(http://multiqc.info)

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

Report generated on 2022-09-19, 16:46 based on data in: `/scratch3/users/katiel/Clinton/CRE_study_August_2022/work/28/d26686a6cedde5db885b4459187fa5`

General Statistics

Copy table | Configure Columns | Plot | Showing $^{46}/_{46}$ rows and $^{3}/_{5}$ columns.

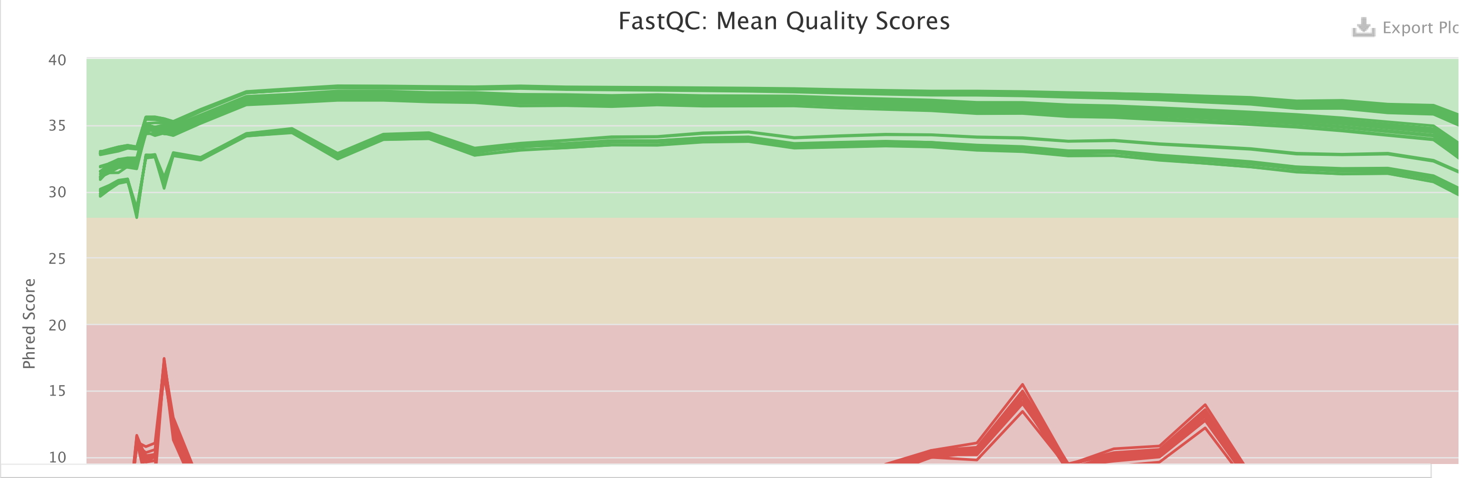
Sample Name	% Dups	% GC	M Seqs
G-10_S6_L001_R2_001			
G-11_S7_L001_R1_001			
G-11_S7_L001_R2_001			
G-13_S8_L001_R1_001			
G-13_S8_L001_R2_001			
G-14_S9_L001_R1_001			
G-14_S9_L001_R2_001			
G-15_S10_L001_R1_001			
G-15_S10_L001_R2_001			
G-16_S11_L001_R1_001			
G-16_S11_L001_R2_001			
G-18_S1_L001_R1_001			
G-18_S1_L001_R2_001			
G-19_S2_L001_R1_001			

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.

