



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 Dades1CUT

File type Conventional base calls Encoding Sanger / Illumina 1.9

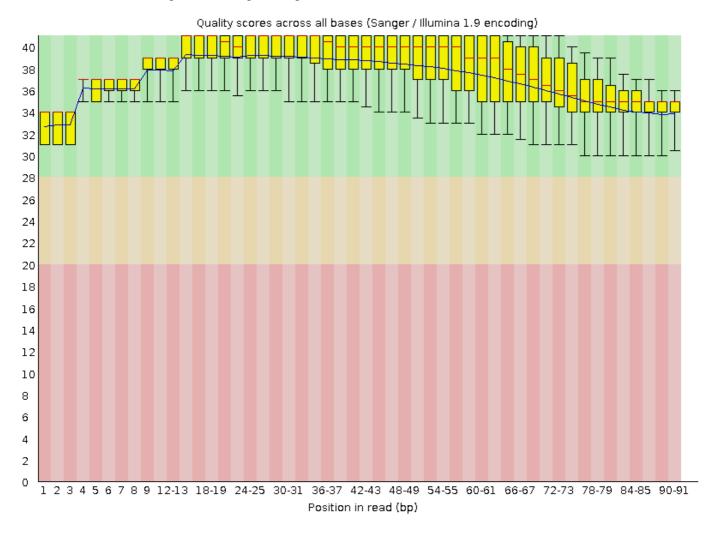
Total Sequences 992332
Total Bases 89.8 Mbp

