












FastQC Report

Wed 13 Jul 2011

ChIP-Seq-pOLs.fastqsanger

Summary

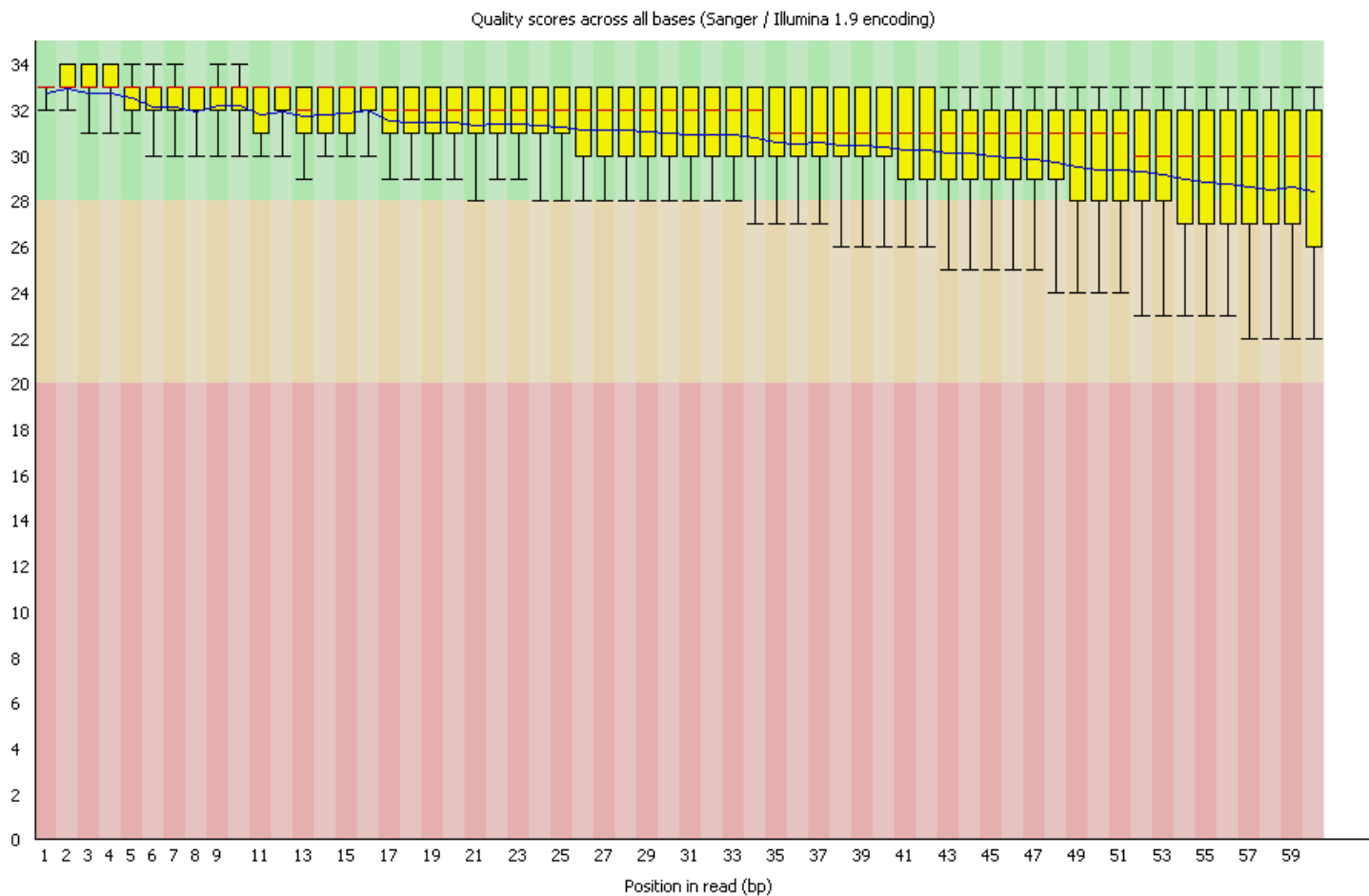
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-  [Per base GC content](#)
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Basic Statistics

Measure	Value
Filename	ChIP-Seq-pOLs.fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	5095659
Sequence length	60
%GC	45

