Summary

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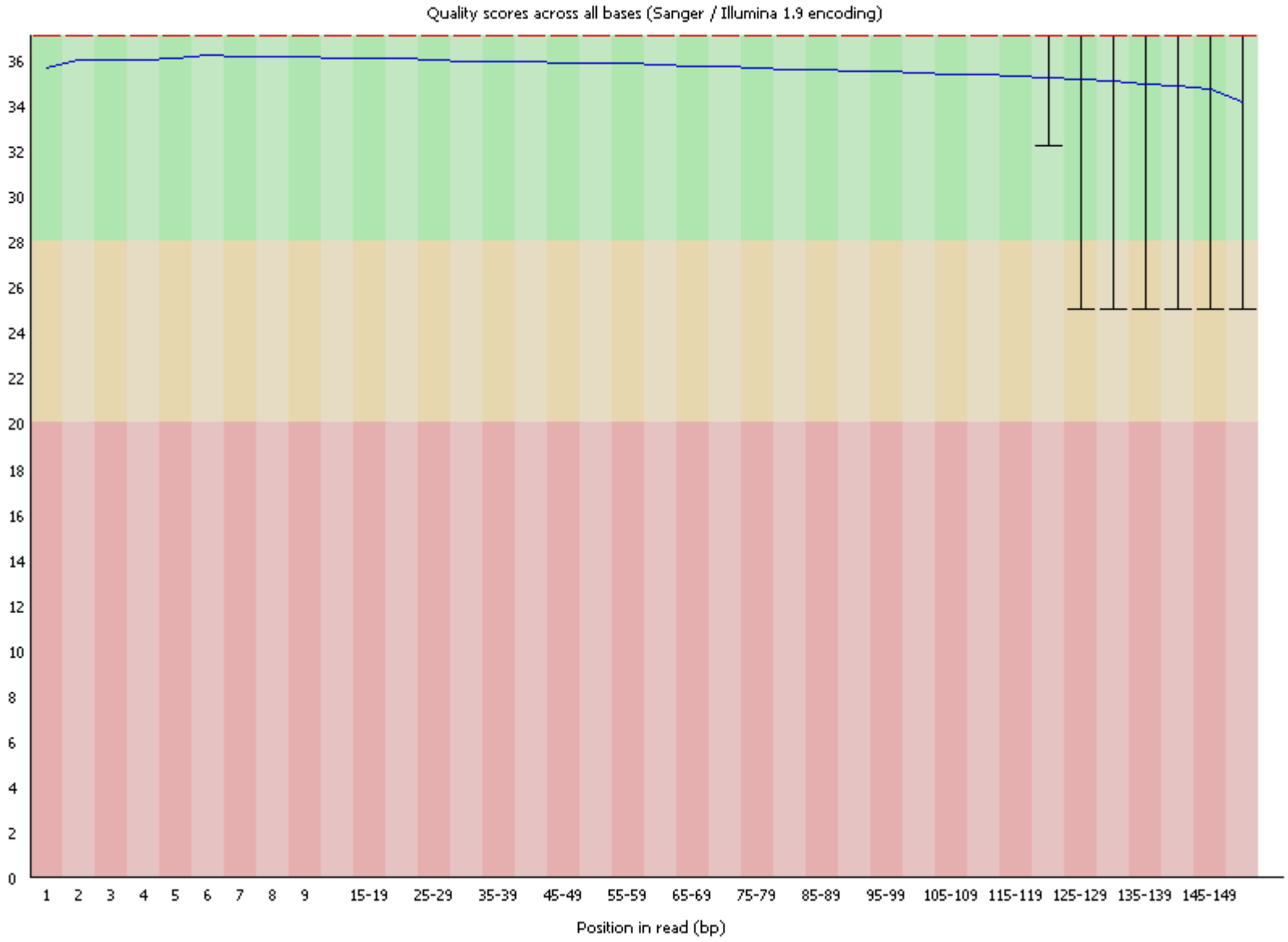
