FastQC Report

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✅ Basic Statistics

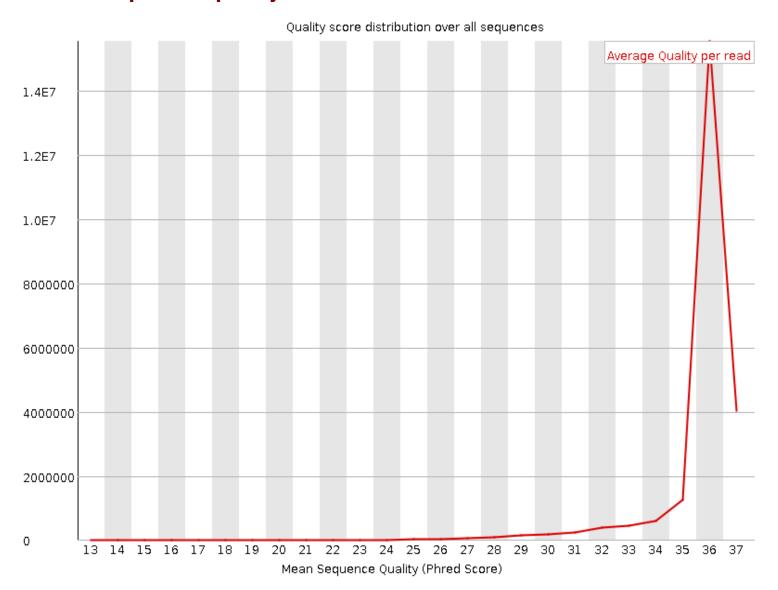| Measure	Value
Filename	SRR14866430_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23255676
Sequences flagged as poor quality	0
Sequence length	151
%GC	51
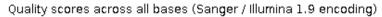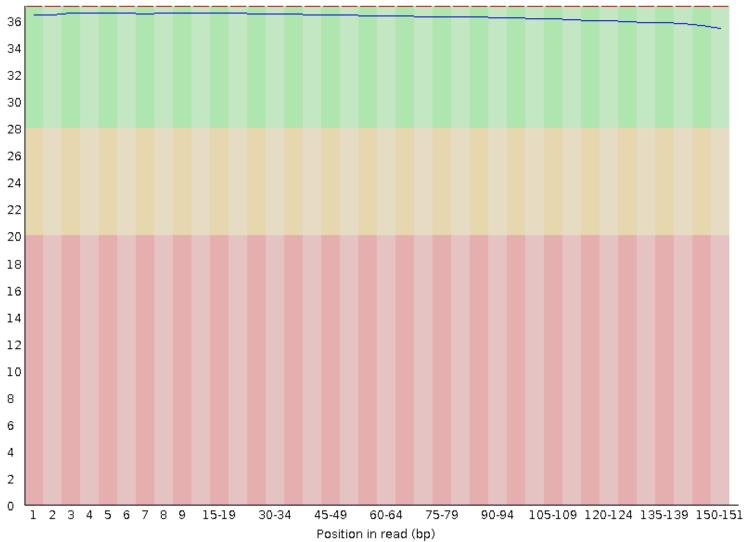
✅ Per base sequence quality

