

FastQC Report

Summary

Mon 24 Apr 2023
gc148-B_trimmed_R2.fastq.gz

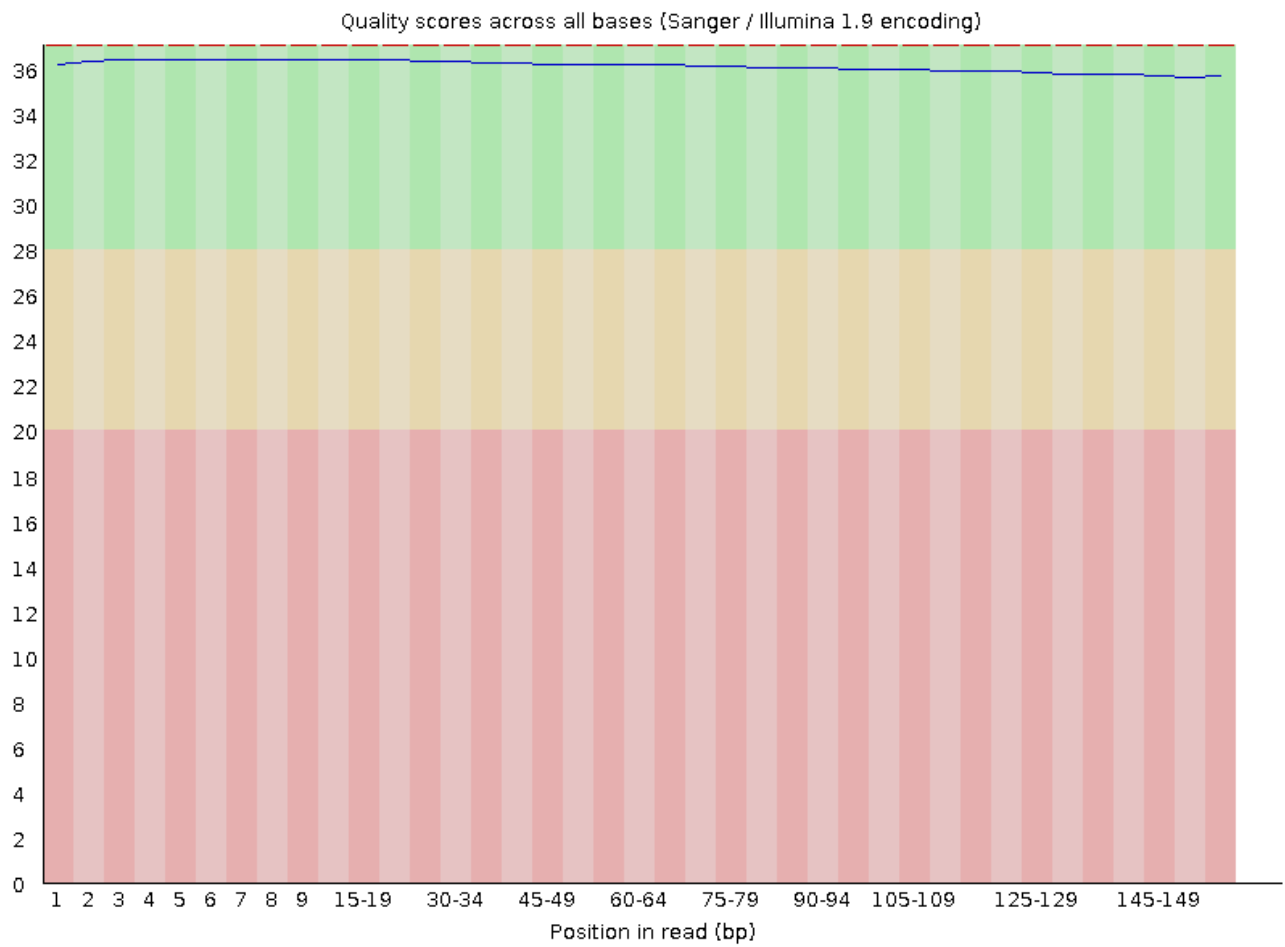
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- ✓ [Per base sequence content](#)
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✓ Basic Statistics

Measure	Value
Filename	gc148-B_trimmed_R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23668708
Sequences flagged as poor quality	0
Sequence length	35-159
%GC	50

