

.mc_f_1 FastQC Report



FastQC Report

Fri 27 Jun 2014

.mc_f_1

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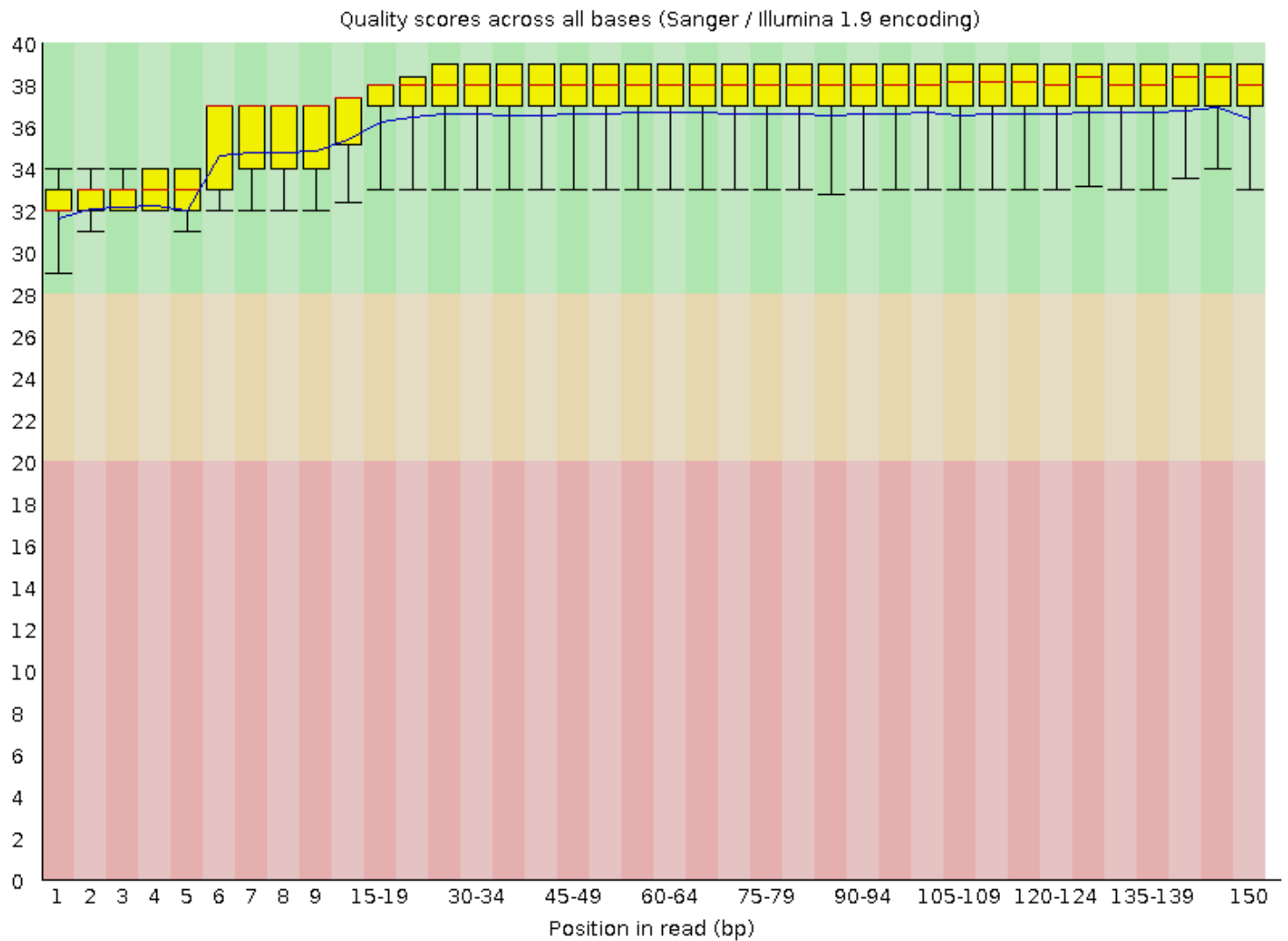


