



MultiQC

(<http://multiqc.info>)

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

Report generated on 2019-10-08, 16:03 based on data in: `/public/home/xijf/project/homework/homework_3/MeRIP_seq_1/data_processing/quality_control`

General Statistics

Copy table

Configure Columns

Plot

Showing 7/7 rows and 3/5 columns.

Sample Name	% Dups	% GC	M Seqs
SRR456551			
SRR456552			
SRR456553			
SRR456554			
SRR456555			
SRR456556			
SRR456557			

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

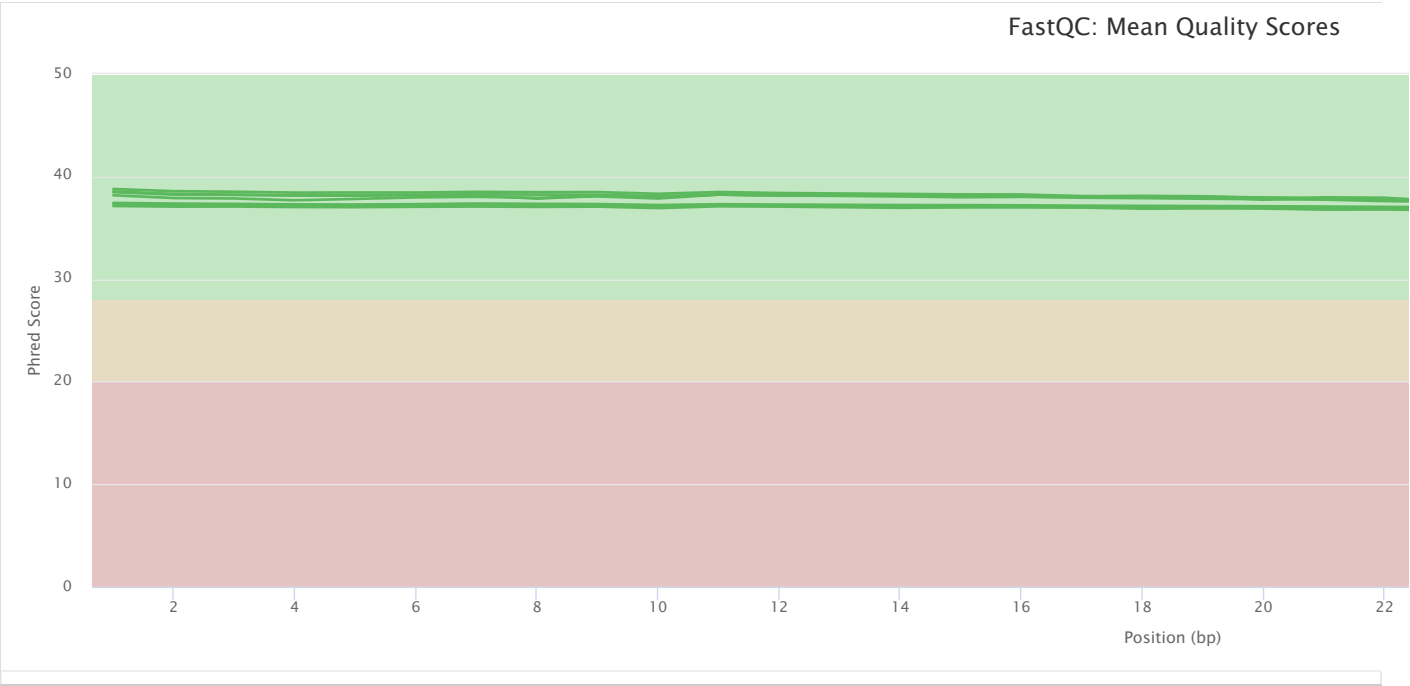


Sequence Quality Histograms

7

Help

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

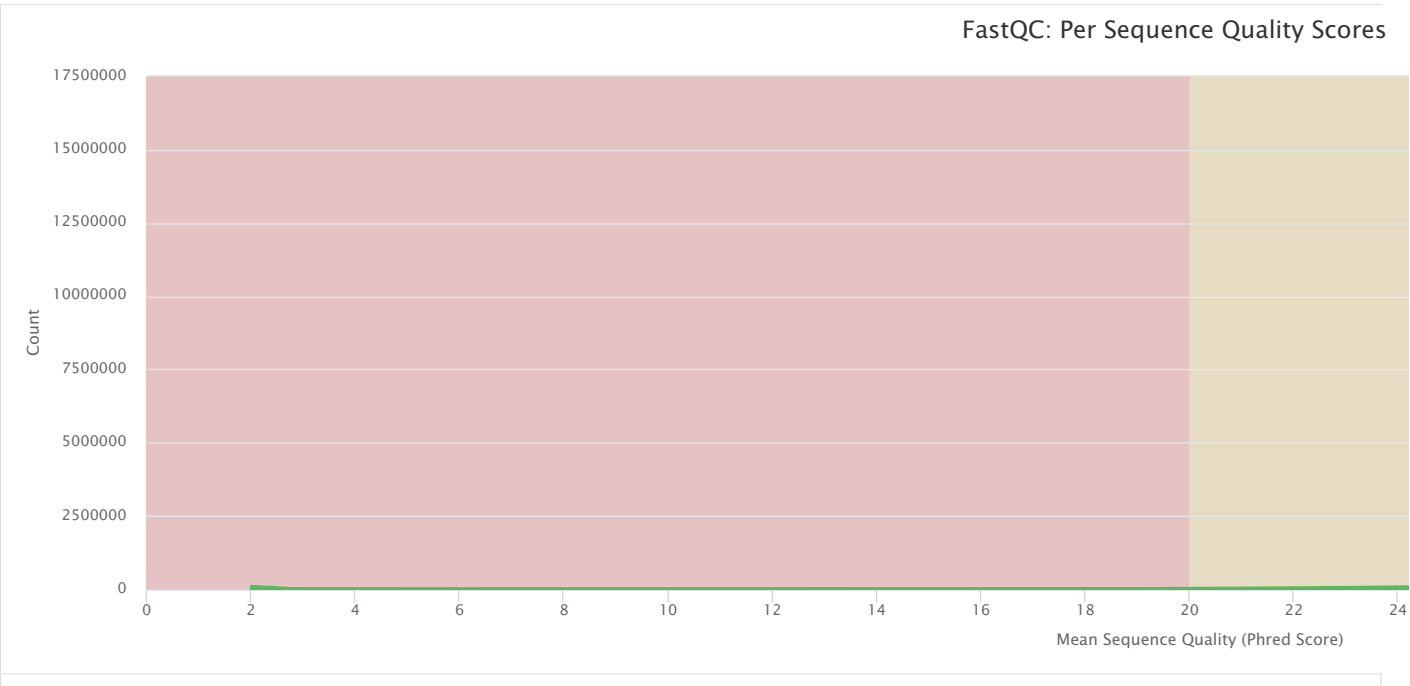


Per Sequence Quality Scores

7

Help

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



Per Base Sequence Content

0

7

Help

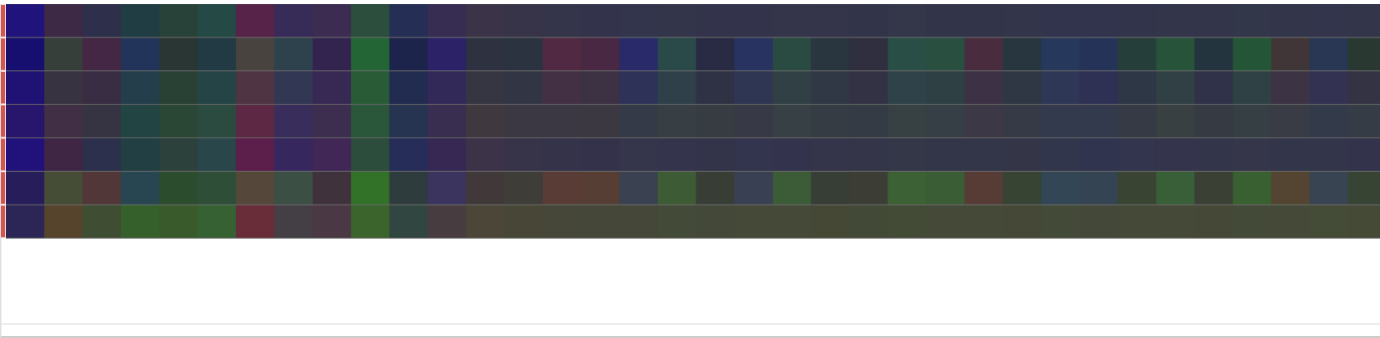
The proportion of each base position for which each of the four normal DNA bases has been called.

