FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per sequence quality scores](#)

⚠️ [Per base sequence content](#)

✅ [Per sequence GC content](#)

✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

⚠️ [Sequence Duplication Levels](#)

❌ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

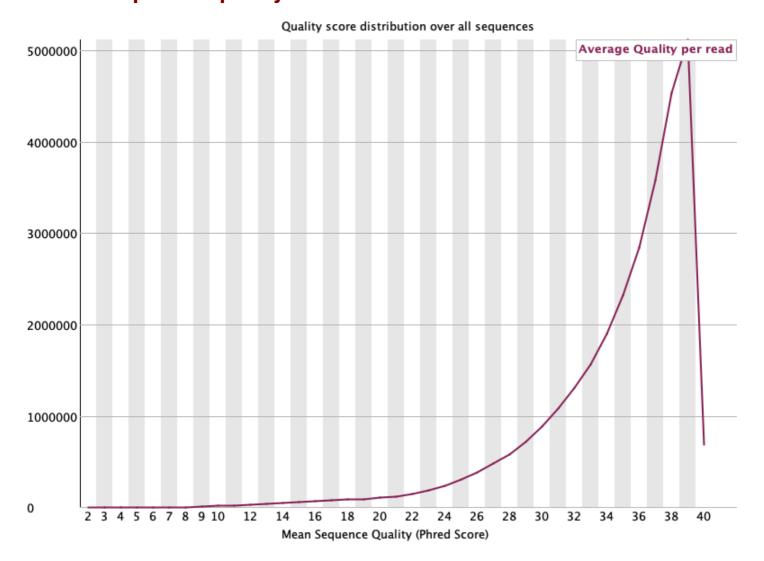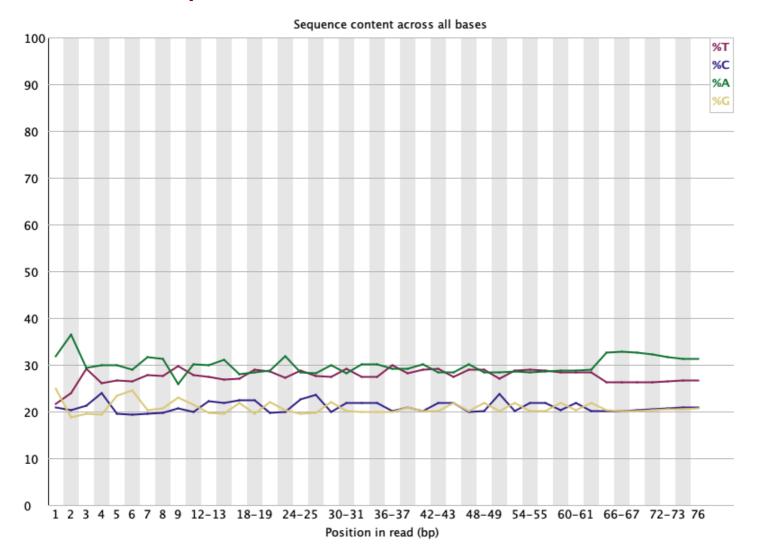| Measure	Value
Filename	SRR13380430_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	29814177
Total Bases	2.2 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	42
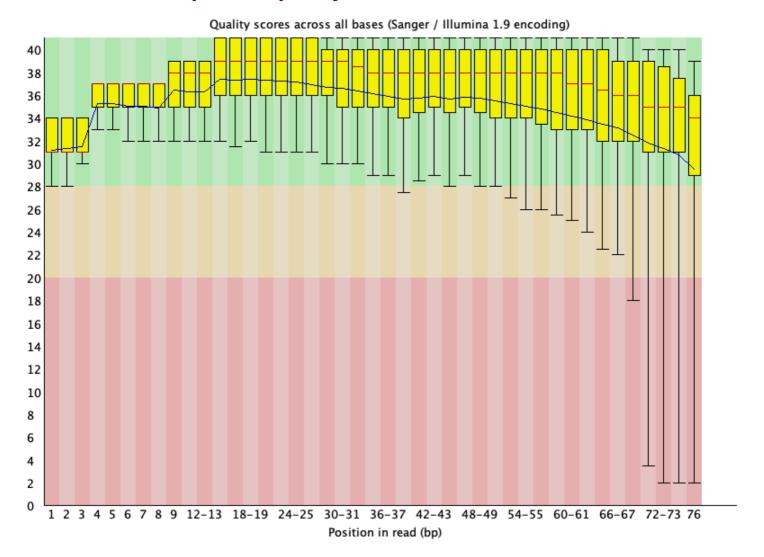
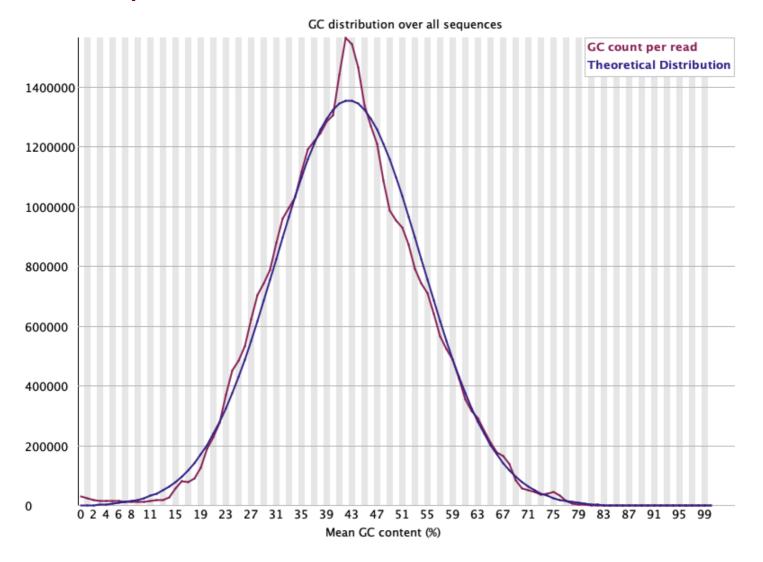# ✅Per base sequence quality

