FastQC Report

Summary

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✅ Basic Statistics

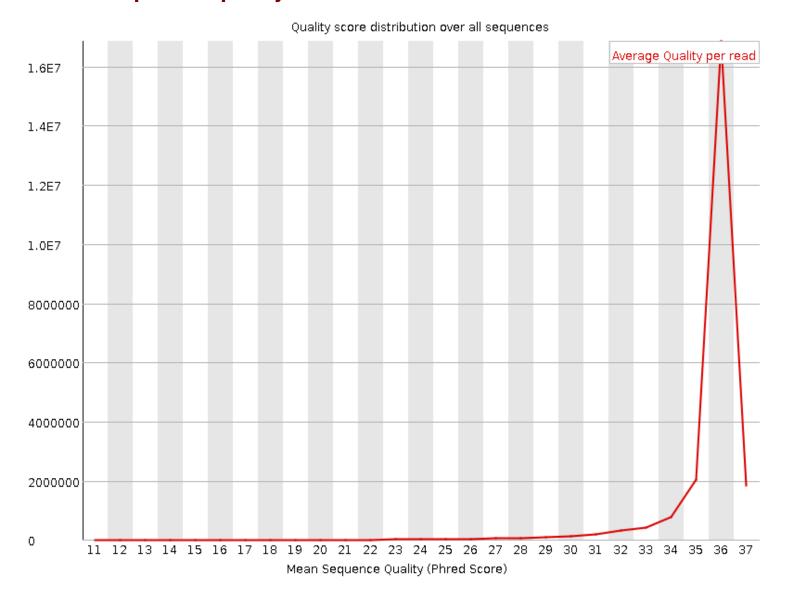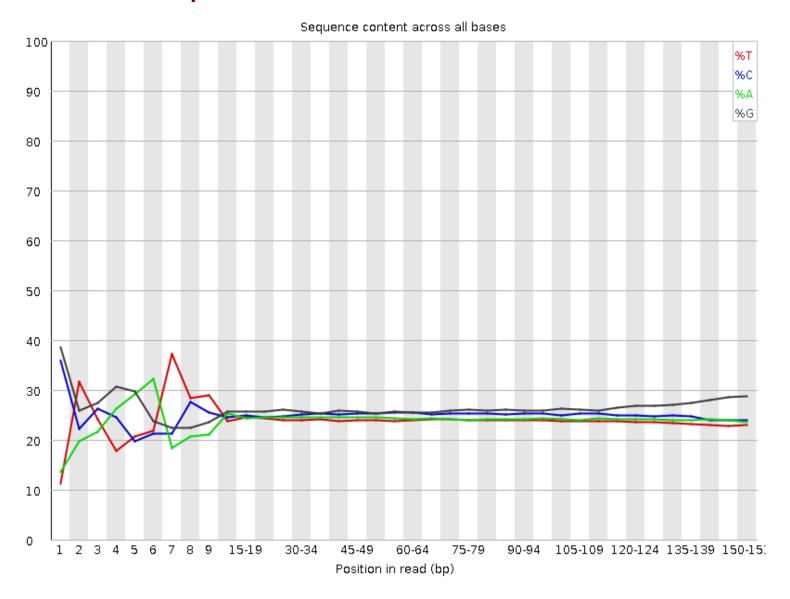| Measure	Value
Filename	SRR14866430_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23255676
Sequences flagged as poor quality	0
Sequence length	151
%GC	51
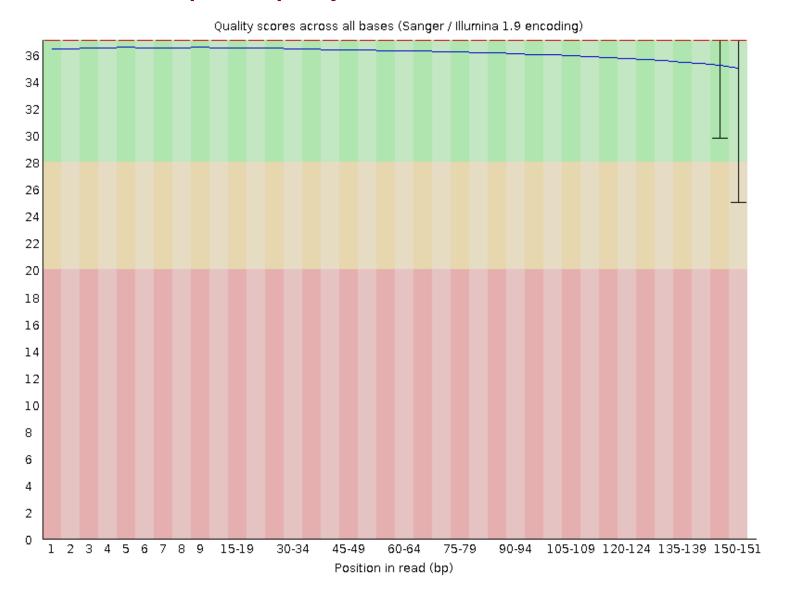
✅ Per base sequence quality

