












FastQC Report

Wed 13 Jul 2011

ChIP-Seq-NSCs.fastqsanger

Summary

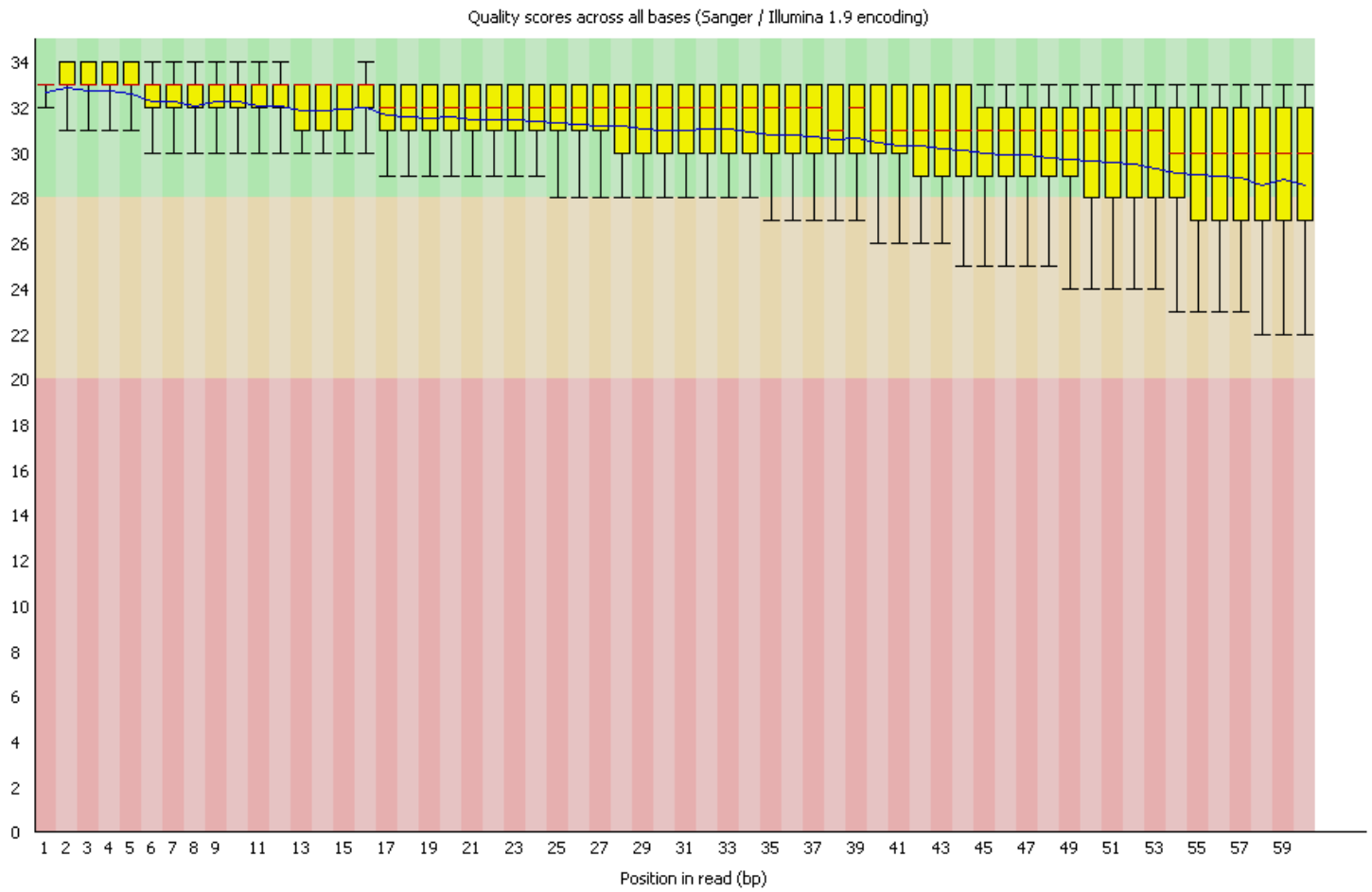
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Basic Statistics

Measure	Value
Filename	ChIP-Seq-NSCs.fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	5548680
Sequence length	60
%GC	43

