












# FastQC Report

Wed 13 Jul 2011

ChIP-Seq IgG control.fastqsanger

## Summary

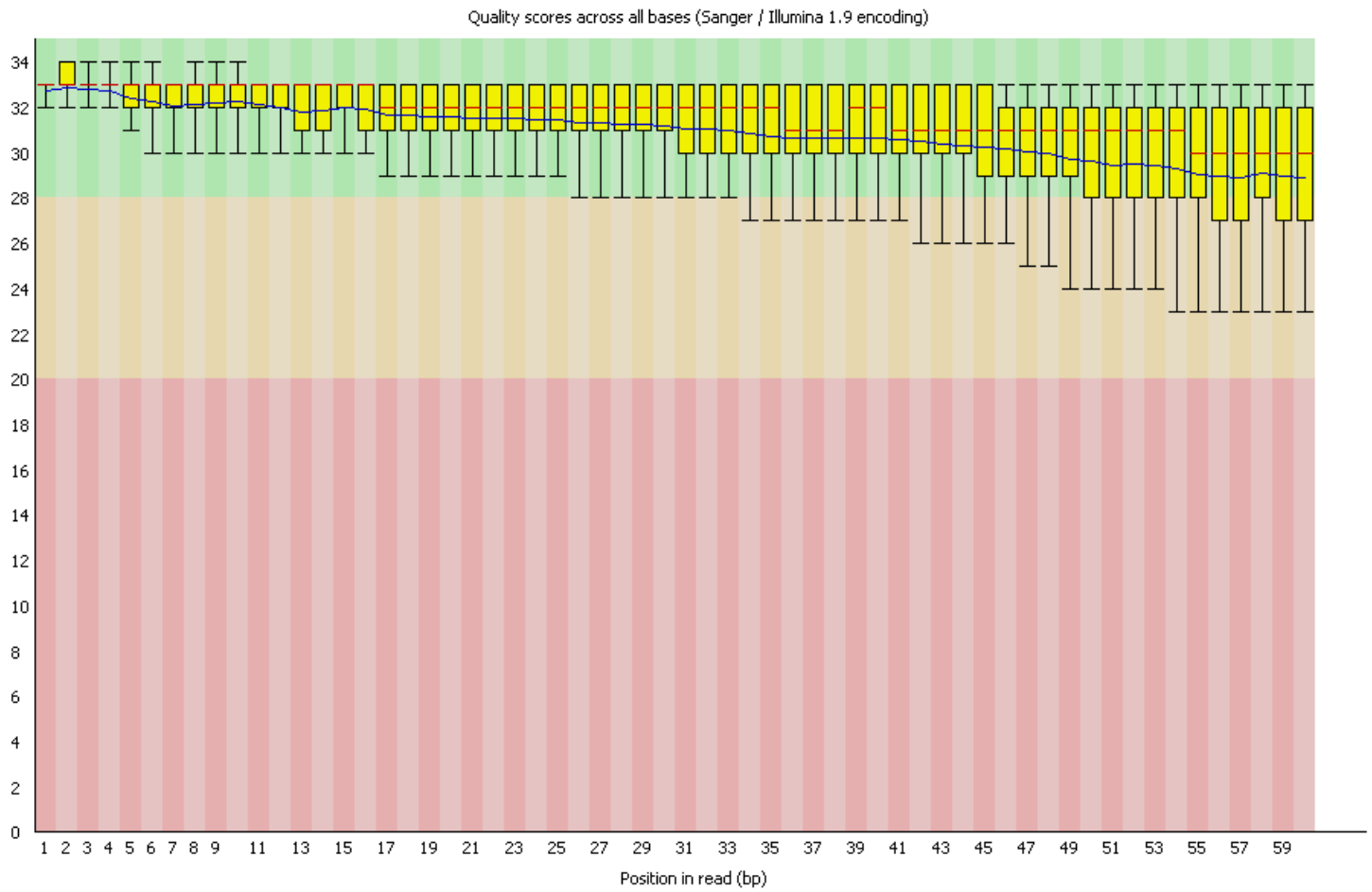
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## Basic Statistics

Measure	Value
Filename	ChIP-Seq IgG control.fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3740234
Sequence length	60
%GC	44

