FastQC Report

Mon 25 Jun 2018
9IRM1_HWC3LBBXX_CGCTCATT-TAAGATTA_L001_R1.fastq.gz

Summary

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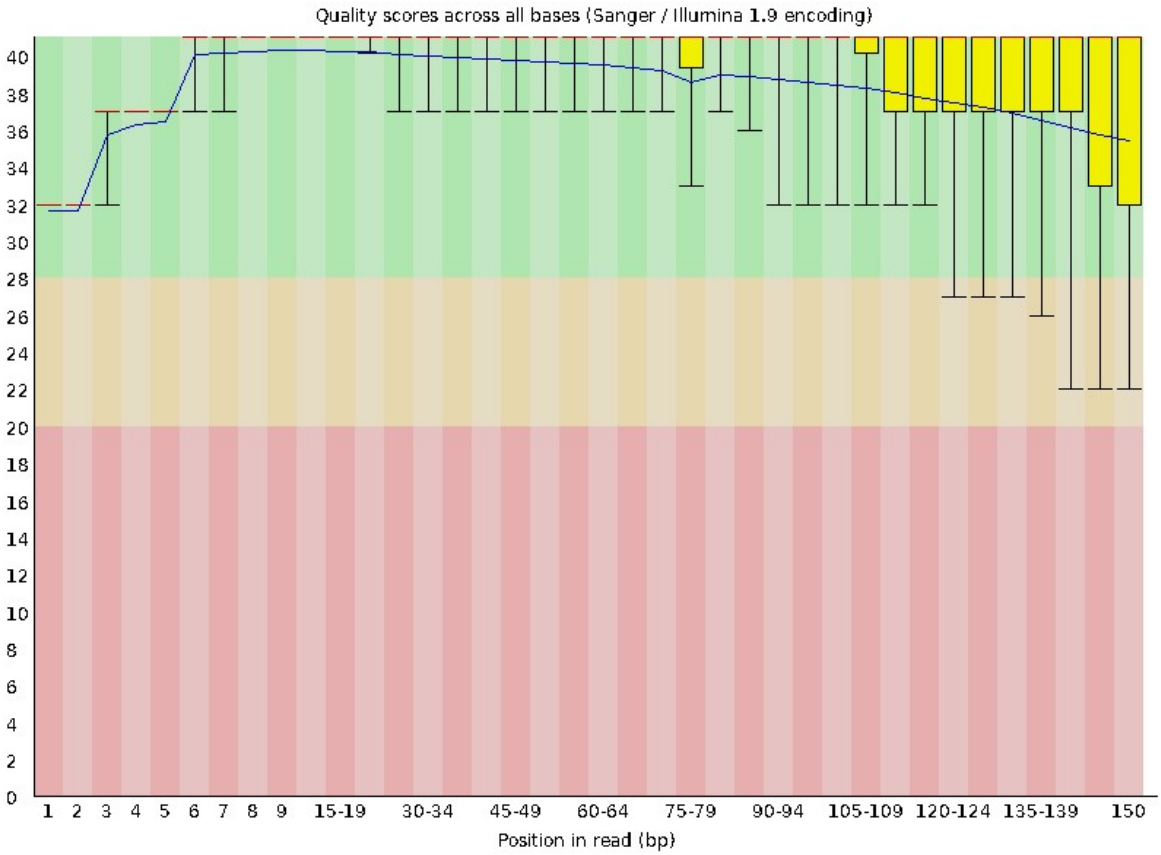
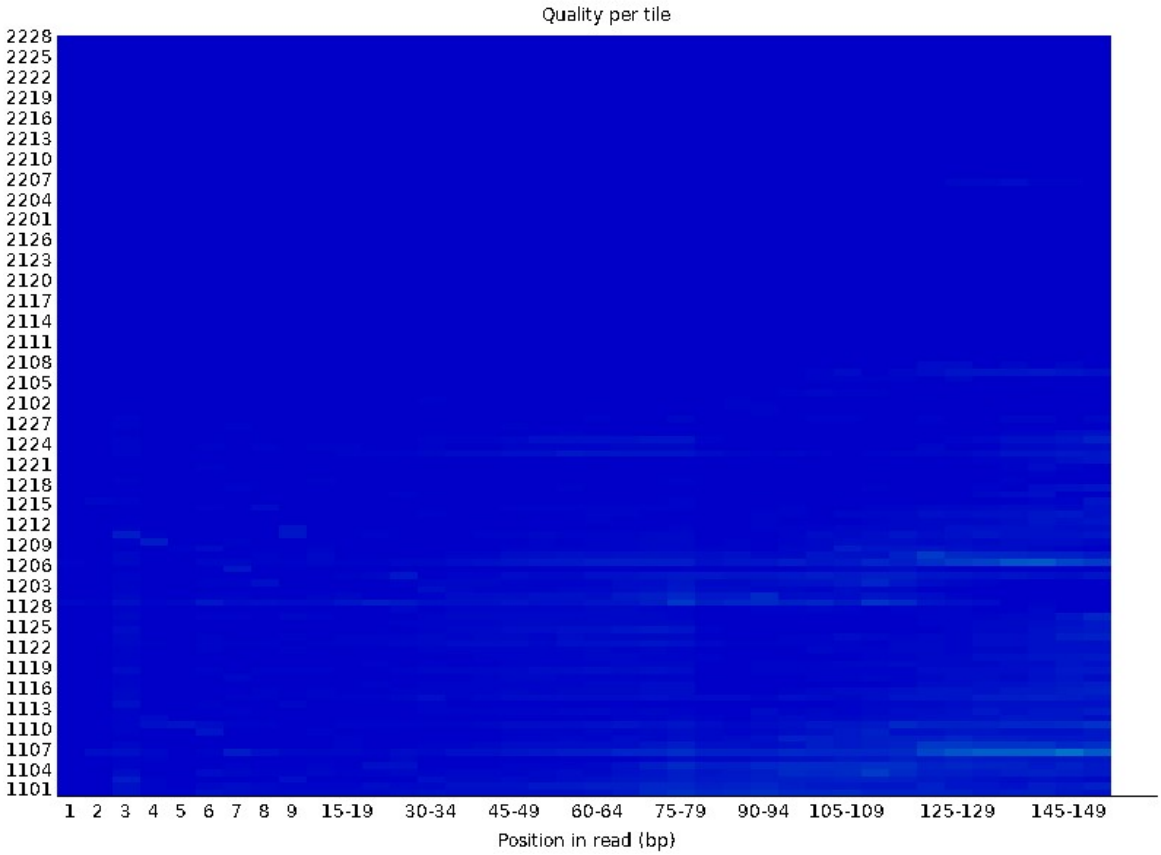
Basic Statistics

