












## Summary

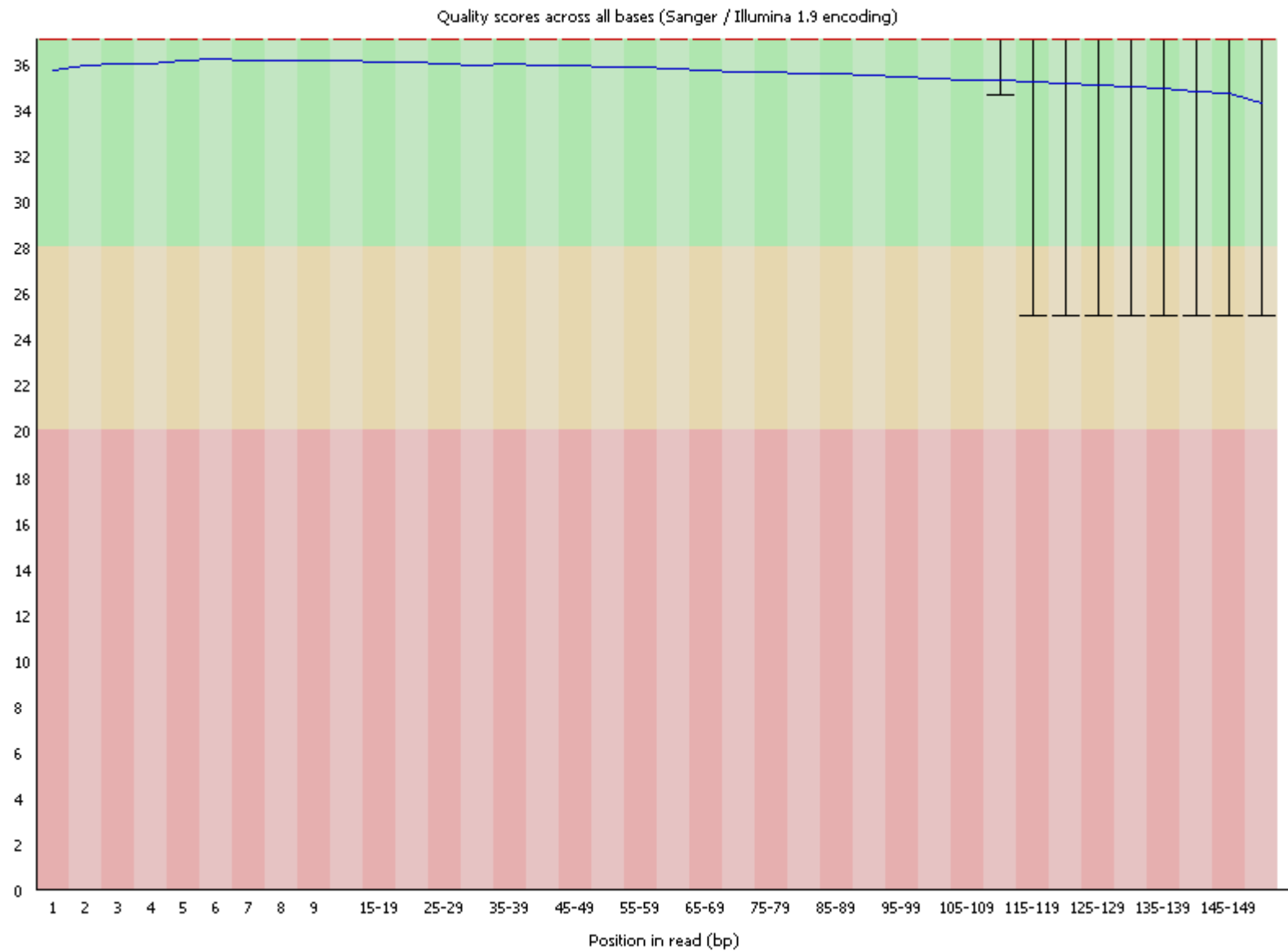
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## Basic Statistics

Measure	Value
Filename	GFX0241451_HMV32DSXY.hg38.sorted.marked.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	195752750
Sequences flagged as poor quality	0
Sequence length	30-151
%GC	42



