MultiQC
v1.8

(http://multiqc.info)

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

Report generated on 2020-03-09, 23:32 based on data in: `/home/bioadmin/fastqc`

General Statistics

Copy table | Configure Columns | Plot | Showing $^{28}/_{28}$ rows and $^{3}/_{5}$ columns.

Sample Name	% Dups	% GC	M Seqs
SRR5054337			
SRR5054338			
SRR5054339			
SRR5054340			
SRR5054341			
SRR5054342			

Sample Name	% Dups	% GC	M Seqs
SRR5054343			
SRR5054344			
SRR5054345			
SRR5054346			
SRR5054347			
SRR5054348			
SRR5054349			
SRR5054350			
SRR5054351			
SRR5054352			
SRR5054353			
SRR5054354			

FastQC

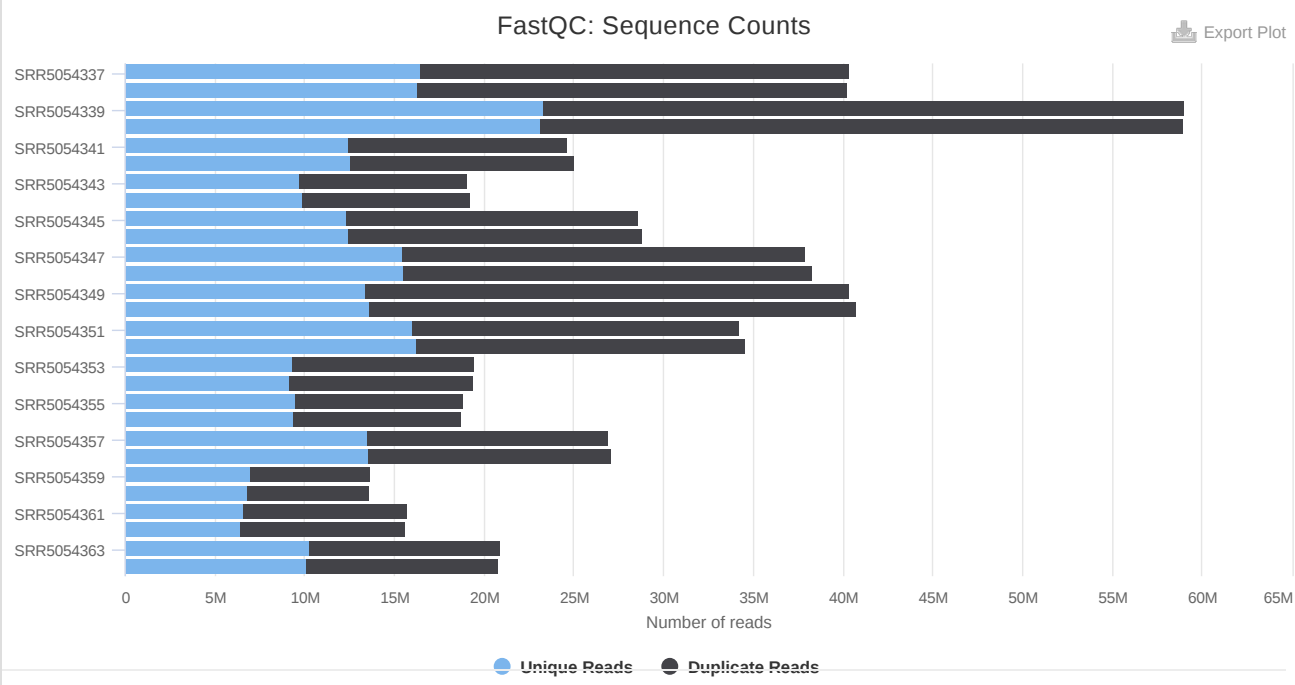
FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

