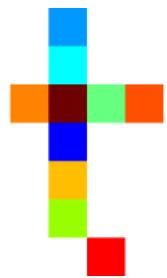




LEVEL^{UP} WORKSHOP I

Part B

0107 - Get Data



This guide will get you set up for module B by downloading cytokine data and donor annotations from the Workshop I project. These Duke University data files detail 18 cytokines measured from a cohort of healthy donors across different age groups, genders, and races.

- 1 Navigate to the top level of the **Workshop I** project.

Click "files" folder.

Workshop I

No description provided.

New data set

New workflow

New file

Upload file

Upload

 faris.naji updated file README.md

 README.md

 Part-B

 Part-A

 files

 README.md

2 Click **Export** icon of the **grifols_cytokine_data.csv** file

The screenshot shows the 'Workshop 1' section of the 'LevelUpWorkshopsTeam' project. The 'grifols_cytokine_data.csv' file is listed with its last update 10 days ago. The 'Export' icon, located at the bottom right of the file card, is circled in orange.

File	Last updated
faris.naji updated file README.md	14 minutes ago
README.md	14 minutes ago
grifols_data_final.csv	10 days ago
grifols_cytokine_data.csv	3 hours ago
donor_annotation.csv	14 minutes ago

Source of files

3 Click "Export" icon of the **donor_annotation.csv** file

The screenshot shows the 'Workshop 1' section of the 'LevelUpWorkshopsTeam' project. The 'donor_annotation.csv' file is listed with its last update 14 minutes ago. The 'Export' icon, located at the bottom right of the file card, is circled in orange.

File	Last updated
faris.naji updated file README.md	14 minutes ago
README.md	14 minutes ago
grifols_data_final.csv	10 days ago
grifols_cytokine_data.csv	3 hours ago
donor_annotation.csv	14 minutes ago

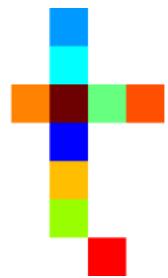
Source of files

4 These two files are downloaded to your download folder



A chrome shortcut to get to the download folder from your browser is to type the **Ctrl + J** keys together.

0108 - Import Data



At the end of the guide. The user knows how to correctly import cytokine data.

1 We will now import the two files downloaded earlier

2 Navigate to the top level of your Workshop I project

3 Click "Workshop I" breadcrumb link

The screenshot shows a user interface for managing projects. At the top, there are tabs for 'Project' and 'Activities'. Below them, a breadcrumb navigation bar shows the path: 'Workshop 1' (with a lock icon) followed by '/ files'. This breadcrumb link is circled in red. The main content area displays a list of files under the heading 'Workshop 1 / files'. The files listed are: 'faris.naji updated file README.md' (highlighted with a blue background), 'README.md', 'grifols_data_final.csv', 'grifols_cytokine_data.csv', and 'donor_annotation.csv'. Above the file list, there are five action buttons: 'New data set', 'New workflow', 'New file', 'Upload file', and 'Upload'.

4 Click on the **Part-B** folder

No description provided.

New data set New workflow New file Upload file Upload

faris.naji updated file README.md

- README.md
- Part-B** (highlighted)
- Part-A
- files

README.md

5 Click on the **New data set** icon.

LevelUpWorkshopsTeam

Project Activities

Workshop 1

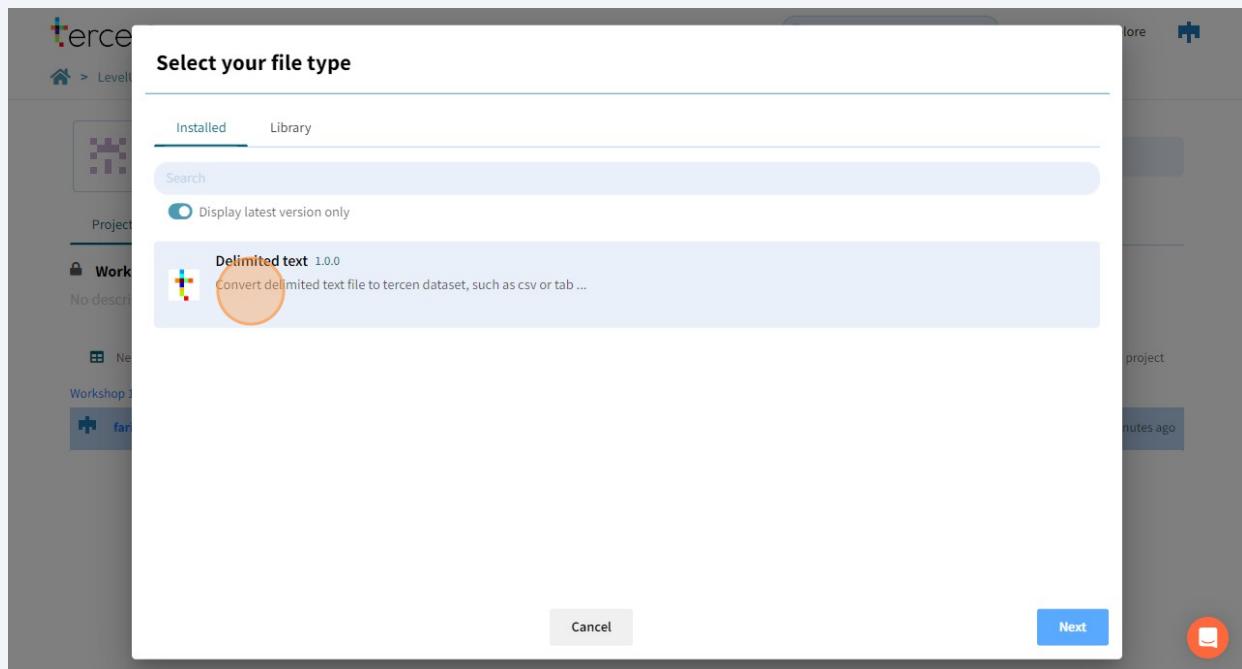
No description provided.

New data set New workflow New file Upload file Upload

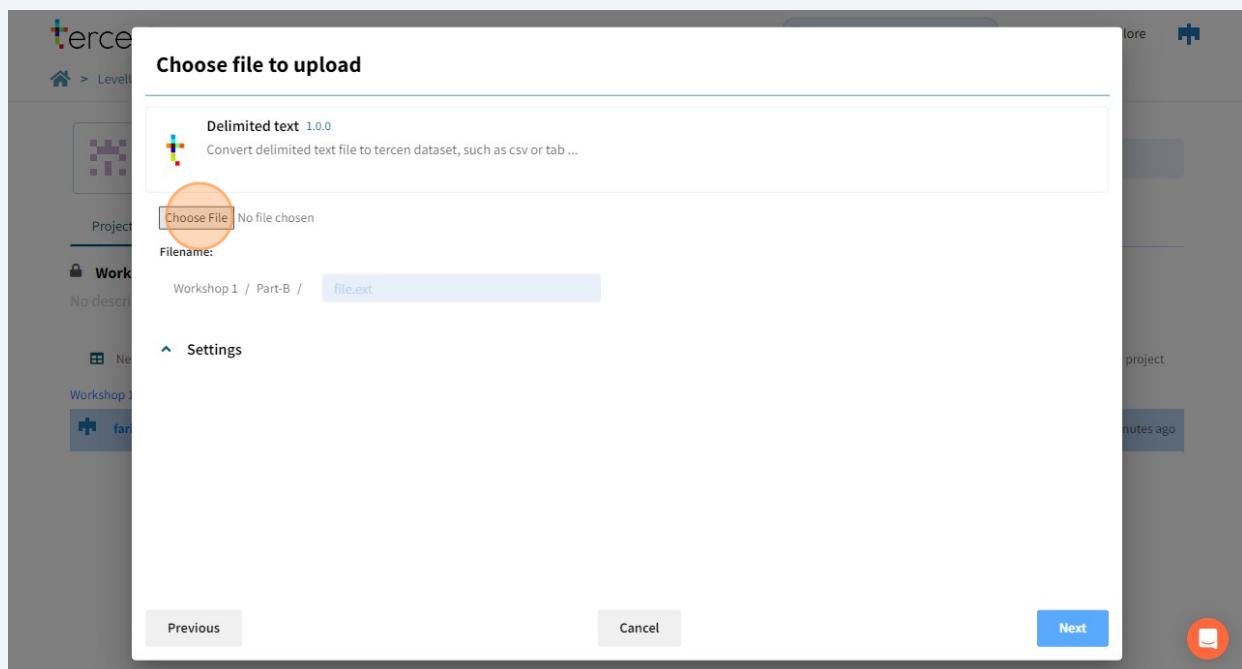
Workshop 1 / Part-B

faris.naji updated file README.md

6 Click on the **Delimited text** reader.

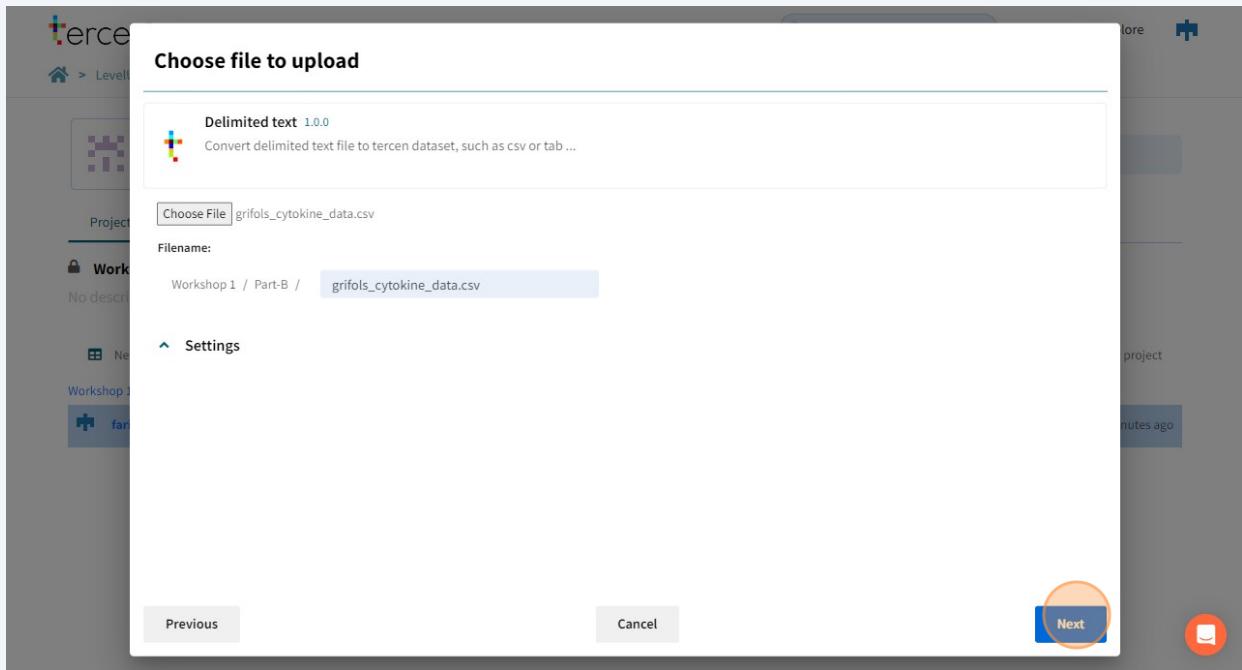


7 Click on the **Choose File** button.



8 Choose the **grifols_cytokine_data.csv** file in your download folder.

9 Click the **Next** button.



10

Click this dropdown under the **Sample ID** column header and choose a **character** type.

Note how **Sample ID** entries lose their decimal places when defined as a **character** type.

This is important as it affects the ordering and coloring of the **Sample ID** factor.

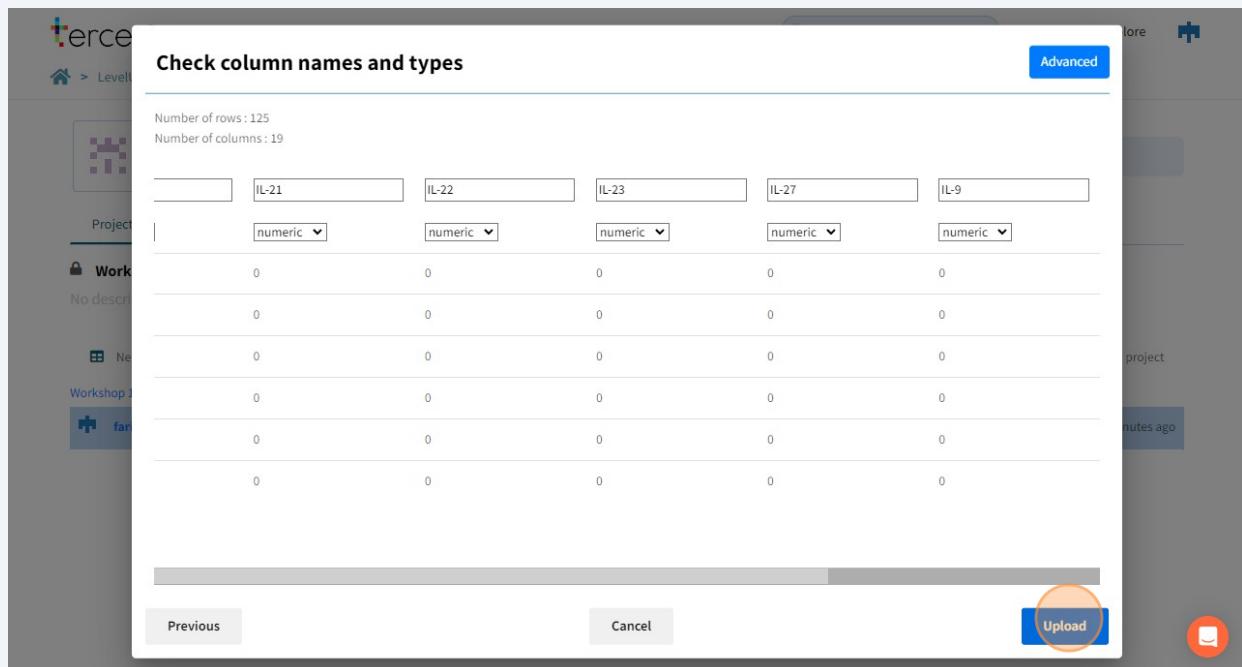
#	Sample ID	IFN-gamma	IL-12p70	IL-13	IL-1beta	IL-2
1	3130035837.0	0	0	0	0	0
2	3130035967.0	0	0	0	0	0
3	3370452578.0	0	0	0	0	0
4	3370452632.0	0	0	0	0	0
5	3370452658.0	0	0	0	0	0
6	3370452662.0	30.06	0	0	0	0

11

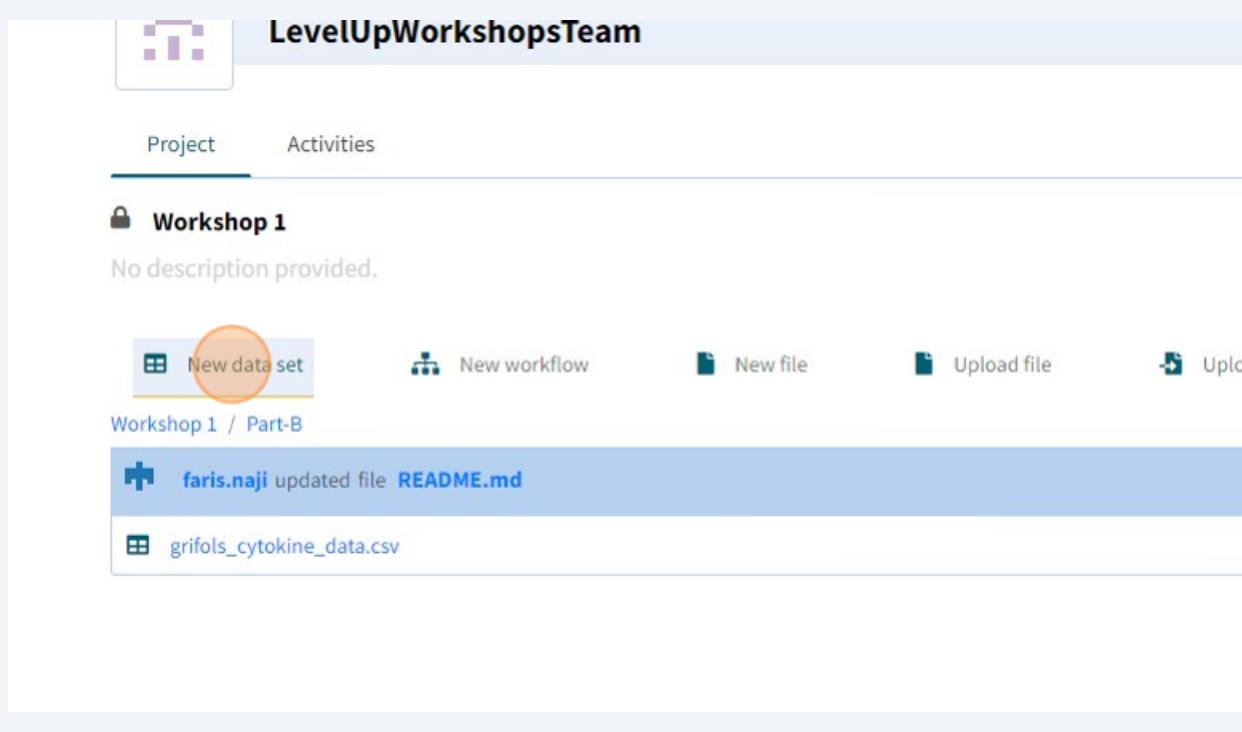
Use the slide bar to check all the other columns. They are all **numeric**, as they should be.

#	Sample ID	IFN-gamma	IL-12p70	IL-13	IL-1beta	IL-2
1	3130035837	0	0	0	0	0
2	3130035967	0	0	0	0	0
3	3370452578	0	0	0	0	0
4	3370452632	0	0	0	0	0
5	3370452658	0	0	0	0	0
6	3370452662	30.06	0	0	0	0

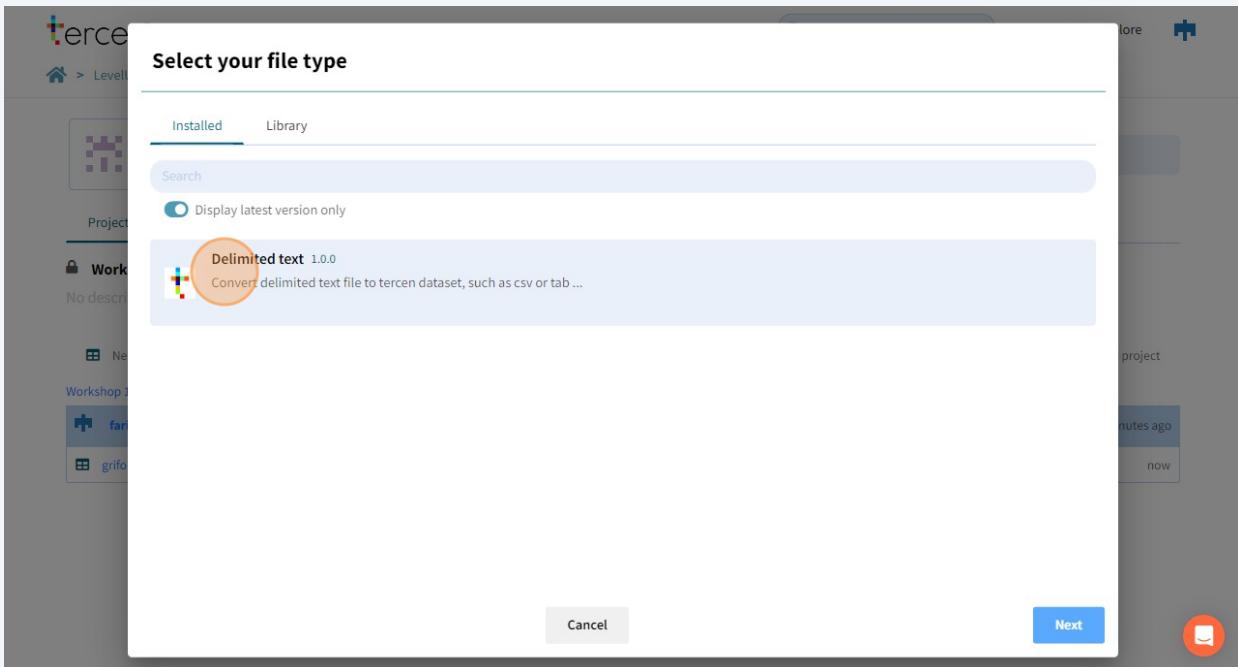
- 12** Click the **Upload** button.



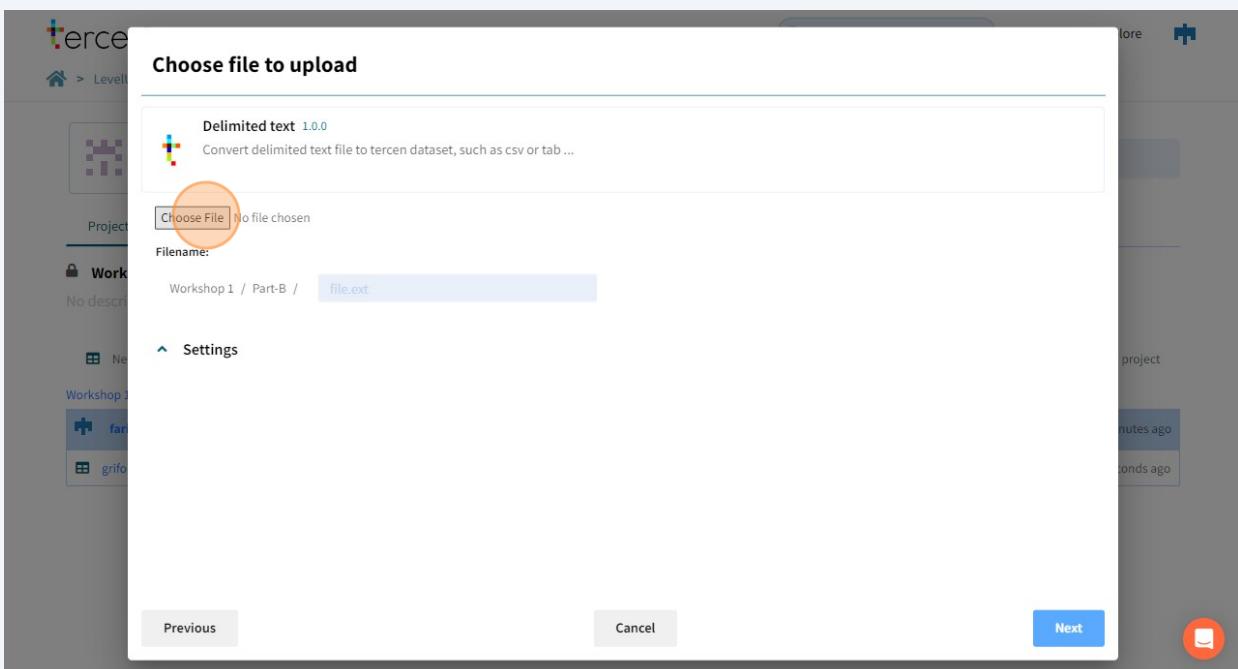
- 13** Click "New data set" icon



14 Click "Delimited text" reader

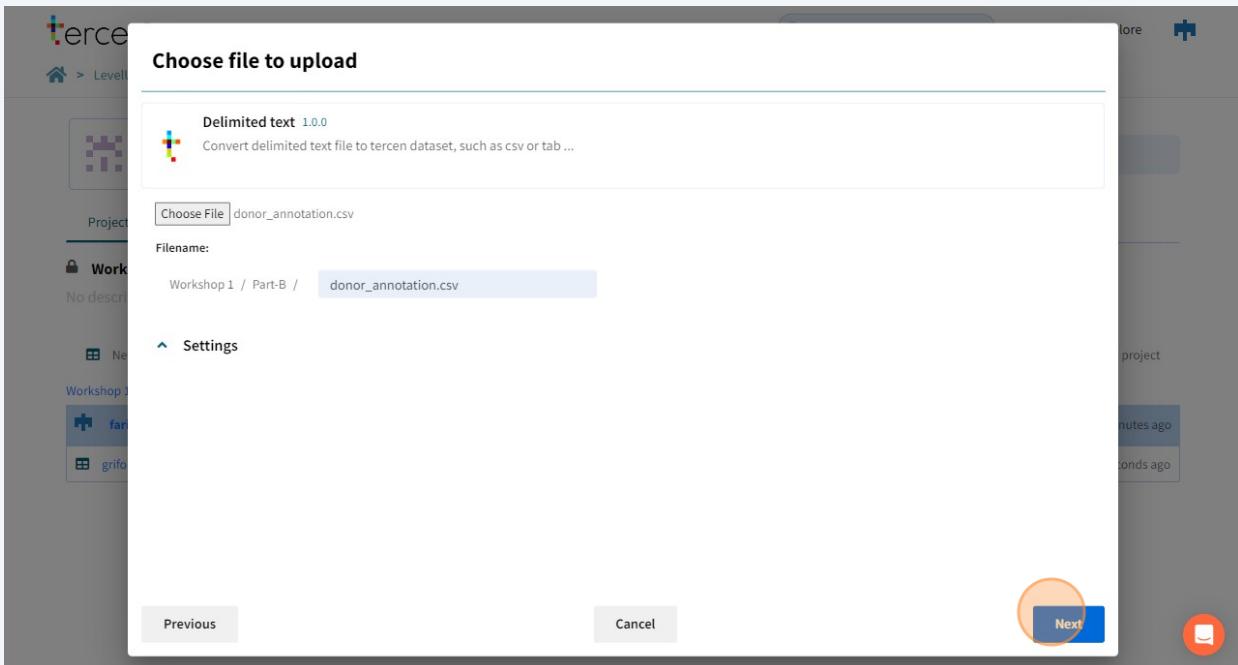


15 Click the **Choose File** button



16 Choose the **donor_annotation.csv** file in your download folder.

17 Click the "Next" button



18 Choose the **donor_annotation.csv** file in your download folder.

19

Click this dropdown under the **Sample ID** column header and choose a **character** type.

The screenshot shows a 'Check column names and types' dialog box. At the top, there are buttons for 'Advanced' and 'Upload'. Below that, it displays 'Number of rows: 127' and 'Number of columns: 7'. The table has columns labeled '#', 'SAMPLE ID', 'AGE', 'AGEGR1N', 'AGEGR1C', 'RACEGRP', and 'SEXN'. The 'SAMPLE ID' column header has a dropdown menu open, with 'numeric' selected and 'character' as an option. The data below includes rows 1 through 6, showing values like 3130035837.0, 23.0, 1.0, etc.

#	SAMPLE ID	AGE	AGEGR1N	AGEGR1C	RACEGRP	SEXN
1	3130035837.0	23.0	1.0	18-29	Caucasian	1.0
2	3130035967.0	27.0	1.0	18-29	Caucasian	1.0
3	3370452578.0	27.0	1.0	18-29	African-American	0
4	3370452632.0	23.0	1.0	18-29	Other	0
5	3370452658.0	40.0	3.0	40-49	African-American	0
6	3370452662.0	38.0	2.0	30-39	African-American	1.0

20

Click here.

The screenshot shows the same 'Check column names and types' dialog box as the previous one, but the dropdown menu for the 'SAMPLE ID' column header is now closed, showing 'character' as the selected type. The other columns ('AGE', 'AGEGR1N', 'AGEGR1C', 'RACEGRP', 'SEXN') and their dropdown menus remain visible.

#	SAMPLE ID	AGE	AGEGR1N	AGEGR1C	RACEGRP	SEXN
1	3130035837	23.0	1.0	18-29	Caucasian	1.0
2	3130035967	27.0	1.0	18-29	Caucasian	1.0
3	3370452578	27.0	1.0	18-29	African-American	0
4	3370452632	23.0	1.0	18-29	Other	0
5	3370452658	40.0	3.0	40-49	African-American	0
6	3370452662	38.0	2.0	30-39	African-American	1.0

21 Click "Upload" Button

The screenshot shows a data upload interface. At the top, it says "Check column names and types". Below that, it displays the number of rows (127) and columns (7). A table shows the first few rows of data with their corresponding column names and types:

	AGEGRIN	AGEGRIC	RACEGRP	SEXN	SEXC
1.0	18-29	Caucasian	1.0	Female	
1.0	18-29	Caucasian	1.0	Female	
1.0	18-29	African-American	0	Male	
1.0	18-29	Other	0	Male	
3.0	40-49	African-American	0	Male	
2.0	30-39	African-American	1.0	Female	

At the bottom right, there is a blue "Upload" button with a white arrow icon, which is circled in red.

22 The two files should now be in your Part-B folder.

Note how the icons of the files look like little tables.

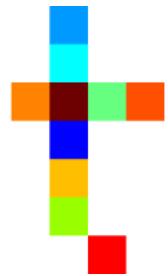
The screenshot shows a project dashboard for "LevelUpWorkshopsTeam". The main navigation bar has tabs for "Project" and "Activities", with "Project" being active. Below the navigation, there is a section for "Workshop I" with the message "No description provided." and four action buttons: "New data set", "New workflow", "New file", and "Upload file".

The "Workshop I / Part-B" section lists the following files:

- faris.naji updated project Workshop I
- grifols_cytokine_data.csv
- donor_annotation.csv

23 You have now successfully imported two files.

0109 - Plot Data



This guide creates a cytokine analysis workflow and shows how to generate plots to visualize all cytokine values across all healthy subjects. The first projection uses one cytokine (TNF-alpha). The second projection introduces a **Gather** to transform data into long format so a projection using all cytokines can be created.

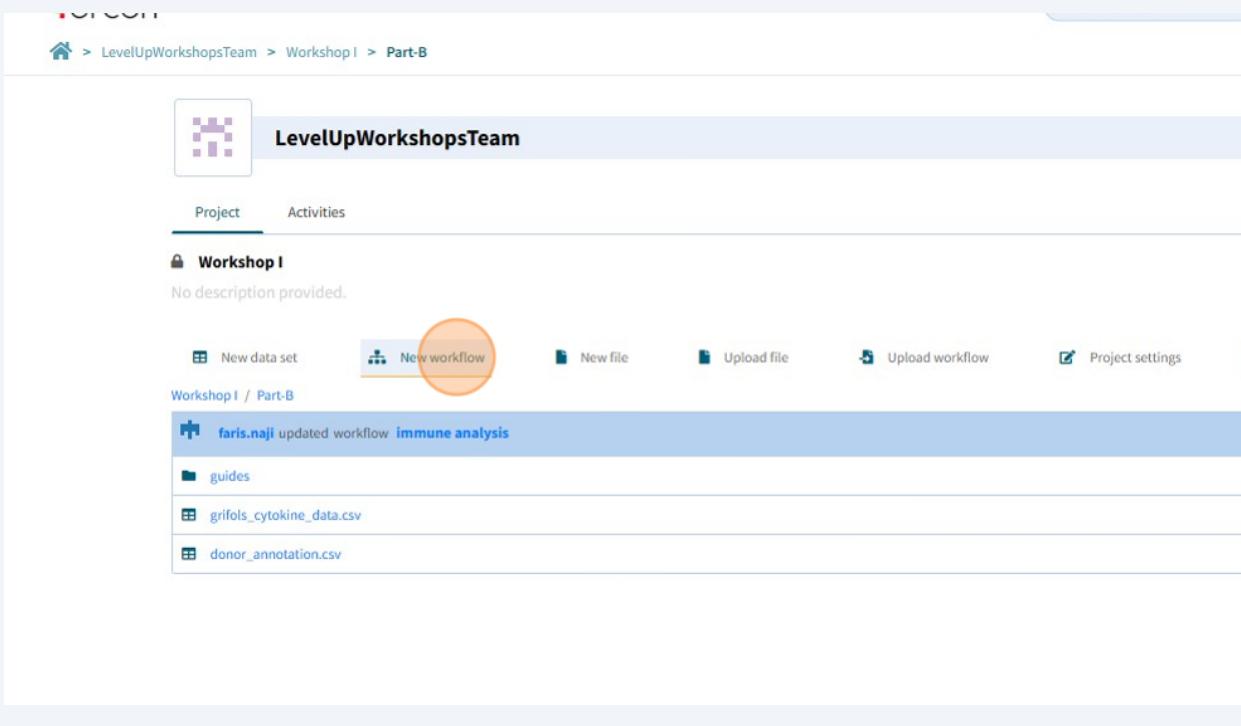
- 1 We begin at the top level of Workshop I project.

Click on the folder **Part-B**.

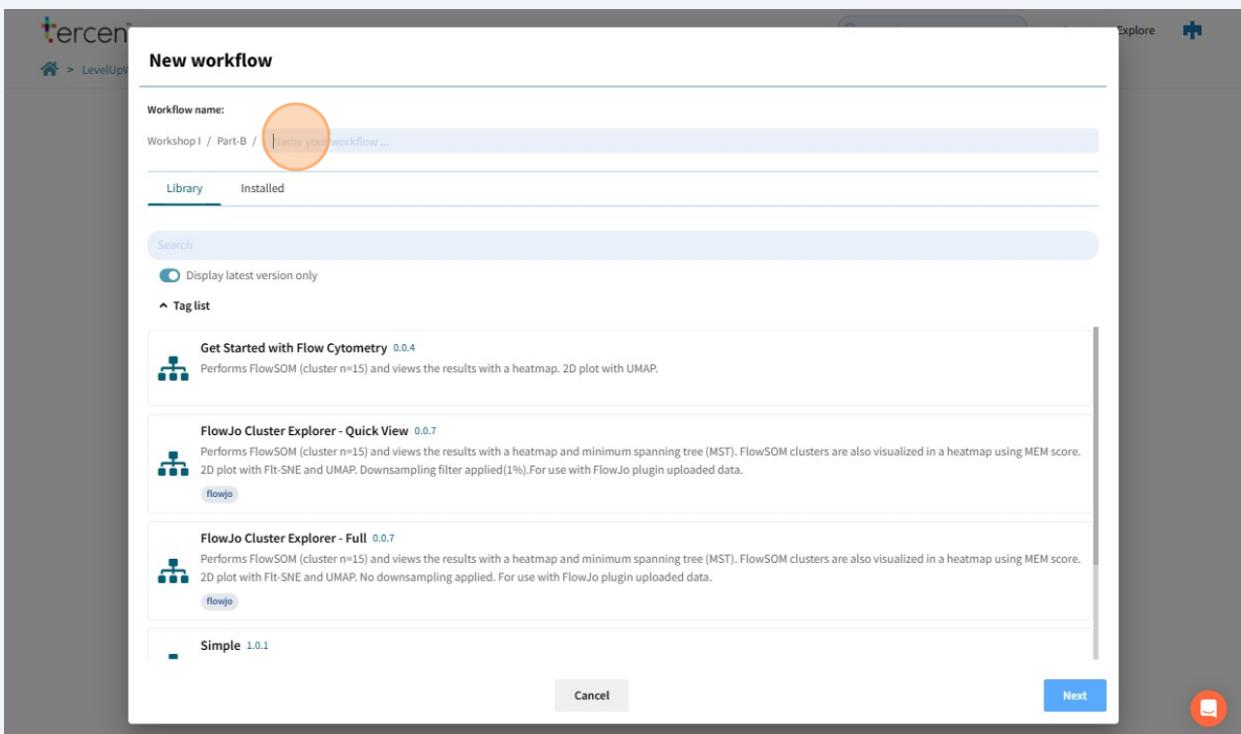
The screenshot shows a project interface with the following details:

- Project Header:** LevelUpWorkshopsTeam
- Navigation:** Home > LevelUpWorkshopsTeam > Workshop I
- Project Tabs:** Project (selected), Activities
- Project Description:** No description provided.
- File Management Buttons:** New data set, New workflow, New file, Upload file, Upload workflow, Proj
- File Tree:** A list of files and folders:
 - faris.naji updated file README.md
 - README.md
 - Part-B (highlighted with a red circle)
 - Part-A
 - files
- Bottom Panel:** A preview area showing README.md.

2 Click "New workflow"

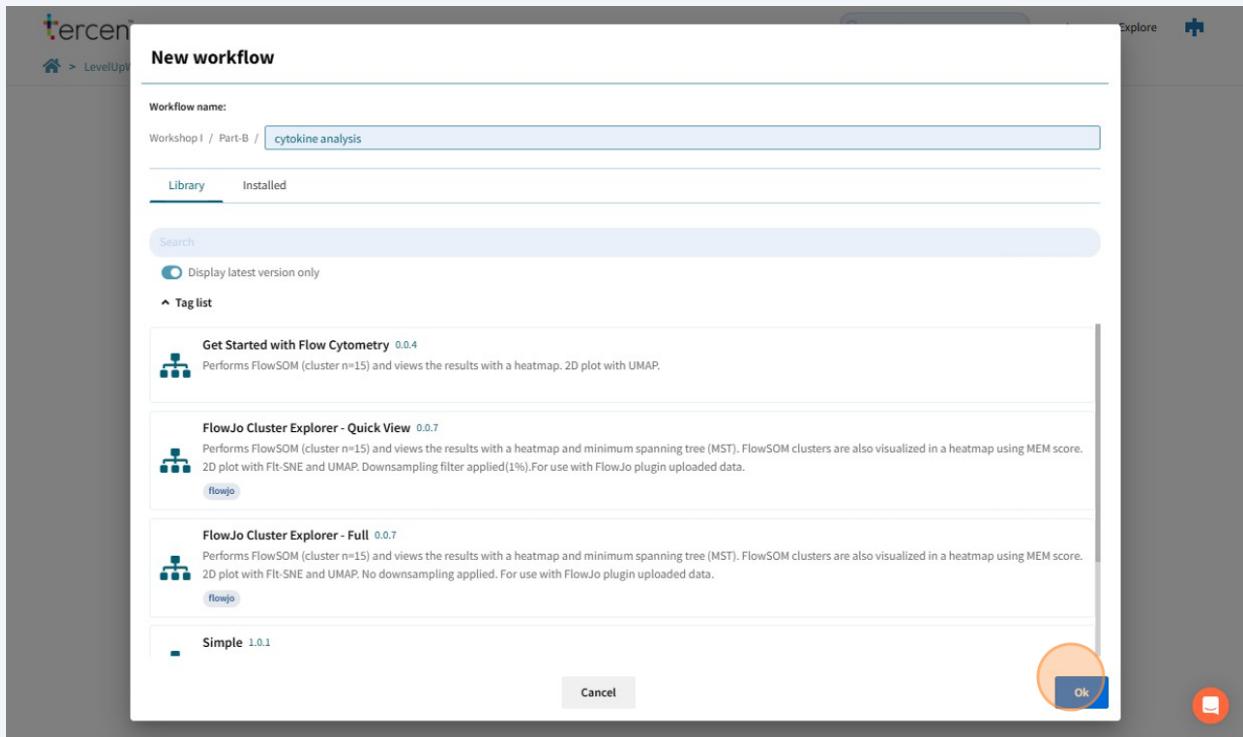


3 Click the "Name your workflow ..." field.

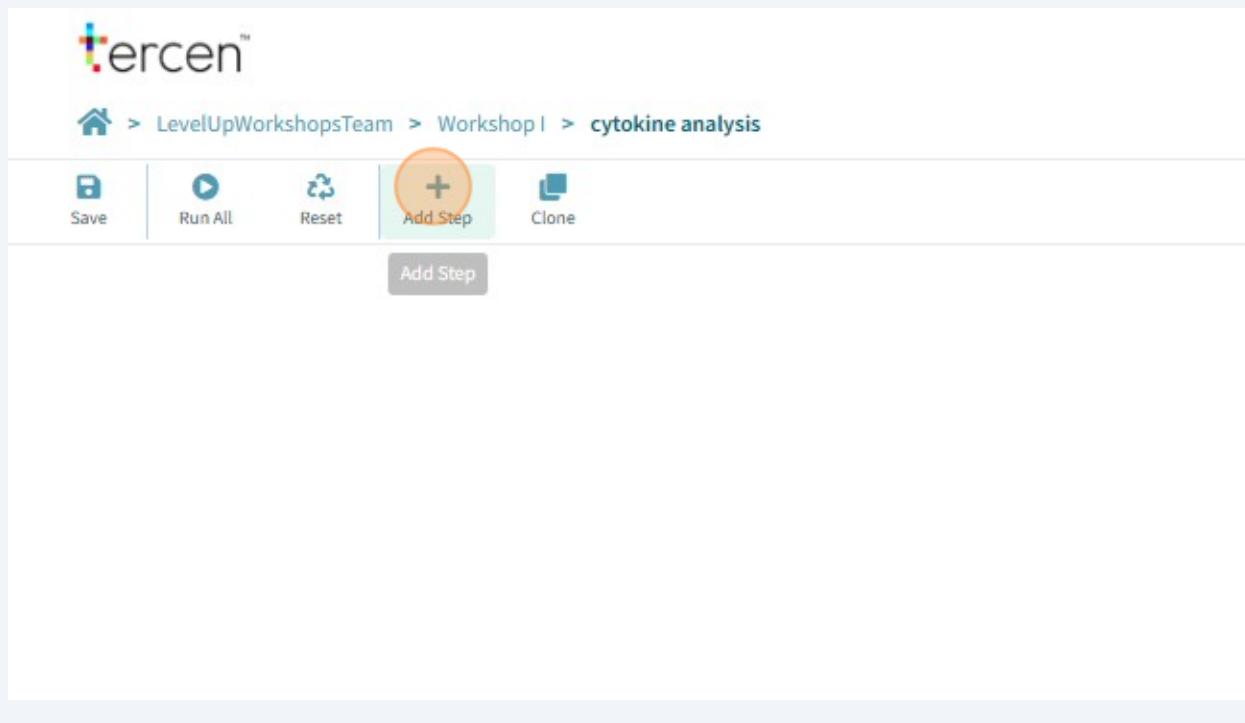


4 Type "cytokine analysis"

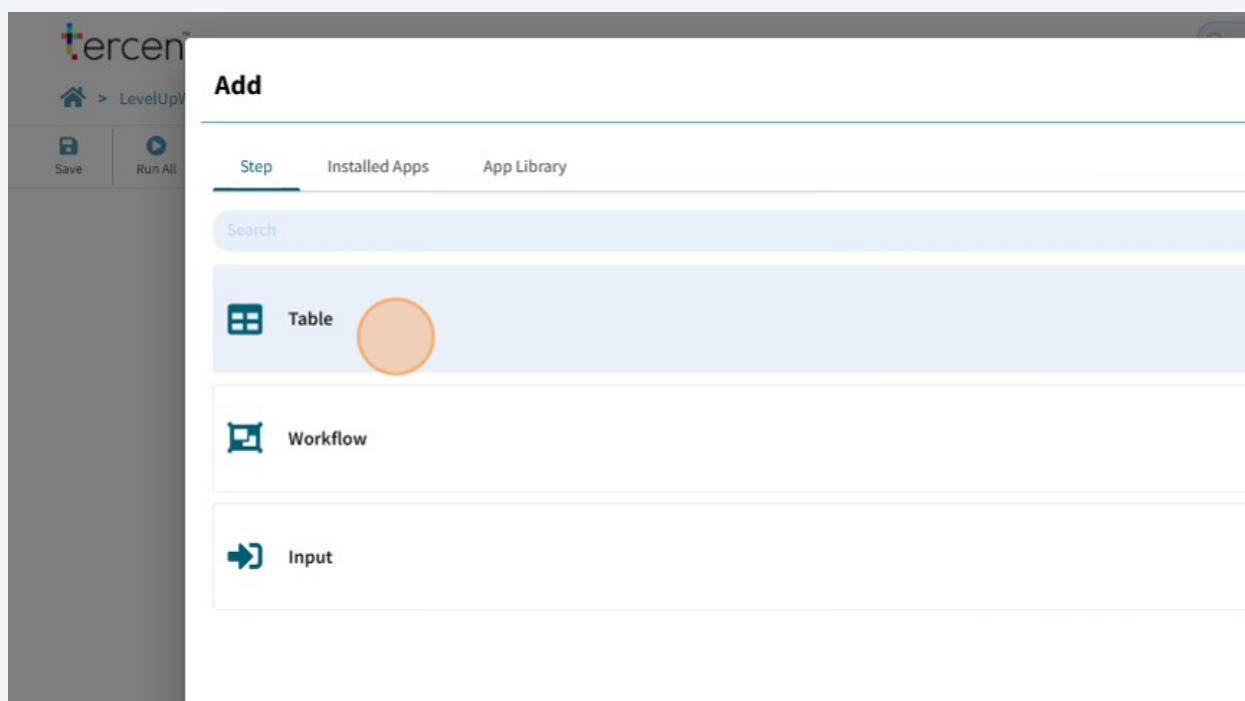
5 Click **Ok** button



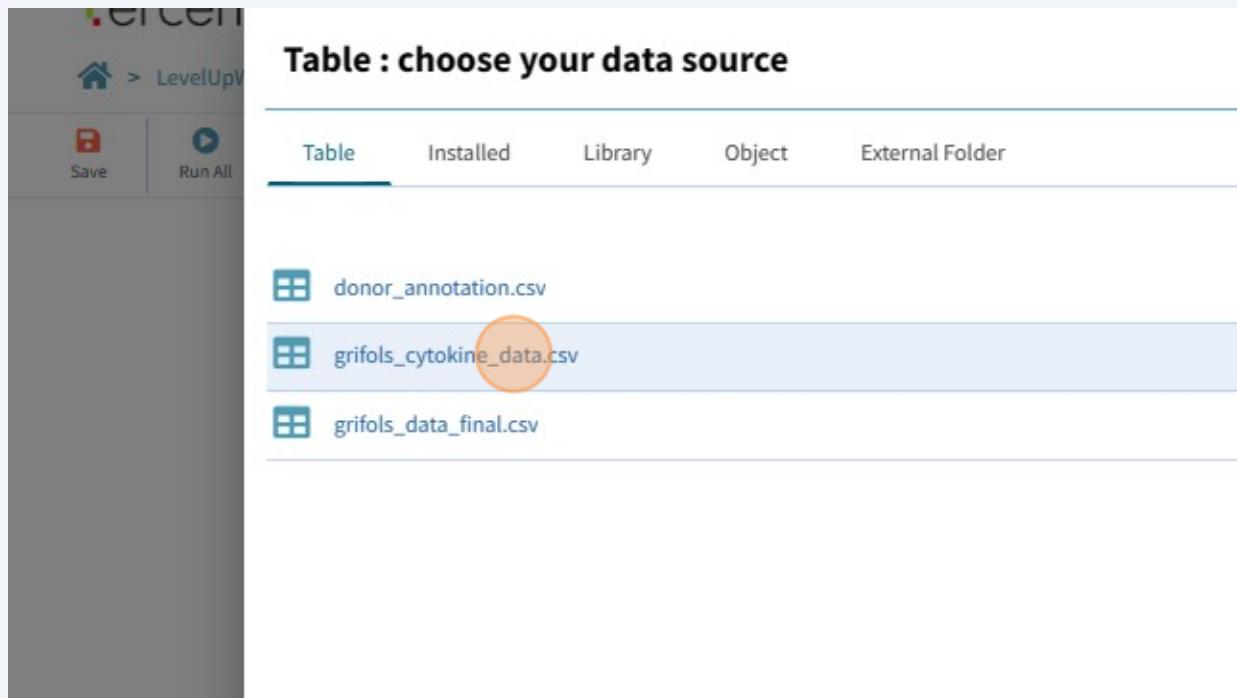
- 6 Click on the **Add Step** icon.



