

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

Report generated on 2025-11-14, 22:47 CST based on data in: /Users/justin/GTMbioinfo/docs

+ Summarize report

• Welcome! Not sure where to start? Watch a tutorial video (6:06)

don't show again

## General Statistics

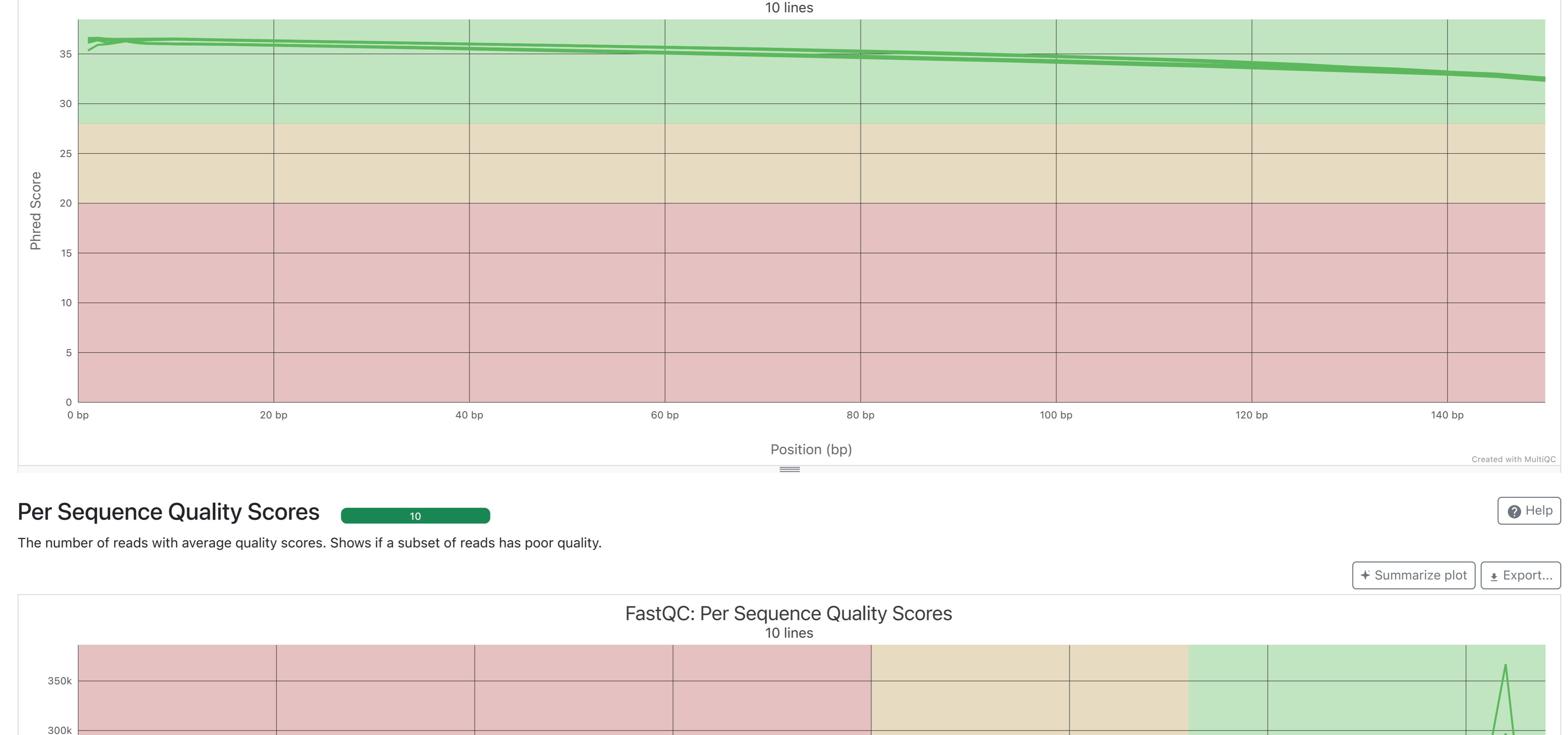
Sample Name	Dups	GC	Seqs
SRR21014913_1	31.9 %	24.0 %	0.4 M
SRR21014913_2	28.0 %	25.0 %	0.4 M
SRR21014914_1	30.9 %	25.0 %	0.5 M
SRR21014914_2	27.3 %	26.0 %	0.5 M
SRR21015008_1	29.9 %	23.0 %	0.7 M
SRR21015008_2	26.0 %	26.0 %	0.7 M
SRR21015019_1	29.8 %	24.0 %	0.6 M
SRR21015019_2	26.0 %	26.0 %	0.6 M
SRR21015062_1	28.0 %	24.0 %	0.5 M
SRR21015062_2	24.9 %	26.0 %	0.5 M

