ℝFastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per sequence quality scores](#)

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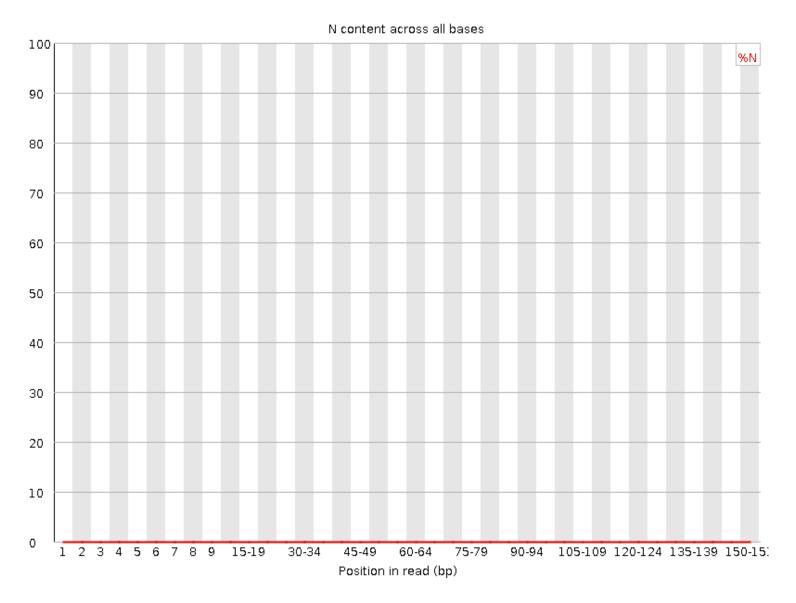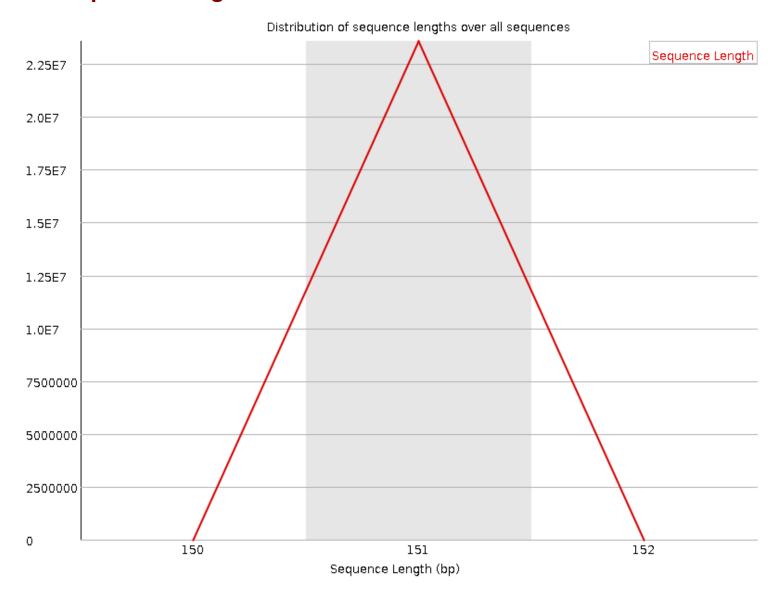
⚠️ [Per sequence GC content](#)

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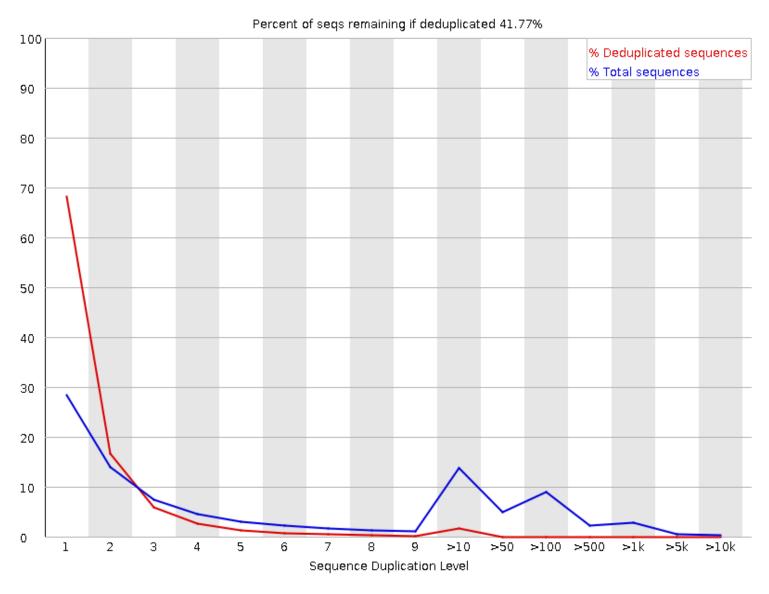
✅ [Sequence Length Distribution](#)
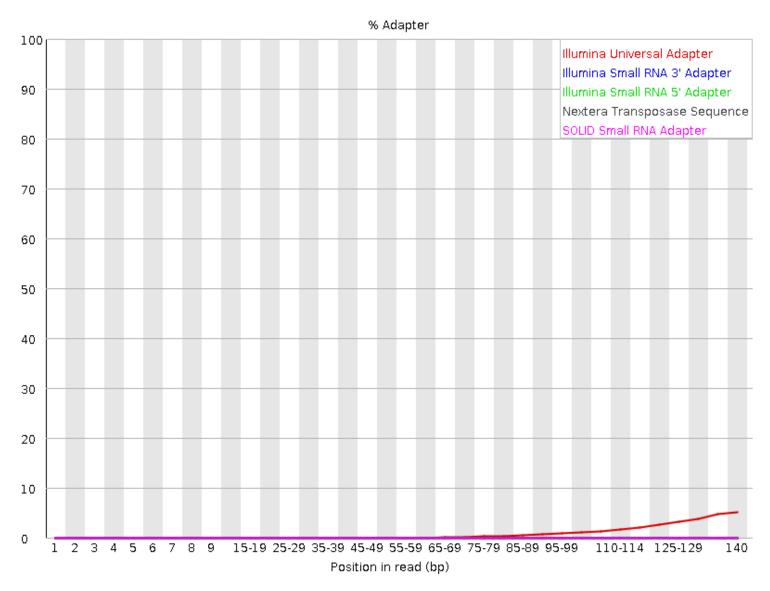
❌ [Sequence Duplication Levels](#)

