Mon 5 Feb 2024 SRR13380525_1.fastq

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 SRR13380525_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

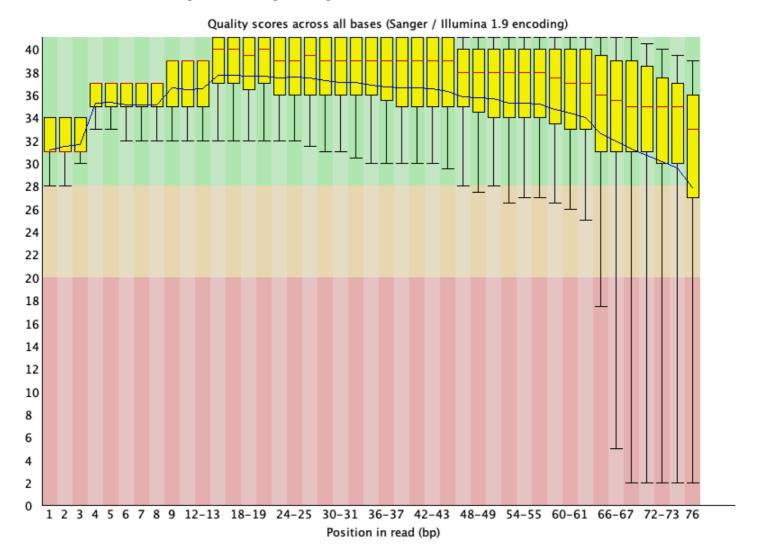
Total Sequences 46570010
Total Bases 3.5 Gbp

