#### Sat 2 Nov 2024 SRR14866426\_1.fastq

# **PastQC Report**Summary





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 SRR14866426\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 22253023

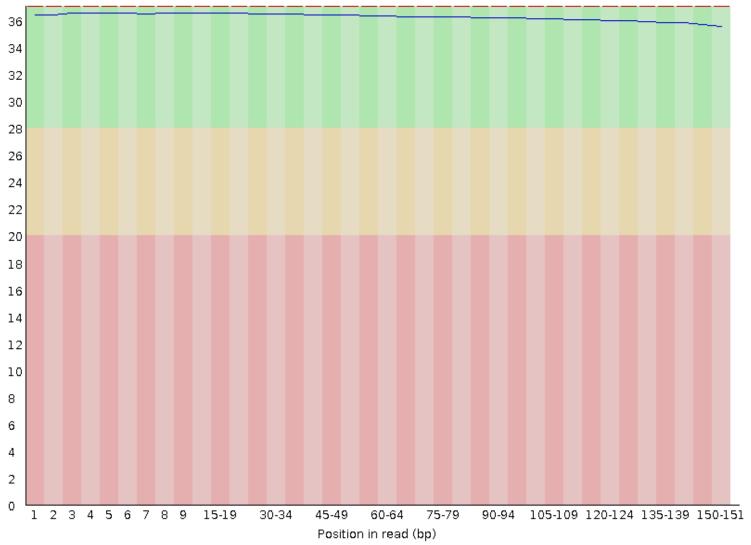
Sequences flagged as poor quality 0

Sequence length 151

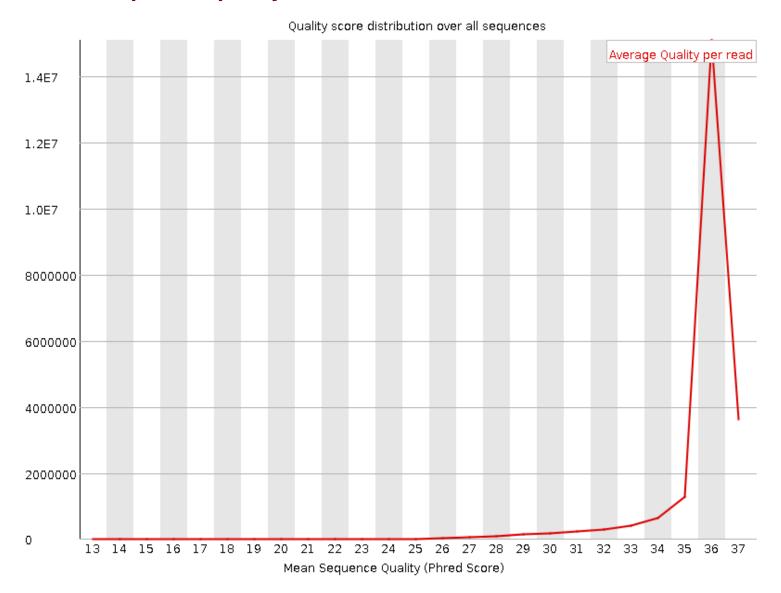
%GC 51

