Mon 5 Feb 2024 SRR13380499_1.fastq

ReportSummary

Basic Statistics

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 SRR13380499_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 40021269

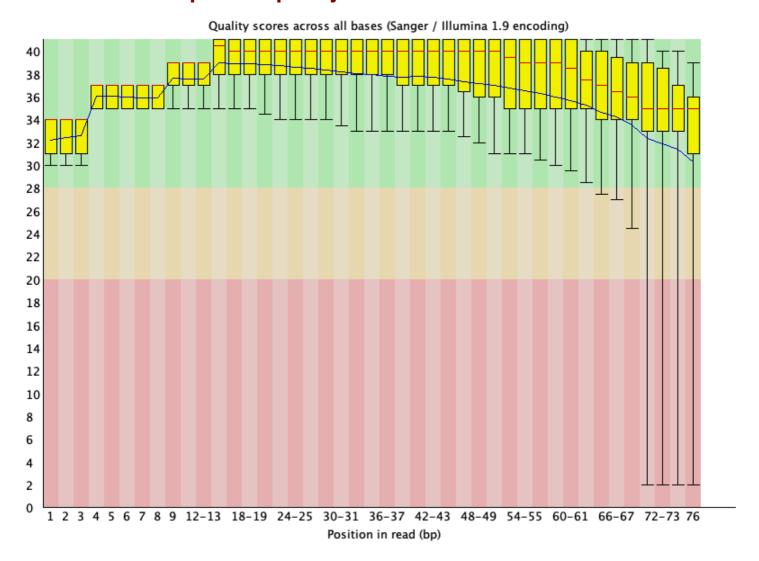
Total Bases 3 Gbp

Sequences flagged as poor quality 0

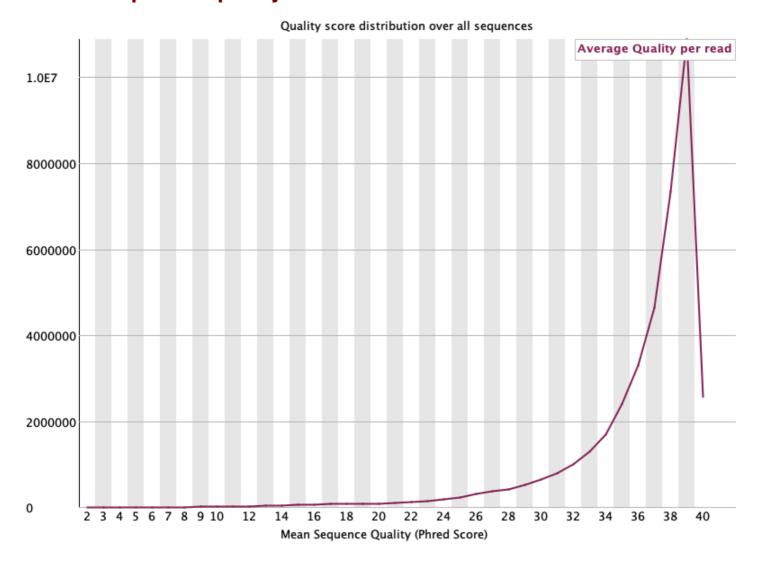
Sequence length 76

