MultiQC
v1.14

MultiQC

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

Report generated on 2024-04-29, 14:44 CEST based on data in: `/home/BCG_2024_vfassi/project/593`

Welcome! Not sure where to start? Watch a tutorial video (6:06) don't show again ×

Toolbox

General Statistics

Copy table | Configure Columns | Plot | Showing 3/3 rows and 8/18 columns.

Sample Name	% GC	≥ 30X	Median cov	Mean cov	% Aligned	% Dups	% GC	M Seqs
case593_child	46%	22.8%	5.0X	24.1X	99.8%	5.4%	43%	3.0
case593_father	52%	31.2%	18.0X	27.3X	99.9%	6.1%	50%	2.2
case593_mother	52%	31.0%	18.0X	26.3X	99.8%	8.5%	50%	2.1

QualiMap

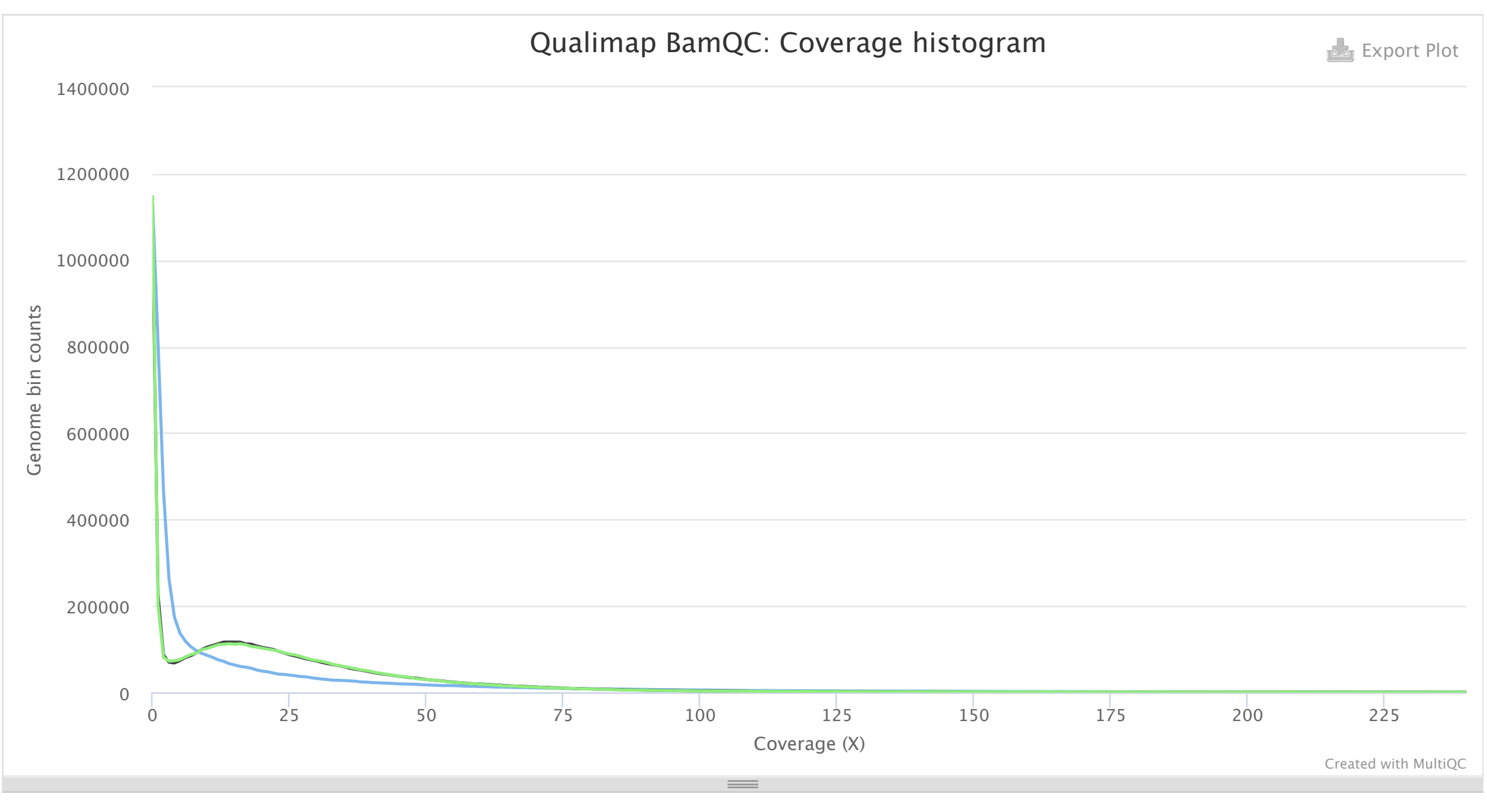
QualiMap is a platform-independent application to facilitate the quality control of alignment sequencing data and its derivatives like feature counts. *DOI: 10.1093/bioinformatics/btv566; 10.1093/bioinformatics/bts503.*