Sequences flagged as poor quality 0

Sequence length 4-91

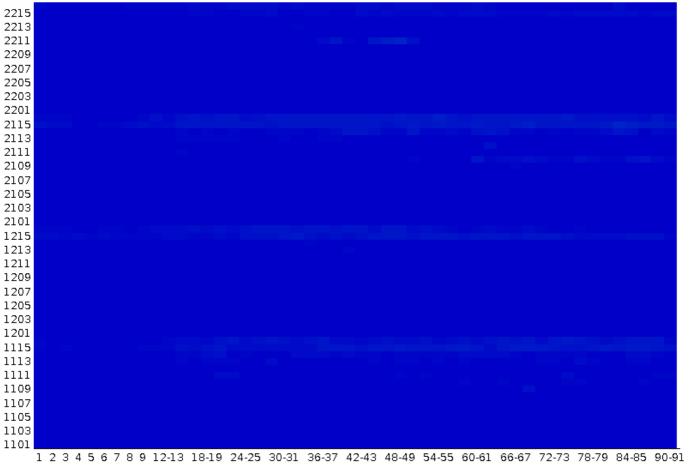
%GC 47

Per base sequence quality



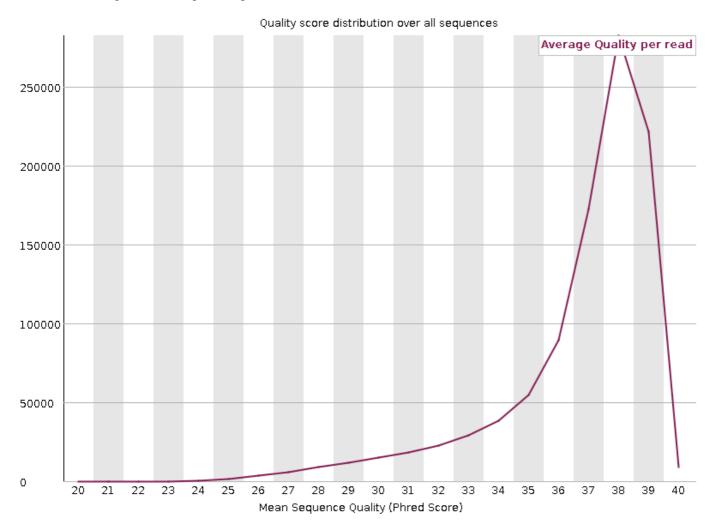
Per tile sequence quality



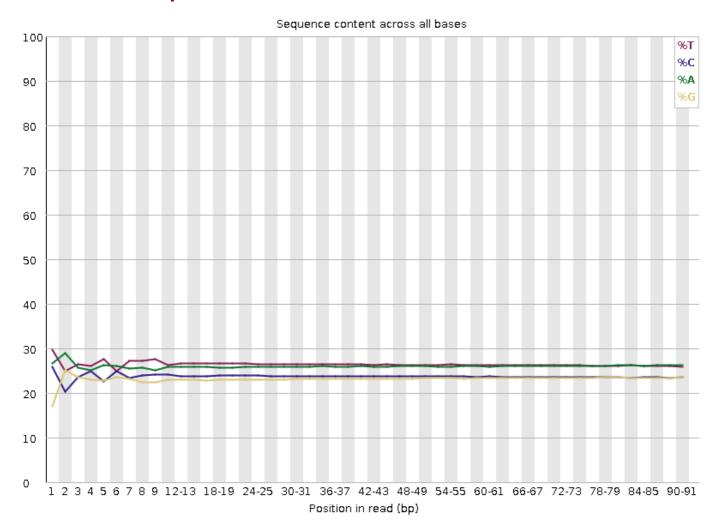


Position in read (bp)

