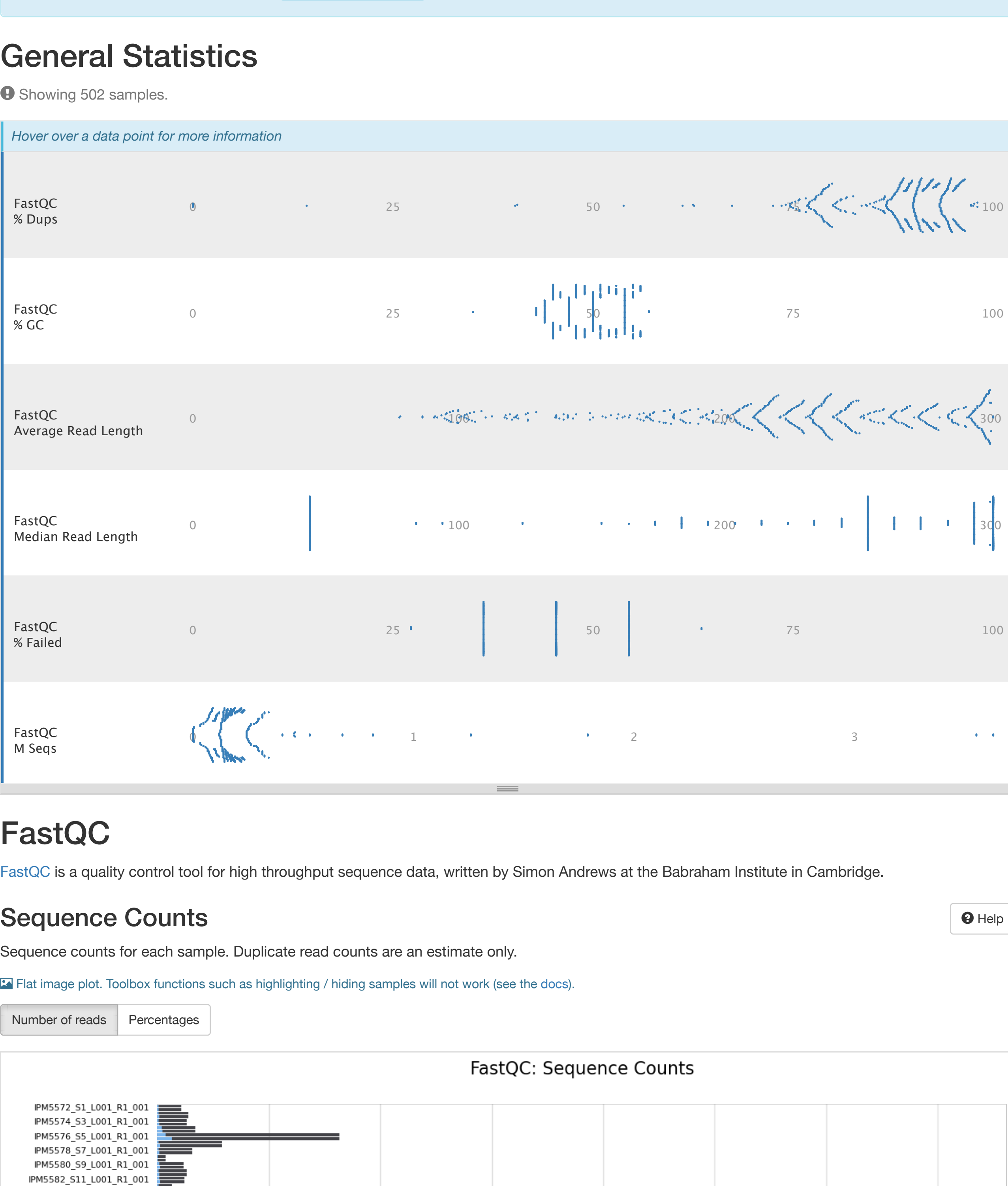


A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2023-06-14, 09:48 UTC based on data in: /mnt/volume_sgp1_01/tung/fastqc



