multiqc
v1.33

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multiqc

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

This report has been generated by the nf-core/rnaseq analysis pipeline. For information about how to interpret these results, please see the documentation.

Report generated on 2026-08-25, 20:51 CDT based on data in: `/bulk/bioinfo/Nextflow_demos/work/10/59876c41a073dd979880bbb1823341`

+ Summarize report

Welcome! Not sure where to start? Watch a tutorial video (6:06) don't show again

General Statistics

View as a violin plot

Copy table | Configure columns | Scatter plot | Violin plot | Export as CSV... Showing 5/5 rows and 28/52 columns. + Summarize table

Sample Name	human Assigned	primary Assigned	dupInt	Duplication	5'-3' bias	M Aligned	Proper Pairs	% Aligned	M Aligned	Library types
RAP1_IAA_30M_REP1	0.0 M	0.1 M	0.0	12.8 %	0.88	0.0 M	82.8 %	81.0 %	0.0 M	ISR
RAP1_UNINDUCED_REP1		0.0 M	0.0	76.1 %	0.95	0.0 M	0.0 %	81.0 %	0.0 M	SR
RAP1_UNINDUCED_REP2	0.0 M	0.1 M	0.0	82.4 %	0.94	0.1 M	0.0 %	80.8 %	0.1 M	SR
WT_REP1		0.2 M	0.0	21.3 %	1.07	0.1 M	74.2 %	79.9 %	0.1 M	ISR
WT_REP2	0.0 M	0.1 M	0.0	13.4 %	1.17	0.0 M	81.7 %	79.8 %	0.0 M	ISR

Strandedness checks

Strandedness declared in the samplesheet versus the values inferred by Salmon and/or RSeQC infer_experiment.

Strandedness: inference summary

One row per sample showing the strandedness declared in the samplesheet (auto means Salmon was asked to infer it) alongside the value each active inference method reported. The Salmon % and RSeQC % columns are a per-method certainty metric for forward / reverse calls: the inferred direction's share of the strand-classified fragment pool (the same quantity the configured stranded_threshold is applied to). Blank for unstranded or undetermined classifications, where different thresholds apply. Per-component Sense / Antisense / Unstranded percentages are hidden by default; toggle them on via the Configure Columns button above the table.

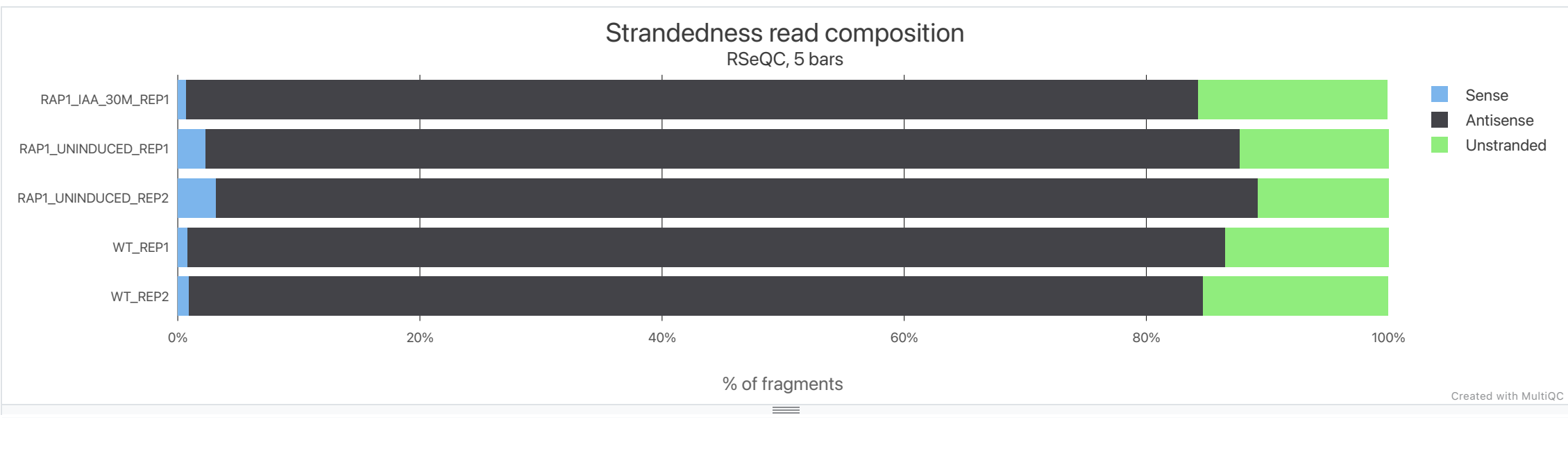
Copy table | Configure columns | Scatter plot | Violin plot | Export as CSV... Showing 5/5 rows and 6/12 columns. + Summarize table

Sample Name	Provided	Salmon inferred	Salmon %	RSeQC inferred	RSeQC %	Status
RAP1_IAA_30M_REP1	reverse	-		reverse	99.1 %	pass
RAP1_UNINDUCED_REP1	reverse	-		reverse	97.4 %	pass
RAP1_UNINDUCED_REP2	reverse	-		reverse	96.4 %	pass
WT_REP1	auto	reverse	89.2 %	reverse	99.1 %	pass
WT_REP2	reverse	-		reverse	98.9 %	pass

Strandedness: read composition

Stacked percentage of sense, antisense and unstranded read fragments per sample. When both Salmon and RSeQC inferred strandedness, use the dataset switcher above the plot to flip between their views.

RSeQC | Salmon + Summarize plot | Export...



FastQC (raw)

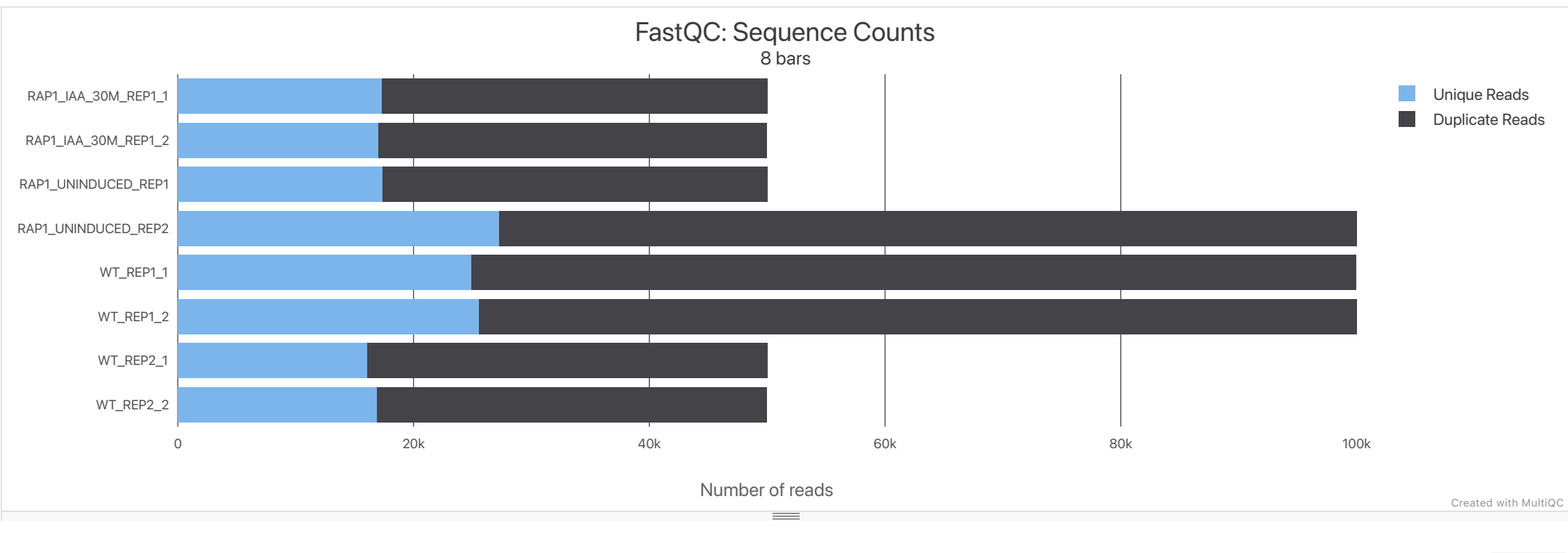
This section of the report shows FastQC results before adapter trimming. http://www.bioinformatics.babraham.ac.uk/projects/fastqc

Sequence Counts

Help

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

Percentages + Summarize plot Export...



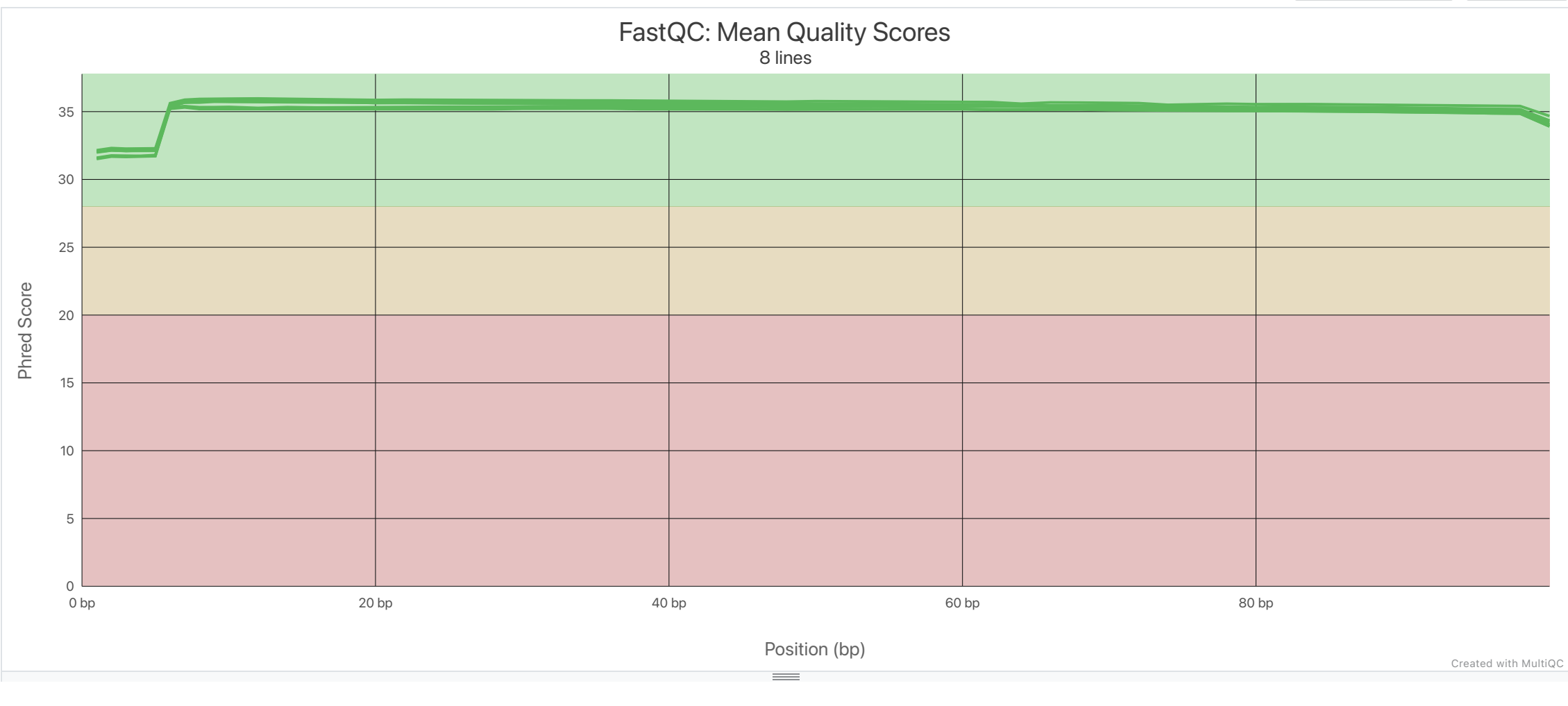
Sequence Quality Histograms

8

Help

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

+ Summarize plot Export...



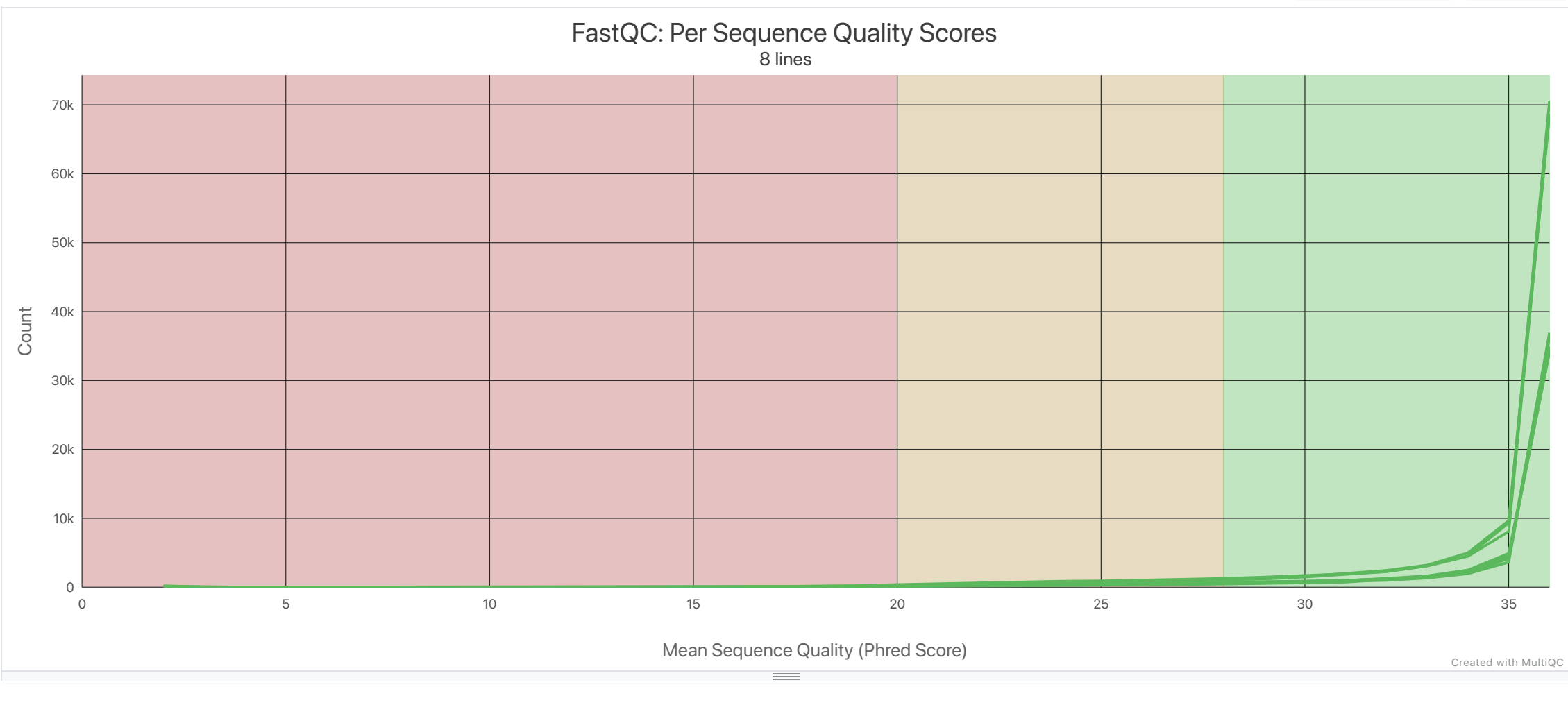
Per Sequence Quality Scores

8

Help

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

+ Summarize plot Export...



Per Base Sequence Content

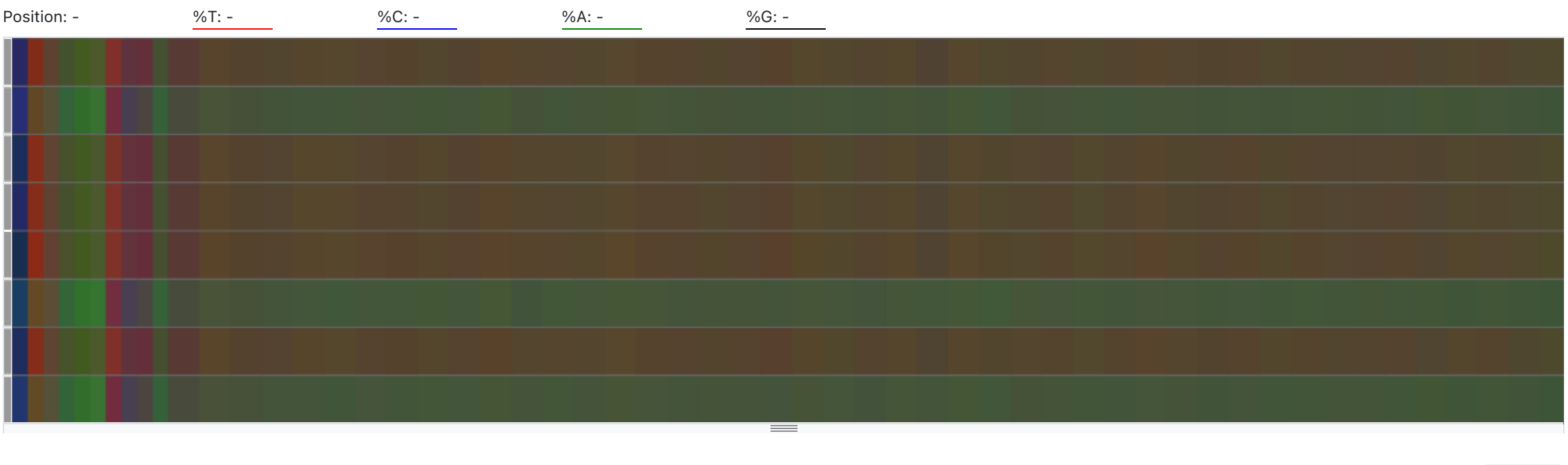
Help

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: -



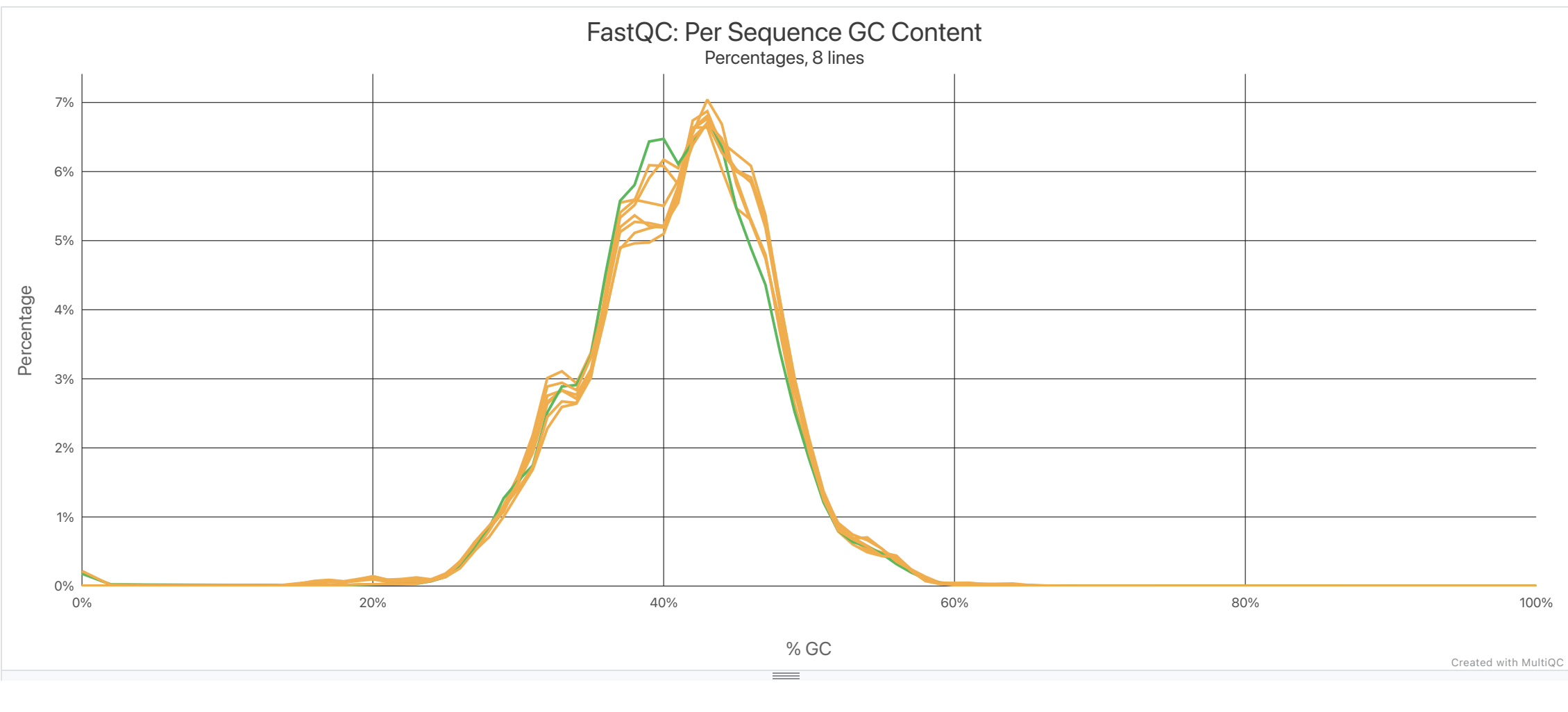
Per Sequence GC Content

1 7

Help

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

Percentages | Counts + Summarize plot Export...



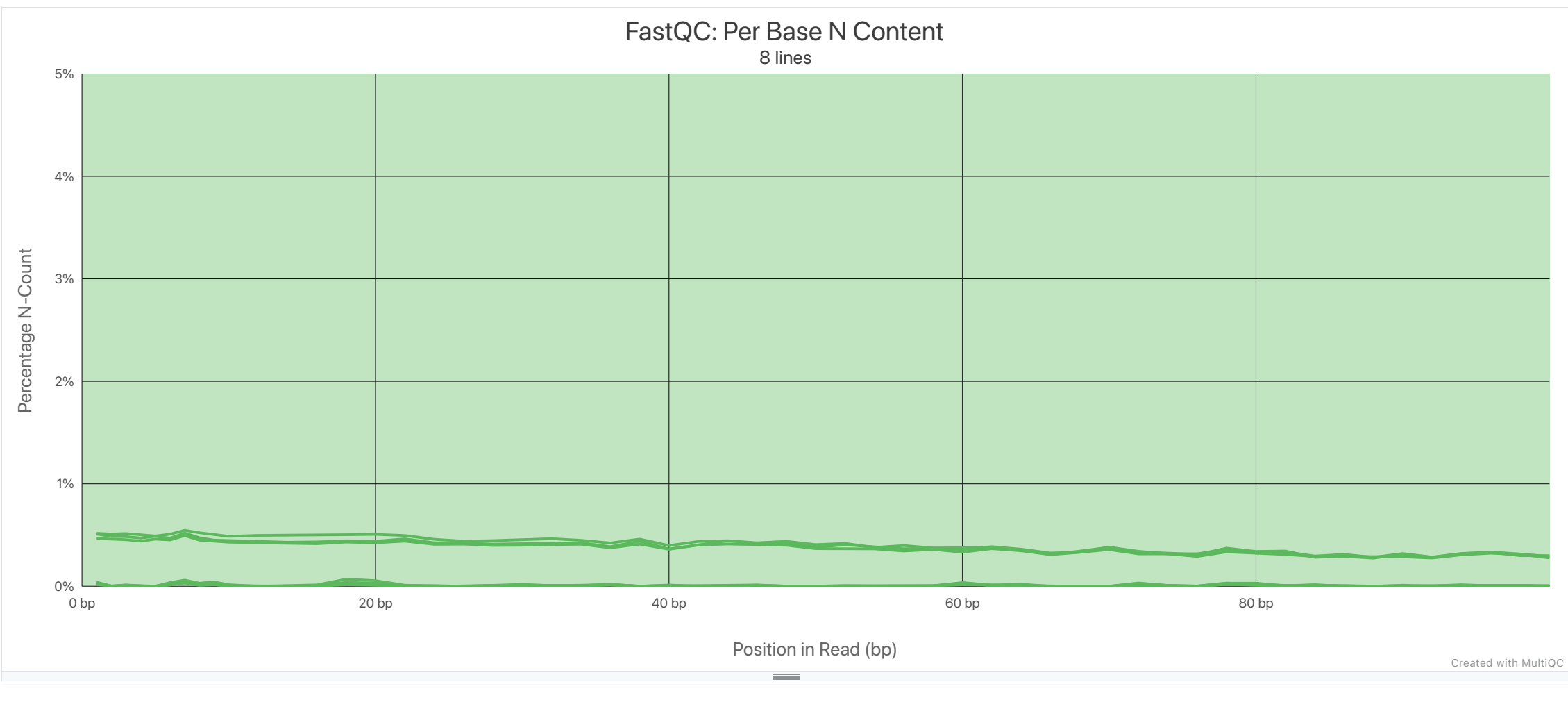
Per Base N Content

8

Help

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

+ Summarize plot Export...



Sequence Length Distribution

8

All samples have sequences of a single length (101bp)

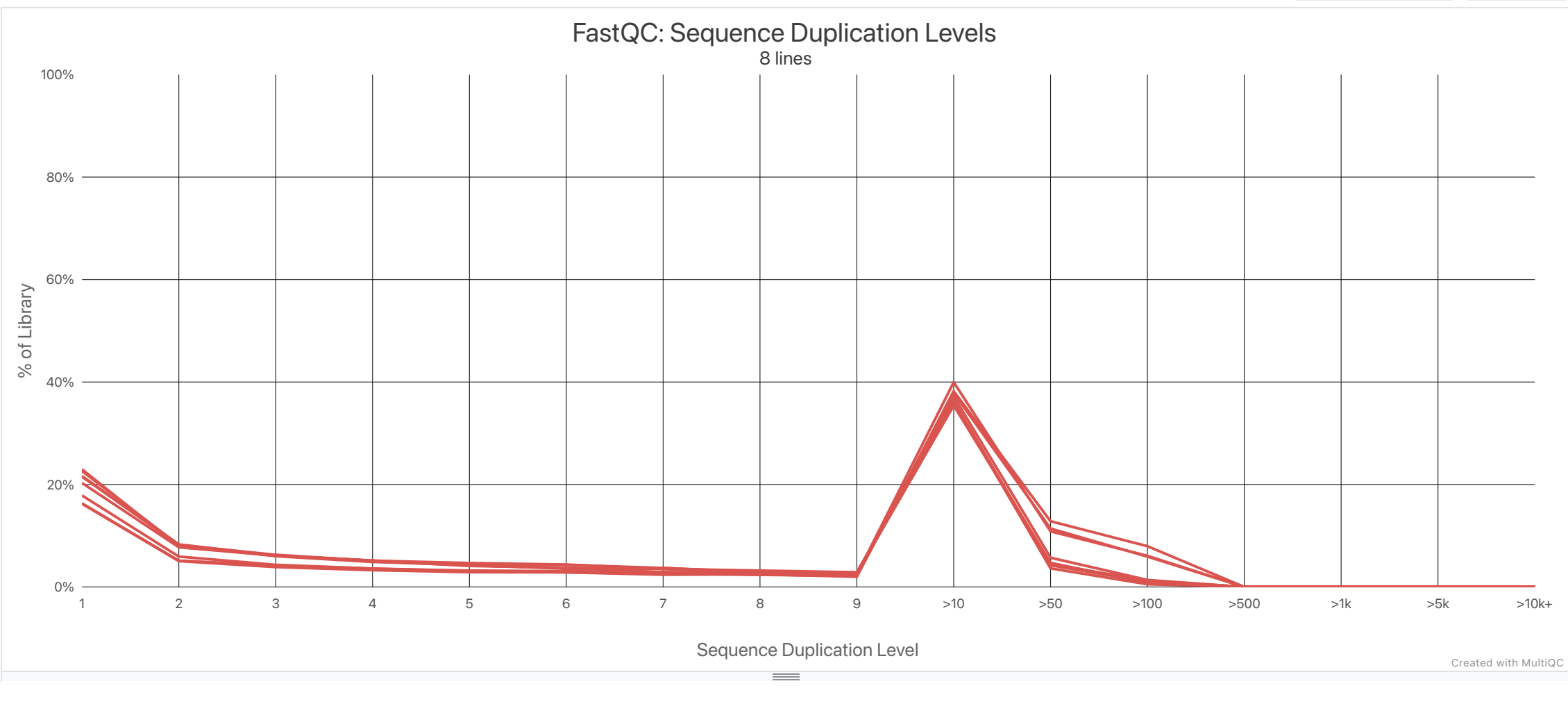
Sequence Duplication Levels

8

Help

The relative level of duplication found for every sequence.

