



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 Dades1\_def

File type Conventional base calls Encoding Sanger / Illumina 1.9

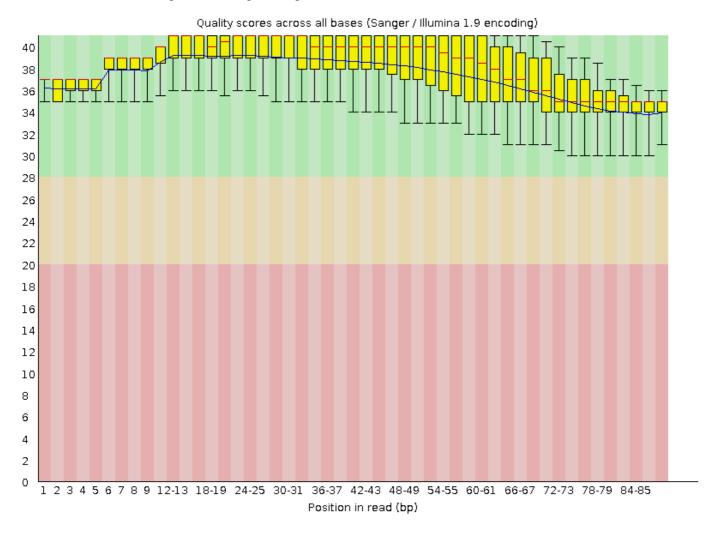
Total Sequences 992175
Total Bases 86.8 Mbp

