



# MultiQC

(<http://multiqc.info>)

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

Report generated on 2021-07-02, 00:46 based on data in:

/home/alejandra/Dados/02\_Sequencias/03\_Reads\_LimpezaDosReads/05\_Estasticas/02\_LimposPelo\_FastP/03\_Fastqc

## General Statistics

Copy table

Configure Columns

Plot

Showing  $\frac{4}{4}$  rows and  $\frac{4}{5}$  columns.

Sample Name	% Dups	% GC	Length	M Seqs
10_EC092_R1_PE_fastpCleaned				
10_EC092_R1_SingleEnd_fastpCleaned				
10_EC092_R2_PE_fastpCleaned				
10_EC092_R2_SingleEnd_fastpCleaned				

## 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.

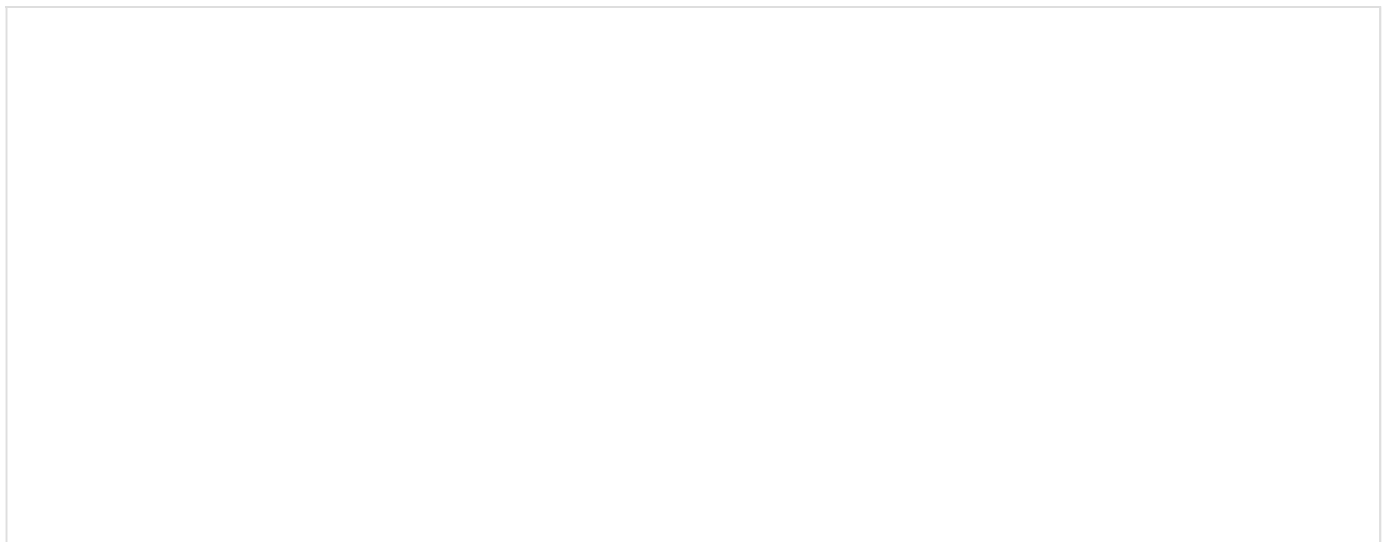
## Sequence Counts

Help

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

Number of reads

Percentages



## FastQC: Sequence Counts

[Export Plot](#)

