Mon 5 Feb 2024 SRR13380501_1.fastq

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

Basic Statistics

Measure Value

Filename SRR13380501_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

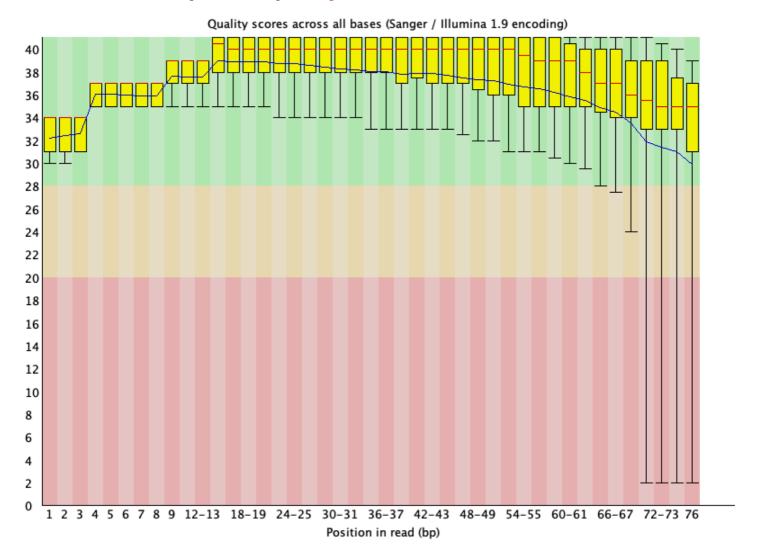
Total Sequences 36482122
Total Bases 2.7 Gbp

