

# 10 years of multiqc

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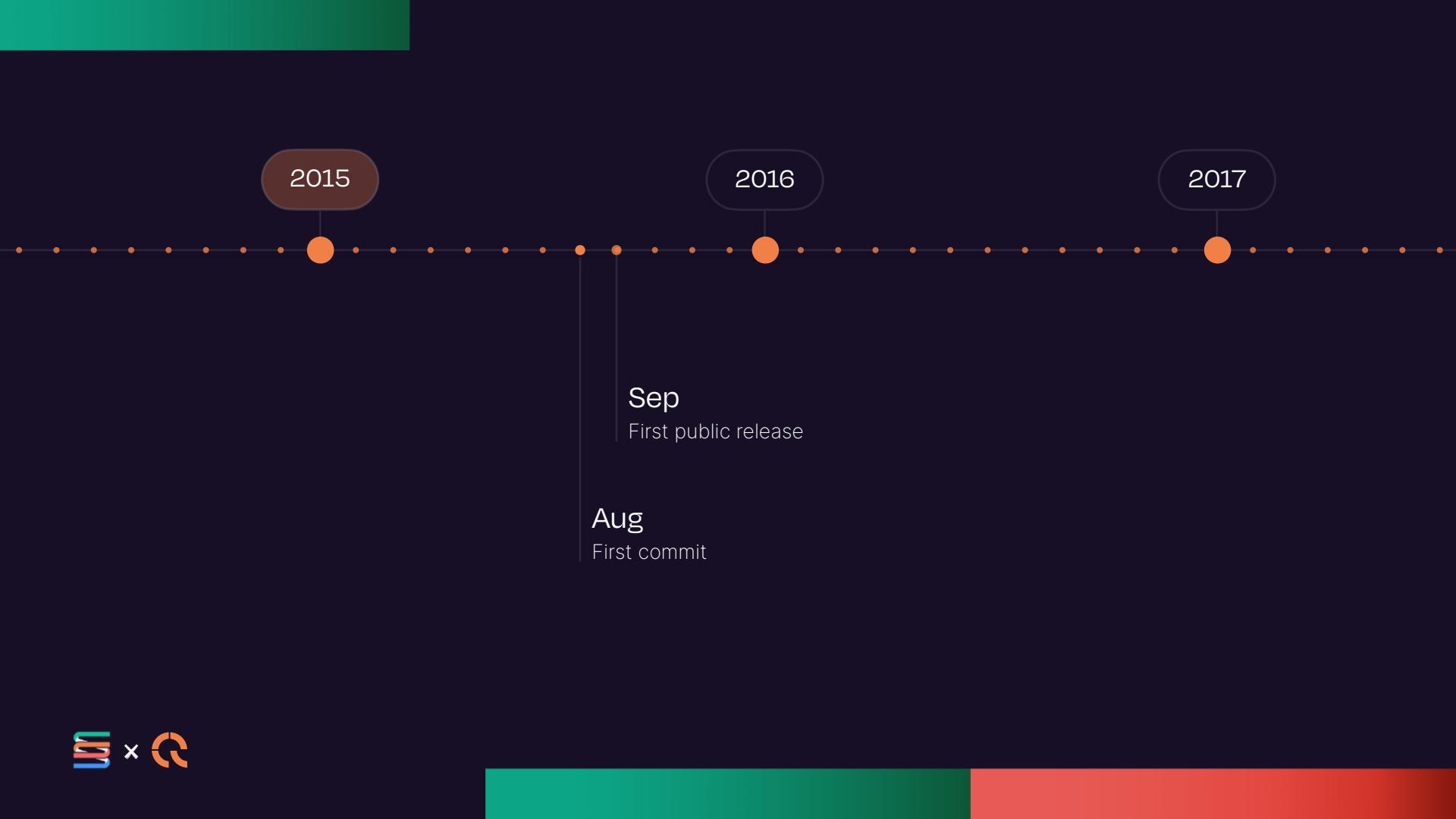
# Celebrating 10 years

