Mon 5 Feb 2024 SRR13380529_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 SRR13380529_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 36649603

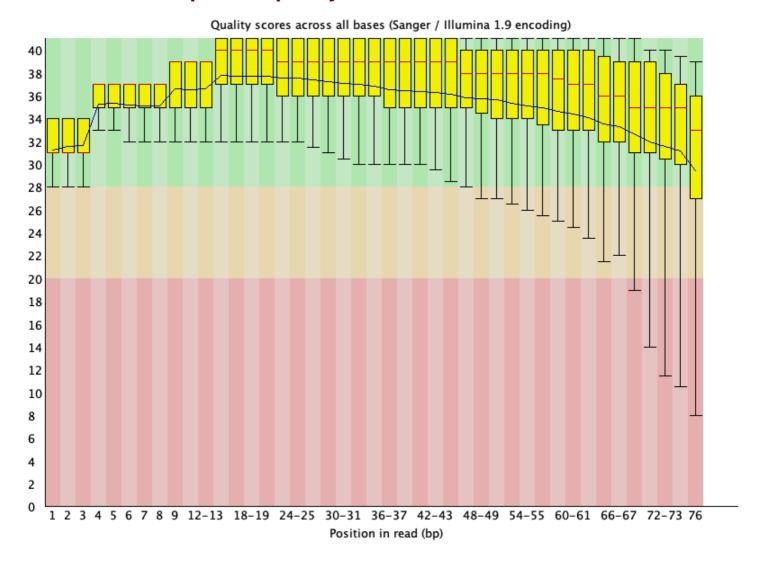
Total Bases 2.7 Gbp

Sequences flagged as poor quality 0

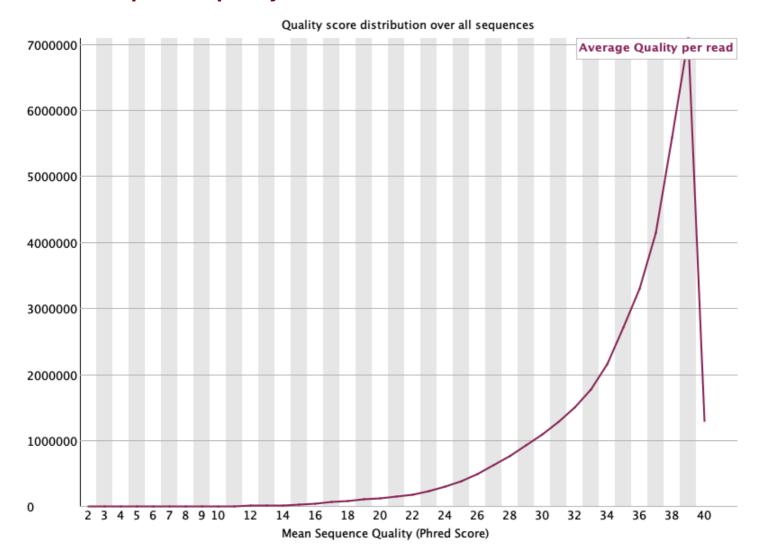
Sequence length 76

%GC 43

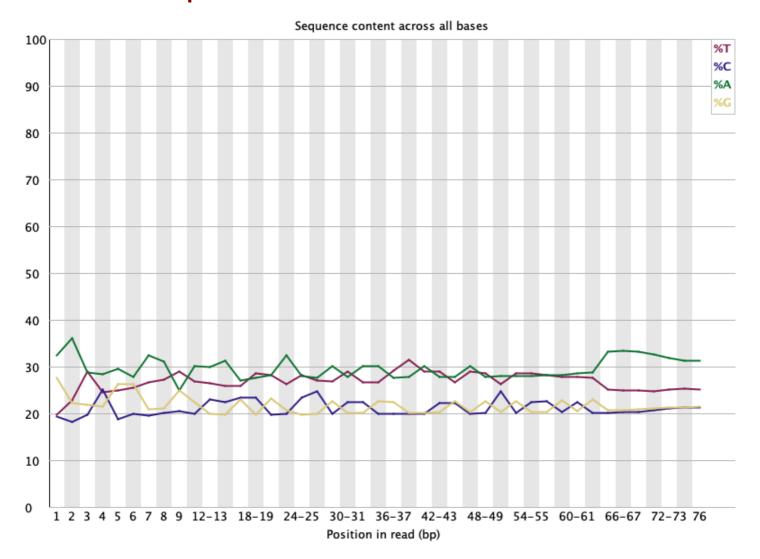
