

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

Report generated on 2020-04-20, 16:34 based on data in: /Users/u6567349/Desktop/ChIP-Seq01(Jan2020)/Data -- April 2020

🔍 Welcome! Not sure where to start?

Watch a tutorial video (6:06)

General Statistics

📄 Copy table

⚙️ Configure Columns

📊 Plot

Showing 54/54 rows and 3/5 columns.

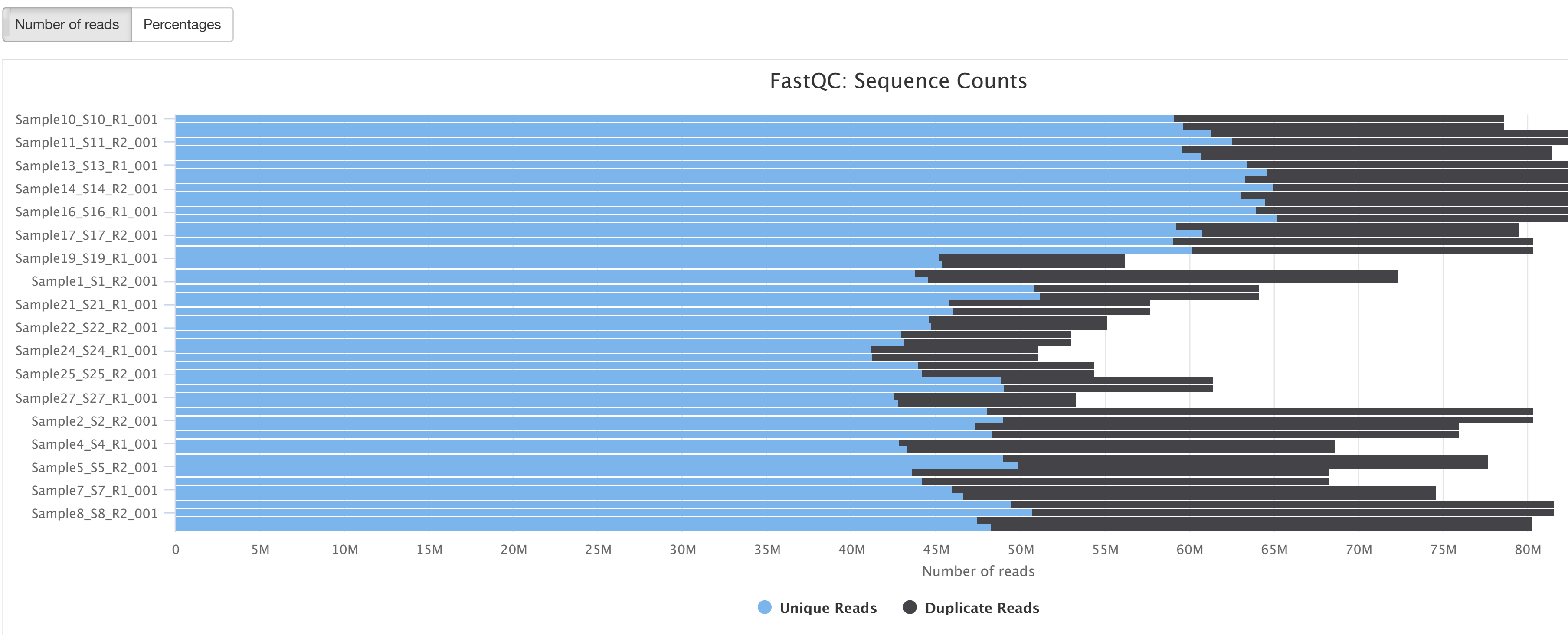
Sample Name	% Dups	% GC	M Seqs
Sample10_S10_R1_001	24.8%	42%	78.6
Sample10_S10_R2_001	24.1%	42%	78.6
Sample11_S11_R1_001	26.5%	41%	83.4
Sample11_S11_R2_001	25.0%	41%	83.4
Sample12_S12_R1_001	26.8%	40%	81.5
Sample12_S12_R2_001	25.5%	40%	81.5
Sample13_S13_R1_001	24.4%	43%	84.0
Sample13_S13_R2_001	23.0%	43%	84.0
Sample14_S14_R1_001	26.4%	43%	86.0
Sample14_S14_R2_001	24.4%	43%	86.0
Sample15_S15_R1_001	25.6%	42%	84.8
Sample15_S15_R2_001	23.9%	42%	84.8
Sample16_S16_R1_001	27.2%	43%	87.9
Sample16_S16_R2_001	25.8%	43%	87.9
Sample17_S17_R1_001	25.4%	43%	79.5

