Mon 5 Feb 2024 SRR13380484_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



Measure Value

Filename SRR13380484_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

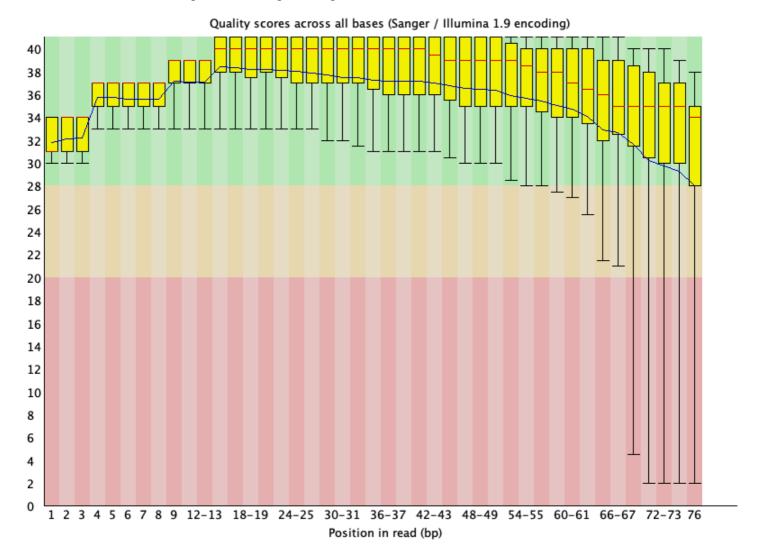
Total Sequences 8369535
Total Bases 636 Mbp

