



# MultiQC

(<http://multiqc.info>)

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

Report generated on 2021-06-17, 15:09 based on data in:

/home/alejandra/Dados/02\_Sequencias/03\_Reads\_LimpezaDosReads/05\_Estatisticas/01\_DadosNaoLimpos/03\_Fa

## General Statistics

Copy table

Configure Columns

Plot

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

**Sample Name**

**% Dups**

**% GC**

**M Seqs**

10\_EC092\_r1

10\_EC092\_r2

## 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.

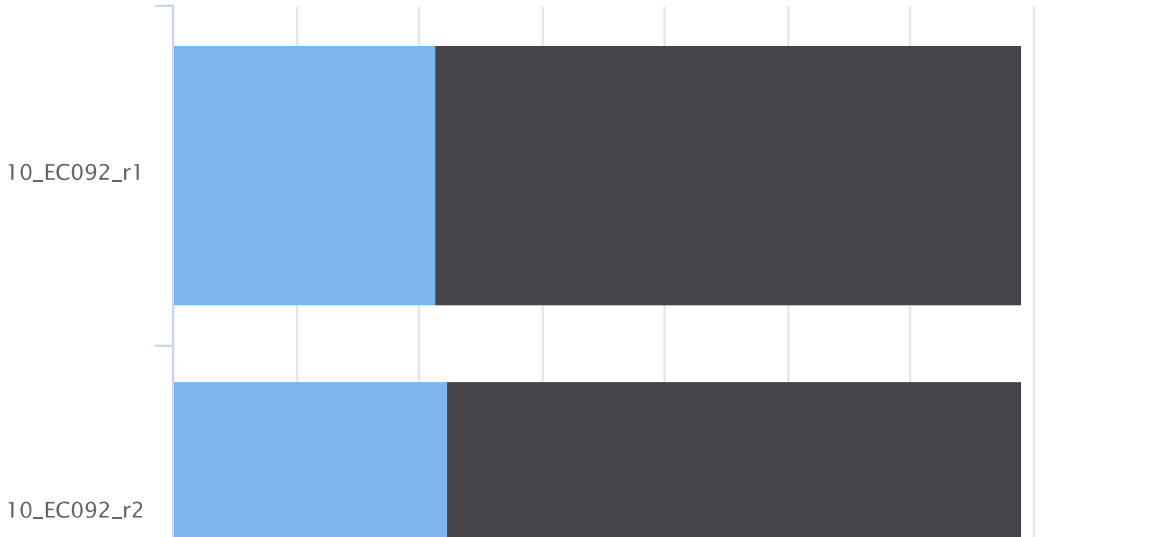
Number of reads

Percentages

--

## FastQC: Sequence Counts

 Export Plot



## Sequence Quality Histograms

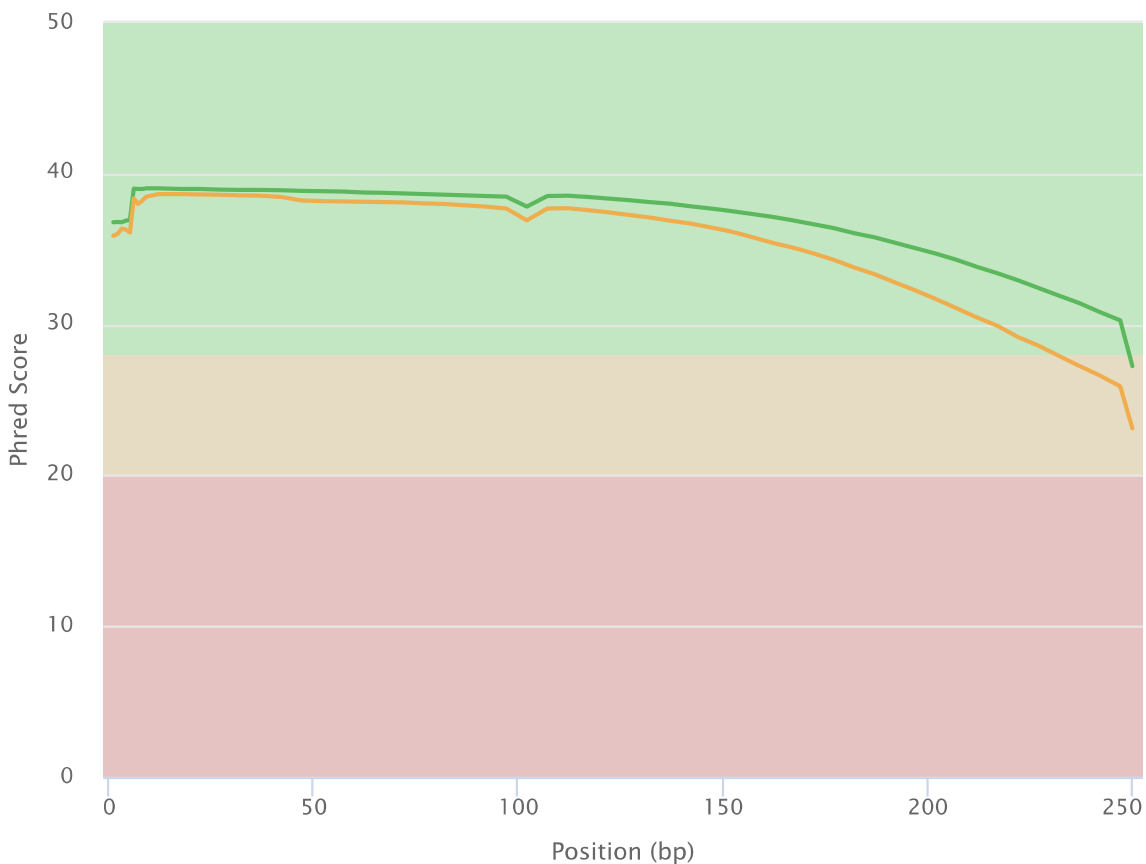
1 1

 Help

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

## FastQC: Mean Quality Scores

 Export Plot



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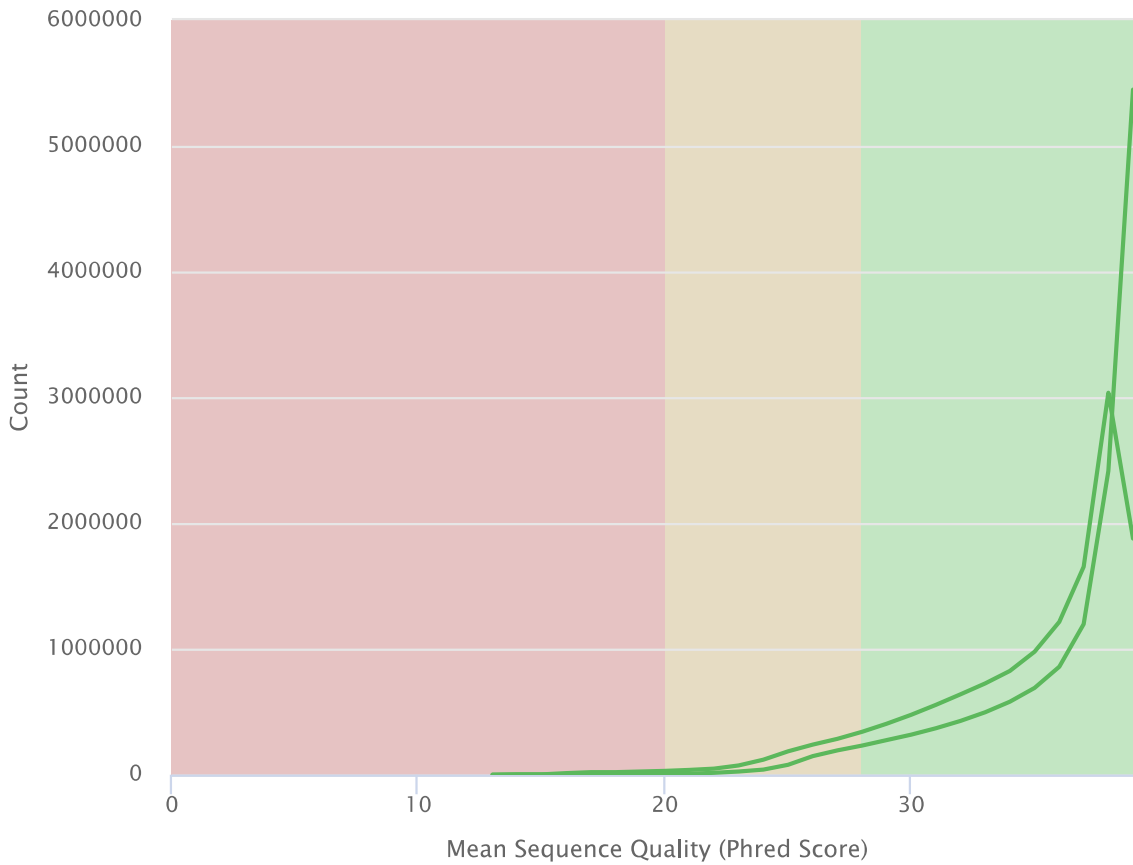
## Per Sequence Quality Scores

