



MultiQC

(<http://multiqc.info>)

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

Report generated on 2021-08-11, 14:47 based on data in: /home/sadaf

General Statistics

Copy table

Configure Columns

Plot

Showing $2\frac{1}{2}$ rows and $3\frac{3}{5}$ columns.

Sample Name	% Dups	% GC	M Seqs
SRR12740661_1			
SRR12740661_2			

FastQC

FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

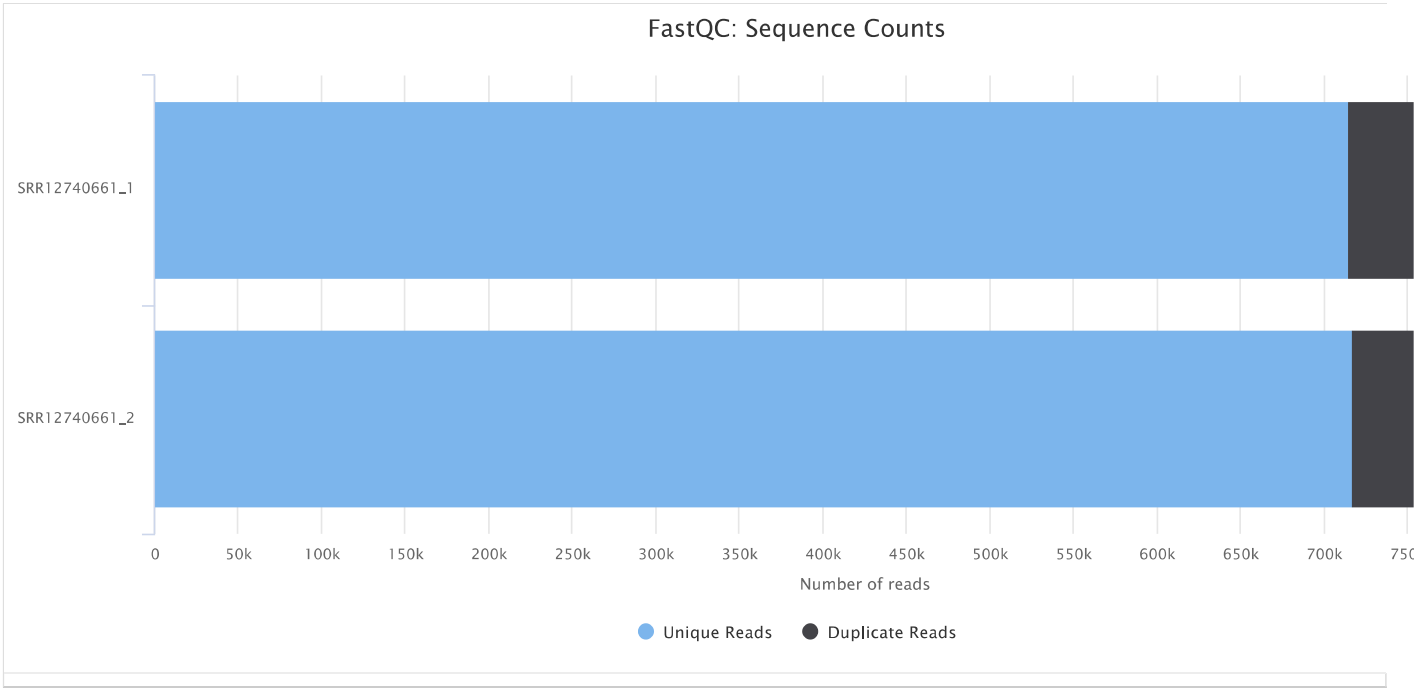
Sequence Counts



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

Number of reads

Percentages

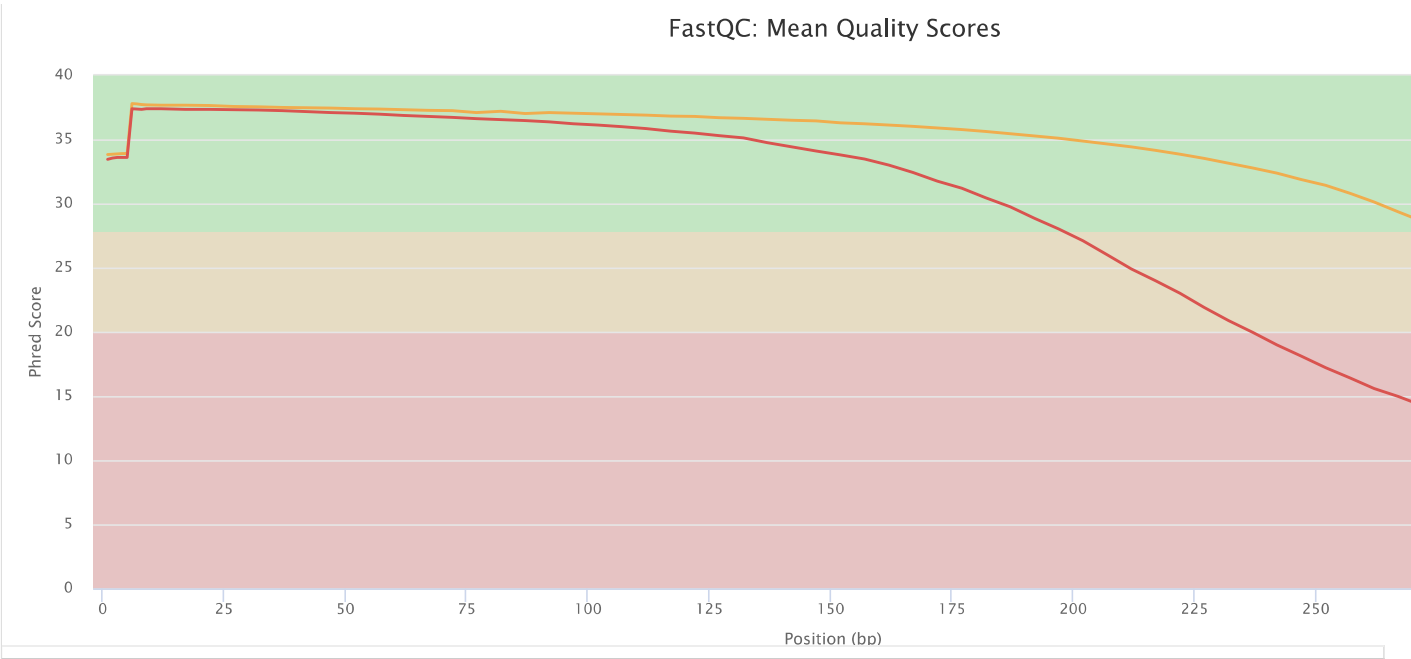


Sequence Quality Histograms

0 1 1



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

