Report

Tue 6 Feb 2024 SRR13380490_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

SRR13380490_1.fastq Filename

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

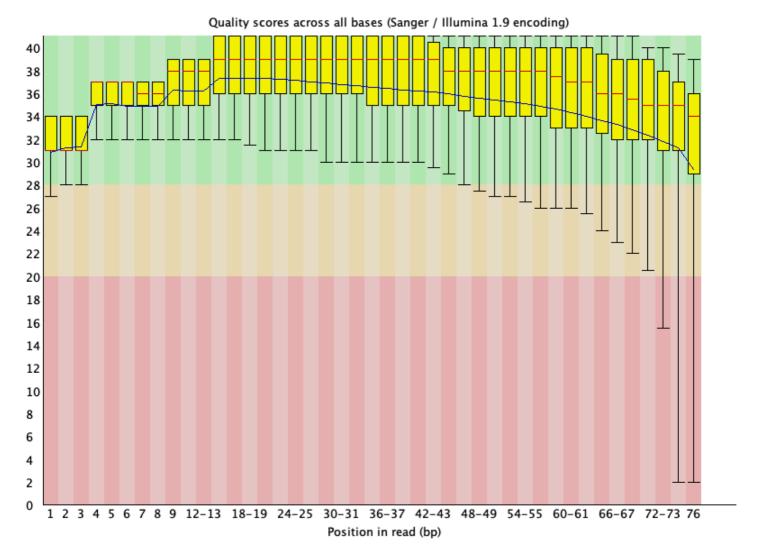
Total Sequences 17080011 Total Bases 1.2 Gbp