Help

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

Number of reads | Percentages

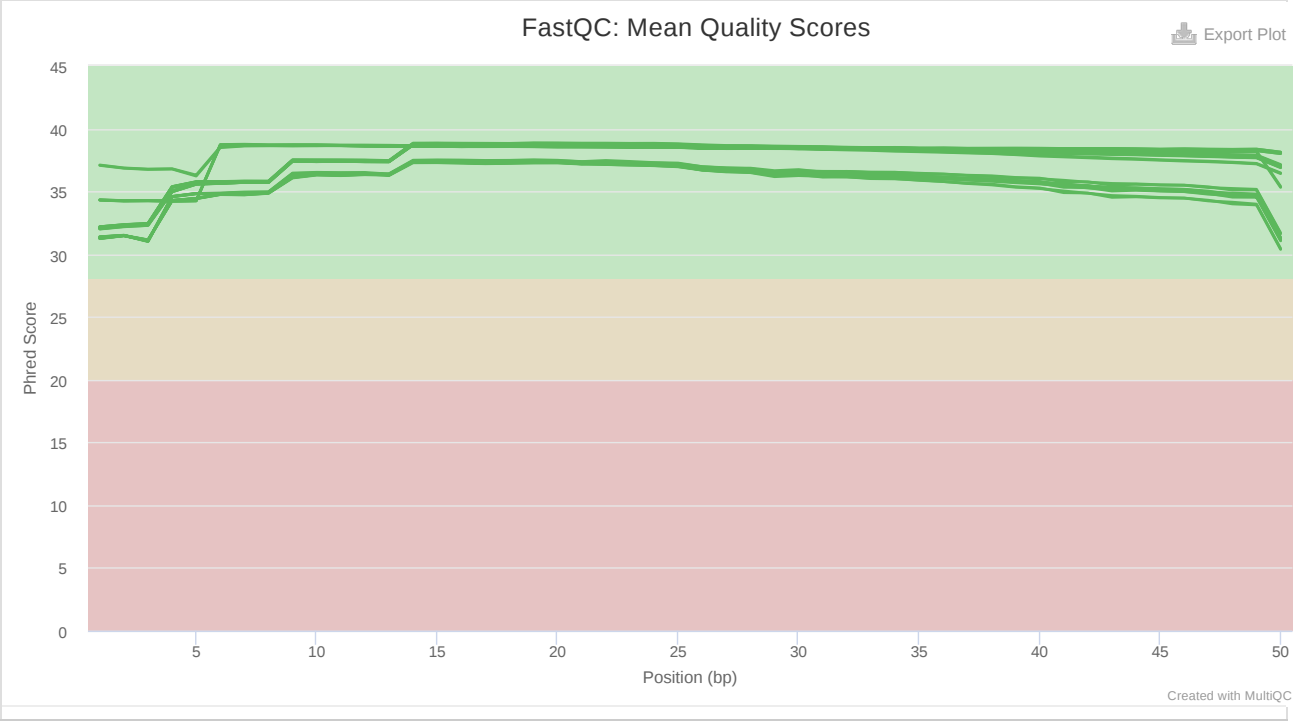


Sequence Quality Histograms 28

Help

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

Y-Limits: on

