












## Summary

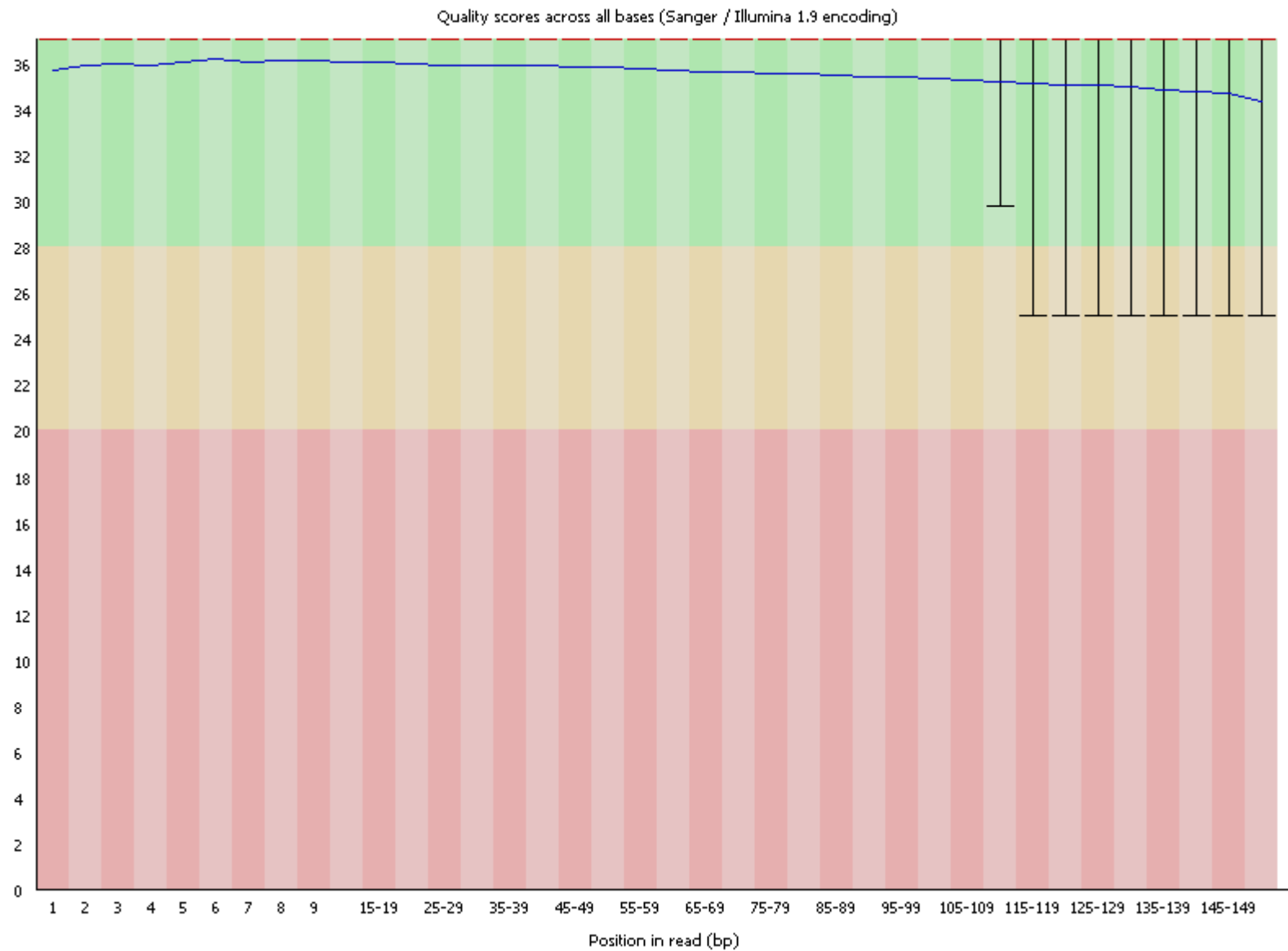
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## Basic Statistics

Measure	Value
Filename	GFX0241451_HMVJLDSXY.hg38.sorted.marked.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	214912996
Sequences flagged as poor quality	0
Sequence length	30-151
%GC	42