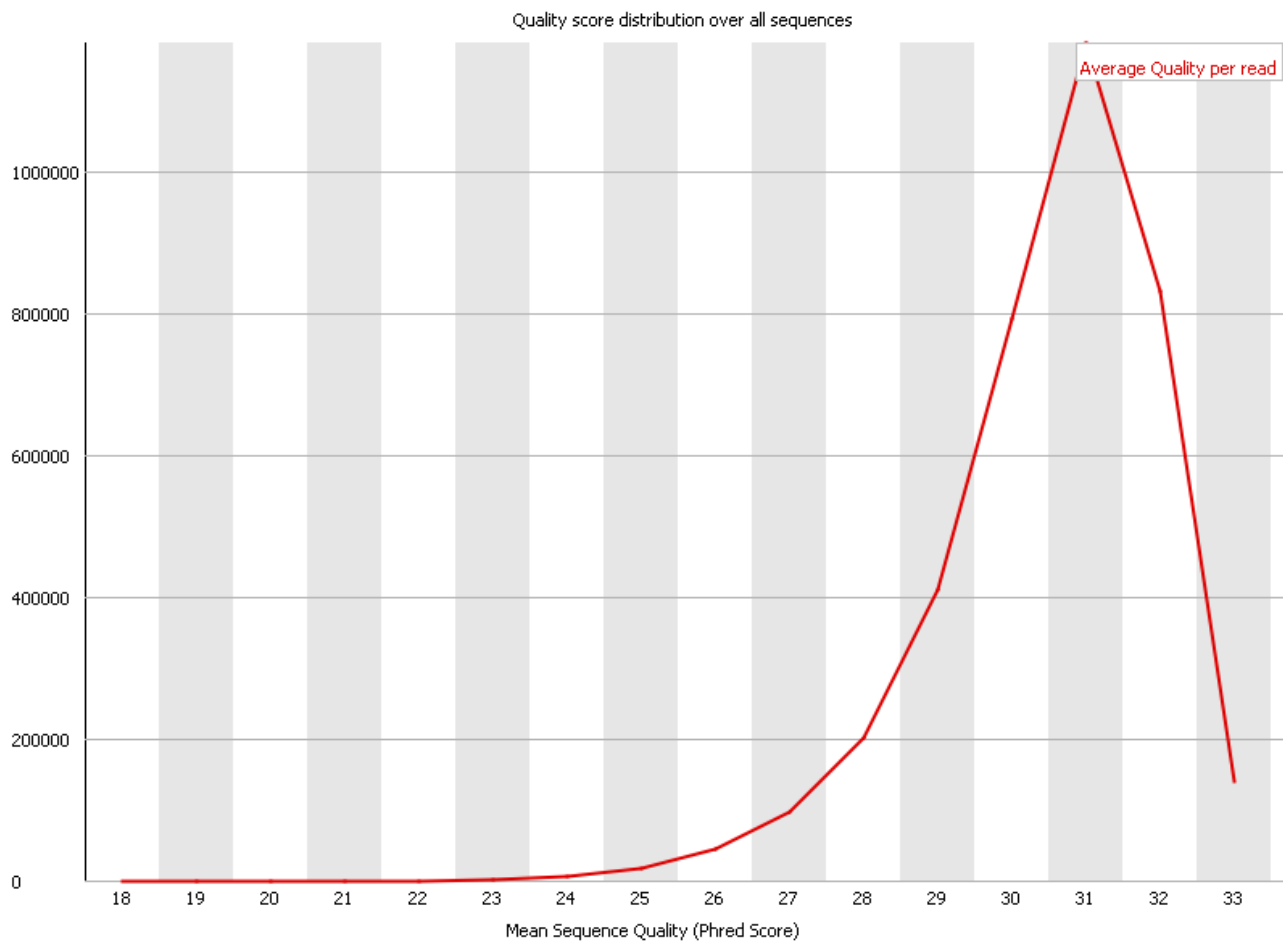
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## Per base sequence quality