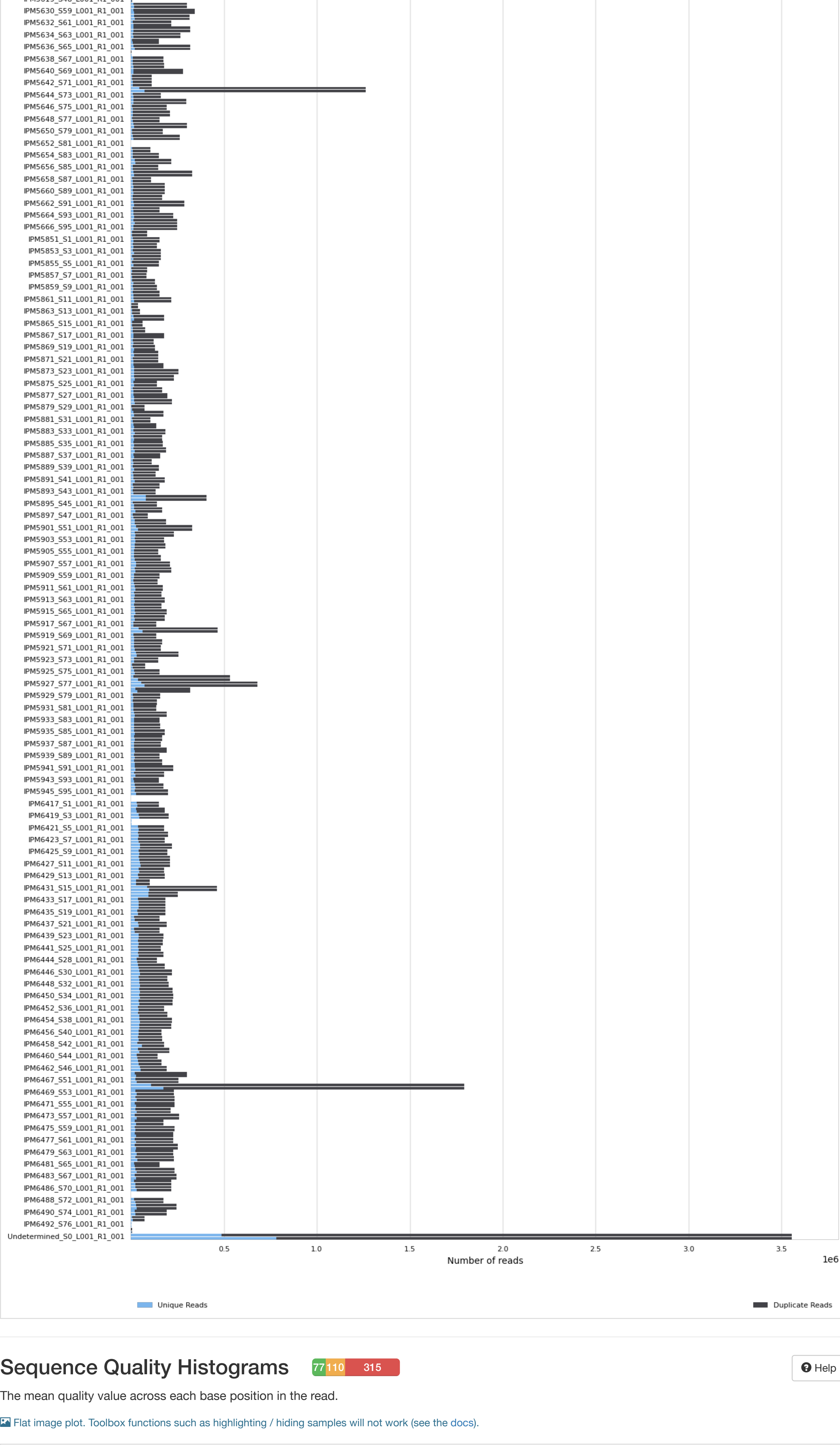
FastQC

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.