Coverage histogram

Help

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

Y-Limits: on

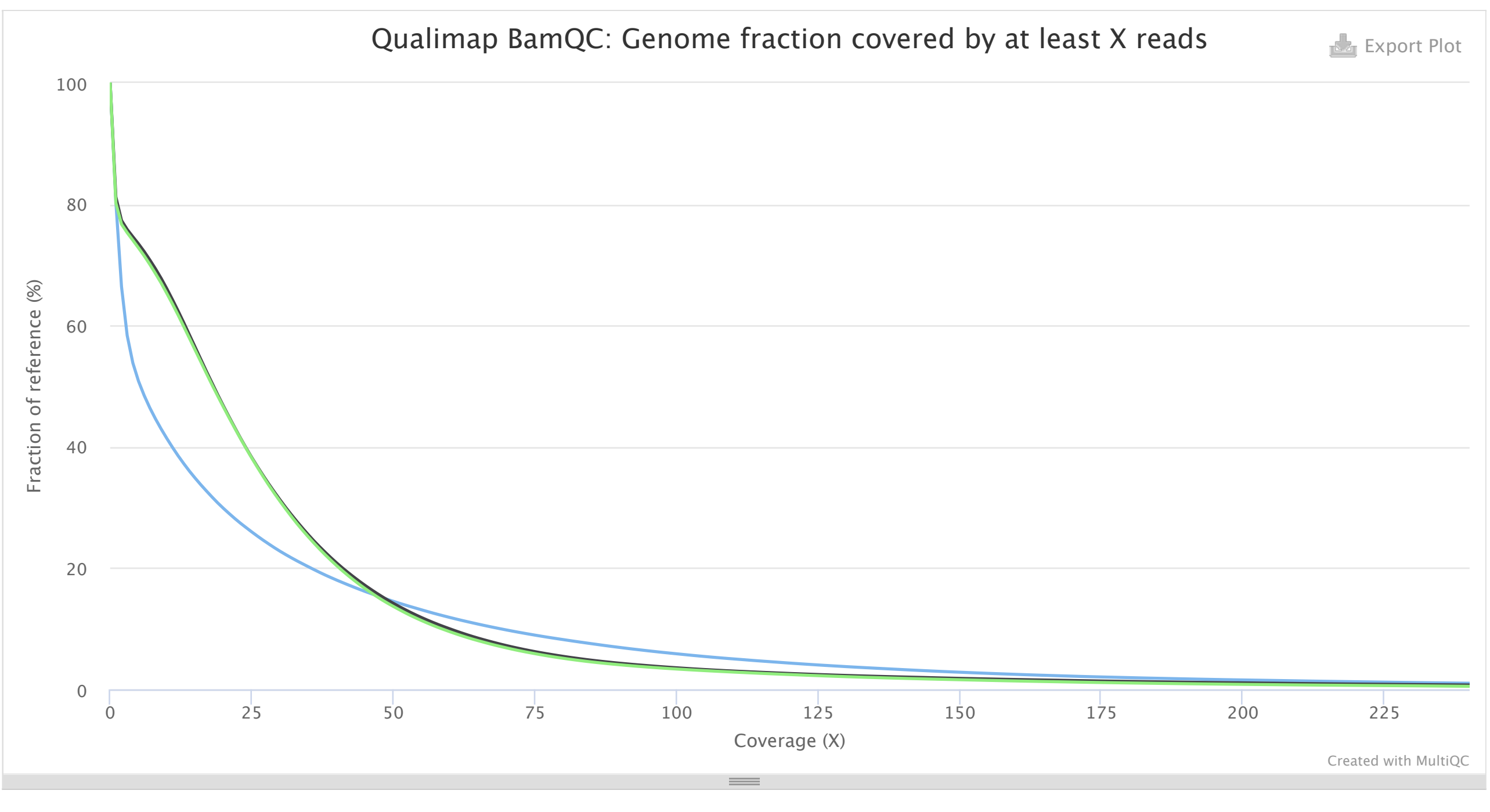


Cumulative genome coverage

Help

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

Y-Limits: on