⚠️ [Overrepresented sequences](#)

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✅ Basic Statistics

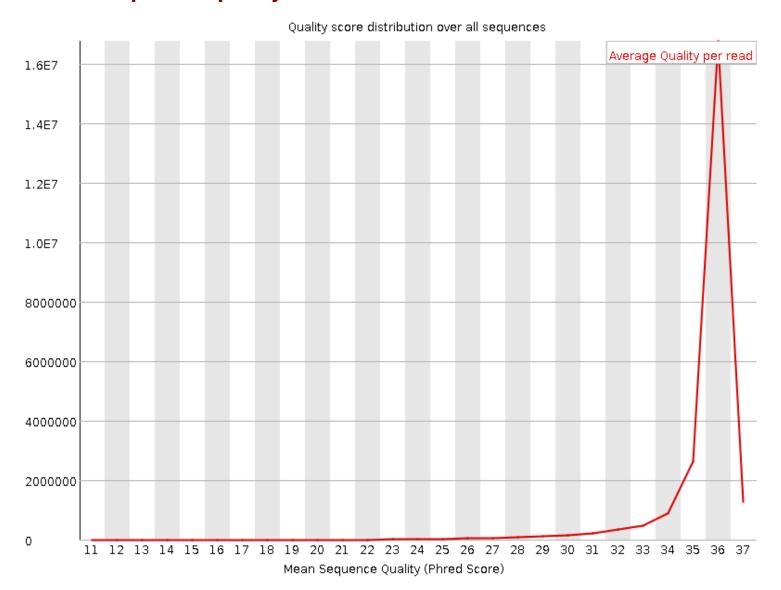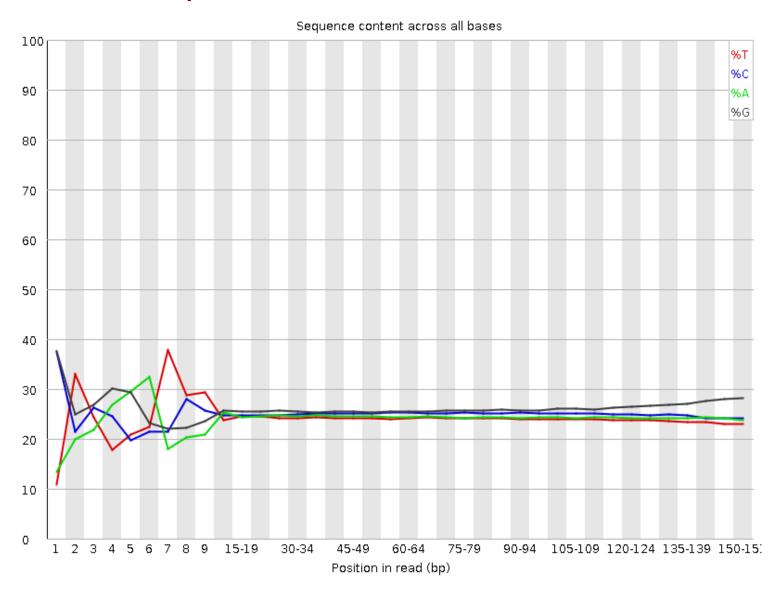| Measure	Value
Filename	SRR14866427_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23558674
Sequences flagged as poor quality	0
Sequence length	151
%GC	51

✅ 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 41.77%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	33899	0.14389179968278348	No Hit
CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	24003	0.10188603993586395	No Hit

⚠️ Adapter Content

Produced by FastQC (version 0.11.7)