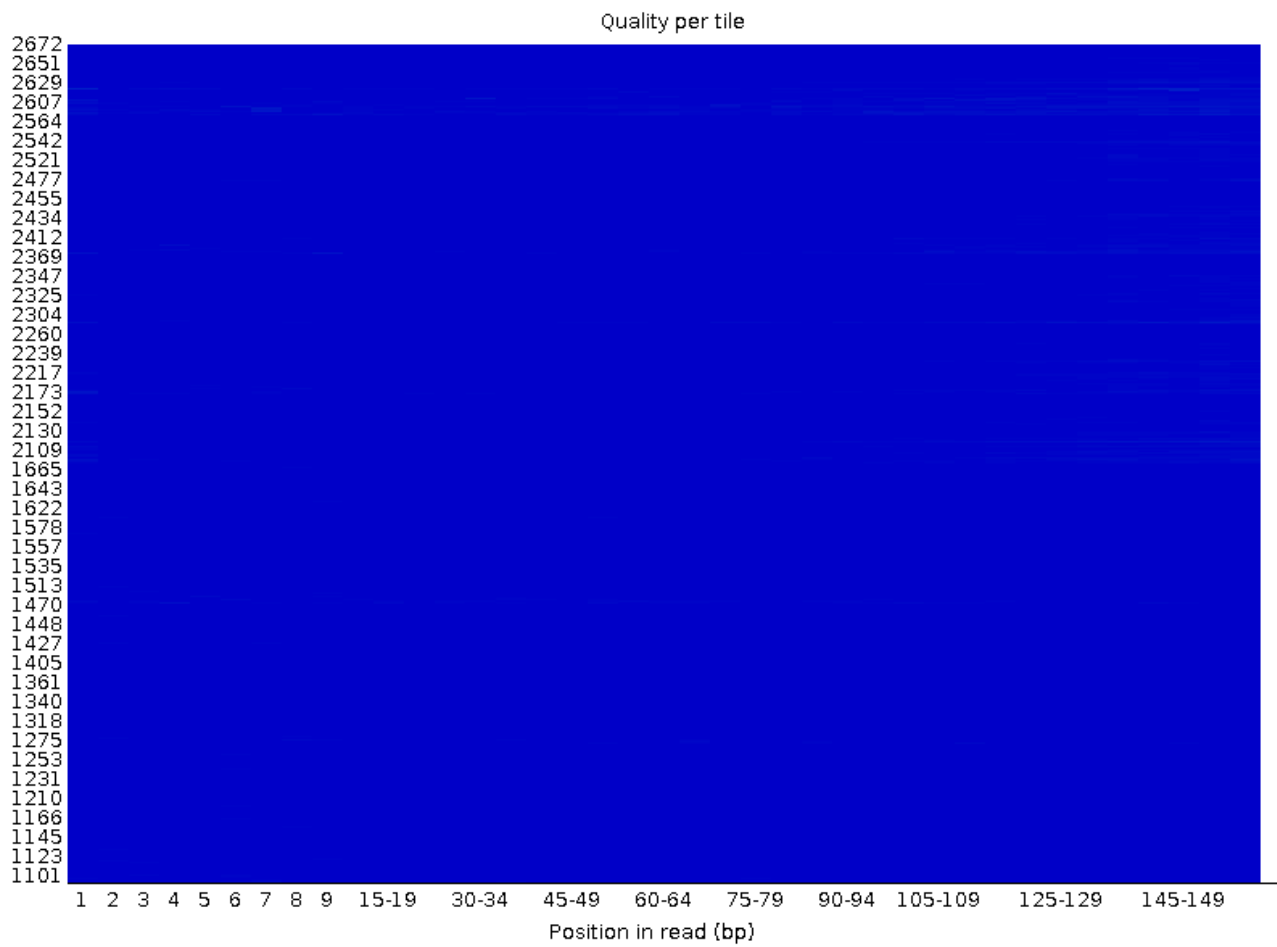


Per base sequence quality



