

General Statistics

Copy table

Configure columns

Scatter plot

Violin plot

Export as CSV...

Showing 12/12 rows and 3/6 columns.

Copy Prompt

Summarize table

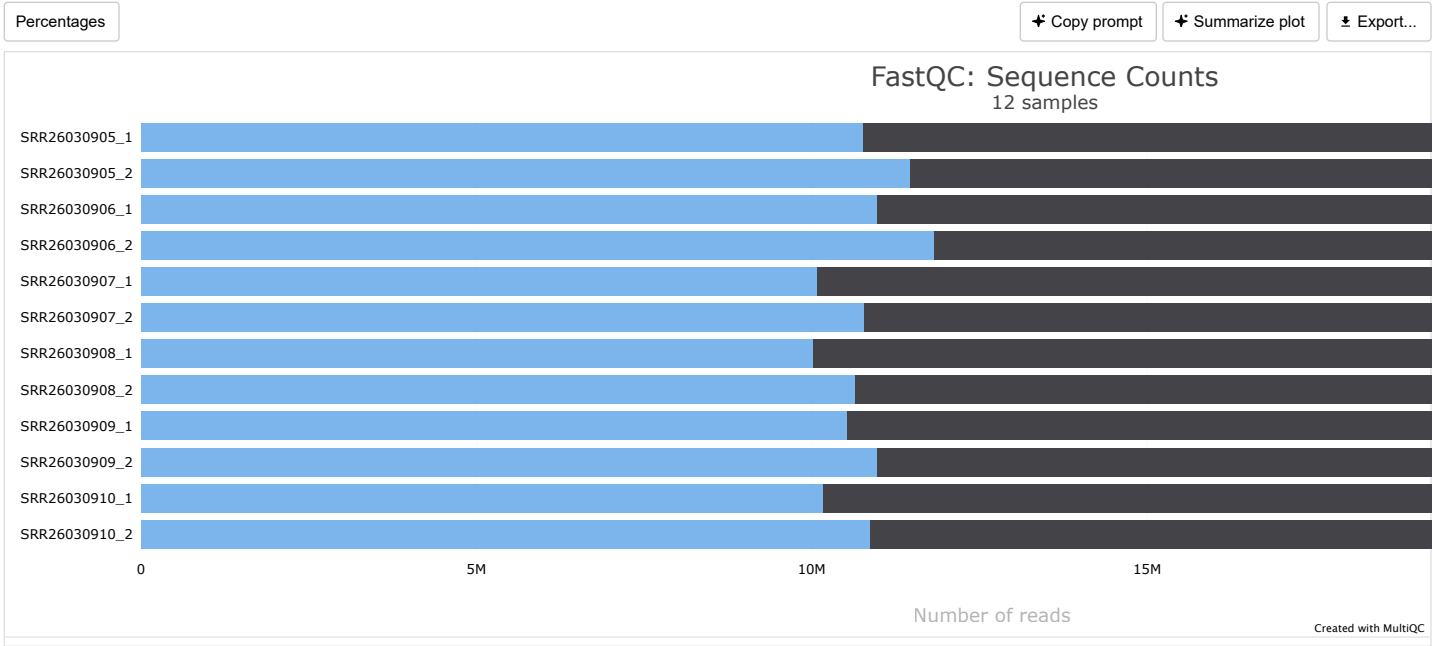
Sample Name	Dups	GC	Seqs
SRR26030905_1	57.6 %	49.0 %	25.4 M
SRR26030905_2	54.8 %	49.0 %	25.4 M
SRR26030906_1	56.4 %	48.0 %	25.2 M
SRR26030906_2	53.0 %	48.0 %	25.2 M
SRR26030907_1	58.0 %	49.0 %	24.0 M
SRR26030907_2	55.1 %	49.0 %	24.0 M
SRR26030908_1	56.9 %	49.0 %	23.2 M
SRR26030908_2	54.2 %	49.0 %	23.2 M
SRR26030909_1	58.0 %	49.0 %	25.1 M
SRR26030909_2	56.2 %	49.0 %	25.1 M
SRR26030910_1	57.8 %	49.0 %	24.1 M
SRR26030910_2	54.9 %	49.0 %	24.1 M

