Nextflow Summit
by seqera

10 years of multiqc

Phil Ewels

Product Manager for OSS, Seqera

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

Mar

Static image plots

Jul

Published in *Bioinformatics*

2019

2020

2021

202

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

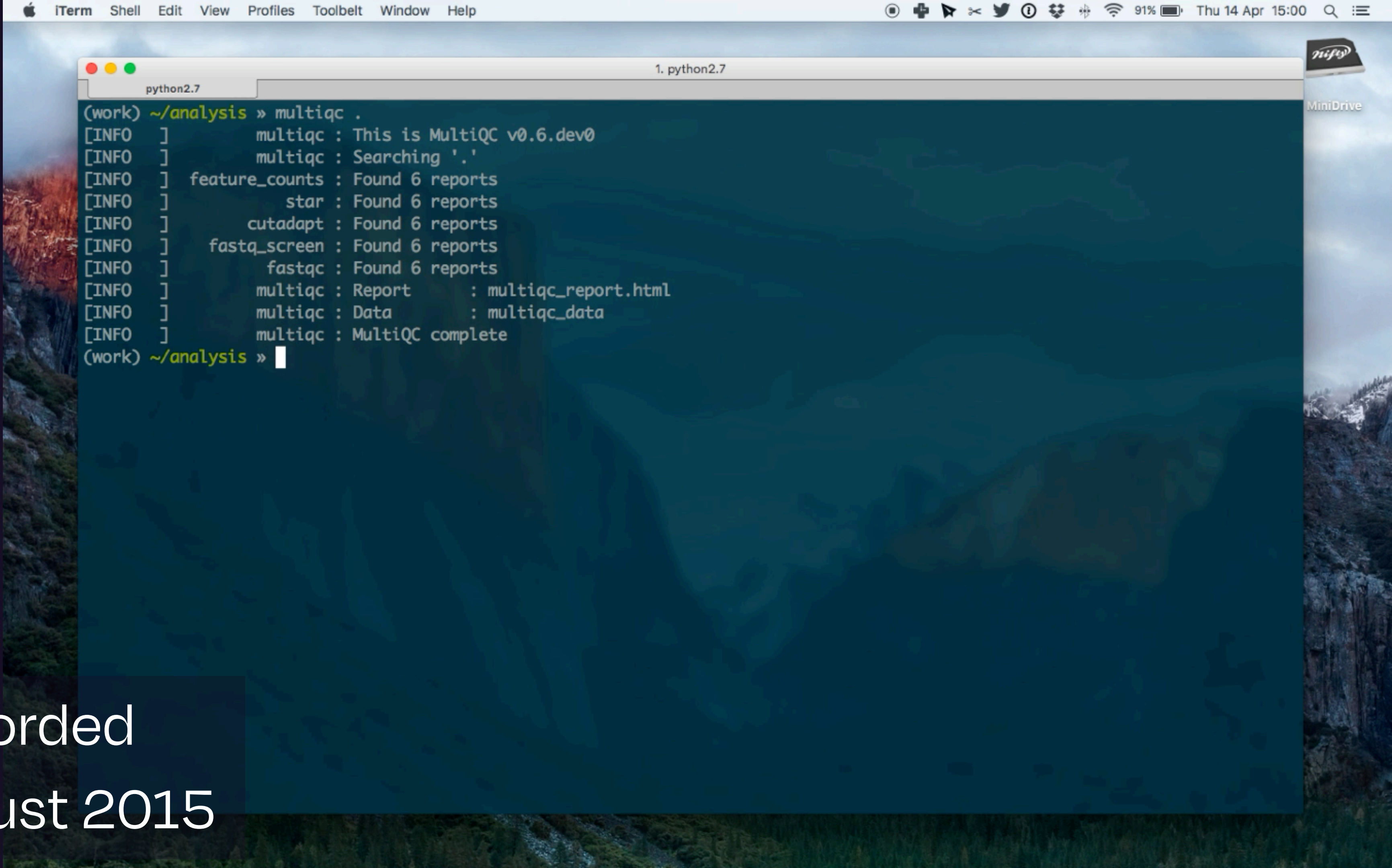
1.5M+
Downloads

7k+
Journal citations

235
Contributors

1,370
GitHub Stars ★

25k+
Daily runs



```
(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

1 2 3

Dark Mode / Themes

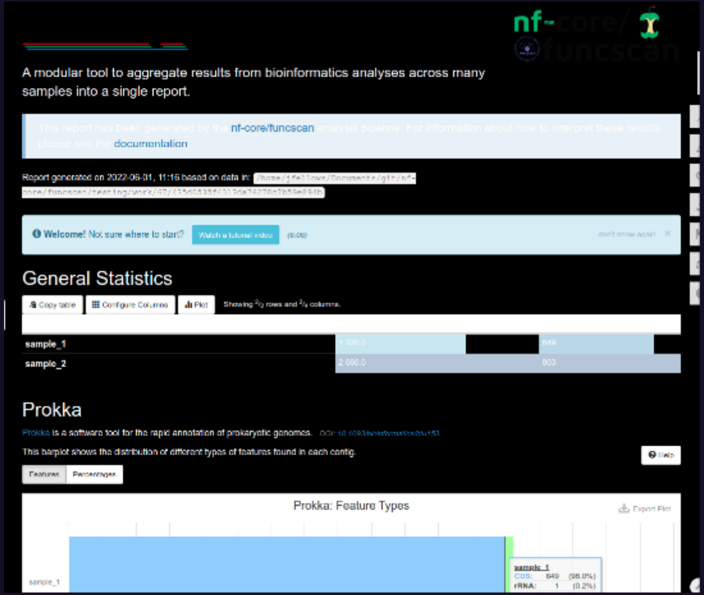
`Custom colours in a few lines of code` 😎

1

2

3

Dark Mode / Themes