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

Rollover for sample name

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

Export Plot



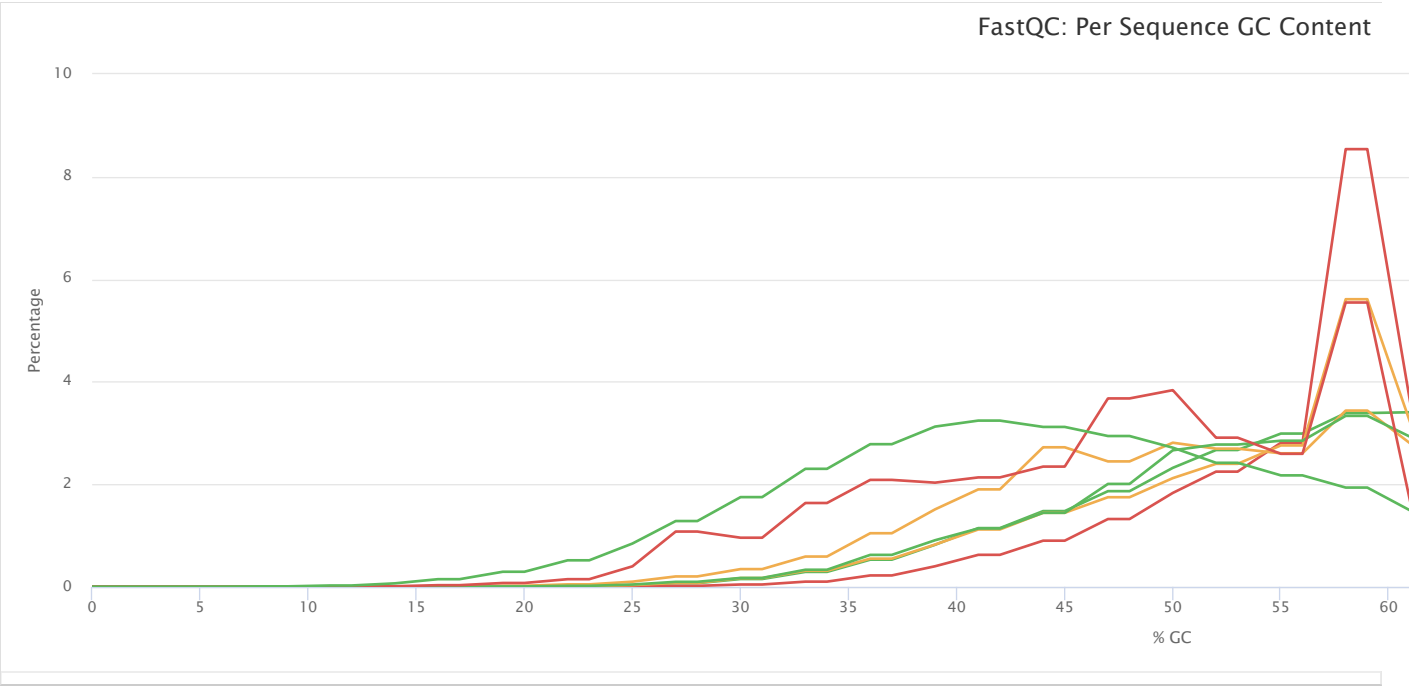
Per Sequence GC Content

3 2 2

Help

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