2

 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 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: -

[Export Plot](#)

%G: -

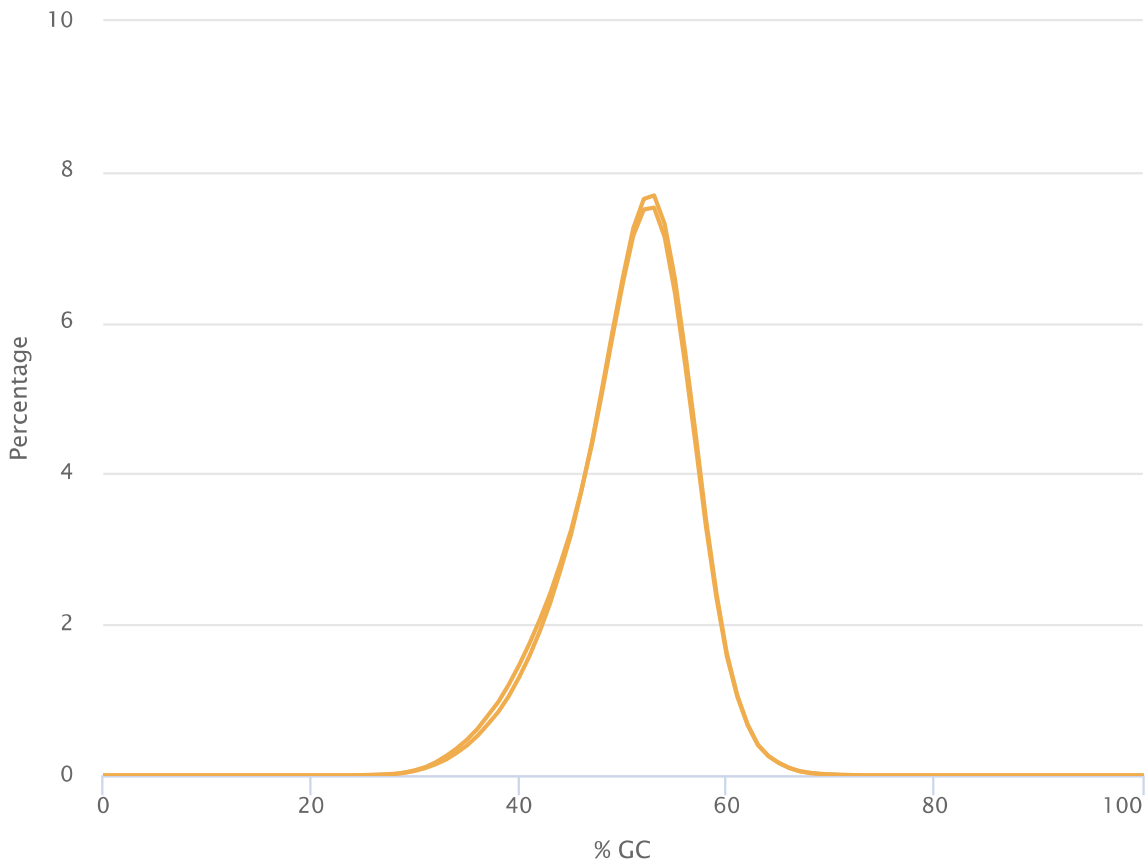


Percentages

Counts

### FastQC: Per Sequence GC Content

Export Plot



