



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

Report generated on 2023-10-03, 12:39 CEST based on data in: /DISK1/research/inea0001/TRIMMED_FASTQ/TRIM_FASTQC

General Statistics

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

Showing 92/92 rows and 3/6 columns.

Sample Name	% Dups	% GC	M Seqs
1003L_trim	68.8%	53%	24.8
1003M_trim	69.8%	52%	30.1
1010L_trim	70.4%	51%	32.9
1010M_trim	62.4%	51%	27.8
1012L_trim	67.2%	51%	27.2
1012M_trim	64.9%	52%	23.3
1014L_trim	66.6%	51%	27.6
1014M_trim	72.1%	51%	35.5
1015L_trim	70.5%	52%	30.0
1015M_trim	71.2%	52%	26.6
1016L_trim	65.3%	51%	29.1
1016M_trim	61.5%	52%	31.3
1017L_trim	71.8%	50%	28.5
1017M_trim	64.5%	51%	27.5
1018L_trim	64.3%	51%	22.9
1018M_trim	66.4%	51%	25.6
1022L_trim	65.7%	50%	25.4
1022M_trim	52.9%	51%	20.4
1025L_trim	65.6%	51%	24.8
1025M_trim	70.7%	53%	26.3
1029L_trim	65.0%	51%	28.0
1029M_trim	67.3%	52%	28.3
1031L_trim	61.9%	51%	29.5
1031M_trim	65.7%	52%	27.2
1032L_trim	69.4%	52%	29.1
1032M_trim	65.9%	51%	29.6
1034L_trim	65.0%	51%	29.5

Sample Name	% Dups	% GC	M Seqs
1034M_trim	66.8%	52%	26.7
1045L_trim	77.2%	50%	27.2
1045M_trim	68.2%	51%	27.0
1047L_trim	69.7%	52%	24.7
1047M_trim	79.6%	51%	25.9
1049L_trim	78.5%	53%	26.6
1049M_trim	75.7%	55%	29.0
1051L_trim	83.5%	53%	24.9
1051M_trim	73.7%	52%	26.7
1052L_trim	82.6%	52%	25.2
1052M_trim	83.6%	57%	26.6
10555L_trim	64.8%	51%	26.1
1055M_trim	78.3%	53%	28.8
1056L_trim	77.7%	53%	27.4
1056M_trim	78.6%	51%	25.4
1060L_trim	79.4%	54%	27.3
1060M_trim	76.9%	54%	31.0
1061L_trim	69.0%	51%	26.0
1061M_trim	80.4%	53%	29.1
1064L_trim	83.3%	52%	26.0
1064M_trim	83.4%	53%	25.7
1067L_trim	72.5%	52%	29.1
1067M_trim	68.3%	51%	25.0
1068L_trim	73.2%	51%	29.8
1068M_trim	70.2%	51%	27.8
1070L_trim	73.0%	53%	28.3
1070M_trim	66.3%	52%	26.8
1071L_trim	65.9%	52%	22.1
1071M_trim	63.9%	52%	27.3
1074L_trim	70.3%	52%	29.5
1074M_trim	71.1%	51%	25.1
1077L_trim	72.5%	50%	29.7
1077M_trim	86.4%	51%	27.6
1079L_trim	83.3%	52%	26.5

Sample Name	% Dups	% GC	M Seqs
1079M_trim	74.8%	51%	35.7
1082L_trim	78.0%	53%	27.6
1082M_trim	72.8%	52%	26.5
1084L_trim	73.4%	52%	26.3
1084M_trim	89.4%	53%	23.7
1088L_trim	67.2%	52%	27.7
1088M_trim	66.5%	52%	26.1
1092L_trim	69.5%	51%	21.8
1092M_trim	76.5%	55%	27.7
3001L_trim	68.1%	51%	29.7
3001M_trim	67.4%	52%	28.9
3005L_trim	90.3%	52%	23.8
3005M_trim	82.7%	51%	27.5
3007L_trim	71.4%	52%	28.1
3007M_trim	78.4%	52%	31.7
3013L_trim	95.6%	52%	47.7
3013M_trim	96.2%	52%	63.7
3015L_trim	75.1%	52%	29.8
3015M_trim	77.8%	53%	25.3
3016L_trim	71.7%	52%	29.6
3016M_trim	40.9%	53%	20.5
3018L_trim	76.8%	53%	26.9
3018M_trim	80.8%	52%	26.1
3019L_trim	82.7%	52%	45.2
3019M_trim	77.9%	51%	30.3
3028L_trim	73.0%	51%	27.0
3028M_trim	70.0%	53%	30.5
3031L_trim	73.9%	52%	27.7
3031M_trim	70.8%	52%	30.1
3032L_trim	69.4%	51%	25.7
3032M_trim	78.2%	56%	22.9

