# **€**FastQC Report

Wed 11 Aug 2021 SRR12740661\_2.fastq.gz

#### **Summary**







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 SRR12740661\_2.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

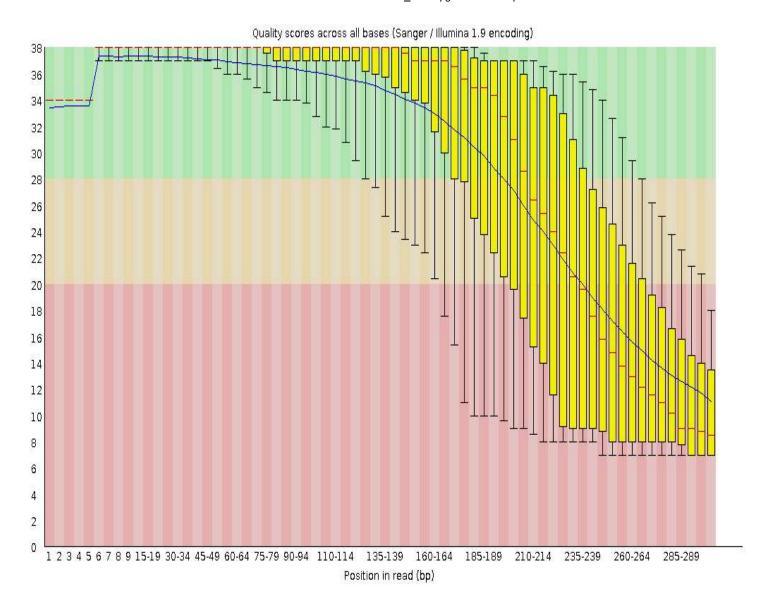
Total Sequences 797777

