8/13/2021 MultiQC Report

Multi⊕C



(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	Ⅲ Configure Columns	⊪ Plot	Showing $^2/_2$ rows and $^3/_5$ columns.			
Sample Name		% Dups	% GC	M Seqs		
SRR12740661_1						
SRR12740661_2						

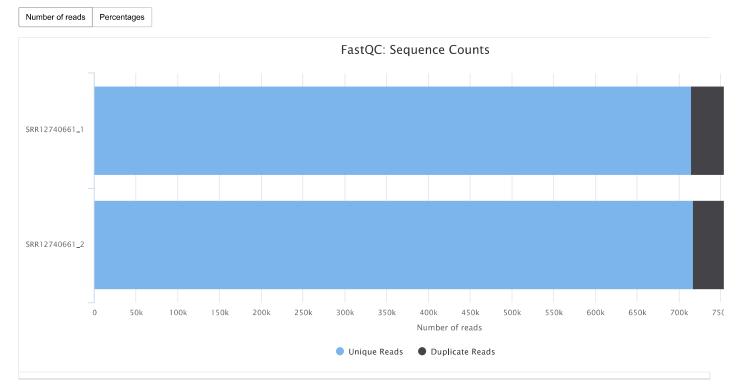
FastQC

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

9 Help

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



Sequence Quality Histograms

6 Help

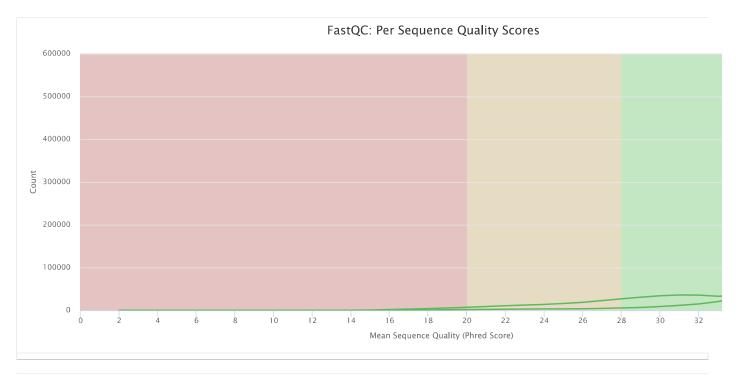
The mean quality value across each base position in the read.



