Report

Thu 1 Jul 2021 SRR1554567_2_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 SRR1554567_2_fastq_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

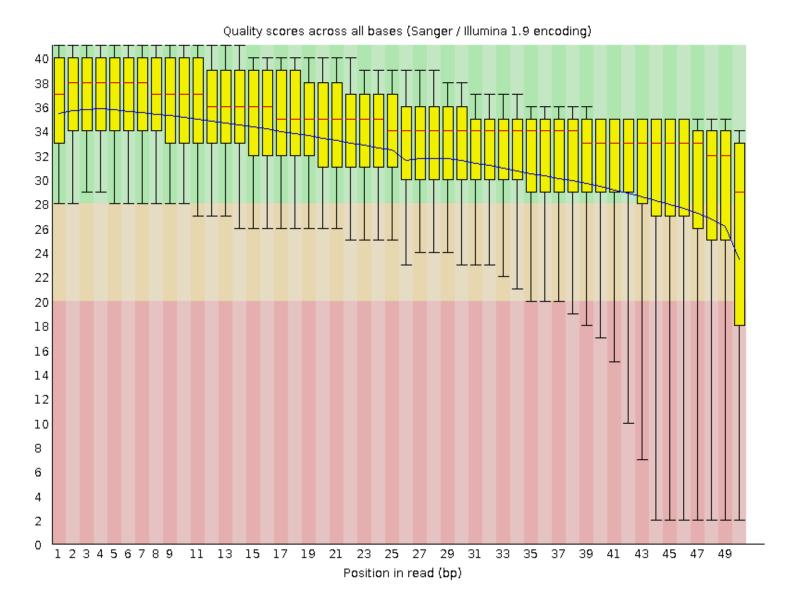
Total Sequences 136312421

Sequences flagged as poor quality 0

