MultiQC

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

Report generated on 2023-06-10, 15:59 ora legale Europa occidentale based on data in: `C:\Users\Ilaria\Desktop\UNI\not_passed\BI1\multiqc`

General Statistics

Copy table | Configure Columns | Plot   Showing $^2/_2$ rows and $^3/_6$ columns.

Sample Name	% Dups	% GC	M Seqs
SRR12816729	28.3%	40%	87.7
SRR12951228	40.2%	42%	94.3

FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.
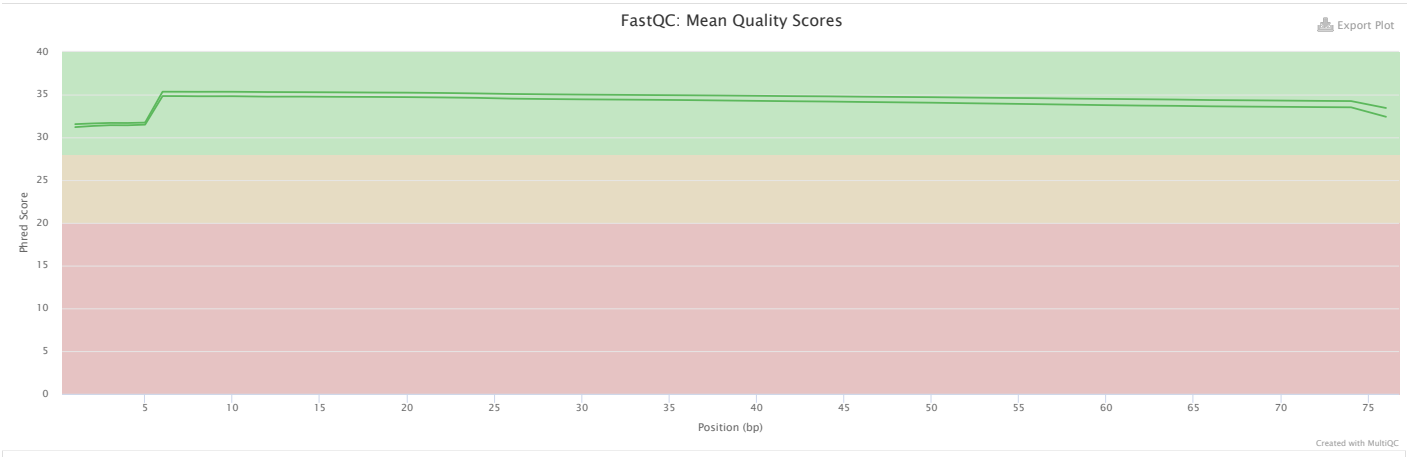
Sequence Counts

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

Number of reads | Percentages

FastQC: Sequence Counts
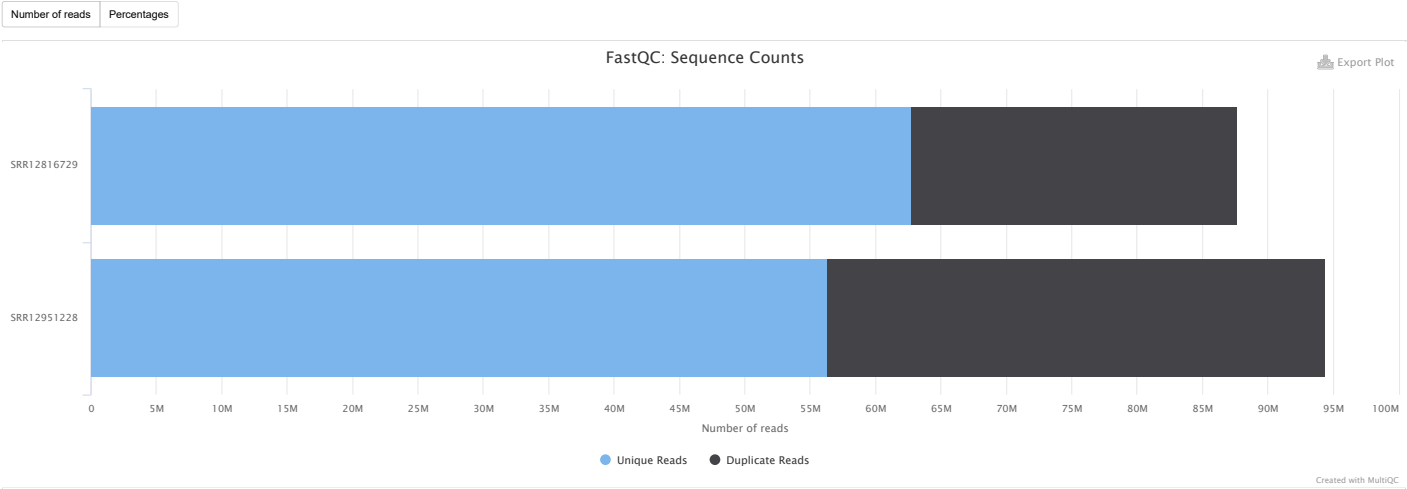
Sequence Quality Histograms 2

