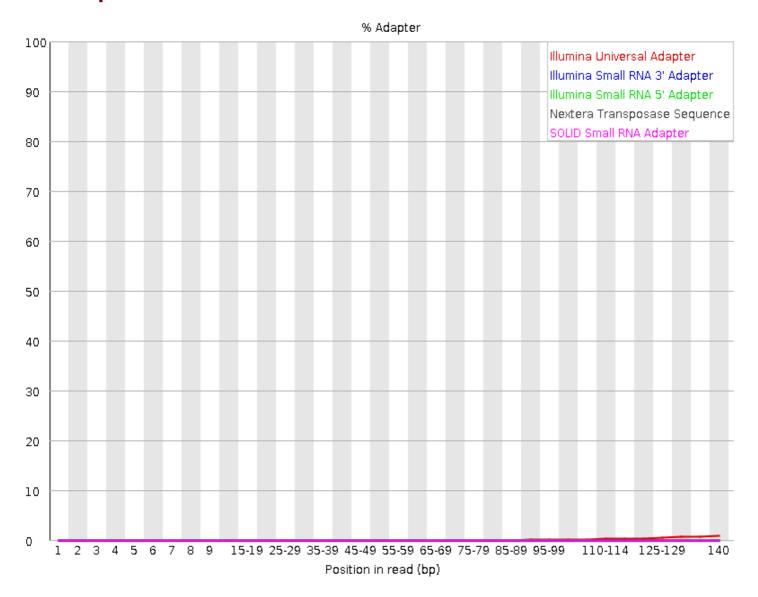
## Sequence Duplication Levels





No overrepresented sequences

## Adapter Content



Produced by FastQC (version 0.11.9)