Mon 5 Feb 2024 SRR13380458_1.fastq

ReportSummary



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 SRR13380458_1.fastq

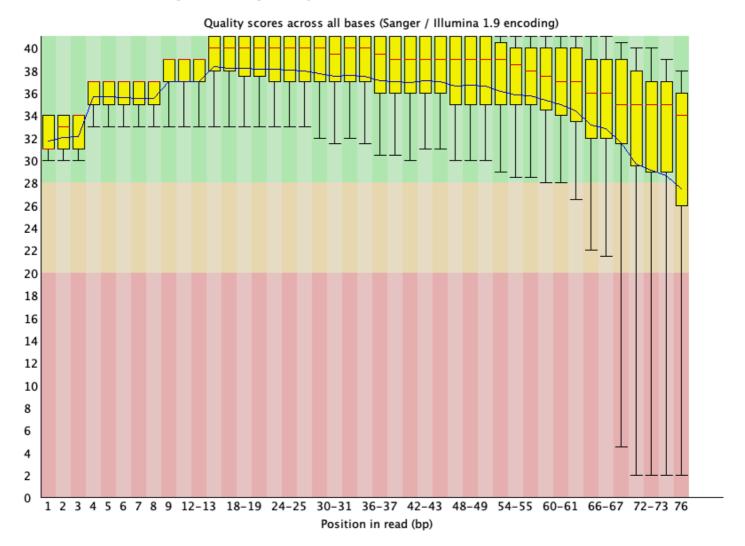
File type Conventional base calls

Encoding Sanger / Illumina 1.9

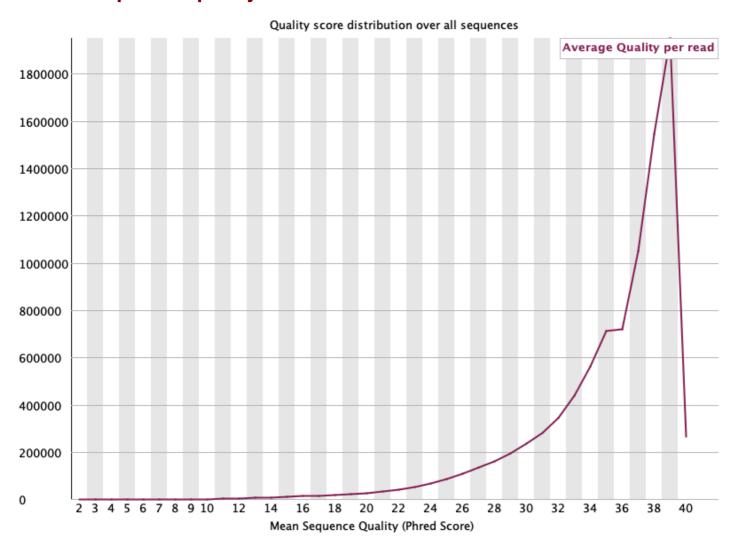
Total Sequences 9176804
Total Bases 697.4 Mbp