How MultiQC became a cornerstone of bioinformatics

1

2 3





2015

2016

2017

Sep

First public release

Aug

First commit



2015

2016

2017

Jul

Published in *Bioinformatics*

Mar

Static image plots



2019

2020

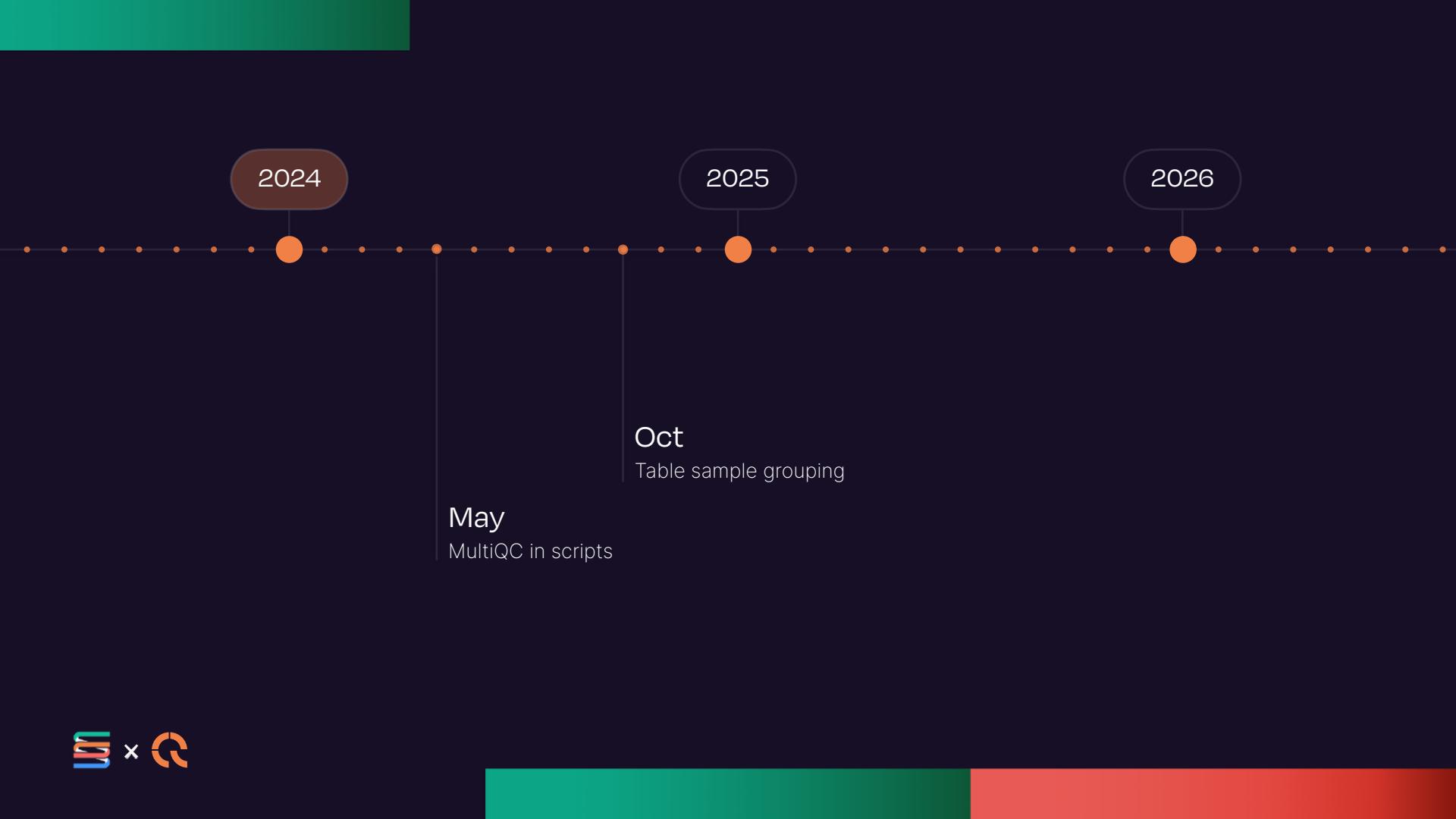
2021

2022

Sep

Support for > 100 tools





2024

2025

2026

May  
MultiQC in scripts

Oct  
Table sample grouping

2024

2025

2026

Jan  
AI Summaries

Oct  
*[insert feature announcement here]*



167

Tools supported

1.5M+

Downloads

7k+

Journal citations

235

Contributors

1,370

GitHub Stars ★

25k+

Daily runs



```
python2.7
1. python2.7
(work) ~/analysis » multiqc .
[INFO]     multiqc : This is MultiQC v0.6.dev0
[INFO]     multiqc : Searching '.'
[INFO]     feature_counts : Found 6 reports
[INFO]     star : Found 6 reports
[INFO]     cutadapt : Found 6 reports
[INFO]     fastq_screen : Found 6 reports
[INFO]     fastqc : Found 6 reports
[INFO]     multiqc : Report      : multiqc_report.html
[INFO]     multiqc : Data       : multiqc_data
[INFO]     multiqc : MultiQC complete
(work) ~/analysis »
```

Recorded  
August 2015

123



# Dark Mode / Themes

Custom colours in a few lines of code 😎

1

2 3



# Dark Mode / Themes



A screenshot of the nf-core/funcscan web interface. The top navigation bar includes the nf-core logo and a search bar. Below the header, a section titled "General Statistics" displays a table and a bar chart comparing two samples. The bar chart shows sample\_1 with a value of 1,930.0 and sample\_2 with a value of 2,666.5. The "Prokka" section shows a bar chart of feature types for sample\_1, with a tooltip indicating 649 (98.0%) for CDS and 1 (0.2%) for RNA.

file:///home/user/multiqc\_report.html  
This page is protected by browser



