FastQC Report

Summary
Mon 13 Jan 2025
HG008-T_TTCCTGTT-AAGATACT_subset_HJVY2DSX7_L001_001.R2.fastq.gz

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✅ Basic Statistics

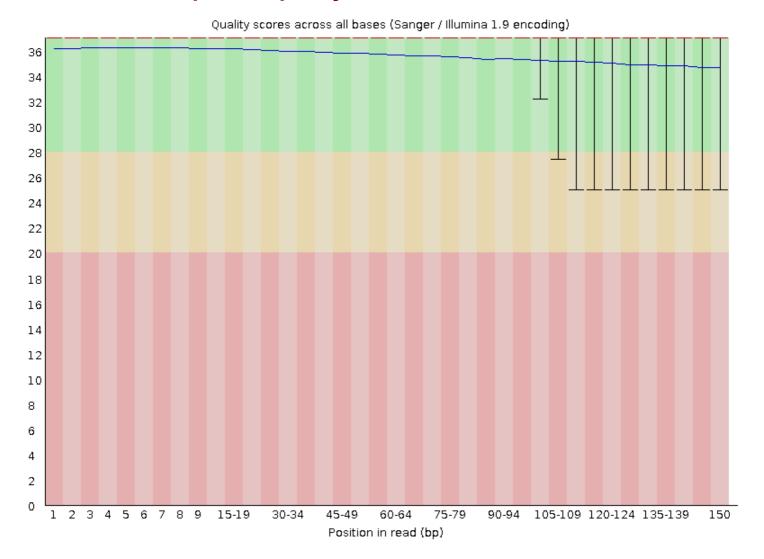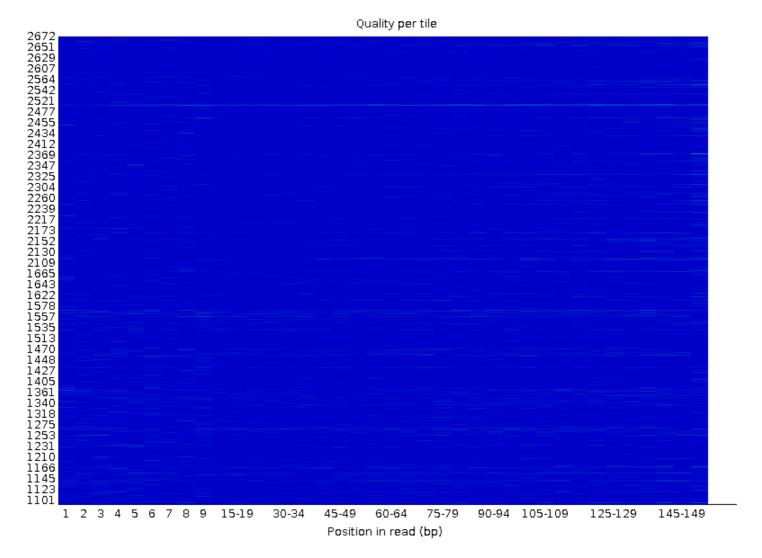| Measure	Value
Filename	HG008-T_TTCCTGTT-AAGATACT_subset_HJVY2DSX7_L001_001.R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Total Bases	150 Mbp
Sequences flagged as poor quality	0
Sequence length	150
%GC	41

