Fri 1 Nov 2024 SRR14866427_1.fastq

ReportSummary





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 SRR14866427_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 23558674

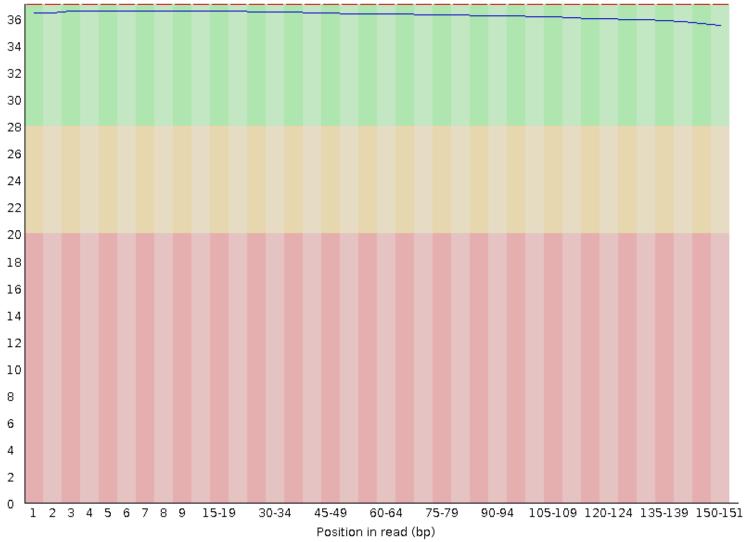
Sequences flagged as poor quality 0

Sequence length 151

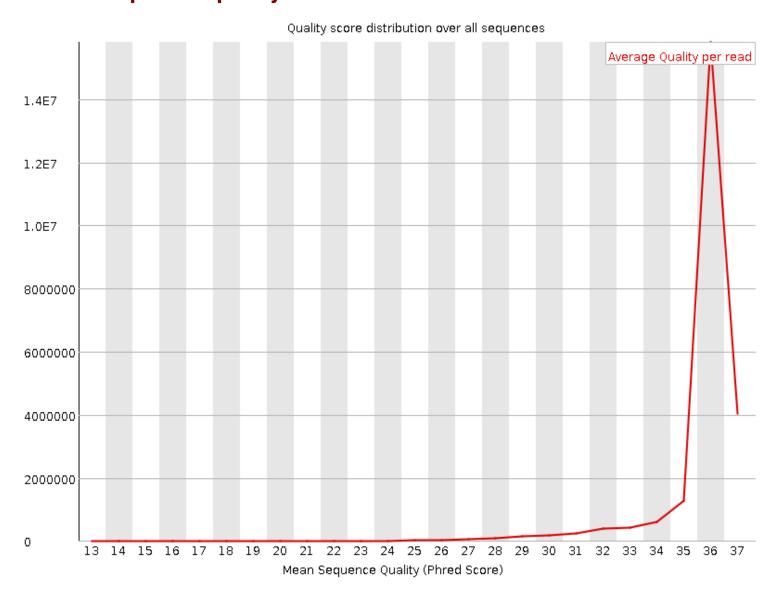