FastQC Version: 0.12.1

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

Sequence Counts

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



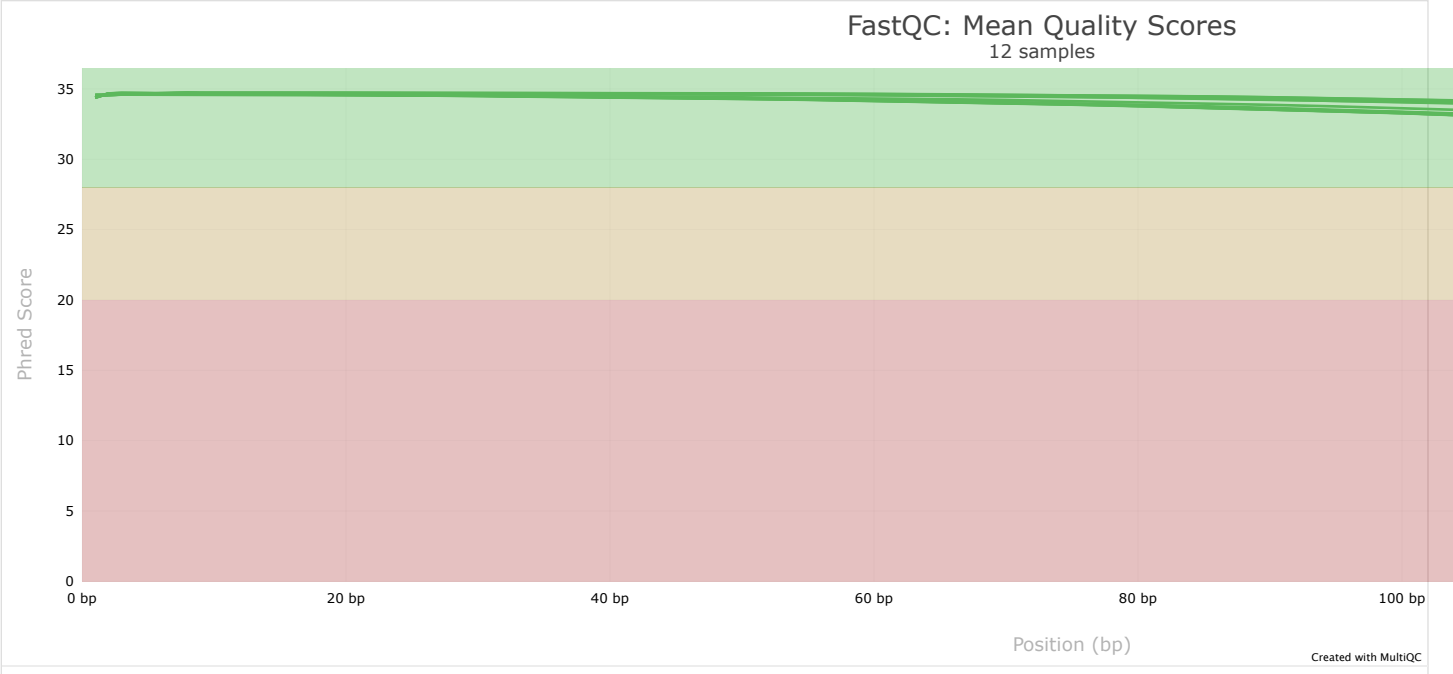