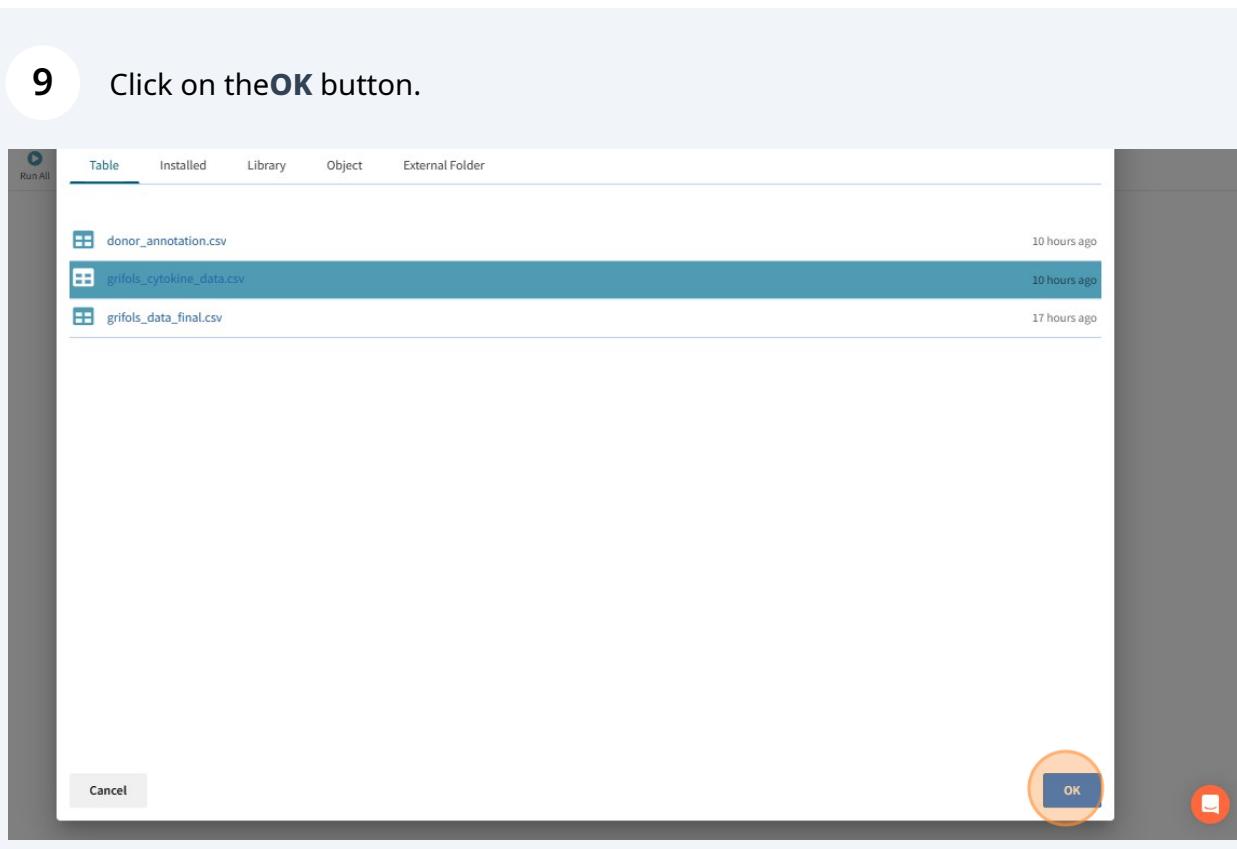
- 7 Click on the **Table** icon



- 8 Click on "grifols_cytokine_data.csv"

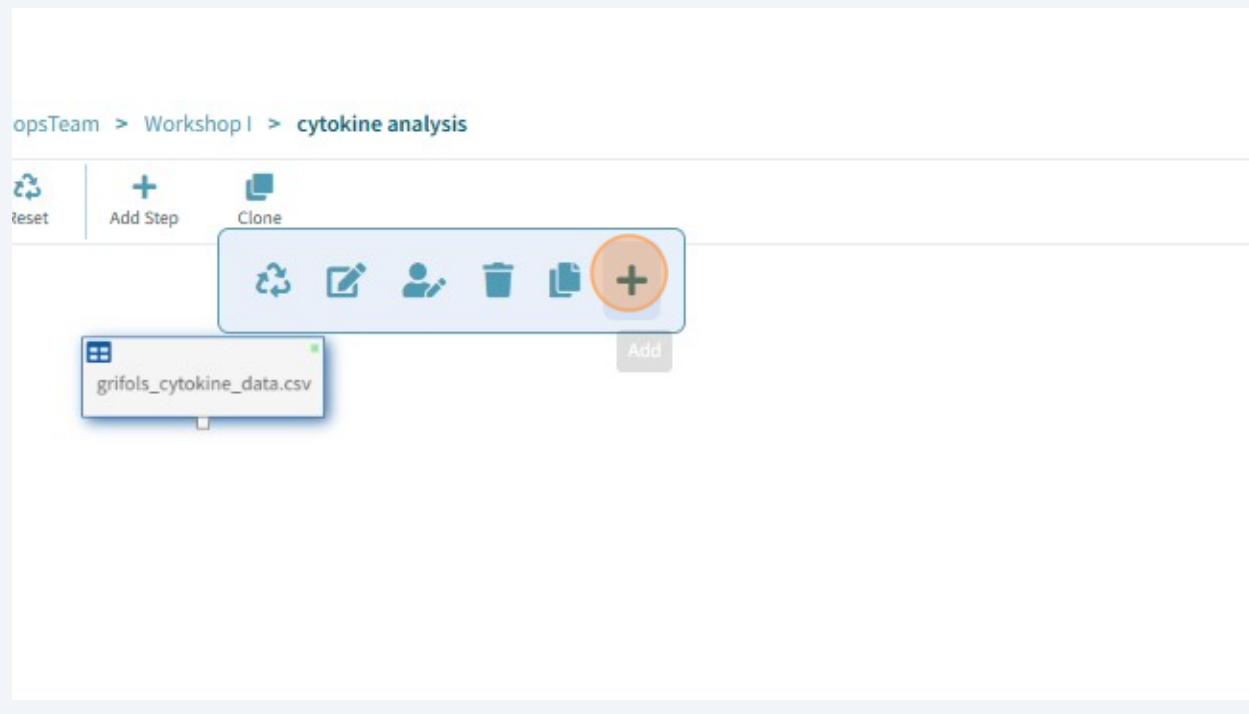


- 9 Click on the OK button.

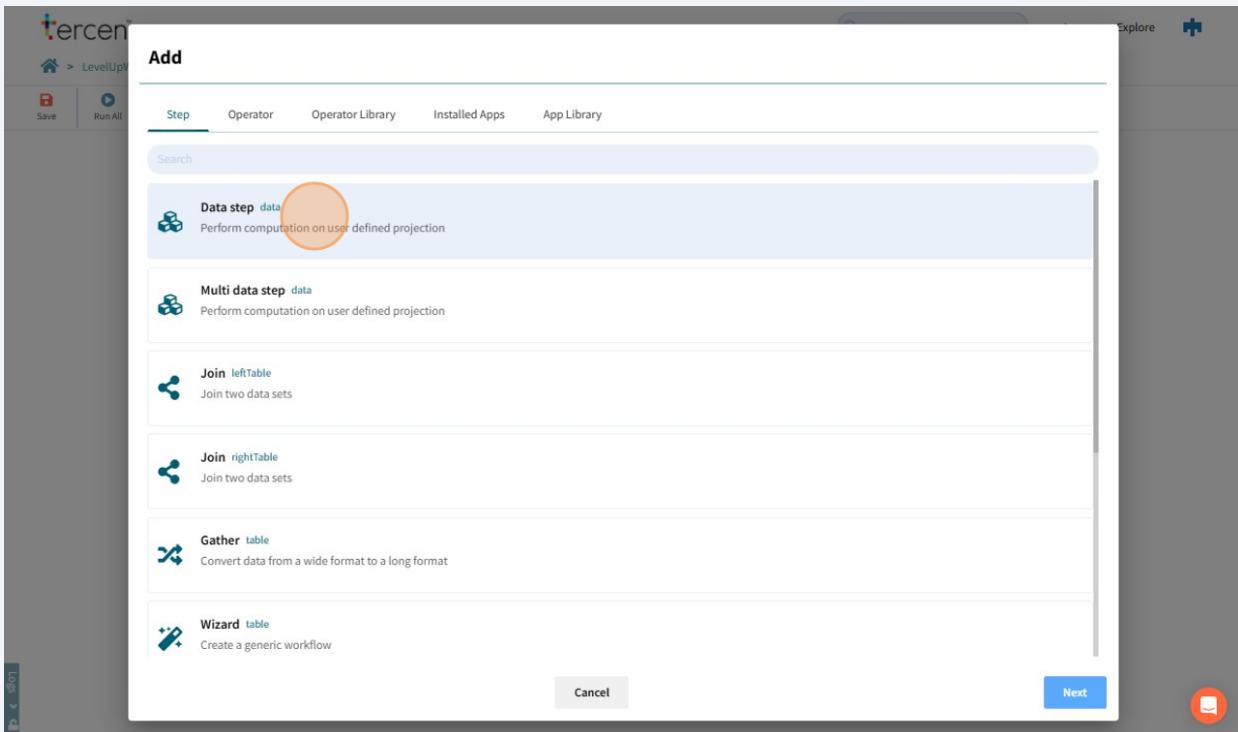


10 We will now create our first plot of the imported cytokine data.

11 Click the Data Table and add a step from the local toolbar.



12 Click on the **Data step**



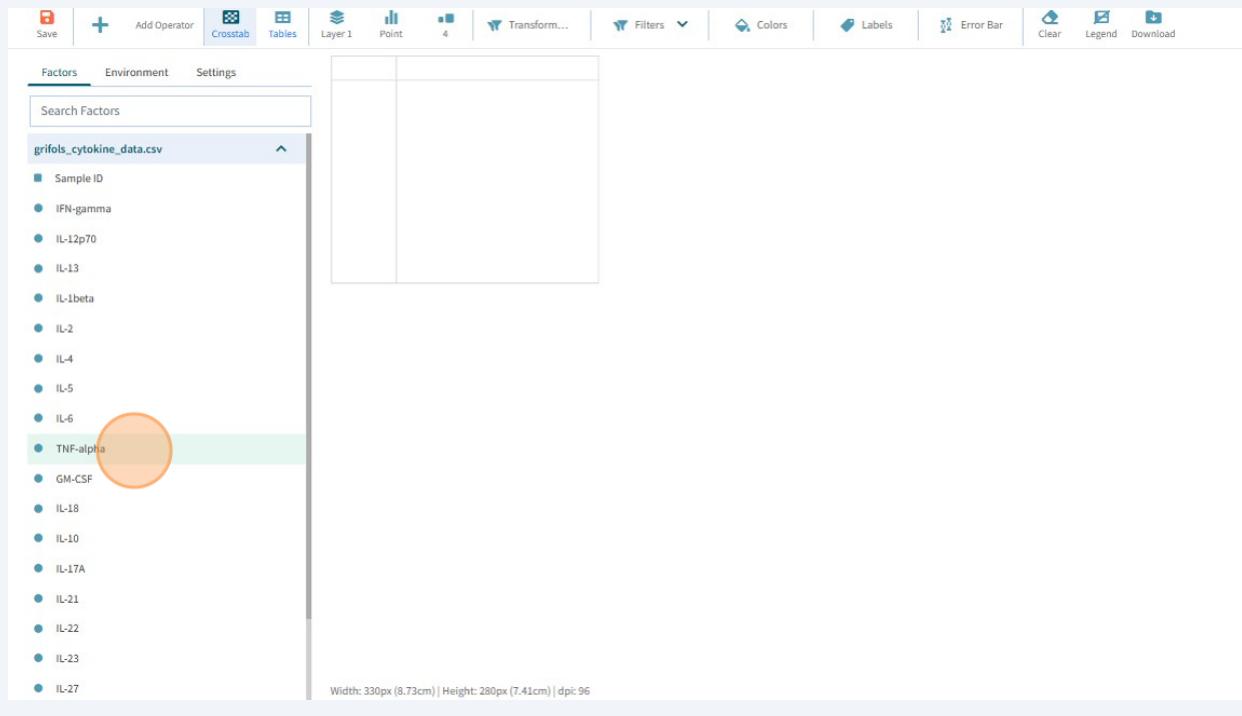
13 This opens the Crosstab Window.

It is one of the most important windows in Tercen.

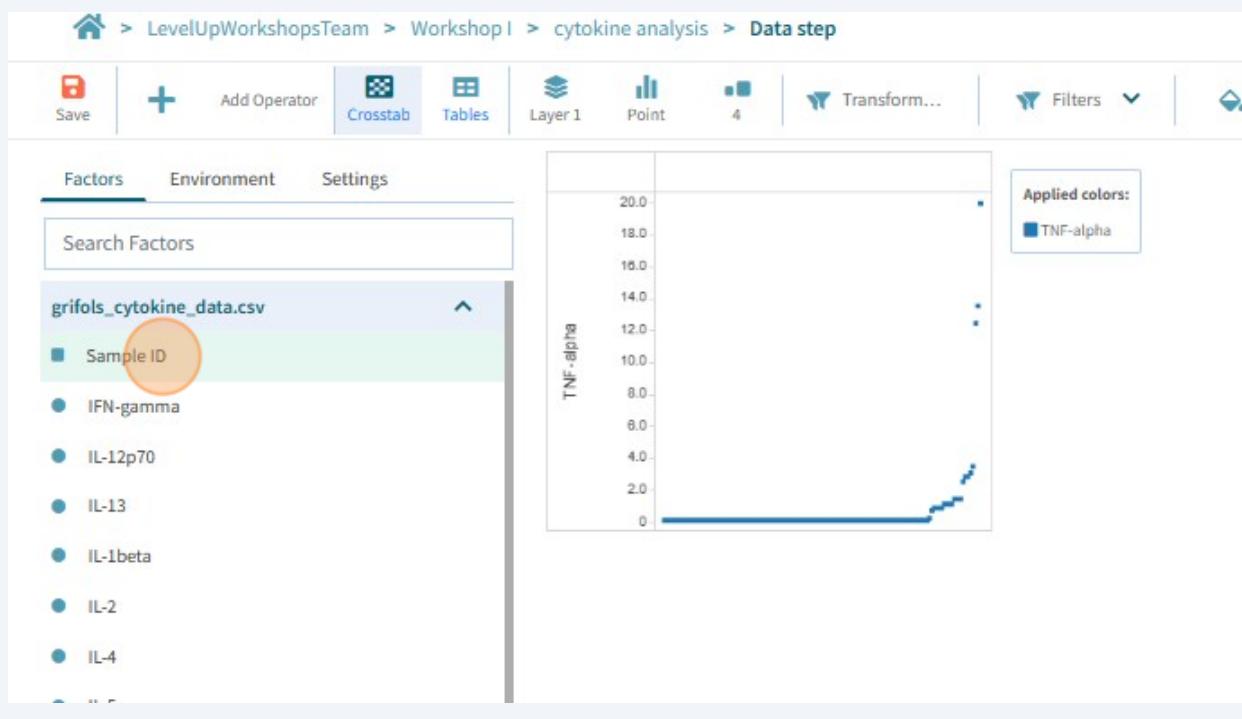
We use it to define a wide variety of plots of the data. We call these plots, projections.

We will now start defining a projection (i.e. plot) of the cytokine data.

14 Drag **TNF-alpha** and drop it onto the Y-Axis.



15 Drag "**Sample ID**" and drop it onto the X-Axis zone





Alert!

When dragging the **Sample ID** onto the X-Axis, it is easy to drop it into the wrong area, such as the Columns, by mistake. This is because the X-Axis is just under the Column area, and it is easy to confuse the two.

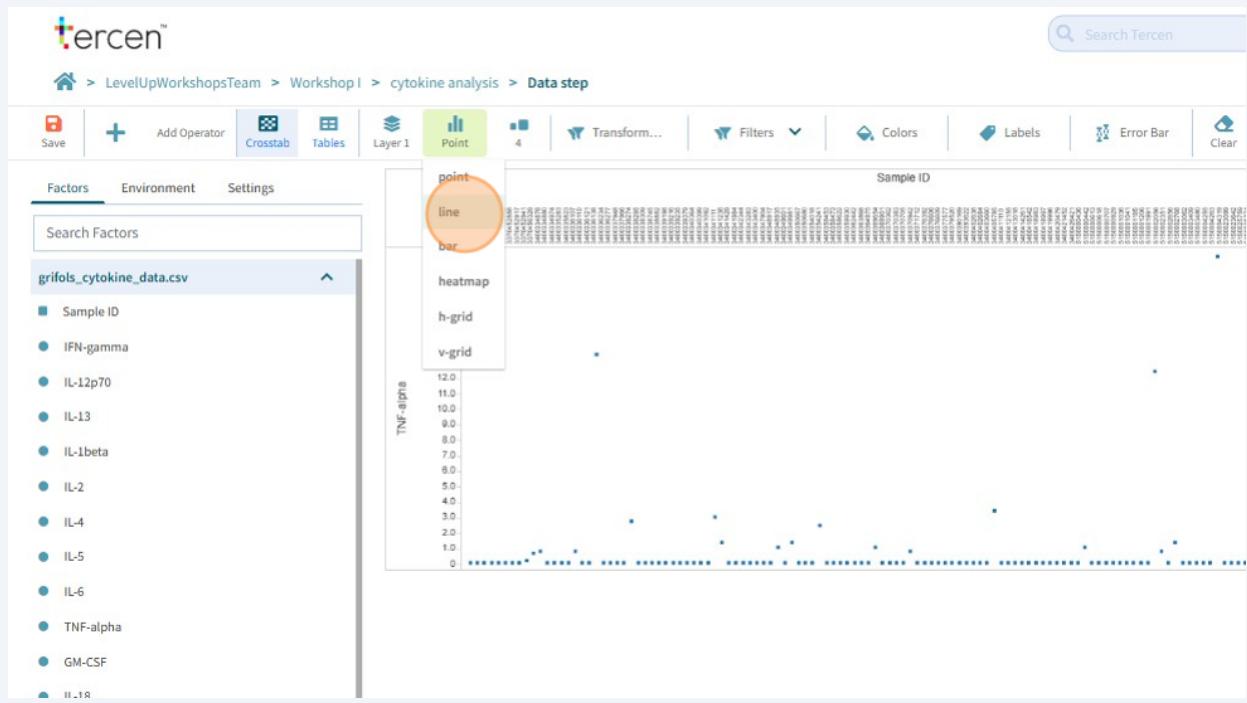
The consequence of a mistake such as this results in a plot where there are individual data points in each data cell instead of having all the data points in one single data cell (see previous screenshot to check you got it right).

16

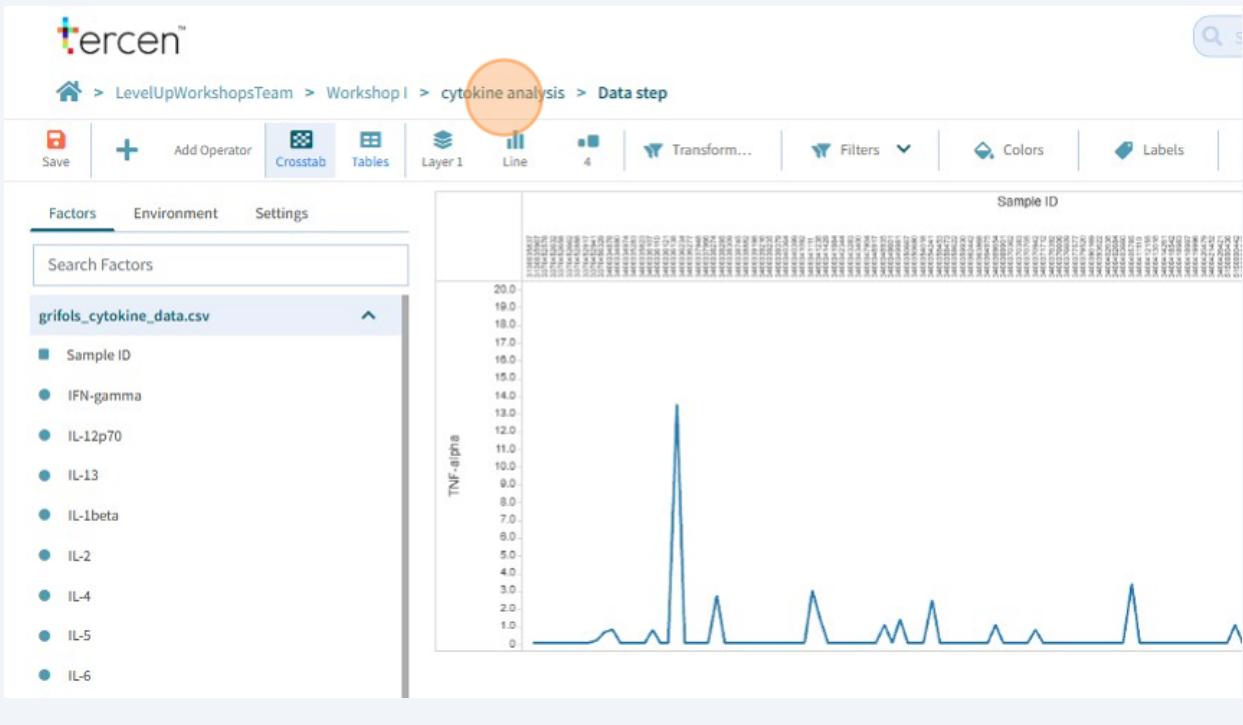
Drag the black lines to adjust the graph on screen.

Click on the **Graph Style** button to change the viewing mode.

Choose the **line** mode.



17 Click "cytokine analysis" in the breadcrumb to navigate to the workflow level.



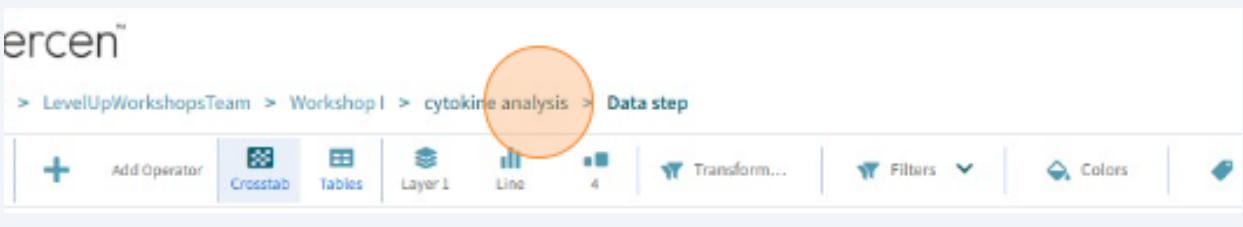
Alert!

Did you notice each cytokine factor on the left of the Crosstab is separate?

In the Crosstab, dragging multiple cytokines to the Rows is impossible. This will limit our ability to plot all the data in one graph.

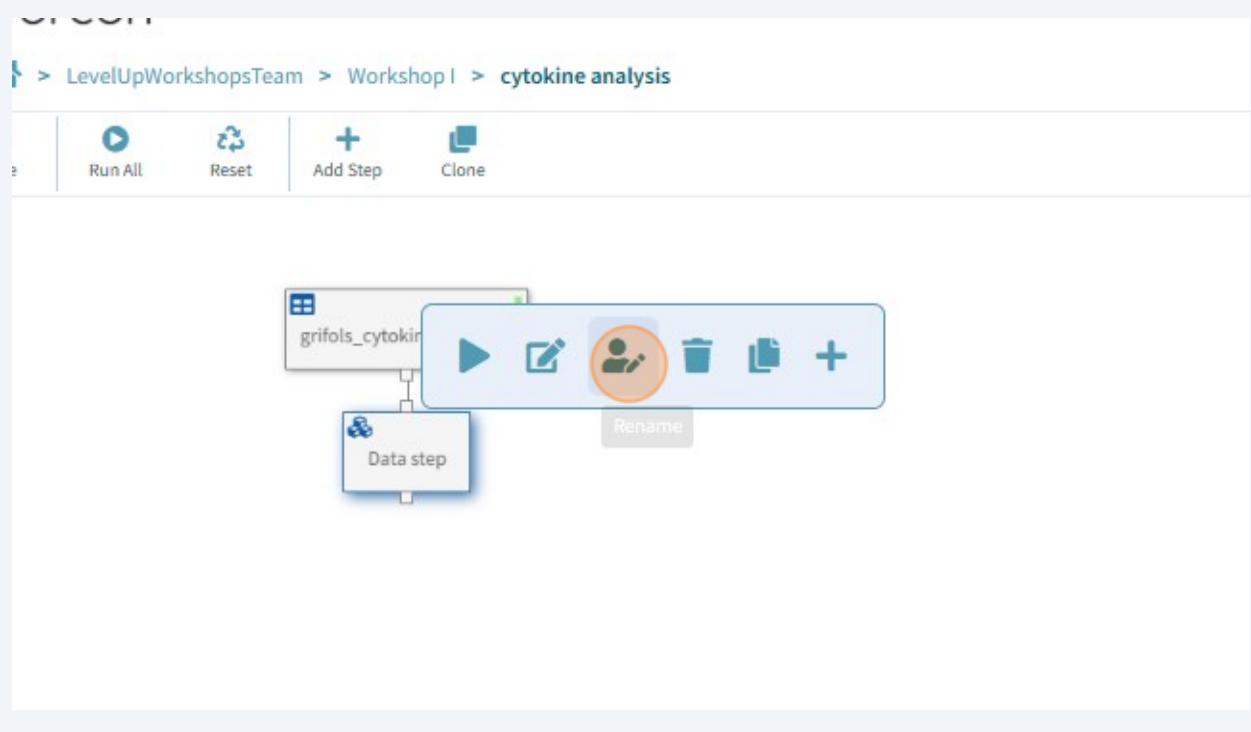
Later, we will use a Gather Step to resolve this issue.

18 Navigate one level up to the workflow, use the breadcrumb at the top.

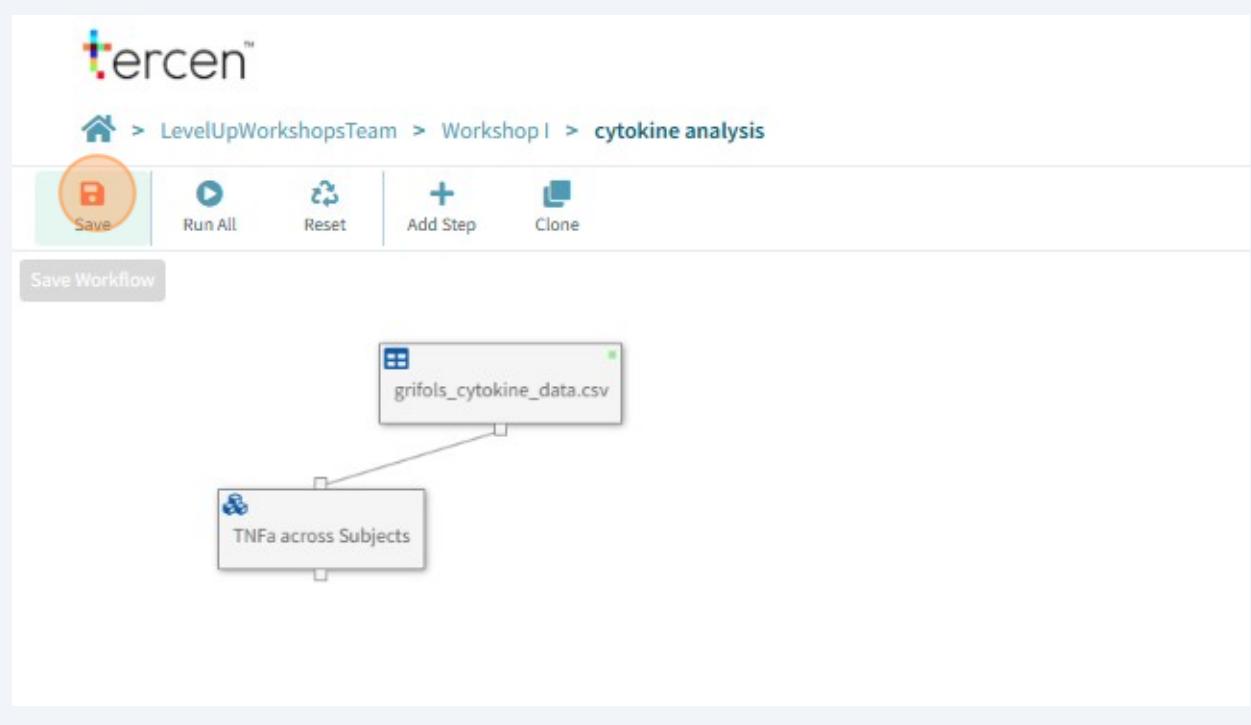


- 19 Rename the data step.

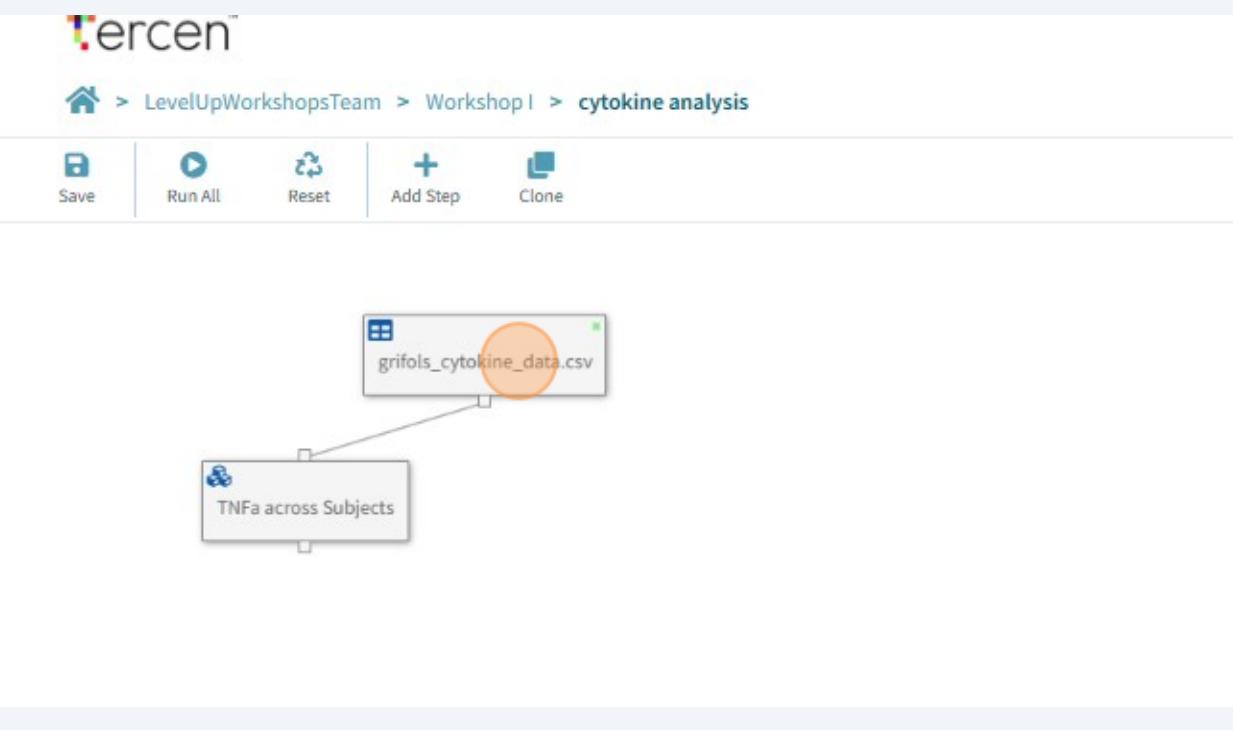
"TNFa across Subjects"



- 20 Click on the **Save** icon to save your work



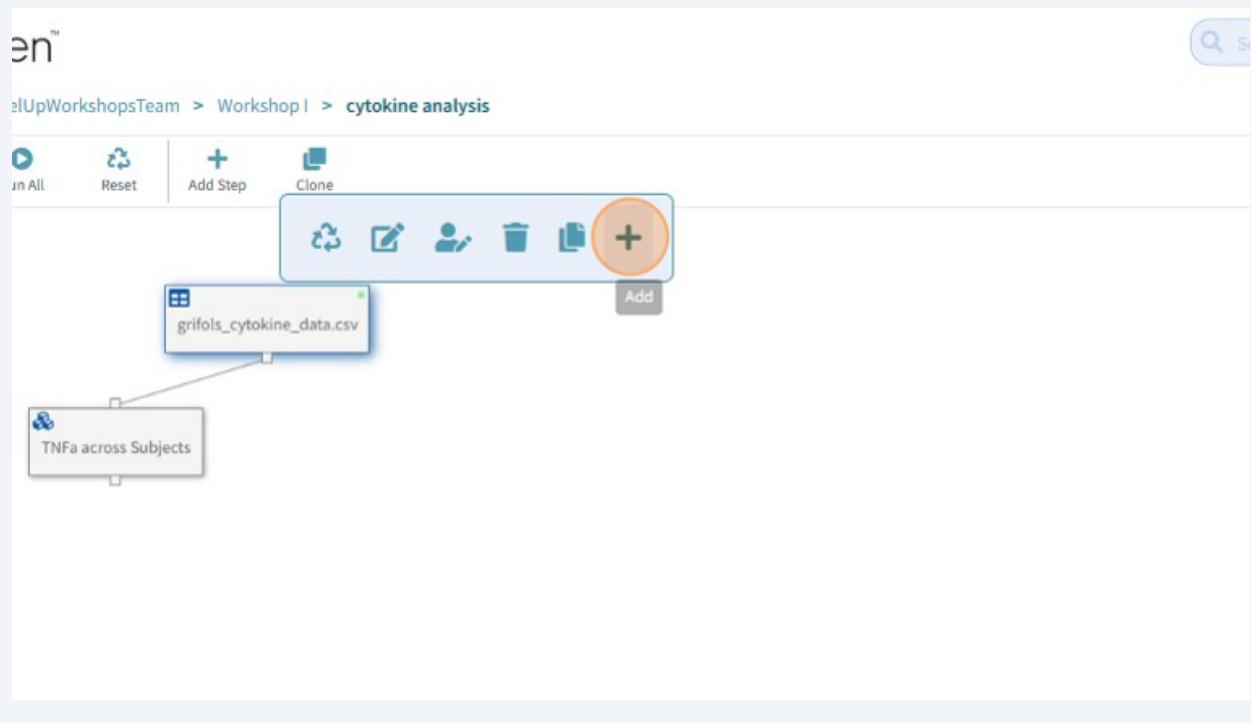
21 Click here.



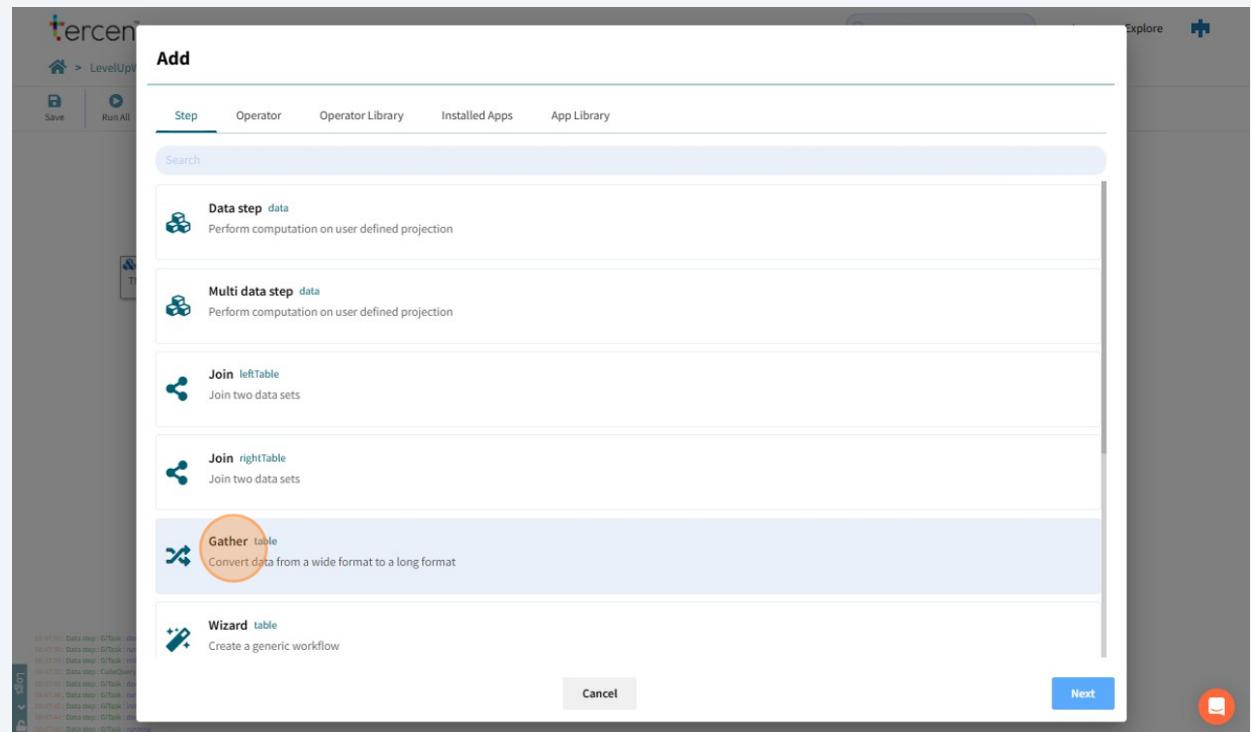
22 Lets add a Gather Step. This will allow us to bundle the cytokines together into a single Factor that can be used to make plots.

A **Gather** will convert data to a long format. This allows us to do a greater variety of plots and computations.

23 Click here.

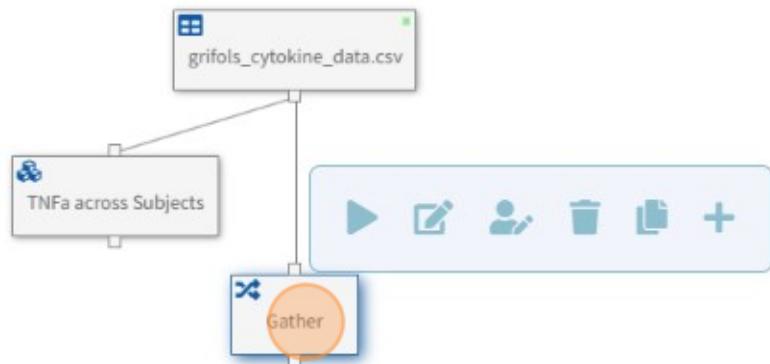


24 Click on the Gather Step.



25 Click the Gather step to open the local tool bar

Choose Edit to open the step.



26 This opens the Gather window. Click into this text field.

Namespace
850

Selection pattern

Factor type
 Numeric
 Character

Factors
 Select all

- IFN-gamma (numeric)
- IL-12p70 (numeric)
- IL-13 (numeric)
- IL-1beta (numeric)
- IL-2 (numeric)
- IL-4 (numeric)
- IL-5 (numeric)
- IL-6 (numeric)
- TNF-alpha (numeric)
- GM-CSF (numeric)
- IL-18 (numeric)
- IL-10 (numeric)
- IL-17A (numeric)
- IL-21 (numeric)
- IL-22 (numeric)



Tip!

A namespace is a text that is used to prefix the output. It requires to be unique in the workflow. The default name is automatically filled, i.e., **gs0**.

The default name is perfectly fine.

However, changing it to a name that best describes your gathering concept is helpful. In this case, it is "cytokine" factors.

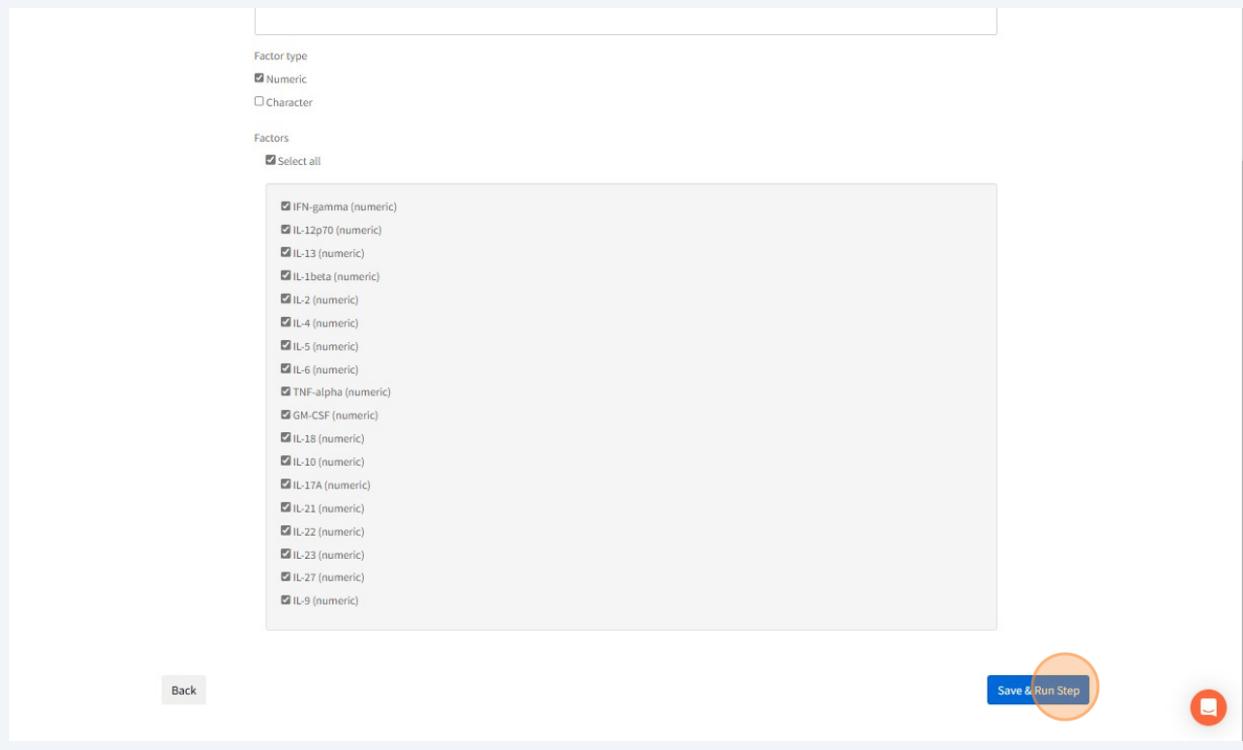
27

Click the "Select all" field. This selects all the cytokines and lets the Gather Step bundle all the cytokines together.

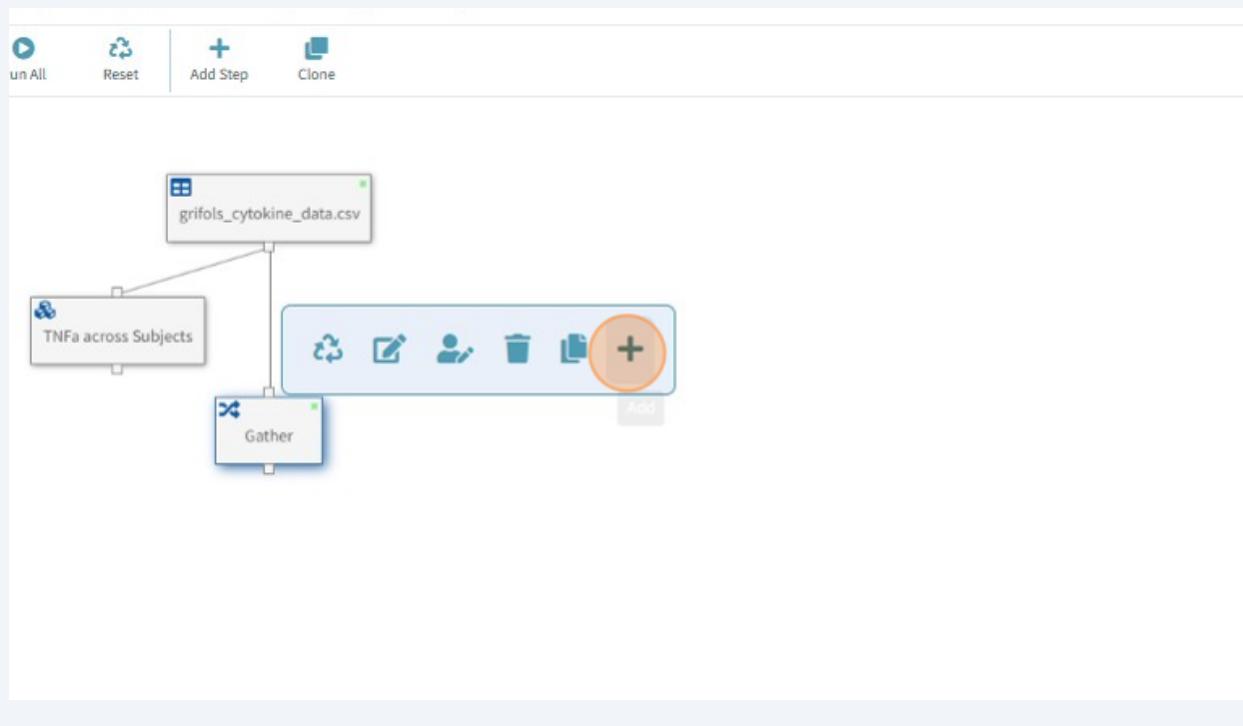
The screenshot shows a software interface for selecting factors. At the top, there is a section labeled "Selection pattern" with a large empty text input field. Below this is a "Factor type" section with two checkboxes: "Numeric" (which is checked) and "Character". Under the "Factors" section, there is a button labeled "Select all" which is highlighted with an orange circle. A dropdown menu is open, listing six cytokines, each preceded by an empty checkbox:

- IFN-gamma (numeric)
- IL-12p70 (numeric)
- IL-13 (numeric)
- IL-1beta (numeric)
- IL-2 (numeric)
- IL-4 (numeric)

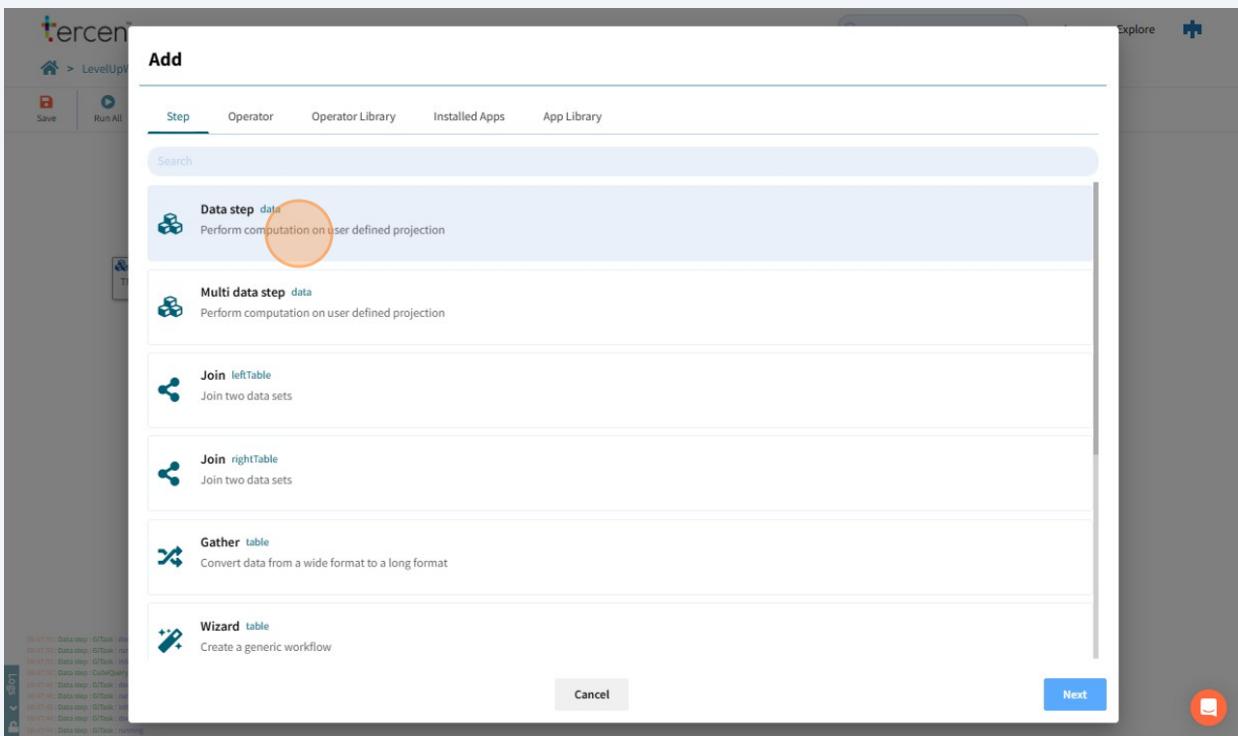
28 Click "Save & Run Step"



29 Click here.



30 Click here.



- 31 A Crosstab window opens.

You will notice two new factors **cytokine.value** and **cytokine.variable**.

The **cytokine.value** factor represents all the cytokine values.

The **cytokine.variable** factor represents all the names of the cytokines.

These two factors were created by the **Gather step**

The screenshot shows the tercen software interface. At the top, there is a navigation bar with icons for Save, Add Operator, Crosstab (which is selected), Tables, Layer 1, Point, Transform..., Filters, and a download icon. Below the navigation bar, there is a breadcrumb trail: Home > LevelUpWorkshopsTeam > Workshop I > cytokine analysis > Data step. On the left, there are tabs for Factors, Environment, and Settings, with Factors selected. Under the Factors tab, there is a search bar labeled 'Search Factors' and a dropdown menu showing 'grifols_cytokine_data.csv'. Below this, under the 'Gather' section, there is a list of factors: 'cytokine.value' (highlighted with a red box) and 'cytokine.variable'.

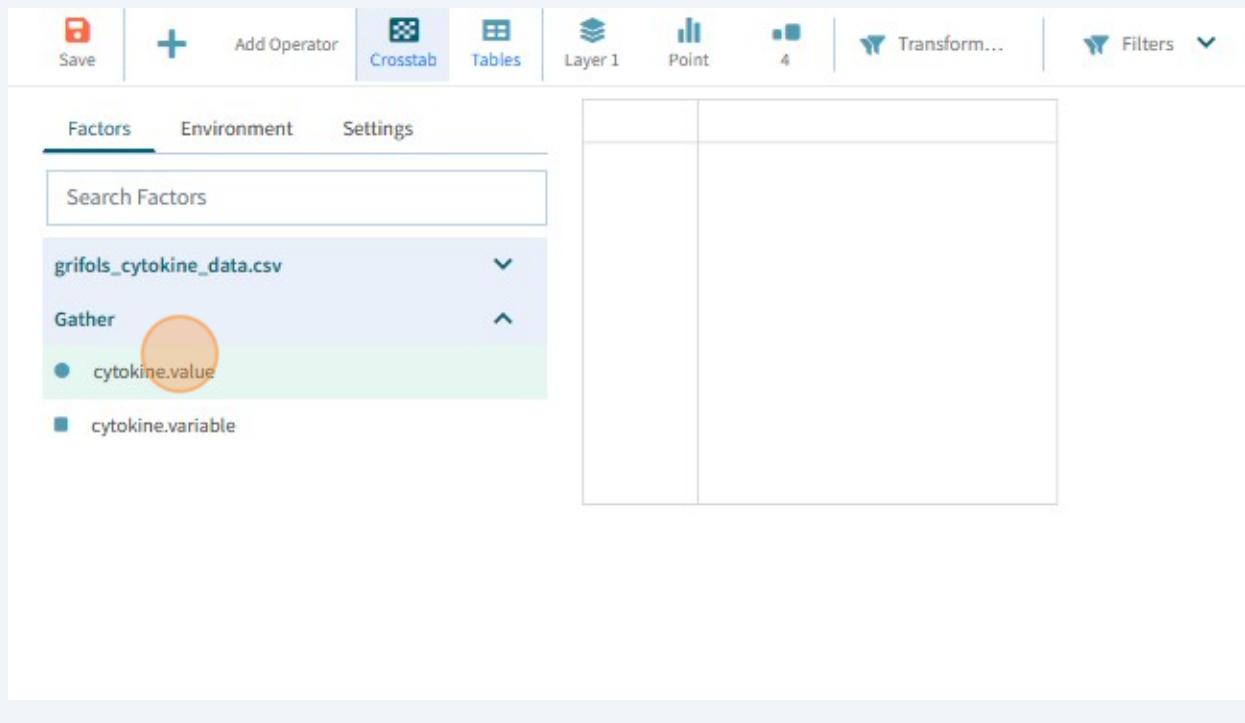
- Note:

The **Gather step** output is always a **value** and a **variable**.

