# **<sup>№</sup>FastQC Report**

Tue 6 Feb 2024 SRR13380503\_1.fastq

#### **Summary**



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

**Adapter Content** 



Measure Value

Filename SRR13380503\_1.fastq

Conventional base calls File type

Encoding Sanger / Illumina 1.9

**Total Sequences** 38198578

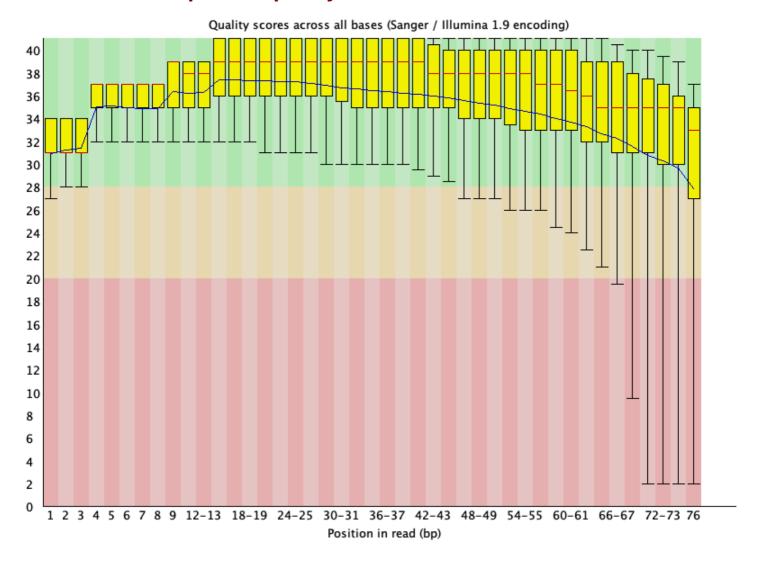
Total Bases 2.9 Gbp

Sequences flagged as poor quality 0

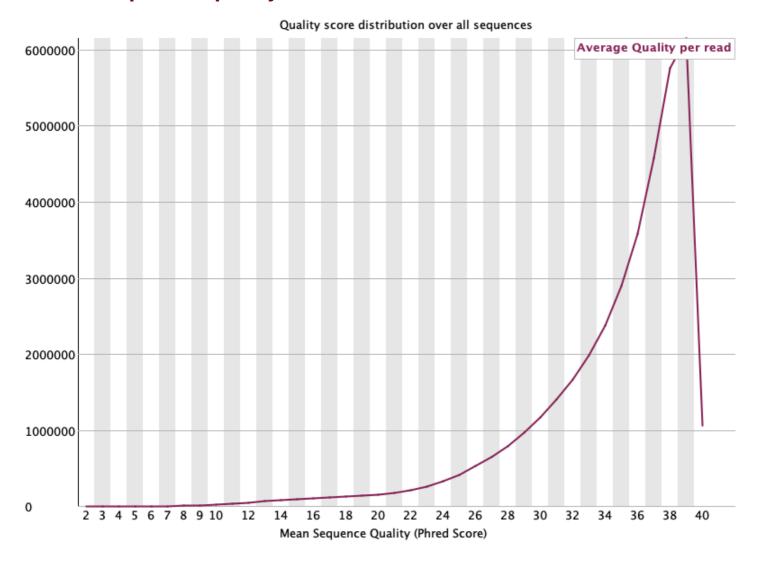
