

Fri 2 Jul 2021 SRR1554539\_1\_adapt\_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 SRR1554539\_1\_adapt\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

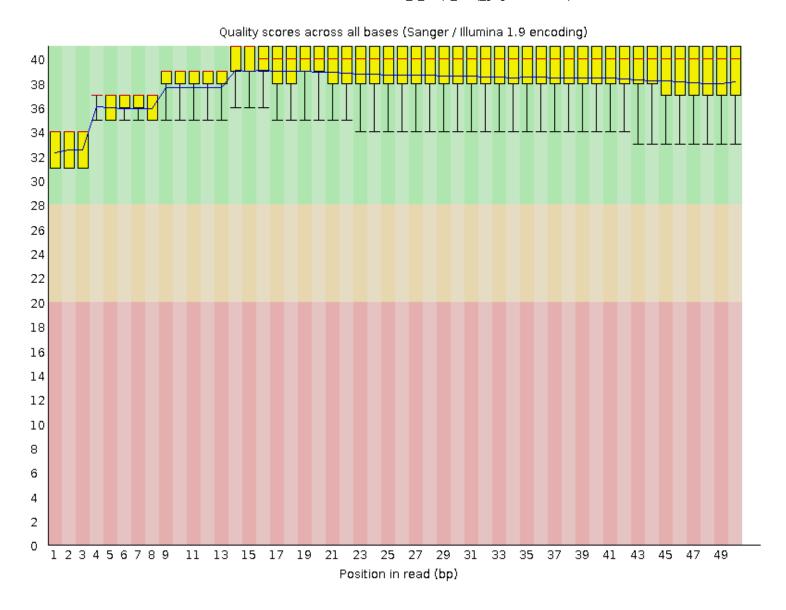
Total Sequences 75954647

Sequences flagged as poor quality 0

