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

Kmer Content

Basic Statistics

Measure Value

Filename carnea_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

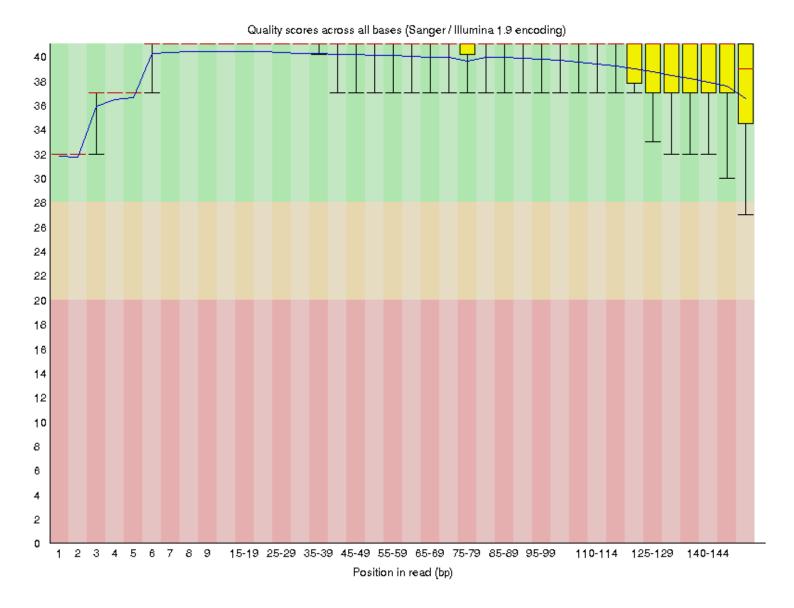
Total Sequences 284155733

Sequences flagged as poor quality 0

Sequence length 45-151

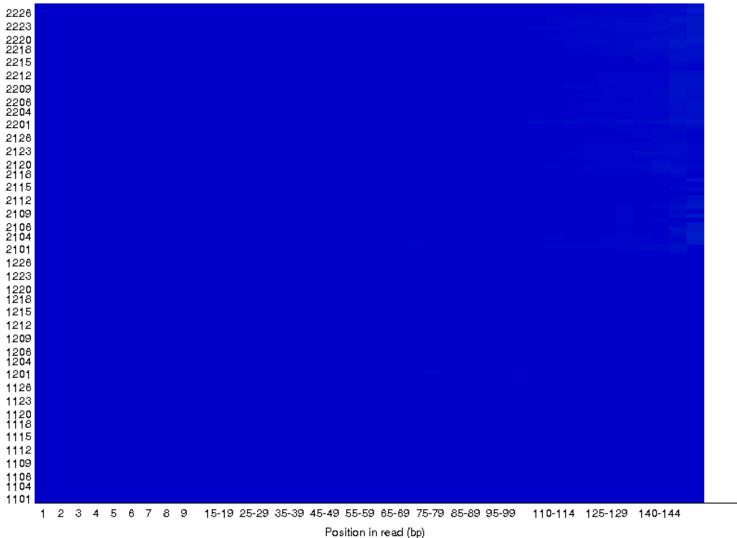
