












FastQC Report

Wed 23 Dec 2020

ERR486827_1.fastq

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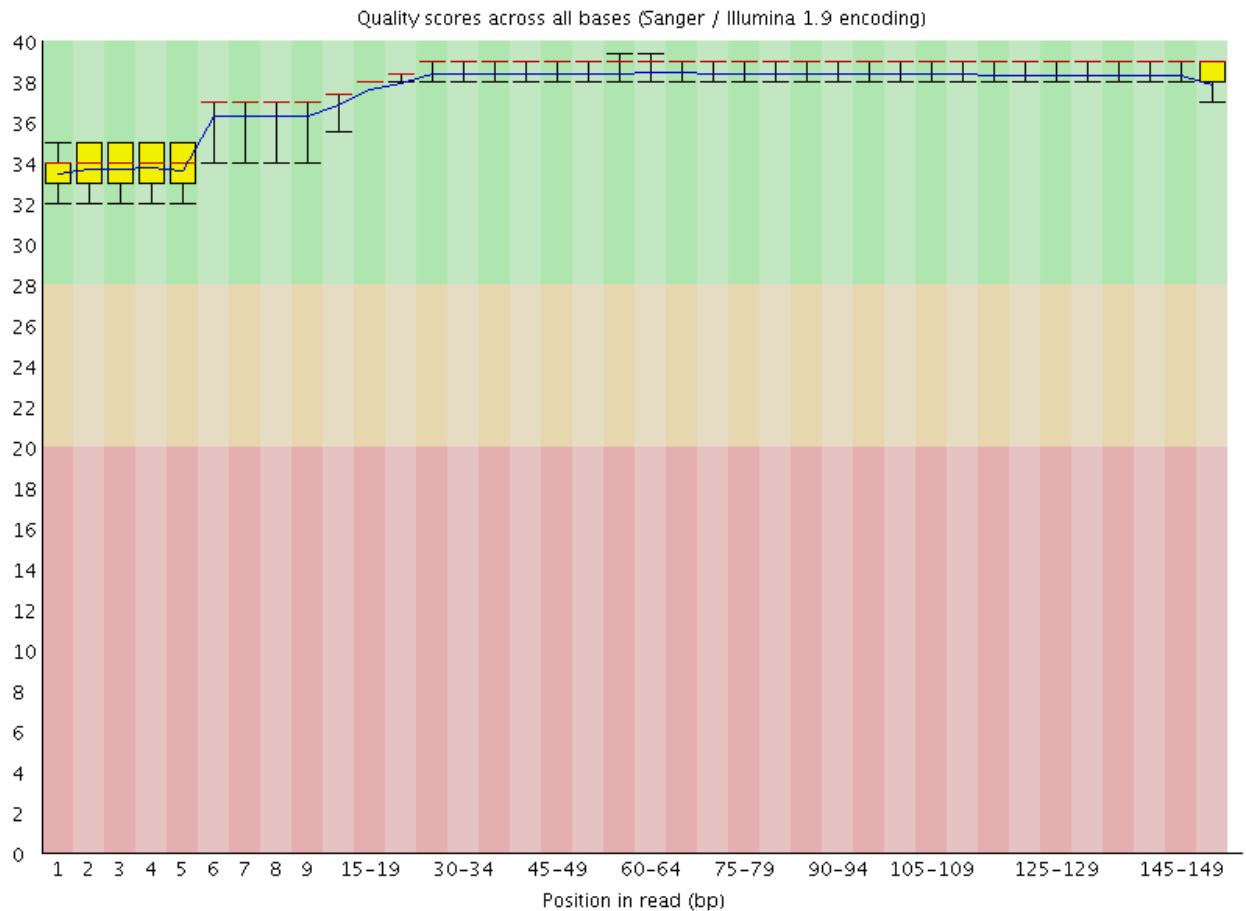
Basic Statistics

	Filename	ERR486827_1.fastq
	File type	Conventional base calls
	Encoding	Sanger / Illumina 1.9

