MultiQC
v1.0

MultiQC

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/Sayres/RNA/raw_FastQC`

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

General Statistics

Copy table | Configure Columns | Plot | Showing 24/24 rows and 3/5 columns.

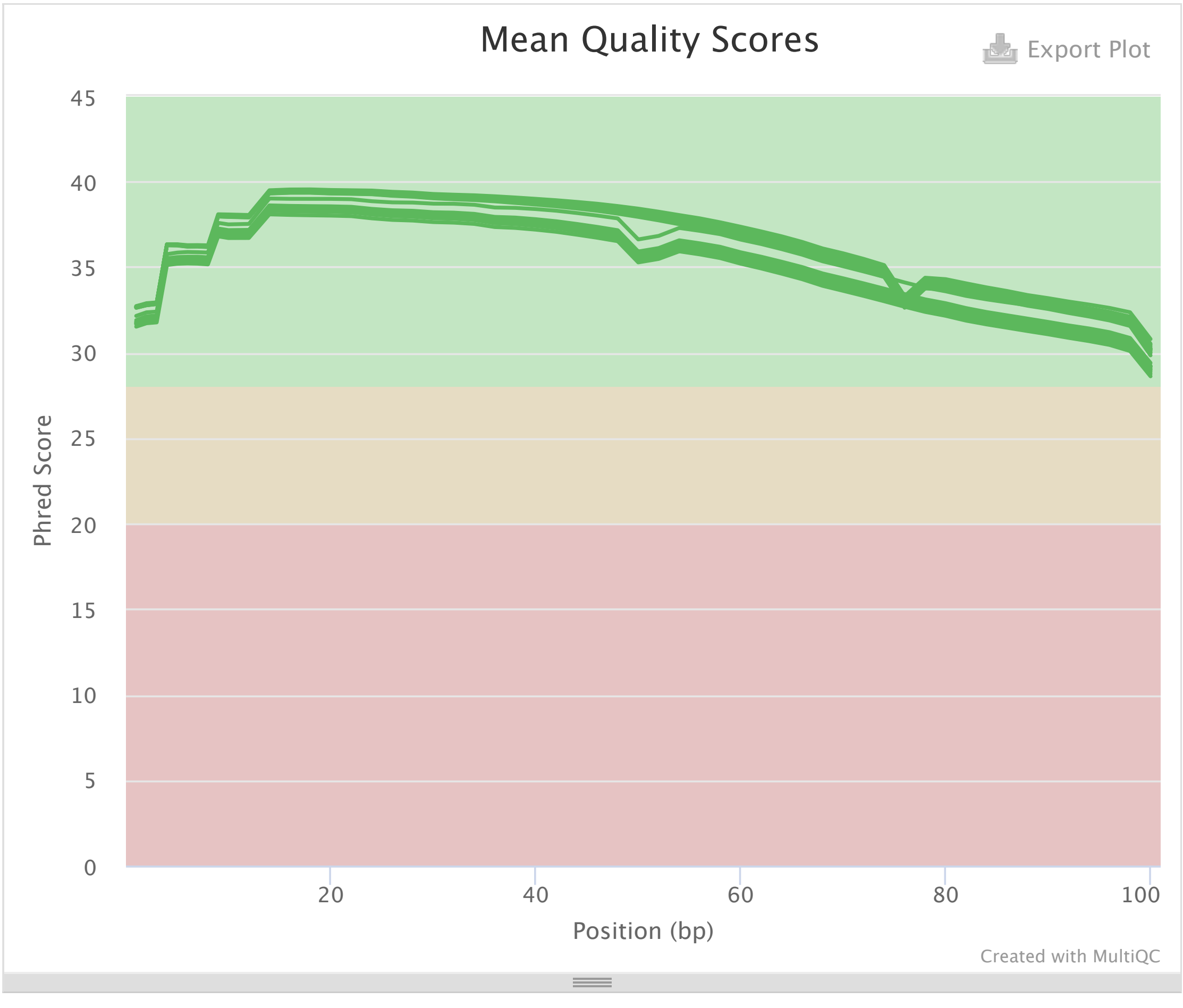
Sample Name	% Dups	% GC	M Seqs
014444_A2_ATCACG_run384_L002_R1_001	66.6%	40%	16.6
014444_A2_ATCACG_run384_L002_R2_001	58.9%	41%	16.6
014445_A4_CGATGT_run384_L002_R1_001	66.6%	40%	16.1
014445_A4_CGATGT_run384_L002_R2_001	59.0%	41%	16.1
014446_A5_TTAGGC_run384_L002_R1_001	61.9%	41%	12.7
014446_A5_TTAGGC_run384_L002_R2_001	55.0%	42%	12.7
014447_B2_TGACCA_run384_L002_R1_001	65.2%	40%	17.9
014447_B2_TGACCA_run384_L002_R2_001	59.2%	41%	17.9
014448_B4_ACAGTG_run384_L002_R1_001	66.2%	40%	15.6
014448_B4_ACAGTG_run384_L002_R2_001	59.8%	41%	15.6
014449_B6_GCCAAT_run384_L002_R1_001	69.4%	40%	21.5
014449_B6_GCCAAT_run384_L002_R2_001	63.4%	41%	21.5