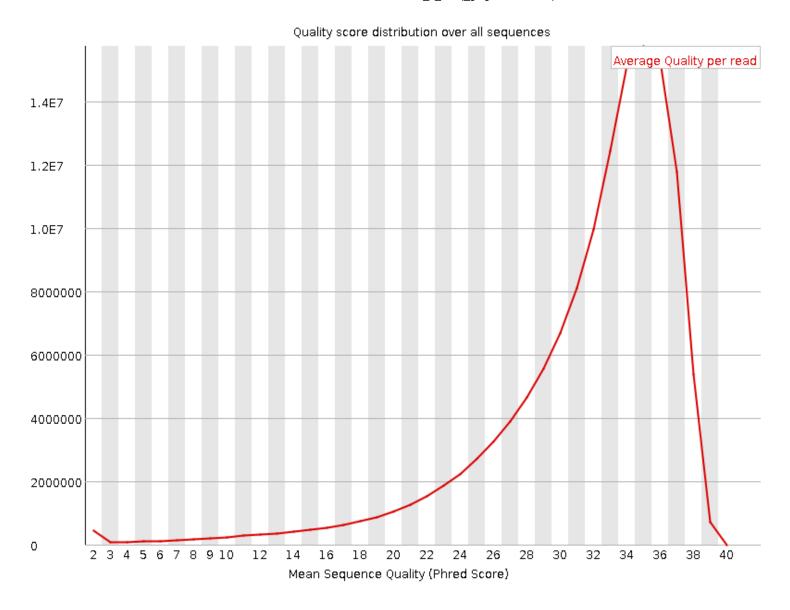
Sequence length 50

%GC 46

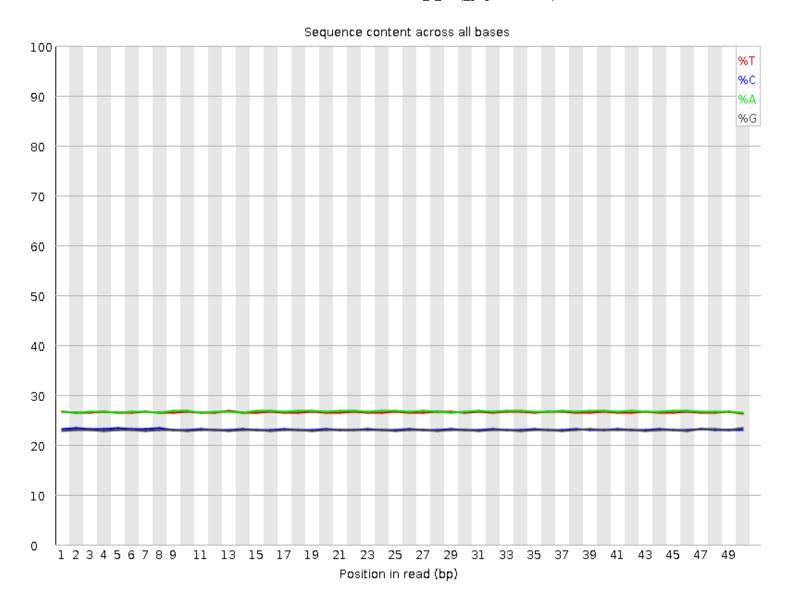
Per base sequence quality



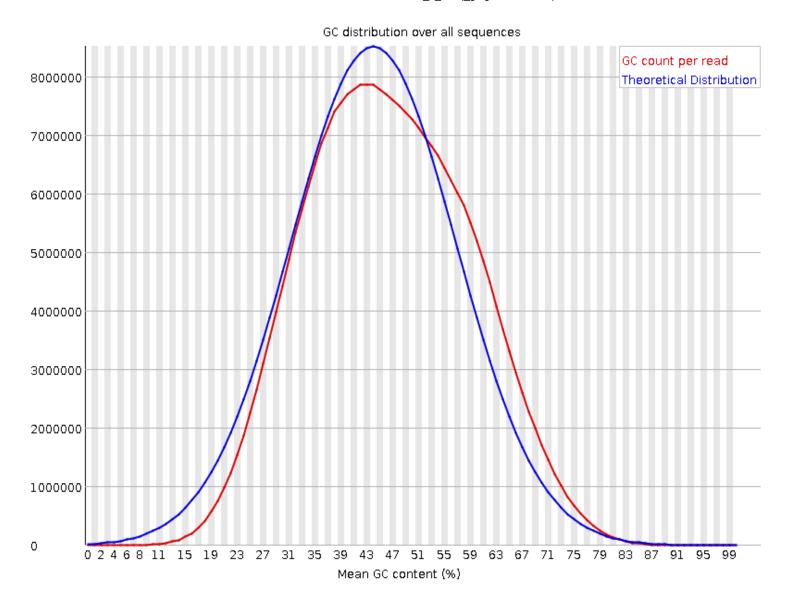
Per sequence quality scores



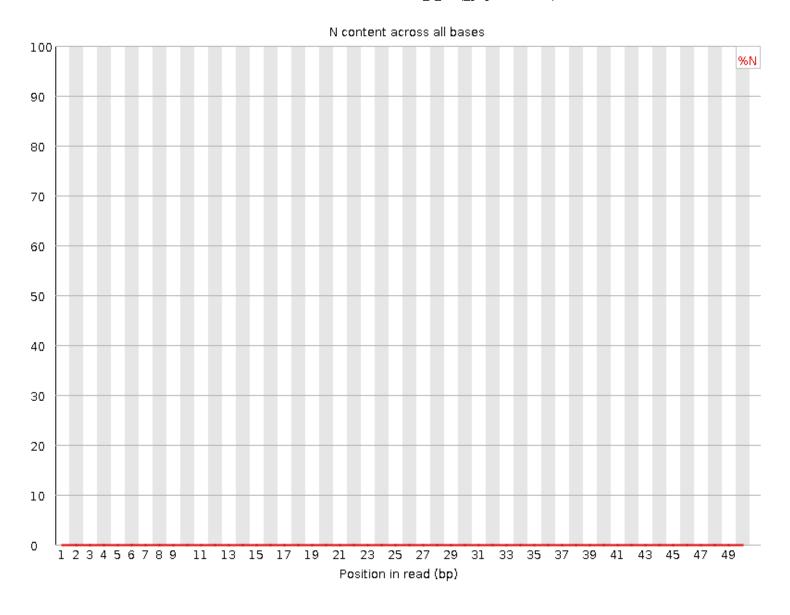
Per base sequence content



