



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

Report generated on 2023-10-02, 13:29 CEST based on data in: /DISK1/research/inea0001/RAW_FASTQ/FASTQC

General Statistics

[Copy table](#)[Configure Columns](#)[Plot](#)

Showing 92/92 rows and 3/6 columns.

Sample Name	% Dups	% GC	M Seqs
1003L	68.6%	53%	24.9
1003M	69.7%	52%	30.3
1010L	70.3%	51%	33.1
1010M	62.4%	51%	27.9
1012L	67.1%	51%	27.3
1012M	64.8%	52%	23.4
1014L	66.5%	51%	27.7
1014M	72.1%	51%	35.7
1015L	70.5%	52%	30.1
1015M	71.1%	52%	26.7
1016L	65.2%	51%	29.3
1016M	61.4%	52%	31.5
1017L	71.7%	50%	28.6
1017M	64.3%	51%	27.7
1018L	64.1%	51%	23.0
1018M	66.3%	51%	25.7
1022L	65.7%	50%	25.6
1022M	52.8%	51%	20.5
1025L	65.5%	51%	24.9
1025M	70.6%	53%	26.4
1029L	64.9%	51%	28.1
1029M	67.2%	52%	28.4
1031L	61.8%	51%	29.6
1031M	65.5%	52%	27.3
1032L	69.3%	52%	29.3
1032M	65.9%	51%	29.7
1034L	65.0%	51%	29.7

Sample Name	% Dups	% GC	M Seqs
1034M	66.7%	52%	26.8
1045L	77.1%	50%	27.3
1045M	68.2%	51%	27.2
1047L	69.7%	52%	24.9
1047M	79.7%	51%	26.1
1049L	78.5%	53%	26.8
1049M	75.7%	55%	29.1
1051L	83.6%	53%	25.2
1051M	73.6%	52%	26.9
1052L	82.7%	52%	25.4
1052M	83.6%	57%	26.8
10555L	64.8%	51%	26.3
1055M	78.3%	53%	29.0
1056L	77.7%	53%	27.6
1056M	78.6%	51%	25.6
1060L	79.4%	54%	27.5
1060M	76.8%	54%	31.2
1061L	69.0%	51%	26.1
1061M	80.4%	53%	29.2
1064L	83.4%	52%	26.2
1064M	83.4%	53%	25.9
1067L	72.5%	52%	29.3
1067M	68.3%	51%	25.1
1068L	73.2%	51%	29.9
1068M	70.2%	51%	28.0
1070L	73.0%	53%	28.5
1070M	66.3%	52%	26.9
1071L	65.9%	52%	22.2
1071M	63.8%	52%	27.5
1074L	70.3%	52%	29.7
1074M	71.1%	51%	25.3
1077L	72.6%	50%	29.9
1077M	86.4%	51%	27.7
1079L	83.3%	52%	26.7

Sample Name	% Dups	% GC	M Seqs
1079M	74.7%	51%	35.9
1082L	78.0%	53%	27.7
1082M	72.8%	52%	26.7
1084L	73.3%	52%	26.4
1084M	89.4%	53%	23.8
1088L	67.2%	52%	27.9
1088M	66.4%	52%	26.3
1092L	69.8%	51%	21.9
1092M	76.5%	55%	27.8
3001L	68.1%	51%	29.8
3001M	67.4%	52%	29.0
3005L	90.4%	52%	24.2
3005M	82.8%	51%	27.7
3007L	71.4%	52%	28.2
3007M	78.4%	52%	31.8
3013L	95.5%	52%	48.0
3013M	96.1%	52%	64.0
3015L	75.0%	52%	29.9
3015M	77.8%	53%	25.4
3016L	71.7%	52%	29.8
3016M	45.8%	53%	21.4
3018L	76.7%	53%	27.1
3018M	80.8%	52%	26.3
3019L	82.8%	52%	45.8
3019M	78.0%	51%	30.6
3028L	73.1%	51%	27.2
3028M	69.9%	53%	30.7
3031L	73.8%	52%	27.8
3031M	70.8%	52%	30.3
3032L	69.4%	51%	25.8
3032M	78.1%	56%	23.0

