



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

Report generated on 2025-09-08, 07:35 PDT based on data in: /scratch/mdesmarais/PRT\_BONCAT-FACS-SEQ/trimmed\_reads/postfastqc

General Statistics

Copy tableConfigure ColumnsPlotShowing 124/124 rows and 3/6 columns.

Sample Name	% Dups	% GC	M Seqs
260ATALL_S4_L003_paired_R1	87.3%	40%	30.4
260ATALL_S4_L003_paired_R2	82.4%	40%	30.4
260ATALL_S4_L003_unpaired_R1	46.4%	40%	1.7
260ATALL_S4_L003_unpaired_R2	30.4%	50%	0.1
260ATBON_S5_L003_paired_R1	93.7%	39%	31.0
260ATBON_S5_L003_paired_R2	90.9%	40%	31.0
260ATBON_S5_L003_unpaired_R1	70.0%	40%	1.7
260ATBON_S5_L003_unpaired_R2	36.4%	49%	0.1
260PRALL_S6_L003_paired_R1	91.4%	41%	44.4
260PRALL_S6_L003_paired_R2	86.8%	41%	44.4
260PRALL_S6_L003_unpaired_R1	53.6%	41%	2.0
260PRALL_S6_L003_unpaired_R2	34.7%	51%	0.2
260PRBON_S7_L003_paired_R1	92.4%	39%	38.6
260PRBON_S7_L003_paired_R2	88.2%	40%	38.6
260PRBON_S7_L003_unpaired_R1	61.8%	40%	1.9
260PRBON_S7_L003_unpaired_R2	31.5%	50%	0.2
50PRALL_S2_L003_paired_R1	61.2%	39%	32.4
50PRALL_S2_L003_paired_R2	57.4%	40%	32.4
50PRALL_S2_L003_unpaired_R1	23.0%	40%	2.0
50PRALL_S2_L003_unpaired_R2	26.5%	52%	0.1
50PRBON_S3_L003_paired_R1	79.8%	42%	41.2
50PRBON_S3_L003_paired_R2	74.6%	43%	41.2
50PRBON_S3_L003_unpaired_R1	43.1%	43%	2.7
50PRBON_S3_L003_unpaired_R2	29.8%	53%	0.2
530ATALL_S8_L003_paired_R1	89.8%	41%	41.7
530ATALL_S8_L003_paired_R2	85.1%	42%	41.7
530ATALL_S8_L003_unpaired_R1	50.5%	41%	2.1
530ATALL_S8_L003_unpaired_R2	28.4%	51%	0.2
530ATBON_S9_L003_paired_R1	56.6%	38%	48.2
530ATBON_S9_L003_paired_R2	53.0%	39%	48.2
530ATBON_S9_L003_unpaired_R1	20.2%	40%	2.4
530ATBON_S9_L003_unpaired_R2	30.4%	48%	0.2
530PR1ALL_S10_L003_paired_R1	73.7%	41%	39.7
530PR1ALL_S10_L003_paired_R2	69.3%	41%	39.7
530PR1ALL_S10_L003_unpaired_R1	34.2%	42%	2.1
530PR1ALL_S10_L003_unpaired_R2	27.4%	51%	0.2
530PR1BON_S11_L003_paired_R1	78.7%	40%	60.8
530PR1BON_S11_L003_paired_R2	72.8%	41%	60.8

Sample Name	% Dups	% GC	M Seqs
530PR1BON_S11_L003_unpaired_R1	39.8%	41%	3.5
530PR1BON_S11_L003_unpaired_R2	35.1%	52%	0.2
540AT1ALL_S12_L003_paired_R1	94.3%	42%	42.5
540AT1ALL_S12_L003_paired_R2	91.3%	43%	42.5
540AT1ALL_S12_L003_unpaired_R1	70.1%	41%	2.2
540AT1ALL_S12_L003_unpaired_R2	38.8%	52%	0.2
540AT1BON_S13_L003_paired_R1	93.7%	39%	49.4
540AT1BON_S13_L003_paired_R2	89.5%	39%	49.4
540AT1BON_S13_L003_unpaired_R1	69.6%	39%	2.9
540AT1BON_S13_L003_unpaired_R2	37.3%	52%	0.2
540AT2ALL_S14_L003_paired_R1	89.9%	39%	43.1
540AT2ALL_S14_L003_paired_R2	84.8%	40%	43.1
540AT2ALL_S14_L003_unpaired_R1	55.1%	40%	2.8
540AT2ALL_S14_L003_unpaired_R2	30.5%	51%	0.2
540AT2BON_S15_L003_paired_R1	74.6%	36%	43.9
540AT2BON_S15_L003_paired_R2	70.0%	37%	43.9
540AT2BON_S15_L003_unpaired_R1	30.3%	37%	2.5
540AT2BON_S15_L003_unpaired_R2	30.7%	49%	0.2
540PR1ALL_S16_L003_paired_R1	89.3%	40%	33.5
540PR1ALL_S16_L003_paired_R2	84.1%	41%	33.5
540PR1ALL_S16_L003_unpaired_R1	52.5%	41%	2.1
540PR1ALL_S16_L003_unpaired_R2	31.1%	53%	0.1
540PR1BON_S17_L003_paired_R1	86.8%	41%	44.5
540PR1BON_S17_L003_paired_R2	81.8%	41%	44.5
540PR1BON_S17_L003_unpaired_R1	44.5%	42%	2.1
540PR1BON_S17_L003_unpaired_R2	24.6%	50%	0.1
540PR2ALL_S18_L003_paired_R1	83.0%	44%	58.7
540PR2ALL_S18_L003_paired_R2	77.1%	45%	58.7
540PR2ALL_S18_L003_unpaired_R1	37.1%	46%	2.5
540PR2ALL_S18_L003_unpaired_R2	26.1%	52%	0.2
540PR2BON_S19_L003_paired_R1	79.7%	42%	53.1
540PR2BON_S19_L003_paired_R2	74.3%	43%	53.1
540PR2BON_S19_L003_unpaired_R1	38.6%	43%	2.8
540PR2BON_S19_L003_unpaired_R2	35.1%	52%	0.2
830AT1ALL_S20_L003_paired_R1	93.1%	42%	52.5
830AT1ALL_S20_L003_paired_R2	88.5%	42%	52.5
830AT1ALL_S20_L003_unpaired_R1	58.5%	42%	2.1
830AT1ALL_S20_L003_unpaired_R2	35.2%	49%	0.2
830AT1BON_S21_L003_paired_R1	87.0%	39%	49.4
830AT1BON_S21_L003_paired_R2	81.9%	40%	49.4
830AT1BON_S21_L003_unpaired_R1	43.4%	40%	2.3
830AT1BON_S21_L003_unpaired_R2	31.9%	49%	0.2
830AT2ALL_S22_L003_paired_R1	91.5%	40%	46.6
830AT2ALL_S22_L003_paired_R2	85.9%	40%	46.6
830AT2ALL_S22_L003_unpaired_R1	56.7%	40%	2.3
830AT2ALL_S22_L003_unpaired_R2	32.9%	51%	0.2

