



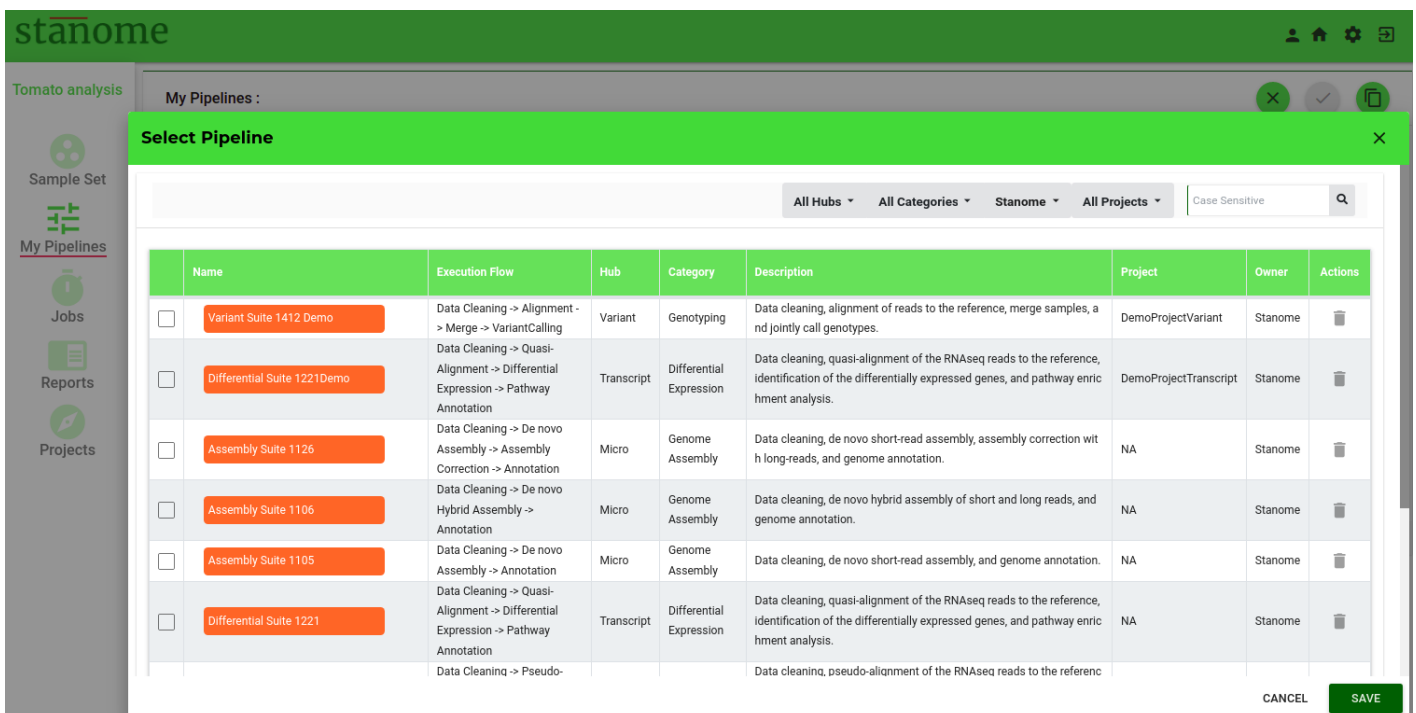








Copy Pipeline

A new pipeline can be created by copying an existing pipeline from other projects or a pre-configured pipeline from **Pipeline Library**.

Click  in the upper right corner of the pipeline creation window to see the existing pipelines via the **Select pipeline** dialog box (Fig.). Using the project setup information, a list of prefiltered pipelines is listed. Users can use multiple field combinations to filter the pipelines. Pipelines from the  can be viewed by selecting the owner as “Stanome”. Select a pipeline and click on  to copy a pipeline into the current project. The pipeline steps, tools, parameters, and other details are auto-populated (except the pipeline name). Name the new pipeline uniquely (duplicate names are not allowed) and verify the tools and commands before saving the pipeline.

 **HINT:** Pipeline name should be less than 50 characters long and only alphanumeric characters and spaces are allowed.



	Name	Execution Flow	Hub	Category	Description	Project	Owner	Actions
<input type="checkbox"/>	Variant Suite 1412 Demo	Data Cleaning -> Alignment -> Merge -> Variant Calling	Variant	Genotyping	Data cleaning, alignment of reads to the reference, merge samples, and jointly call genotypes.	DemoProjectVariant	Stanome	
<input type="checkbox"/>	Differential Suite 1221 Demo	Data Cleaning -> Quasi-Alignment -> Differential Expression -> Pathway Annotation	Transcript	Differential Expression	Data cleaning, quasi-alignment of the RNAseq reads to the reference, identification of the differentially expressed genes, and pathway enrichment analysis.	DemoProjectTranscript	Stanome	
<input type="checkbox"/>	Assembly Suite 1126	Data Cleaning -> De novo Assembly -> Assembly Correction -> Annotation	Micro	Genome Assembly	Data cleaning, de novo short-read assembly, assembly correction with long-reads, and genome annotation.	NA	Stanome	
<input type="checkbox"/>	Assembly Suite 1106	Data Cleaning -> De novo Hybrid Assembly -> Annotation	Micro	Genome Assembly	Data cleaning, de novo hybrid assembly of short and long reads, and genome annotation.	NA	Stanome	
<input type="checkbox"/>	Assembly Suite 1105	Data Cleaning -> De novo Assembly -> Annotation	Micro	Genome Assembly	Data cleaning, de novo short-read assembly, and genome annotation.	NA	Stanome	
<input type="checkbox"/>	Differential Suite 1221	Data Cleaning -> Quasi-Alignment -> Differential Expression -> Pathway Annotation	Transcript	Differential Expression	Data cleaning, quasi-alignment of the RNAseq reads to the reference, identification of the differentially expressed genes, and pathway enrichment analysis.	NA	Stanome	
		Data Cleaning -> Pseudo-			Data cleaning, pseudo-alignment of the RNAseq reads to the reference			

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