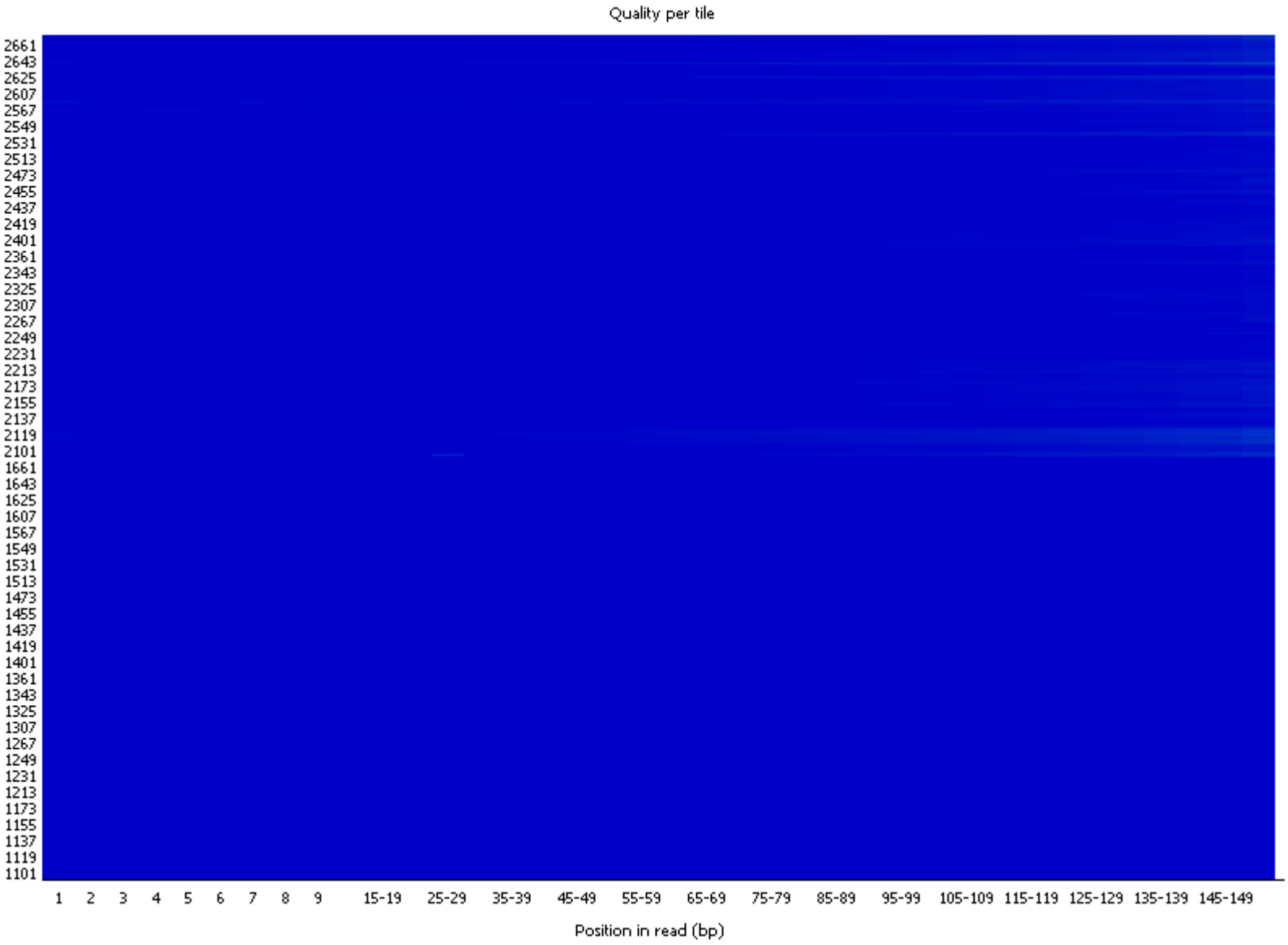
Basic Statistics

Measure	Value
Filename	GFX0241451_HLC5KDSXY.hg38.sorted.marked.