FastQC Report

Tue 13 May 2025
SRR33285751_1_paired.fastq

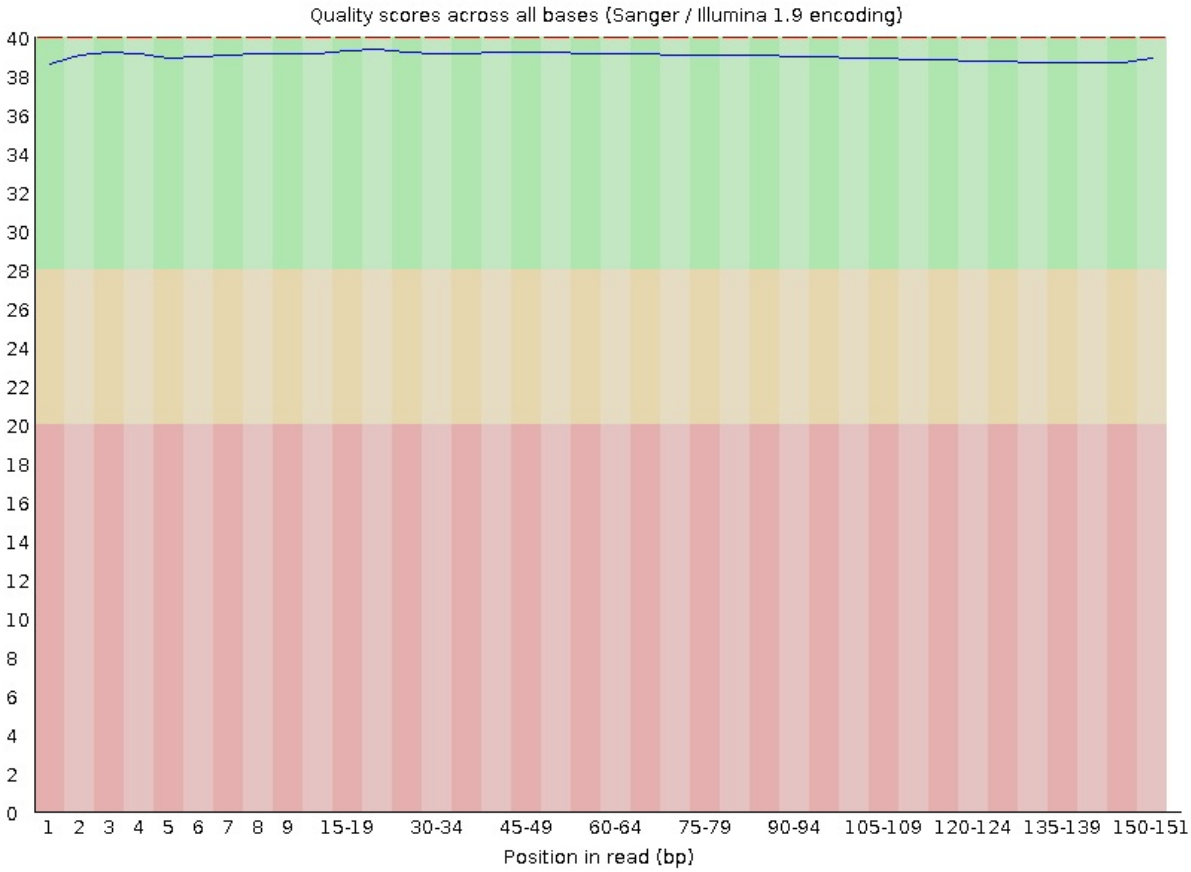
Summary

- Basic Statistics
