



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

Report generated on 2024-04-11, 10:36 CEST based on data in: /DISK1/research/inea0001/MASTERS\_THESIS/FASTQC

## General Statistics

Sample Name	% Dups	% GC	M Seqs
1003L	68.6%	53%	24.9
1003L_trim	68.8%	53%	24.8
1003M	69.7%	52%	30.3
1003M_trim	69.8%	52%	30.1
1010L	70.3%	51%	33.1
1010L_trim	70.4%	51%	32.9
1010M	62.4%	51%	27.9
1010M_trim	62.4%	51%	27.8
1012L	67.1%	51%	27.3
1012L_trim	67.2%	51%	27.2
1012M	64.8%	52%	23.4
1012M_trim	64.9%	52%	23.3
1014L	66.5%	51%	27.7
1014L_trim	66.6%	51%	27.6
1014M	72.1%	51%	35.7
1014M_trim	72.1%	51%	35.5
1015L	70.5%	52%	30.1
1015L_trim	70.5%	52%	30.0
1015M	71.1%	52%	26.7
1015M_trim	71.2%	52%	26.6
1016L	65.2%	51%	29.3
1016L_trim	65.3%	51%	29.1
1016M	61.4%	52%	31.5
1016M_trim	61.5%	52%	31.3
1017L	71.7%	50%	28.6
1017L_trim	71.8%	50%	28.5
1017M	64.3%	51%	27.7

Sample Name	% Dups	% GC	M Seqs
1017M_trim	64.5%	51%	27.5
1018L	64.1%	51%	23.0
1018L_trim	64.3%	51%	22.9
1018M	66.3%	51%	25.7
1018M_trim	66.4%	51%	25.6
1022L	65.7%	50%	25.6
1022L_trim	65.7%	50%	25.4
1022M	52.8%	51%	20.5
1022M_trim	52.9%	51%	20.4
1025L	65.5%	51%	24.9
1025L_trim	65.6%	51%	24.8
1025M	70.6%	53%	26.4
1025M_trim	70.7%	53%	26.3
1029L	64.9%	51%	28.1
1029L_trim	65.0%	51%	28.0
1029M	67.2%	52%	28.4
1029M_trim	67.3%	52%	28.3
1031L	61.8%	51%	29.6
1031L_trim	61.9%	51%	29.5
1031M	65.5%	52%	27.3
1031M_trim	65.7%	52%	27.2
1032L	69.3%	52%	29.3
1032L_trim	69.4%	52%	29.1
1032M	65.9%	51%	29.7
1032M_trim	65.9%	51%	29.6
1034L	65.0%	51%	29.7
1034L_trim	65.0%	51%	29.5
1034M	66.7%	52%	26.8
1034M_trim	66.8%	52%	26.7
1045L	77.1%	50%	27.3
1045L_trim	77.2%	50%	27.2
1045M	68.2%	51%	27.2
1045M_trim	68.2%	51%	27.0
1047L	69.7%	52%	24.9

Sample Name	% Dups	% GC	M Seqs
1047L_trim	69.7%	52%	24.7
1047M	79.7%	51%	26.1
1047M_trim	79.6%	51%	25.9
1049L	78.5%	53%	26.8
1049L_trim	78.5%	53%	26.6
1049M	75.7%	55%	29.1
1049M_trim	75.7%	55%	29.0
1051L	83.6%	53%	25.2
1051L_trim	83.5%	53%	24.9
1051M	73.6%	52%	26.9
1051M_trim	73.7%	52%	26.7
1052L	82.7%	52%	25.4
1052L_trim	82.6%	52%	25.2
1052M	83.6%	57%	26.8
1052M_trim	83.6%	57%	26.6
1055L	64.8%	51%	26.3
1055L_trim	64.8%	51%	26.1
1055M	78.3%	53%	29.0
1055M_trim	78.3%	53%	28.8
1056L	77.7%	53%	27.6
1056L_trim	77.7%	53%	27.4
1056M	78.6%	51%	25.6
1056M_trim	78.6%	51%	25.4
1060L	79.4%	54%	27.5
1060L_trim	79.4%	54%	27.3
1060M	76.8%	54%	31.2
1060M_trim	76.9%	54%	31.0
1061L	69.0%	51%	26.1
1061L_trim	69.0%	51%	26.0
1061M	80.4%	53%	29.2
1061M_trim	80.4%	53%	29.1
1064L	83.4%	52%	26.2
1064L_trim	83.3%	52%	26.0
1064M	83.4%	53%	25.9

Sample Name	% Dups	% GC	M Seqs
1064M_trim	83.4%	53%	25.7
1067L	72.5%	52%	29.3
1067L_trim	72.5%	52%	29.1
1067M	68.3%	51%	25.1
1067M_trim	68.3%	51%	25.0
1068L	73.2%	51%	29.9
1068L_trim	73.2%	51%	29.8
1068M	70.2%	51%	28.0
1068M_trim	70.2%	51%	27.8
1070L	73.0%	53%	28.5
1070L_trim	73.0%	53%	28.3
1070M	66.3%	52%	26.9
1070M_trim	66.3%	52%	26.8
1071L	65.9%	52%	22.2
1071L_trim	65.9%	52%	22.1
1071M	63.8%	52%	27.5
1071M_trim	63.9%	52%	27.3
1074L	70.3%	52%	29.7
1074L_trim	70.3%	52%	29.5
1074M	71.1%	51%	25.3
1074M_trim	71.1%	51%	25.1
1077L	72.6%	50%	29.9
1077L_trim	72.5%	50%	29.7
1077M	86.4%	51%	27.7
1077M_trim	86.4%	51%	27.6
1079L	83.3%	52%	26.7
1079L_trim	83.3%	52%	26.5
1079M	74.7%	51%	35.9
1079M_trim	74.8%	51%	35.7
1082L	78.0%	53%	27.7
1082L_trim	78.0%	53%	27.6
1082M	72.8%	52%	26.7
1082M_trim	72.8%	52%	26.5
1084L	73.3%	52%	26.4