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	546351097
Sequences flagged as poor quality	0
Sequence length	30-151
%GC	42

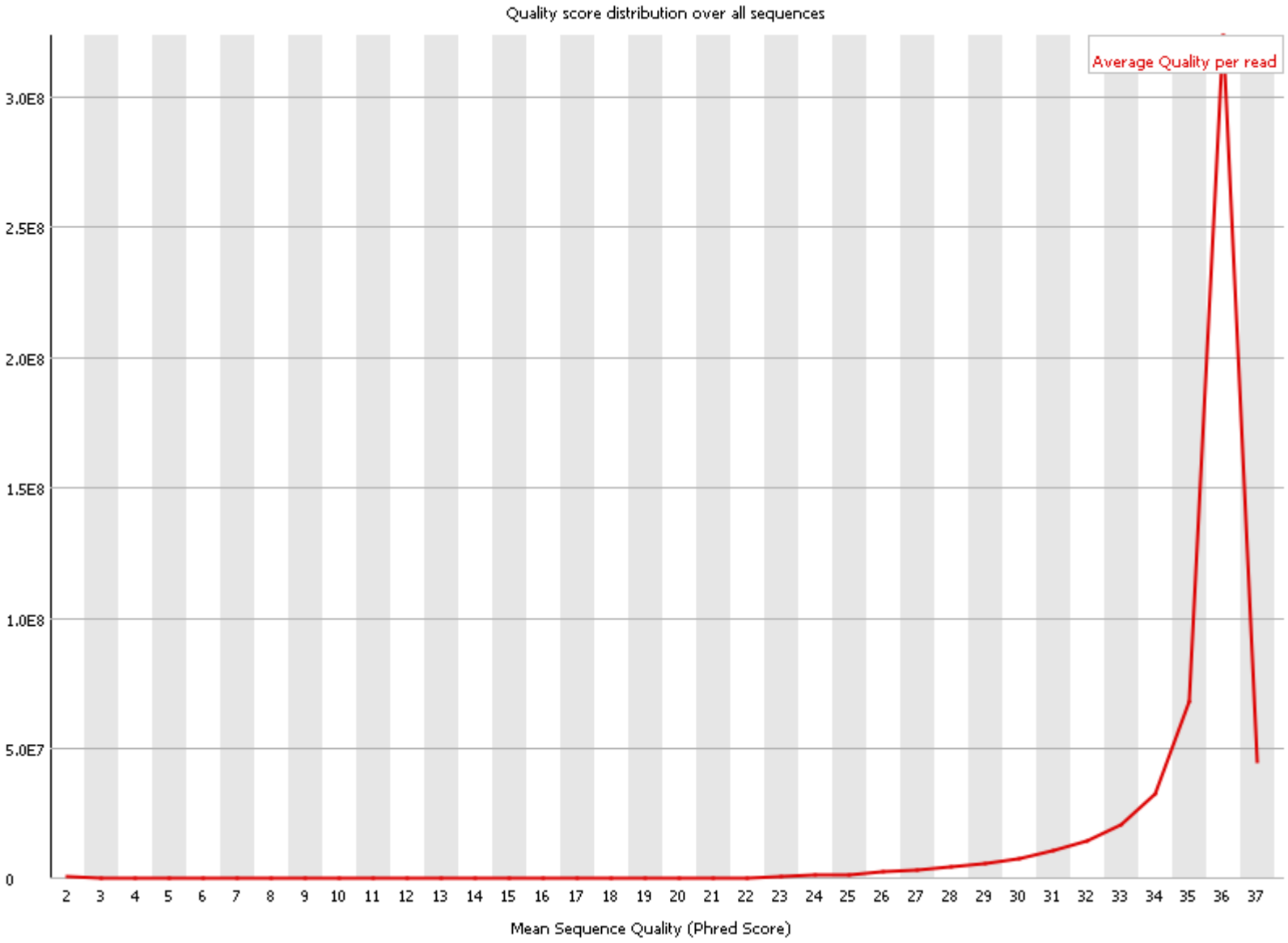
Per base sequence quality



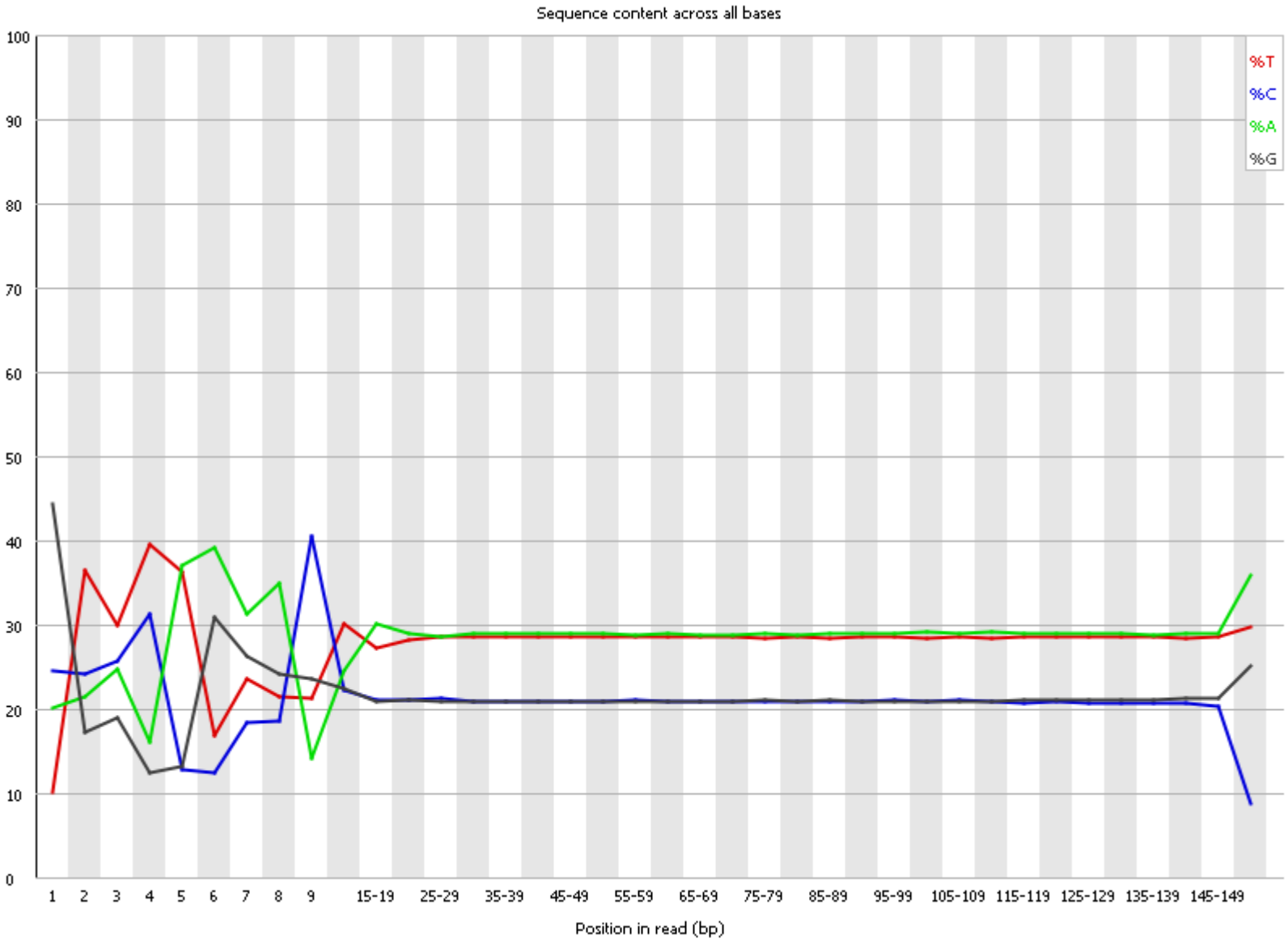
Per tile sequence quality



