

Wed 30 Jun 2021 SRR1554535_2_adapt_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 SRR1554535_2_adapt_fastq_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

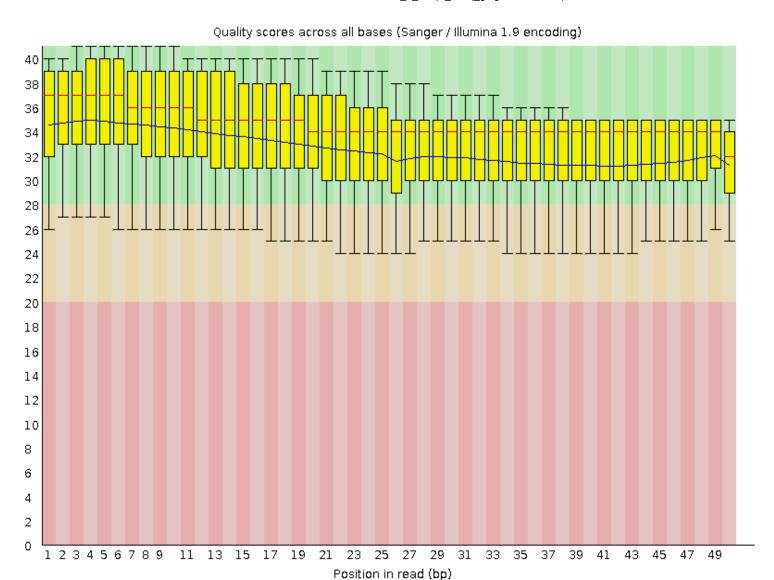
Total Sequences 87566336

Sequences flagged as poor quality 0

