












Summary

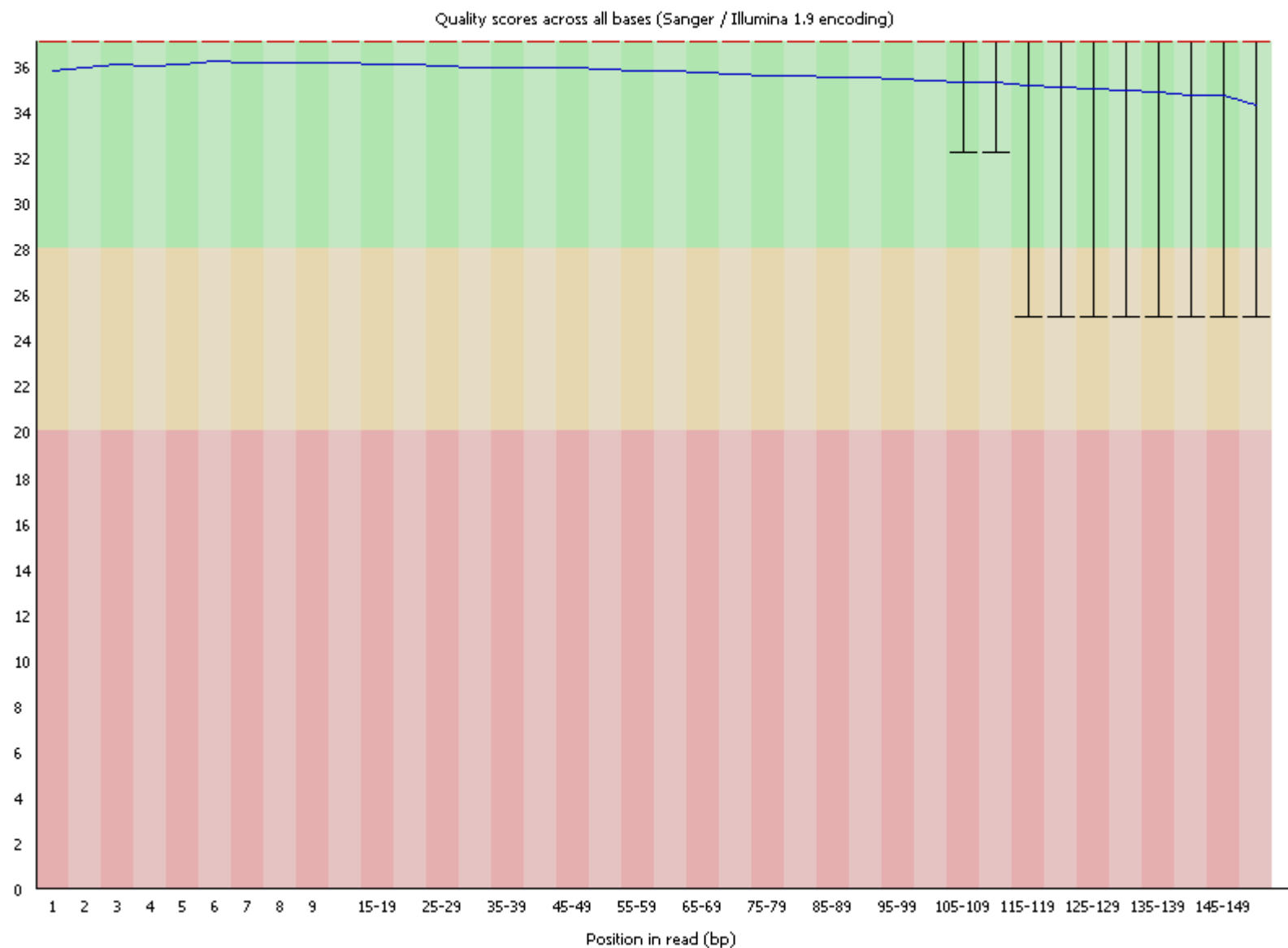
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Basic Statistics

Measure	Value
Filename	GFX0241451_HHVJGDSXY.hg38.sorted.marked.bam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	125878782
Sequences flagged as poor quality	0
Sequence length	30-151
%GC	42