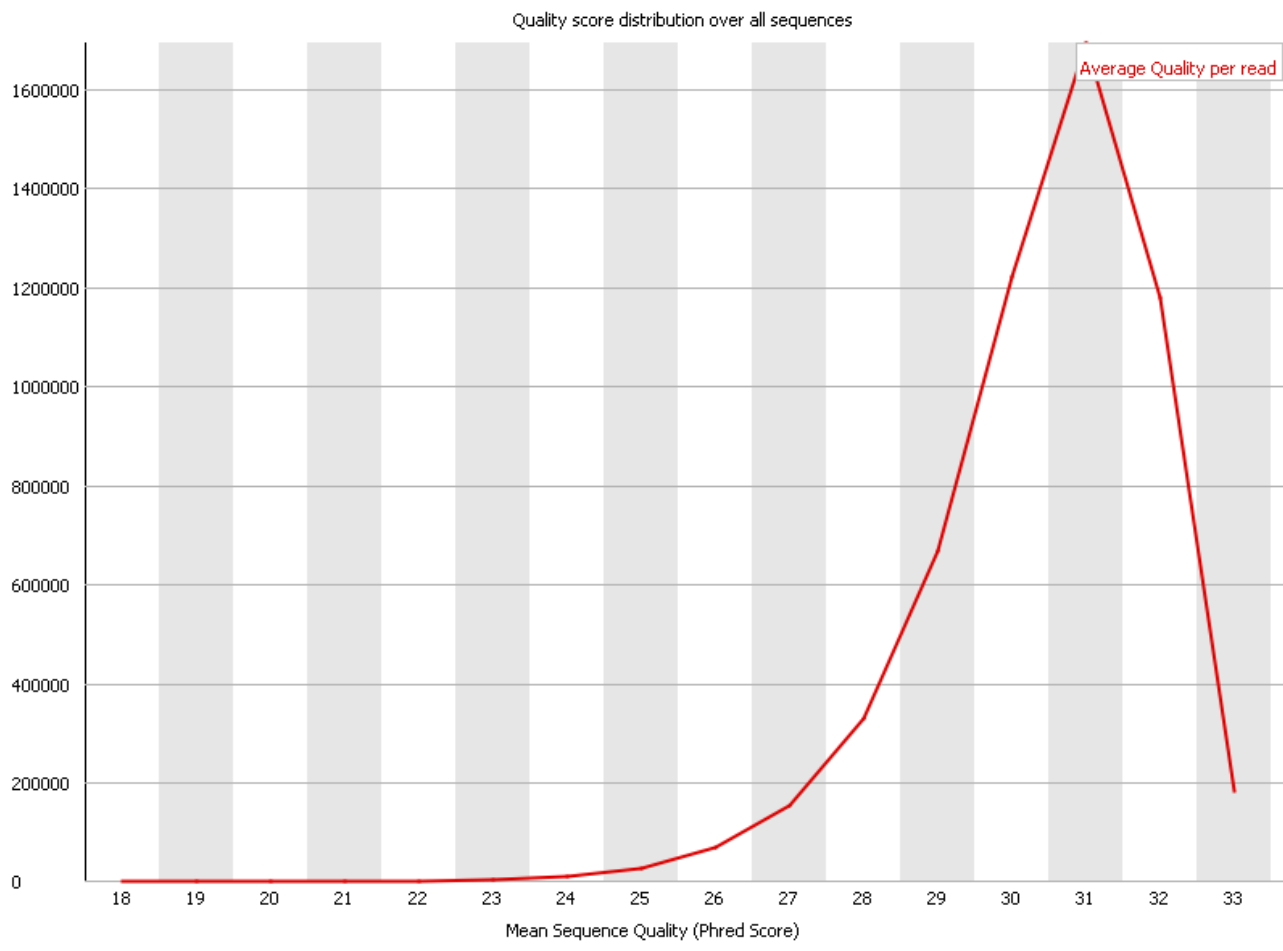
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Per base sequence quality