Sequences flagged as poor quality 0

Sequence length 1-88

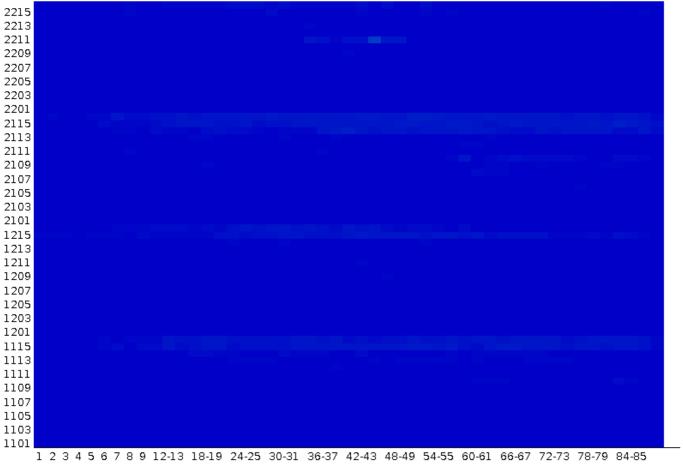
%GC 47

## Per base sequence quality



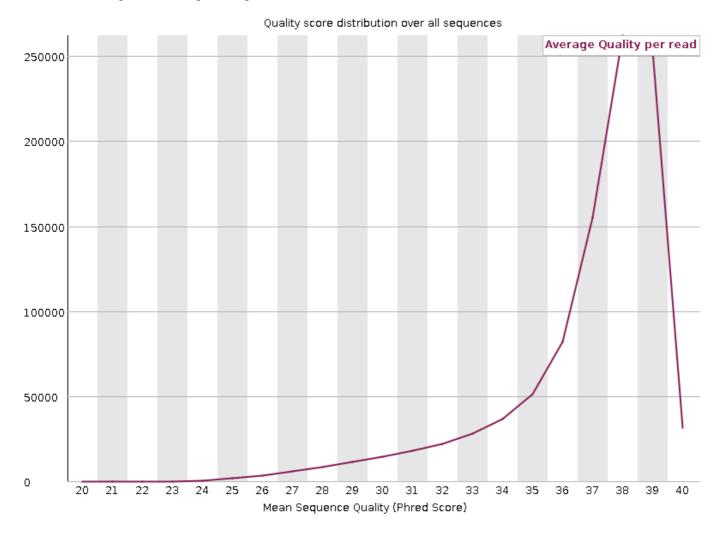
# Per tile sequence quality



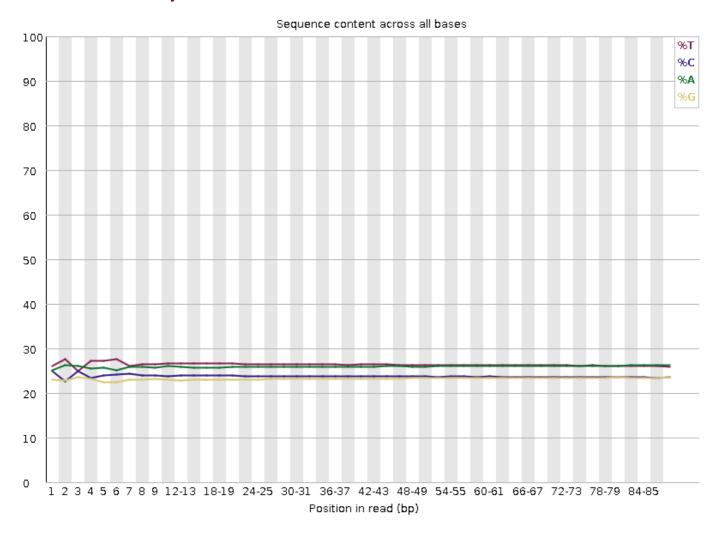


Position in read (bp)

