#### Mon 5 Feb 2024 SRR13380508\_1.fastq

# **№**FastQC 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 SRR13380508\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 17798490

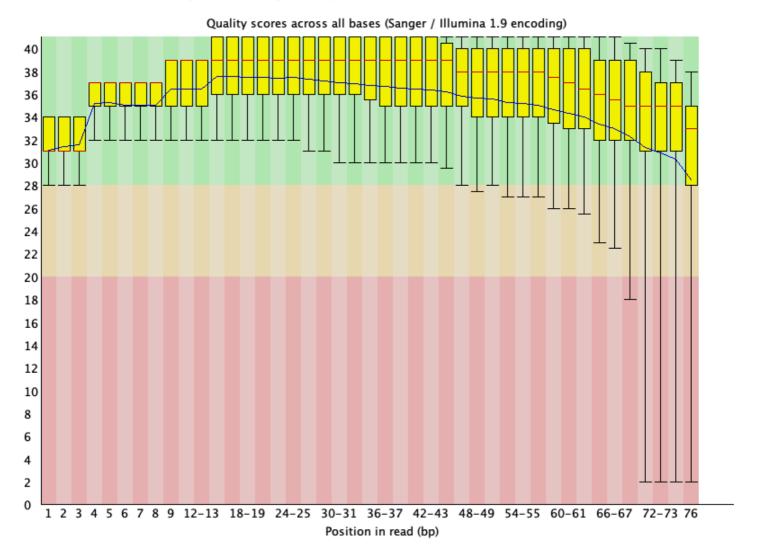
Total Bases 1.3 Gbp

Sequences flagged as poor quality  $\, {\bf 0} \,$ 

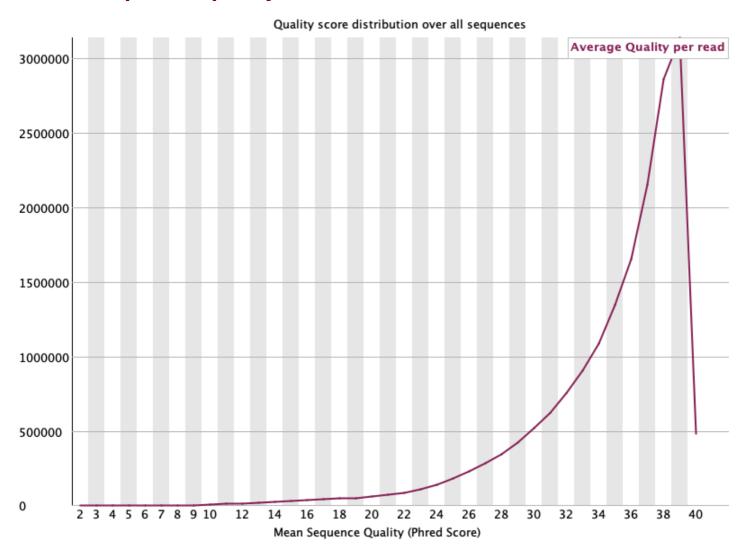
Sequence length 76

%GC 46

