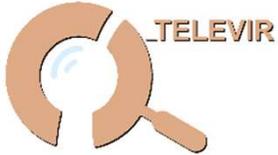


# Hypothesis-Free Detection

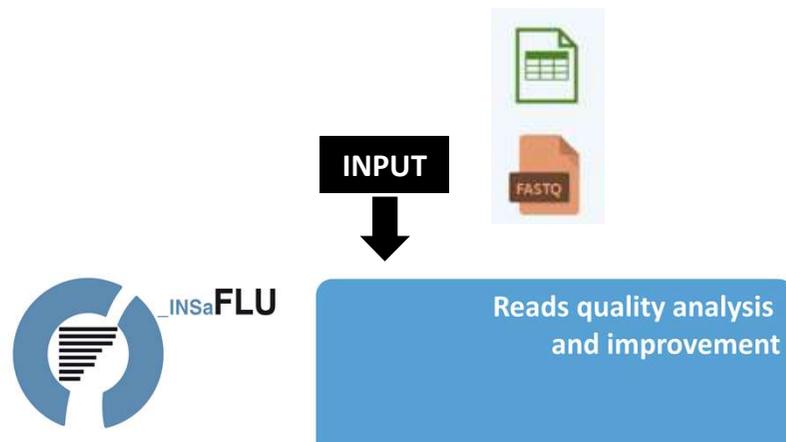


**Virus Detection**  
From Reads to viral  
detection

Settings

# TELEVIR | Basics

## Bioinformatics Diagnostics



### VIRUS DETECTION (*TELEVIR module*)

Hypothesis-free Virus  
Detection

Validation

Investigatory Mapping

# TELEVIR | Virus Detection

## Project Planning

Check Settings

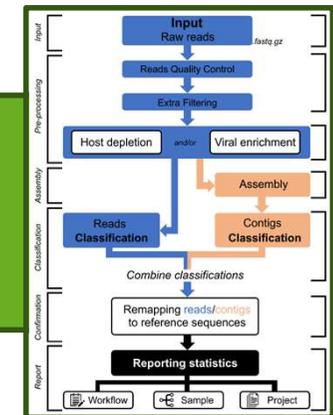
Create Project

Deploy

Prepare analysis

Setup Experiment

Manage Workflows



# TELEVIR | Virus Detection

## Settings | Setup

## | Modular Deployment

**Software** can be turned **ON/OFF**

**Pipeline Steps** can be turned **ON/OFF**

- *Some combinations are not allowed, e.g.*

*Contig classification ON & Assembly OFF*

- *At least one classifier must be ON*

## | Benchmarked Default Settings

Settings are modifiable

# TELEVIR | Virus Detection

## Settings | Classification Software

Software	Algorithm	Substrate	Database
<b>Kaiju</b>	Mod. BWT	Protein	NCBI viral Refseq protein
<b>Diamond</b>	Diamond Framework	Protein	NCBI viral Refseq protein
<b>KrakenUniq</b>	Probabilistic	DNA	NCBI viral Refseq
<b>Centrifuge</b>	Mod. BWT	DNA	NCBI viral Refseq

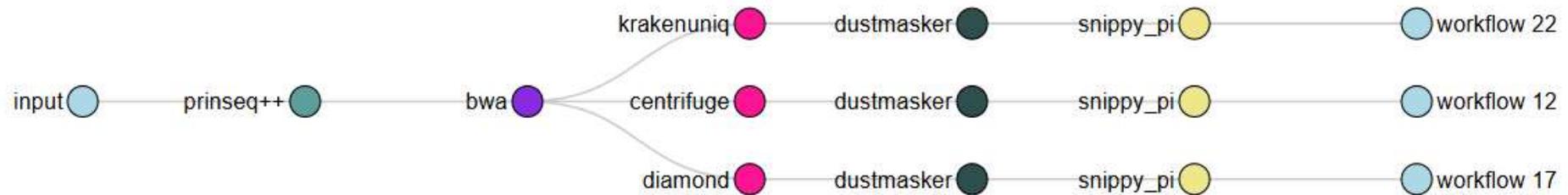
# TELEVIR | Virus Detection

## Settings | Classification Software

Software	Algorithm	Substrate	Database
<b>Kraken2</b>	Hash	DNA	NCBI viral Refseq +
<b>FastviromeExplorer</b>	EM	DNA	NCBI viral Refseq; Virosaurus
<b>BWA</b>	BWA	DNA	NCBI viral Refseq