Percentages Counts

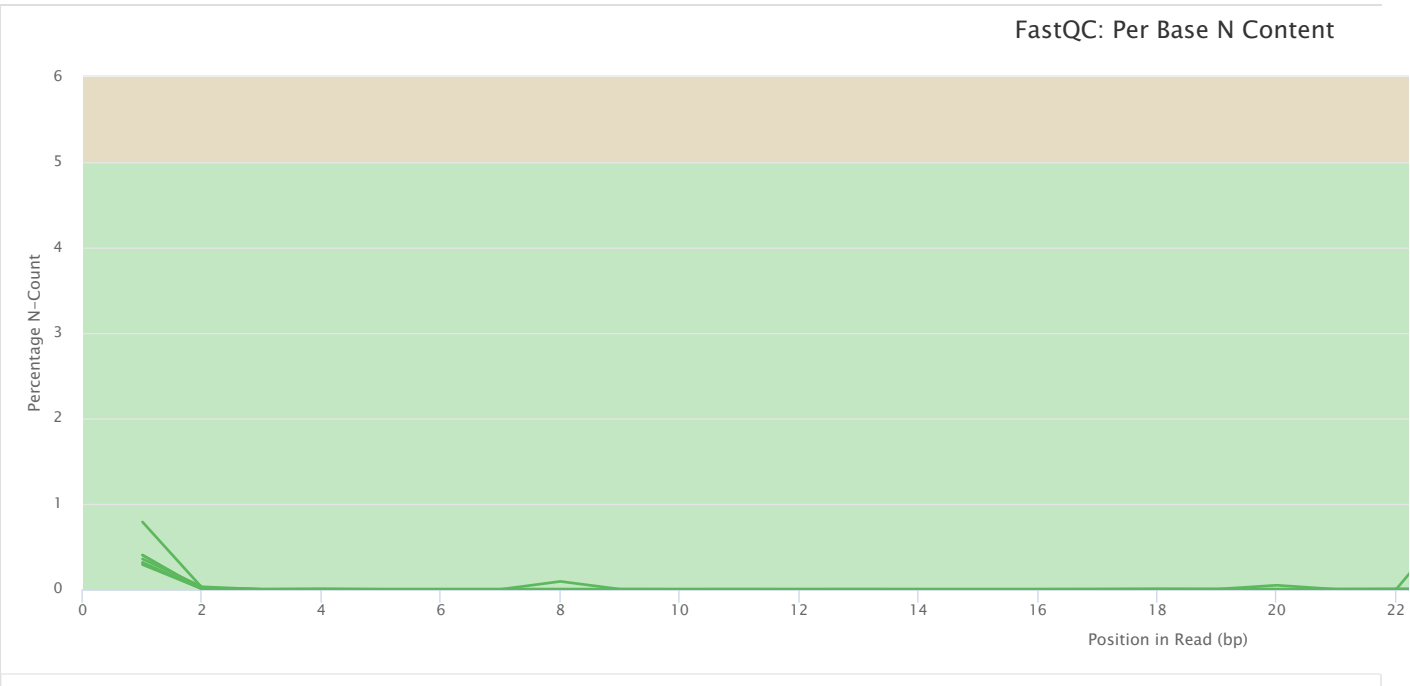


Per Base N Content

7

Help

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



Sequence Length Distribution

7

All samples have sequences of a single length (36bp).

