












# FastQC Report

## Summary

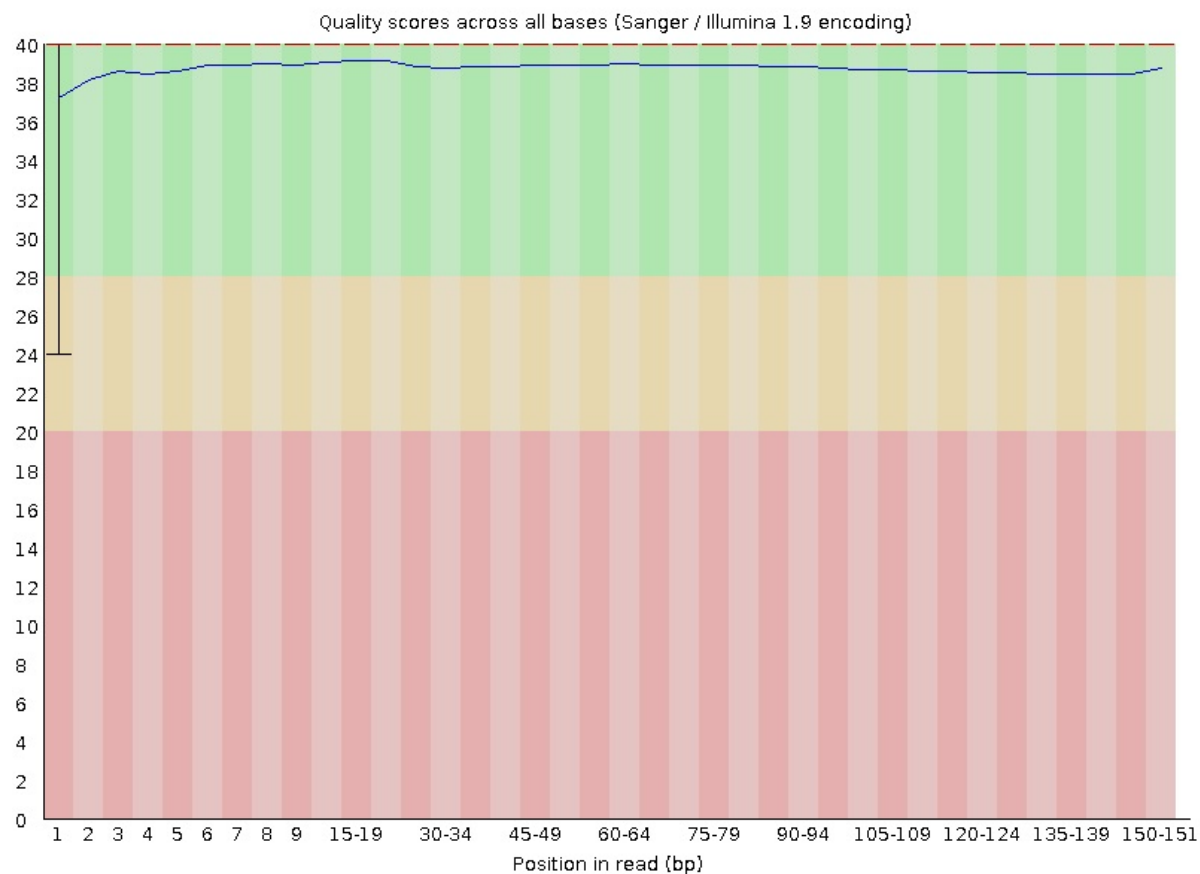
Tue 13 May 2025  
SRR33285751\_2\_paired.fastq