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

FastQC: Mean Quality Scores

Per Sequence Quality Scores   `2`

The number of reads with average quality scores. Shows if a subset of reads has poor quality.
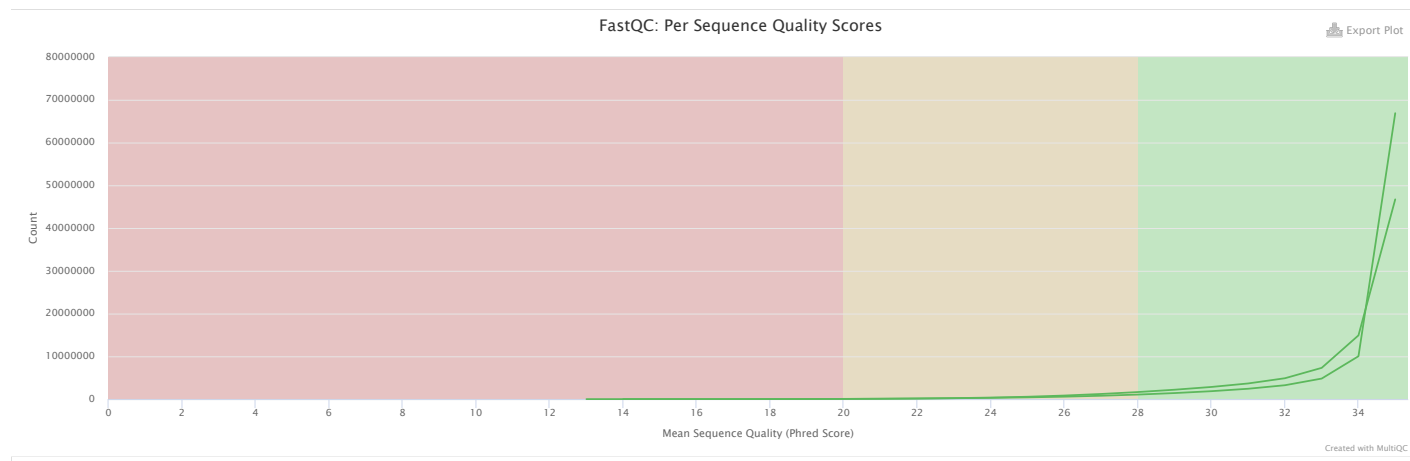
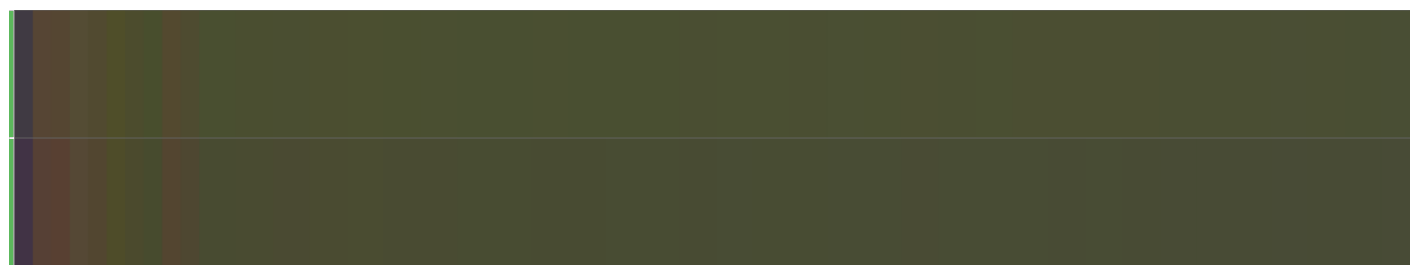## Per Base Sequence Content   `2`

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.

