












FastQC Report

Summary

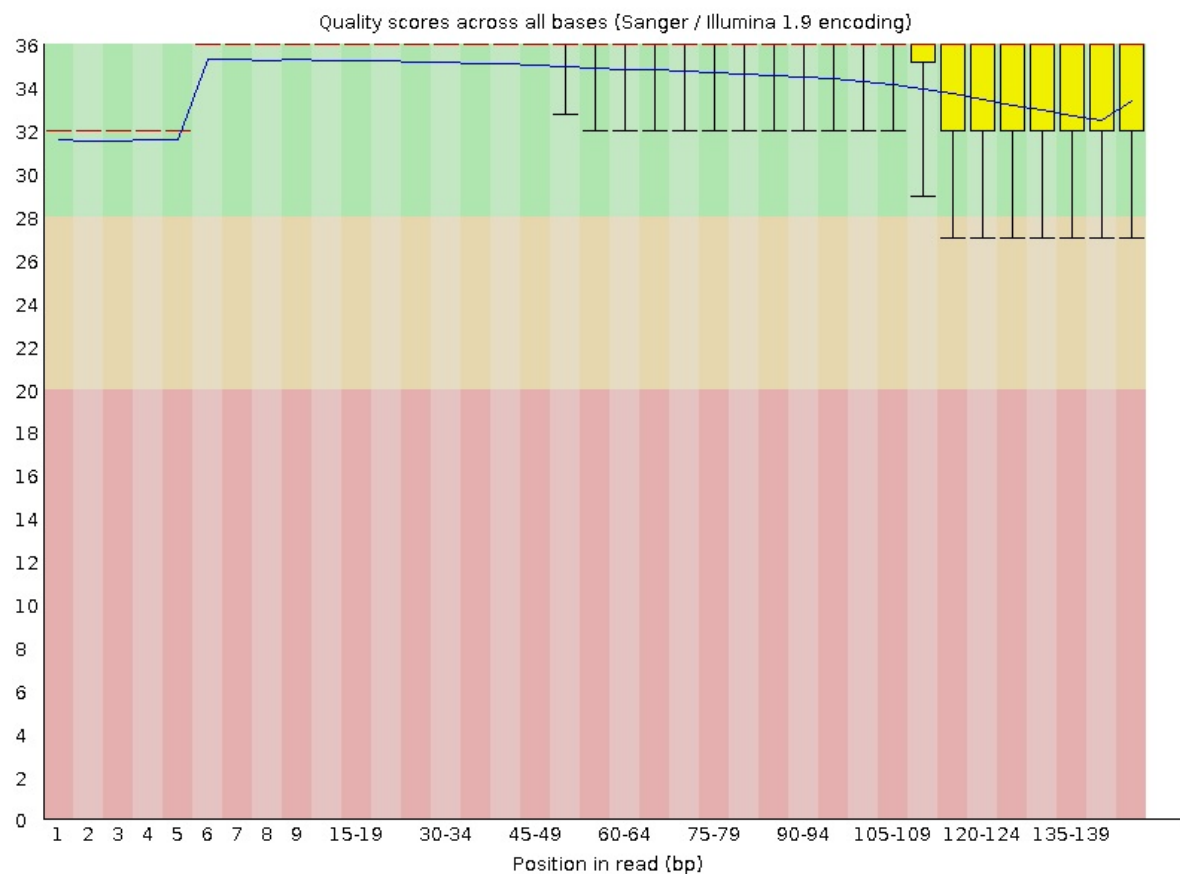
Wed 2 Apr 2025
SRR31001868_2_paired.fastq

