Report

Tue 6 Feb 2024 SRR13380539_1.fastq

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



Measure Value

SRR13380539_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

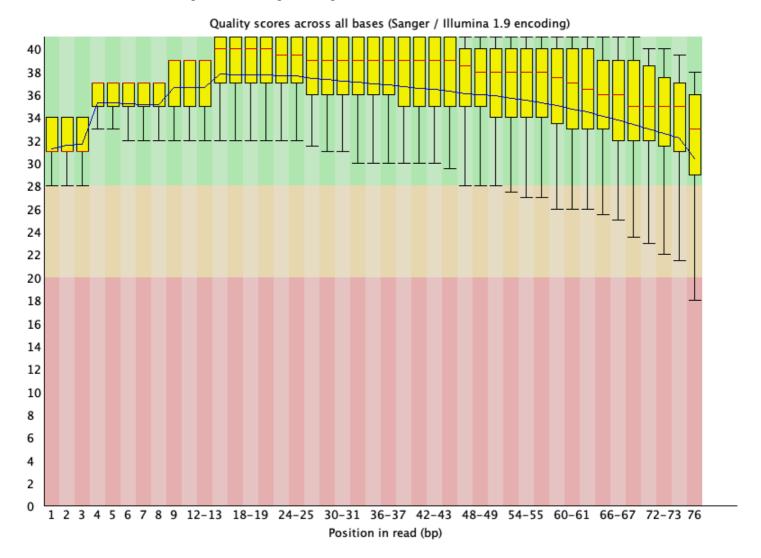
Total Sequences 32503721 Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