FastQC

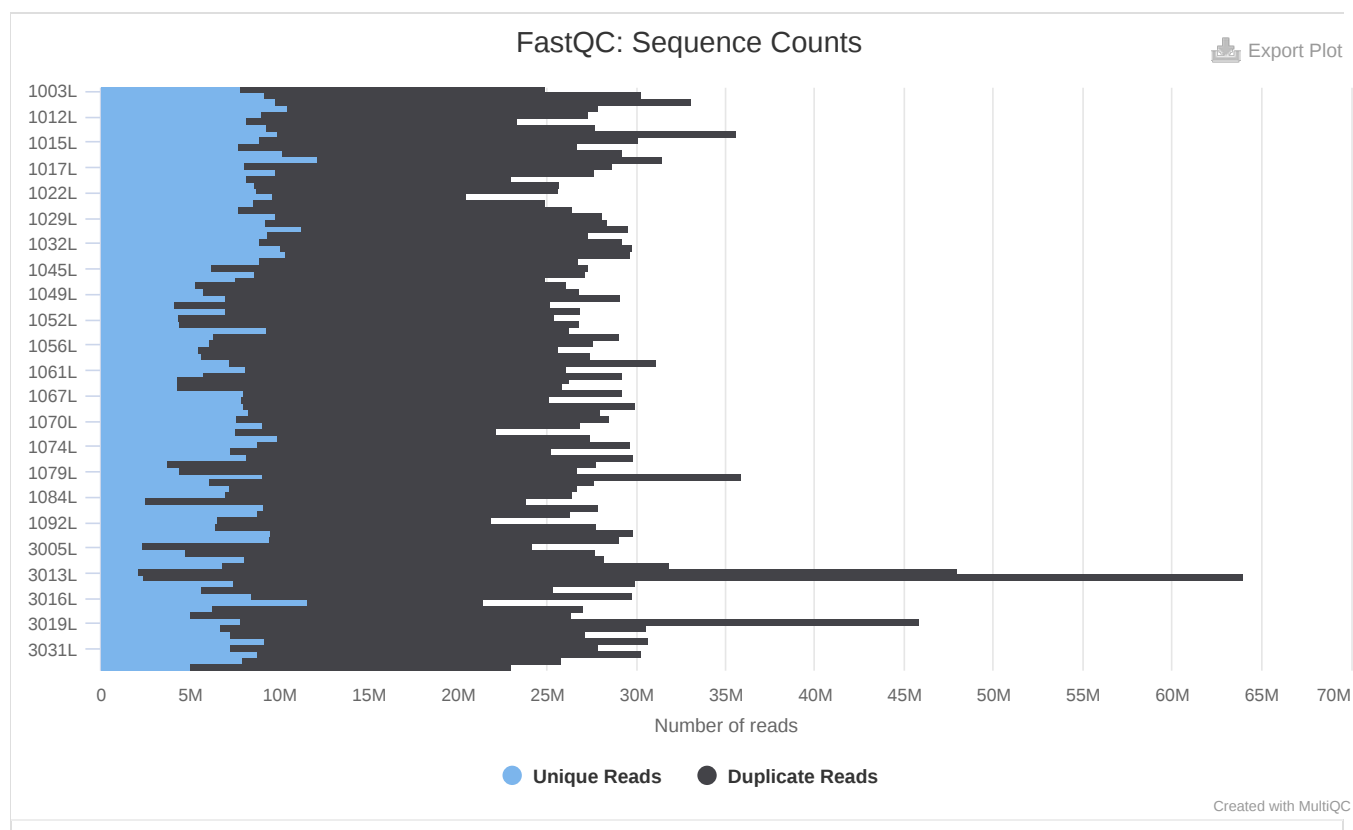
FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

