# MultiQC

v1.11

# MultiQC

(http://multiqc.info)

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

Report generated on 2022-07-02, 15:49 based on data in: `/data/jwd/main/048/015/48015714/working/multiqc_WDir`

## General Statistics

Copy table | Configure Columns | Plot  Showing $^8/_8$ rows and $^4/_5$ columns.

| Sample Name | % Dups | % GC | Length | M Seqs |
|---|---|---|---|---|
| **Trimmomatic on SLGFSK-N_231335_r1_chr5_12_17_fastq_gz _R1 paired** | | | | |
| **Trimmomatic on SLGFSK-N_231335_r1_chr5_12_17_fastq_gz _R1 unpaired** | | | | |
| **Trimmomatic on SLGFSK-N_231335_r2_chr5_12_17_fastq_gz _R2 paired** | | | | |
| **Trimmomatic on SLGFSK-N_231335_r2_chr5_12_17_fastq_gz _R2 unpaired** | | | | |
| **Trimmomatic on SLGFSK-T_231336_r1_chr5_12_17_fastq_gz _R1 paired** | | | | |
| **Trimmomatic on SLGFSK-T_231336_r1_chr5_12_17_fastq_gz _R1 unpaired** | | | | |
| **Trimmomatic on SLGFSK-T_231336_r2_chr5_12_17_fastq_gz _R2 paired** | | | | |
| **Trimmomatic on SLGFSK-T_231336_r2_chr5_12_17_fastq_gz _R2 unpaired** | | | | |

## 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

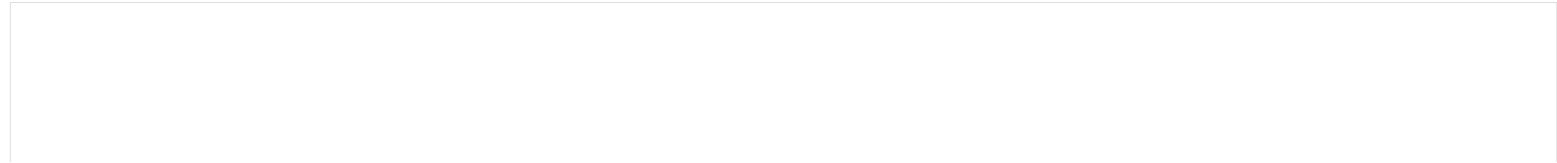Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads | Percentages
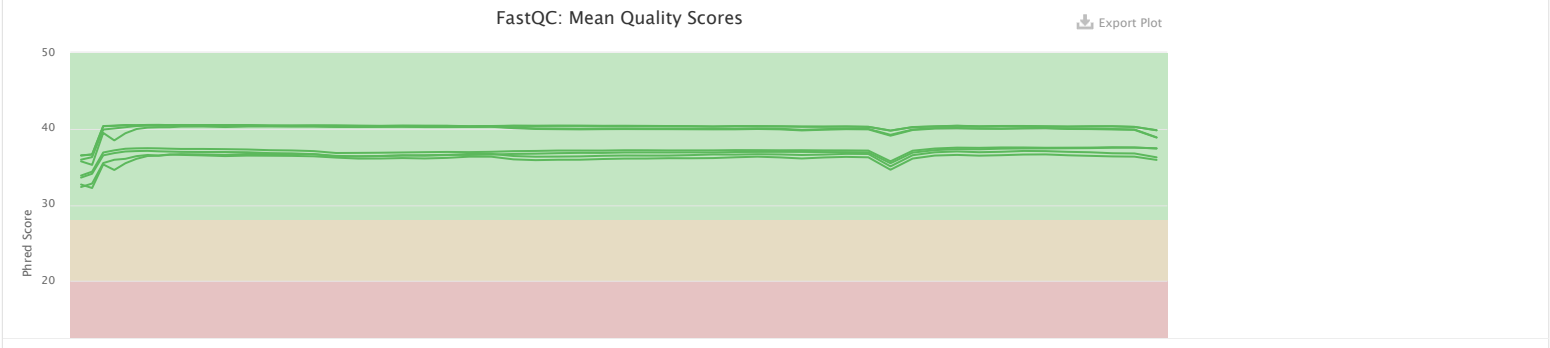