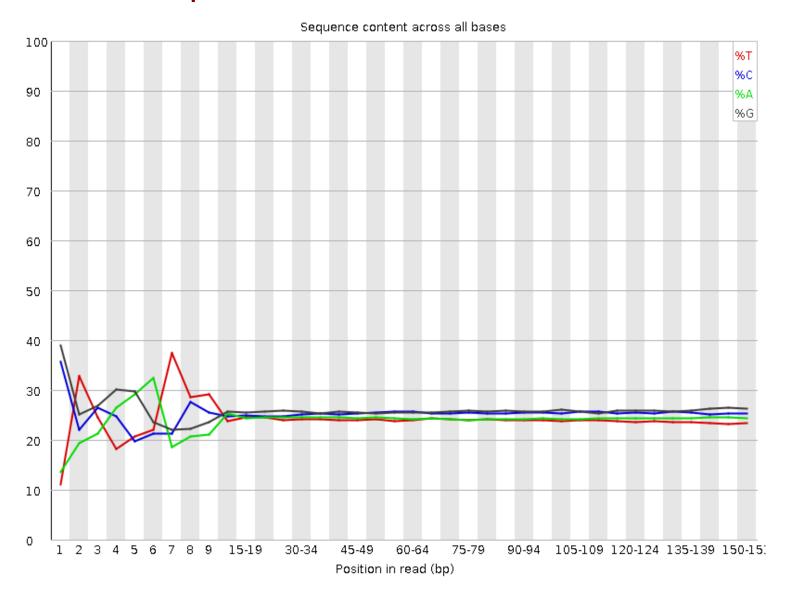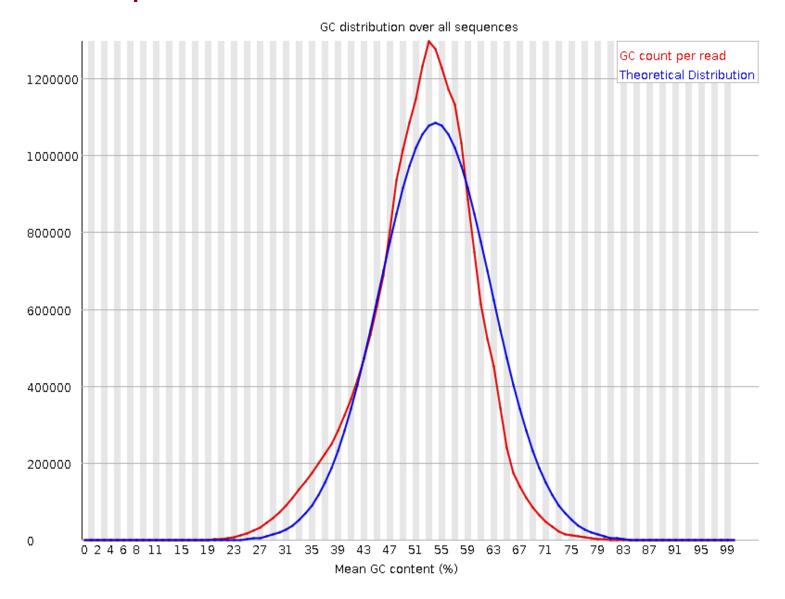Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅ 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
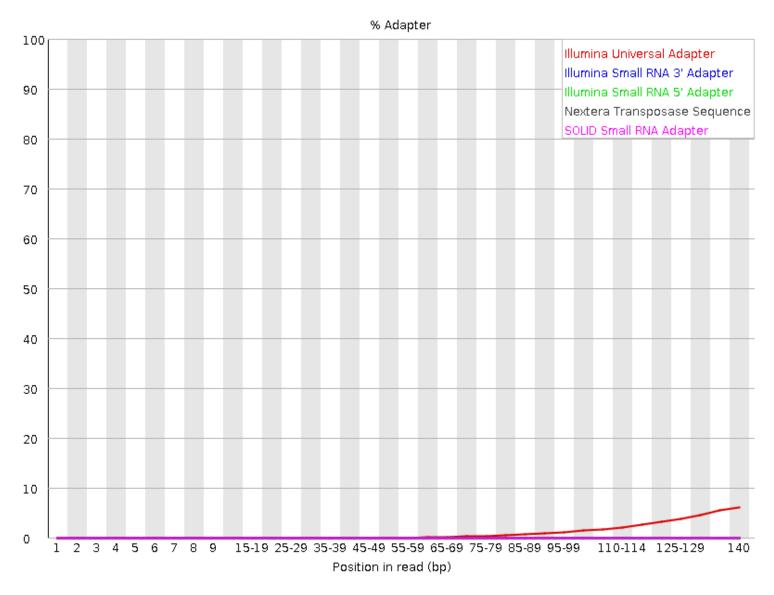
❌ Sequence Duplication Levels

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	42624	0.18328428724239193	No Hit
GTCTCTTTCTGCTGACGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGG	38451	0.1653402807985457	No Hit
CGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTG	33521	0.14414115504533173	No Hit
AAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTGATGC	27653	0.11890860536584702	No Hit

⚠️ Adapter Content

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