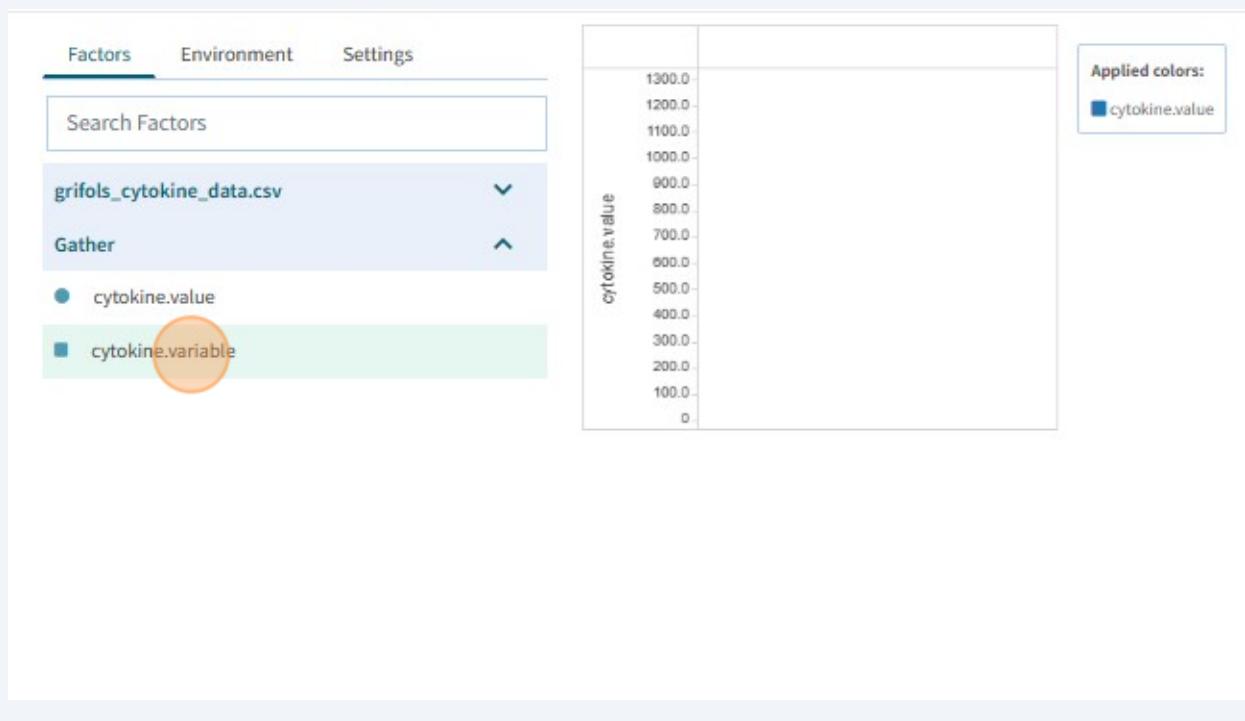
The **Gather step** is convenient and can be applied to other situations where, for example, there are separate sample columns in the dataset and who like to gather them into one concept.

Hint: There is a question about this in the quiz.

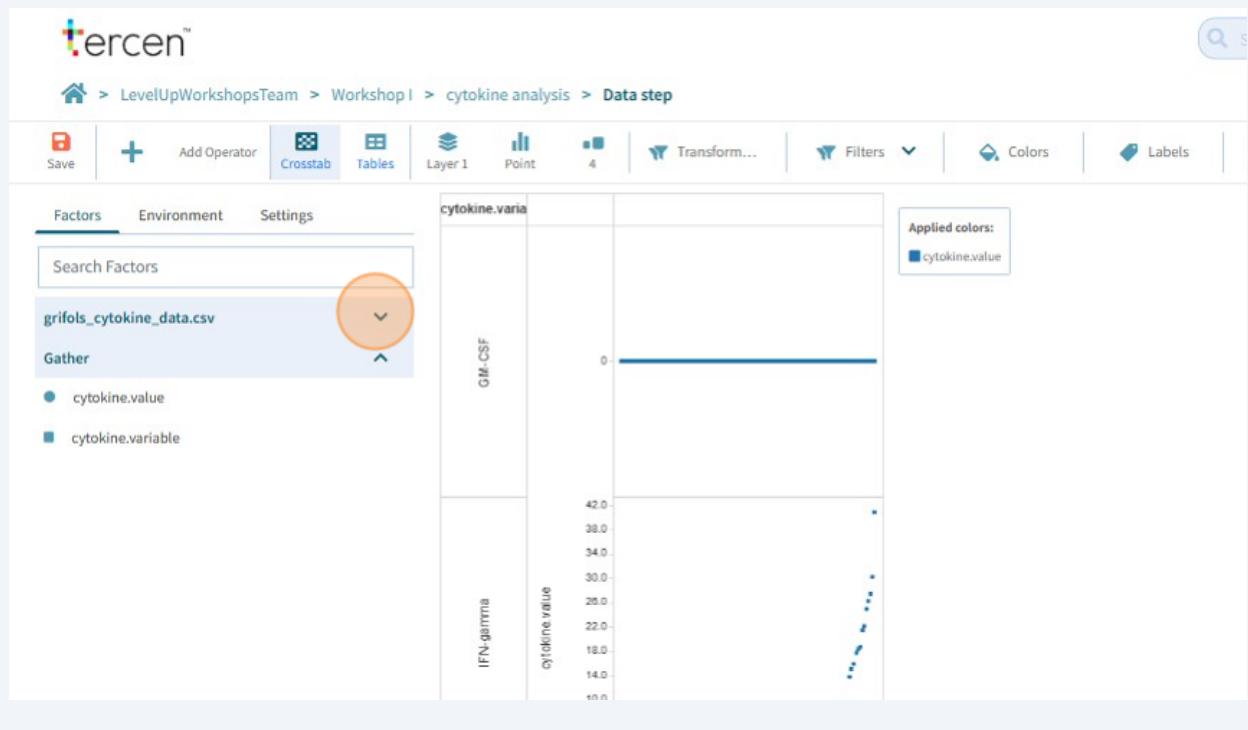
32 Drag **cytokine.value** and drop it onto the Y-Axis.



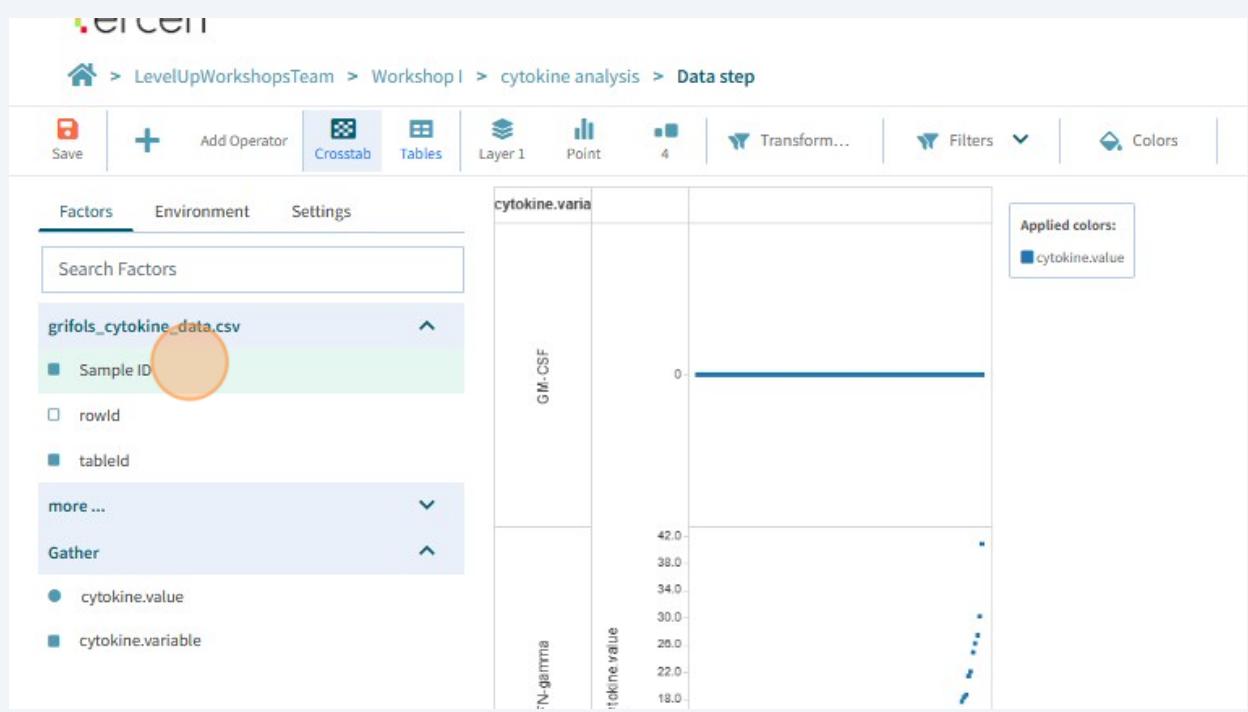
33 Drag **cytokine.variable** and drop it onto the Rows.



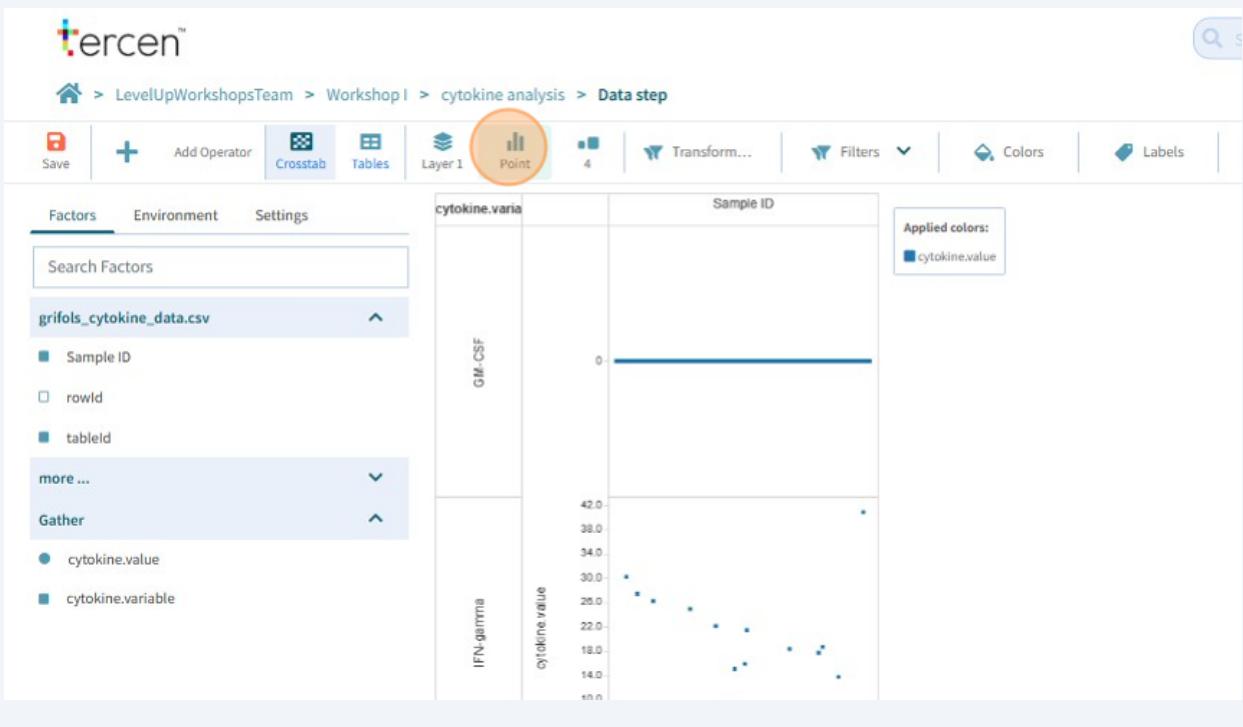
34 Click here to expand the factor list.



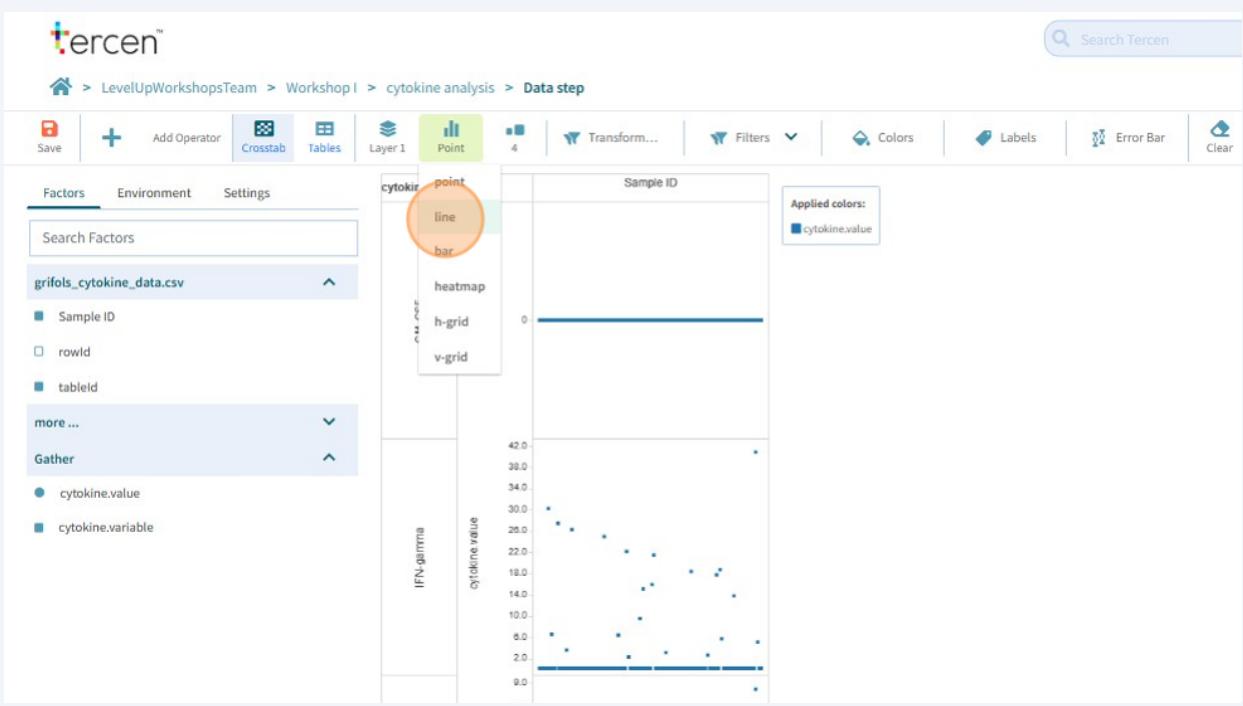
35 Drag Sample ID and drop it onto the Columns.



36 Click on the Graph Style.

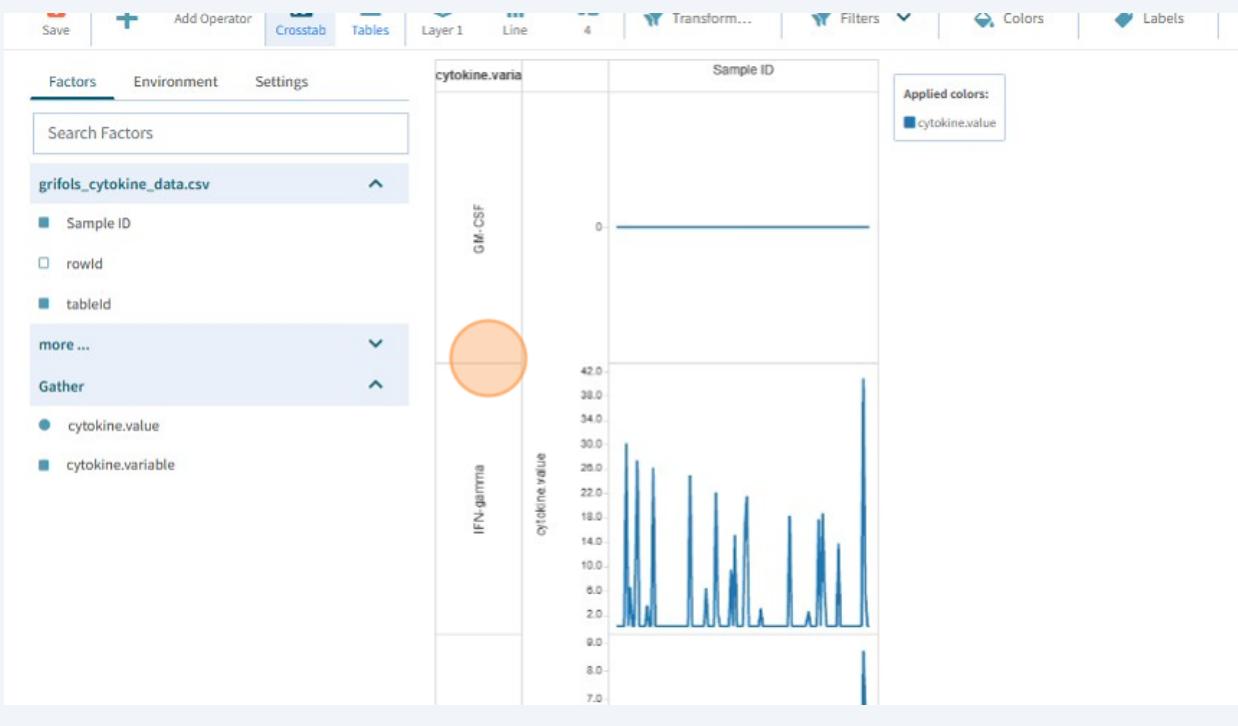


37 Click "line"



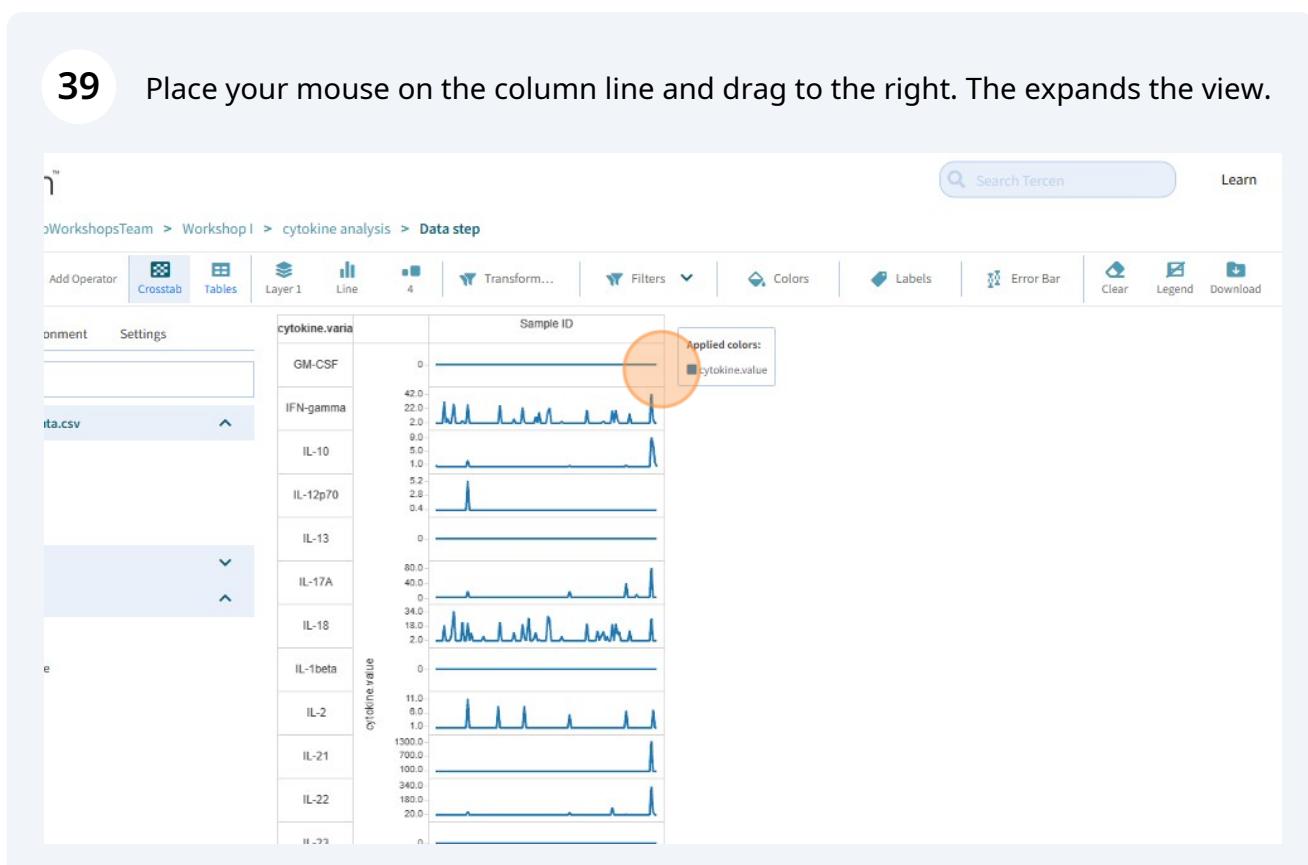
38

Place your mouse on the row line and drag it upwards. This compresses the view.

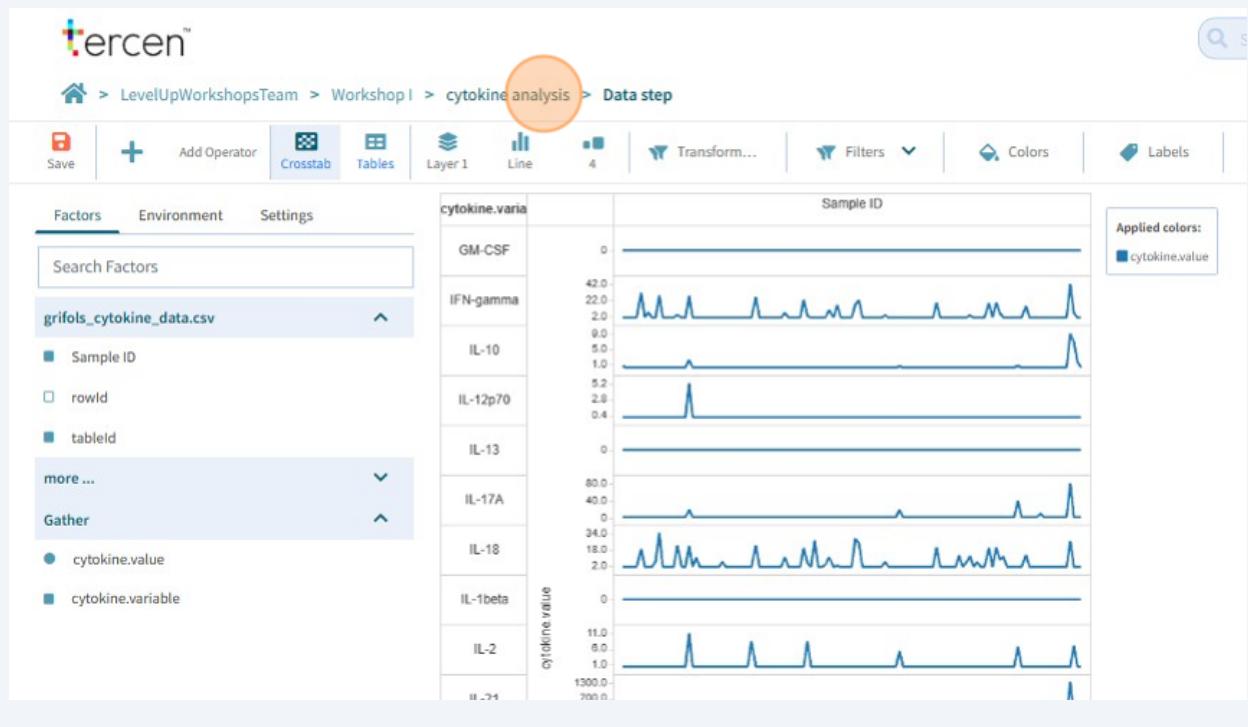


39

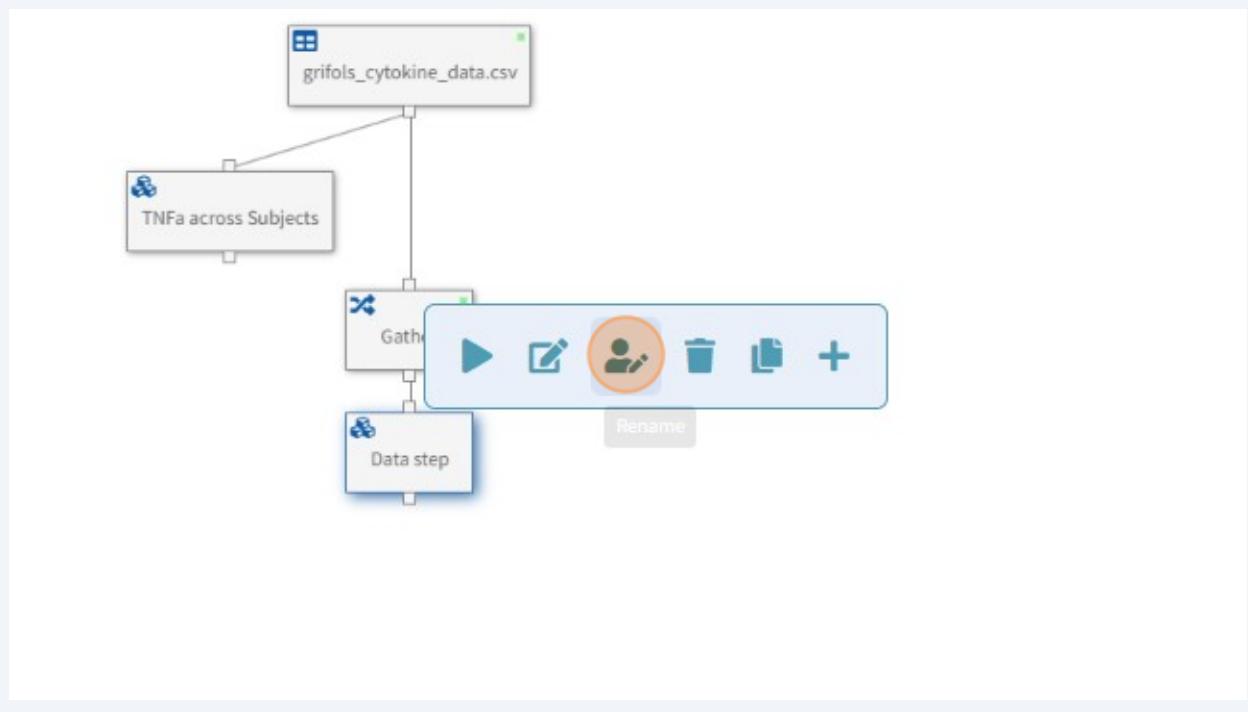
Place your mouse on the column line and drag to the right. The expands the view.



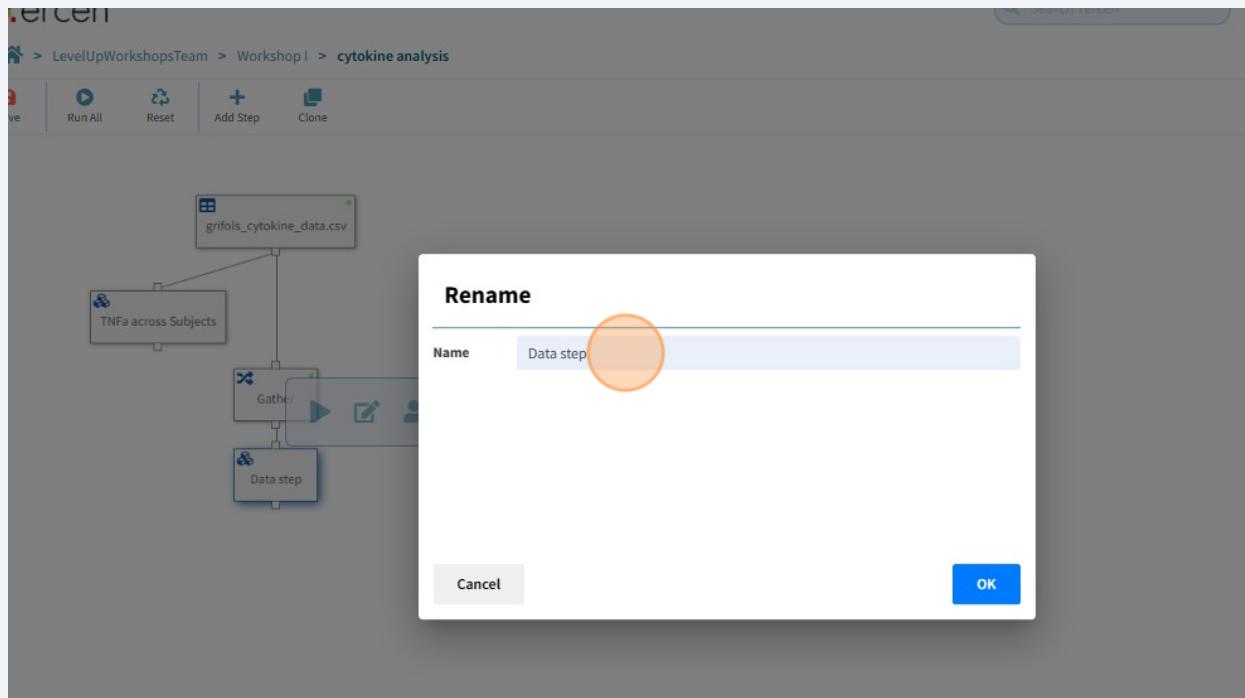
40 Click "cytokine analysis", this returns you to the workflow level.



41 Click on the Data Step

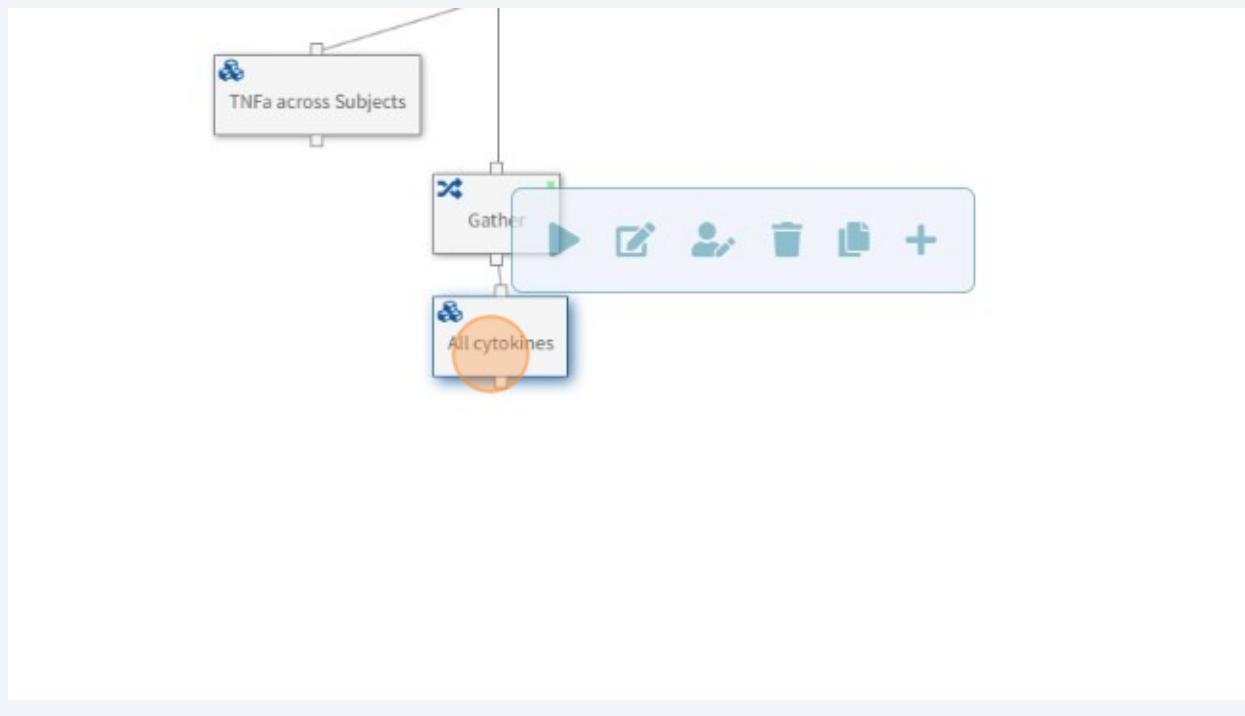


42 Click this text field.



43 Type "All cytokines"

44 Drag the "All cytokines" data step to the left to make room.



45 Click on the **Save** icon to save your work.

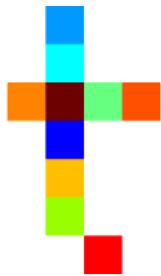


46

You have now imported, gathered, and plotted all 18 cytokines against all 127 donor subjects.

Well done!

0110 - Join Donor Information



This guide provides step-by-step instructions on how to use the Join step to merge donor annotations and cytokine data and then analyse them together in new projections.

- 1 We wish to add the donor information to the cytokine measurements.

The extra information is contained in the donor annotation file.

This requires merging them. This first requires to identify the commonalities between the two files.

We call this process identifying the keys.

If you open the **grifols_cytokine_data.csv** and the **donor_annotation.csv** file side by side, you will notice they each have one column containing the same type of information. However, the column names differ.

In the cytokine file, the column is called **Sample ID**; in the donor file, it is called the **SUBJECT ID**.

We call these common column headers keys.

Key

grifol_cytokine_data.csv

A	B	C	D	E	F	G	H
1 Sample ID	FN-gamma	IL-12p70	IL-13	IL-1beta	IL-2	IL-4	IL-5
2 3130035837	0	0	0	0	0	0	0
3 3130035967	0	0	0	0	0	0	0
4 3370452578	0	0	0	0	0	0	0
5 3370452632	0	0	0	0	0	0	0
6 3370452658	0	0	0	0	0	0	0
7 3370452662	30.06	0	0	0	0	0	0
8 3370452888	0	0	0	0	0	0	0
9 3370452917	6.39	0	0	0	0	0	0
10 3370452941	0	0	0	0	0	0	0
11 3370456329	0	0	0	0	0	0	0
12 3400334878	27.22	0	0	0	0	0	0
13 3400334880	0	0	0	0	0	0	0
14 3400334974	0	0	0	0	0	0	0
15 3400335283	0	0	0	0	0	0	0
16 3400335823	0	0	0	0	0	0	0
17 3400336107	3.44	0	0	0	0	0	0
18 3400336110	0	0	0	0	0	0	0
19 3400336121	0	0	0	0	0	0	0
20 3400336138	26.15	5.12	0	0	10.7	0	2.55
21 3400336234	0	0	0	0	0	0	0

donor_annotation.csv

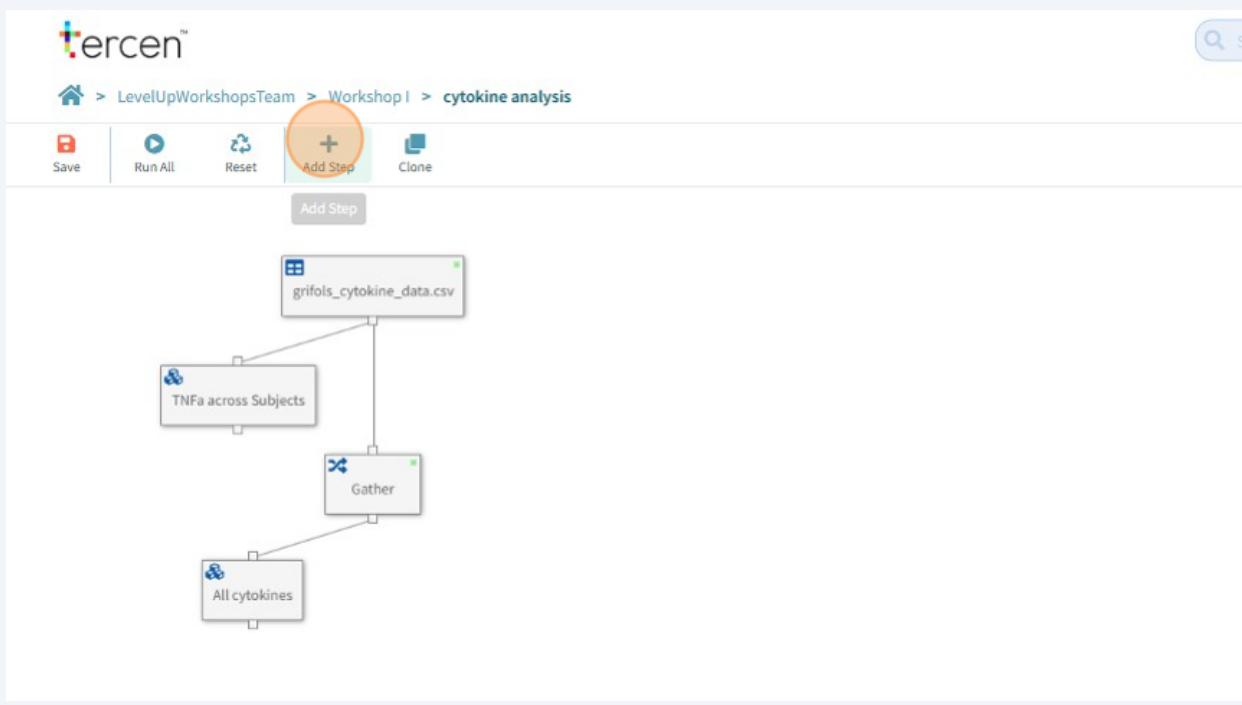
A	B	C	D	E	F	G
1 SUBJECT ID	AGE	AGEG	AGEGR1C	RACEGRP	SEXN	SEX
2 3130035837	23	1	18-29	Caucasian	1	Female
3 3130035967	27	1	18-29	Caucasian	1	Female
4 3370452578	27	1	18-29	African-Ar	0	Male
5 3370452632	23	1	18-29	Other	0	Male
6 3370452658	40	3	40-49	African-Ar	0	Male
7 3370452662	38	2	30-39	African-Ar	1	Female
8 3370452888	24	1	18-29	African-Ar	0	Male
9 3370452917	35	2	30-39	African-Ar	0	Male
10 3370452941	26	1	18-29	African-Ar	0	Male
11 3370456329	28	1	18-29	Caucasian	0	Male
12 3400334878	46	3	40-49	Caucasian	0	Male
13 3400334880	35	2	30-39	Caucasian	0	Male
14 3400334974	20	1	18-29	Caucasian	0	Male
15 3400335283	19	1	18-29	Other	0	Male
16 3400335823	29	1	18-29	Caucasian	1	Female
17 3400336107	38	2	30-39	Caucasian	0	Male
18 3400336110	19	1	18-29	Caucasian	1	Female
19 3400336121	25	1	18-29	Caucasian	0	Male
20 3400336138	21	1	18-29	African-Ar	1	Female
21 3400336234	18	1	18-29	Caucasian	0	Male

- 2** We will use a **Join Step** in Tercen to merge these two files together using the keys **Sample ID** and **SUBJECT ID**

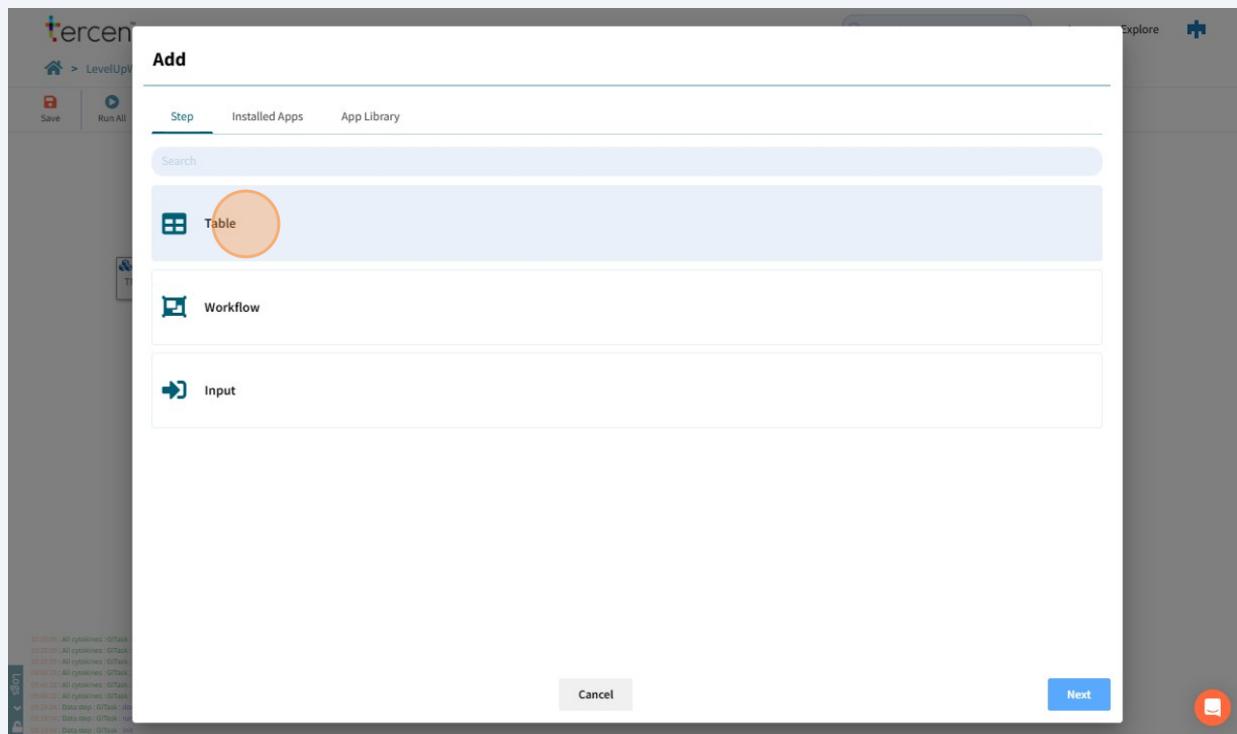
But first, we need to add the donor information to our workflow.

- 3** Starting at the **cytokine analysis** workflow

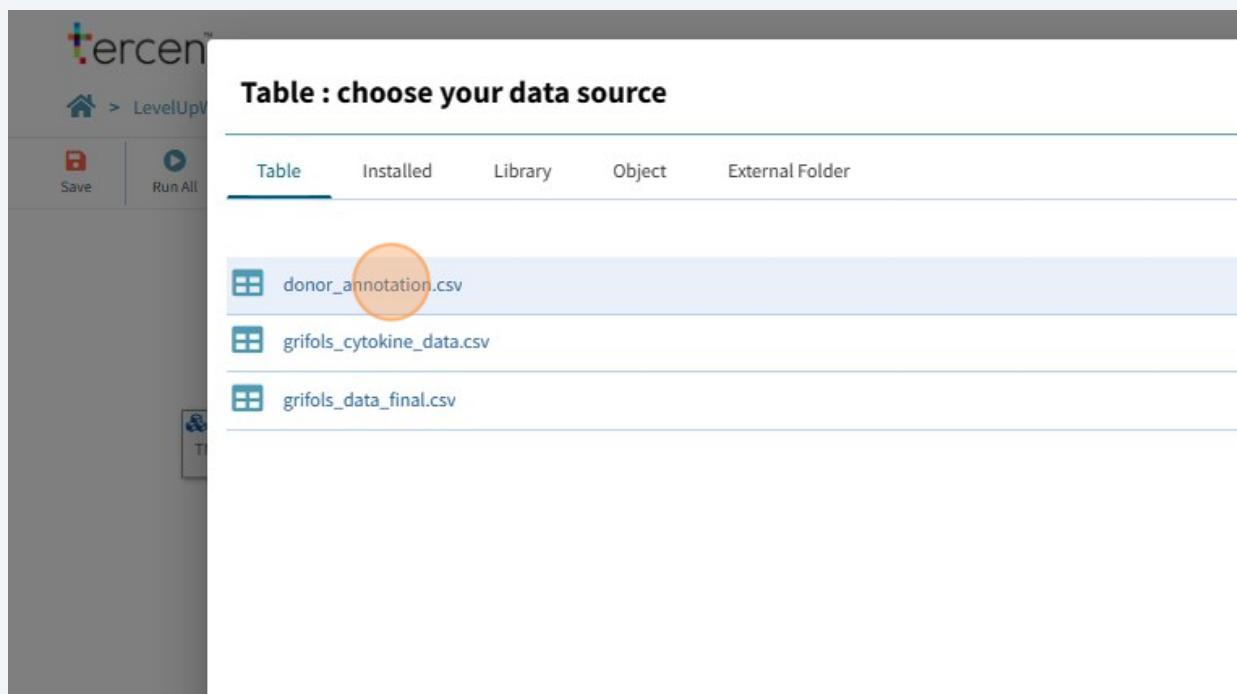
Click **Add Step** in the global toolbar.



