FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

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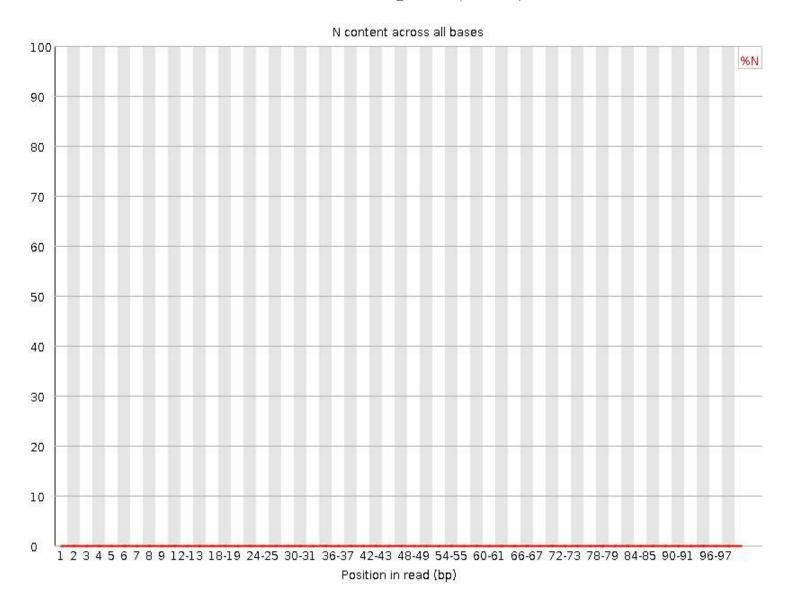
✅ [Per base sequence content](#)

⚠️ [Per sequence GC content](#)
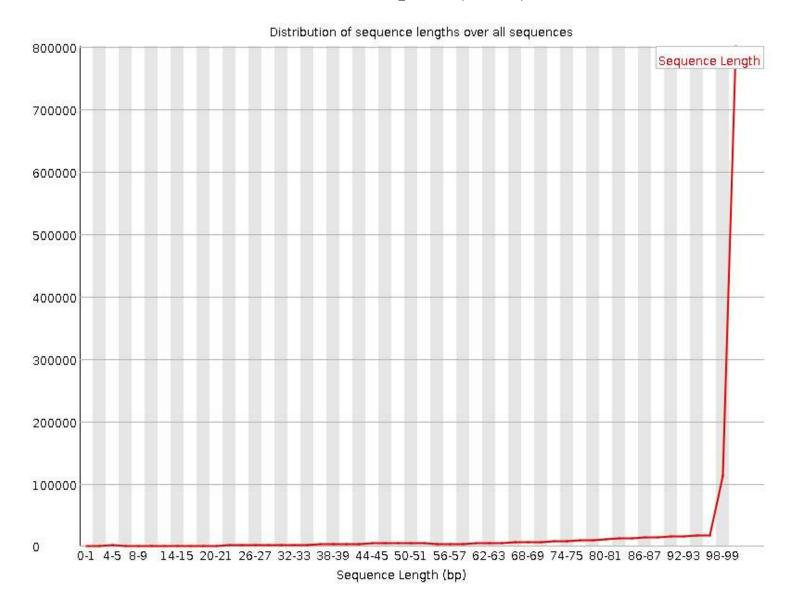
✅ [Per base N content](#)
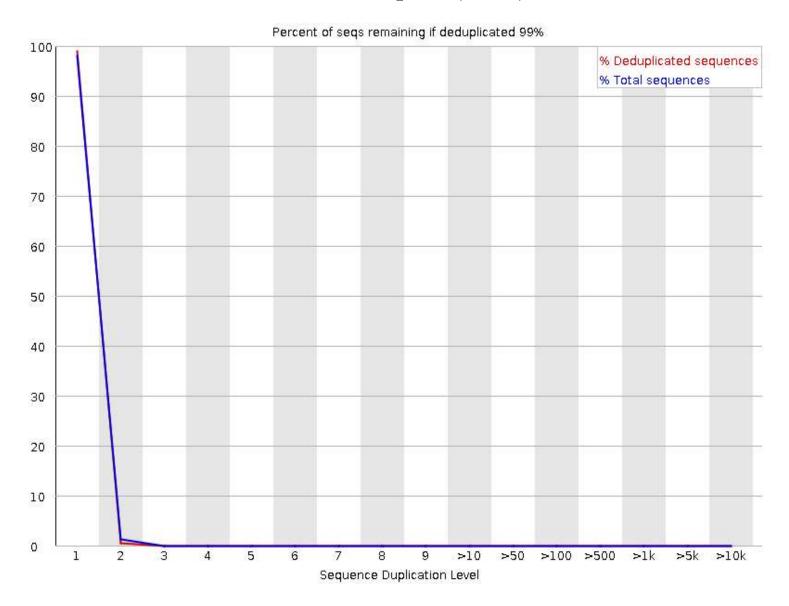
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✅ Basic Statistics

Measure	Value
Filename	A0167658L_2.trimmed.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1205389
Sequences flagged as poor quality	0
Sequence length	2-100
%GC	38

✅ 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

Percent of seqs remaining if deduplicated 99%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

⚠️Kmer Content

Log2 Obs/Exp

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCCCGGA	120	0.008049086	13.370872	84-85

Produced by [FastQC](#) (version 0.11.5)