**MultiQC**

# (http://multiqc.info)

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

Report generated on 2022-01-23, 19:58 based on data in: `/media/data04/gaye/workspace/rnaseq/data2`

## General Statistics

[Copy table] [Configure Columns] [Plot]  Showing ⁶/₆ rows and ³/₅ columns.

| Sample Name | % Dups | % GC | M Seqs |
|---|---|---|---|
| SRR12424243_1 | | | |
| SRR12424244_1 | | | |
| SRR12424245_1 | | | |
| SRR12424255_1 | | | |
| SRR12424256_1 | | | |
| SRR12424257_1 | | | |

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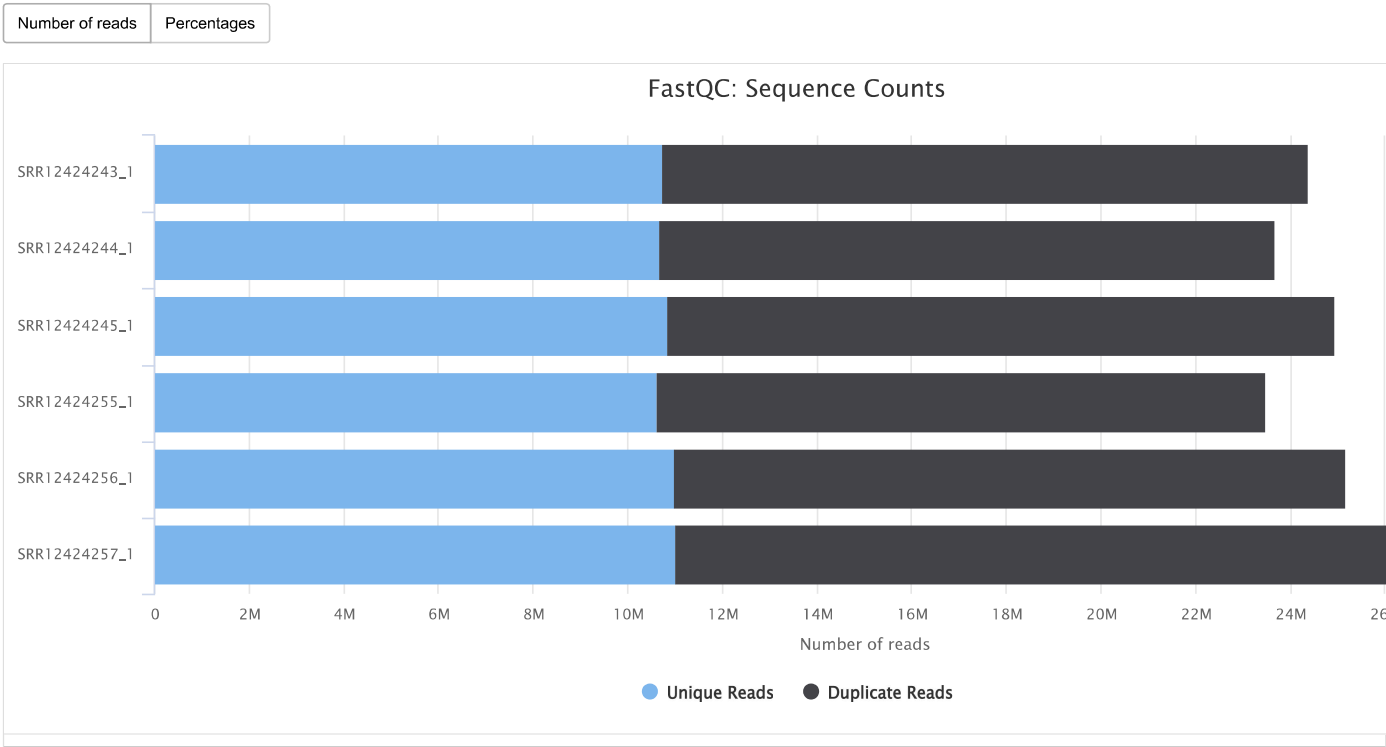
FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.
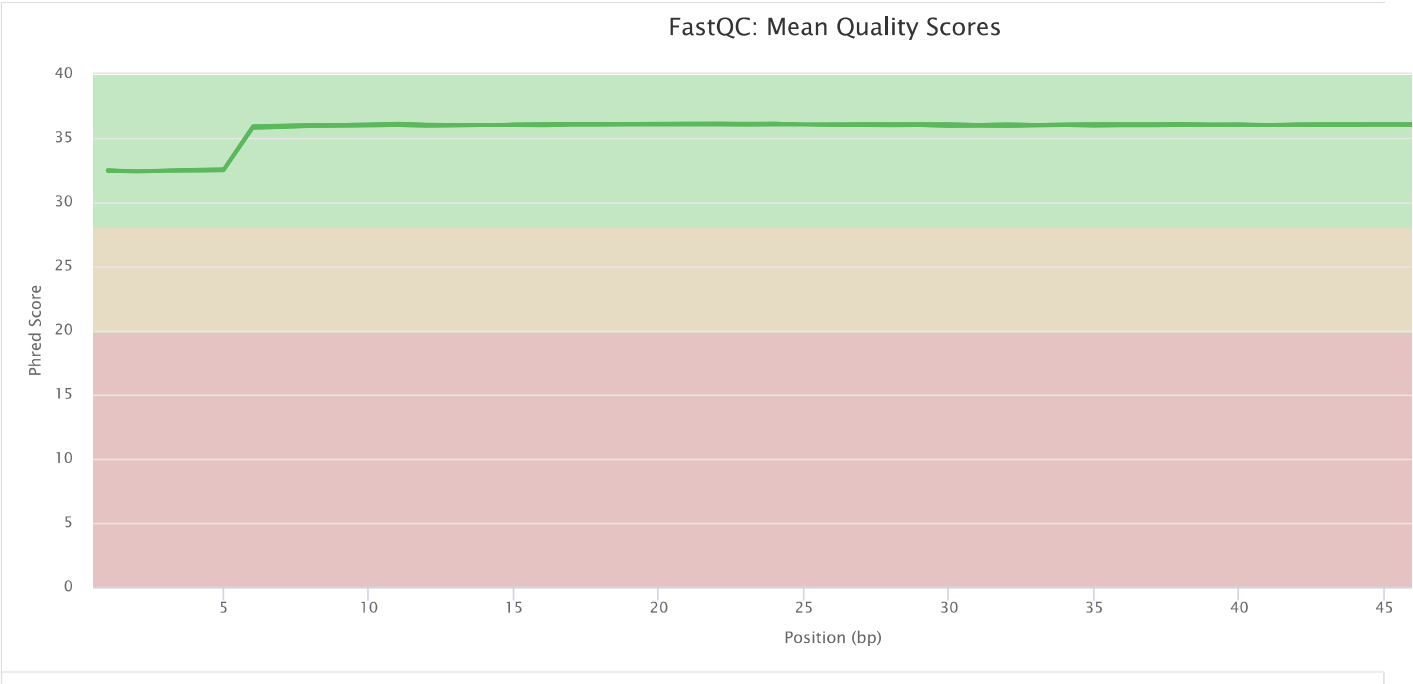
### Sequence Counts　　　　　　　　　　　　　　　　　　　　　[? Help]

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

[Number of reads] [Percentages]



