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v1.14
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# MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2024-04-29, 15:21 CEST based on data in: `/home/BCG_2024_vfassi/project/737`

📘 Welcome! Not sure where to start?

[Watch a tutorial video](#)

(6:06)

don't show again ✕

## General Statistics

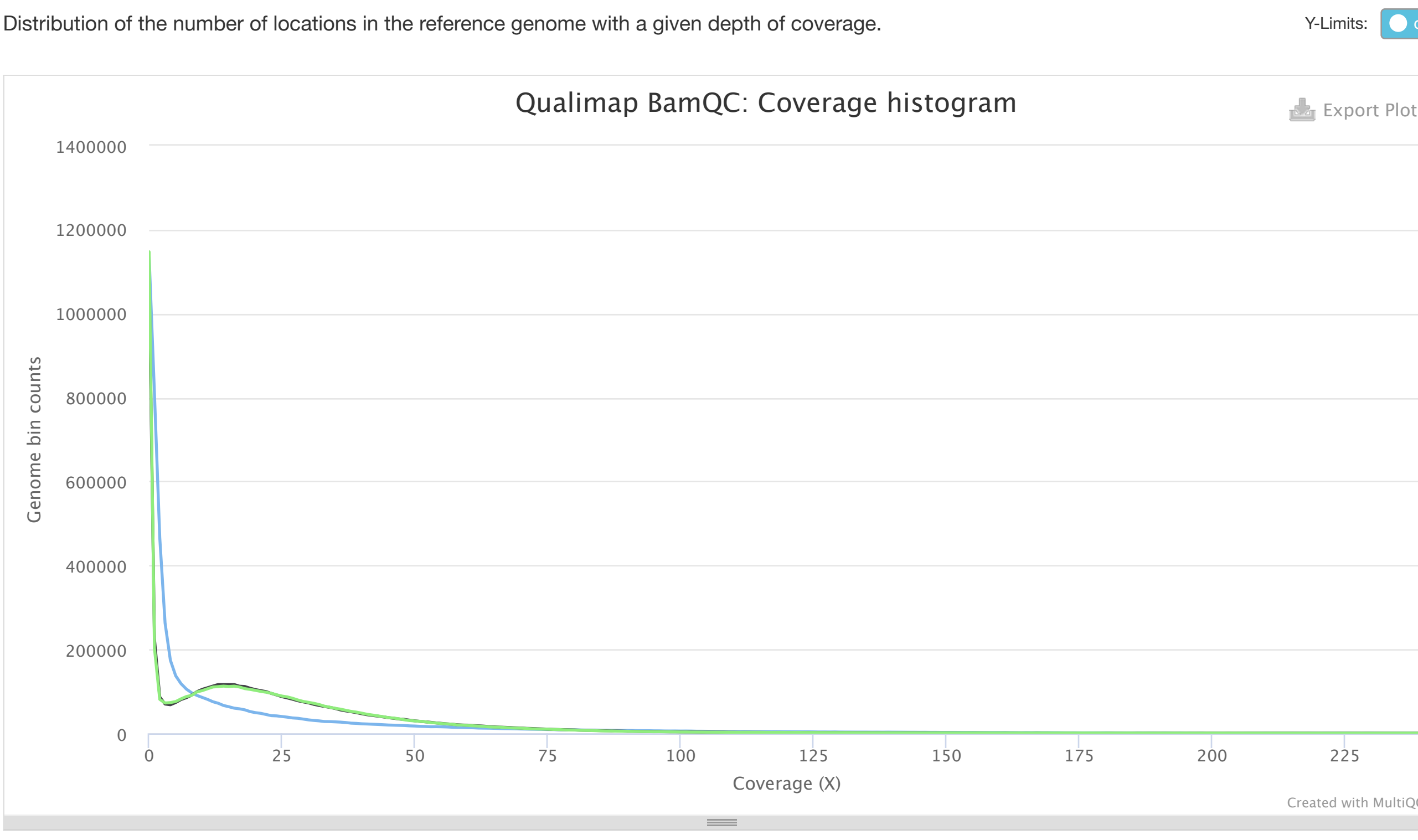
Sample Name	% GC	≥ 30X	Median cov	Mean cov	% Aligned	% Dups	% GC	M Seqs
case737_child	46%	22.8%	5.0X	24.1X	99.8%	5.4%	43%	3.0
case737_father	52%	31.2%	18.0X	27.3X	99.9%	6.1%	50%	2.2
case737_mother	52%	31.0%	18.0X	26.3X	99.8%	8.5%	50%	2.1

## QualiMap

QualiMap is a platform-independent application to facilitate the quality control of alignment sequencing data and its derivatives like feature counts. DOI: [10.1093/bioinformatics/btv566](https://doi.org/10.1093/bioinformatics/btv566); [10.1093/bioinformatics/bts503](https://doi.org/10.1093/bioinformatics/bts503).

