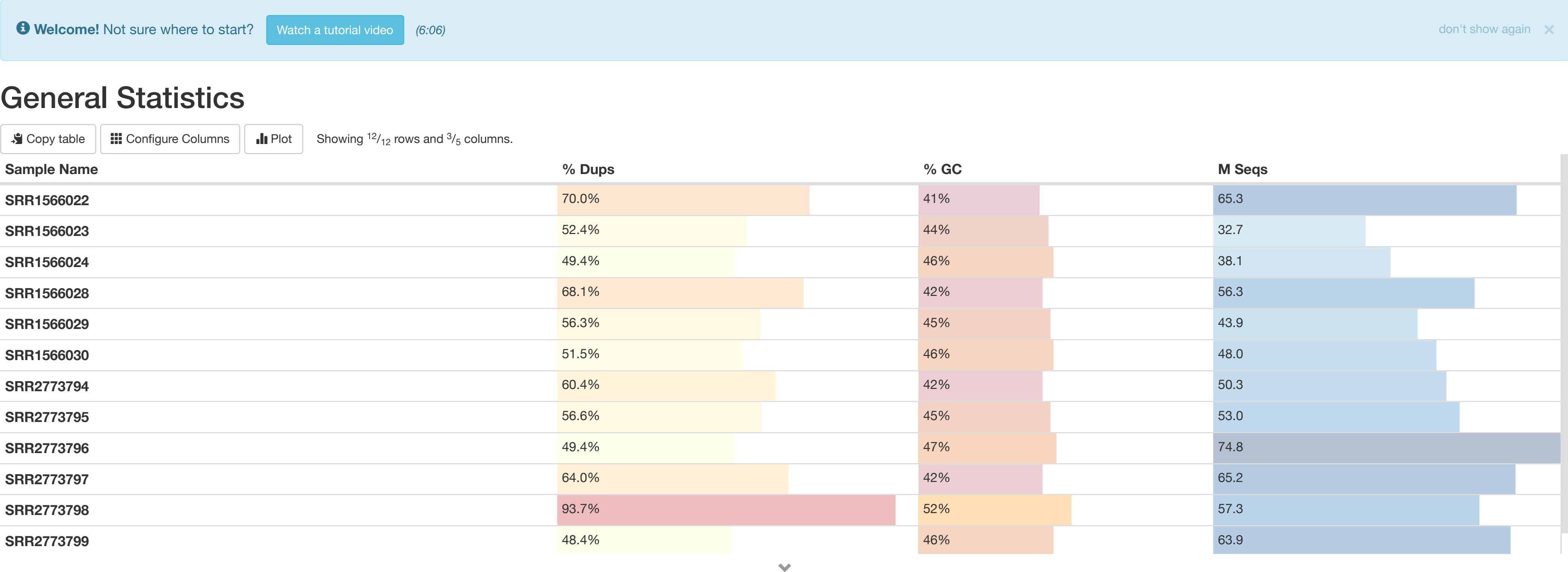


A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2019-10-23, 13:24 based on data in: `./data/storage/SAYRES/NASDNIA/Heini/Processing/Clark/RNA/raw_FastQC`