Sample Name	% Dups	% GC	M Seqs
830AT2BON_S23_L003_paired_R1	91.4%	41%	49.1
830AT2BON_S23_L003_paired_R2	86.0%	41%	49.1
830AT2BON_S23_L003_unpaired_R1	51.0%	41%	2.0
830AT2BON_S23_L003_unpaired_R2	30.1%	51%	0.2
830AT3ALL_S24_L003_paired_R1	82.7%	41%	48.1
830AT3ALL_S24_L003_paired_R2	77.0%	41%	48.1
830AT3ALL_S24_L003_unpaired_R1	32.0%	41%	2.1
830AT3ALL_S24_L003_unpaired_R2	21.2%	49%	0.1
830AT3BON_S25_L003_paired_R1	63.8%	40%	54.0
830AT3BON_S25_L003_paired_R2	59.6%	41%	54.0
830AT3BON_S25_L003_unpaired_R1	28.0%	42%	2.3
830AT3BON_S25_L003_unpaired_R2	32.6%	49%	0.2
830PR1ALL_S26_L003_paired_R1	91.6%	41%	48.4
830PR1ALL_S26_L003_paired_R2	86.3%	42%	48.4
830PR1ALL_S26_L003_unpaired_R1	57.8%	41%	2.7
830PR1ALL_S26_L003_unpaired_R2	38.5%	53%	0.2
830PR1BON_S27_L003_paired_R1	91.4%	40%	38.8
830PR1BON_S27_L003_paired_R2	87.9%	40%	38.8
830PR1BON_S27_L003_unpaired_R1	58.2%	40%	2.2
830PR1BON_S27_L003_unpaired_R2	40.9%	52%	0.2
830PR2ALL_S28_L003_paired_R1	91.4%	40%	50.3
830PR2ALL_S28_L003_paired_R2	86.1%	40%	50.3
830PR2ALL_S28_L003_unpaired_R1	55.7%	40%	2.6
830PR2ALL_S28_L003_unpaired_R2	32.4%	51%	0.2
830PR2BON_S29_L003_paired_R1	88.8%	40%	51.6
830PR2BON_S29_L003_paired_R2	83.6%	41%	51.6
830PR2BON_S29_L003_unpaired_R1	52.5%	41%	2.6
830PR2BON_S29_L003_unpaired_R2	36.2%	50%	0.2
830PR3ALL_S30_L003_paired_R1	78.8%	37%	47.2
830PR3ALL_S30_L003_paired_R2	73.7%	38%	47.2
830PR3ALL_S30_L003_unpaired_R1	30.8%	39%	2.2
830PR3ALL_S30_L003_unpaired_R2	26.0%	47%	0.2
830PR3BON_S31_L003_paired_R1	89.0%	39%	48.5
830PR3BON_S31_L003_paired_R2	83.0%	39%	48.5
830PR3BON_S31_L003_unpaired_R1	47.7%	39%	2.4
830PR3BON_S31_L003_unpaired_R2	29.0%	48%	0.2
NC_S32_L003_paired_R1	95.8%	43%	36.2
NC_S32_L003_paired_R2	93.4%	44%	36.2
NC_S32_L003_unpaired_R1	81.7%	44%	2.7
NC_S32_L003_unpaired_R2	51.9%	52%	0.2