10\_EC092\_R1\_PE\_fastpCleaned



## Sequence Quality Histograms

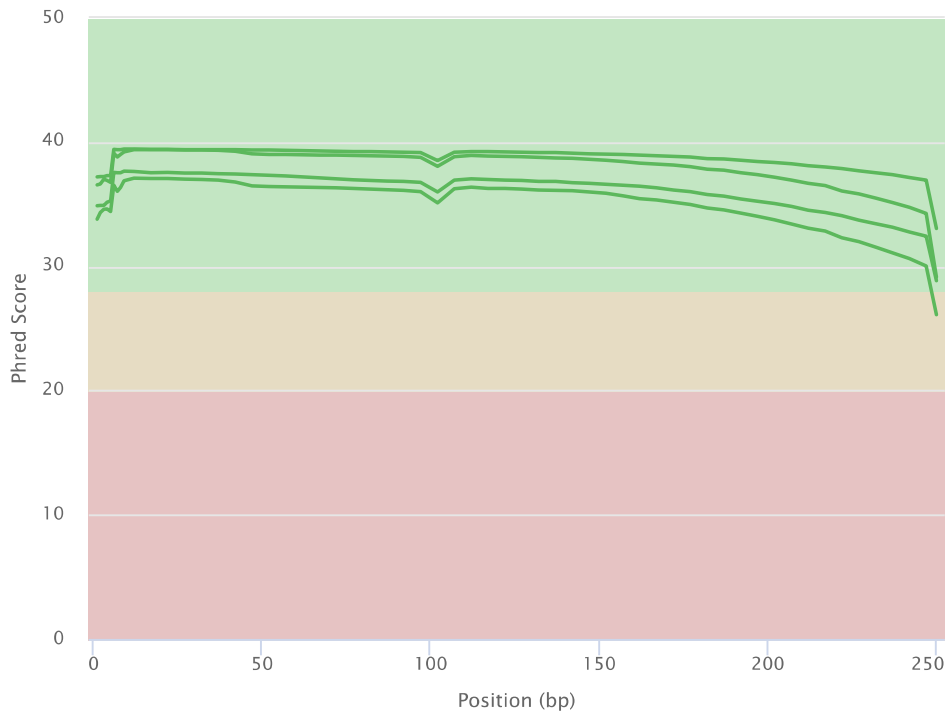
4

[Help](#)

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

## FastQC: Mean Quality Scores

[Export Plot](#)

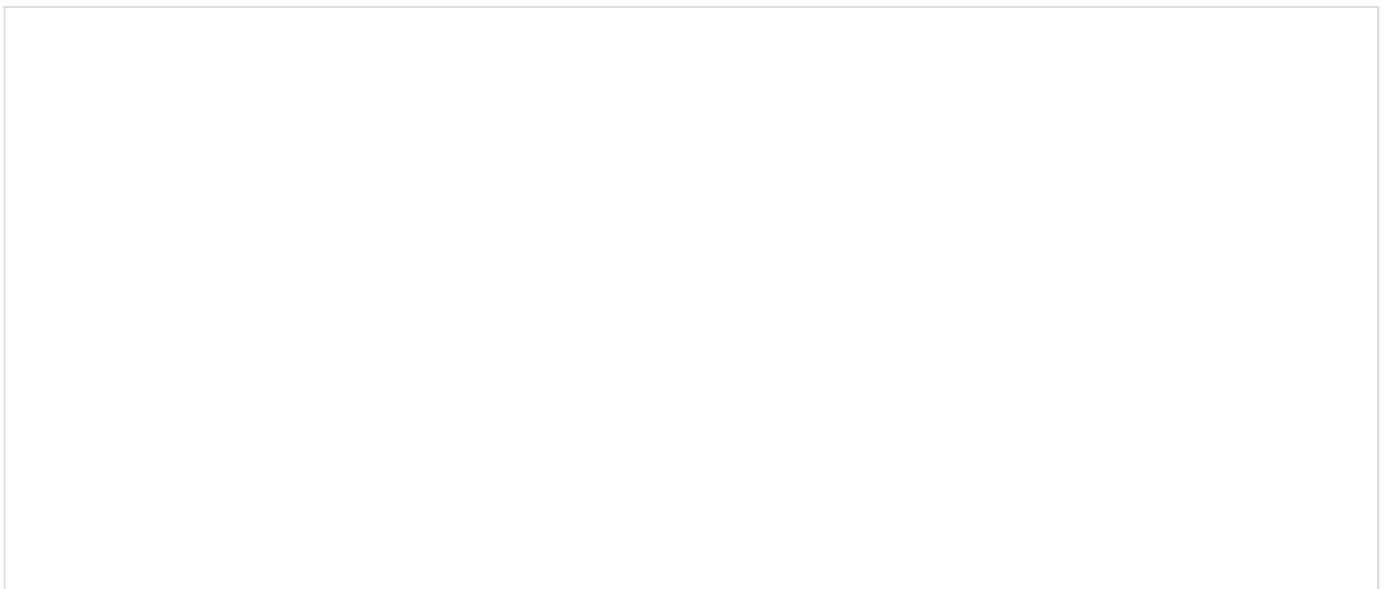


## Per Sequence Quality Scores

4

[Help](#)

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



## FastQC: Per Sequence Quality Scores [Export Plot](#)



## Per Base Sequence Content 0 4

[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.](#)