Sequences flagged as poor quality \emptyset

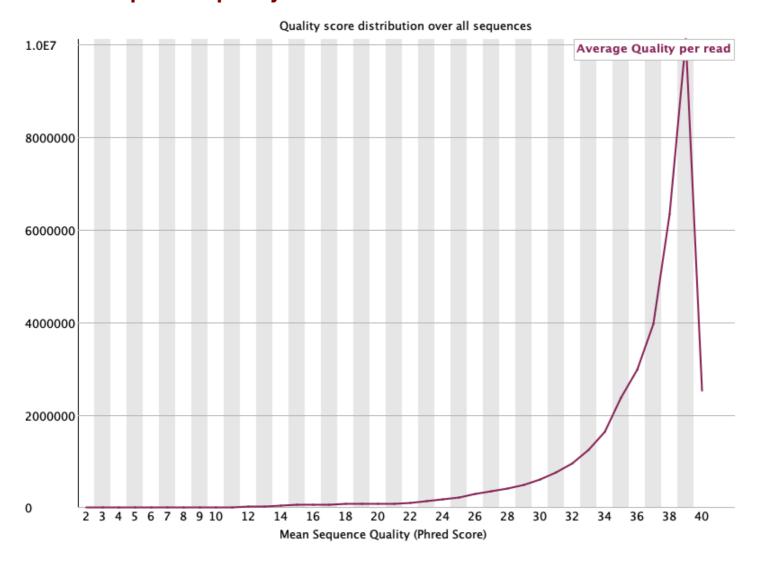
Sequence length 76

%GC 44

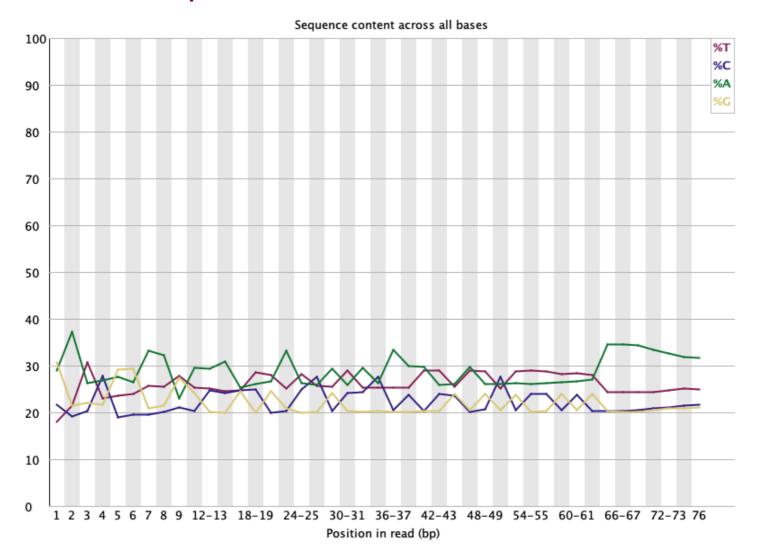
Per base sequence quality



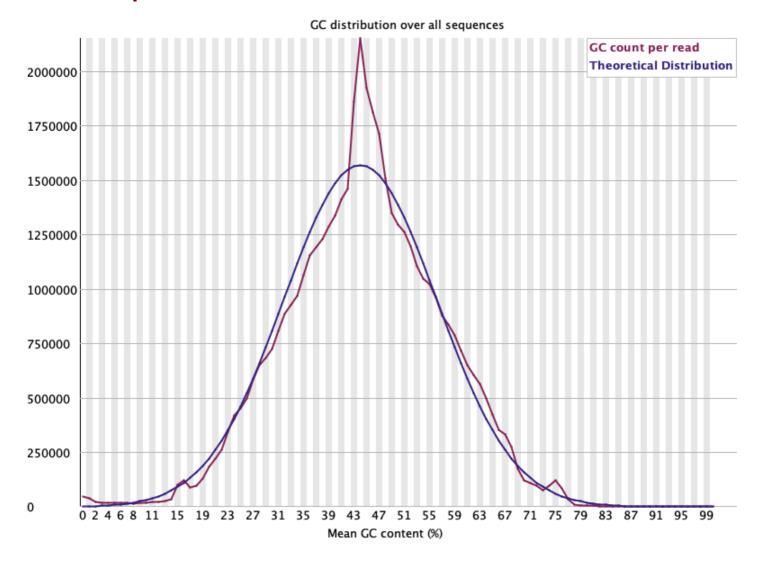
Per sequence quality scores



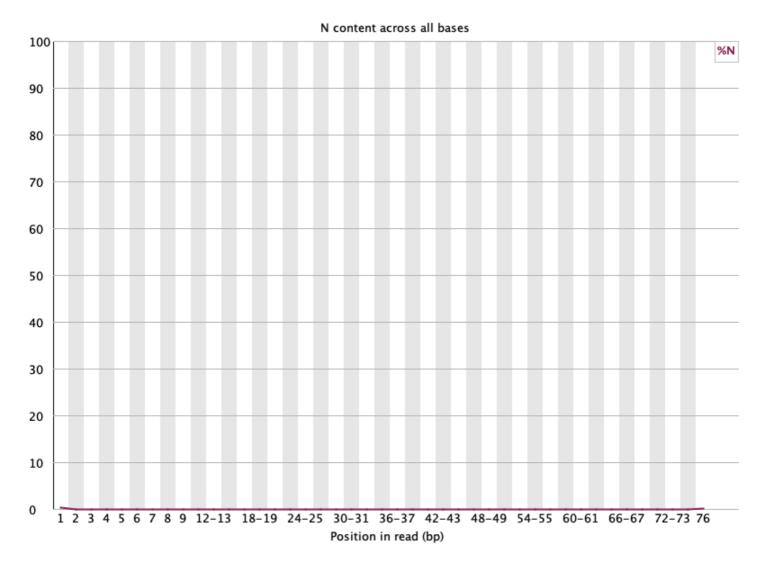
Per base sequence content



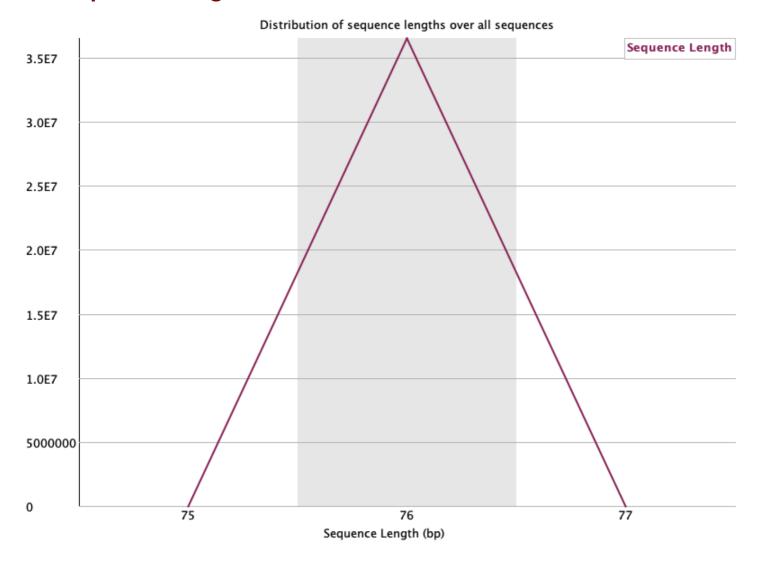
Per sequence GC content



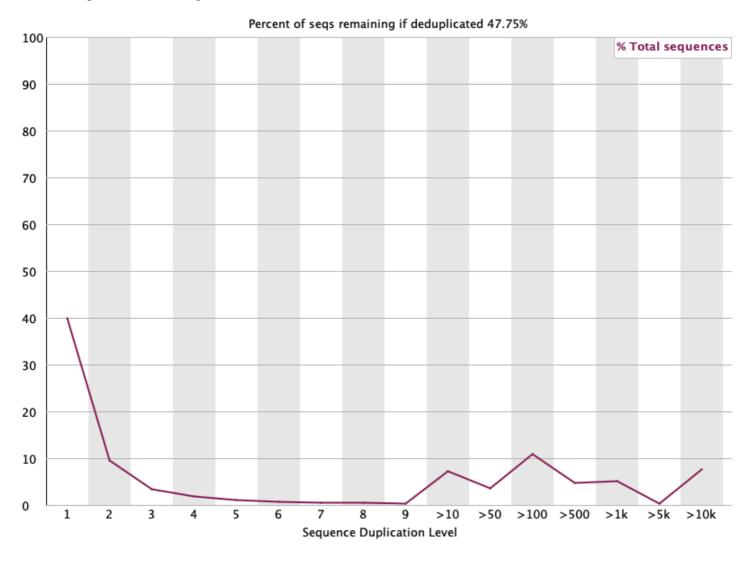
