№FastQC Report

Summary HG008-N-D_CGGACAAC-AATCCGGA_subset_H3LLJDSXC_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-N-D_CGGACAAC-

AATCCGGA_subset_H3LLJDSXC_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

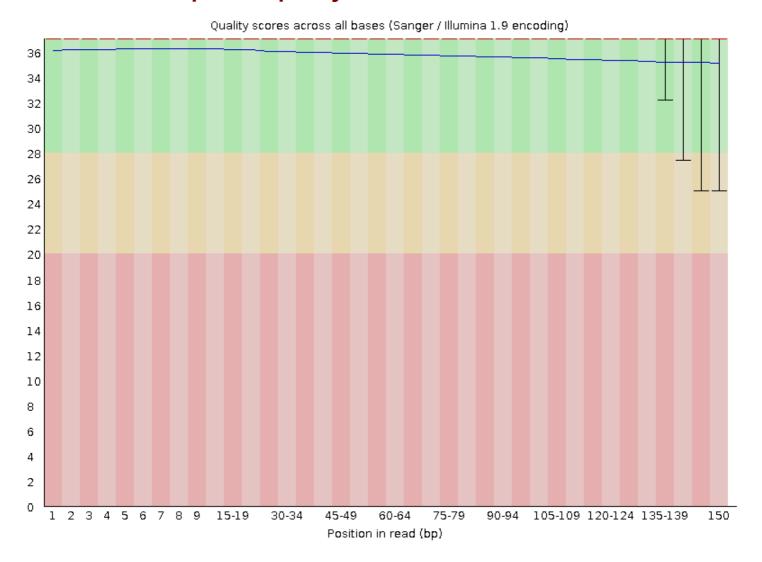
quality

0

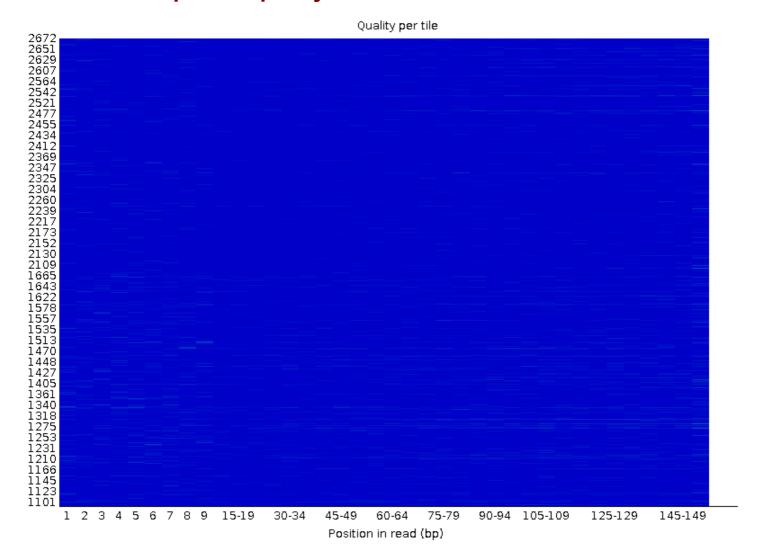
