

#### Thu 13 Apr 2023 Trimmomatic on SAMN26643022\_reverse \_R2 paired\_.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 Trimmomatic on SAMN26643022\_reverse \_R2 paired\_.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

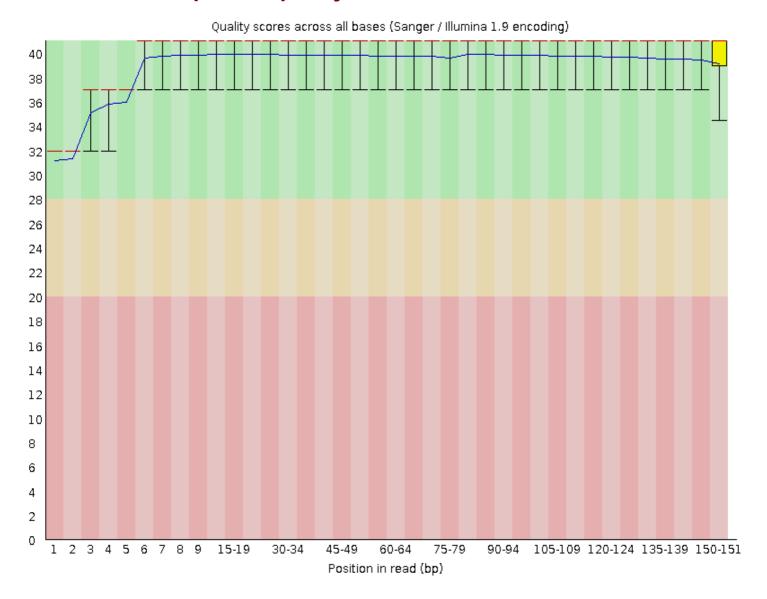
Total Sequences 71743604