# TELEVIR | Virus Detection

## Settings | Cross Validation



## | Modular Deployment

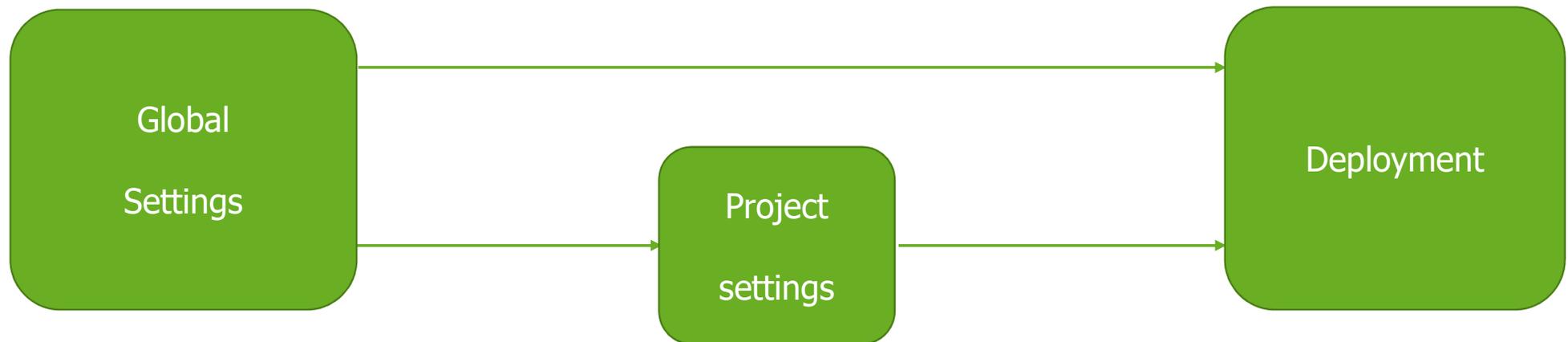
All possible combinations are deployed

*Ensemble Ranking*

# TELEVIR | Virus Detection

## Settings | Project Setup

Global Settings get replicated at Project level



# TELEVIR | Global Settings

 Video tutorial



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## From “reads” to viral metagenomics detection and routine genomic surveillance

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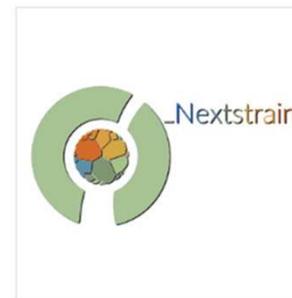
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Virus Detection



Reference-based  
genome assembly



Nextstrain



### News

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# TELEVIR | Global Settings



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Virus Detection



Reference-based genome assembly



Nextstrain

# TELEVIR | Global Settings

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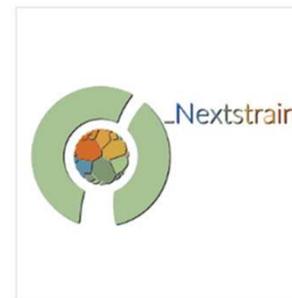
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Virus Detection



