multiqc

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

Report generated on 2025-11-21, 21:57 EST based on data in: `/projectnb/bf528/students/addisony/project-3-addddisonnnn/work/ab/551496f0753ca6ff6b137b3496f3b2`

General Statistics

Copy table | Configure columns | Scatter plot | Violin plot   Showing $^0/_8$ rows and $^5/_{10}$ columns.   Export as CSV

Sample Name	Reads mapped	% Dropped	Dups	GC	Seqs
INPUT_rep1		1.1 %	10.6 %	43.0 %	30.1 M
INPUT_rep1_flagstat	28.6 M				
INPUT_rep2		1.4 %	12.9 %	43.0 %	10.7 M
INPUT_rep2_flagstat	10.1 M				
IP_rep1		3.4 %	89.1 %	47.0 %	29.7 M
IP_rep1_flagstat	27.8 M				
IP_rep2		4.3 %	74.3 %	46.0 %	30.0 M
IP_rep2_flagstat	28.2 M				

Samtools

Toolkit for interacting with BAM/CRAM files.   *URL: http://www.htslib.org   DOI: 10.1093/bioinformatics/btp352*
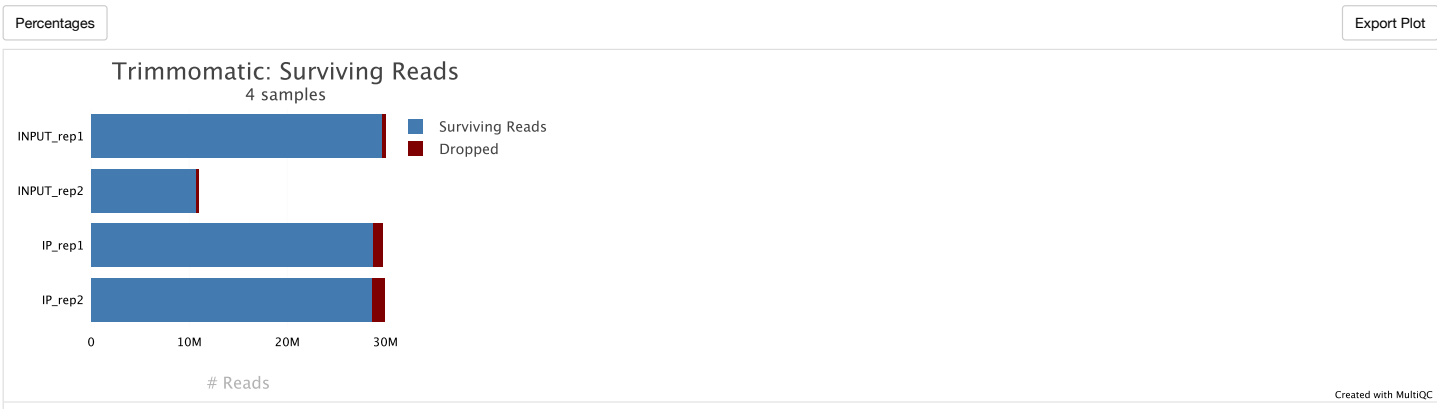
Flagstat

This module parses the output from `samtools flagstat`

Configure columns | Table | Read counts | Percentage of total   Export Plot

Samtools flagstat: read count
Read counts, 4 samples

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Trimmomatic

Read trimming tool for Illumina NGS data. *URL: http://www.usadellab.org/cms/?page=trimmomatic   DOI: 10.1093/bioinformatics/btu170*