# Dark Mode / Themes



Bootstrap v5.3



vladsavelyev on Aug 13, 2024

It sounds like it would be a rewrite, rather than an upgrade

# Dark Mode / Themes



Bootstrap v5.3



Vite



# Dark Mode / Themes



MultiQC Report x MultiQC Report x MultiQC Report x +

File /Users/ewels/GitHub/MultiQC/website/public/examples/rna-seq/multiqc\_original.html/multiqc\_report.html

multic v1.31

**multic**

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

Report generated on 2025-10-21, 10:57 CEST based on data in: /Users/ewels/GitHub/MultiQC/website/public/examples/rna-seq

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

**Report AI Summary**

- All samples show good alignment rates (82-98%), but high duplication rates (57-81%) across all samples
- SRR3192398 and SRR3192399 have lower assignment rates (~51%) compared to other samples (56-73%)

Provider: Segera AI, model: claude-sonnet-4-0 Chat with Segera AI

**General Statistics**

Copy table Configure columns Scatter plot Violin plot Export as CSV... Showing 8/8 rows and 7/15 columns. + Summarize table

Sample Name	Assigned	Aligned	Uniq aligned	Trimmed bases	Dups	GC	Sqs
SRR3192396	67.5%	97.2%	93.7%	3.2%	75.9%	50.5%	208.8M
SRR3192397	66.6%	98.1%	94.7%	2.8%	74.7%	48.5%	183.9M
SRR3192398	50.9%	95.9%	88.2%	5.0%	57.6%	47.0%	133.1M
SRR3192399	52.3%	96.3%	88.2%	5.0%	59.3%	47.0%	148.7M
SRR3192400	70.3%	83.1%	77.3%	6.2%	75.1%	45.0%	189.9M
SRR3192401	71.2%	82.2%	76.4%	6.2%	75.9%	45.0%	190.5M
SRR3192657	73.1%	94.1%	91.2%	2.5%	81.4%	50.5%	186.3M
SRR3192658	71.2%	92.5%	89.7%	2.8%	81.4%	52.0%	194.1M

**featureCounts**

Counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations. URL: <http://subread.sourceforge.net> DOI: 10.1093/bioinformatics/btt656

**Assignments**

Percentages + Summarize plot Export...

