#### Tue 16 Sep 2025 evol1\_R1.fastq

# **Report**

#### **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 evol1\_R1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 988653

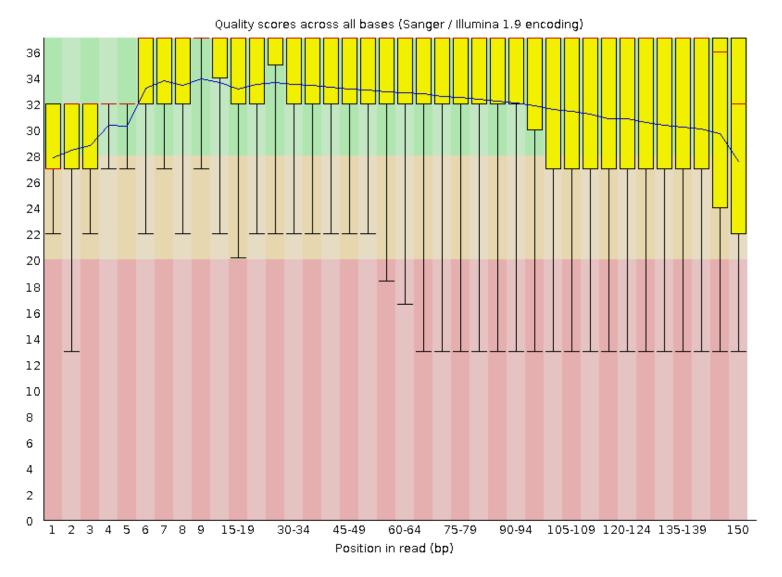
Total Bases 139.3 Mbp

Sequences flagged as poor quality 0

Sequence length 35-150

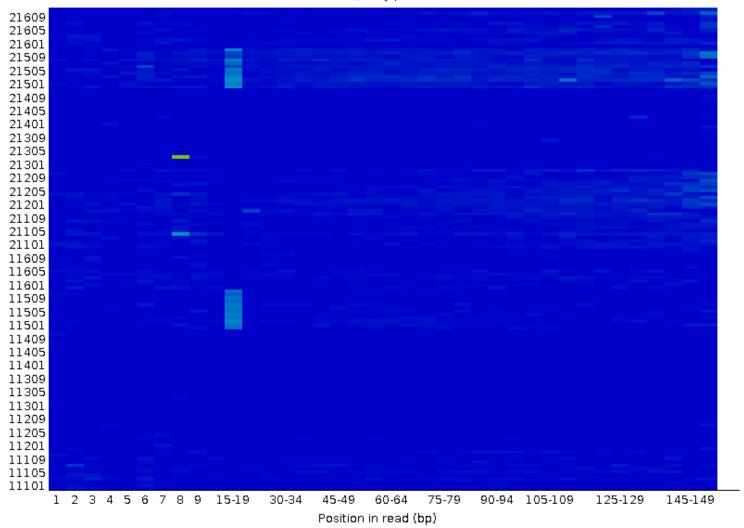
