

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

Report generated on 2019-10-23, 13:24 based on data in:
/data/storage/SAYRES/NASONIA/Heini/Processing/Clark/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 12/12 rows and 3/5 columns.

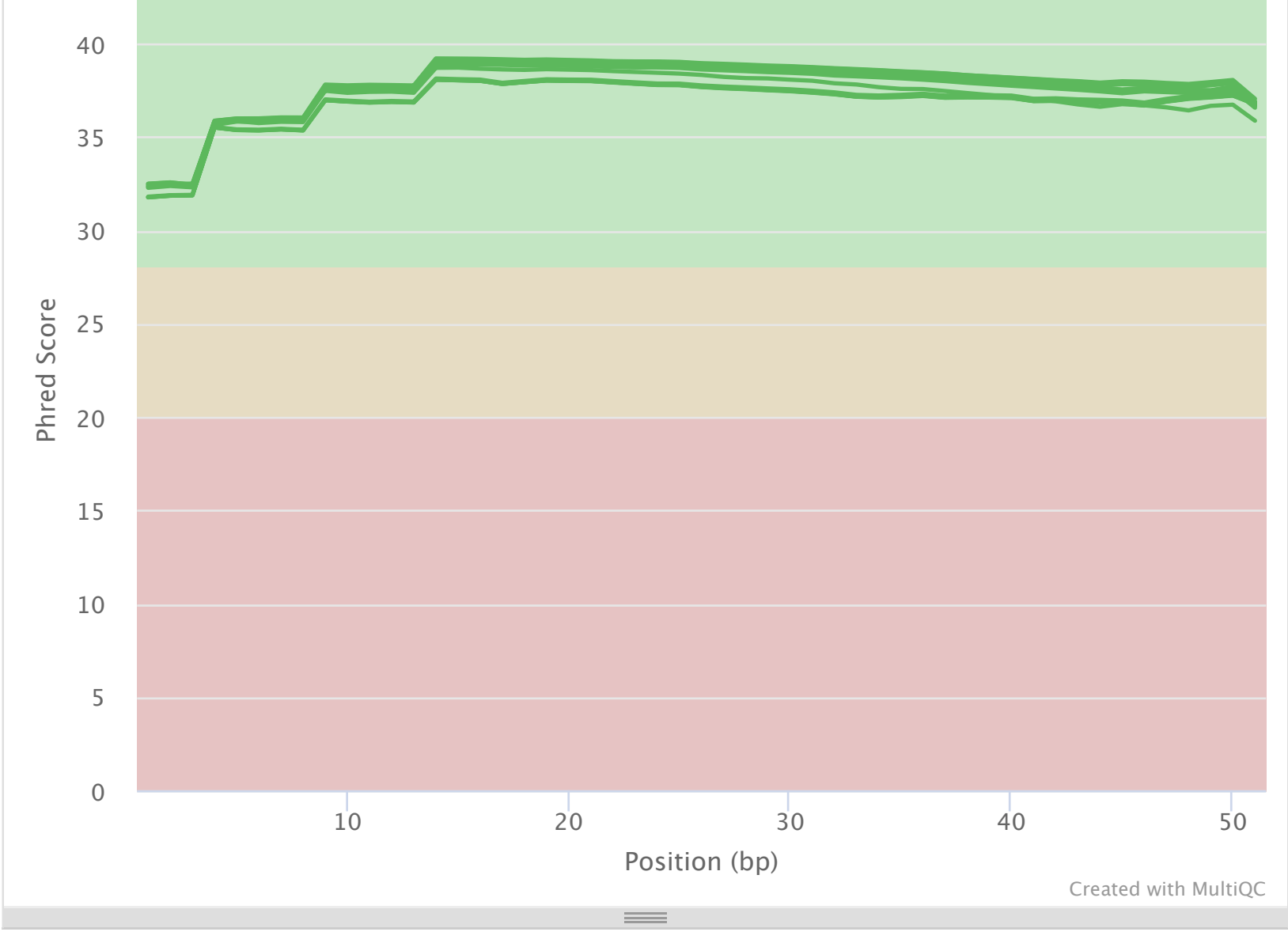
Sample Name	% Dups	% GC	M Seqs
SRR1566022_trimmomatic	68.6%	41%	63.6
SRR1566023_trimmomatic	52.2%	44%	32.3
SRR1566024_trimmomatic	49.1%	46%	37.2
SRR1566028_trimmomatic	66.6%	42%	54.7
SRR1566029_trimmomatic	56.1%	45%	43.3
SRR1566030_trimmomatic	51.3%	46%	46.7
SRR2773794_trimmomatic	58.8%	42%	48.9
SRR2773795_trimmomatic	56.2%	45%	52.2
SRR2773796_trimmomatic	49.2%	46%	72.9
SRR2773797_trimmomatic	62.4%	42%	63.3
SRR2773798_trimmomatic	93.9%	52%	55.9
SRR2773799_trimmomatic	48.2%	46%	62.4