ℹ Rollover for sample name

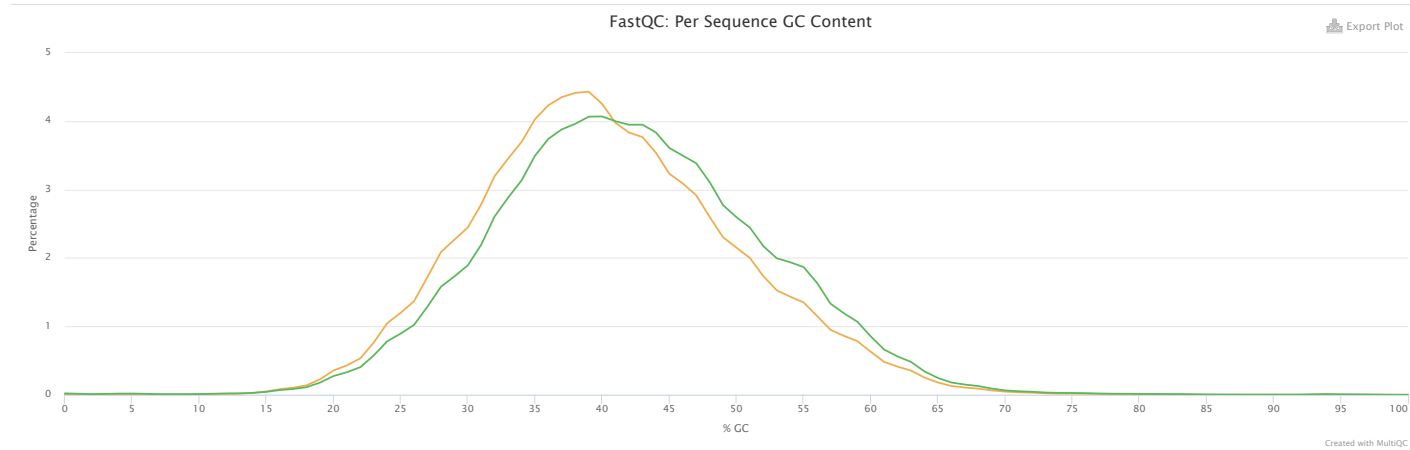Position: -   %T: -   %C: -   %A: -   %G: -   ⬇ Export Plot
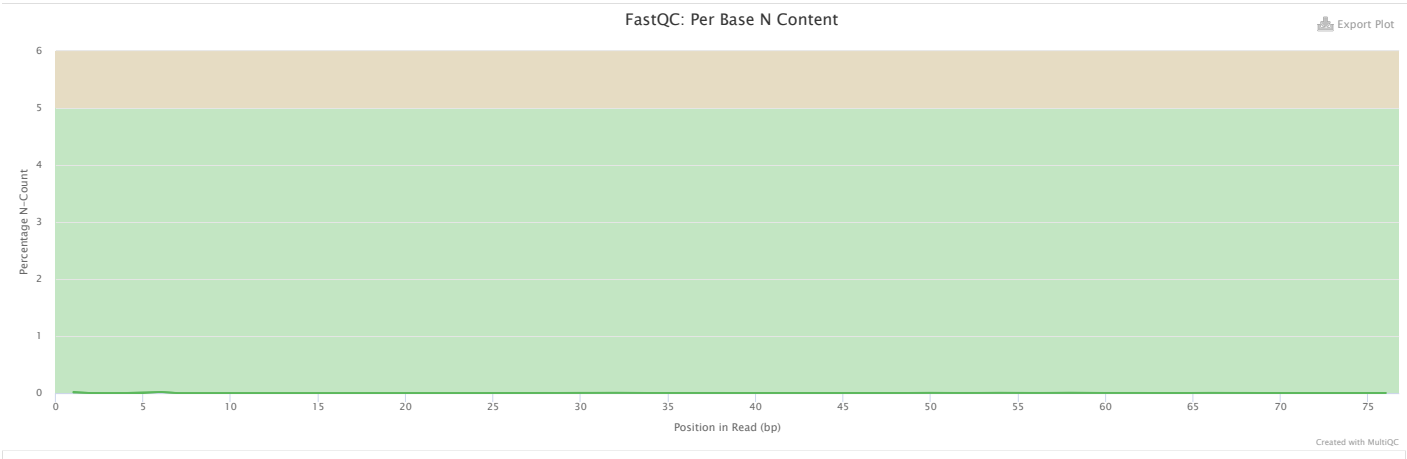