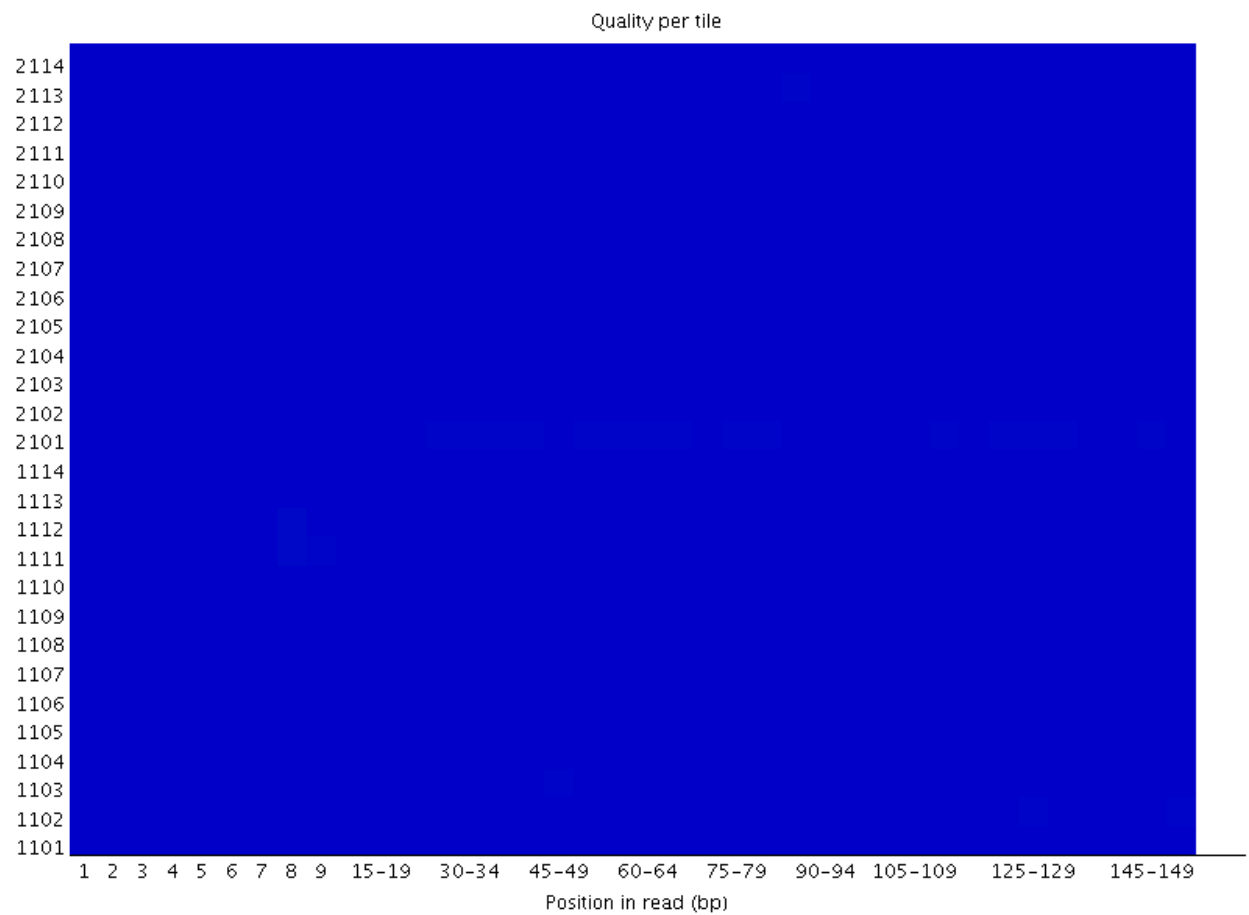
Total Sequences	398824
Sequences flagged as poor quality	0
Sequence length	150
%GC	31