- 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
- Adapter Content

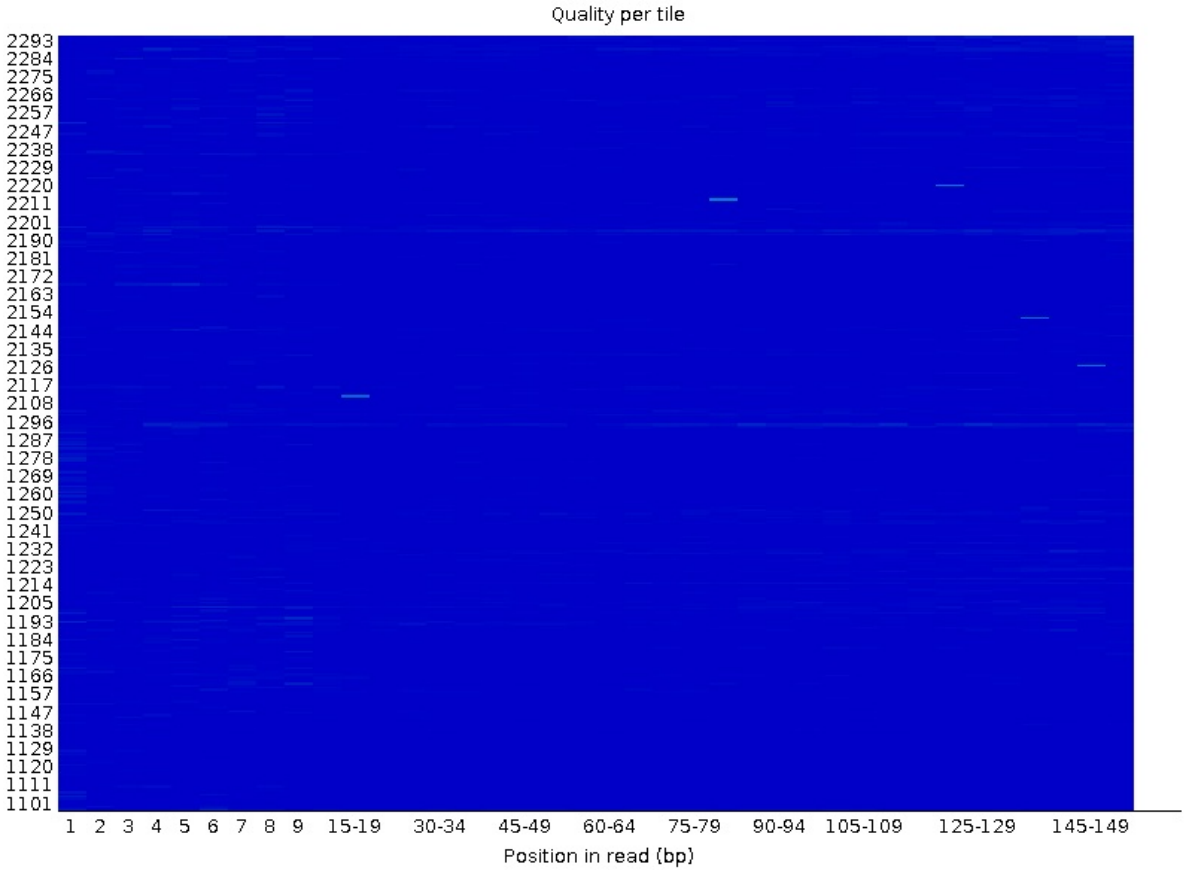
