# **№**FastQC Report

Sun 18 Jul 2021 SRR1554555\_2\_fastq\_gz.gz

#### Summary







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 SRR1554555\_2\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

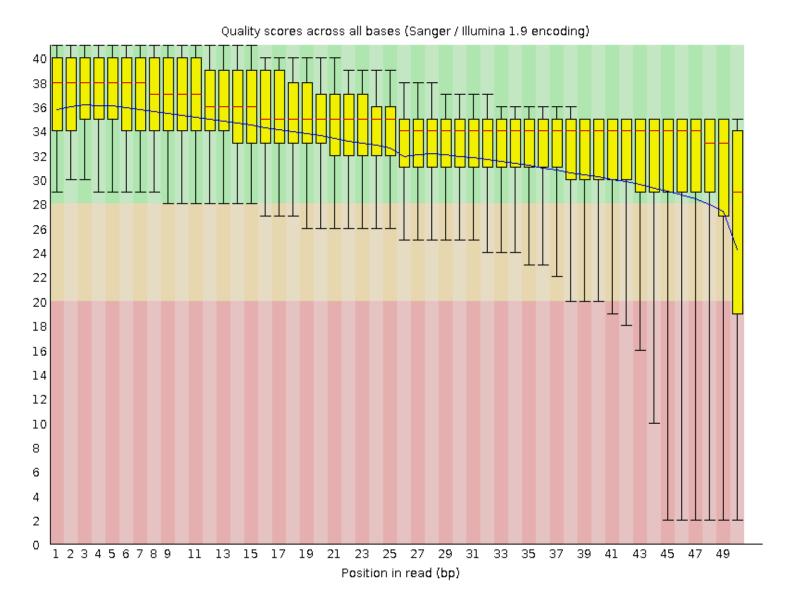
Total Sequences 52095300