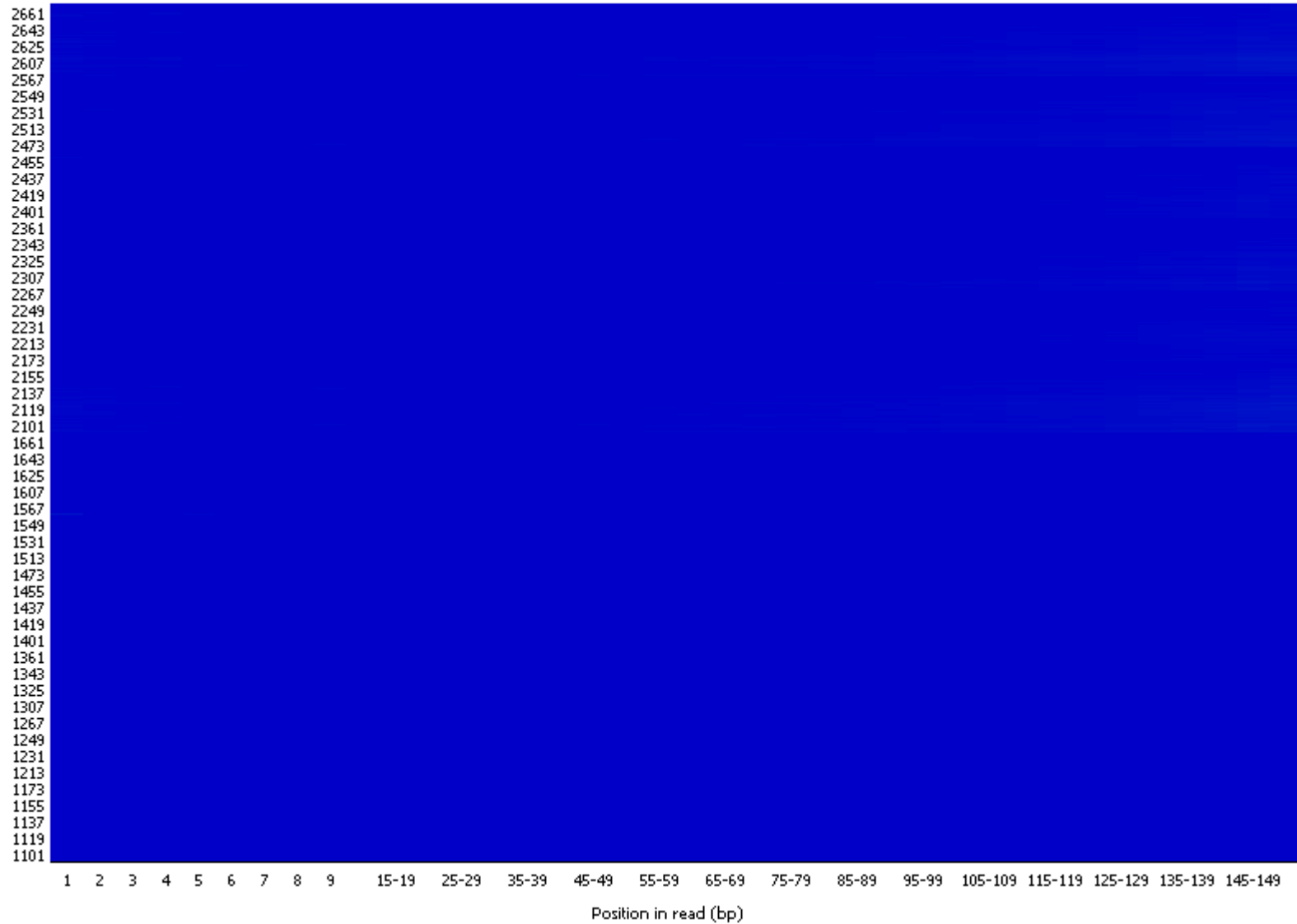
## Per base sequence quality





## Per