Mon 5 Feb 2024 SRR13380516_1.fastq

PastQC 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 SRR13380516_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

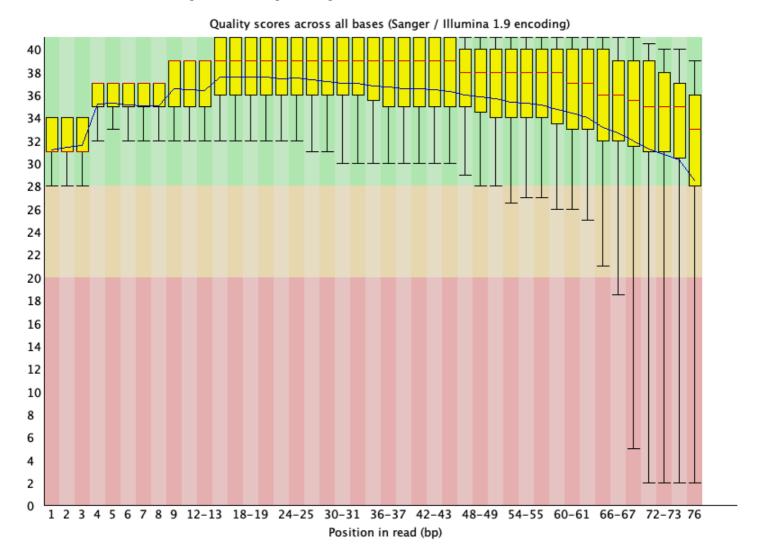
Total Sequences 32665015
Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

