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

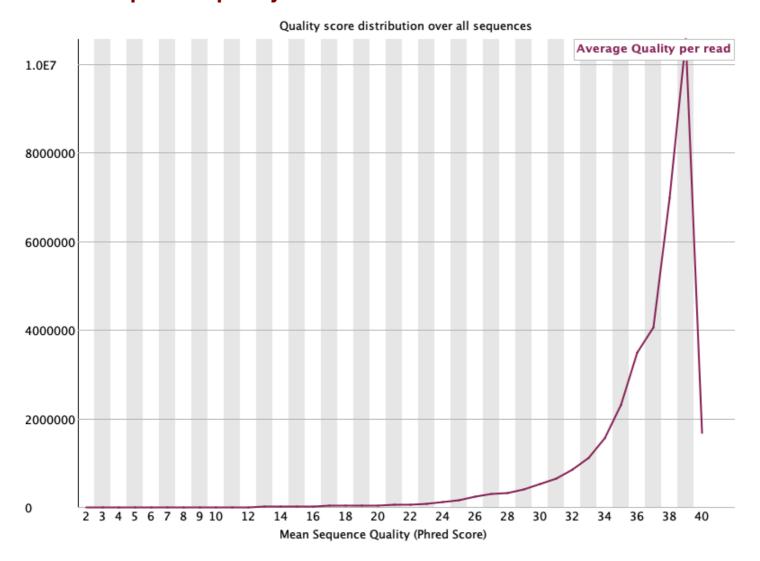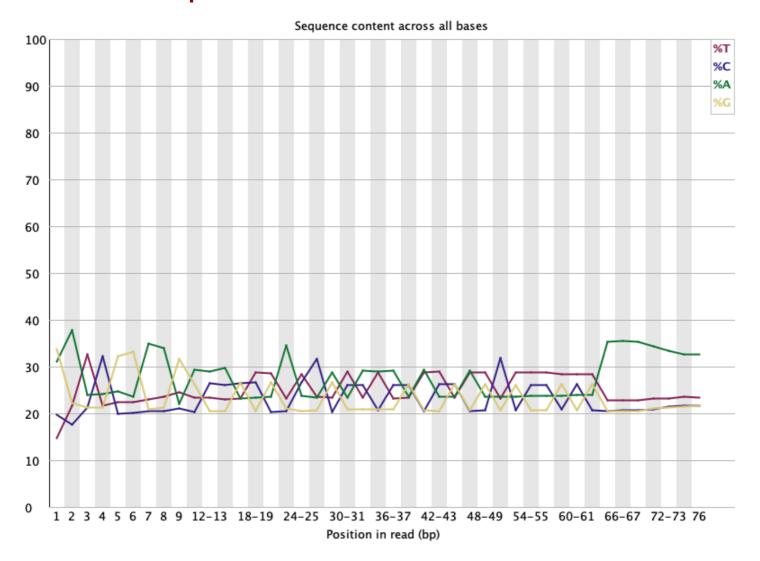| Measure	Value
Filename	SRR13380452_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36173999
Total Bases	2.7 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	46
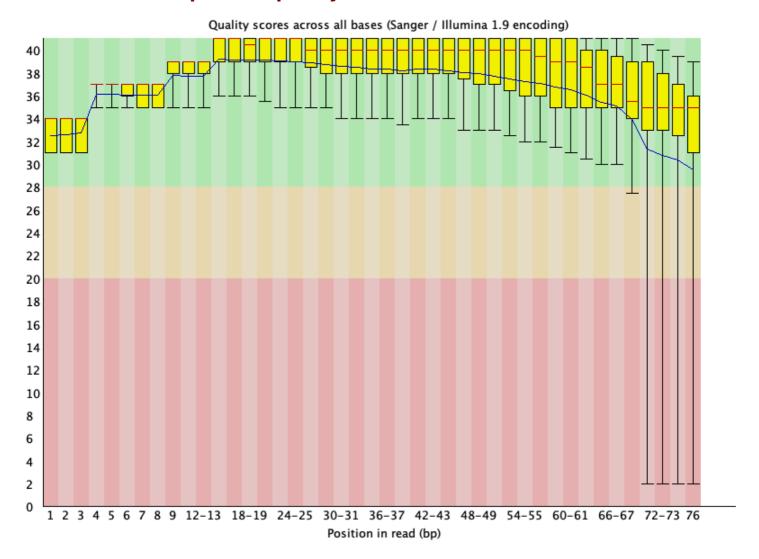
✅Per base sequence quality

