# **Report**

Tue 6 Feb 2024 SRR13380533\_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



Measure Value

Filename SRR13380533\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

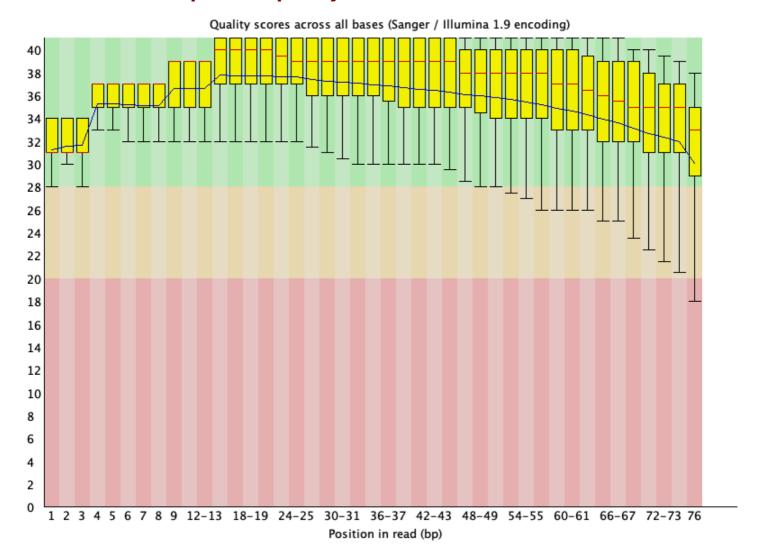
Total Sequences 32865467
Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

