#### Mon 5 Feb 2024 SRR13380446\_1.fastq

# **Report**

#### 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 SRR13380446\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

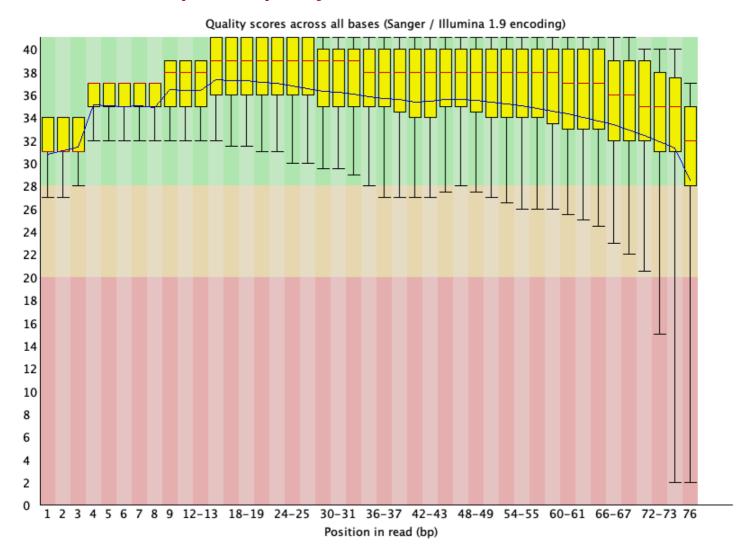
Total Sequences 31687911
Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