FastQC

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

Sequence Counts

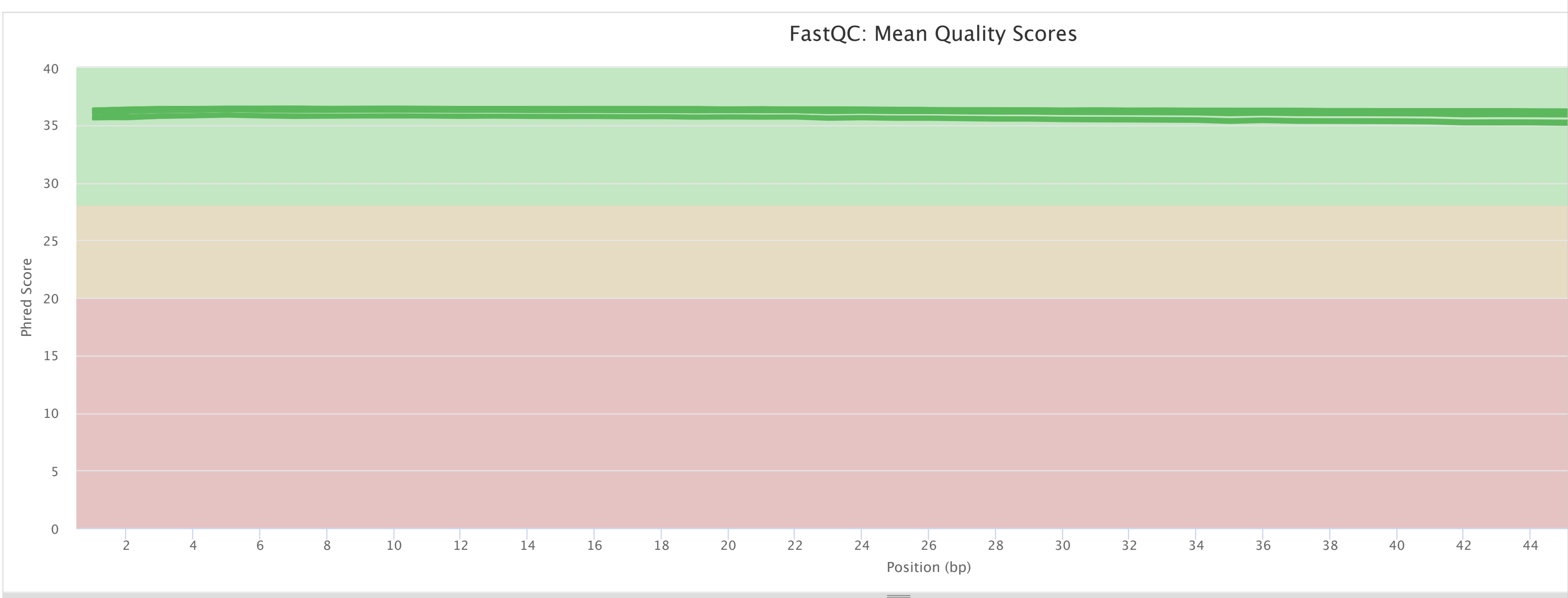
Sequence counts for each sample. Duplicate read counts are an estimate only.