tile sequence quality

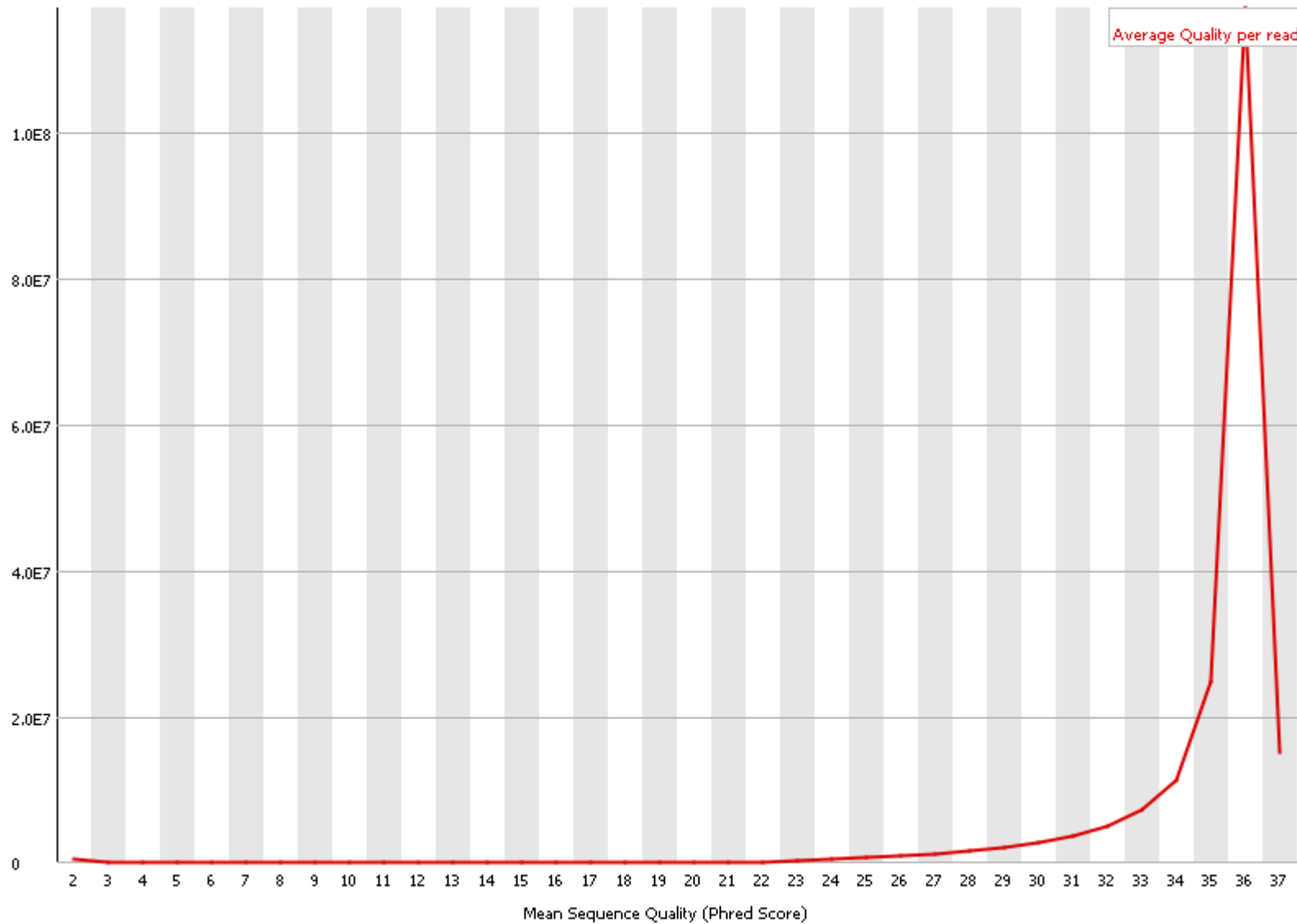
Quality per tile



