餐FastQC Report

Wed 11 Aug 2021 SRR12740661_1P.fastq

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 SRR12740661_1P.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

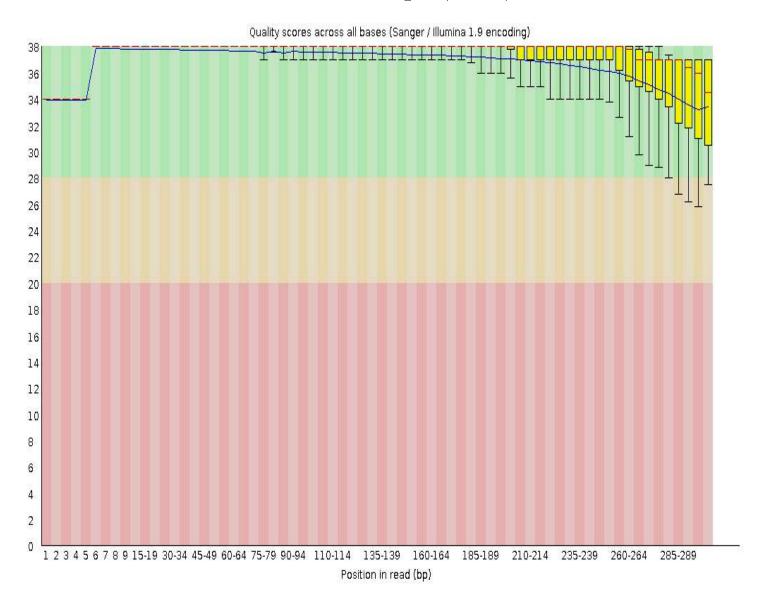
Total Sequences 738970

Sequences flagged as poor quality 0