Measure	Value
Filename	9IRM1_HWC3LBBXX_CGCTCATT-TAAGATTA_L001_R1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	94005512
Sequences flagged as poor quality	0
Sequence length	150
%GC	38

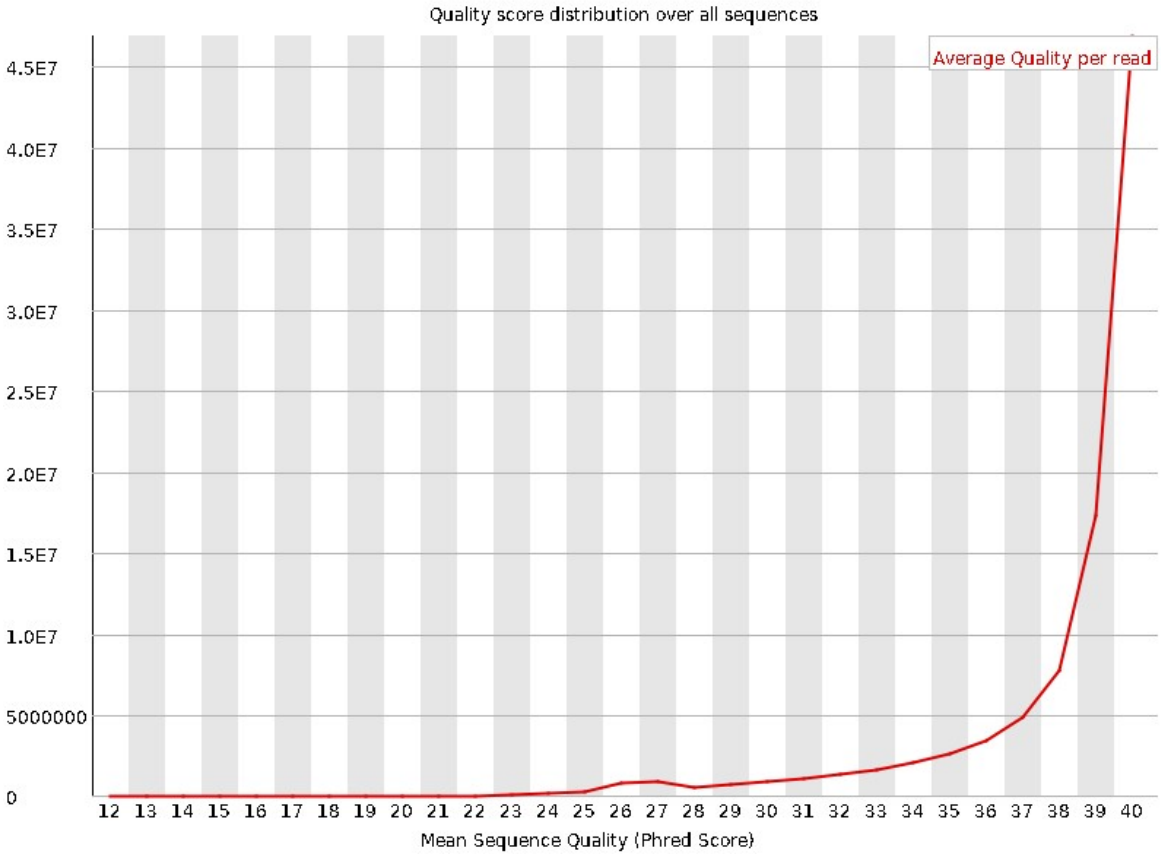
Per base sequence quality



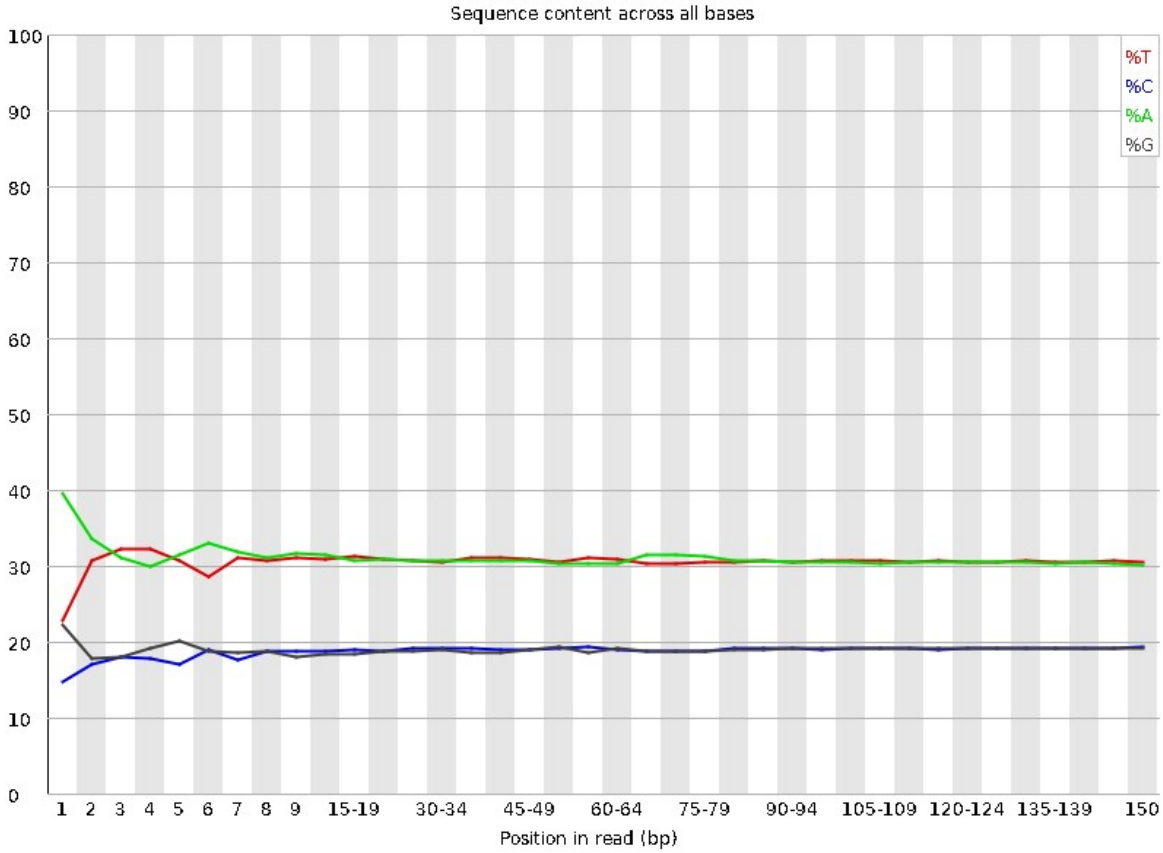
Per tile sequence quality



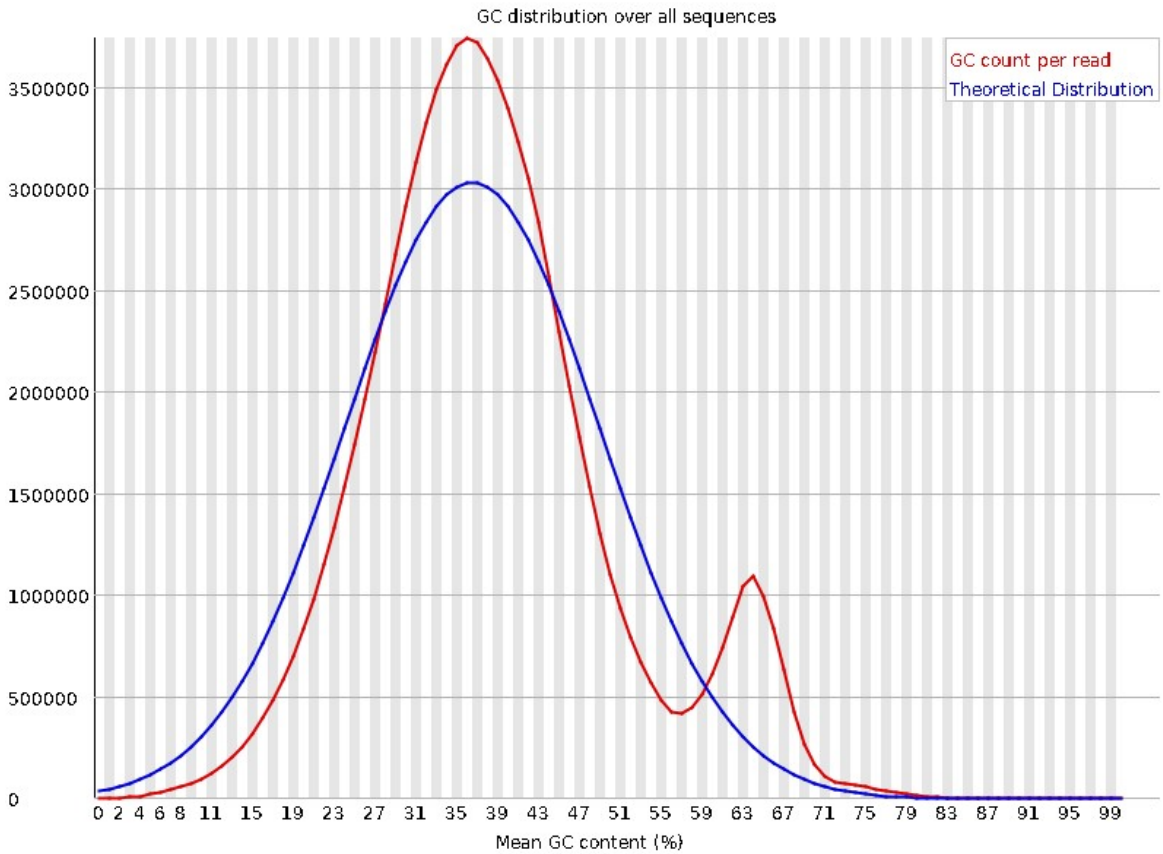