Sequences flagged as poor quality 0

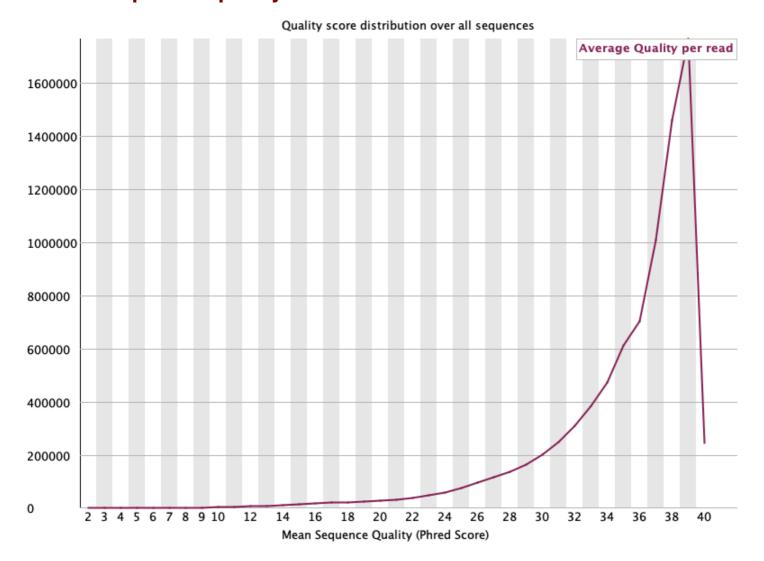
Sequence length 76

%GC 46

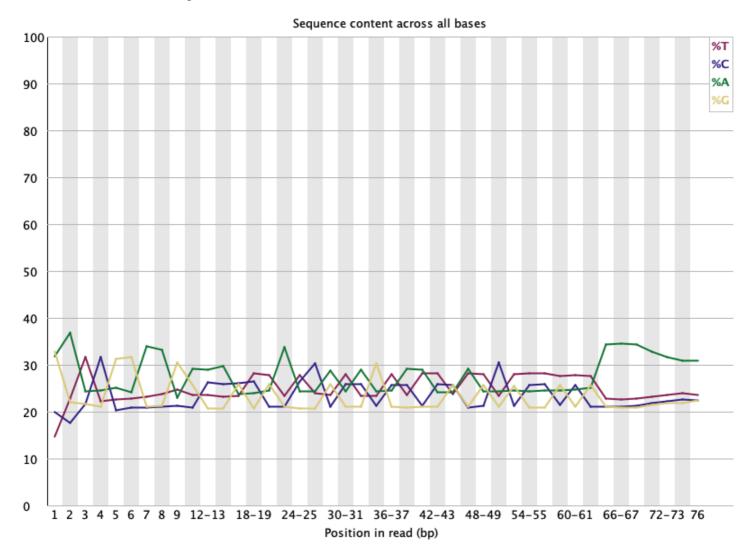
Per base sequence quality



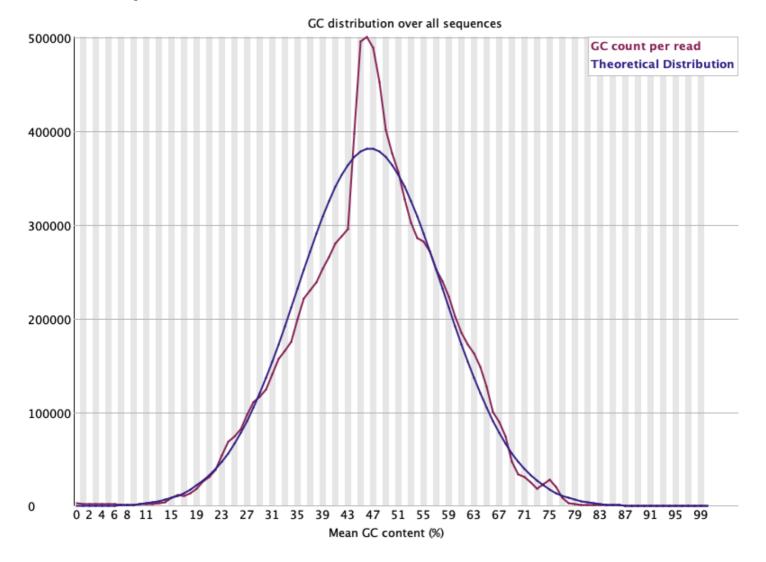
Per sequence quality scores



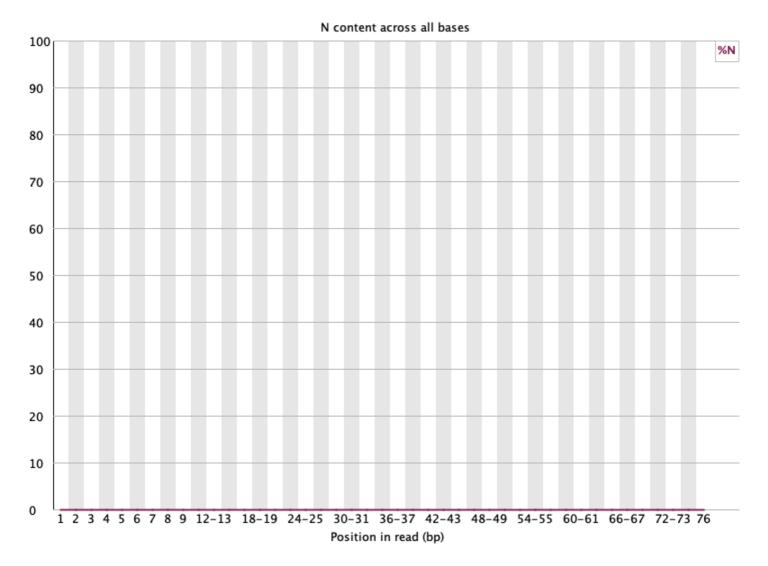
Per base sequence content



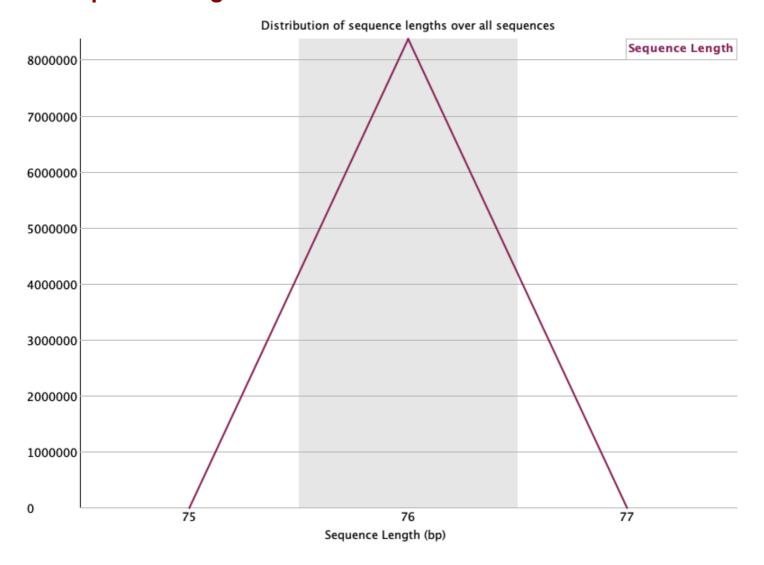
Per sequence GC content



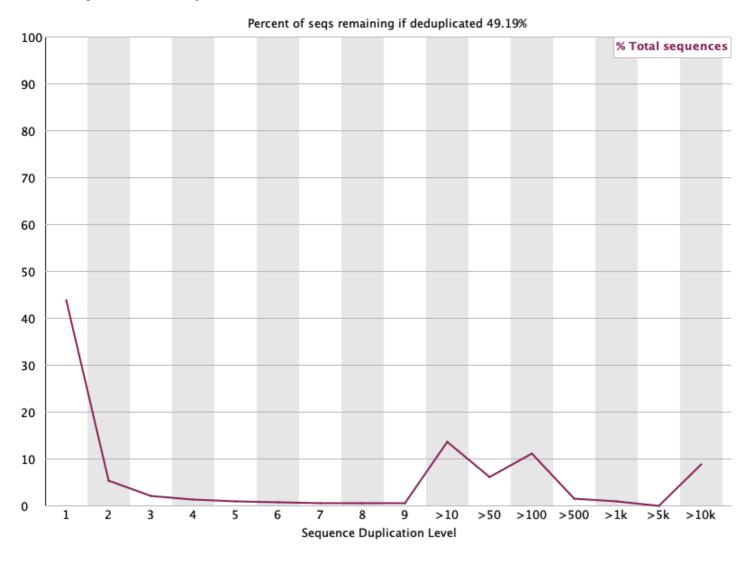