FastQC

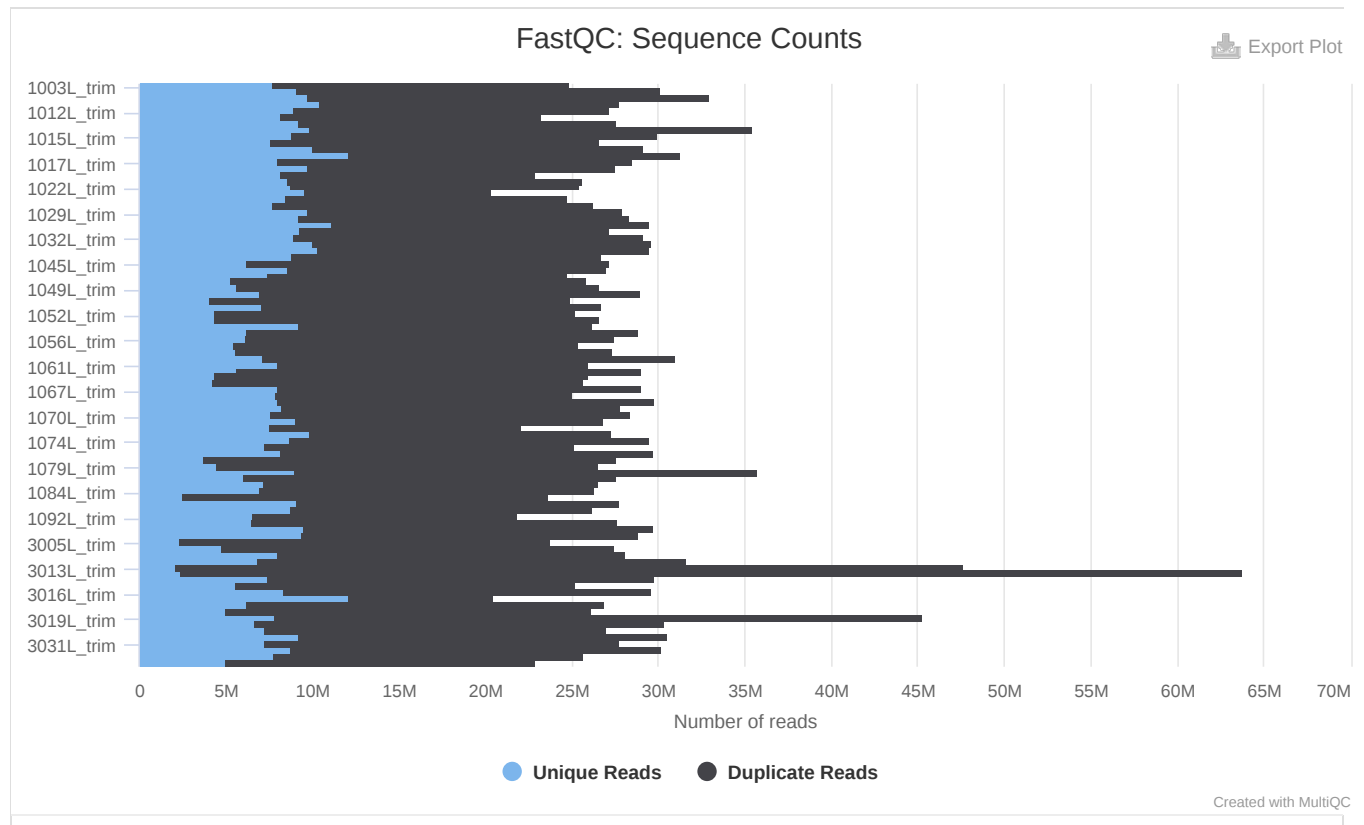
FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