Sequence Quality Histograms

54

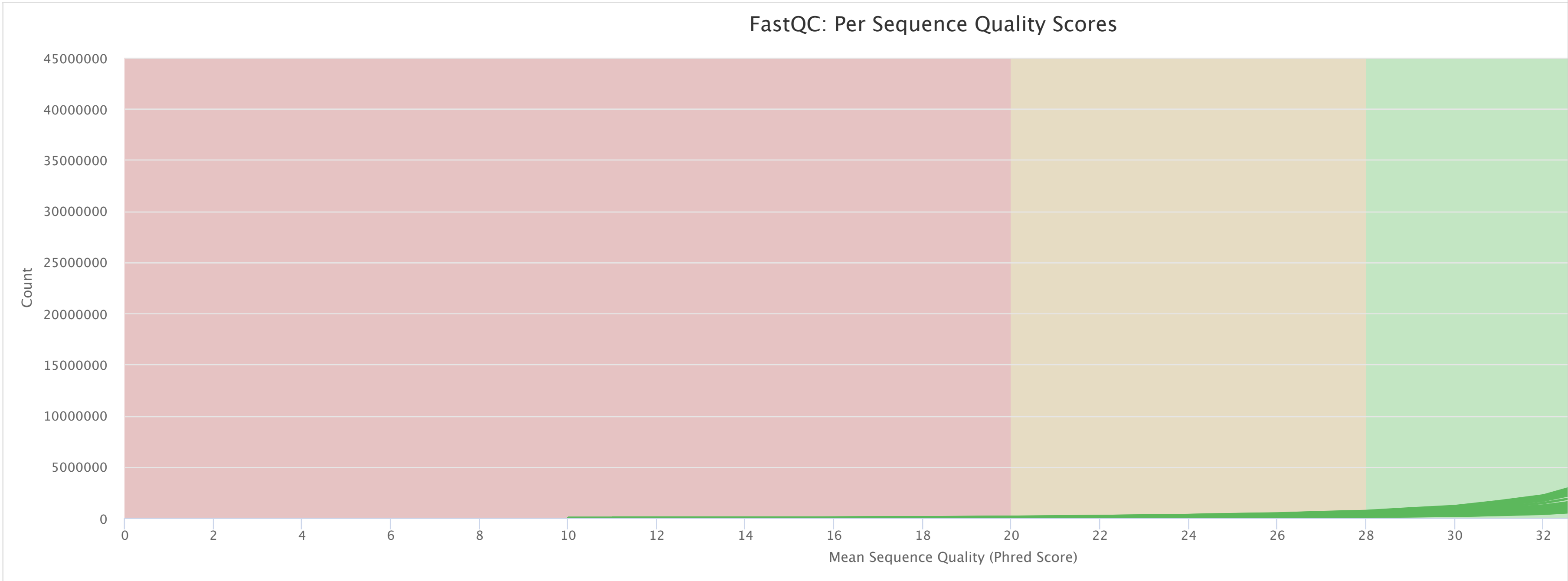
The mean quality value across each base position in the read.