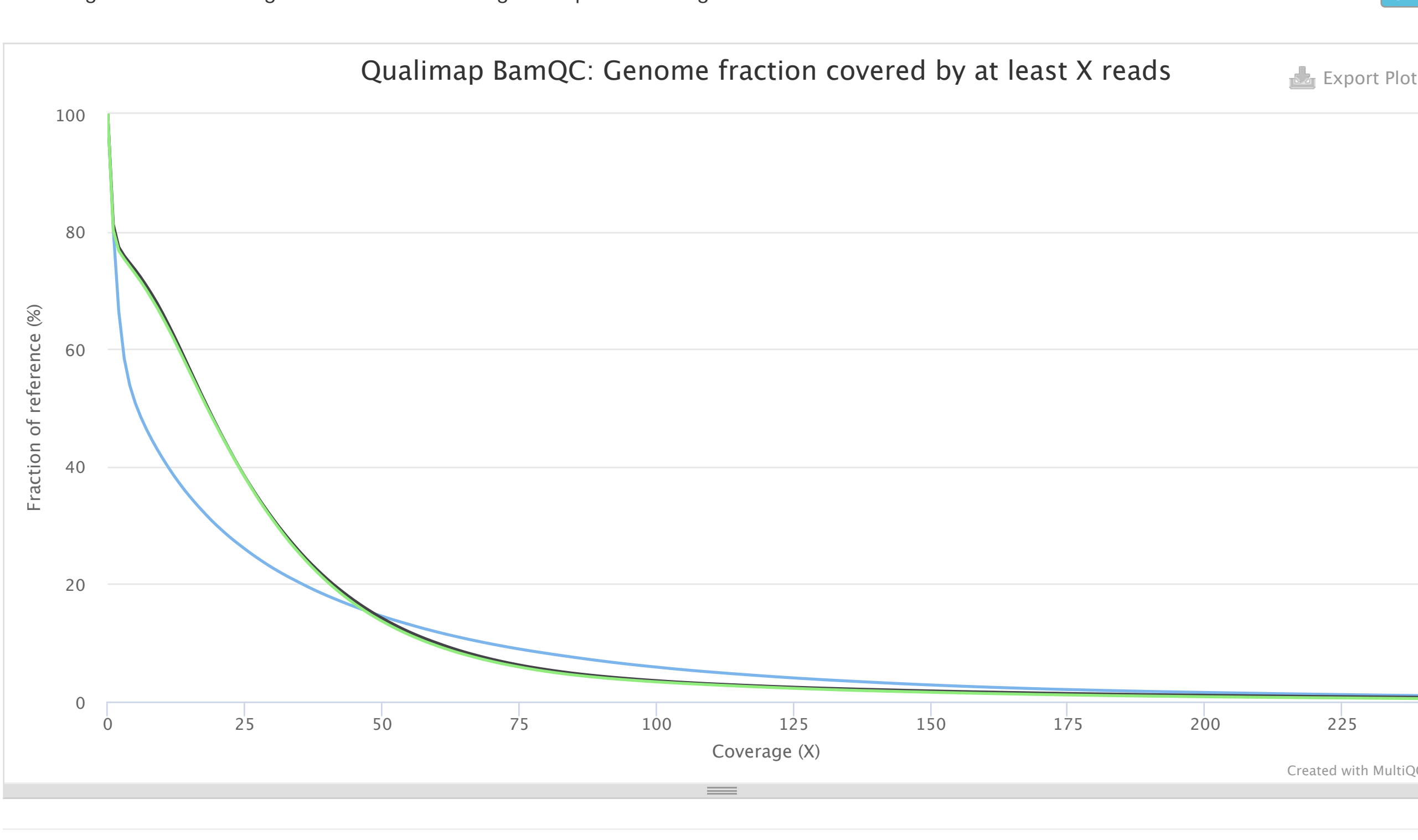
## Coverage histogram

Distribution of the number of locations in the reference genome with a given depth of coverage.



