



General Stats
FastQC
Sequence Quality Histograms
Per Sequence Quality Scores
Per Base Sequence Content
Per Sequence GC Content
Per Base N Content
Sequence Length Distribution
Sequence Duplication Levels
Overrepresented sequences
Adapter Content



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

Report generated on 2023-03-24, 09:17 based on data in: /scratch3/users/katiel/Clinton/CRE_study_August_2022/work/90/2b2bafbae14eadbcb6e165699d8af

General Statistics

Copy table Configure Columns Plot Showing 48/48 rows and 3/5 columns.

Sample Name	% Dups	% GC	M Seqs
KLEB-CRE-TBH-0065_S9_L001_trimmed_R2			
KLEB-CRE-TBH-0066_S10_L001_trimmed_R1			
KLEB-CRE-TBH-0066_S10_L001_trimmed_R2			
KLEB-CRE-TBH-0075_S11_L001_trimmed_R1			
KLEB-CRE-TBH-0075_S11_L001_trimmed_R2			
KLEB-CRE-TBH-0077_S13_L001_trimmed_R1			
KLEB-CRE-TBH-0077_S13_L001_trimmed_R2			
KLEB-CRE-TBH-0080_S23_L001_trimmed_R1			
KLEB-CRE-TBH-0080_S23_L001_trimmed_R2			
PROV-CRE-TBH-0058_S8_L001_trimmed_R1			
PROV-CRE-TBH-0058_S8_L001_trimmed_R2			
SERR-CRE-N05-0001_S22_L001_trimmed_R1			
SERR-CRE-N05-0001_S22_L001_trimmed_R2			
Undetermined_S0_L001_trimmed_R1			
Undetermined_S0_L001_trimmed_R2			



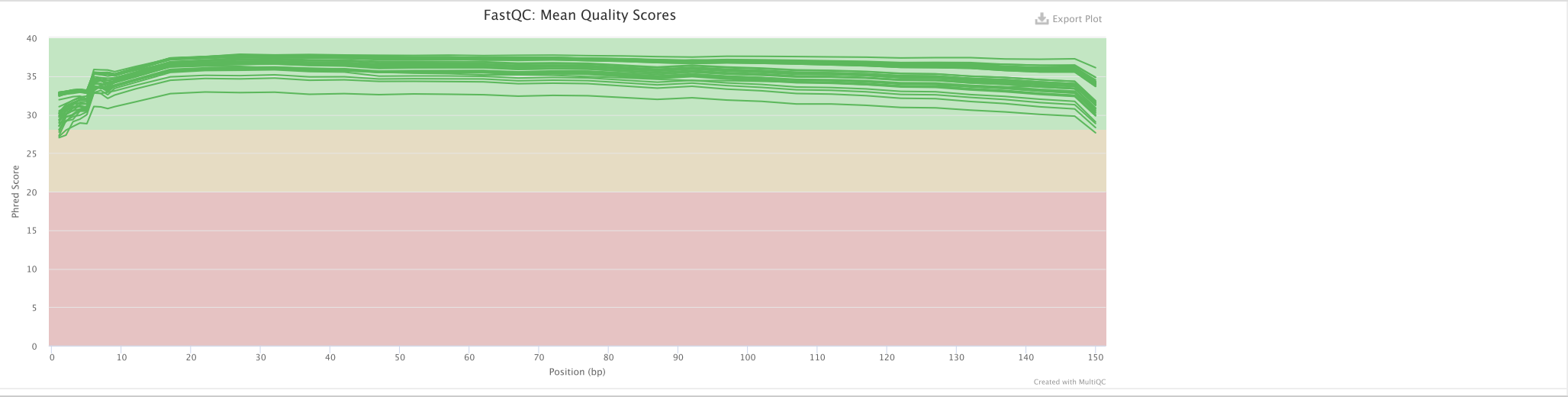
FastQC

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 Quality Histograms 48

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>).

