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](#)

❌ [Sequence Duplication Levels](#)

⚠️ [Overrepresented sequences](#)

⚠️ [Adapter Content](#)

✅ Basic Statistics

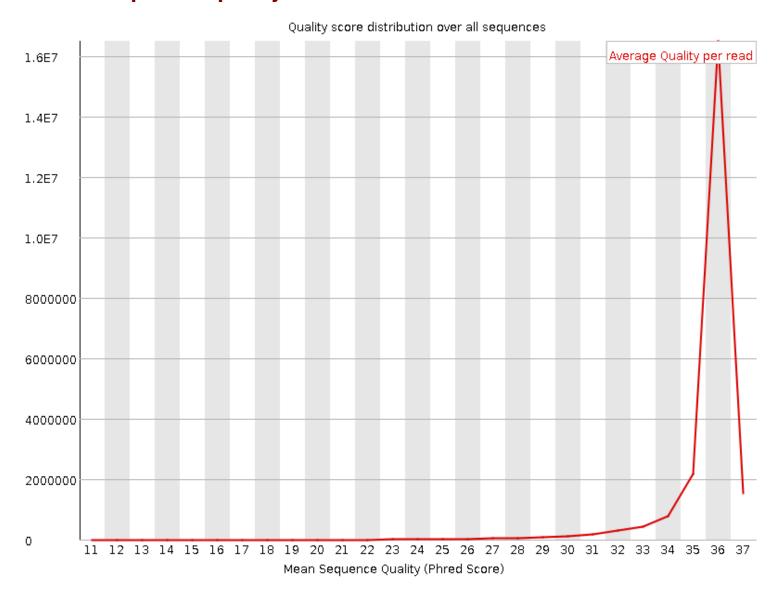| Measure	Value
Filename	SRR14866428_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	22794073
Sequences flagged as poor quality	0
Sequence length	151
%GC	51
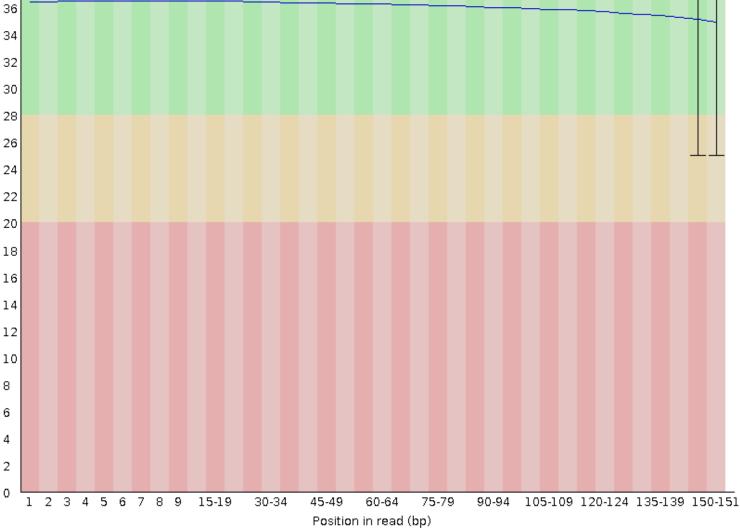
✅Per base sequence quality

