

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

Report generated on 2019-10-23, 13:26 based on data in:  
/data/storage/SAYRES/NASONIA/Heini/Processing/Sayres/RNA/trimmed\_FastQC

!

Welcome! Not sure where to start?

Watch a tutorial video

don't show again

✕

(6:06)

## General Statistics

Copy table

Configure Columns

Plot

Showing 24/24 rows and 3/5 columns.

Sample Name	% Dups	% GC	M Seqs
014444_trimmomatic_trimmed_pair_1	66.3%	40%	14.7
014444_trimmomatic_trimmed_pair_2	60.5%	41%	14.7
014445_trimmomatic_trimmed_pair_1	66.4%	40%	14.4
014445_trimmomatic_trimmed_pair_2	60.3%	41%	14.4
014446_trimmomatic_trimmed_pair_1	61.5%	40%	11.3
014446_trimmomatic_trimmed_pair_2	56.0%	41%	11.3
014447_trimmomatic_trimmed_pair_1	64.7%	40%	16.2
014447_trimmomatic_trimmed_pair_2	60.1%	40%	16.2
014448_trimmomatic_trimmed_pair_1	65.9%	40%	14.1
014448_trimmomatic_trimmed_pair_2	61.0%	40%	14.1
014449_trimmomatic_trimmed_pair_1	69.2%	39%	19.4
014449_trimmomatic_trimmed_pair_2	64.8%	40%	19.4

