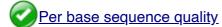
Report

Mon 5 Feb 2024 SRR13380438_1.fastq

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

Basic Statistics

Measure Value

Filename SRR13380438_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 35760507

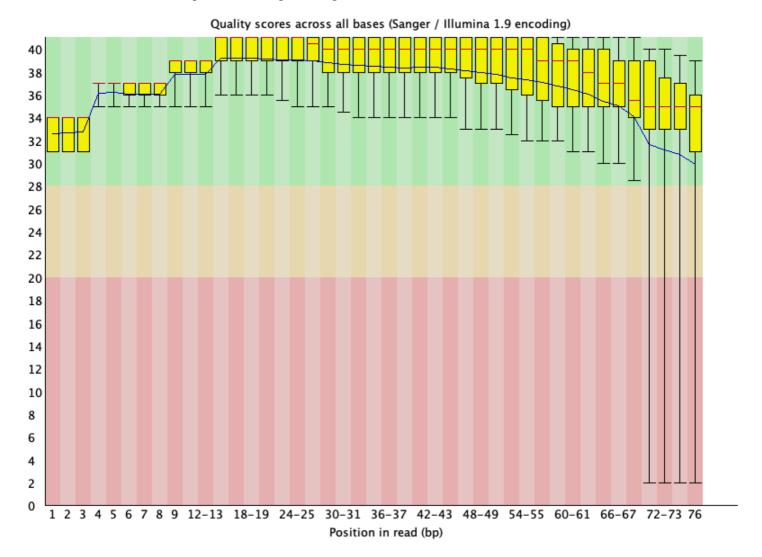
Total Bases 2.7 Gbp

Sequences flagged as poor quality \emptyset