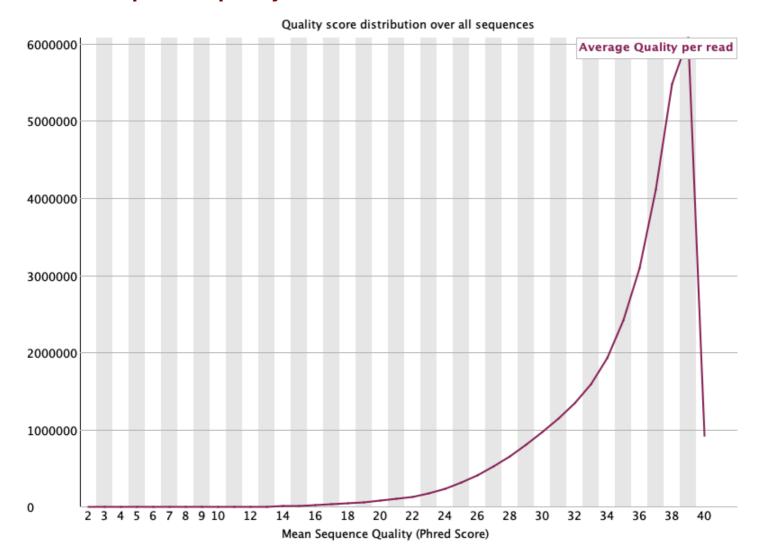
Sequence length 76

%GC 47

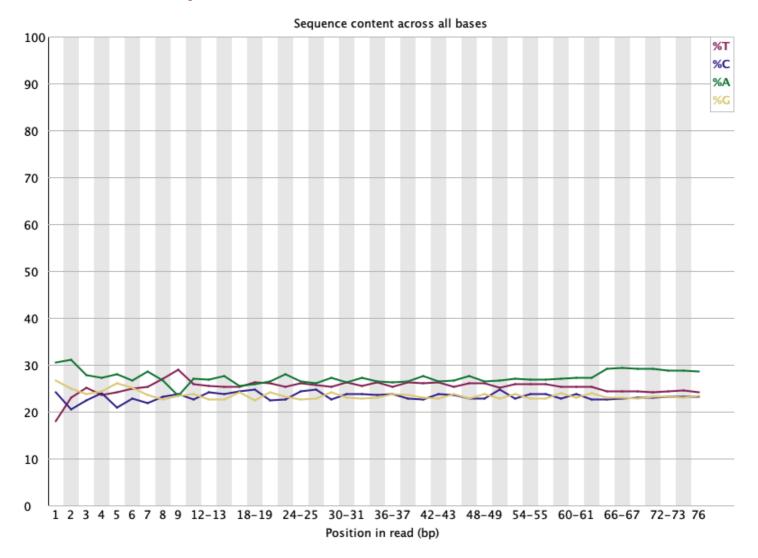
## Per base sequence quality



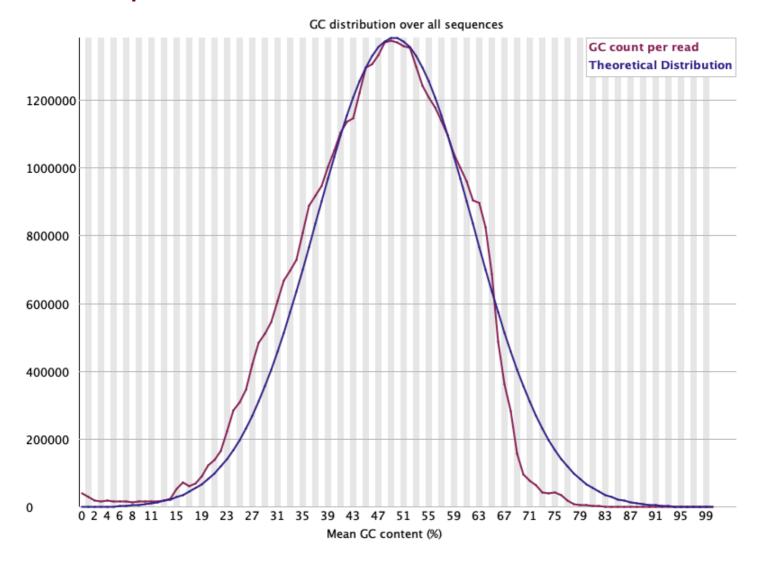
## Per sequence quality scores



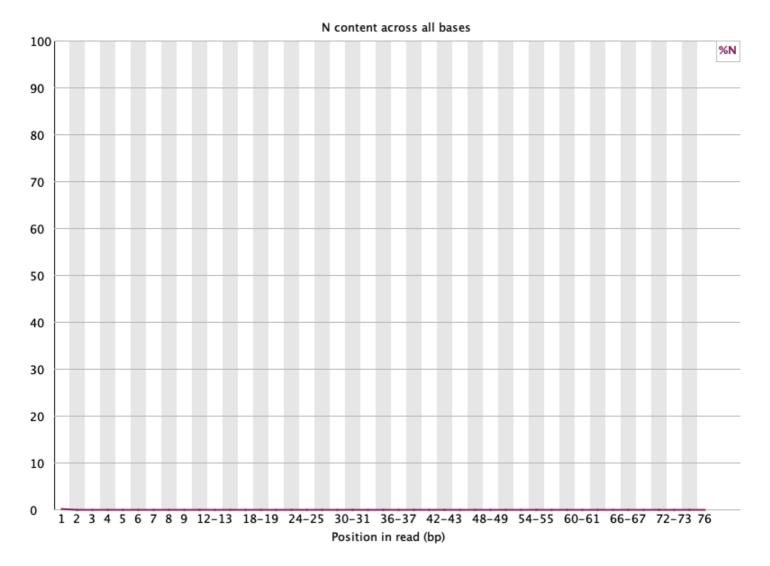
## Per base sequence content



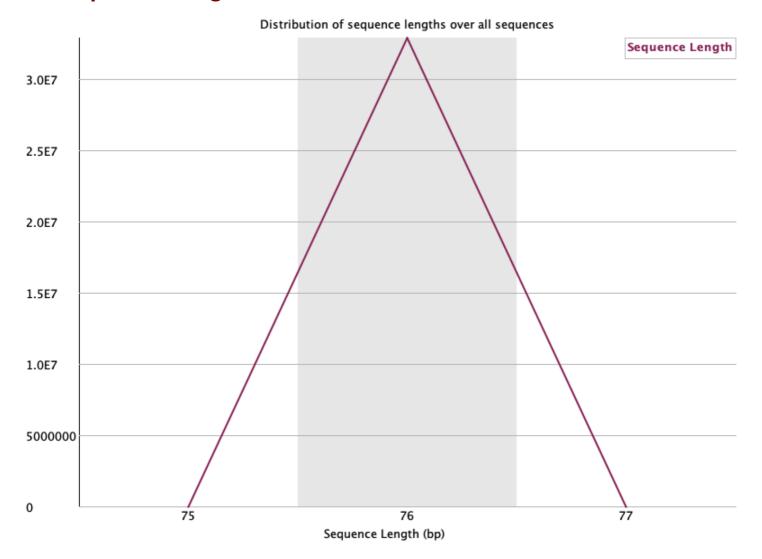
## Per sequence GC content



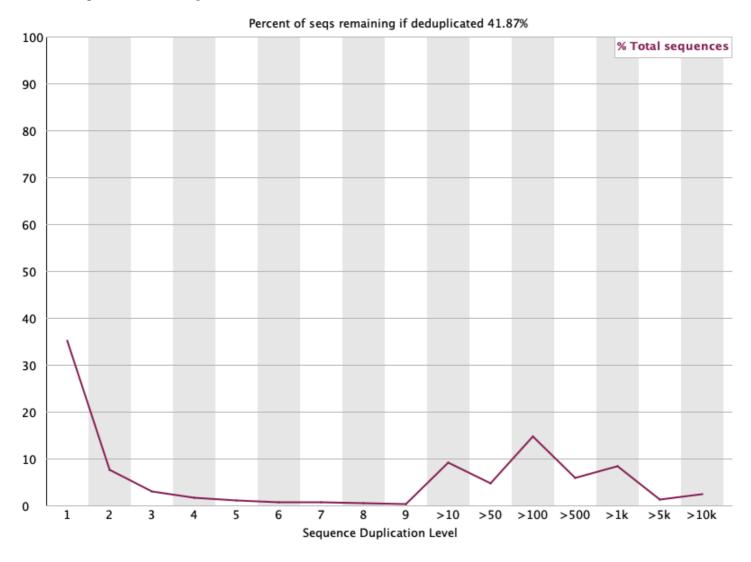
### Per base N content



## Sequence Length Distribution



### Sequence