

FastQC Report

Summary

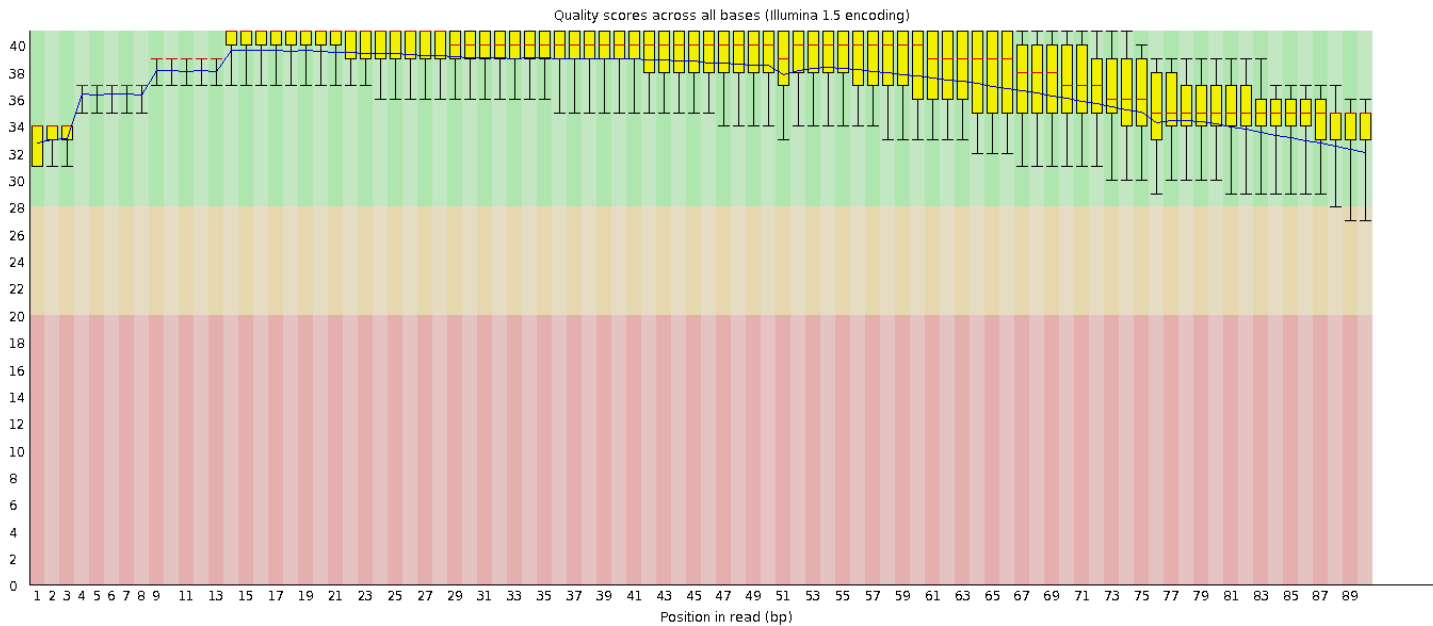
Sat 17 Aug 2013
file3.fastq

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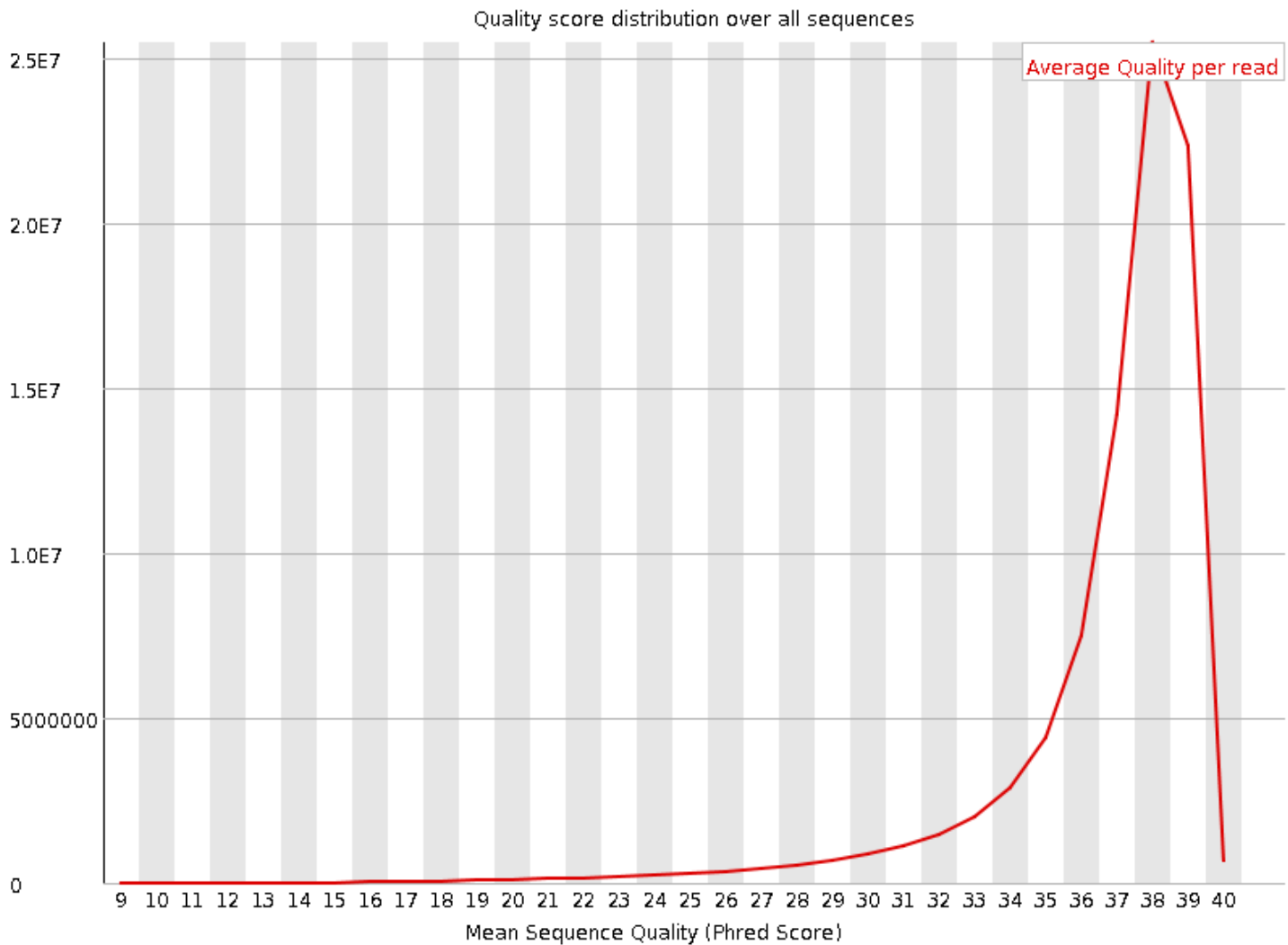
Basic Statistics

Measure	Value
Filename	file3.fastq
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	86875298
Filtered Sequences	0
Sequence length	90
%GC	44

