№FastQC Report

Summary



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 16S_sequences_reverse.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

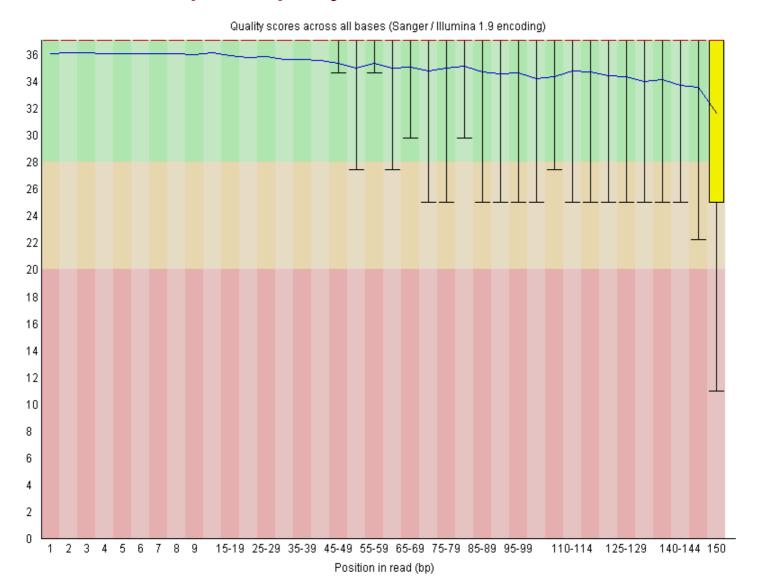
Total Sequences 57976189

Sequences flagged as poor quality 0

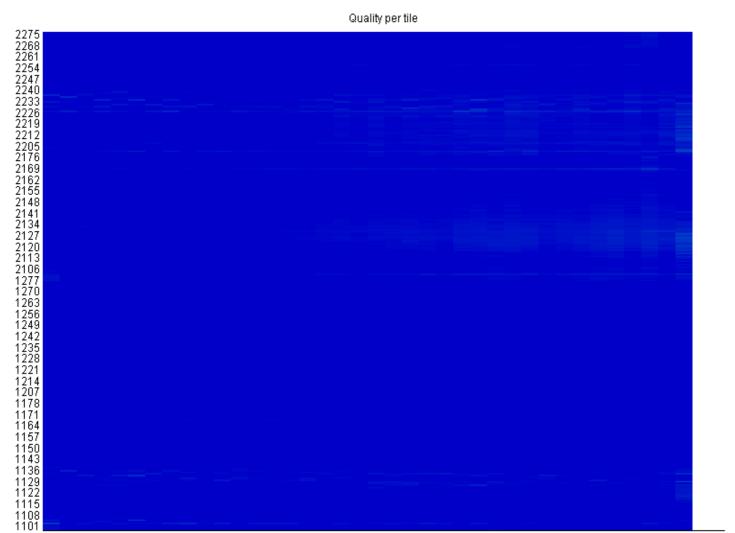
Sequence length 150

%GC 48

Per base sequence quality

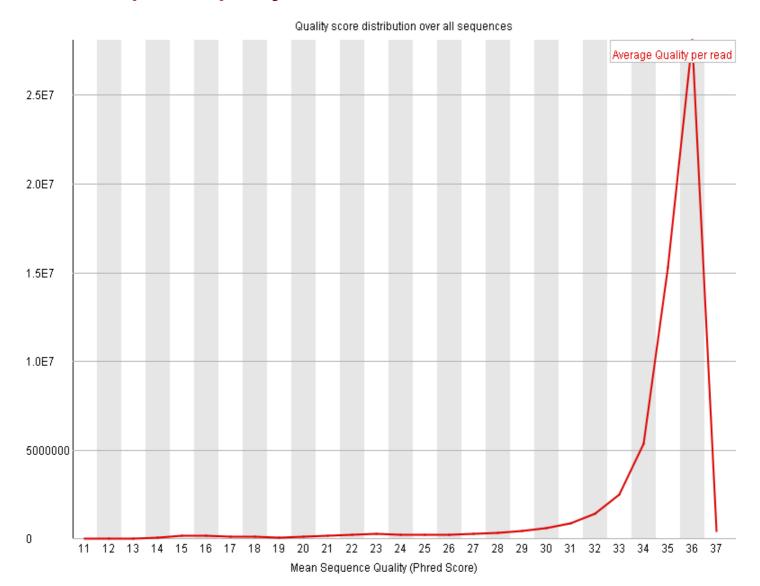


Per tile sequence quality

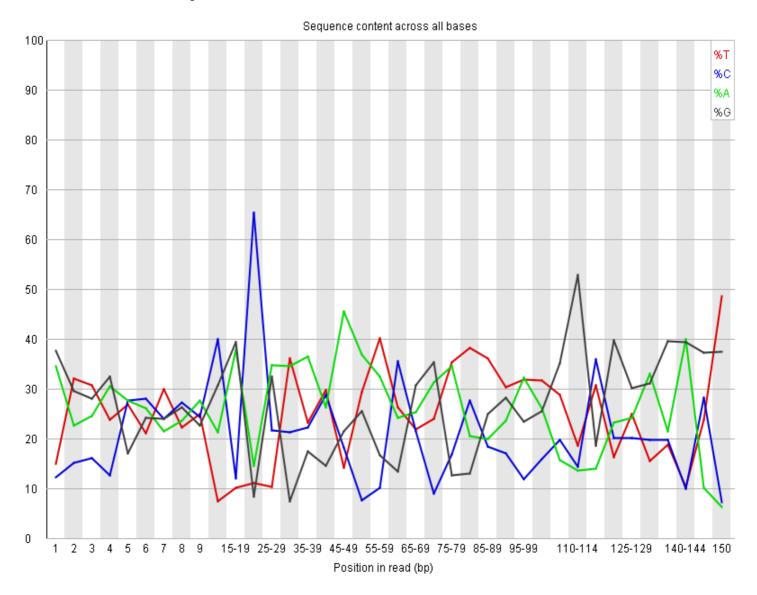


1 2 3 4 5 6 7 8 9 15-19 25-29 35-39 45-49 55-59 65-69 75-79 85-89 95-99 110-114 125-129 140-144 Position in read (bp)