+ Summarize plot Export...

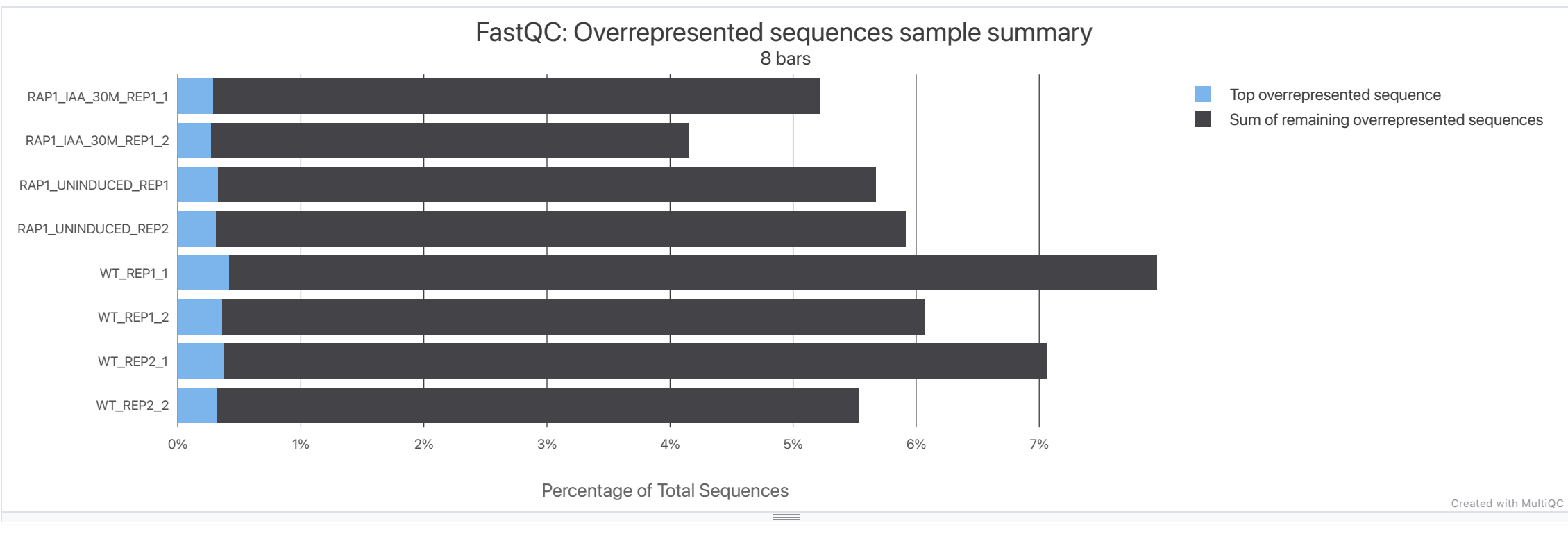


Overrepresented sequences by sample

Help

The total amount of overrepresented sequences found in each library.

+ Summarize plot Export...



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 | Scatter plot | Violin plot | Export as CSV... Showing 20/20 rows and 3/3 columns. + Summarize table

Overrepresented sequence	Reports	Occurrences	% of all reads
CTTTAAATGGGTCAGGGAATTCGGTAGGAGATTCTGGAGGTAGATCAGGG	5	691	0.1256 %
CTGGAAGTGAAATTGTAGGTCACCAATAGCGTTAATTGGTATATTTCTTT	5	633	0.1151 %
GTTTGATTGATTTTACTGCTTTTACAGCTGCAATCAGGTGAATTCGTTTC	5	624	0.1135 %
GTCAACTTCTCTGGGTGCGCGAATATTGGTTTTAGAAACACGTTTCGAAT	5	613	0.1115 %
CTAAAACTTGCCTAGAGGGGAATAGTATATGTTGAGCAAGTGTGTTGATG	5	592	0.1076 %
AGAGAATCTAGCAGCTCTTGGGCATCTGGTAACCAAGATGATTGGACAGT	5	578	0.1051 %
CTCATTTTCACTGTACGAGTCTGAGTGTCTGAAATCTTTAGATTTACTGG	5	560	0.1018 %
CAATGGTCTACCTGGGTACAATTCTTCGGACTTTCTGGCGTTGTCAATGA	5	551	0.1002 %
GTTCAGTCTGTCGATAATGTTTGTGACTTTTGTTTCAAATGCATCTGCAG	5	535	0.0973 %
GTGATATCTACTGCAGCCAATTCATTCAAACTGAGTAAGTCATAGGCTAT	5	526	0.0956 %
CTTTTCTGTCATAATATTCGTCAGTGTCCCAAGTTTTCATCTTCAACAGT	5	505	0.0918 %
GTTCGCTCCACTTTGTTTCAATCCATAAAGTGATTTCTTCAAACGTATCA	5	467	0.0849 %
GTCAAAATAGCAGCTTGAACAGCAGCACCGTAAGCAACAGCTTCATCTGG	5	455	0.0827 %
CTTTGATGTCTGCATACAAATATGCCGAAGATATGTCTAATTGTGTAATA	5	445	0.0809 %
CTTATGTATAATTCTTCTTTGATGTCTGCATACAAATATGCCGAAGATAT	5	397	0.0722 %

Expand table

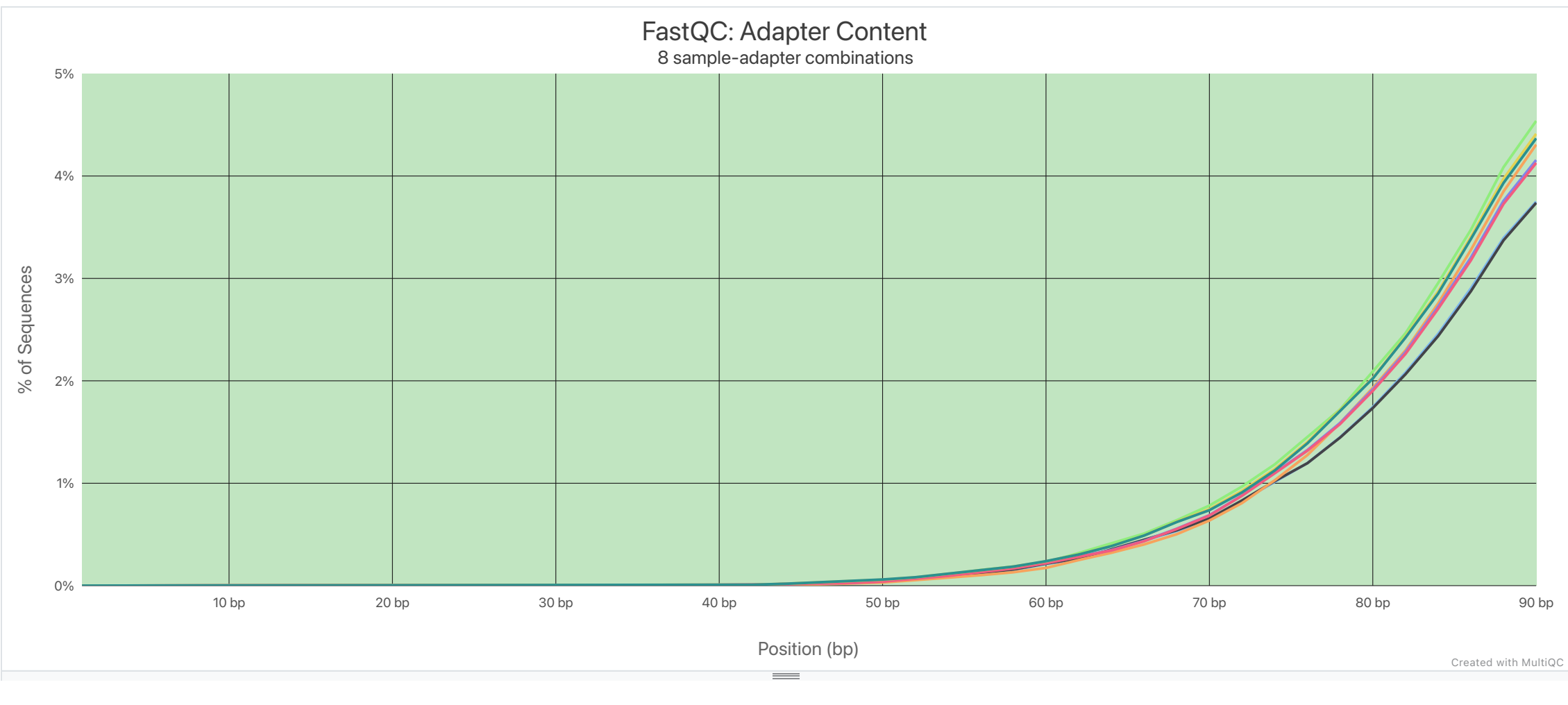
Adapter Content

8

Help

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

+ Summarize plot Export...

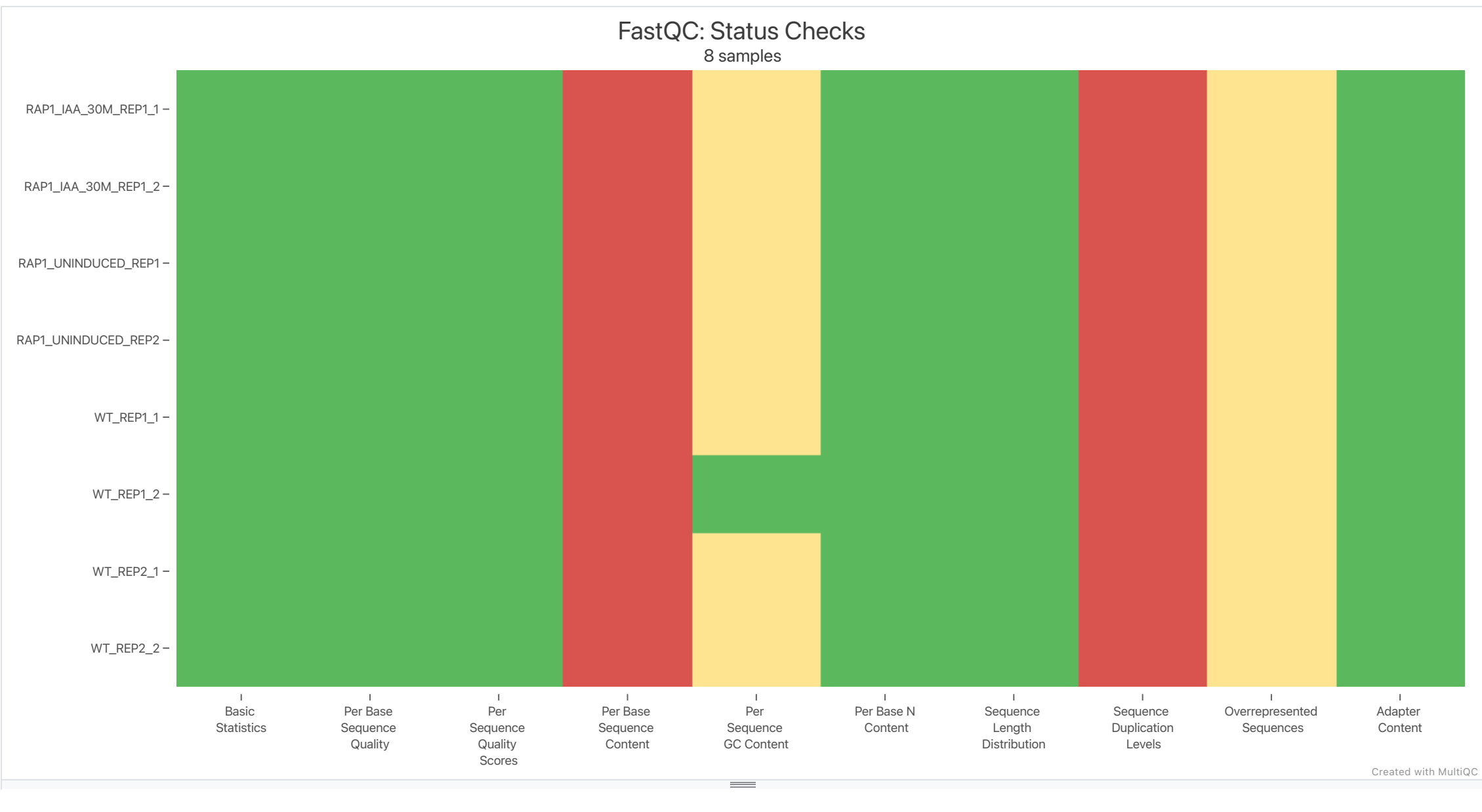


Status Checks

Help

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

Sorted by sample | Clustered + Summarize plot Export...



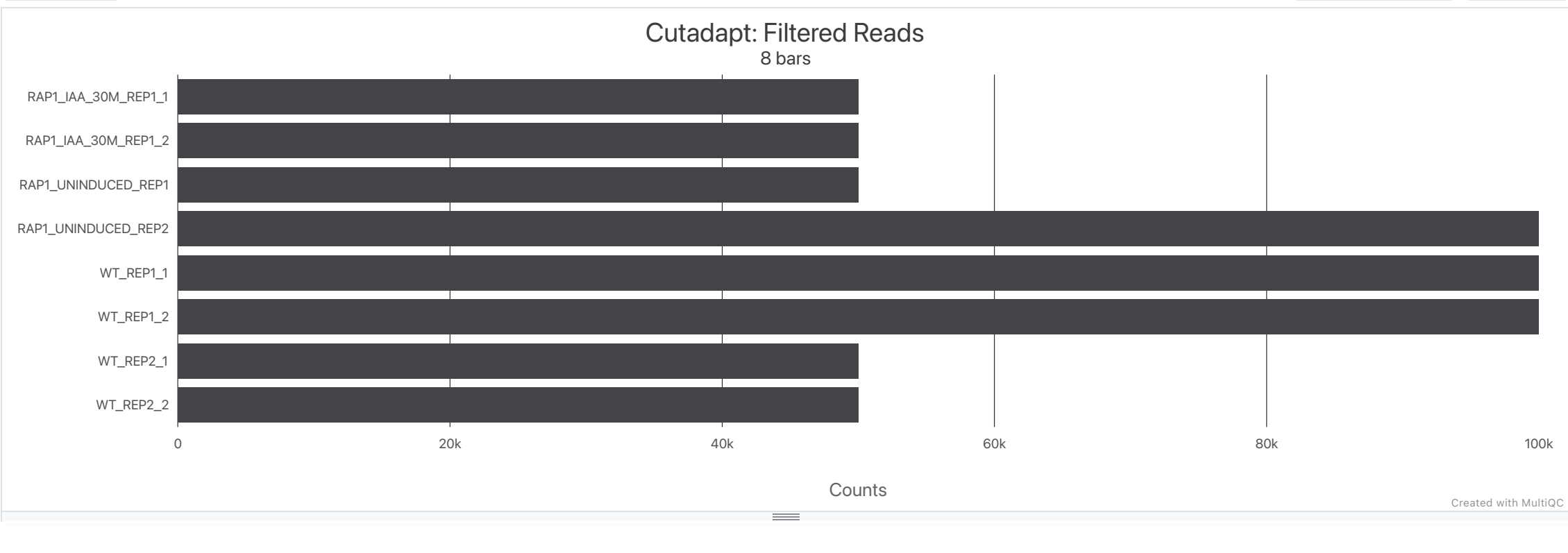
Cutadapt

Finds and removes adapter sequences, primers, poly-A tails, and other types of unwanted sequences. https://cutadapt.readthedocs.io DOI: 10.14806/ej.17.1.200

Filtered Reads

This plot shows the number of reads (SE) / pairs (PE) removed by Cutadapt.

Percentages + Summarize plot Export...

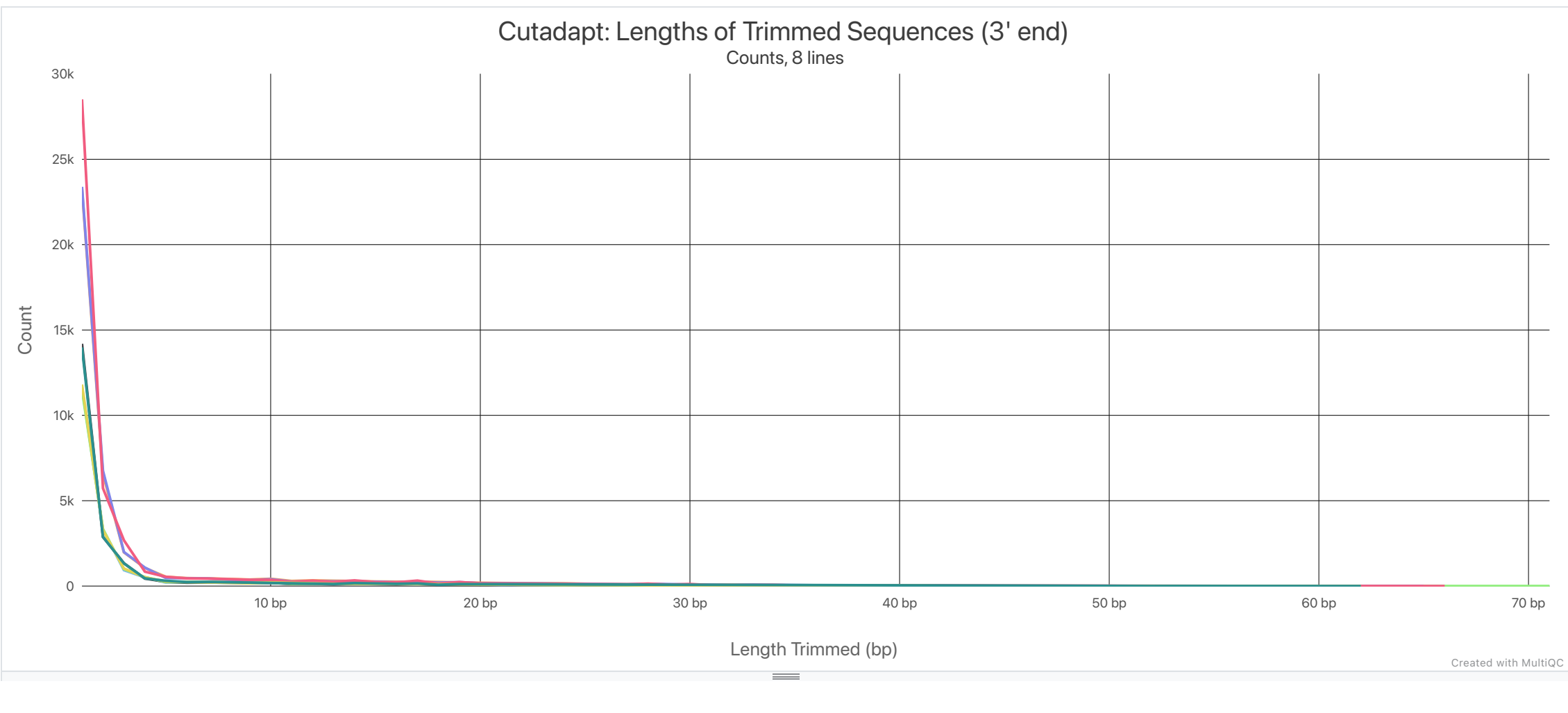


Trimmed Sequence Lengths (3')

Help

This plot shows the number of reads with certain lengths of adapter trimmed for the 3' end.

Counts | Obs/Exp + Summarize plot Export...



FastQC (trimmed)

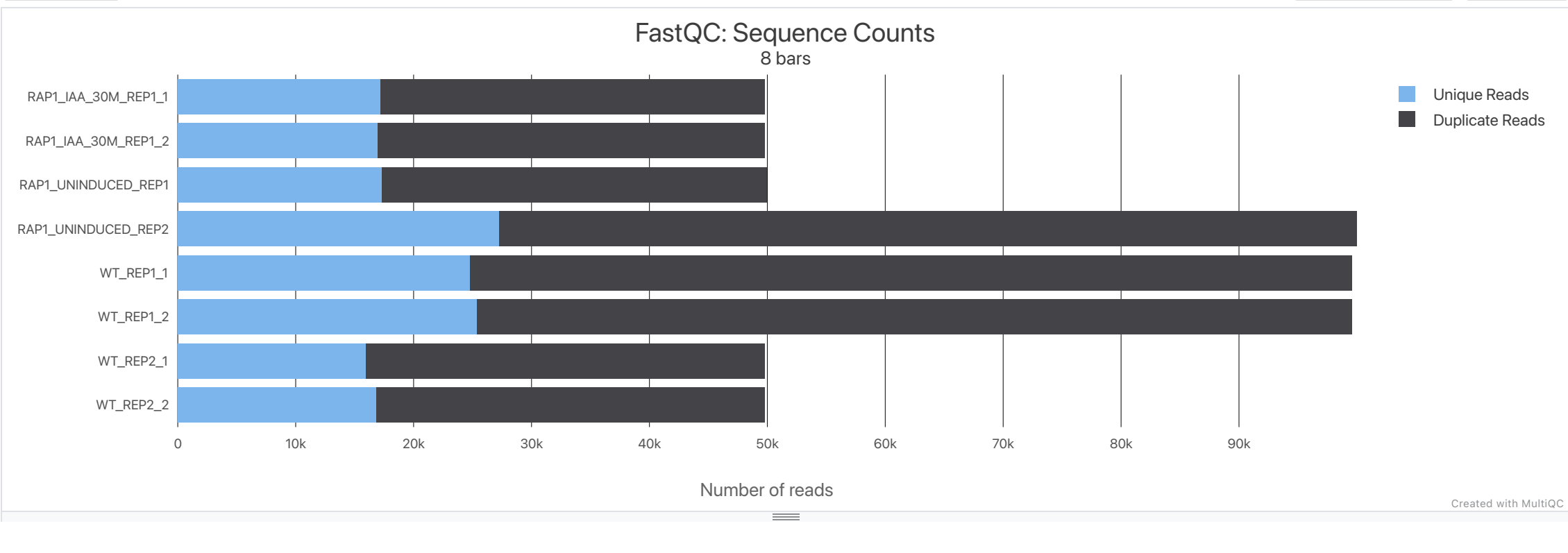
This section of the report shows FastQC results after adapter trimming. http://www.bioinformatics.babraham.ac.uk/projects/fastqc

Sequence Counts

Help

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

Percentages + Summarize plot Export...



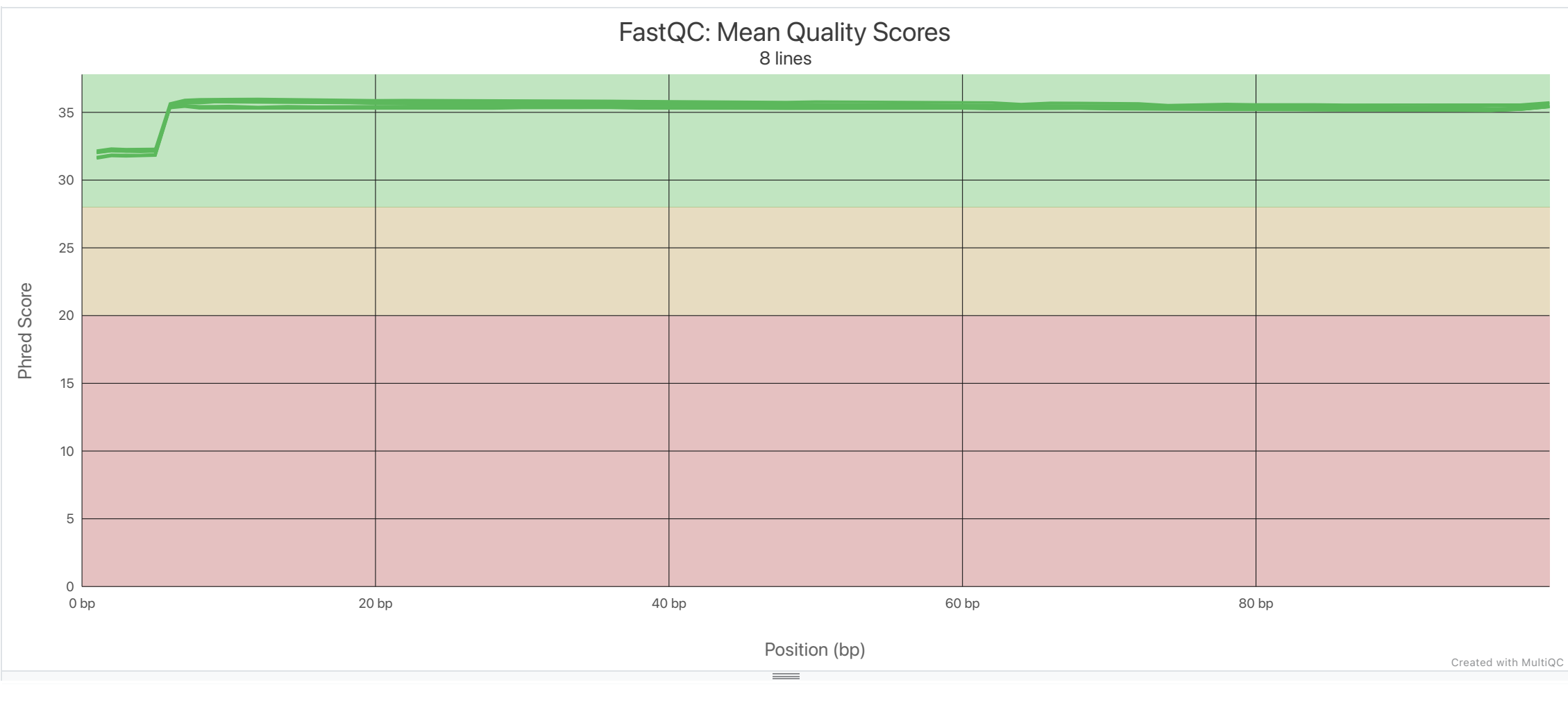
Sequence Quality Histograms

8

Help

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

+ Summarize plot Export...