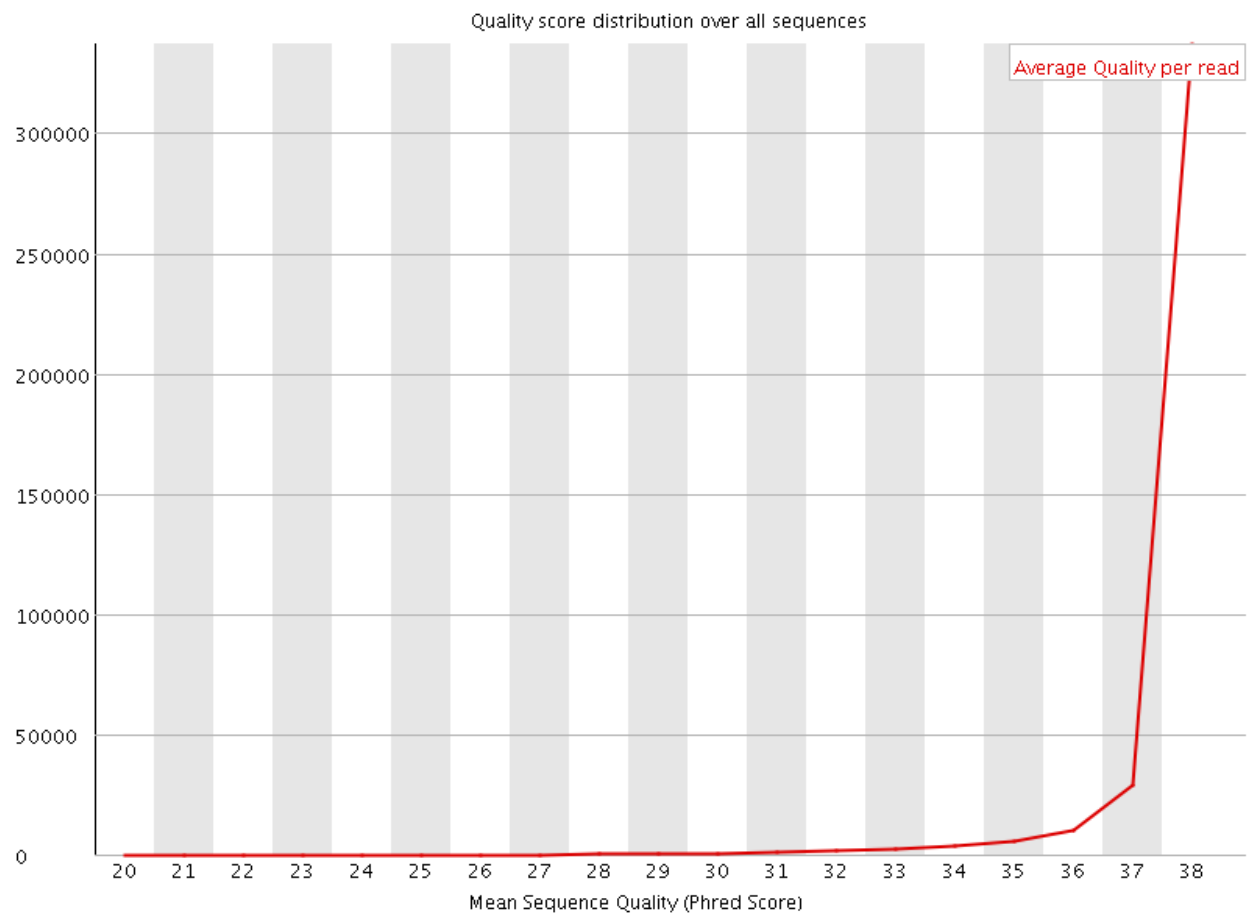
Per base sequence quality