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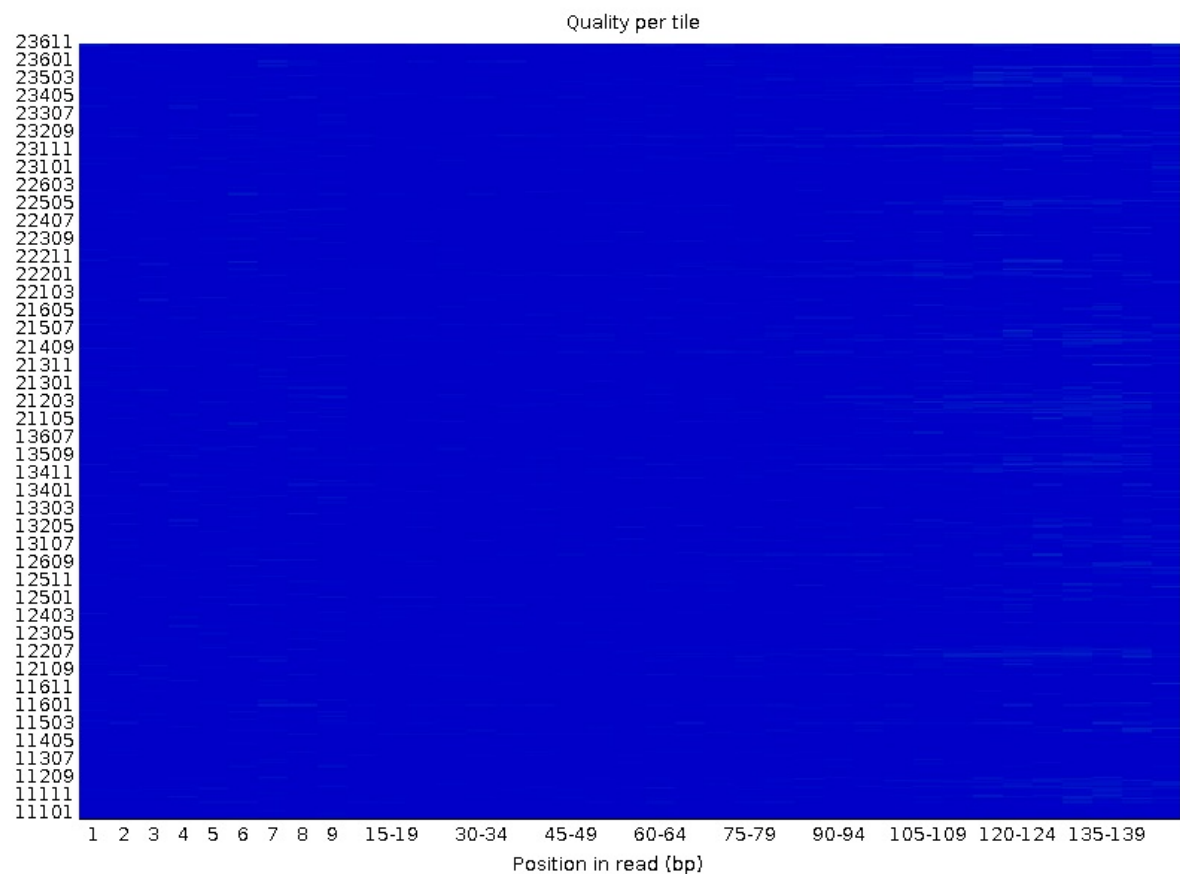
Basic Statistics

Measure	Value
Filename	SRR31001868_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1124937
Total Bases	135.4 Mbp
Sequences flagged as poor quality	0
Sequence length	36-145
%GC	33

