# **€**FastQC Report

Thu 1 Jul 2021 SRR1554538\_2\_fastq\_gz.gz

#### Summary





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 SRR1554538\_2\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

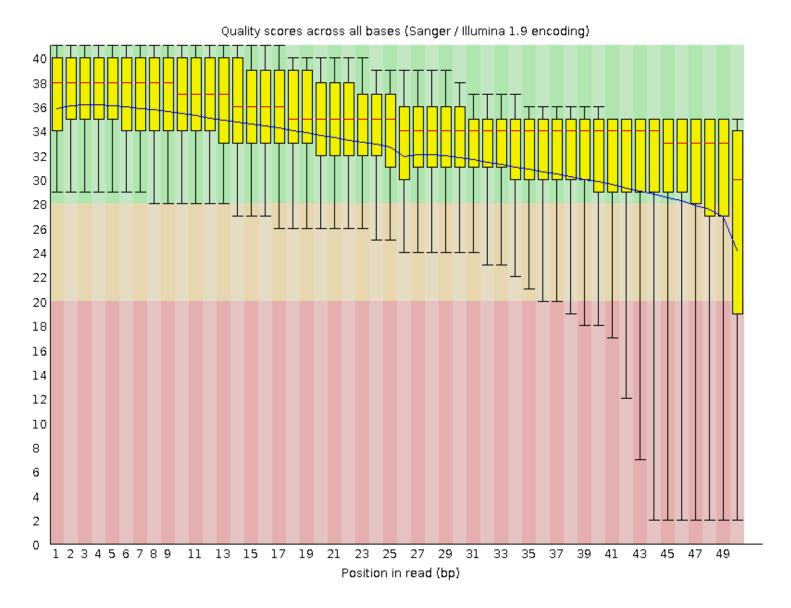
Total Sequences 147333336