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

Number of reads

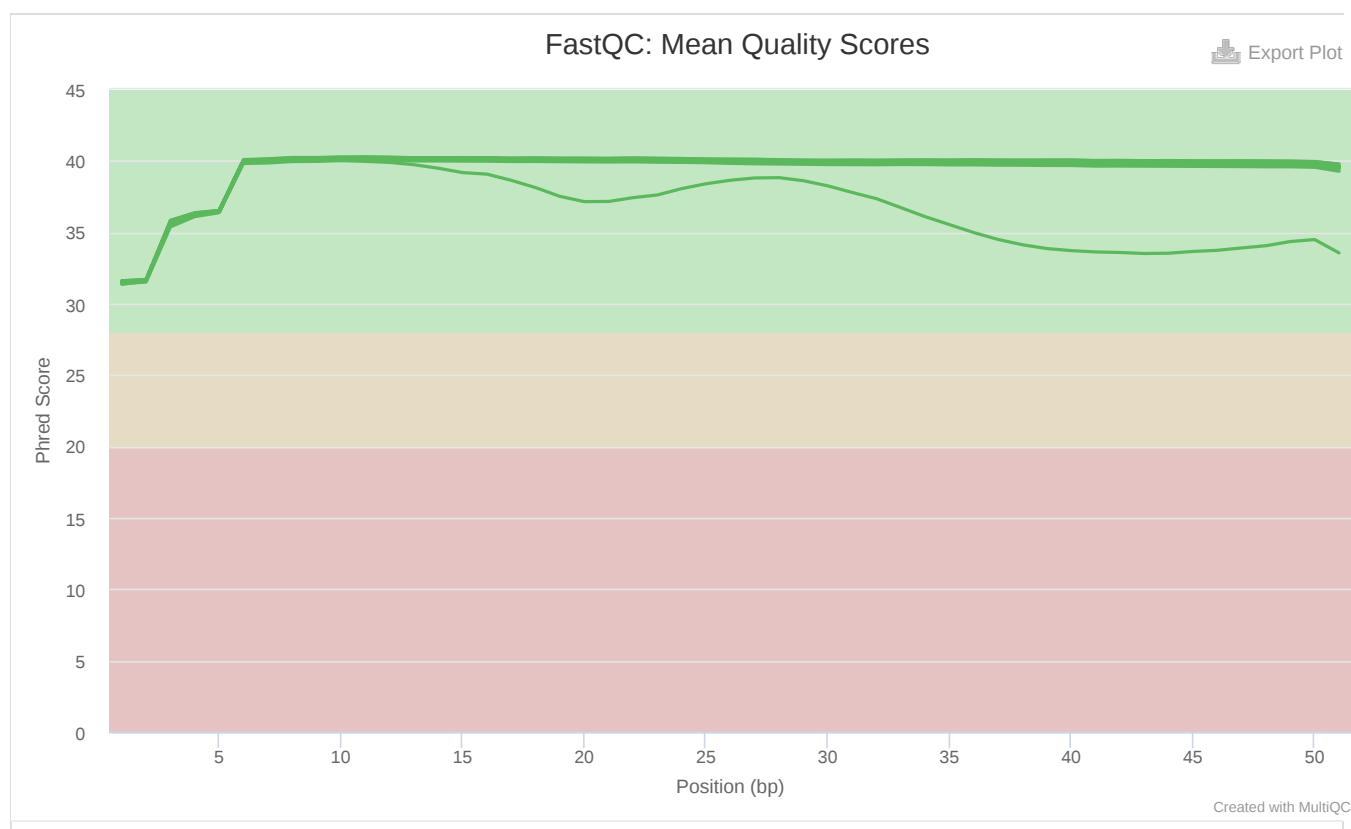
Percentages