Sequences flagged as poor quality 0

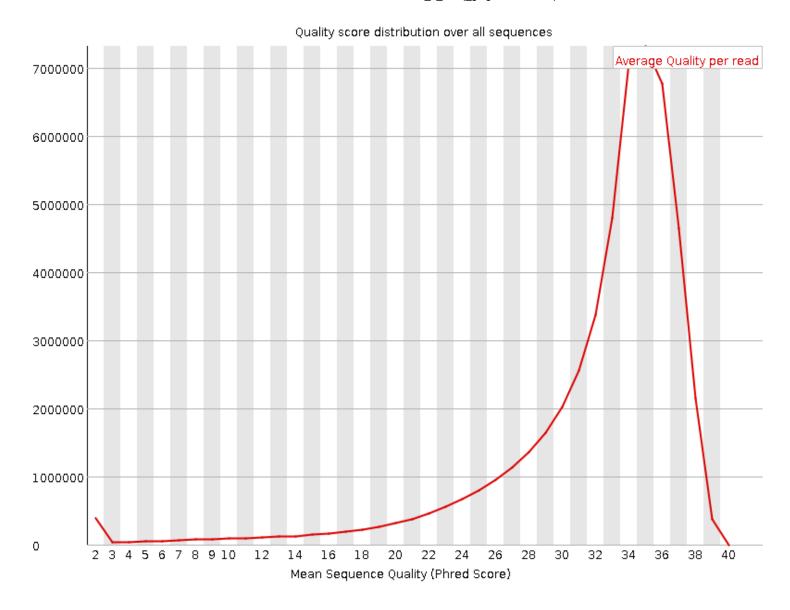
Sequence length 50

%GC 48

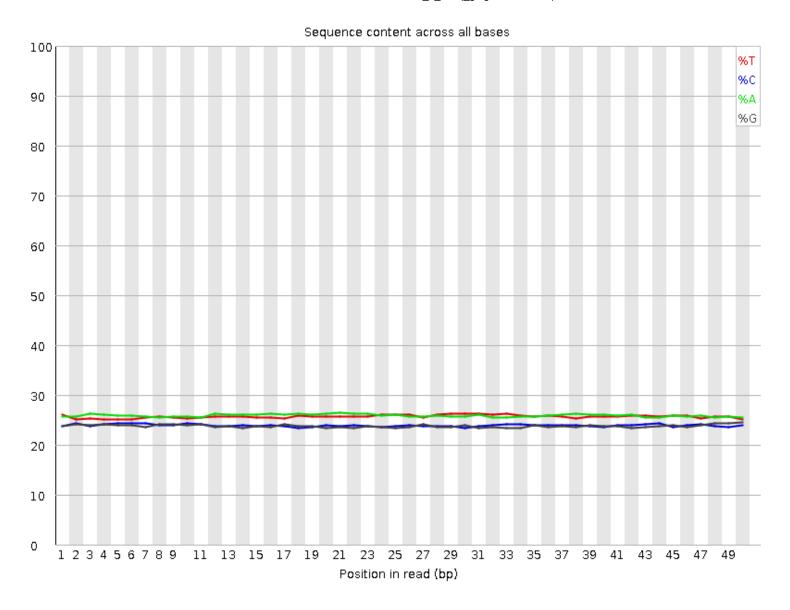
#### Per base sequence quality



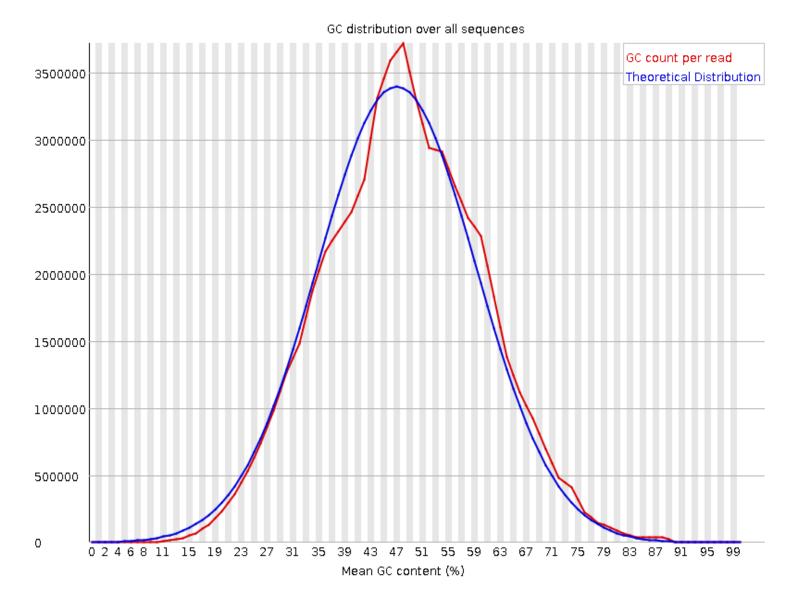
# Per sequence quality scores



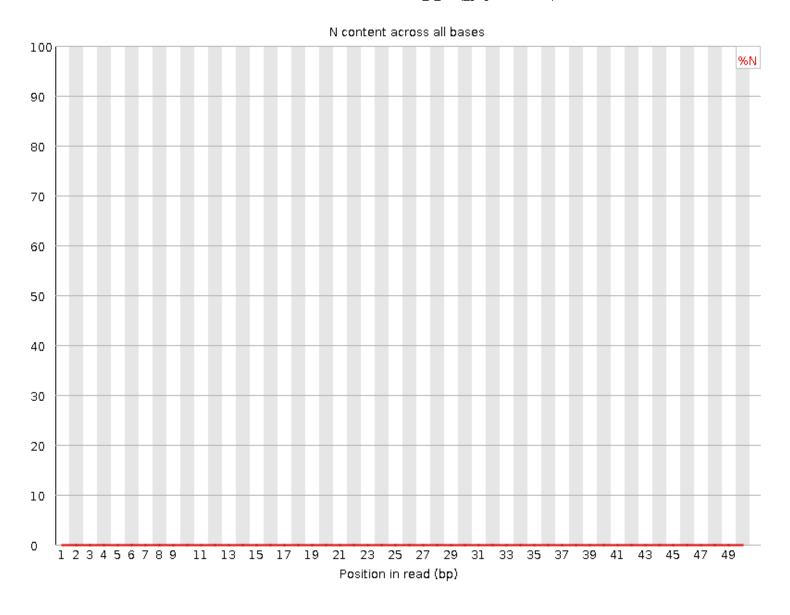