#### Per base sequence quality

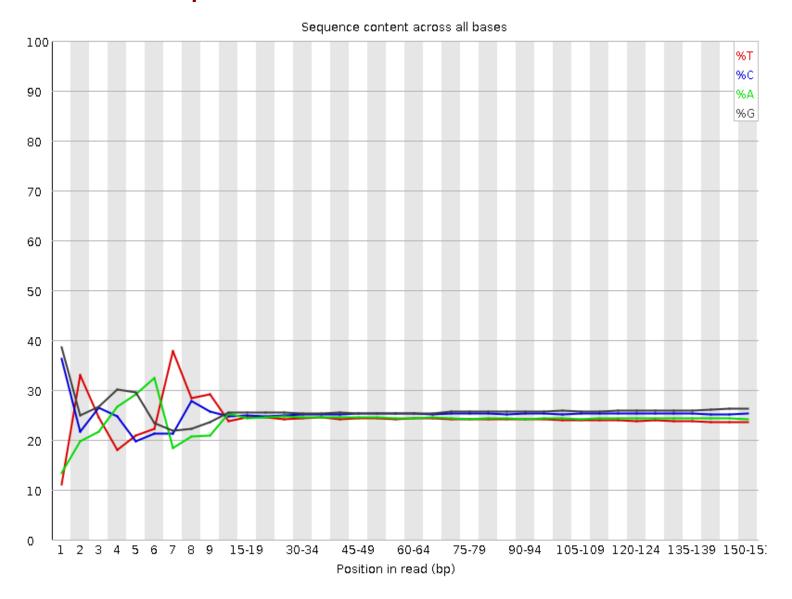




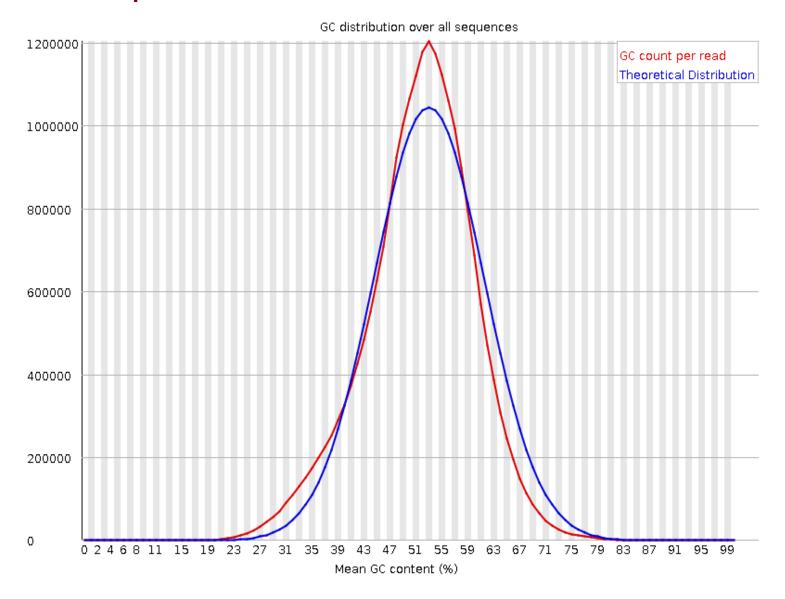
#### Per sequence quality scores



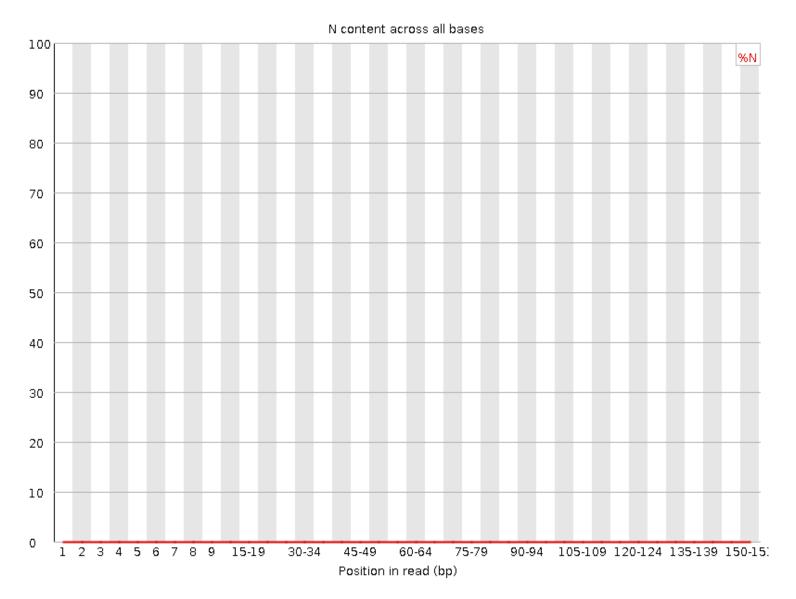
### Per base sequence content



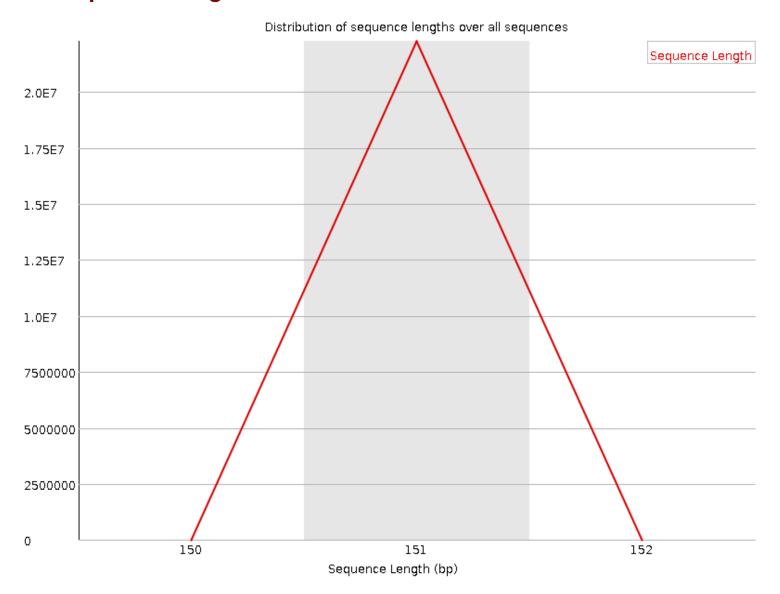
#### Per sequence GC content



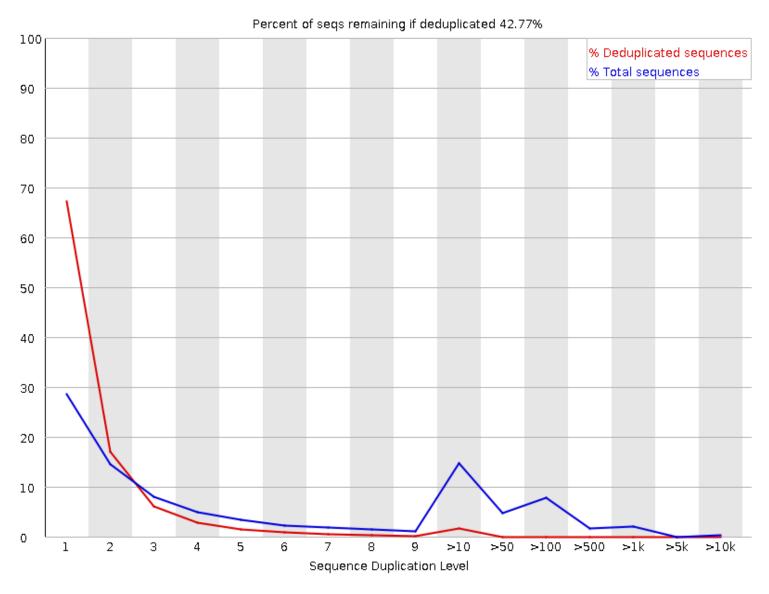
