# **Report**

Mon 5 Feb 2024 SRR13380421\_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

#### Basic Statistics

Measure Value

Filename SRR13380421\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

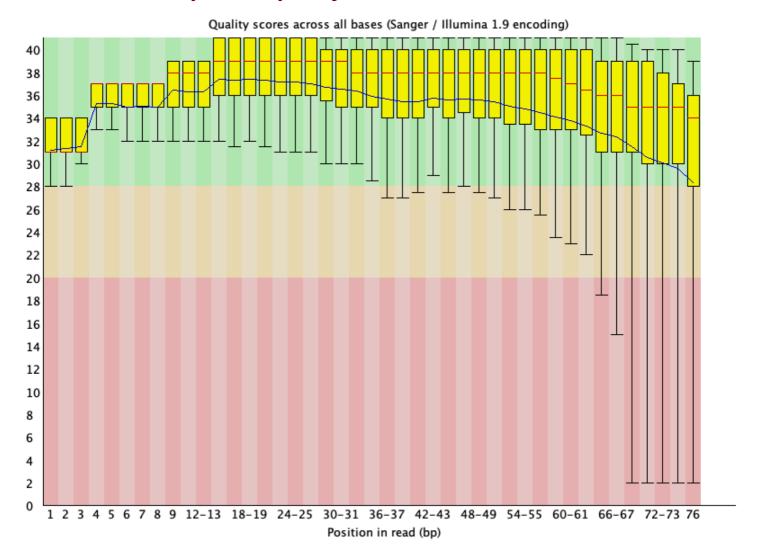
Total Sequences 30317564
Total Bases 2.3 Gbp

