### Thu 18 Sep 2025 evol1\_R2.clean.fq

# **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\_R2.clean.fq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 706085

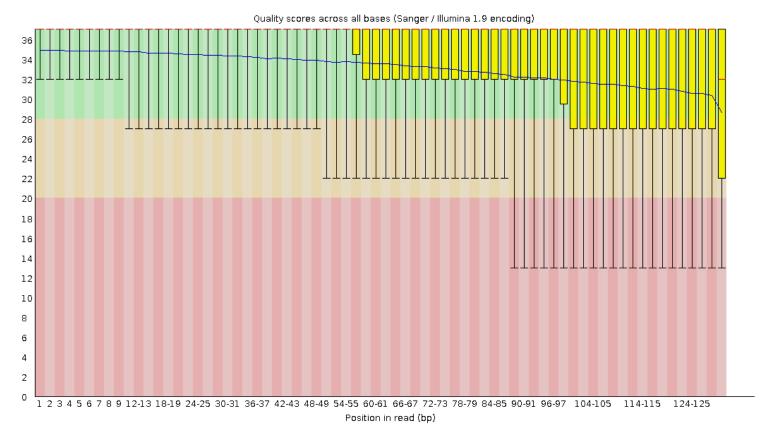
Total Bases 88.2 Mbp

Sequences flagged as poor quality 0

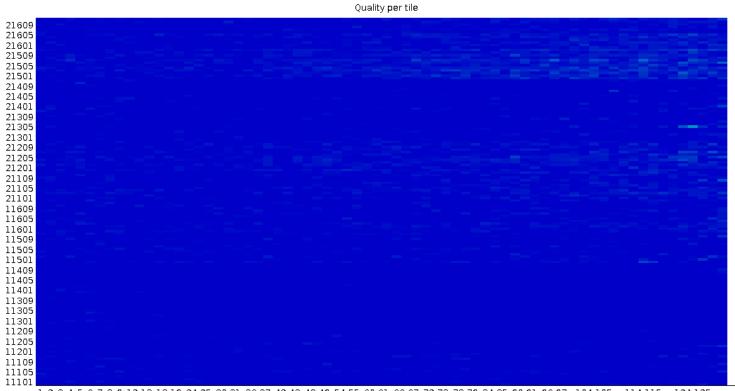
Sequence length 80-130

%GC 51

## Per base sequence quality

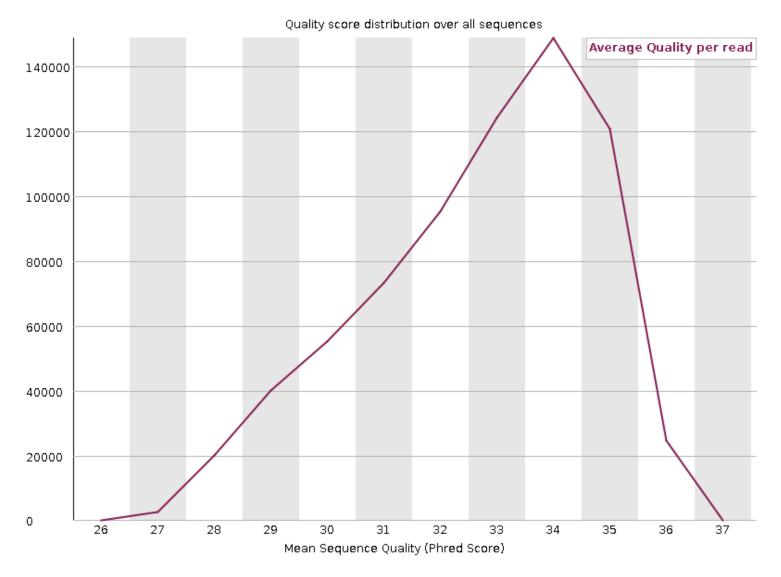


## Per tile sequence quality

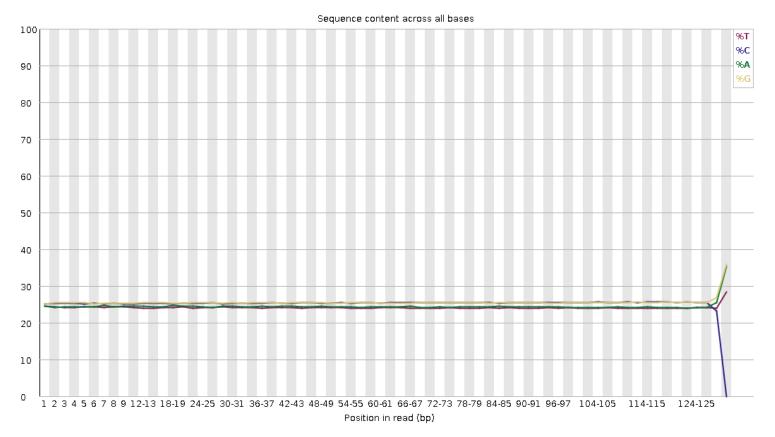


1 2 3 4 5 6 7 8 9 12-13 18-19 24-25 30-31 36-37 42-43 48-49 54-55 60-61 66-67 72-73 78-79 84-85 90-91 96-97 104-105 114-115 124-125 Position in read (bp)