#### Per base N content



#### Sequence Length Distribution



#### Sequence Duplication Levels

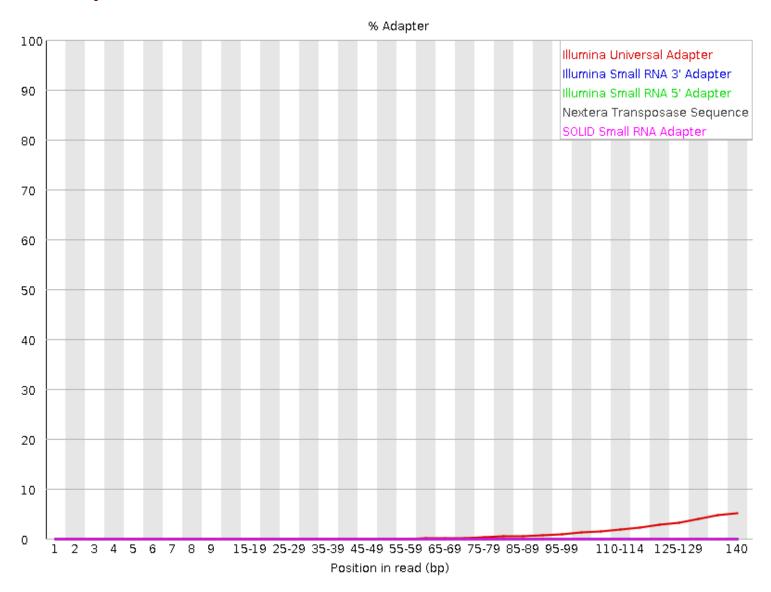


## **Overrepresented sequences**

Sequence Count Percentage Possible Source

GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCTGTCAATCTCGTAT 28753 0.1292094112337007 TruSeq Adapter, Index 18 (97% over 38bp)

#### Adapter Content



Produced by FastQC (version 0.11.7)