

FastQC Report

Summary

Mon 24 Apr 2023
gc148-B_Raw_Reads_R1.fastq.gz

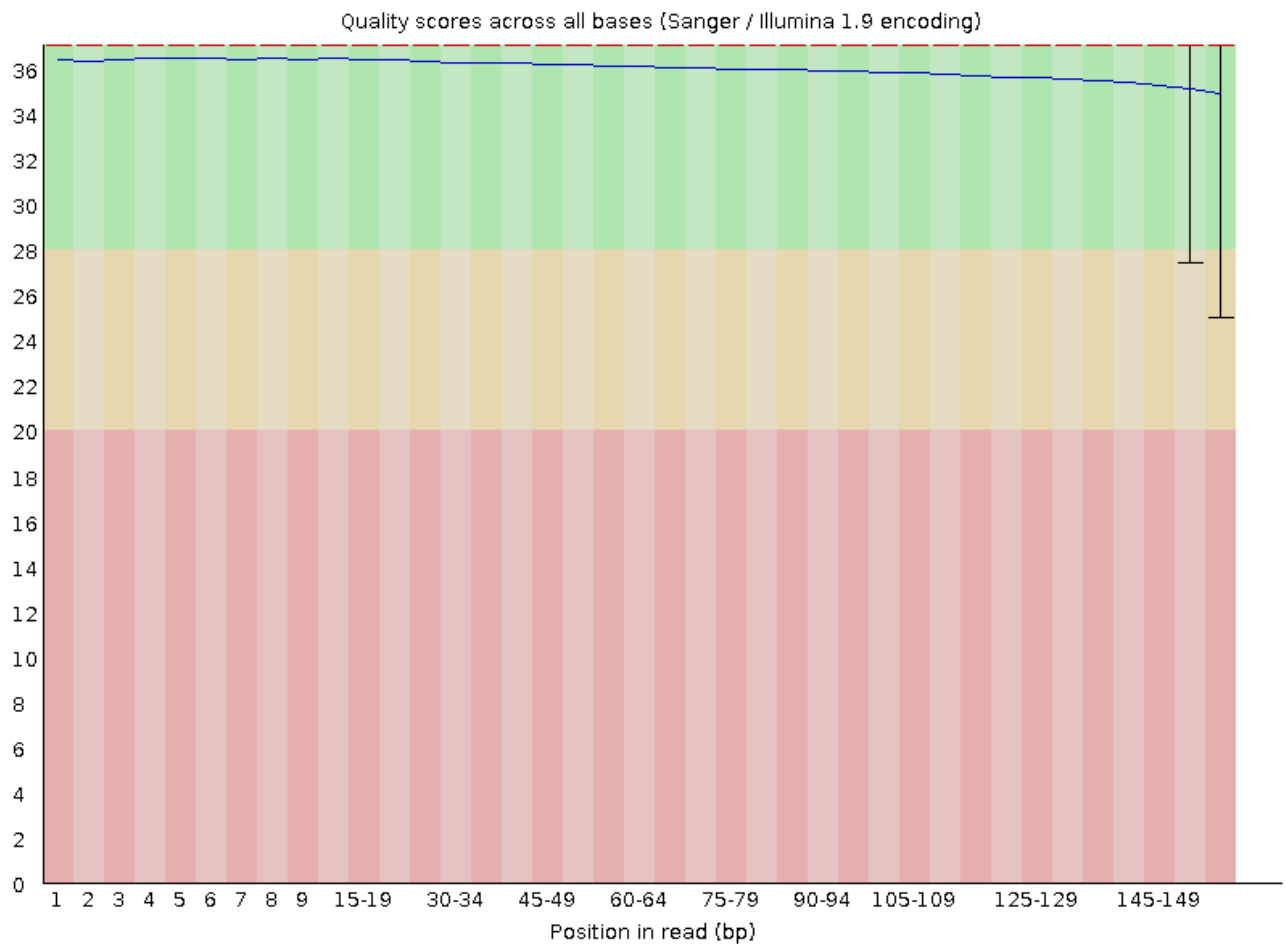
- ✓ [Basic Statistics](#)
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- ✓ [Per base sequence content](#)
- ! [Per sequence GC content](#)
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✓ Basic Statistics

Measure	Value
Filename	gc148-B_Raw_Reads_R1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	30406085
Sequences flagged as poor quality	0
Sequence length	159
%GC	50

