Mon 5 Feb 2024 SRR13380486_1.fastq

PastQC ReportSummary



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

Adapter Content

Basic Statistics

Measure Value

Filename SRR13380486_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 28014099

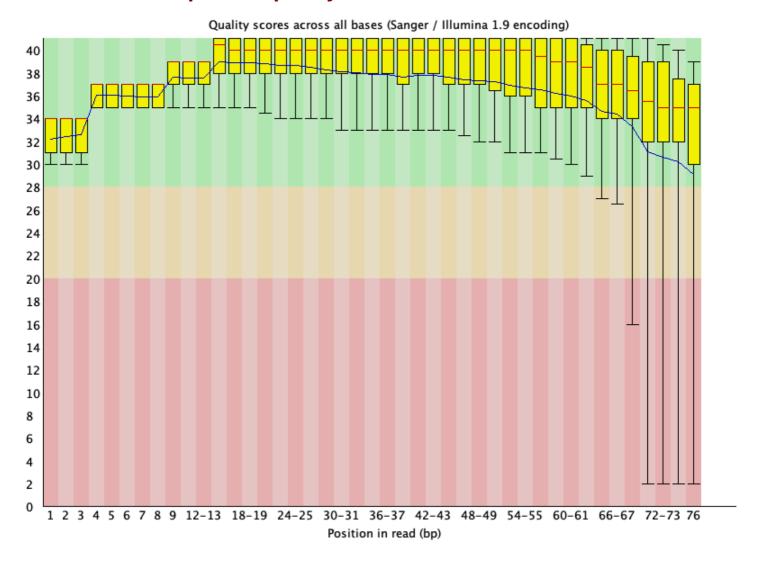
Total Bases 2.1 Gbp

Sequences flagged as poor quality 0

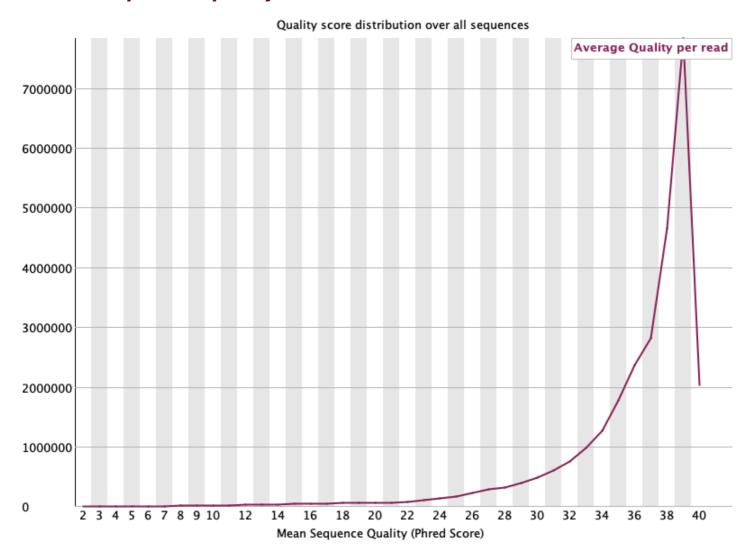
