FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

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⚠️ [Per base sequence content](#)
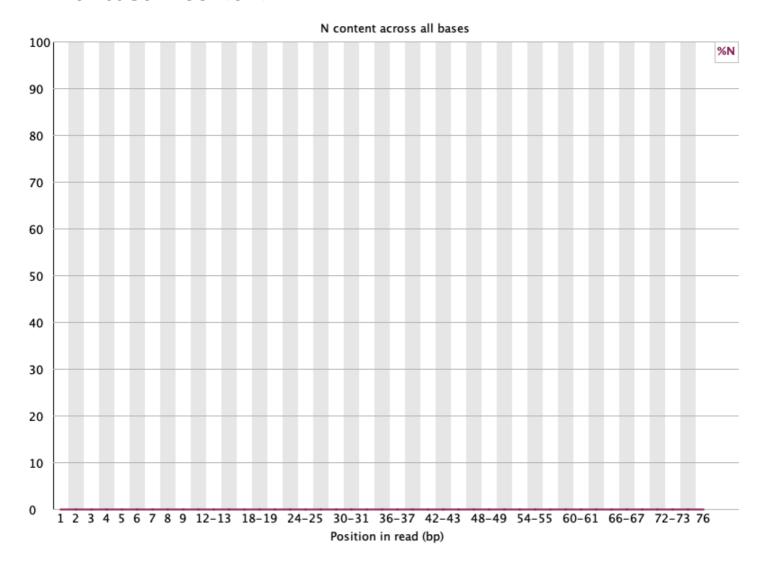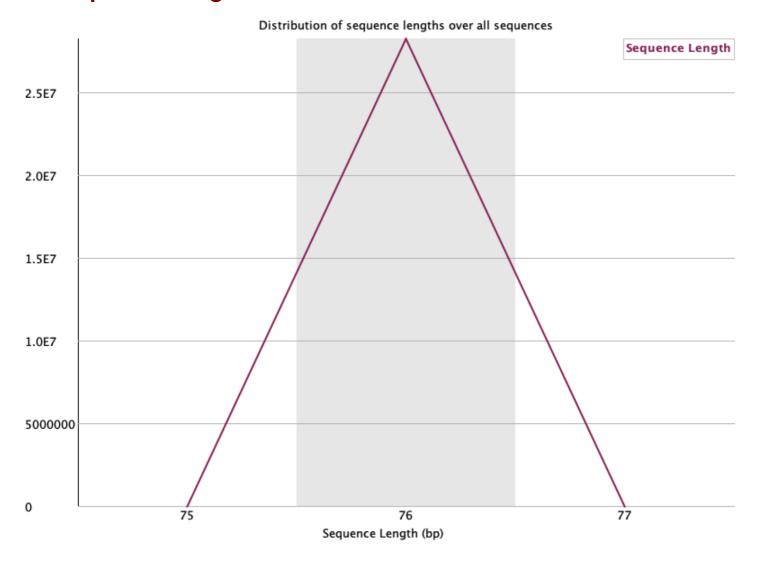
✅ [Per sequence GC content](#)

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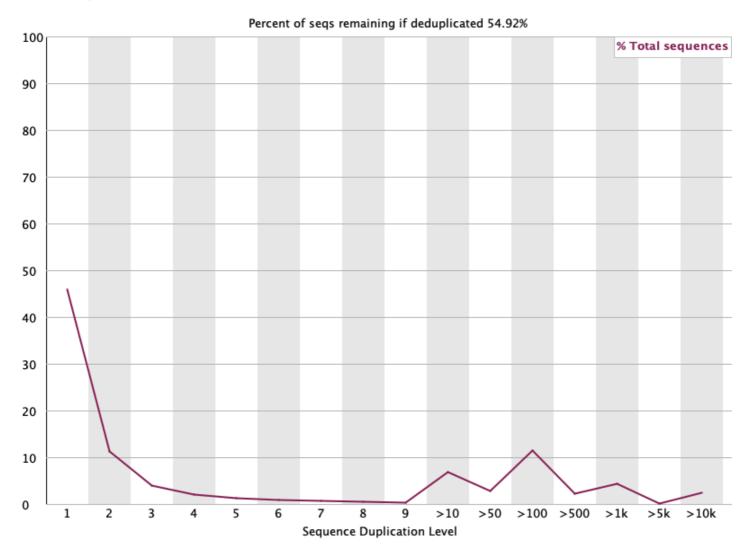
✅ [Sequence Length Distribution](#)
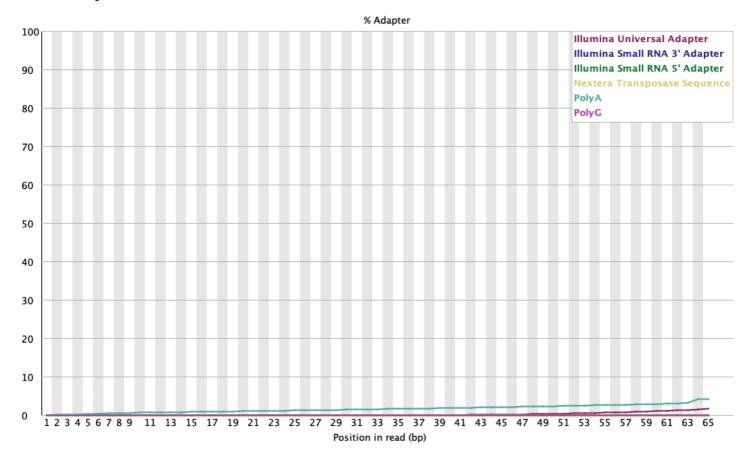
⚠️ [Sequence Duplication Levels](#)

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Basic Statistics

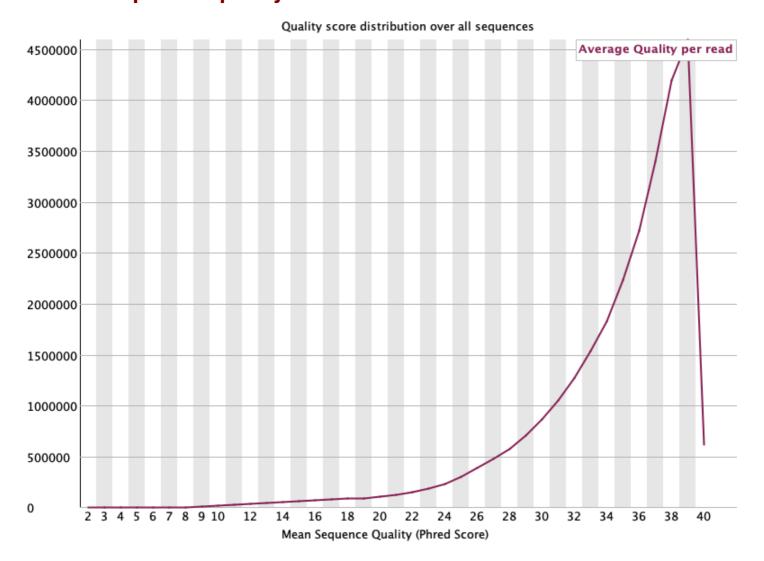| Measure	Value
Filename	SRR13380425_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	28234484
Total Bases	2.1 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	42

✅ 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

Percent of seqs remaining if deduplicated 54.92%

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATGC	476348	1.68711423945272	TruSeq Adapter, Index 2 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTT	199008	0.7048402230407327	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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