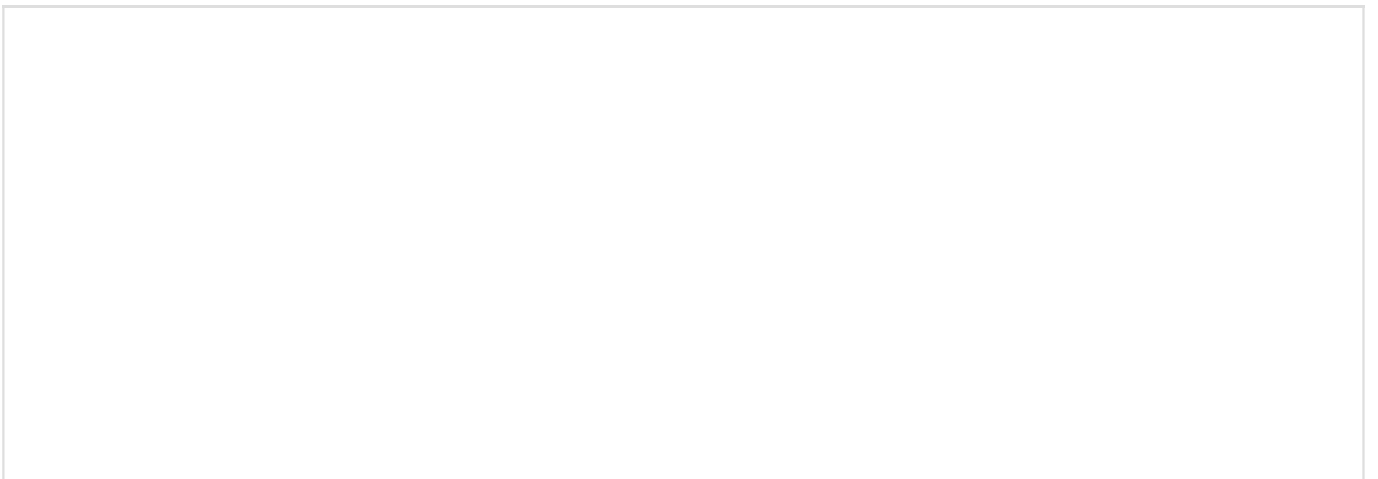
Created with MultiQC

## Per Base N Content

2

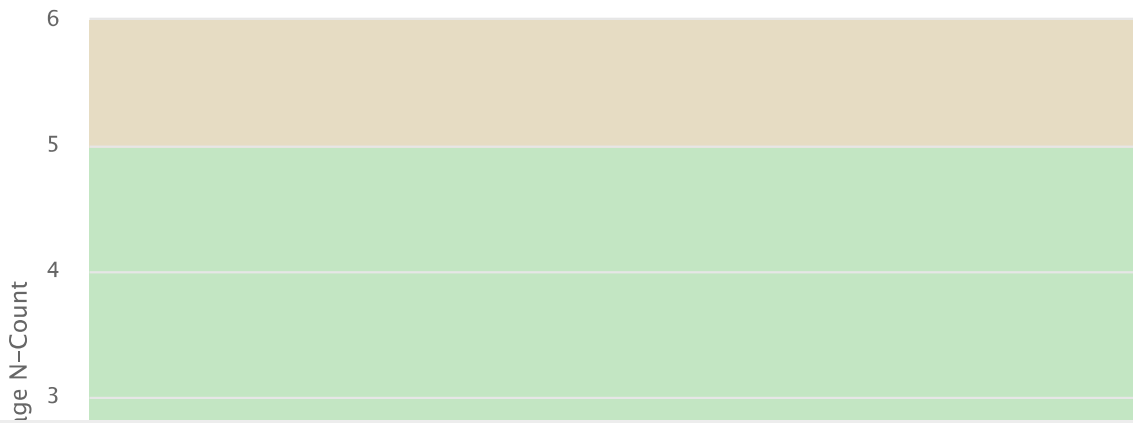
Help

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



## FastQC: Per Base N Content

 Export Plot