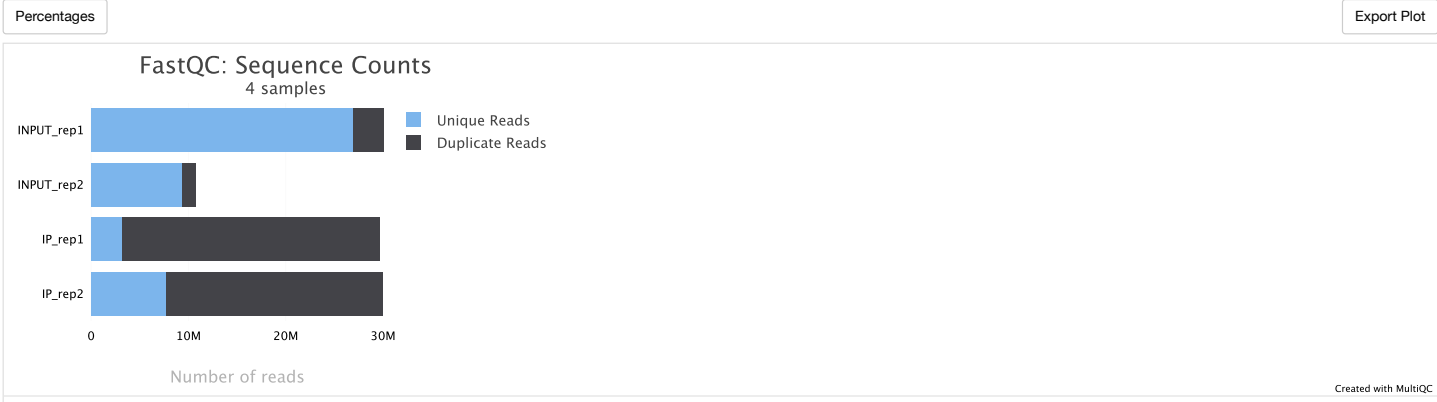Percentages   Export Plot

FastQC *Version:* `0.12.1`

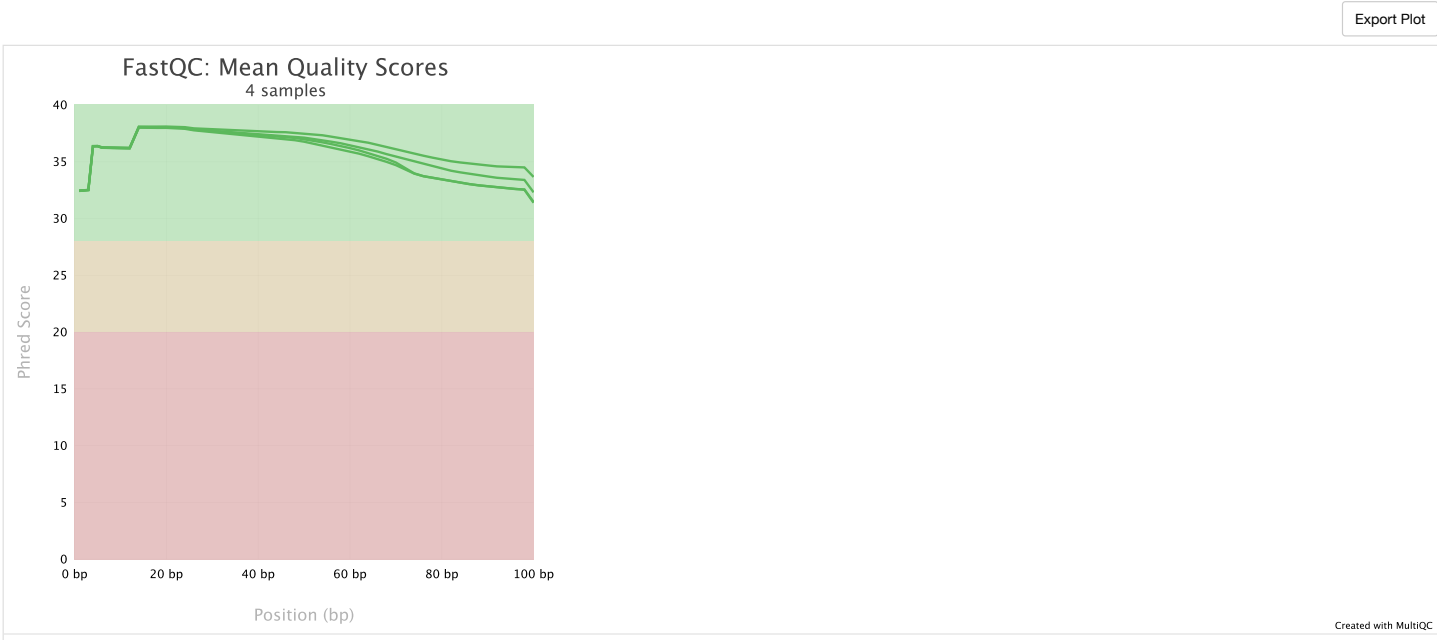Quality control tool for high throughput sequencing data. *URL: http://www.bioinformatics.babraham.ac.uk/projects/fastqc*