%GC 51

Per base sequence quality

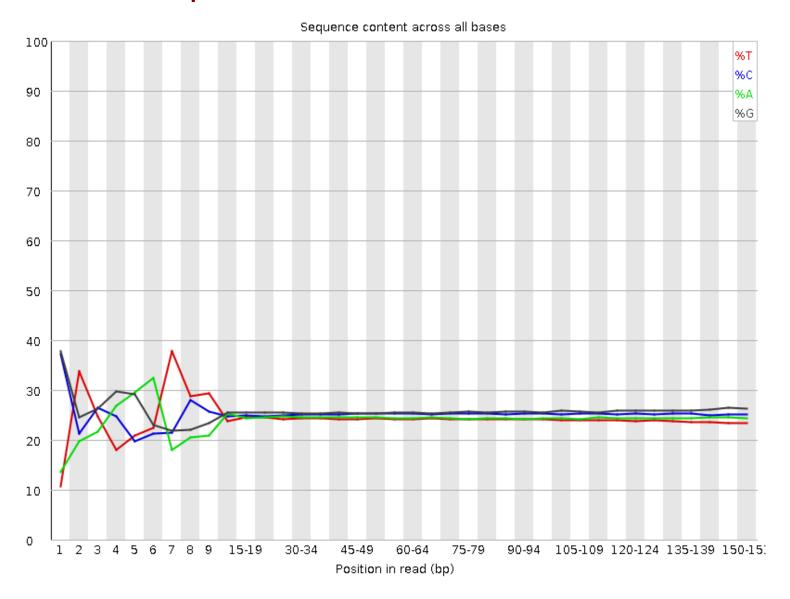




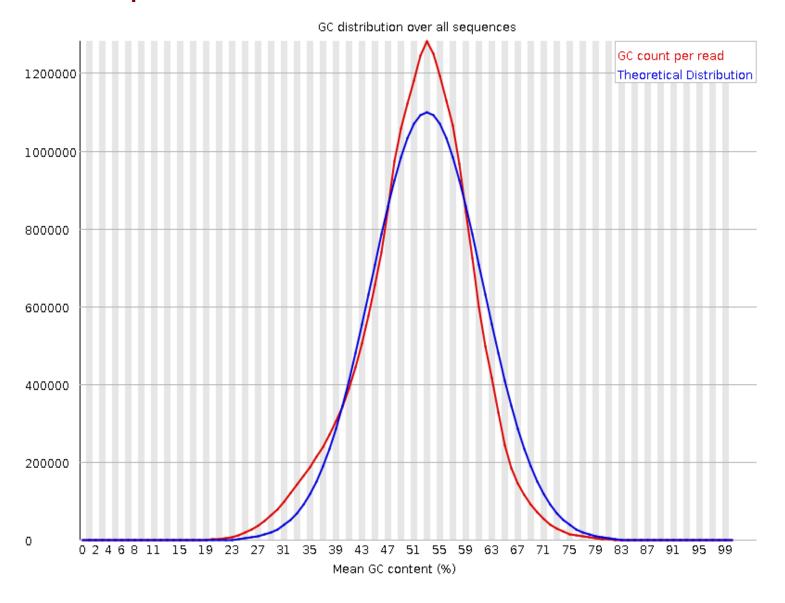
Per sequence quality scores



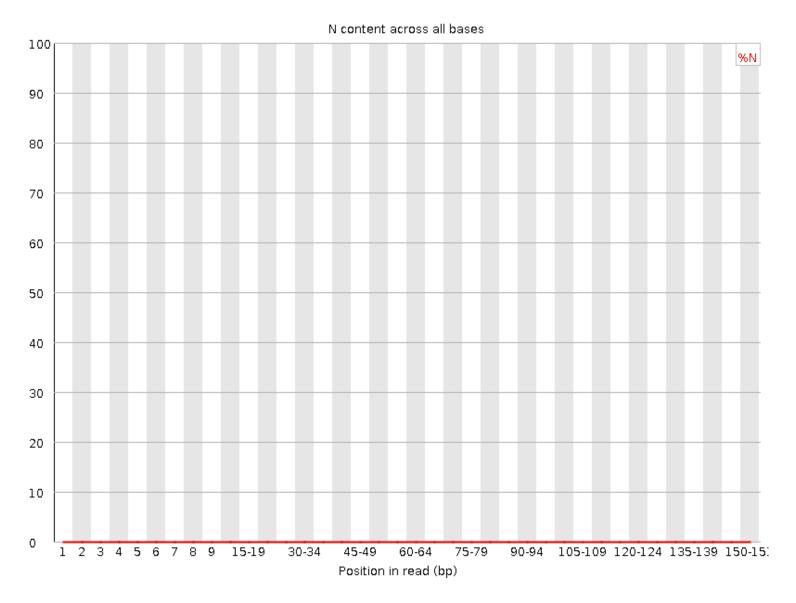
Per base sequence content



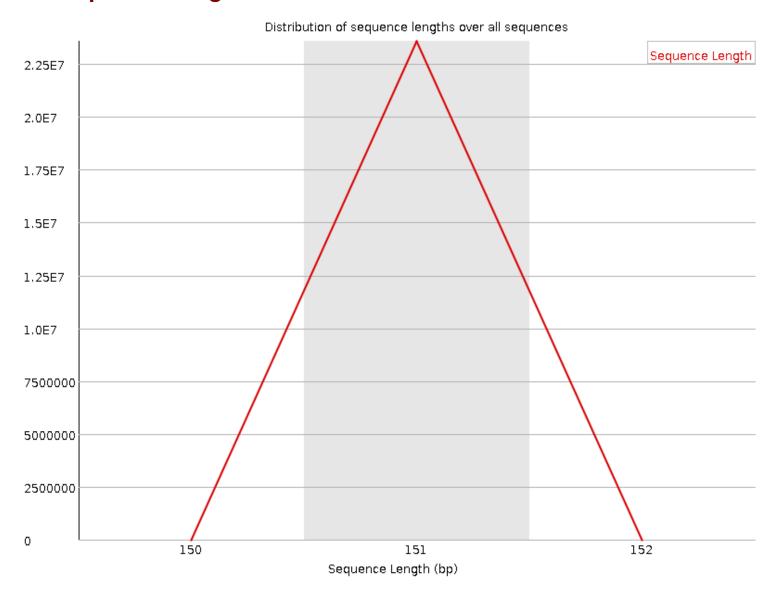
Per sequence GC content



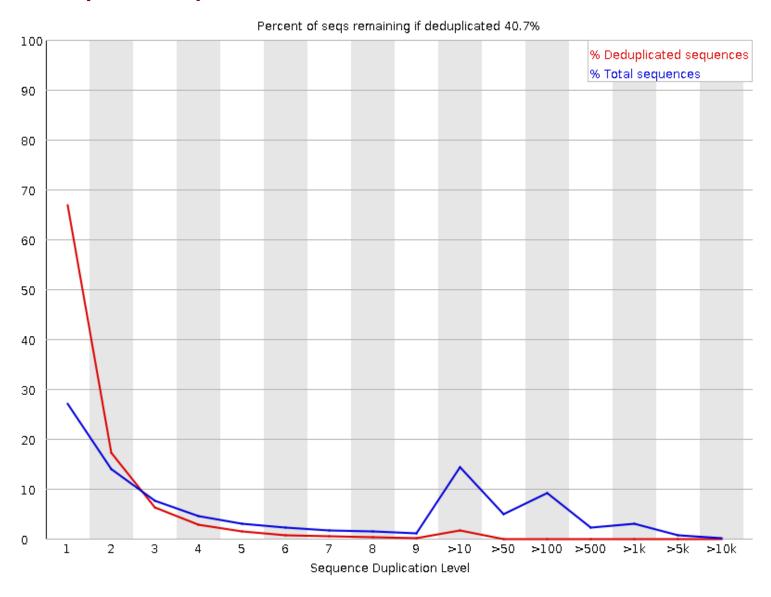
