

Summary

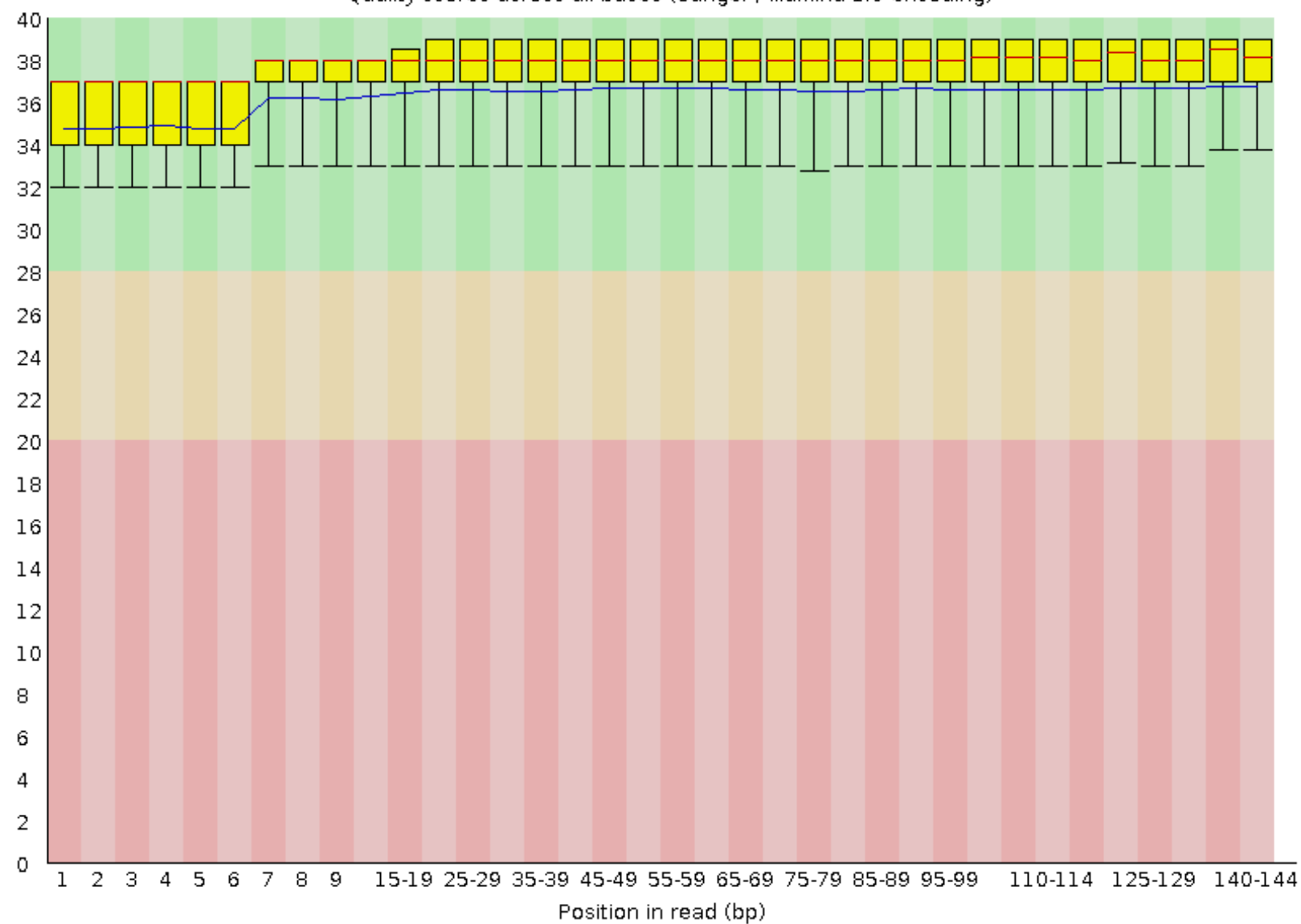
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Basic Statistics

Measure	Value
Filename	Trim_sequences_on_data_10
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	5331604
Filtered Sequences	0
Sequence length	30-144
%GC	48

