FastQC Report

Summary

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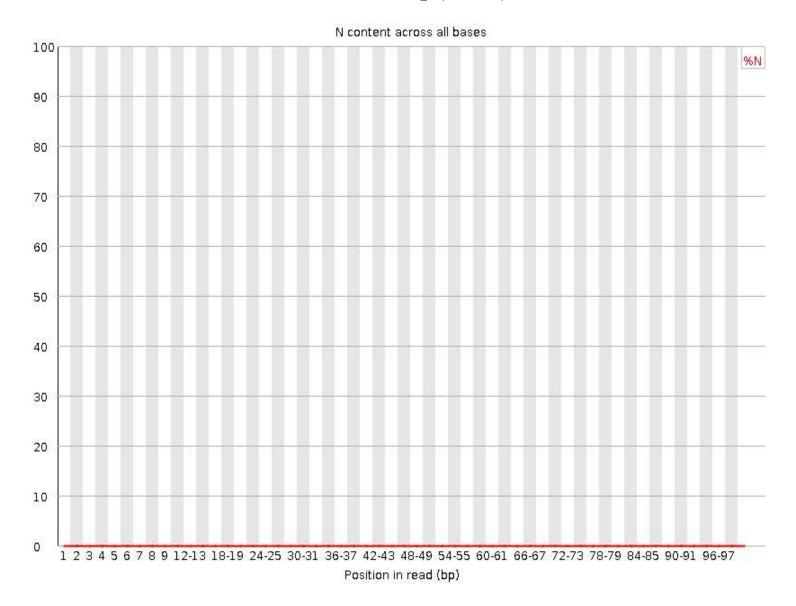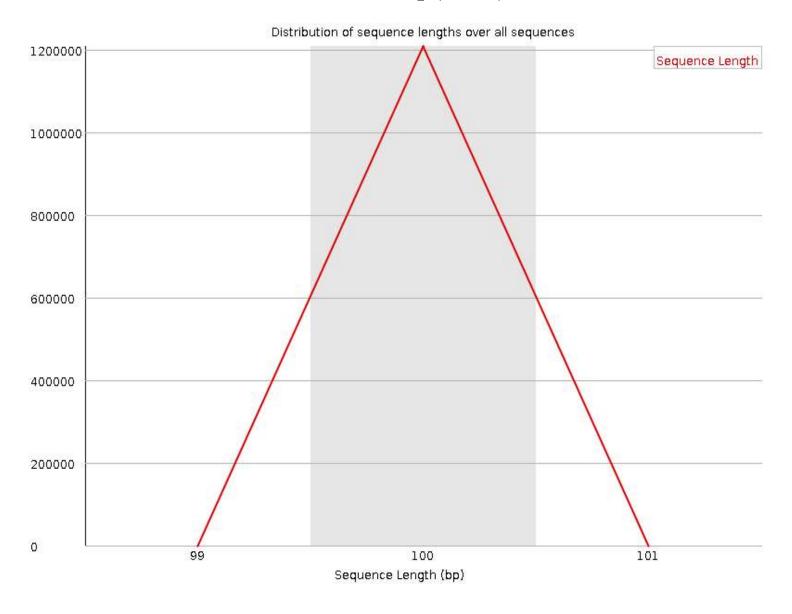
✅ [Per base N content](#)
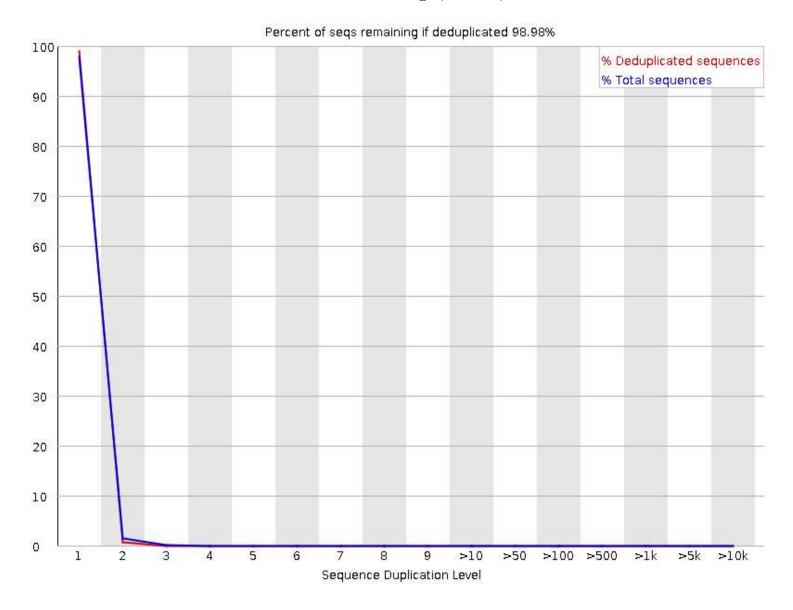
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✅ Basic Statistics