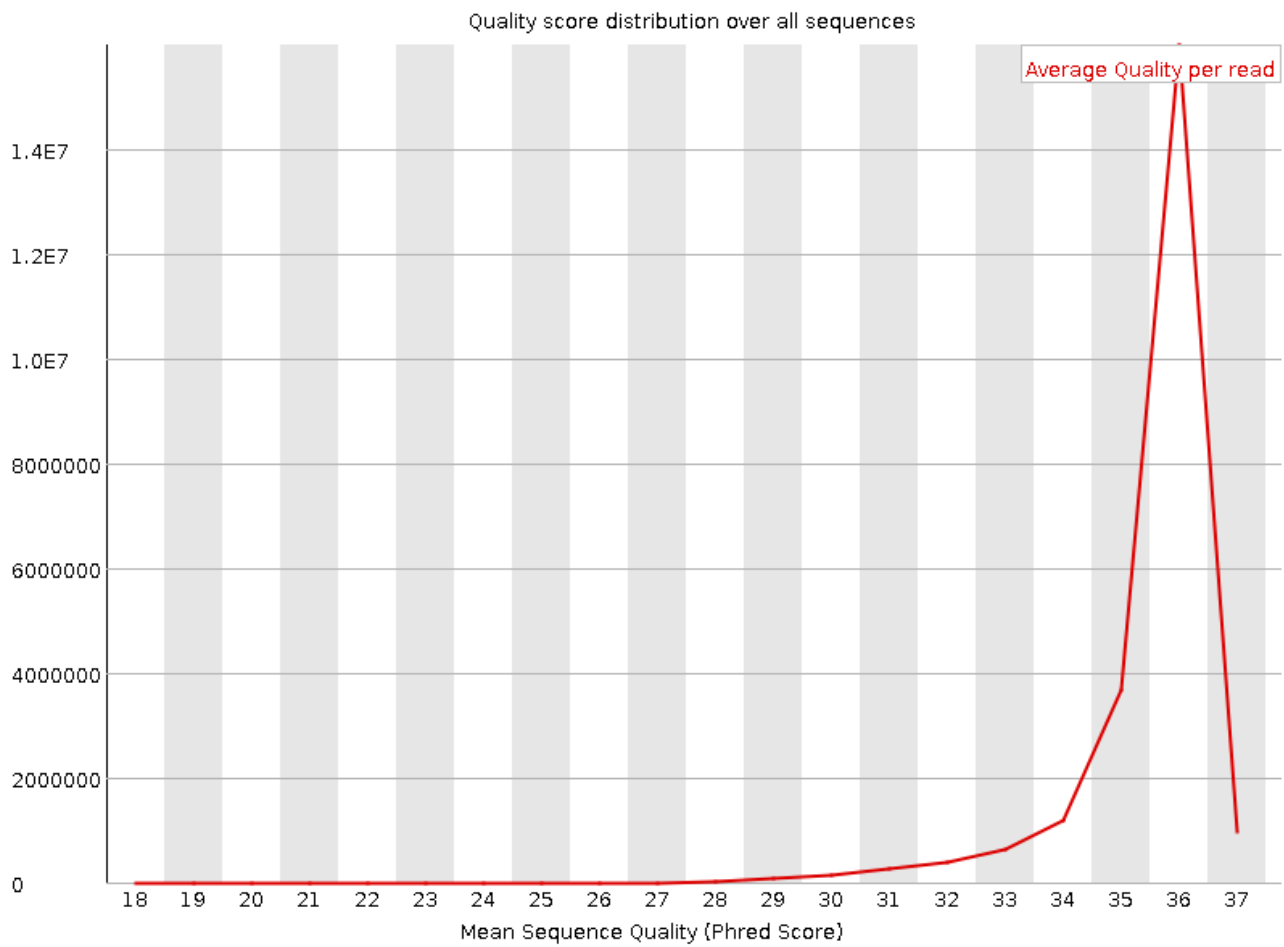


Per tile sequence quality



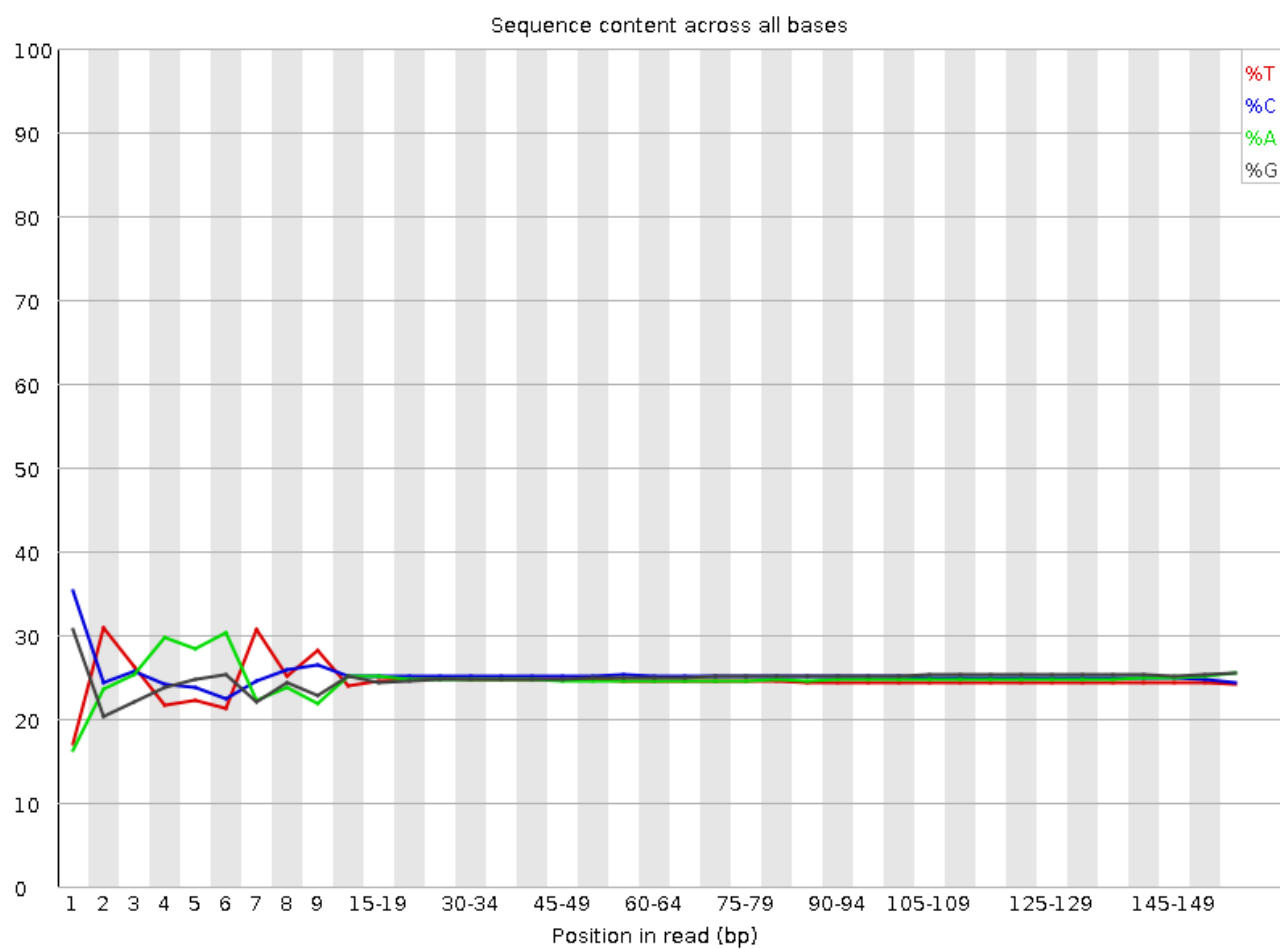