Sequence Quality Histograms

12

Help

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

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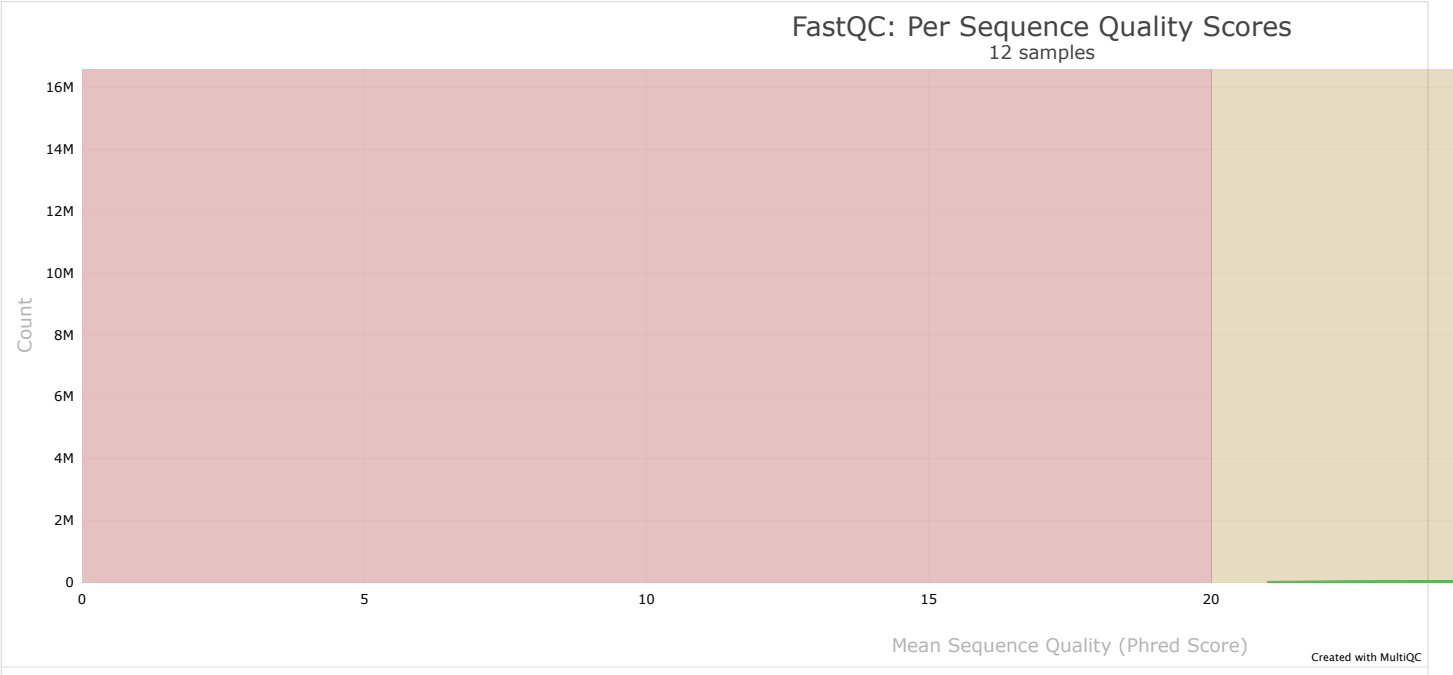
Per Sequence Quality Scores