## FastQC

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

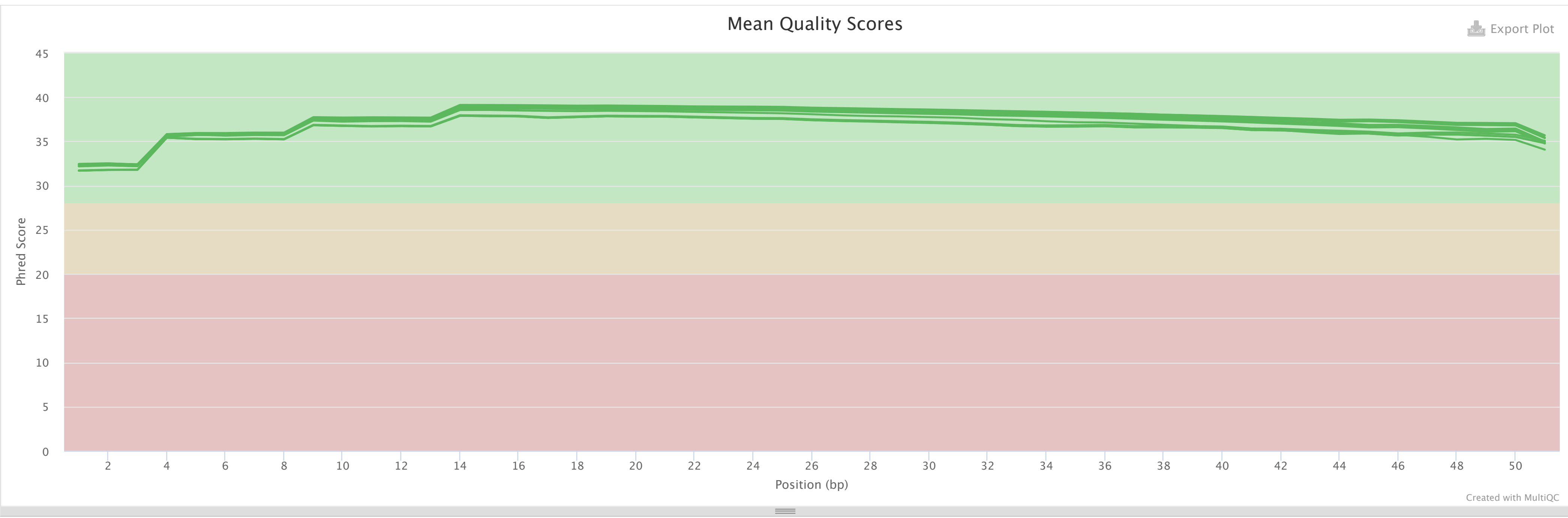
### Sequence Quality Histograms

12

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

Y-Limits: 

on



### Per Sequence Quality Scores

12

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

66

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.