Per base sequence quality



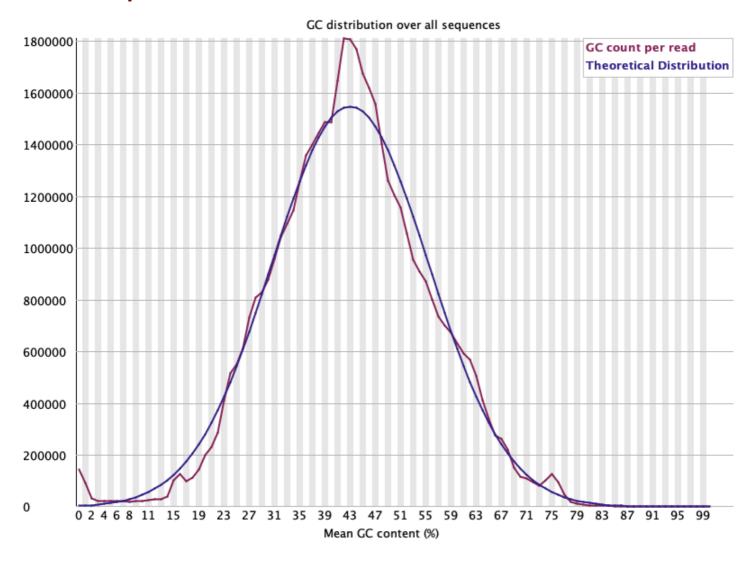
Per sequence quality scores



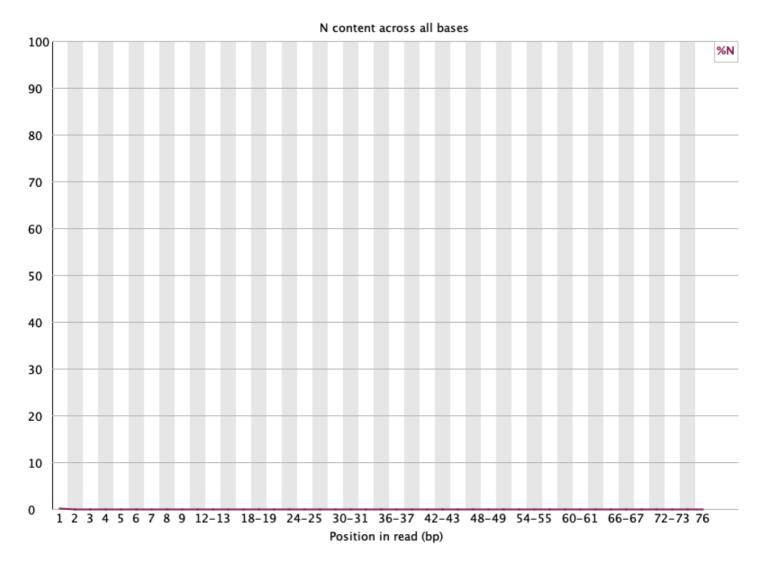
Per base sequence content



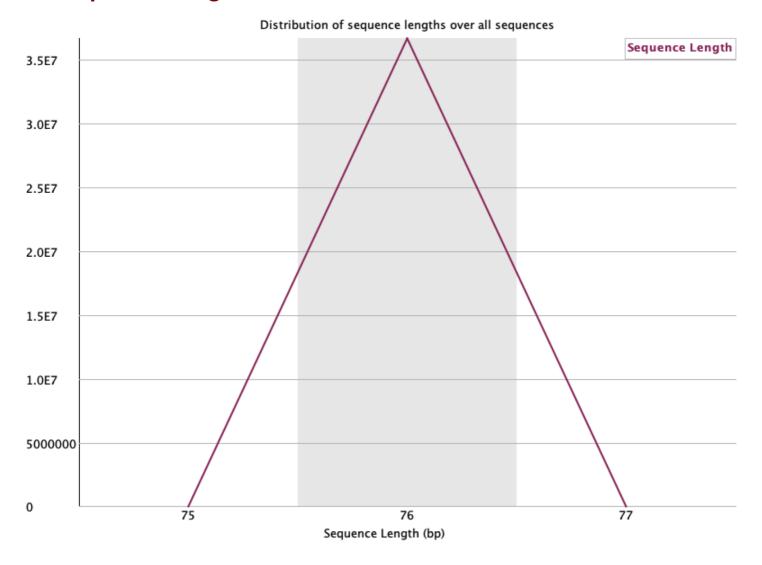
Per sequence GC content



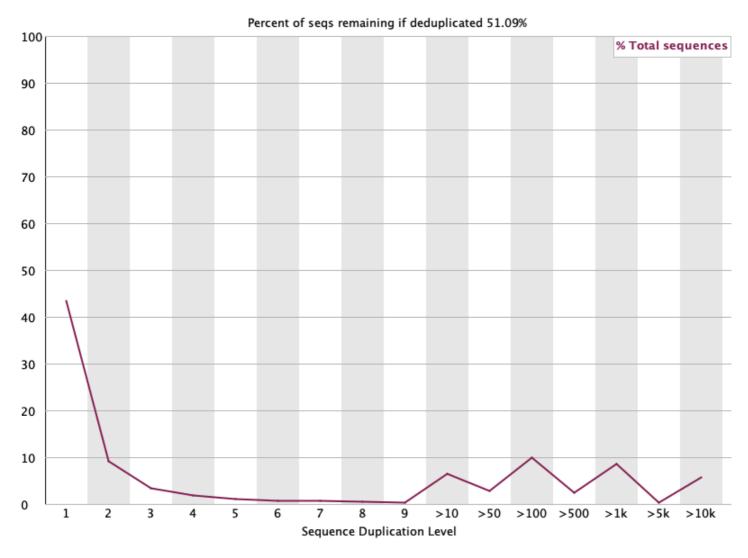
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGGTTTATCTCGTATGC	1537637	4.195507929512907	TruSeq Adapter, Index 14 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	394106	1.0753349770255356	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	115525	0.3152148742238763	No Hit

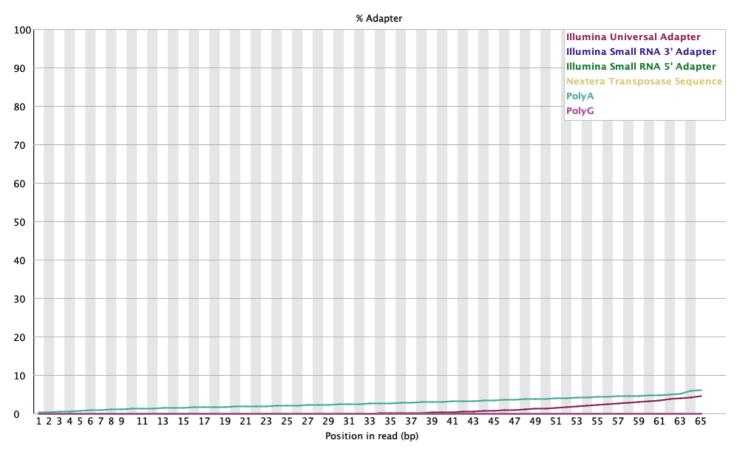
Sequence

Count

Percentage

Possible Source

Adapter Content



Produced by FastQC (version 0.12.1)