Per Sequence GC Content   `1` `1`

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

Percentages   Counts

Per Base N Content   2

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

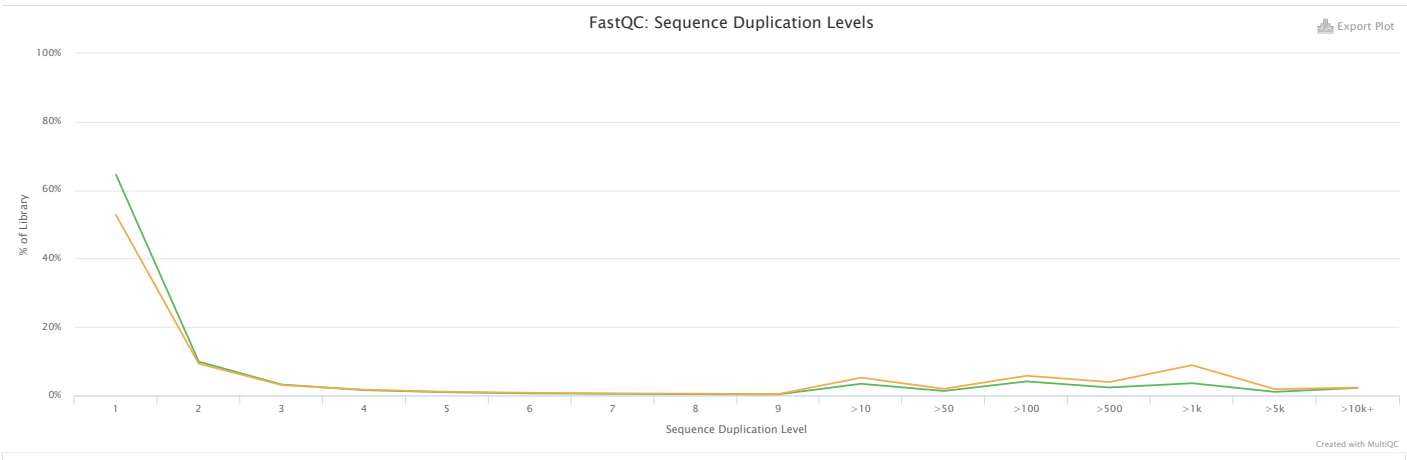### FastQC: Per Base N Content

Sequence Length Distribution   2

All samples have sequences of a single length (76bp).

Sequence Duplication Levels   1   1

The relative level of duplication found for every sequence.

FastQC: Sequence Duplication Levels

Overrepresented sequences   2

The total amount of overrepresented sequences found in each library.

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

Adapter Content `2`

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

FastQC: Adapter Content

Created with MultiQC
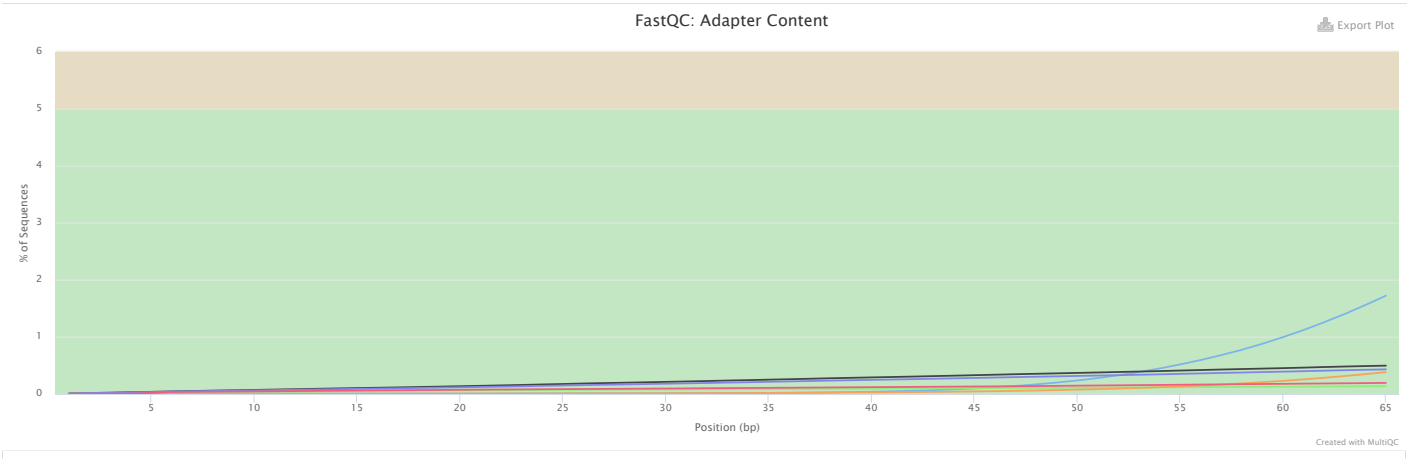
Status Checks

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

Sort by highlight   **Min:** 0   **Max:** 1

FastQC: Status Checks

Created with MultiQC

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seqeralabs