Sample Name	% Dups	% GC	M Seqs
1084L_trim	73.4%	52%	26.3
1084M	89.4%	53%	23.8
1084M_trim	89.4%	53%	23.7
1088L	67.2%	52%	27.9
1088L_trim	67.2%	52%	27.7
1088M	66.4%	52%	26.3
1088M_trim	66.5%	52%	26.1
1092L	69.8%	51%	21.9
1092L_trim	69.5%	51%	21.8
1092M	76.5%	55%	27.8
1092M_trim	76.5%	55%	27.7
3001L	68.1%	51%	29.8
3001L_trim	68.1%	51%	29.7
3001M	67.4%	52%	29.0
3001M_trim	67.4%	52%	28.9
3005L	90.4%	52%	24.2
3005L_trim	90.3%	52%	23.8
3005M	82.8%	51%	27.7
3005M_trim	82.7%	51%	27.5
3007L	71.4%	52%	28.2
3007L_trim	71.4%	52%	28.1
3007M	78.4%	52%	31.8
3007M_trim	78.4%	52%	31.7
3013L	95.5%	52%	48.0
3013L_trim	95.6%	52%	47.7
3013M	96.1%	52%	64.0
3013M_trim	96.2%	52%	63.7
3015L	75.0%	52%	29.9
3015L_trim	75.1%	52%	29.8
3015M	77.8%	53%	25.4
3015M_trim	77.8%	53%	25.3
3016L	71.7%	52%	29.8
3016L_trim	71.7%	52%	29.6
3016M	45.8%	53%	21.4

Sample Name	% Dups	% GC	M Seqs
3016M_trim	40.9%	53%	20.5
3018L	76.7%	53%	27.1
3018L_trim	76.8%	53%	26.9
3018M	80.8%	52%	26.3
3018M_trim	80.8%	52%	26.1
3019L	82.8%	52%	45.8
3019L_trim	82.7%	52%	45.2
3019M	78.0%	51%	30.6
3019M_trim	77.9%	51%	30.3
3028L	73.1%	51%	27.2
3028L_trim	73.0%	51%	27.0
3028M	69.9%	53%	30.7
3028M_trim	70.0%	53%	30.5
3031L	73.8%	52%	27.8
3031L_trim	73.9%	52%	27.7
3031M	70.8%	52%	30.3
3031M_trim	70.8%	52%	30.1
3032L	69.4%	51%	25.8
3032L_trim	69.4%	51%	25.7
3032M	78.1%	56%	23.0
3032M_trim	78.2%	56%	22.9

# FastQC

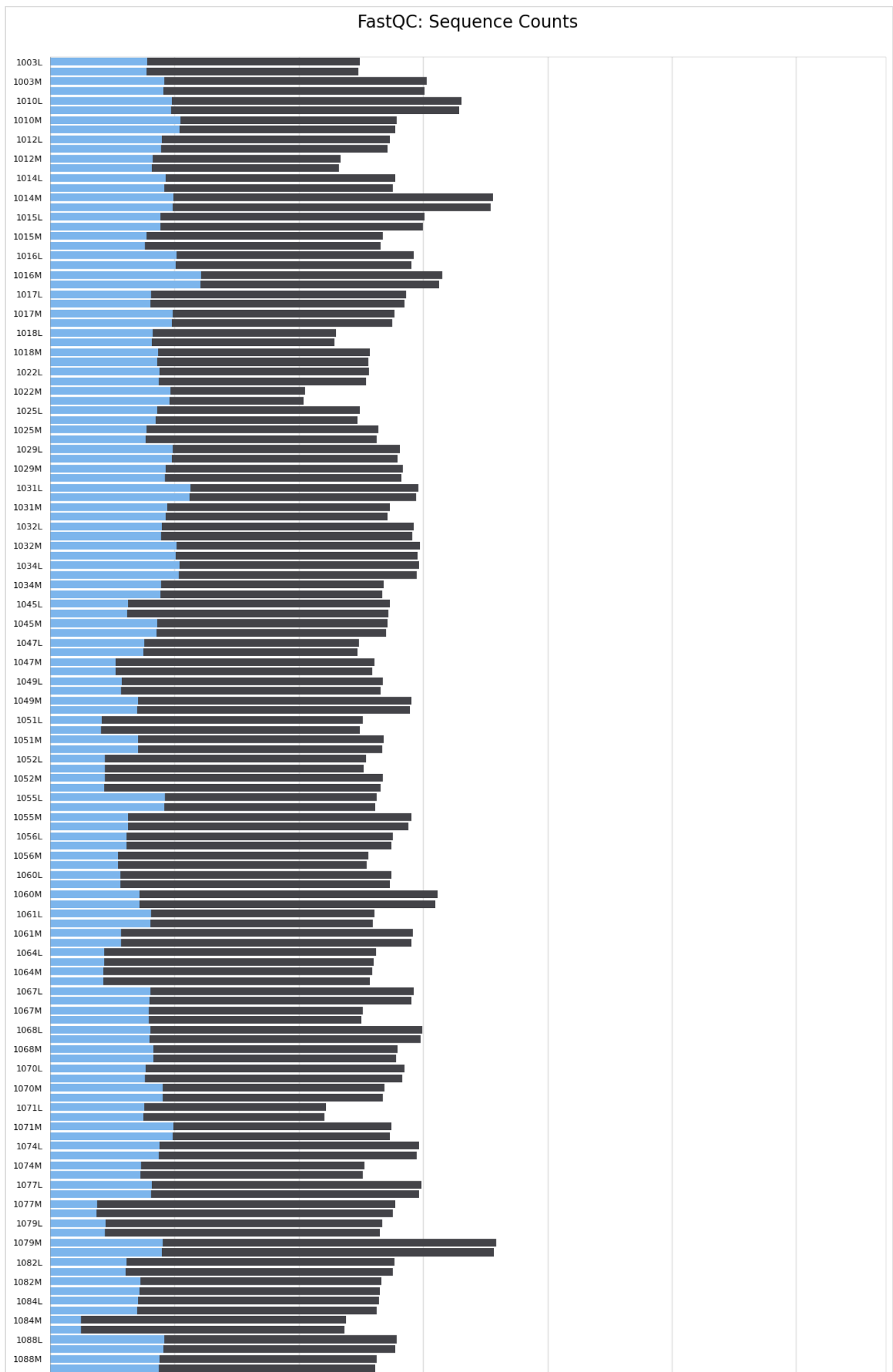
FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