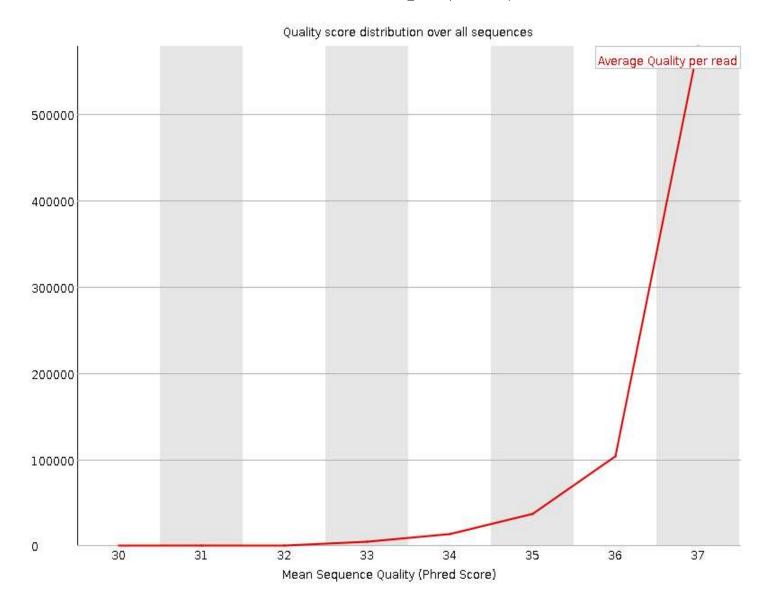
Sequence length 50-301

%GC 29

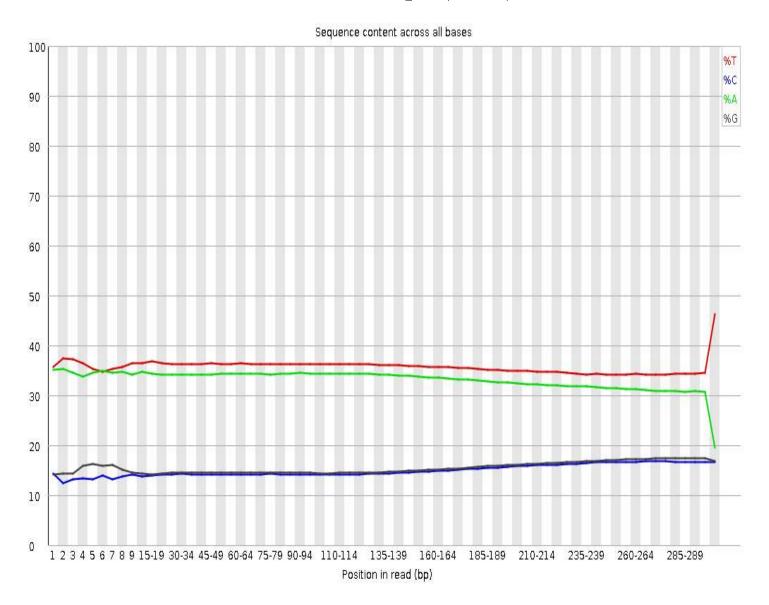
Per base sequence quality



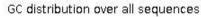


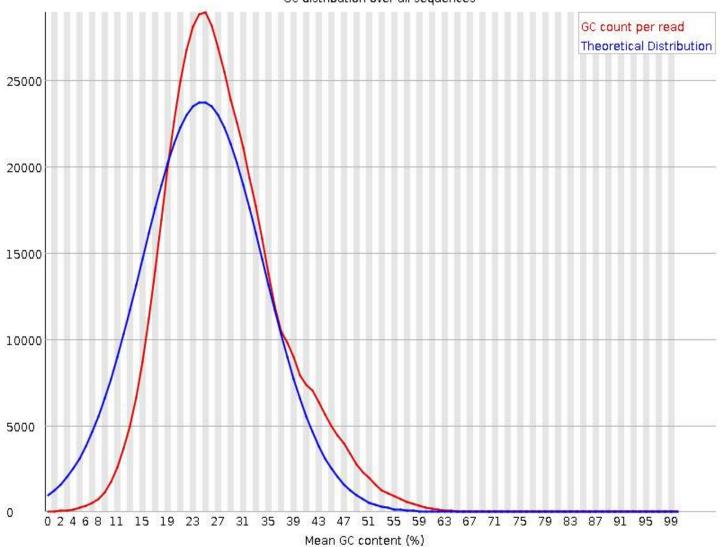


②Per base sequence content

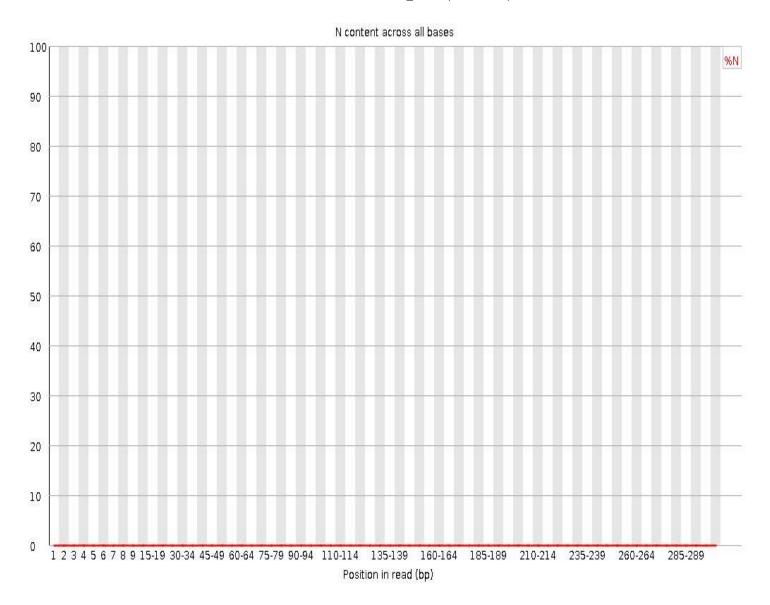


