Mon 5 Feb 2024 SRR13380435_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 SRR13380435_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

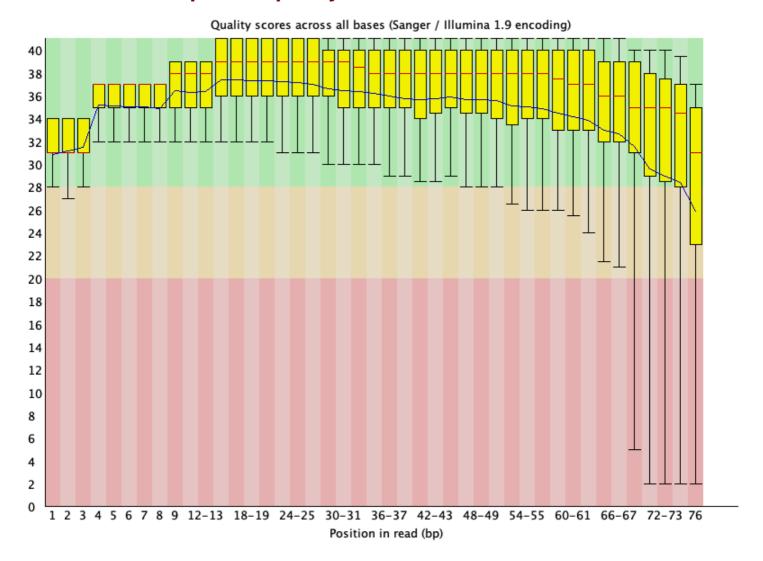
Total Sequences 31966570
Total Bases 2.4 Gbp