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

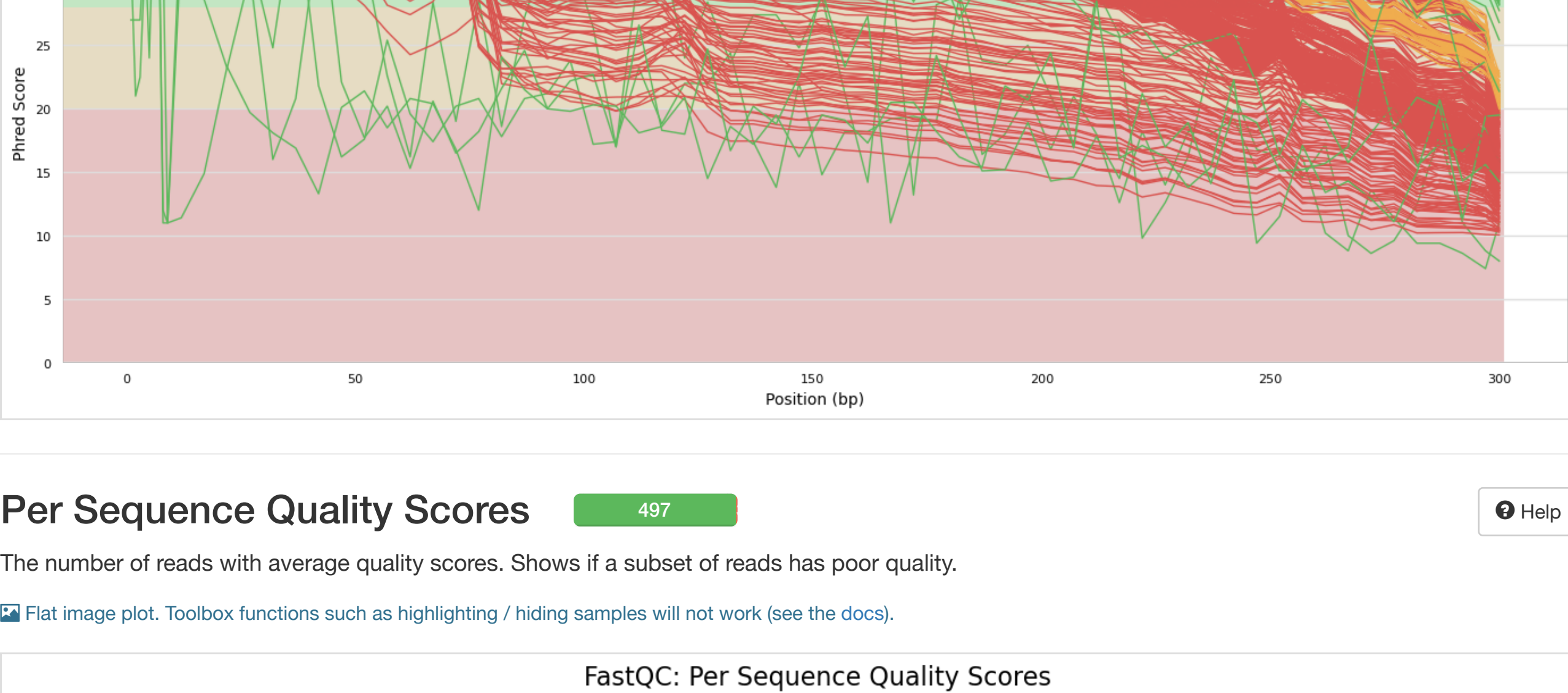


Sequence Quality Histograms

77 110 315

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

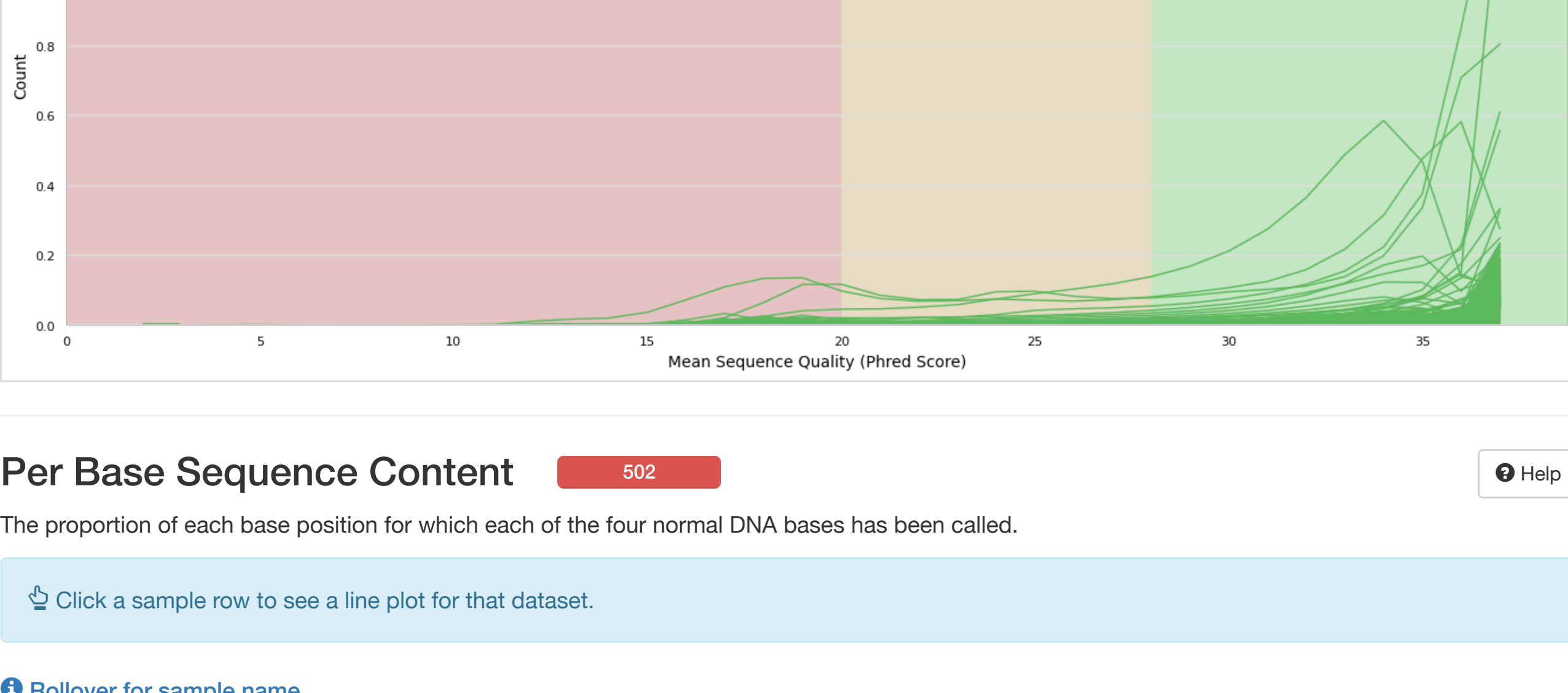


