

Mon 19 Jul 2021 SRR1554555\_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 SRR1554555\_1\_adapt\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

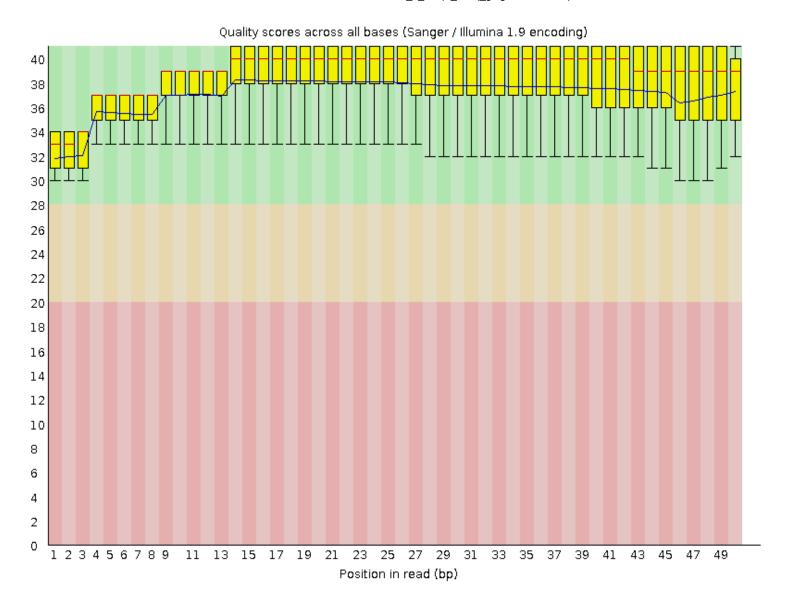
Total Sequences 50987496

Sequences flagged as poor quality 0

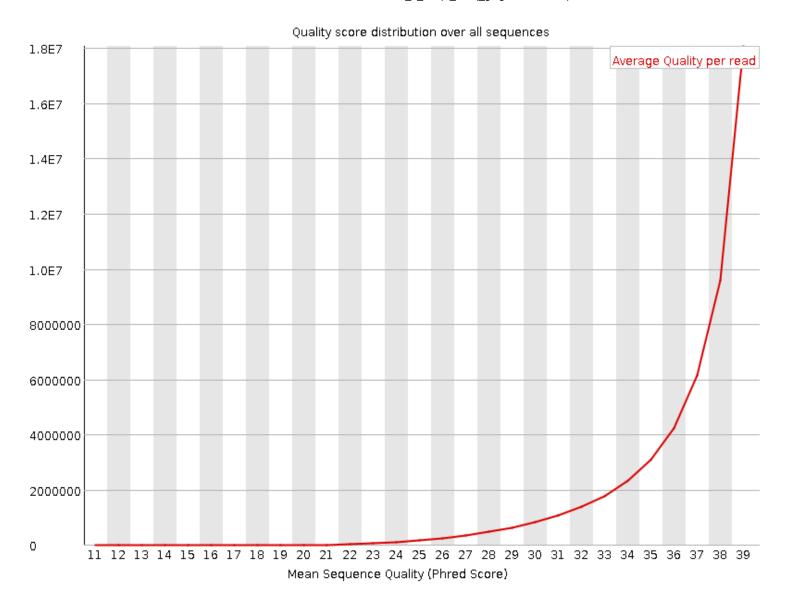
