

General Statistics

Copy table

Configure Columns

Plot

Showing $\frac{3}{3}$ rows and $\frac{3}{5}$ columns.

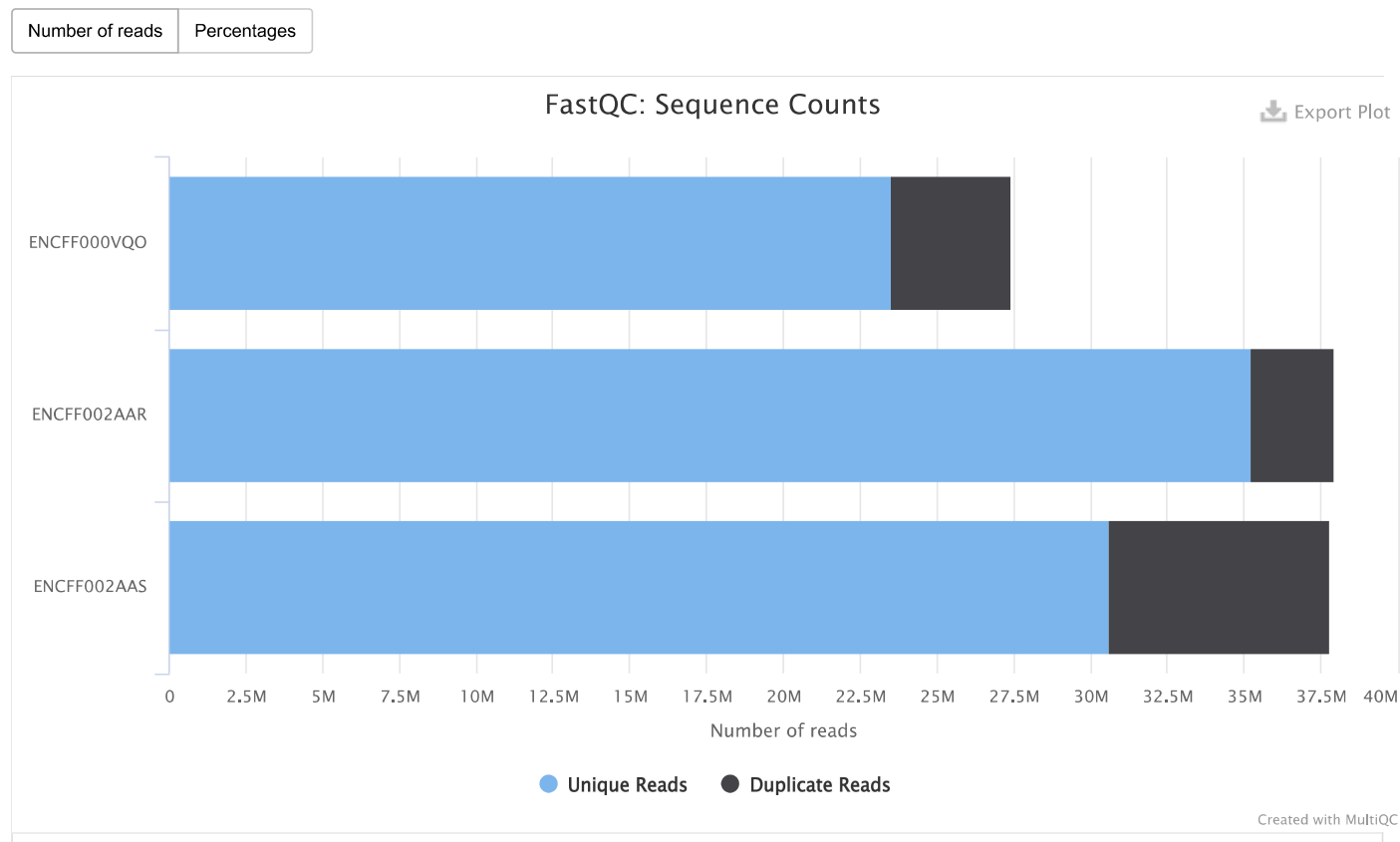
| Sample Name | % Dups | % GC | M Seqs |
|-------------|--------|------|--------|
| ENCFF000VQO | 14.1% | 48% | 27.4 |
| ENCFF002AAR | 7.1% | 40% | 37.9 |
| ENCFF002AAS | 19.0% | 53% | 37.8 |