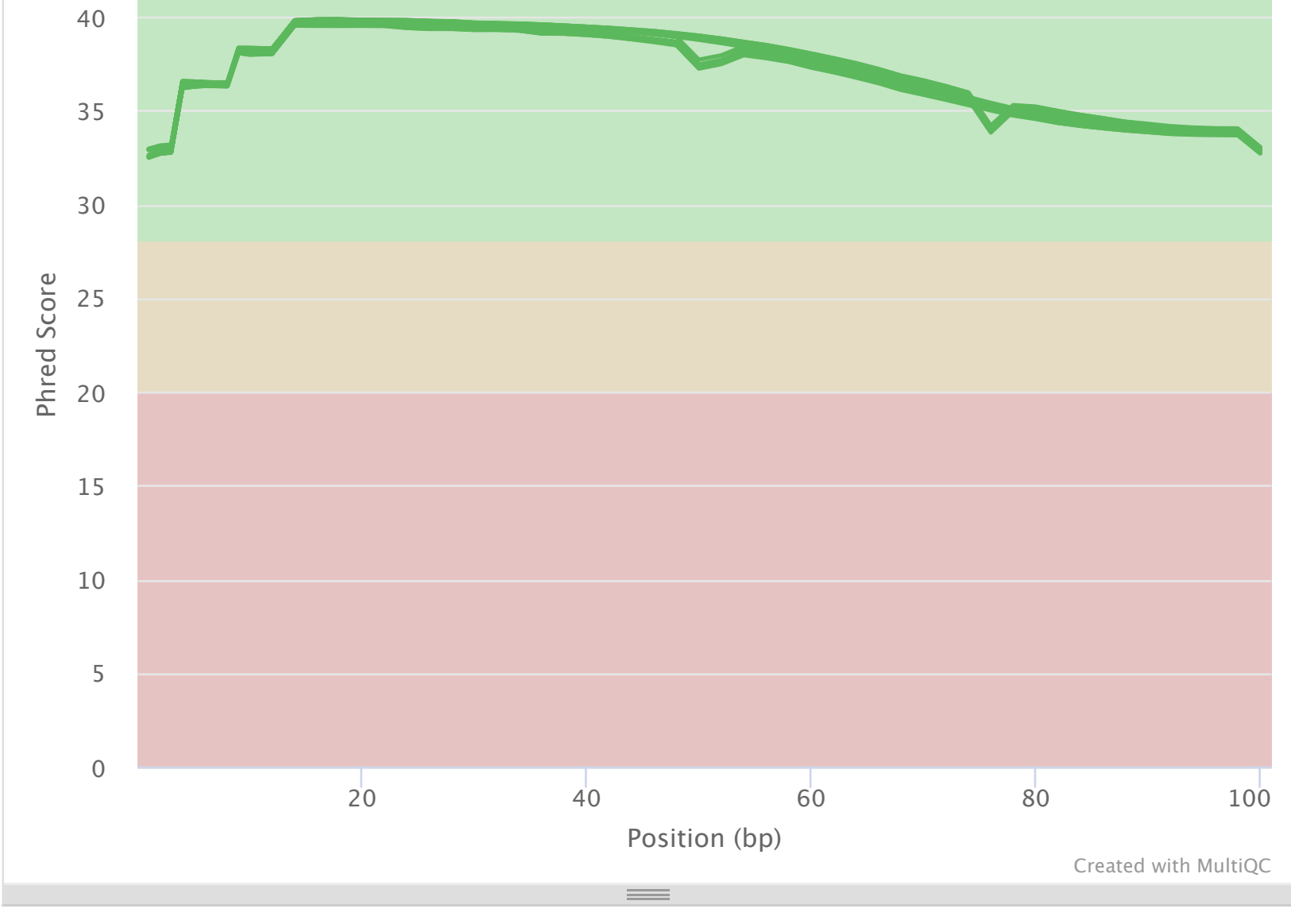
## FastQC

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

## Sequence Quality Histograms

The mean quality value across each base position in the read. See the [FastQC help](#)-Limits: 

