᠙FastQC Report

Wed 11 Aug 2021 SRR12740661_1.fastq.gz

Summary







Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content



Measure Value

Filename SRR12740661_1.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

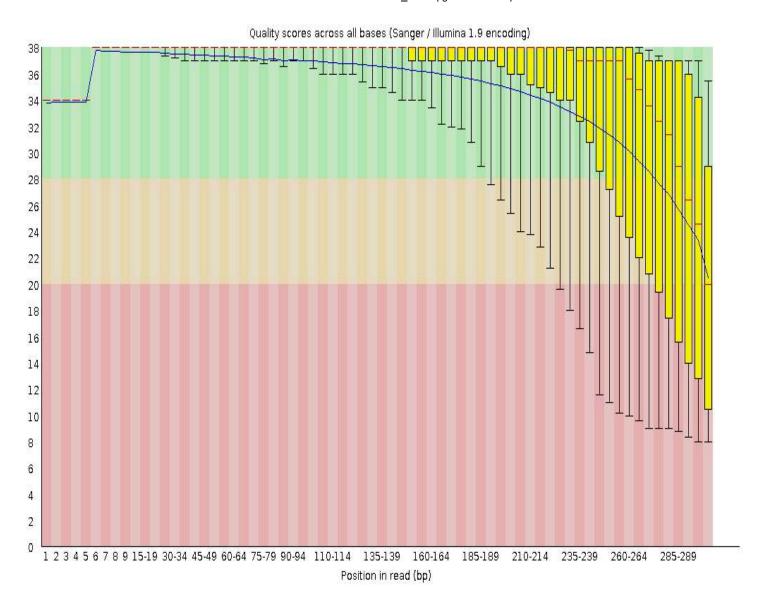