Sequence length 20-50

%GC 48

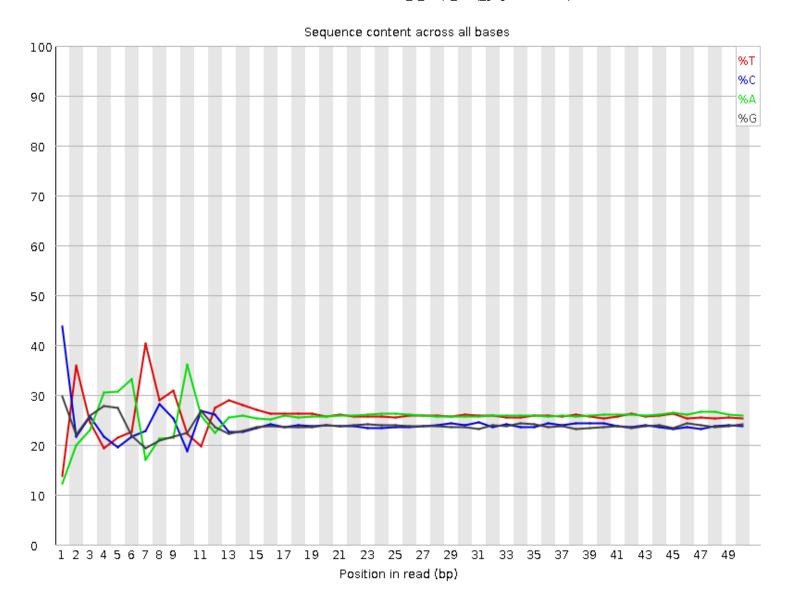
## Per base sequence quality



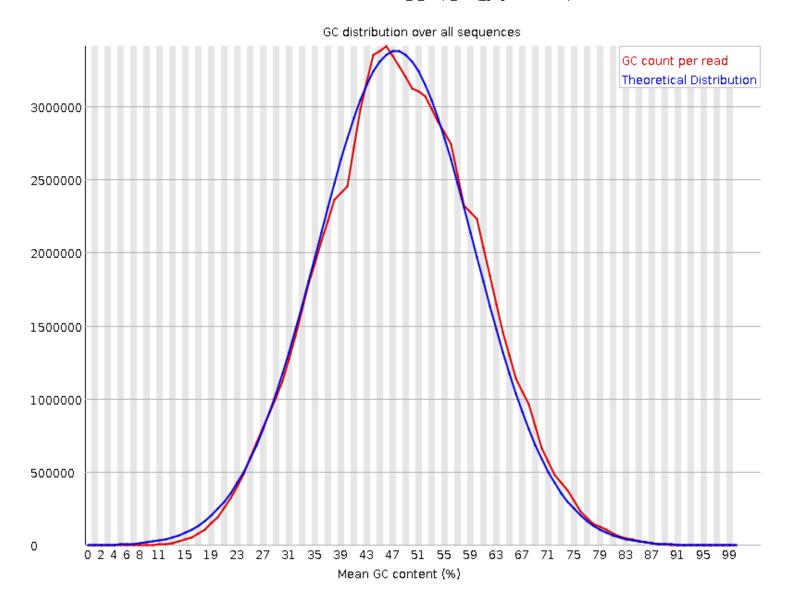
# Per sequence quality scores



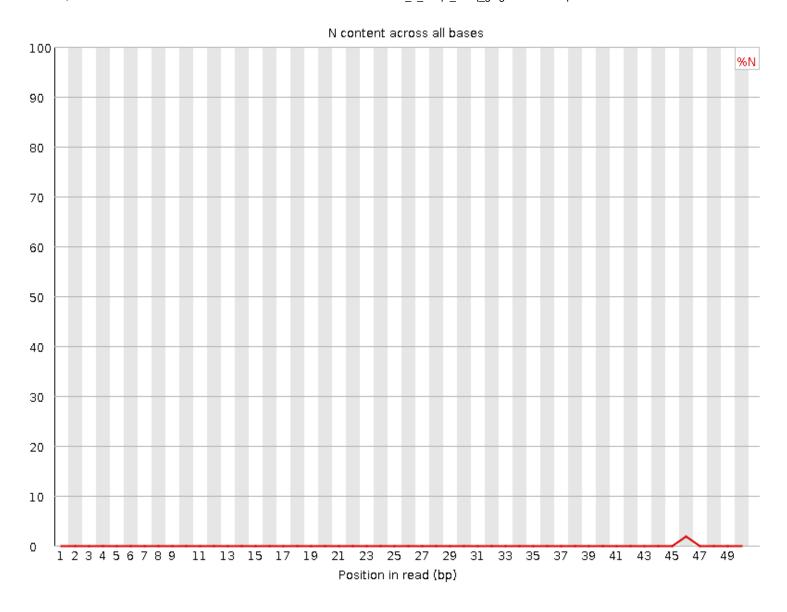
## ②Per base sequence content



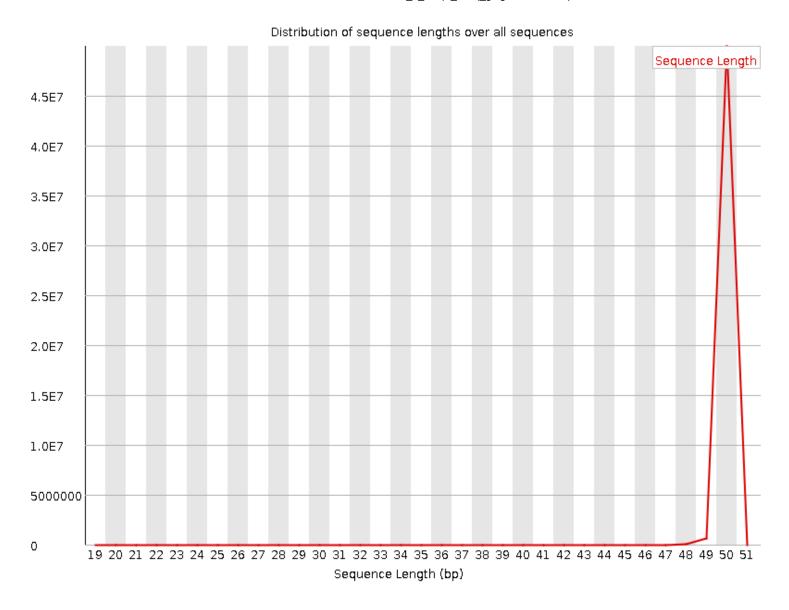