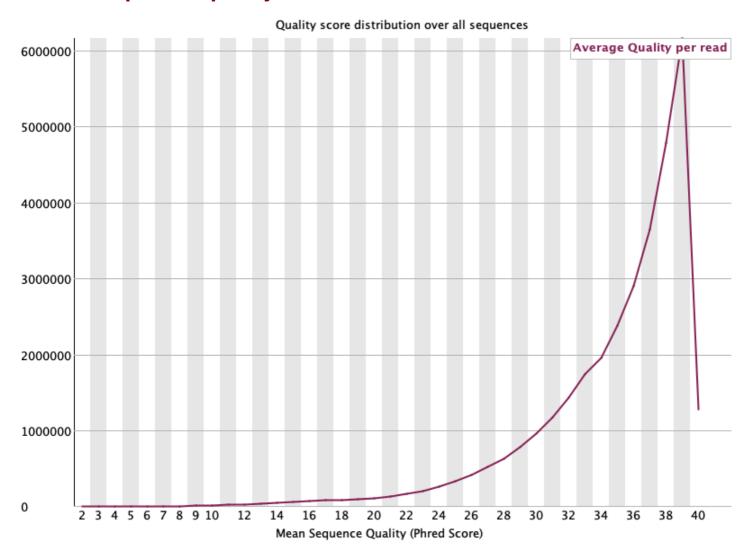
Sequence length 76

%GC 43

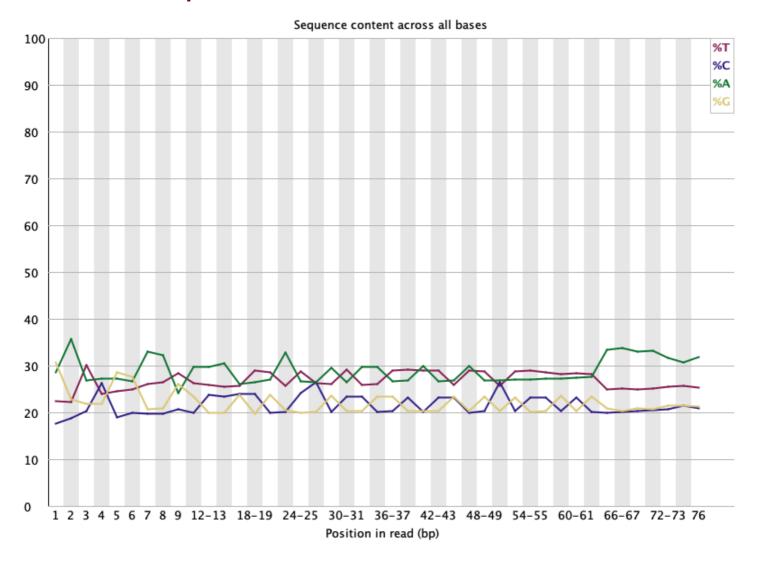
Per base sequence quality



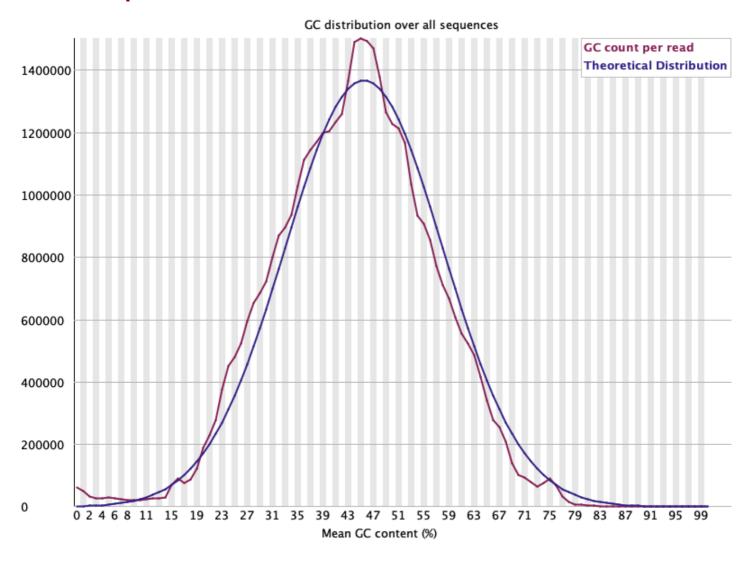
Per sequence quality scores



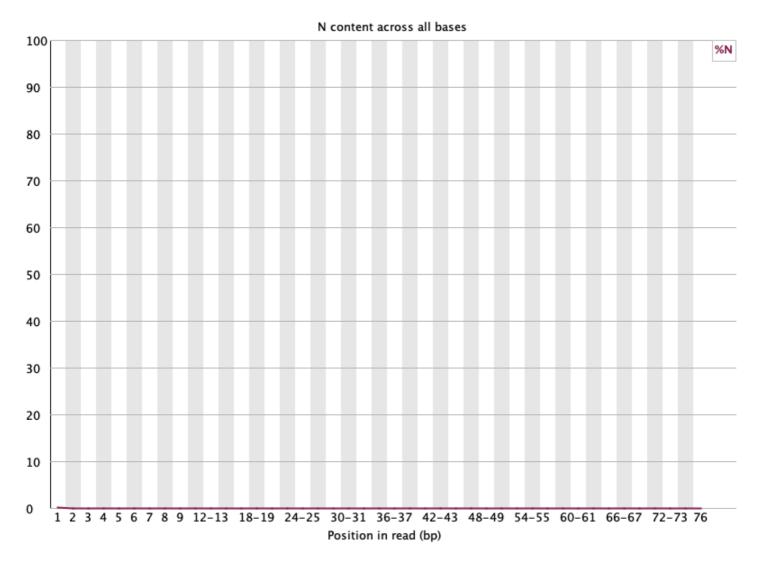
Per base sequence content



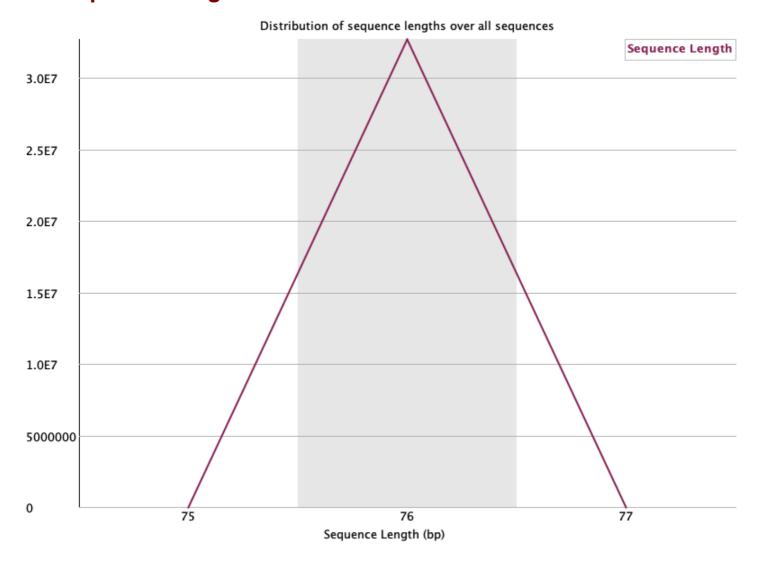
Per sequence GC content



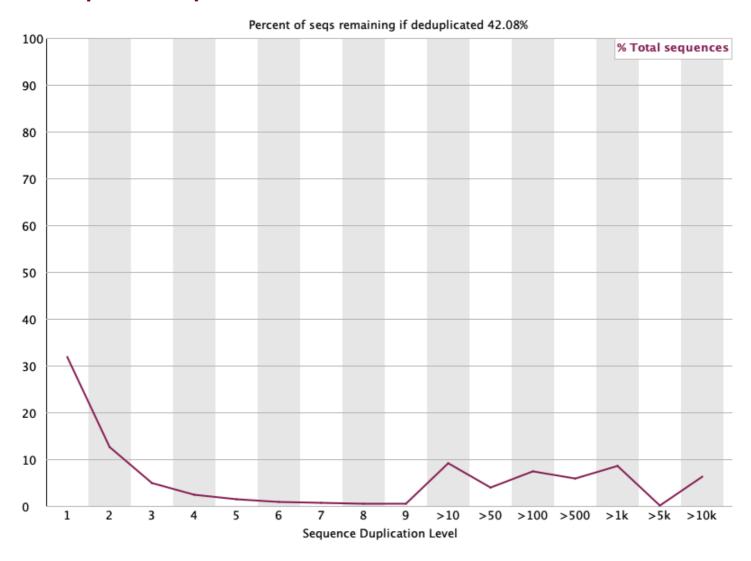