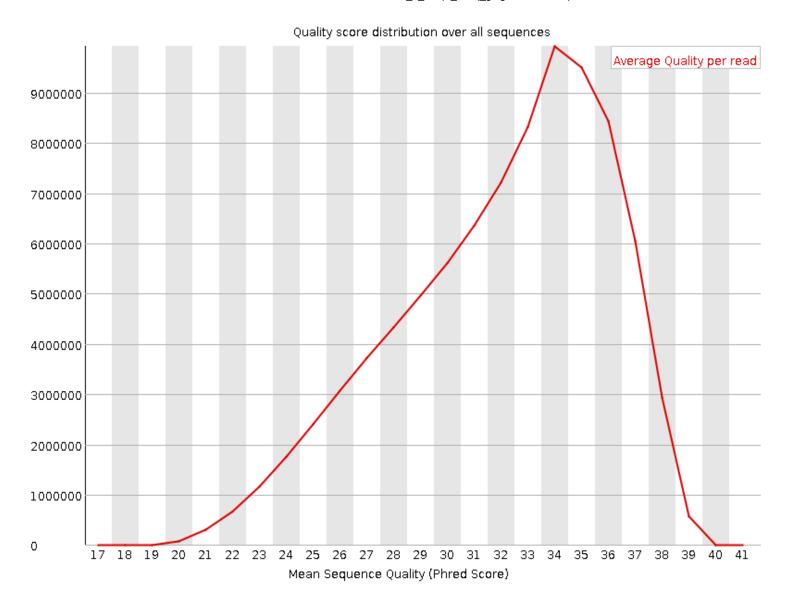
Sequence length 20-50

%GC 47

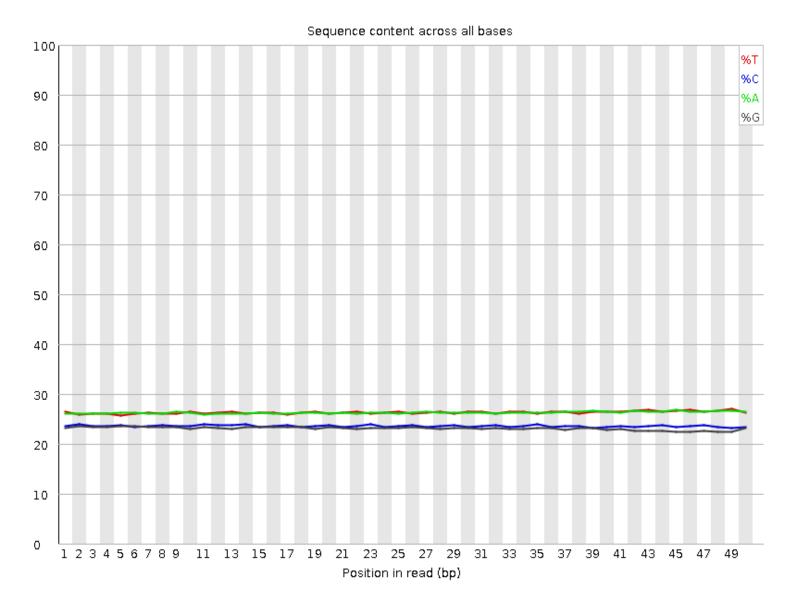
Per base sequence quality



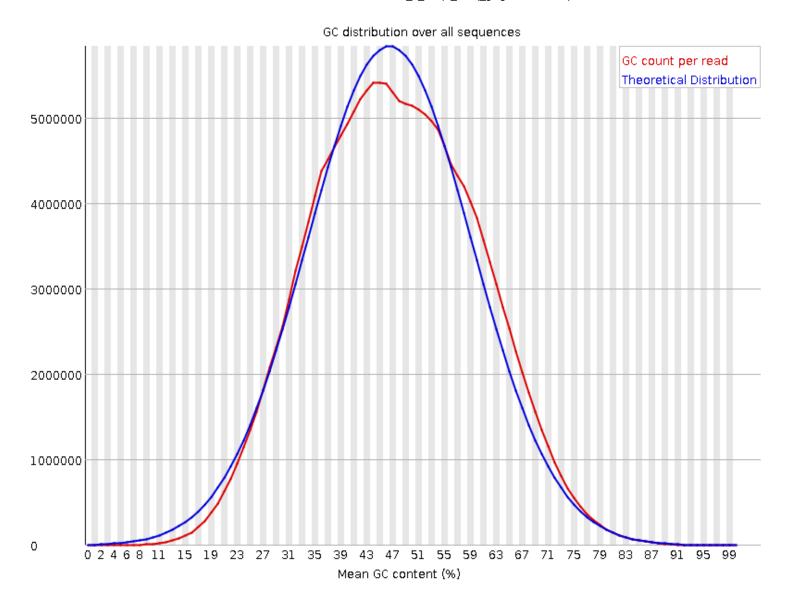
Per sequence quality scores



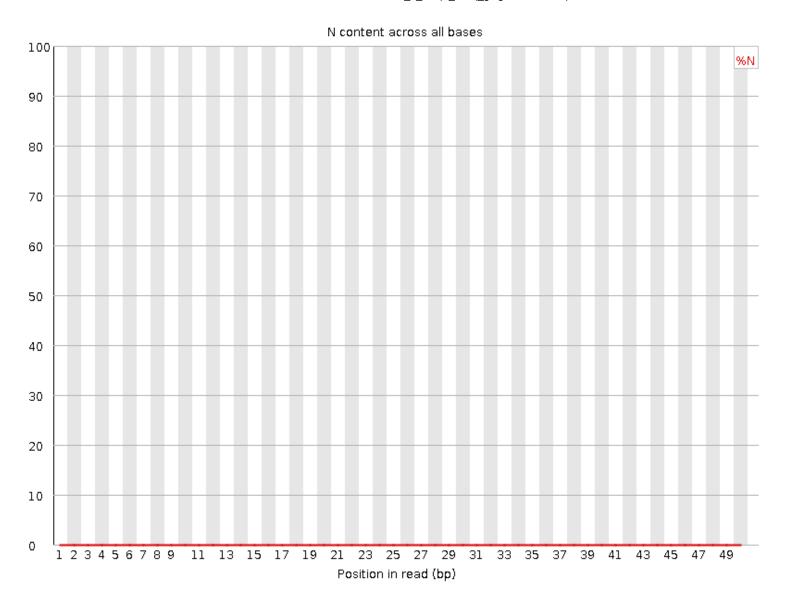




