FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

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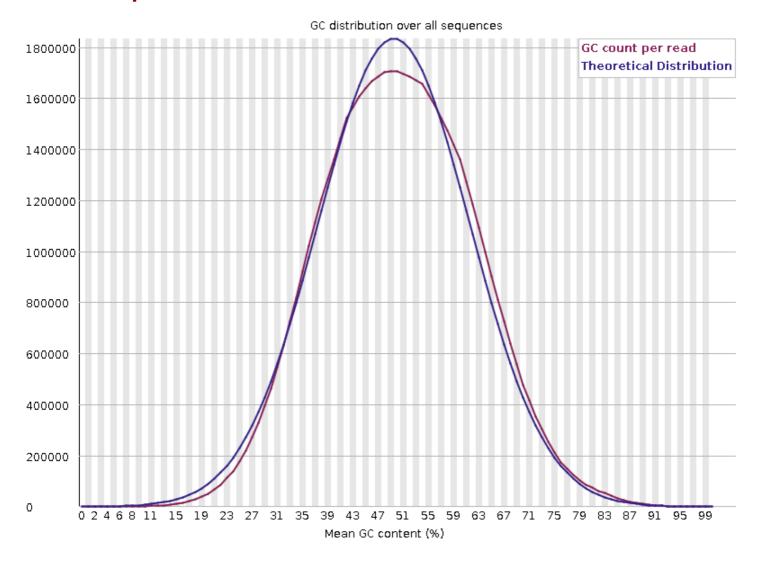
✅ [Per sequence quality scores](#)
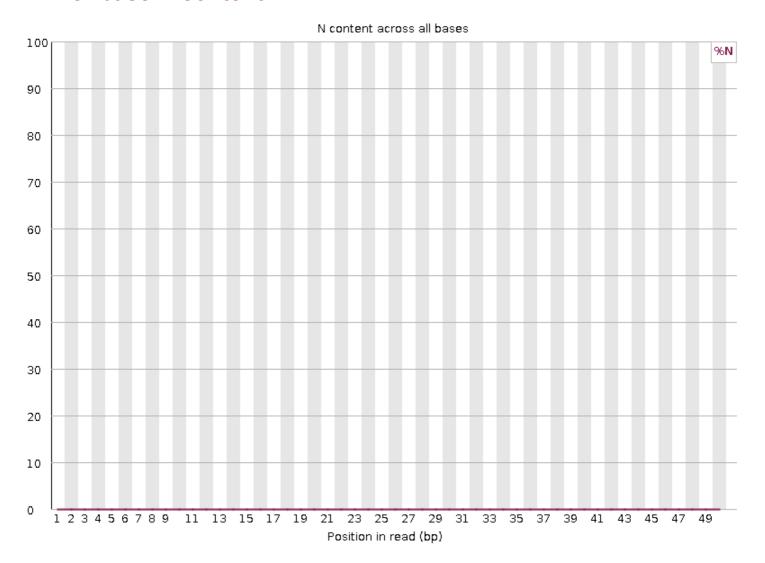
❌ [Per base sequence content](#)

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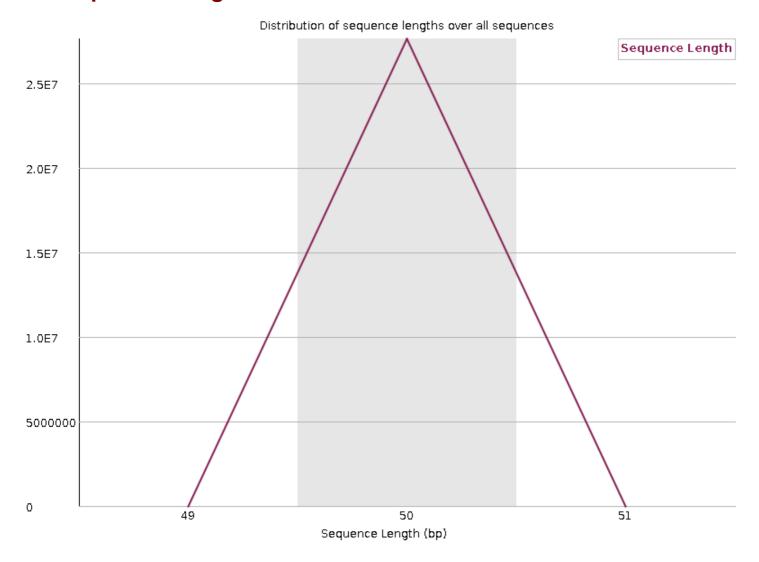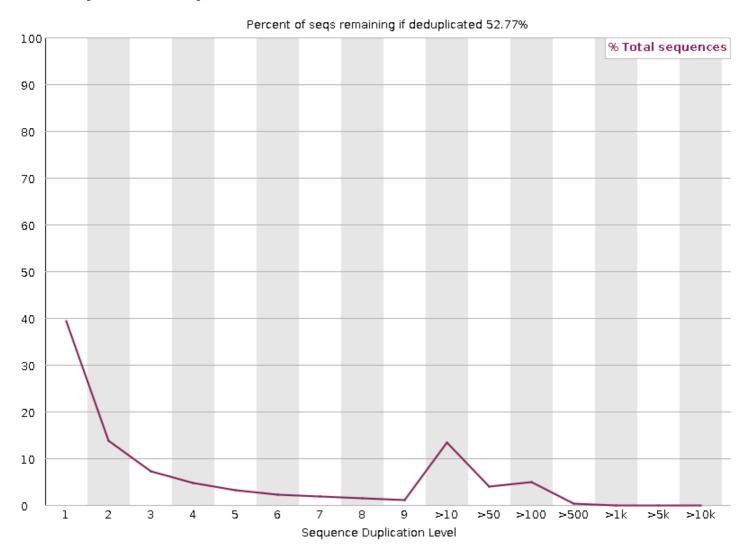
✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

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✅ Basic Statistics

Measure	Value
Filename	SRR827457_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	27640449
Total Bases	1.3 Gbp
Sequences flagged as poor quality	0
Sequence length	50
%GC	50

✅ Per base sequence quality

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

⚠️ Per tile sequence quality

Quality per tile

✅Per sequence quality scores

Quality score distribution over all sequences

❌Per base sequence content

Sequence content across all bases

✅Per sequence GC content

✅ Per base N content

N content across all bases

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠️ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 52.77%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

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