FastQC Report

Summary

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✅ Basic Statistics

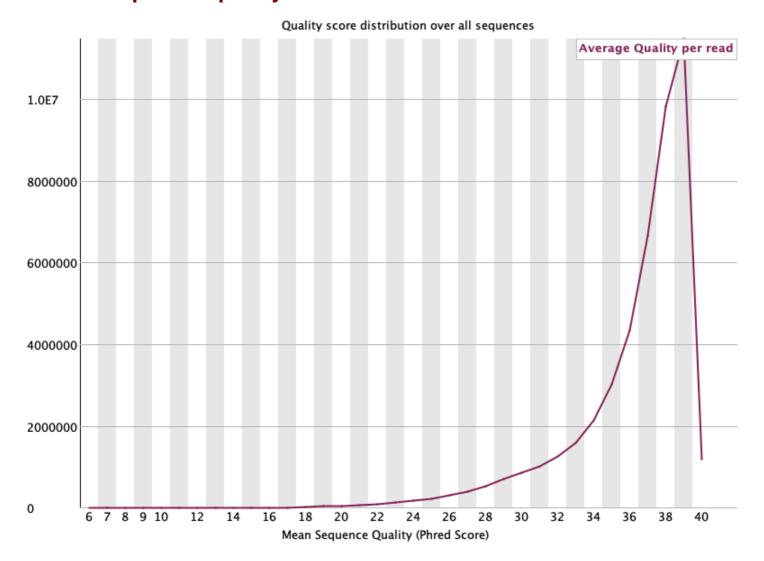| Measure	Value
Filename	SRR13380443_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	46436582
Total Bases	3.5 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	45
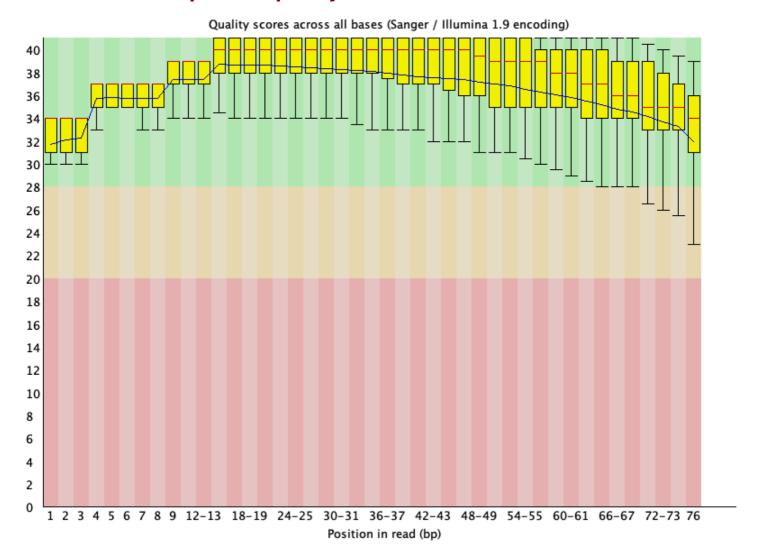
✅ Per base sequence quality

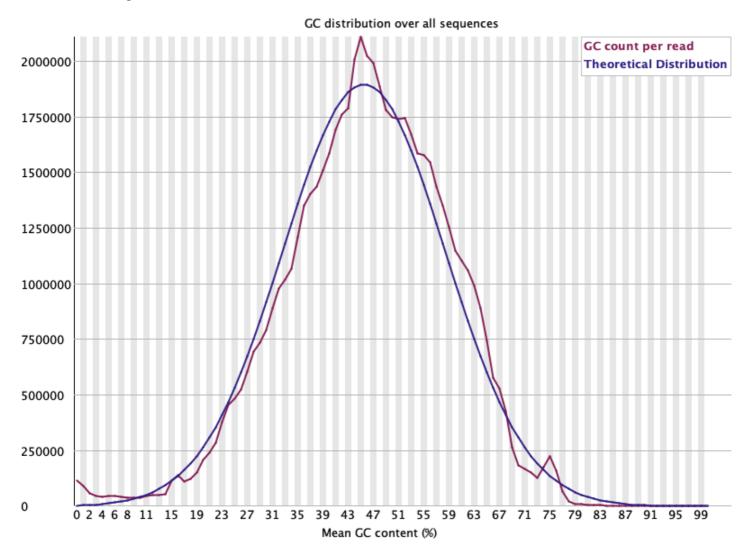Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅ 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
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTAGATCGATCTCGTAT	702406	1.5126134821895376	TruSeq Adapter, Index 3 (97% over 37bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	334713	0.7207959448867275	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	86433	0.18613127038505978	No Hit

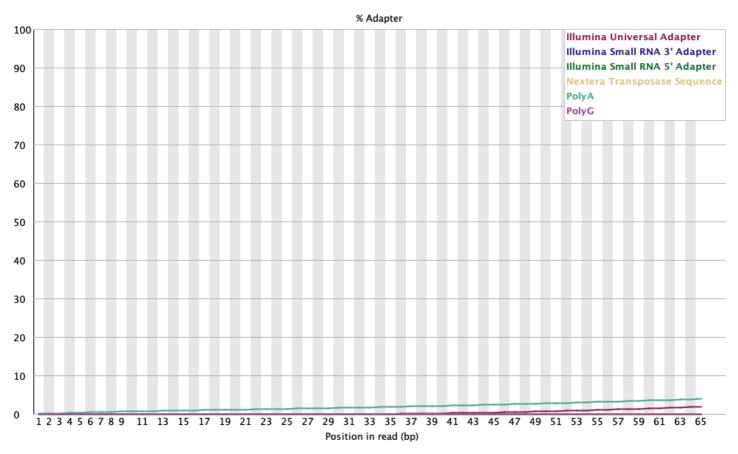## ✅ Adapter Content

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