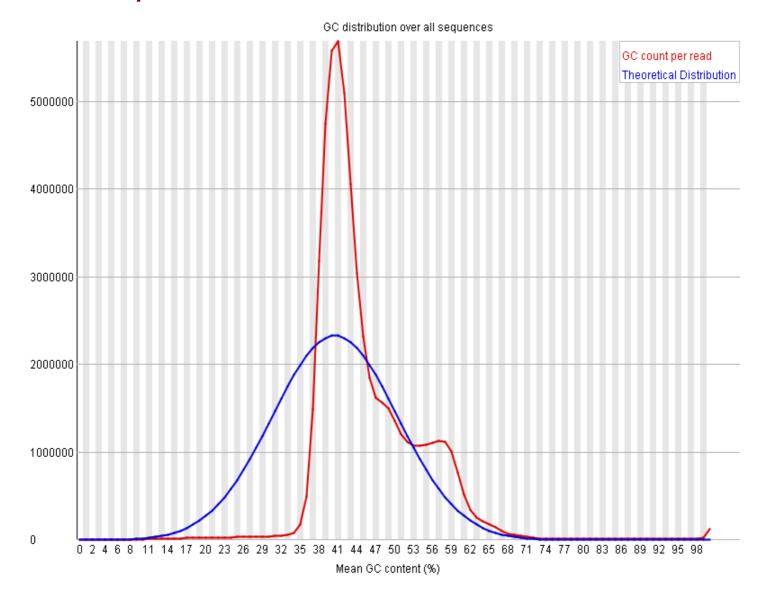
Per sequence quality scores



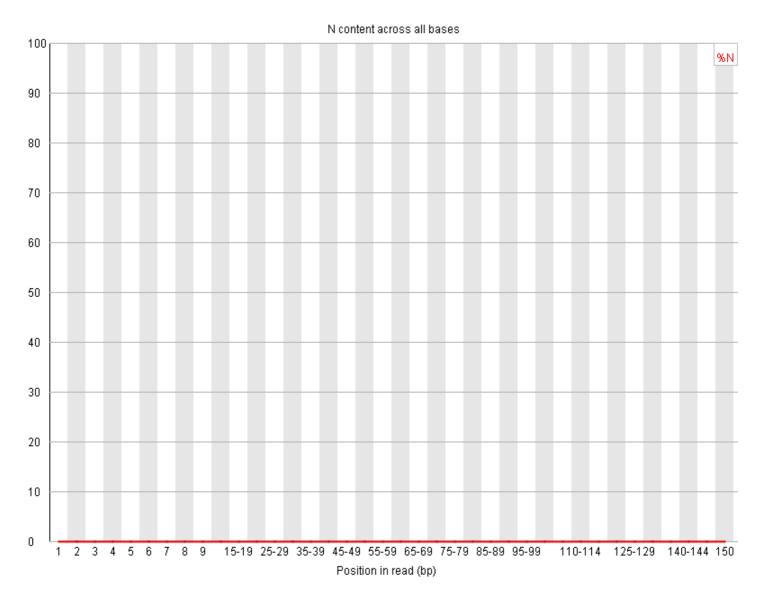
Per base sequence content



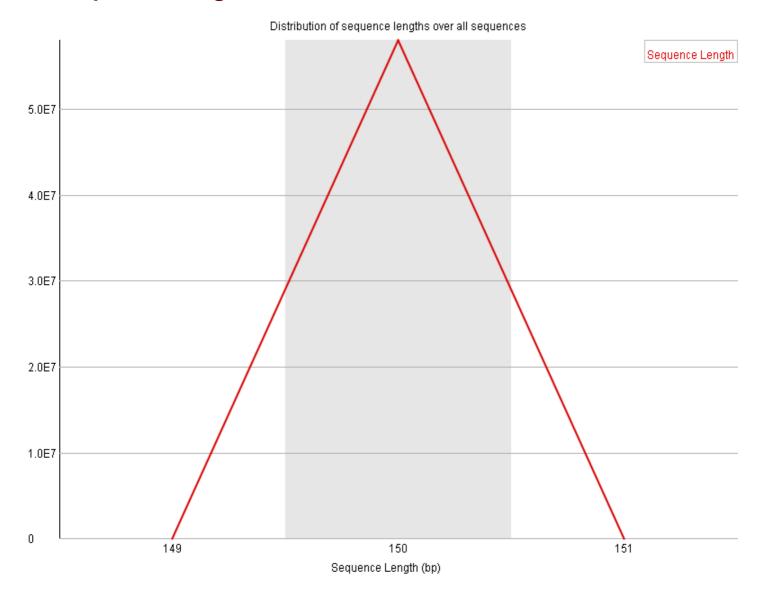
Per sequence GC content



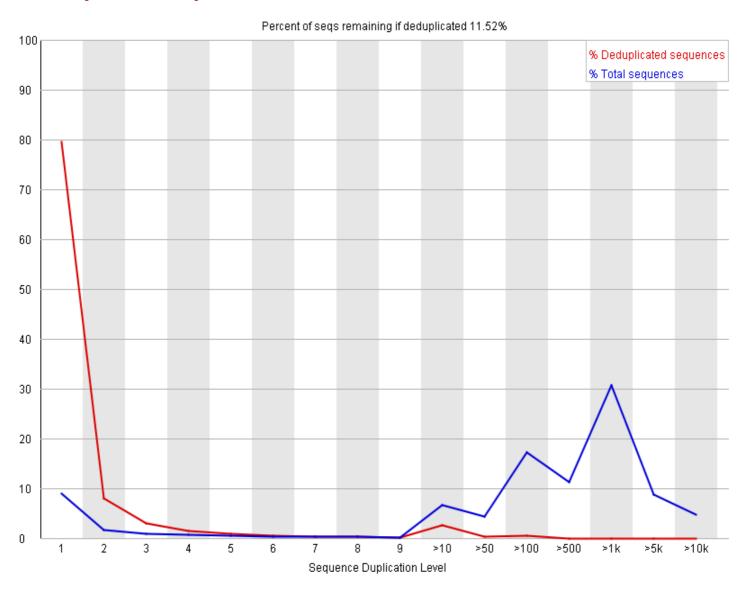