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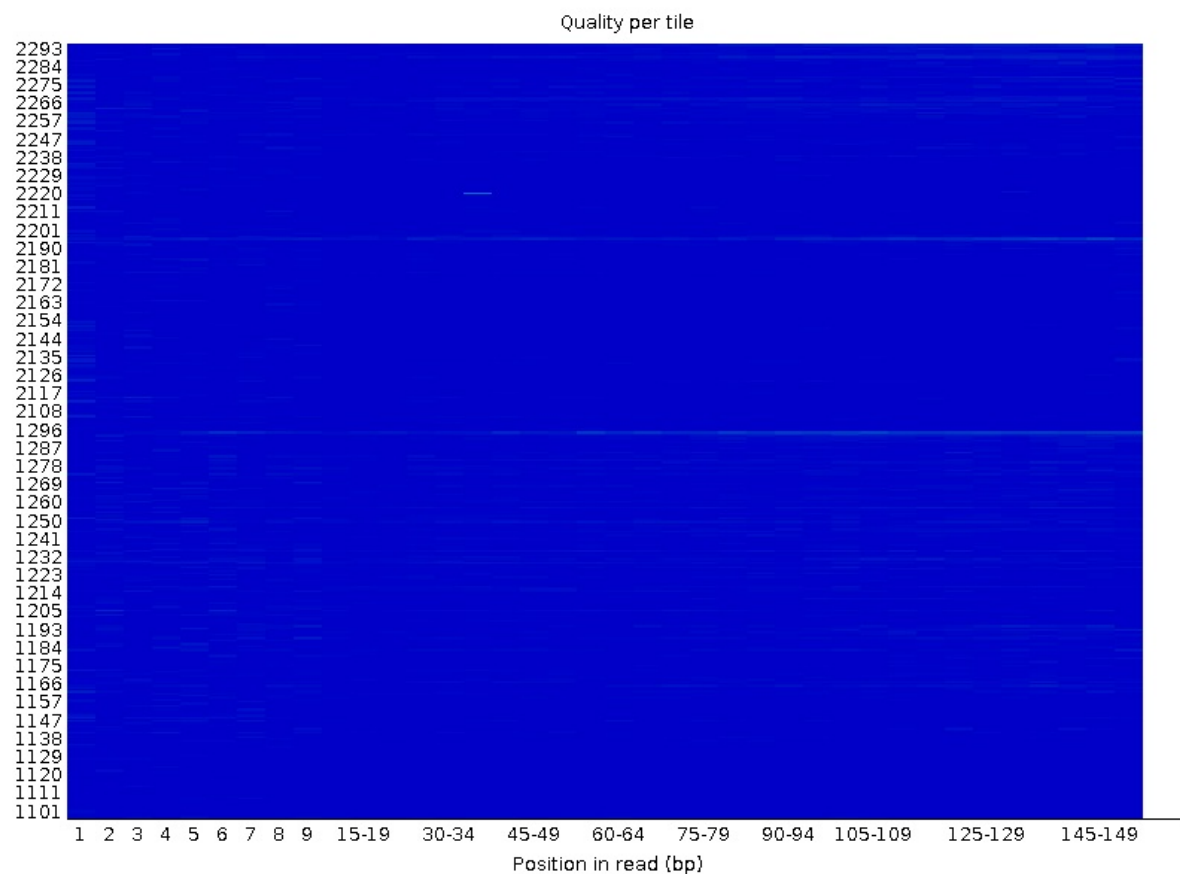
### Basic Statistics

Measure	Value
Filename	SRR33285751_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1929156
Total Bases	280.8 Mbp
Sequences flagged as poor quality	0
Sequence length	36-151
%GC	51