Per Sequence Quality Scores

497

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

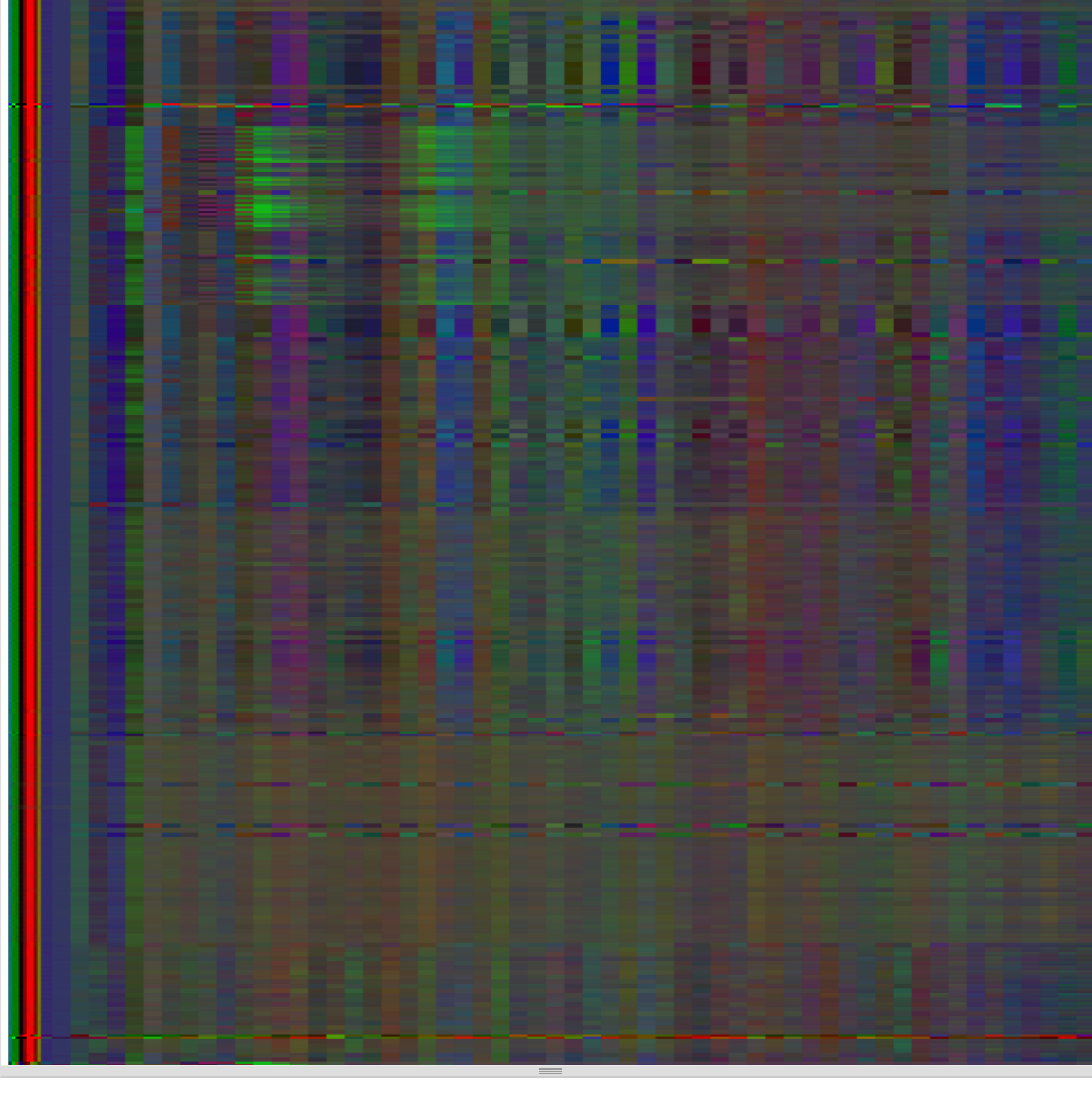


Per Base Sequence Content

502

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.](#)