Reference-based  
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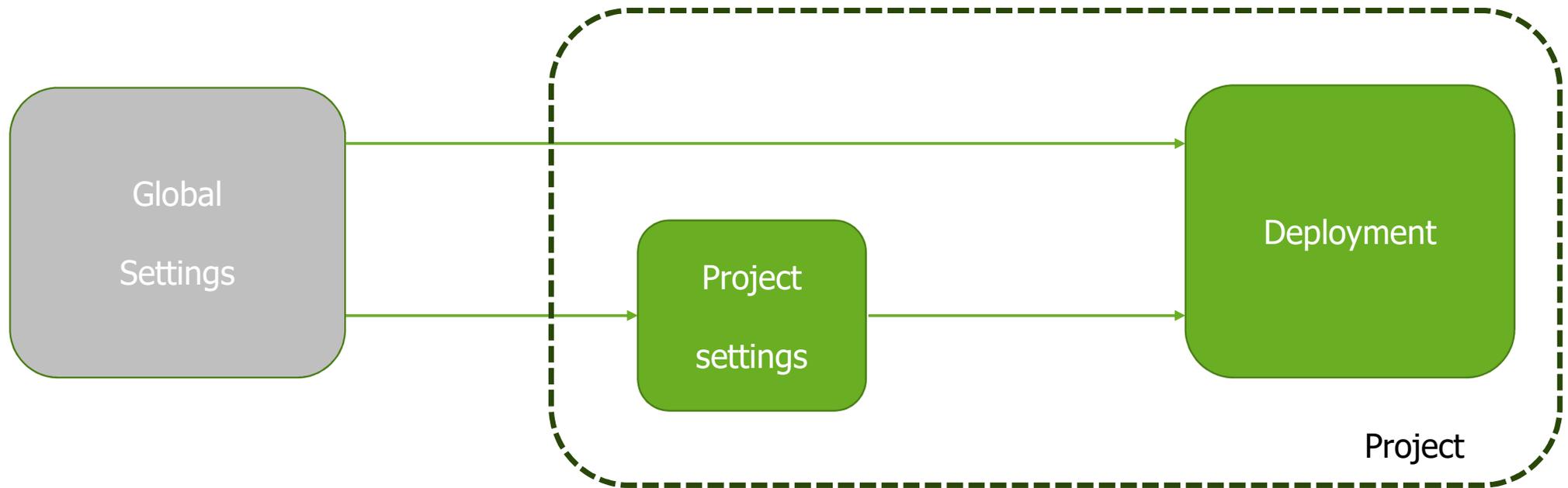
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# TELEVIR | Virus Detection

## Settings | Project Setup

Global Settings get replicated at Project level



# TELEVIR | Virus Detection

## Projects | Workflow Management



### | Workflow Management

**Deploy** workflows – single OR multiple

**Stop** Workflows – single OR multiple



**Project Specific Settings**

### | Set Controls

Flag in reports

### | Access Workflow Reports

**Individual** Workflows, **Sample** Workflow-Comparison

**Across Samples**

# TELEVIR | Virus Detection

## Projects | Creation

1. Create Project
2. Change settings (i.e., select workflows)
3. Add Samples to the project. 
4. Deploy Workflows

# TELEVIR | Project Setup



## From "reads" to viral metagenomics detection and routine genomic surveillance

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### Virus Detection

From Reads to viral detection

### Reference-based genome assembly

From reads to consensus sequence, mutations list, alignments, Pango lineage classification, etc.

### Nextstrain

From consensus sequences to phylogeographic and temporal analysis and metadatada navigation

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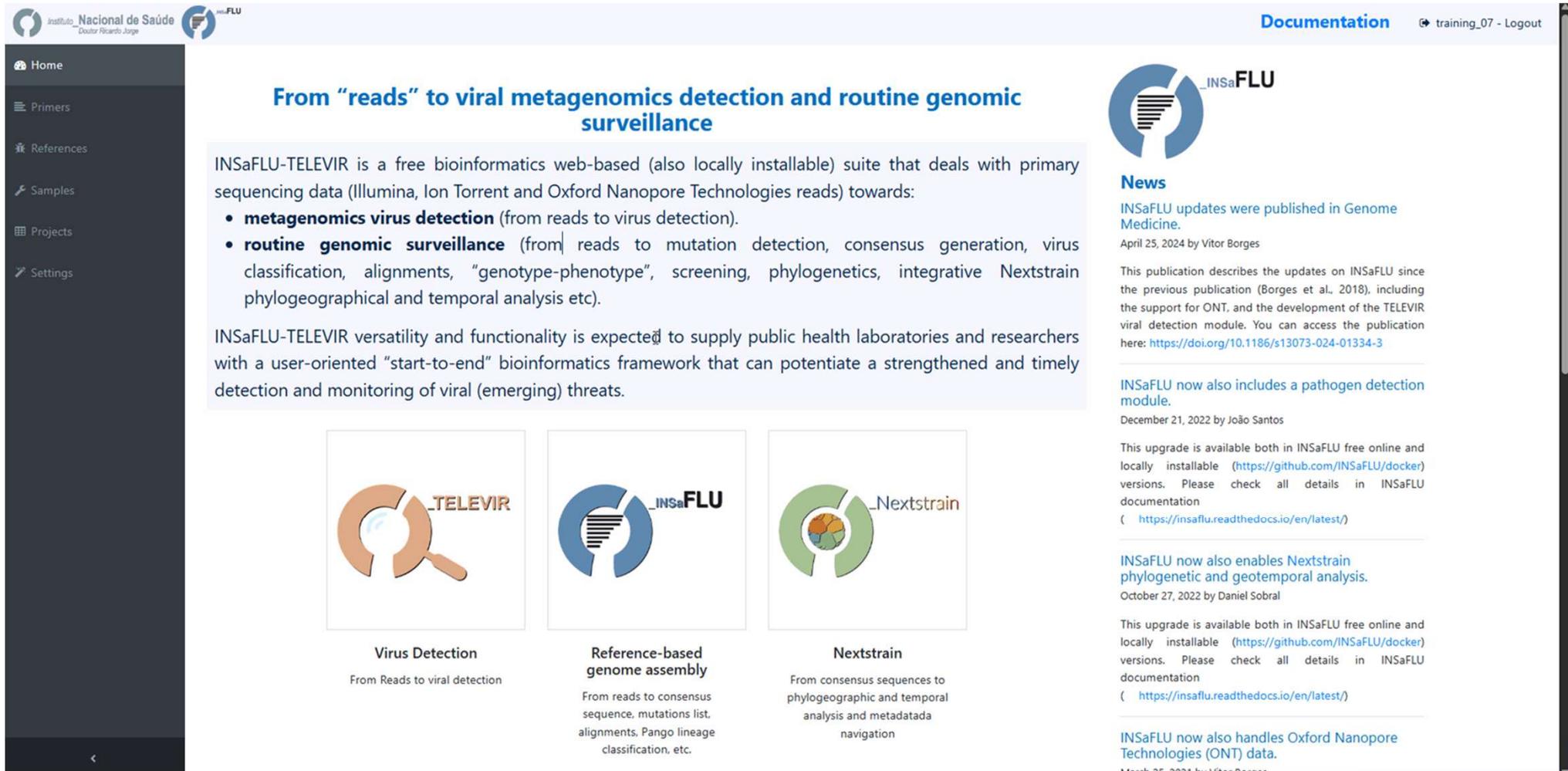
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INSaFLU now also handles Oxford Nanopore Technologies (ONT) data.  
March 25, 2021 by Vítor Borges