Per base sequence quality

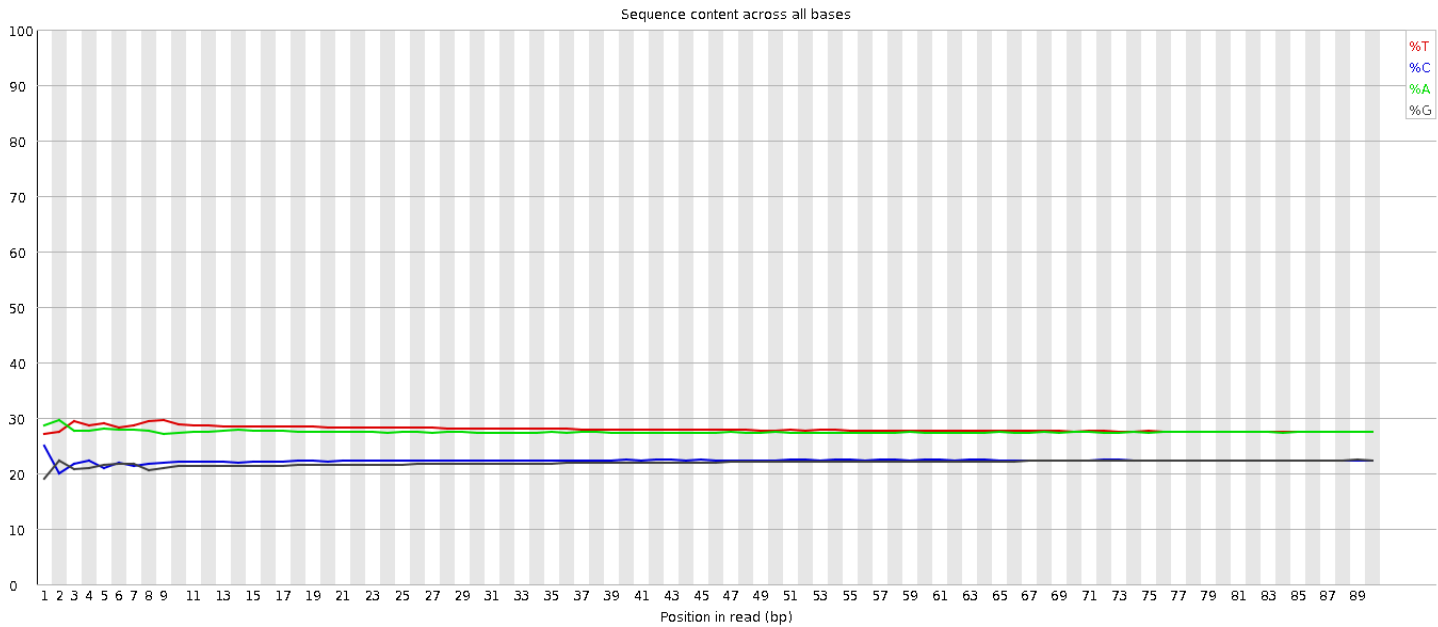


 Per sequence quality scores





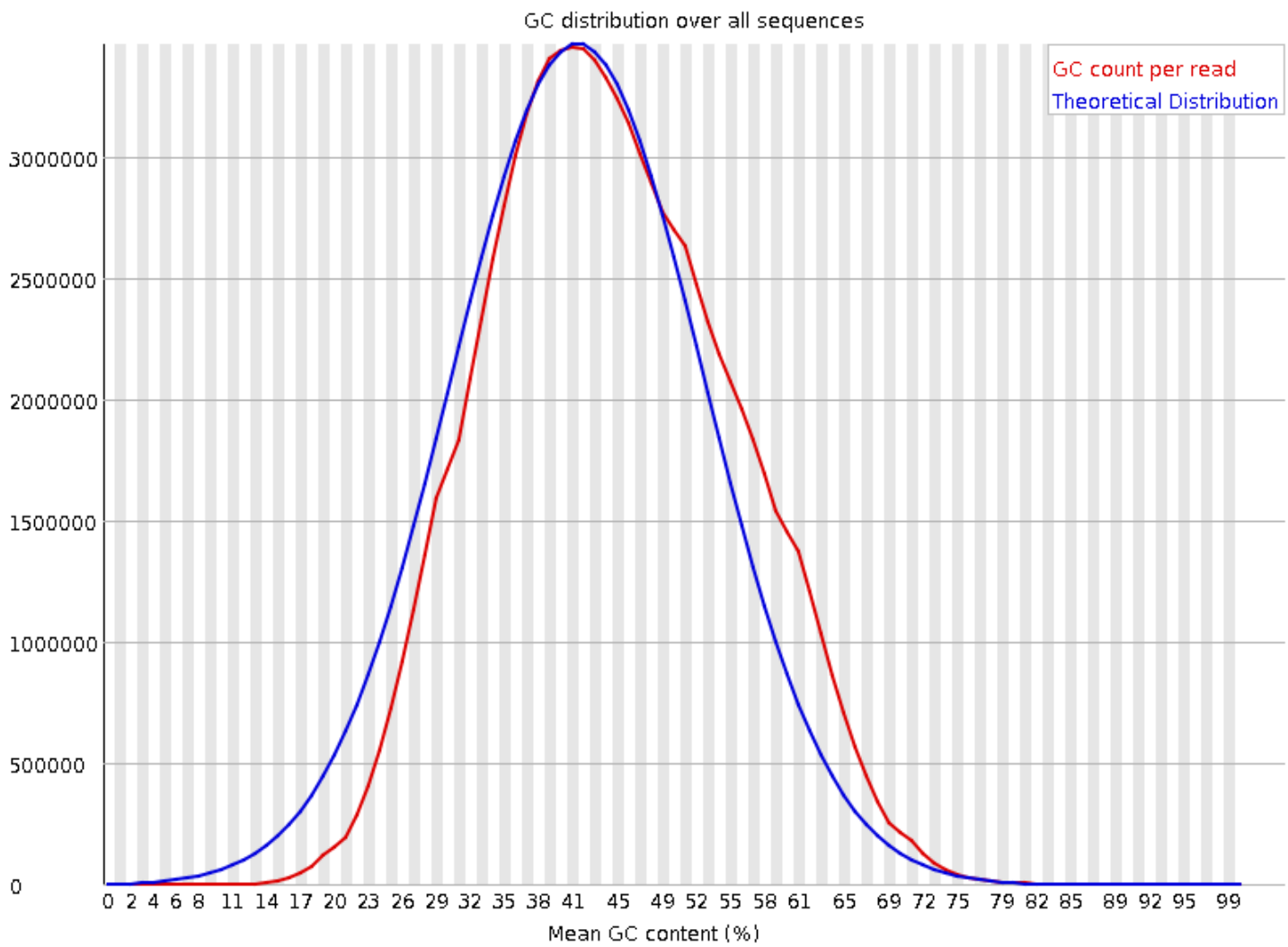