Sequence length 76

%GC 44

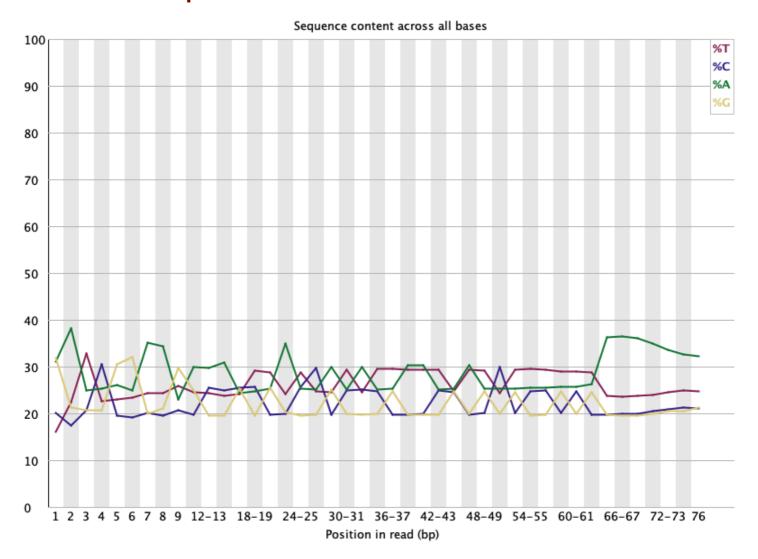
Per base sequence quality



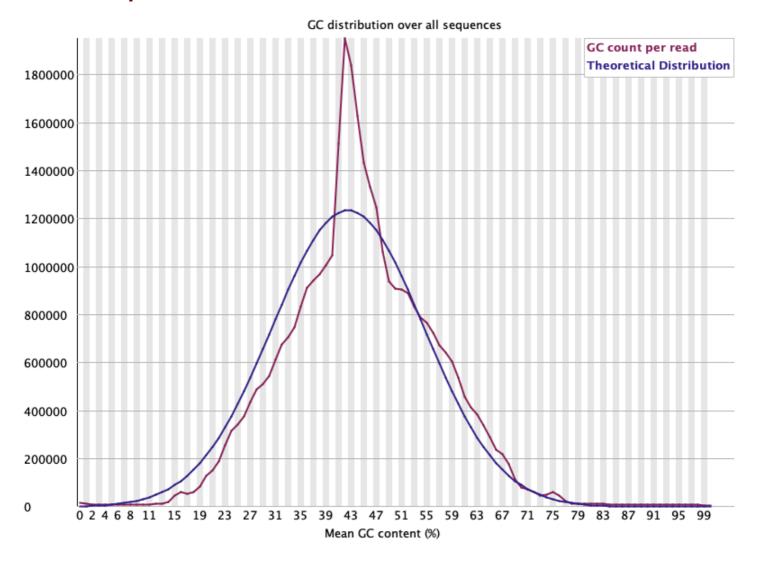
Per sequence quality scores



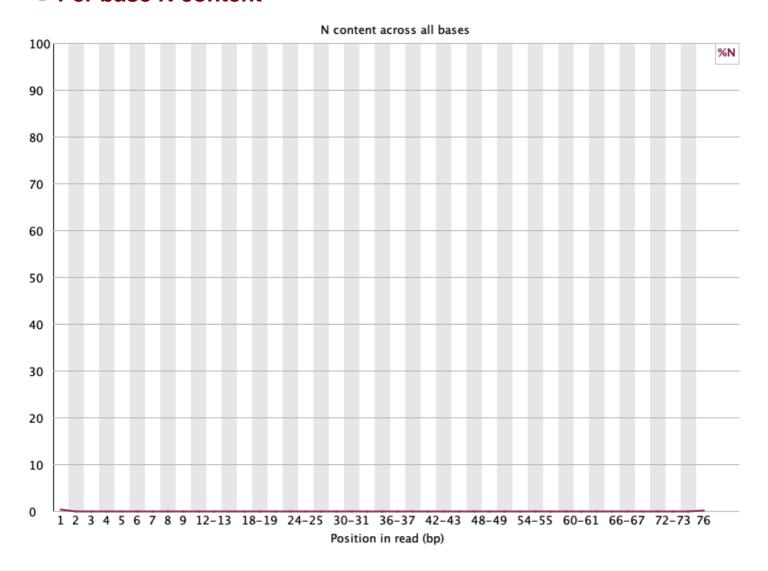
Per base sequence content



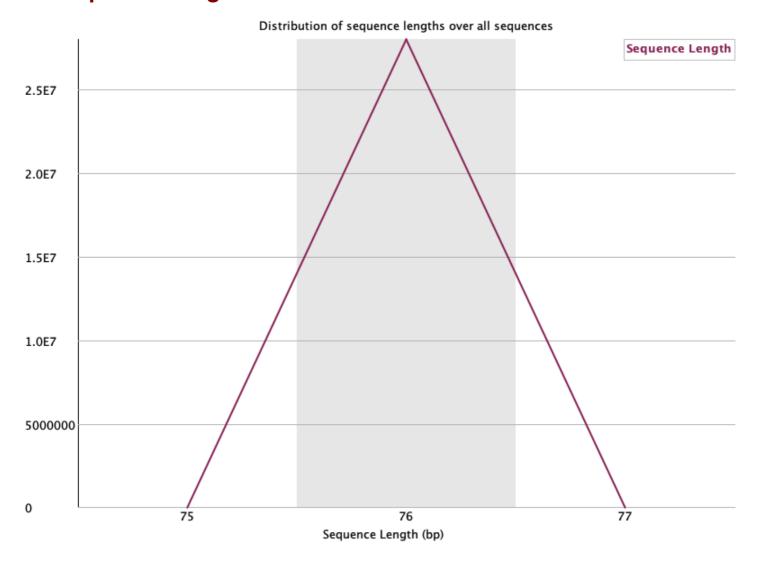
Per sequence GC content



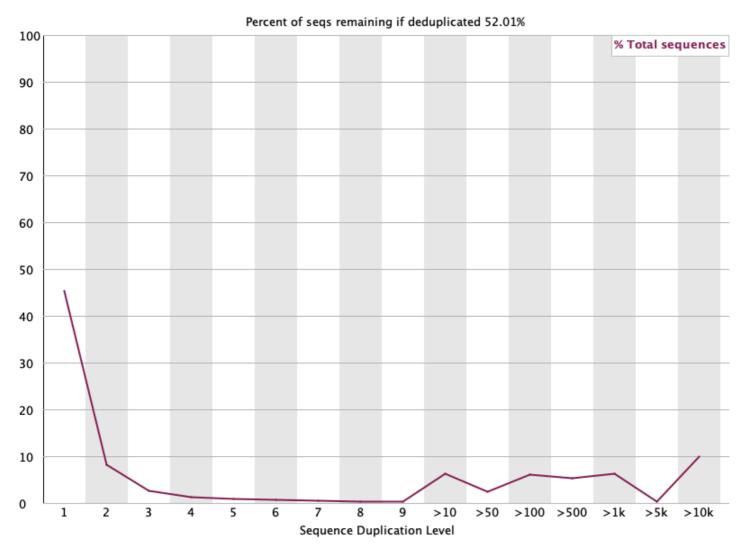