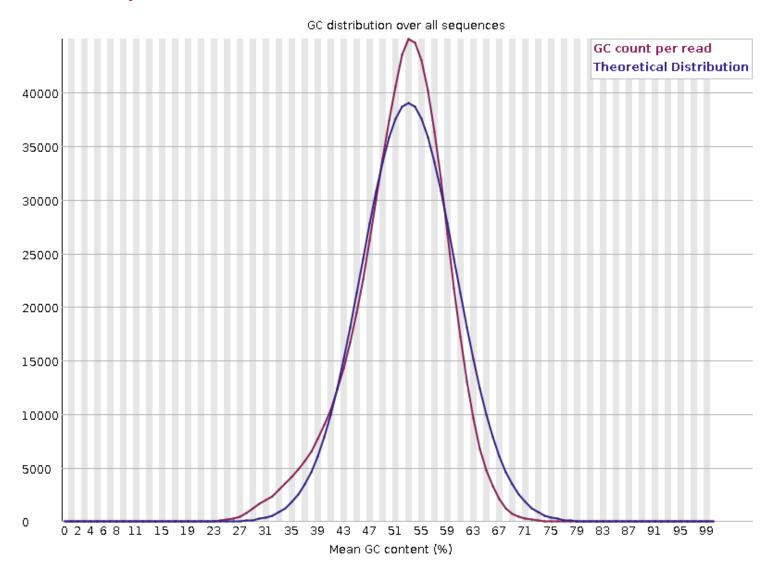
## Per sequence quality scores



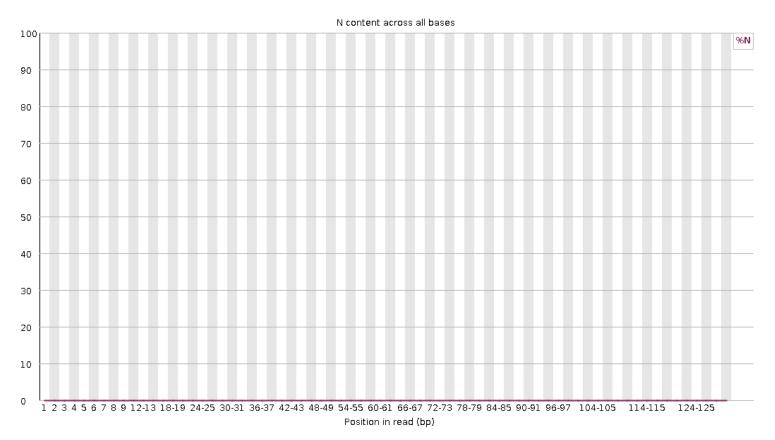
## **OPER** Per base sequence content



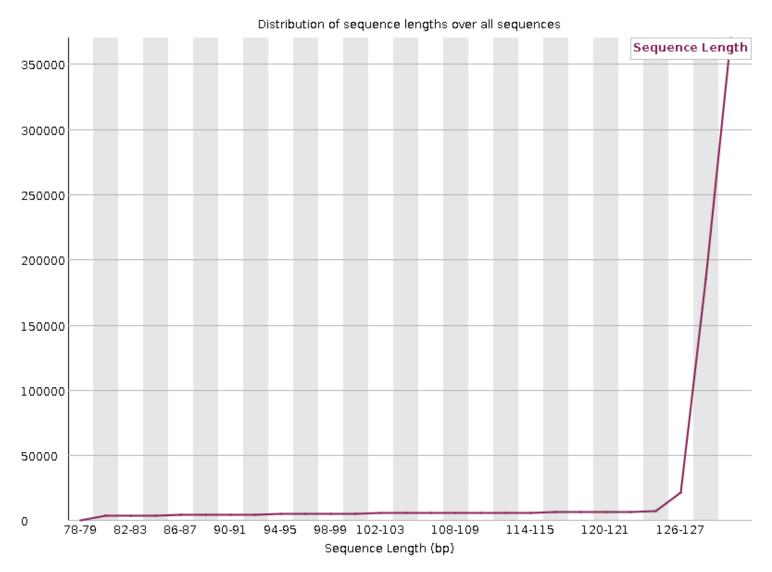
### Per sequence GC content



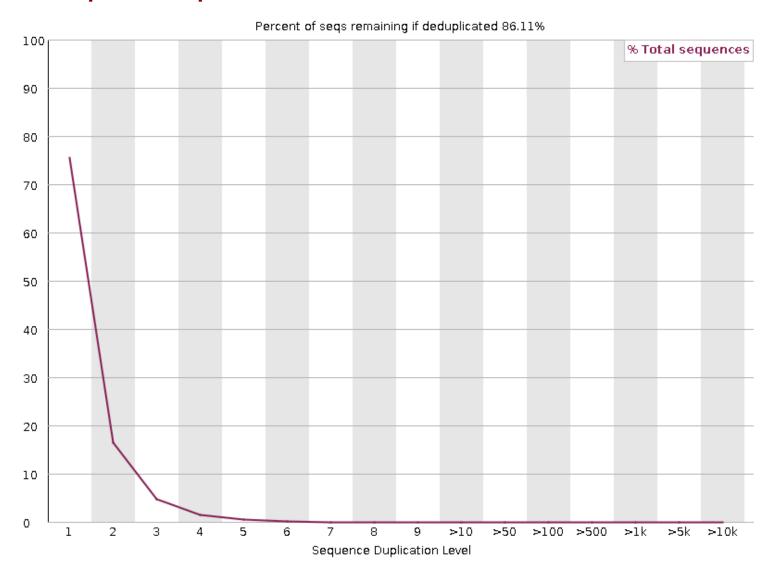