FastQC: Sequence Counts

- Unique Reads
- Duplicate Reads

Created with MultiQC
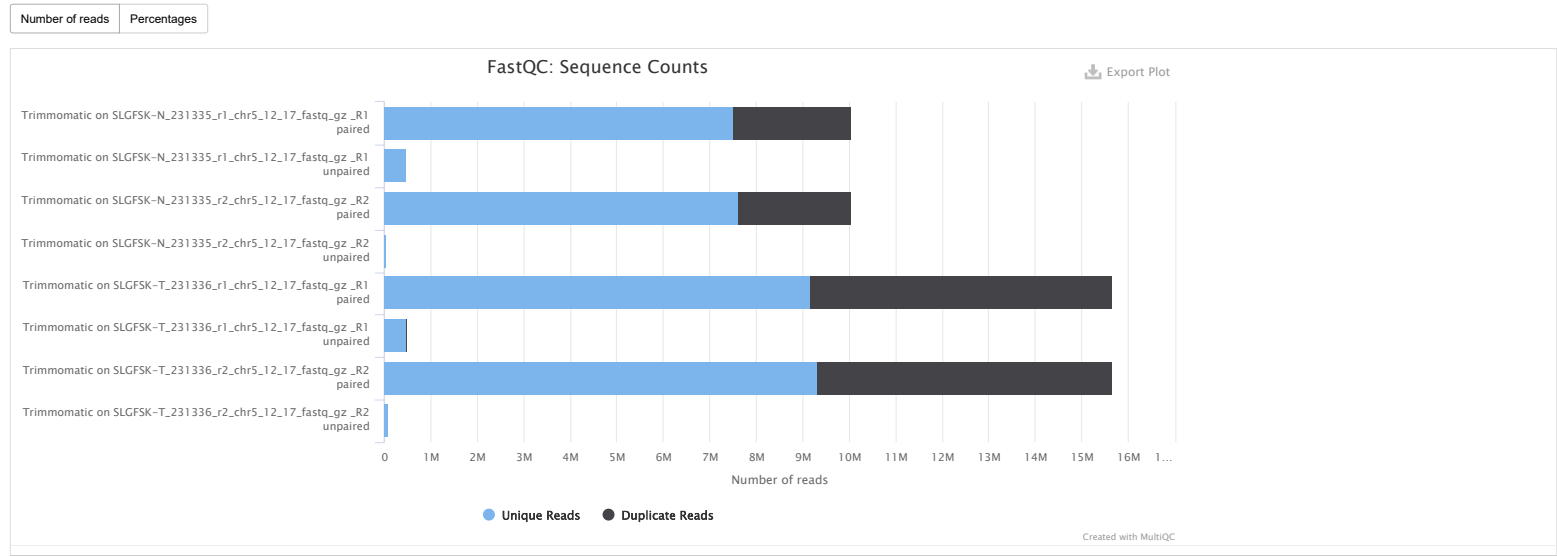
### Sequence Quality Histograms 8

Help

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

Y-Limits: on

## FastQC: Mean Quality Scores



## Per Sequence Quality Scores    8

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

Y-Limits: [on]



FastQC: Per Sequence Quality Scores

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## Per Base Sequence Content    8

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
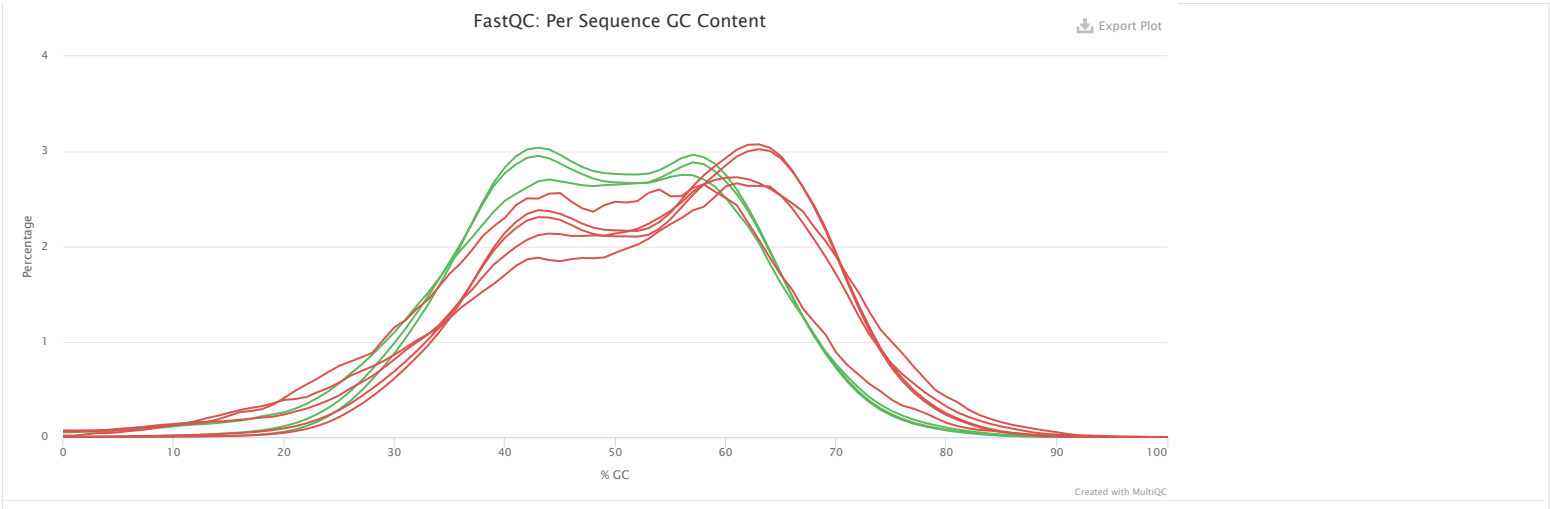


