#### Mon 5 Feb 2024 SRR13380528\_1.fastq

# **PastQC Report**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 SRR13380528\_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 38590455

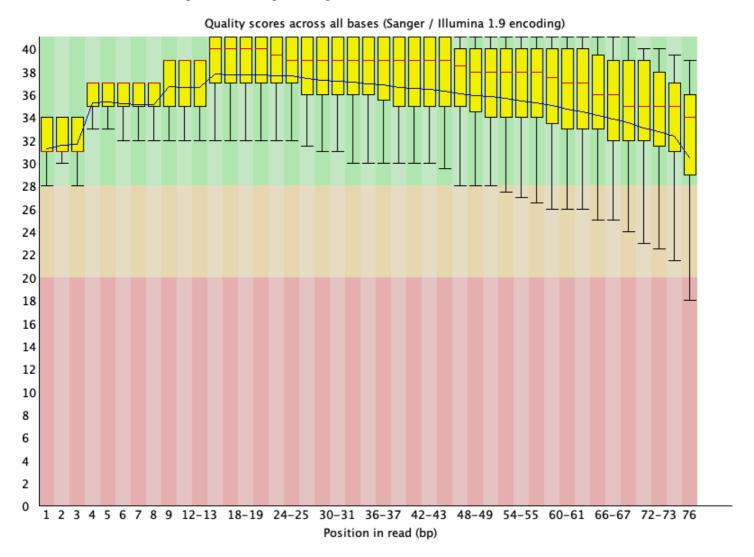
Total Bases 2.9 Gbp

Sequences flagged as poor quality  $\, {\bf 0} \,$ 

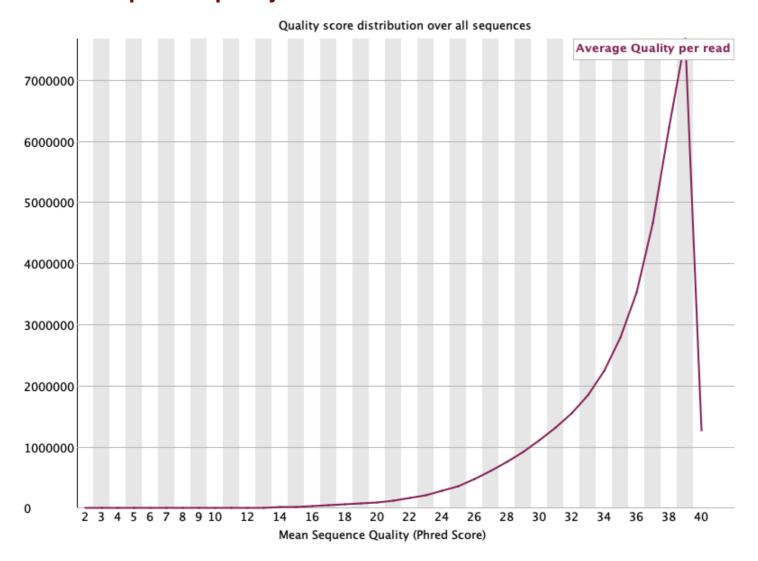
Sequence length 76

%GC 45

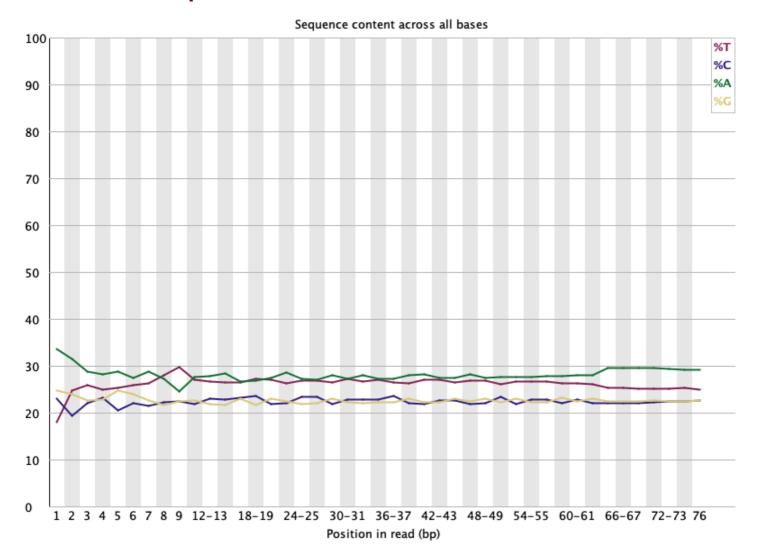
