Mon 5 Feb 2024 SRR13380466_1.fastq

PastQC 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



Measure Value

Filename SRR13380466_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 9776534

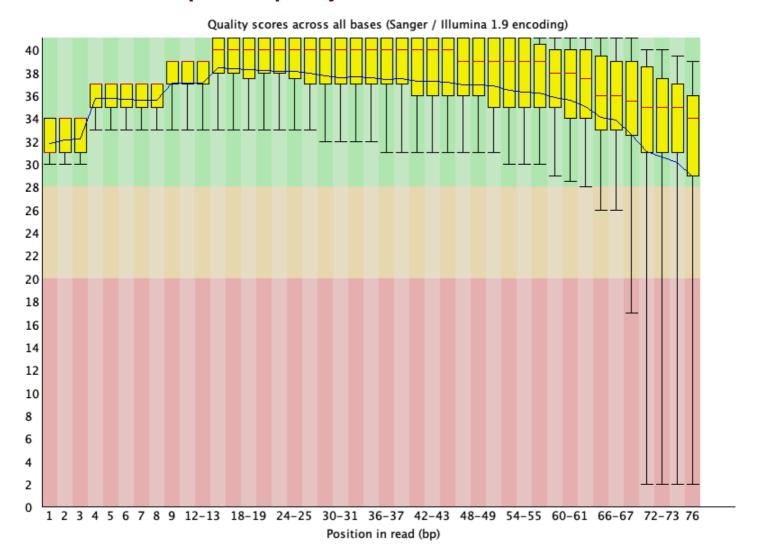
Total Bases 743 Mbp

Sequences flagged as poor quality $\, {\tt 0} \,$

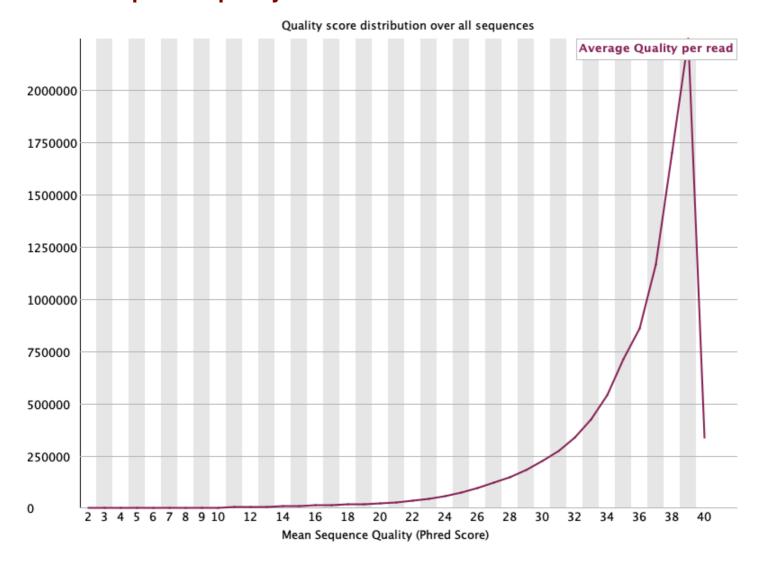
Sequence length 76

%GC 46

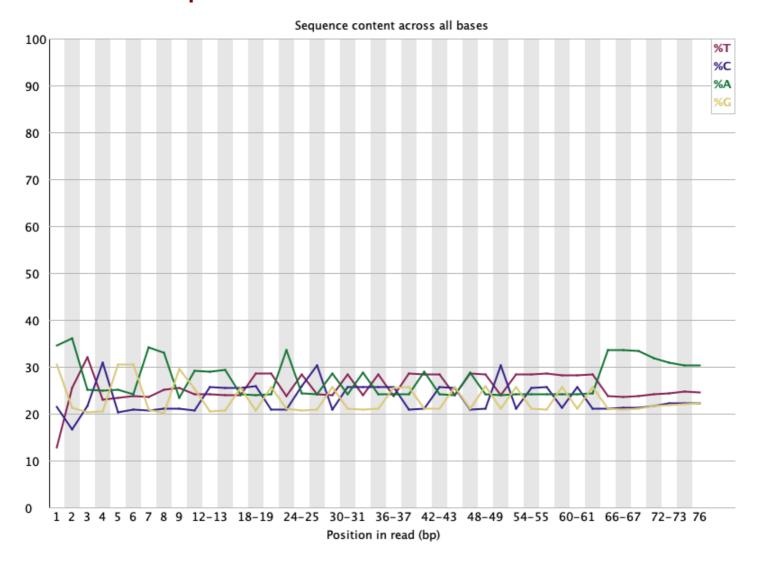