## Sequence Length Distribution

2

All samples have sequences of a single length (251bp).

## Sequence Duplication Levels

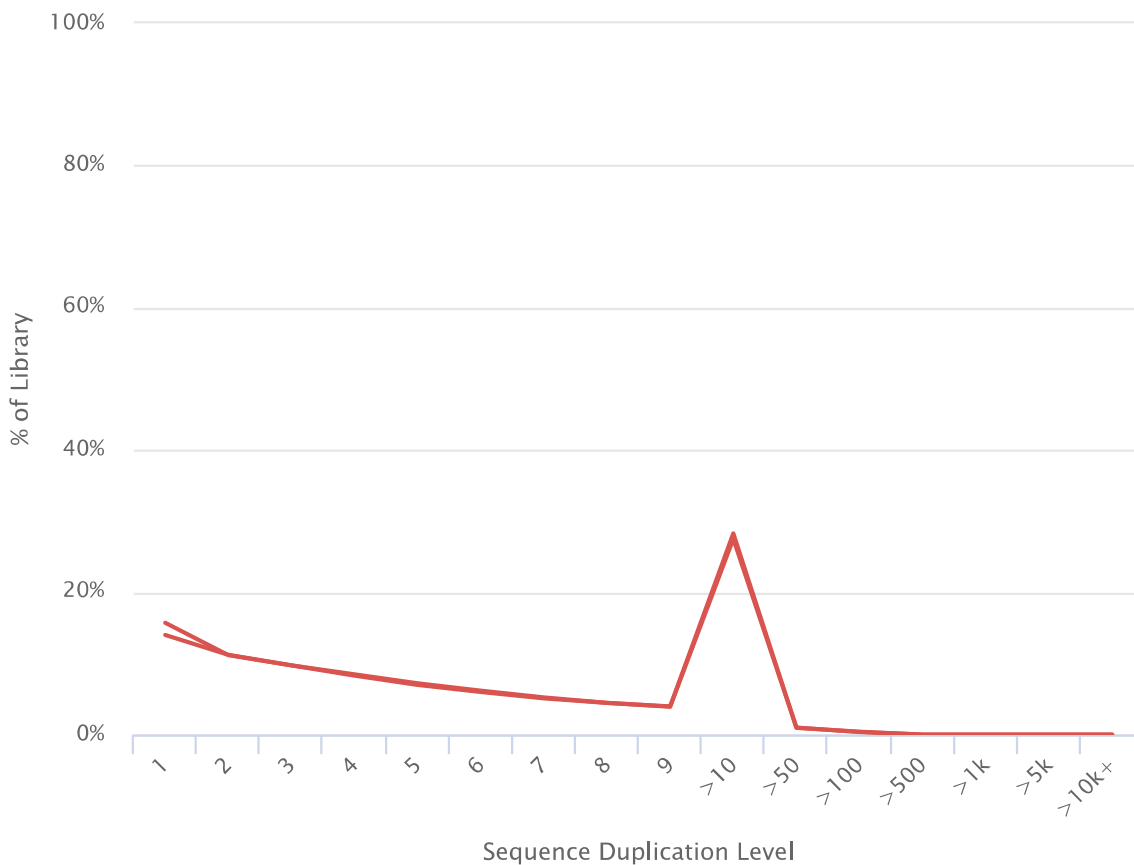
0 2

 Help

The relative level of duplication found for every sequence.