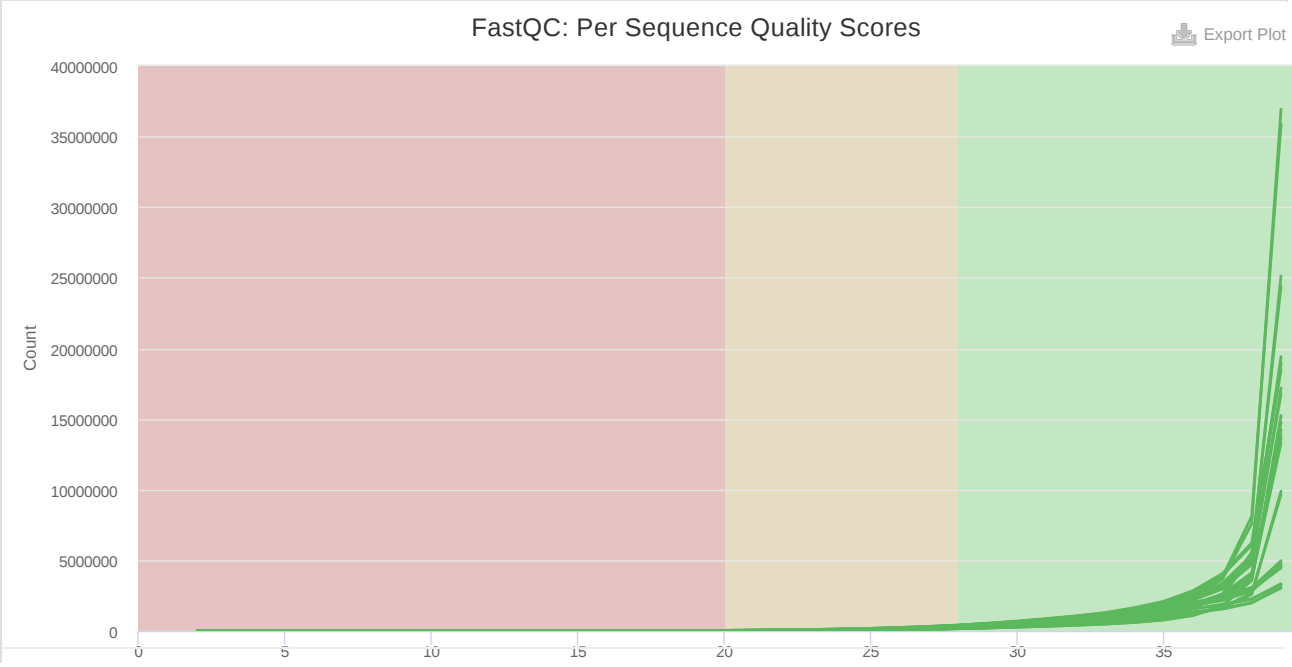


Per Sequence Quality Scores 28

Help

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

Y-Limits: on



Per Base Sequence Content 0 28

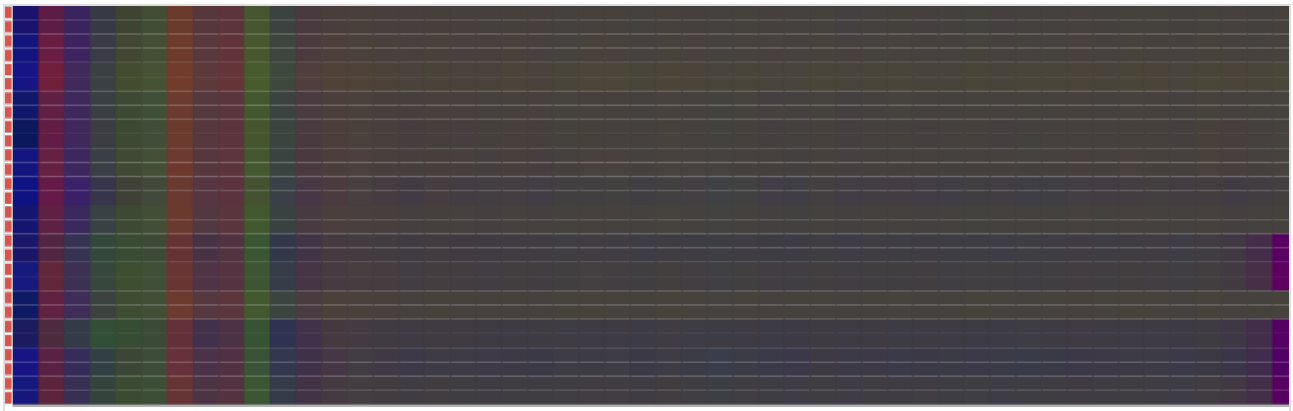
Help