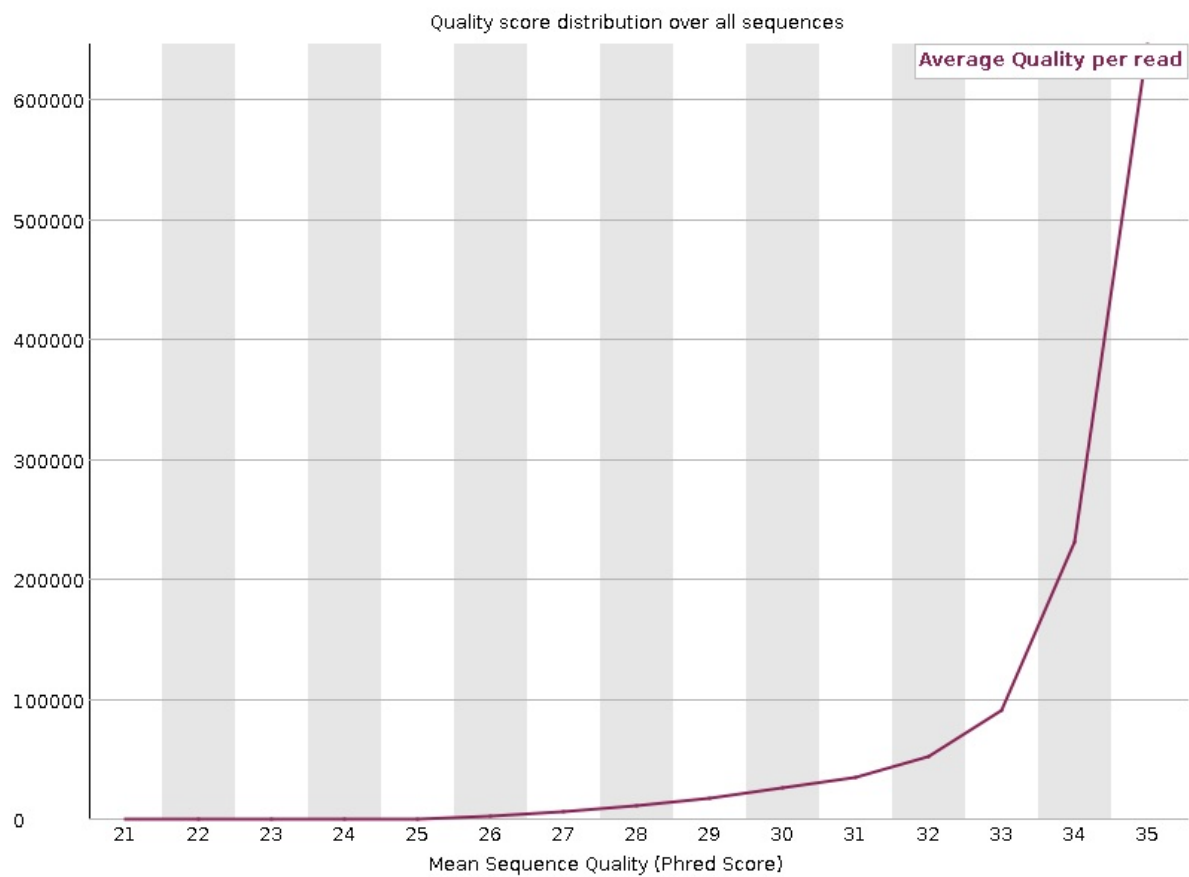
Per base sequence quality



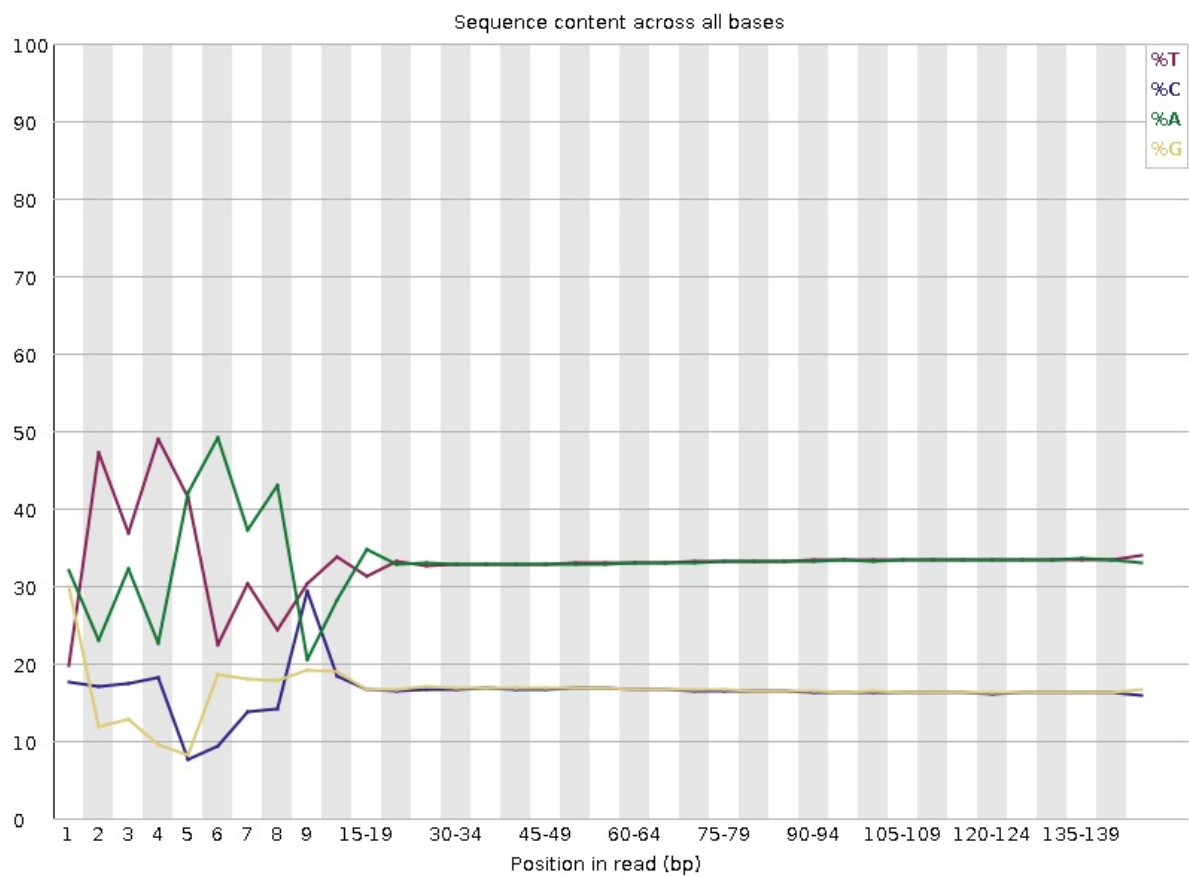