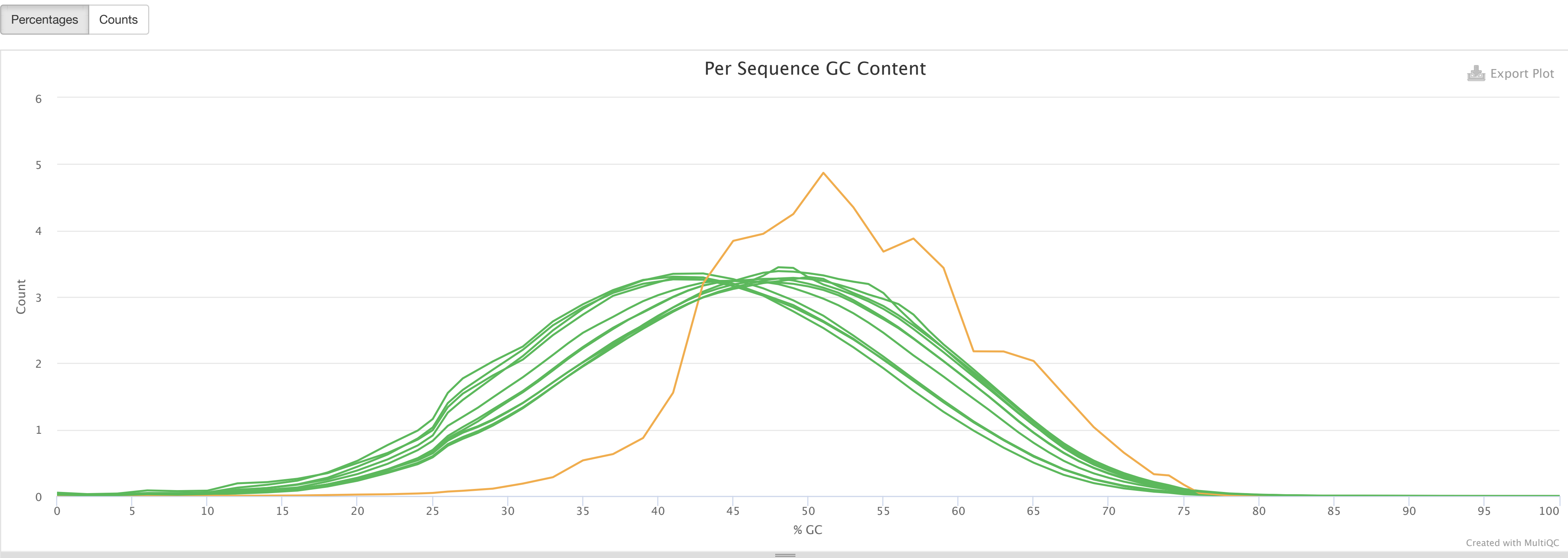
### Per Sequence GC Content

111

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



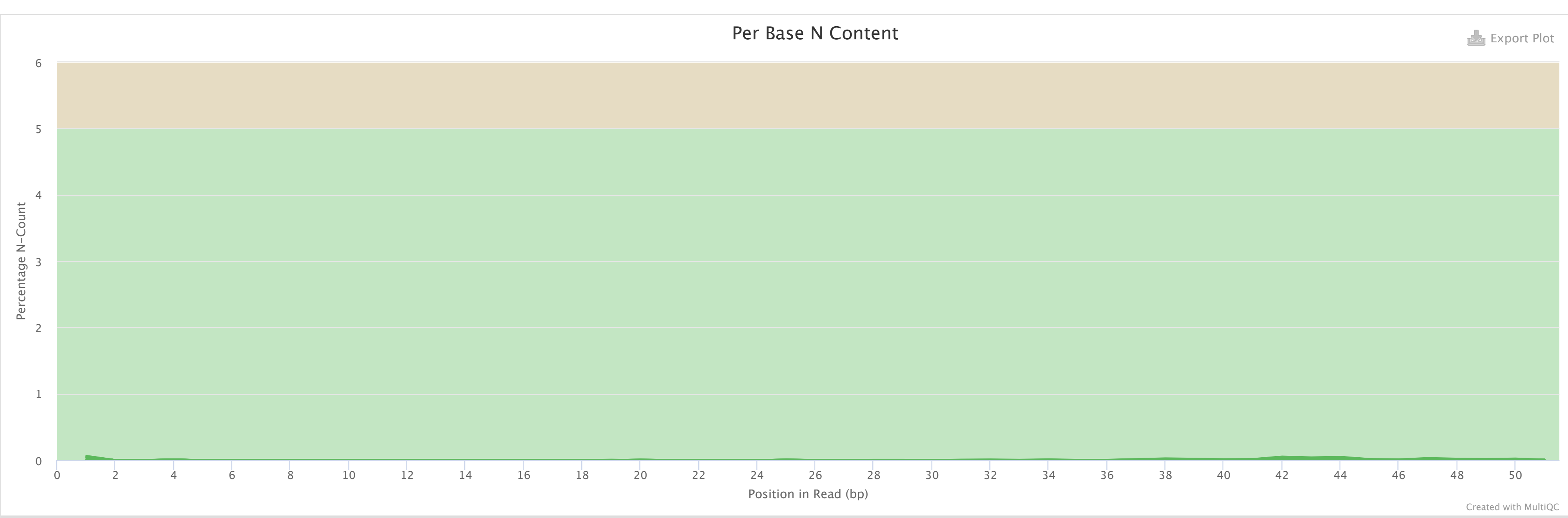
### Per Base N Content

12

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

Y-Limits: 