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

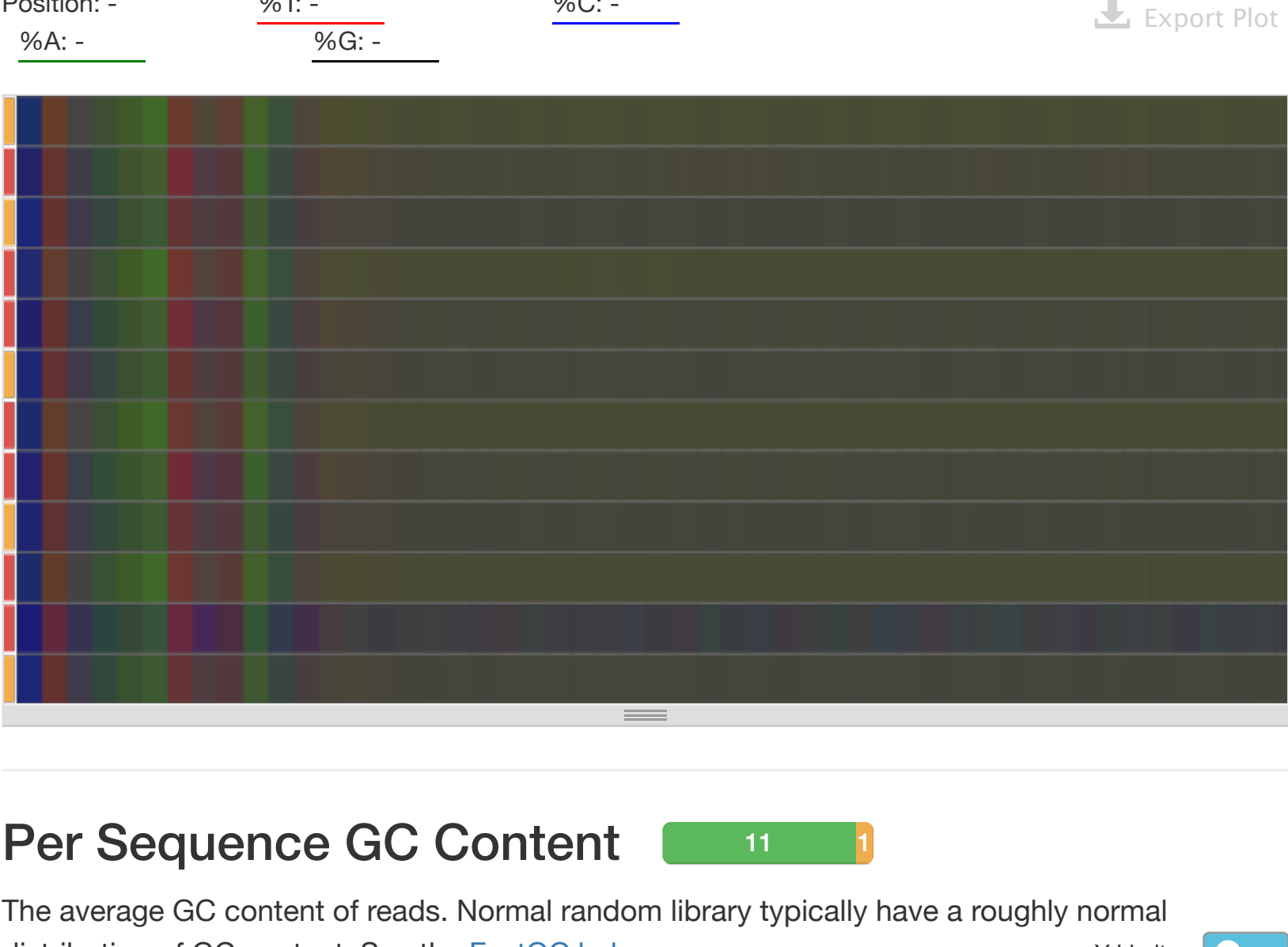
The number of reads with average quality scores. Shows if a subset of reads has poor quality. See the [FastQC help](#). Y-Limits: ☒ on