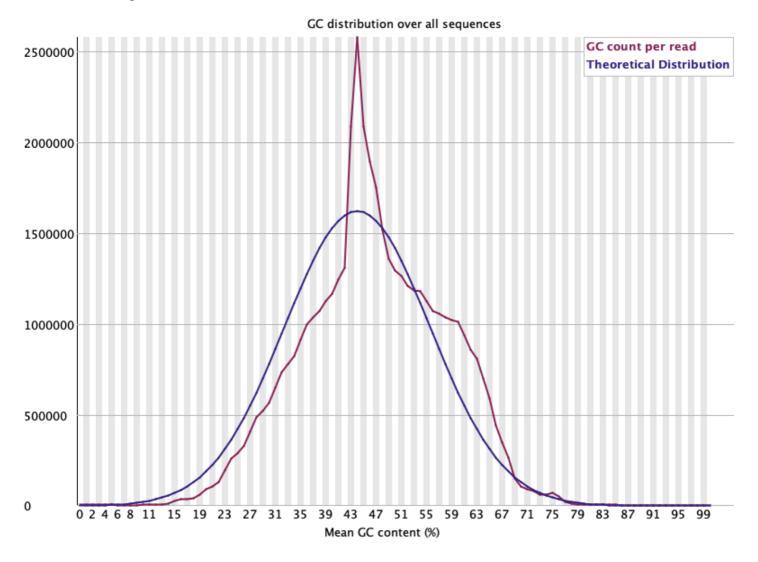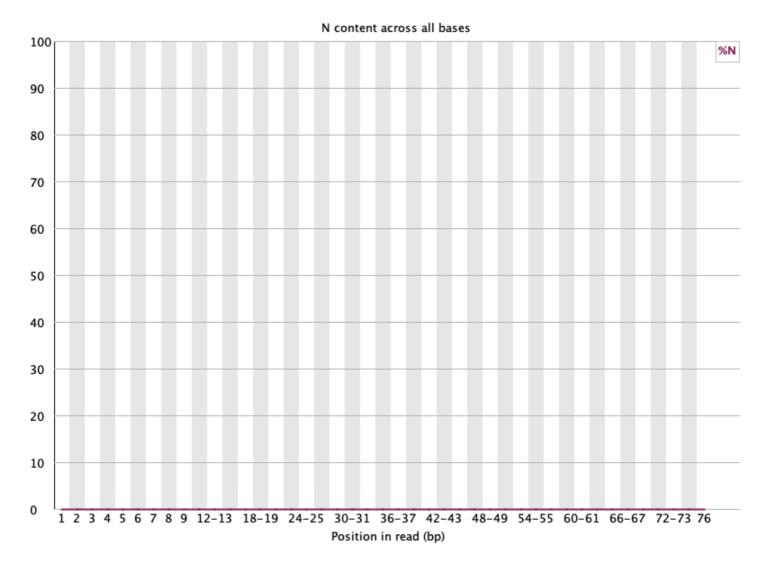Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅Per sequence quality scores

⚠️Per base sequence content

⚠️Per sequence GC content

✅Per base N content
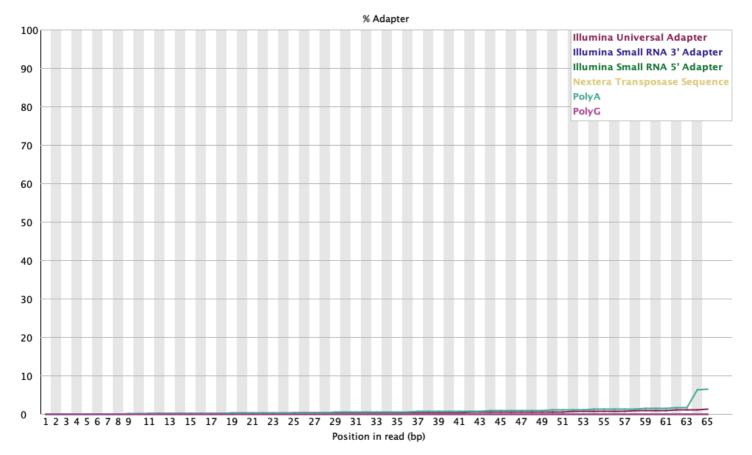
✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTACAGCATCTCGTATGC	3491201	9.651133677534517	TruSeq Adapter, Index 7 (97% over 35bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	186900	0.5166694453659934	Clontech SMART CDS Primer II A (100% over 26bp)

⚠️ Adapter Content

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