Sat 2 Nov 2024 SRR14866426_2.fastq

ReportSummary





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 SRR14866426_2.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

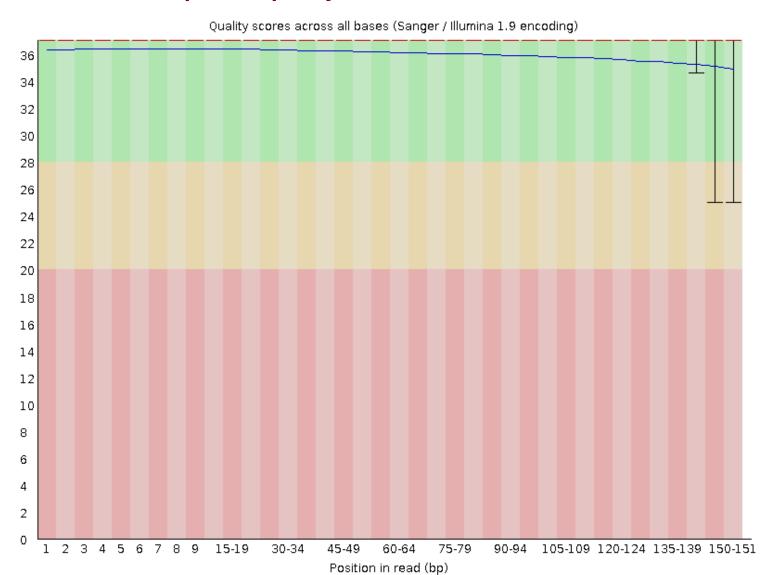
Total Sequences 22253023

Sequences flagged as poor quality 0

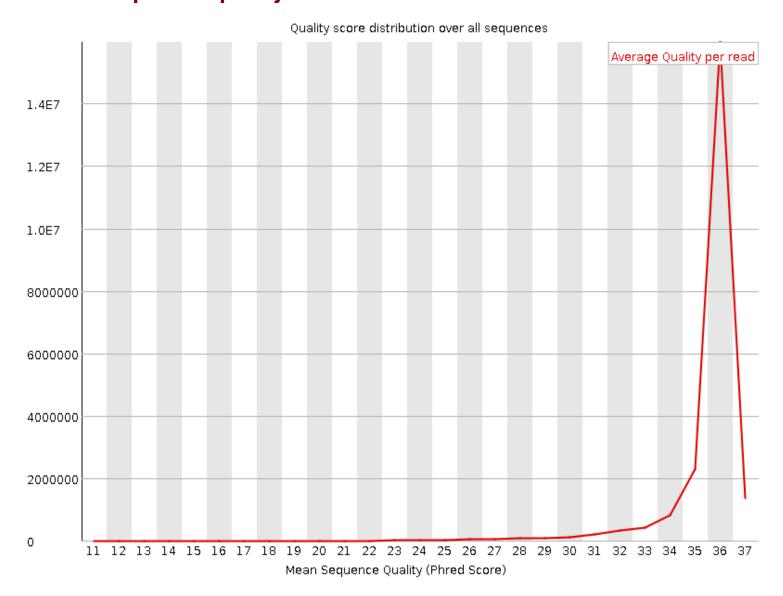
