












# FastQC Report

Wed 23 Dec 2020

ERR486827\_2.fastq

## Summary

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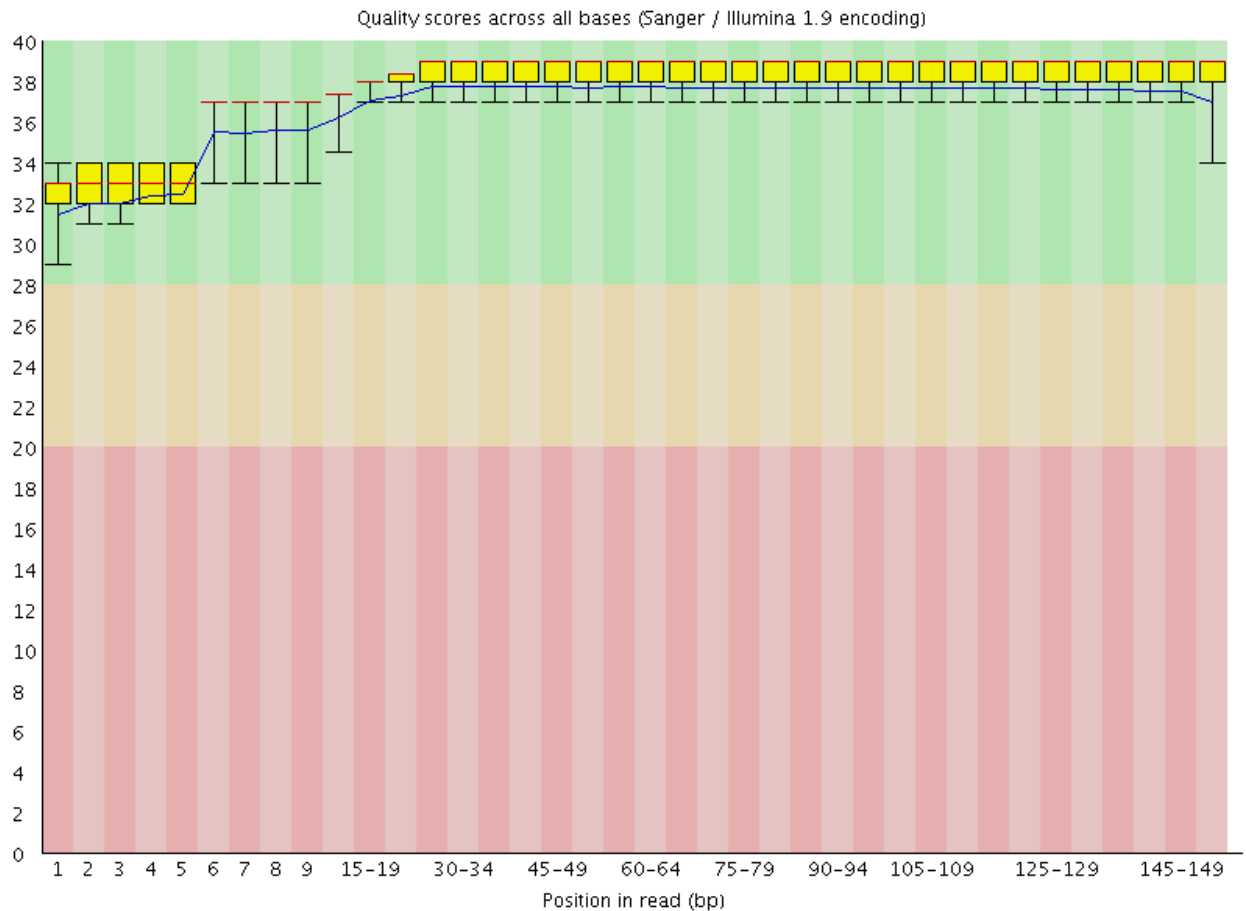
## Basic Statistics

	Filename	ERR486827_2.fastq
	File type	Conventional base calls
	Encoding	Sanger / Illumina 1.9

