



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

 Loading report..

Report generated on 2025-01-20, 12:57 GMT based on data in: /home/shali/compbio/sratoolkit/test_fastqc_files

General Statistics

 Copy table

 Configure Columns

 Plot

Showing ¹²/₁₂ rows and ³/₆ columns.

Sample Name	% Dups	% GC	M Seqs
SRR827457_1	47.2%	50%	27.6
SRR827457_2	45.1%	50%	27.6
SRR827459_1	44.2%	50%	26.8
SRR827459_2	45.1%	50%	26.8
SRR827461_1	45.0%	50%	27.3
SRR827461_2	45.6%	50%	27.3
SRR827474_1	43.5%	50%	24.5
SRR827474_2	44.9%	50%	24.5
SRR827476_1	44.2%	50%	25.0
SRR827476_2	44.7%	50%	25.0
SRR827478_1	51.3%	50%	29.0
SRR827478_2	48.2%	50%	29.0

FastQC

Version: 0.12.1

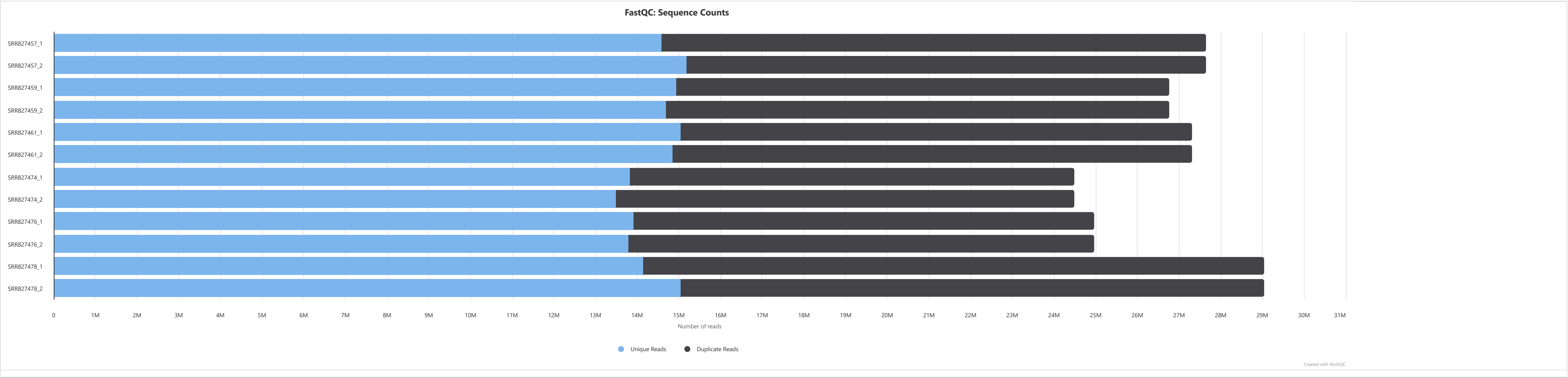
FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

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

Number of reads

Percentages



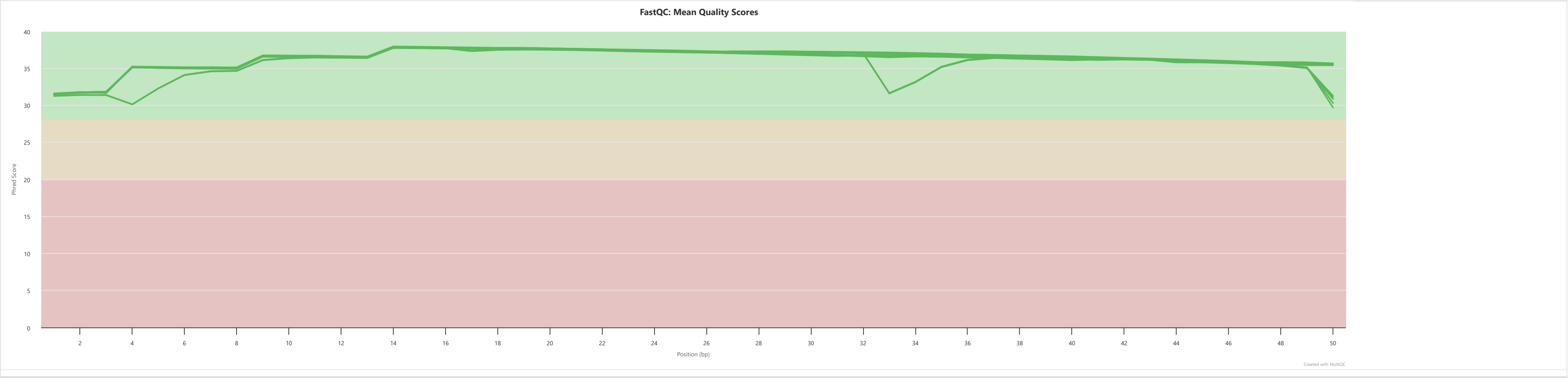
Sequence Quality Histograms

12

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

Y-Limits:

on



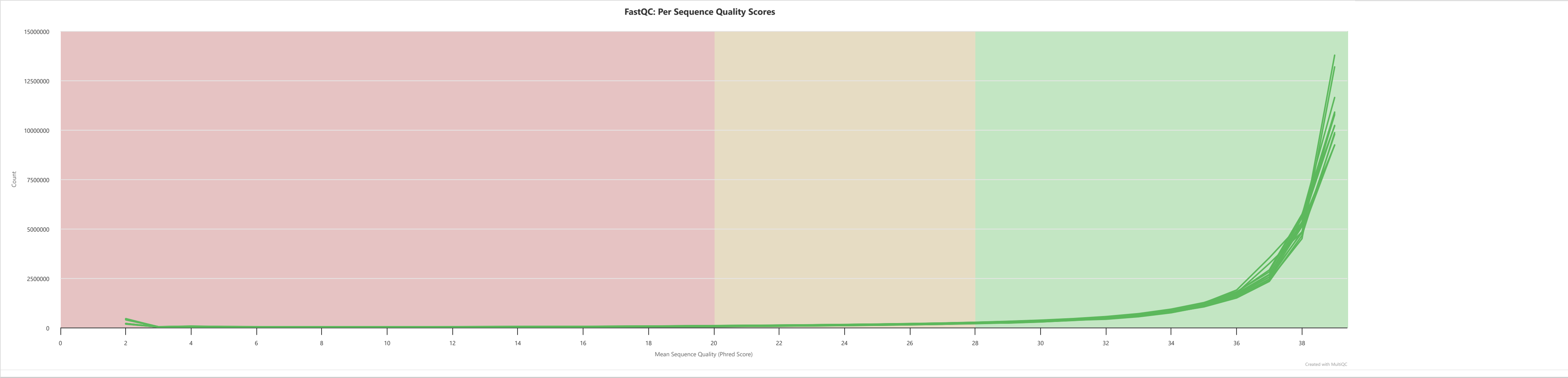
Per Sequence Quality Scores

12

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

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.

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

📘 Rollover for sample name

Position: -

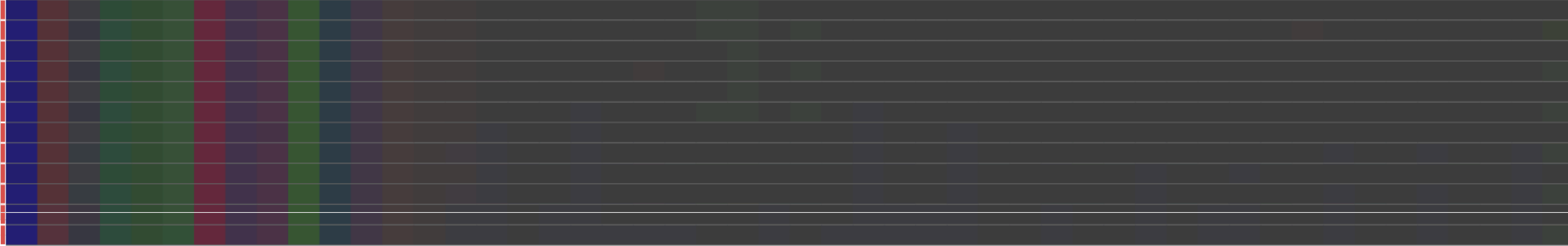
%T: -

%C: -

%A: -

%G: -

📄 Export Plot



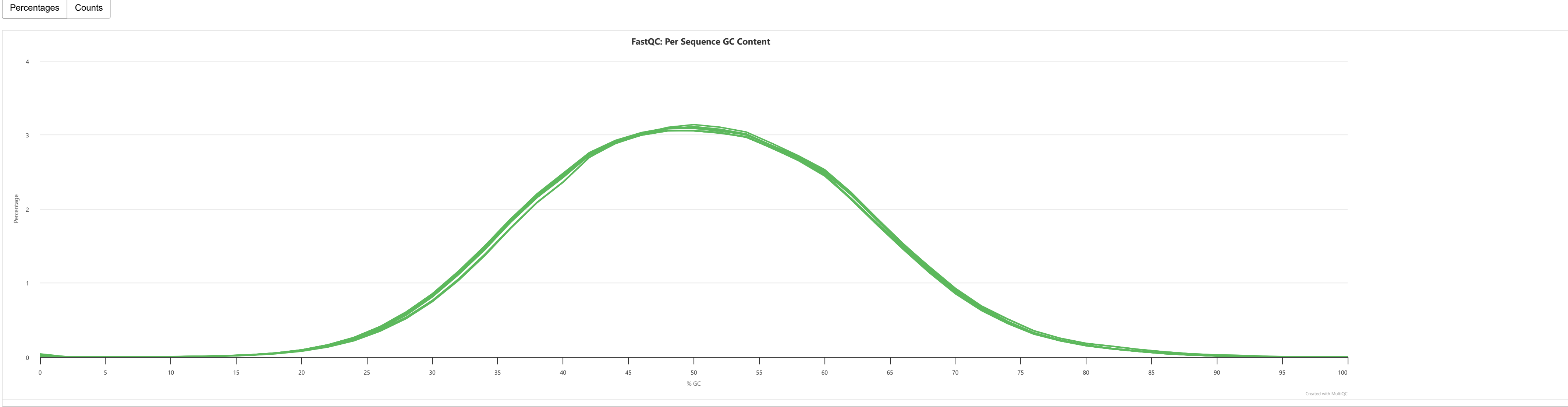
Per Sequence GC Content

12

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

Y-Limits:

on



Per Base N Content

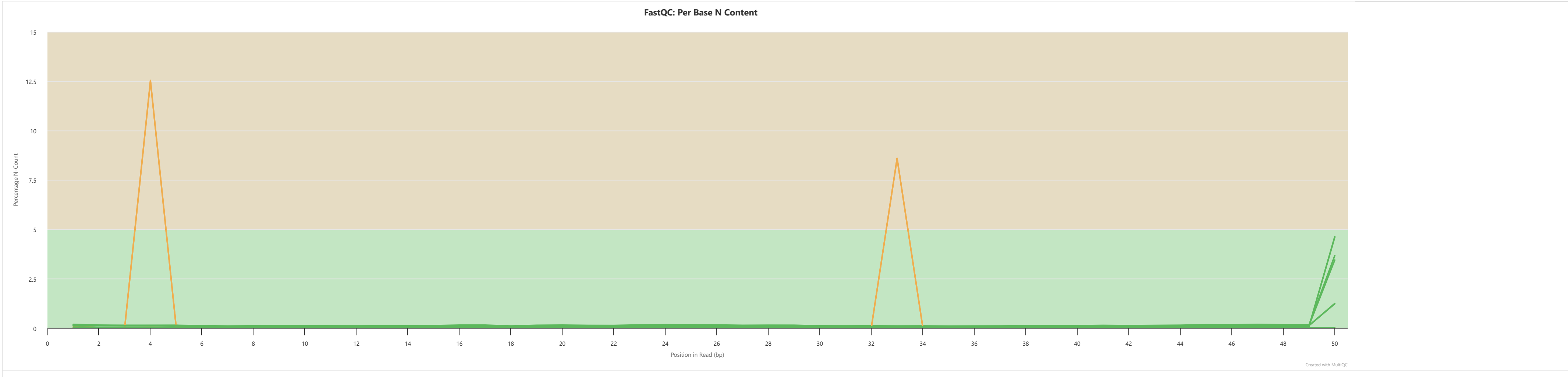
8

4

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

Y-Limits:

on



Sequence Length Distribution

12

All samples have sequences of a single length (50bp).

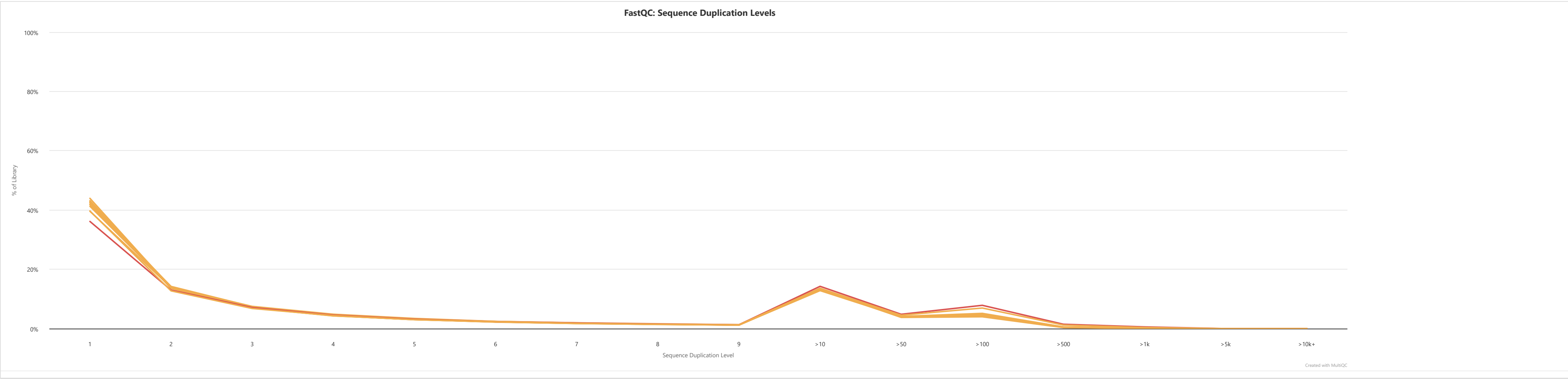
Sequence Duplication Levels

11

The relative level of duplication found for every sequence.

Y-Limits:

on



Overrepresented sequences by sample

12

The total amount of overrepresentation found in each library.

12 samples had less than 1% of reads made up of overrepresented sequences

Top overrepresented sequences

Top overrepresented sequences across all samples. The table shows 20 most overrepresented sequences across all samples, ranked by the number of samples they occur in.

📄 Copy table

Showing 0/0 rows.

Overrepresented sequence

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

Min:	0
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Max:

1

Software Versions

Software Versions lists versions of software tools extracted from file contents.

 Copy table

Software	Version
FastQC	0.12.1

