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

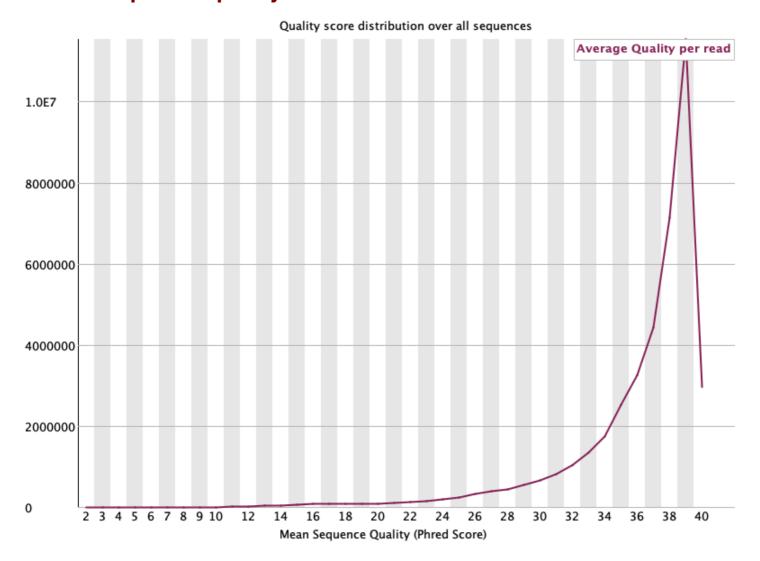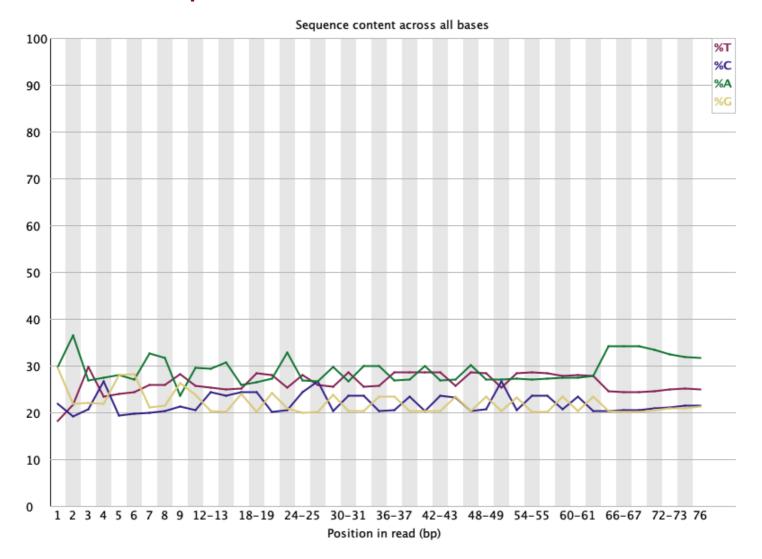| Measure	Value
Filename	SRR13380502_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41032192
Total Bases	3.1 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	44
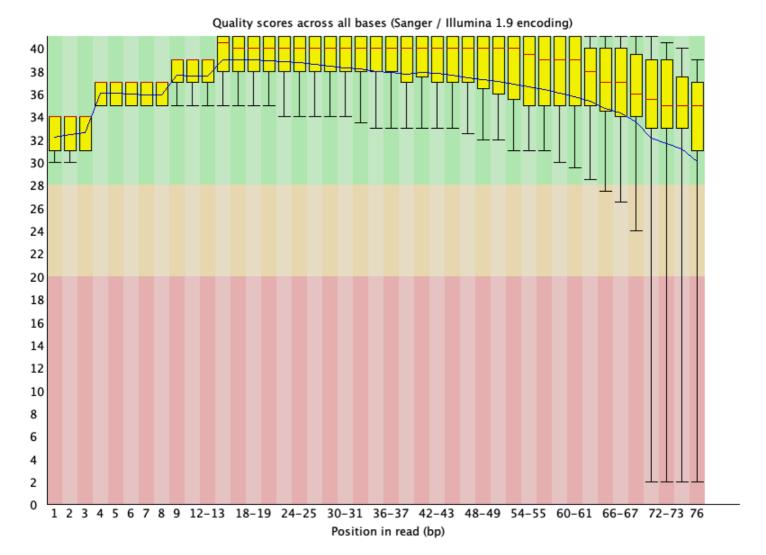
✅ Per base sequence quality
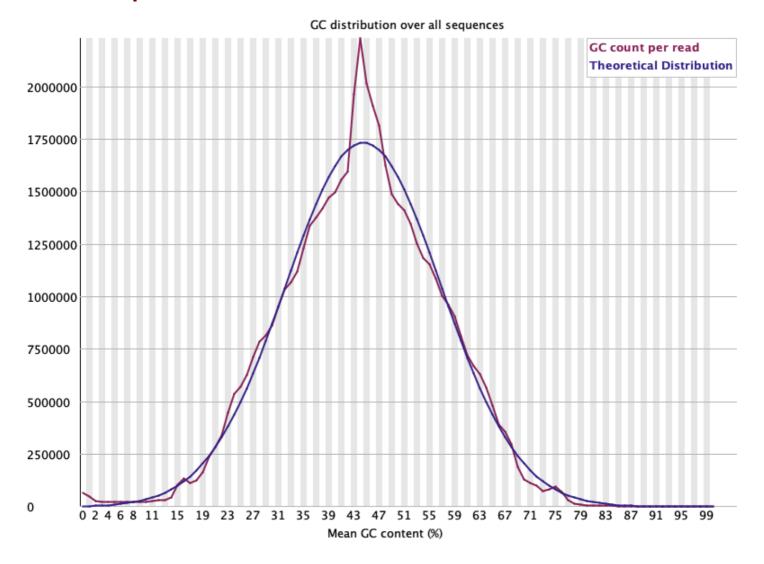
✅Per sequence quality scores

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 48.14%

❌ Overrepresented sequences

| Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATGCTATCTCGTATGC	2305004	5.617550239577744	TruSeq Adapter, Index 9 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	321029	0.7823832565415955	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	51521	0.1255623876979324	No Hit
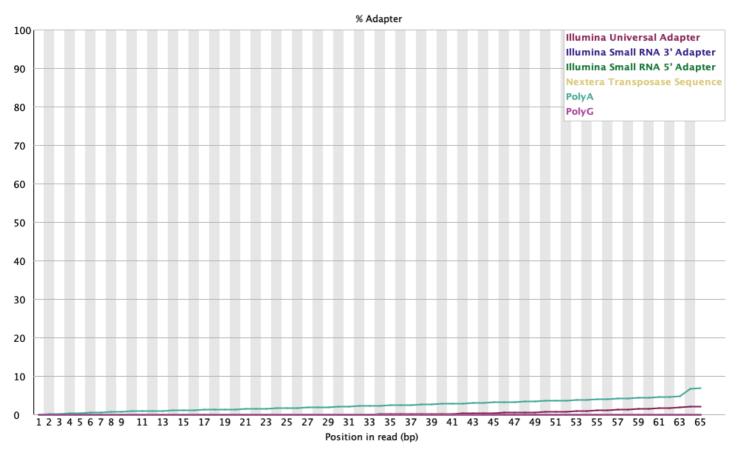
⚠️ Adapter Content

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