

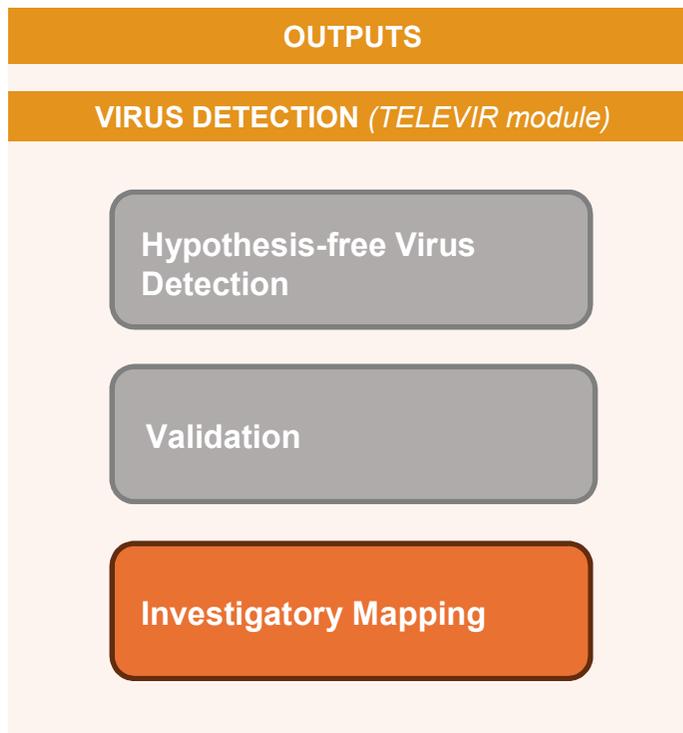
Investigatory Mapping



Virus Detection
From Reads to viral
detection

Settings

TELEVIR | Investigatory Mapping Bioinformatics Diagnostics

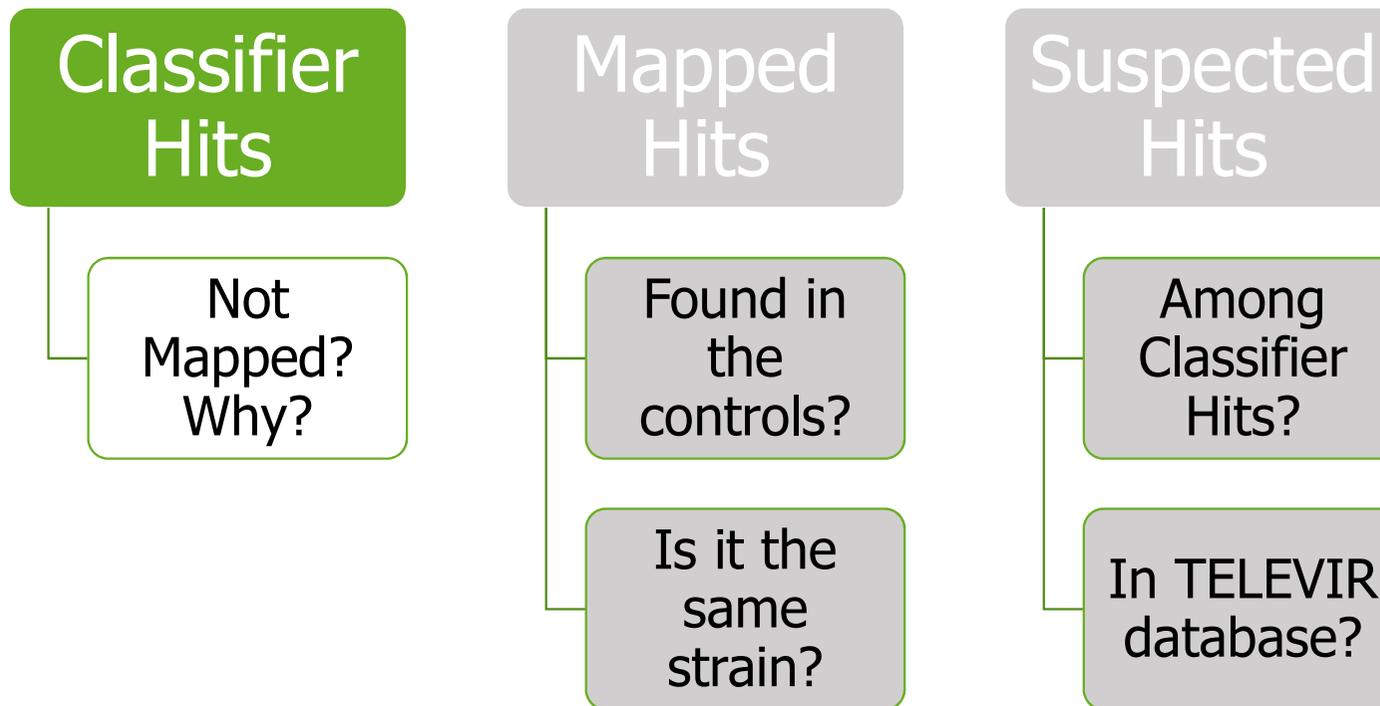


I don't know what I have

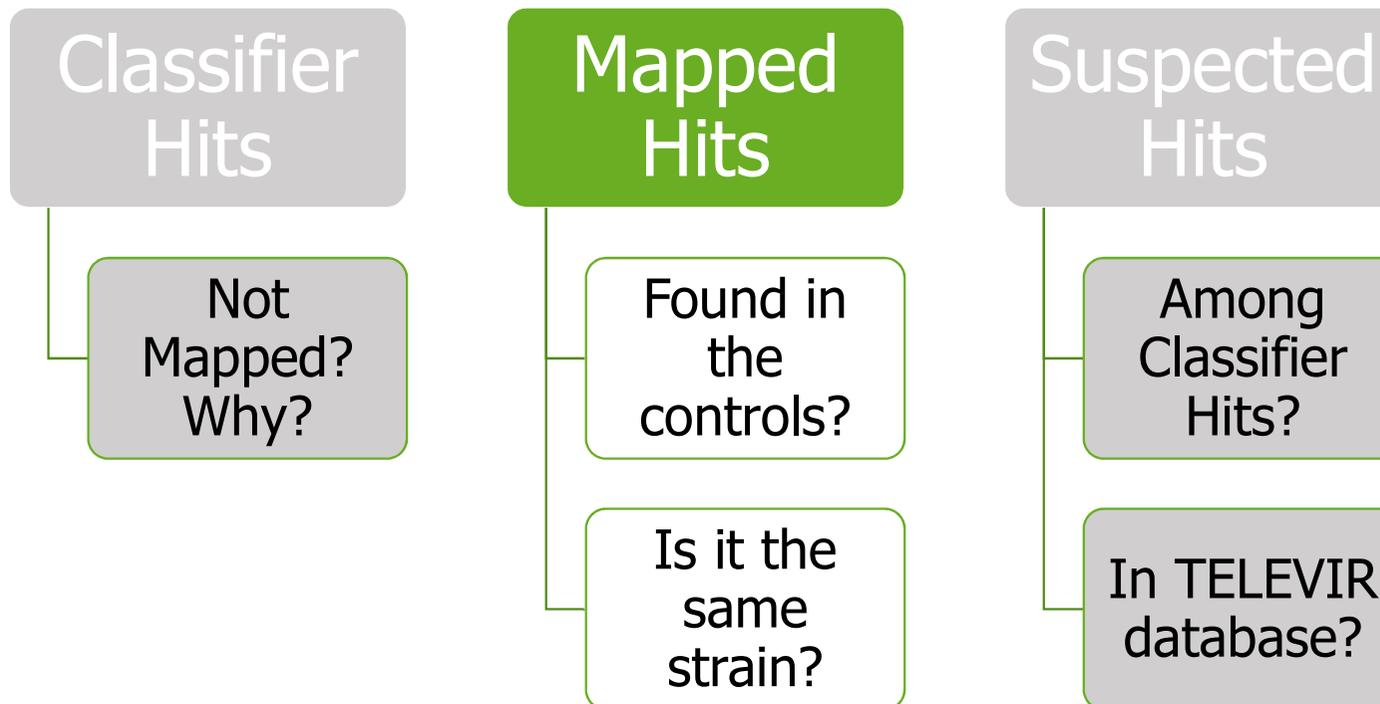
Any guess needs to be looked into

Suspected, Contaminants and False Positives

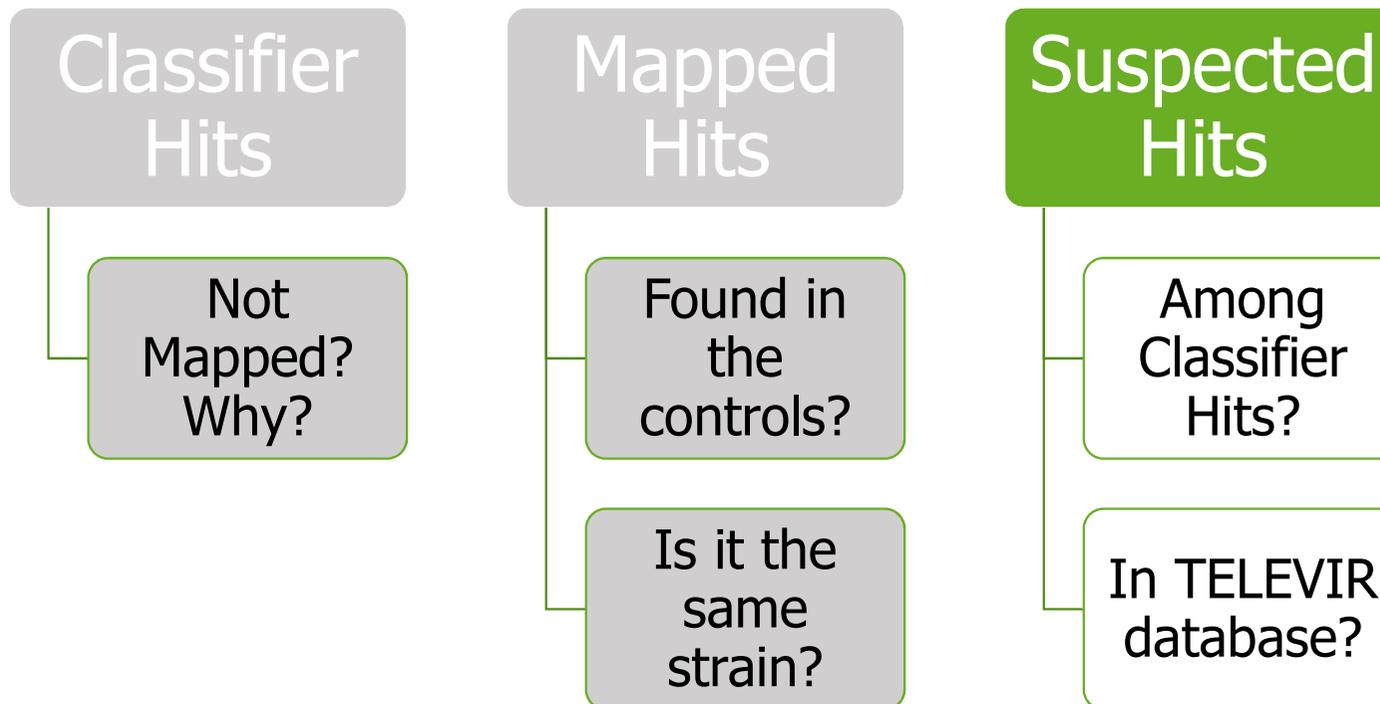
TELEVIR | Investigatory Mapping



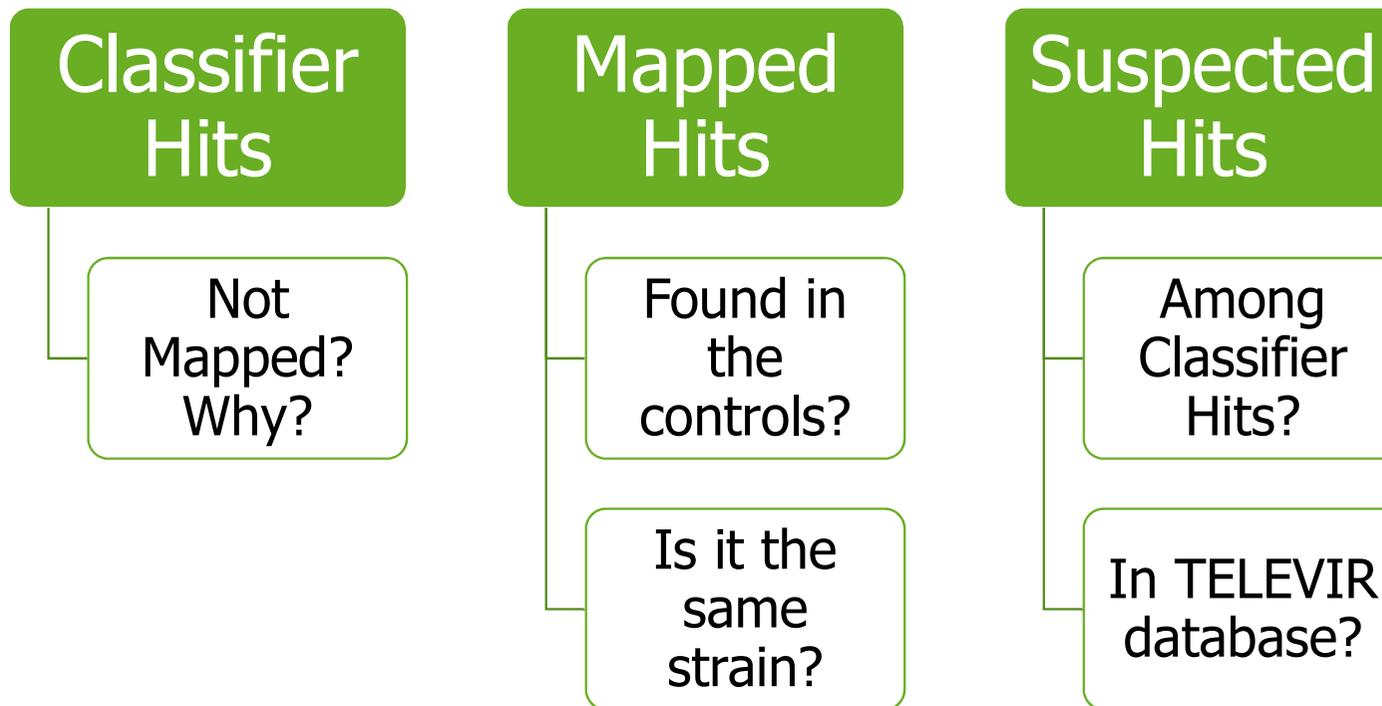
TELEVIR | Investigatory Mapping