# FastQC

Version: 0.12.1

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

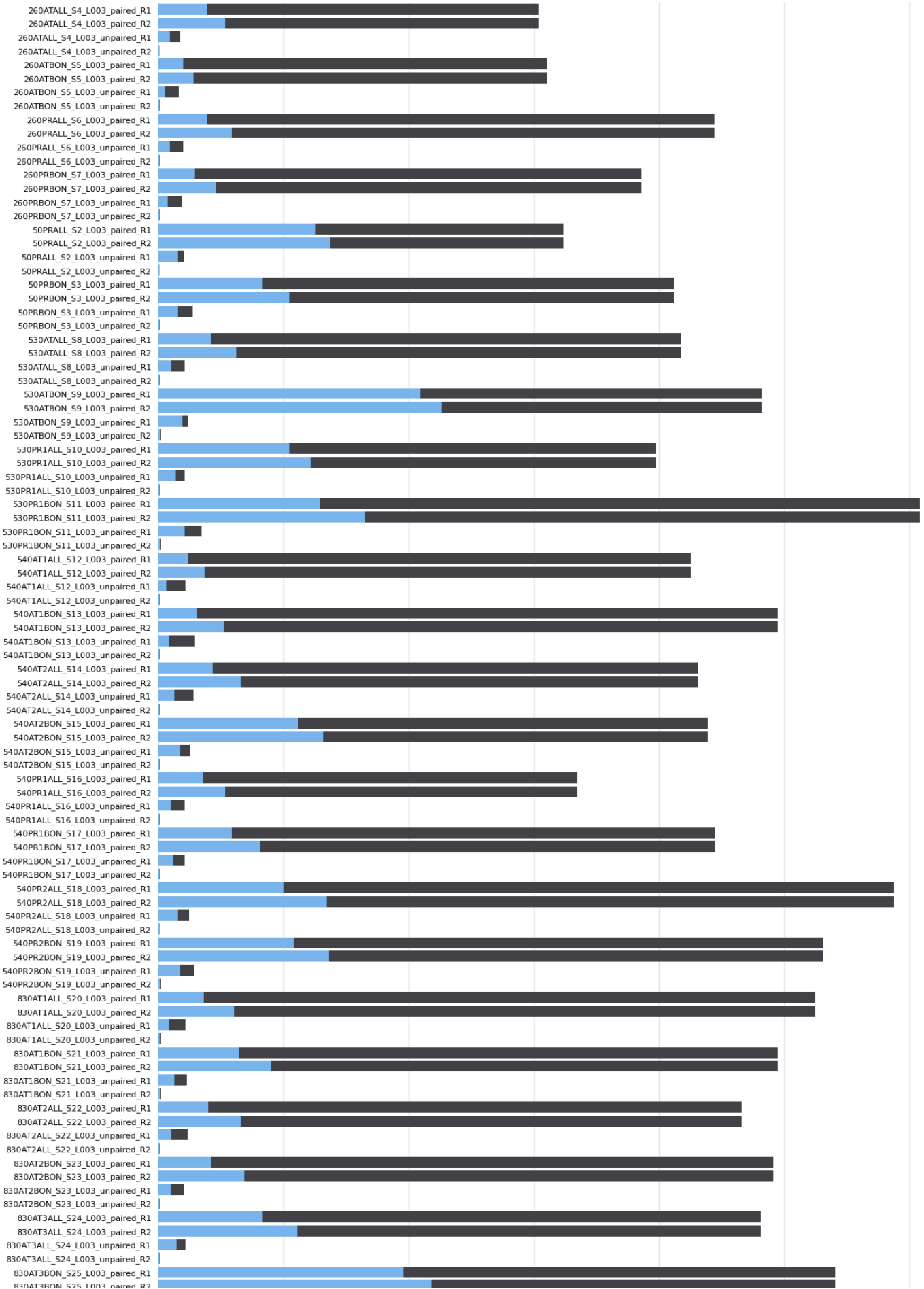
## Sequence Counts

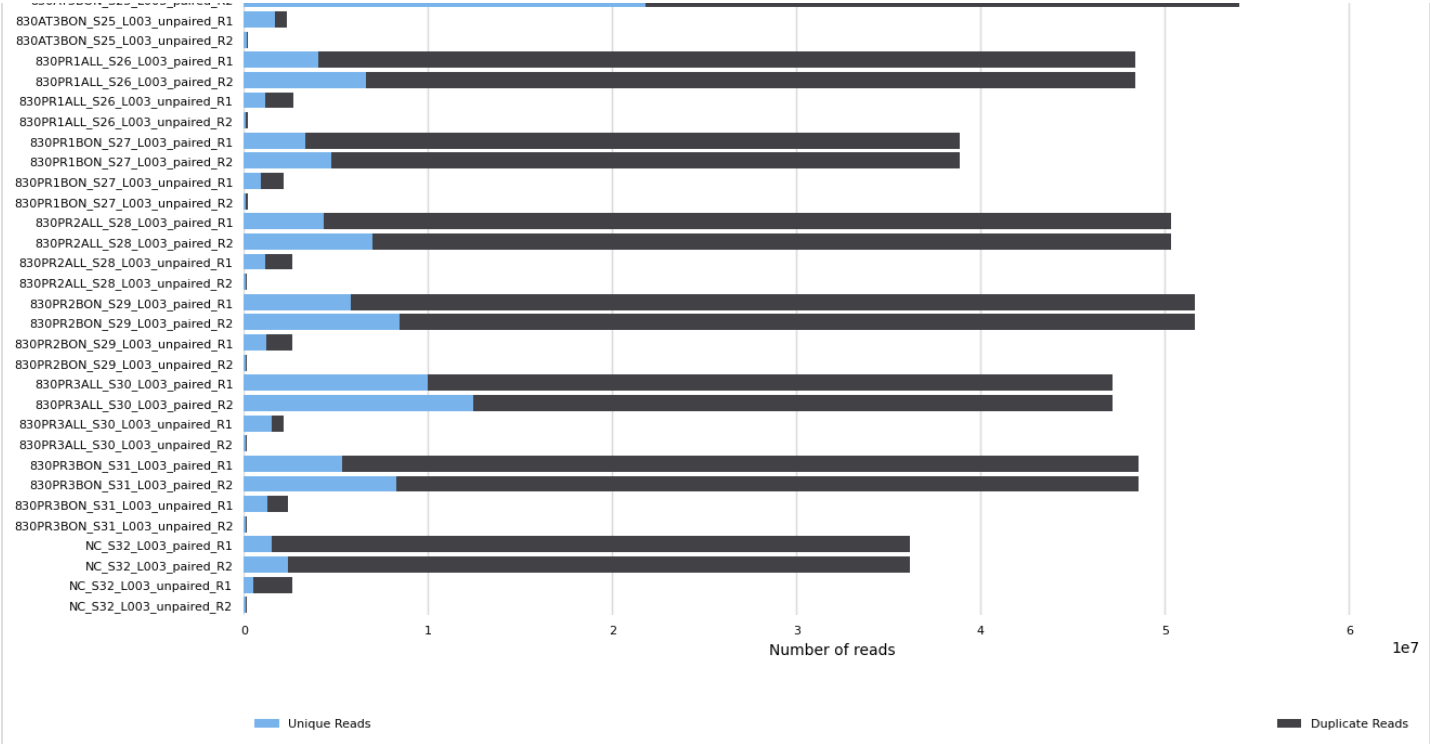
Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads	Percentages
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FastQC: Sequence Counts