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

Number of reads

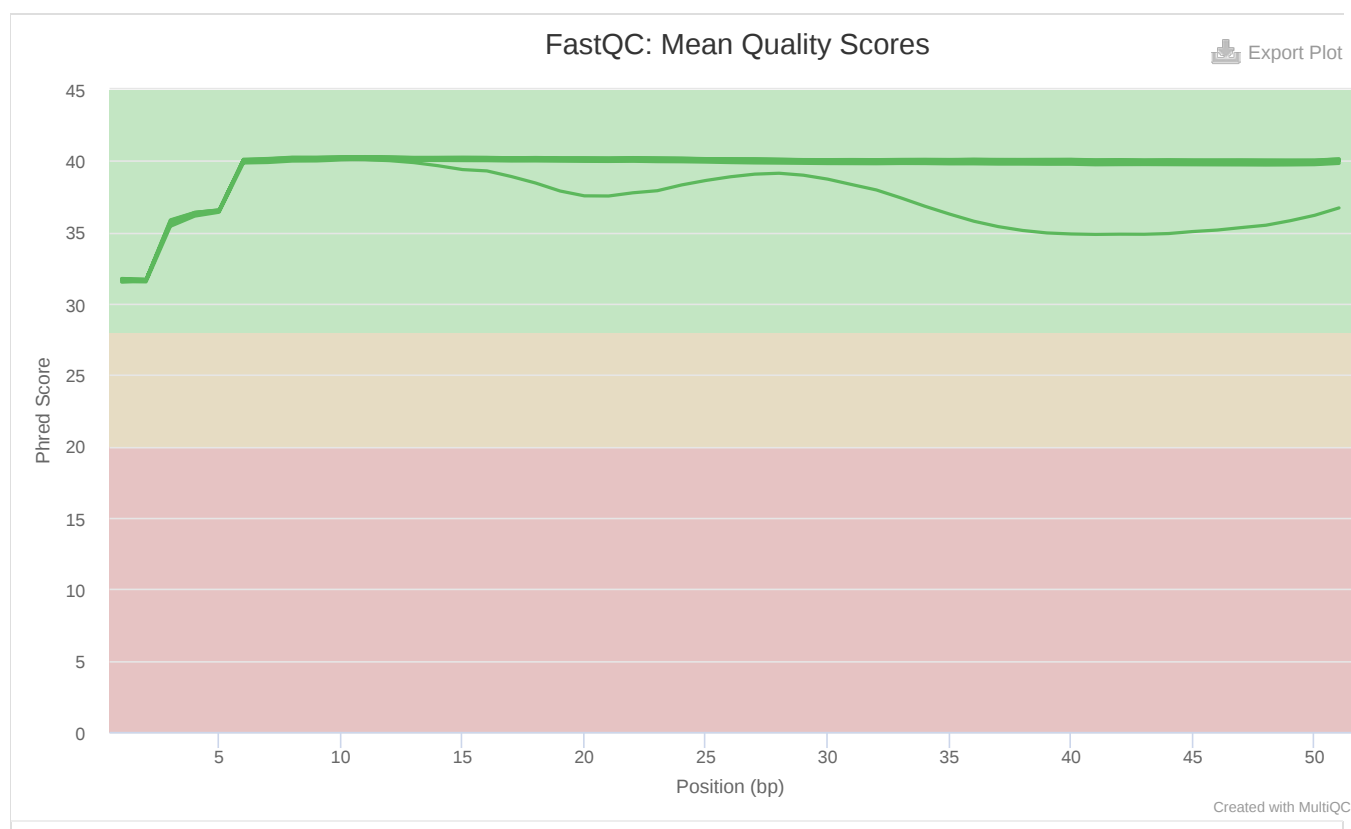
Percentages