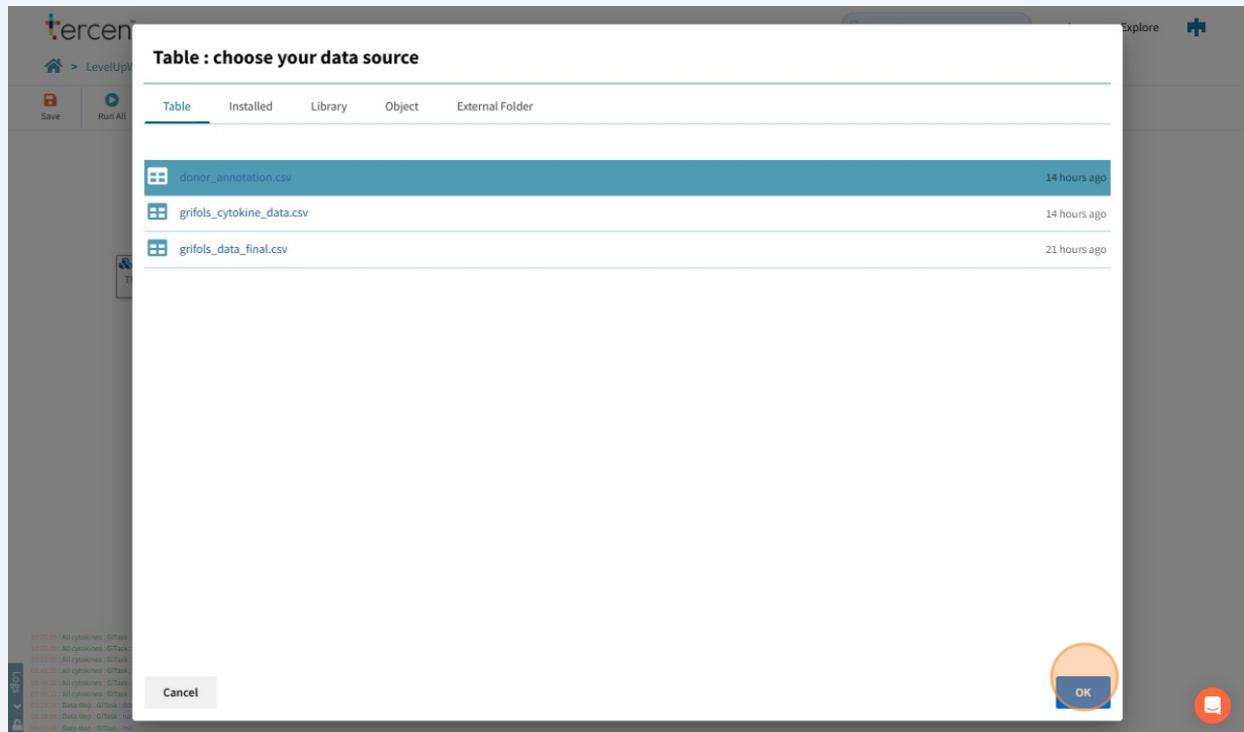
4 Click on Table



5 Click "donor_annotation.csv"



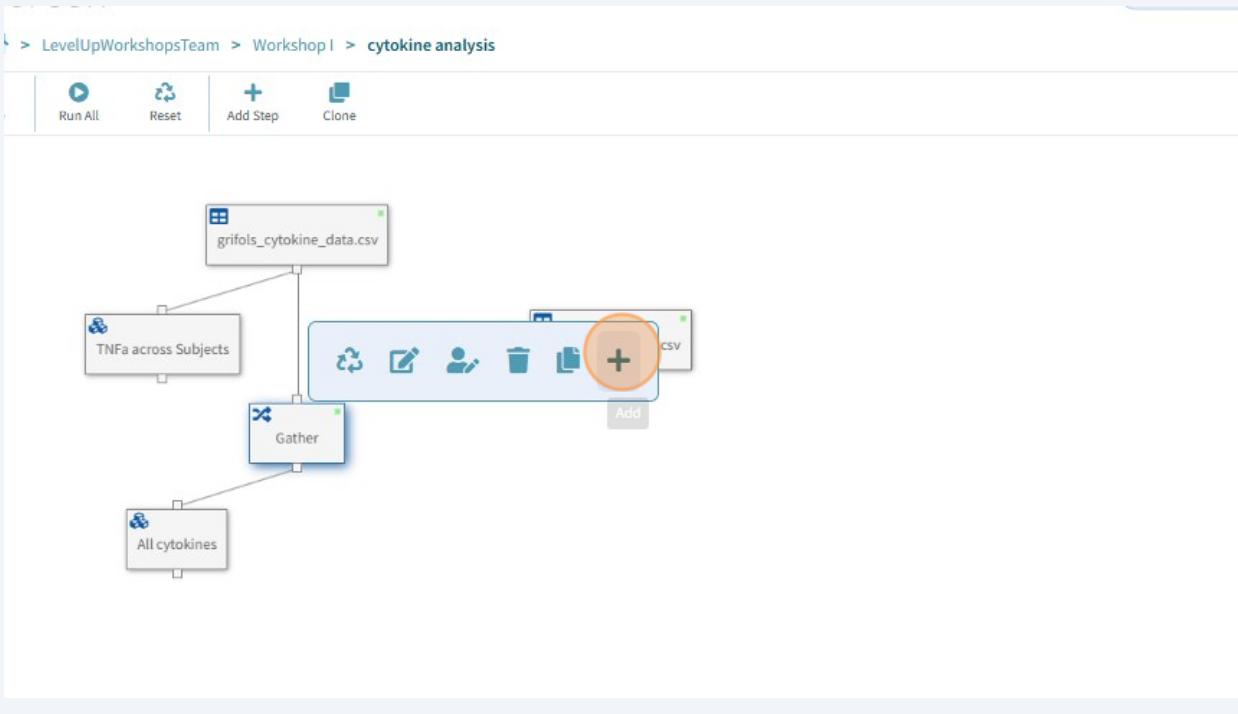
6 Click "OK"



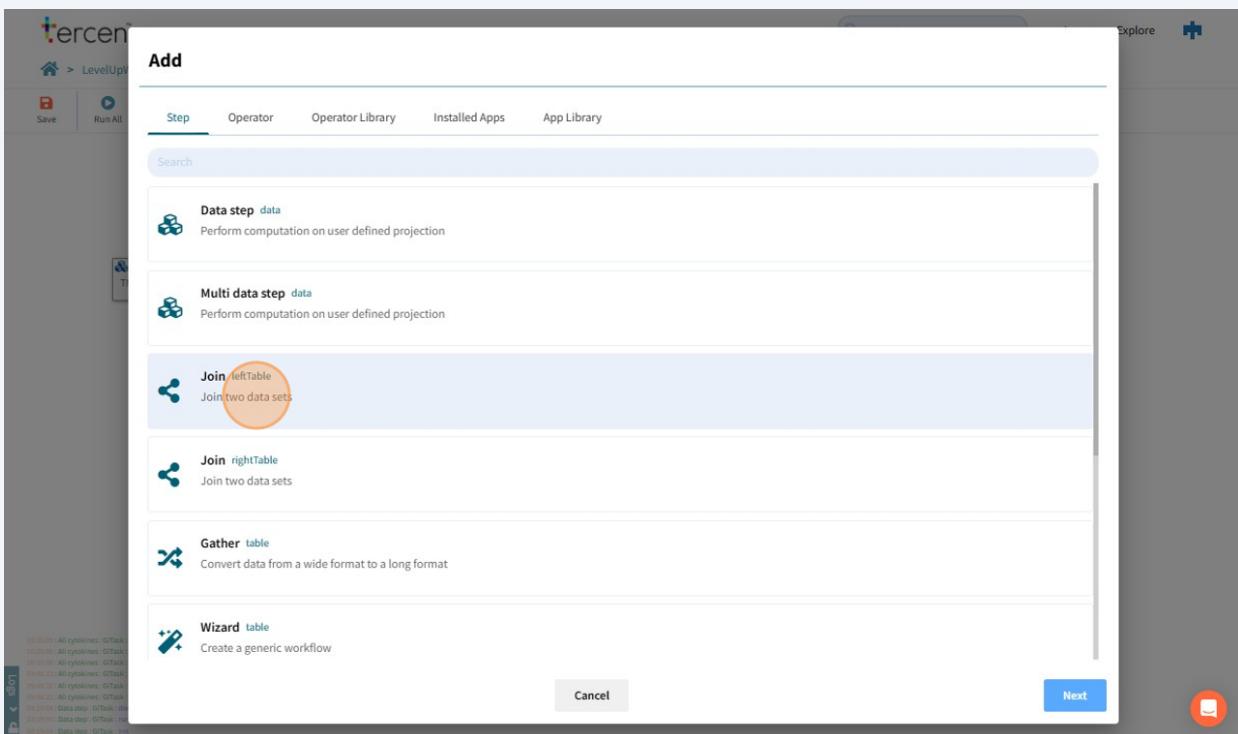
7 Click on the **Gather** step



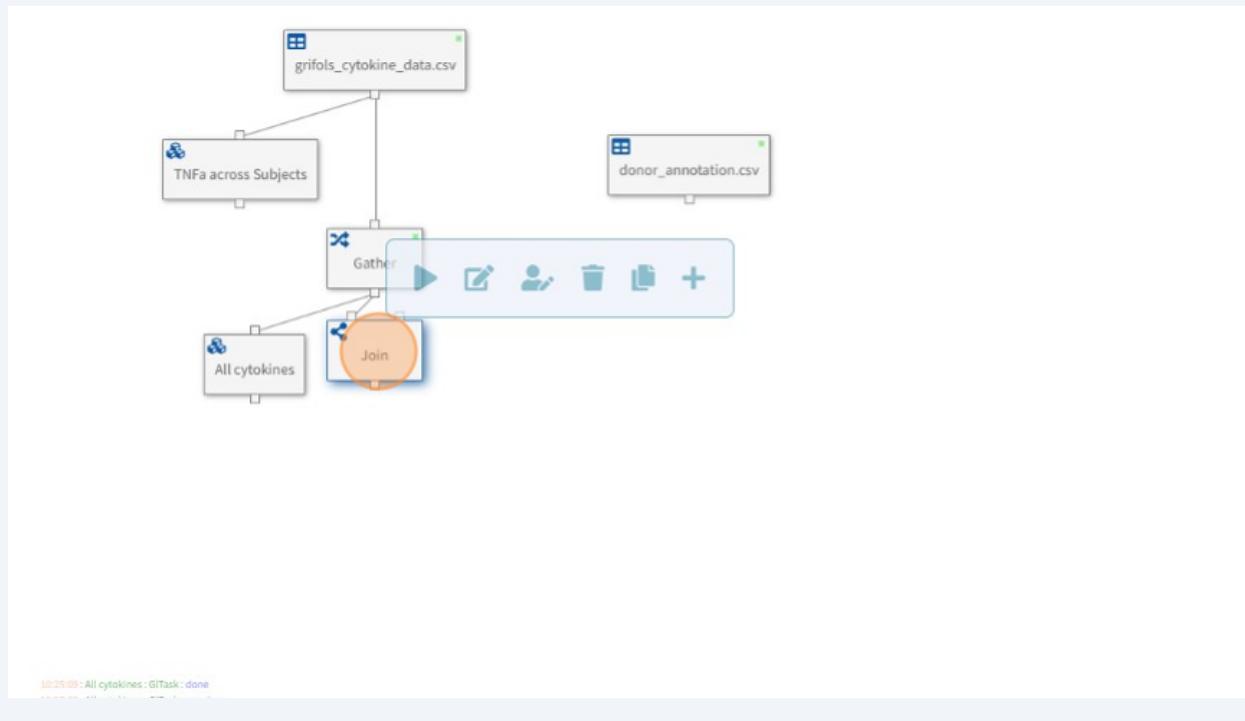
8 Click here.



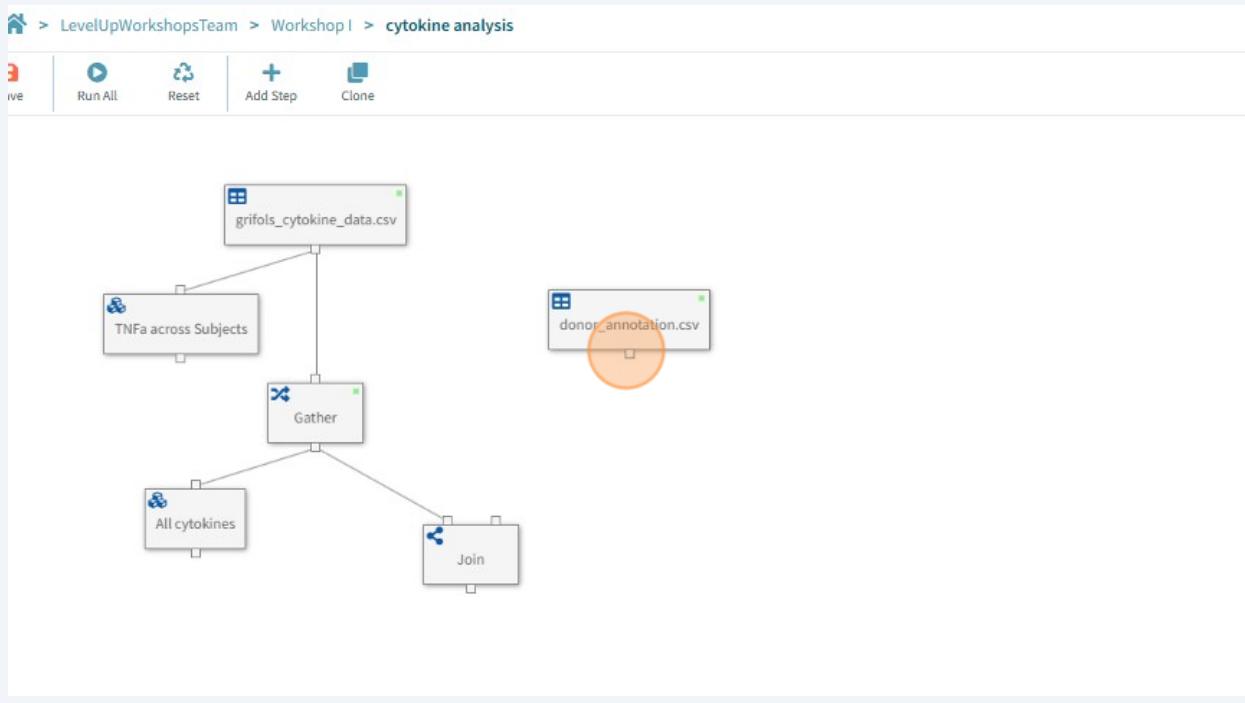
9 Click on **Join left Table**



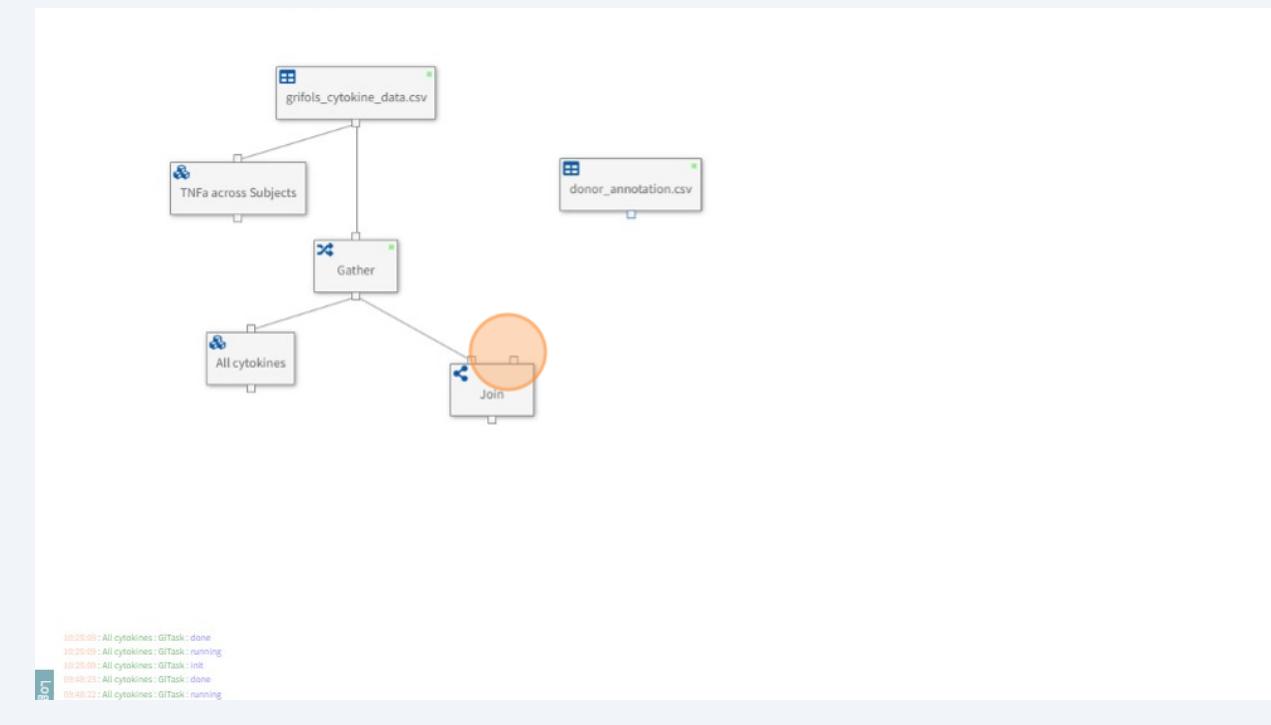
10 Click on the **Join** step



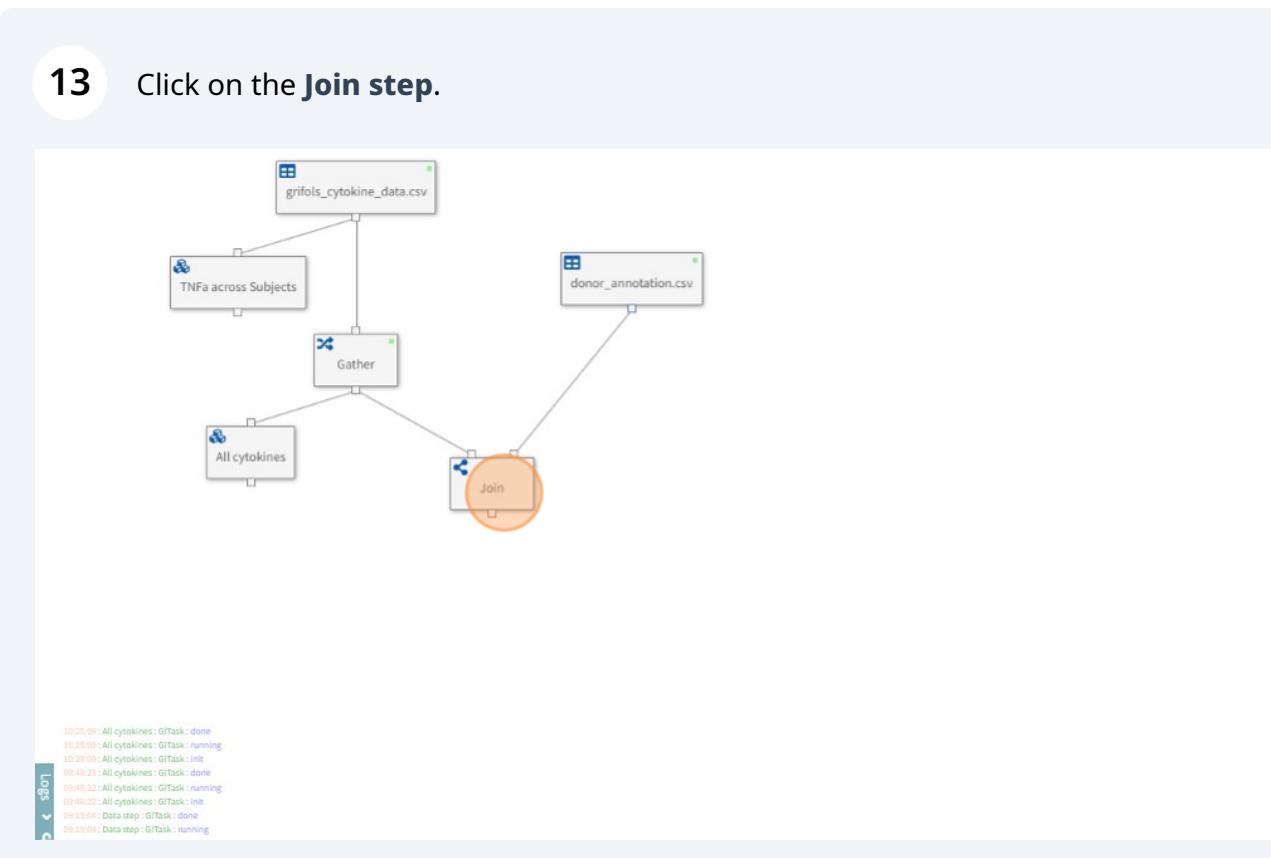
11 Click on the output port of the **donor_annotation.csv**.



12 Click on the input port of **Join step**.



13 Click on the **Join step**.



14 Click on Sample ID.

The screenshot shows the Tercen platform's 'Join' interface. At the top, there is a search bar labeled 'Search Tercen' and navigation links for 'Learn' and 'Explore'. Below the header, the URL path is shown: 'LevelUpWorkshopsTeam > Workshop I > cytokine analysis > Join'. The main area is titled 'Namespace' with the value 'js0'. Under 'Join keys', there are two sections: 'Join keys' and 'Select all'. The 'Join keys' section contains a list of checkboxes for various variables, with the first one, 'Sample ID (character)', highlighted by a red circle. The 'Select all' section contains a list of checkboxes for other variables like 'AGE' and 'SEXN'.

15 Click on SUBJECT ID.

The screenshot shows the Tercen platform's 'Join' interface, similar to the previous one but with different selected checkboxes. The 'Namespace' is still 'js0'. In the 'Join keys' section, the 'Select all' checkbox is checked. In the 'Select all' section, the 'SUBJECT ID (character)' checkbox is highlighted by a red circle. Other checkboxes like 'AGE' and 'SEXN' are also present in this section.

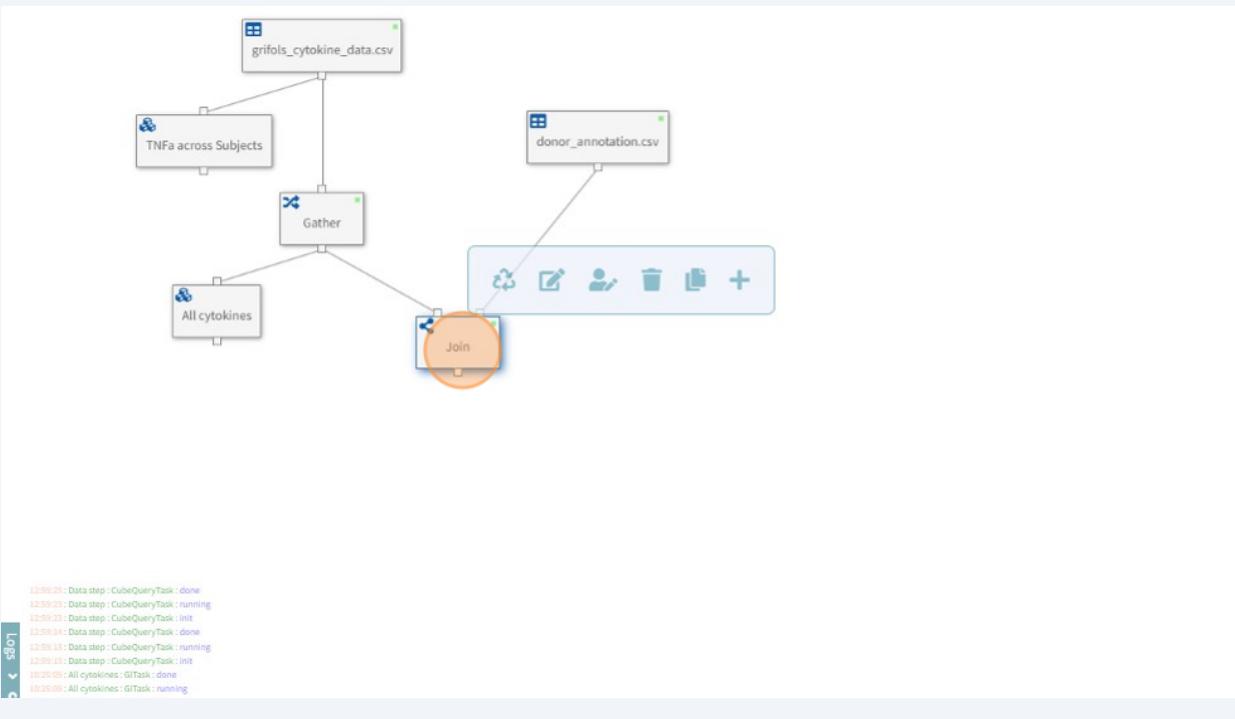
16 The factors **Sample ID** and **SUBJECT ID** are called the keys

17 Click **Save & Run Step** button.

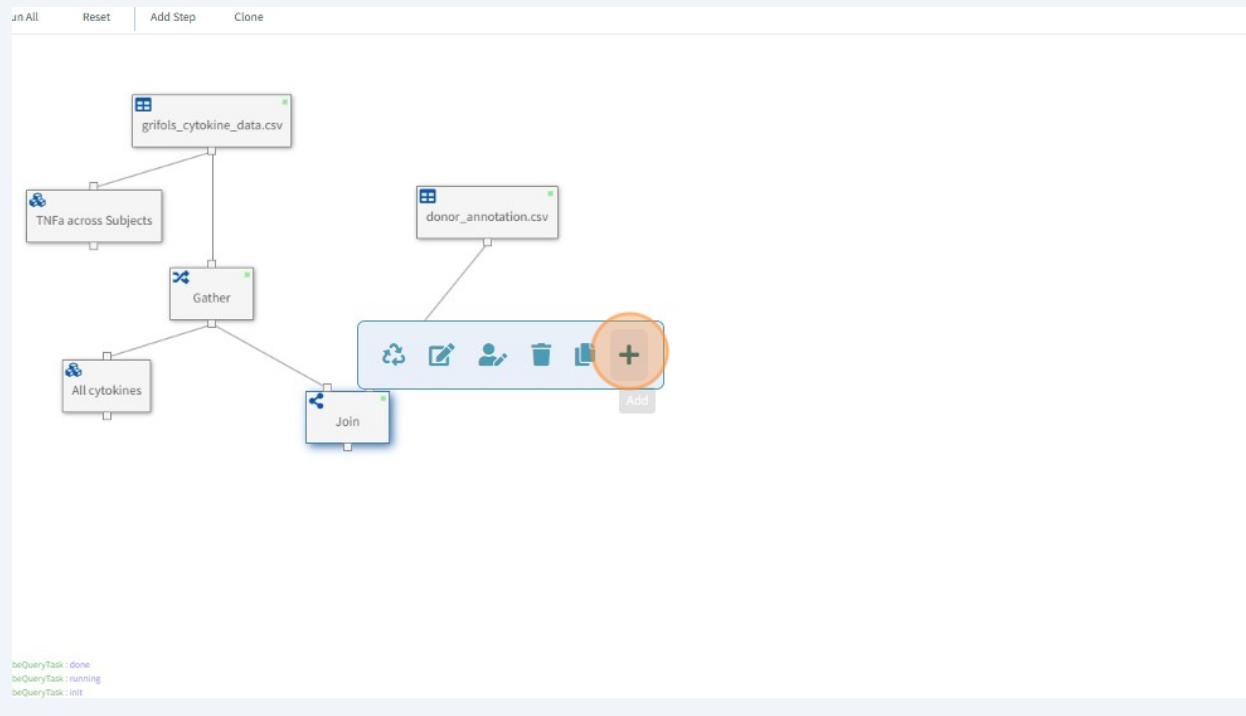
The screenshot shows a software interface with two columns of variables. The left column contains variables: IFN-gamma (numeric), IL-12p70 (numeric), IL-13 (numeric), IL-1beta (numeric), IL-2 (numeric), IL-4 (numeric), IL-5 (numeric), IL-6 (numeric), TNF-alpha (numeric), GM-CSF (numeric), IL-18 (numeric), IL-10 (numeric), IL-17A (numeric), IL-21 (numeric), IL-22 (numeric), IL-23 (numeric), IL-27 (numeric), IL-9 (numeric), rowId (numeric), tableId (character), cytokine.value (numeric), and cytokine.variable (character). The right column contains variables: AGE (numeric), AGEGR1N (numeric), AGEGR1C (character), RACEGRP (character), SEXN (numeric), SEXC (character), rowId (numeric), and tableId (character).

At the bottom of the interface, there is a control panel with three buttons: "Back" (disabled), "Save & Run Step" (highlighted with an orange circle), and a red "Cancel" button.

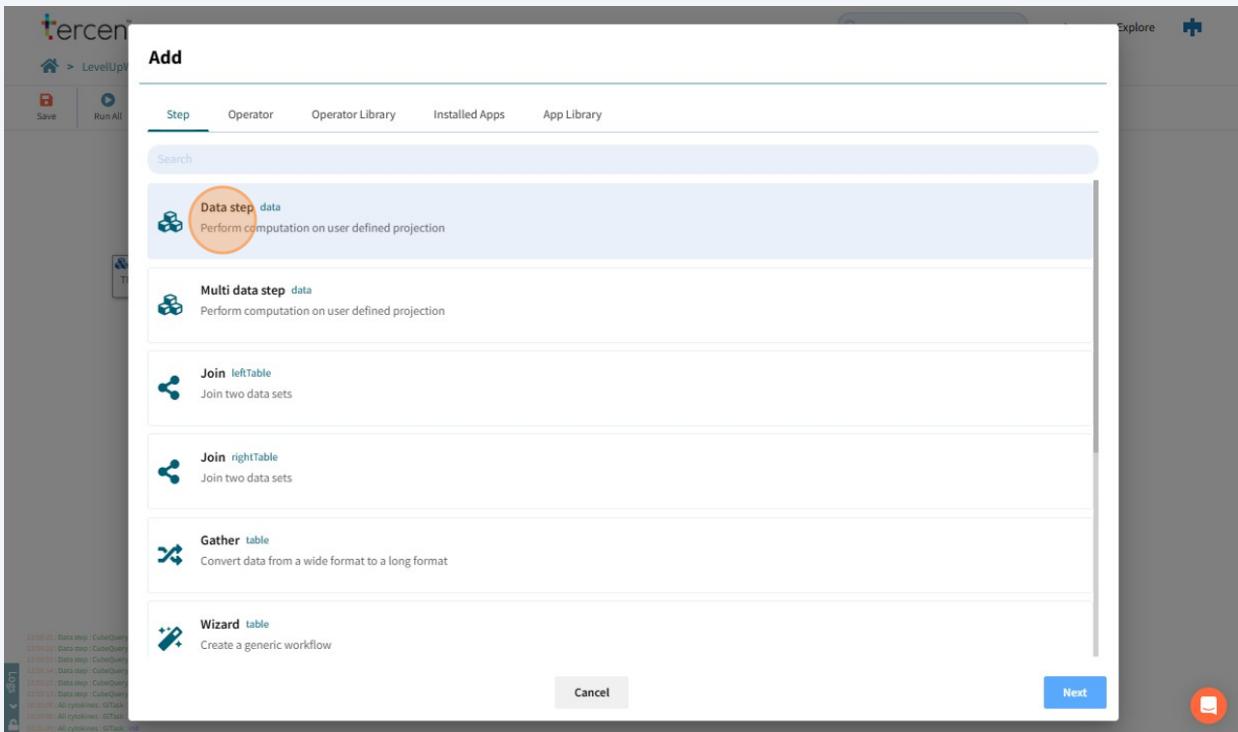
18 Click on the **Join** step.



19 Click here.



20 Click Data step.



- 21 A crosstab window opens.

Notice that new factors have appeared on the bottom left of the window. These are all the column headers from the donor annotation file.

Each new factor name has been prefixed with **js0**. This is to identify them as originating from the donor file.

If the merging was correct, then the factor **Sample ID** and **js0.SUBJECT ID** should have equivalent values.

Let's check this using another projection in Tercen.

The screenshot shows the Tercen software interface. At the top, there are several tabs: Save, Add Operator, Crosstab (which is selected and highlighted in blue), Tables, Layer 1, Point, and Tran. Below these are three buttons: Factors, Environment, and Settings. The Factors button is underlined, indicating it is active. In the main area, there is a search bar labeled "Search Factors" and a dropdown menu showing "grifols_cytokine_data.csv". Underneath this, there are two sections: "Gather" and "Join". The "Join" section is expanded and highlighted with a red box. It contains a list of columns from the donor annotation file, each preceded by a small blue square icon:

- js0.SUBJECT ID
- js0.AGE
- js0.AGEGR1N
- js0.AGEGR1C
- js0.RACEGRP
- js0.SEXN
- js0.SEXC
- js0.rowId
- js0.tableId

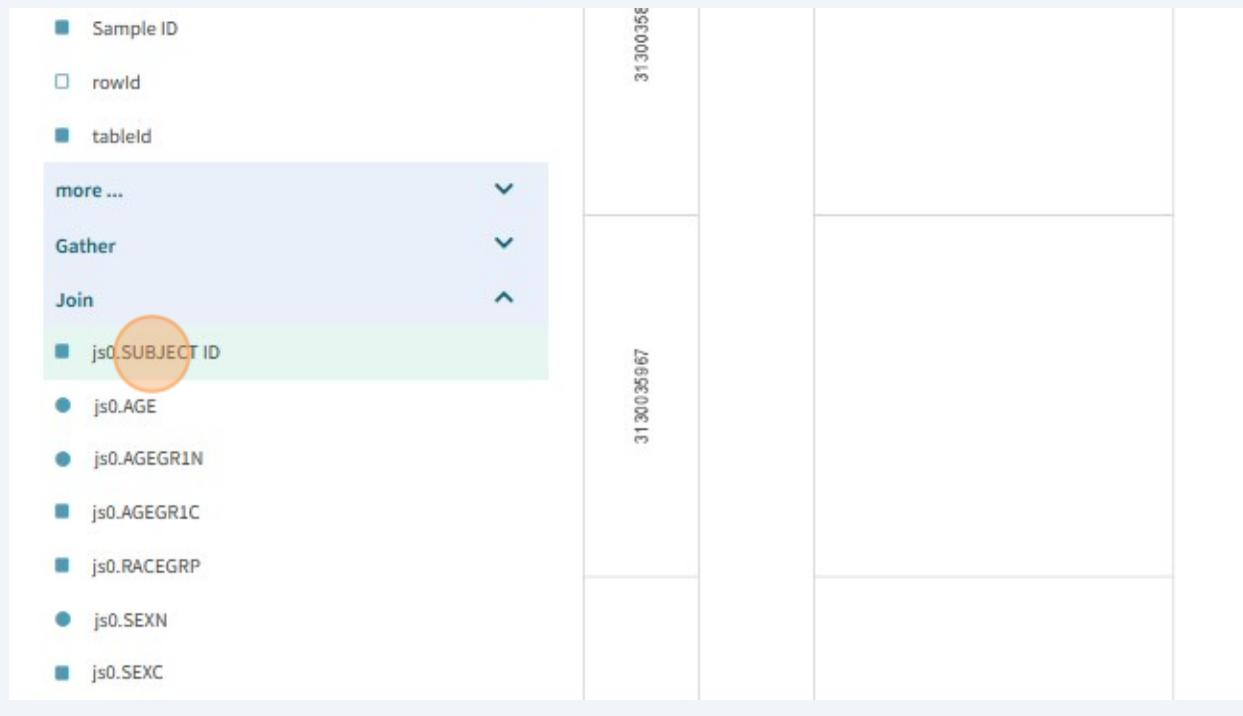
22 Click **grifols_cytokine_data.csv** to expand the menu.

The screenshot shows the Data step interface with the 'Factors' tab selected. At the top, there are navigation links: Home > LevelUpWorkshopsTeam > Workshop I > cytokine analysis > Data step. Below the navigation are various operators: Save, Add Operator, Crosstab (selected), Tables, Layer 1, Point, Transform..., and Filters. The 'Factors' tab is active, showing a search bar and a list of factors. The 'grifols_cytokine_data.csv' file is listed and has a dropdown arrow next to it, which is circled in orange. Below it are 'Gather' and 'Join' sections, each with a dropdown arrow. A list of variables follows: js0.SUBJECT ID, js0.AGE, js0.AGEGR1N, and js0.AGEGR1C. The main workspace area is empty.

23 Drag **Sample ID** and drop it onto the **Rows**.

The screenshot shows the Data step interface with the 'Factors' tab selected. The layout is identical to the previous screenshot, with the same navigation and operator buttons. The 'grifols_cytokine_data.csv' file is selected and expanded, showing its contents. The 'Sample ID' variable is highlighted with a green background and circled in orange, indicating it has been moved to the Rows section. The other variables listed are 'rowId' and 'tableId'. The 'more ...' section, 'Gather' section, and 'Join' section are also visible. The main workspace area is empty.

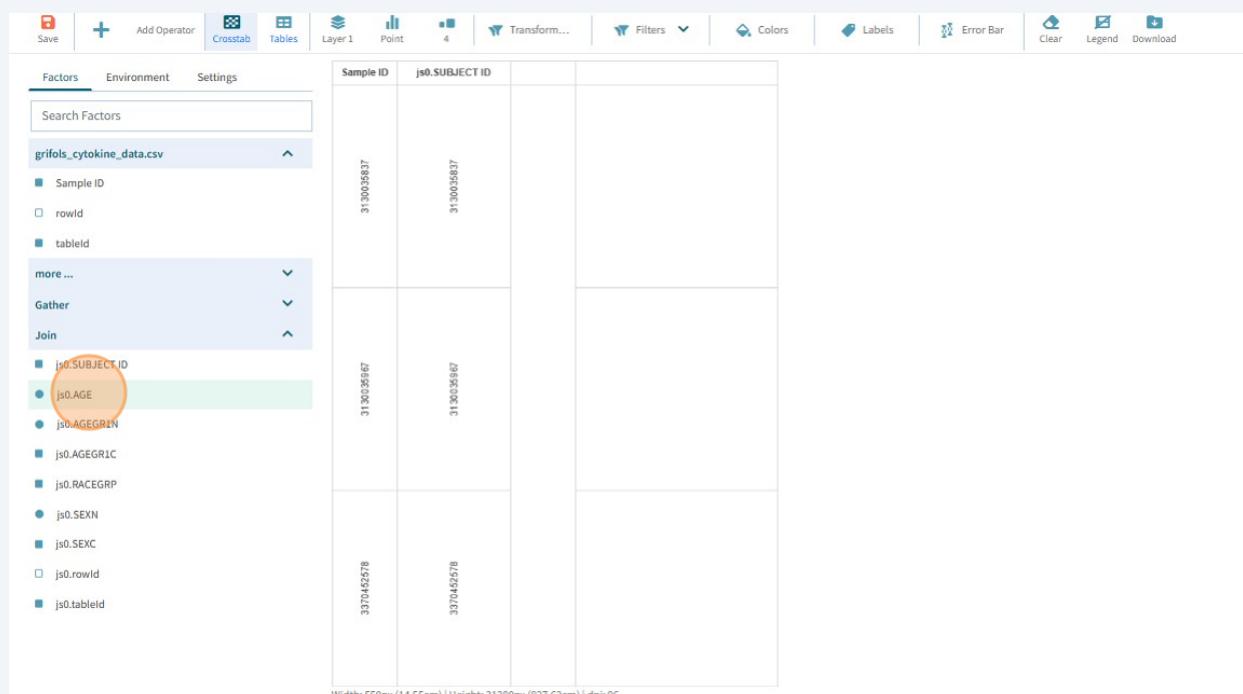
24 Drag **js0.SUBJECT ID** and drop it onto the **Rows**.



25 Drag **js0.AGE** and drop it onto the **Rows**.

Note how the values match up to each other.

For each entry in the **Sample ID** there is an equivalent one in the **js0.SUBJECT ID**. This indicates a successful merging of the donor information.





Alert!

If you do not see matching values, something is amiss with the settings in the **Join Step**. Check the keys!



Tip!

In the last Crosstab projection, you may have noticed no Y-axis was used.

The Crosstab window does not always need a Y-axis defined. It depends on what you want to do.

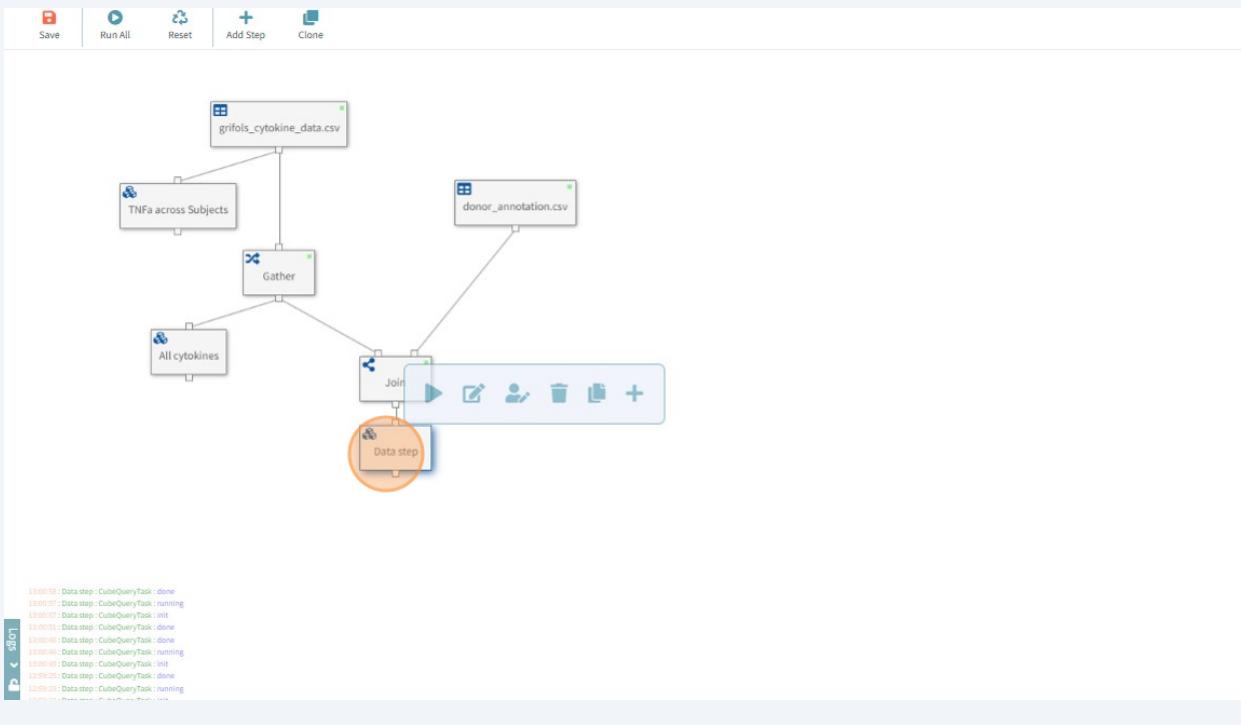
Hint: This could be in the quiz.

26

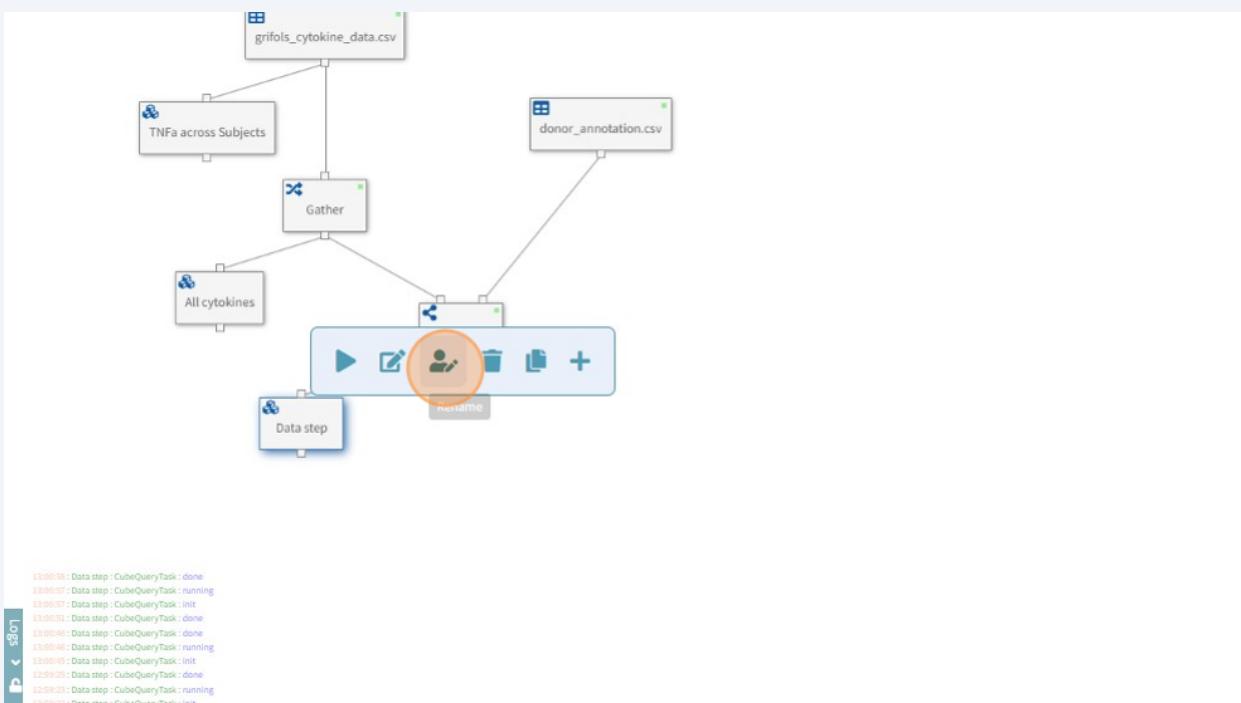
Click "cytokine analysis" to navigate back to the workflow view.

Sample ID	js0.SUBJECT ID	js0.AGE	js0.RACEGRP
3130025837	3130025837	23	
3130035967	3130035967	27	
1370452578			

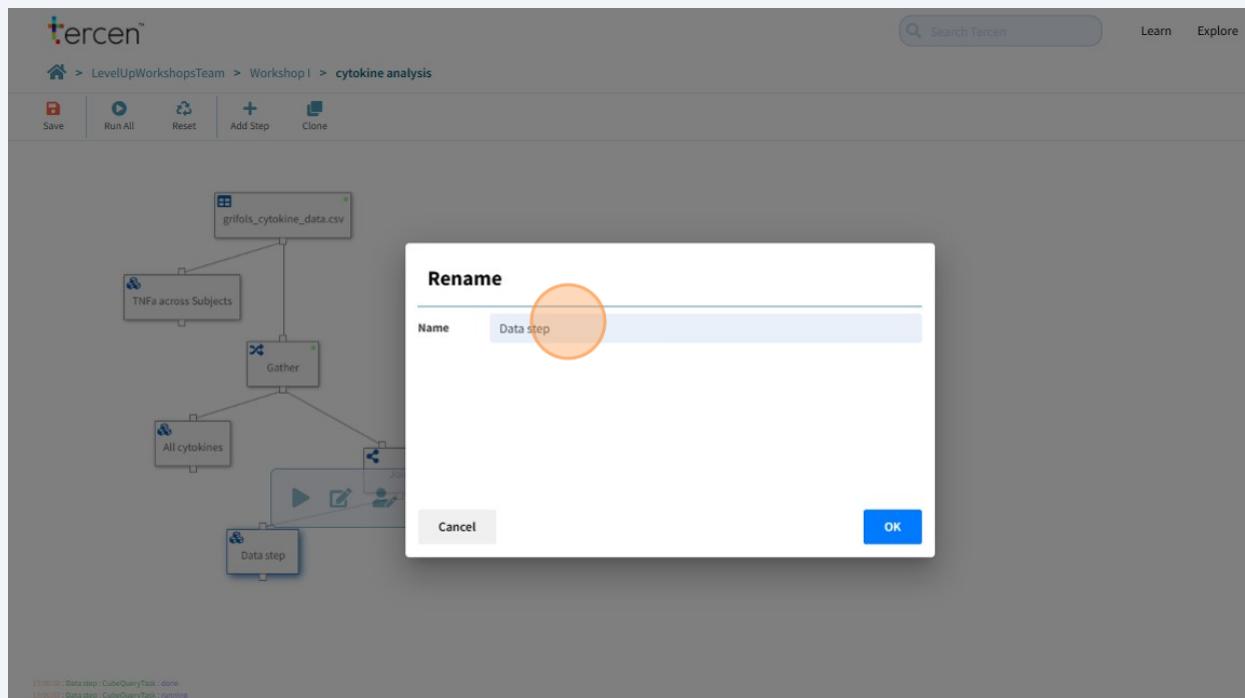
27 Click on the Data step



28 Click Rename icon.

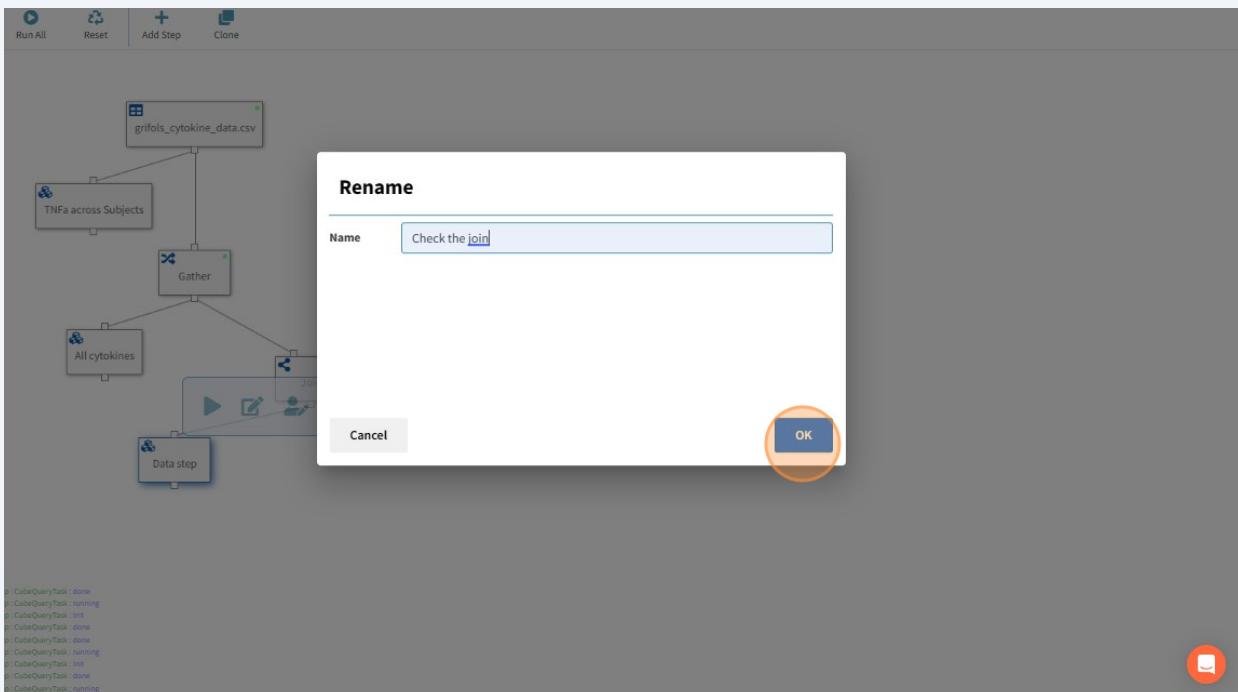


29 Click this text field.



30 Type "Check the join"

31 Click "OK"



32 Please save your workflow.

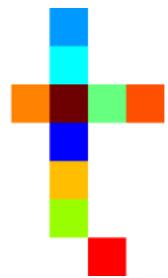
33 You are at the end of the guide.

Here is a recap of what you have achieved:

- Joined donor annotation
- Checked if the join was successful
- Created a plot with the new donor information

Well done!