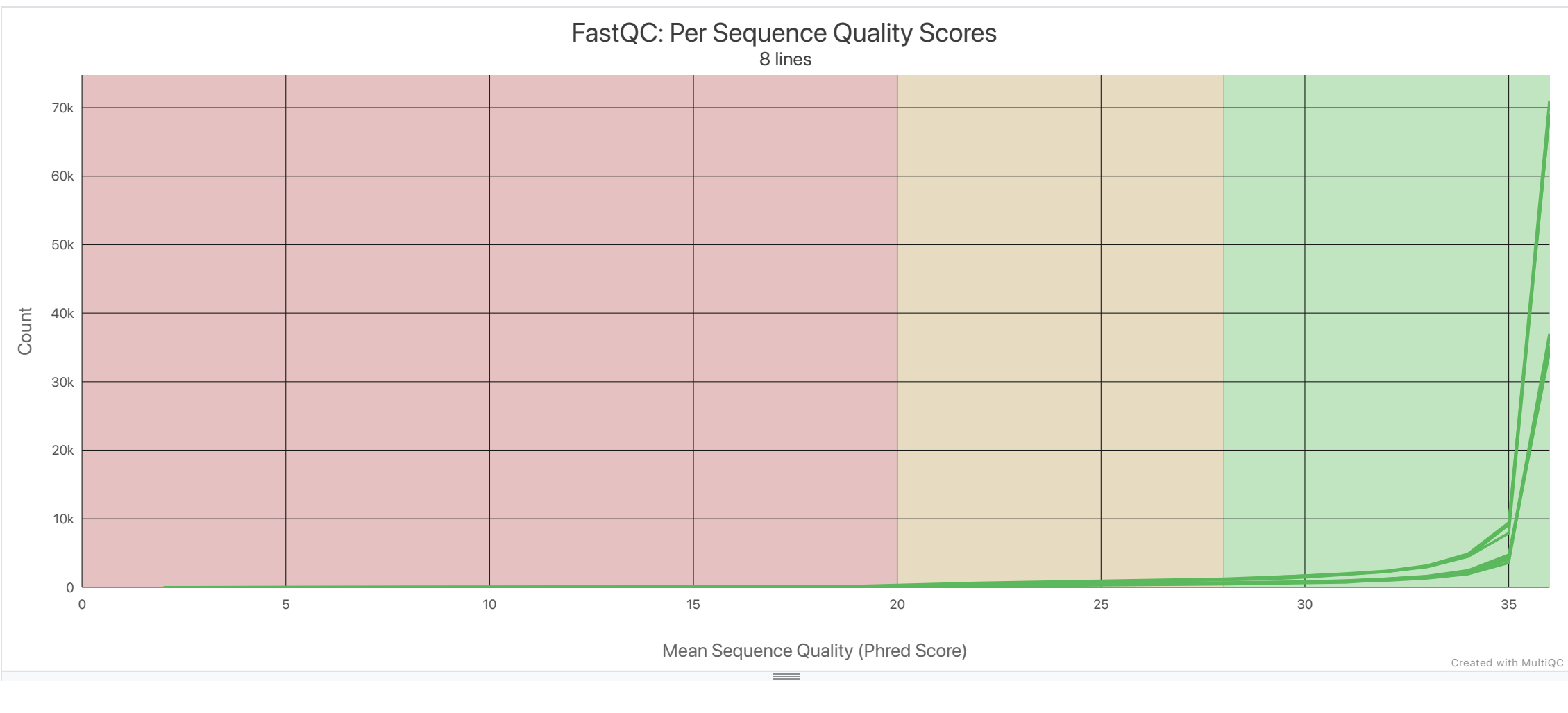
Per Sequence Quality Scores

8

Help

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

+ Summarize plot Export...



Per Base Sequence Content

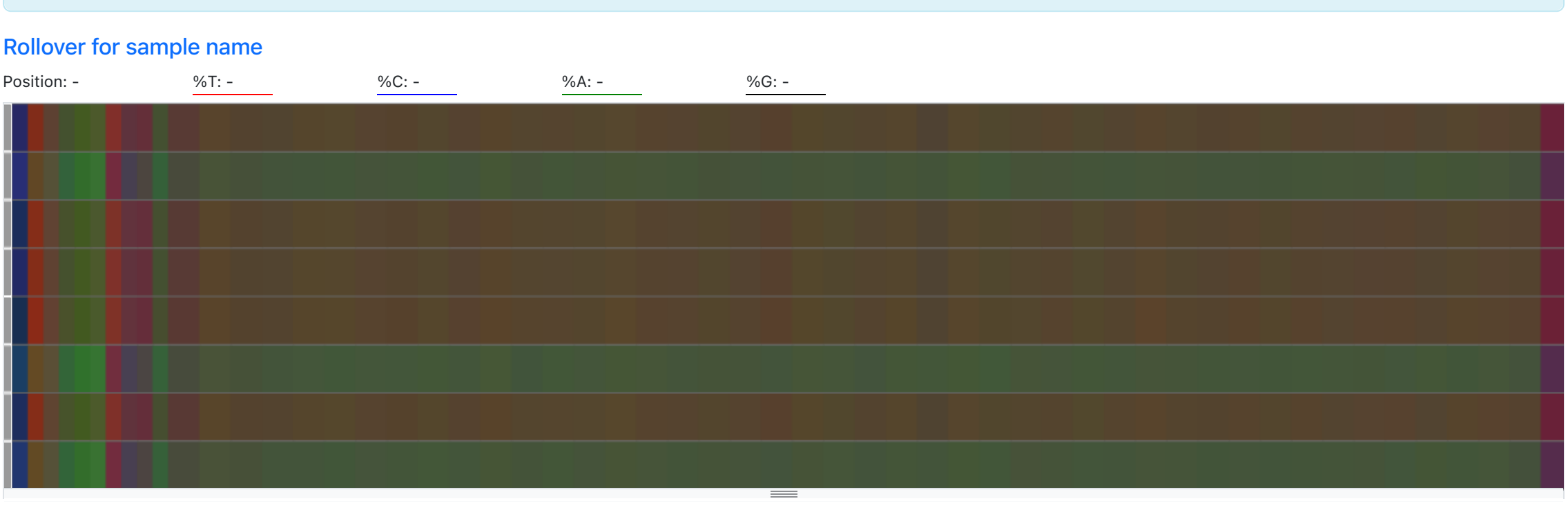
Help

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: -



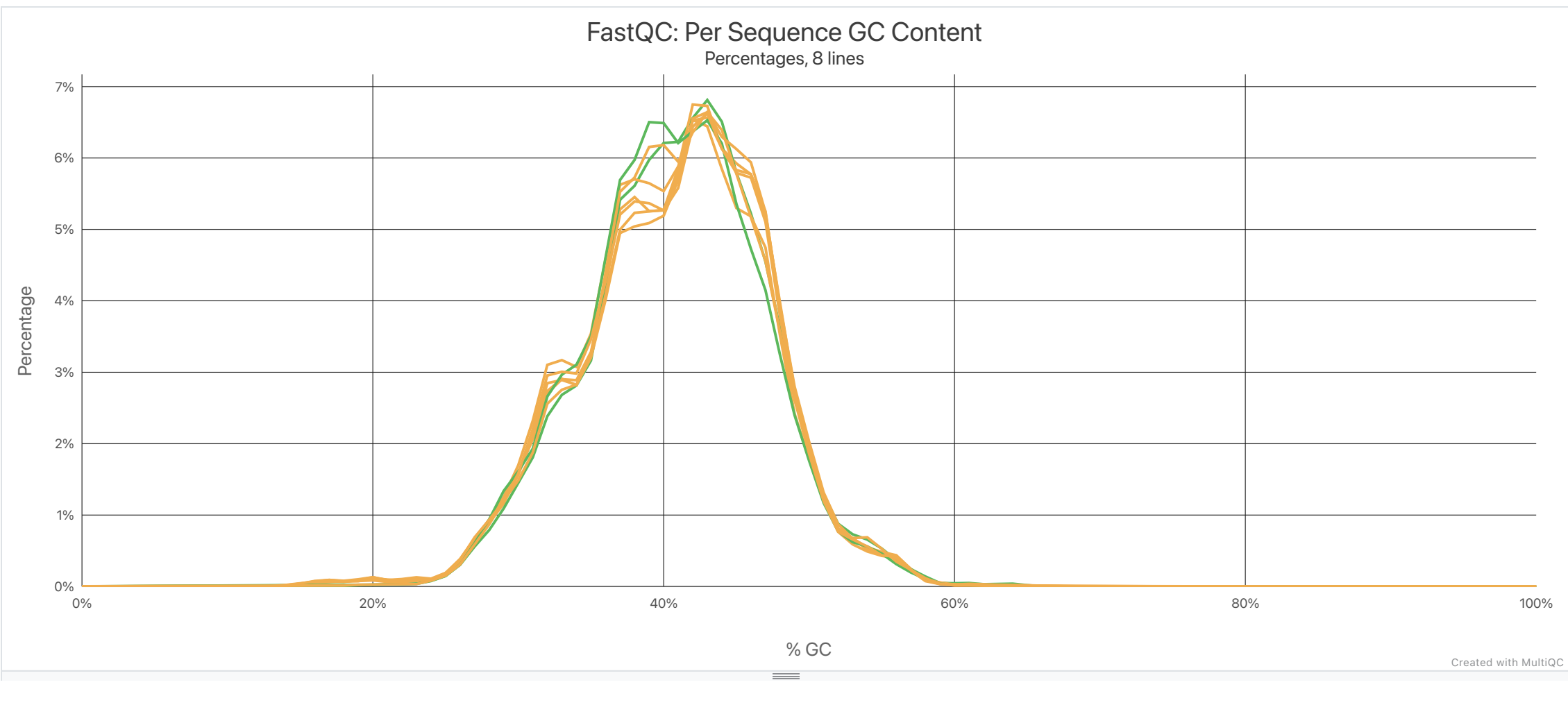
Per Sequence GC Content

2 6

Help

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

Percentages | Counts + Summarize plot Export...



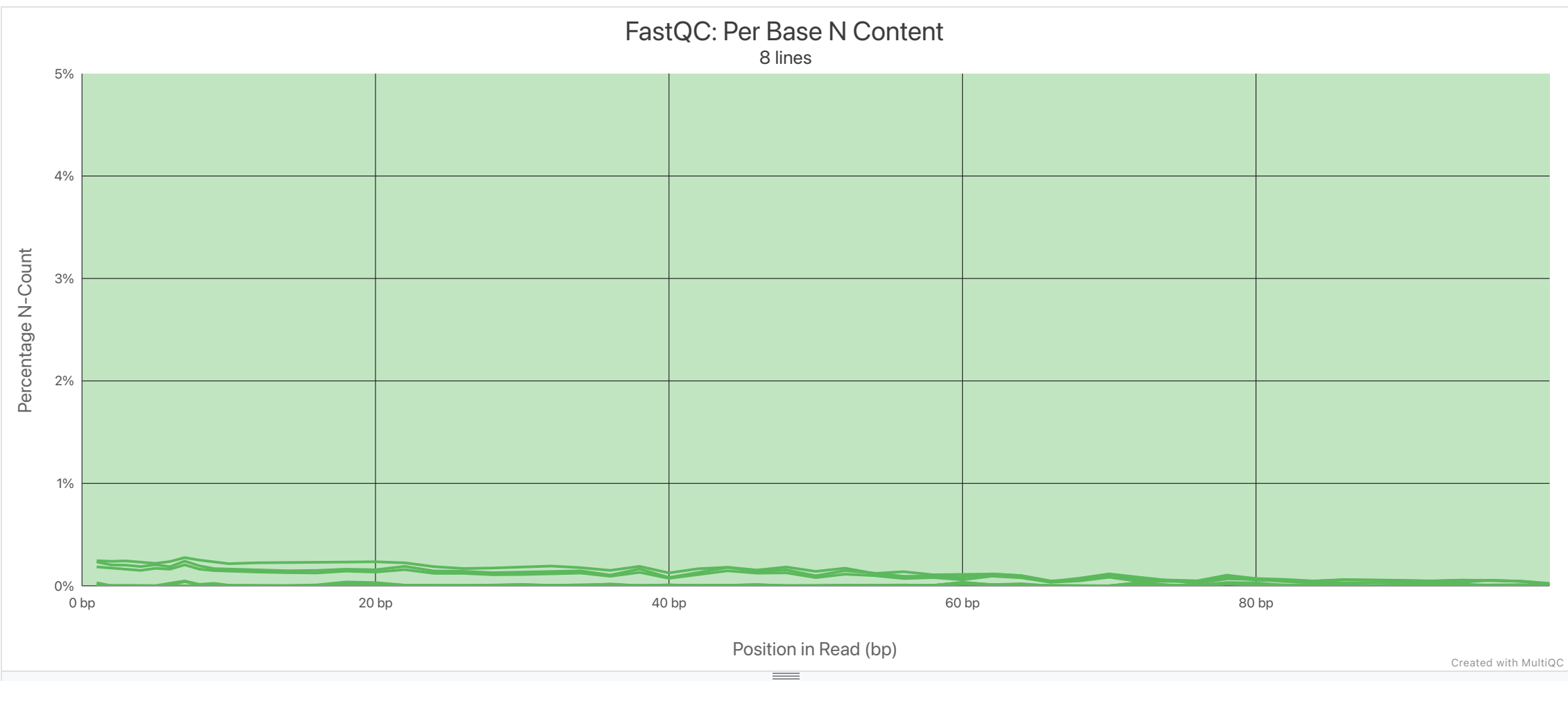
Per Base N Content

8

Help

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

+ Summarize plot Export...

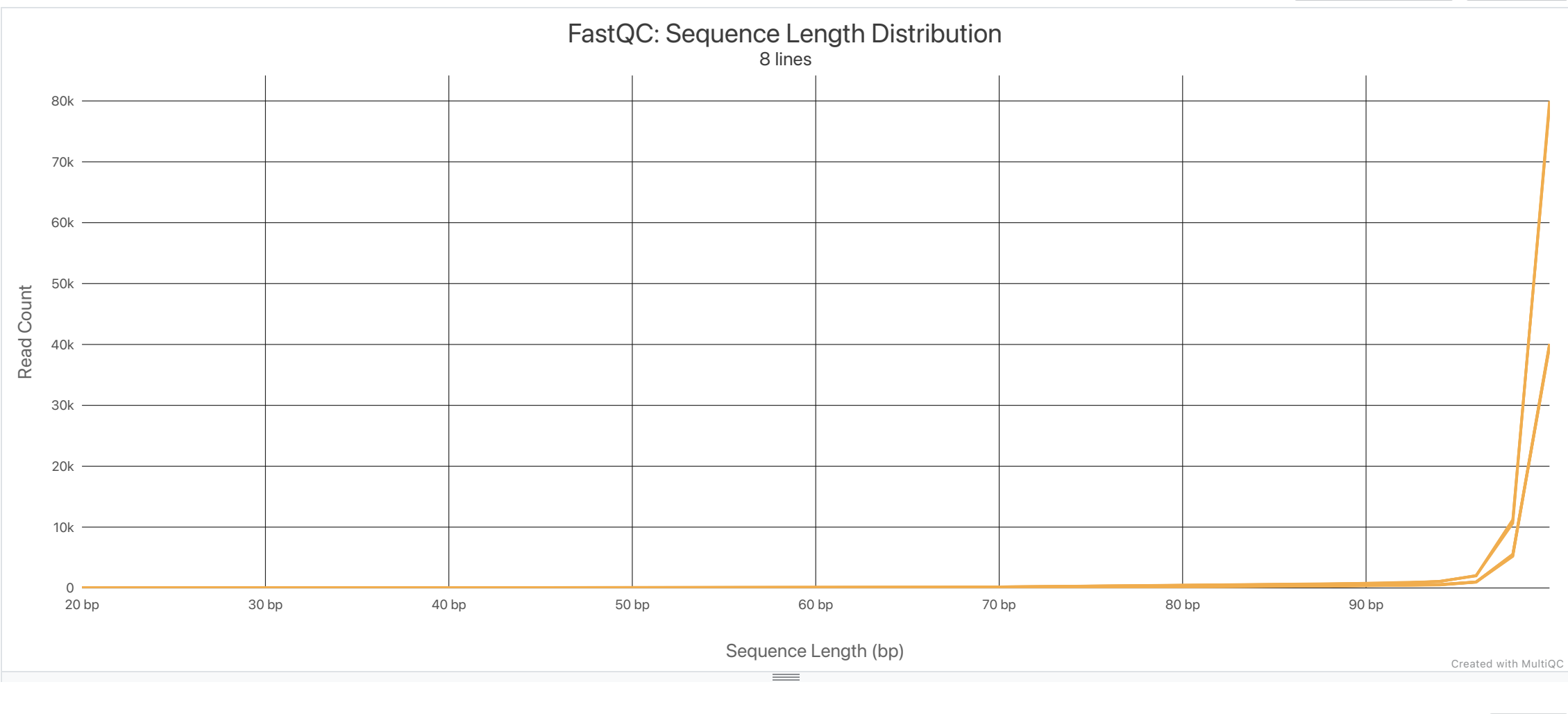


Sequence Length Distribution

8

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

+ Summarize plot Export...



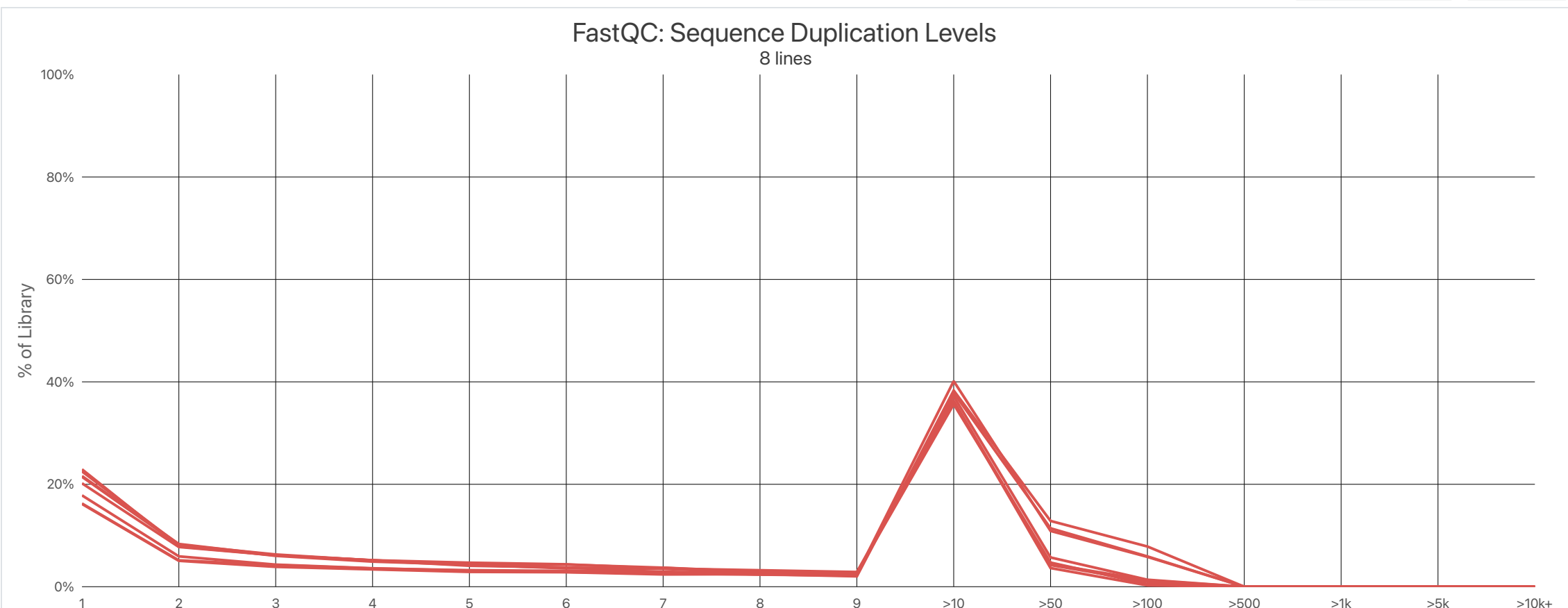
Sequence Duplication Levels

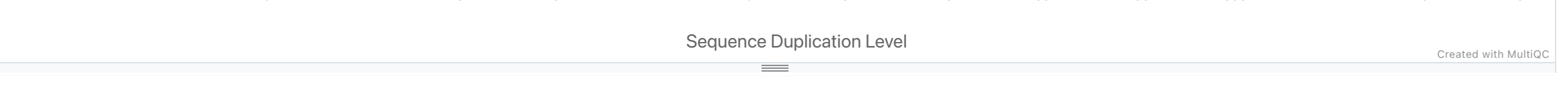
8

Help

The relative level of duplication found for every sequence.

+ Summarize plot Export...



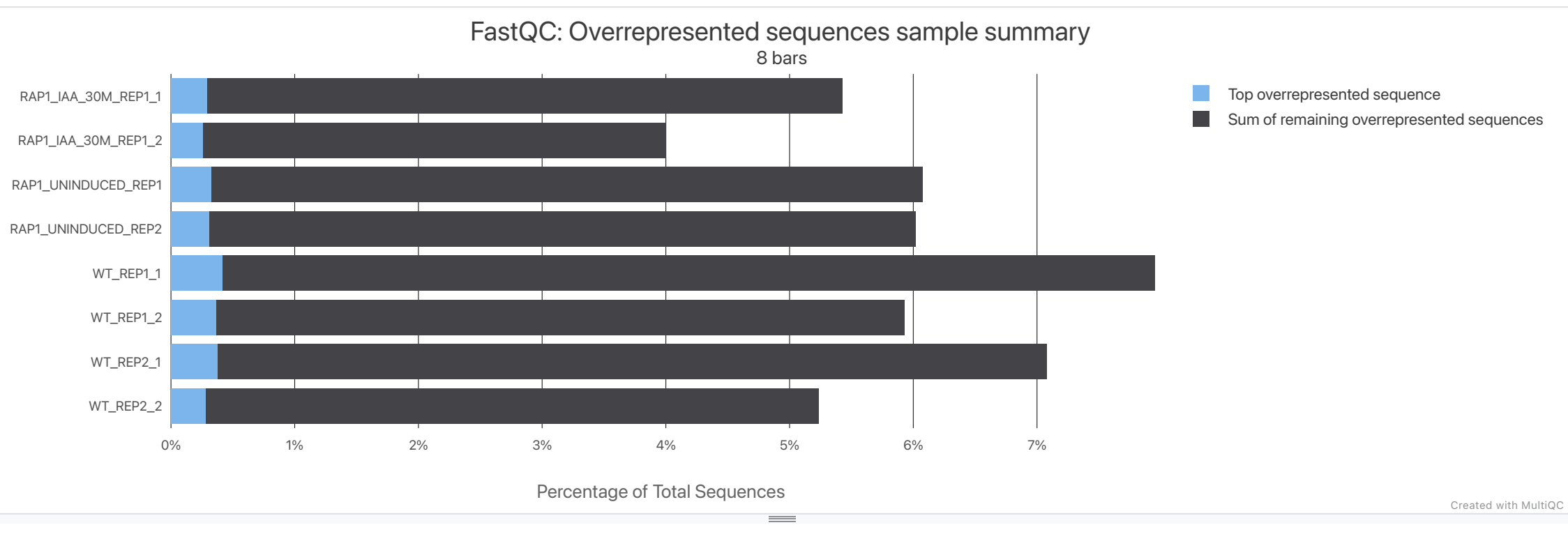


Overrepresented sequences by sample

❓ Help

The total amount of overrepresented sequences found in each library.

+ Summarize plot ⇩ Export...