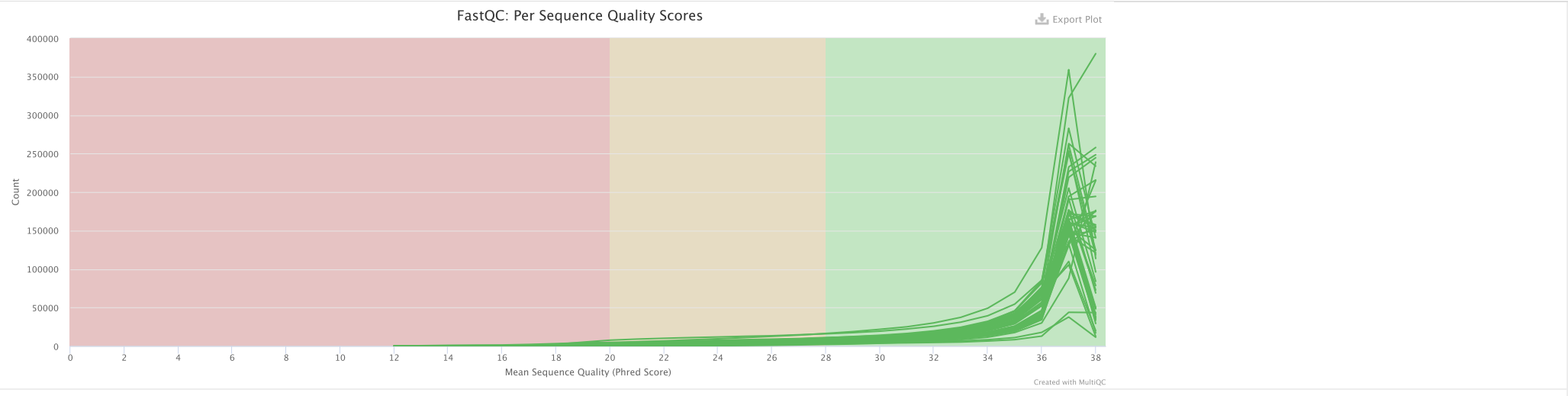
Y-Limits:



Per Sequence Quality Scores 48

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>).

Y-Limits:



Per Base Sequence Content 0 48

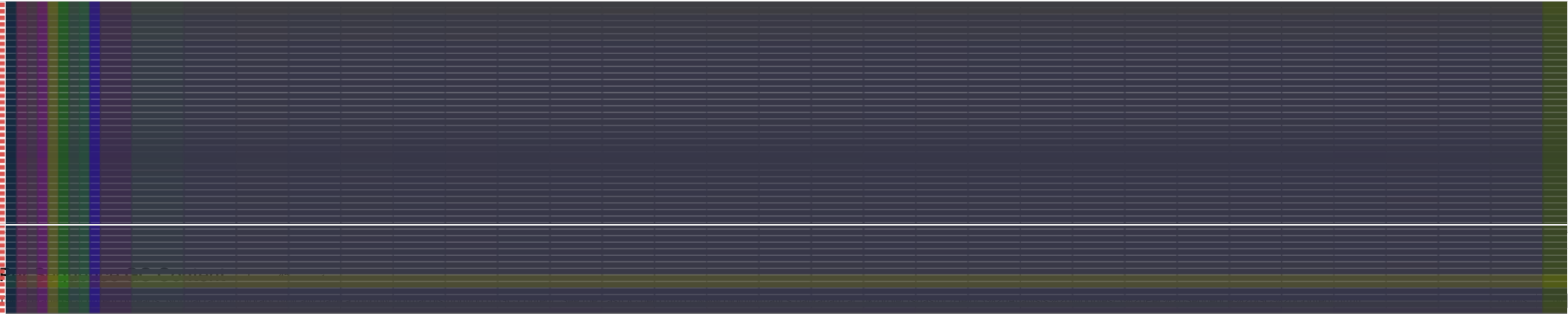
The proportion of each base position for which each of the four normal DNA bases has been called. See the FastQC help (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/4%20Per%20Base%20Sequence%20Content.html>).