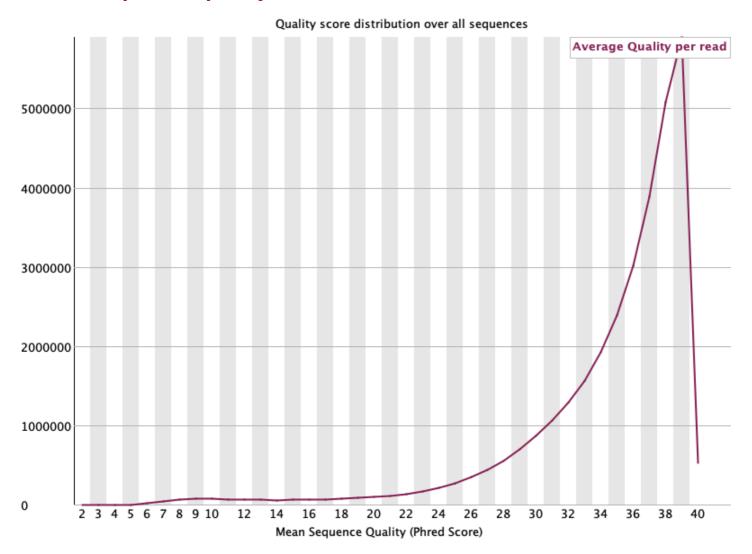
Sequence length 76

%GC 44

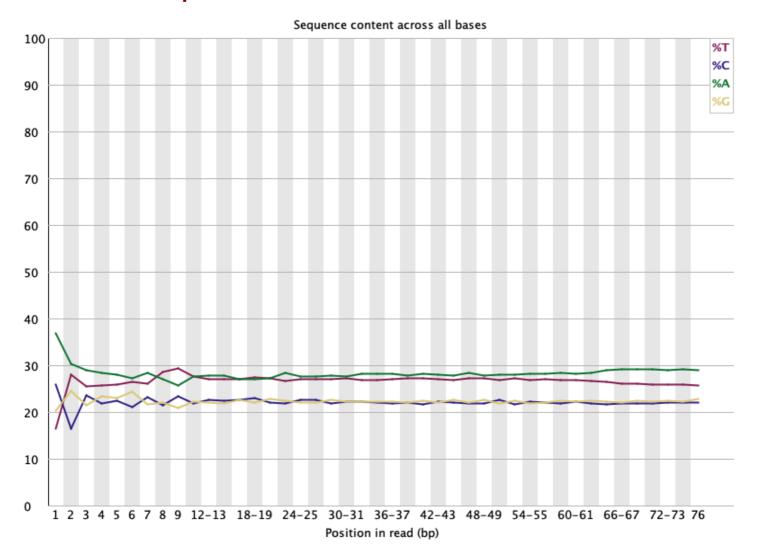
#### Per base sequence quality



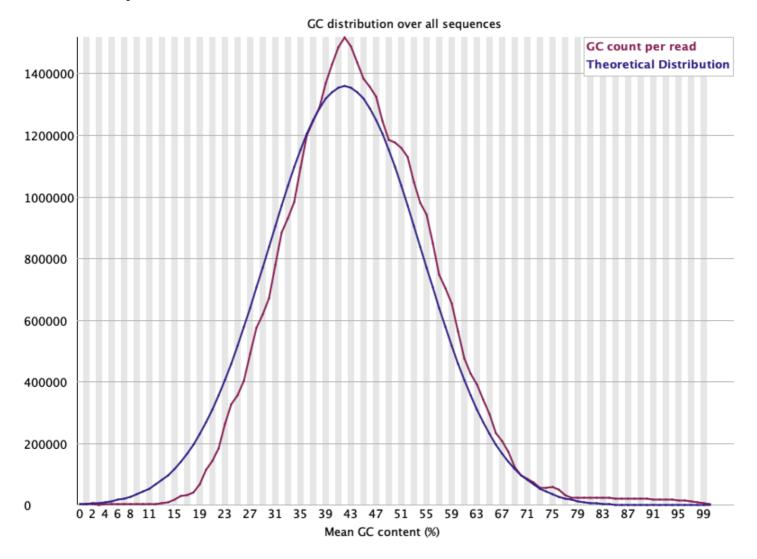
### Per sequence quality scores



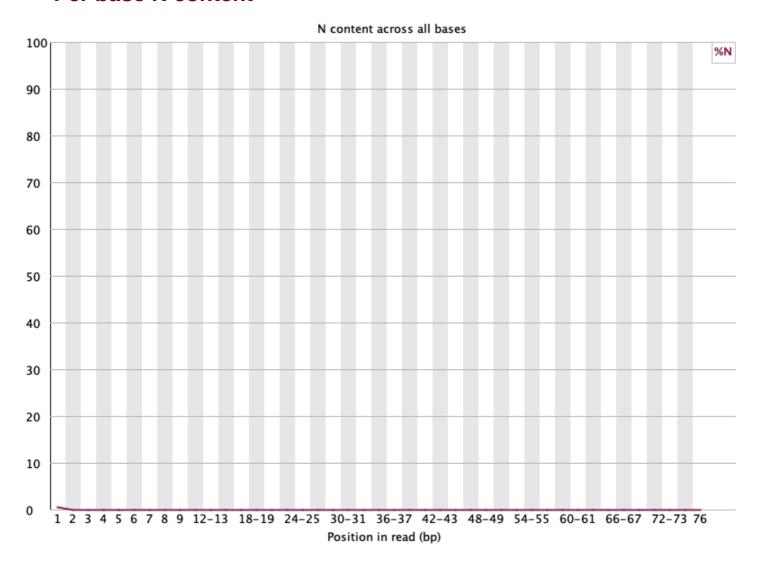
## Per base sequence content



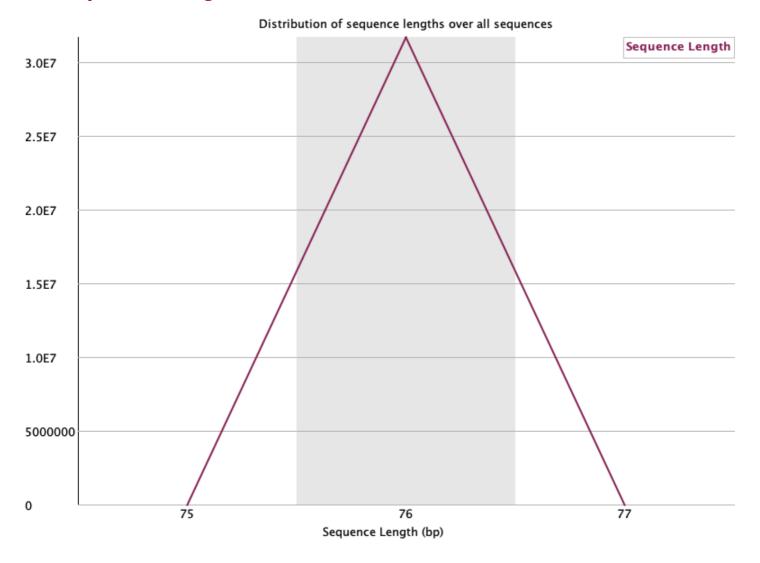
#### Per sequence GC content



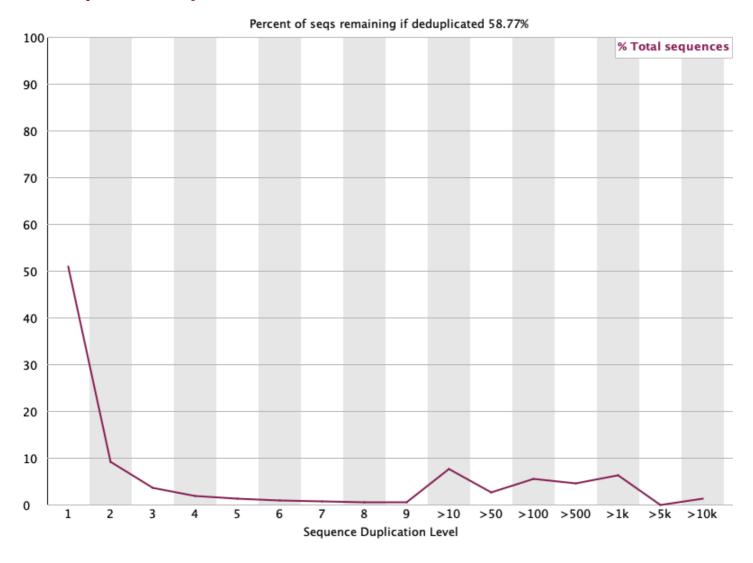
#### Per base N content



## Sequence Length Distribution



#### Sequence Duplication Levels



#### Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACATCTATCT	181555	0.5729472037459332	TruSeq Adapter, Index 8 (97% over 37bp)