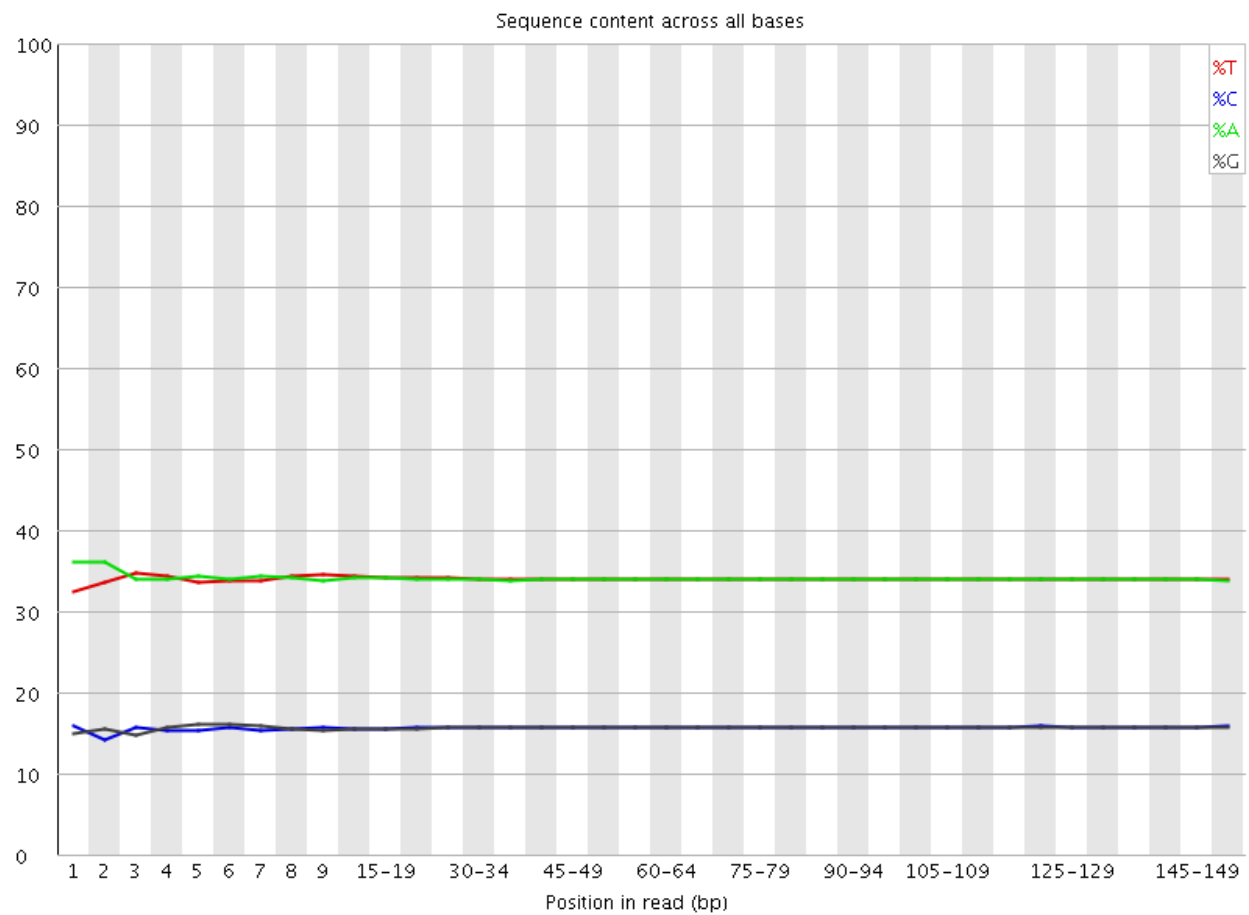
Per tile sequence quality



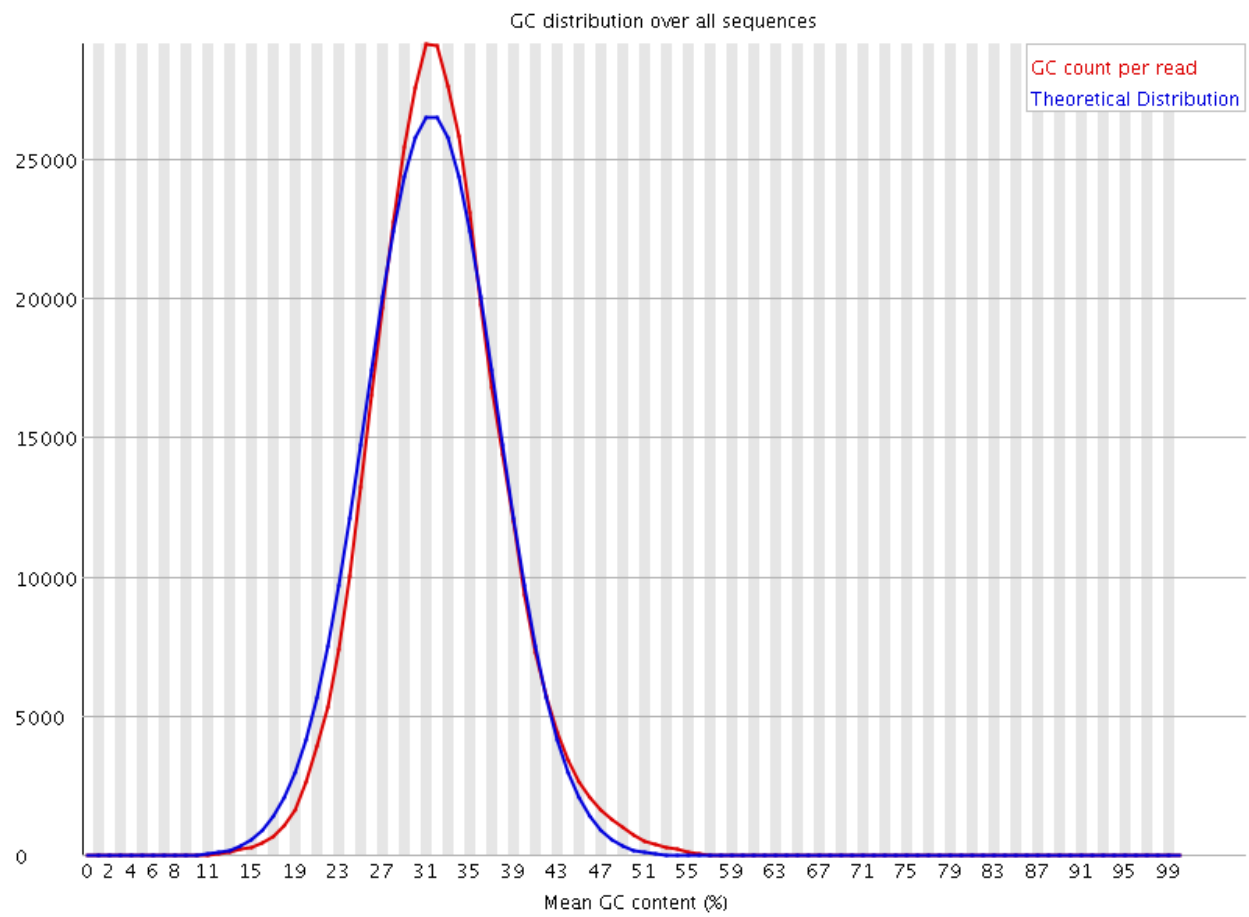
