Report

Mon 19 Jul 2021 SRR1554566_1_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 SRR1554566_1_adapt_fastq_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

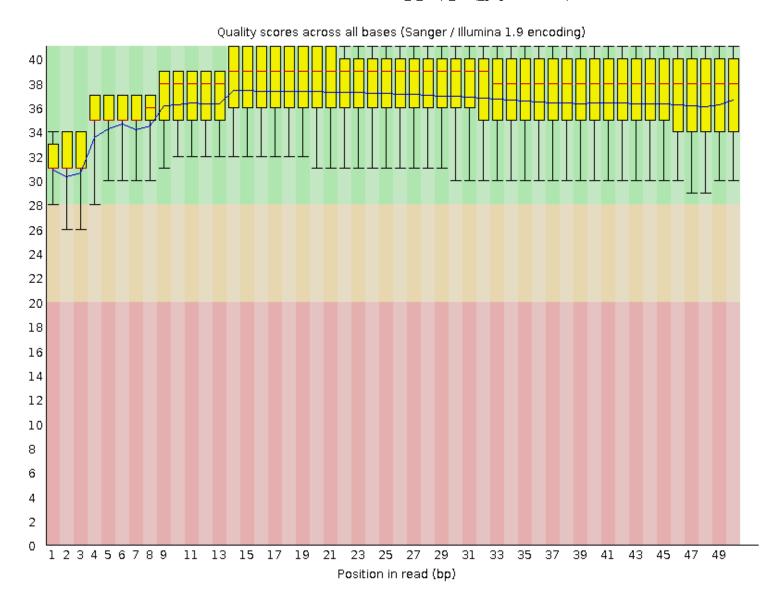
Total Sequences 114321281

Sequences flagged as poor quality 0