## FastQC Version: 0.12.1

Quality control tool for high throughput sequencing data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>

### Sequence Counts

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



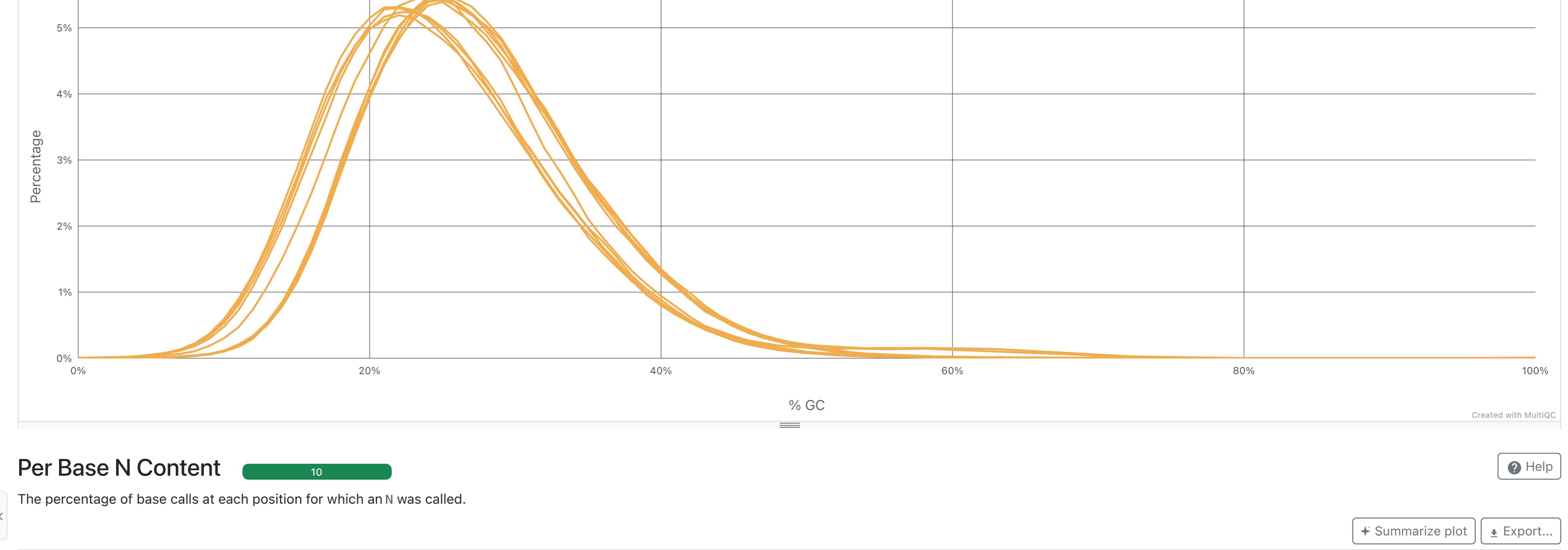
### Sequence Quality Histograms

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



