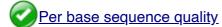
Report

Mon 5 Feb 2024 SRR13380427_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

Filename SRR13380427_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 29060409

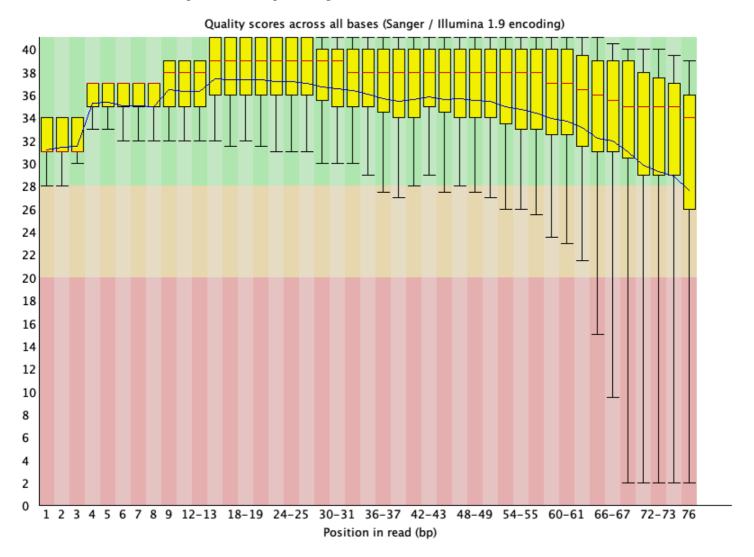
Total Bases 2.2 Gbp

Sequences flagged as poor quality \emptyset

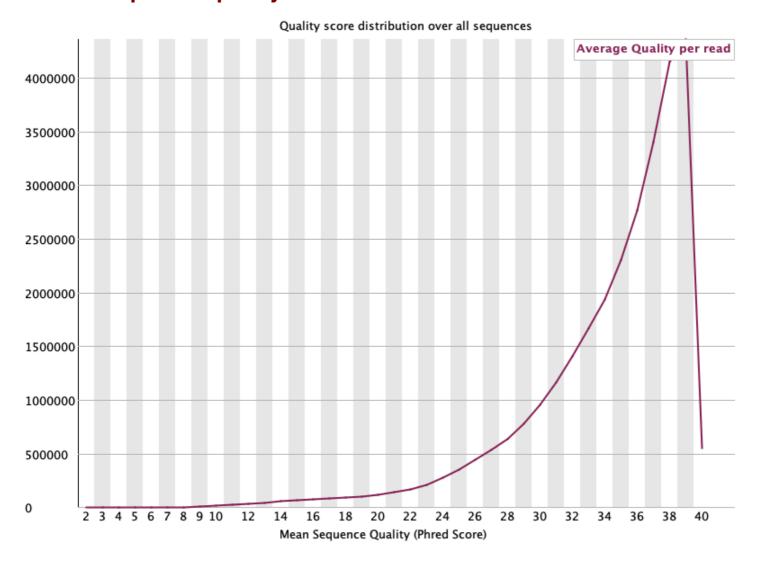
Sequence length 76

%GC 43

