# **Report**

Tue 6 Feb 2024 SRR13380537\_1.fastq

#### **Summary**







Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content



Measure Value

SRR13380537\_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

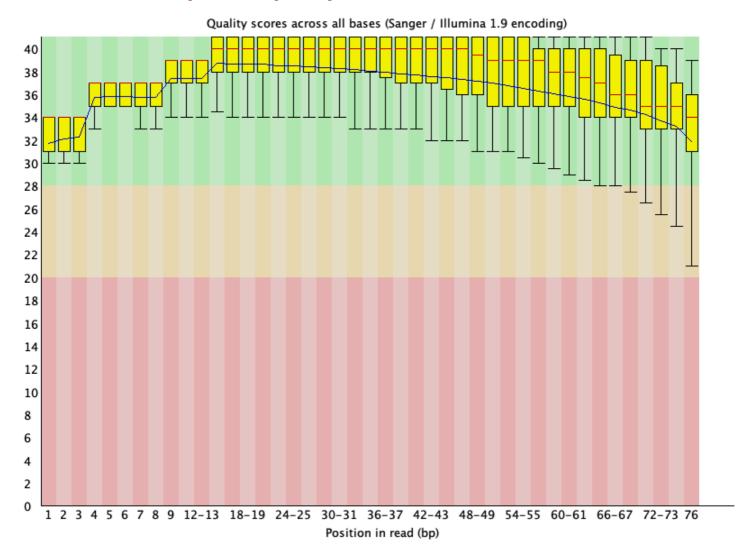
**Total Sequences** 35179626 Total Bases 2.6 Gbp