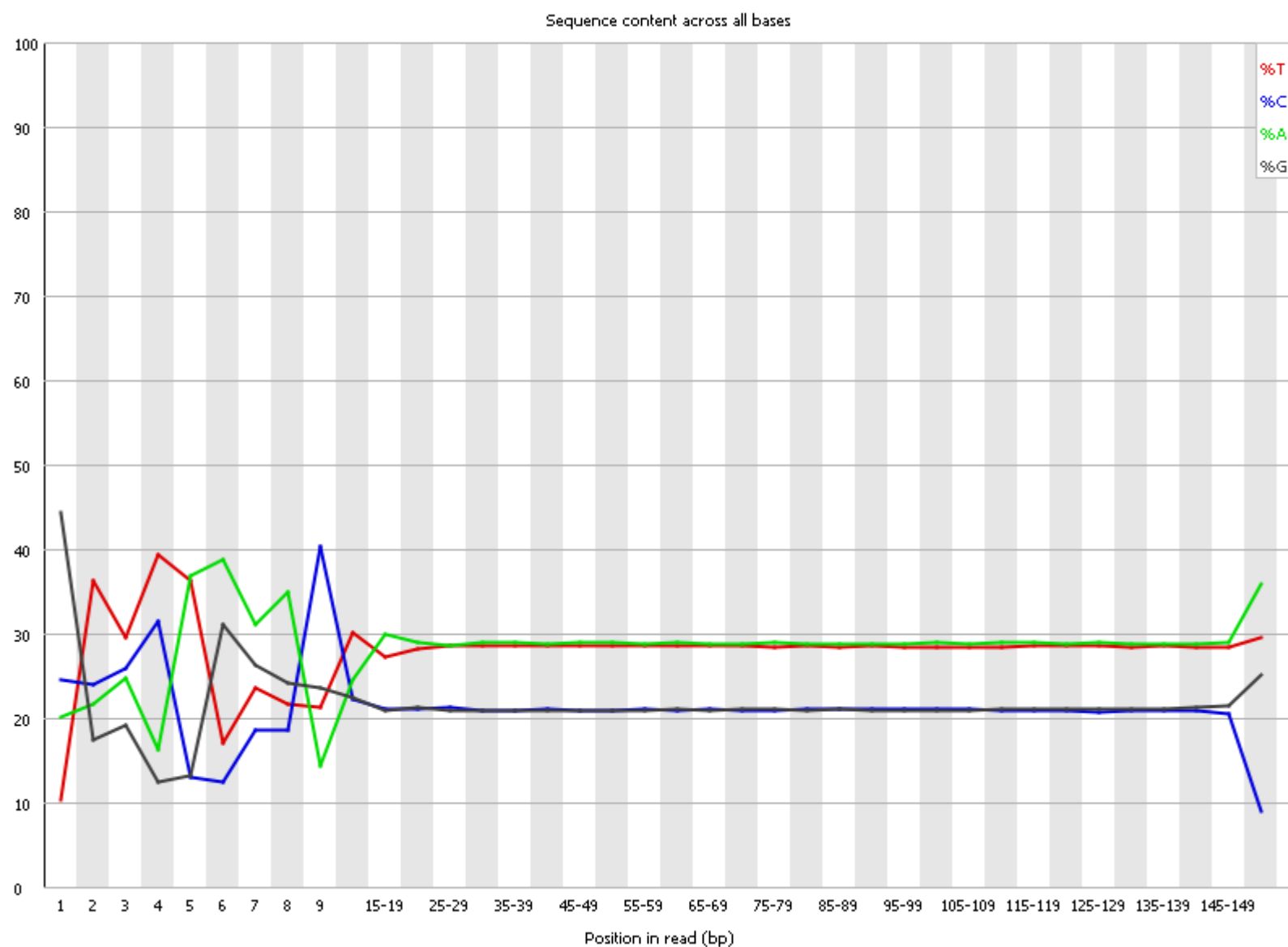


## Per sequence quality scores

