FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per tile sequence quality
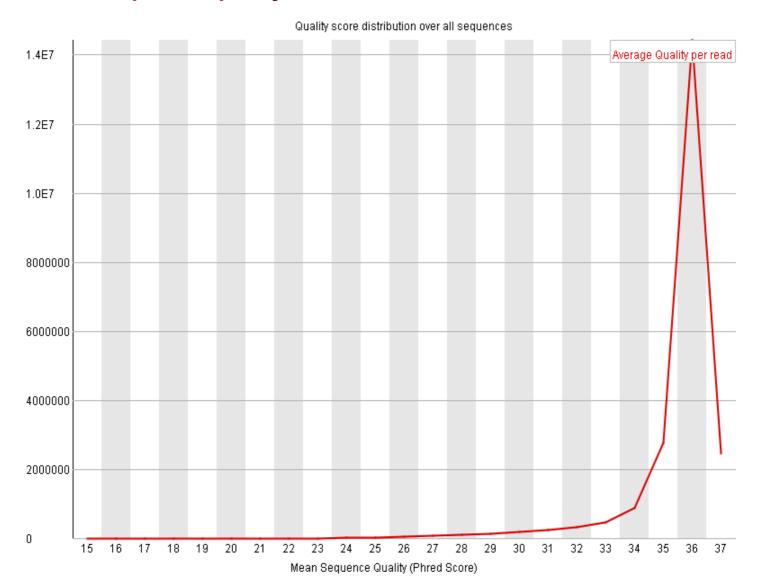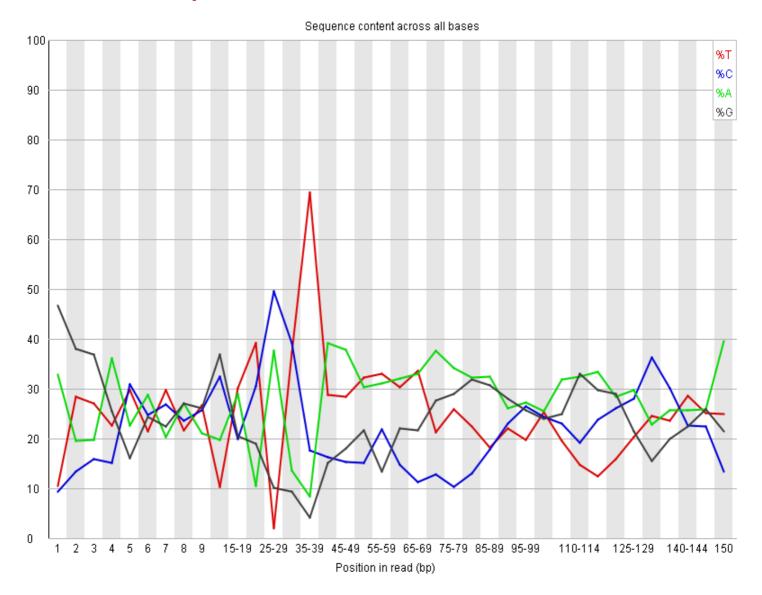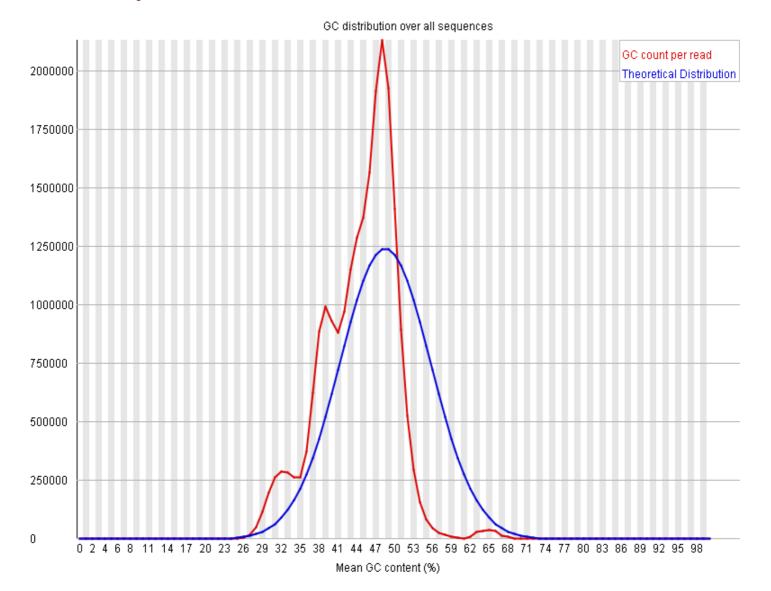
✅ Per sequence quality scores
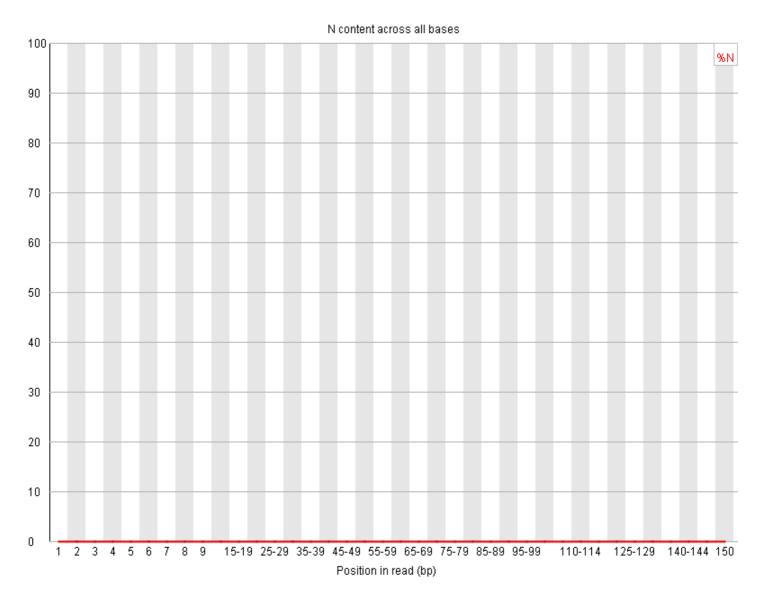
❌ Per base sequence content
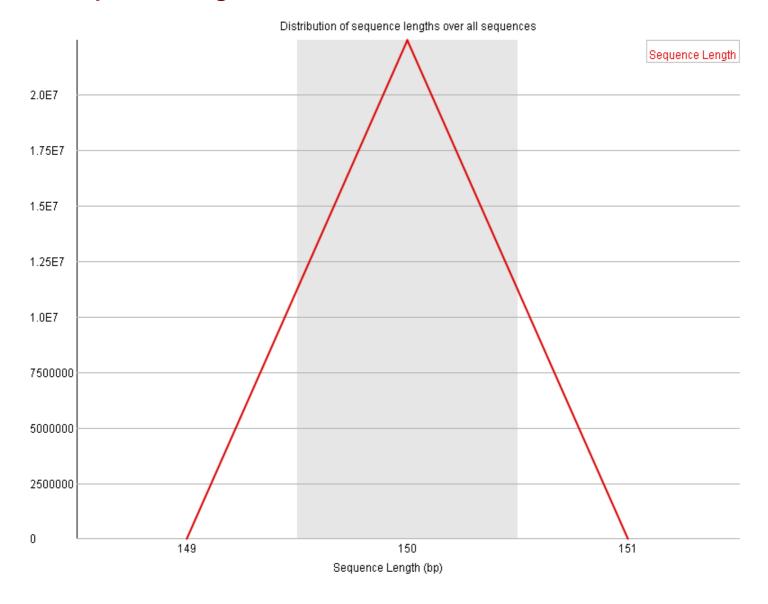
❌ Per sequence GC content
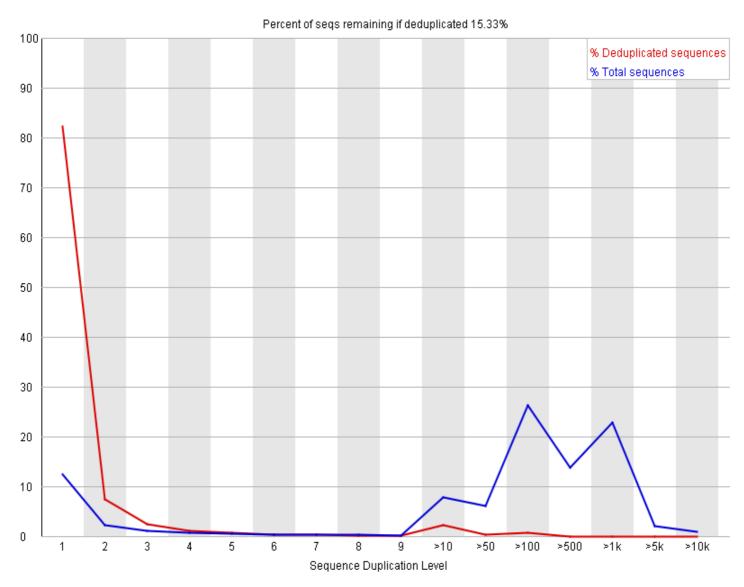
✅ Per base N content