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Tool for investigating



Something to Investigate

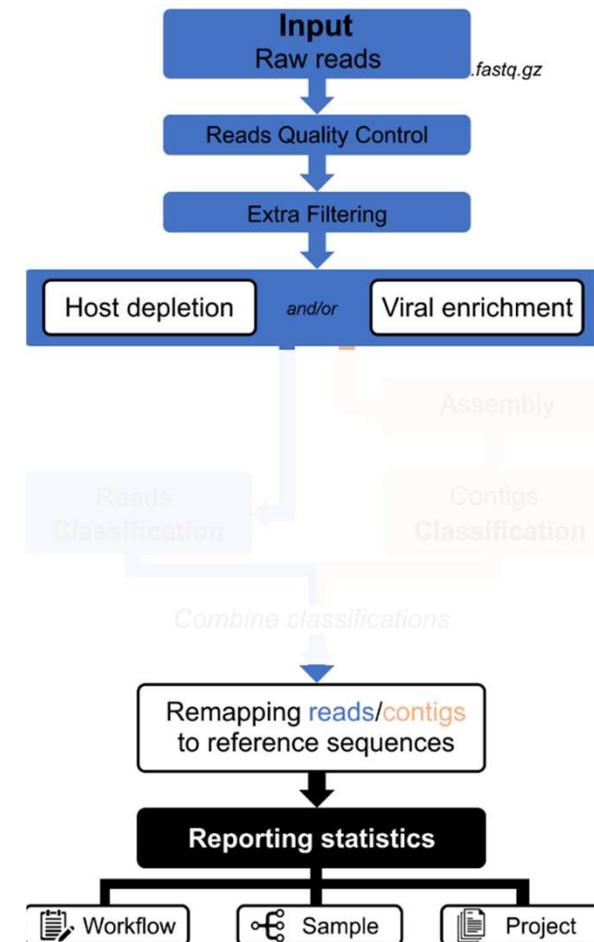
TELEVIR | Investigatory Mapping

Workflows

| Pre-processing

| Mapping

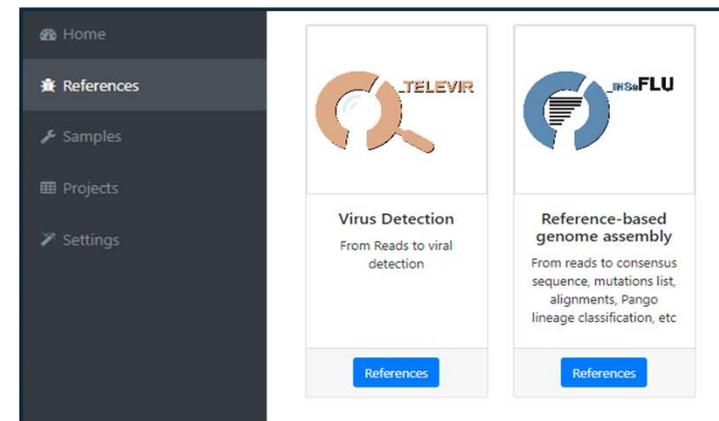
No classification
Provided references



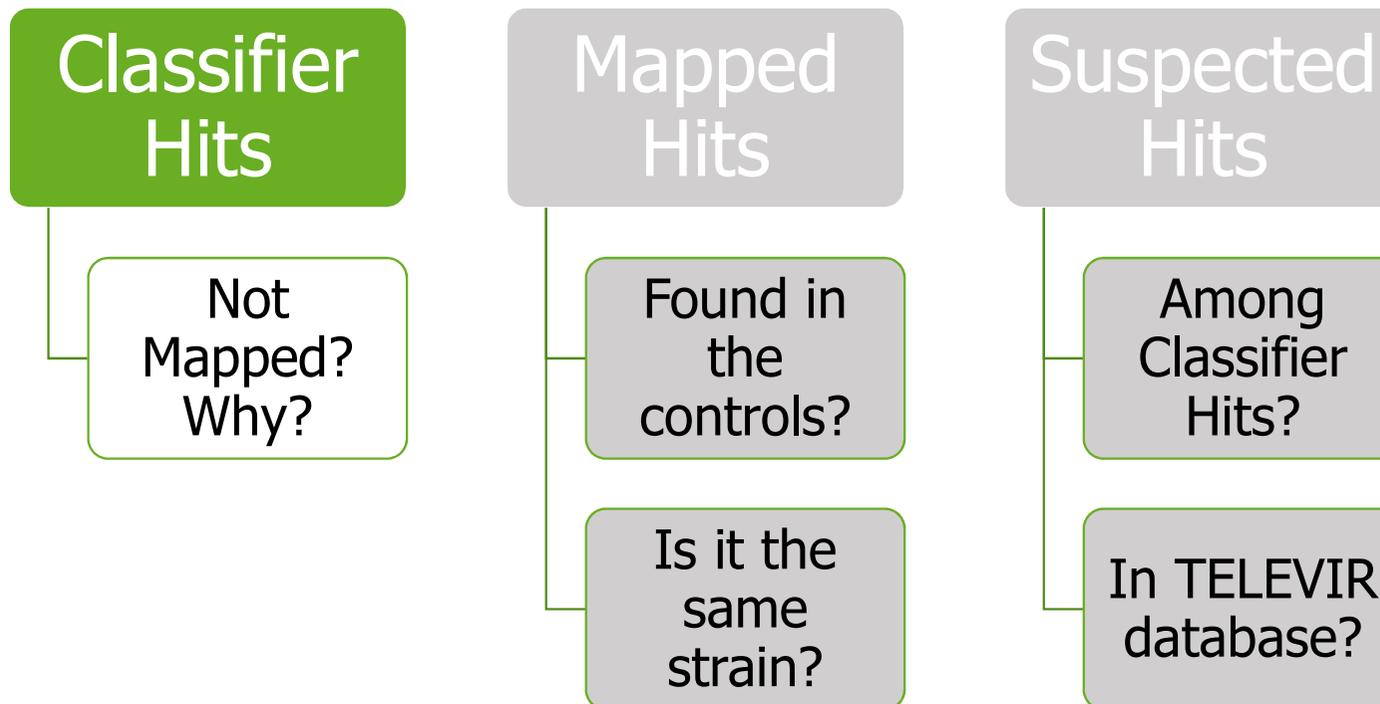
TELEVIR | Investigatory Mapping

Reference Selection

- **Add references**
- **Explore existing references**
- **Create Reference Panels to streamline mappings**