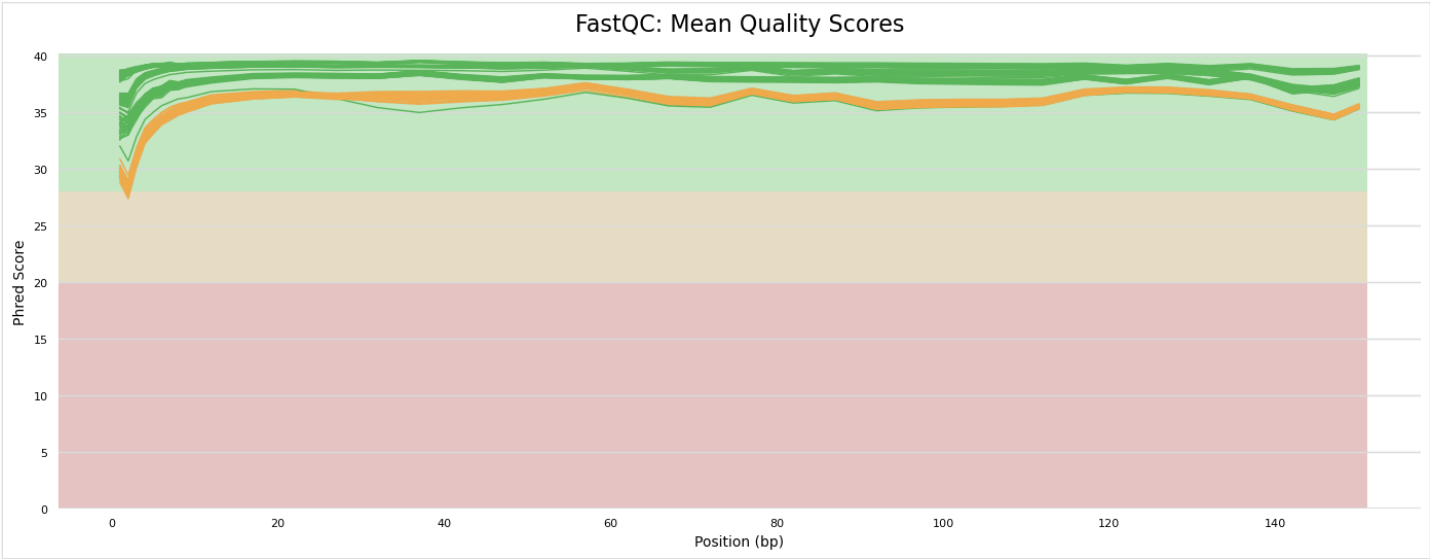




Sequence Quality Histograms

94 30

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





Per Sequence Quality Scores

124

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



Per Base Sequence Content

8322

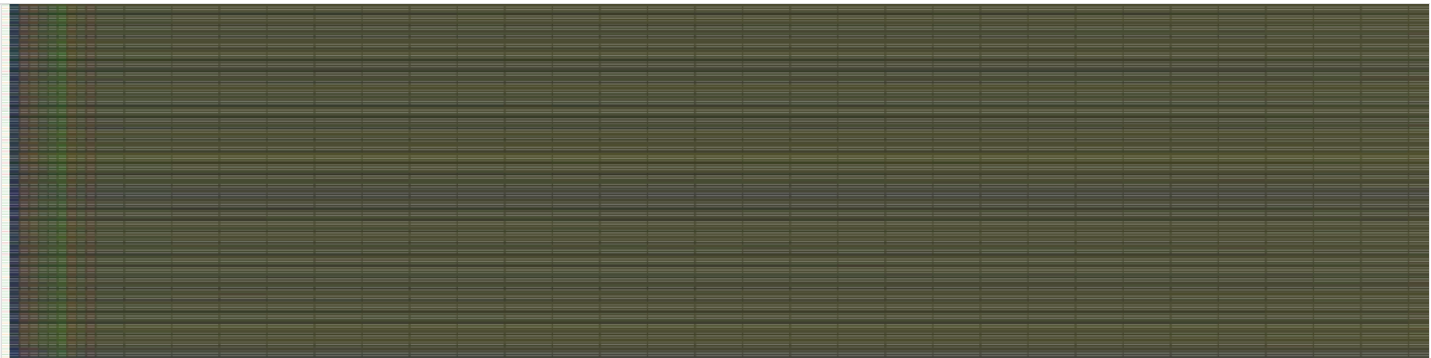
The proportion of each base position for which each of the four normal DNA bases has been called.

🔗 Click a sample row to see a line plot for that dataset.