Per Sequence Quality Scores

54

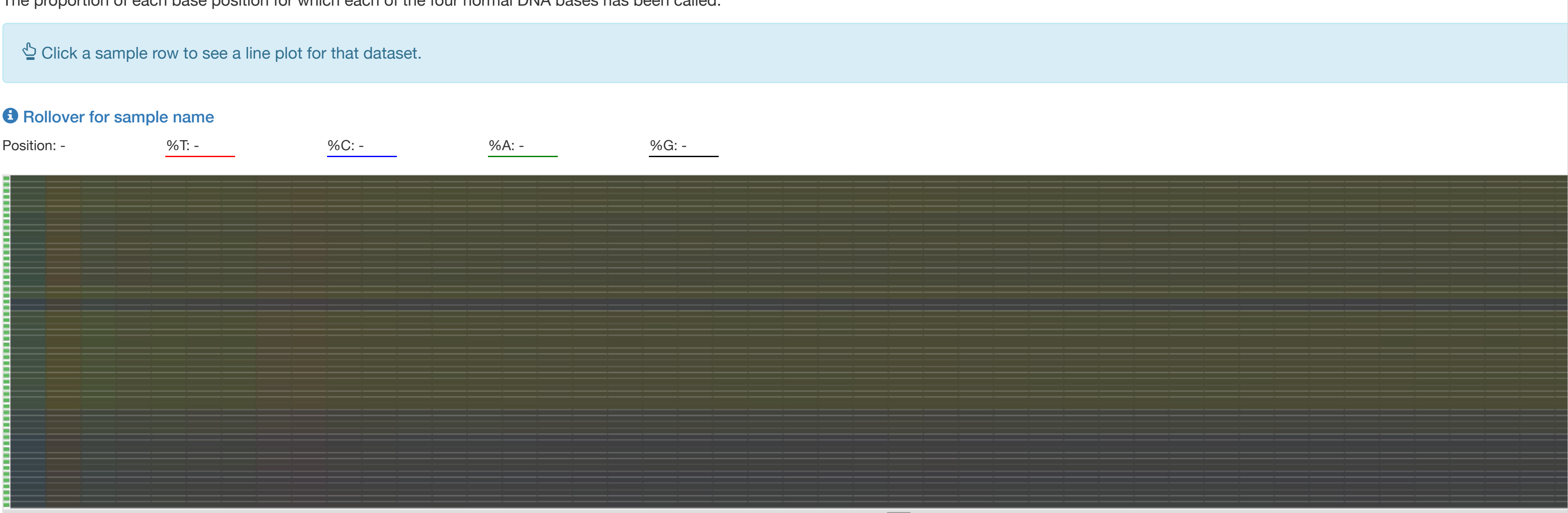
The number of reads with average quality scores. Shows if a subset of reads has poor quality.



Per Base Sequence Content

54

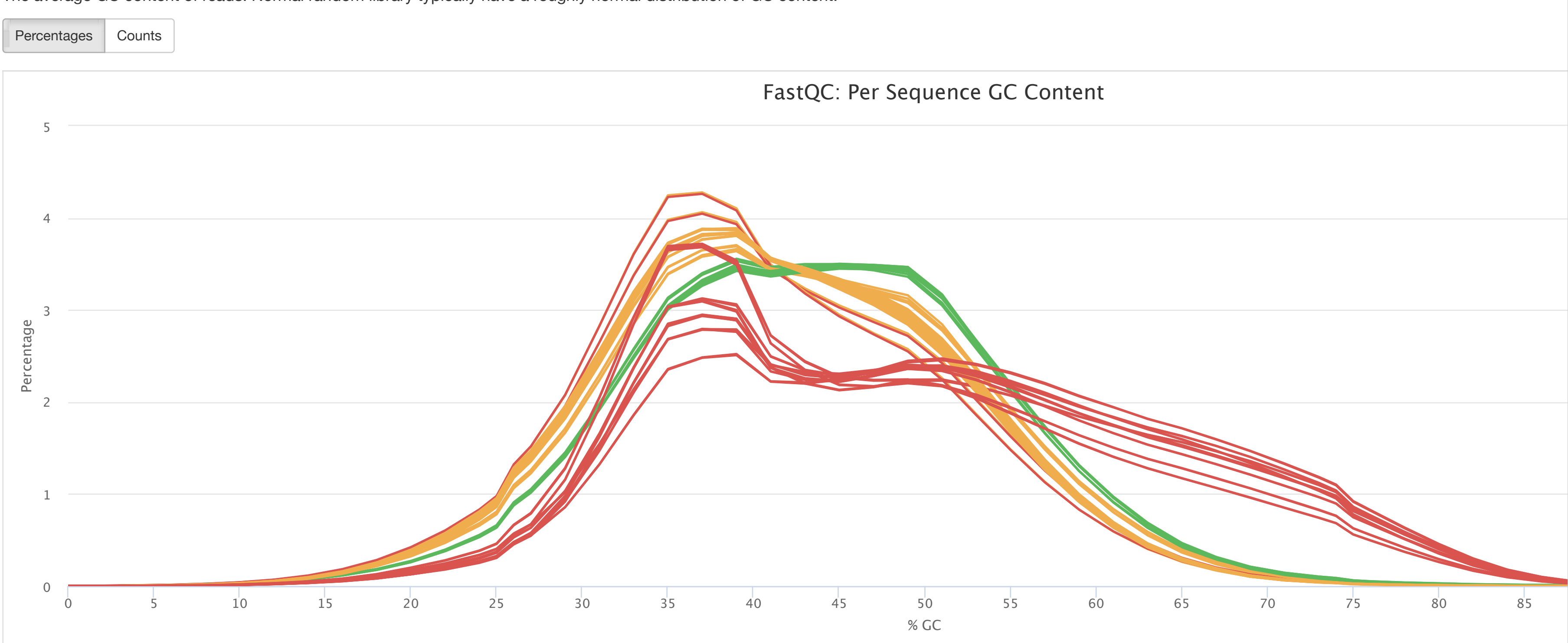
The proportion of each base position for which each of the four normal DNA bases has been called.