Sequence Quality Histograms

92

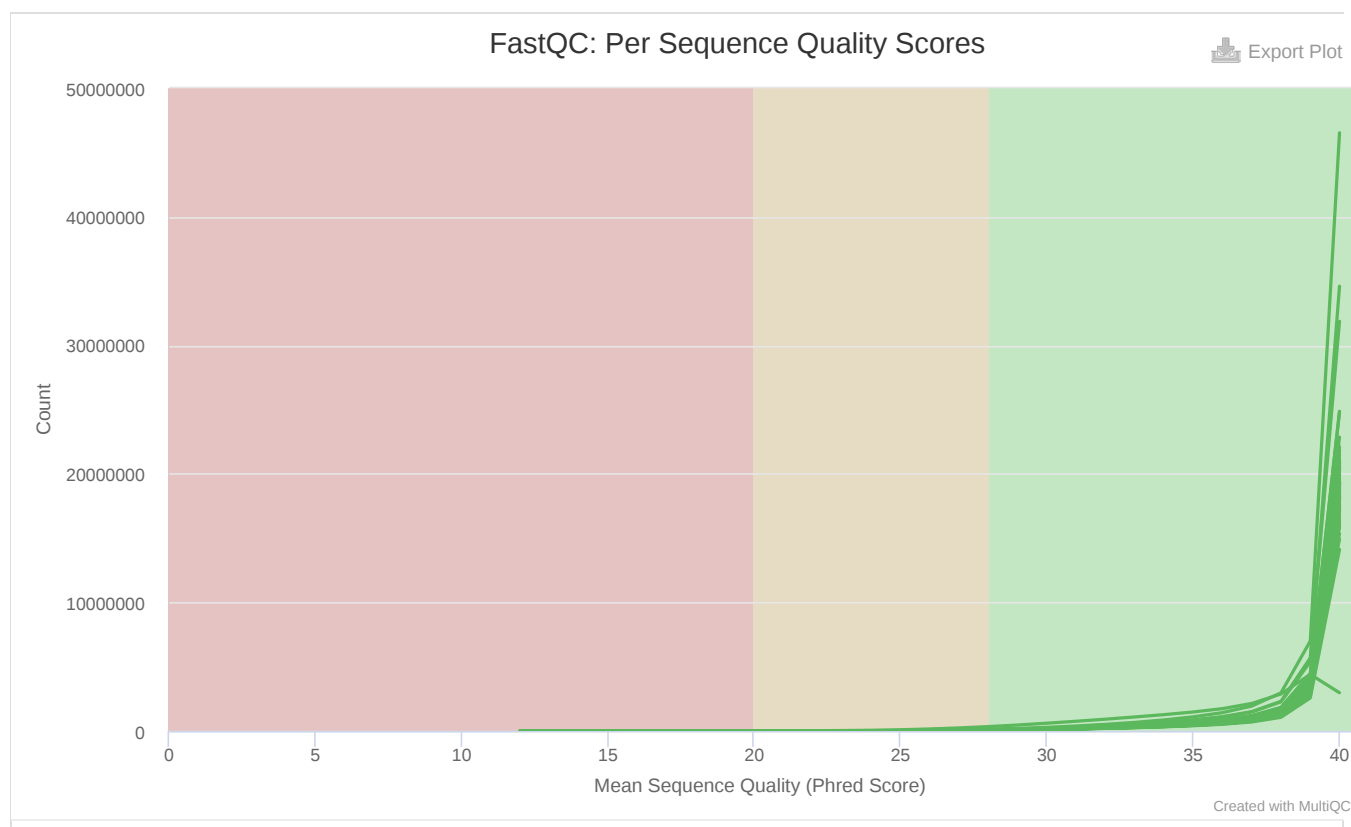
The mean quality value across each base position in the read.



