Fri 3 Apr 2020 A0167658L_1.trimmed.fq

№FastQC Report

Summary



Per base 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

Example 2 Kmer Content

Basic Statistics

Measure Value

File type

A0167658L_1.trimmed.fq

Conventional base calls

Encoding Sanger / Illumina 1.9

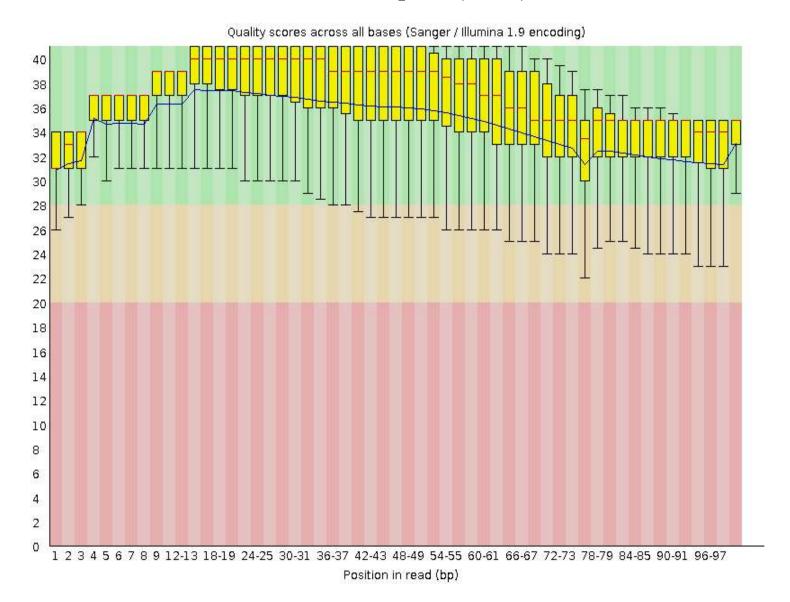
Total Sequences 1205389