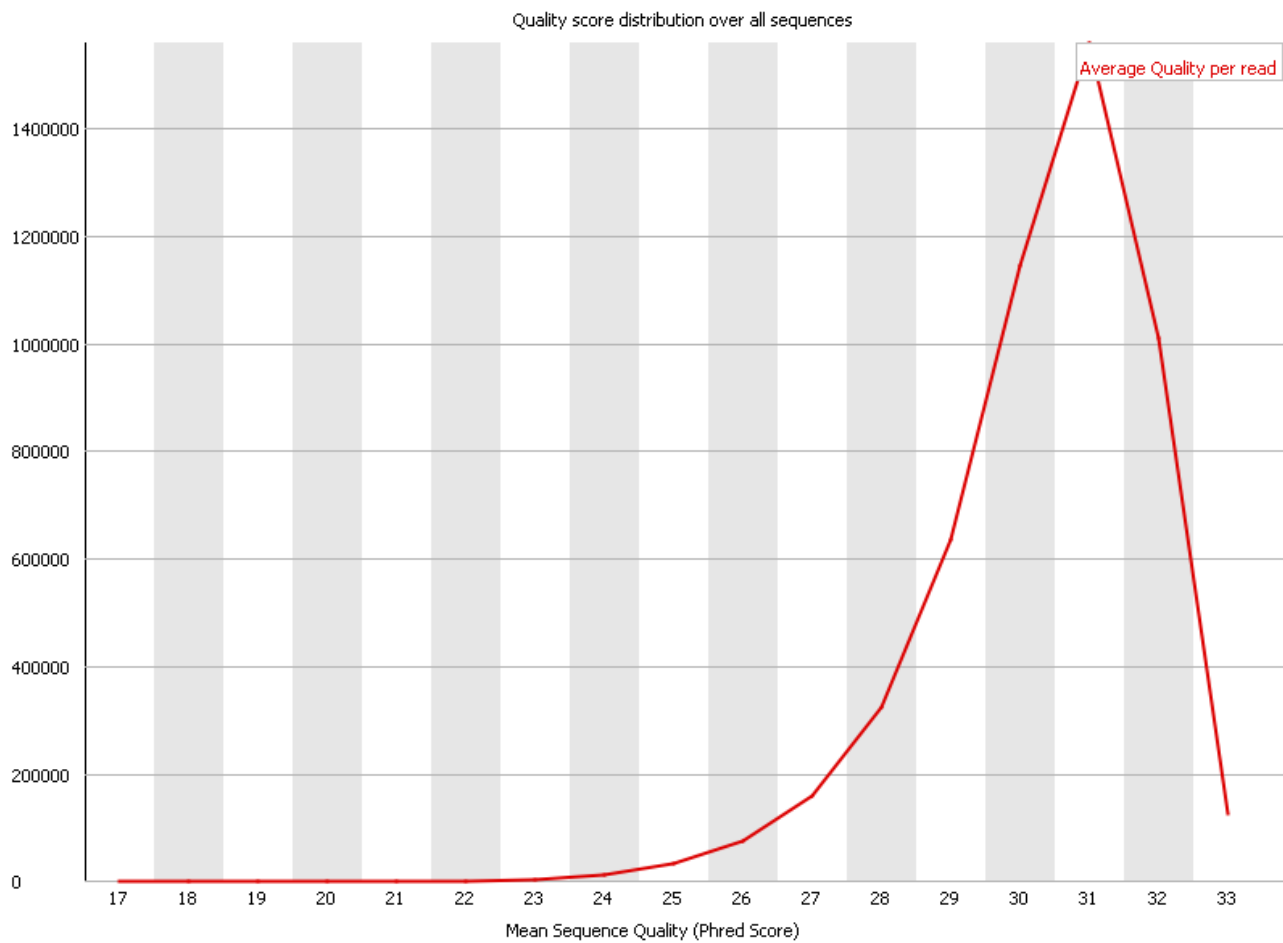
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Per base sequence quality