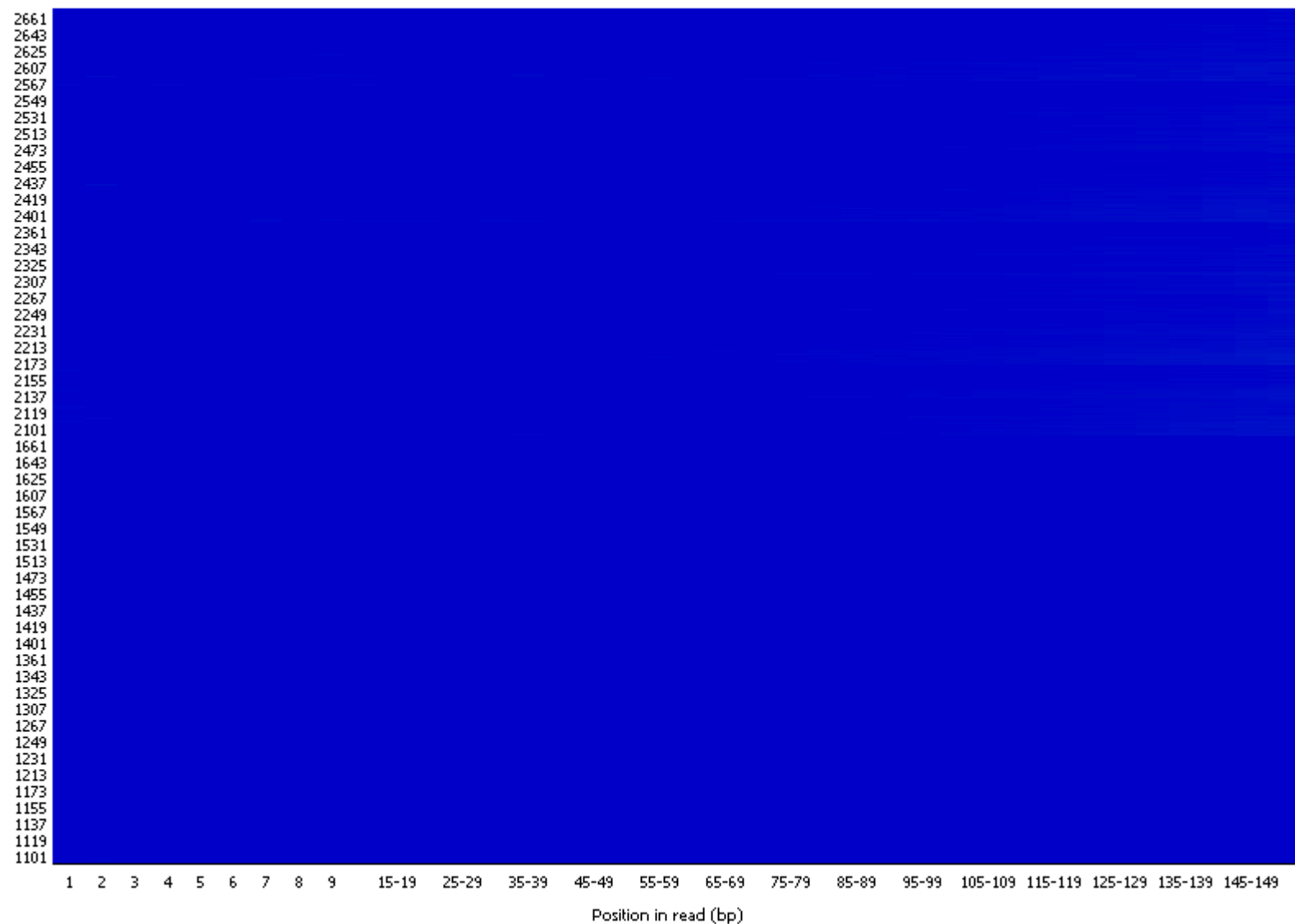
Per base sequence quality





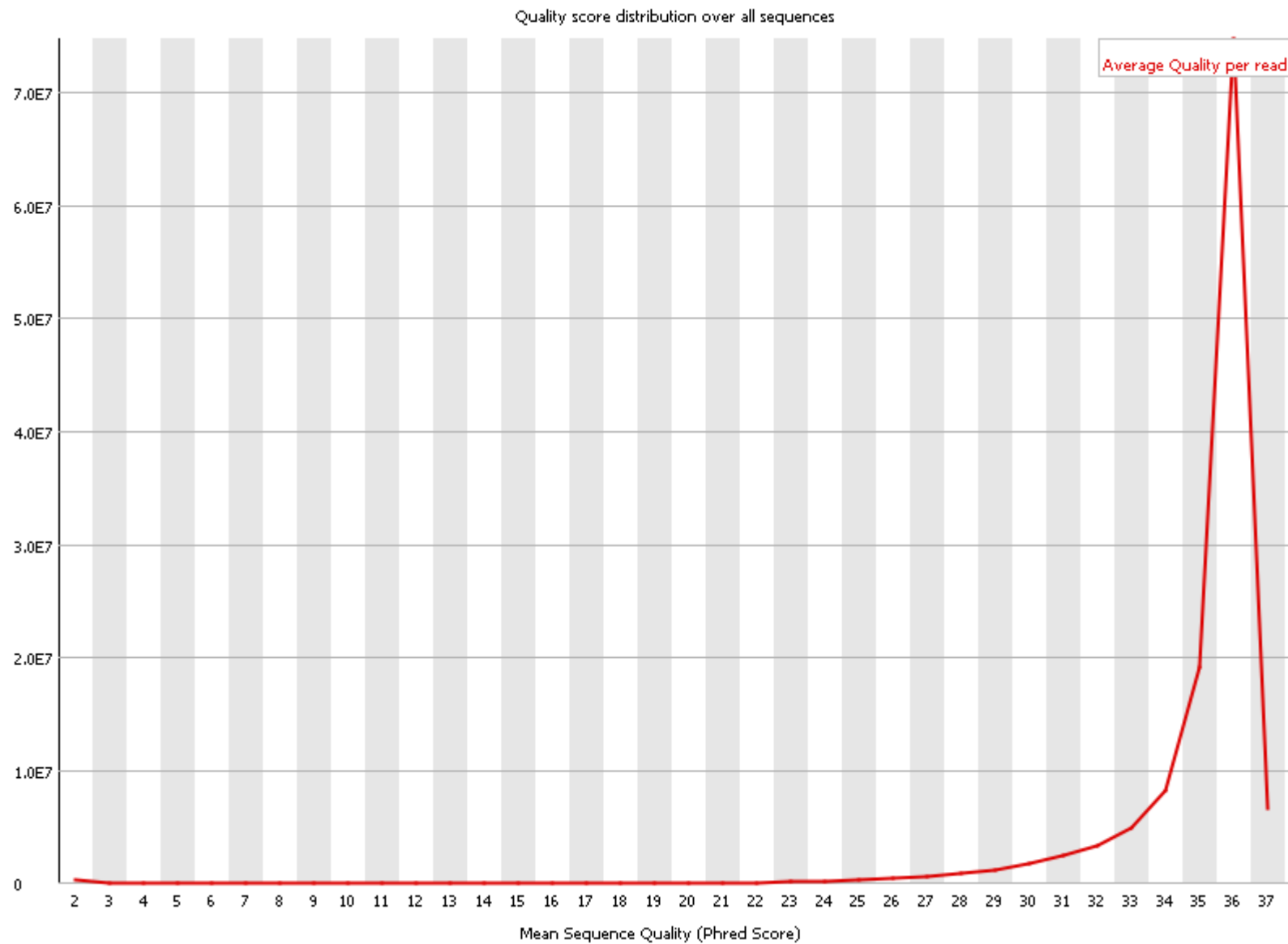