0111 - Calculate Mean

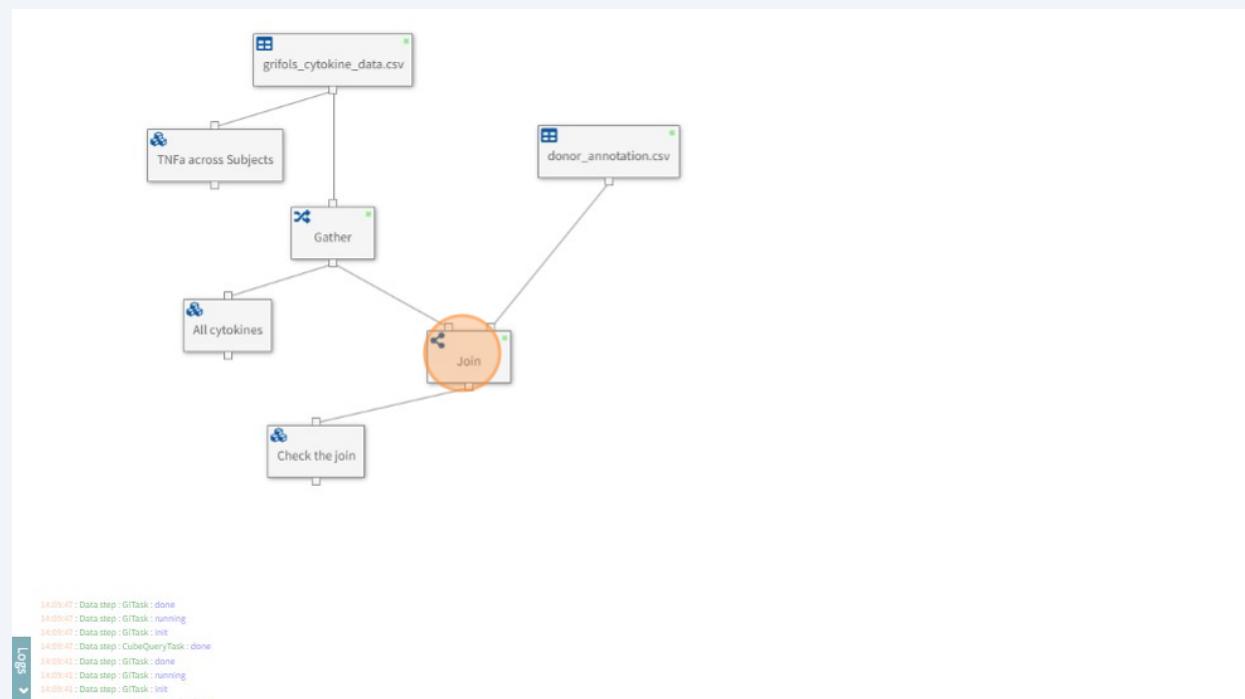


1 If you follow this guide, you will learn how to:

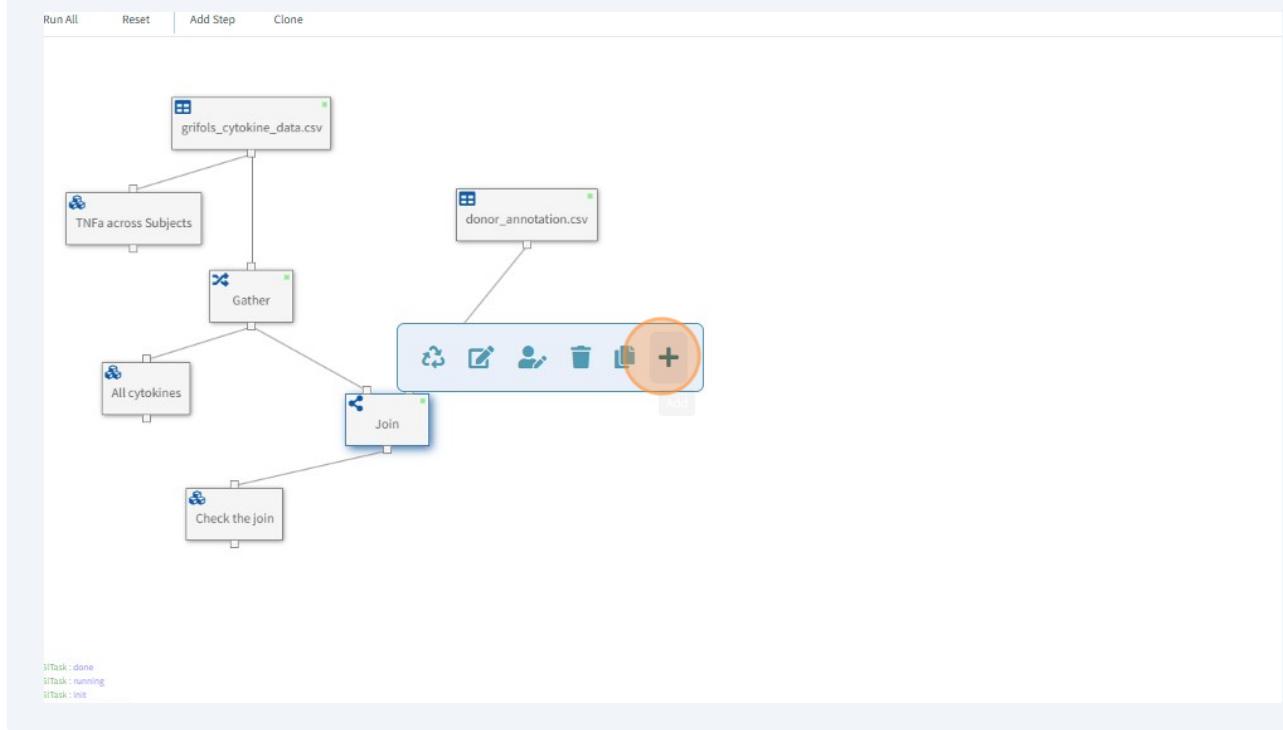
- Create plots by grouping subjects by cohort groups
- Calculate the mean and standard deviation per Gender cohort
- Check the output of the Join step
- Create new plots with the extra donor annotations

2 We will now calculate the mean value of each cytokine per gender.

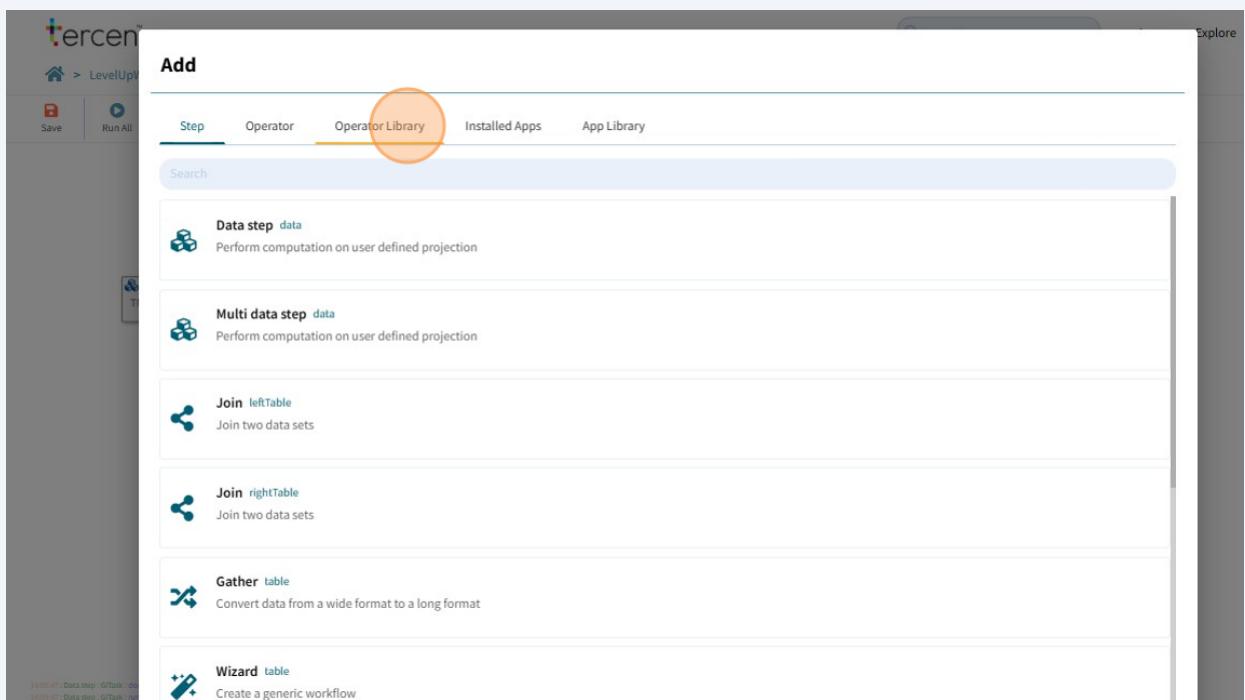
3 Click here.



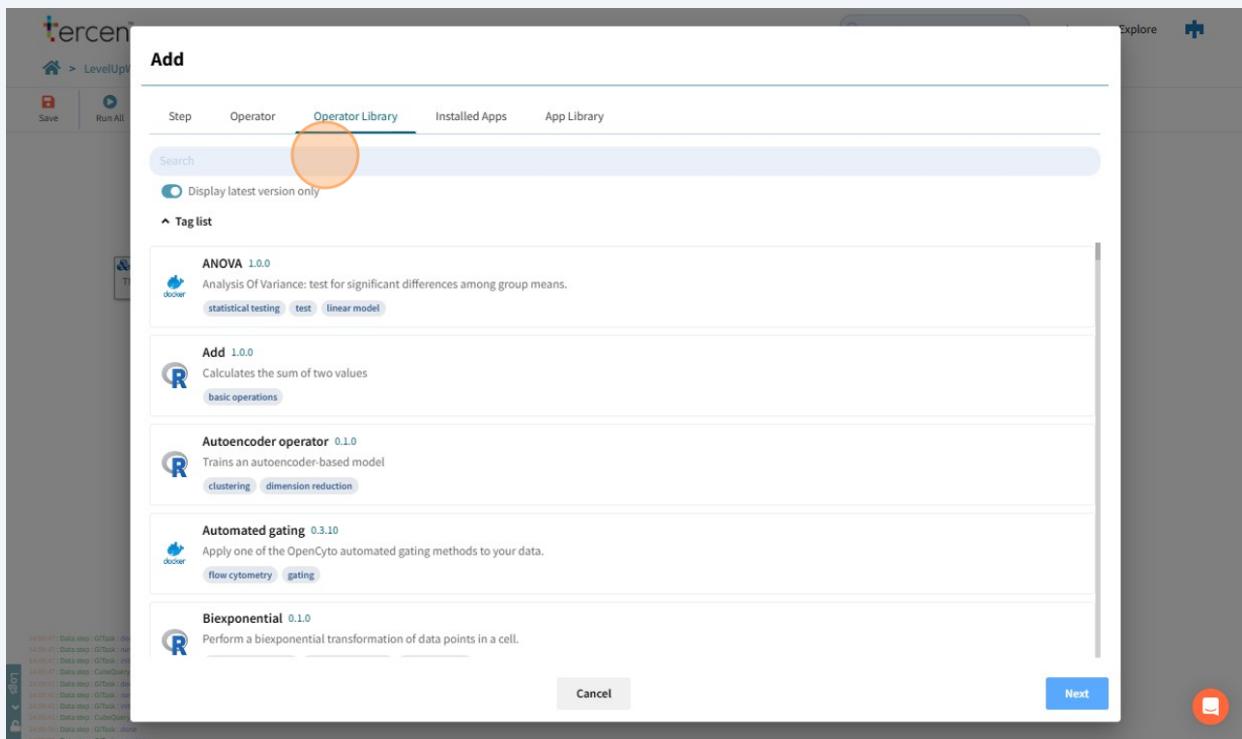
4 Click here.



5 Click Operator Library

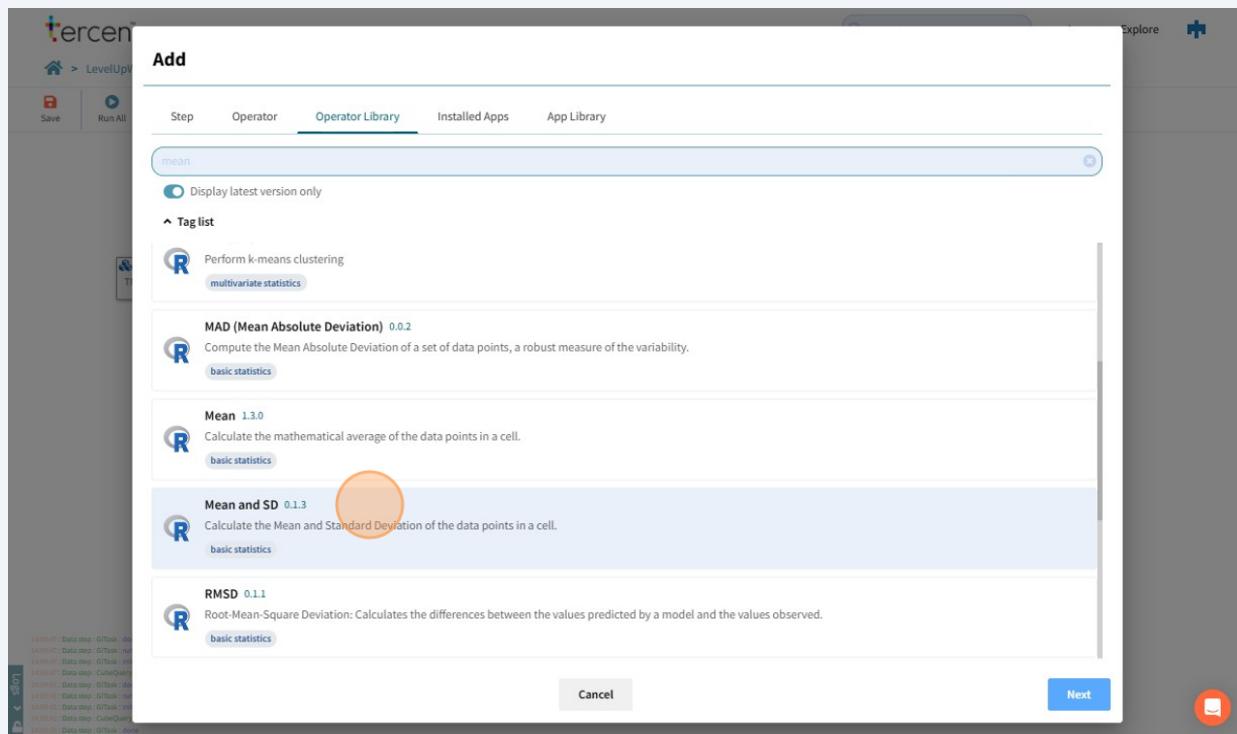


6 Click the **Search** field.

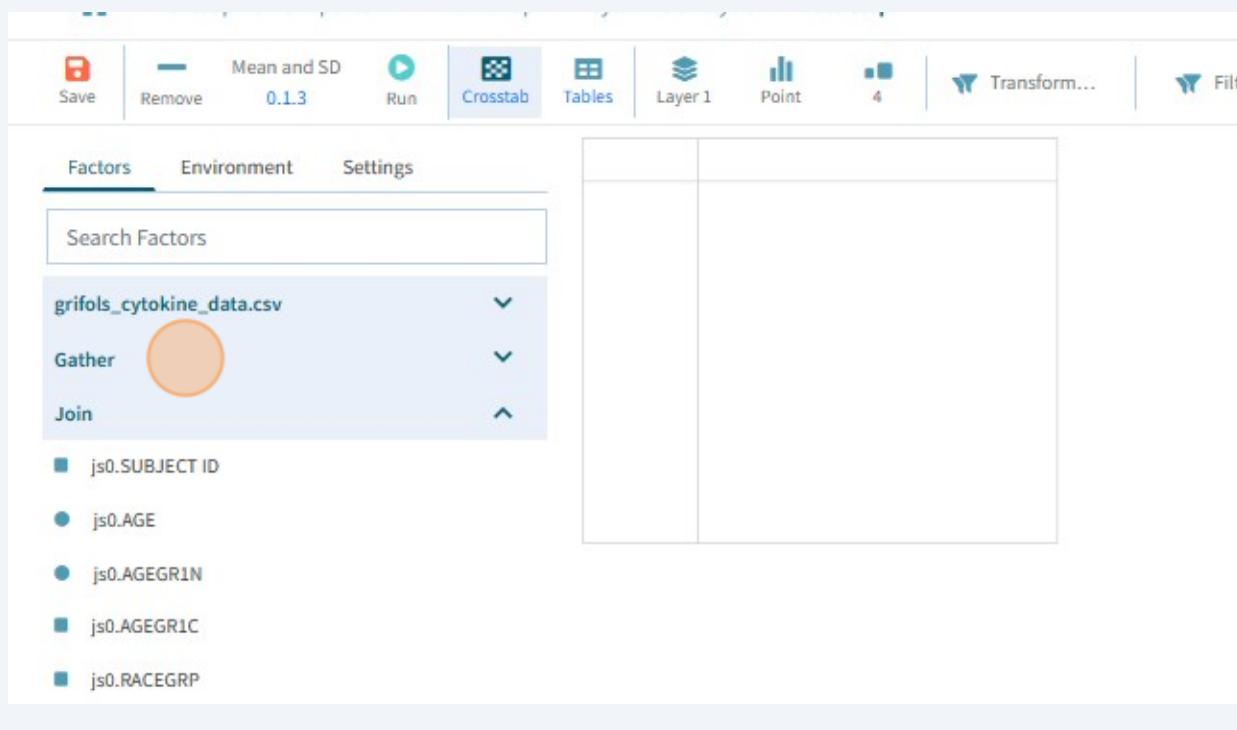


7 Type "mean"

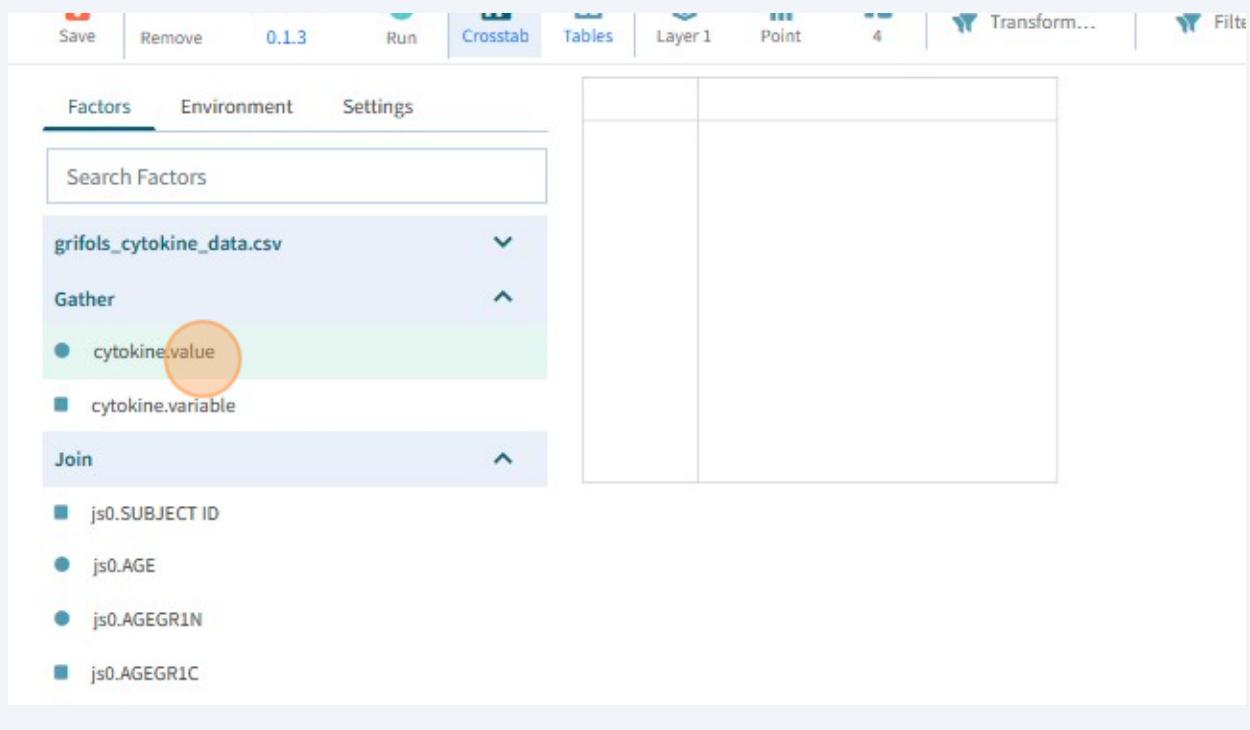
8 Click Mean and SD



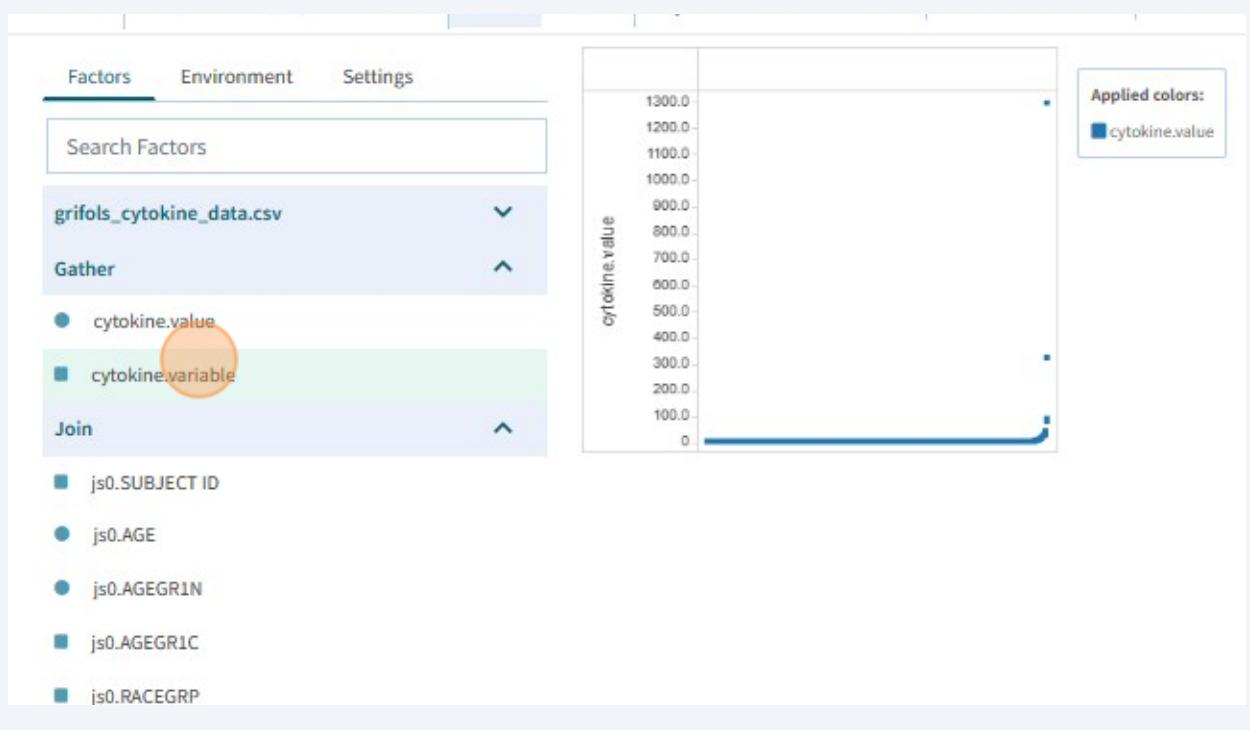
9 Click Gather



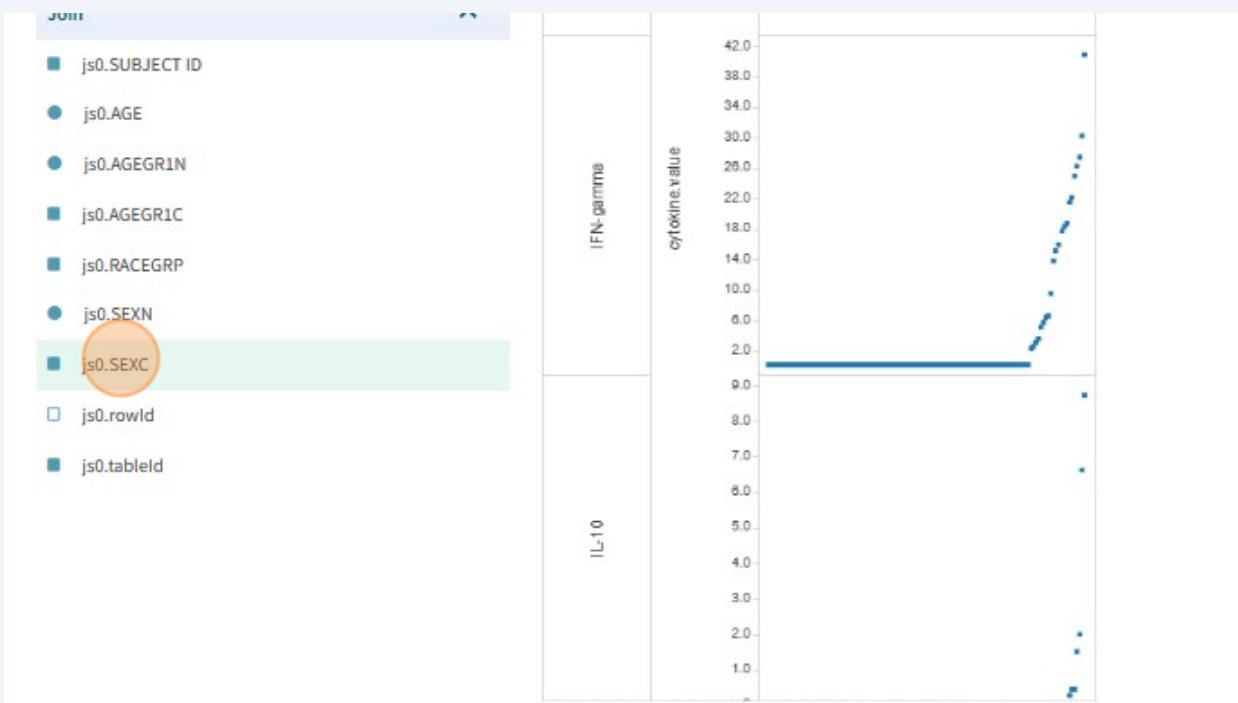
10 Drag **cytokine.value** and drop it onto the **Y-Axis**.



11 Drag **cytokine.variable** and drop it onto the **Rows**.



12 Drag the **js0.SEXC** factor and drop onto **Columns**.

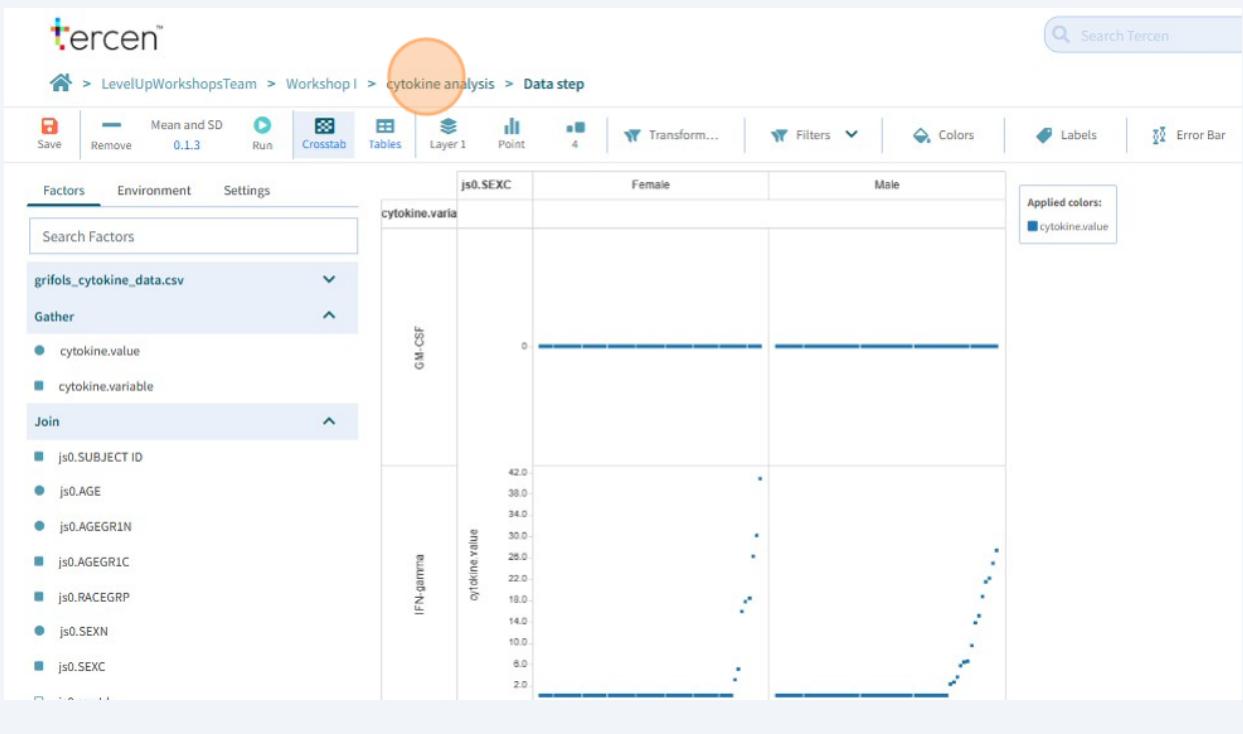


Tip!

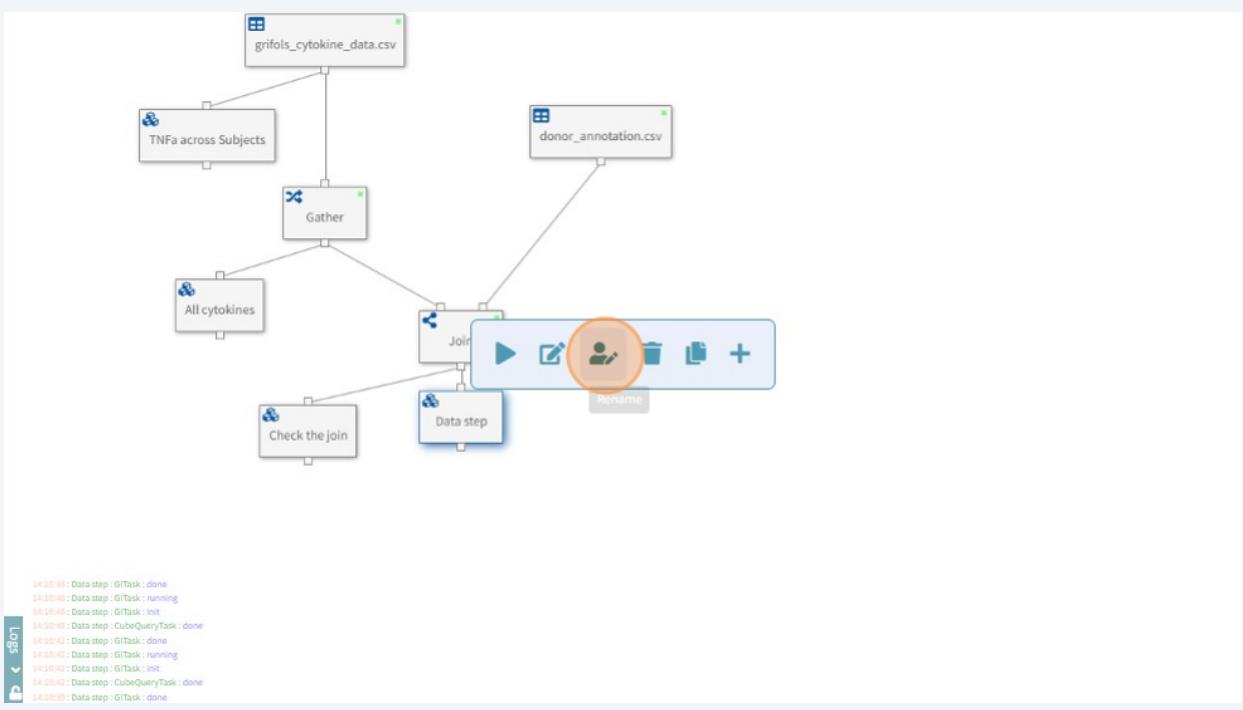
If you drag the **js0.RACEGRP** instead of the **js0.SEXC** to the Columns, you are ready to calculate the mean per race instead of gender.

Hint: This question is in the quiz.

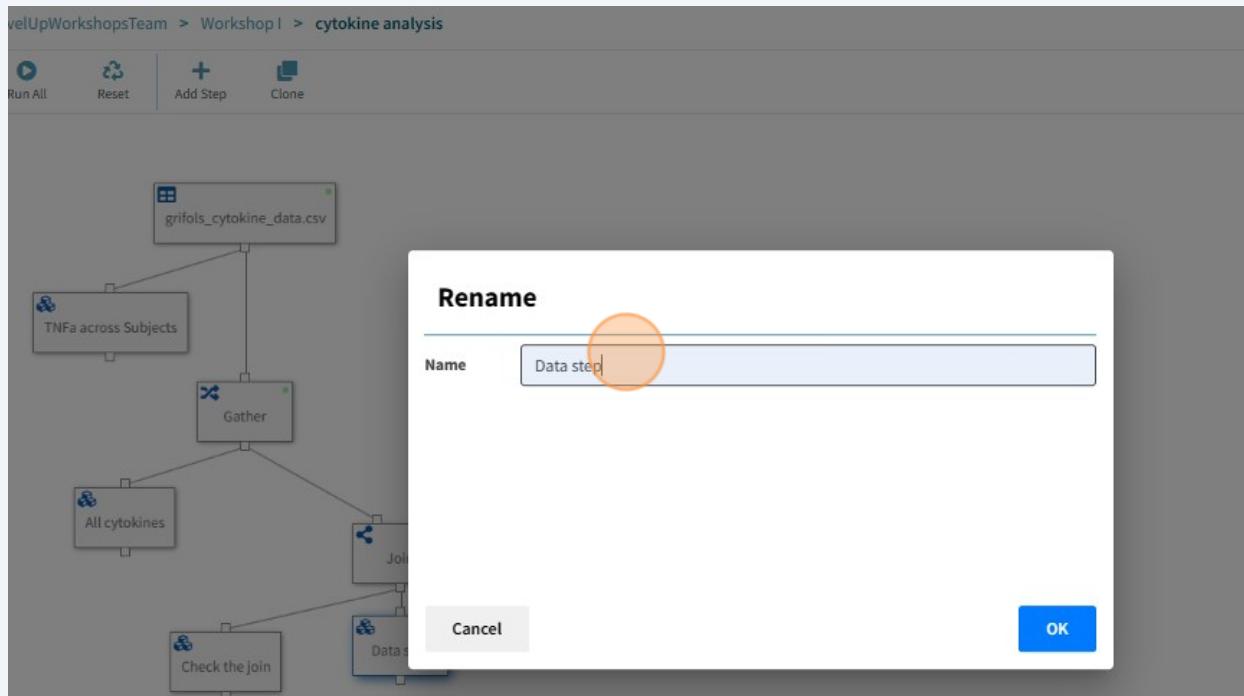
13 Click **cytokine analysis** to navigate back to the workflow view.



14 Click on the **Rename** icon.

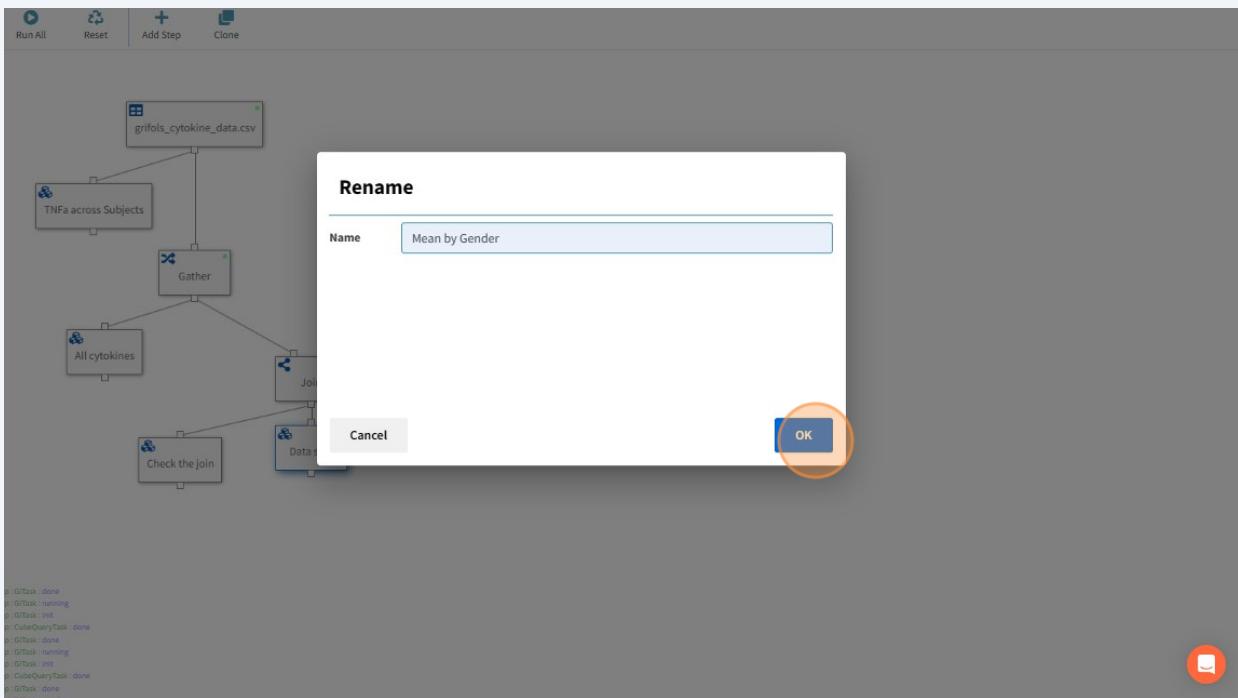


15 Click this text field.

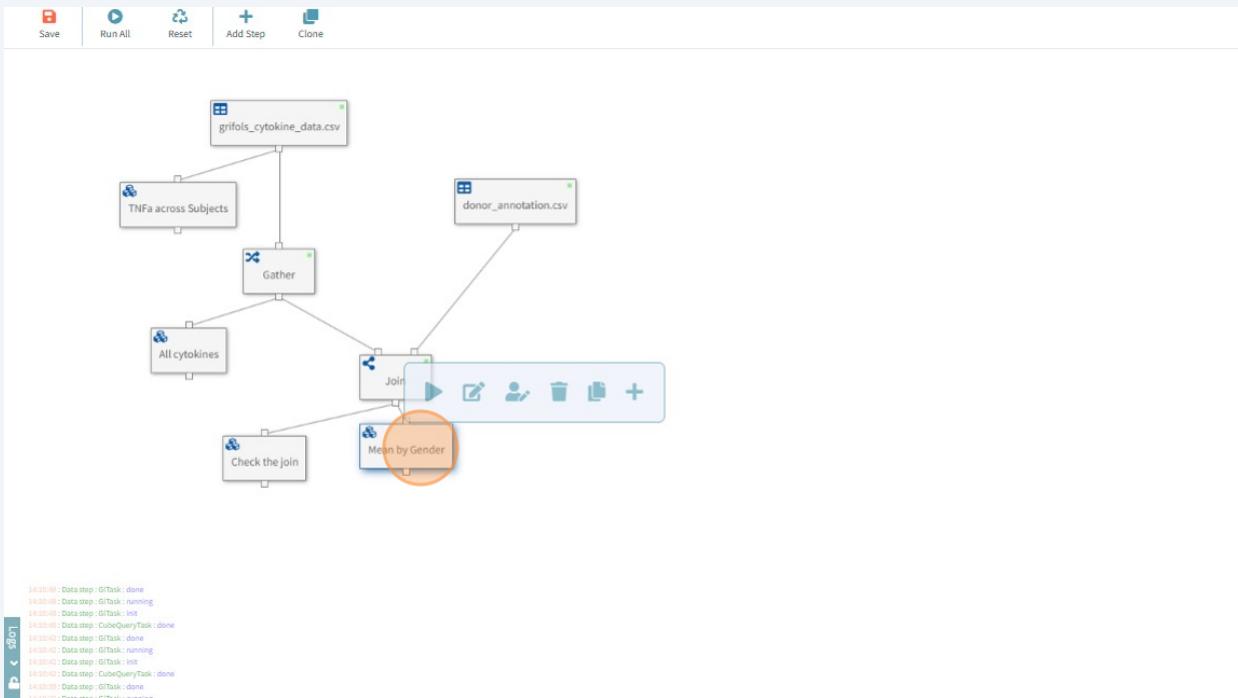


16 Type "Mean by Gender"

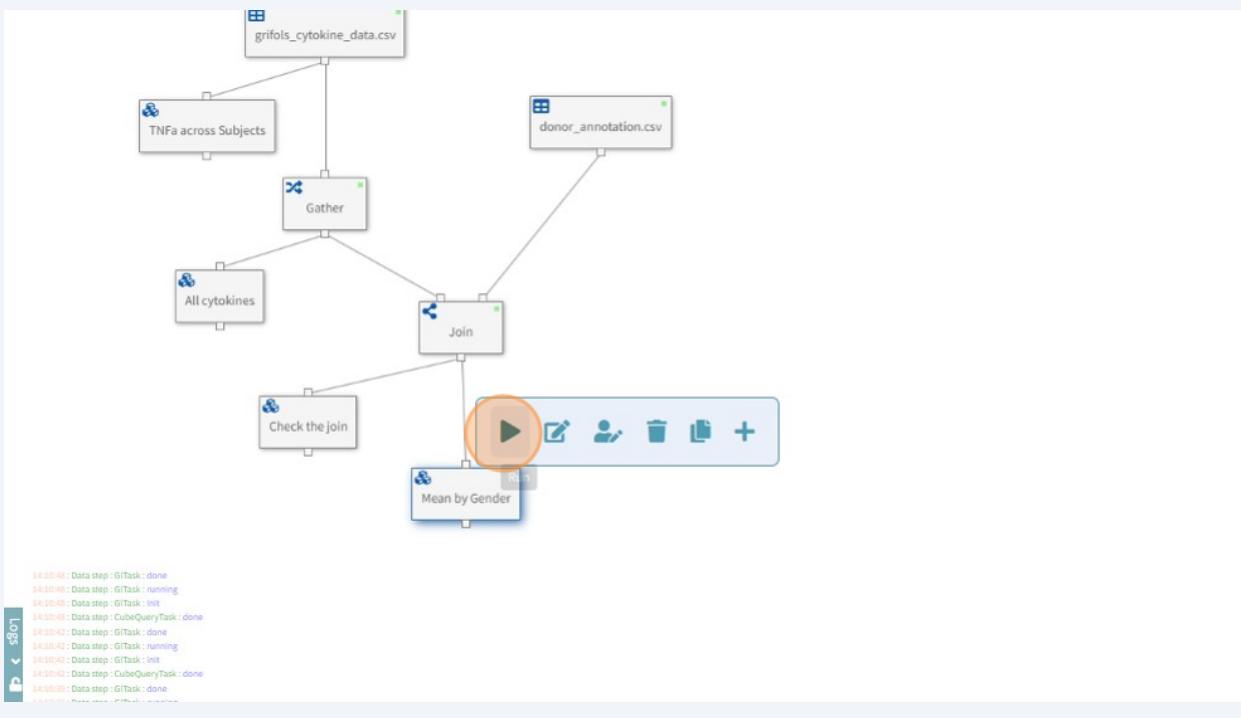
17 Click "OK"



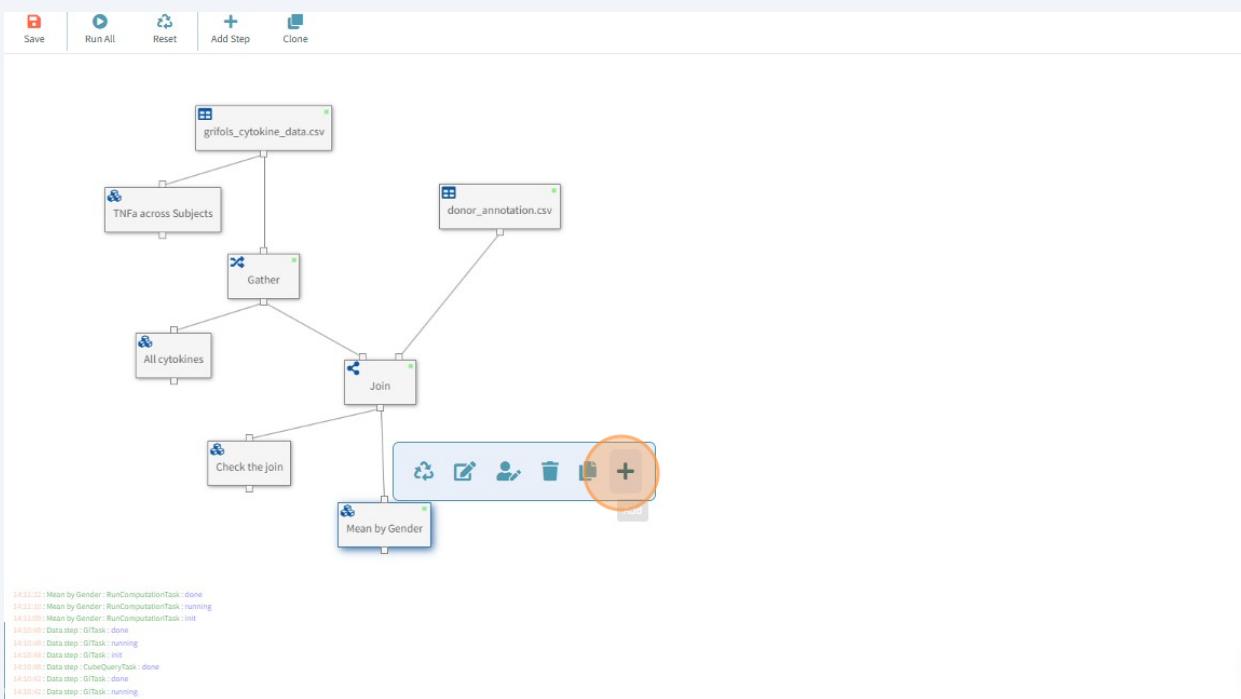
18 Click on Mean by Gender



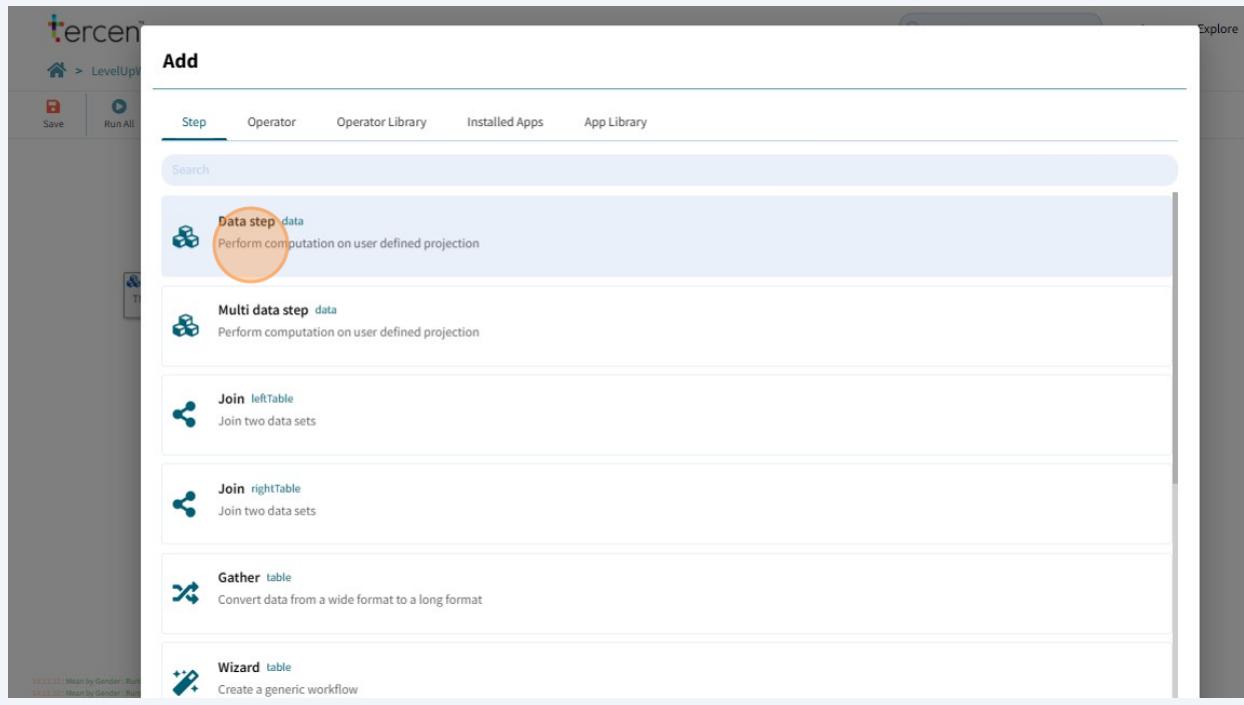
19 Click on the **Run** icon.



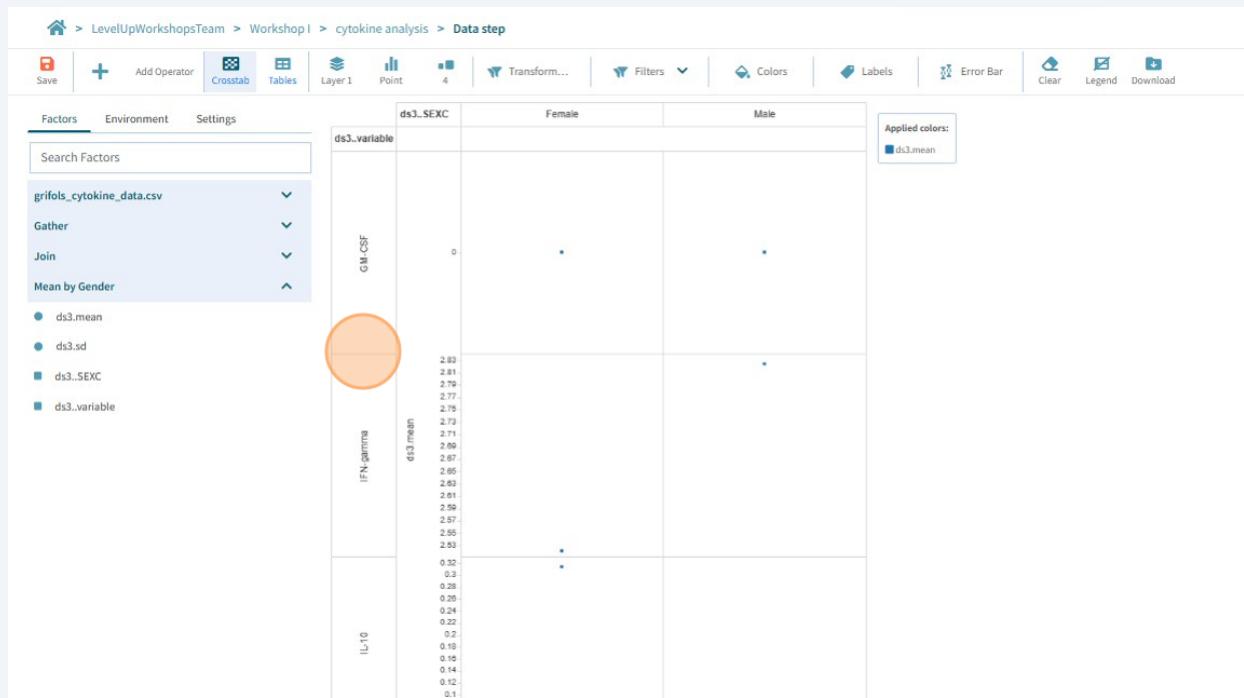
20 Click on the "+" icon.