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 24

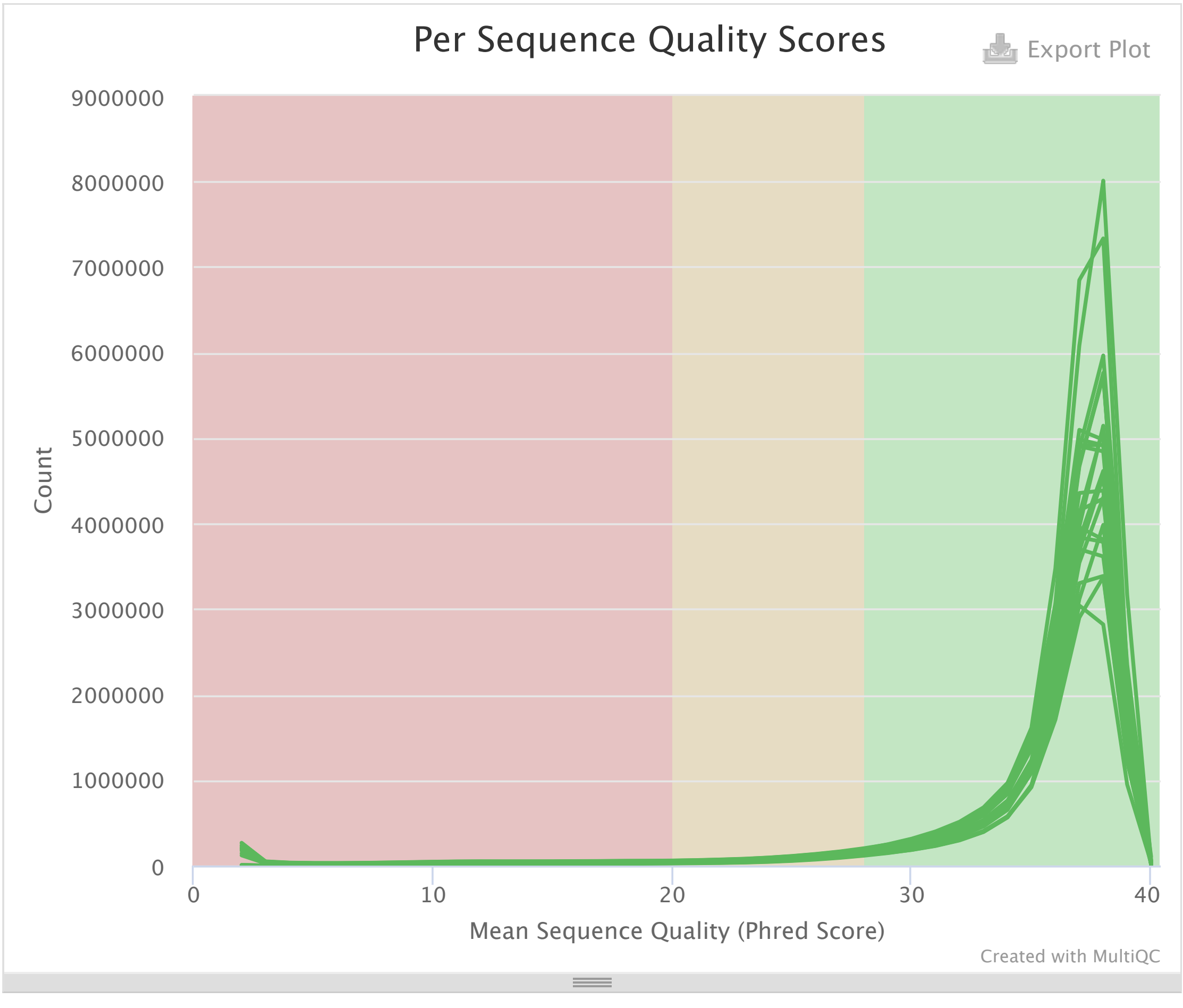
The mean quality value across each base position in the read. See the FastQC help Y-Limits: on