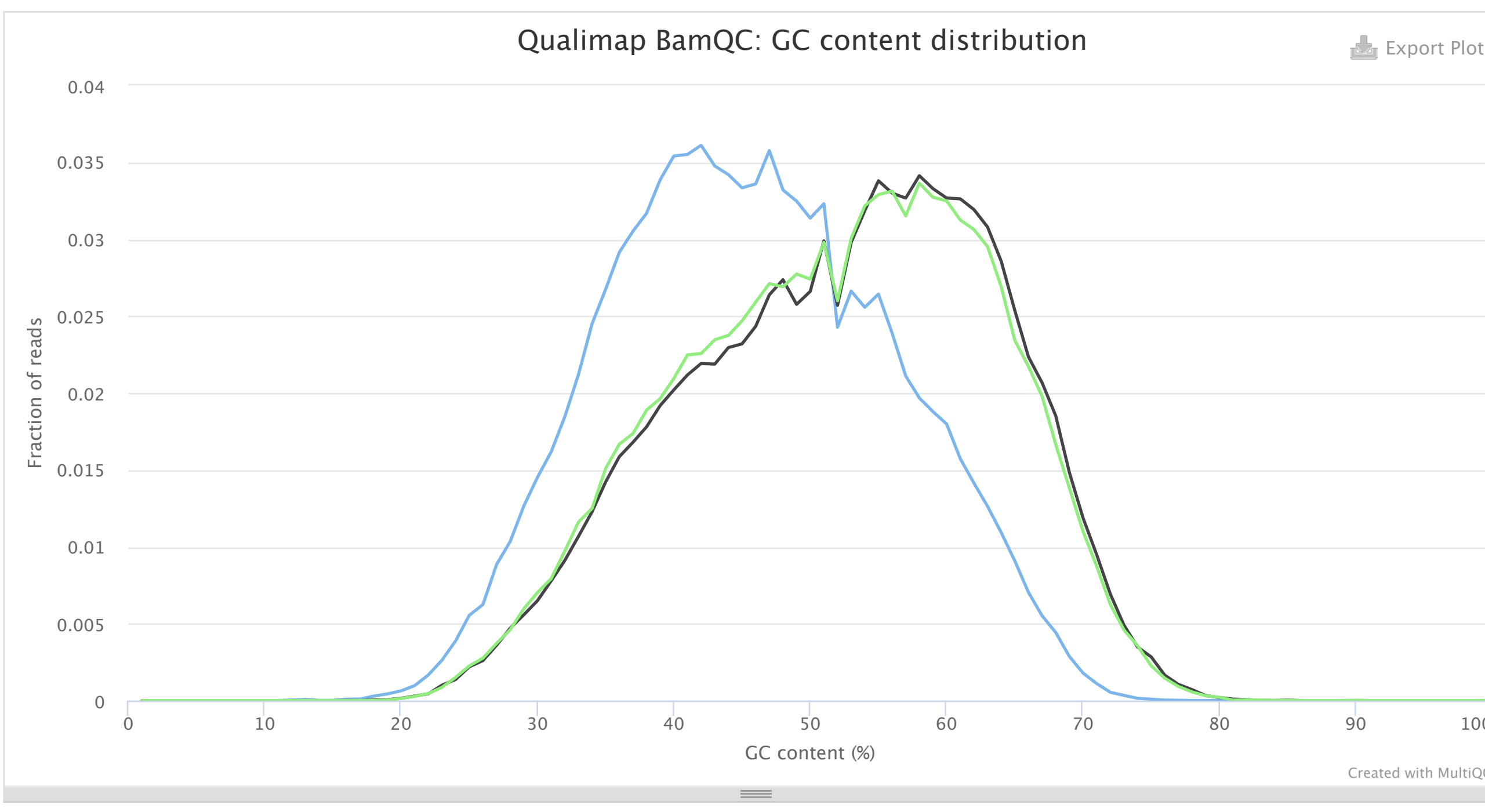
## Cumulative genome coverage

Percentage of the reference genome with at least the given depth of coverage.



## GC content distribution

Each solid line represents the distribution of GC content of mapped reads for a given sample.