Per Sequence Quality Scores

92

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



Per Base Sequence Content

90

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

73

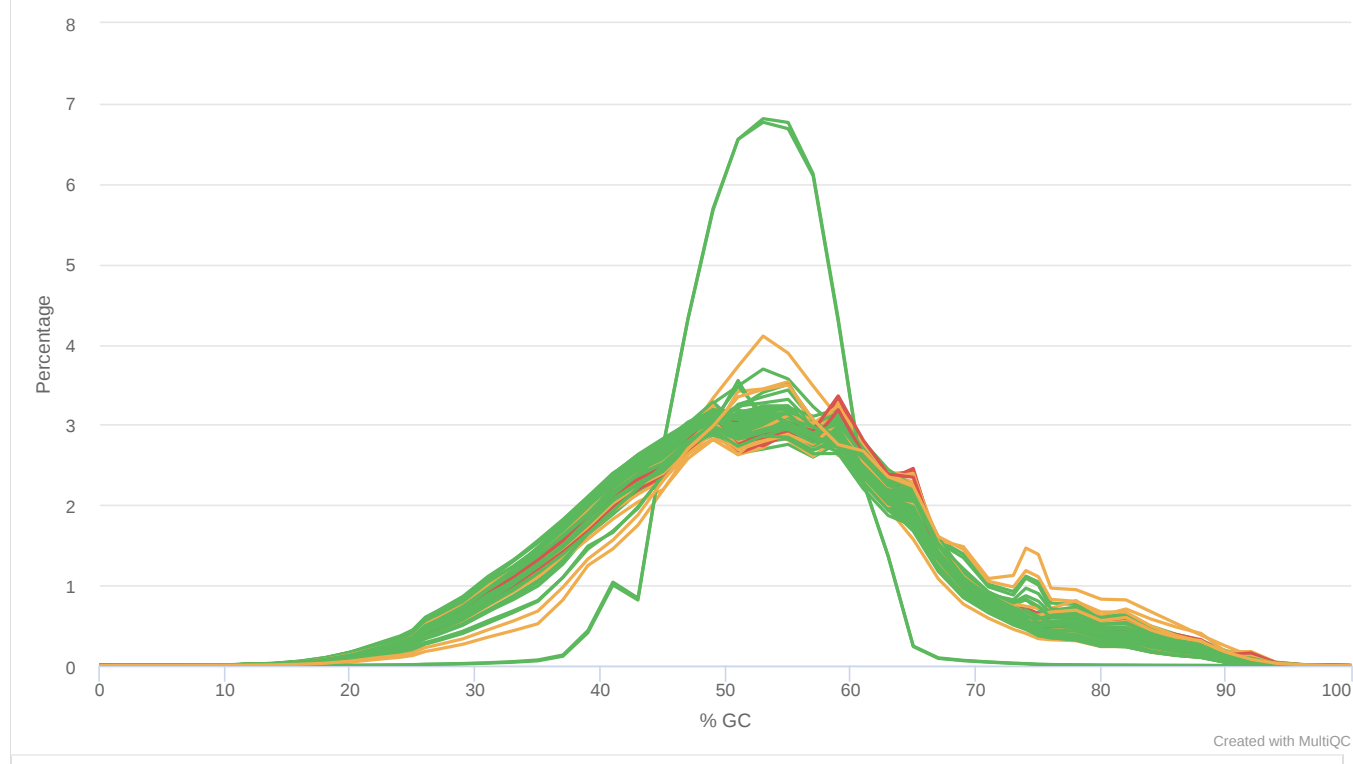
11