Sequences flagged as poor quality

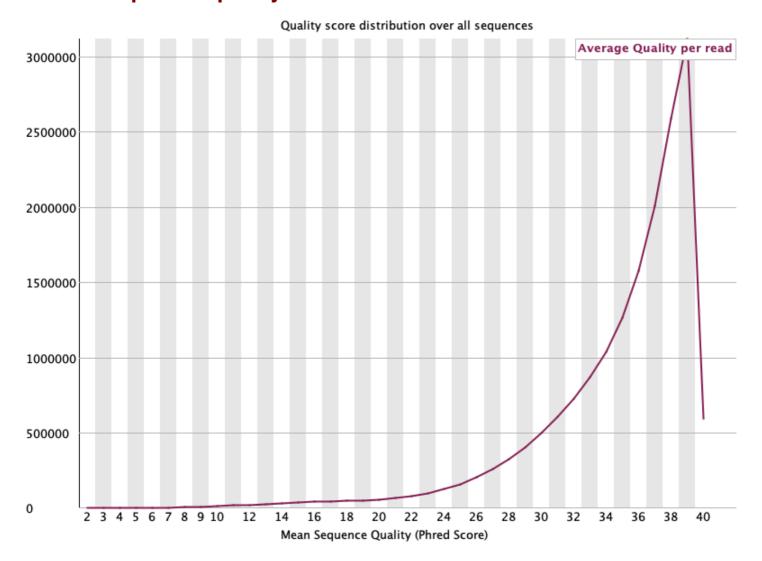
Sequence length 76

%GC 44

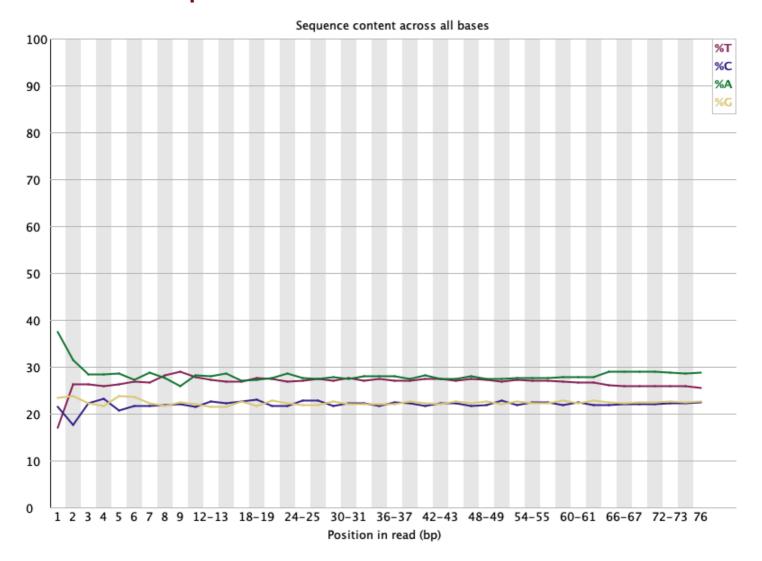
Per base sequence quality



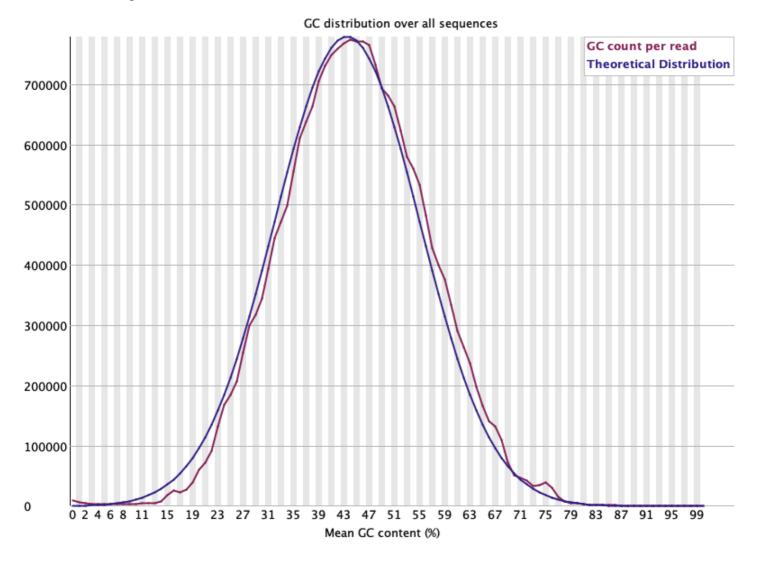
Per sequence quality scores



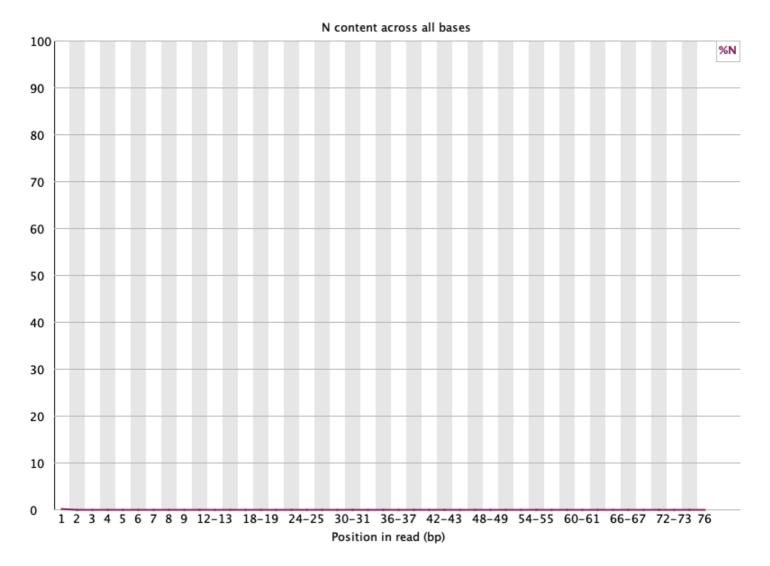
Per base sequence content



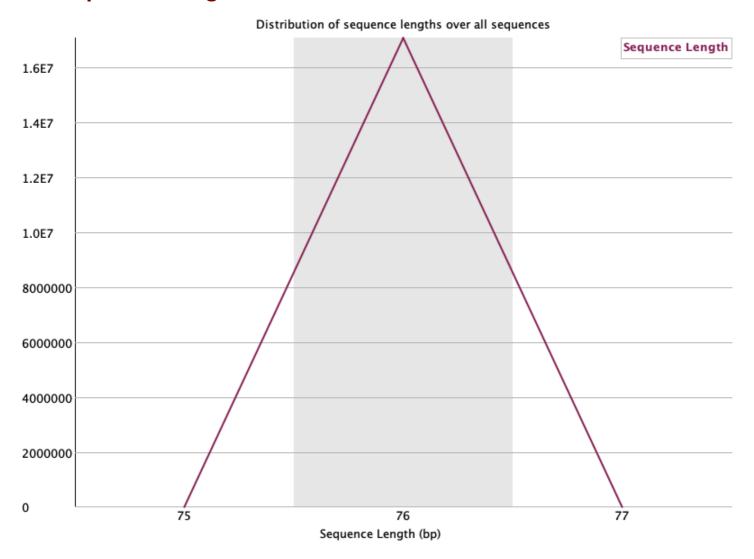
Per sequence GC content



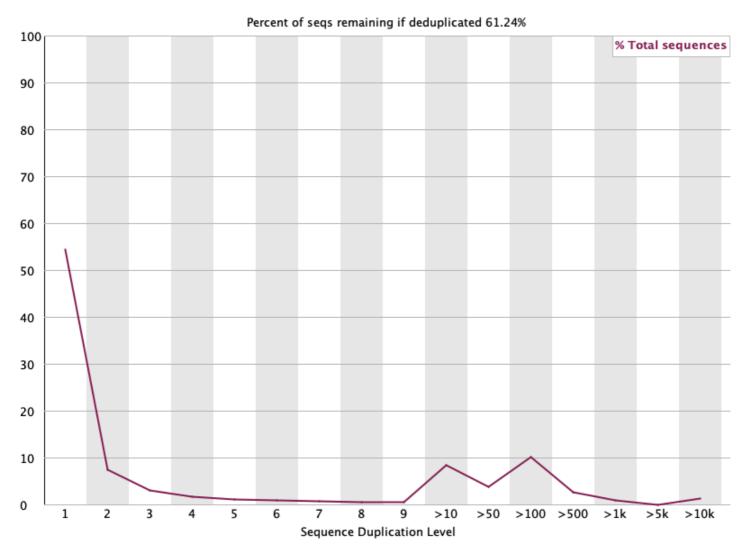
Per base N content