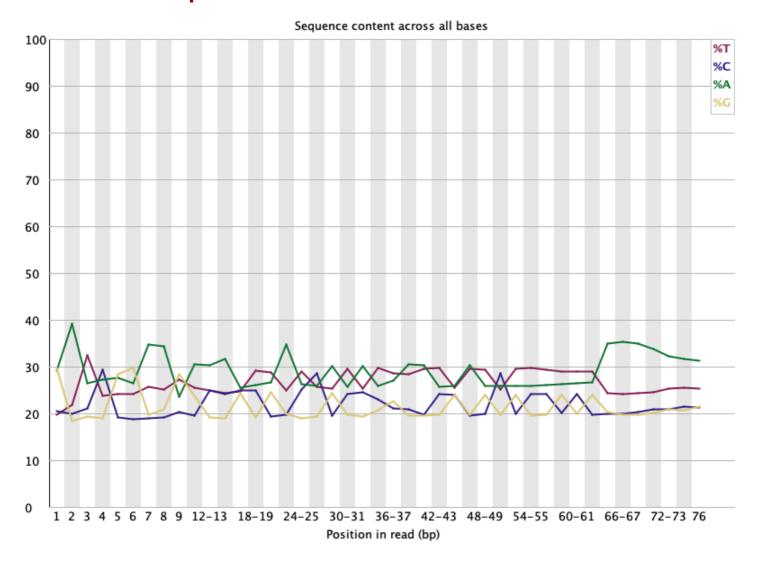
Per base sequence quality



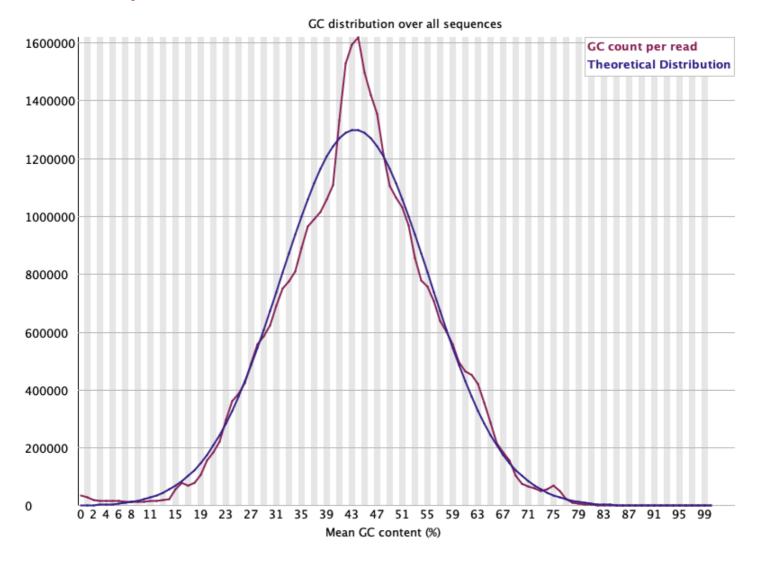
Per sequence quality scores



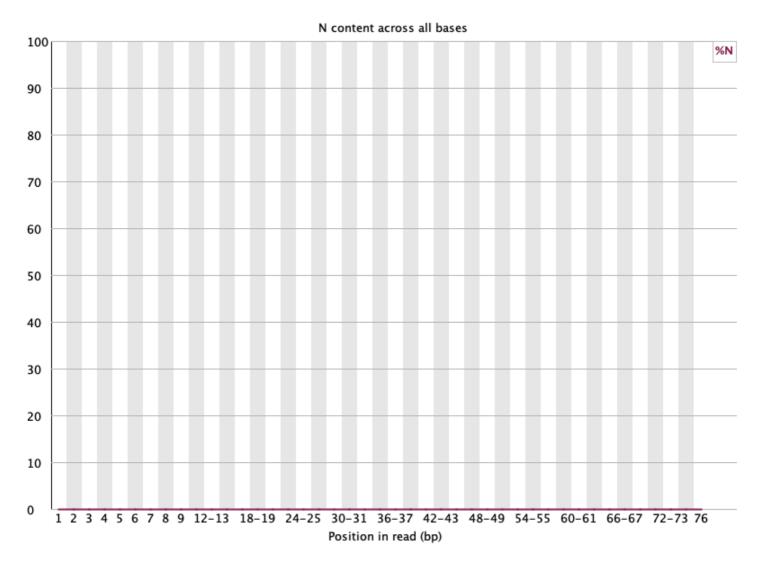
Per base sequence content



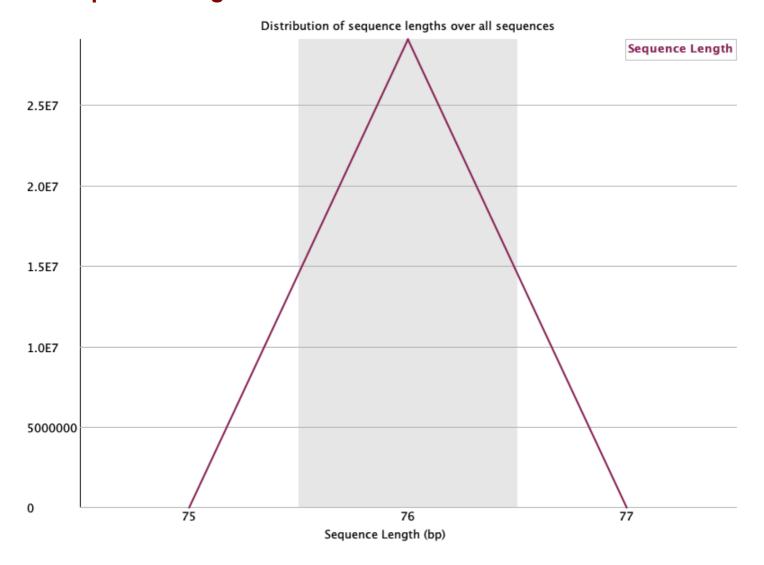
Per sequence GC content



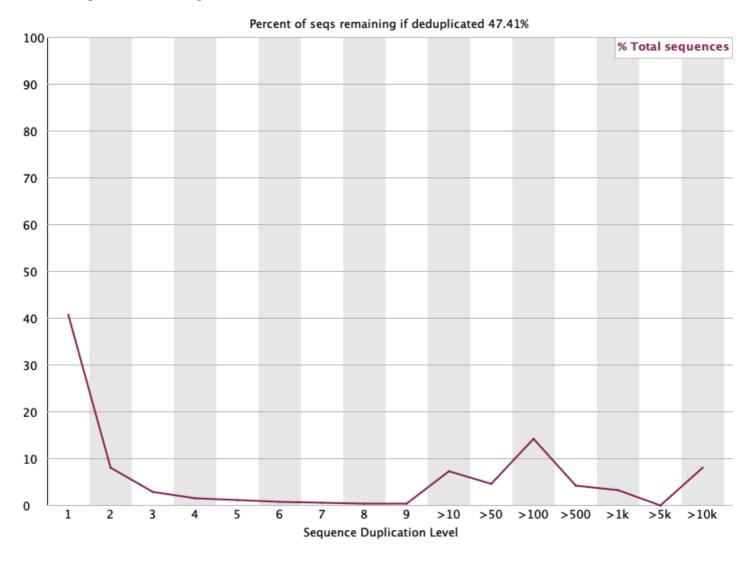
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGC	1556070	5.354604610003941	