Basic Statistics

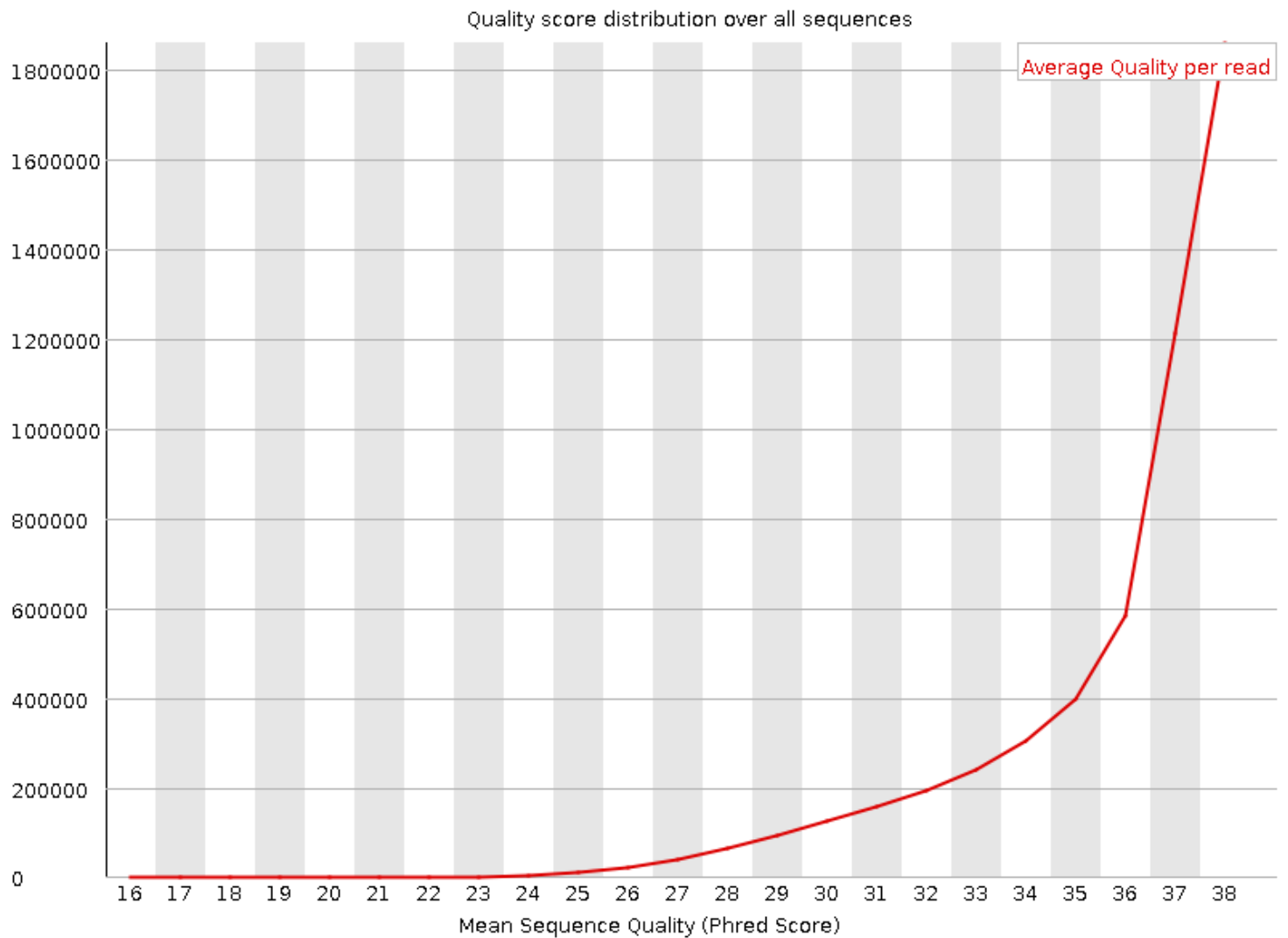
Measure	Value
Filename	.mc_f_1
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	5331604
Filtered Sequences	0
Sequence length	36-150
%GC	48