FastQC: Sequence Counts

# Sequence Quality Histograms    6
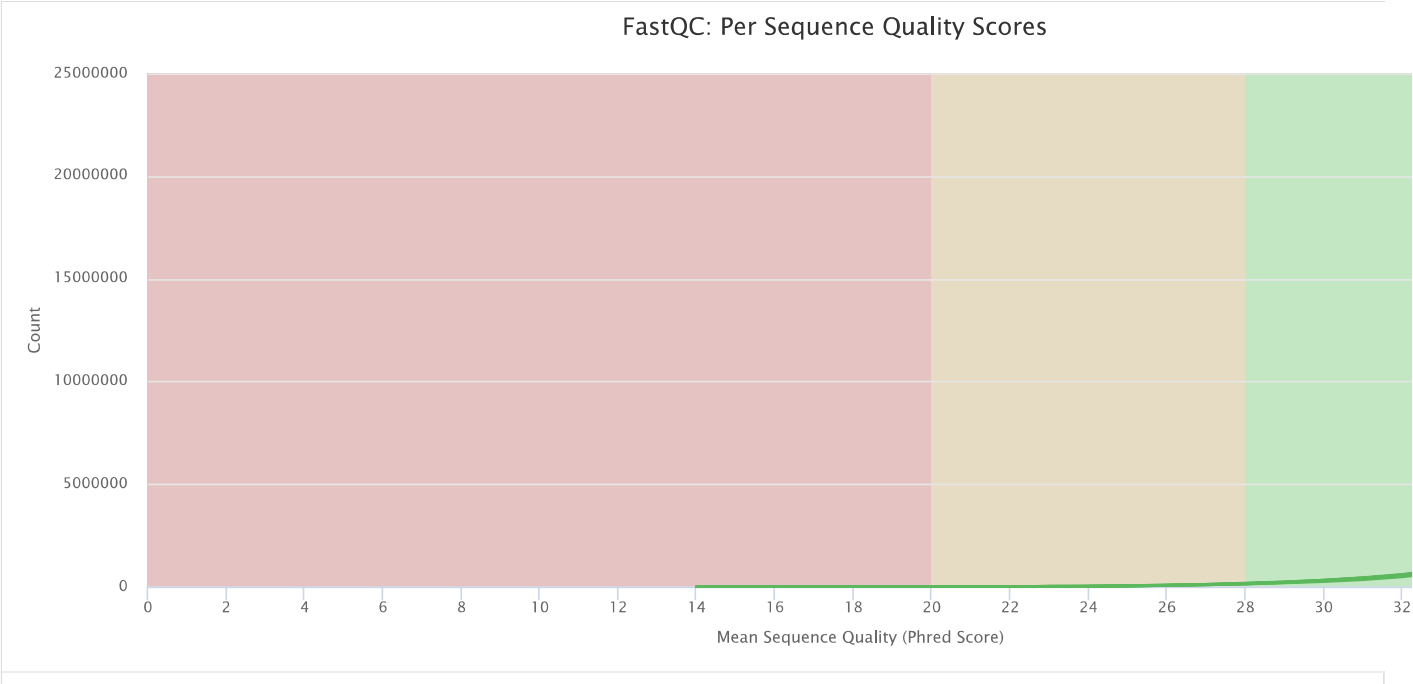
[? Help]

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



# Per Sequence Quality Scores    6

[? Help]

