Tue 16 Sep 2025 evol1_R2.fastq

№FastQC 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.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 988653

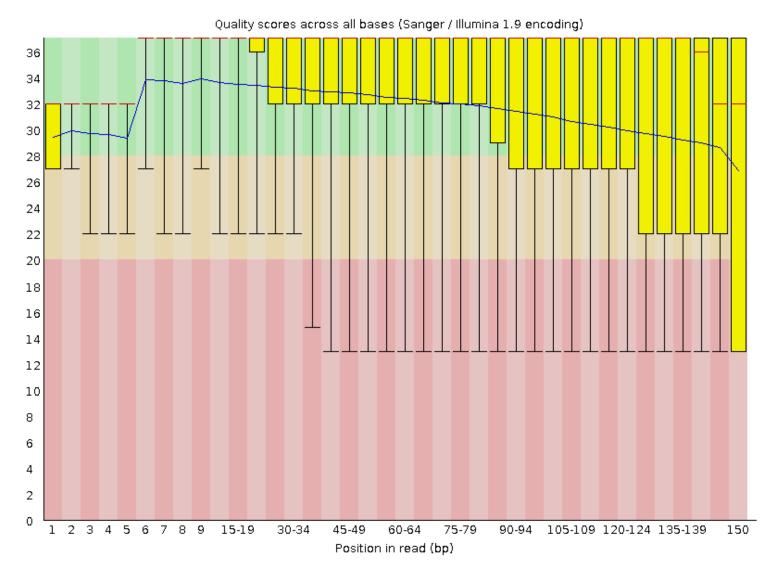
Total Bases 139.4 Mbp

Sequences flagged as poor quality 0

Sequence length 35-150

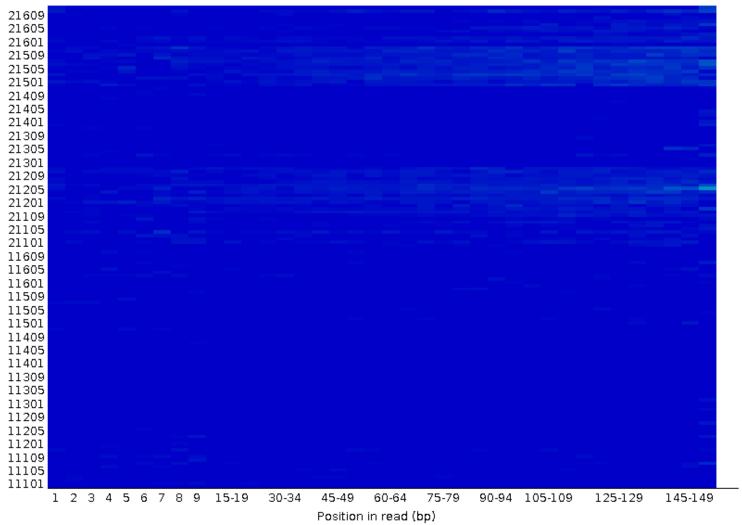
