# **Report**

Mon 25 Aug 2025 GG20-leaf\_R2.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\_R2.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 344148221

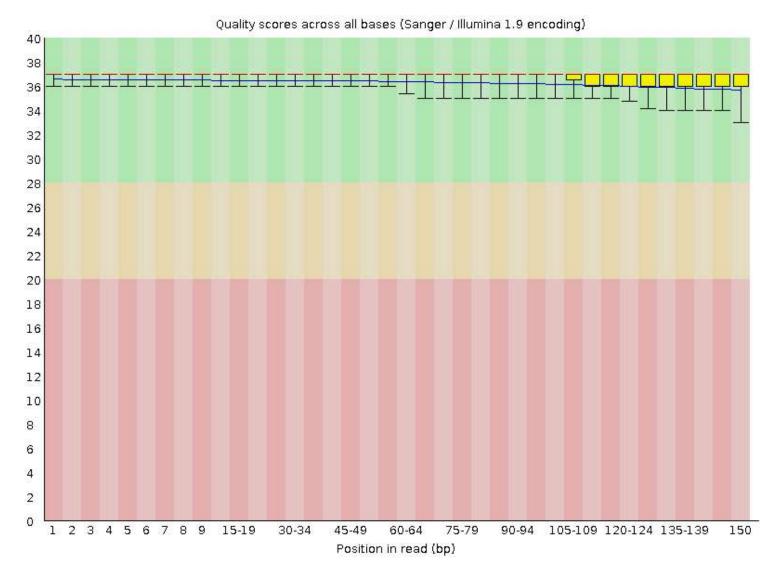
Total Bases 47 Gbp

Sequences flagged as poor quality 0

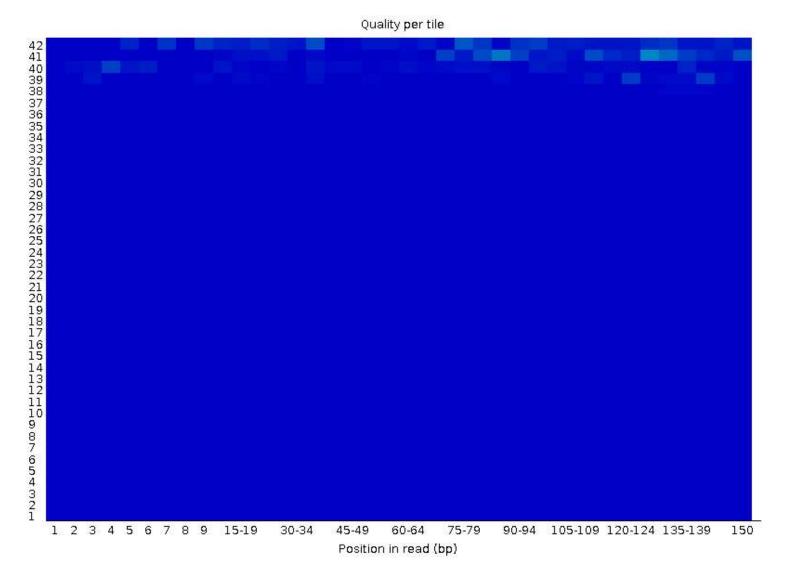
Sequence length 50-150

