Cultivar_M_Pisum_Ensembl

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 2023-07-25, 01:39 UTC based on data in:
`/gpfs/fs7/aafc/phenocart/nathaniel_rnaseq_temp/Sijan_Fusarium_Results/Cultivar_M/ensembl_pisum/work/3e/5c4b5acea6362cd3fd24f06f5ac613`

General Statistics

Copy table | Configure Columns | Plot | Showing $^{72}/_{72}$ rows and $^{21}/_{30}$ columns.

Sample Name	% rRNA	dupInt % Dups	5'-3' bias	M Aligned	% Aligned	% Proper Pairs	Error rate	M Non-Primary	M Reads Mapped	% Mapped	% Proper Pairs	M Total seqs	M Reads Mapped	% Dups	% GC	M Seqs	% BP Trimmed	% Dups	% GC	M Seqs
M-C-2H-R1	0.00%	0.19%	35.8%	1.00	34.7	94.2%	54.1%	0.45%	6.3	69.3	95.5%	95.4%	72.6	75.6						
M-C-2H-R1_1															54.1%	42%	36.4	1.8%	53.5%	41%	36.3
M-C-2H-R1_2															47.9%	42%	36.4	2.0%	47.4%	42%	36.3
M-C-2H-R2	0.00%	0.18%	34.9%	0.98	30.3	92.1%	49.2%	0.45%	12.0	60.7	93.9%	93.9%	64.7	72.7						
M-C-2H-R2_1															49.7%	42%	32.4	1.7%	49.2%	41%	32.3
M-C-2H-R2_2															47.3%	42%	32.4	1.9%	46.9%	42%	32.3
M-C-2H-R3	0.00%	0.19%	35.9%	1.02	32.6	94.0%	51.9%	0.43%	8.6	65.2	95.2%	95.2%	68.5	73.9						
M-C-2H-R3_1															52.7%	42%	34.3	1.7%	52.3%	41%	34.3
M-C-2H-R3_2															49.6%	42%	34.3	1.8%	49.1%	42%	34.3
M-C-3D-R1	0.00%	0.18%	35.1%	0.98	26.7	91.7%	45.5%	0.45%	15.6	53.3	93.5%	93.5%	57.0	69.0						
M-C-3D-R1_1															49.8%	42%	28.6	1.8%	49.3%	42%	28.5
M-C-3D-R1_2															47.7%	42%	28.6	2.0%	47.2%	42%	28.5
M-C-3D-R2	0.00%	0.20%	34.6%	1.02	25.8	92.7%	50.1%	0.45%	9.7	51.7	94.2%	94.2%	54.9	61.3						

Sample Name	% rRNA	% dups	Int Dups	5'-3' bias	M Aligned	% Aligned	% Proper Pairs	Error rate	M Non-Primary	M Reads Mapped	% Mapped	% Proper Pairs	M Total seqs	M Reads Mapped	% Dups	% GC	M Seqs	% BP Trimmed	% Dups	% GC	M Seqs
M-C-3D-R2_1															49.9%	42%	27.5	1.6%	49.5%	42%	27.4
M-C-3D-R2_2															45.8%	42%	27.5	1.8%	45.3%	42%	27.4
M-C-3D-R3	0.00%	0.24%	38.9%	0.98	33.6	94.9%	51.0%	0.46%	7.2	67.2	96.0%	96.0%	70.0	74.4							
M-C-3D-R3_1															53.3%	41%	35.0	1.8%	52.7%	41%	35.0
M-C-3D-R3_2															48.0%	42%	35.0	1.9%	47.5%	41%	35.0
M-C-6D-R1	0.00%	0.18%	34.0%	0.99	29.2	93.0%	51.1%	0.46%	10.3	58.5	94.5%	94.5%	61.9	68.8							
M-C-6D-R1_1															51.8%	42%	31.0	1.5%	51.4%	41%	30.9
M-C-6D-R1_2															47.8%	42%	31.0	1.6%	47.4%	42%	30.9
M-C-6D-R2	0.00%	0.17%	32.4%	0.99	26.3	91.8%	47.8%	0.46%	14.8	52.7	93.6%	93.6%	56.3	67.4							
M-C-6D-R2_1															49.3%	42%	28.2	1.6%	48.8%	41%	28.1
M-C-6D-R2_2															46.4%	42%	28.2	1.8%	45.9%	42%	28.1
M-C-6D-R3	0.00%	0.20%	35.3%	1.00	27.7	91.4%	44.4%	0.45%	17.6	55.4	93.3%	93.3%	59.4	73.0							
M-C-6D-R3_1															51.6%	42%	29.7	1.9%	51.0%	41%	29.7
M-C-6D-R3_2															48.3%	42%	29.7	2.1%	47.7%	42%	29.7
M-C-9D-R1	0.00%	0.19%	35.3%	1.03	27.9	92.9%	48.7%	0.47%	11.8	55.9	94.5%	94.5%	59.1	67.7							
M-C-9D-R1_1															52.7%	41%	29.6	1.6%	52.3%	41%	29.5
M-C-9D-R1_2															47.8%	42%	29.6	1.7%	47.4%	41%	29.5
M-C-9D-R2	0.00%	0.22%	38.9%	1.04	38.0	92.9%	47.1%	0.46%	13.8	76.1	94.5%	94.5%	80.5	89.9							
M-C-9D-R2_1															53.4%	42%	40.3	1.5%	53.0%	41%	40.2

Sample Name	% rRNA	% dupInt	% Dups	5'-3' bias	M Aligned	% Aligned	% Proper Pairs	Error rate	M Non-Primary	M Reads Mapped	% Mapped	% Proper Pairs	M Total seqs	M Reads Mapped	% Dups	% GC	M Seqs	% BP Trimmed	% Dups	% GC	M Seqs
M-C-9D-R2_2															51.4%	42%	40.3	1.6%	51.0%	41%	40.2
M-C-9D-R3	0.00%	0.17%	36.3%	1.04	32.7	92.8%	47.6%	0.46%	14.4	65.4	94.4%	94.4%	69.2	79.8							
M-C-9D-R3_1															52.9%	42%	34.7	2.0%	52.3%	41%	34.6
M-C-9D-R3_2															51.0%	42%	34.7	2.1%	50.4%	41%	34.6
M-Fa-2H-R1	0.00%	0.20%	36.3%	1.01	27.9	92.8%	47.4%	0.45%	12.7	55.9	94.4%	94.4%	59.2	68.5							
M-Fa-2H-R1_1															51.4%	42%	29.6	1.8%	50.9%	42%	29.6
M-Fa-2H-R1_2															49.2%	42%	29.6	1.9%	48.7%	42%	29.6
M-Fa-2H-R2	0.00%	0.19%	34.7%	1.06	26.5	92.8%	51.5%	0.45%	8.1	53.0	94.3%	94.3%	56.2	61.1							
M-Fa-2H-R2_1															52.0%	42%	28.1	1.6%	51.5%	41%	28.1
M-Fa-2H-R2_2															46.9%	42%	28.1	1.8%	46.5%	42%	28.1
M-Fa-2H-R3	0.00%	0.22%	38.2%	0.99	32.8	92.8%	46.4%	0.44%	14.1	65.6	94.3%	94.3%	69.5	79.7							
M-Fa-2H-R3_1															55.3%	42%	34.8	1.5%	54.9%	41%	34.8
M-Fa-2H-R3_2															50.8%	42%	34.8	1.7%	50.4%	42%	34.8
M-Fa-3D-R1	0.00%	0.19%	35.4%	0.99	27.5	92.6%	47.2%	0.45%	13.6	54.9	94.2%	94.2%	58.3	68.5							
M-Fa-3D-R1_1															52.4%	42%	29.2	1.7%	51.9%	41%	29.2

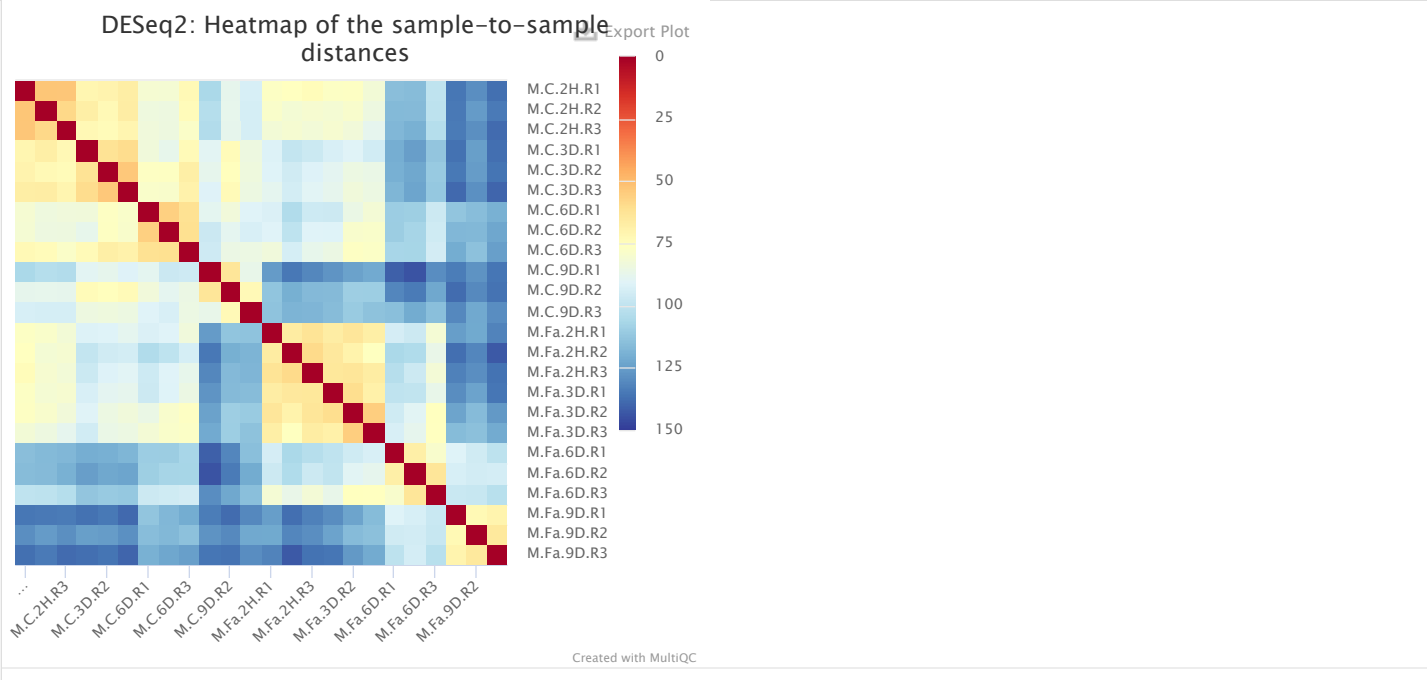
Sample Name	% rRNA	% dupInt	% Dups	5'-3' bias	M Aligned	% Aligned	% Proper Pairs	Error rate	M Non-Primary	M Reads Mapped	% Mapped	% Proper Pairs	M Total seqs	M Reads Mapped	% Dups	% GC	M Seqs	% BP Trimmed	% Dups	% GC	M Seqs
M-Fa-3D-R1_2															47.4%	42%	29.2	1.9%	47.0%	42%	29.2
M-Fa-3D-R2	0.00%	0.20%	36.4%	0.96	30.6	93.8%	49.2%	0.46%	11.3	61.2	95.1%	95.1%	64.4	72.5							
M-Fa-3D-R2_1															53.4%	42%	32.2	1.7%	53.0%	41%	32.2
M-Fa-3D-R2_2															49.2%	42%	32.2	1.9%	48.8%	42%	32.2
M-Fa-3D-R3	0.00%	0.19%	34.7%	1.01	29.4	94.1%	54.2%	0.45%	6.3	58.8	95.3%	95.3%	61.7	65.1							
M-Fa-3D-R3_1															52.0%	42%	30.9	1.6%	51.6%	41%	30.9
M-Fa-3D-R3_2															48.0%	42%	30.9	1.8%	47.6%	42%	30.9
M-Fa-6D-R1	0.00%	0.19%	35.3%	0.96	27.2	91.9%	46.1%	0.46%	14.7	54.3	93.6%	93.6%	58.0	69.1							
M-Fa-6D-R1_1															51.7%	42%	29.1	1.6%	51.3%	42%	29.0
M-Fa-6D-R1_2															50.2%	42%	29.1	1.7%	49.8%	42%	29.0
M-Fa-6D-R2	0.00%	0.22%	40.1%	0.98	36.0	88.1%	35.9%	0.46%	35.0	72.0	90.7%	90.7%	79.4	107.1							
M-Fa-6D-R2_1															58.6%	42%	39.8	2.0%	57.9%	42%	39.7
M-Fa-6D-R2_2															54.3%	42%	39.8	2.2%	53.7%	42%	39.7
M-Fa-6D-R3	0.00%	0.22%	40.0%	0.97	40.1	92.3%	43.3%	0.46%	21.1	80.3	94.0%	94.0%	85.4	101.3							
M-Fa-6D-R3_1															58.6%	42%	42.8	1.7%	58.1%	41%	42.7

Sample Name	% rRNA	% dup	Int	% Dups	5'-3' bias	M Aligned	% Aligned	% Proper Pairs	Error rate	M Non-Primary	M Reads Mapped	% Mapped	% Proper Pairs	M Total seqs	M Reads Mapped	% Dups	% GC	M Seqs	% BP Trimmed	% Dups	% GC	M Seqs
M-Fa-6D-R3_2																54.7%	42%	42.8	1.9%	54.1%	42%	42.7
M-Fa-9D-R1	0.00%	0.20%	35.7%	0.99	27.5	92.5%	50.7%	0.46%	8.3	55.0	94.1%	94.1%	58.4	63.3								
M-Fa-9D-R1_1																54.3%	41%	29.3	1.7%	53.8%	41%	29.2
M-Fa-9D-R1_2																49.7%	42%	29.3	1.8%	49.2%	41%	29.2
M-Fa-9D-R2	0.00%	0.22%	38.2%	0.97	33.9	92.8%	45.6%	0.47%	16.0	67.8	94.4%	94.4%	71.9	83.8								
M-Fa-9D-R2_1																54.6%	42%	36.0	1.6%	54.2%	42%	35.9
M-Fa-9D-R2_2																51.0%	42%	36.0	1.6%	50.7%	41%	35.9
M-Fa-9D-R3	0.00%	0.22%	36.1%	1.01	22.9	93.5%	47.9%	0.47%	10.1	45.8	95.0%	95.0%	48.3	55.9								
M-Fa-9D-R3_1																50.8%	42%	24.2	1.6%	50.4%	41%	24.1
M-Fa-9D-R3_2																45.2%	42%	24.2	1.7%	44.8%	42%	24.1

STAR_RSEM DESeq2 sample similarity

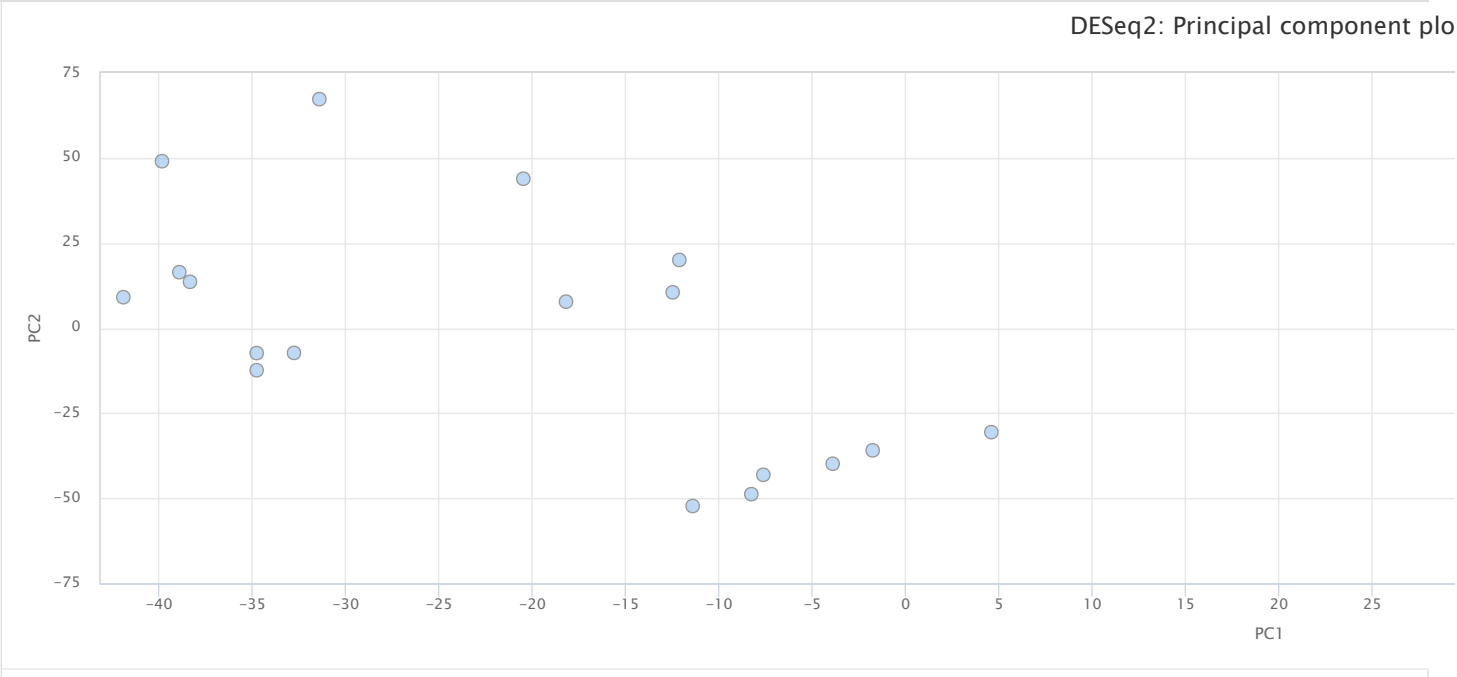
is generated from clustering by Euclidean distances between DESeq2 rlog values for each sample in the `deseq2_qc.r` script.