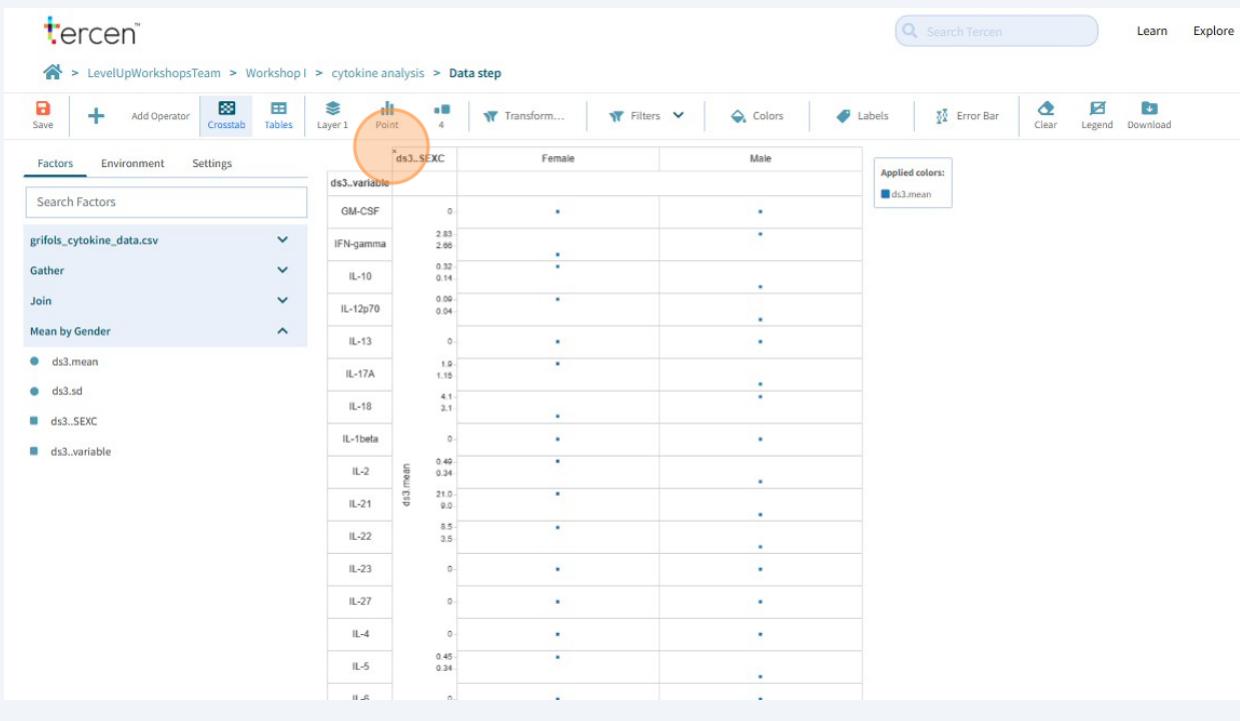
21 Click on Data Step.



22 Drag the row line upward to compress the view vertically.



23 Click on the little "x" icon to remove the factor.

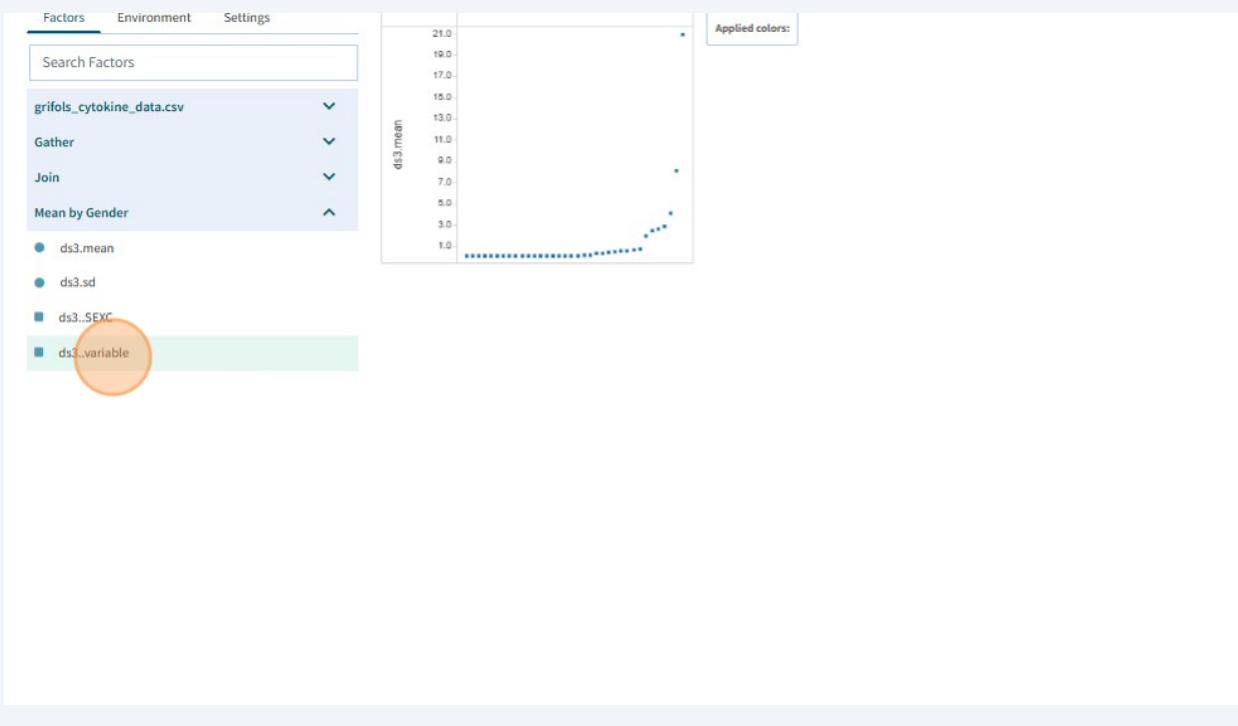


Tip!

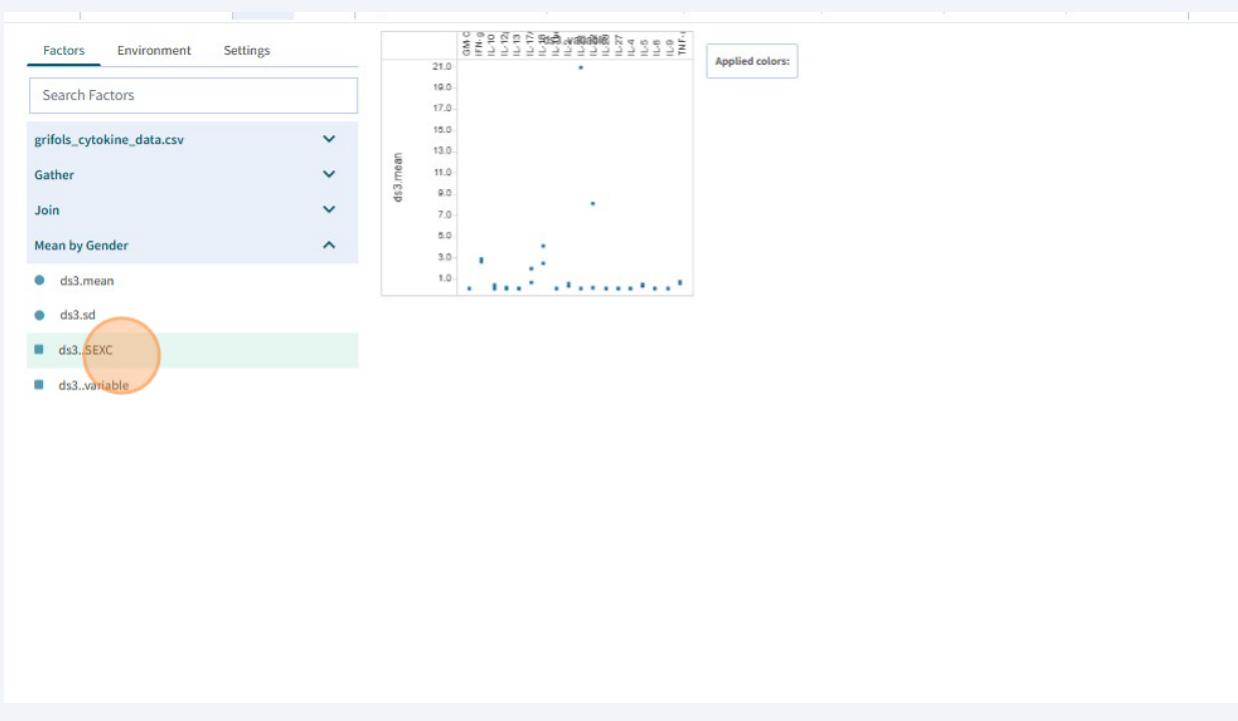
The little "x" only appears when you put your mouse over the factor. This is how we remove factors from Grid area of the Crosstab Window.

There is also a "Clear" button on the top right of the Crosstab, this resets the view and removes every factor in the Grid area.

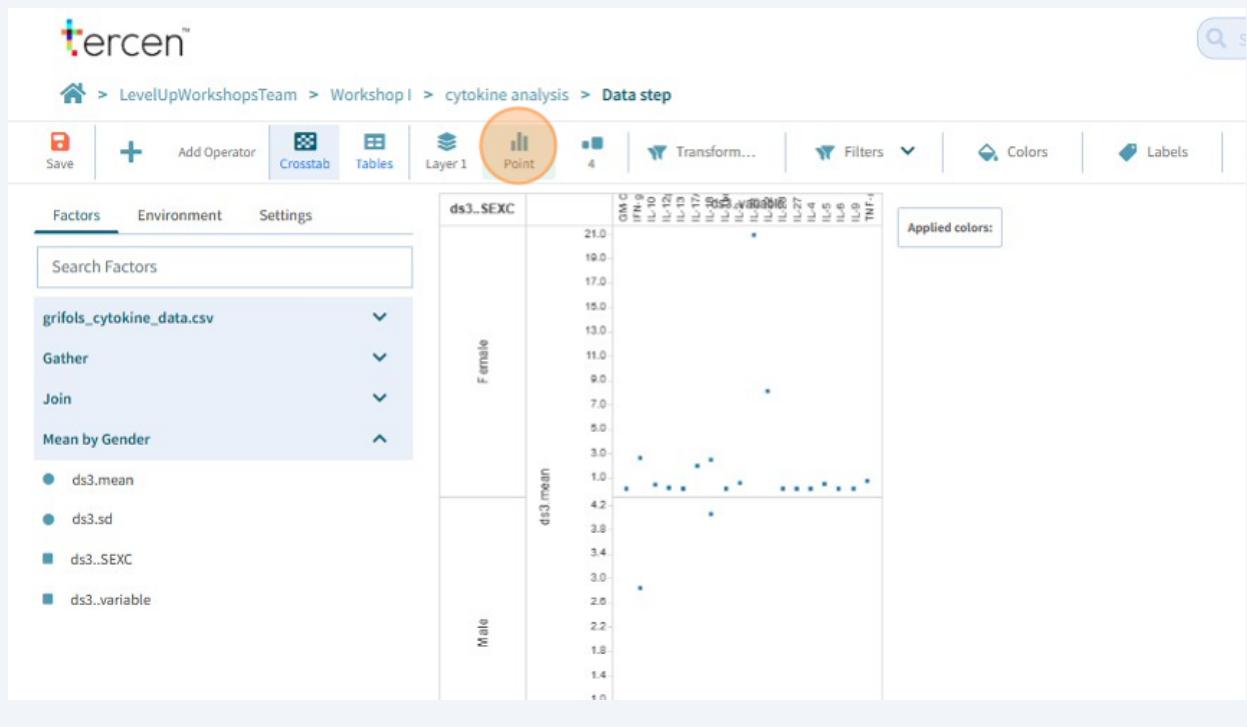
24 Drag **ds3..variable** and drop it onto the **X-Axis**.



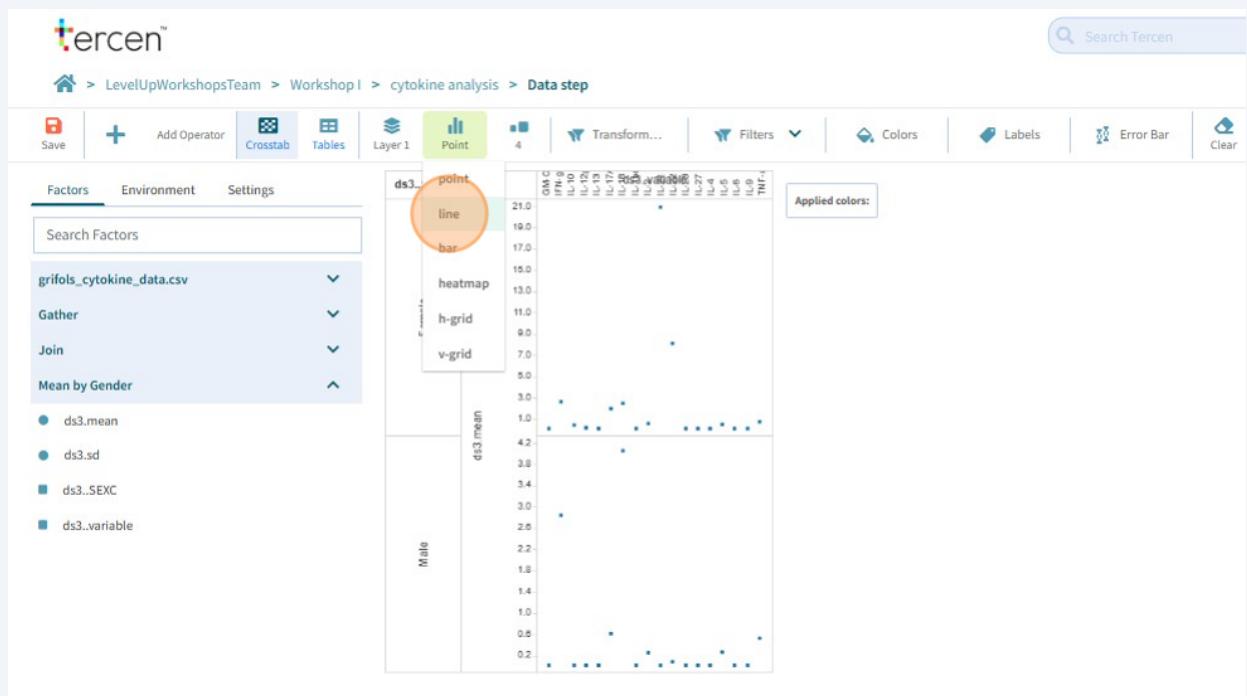
25 Drag **ds3..SEXC** and drop it onto the **Columns**.



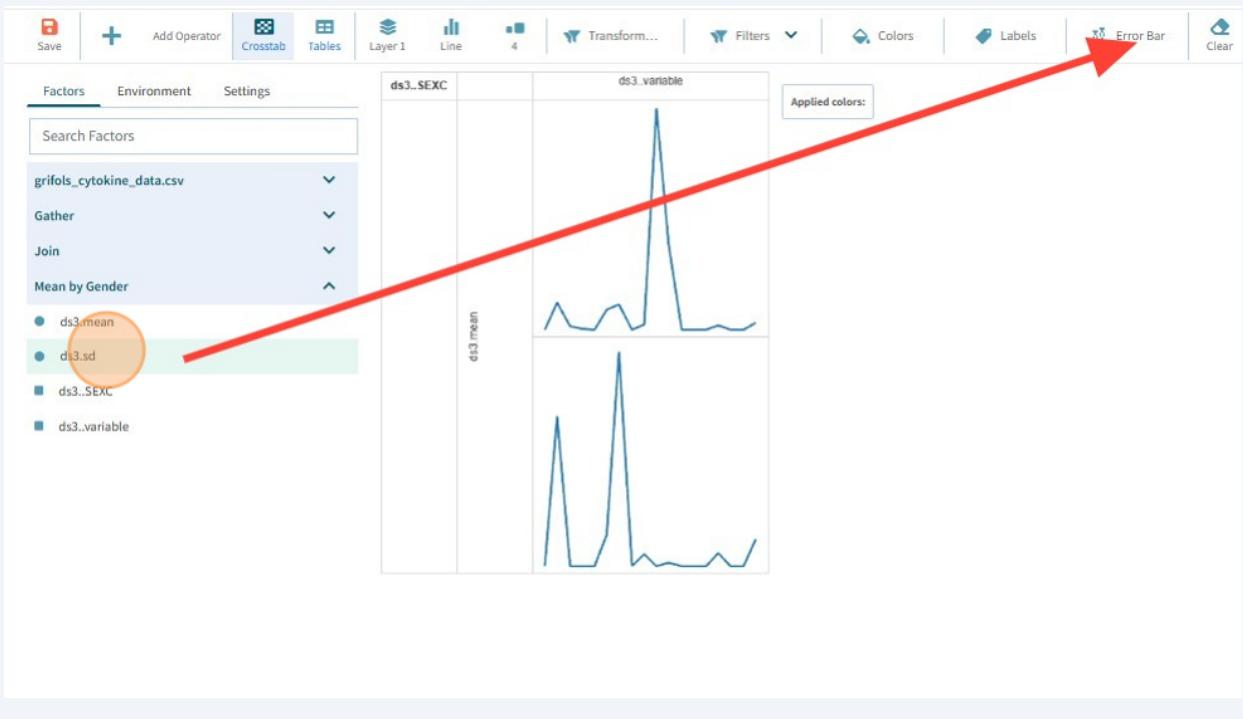
26 Click on the Style.



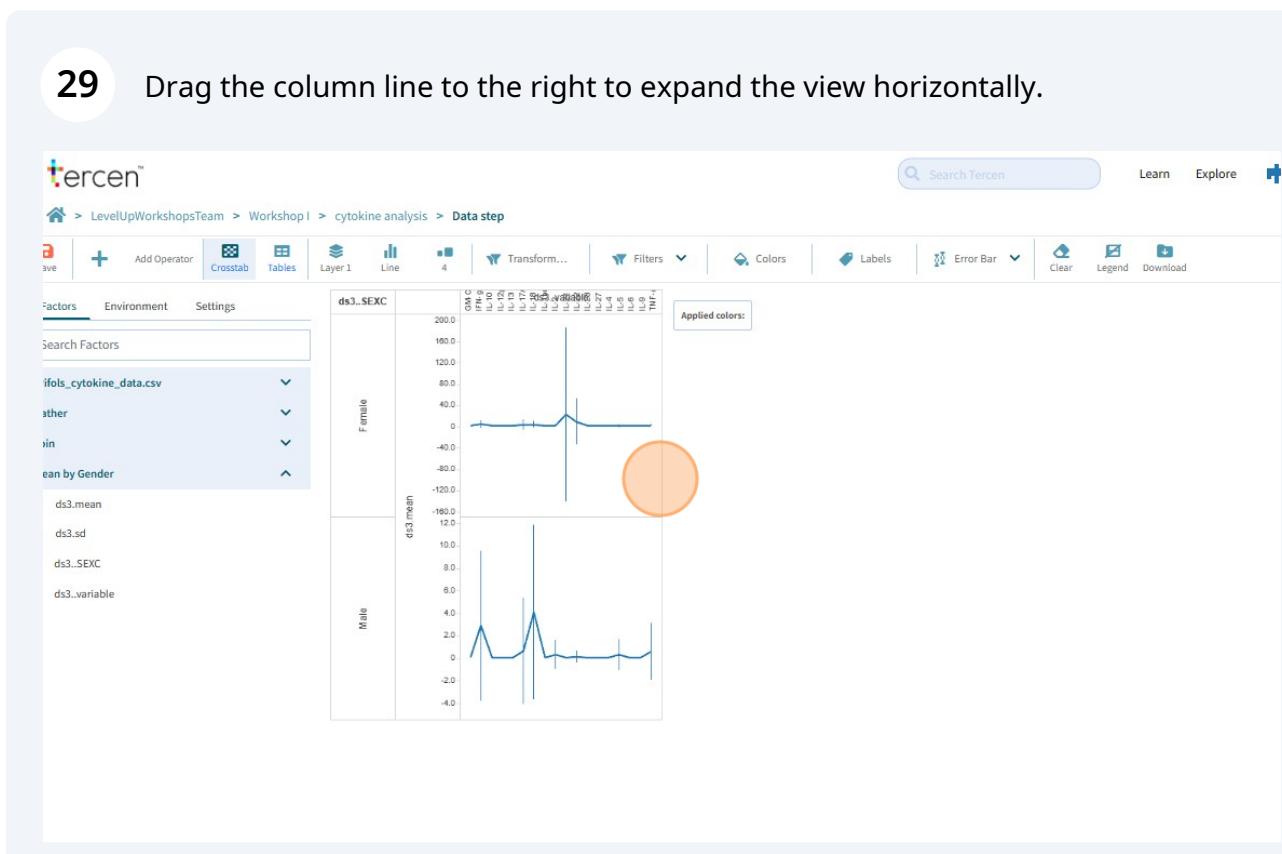
27 Click "line"



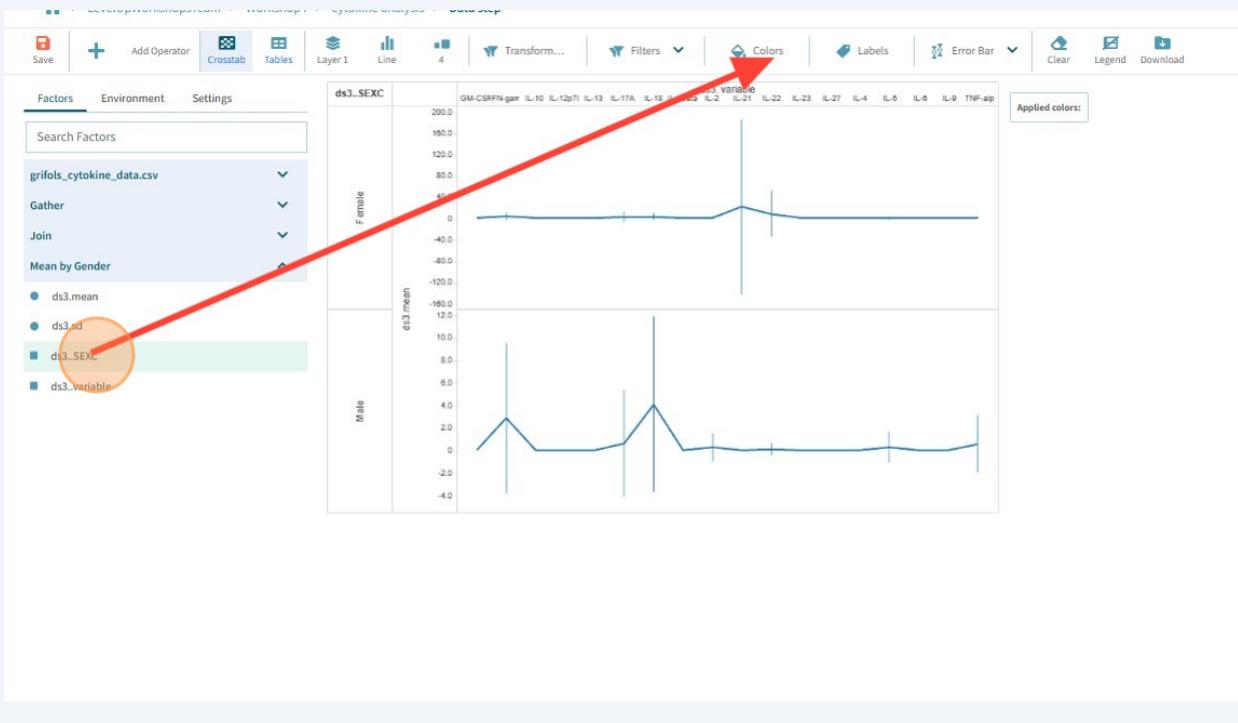
28 Drag **ds3..sd** and drop it onto the **Error Bar**.



29 Drag the column line to the right to expand the view horizontally.



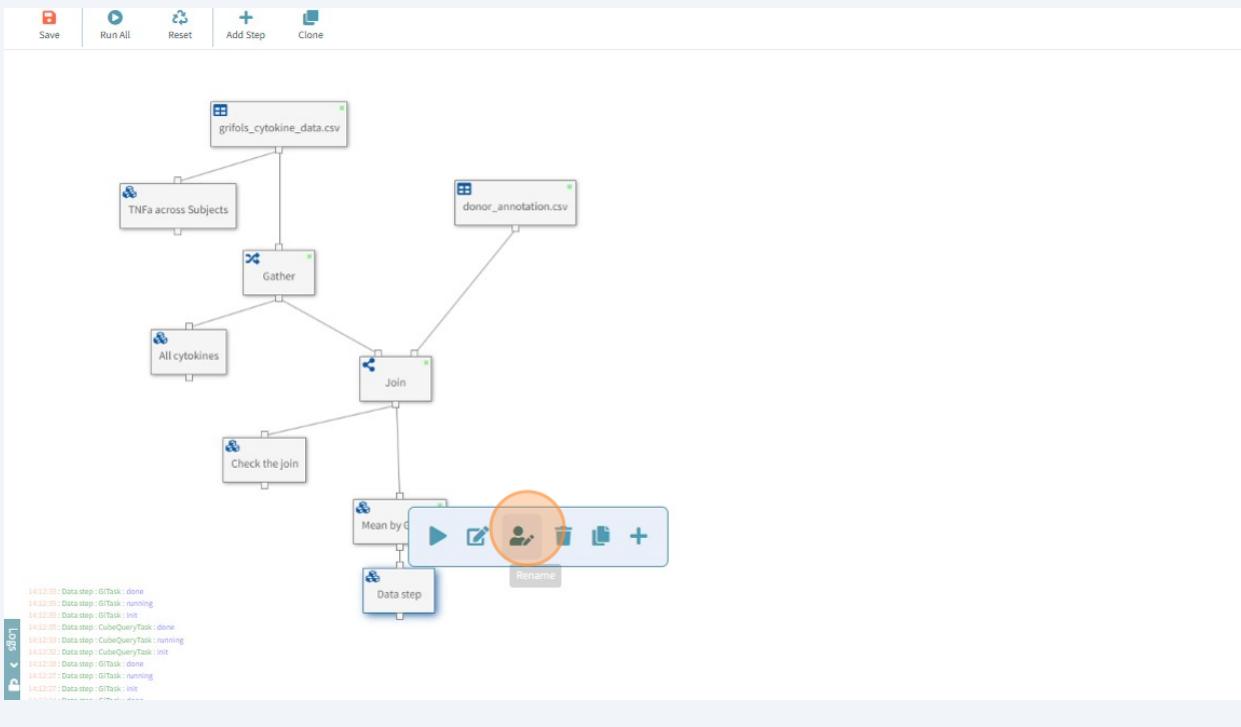
30 Drag ds3..SEX and drop it onto the Color.



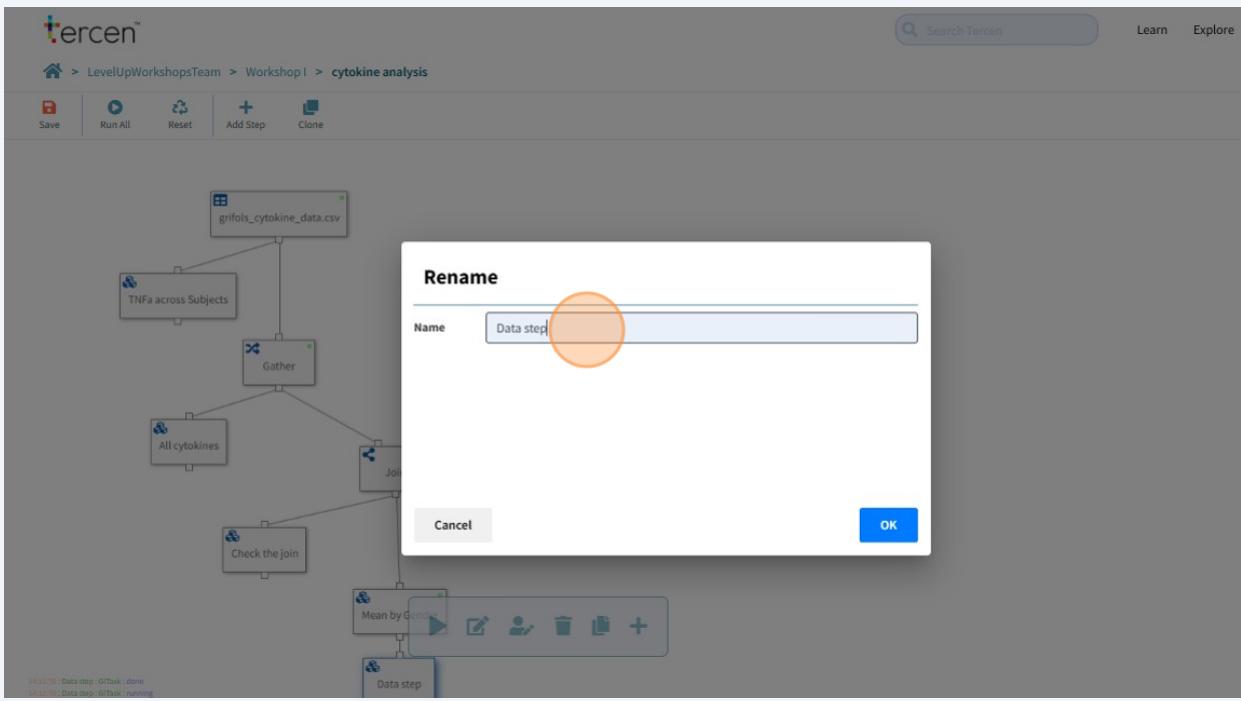
31 Click cytokine analysis to navigate to the workflow view.



32 Click on the Rename icon.

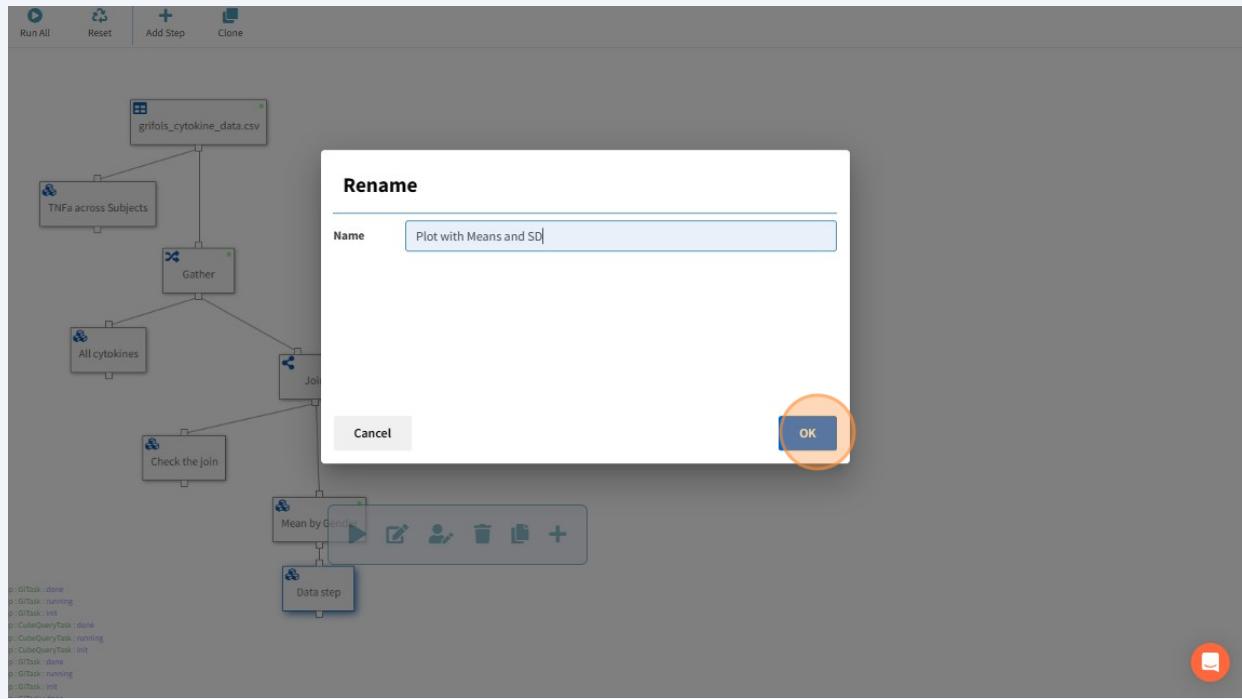


33 Click this text field.

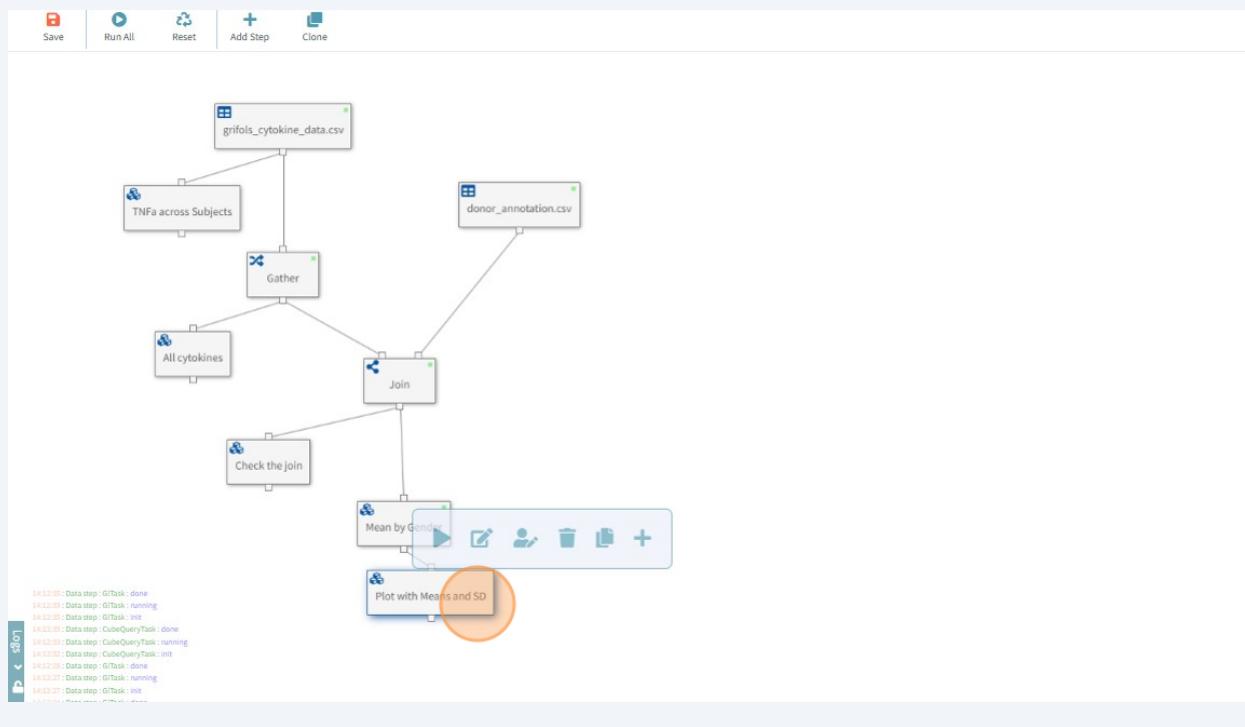


34 Type "Plot with Means and SD"

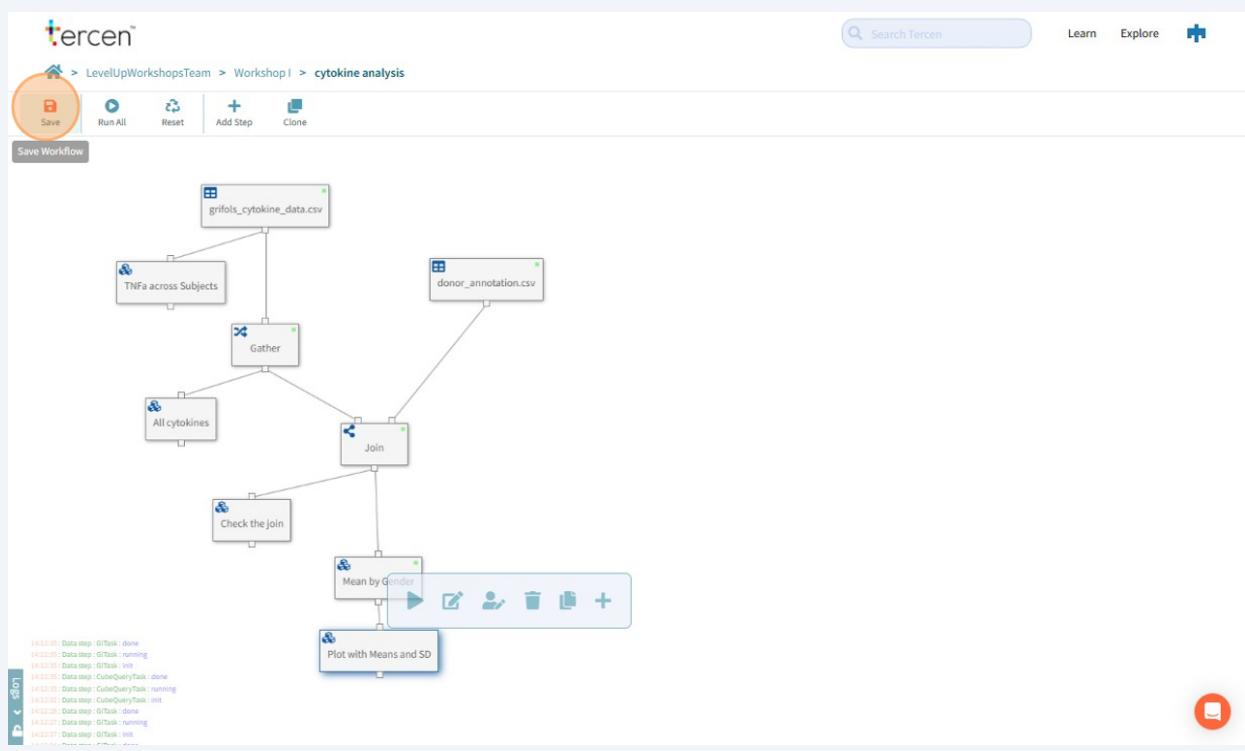
35 Click "OK"



36 Move the step the left to organize the workflow.



37 Click here.



38

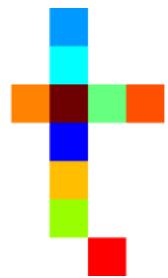
You are at the end of the guide.

Here is a recap of what you have achieved:

- Calculated the mean of a cohort group
- Created a plot with the the mean values

Well done!

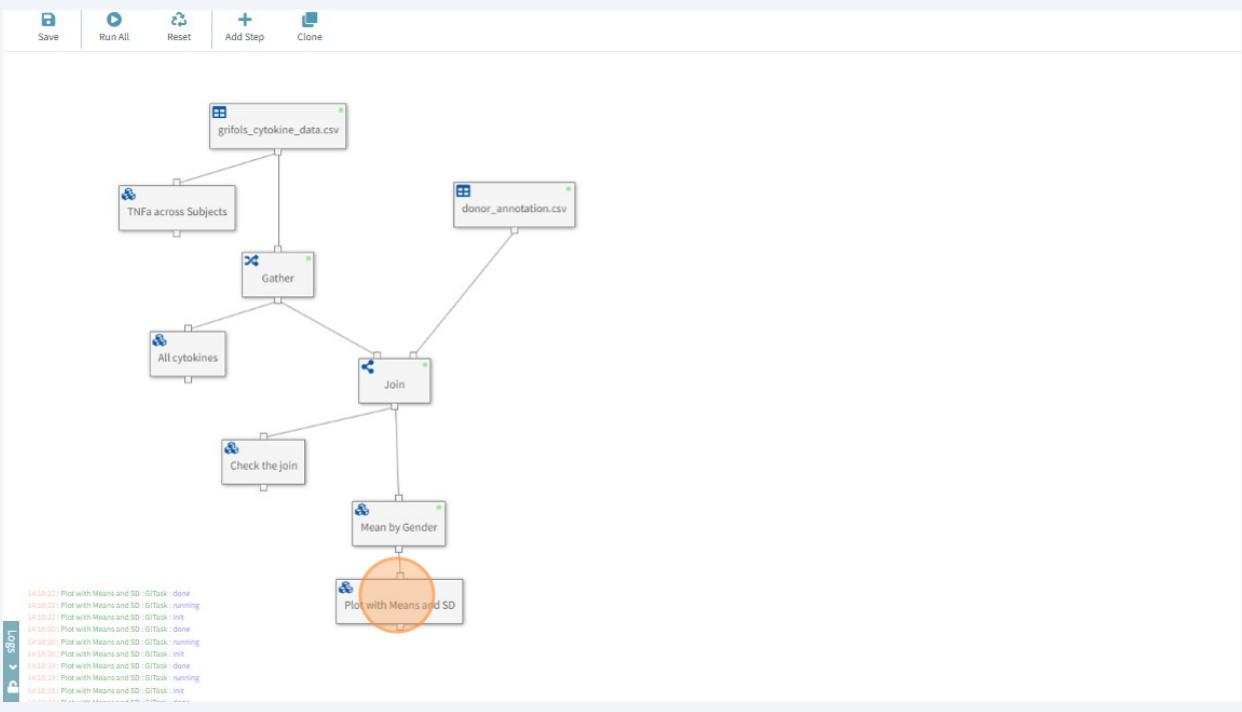
0112 - Export Plots



The guide explains how to use the Filter control to isolate data in projections. It will also investigate more functionality of the plot operator for making graphs to be exported for reports.

1 Starting on the cytokine analysis workflow

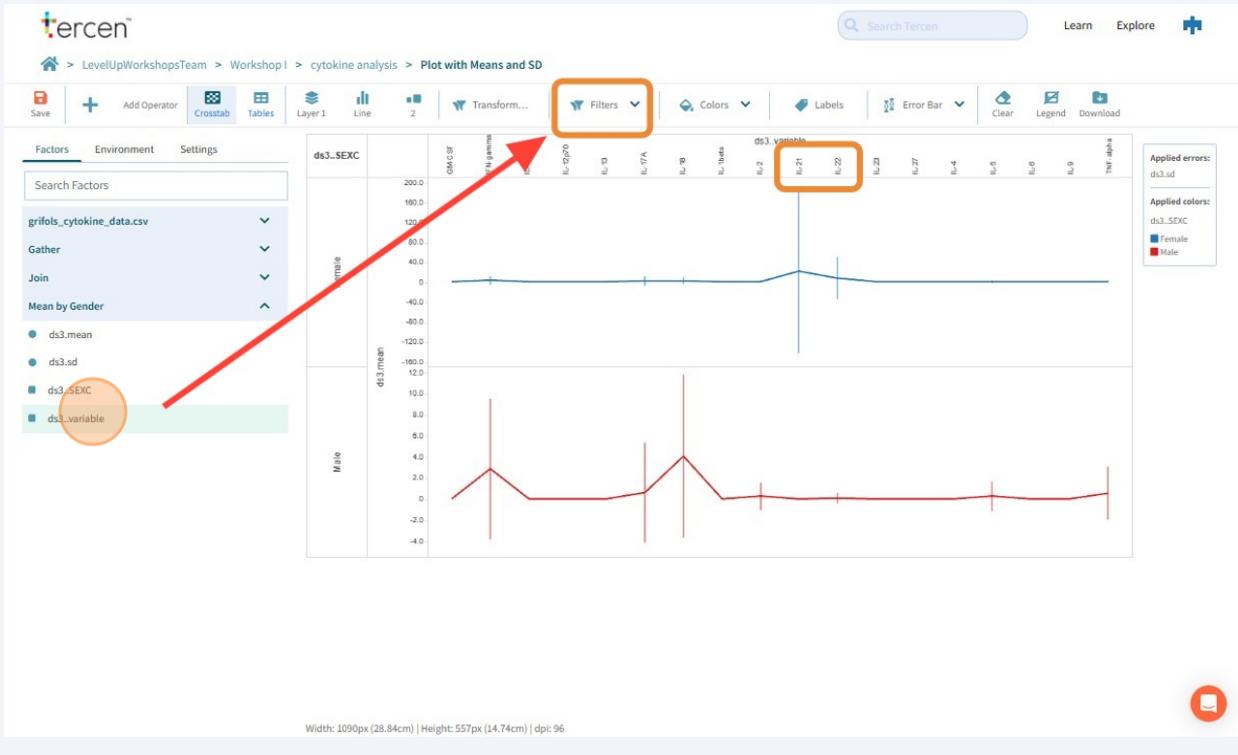
Click **Plot with Means and SD** and select Edit on the local toolbar.



- 2 Take a moment to note cytokines IL-21 and IL-22 on the graph.

We will use a **Filter** to remove them

Drag "ds3..variable" to the **Filters**.

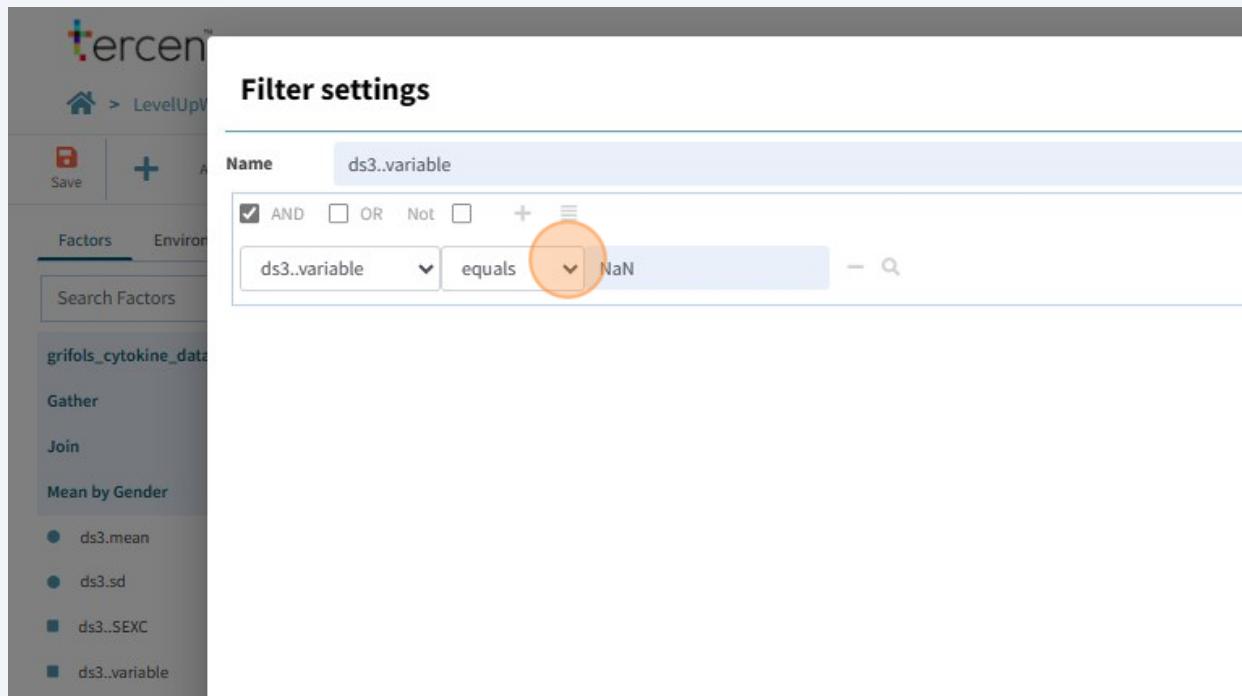


- 3 The Filter control panel will open.

A Filter uses logical rules to include or exclude data from the projection.

Tercen starts with a placeholder rule for you to modify

"ds3.variable equals NaN"



- 4 Change the setting from "equals" to "not equals"

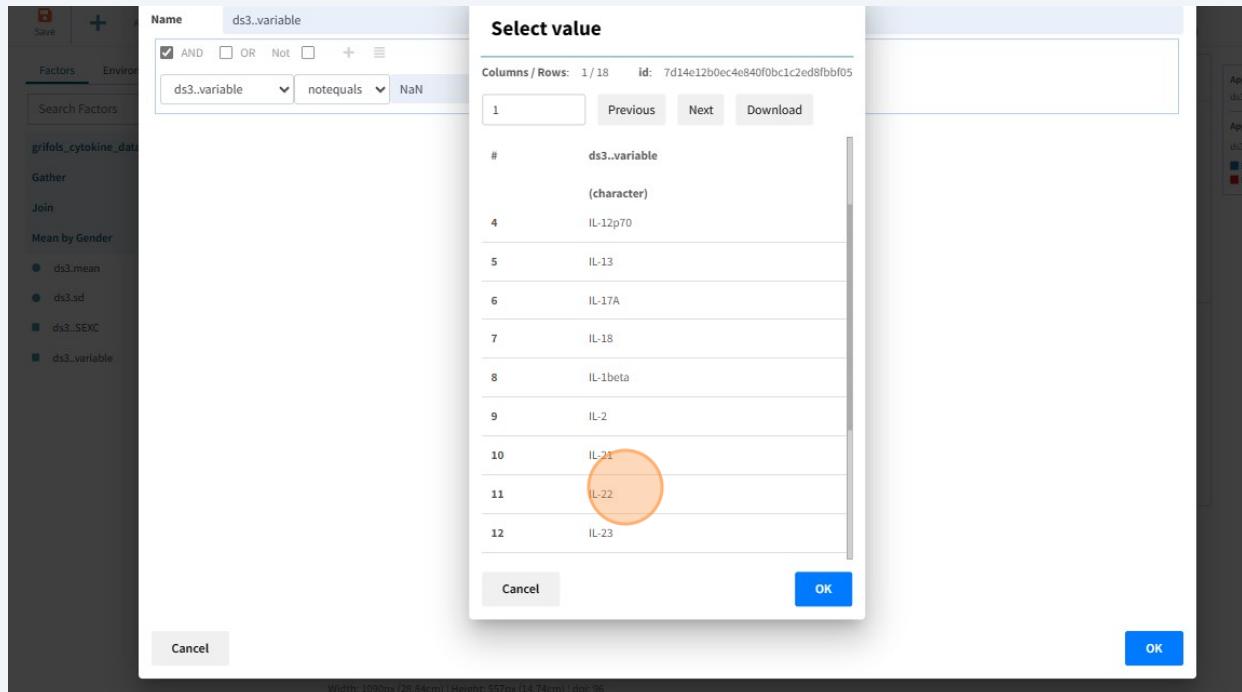
Click the Search icon.

