

Thu 1 Jul 2021 SRR1554561\_2\_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 SRR1554561\_2\_adapt\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

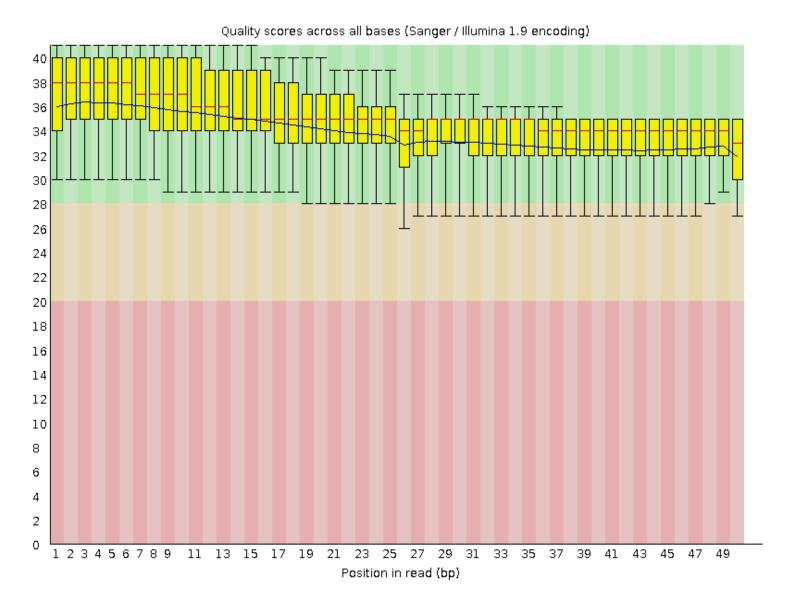
Total Sequences 87005655

Sequences flagged as poor quality  $\,\,$  0  $\,$ 