Basic Statistics

Measure	Value
Filename	SRR33285751_1_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1929156
Total Bases	281.8 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	51

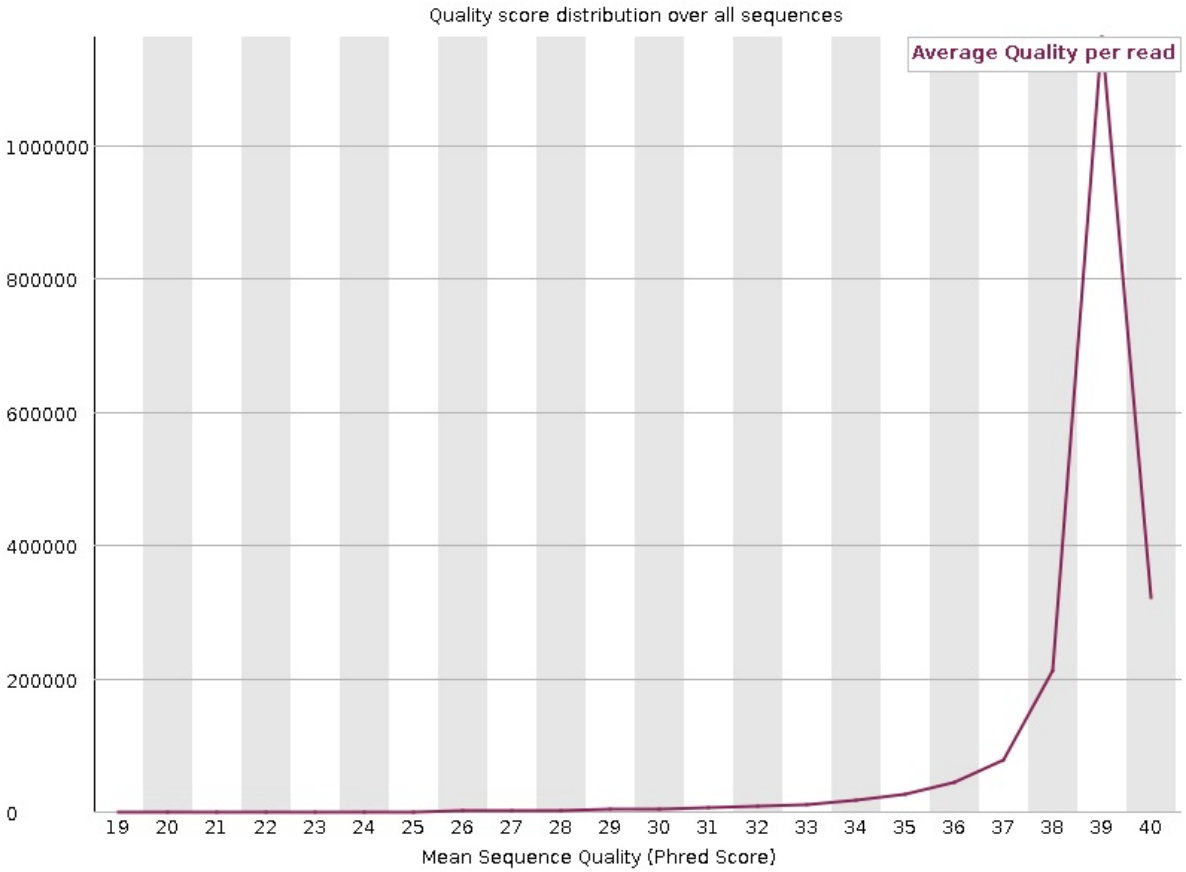