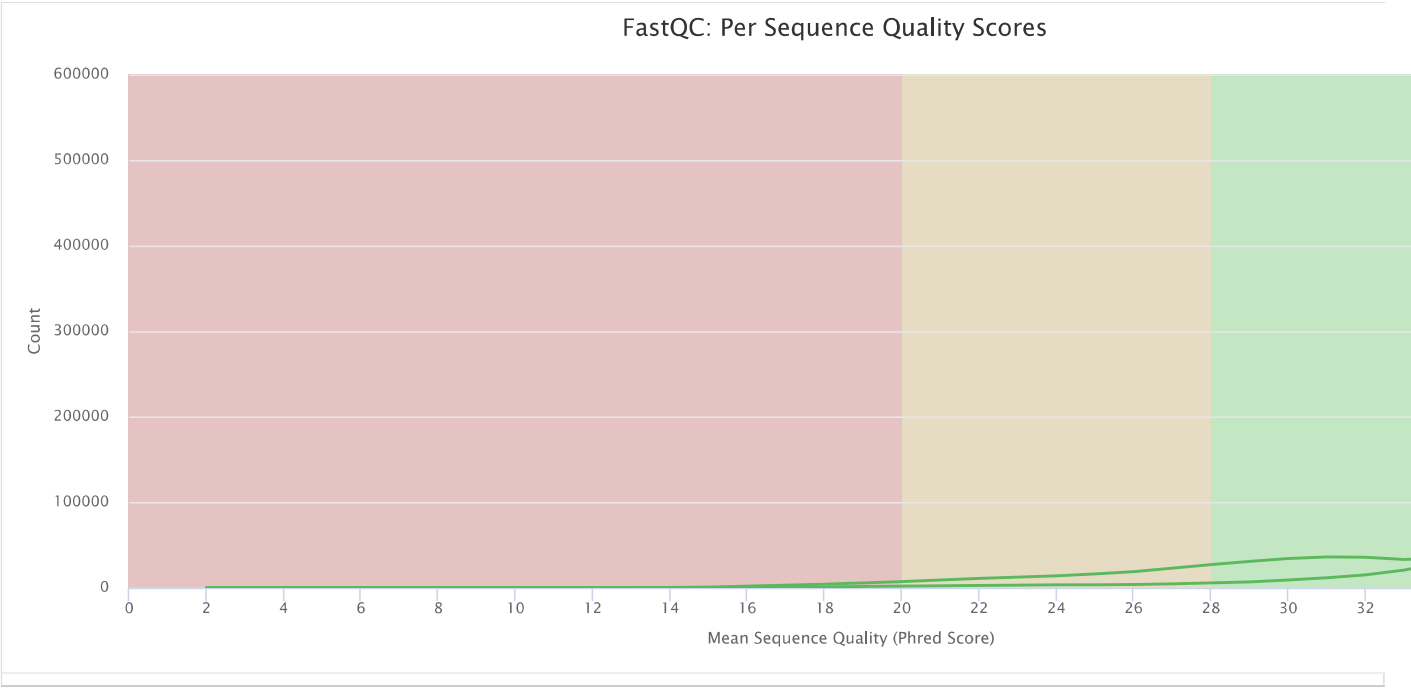


Per Sequence Quality Scores

2

Help

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



Per Base Sequence Content

0 1 1

Help

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

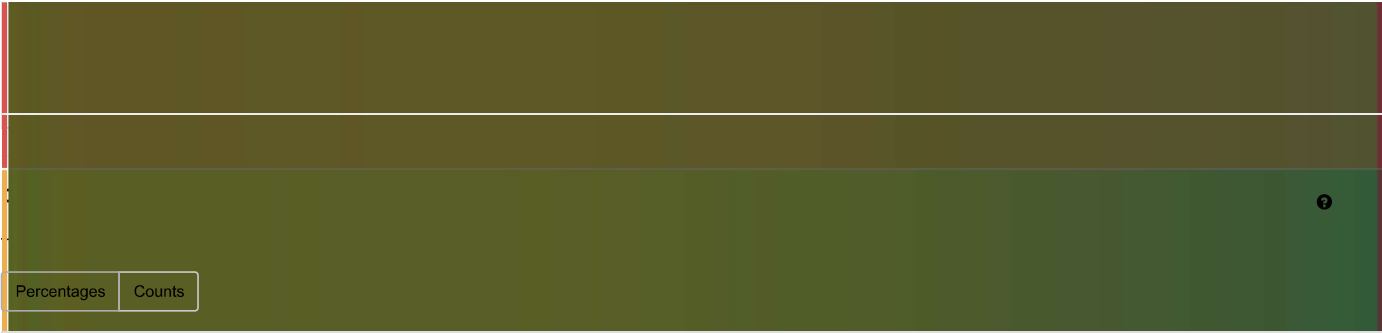
Click a sample row to see a line plot for that dataset.

