# 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

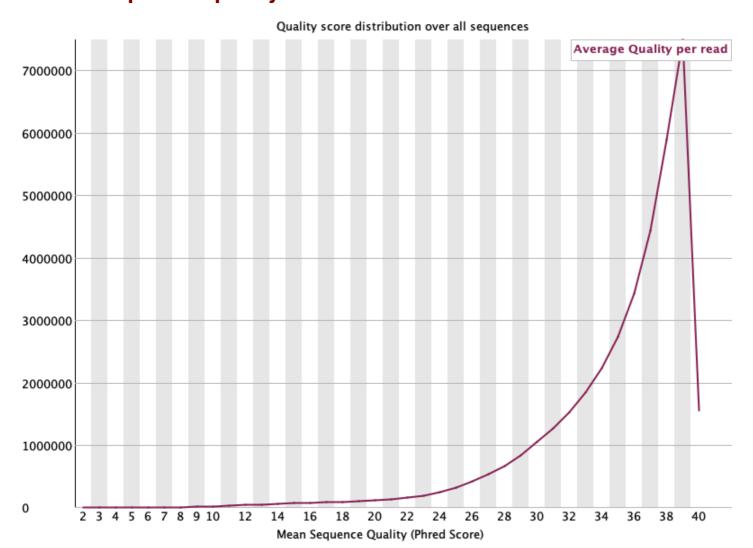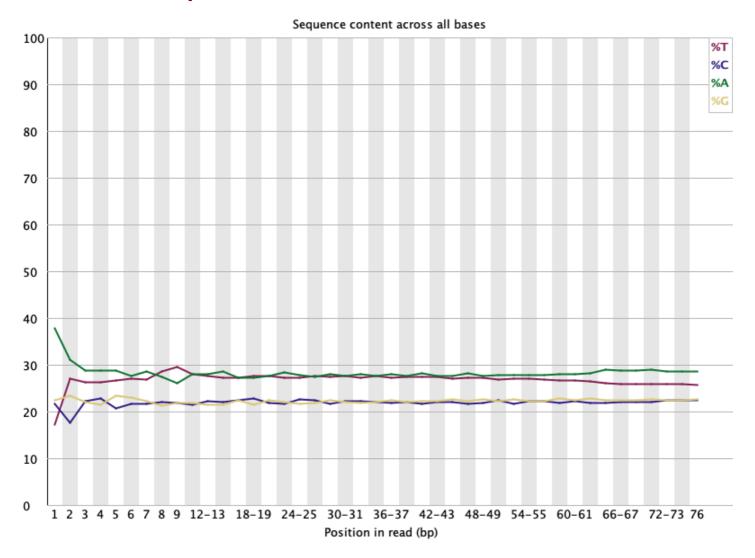| Measure | Value |
|---------|-------|
| Filename | SRR13380477_1.fastq |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 37909467 |
| Total Bases | 2.8 Gbp |
| Sequences flagged as poor quality | 0 |
| Sequence length | 76 |
| %GC | 44 |
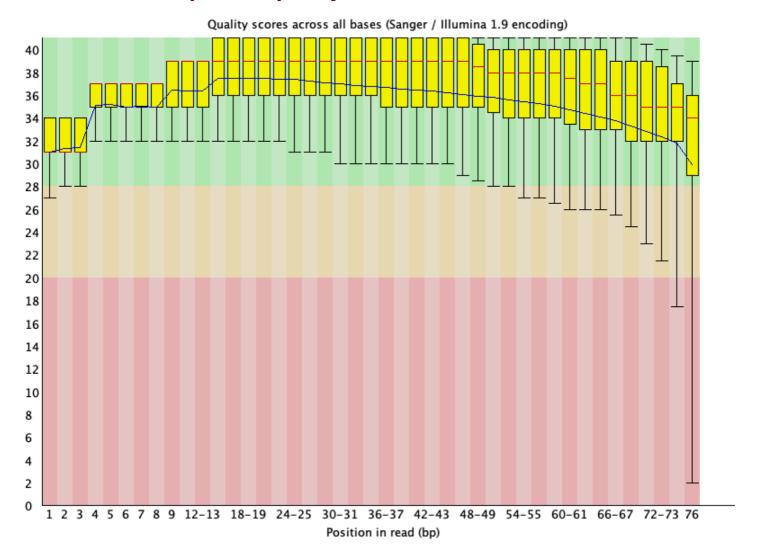
# ✅ Per base sequence quality