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



# Per Base Sequence Content    0 2      4

[? 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
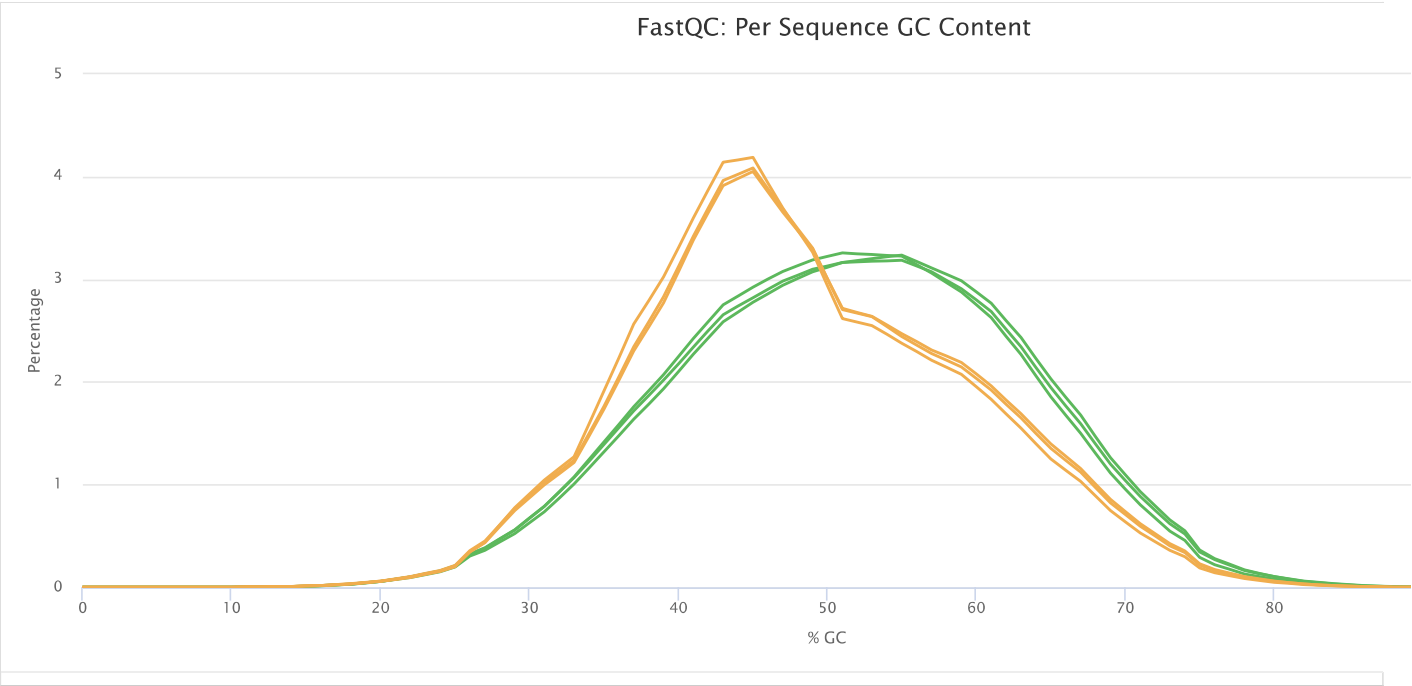
## Per Sequence GC Content       3       3

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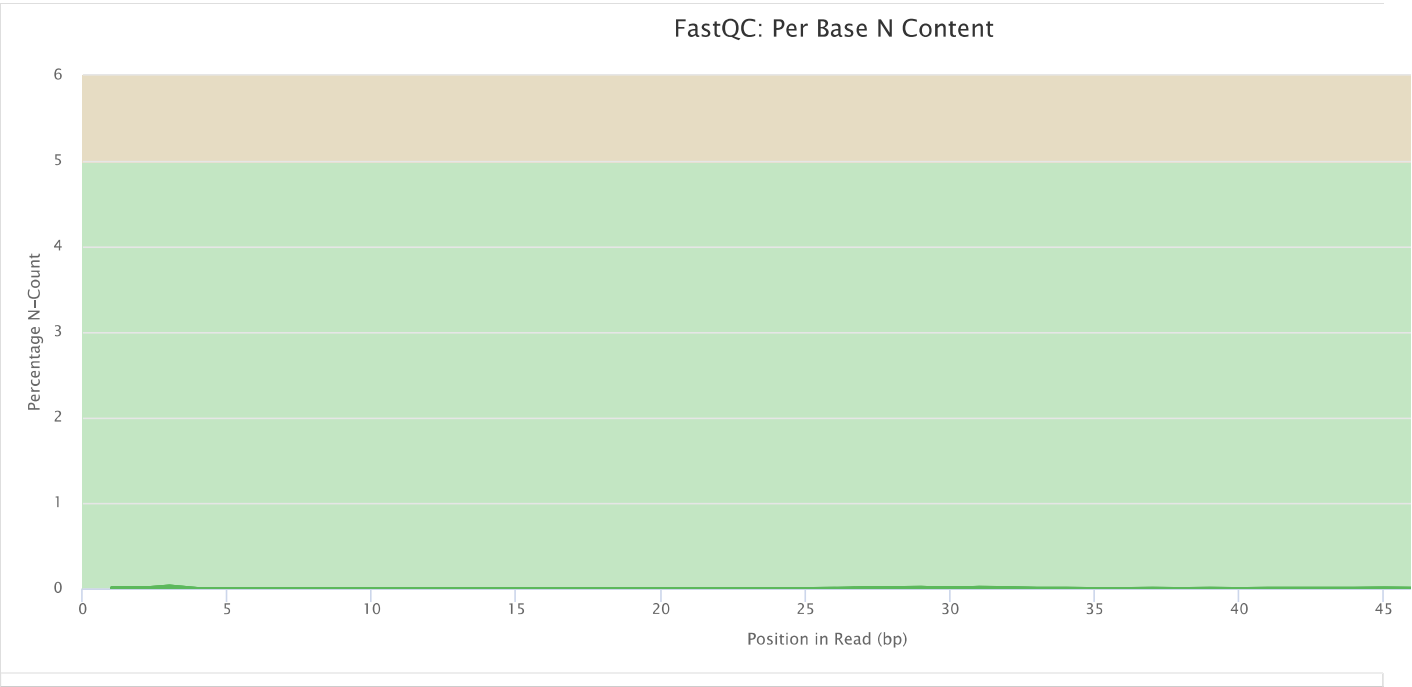
Percentages | Counts