📄 Rollover for sample name

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

📄 Export Plot

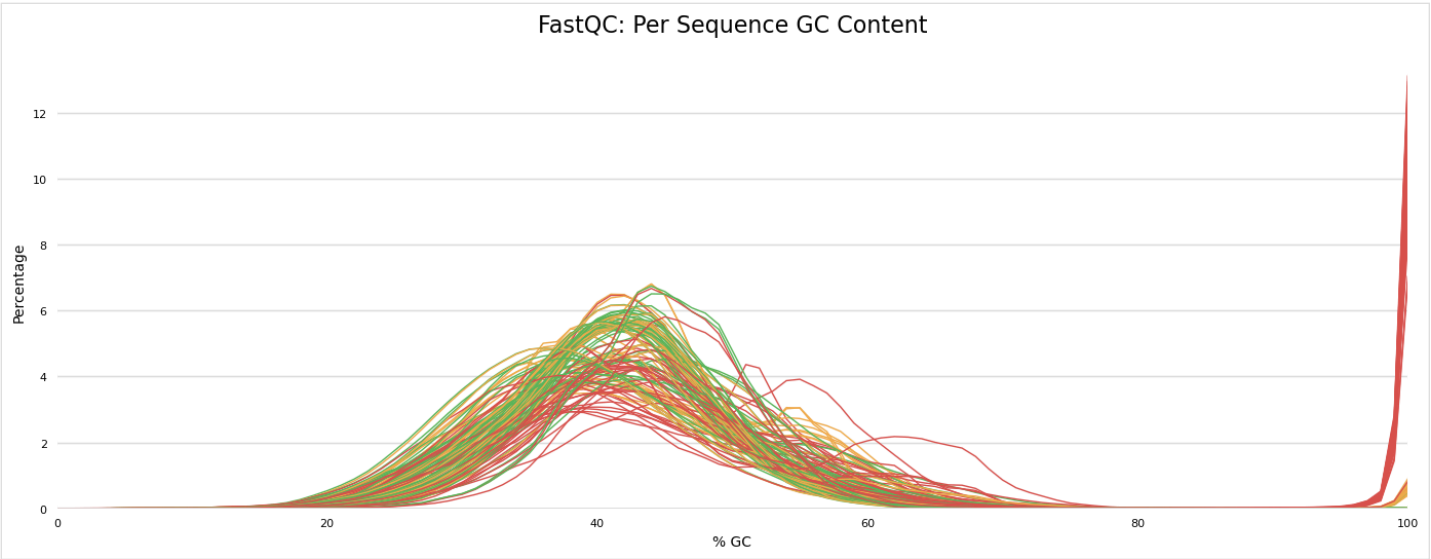


Per Sequence GC Content 47 42

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

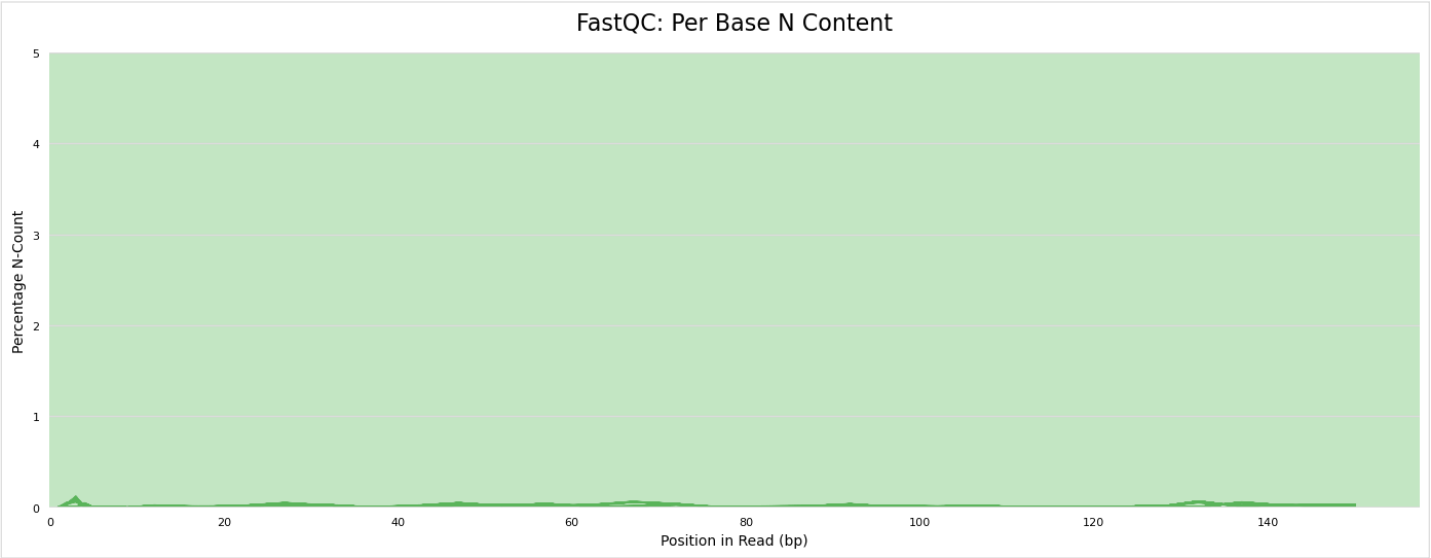
Percentages

Counts



Per Base N Content 124

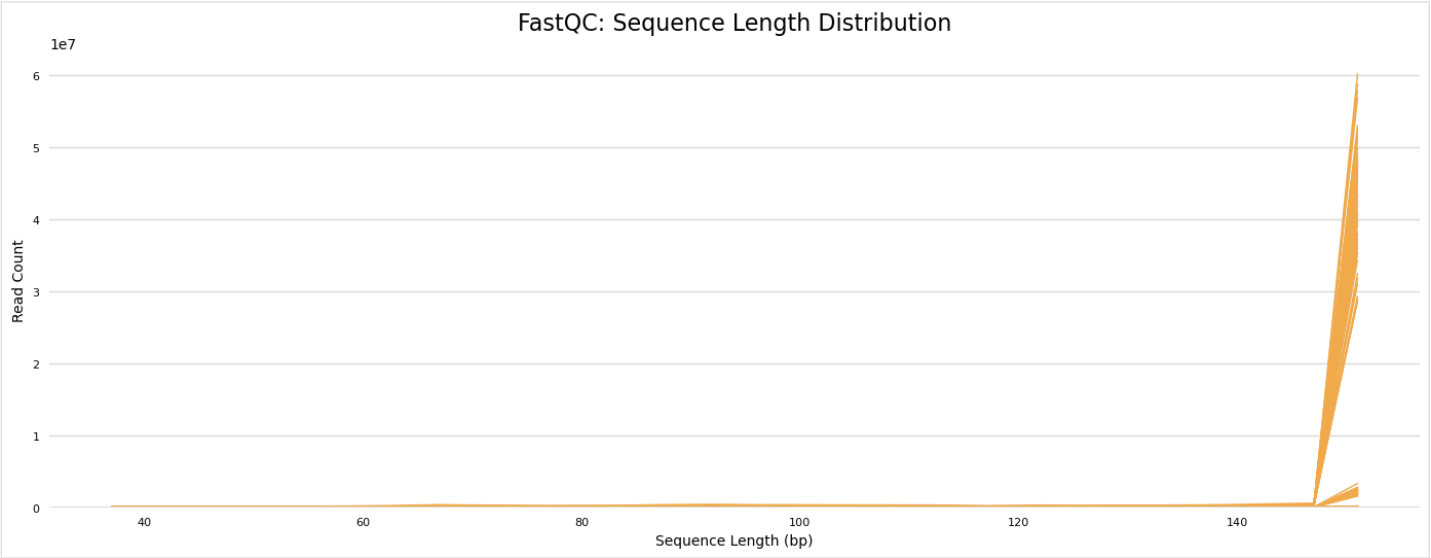
The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

