# **Report**

Mon 5 Feb 2024 SRR13380426\_1.fastq

#### **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 SRR13380426\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 26571106

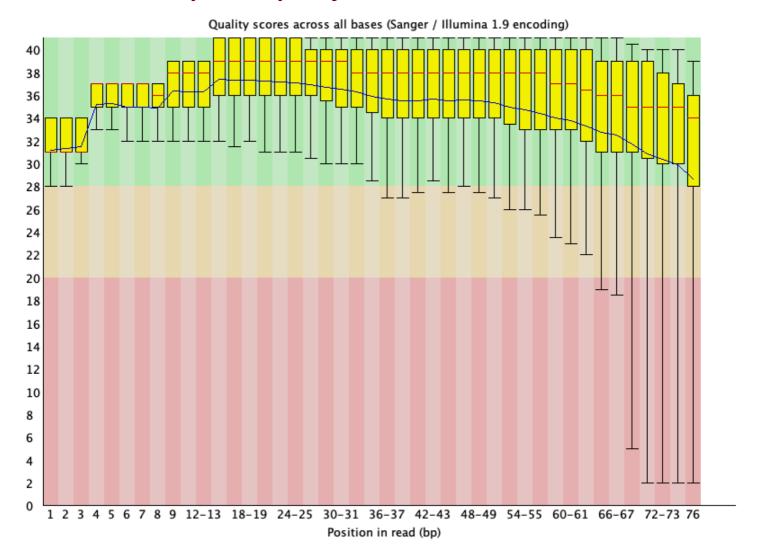
Total Bases 2 Gbp

Sequences flagged as poor quality 0

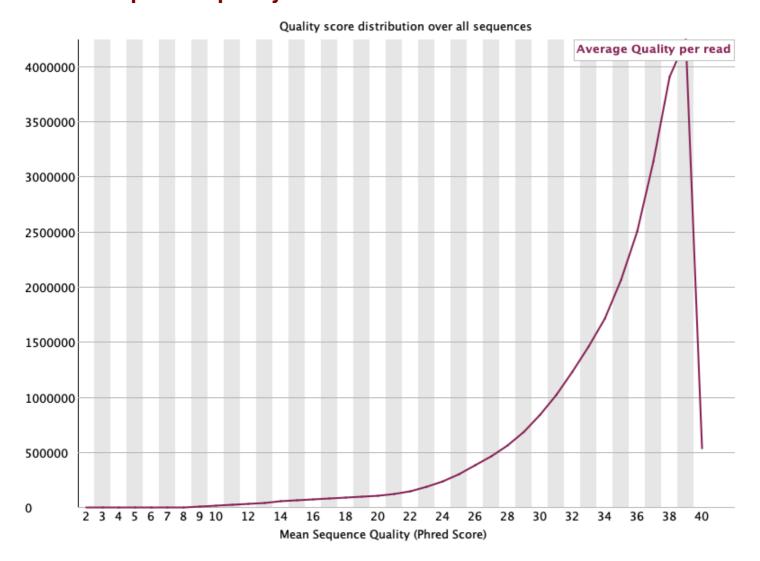
Sequence length 76

%GC 42

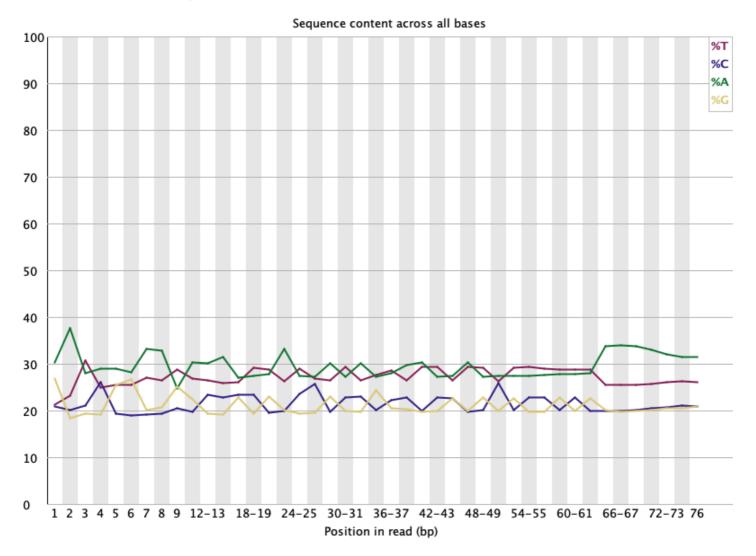