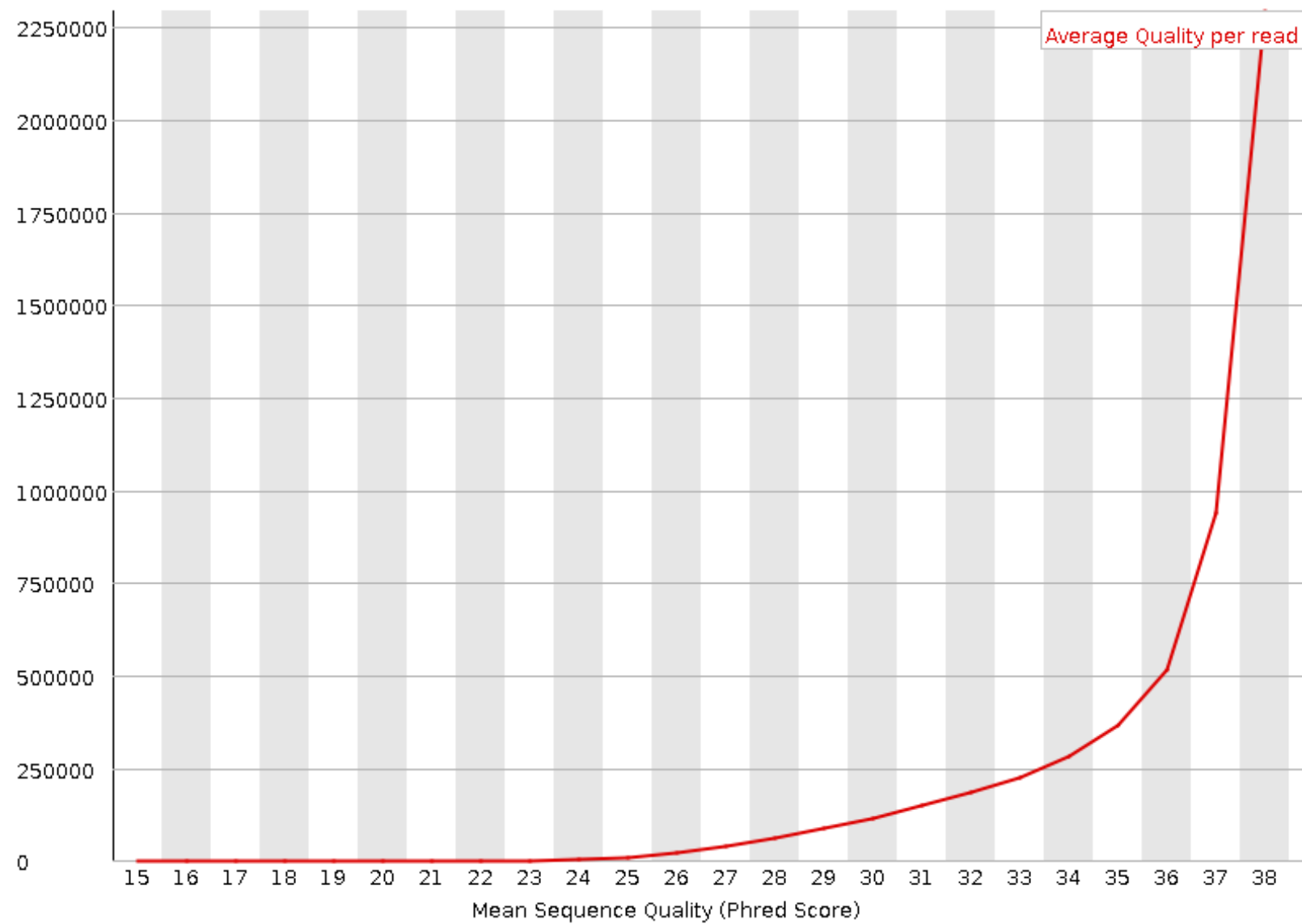
Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)