Sequences flagged as poor quality 0

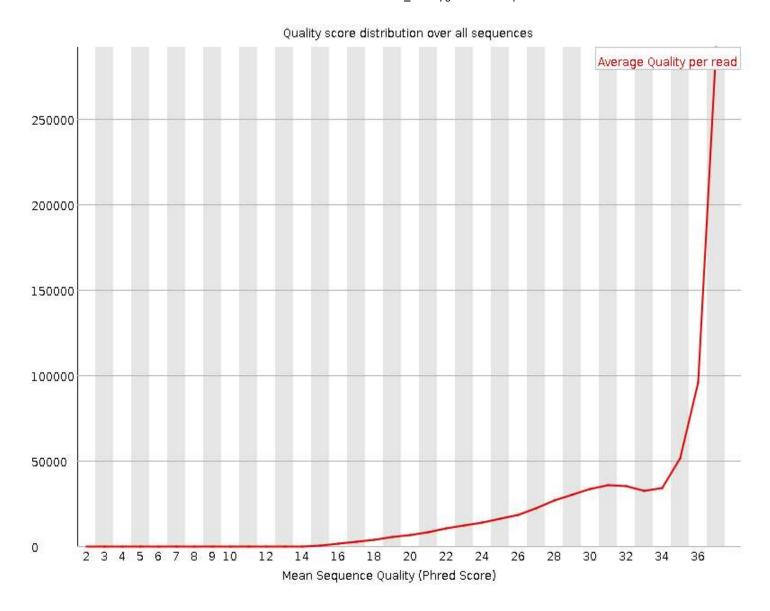
Sequence length 35-301

%GC 30

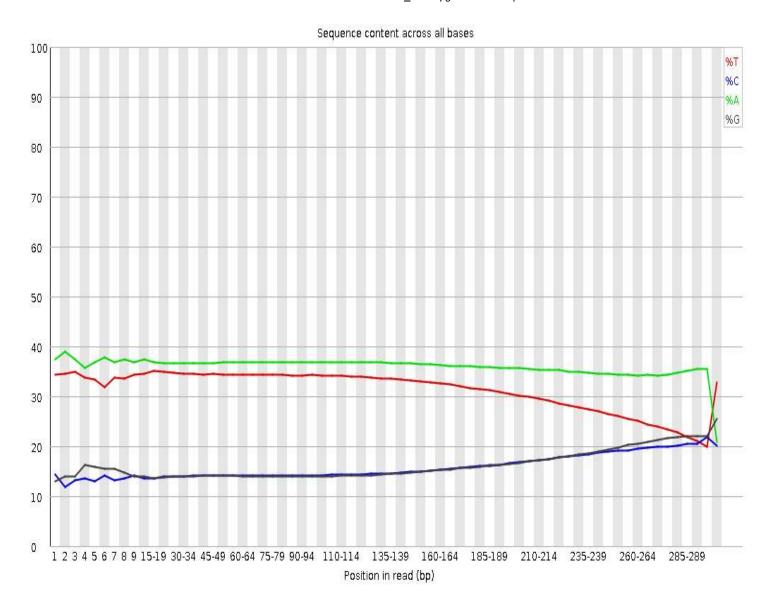
### ②Per base sequence quality



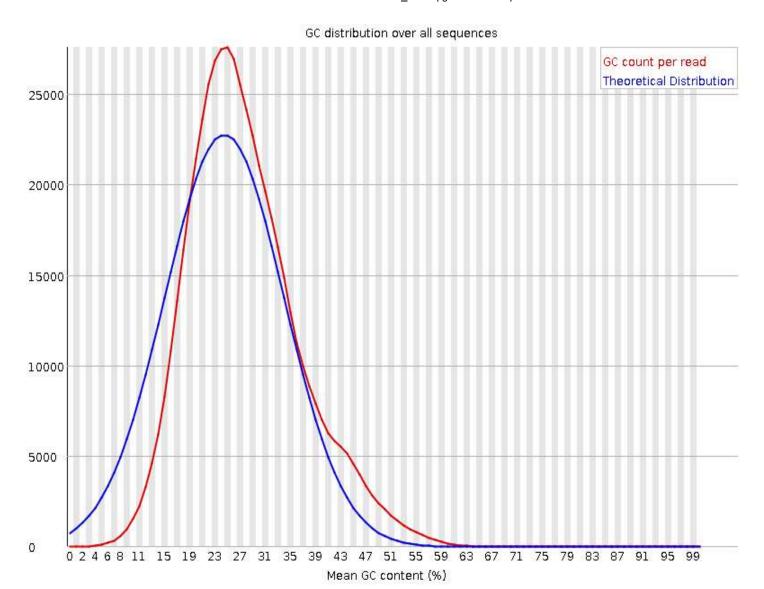




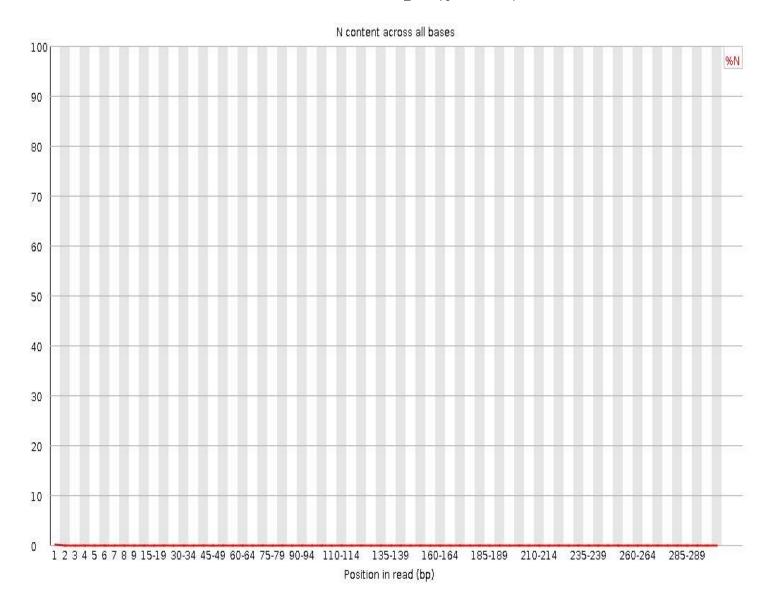