Per sequence quality scores



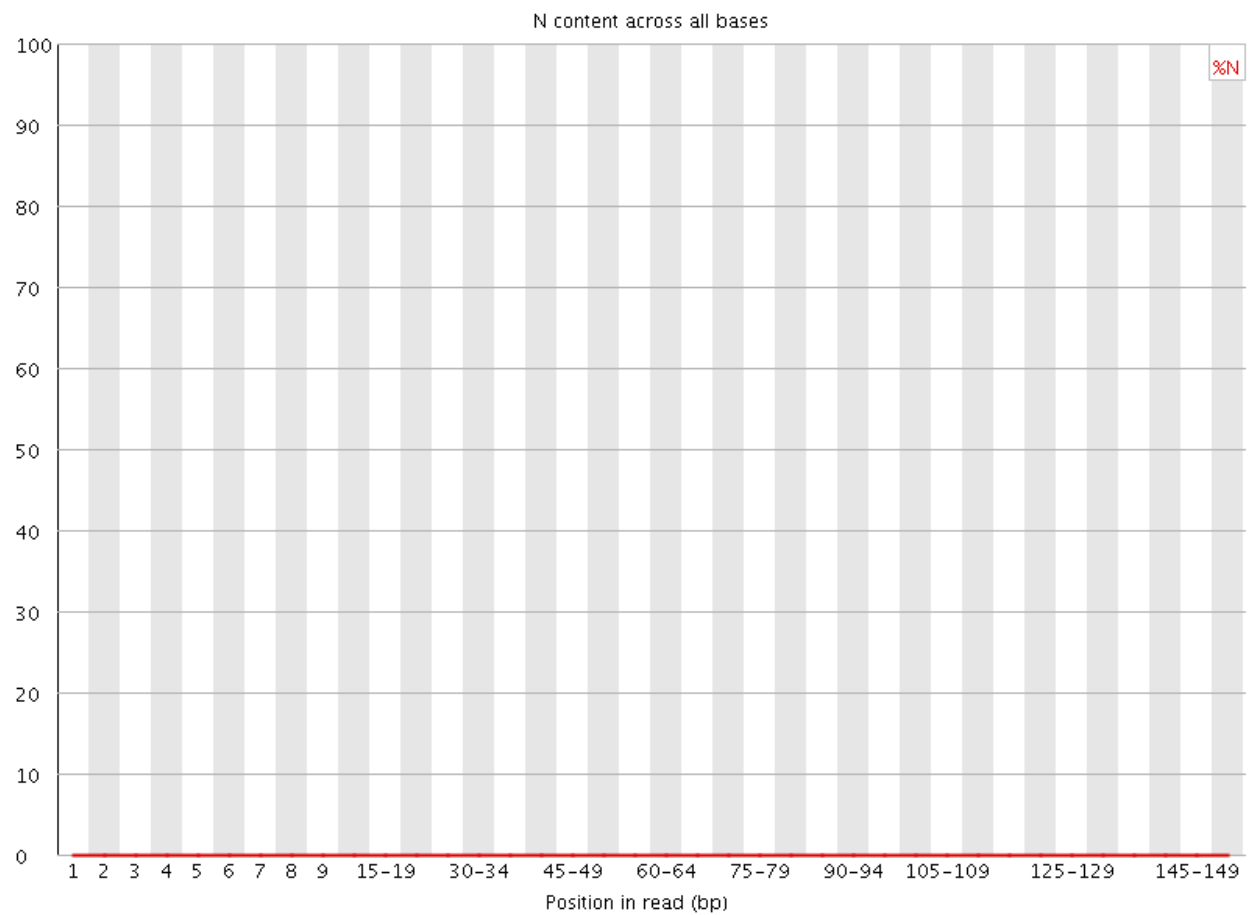
Per base sequence