Mon 5 Feb 2024 SRR13380481_1.fastq

Report

Summary







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 SRR13380481_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

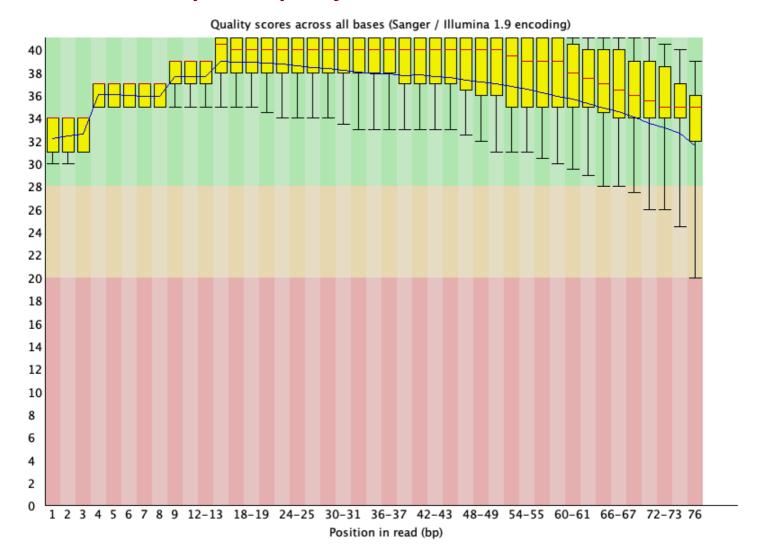
Total Sequences 32434601
Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