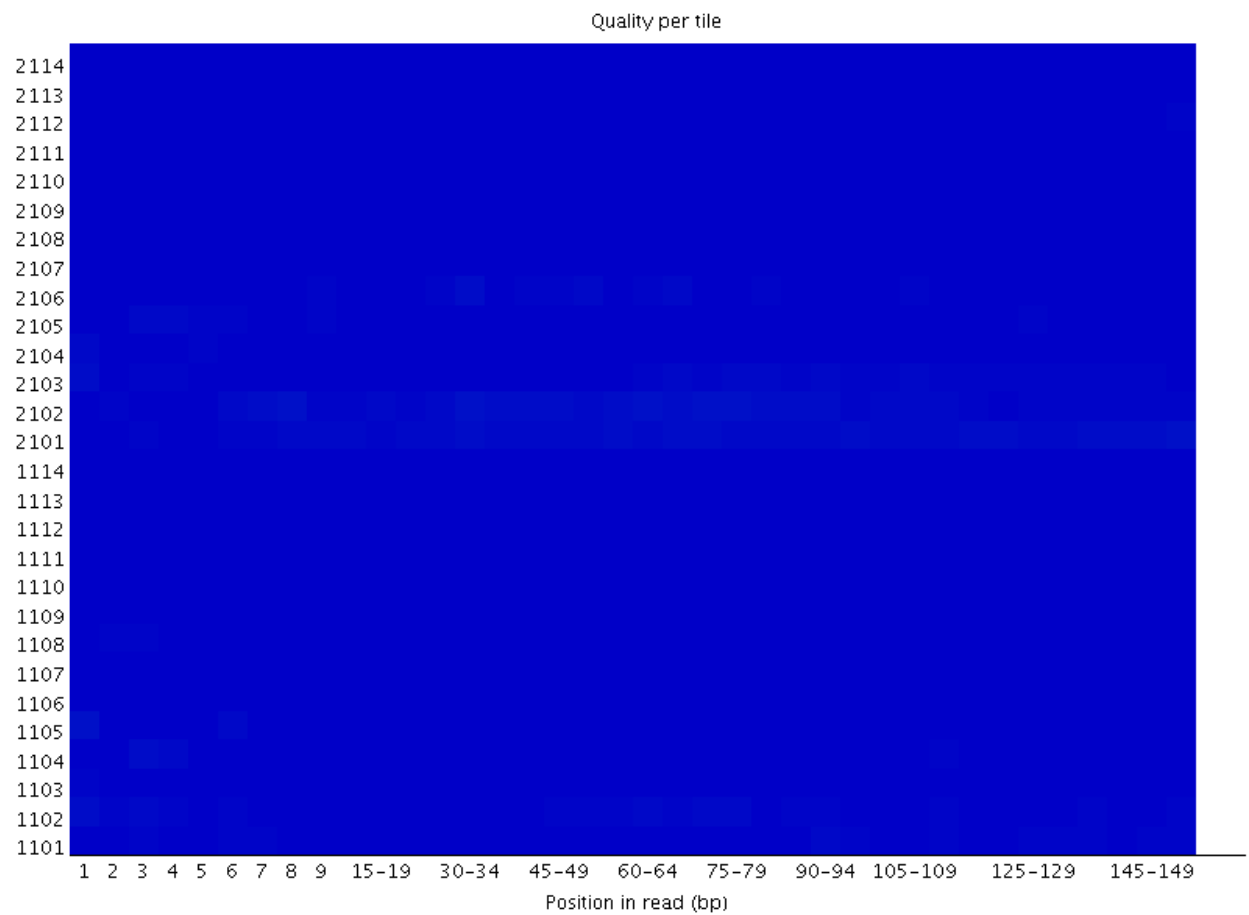
Total Sequences	398824
Sequences flagged as poor quality	0
Sequence length	150
%GC	31