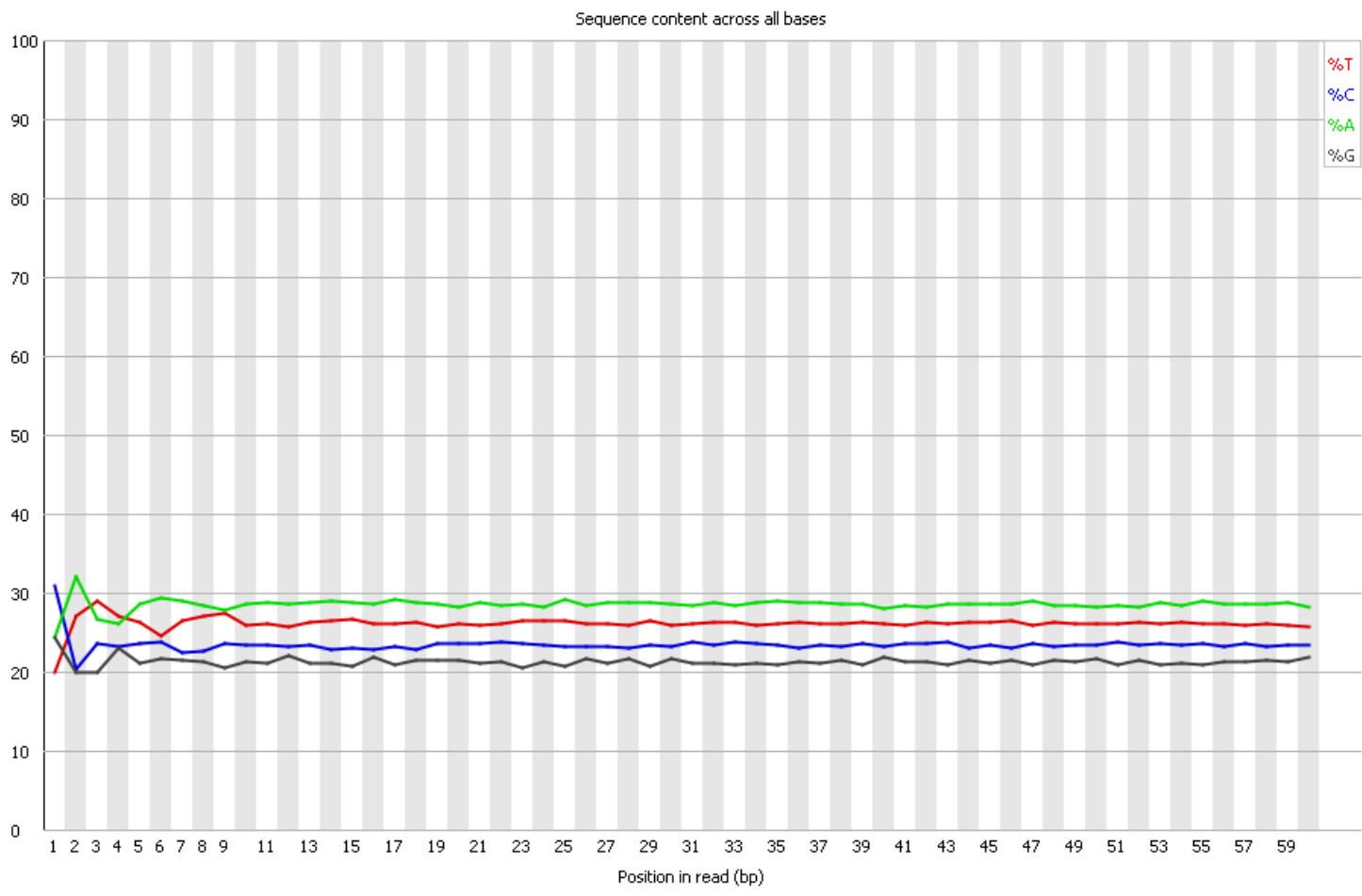
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Per sequence quality scores