# TELEVIR | Project Setup

 Video tutorial



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From Reads to viral detection

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# TELEVIR | Virus Detection

## Projects | Workflow Management

### Metagenomics Management

 Run Metagenomics workflows, and validation by mapping.  Change settings (workflows, validation and reporting).  Add and manage targets for validation.  Focus on selected targets for validation (multi-sample and INSaFLU connection).

Run Sort sample reports View Project reports Project Settings Power Actions Sample Select  Search

Control	Sample Name	Report	Workflows	Run	Sorting	References	<input type="checkbox"/>	Combinations	Mapping Runs	Running	Queued
<input type="radio"/>	17	<a href="#">Combined Report</a>	<a href="#">Workflow Panel</a>		<input type="checkbox"/>	 (0)	<input type="checkbox"/>	0	0	3	0
<input type="radio"/>	barcode_09	<a href="#">Combined Report</a>	<a href="#">Workflow Panel</a>		<input type="checkbox"/>	 (0)	<input type="checkbox"/>	0	0	0	0

**Note:** You can change parameters to run new workflows. Results will be integrated to the Combined Report cumulatively.

Refresh Total samples: 2



# TELEVIR | Virus Detection

## Projects | Workflow Management

### Sample Table

#### Metagenomics Management

Run Metagenomics workflows, and validation by mapping. Change settings (workflows, validation and reporting). Add and manage targets for validation. Focus on selected targets for validation (multi-sample and INSaFLU connection).

Run | Sort sample reports | View Project reports | Project Settings | Actions | Sample Select | Sample Name Search

Control	Sample Name	Report	Workflows	Run	Sorting	References	Sample Select	Combinations	Mapping Runs	Running	Queued
<input type="radio"/>	17	Combined Report	Workflow Panel	<input type="checkbox"/>	<input type="checkbox"/>	(0)	<input type="checkbox"/>	0	0	3	0
<input type="radio"/>	barcode_09	Combined Report	Workflow Panel	<input type="checkbox"/>	<input type="checkbox"/>	(0)	<input type="checkbox"/>	0	0	0	0

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Refresh

Total samples: 2

# TELEVIR | Virus Detection

## Projects | Workflow Management

Deployment

### Metagenomics Management

Run Metagenomics workflows, and validation by mapping. Change settings (workflows, validation and reporting). Add and manage targets for validation. Focus on selected targets for validation (multi-sample and INSaFLU connection).