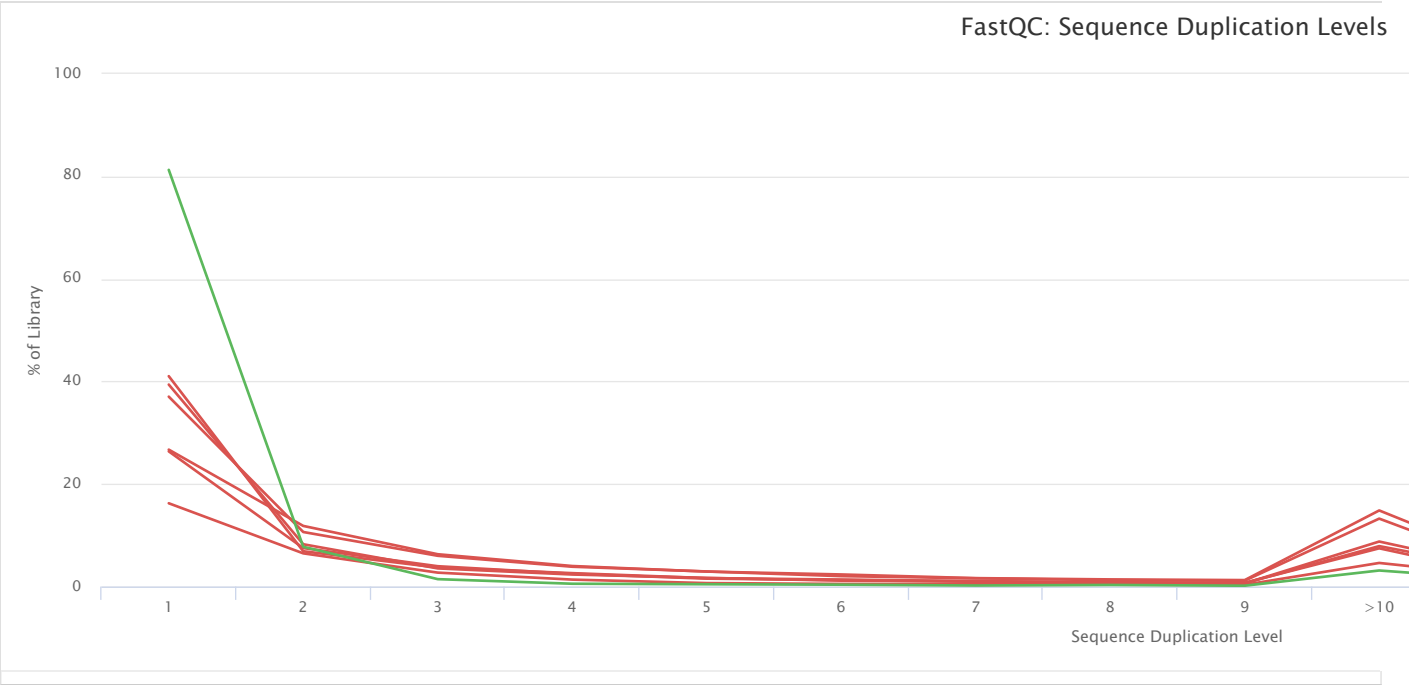
Sequence Duplication Levels

10

6

Help

The relative level of duplication found for every sequence.