Sequence length 150

%GC 40

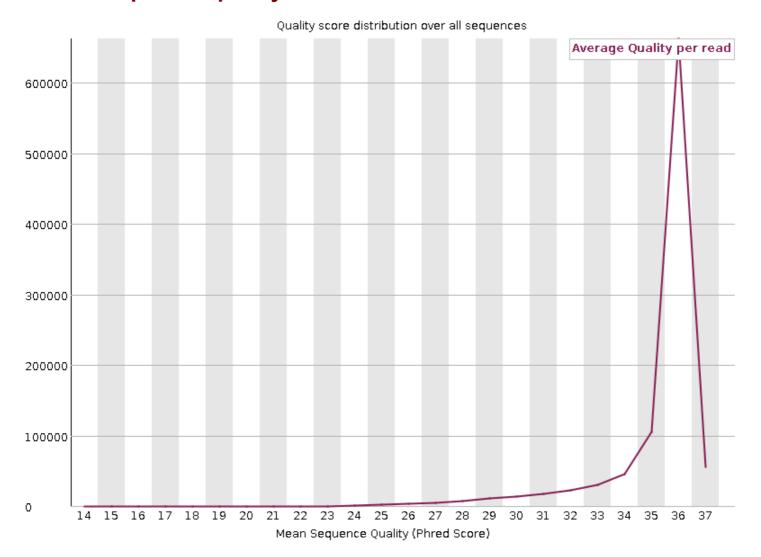
Per base sequence quality



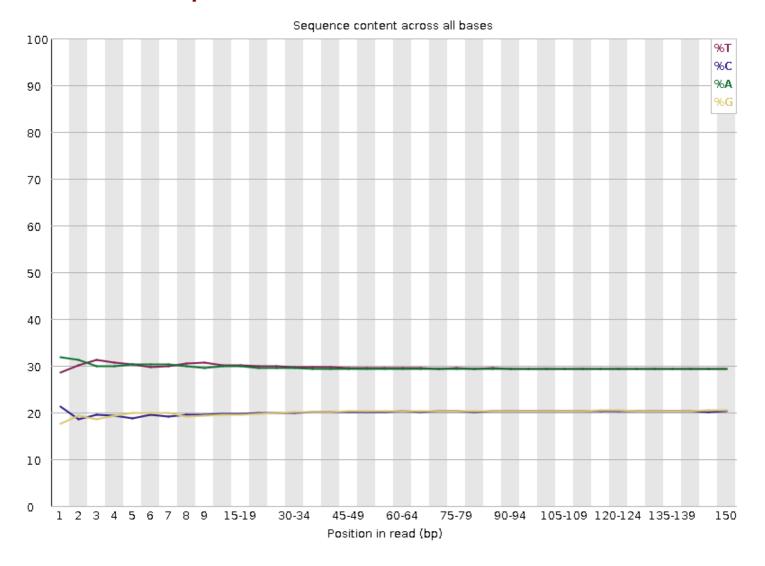
Per tile sequence quality



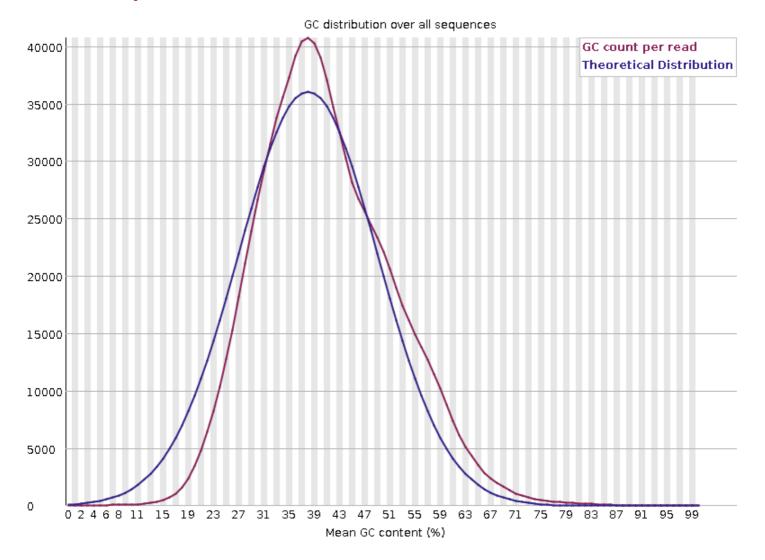
Per sequence quality scores



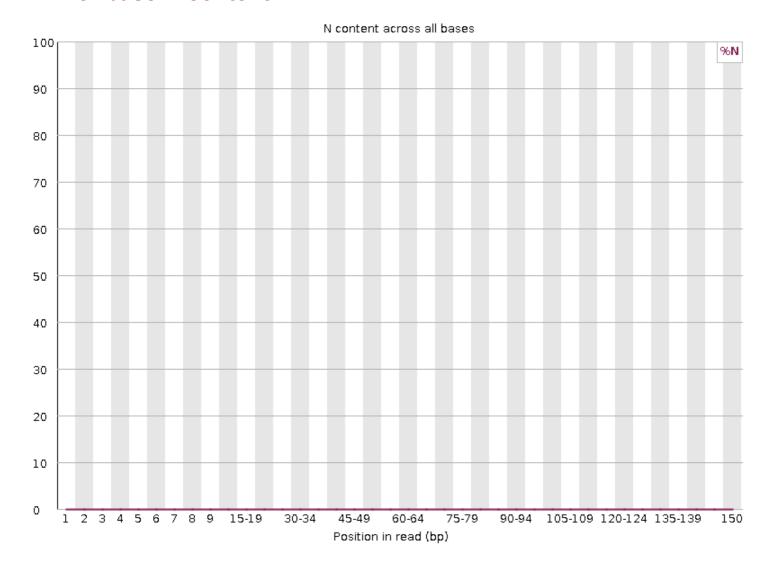
Per base sequence content