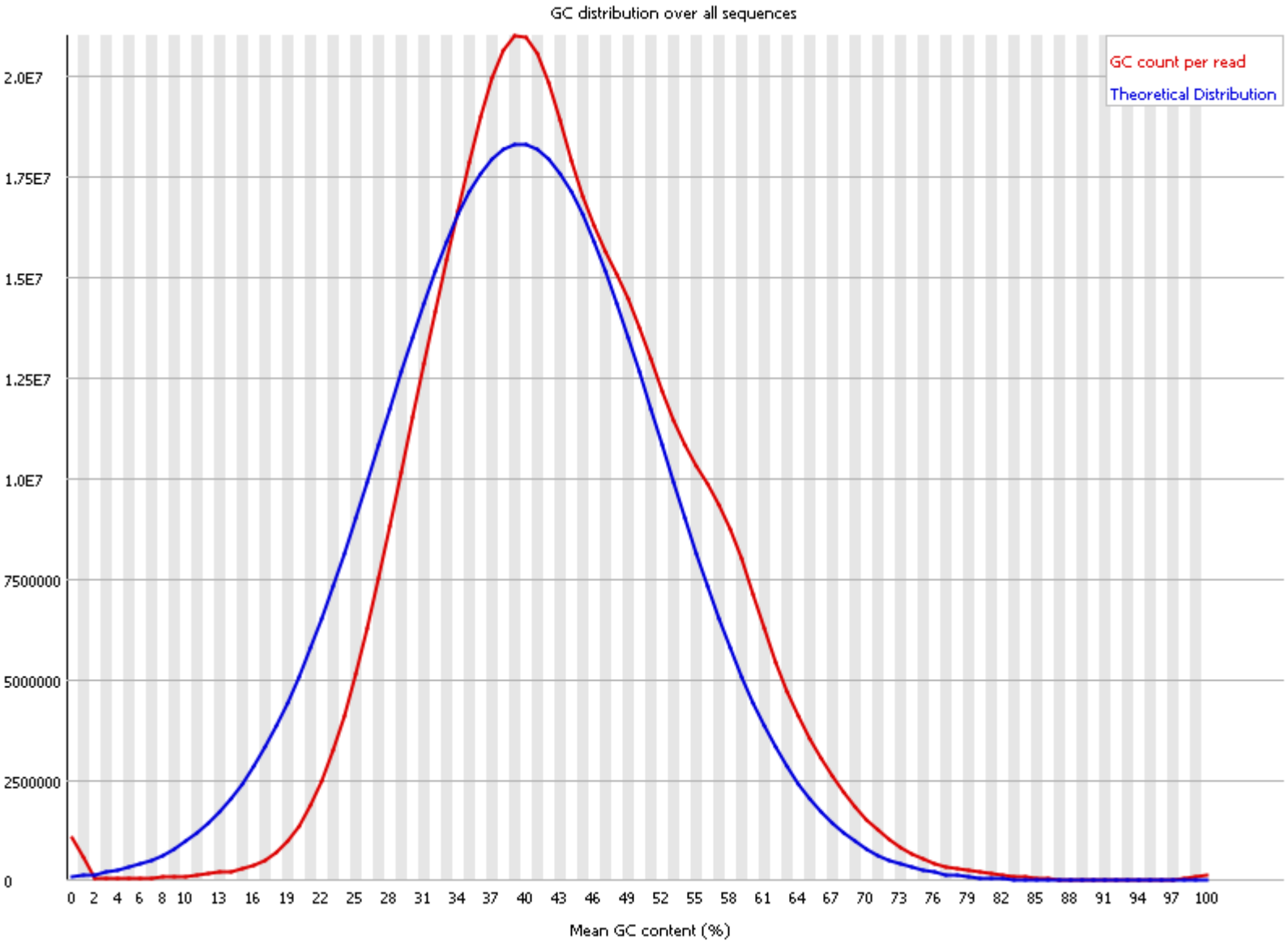
Per sequence quality scores



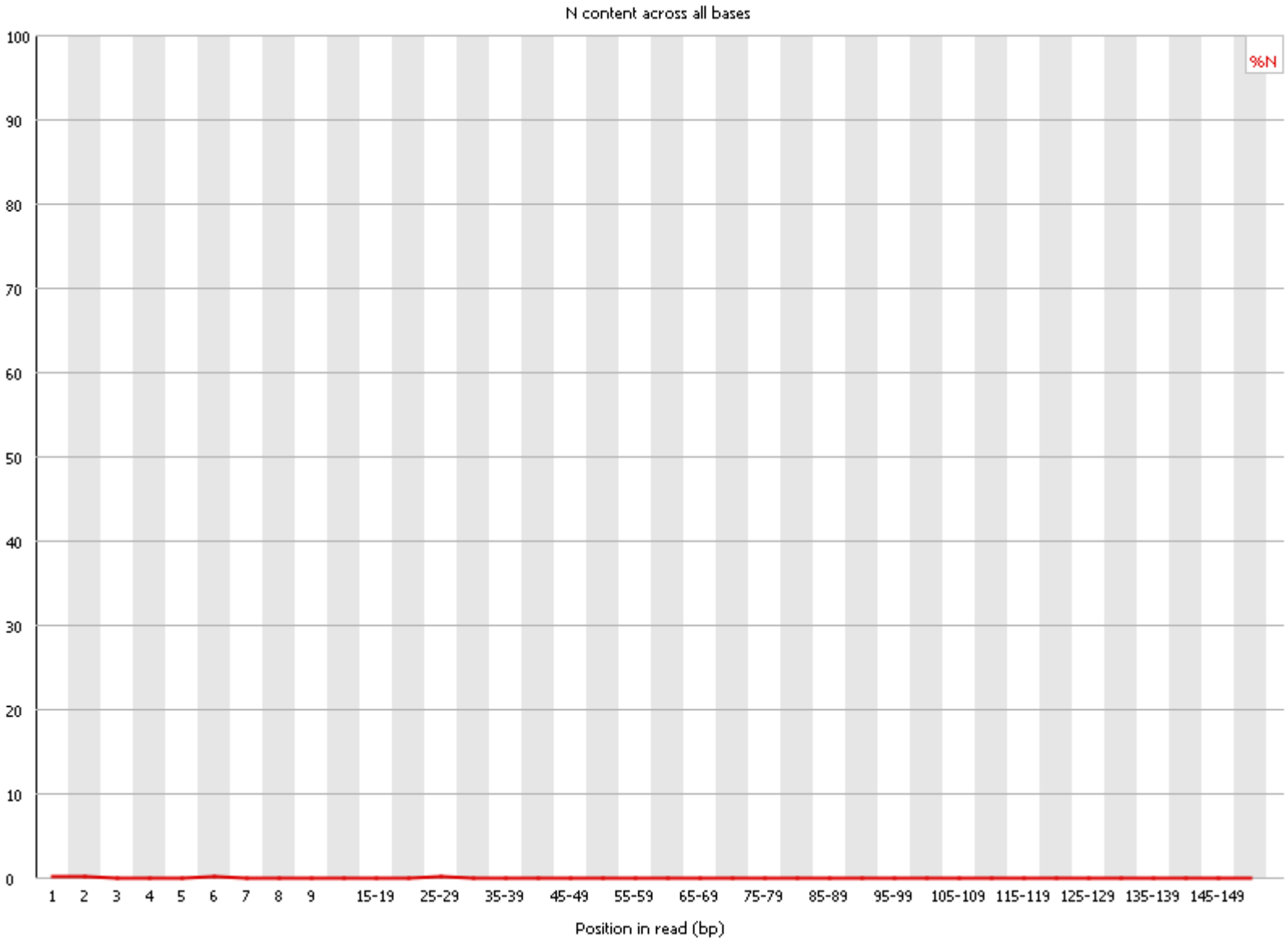
