Mon 5 Feb 2024 SRR13380457_1.fastq

PastQC Report Summary



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 SRR13380457_1.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 7629327

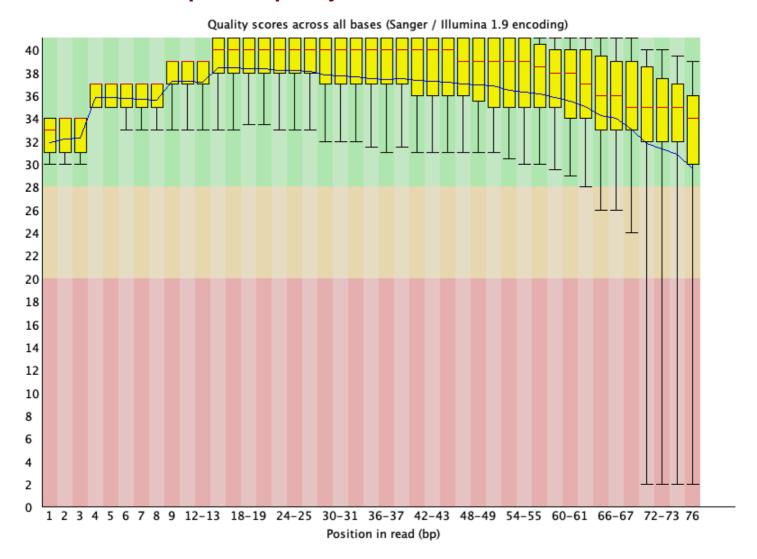
Total Bases 579.8 Mbp

Sequences flagged as poor quality 0

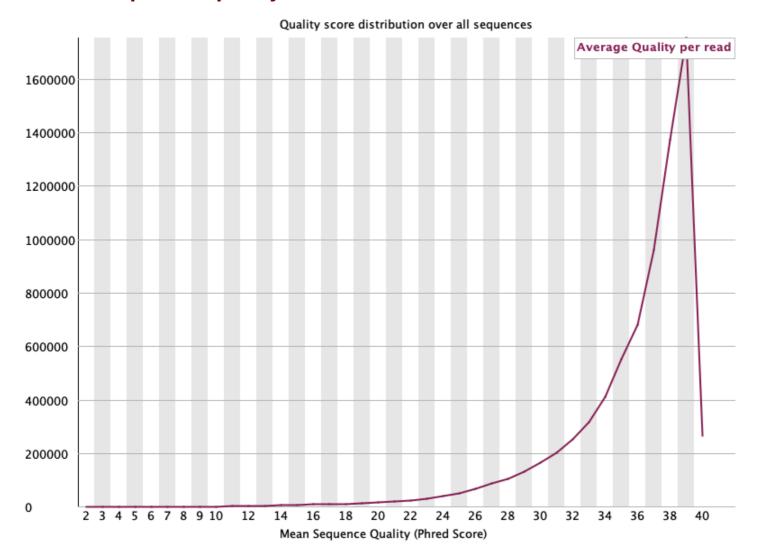
Sequence length 76

%GC 47

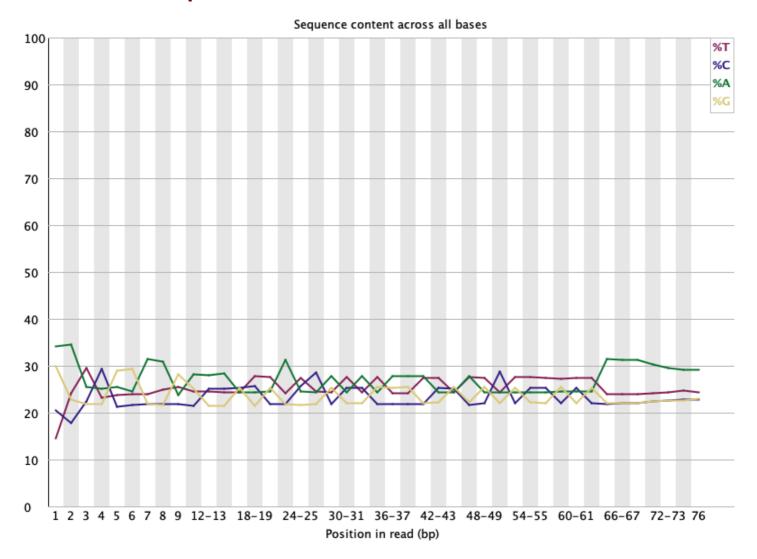