Sequences flagged as poor quality 0

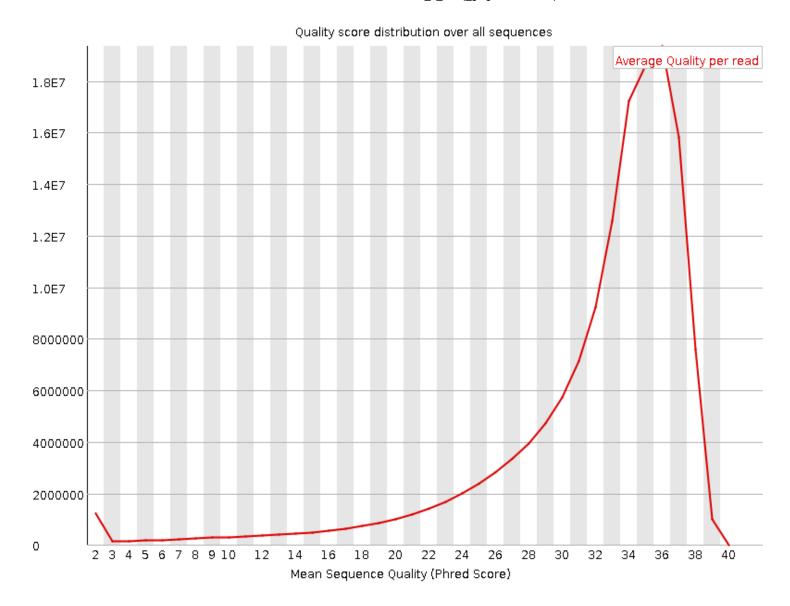
Sequence length 50

%GC 47

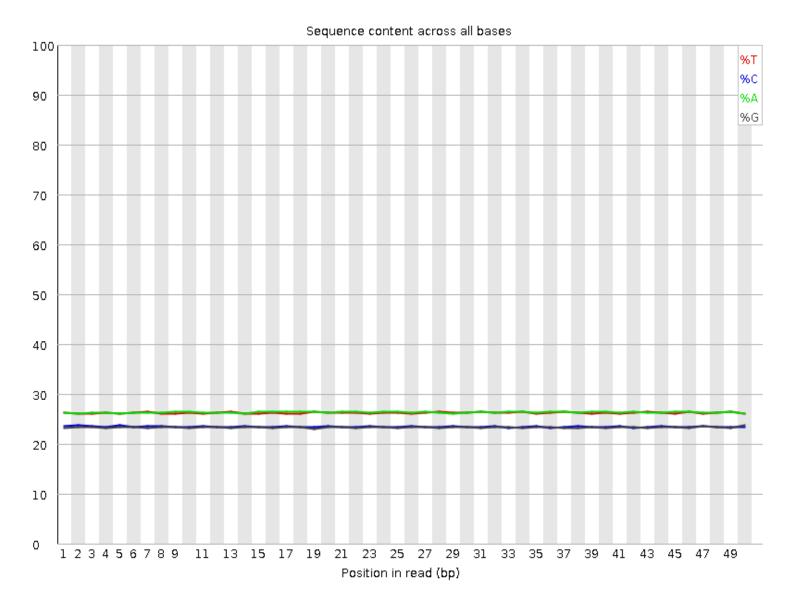
#### Per base sequence quality



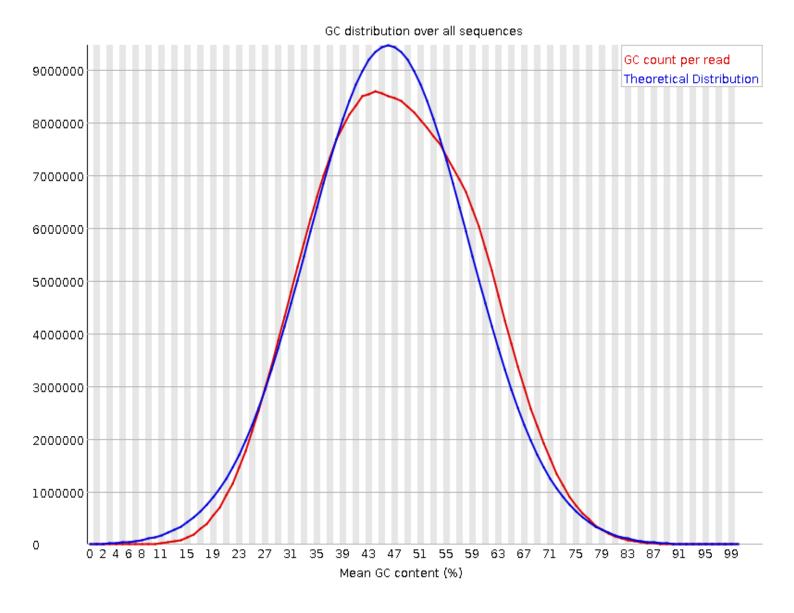
## Per sequence quality scores



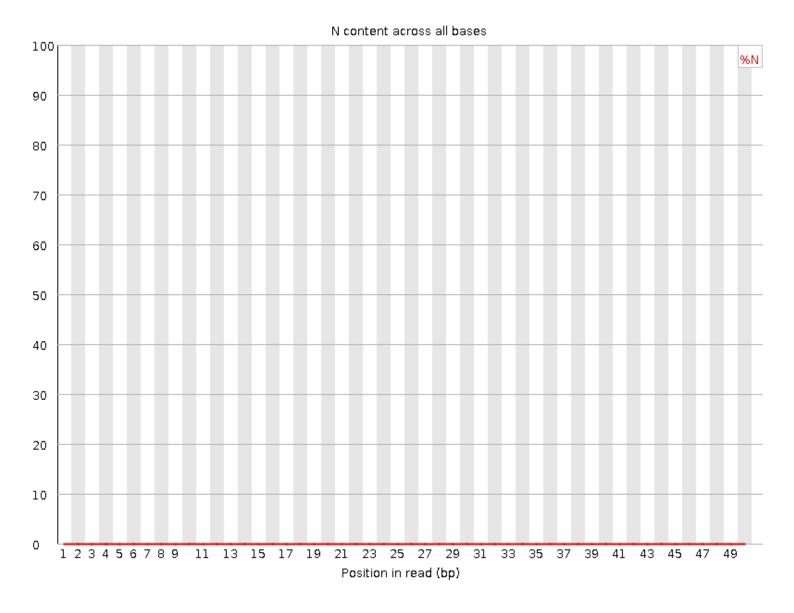