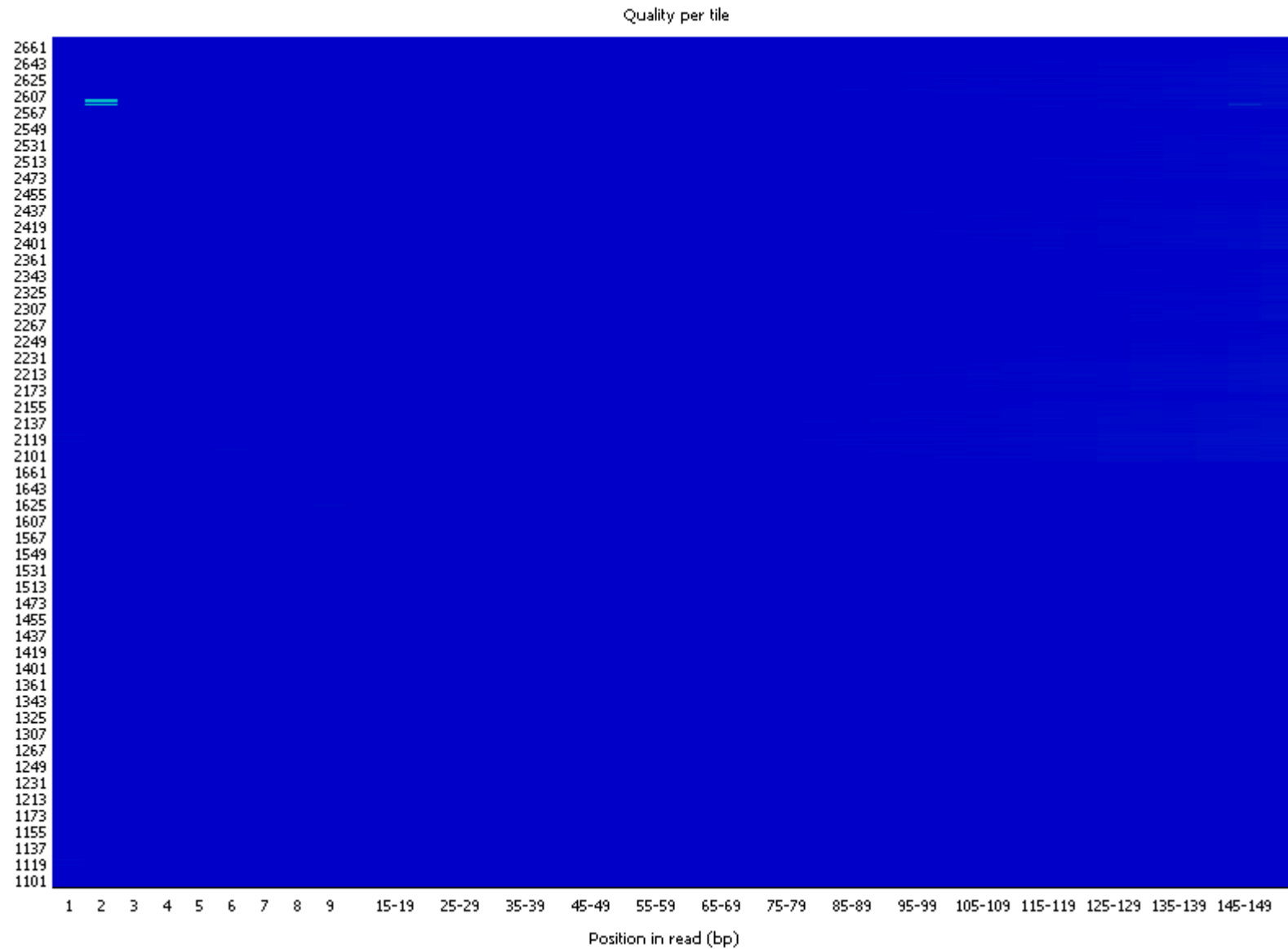


## Per base sequence quality





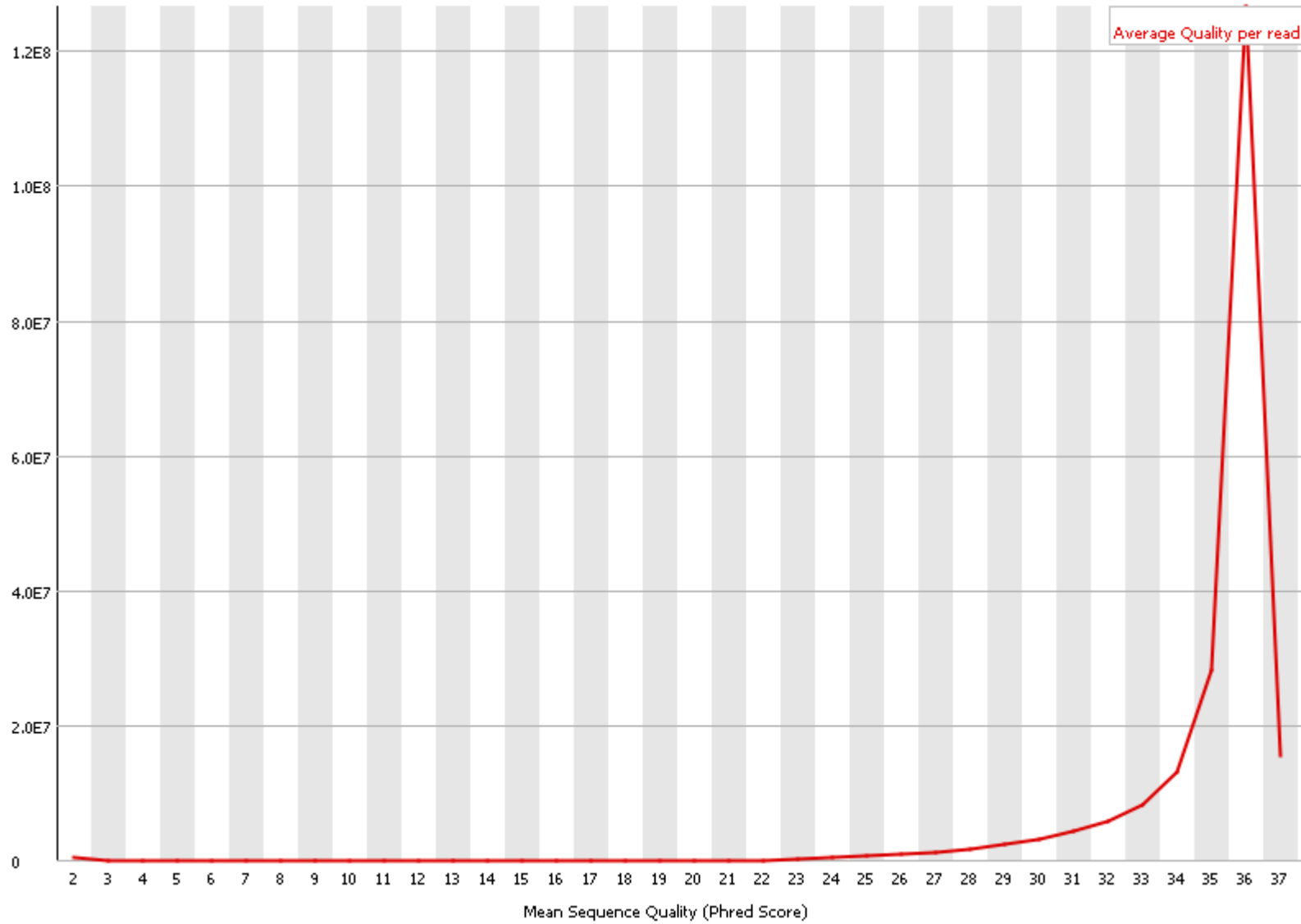