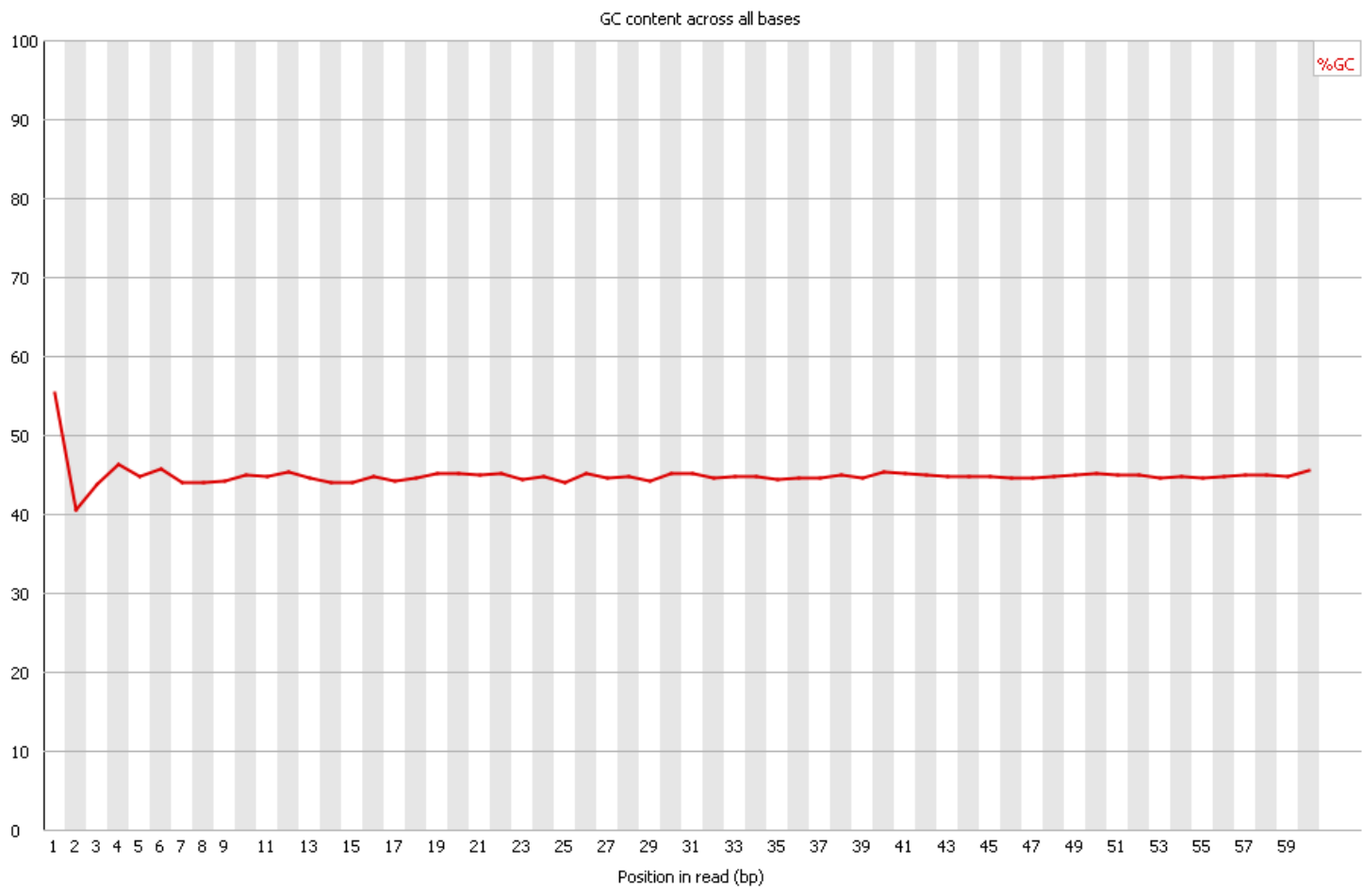
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 Per base sequence content



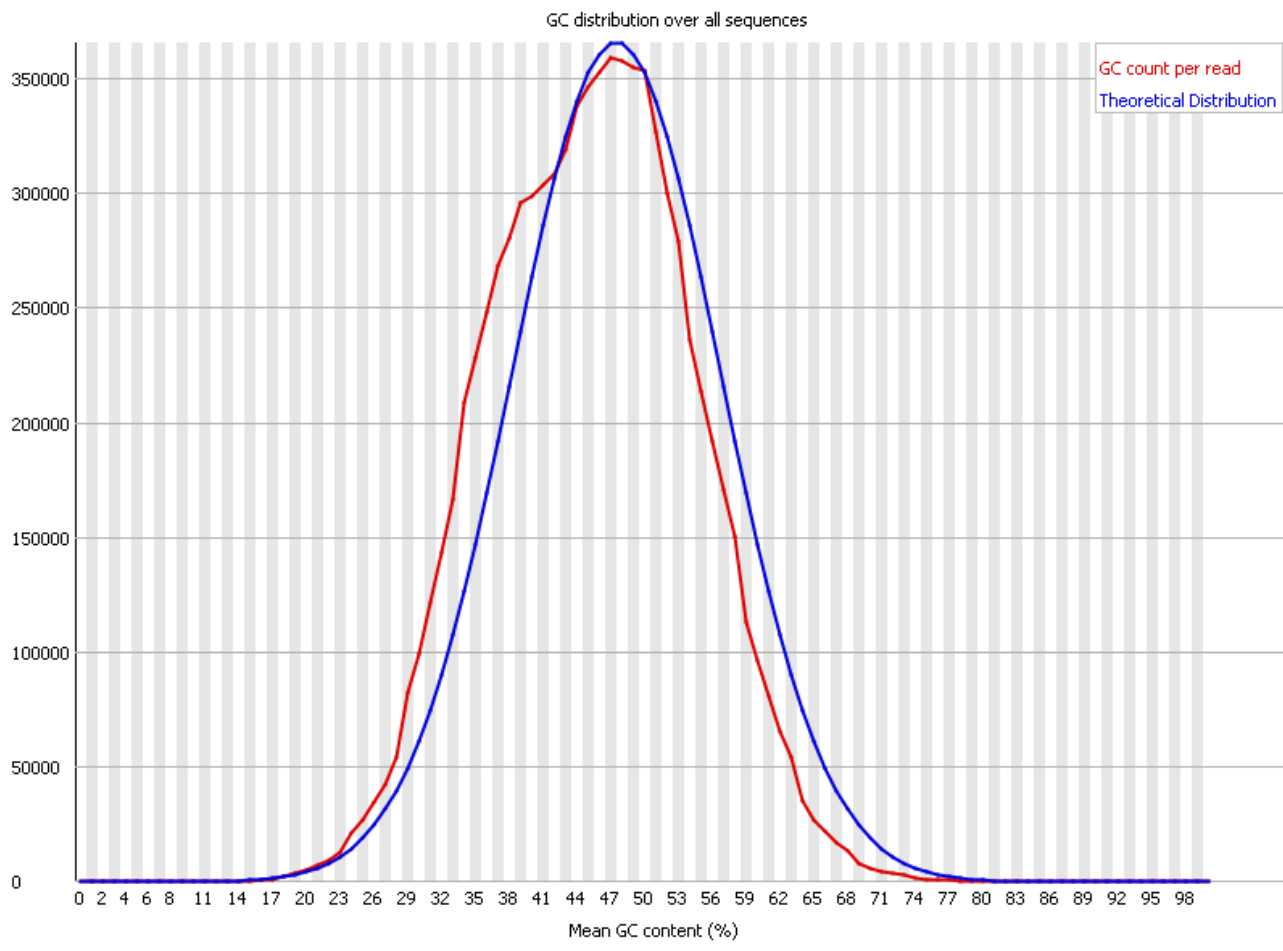
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 Per base GC content



