Report

Mon 25 Aug 2025 GG20-leaf_R1.fastq.gz

Summary





Per tile 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

Adapter Content

Basic Statistics

Measure Value

Filename GG20-leaf_R1.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 344148221

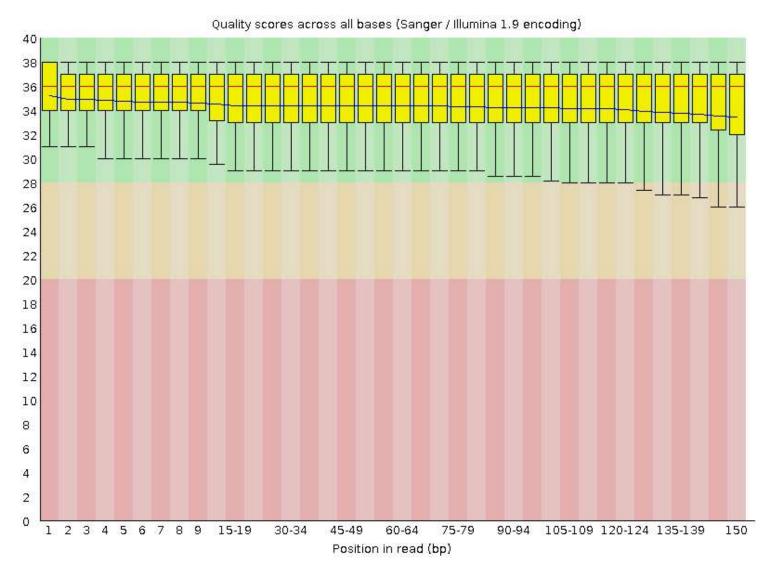
Total Bases 47 Gbp