Sequences flagged as poor quality 0
Sequence length 76
%GC 46

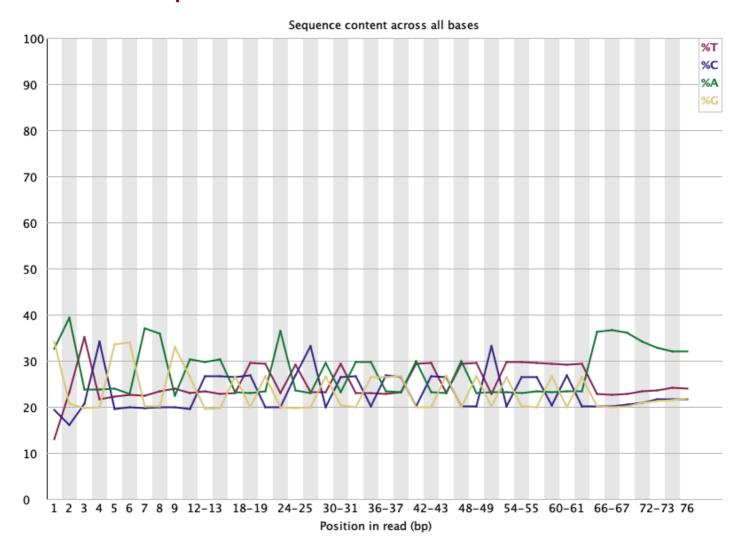
Per base sequence quality



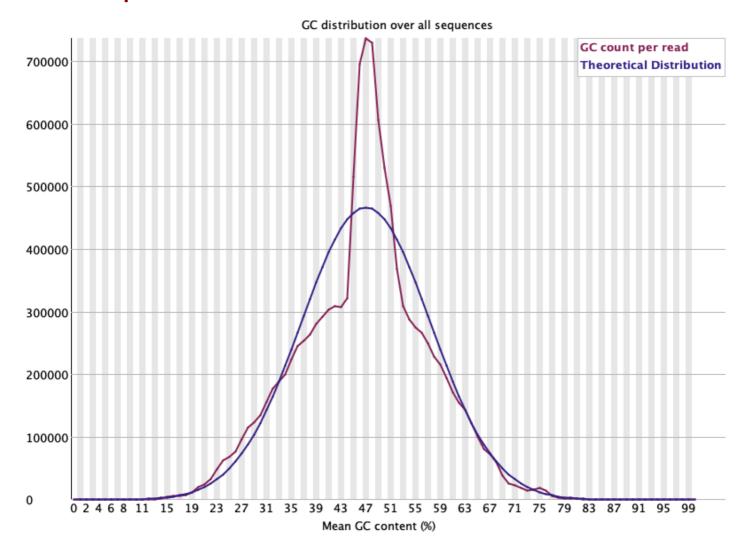
Per sequence quality scores



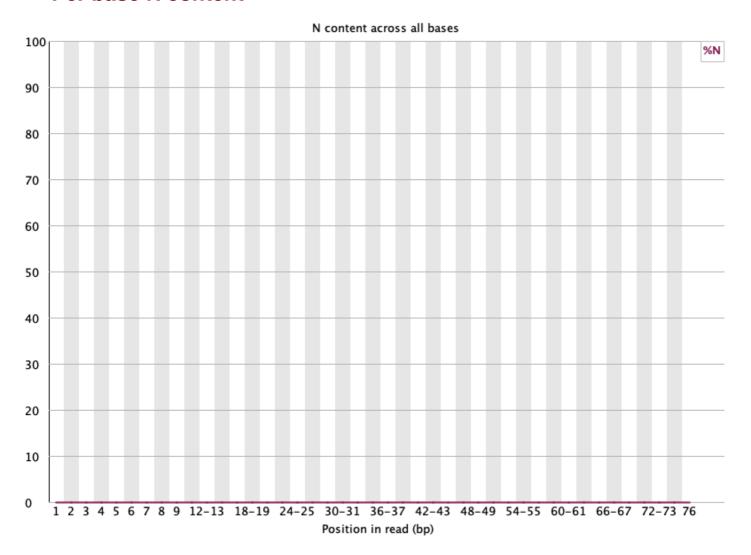
Per base sequence content



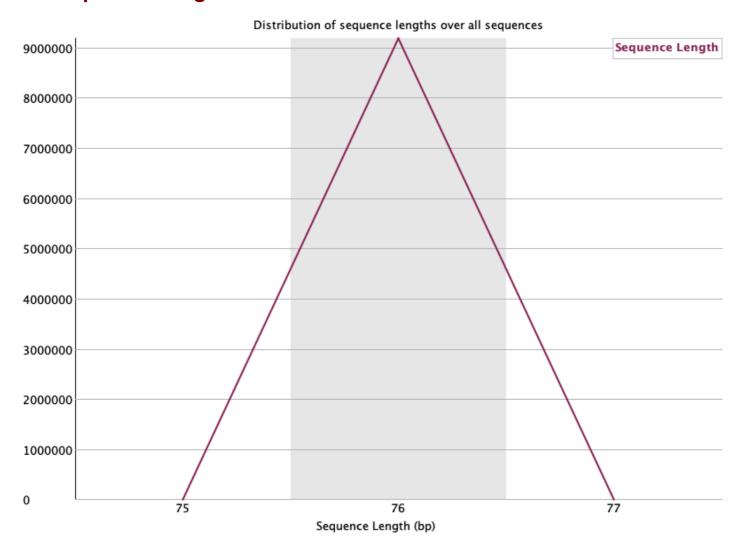
Per sequence GC content



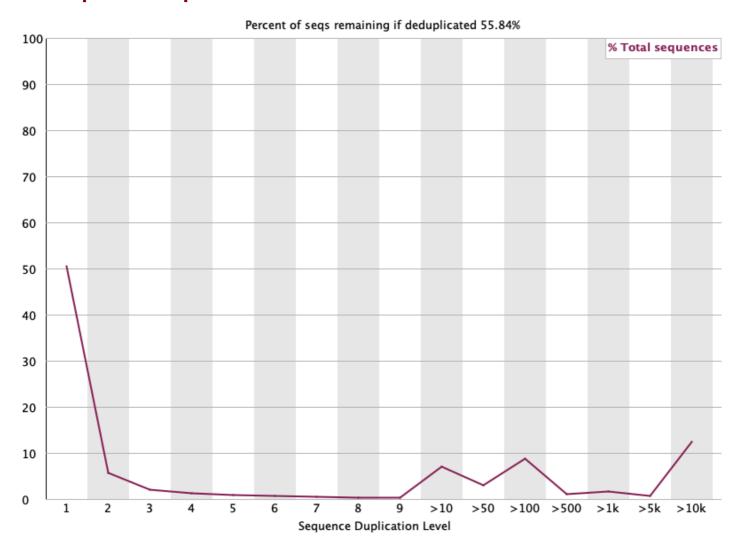
Per base N content



Sequence Length Distribution



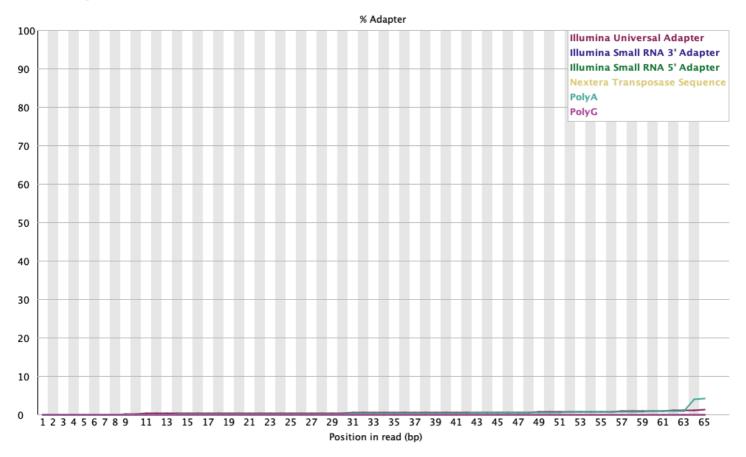
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGGCCGATCTCGTATGC	1101485	12.002926073173189	TruSeq Adapter, Index 13 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	28403	0.3095086263147824	Clontech SMART CDS Primer II A (100% over 26bp)
CGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACAGGCCGAT	21357	0.23272808267453463	TruSeq Adapter, Index 13 (97% over 37bp)
AGCAGTGGTATCAACGCAGAGTAAGCAGTGGTATCAACGCAGAGTAAGCA	9410	0.10254114613322896	Clontech SMARTer II A Oligonucleotide (95% over 24bp)

Adapter Content



Produced by FastQC (version 0.12.1)