## Per Base N Content       6

The percentage of base calls at each position for which an `N` was called.
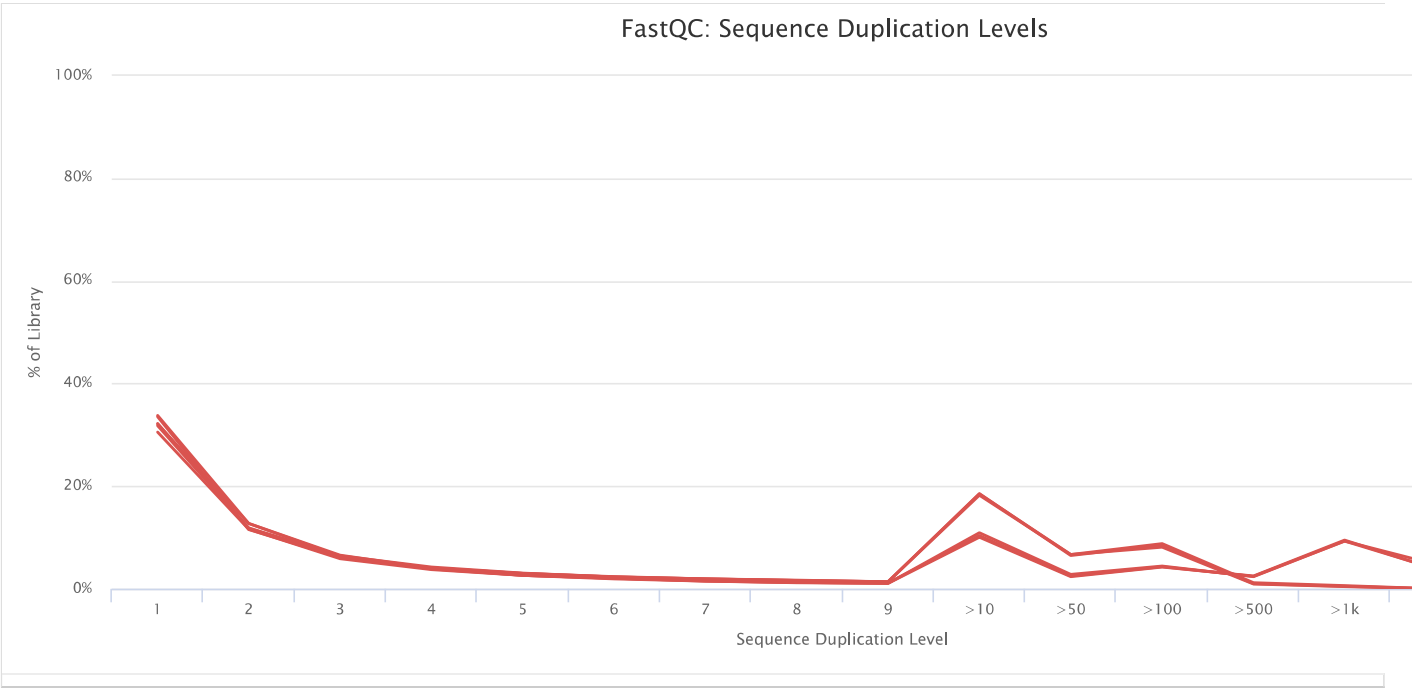
## Sequence Length Distribution  6

