# **<sup>№</sup>FastQC Report**

Mon 5 Feb 2024 SRR13380431\_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 SRR13380431\_1.fastq

Conventional base calls File type

Encoding Sanger / Illumina 1.9

**Total Sequences** 27779395

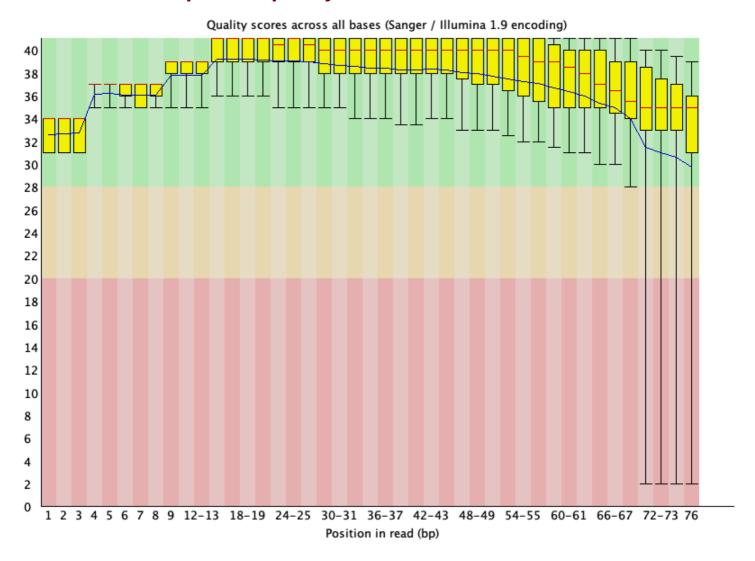
Total Bases 2.1 Gbp

Sequences flagged as poor quality 0

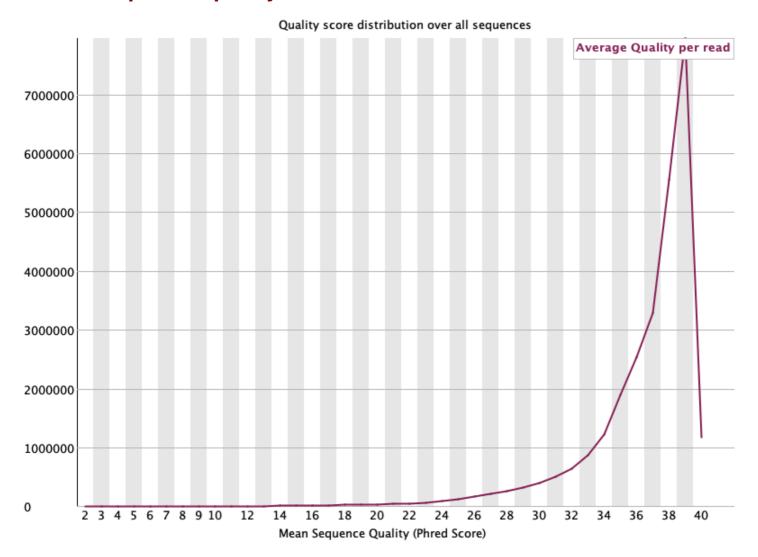
Sequence length 76

