FastQC Report

Summary

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✅ Basic Statistics

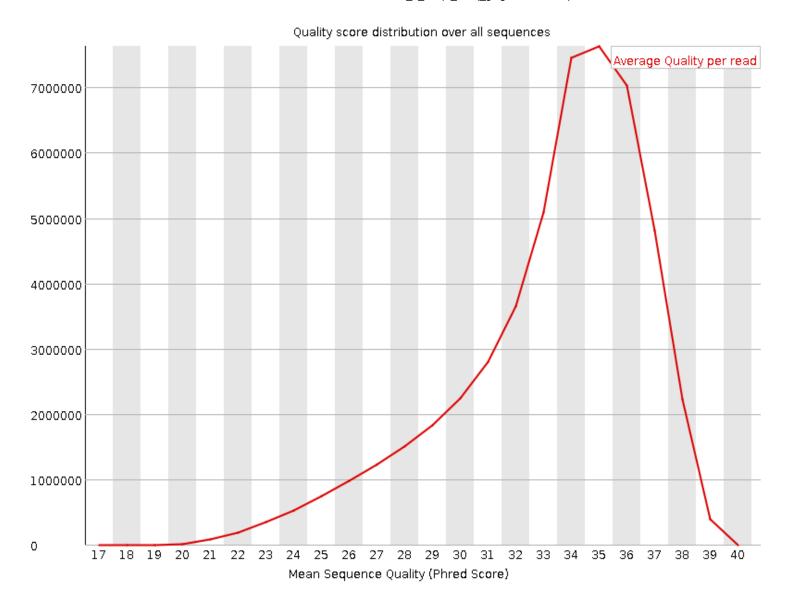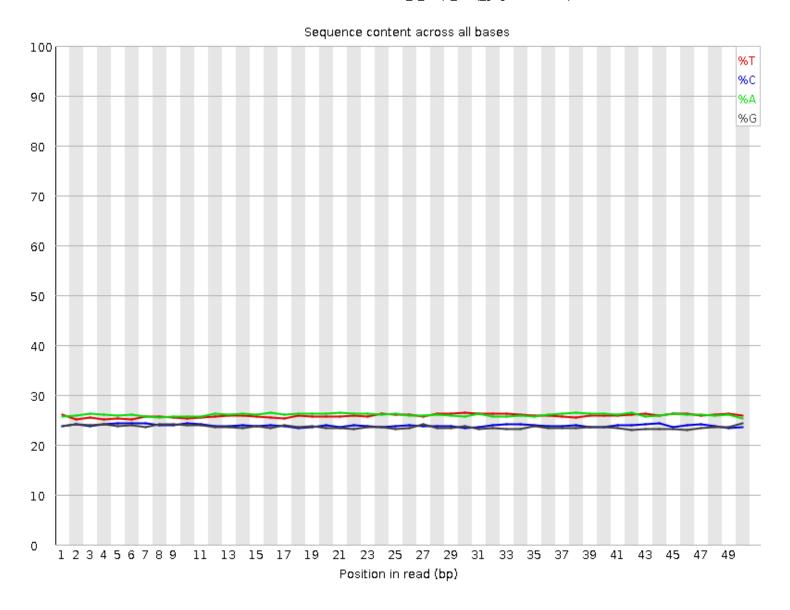| Measure	Value
Filename	SRR1554555_2_adapt_fastq_gz.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	50987496
Sequences flagged as poor quality	0
Sequence length	20-50
%GC	47
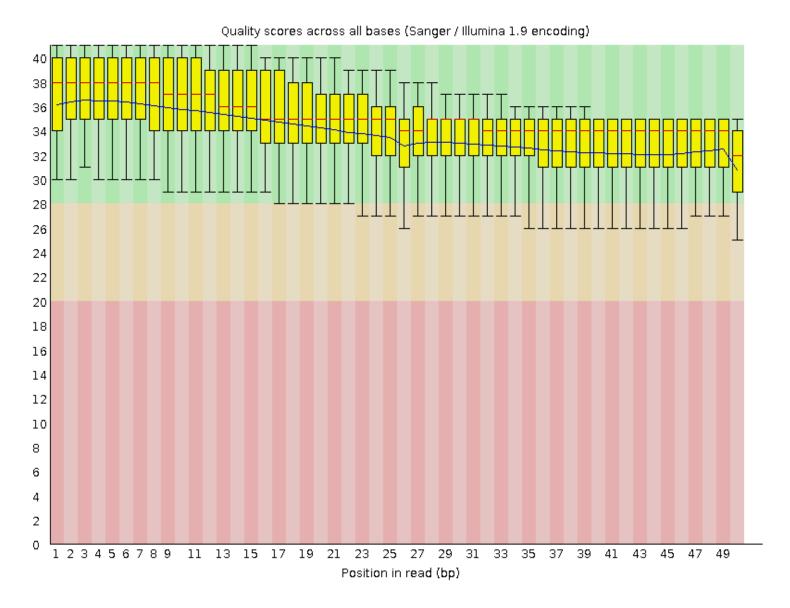
✅ Per base sequence quality

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

⚠️ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 65.31%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

% Adapter

Produced by [FastQC](version 0.11.8)