Per base N content



Sequence Length Distribution



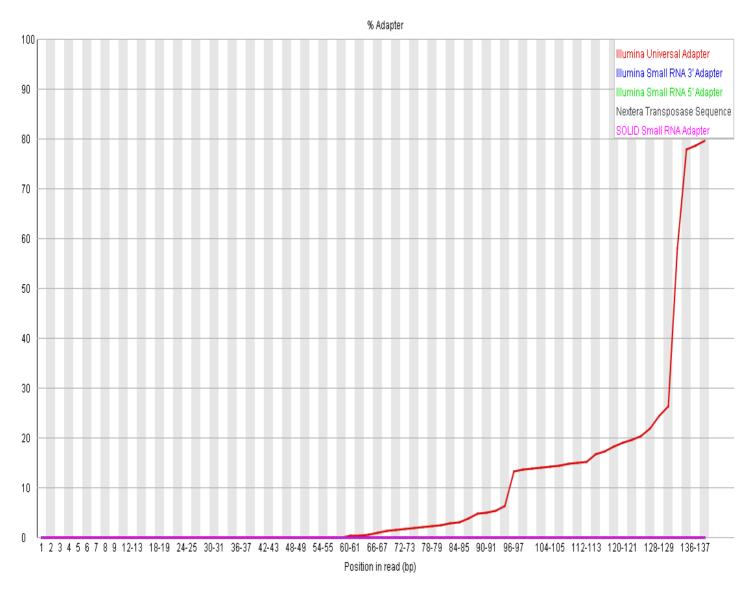
Sequence Duplication Levels



Overrepresented sequences

Sequence Count Percentage Possible Source

Adapter Content



Produced by <u>FastQC</u> (version 0.11.8)