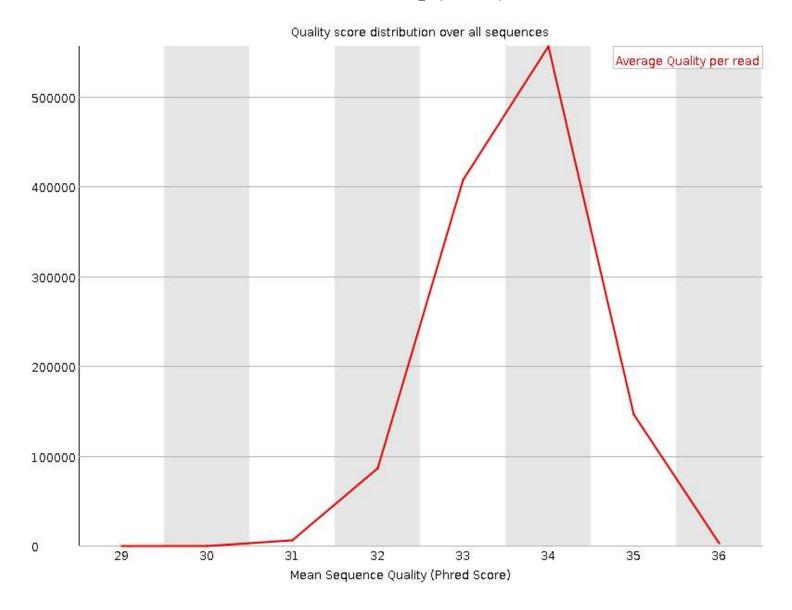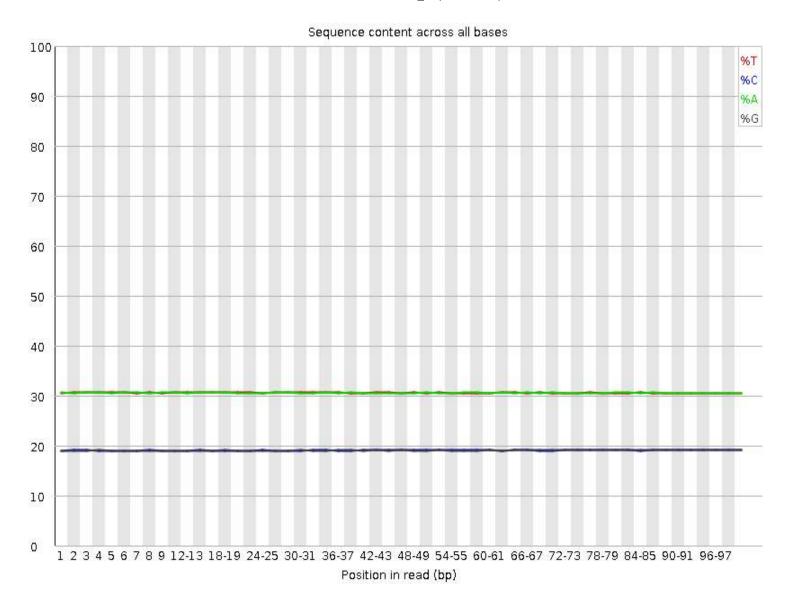| Measure	Value
Filename	A0167658L_2.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1208670
Sequences flagged as poor quality	0
Sequence length	100
%GC	38

✅ 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

✅ Per sequence GC content

GC distribution over all sequences

Legend: GC count per read / Theoretical Distribution

Mean GC content (%)

✅ **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 98.98%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

⚠️Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGACTTT	635	0.0030108402	5.1811023	78-79

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