Sequence Length Distribution



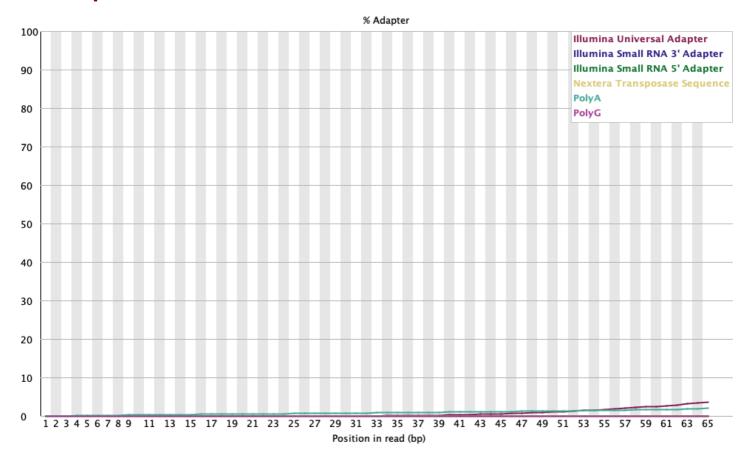
Sequence Duplication Levels



Overrepresented sequences

	Sequence	Count	Percentage	Possible Source
GA	TCGGAAGAGCACACGTCTGAACTCCAGTCACTACAGCATCTCGTATGC	161008	0.9426691821217211	TruSeq Adapter, Index 7 (97% over 35bp)
AA	GCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTT	82646	0.48387556659067726	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)