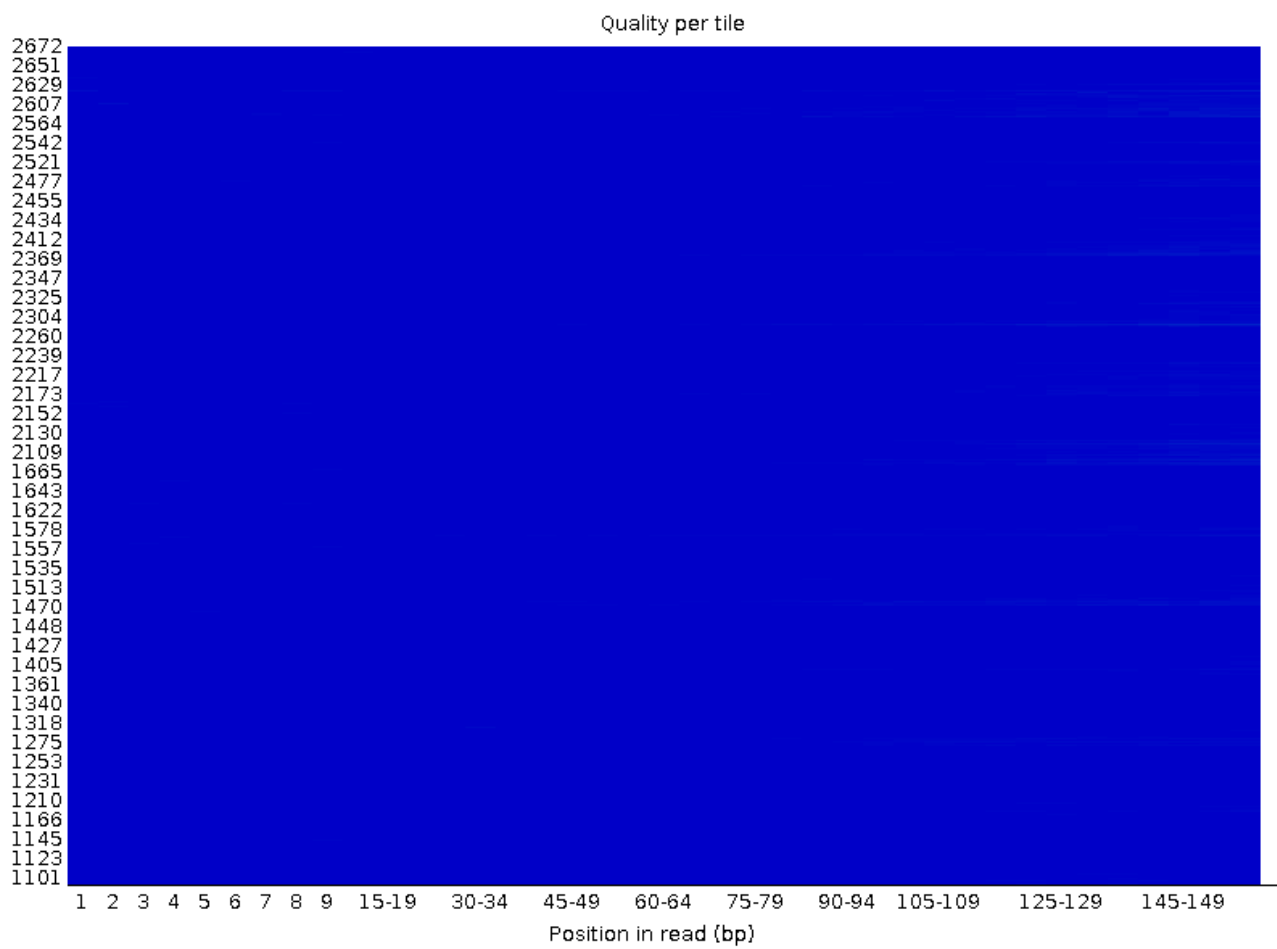


Per base sequence quality



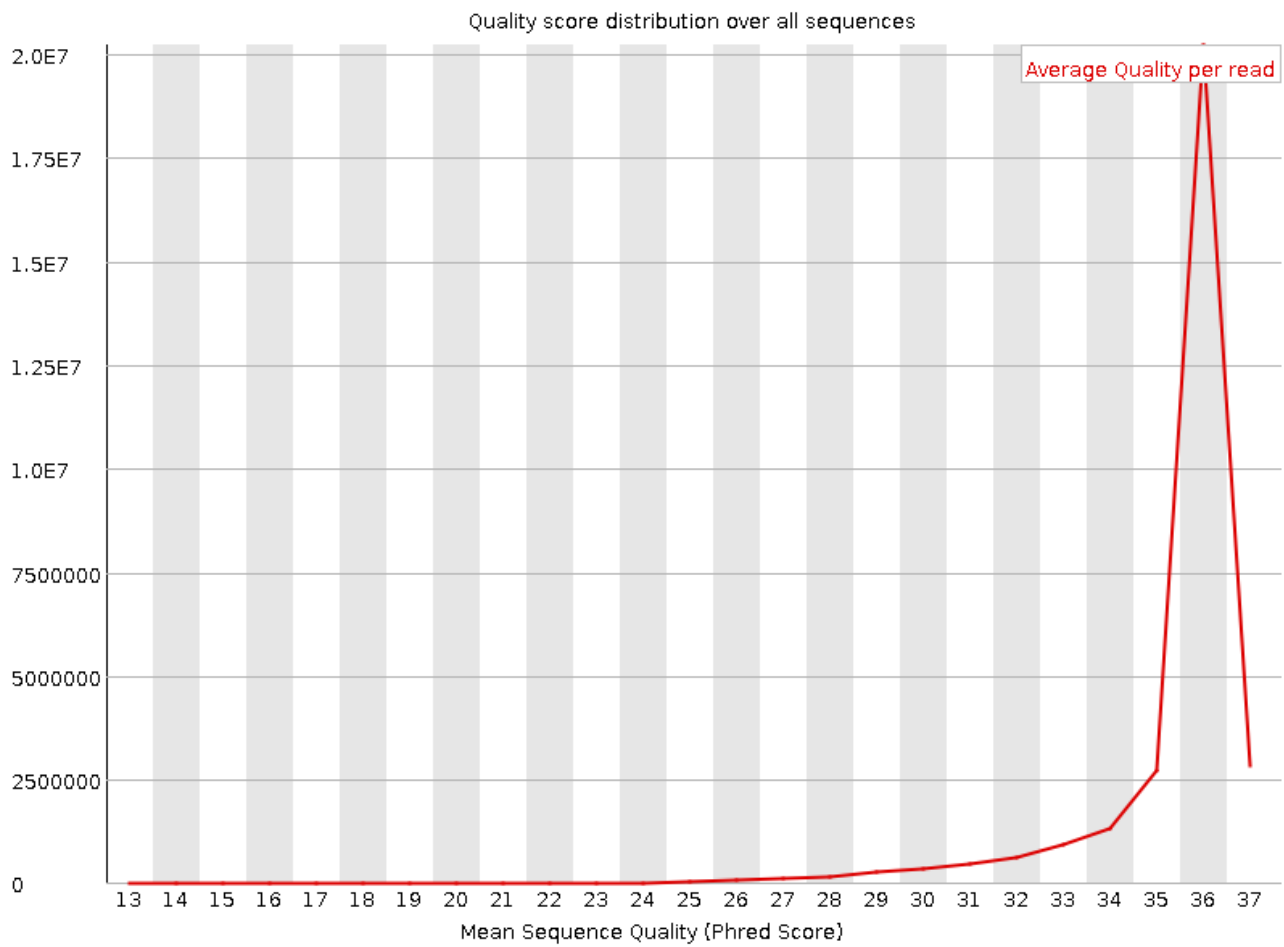