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 | Scatter plot | Violin plot | Export as CSV... Showing $^{20}/_{20}$ rows and $^{3}/_{3}$ columns. + Summarize table

Overrepresented sequence	Reports	Occurrences	% of all reads
CTTTGACCCAGGTAGGTAGGAATTGAGAGGGAGCAAATATTTGAAAAGTG	5	1214	0.2215 %
GTTAGGAGTGTGCAATACCTTTATTGATGTTTTGGTGTTGTCCTGGAAGT	5	1031	0.1881 %
CTTCGATCTCGGAGGTTCTAAACTACGCATATTCTTAGTATTCCATGTGT	5	823	0.1501 %
CGAGATTCGAGTTTTGTAAAAATTTGATGTATGTTTTAACCCAATTTGGA	5	783	0.1428 %
CCTCATTCCGTTTTATATGTTTATATTCATTGATCCTATTACATTATCAA	5	736	0.1343 %
CTTTAAATGGGTCAGGGAATTCGGTAGGAGATTCTGGAGGTAGATCAGGG	5	691	0.1261 %
CTGGAAGTGAAATTGTAGGTCACCAATAGCGTTAATTGGTATATTTCTTT	5	633	0.1155 %
GTTTGATTGATTTTACTGCTTTTACAGCTGCAATCAGGTGAATTCGTTTC	5	620	0.1131 %
GTCAACTTCTCTGGGTGCGCGAATATTGGTTTTAGAAACACGTTTCGAAT	5	613	0.1118 %
CTAAAACTTGCCTAGAGGGGAATAGTATATGTTGAGCAAGTGTGTTGATG	5	590	0.1076 %
AGAGAATCTAGCAGCTCTTGGGCATCTGGTAACCAAGATGATTGGACAGT	5	578	0.1054 %
CTCATTTTCACTGTACGAGTCTGAGTGTCTGAAATCTTTAGATTTACTGG	5	560	0.1022 %
CAATGGTCTACCTGGGTACAATTCTTCGGACTTTCTGGCGTTGTCAATGA	5	551	0.1005 %
GTTCAGTCTGTCGATAATGTTTGTGACTTTTGTTTCAAATGCATCTGCAG	5	534	0.0974 %
GTGATATCTACTGCAGCCAATTCATTCAAACTGAGTAAGTCATAGGCTAT	5	525	0.0958 %

Expand table ⌄

Adapter Content

8

❓ Help

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%

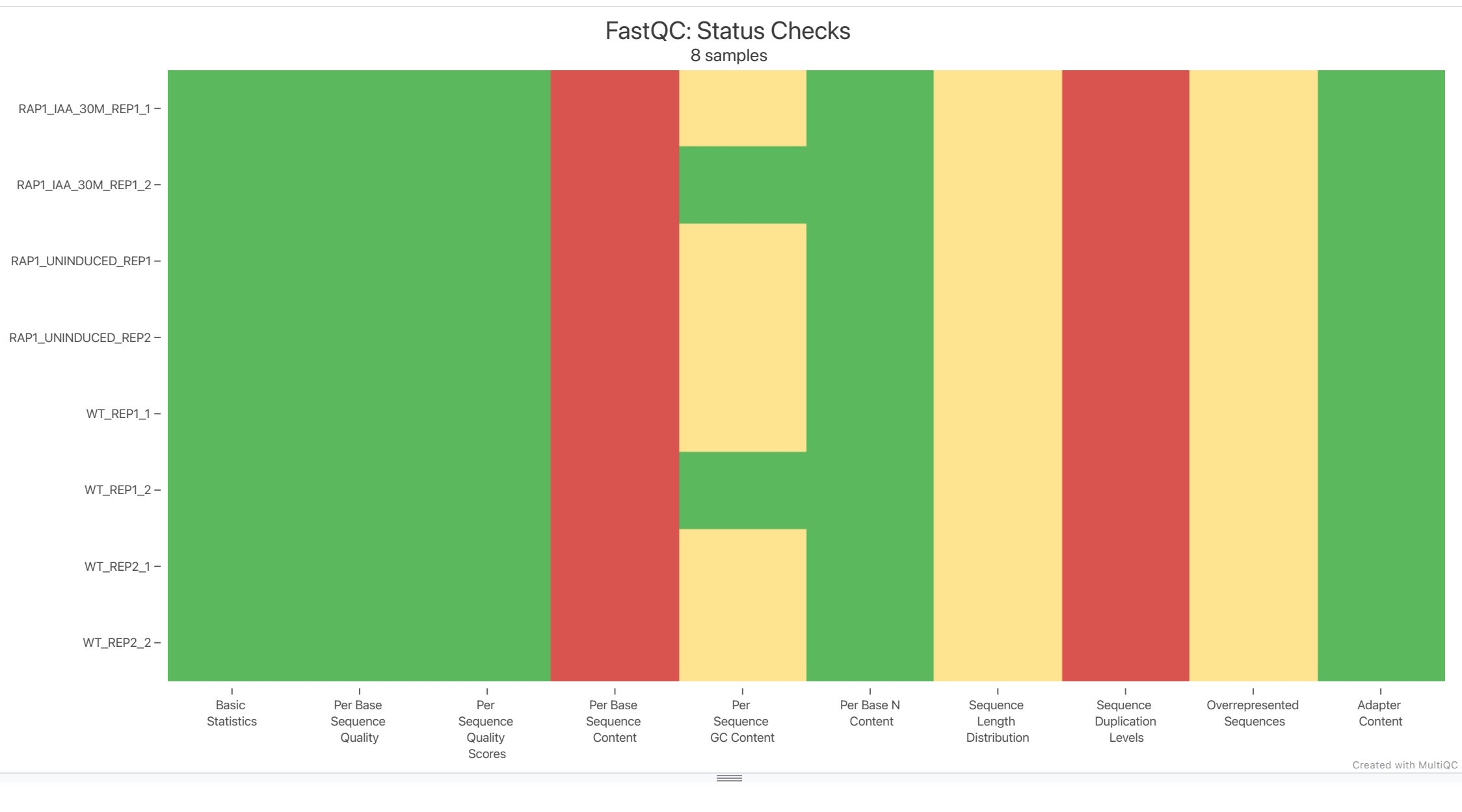
Status Checks

❓ Help

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

Sorted by sample | Clustered

+ Summarize plot ⇩ Export...



BBTools

Pre-processing, assembly, alignment, and statistics tools for DNA/RNA sequencing reads. http://jgi.doe.gov/data-and-tools/bbtools

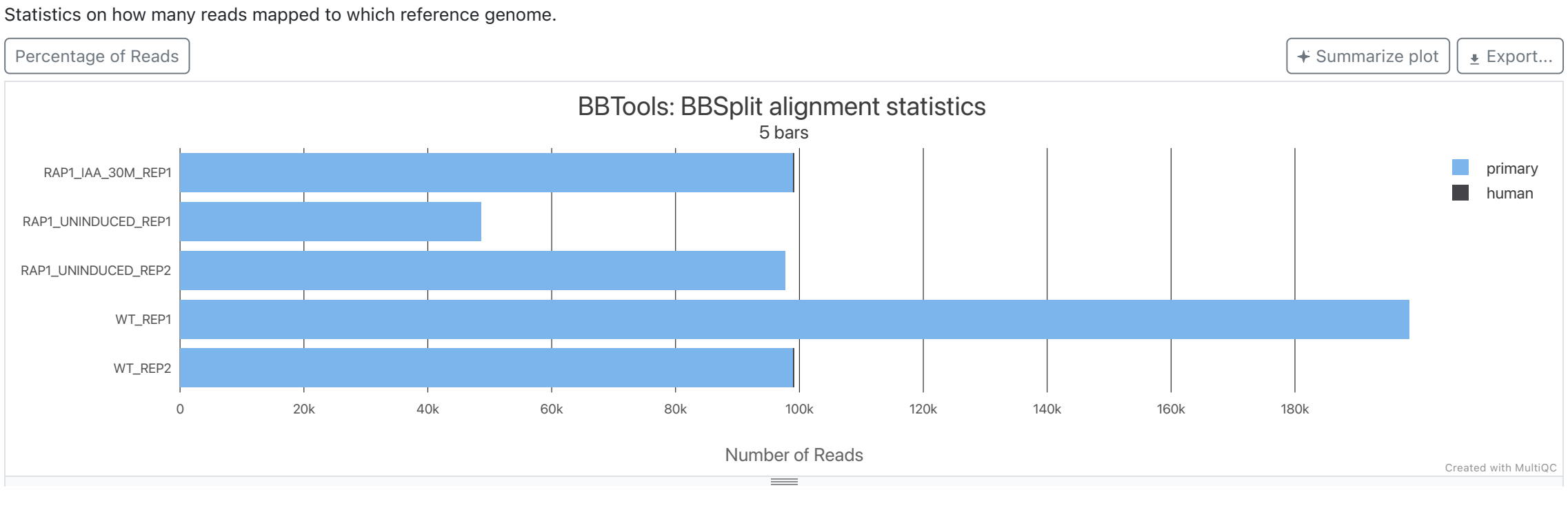
BBSplit alignment statistics

❓ Help

Statistics on how many reads mapped to which reference genome.

Percentage of Reads

+ Summarize plot ⇩ Export...



BBSplit Statistics

Statistics on how many reads mapped to which reference genome.

Copy table | Configure columns | Scatter plot | Violin plot | Export as CSV... Showing $^{5}/_{5}$ rows and $^{4}/_{10}$ columns. + Summarize table

Sample Name	human % Unambig	human % Ambig	primary % Unambig	primary % Ambig
RAP1_IAA_30M_REP1	0.0 %	0.0 %	99.6 %	0.0 %
RAP1_UNINDUCED_REP1			97.2 %	0.0 %
RAP1_UNINDUCED_REP2	0.0 %	0.0 %	97.7 %	0.0 %
WT_REP1			99.7 %	0.0 %
WT_REP2	0.0 %	0.0 %	99.6 %	0.0 %

FastQC (filtered)

This section of the report shows FastQC results after contaminant removal (BBSplit) and/or ribosomal RNA removal. http://www.bioinformatics.babraham.ac.uk/projects/fastqc

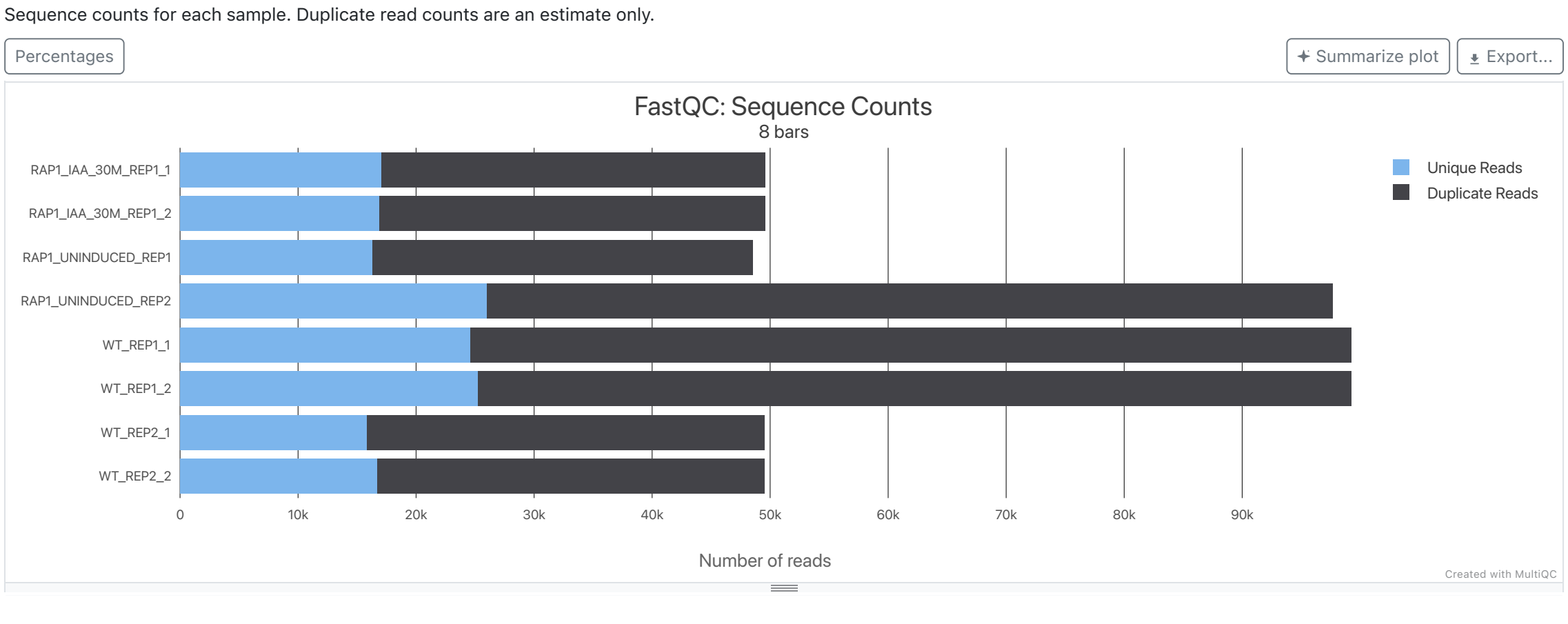
Sequence Counts

❓ Help

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

Percentages

+ Summarize plot ⇩ Export...



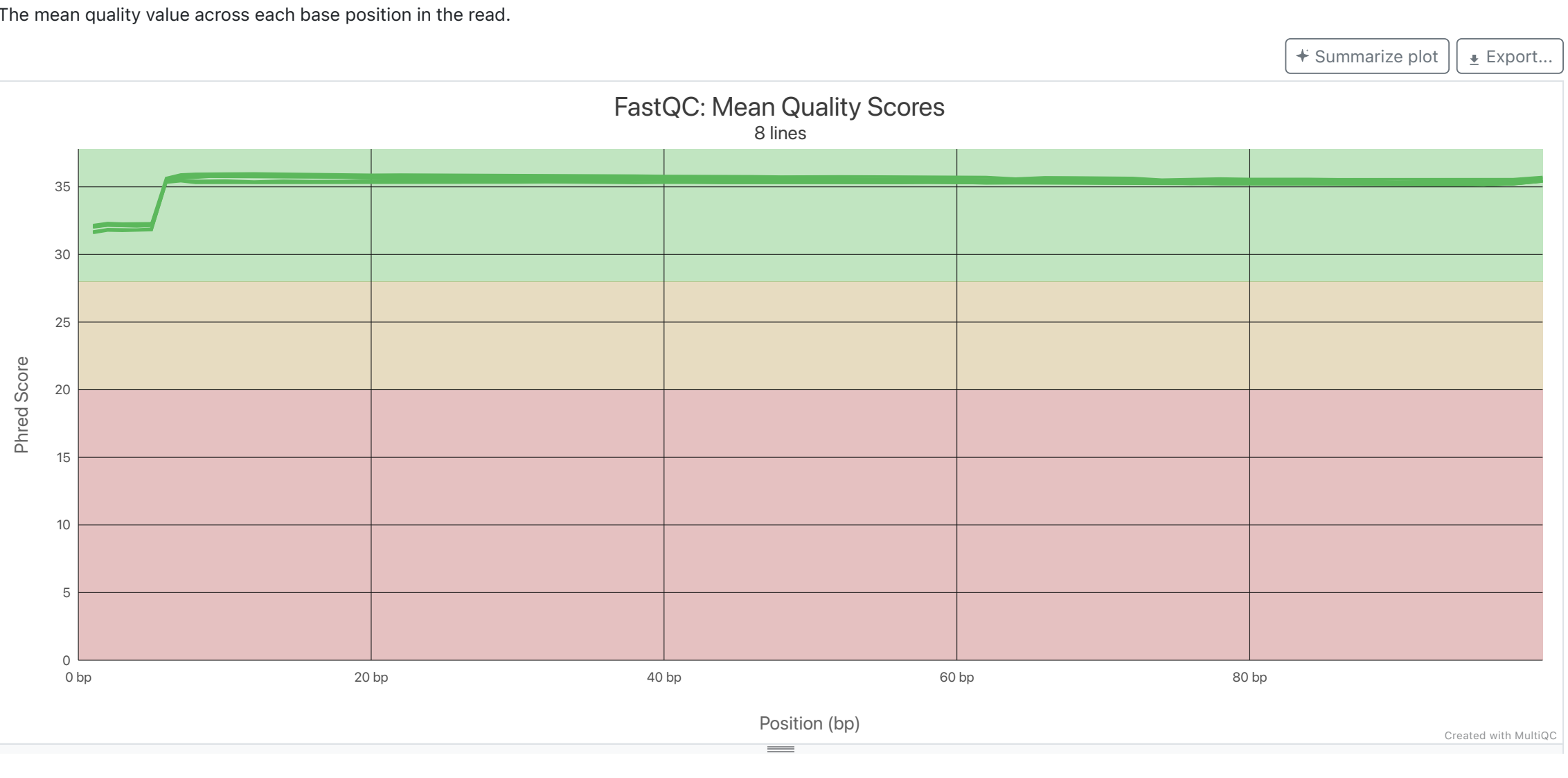
Sequence Quality Histograms

8

❓ Help

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

+ Summarize plot ⇩ Export...



Per Sequence Quality Scores

8

❓ Help

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

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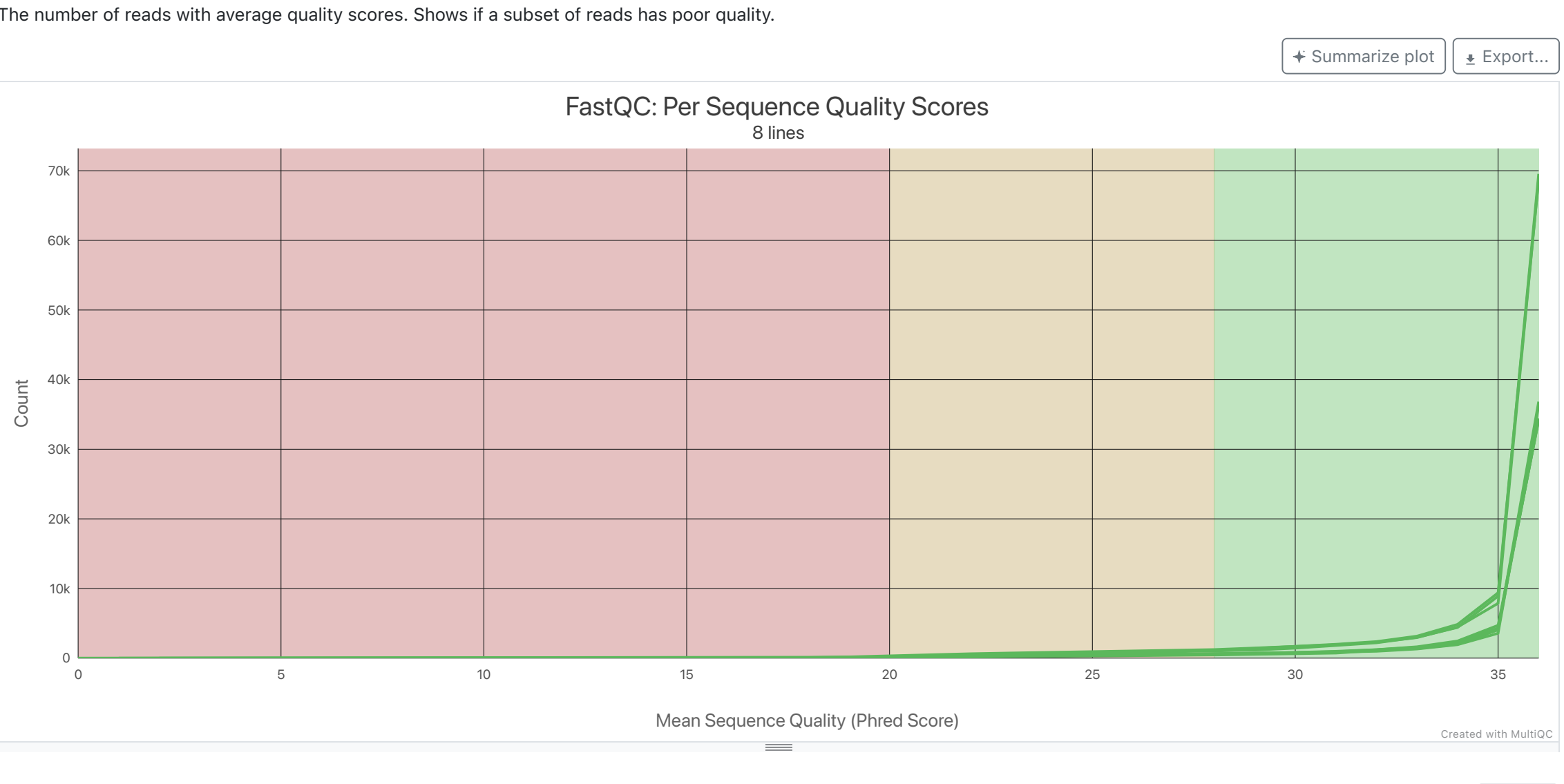

Per Base Sequence Content

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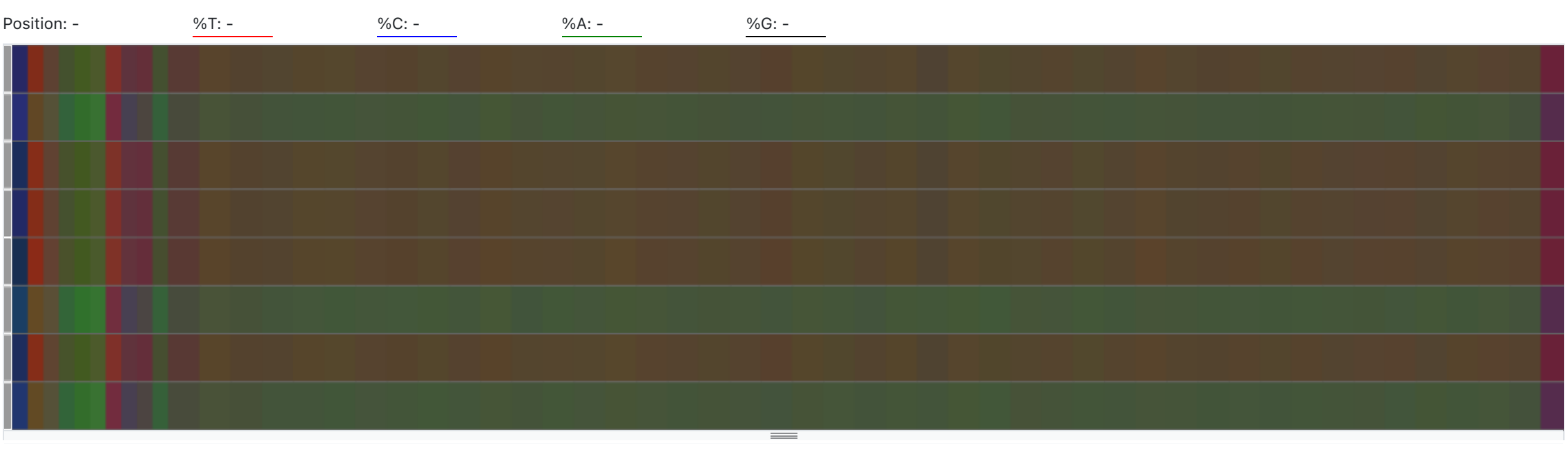
The proportion of each base position for which each of the four normal DNA bases has been called.

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

Rollover for sample name

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



Per Sequence GC Content

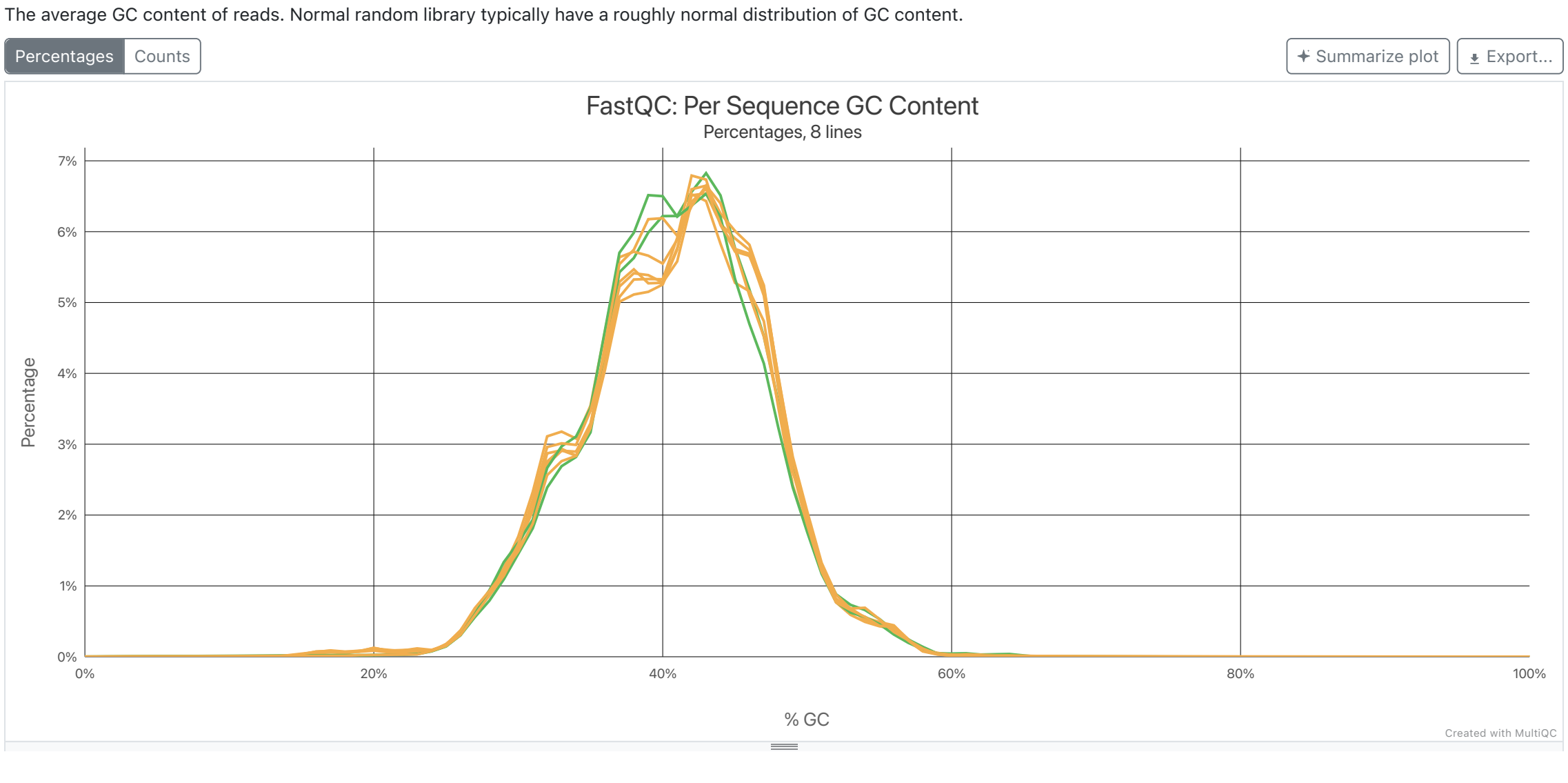
2 6

❓ Help

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

Percentages | Counts

+ Summarize plot ⇩ Export...



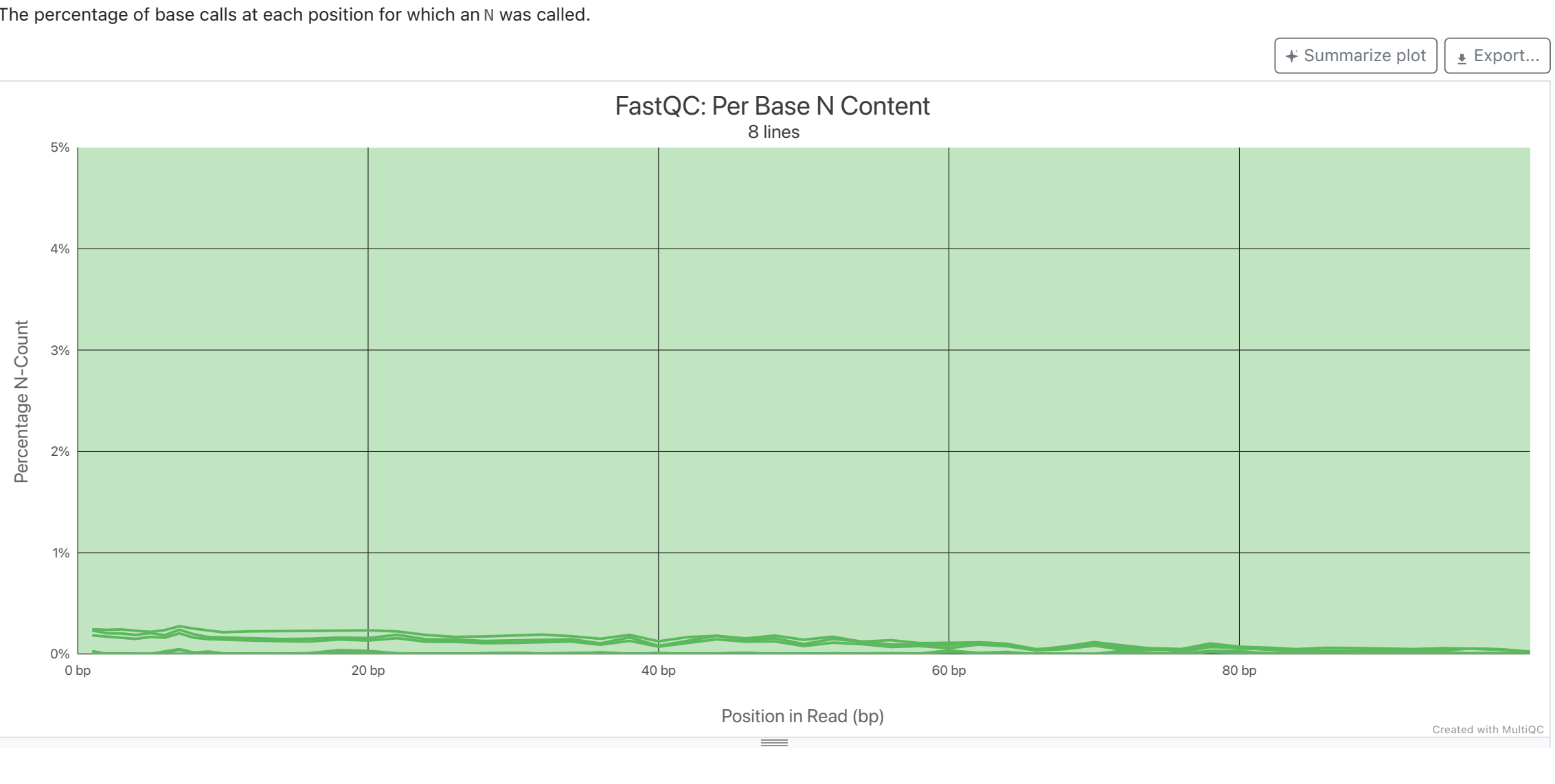
Per Base N Content

8

❓ Help

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

+ Summarize plot ⇩ Export...

