Mon 5 Feb 2024 SRR13380434_1.fastq

Report

Summary





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 SRR13380434_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 26445262

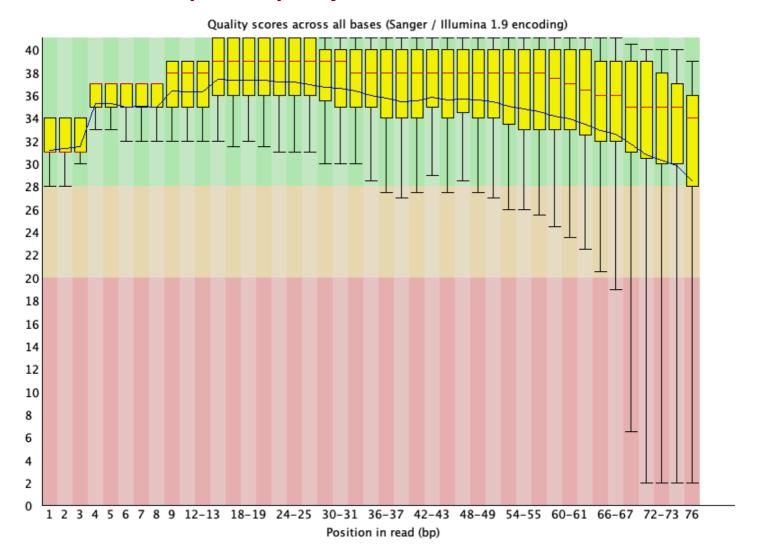
Total Bases 2 Gbp

Sequences flagged as poor quality 0

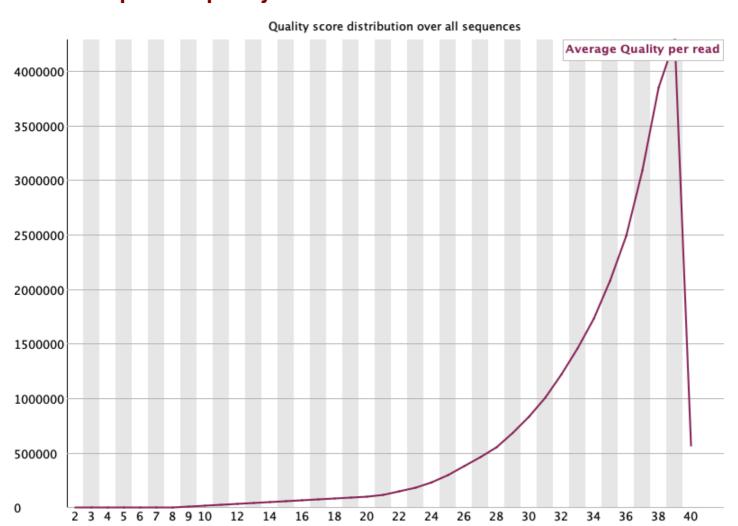
Sequence length 76

%GC 42

Per base sequence quality

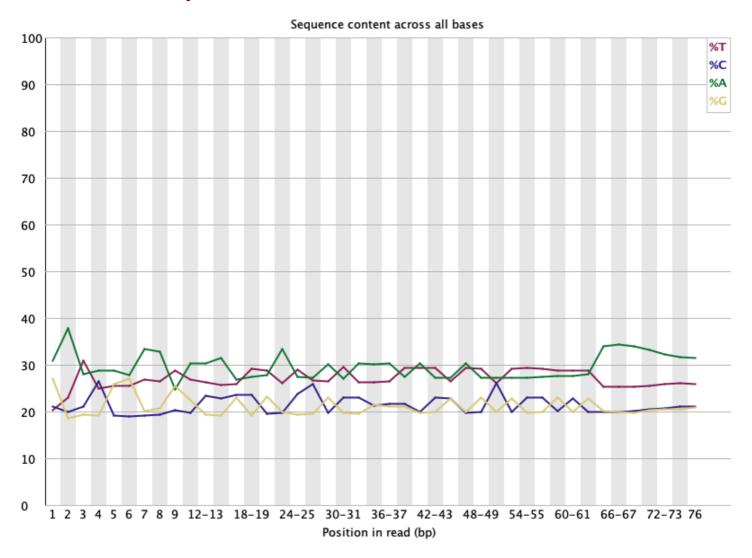


Per sequence quality scores

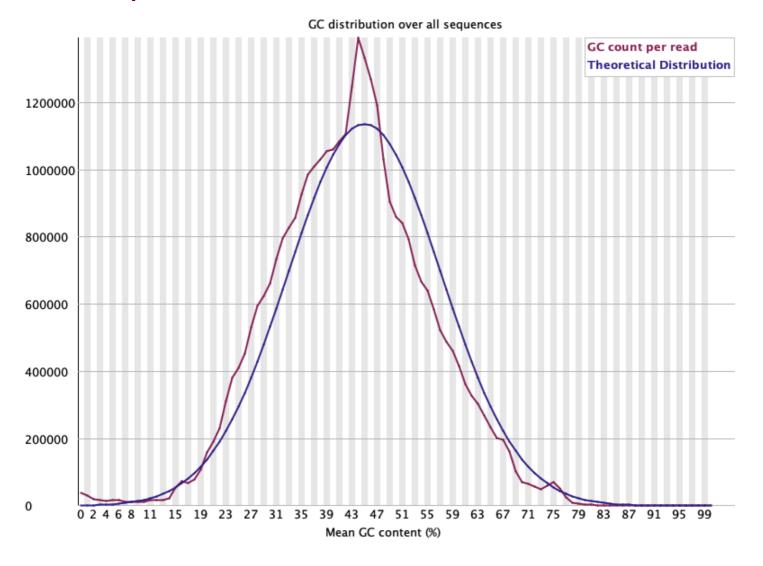


Mean Sequence Quality (Phred Score)

