FastQC Report

Summary

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✅ Basic Statistics

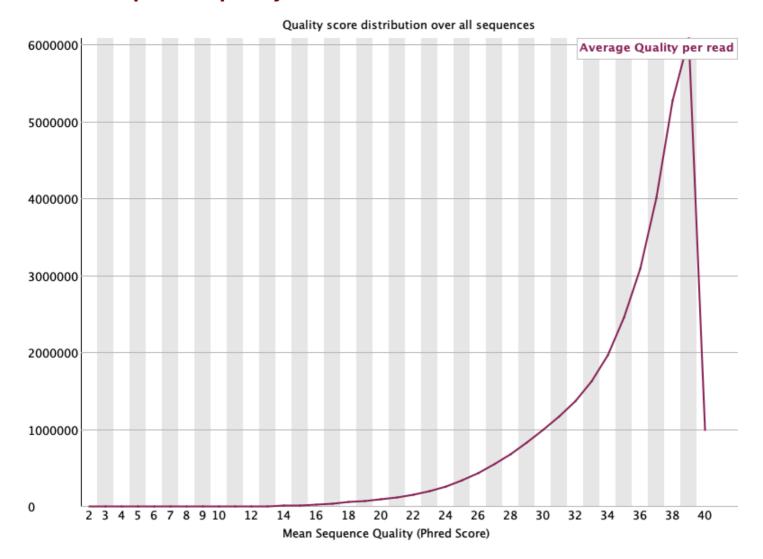| Measure	Value
Filename	SRR13380538_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	33041518
Total Bases	2.5 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	45
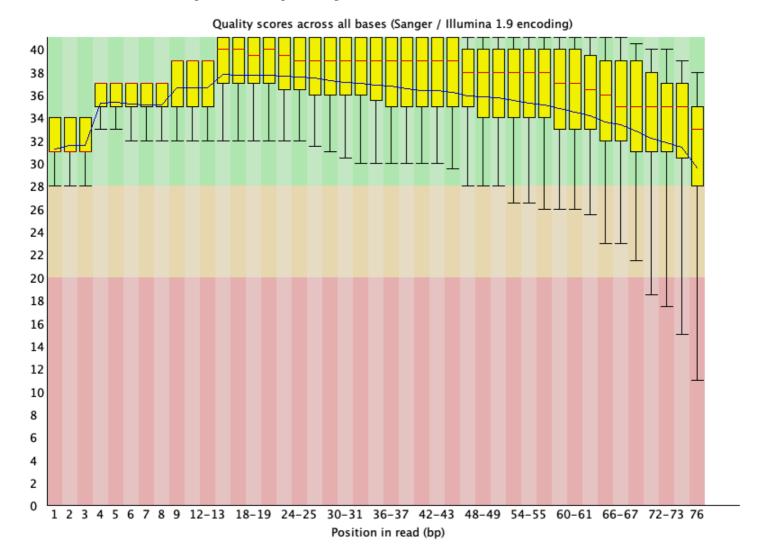
✅ Per base sequence quality

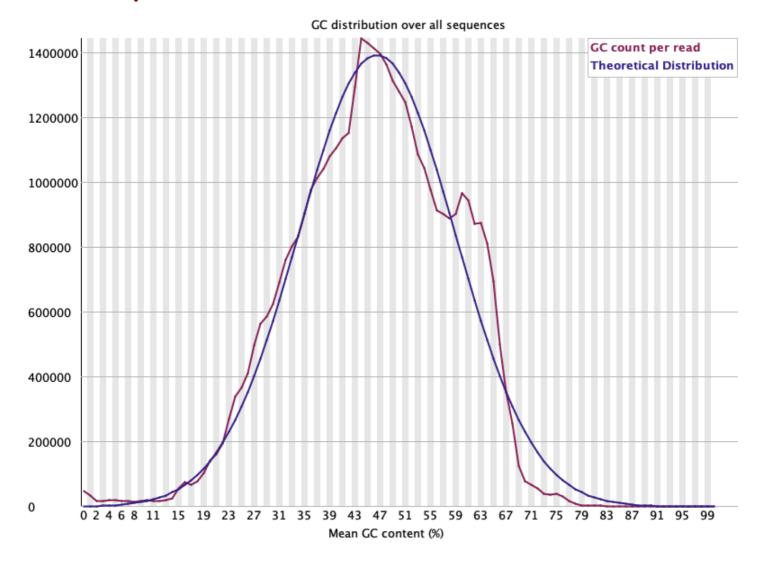Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅ Per sequence quality scores

⚠️ 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 46.07%

❌ Overrepresented sequences

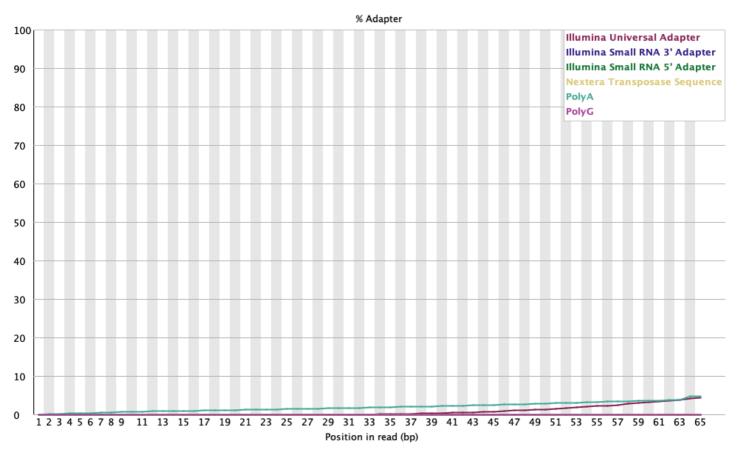| Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTTTCGATCTCGTATGC	1252192	3.7897532431772656	TruSeq Adapter, Index 21 (98% over 50bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	183647	0.5558067882958646	Clontech SMART CDS Primer II A (100% over 26bp)

Sequence	Count	Percentage	Possible Source
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	43792	0.1325362835932659	No Hit

✅ Adapter Content

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