FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per sequence quality scores](#)
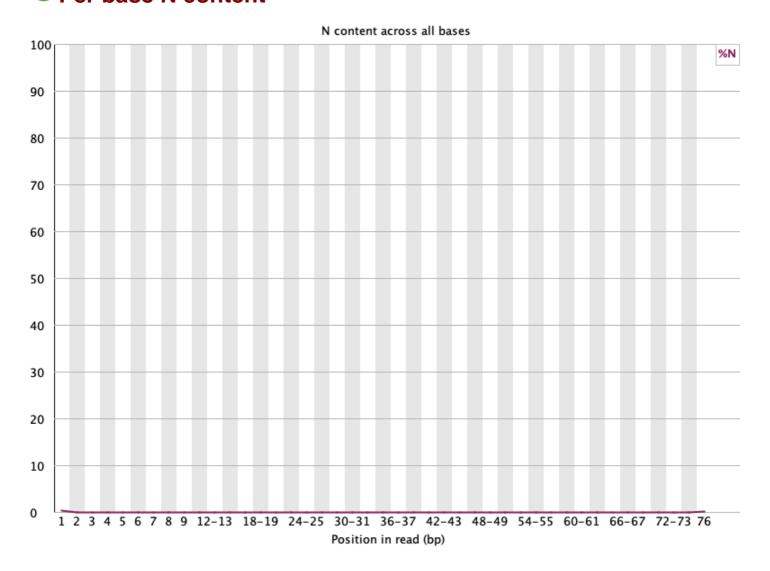
❌ [Per base sequence content](#)

⚠️ [Per sequence GC content](#)

✅ [Per base N content](#)
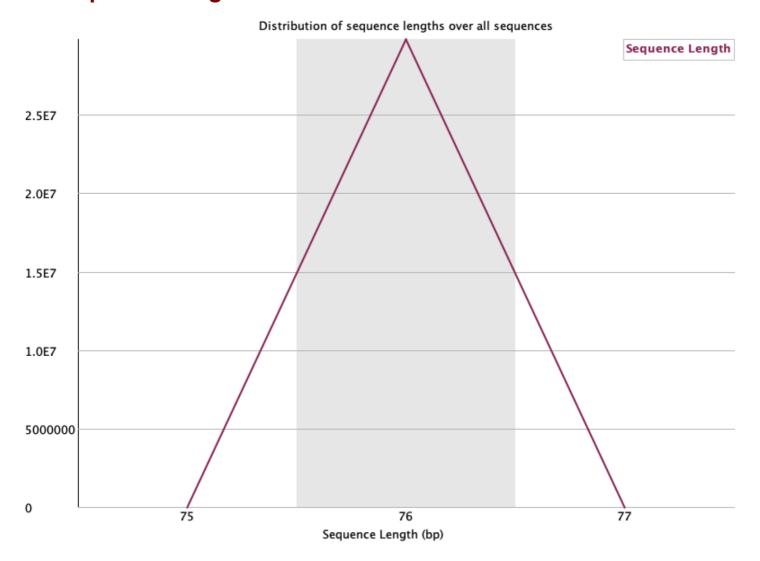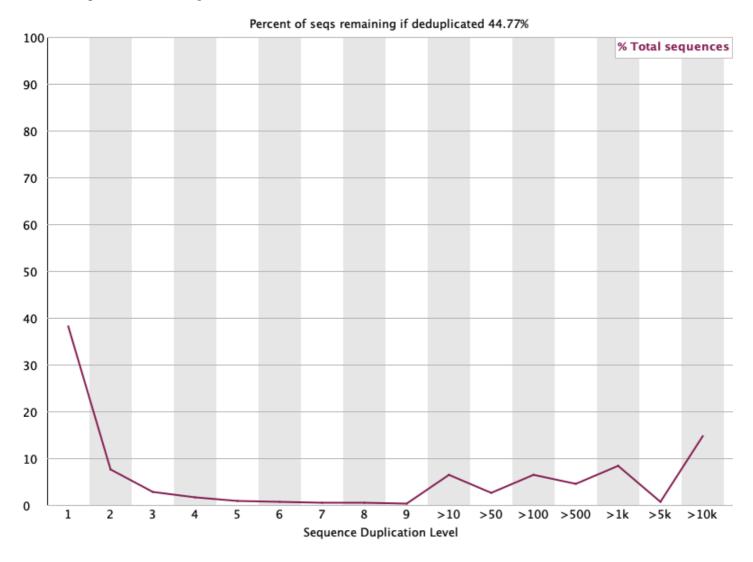
✅ [Sequence Length Distribution](#)