Per tile sequence quality



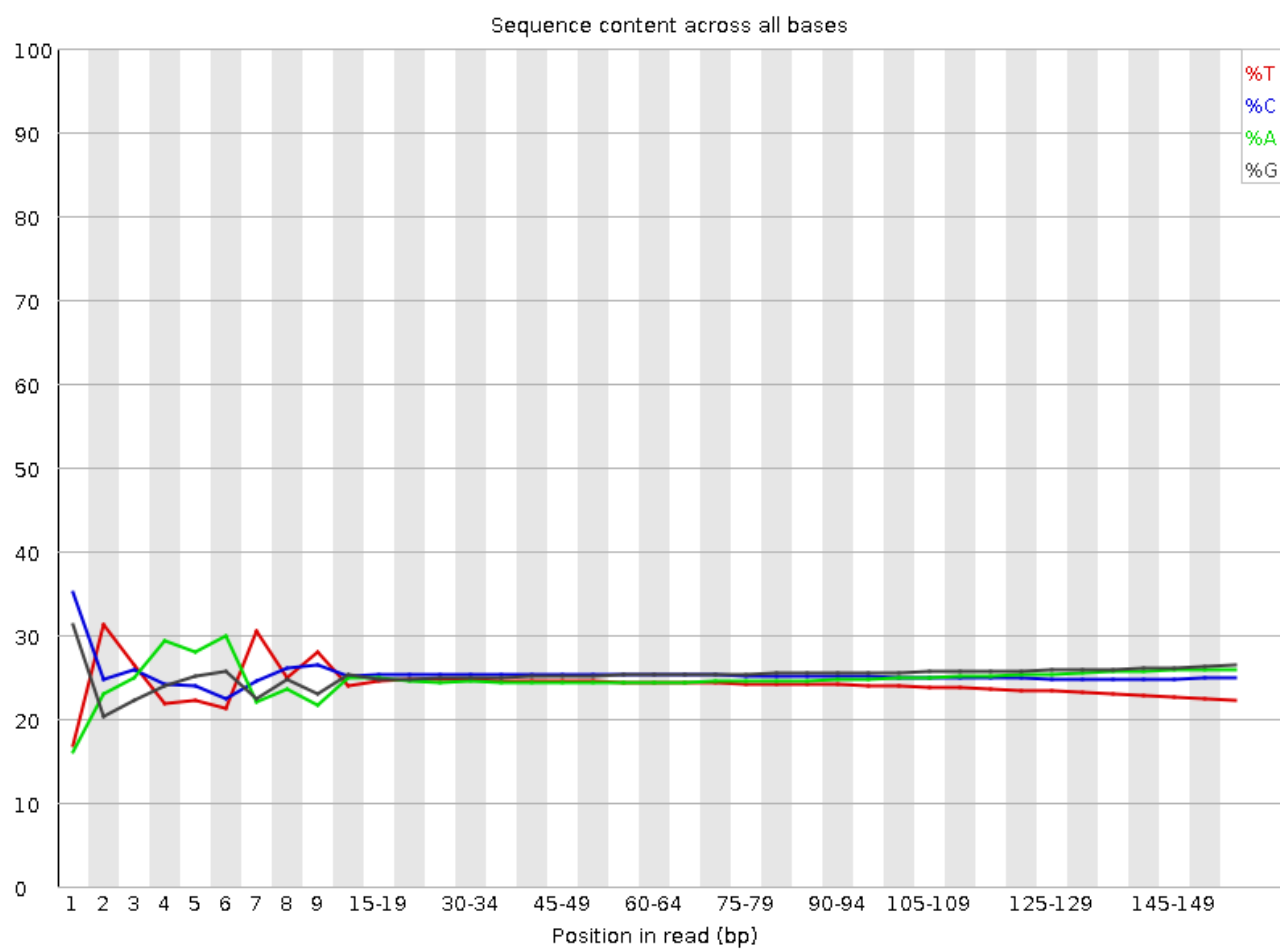


