Mon 5 Feb 2024 SRR13380497_1.fastq

Report

Summary



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 SRR13380497_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

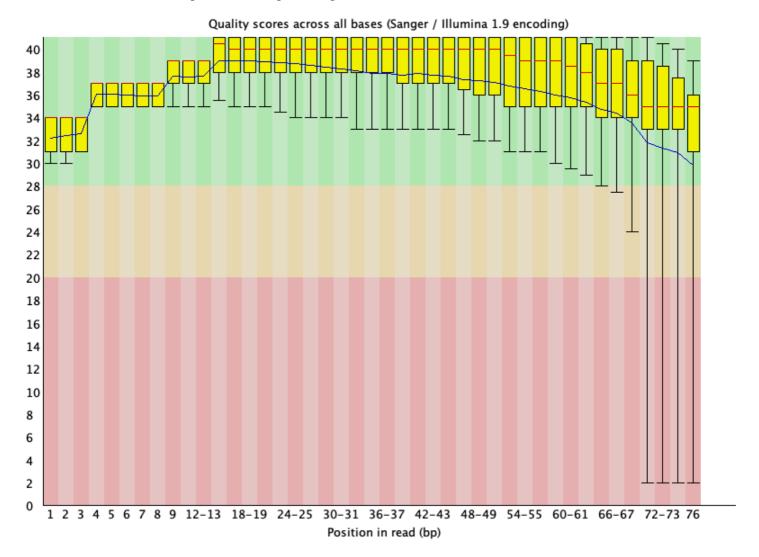
Total Sequences 36121631
Total Bases 2.7 Gbp