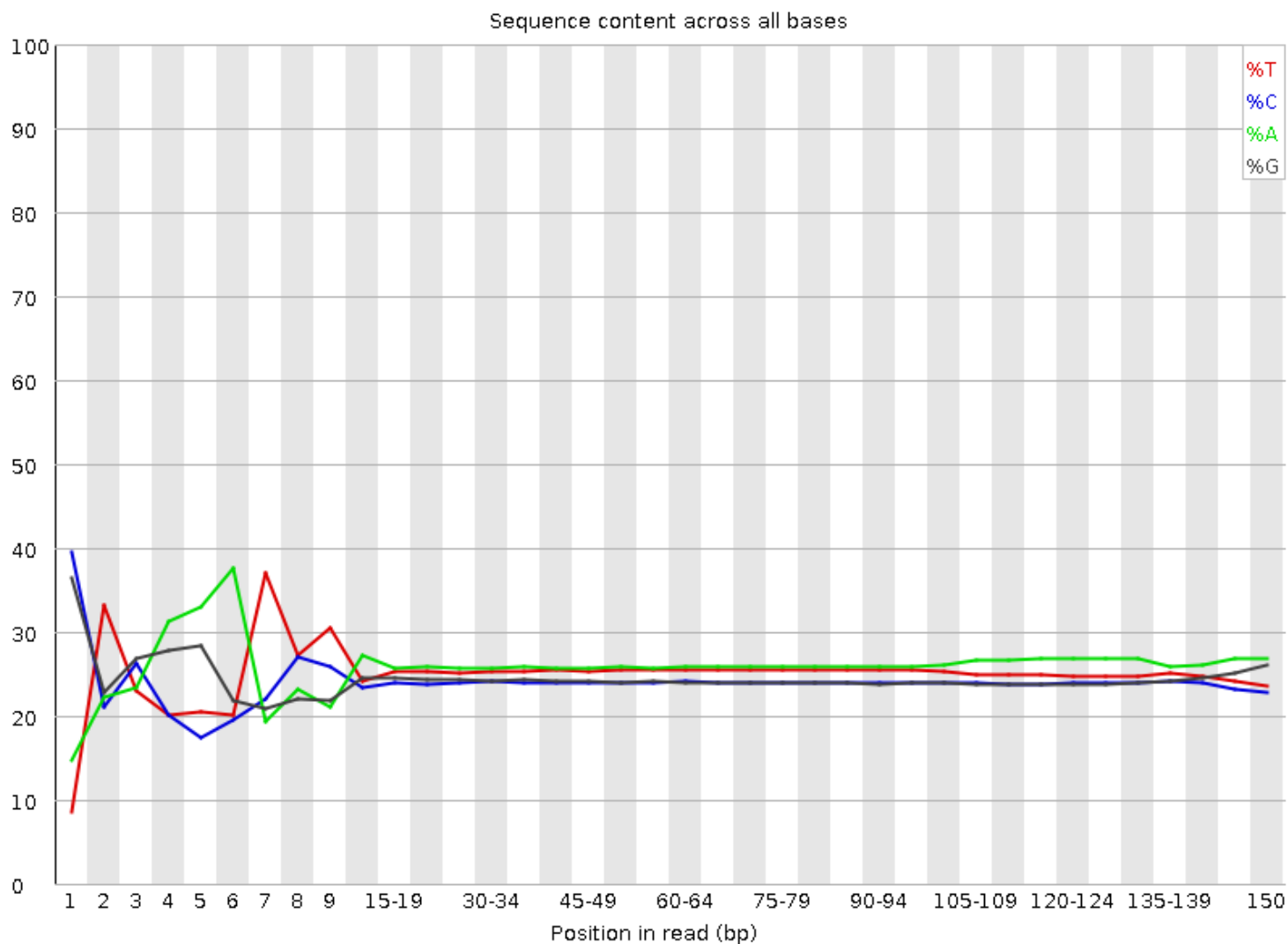
Per base sequence quality