## Per base N content



### Sequence Length Distribution



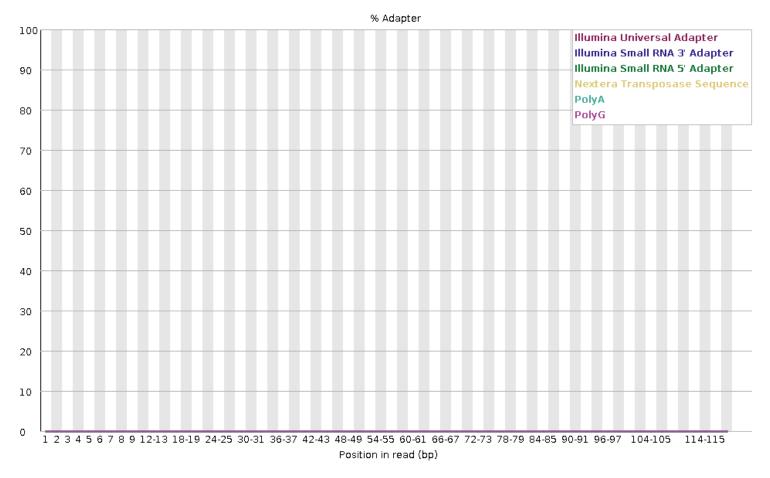
## Sequence Duplication Levels





No overrepresented sequences

## Adapter Content



Produced by FastQC (version 0.12.1)