Sort by highlight **Min:** 0.0 **Max:** 143.0958



STAR_RSEM DESeq2 PCA plot

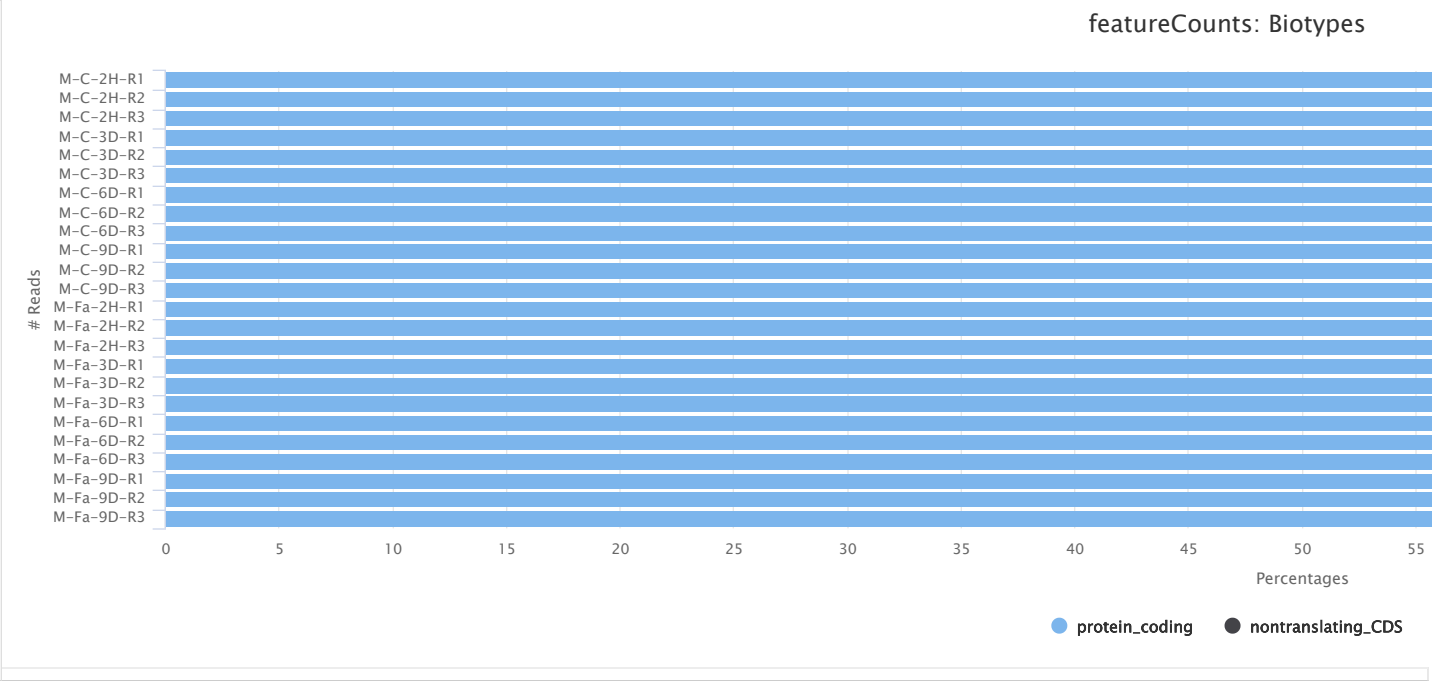
PCA plot between samples in the experiment. These values are calculated using DESeq2 in the `deseq2_qc.r` script.



Biotype Counts

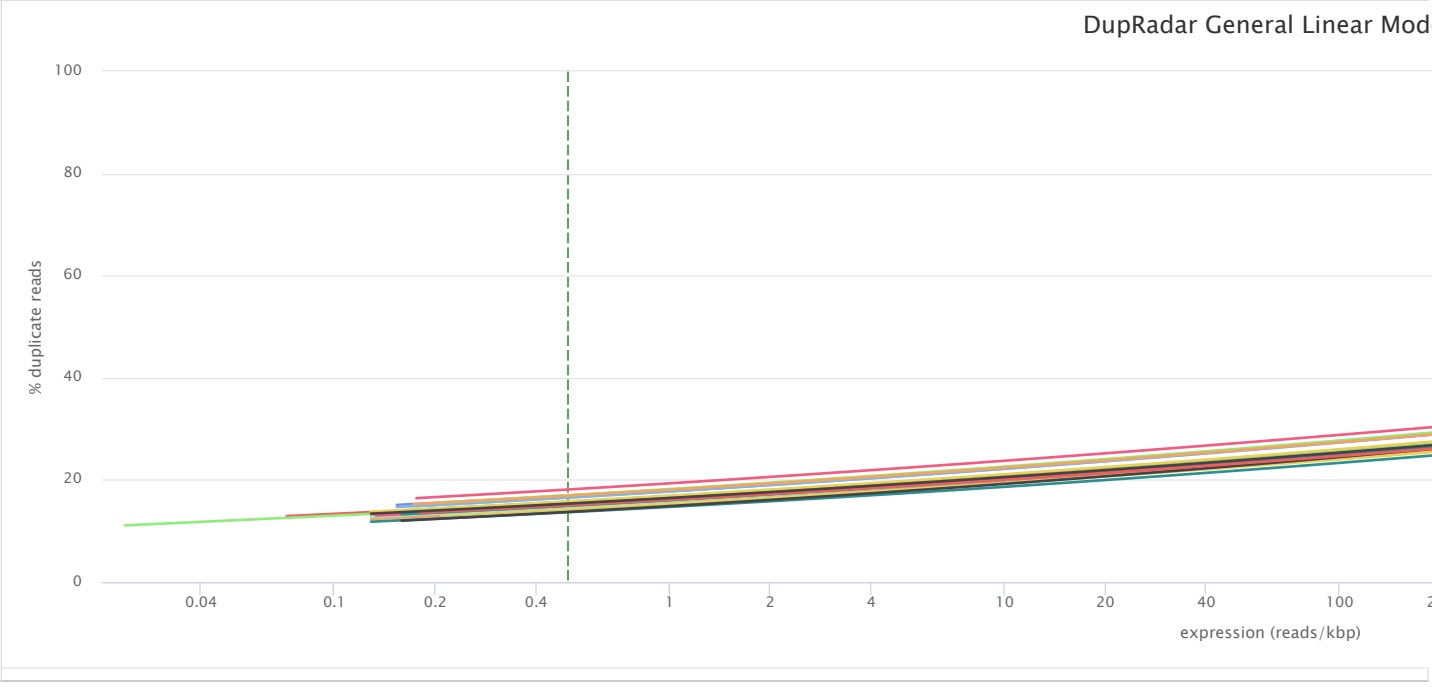
shows reads overlapping genomic features of different biotypes, counted by featureCounts.

Number of Reads | Percentages



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. .



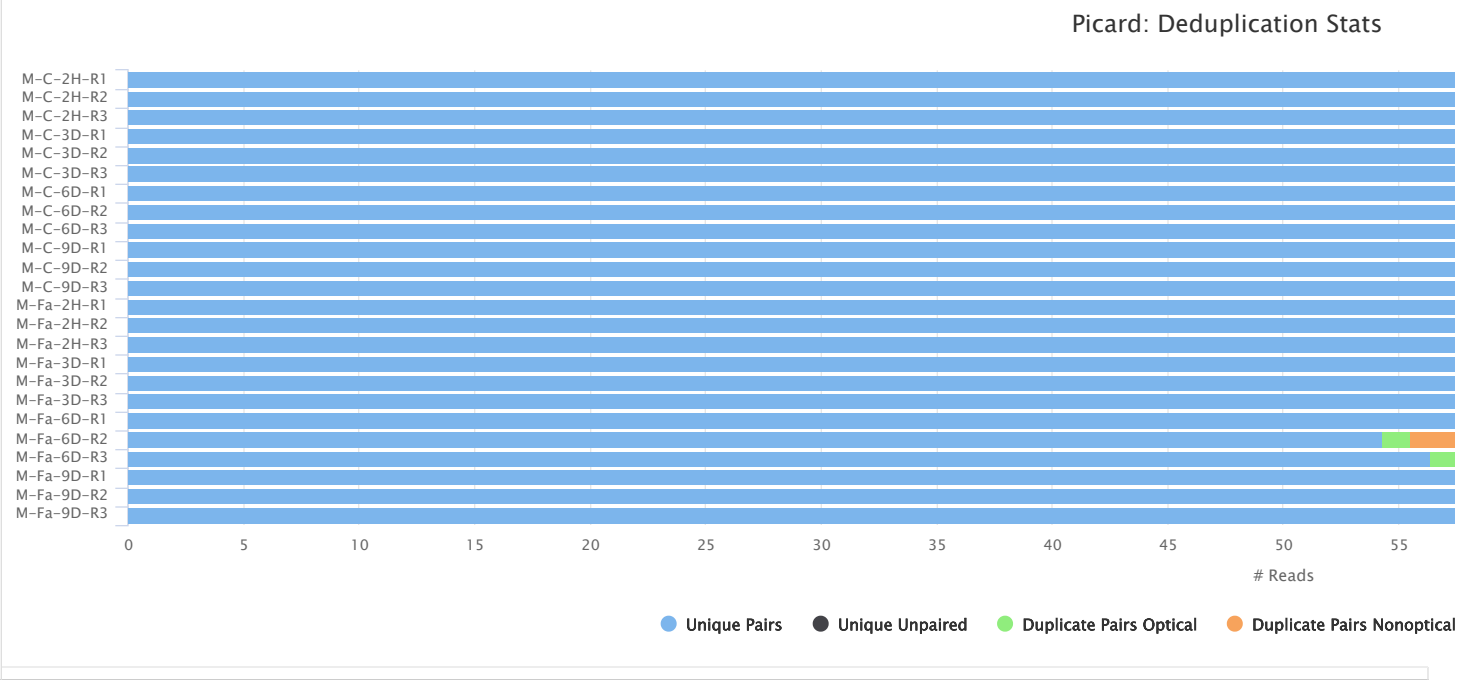
Picard

Picard is a set of Java command line tools for manipulating high-throughput sequencing data.

Mark Duplicates

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

Number of Reads | Percentages



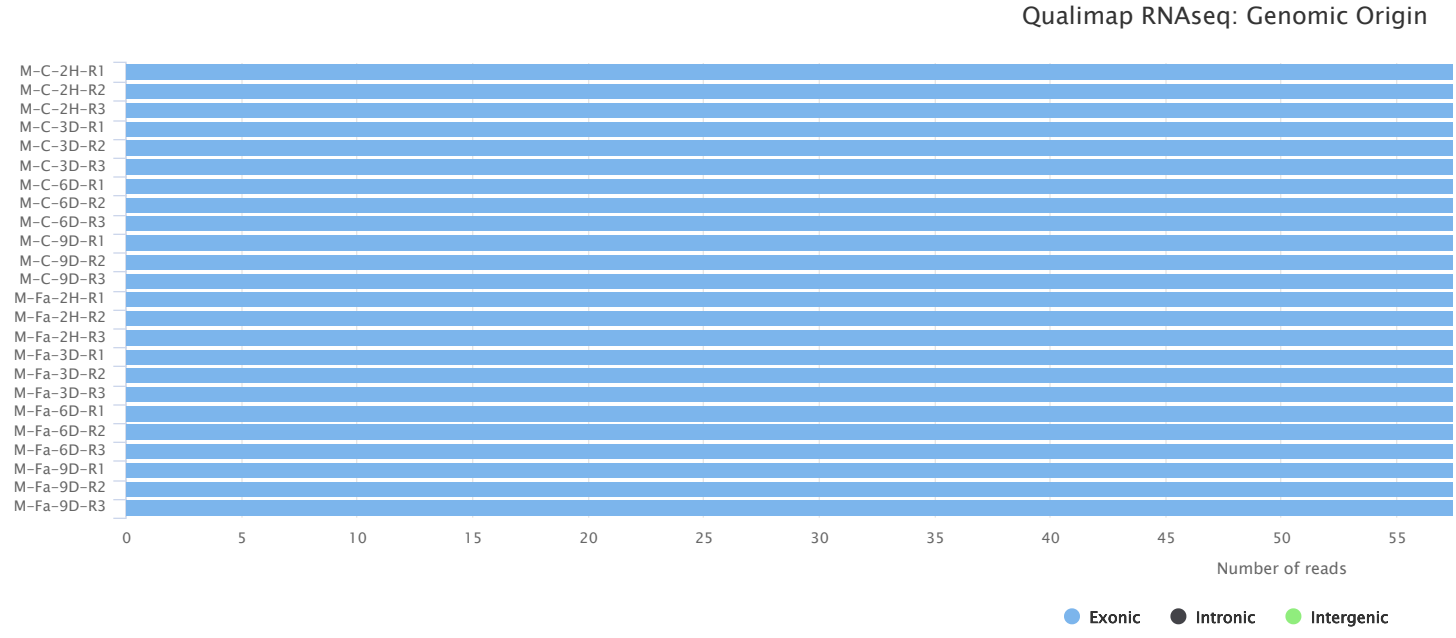
QualiMap

QualiMap is a platform-independent application to facilitate the quality control of alignment sequencing data and its derivatives like feature counts. *DOI: 10.1093/bioinformatics/btv566; 10.1093/bioinformatics/bts503.*

Genomic origin of reads

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.