**featureCounts: Assignments**  
8 bars

Legend:

- Assigned (blue)
- Unassigned: Ambiguity (dark blue)
- Unassigned: Multi Mapping (green)
- Unassigned: No Features (orange)

MultiQC Report MultiQC Report MultiQC Report

File /Users/ewels/GitHub/MultiQC/website/public/examples/rna-seq/multiqc\_report.html#star

**multic** v1.30.dev0

General Stats

featureCounts

STAR

Summary Statistics

Alignment Scores

Cutadapt

Filtered Reads

Trimmed Sequence Lengths (3')

FastQC: trimmed

Sequence Counts

Sequence Quality Histograms

Per Sequence Quality Scores

Per Base Sequence Content

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences by sample

Top overrepresented sequences

Adapter Content

Status Checks

FastQC: raw

Sequence Counts

Sequence Quality Histograms

Per Sequence Quality Scores

Per Base Sequence Content

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences by sample

**multic** v1.30.dev0

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

Report generated on 2025-10-21, 11:29 CEST based on data in: /Users/ewels/GitHub/MultiQC/website/public/examples/rna-seq

Welcome! Not sure where to start? Watch a tutorial video (6:06)

don't show again

**Report AI Summary**

- All samples show good alignment rates (82-98%), but high duplication levels (55-82%) across all samples
- SRR3192398 and SRR3192399 show lower assignment rates (~51%) compared to other samples (66-73%)

More details...

Provider: Seqera AI, model: claude-3-5-sonnet-latest Chat with Seqera AI

**General Statistics**

Copy table Configure columns Scatter plot Violin plot Export as CSV... Showing 8/8 rows and 7/15 columns. + Summarize table

Sample Name	Assigned	Aligned	Uniq aligned	Trimmed bases	Dups	GC	Seqs
SRR3192396	87.5%	97.2%	93.7%	3.2%	75.9%	50.5%	208.8 M
SRR3192397	66.6%	98.1%	94.7%	2.8%	74.7%	48.5%	183.9 M
SRR3192398	50.9%	95.9%	88.2%	5.0%	57.6%	47.0%	133.1 M
SRR3192399	52.3%	96.3%	88.2%	5.0%	59.3%	47.0%	148.7 M
SRR3192400	70.3%	83.1%	77.3%	6.2%	75.1%	45.0%	189.9 M
SRR3192401	71.2%	62.2%	76.4%	6.2%	75.9%	45.0%	190.5 M
SRR3192657	73.1%	94.1%	91.2%	2.5%	81.4%	50.5%	186.3 M
SRR3192668	71.2%	92.5%	89.7%	2.8%	81.4%	52.0%	194.1 M

**featureCounts**

Counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations. <http://subread.sourceforge.net> DOI: 10.1093/bioinformatics/btt856

**Assignments**

Percentages + Summarize plot + Export...

**featureCounts: Assignments**  
8 samples

Assigned  
Unassigned: Ambiguity  
Unassigned: Multi Mapping  
Unassigned: No Features

file:///Users/ewels/GitHub/MultiQC/website/public/examples/rna-seq/multiqc\_report.html#general\_stats

MultiQC Report | MultiQC Report | MultiQC Report

File / Users/ewels/GitHub/MultiQC/website/public/examples/na-seq/disco/multiqc\_report.html#

**multic** VERSION 0.10.0

**GENERAL STATS**

**FEATURE COUNTS**

**STAR**

SUMMARY STATISTICS  
ALIGNMENT SCORES  
CUTADAPT  
FILTERED READS  
TRIMMED SEQUENCE LENGTHS (3)  
FASTQC: TRIMMED  
SEQUENCE COUNTS  
SEQUENCE QUALITY HISTOGRAMS  
PER-BASE SEQUENCE QUALITY SCORES  
PER-BASE SEQUENCE CONTENT  
PER-BASE SEQUENCE GC CONTENT  
PER-BASE N CONTENT  
SEQUENCE LENGTH DISTRIBUTION  
SEQUENCE DUPLICATION LEVELS  
OVERREPRESENTED SEQUENCES IN SAMPLE  
TOP OVERREPRESENTED SEQUENCES  
ADAPTER CONTENT  
STATUS CHECKS

**FASTQC RAW**

SEQUENCE COUNTS  
SEQUENCE QUALITY HISTOGRAMS  
PER-BASE SEQUENCE QUALITY SCORES  
PER-BASE SEQUENCE CONTENT  
PER-BASE SEQUENCE GC CONTENT  
PER-BASE N CONTENT

**multic**

A MODULAR TOOL TO AGGREGATE RESULTS FROM BIOINFORMATICS ANALYSES ACROSS MANY SAMPLES INTO A SINGLE REPORT.

