FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per sequence quality scores

⚠️ Per base sequence content

⚠️ Per sequence GC content
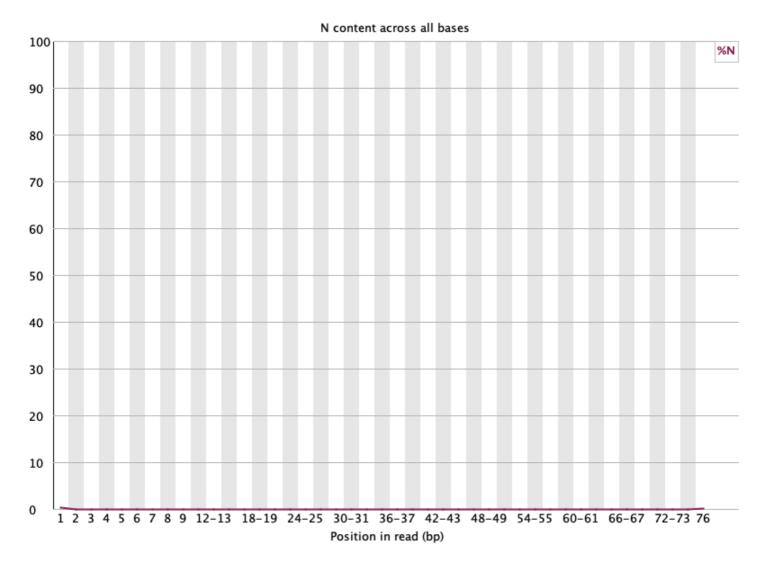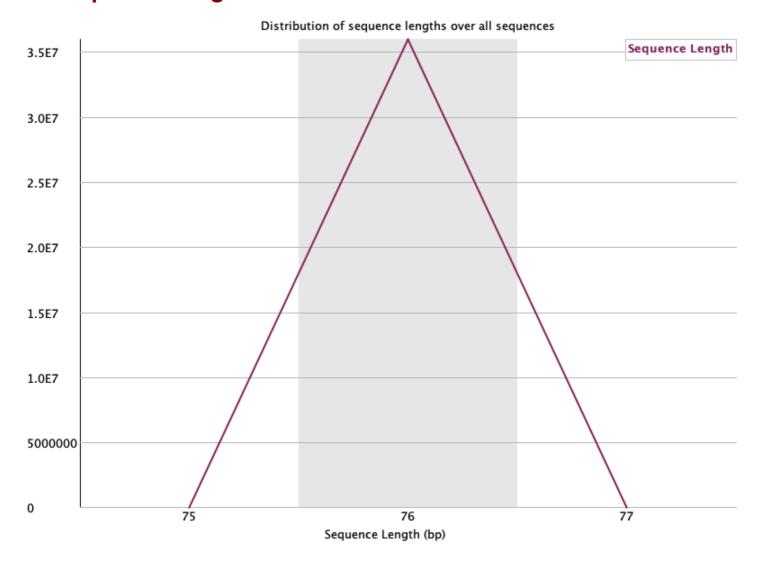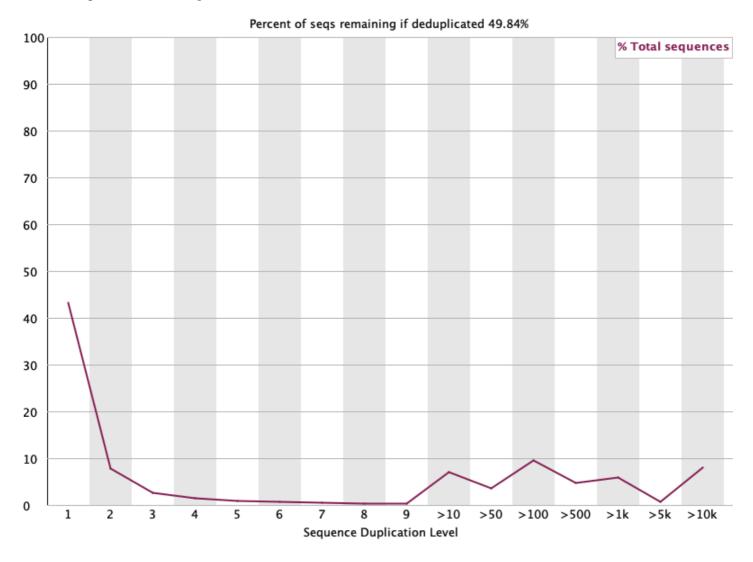
✅ Per base N content