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

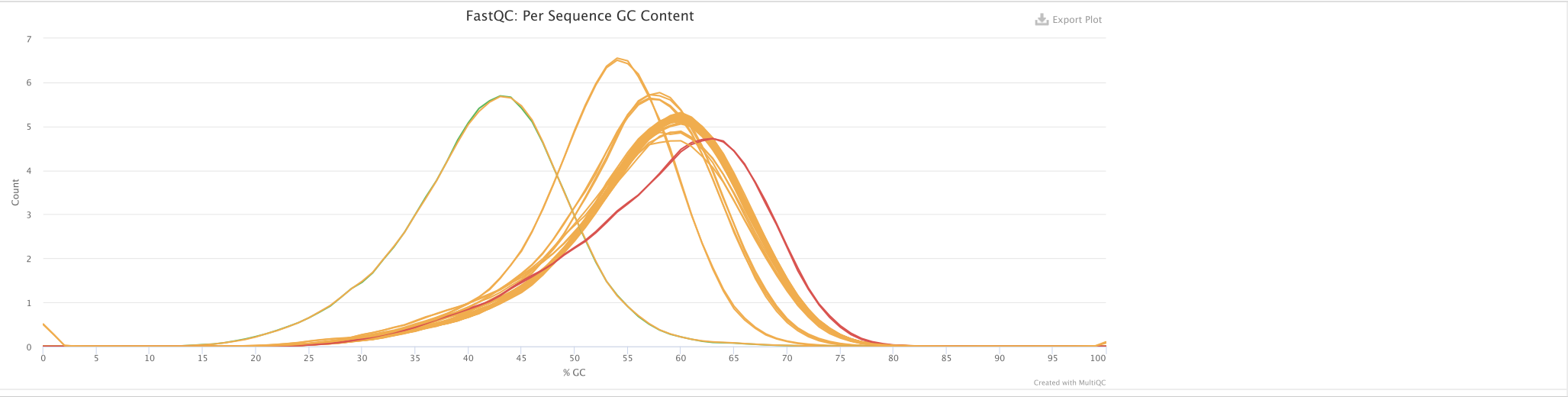
Rollover for sample name

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

Export Plot



Counts

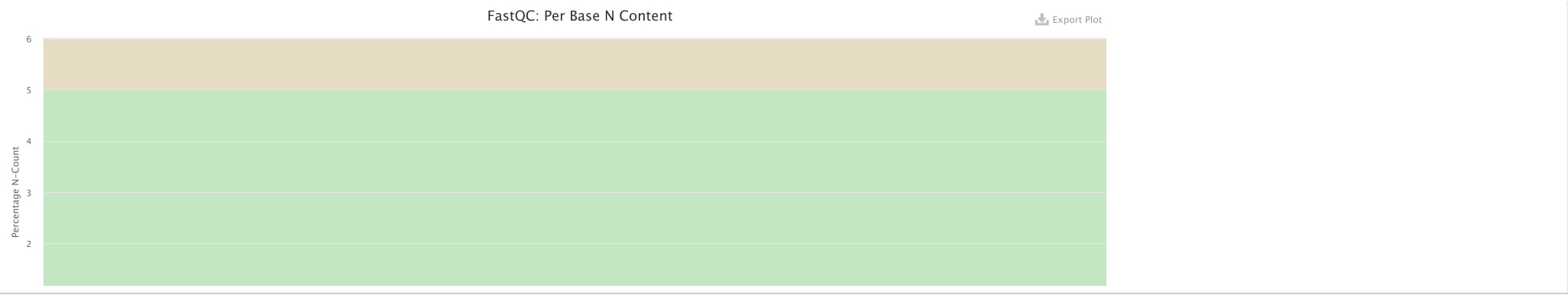


Per Base N Content 48

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>).