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

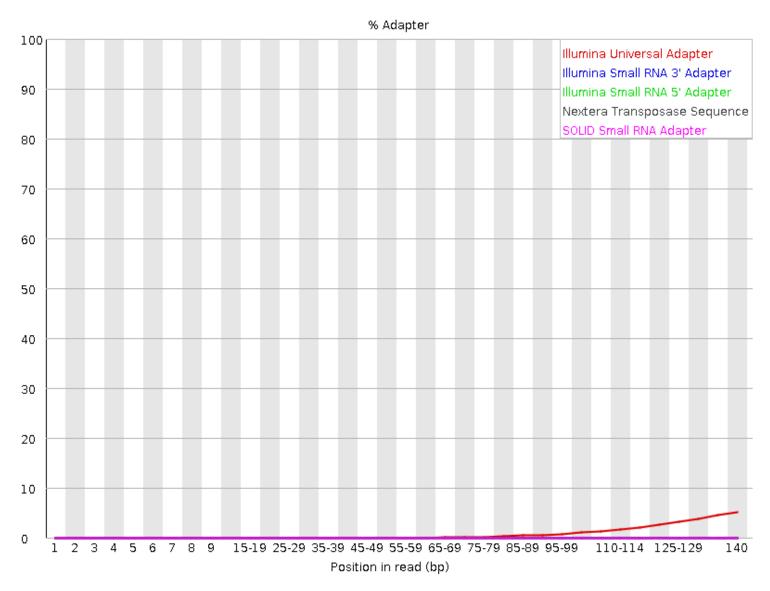


Overrepresented sequences

Sequence Count Percentage Possible Source

CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA 25091 0.10650429646422375 No Hit

Adapter Content



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