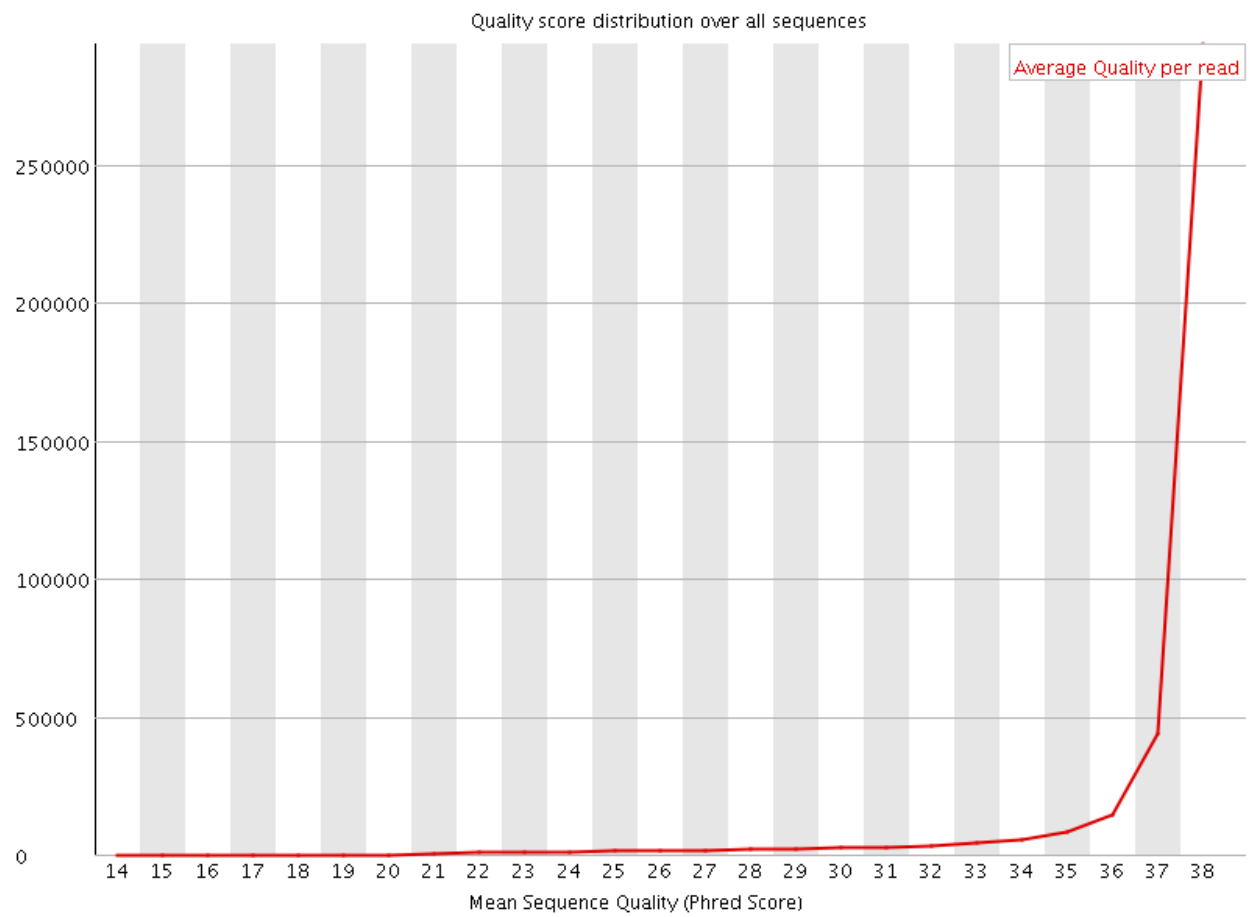
## Per base sequence quality



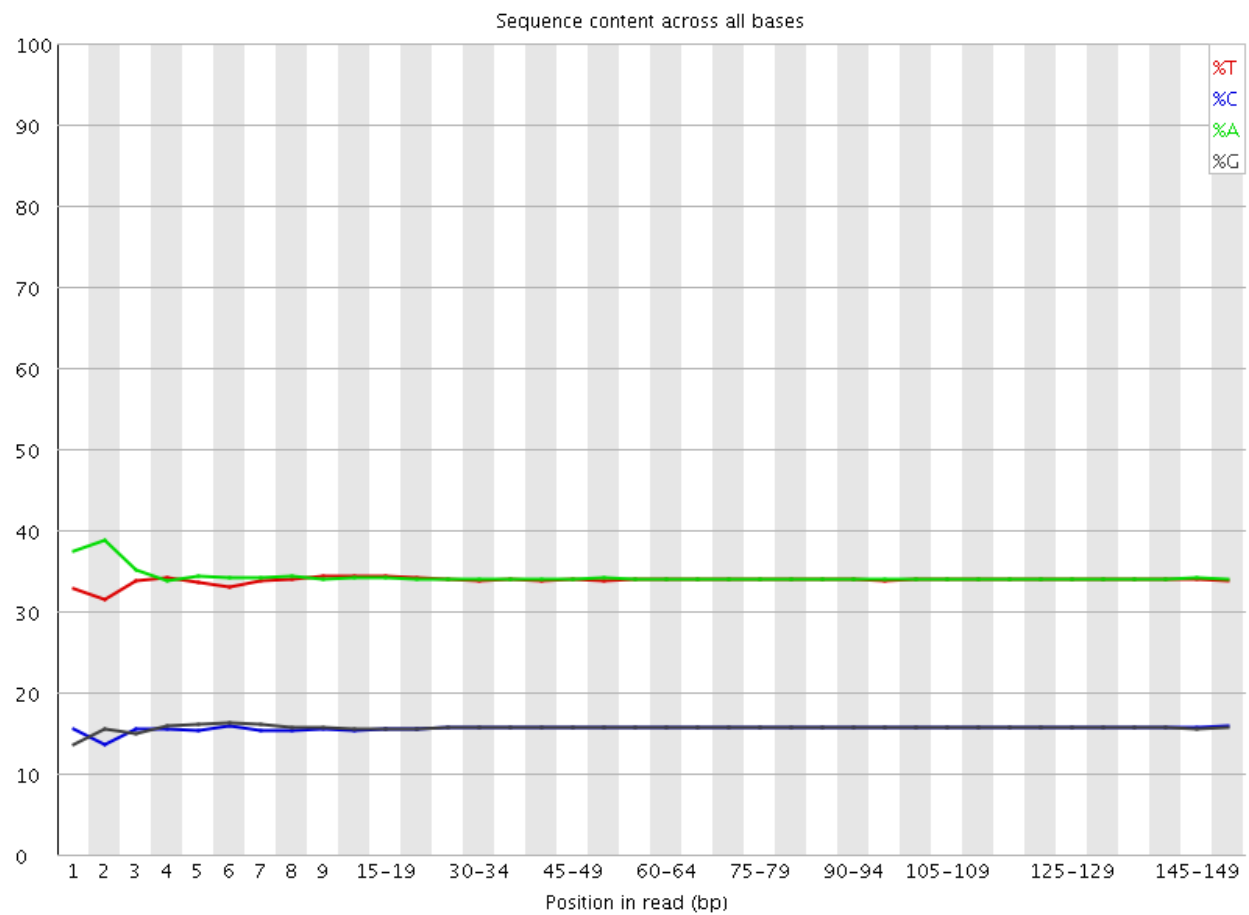