Sequences flagged as poor quality 0

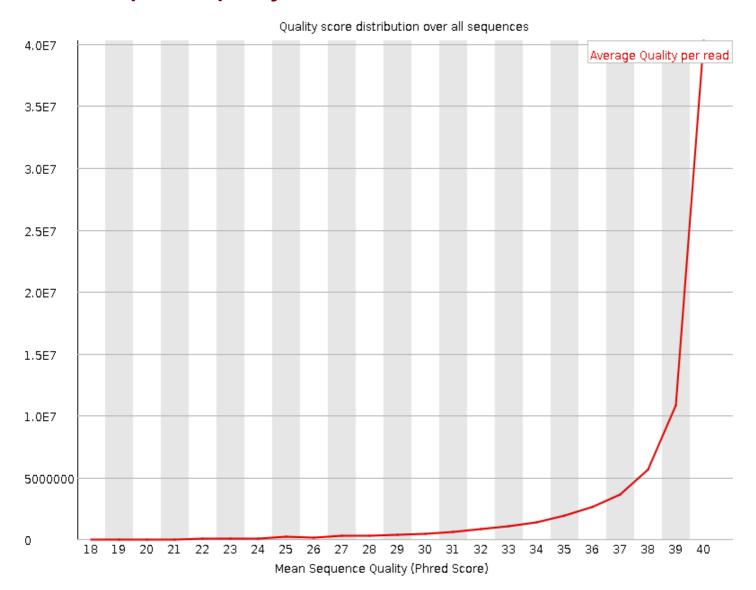
Sequence length 2-151

%GC 39

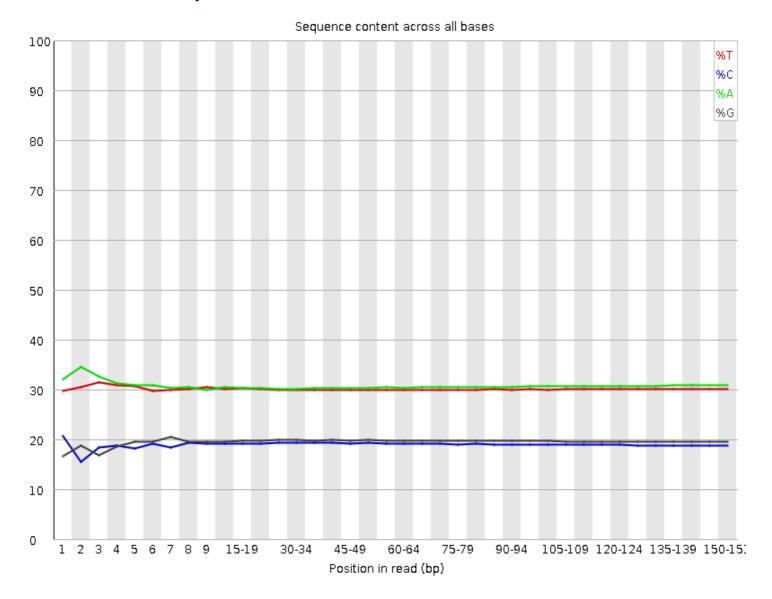
## Per base sequence quality



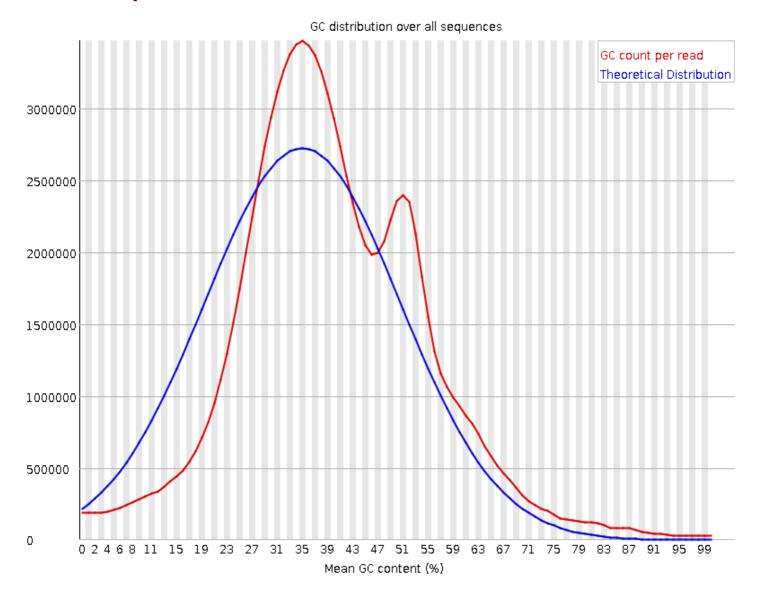
# Per sequence quality scores



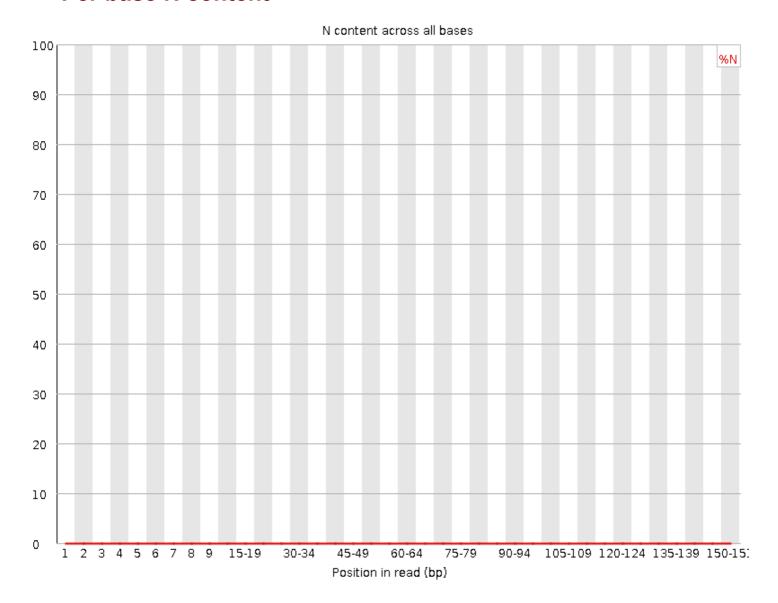