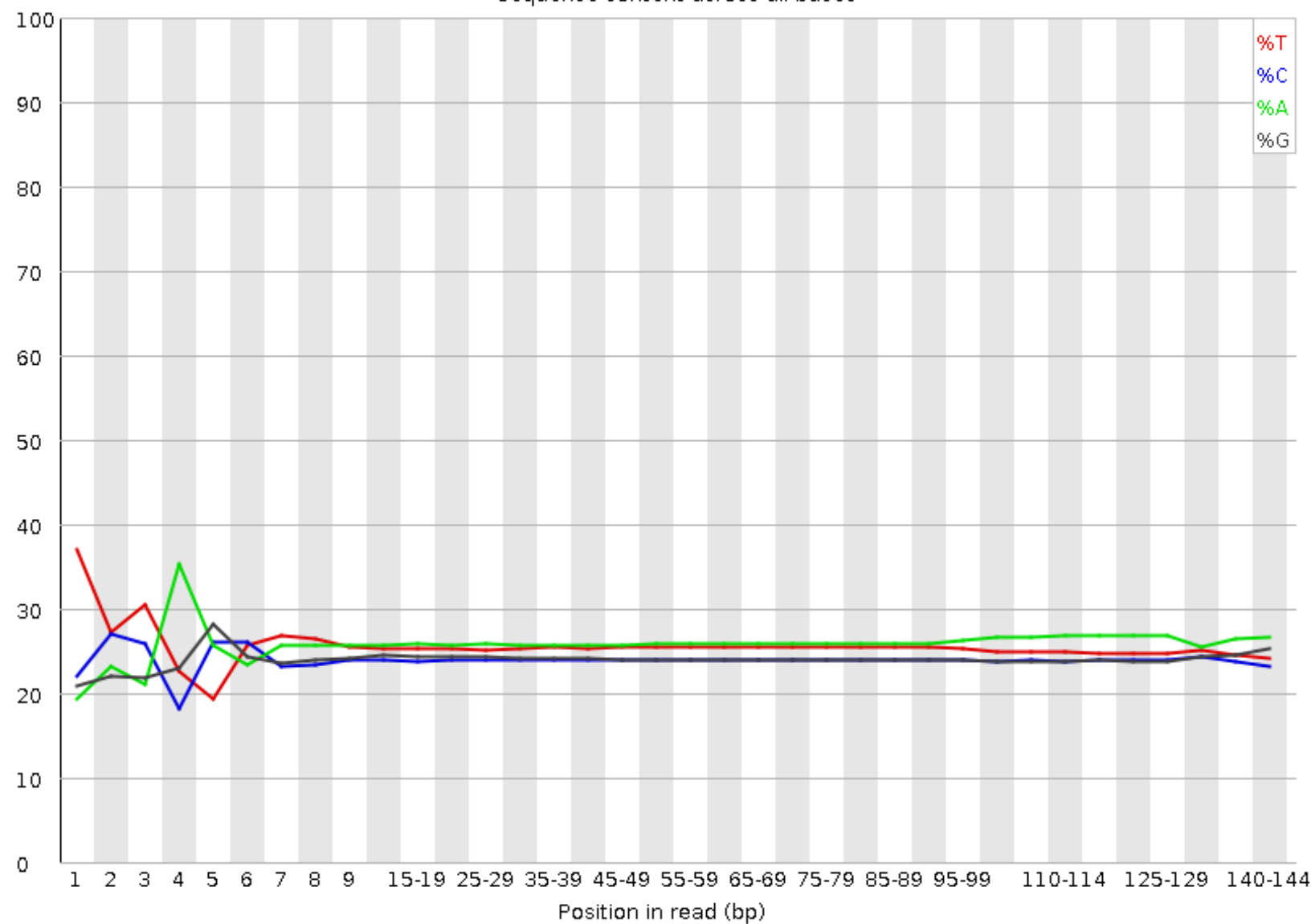
✓ **Per sequence quality scores**

Quality score distribution over all sequences