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



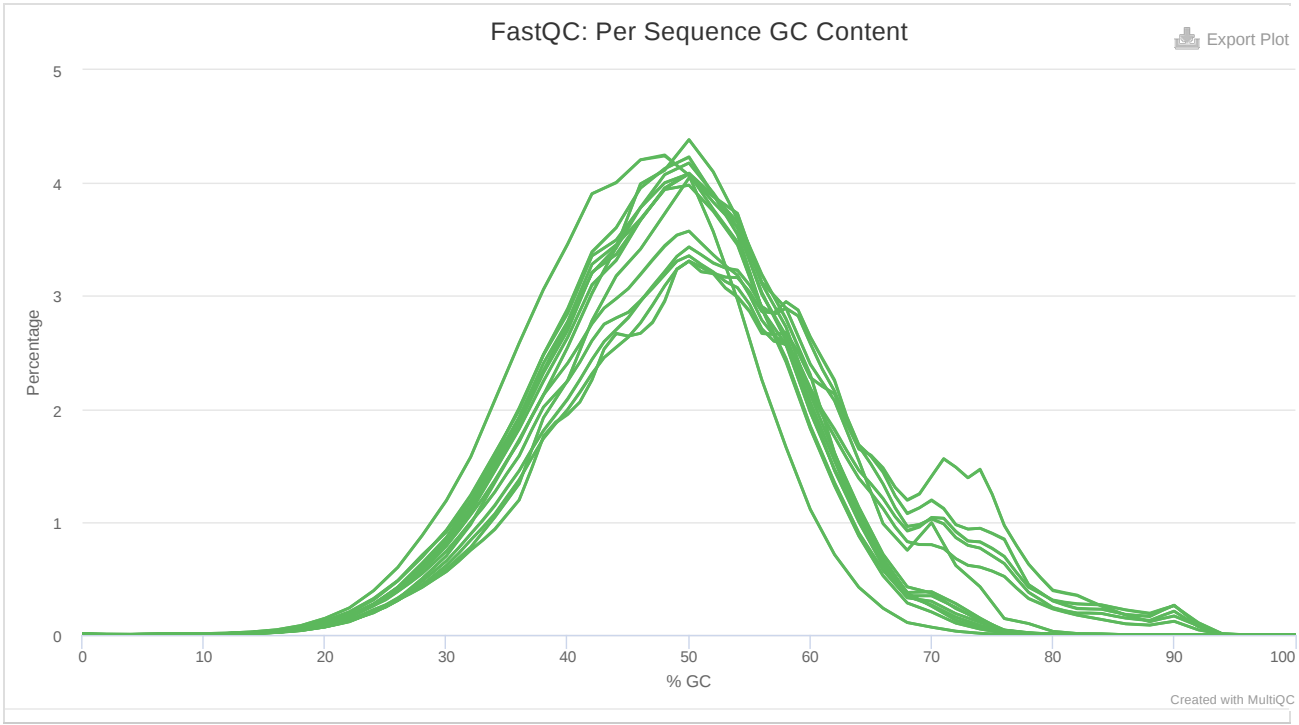
Per Sequence GC Content 28

Help

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

Y-Limits: on

Percentages | Counts

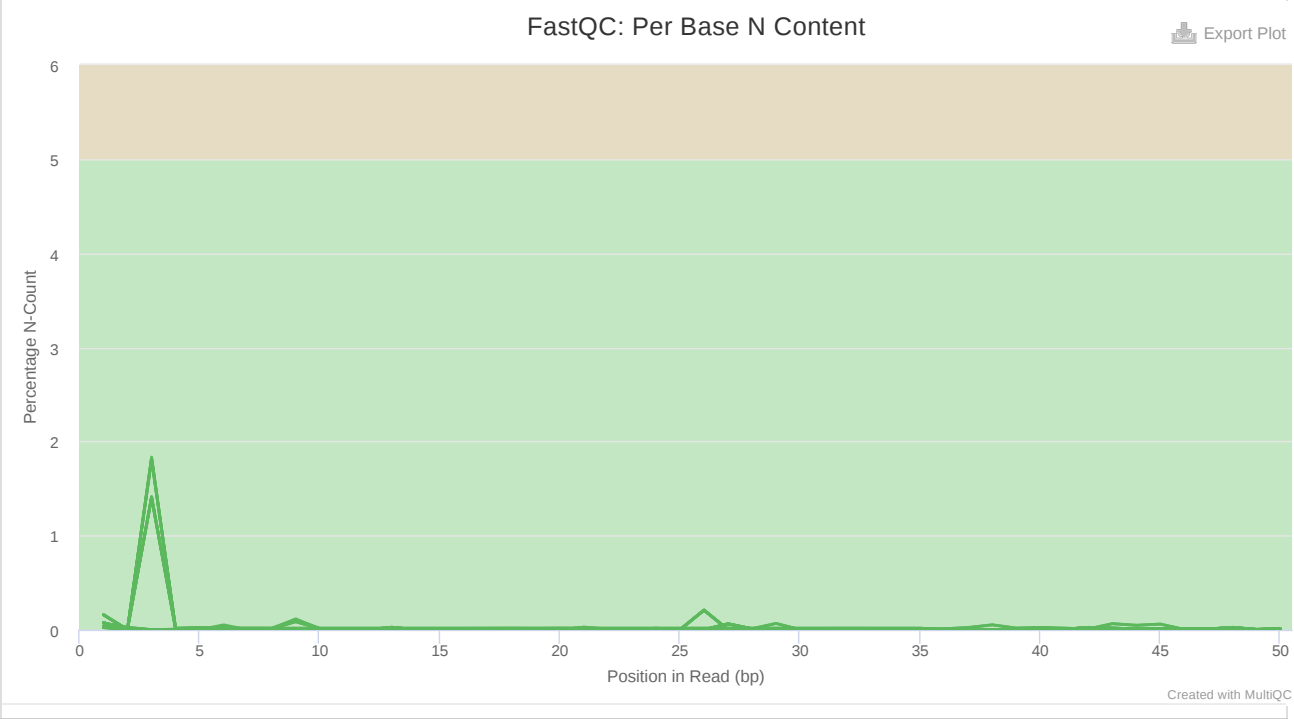