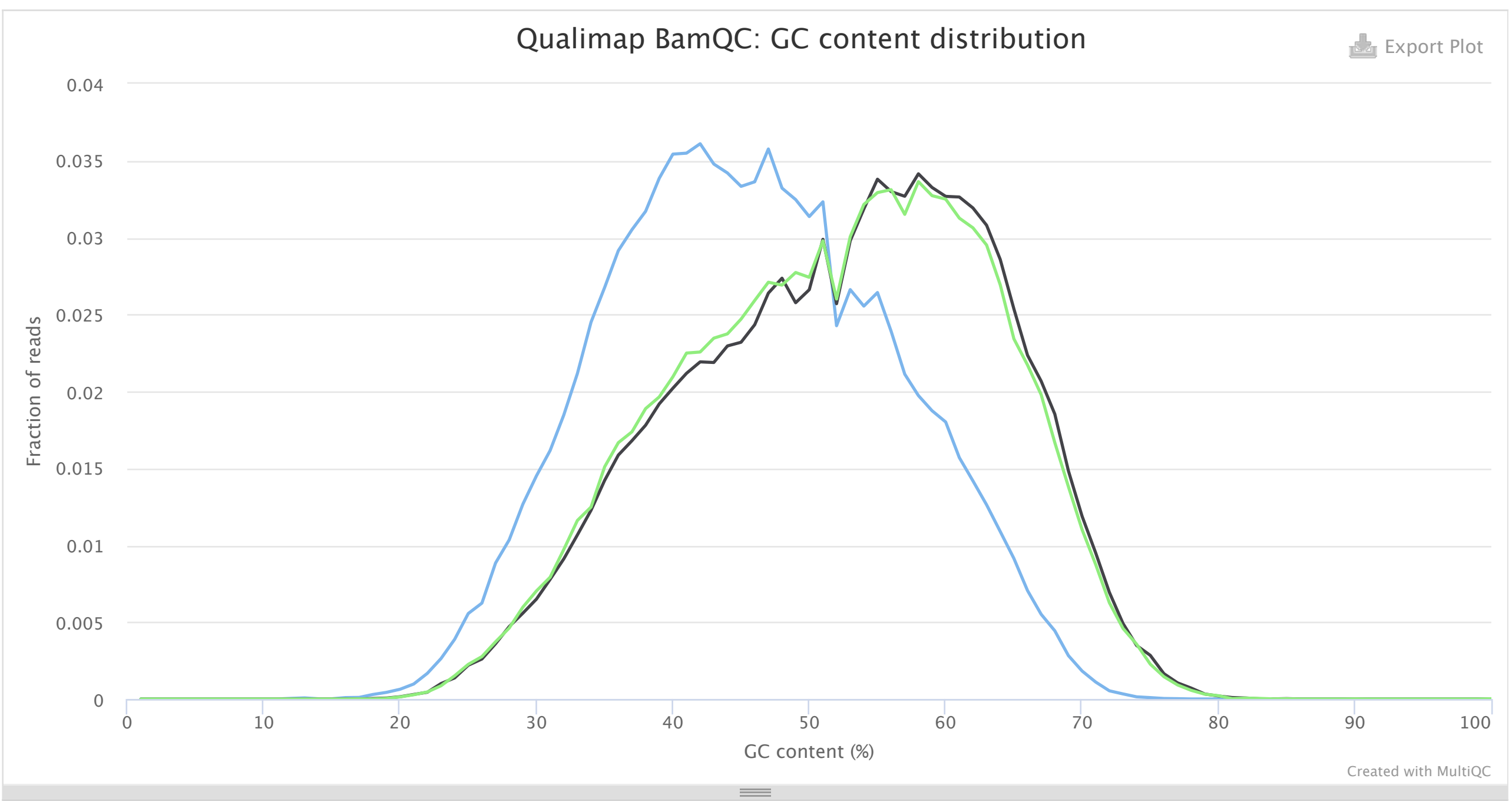


GC content distribution

Help

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

Y-Limits: on



FastQC

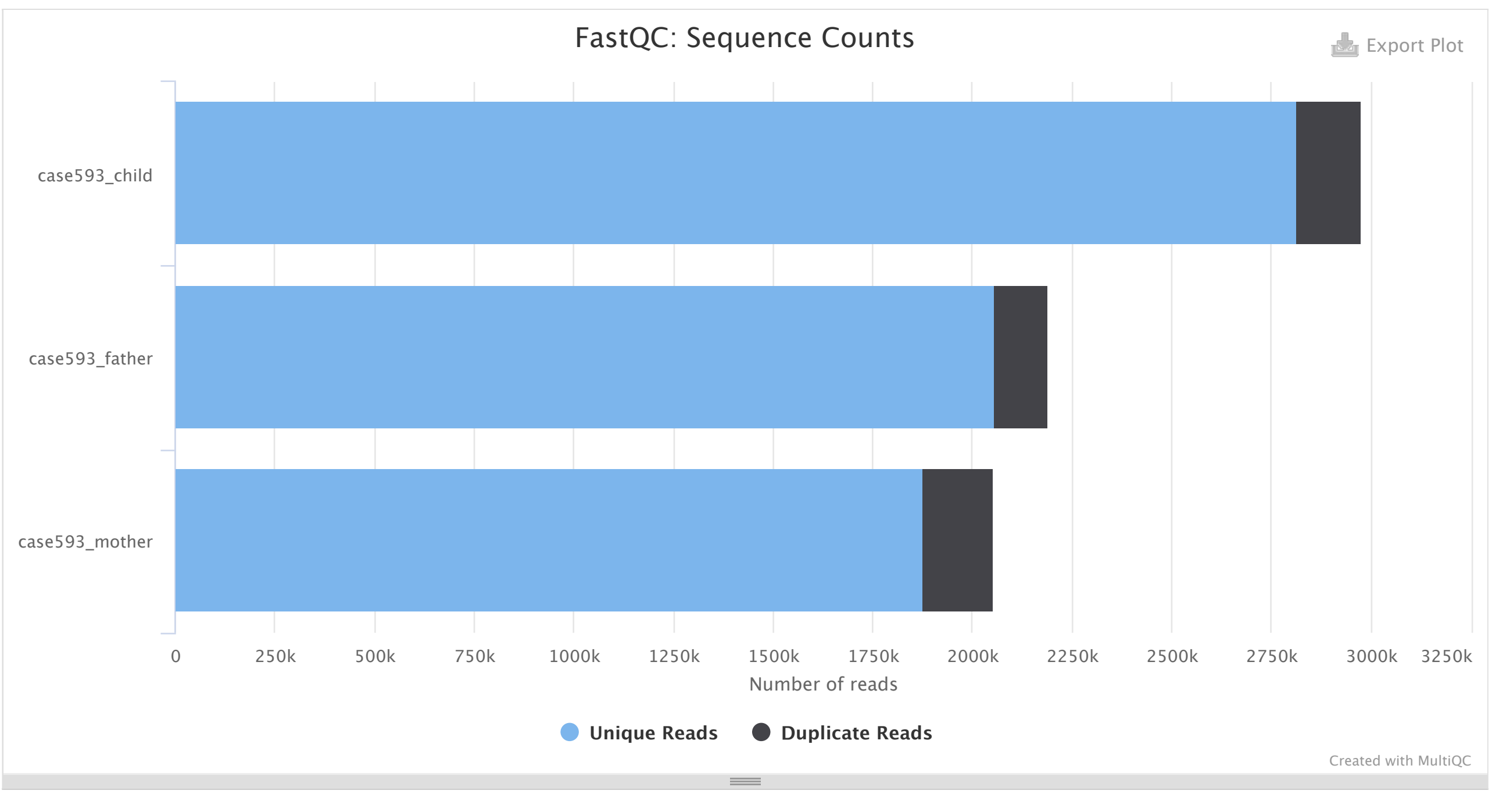
FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