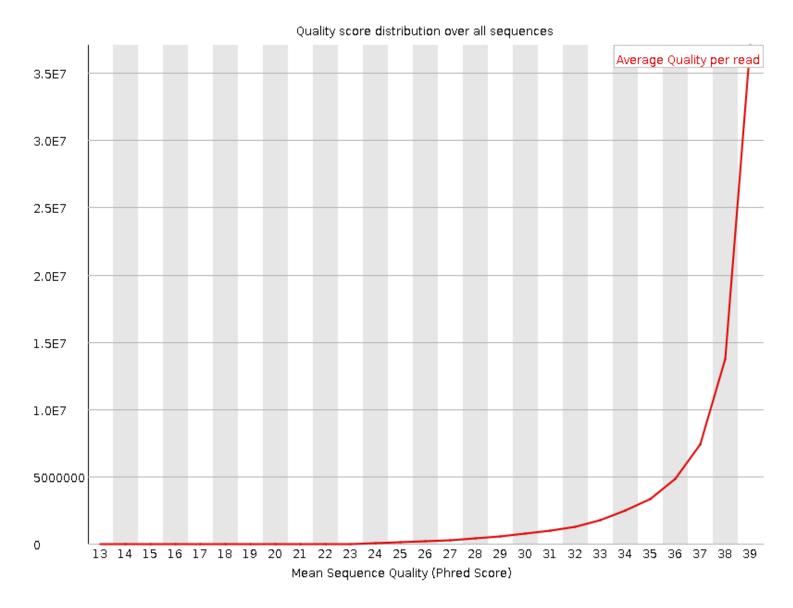
Sequence length 20-50

%GC 48

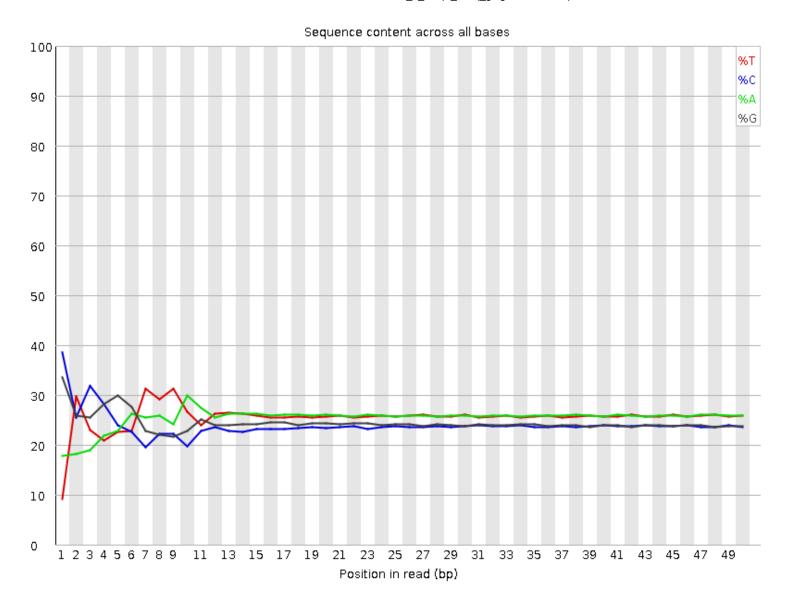
## Per base sequence quality



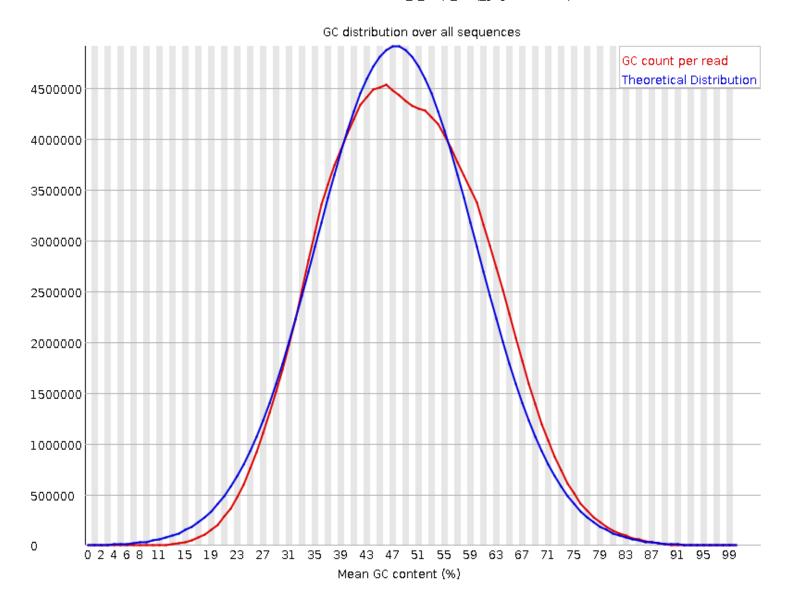
## Per sequence quality scores



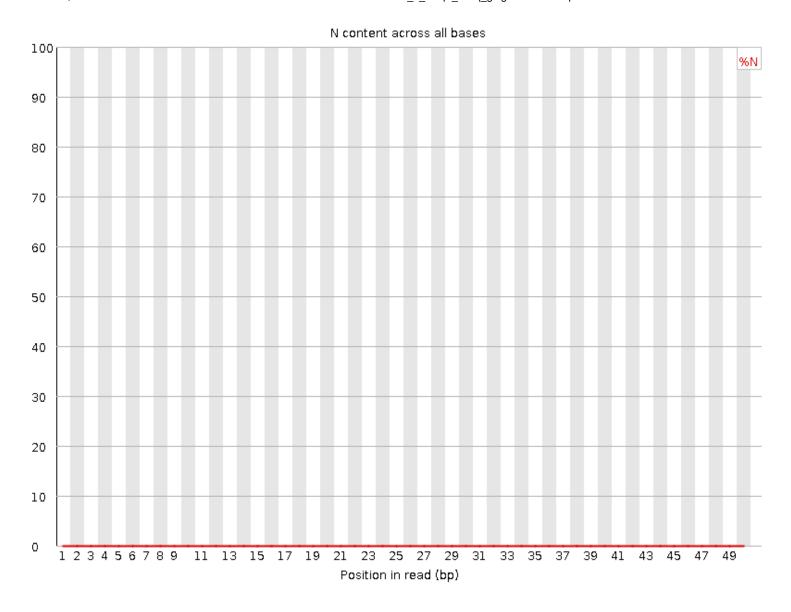