## Per tile sequence quality



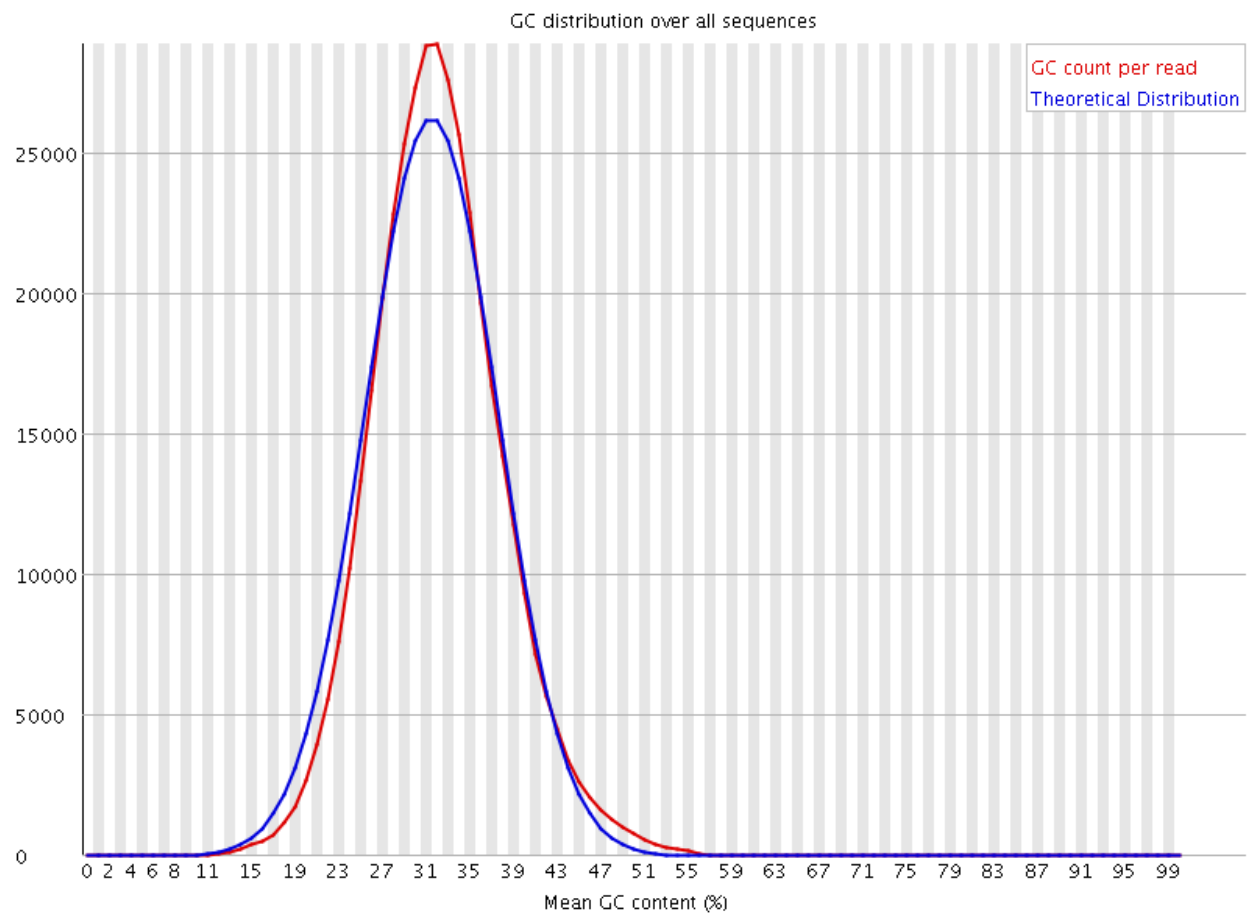
**Per sequence quality scores**