Run Sort sample reports View Project reports Project Settings Actions Sample Select Sample Name Search

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<input type="radio"/>	17	Combined Report	Workflow Panel	 	<input type="checkbox"/>	(0)	<input type="checkbox"/>	0	0	3	0
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Note: You can change parameters to run new workflows. Results will be integrated to the Combined Report cumulatively.

Refresh

Total samples: 2

 Run - Classical workflows” (for all samples)

the individual  (user-selected samples)

 Stop Workflows

# TELEVIR | Virus Detection

## Projects | Workflow Management

Controls

### Metagenomics Management

Run Metagenomics workflows, and validation by mapping. Change settings (workflows, validation and reporting). Add and manage targets for validation. Focus on selected targets for validation (multi-sample and INSaFLU connection).

Run | Sort sample reports | View Project reports | Project Settings | Actions | Sample Select | Sample Name Search

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<input type="radio"/>	17	Combined Report	Workflow Panel		<input type="checkbox"/>	(0)	<input type="checkbox"/>	0	0	3	0
<input type="radio"/>	barcode_09	Combined Report	Workflow Panel		<input type="checkbox"/>	(0)	<input type="checkbox"/>	0	0	0	0

Note: You can change parameters to run new workflows. Results will be integrated to the Combined Report cumulatively.

Refresh

Total samples: 2

# TELEVIR | Virus Detection

## Projects | Workflow Management

### Monitoring

#### Metagenomics Management

▲ Run Metagenomics workflows, and validation by mapping. ⚙️ Change settings (workflows, validation and reporting). 📄 Add and manage targets for validation. 🔍 Focus on selected targets for validation (multi-sample and INSaFLU connection).

Run | Sort sample reports | View Project reports | Project Settings | Actions | Sample Select | Sample Name Search

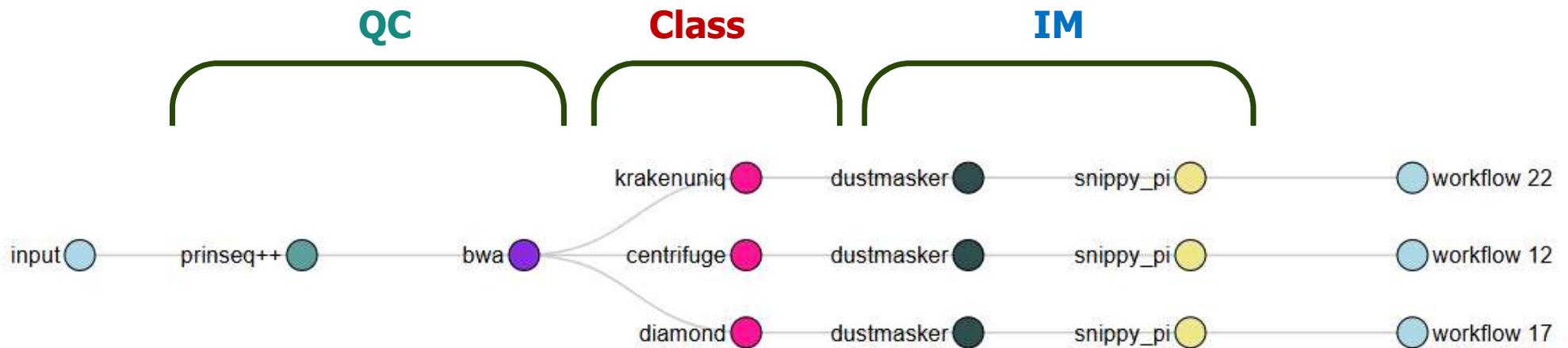
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Note: You can change parameters to run new workflows. Results will be integrated to the Combined Report cumulatively.

Refresh

Total samples: 2

# TELEVIR | Virus Detection



## | Modular Deployment

All possible combinations are deployed

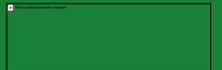


# Slido questions

**Do not edit**  
*How to change the  
design*

**4. I sequenced a human blood sample using a shotgun approach. Which steps will help filter out host reads?**

The [Slido app](#) must be installed on every computer you're presenting from



**Do not edit**  
*How to change the  
design*

## 5. What is the main purpose of the assemblies produced in TELEVIR workflows?

The [Slido app](#) must be installed on every computer you're presenting from



## Questions from chat