Sequence length 151

%GC 51

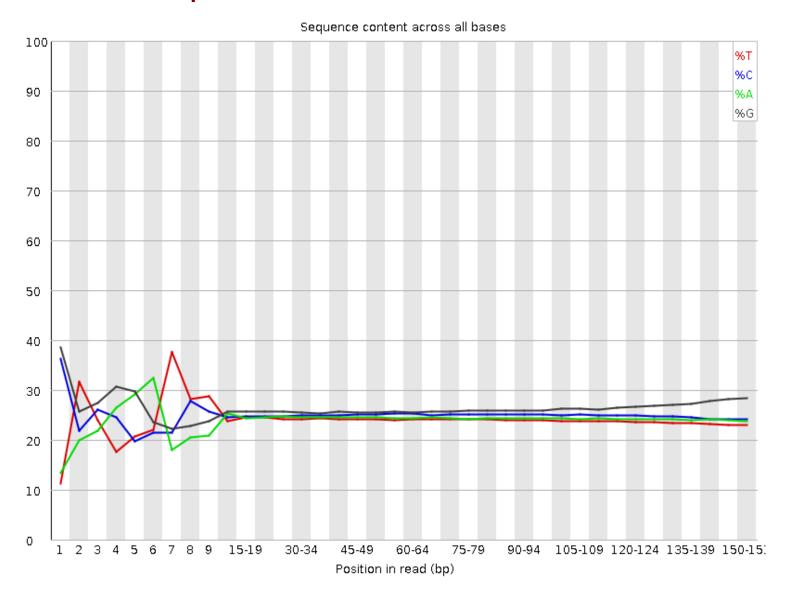
Per base sequence quality



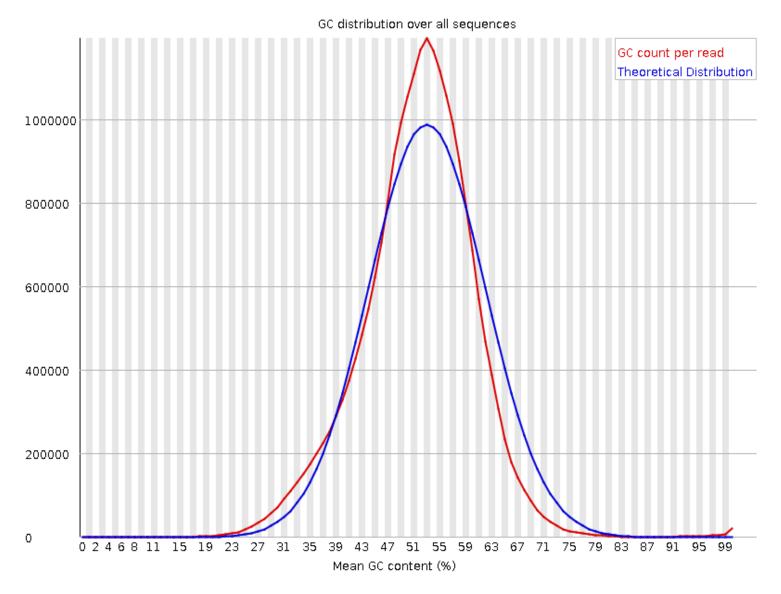
Per sequence quality scores



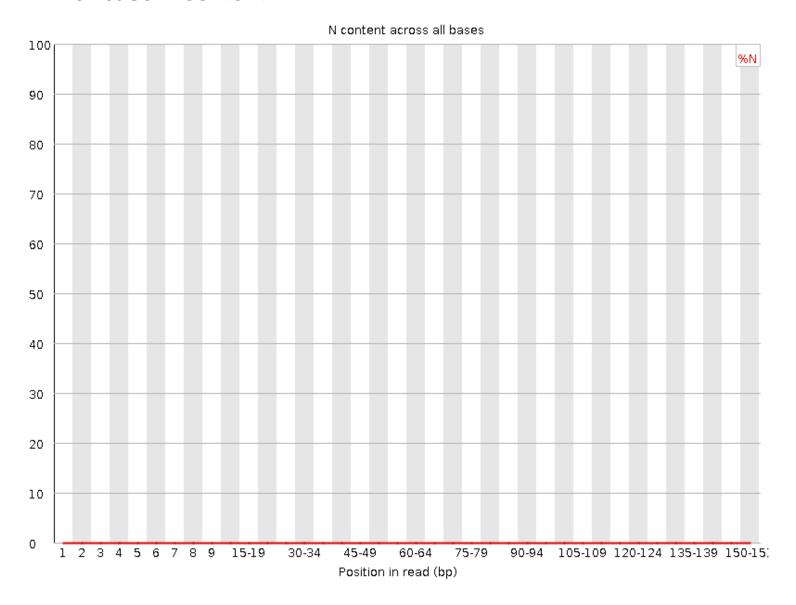
Per base sequence content



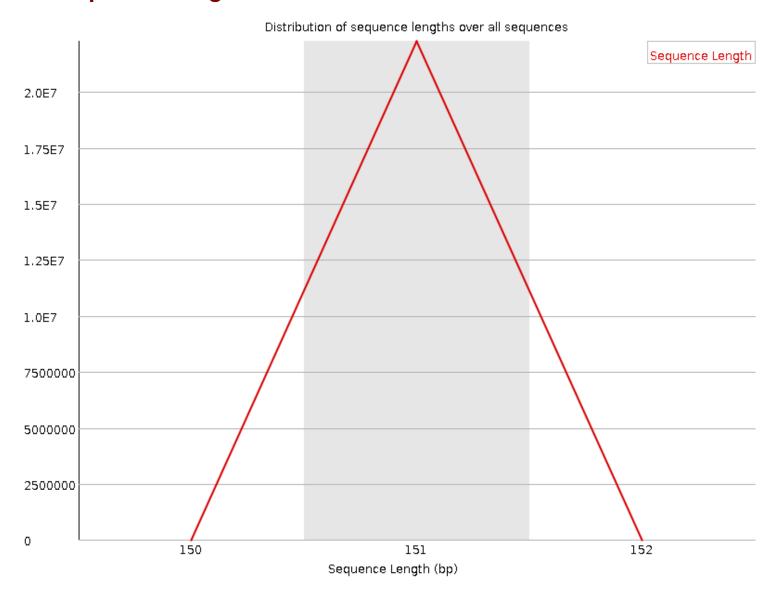