Overrepresented sequences

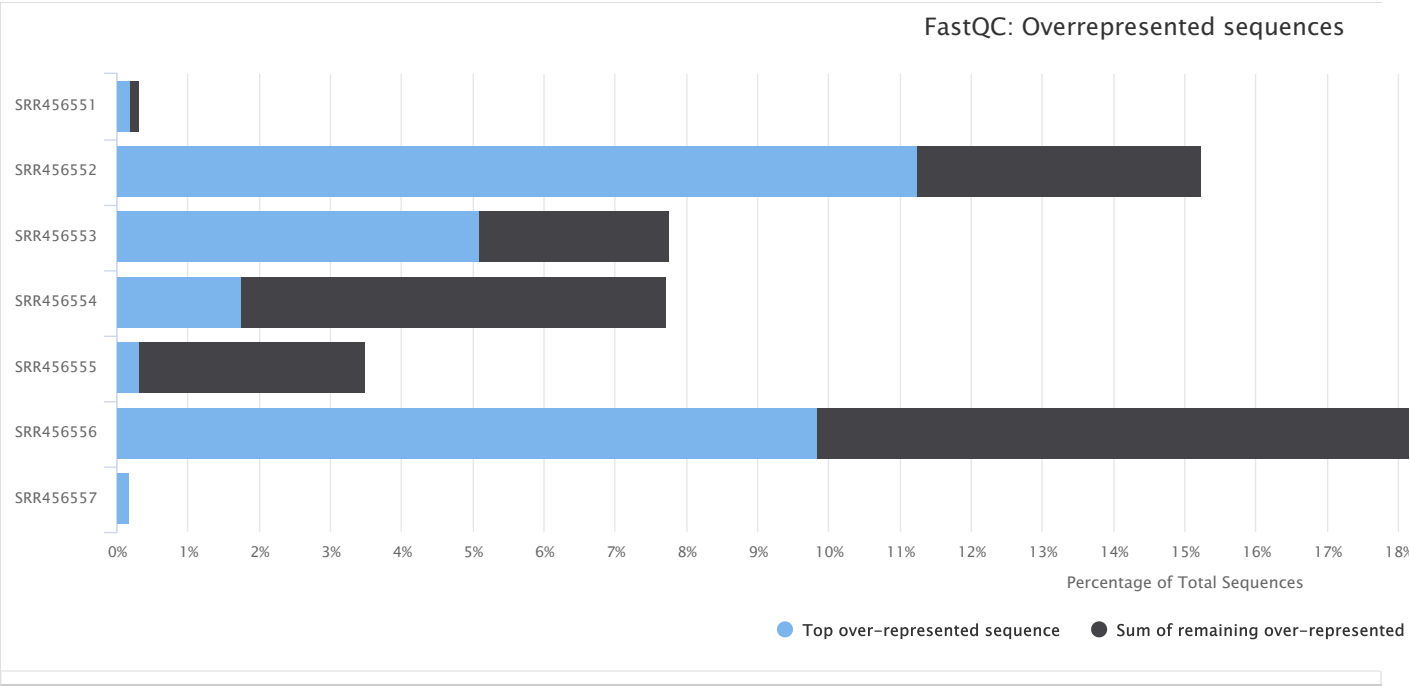
0

3

4

Help

The total amount of overrepresented sequences found in each library.



Adapter Content

6

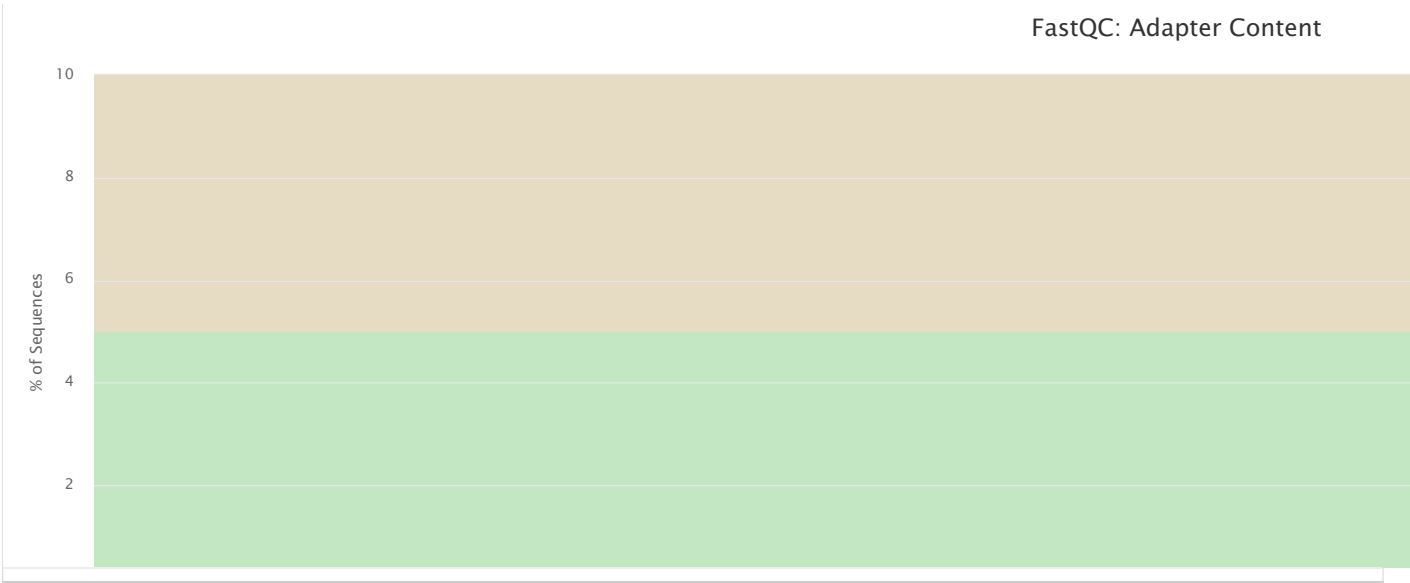
1

Help

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



FastQC: Adapter Content



MultiQC v1.7 (<http://multiqc.info>) - Written by [Phil Ewels](http://phil.ewels.co.uk), available on [GitHub](https://github.com/ewels/MultiQC). This report uses [HighCharts](http://www.highcharts.com/), [jQuery](https://jquery.com/), [jQuery UI](https://jqueryui.com/), [Bootstrap](http://getbootstrap.com/), [FileSaver.js](https://github.com/eligrey/FileSaver.js) and [clipboard.js](https://clipboardjs.com/). **SciLifeLab** (<http://www.scilifelab.se/>)