Sequences flagged as poor quality 0

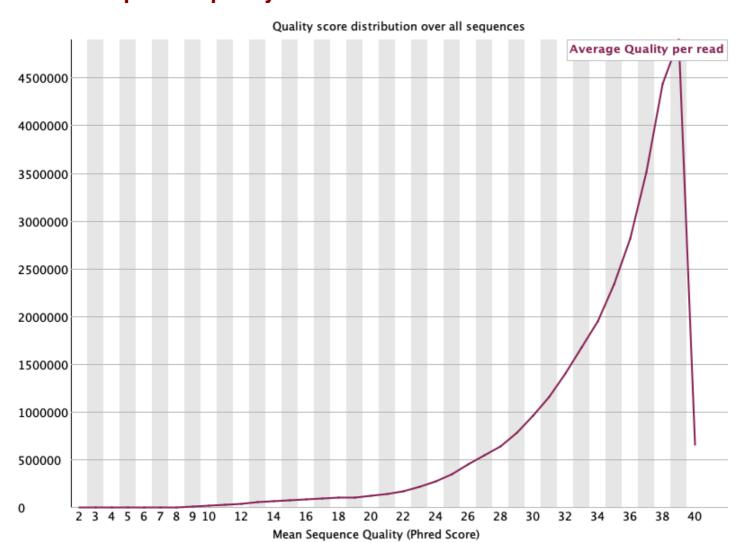
Sequence length 76

%GC 42

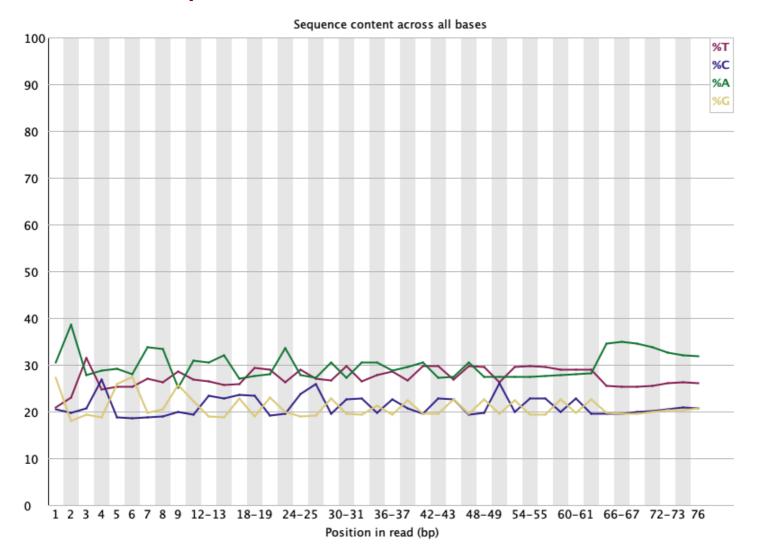
## Per base sequence quality



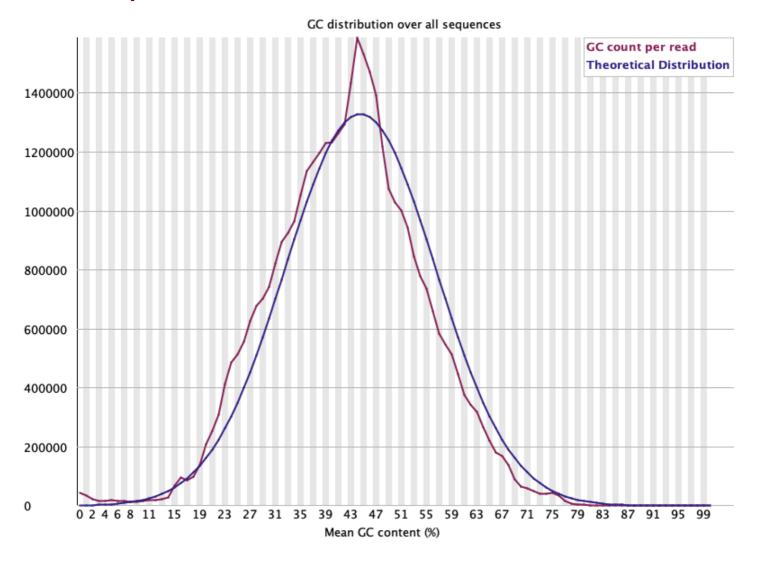
## Per sequence quality scores



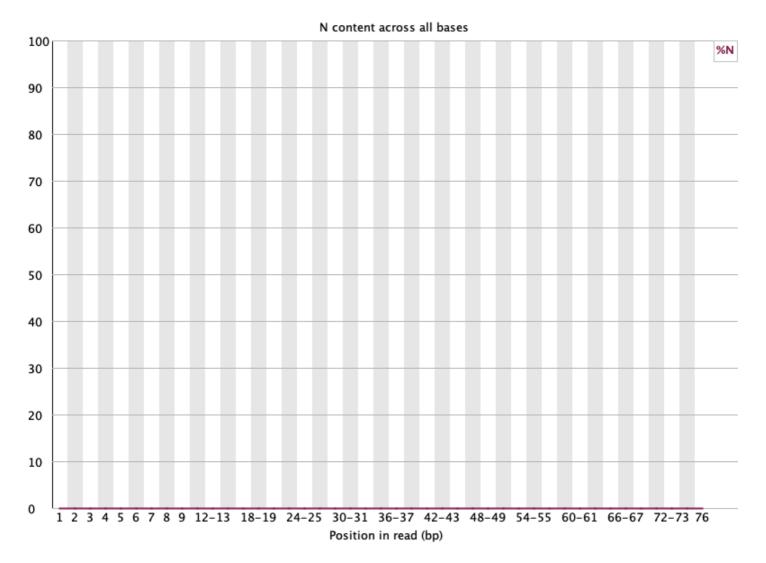
## Per base sequence content



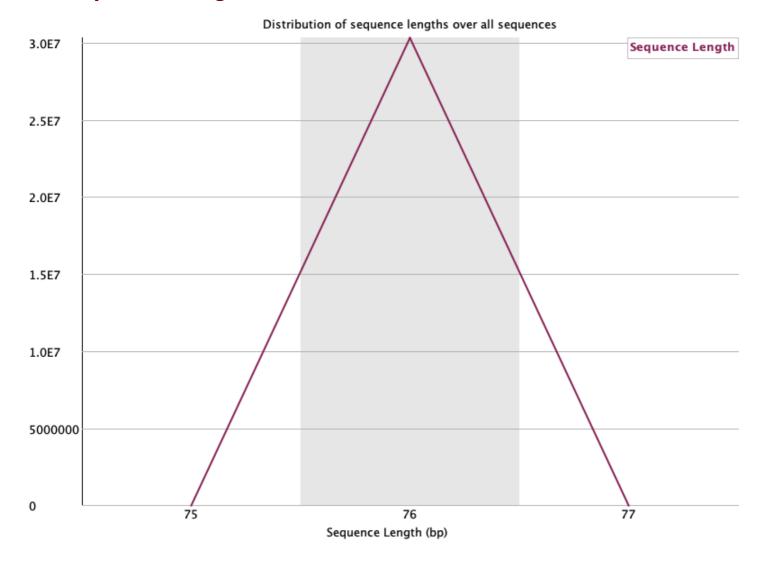
#### Per sequence GC content



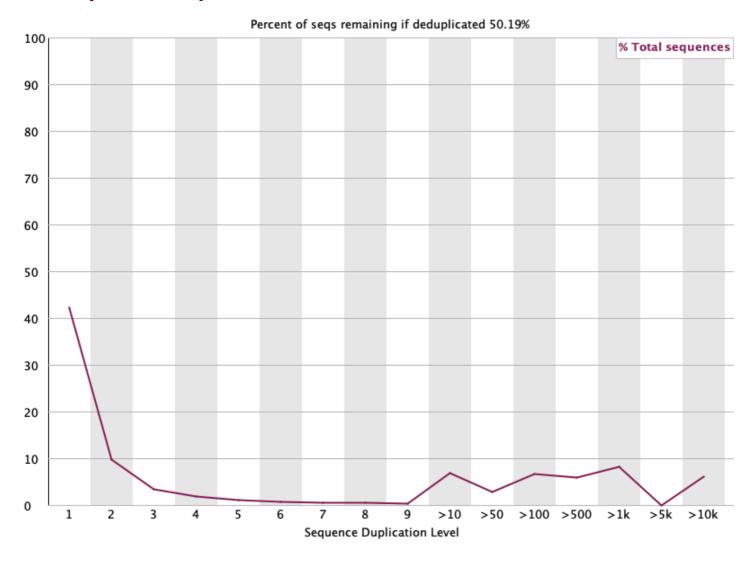