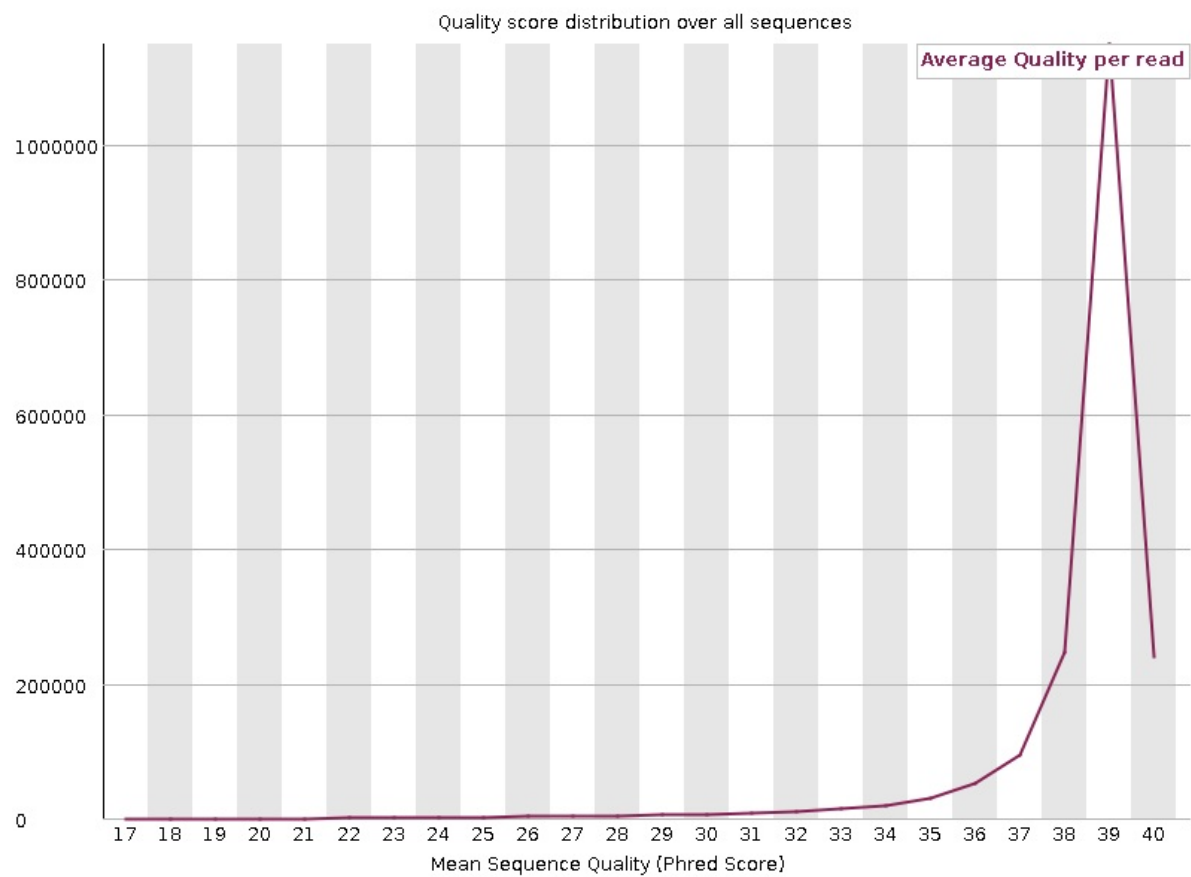
### Per base sequence quality



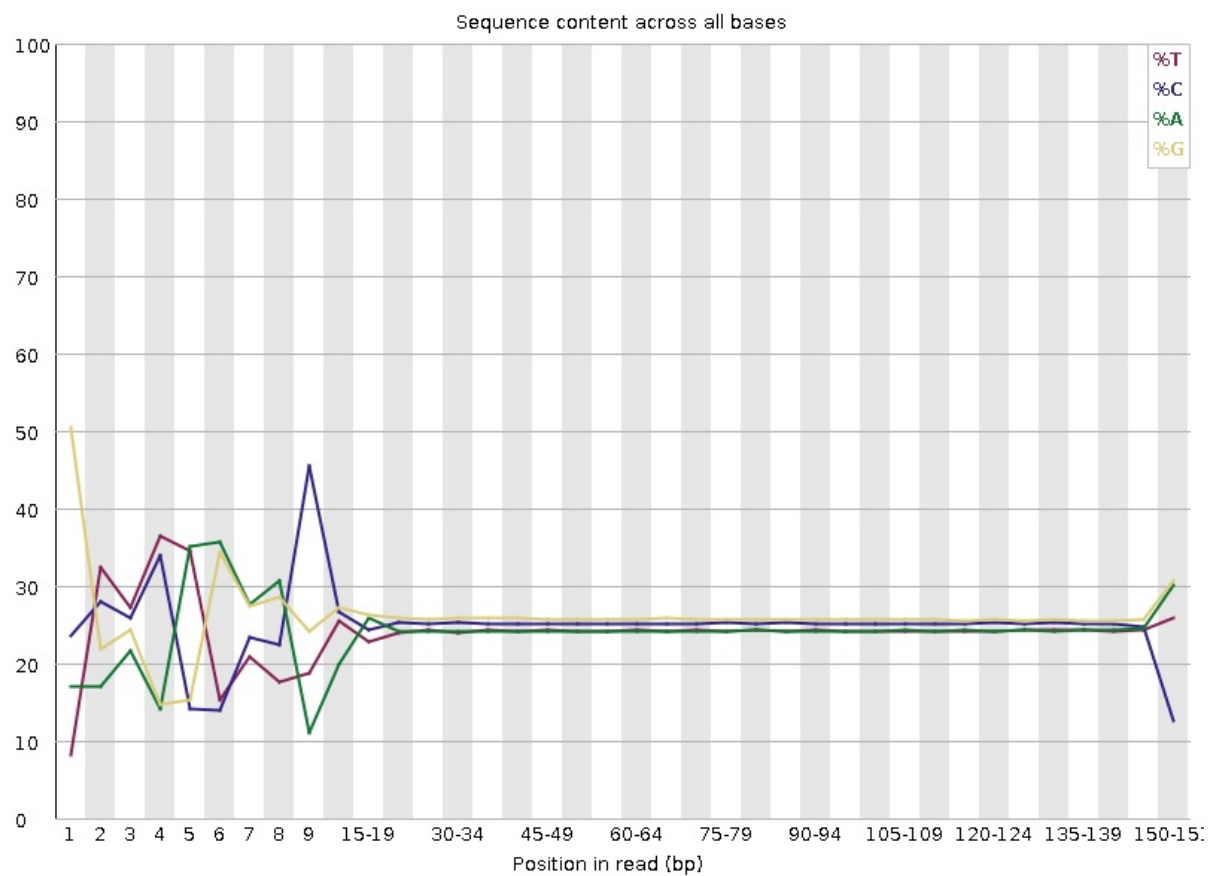