The screenshot shows the 'Filter settings' dialog box. At the top, there is a search bar labeled 'Name' containing 'ds3.variable'. Below the search bar are filter operators: 'AND' (checkbox checked), 'OR' (checkbox unselected), 'Not' (checkbox unselected), and a '+' sign. The main query area contains three dropdown menus: 'ds3.variable' (selected), 'notequals' (selected), and 'NaN'. To the right of these dropdowns is a search icon (magnifying glass) enclosed in a red circle. On the left side of the dialog, there is a sidebar with various options: 'Save', 'Factors', 'Environ', 'Search Factors', 'grifols_cytokine_data', 'Gather', 'Join', and 'Mean by Gender'. Under 'Mean by Gender', there is a list of variables: 'ds3.mean' (selected), 'ds3.sd', 'ds3.SEXC', and 'ds3.variable'. The right side of the dialog has a vertical sidebar titled 'Explore' with several items listed.

- 5 A box will open showing a list of all the unique values in the ds3.variable factor.

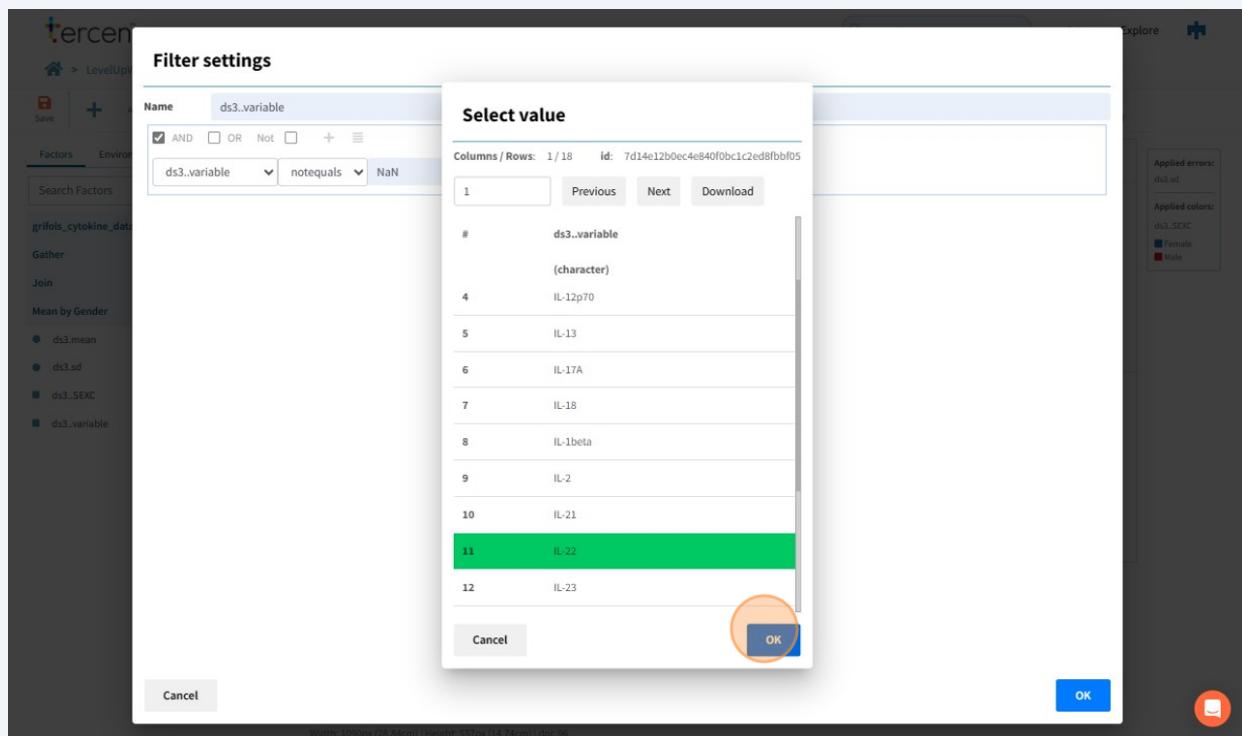
You can see it is the Cytokine Names

Select "IL-22"



The screenshot shows a software interface with a sidebar containing various data analysis tools like 'Search Factors', 'Gather', 'Join', and 'Mean by Gender'. The main area displays a 'ds3.variable' search results table with columns for '#', 'ds3.variable', and '(character)'. The table lists entries from 4 to 12, including IL-12p70, IL-13, IL-17A, IL-18, IL-1beta, IL-2, IL-21, IL-22, and IL-23. The row for 'IL-22' is highlighted with an orange circle. Below the table are 'Cancel' and 'OK' buttons. The entire dialog is titled 'Select value'.

- 6 Click "OK"



The screenshot shows the same software interface after the 'OK' button was clicked. The 'ds3.variable' search results table now highlights the row for 'IL-22' with a green bar, indicating it has been selected. The 'OK' button is also highlighted with an orange circle. The rest of the interface remains the same, with the sidebar and other dialog elements visible.

7 We have built the logical rule

ds3.variable not equals IL-22

The projection will exclude IL-22 and select all the others.

8 Filter rules can be stacked to build more complex selections.

The topmost one is actioned first with the following filters further refining that selection.

Click the + (plus) icon to add another filter rule.

The screenshot shows the Tercen software interface with the 'LevelUp!' project selected. On the left, there's a sidebar with 'Factors' and 'Environ' tabs, and sections for 'Search Factors', 'Gather', 'Join', and 'Mean by Gender' (with options for 'ds3.mean', 'ds3.sd', 'ds3.SEXC', and 'ds3.variable'). The main area is titled 'Filter settings' and contains a configuration for a filter named 'ds3.variable'. The filter is set to 'not equals' and is configured to exclude 'IL-22'. A plus sign (+) button is highlighted with a red circle, indicating where to add another filter rule. The overall interface is clean and modern, with a light gray background and white text.

9 Let's deselect another cytokine

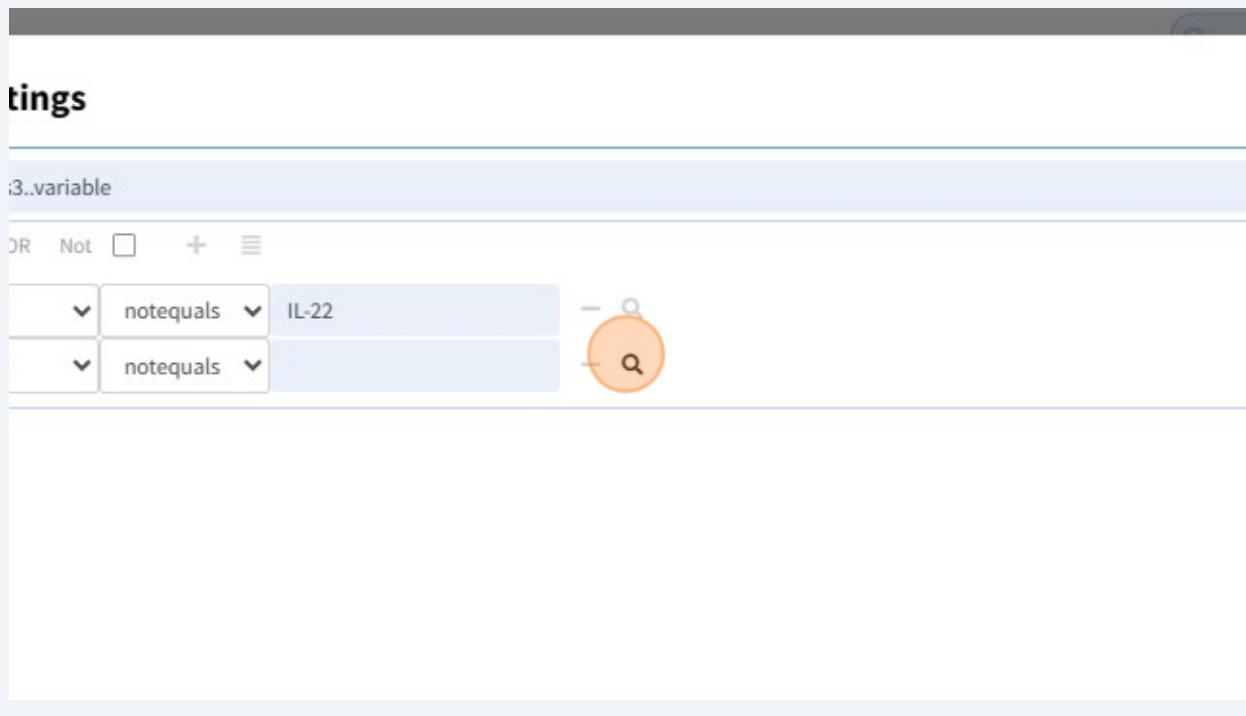
Change the Factor to ds3.variable

The screenshot shows the Tercen software interface with the 'Factors' tab selected. On the left, there is a sidebar with options like 'Search Factors', 'Gather', 'Join', and 'Mean by Gender'. Under 'Mean by Gender', there are two items: 'ds3.mean' and 'ds3.sd'. The main area displays the 'Filter settings' dialog. The 'Name' field is set to 'ds3..variable'. The logic is set to 'AND'. There are two filter conditions: 1) 'ds3..variable notequals IL-22' and 2) 'ds3.mean equals NaN'. The second condition's dropdown menu is highlighted with an orange circle.

10 Change the logic to "not equals"

The screenshot shows the Tercen software interface with the 'Factors' tab selected. The sidebar and 'Mean by Gender' section are identical to the previous screenshot. The main area displays the 'Filter settings' dialog. The 'Name' field is set to 'ds3..variable'. The logic is set to 'AND'. There are two filter conditions: 1) 'ds3..variable notequals IL-22' and 2) 'ds3..variable equals NaN'. The second condition's dropdown menu is highlighted with an orange circle, indicating it has been modified.

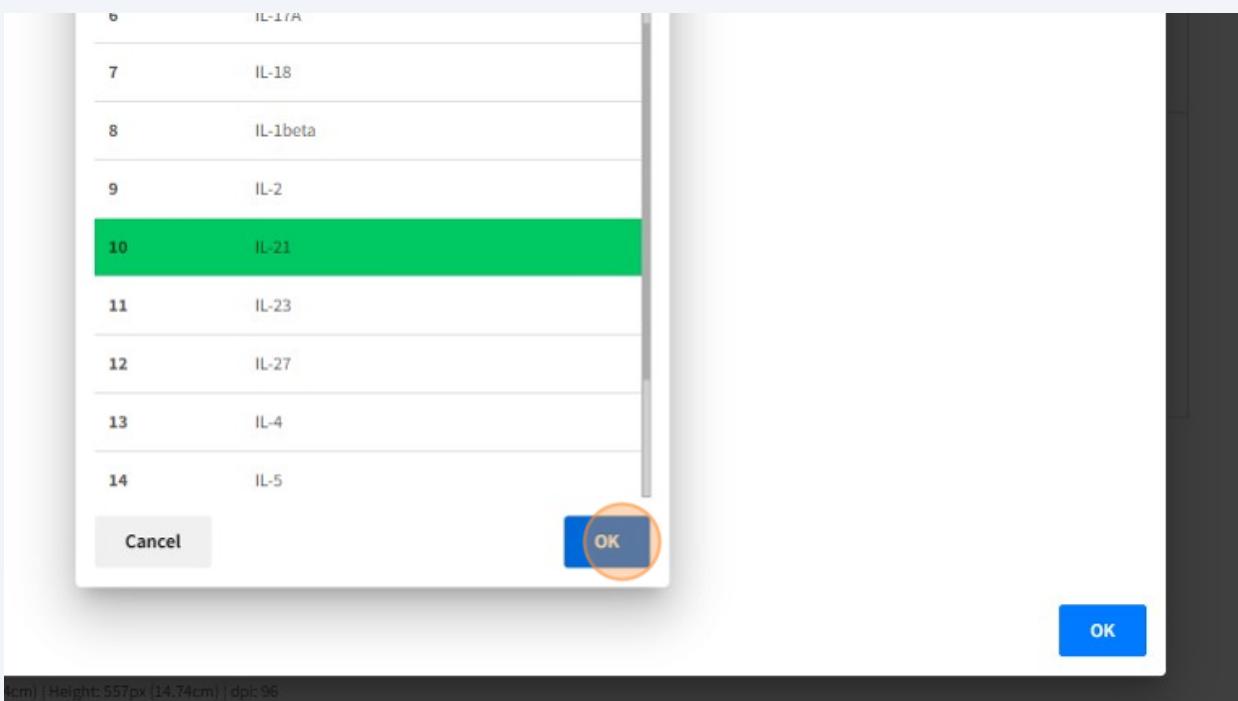
11 Select the search icon.



12 Click "IL-21"

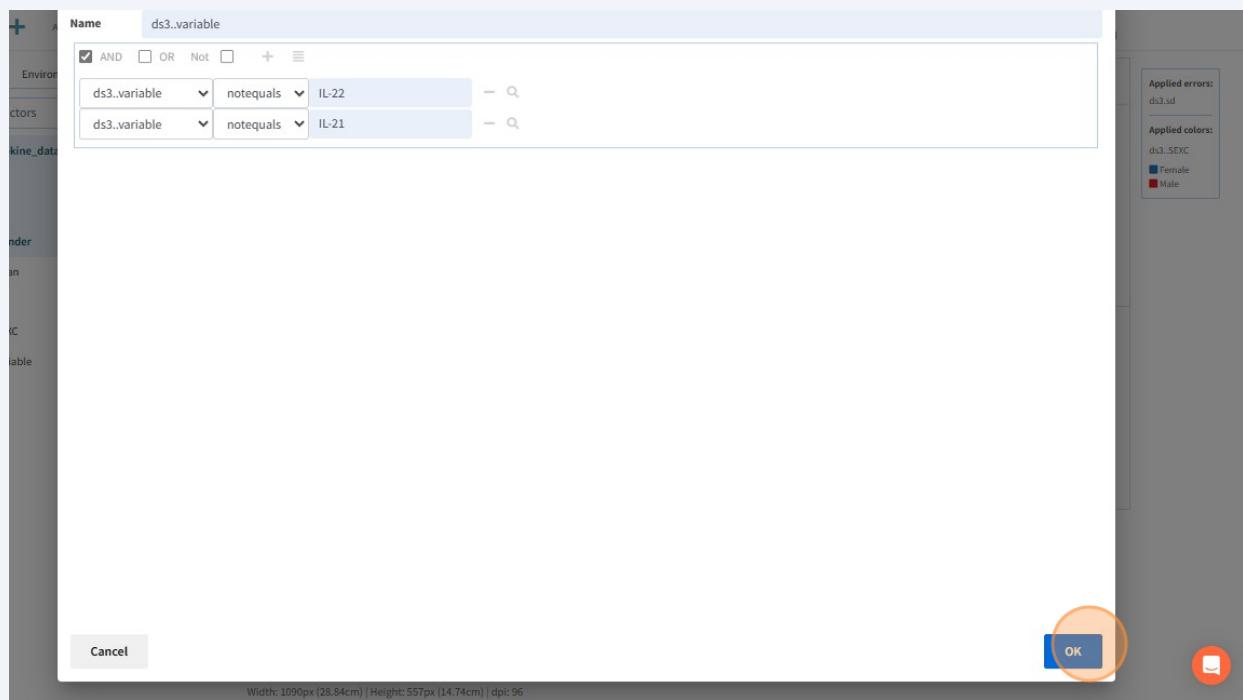
6	IL-17A
7	IL-18
8	IL-1beta
9	IL-2
10	IL-21
11	IL-23
12	IL-27
13	IL-4
14	IL-5

13 Click "OK"



14 We have made a filter that excludes two cytokines.

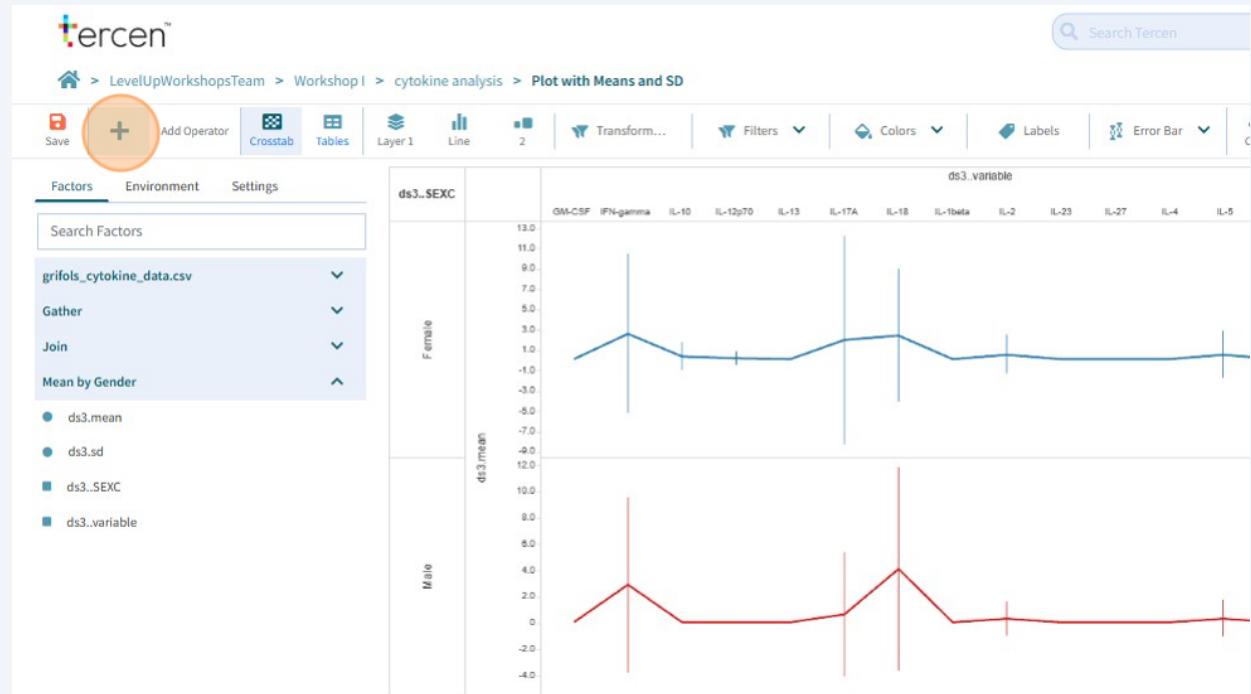
Click "OK" to apply it.



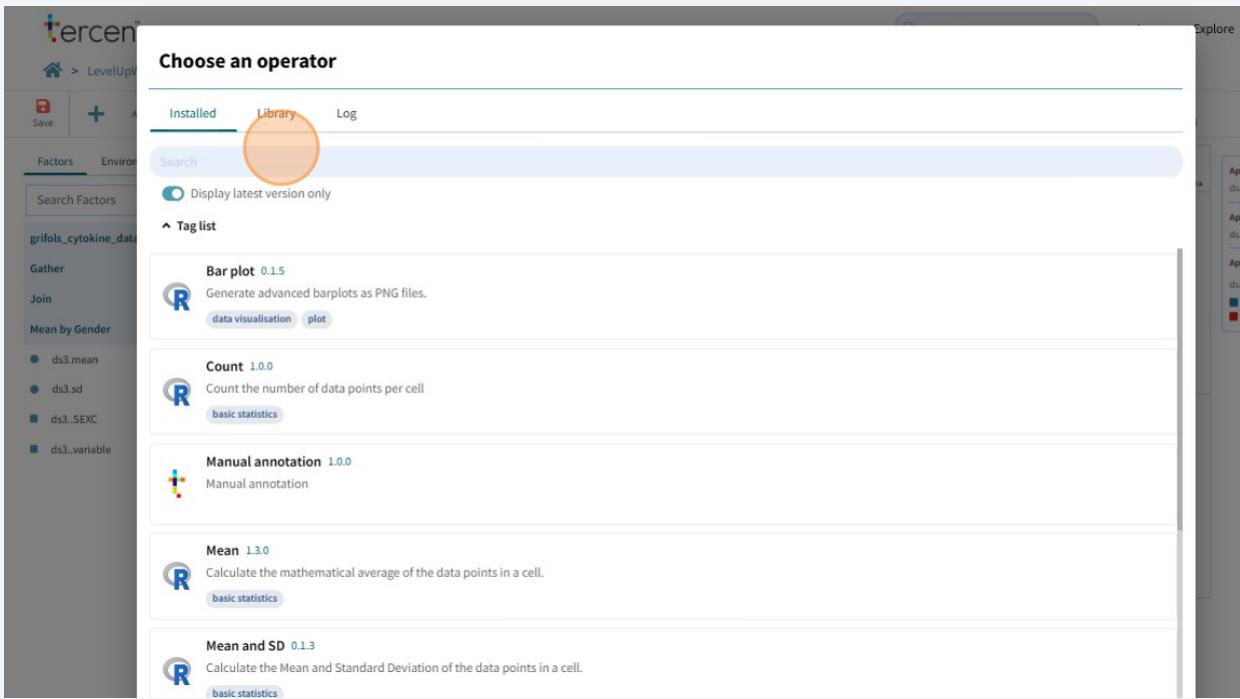
15 Take a moment to check that IL-21 and IL-22 are now missing from the graph.

16 Now lets use the plot operator again and experiment some more with its settings.

Click the Add Operator button.

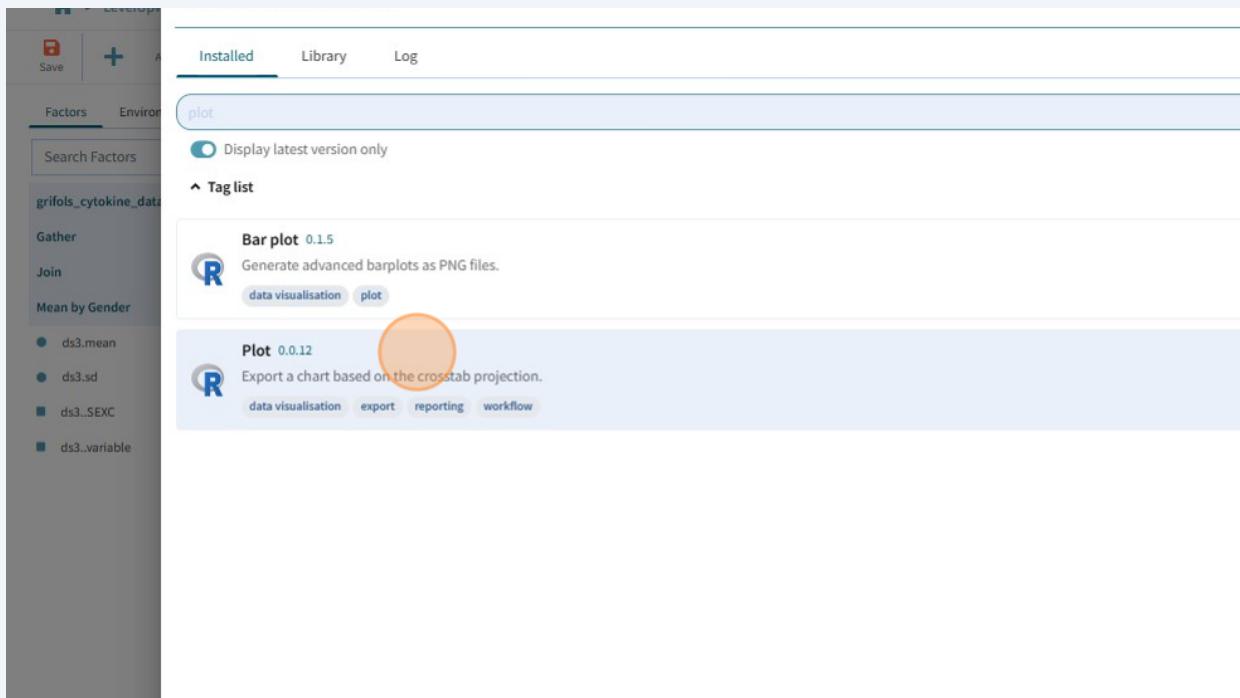


17 Click the "Search" field.

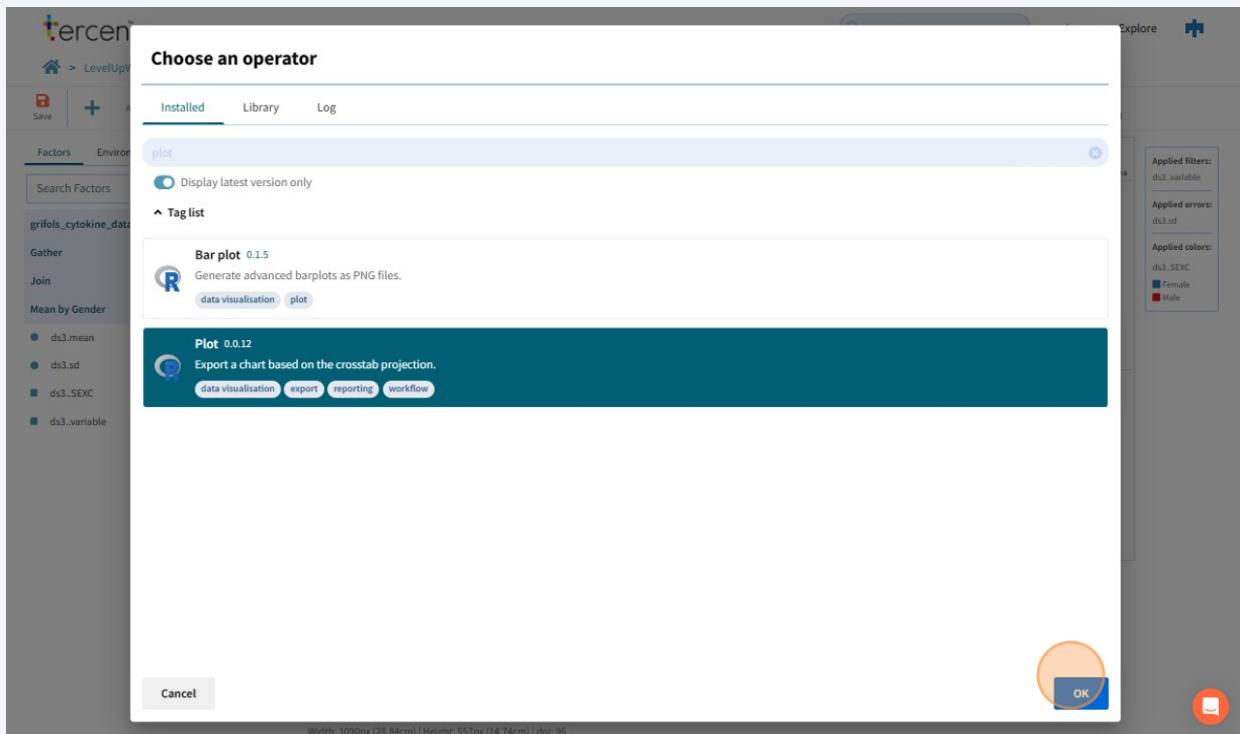


18 Type "plot"

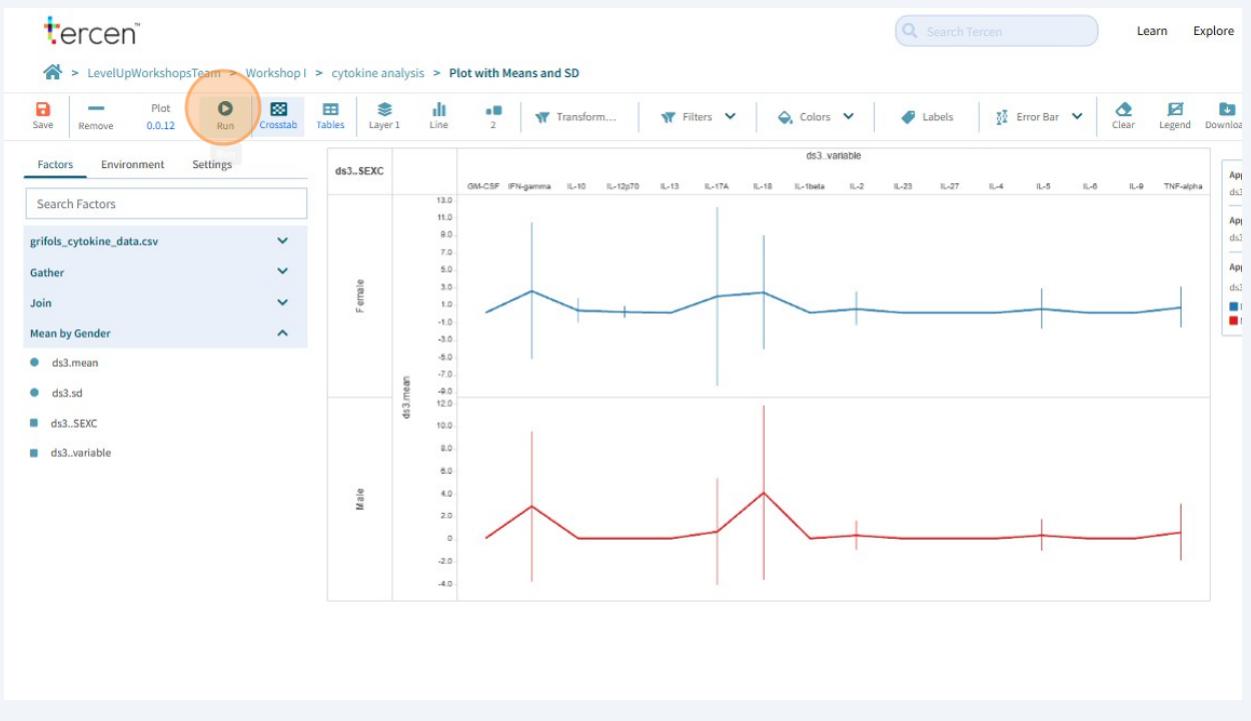
19 Click here.



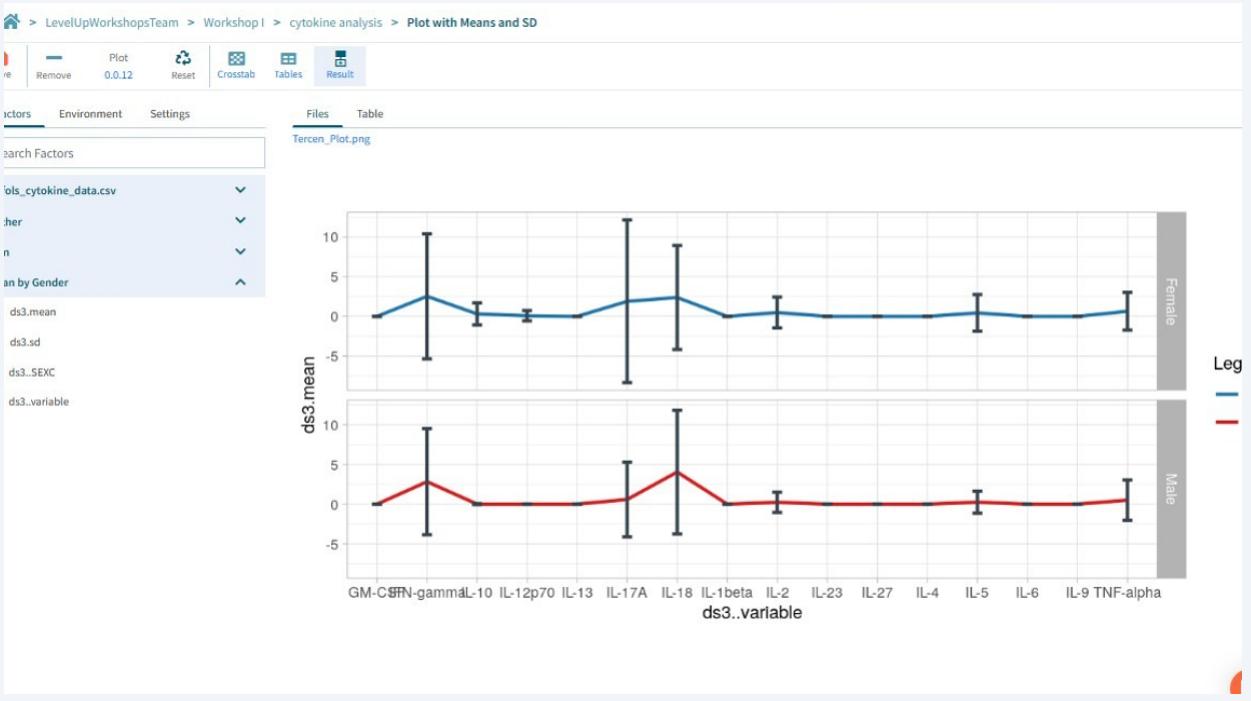
20 Click "OK"



21 Click on the Run icon.



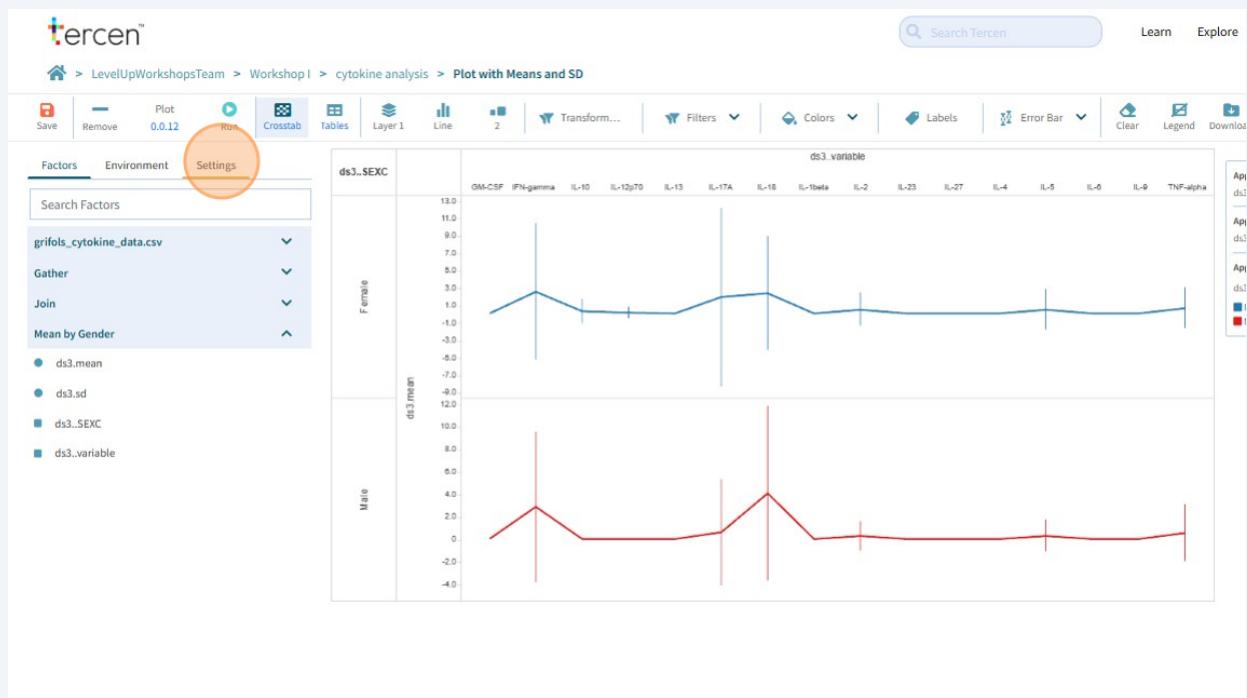
22 A generated image appears, by default its in **png** format.



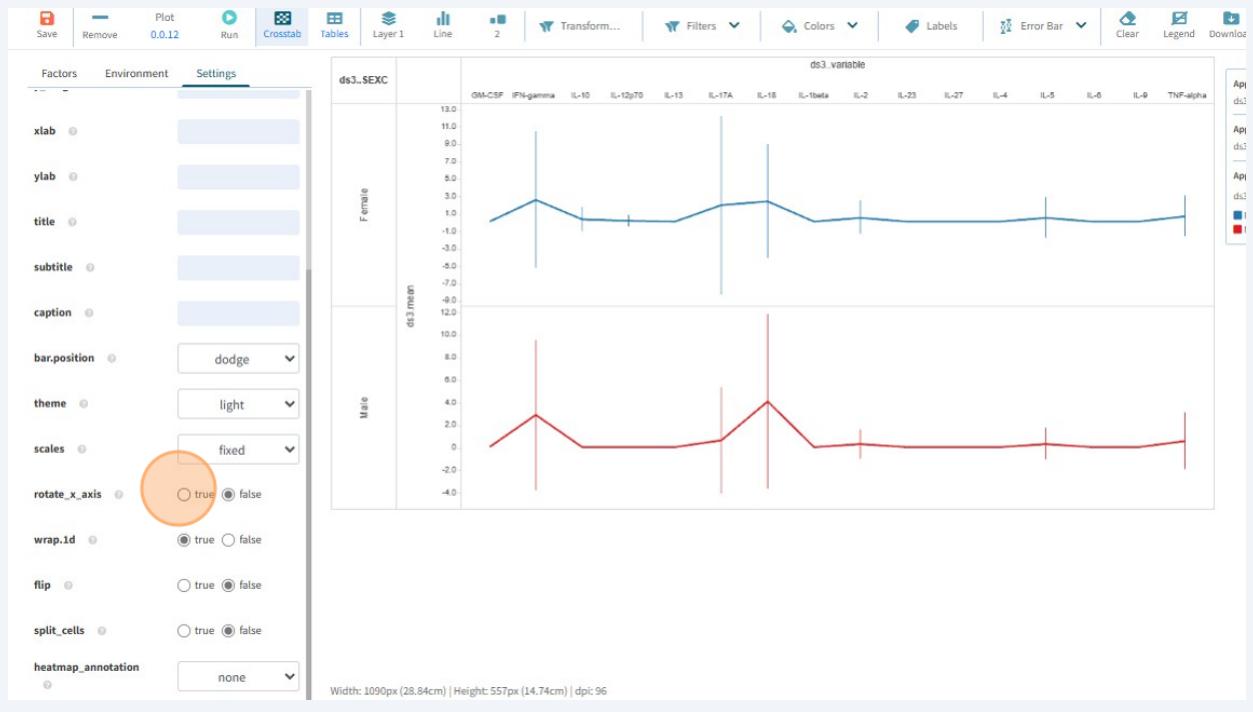
23 Click Reset icon



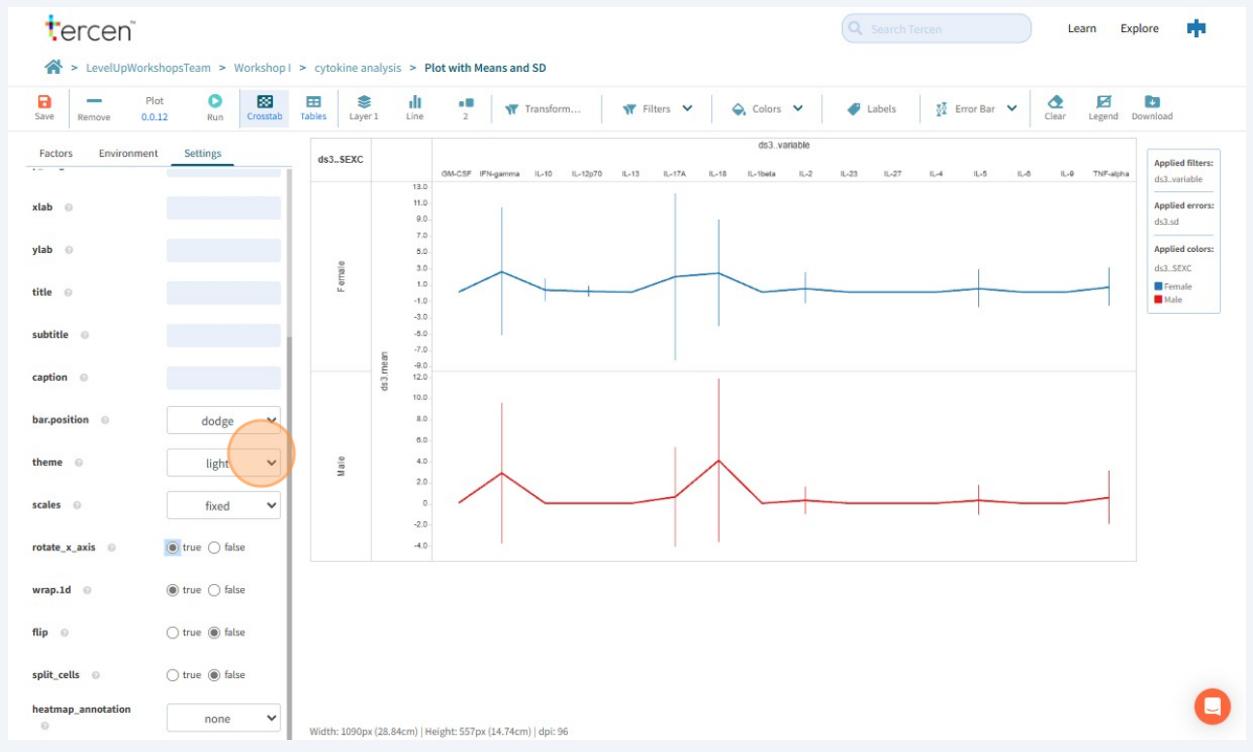
24 Click "Settings"



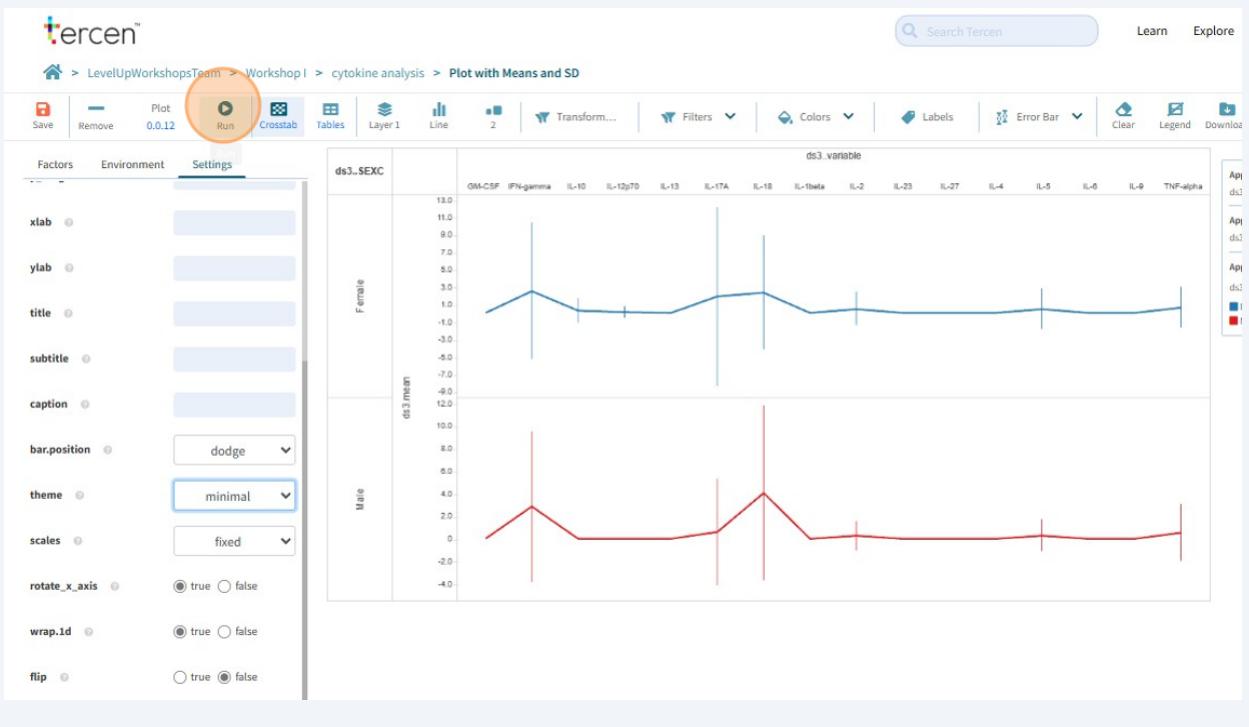
25 Click this radio button for `rotate_x_axis`.



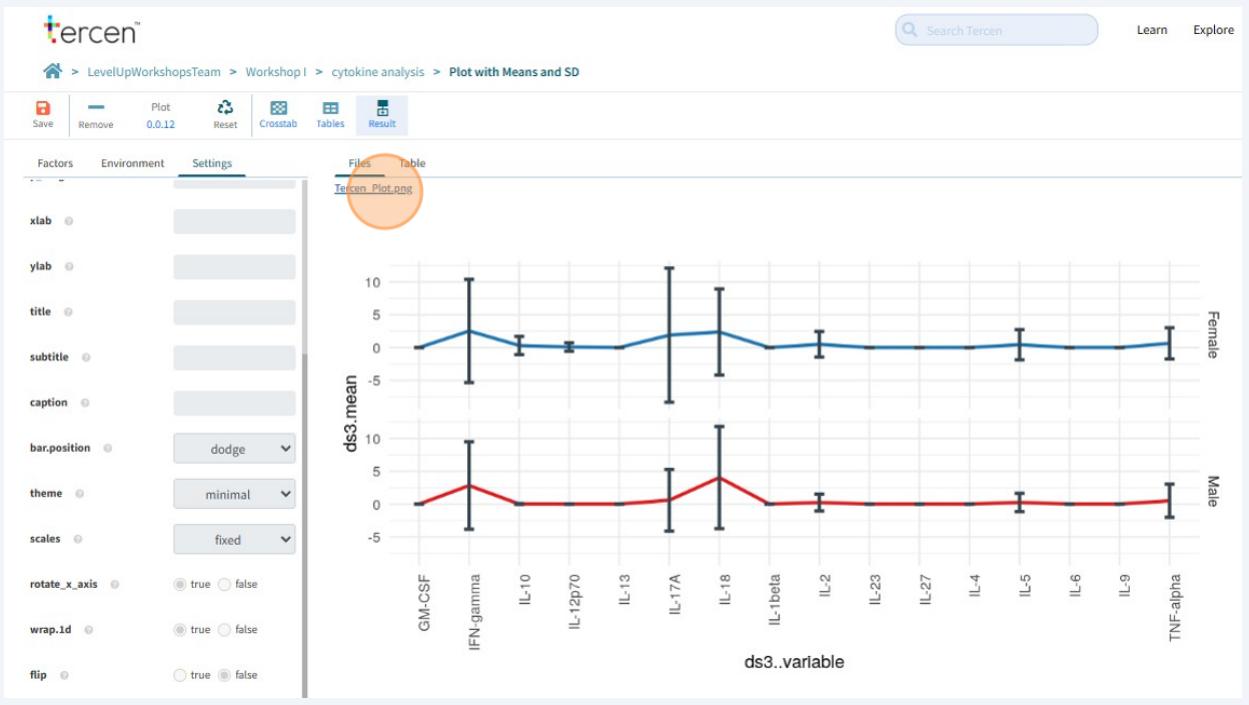
26 Click this dropdown menu for `theme` and choose **minimal**



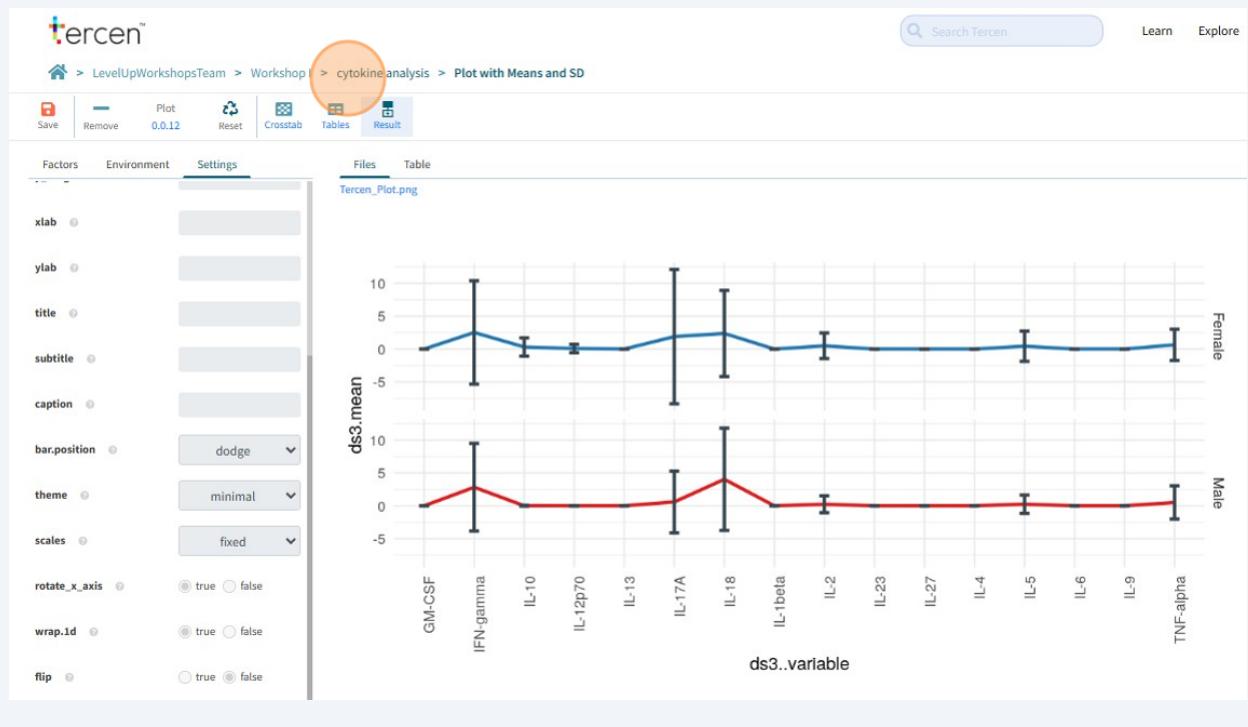
27 Click Run icon.