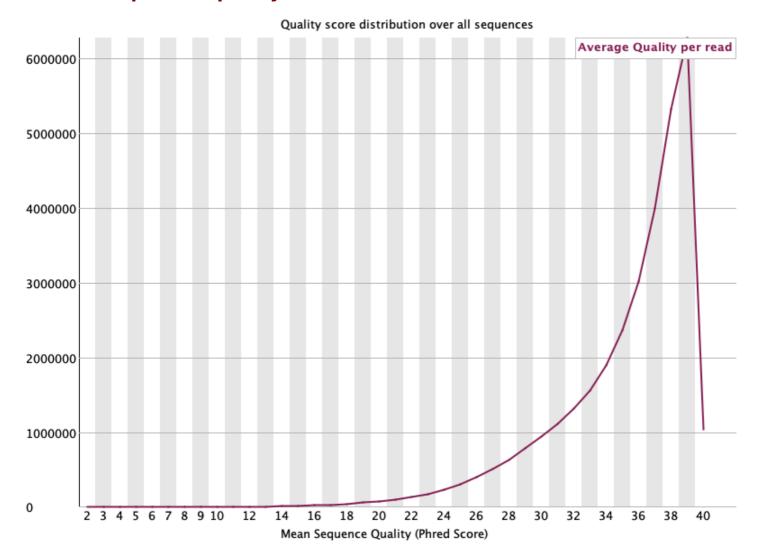
Sequence length 76

%GC 45

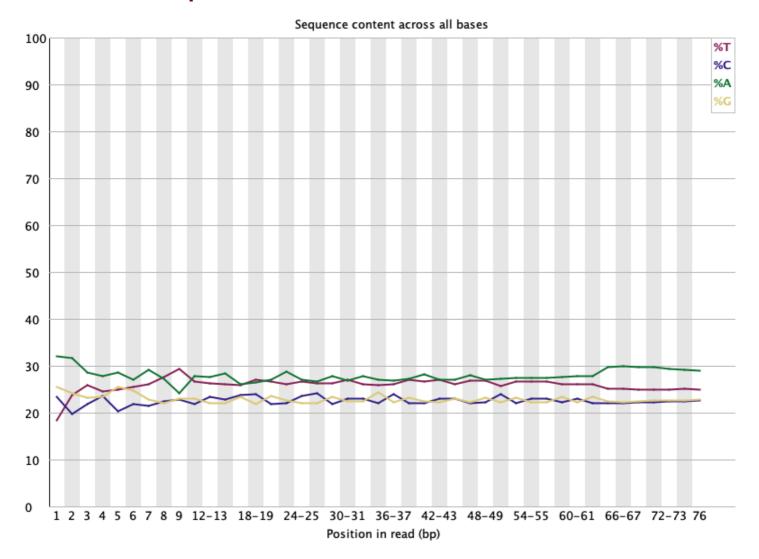
Per base sequence quality



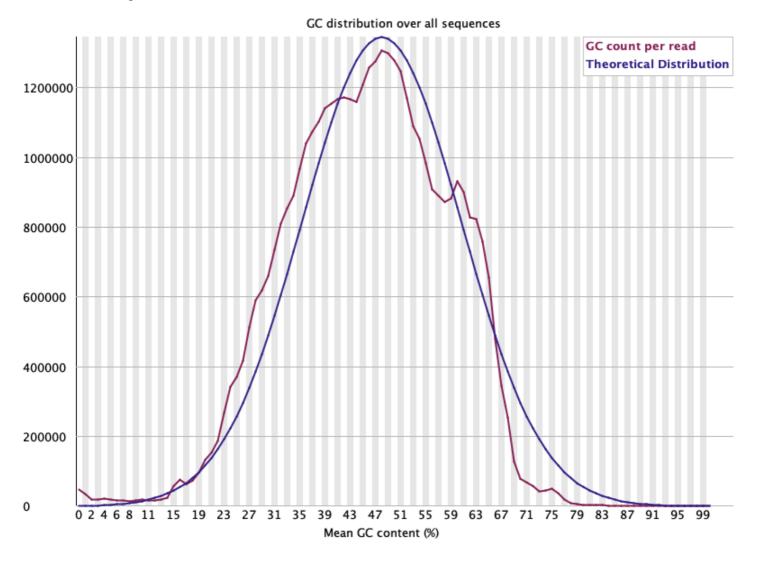
Per sequence quality scores



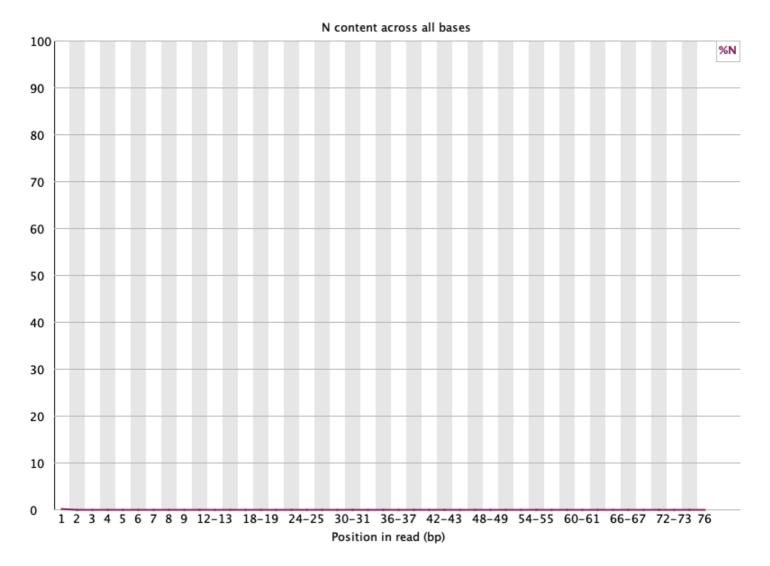
Per base sequence content



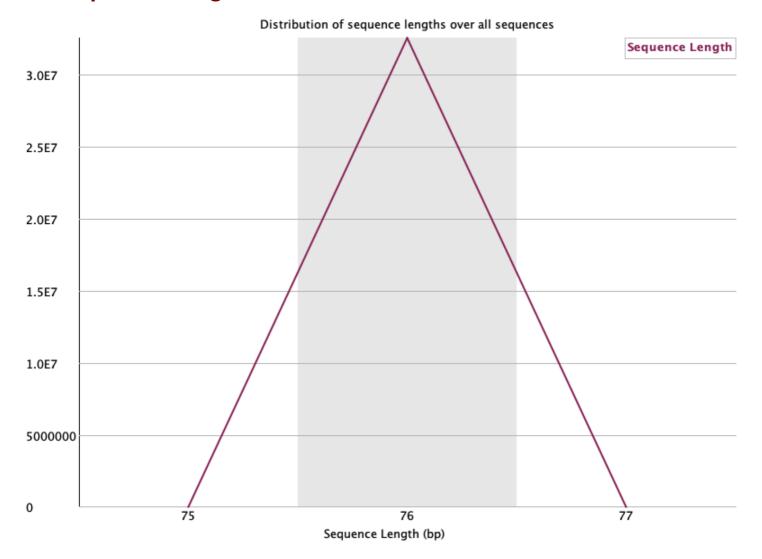
Per sequence GC content



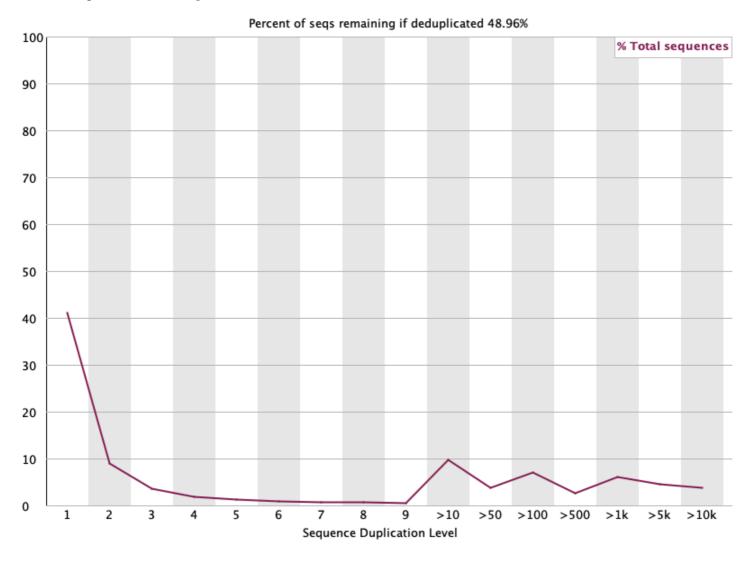