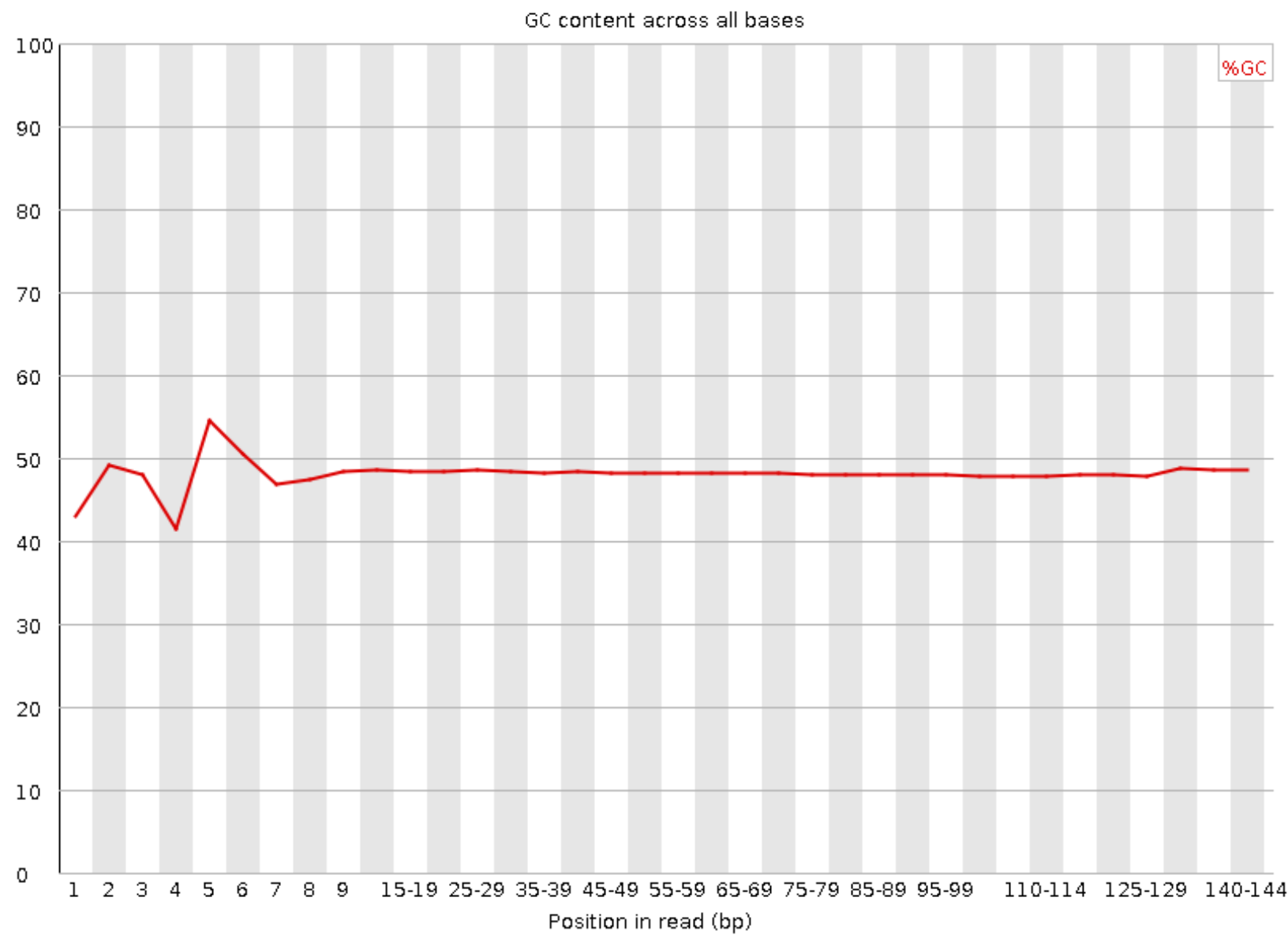


⚠ **Per base sequence content**

Sequence content across all bases