Per tile sequence quality

Quality per tile

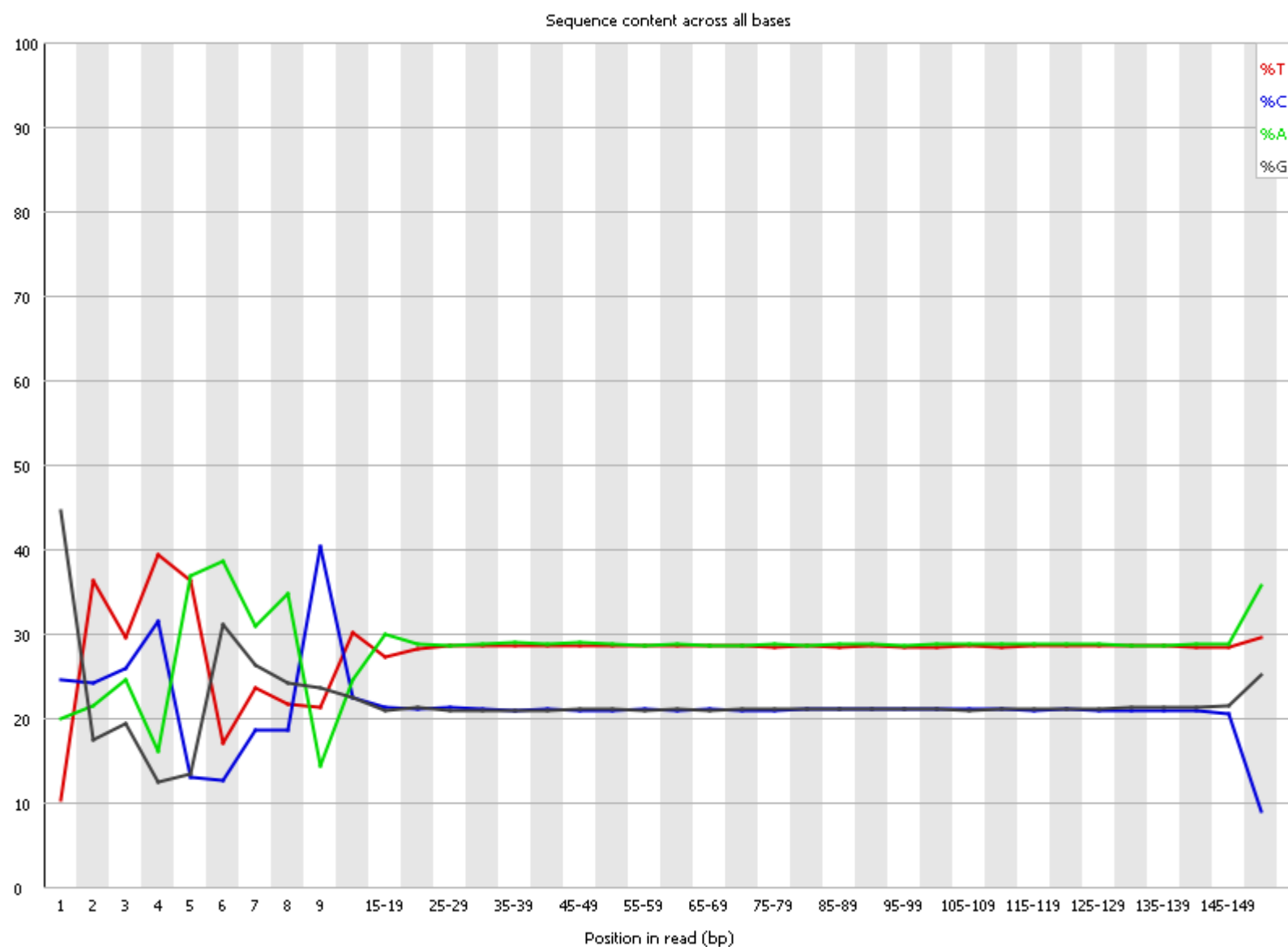




Per sequence quality scores