✅Per base sequence quality

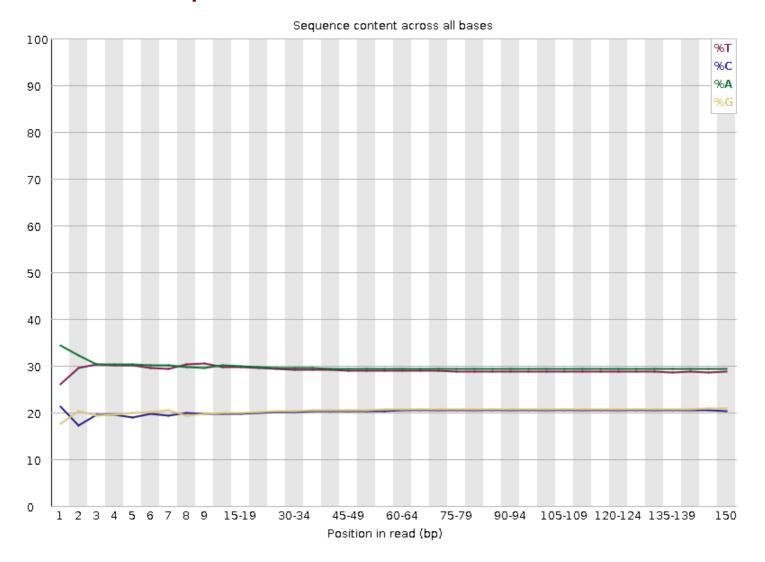Quality scores across all bases (Sanger / Illumina 1.9 encoding)
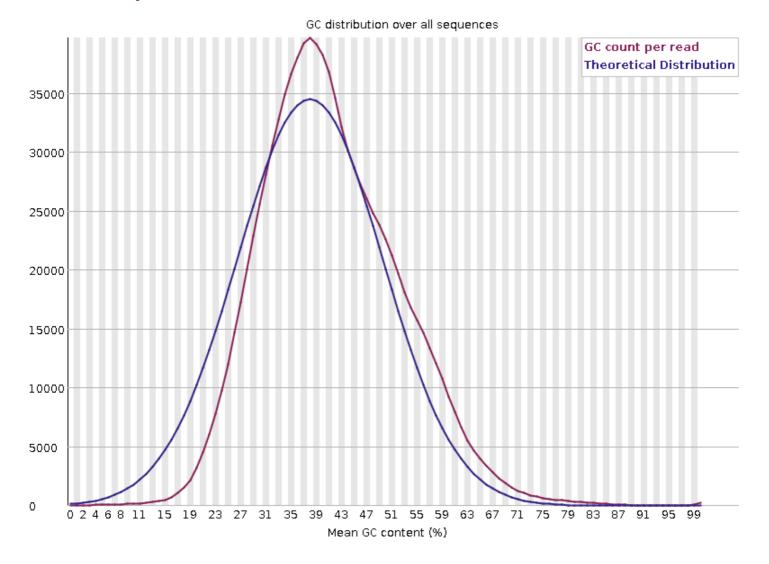
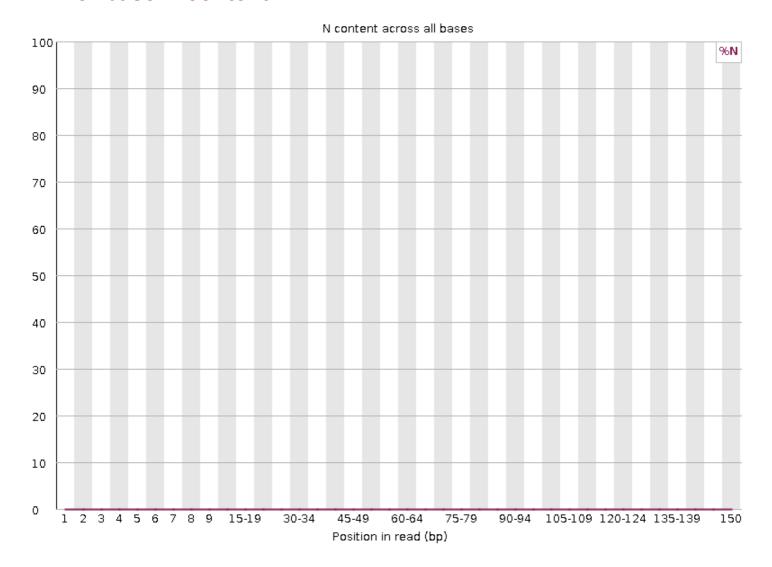# ✅ Per tile sequence quality

✅ Per sequence quality scores

✔ Per base sequence content
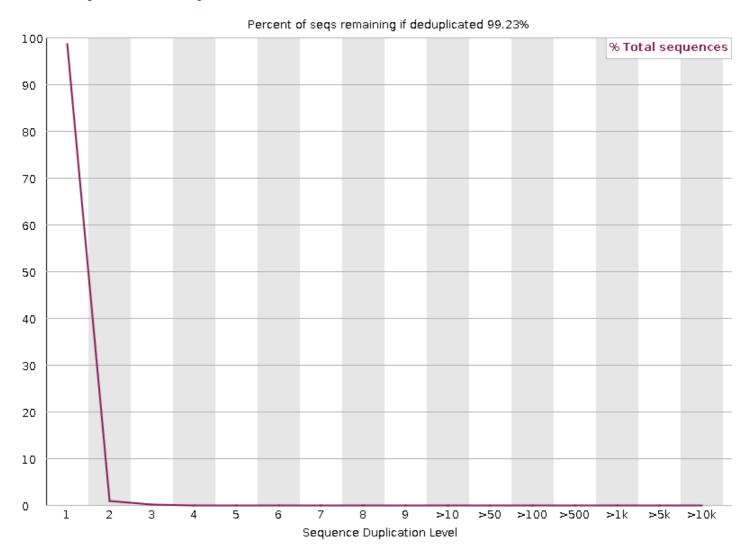
⚠️Per sequence GC content
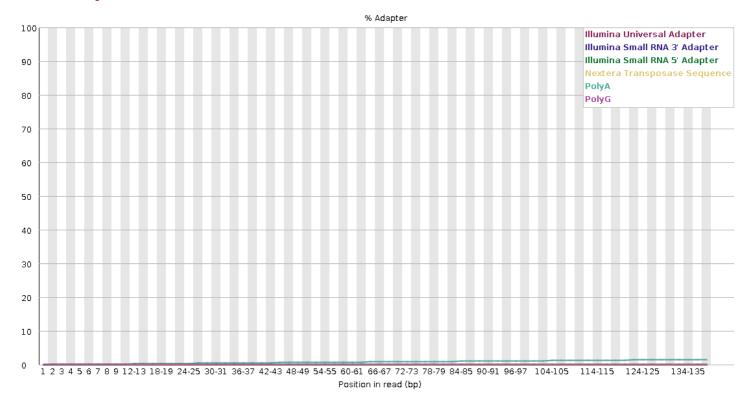
✅Per base N content

✅Sequence Length Distribution

Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99.23%

Overrepresented sequences

No overrepresented sequences

✅Adapter Content

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