The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Y-Limits: [on]

[Percentages] [Counts]
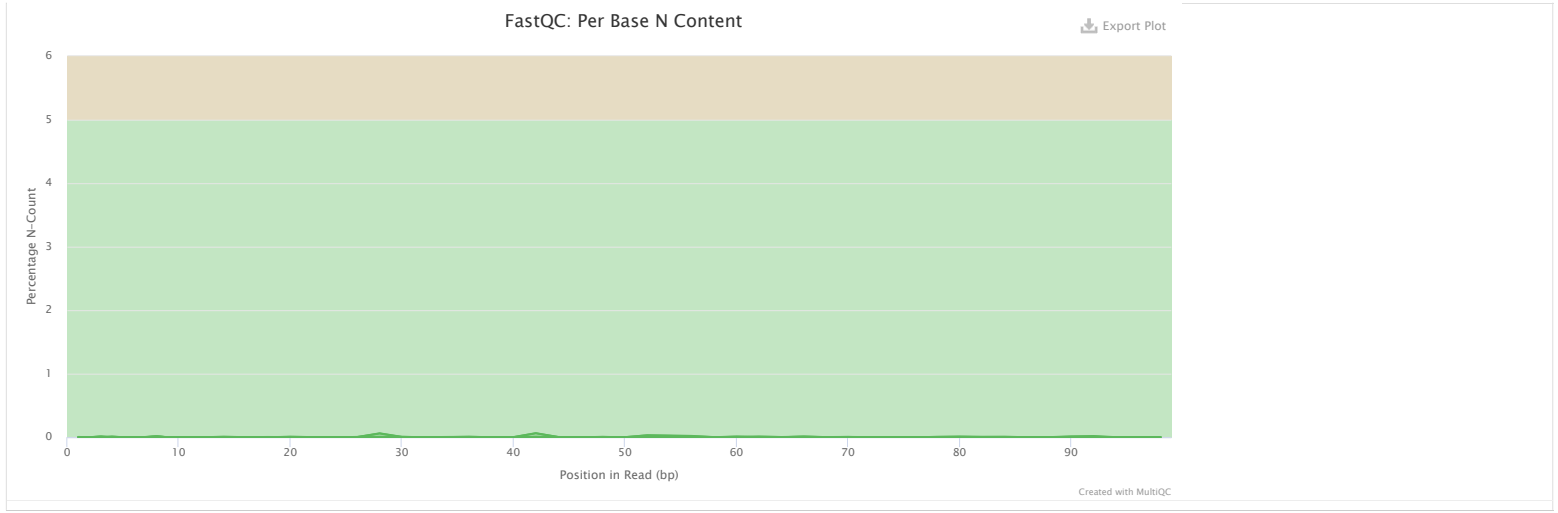
FastQC: Per Sequence GC Content