Sequences flagged as poor quality 0

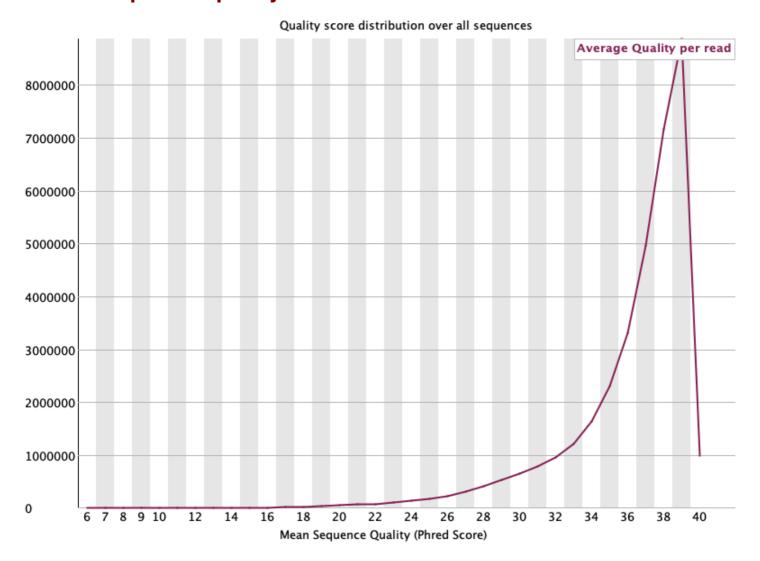
Sequence length 76

%GC 45

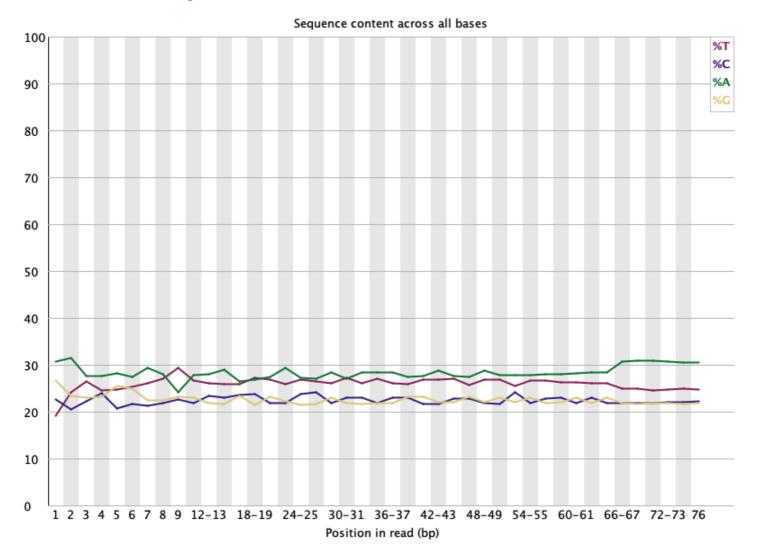
## Per base sequence quality



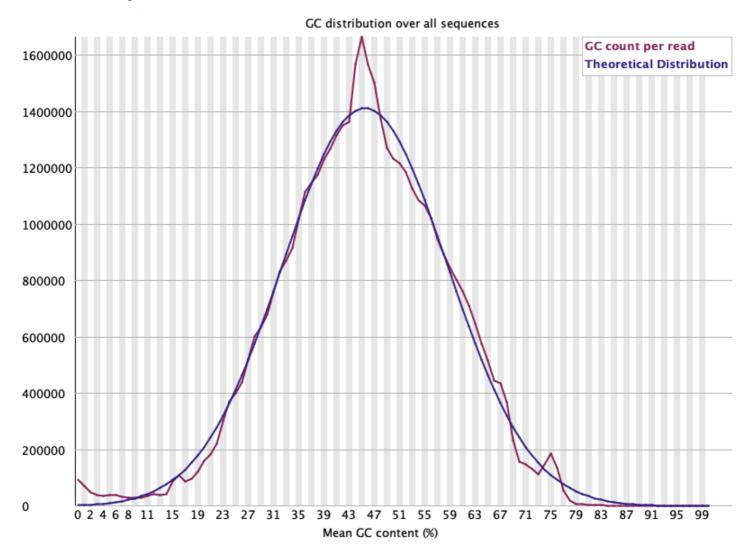
## Per sequence quality scores



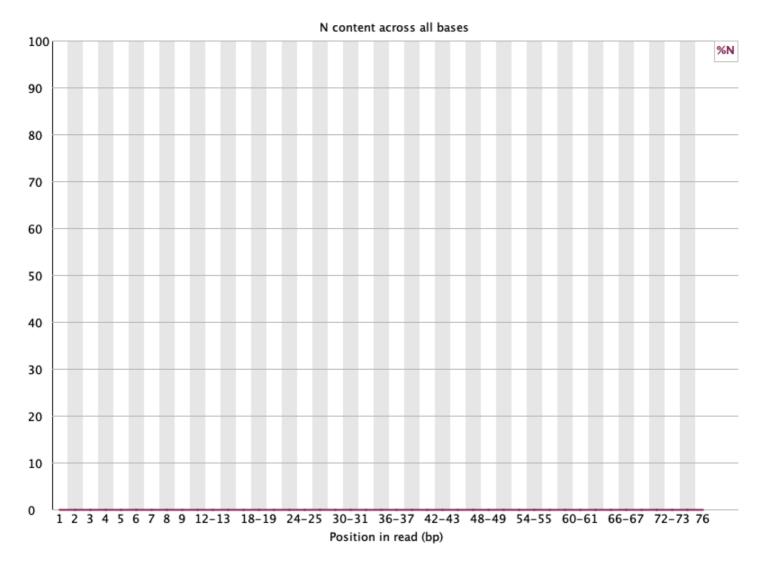
## Per base sequence content



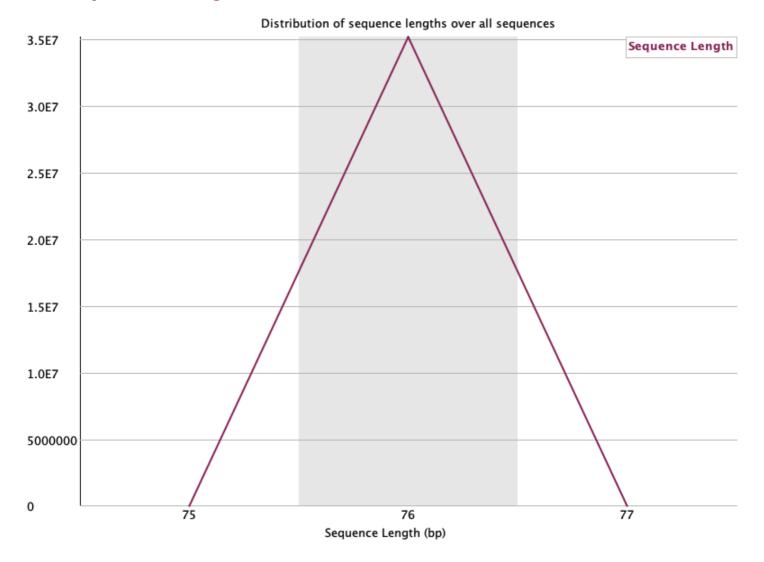
## Per sequence GC content



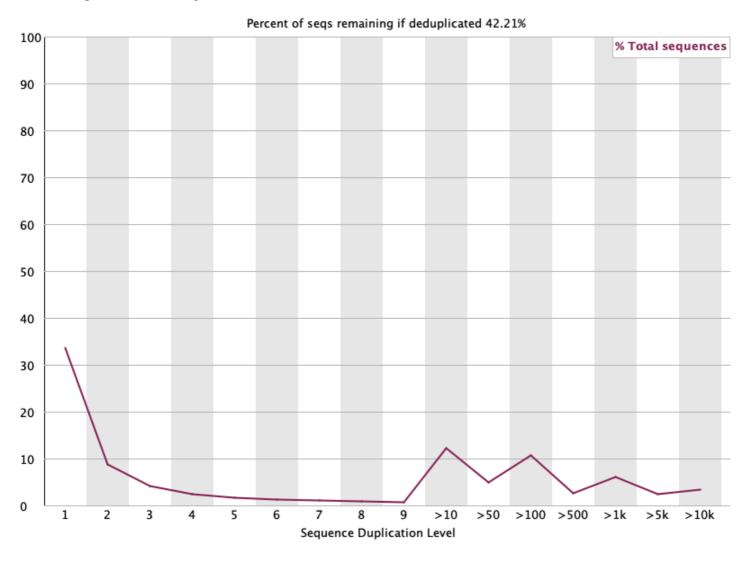