Per Base Sequence Content

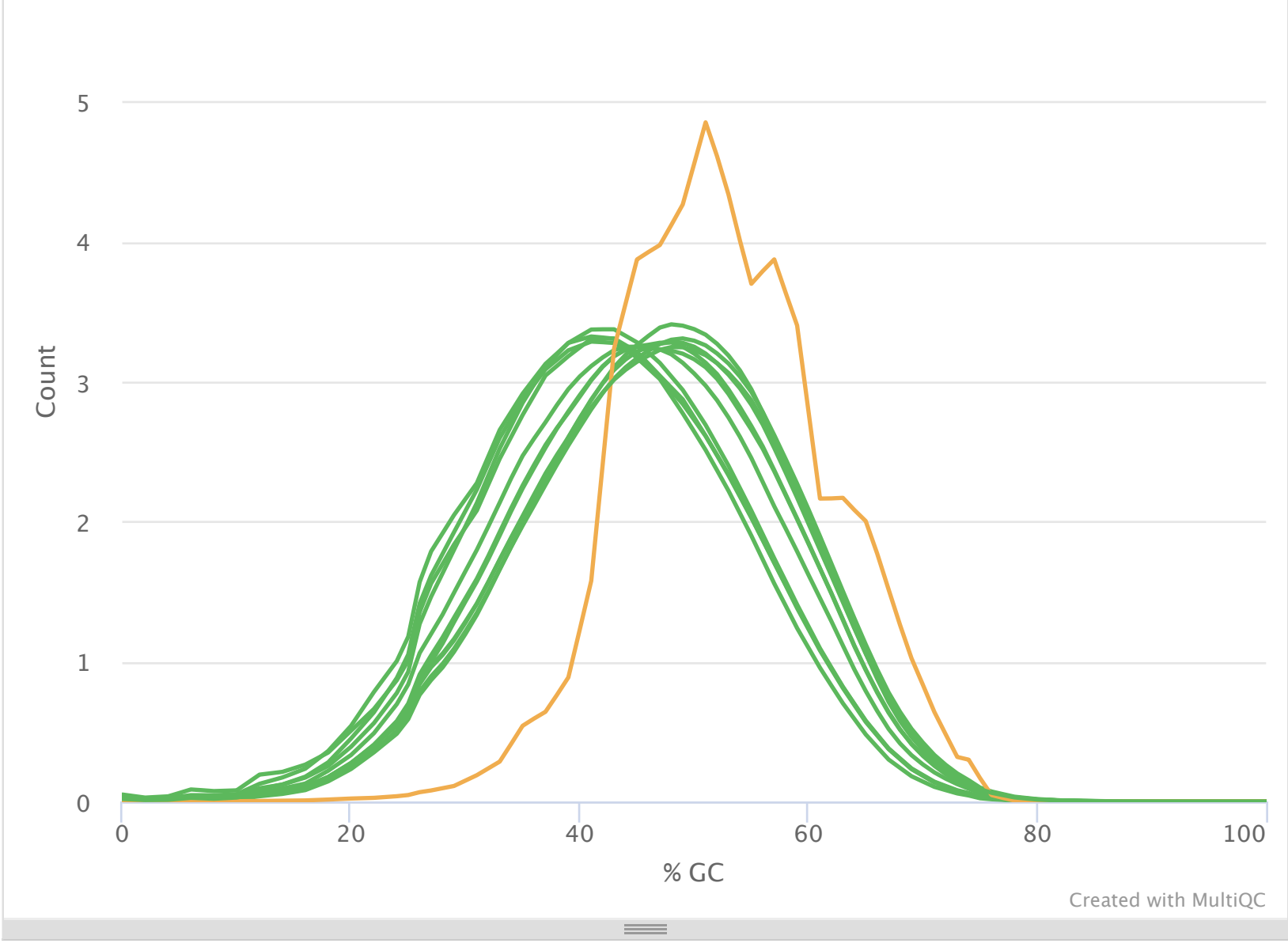
The proportion of each base position for which each of the four normal DNA bases has been called. See the [FastQC help](#).