124

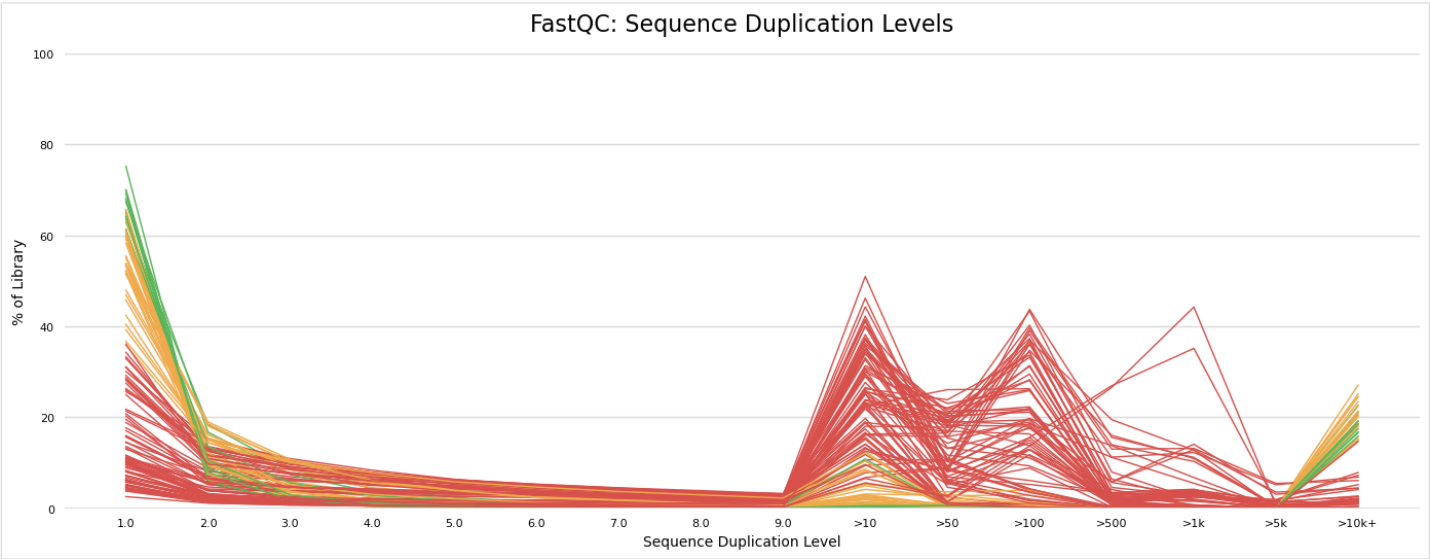
The distribution of fragment sizes (read lengths) found. See the FastQC help



Sequence Duplication Levels

1: 33

The relative level of duplication found for every sequence.