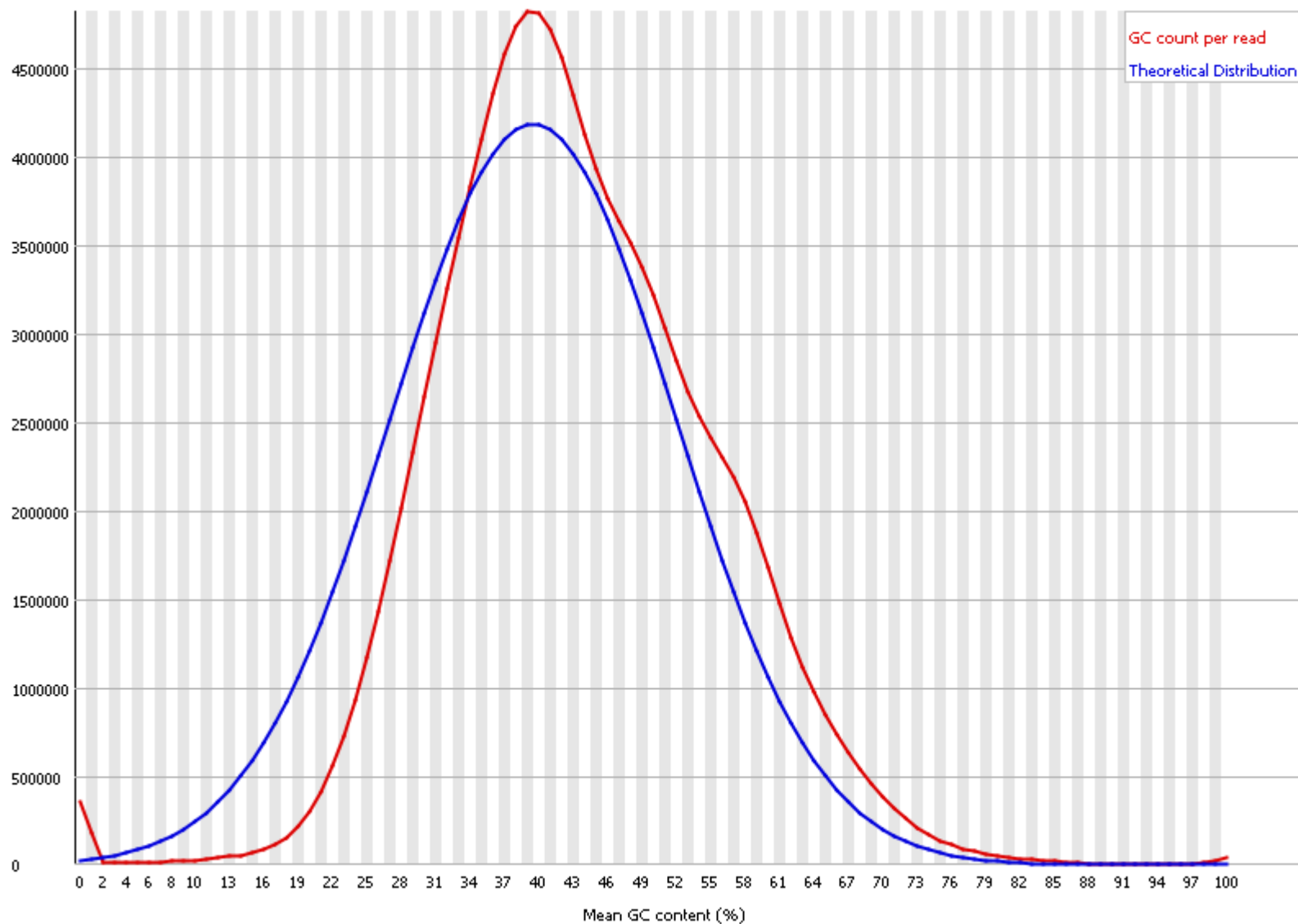
✖ Per base sequence content





Per sequence GC content

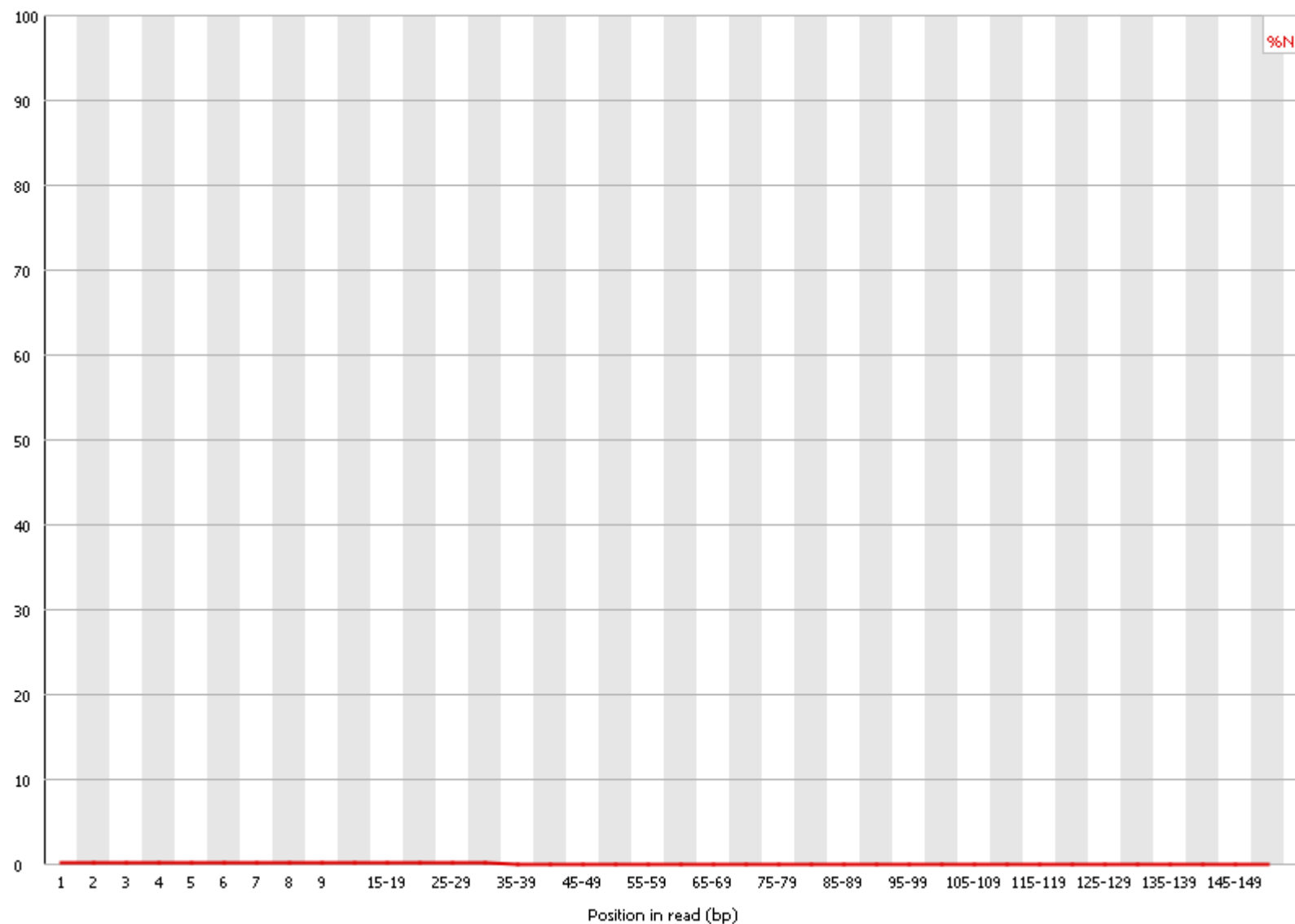