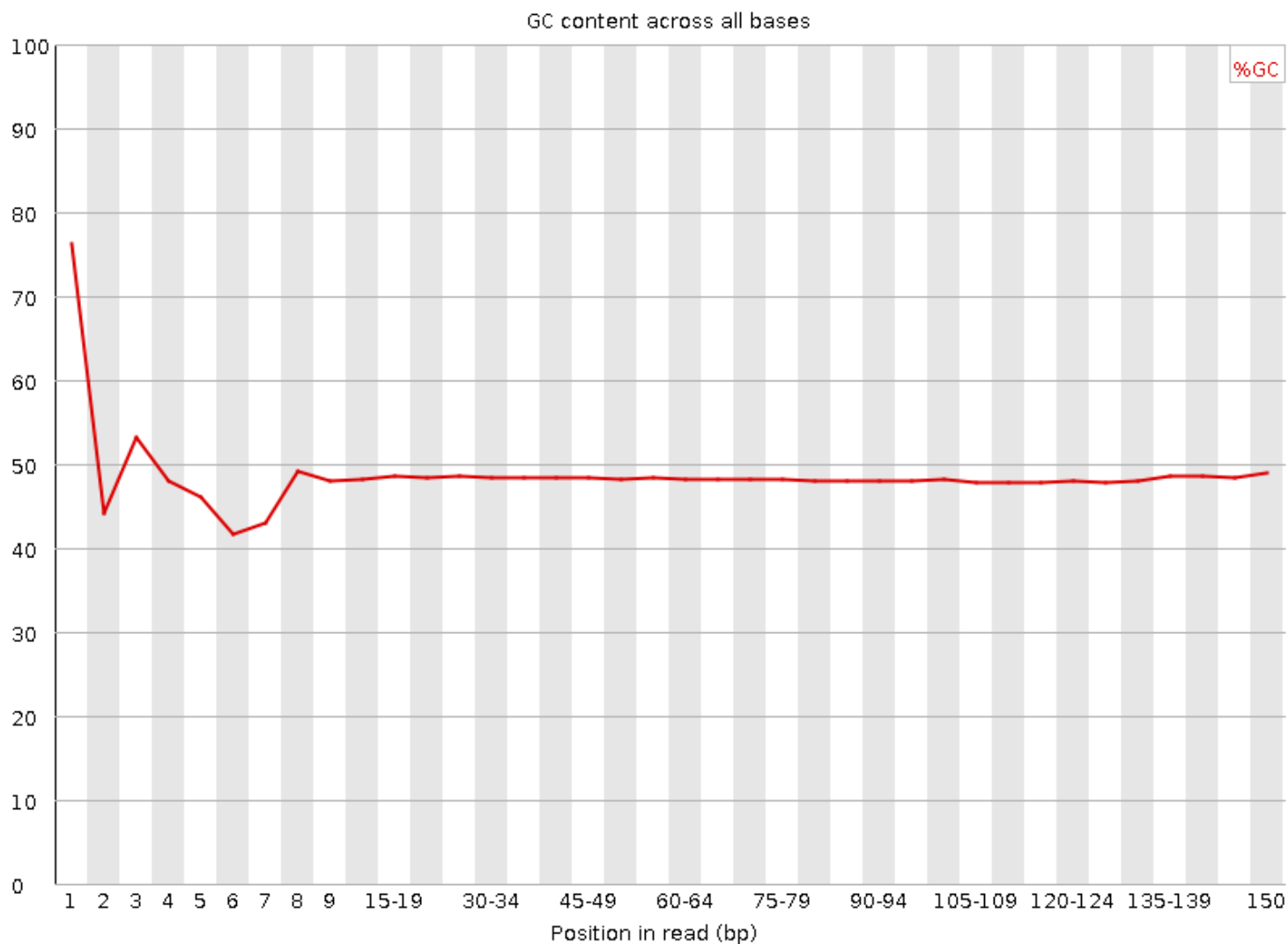
Per sequence quality scores



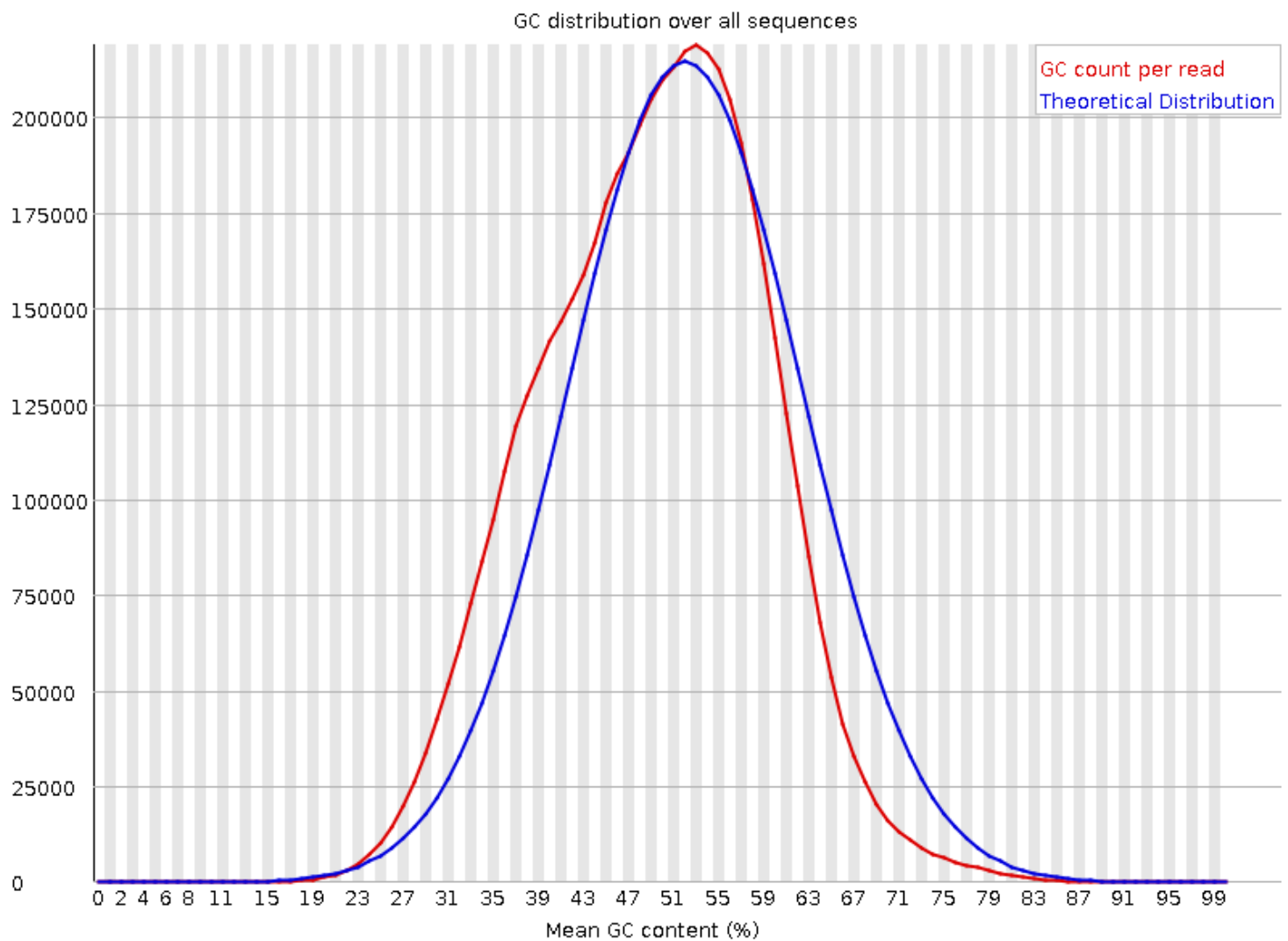
