FastQC Report

Summary

✅ Basic Statistics

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✅ Basic Statistics

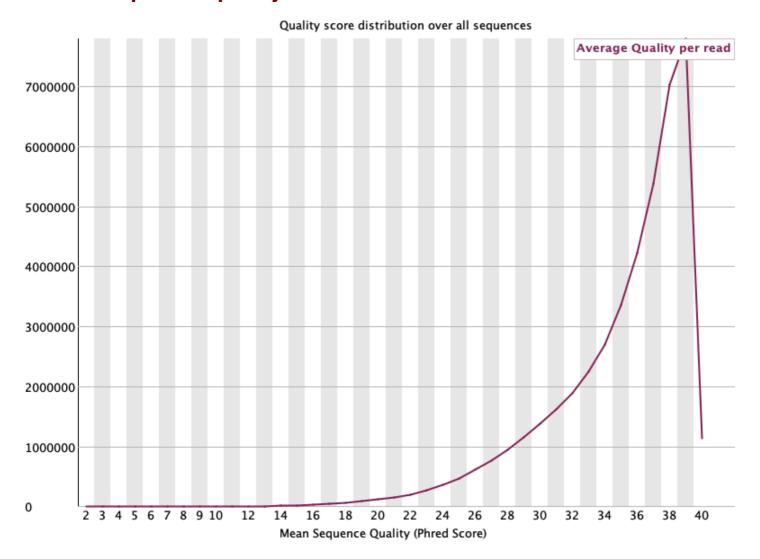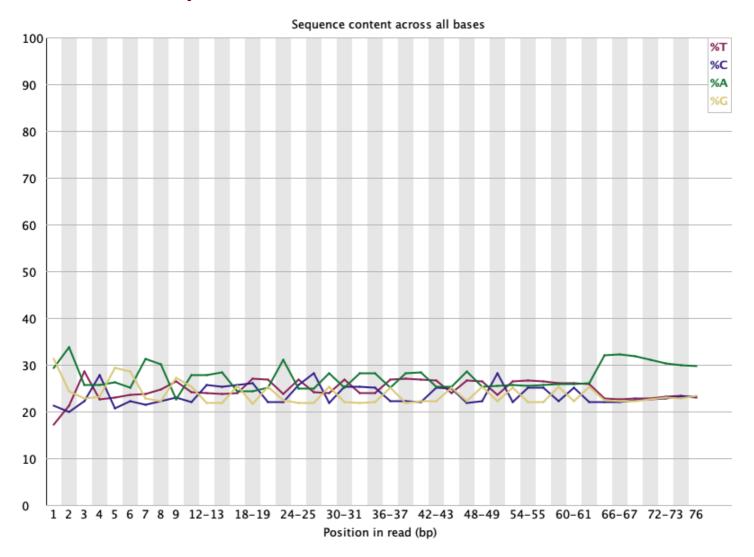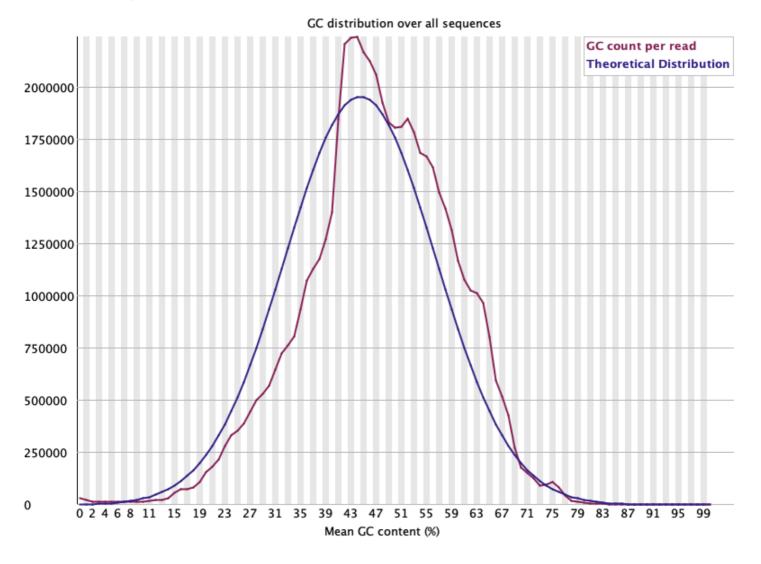| Measure	Value