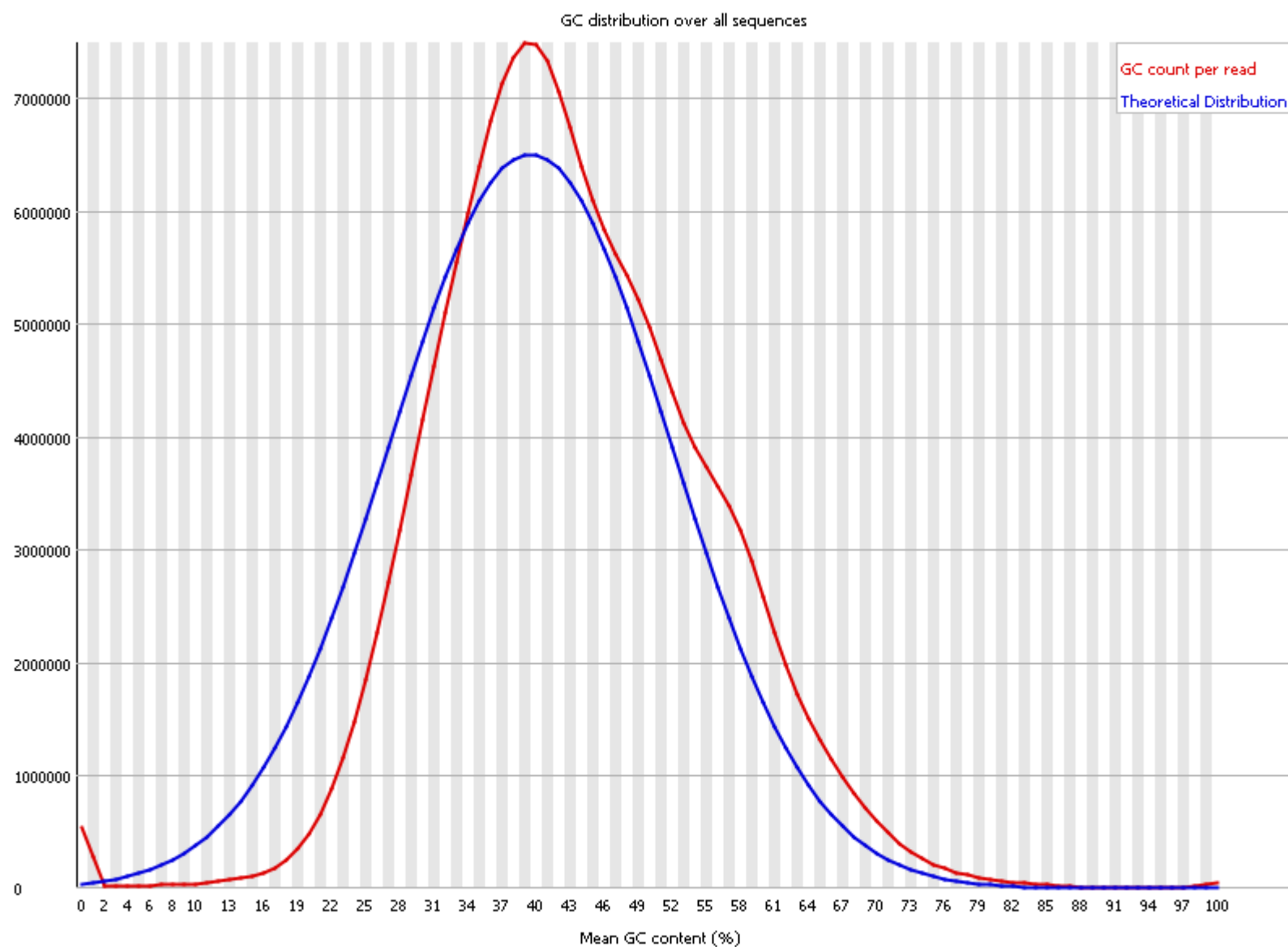
Quality score distribution over all sequences