Per sequence quality scores



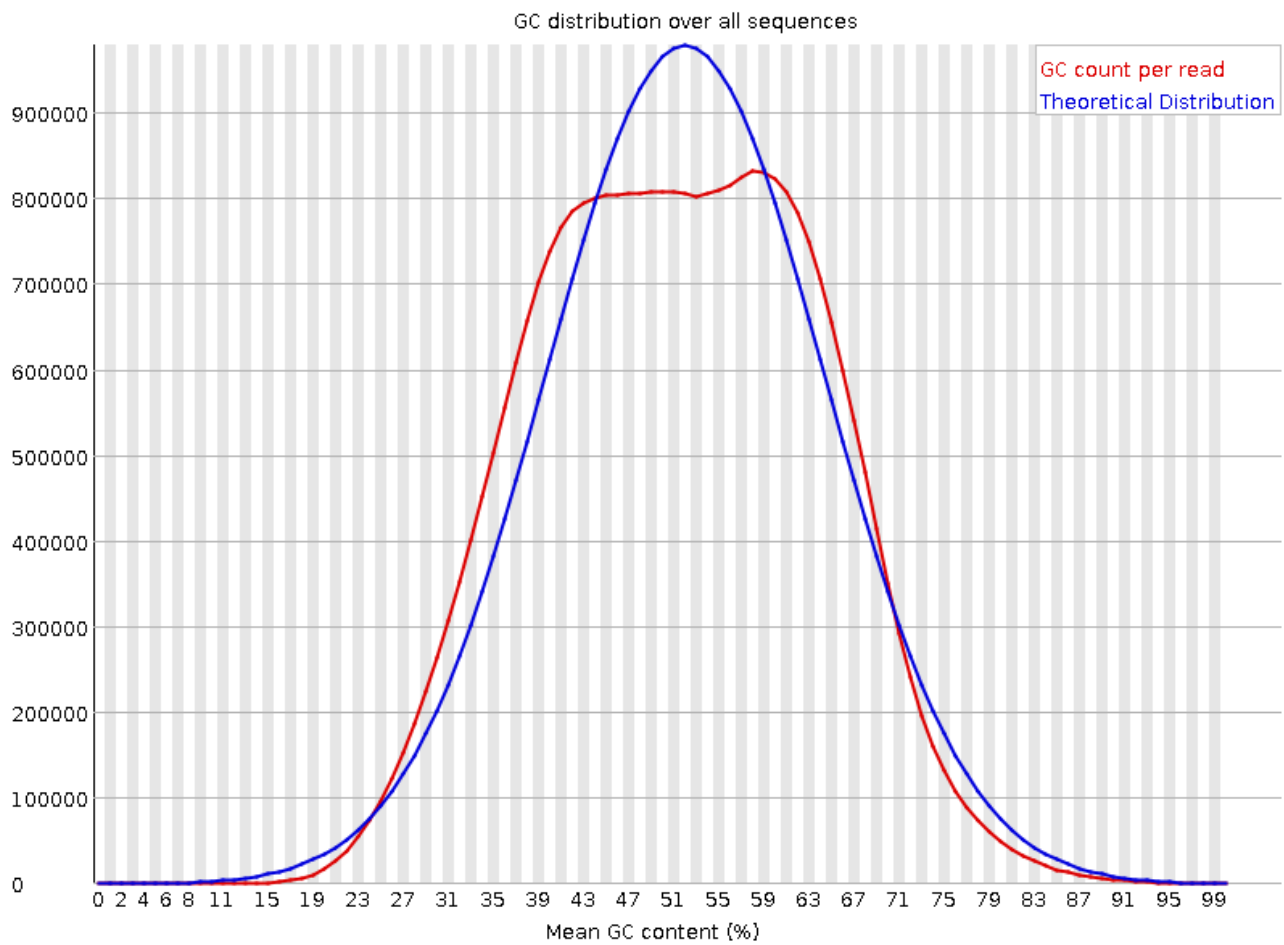


Per base sequence content