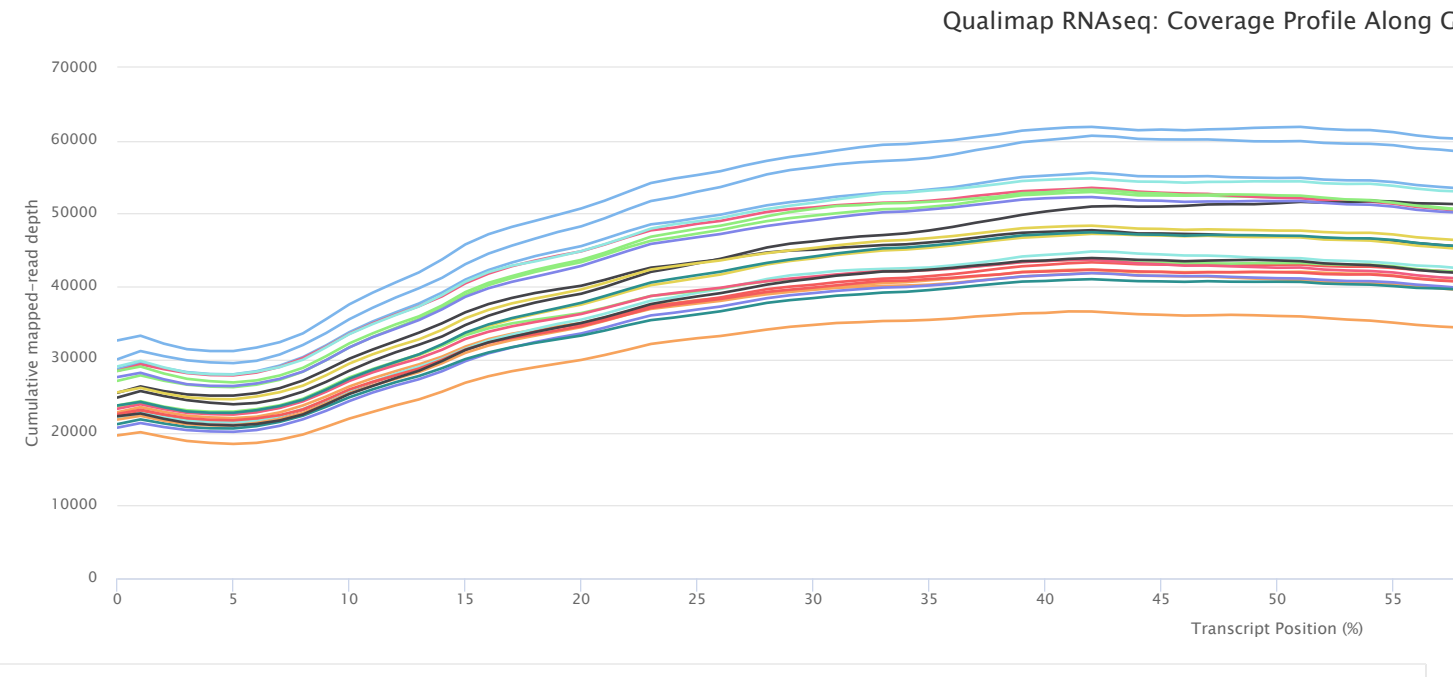
Counts | Percentages



Gene Coverage Profile

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

Counts | Normalised



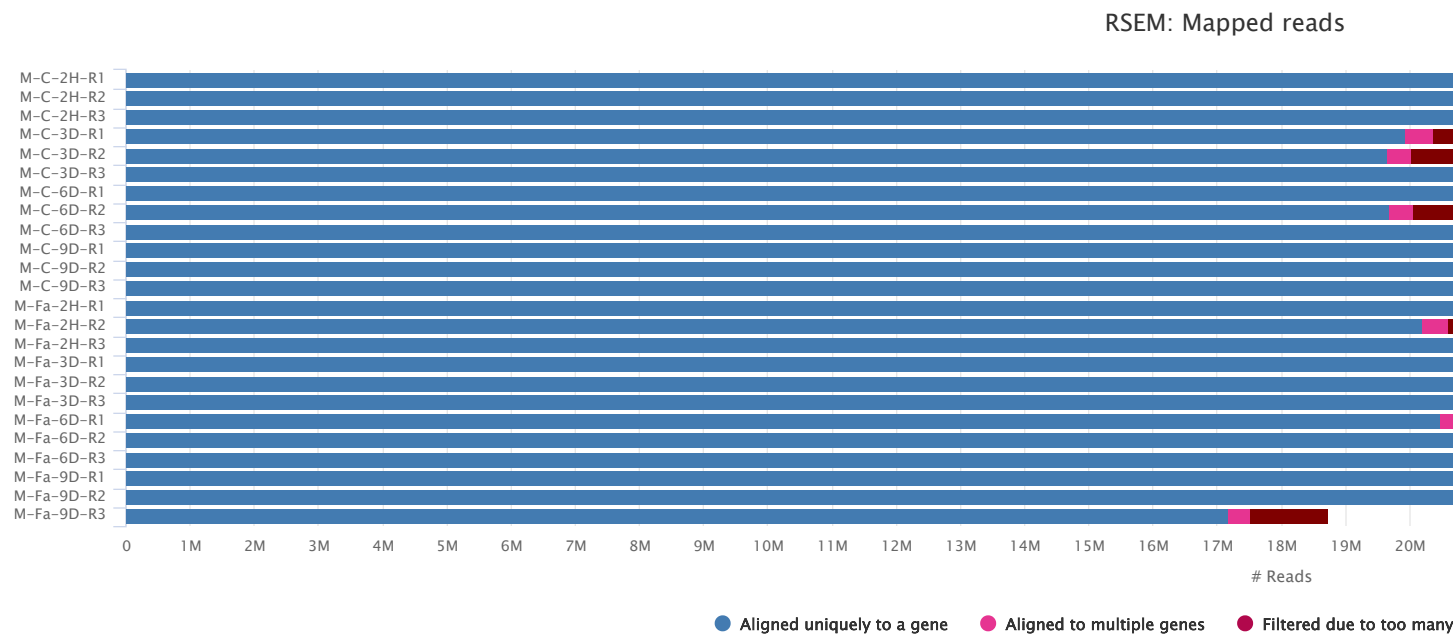
Rsem

Rsem RSEM (RNA-Seq by Expectation-Maximization) is a software package forestimating gene and isoform expression levels from RNA-Seq data. *DOI: 10.1186/1471-2105-12-323.*

Mapped Reads

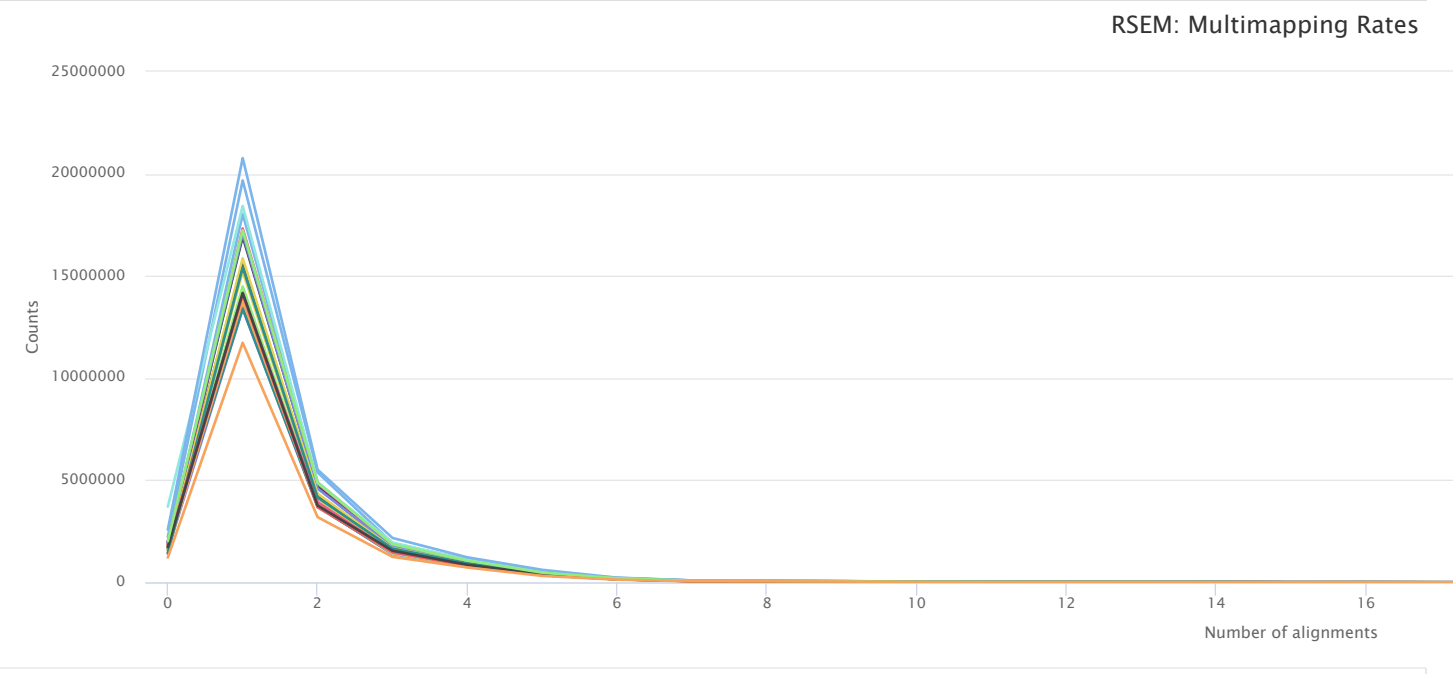
A breakdown of how all reads were aligned for each sample.

Number of Reads | Percentages



Multimapping rates

A frequency histogram showing how many reads were aligned to n reference regions.

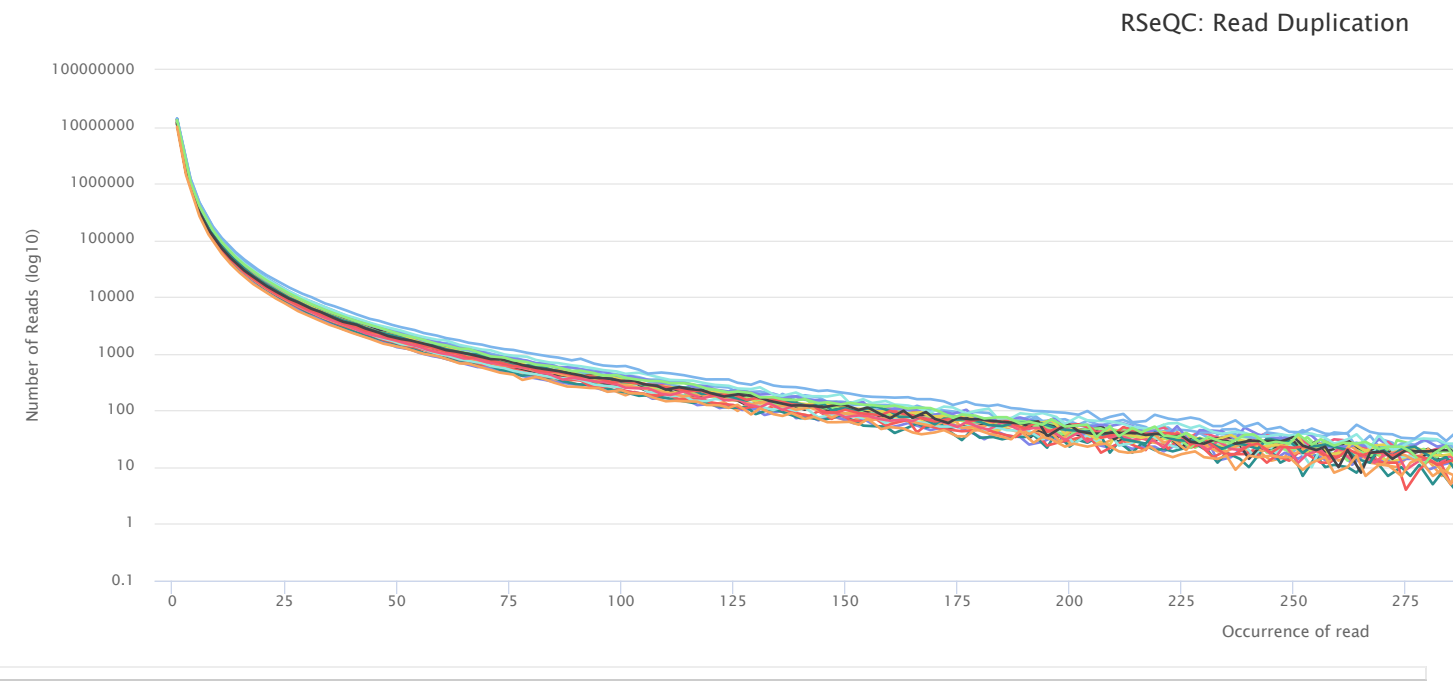


RSeQC

RSeQC package provides a number of useful modules that can comprehensively evaluate high throughput RNA-seq data. *DOI: 10.1093/bioinformatics/bts356.*

Read Duplication

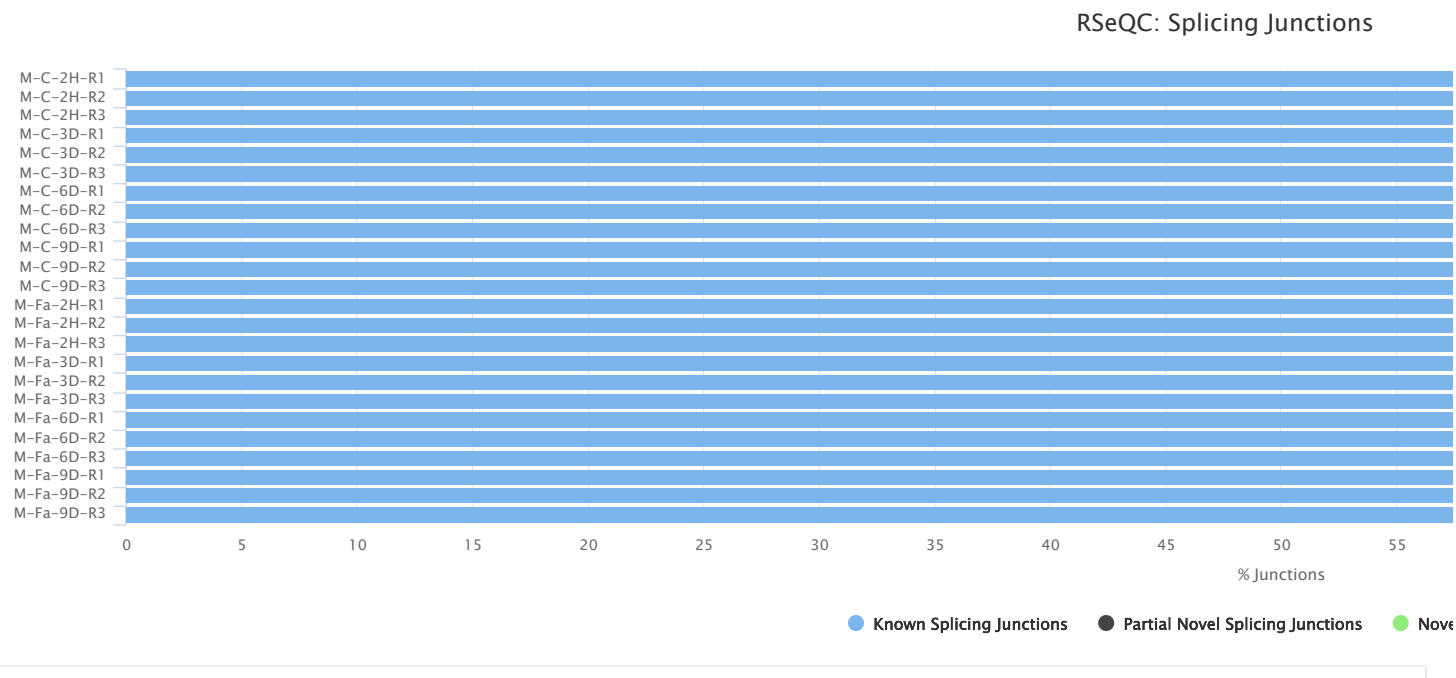
read_duplication.py calculates how many alignment positions have a certain number of exact duplicates. Note - plot truncated at 500 occurrences and binned.



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.

Counts | Percentages | Junctions | Events

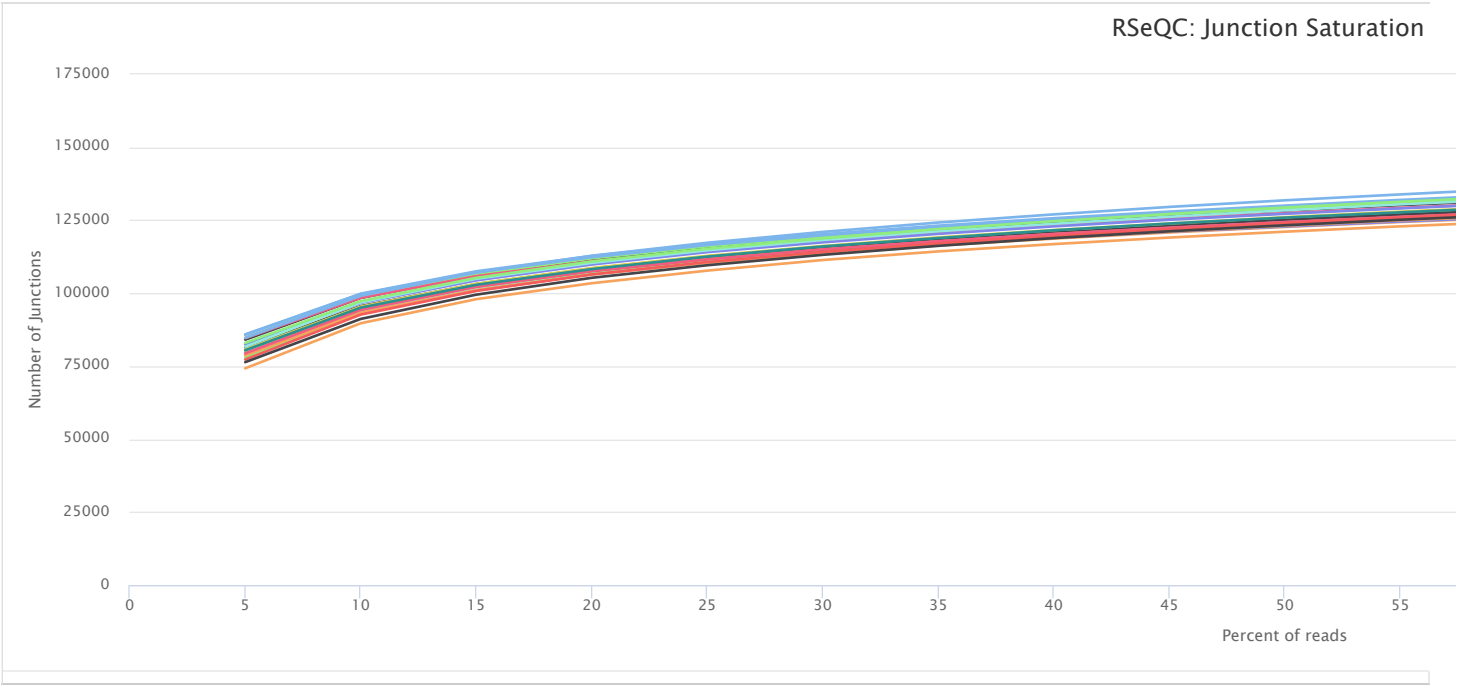


Junction Saturation

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.

