# **Report**

Mon 5 Feb 2024 SRR13380470\_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

SRR13380470\_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

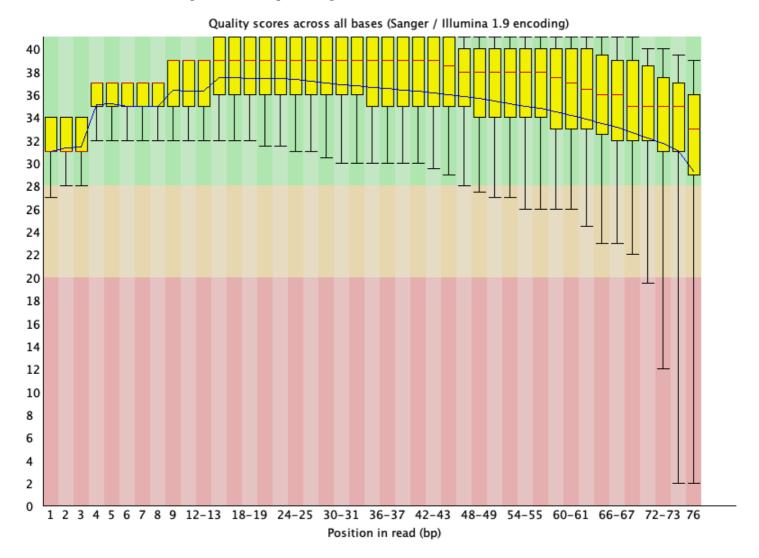
**Total Sequences** 35748776 Total Bases 2.7 Gbp