Per Sequence Quality Scores 24

The number of reads with average quality scores. Shows if a subset of reads has poor quality. See the FastQC help.

Y-Limits: on

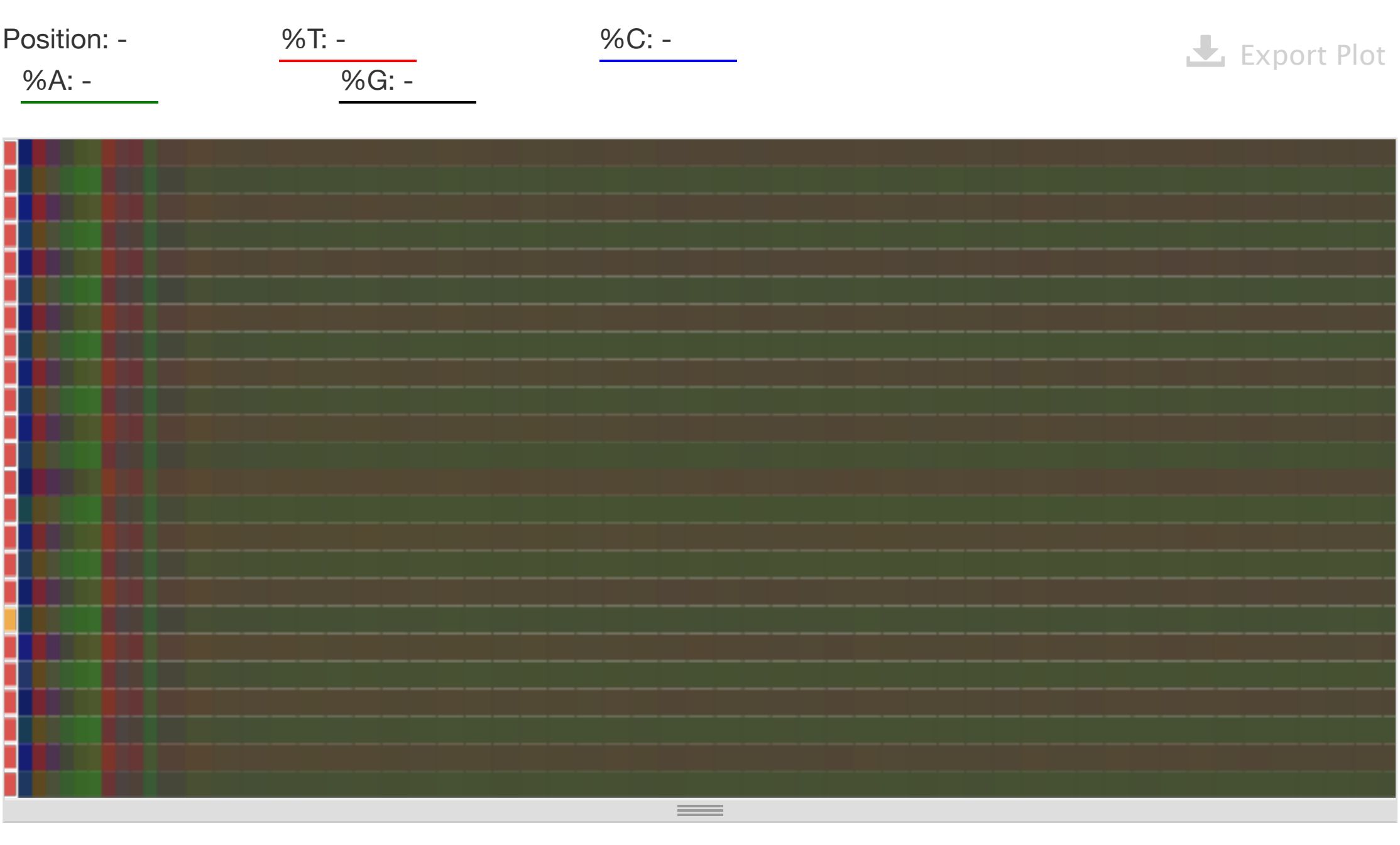


Per Base Sequence Content 1 23

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.