## ✔ Per tile sequence quality



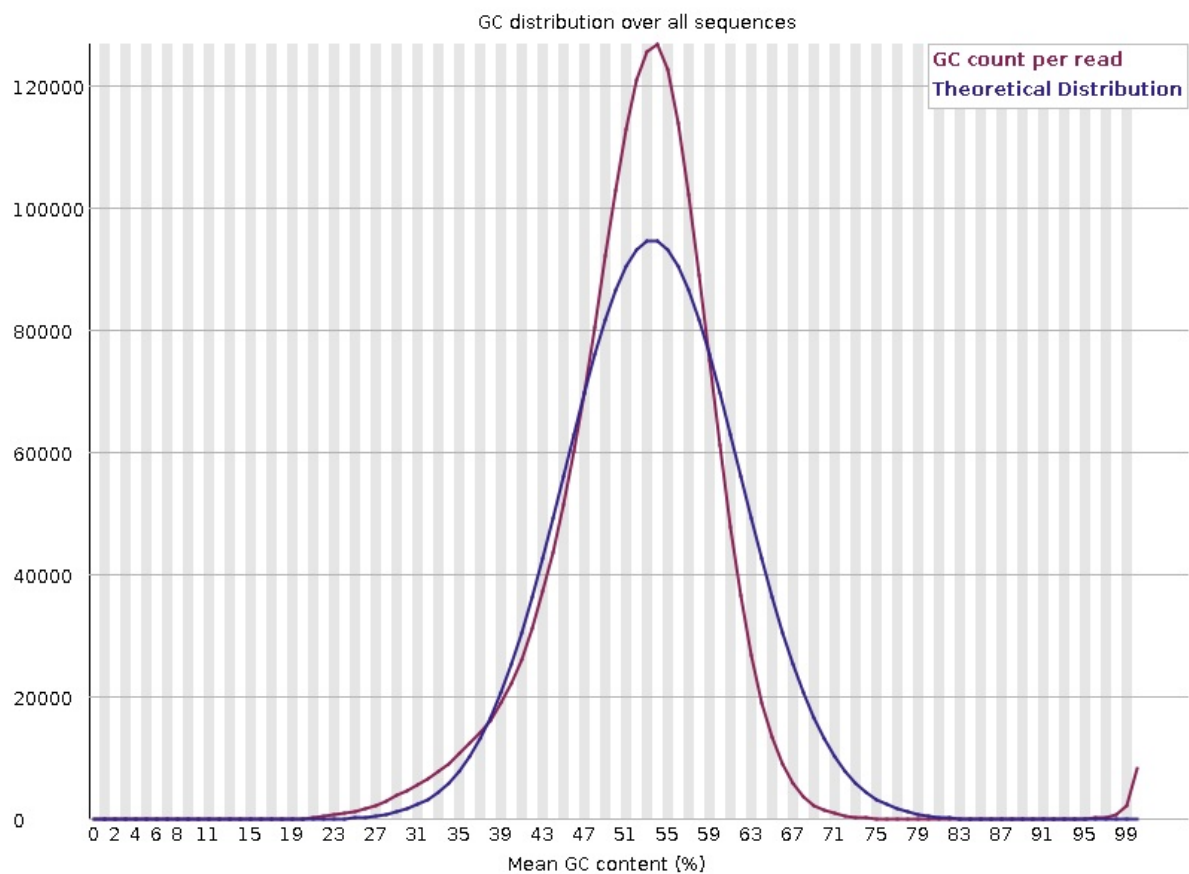
## ✔ Per sequence quality