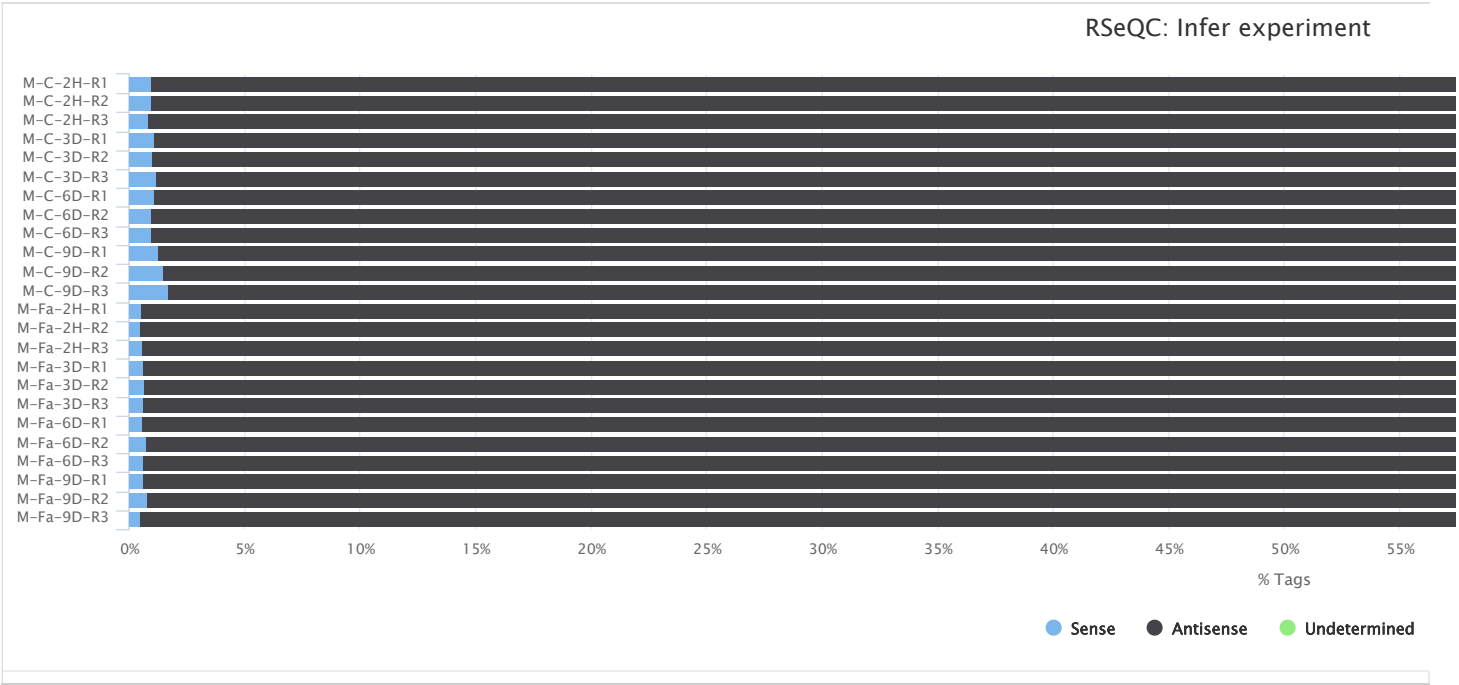
Click a line to see the data side by side (as in the original RSeQC plot).

All Junctions | Known Junctions | Novel Junctions



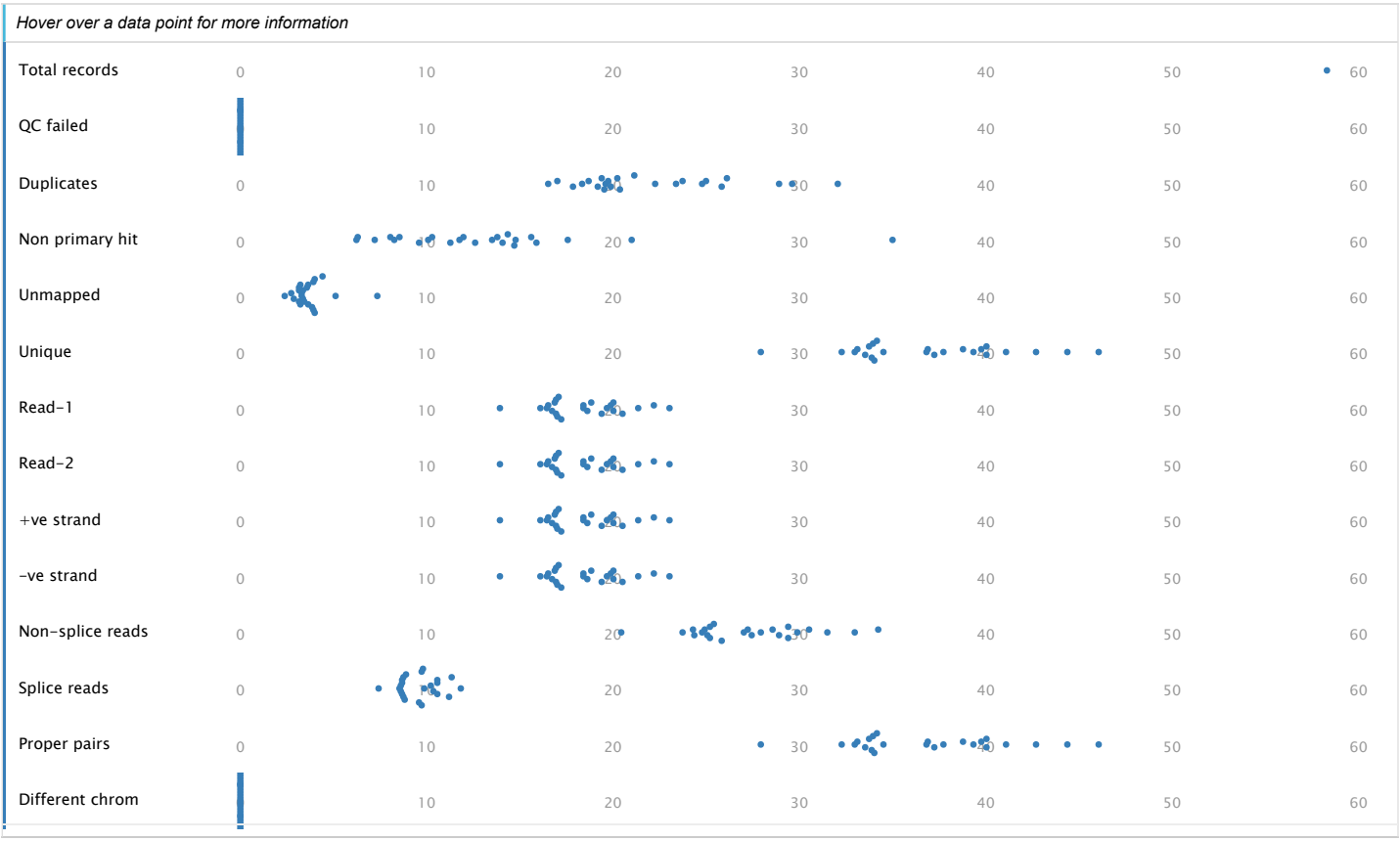
Infer experiment

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).



Bam Stat

All numbers reported in millions.



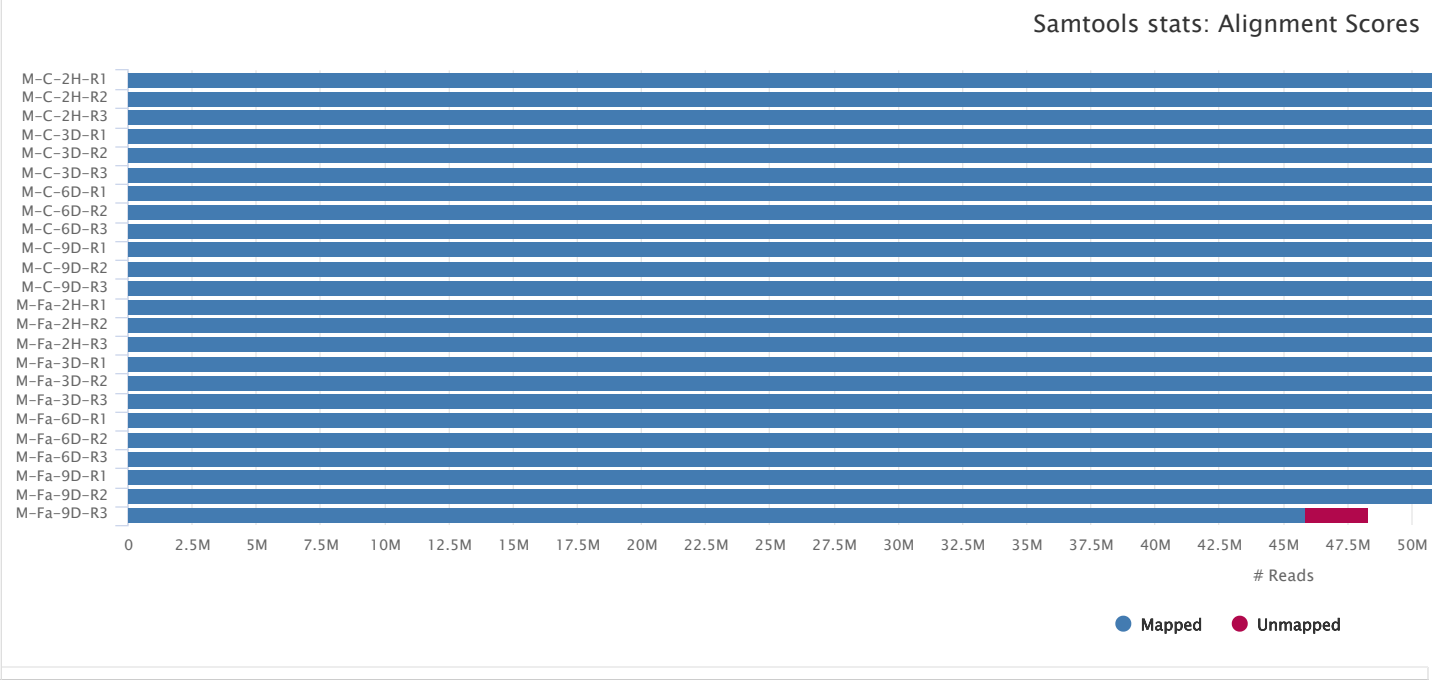
Samtools

Samtools is a suite of programs for interacting with high-throughput sequencing data. *DOI: 10.1093/bioinformatics/btp352.*

Percent Mapped

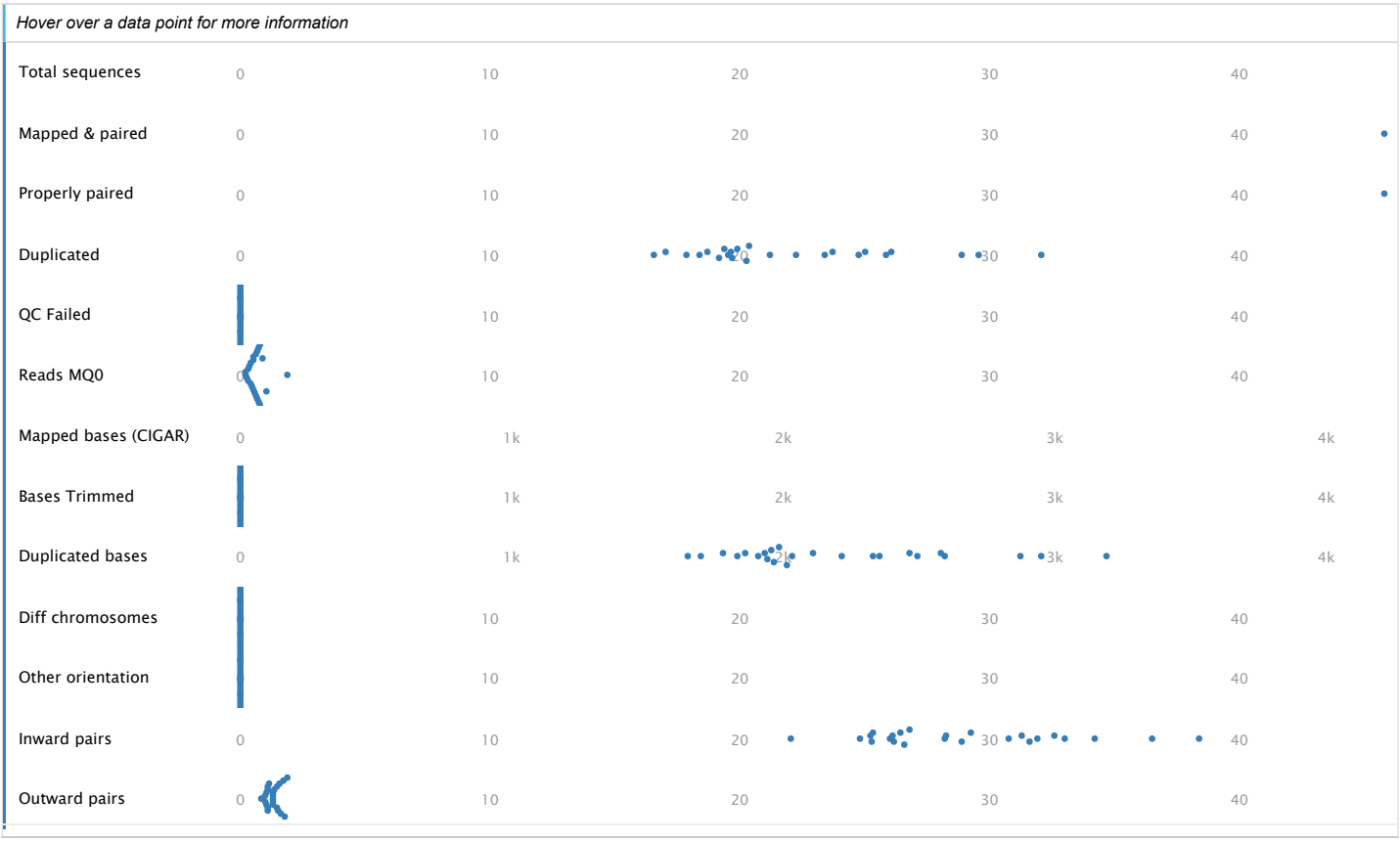
Alignment metrics from `samtools stats` ; mapped vs. unmapped reads.

