Report

Tue 6 Feb 2024 SRR13380535_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

Basic Statistics

Measure Value

Filename SRR13380535_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 35697219

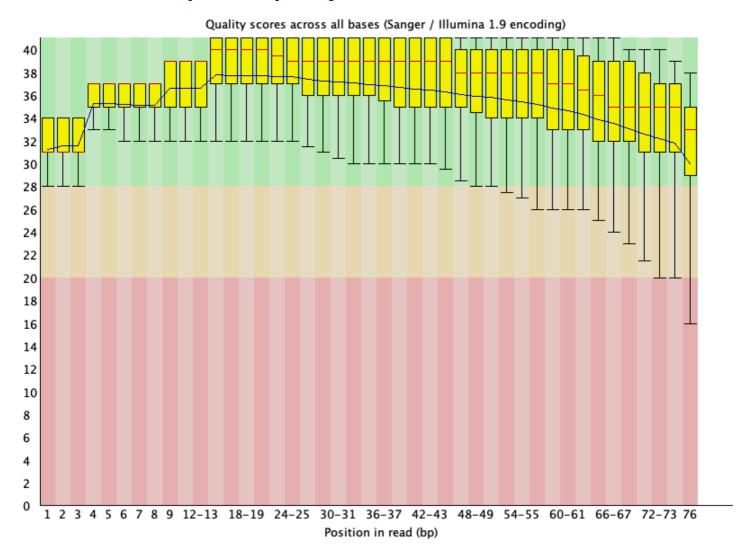
Total Bases 2.7 Gbp

Sequences flagged as poor quality $\, {\tt 0} \,$

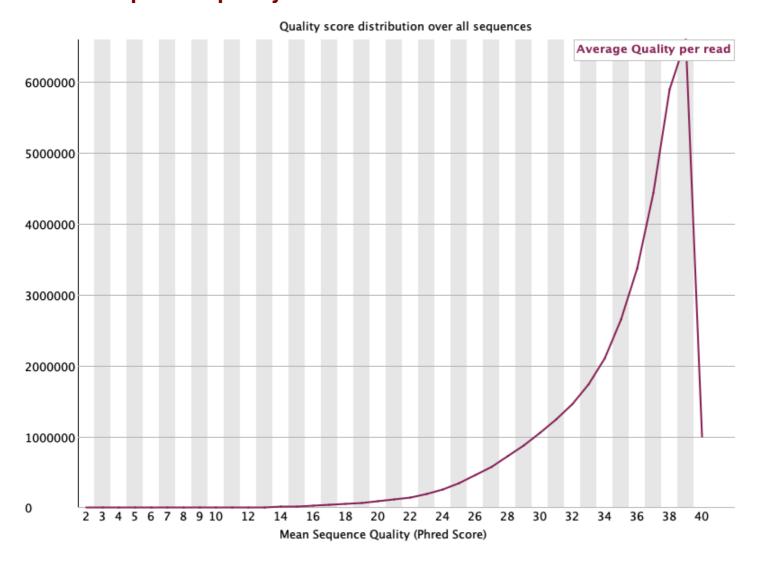
Sequence length 76

%GC 46