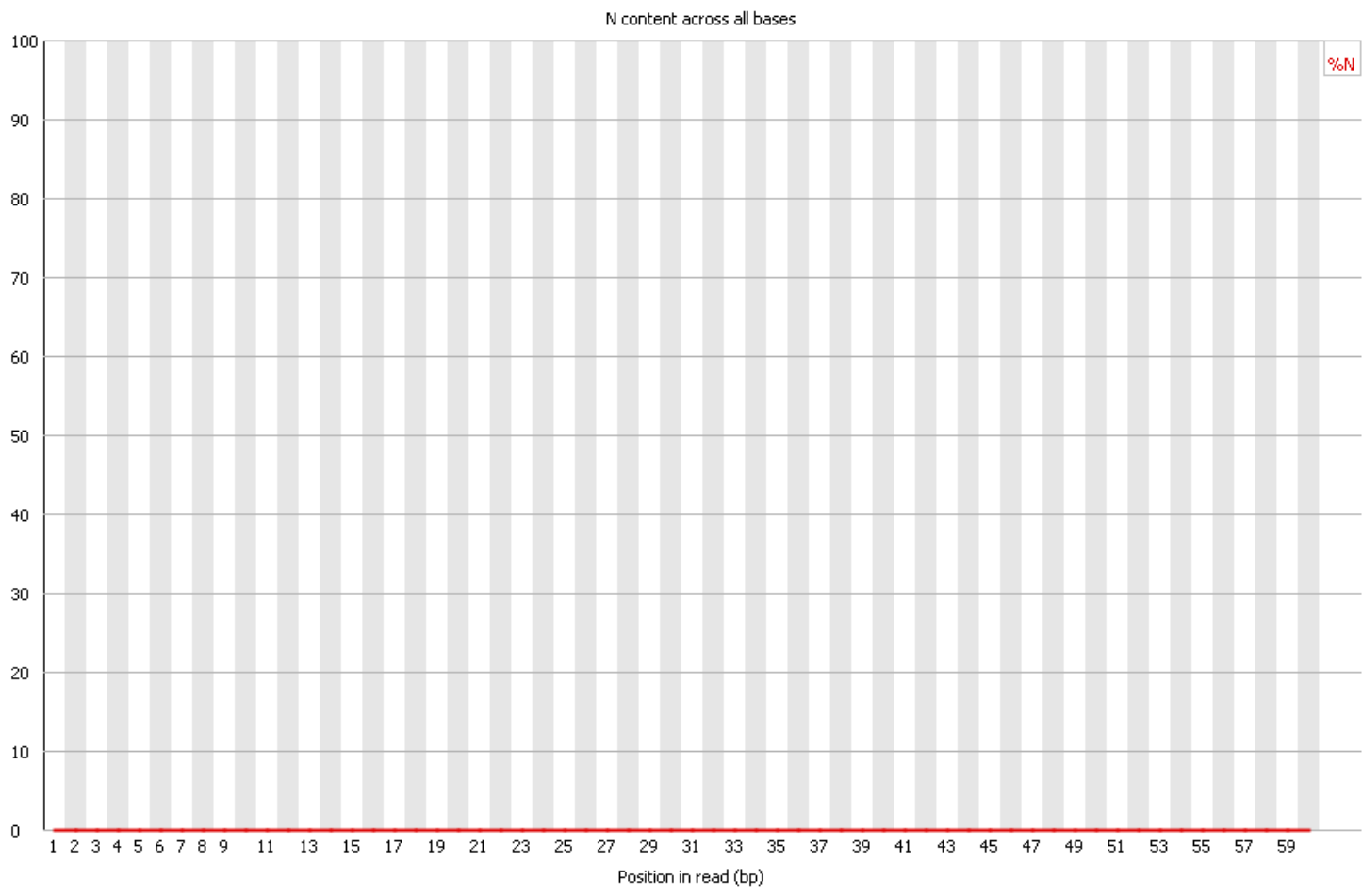
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! Per sequence GC content