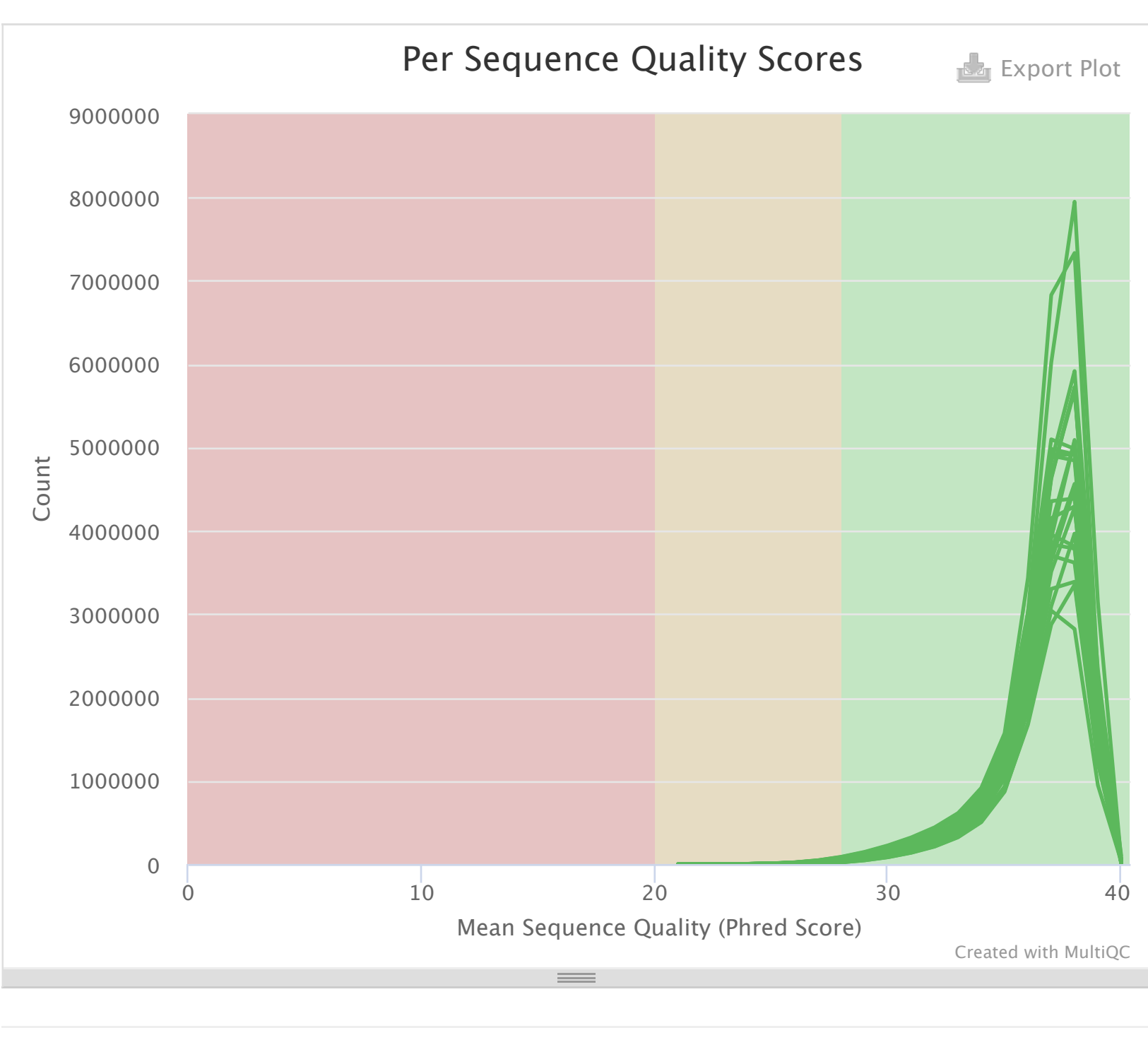
on



## Per Sequence Quality Scores

The number of reads with average quality scores. Shows if a subset of reads has poor quality. See the [FastQC help](#). Y-Limits: 