Per sequence quality scores



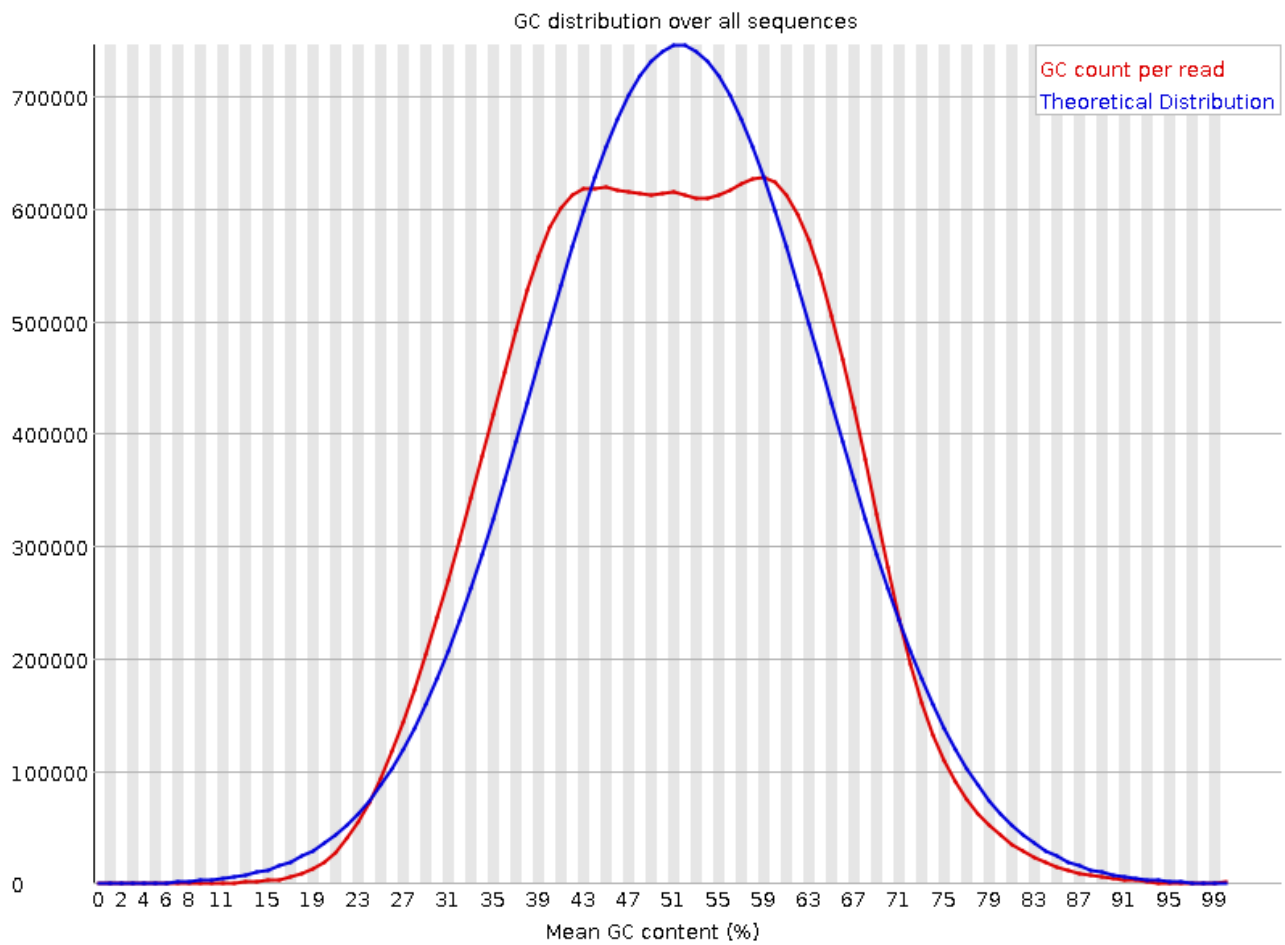


Per base sequence content