Per base sequence content



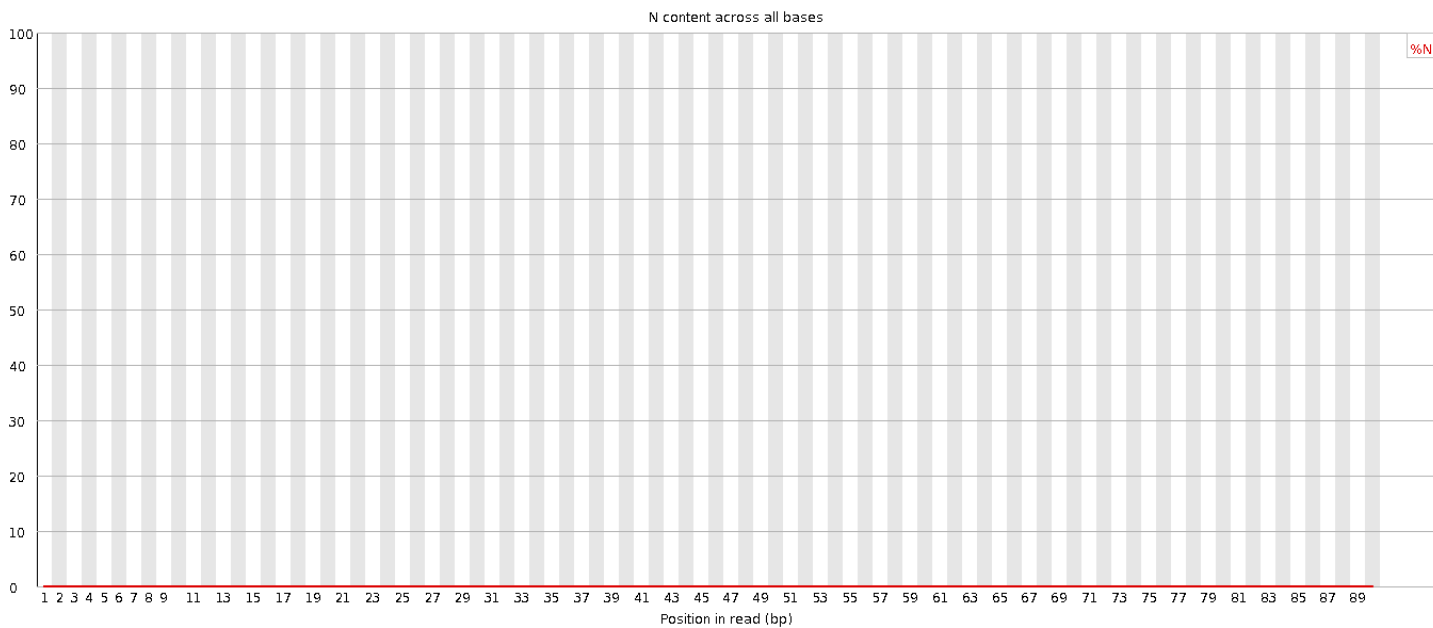
Per base GC content



Per sequence GC content

