Report

Mon 5 Feb 2024 SRR13380471_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



Measure Value

SRR13380471_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

Total Sequences 6450215

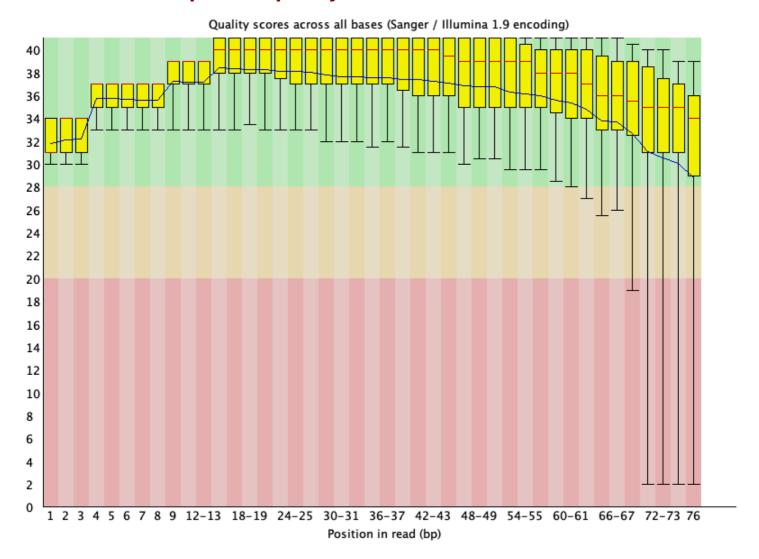
Total Bases 490.2 Mbp

Sequences flagged as poor quality 0

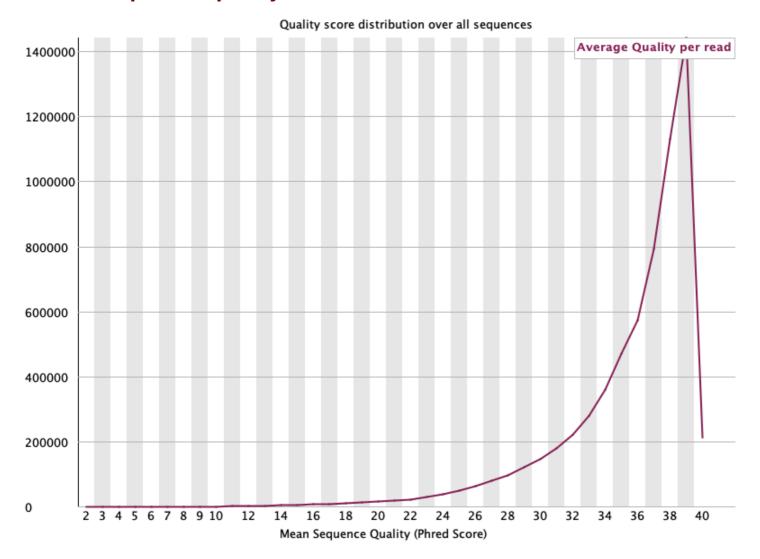
Sequence length 76

%GC 47

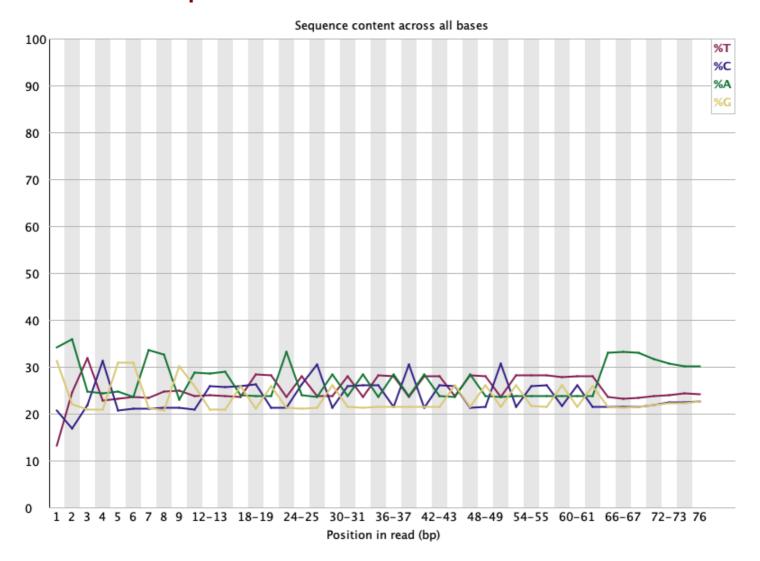