## ✓ Per tile sequence quality



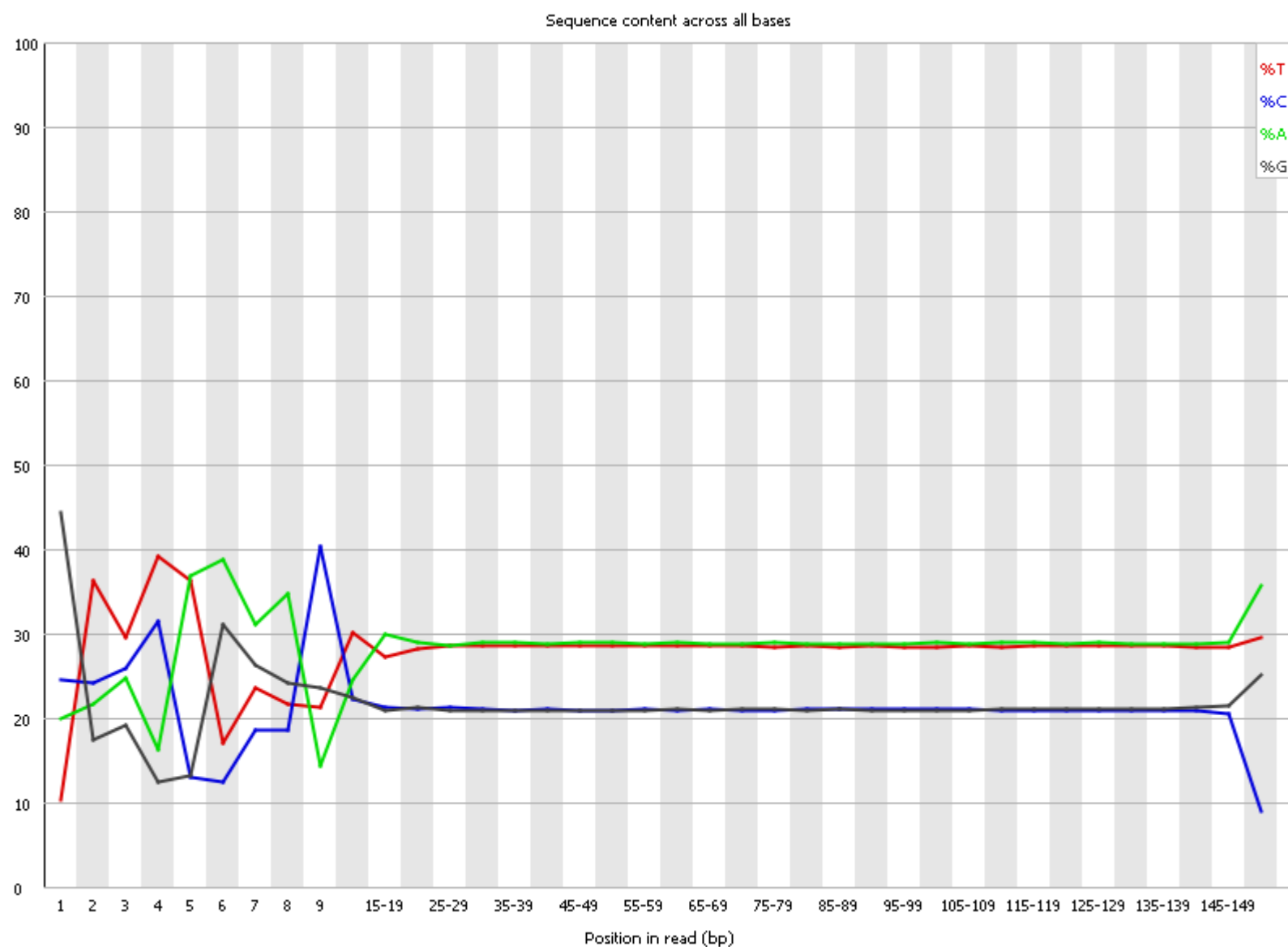


## Per sequence quality scores

Quality