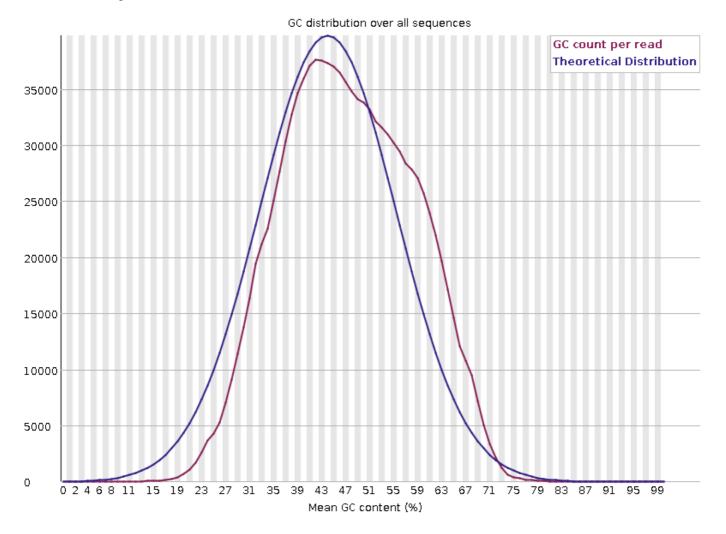
#### Per sequence quality scores



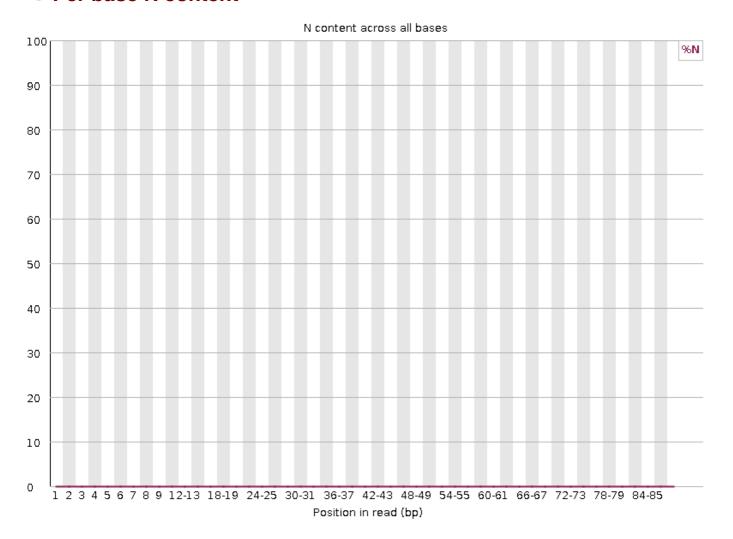
# Per base sequence content



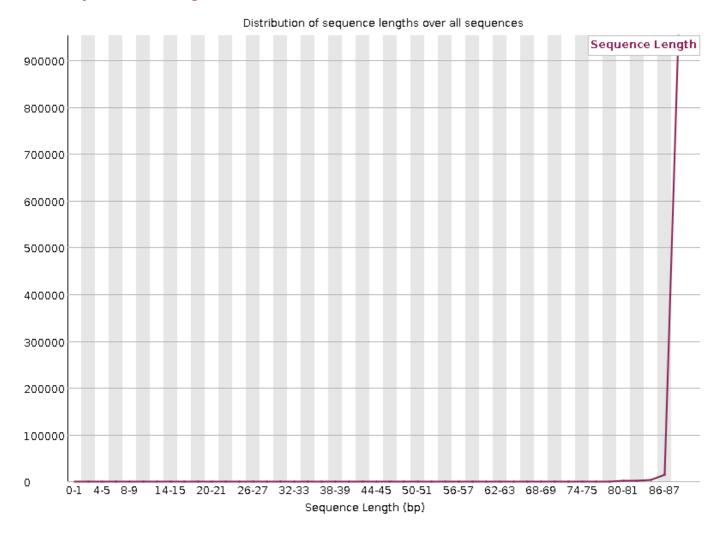
#### Per sequence GC content



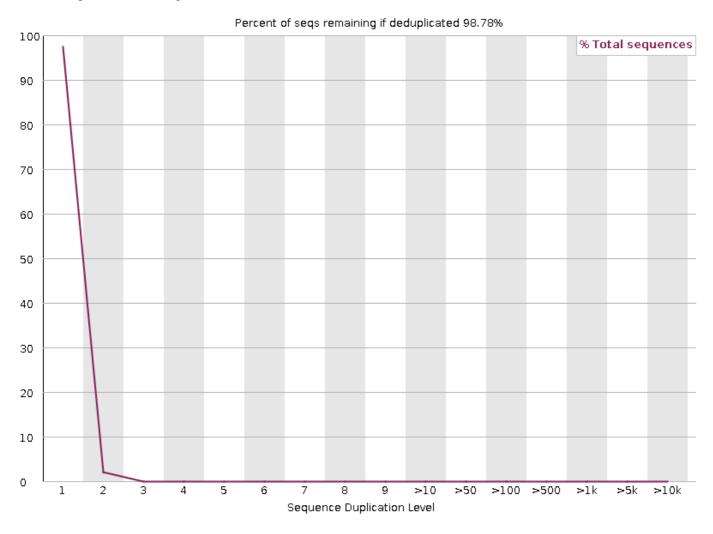
#### Per base N content



#### Sequence Length Distribution

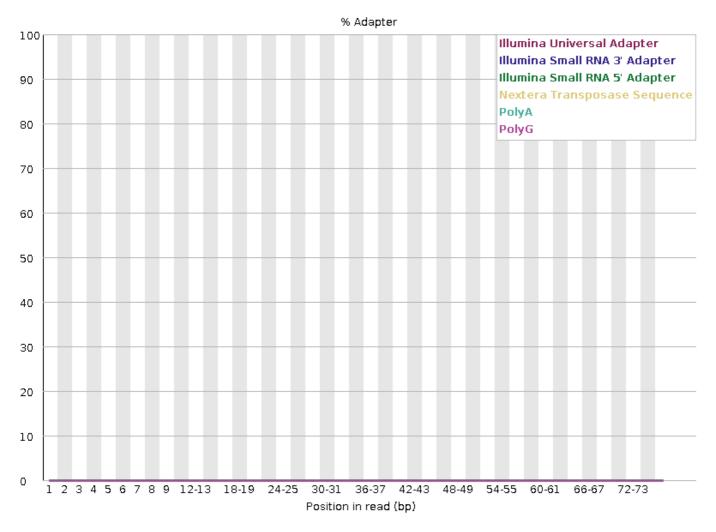


# Sequence Duplication Levels





## Adapter Content



Produced by FastQC (version 0.12.1)