

Wed 30 Jun 2021 SRR1554568_1_adapt_fastq_gz.gz

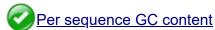
Summary











Per base N content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content

Basic Statistics

Measure Value

Filename SRR1554568_1_adapt_fastq_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

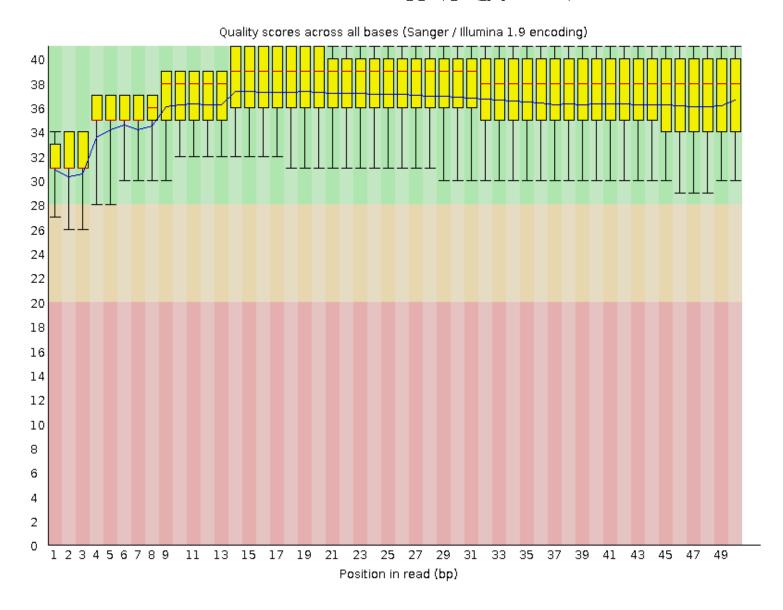
Total Sequences 104969561

Sequences flagged as poor quality 0

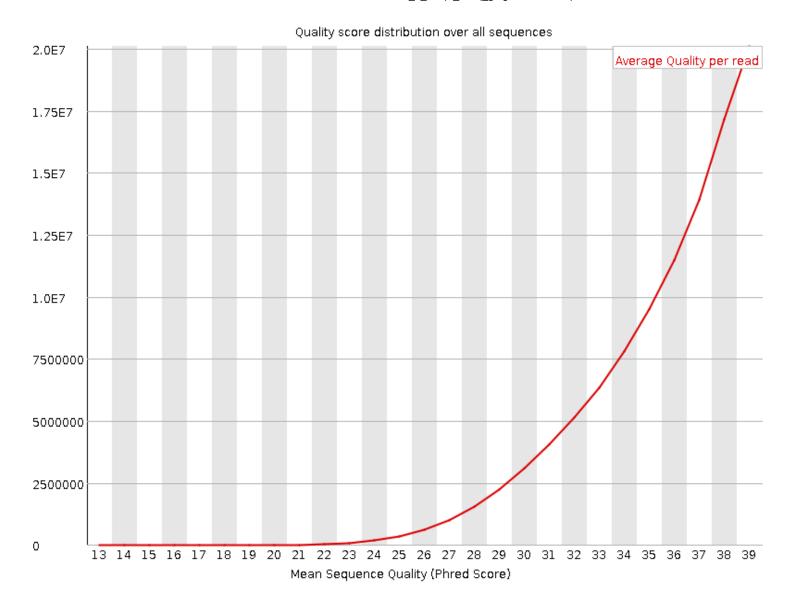
Sequence length 20-50

%GC 47

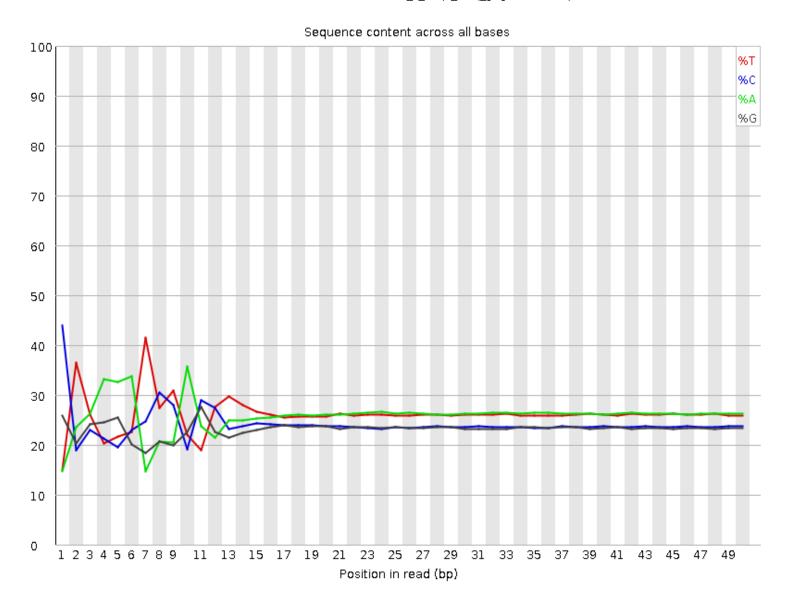
Per base sequence quality



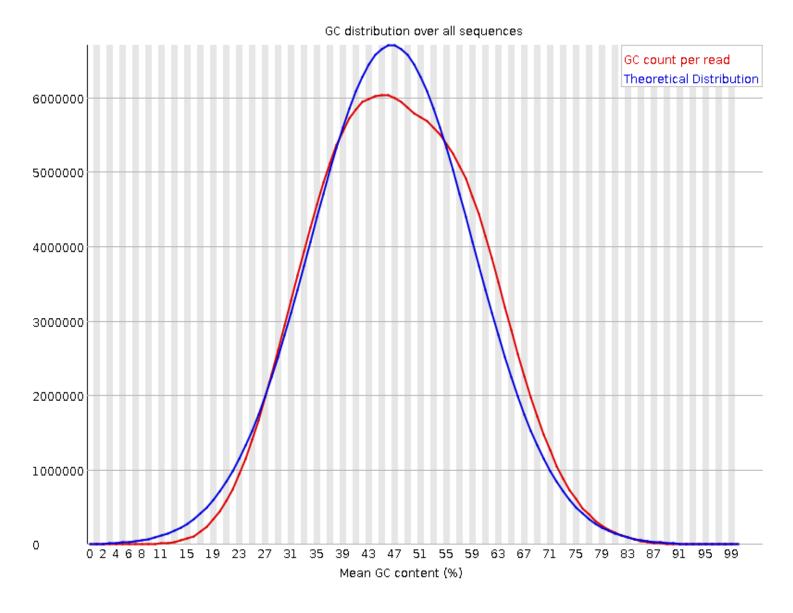
Per sequence quality scores