%GC 50

## Per base sequence quality

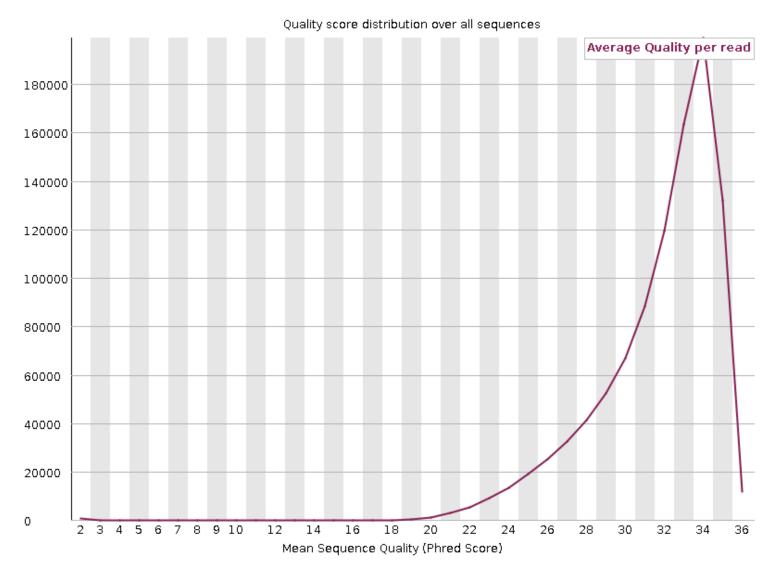


#### Per tile sequence quality

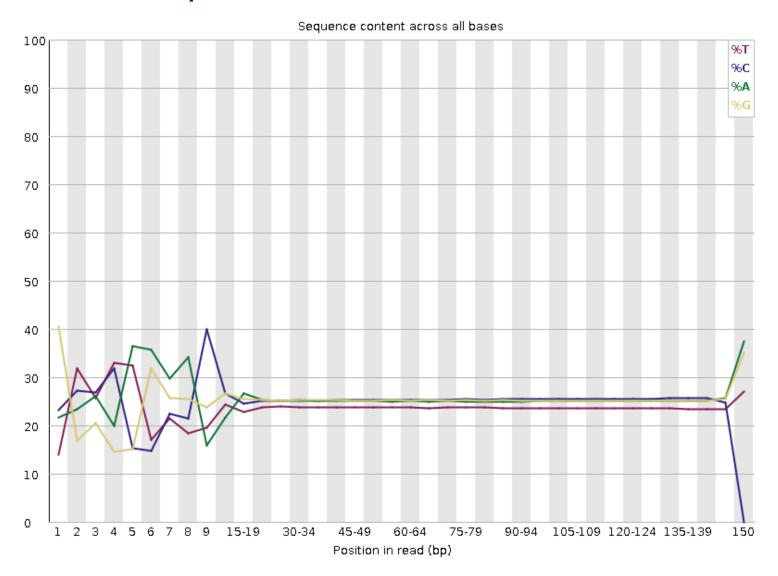




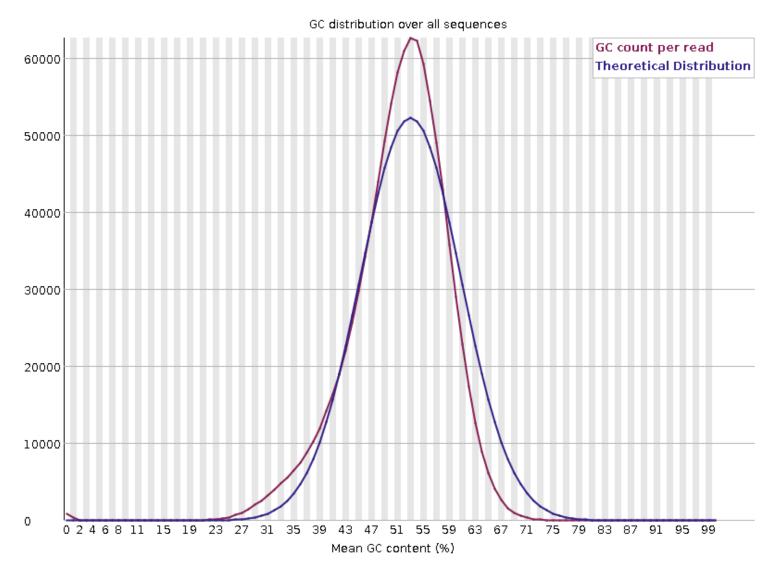
## Per sequence quality scores



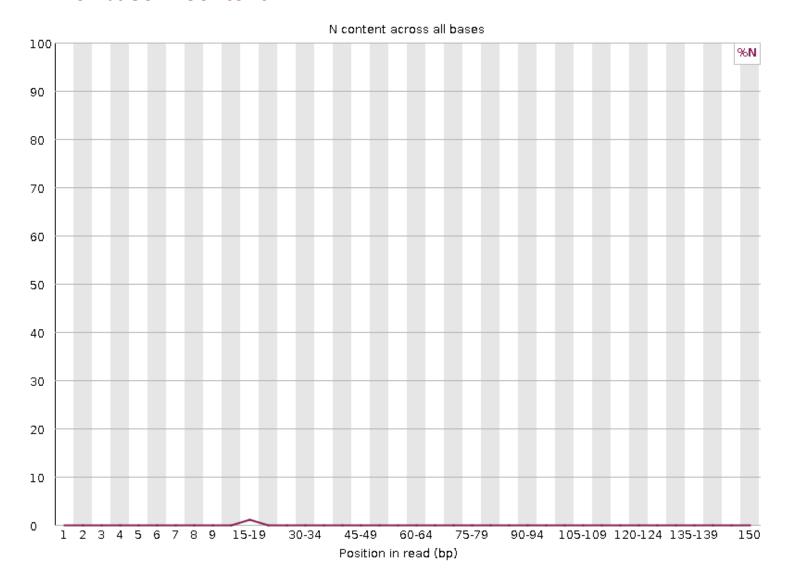
## Per base sequence content



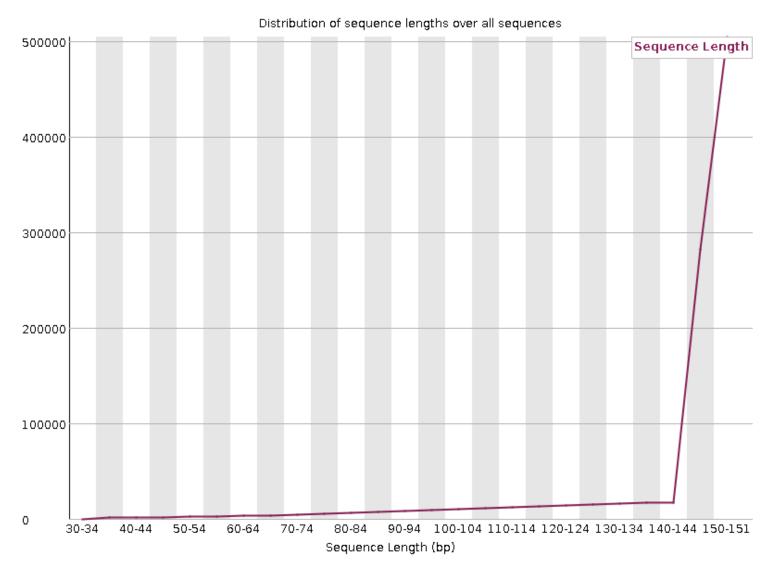