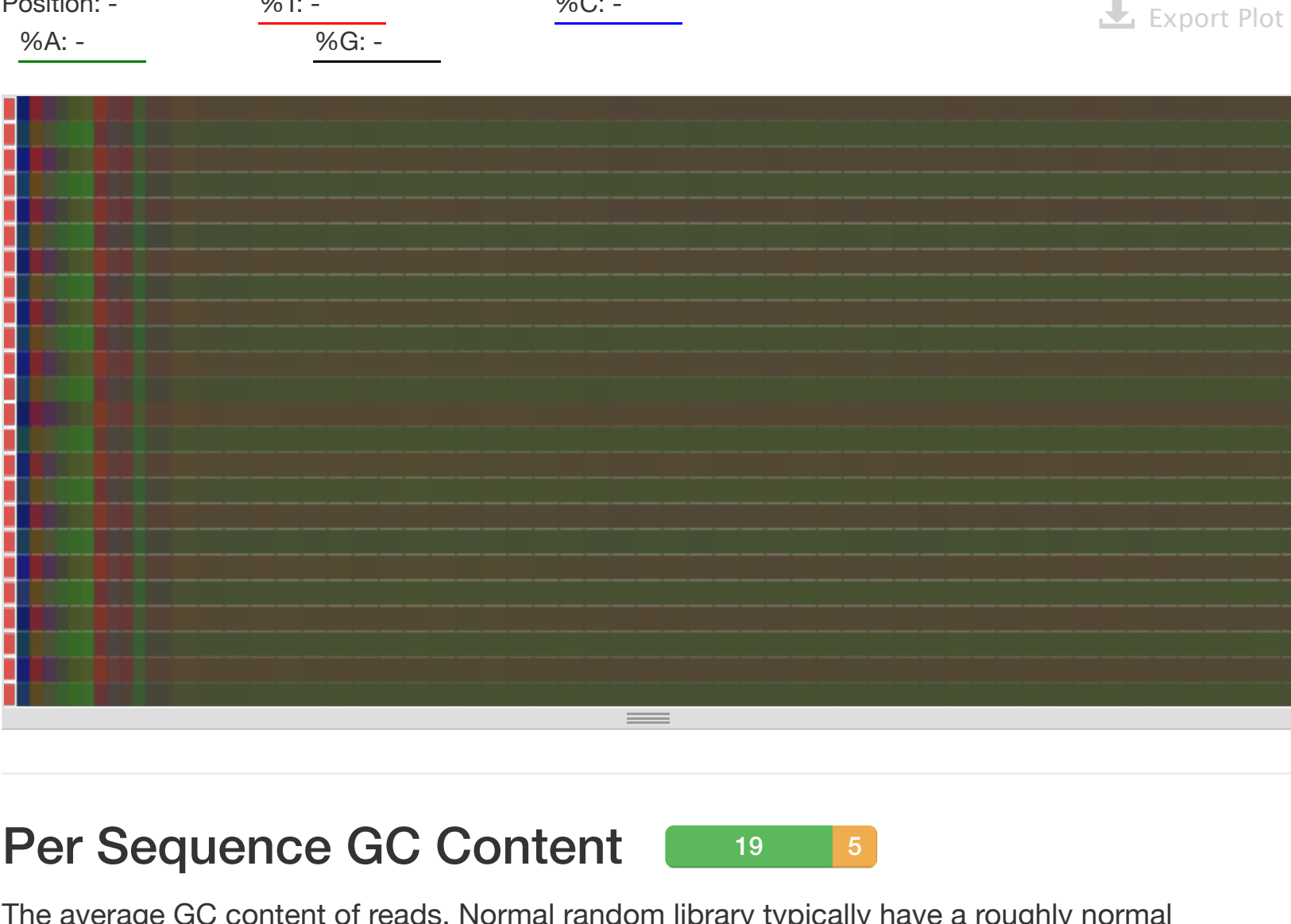
on



## Per Base Sequence Content

The proportion of each base position for which each of the four normal DNA bases has been called. See the [FastQC help](#).

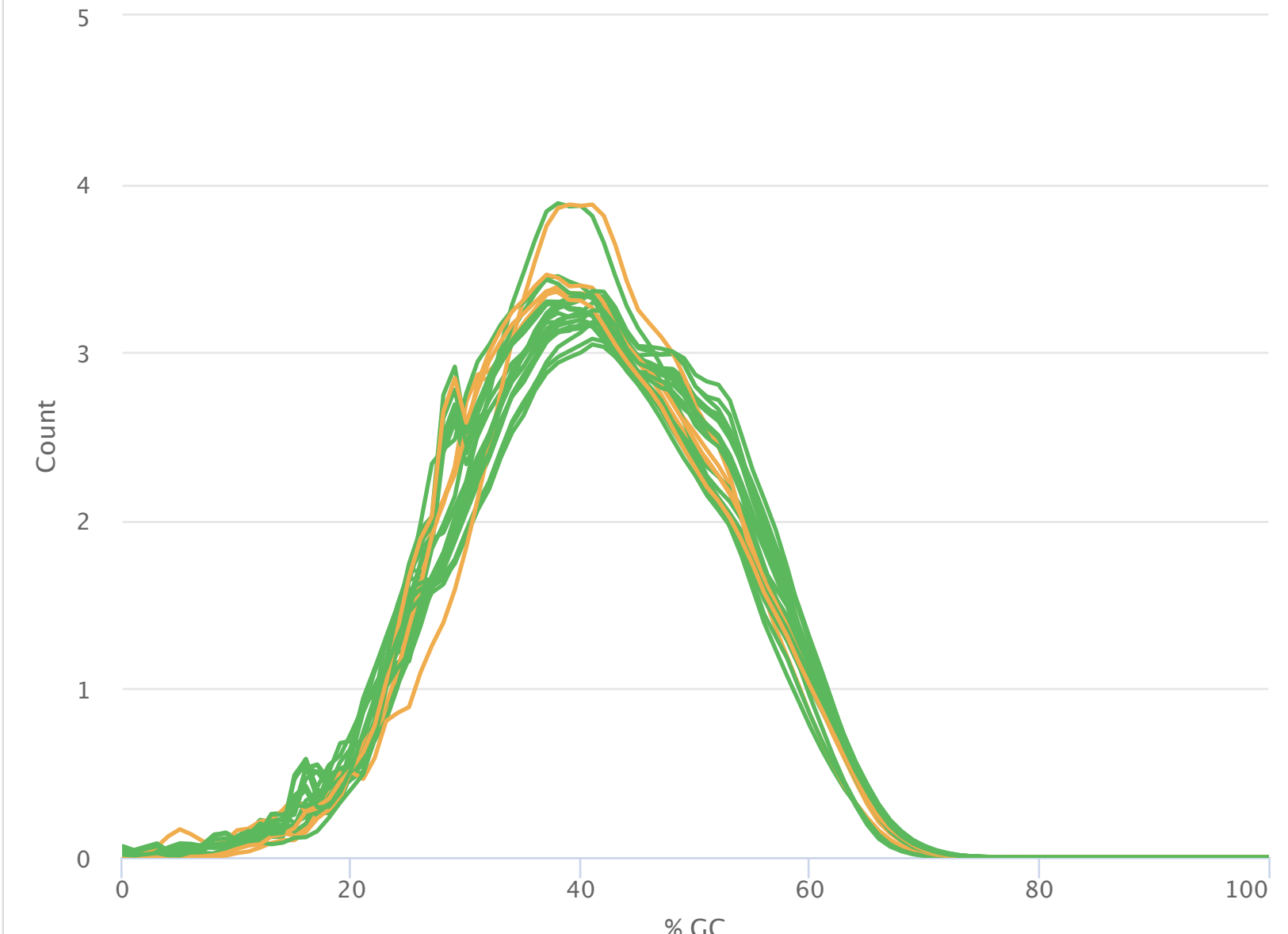
[Click a sample row to see a line plot for that dataset.](#)