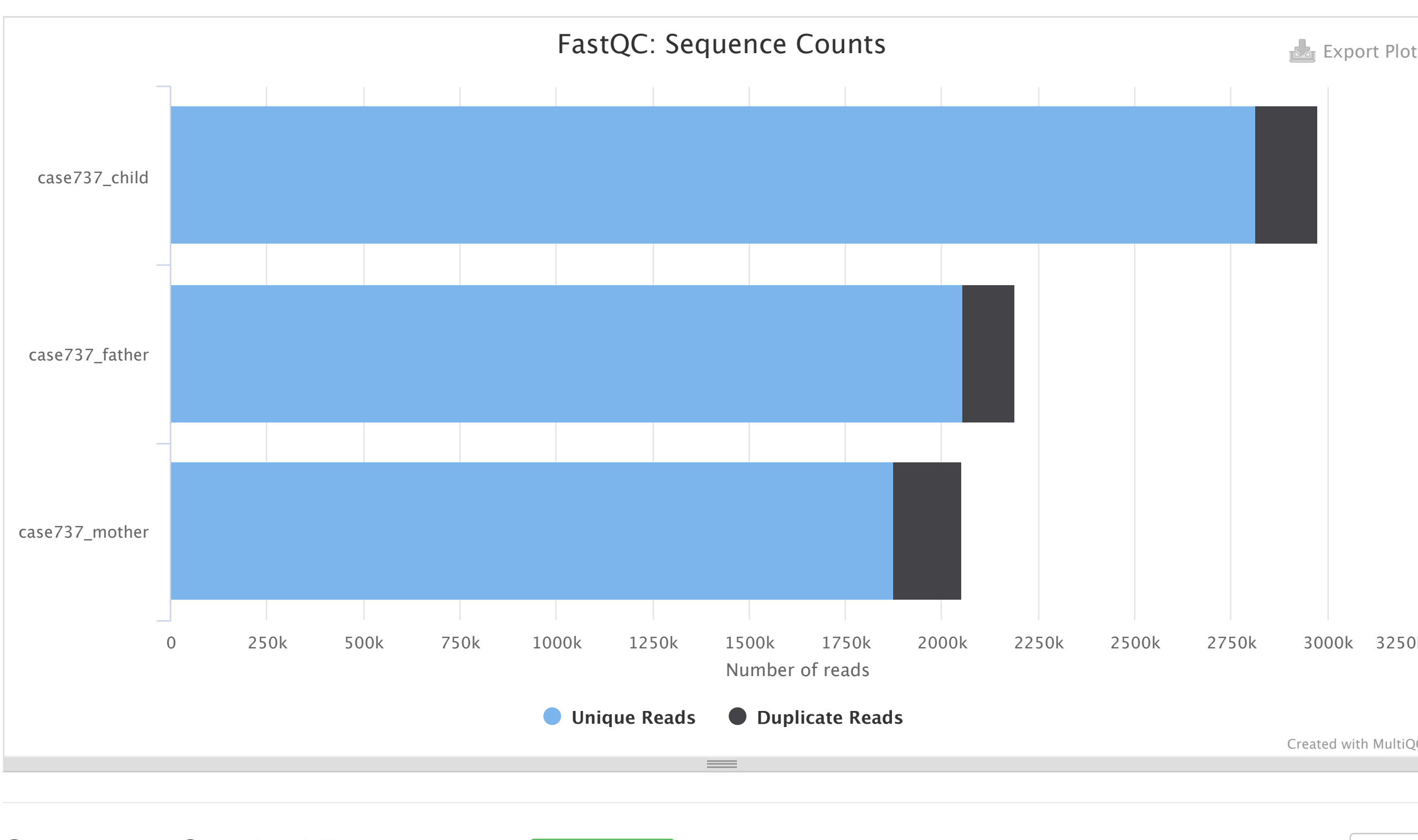


## FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

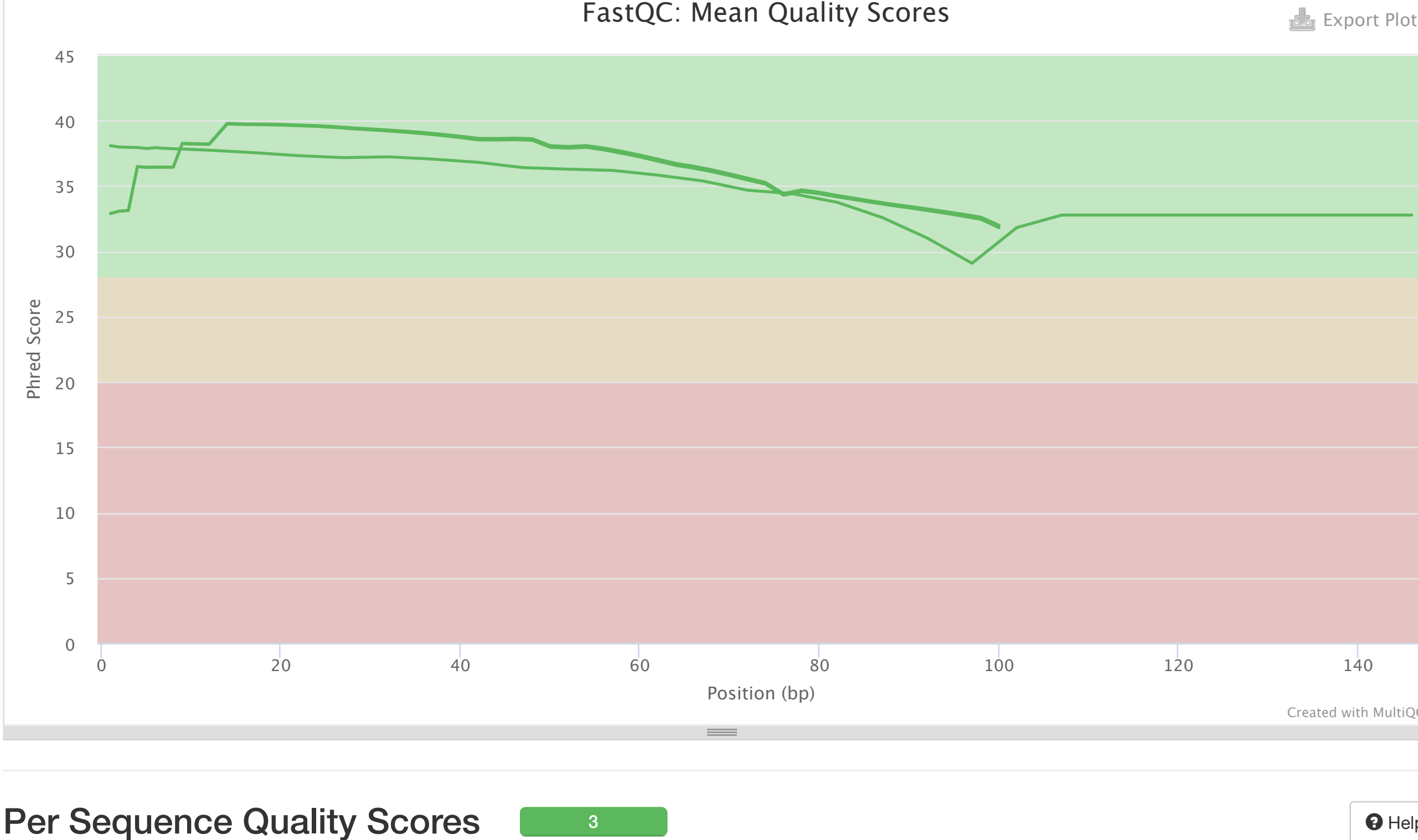
## Sequence Counts

Sequence counts for each sample. Duplicate read counts are an estimate only.