scores



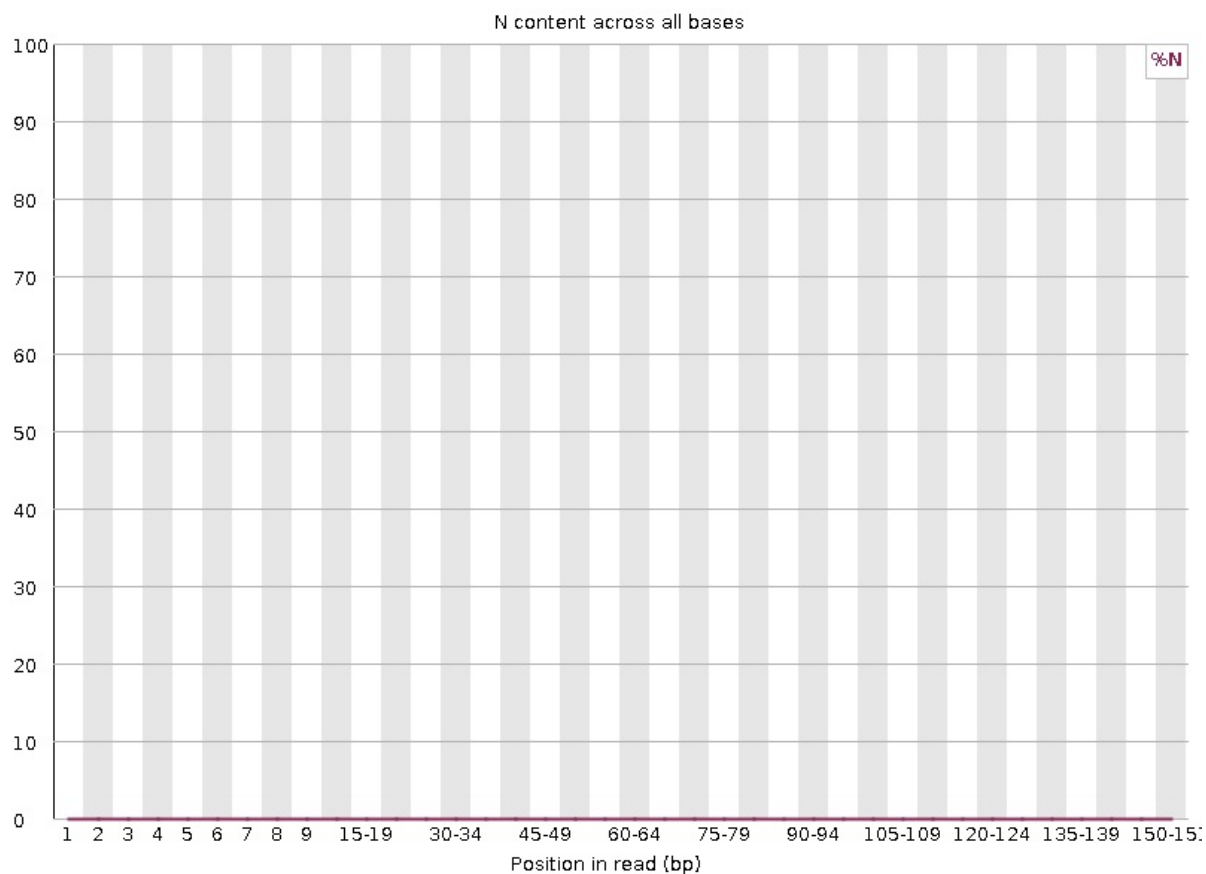
## ✖ Per base sequence content



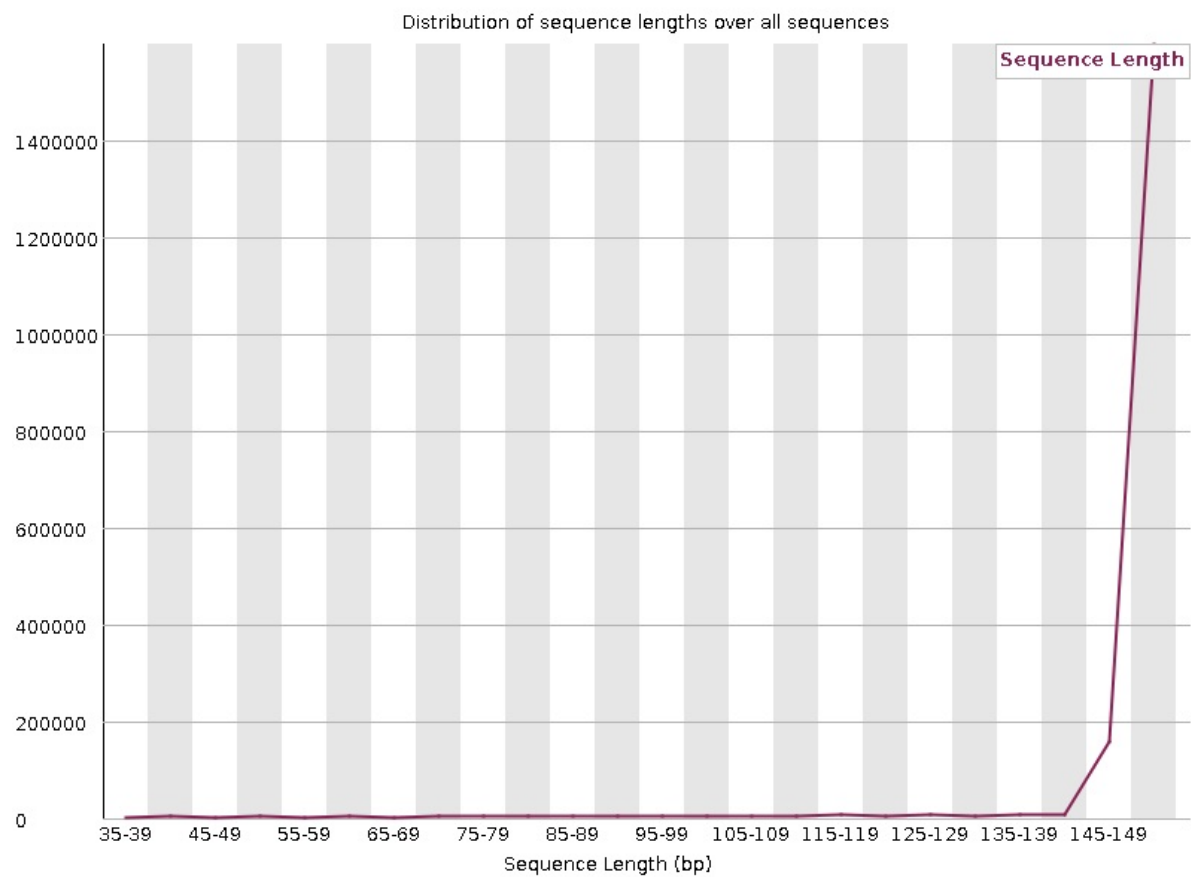