GC distribution over all sequences



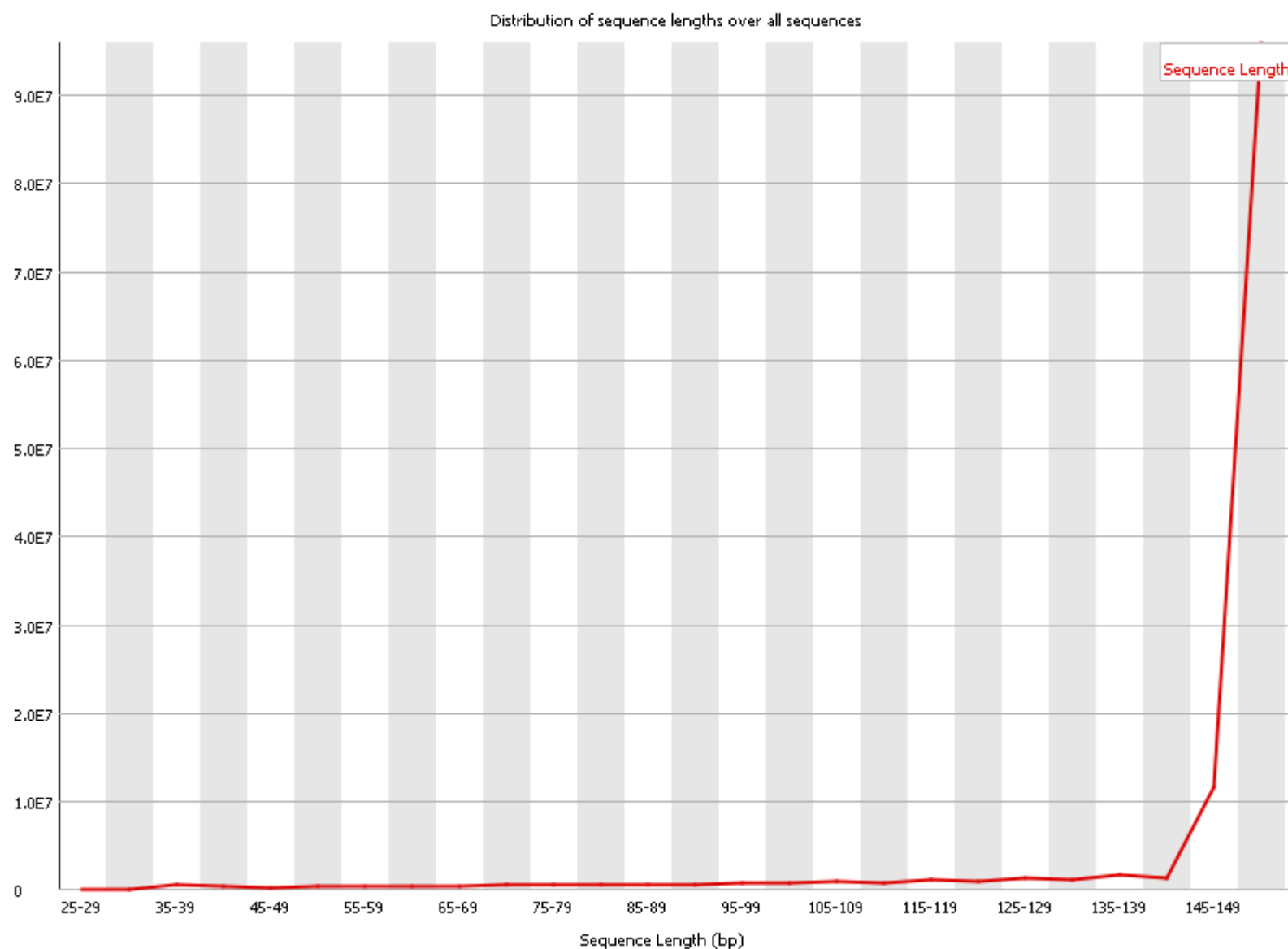


Per base N content

