FastQC Report

Summary

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✅ Basic Statistics

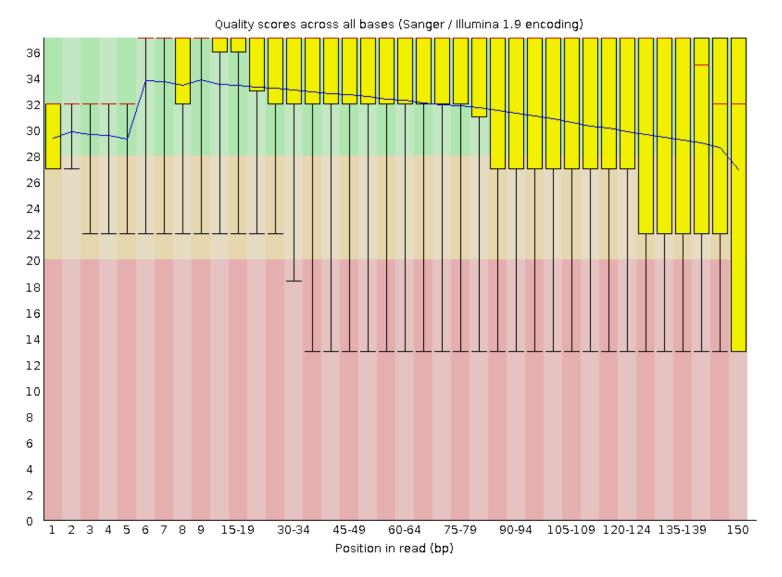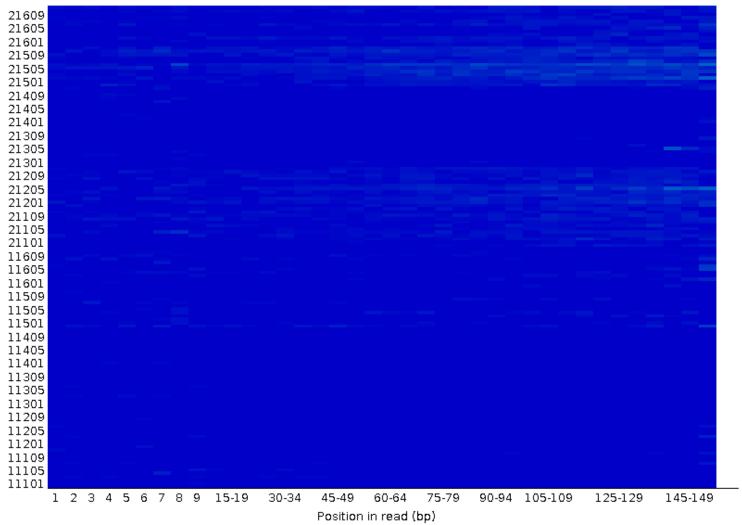| Measure	Value
Filename	evol2_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	926261
Total Bases	133.9 Mbp
Sequences flagged as poor quality	0
Sequence length	35-150
%GC	50