Sequence Counts

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

Percentages   Export Plot

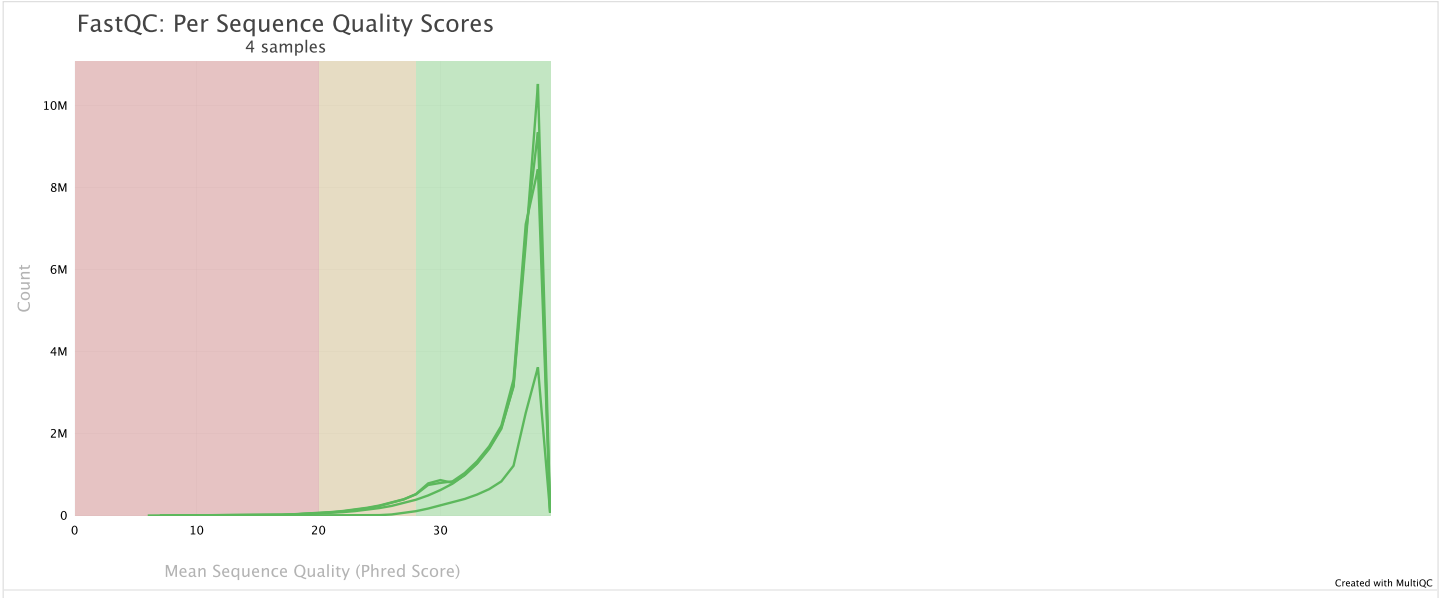
Sequence Quality Histograms   4

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

Export Plot

Per Sequence Quality Scores `4`

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

Export Plot

FastQC: Per Sequence Quality Scores
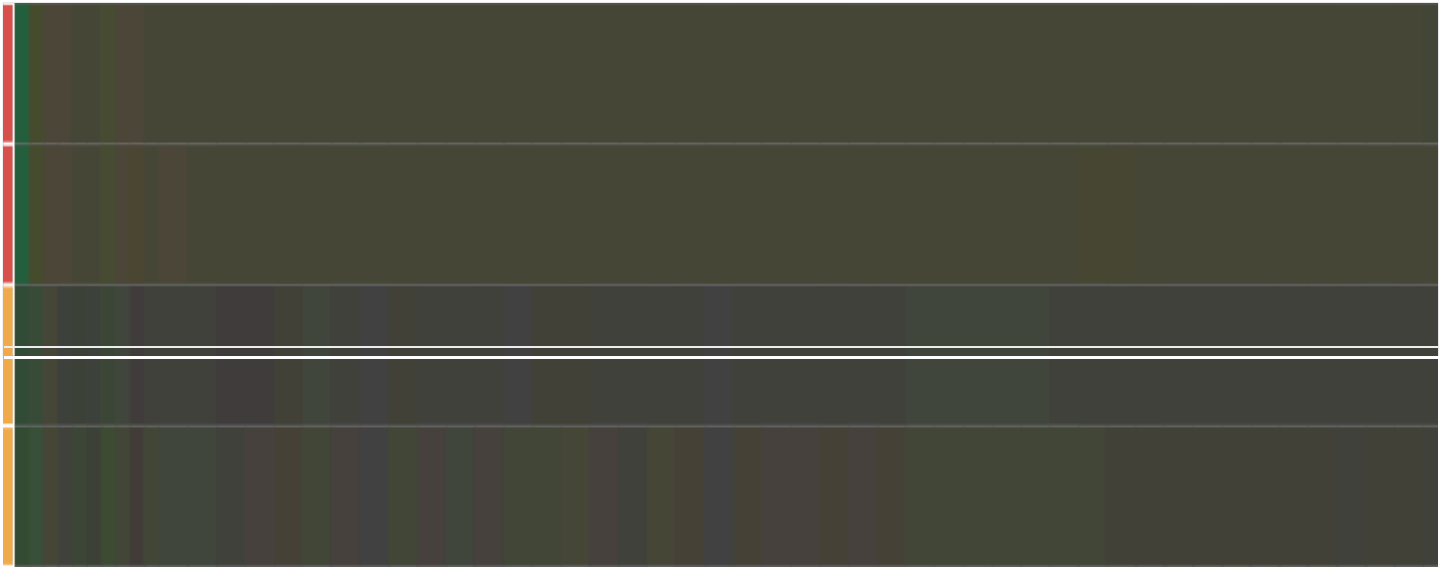4 samples

