#### Thu 26 Oct 2017 carnea\_1\_filtered.fastq

# **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\_filtered.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

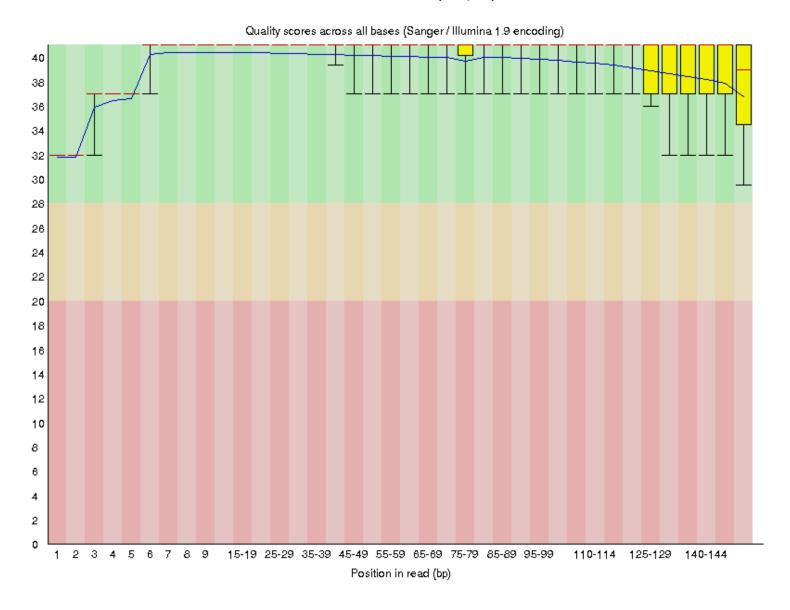
Total Sequences 213735465

Sequences flagged as poor quality 0

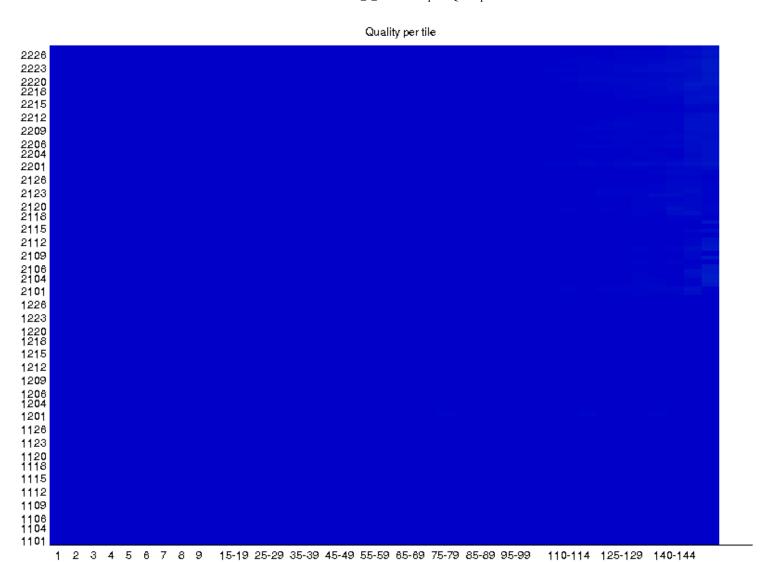
Sequence length 45-151

%GC 30

#### Per base sequence quality

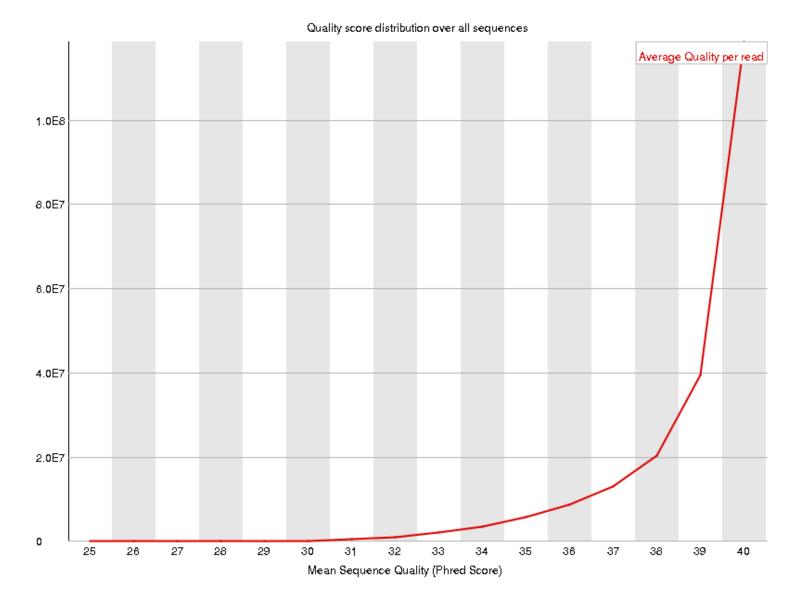


## Per tile sequence quality

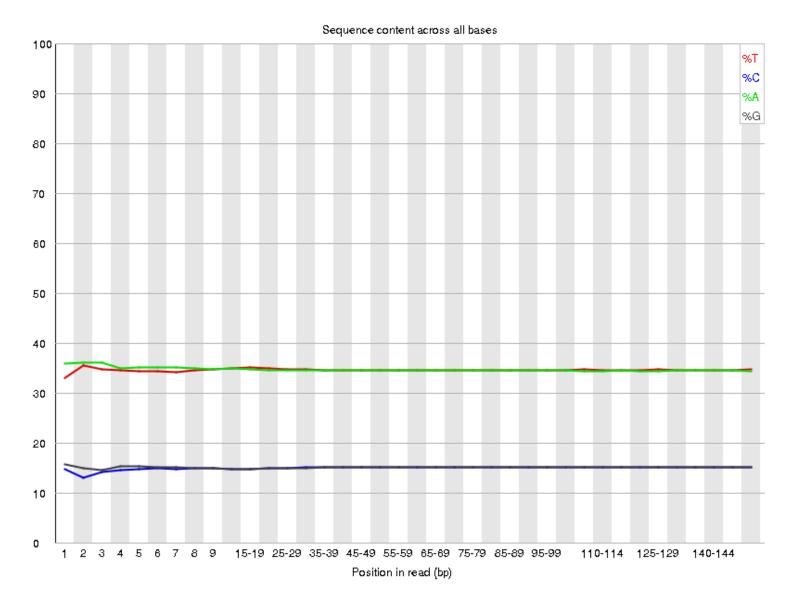


Position in read (bp)