**i** Rollover for sample name

Position: -

%T: -

%C: -

%A: -

%G: -

[Export Plot](#)



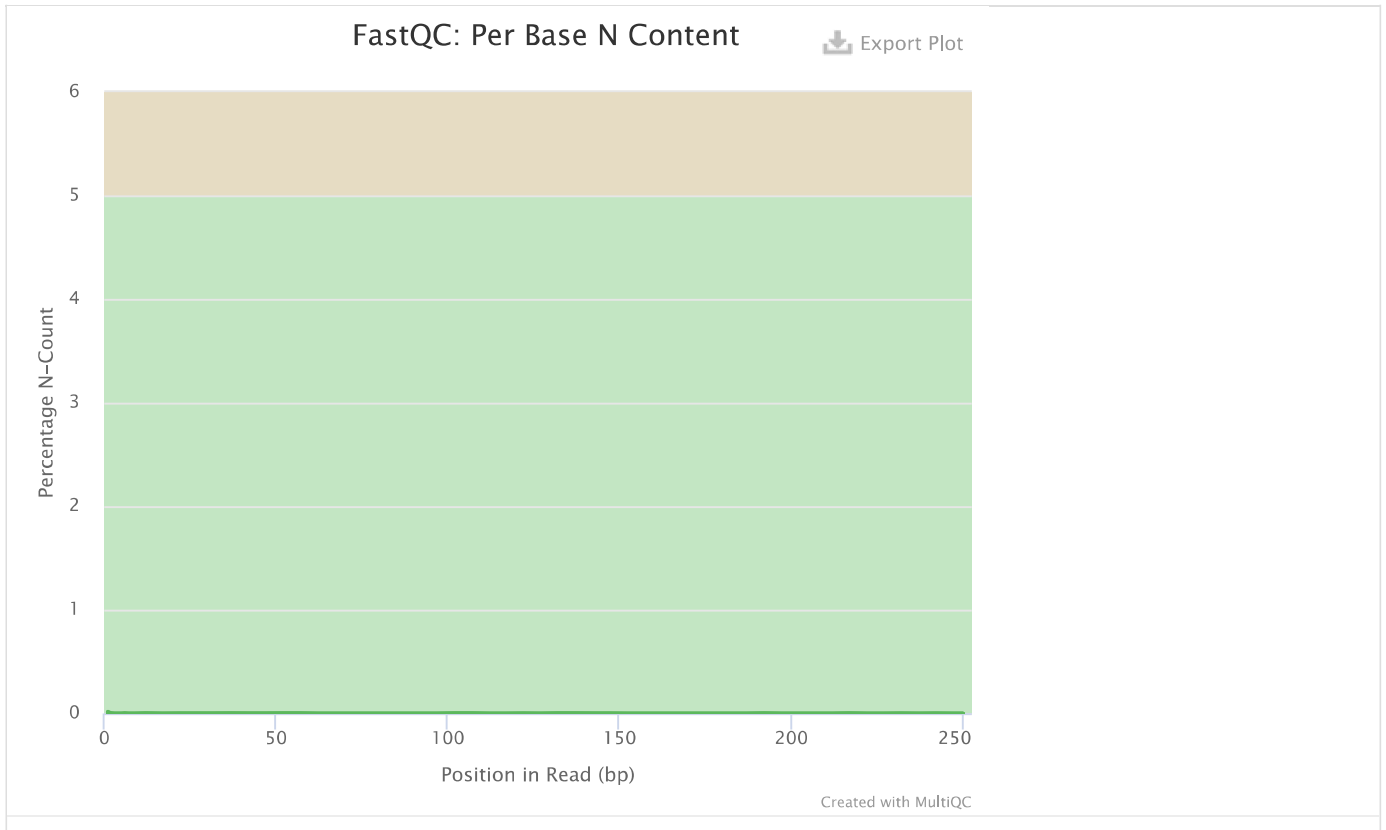
Percentages

Counts

## Per Base N Content 4

[Help](#)