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

Percentages

Counts

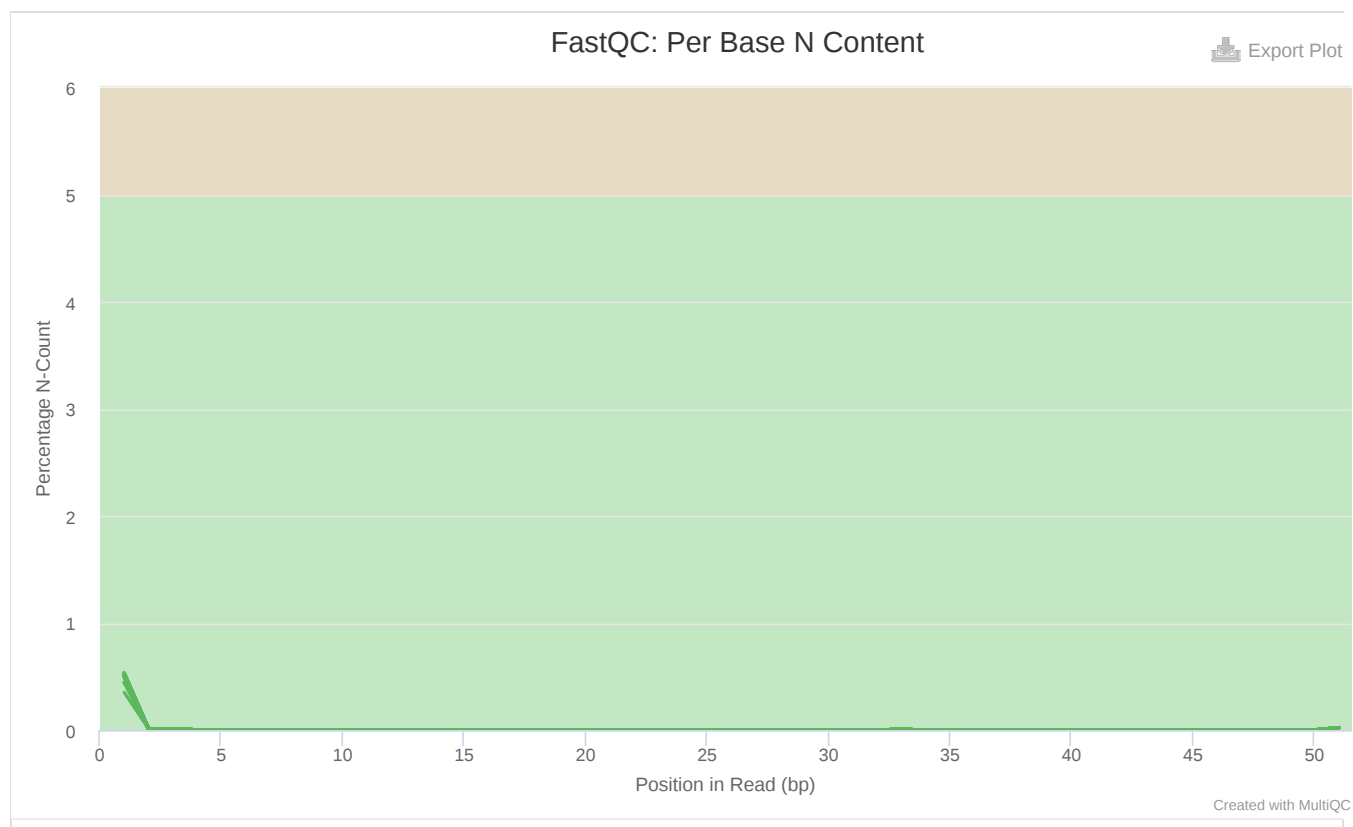
FastQC: Per Sequence GC Content

 Export Plot

Per Base N Content

92

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