## Per base sequence quality



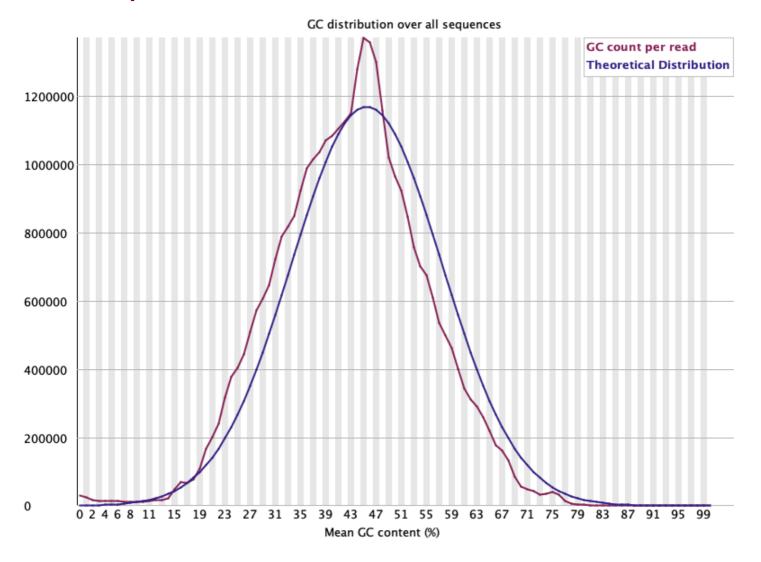
## Per sequence quality scores



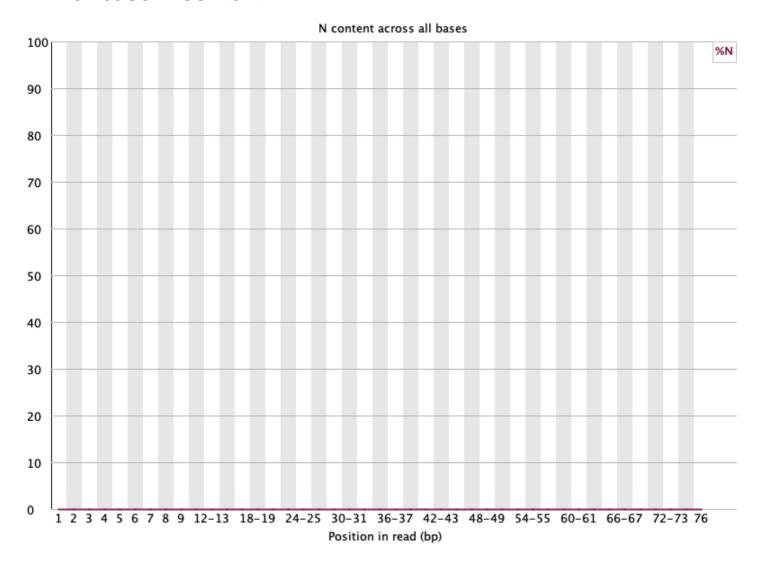
## Per base sequence content



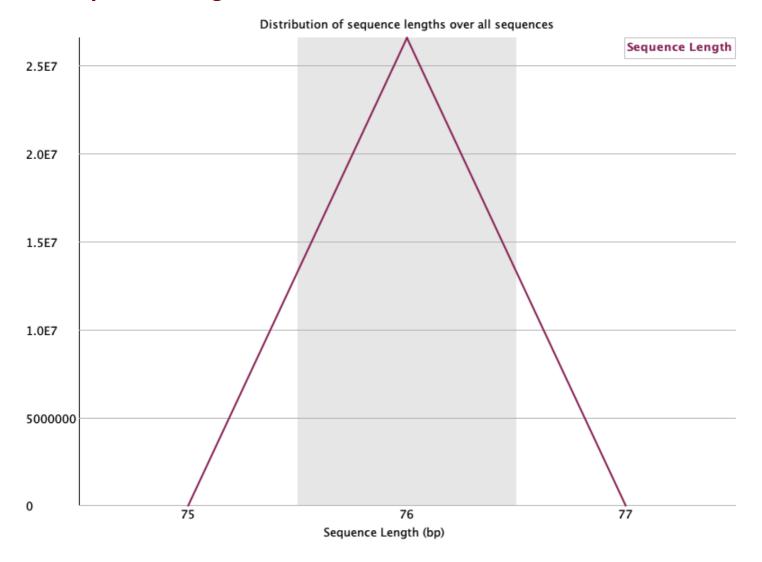
#### Per sequence GC content



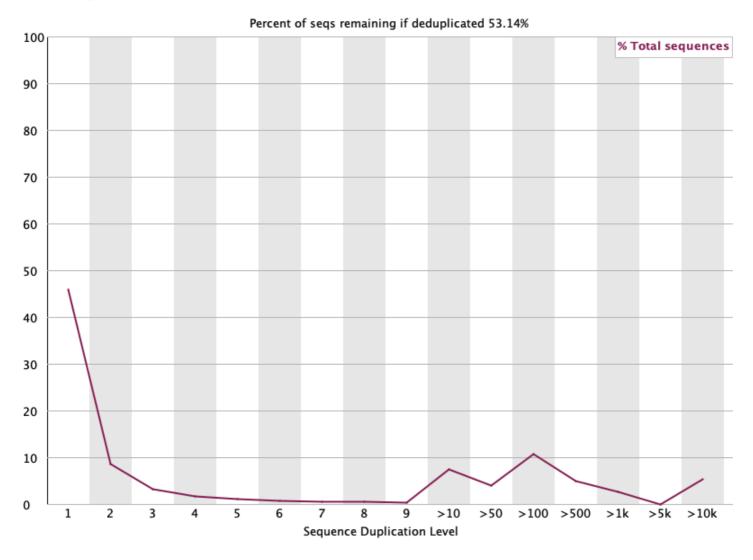
## Per base N content



## Sequence Length Distribution



#### Sequence Duplication Levels



#### **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGC	978246	