%GC 50

Per base sequence quality

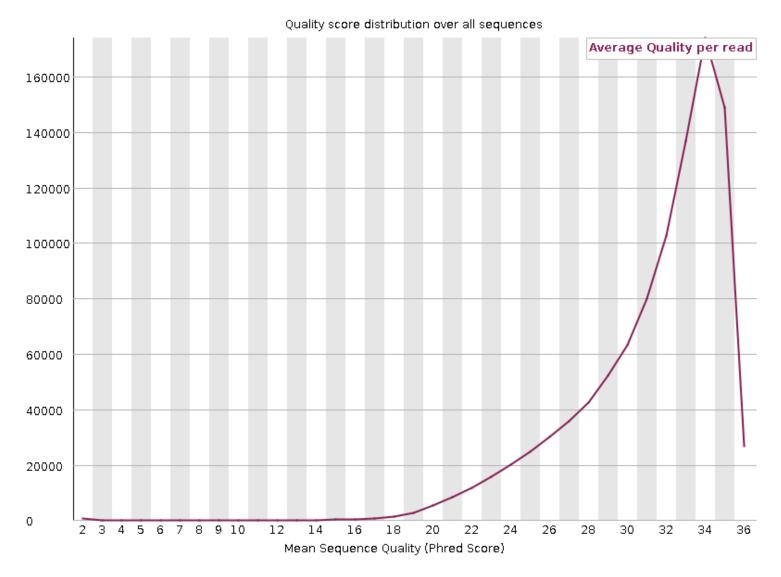


Per tile sequence quality

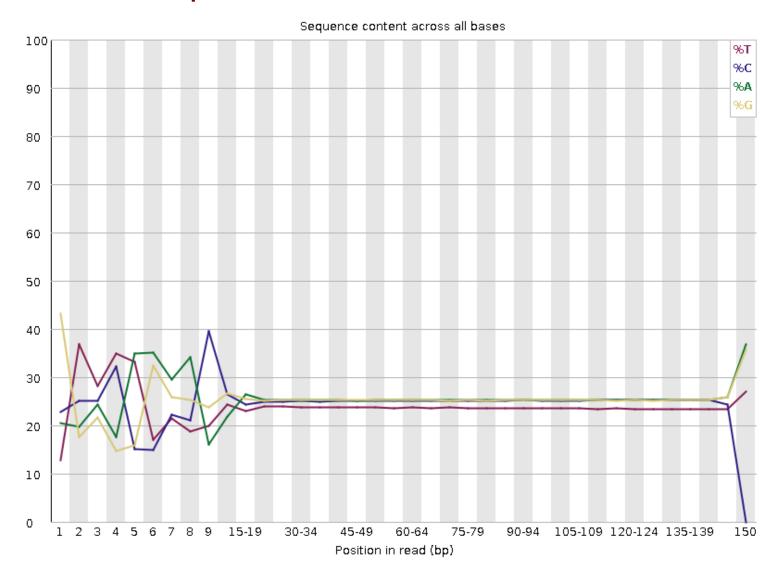




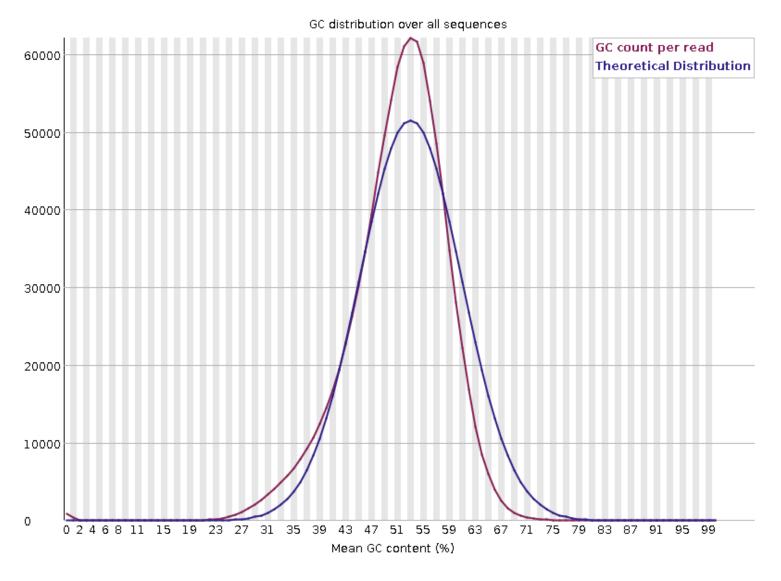
Per sequence quality scores



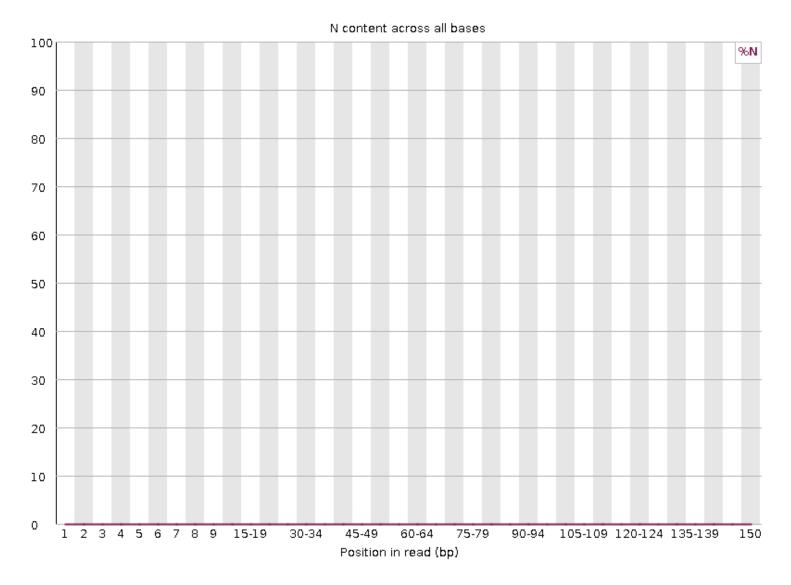
Per base sequence content



