Report

Sat 2 Nov 2024 SRR14866429_1.fastq

Summary







Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content

Basic Statistics

Value Measure

Filename SRR14866429_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

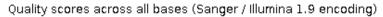
Total Sequences 21908548

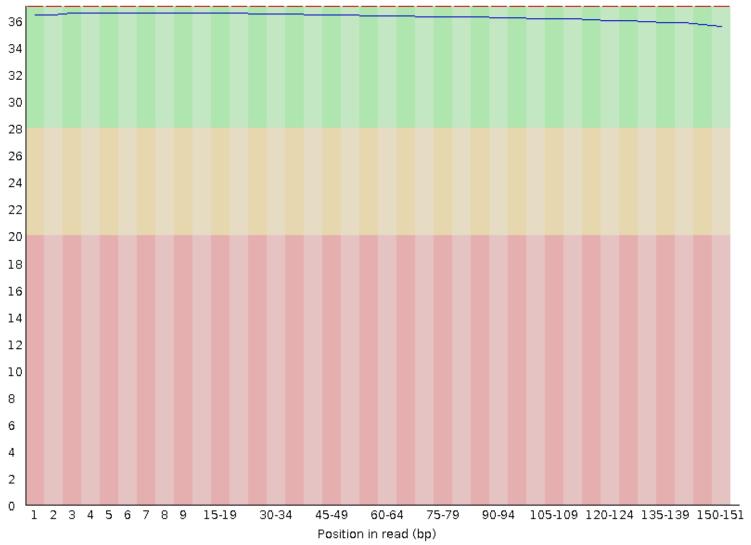
Sequences flagged as poor quality 0

Sequence length 151

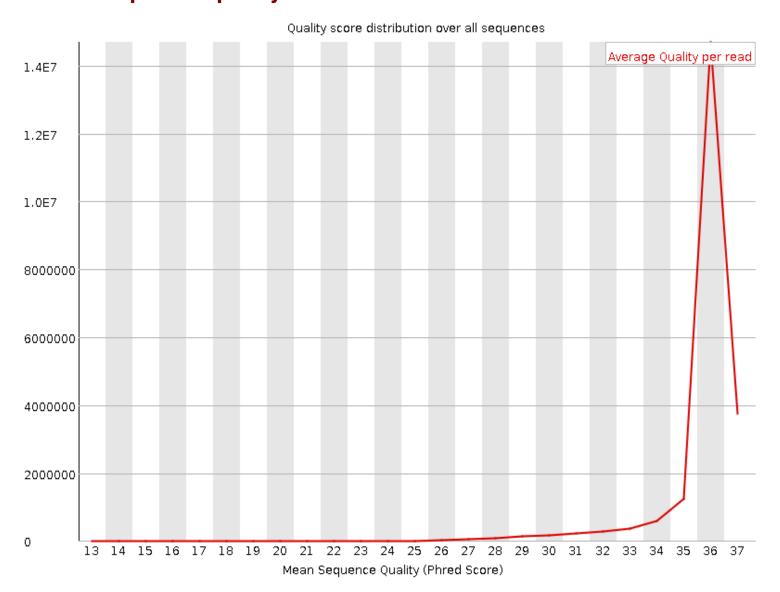
%GC 51