Per base sequence quality



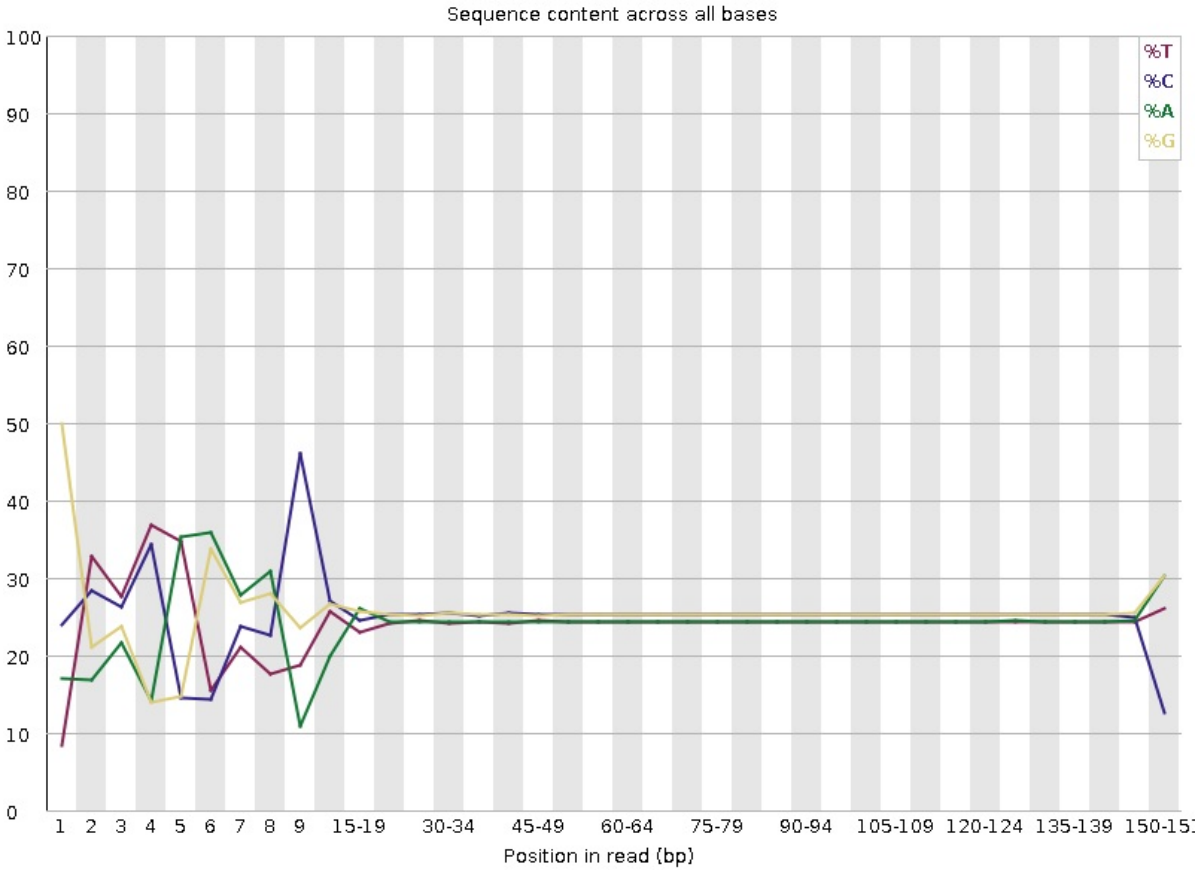
Per tile sequence quality



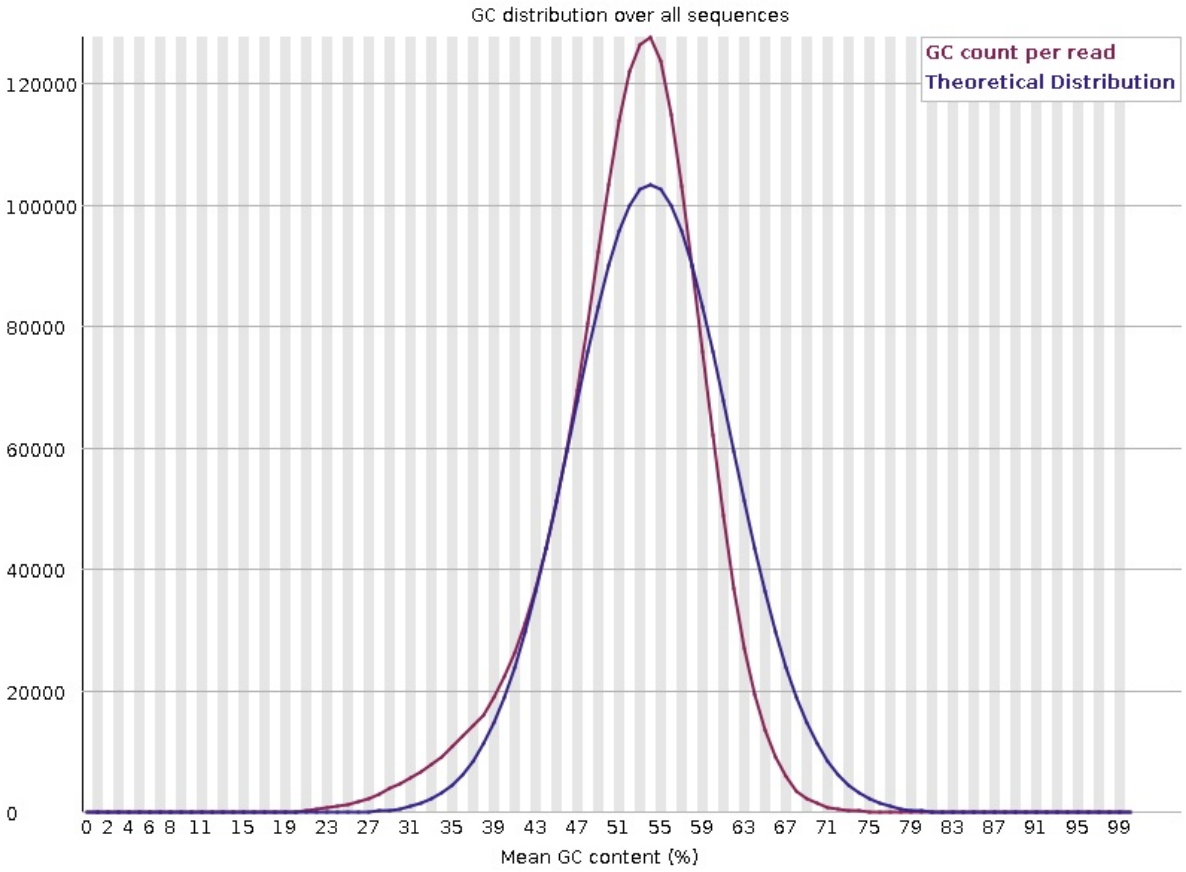