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGC	713801	8.52856222000386	TruSeq Adapter, Index 11 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	38338	0.4580660693813934	Clontech SMART CDS Primer II A (100% over 26bp)
CGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC	8620	0.10299257963554725	Illumina Single

Sequence

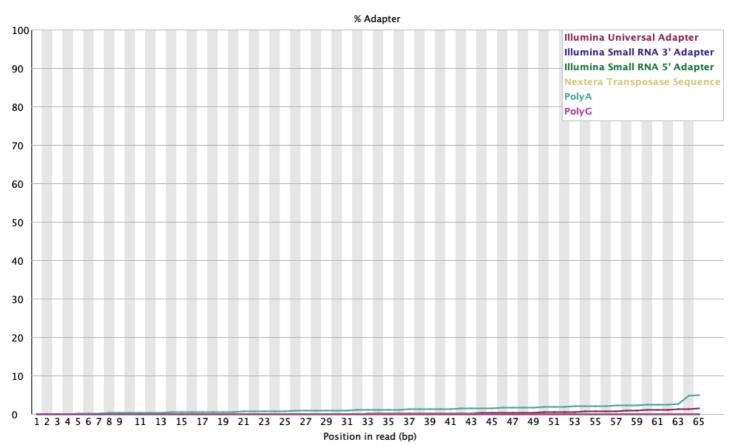
Count

Percentage

Possible Source

End PCR Primer 1 (100% over 50bp)

Adapter Content



Produced by FastQC (version 0.12.1)