Help

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

Number of reads | Percentages



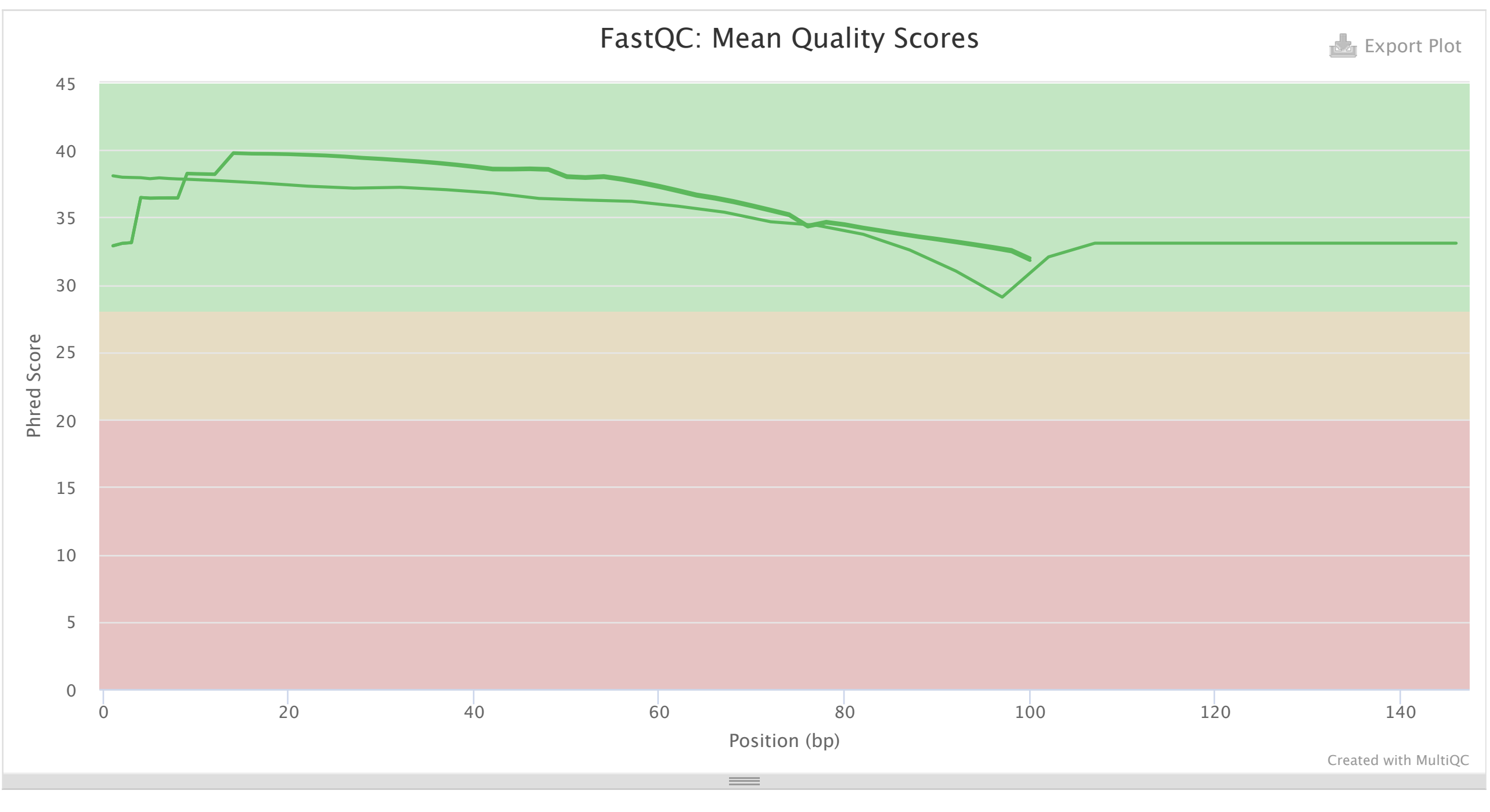
Sequence Quality Histograms

3

Help

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

Y-Limits: on



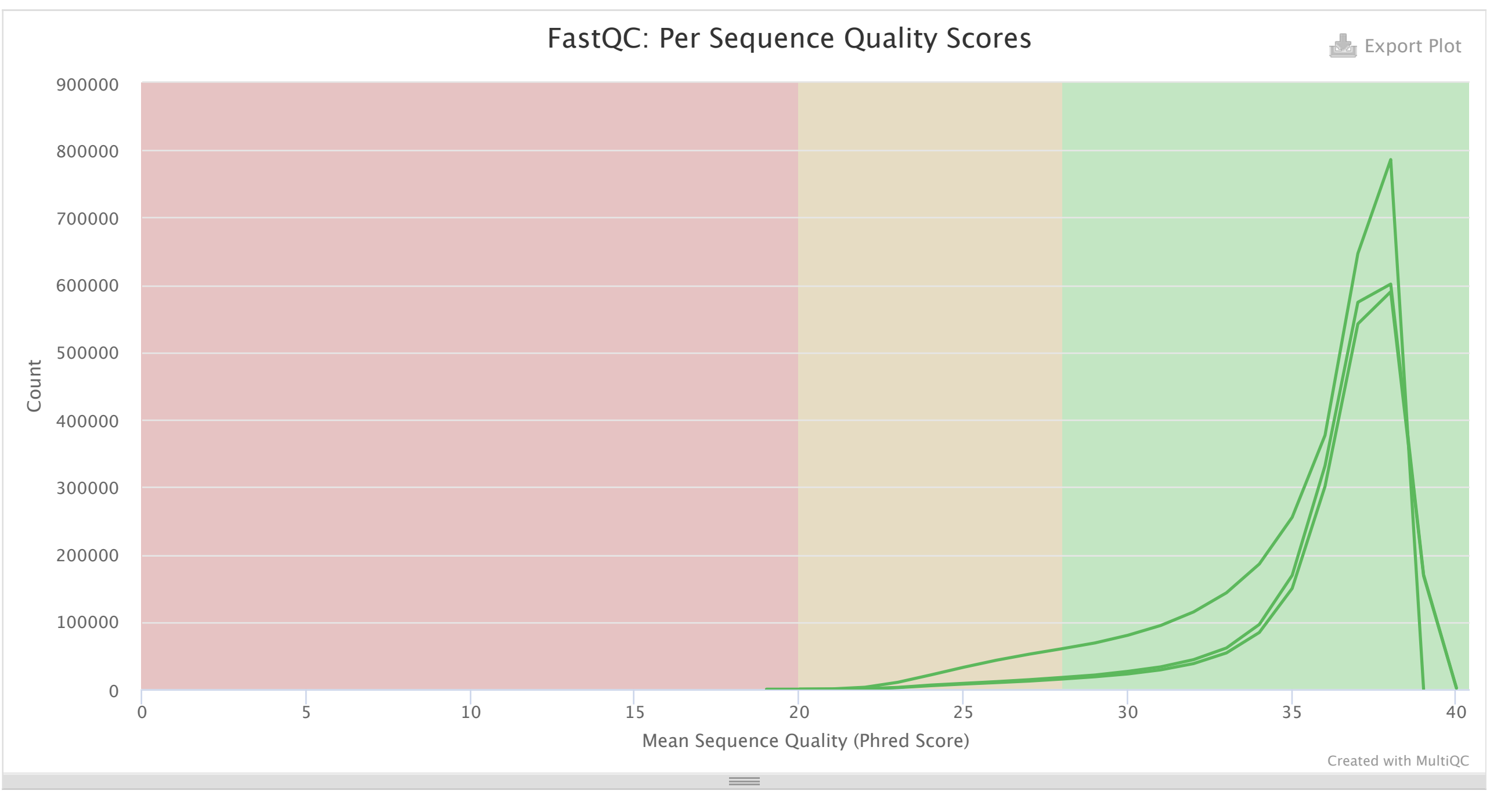
Per Sequence Quality Scores

3

Help

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

Y-Limits: on



Per Base Sequence Content

1 2

Help

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

Click a sample row to see a line plot for that dataset.