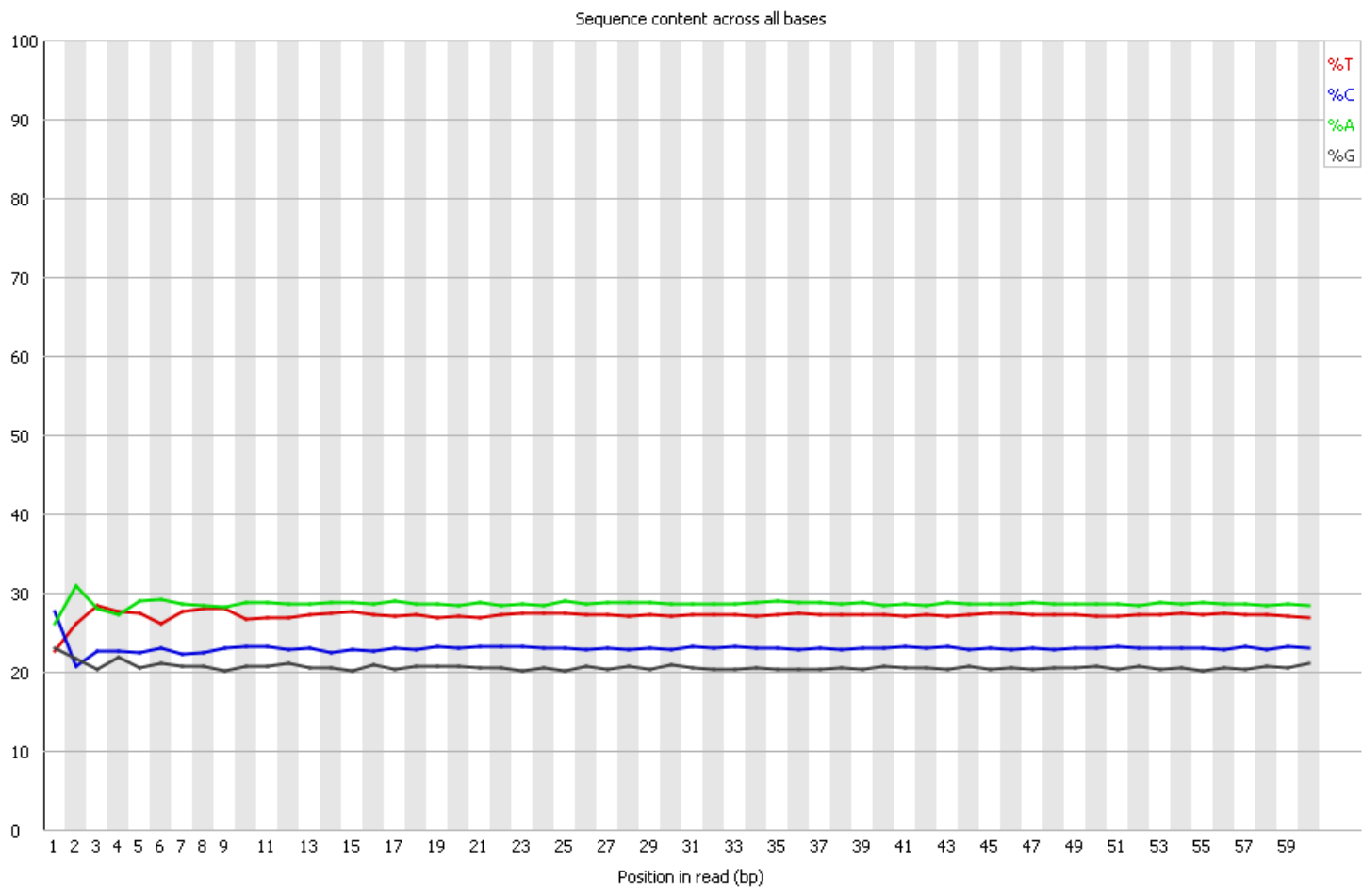
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Per sequence quality scores