on



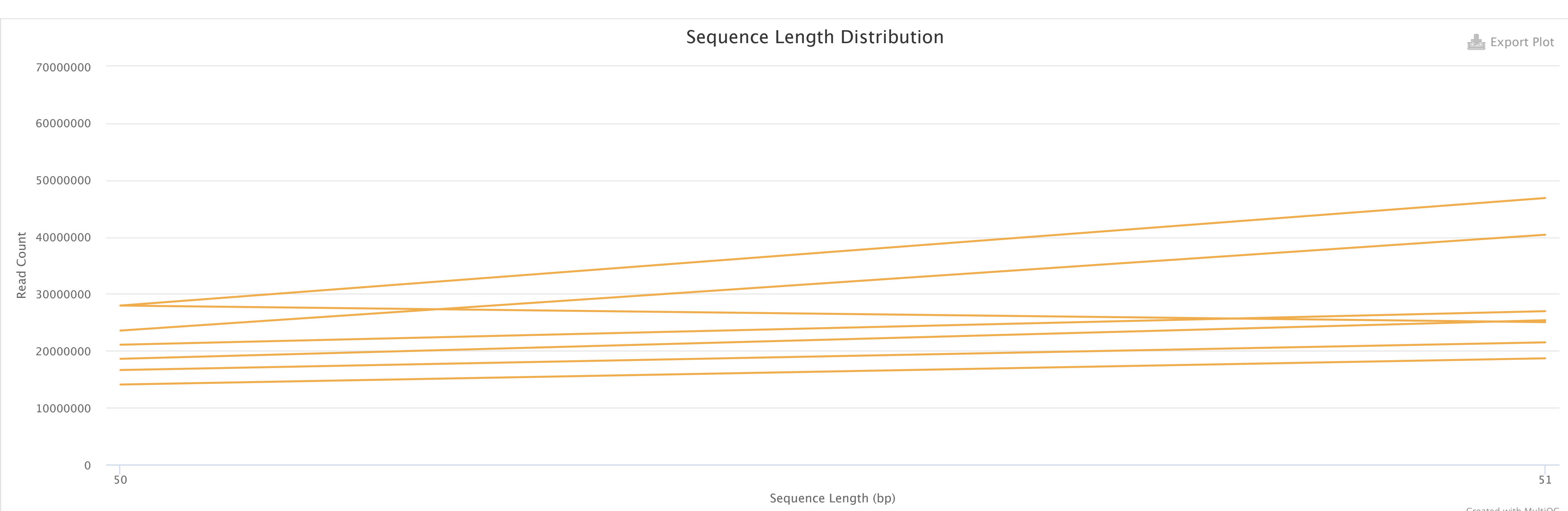
### Sequence Length Distribution

67

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

Y-Limits: 