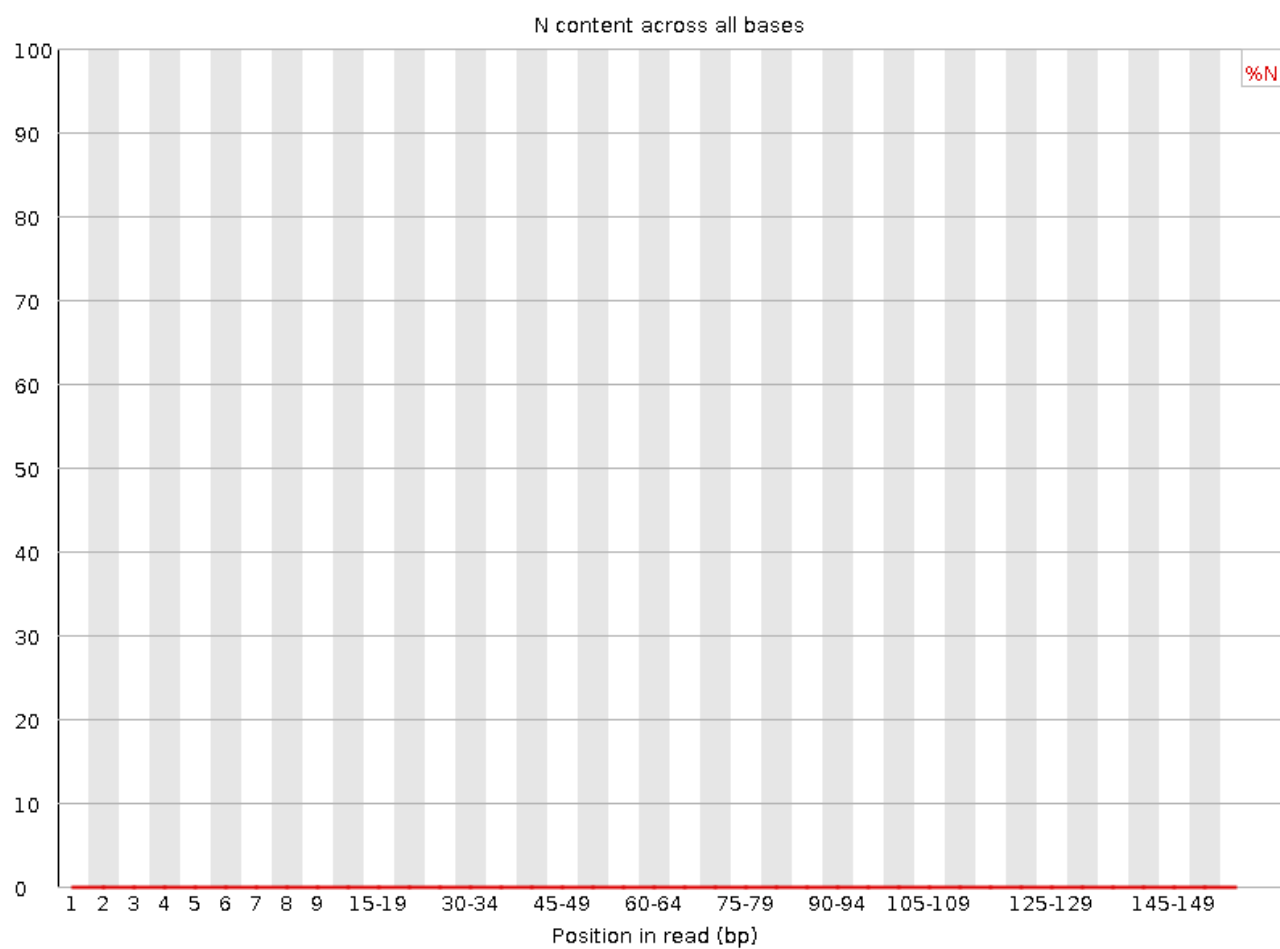




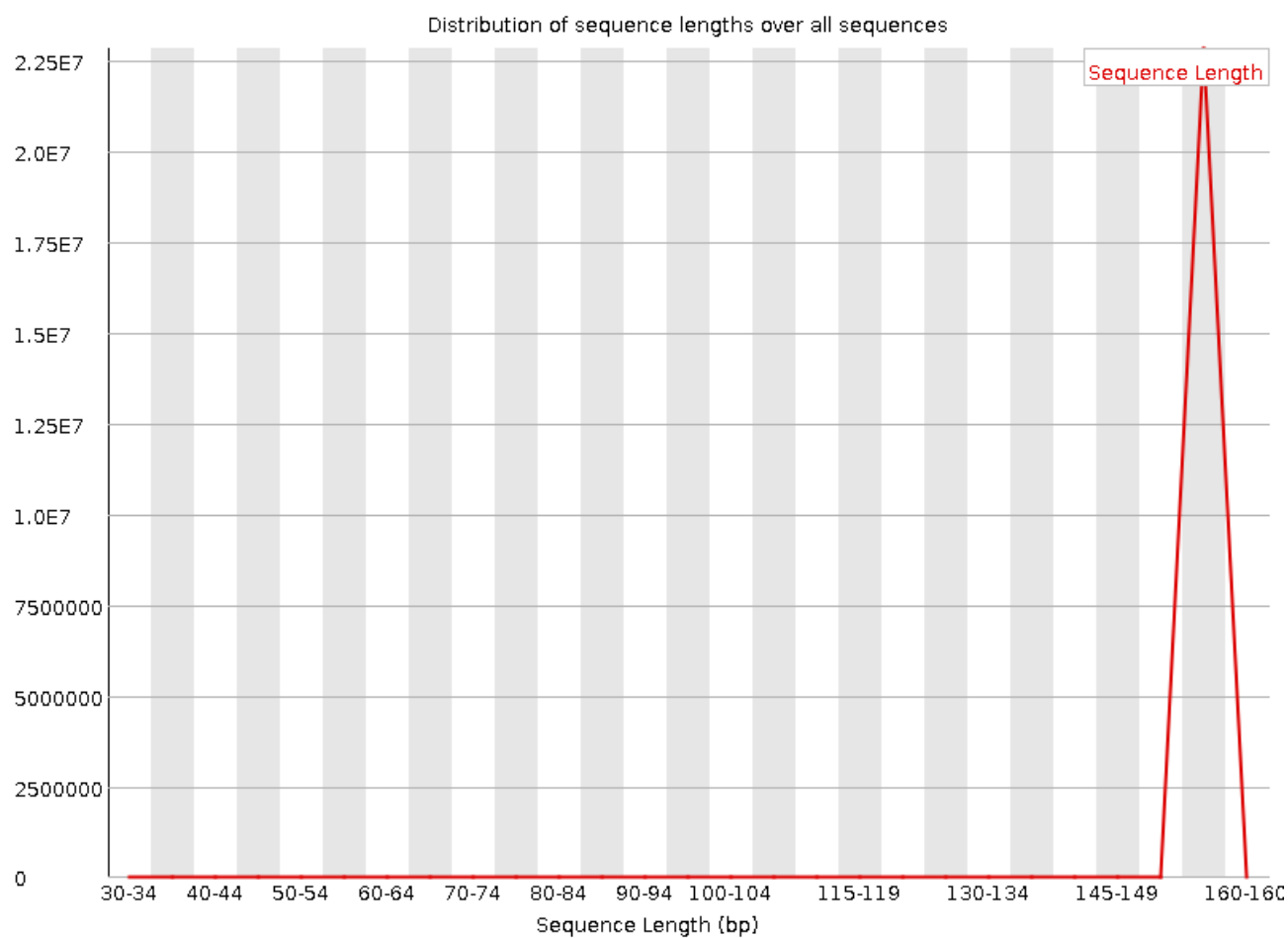