## Per Sequence GC Content

The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content. See the [FastQC help](#). Y-Limits: 

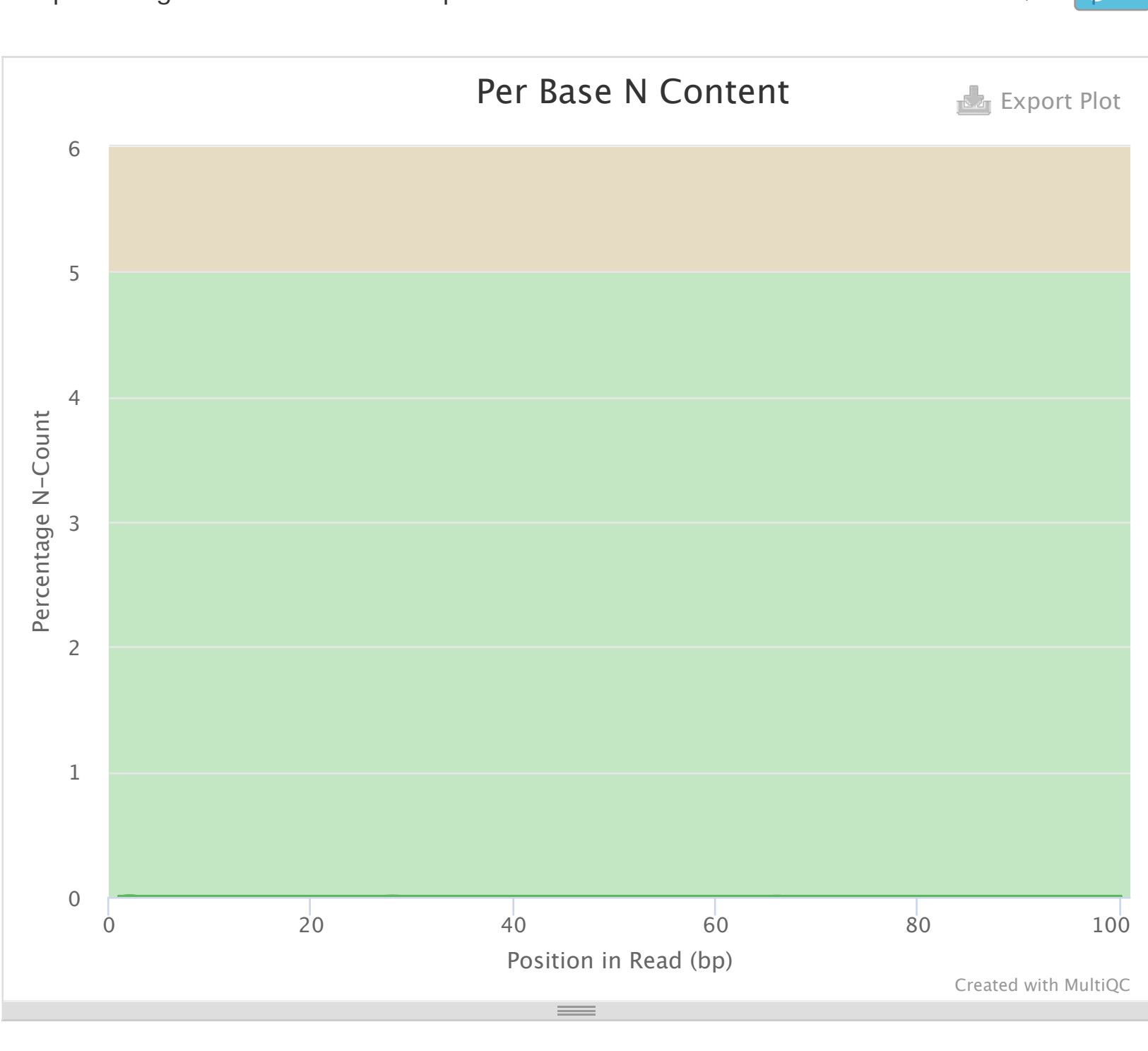
on



## Per Base N Content

The percentage of base calls at each position for which an N was called. See the [FastQC help](#). Y-Limits: 