Per base sequence quality

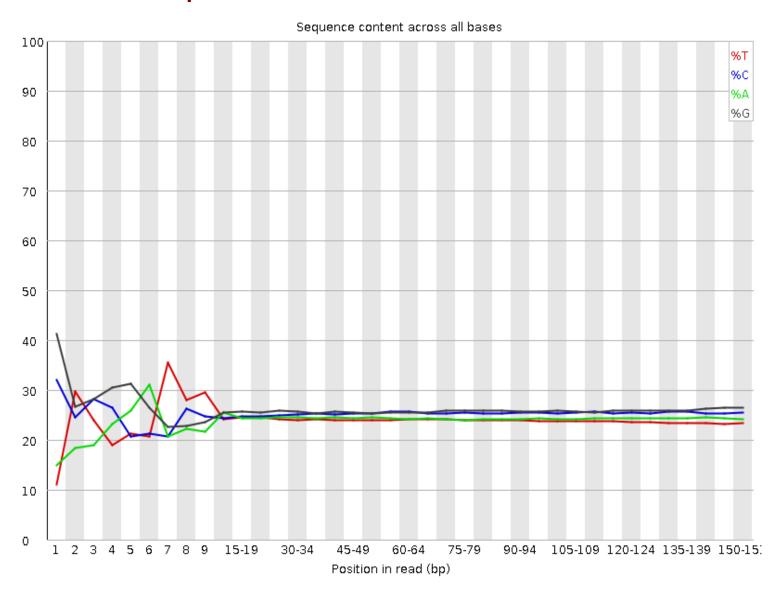




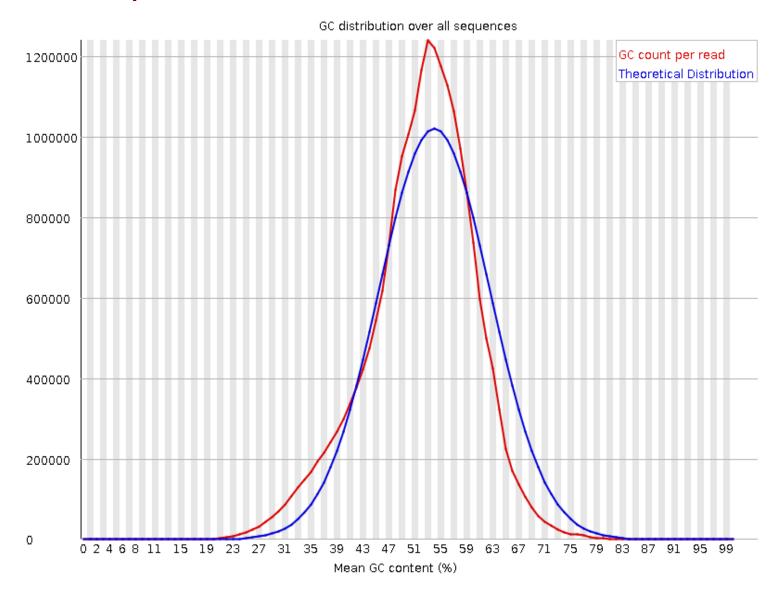
Per sequence quality scores



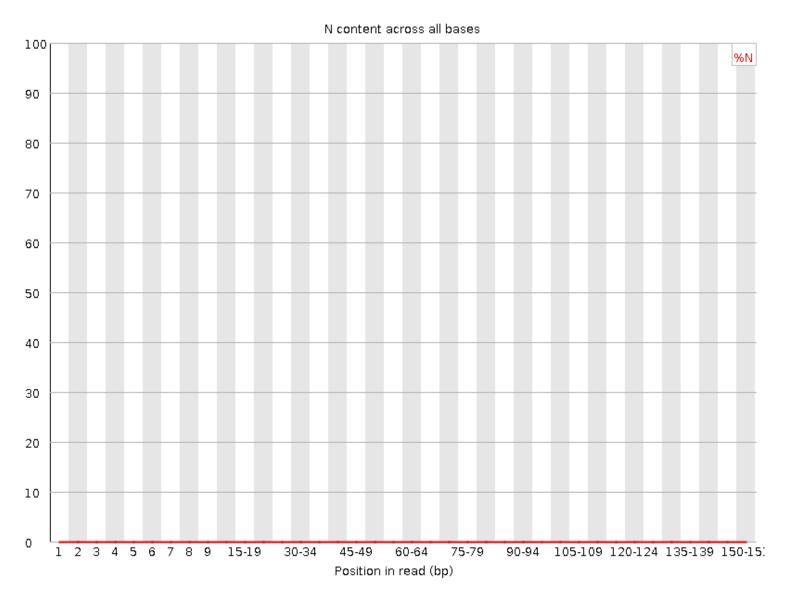
Per base sequence content



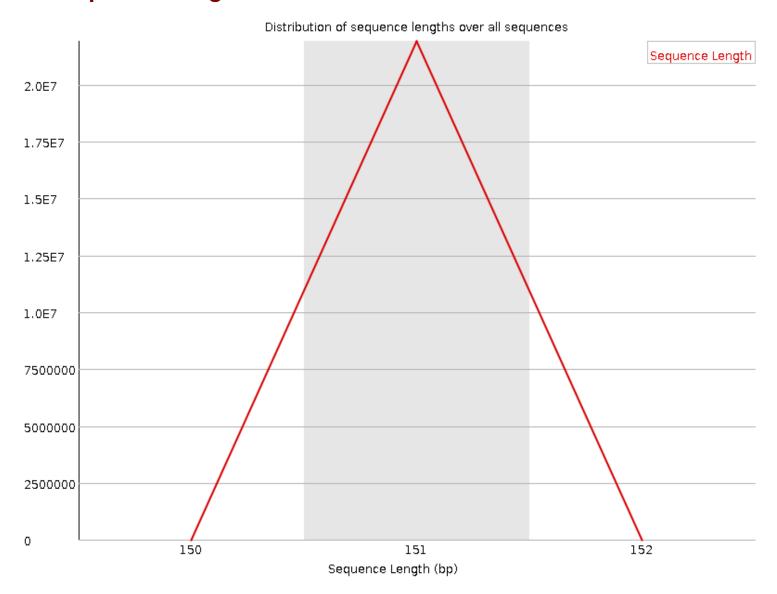
Per sequence GC content



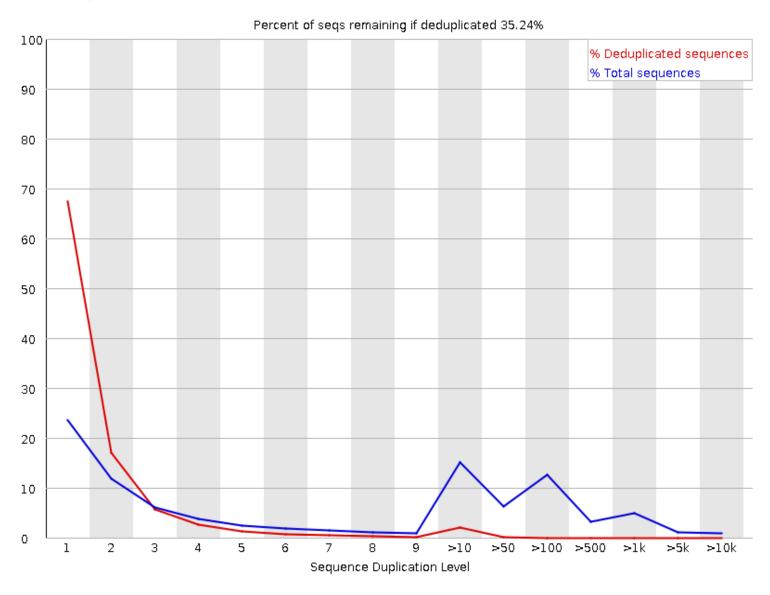
Per base N content



Sequence Length Distribution



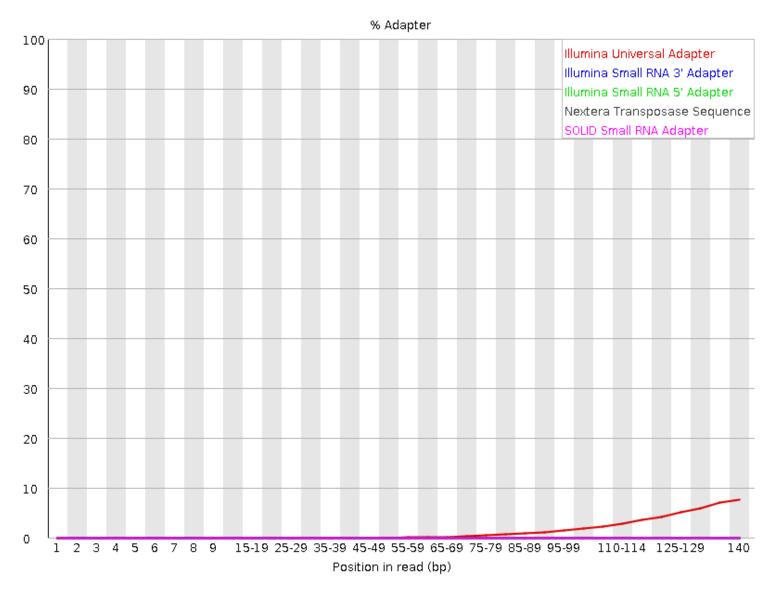
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GTCTCTTTCTGCTGACGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGG}$	27420	0.12515662836259164	No Hit
${\tt CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA}$	25695	0.117282989269759	No Hit
${\tt CGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTG}$	25517	0.11647052100394786	No Hit
AAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTGATGC	24247	0.11067369686023922	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)