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence		Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCCTGAT	rctcgtatgc	521187	1.6034687228579152	TruSeq Adapter, Index 18 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	тттттттт	189211	0.5821210439260169	Clontech SMART CDS Primer II A (100% over 26bp)

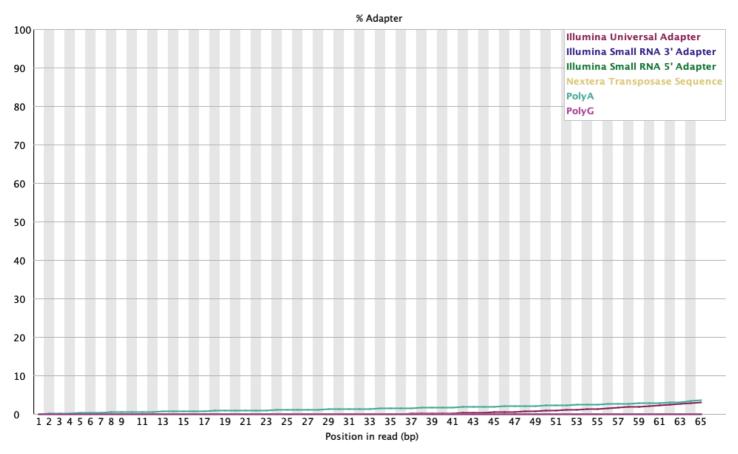
Sequence

Count

Percentage

Possible Source

Adapter Content



Produced by FastQC (version 0.12.1)