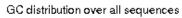


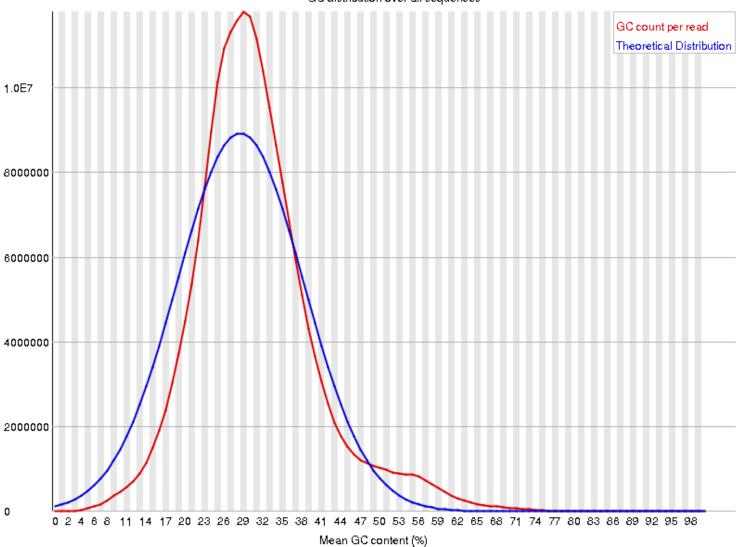


## Per base sequence content

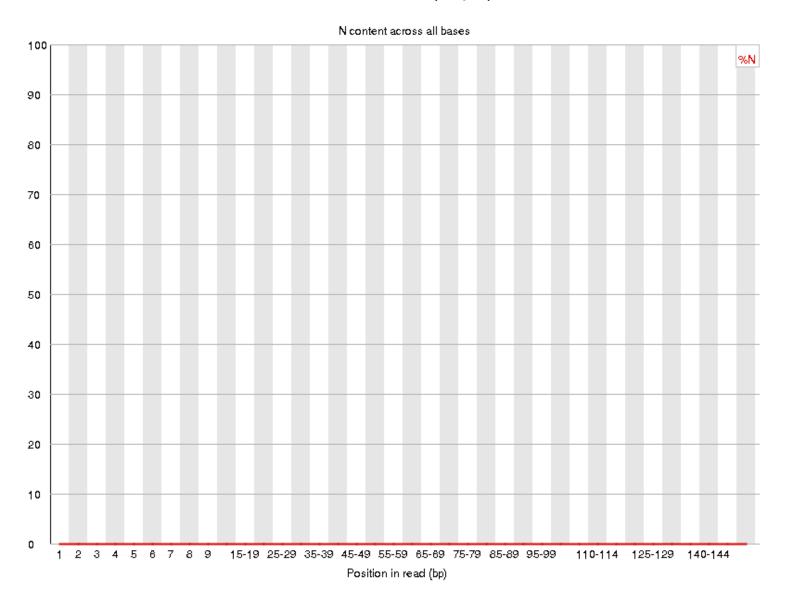


## Per sequence GC content

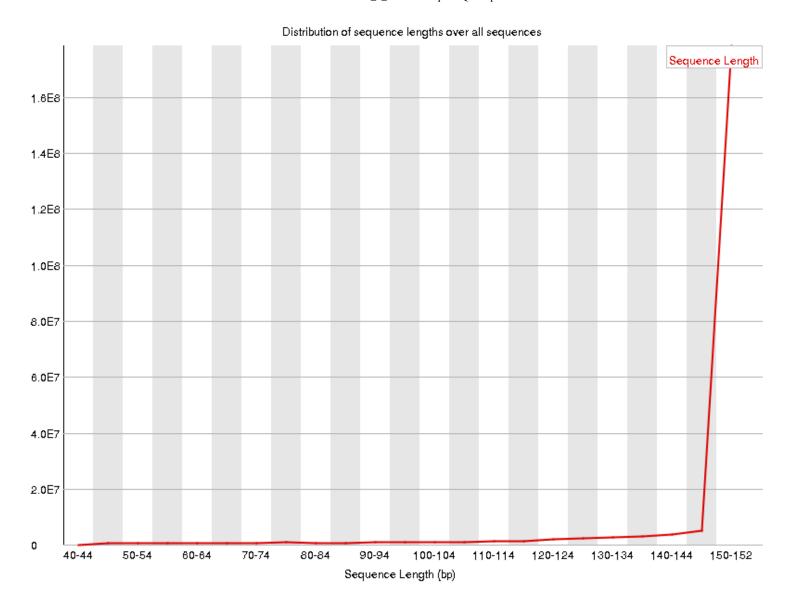