Filename	SRR13380512_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	44327530
Total Bases	3.3 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	47
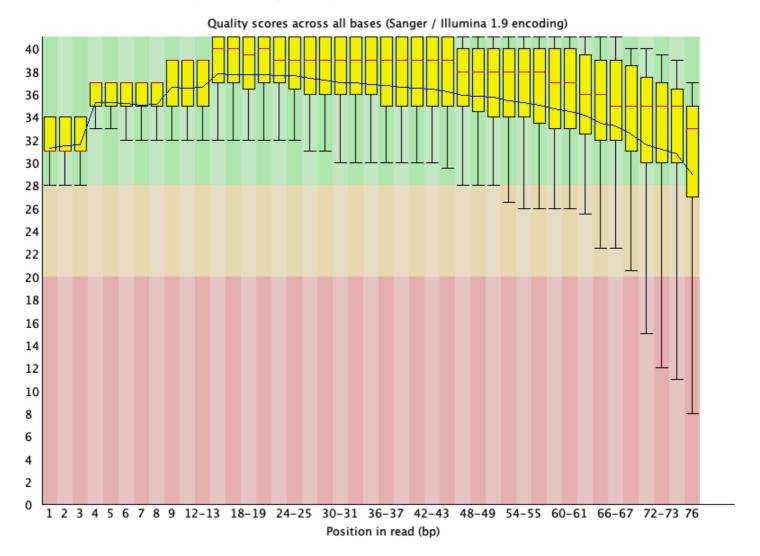
✅ Per base sequence quality