Per base sequence quality



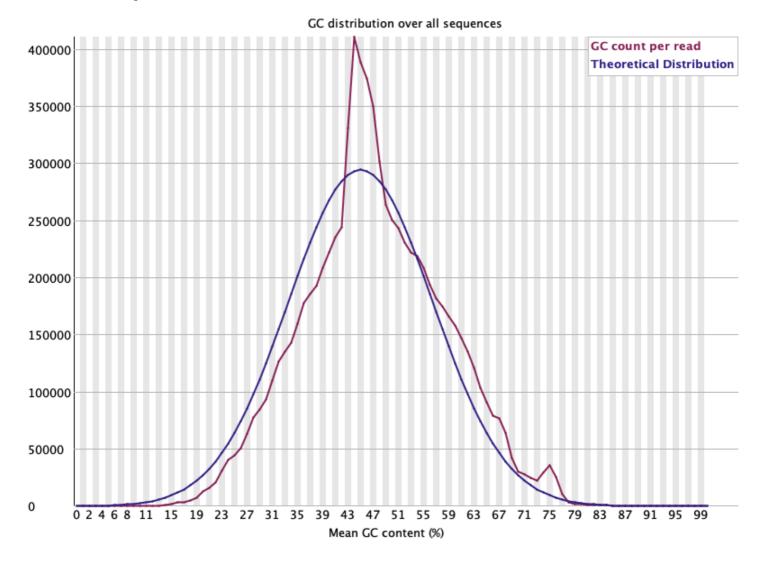
Per sequence quality scores



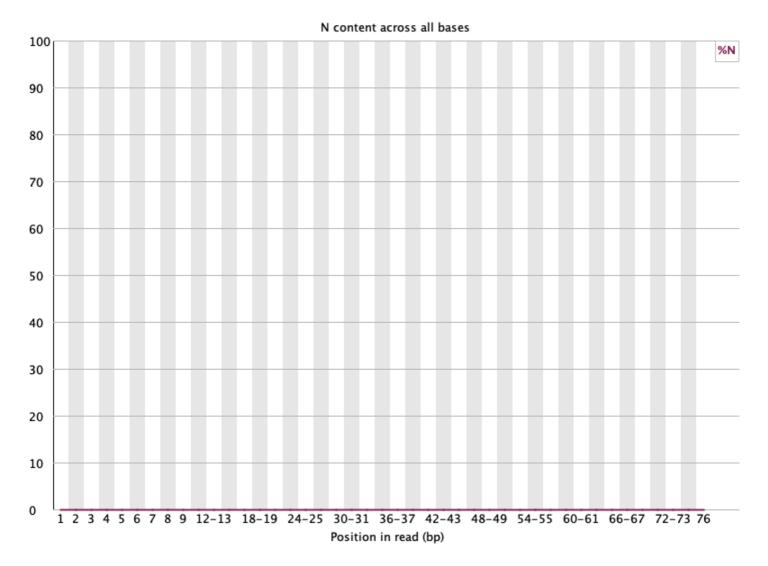
Per base sequence content



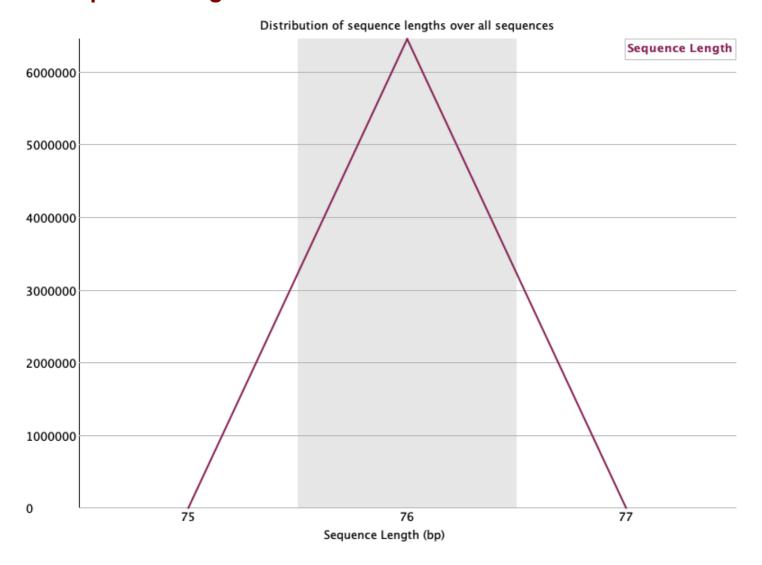
Per sequence GC content



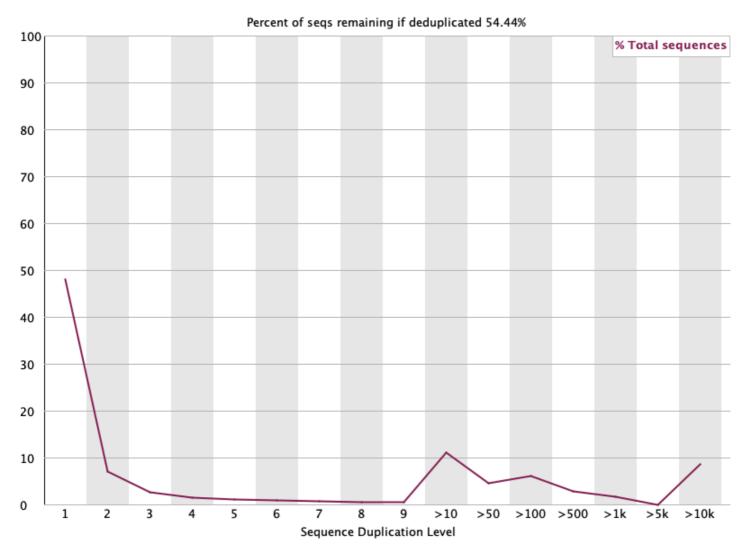
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTCTACCATCTCGTAT	GC 545646	8.459345928779118	TruSeq Adapter, Index 8 