Per Base Sequence Content `2`

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

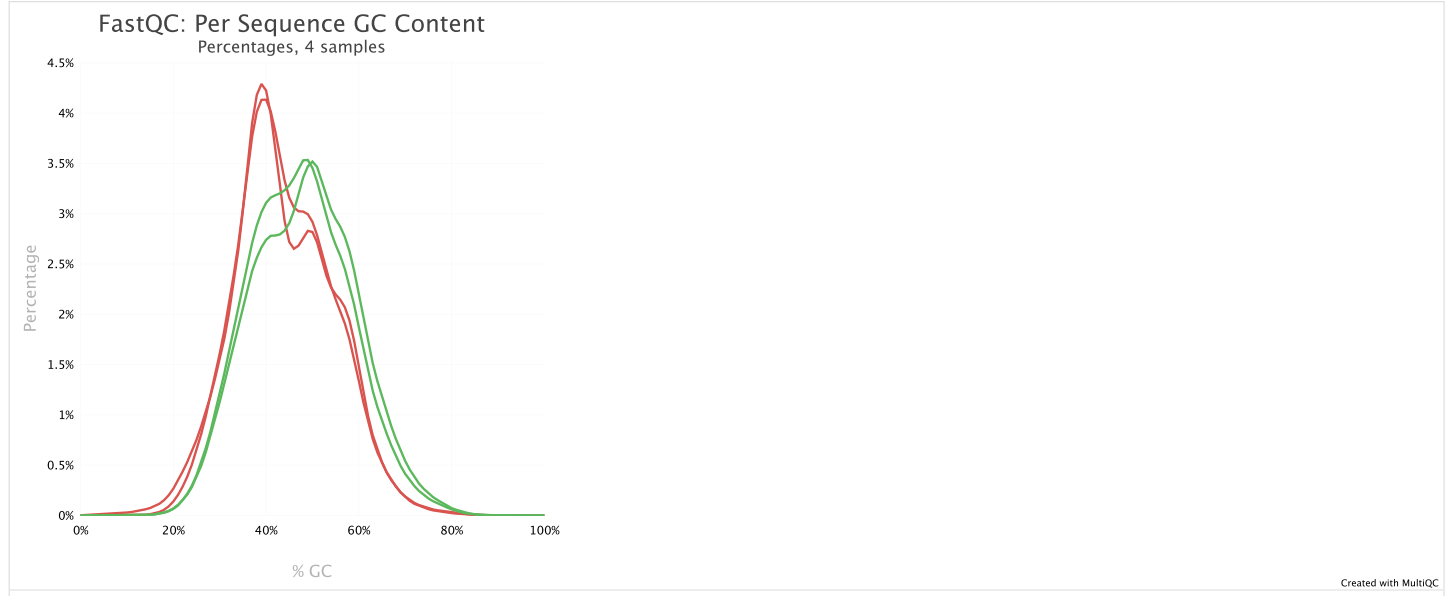Position: -   %T: -   %C: -   %A: -   %G: -