### Per base N content



## Sequence Length Distribution



### Sequence Duplication Levels



#### **Overrepresented sequences**

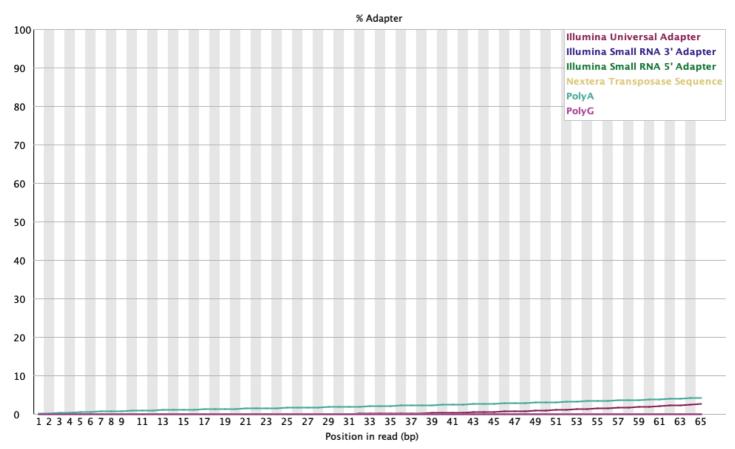
Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCAGCTGATCTCGTAT	728052	2.0695274020252517	TruSeq Adapter, Index 1 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	223881	0.6363939173202126	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	74802	0.2126287527900382	No Hit

Sequence Count

Percentage

Possible Source

#### Adapter Content



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