Per base sequence quality



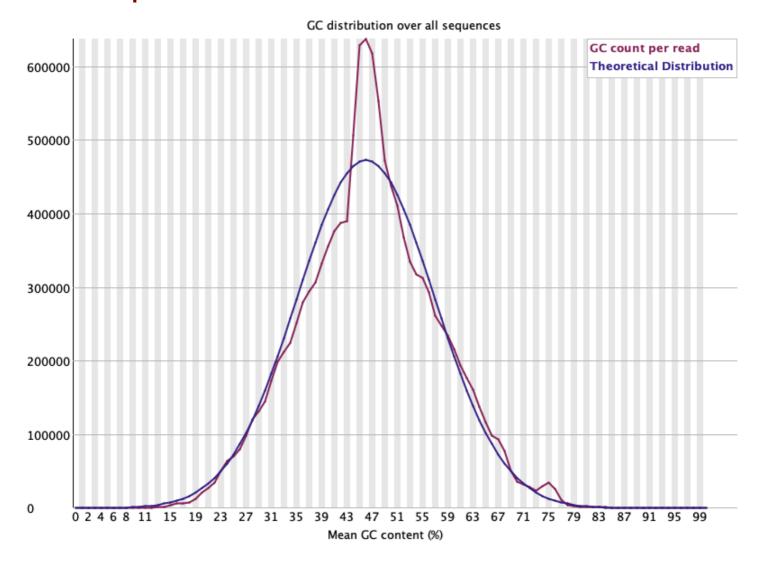
Per sequence quality scores



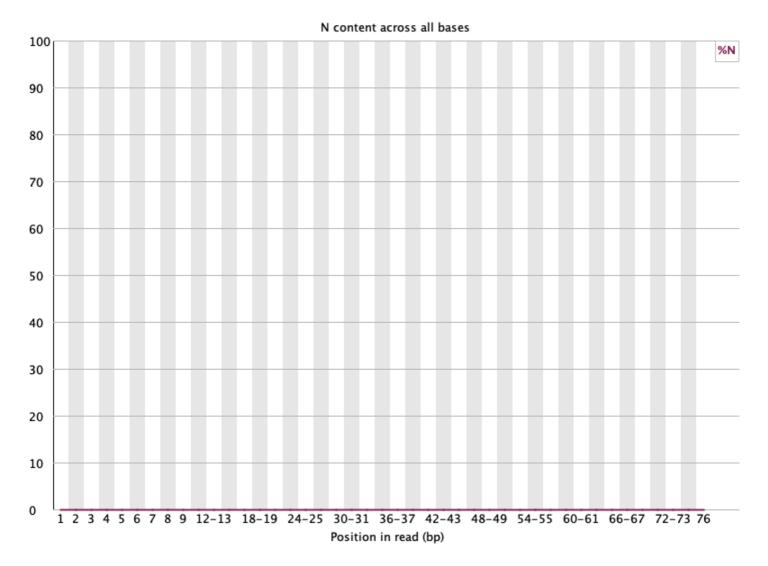
Per base sequence content



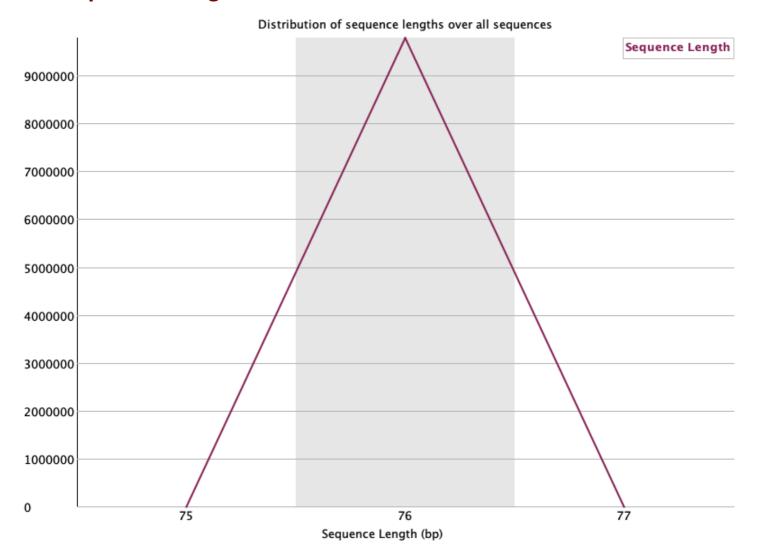
Per sequence GC content



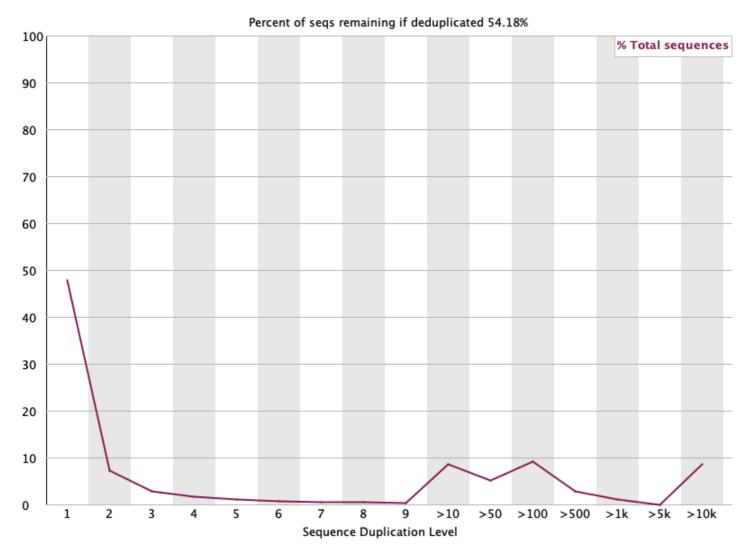
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTGCTGATCTCGTATGC	826005	8.4488531416144	TruSeq Adapter, Index 