All samples have sequences of a single length (51bp).

## Sequence Duplication Levels  0  6

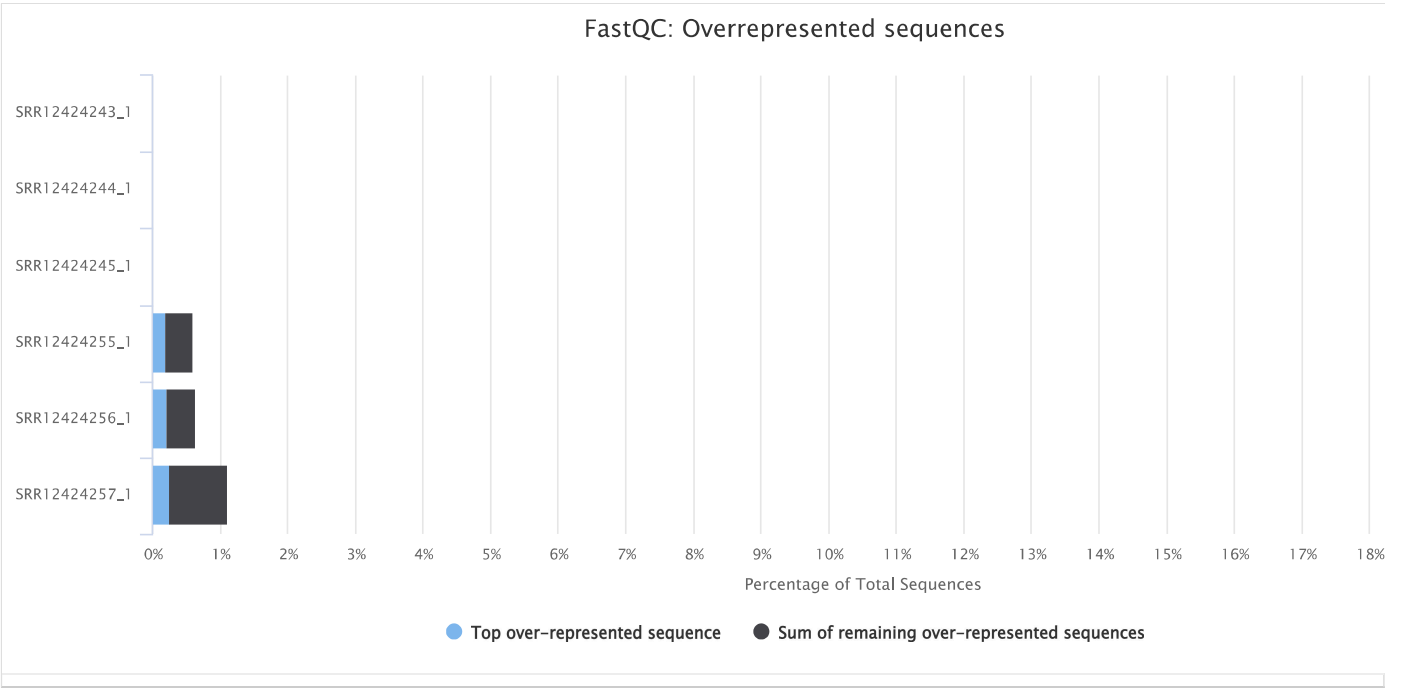The relative level of duplication found for every sequence.