FastQC

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

Sequence Counts

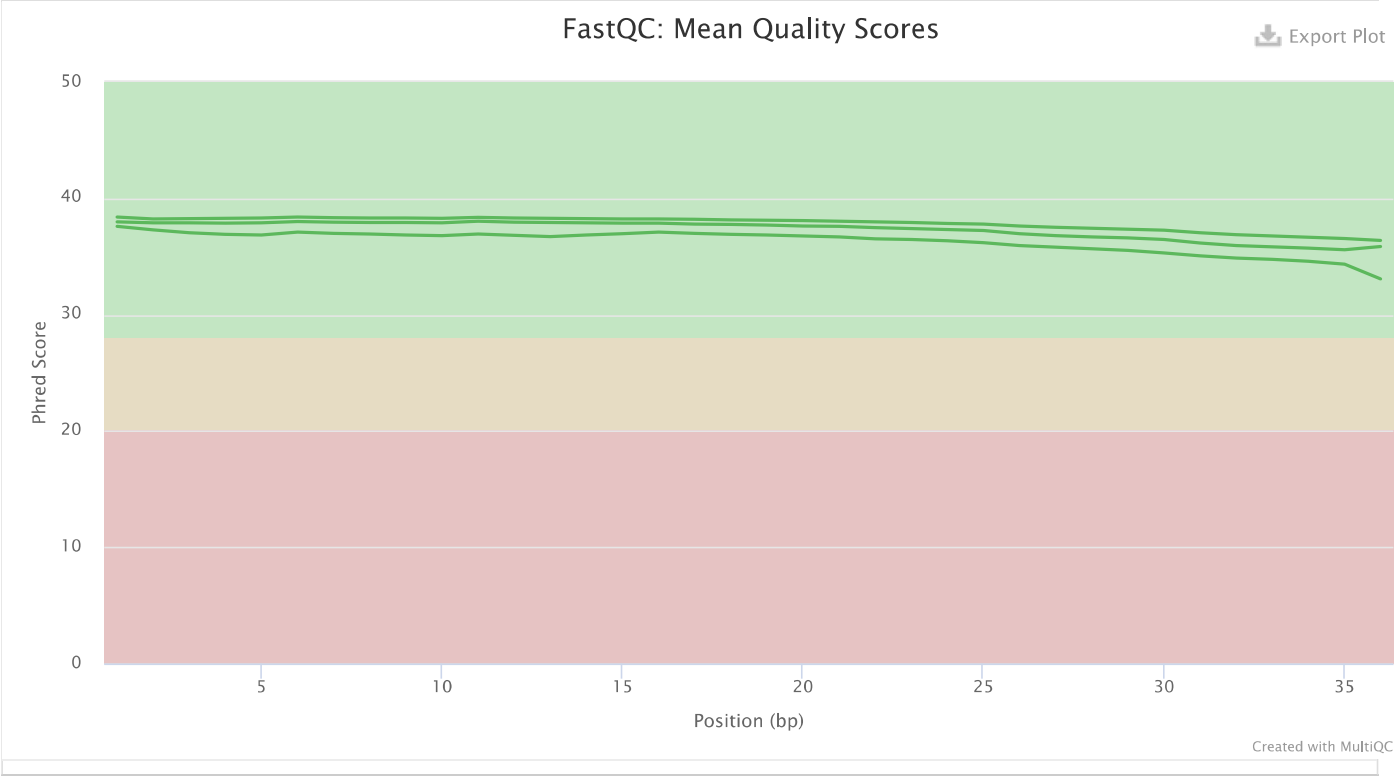
Sequence counts for each sample. Duplicate read counts are an estimate only.