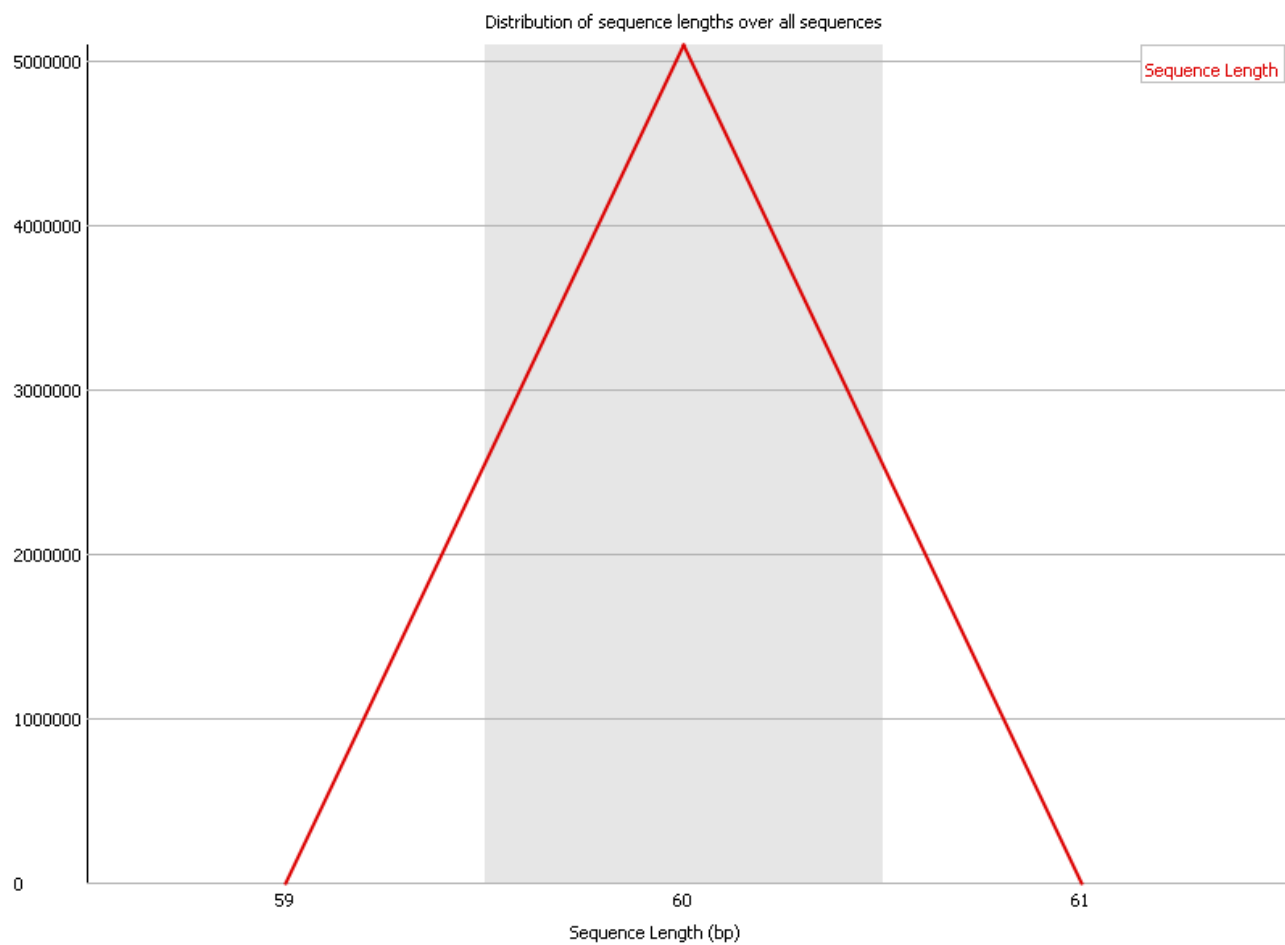
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 Per base N content