%GC 35

Per base sequence quality

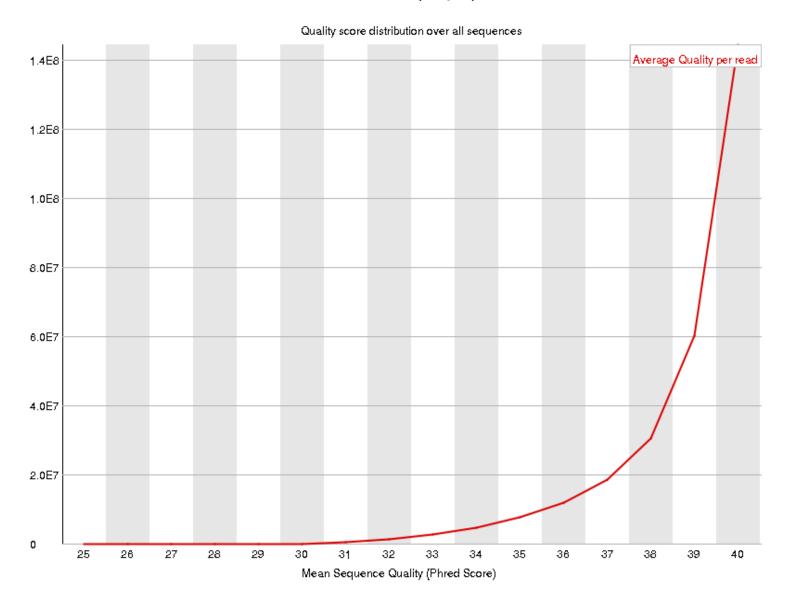


Per tile sequence quality

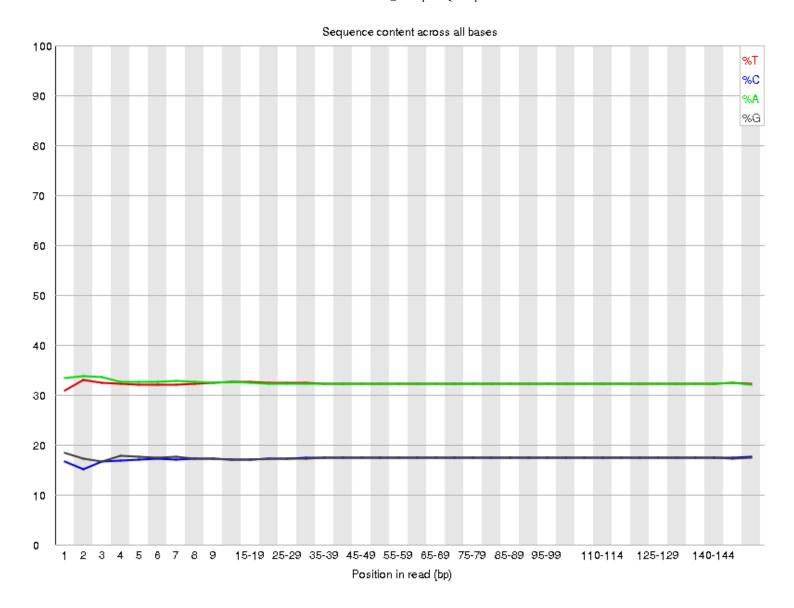




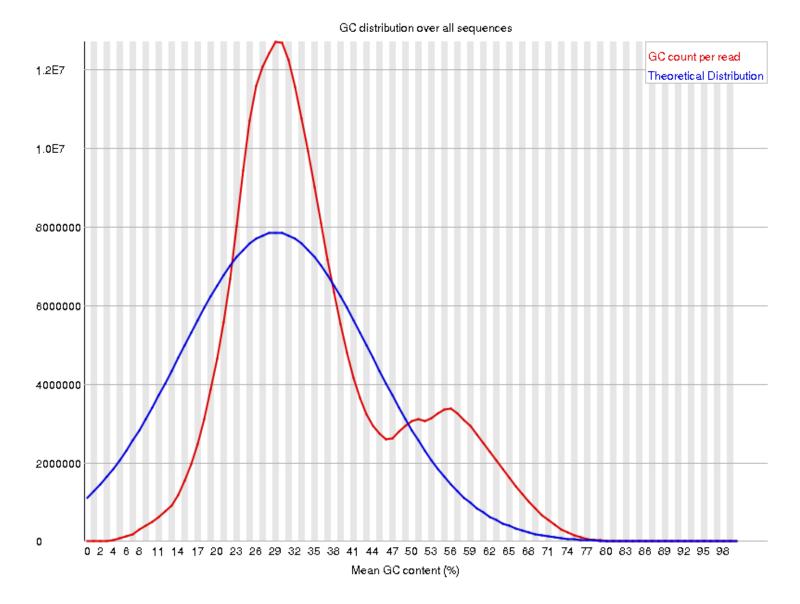
Per sequence quality scores



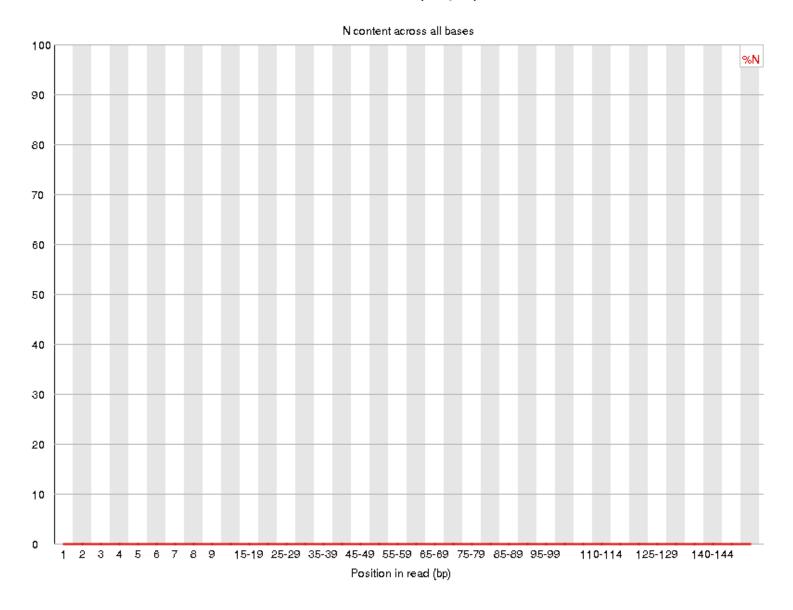




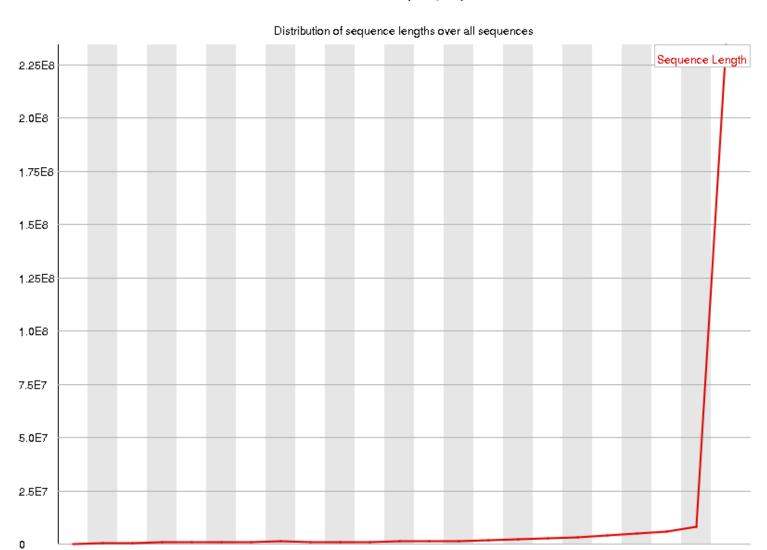