Sequence length 76

%GC 47

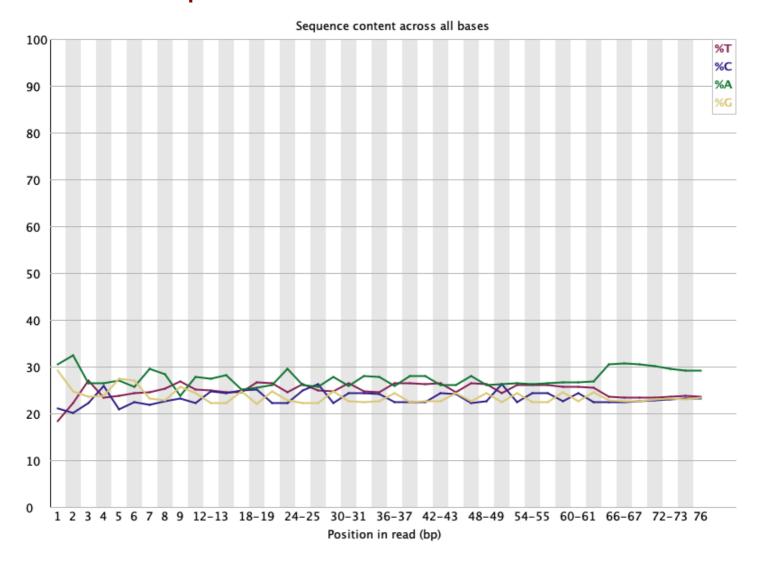
# Per base sequence quality



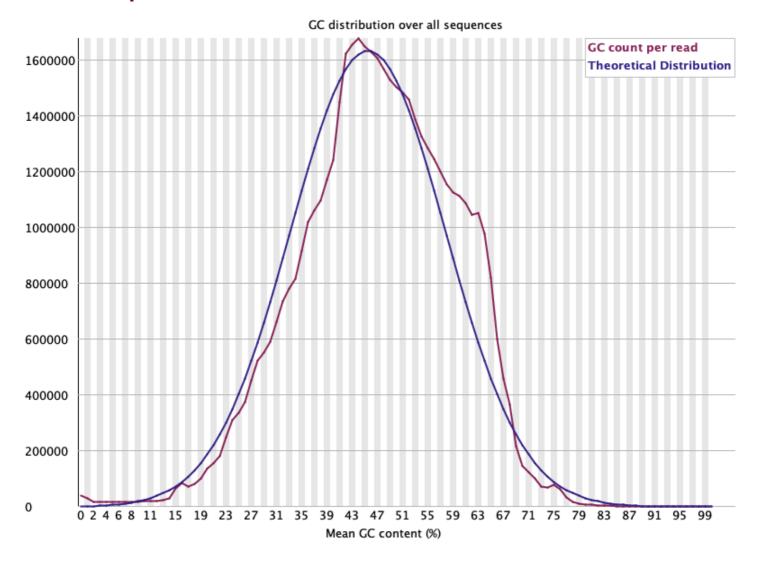
# Per sequence quality scores



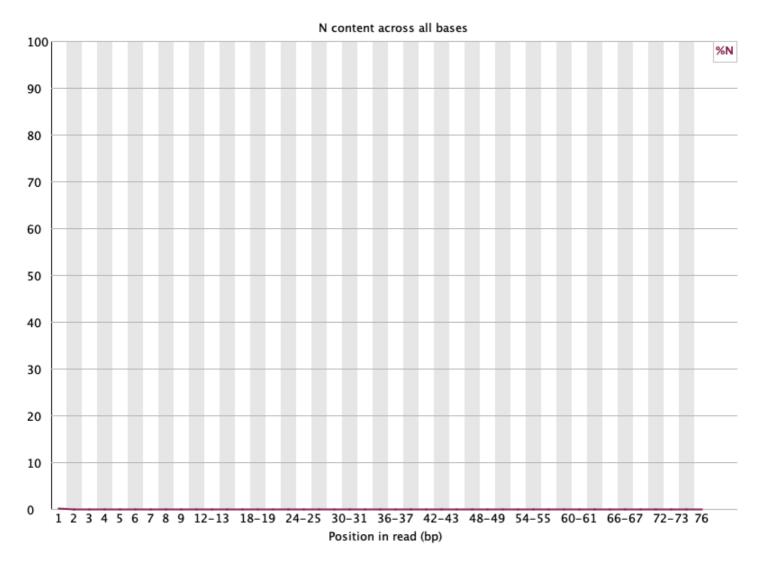
# Per base sequence content



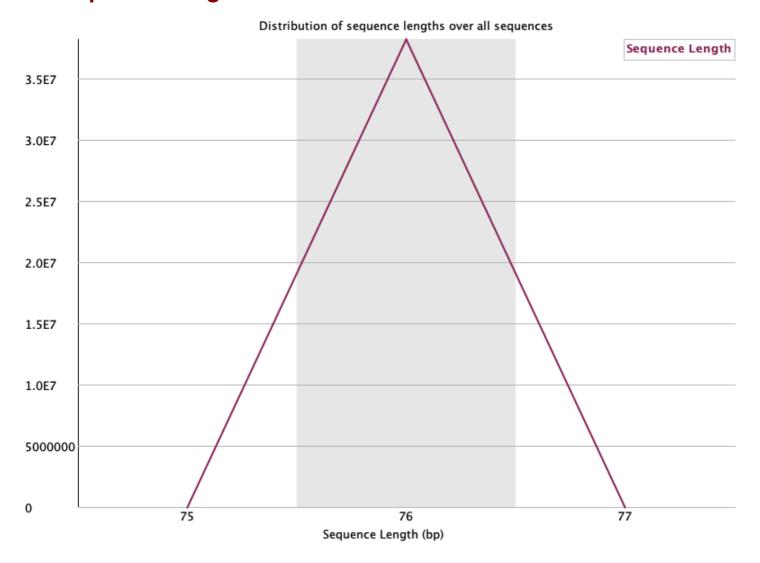
### Per sequence GC content



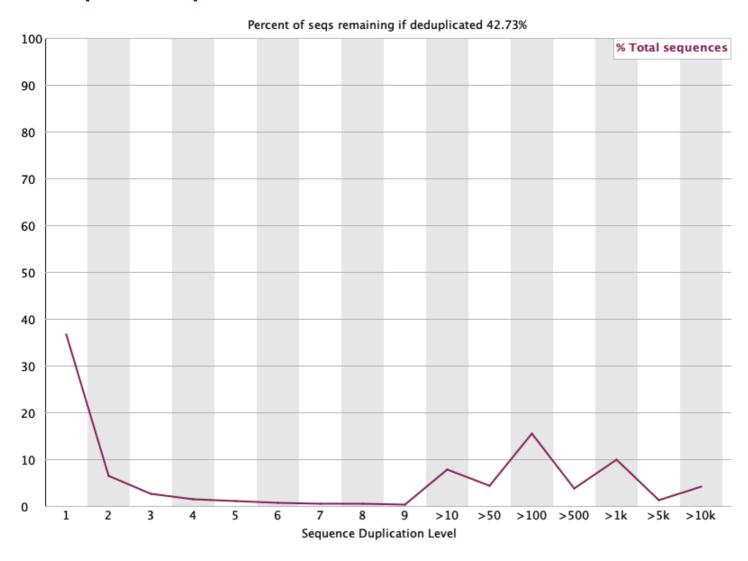
### Per base N content



# Sequence Length Distribution



### Sequence