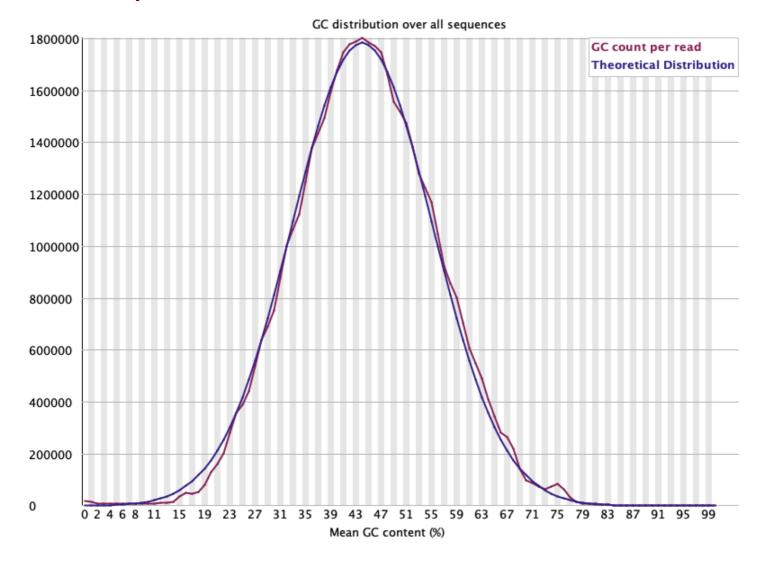Quality scores across all bases (Sanger / Illumina 1.9 encoding)
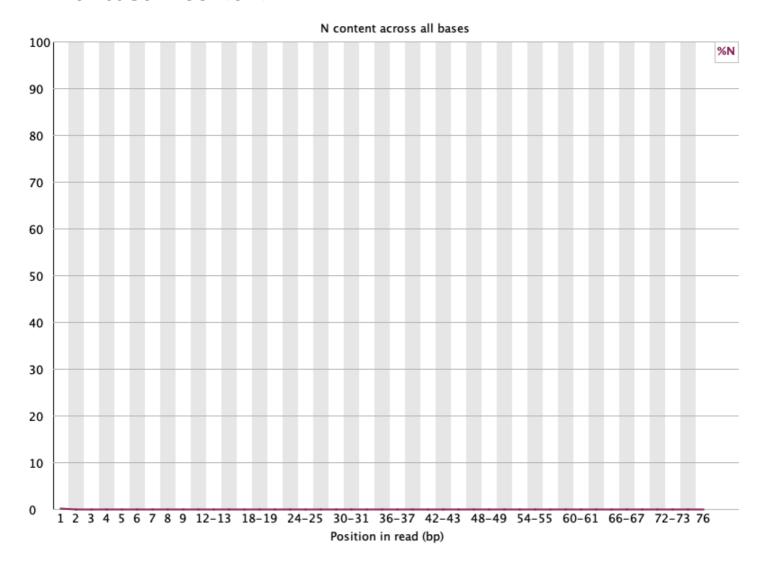
# ✅Per sequence quality scores

# ❌Per base sequence content

# ✅Per sequence GC content

# Per base N content

# ✅ Sequence Length Distribution



Distribution of sequence lengths over all sequences
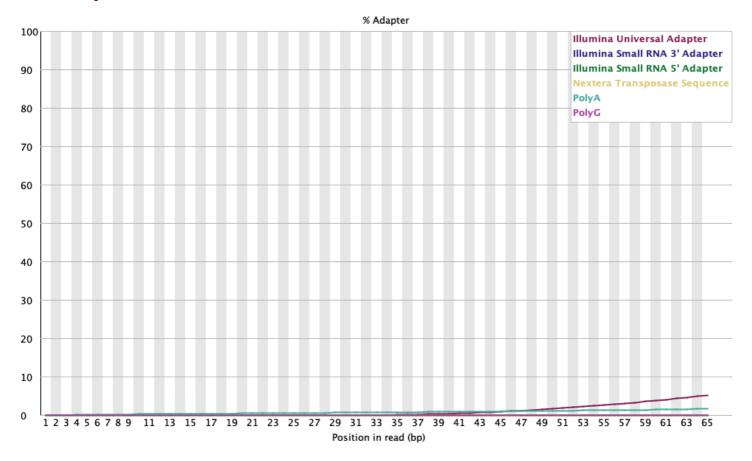
# ⚠️ Sequence Duplication Levels



# ⚠️ Overrepresented sequences

| Sequence | Count | Percentage | Possible Source |
|---|---|---|---|
| GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTAGCTATCTCGTATGC | 237908 | 0.6275688339274198 | TruSeq Adapter, Index 3 (97% over 37bp) |
| AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT | 140000 | 0.3693008925712408 | Clontech SMART CDS Primer II A (100% over 26bp) |

# ⚠️ Adapter Content



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