Per sequence GC content

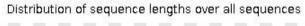


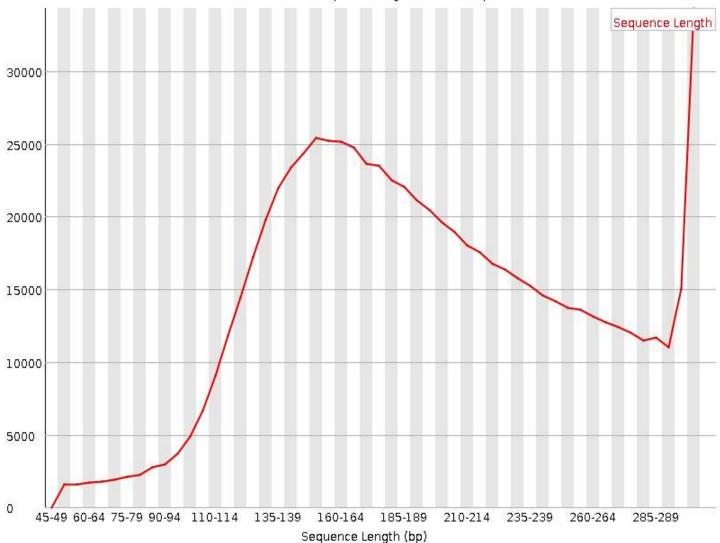




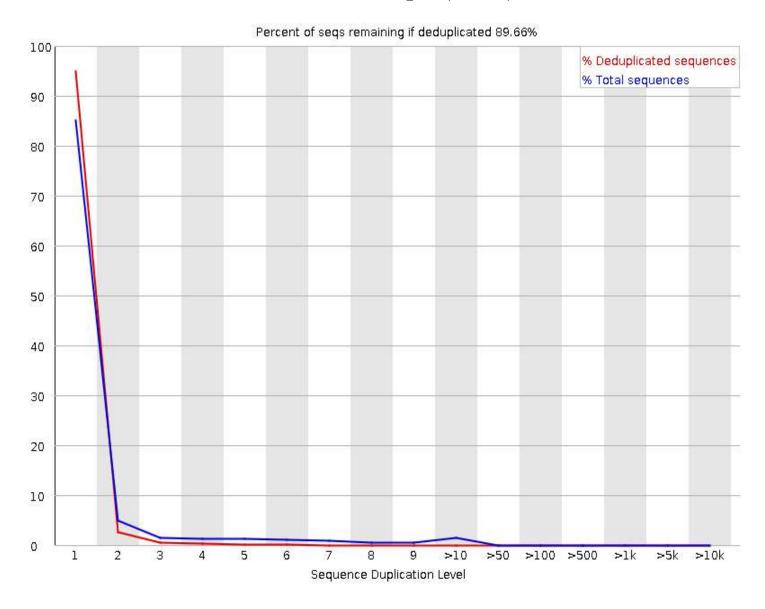


Sequence Length Distribution



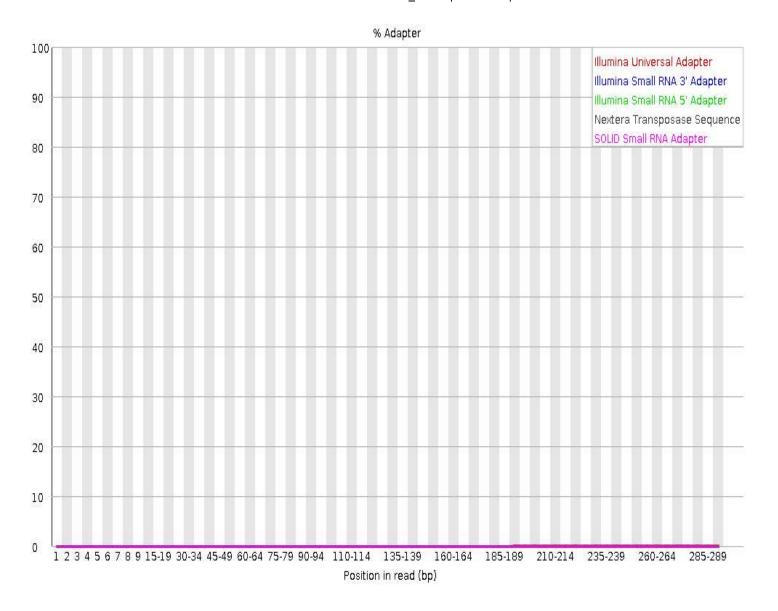












Produced by FastQC (version 0.11.9)