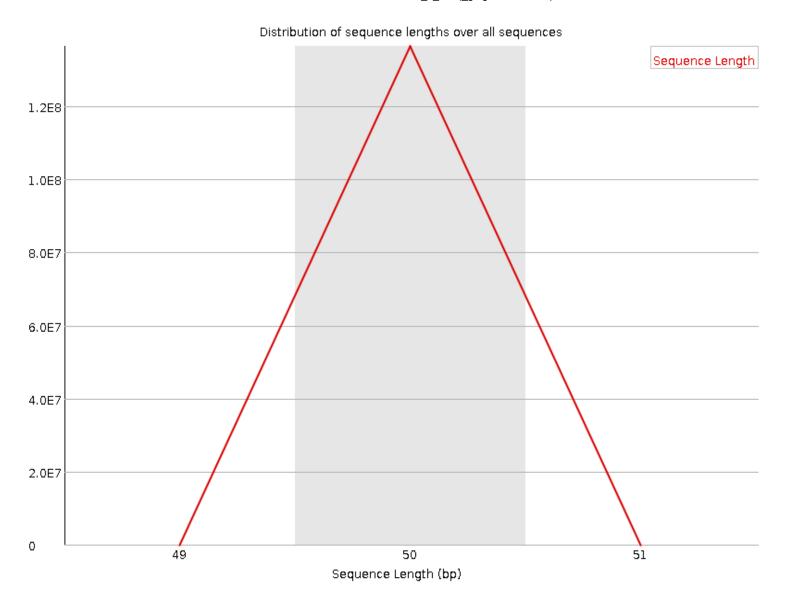




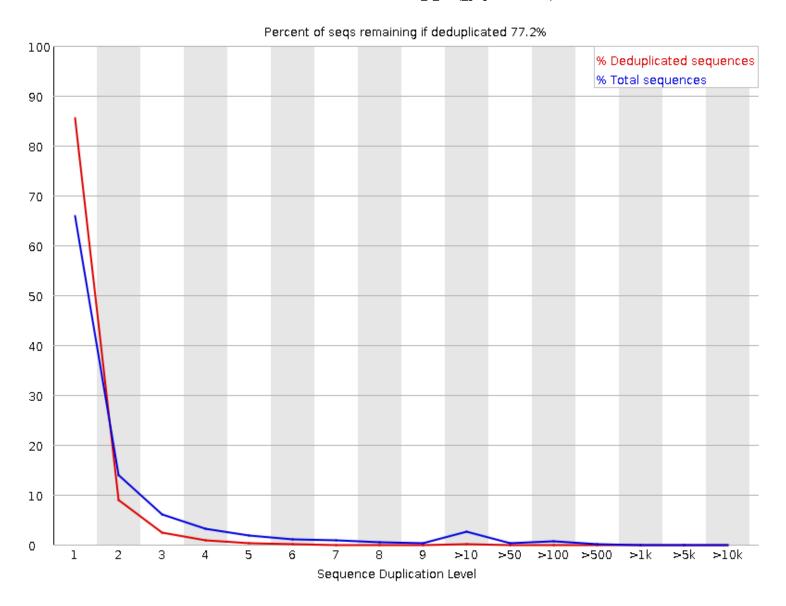




Sequence Length Distribution



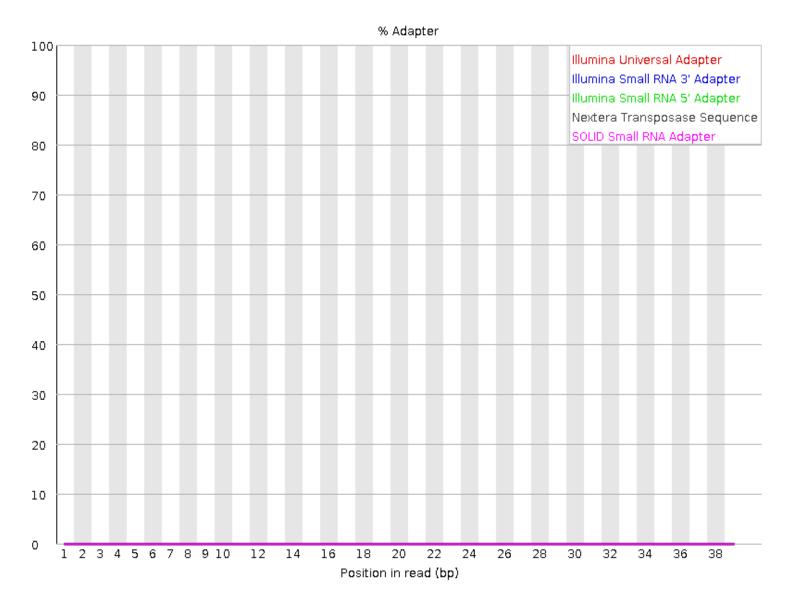
Sequence Duplication Levels





No overrepresented sequences





Produced by FastQC (version 0.11.8)