Per base sequence content



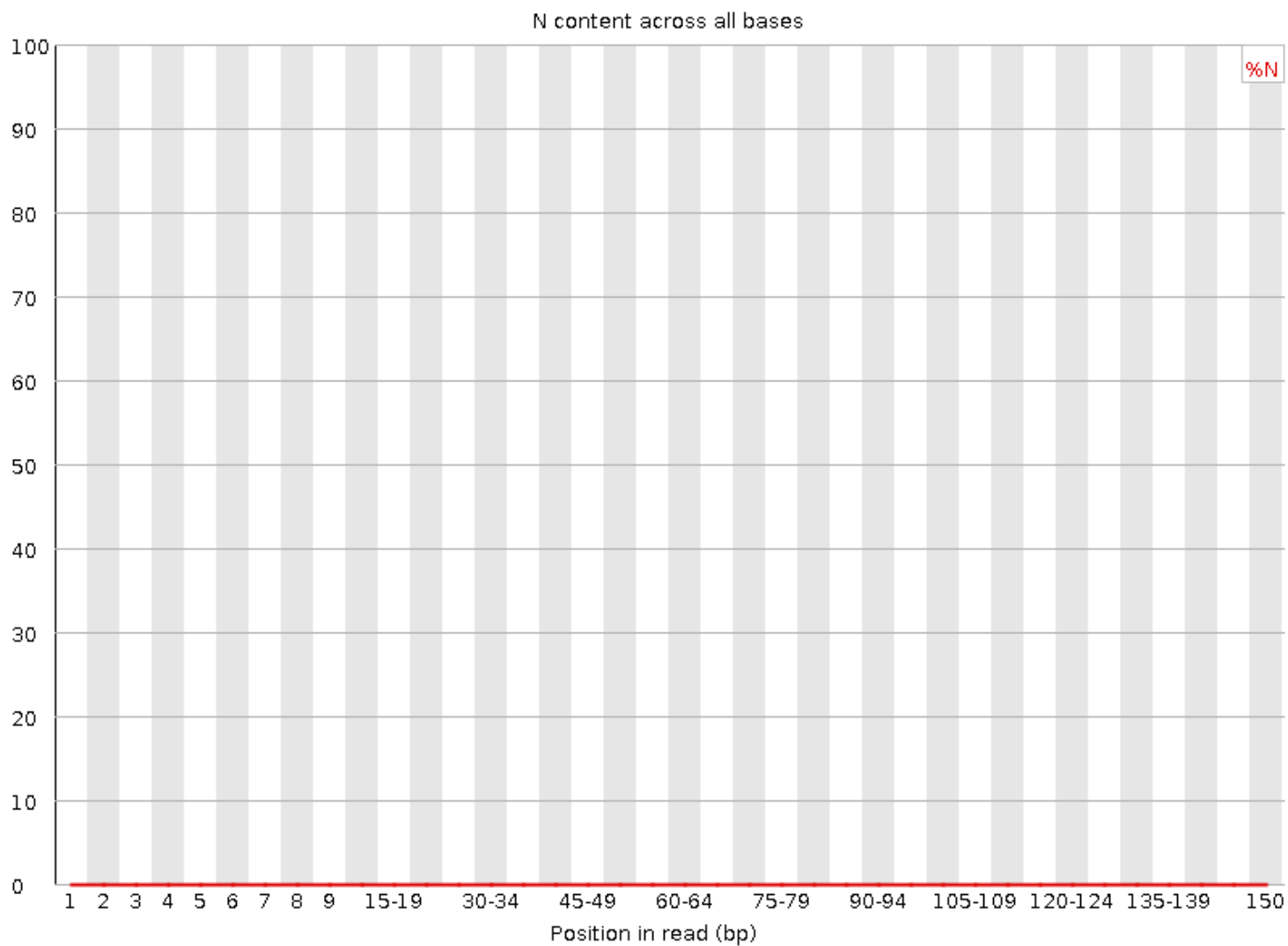