Total Sequences 797777

Sequences flagged as poor quality 0

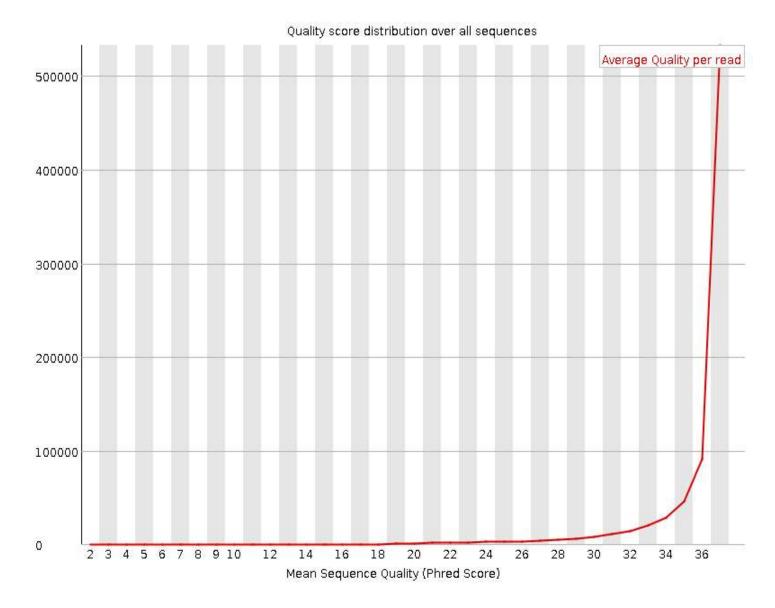
Sequence length 35-301

%GC 30

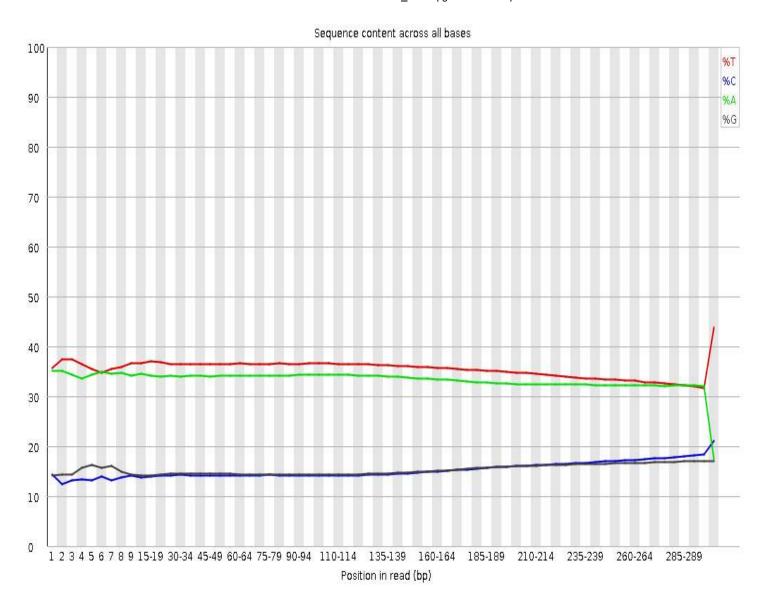
Per base sequence quality



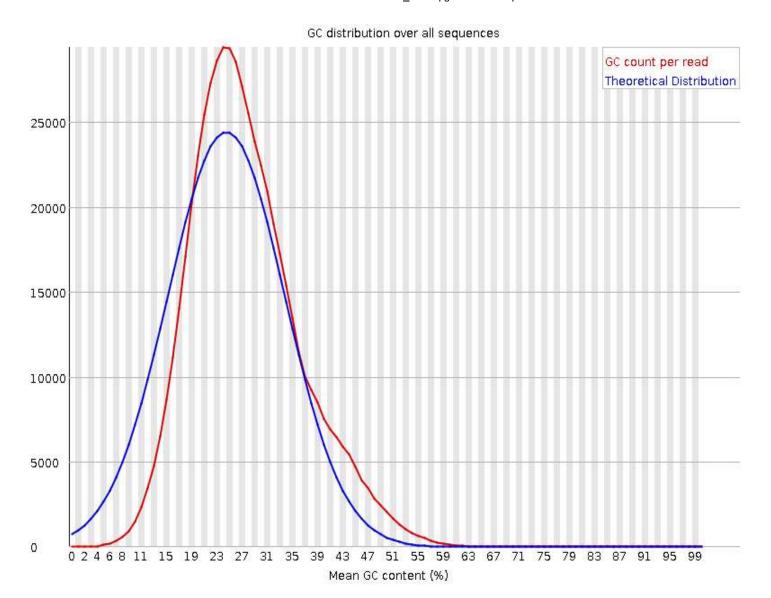




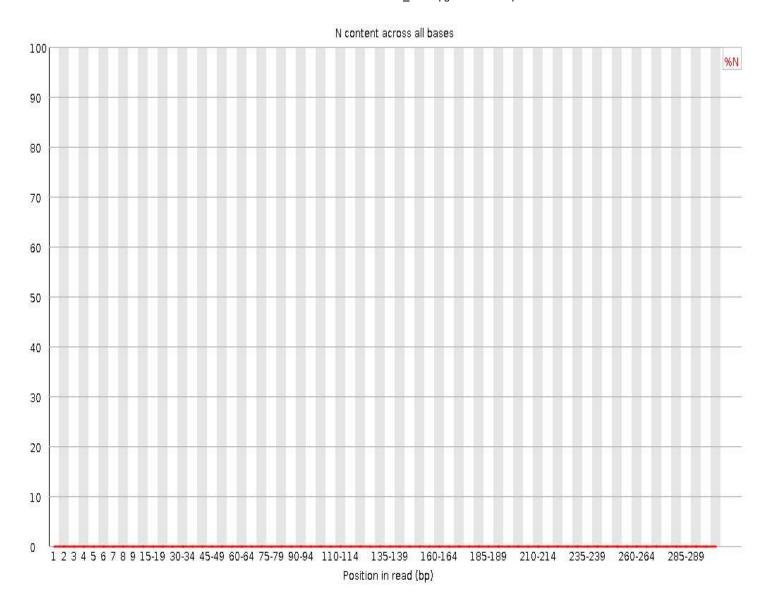