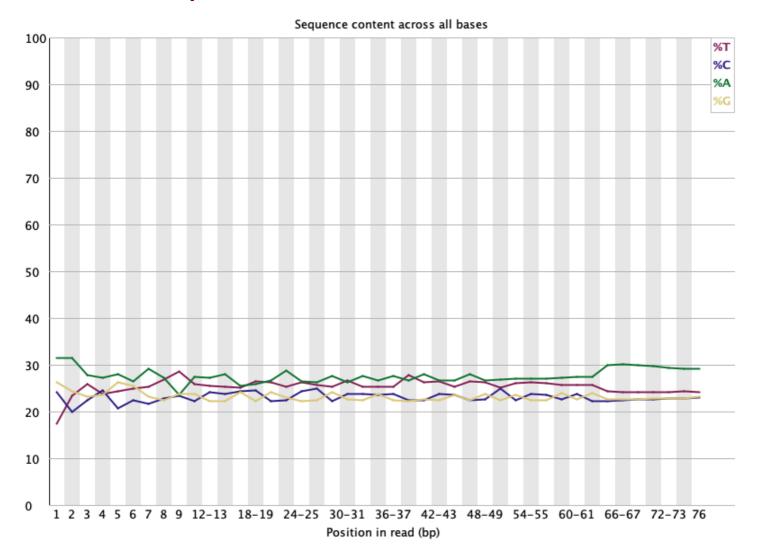
Per base sequence quality



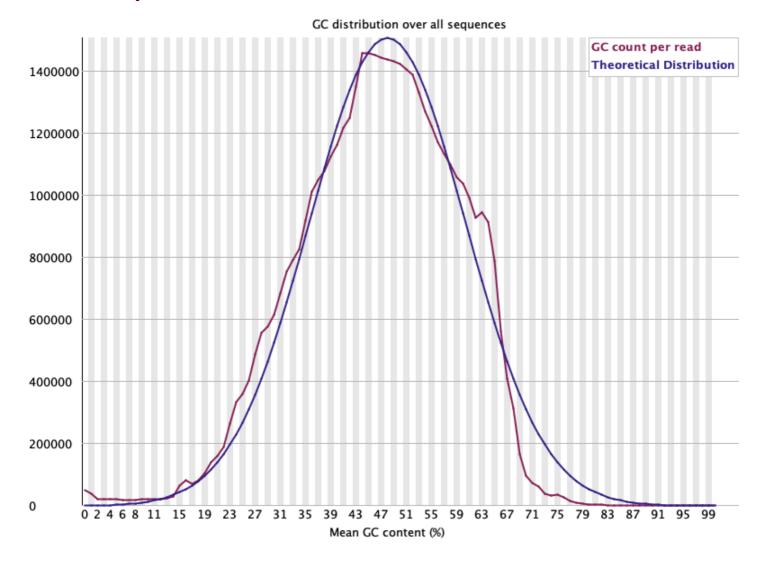
Per sequence quality scores



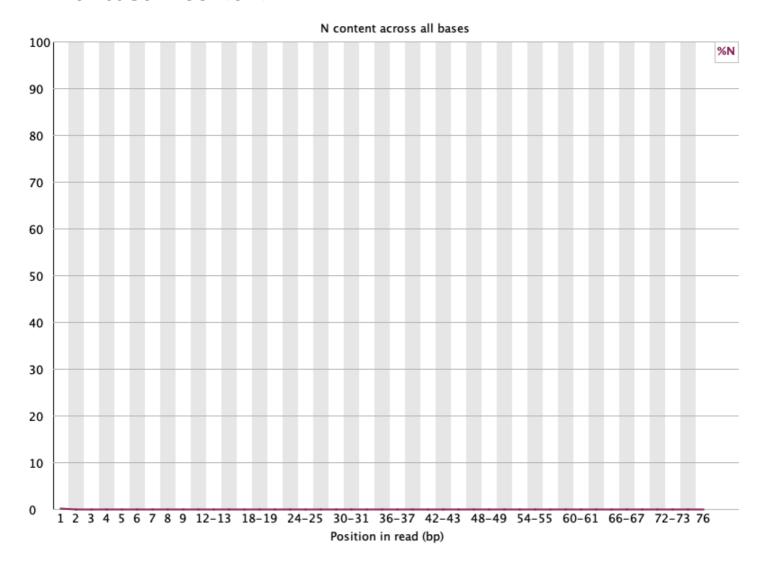
Per base sequence content



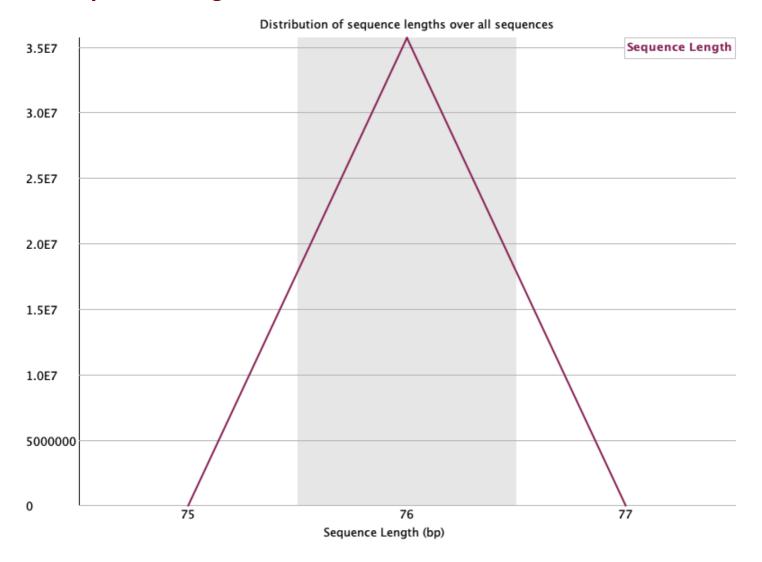
Per sequence GC content



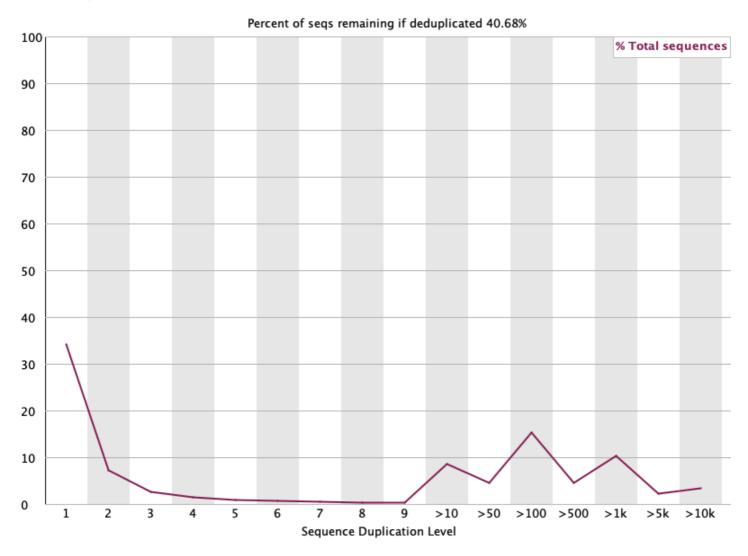
Per base N content



Sequence Length Distribution



