FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per sequence quality scores](#)

❌ [Per base sequence content](#)

✅ [Per sequence GC content](#)
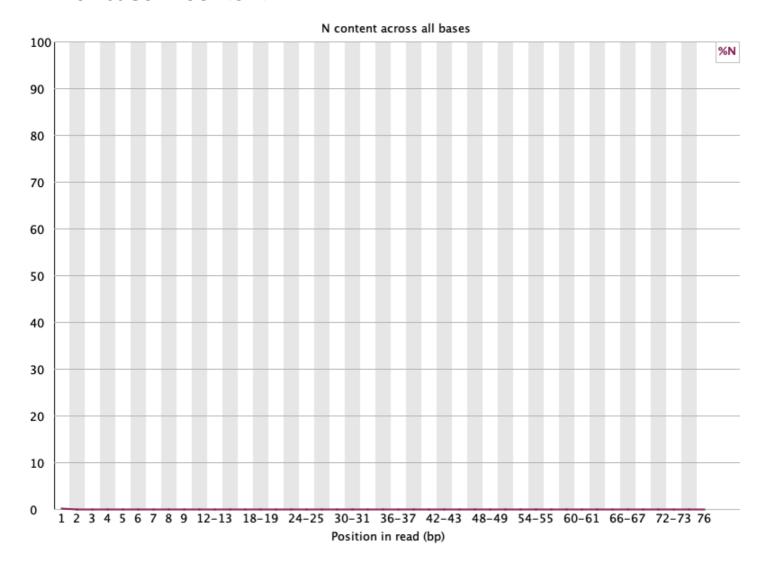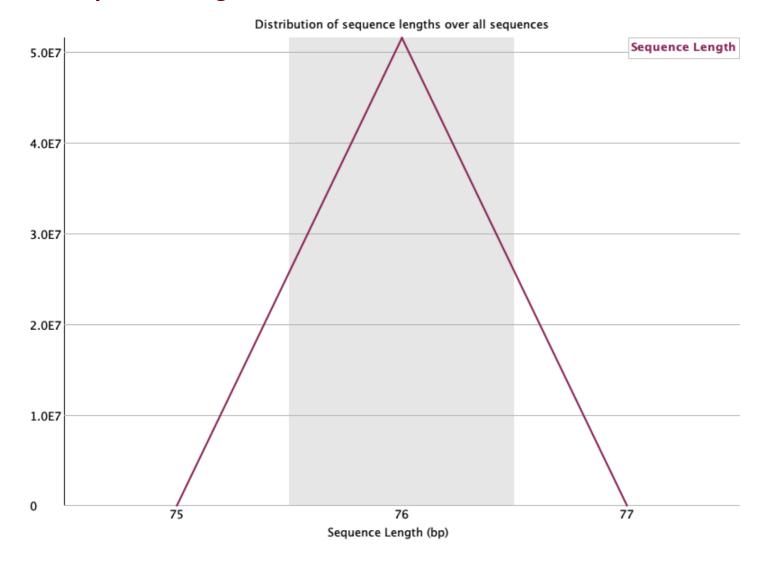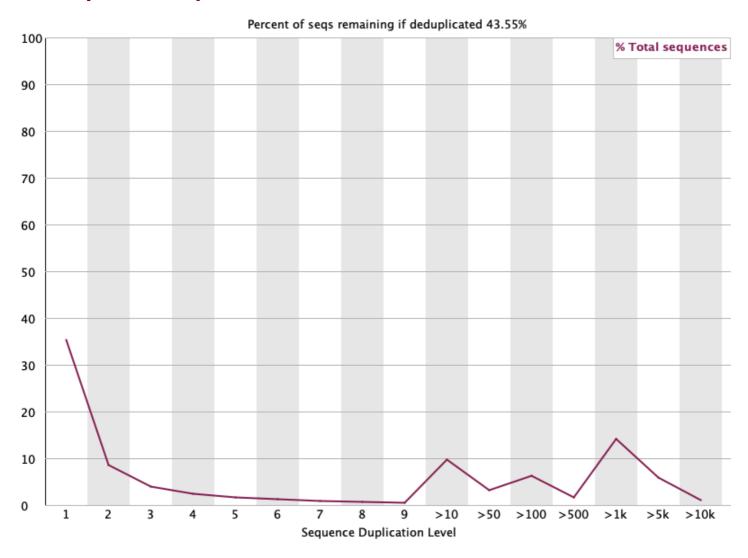
✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