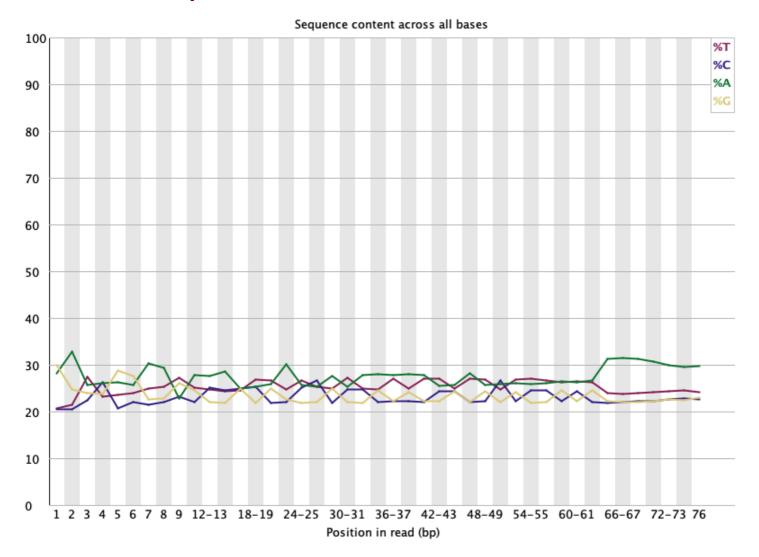
### Per base sequence quality



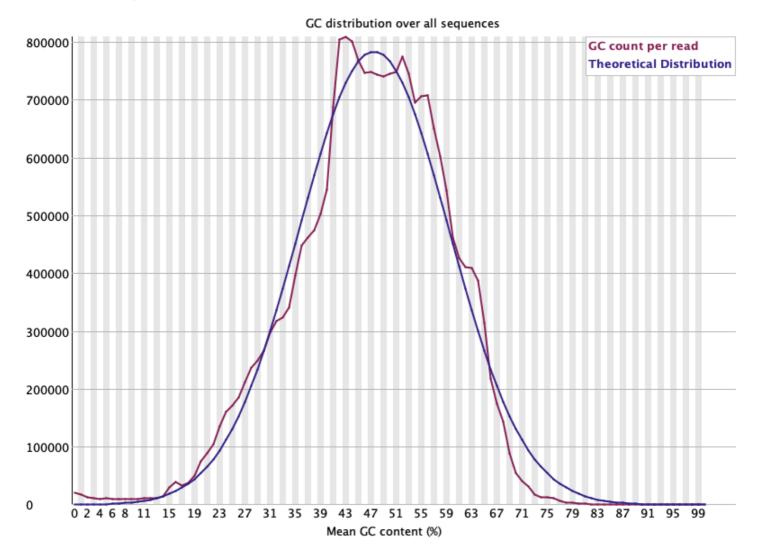
## Per sequence quality scores



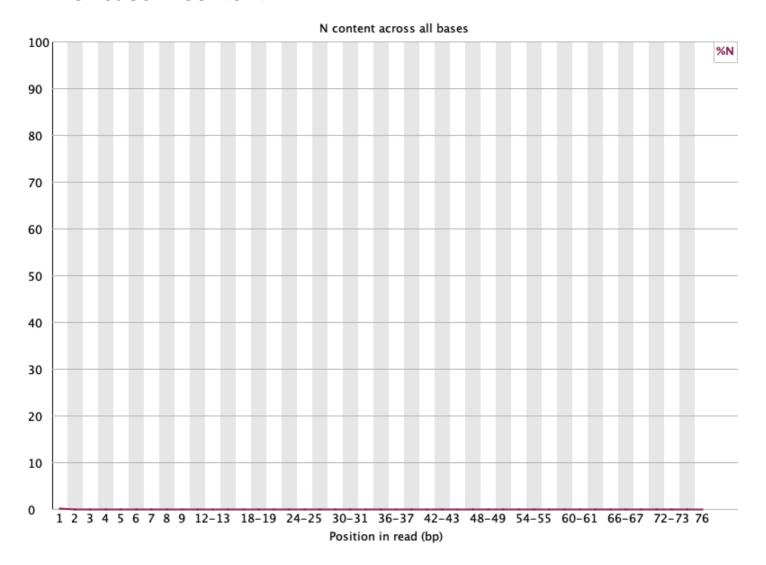
## Per base sequence content



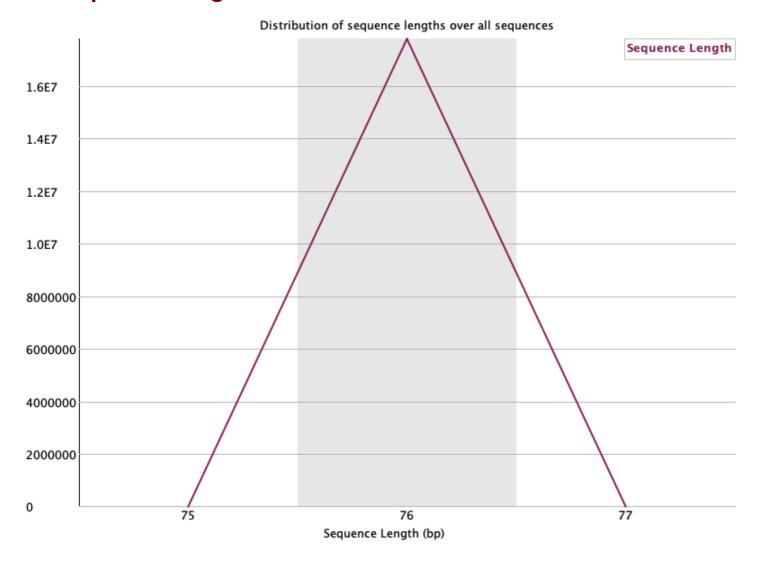
## Per sequence GC content



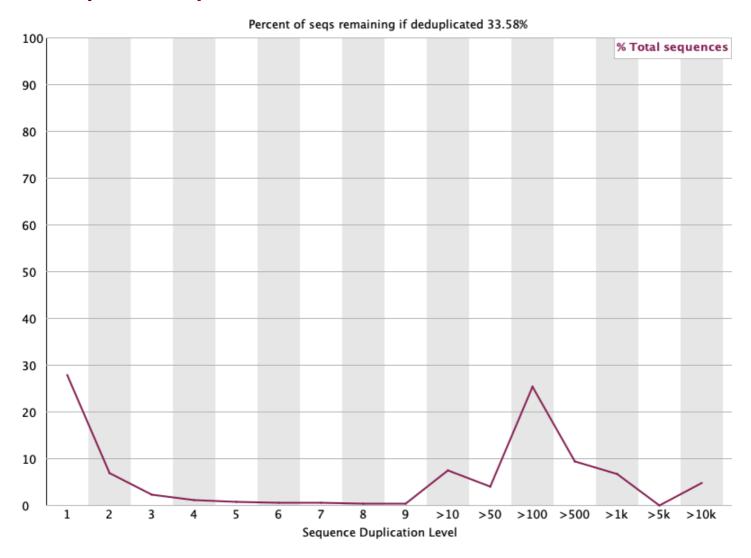
### Per base N content



## Sequence Length Distribution



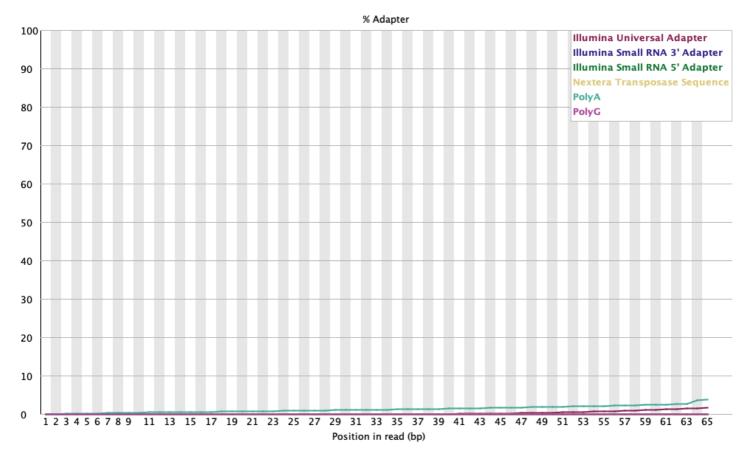
#### Sequence Duplication Levels



#### **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGATAGAT	711684	3.998563923119321	TruSeq Adapter, Index 2 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	116659	0.6554432426571017	Clontech SMART CDS Primer II A (100% over 26bp)

## Adapter Content



Produced by FastQC (version 0.12.1)