## FastQC: Sequence Duplication Levels

 Export Plot



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# Overrepresented sequences

2

[Help](#)

The total amount of overrepresented sequences found in each library.

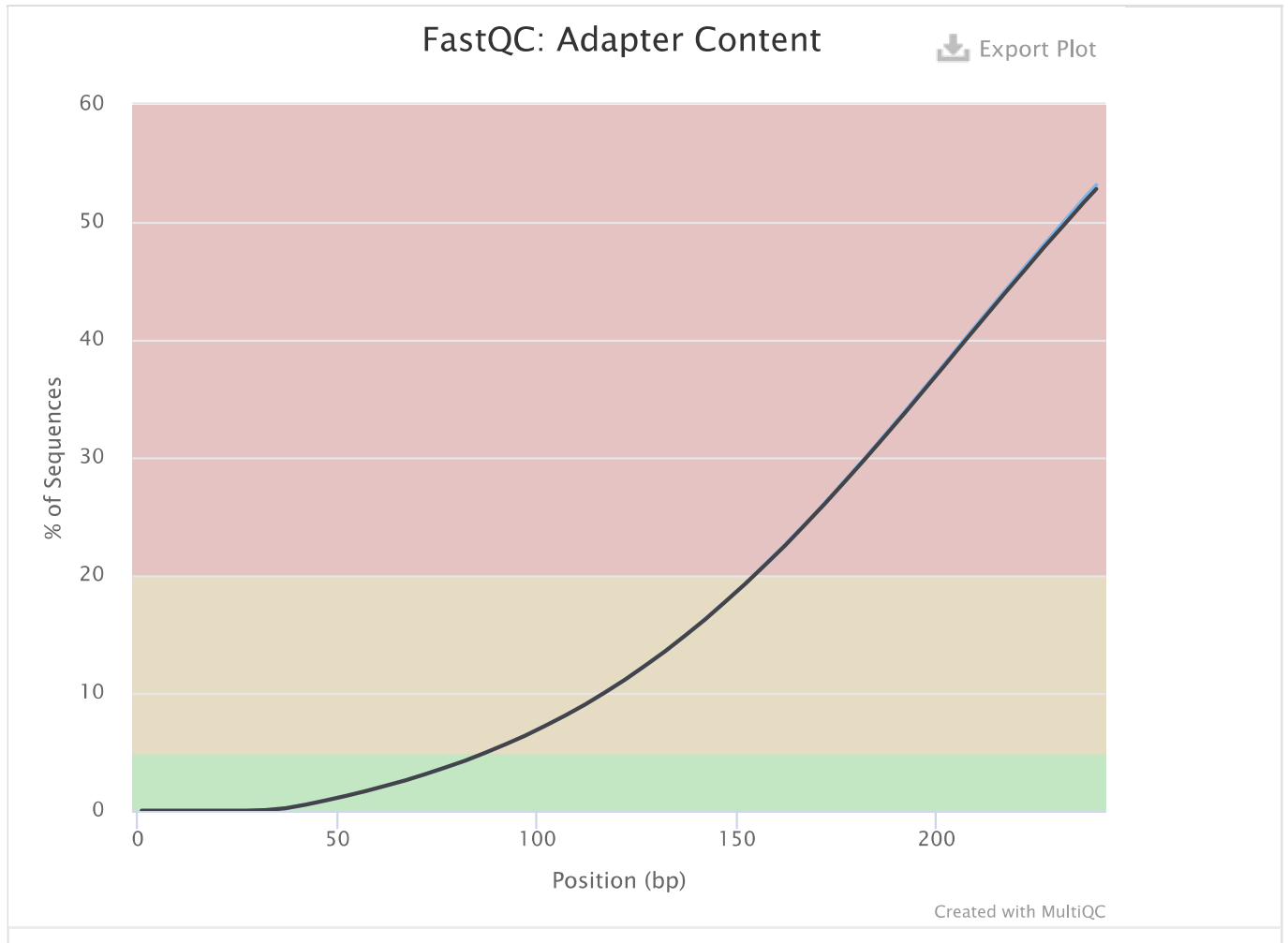
2 samples had less than 1% of reads made up of overrepresented sequences

# Adapter Content

0 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).