## ✖ Per base sequence content



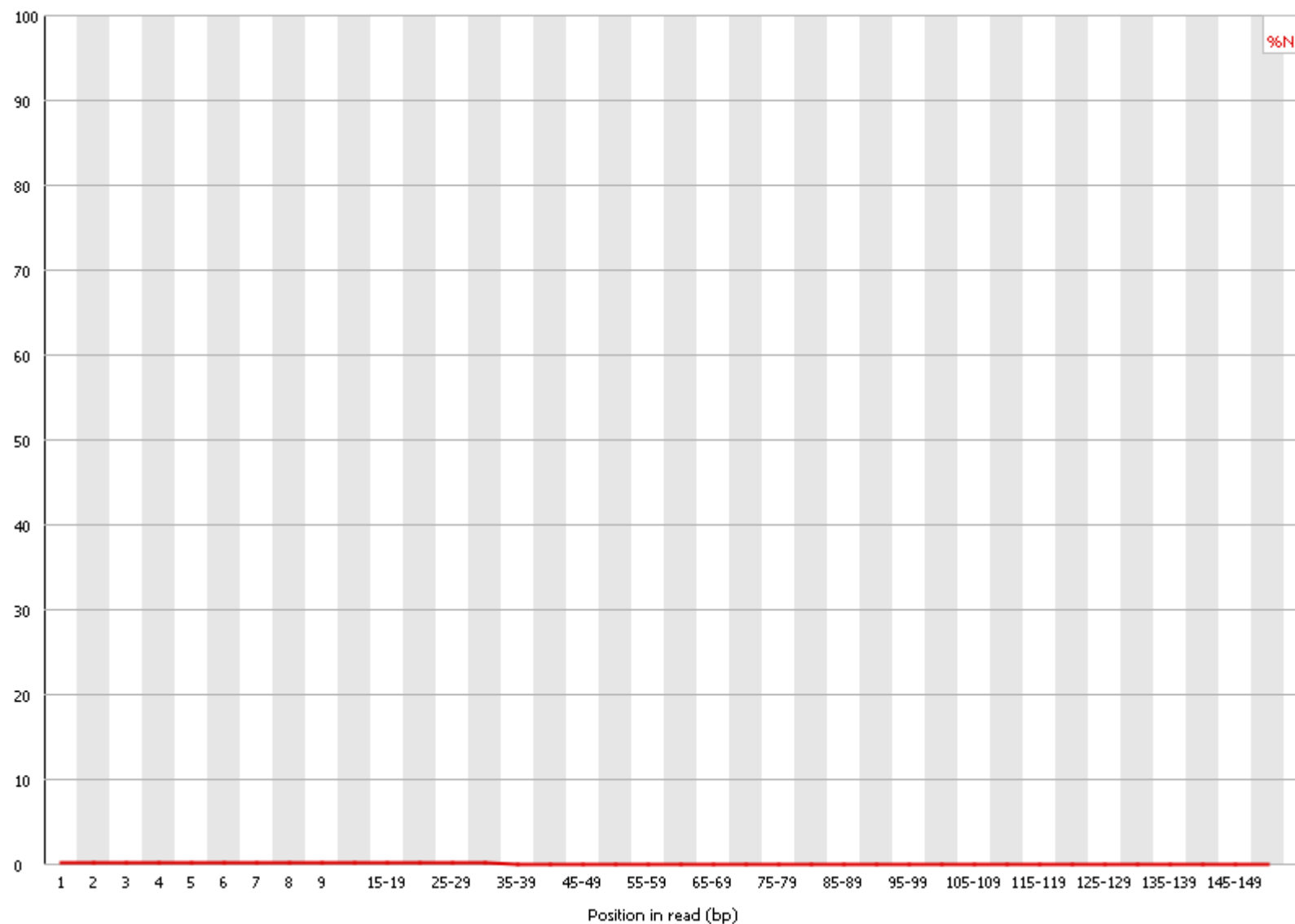
## ! Per sequence GC content



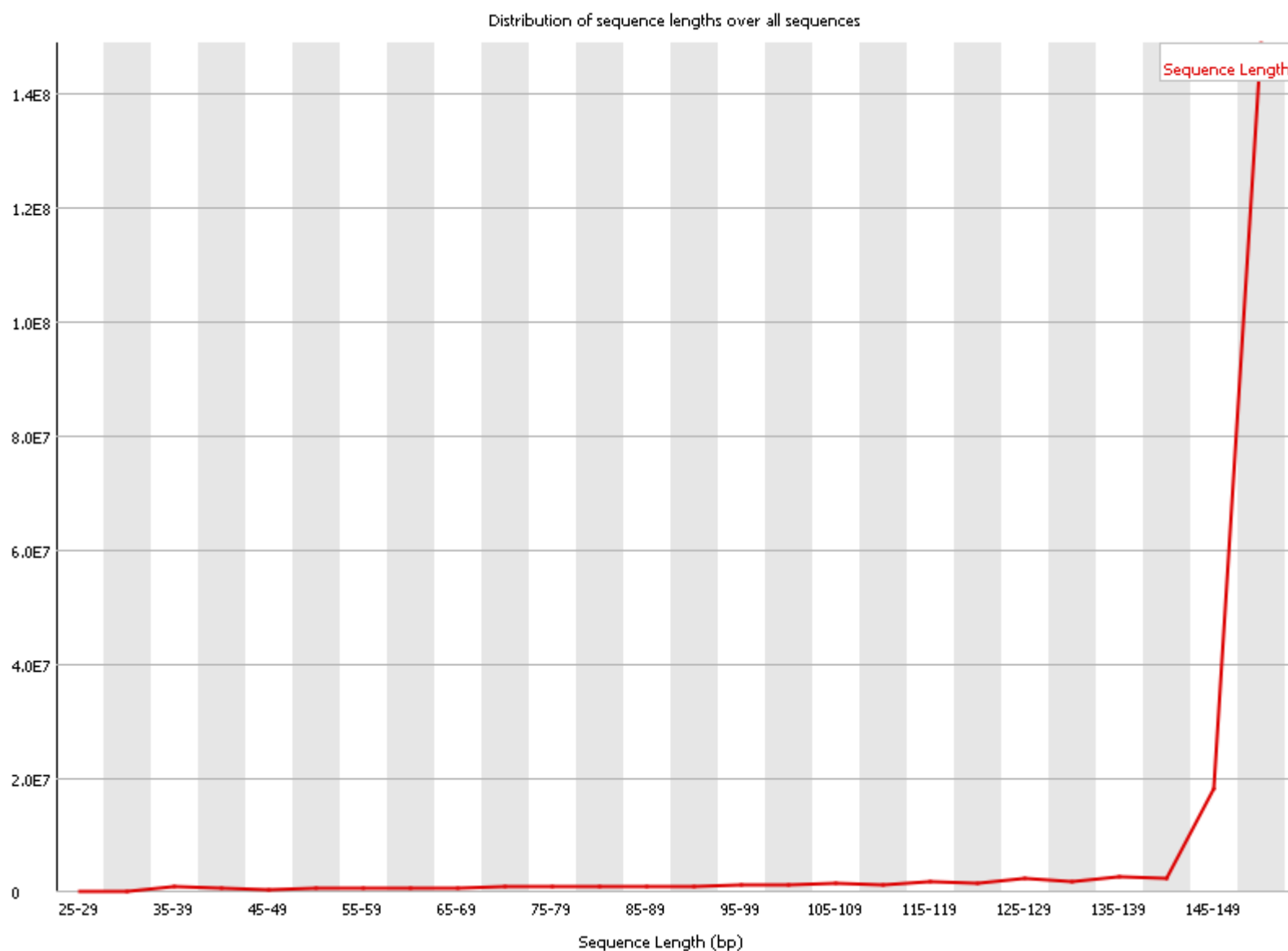