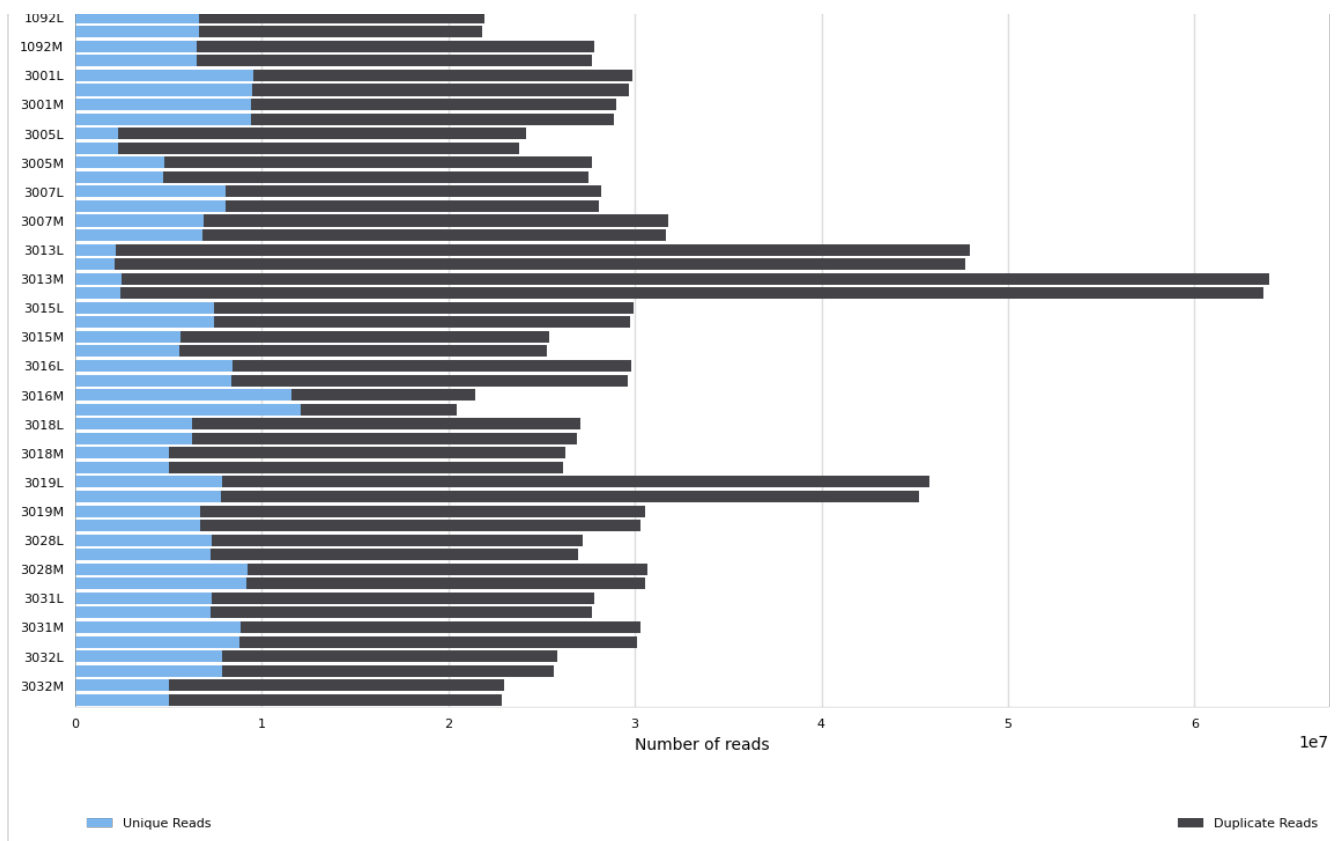
## Sequence Counts

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

Number of reads	Percentages
-----------------	-------------







## Sequence Quality Histograms

184

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



## Per Sequence Quality Scores

184

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