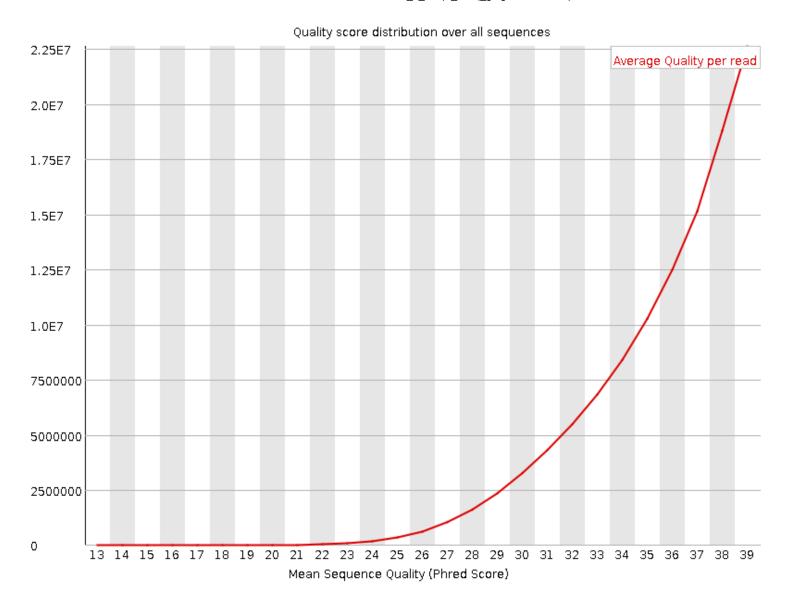
Sequence length 20-50

%GC 48

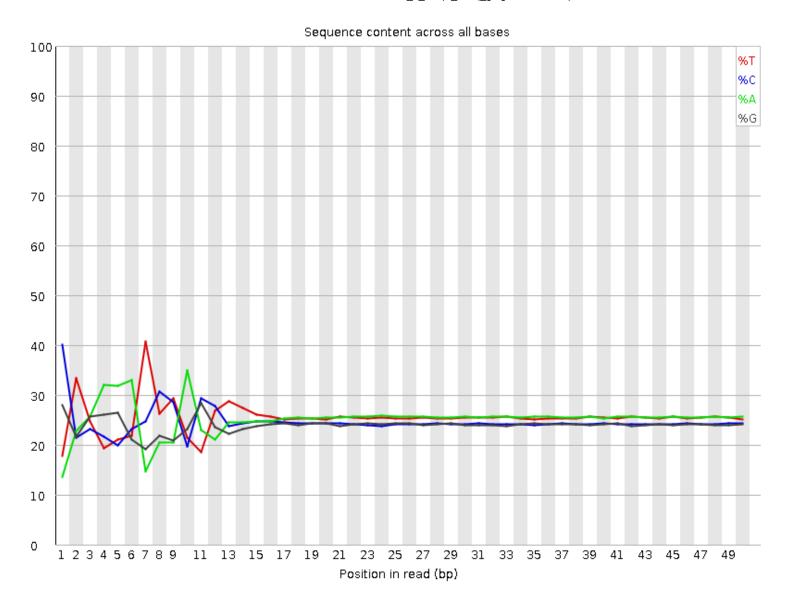
Per base sequence quality



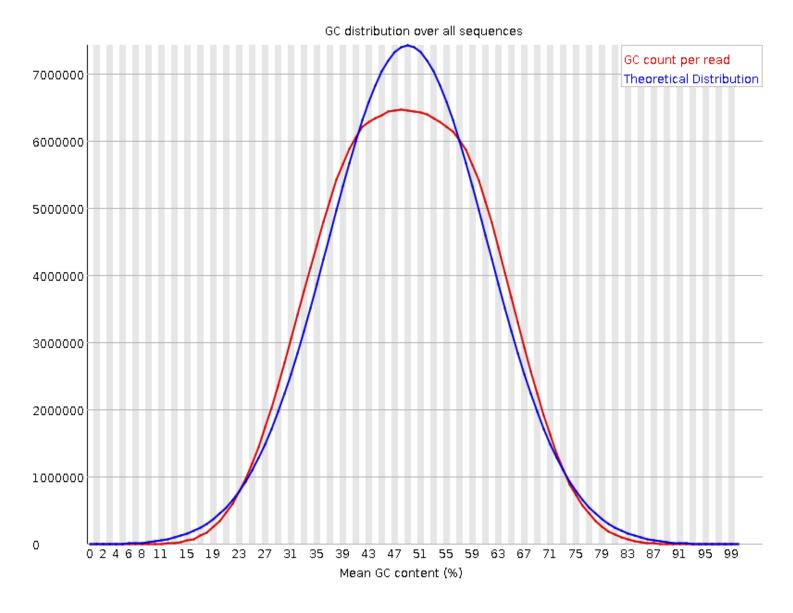
Per sequence quality scores



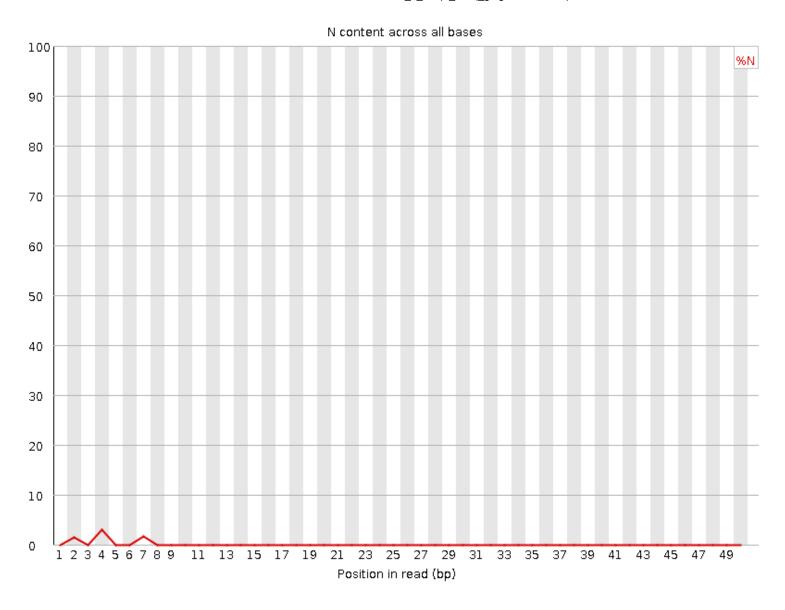
②Per base sequence content