# Per sequence GC content



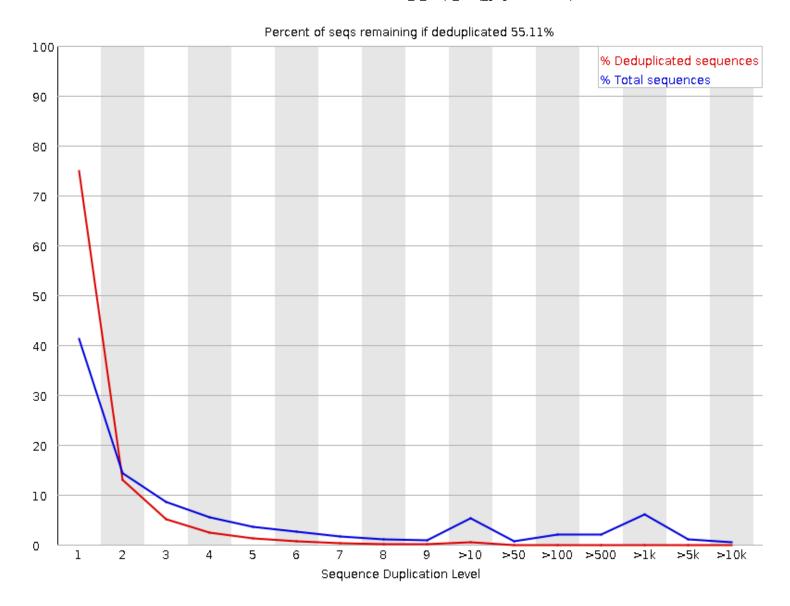




### Sequence Length Distribution



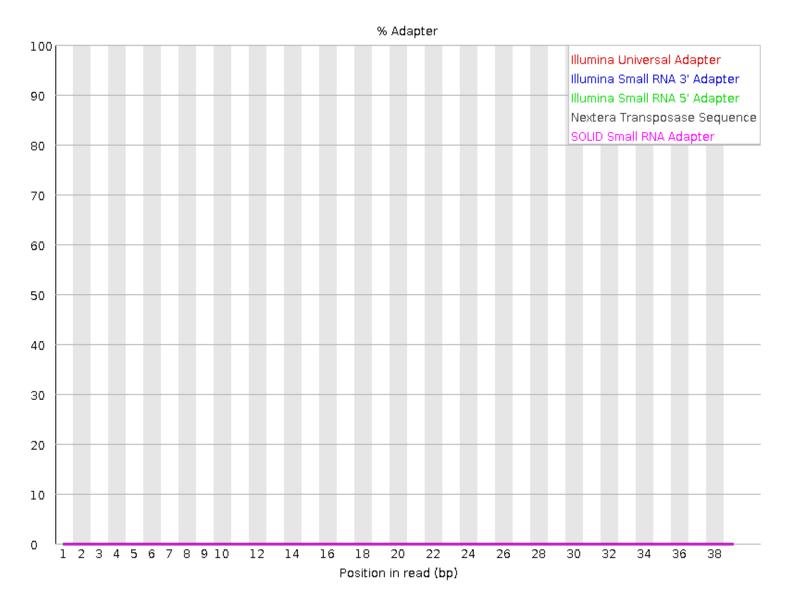
#### Sequence Duplication Levels





TWO OVERTEPIESERIEU SEQUERICES





Produced by FastQC (version 0.11.8)