Per sequence GC content







Sequence Length Distribution



Sequence Duplication Levels

60-64

70-74

80-84

90-94

Sequence Length (bp)

100-104

110-114

120-124

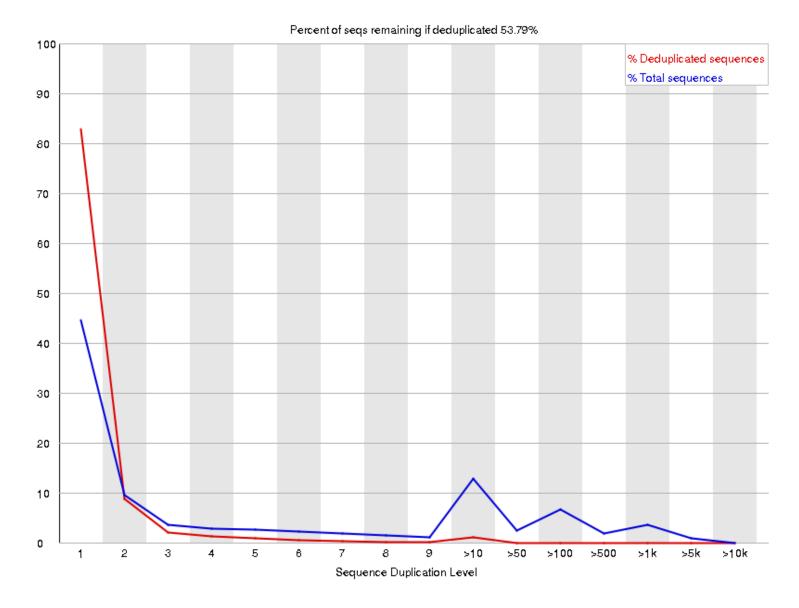
130-134

140-144

150-152

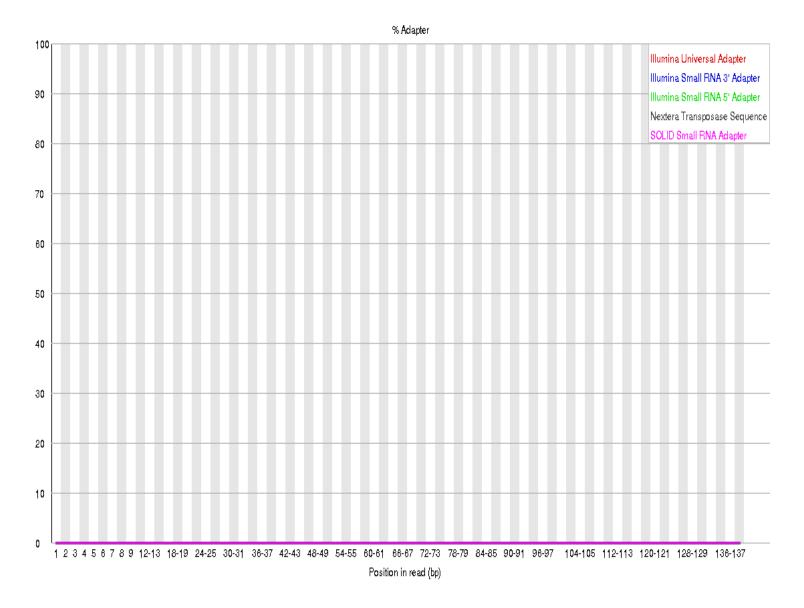
40-44

50-54











Produced by FastQC (version 0.11.5)