Sequences flagged as poor quality 0

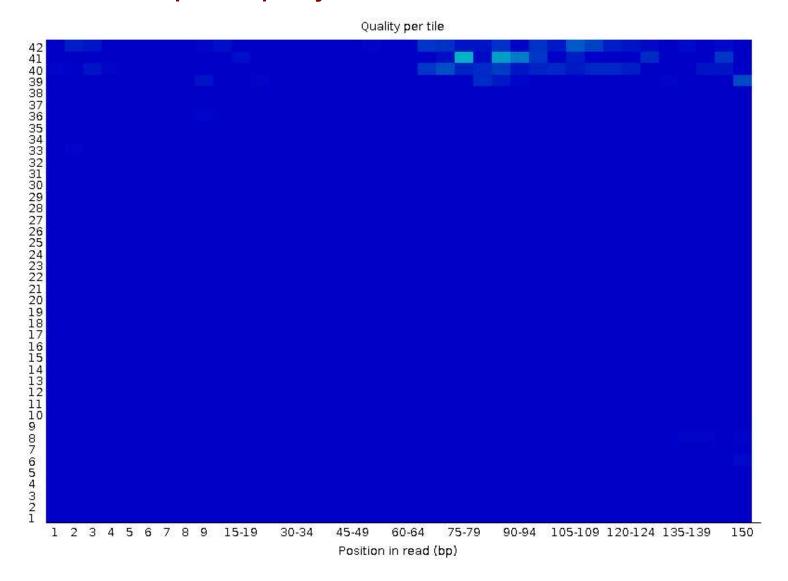
Sequence length 50-150

%GC 37

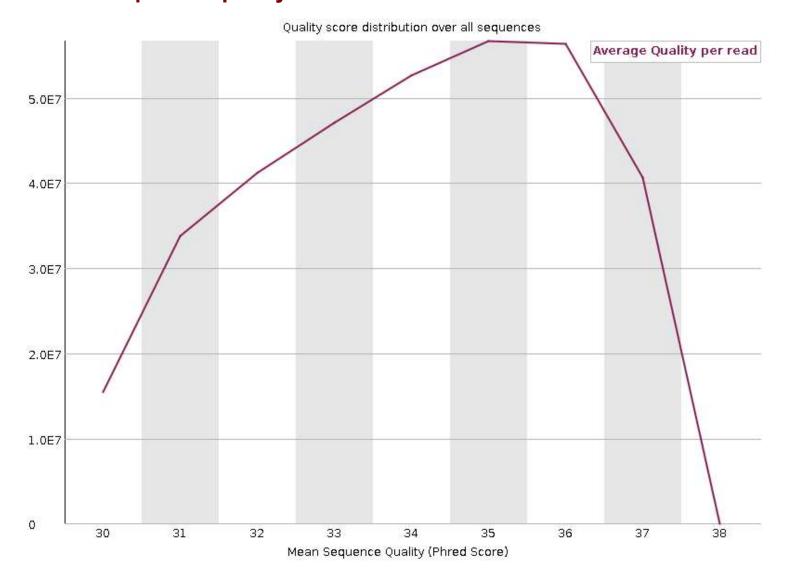
Per base sequence quality



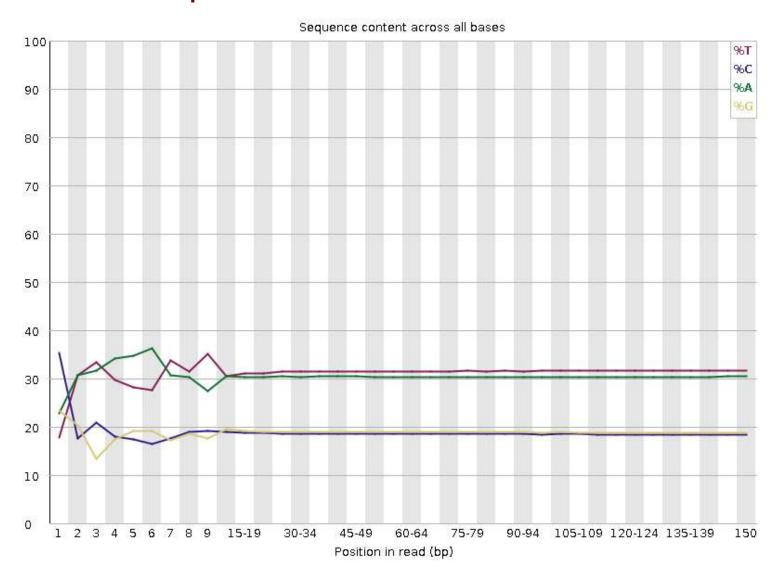
Per tile sequence quality



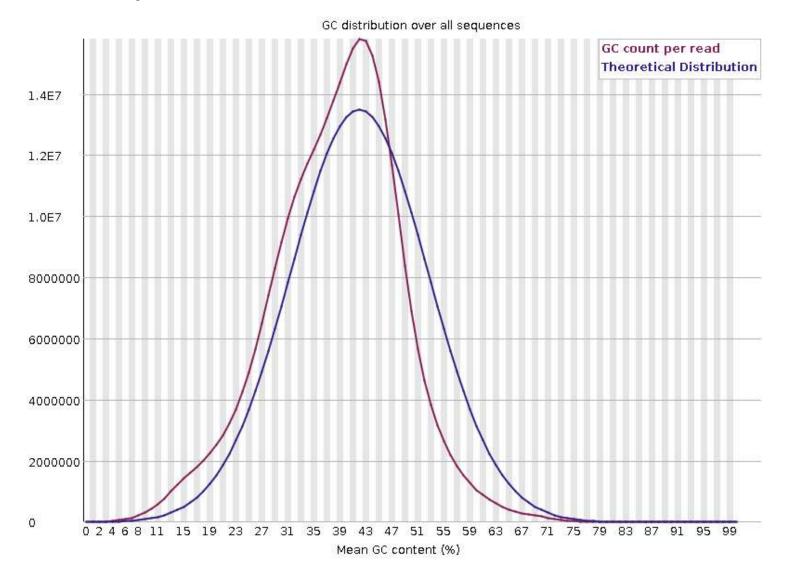
Per sequence quality scores



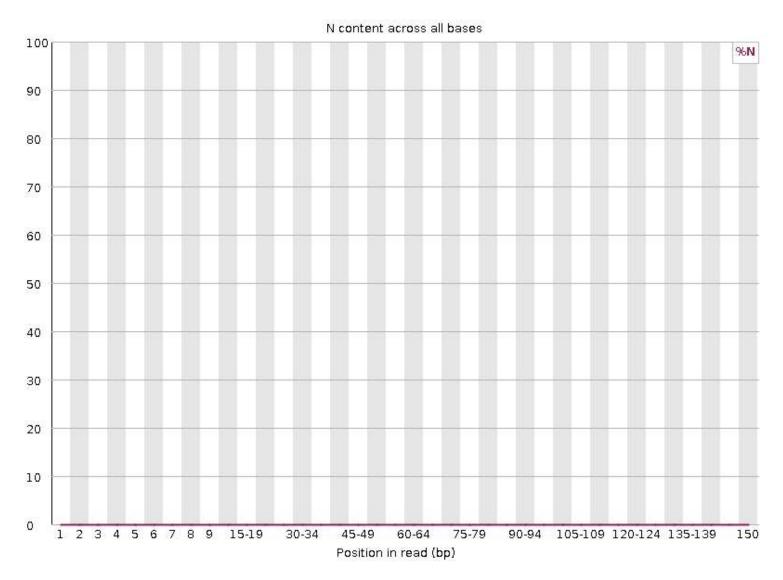