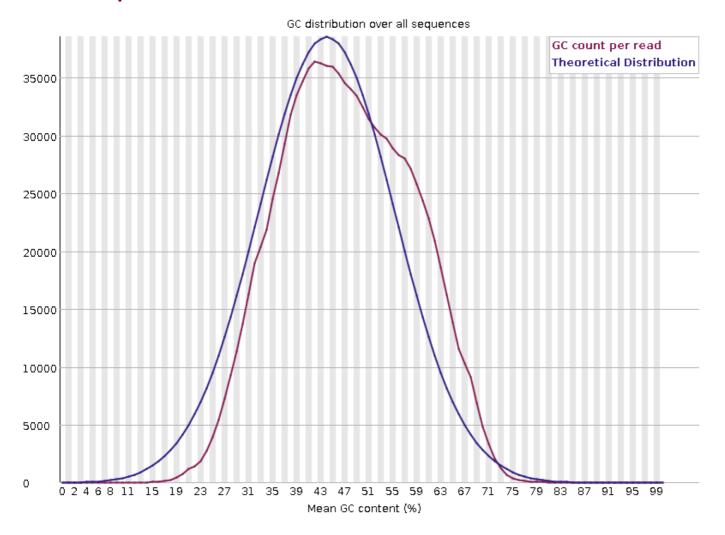
Per sequence quality scores



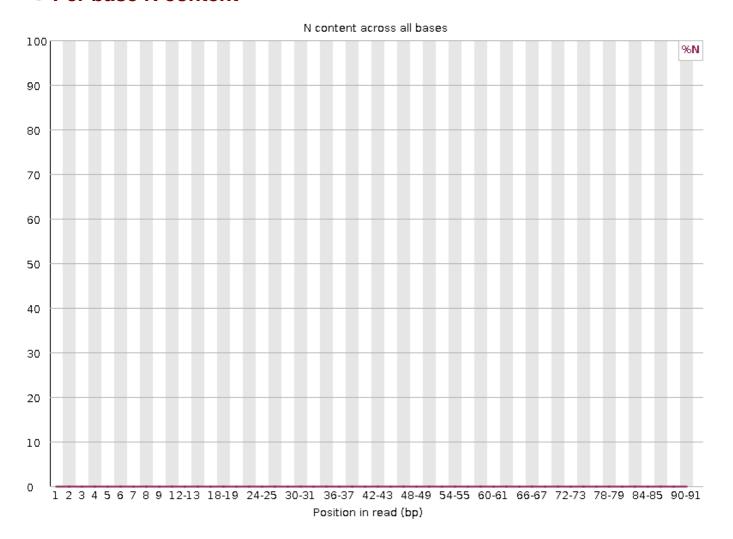
Per base sequence content



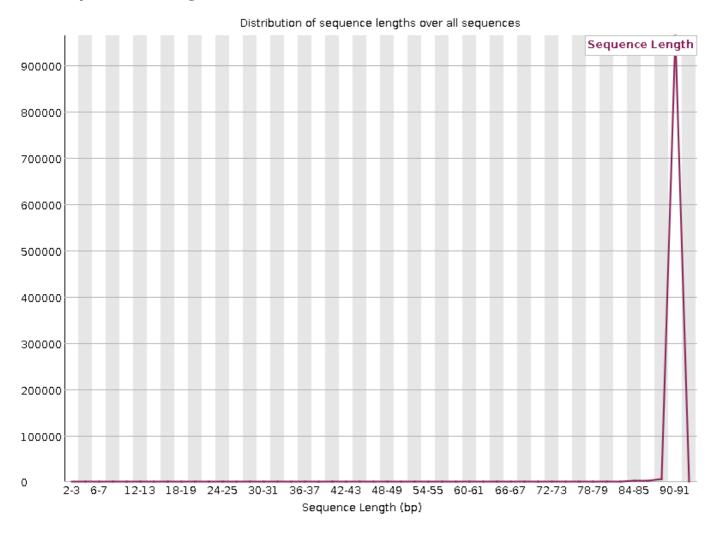
Per sequence GC content



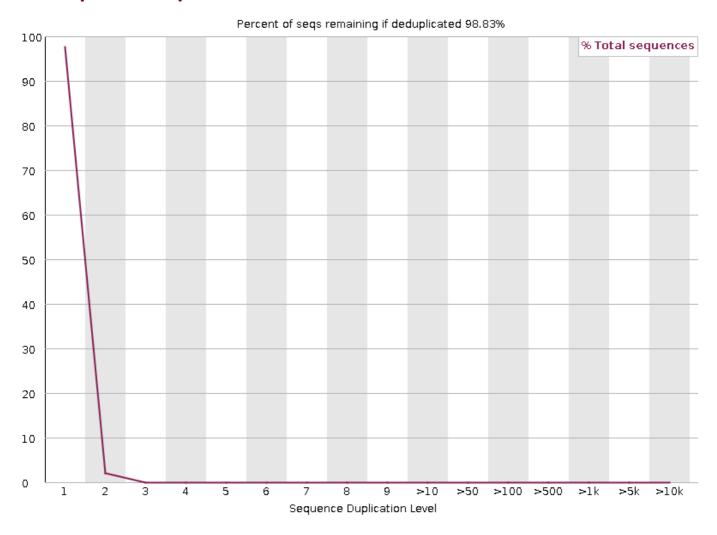
Per base N content



Sequence Length Distribution

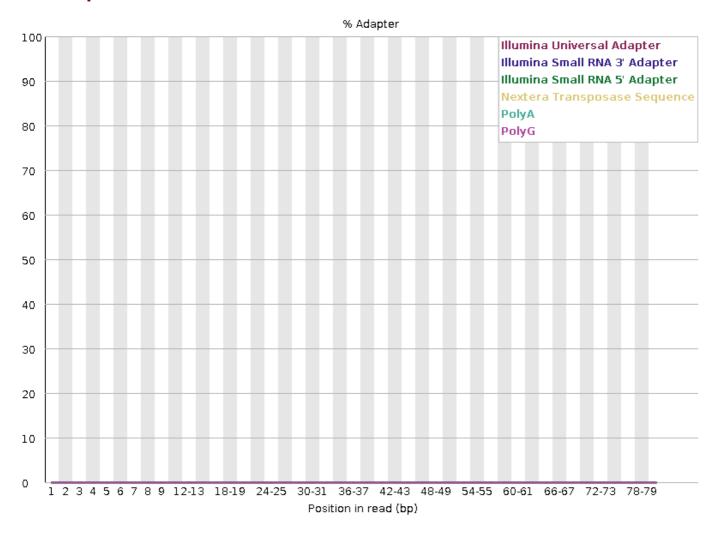


Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.12.1)