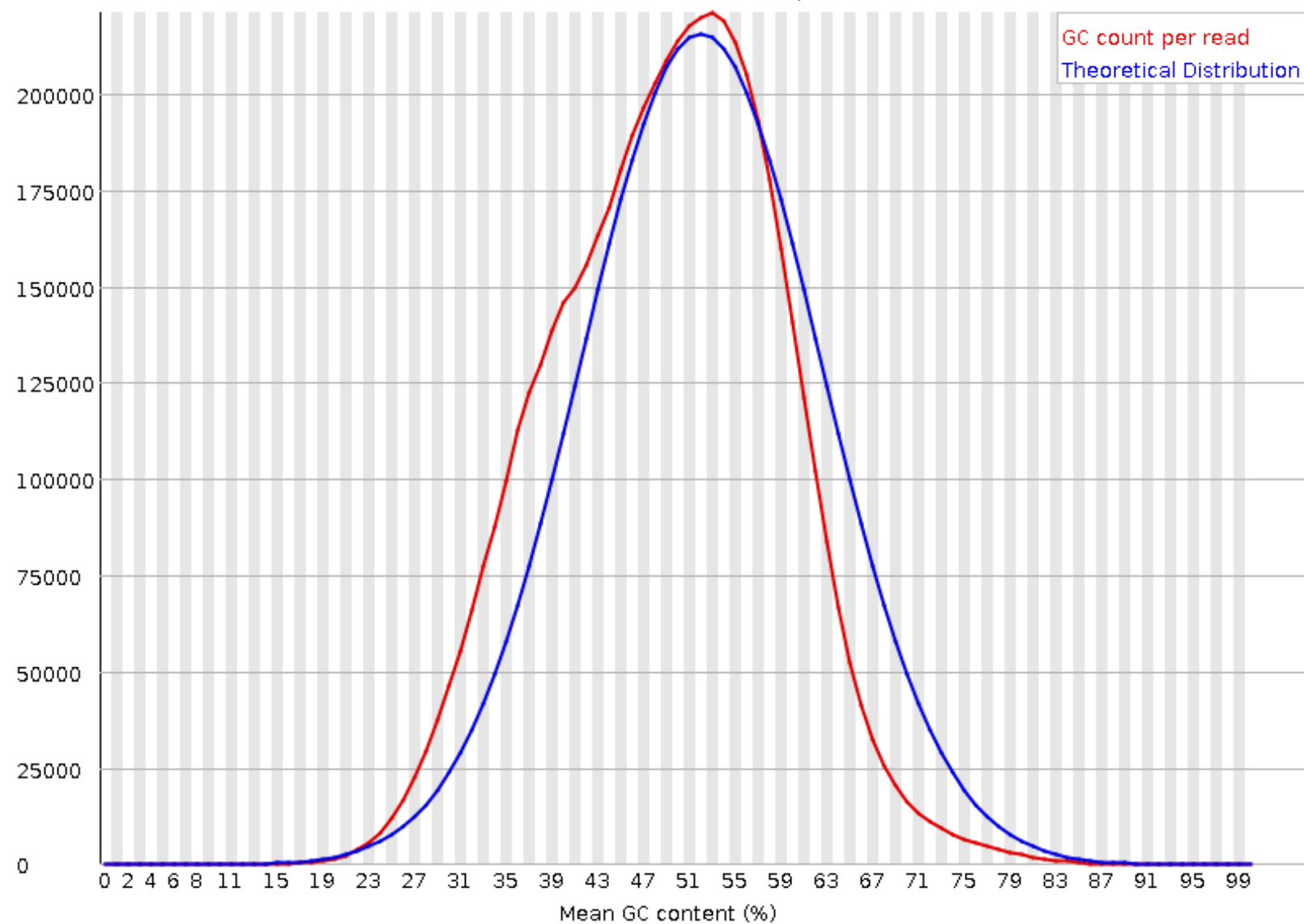


Per base GC content

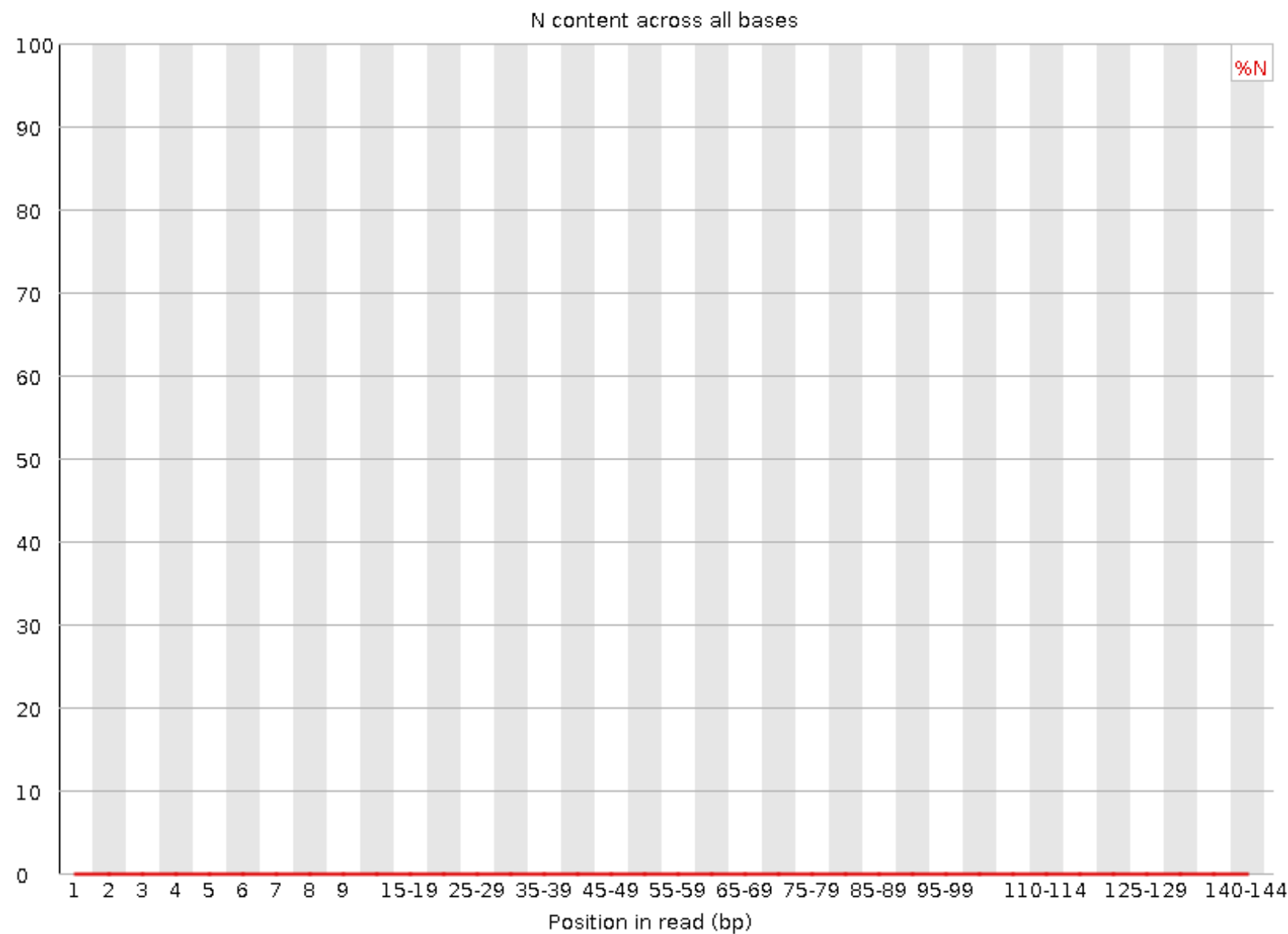


Per sequence GC content