Per Base N Content 28

Help

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

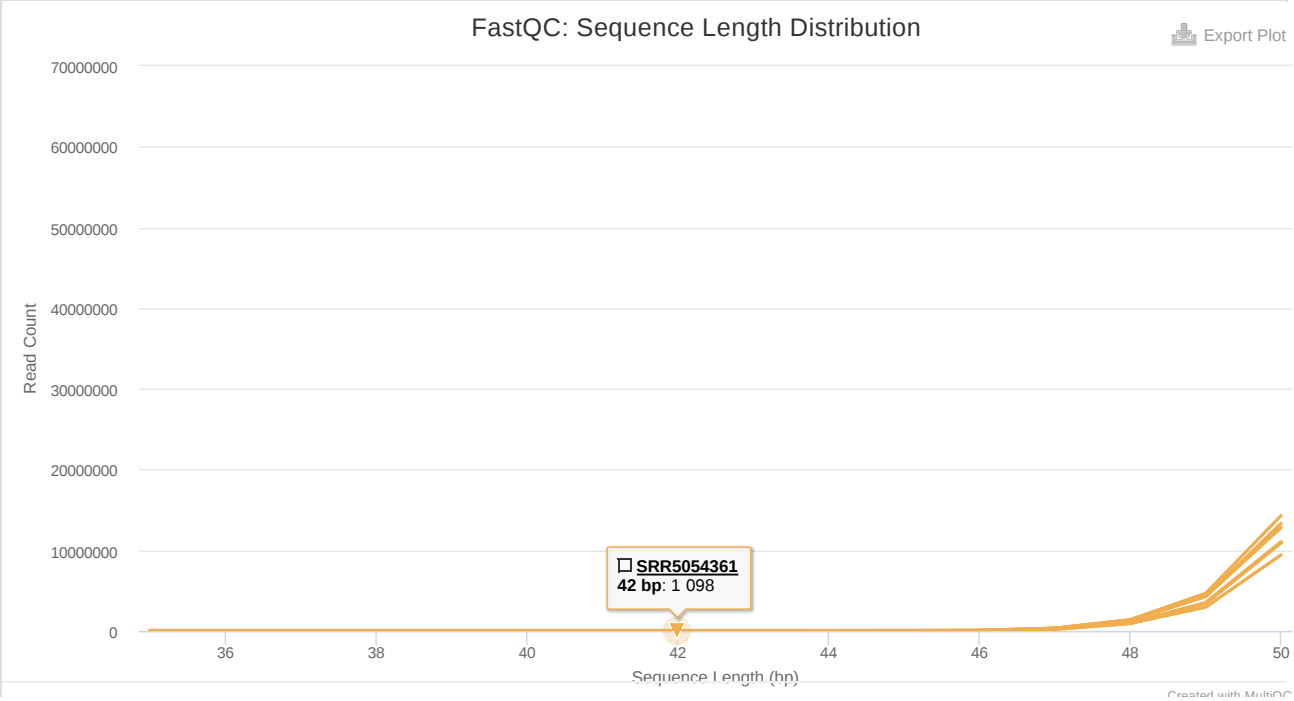
Y-Limits: on



Sequence Length Distribution 18 10

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)

