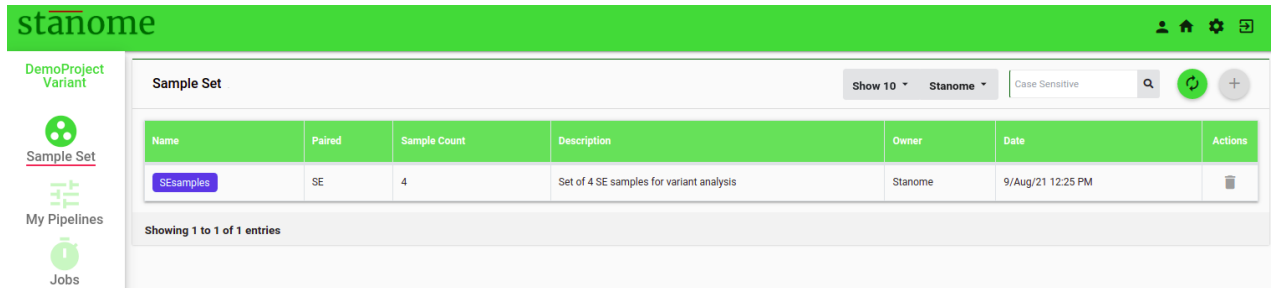

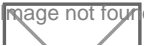



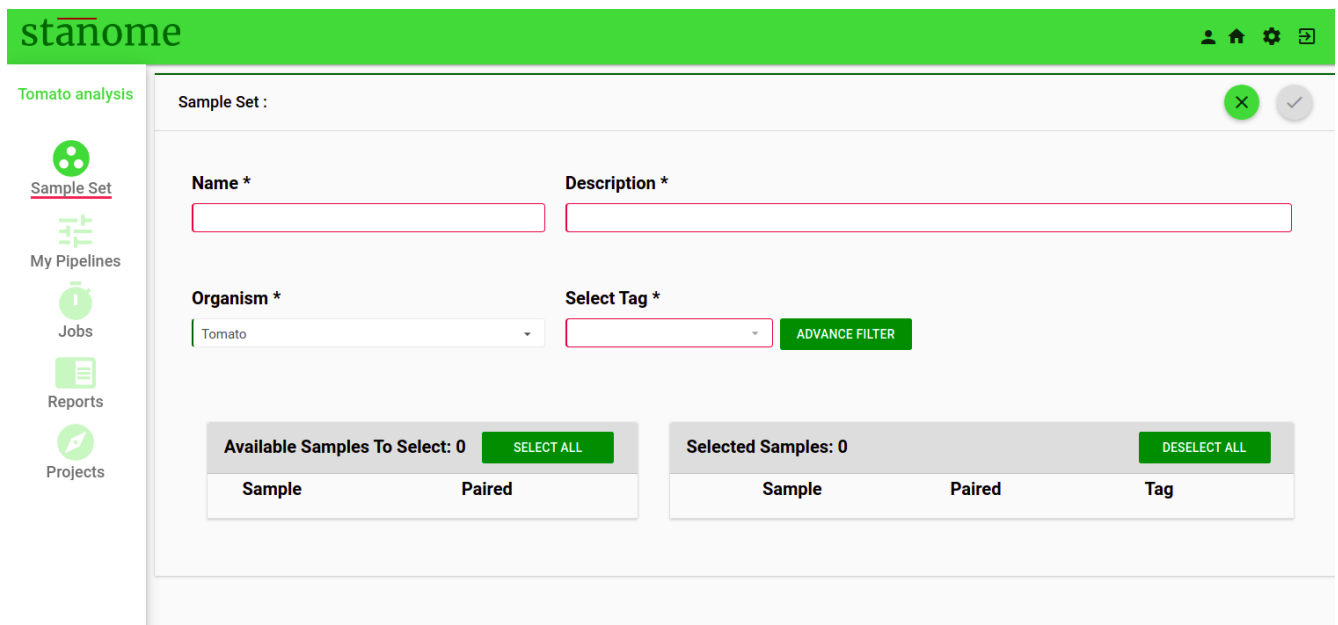
# SAMPLE SET MANAGEMENT

**Sample Set** is a group of sequence files that belong to an experiment and can be analyzed together. **Sample Set** window allows new sample set creation and provides a list view of the existing **Sample Sets** within a project (Fig. 1).



## Sample Set Creation

**Sample Set** can be created by selecting the samples available in the . Click  from the **Project Main** window or click  on the **Sample Set** window to create a new **Sample Set** (Fig. 2).



Fill in the following details on the **Sample Set** creation window:

- **Name\*** - Provide a unique name for the **Sample Set**.



Only alphanumeric characters and spaces are allowed.



**Sample Set** names are helpful while executing the pipelines.

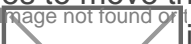
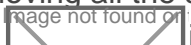
**CAUTION - Names shouldn't be reused.**

- **Description\*** - Provide a description for the **Sample Set** that can be included in the final report (Example: experiment type).
- **Organism** - Select organism name from the drop-down list.



Samples from different organisms can be selected to form a single sample set

**CAUTION - Unless intended, samples from multiple organisms in a sample set are not recommended.**

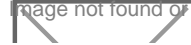
- **Select Tag** - Using the tags given during sample upload samples can be filtered. A list of samples uploaded under the corresponding tag would appear in the table on the left. Click on the samples to move them to the selected samples table and to add to the sample set (Fig. 2).  icon allows moving all the samples listed under the selected tag to the selected samples table.  icons allow deselection of the selected samples (Fig. 2).



Samples from different tags can be selected to create one sample set.


**CAUTION - Select either SE or PE samples only. The platform doesn't allow mixed selection.**

## Sample Filter


Click on the  to filter samples based on the sample quality. Six filters are supported.

1. **The total number of reads:** This shows the samples with the total number of reads greater than the number entered.
2. **Number of poor quality reads:** This shows the samples which contain, number of poor quality reads less than the number entered. The quality of reads is determined by the fastqc tool.
3. **Sequence length:** Shows the samples with reads whose sequence length ranges the number entered.

4. **Per base sequence quality:** Shows the samples with reads per base sequence quality tagged as Pass/Fail/Warn.
5. **Sequence length distribution:** This shows the samples with reads sequence length distribution tagged as Pass/Fail/Warn.
6. **Adapter content:** Shows the samples with read adapter content tagged as Pass/Fail/Warn.

Click  on the upper right corner of the window to save the **Sample Set**. Multiple sample sets can be created under one project with different sequence files.

## Sample Set Deletion

A sample set can be deleted by clicking  icon on the **Sample Set** window. This action deletes the sample set only, however, the samples are still available in the **Sequence Data** for future usage.

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Revision #5

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