Per sequence quality scores



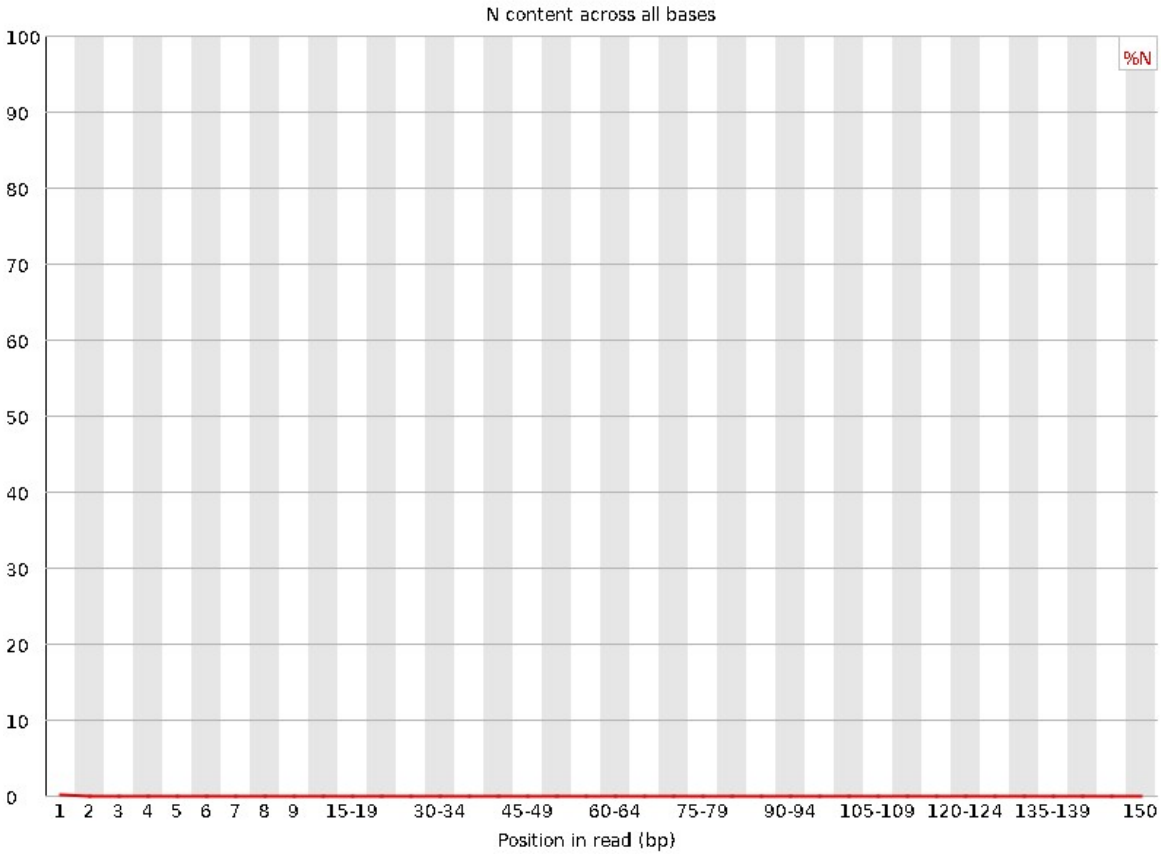
Per base sequence content



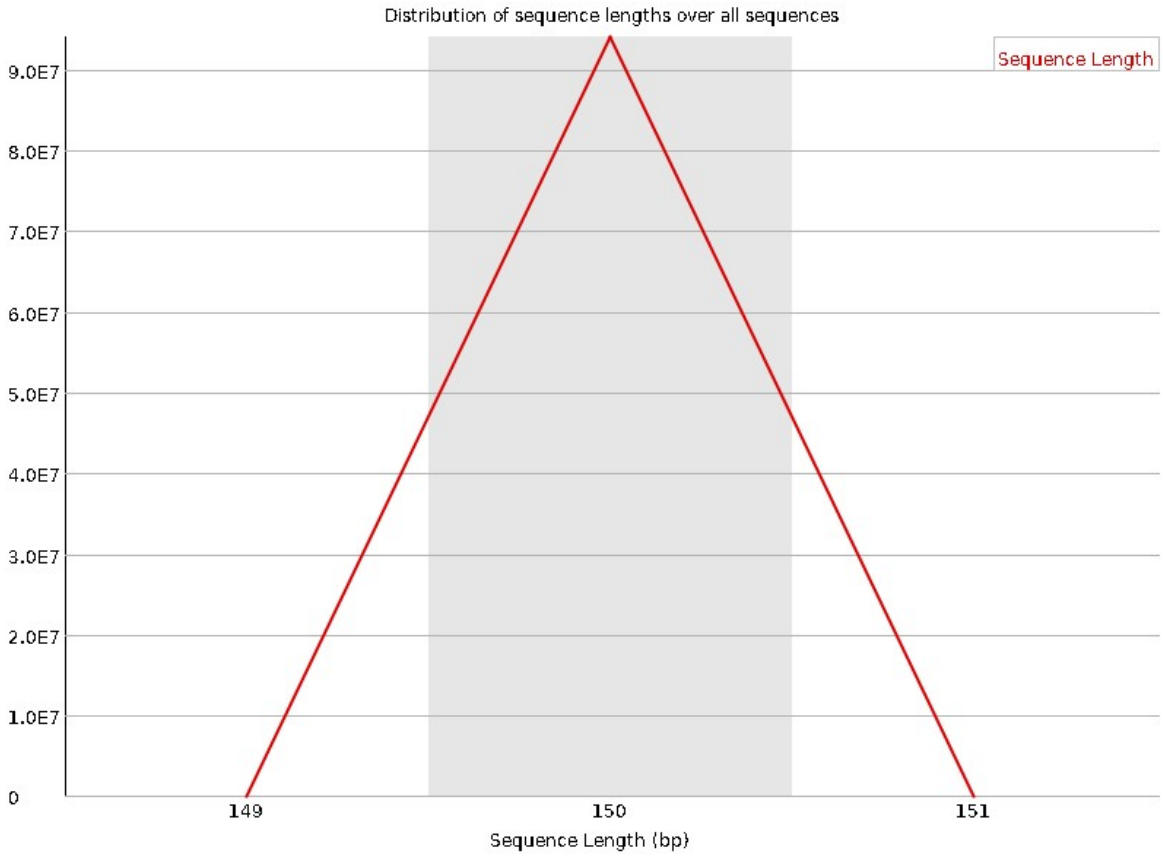
Per sequence GC content