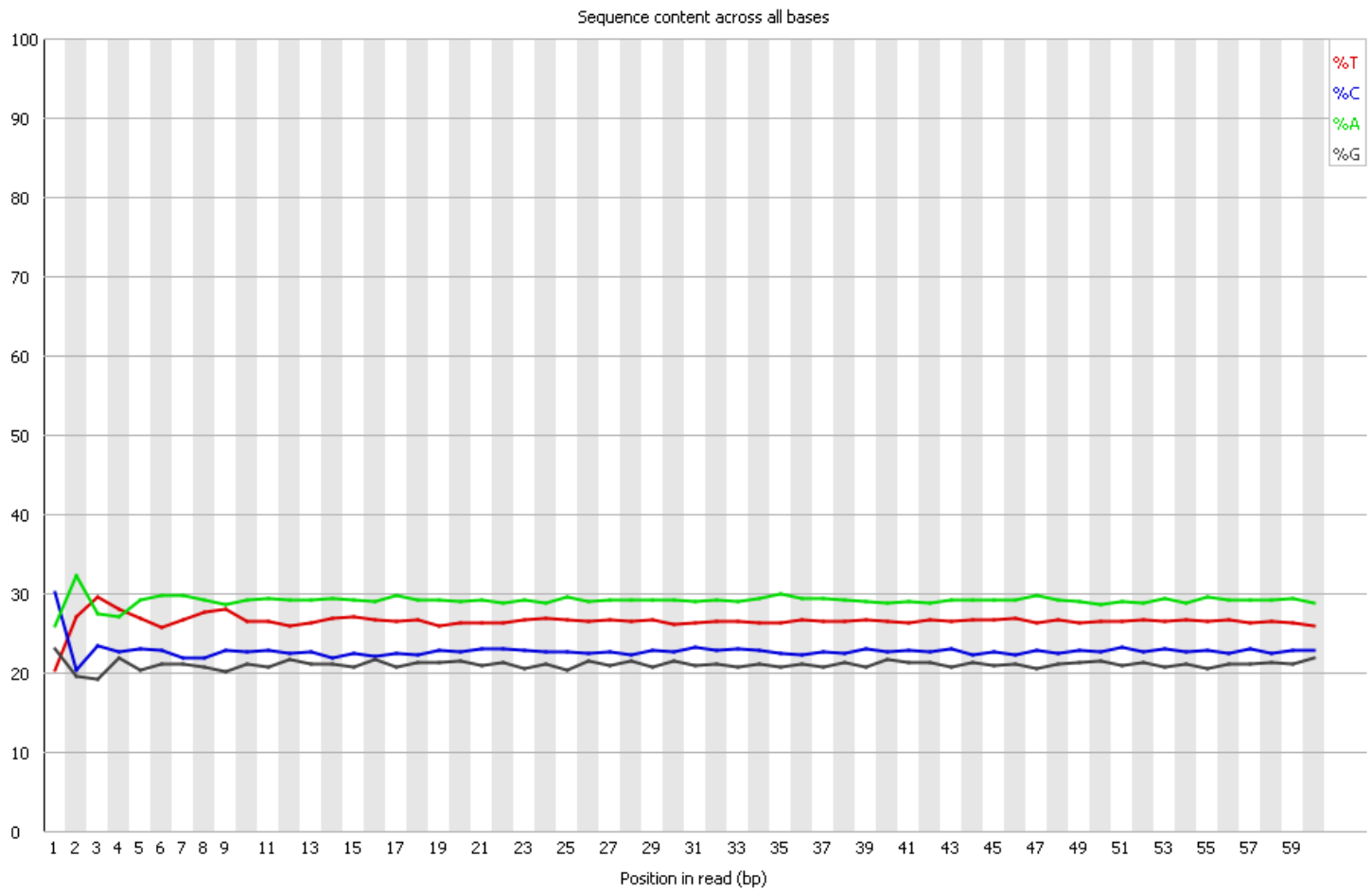
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## Per sequence quality scores