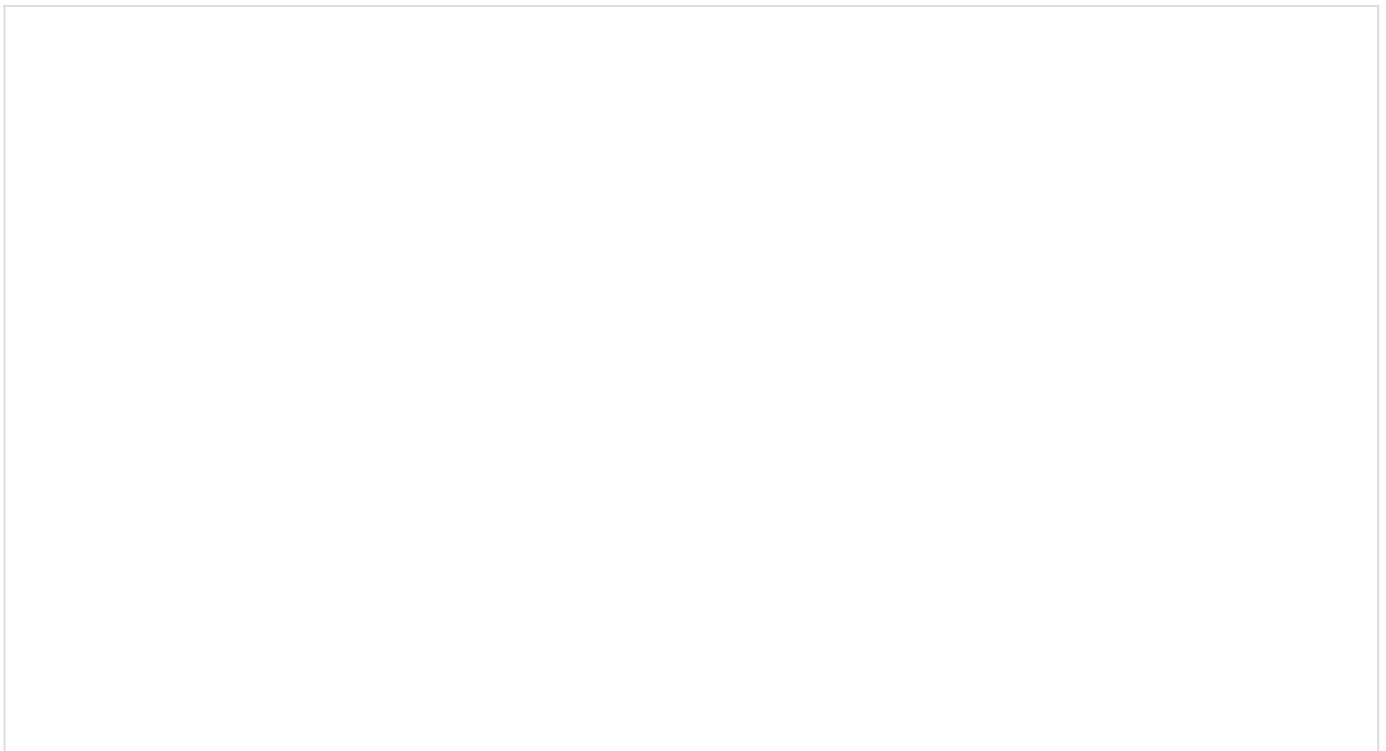
The percentage of base calls at each position for which an N was called.



