

# Pipeline Execution

Once a pipeline is successfully created and validated within a project, it's ready for execution. A newly created pipeline is shown in Fig. 1.

**stanome**

DemoProject  
Variant

Sample Set

**My Pipelines**

Jobs

Reports

Projects

My Pipelines : 5708635328 , Variant Suite 1412 Demo

← ↻ INITIALIZE PIPELINE

**Name \***  
Variant Suite 1412 Demo

**Hub**  
Variant

**Description \***  
Data cleaning, alignment of reads to the reference, merge samples, and jointly call genotypes.

**Execution Flow \***  
Data Cleaning -> Alignment -> Merge -> VariantCalling

**Category**  
Genotyping

**Date \***  
9/Aug/21 12:28 PM

**Details**  
An optimized pipeline for joint genotyping from the targeted sequencing data. Sequencing reads are aligned to the reference genome with Bowtie2 and the aligned BAM files are merged to facilitate the joint genotyping of all samples. The SNP and INDEL variants, defined in the target file, are called by splitting them for parallel executions of FreeBayes.  
Input data:  
Reference genome (Fasta)  
Targeted sequencing data (Fastq)  
Targets file (BED)  
Regions file (optional for genome browser)

▼ Pipeline Steps

Step	Name	Tool	Command	Predecessor	Merge	Input Source	Actions
1	DataCleaning	Trimmomatic	Trimmomatic	NA	No	Data Store	↻

- The following actions are allowed on the **Pipeline** window: view/delete/edit/initialize.


-  **Pipeline** deletion

-  **Pipeline** edit

-  Page refresh

-  Back navigation



 Pipeline initialization

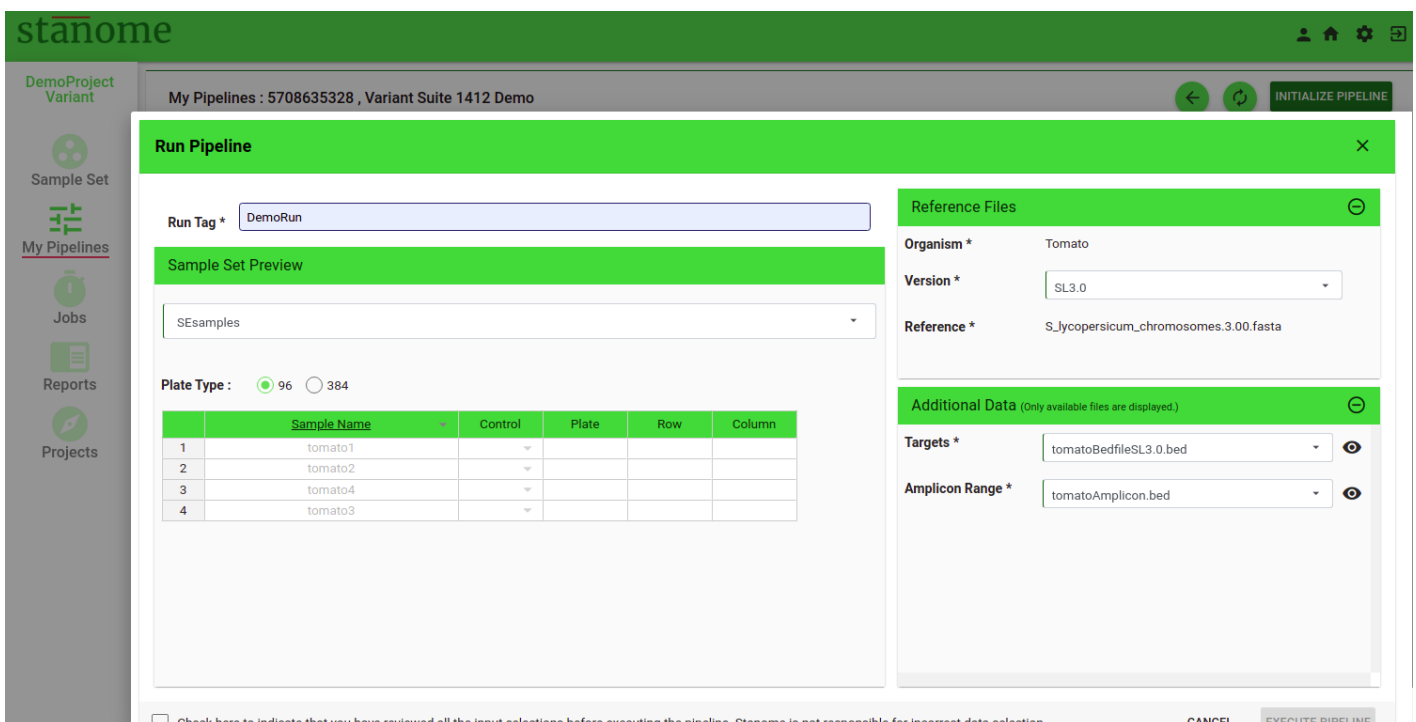
- Click  to access the **Run Pipeline** dialog box (Fig. 2). Final data selections happen during this stage and all fields are required to be filled. The contents of the dialog box change dynamically based on the analysis type and the tools in the pipeline.
- Provide a unique Run Tag
- Sample Set selection from the drop-down shows the sample names in a tabular format

- Select the plate format: 96-well or 384-well (This information is extensively used in the **Reports** to show the results in the plate format)
- Fill in the sample set table with the plate format details and control sample information.
- Latest reference genomes and corresponding additional files are preselected based on the organism of the project. Please confirm or change the selections using the drop-downs.

 **HINT:** The contents of the metadata files can be viewed by clicking the  icon

**CAUTION - Differential Suite pipelines need at least two conditions with two replicates for each. Variant Suite pipelines need properly formatted target files.**

- Agree to the terms and conditions to enable .
- Click  to run the **Pipeline**.



**stanome**

DemoProject Variant

My Pipelines : 5708635328 , Variant Suite 1412 Demo

**Run Pipeline**

Run Tag \* DemoRun

**Sample Set Preview**

SEsamples

Plate Type : ☒ 96 ☐ 384

	Sample Name	Control	Plate	Row	Column
1	tomato1				
2	tomato2				
3	tomato4				
4	tomato3				

**Reference Files**

Organism \* Tomato

Version \* SL3.0

Reference \* S\_lycopersicum\_chromosomes.3.00.fasta

**Additional Data** (Only available files are displayed.)

Targets \* tomatoBedfileSL3.0.bed

Amplicon Range \* tomatoAmplicon.bed

☐ Check here to indicate that you have reviewed all the input selections before executing the pipeline. Stanome is not responsible for incorrect data selection.


CANCEL EXECUTE PIPELINE

Computing resources are initialized upon pipeline execution. The pipeline window automatically refreshes and redirects to the jobs window. Executed jobs appear in the jobs table. Refresh the window if the job is not visible. Jobs wait in the queue until computing resources are available and the status appears as pending and changes to Running. An email is sent when the job starts and also upon completion.

## Pipeline Cancellation

Click the **STOP** button on the **JOBS** window to cancel an active pipeline execution and this will abort the run.

## Pipeline Deletion

Click  to delete a **Pipeline** from the **Pipeline** window (Fig. 1). This action deletes the pipeline records entirely from a project and can't be retrieved.

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Revision #2

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