Sequences flagged as poor quality 0

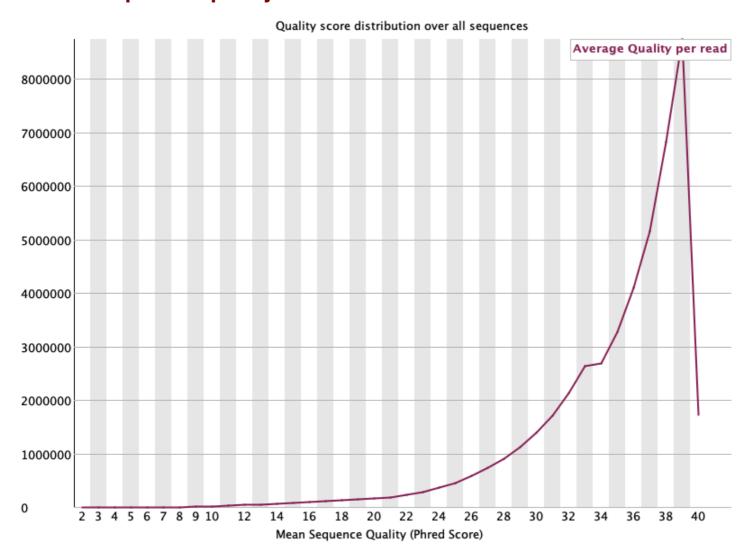
Sequence length 76

%GC 45

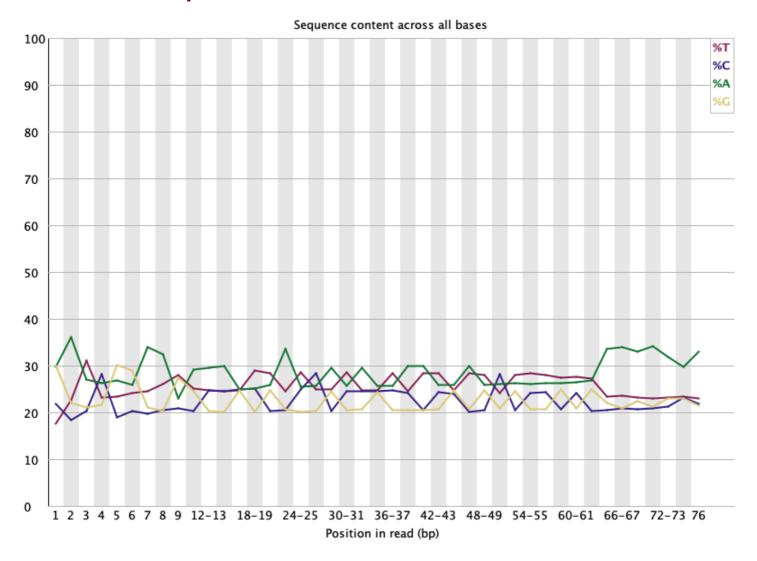
Per base sequence quality



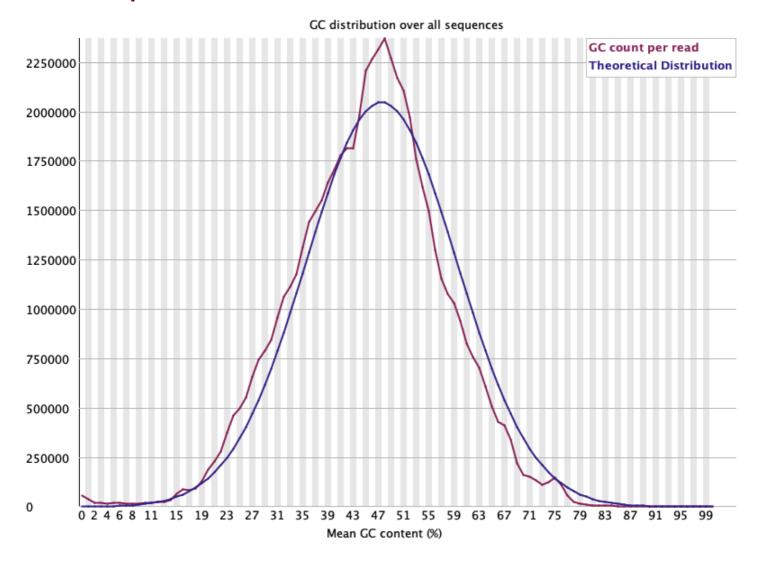
Per sequence quality scores



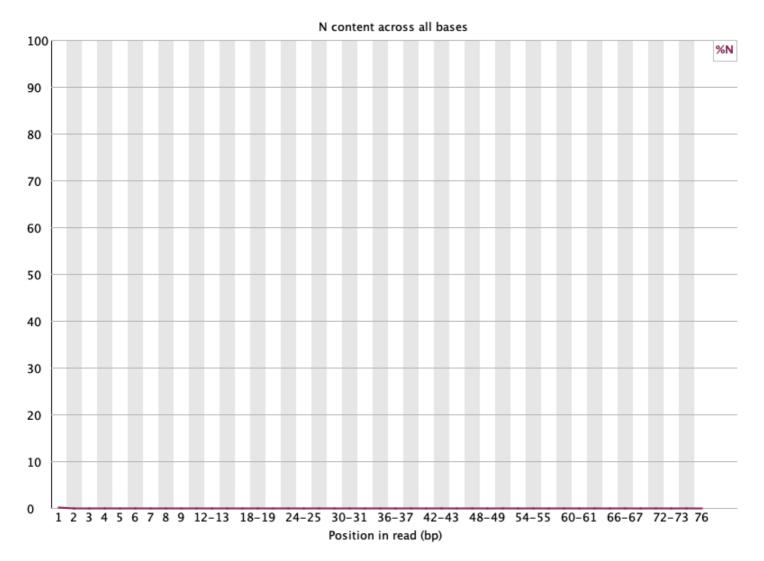
Per base sequence content



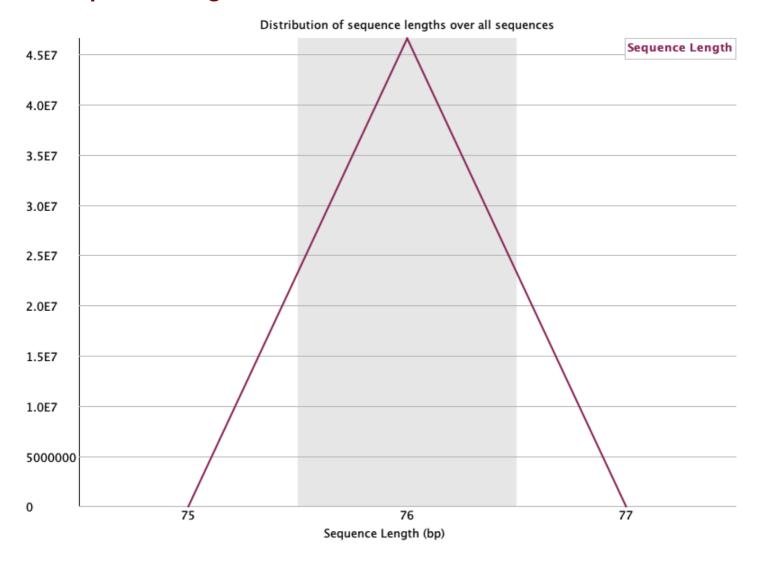
Per sequence GC content



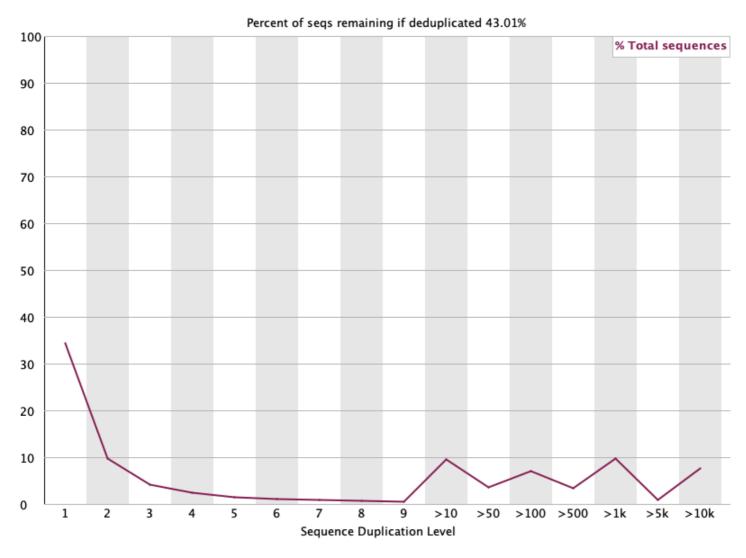