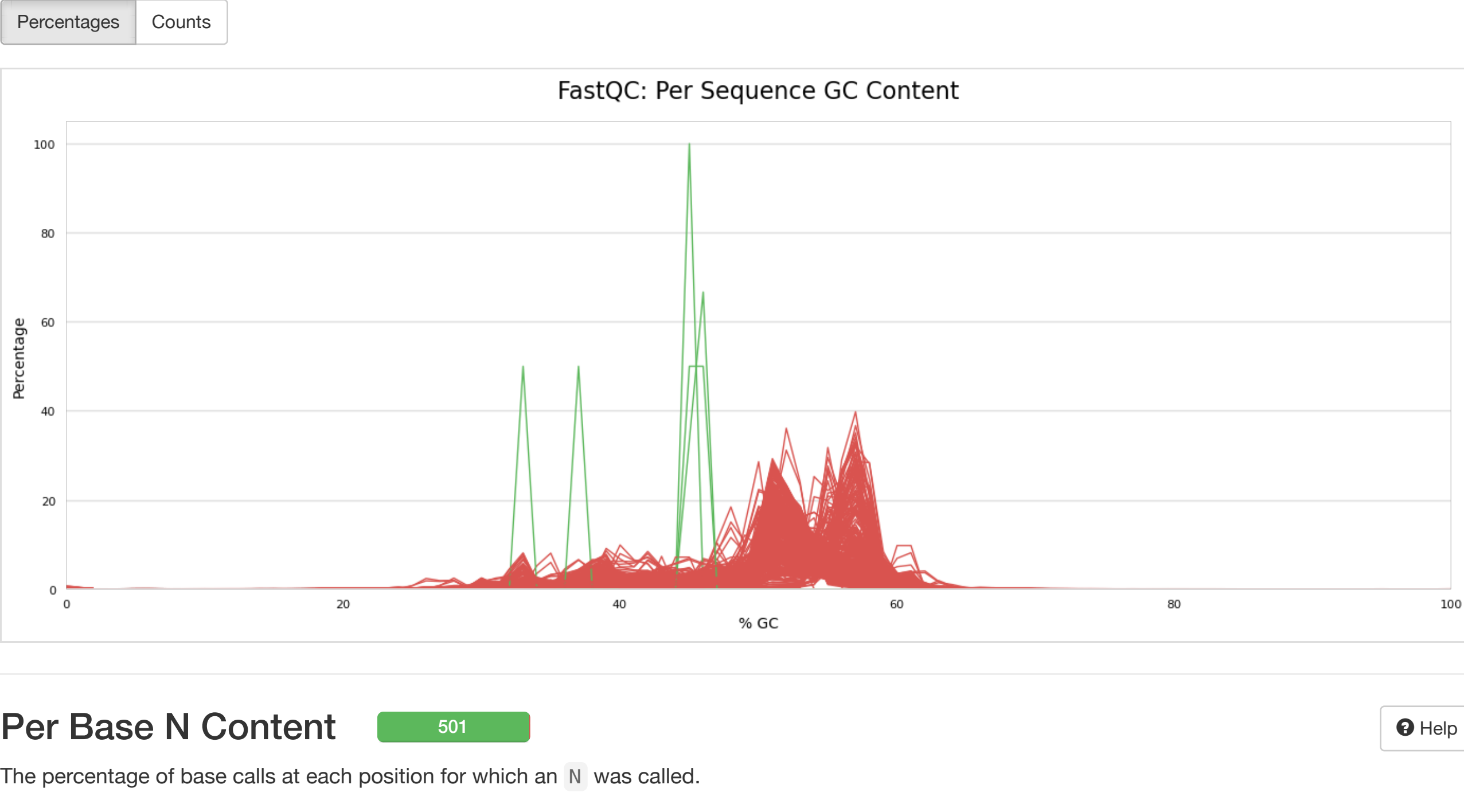


Per Sequence GC Content

498

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

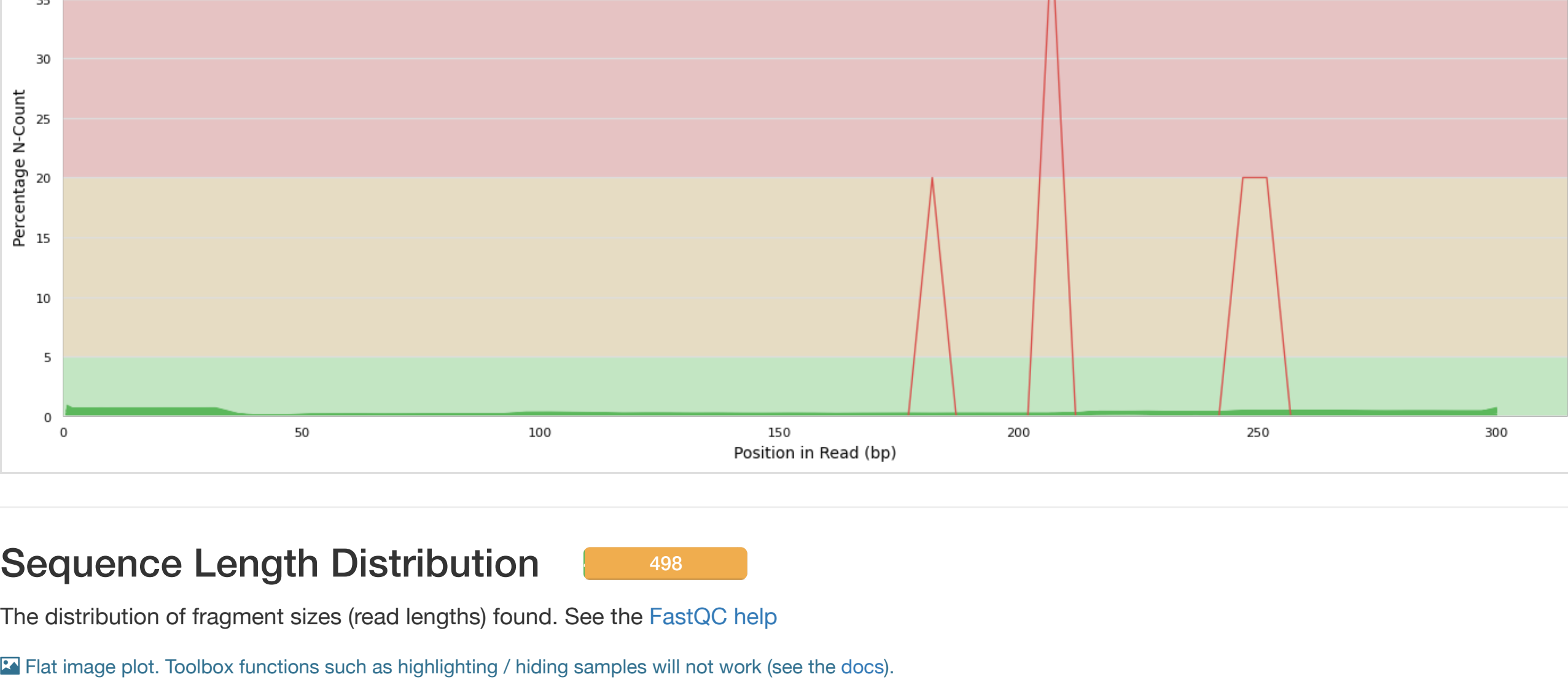