Per sequence quality scores



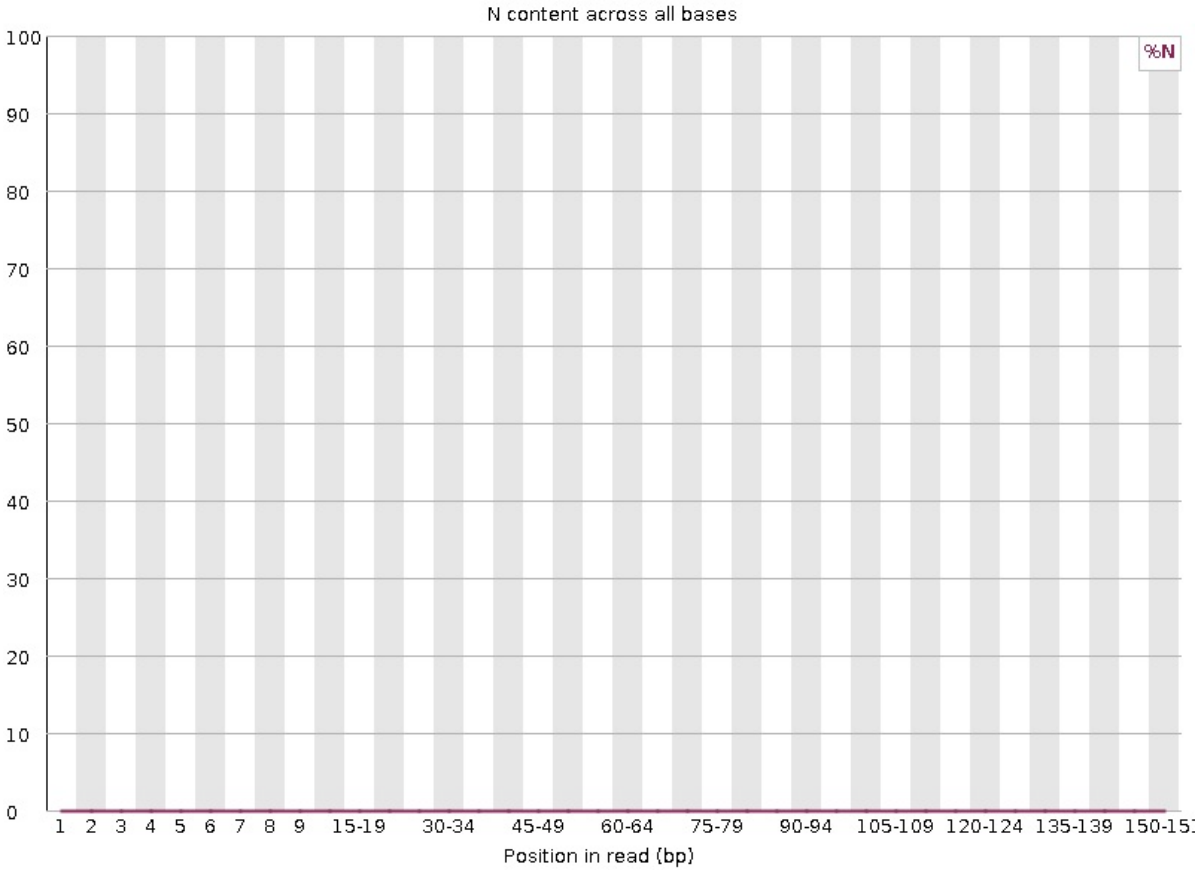
Per base sequence content