TELEVIR | Investigatory Mapping



TELEVIR | Investigatory Mapping Projects | Reference Panel

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

Control	Sample Name	Report	Workflows	Run	Sorting	References	Sample Select	Combinations	Mapping Runs	Running	Queued
<input type="radio"/>	i7	Combined Report	Workflow Panel	<input type="checkbox"/>	<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"/>	<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 | Investigatory Mapping

Investigatory Mapping | Reference Panel

Changing of Parameters

Add references manually
- not reported by classifiers

Deploy Mapping of selected references

Workflows sample: Met_0037b_VSP_2024_DNA Combined Report

Workflow report 16
Workflow report 23
Workflow report 30

1 Added References Add References

Added Panels Add Panels

Actions		Description, Accession, Taxid						Search
<input checked="" type="checkbox"/>	Description	Accession Id	Taxid	Runs	Global Ranking	Ensemble Ranking	Best Mapping	
<input type="checkbox"/>	human gammaherpesvirus 4	NC_007605.1	10376	16, 23, 30	6	1	Mapped	
<input type="checkbox"/>	Human herpesvirus 4 type 2	NC_009334.1	12509	16, 23, 30	13	1	Mapped	

TELEVIR | Investigatory Mapping

Investigatory Mapping | Reference Panel

Was it suggested by classifiers?

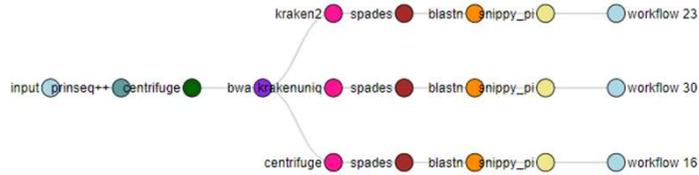
If Yes,

Was it mapped and failed?

Yes and Yes? Stop

Yes and No? Map, compare Mappings.

Workflows sample: Met_0037b_VSP_2024_DNA Combined Report



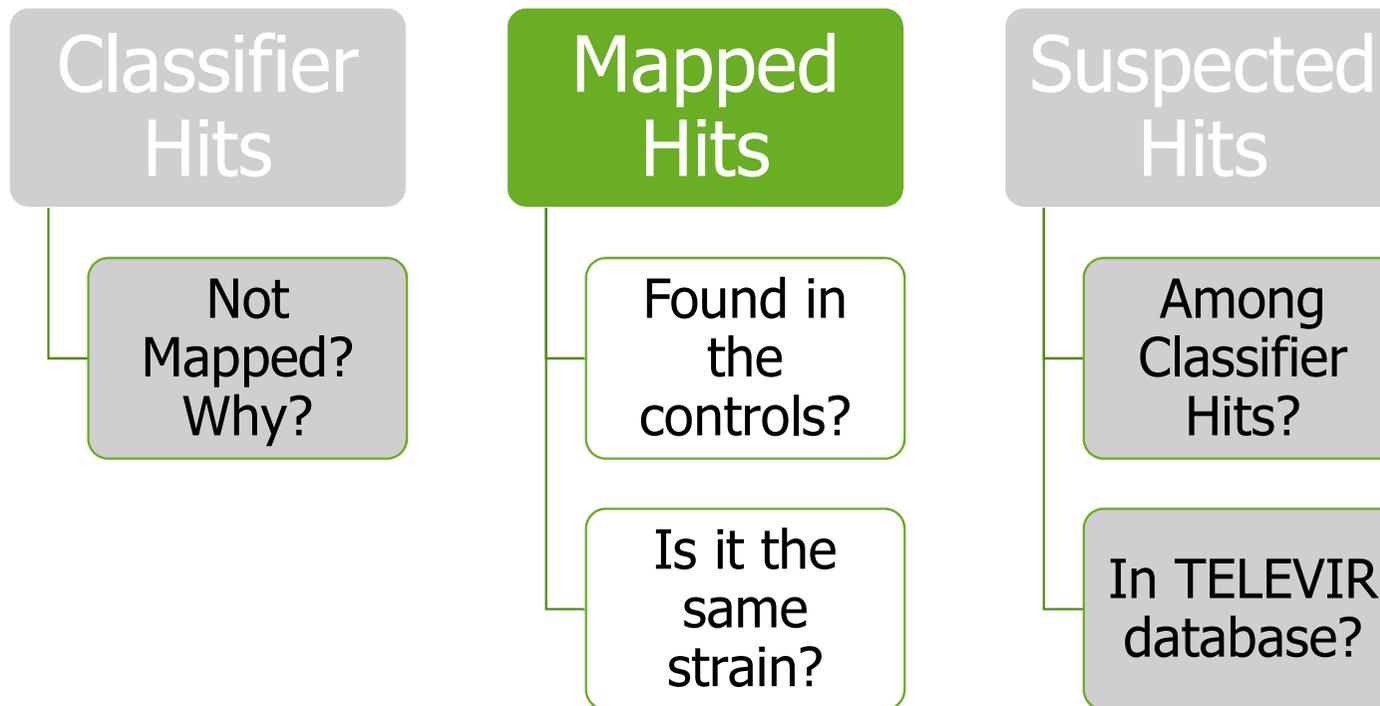
Workflow report 16
Workflow report 23
Workflow report 30