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

✅ Per sequence quality scores

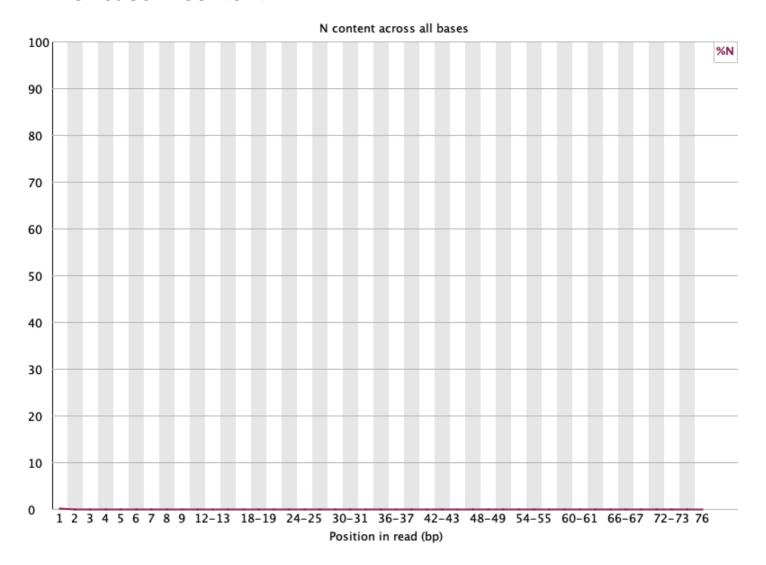Quality score distribution over all sequences
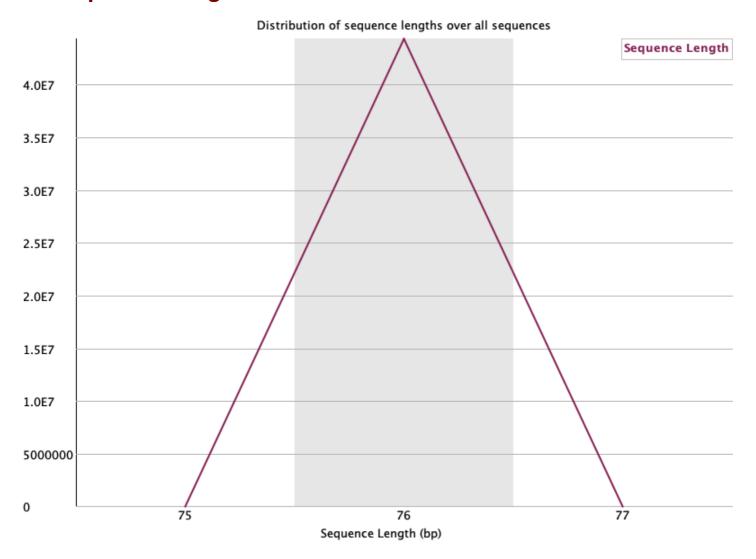
Per base sequence content
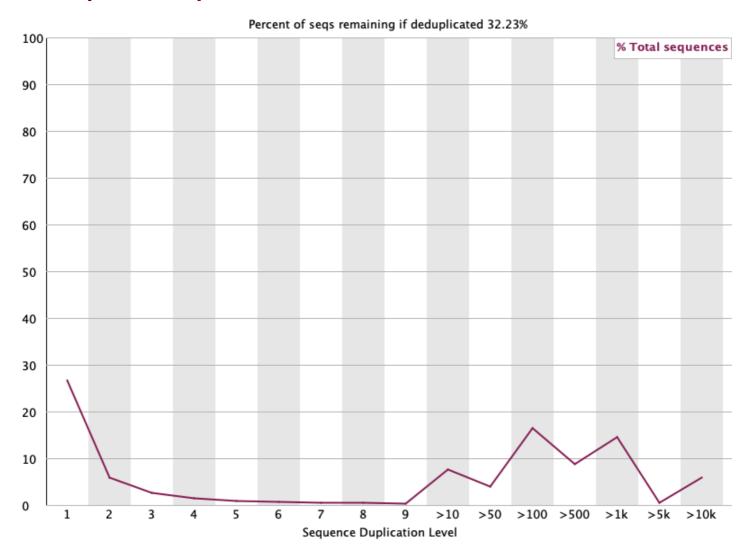
⚠️ Per sequence GC content

Per base N content

✅ Sequence Length Distribution
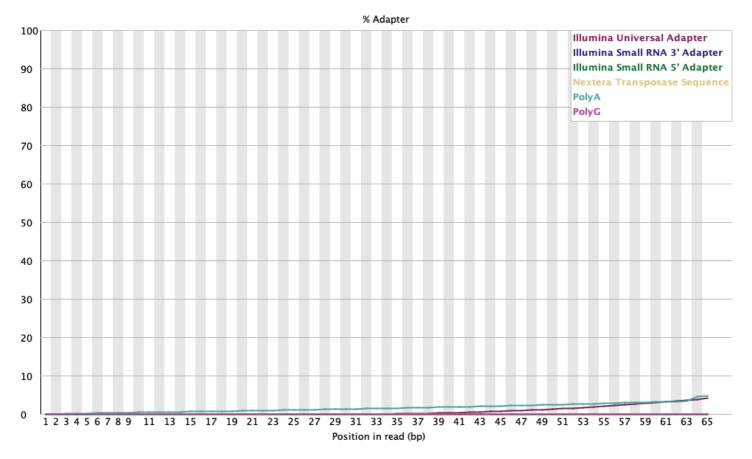
❌Sequence Duplication Levels

❌Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATCTCGTATGC	2416104	5.450572138804034	TruSeq Adapter, Index 25 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTT	175399	0.395688638640592	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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