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/funcscan analysis pipeline. For information about how to interpret these results, please see the documentation

Report generated on 2022-06-01, 11:16 based on data in: `/home/jfellows/Documents/git/nf-core/funcscan/testing/work/47/[illegible]`

General Statistics

Showing $^2/_2$ rows and $^2/_4$ columns.

sample_1	1 320.0	849
sample_2	2 080.0	803

Prokka

Prokka is a software tool for the rapid annotation of prokaryotic genomes.

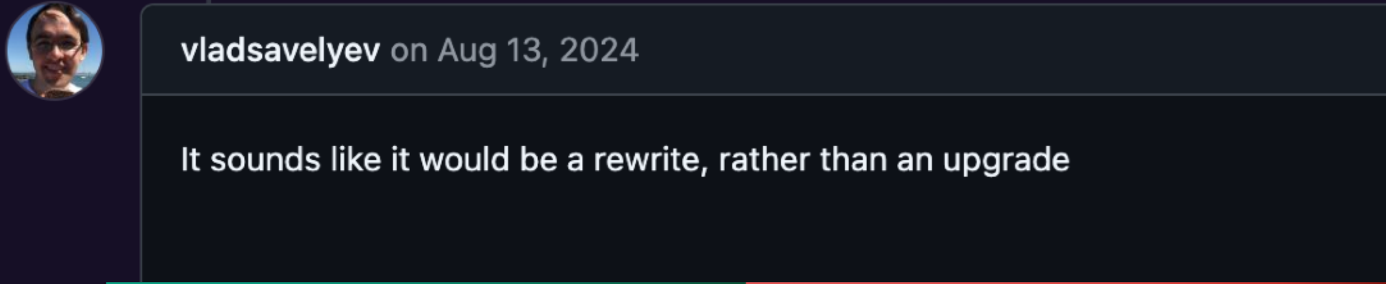
This barplot shows the distribution of different types of features found in each contig.

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

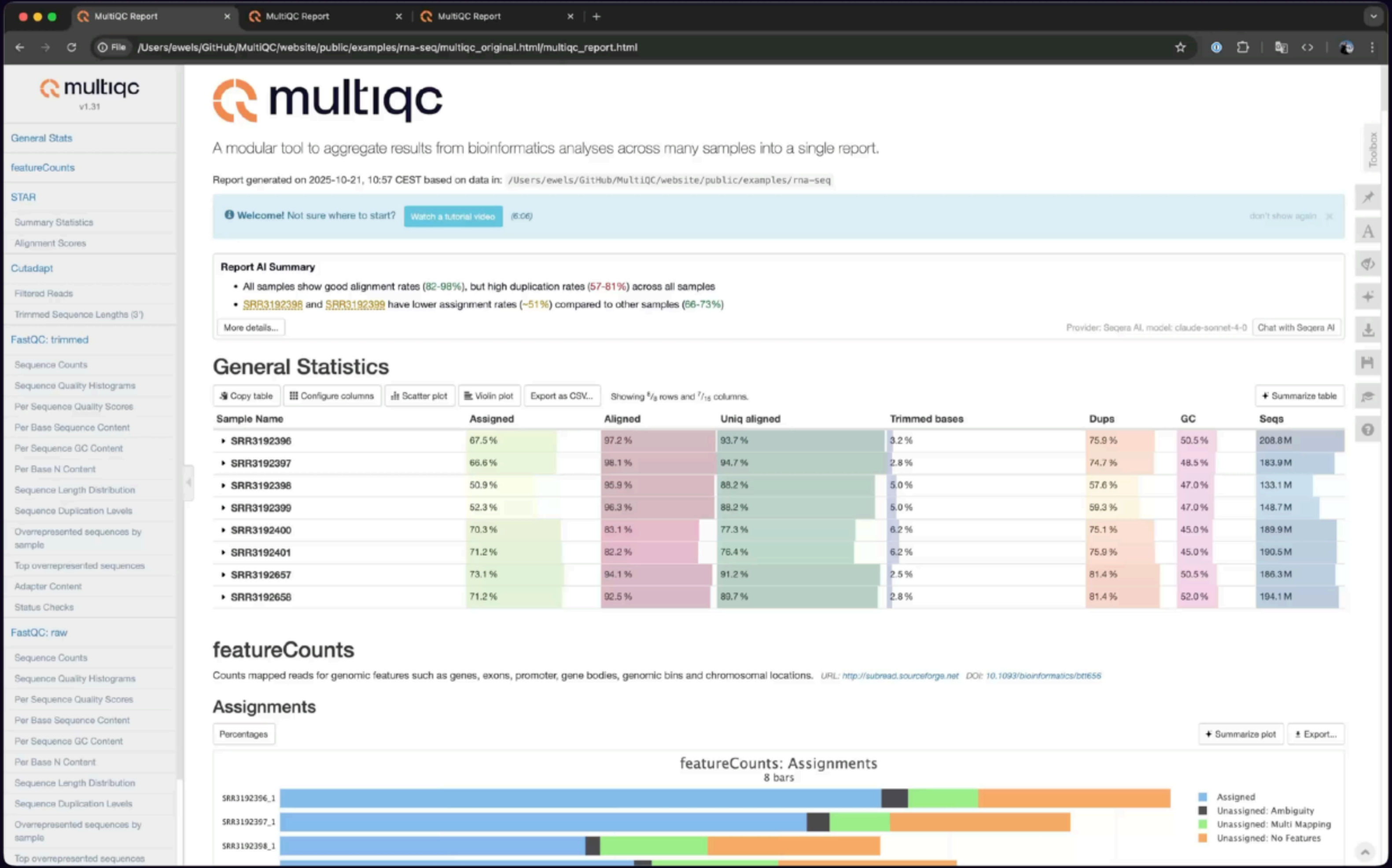
Bootstrap v5.3

Vite