✅ Sequence Length Distribution

❌ Sequence Duplication Levels

❌ Overrepresented sequences

⚠️ Adapter Content

✅ Basic Statistics

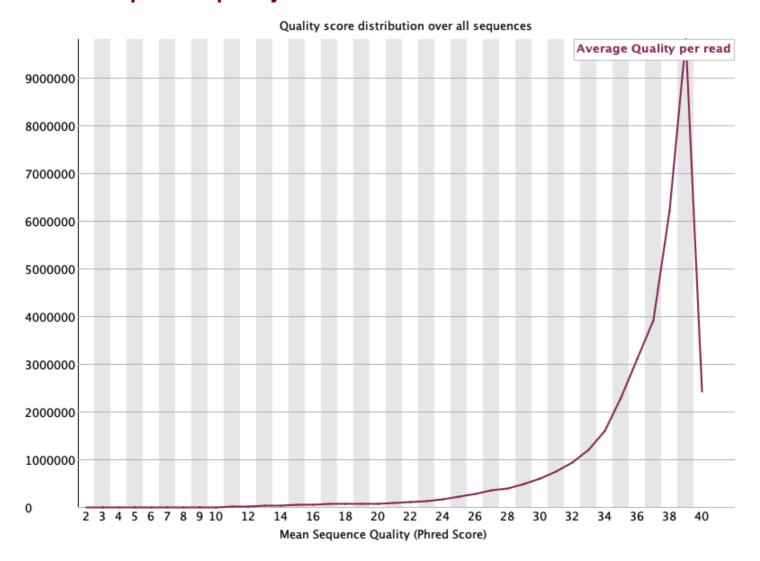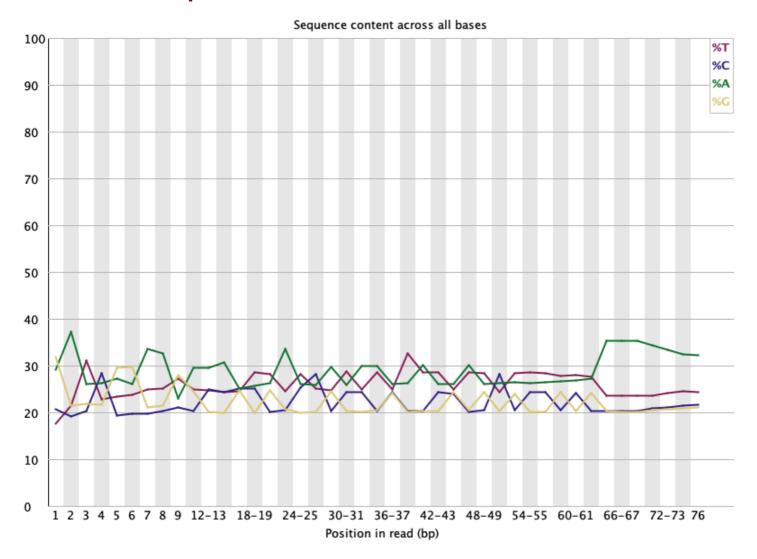| Measure	Value
Filename	SRR13380483_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	35957208
Total Bases	2.7 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	44

✅ Per base sequence quality

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

✅ 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
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGCTTATCTCGTATGC	2566012	7.136293785657663	TruSeq Adapter, Index 10 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	251746	0.7001266616696158	Clontech SMART CDS Primer II A (100% over 26bp)

⚠️ Adapter Content

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