FastQC Report

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✅ Basic Statistics

Measure	Value
Filename	SRR1554535_2_fastq_gz.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	91185969
Sequences flagged as poor quality	0
Sequence length	50
%GC	47

❌ Per base sequence quality

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

Position in read (bp)

✅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

Percent of seqs remaining if deduplicated 62.1%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

Produced by [FastQC](#) (version 0.11.8)