Rollover for sample name

Position: - %T: - %C: - %A: - %G: -

Export Plot



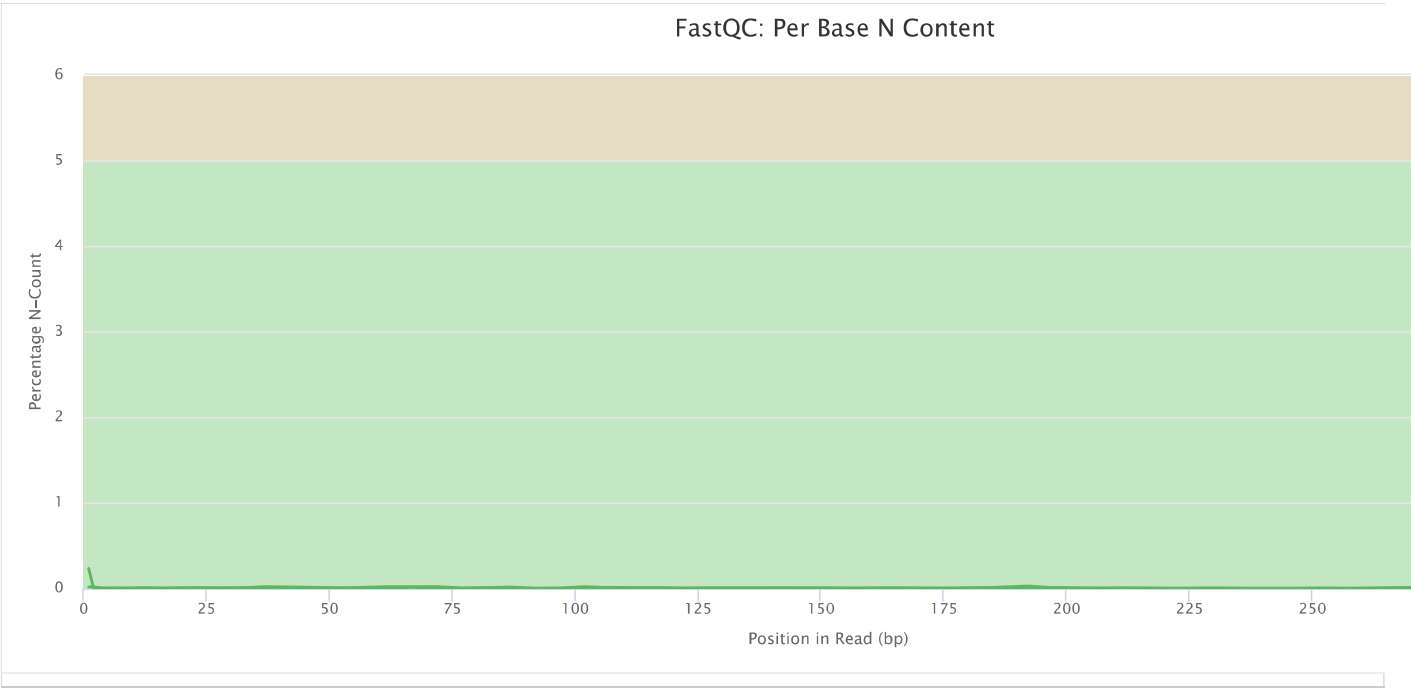


Per Base N Content

2

Help

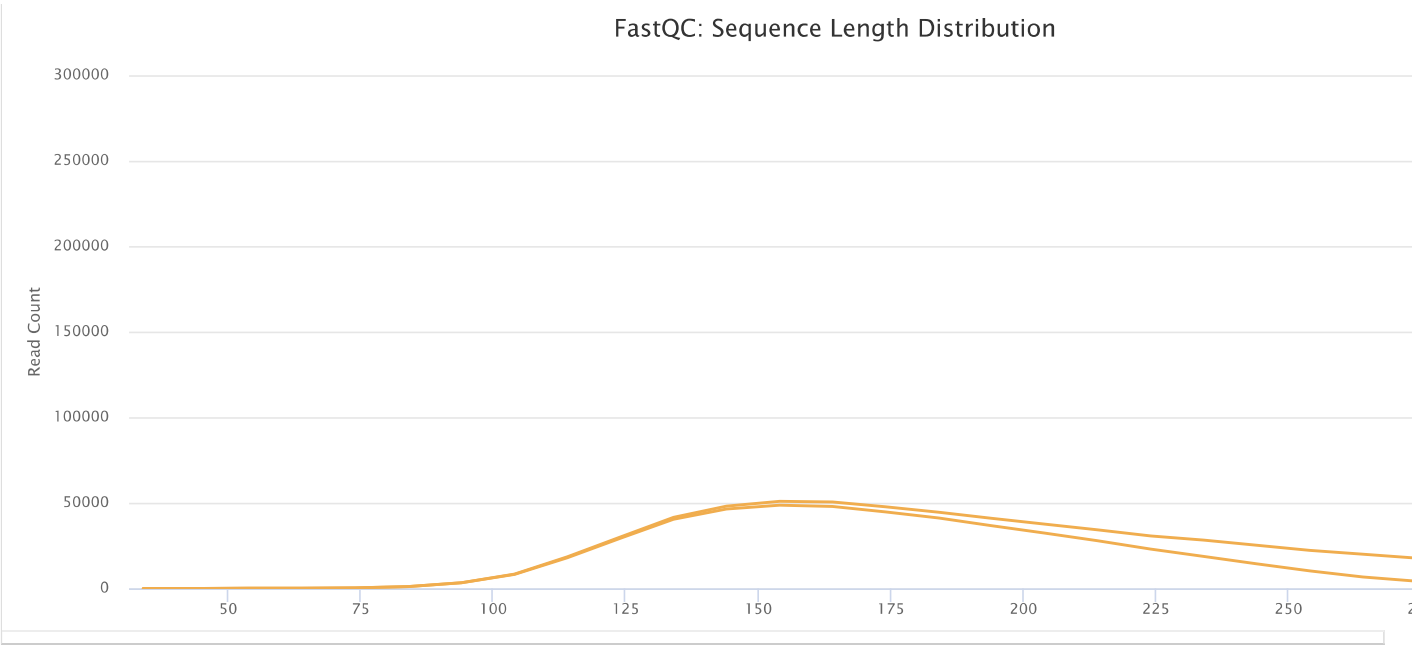
The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