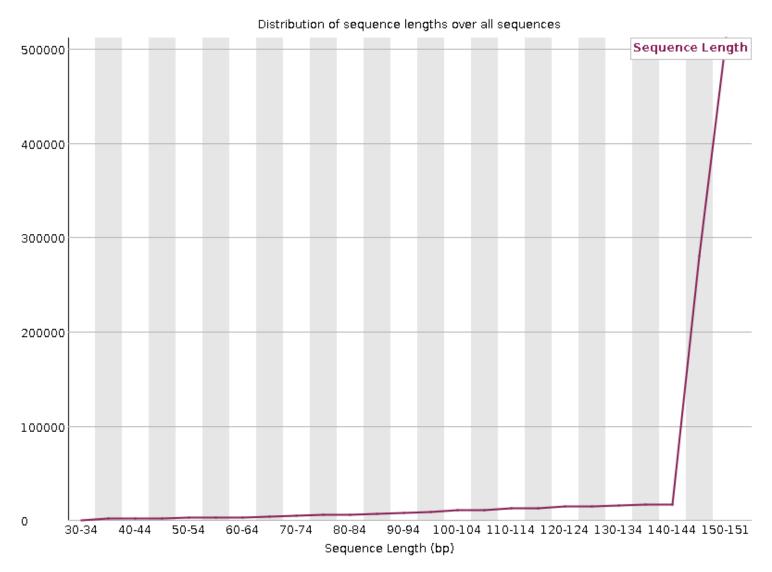
Per sequence GC content



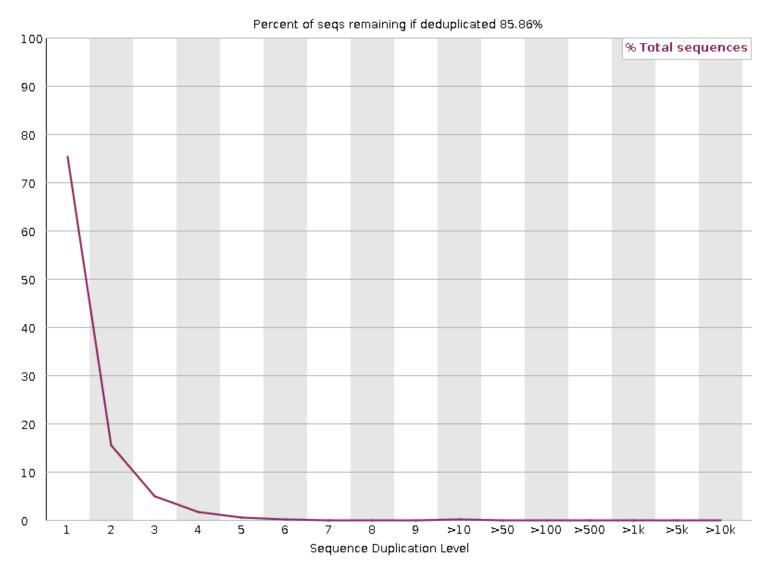
Per base N content



Sequence Length Distribution



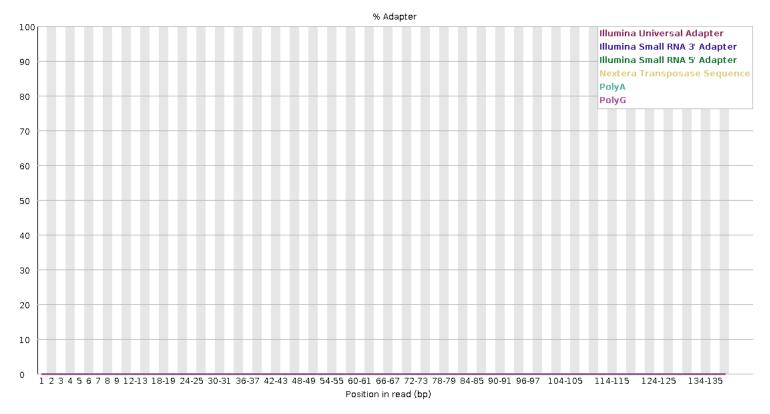
Sequence Duplication Levels





No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.12.1)