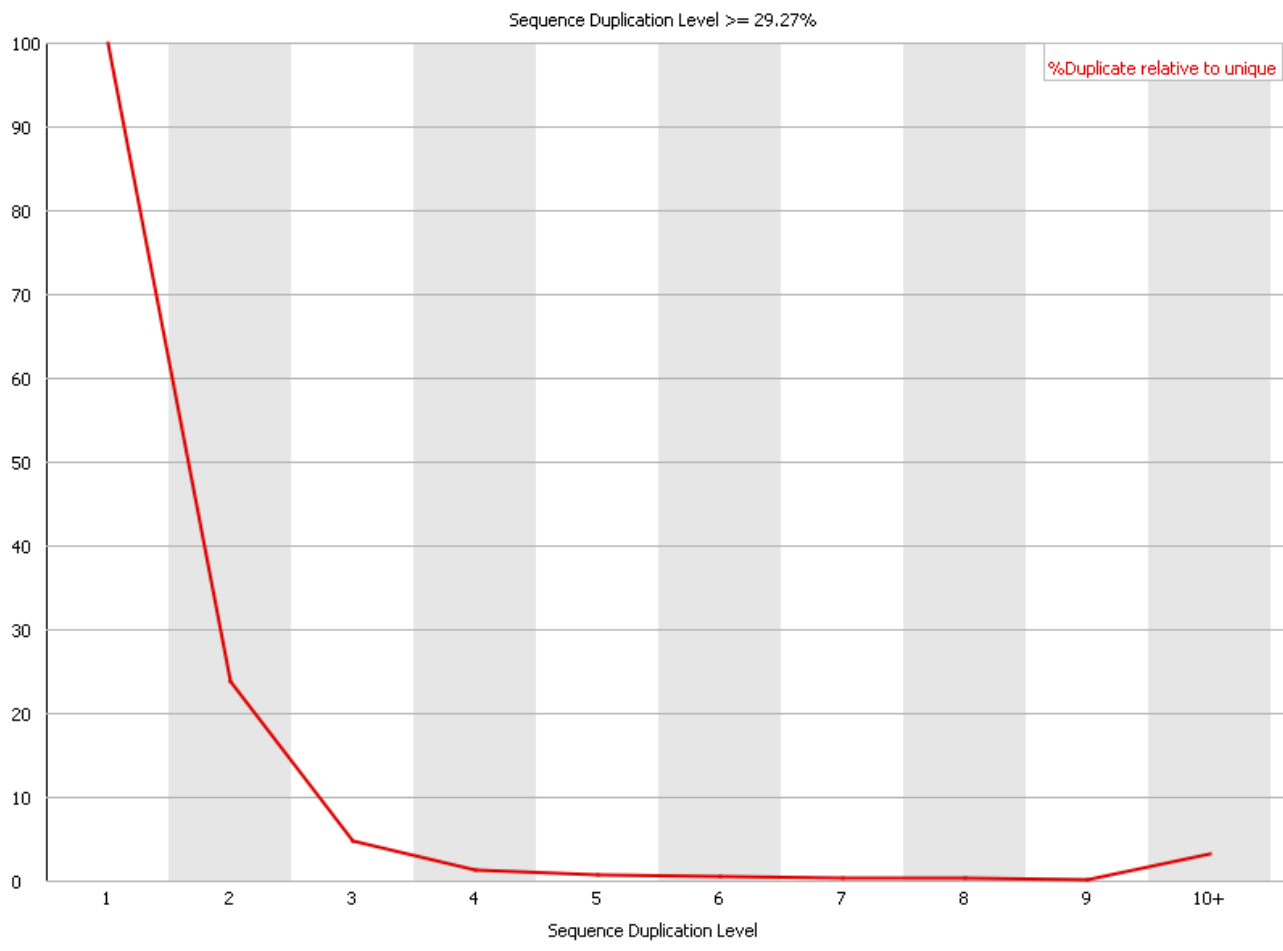
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Sequence Length Distribution



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! Sequence Duplication Levels



