# **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\_2.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

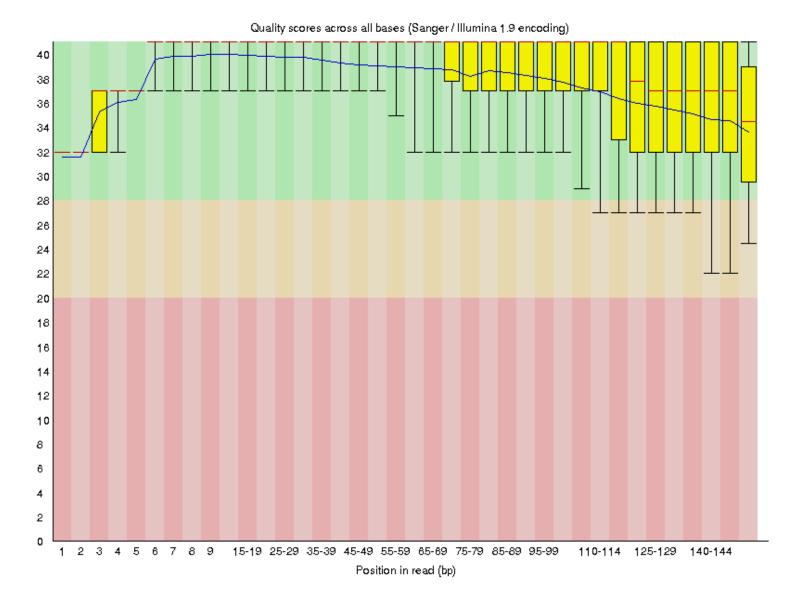
Total Sequences 284155733

Sequences flagged as poor quality 0

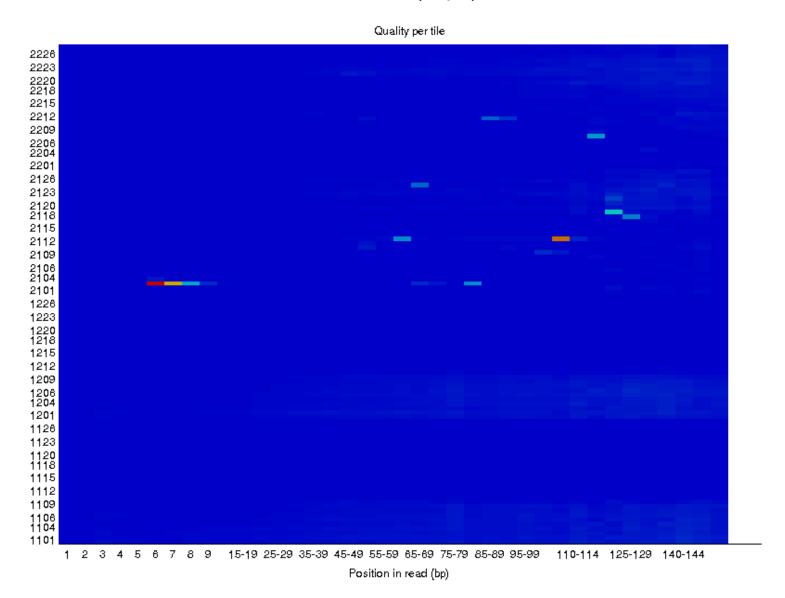