1 Added References Add References

Added Panels Add Panels

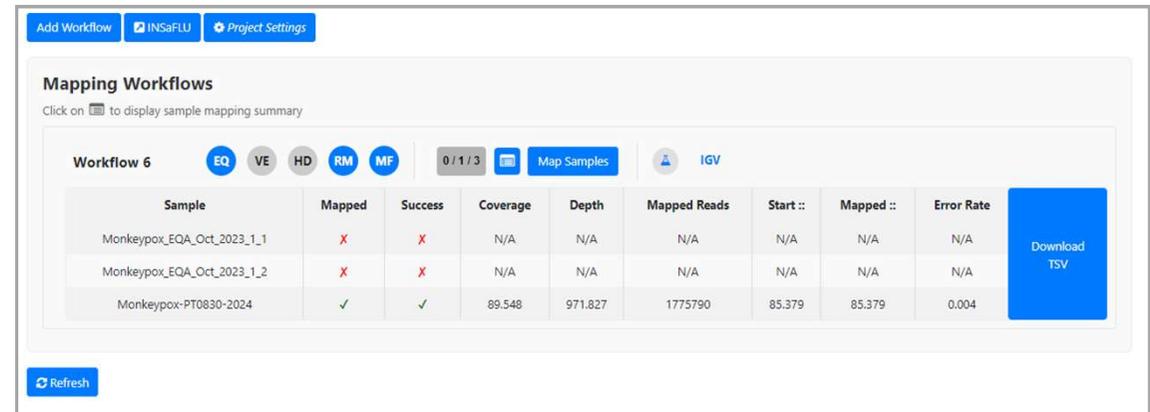
Actions		Description, Accession, Taxid						Search
<input type="checkbox"/>	Description	Accession Id	Taxid	Runs	Global Ranking	Ensemble Ranking	Best Mapping	
<input type="checkbox"/>	human gammaherpesvirus 4	NC_007605.1	10376	16, 23, 30	6	1	Mapped	
<input type="checkbox"/>	Human herpesvirus 4 type 2	NC_009334.1	12509	16, 23, 30	13	1	Mapped	

TELEVIR | Investigatory Mapping



TELEVIR | Investigatory Mapping Projects | Reference Panel

| Mapping Workflows



The screenshot shows a web interface for 'Mapping Workflows'. At the top, there are buttons for 'Add Workflow', 'INSaFLU', and 'Project Settings'. Below this is a section for 'Workflow 6' with filters for 'EQ', 'VE', 'HD', 'RM', and 'MF'. A 'Map Samples' button and a '0 / 1 / 3' indicator are also present. The main part of the interface is a table with the following data:

Sample	Mapped	Success	Coverage	Depth	Mapped Reads	Start ::	Mapped ::	Error Rate	Download TSV
Monkeypox_EQA_Oct_2023_1_1	X	X	N/A	N/A	N/A	N/A	N/A	N/A	Download TSV
Monkeypox_EQA_Oct_2023_1_2	X	X	N/A	N/A	N/A	N/A	N/A		
Monkeypox-PT0830-2024	✓	✓	89.548	971.827	1775790	85.379	85.379	0.004	

A 'Refresh' button is located at the bottom left of the table area.

| Tabular result statistics

Compare with Controls

| Stacked IGVs

Compare mappings



TELEVIR | Investigatory Mapping Projects | Reference Focus

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"/>	i7	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

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

Refresh

Total samples: 2

Explore References

TELEVIR | Investigatory Mapping Projects | Reference Focus

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

Control	Sample Name	Report	Workflows	Run	Sorting	References	Sample Select	Combinations	Mapping Runs	Running	Queued
<input type="radio"/>	i7	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

Add References – Explore References

TELEVIR | Investigatory Mapping Projects | Reference Focus

Actions - Focus

The screenshot displays the 'Metagenomics Management' interface. At the top, there are buttons for 'Run', 'Sort sample reports', 'View Project reports', and 'Project Settings'. Below these is a table with columns: Control, Sample Name, Report, Workflows, Run, and Sorting. Two rows are visible: one for sample 'i7' and another for 'barcode_09'. An 'Actions' dropdown menu is open, showing options: 'Add Targets', 'Add Panels', 'Focus', and '(0)'. A callout box highlights the 'Focus' option, which opens a 'Reference Targeted Analysis' dialog. This dialog has a search bar containing 'monkeypox' and a 'Search' button. Below the search bar is a table with columns: Description, Accession Id, Taxid, and E Rank. The table lists four entries for 'Monkeypox virus, complete genome' with various accession IDs and E Ranks. A 'Create Project' button is located at the bottom right of the dialog.