12

Help

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

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Per Base Sequence Content

6

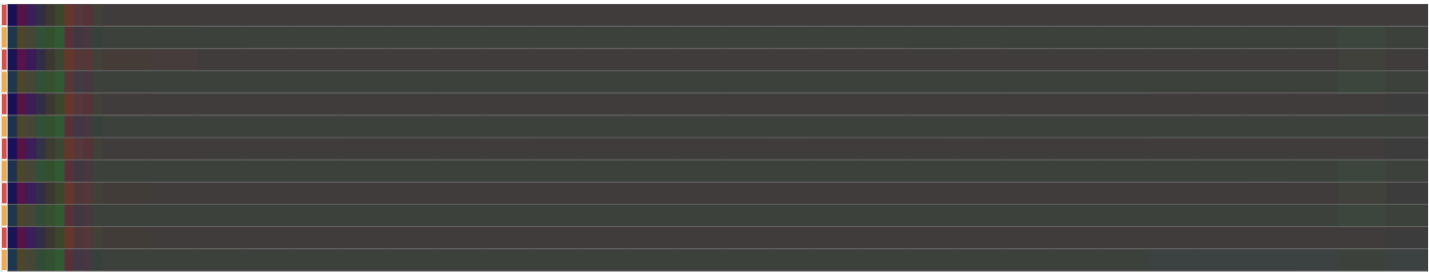
Help

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: -



Per Sequence GC Content

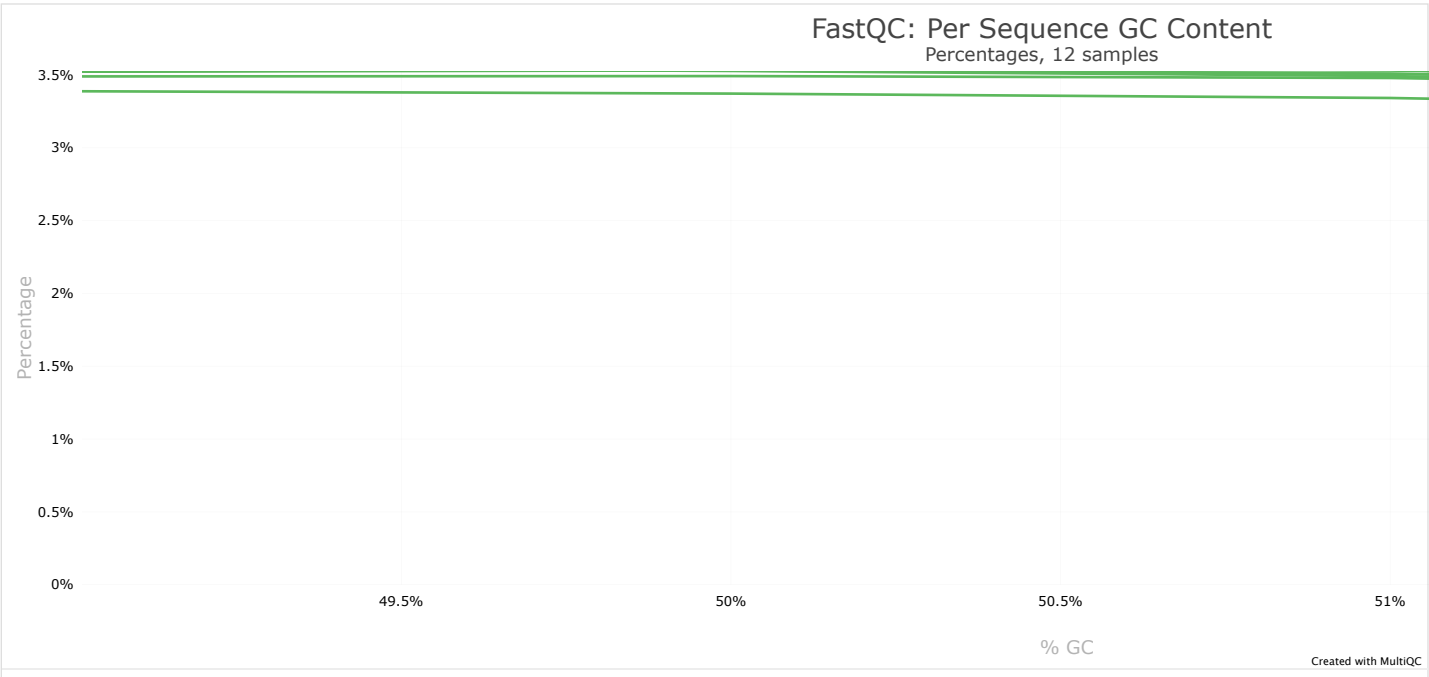
12

Help

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

Percentages Counts

Copy prompt Summarize plot Export...