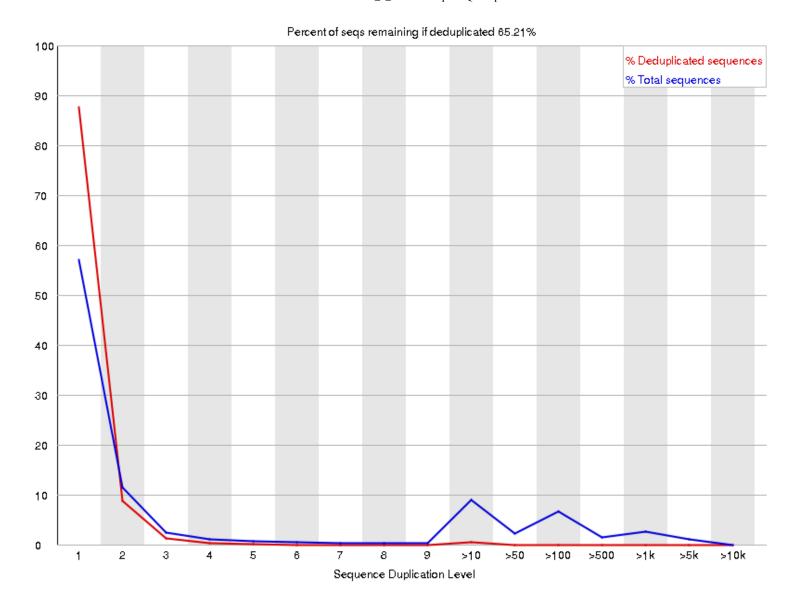




## Sequence Length Distribution

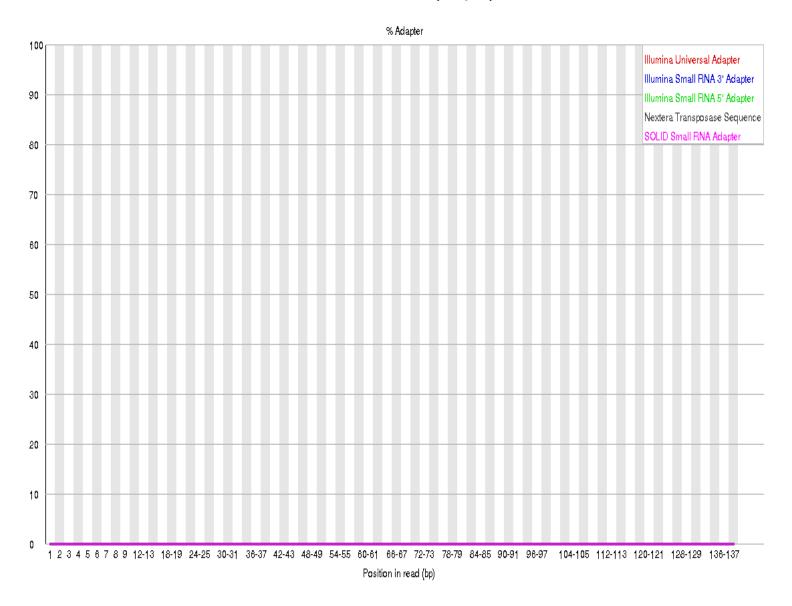


#### Sequence Duplication Levels











Produced by FastQC (version 0.11.5)