Sequences flagged as poor quality

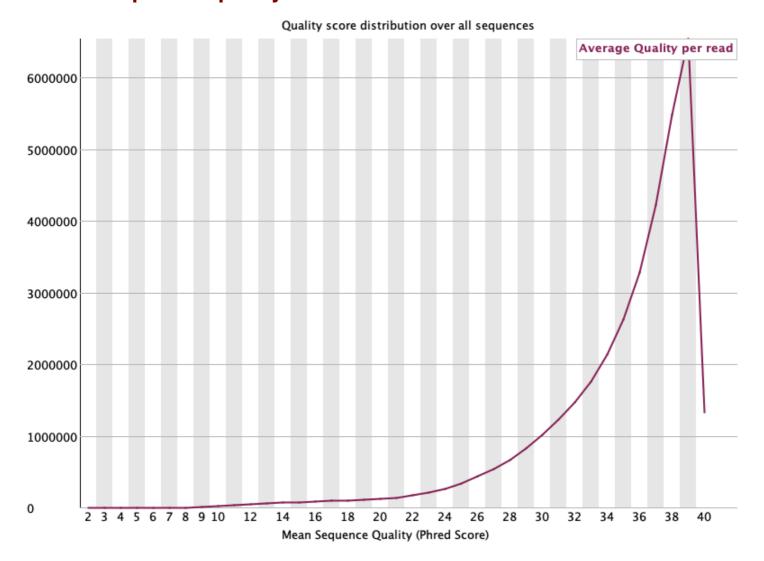
Sequence length 76

%GC 44

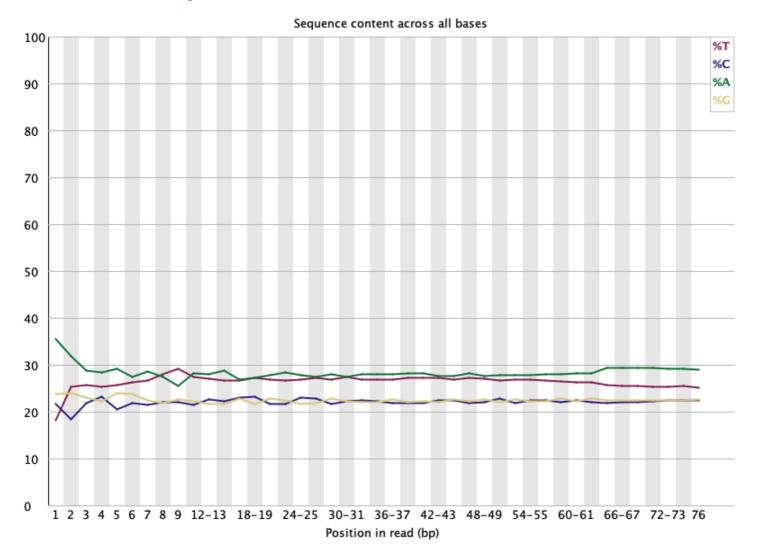
# Per base sequence quality



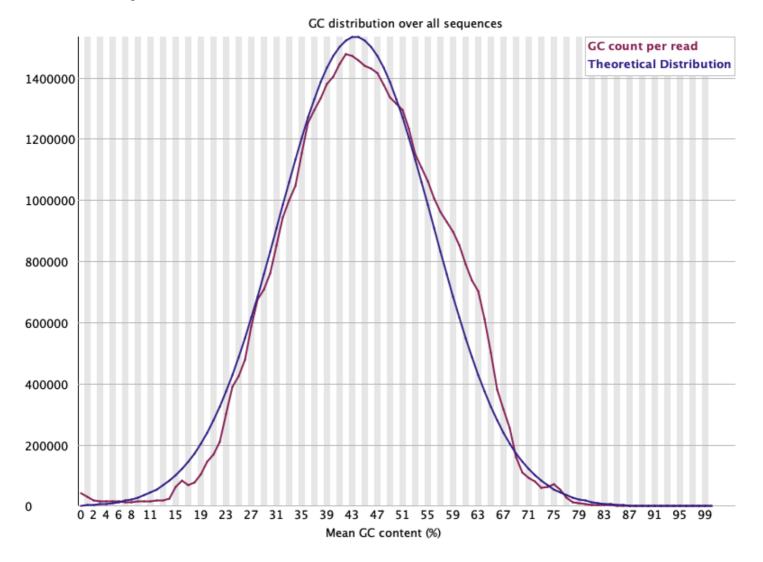
# Per sequence quality scores



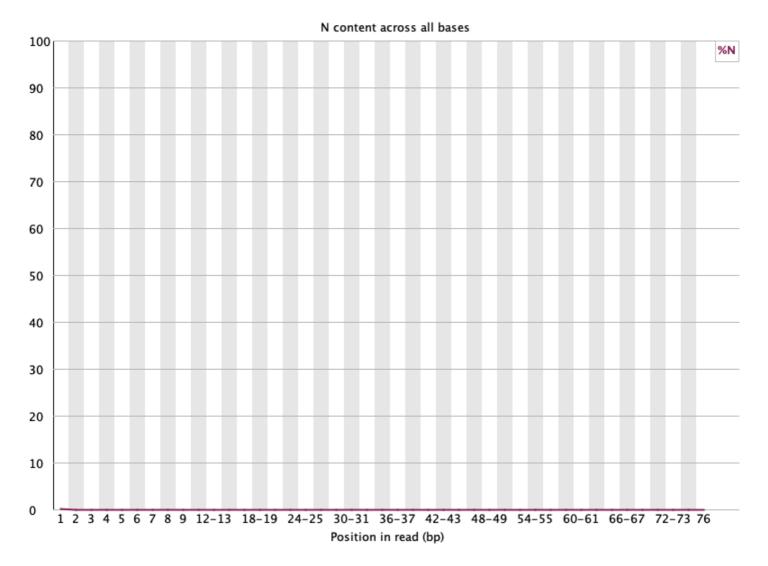
## Per base sequence content



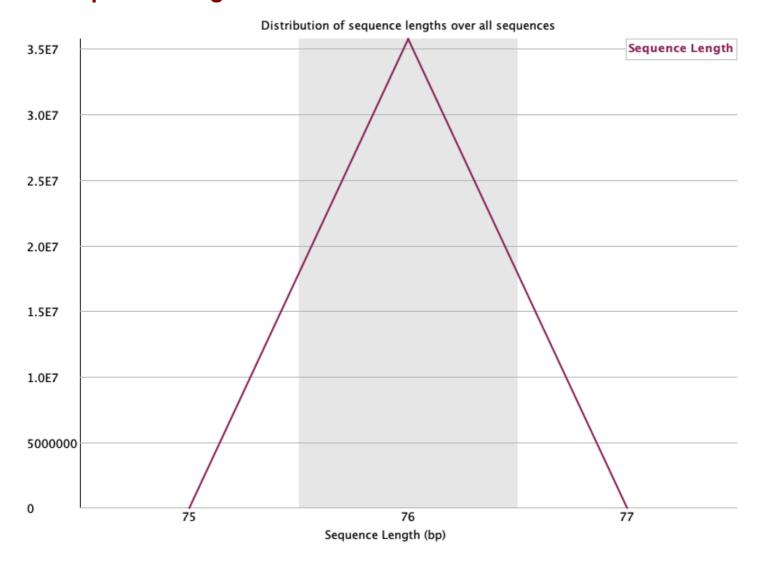
# Per sequence GC content



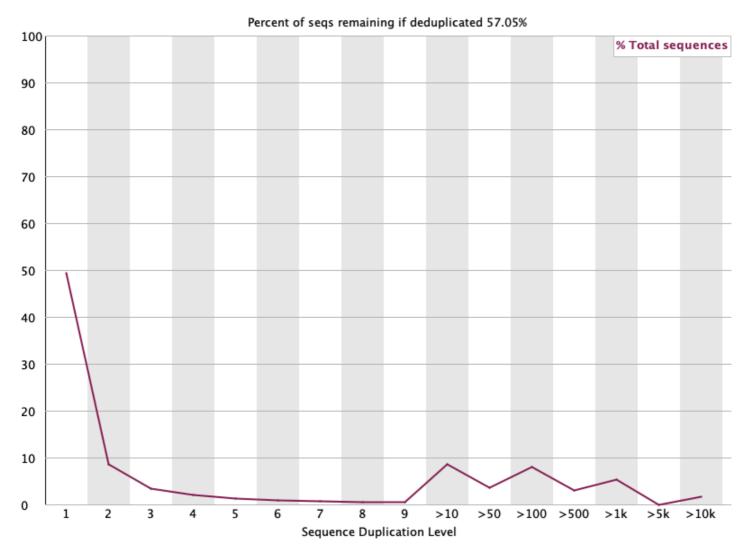