Per Sequence GC Content

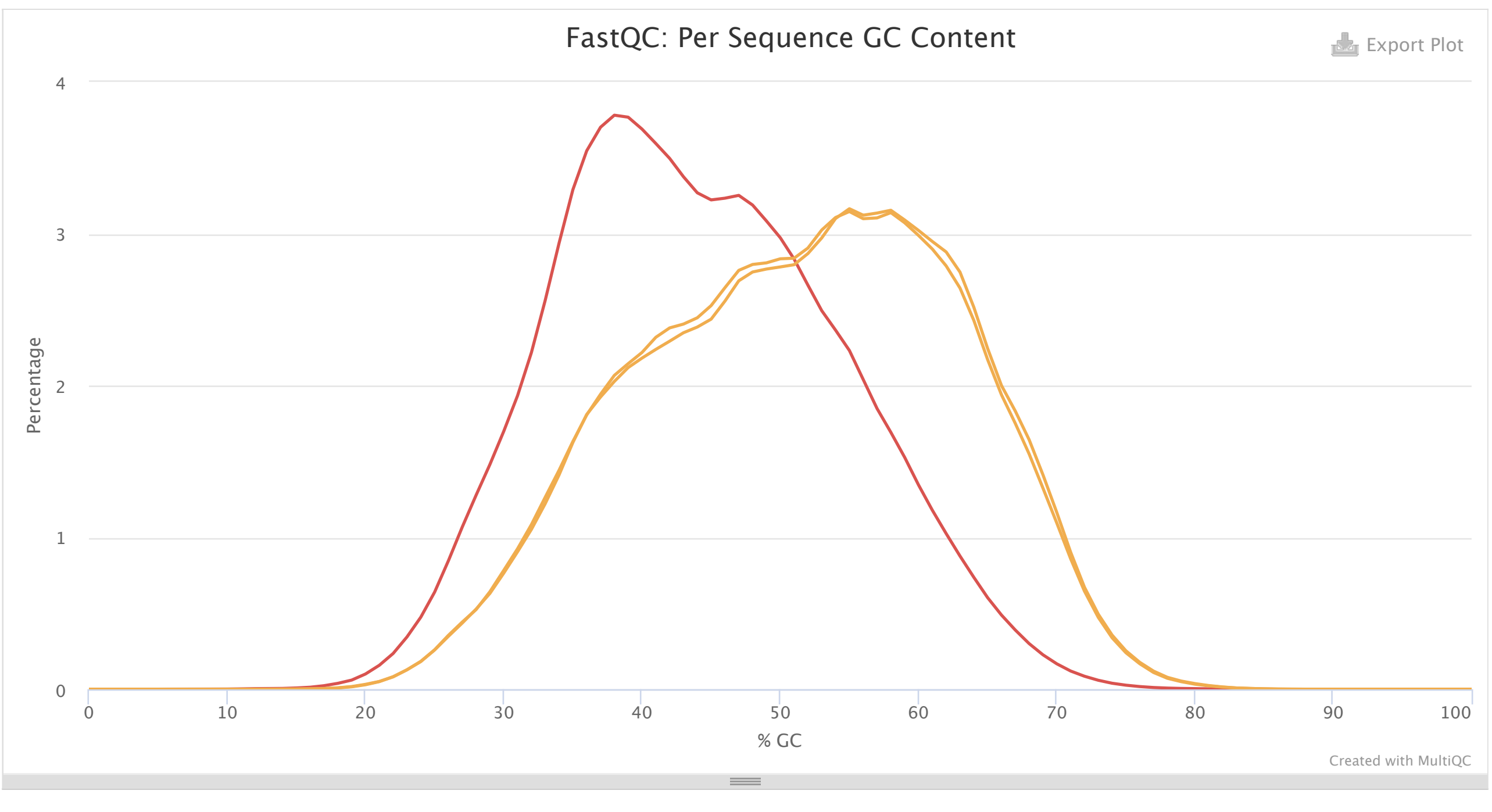
2 1

Help

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

Y-Limits: on

Percentages | Counts



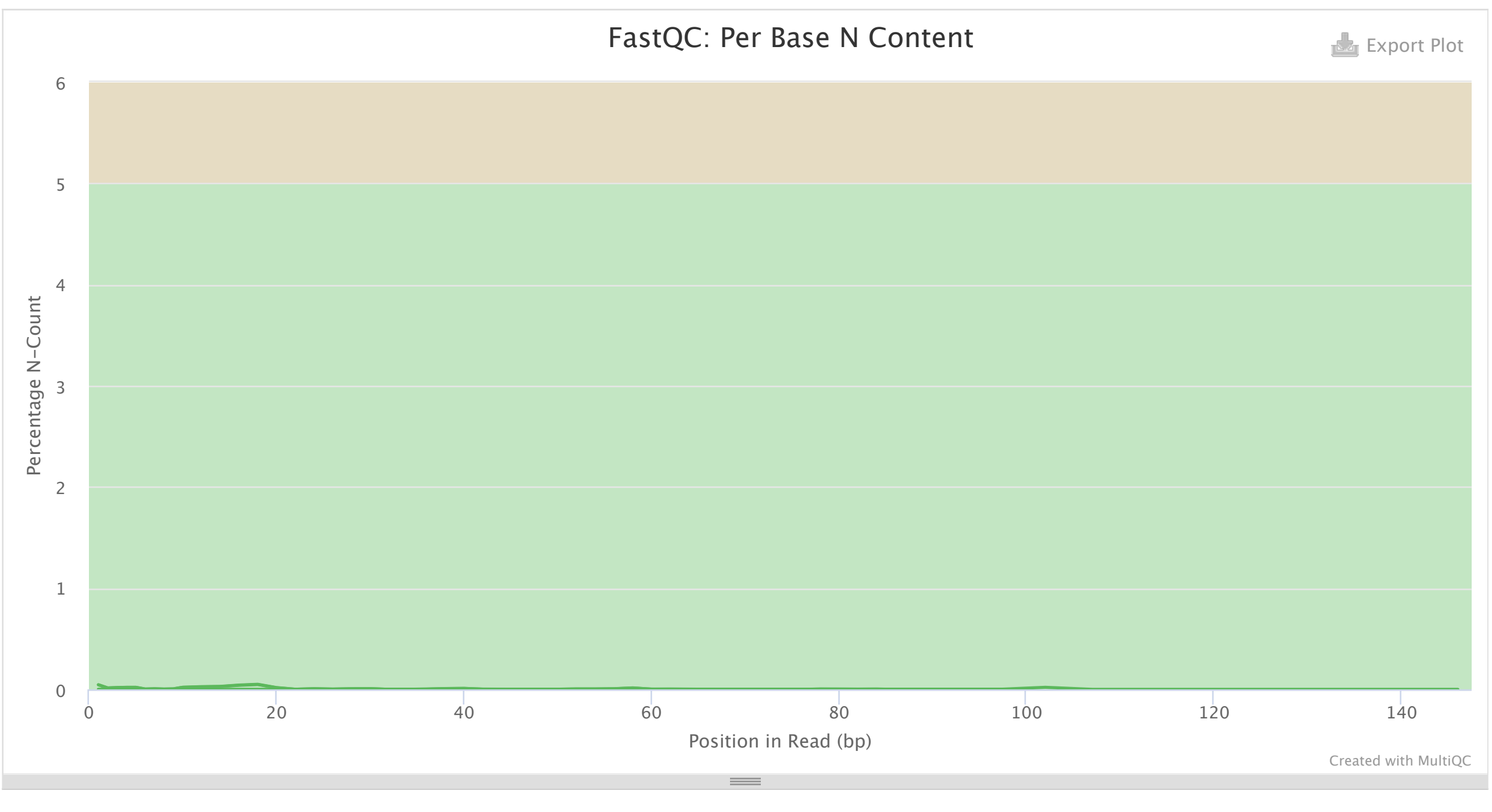
Per Base N Content

3

Help

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