N content across all bases



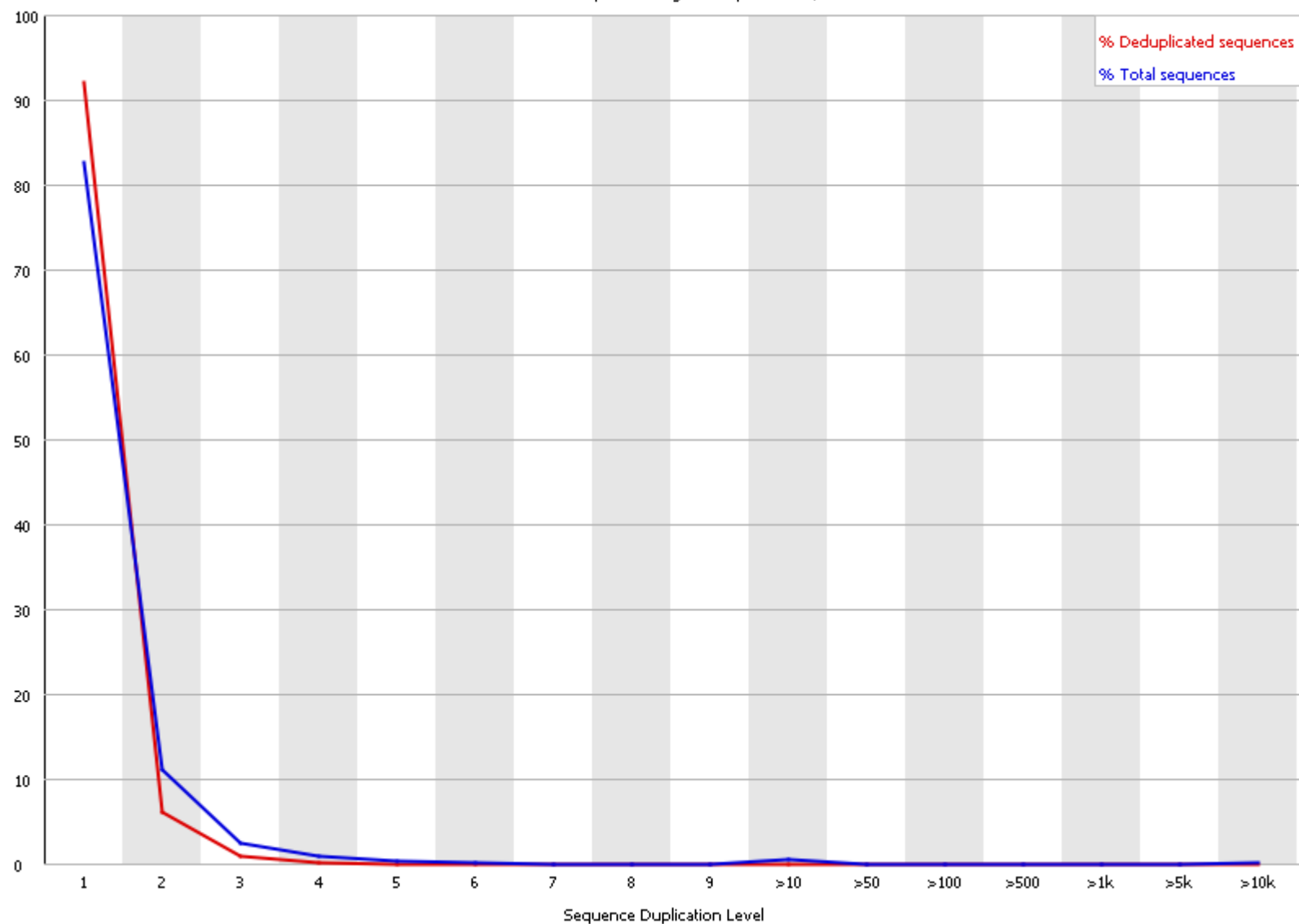
Sequence Length Distribution