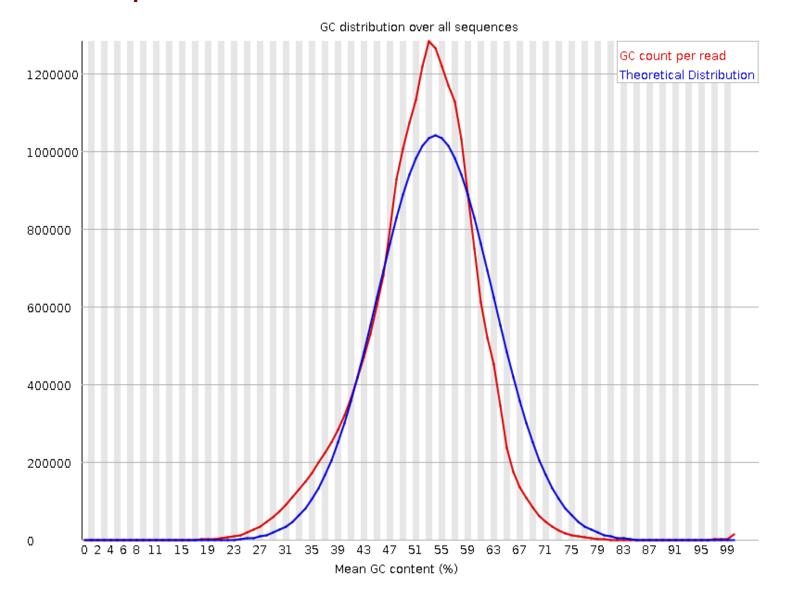# ✅Per sequence quality scores
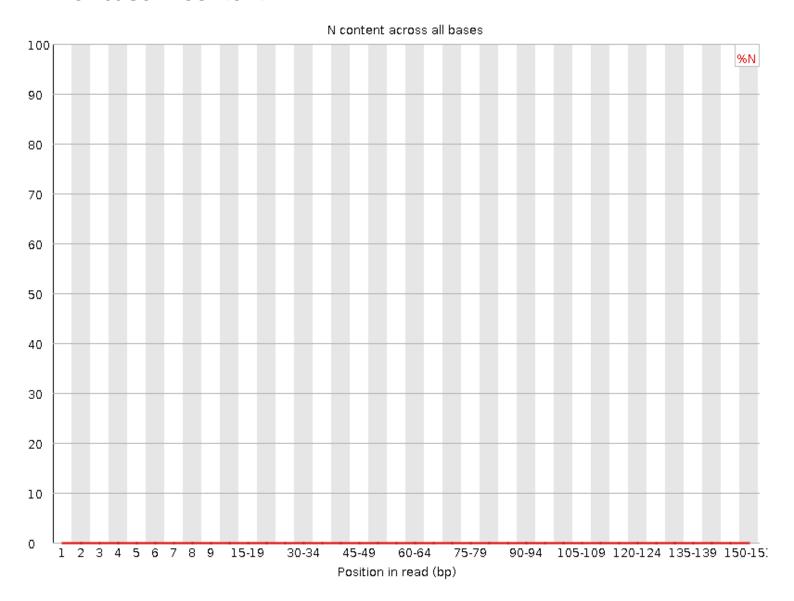
Quality score distribution over all sequences

⚠️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

Percent of seqs remaining if deduplicated 39.2%

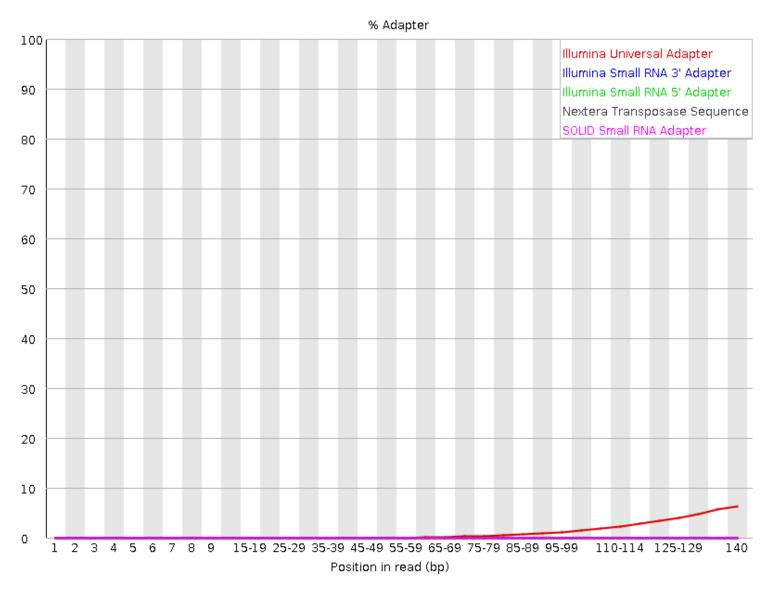# ⚠️Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	42141	0.18120737492214803	No Hit
GTCTCTTTCTGCTGACGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGG	35275	0.15168339978592751	No Hit
CGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTG	33237	0.14291994780113038	No Hit
AAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTGATGC	28354	0.1219229232467807	No Hit
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	27843	0.11972561021231978	No Hit

⚠️ Adapter Content

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