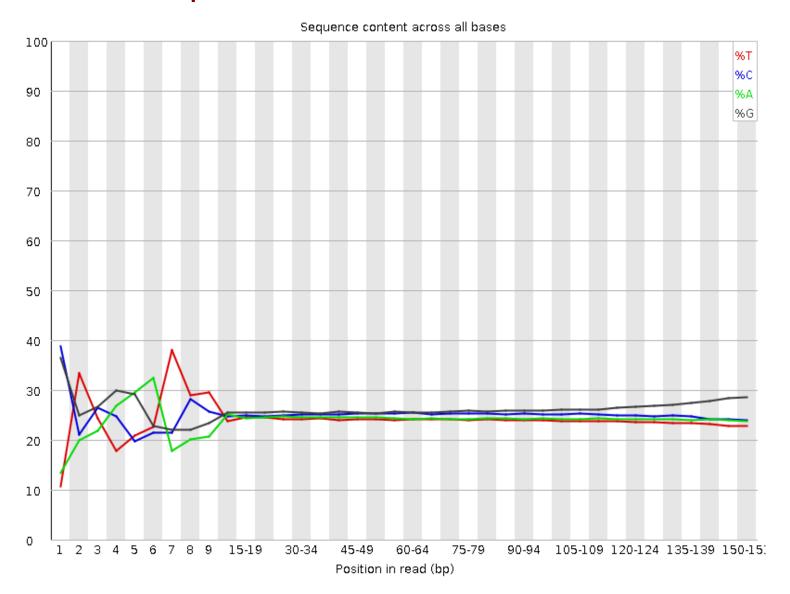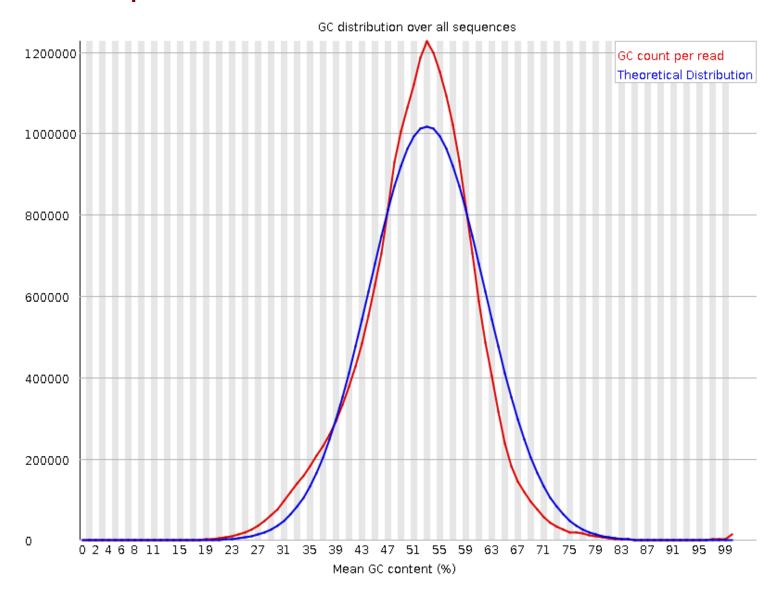Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅ Per sequence quality scores

❌Per base sequence content

⚠️Per sequence GC content

✅ Per base N content

✅ Sequence Length Distribution

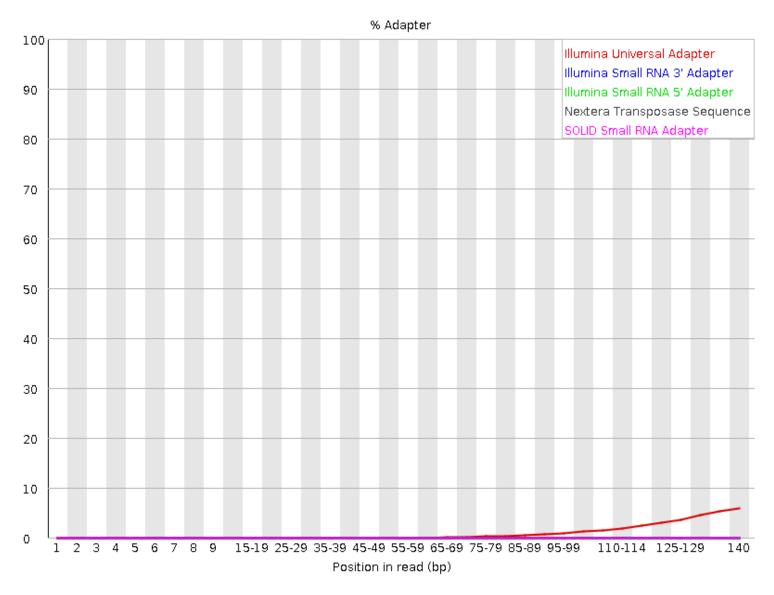Distribution of sequence lengths over all sequences

❌ Sequence Duplication Levels

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	25602	0.11231867161257227	No Hit
CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	25058	0.10993208629278323	No Hit

⚠️ Adapter Content

Produced by [FastQC](#) (version 0.11.7)