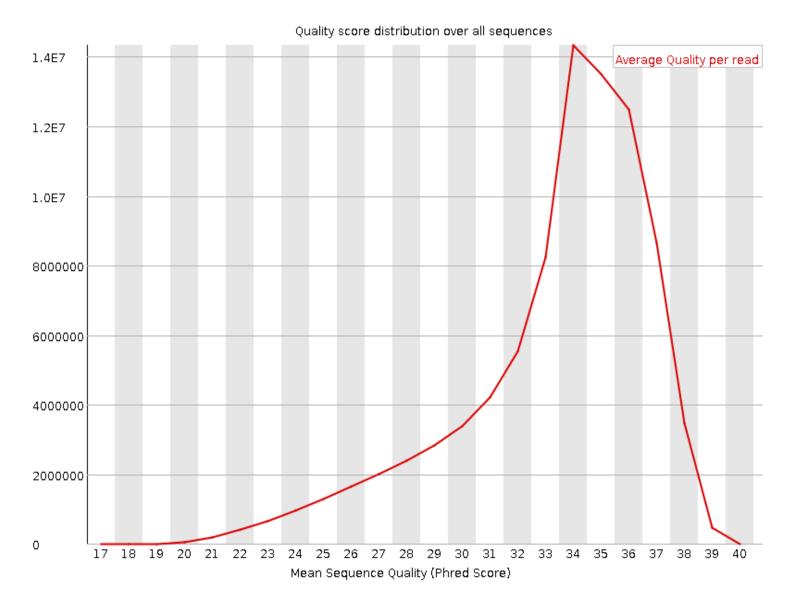
Sequence length 20-50

%GC 51

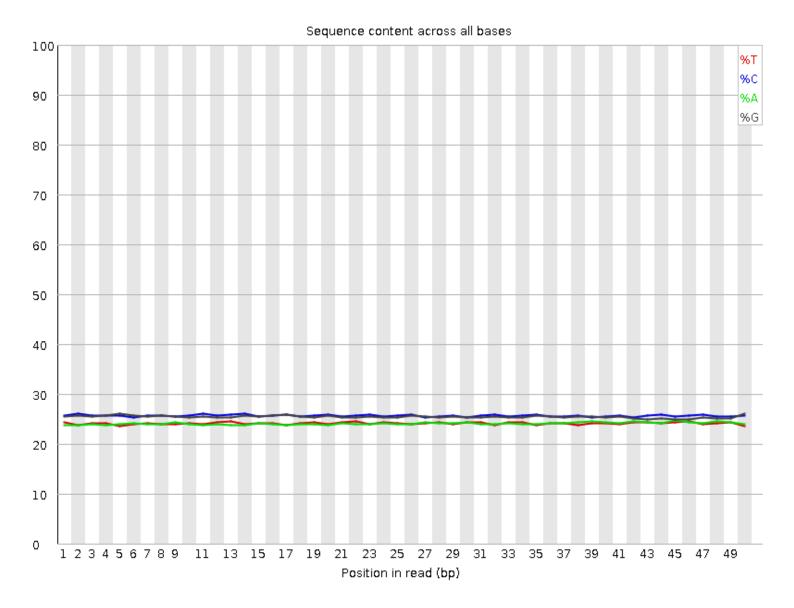
# Per base sequence quality



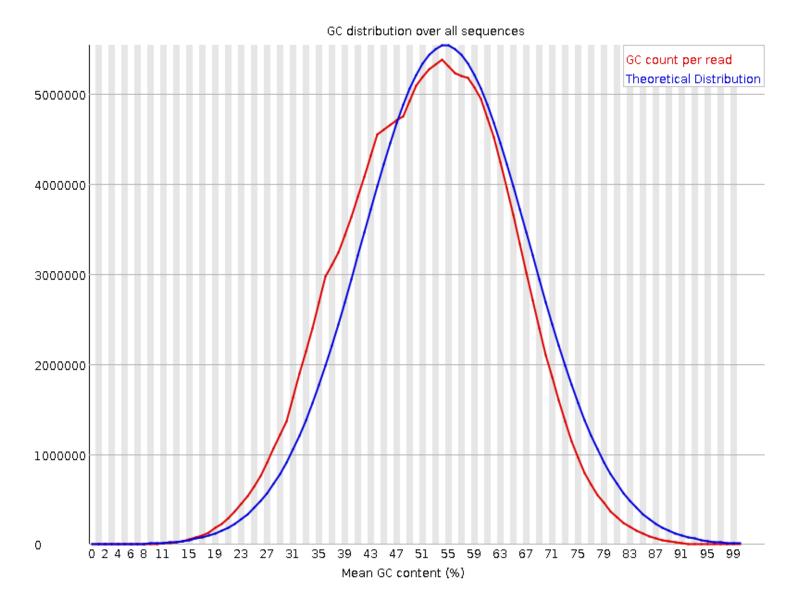
# Per sequence quality scores



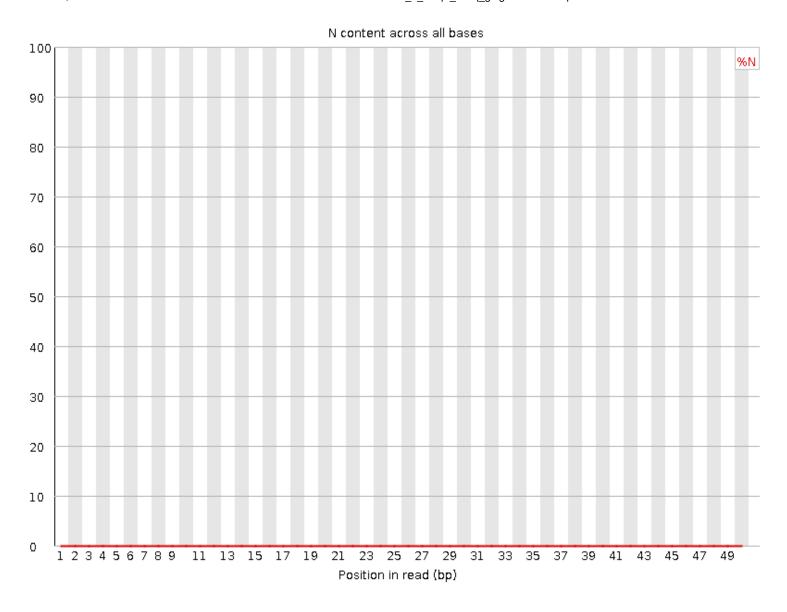