7 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT	⁻ 19519	0.19965153294613408	Clontech SMART CDS Primer II A (100% over 26bp)
CGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACCTGCTGAT	9821	0.10045482376474116	TruSeq Adapter,

Sequence

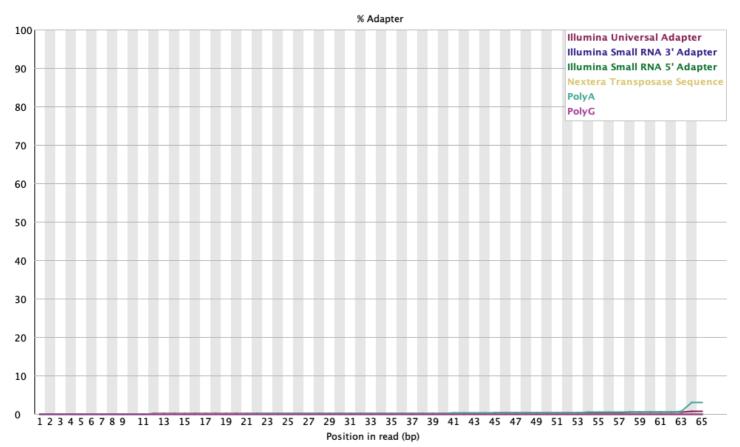
Count

Percentage

Possible Source

Index 7 (97% over 36bp)

Adapter Content



Produced by FastQC (version 0.12.1)