Per sequence GC content



✔ Per base N content

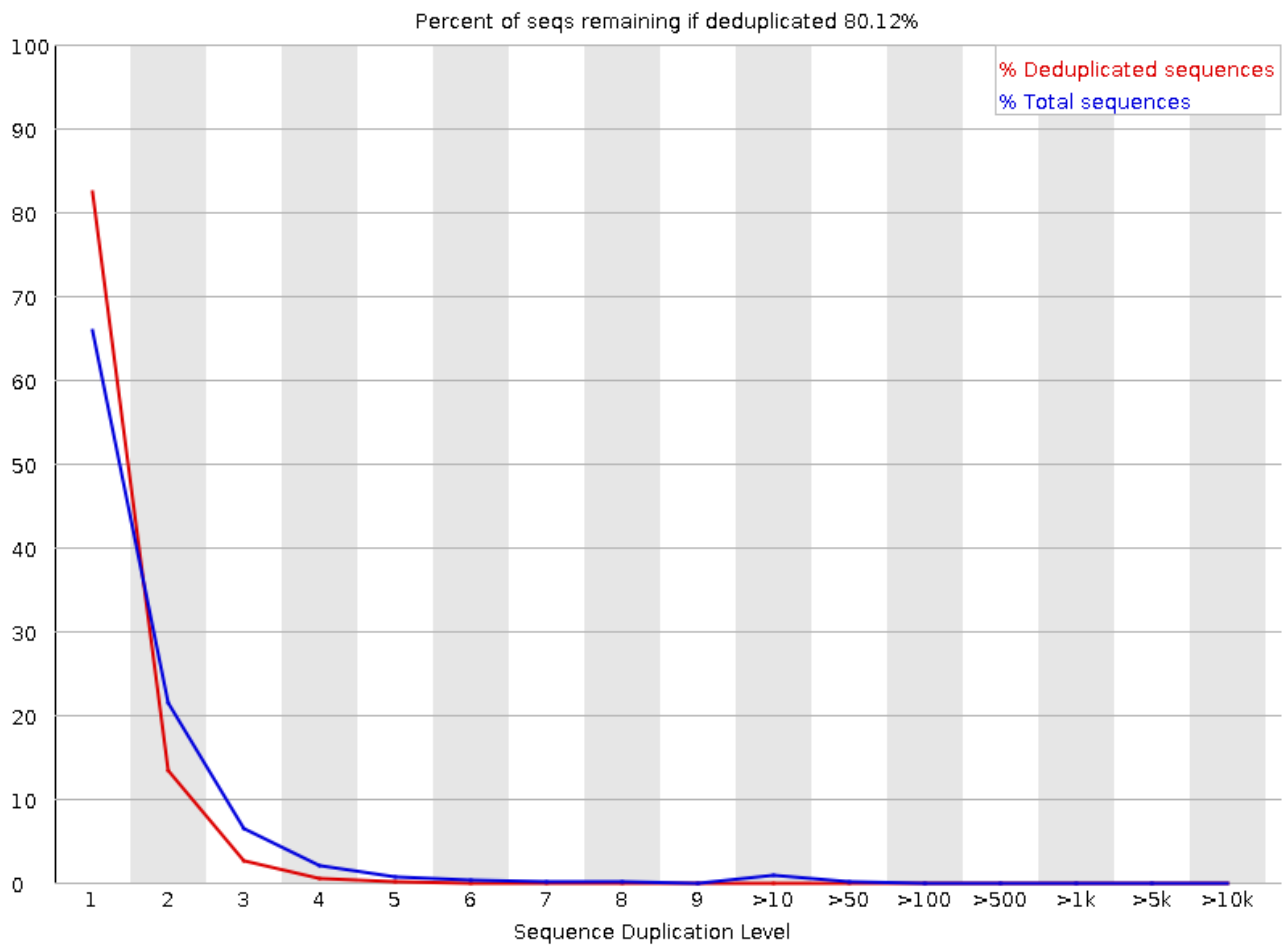


