Report

Tue 6 Feb 2024 SRR13380541_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

SRR13380541_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

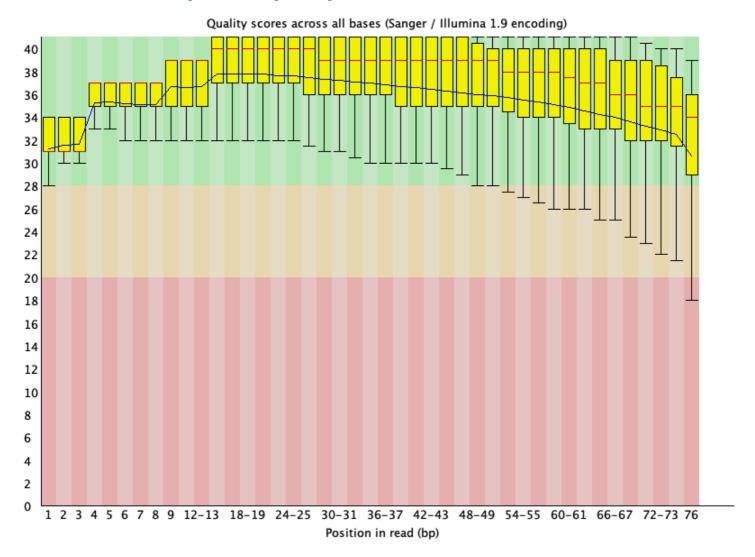
Total Sequences 33765974 Total Bases 2.5 Gbp