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

@ Help

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

• Rollover for sample name

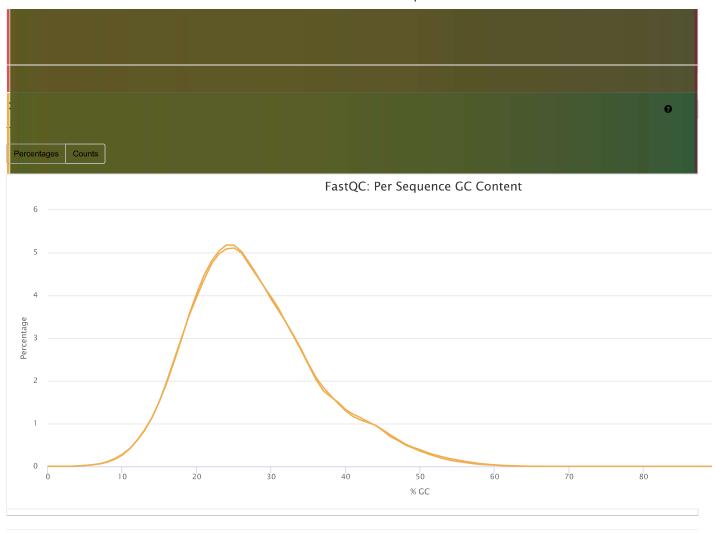
Position: - %T: -

%T: - <u>%</u>C: -

%G: -

%A: -

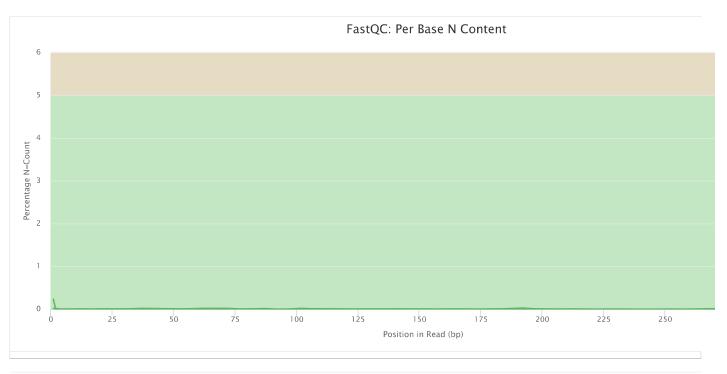
♣ Export Plot



Per Base N Content

2

The percentage of base calls at each position for which an $\,{\,{\rm N}\,}$ was called.

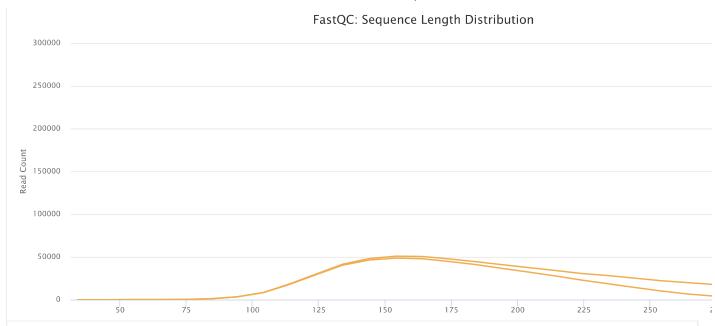


Sequence Length Distribution 0 2

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)

9 Help

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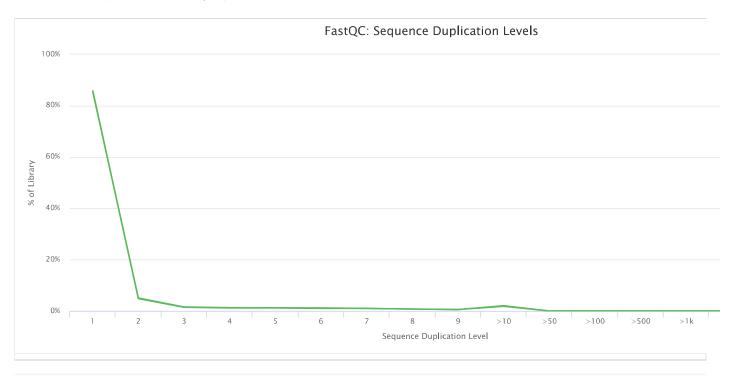


Sequence Duplication Levels

2



The relative level of duplication found for every sequence.



Overrepresented sequences

2



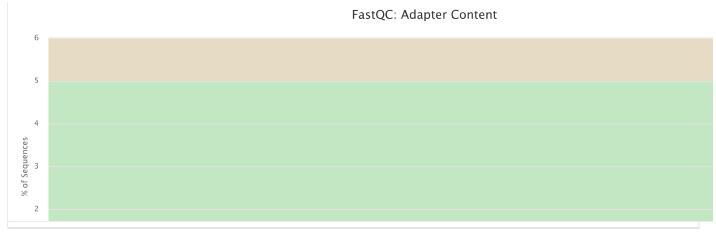
The total amount of overrepresented sequences found in each library.

 $2\ \text{samples}$ had less than 1% of reads made up of overrepresented sequences

Adapter Content

9 Help

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



Status Checks **9** Help Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red). Min: 0 ↓ Sort by highlight FastQC: Status Checks Basic Statistics Per Base Per Sequence Quality Per Base Per Sequence GC Per Base N Sequence Length Sequence Duplication Overrepresented Adapter Conter Sequence Co Sequence Qu Cont Content Dist Section Name

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

SciLifeLab

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

This report uses <u>HighCharts (http://www.highcharts.com/)</u>, <u>jQuery (https://jguery.com/)</u>, <u>jQuery UI (https://jgueryui.com/</u>), <u>Bootstrap (http://getbootstrap.com/</u>). <u>FileSaver.js (https://github.com/eligrey/FileSaver.js)</u> and <u>clipboard.js (https://clipboard.js (https://clipboard.j</u>