## Per Base Sequence Content

180

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: -

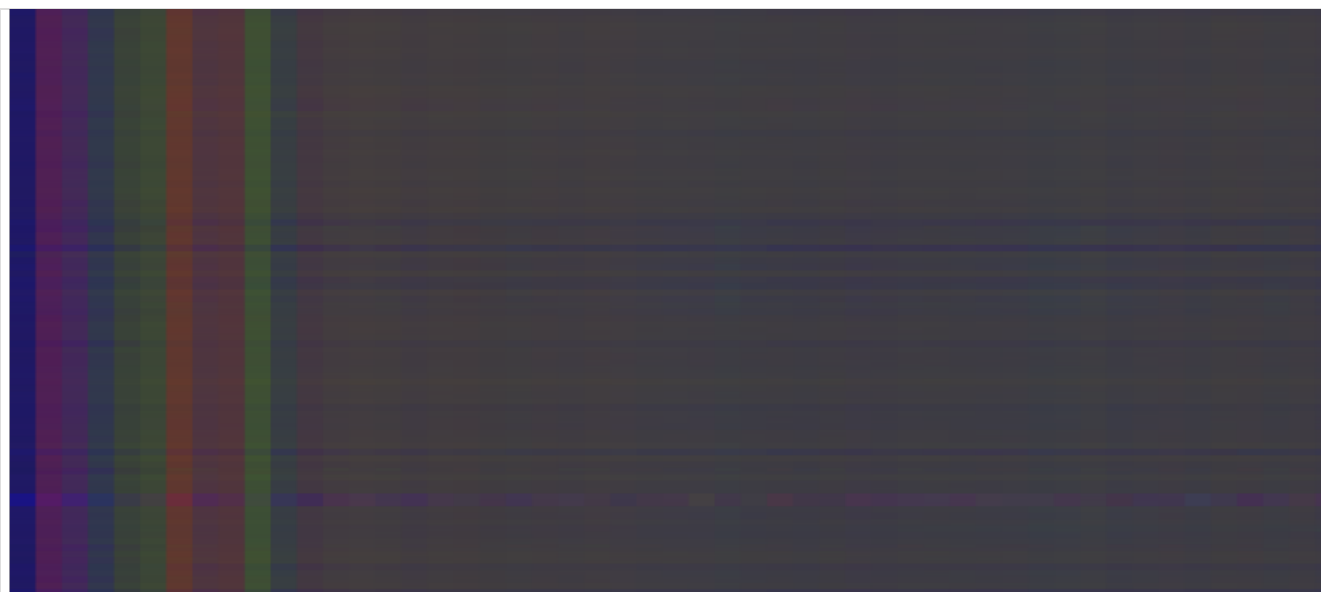
%T: -

%C: -

%A: -

%G: -

📄 Export Plot



## Per Sequence GC Content

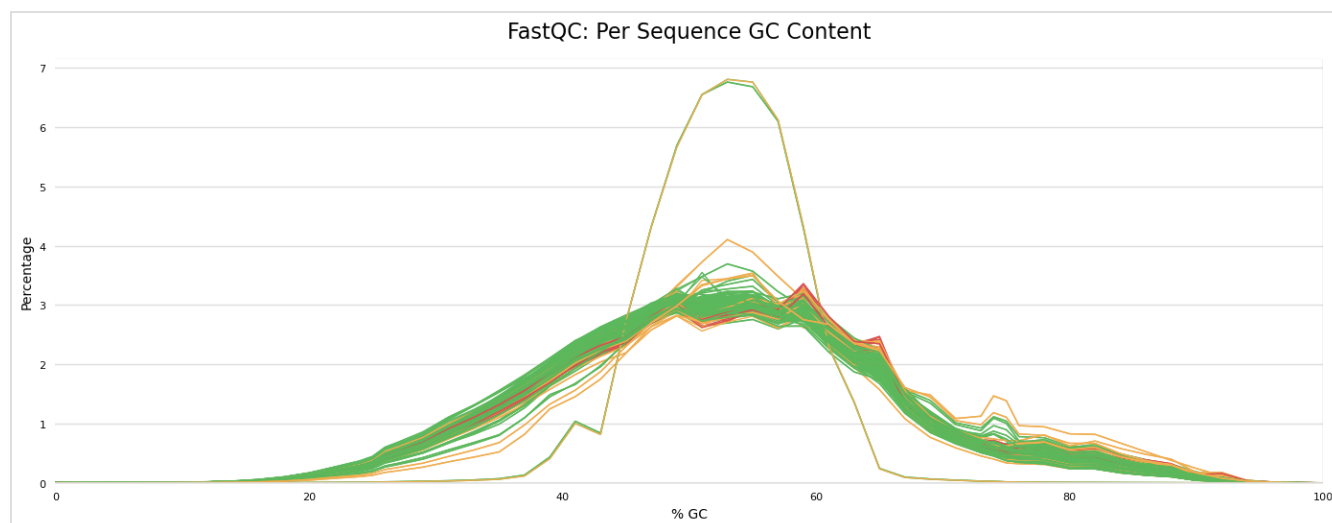
146

22

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

Percentages

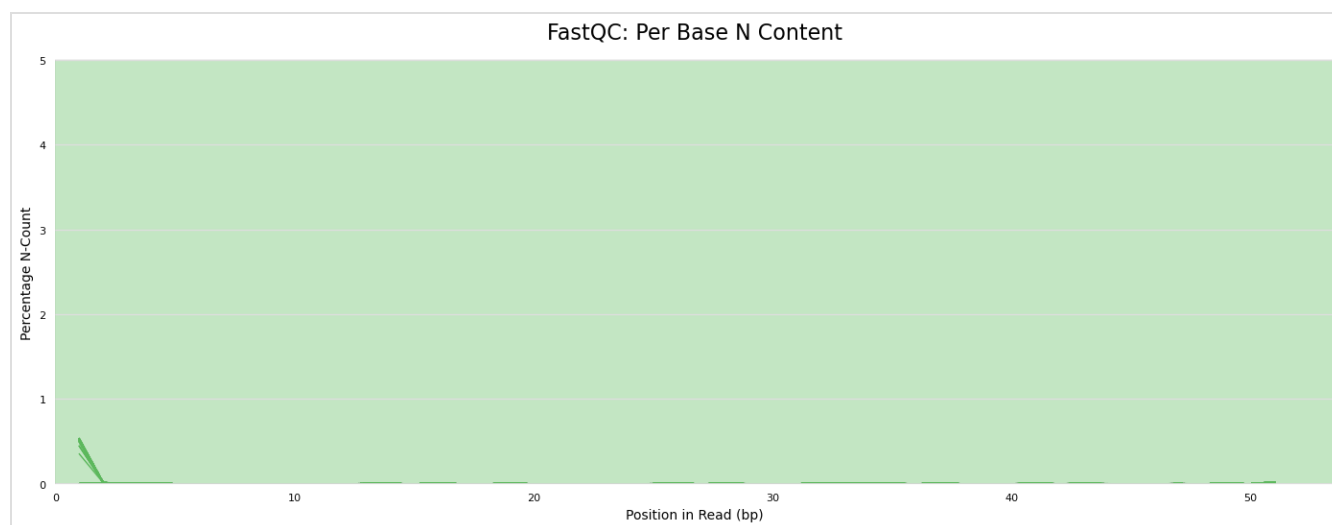