Dark Mode / Themes

`multiqc.min.js`

`multiqc.min.css`



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? (6:06)

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 (66-73%)

Provider: Seqera AI, model: claude-sonnet-4-0

General Statistics

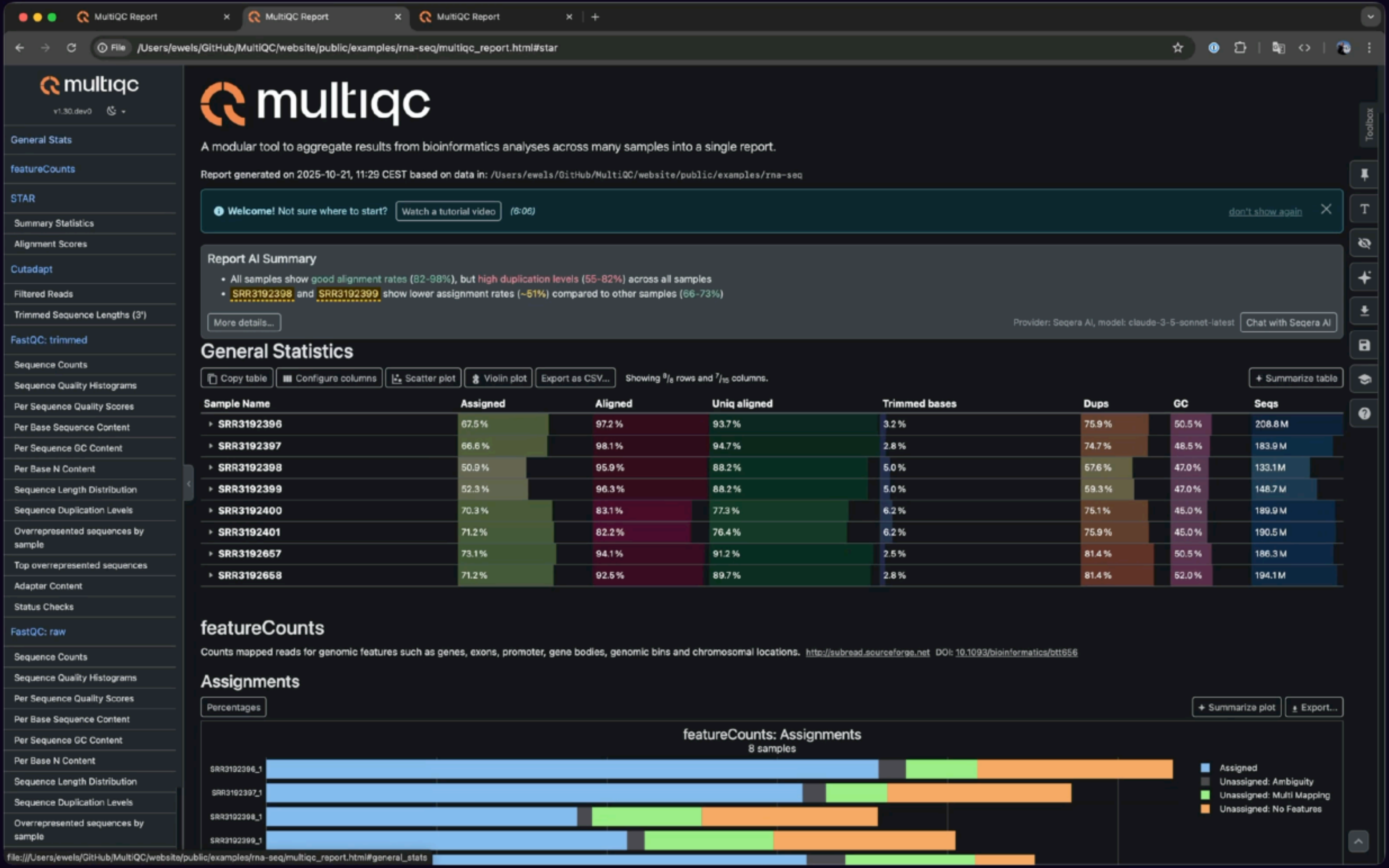
Showing 8/8 rows and 7/15 columns.

Sample Name	Assigned	Aligned	Uniq aligned	Trimmed bases	Dups	GC	Seqs
SRR3192396	67.5 %	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 %	82.2 %	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
SRR3192658	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. *URL: http://subread.sourceforge.net DOI: 10.1093/bioinformatics/btt656*

Assignments