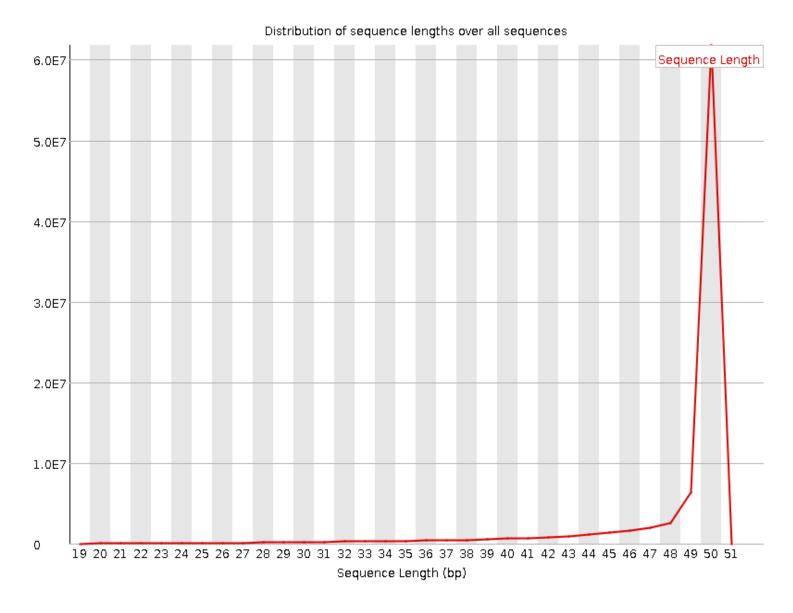
Per sequence GC content



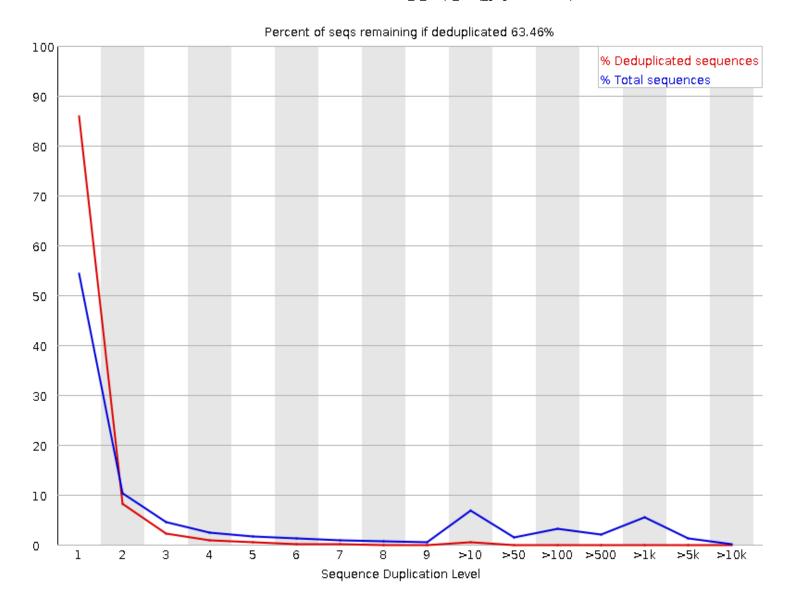




Sequence Length Distribution

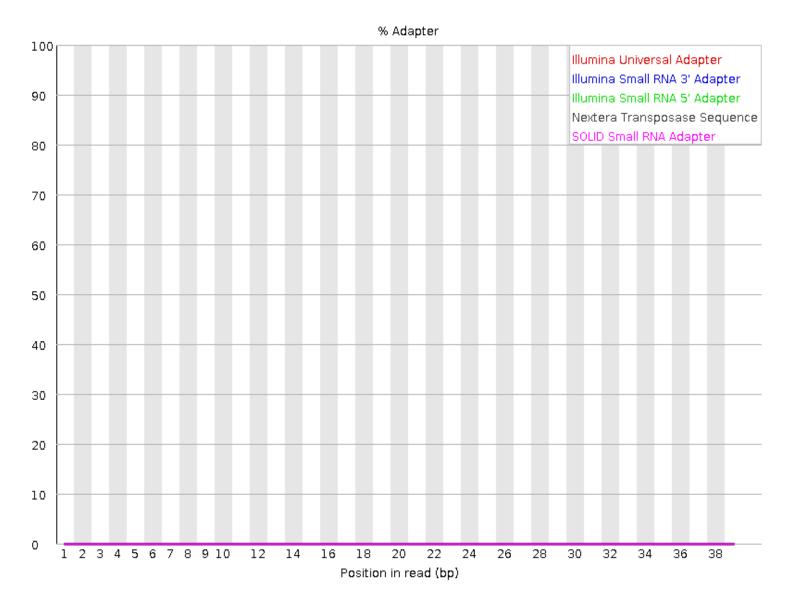


Sequence Duplication Levels









Produced by FastQC (version 0.11.8)