Rollover for sample name

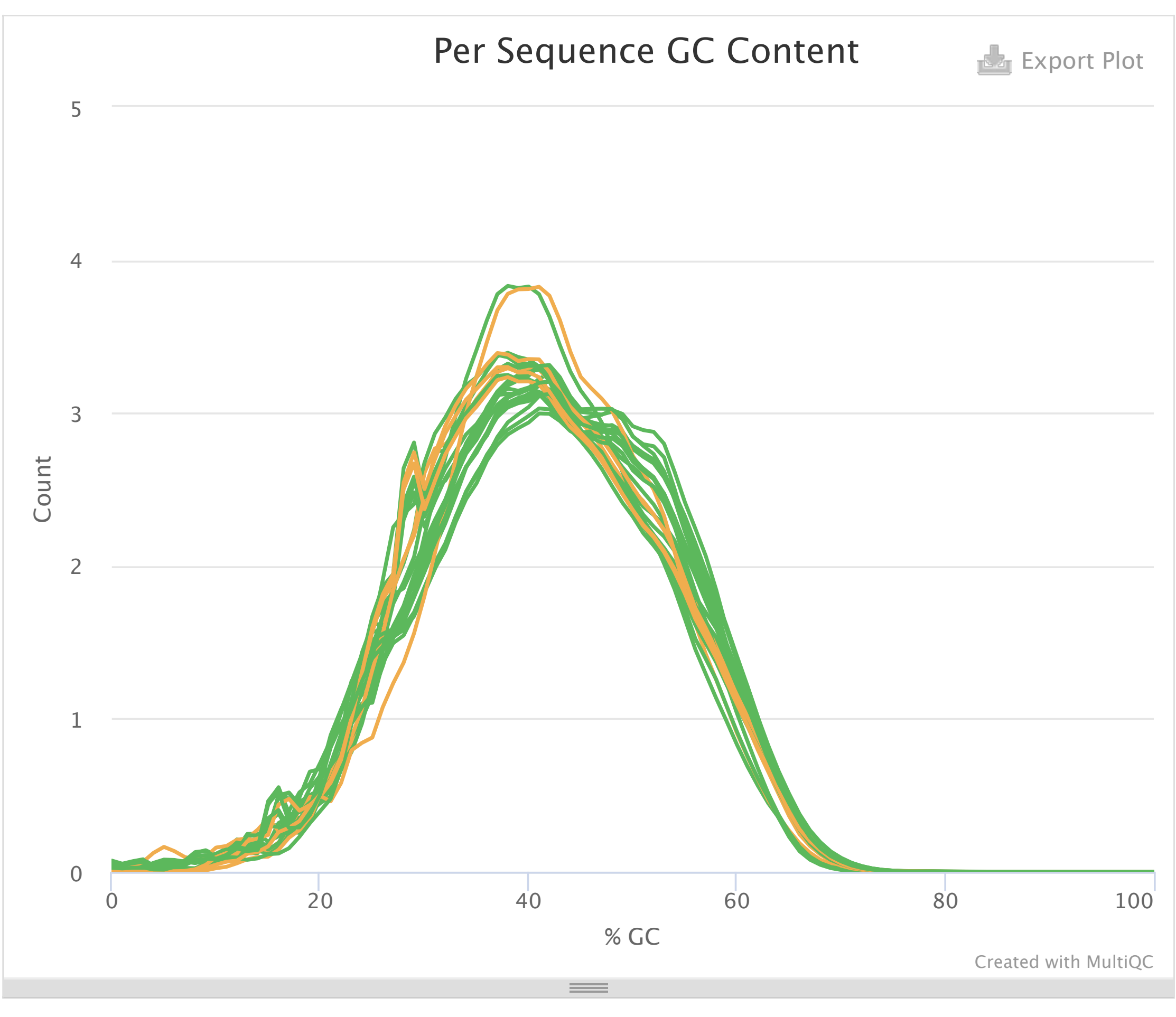


Per Sequence GC Content 19 5

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