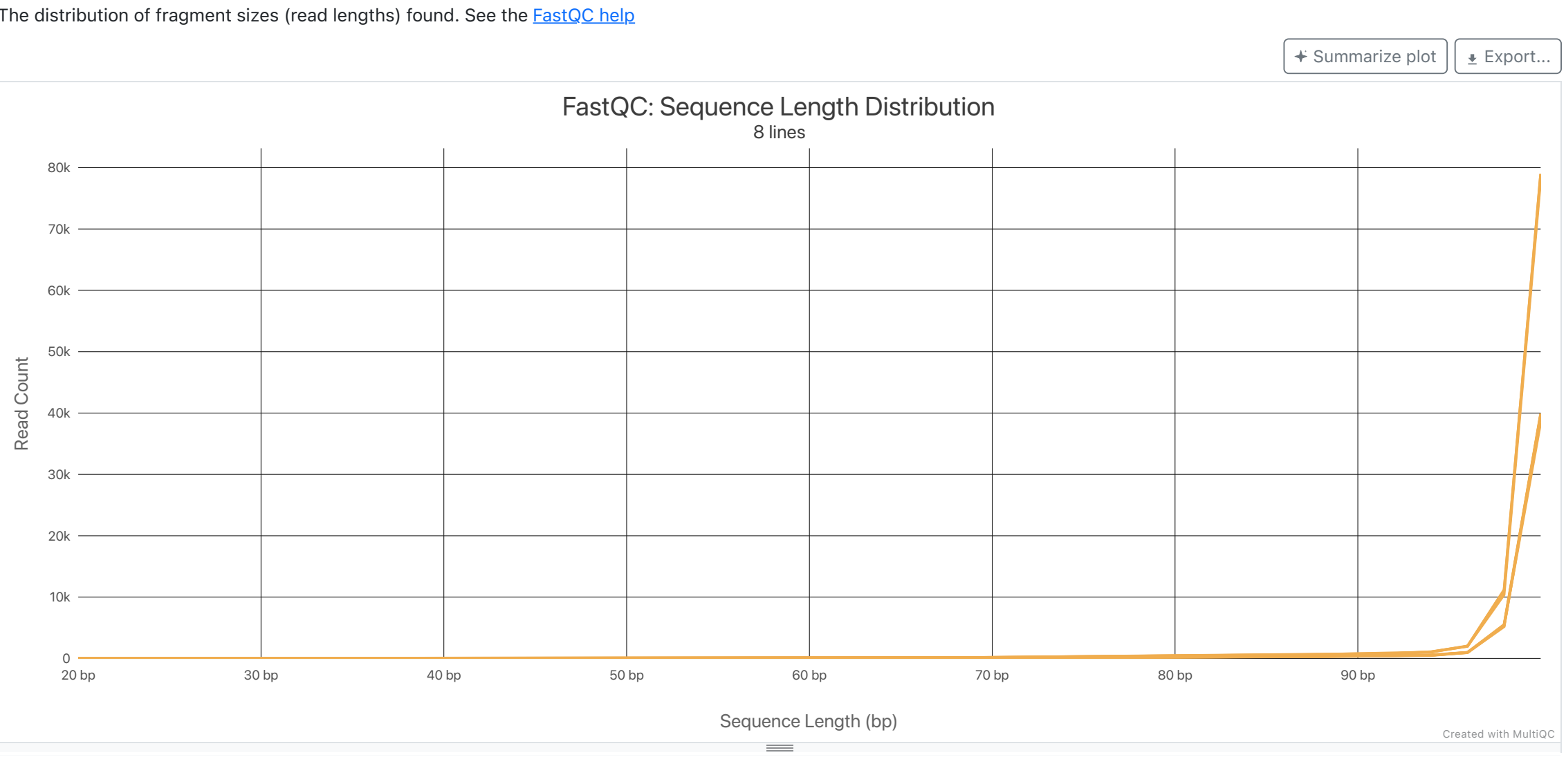


Sequence Length Distribution

8

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

+ Summarize plot ⇩ Export...



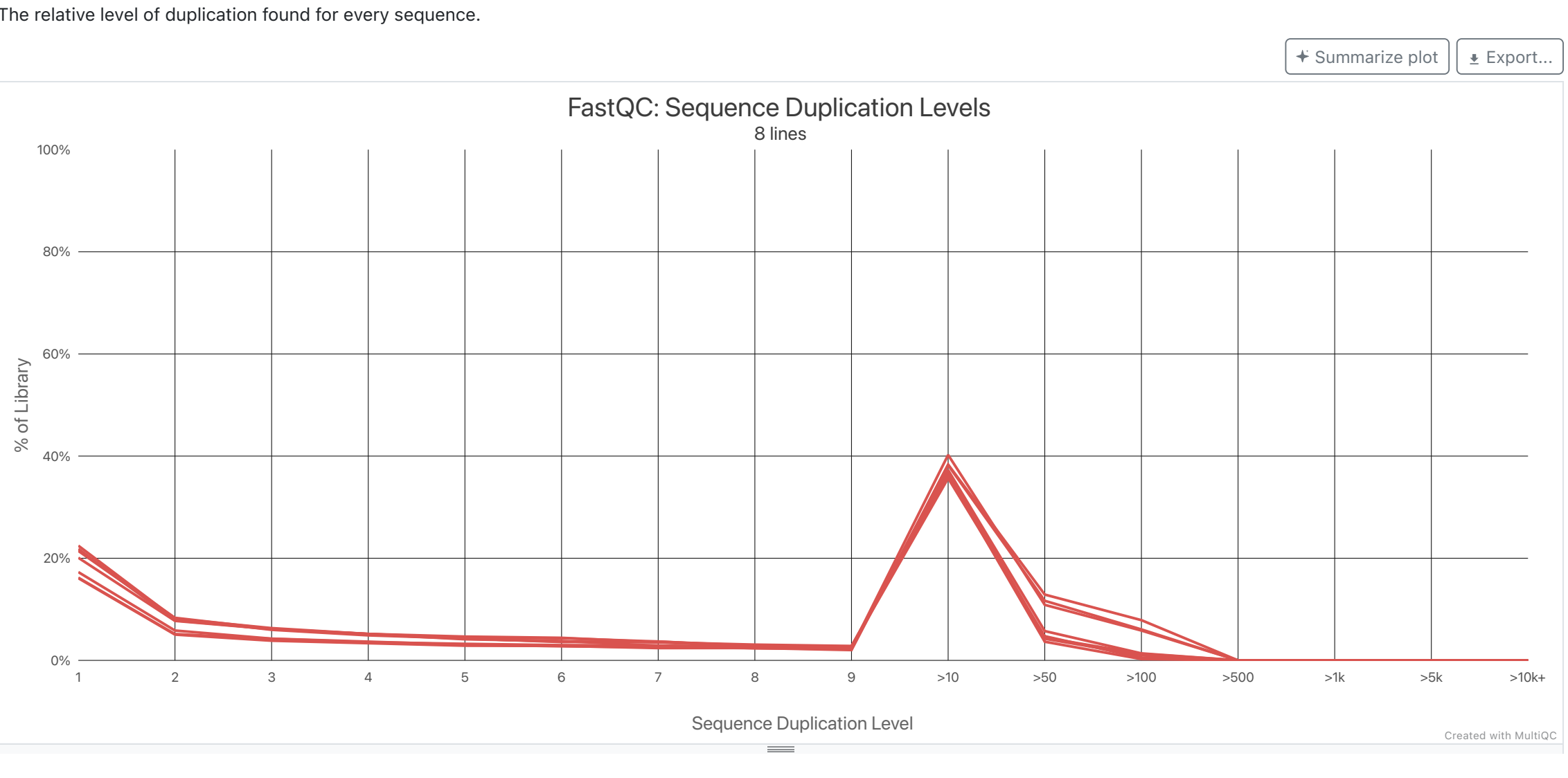
Sequence Duplication Levels

8

❓ Help

The relative level of duplication found for every sequence.

+ Summarize plot ⇩ Export...

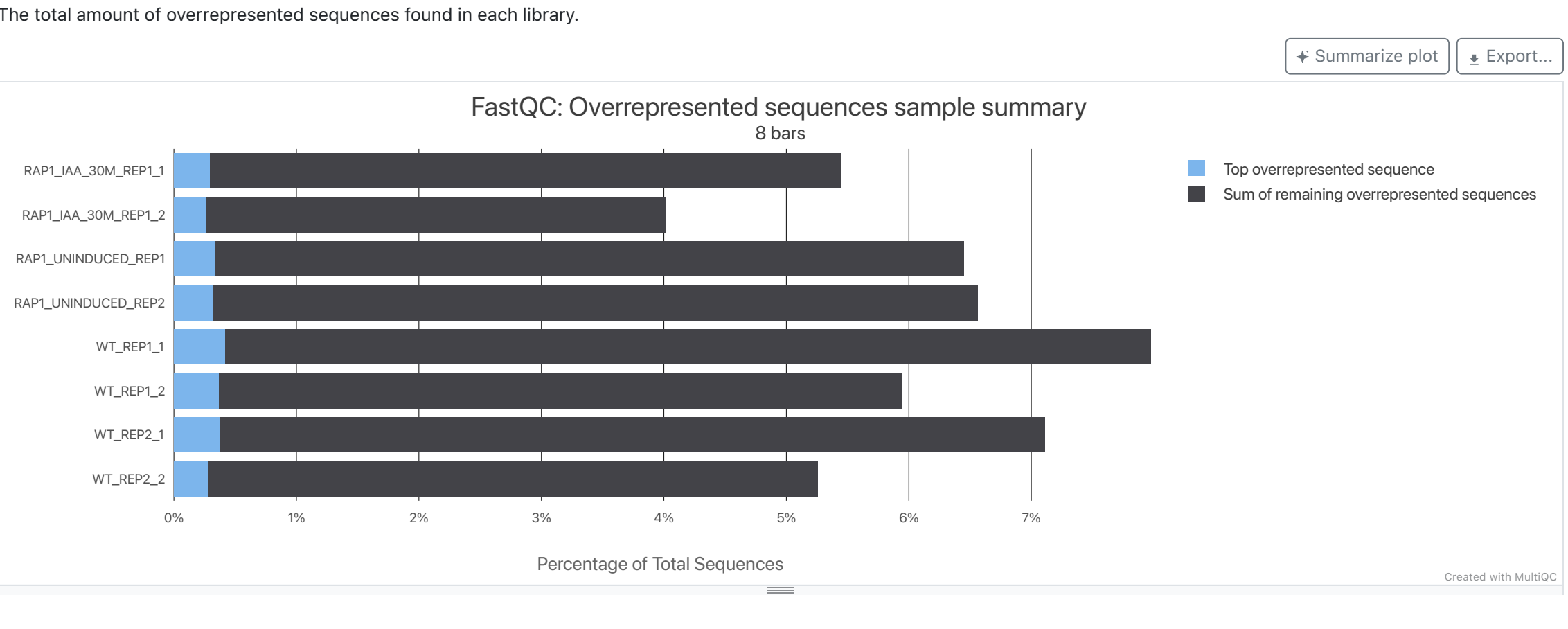


Overrepresented sequences by sample

❓ Help

The total amount of overrepresented sequences found in each library.

+ Summarize plot ⇩ Export...



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 | Scatter plot | Violin plot | Export as CSV... Showing $^{20}/_{20}$ rows and $^{3}/_{3}$ columns. + Summarize table

Overrepresented sequence	Reports	Occurrences	% of all reads
CTTTGACCCAGGTAGGTAGGAATTGAGAGGGAGCAAATATTTGAAAAGTG	5	1214	0.2236 %
GTTAGGAGTGTGCAATACCTTTATTGATGTTTTGGTGTTGTCCTGGAAGT	5	1030	0.1897 %
CTTCGATCTCGGAGGTTCTAAACTACGCATATTCTTAGTATTCCATGTGT	5	823	0.1516 %
CGAGATTCGAGTTTTGTAAAAATTTGATGTATGTTTTAACCCAATTTGGA	5	783	0.1442 %
CCTCATTCCGTTTTATATGTTTATATTCATTGATCCTATTACATTATCAA	5	736	0.1356 %
CTTTAAATGGGTCAGGGAATTCGGTAGGAGATTCTGGAGGTAGATCAGGG	5	691	0.1273 %
CTGGAAGTGAAATTGTAGGTCACCAATAGCGTTAATTGGTATATTTCTTT	5	633	0.1166 %
GTTTGATTGATTTTACTGCTTTTACAGCTGCAATCAGGTGAATTCGTTTC	5	620	0.1142 %
GTCAACTTCTCTGGGTGCGCGAATATTGGTTTTAGAAACACGTTTCGAAT	5	613	0.1129 %
CTAAAACTTGCCTAGAGGGGAATAGTATATGTTGAGCAAGTGTGTTGATG	5	590	0.1087 %
AGAGAATCTAGCAGCTCTTGGGCATCTGGTAACCAAGATGATTGGACAGT	5	578	0.1065 %
CTCATTTTCACTGTACGAGTCTGAGTGTCTGAAATCTTTAGATTTACTGG	5	560	0.1031 %
CAATGGTCTACCTGGGTACAATTCTTCGGACTTTCTGGCGTTGTCAATGA	5	551	0.1015 %
GTTCAGTCTGTCGATAATGTTTGTGACTTTTGTTTCAAATGCATCTGCAG	5	534	0.0984 %
GTGATATCTACTGCAGCCAATTCATTCAAACTGAGTAAGTCATAGGCTAT	5	525	0.0967 %

Expand table ⌄

Adapter Content

8

❓ Help

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%

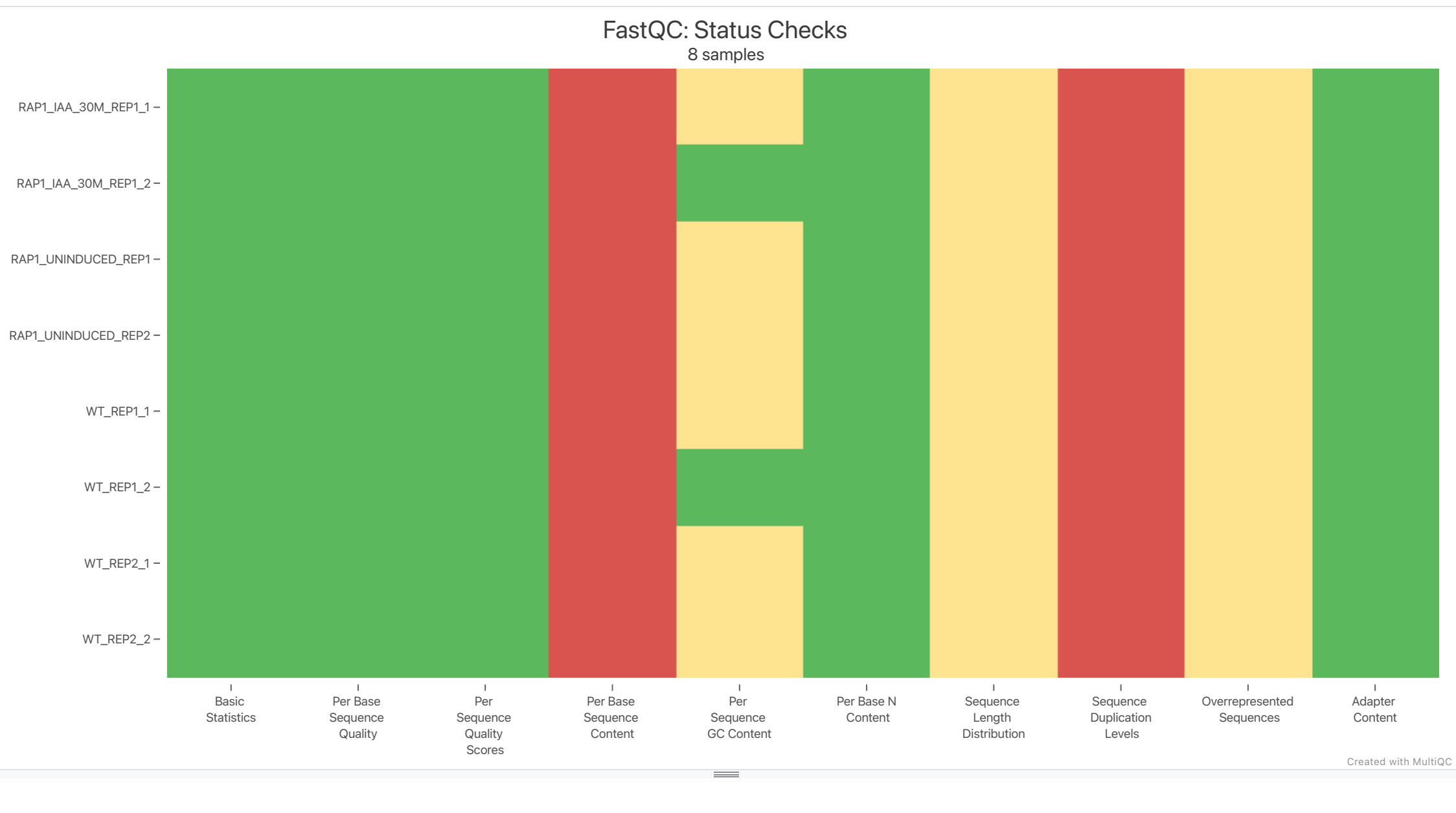
Status Checks

❓ Help

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

Sorted by sample | Clustered

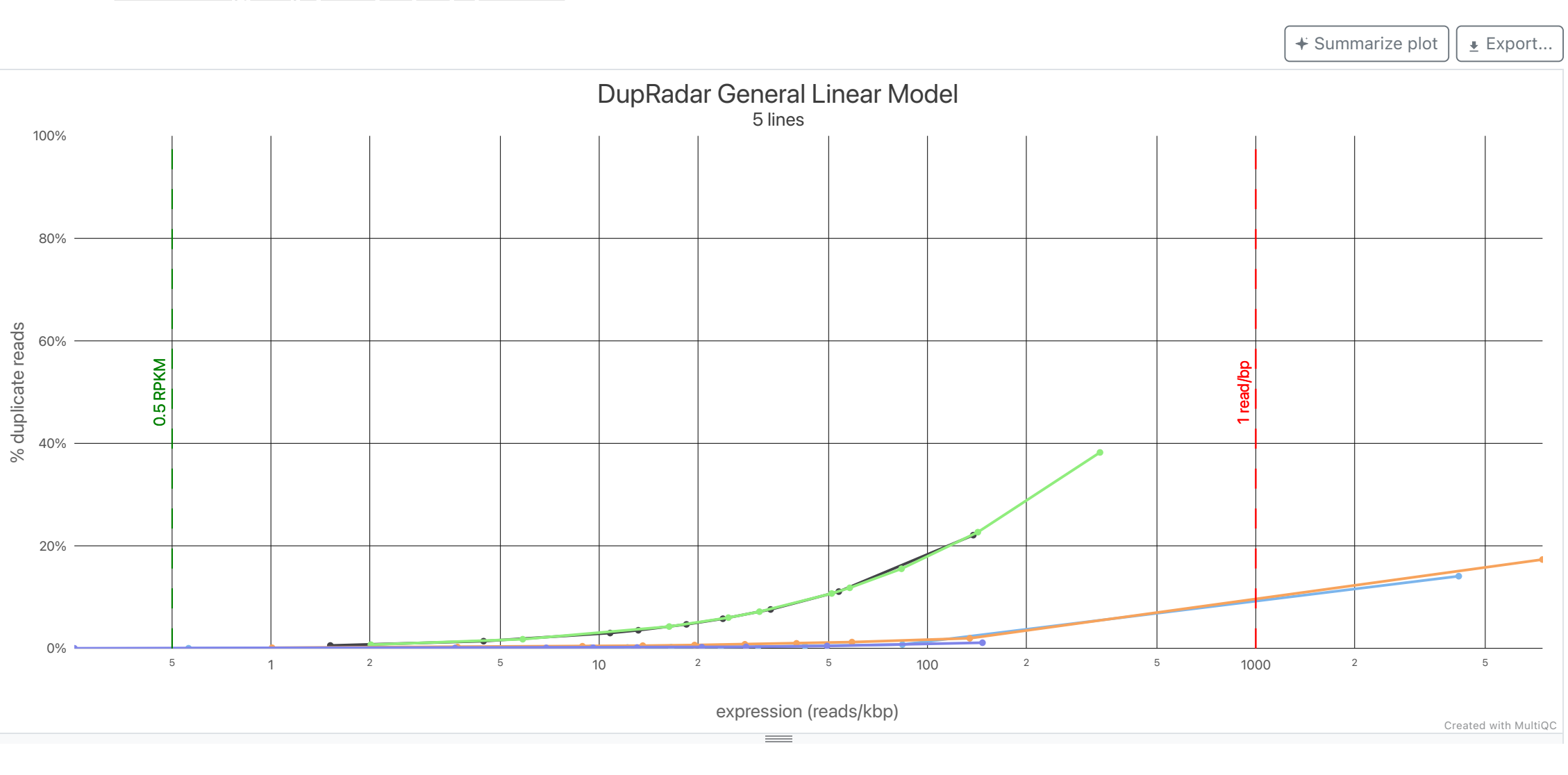
+ Summarize plot ⇩ Export...



DupRadar

DupRadar provides duplication rate quality control for RNA-Seq datasets. Highly expressed genes can be expected to have a lot of duplicate reads, but high numbers of duplicates at low read counts can indicate low library complexity with technical duplication. This plot shows the general linear models - a summary of the gene duplication distributions. bioconductor.org/packages/release/bioc/html/dupRadar.html

+ Summarize plot ⇩ Export...



Picard

Tools for manipulating high-throughput sequencing data. http://broadinstitute.github.io/picard

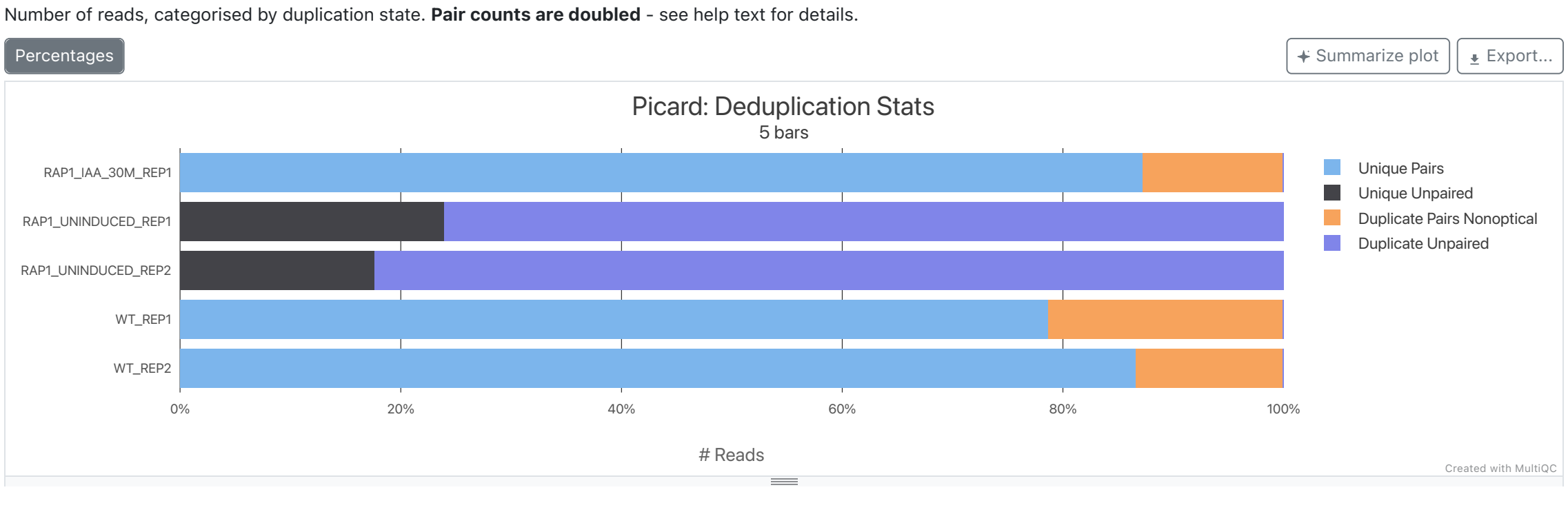
Mark Duplicates

❓ Help

Number of reads, categorised by duplication state. **Pair counts are doubled** - see help text for details.

Percentages

+ Summarize plot ⇩ Export...



QualiMap

Quality control of alignment data and its derivatives like feature counts. http://qualimap.bioinfo.cipf.es DOI: 10.1093/bioinformatics/btv566; 10.1093/bioinformatics/bts503

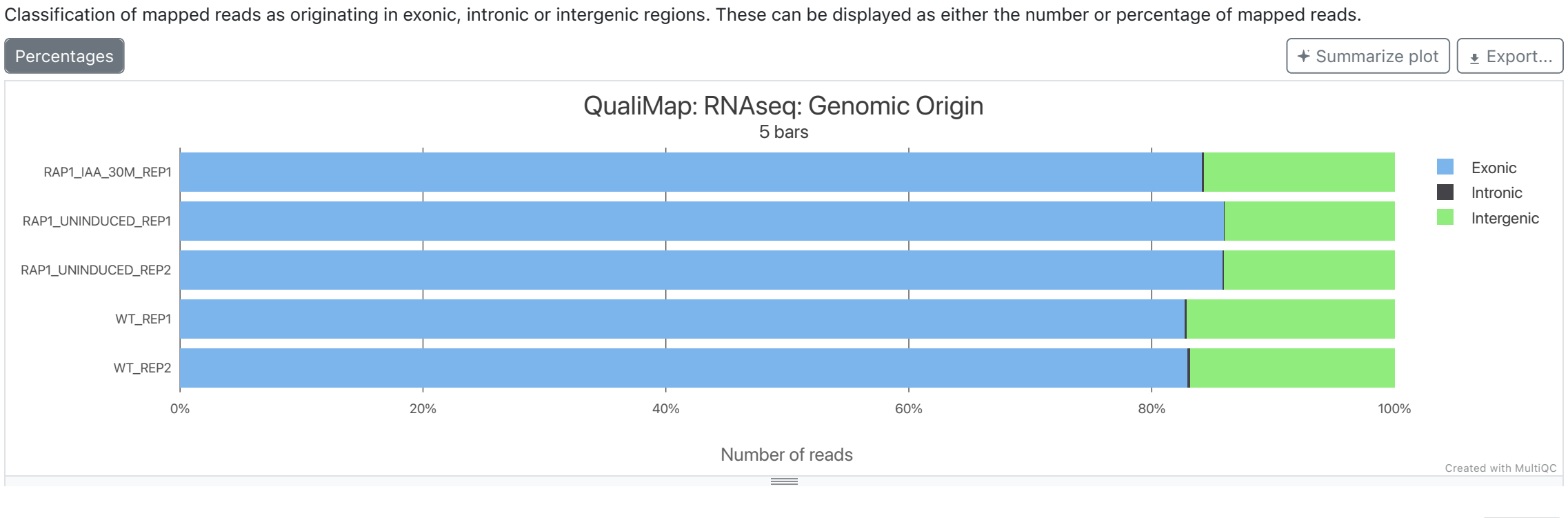
Genomic origin of reads

❓ Help

Classification of mapped reads as originating in exonic, intronic or intergenic regions. These can be displayed as either the number or percentage of mapped reads.