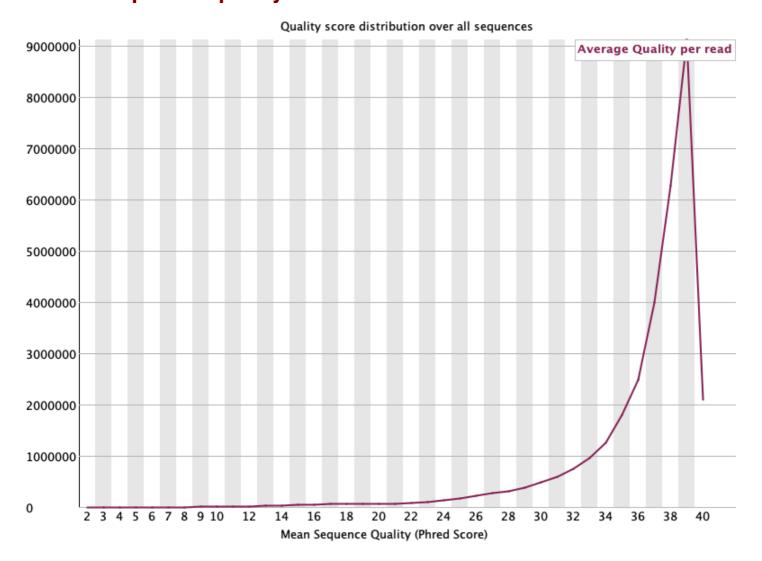
Sequence length 76

%GC 46

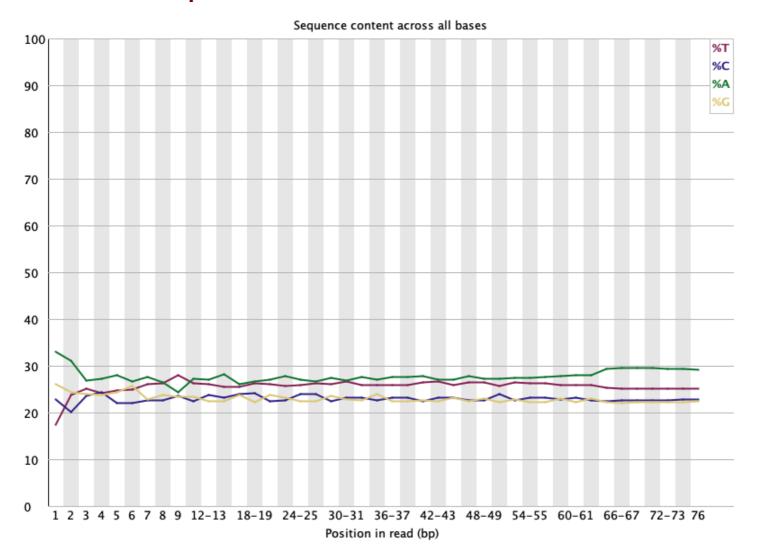
Per base sequence quality



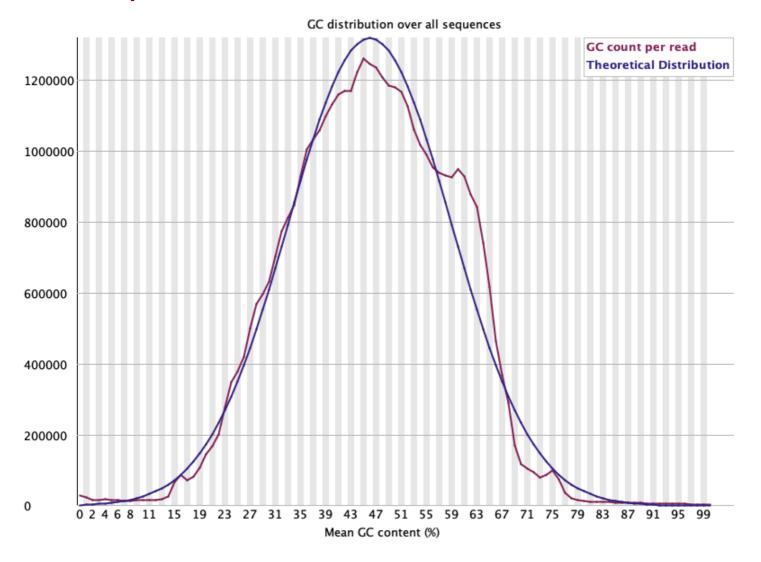
Per sequence quality scores



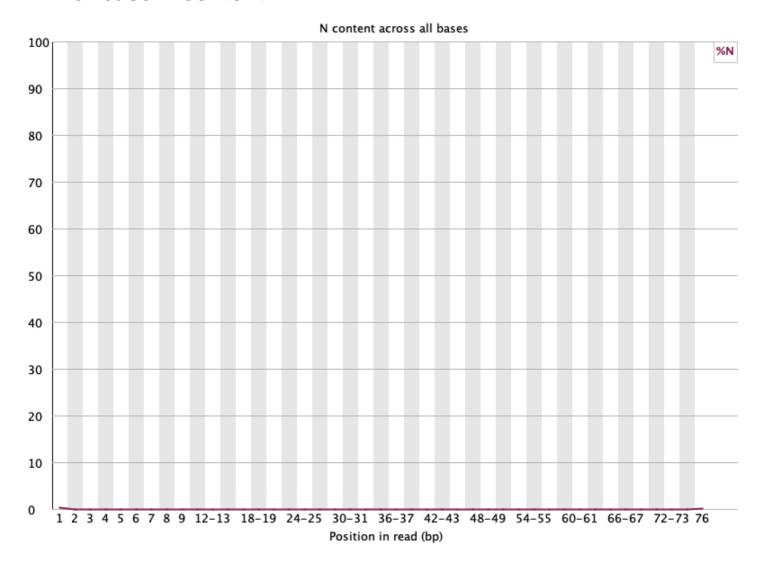
Per base sequence content



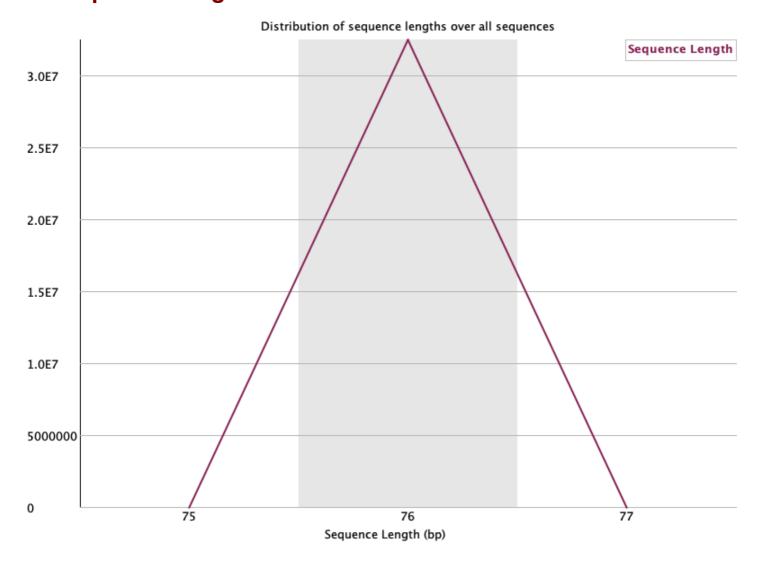
Per sequence GC content