Sequences flagged as poor quality \emptyset

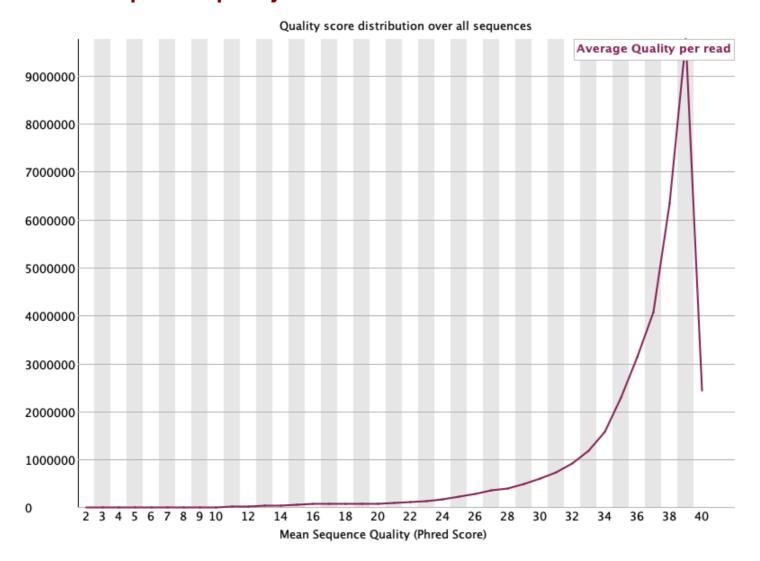
Sequence length 76

%GC 44

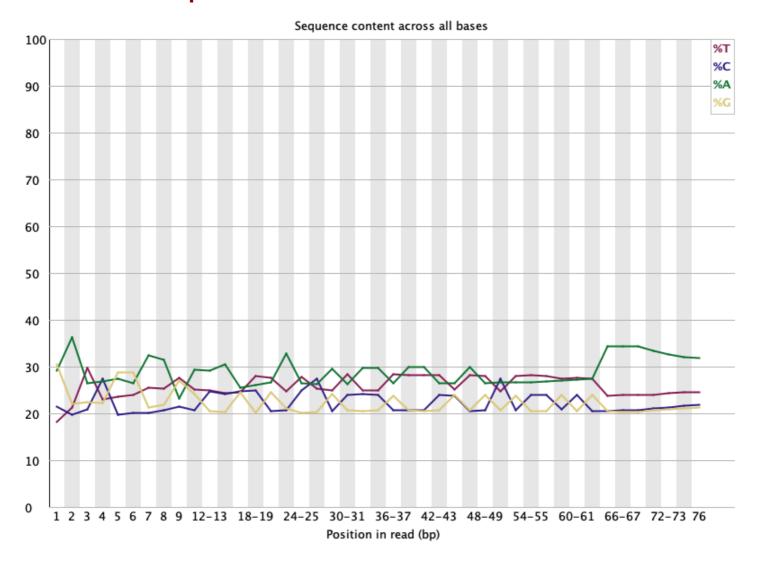
Per base sequence quality



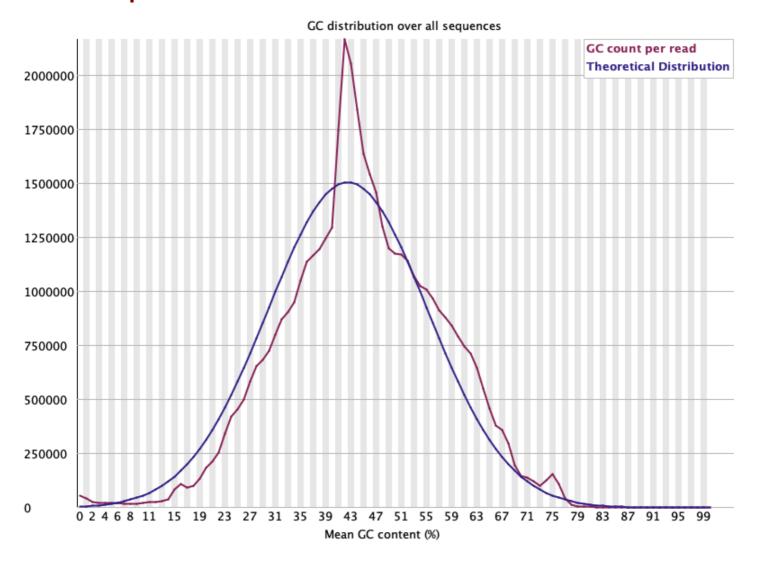
Per sequence quality scores



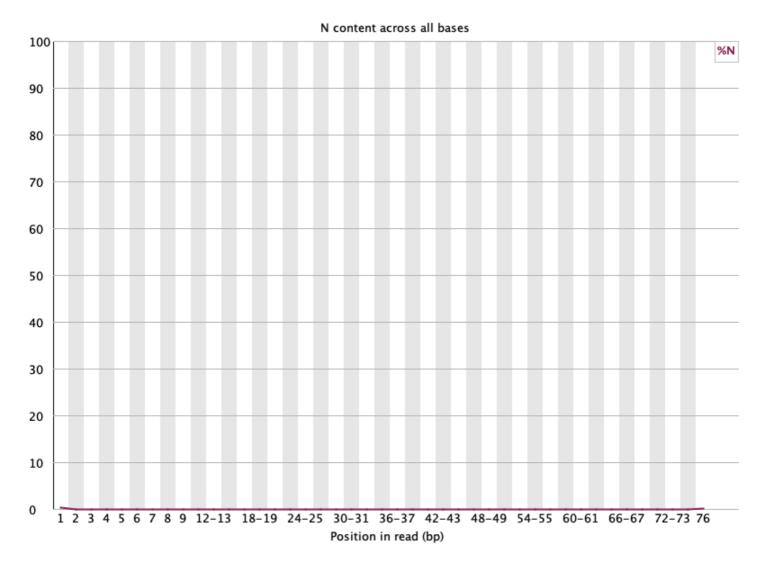
Per base sequence content



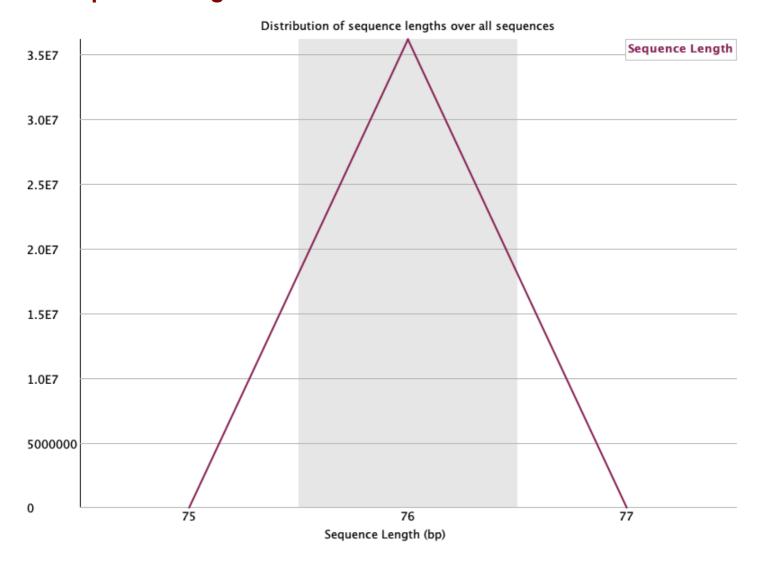
Per sequence GC content