score distribution over all sequences



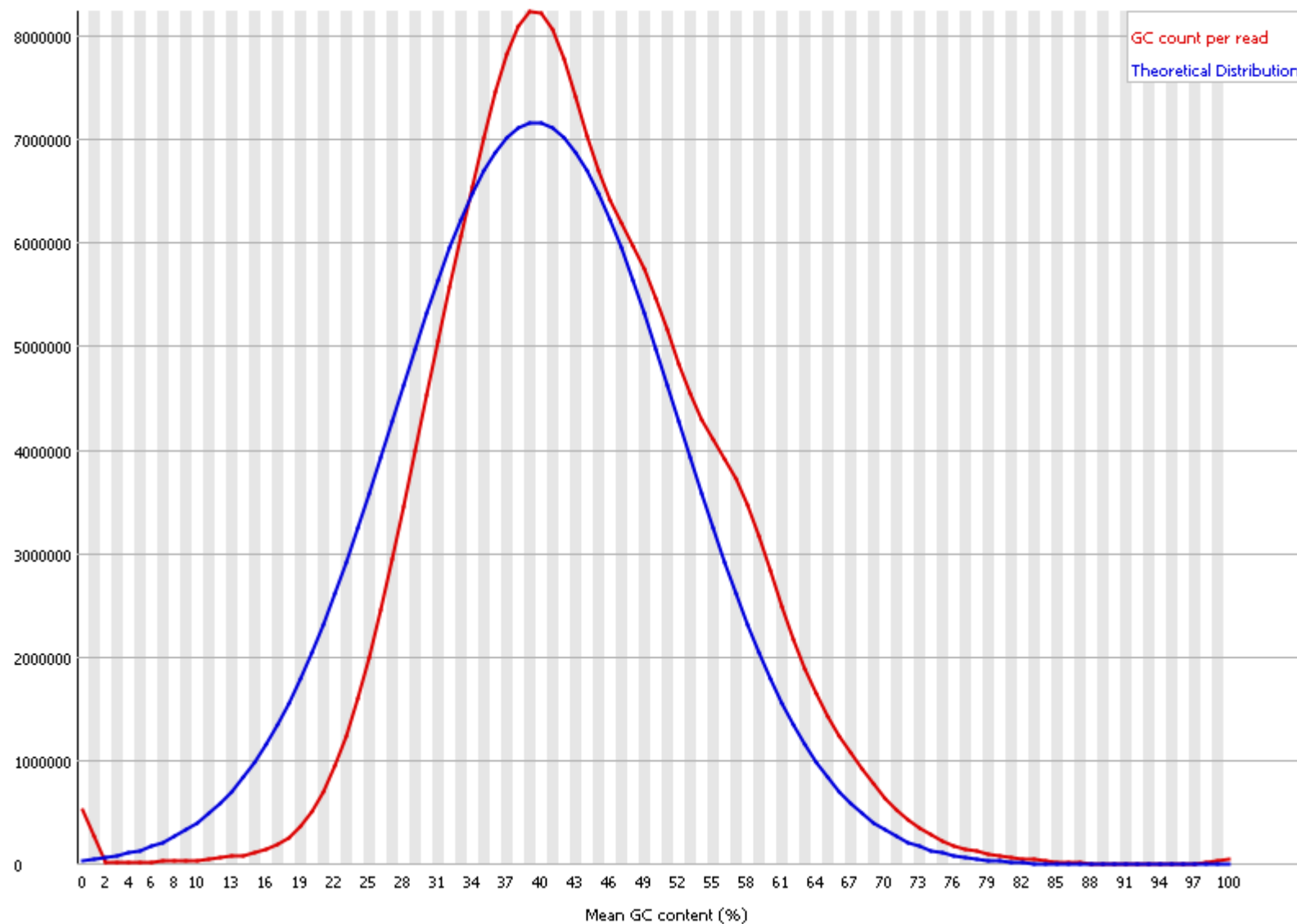
## ✖ Per base sequence content