Y-Limits: on

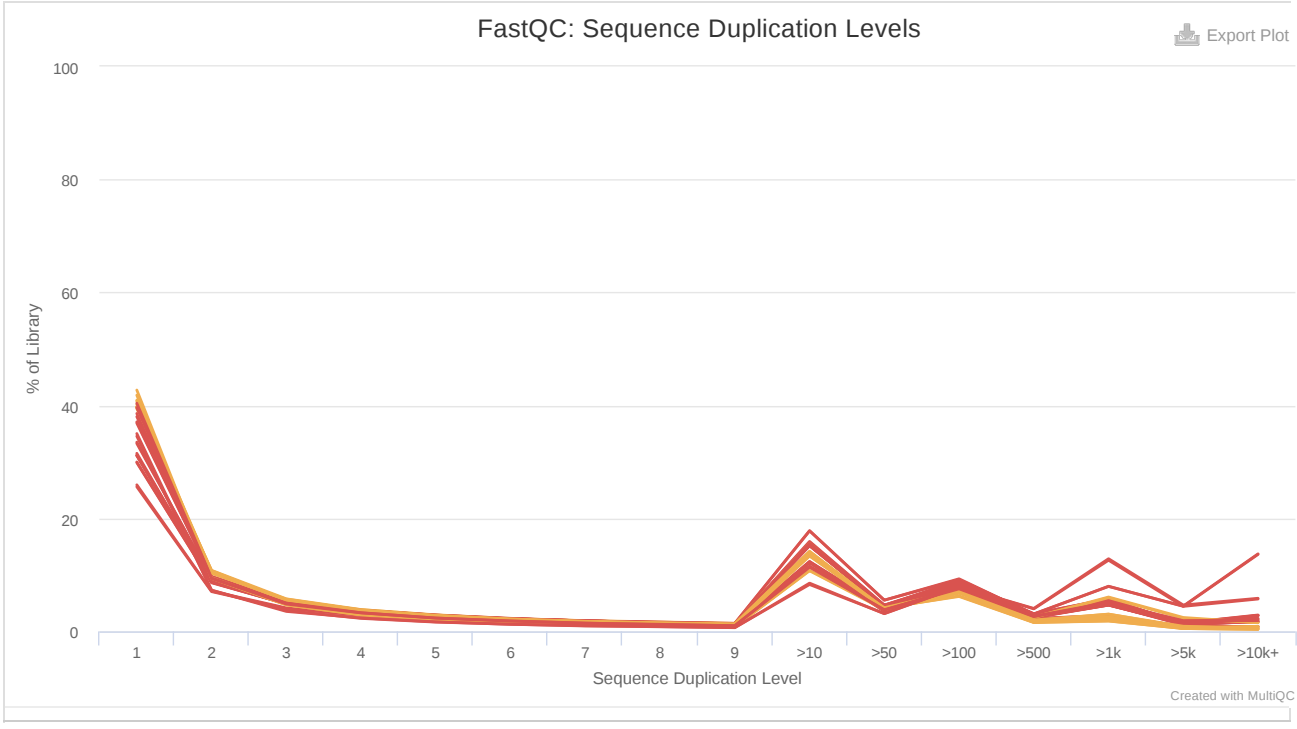


Sequence Duplication Levels 0 10 18

Help

The relative level of duplication found for every sequence.