✅ Per sequence quality scores

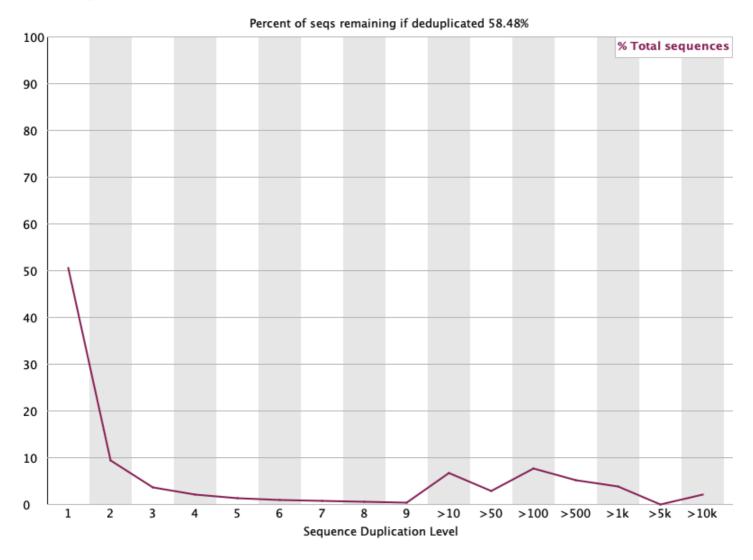# ⚠️Per base sequence content

✅ Per sequence GC content
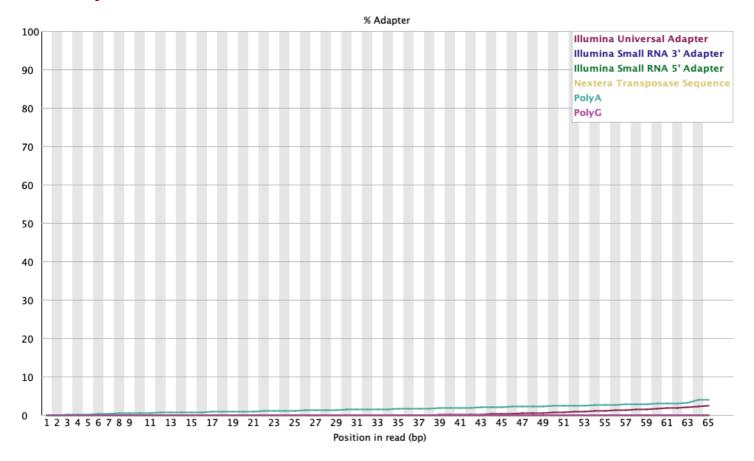
✅ Per base N content

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠️ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 58.48%

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTGAATCTCGTATGC	409441	1.3733097512636354	TruSeq Adapter, Index 8 (100% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	189149	0.6344263670266665	Clontech SMART CDS Primer II A (100% over 26bp)

✅ Adapter Content

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