⥠FastQC Report

Summary

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✅ Basic Statistics

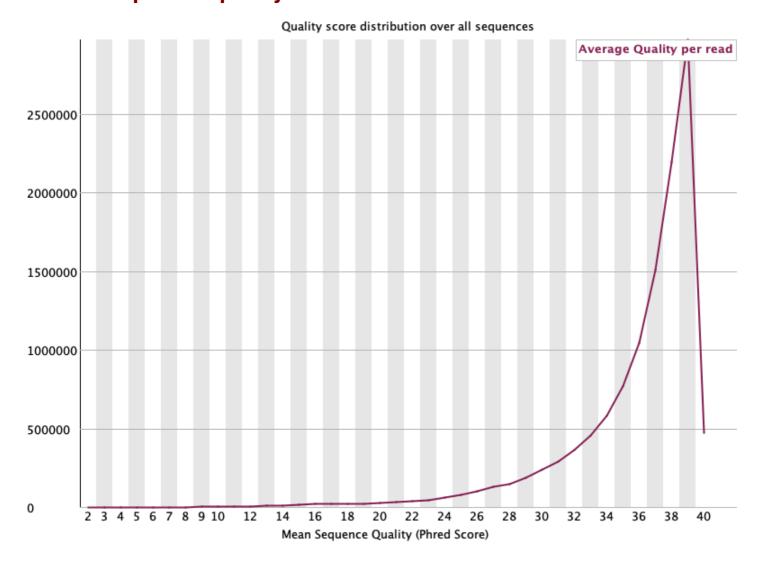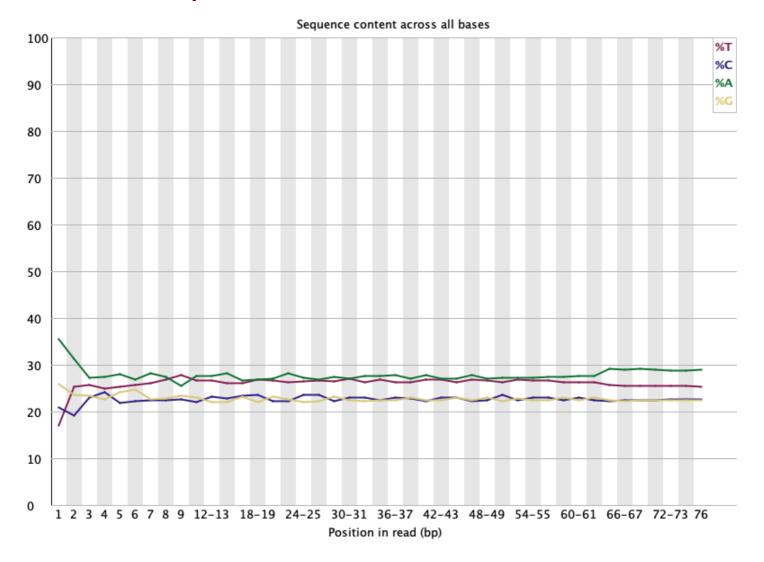| Measure	Value
Filename	SRR13380480_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	12013342
Total Bases	913 Mbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	45
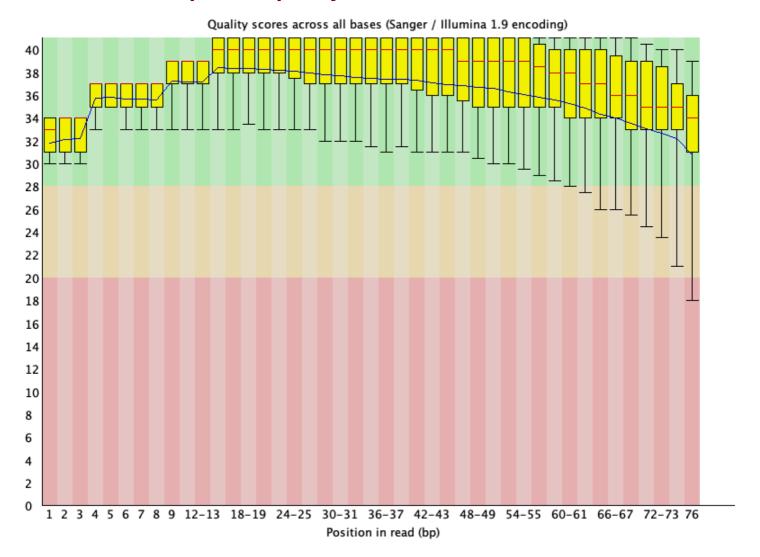
✅ Per base sequence quality

✅ Per sequence quality scores

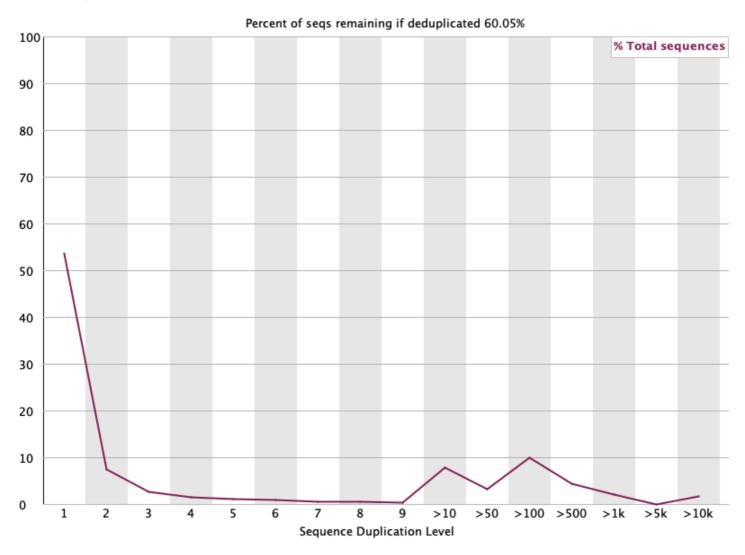# ⚠️ Per base sequence content

✅ Per sequence GC content

✅ Per base N content

N content across all bases

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTACAGCATCTCGTATGC	136302	1.1345885266564457	TruSeq Adapter, Index 7 (97% over 35bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	63218	0.5262315848495781	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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