Sequences flagged as poor quality 0

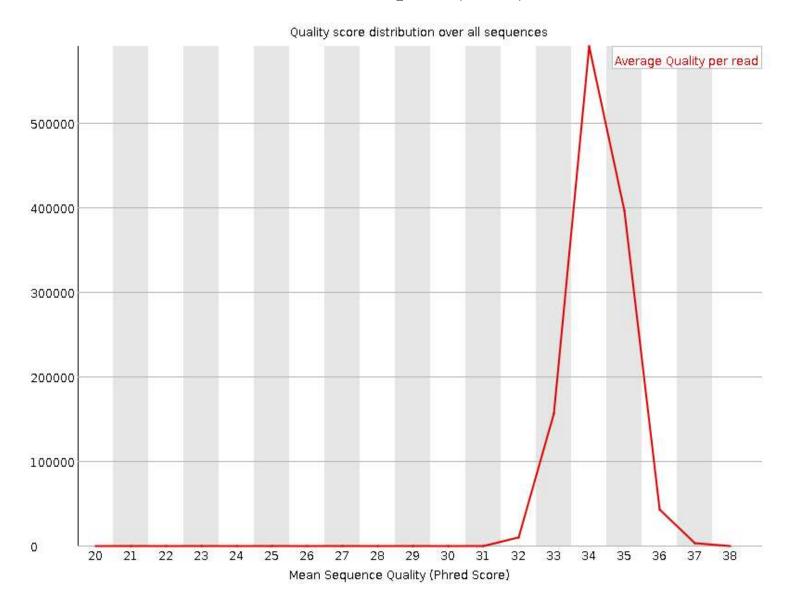
Sequence length 2-100

%GC 38

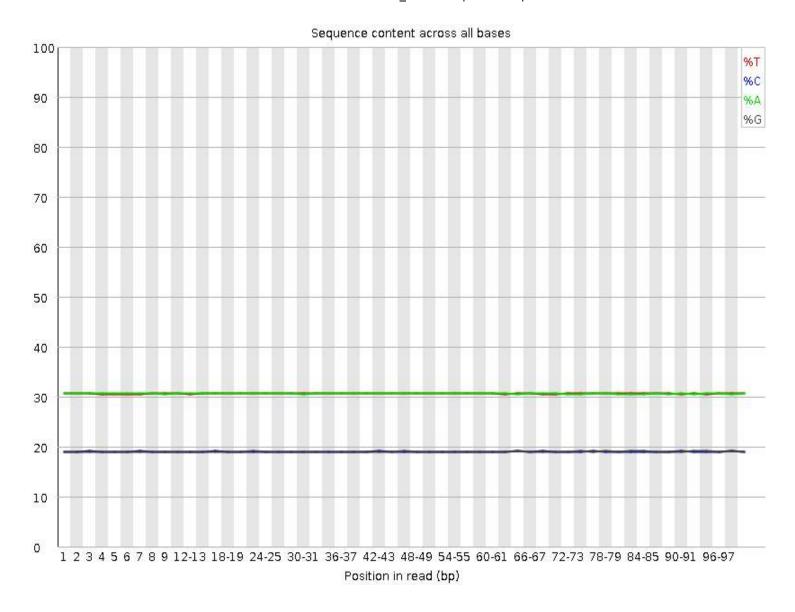
Per base sequence quality



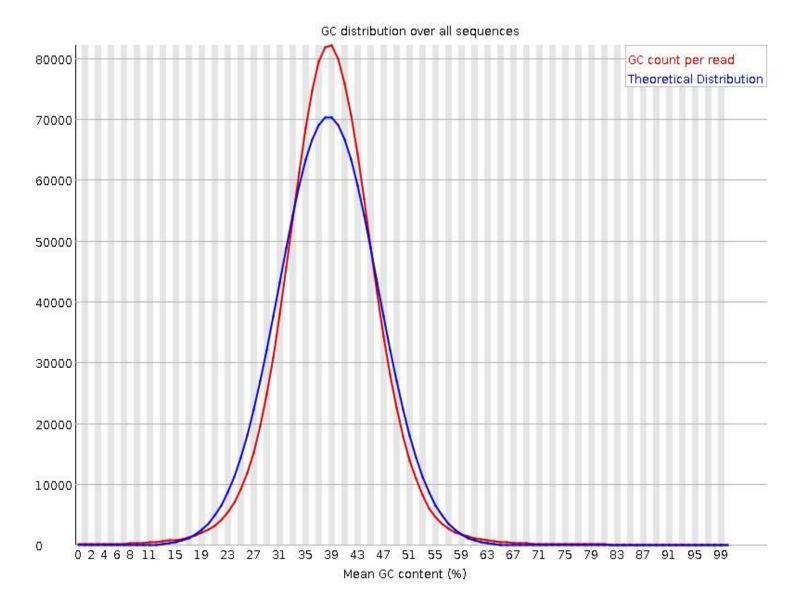
Per sequence quality scores



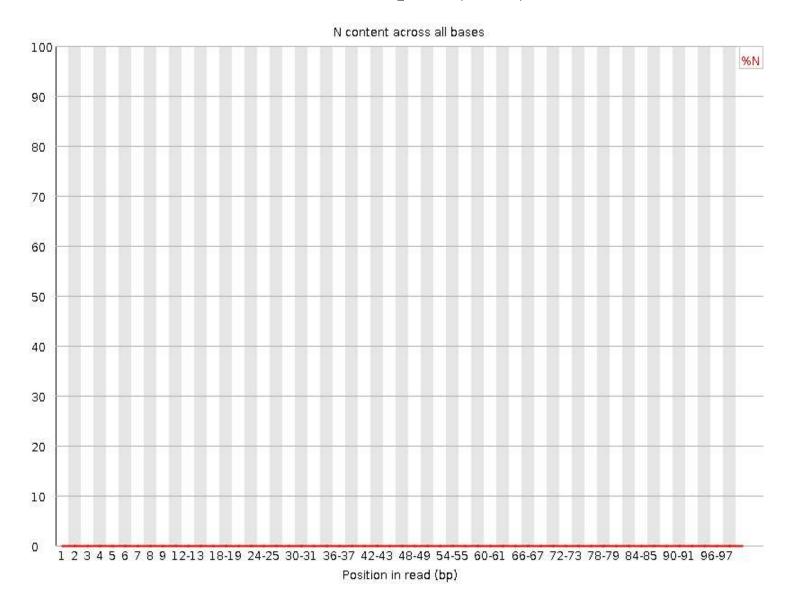




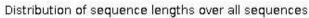