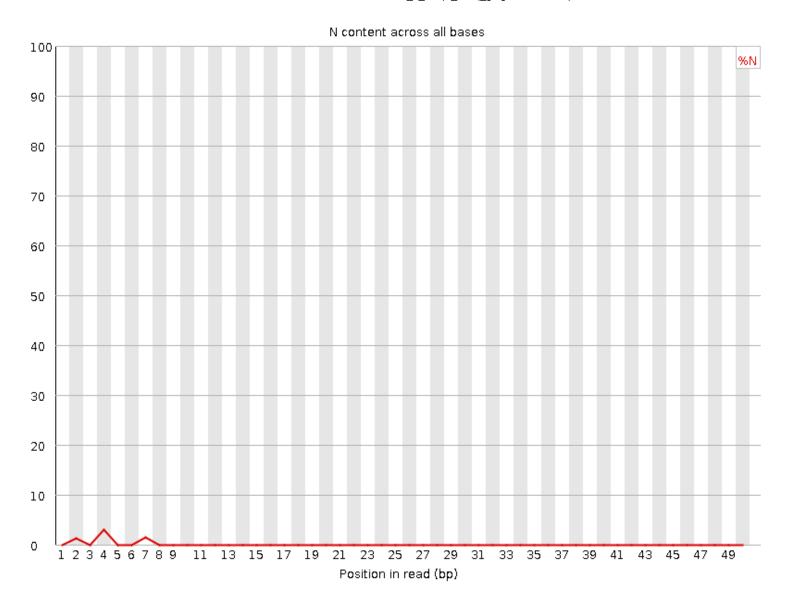
Per base sequence content



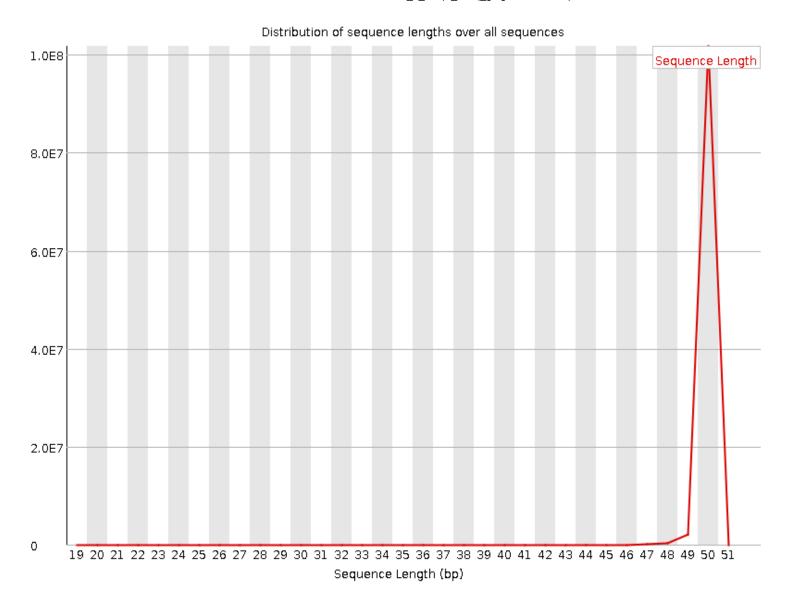
Per sequence GC content



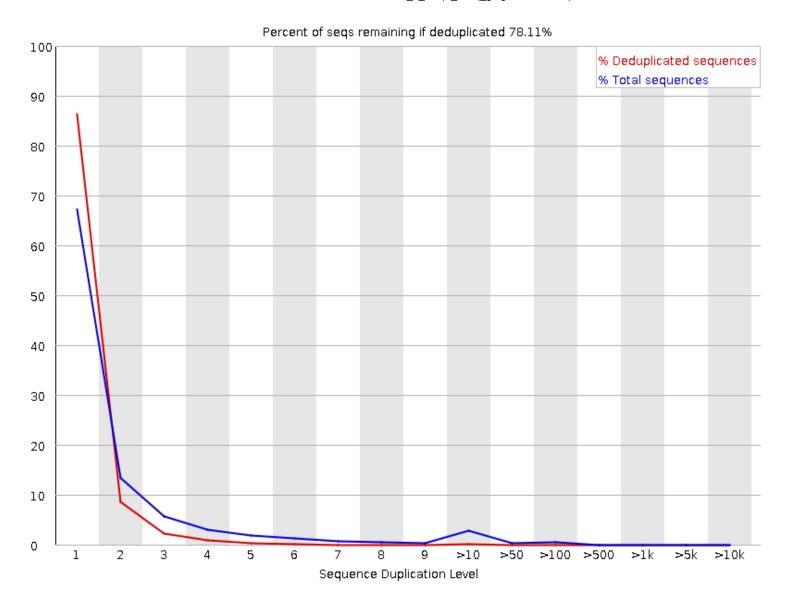




Sequence Length Distribution

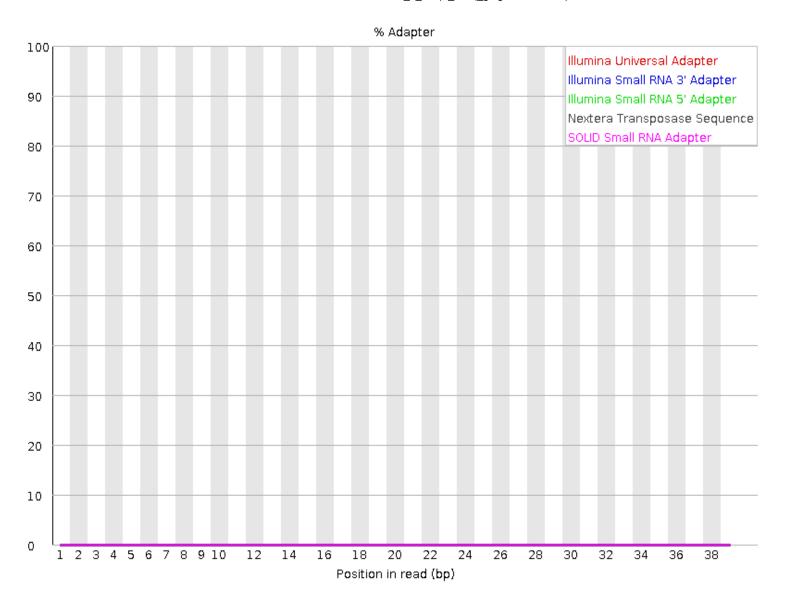


Sequence Duplication Levels









Produced by FastQC (version 0.11.8)