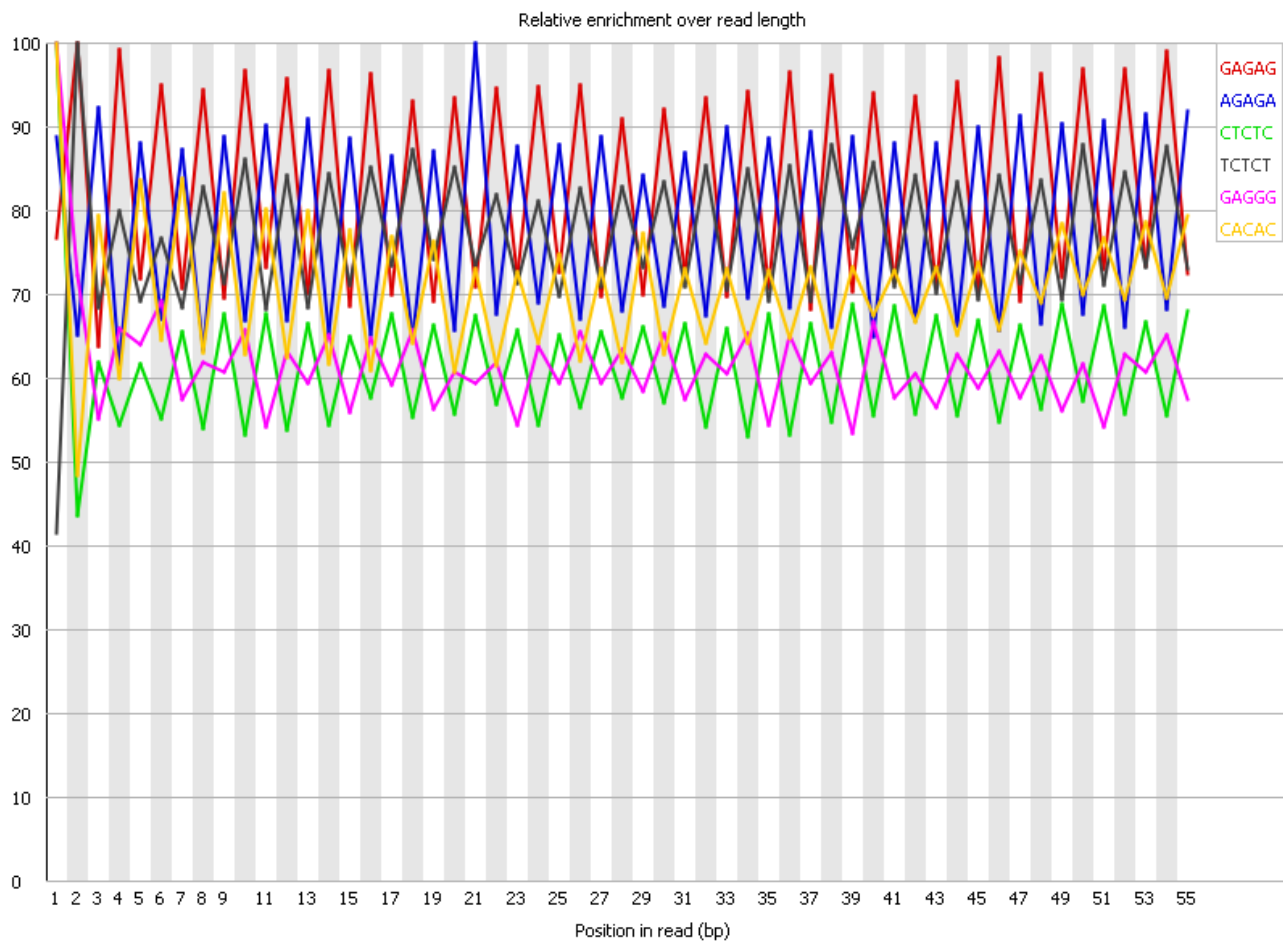
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Overrepresented sequences

No overrepresented sequences

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Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
GAGAG	1995480	8.804197	10.597129	2
AGAGA	2123230	6.993099	8.931539	21
CTCTC	1232670	4.842374	7.8667407	1
TCTCT	1243120	4.381121	5.6668015	2
GAGGG	612870	3.6222668	5.856107	1
CACAC	1097305	3.6217186	5.1173496	1
GGAGA	809570	3.5718794	4.114365	4
AGAGG	794160	3.5038893	3.9942465	27
GGGAG	574860	3.397615	4.344539	3
ACACA	1229790	3.337851	4.182797	2
GGAGG	556070	3.2865598	3.8211792	1
AGGAG	725135	3.1993463	4.121645	2
GAGGA	723495	3.1921103	4.417695	1
CTCTG	633585	2.7417934	6.119199	22
TGTTT	647720	2.255997	5.7210584	11
CTGGT	460675	2.196053	5.1323066	1
TCTGG	405640	1.9336994	5.327636	23
GTTTG	361110	1.5443594	5.646421	12
TGATG	391375	1.5342278	5.0311503	15

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