## Sequence Length Distribution 0 4

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

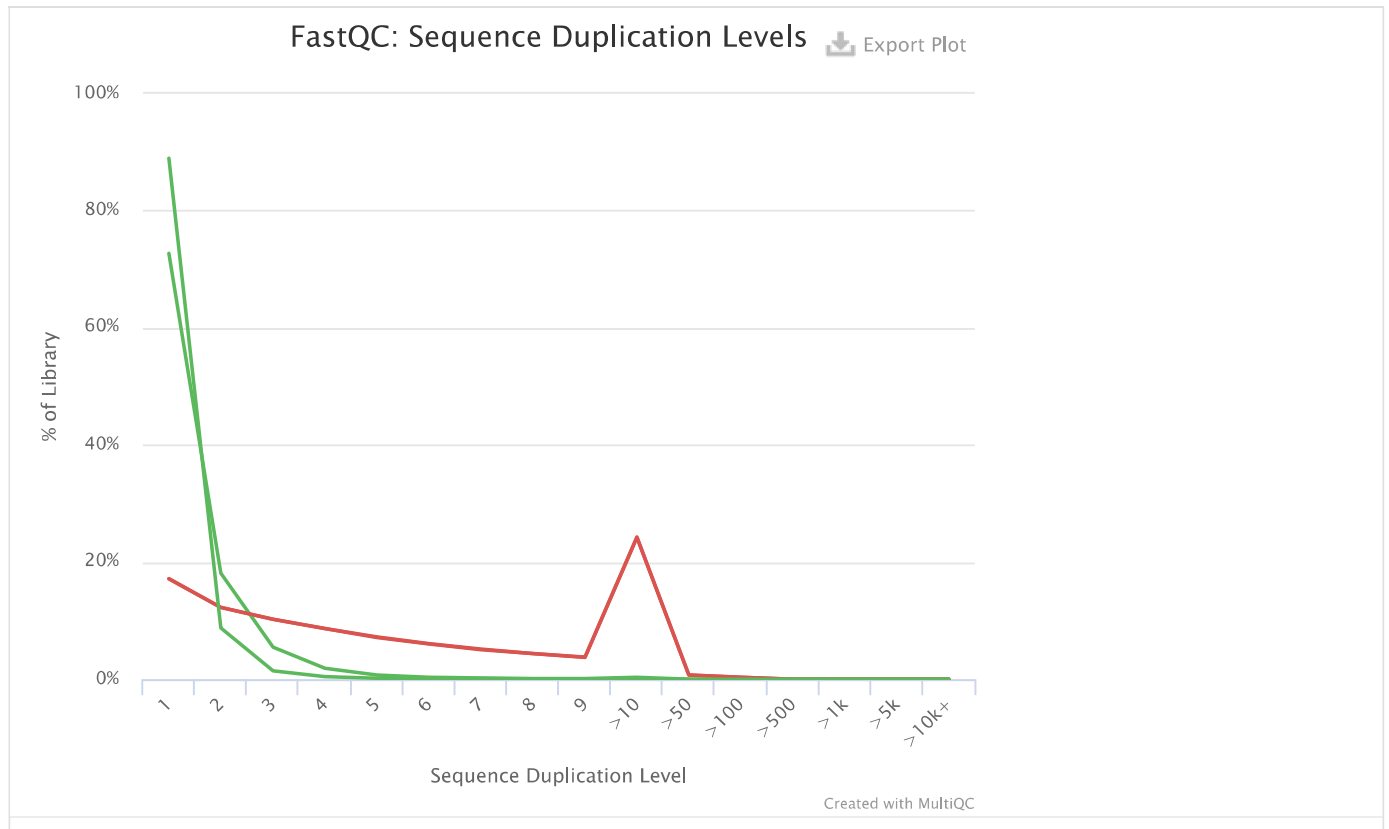
(<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/7%20Sequence%20Length%20Distribution.html>)



## Sequence Duplication Levels 2 0 2

[Help](#)

The relative level of duplication found for every sequence.



## Overrepresented sequences 4

[Help](#)

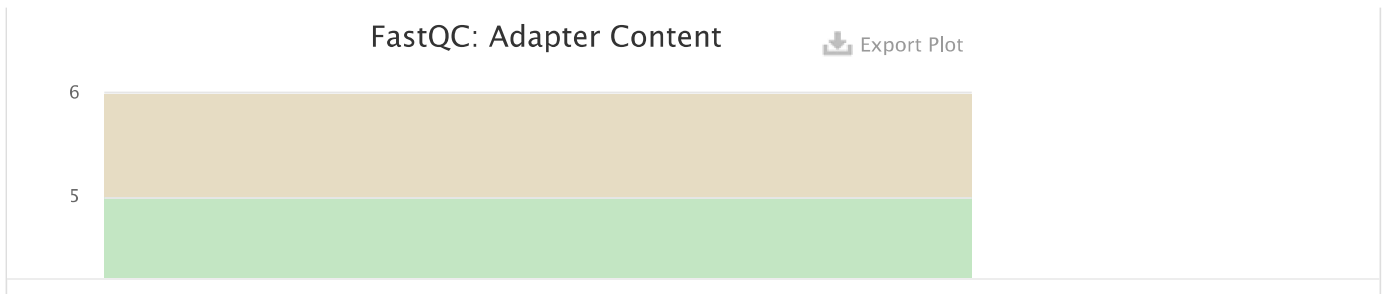
The total amount of overrepresented sequences found in each library.