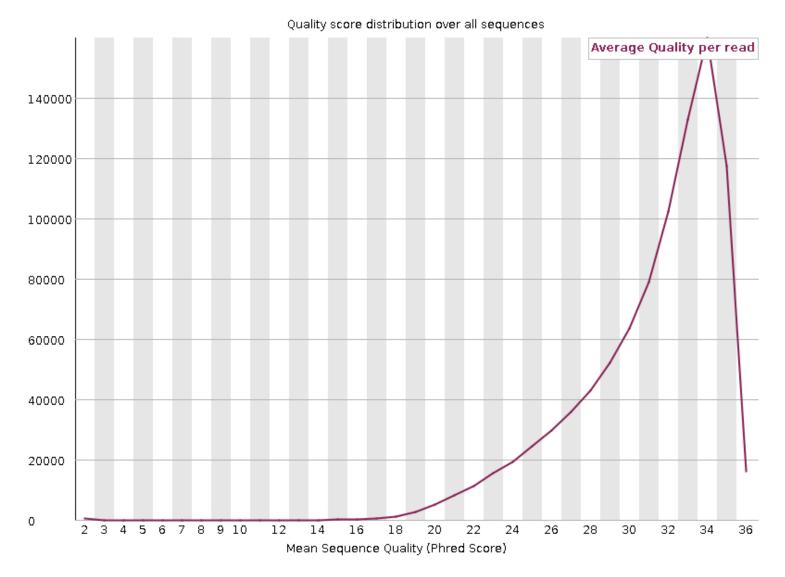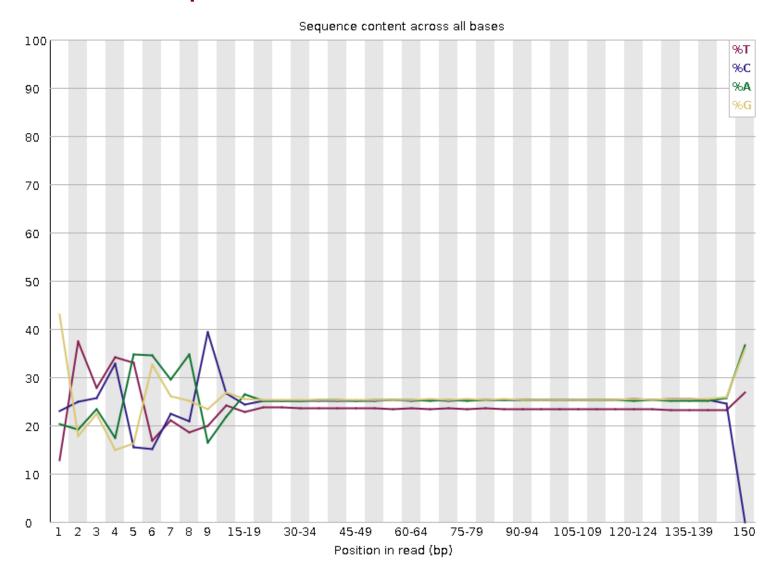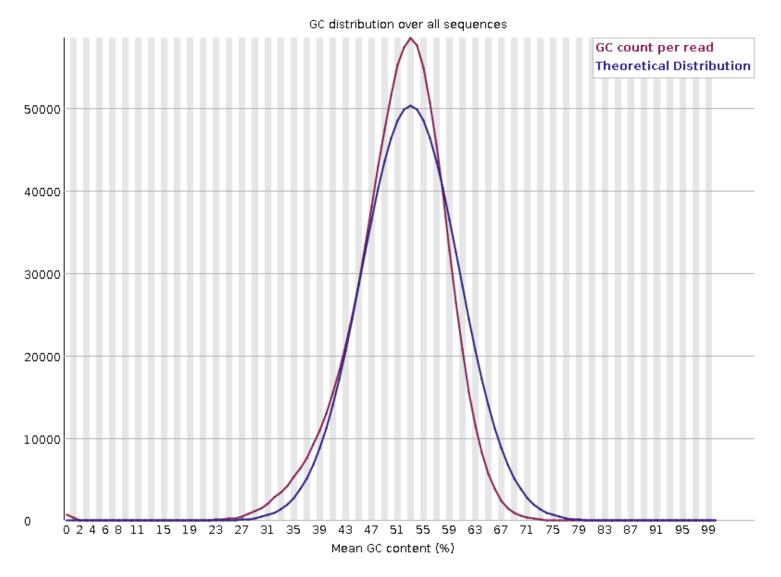# ✅ Per base sequence quality

✅Per tile sequence quality

✅Per sequence quality scores

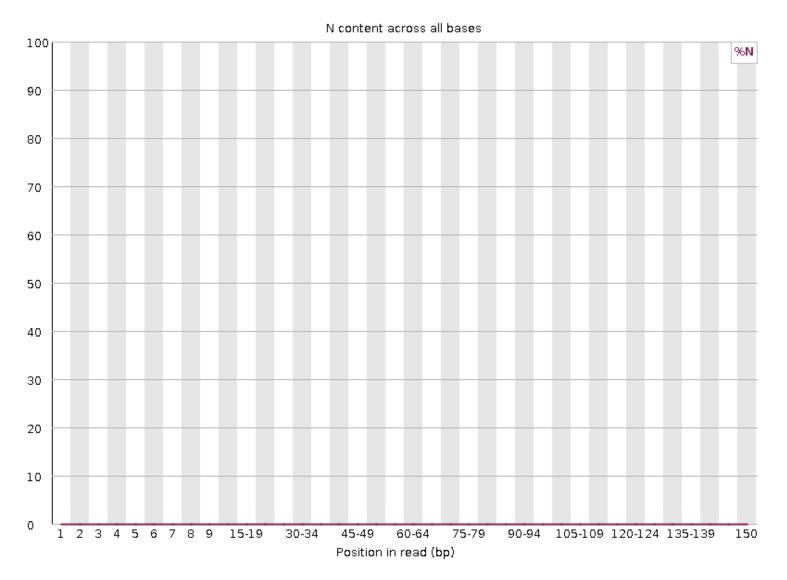# ❌Per base sequence content

⚠️ Per sequence GC content

GC distribution over all sequences

Legend:
GC count per read
Theoretical Distribution

x-axis: 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

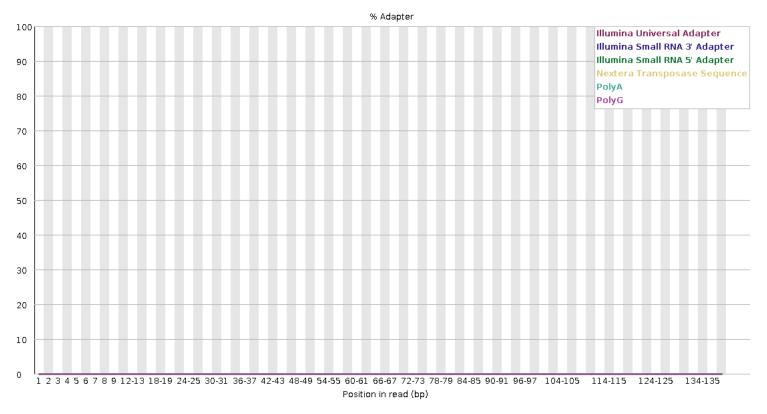Percent of seqs remaining if deduplicated 86.49%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

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