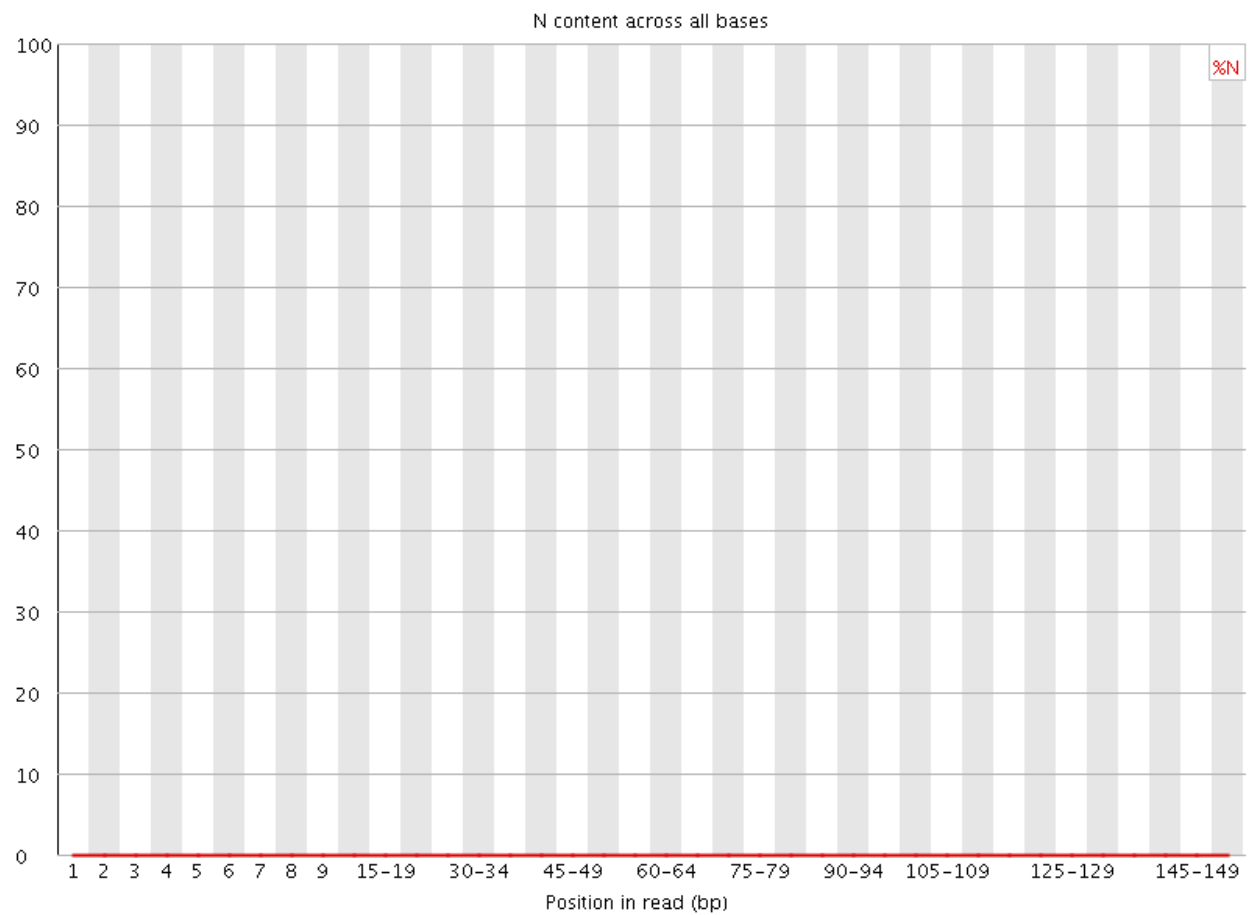
**Per base sequence content**



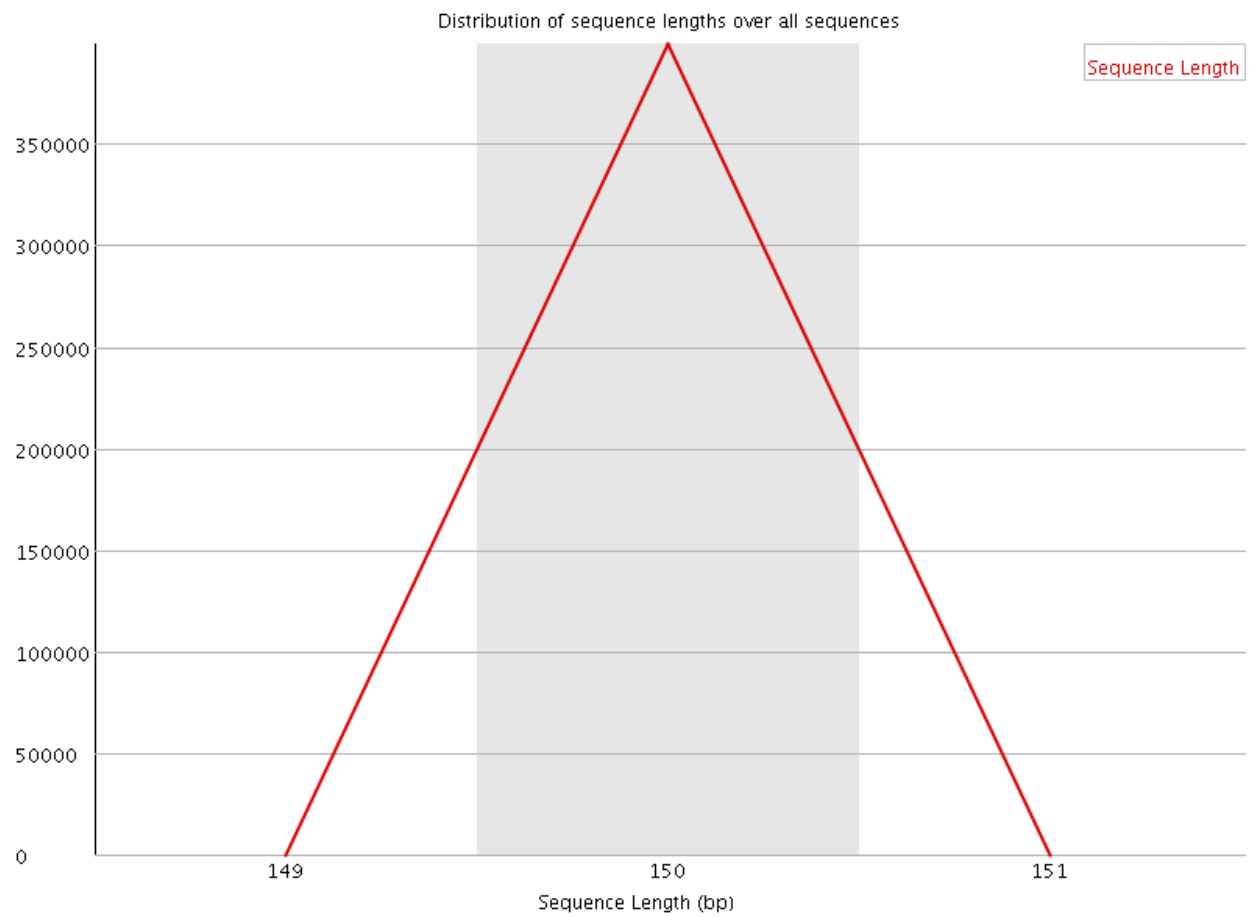