Per base GC content



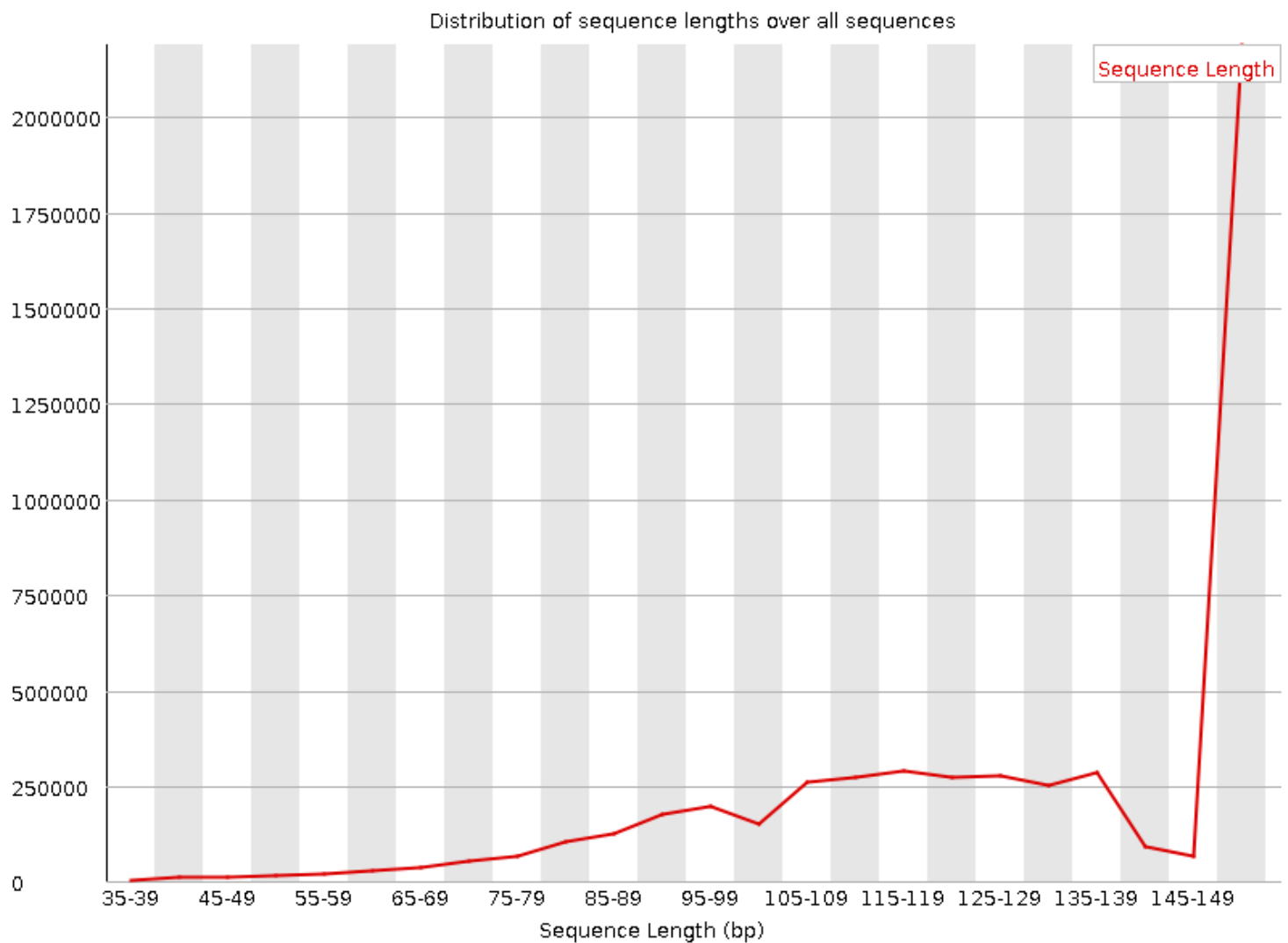
Per sequence GC content