Sequence Quality Histograms

92

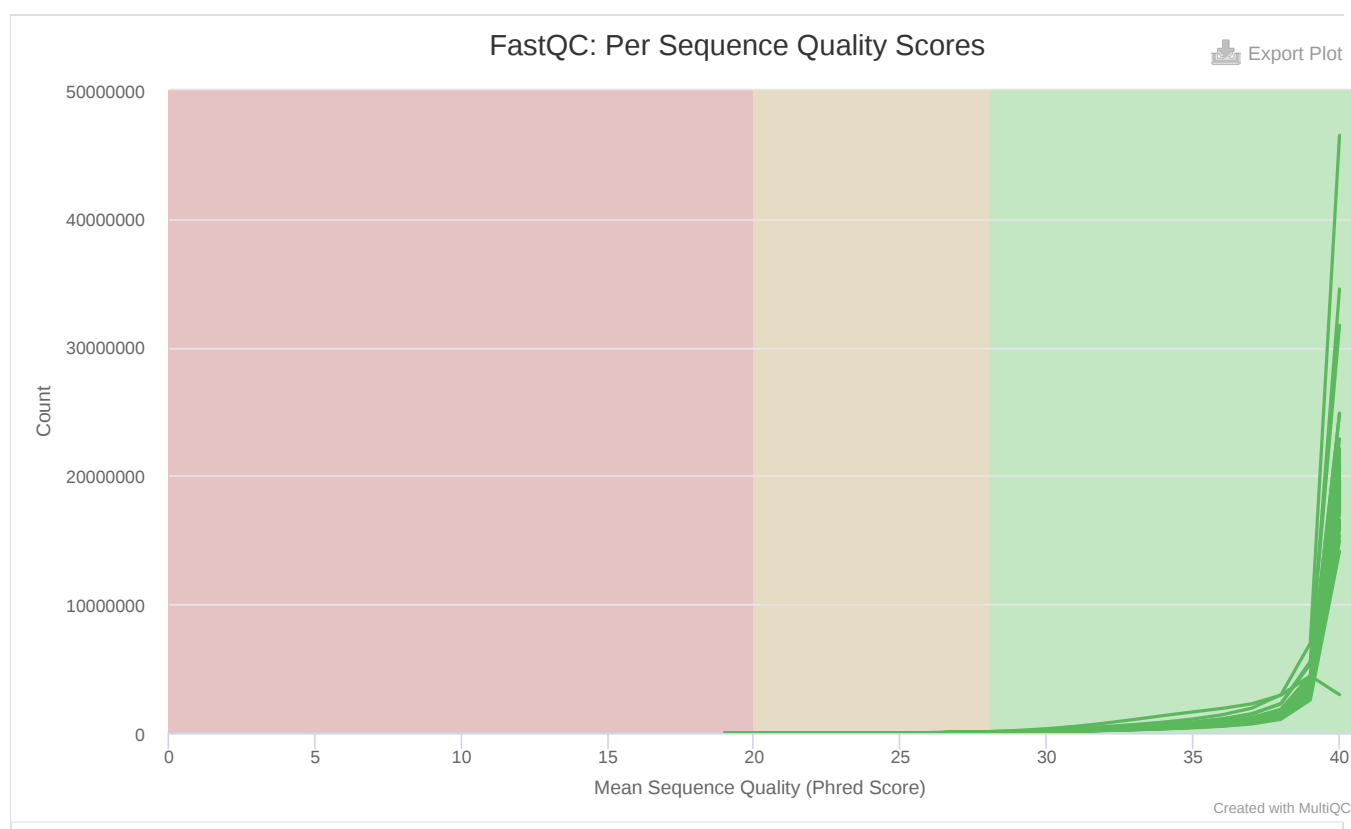
The mean quality value across each base position in the read.