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGC	2499961	8.923938621049352	TruSeq Adapter, Index 12 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	186375	0.6652900027232715	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence

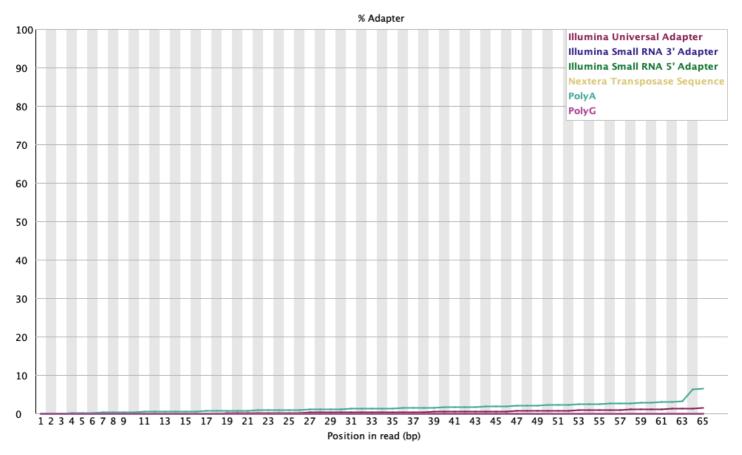
Count

Percentage

Possible Source

0.16650901390760417 No Hit

Adapter Content



Produced by FastQC (version 0.12.1)