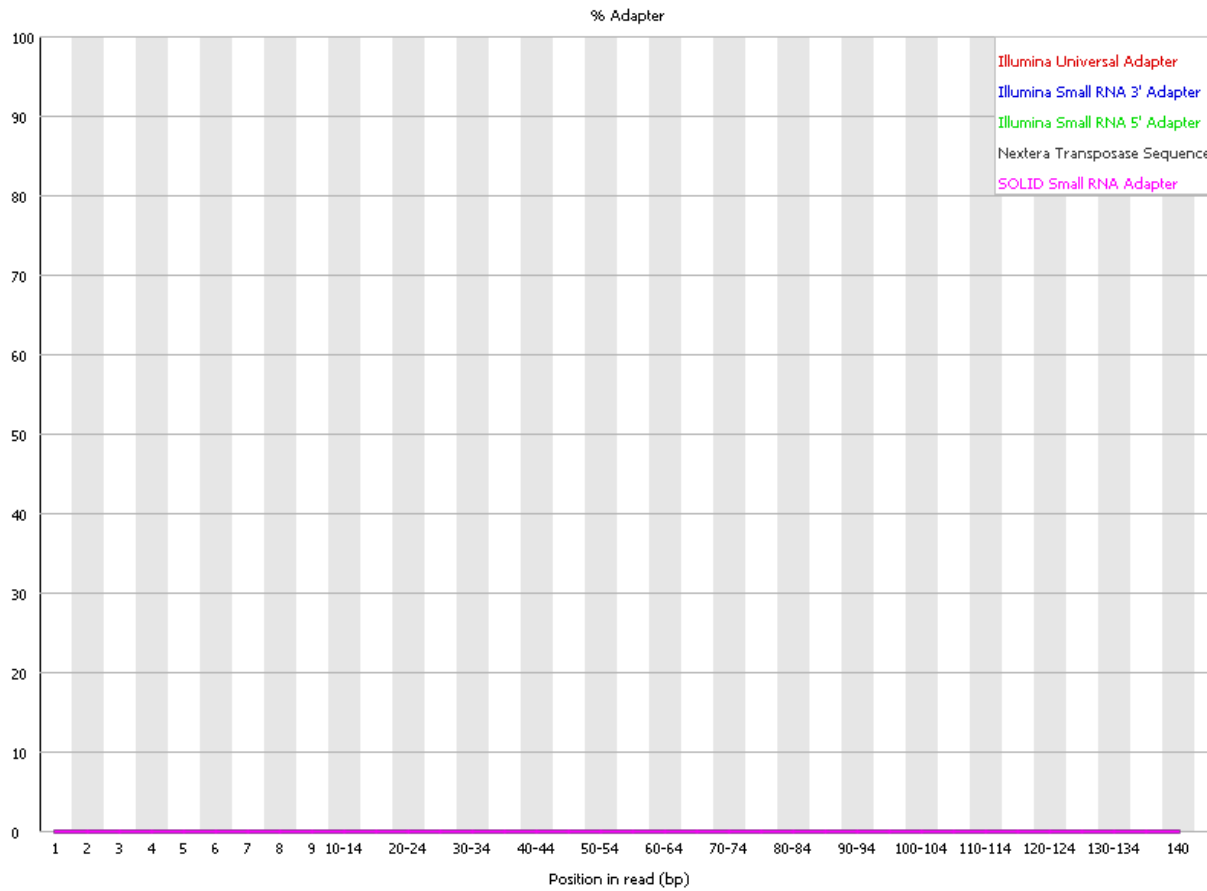
Sequence Duplication Levels

Percent of seqs remaining if deduplicated 89,75%





Sequence	Count	Percentage	Possible Source
NNN	340705	0.270661825970798	No Hit



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