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



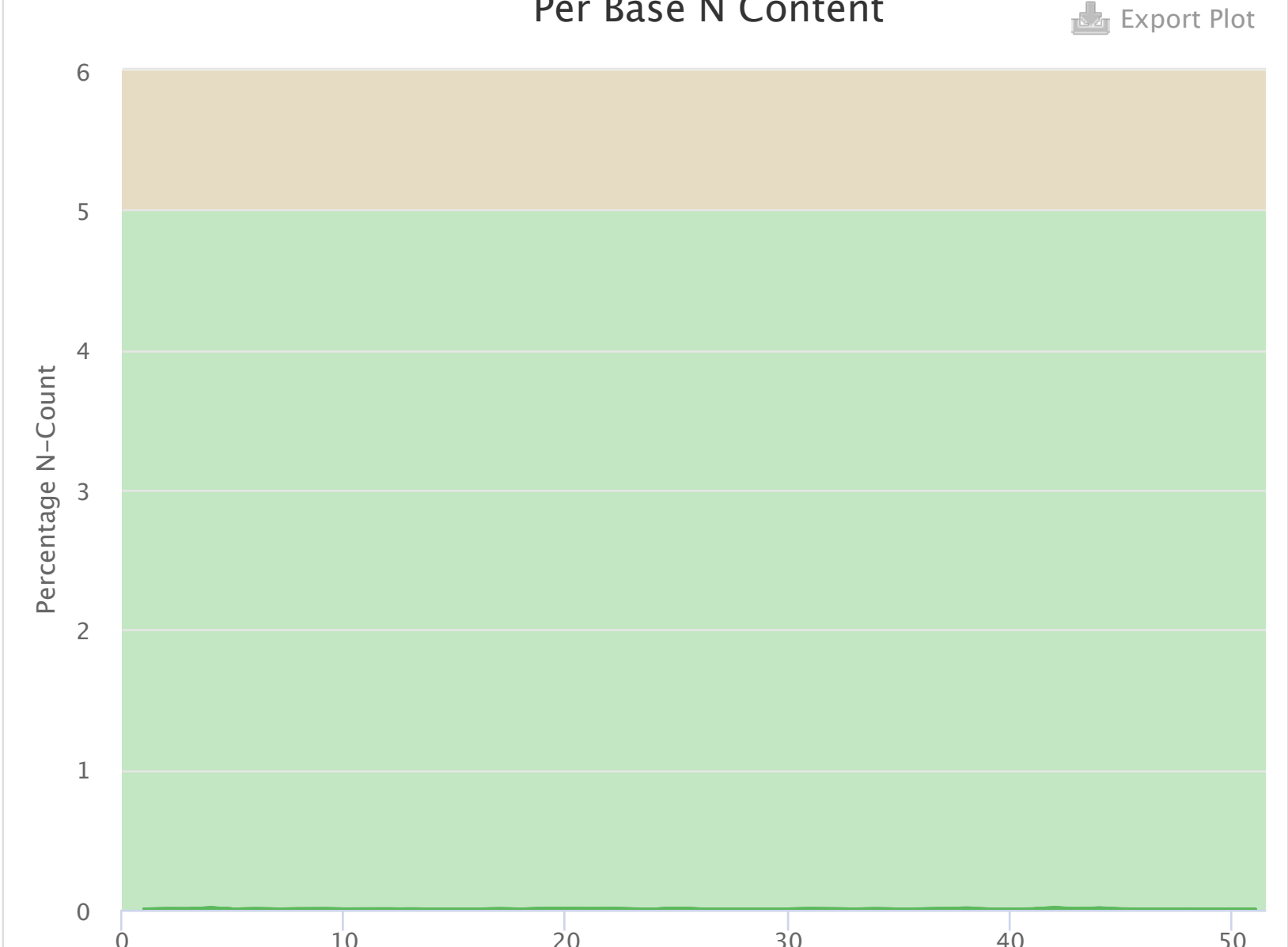
Per Sequence GC Content