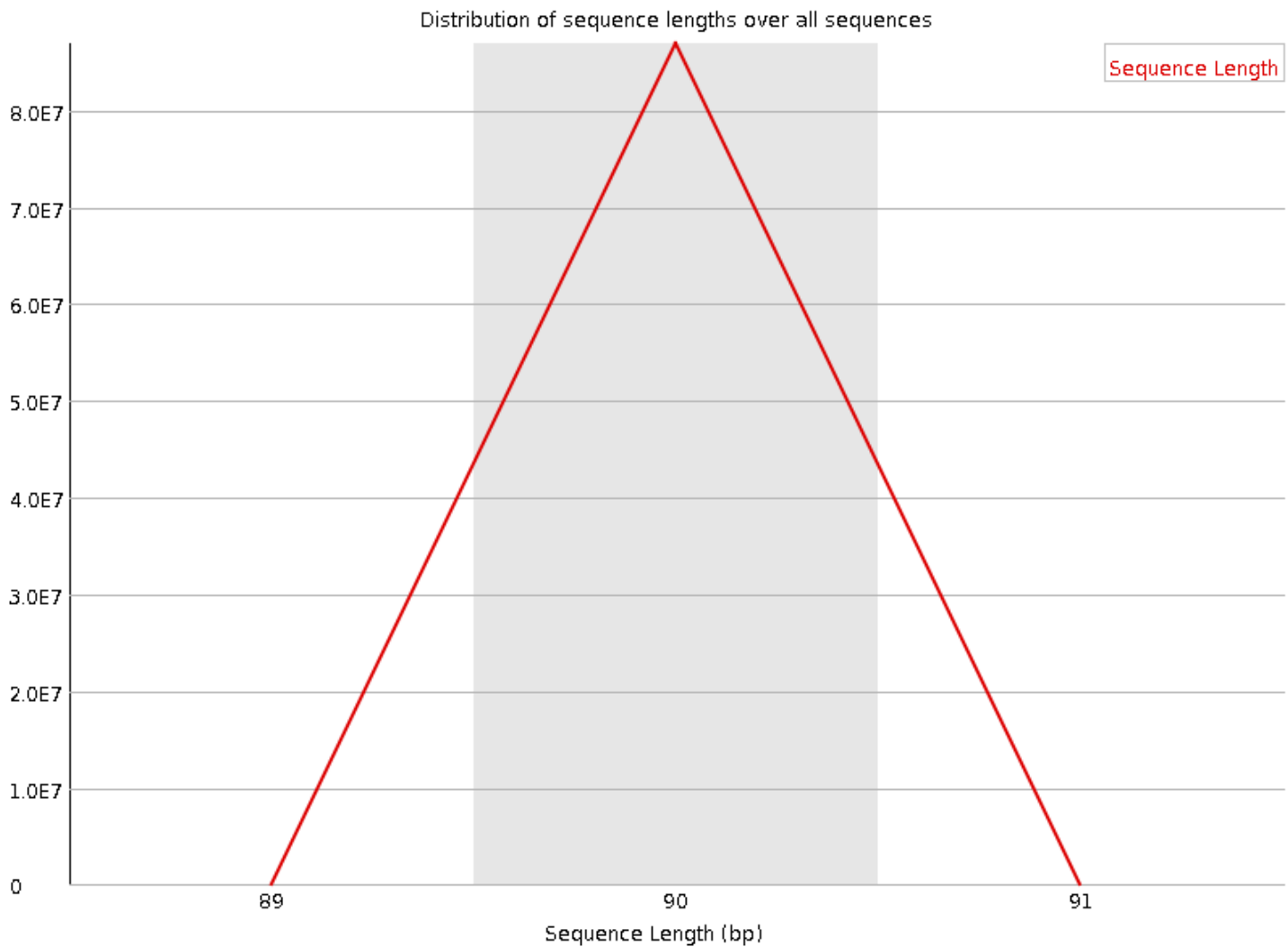


 Per base N content



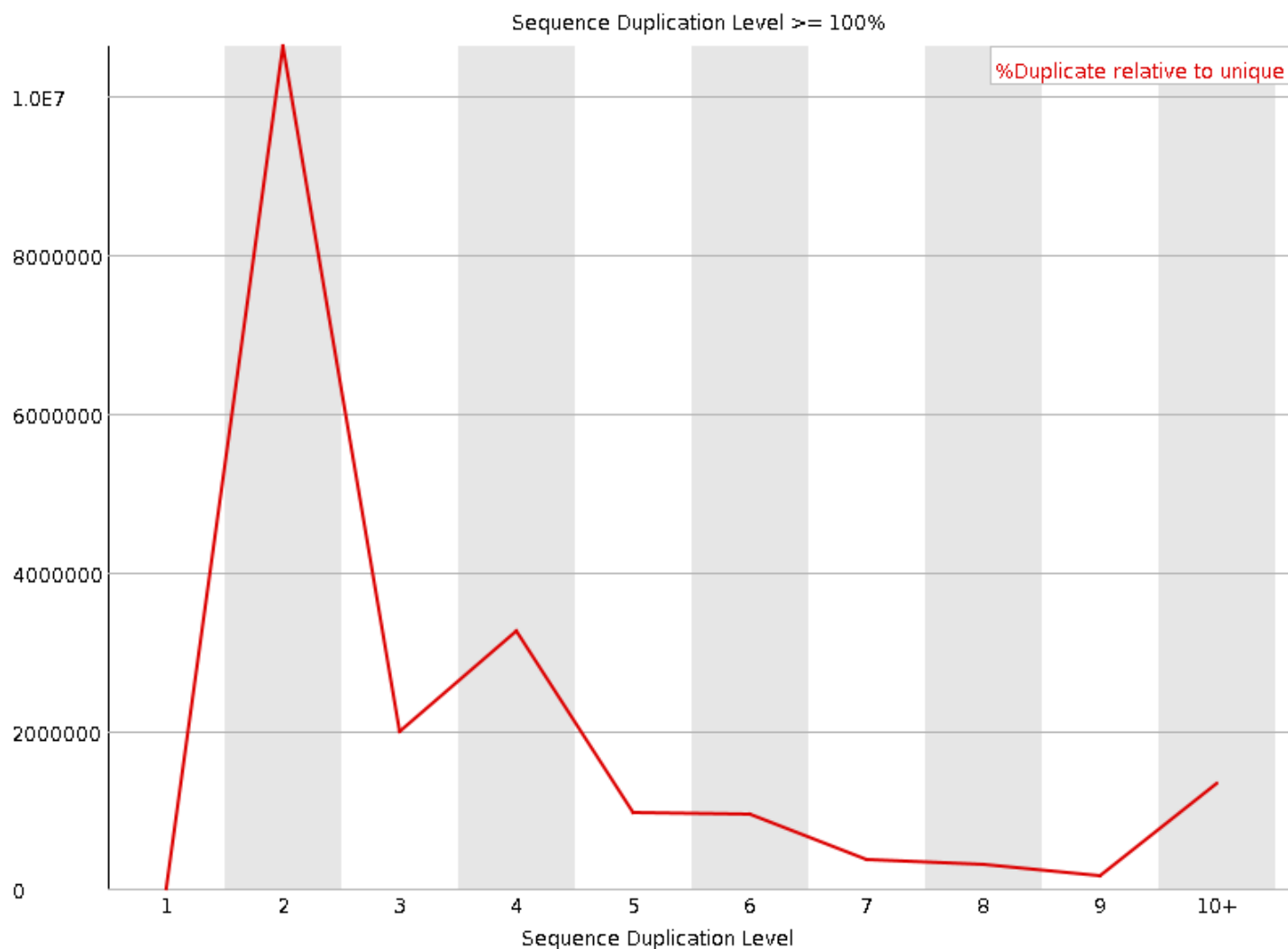


Sequence Length Distribution





Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences



Kmer Content

No overrepresented Kmers

Produced by [FastQC](#) (version 0.10.1)