FastQC Report

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✅ Basic Statistics

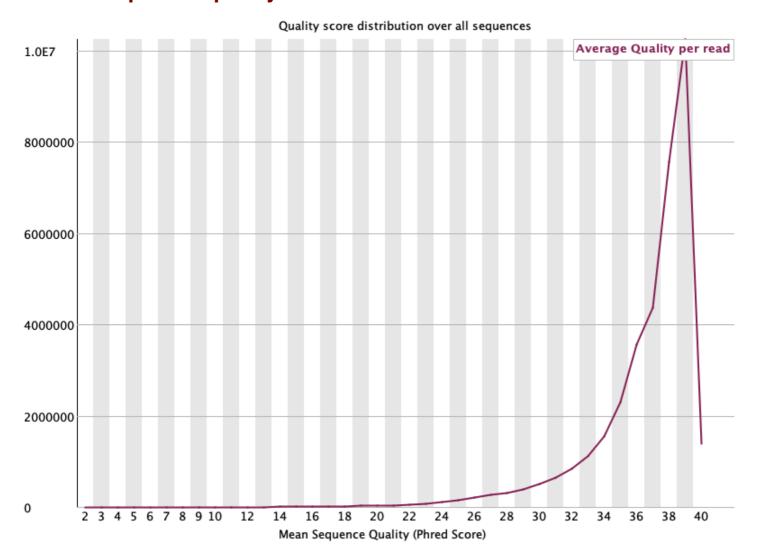| Measure	Value
Filename	SRR13380441_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36257654
Total Bases	2.7 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	48
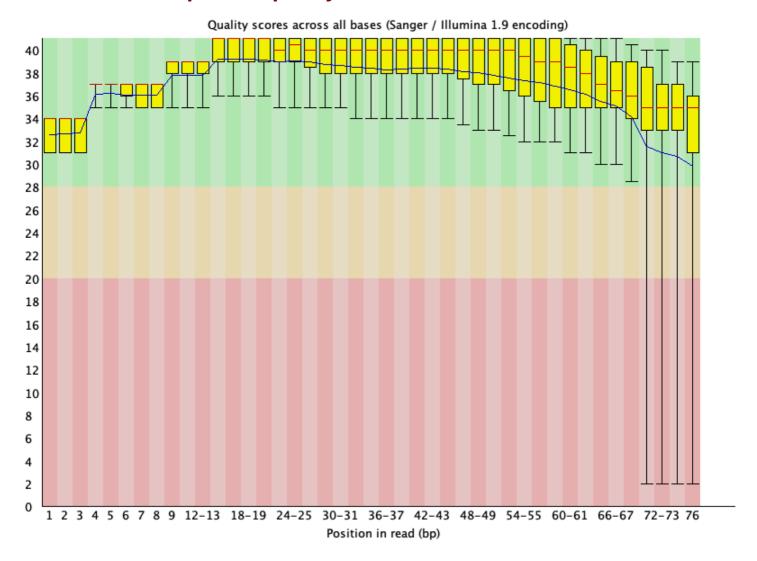
Per base sequence quality

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

Position in read (bp)

✅Per sequence quality scores

⚠️ Per base sequence content

Sequence content across all bases

❌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
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGTGACATCTCGTATGC	3251428	8.96756309716012	TruSeq Adapter, Index 13 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	139940	0.38595988587678615	Clontech SMART CDS Primer II A (100% over 26bp)

⚠️ Adapter Content

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