Sequence Quality Histograms

3

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



Per Sequence Quality Scores

3

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



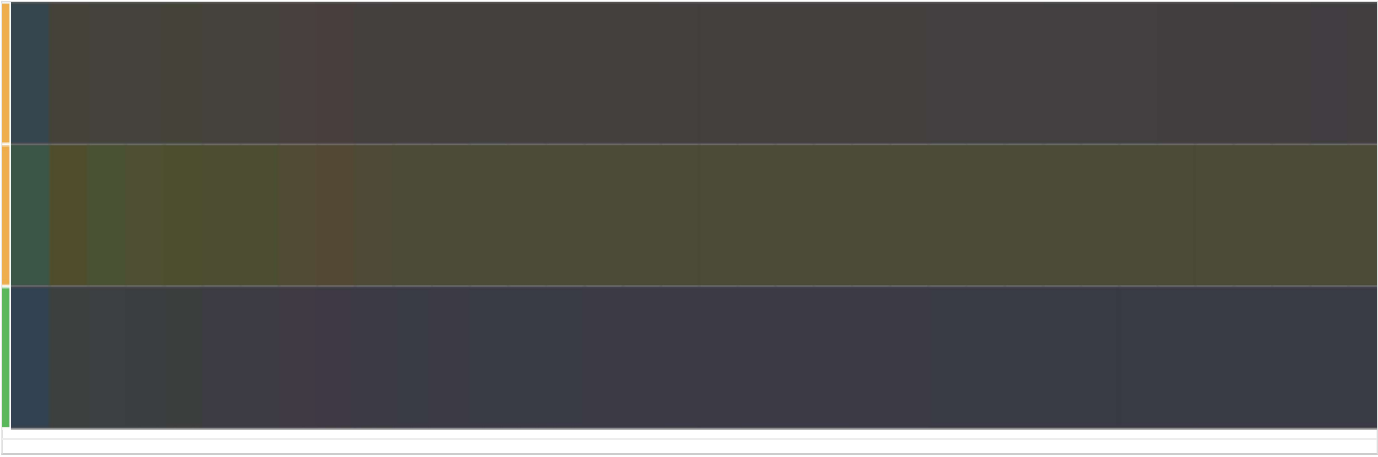
Per Base Sequence Content

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

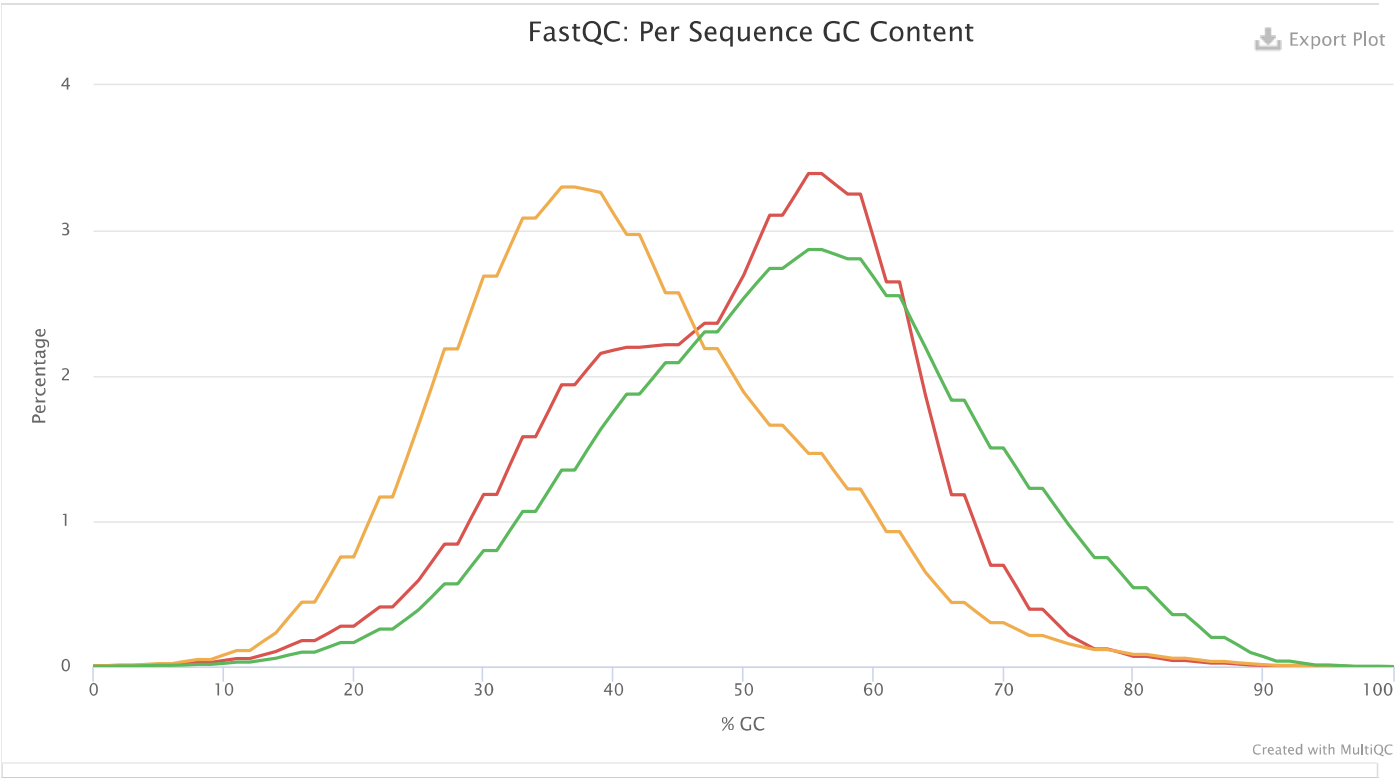
Position: - %T: - %C: - %A: - %G: - Export Plot