REPORT GENERATED ON 2025-10-21, 11:28 CEST BASED ON DATA IN: /Users/ewels/GitHub/MultiQC/website/public/examples/na-seq/disco/multiqc\_report.html#

WELCOME! NOT SURE WHERE TO START? [WATCH A TUTORIAL VIDEO](#) (6:26) [DON'T SHOW AGAIN](#)

**REPORT AI SUMMARY**

- ALL SAMPLES SHOW GOOD ALIGNMENT RATES (82-98%), BUT HIGH DUPLICATION LEVELS (57-82%) ACROSS ALL SAMPLES
- SRR3191396 AND SRR3191397 HAVE LOWER ALIGNMENT RATES (~5%) COMPARED TO OTHER SAMPLES (66-93%)

[MORE DETAILS](#)

PROVIDER: SERENA, MODEL: CLAUDE-3-15-SONNET-LATEST [CHAT WITH SERENA AI](#)

**GENERAL STATISTICS**

[COPY TABLE](#) [CONFIGURE COLUMNS](#) [SCATTER PLOT](#) [VIOLIN PLOT](#) [EXPORT AS CSV](#) Showing 9/16 rows and 9/16 columns [+ SUMMARIZE TABLE](#)

SAMPLE NAME	ASSIGNED	ALIGNED	UNIQUE ALIGNED	TRIMMED TRACES	DUPS	GC	SEQS
SRR3191396	67.5%	97.2%	93.9%	3.2%	75.9%	50.5%	2088M
SRR3191397	66.6%	98.1%	97.9%	2.8%	74.7%	48.5%	1839M
SRR3191398	50.9%	95.9%	88.2%	5.0%	57.6%	47.0%	133.1M
SRR3191399	52.0%	96.3%	88.2%	5.0%	59.9%	47.0%	148.7M
SRR3191400	70.3%	83.1%	77.3%	6.2%	75.1%	45.0%	189.9M
SRR3191401	71.2%	82.2%	76.4%	6.2%	75.9%	45.0%	192.5M
SRR3191657	73.1%	94.1%	91.2%	2.5%	81.4%	50.5%	186.3M
SRR3191658	71.2%	92.5%	89.9%	2.8%	81.4%	52.0%	194.1M

**FEATURE COUNTS**

COUNTS MAPPED READS FOR GENOMIC FEATURES SUCH AS GENES, EXONS, PROMOTER, GENE BODY, GENOMIC TRINIS AND CHROMOSOMAL LOCATIONS [HTTP://SRA.readthedocs.io/en/latest/FORMATS/MTB656](http://SRA.readthedocs.io/en/latest/FORMATS/MTB656)

**ASSIGNMENTS**

[PERCENTAGES](#) [SCATTER PLOT](#) [EXPORT](#) [+ SUMMARIZE TABLE](#)

FEATURE COUNTS: ASSIGNMENTS 8 SAMPLES

Legend: Assigned (blue), Unassigned: Ambiguity (black), Unassigned: Multi Mapping (green), Unassigned: No Features (orange)

♀ \_colors.scss ×

```
multiqc > templates > disco > src > scss > ♀ _colors.scss > ...
1  $body-bg: #833ab4;
2
3  $font-family-base: "Rock Salt", cursive;
4
5  $primary: #7300ff;
6  $secondary: #00ff0d;
7
8  $body-primary-bg: #f00;
9  $body-secondary-bg: #00f;
10 $body-tertiary-bg: #e1ff00;
11 $info: #3300aa;
12
```

♀ custom.scss ×

```
multiqc > templates > disco > src > scss > ♀ custom.scss > ...
1  @import "https://fonts.googleapis.com/css2?family=Rock+Salt&d
2
3  body {
4    background: linear-gradient(
5      90deg,
6      #13182b 0%,
7      #2a2a2a 50%,
8      #3a3a3a 100%
9    );
10 }
11 .side-nav-wrapper {
12   background: linear-gradient(
13     0deg,
14     #3493c4 0%,
15     #2a2a2a 100%
16   );
17 }
18
```



Dark mode



Reduced report file size by 50%



Simple custom colour themes

1

2

3

# Thanks

Phil Ewels <[phil.ewels@seqera.io](mailto:phil.ewels@seqera.io)>



Vlad Savelyev  
(Astra Zeneca)

[vladsavelyev](#)

1,036 commits 391,617 ++ 113,728 --