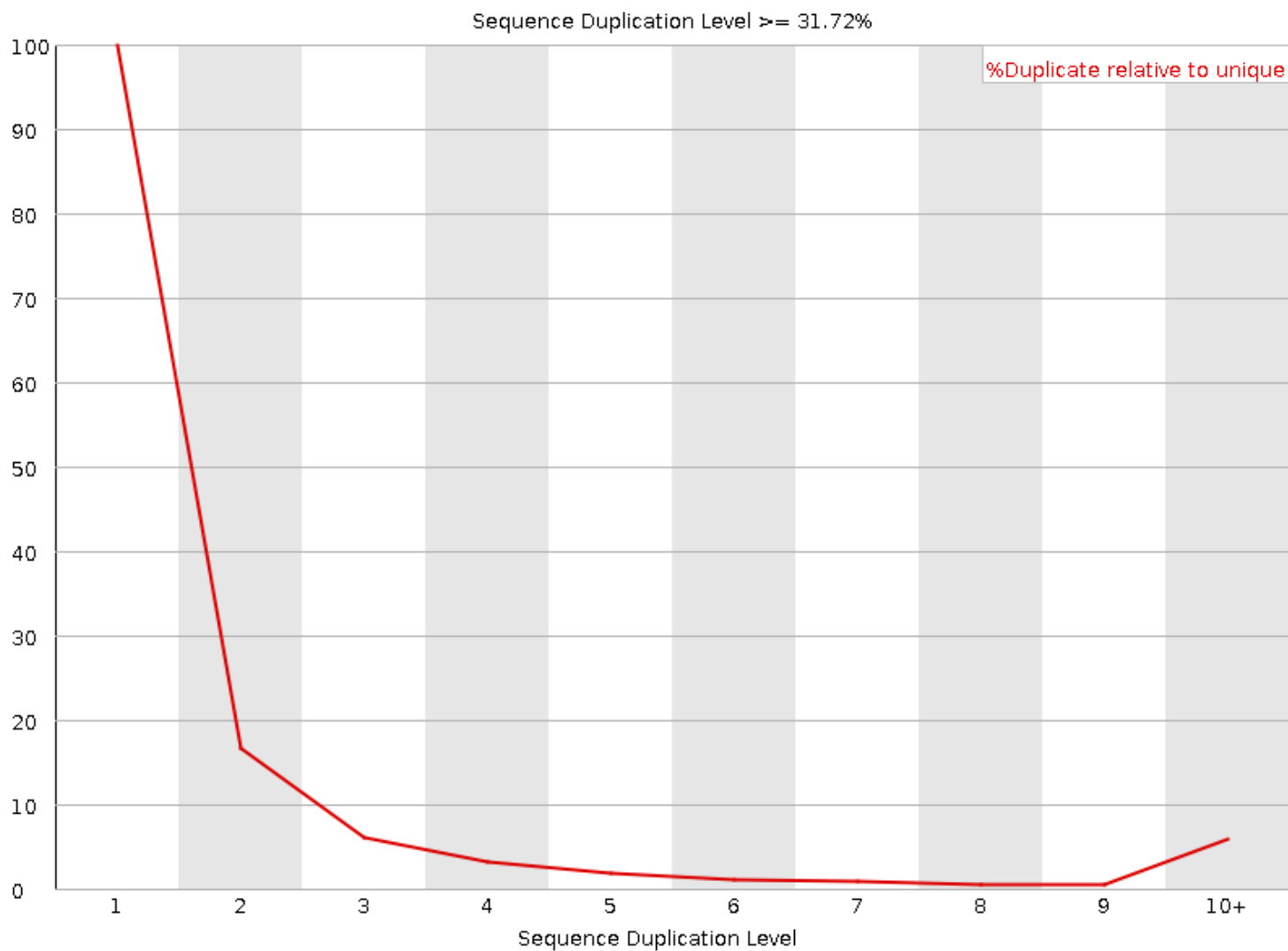
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