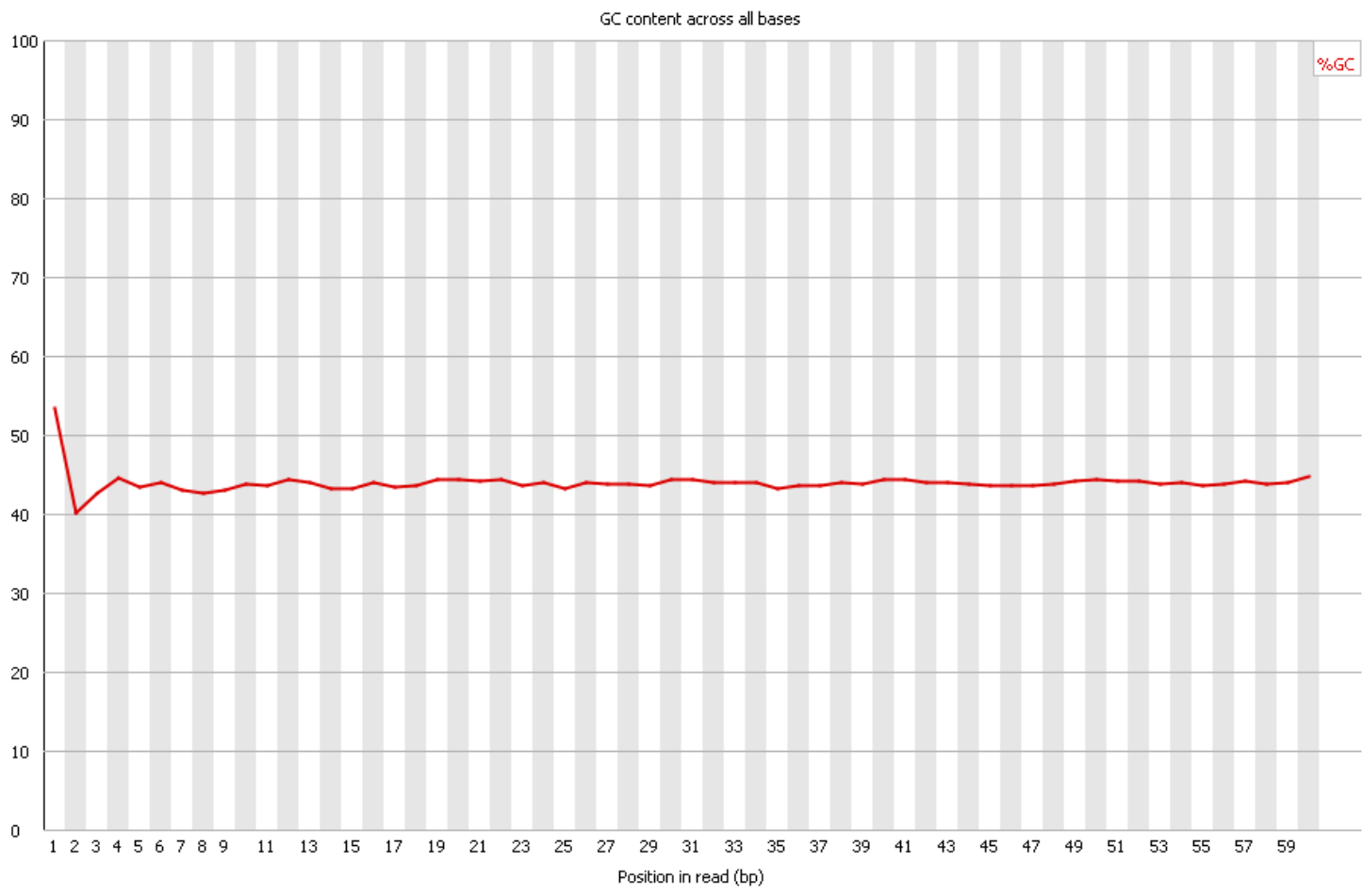
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 Per base sequence content



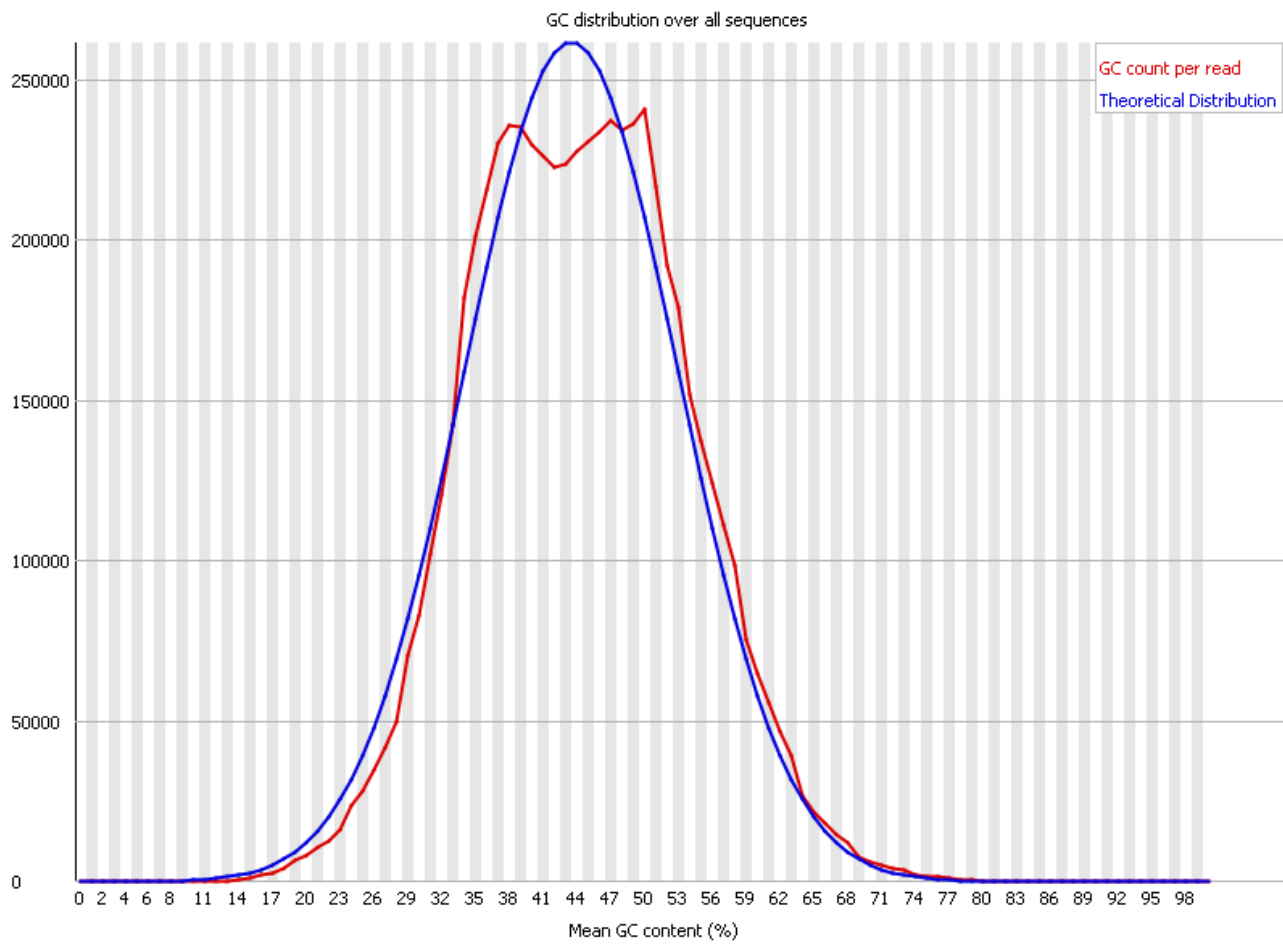
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! Per base GC content