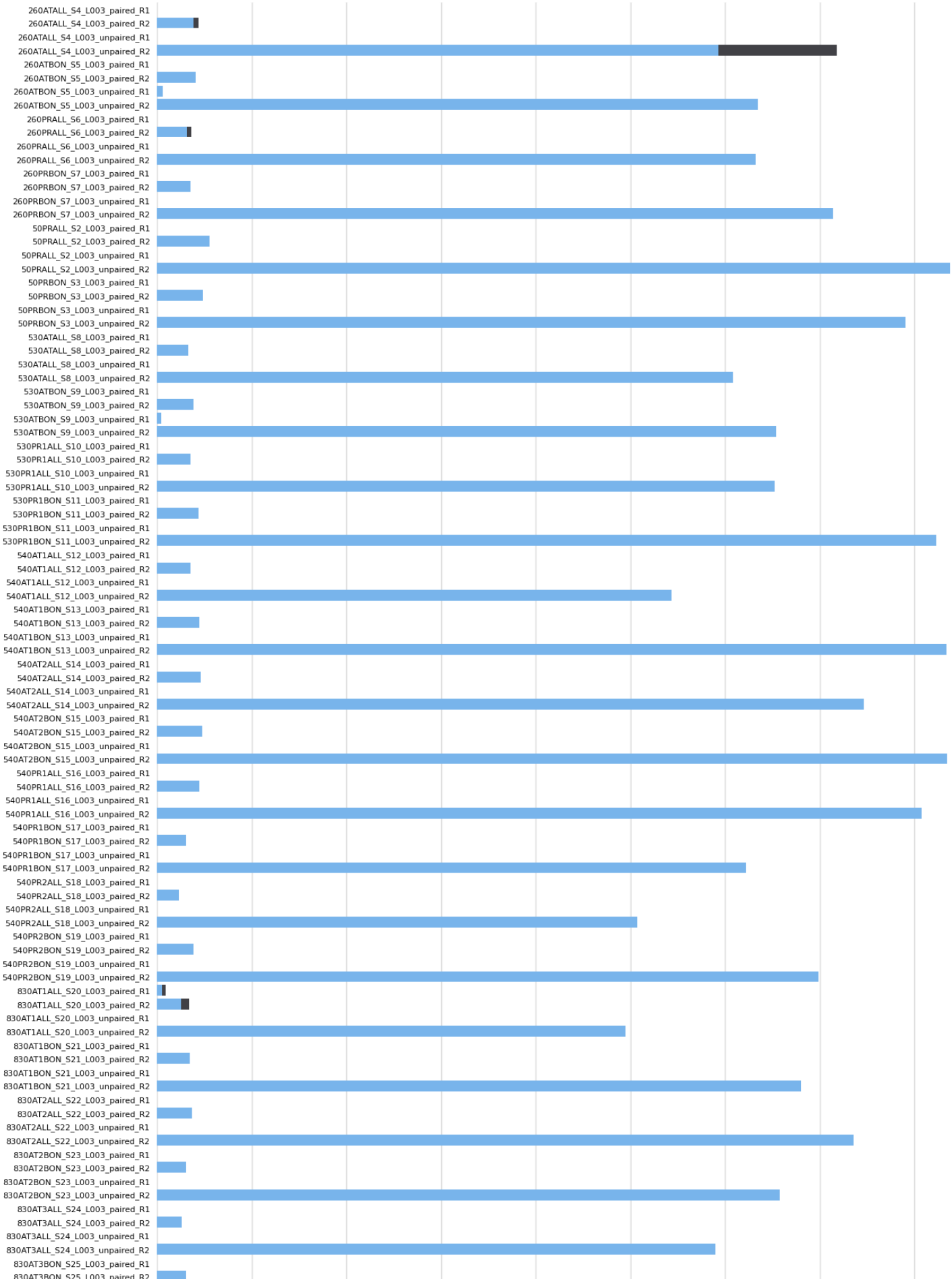
# Overrepresented sequences by sample

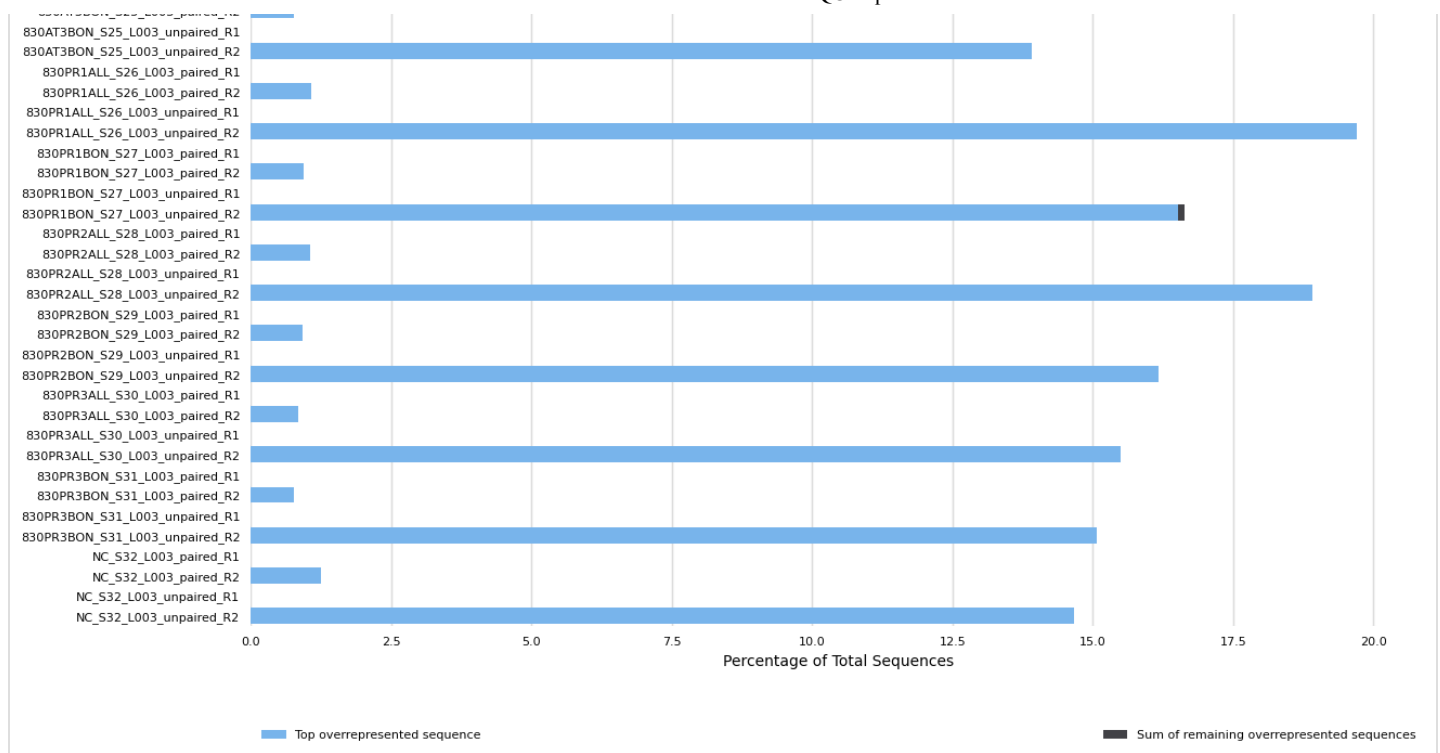
59 23

The total amount of overrepresented sequences found in each library.



FastQC: Overrepresented sequences sample summary





### Top overrepresented sequences

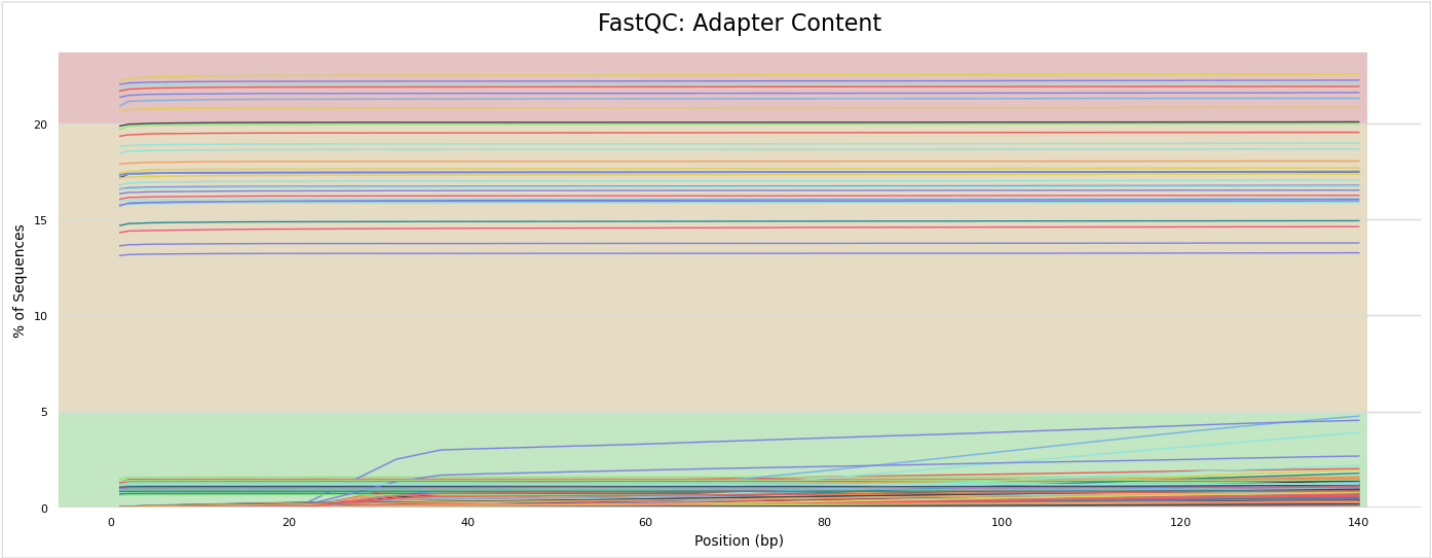
Top overrepresented sequences across all samples. The table shows 20 most overrepresented sequences across all samples, ranked by the number of samples they occur in.

 Copy table
  Configure Columns
  Plot
 Showing 20/20 rows and 3/3 columns.