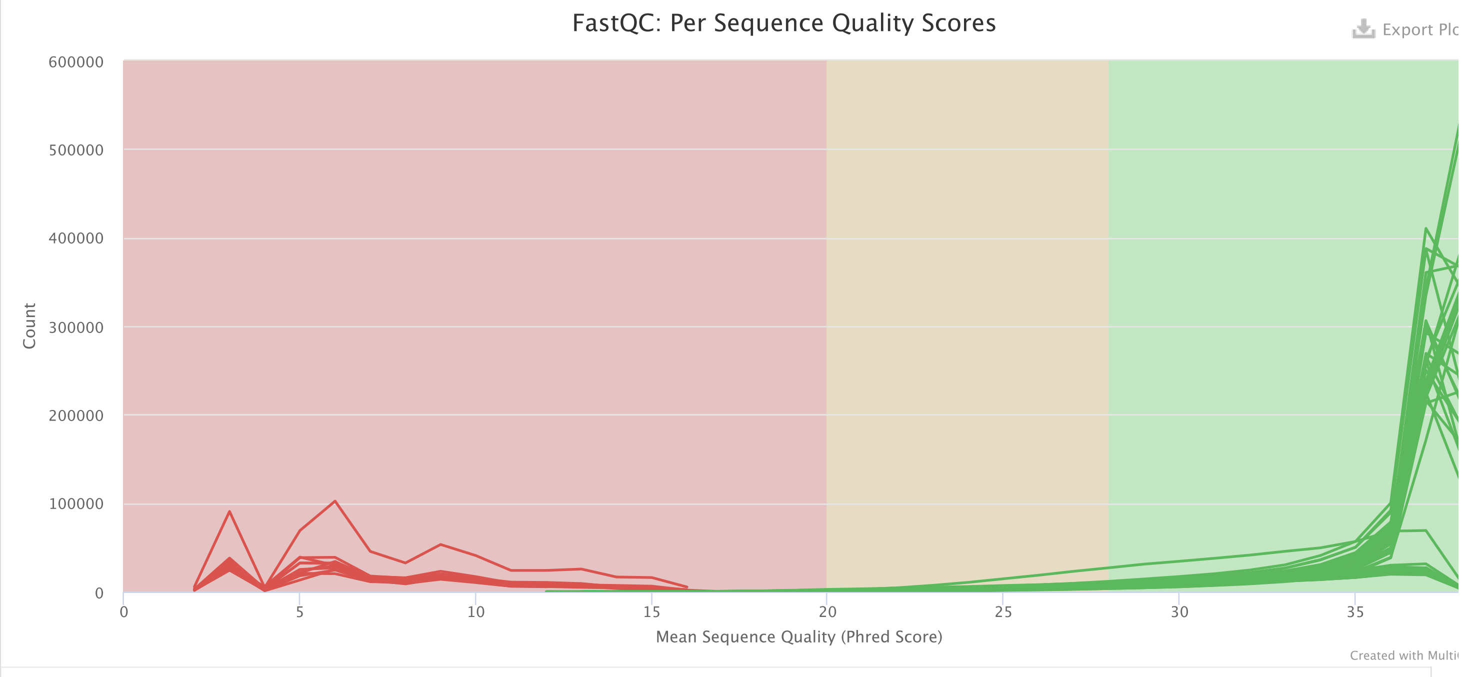
Sequence Quality Histograms 35 011

The mean quality value across each base position in the read. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/2%20Per%20Base%20Sequence%20Quality.html).



Per Sequence Quality Scores 35 011

The number of reads with average quality scores. Shows if a subset of reads has poor quality. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/3%20Per%20Sequence%20Quality%20Scores.html).



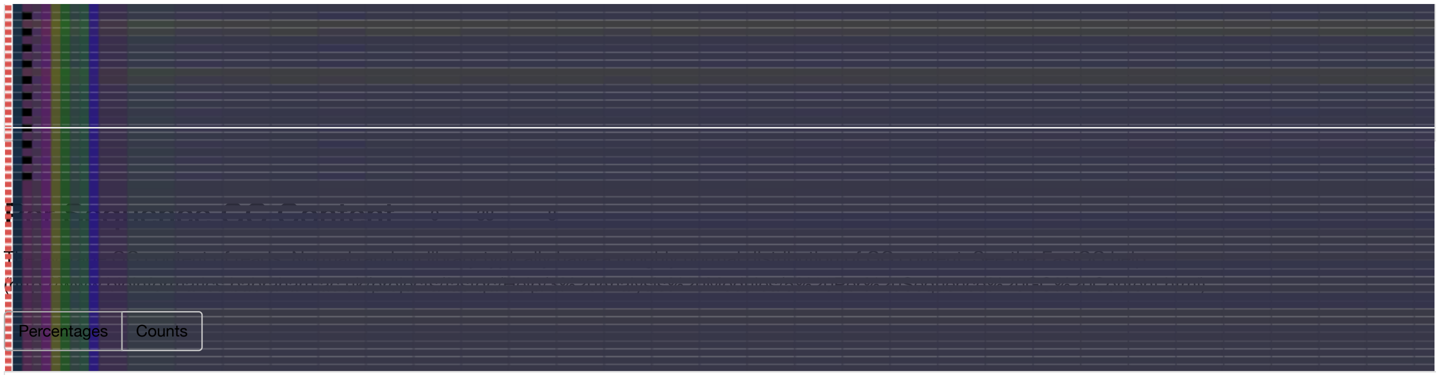
Per Base Sequence Content 0 46

The proportion of each base position for which each of the four normal DNA bases has been called. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/4%20Per%20Base%20Sequence%20Content.html).