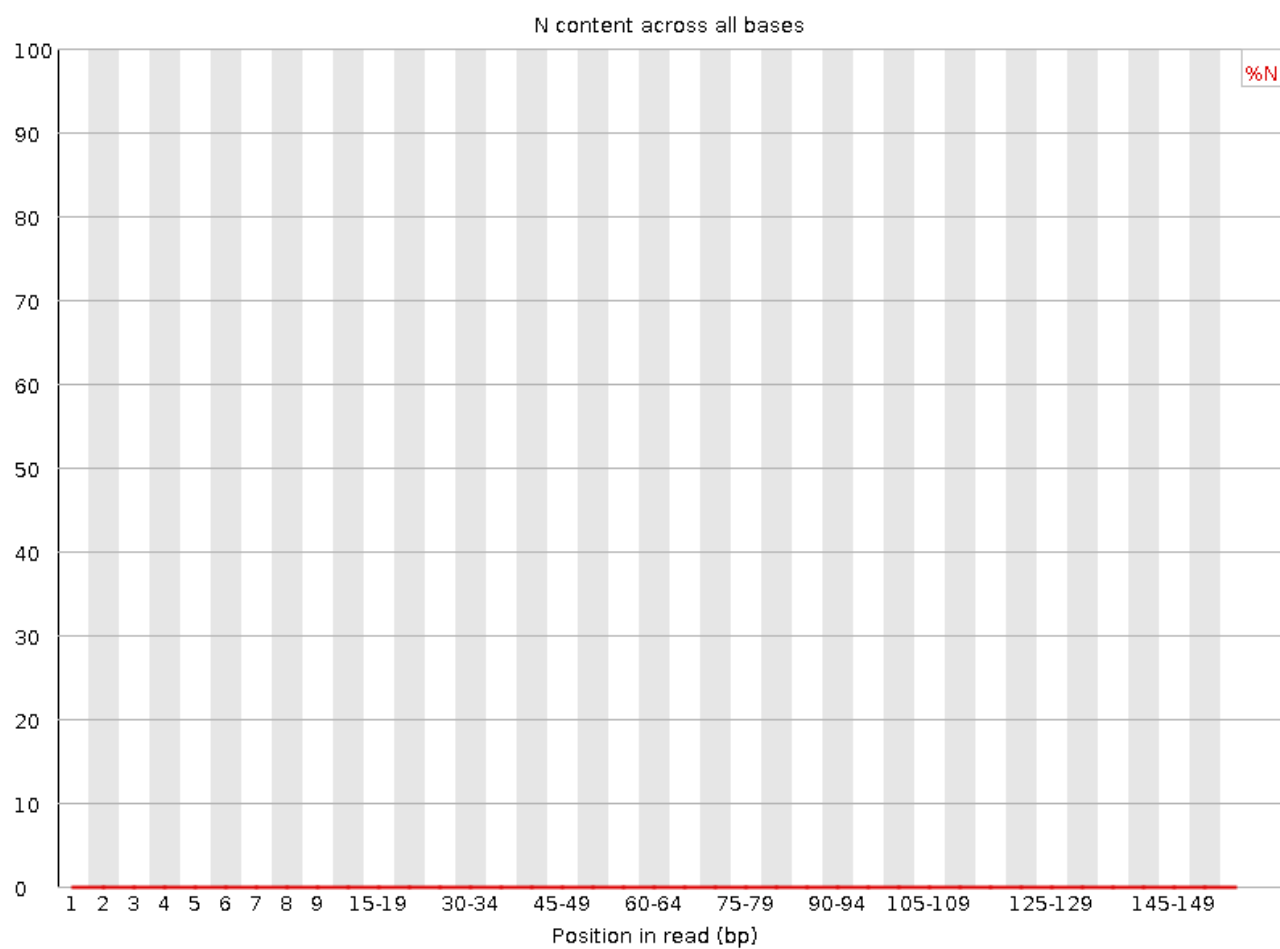




Per sequence GC content

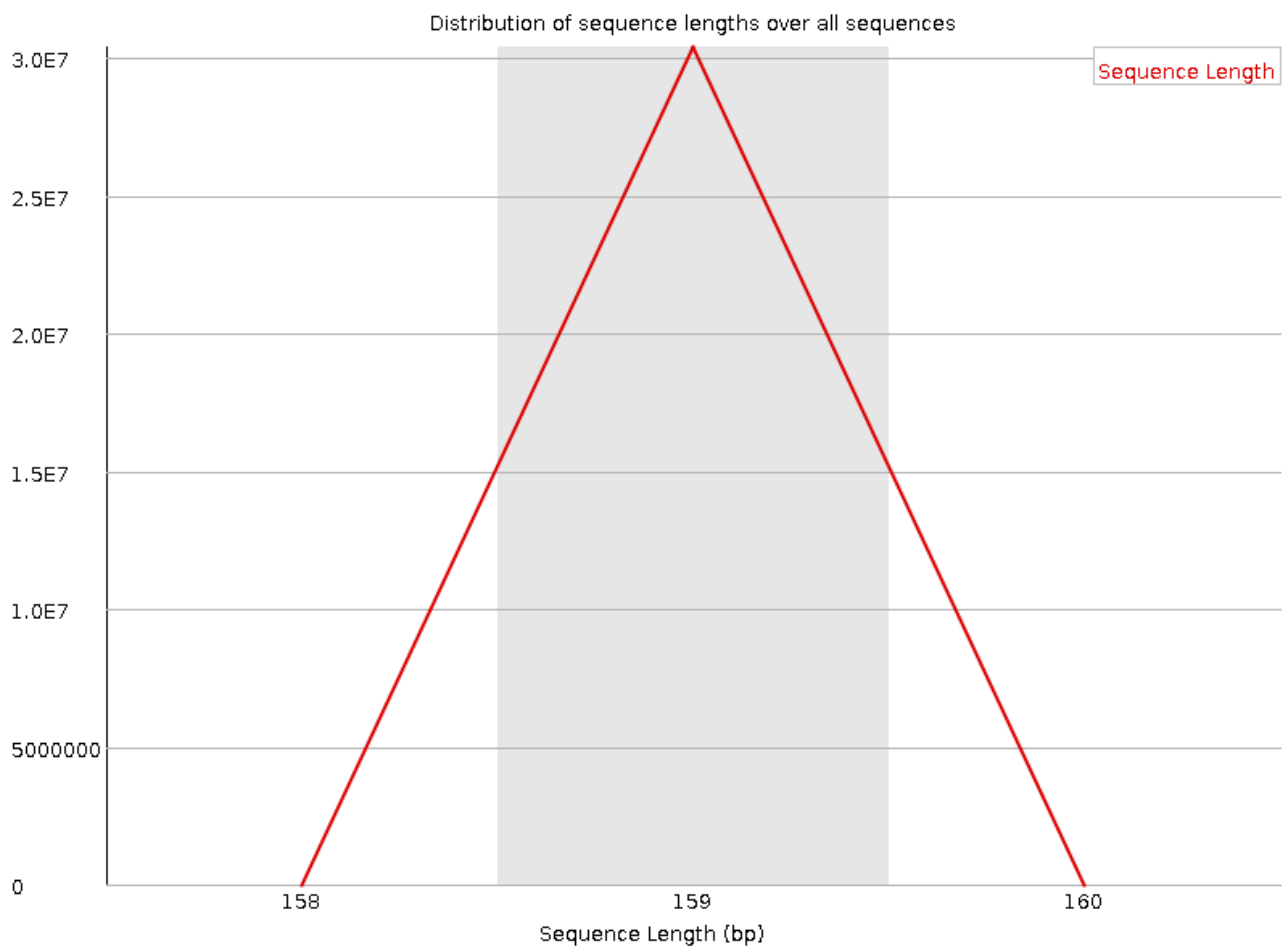