Y-Limits: on

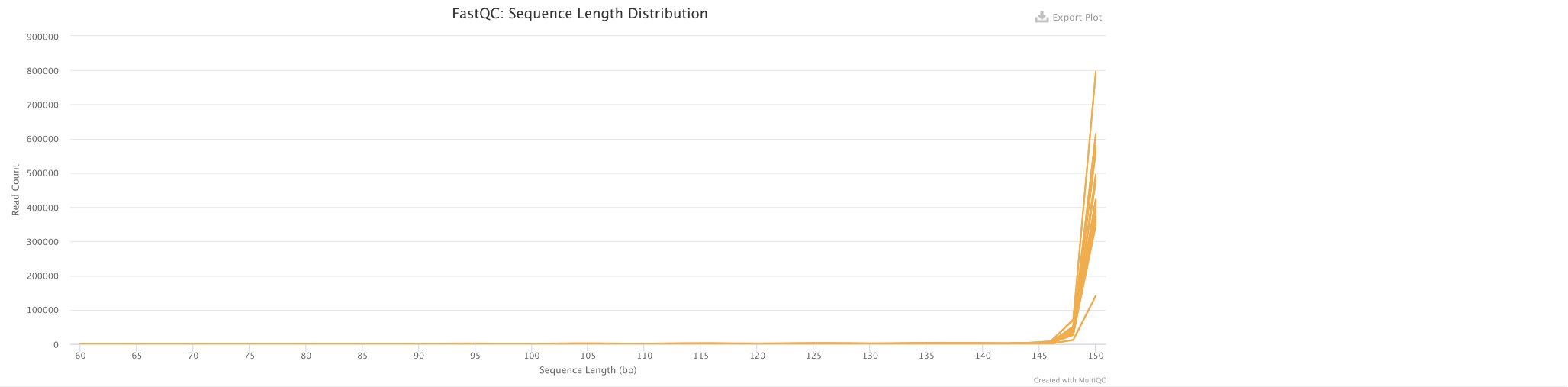




Sequence Length Distribution 0 48

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>).

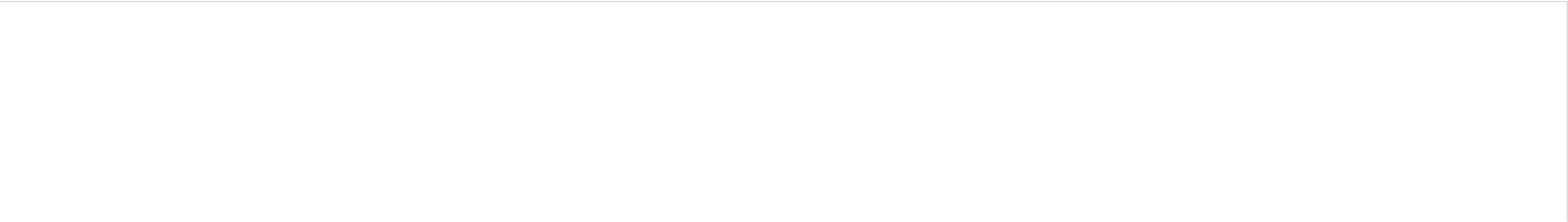
Y-Limits: on

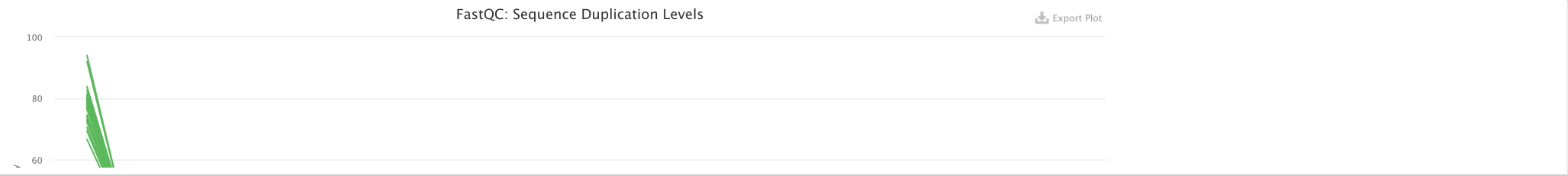


Sequence Duplication Levels 48

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>).

Y-Limits: on





Overrepresented sequences461

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>).

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

Adapter Content48

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 $\geq 0.1\%$ adapter contamination are shown.

No samples found with any adapter contamination > 0.1%