Per Base N Content

501

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

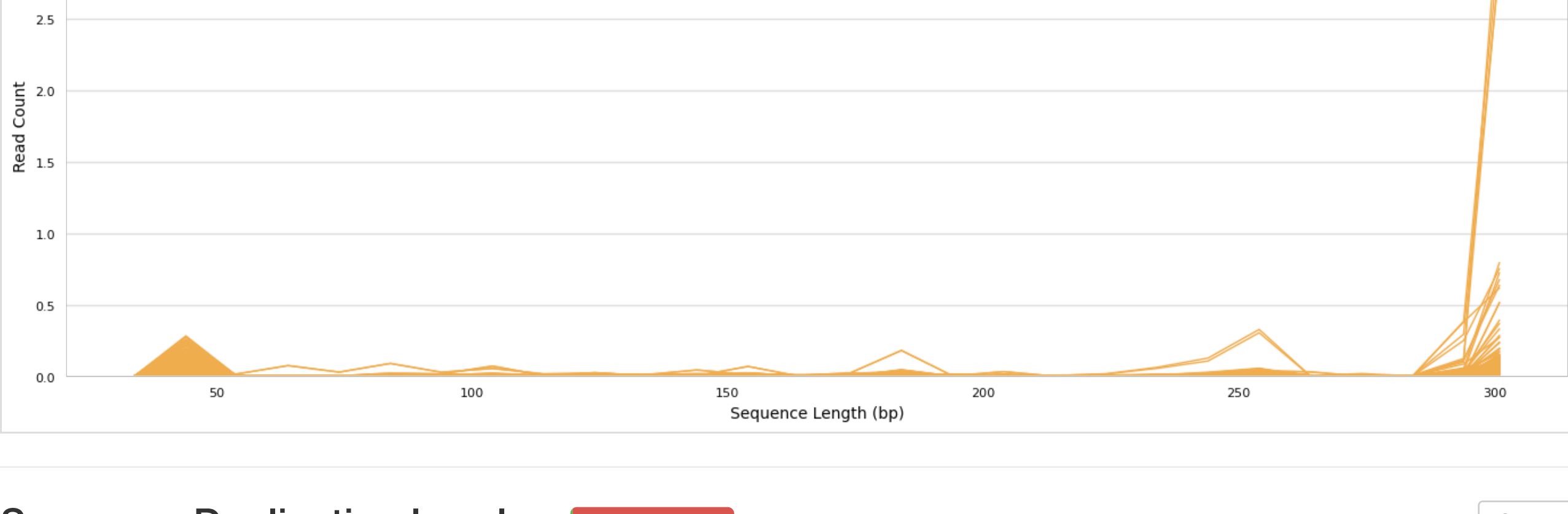


Sequence Length Distribution

498