Counts



## Per Base N Content

184

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

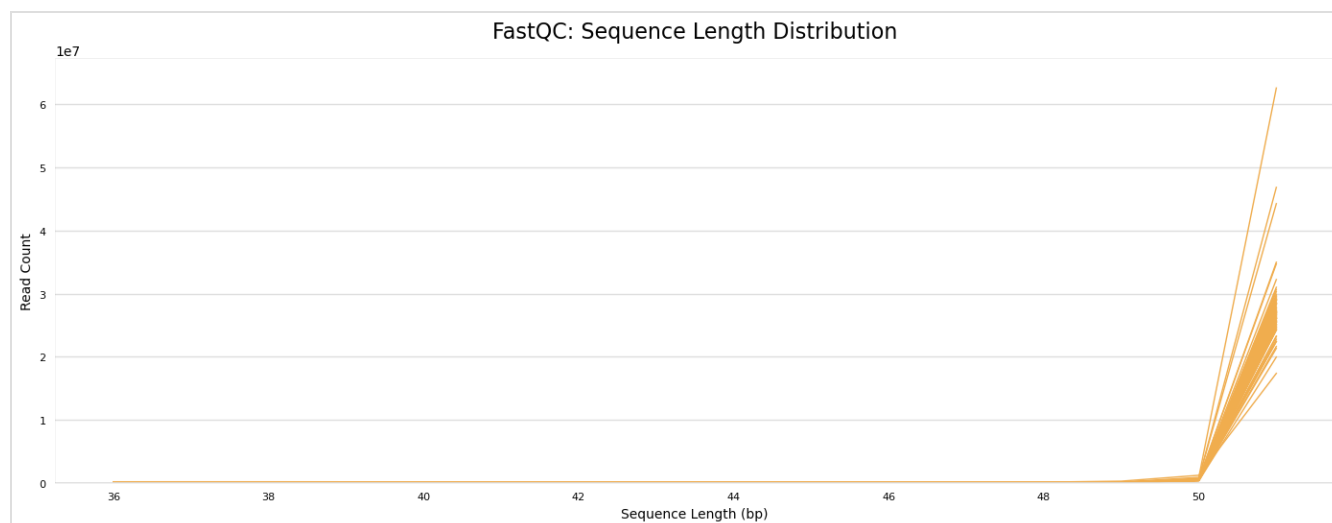


## Sequence Length Distribution

92

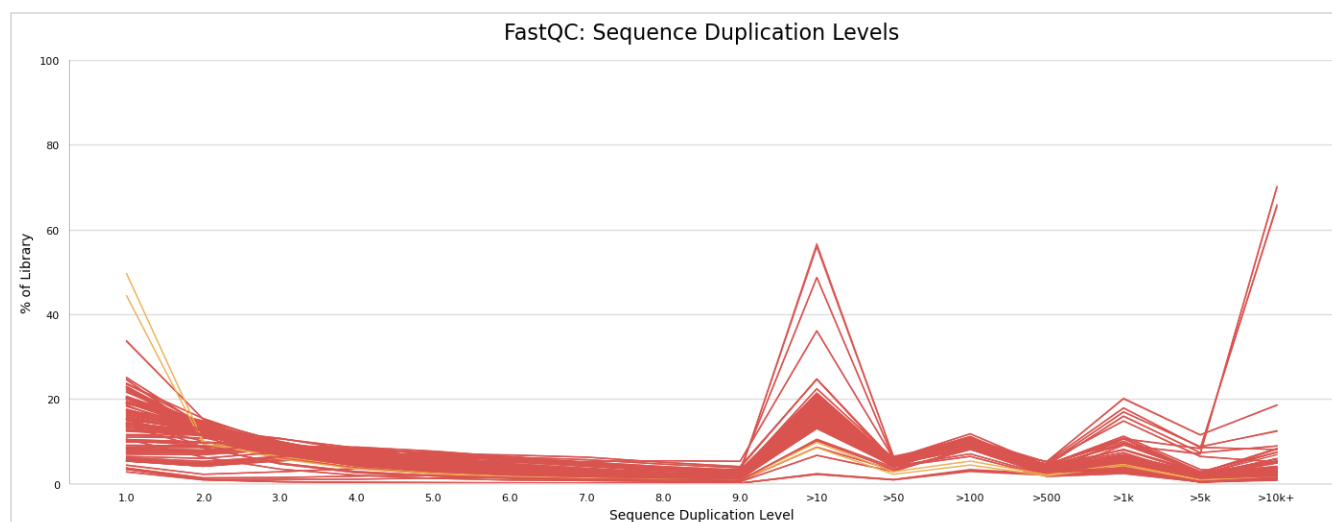
92

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



## Sequence Duplication Levels

The relative level of duplication found for every sequence.