## Sequence Quality Histograms

The mean quality value across each base position in the read.



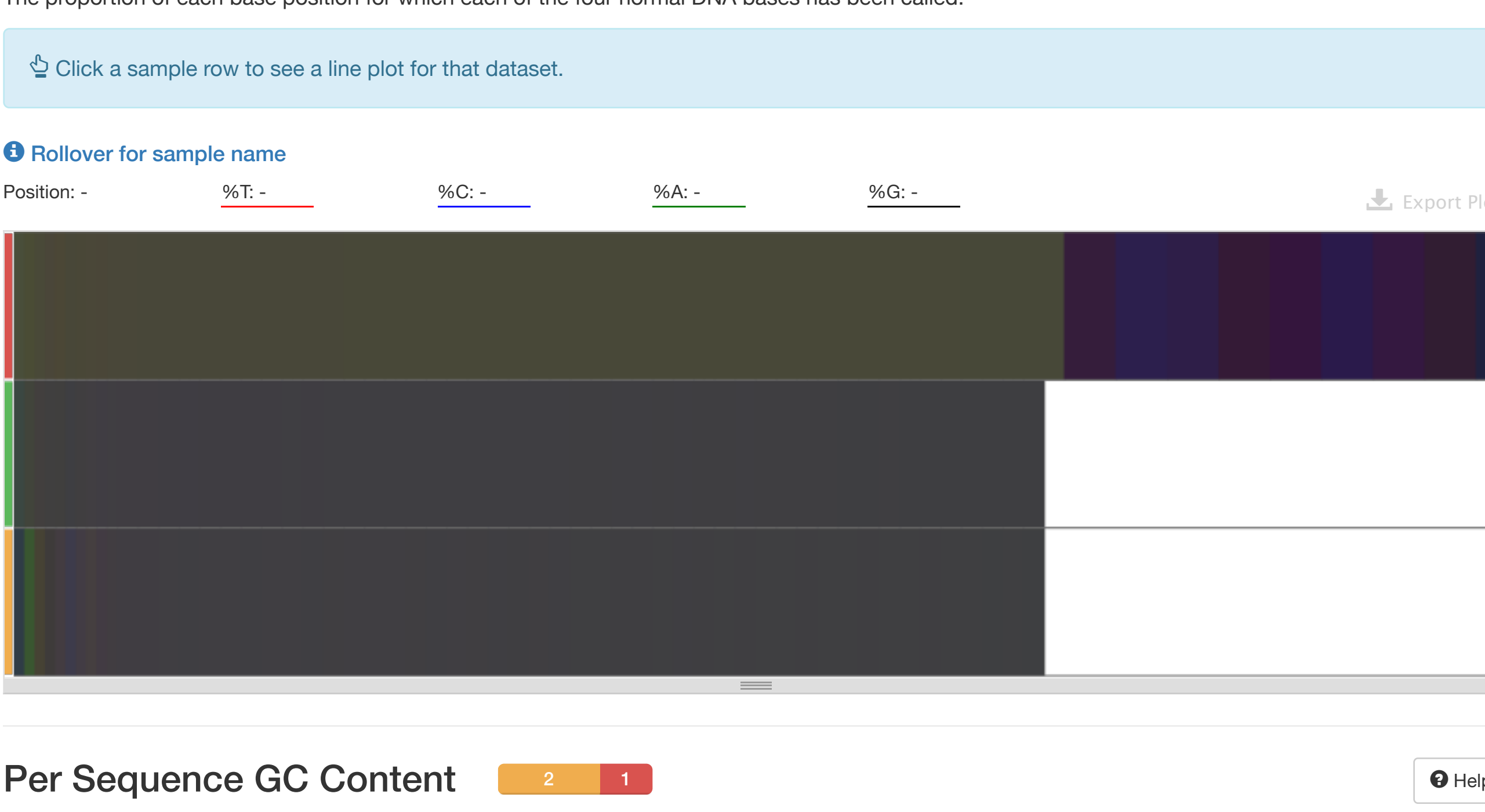
## Per Sequence Quality Scores

The number of reads with average quality scores. Shows if a subset of reads has poor quality.