Overrepresented sequence	Samples	Occurrences	% of all reads
GGGGGGGGGGGGGGGGGGGGGGG	62	13 825 946	0.4811%
CTCCGGCATTCACTAACCGAAGGAGTG 2CATTTATCATGAAATTGCACCA		120 737	0.0042%
C CGGAGCATTCTATGGTGAATTCATG 2TAATGGCACTCCTTCGGTTA		110 666	0.0039%
CAACAGATT CAGCAGGAAGATGCCACT 2AATTGCGGCACATTTGCCTGAC		40 641	0.0014%
GATCGGAAGAGCACACGTCTGAACTCC AGTCACGAATTACGATCTGGGGG		2 487	0.0001%
CAACAATGTGGATT TGCCAACGTTCTGG. TCGTCCGACGATGGCAATAACTG		48 681	0.0017%
GACA ACTGGCGACAGCCAGTTGGACA 1ACC GTGAACGCAGTGAGCGGGCT		227	0.0000%
GATCGGAAGAGCACACGTCTGAACTCC AGTCACTGATCTAAATCTGGGGG		2 499	0.0001%
ACATAGGCGAACTCAGCCATCATCAG 2GGGAAGTGCCACATCTGTCAGG		559	0.0000%
ATAGGCGAACTCAGCCATCATCAGCG 3GAAGTGCCACATCTGTCAGGCA		333	0.0000%
CATAGGCGAACTCAGCCATCATCAGC 3GGAAGTGCCACATCTGTCAGGC		295	0.0000%
CCGCAATTGAGTGGCATCTTCCTGCTG. ATCTGTTGATACATAGGCGAAC		281	0.0000%
GCATCTTCCTGCTGAATCTGTTGATACA 2AGGCGAACTCAGCCATCATC		226	0.0000%
GCCACATCTGTCAGGCAAATGTGCCGC AATTGAGTGGCATCTTCCTGCTG		186	0.0000%
ATCAACAGATT CAGCAGGAAGATGCCA 2TCAATTGCGGCACATTTGCCTG		180	0.0000%
AGGCGAACTCAGCCATCATCAGCGG 1AAGTGCCACATCTGTCAGGCAAA		177	0.0000%
TACATAGGCGAACTCAGCCATCATCA 1CGGGAAGTGCCACATCTGTCAG		162	0.0000%
GTGGCATCTTCCTGCTGAATCTGTTGAT 1CATAGGCGAACTCAGCCATC		162	0.0000%
GGCAAATGTGCCGCAATTGAGTGGCAT 2TTCCTGCTGAATCTGTTGATAC		147	0.0000%
TCAACAGATT CAGCAGGAAGATGCCAC 1CAATTGCGGCACATTTGCCTGA		145	0.0000%

Adapter Content 93

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



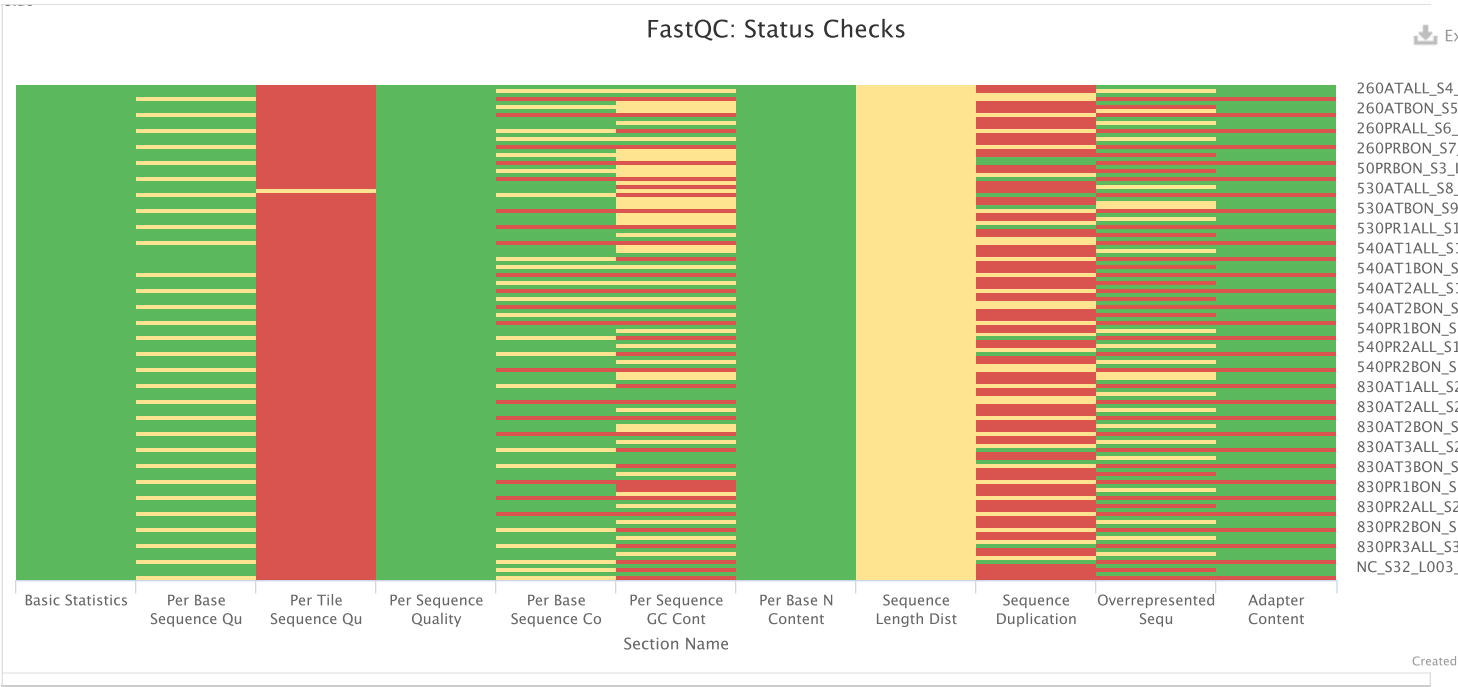
Status Checks

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

Sort by highlight

Min: 0

Max: 1



Software Versions

Software Versions lists versions of software tools extracted from file contents.

Copy table

Software	Version
FastQC	0.12.1



**MultiQC v1.19** - Written by [Phil Ewels](#), available on [GitHub](#).

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