✓ Per tile sequence quality



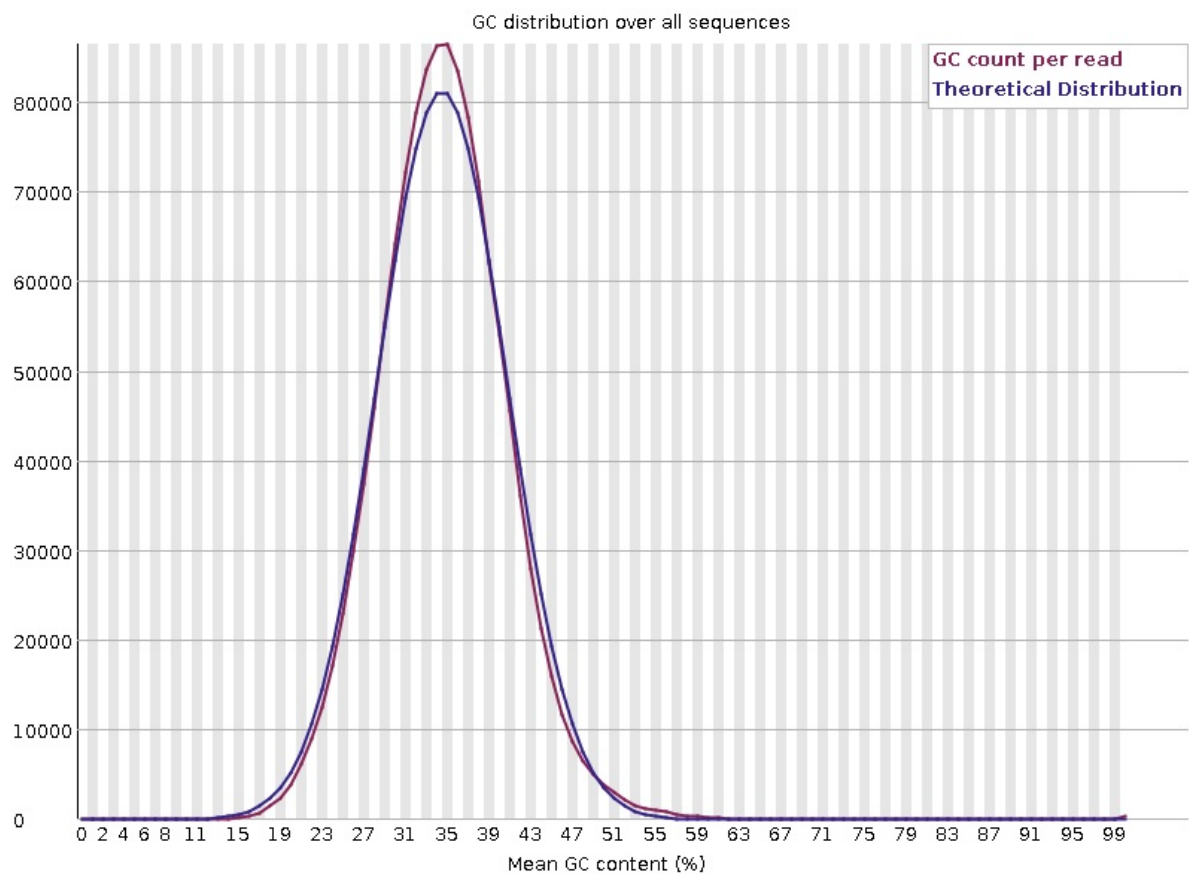
✓ Per sequence quality scores