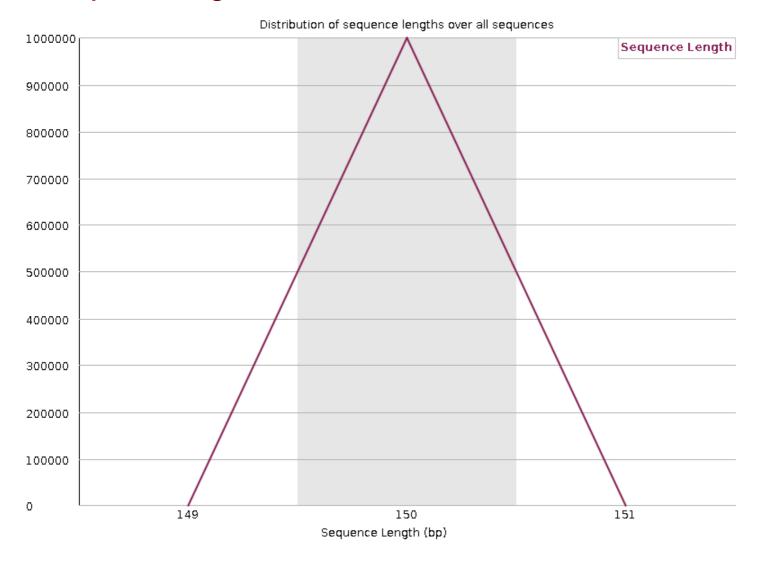
Per sequence GC content



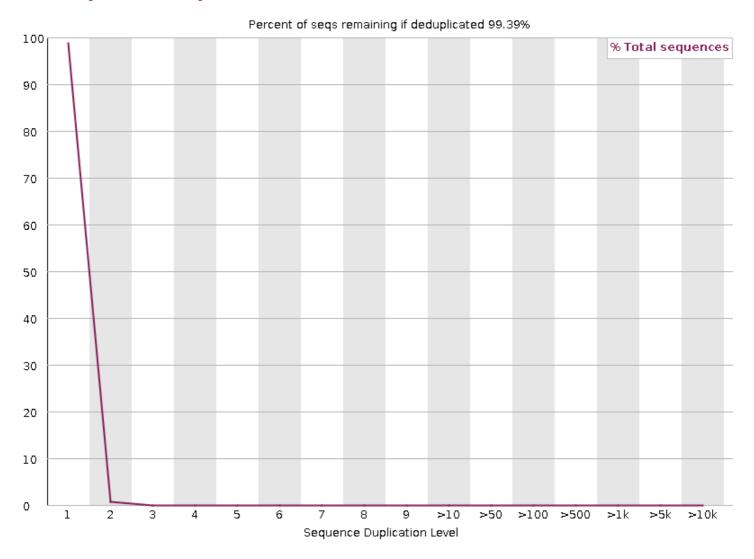
Per base N content



Sequence Length Distribution



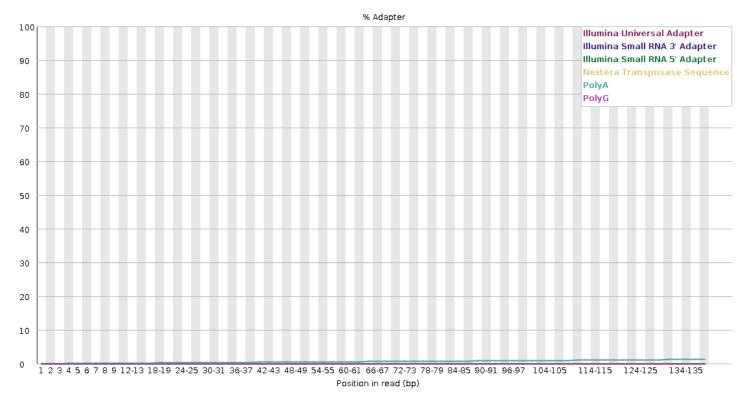
Sequence Duplication Levels





No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.12.1)