№FastQC Report

Summary

Mon 13 Jan 2025 HG008-T_TTCCTGTT-AAGATACT_subset_HJVY2DSX7_L001_001.R1.fastq.gz



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

Overrepresented sequences

Adapter Content

Basic Statistics

Measure Value

Filename HG008-T_TTCCTGTT-

AAGATACT_subset_HJVY2DSX7_L001_001.R1.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 1000000

Total Bases 150 Mbp

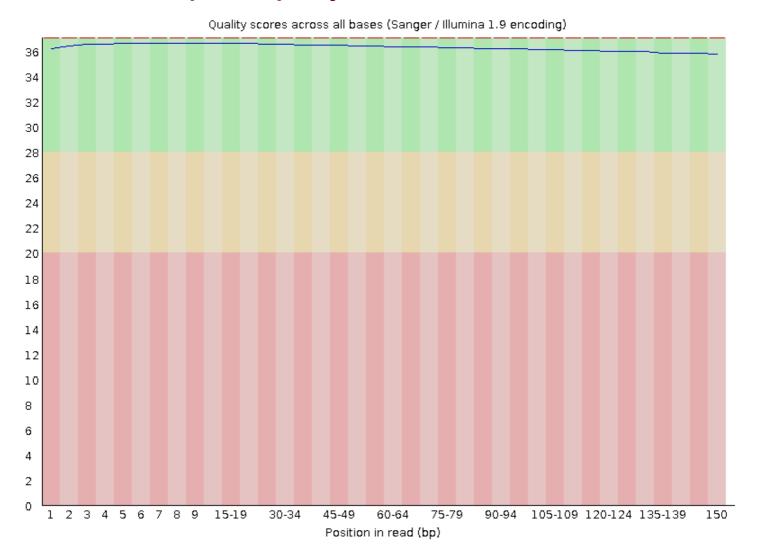
Sequences flagged as poor

quality

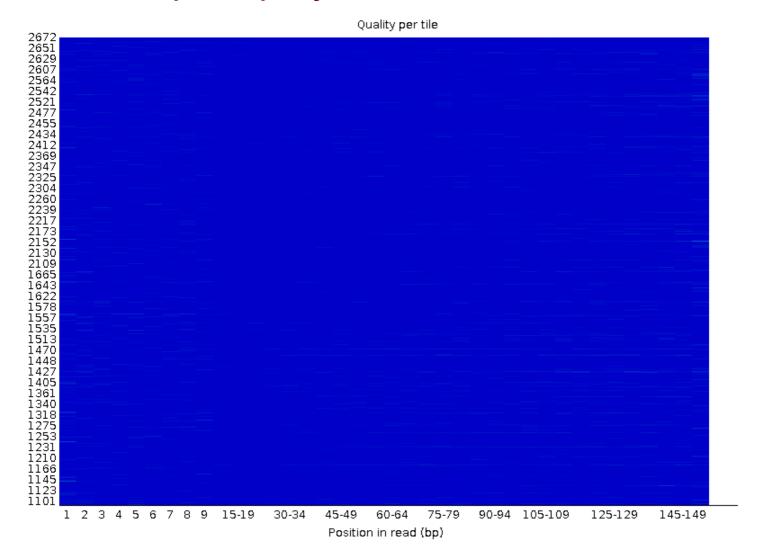
Sequence length 150

%GC 41

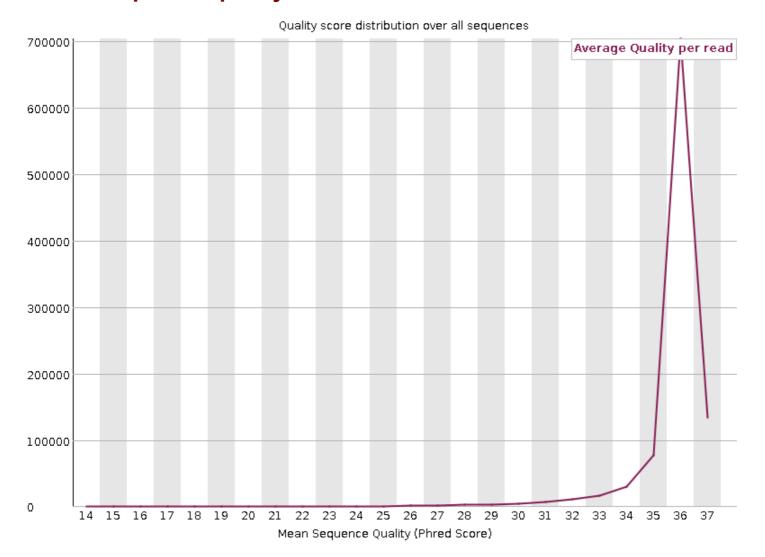
Per base sequence quality



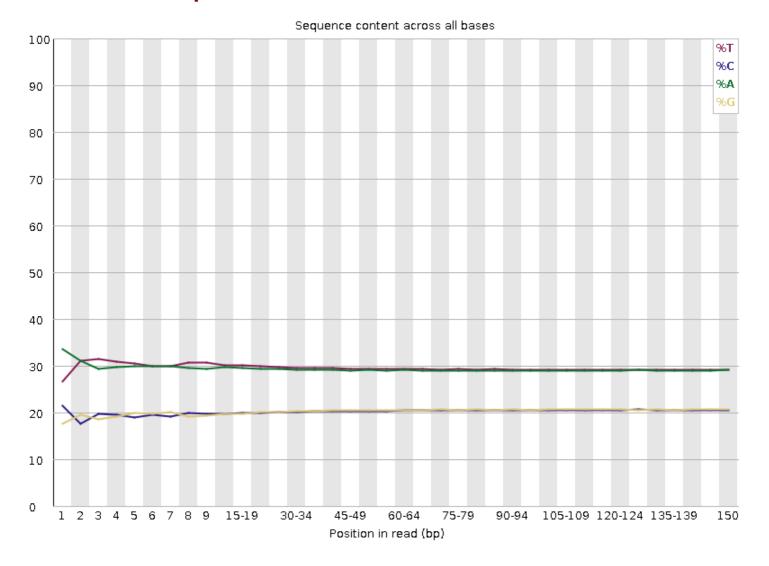
Per tile sequence quality



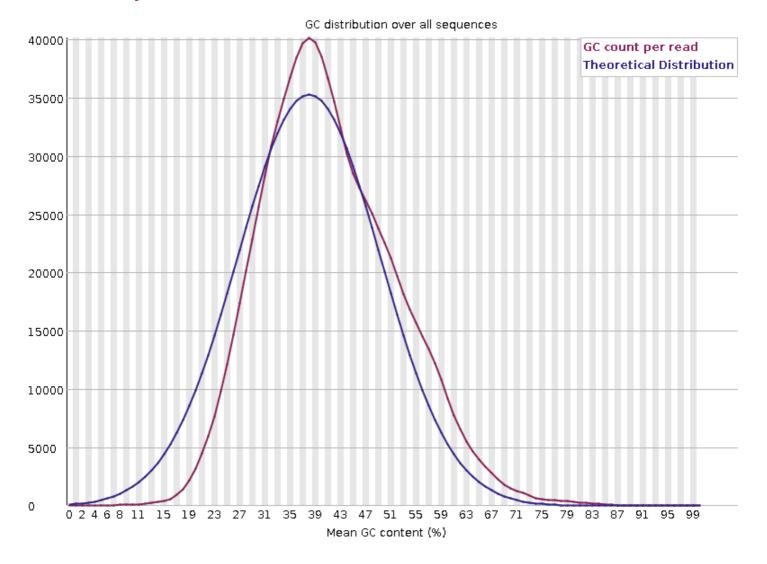
Per sequence quality scores