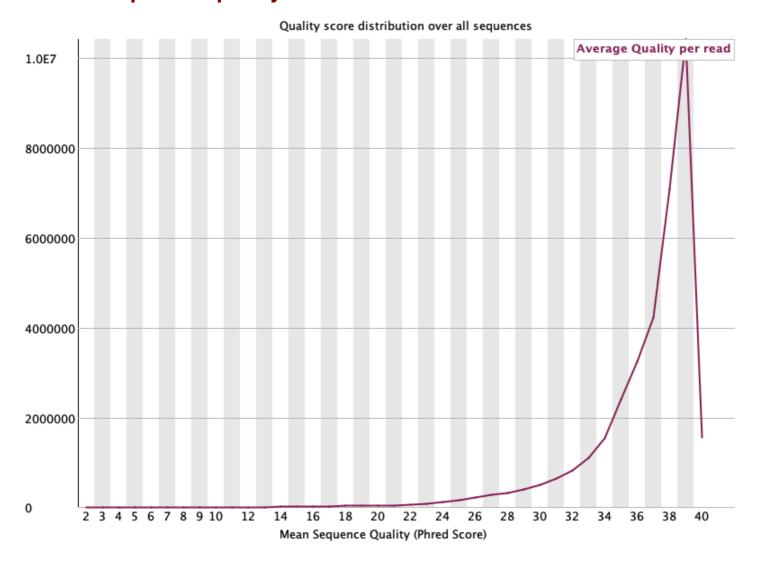
Sequence length 76

%GC 47

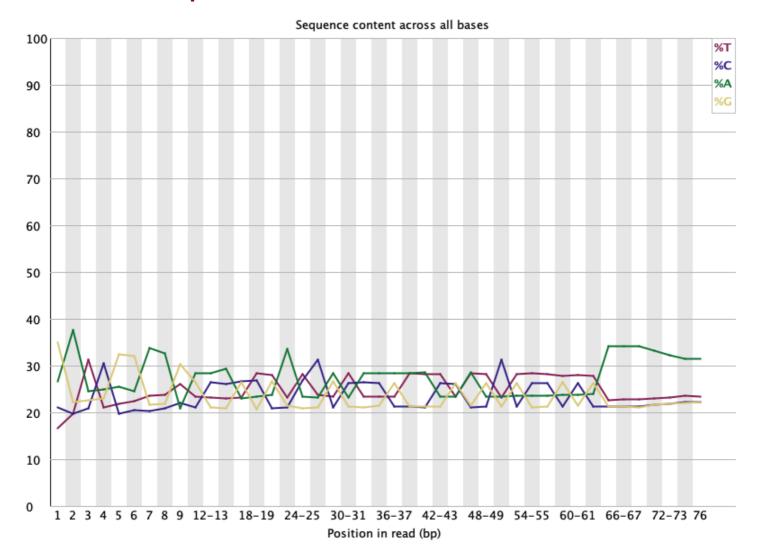
Per base sequence quality



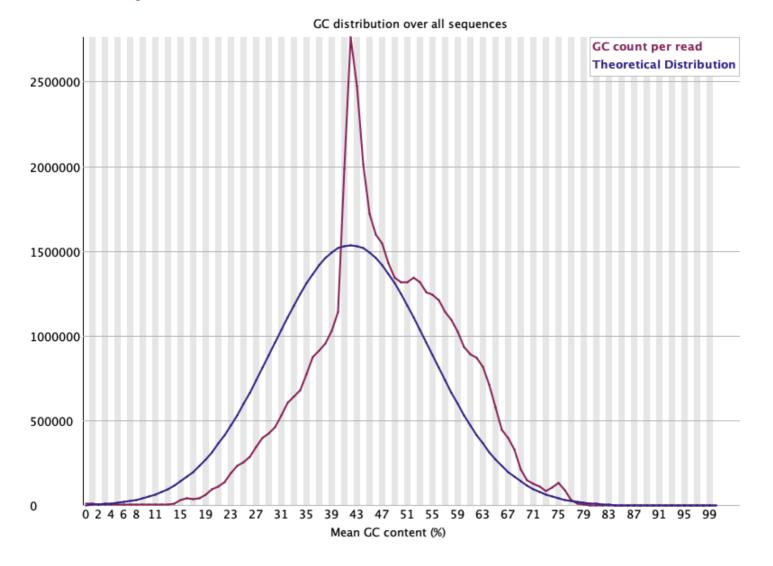
Per sequence quality scores



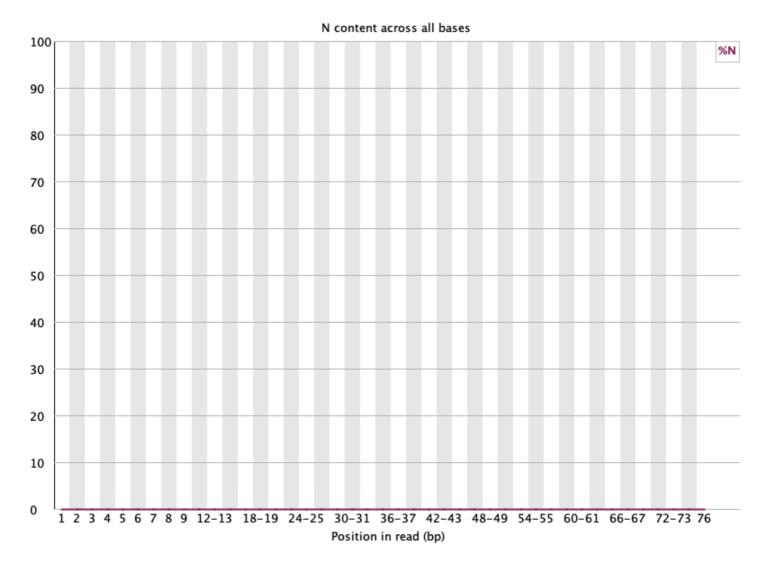
Per base sequence content



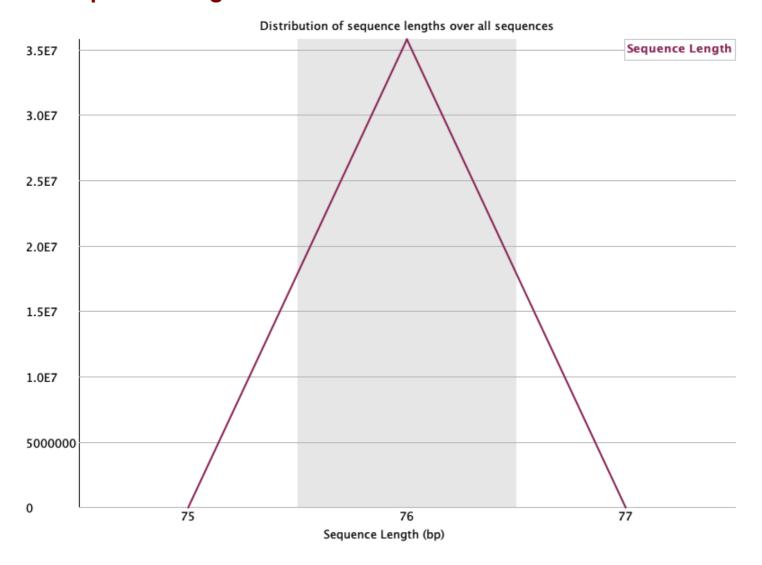
Per sequence GC content



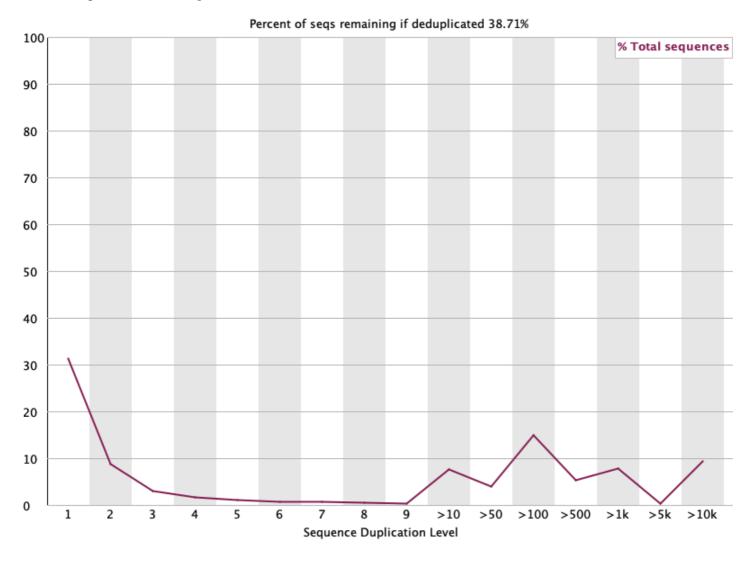