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

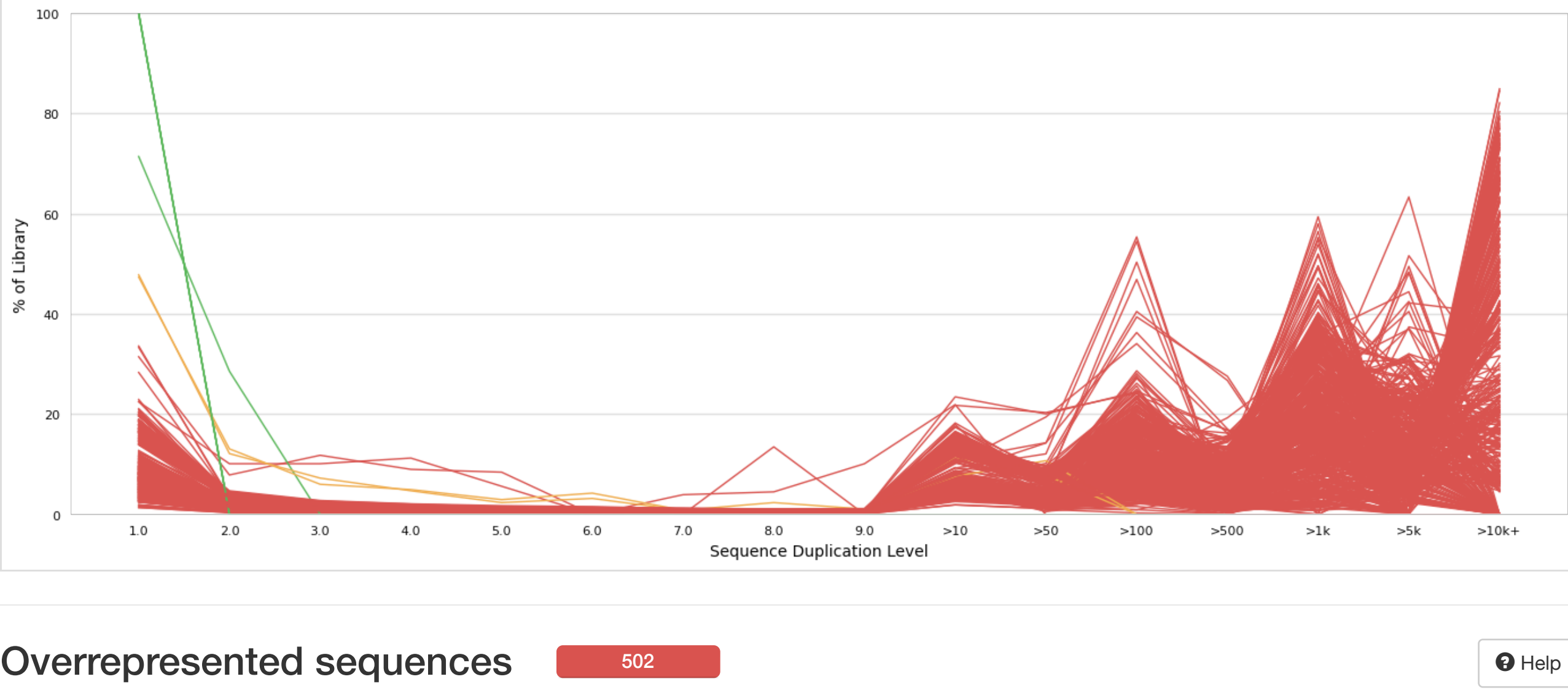


Sequence Duplication Levels

494

The relative level of duplication found for every sequence.