### Per base sequence content



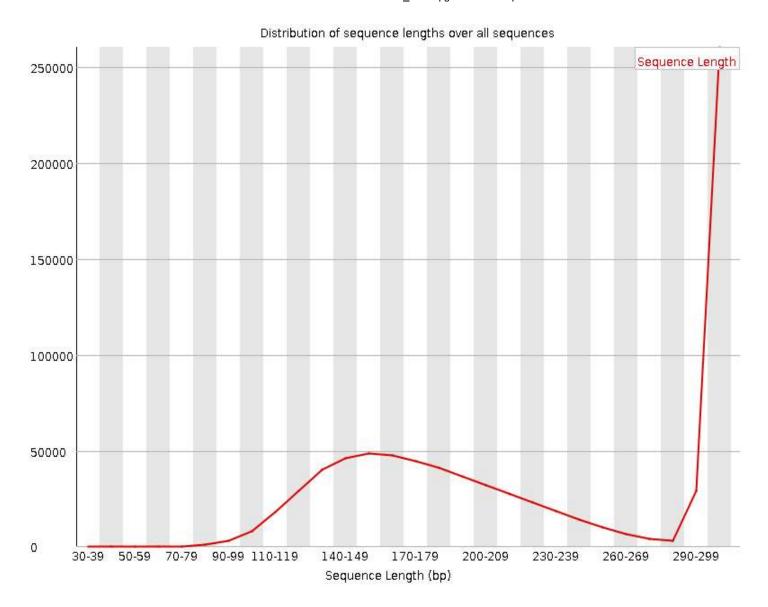
## Per sequence GC content



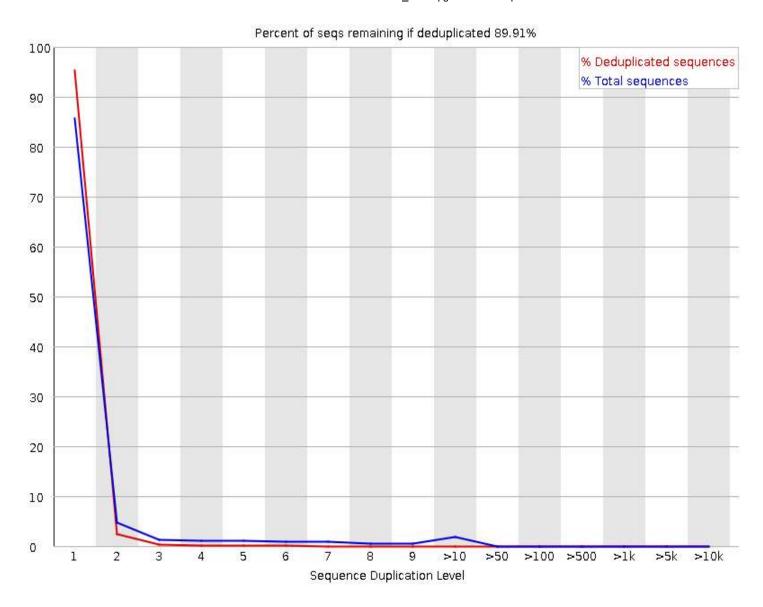




## Sequence Length Distribution

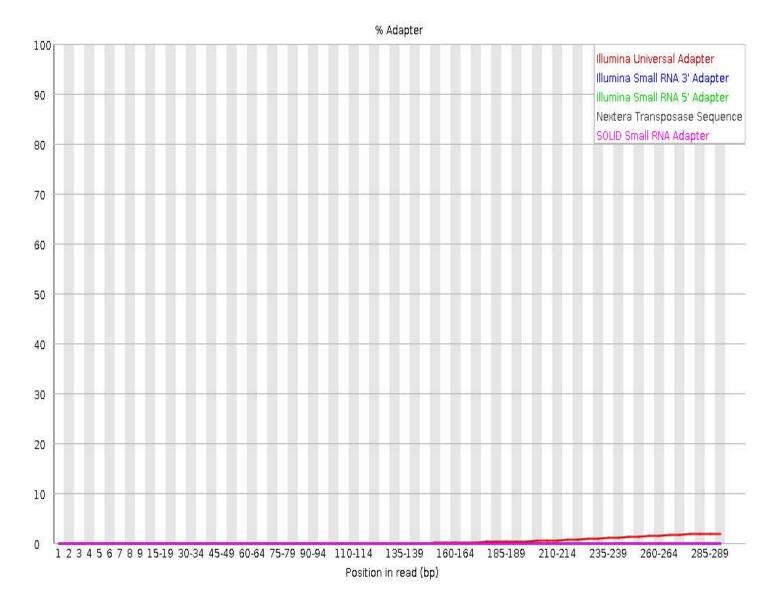








Adapter Content



#### Produced by FastQC (version 0.11.9)