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?

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%)

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

General Statistics

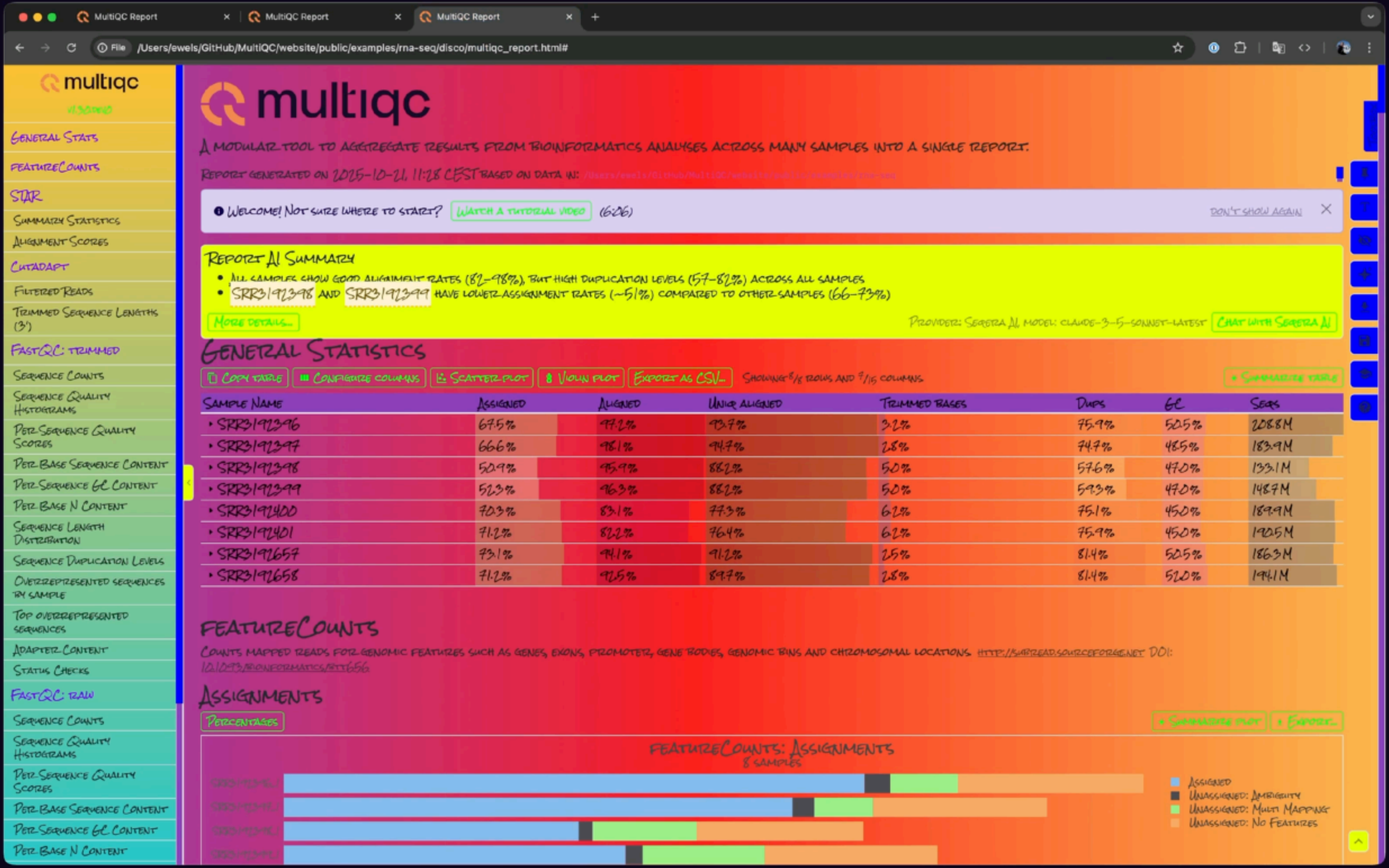
Showing 8/8 rows and 7/15 columns.

Sample Name	Assigned	Aligned	Uniq aligned	Trimmed bases	Dups	GC	Seqs
SRR3192396	67.5 %	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 %	82.2 %	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
SRR3192658	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/btt656

Assignments



multiqc

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/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 (57–82%) across all samples