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

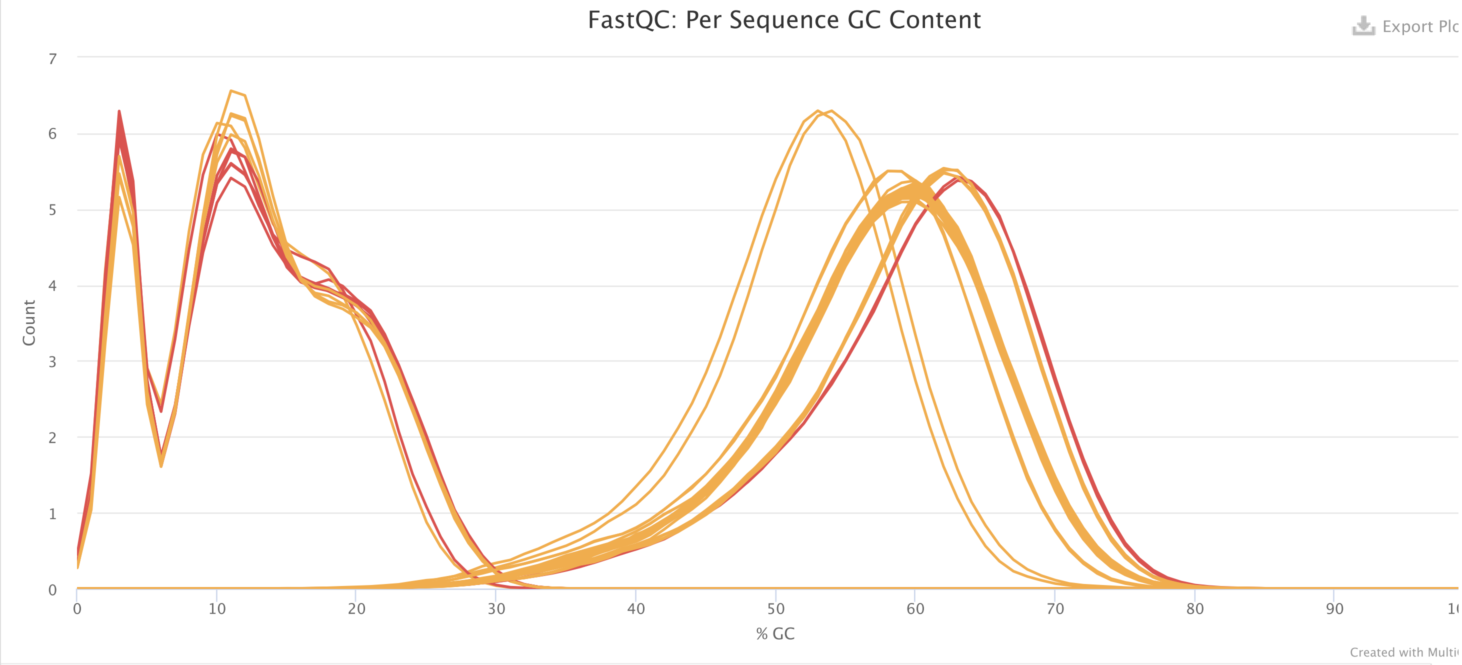
Rollover for sample name

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



Per Sequence GC Content

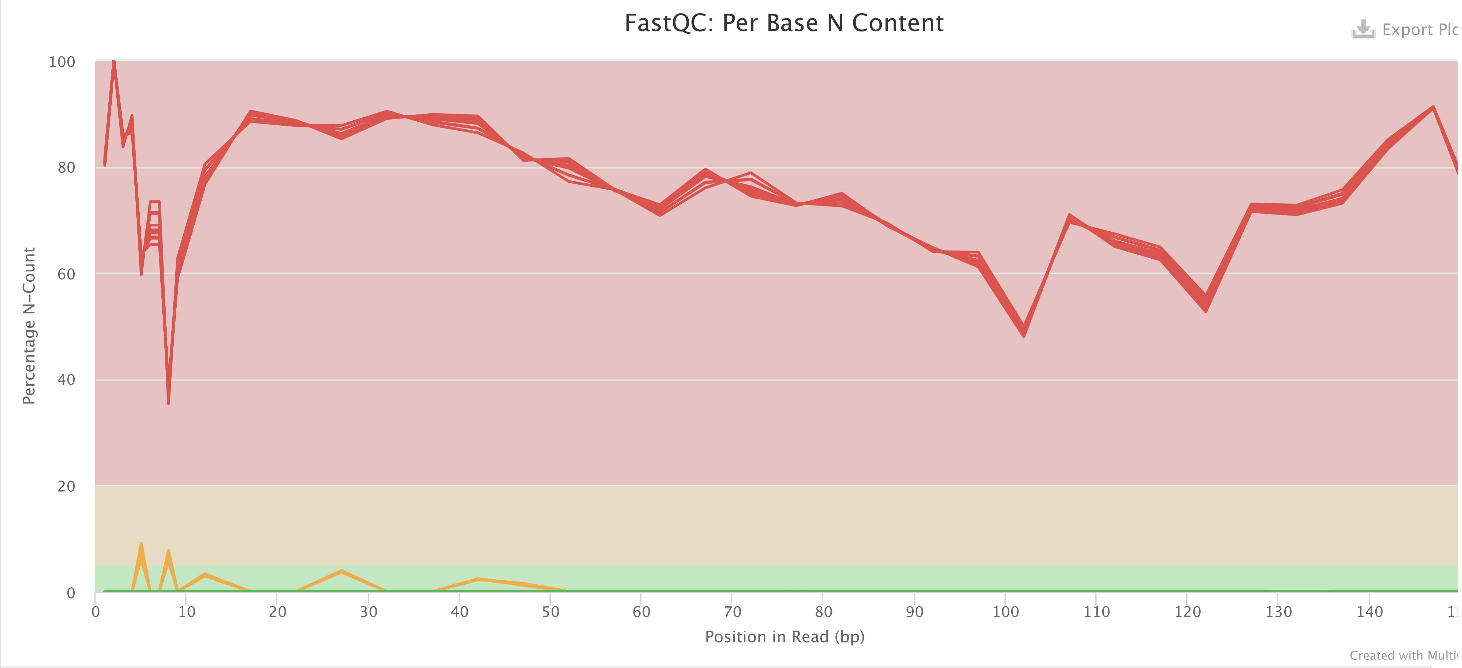
[illegible]



Per Base N Content

24 11 11

The percentage of base calls at each position for which an N was called. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/6%20Per%20Base%20N%20Content.html).