0 2

The distribution of fragment sizes (read lengths) found. See the FastQC help (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/7%20Sequence%20Length%20Distribution.html>)

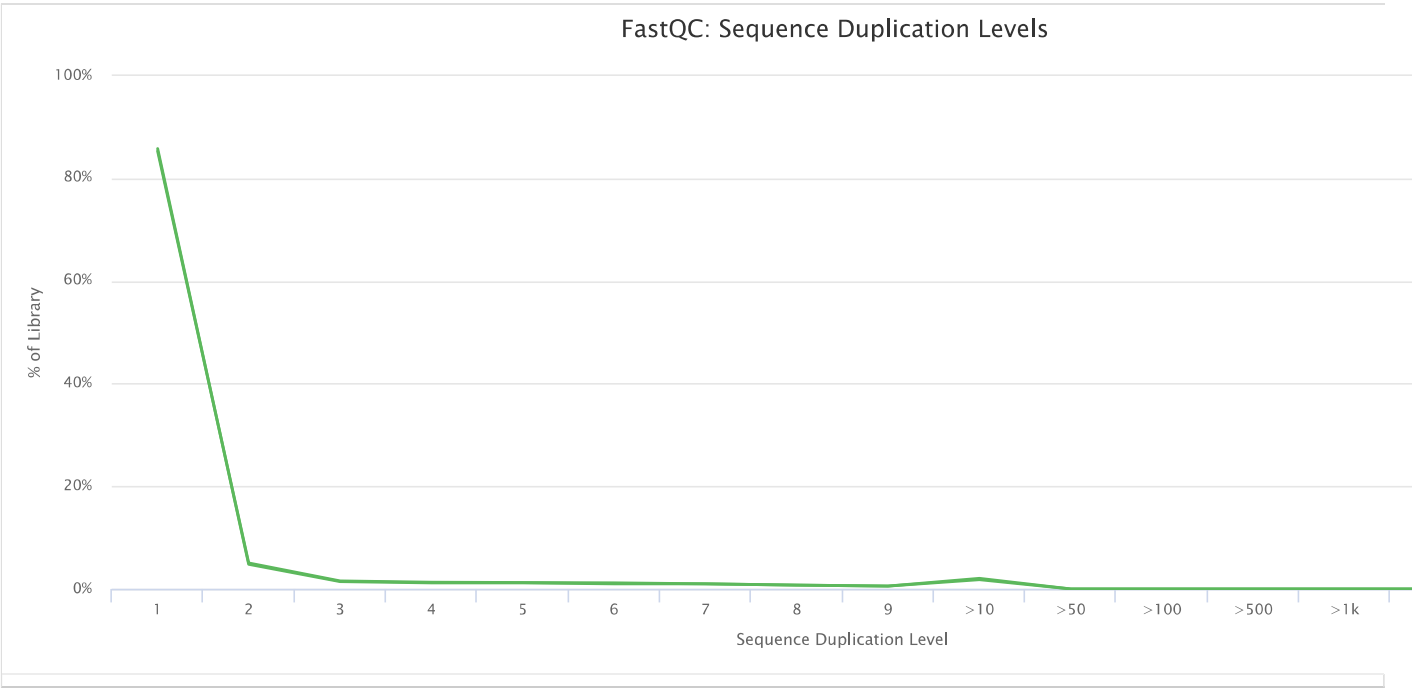


Sequence Duplication Levels

2

[Help](#)

The relative level of duplication found for every sequence.