%GC 47

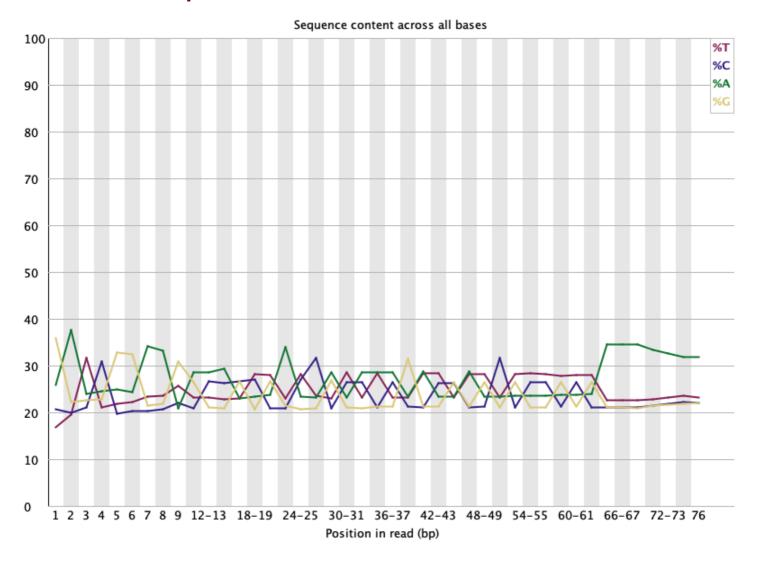
#### Per base sequence quality



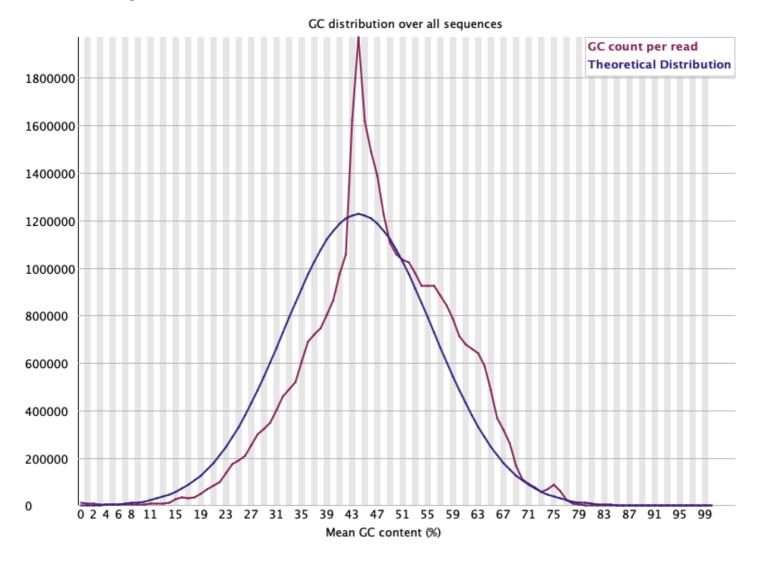
## Per sequence quality scores



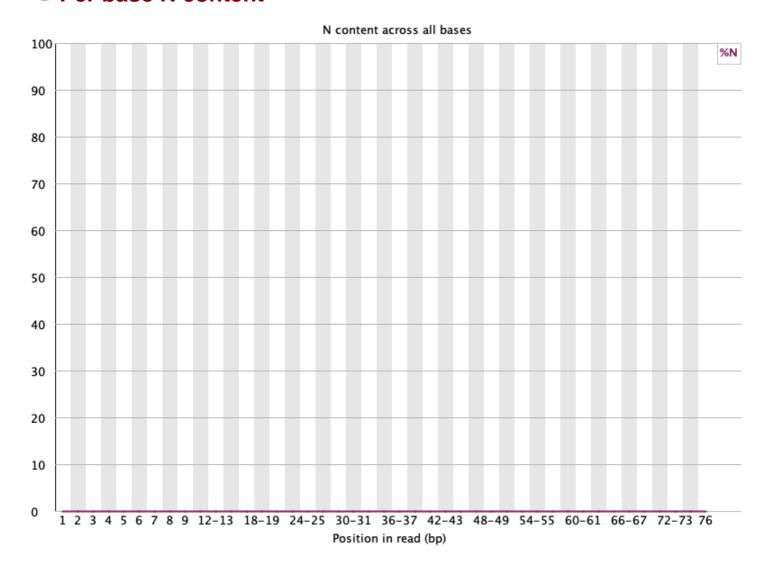
#### Per base sequence content



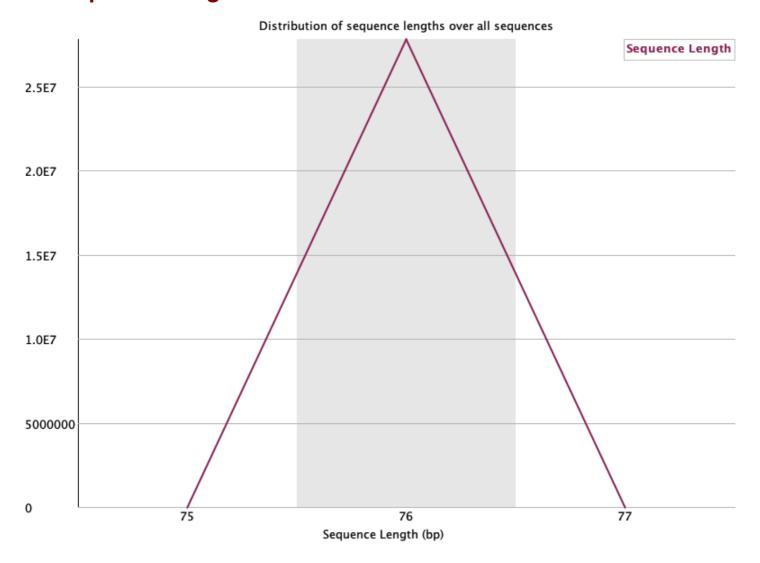
## Per sequence GC content



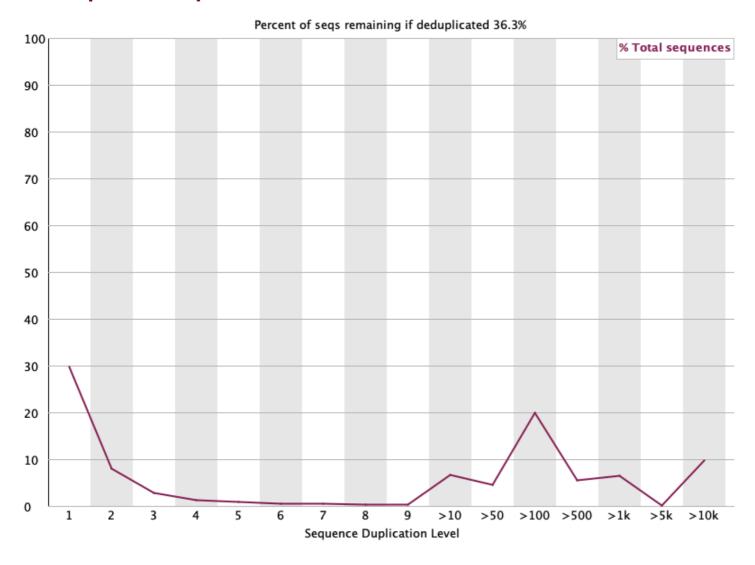
#### Per base N content



## Sequence Length Distribution



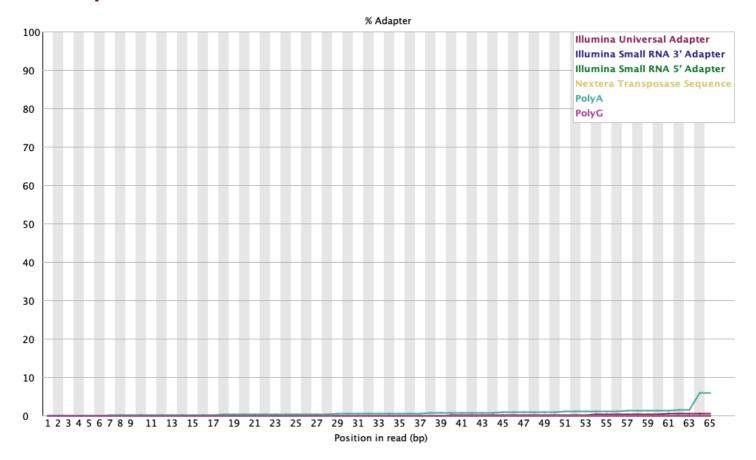
#### Sequence Duplication Levels



## **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATACGGATCTCGTATGC	2572069	9.258909346297859	TruSeq Adapter, Index 27 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	129413	0.46585967764956726	Clontech SMART CDS Primer II A (100% over 26bp)

#### Adapter Content



Produced by FastQC (version 0.12.1)