**Per sequence GC content**



**Per base N content**

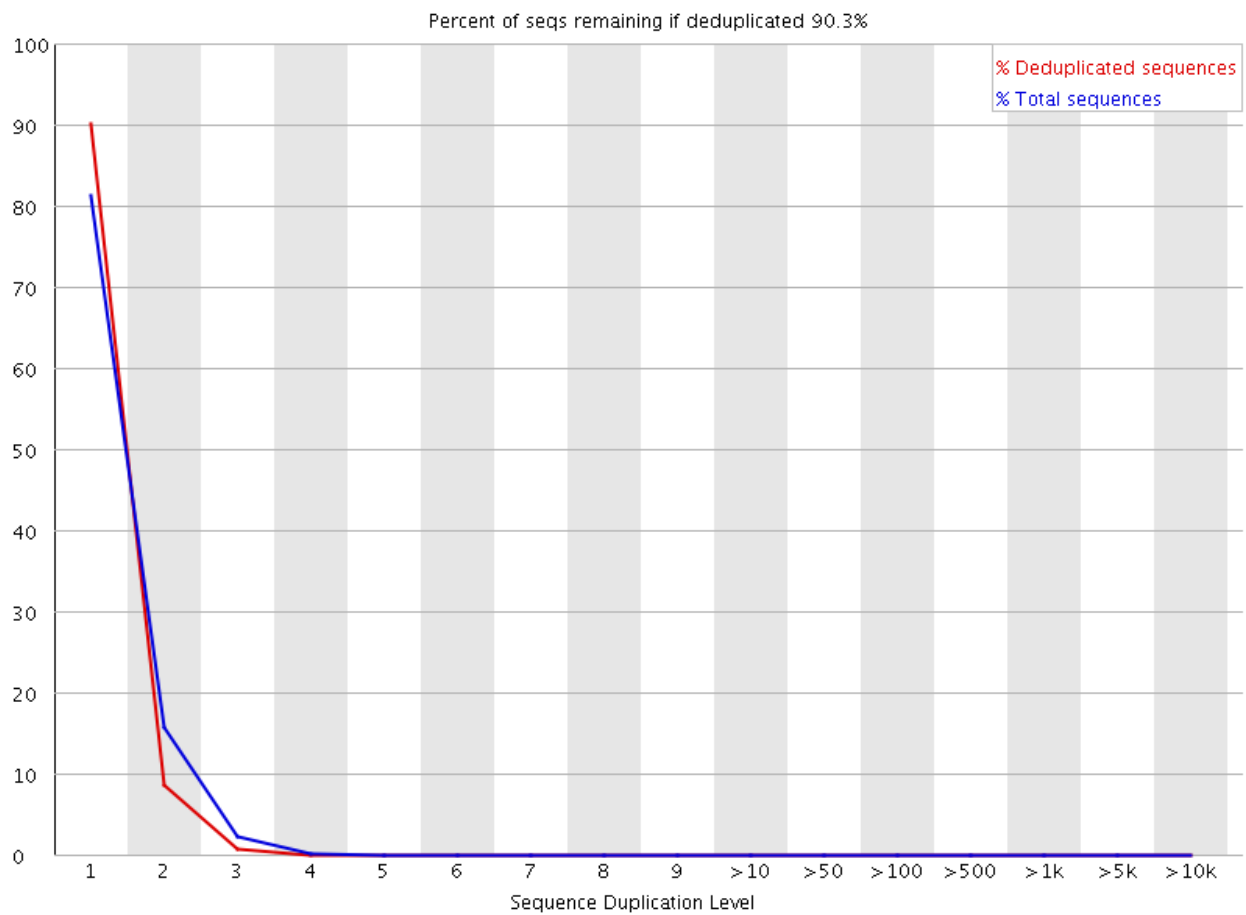