%GC 45

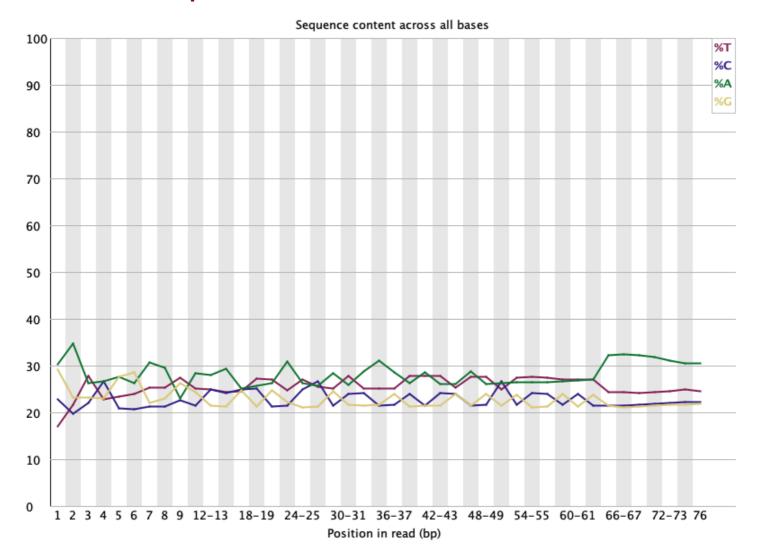
Per base sequence quality



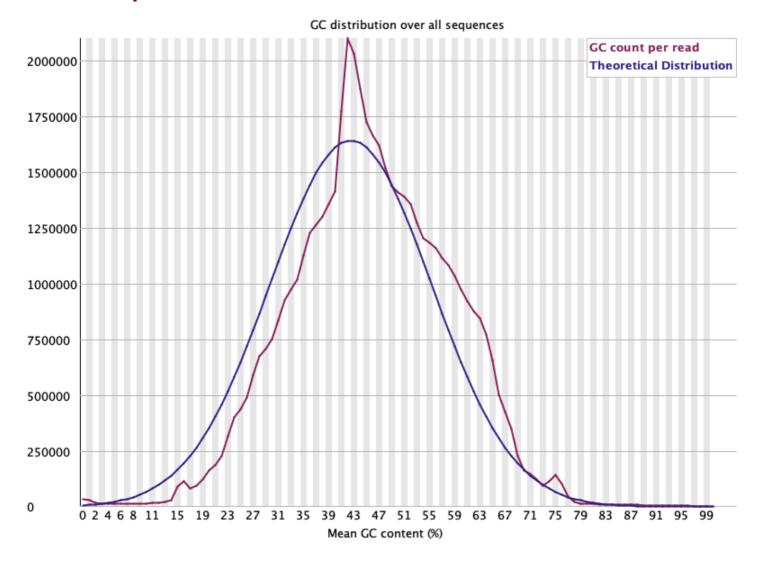
Per sequence quality scores



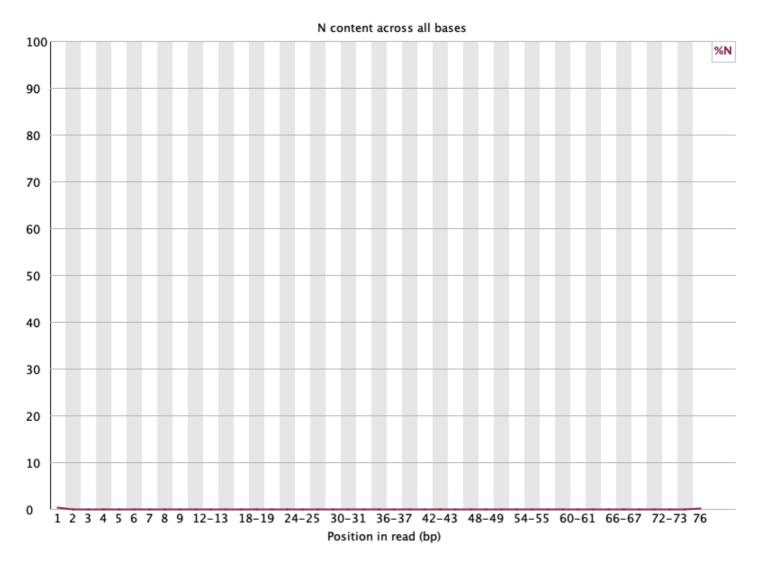
Per base sequence content



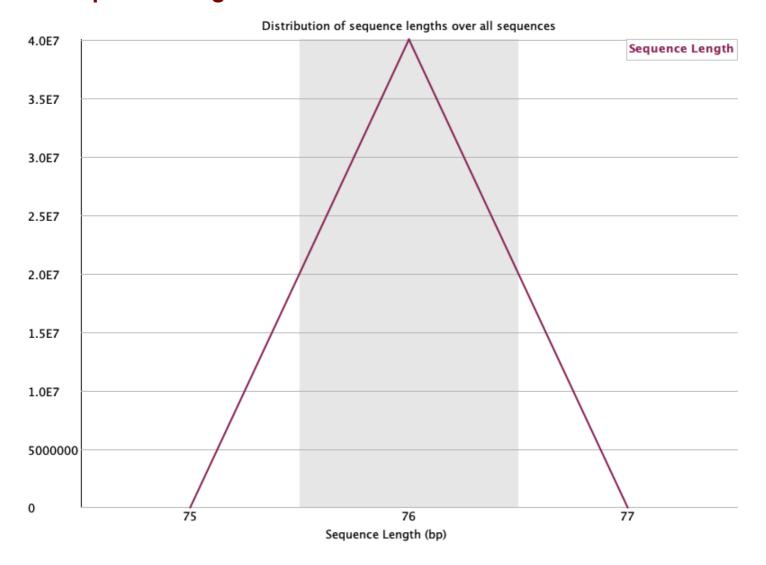
Per sequence GC content



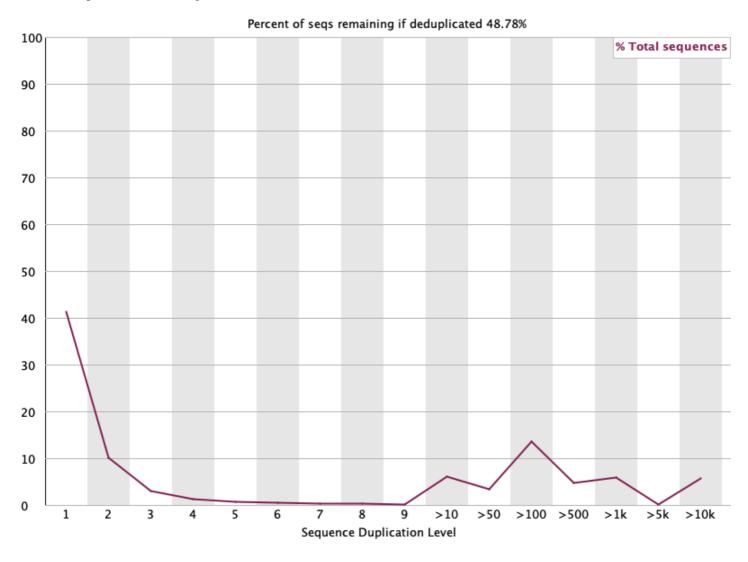
Per base N content