## Per base N content

N content across all bases



## Sequence Length Distribution

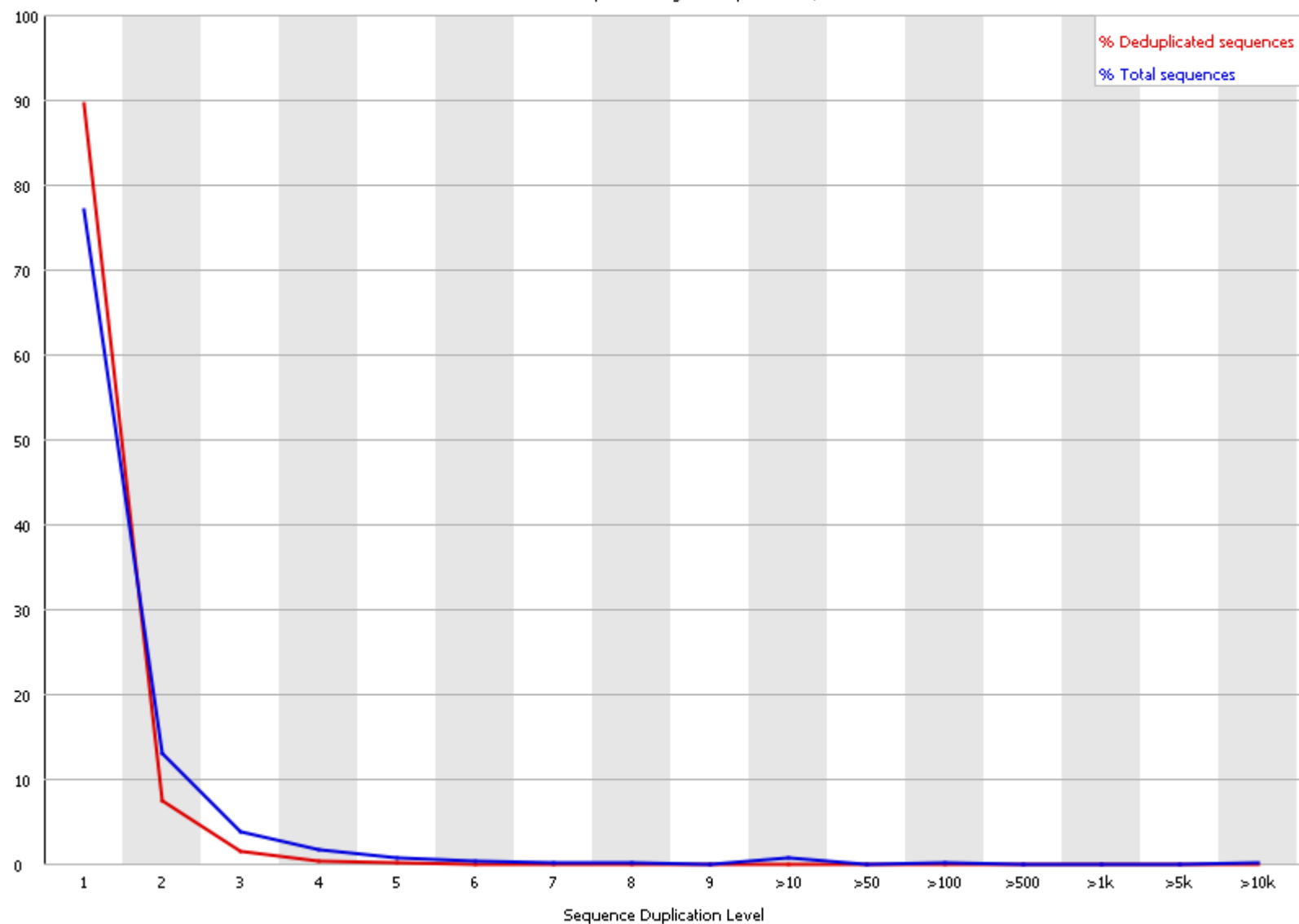


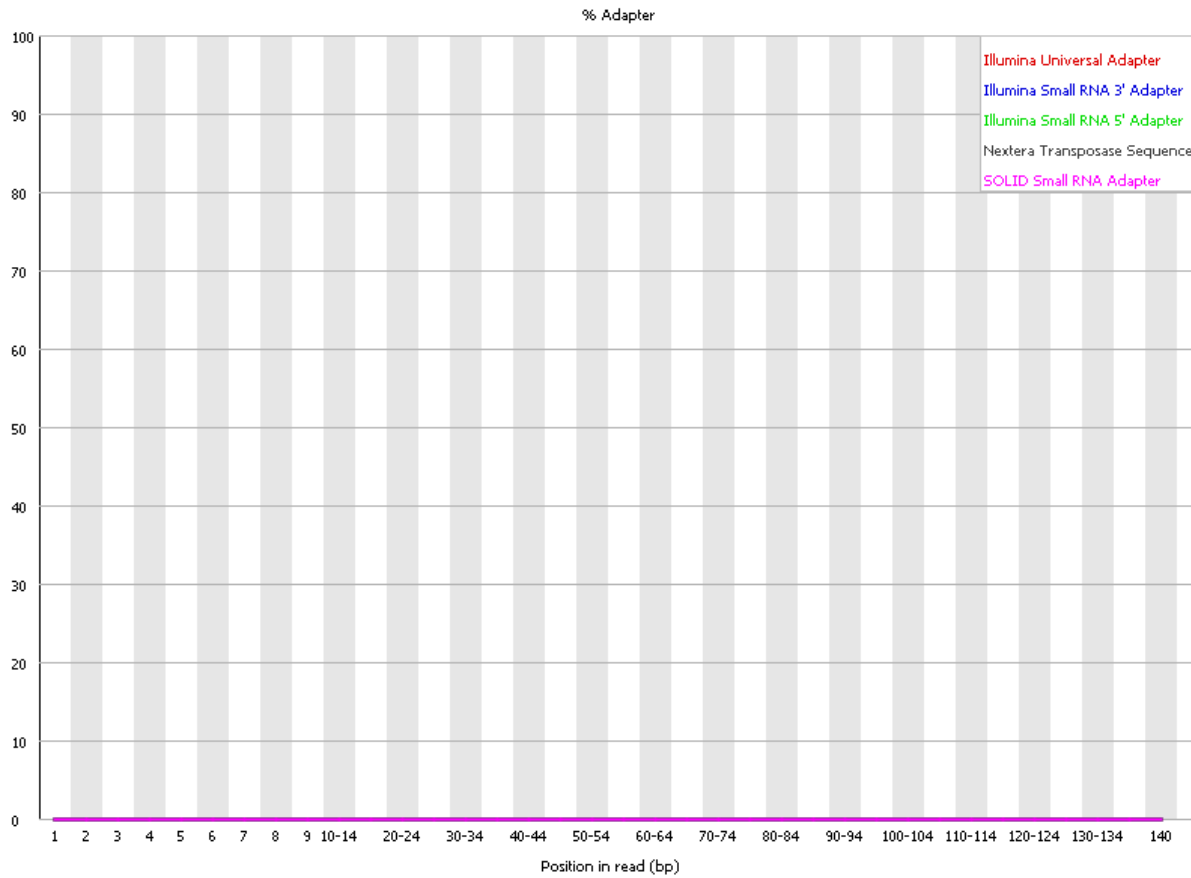




## Sequence Duplication Levels

Percent of seqs remaining if deduplicated 86,03%



[illegible]

Produced by [FastQC](#) (version 0.11.9)