Per base sequence content



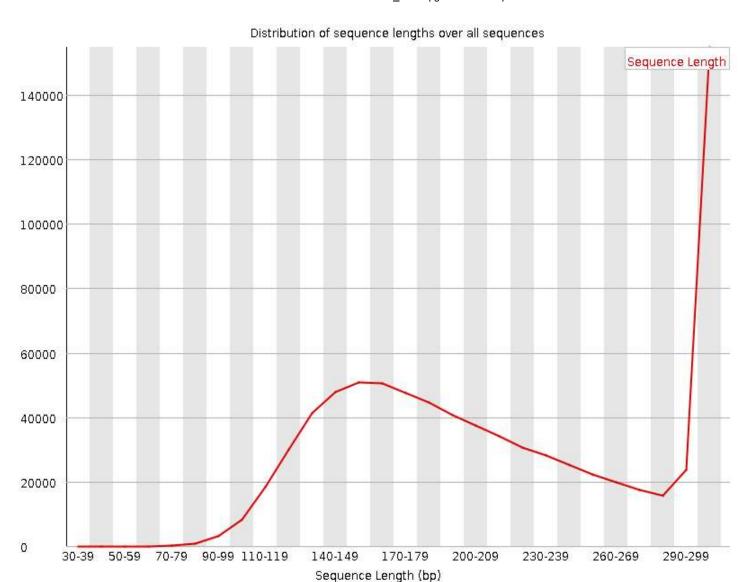
Per sequence GC content



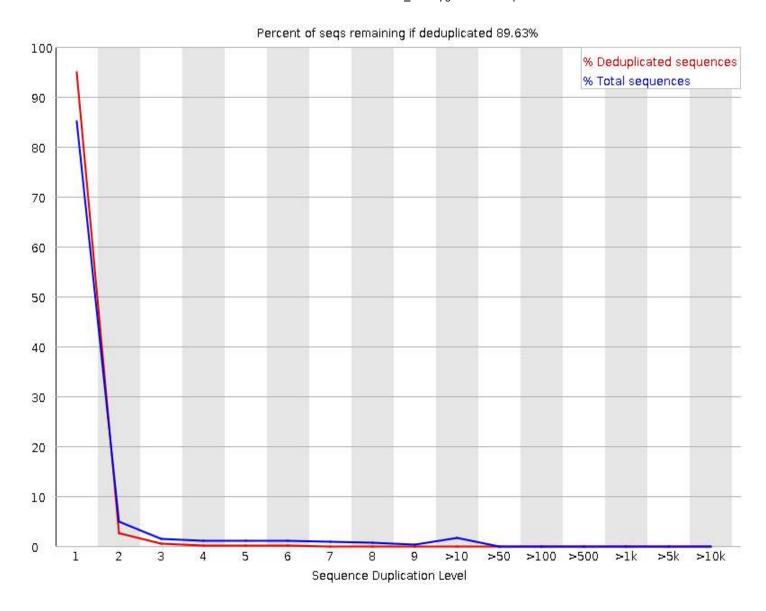




Sequence Length Distribution

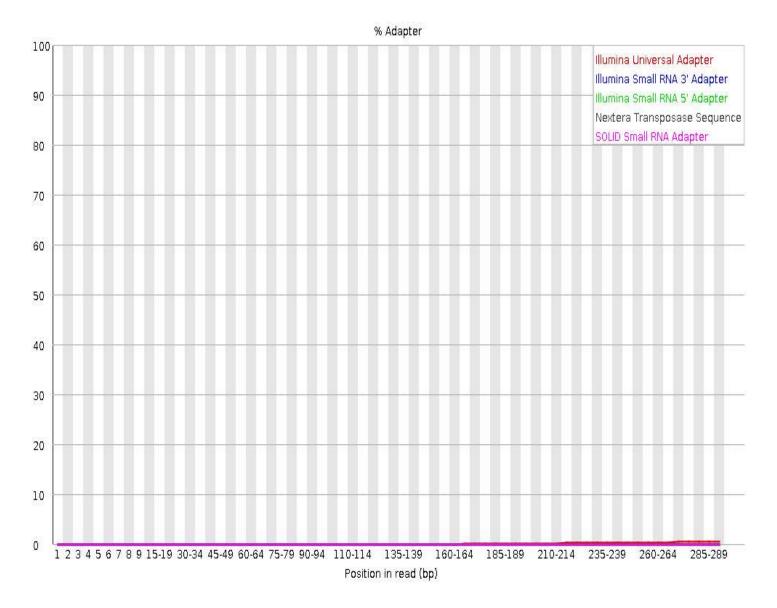








Adapter Content



Produced by <u>FastQC</u> (version 0.11.9)