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## Per Base N Content    8

Help

The percentage of base calls at each position for which an `N` was called.
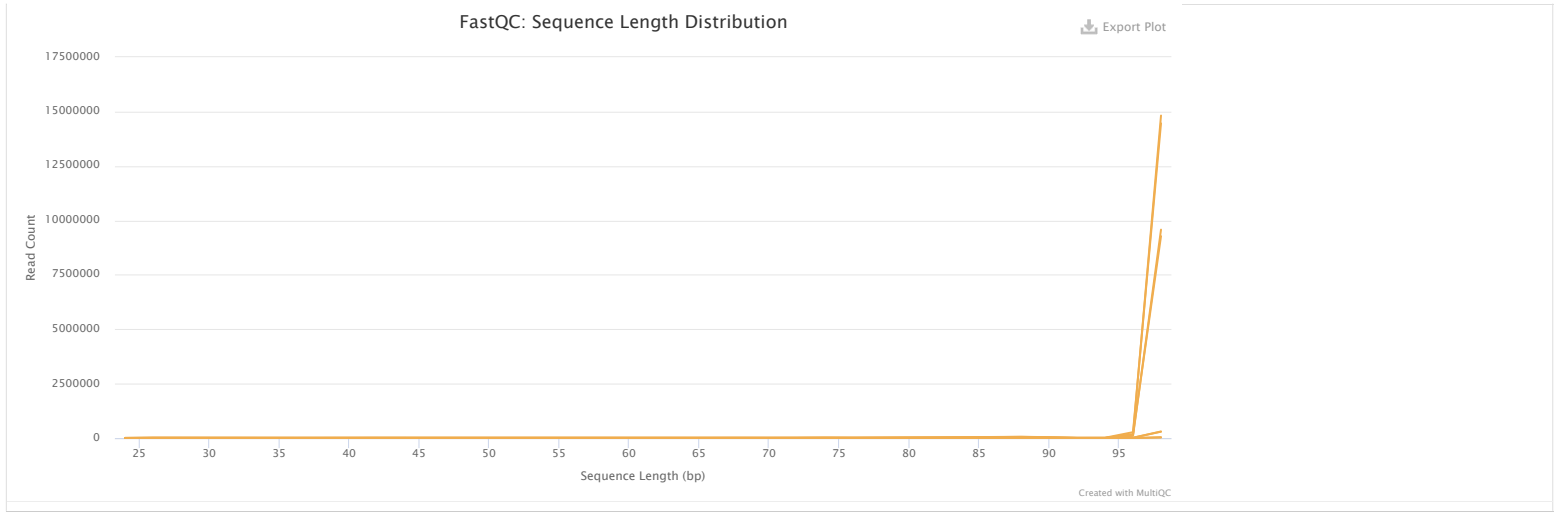
## Sequence Length Distribution  0  8

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)
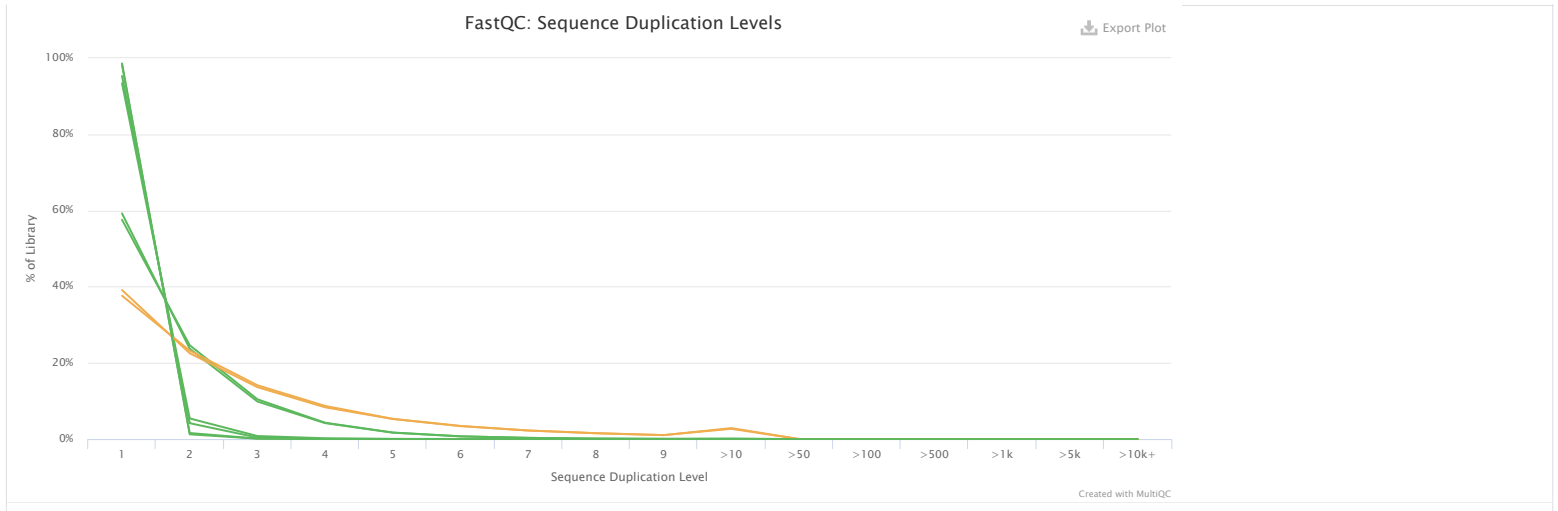
Y-Limits: on



## Sequence Duplication Levels  6  2

The relative level of duplication found for every sequence.

❓ Help

Y-Limits: on



## Overrepresented sequences  8

The total amount of overrepresented sequences found in each library.

❓ Help

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

## Adapter Content  8

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

❓ Help

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).

❓ Help

Sort by highlight

## FastQC: Status Checks

Export Plot



| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Basic Statistics | Per Base Sequence Qu | Per Tile 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 Content |

Trimmomatic on SLGFS

Section Name

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