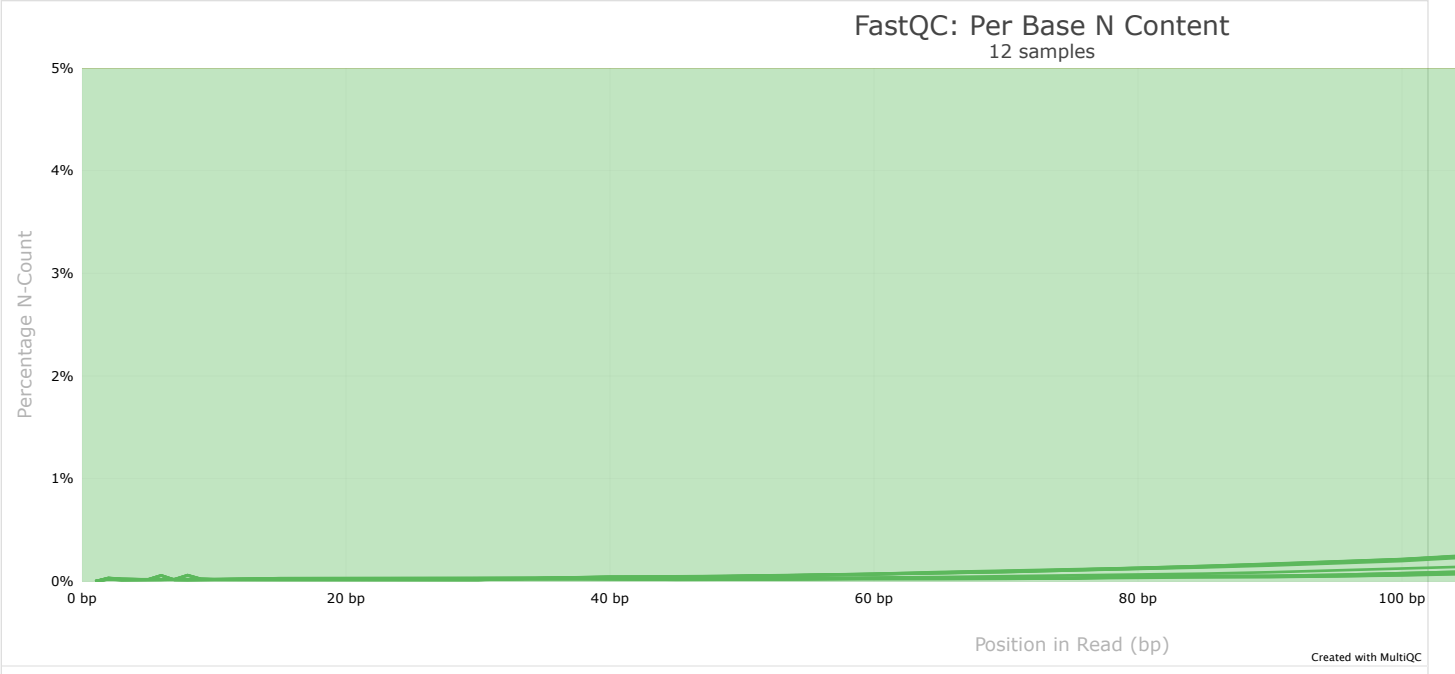
Per Base N Content

12

Help

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

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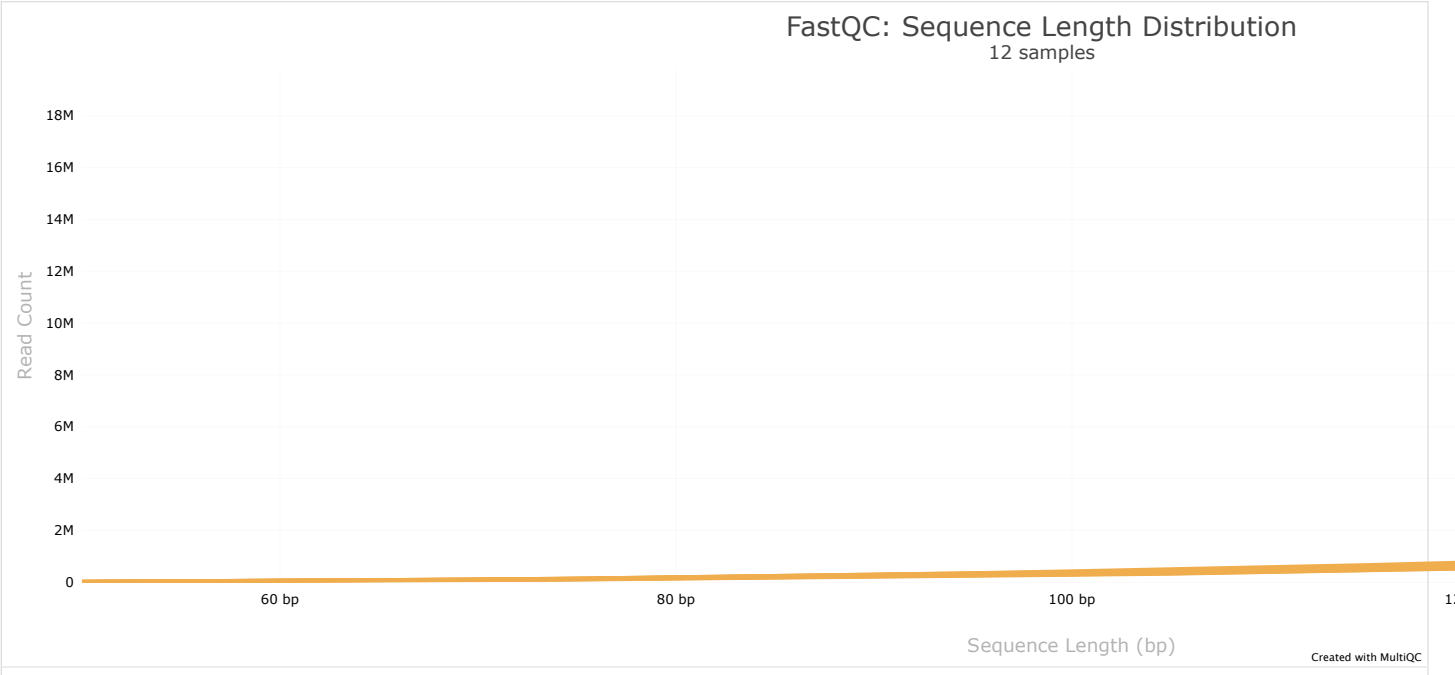