Per Sequence GC Content   `2`

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

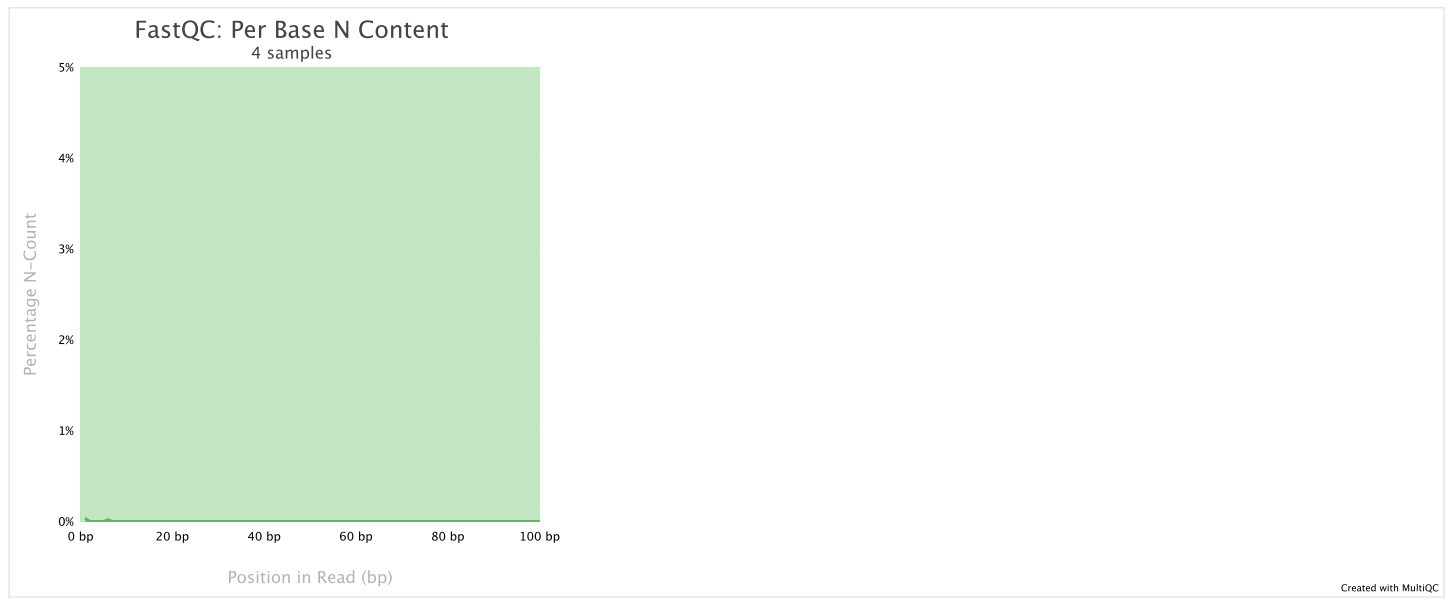| Percentages	Counts	Export Plot

Per Base N Content   `4`

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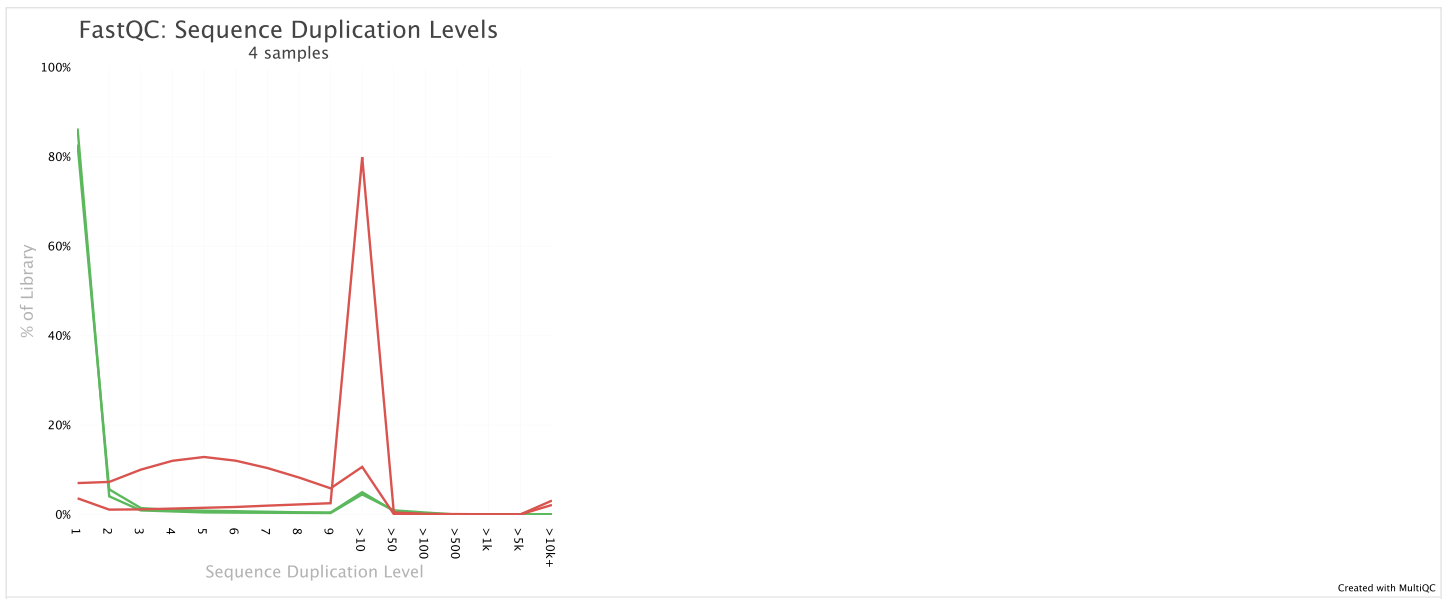
Export Plot

