FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per sequence quality scores

⚠️ Per base sequence content
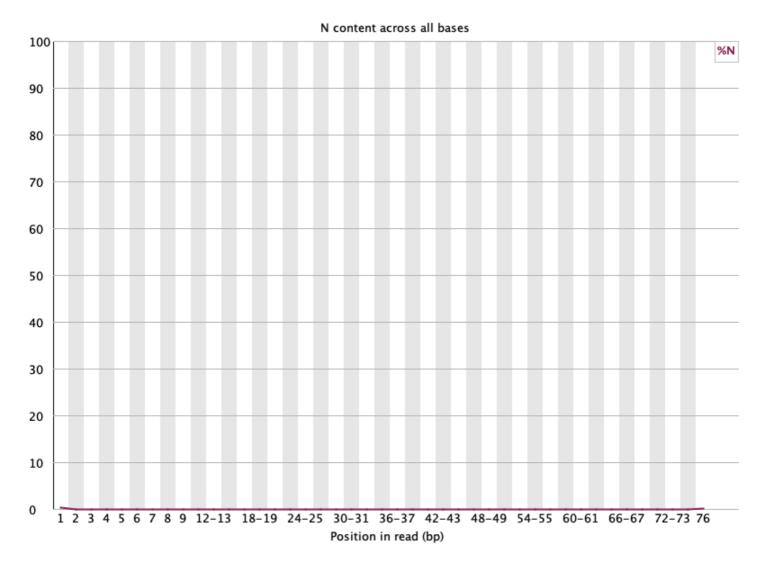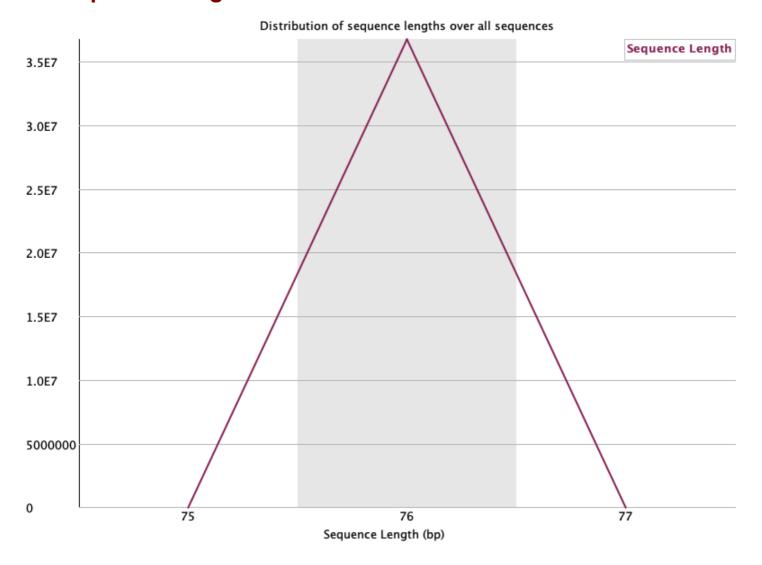
❌ Per sequence GC content
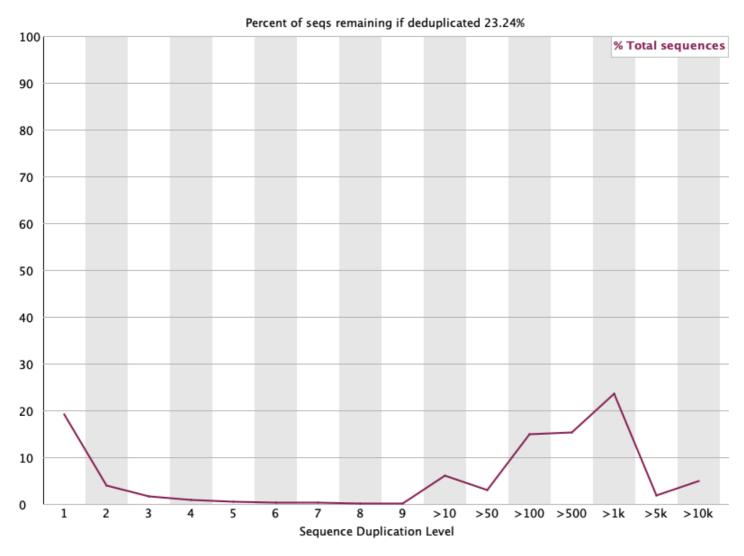
✅ Per base N content