Per base sequence content



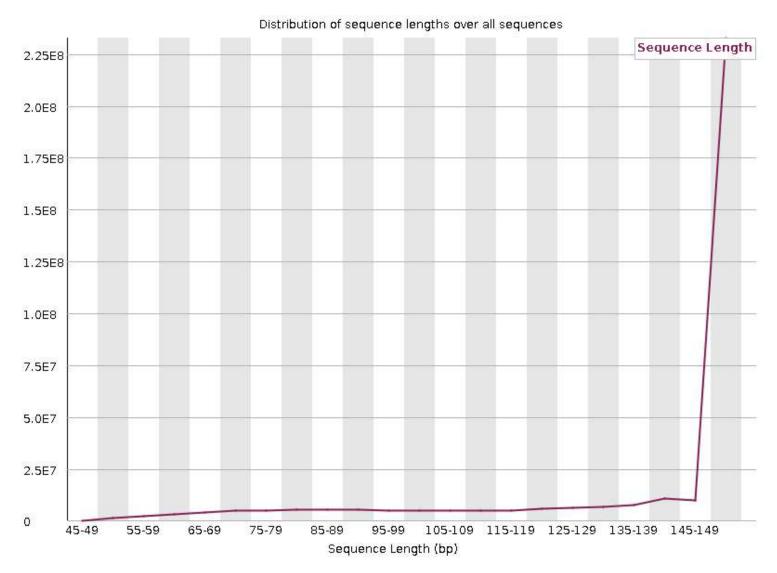
Per sequence GC content



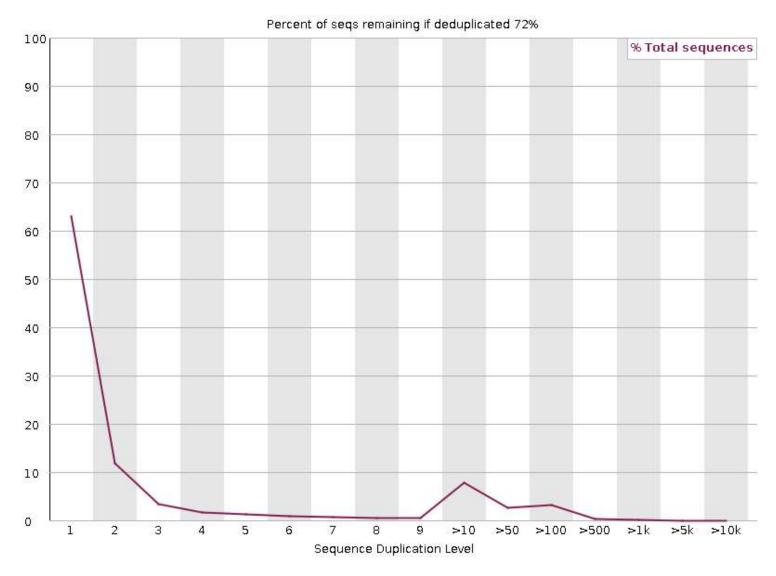
Per base N content



Sequence Length Distribution



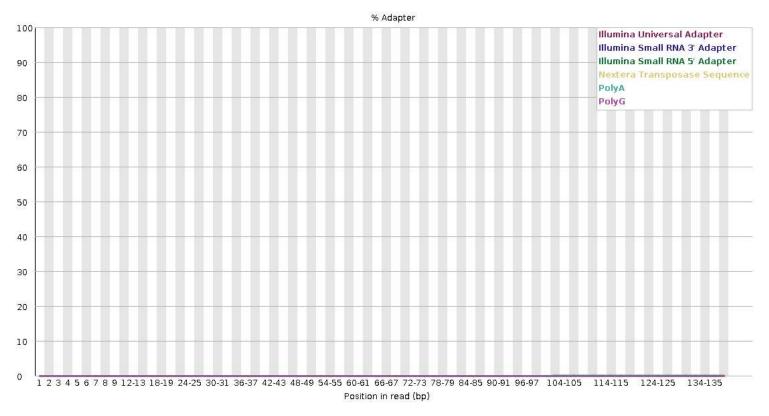
Sequence Duplication Levels





No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.12.1)