- SRR3192398 and SRR3192399 have 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

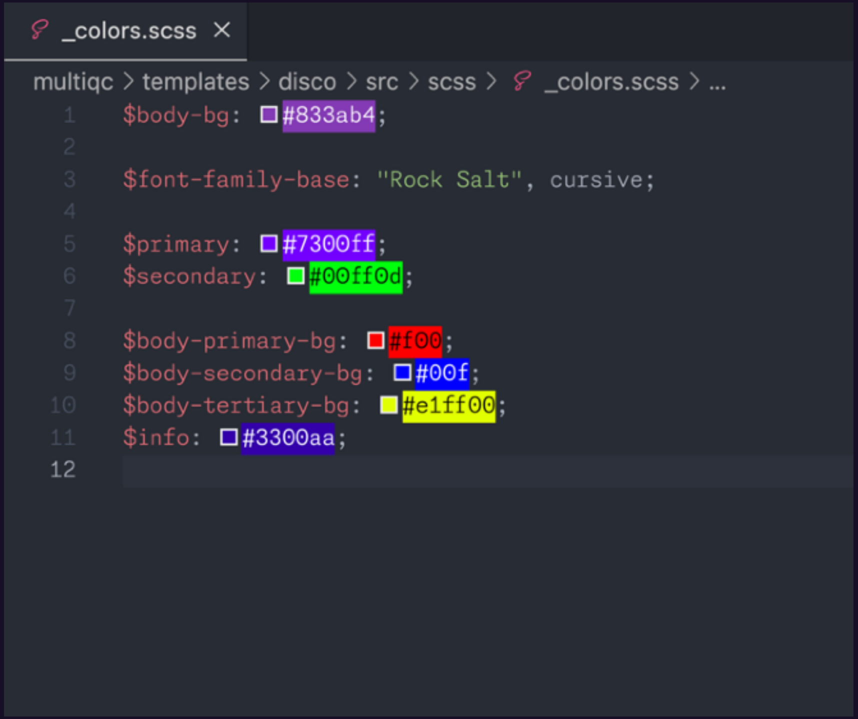
Copy table Configure columns Scatter plot Violin plot Export as CSV... Showing 8/8 rows and 7/15 columns. Summarize table

Sample Name	Assigned	Aligned	Uniq aligned	Trimmed Bases	Dups	GC	Seqs
SRR3192396	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. http://subread.sourceforge.net DOI: 10.1093/bioinformatics/btt656

Assignments



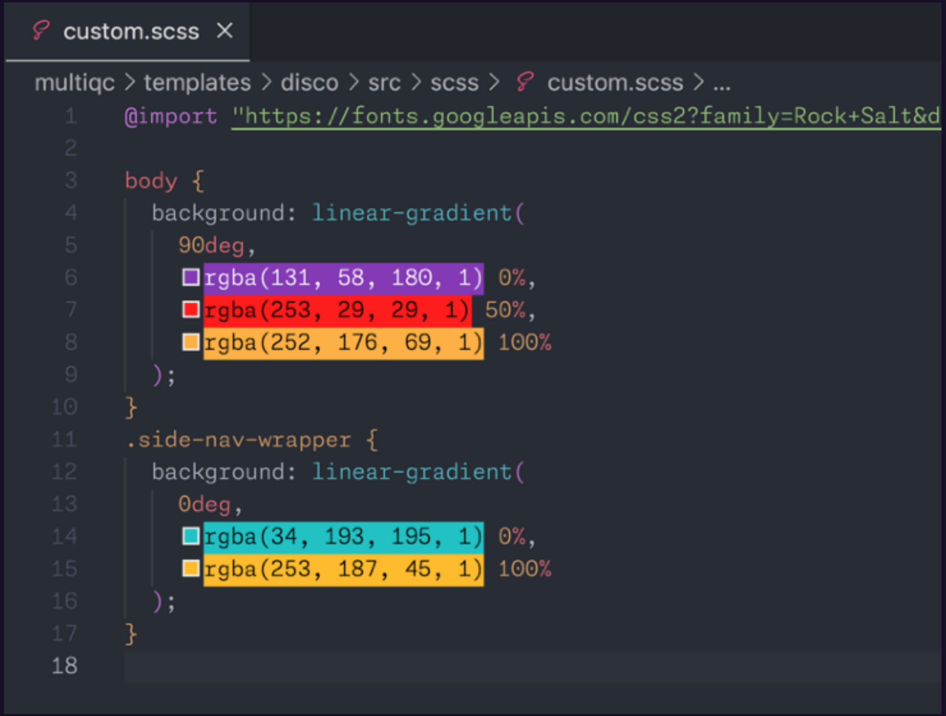
```scss
$body-bg: #833ab4;

$font-family-base: "Rock Salt", cursive;

$primary: #7300ff;
$secondary: #00ff0d;

$body-primary-bg: #f00;
$body-secondary-bg: #00f;
$body-tertiary-bg: #e1ff00;
$info: #3300aa;

```



```scss
@import "https://fonts.googleapis.com/css2?family=Rock+Salt&d

body {
  background: linear-gradient(
    90deg,
    rgba(131, 58, 180, 1) 0%,
    rgba(253, 29, 29, 1) 50%,
    rgba(252, 176, 69, 1) 100%
  );
}
.side-nav-wrapper {
  background: linear-gradient(
    0deg,
    rgba(34, 193, 195, 1) 0%,
    rgba(253, 187, 45, 1) 100%
  );
}

```

Dark mode

Reduced report file size by 50%

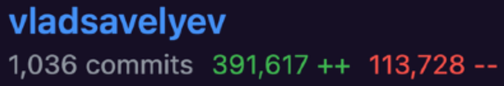
Simple custom colour themes

Thanks

Phil Ewels <phil.ewels@seqera.io>

Vlad Savelyev

(Astra Zeneca)



vladsavelyev

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

1 2 3