GC distribution over all sequences

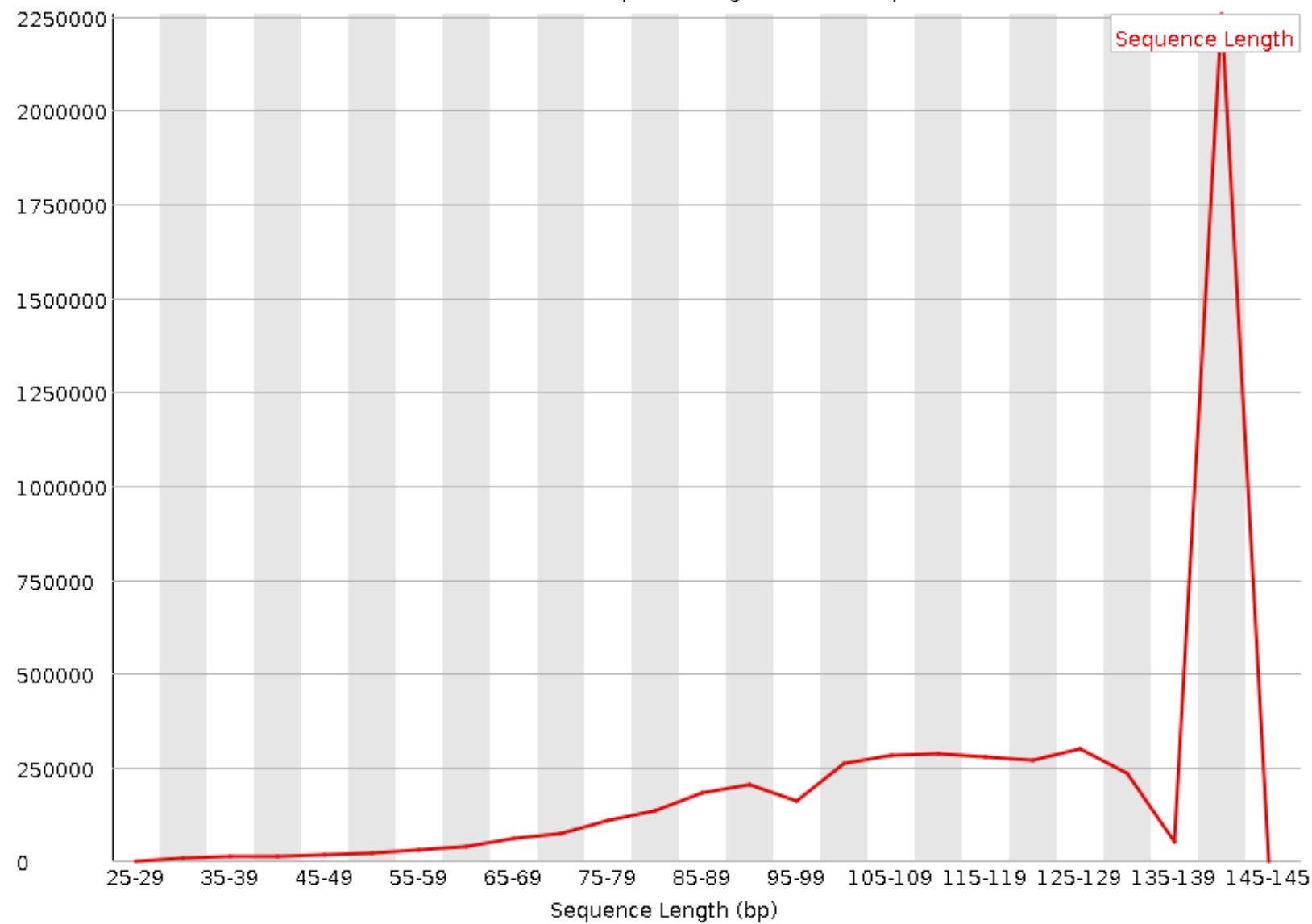


Per base N content