Sequence Length Distribution `3` `1`

The distribution of fragment sizes (read lengths) found. See the FastQC help

Export Plot

FastQC: Sequence Length Distribution
4 samples

Sequence Duplication Levels `2`

The relative level of duplication found for every sequence.
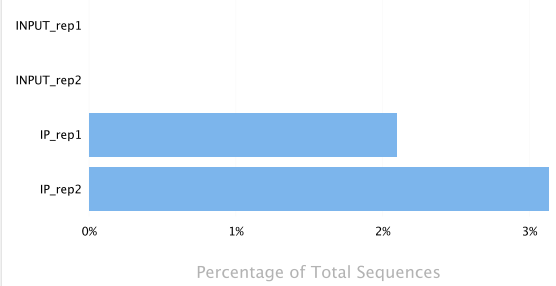
Export Plot

FastQC: Sequence Duplication Levels
4 samples

Overrepresented sequences by sample `2`

The total amount of overrepresented sequences found in each library.

Export Plot

stQC: Overrepresented sequences sample summa
4 samples

Percentage of Total Sequences

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Top overrepresented sequences

Top overrepresented sequences across all samples. The table shows 20 most overrepresented sequences across all samples, ranked by the number of samples they occur in.

Copy table   Configure columns   Scatter plot   Violin plot   Showing $^0/_2$ rows and $^3/_3$ columns.   Export as CSV
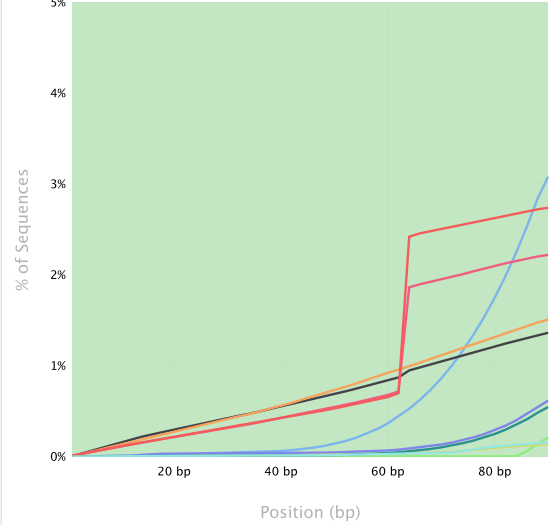
Overrepresented sequence	Reports	Occurrences	% of all reads
GATCGGAAGAGCACACGTCTGAACTCCAGT(	1	623 488	0.6201 %
GATCGGAAGAGCACACGTCTGAACTCCAGT(	1	937 732	0.9326 %

Adapter Content `4`

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

Export Plot

FastQC: Adapter Content
10 samples

% of Sequences

Position (bp)

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Status Checks

Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red).

Min: [0.0] ●———————————   **Max:** [1.0] ————————————●   [Export Plot]

FastQC: Status Checks
11 samples

Software Versions

Software Versions lists versions of software tools extracted from file contents.

[📋 Copy table]

Software	Version
FastQC	0.12.1

MultiQC v1.25 - Written by Phil Ewels, available on GitHub.
This report uses Plotly, jQuery, jQuery UI, Bootstrap and FileSaver.js.

seqera