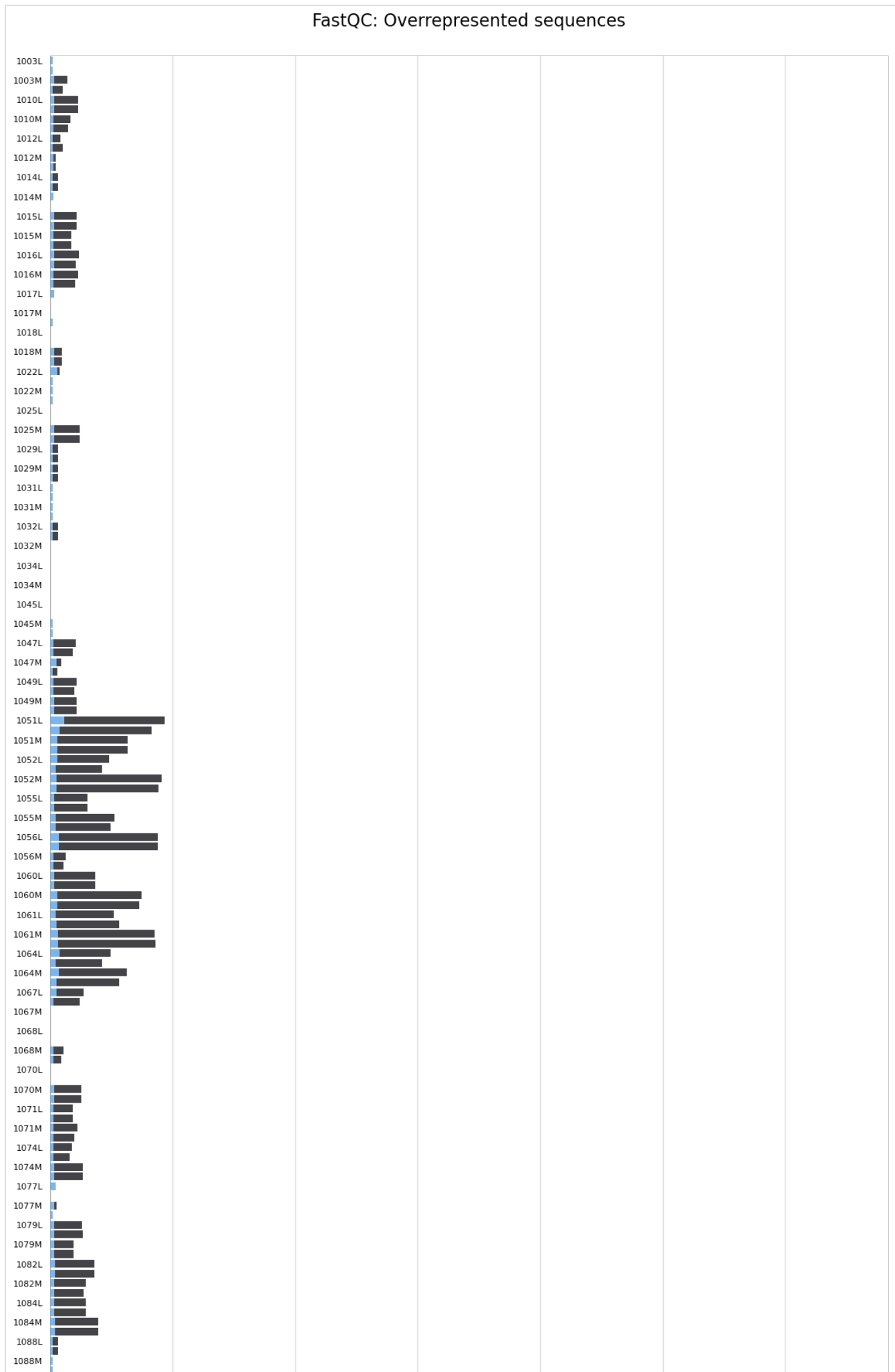


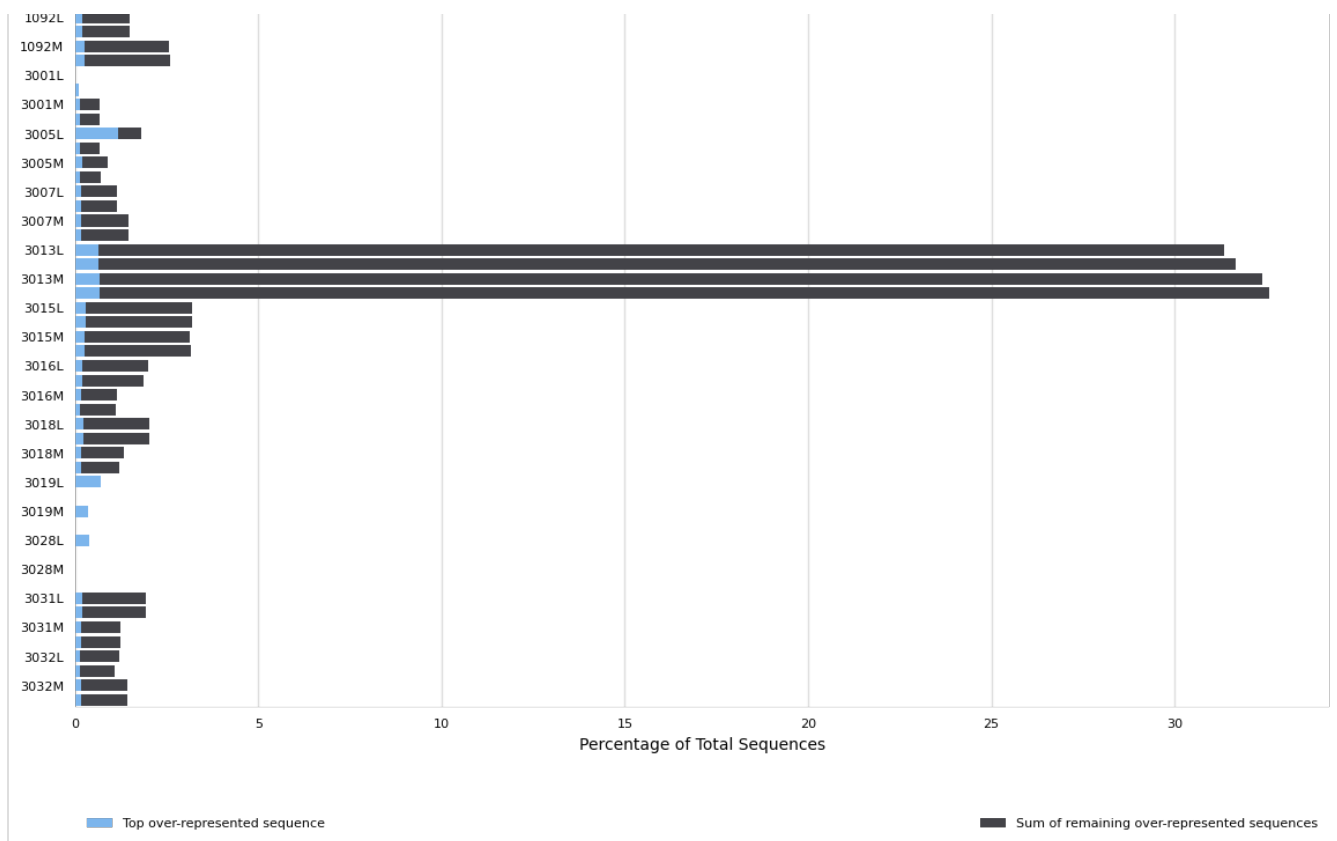
## Overrepresented sequences

28

155

The total amount of overrepresented sequences found in each library.