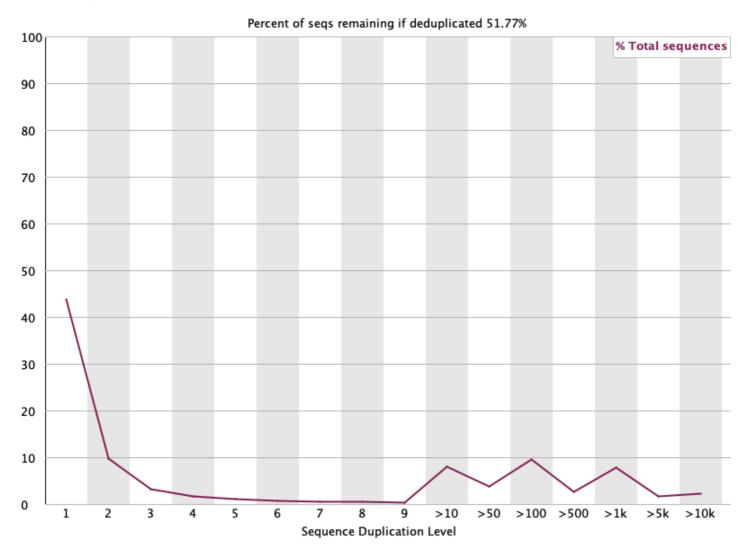
Per base N content



Sequence Length Distribution



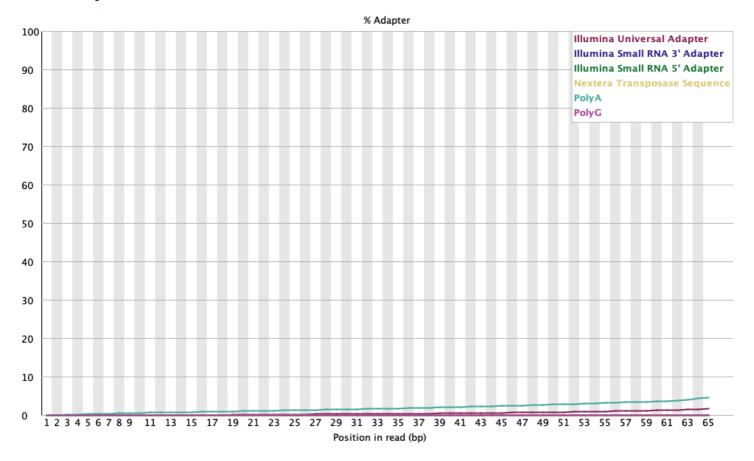
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCACAATCTCGTATGC	368358	1.1356945627294752	TruSeq Adapter, Index 6 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	242780	0.7485216173924878	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)