# Per base sequence content



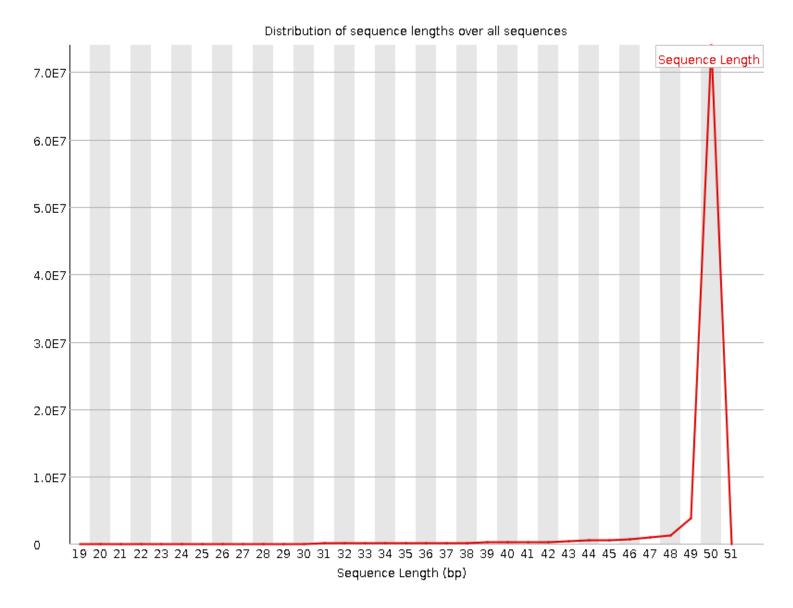
## Per sequence GC content



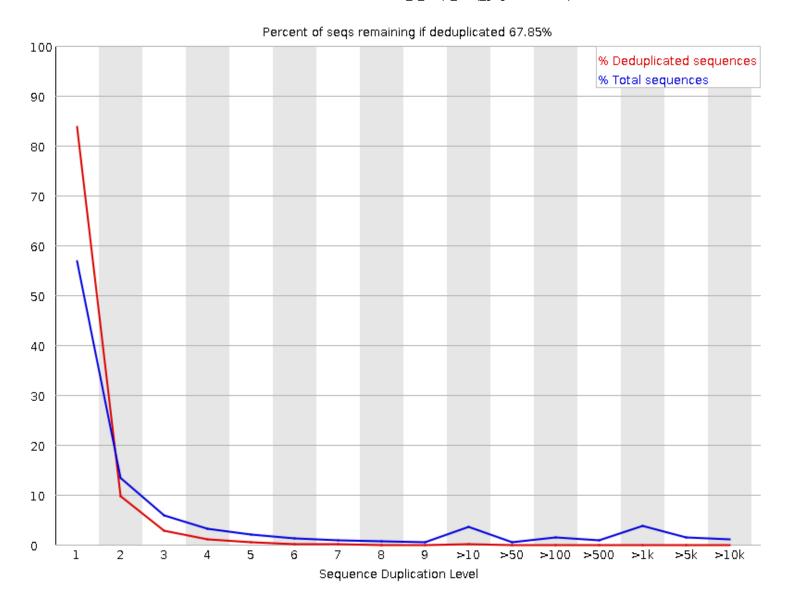




## Sequence Length Distribution

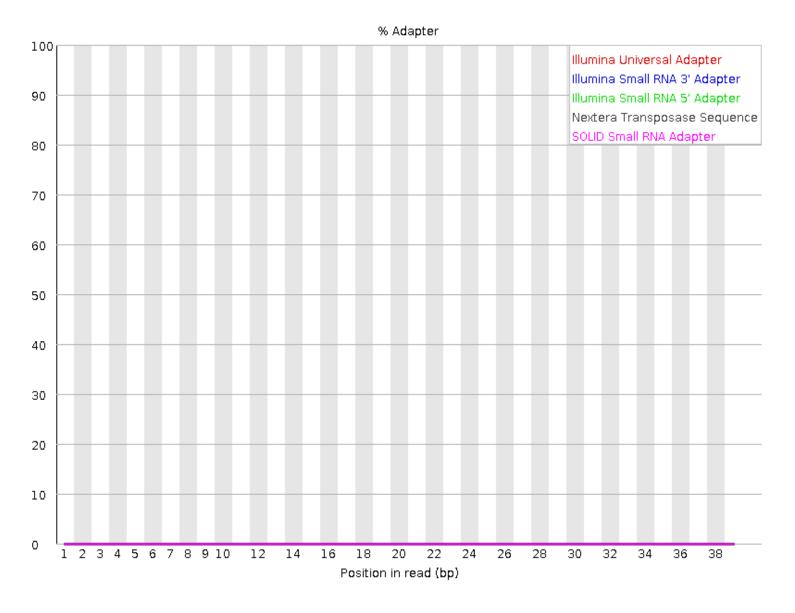


### Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.11.8)