✅ Sequence Length Distribution
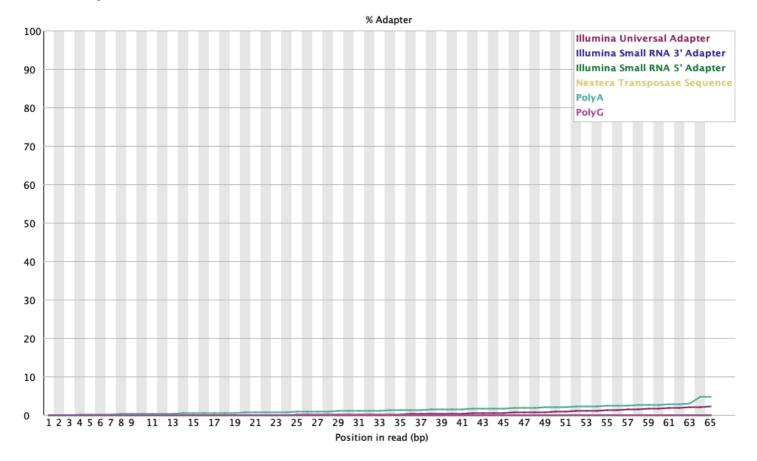
❌ Sequence Duplication Levels

❌ Overrepresented sequences

✅ Adapter Content

✅ Basic Statistics

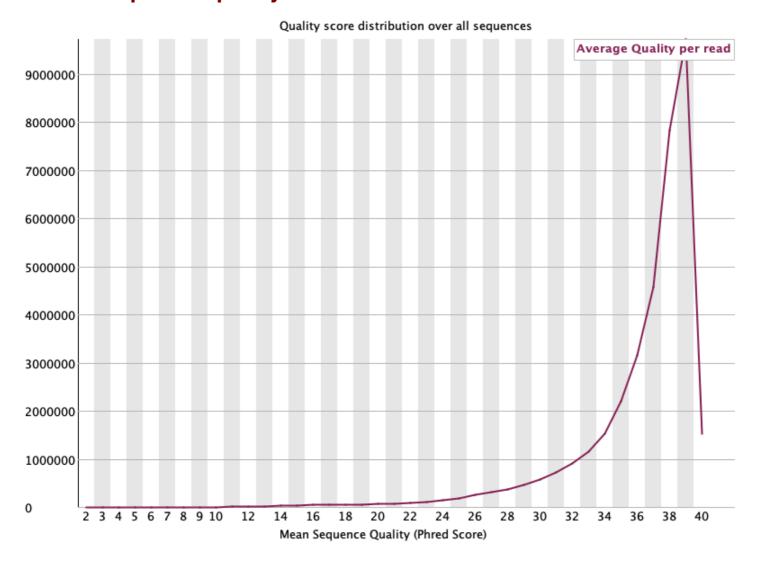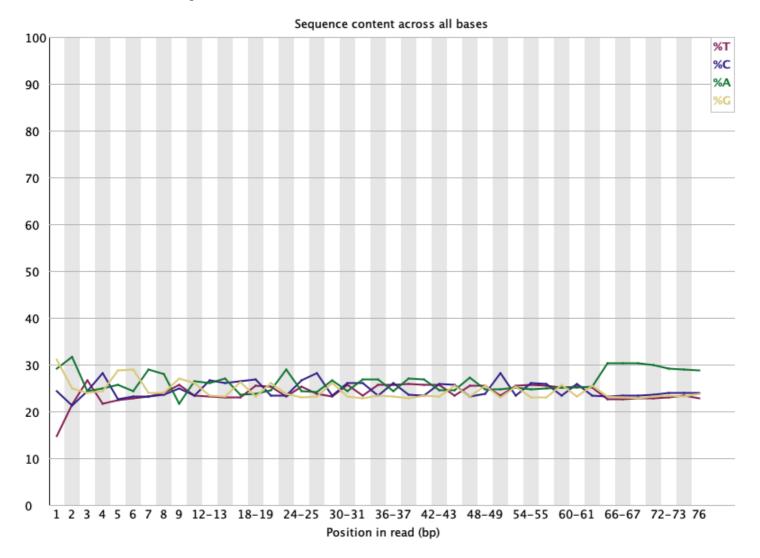| Measure	Value
Filename	SRR13380495_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36733246
Total Bases	2.7 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	49

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

GC distribution over all sequences

✅ Per base N content

N content across all bases

✅ Sequence Length Distribution

❌ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 23.24%

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCTATATCTCGTATGC	1570115	4.274370416379756	TruSeq Adapter, Index 15 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	176063	0.4793015025135541	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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