✔ Per base N content



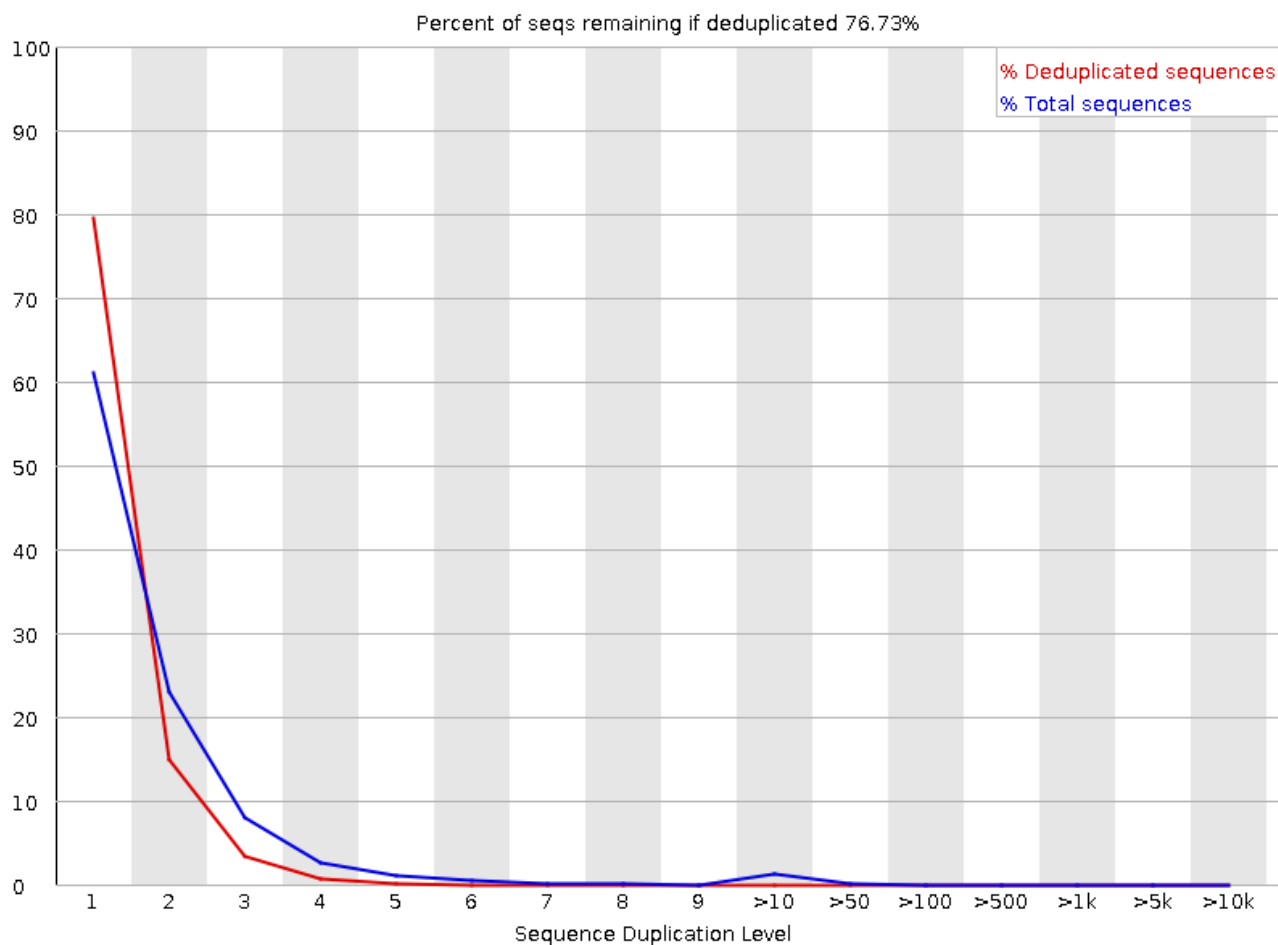