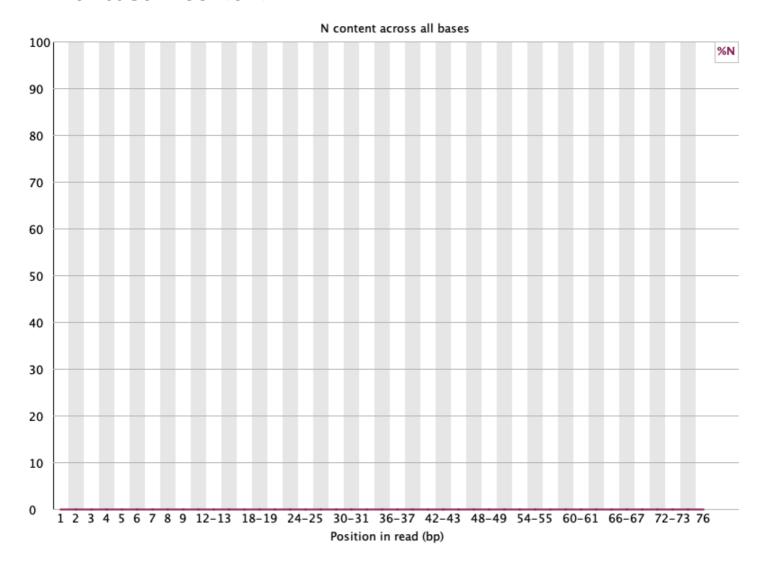
Per base sequence content



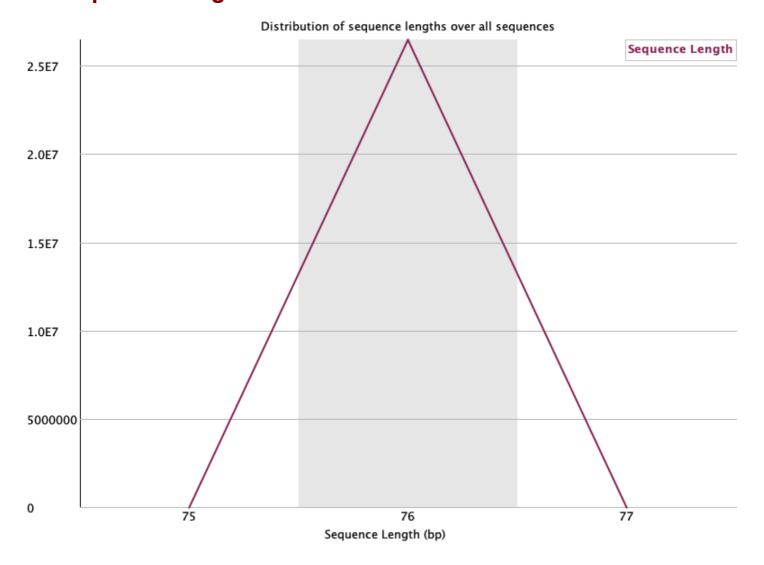
Per sequence GC content



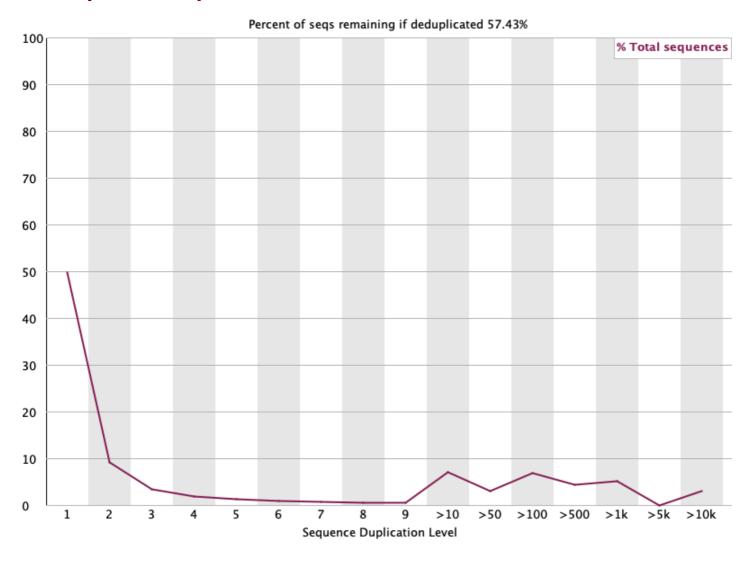
Per base N content



Sequence Length Distribution



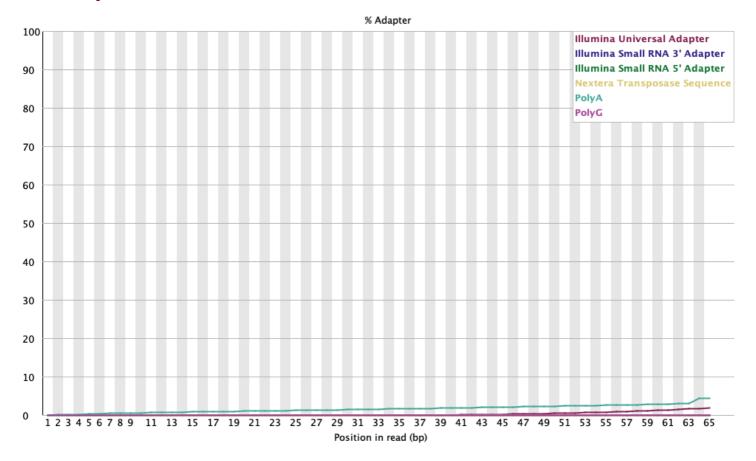
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGT	ATGC 555637	2.101083362305127	TruSeq Adapter, Index 5 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	TTTT 191941	0.7258048719653448	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAA 27533	0.1041131677954259	No Hit

Adapter Content



Produced by FastQC (version 0.12.1)