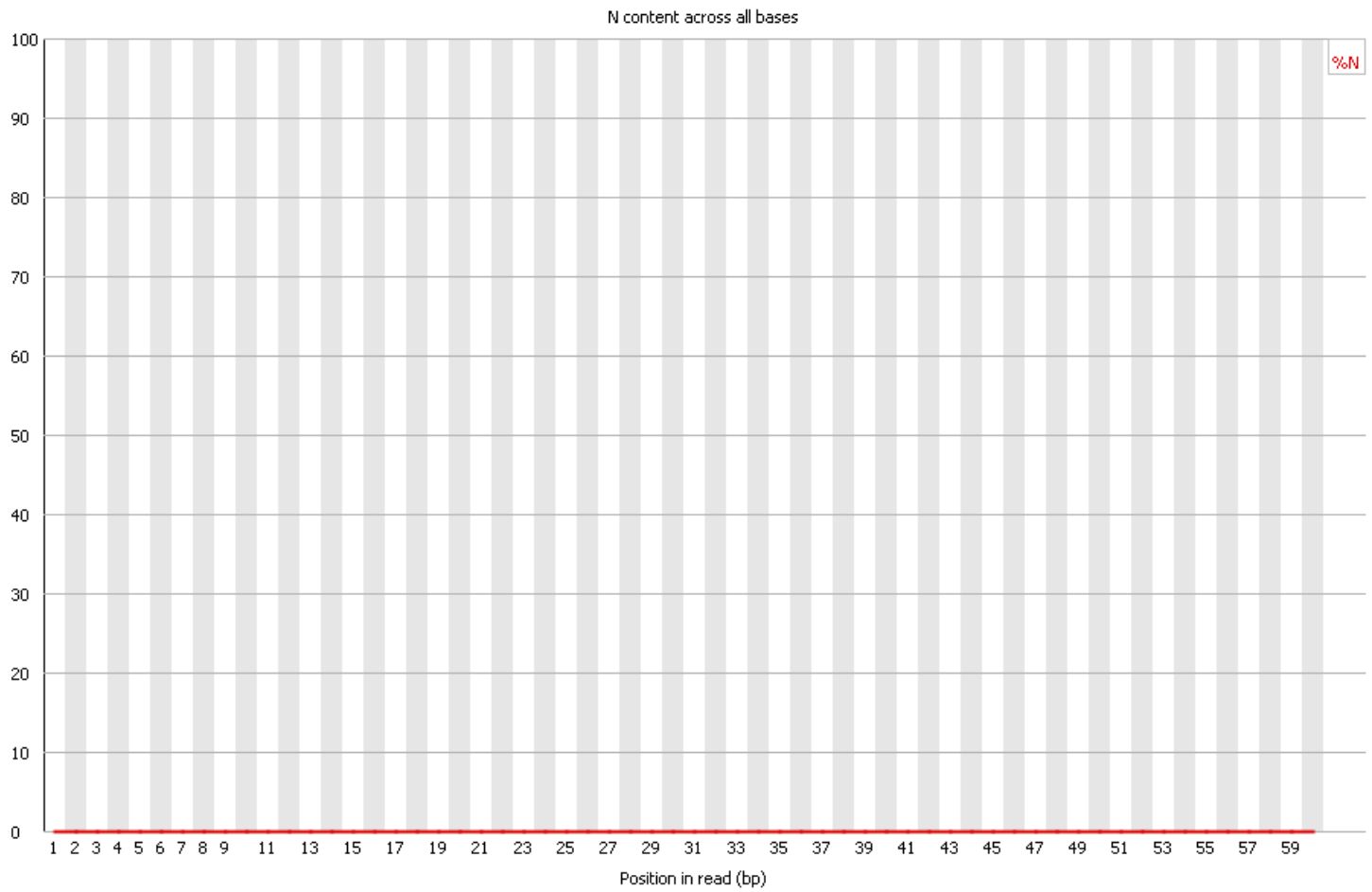
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 Per sequence GC content