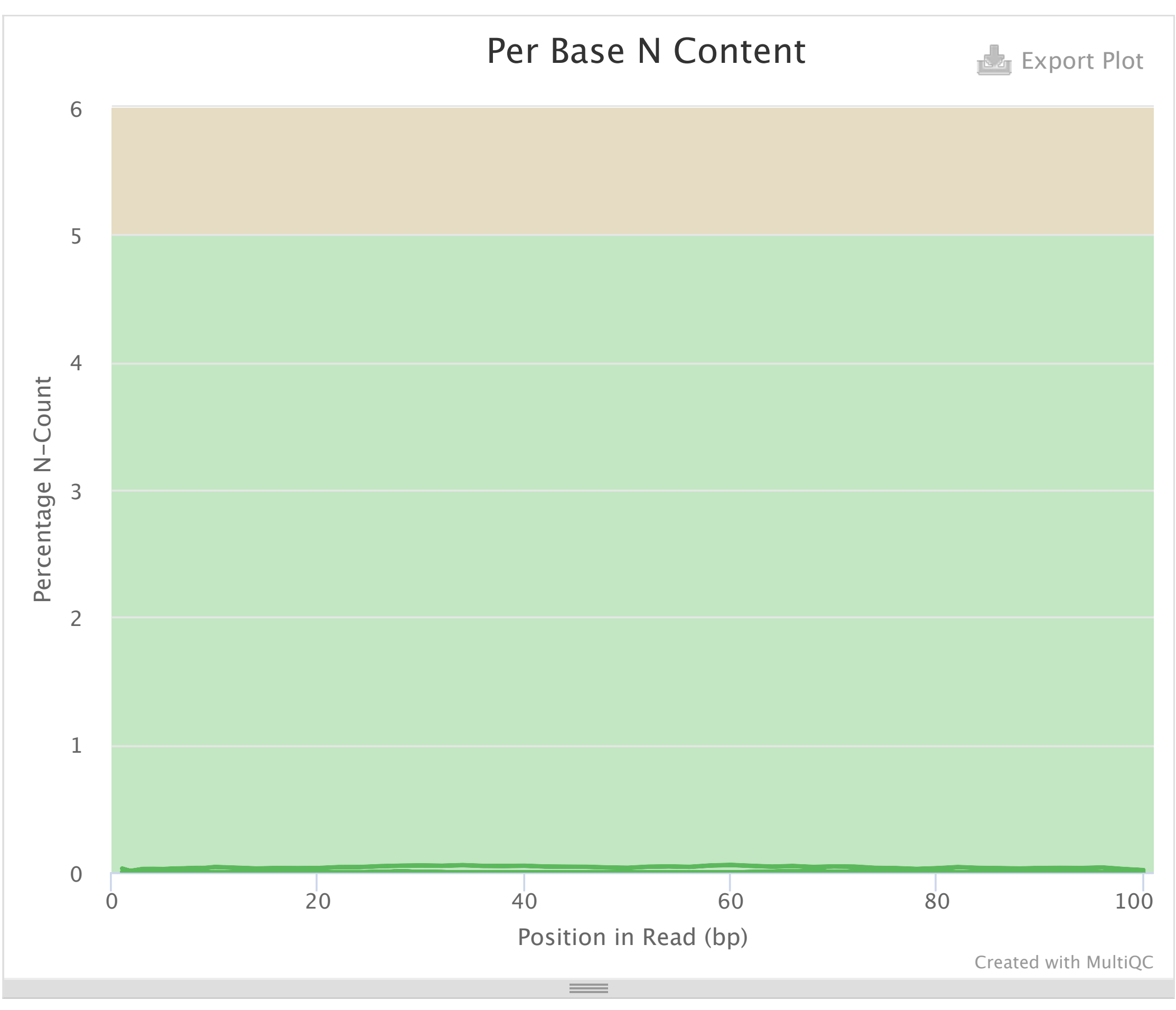
Y-Limits: on

Percentages | Counts



Per Base N Content 24

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

