





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 Dades2CUT

File type Conventional base calls Encoding Sanger / Illumina 1.9

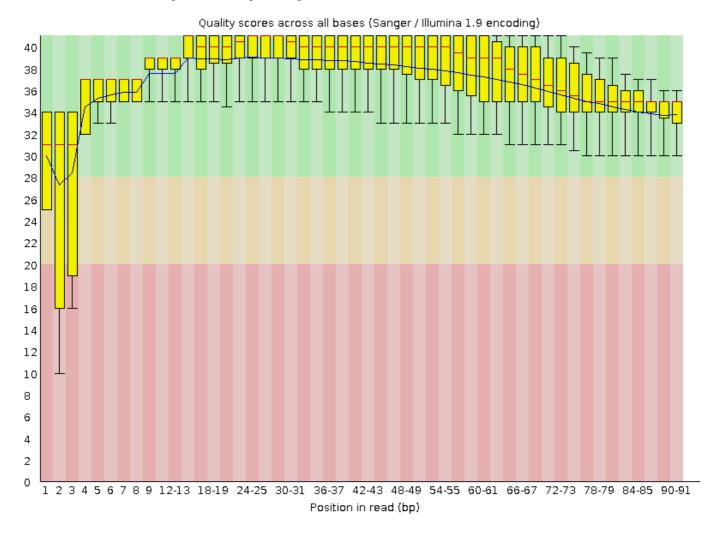
Total Sequences 992332
Total Bases 88.9 Mbp