✅ Sequence Length Distribution
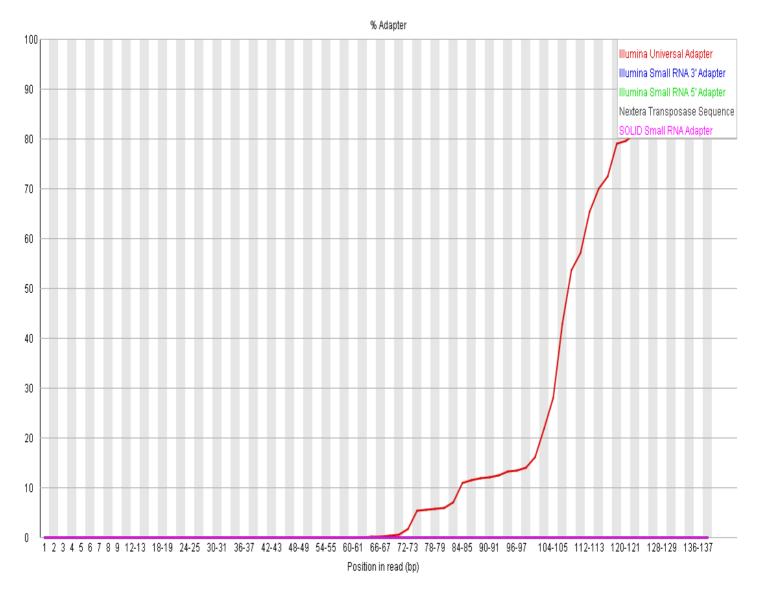
❌ Sequence Duplication Levels