### Per Sequence Quality Scores

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



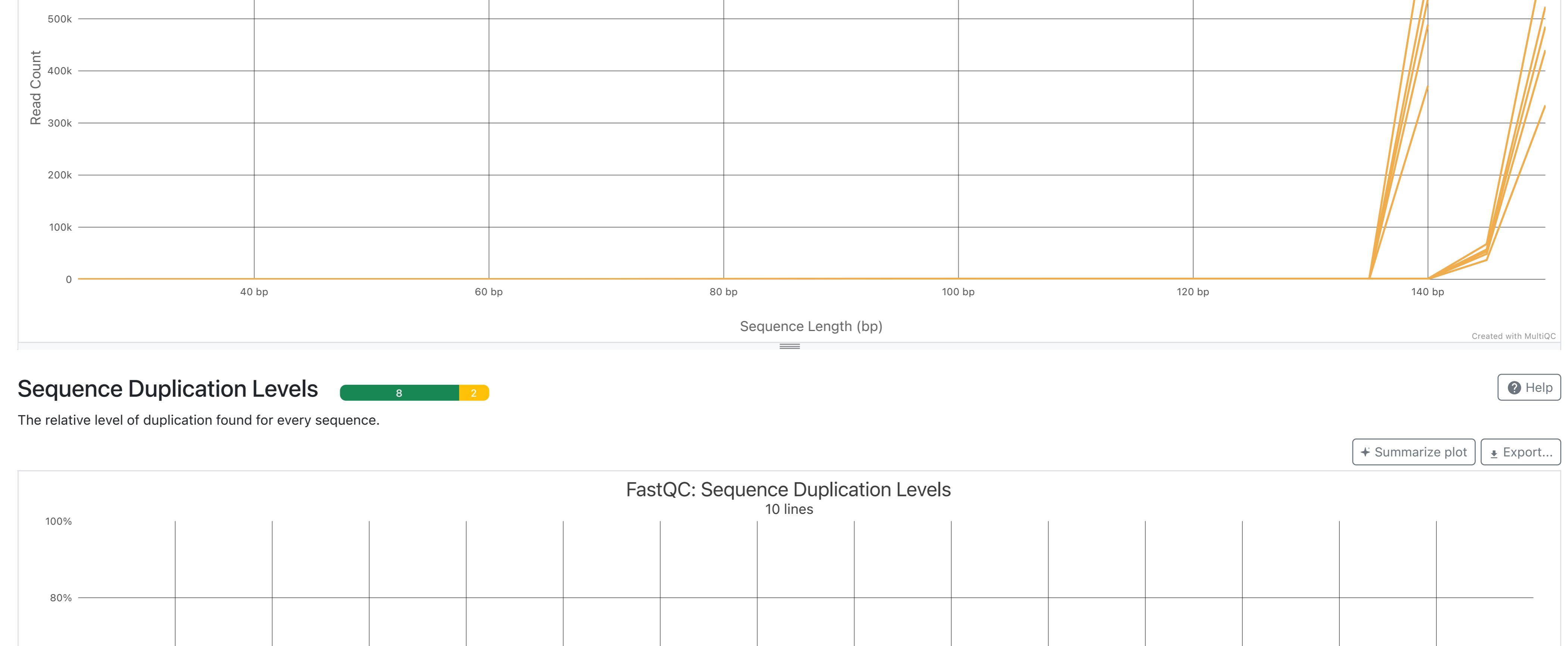
### Per Base Sequence Content

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



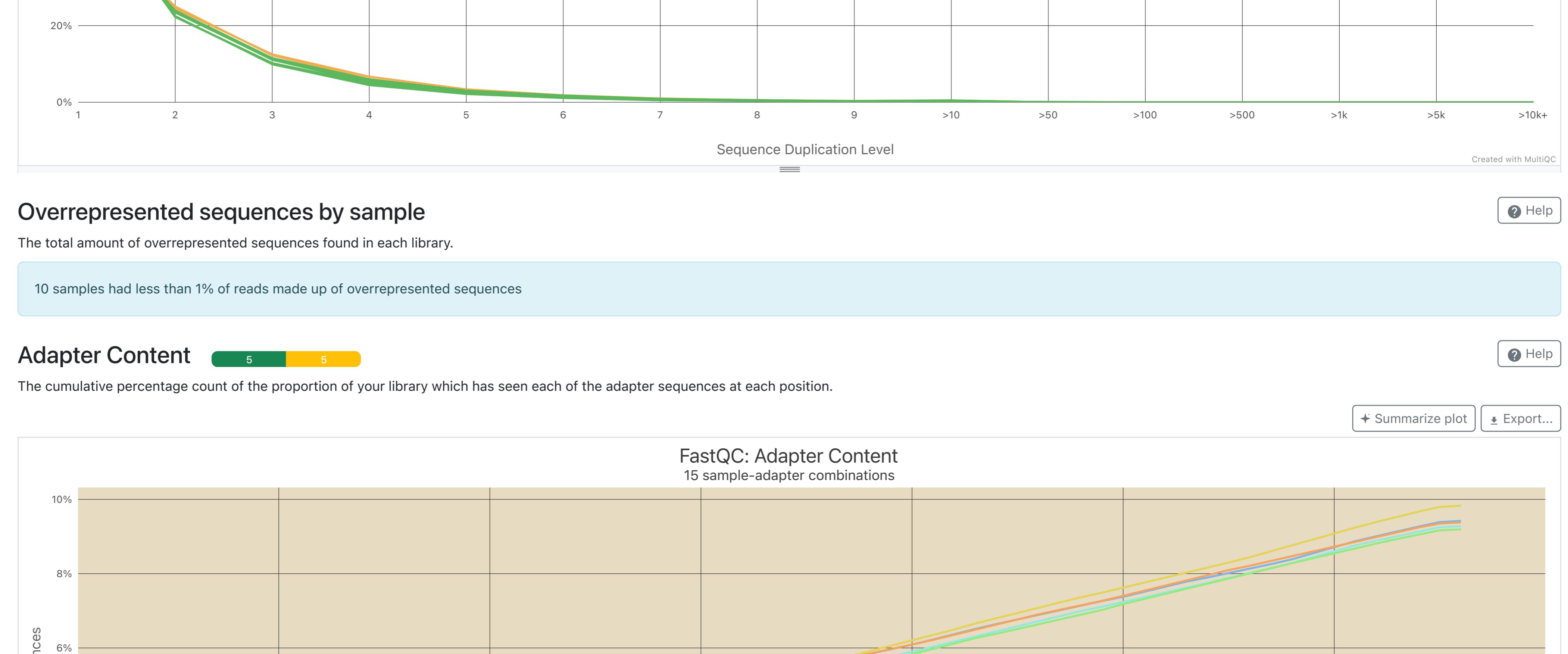