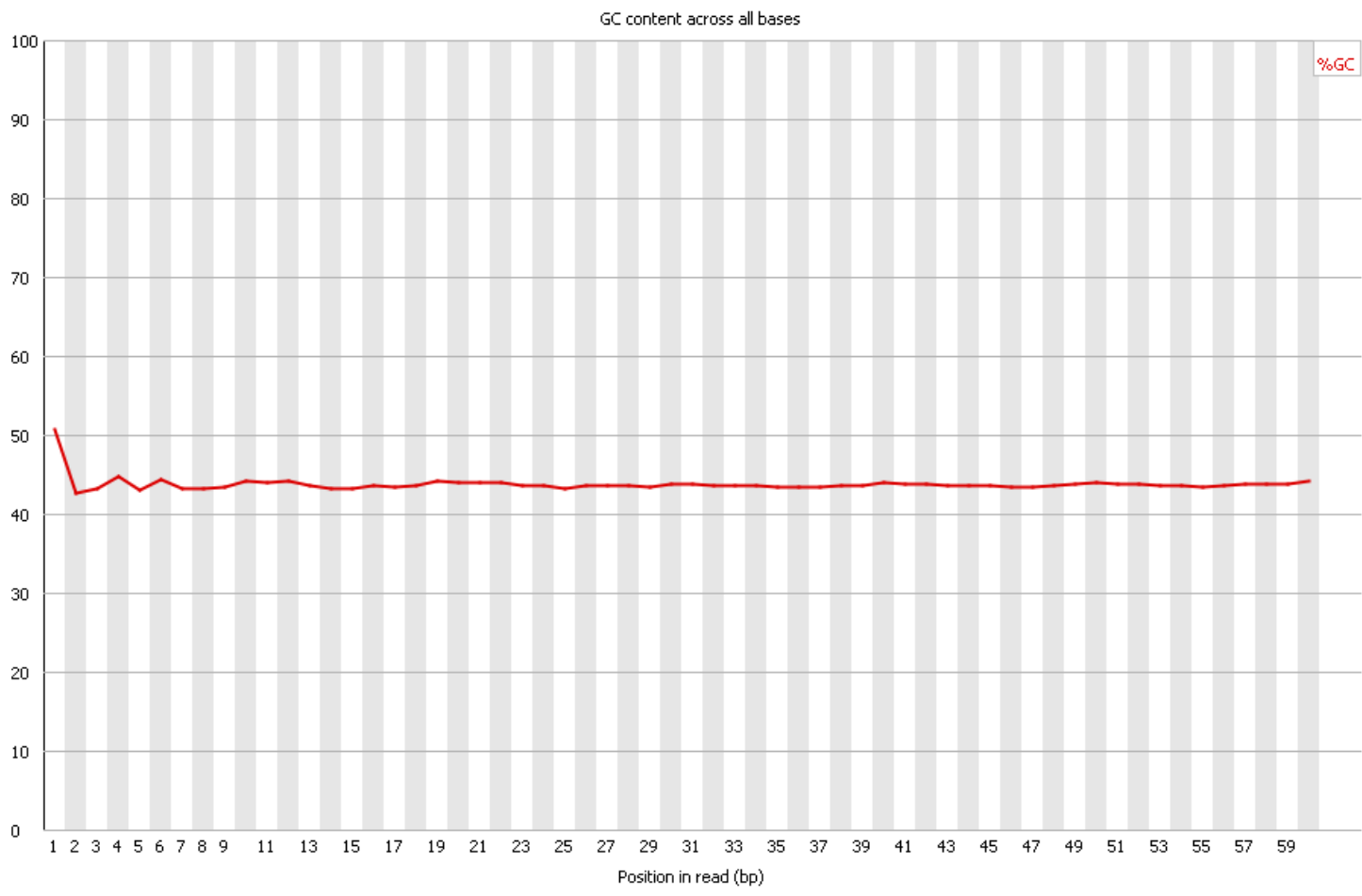
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 Per base sequence content



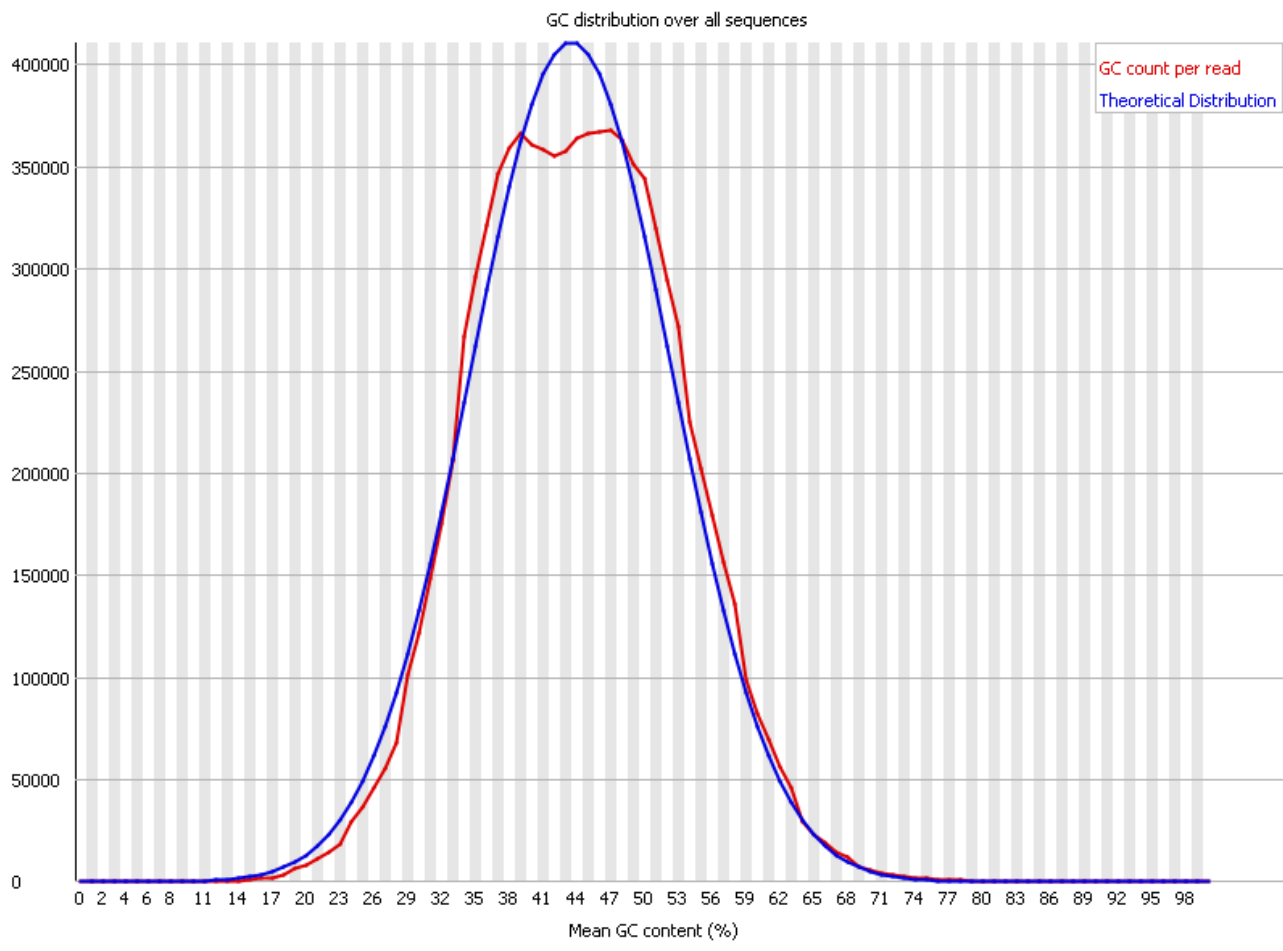
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 Per base GC content