content



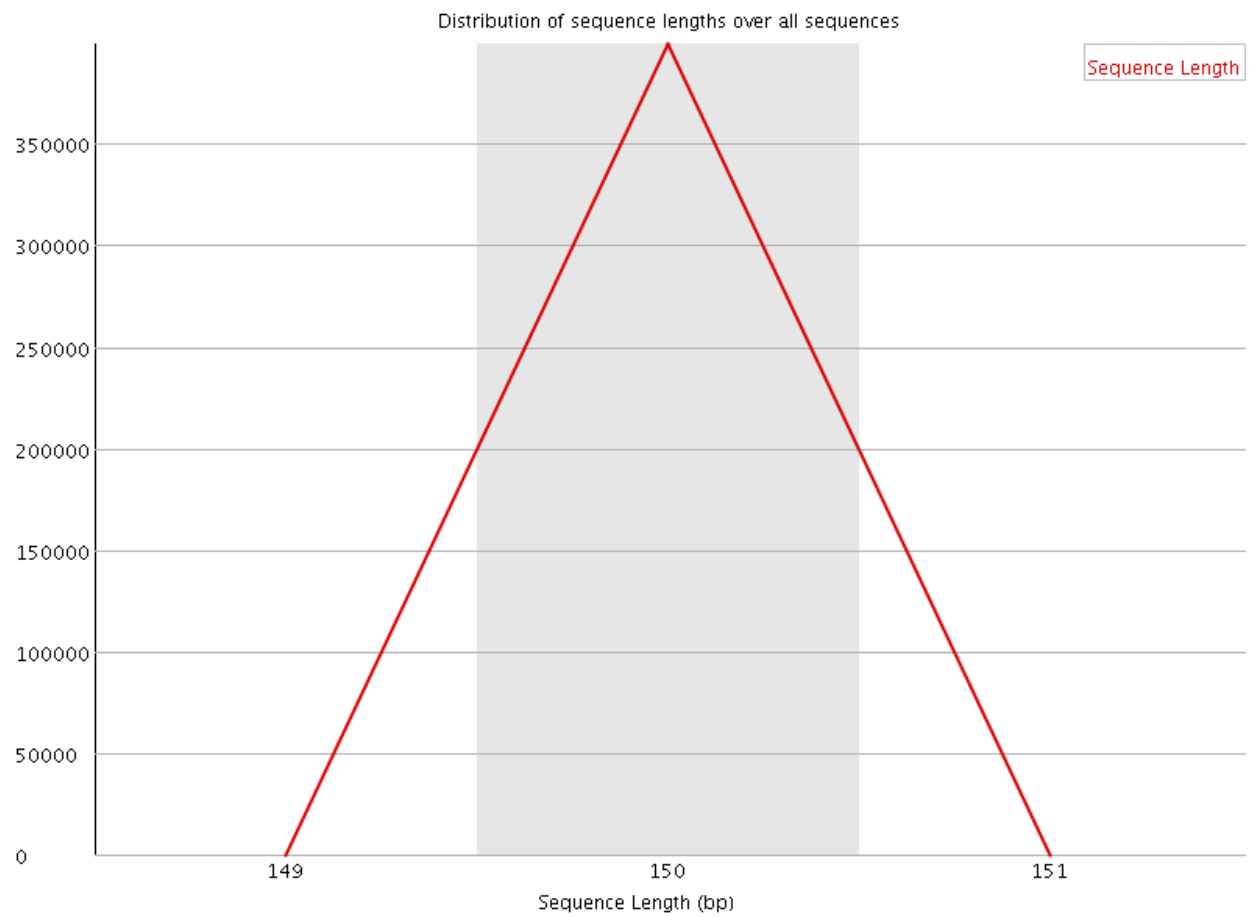
Per sequence GC content