Percentages

+ Summarize plot ⇩ Export...



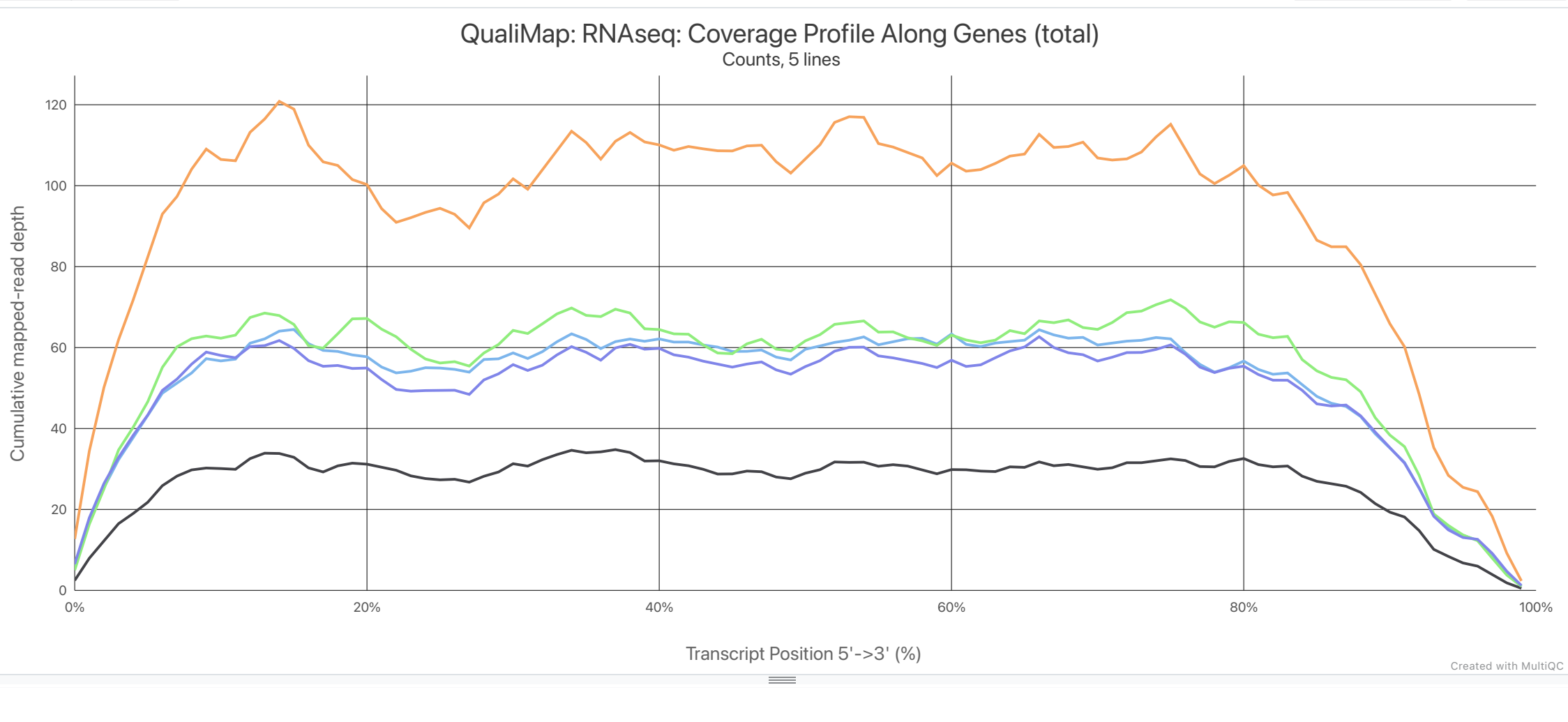
Gene Coverage Profile

❓ Help

Mean distribution of coverage depth across the length of all mapped transcripts.

Counts | Normalised

+ Summarize plot ⇩ Export...



RSeQC

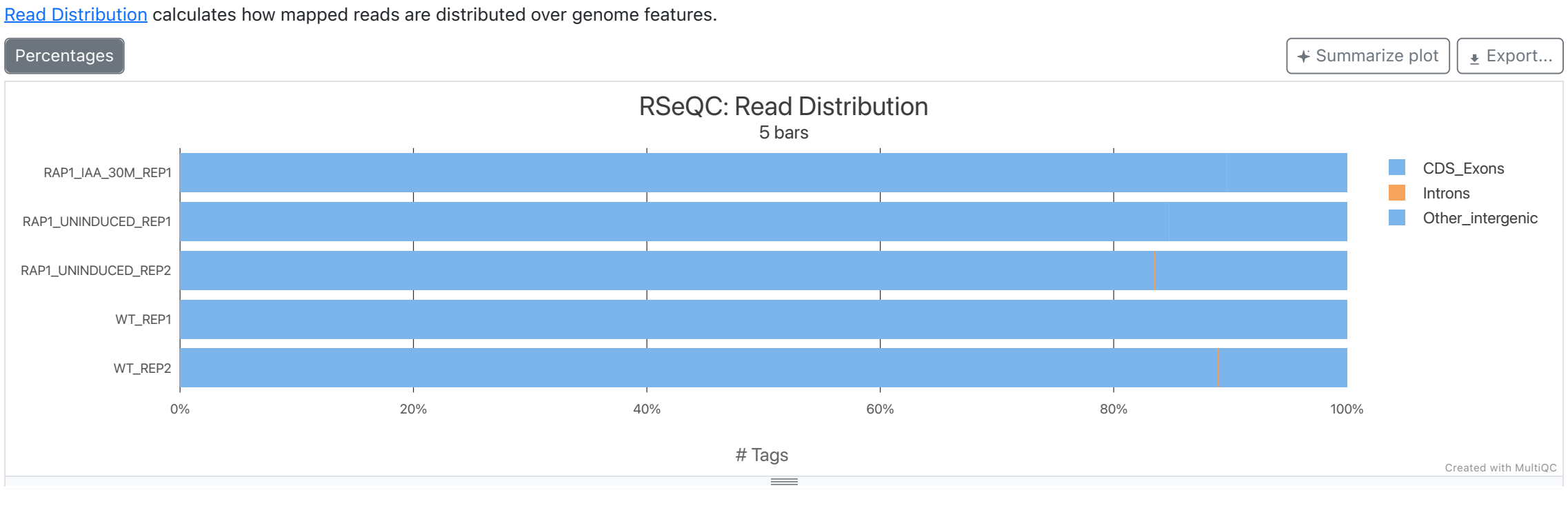
Evaluates high throughput RNA-seq data. http://rseqc.sourceforge.net DOI: 10.1093/bioinformatics/bts356

Read Distribution

Read Distribution calculates how mapped reads are distributed over genome features.

Percentages

+ Summarize plot ⇩ Export...

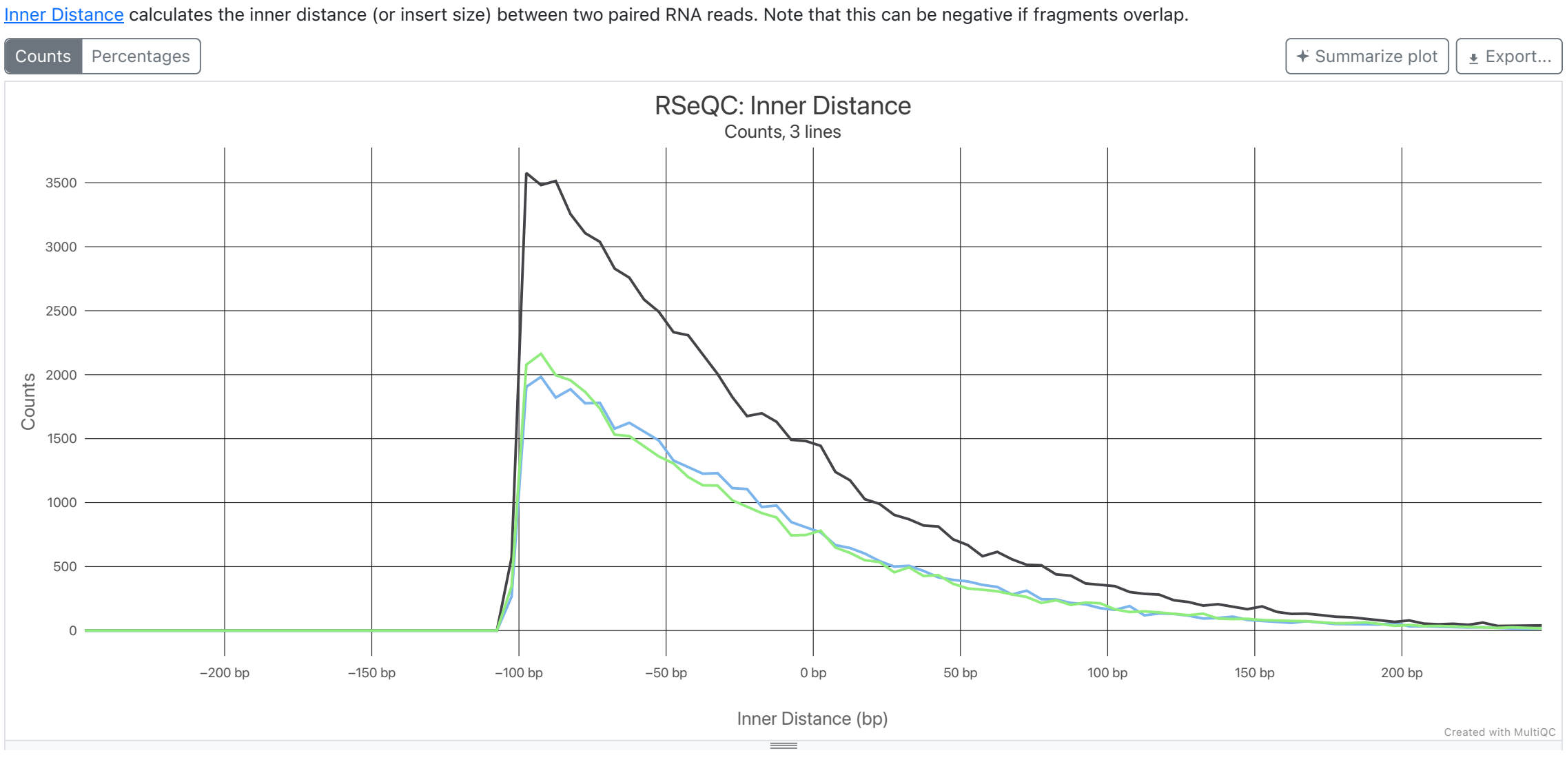


Inner Distance

Inner Distance calculates the inner distance (or insert size) between two paired RNA reads. Note that this can be negative if fragments overlap.

Counts | Percentages

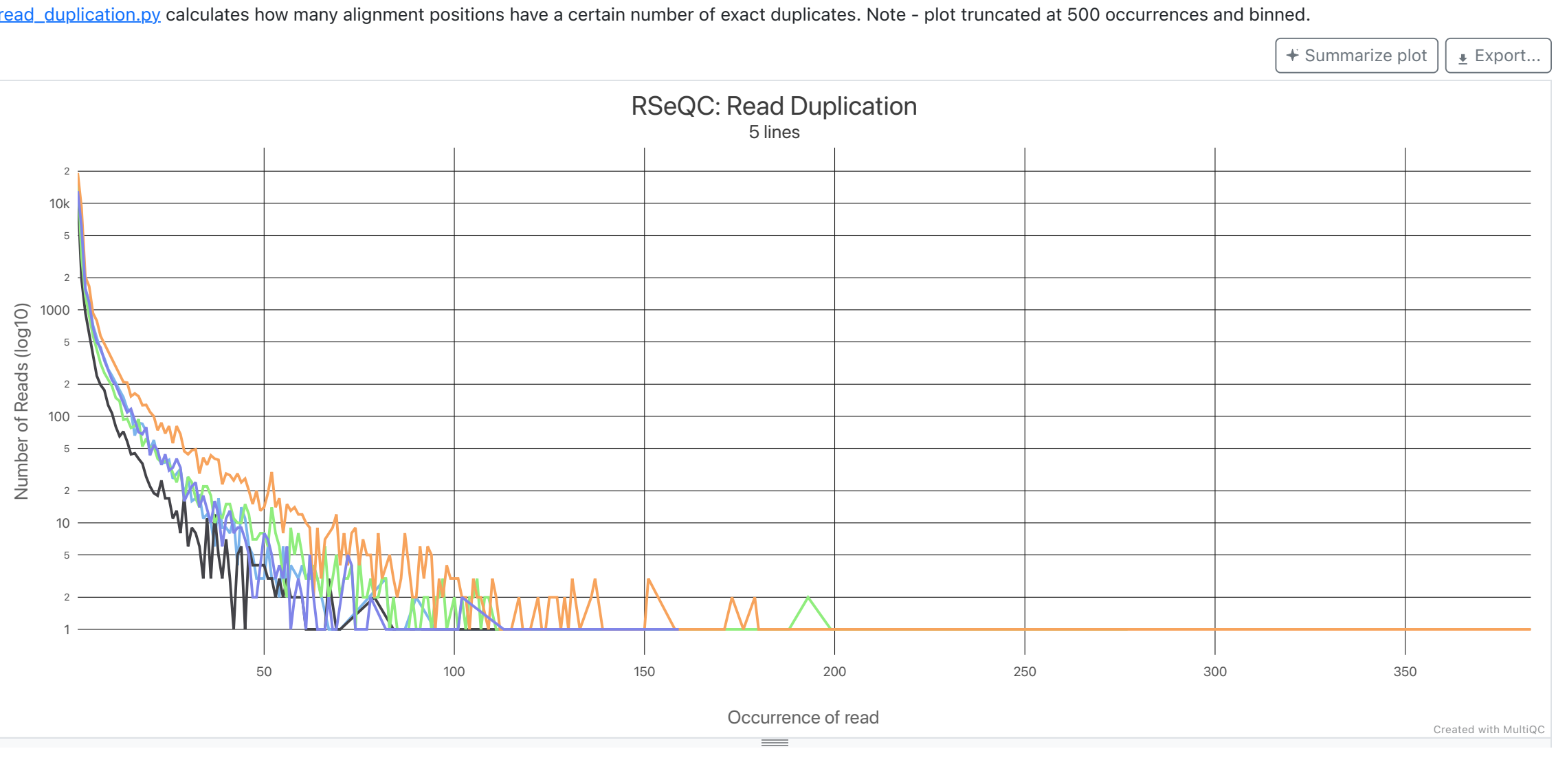
+ Summarize plot ⇩ Export...



Read Duplication

read_duplication.py calculates how many alignment positions have a certain number of exact duplicates. Note - plot truncated at 500 occurrences and binned.

+ Summarize plot ⇩ Export...

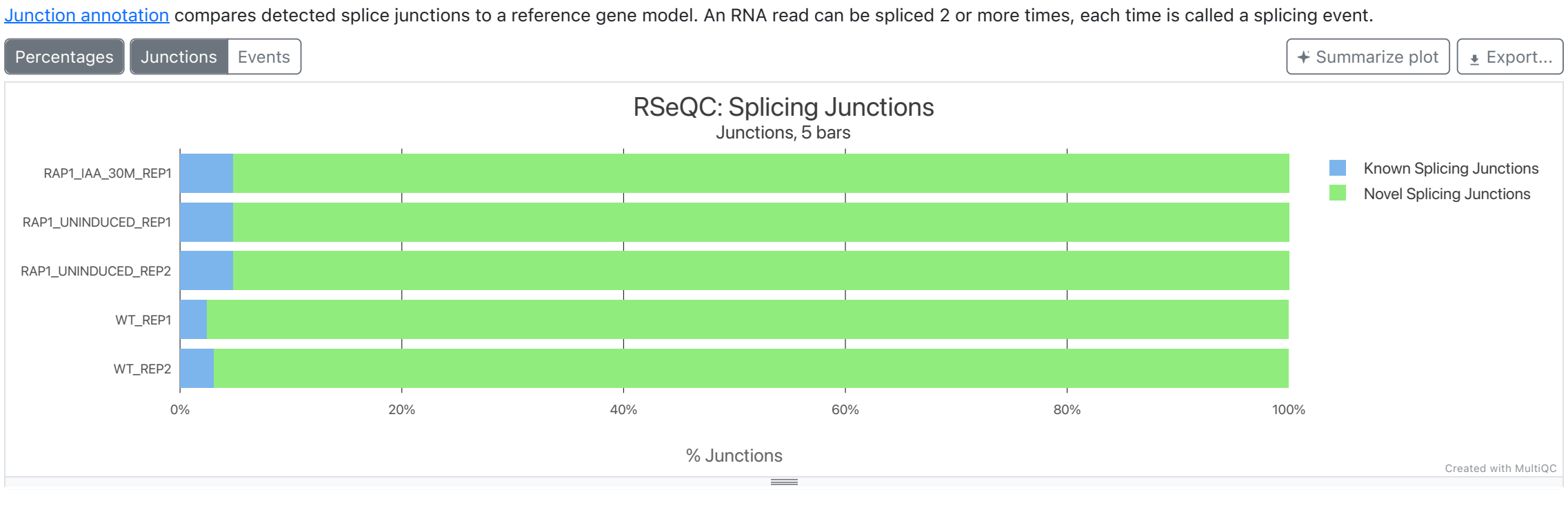


Junction Annotation

Junction annotation compares detected splice junctions to a reference gene model. An RNA read can be spliced 2 or more times, each time is called a splicing event.

Percentages | Junctions | Events

+ Summarize plot ⇩ Export...

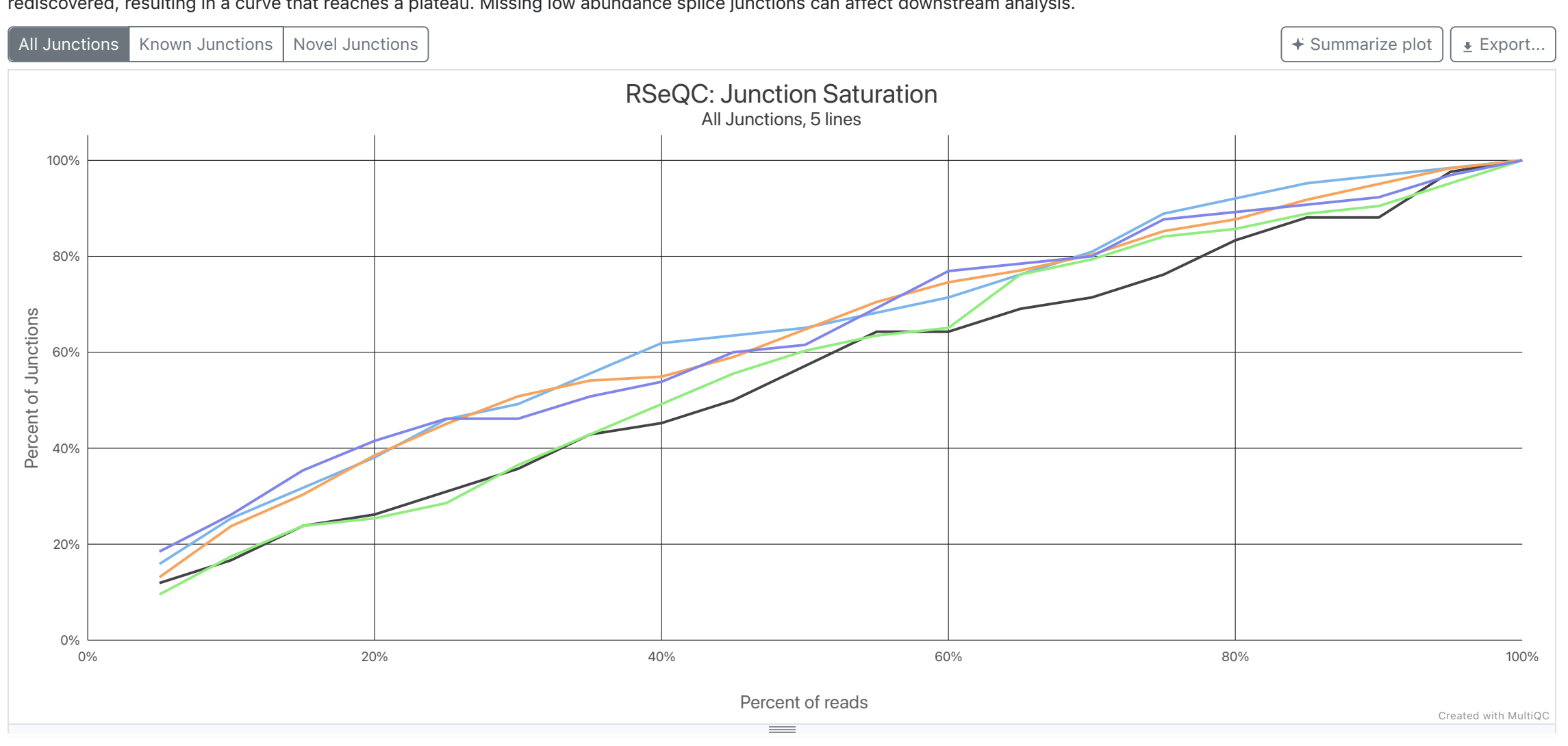


Junction Saturation

Junction Saturation counts the number of known splicing junctions that are observed in each dataset. If sequencing depth is sufficient, all (annotated) splice junctions should be rediscovered, resulting in a curve that reaches a plateau. Missing low abundance splice junctions can affect downstream analysis.

All Junctions | Known Junctions | Novel Junctions

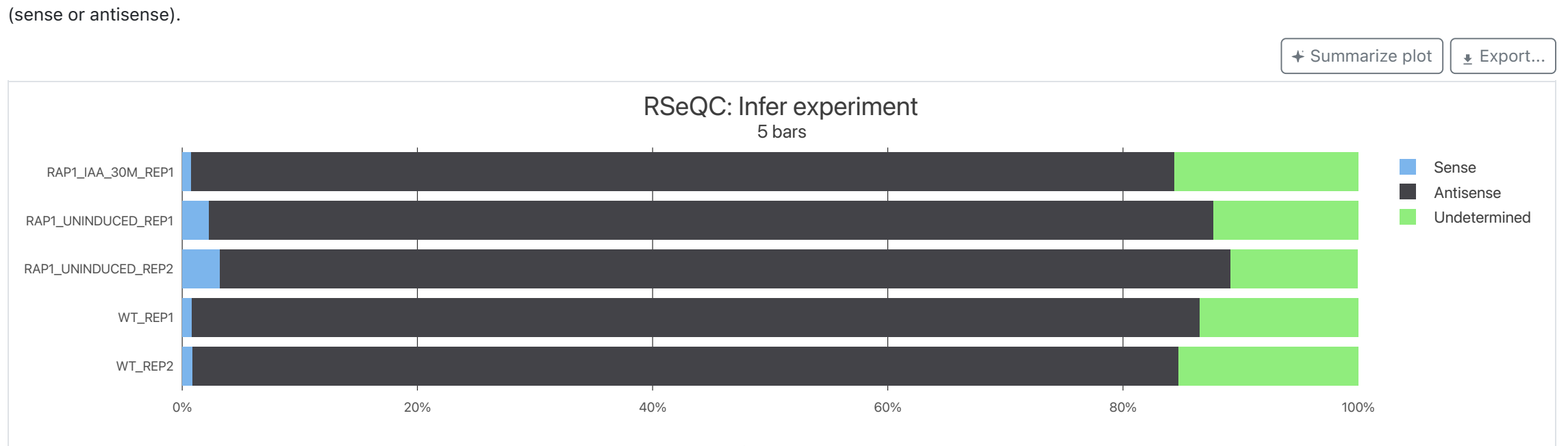
+ Summarize plot Export...



Infer experiment

Infer experiment counts the percentage of reads and read pairs that match the strandedness of overlapping transcripts. It can be used to infer whether RNA-seq library preps are stranded (sense or antisense).

+ Summarize plot Export...

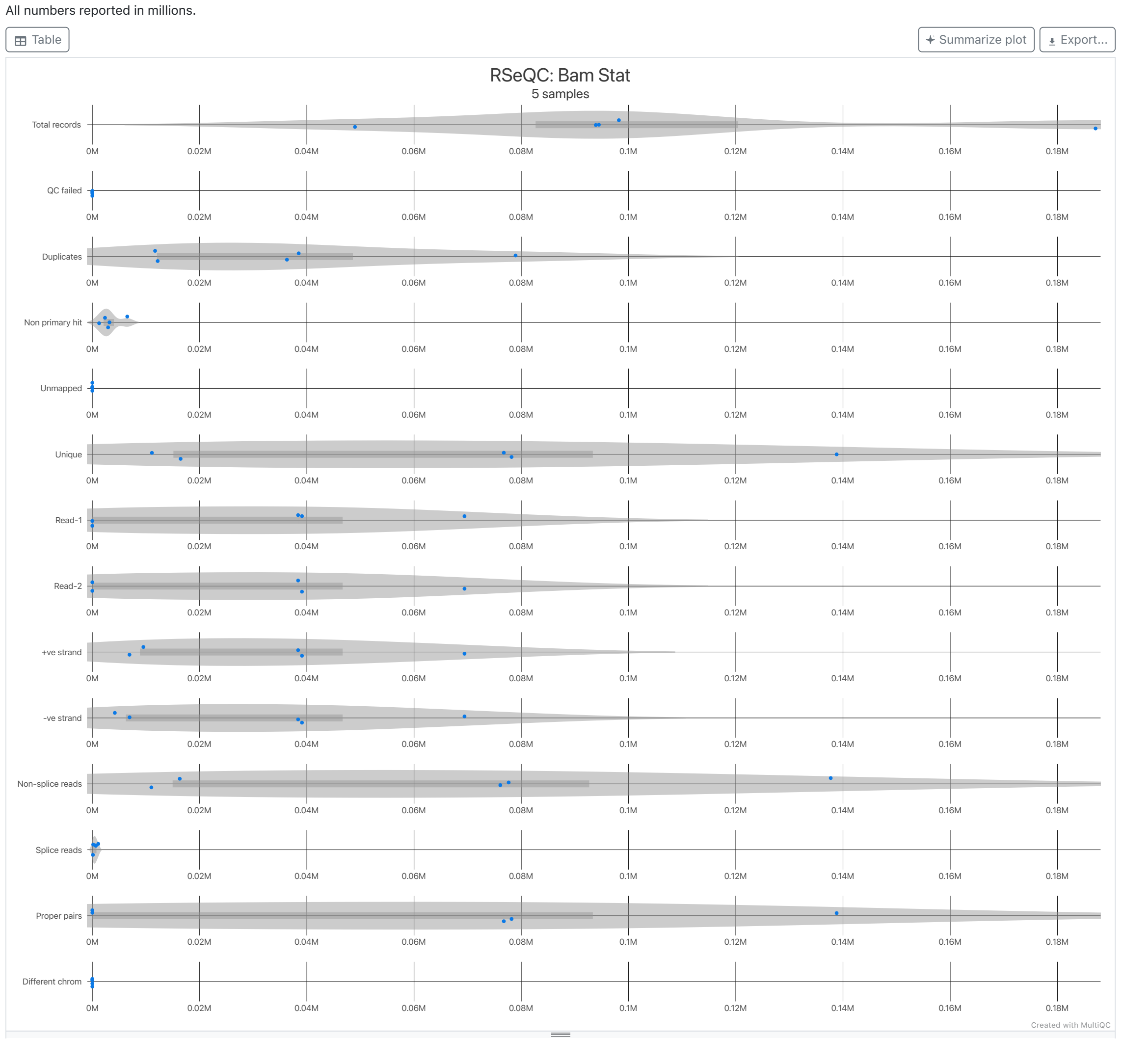


Bam Stat

All numbers reported in millions.