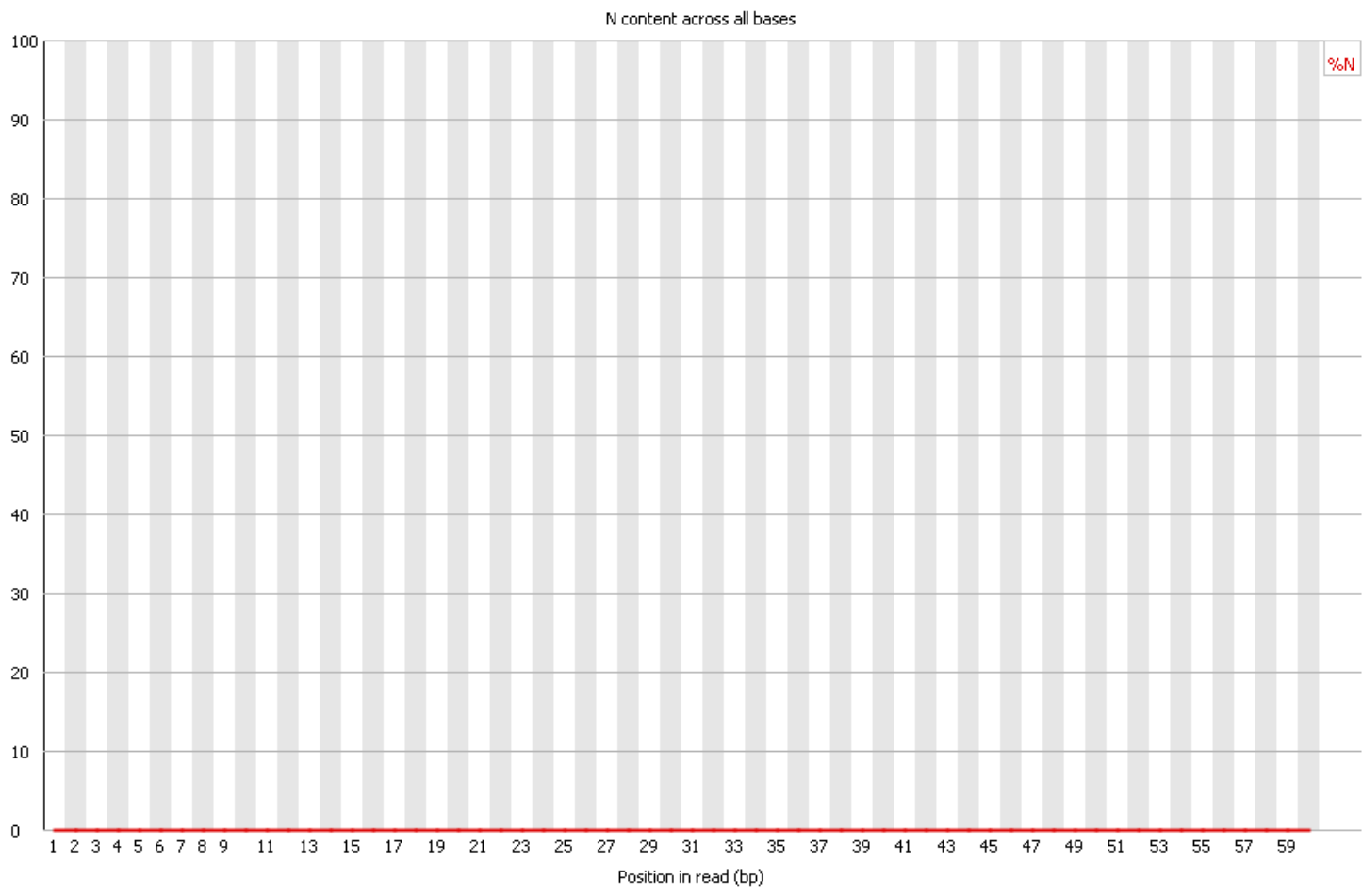
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 Per sequence GC content