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



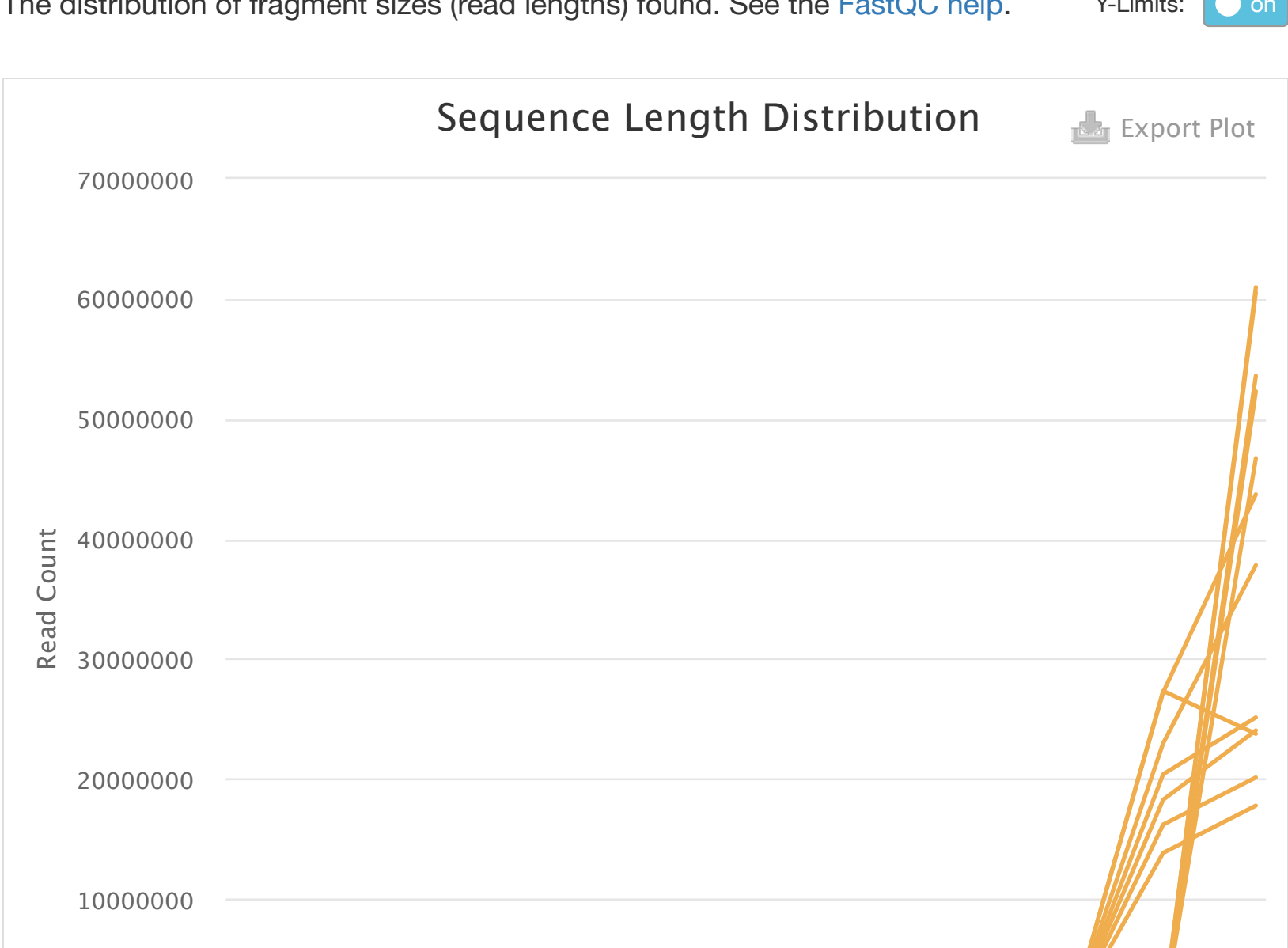
Per Base N Content

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