### Per base sequence content



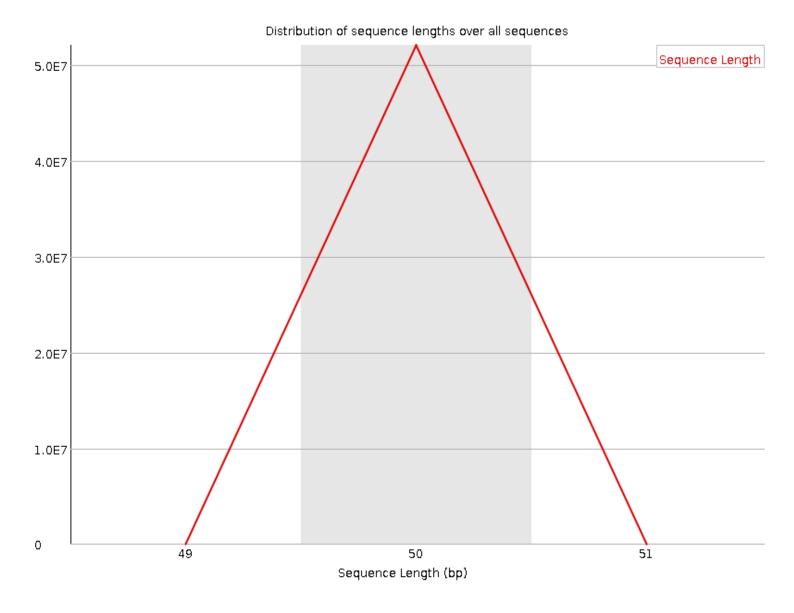
# Per sequence GC content



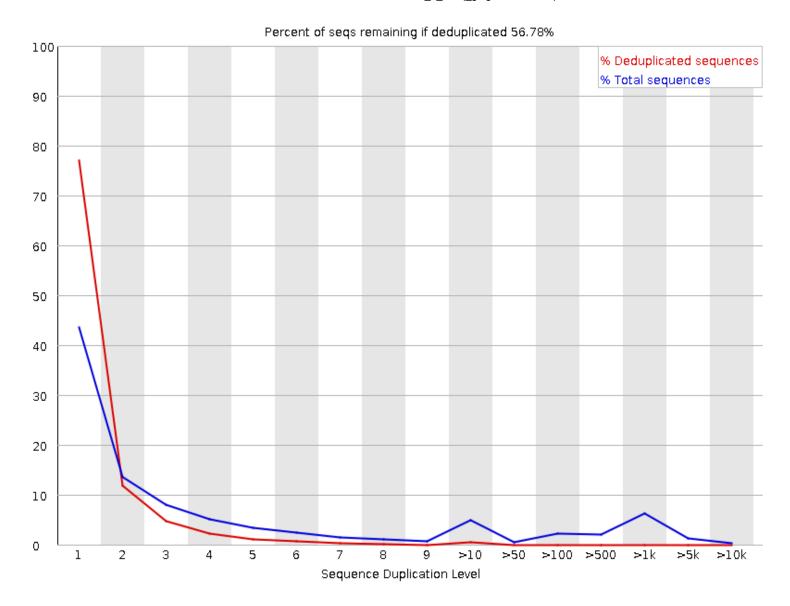




# Sequence Length Distribution

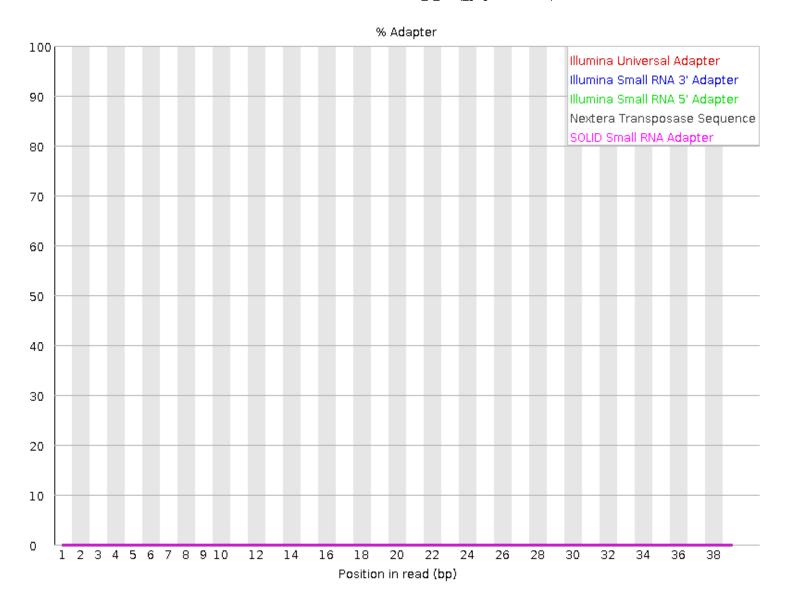


#### Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.11.8)