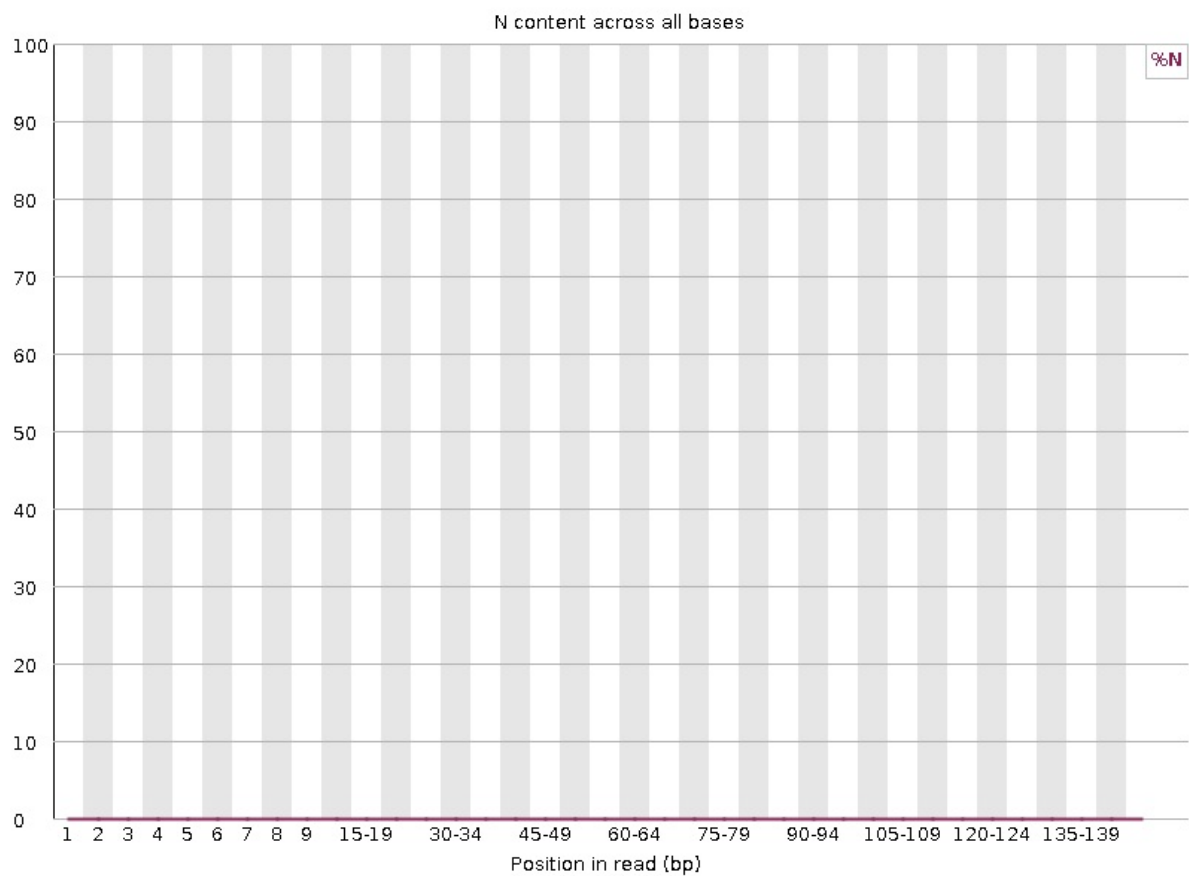
❌ Per base sequence content



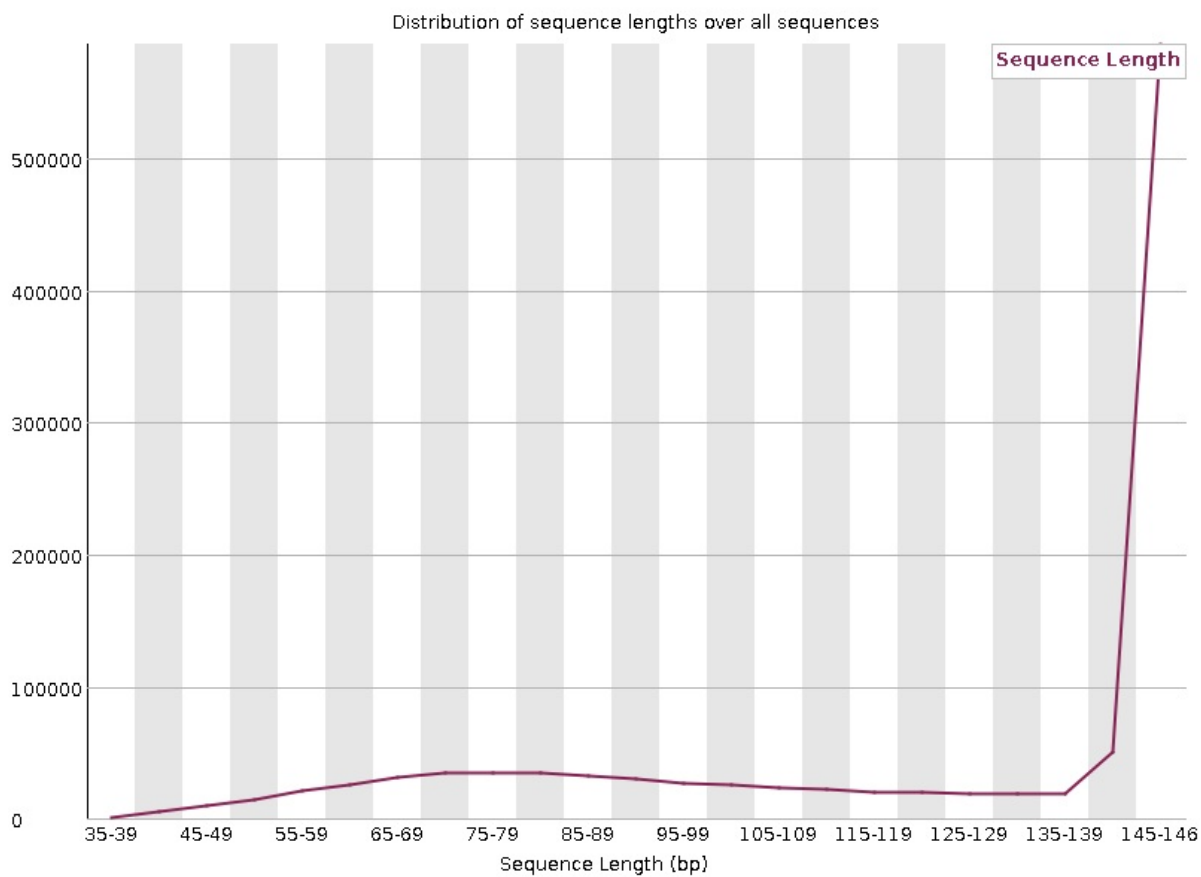