Overrepresented sequences

2

[Help](#)

The total amount of overrepresented sequences found in each library.

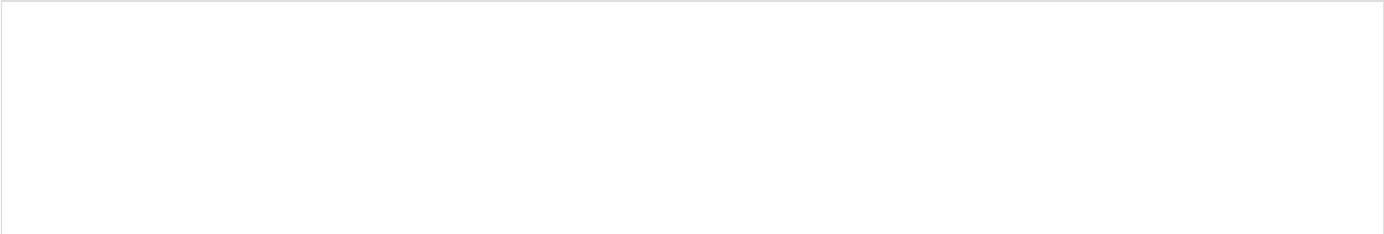
2 samples had less than 1% of reads made up of overrepresented sequences

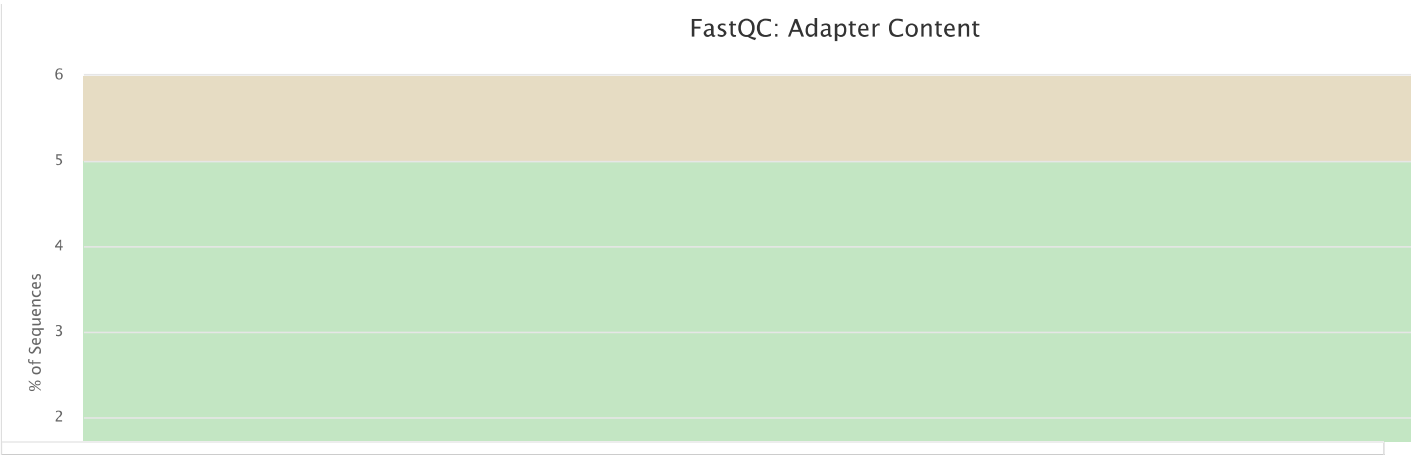
Adapter Content

2

[Help](#)

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





Status Checks

Help

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

Sort by highlight

Min: 0

Max: 1