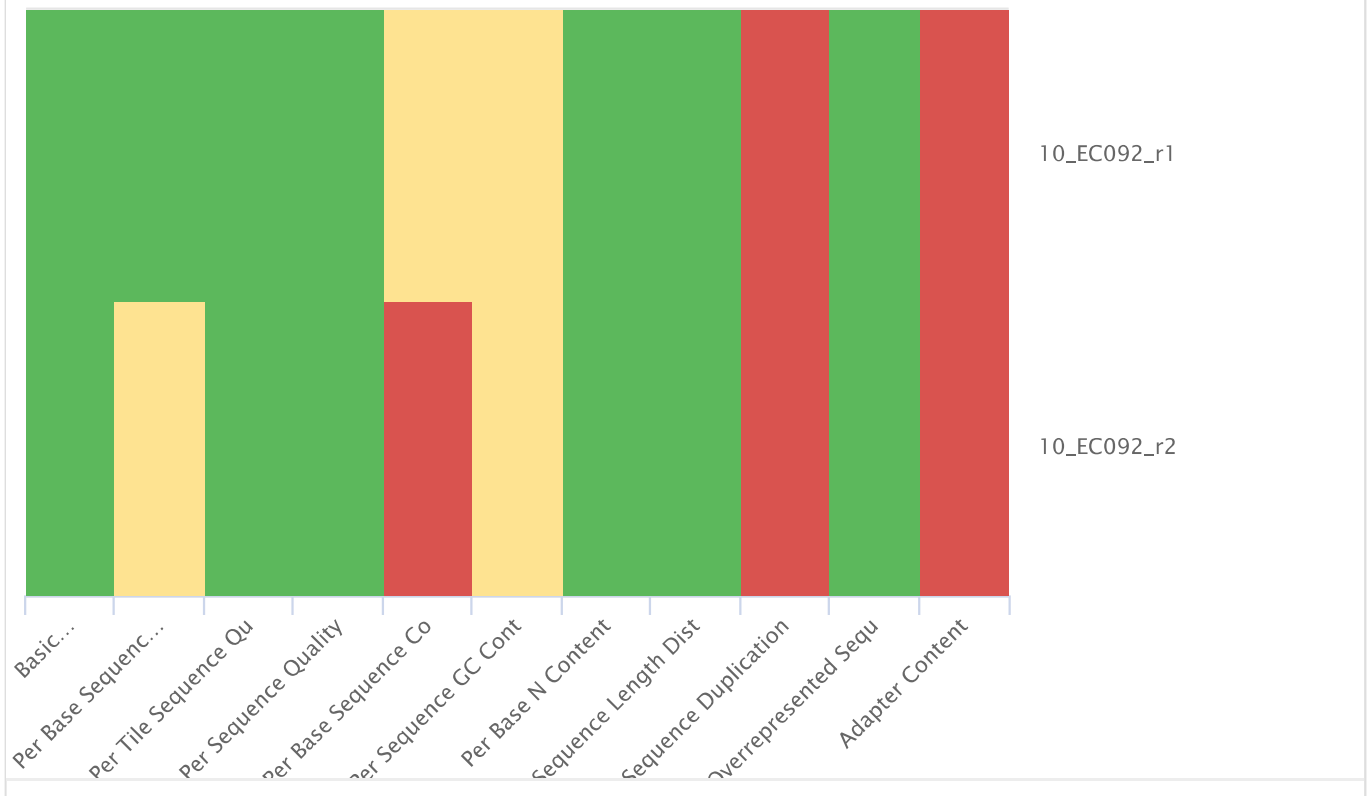
Sort by highlight

Min: 0

Max: 1

## FastQC: Status Checks

 Export Plot



**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>).



SciLifeLab

<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/>).