3.6816156617643236	TruSeq Adapter, Index 11 (100% over 50bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCATCTCGTATGC	277571	1.0446347246516572	TruSeq Adapter, Index 3 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	175646	0.6610413582332628	Clontech SMART CDS Primer II A (100%

Sequence

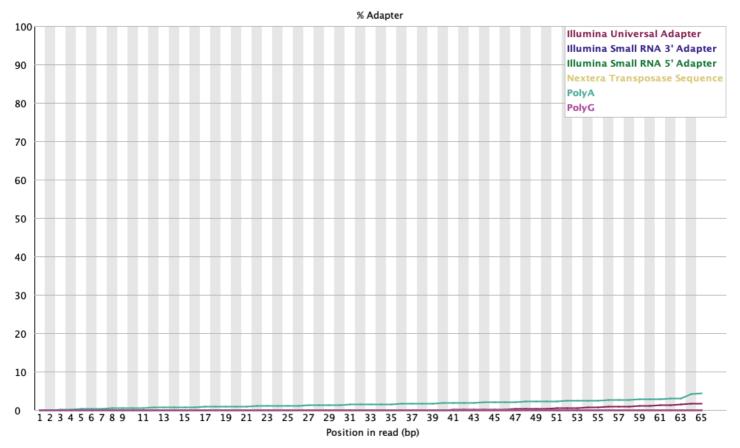
Count

Percentage

Possible Source

over 26bp)





Produced by FastQC (version 0.12.1)