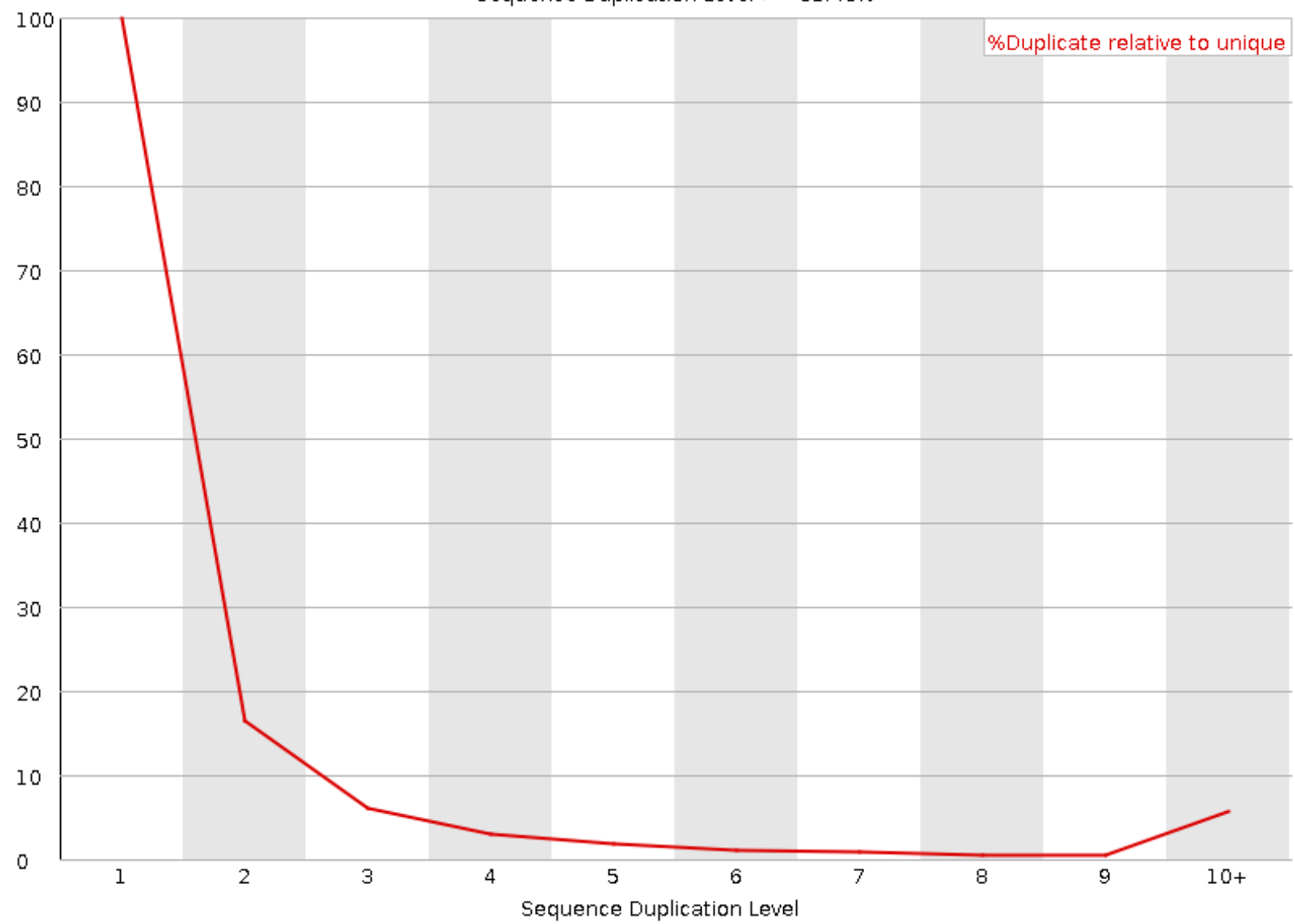
 Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Sequence Duplication Level $\geq$ 31.46%