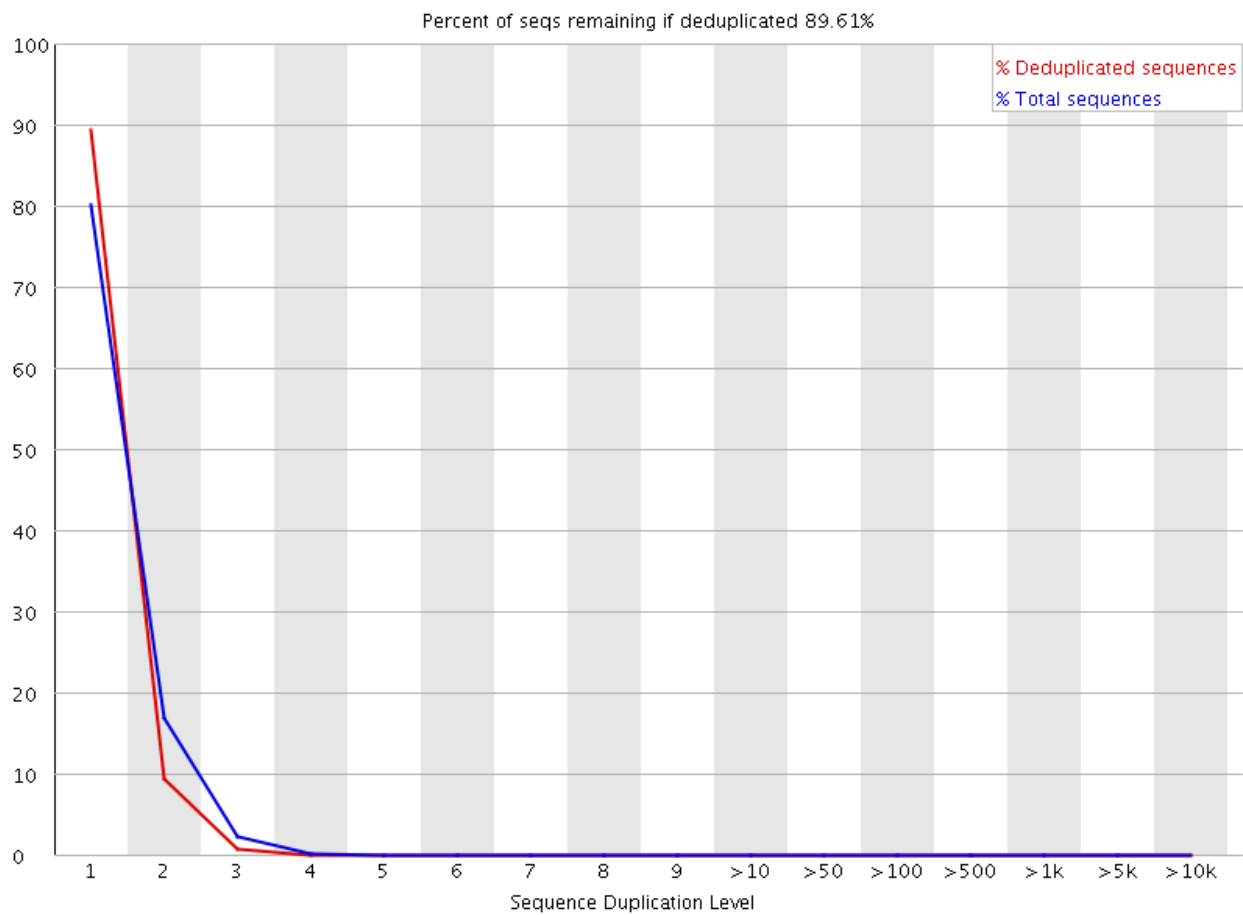
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