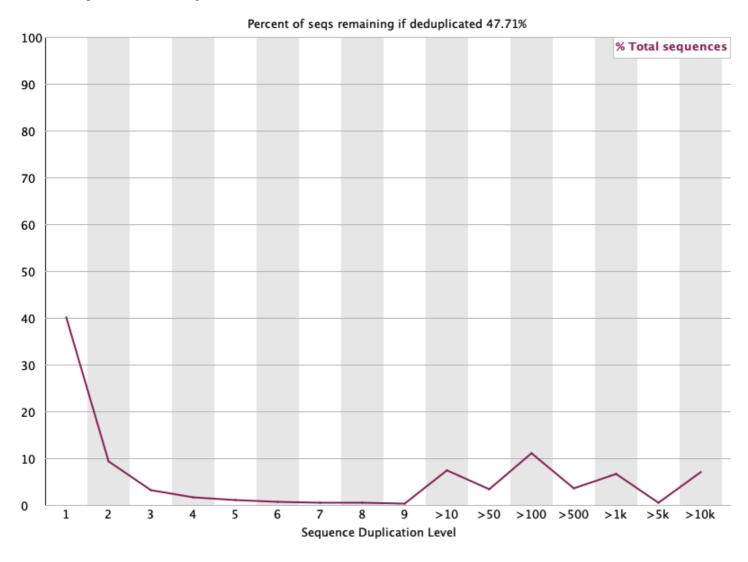
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATCTCGTATGC	2192094	6.068646235824733	TruSeq Adapter, Index 25 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	269682	0.7465941944869544	Clontech SMART CDS Primer II A (100% over 26bp)

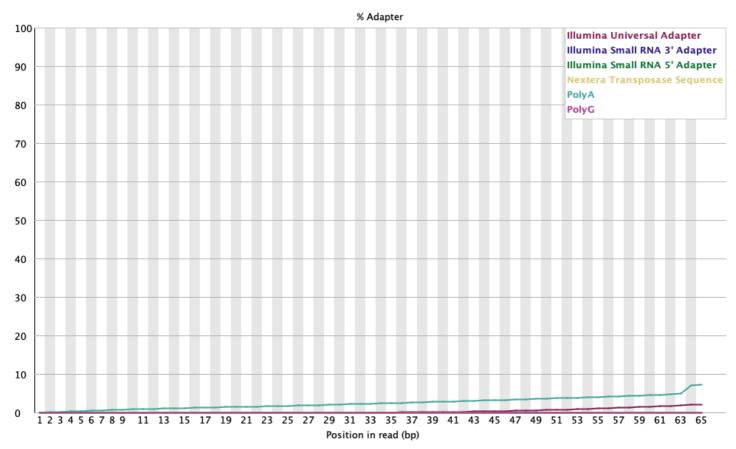
Sequence

Count

Percentage

Possible Source

Adapter Content



Produced by FastQC (version 0.12.1)