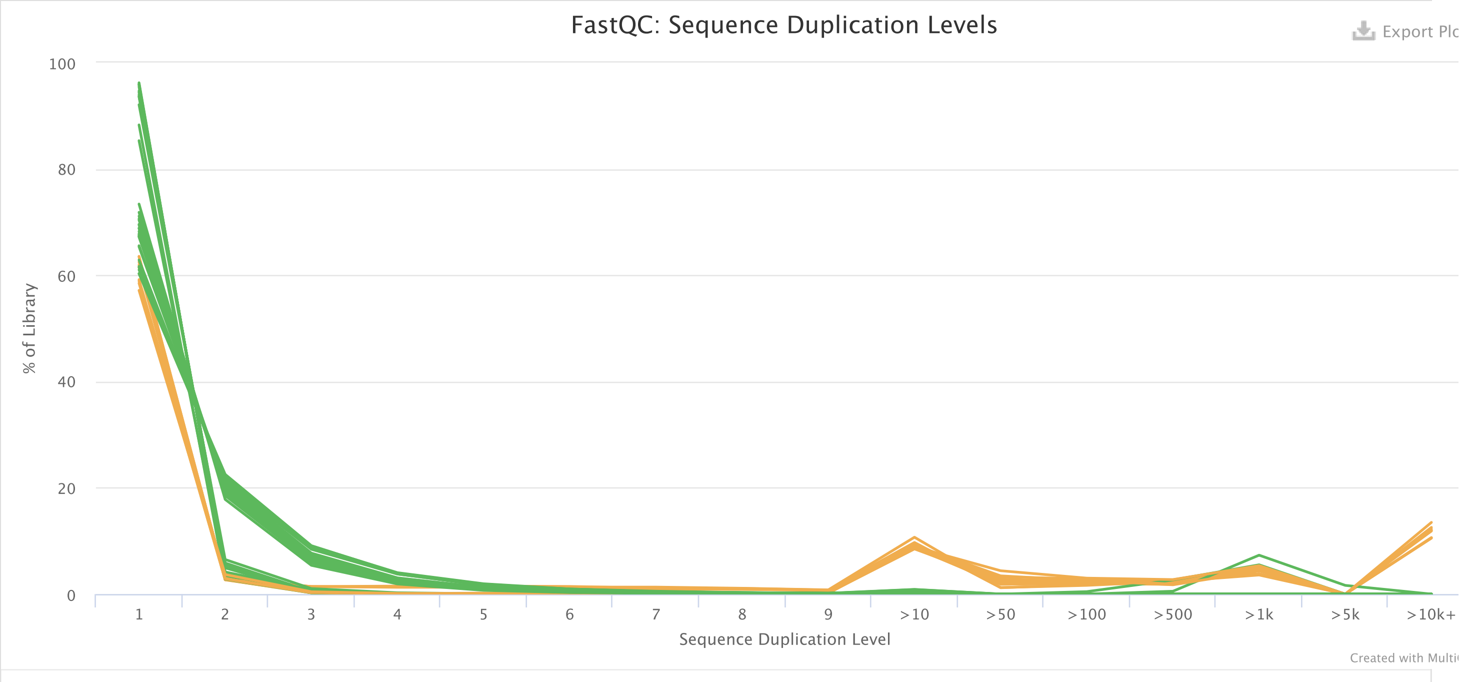


Sequence Length Distribution 46

All samples have sequences of a single length (151bp).