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCAACAATCTCGTATGC	2385396	6.538534134609823	TruSeq Adapter, Index 2 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	319250	0.875086158639566	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence

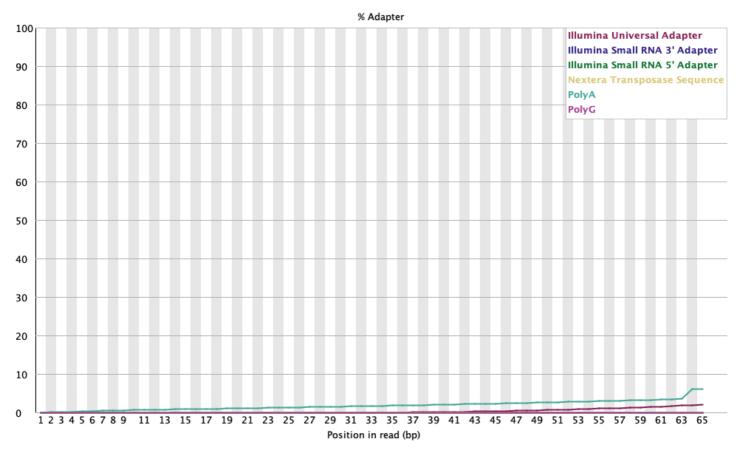
Count

Percentage

Possible Source

0.1006547809910838 No Hit

Adapter Content



Produced by FastQC (version 0.12.1)