FastQC: Sequence Duplication Levels

## Overrepresented sequences  3  3

The total amount of overrepresented sequences found in each library.



FastQC: Overrepresented sequences

## Adapter Content  6

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

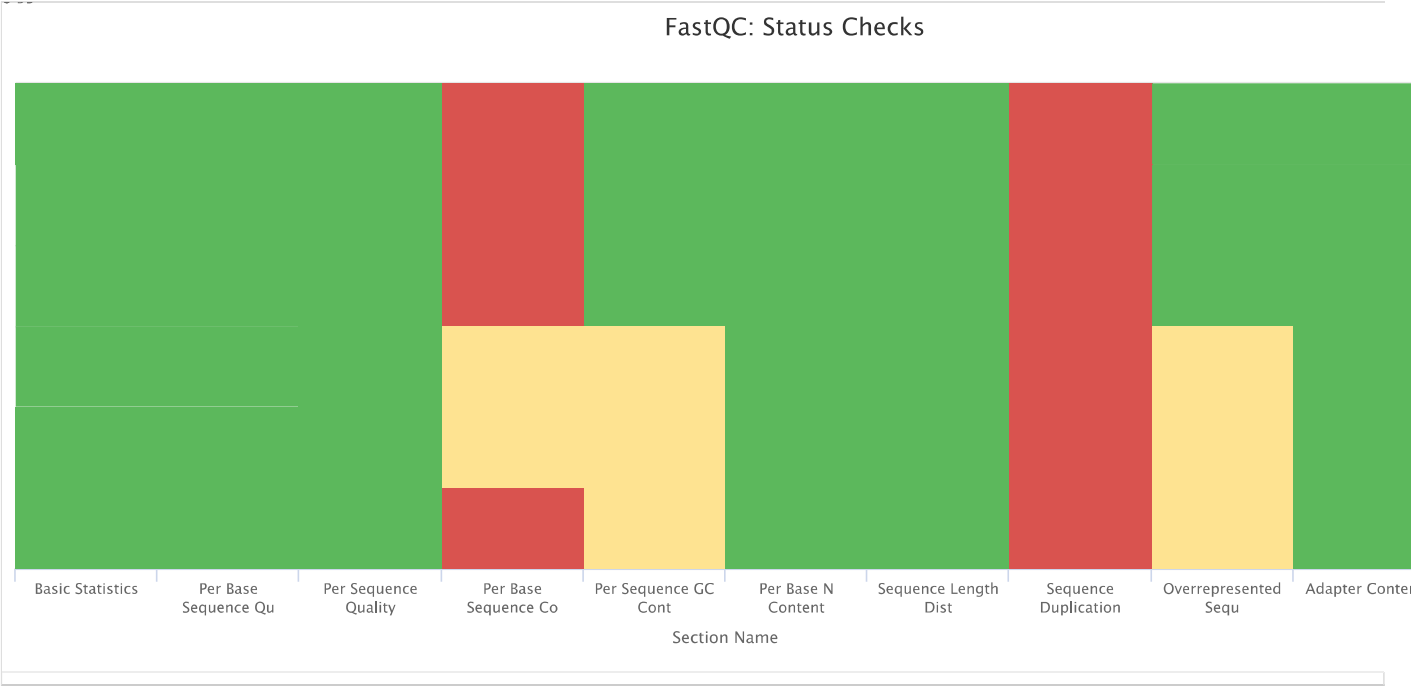No samples found with any adapter contamination > 0.1%

# Status Checks

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

⬇ Sort by highlight

### FastQC: Status Checks



Basic Statistics | Per Base Sequence Qu | Per Sequence Quality | Per Base Sequence Co | Per Sequence GC Cont | Per Base N Content | Sequence Length Dist | Sequence Duplication | Overrepresented Sequ | Adapter Conter

Section Name

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