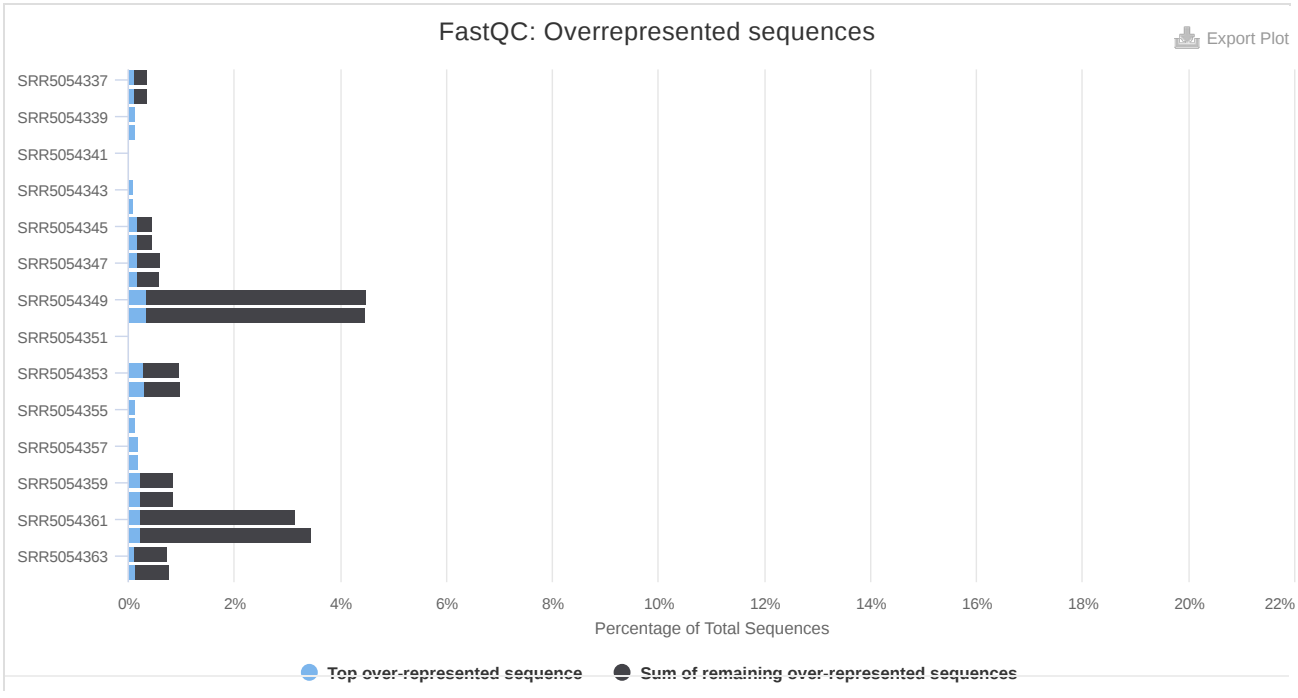
Y-Limits: on



Overrepresented sequences 4 24

Help

The total amount of overrepresented sequences found in each library.



Adapter Content 28

Help

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

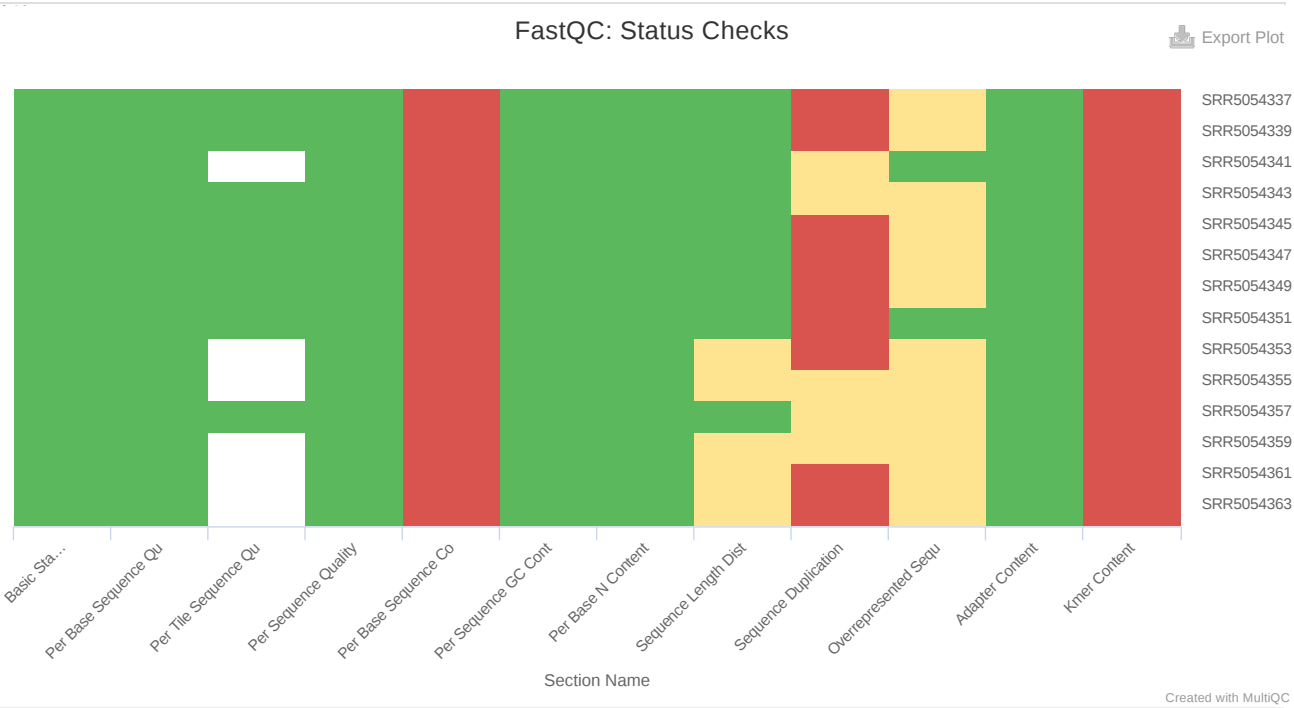
No samples found with any adapter contamination > 0.1%

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



MultiQC v1.8 (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/)