Per Sequence GC Content

102420

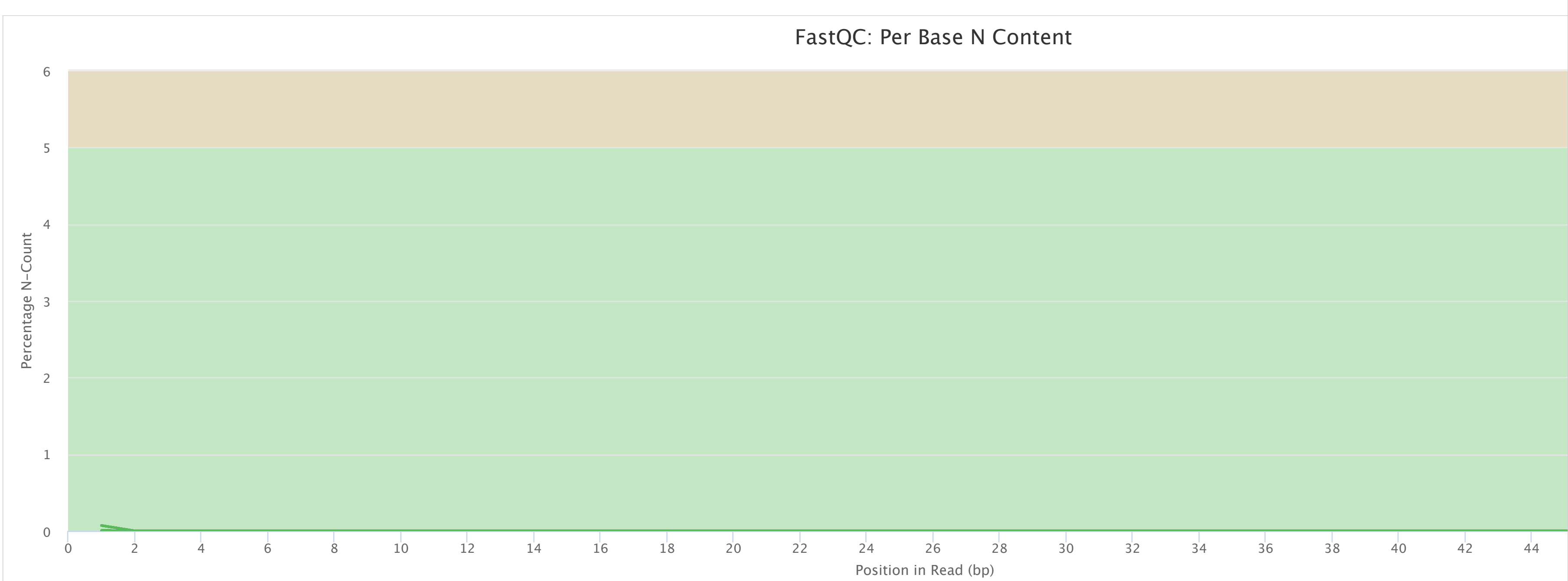
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.