## Per sequence GC content

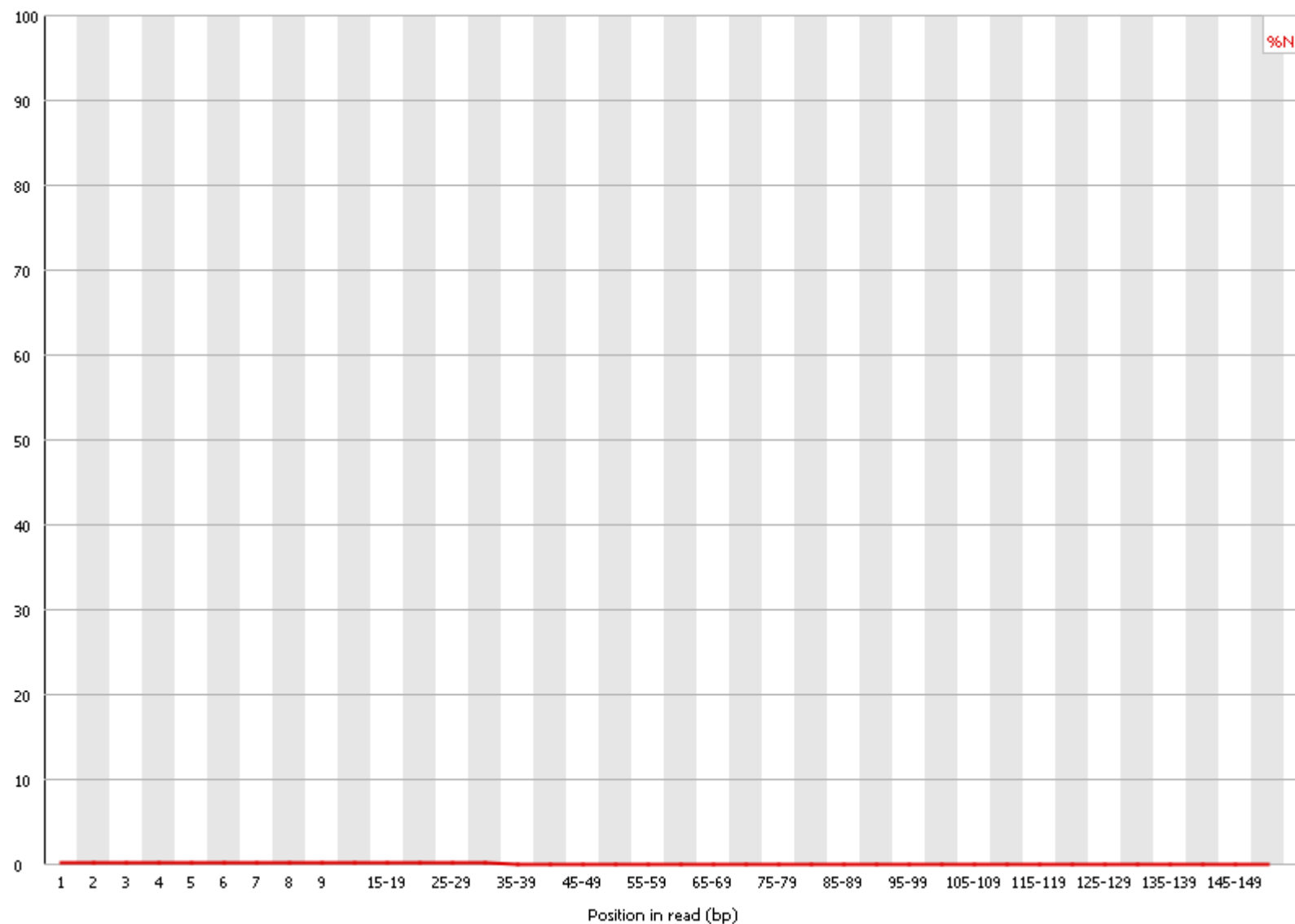
GC distribution over all sequences