Sequence Length Distribution

12

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

Copy prompt Summarize plot Export...

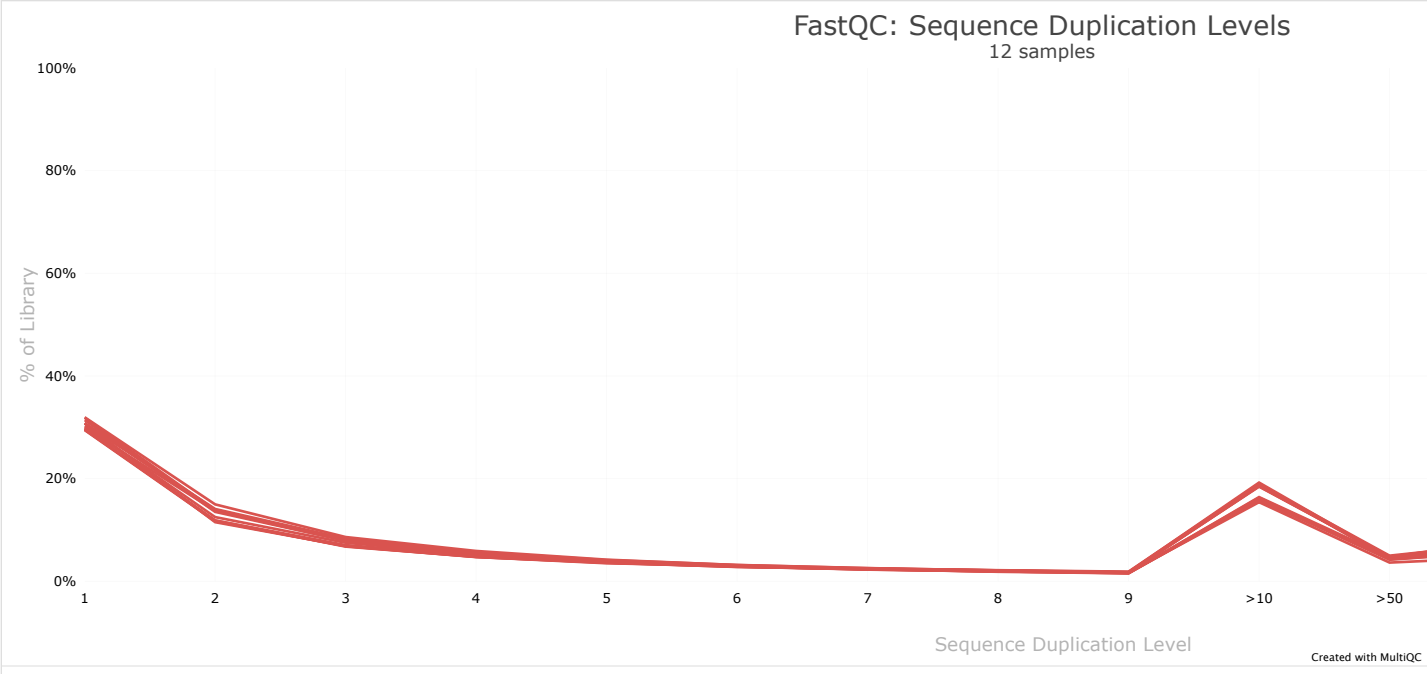


Sequence Duplication Levels

Help

The relative level of duplication found for every sequence.

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Overrepresented sequences by sample

12

Help

The total amount of overrepresented sequences found in each library.