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

## Adapter Content 4

[Help](#)

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



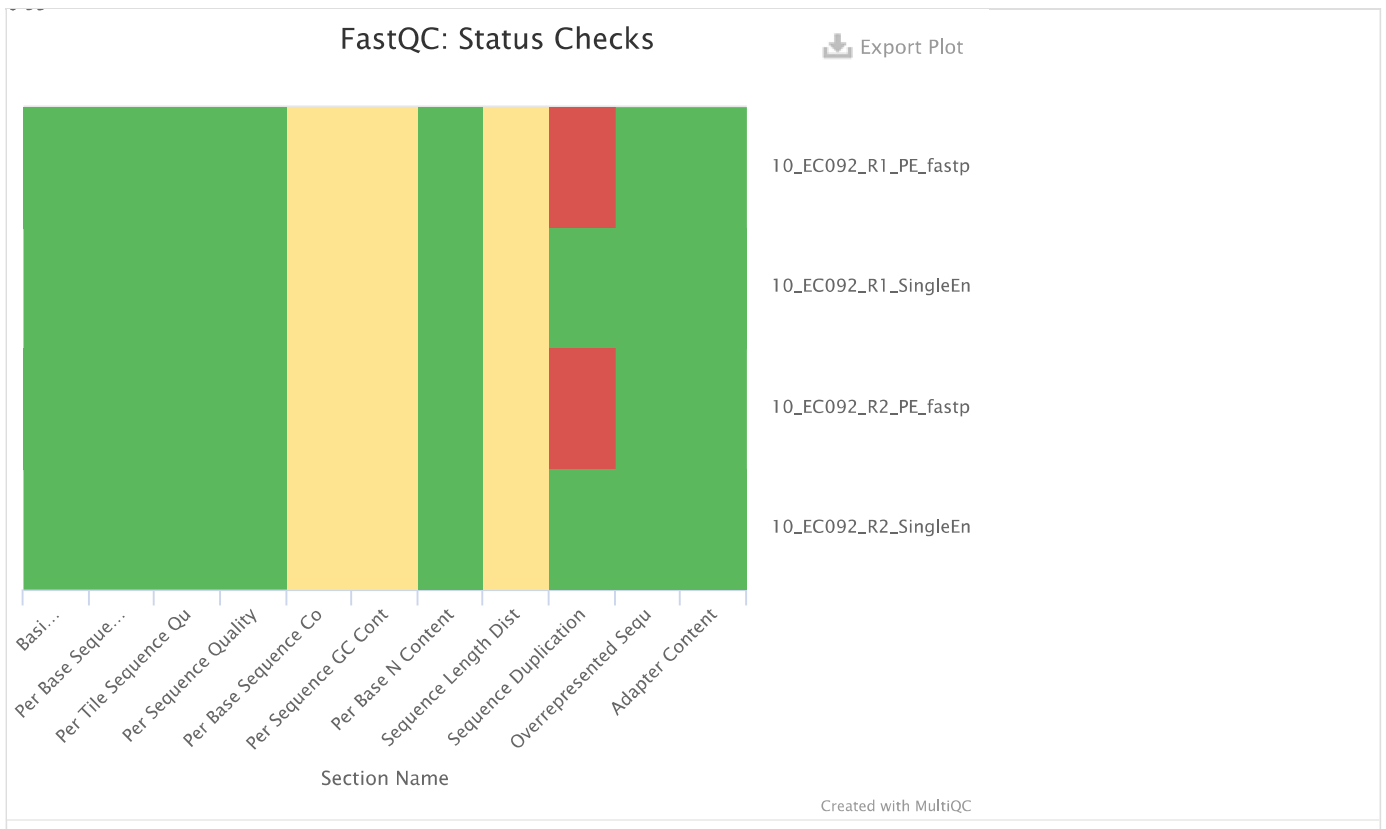
## Status Checks

[Help](#)

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

Sort by highlight

Min:   Max:



**MultiQC v1.11.dev0** (<http://multiqc.info>) - Written by [Phil Ewels](http://phil.ewels.co.uk) (<http://phil.ewels.co.uk>), available on [GitHub](https://github.com/ewels/MultiQC) (<https://github.com/ewels/MultiQC>).



(<http://www.scilifelab.se/>)

This report uses [HighCharts](http://www.highcharts.com/) (<http://www.highcharts.com/>), [jQuery](https://jquery.com/) (<https://jquery.com/>), [jQuery UI](https://jqueryui.com/) (<https://jqueryui.com/>), [Bootstrap](http://getbootstrap.com/) (<http://getbootstrap.com/>), [FileSaver.js](https://github.com/eligrey/FileSaver.js) (<https://github.com/eligrey/FileSaver.js>) and [clipboard.js](https://clipboardjs.com/) (<https://clipboardjs.com/>).