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATGCTATCTCGTATGC	1801161	5.514036959725872	TruSeq Adapter, Index 9 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	188608	0.5774006226539311	Clontech SMART CDS Primer II A (100% over 26bp)

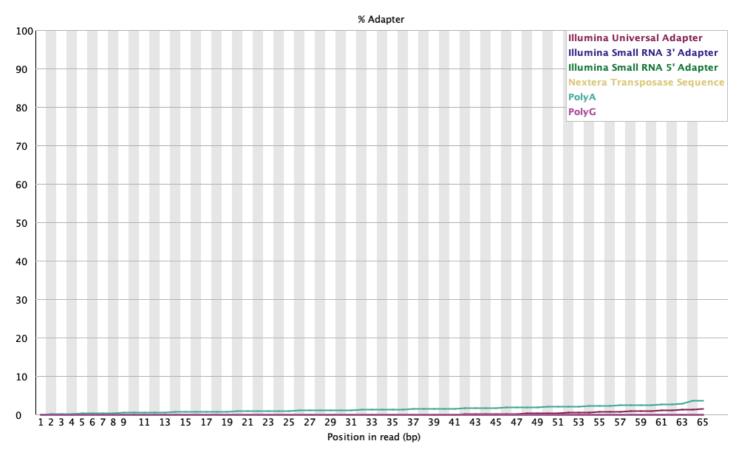
Sequence

Count

Percentage

Possible Source

Adapter Content



Produced by FastQC (version 0.12.1)