Duplication Levels



#### **Overrepresented sequences**

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTGCTGATCTCGTATGC	556672	1.693790019779728	TruSeq Adapter, Index 7 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	173478	0.5278427962091639	Clontech SMART CDS Primer II A (100% over 26bp)

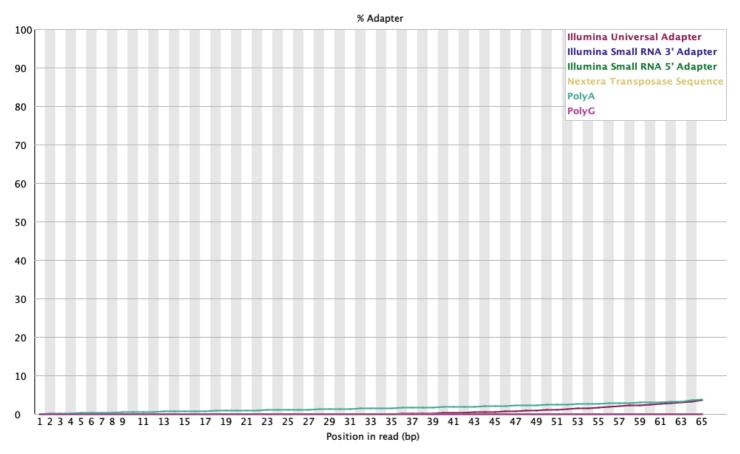
Sequence

Count

Percentage

Possible Source

#### Adapter Content



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