TruSeq Adapter, Index 12 (100% over 50bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGC	567880	1.954136295879387	TruSeq Adapter, Index 4 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	235864	0.8116334494810449	Clontech SMART CDS Primer

Sequence

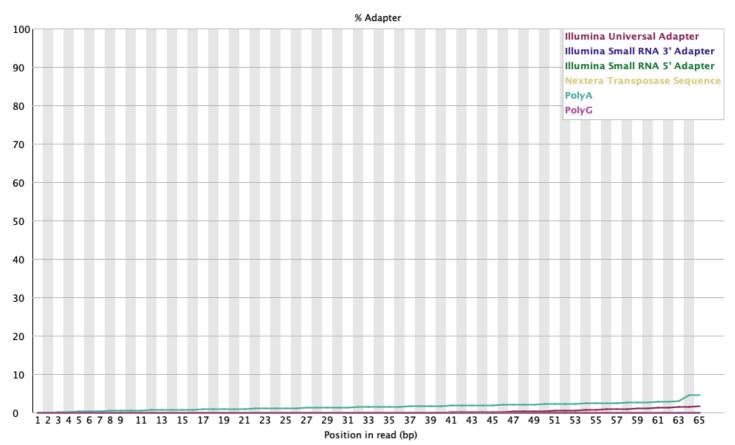
Count

Percentage

Possible Source

II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)