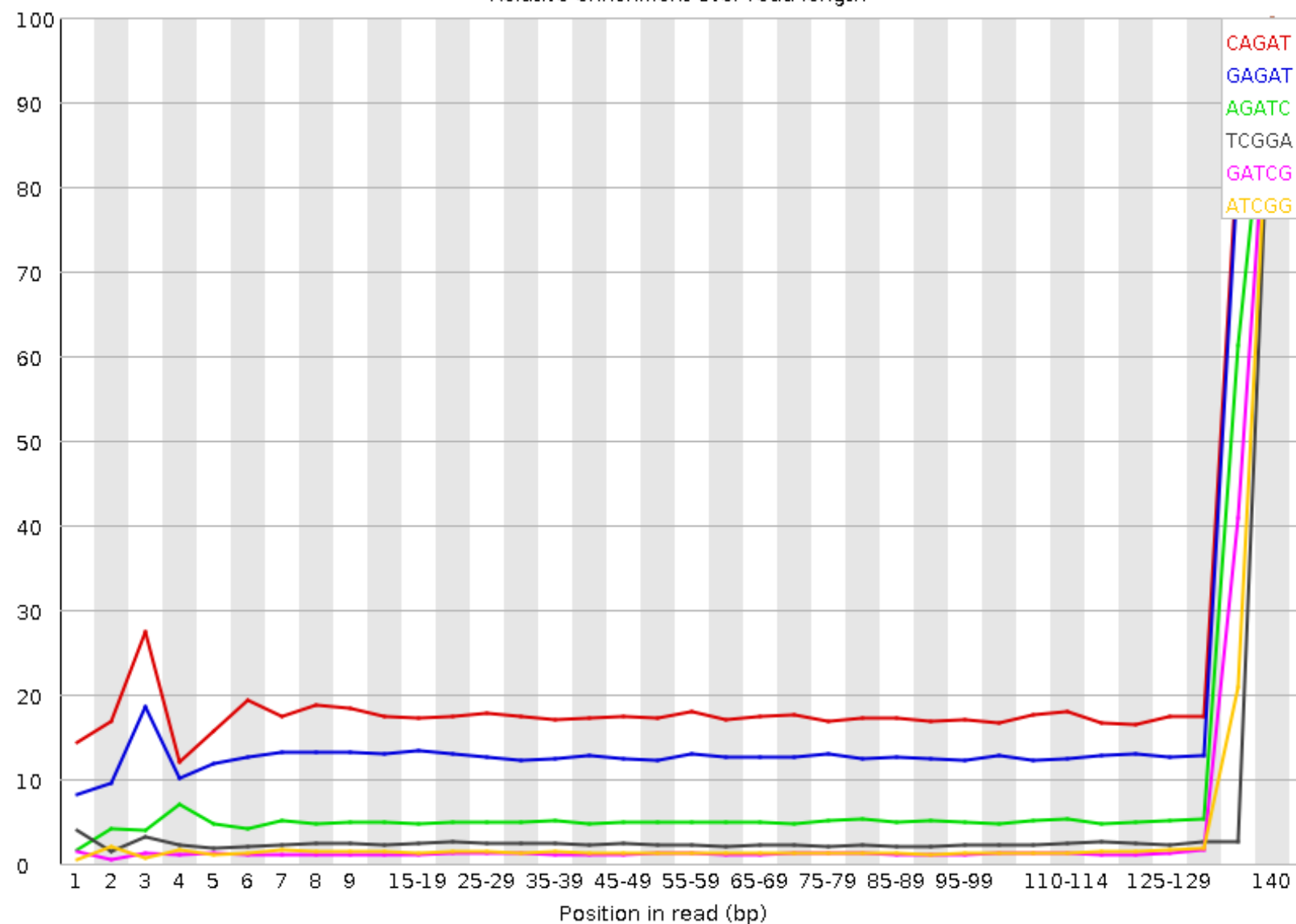


 **Overrepresented sequences**

No overrepresented sequences

 **Kmer Content**

Relative enrichment over read length



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CAGAT	875530	1.3787261	7.255835	140
GAGAT	772520	1.2133123	8.437641	140
AGATC	767665	1.2088675	18.779808	140
TCGGA	303515	0.5158999	18.260632	140
GATCG	276965	0.47077152	19.475422	140
ATCGG	255190	0.43375945	19.66455	140

Files created by FastQC

[Trim_sequences_on_data_10_fastqc.zip \(148.6 KB\)](#)

[duplication_levels.png \(17.4 KB\)](#)

[fastqc_data.txt \(8.6 KB\)](#)

[fastqc_report.html \(7.3 KB\)](#)

[kmer_profiles.png \(38.6 KB\)](#)

[per_base_gc_content.png \(10.9 KB\)](#)

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

[per_base_quality.png \(8.4 KB\)](#)

[per_base_sequence_content.png \(19.6 KB\)](#)

[per_sequence_gc_content.png \(30.0 KB\)](#)

[per_sequence_quality.png \(15.9 KB\)](#)

[rgFastQCgenRRY.log \(1.4 KB\)](#)

[sequence_length_distribution.png \(23.0 KB\)](#)

[summary.txt \(597 B\)](#)

[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)