❌ [Sequence Duplication Levels](#)

⚠️ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

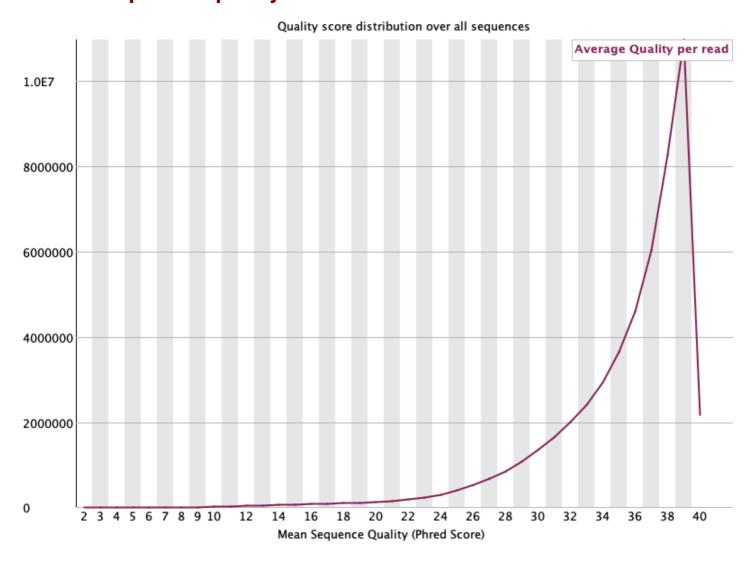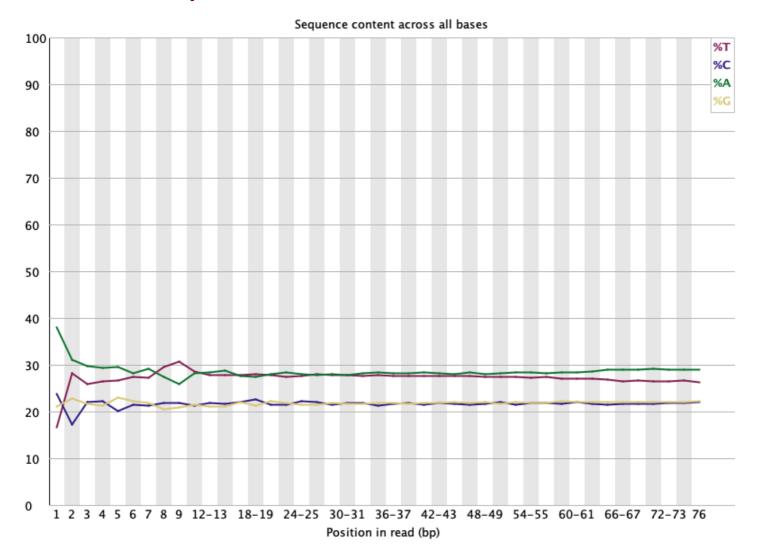| Measure	Value
Filename	SRR13380520_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	51506458
Total Bases	3.9 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	43

✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

Position in read (bp)

✅ Per sequence quality scores

Quality score distribution over all sequences

❌Per base sequence content

✅ Per sequence GC content

Per base N content

N content across all bases

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

❌ Sequence Duplication Levels

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAATCTCGTATGC	211259	0.4101602171906288	TruSeq Adapter, Index 15 (98% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTT	174774	0.3393244396654105	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

Produced by [FastQC](#) (version 0.12.1)