Mon 5 Feb 2024 SRR13380500_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 SRR13380500_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 45158118

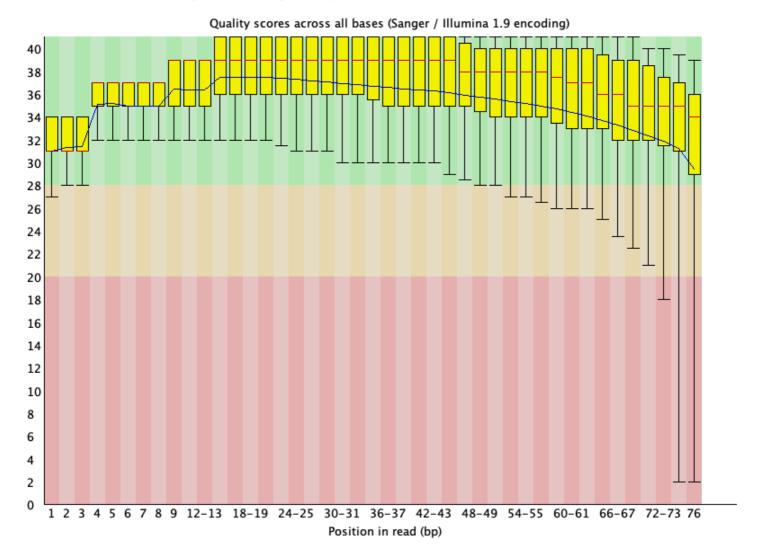
Total Bases 3.4 Gbp

Sequences flagged as poor quality 0

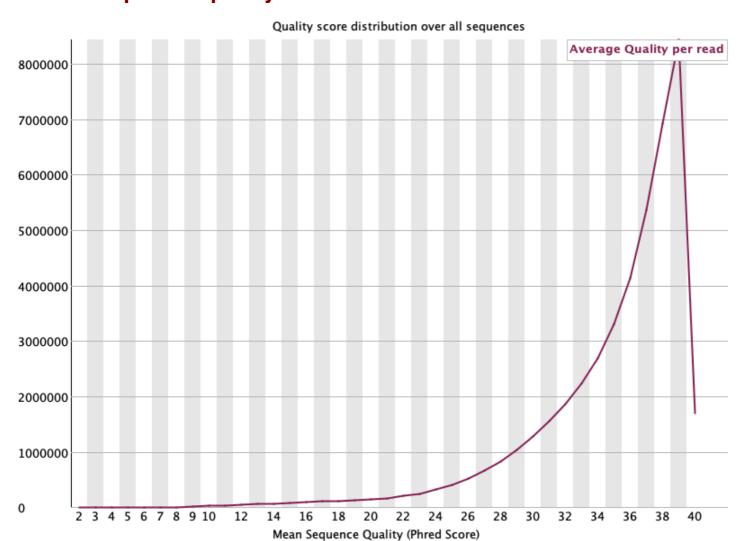
Sequence length 76

%GC 45

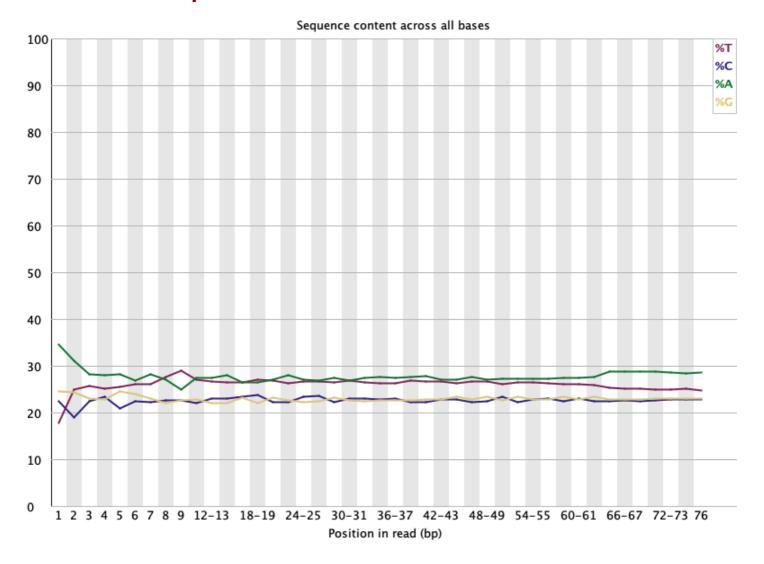