Sequences flagged as poor quality 0

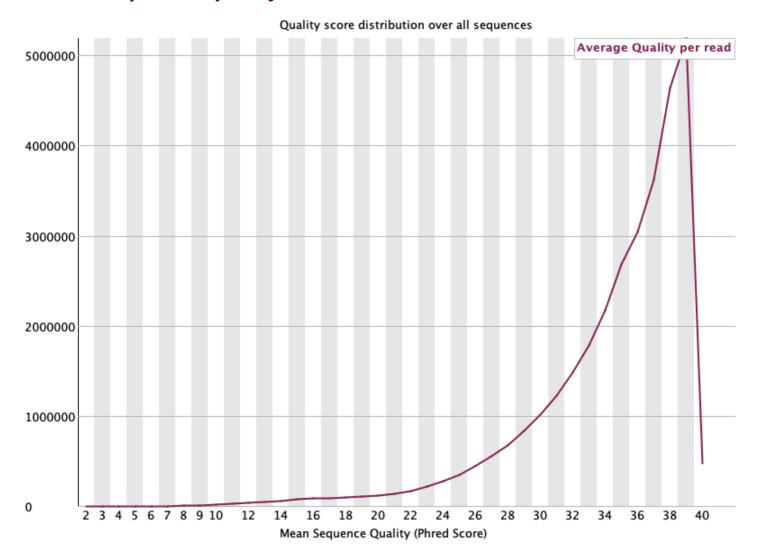
Sequence length 76

%GC 43

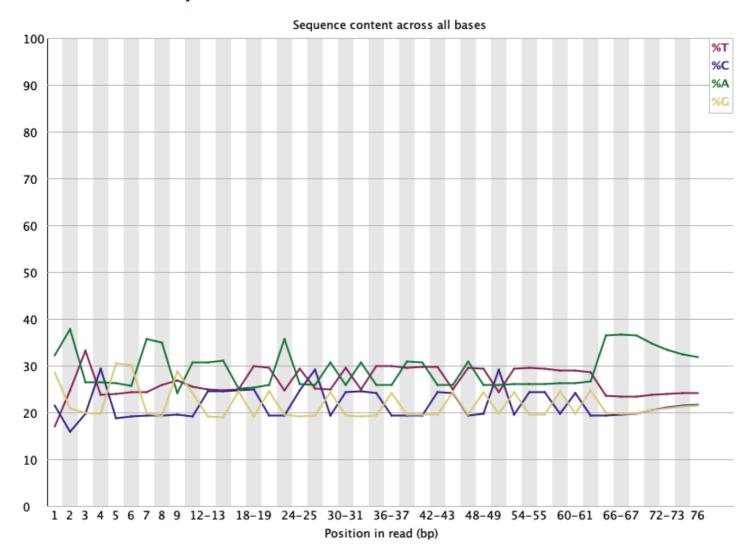
Per base sequence quality



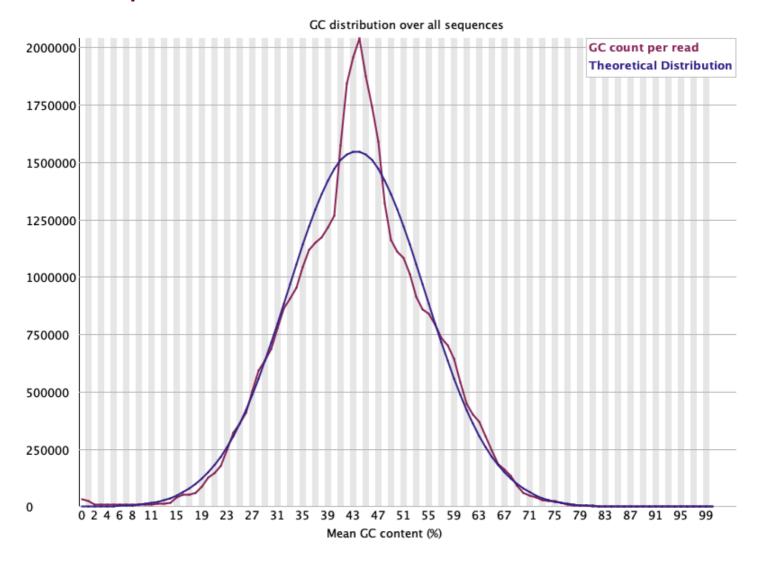
Per sequence quality scores



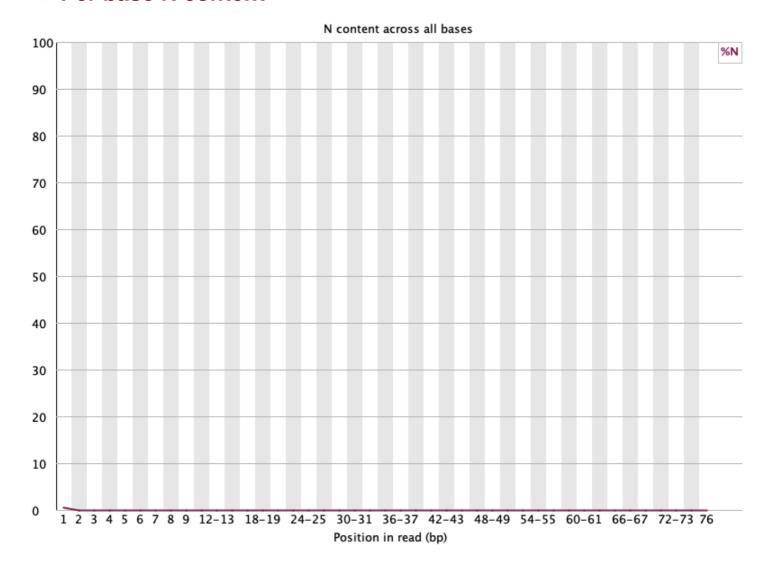
Per base sequence content



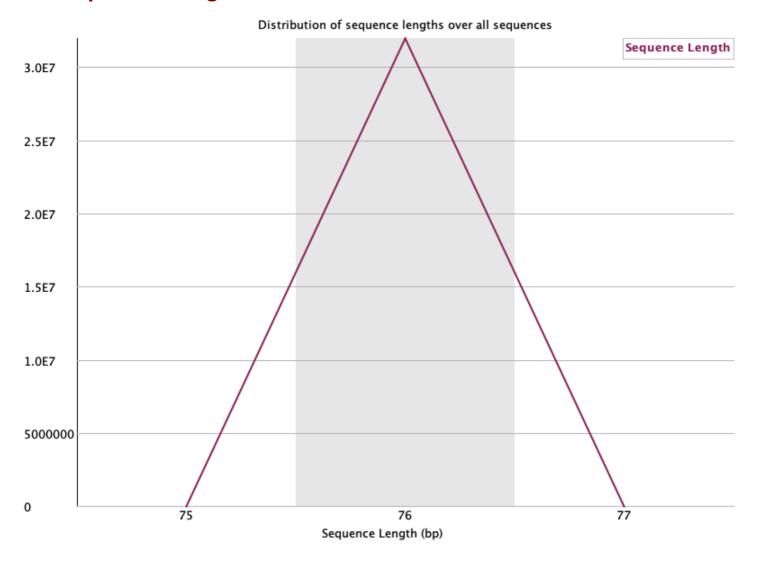
Per sequence GC content



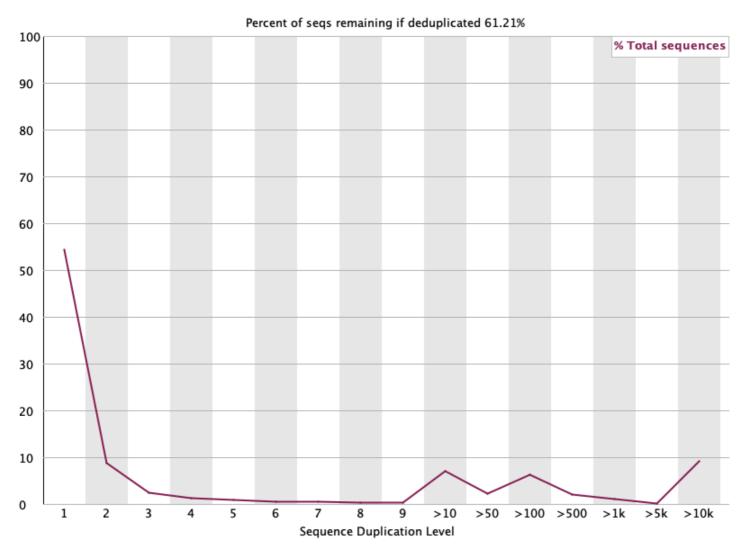
Per base N content