Per base N content



Sequence Length Distribution



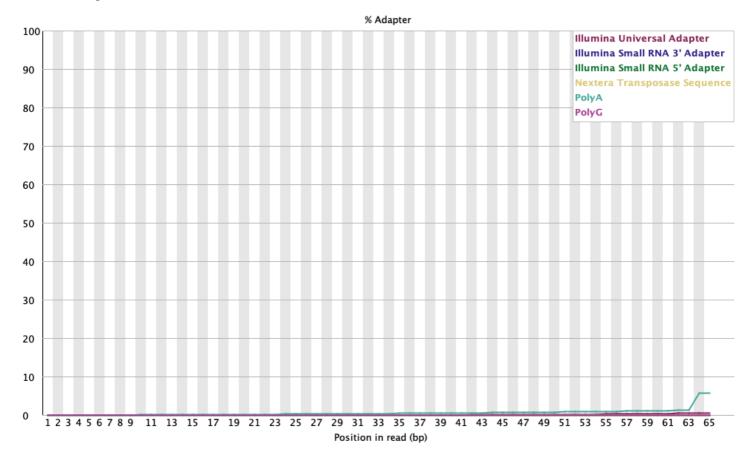
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACGATAATCTCGTATGC	3189654	8.919487634781017	TruSeq Adapter, Index 15 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	179857	0.5029486858226031	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)