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

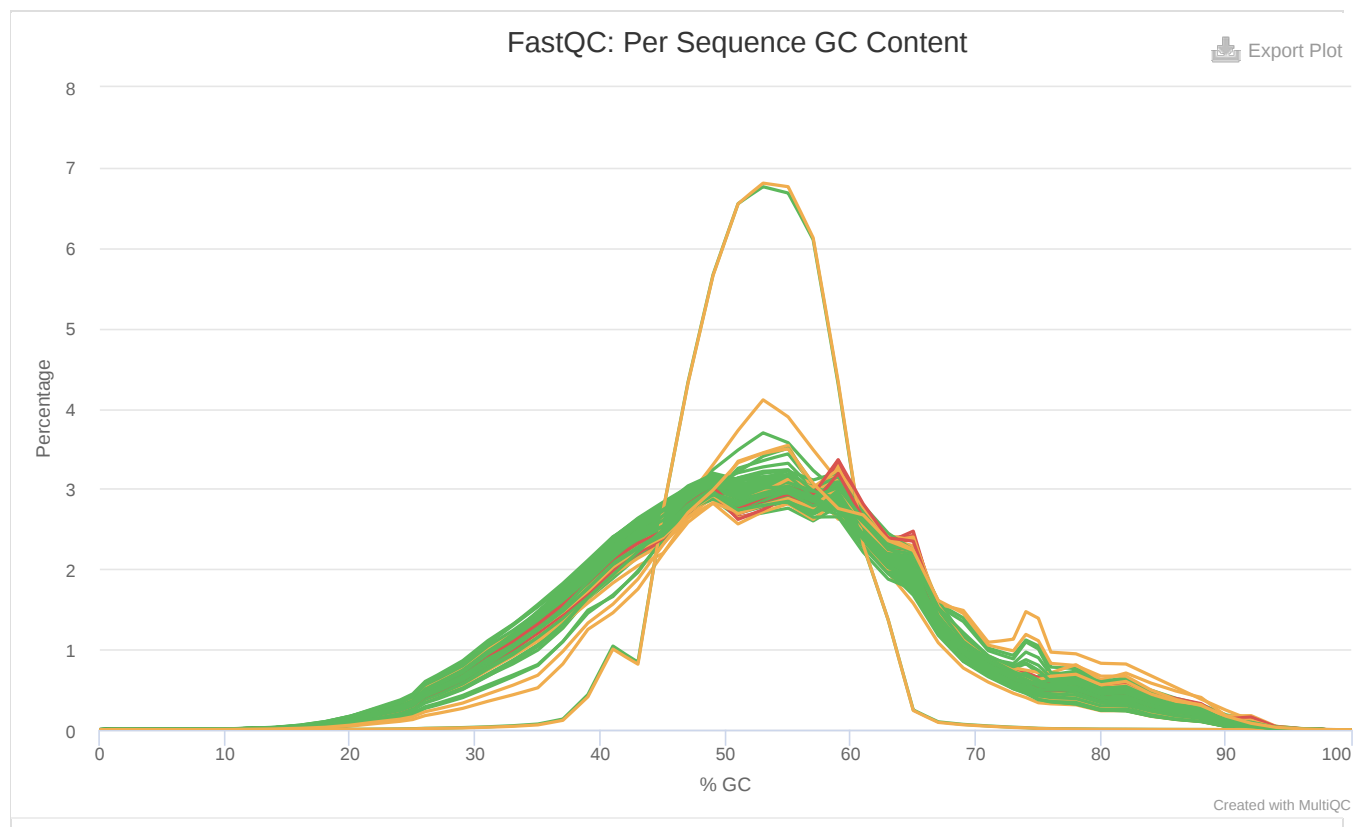
73

11

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

Percentages

