Mon 5 Feb 2024 SRR13380488_1.fastq

PastQC ReportSummary





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 SRR13380488_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 36867306

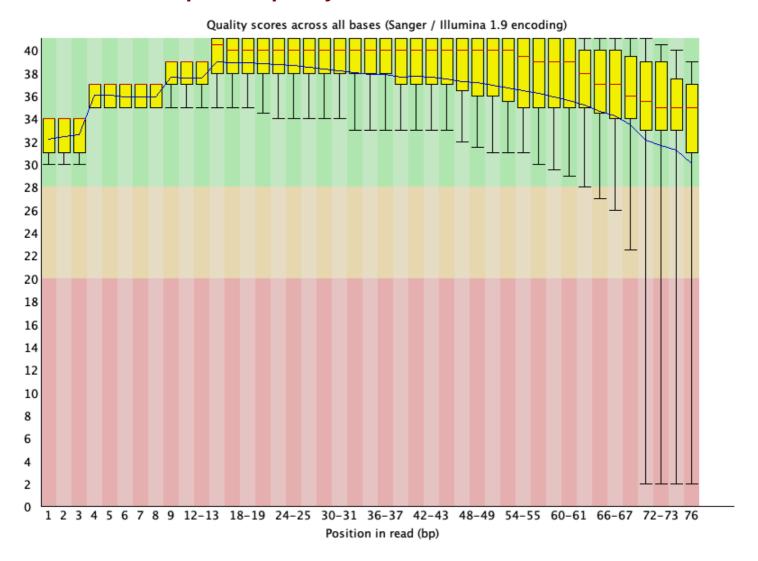
Total Bases 2.8 Gbp

Sequences flagged as poor quality 0

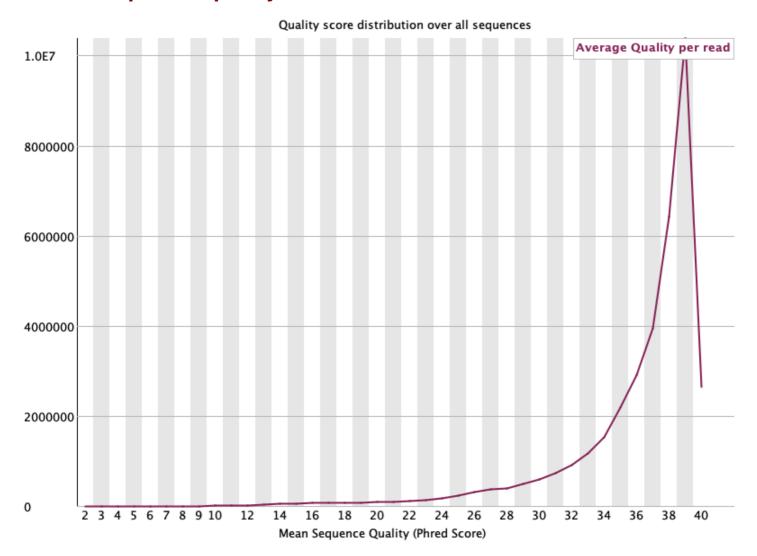
Sequence length 76

%GC 43