Number of Reads | Percentages



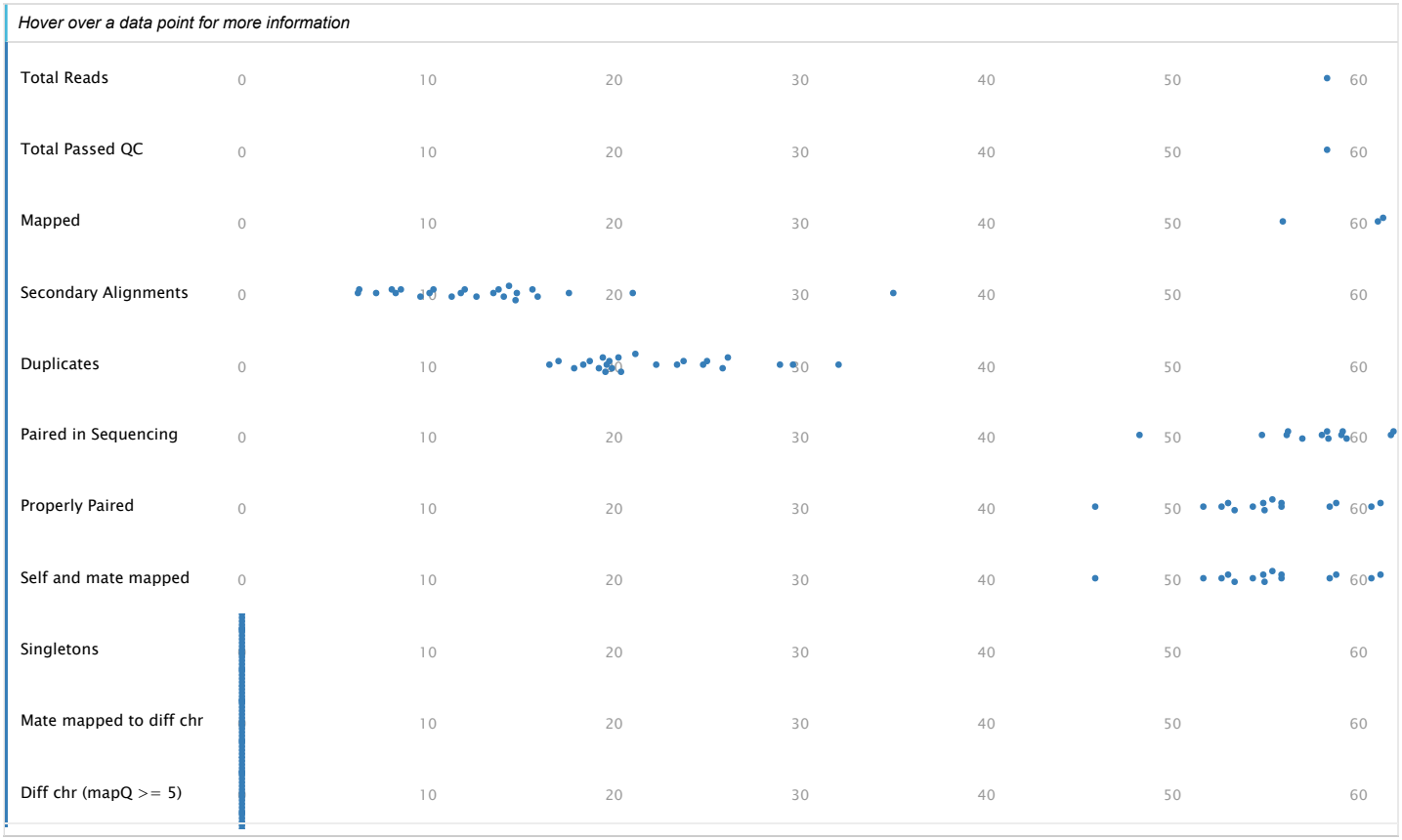
Alignment metrics

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



Samtools Flagstat

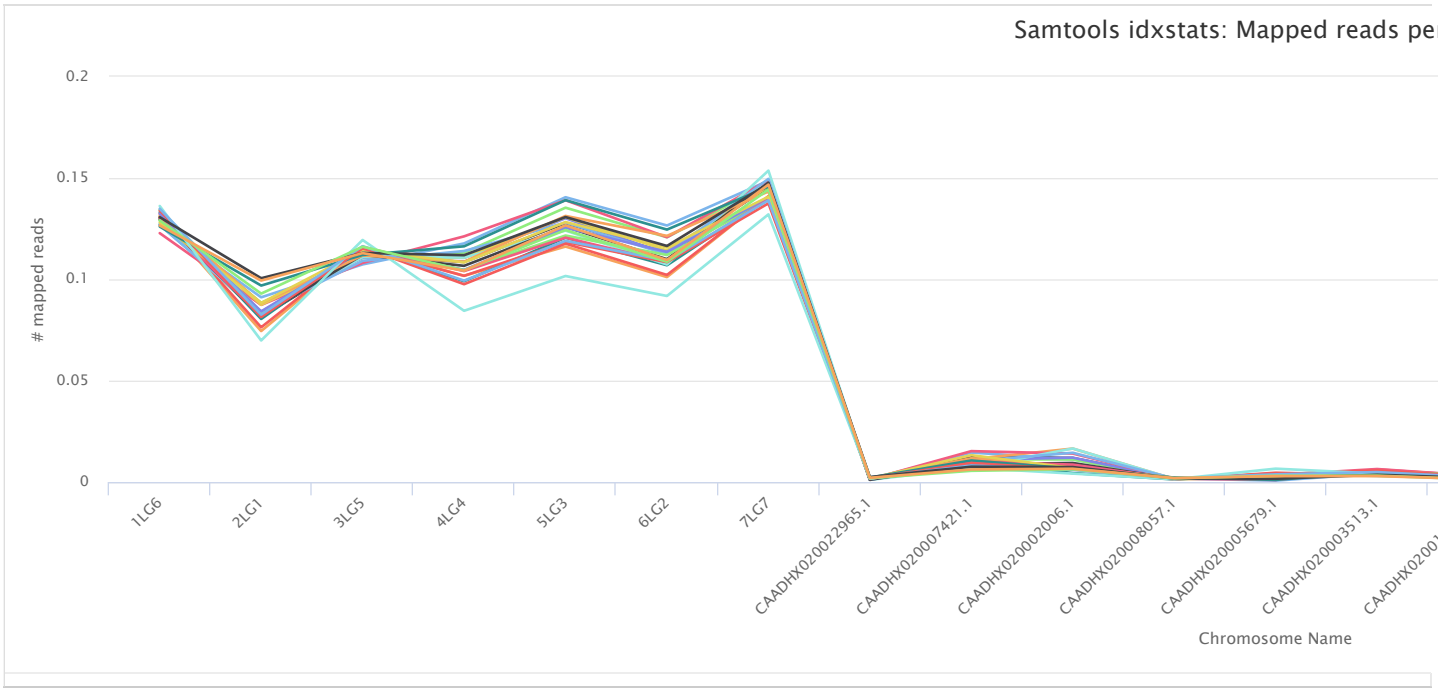
This module parses the output from `samtools flagstat`. All numbers in millions.



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.

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



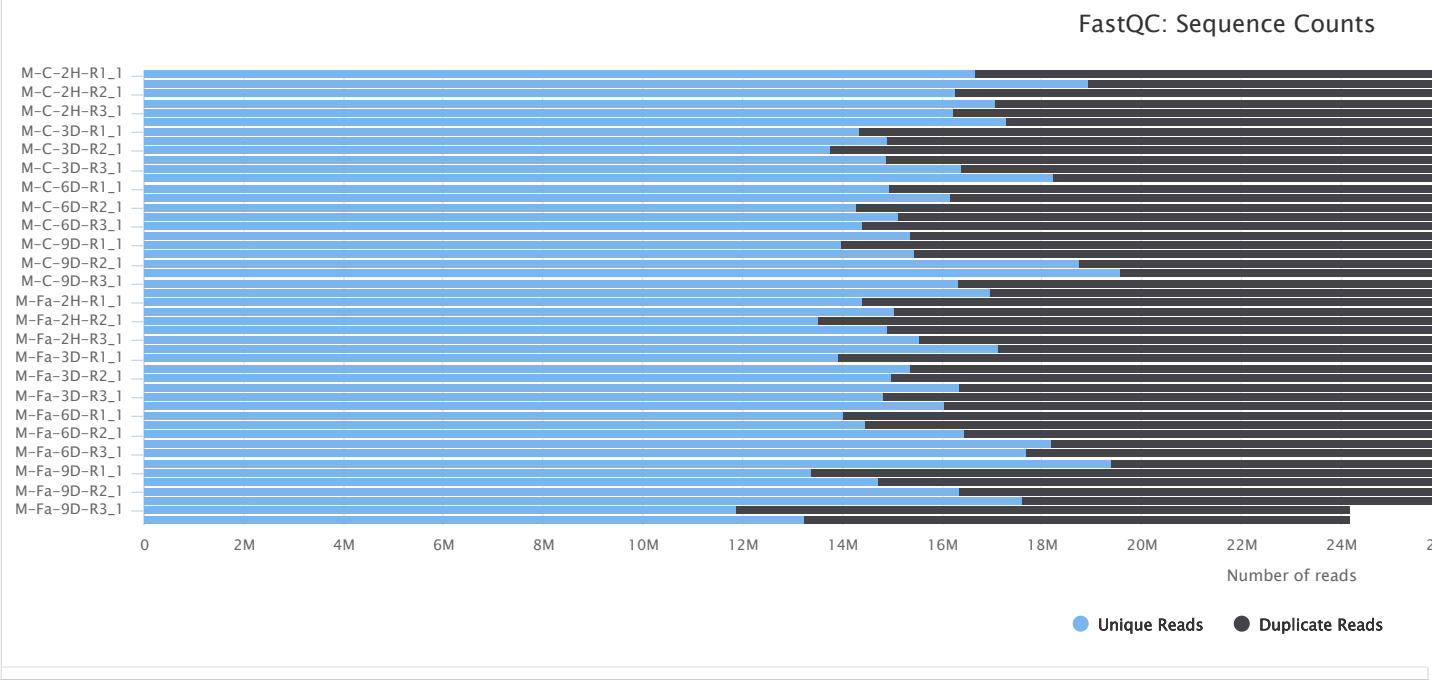
FastQC (raw)

FastQC (raw) This section of the report shows FastQC results before adapter trimming.

Sequence Counts

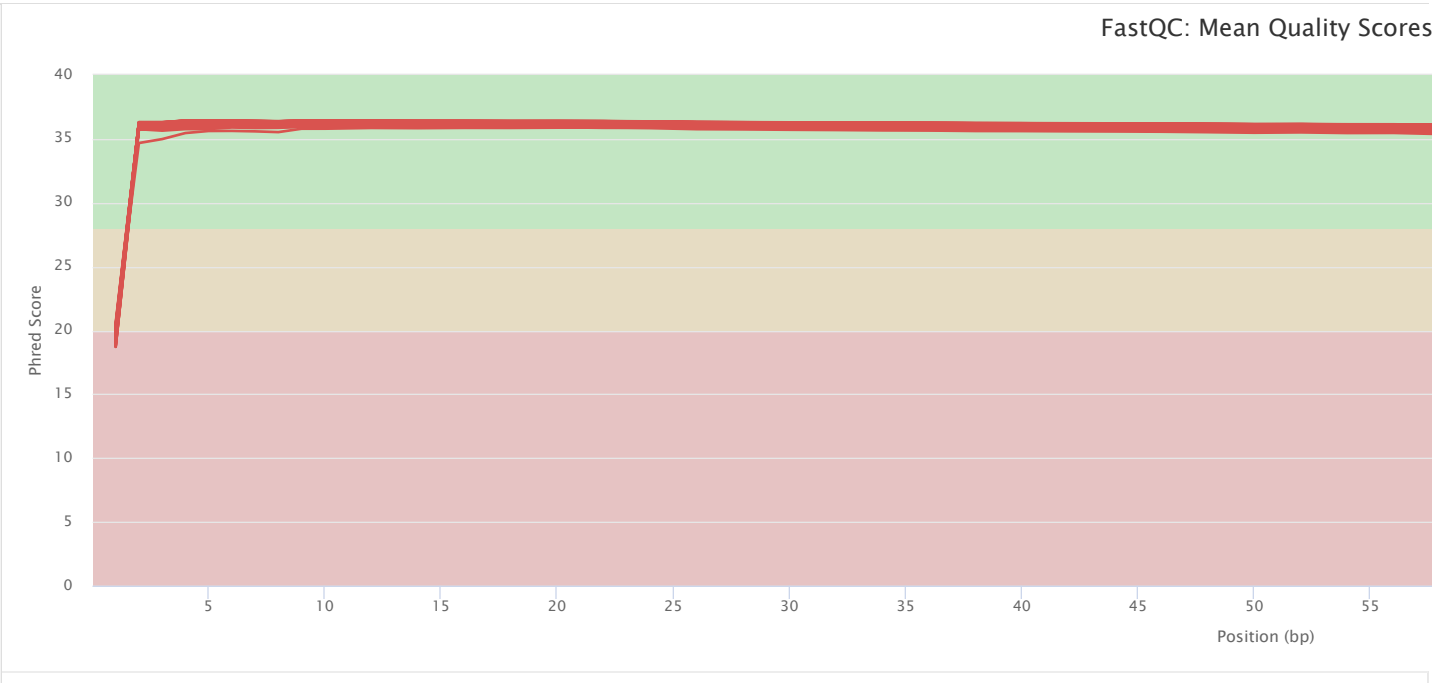
Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads | Percentages



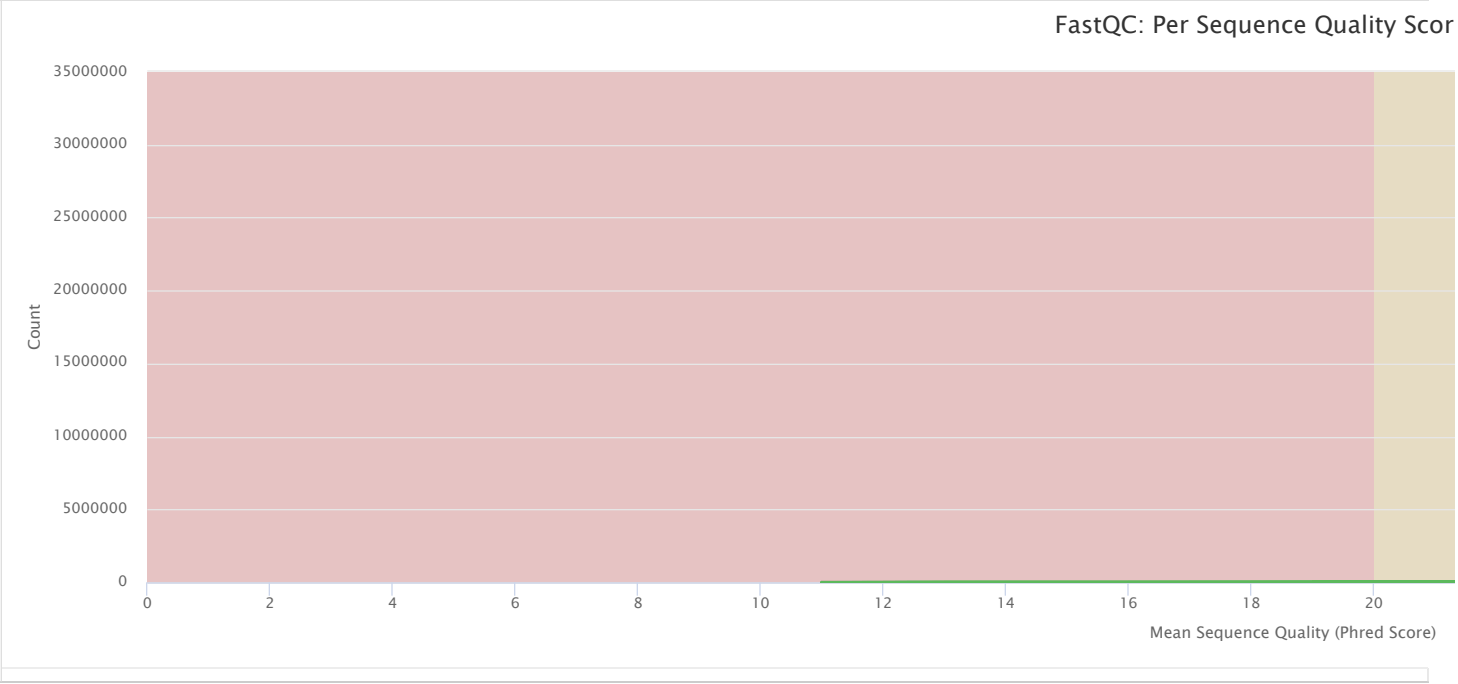
Sequence Quality Histograms

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



Per Sequence Quality Scores 48

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



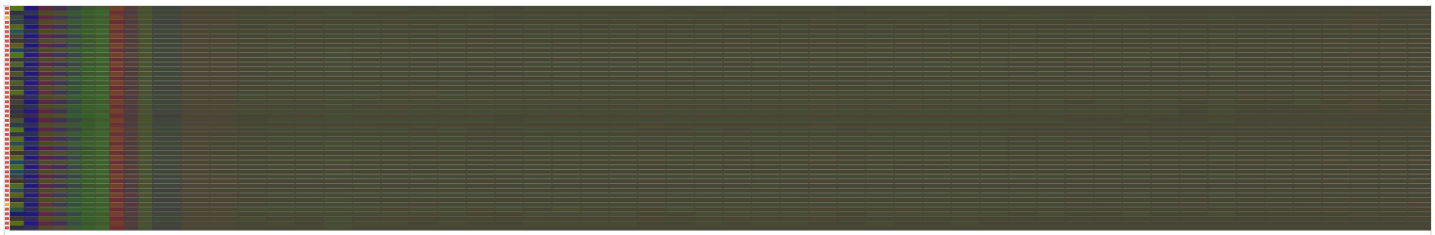
Per Base Sequence Content

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

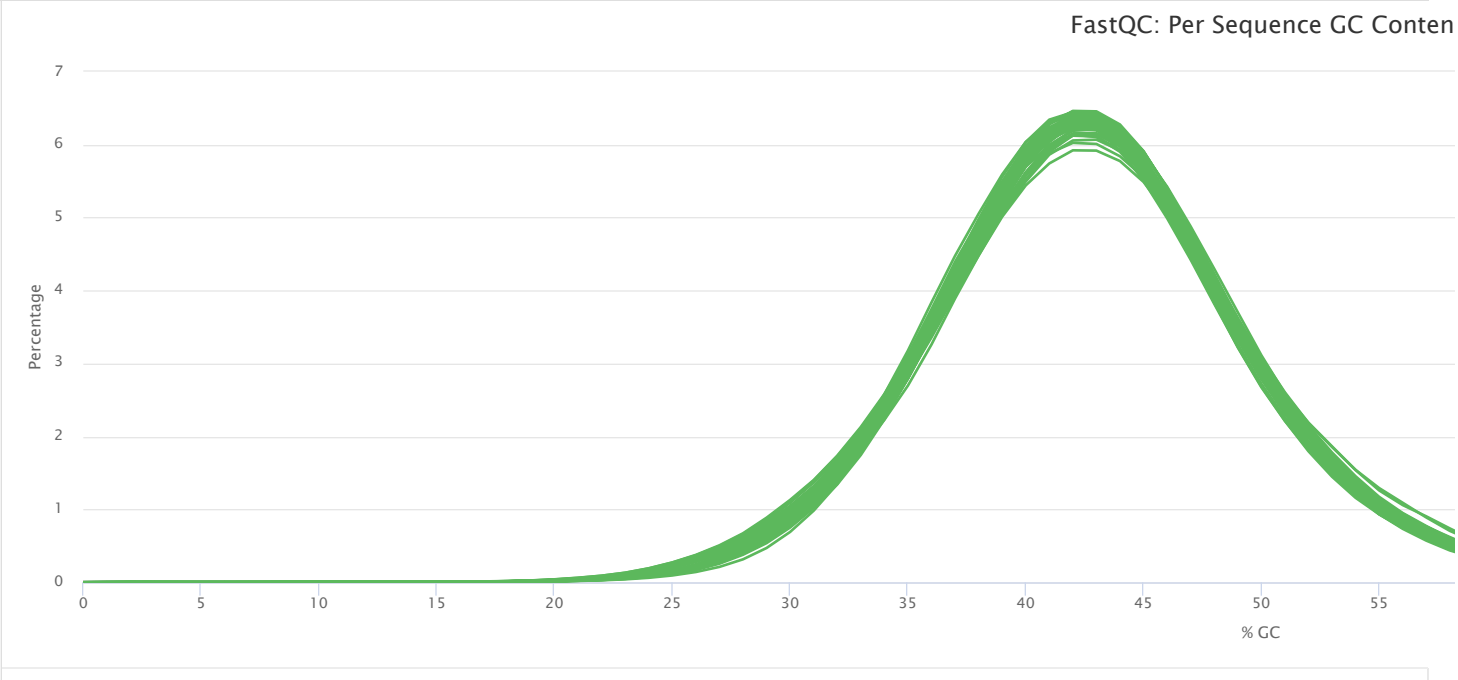
Position: - %T: - %C: - %A: - %G: - Export Plot