Table

+ Summarize plot Export...



Samtools

Toolkit for interacting with BAM/CRAM files. http://www.htslib.org DOI: 10.1093/bioinformatics/btp352

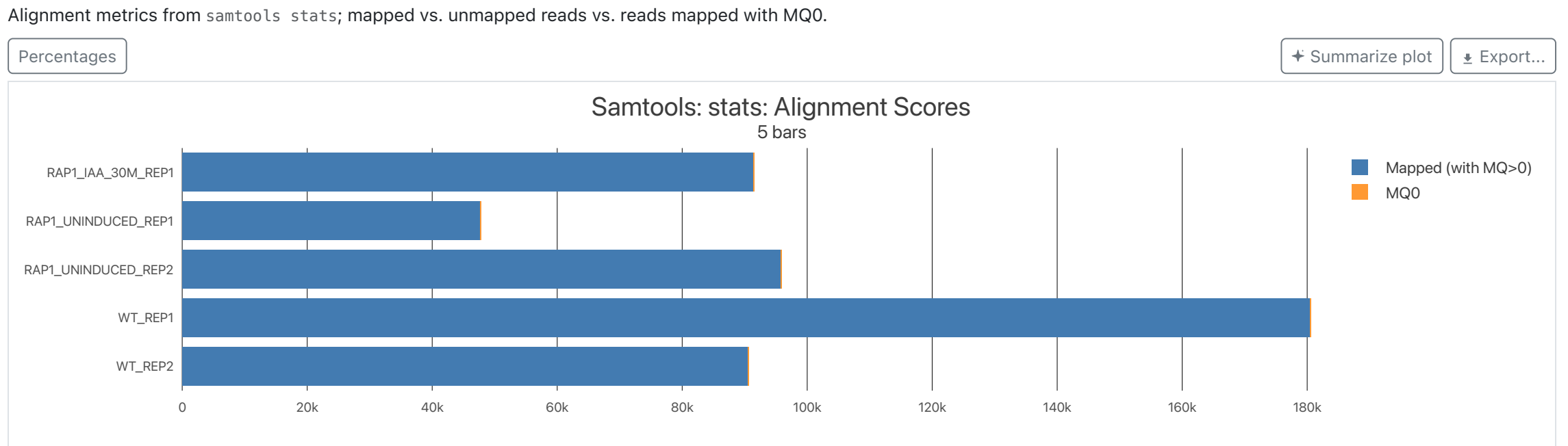
Percent mapped

Help

Alignment metrics from `samtools stats`; mapped vs. unmapped reads vs. reads mapped with MQ0.

Percentages

+ Summarize plot Export...

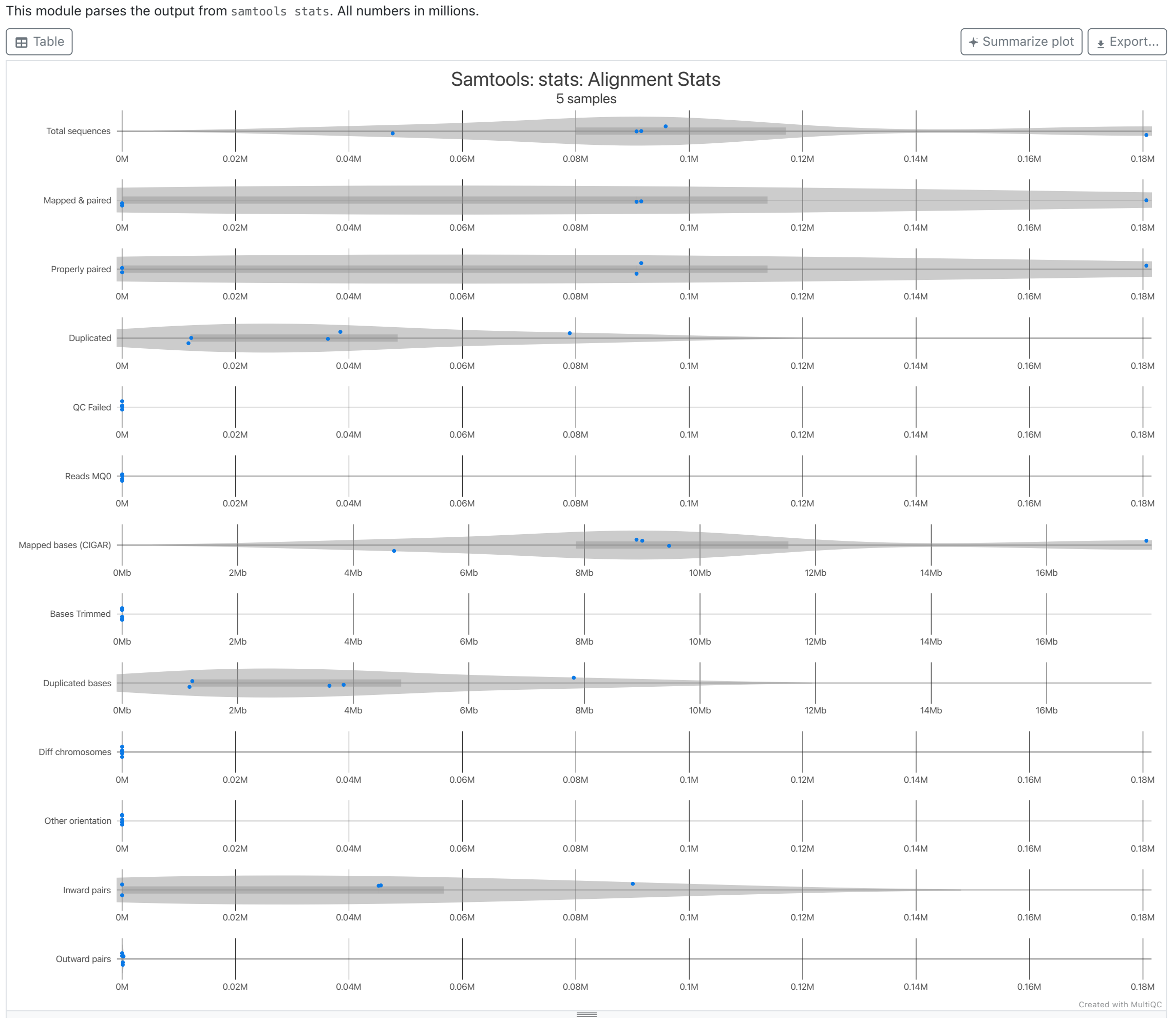


Alignment stats

This module parses the output from `samtools stats`. All numbers in millions.

Table

+ Summarize plot Export...

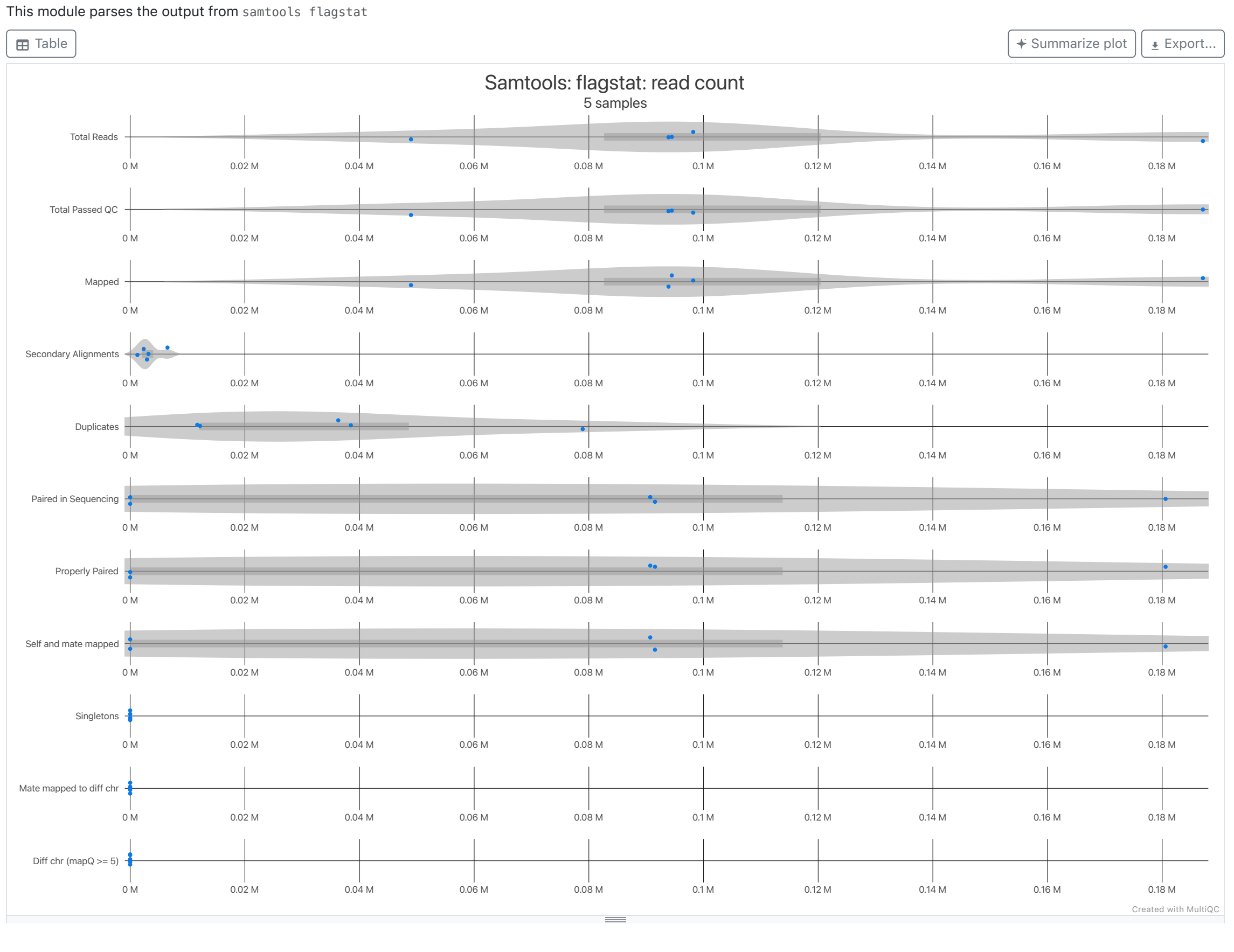


Flagstat

This module parses the output from `samtools flagstat`

Table

+ Summarize plot Export...

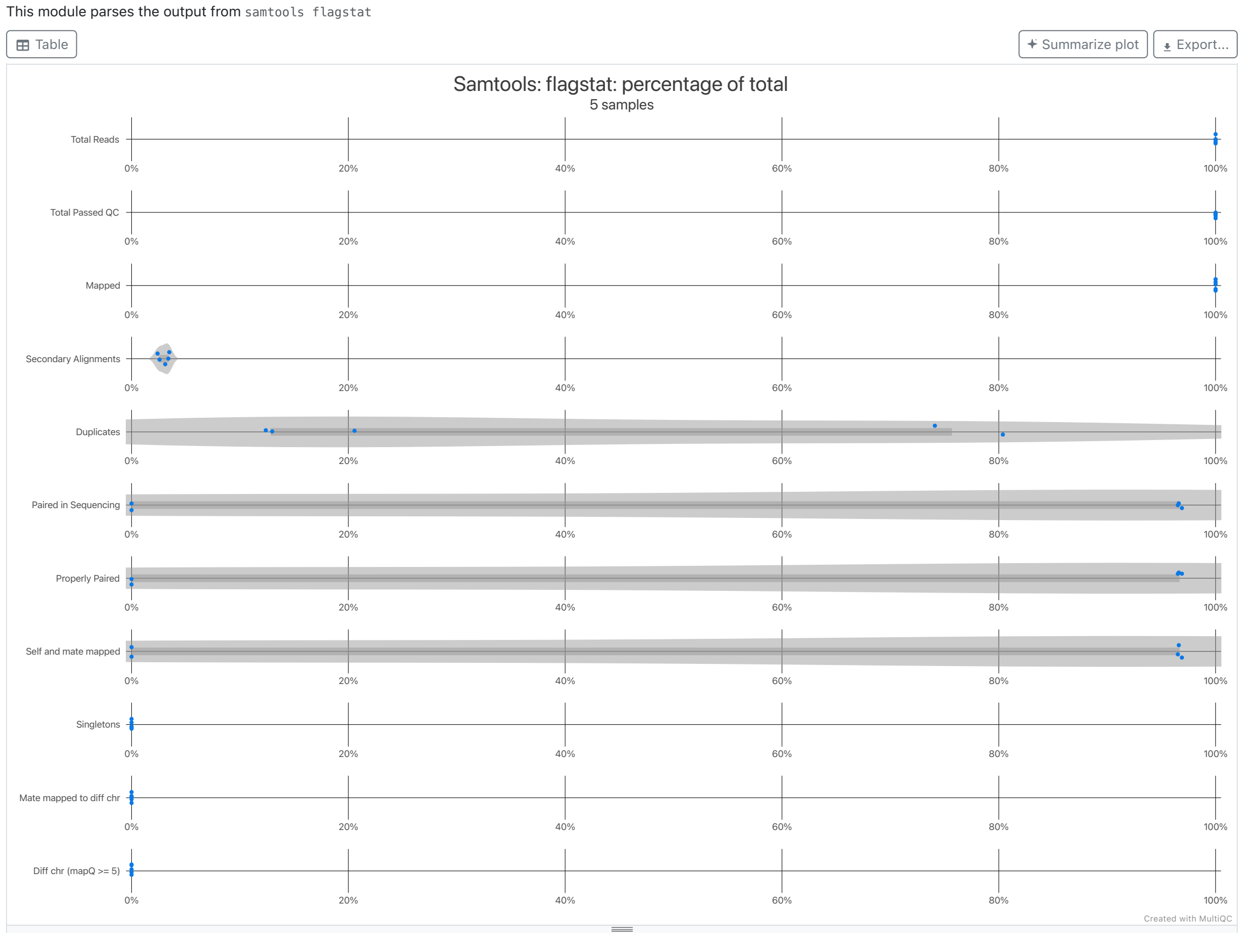


Flagstat: Percentage of total

This module parses the output from `samtools flagstat`

Table

+ Summarize plot Export...

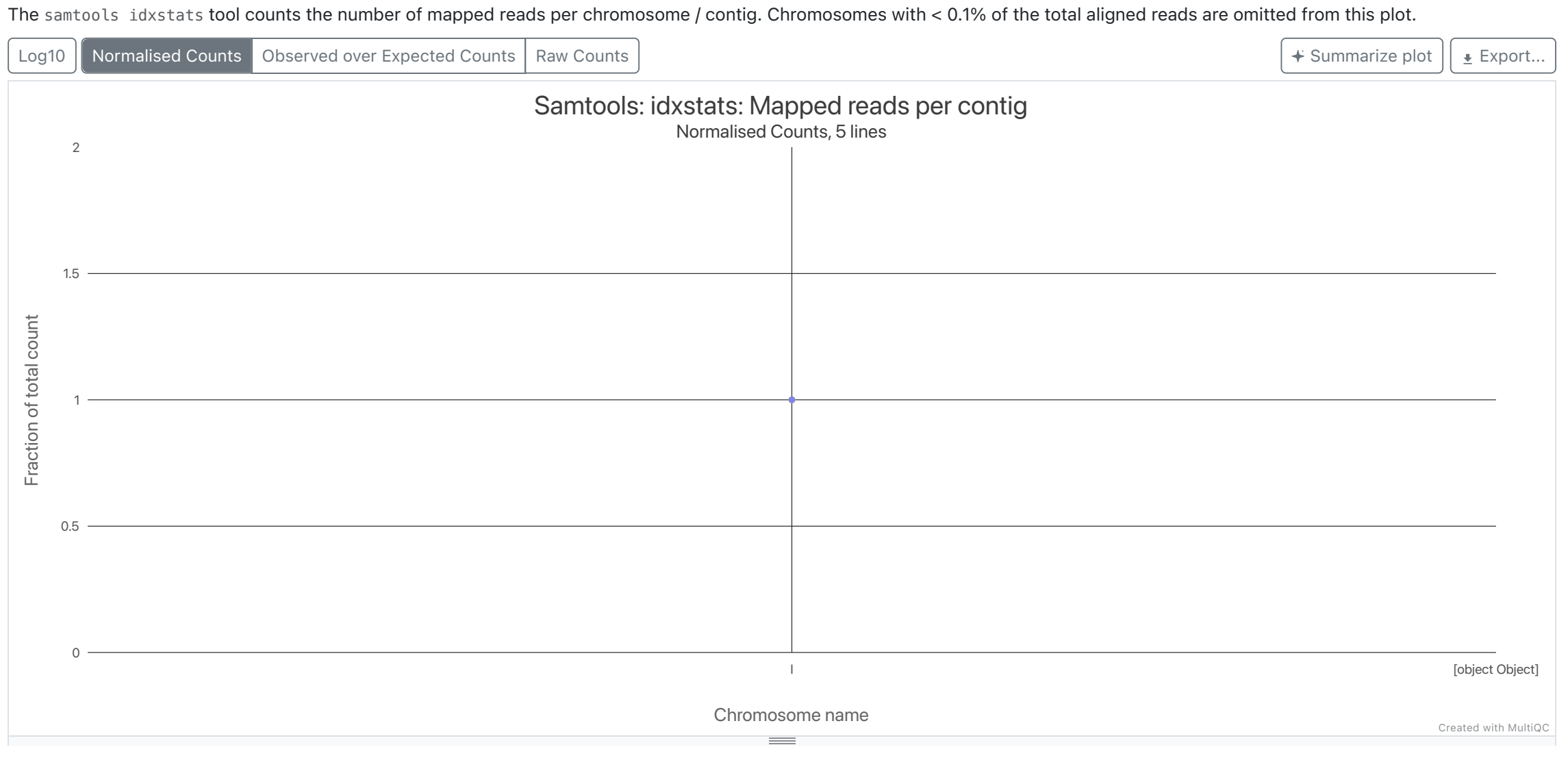


Mapped reads per contig

The `samtools idxstats` tool counts the number of mapped reads per chromosome / contig. Chromosomes with < 0.1% of the total aligned reads are omitted from this plot.

Log10 | Normalised Counts | Observed over Expected Counts | Raw Counts

+ Summarize plot Export...



STAR

Universal RNA-seq aligner. https://github.com/alexdobin/STAR DOI: 10.1093/bioinformatics/bts635

Summary Statistics

Summary statistics from the STAR alignment

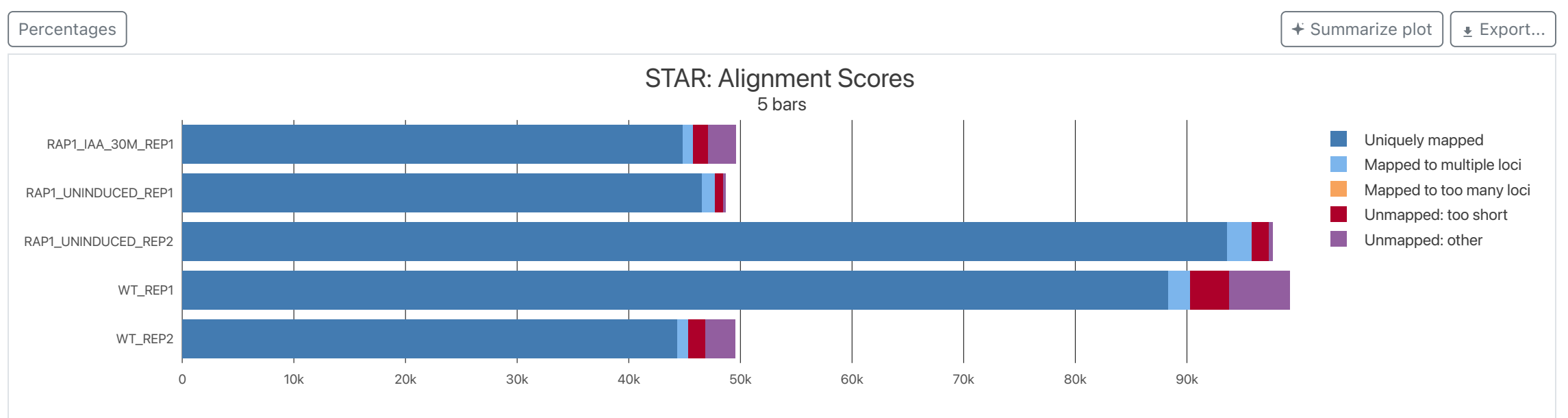
Copy table | Configure columns | Scatter plot | Violin plot | Export as CSV... Showing 5/5 rows and 10/19 columns. + Summarize table

Sample Name	Total reads	Aligned	Uniq aligned	Avg. mapped len	Annotated splices	Mismatch rate	Del rate	Del len	Ins rate	Ins len
RAP1_IAA_30M_REP1	0.0 M	92.3 %	90.4 %	196.8 bp	0.0 M	0.8 %	0.0 %	1.2 bp	0.0 %	1.1 bp
RAP1_UNINDUCED_REP1	0.0 M	98.2 %	96.0 %	98.7 bp	0.0 M	1.1 %	0.0 %	1.2 bp	0.0 %	1.2 bp
RAP1_UNINDUCED_REP2	0.1 M	98.1 %	95.8 %	98.8 bp	0.0 M	1.1 %	0.0 %	1.3 bp	0.0 %	1.2 bp
WT_REP1	0.1 M	91.0 %	89.0 %	196.5 bp	0.0 M	0.9 %	0.0 %	1.2 bp	0.0 %	1.1 bp
WT_REP2	0.0 M	91.5 %	89.5 %	196.4 bp	0.0 M	0.9 %	0.0 %	1.2 bp	0.0 %	1.1 bp

Alignment Scores

Percentages

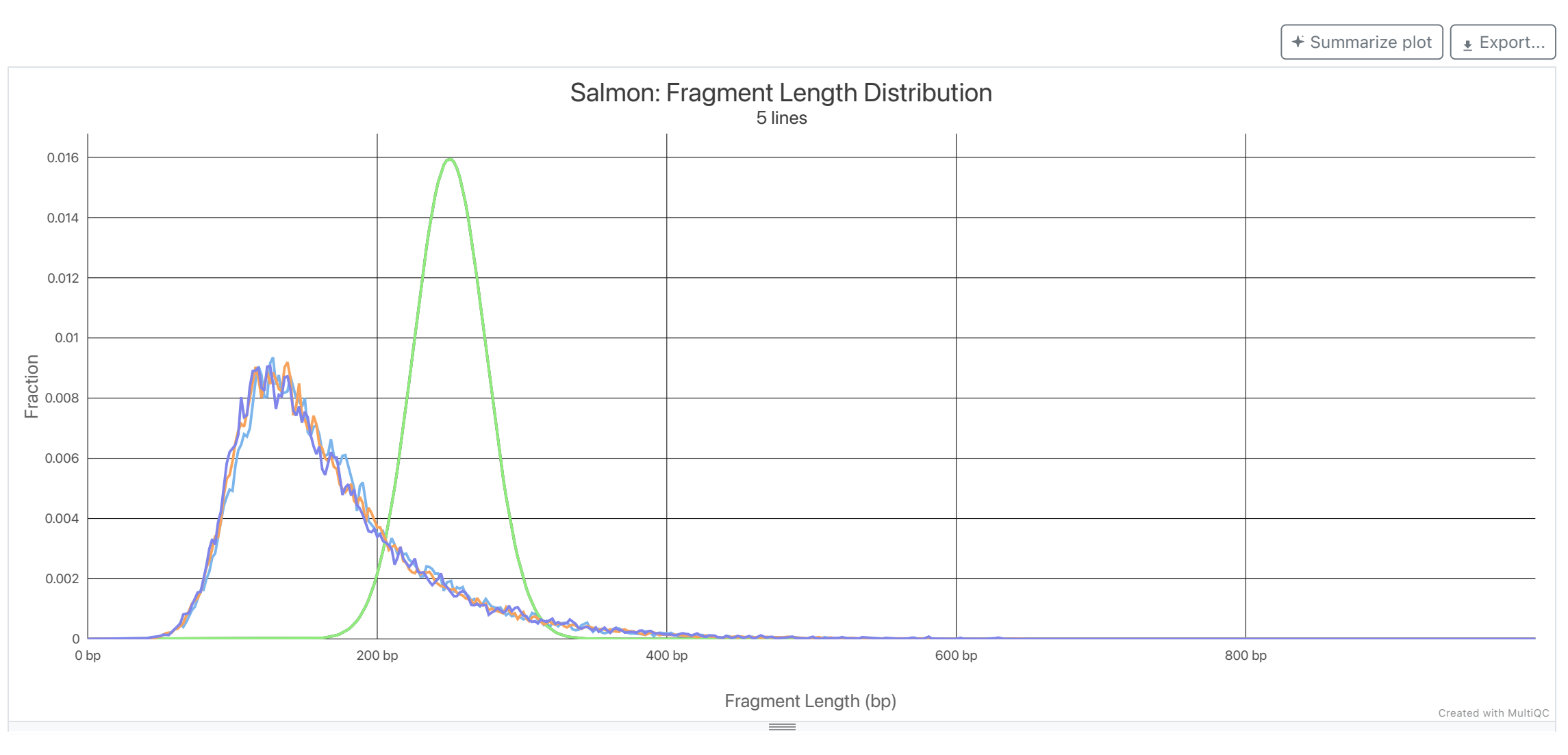
+ Summarize plot Export...