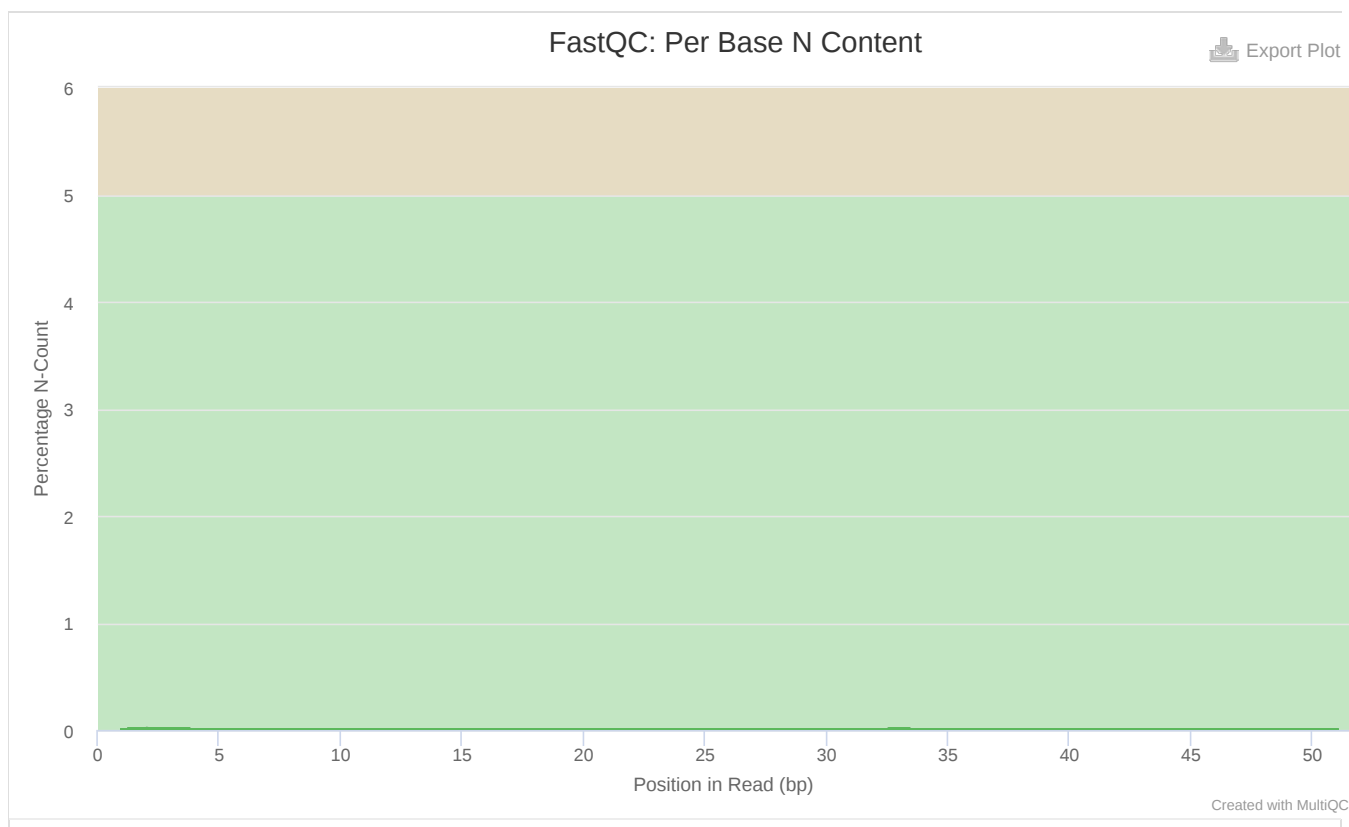
Counts



Per Base N Content

92

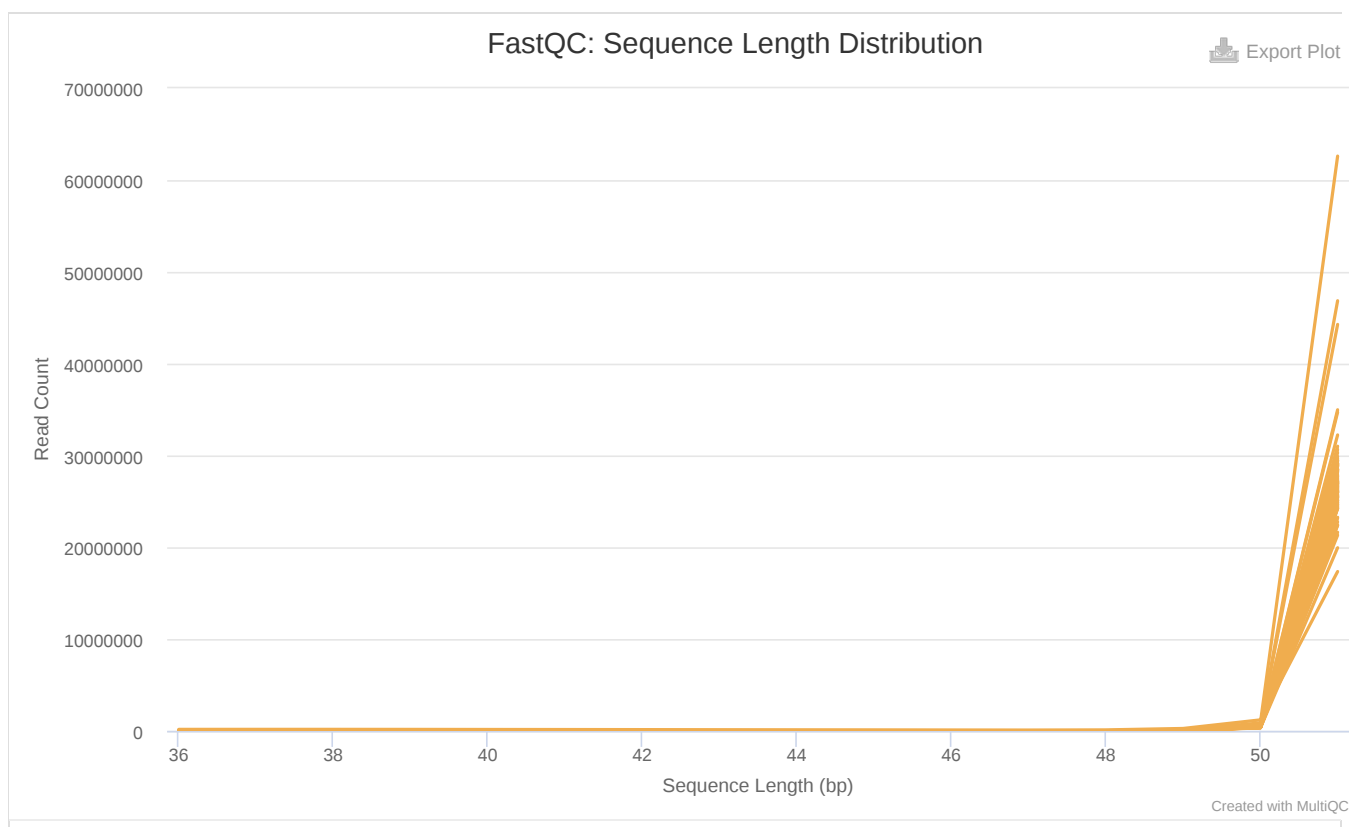
The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