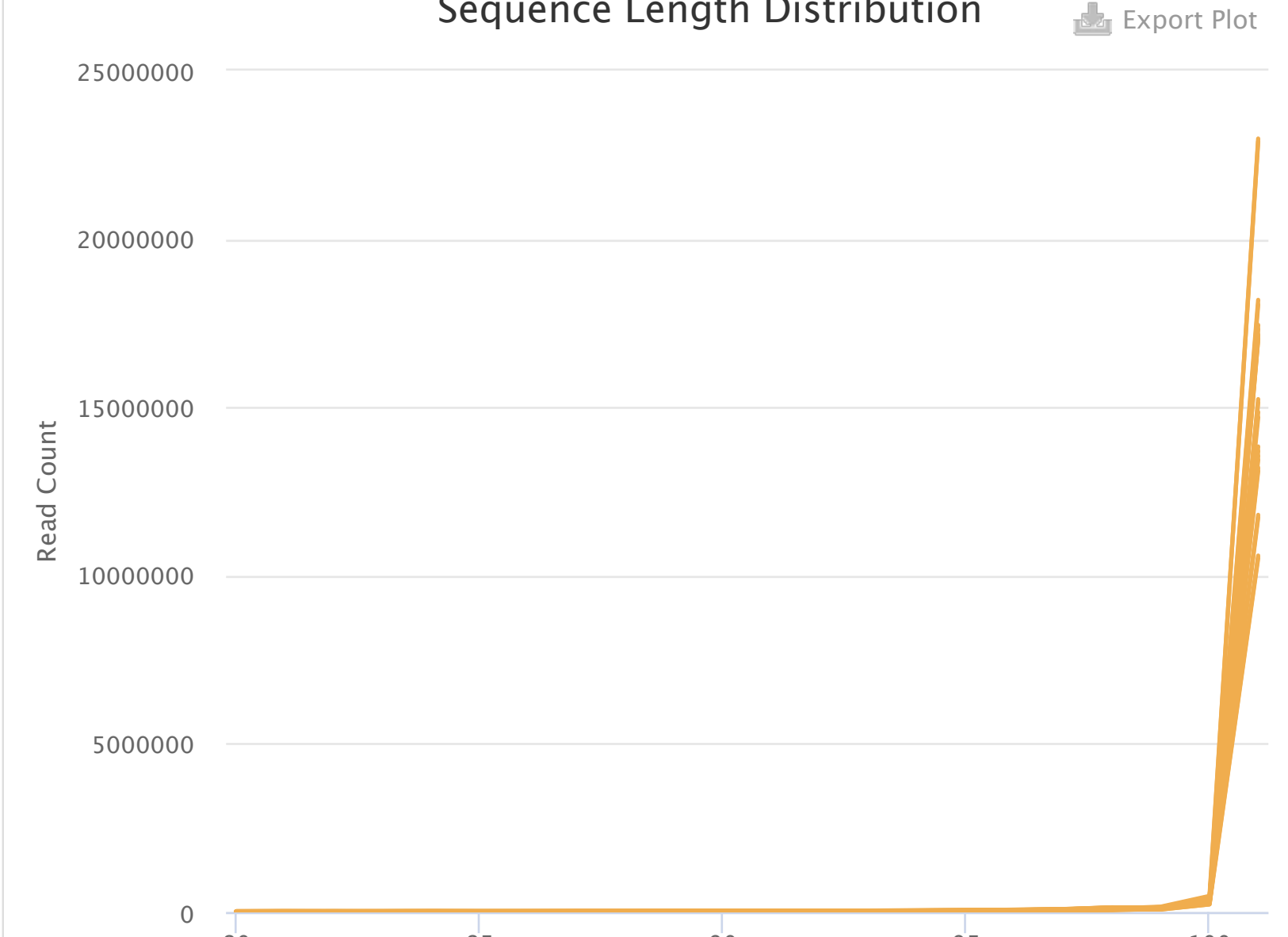
on



## Sequence Length Distribution

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

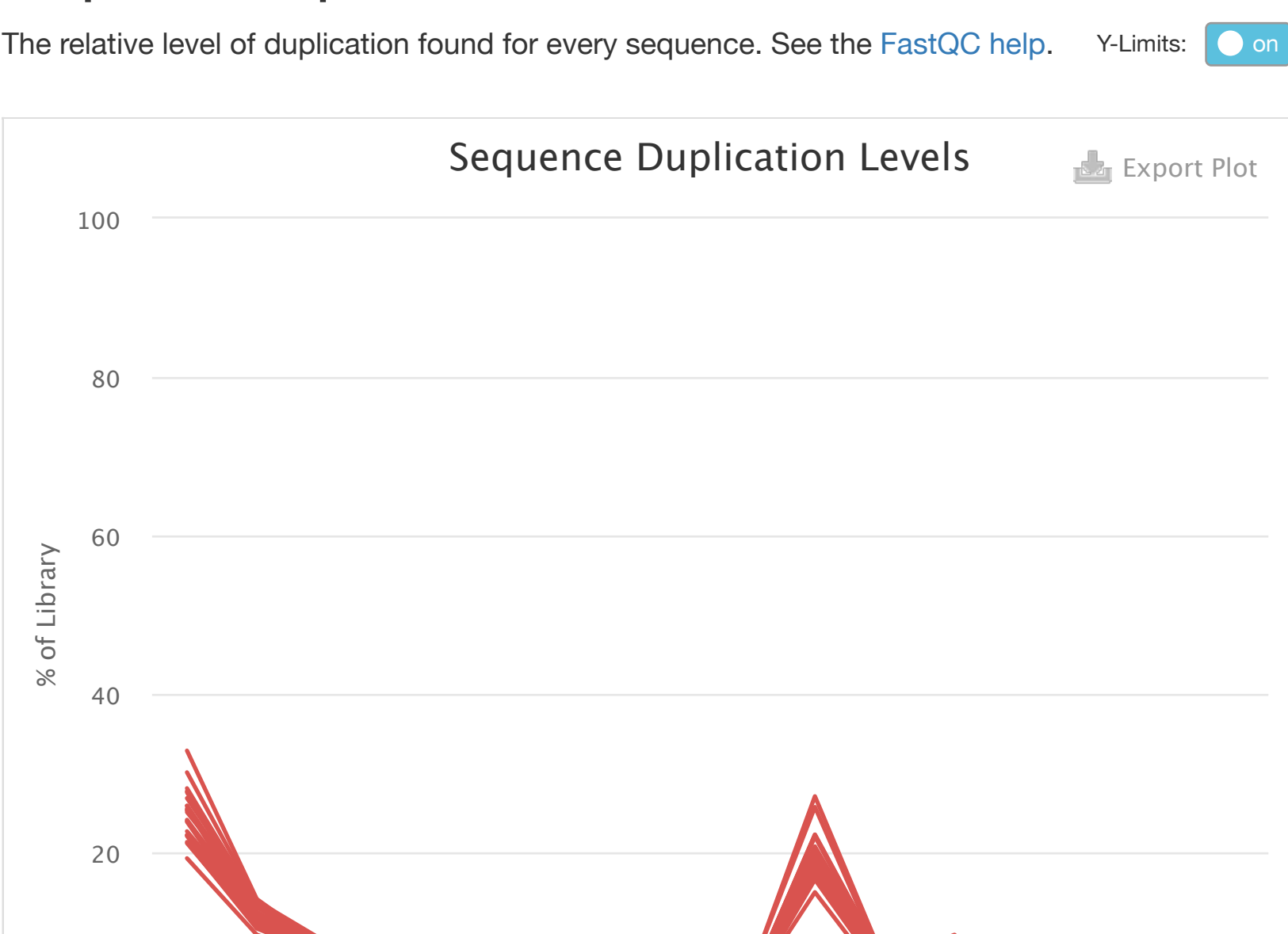
on



## Sequence Duplication Levels

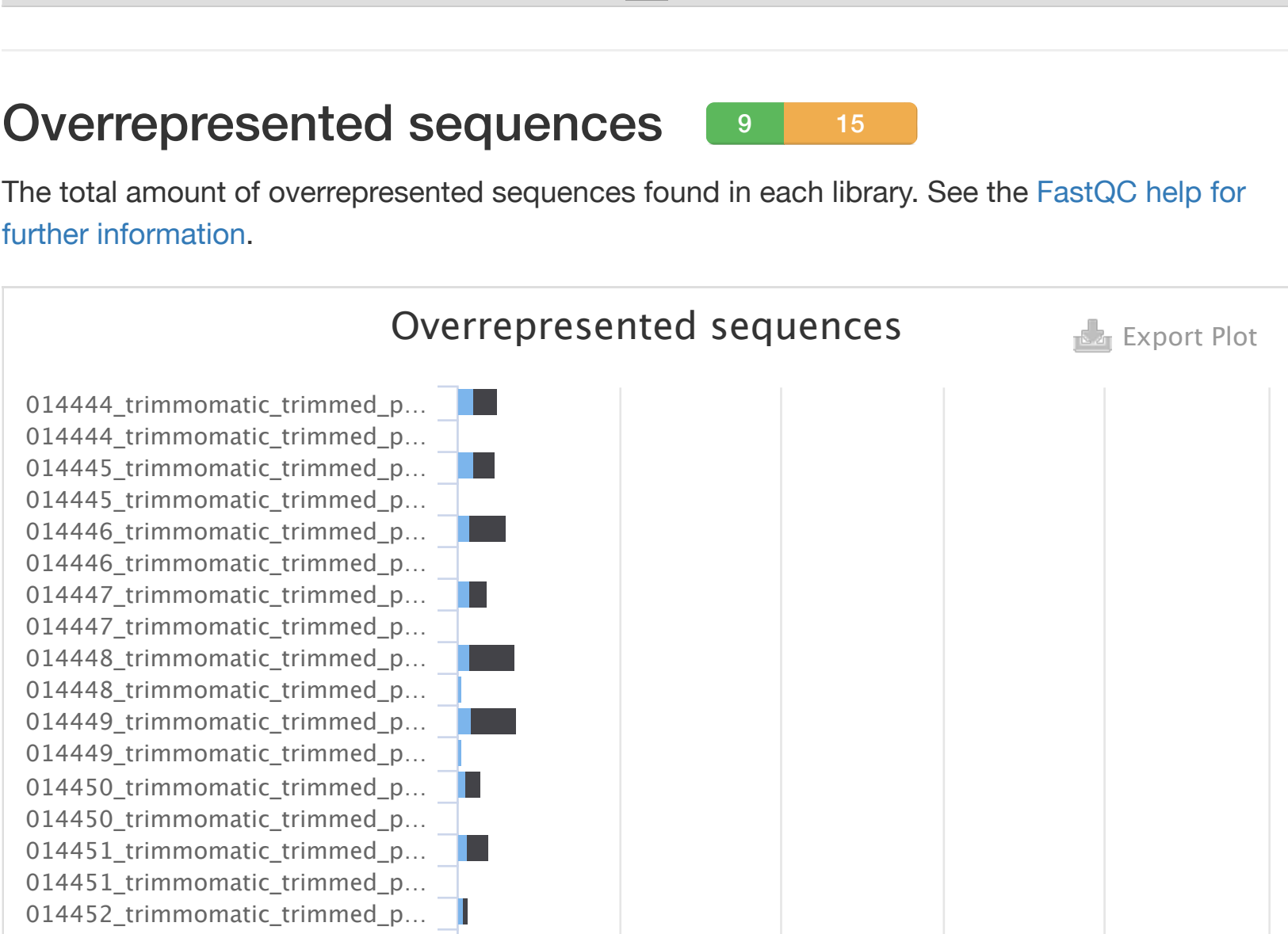
The relative level of duplication found for every sequence. See the [FastQC help](#). Y-Limits: 

on



## Overrepresented sequences

The total amount of overrepresented sequences found in each library. See the [FastQC help](#) for further information.



## Adapter Content

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position. See the [FastQC help](#). Only samples with  $\geq 0.1\%$  adapter contamination are shown.

No samples found with any adapter contamination  $> 0.1\%$