Sequence Length Distribution





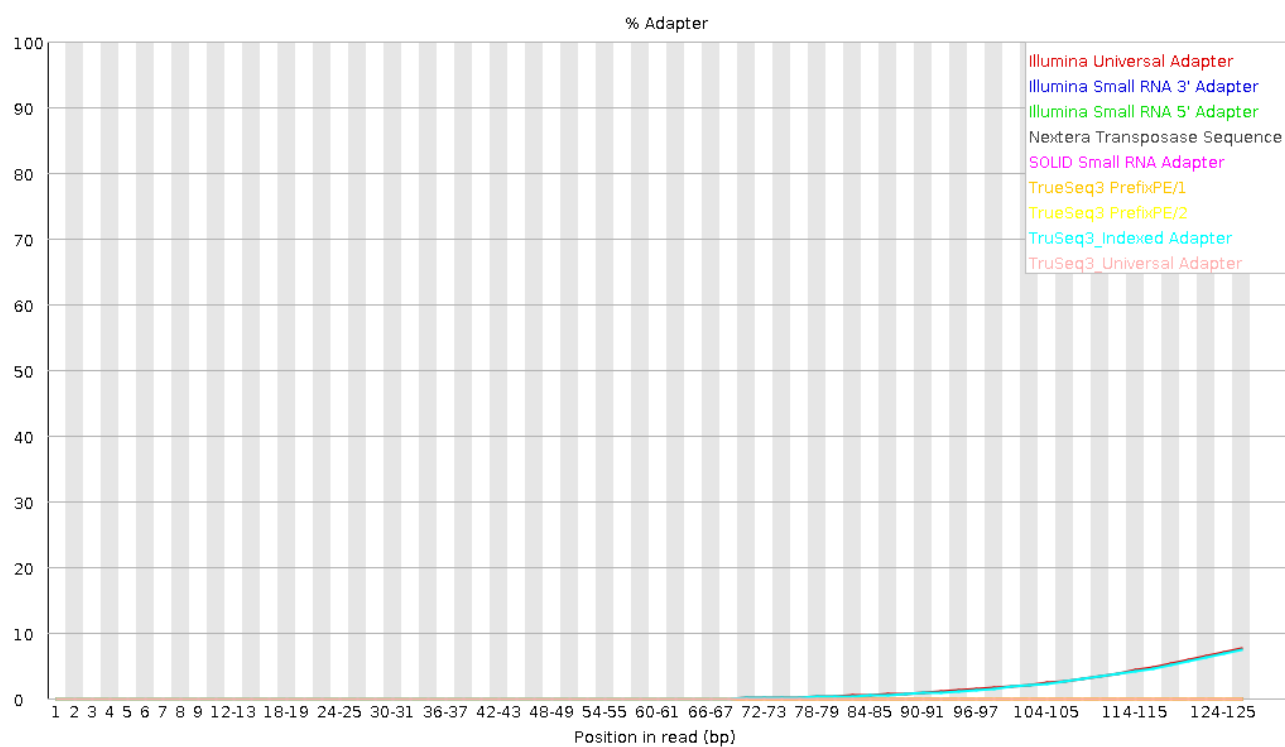
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

! Adapter Content



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