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	TT 13054	0.20238085087086244	Clontech SMART CDS Primer II A (100% over 26bp)
CGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACTCTACC	AT 6616	0.1025702244033726	TruSeq Adapter,

Sequence

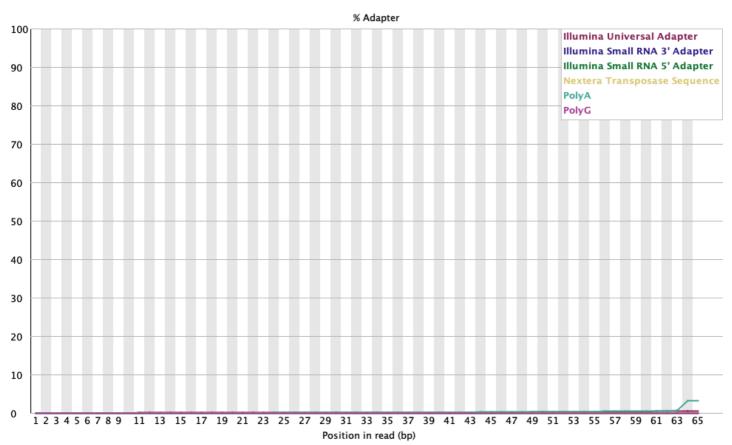
Count

Percentage

Possible Source

Index 8 (97% over 36bp)

Adapter Content



Produced by FastQC (version 0.12.1)