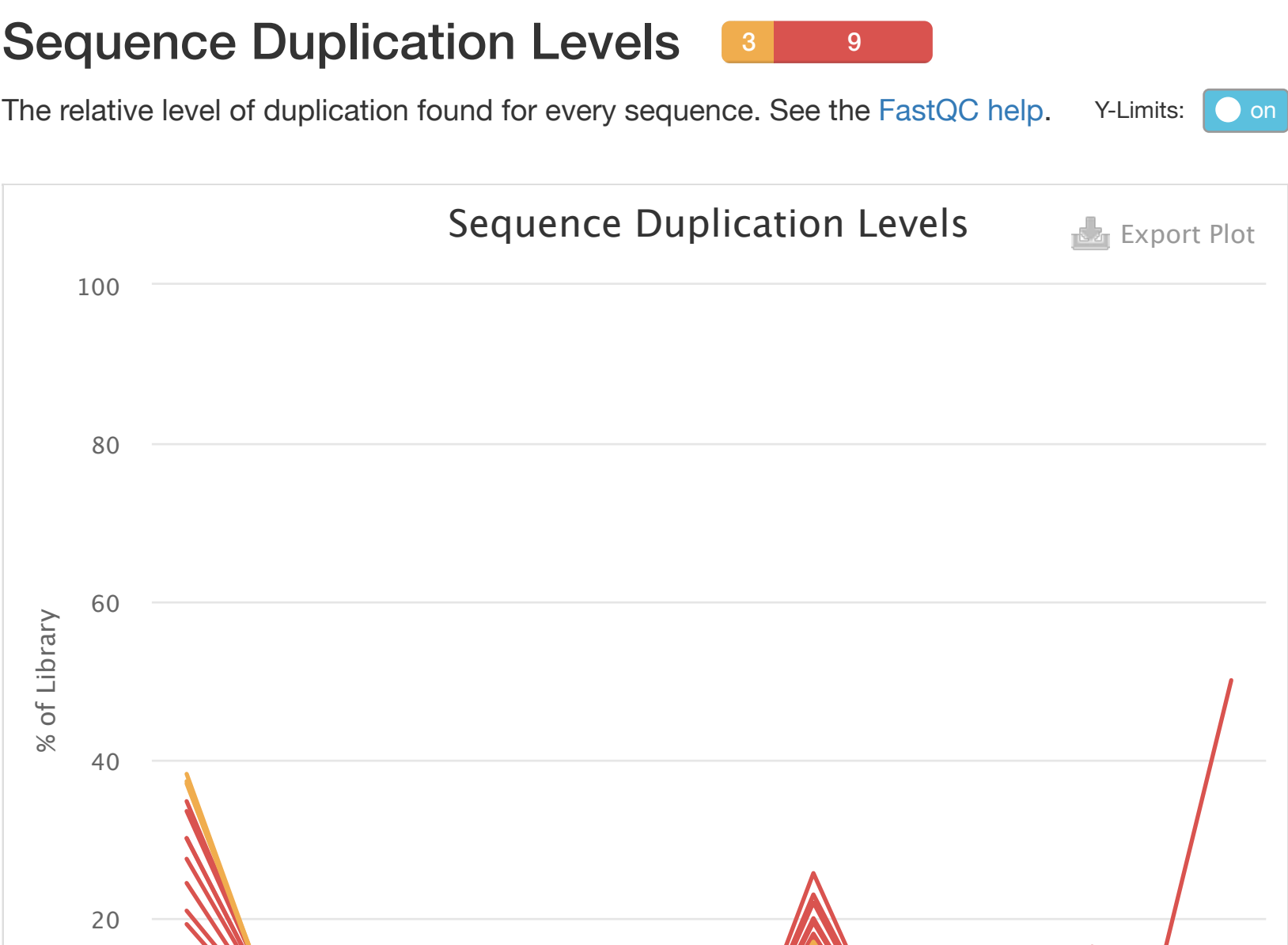
Sequence Length Distribution

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