%GC 37

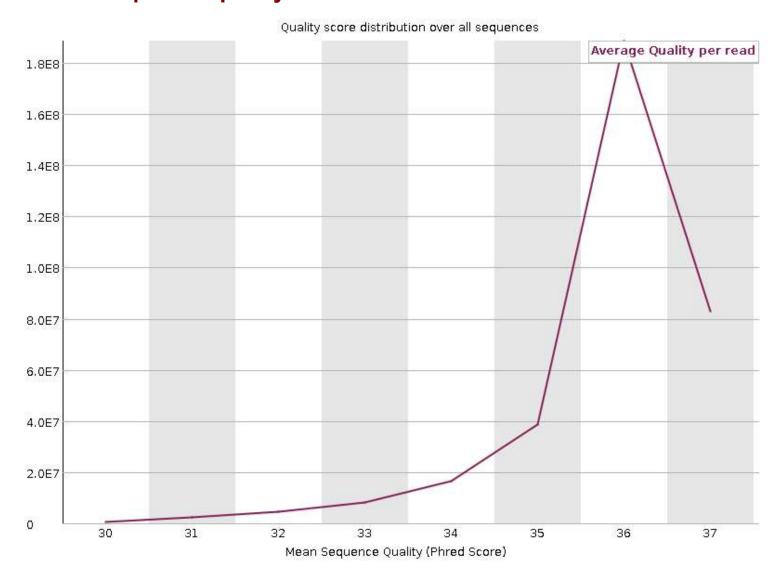
#### Per base sequence quality



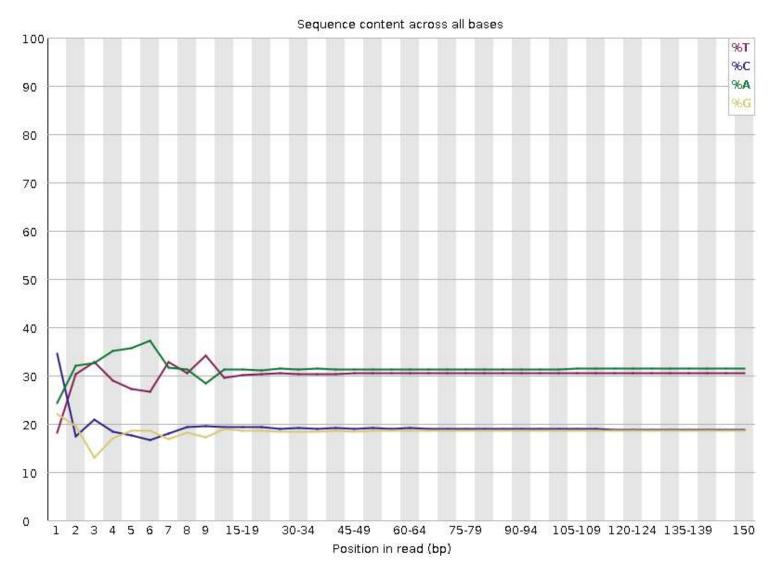
#### Per tile sequence quality



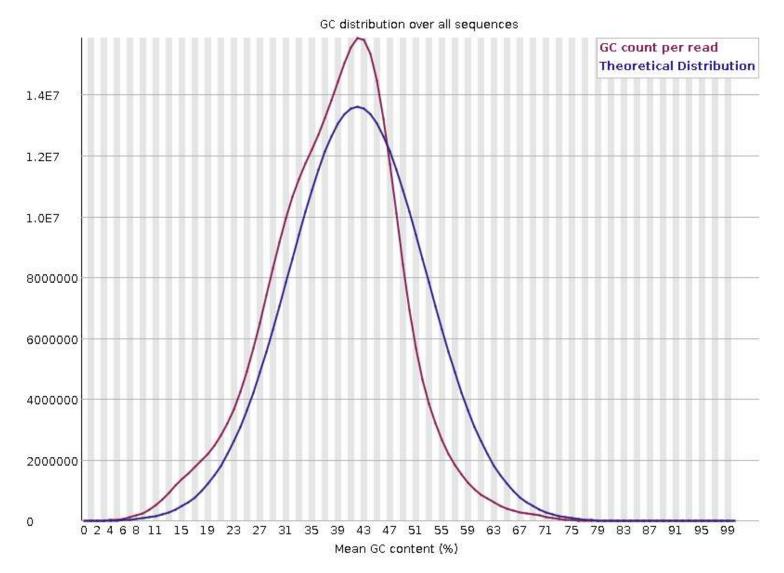
## Per sequence quality scores



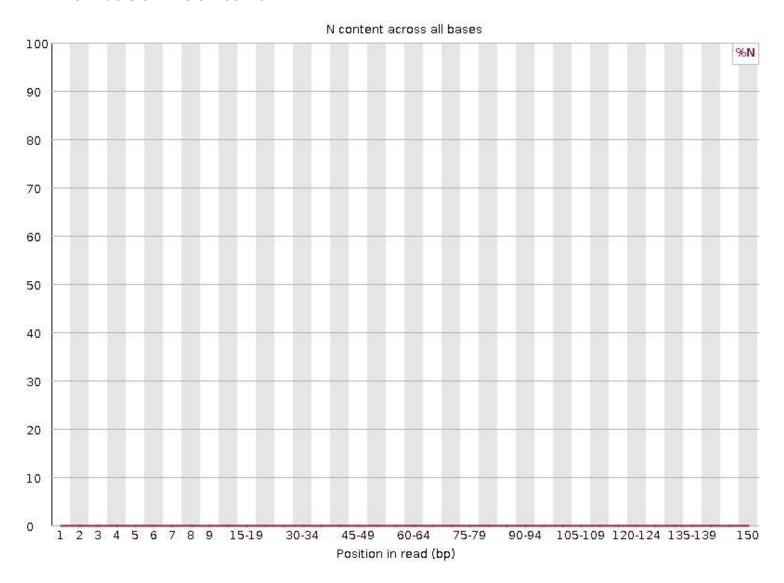
#### Per base sequence content



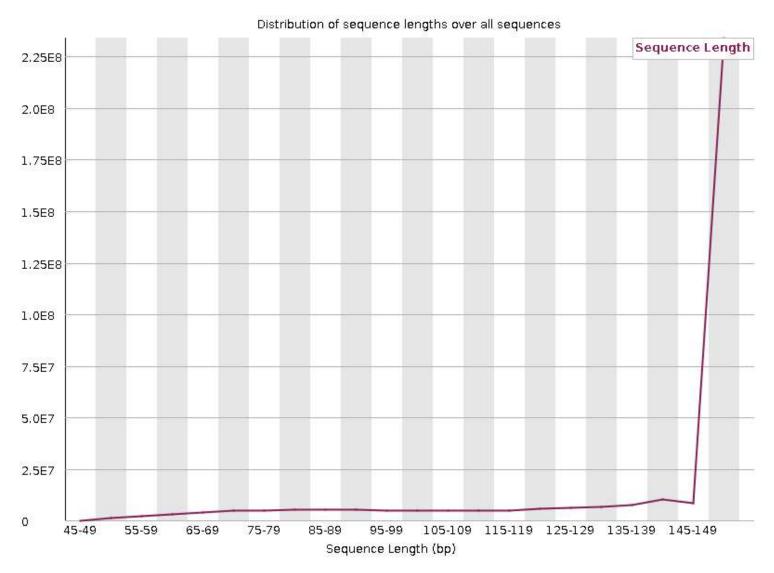