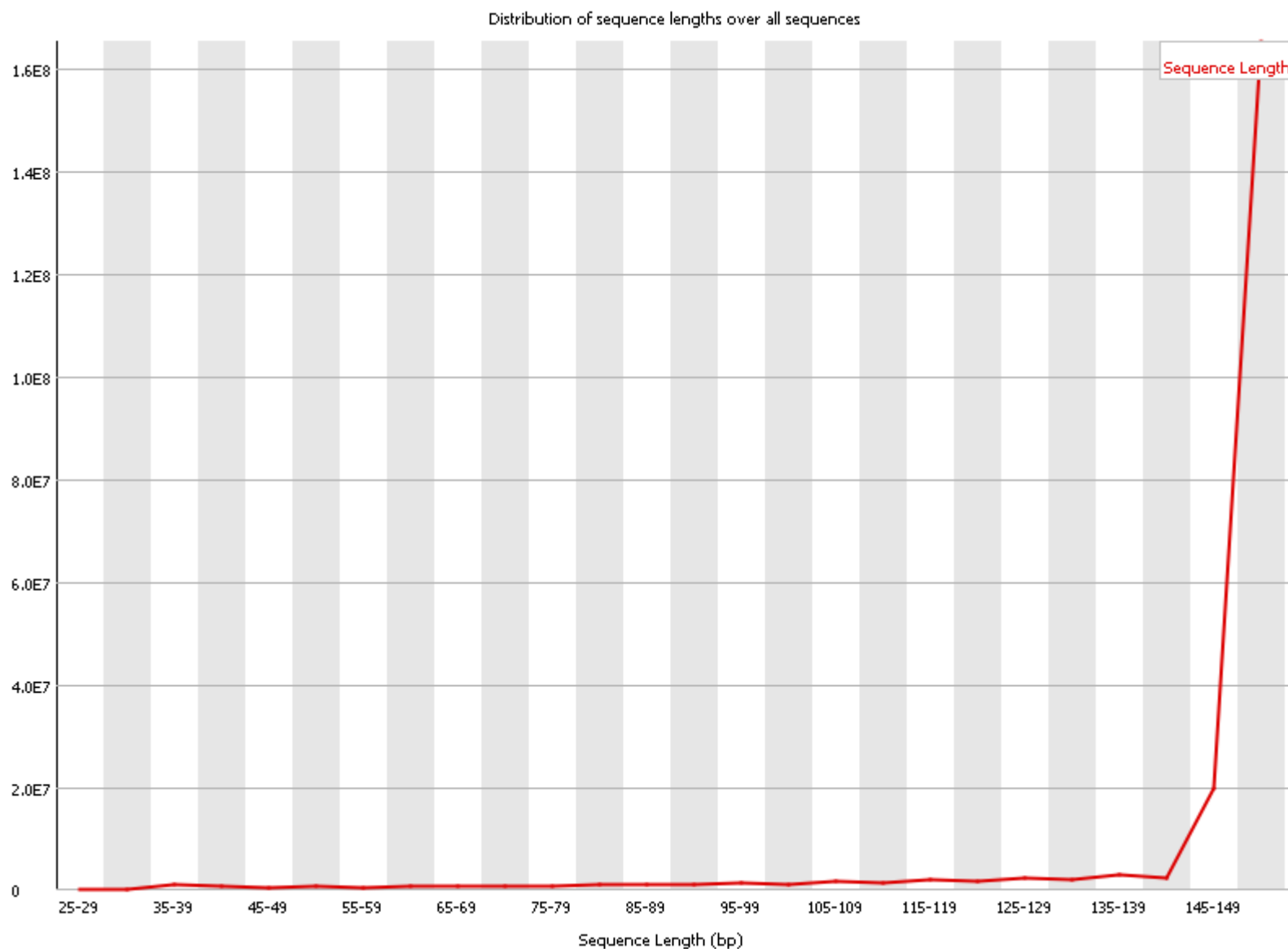


## Per base N content

N content across all bases



## Sequence Length Distribution