Sequence Length Distribution



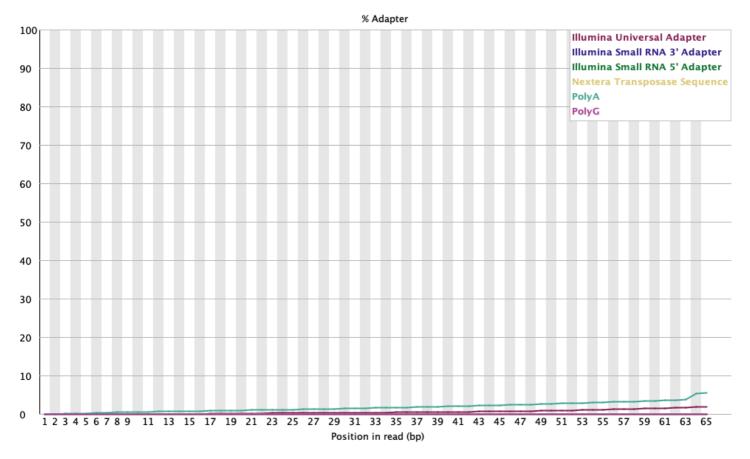
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGACCACGTCTGAACTCCAGTCACAAGACTATCTCGTATGC	1847366	4.615960578361471	TruSeq Adapter, Index 7 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	335511	0.8383317380565818	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)