Sequence Length Distribution



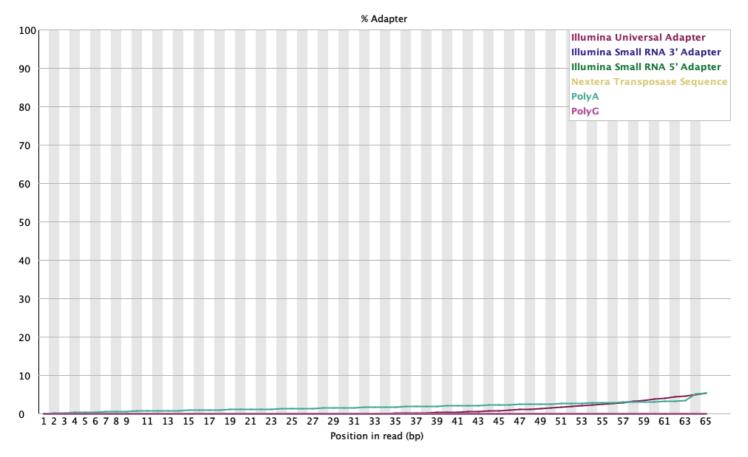
Sequence Duplication Levels



Overrepresented sequences

Sequence		Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGA	ACTCCAGTCACCTTGTAATCTCGTATGC	2656498	8.3102378516056	TruSeq Adapter, Index 12 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAG	TACTTTTTTTTTTTTTTTTTTTTTTT	103386	0.32341912191392447	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)