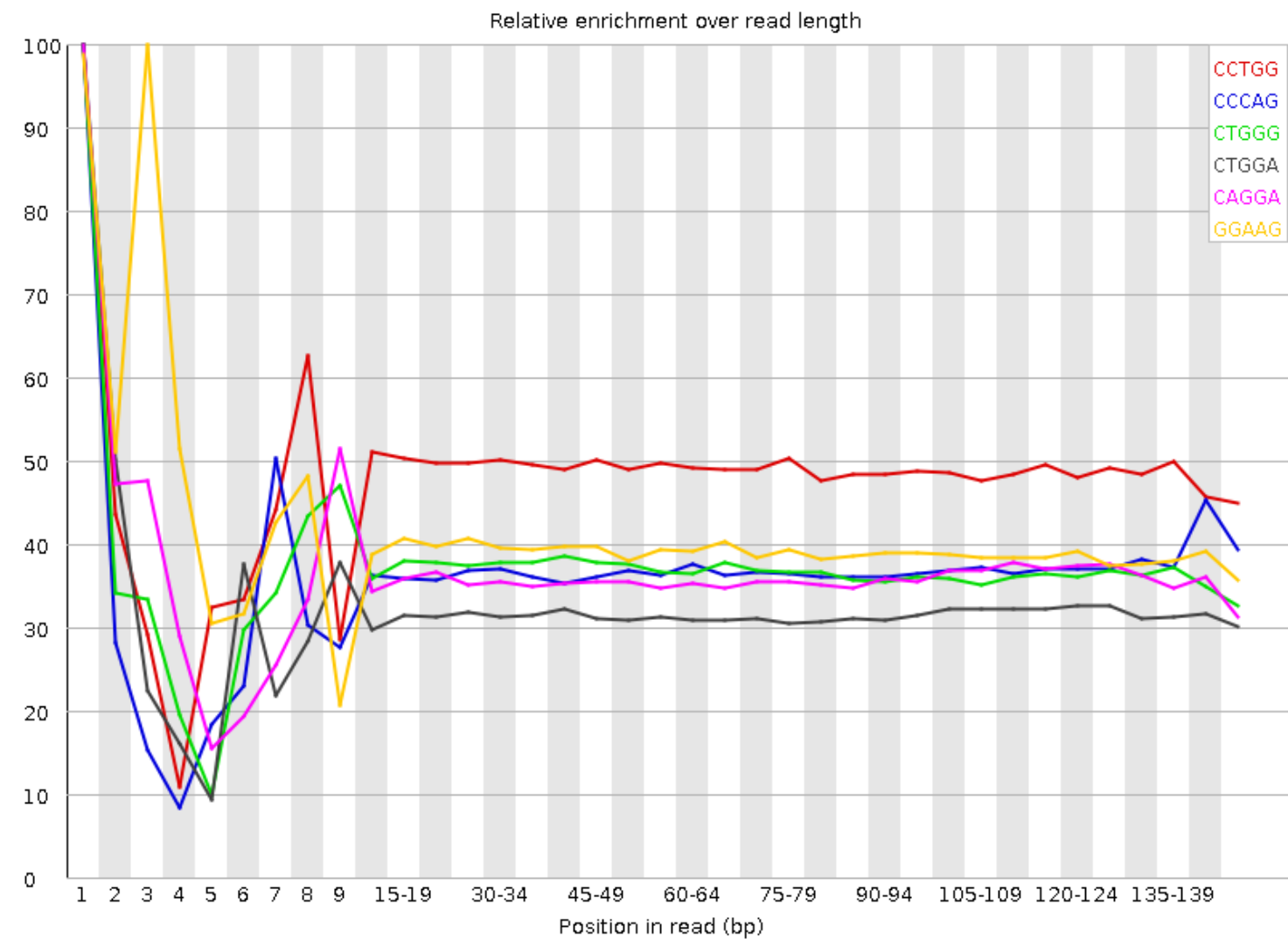


Overrepresented sequences

No overrepresented sequences



Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp	Position
CCTGG	1406800	2.4498837	5.017741	1	
CCCAG	1366605	2.3242958	6.3471613	1	
CTGGG	1333320	2.3009083	6.193922	1	
CTGGA	1391285	2.2343729	7.0146456	1	
CAGGA	1394410	2.1672902	5.9858418	1	
GGAAG	1329775	2.0481255	5.088619	3	
CTCAG	1179690	1.9118581	5.810879	1	
GCCAG	1124525	1.8952622	5.5952387	1	
TGGAA	1099815	1.6288669	5.181881	2	
GTGGA	949680	1.5113624	5.0220256	1	
CAGAT	928700	1.3880004	7.2735047	145-146	
GAGAT	823630	1.2198267	8.258251	145-146	
AGATC	809520	1.2098786	18.773237	145-146	
TCGGA	318595	0.51165646	9.272223	145-146	
GATCG	286915	0.46077907	19.44268	145-146	
ATCGG	265980	0.42715797	19.34606	145-146	

Files created by FastQC

[.mc_f_1_fastqc.zip \(173.5 KB\)](#)

[duplication_levels.png \(17.5 KB\)](#)

[fastqc_data.txt \(9.3 KB\)](#)

[fastqc_report.html \(8.1 KB\)](#)

[kmer_profiles.png \(60.3 KB\)](#)

[per_base_gc_content.png \(12.7 KB\)](#)

[per_base_n_content.png \(7.4 KB\)](#)

[per_base_quality.png \(8.7 KB\)](#)

[per_base_sequence_content.png \(24.9 KB\)](#)

[per_sequence_gc_content.png \(30.1 KB\)](#)

[per_sequence_quality.png \(16.7 KB\)](#)

[rgFastQC9V6o1y.log \(986 B\)](#)

[sequence_length_distribution.png \(17.7 KB\)](#)

[summary.txt \(399 B\)](#)

[FastQC documentation and full attribution is here](#)

FastQC was run by Galaxy using the rgenetics rgFastQC wrapper - see <http://bitbucket.org/rgenetics> for details and licensing
Produced by [FastQC](#) (version 0.10.1)