#### Per base sequence content



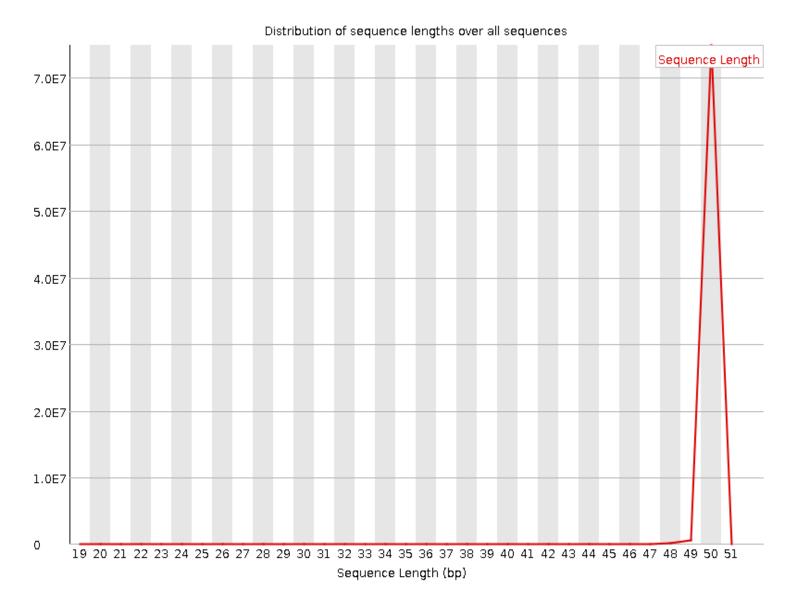
# Per sequence GC content



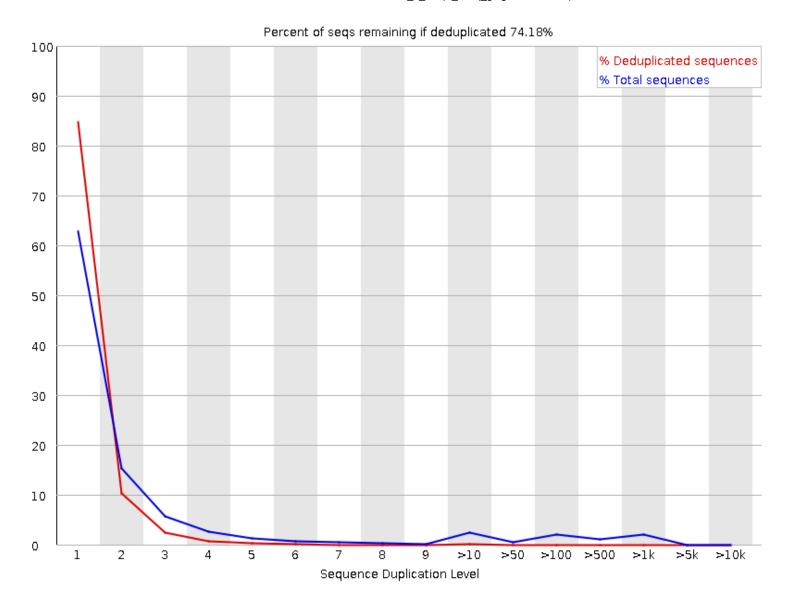




### Sequence Length Distribution

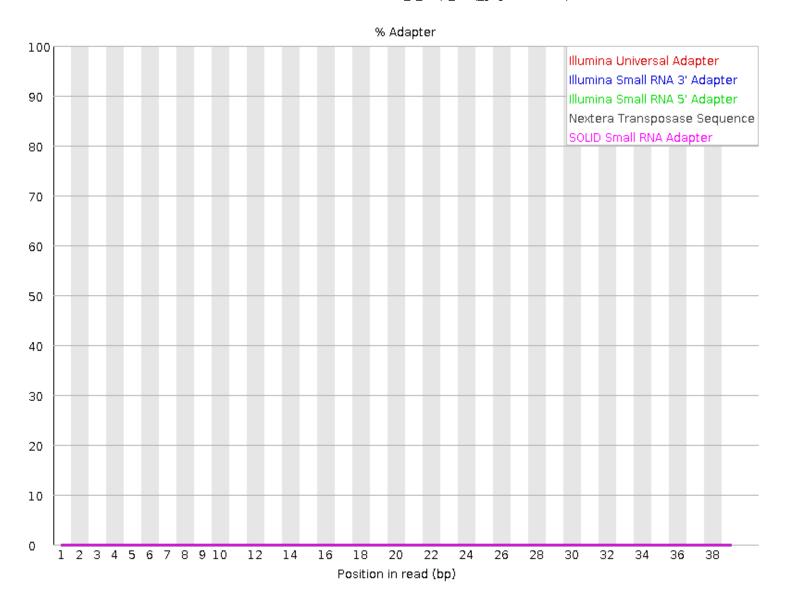


## Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.11.8)