FastQC Report

Summary

HG008-N-D_CGGACAAC-AATCCGGA_subset_H3LLJDSXC_L001_001.R2.fastq.gz

Mon 13 Jan 2025

✅ 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

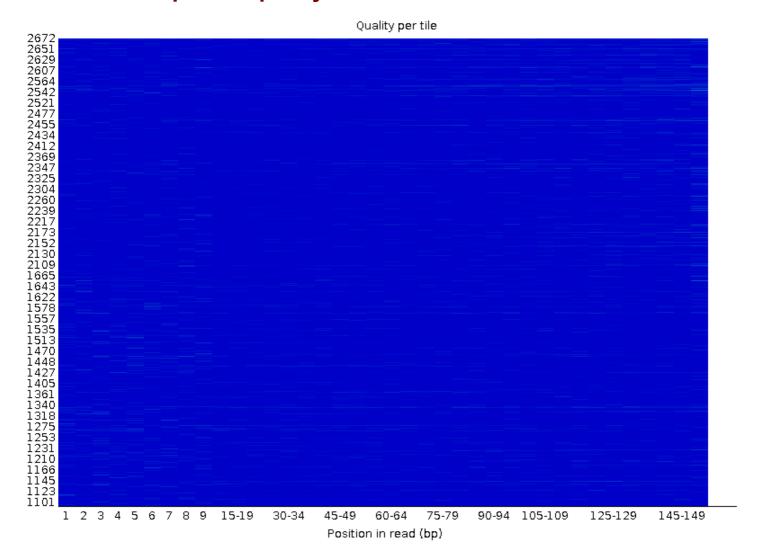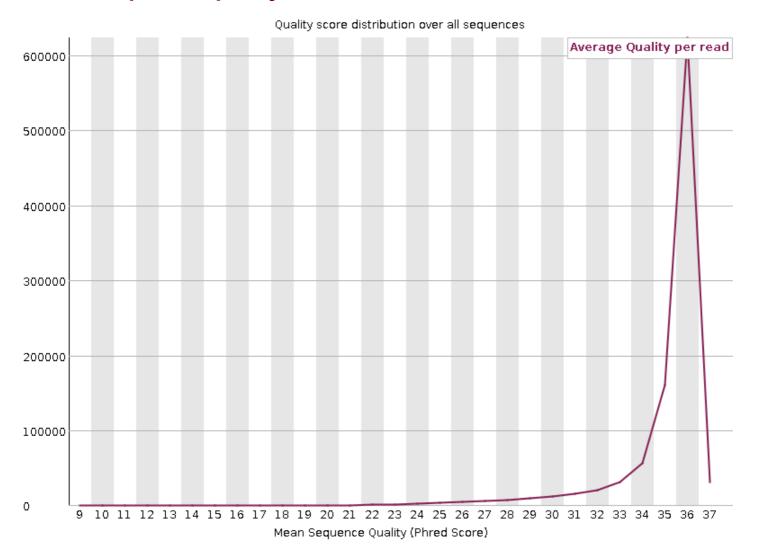| Measure	Value
Filename	HG008-N-D_CGGACAAC-AATCCGGA_subset_H3LLJDSXC_L001_001.R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Total Bases	150 Mbp