## Sequence Length Distribution



## Sequence Duplication Levels



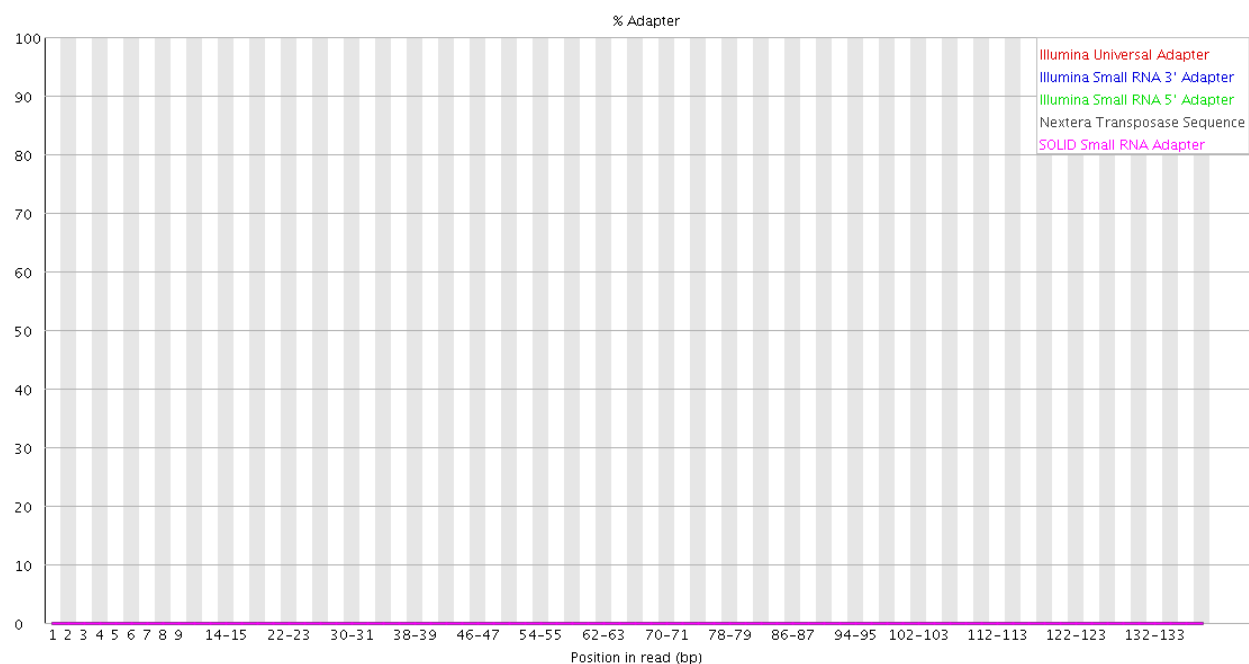


**Overrepresented sequences**

No overrepresented sequences



**Adapter Content**



Produced by [FastQC](#) (version 0.11.7)