Per Sequence GC Content 48

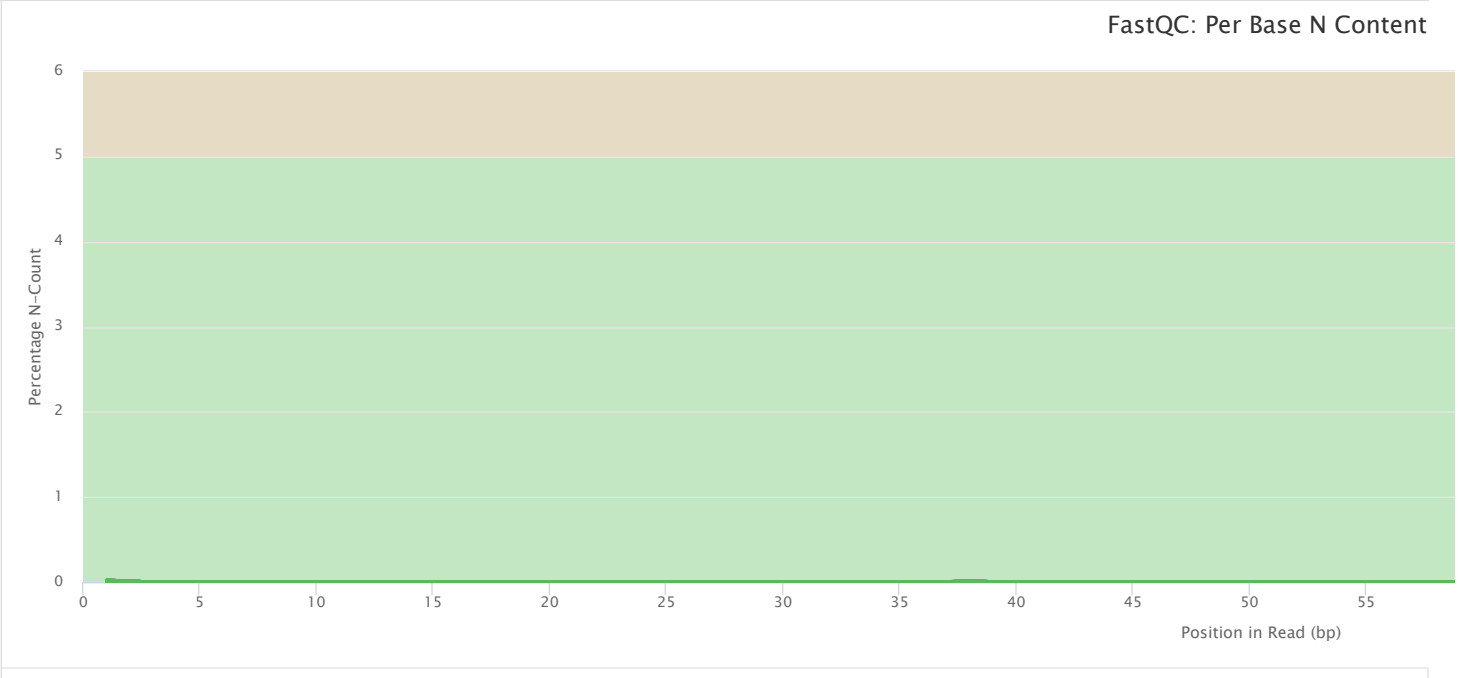
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Percentages | Counts



Per Base N Content 48

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

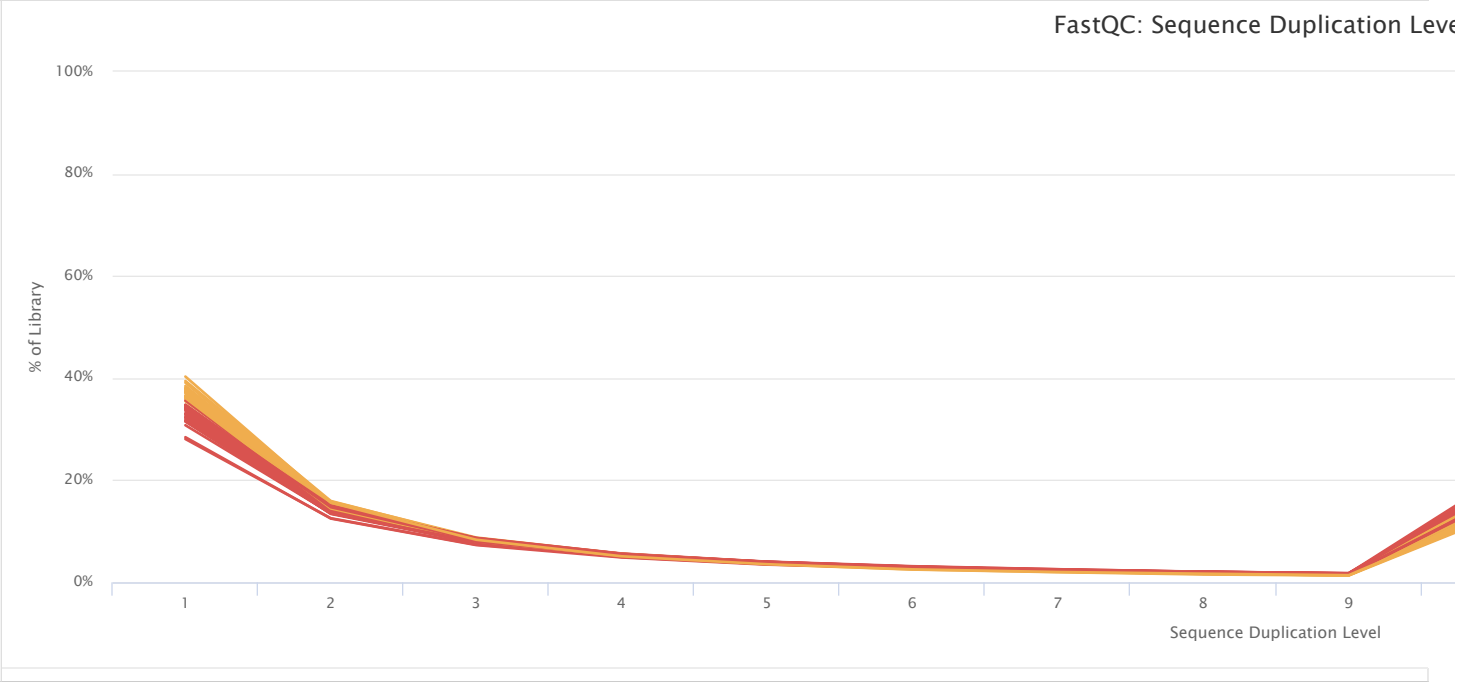


Sequence Length Distribution 48

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

Sequence Duplication Levels 21

The relative level of duplication found for every sequence.



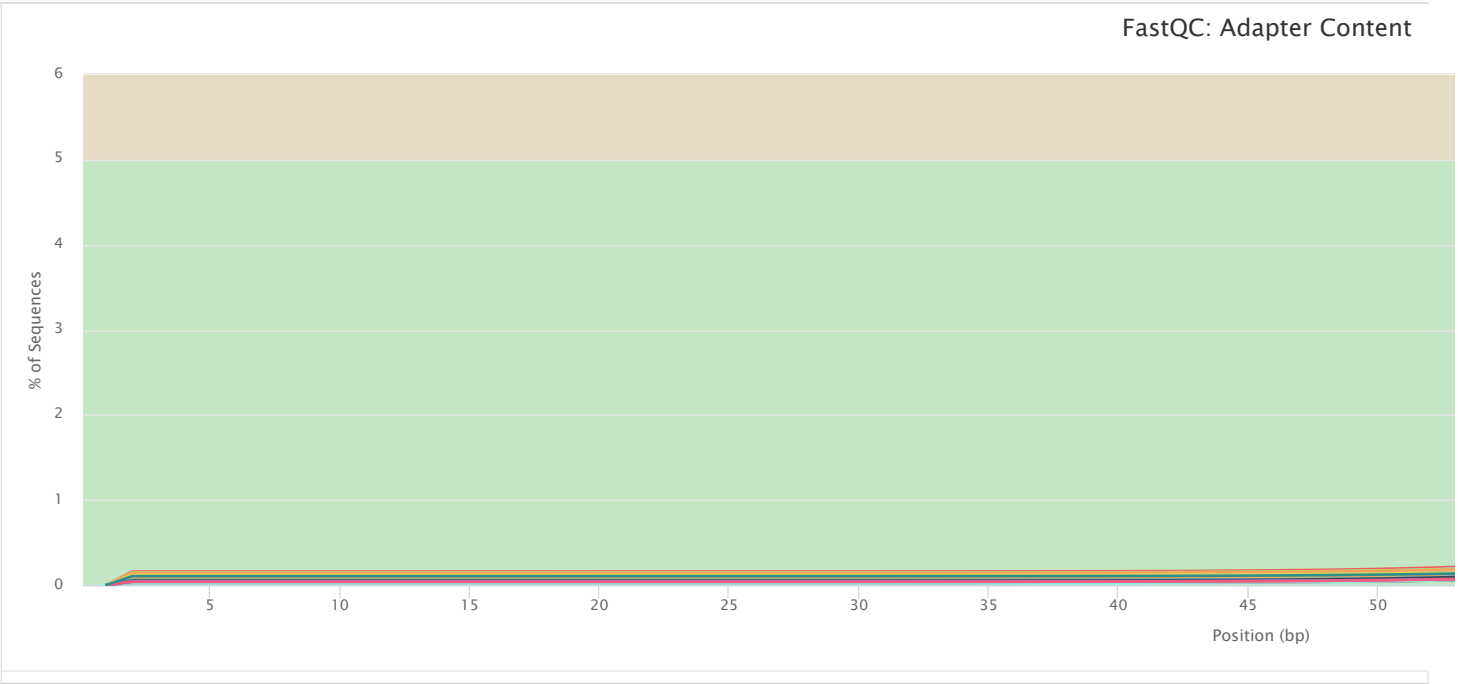
Overrepresented sequences 46

The total amount of overrepresented sequences found in each library.

48 samples had less than 1% of reads made up of overrepresented sequences

Adapter Content 48

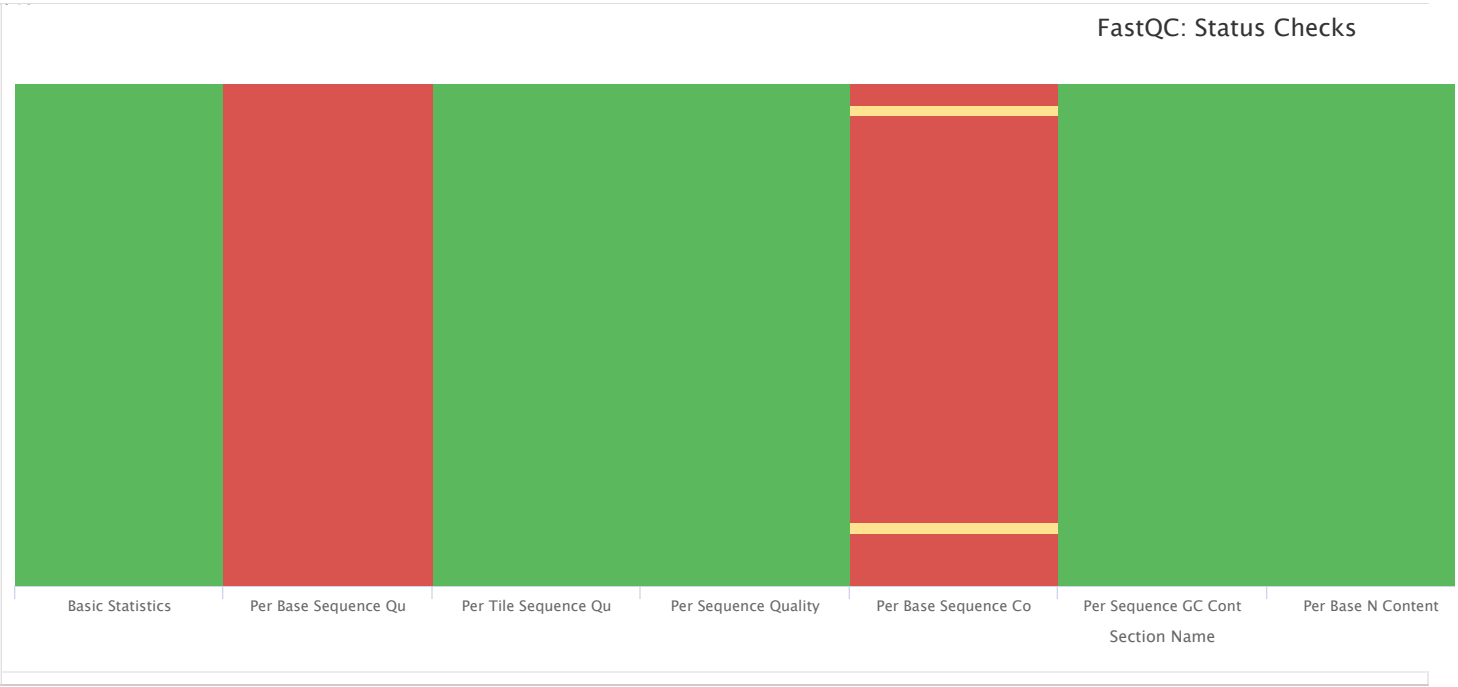
The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.



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



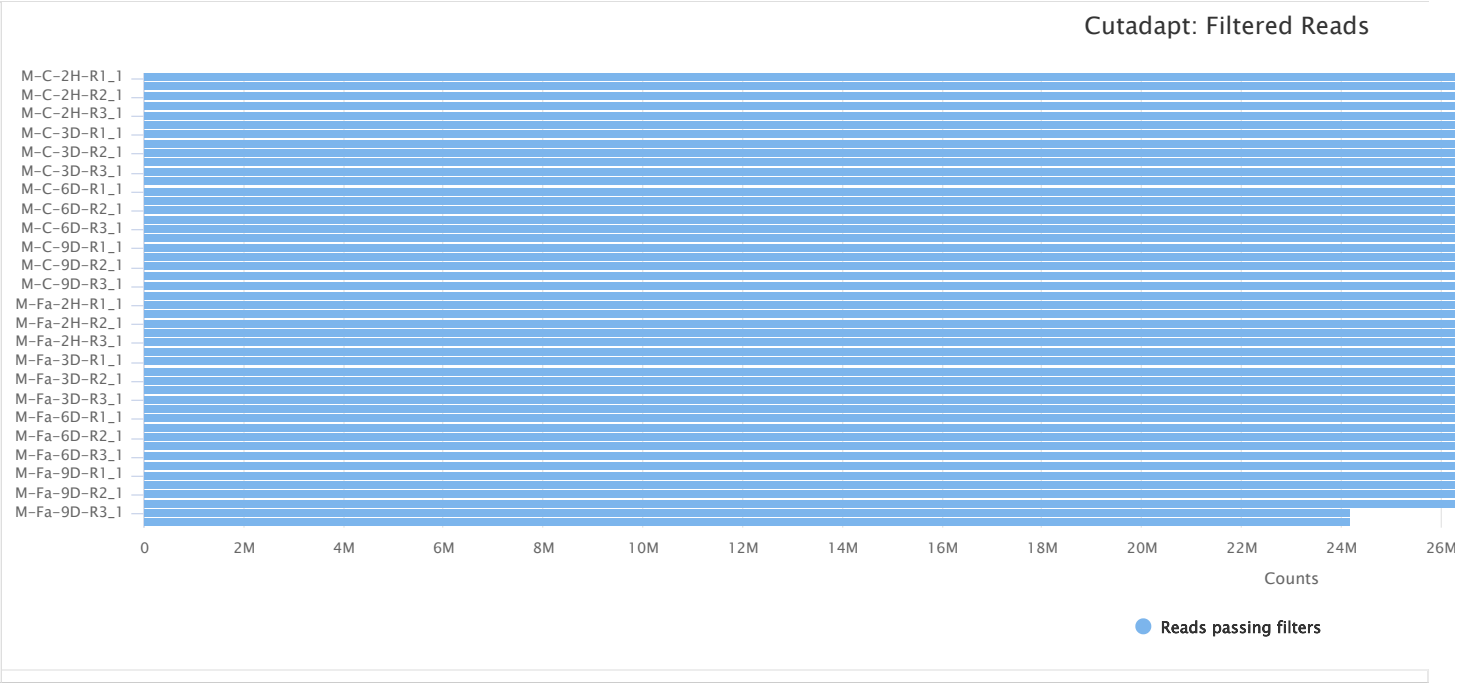
Cutadapt

Cutadapt is a tool to find and remove adapter sequences, primers, poly-A tails and other types of unwanted sequence from your high-throughput sequencing reads. *DOI: 10.14806/ej.17.1.200.*