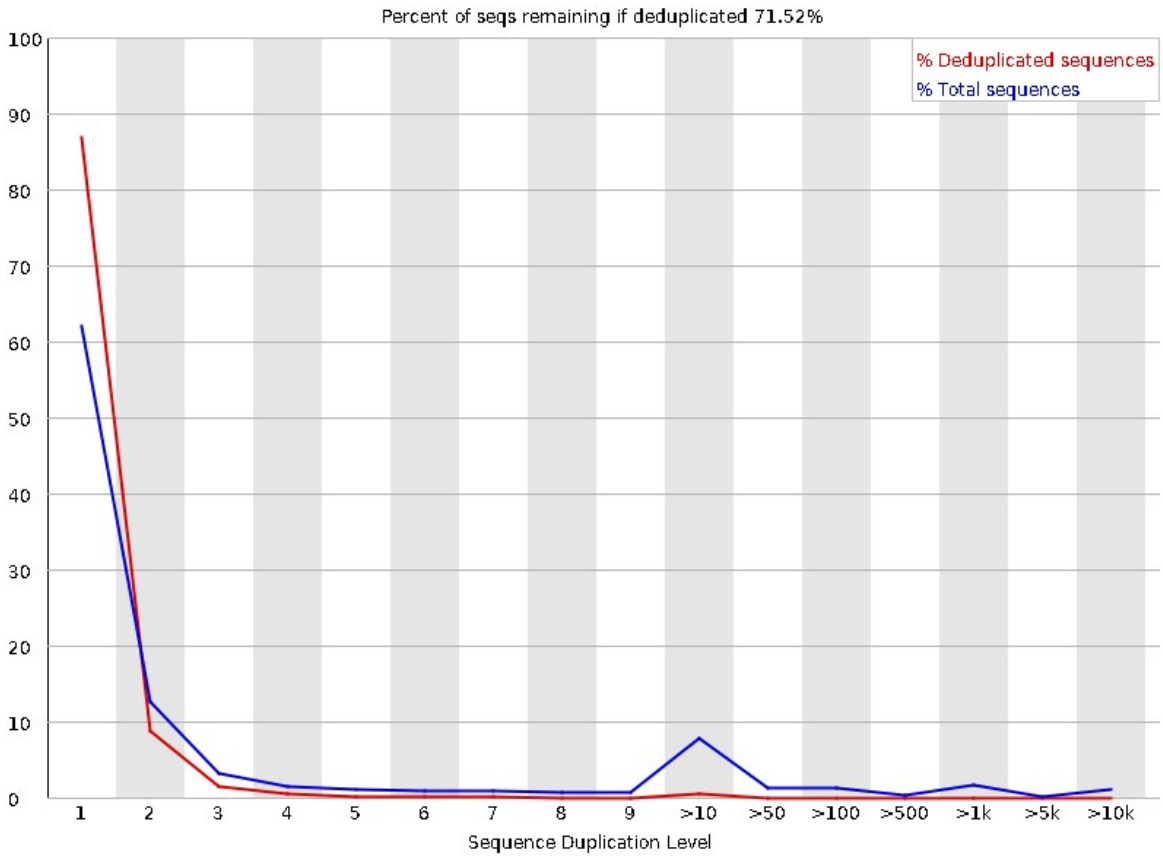
Per base N content



Sequence Length Distribution



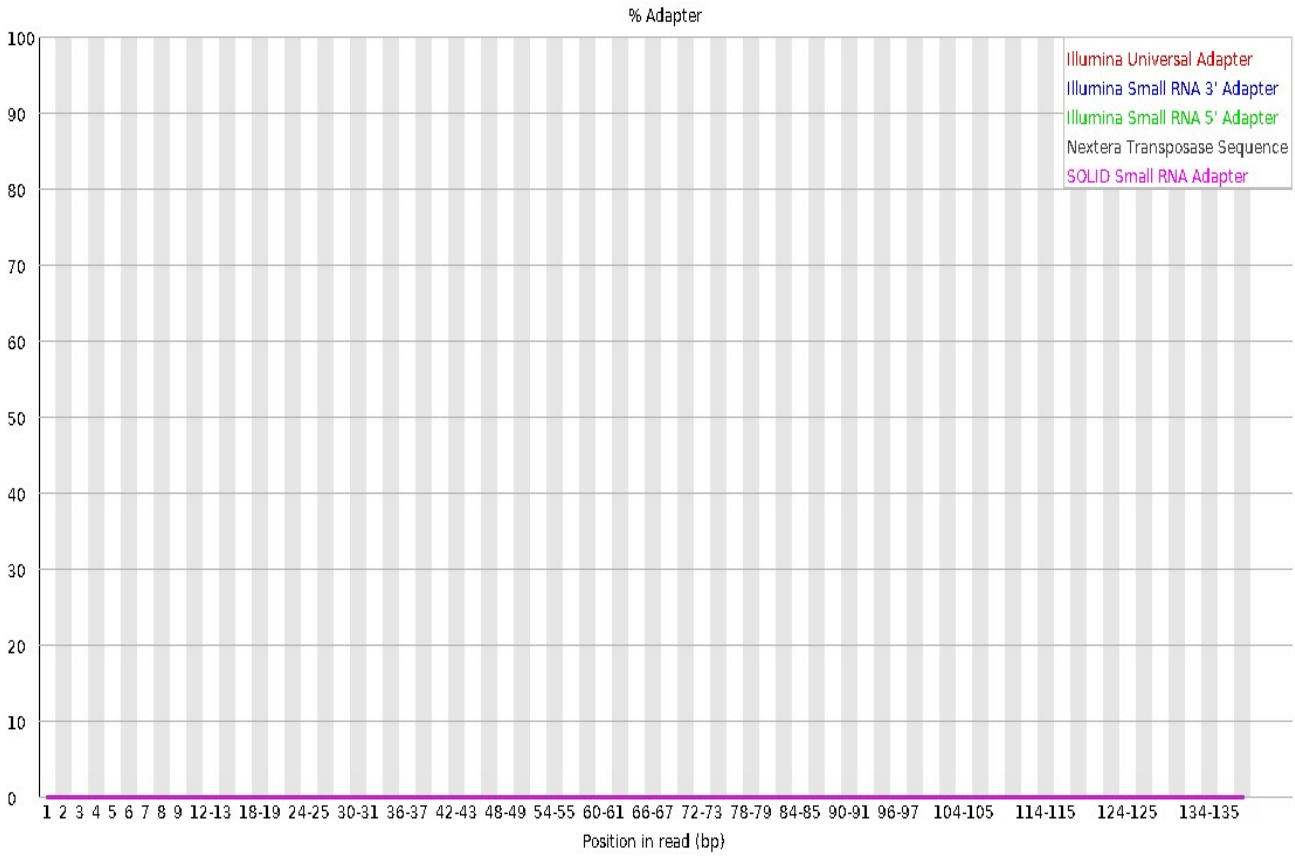
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
ATCGGAAGAGCACACGTCTGAACTCCAGTCACCGCTCATTATCTCGTATG	981789	1.044395141425324	TruSeq Adapter, Index 2 (97% over 36bp)

Adapter Content



Produced by FastQC (version 0.11.7)