#### Per base sequence content



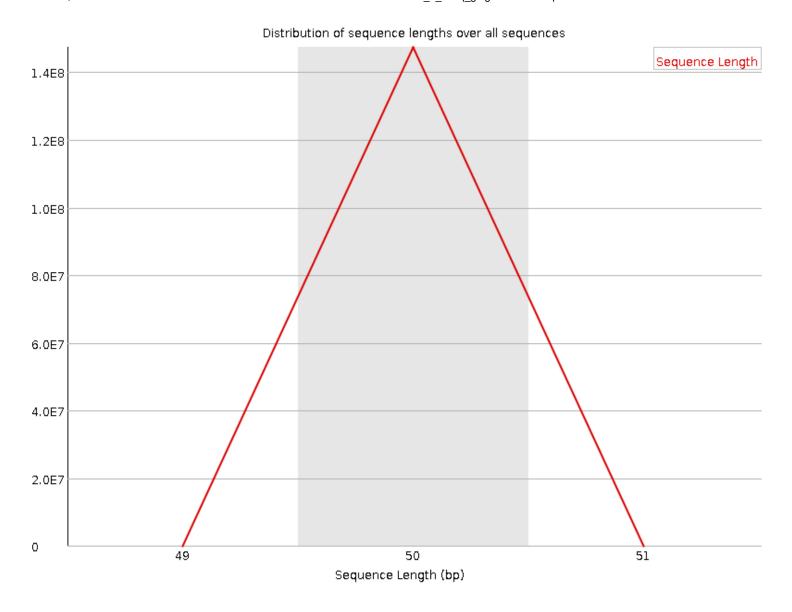
## Per sequence GC content



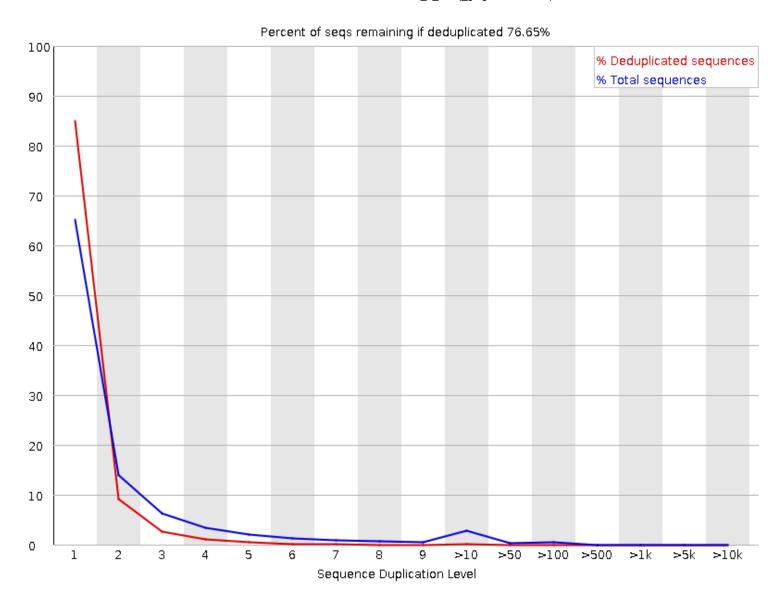




## Sequence Length Distribution

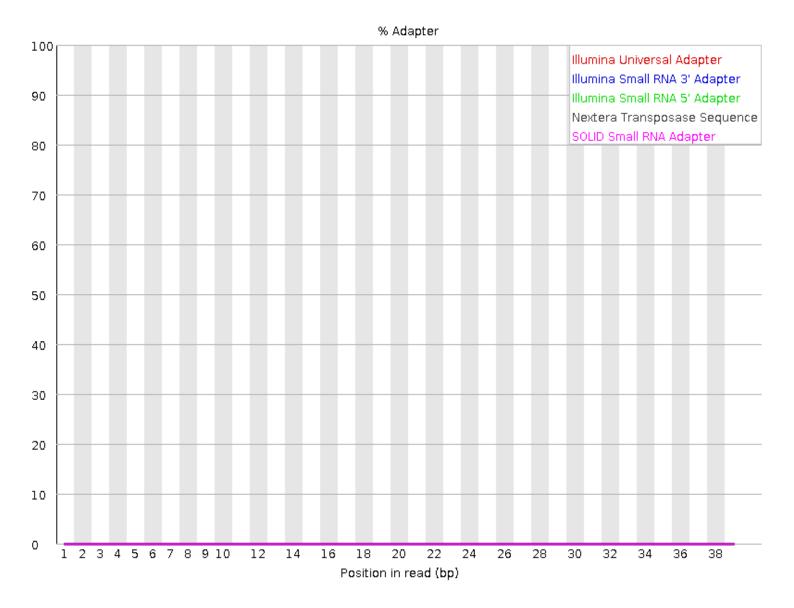


#### Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.11.8)