## Per base N content



## Sequence Length Distribution



#### Sequence Duplication Levels



### **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATGC	971626	3.204828725685217	TruSeq Adapter, Index 9 (100% over 50bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGATCTCGTATGC	569820	1.8795045670555854	TruSeq Adapter, Index 1 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	271462	0.8953951577376073	Clontech SMART CDS Primer II A (100%

Sequence

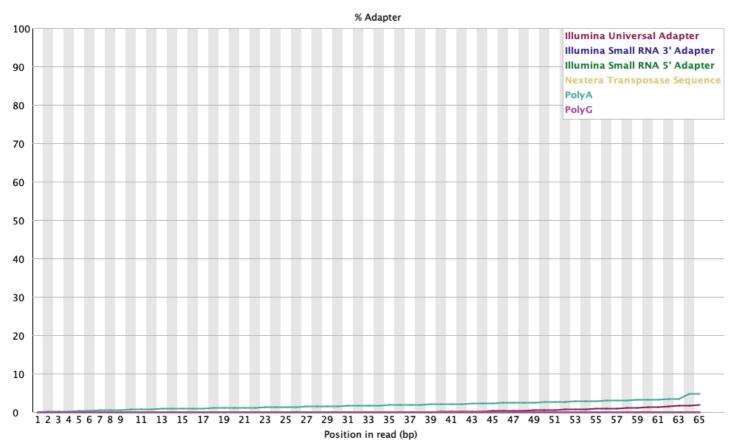
Count

Percentage

Possible Source

over 26bp)





Produced by FastQC (version 0.12.1)