Per base sequence quality



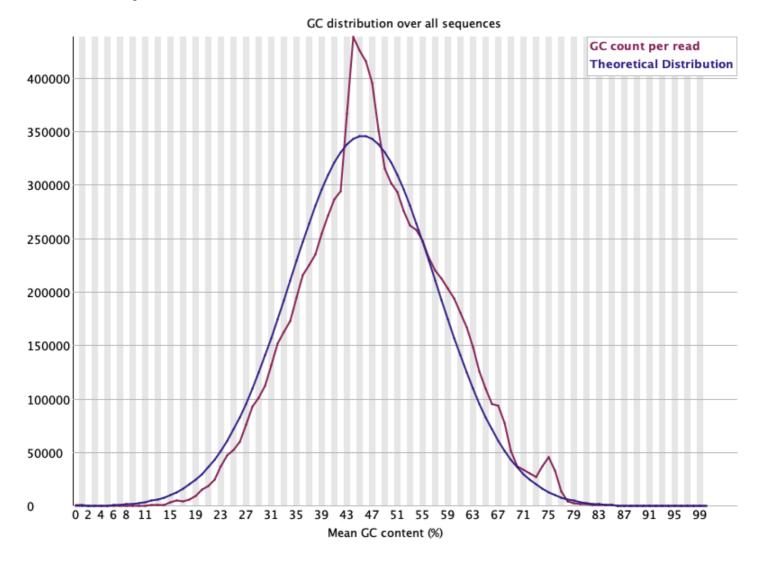
Per sequence quality scores



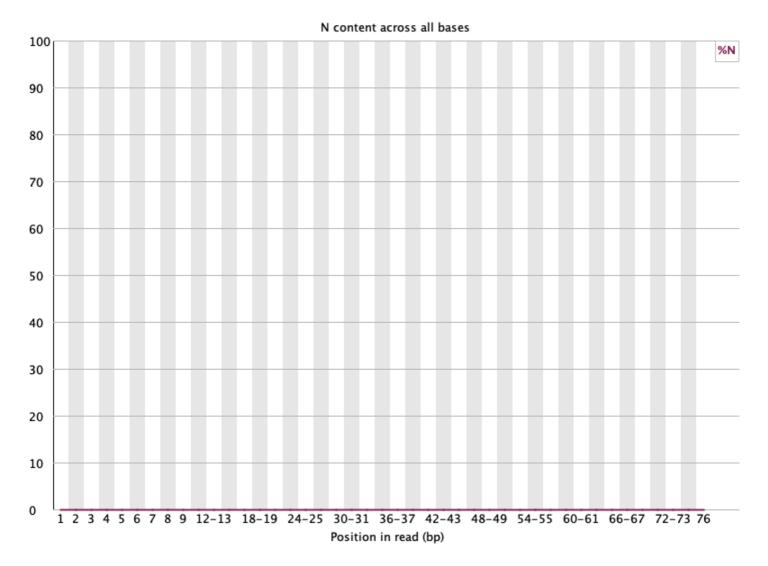
Per base sequence content



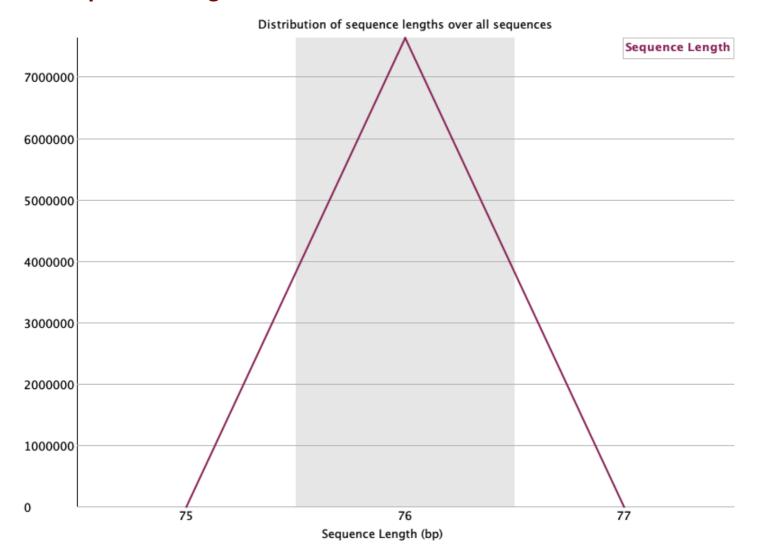
Per sequence GC content



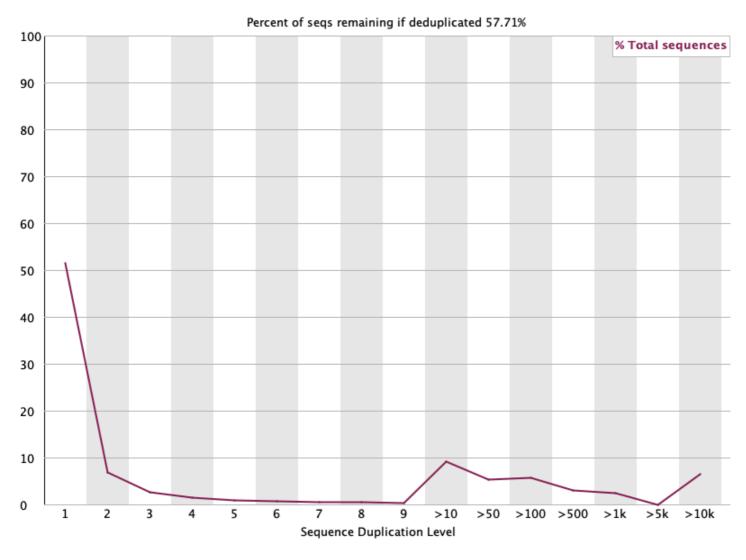
Per base N content



Sequence Length Distribution



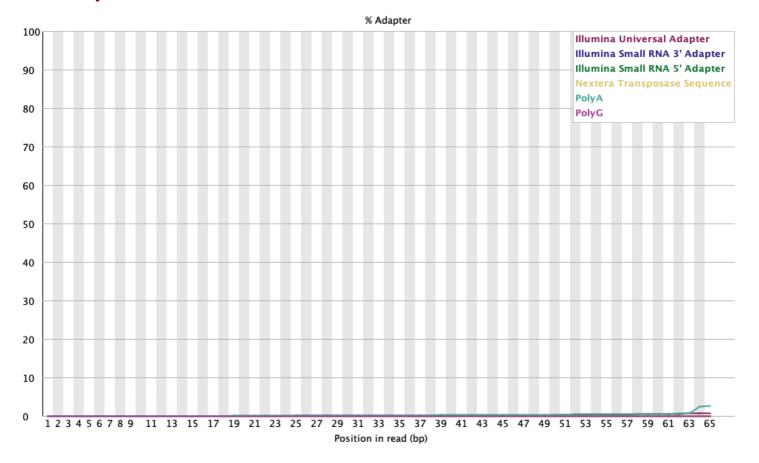
Sequence Duplication Levels



Overrepresented sequences

	Sequence	Count	Percentage	Possible Source
GATC	GGAAGAGCACACGTCTGAACTCCAGTCACGTAGAGATCTCGTATGC	475460	6.232004474313396	TruSeq Adapter, Index 3 (97% over 37bp)
AAGC	AGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTT	22102	0.28969789864820317	Clontech SMART CDS Primer II A (100% over 26bp)

Adapter Content



Produced by FastQC (version 0.12.1)