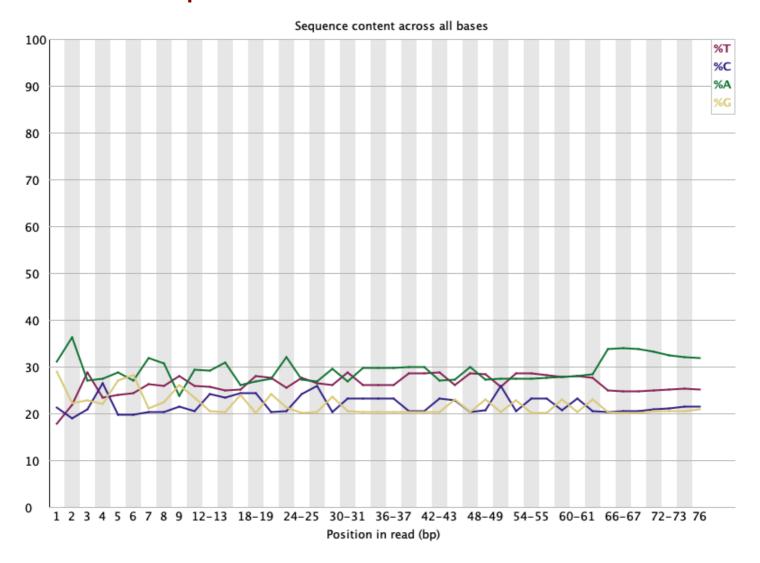
Per base sequence quality



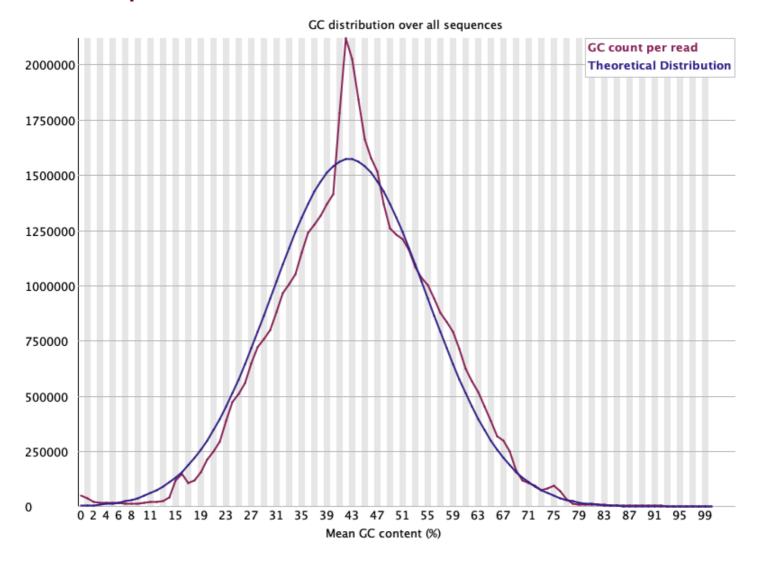
Per sequence quality scores



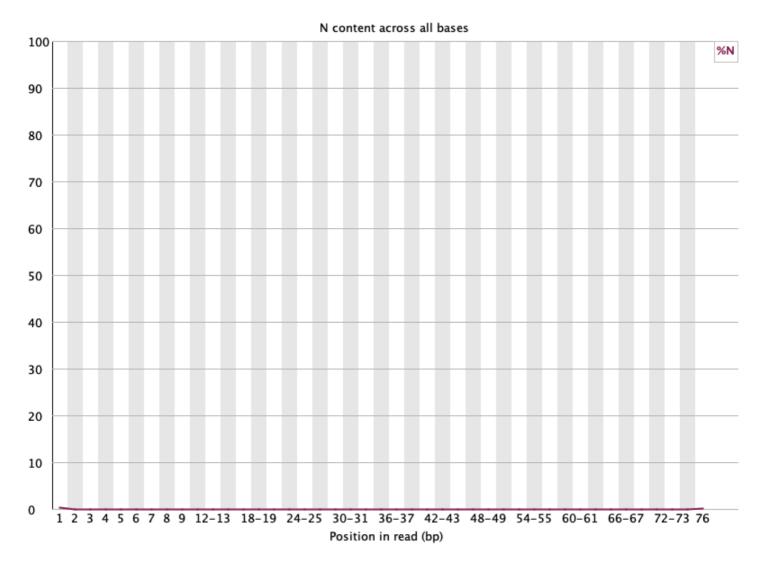
Per base sequence content



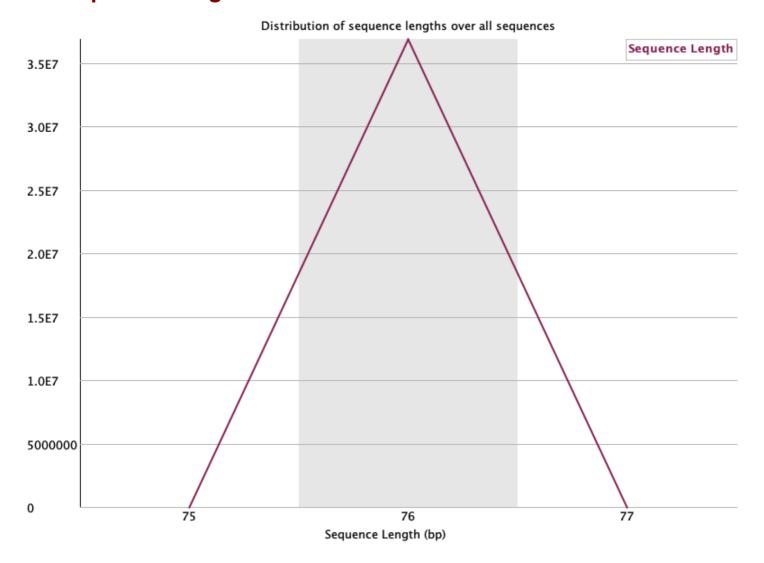
Per sequence GC content



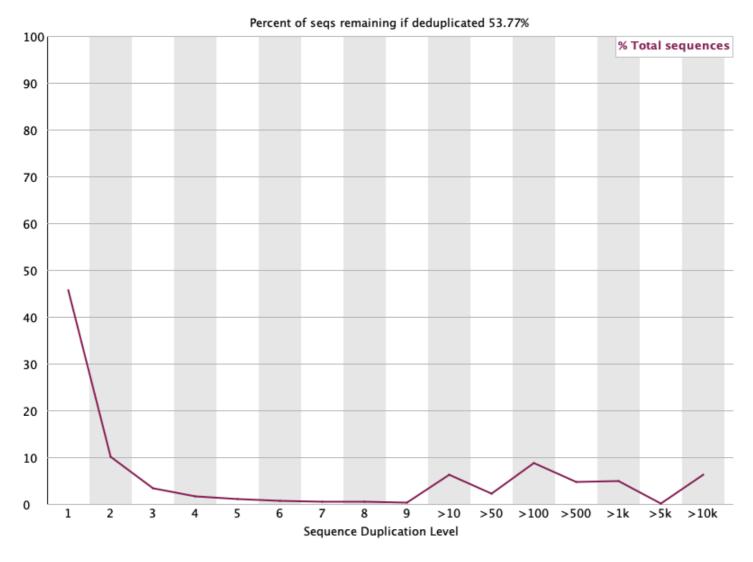
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCAACTAATCTCGTATGC	1802019	4.887851040702567	TruSeq Adapter, Index 23 (97% over 38bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	412742	1.119533930686446	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence

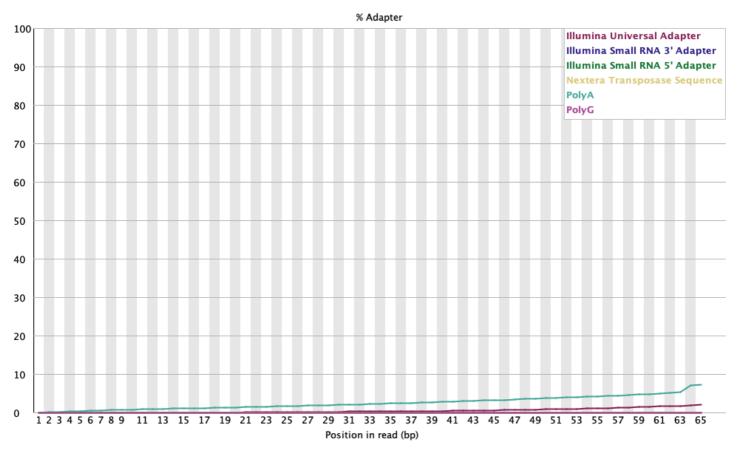
Count

Percentage

Possible Source

0.11021418272330503 No Hit

Adapter Content



Produced by FastQC (version 0.12.1)