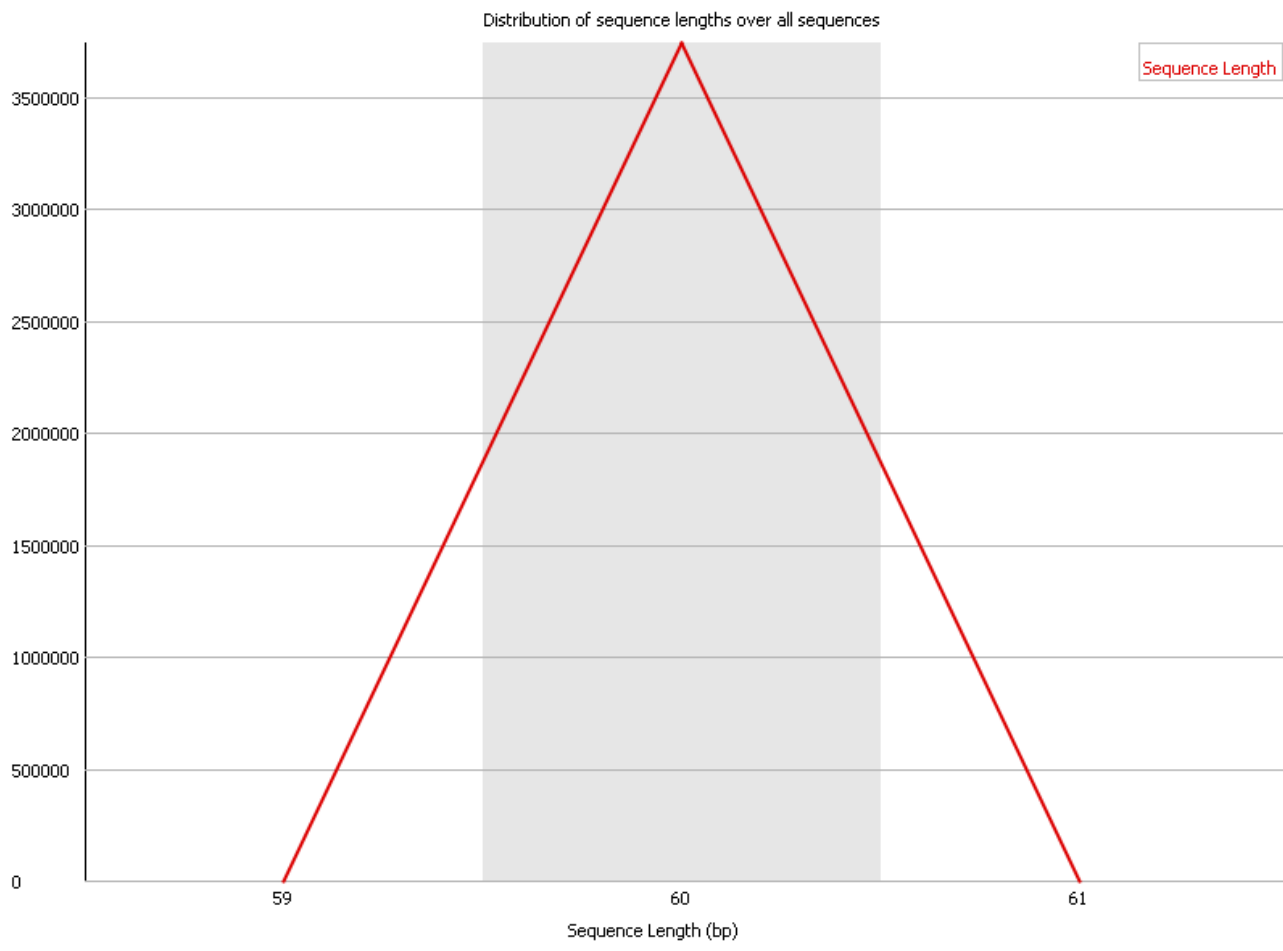
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 Per base N content