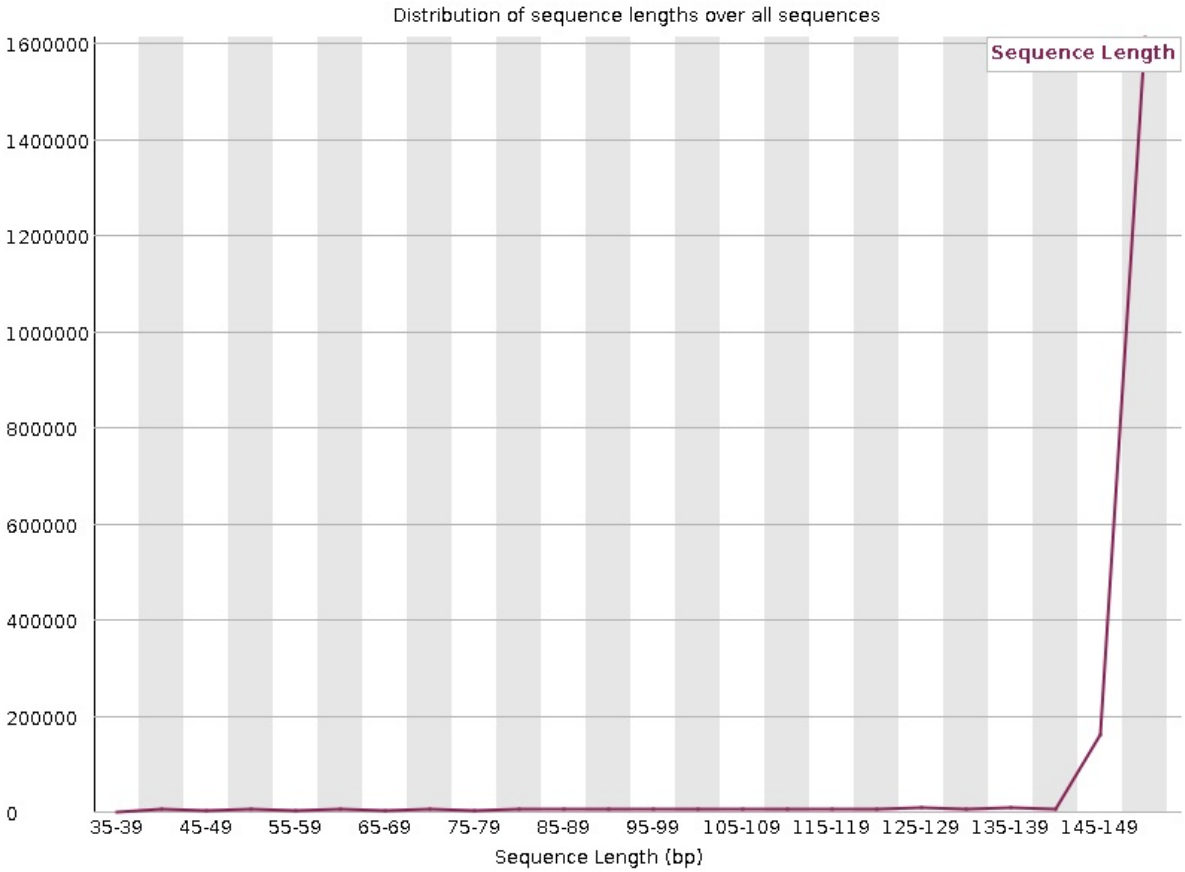
Per sequence GC content



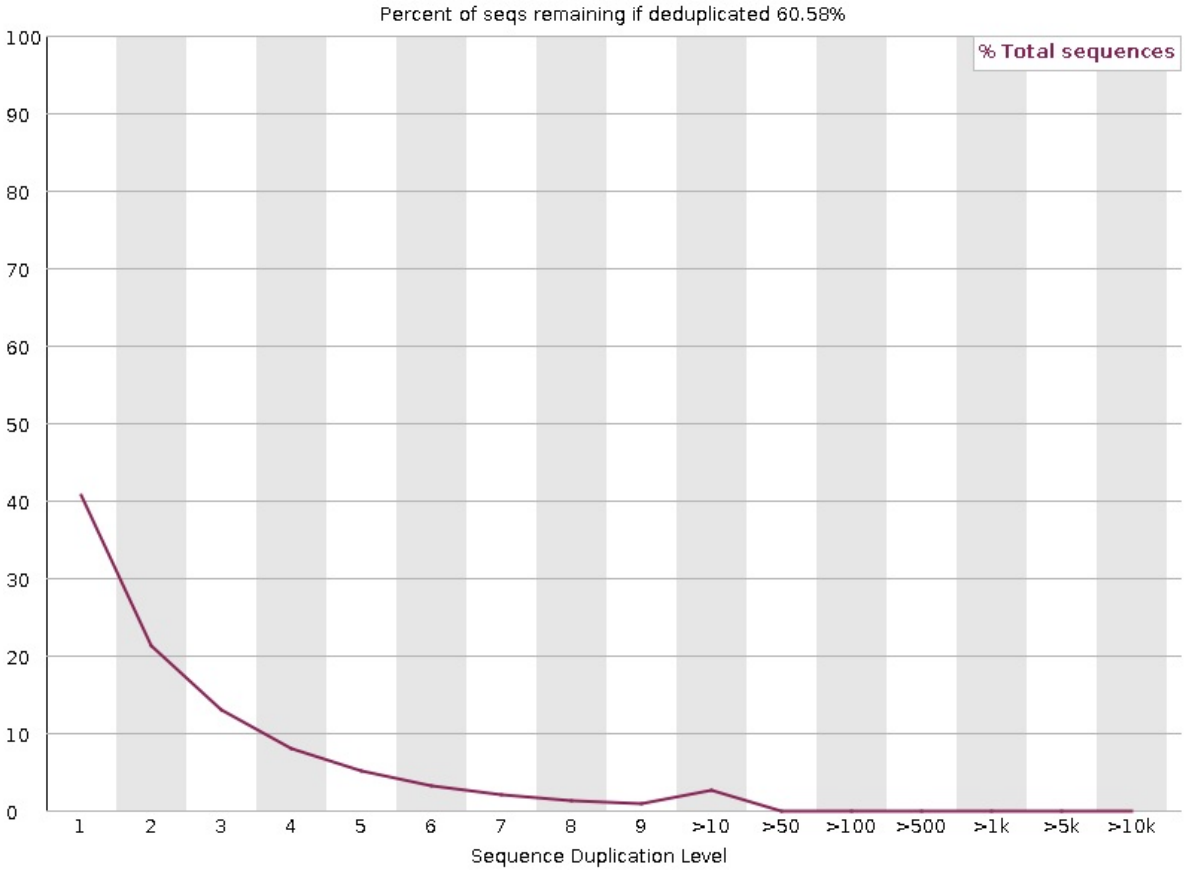
Per base N content