Y-Limits: on

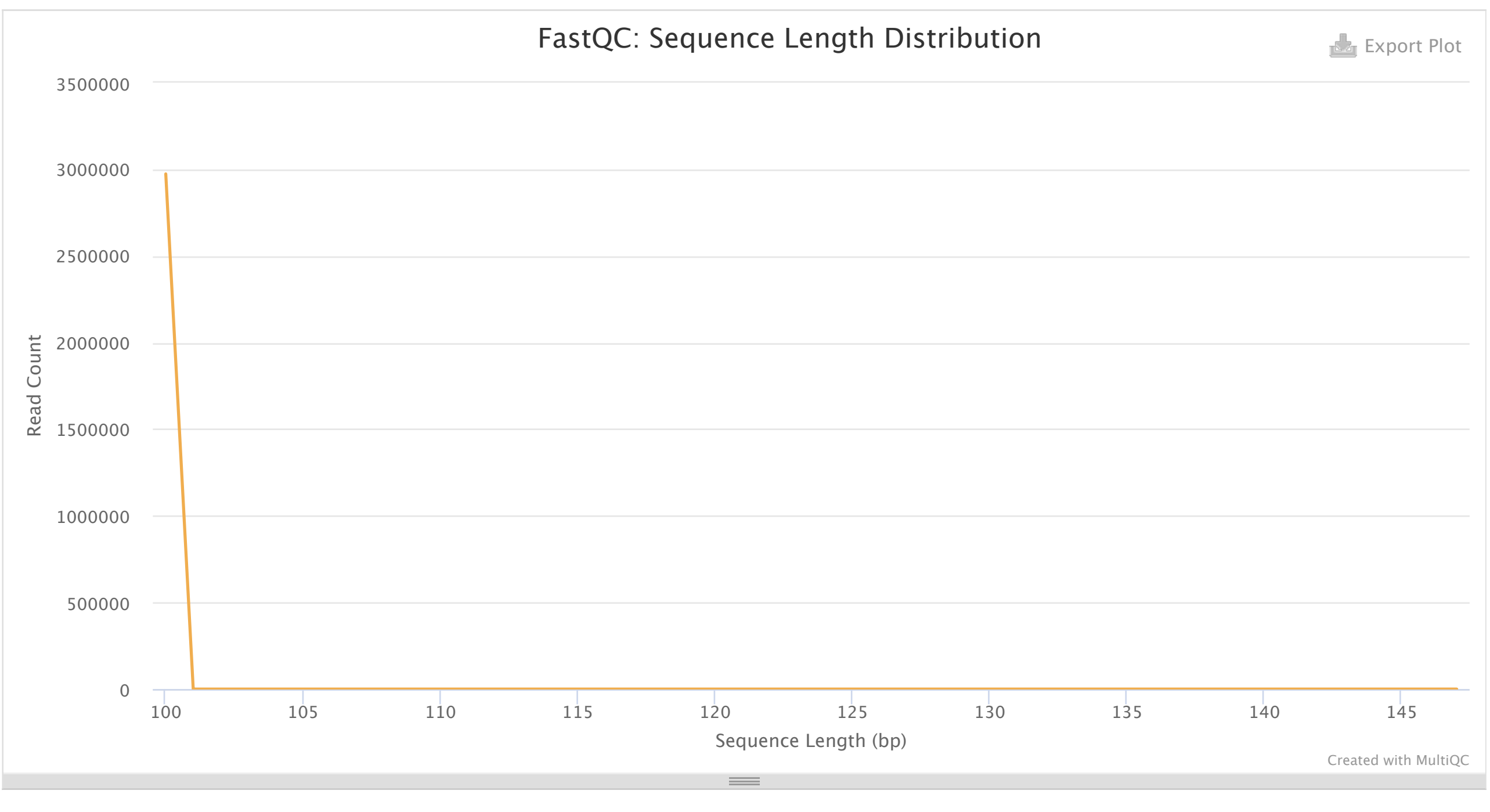


Sequence Length Distribution

2 1

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

Y-Limits: on



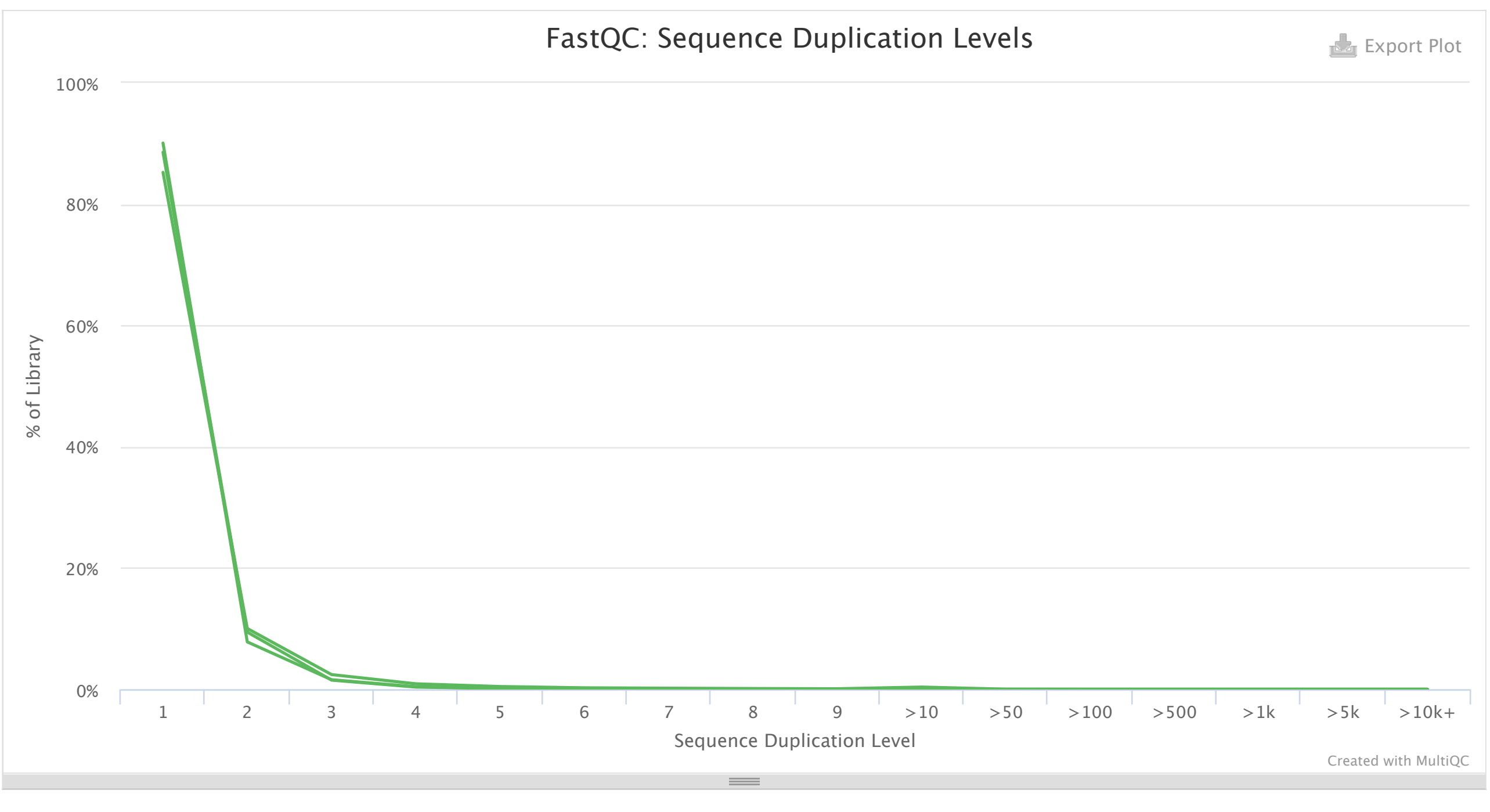
Sequence Duplication Levels

3

Help

The relative level of duplication found for every sequence.