Sequences flagged as poor quality	0
Sequence length	150
%GC	40
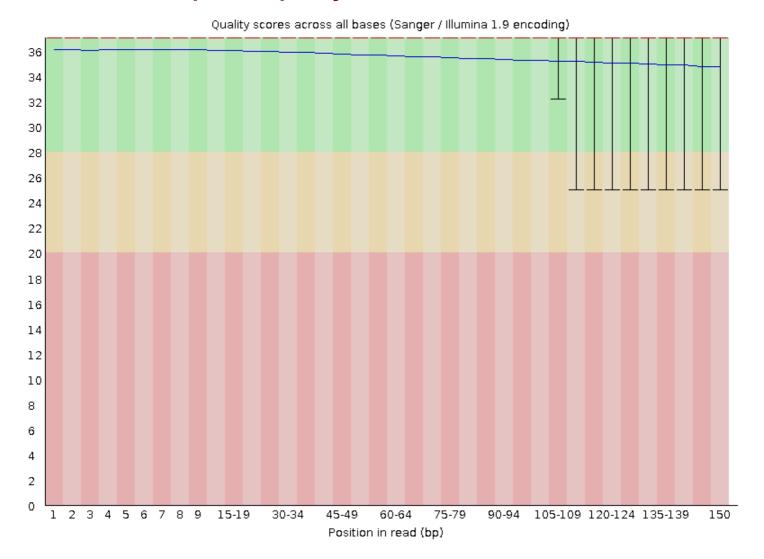
✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)
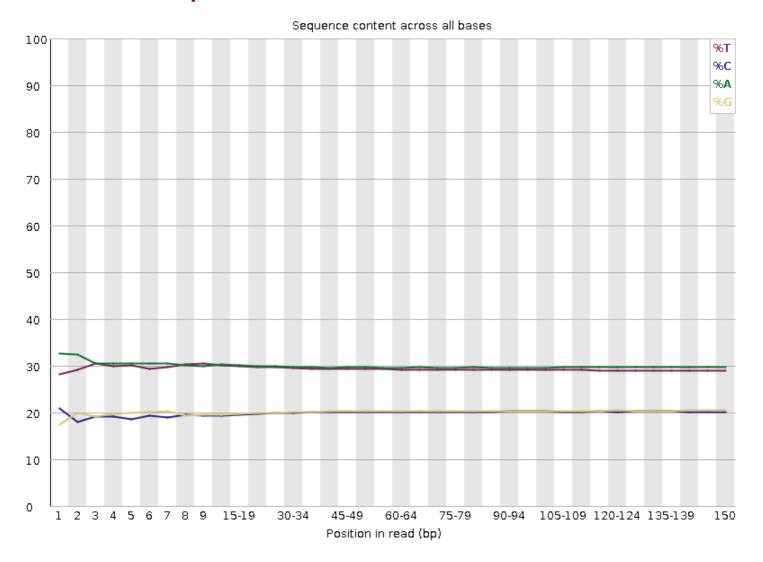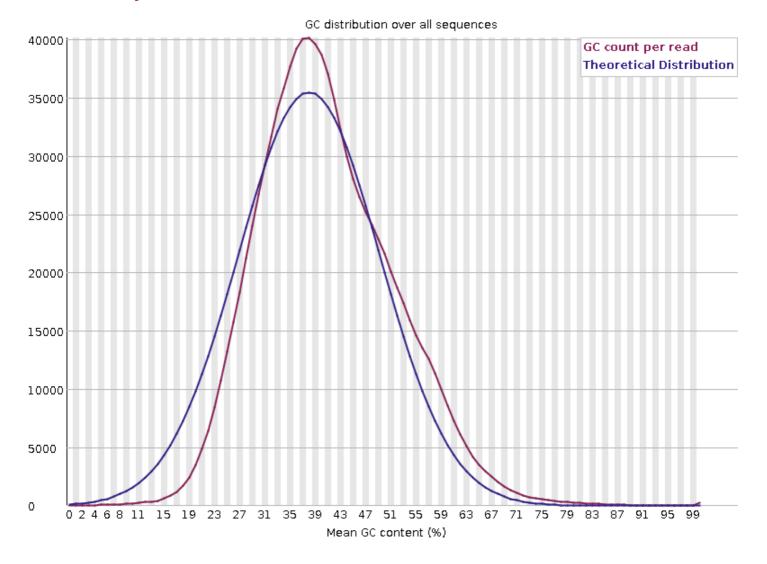
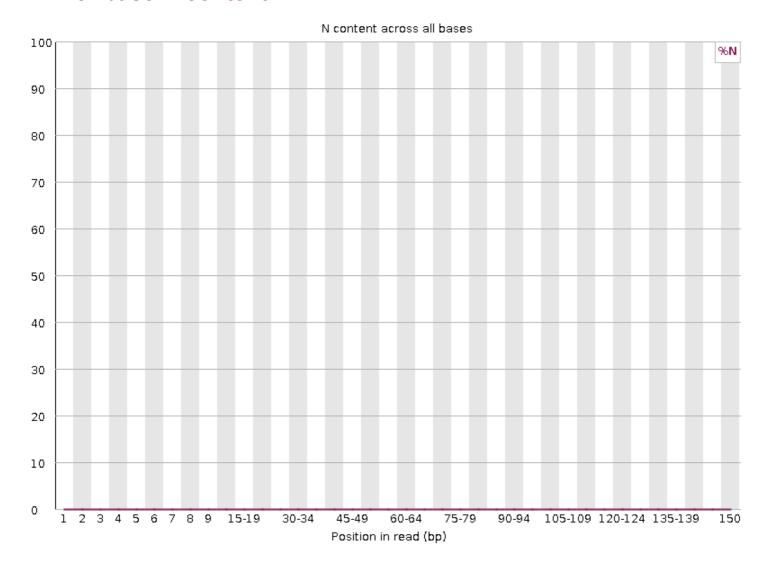# Per tile sequence quality