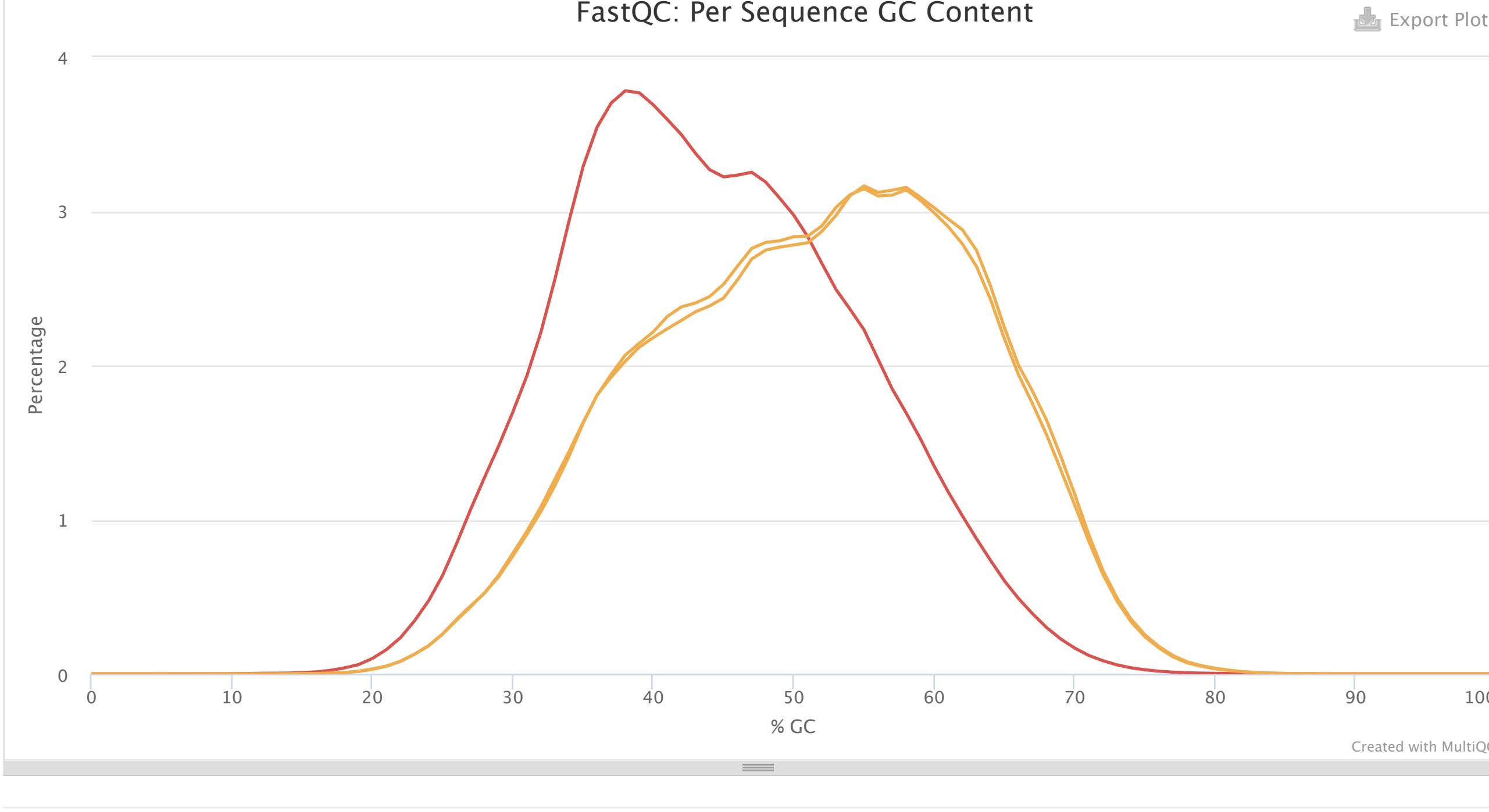
## Per Base Sequence Content

The proportion of each base position for which each of the four normal DNA bases has been called.