Sequence length 45-151

%GC 34

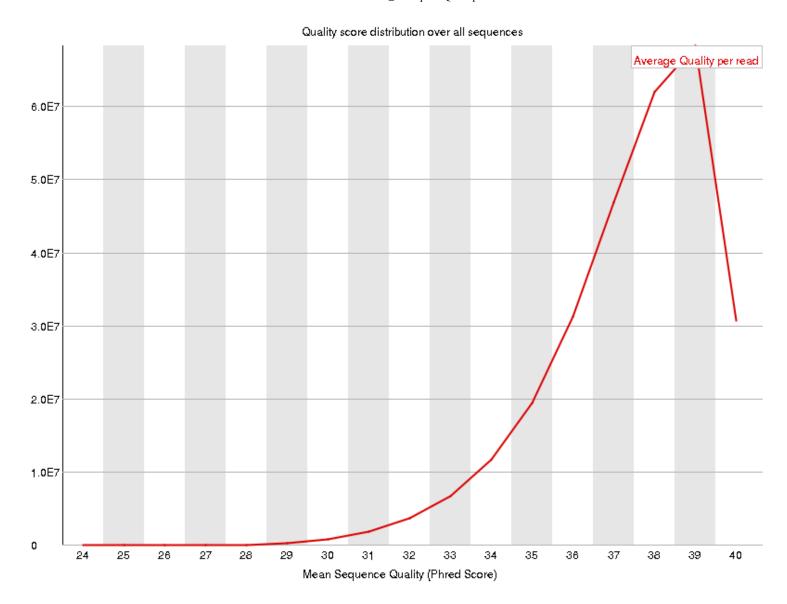
#### Per base sequence quality



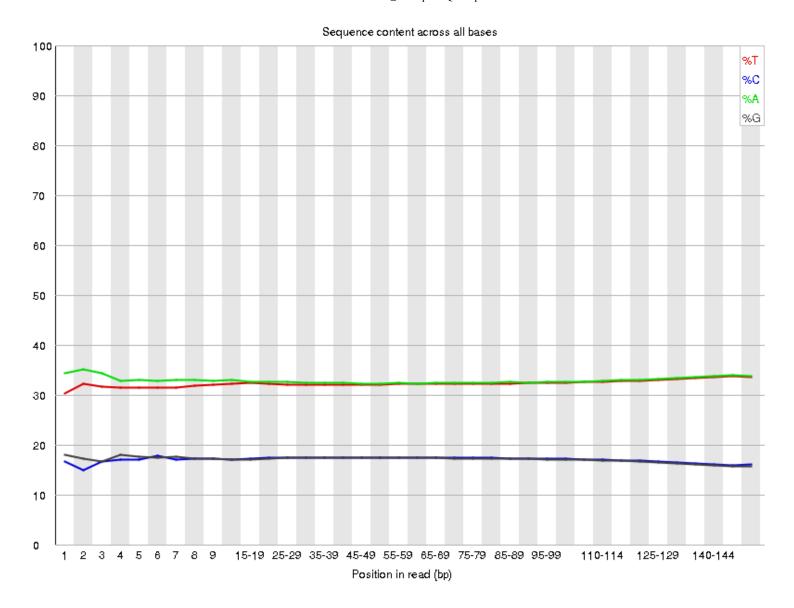
#### ②Per tile sequence quality



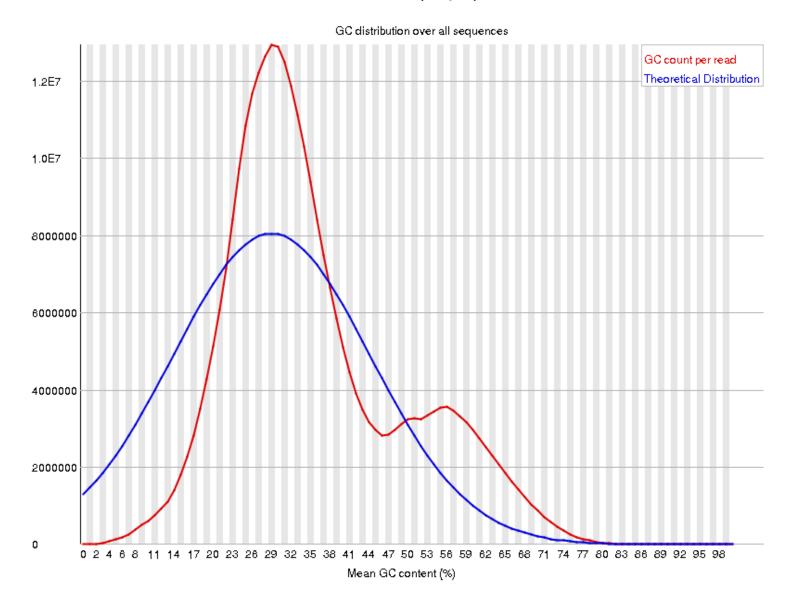




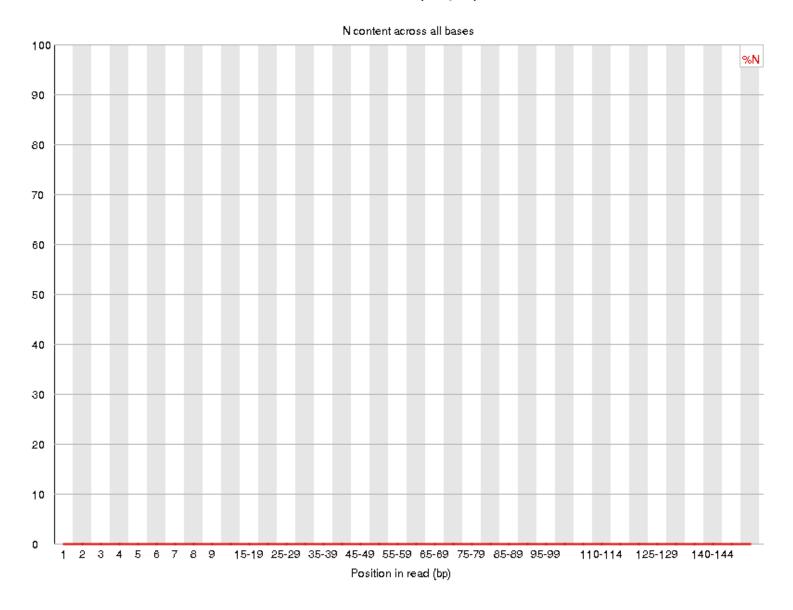