Metagenomics Management

Run Metagenomics workflows, and validation by mapping. Change settings (workflows, validation and reporting). Add validation (multi-sample and INSaFLU connection).

Run | Sort sample reports | View Project reports | Project Settings

Control	Sample Name	Report	Workflows	Run	Sorting
<input type="radio"/>	i7	Combined Report	Workflow Panel	<input type="checkbox"/>	<input type="checkbox"/>
<input type="radio"/>	barcode_09	Combined Report	Workflow Panel	<input type="checkbox"/>	<input type="checkbox"/>

Actions

- Add Targets
- Add Panels
- Focus
- (0)

Reference Targeted Analysis

Map selected samples and connect to an INSaFLU project. Select Televir hits below to use as reference.

monkeypox Search

	Description	Accession Id	Taxid	E Rank
<input type="checkbox"/>	Monkeypox virus, complete genome	NC_003310.1	10244	1
<input type="checkbox"/>	Monkeypox virus, complete genome	KJ642617.1	10244	1
<input type="checkbox"/>	Monkeypox virus, complete genome	NC_063383.1	10244	2
<input type="checkbox"/>	Monkeypox virus, complete genome	KJ642617.1	10244	2

Create Project

TELEVIR | Investigatory Mapping Projects | Reference Focus

Total samples: 4

Reference Analysis

✦ Focus on selected targets for validation. Coordinate processing and mapping workflows against selected references across multiple samples.



Influenza A virus (A/goose/Guangdong/1/1996(H5N1)) hemagglutinin (HA) gene, complete cds

Taxid: 93838 Accid: NC_007362.1

[View Details](#)

+ Samples: 0

W.2



Human rhinovirus 1 strain ATCC VR-1559, complete genome

Taxid: 573824 Accid: NC_038311.1

[View Details](#)

+ Samples: 0

W.1

[Refresh](#)

Target a single reference

Compare mapping results across samples

TELEVIR | Investigatory Mapping Projects | Reference Focus

[Add Workflow](#) [INSaFLU](#) [Project Settings](#)

Mapping Workflows

Click on  to display sample mapping summary

Workflow 13-8	EQ VE HD RM MF	0 / 0 / 0	 Map Samples	
Workflow 7-10	EQ VE HD RM MF	0 / 0 / 0	 Map Samples	

[Refresh](#)

**Standardized Mapping across samples
&
Relax Filtering – Depletion and Enrichment – Maximize mapped reads**

TELEVIR | Investigatory Mapping

 Video tutorial

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

INSaFLU-TELEVIR is a free bioinformatics web-based (also locally installable) suite that deals with primary sequencing data (Illumina, Ion Torrent and Oxford Nanopore Technologies reads) towards:

- **metagenomics virus detection** (from reads to virus detection).
- **routine genomic surveillance** (from reads to mutation detection, consensus generation, virus classification, alignments, “genotype-phenotype”, screening, phylogenetics, integrative Nextstrain phylogeographical and temporal analysis etc).

INSaFLU-TELEVIR versatility and functionality is expected to supply public health laboratories and researchers with a user-oriented “start-to-end” bioinformatics framework that can potentiate a strengthened and timely detection and monitoring of viral (emerging) threats.



Virus Detection

From Reads to viral detection



Reference-based genome assembly

From reads to consensus sequence, mutations list,



Nextstrain

From consensus sequences to phylogeographic and temporal analysis and metadata



News

INSaFLU updates were published in Genome Medicine.

April 25, 2024 by Vitor Borges

This publication describes the updates on INSaFLU since the previous publication (Borges et al., 2018), including the support for ONT, and the development of the TELEVIR viral detection module. You can access the publication here: <https://doi.org/10.1186/s13073-024-01334-3>

INSaFLU now also includes a pathogen detection module.