Per Sequence GC Content

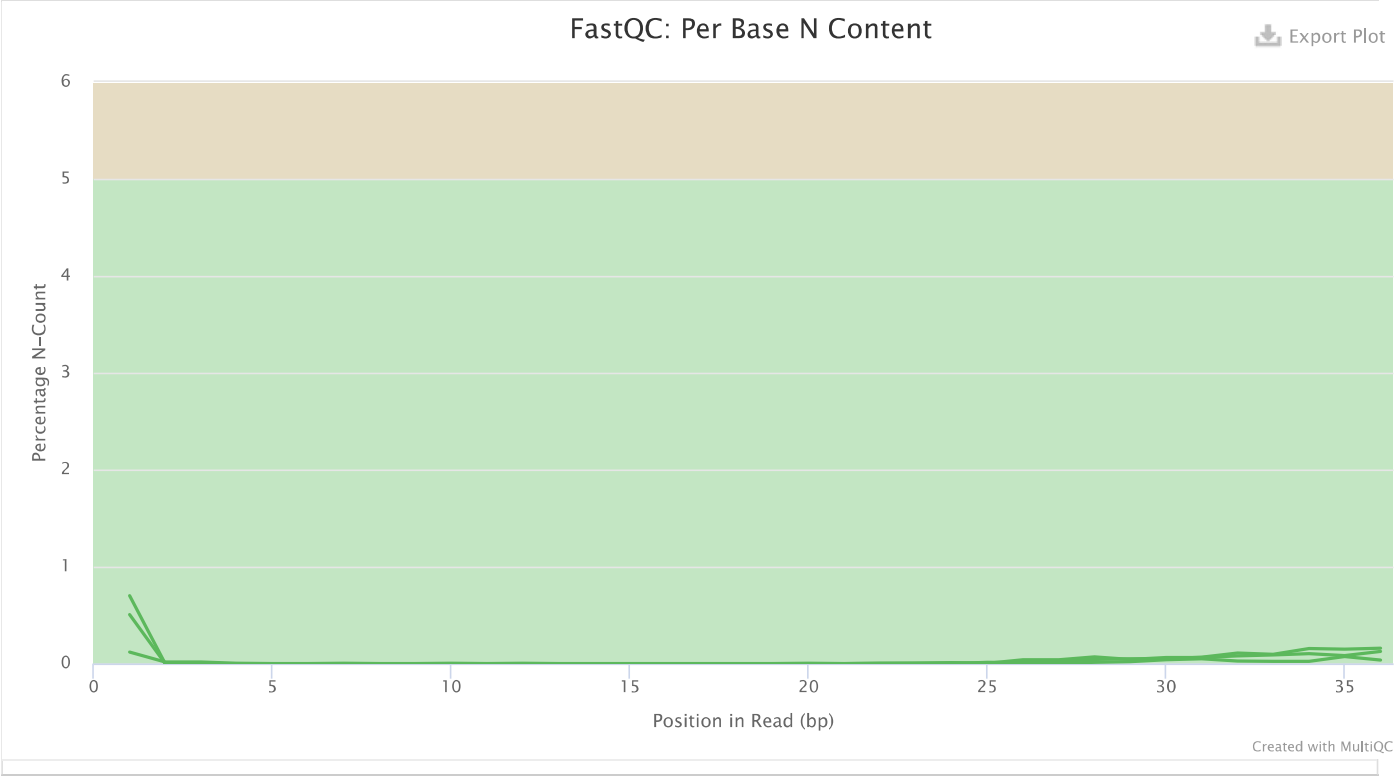
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Percentages Counts



