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

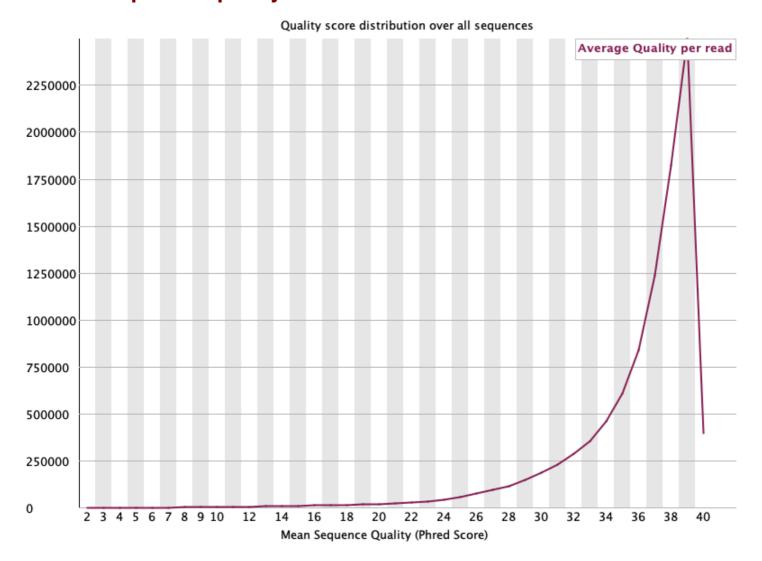| Measure	Value
Filename	SRR13380448_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	9754890
Total Bases	741.3 Mbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	45
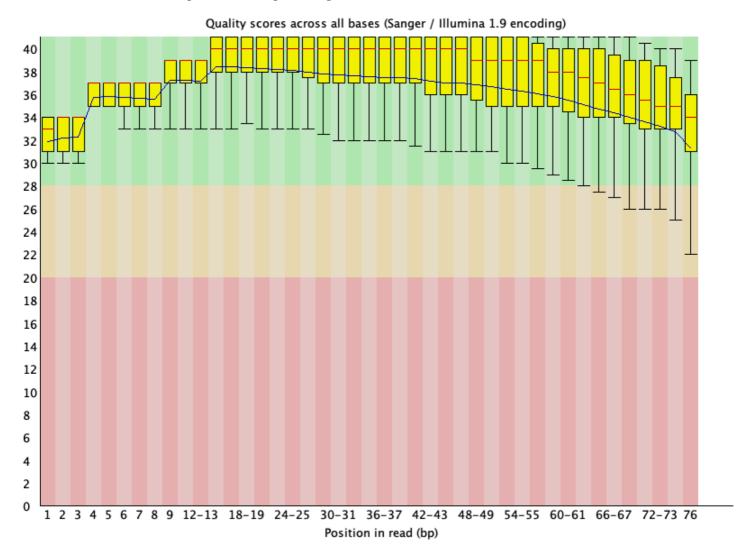
Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅Per sequence quality scores

Quality score distribution over all sequences

❌Per base sequence content

Sequence content across all bases

✅ Per sequence GC content

GC distribution over all sequences

Per base N content

N content across all bases

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Overrepresented sequences

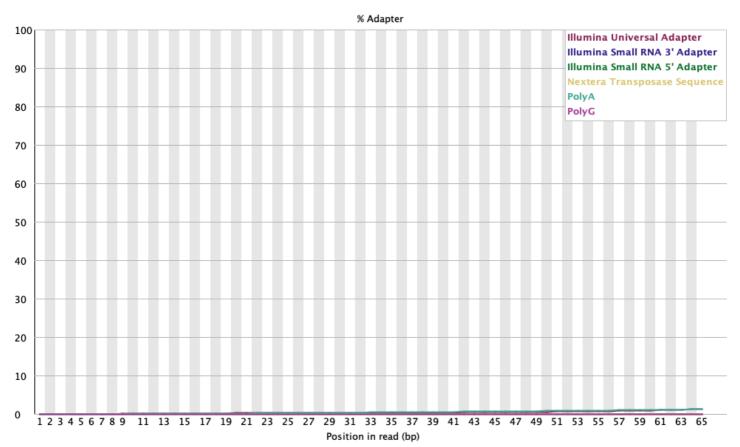| Sequence	Count	Percentage	Possible Source
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTT	38372	0.3933616883429747	Clontech SMART CDS Primer II A (100% over 26bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGACGGAATCTCGTATGC	37468	0.3840945413018496	TruSeq Adapter, Index 6 (97% over 36bp)
CGCGCGCGAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGACGGAAT	15810	0.16207256053117974	TruSeq Adapter,

Sequence	Count	Percentage	Possible Source
			Index 6 (97% over 36bp)

✅ Adapter Content

Produced by FastQC (version 0.12.1)