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCTCCAATCTCGTATGC	3198777	6.868748793483189	TruSeq Adapter, Index 9 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	160902	0.3455056161680017	Clontech SMART CDS Primer II A (100% over 26bp)

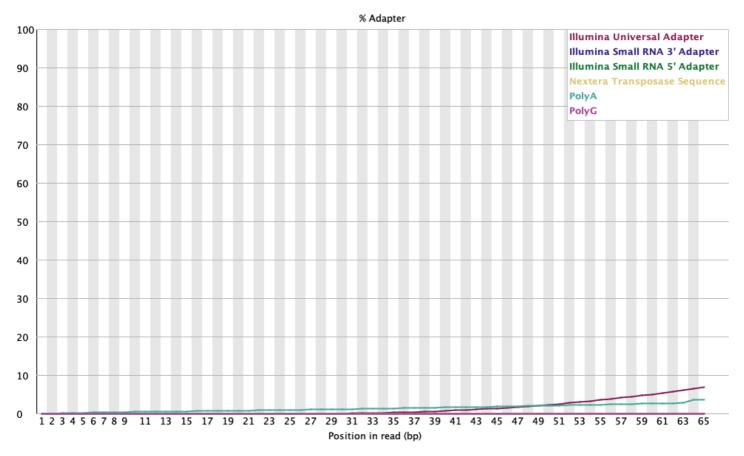
Sequence

Count

Percentage

Possible Source

Adapter Content



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