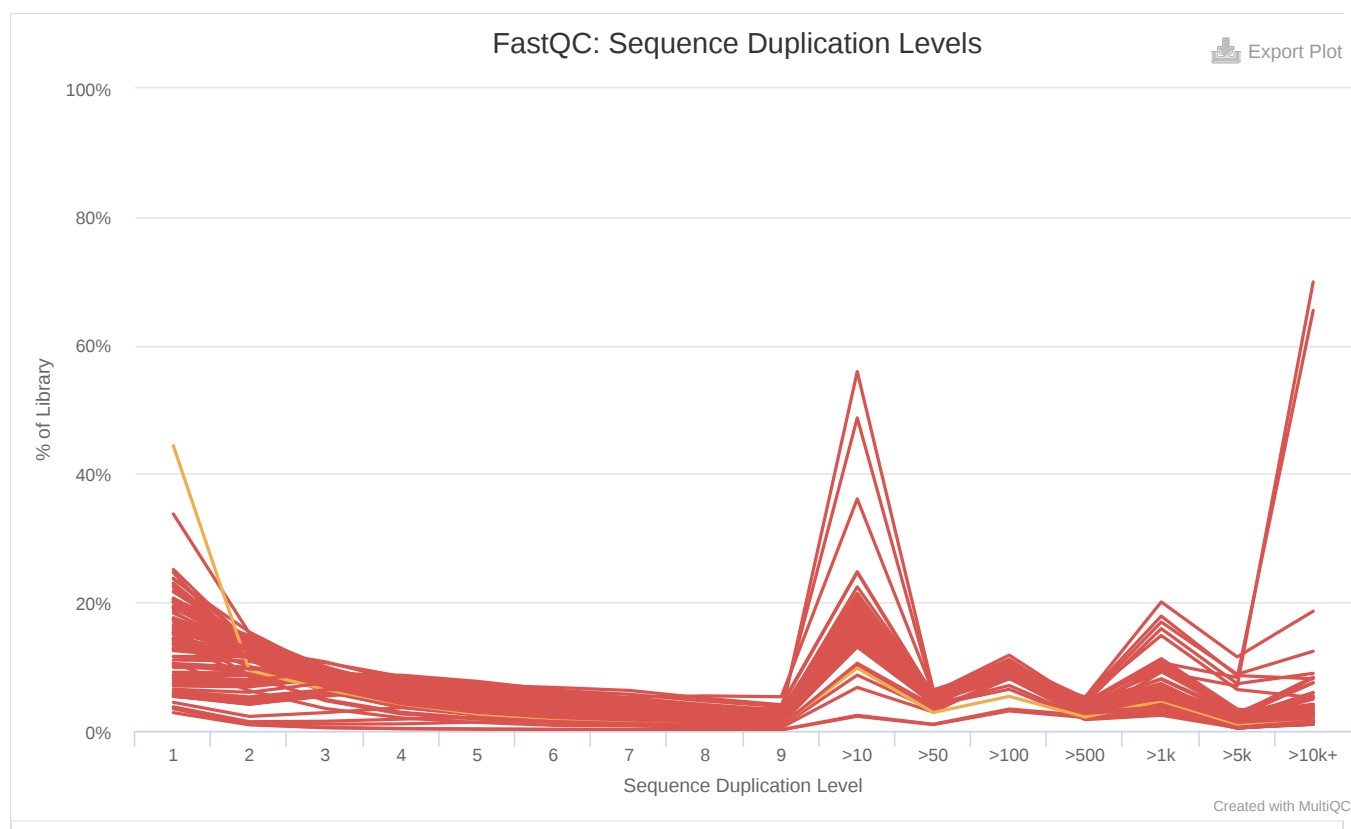
Sequence Length Distribution

92

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

Sequence Duplication Levels

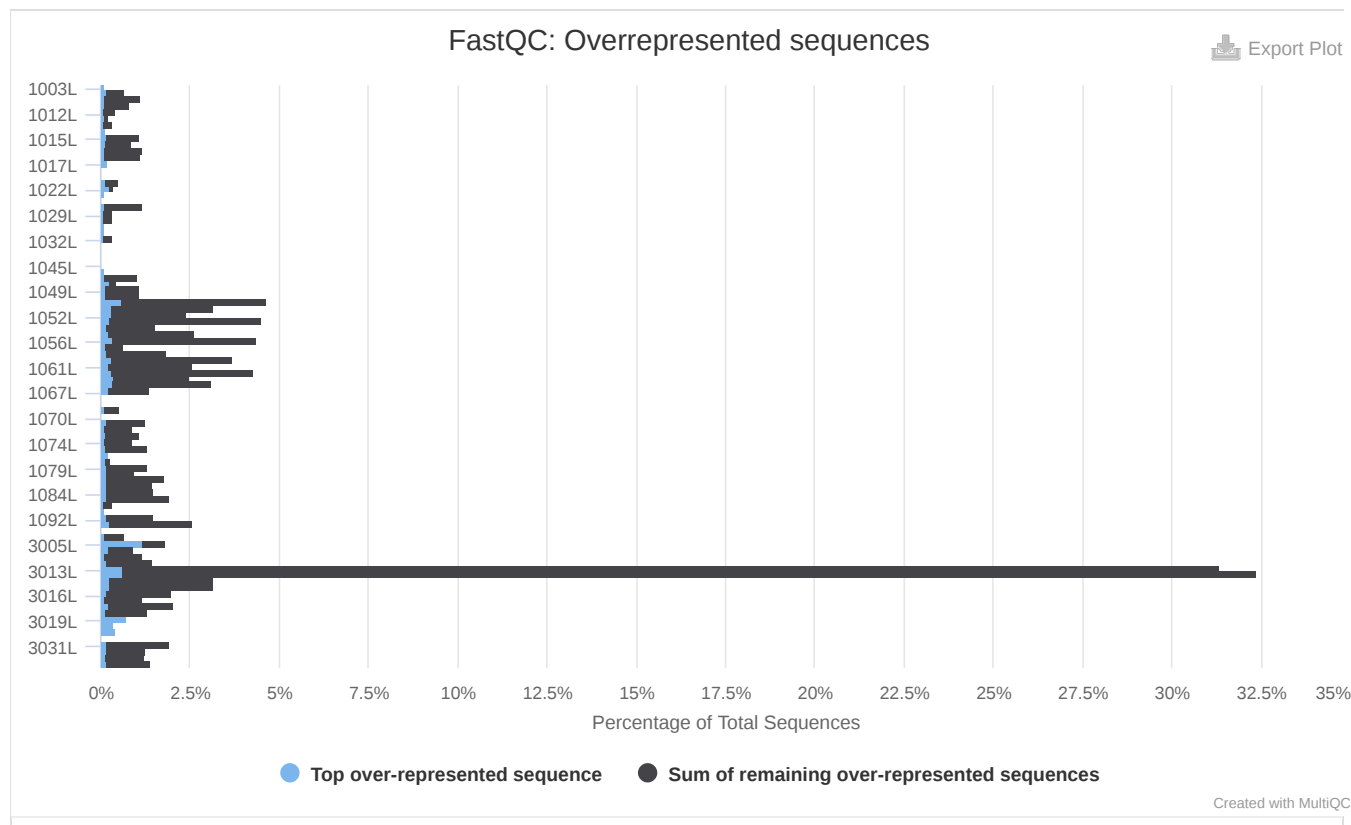
The relative level of duplication found for every sequence.