Sequences flagged as poor quality 0

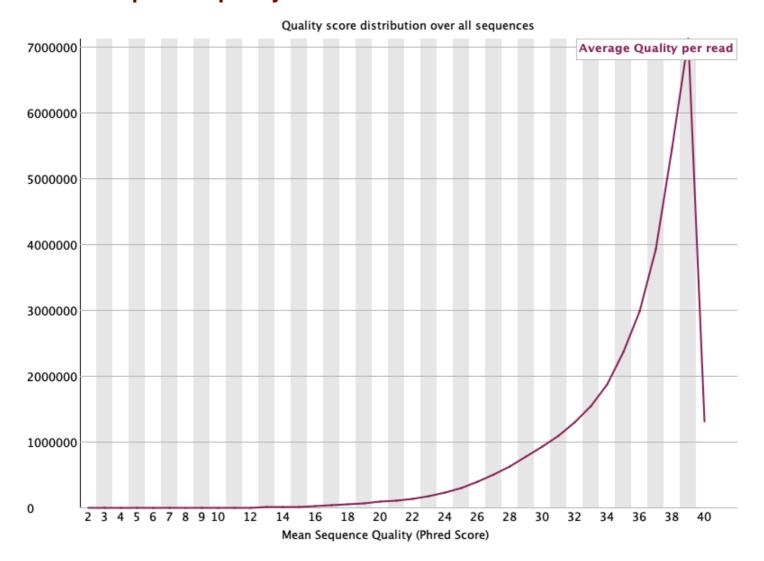
Sequence length 76

%GC 42

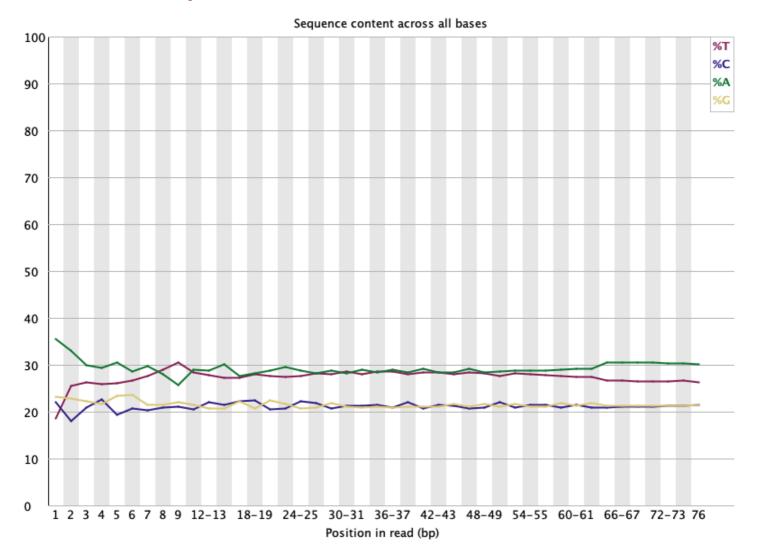
Per base sequence quality



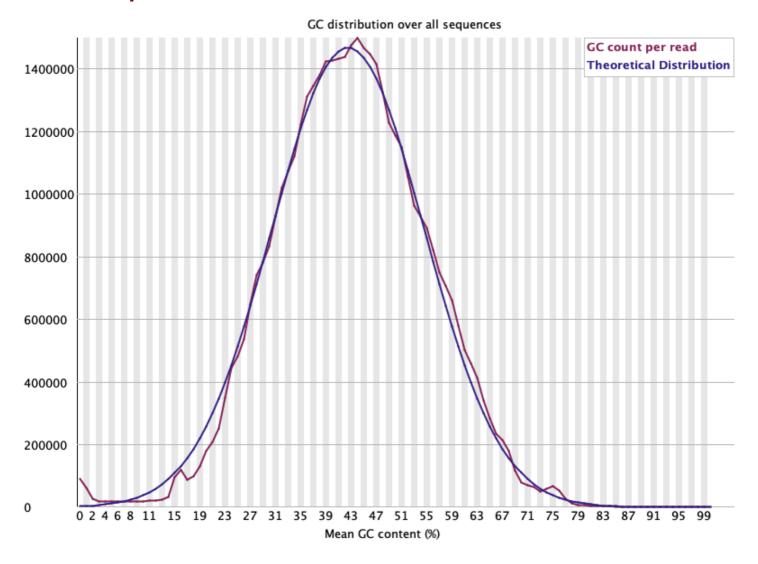
Per sequence quality scores



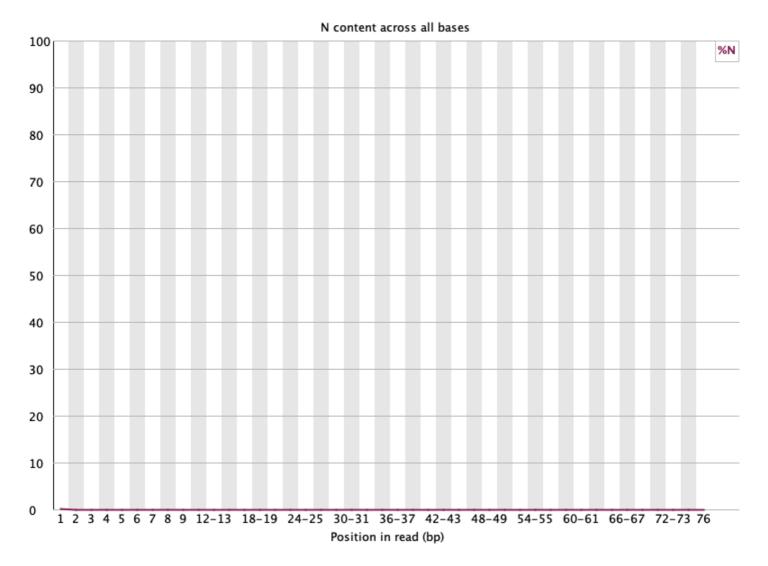
Per base sequence content



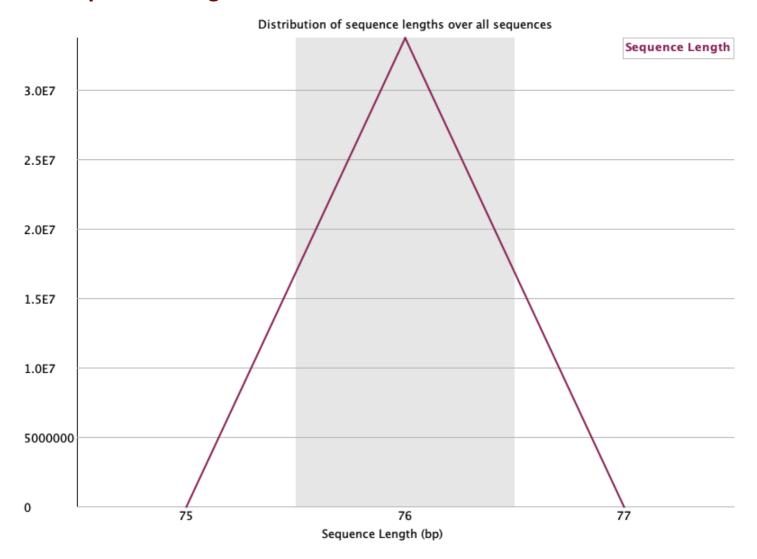
Per sequence GC content



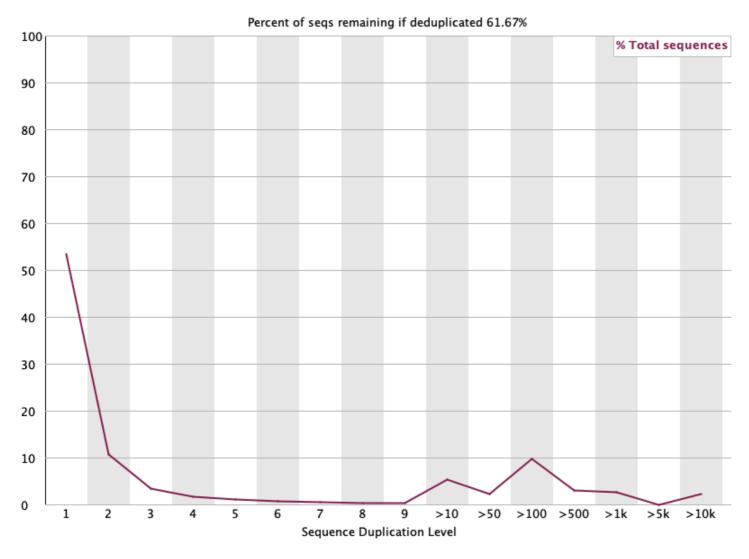
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