Per base sequence quality



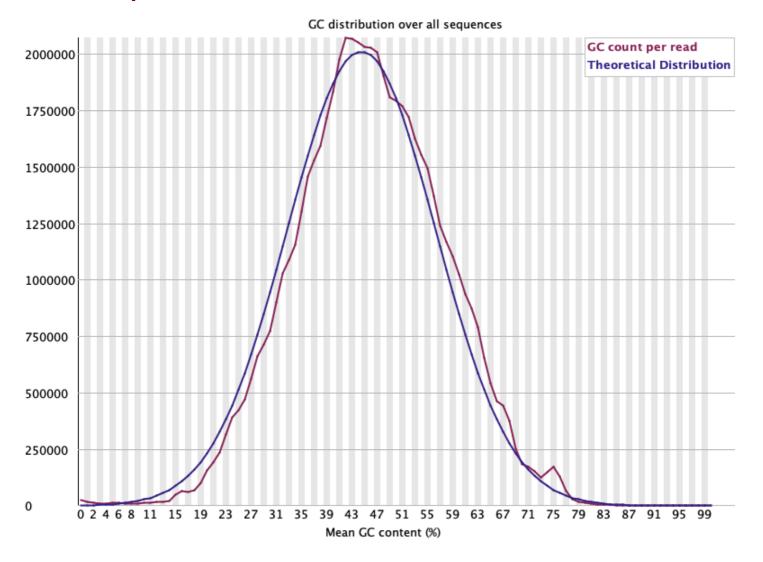
Per sequence quality scores



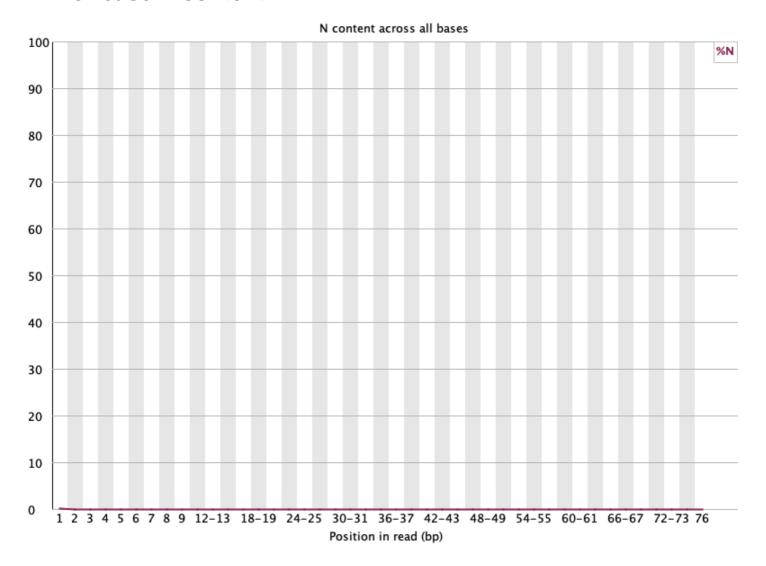
Per base sequence content



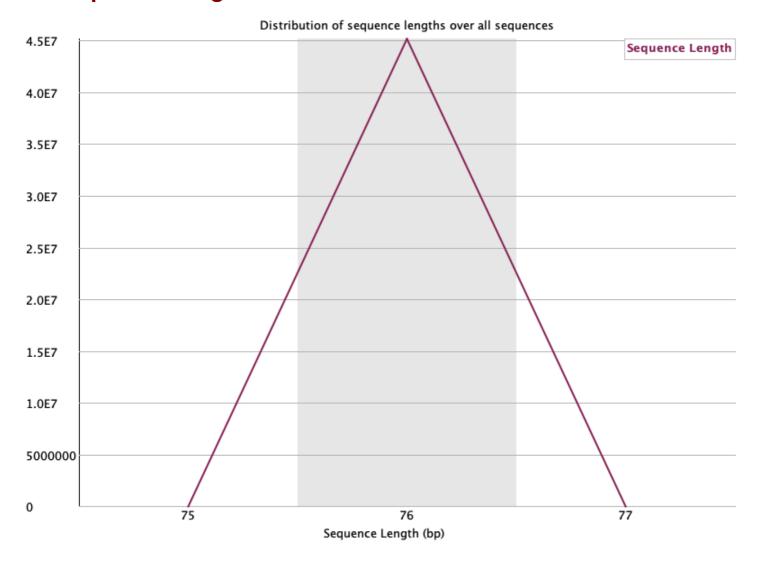
Per sequence GC content



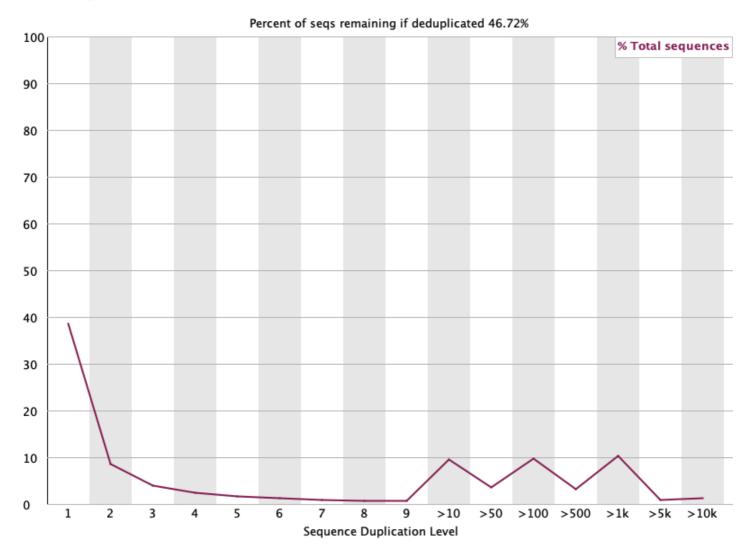
Per base N content



Sequence Length Distribution



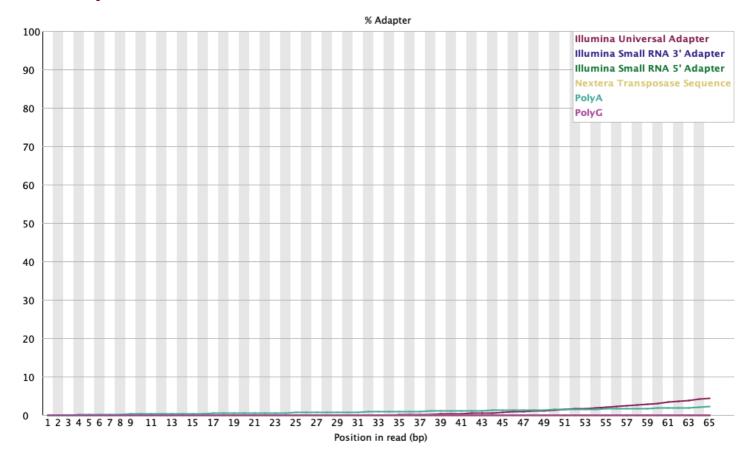
Sequence Duplication Levels



Overrepresented sequences

	Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTC	CTGAACTCCAGTCACCAACTAATCTCGTATGC	456607	1.011129383204145	TruSeq Adapter, Index 23 (97% over 38bp)
AAGCAGTGGTATCAACGCA	AGAGTACTTTTTTTTTTTTTTTTTTTTTT	168327	0.372750255003984	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)