Per base sequence content



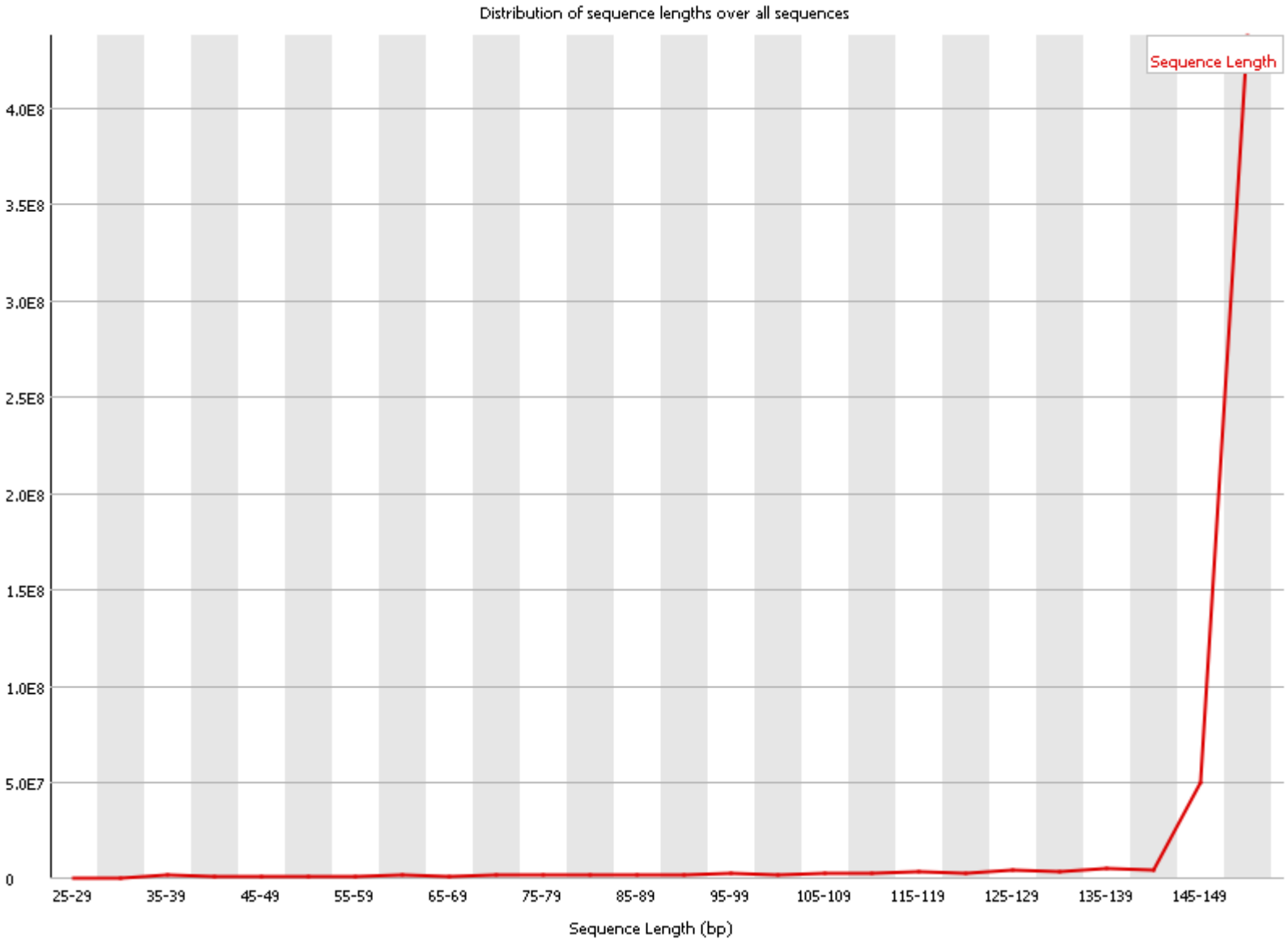
Per sequence GC content



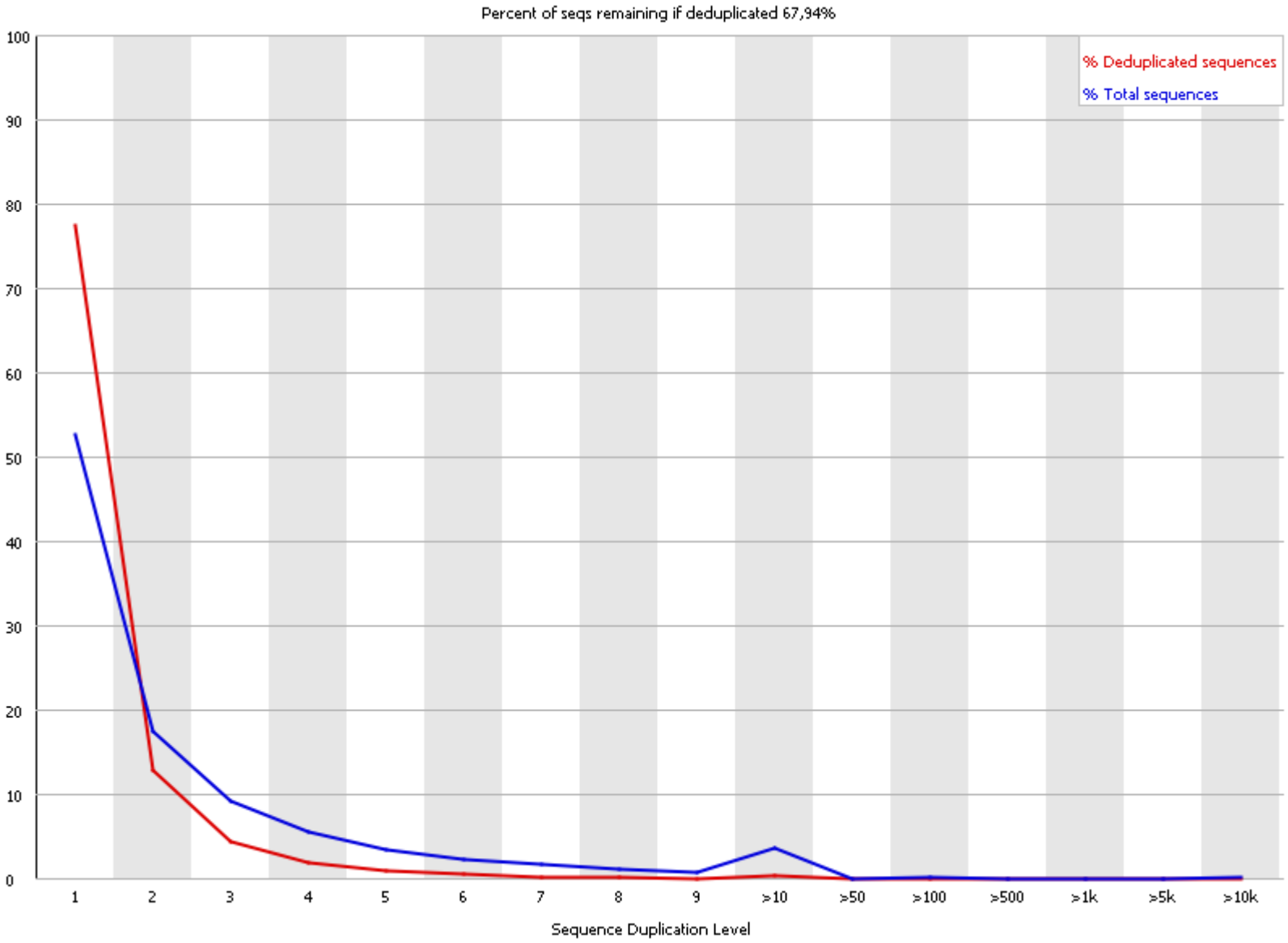