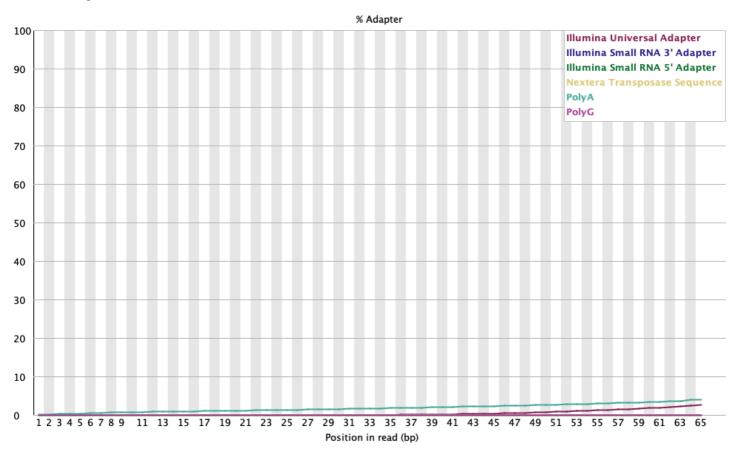


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTCTACCATCTCGTATGC	356031	1.0544076116388645	TruSeq Adapter, Index 8 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	341304	1.0107926991829113	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	73597	0.21796202295245506	No Hit

Sequence Count Percentage

Adapter Content



Produced by FastQC (version 0.12.1)

Possible

Source