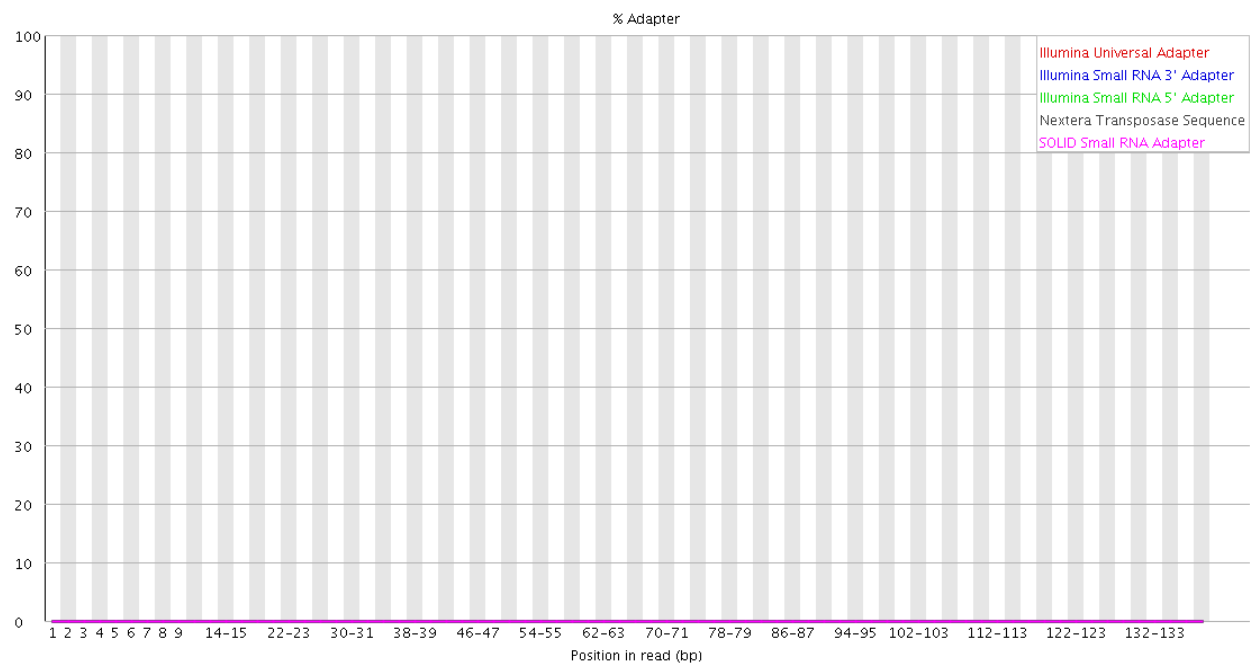


Overrepresented sequences

No overrepresented sequences



Adapter Content



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