! Sequence Length Distribution





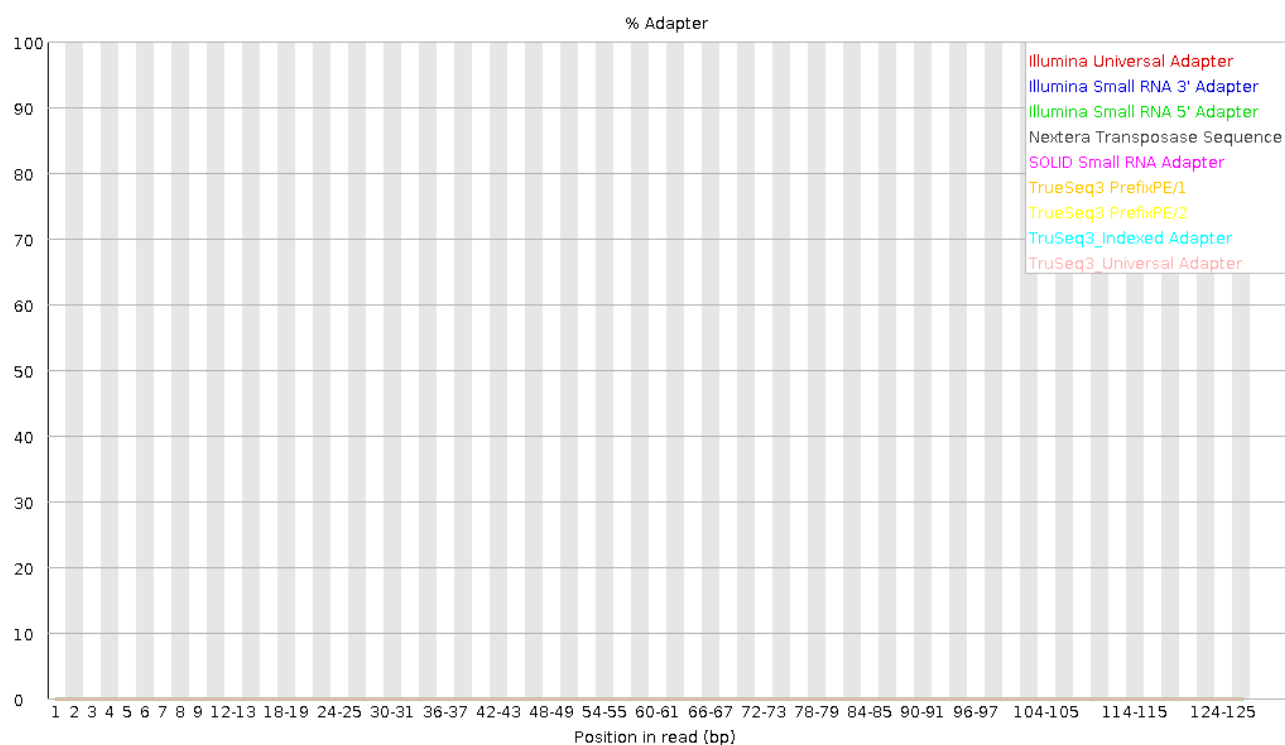
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content



Produced by [FastQC](#) (version 0.11.9)