Per sequence GC content

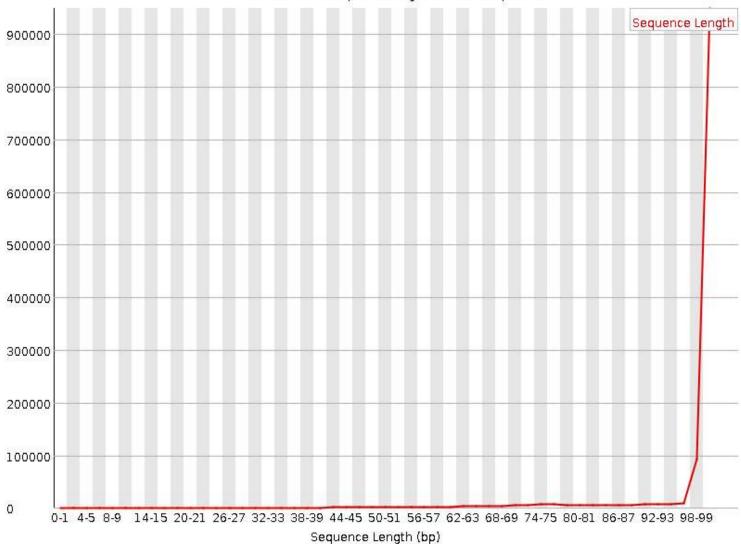




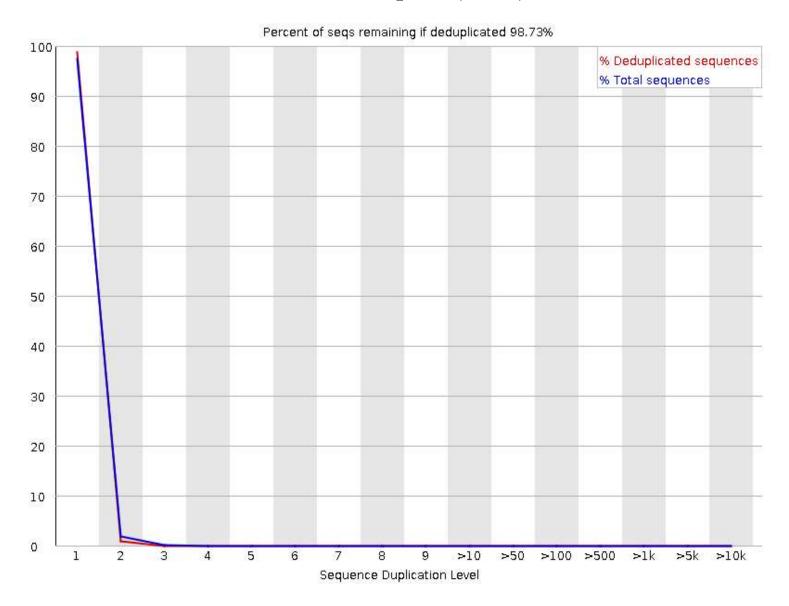


Sequence Length Distribution





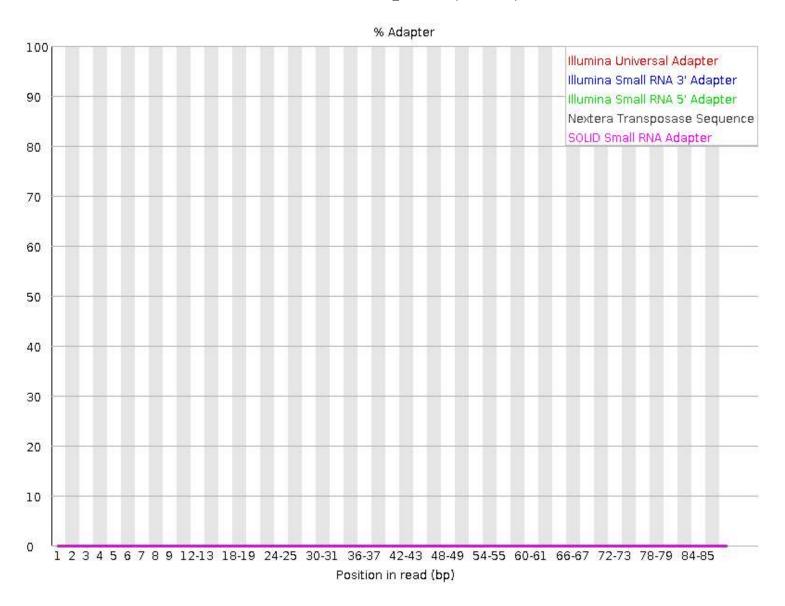
Sequence Duplication Levels



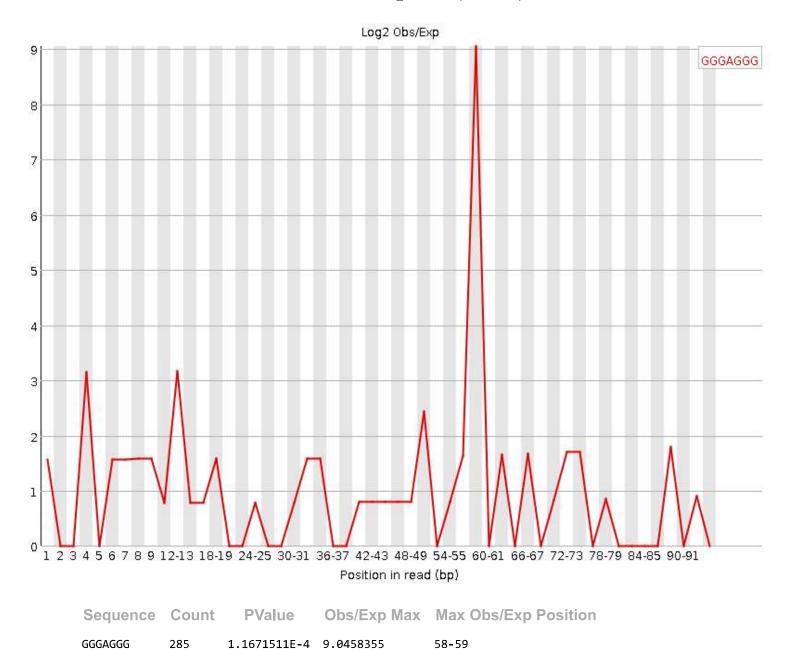


No overrepresented sequences









Produced by <u>FastQC</u> (version 0.11.5)