Y-Limits: on



Overrepresented sequences

3

Help

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

3

Help

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

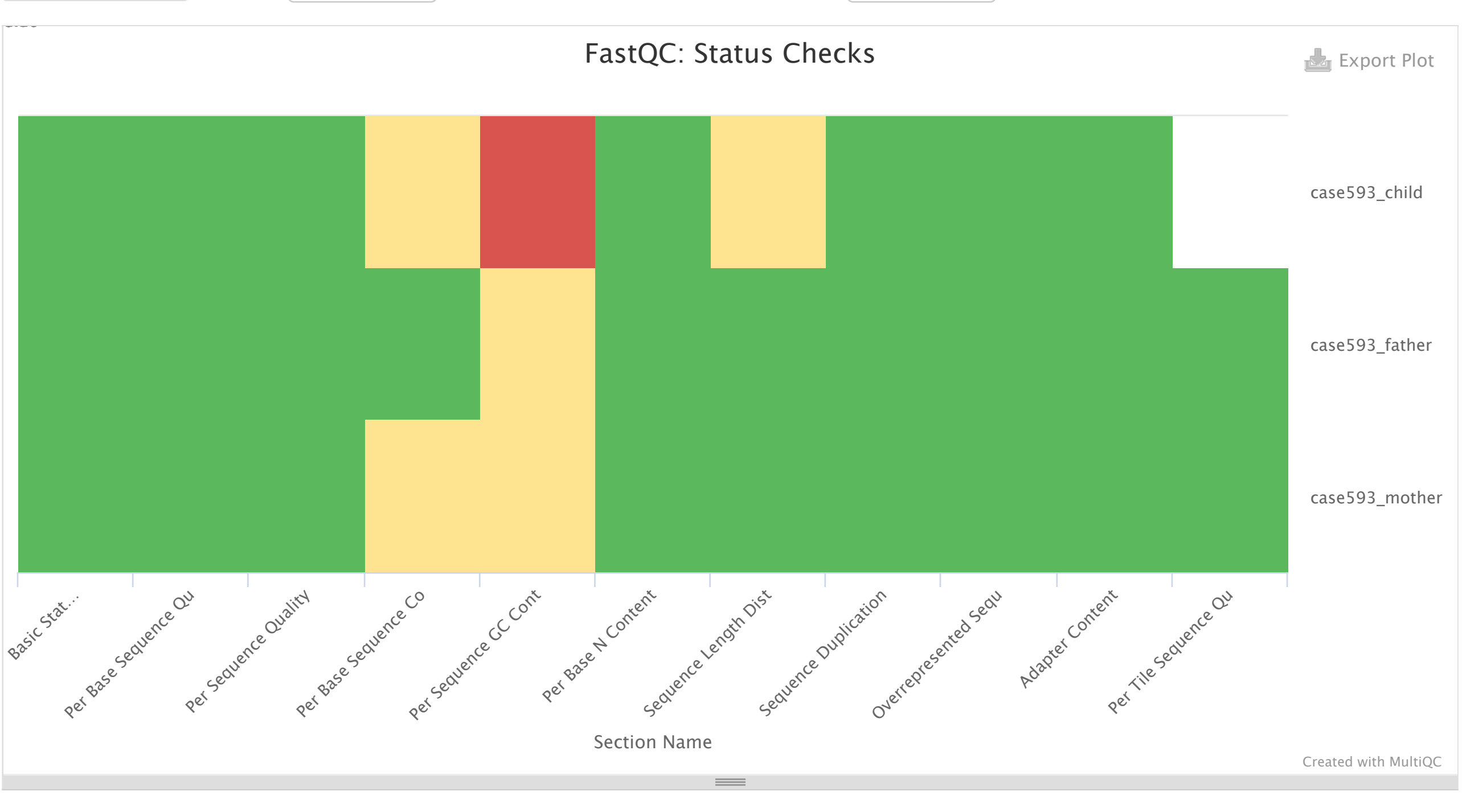
No samples found with any adapter contamination > 0.1%

Status Checks

Help

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

Sort by highlight | **Min:** 0 | **Max:** 1



MultiQC v1.14 - Written by Phil Ewels, available on GitHub.
This report uses HighCharts, jQuery, jQuery UI, Bootstrap, FileSaver.js and clipboard.js.
seqeralabs