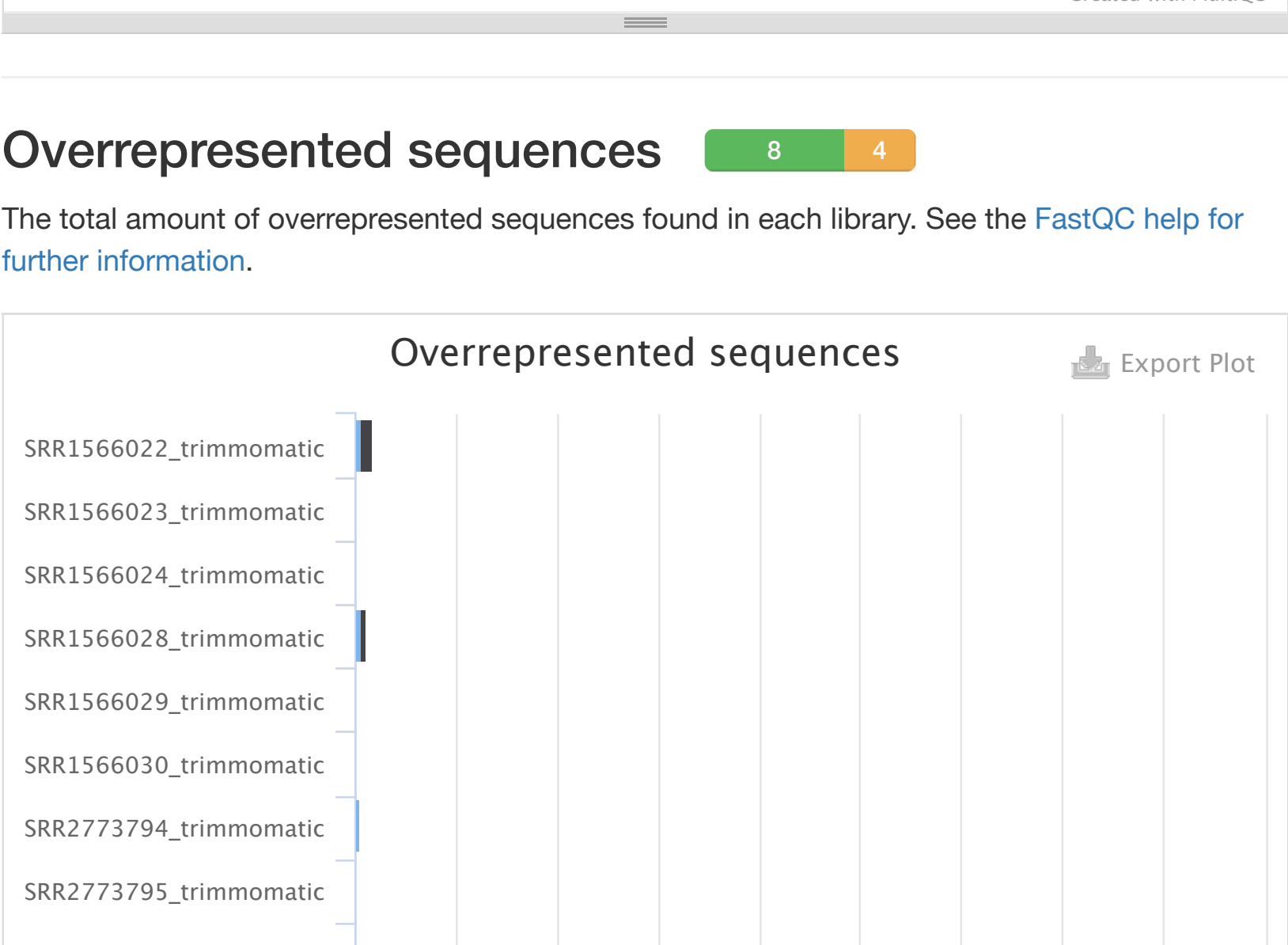
Sequence Duplication Levels

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 $> 0.1\%$