December 21, 2022 by João Santos

This upgrade is available both in INSaFLU free online and locally installable (<https://github.com/INSaFLU/docker>) versions. Please check all details in INSaFLU documentation (<https://insaflu.readthedocs.io/en/latest/>)

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training_07 - Logout



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TELEVIR | Investigatory Mapping

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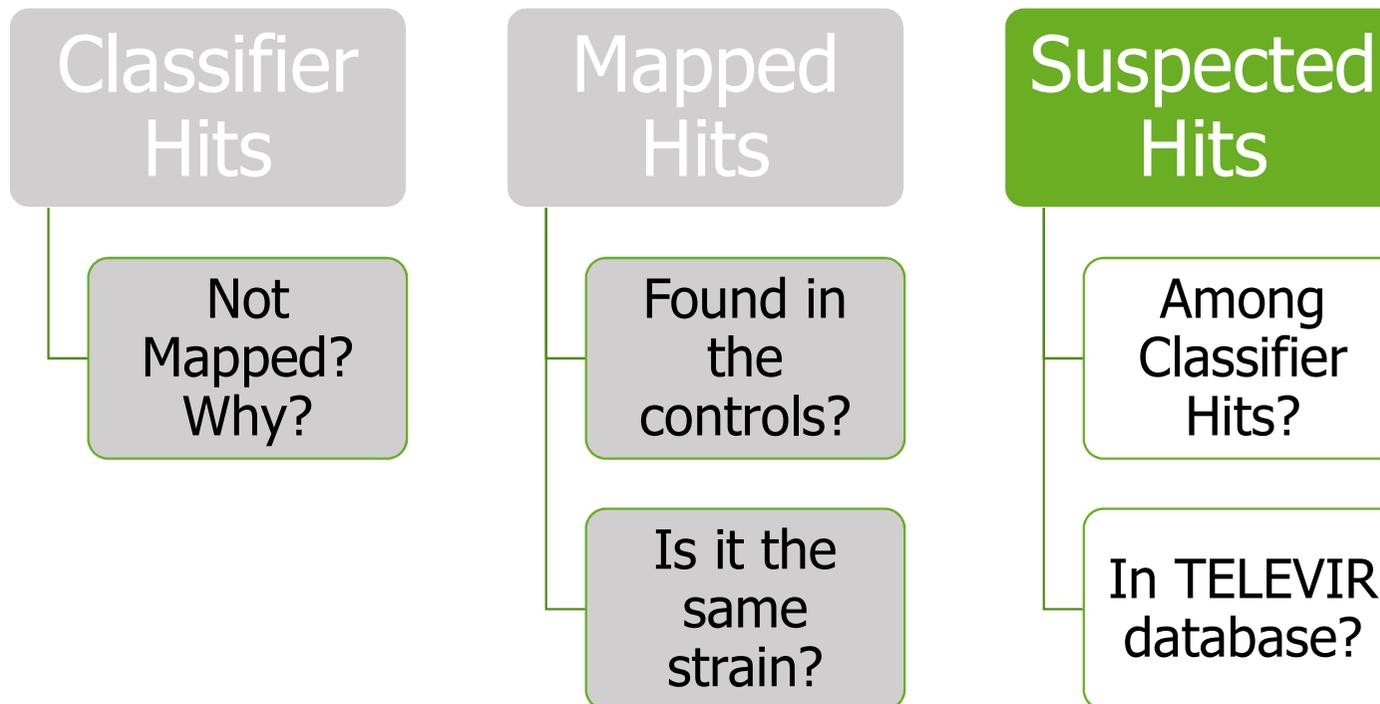
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TELEVIR | Investigatory Mapping



TELEVIR | Hypothesis Free Follow up Workflows | Panel Mapping

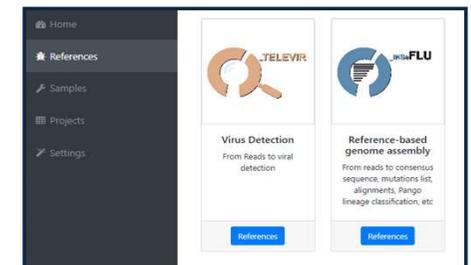
One Sample – One Reference – No classifiers

Panels created in TELE VIR References section

Can be added to single sample, multiple samples, whole project

Can be deployed individually or in group

Comparable validation statistics and grouping



Description	taxid	accid	Cov (%)	Depth	Duplic.	Mapped reads	start emp (%)	mapped_avg (x)	Steps	Windows Covered	Private reads	Mismatch rate	class. success	mapping len (bp)	Warning	Control
NC_023877.1		private reads: 1041				private reads proportion: 1.0				Group size 1						Read Overlay
Porcine stool-associated circular virus 4 isolate CP2, complete genome	1475062	NC_023877.1	100.0	95.39	95.48	2082	0.09152	1.19207	0	3/3	1041	0.03369981	reads	reads		
Inzev30		private reads: 1672				private reads proportion: 1.0				Group size 4						Read Overlay
Human parvovirus B19 isolate B1 311-406-851 non-structural protein NS1 (NS1) 7.5 kDa protein (7.5 kDa), capsid protein 1 (VP1), protein X (X), and capsid protein 2 (VP2) genes, complete cds	10798	K0055643.1	99.78	81.24	81.58	3320	0.14594	1.9009	3	3/3	1672	0.01919471	reads	reads		
Inzev27		private reads: 7196				private reads proportion: 1.0				Group size 5						Read Overlay
Primate bocaparvovirus 1 isolate st2, complete genome	3052040	NC_007455.1	99.62	201.15	201.91	10932	0.48054	6.25923	3	3/3	1487	0.09941666	reads	reads		



Slido questions

Do not edit
*How to change the
design*

8. What is one of the main purposes of the 'TELEVIR-Focus' feature?

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



Questions from chat