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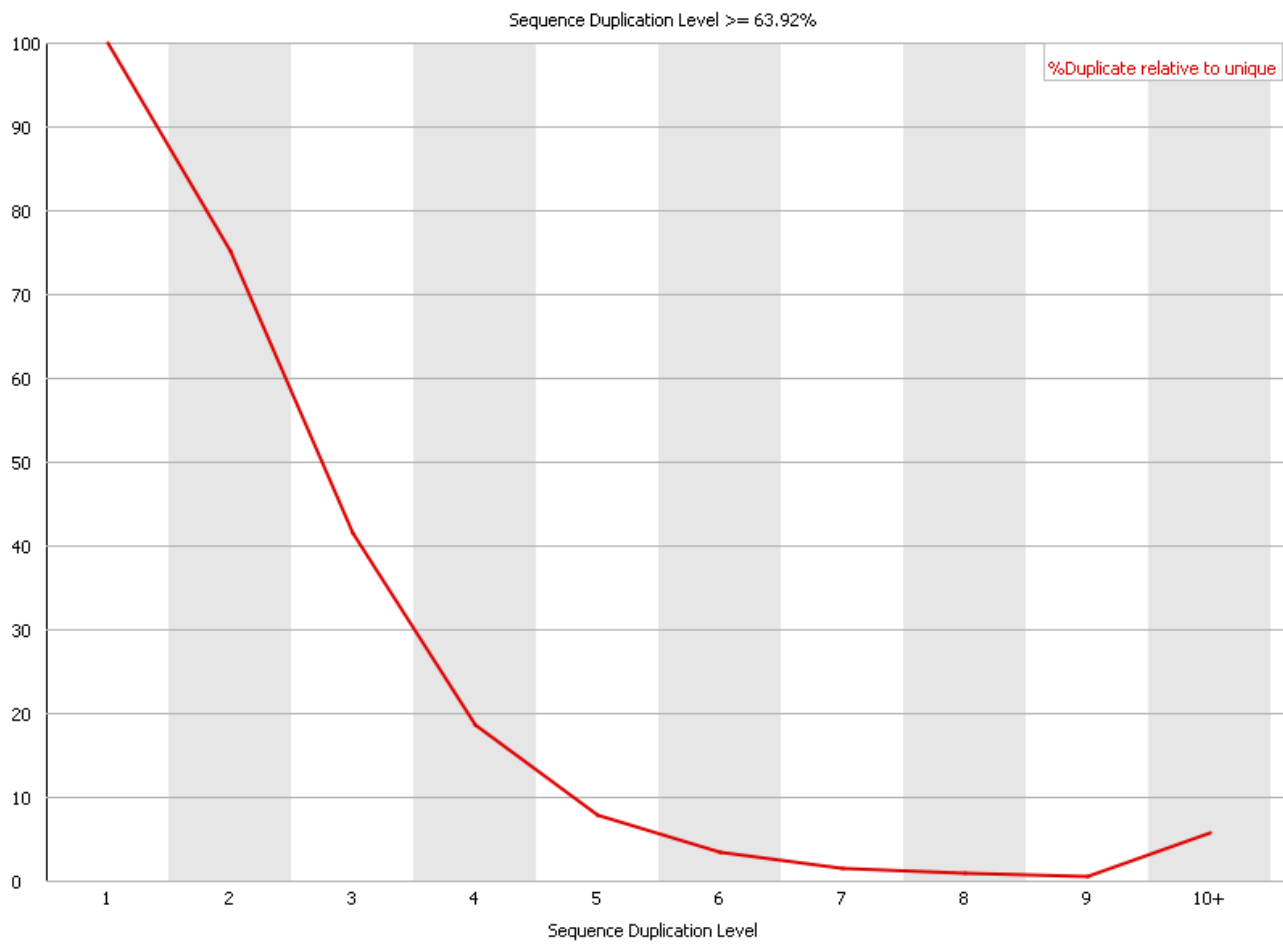
## Sequence Length Distribution



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## Sequence Duplication Levels