Sequences flagged as poor quality $\, {\tt 0} \,$

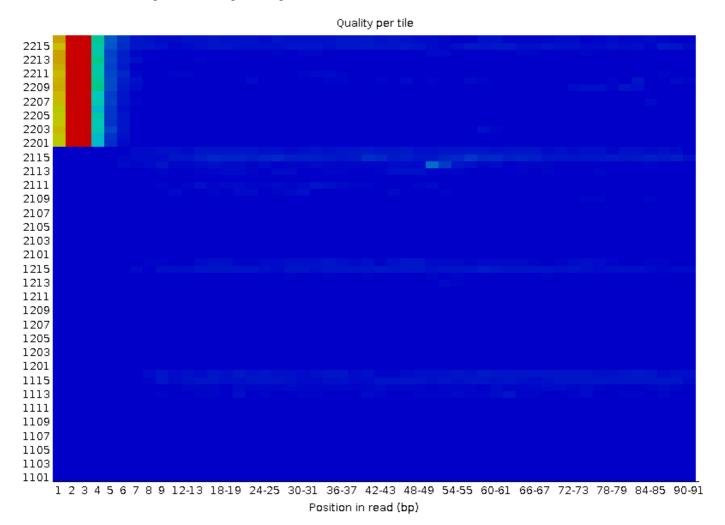
Sequence length 1-91

%GC 47

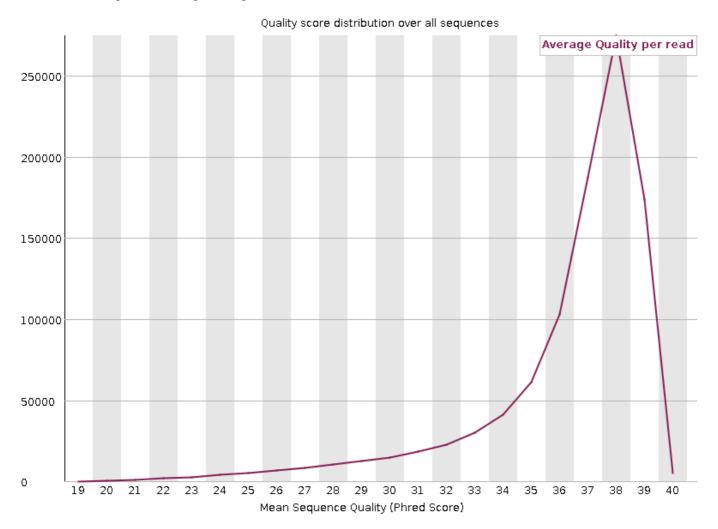
Per base sequence quality



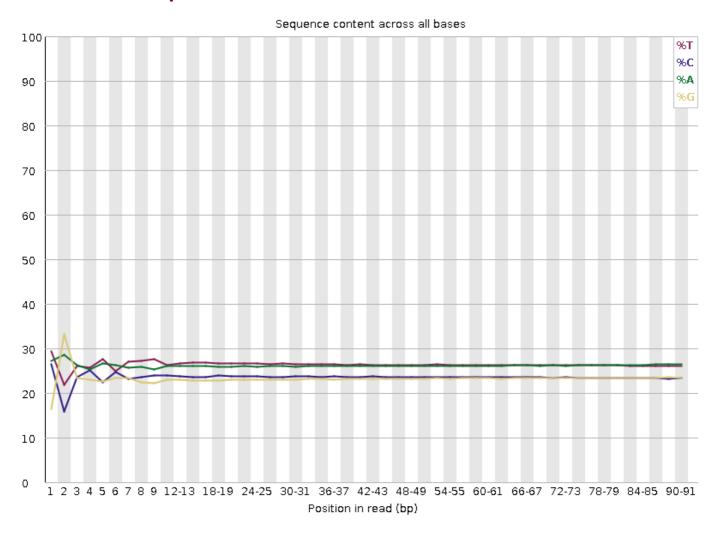
②Per tile sequence quality



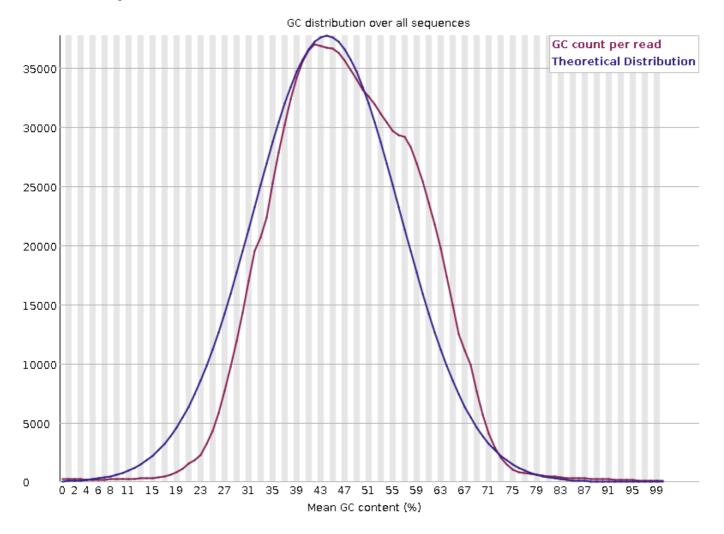
Per sequence quality scores