Per sequence GC content



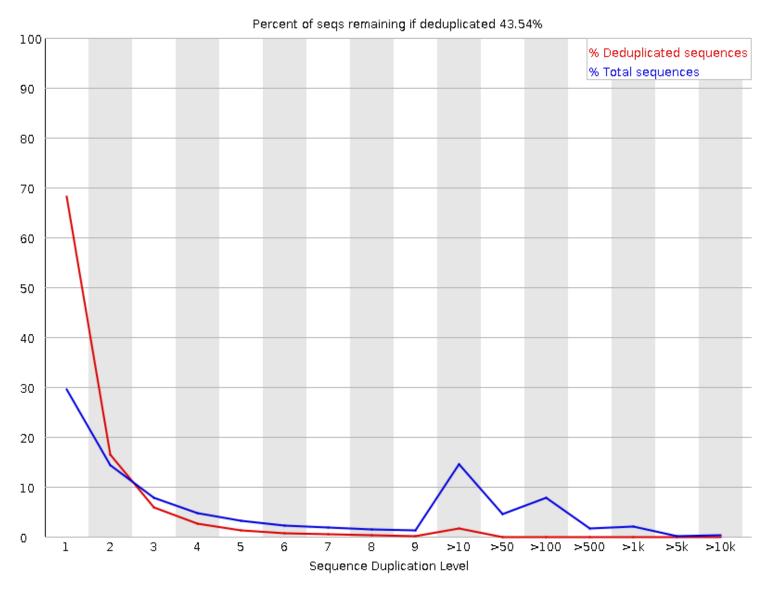
Per base N content



Sequence Length Distribution



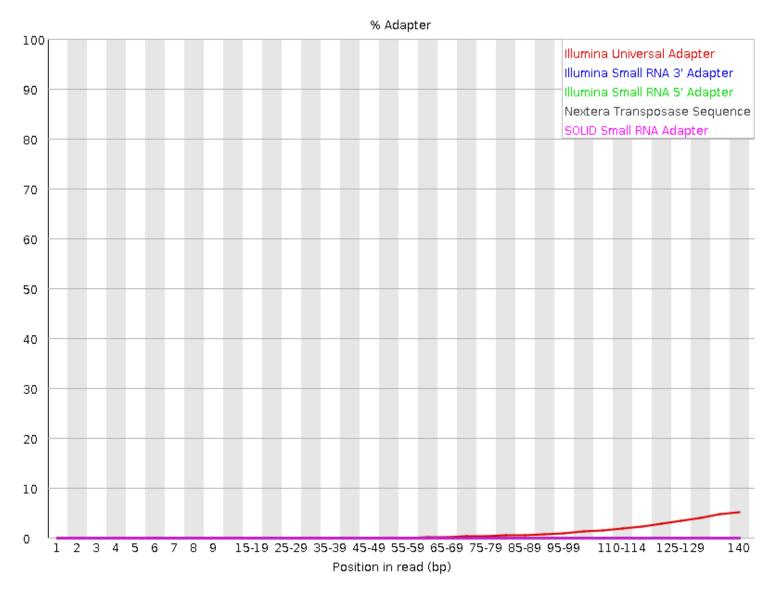
Sequence Duplication Levels



Overrepresented sequences

Sequence Count Percentage Possible Source

Adapter Content



Produced by FastQC (version 0.11.7)