Duplication Levels



# **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATCTCGTATGC	1287723	3.371128108486133	TruSeq Adapter, Index 25 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	212524	0.5563662605450914	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence

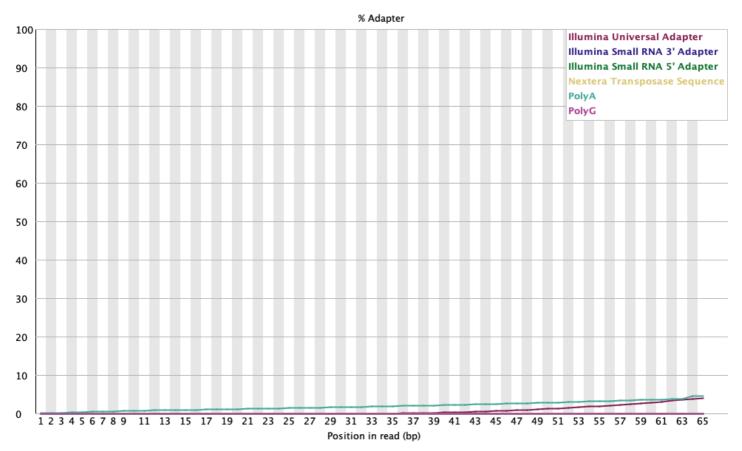
Count

Percentage

Possible Source

0.11705409557392424 No Hit

#### Adapter Content



Produced by FastQC (version 0.12.1)