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

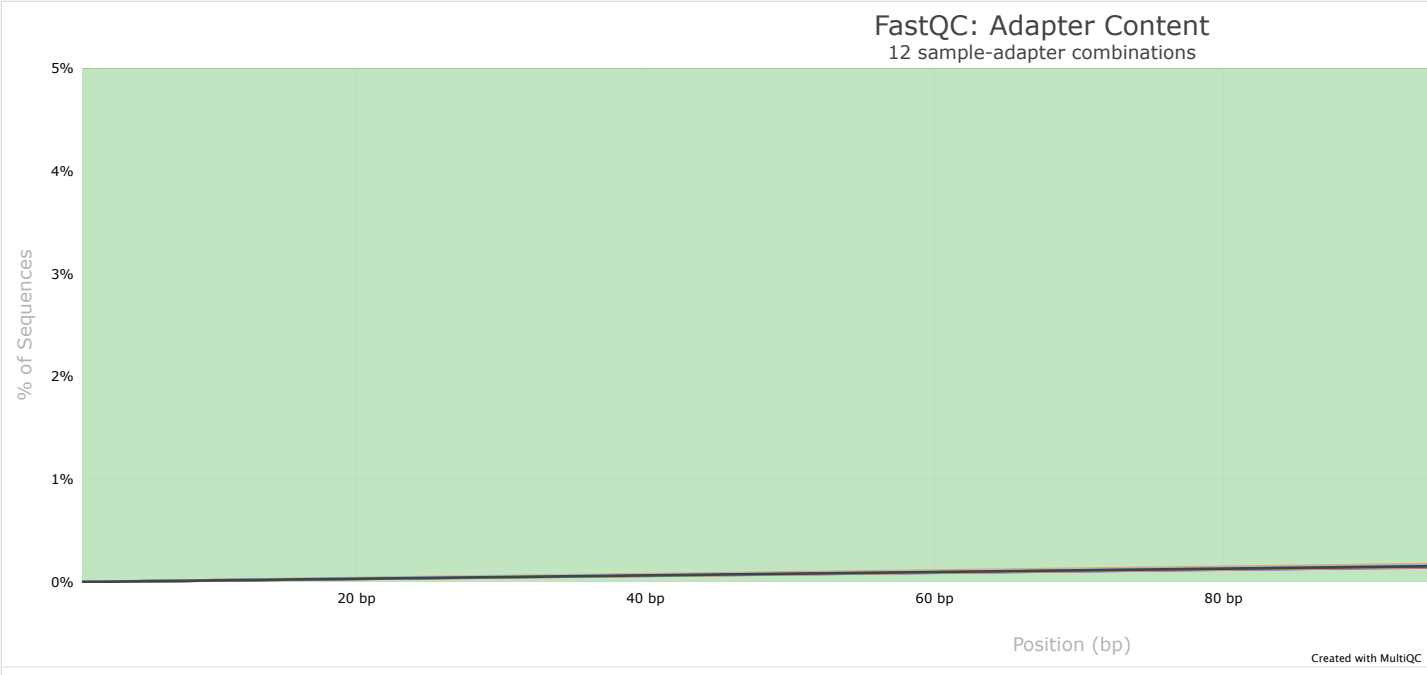
Adapter Content

12

Help

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

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Status Checks

Help