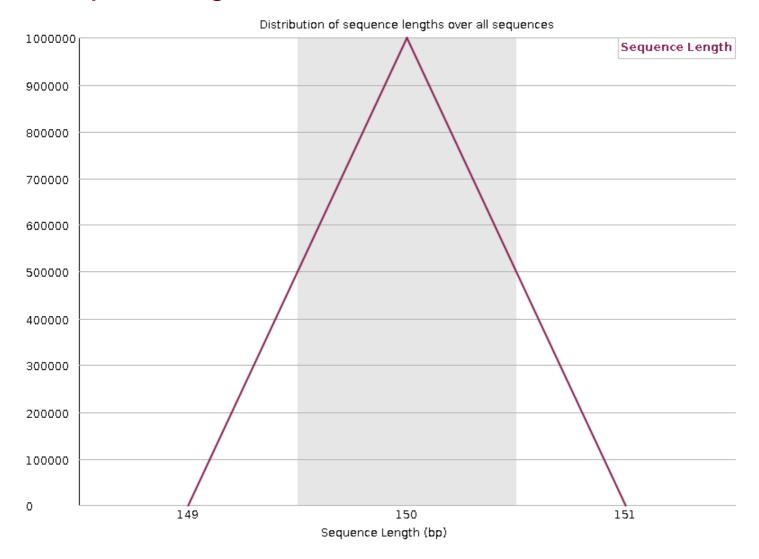# Per sequence quality scores

✅ Per base sequence content
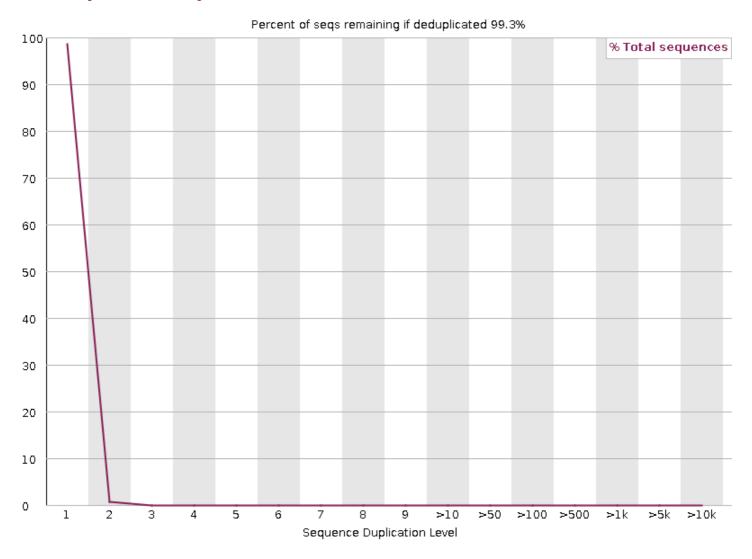
⚠️Per sequence GC content

✅Per base N content

✅Sequence Length Distribution

✅ Sequence Duplication Levels

✅ Overrepresented sequences
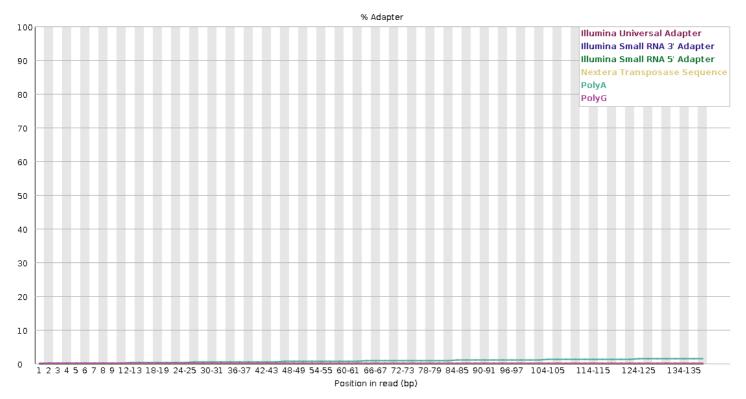
No overrepresented sequences

✅ Adapter Content

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