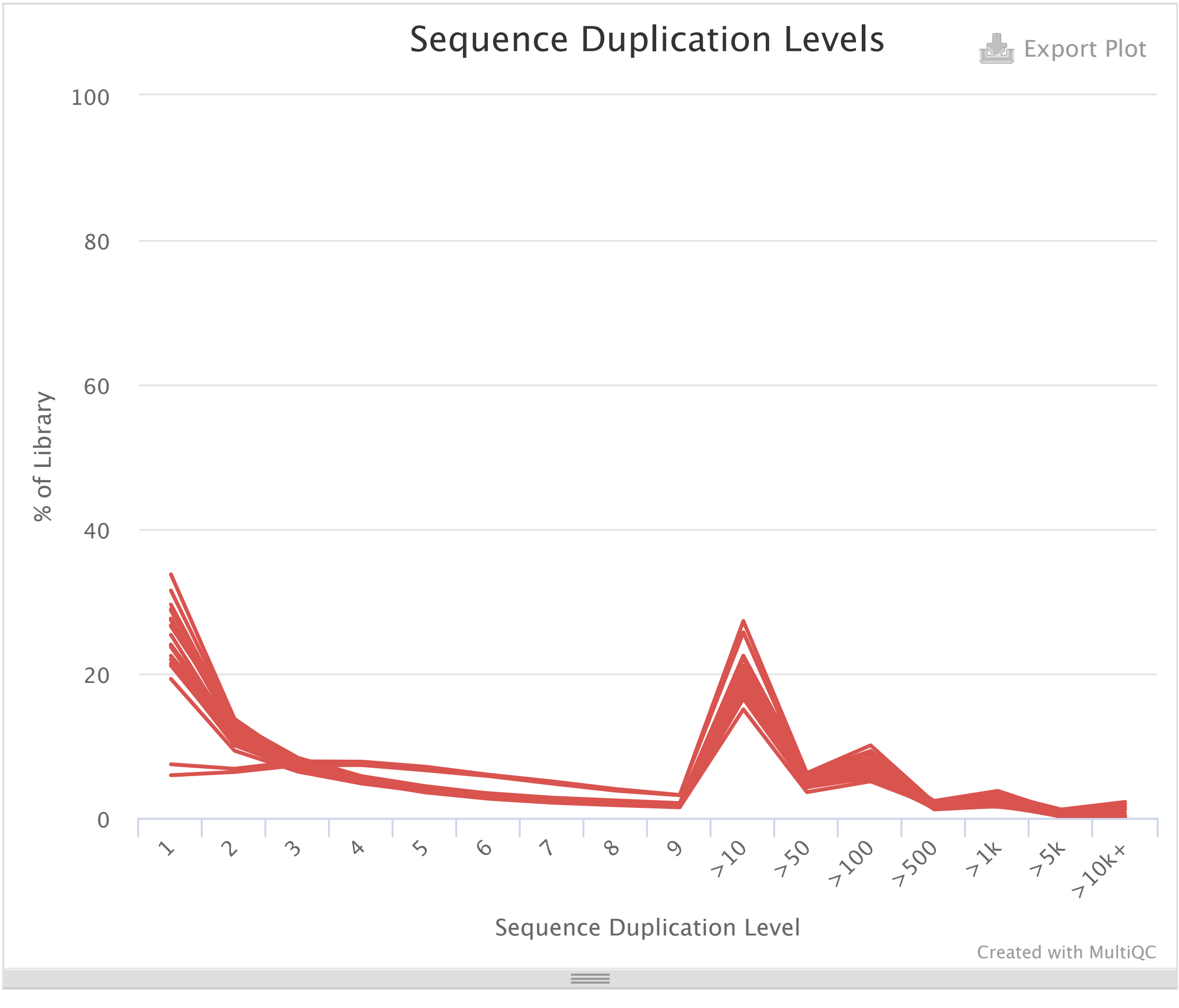


Sequence Length Distribution 24

All samples have sequences of a single length (101bp).