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

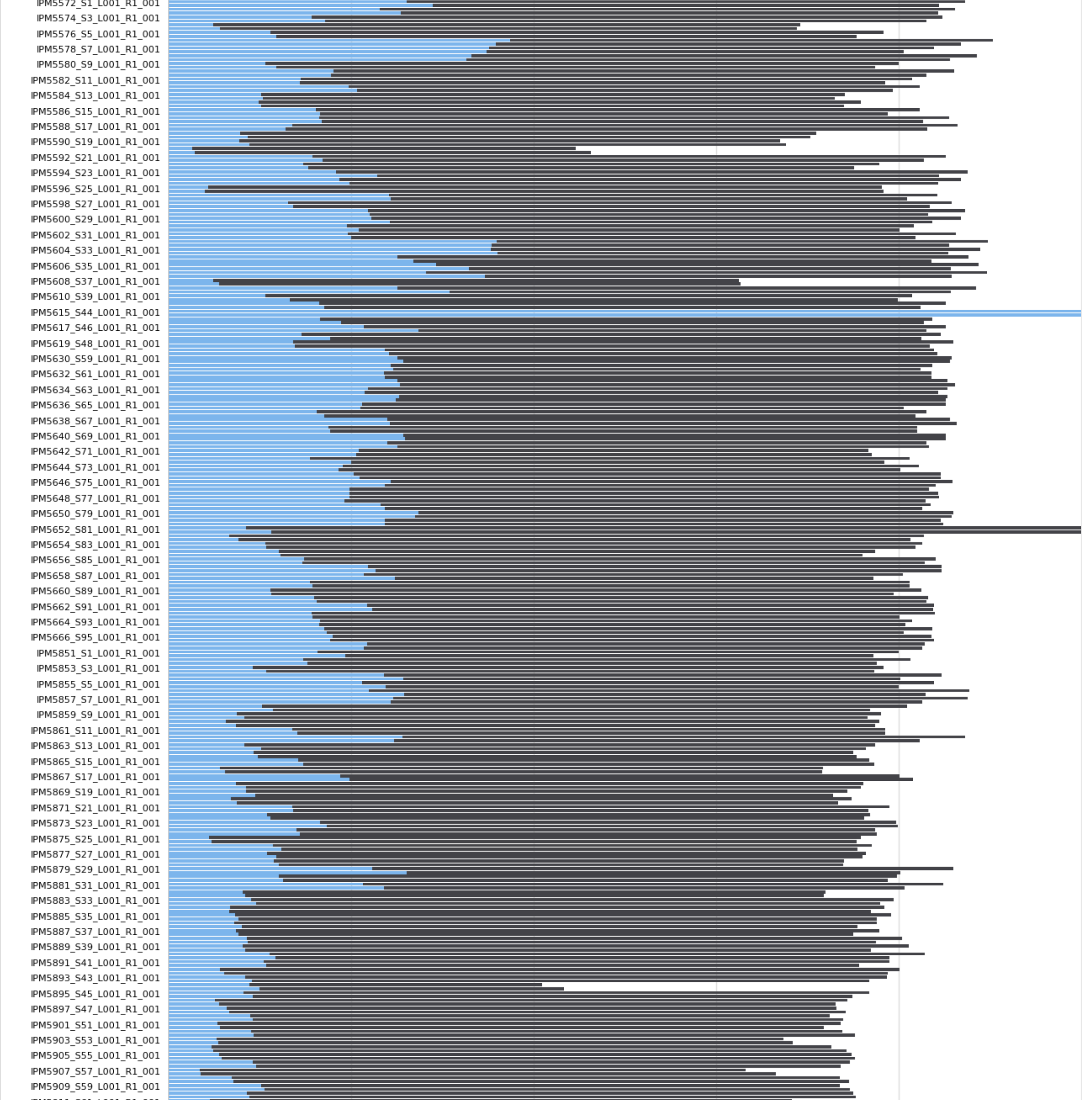


Overrepresented sequences

502

The total amount of overrepresented sequences found in each library.

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).



Adapter Content

441

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

☒ Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).



Status Checks

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