Filtered Reads

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

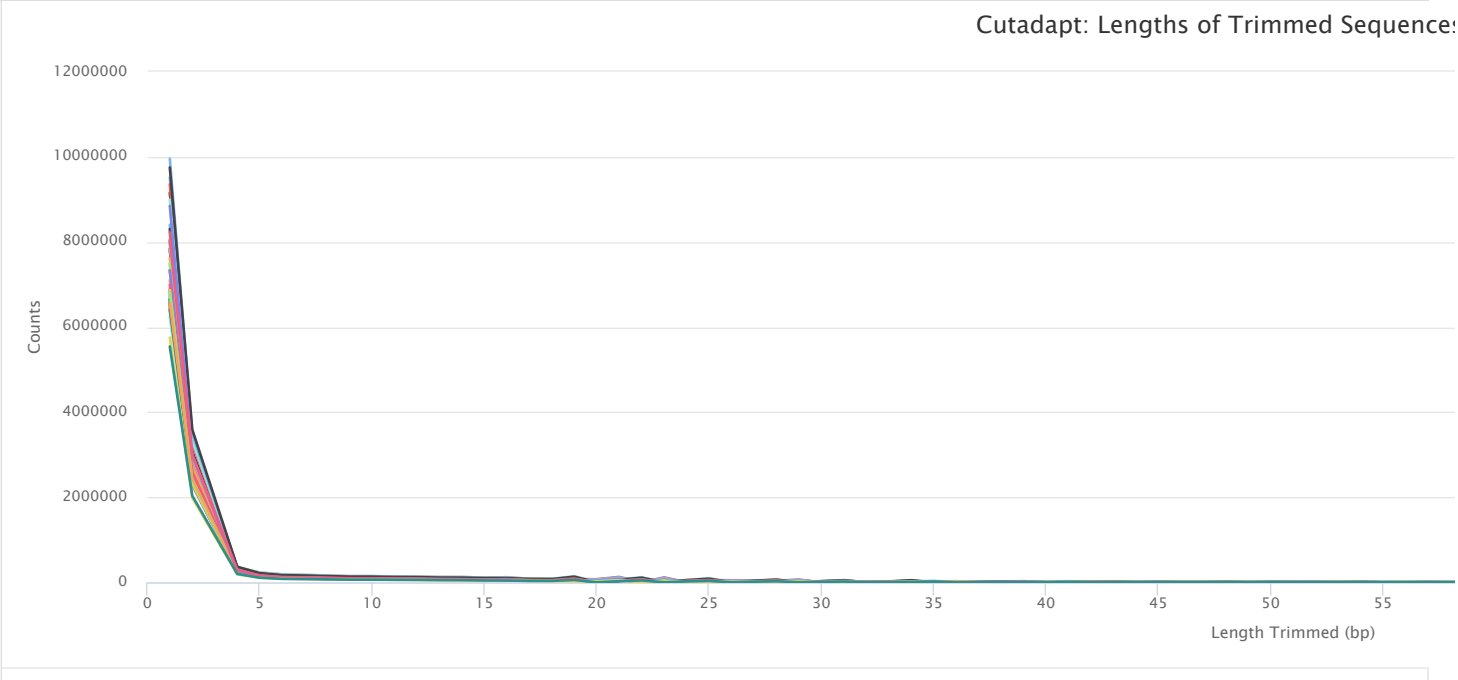
Counts | Percentages



Trimmed Sequence Lengths (3')

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

Counts | Obs/Exp



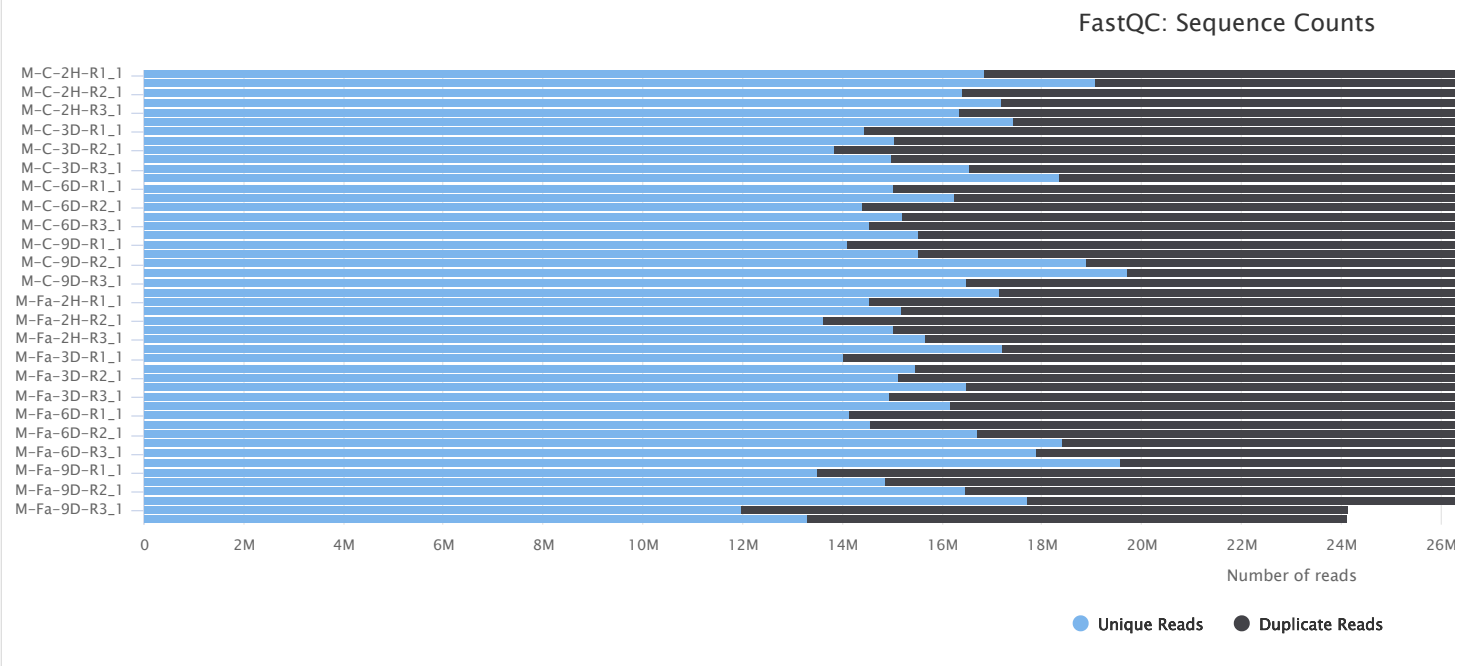
FastQC (trimmed)

FastQC (trimmed) This section of the report shows FastQC results after adapter trimming.

Sequence Counts

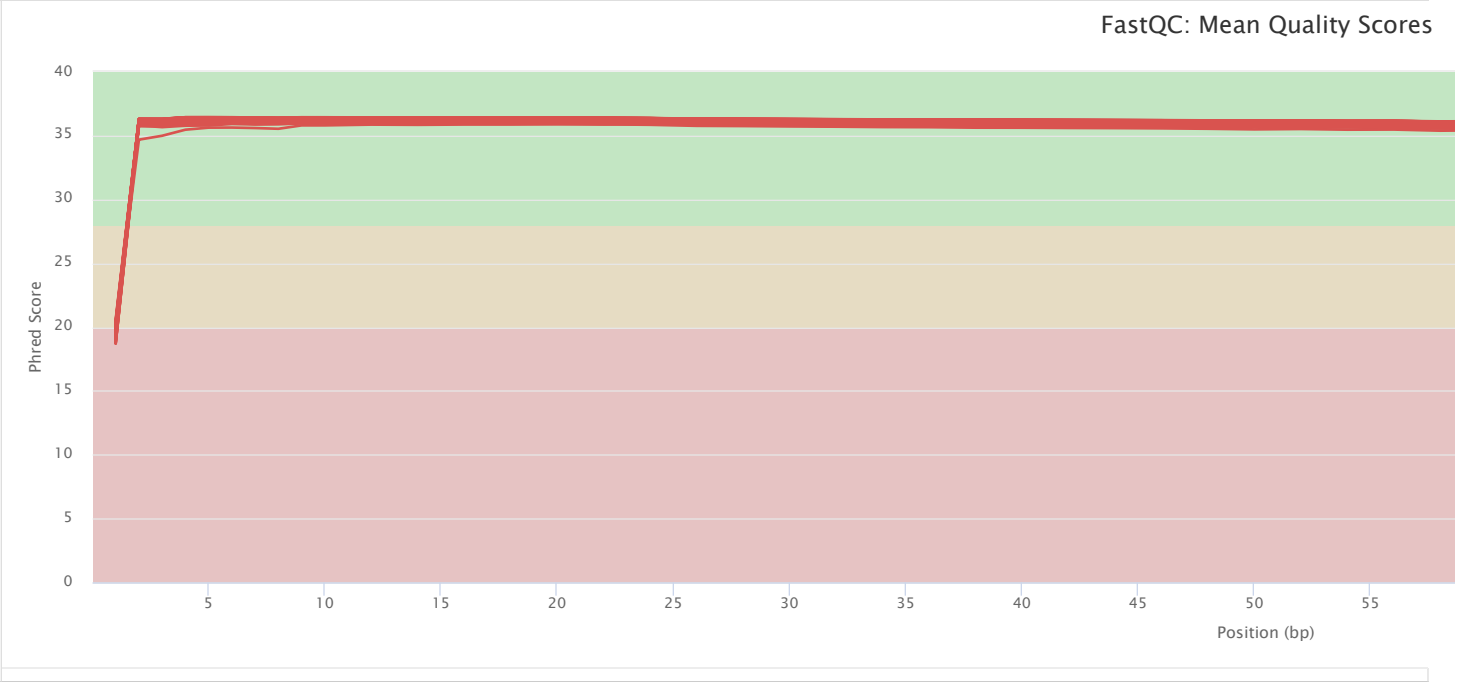
Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads | Percentages