on



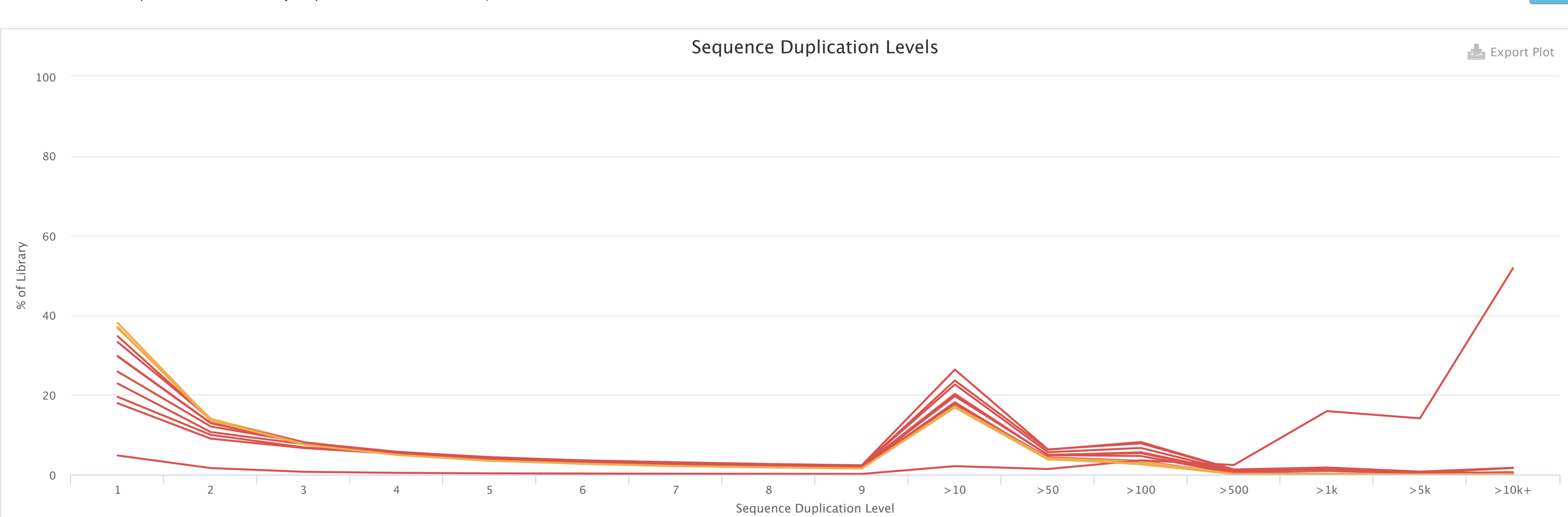
### Sequence Duplication Levels

39

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

Y-Limits: 

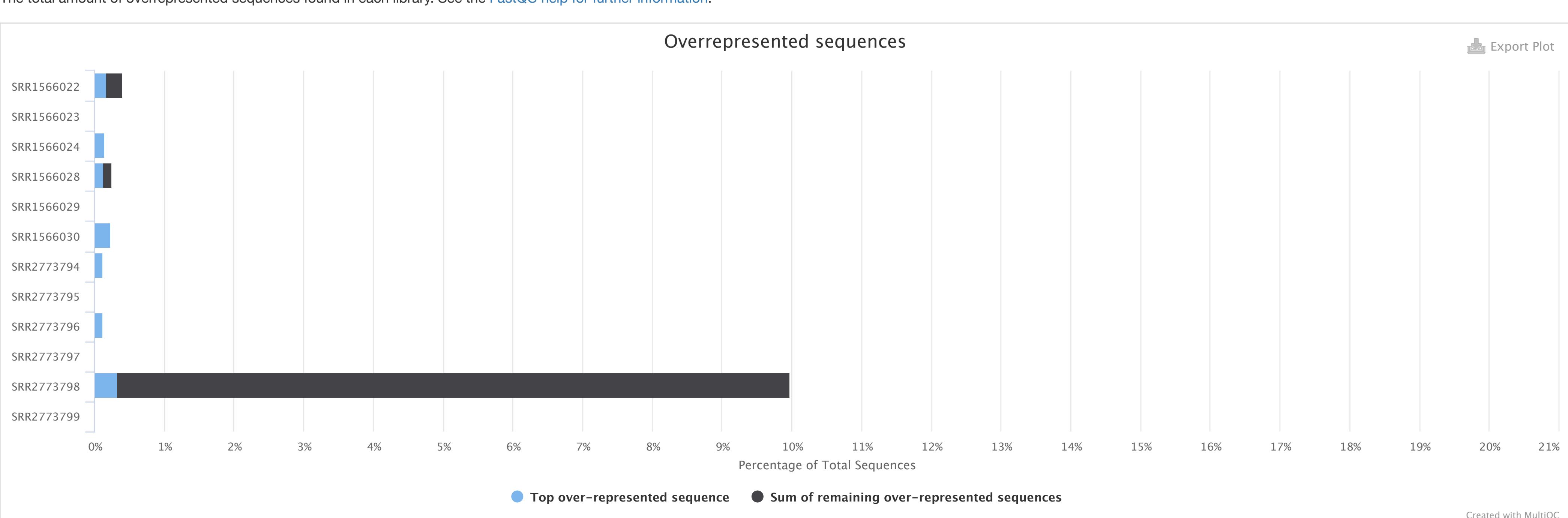
on



### Overrepresented sequences

57

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



### Adapter Content

12

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.

Y-Limits: 

on