#### Per sequence GC content



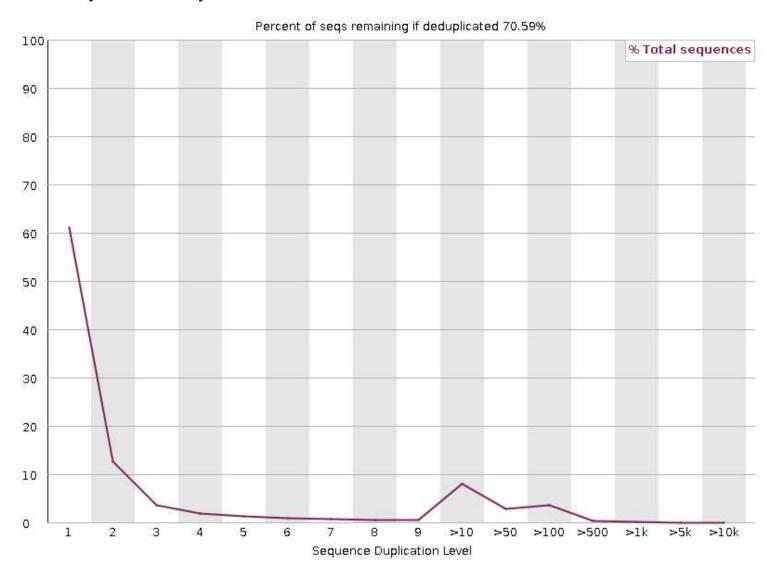
#### Per base N content



#### Sequence Length Distribution



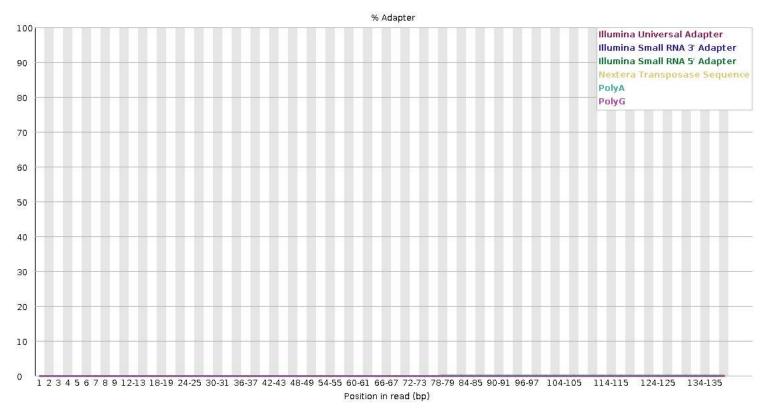
### Sequence Duplication Levels





No overrepresented sequences

#### Adapter Content



Produced by FastQC (version 0.12.1)