✅ Per sequence GC content



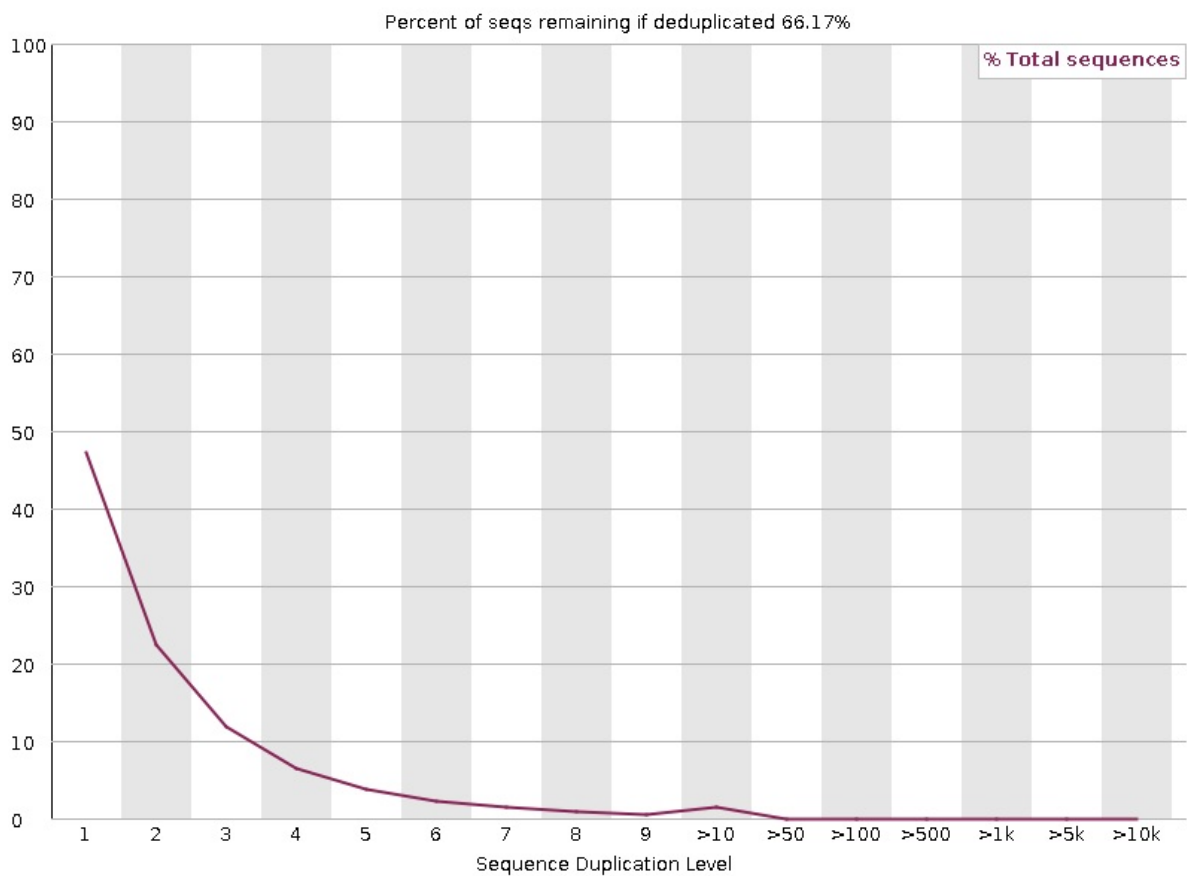
✅ Per base N content



⚠️ Sequence Length Distribution



⚠️ Sequence Duplication Levels



✅ Overrepresented sequences

No overrepresented sequences

Adapter Content