# Per base sequence content



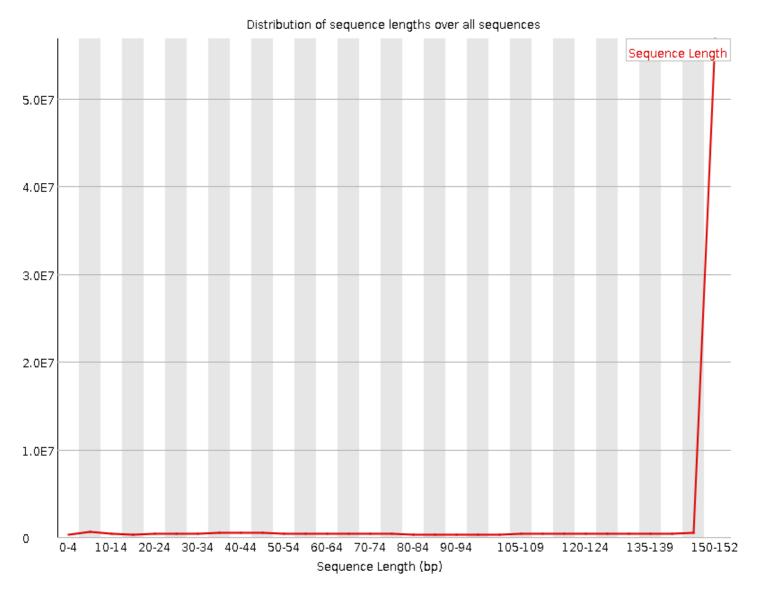
### Per sequence GC content



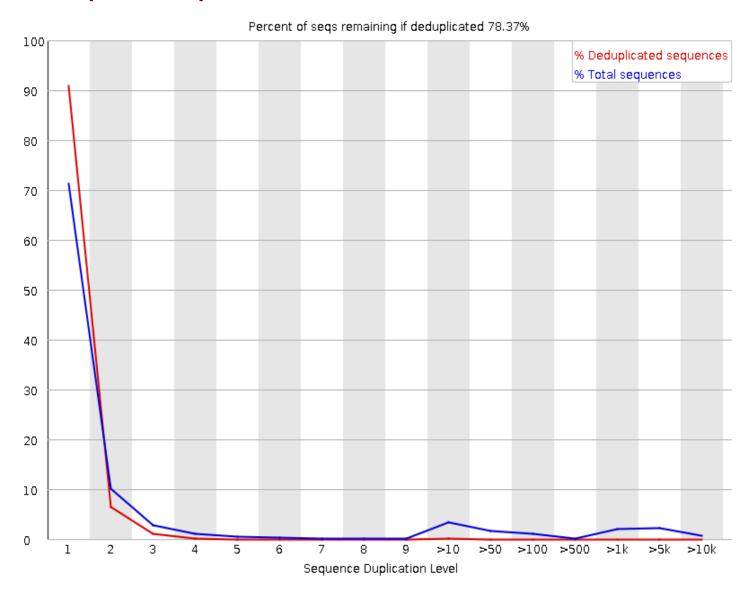
## Per base N content



#### Sequence Length Distribution

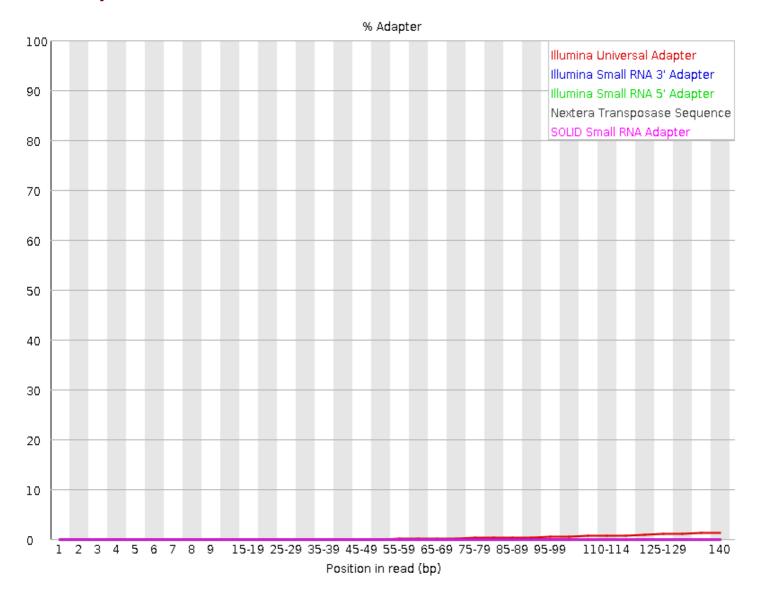


## Sequence Duplication Levels





# Adapter Content



Produced by FastQC (version 0.11.9)