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

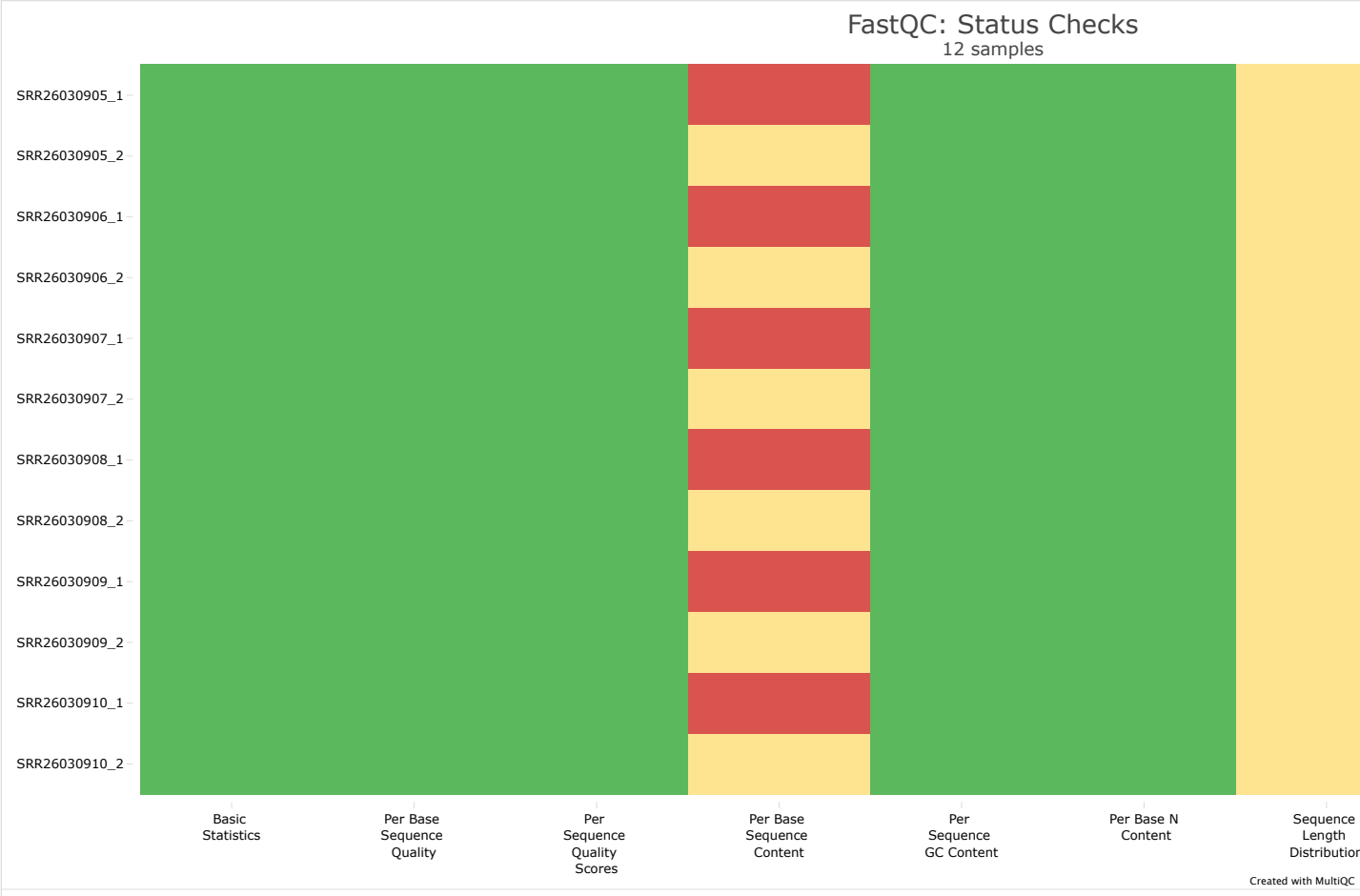
Sorted by sample

Clustered

Copy prompt

Summarize plot

Export...



Software Versions

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

Copy table

Software	Version
FastQC	0.12.1