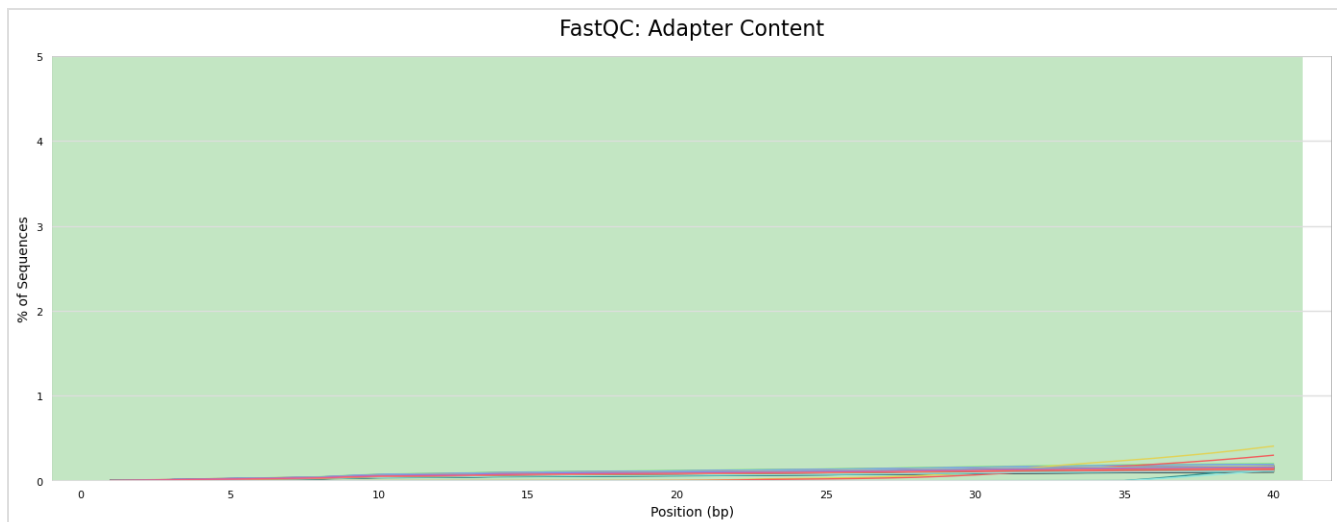




## Adapter Content

184

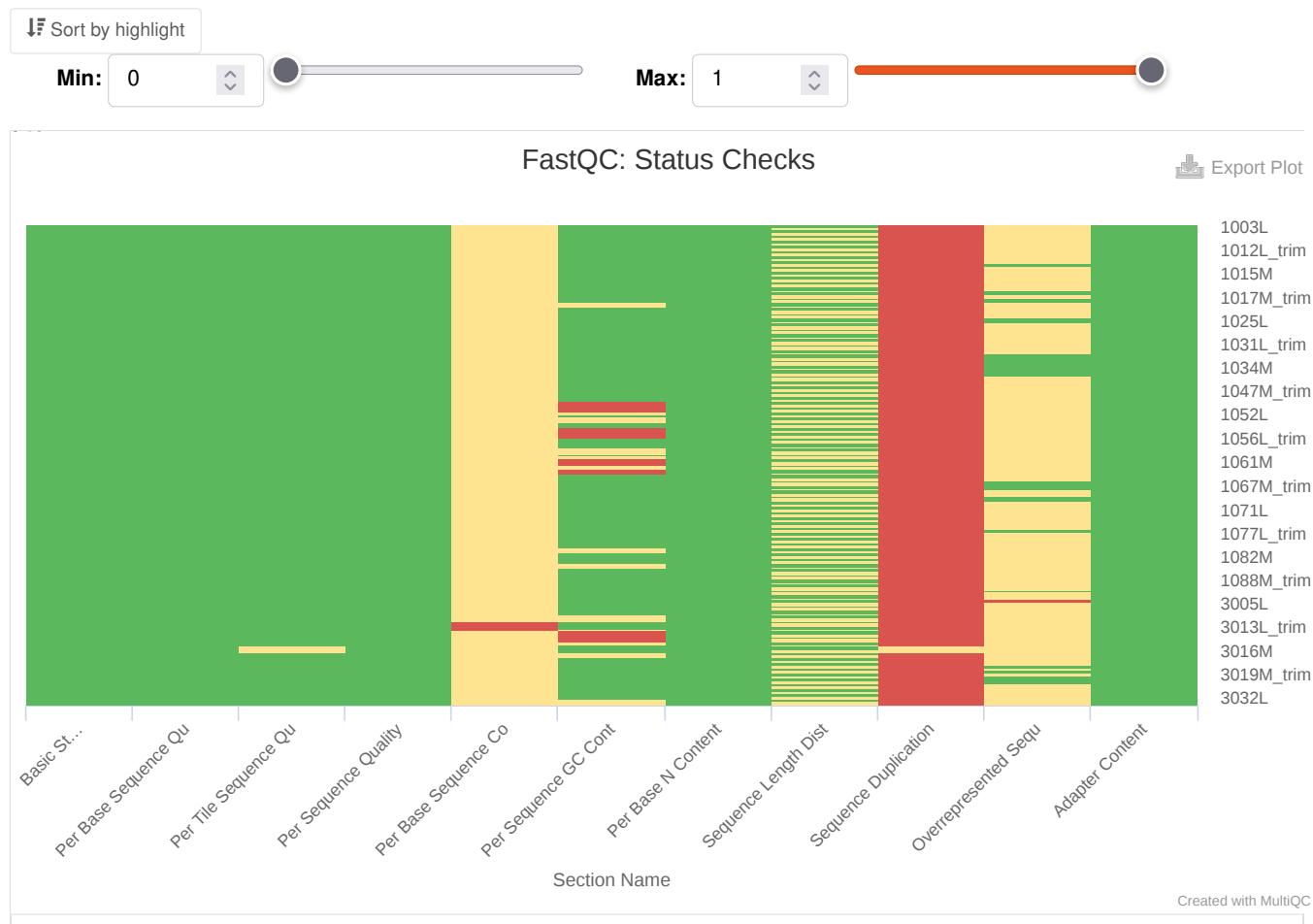
The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.





## Status Checks

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



**MultiQC v1.15** - Written by [Phil Ewels](#), available on [GitHub](#).

This report uses [HighCharts](#), [jQuery](#), [jQuery UI](#), [Bootstrap](#), [FileSaver.js](#) and [clipboard.js](#).