Sequence Length Distribution



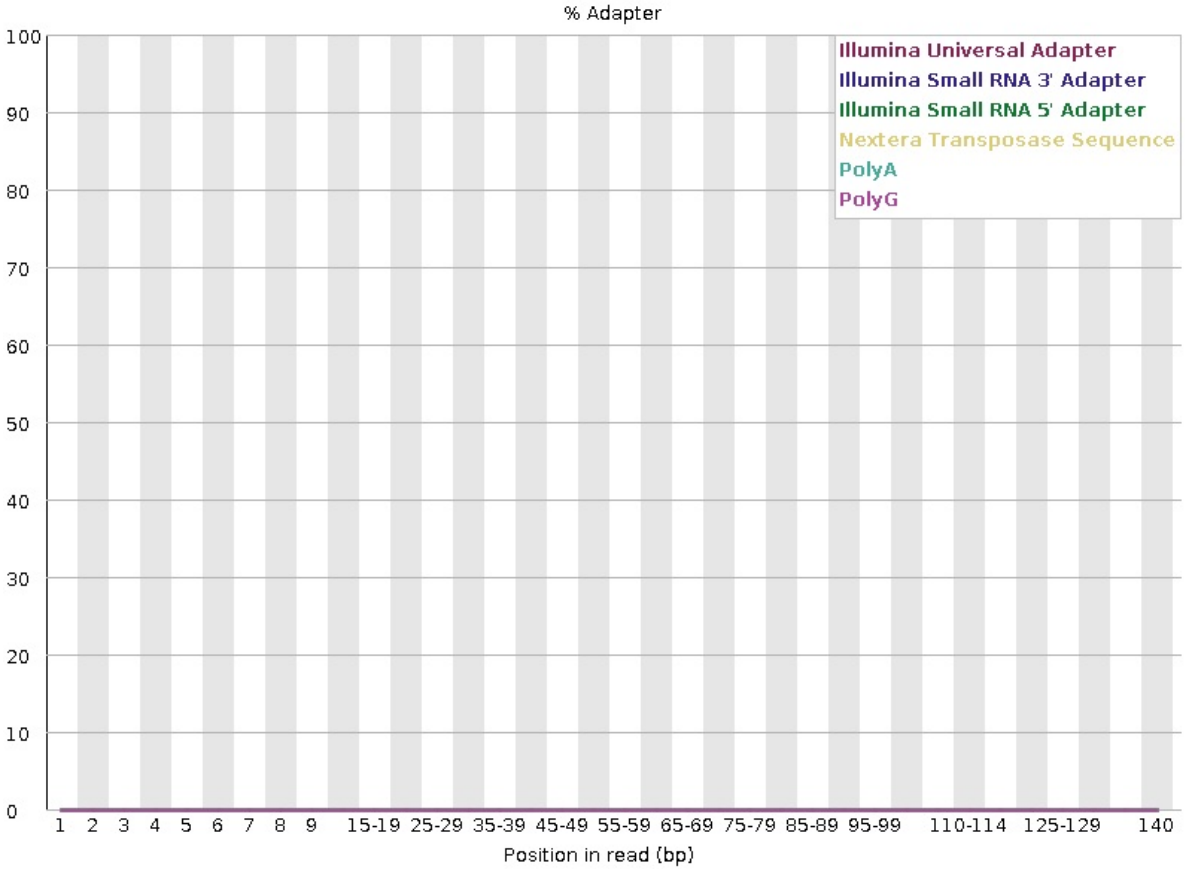
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.12.1)