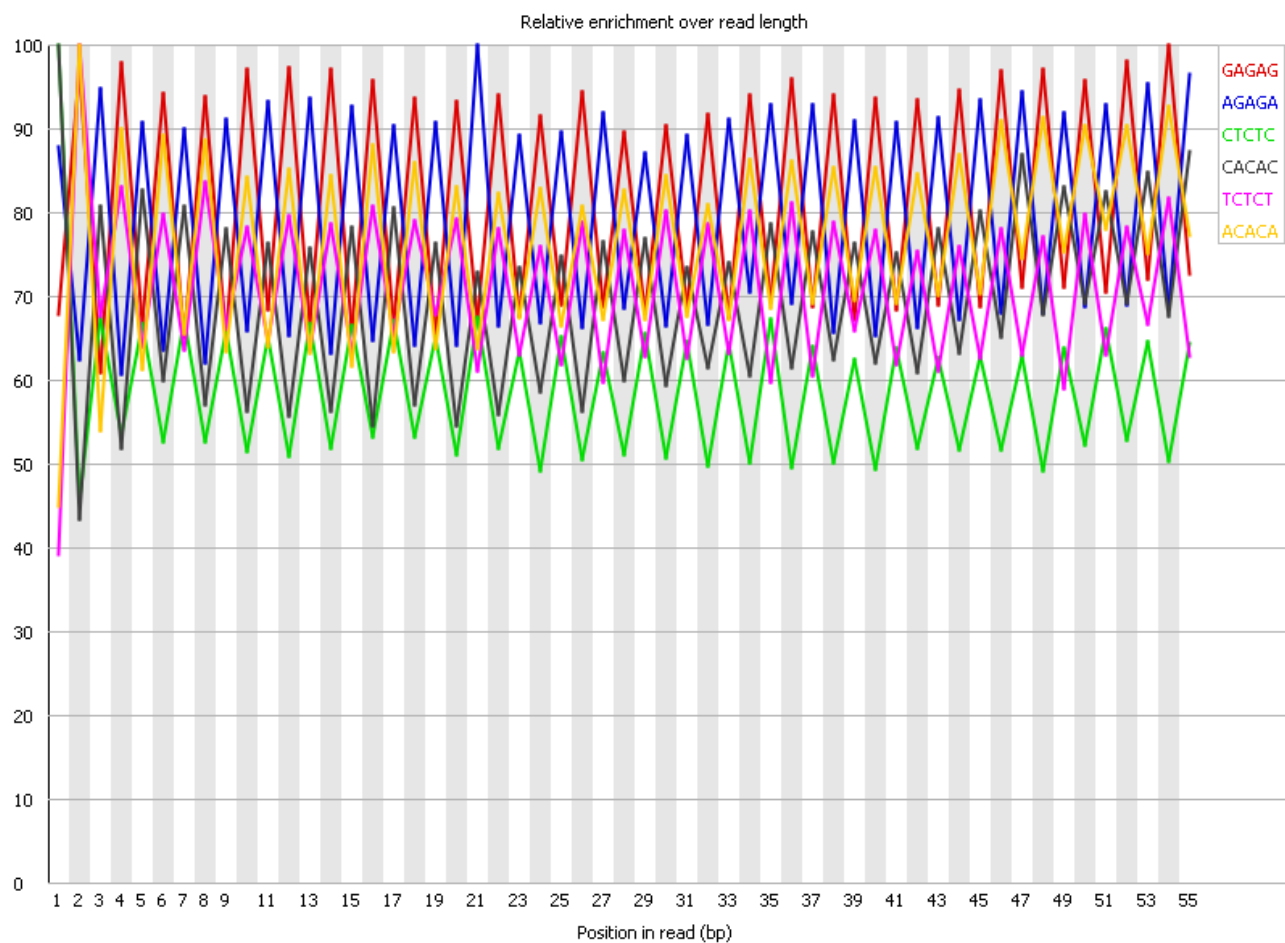
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### Overrepresented sequences

No overrepresented sequences

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### Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
GAGAG	1428690	8.5290985	10.483994	54
AGAGA	1546595	6.6827054	8.415197	21
CTCTC	816125	4.6517086	7.8920164	1
CACAC	888970	4.2003827	6.0200033	1
TCTCT	842050	4.124638	5.804397	2
ACACA	950610	3.5145457	4.581321	2
TTTTT	957515	3.4639993	5.1673374	42
GAGGG	375165	3.0944028	4.550071	1
GGGAG	368255	3.0374086	3.8401148	3
GGAGA	503550	3.0061297	3.587148	1
CTCTG	418740	2.5802083	5.3766656	22

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