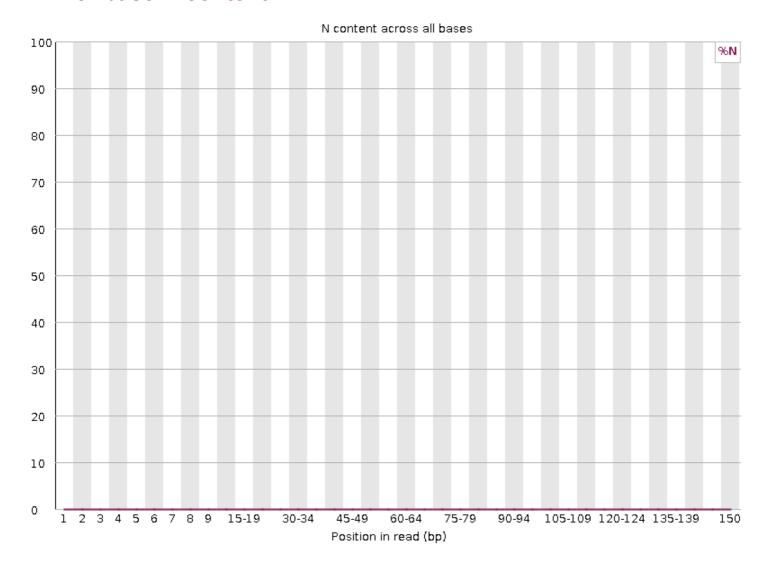
Per base sequence content



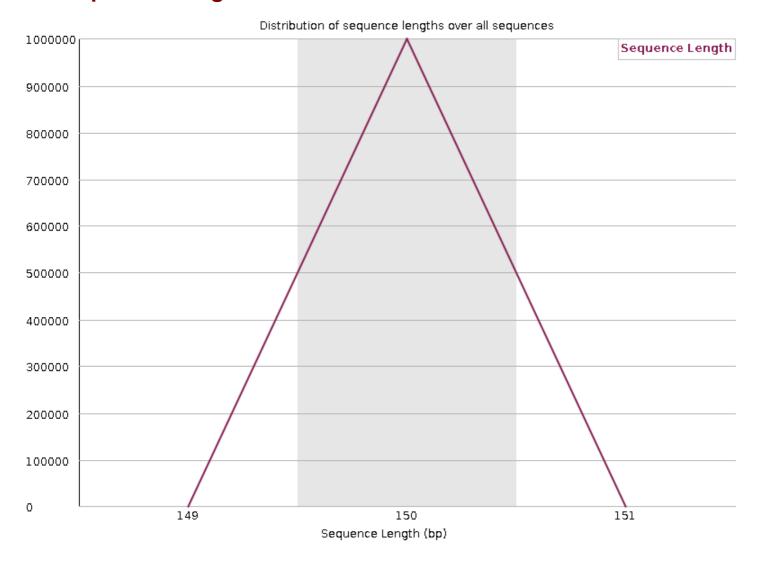
Per sequence GC content



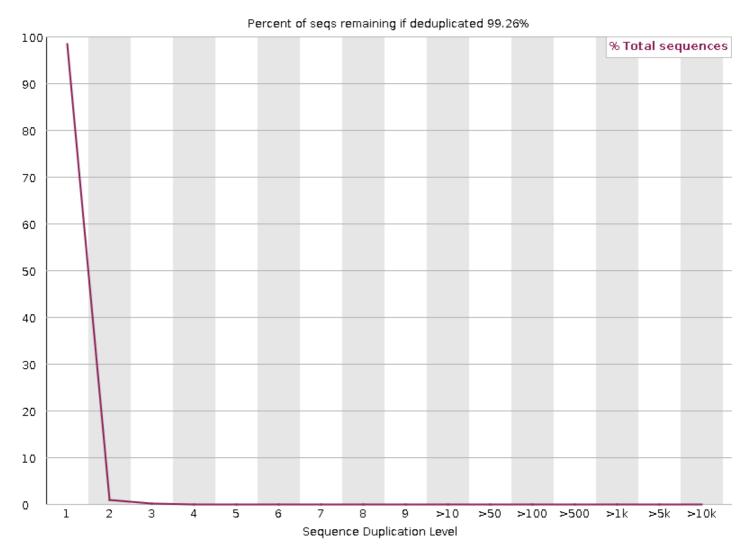
Per base N content



Sequence Length Distribution



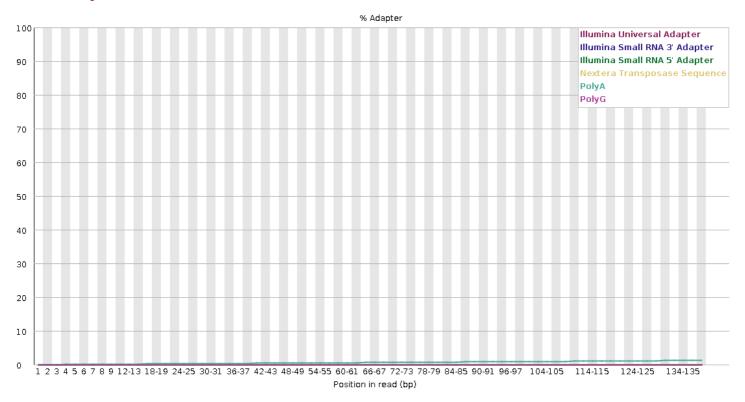
Sequence Duplication Levels





No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.12.1)