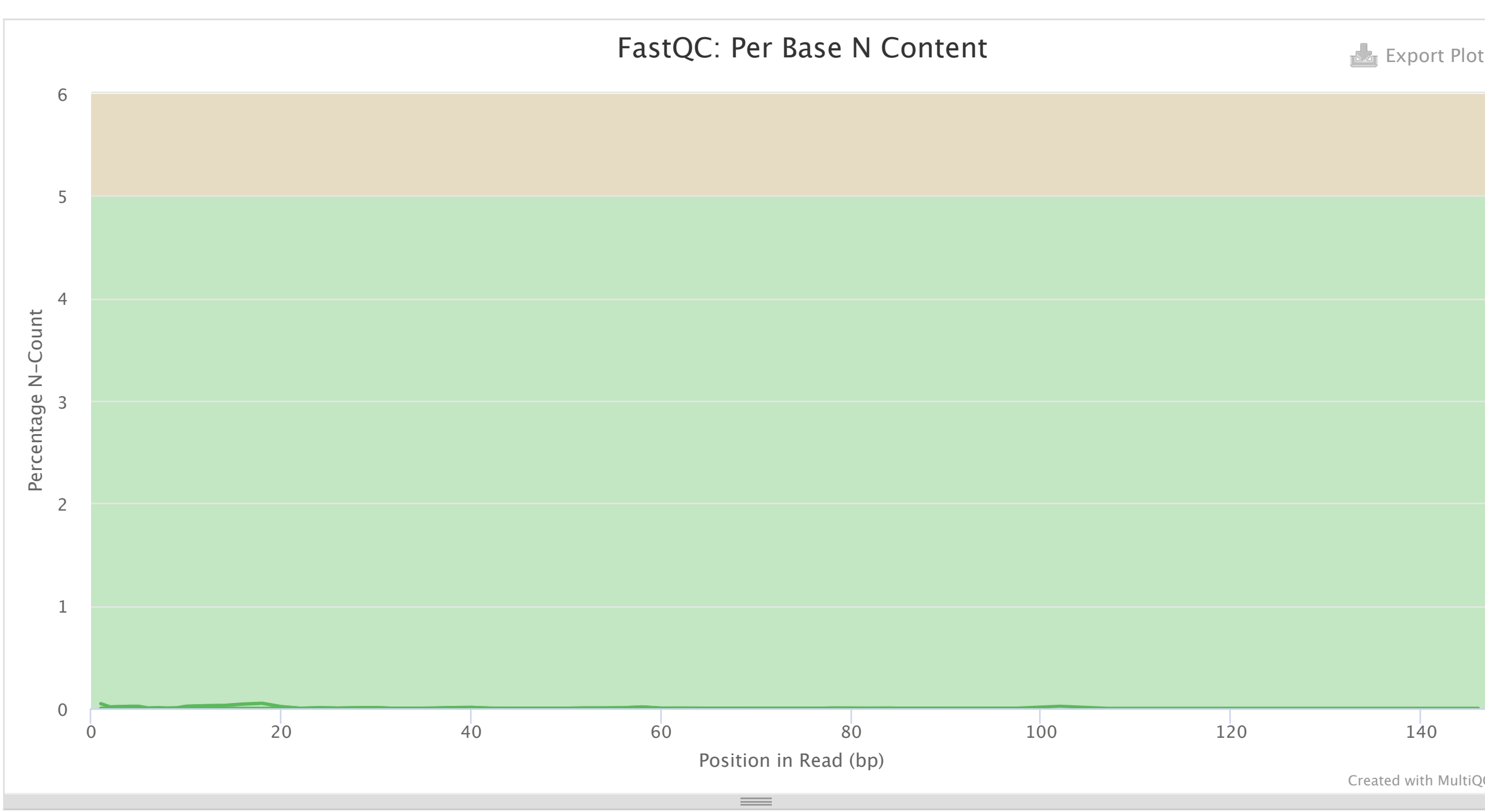
## Per Sequence GC Content

The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.