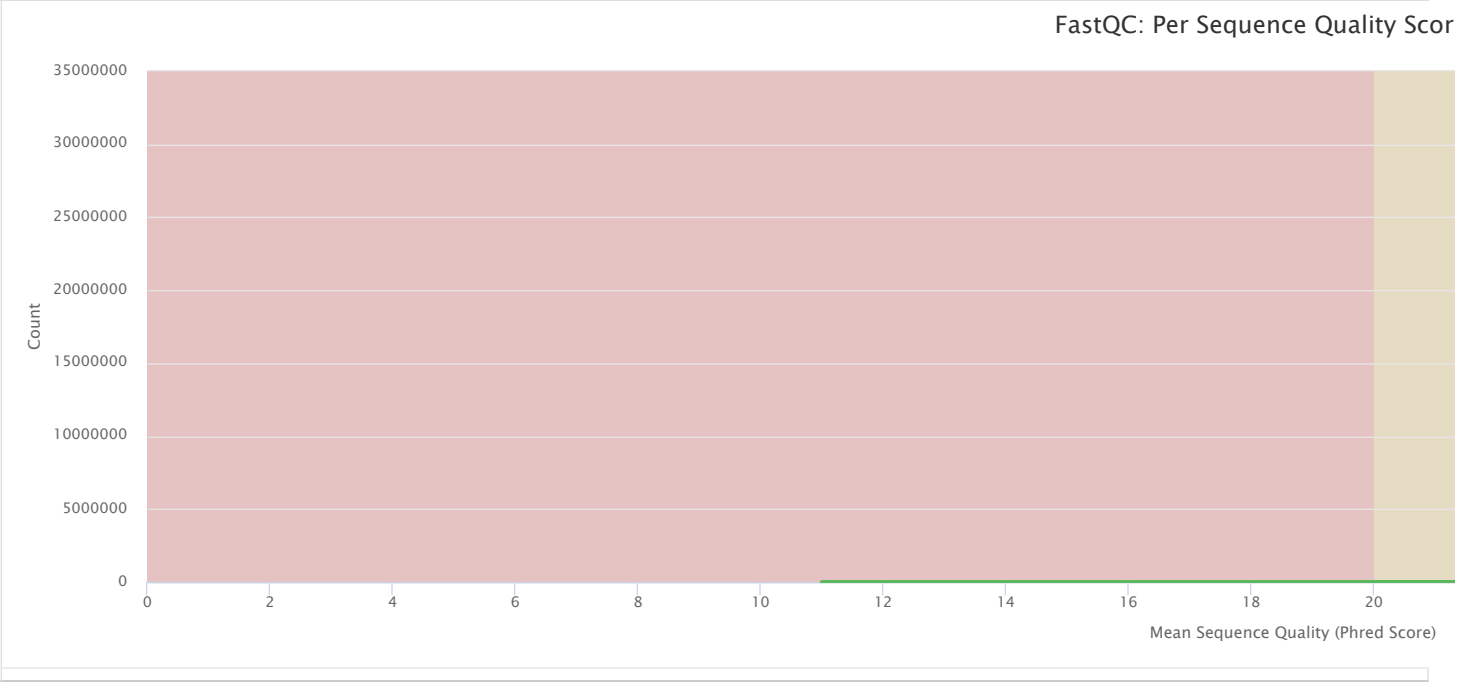
Sequence Quality Histograms

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



Per Sequence Quality Scores 48

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



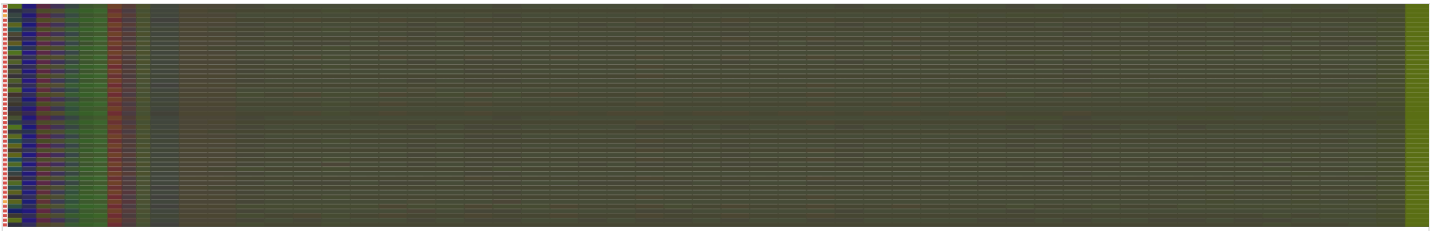
Per Base Sequence Content

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

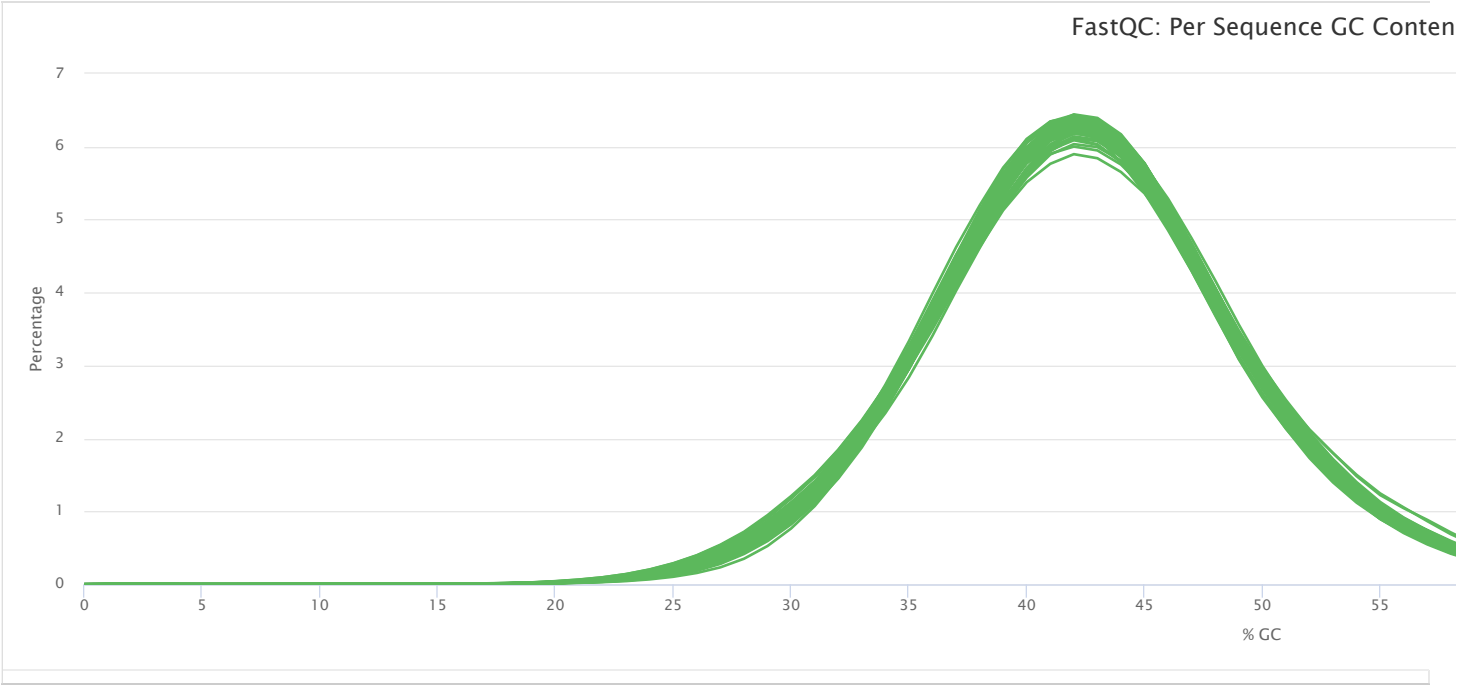


Per Sequence GC Content

48

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

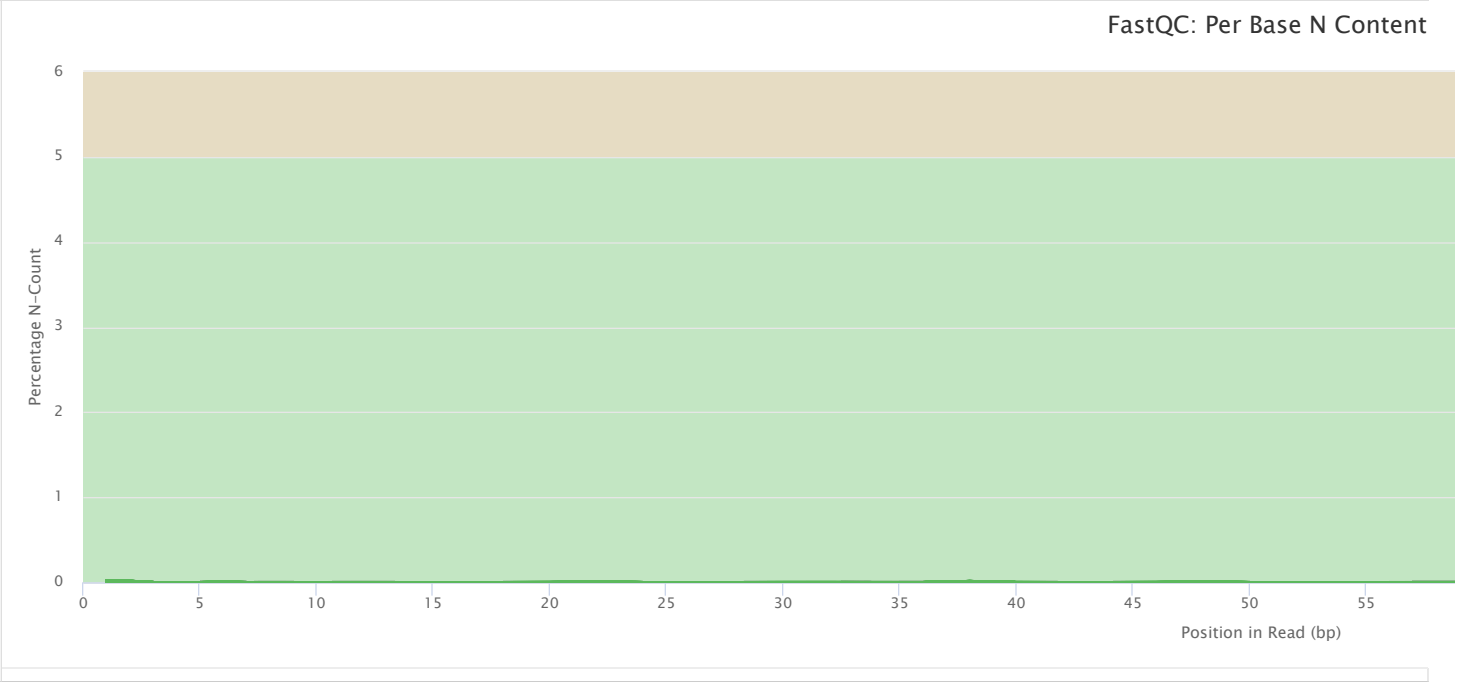
Percentages | Counts



Per Base N Content

48

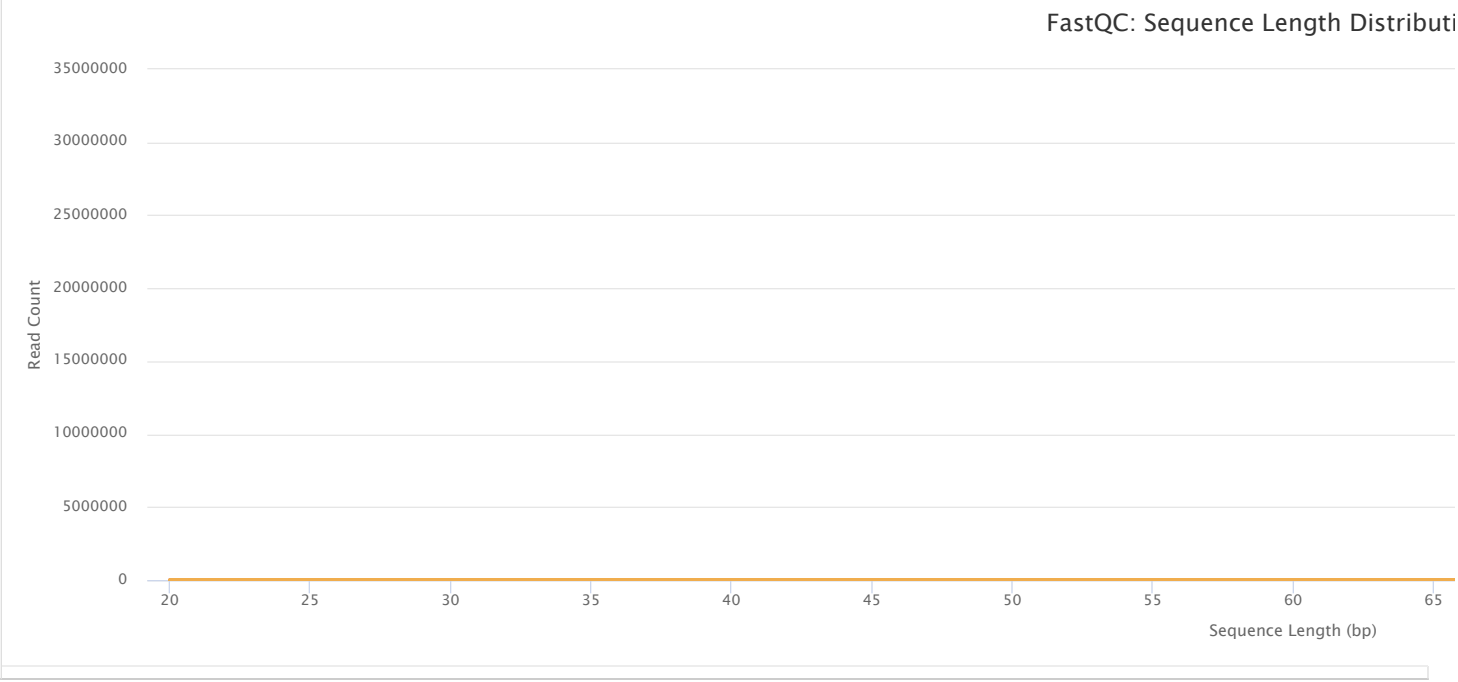
The percentage of base calls at each position for which an `N` was called.



Sequence Length Distribution

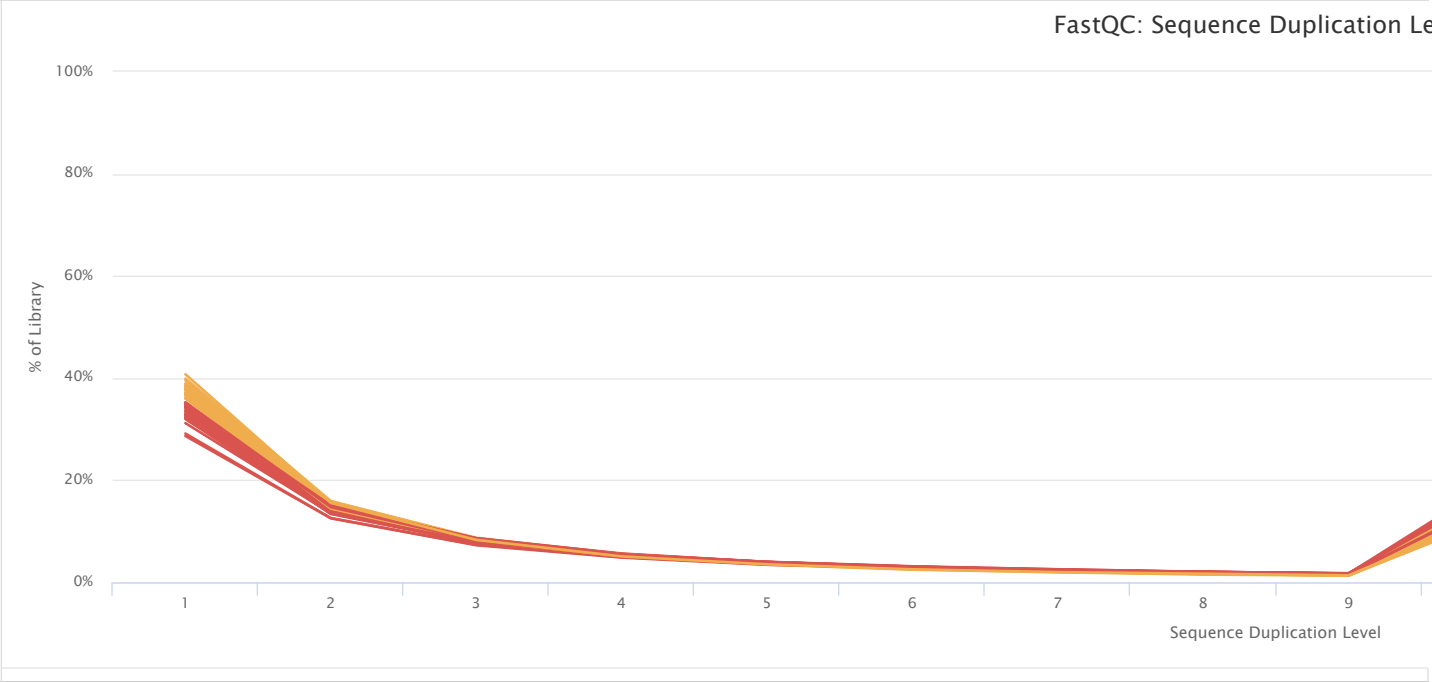
48

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



Sequence Duplication Levels 22

The relative level of duplication found for every sequence.



Overrepresented sequences 48

The total amount of overrepresented sequences found in each library.

48 samples had less than 1% of reads made up of overrepresented sequences

Adapter Content 48

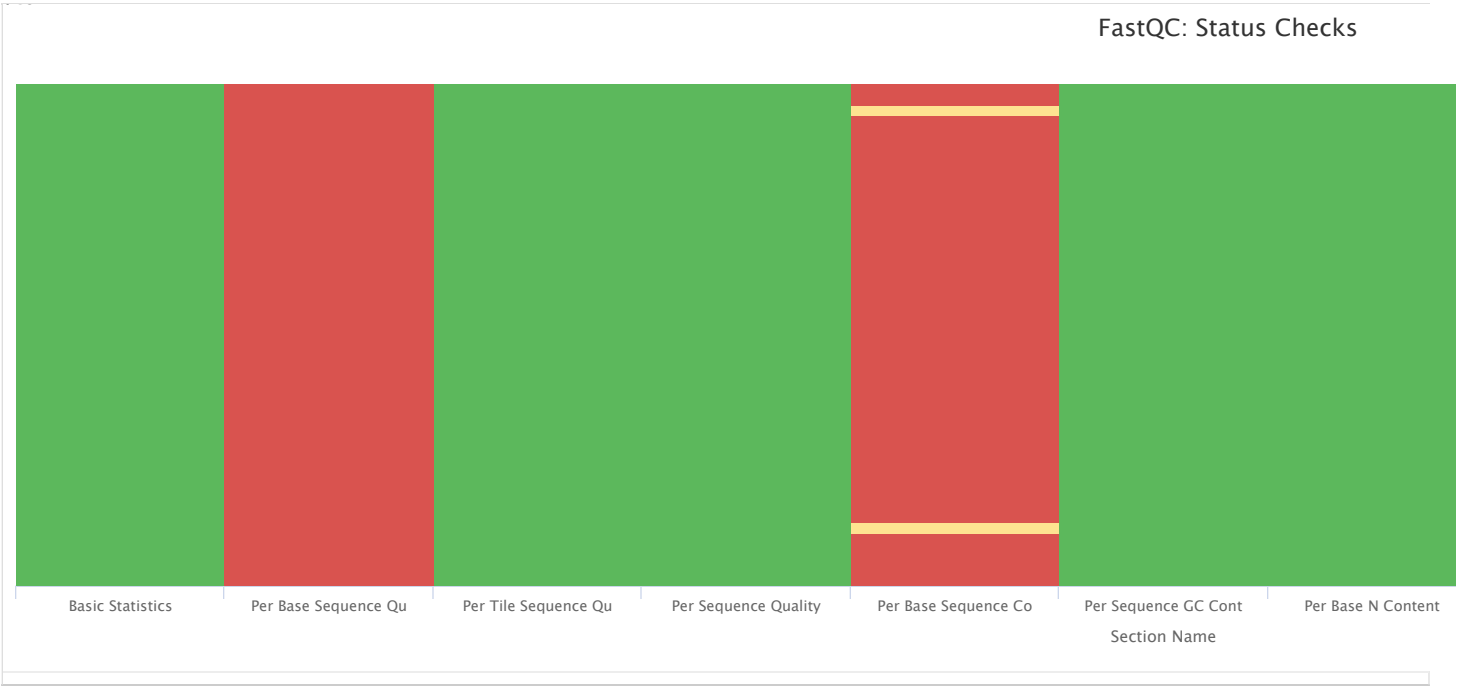
The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

Status Checks

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



nf-core/rnaseq Methods Description

Suggested text and references to use when describing pipeline usage within the methods section of a publication.

Methods

Data was processed using nf-core/rnaseq v3.11.1 (doi: https://doi.org/10.5281/zenodo.1400710) of the nf-core collection of workflows (Ewels *et al.*, 2020).

The pipeline was executed with Nextflow v22.10.6 (Di Tommaso *et al.*, 2017) with the following command:

```
nextflow run /gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/nf-core-rnaseq-3.11.1/workflow -profile singularity -c /gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/gpsc_slurm.conf -w ./work -resume -params-file ./nf-params.json
```

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. https://doi.org/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. https://doi.org/10.1038/s41587-020-0439-x

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 Software Versions

are collected at run time from the software output.

Process Name	Software	Version
CUSTOM_DUMPSOFTWAREVERSIONS	python	3.11.0
	yaml	6.0
CUSTOM_GETCHROMSIZES	getchromsizes	1.16.1
DESEQ2_QC_RSEM	bioconductor-deseq2	1.28.0
	r-base	4.0.3
DUPRADAR	bioconductor-dupradar	1.28.0
	r-base	4.2.1
FASTQC	fastqc	0.11.9
GTF2BED	perl	5.26.2
GTF_GENE_FILTER	python	3.9.5
GUNZIP_FASTA	gunzip	1.10
GUNZIP_GTF	gunzip	1.10
MAKE_TRANSCRIPTS_FASTA	rsem	1.3.1
	star	2.7.10a
MULTIQC_CUSTOM_BIOTYPE	python	3.9.5
PICARD_MARKDUPLICATES	picard	3.0.0
QUALIMAP_RNASEQ	qualimap	2.2.2-dev
RSEM_CALCULATEEXPRESSION	rsem	1.3.1
	star	2.7.10a
RSEM_MERGE_COUNTS	sed	4.7
RSEM_PREPAREREFERENCE_GENOME	rsem	1.3.1
	star	2.7.10a
RSEQC_BAMSTAT	rseqc	3.0.1
RSEQC_INFEREXPERIMENT	rseqc	3.0.1
RSEQC_JUNCTIONANNOTATION	rseqc	3.0.1
RSEQC_JUNCTIONSATURATION	rseqc	3.0.1
RSEQC_READDUPLICATION	rseqc	3.0.1
SAMPLESHEET_CHECK	python	3.9.5
SAMTOOLS_FLAGSTAT	samtools	1.16.1
SAMTOOLS_IDXSTATS	samtools	1.16.1
SAMTOOLS_INDEX	samtools	1.16.1
SAMTOOLS_SORT	samtools	1.16.1
SAMTOOLS_STATS	samtools	1.16.1
SUBREAD_FEATURECOUNTS	subread	2.0.1
TRIMGALORE	cutadapt	3.4
	trimgalore	0.6.7
Workflow	Nextflow	22.10.6
	nf-core/rnaseq	3.11.1

nf-core/rnaseq Workflow Summary

- this information is collected when the pipeline is started.

Core Nextflow options

runName	scruffy_celsius
containerEngine	singularity
launchDir	/gpfs/fs7/aafc/phenocart/nathaniel_rnaseq_temp/Sijan_Fusarium_Results/Cultivar_M/ensembl_pisum
workDir	/gpfs/fs7/aafc/phenocart/nathaniel_rnaseq_temp/Sijan_Fusarium_Results/Cultivar_M/ensembl_pisum/work
projectDir	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/nf-core-rnaseq-3.11.1/workflow
userName	nal000
profile	singularity
configFiles	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/nf-core-rnaseq-3.11.1/workflow/nextflow.config, /gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/gpsc_slurm.conf

Input/output options

input	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/projects/Sijan_Pandit/Pea_Fusarium/mapping_csv/mapping_Cultivar_M.csv
outdir	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/projects/Sijan_Pandit/Pea_Fusarium/results/Cultivar_M/ensembl_pisum/output
multiqc_title	Cultivar_M_Pisum_Ensembl

Reference genome options

fasta	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/reference_genomes/Pisum_sativum_3888/Ensembl/release_56/Pisum_sativum.Pisum_sativum_v1a.dna.to
gtf	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/reference_genomes/Pisum_sativum_3888/Ensembl/release_56/Pisum_sativum.Pisum_sativum_v1a.56.gtf

Read trimming options

extra_trimgalore_args	--nextseq 20

Alignment options

aligner	star_rsem
bam_csi_index	true
seq_center	AAFC-AAC

Process skipping options

skip_bigwig	true
skip_stringtie	true

Institutional config options

custom_config_base	/gpfs/fs7/aafc/pilot/aafc_leth/nathaniel_rnaseq/nf-core-rnaseq-3.11.1/workflow/../configs/

Max job request options

max_memory	192.GB