Per base N content



Sequence Length Distribution



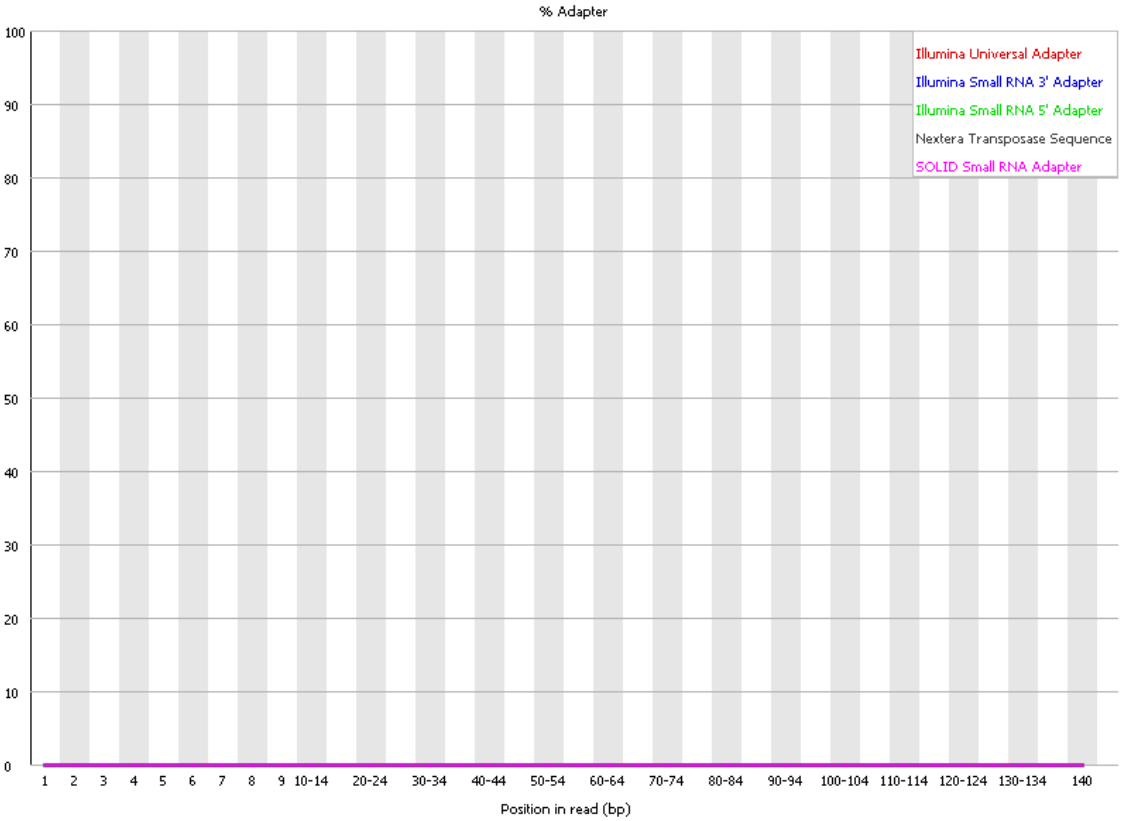
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1032903	0.18905480480805184	No Hit

Adapter Content



Produced by FastQC (version 0.11.9)