## Per sequence GC content



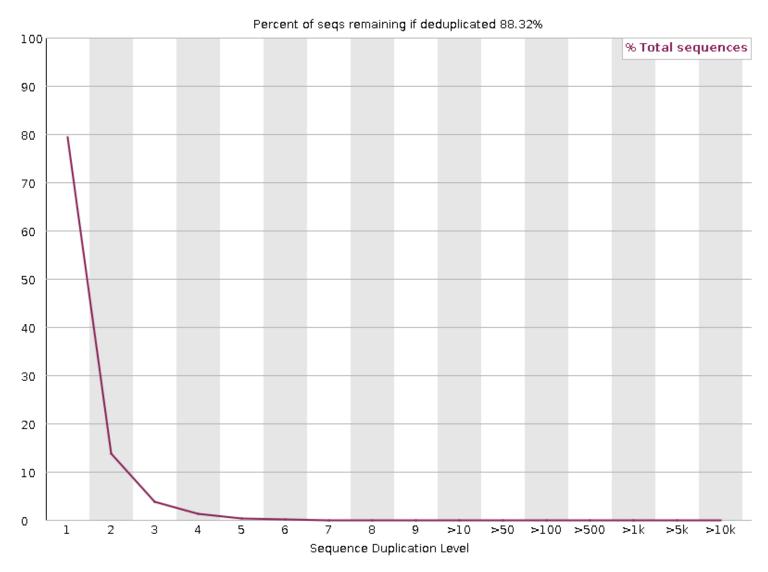
### Per base N content



### Sequence Length Distribution



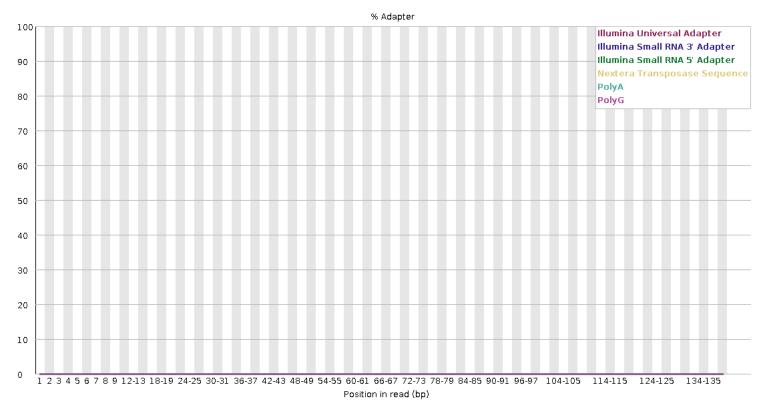
## Sequence Duplication Levels





No overrepresented sequences

## Adapter Content



Produced by FastQC (version 0.12.1)