FastQC Report

Summary

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✅ [Per base sequence quality](#)

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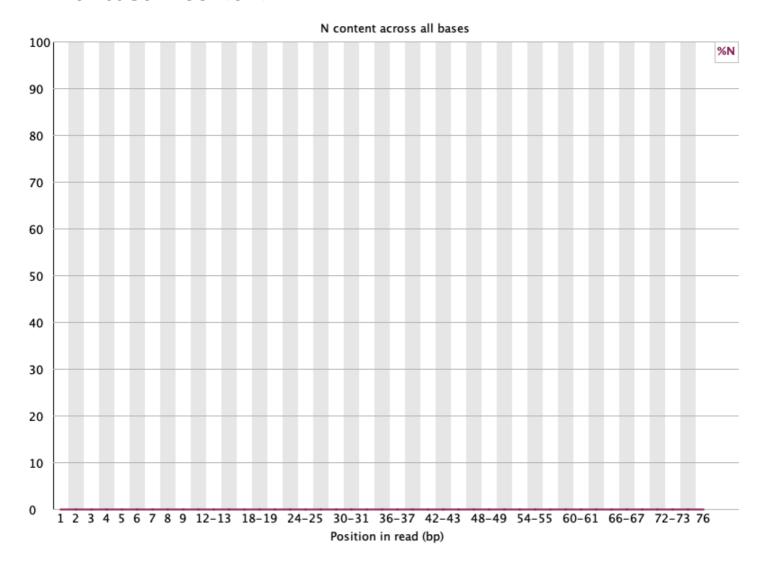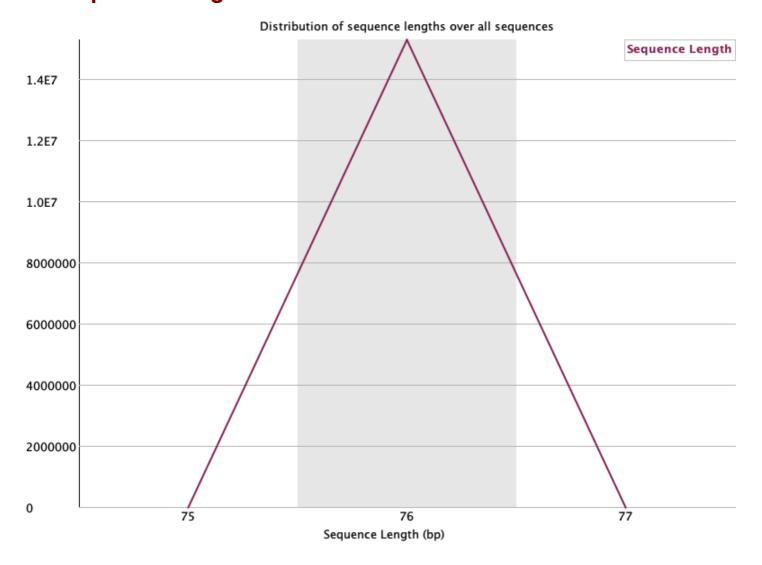
✅ [Per sequence GC content](#)

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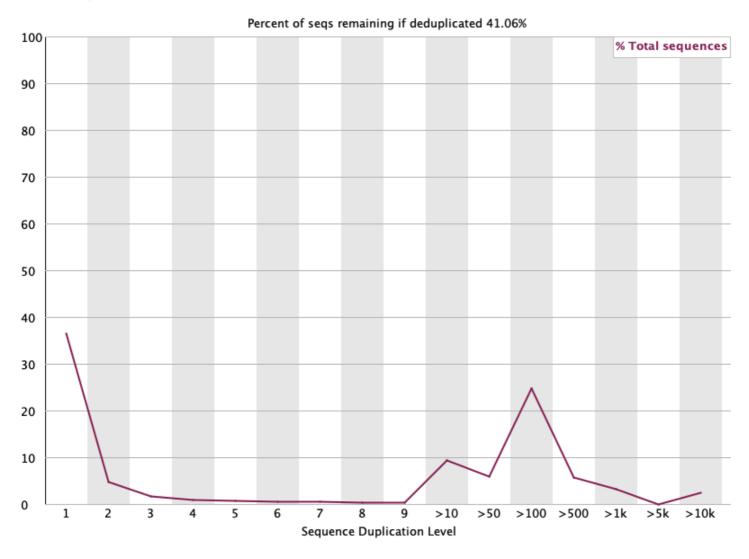
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✅ Basic Statistics

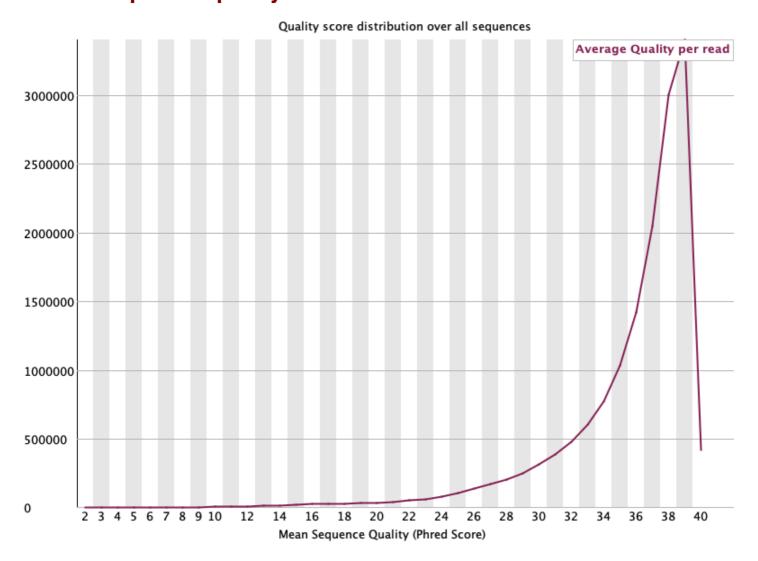| Measure	Value
Filename	SRR13380482_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	15292306
Total Bases	1.1 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	48

✅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

GC distribution over all sequences

✅ Per base N content

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

❌ Sequence Duplication Levels

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGCCATATCTCGTATGC	323931	2.1182613008136246	TruSeq Adapter, Index 4 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	79155	0.5176132363555895	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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