Per Base N Content 3

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

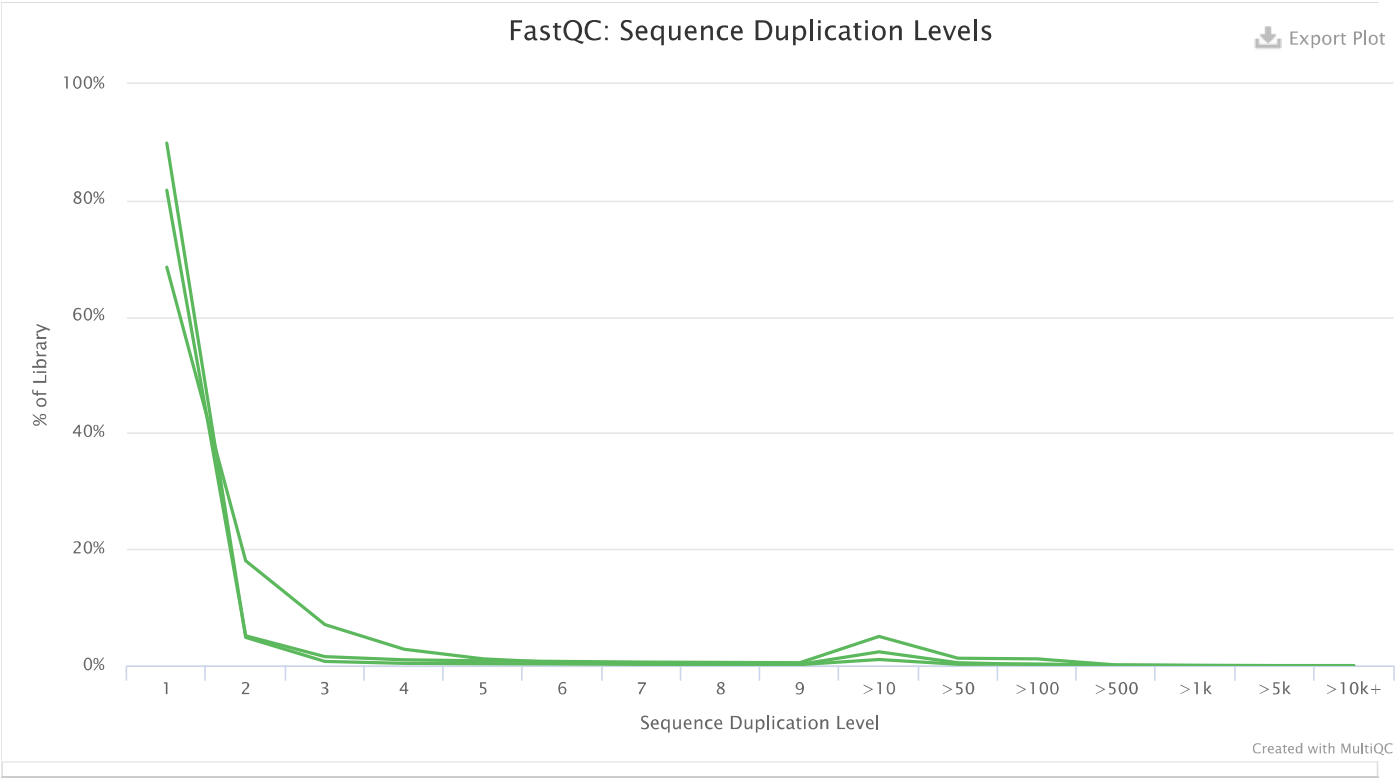


Sequence Length Distribution 3

All samples have sequences of a single length (36bp).

Sequence Duplication Levels 3

The relative level of duplication found for every sequence.



Overrepresented sequences 3

The total amount of overrepresented sequences found in each library.

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

Adapter Content 3

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).

