
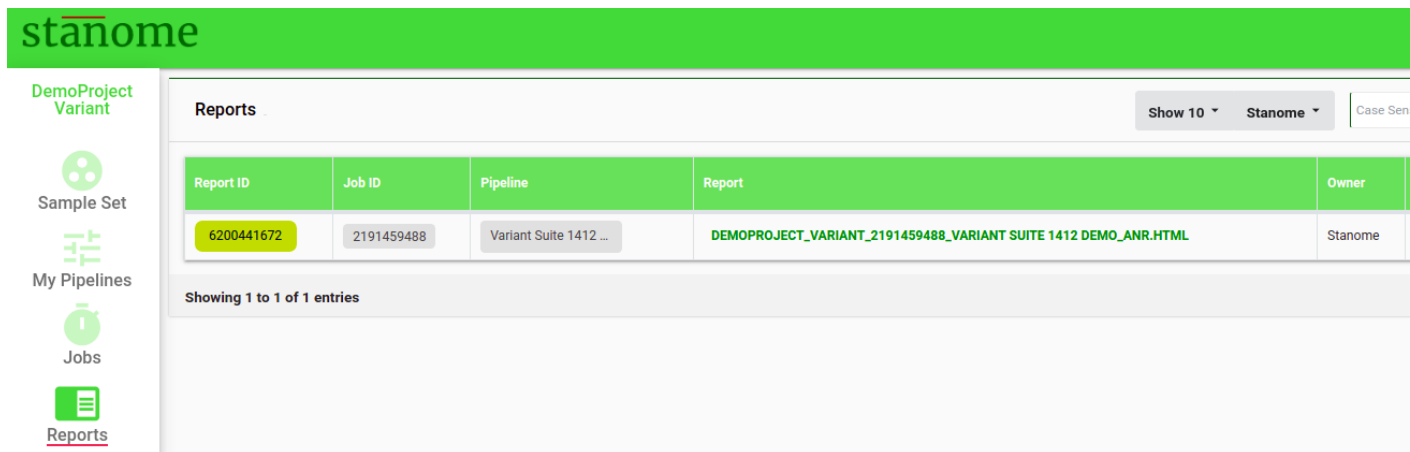


# Overview

Each pipeline execution generates an HTML report. The final report and other files can be accessed through the Reports window  (Fig.). Reports can also be accessed through the ReportID on the job details page.



The screenshot shows the Stanome web interface. On the left is a sidebar with navigation icons for DemoProject Variant, Sample Set, My Pipelines, Jobs, and Reports (which is highlighted with a red underline). The main content area is titled 'Reports' and includes a table with the following data:

Report ID	Job ID	Pipeline	Report	Owner
6200441672	2191459488	Variant Suite 1412 ...	DEMOPROJECT_VARIANT_2191459488_VARIANT SUITE 1412 DEMO_ANR.HTML	Stanome

Below the table, it says 'Showing 1 to 1 of 1 entries'.

- Click **Report ID** to access intermediate files from a few important steps in the pipeline.
- Click the **PREFIX\_ANR.HTML** to access the final downloadable report. Default: NO REPORT AVAILABLE.

Reports are generated dynamically based on the analysis type and each report is divided into sections based on the tools used in the pipeline. The first two sections are generated for all the jobs to provide the job overview: analysis summary and sample quality.

- **Analysis Summary:**

This section consolidates the information related to the job: project, samples, and the experiment in four sub-sections:

- Project Details: This shows the information provided during the project creation and the pipeline details.
- Run Summary: Displays the job status, runtimes, and the files used for the analysis: reference, annotation or metadata files, and the samples.
- Tools: A brief summary of the tools, versions, descriptions, and citations is shown.

- Commands: A complete list of the commands used in the pipeline.

- **Sample Quality:**

Details of sample (sequencing) quality are provided in this section. It has two sub-sections:

- Metrics Table: This shows the sequence quality details of each sample in a tabular format.
- Sample Quality Plot: The average quality scores (Phred scale) of all the reads in a sample are displayed in a 96-Well plate format, each circle representing a sample. The higher the score, the better, and scores above 30 are generally considered good for the majority of the applications. Average scores are calculated using all the reads in a sample with the FastQC tool. The 96-Well plate format helps to visualize the low-quality samples, plate effects, and pooling errors easily.

The remaining sections are dynamically generated based on the pipeline type and the tools used. Two sample reports are provided below to understand the features of each report.

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