Salmon

Quantifies expression of transcripts using RNA-seq data. https://combine-lab.github.io/salmon DOI: 10.1038/nmeth.4197

+ Summarize plot Export...



Sample relationships

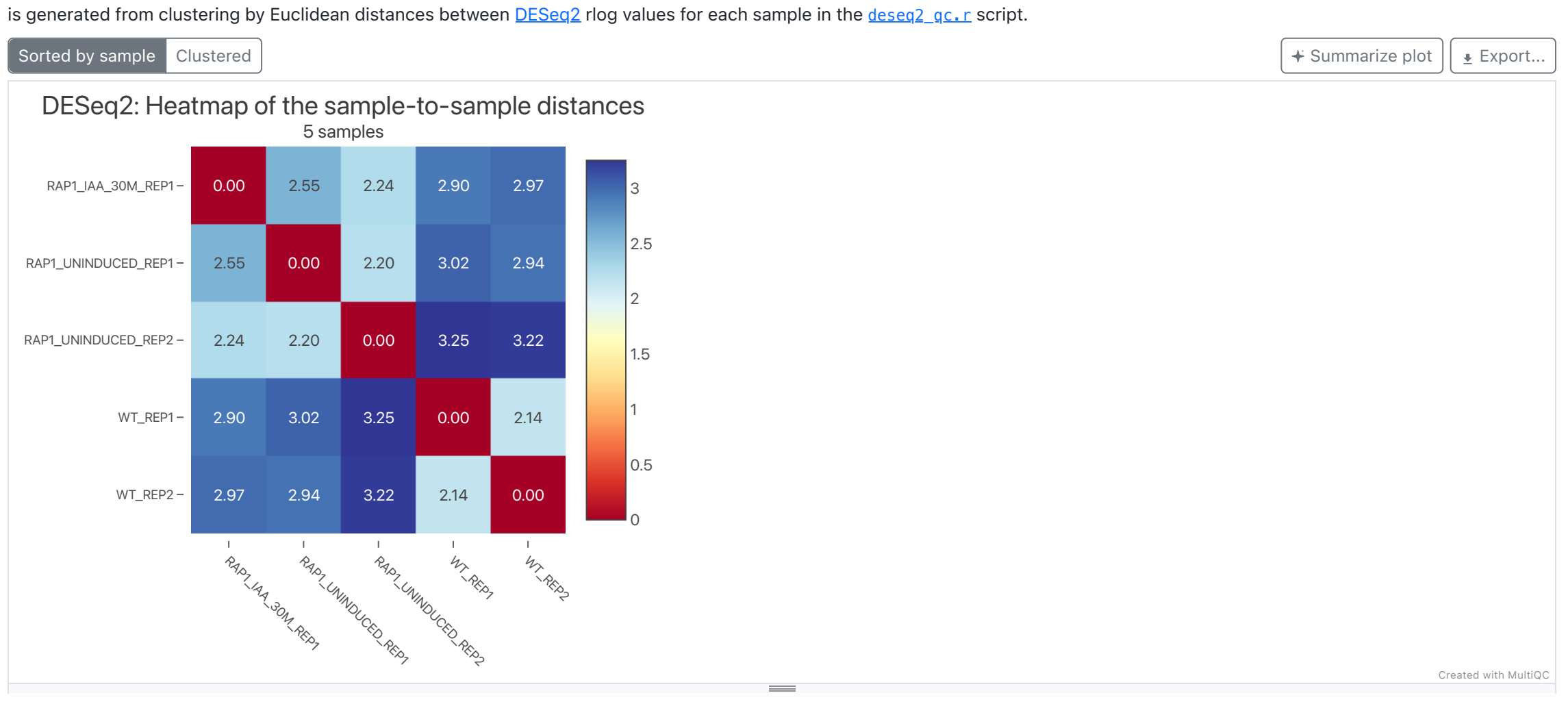
Plots interrogating sample relationships, based on final count matrices.

SALMON DESeq2 sample similarity

is generated from clustering by Euclidean distances between DESeq2 rlog values for each sample in the `deseq2_qc.r` script.

Sorted by sample | Clustered

+ Summarize plot Export...

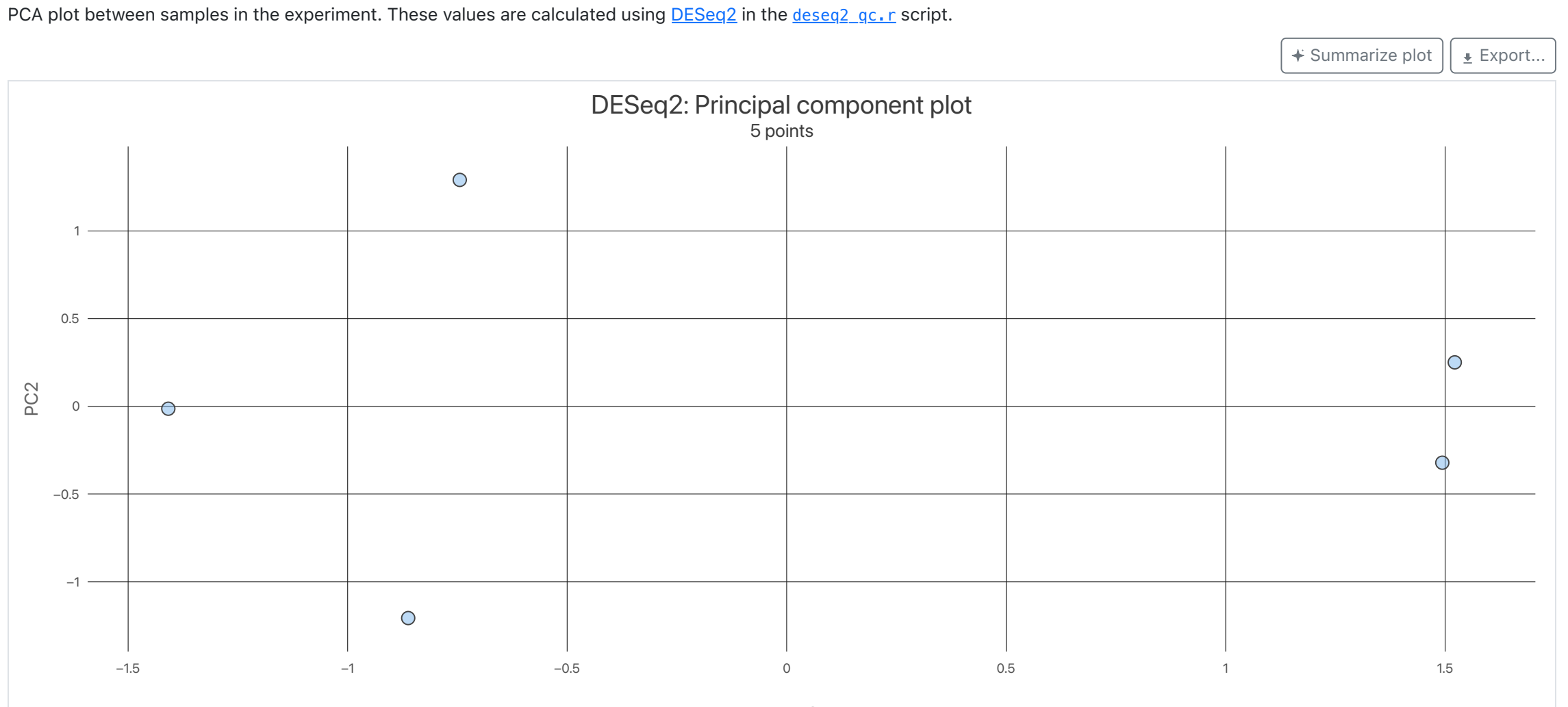


	RAP1_IAA_30M_REP1	RAP1_UNINDUCED_REP1	RAP1_UNINDUCED_REP2	WT_REP1	WT_REP2
RAP1_IAA_30M_REP1	0.00	2.55	2.24	2.90	2.97
RAP1_UNINDUCED_REP1	2.55	0.00	2.20	3.02	2.94
RAP1_UNINDUCED_REP2	2.24	2.20	0.00	3.25	3.22
WT_REP1	2.90	3.02	3.25	0.00	2.14
WT_REP2	2.97	2.94	3.22	2.14	0.00

SALMON DESeq2 PCA plot

PCA plot between samples in the experiment. These values are calculated using DESeq2 in the `deseq2_qc.r` script.

+ Summarize plot Export...

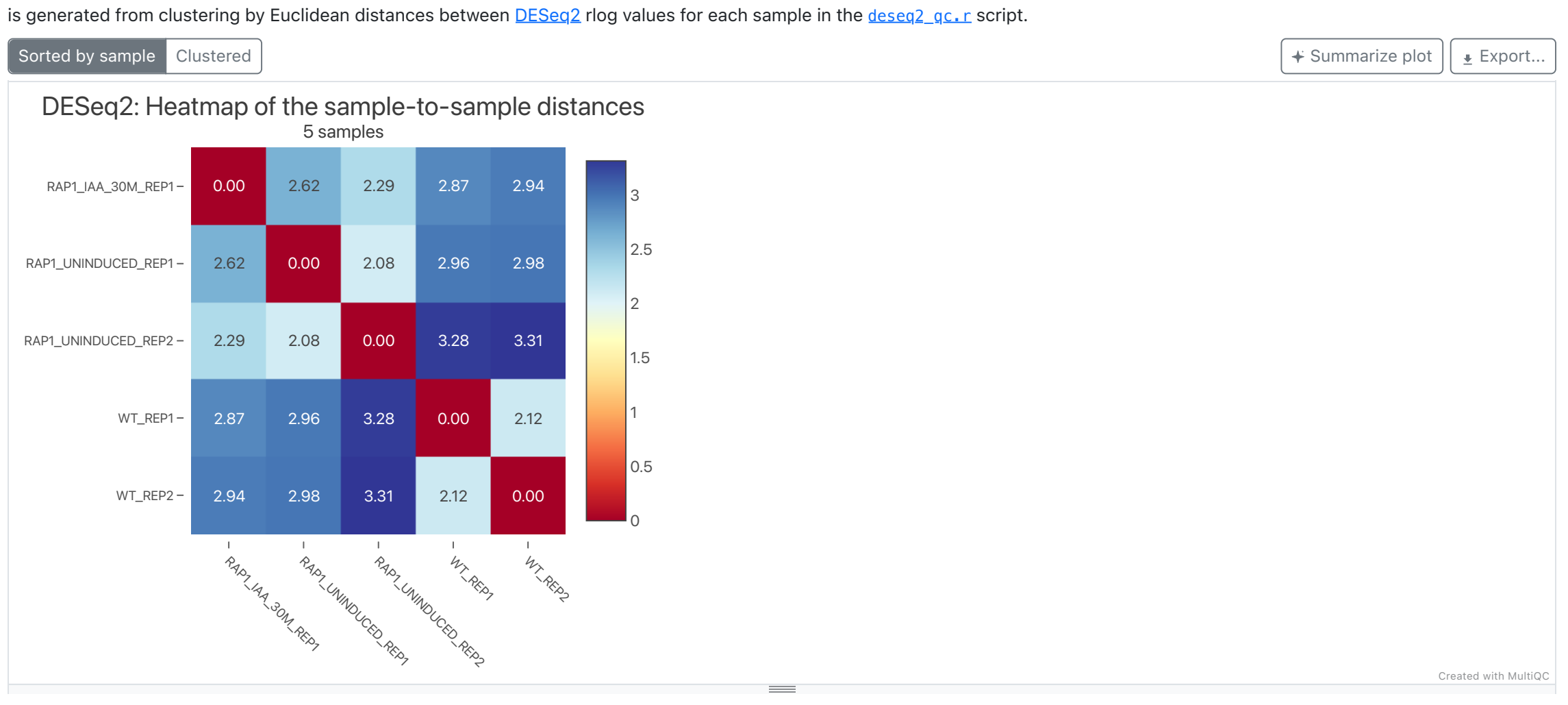


STAR_SALMON DESeq2 sample similarity

is generated from clustering by Euclidean distances between DESeq2 rlog values for each sample in the `deseq2_qc.r` script.

Sorted by sample | Clustered

+ Summarize plot Export...

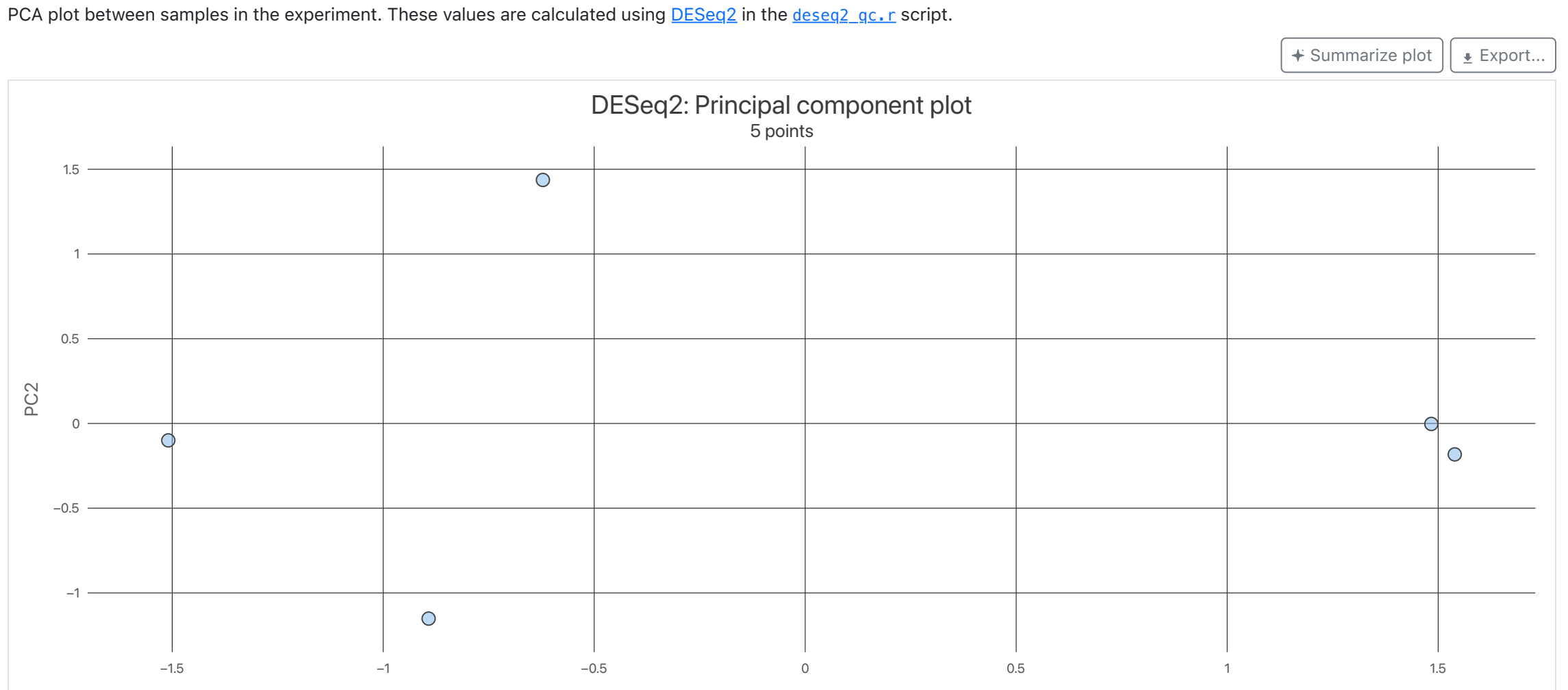


	RAP1_IAA_30M_REP1	RAP1_UNINDUCED_REP1	RAP1_UNINDUCED_REP2	WT_REP1	WT_REP2
RAP1_IAA_30M_REP1	0.00	2.62	2.29	2.87	2.94
RAP1_UNINDUCED_REP1	2.62	0.00	2.08	2.96	2.98
RAP1_UNINDUCED_REP2	2.29	2.08	0.00	3.28	3.31
WT_REP1	2.87	2.96	3.28	0.00	2.12
WT_REP2	2.94	2.98	3.31	2.12	0.00

STAR_SALMON DESeq2 PCA plot

PCA plot between samples in the experiment. These values are calculated using DESeq2 in the `deseq2_qc.r` script.

+ Summarize plot Export...

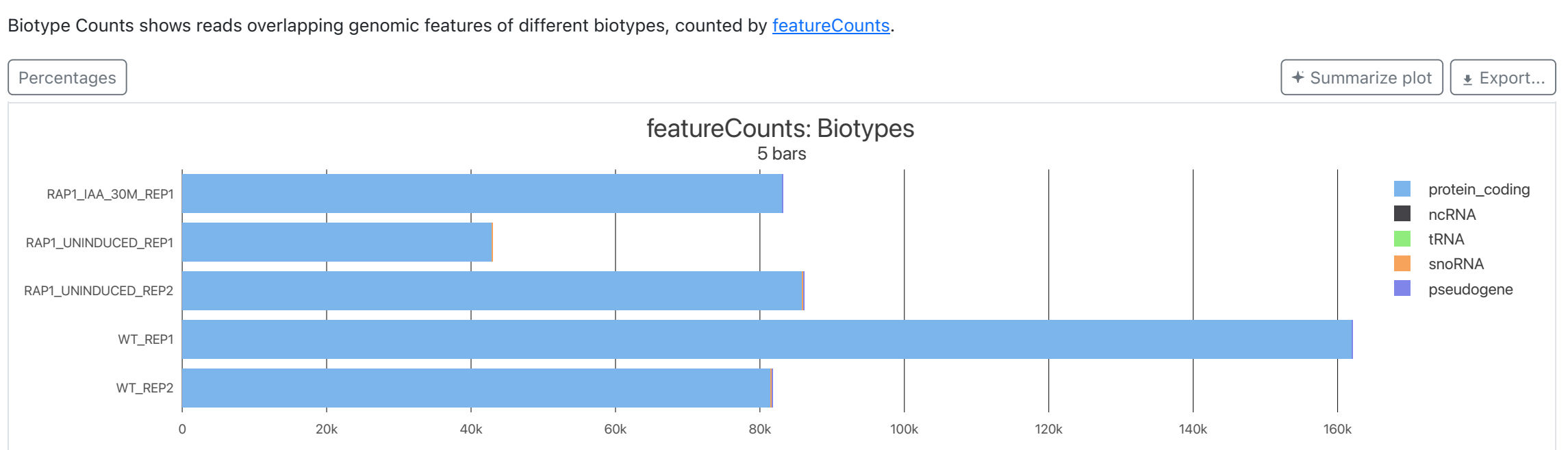


Biotype Counts

Biotype Counts shows reads overlapping genomic features of different biotypes, counted by featureCounts.

Percentages

+ Summarize plot Export...



Software Versions

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

Copy table

Group	Software	Version
BBMAP_BBSPLIT	bbmap	39.18
BEDTOOLS_GENOMECOV_COMBINED	bedtools	2.31.1
BEDTOOLS_GENOMECOV_FW	bedtools	2.31.1
BEDTOOLS_GENOMECOV_REV	bedtools	2.31.1
CAT_FASTQ	cat	9.5
CUSTOM_CATADDITIONALFASTA	python	3.12.2
CUSTOM_GTFFILTER	python	3.9.5
CUSTOM_MULTIQCCUSTOMBIOTYPE	python	3.12.12
CUSTOM_TX2GENE	python	3.10.4
DESEQ2_QC_BAM_SALMON	bioconductor-deseq2	1.46.0
	r-base	4.4.2
DESEQ2_QC_PSEUDO	bioconductor-deseq2	1.46.0
	r-base	4.4.2
DupRadar	bioconductor-dupradar	1.38.0
EAUTILS_GTF2BED	perl	5.26.2
FASTQC	fastqc	0.12.1
FASTQC_FILTERED	fastqc	0.12.1
FQ_LINT	fq	0.12.0
FQ_LINT_AFTER_BBSPLIT	fq	0.12.0
FQ_LINT_AFTER_TRIMMING	fq	0.12.0
FQ_SUBSAMPLE	fq	0.12.0
GUNZIP_ADDITIONAL_FASTA	gunzip	1.13
GUNZIP_GTF	gunzip	1.13
PICARD_MARKDUPLICATES	picard	3.4.0
QUALIMAP_RNASEQ	qualimap	2.3
RSEQC_BAMSTAT	rseqc	5.0.4
RSEQC_INFEREXPERIMENT	rseqc	5.0.4
RSEQC_INNERDISTANCE	rseqc	5.0.4
RSEQC_JUNCTIONANNOTATION	rseqc	5.0.4
RSEQC_JUNCTIONSATURATION	rseqc	5.0.4
RSEQC_READDISTRIBUTION	rseqc	5.0.4
RSEQC_READDUPLICATION	rseqc	5.0.4
SALMON_QUANT	salmon	1.10.3
SAMTOOLS_FAIDX	samtools	1.23.1
SAMTOOLS_FLAGSTAT	samtools	1.23.1
SAMTOOLS_IDXSTATS	samtools	1.23.1
SAMTOOLS_INDEX	samtools	1.23.1
SAMTOOLS_SORT	samtools	1.23.1
SAMTOOLS_SORT_QUALIMAP	samtools	1.23.1
SAMTOOLS_STATS	samtools	1.23.1
SE_GENE_UNIFIED	bioconductor-summarizedexperiment	1.32.0
SE_TRANSCRIPT_UNIFIED	bioconductor-summarizedexperiment	1.32.0
STAR_ALIGN	gawk	5.1.0
	samtools	1.21
	star	2.7.11b
STAR_GENOMEGENERATE	gawk	5.1.0
	samtools	1.21
	star	2.7.11b
STRINGTIE_STRINGTIE	stringtie	2.2.3
SUBREAD_FEATURECOUNTS	subread	2.0.6
TRIMGALORE	trimgalore	2.1.0
TXIMETA_TXIMPORT	bioconductor-tximeta	1.20.1
UCSC_BEDCLIP	ucsc	377
UCSC_BEDGRAPHTOBIGWIG	ucsc	469
UNTAR_SALMON_INDEX	untar	1.34
Workflow	Nextflow	26.04.2
	nf-core/rnaseq	v3.26.0-ge7ca462

nf-core/rnaseq Methods Description

Suggested text and references to use when describing pipeline usage within the methods section of a publication. https://github.com/nf-core/rnaseq

Methods

Data was processed using nf-core/rnaseq v3.26.0 (doi: 10.5281/zenodo.1400710) of the nf-core collection of workflows (Ewels *et al.*, 2020), utilising reproducible software environments from the Bioconda (Grüning *et al.*, 2018) and Biocontainers (da Veiga Leprevost *et al.*, 2017) projects.

The pipeline was executed with Nextflow v26.04.2 (Di Tommaso *et al.*, 2017) with the following command:

```
nextflow run nf-core/rnaseq -r 3.26.0 -profile test,singularity -c beocat_rnaseq.config --outdir rnaseq_test_output
```

References

- Di Tommaso, P., Chatzou, M., Floden, E. W., Barja, P. P., Palumbo, E., & Notredame, C. (2017). Nextflow enables reproducible computational workflows. Nature Biotechnology, 35(4), 316-319. doi: 10.1038/nbt.3820
- Ewels, P. A., Peltzer, A., Fillinger, S., Patel, H., Alneberg, J., Wilm, A., Garcia, M. U., Di Tommaso, P., & Nahnsen, S. (2020). The nf-core framework for community-curated bioinformatics pipelines. Nature Biotechnology, 38(3), 276-278. doi: 10.1038/s41587-020-0439-x
- Grüning, B., Dale, R., Sjödin, A., Chapman, B. A., Rowe, J., Tomkins-Tinch, C. H., Valieris, R., Köster, J., & Bioconda Team. (2018). Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 15(7), 475–476. doi: 10.1038/s41592-018-0046-7
- da Veiga Leprevost, F., Grüning, B. A., Alves Aflitos, S., Röst, H. L., Uszkoreit, J., Barsnes, H., Vaudel, M., Moreno, P., Gatto, L., Weber, J., Bai, M., Jimenez, R. C., Sachsenberg, T., Pfeuffer, J., Vera Alvarez, R., Griss, J., Nesvizhskii, A. I., & Perez-Riverol, Y. (2017). BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics (Oxford, England), 33(16), 2580–2582. doi: 10.1093/bioinformatics/btx192

Notes:

- The command above does not include parameters contained in any configs or profiles that may have been used. Ensure the config file is also uploaded with your publication!
- You should also cite all software used within this run. Check the "Software Versions" of this report to get version information.

nf-core/rnaseq Workflow Summary

- this information is collected when the pipeline is started. https://github.com/nf-core/rnaseq

Input/output options

input
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/samplesheet/v3.10/samplesheet_test.csv`

outdir
`rnaseq_test_output`

Reference genome options

additional_fasta
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/gfp.fa.gz`

fasta
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/genome.fasta`

gff
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/genes.gff.gz`

gtf
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/genes_with_empty_tid.gtf.gz`

hisat2_index
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/hisat2.tar.gz`

salmon_index
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/salmon.tar.gz`

transcript_fasta
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/transcriptome.fasta`

Read filtering options

bbsplit_fasta_list
`https://raw.githubusercontent.com/nf-core/test-datasets/626c8fab639062eade4b10747e919341cbf9b41a/reference/bbsplit_fasta_list.txt`

UMI options

umi_discard_read
`0`

umitools_bc_pattern
`NNNN`

Alignment options

pseudo_aligner
`salmon`

Quality Control

kraken_db
`https://raw.githubusercontent.com/nf-core/test-datasets/eb0cbf73c3f103f8aeda9878ba200e92b4d045d8/data/genomics/sarscov2/genome/db/kraken2.tar.gz`

Process skipping options

skip_bbsplit
`false`

Institutional config options

config_profile_contact
`/Teresa Shippy (tshippy@ksu.edu)`

config_profile_description
`Beocat at Kansas State University cluster profile provided by nf-core/configs.`

config_profile_name
`Test profile`

Generic options

trace_report_suffix
`2026-08-25_20-40-32`

Core Nextflow options

configFiles
`/homes/tshippy/.nextflow/assets/.repos/nf-core/rnaseq/clones/e7ca46272c8f9d5ceee3f71759f4ba551d3217a4/nextflow.config,`
`/bulk/bioinfo/Nextflow_demos/beocat_rnaseq.config`

container
`[.*PARABRICKS_STARGENOMEGENERATE:community.wave.seqera.io/library/htslib_samtools_star_gawk:4de2f983041d42e6]`

containerEngine
`singularity`

launchDir
`/bulk/bioinfo/Nextflow_demos`

profile
`test,singularity`

projectDir
`/homes/tshippy/.nextflow/assets/.repos/nf-core/rnaseq/clones/e7ca46272c8f9d5ceee3f71759f4ba551d3217a4`

revision
`master`

runName
`big_maxwell`

userName
`tshippy`

workDir
`/bulk/bioinfo/Nextflow_demos/work`

MultiQC v1.33 - Written by Phil Ewels, available on GitHub.
This report uses Plotly, jQuery, jQuery UI, Bootstrap and FileSaver.js.