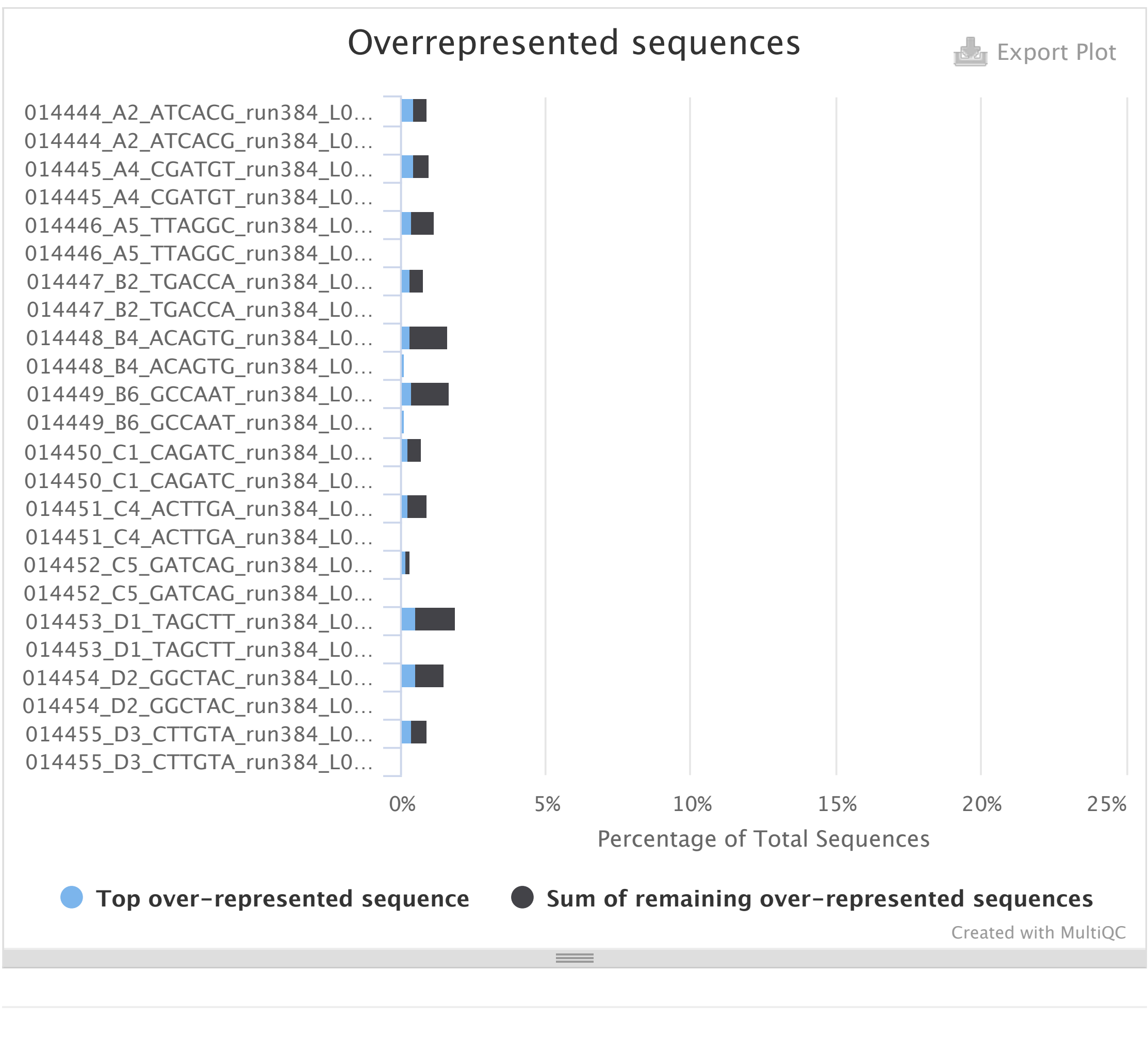
Sequence Duplication Levels 24

The relative level of duplication found for every sequence. See the FastQC help. Y-Limits: on



Overrepresented sequences 10 14

The total amount of overrepresented sequences found in each library. See the FastQC help for further information.



Adapter Content 24

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 ≥ 0.1% adapter contamination are shown.

Y-Limits: on