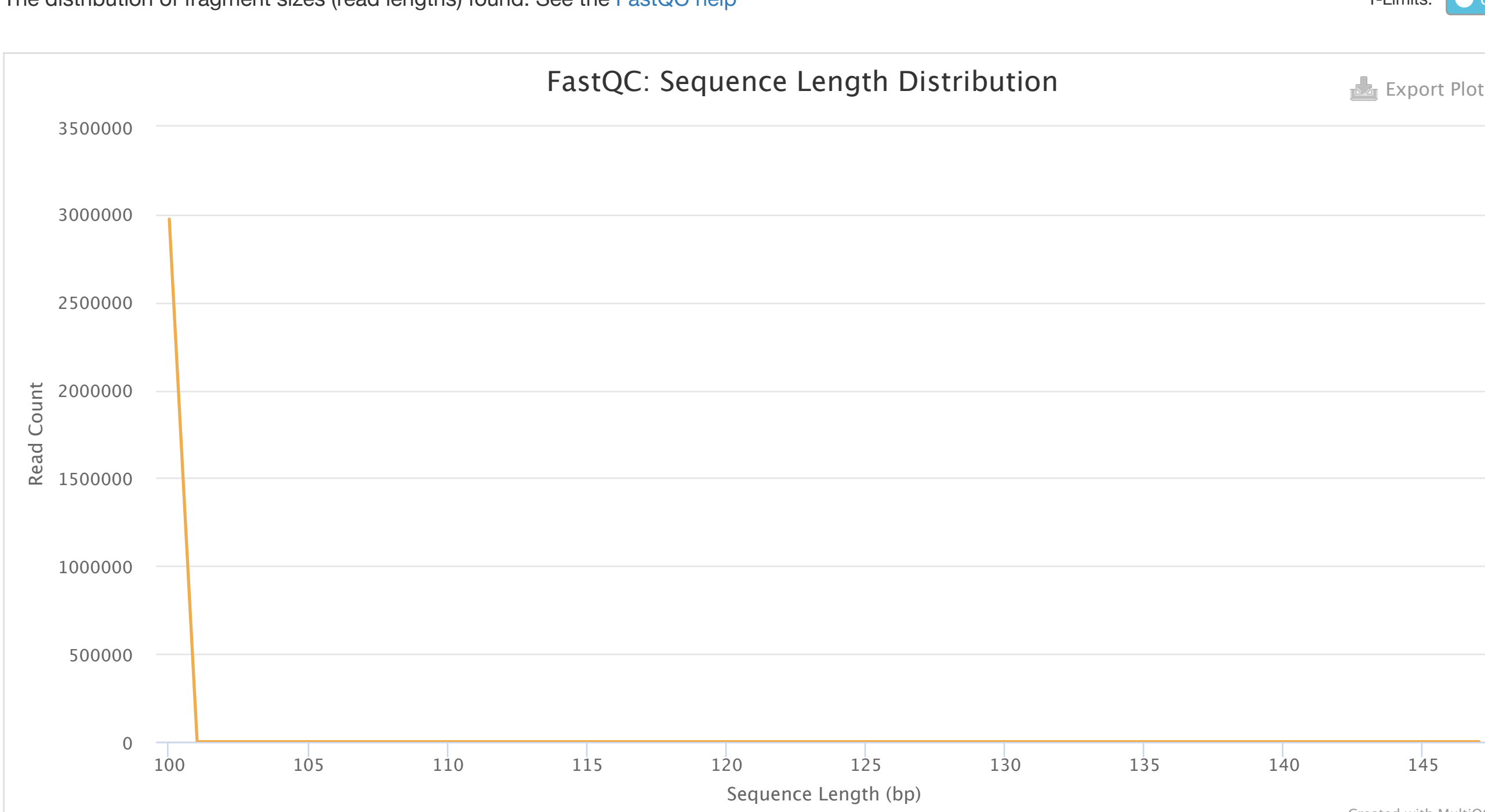
## Per Base N Content

The percentage of base calls at each position for which an N was called.



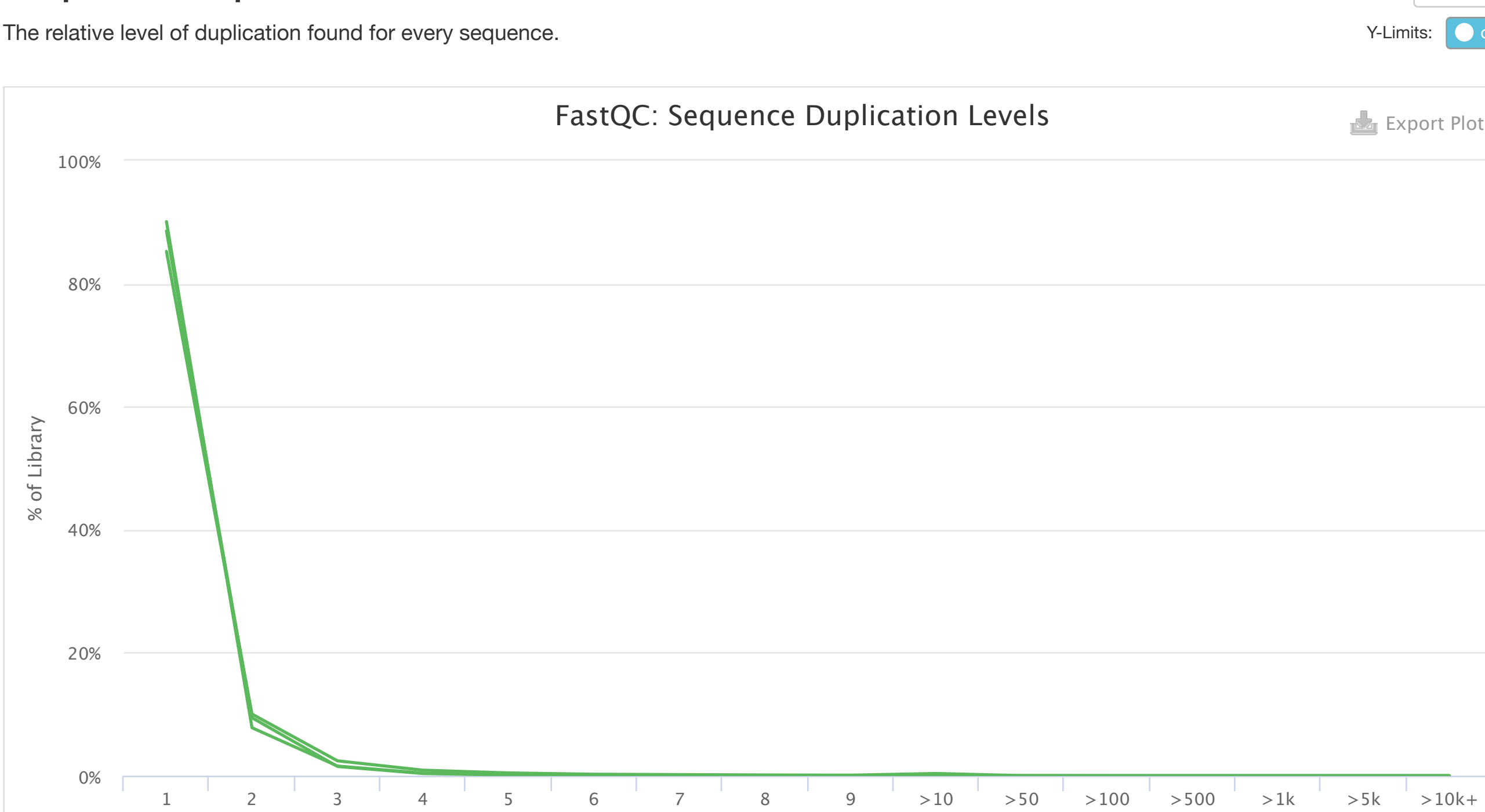
## Sequence Length Distribution

The distribution of fragment sizes (read lengths) found. See the [FastQC help](#)



## Sequence Duplication Levels

The relative level of duplication found for every sequence.



## Overrepresented sequences

The total amount of overrepresented sequences found in each library.

3 samples had less than 1% of reads made up of overrepresented sequences

## Adapter Content

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

## Status Checks

Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red).