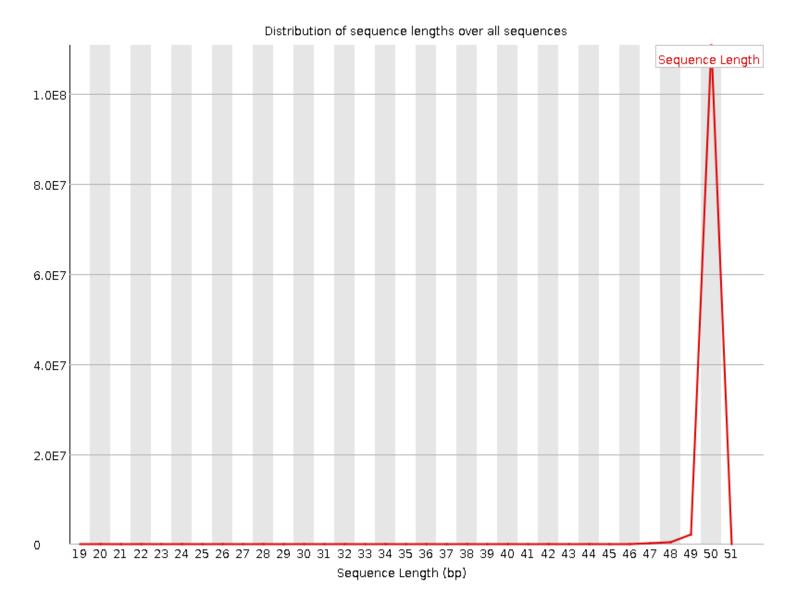
Per sequence GC content



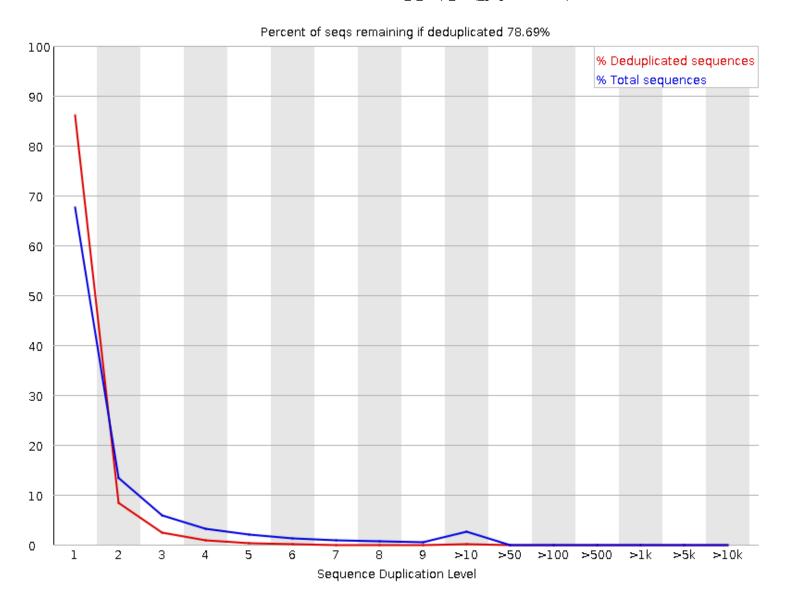




Sequence Length Distribution



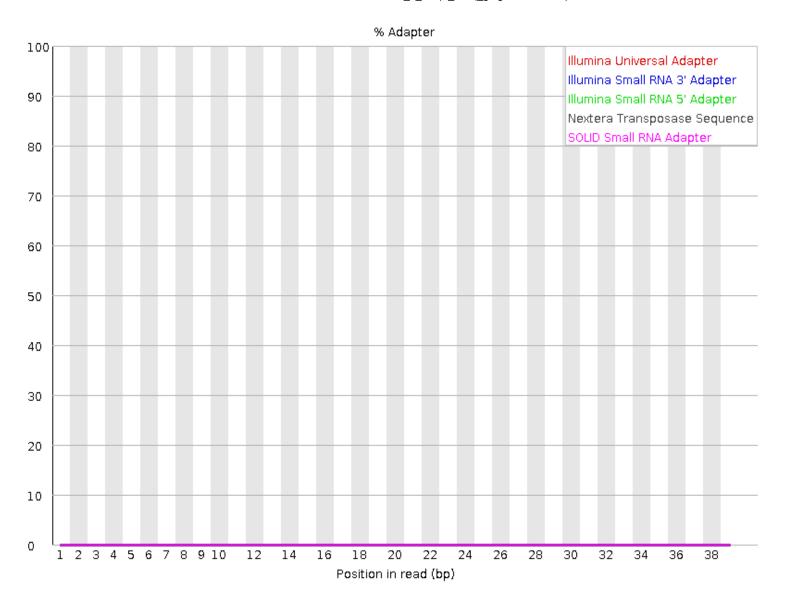
Sequence Duplication Levels





No overrepresented sequences





Produced by FastQC (version 0.11.8)