### Per Sequence GC Content

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



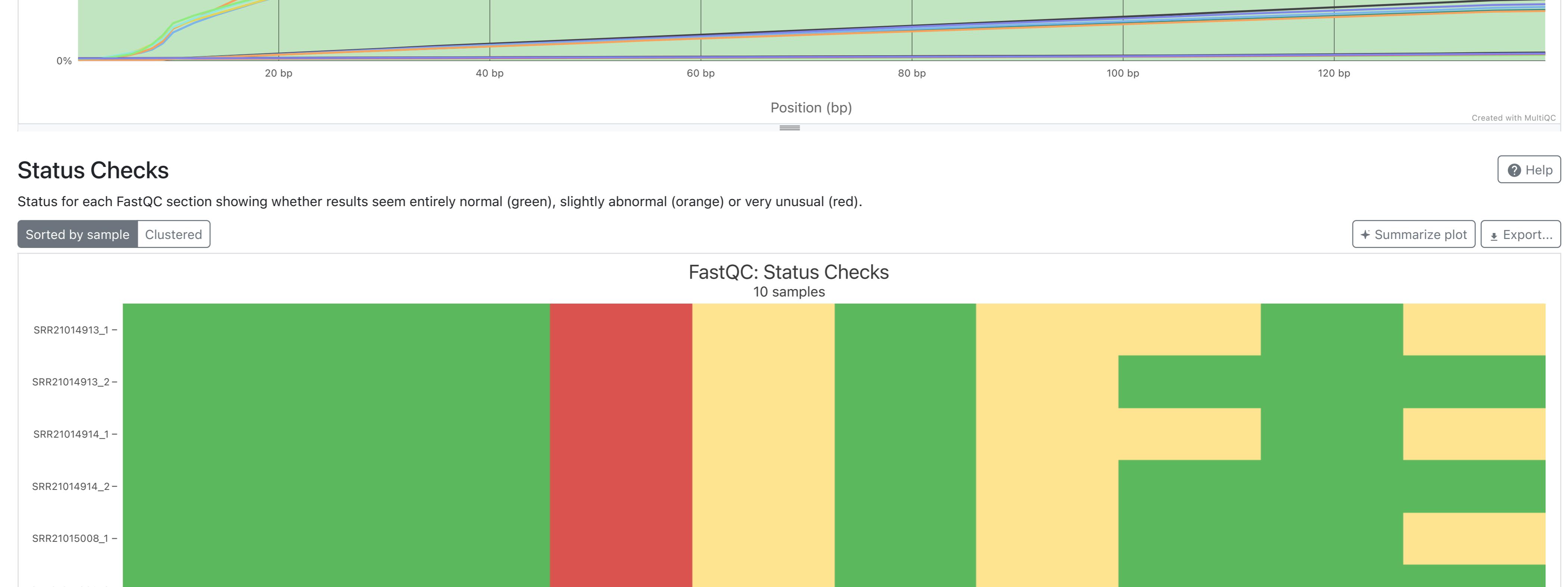
### Per Base N Content

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



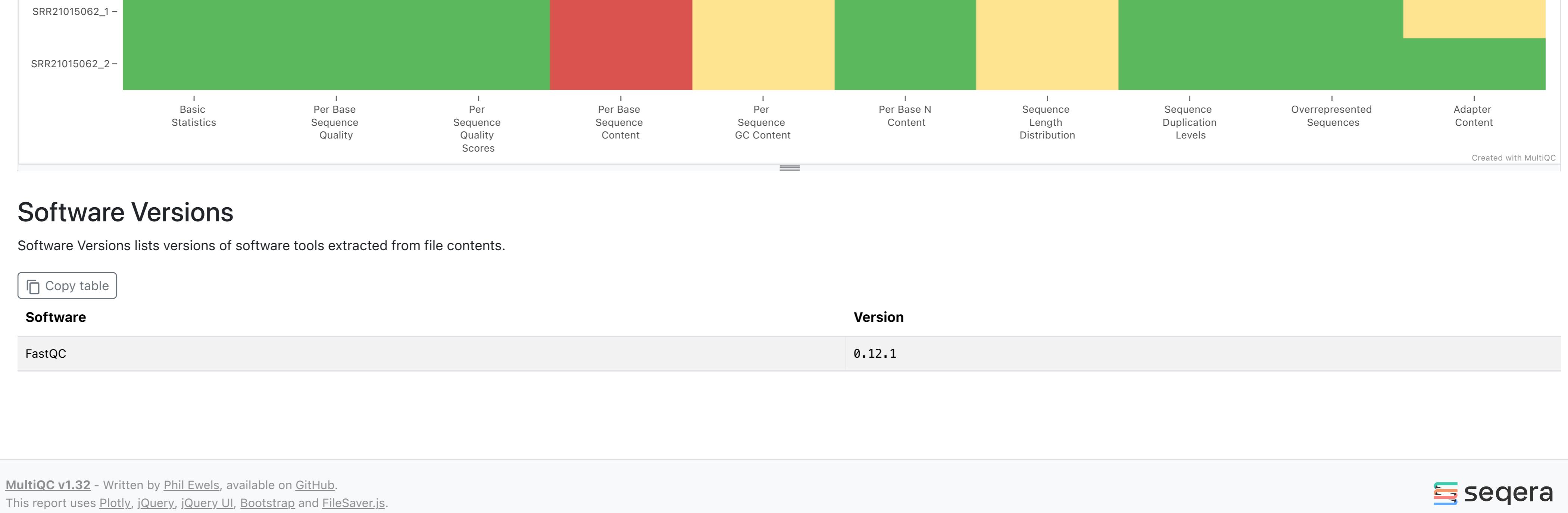
### Sequence Length Distribution

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



### Sequence Duplication Levels

The relative level of duplication found for every sequence.



### Overrepresented sequences by sample

The total amount of overrepresented sequences found in each library.



### Software Versions

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

Software	Version
FastQC	0.12.1