Per Base N Content

54

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



Sequence Length Distribution

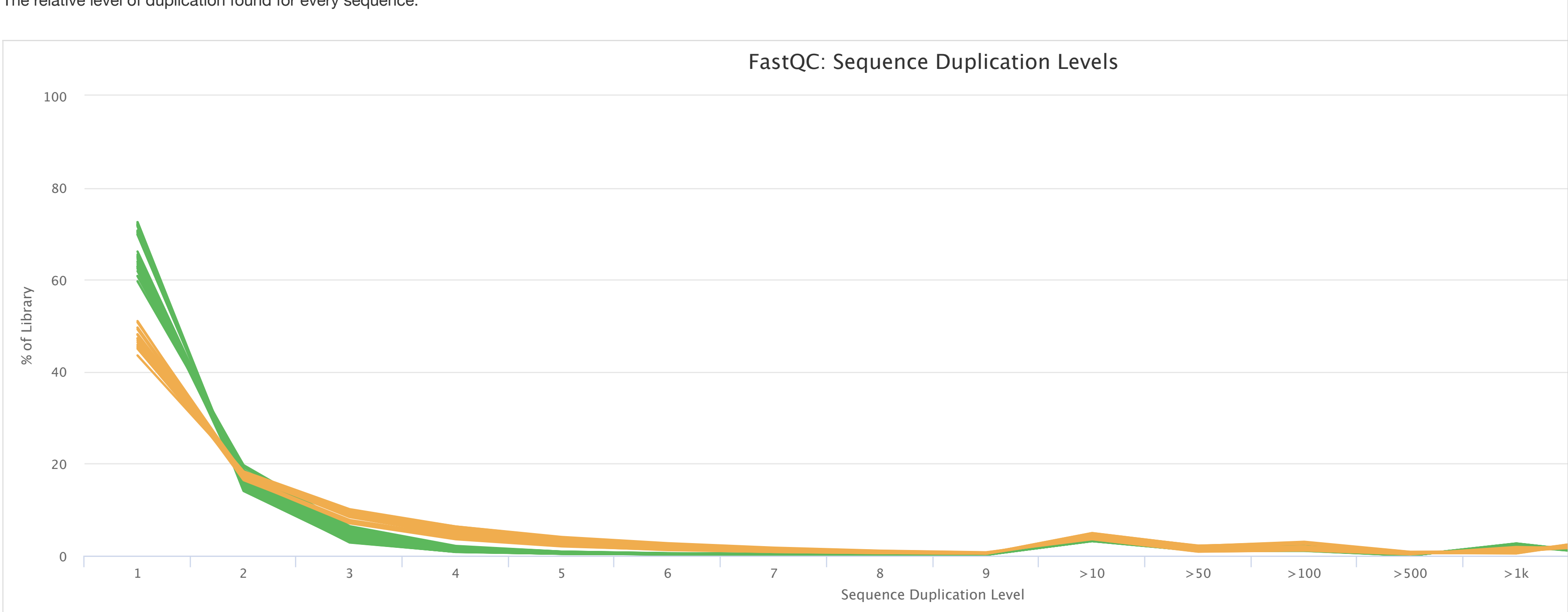
54

All samples have sequences of a single length (51bp).

Sequence Duplication Levels

3616

The relative level of duplication found for every sequence.



Overrepresented sequences

477

The total amount of overrepresented sequences found in each library.