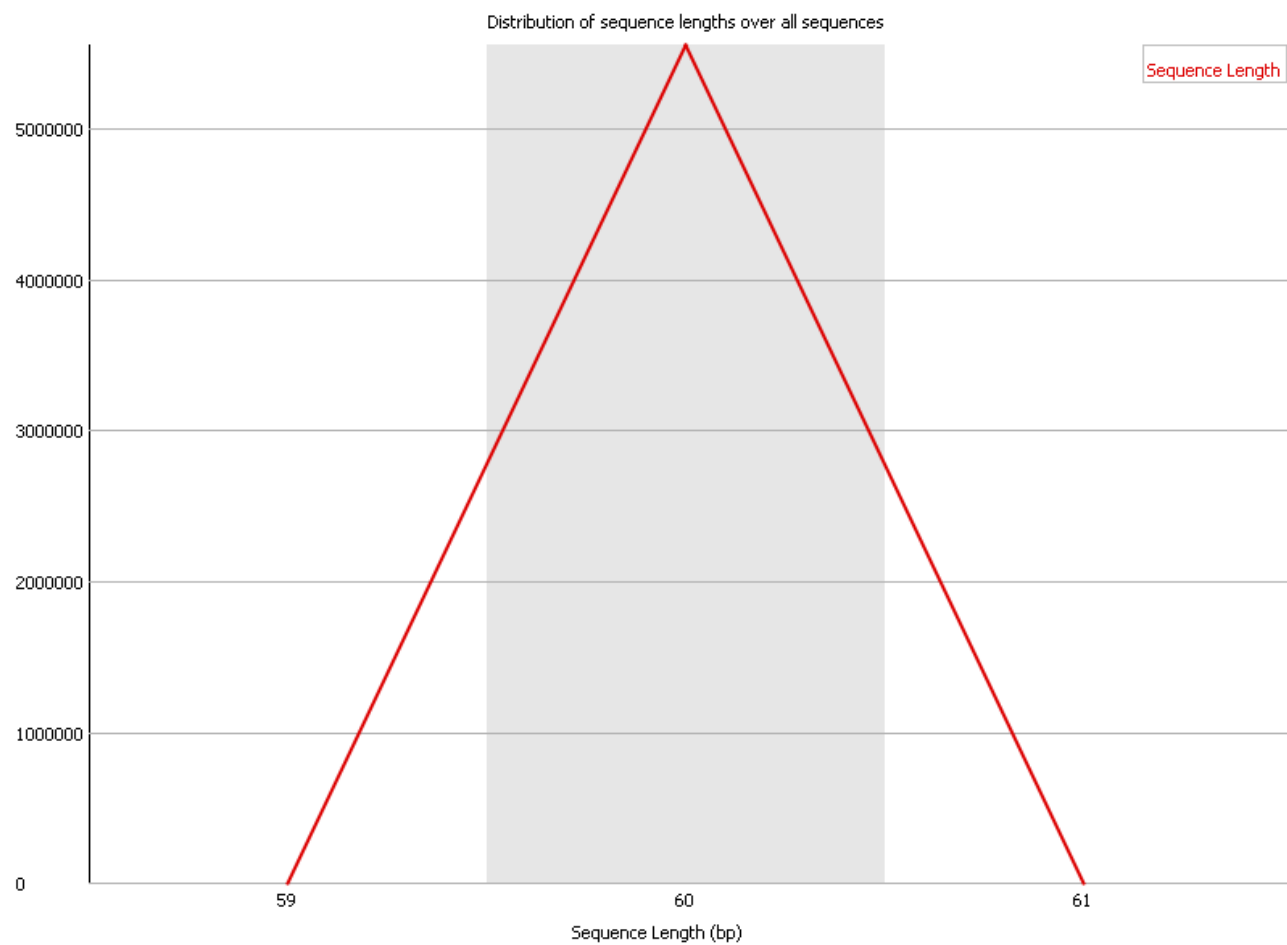
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 Per base N content