CG	61041	0.19263182101212037	No Hit
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	46505	0.14675943769218489	Clontech SMART CDS Primer II A (100% over 26bp)
CGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACACATCTAT	34863	0.11001987477180178	TruSeq Adapter, Index 8 (97% over 37bp)

Sequence

Count

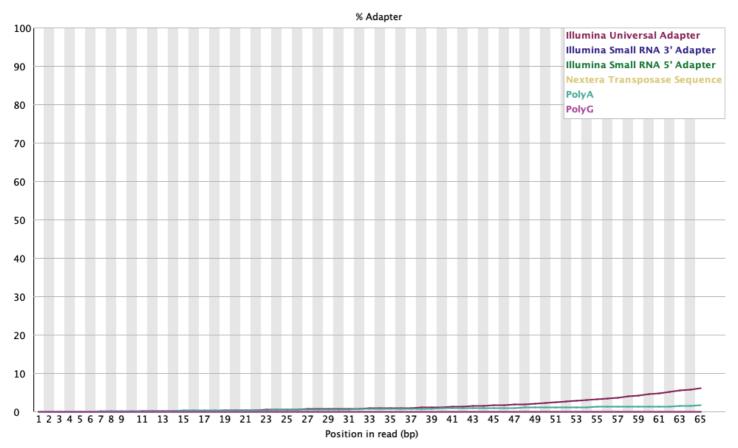
Percentage

Possible Source

MCGCGCGCGCGCGCGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCC 34077 0.10753943357137048 P

Illumina Multiplexing PCR Primer 2.01 (100% over 28bp)

#### Adapter Content



Produced by FastQC (version 0.12.1)