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✅ Basic Statistics

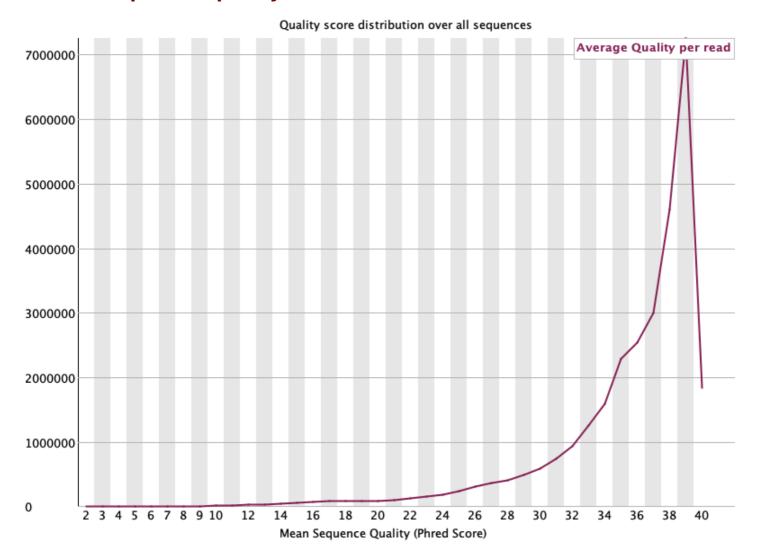| Measure	Value
Filename	SRR13380479_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	29778952
Total Bases	2.2 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	44

✅Per base sequence quality

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

Position in read (bp)
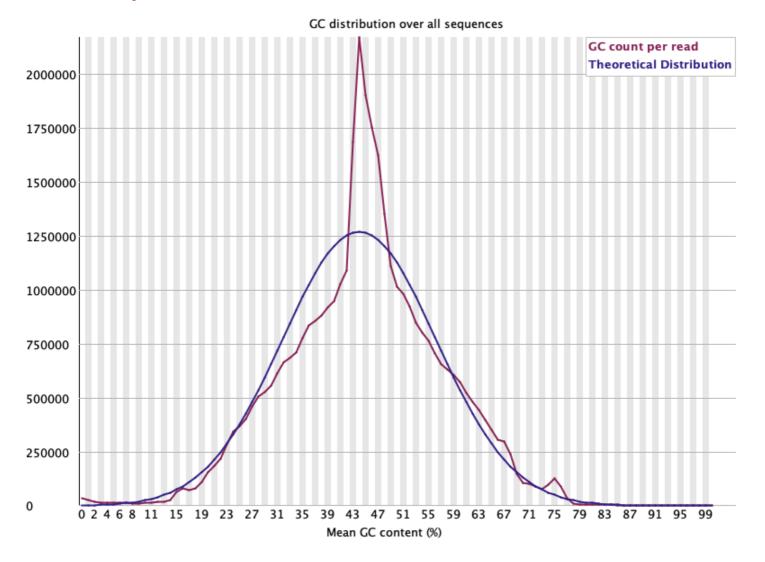
✅ Per sequence quality scores

Quality score distribution over all sequences

⊗ Per base sequence content

⚠️Per sequence GC content

✅ Per base N content

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⊗ Sequence Duplication Levels

⊗ Overrepresented sequences

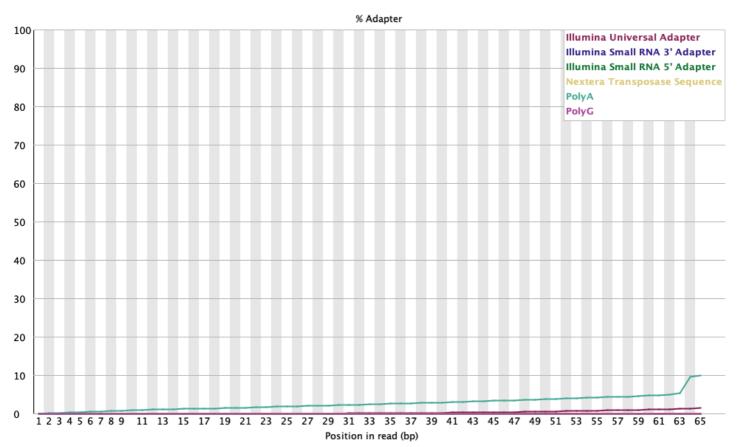| Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATGC	3684320	12.37222854585346	TruSeq Adapter, Index 9 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	284729	0.9561417742303355	Clontech SMART CDS Primer II A (100% over 26bp)
GATCGGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATG	126624	0.4252130833885625	TruSeq Adapter,

Sequence	Count	Percentage	Possible Source
			Index 9 (100% over 45bp)

❌Adapter Content

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