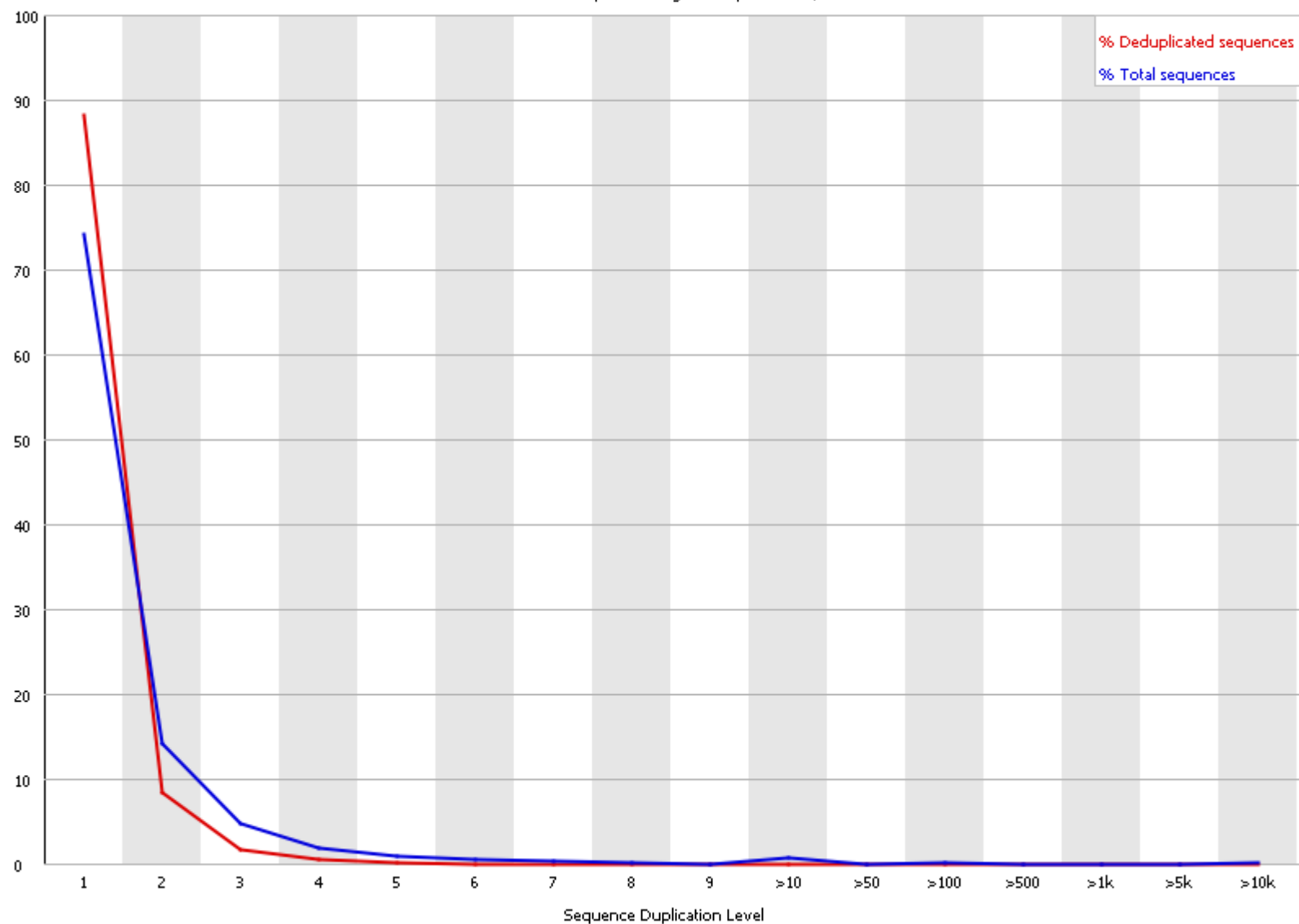


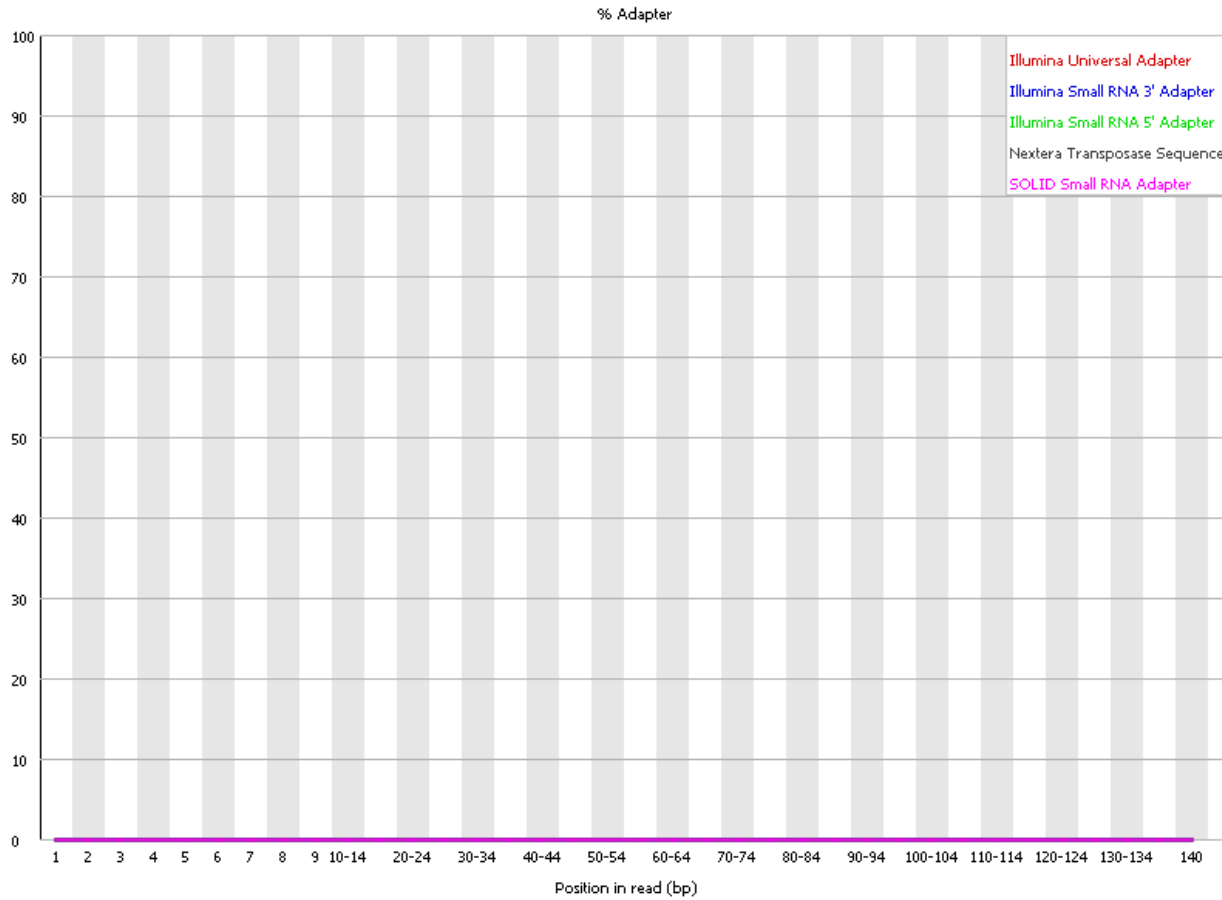




## Sequence Duplication Levels

Percent of seqs remaining if deduplicated 84,19%



[illegible]

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