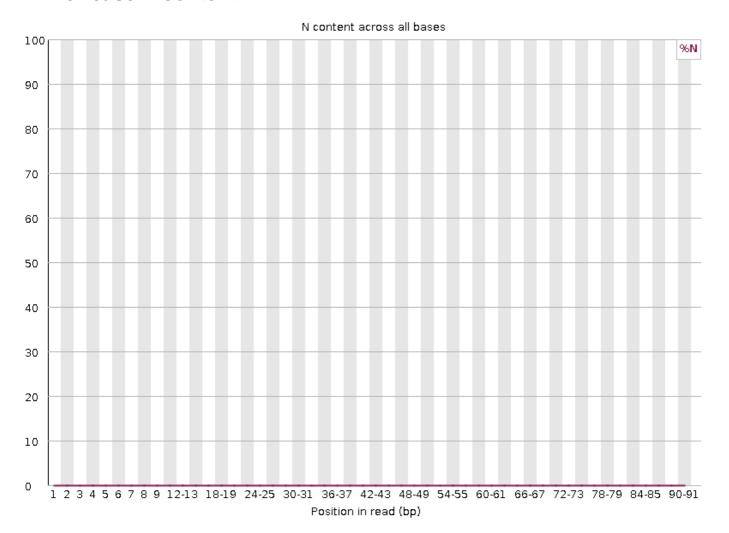
Per base sequence content



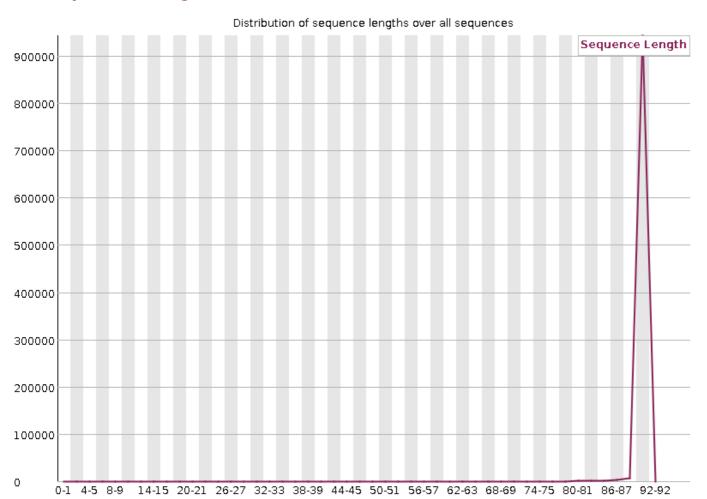
Per sequence GC content



Per base N content

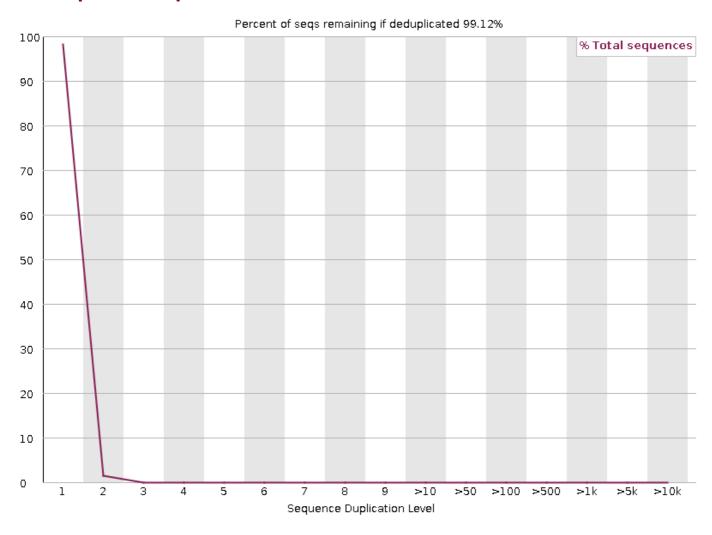


Sequence Length Distribution



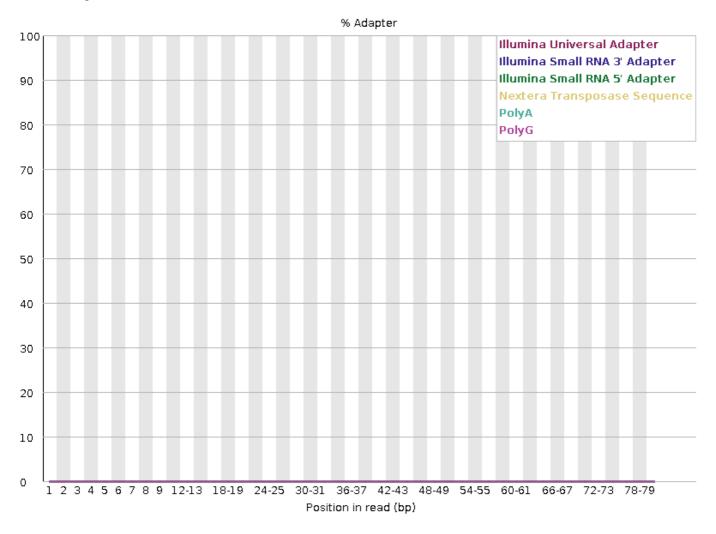
Sequence Length (bp)

Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.12.1)