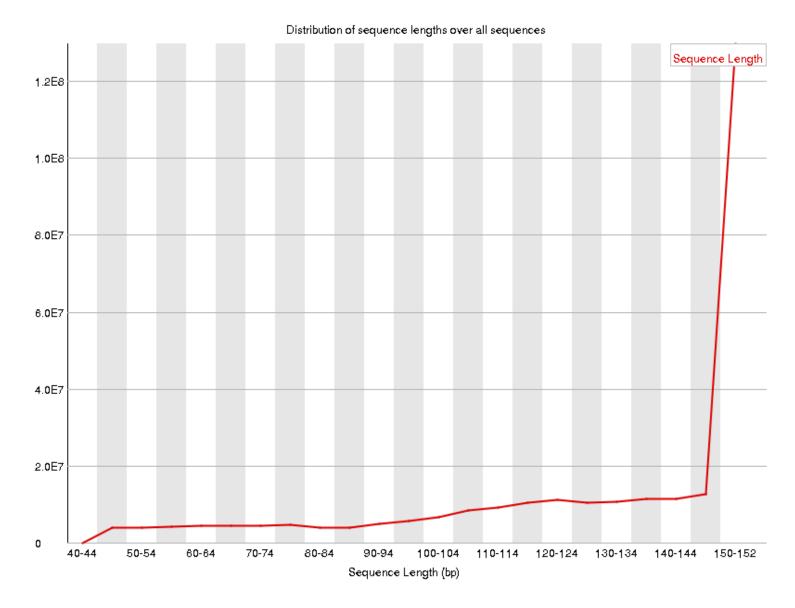
## Per sequence GC content



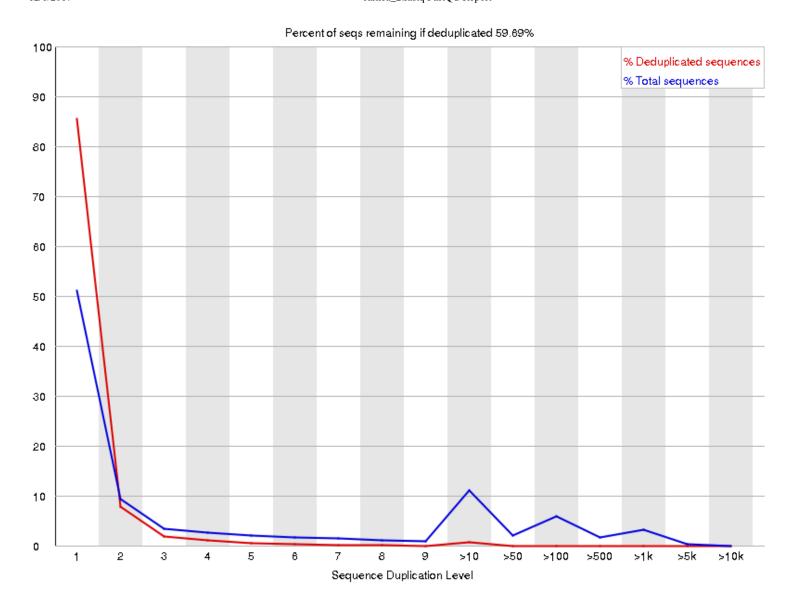




### Sequence Length Distribution

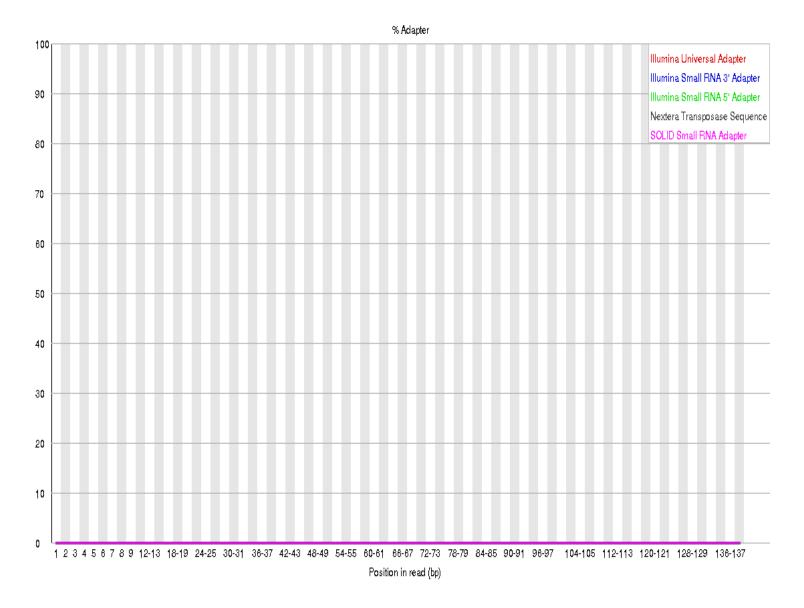


#### Sequence Duplication Levels











Produced by FastQC (version 0.11.5)