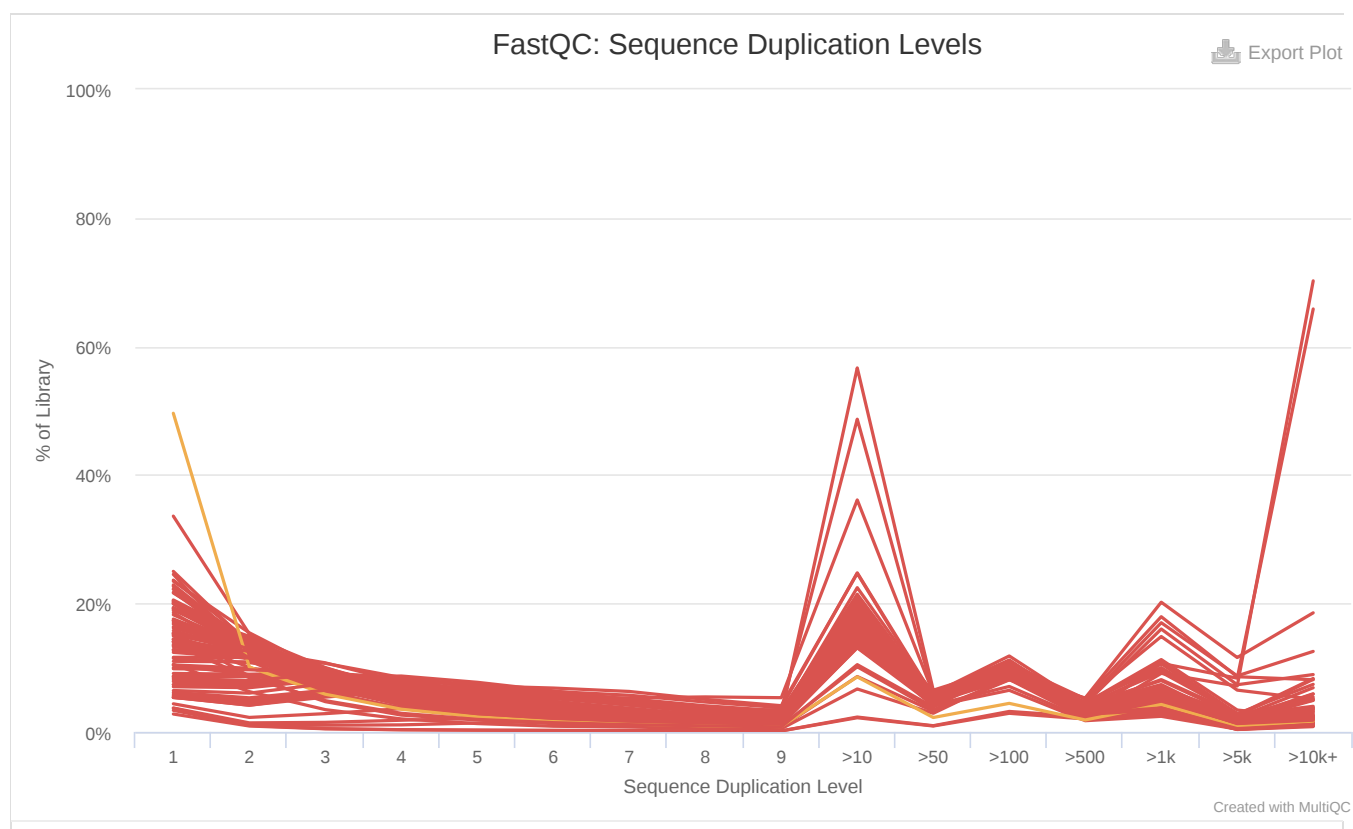
92

The distribution of fragment sizes (read lengths) found. See the FastQC help



Sequence Duplication Levels

The relative level of duplication found for every sequence.