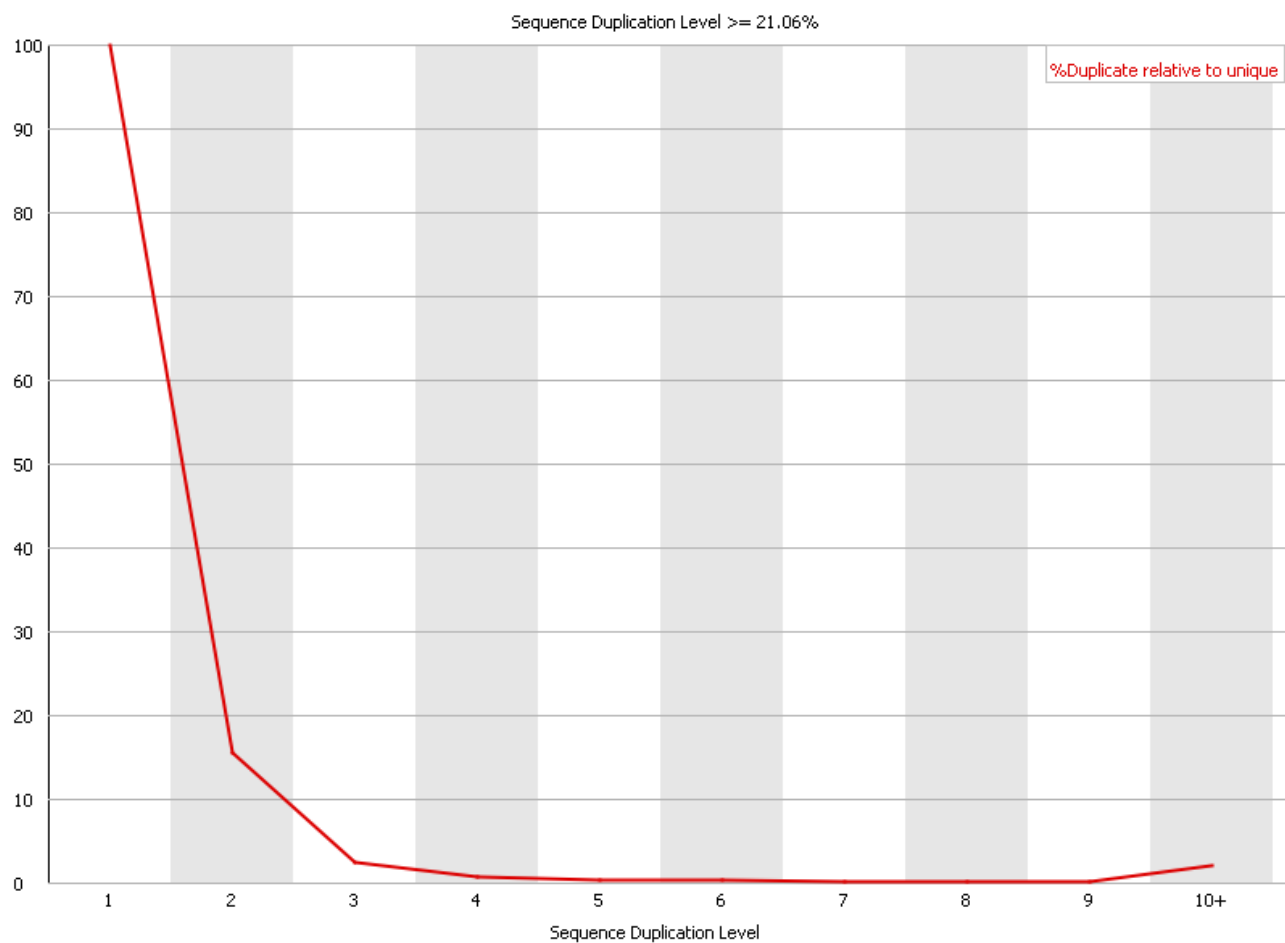
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Sequence Length Distribution