Overrepresented sequences

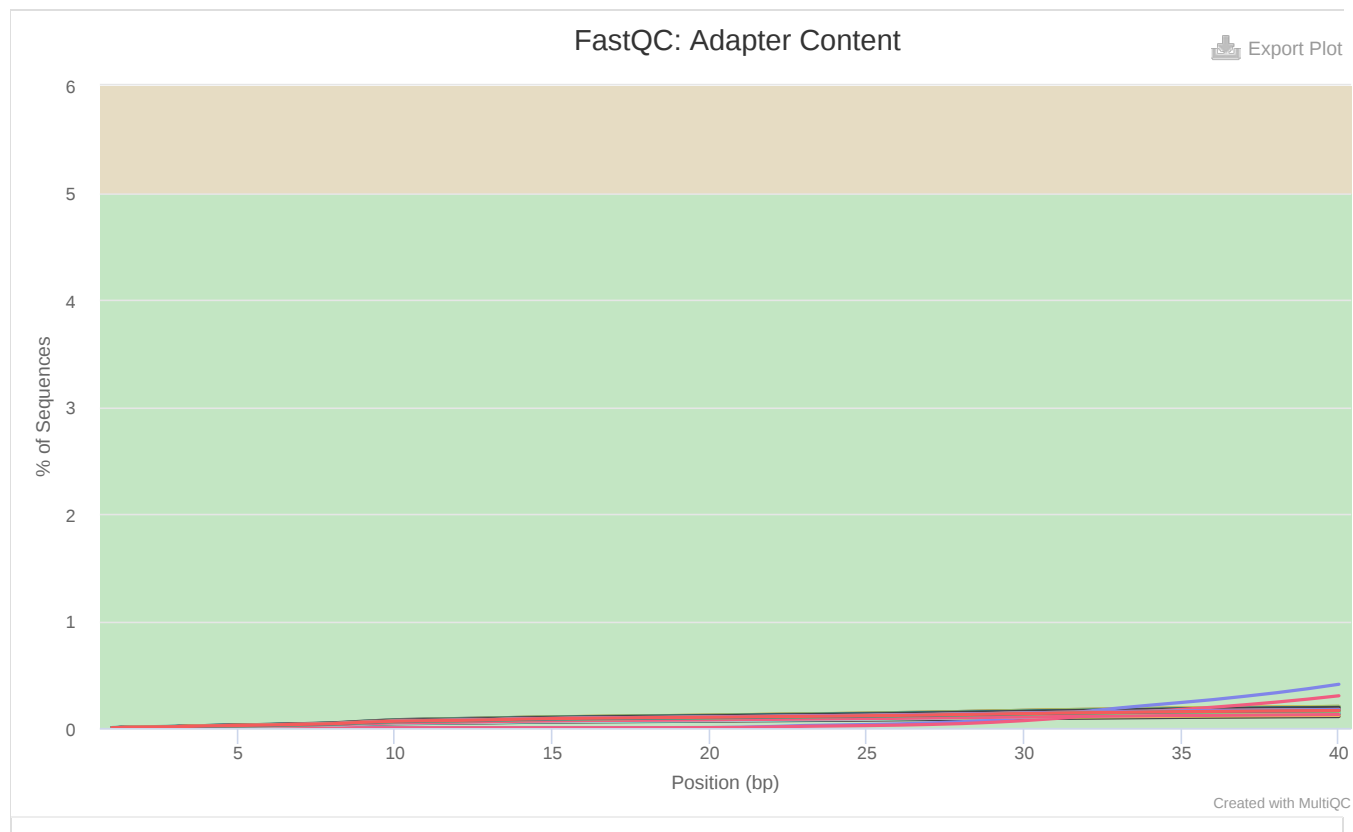
12 79

The total amount of overrepresented sequences found in each library.



Adapter Content 92

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



Status Checks

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