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

Adapter Content

54

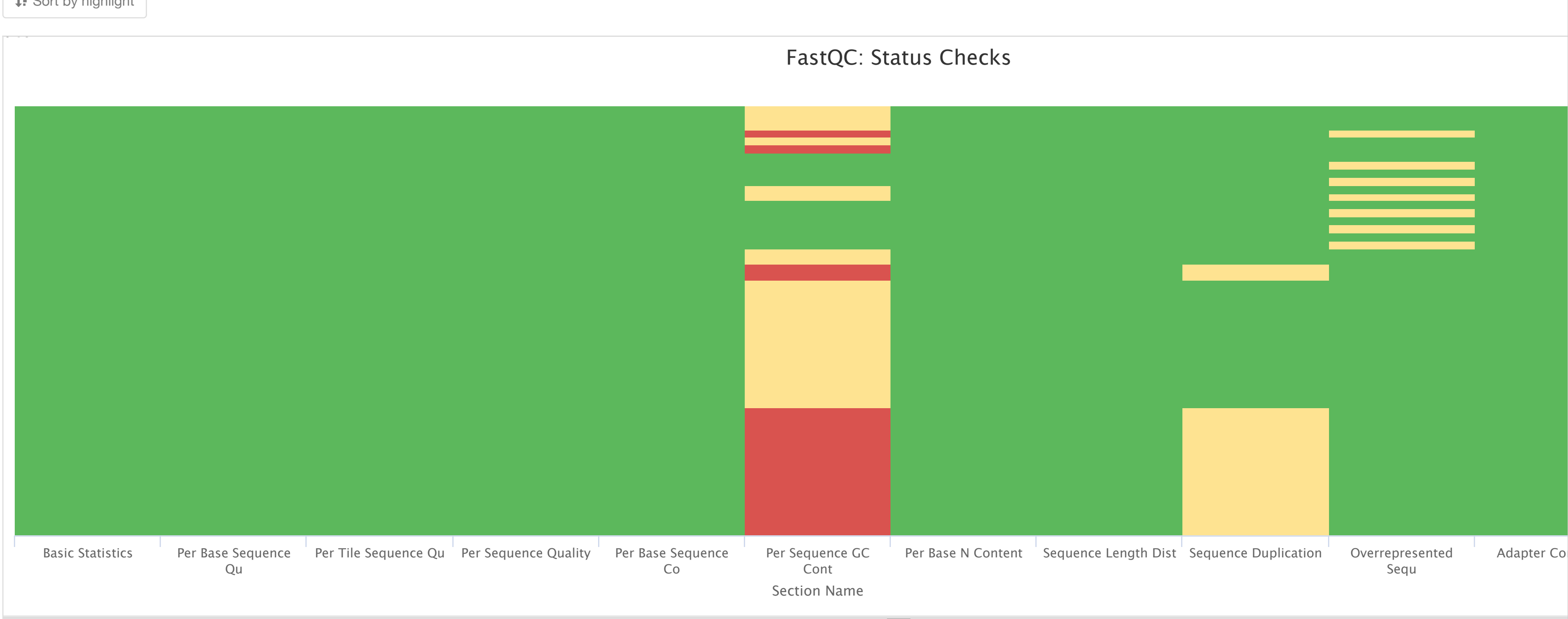
The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

Status Checks

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

⌵ Sort by highlight



Export Plots

Images

Data

1200 px

800 px

px

Aspect ratio

PNG

Plot scaling

2

X

Choose Plots

👁 All

🚫 None

- ☒ fastqc_sequence_counts_plot
- ☒ fastqc_per_base_sequence_quality_plot
- ☒ fastqc_per_sequence_quality_scores_plot
- ☒ fastqc_per_base_sequence_content_plot
- ☒ fastqc_per_sequence_gc_content_plot
- ☒ fastqc_per_base_n_content_plot
- ☒ fastqc_sequence_duplication_levels_plot
- ☒ fastqc_status-check-heatmap
- ☒ tableScatterPlot

Download Plot Images

If you use plots from MultiQC in a publication or presentation, please cite:

MultiQC: Summarize analysis results for multiple tools and samples in a single report
Phil Ewels, Måns Magnusson, Saverio Lundin and Max Käller
Bioinformatics 32(18)
doi:10.1093/bioinformatics/btw354
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