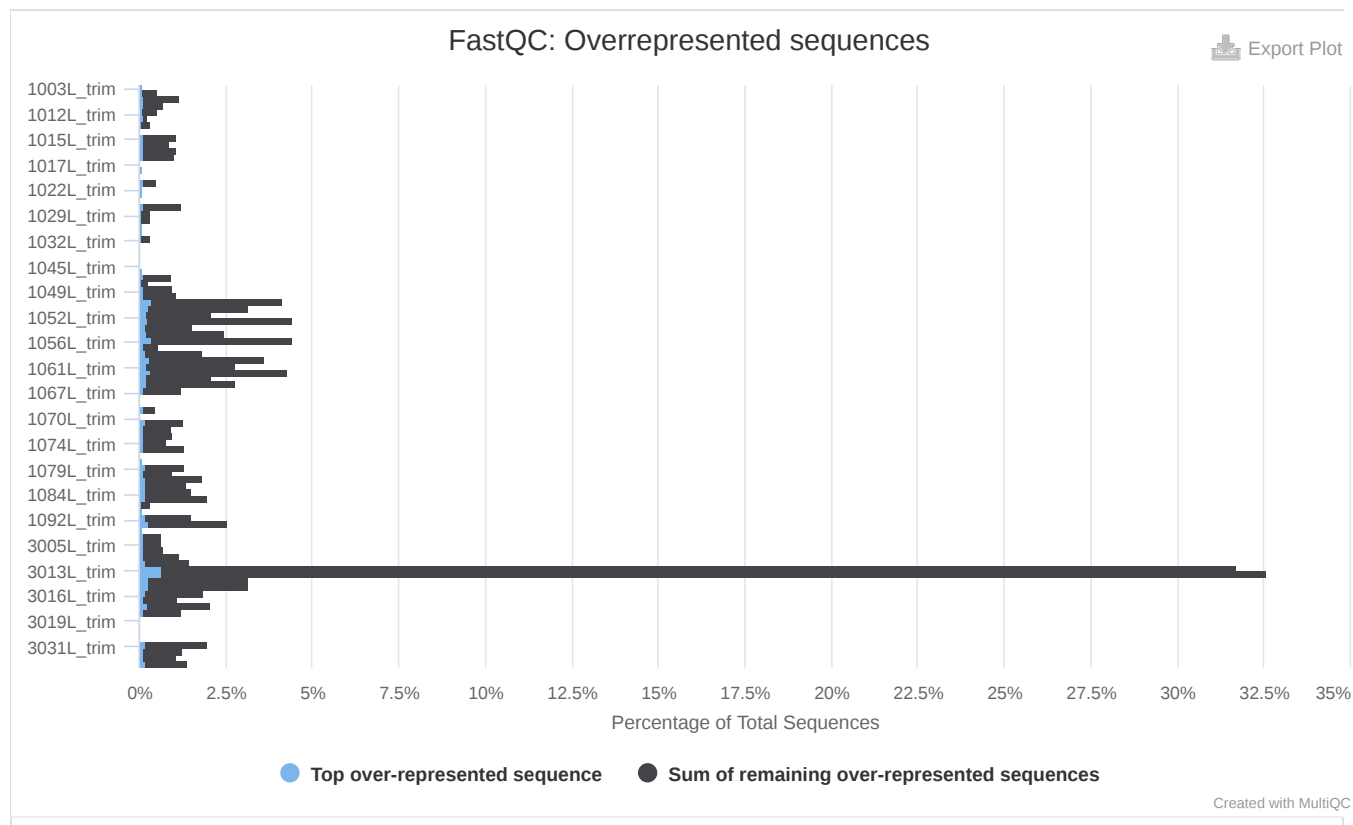


Overrepresented sequences

16

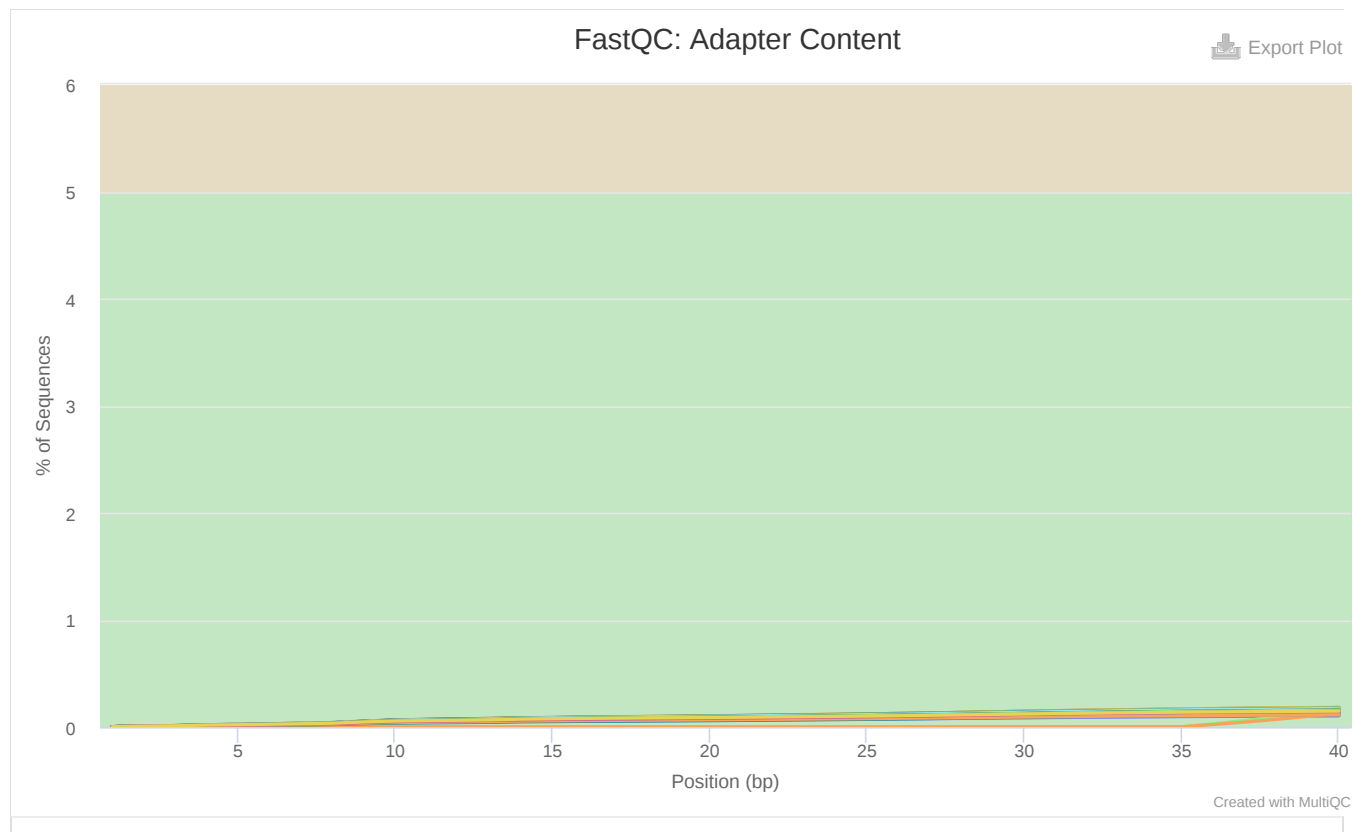
76

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).