### Per base N content



# Sequence Length Distribution



#### Sequence Duplication Levels



#### Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACGATAATCTCGTATGC	308004	0.8615791488916992	TruSeq Adapter, Index 15 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	249976	0.6992575074458494	Clontech SMART CDS Primer II A (100% over 26bp)

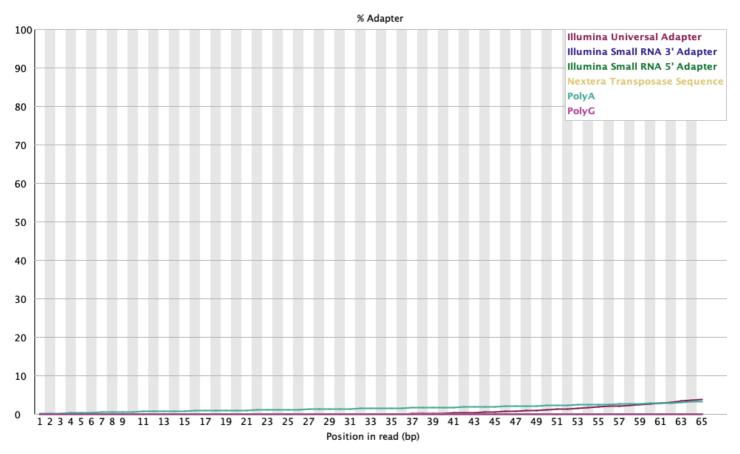
Sequence

Count

Percentage

Possible Source

#### Adapter Content



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