⚠️ Overrepresented sequences

❌ Adapter Content

✅ Basic Statistics

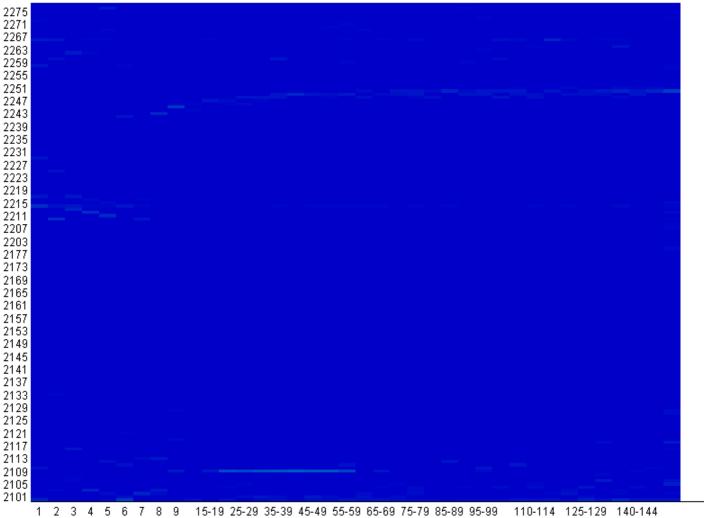| Measure	Value
Filename	250207_A00902_A_L002_BFTV-2_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	22421828
Sequences flagged as poor quality	0
Sequence length	150
%GC	46

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

GC distribution over all sequences

Per base N content

N content across all bases

Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Length

Sequence Duplication Levels

Percent of seqs remaining if deduplicated 15.33%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CGGAAGAGCACACGTCTGAACTCCAGTCACATGTGAGCTAATCTCGTATG	59282	0.2643941430645173	TruSeq Adapter, Index 15 (97% over 37bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTGAGCTAATCTCGT	42785	0.19081851845442754	TruSeq Adapter, Index 15 (97% over 40bp)

⊗ Adapter Content

Produced by [FastQC](#) (version 0.11.8)