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! Sequence Duplication Levels



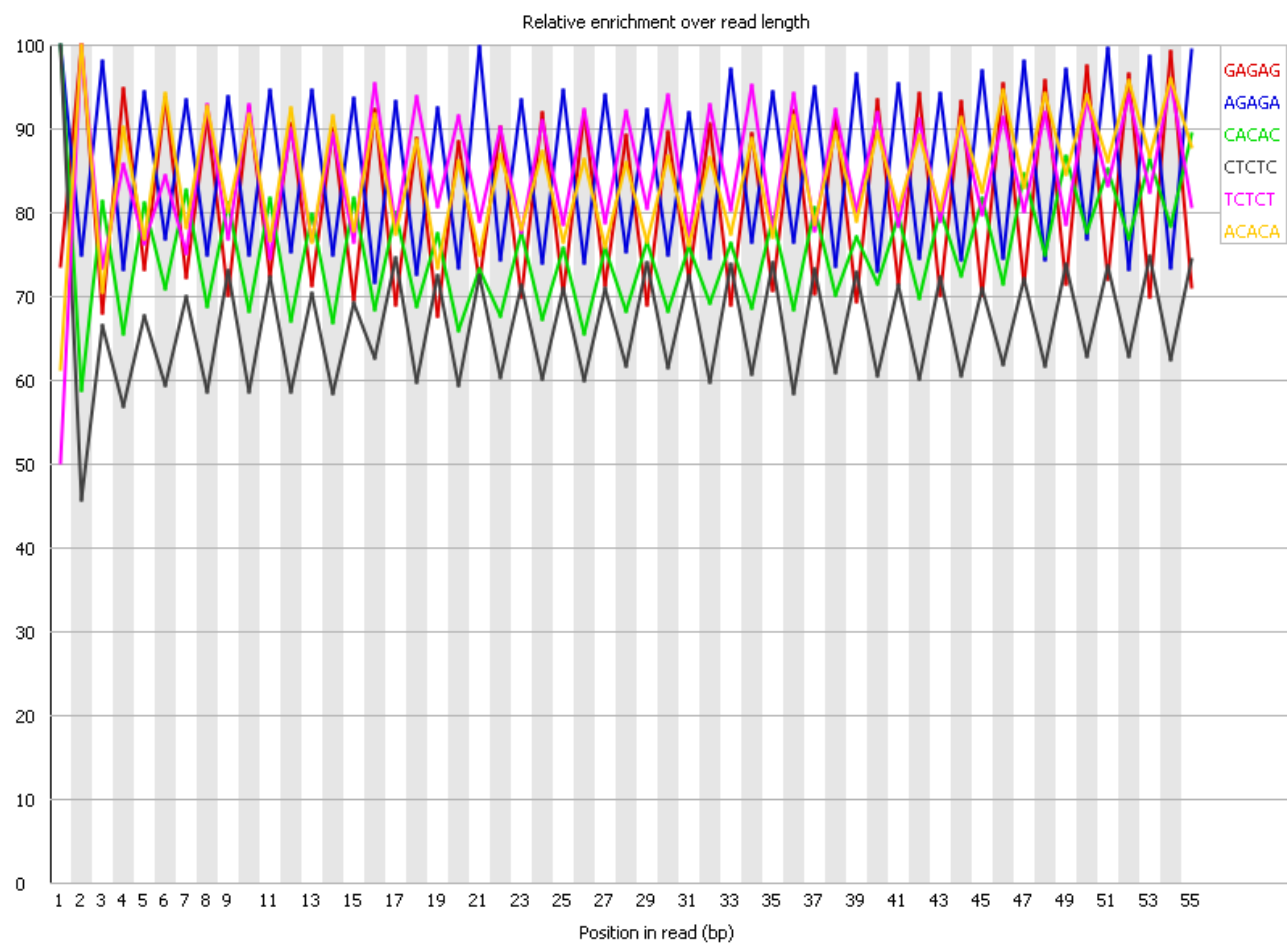
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Overrepresented sequences

No overrepresented sequences

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Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
GAGAG	1250695	5.548921	6.7970896	2
AGAGA	1445660	4.6301126	5.4237266	1
CACAC	1075935	3.4298215	4.5435925	1
CTCTC	969405	3.4188979	5.127703	1
TCTCT	1054250	3.1520834	3.7156014	2
ACACA	1204605	3.094964	3.6599352	2

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