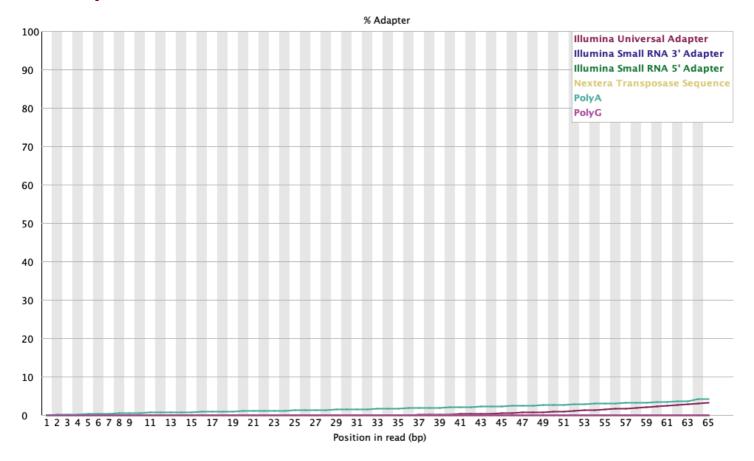
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCACTTATCTCGTATGC	778127	2.179797255354822	TruSeq Adapter, Index 23 (97% over 38bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	209869	0.5879141453568134	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	46734	0.1309177614088089	No Hit

Adapter Content



Produced by FastQC (version 0.12.1)