# Per base sequence quality



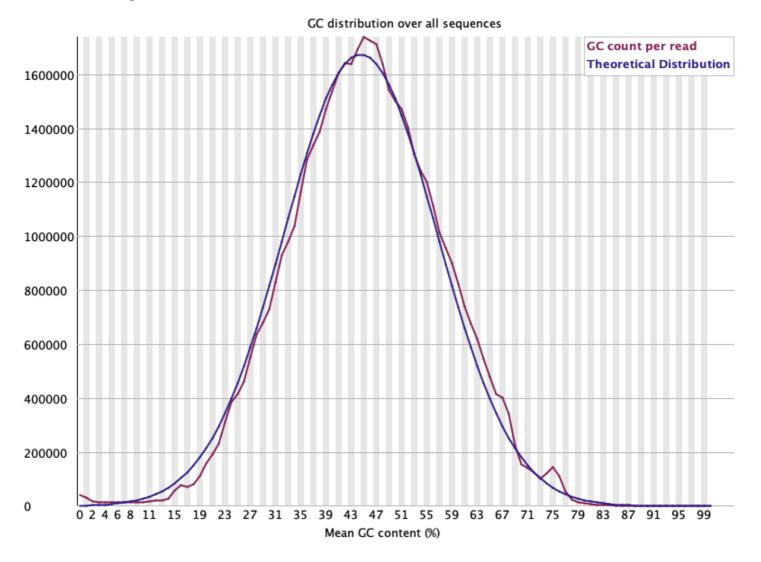
# Per sequence quality scores



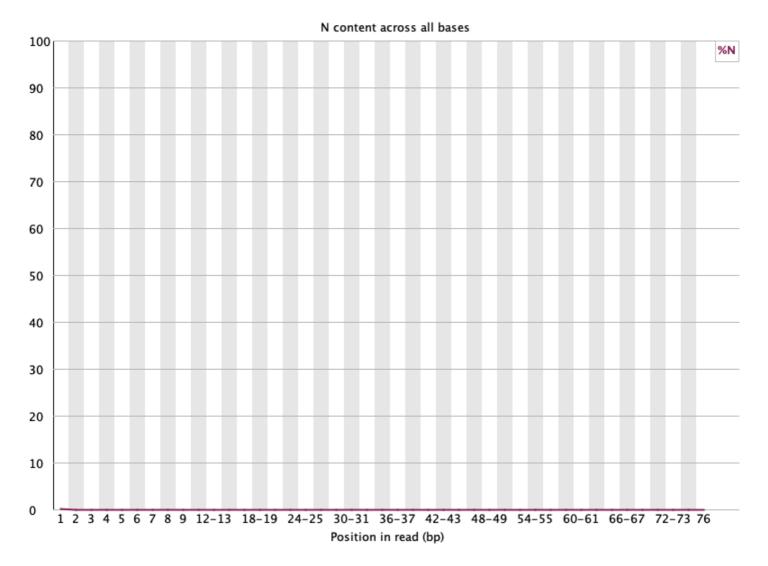
## Per base sequence content



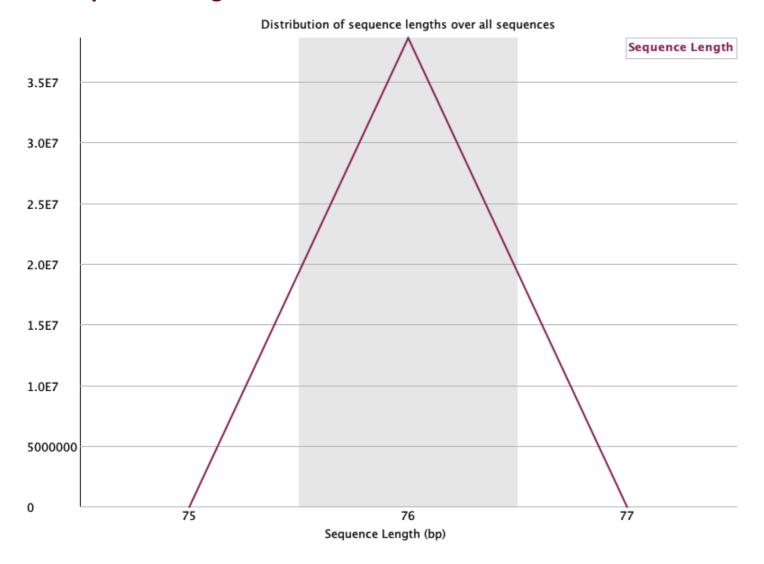
# Per sequence GC content



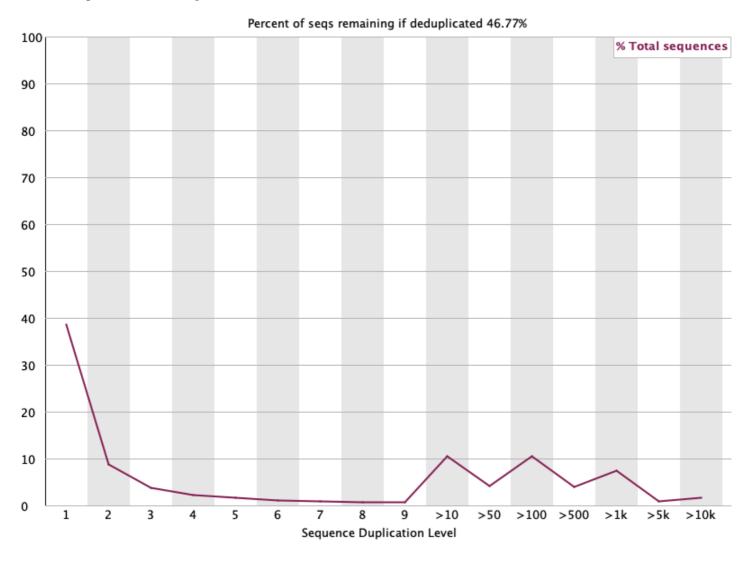
### Per base N content



# Sequence Length Distribution



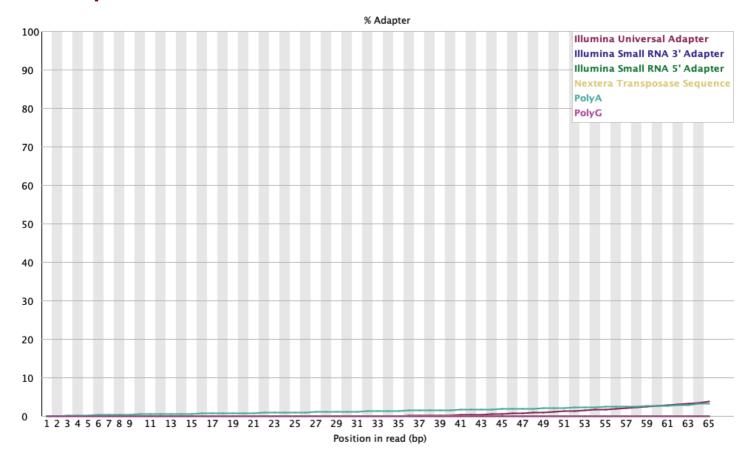
### Sequence Duplication Levels



#### **Overrepresented sequences**

Sequence		Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTC	CACTCCCGAATCTCGTATGC	489478	1.2683913677617948	TruSeq Adapter, Index 6 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	177693	0.46045842164856565	Clontech SMART CDS Primer II A (100% over 26bp)

# Adapter Content



Produced by FastQC (version 0.12.1)