# 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

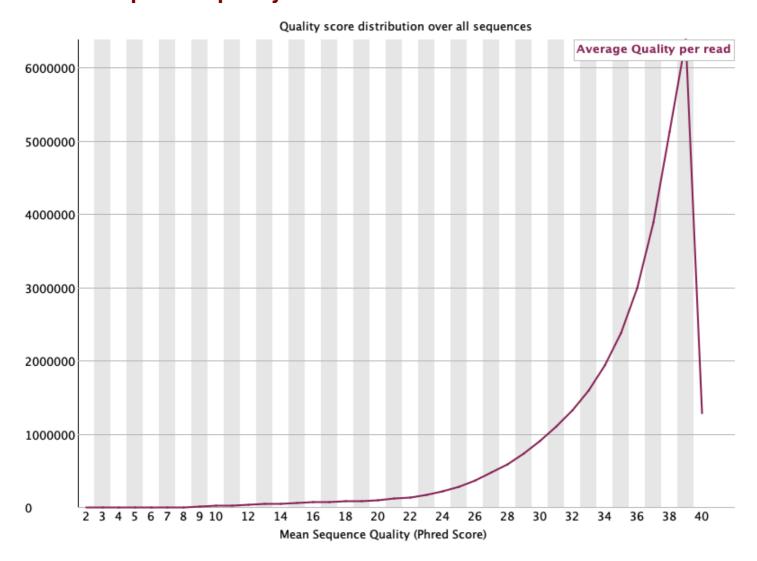| Measure | Value |
| --- | --- |
| Filename | SRR13380521_1.fastq |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 32909344 |
| Total Bases | 2.5 Gbp |
| Sequences flagged as poor quality | 0 |
| Sequence length | 76 |
| %GC | 45 |
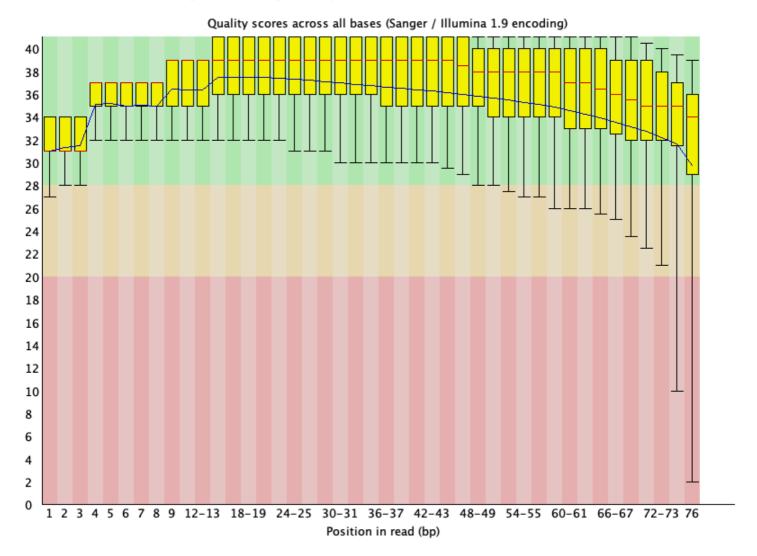
# ✓ Per base sequence quality

# ✅ Per sequence quality scores



Quality score distribution over all sequences

# ⚠️Per base sequence content

# ✅Per sequence GC content

# ✅ Per base N content



*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 |
|---|---|---|---|
| AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTT | 128102 | 0.3892572273698315 | Clontech SMART CDS Primer II A (100% over 26bp) |
| GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTATACATCTCGTATGC | 122418 | 0.3719855369952072 | TruSeq Adapter, Index 2 (97% over 37bp) |

# ✅ Adapter Content



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