## ⚠ Per sequence GC content



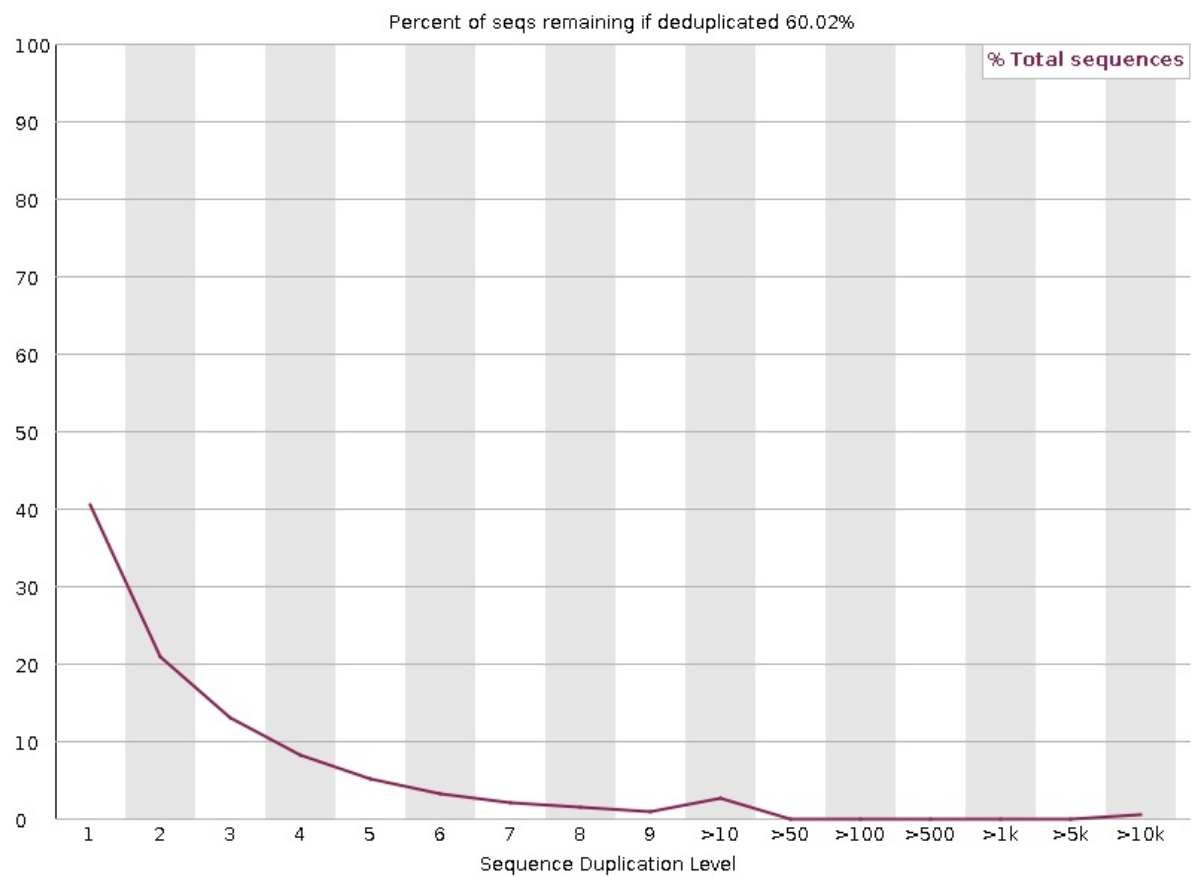
## ✔ Per base N content



## ⚠ Sequence Length Distribution



## ! Sequence Duplication Levels



## ! Overrepresented sequences