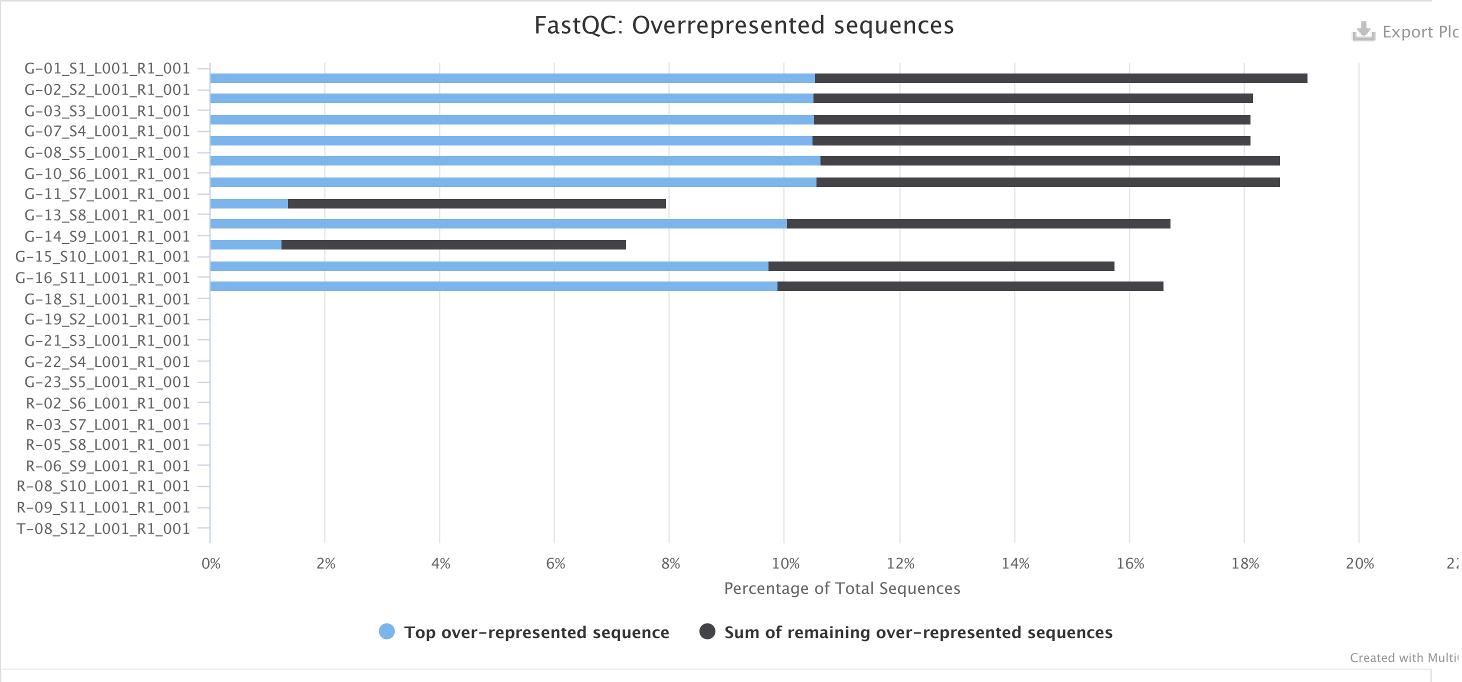
Sequence Duplication Levels 37 9

The relative level of duplication found for every sequence. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/8%20Duplicate%20Sequences.html).



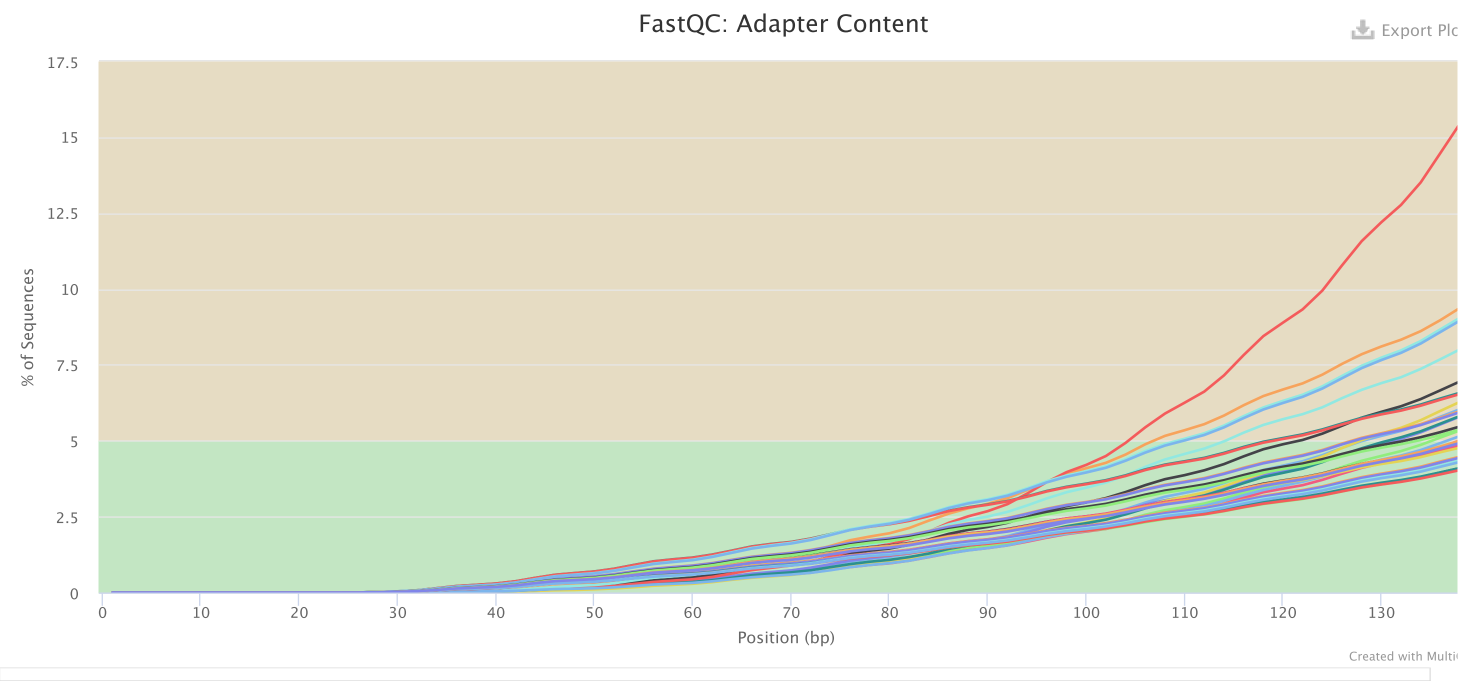
Overrepresented sequences 35 011

The total amount of overrepresented sequences found in each library. See the FastQC help for further information (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/9%20Overrepresented%20Sequences.html).



Adapter Content 27 18 ·

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position. See the FastQC help (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/10%20Adapter%20Content.html). Only samples with ≥ 0.1% adapter contamination are shown.



MultiQC v1.3 (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/).

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