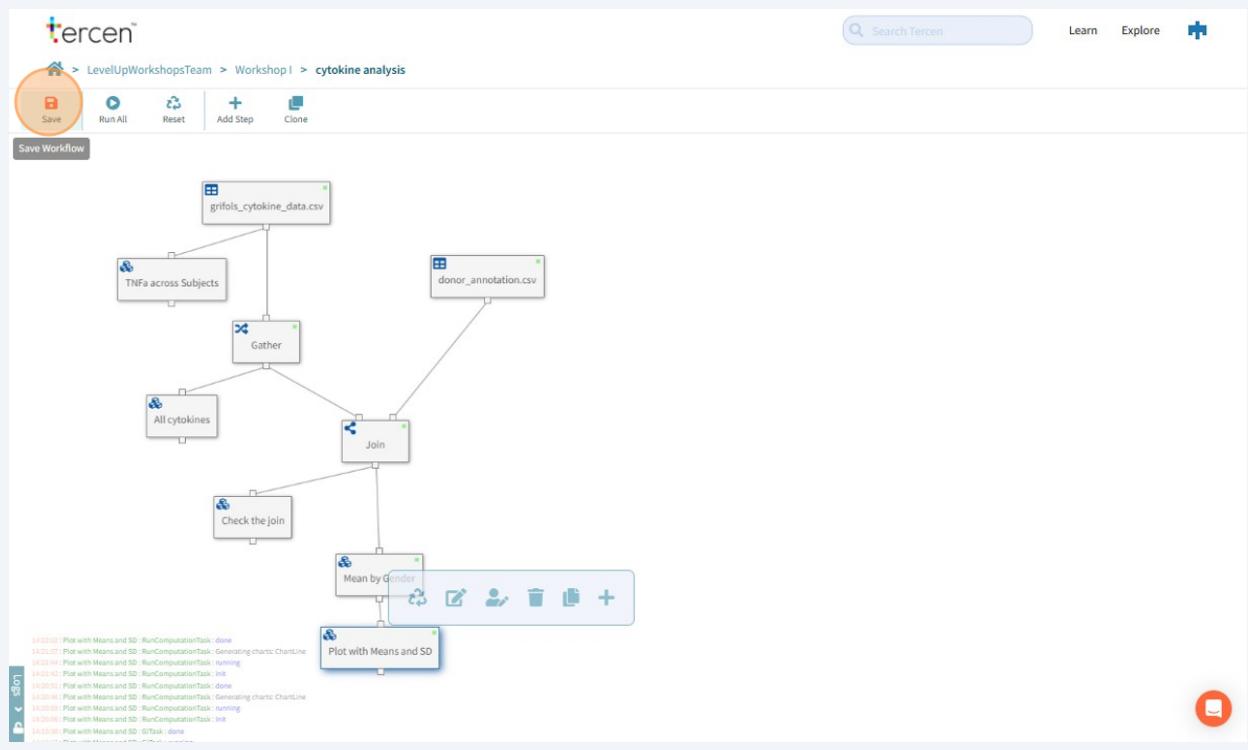
28 Click Tercen_Plot.png this downloads the image.



29 Click **cytokine analysis** to navigate back to the workflow view.



30 Click **Save** icon.



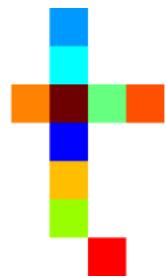
31 You are at the end of the guide.

Here is a recap of what you have achieved:

- Removed data from a projection
- Export a plot as a PNG image

Well done!

0113 - Run a Template



This guide provides a step-by-step walkthrough of how to run a Template workflow. It explains what a Template workflow is and how it can be used to start with a complete pipeline instead of creating one from scratch. Users can easily navigate the process and successfully run a Template workflow.

- 1 This guide outlines the steps necessary to run a Template workflow.

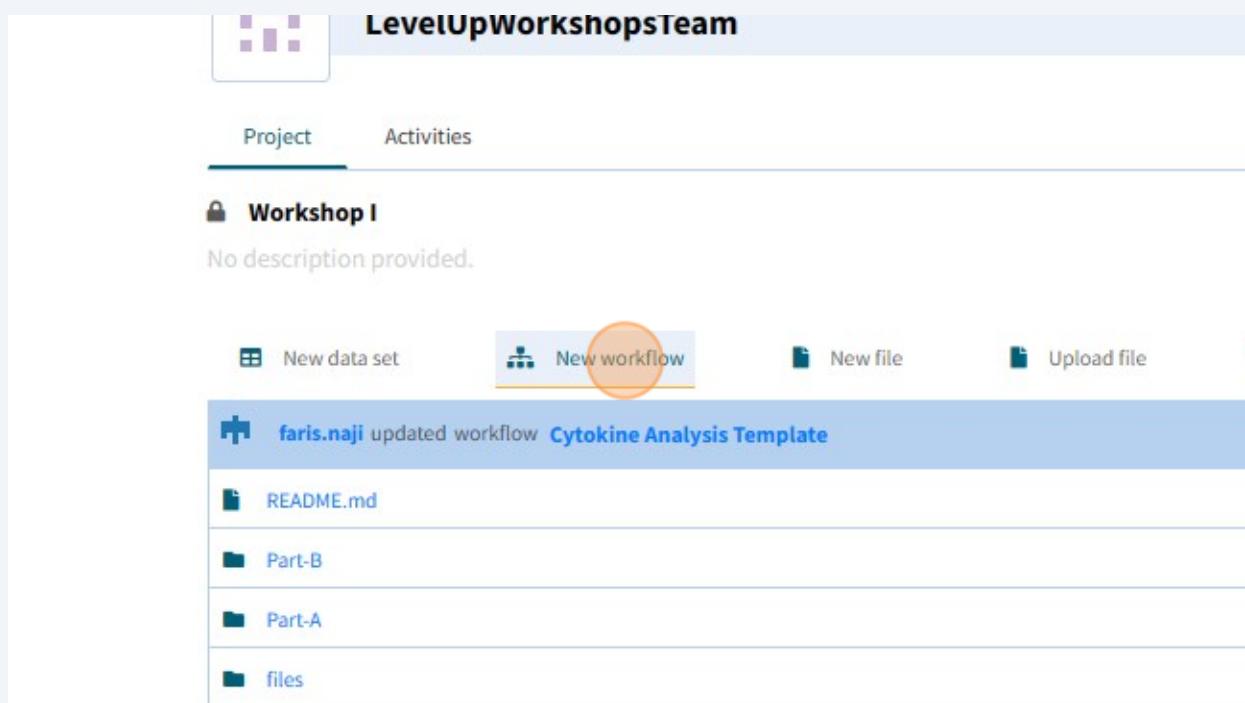
(i) Tip!

A Template workflow is a preexisting pipeline. It allows users to start with a complete pipeline instead of creating a pipeline from scratch.

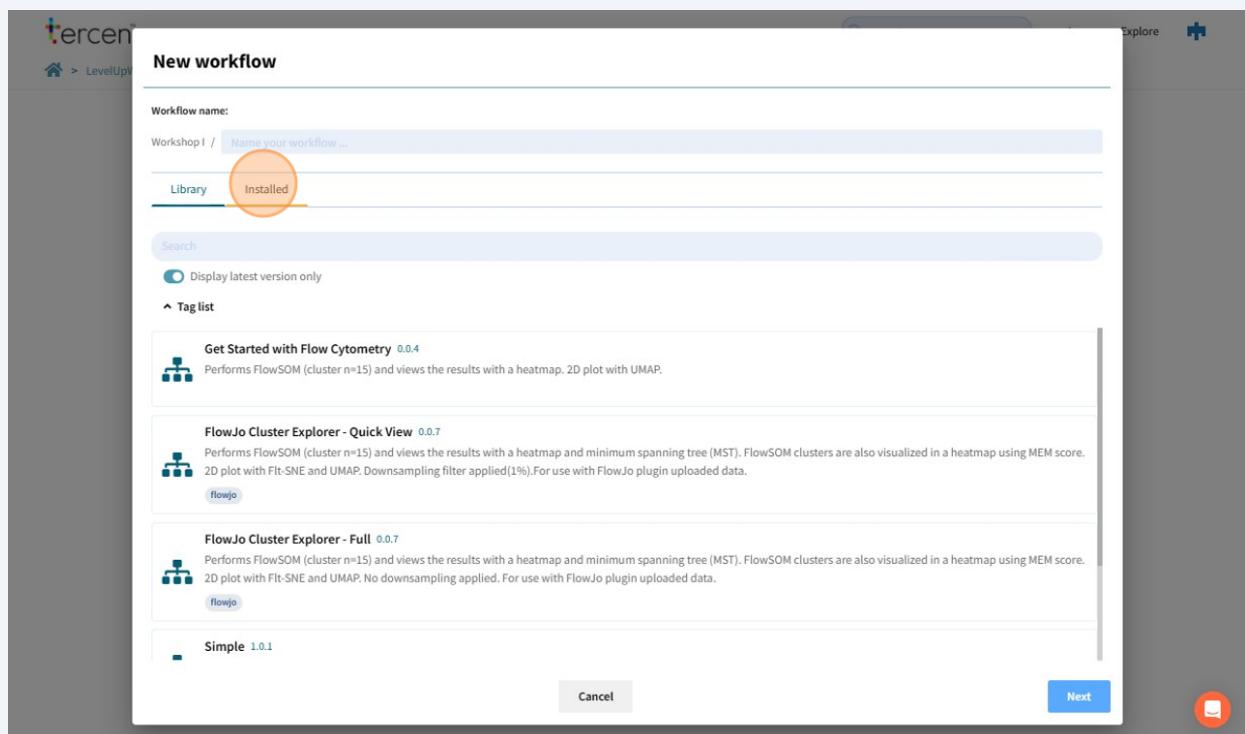
- 2 Click "Workshop I" to navigate to the top level in Workshop I

The screenshot shows the tercen platform interface. At the top, there is a navigation bar with a home icon, the text 'LevelUpWorkshopsTeam', and a search bar containing 'templates'. Below the navigation bar, there is a header for 'LevelUpWorkshopsTeam' with a project icon. The main content area shows a section titled 'Workshop I' with a lock icon, followed by the text 'No description provided.' Below this, there is a toolbar with icons for 'New data set', 'New workflow', 'New file', 'Upload file', 'Upload workflow', and 'Project settings'. A blue header bar displays the text 'faris.naji updated workflow Cytokine Analysis Template'. Underneath this, there is a list of files: 'README.md', 'Part-B', 'Part-A', and 'files'. At the bottom of the list, there is a single file named 'RFADMF.mdf'.

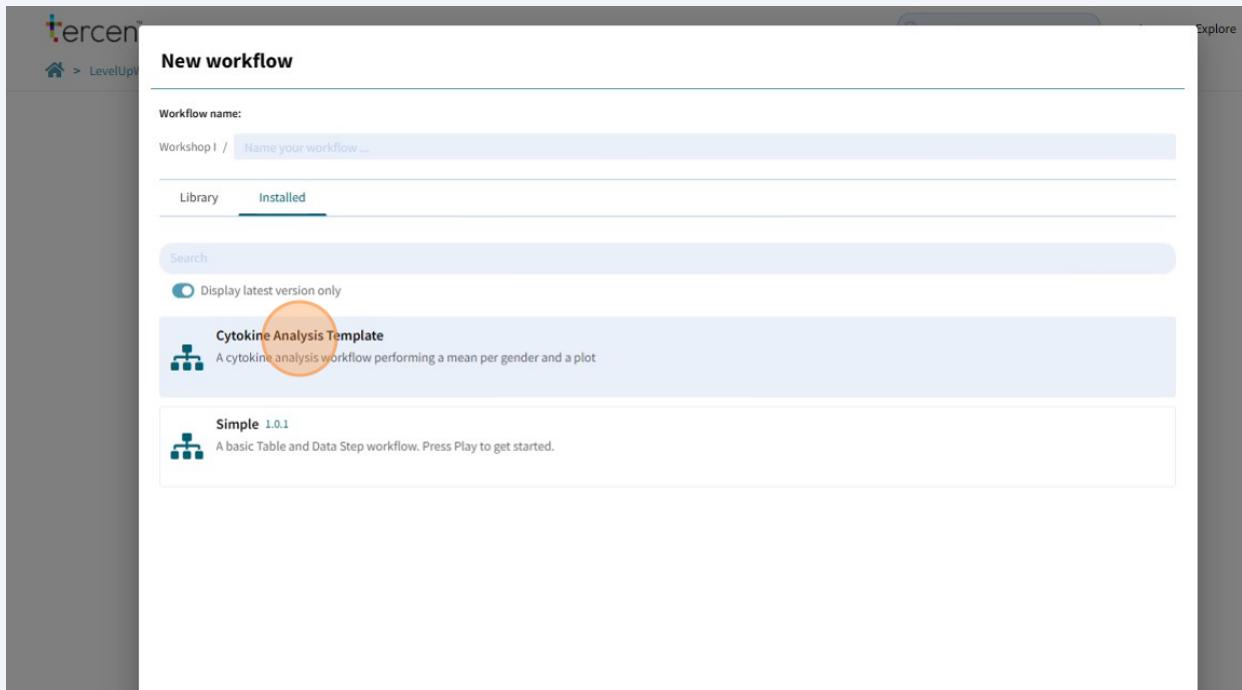
- 3 Click "New workflow"



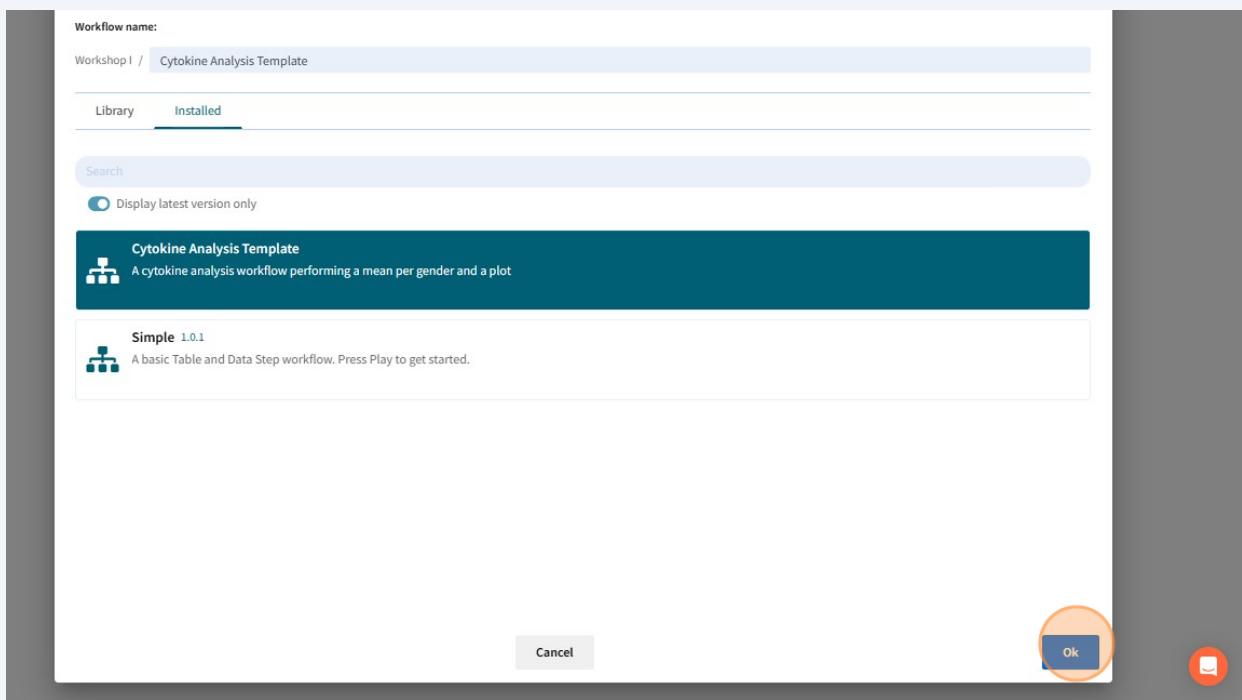
- 4 Click "Installed"



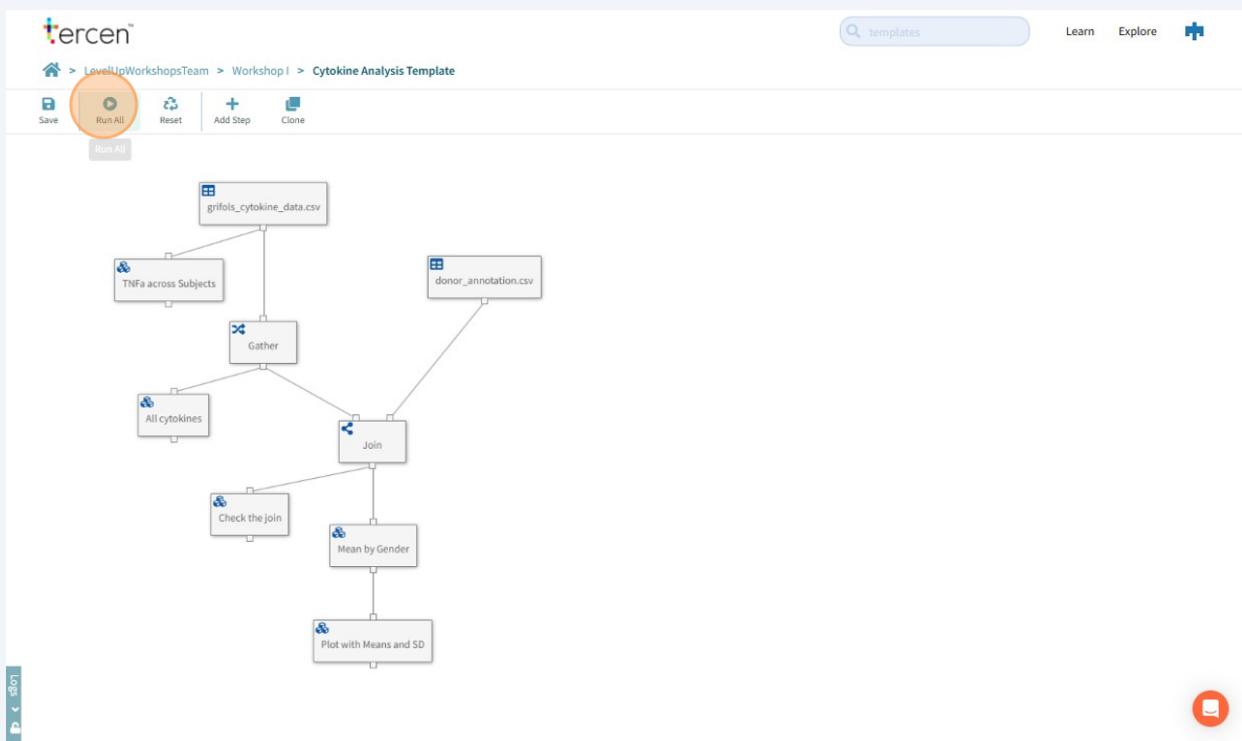
5 Click "Cytokine Analysis Template"



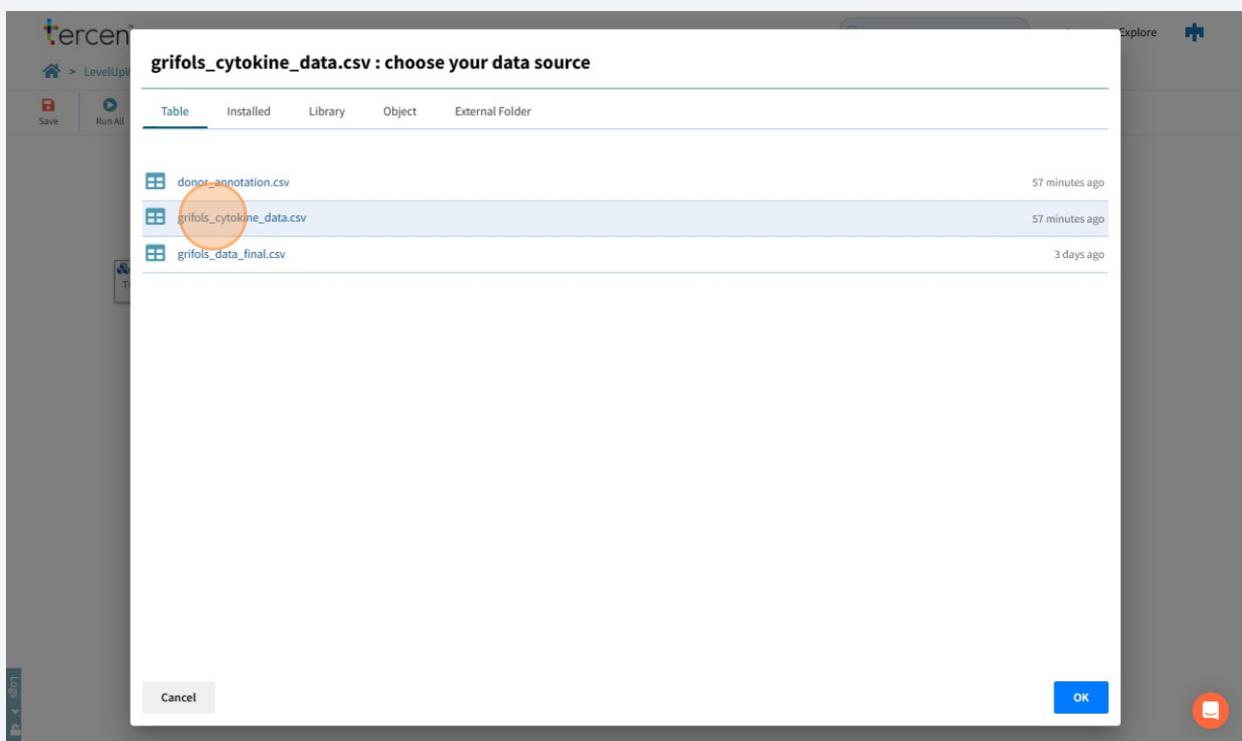
6 Click "Ok"



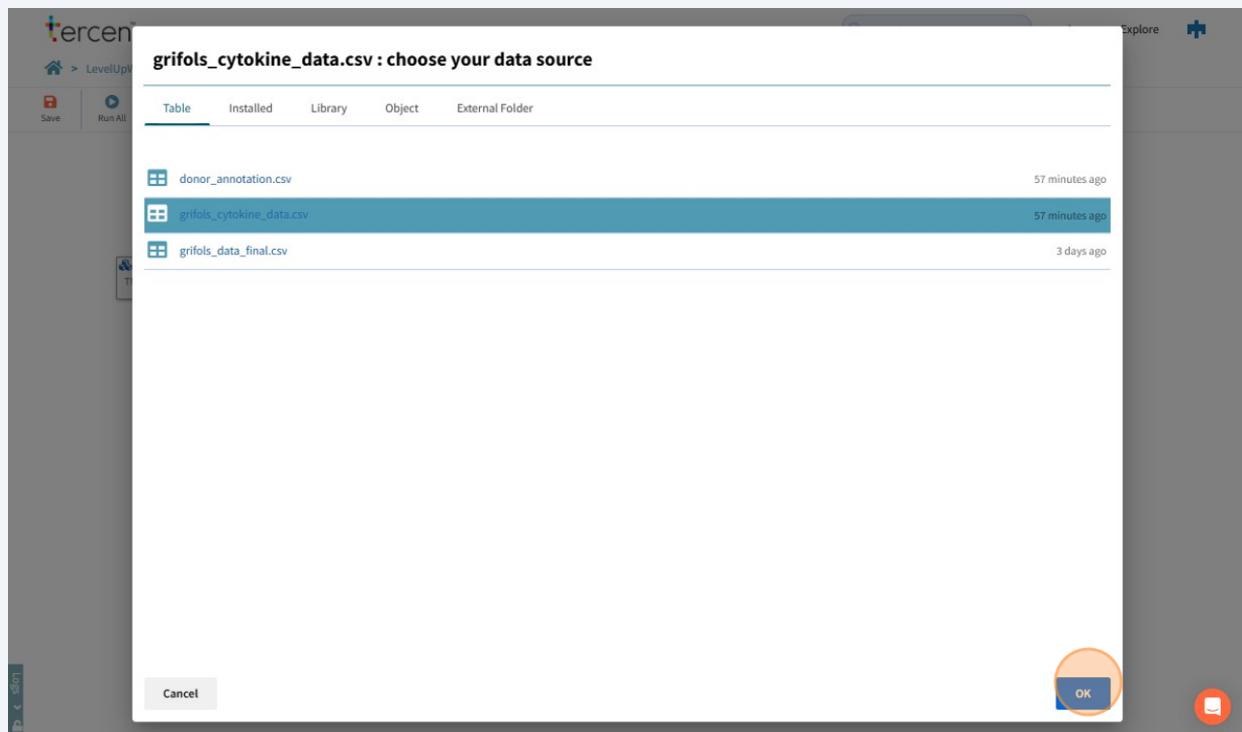
- 7 Click on the **Run All** icon at the top of the window.



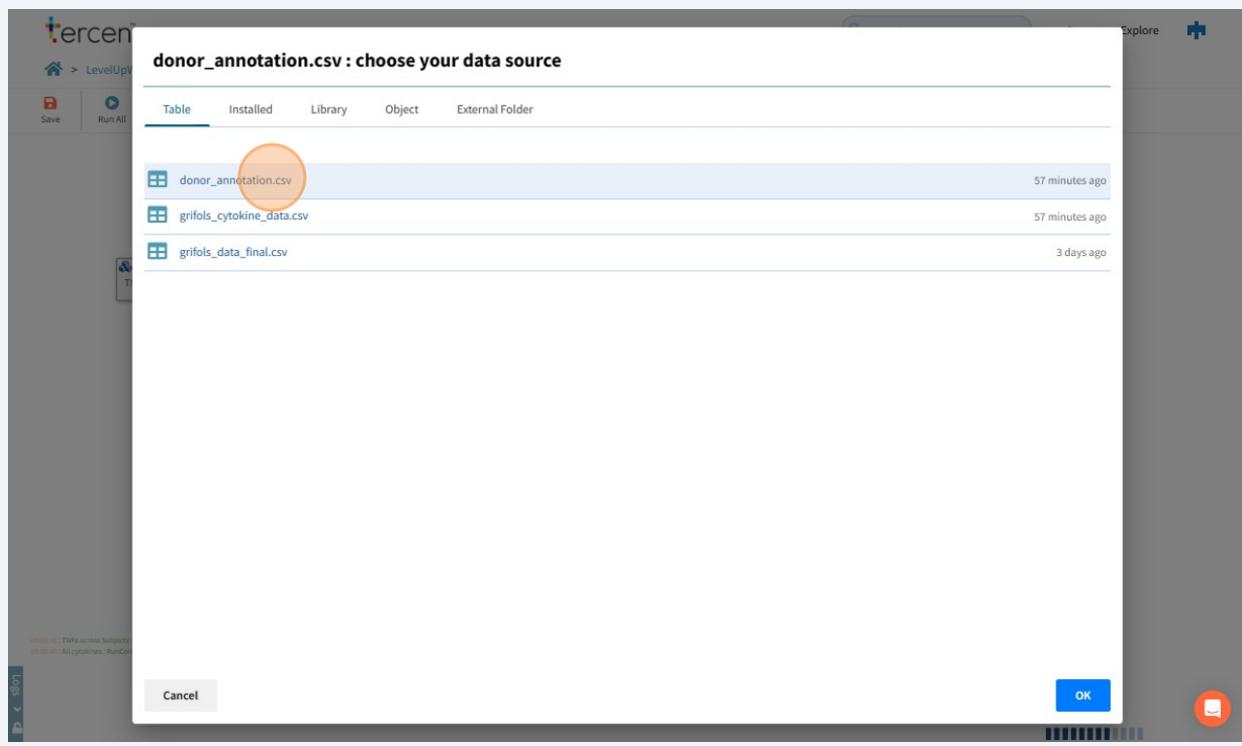
- 8 Click **grifols_cytokine_data.csv**



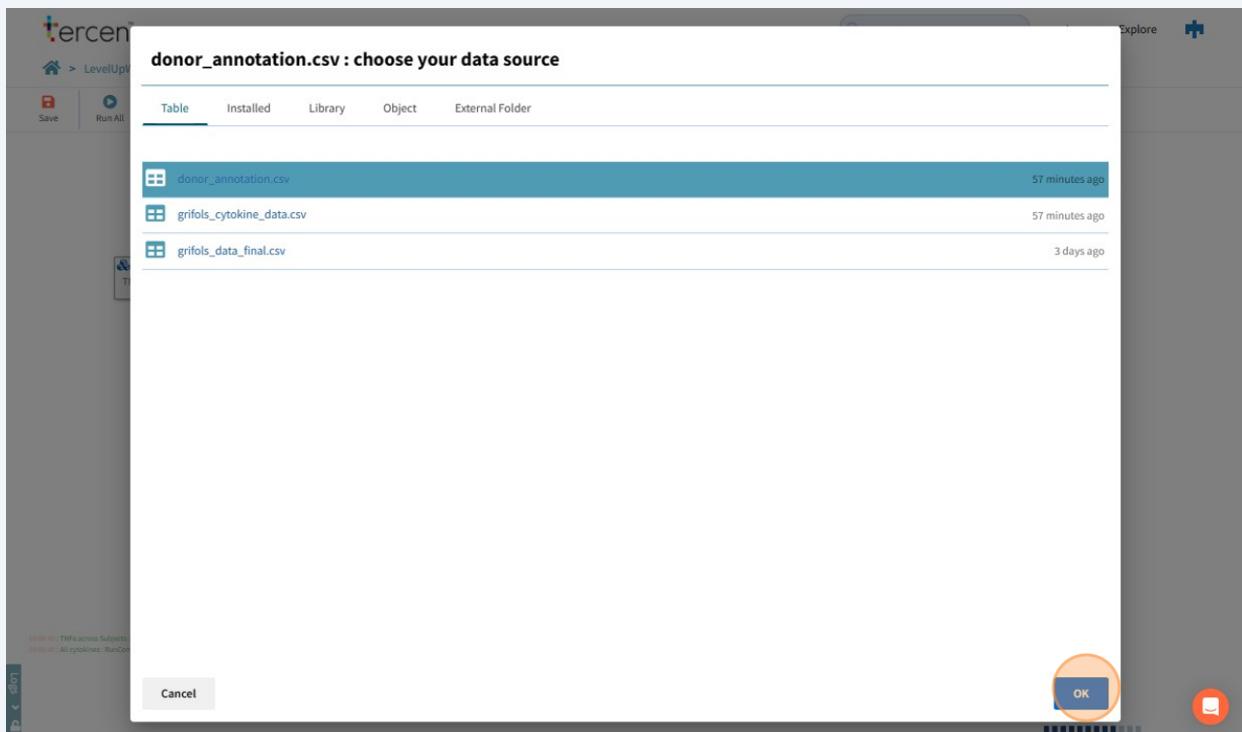
9 Click "OK"



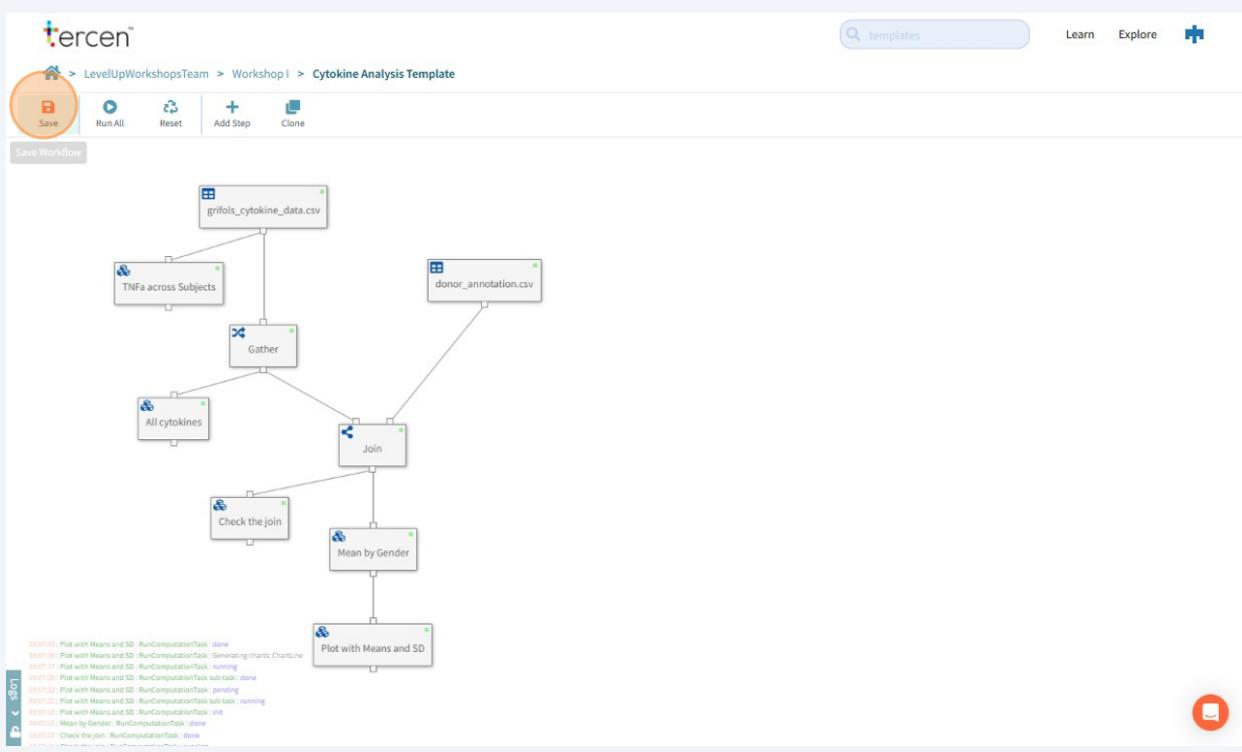
10 Click **donor_annotation.csv**



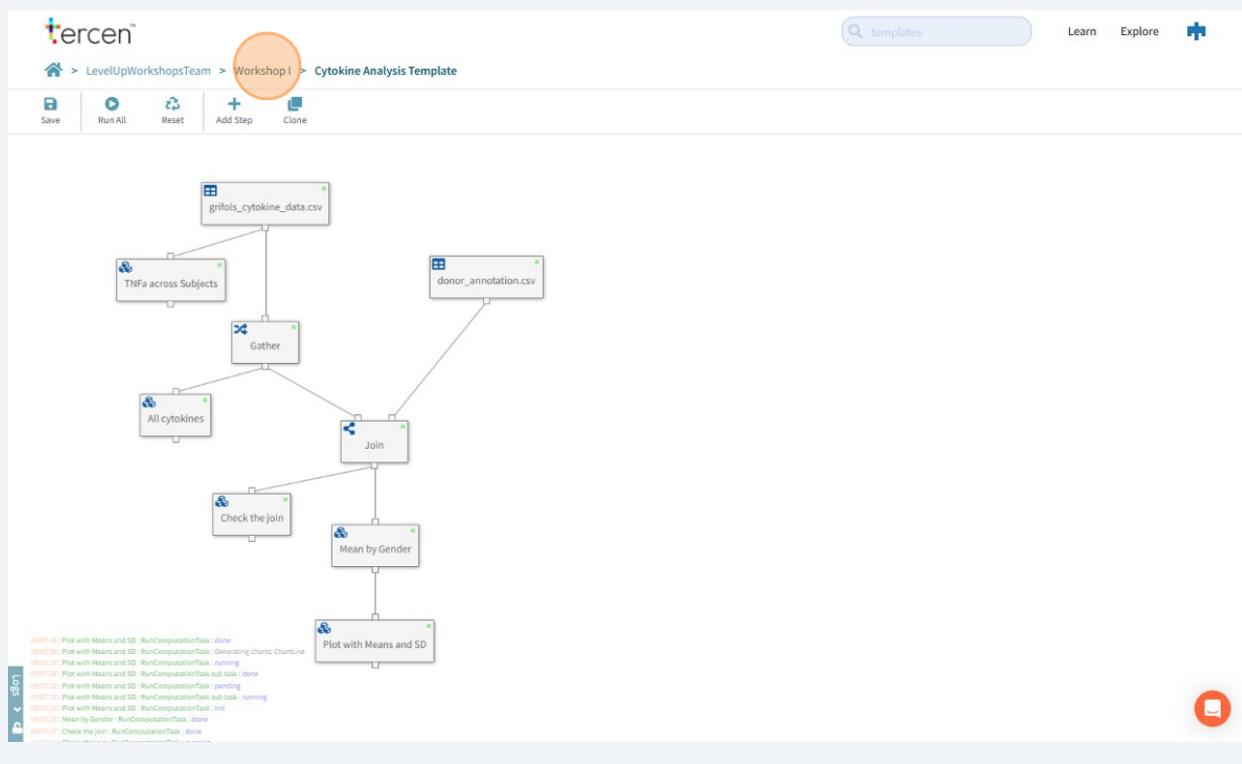
11 Click "OK"



12 Click on **Save** icon.



13 Click **Workshop I** to navigate back to the top level of the workshop I project.



14 Here is the location of completed workflow.

LevelUpWorkshopsTeam

Project Activities

Workshop I

No description provided.

New data set New workflow New file Upload file Upload workflow Project settings

faris.naji updated workflow **Cytokine Analysis Template**

README.md

Part-B

Part-A

files

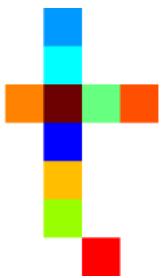
Cytokine Analysis Template

README.md

15 Well done!

You have seen a Template workflow in action.

0114 - Analyze RNA Data



- We will download an RNA dataset of immune cells from the protein atlas website, unzip it, and upload it to Tercen. We will perform a simple plot and look at the CD79A gene to see its transcription value across the different immune cells.

- Click "rna_immune_cell.tsv.zip"

The screenshot shows the "THE HUMAN PROTEIN ATLAS" website with a navigation bar including "SECTIONS", "ABOUT", "NEWS", "LEARN", "DATA", and "HELP". A search bar is present. Below the header, a section titled "DATA : DOWNLOADABLE DATA" shows "Ensembl version 109". There are four listed datasets:

- 19 RNA Allen mouse brain region gene data**: Transcript expression levels summarized per gene in 11 brain regions based on ISH. The tab-separated file includes Ensembl gene identifier ("Gene"), analysed sample ("Tissue") and expression energy ("Expression energy"). The data was obtained from [Allen brain atlas](#) and is based on The Human Protein Atlas version 23.0 and Ensembl version 109. [rna_mouse_brain_allen.tsv.zip](#) (TSV-file (zip compressed), 717.3 KB)
- 20 RNA HPA immune cell gene data**: Transcript expression levels summarized per gene in 18 cell types and total PBMC. The tab-separated file includes Ensembl gene identifier ("Gene"), analysed sample ("Immune cell"), transcripts per million ("TPM"), protein-coding transcripts per million ("pTPM") and normalized expression ("nTPM"). The data is based on The Human Protein Atlas version 23.0 and Ensembl version 109. [rna_immune_cell.tsv.zip](#) (TSV-file (zip compressed), 2.6 MB)
- 21 RNA HPA immune cell sample gene data**: Transcript expression levels summarized per gene in 109 immune cell samples. "rna_immune_cell_sample.tsv.zip" includes Ensembl gene identifier ("Gene"), analysed sample ("Immune cell"), donor ("Donor"), transcripts per million ("TPM"), protein-coding transcripts per million ("pTPM"). "rna_immune_cell_sample_tpm_m.tsv.zip" is in matrix format and only includes TPM. The data is based on The Human Protein Atlas version 23.0 and Ensembl version 109. [rna_immune_cell_sample.tsv.zip](#) (TSV-file (zip compressed), 32.8 MB) [rna_immune_cell_sample_tpm_m.tsv.zip](#) (TSV-file (zip compressed), 5.4 MB)
- 22 RNA Monaco immune cell gene data**: Transcript expression levels summarized per gene in 30 immune cell types. The tab-separated file includes Ensembl gene identifier ("Gene"), analysed sample ("Immune

- The file will download to your download folder on your C: drive

4 Click "Part-B"

No description provided.

New data set New workflow New file Upload file

faris.naji updated workflow Simple

- README.md
- Part-B**
- Part-A
- files

README.md

5 Click "New data set".

Project Activities

Workshop I

No description provided.

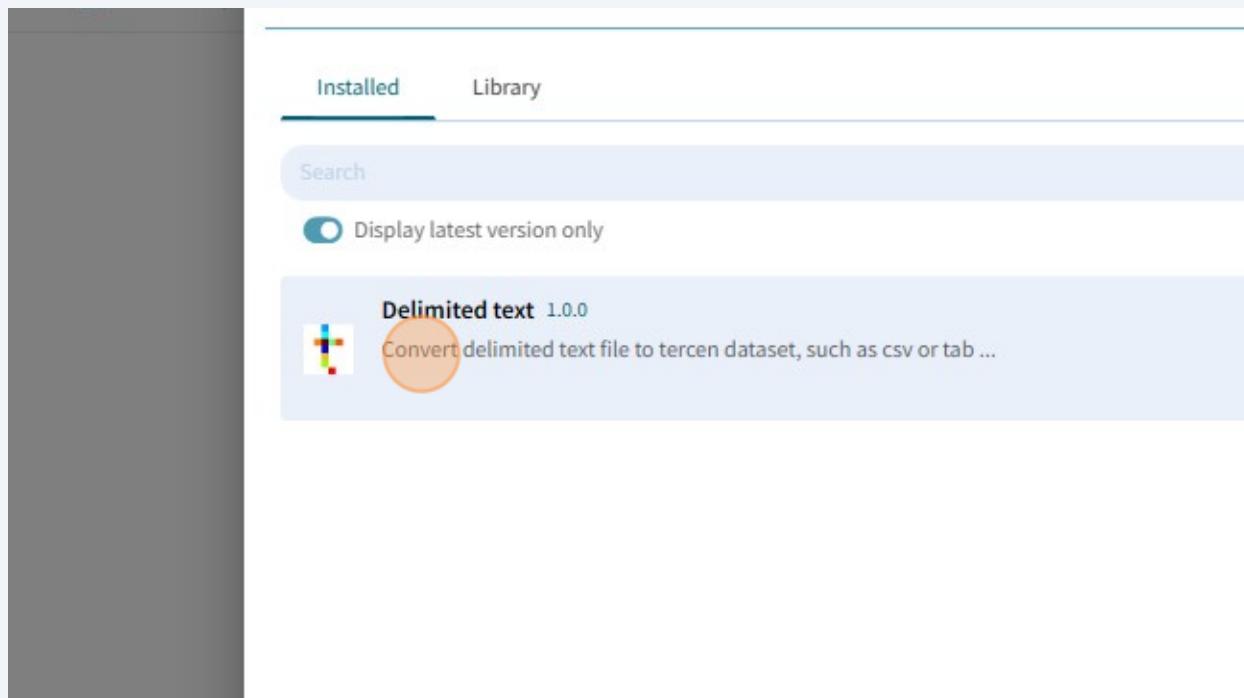
New data set New workflow New file Upload file

Workshop I / Part-B

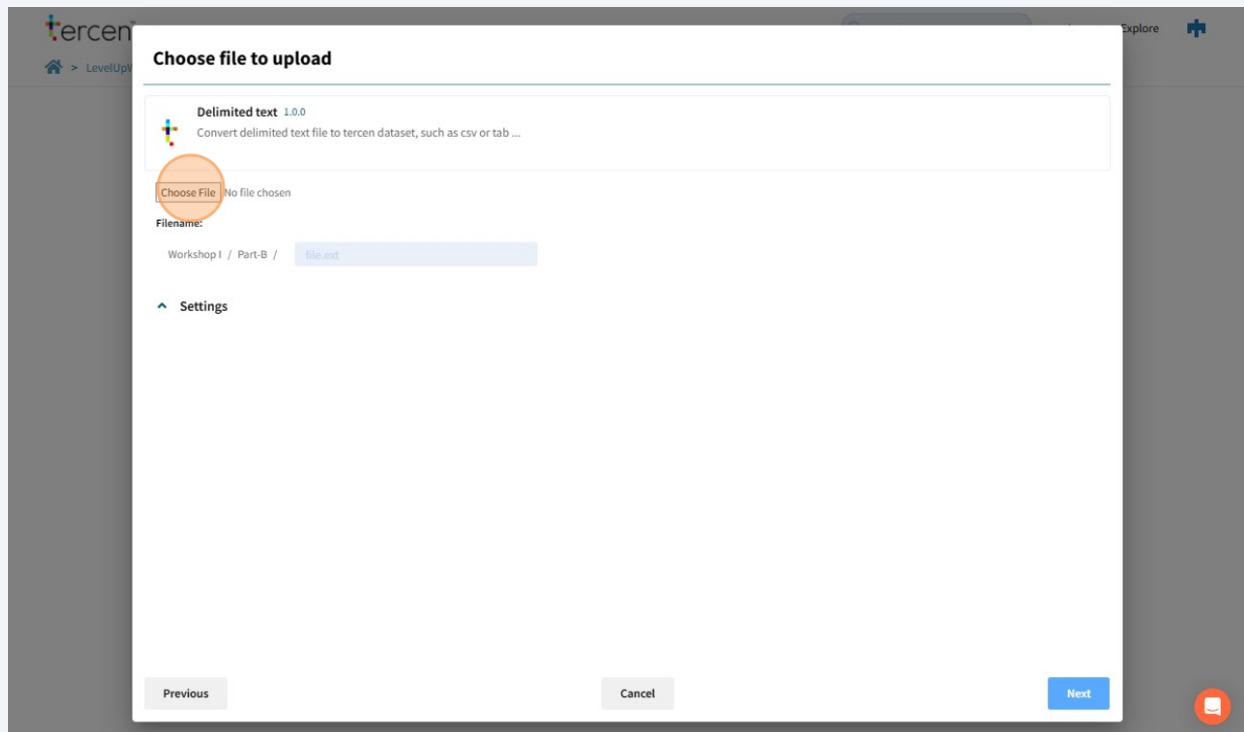
faris.naji updated workflow Simple

- guides
- grifols_cytokine_data.csv
- donor_annotation.csv

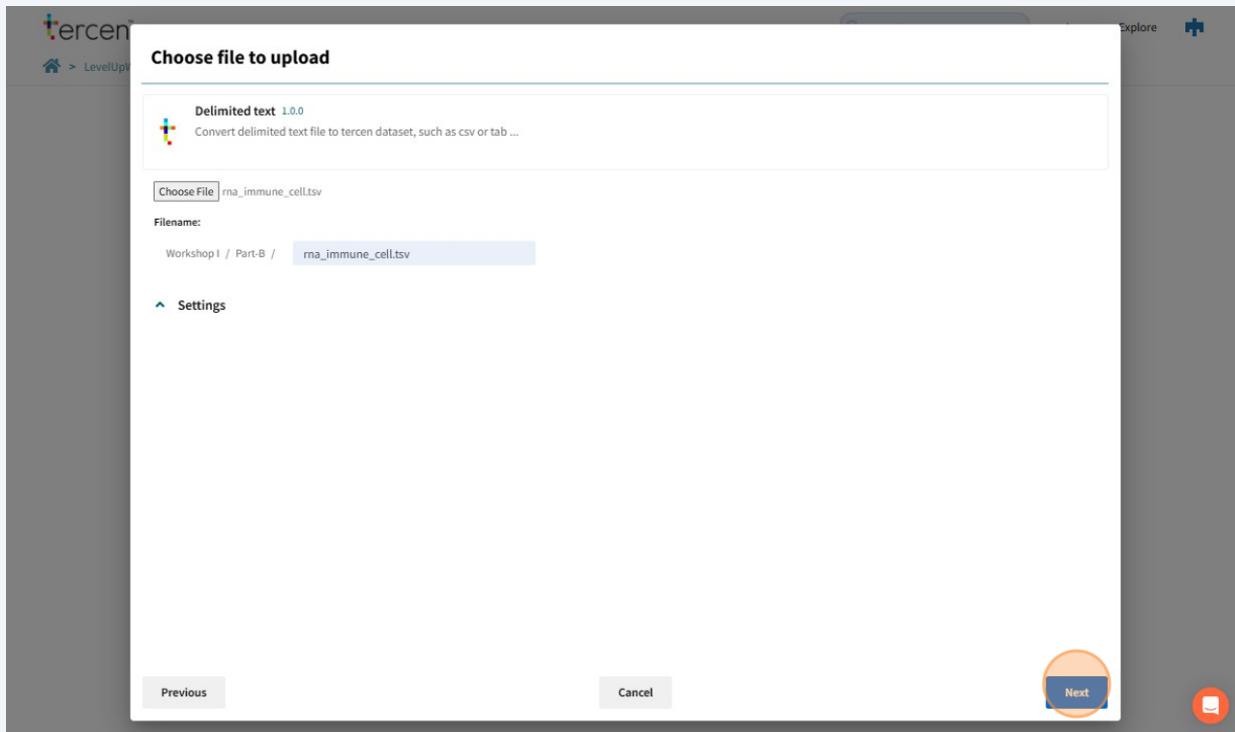
6 Click "Delimited text"



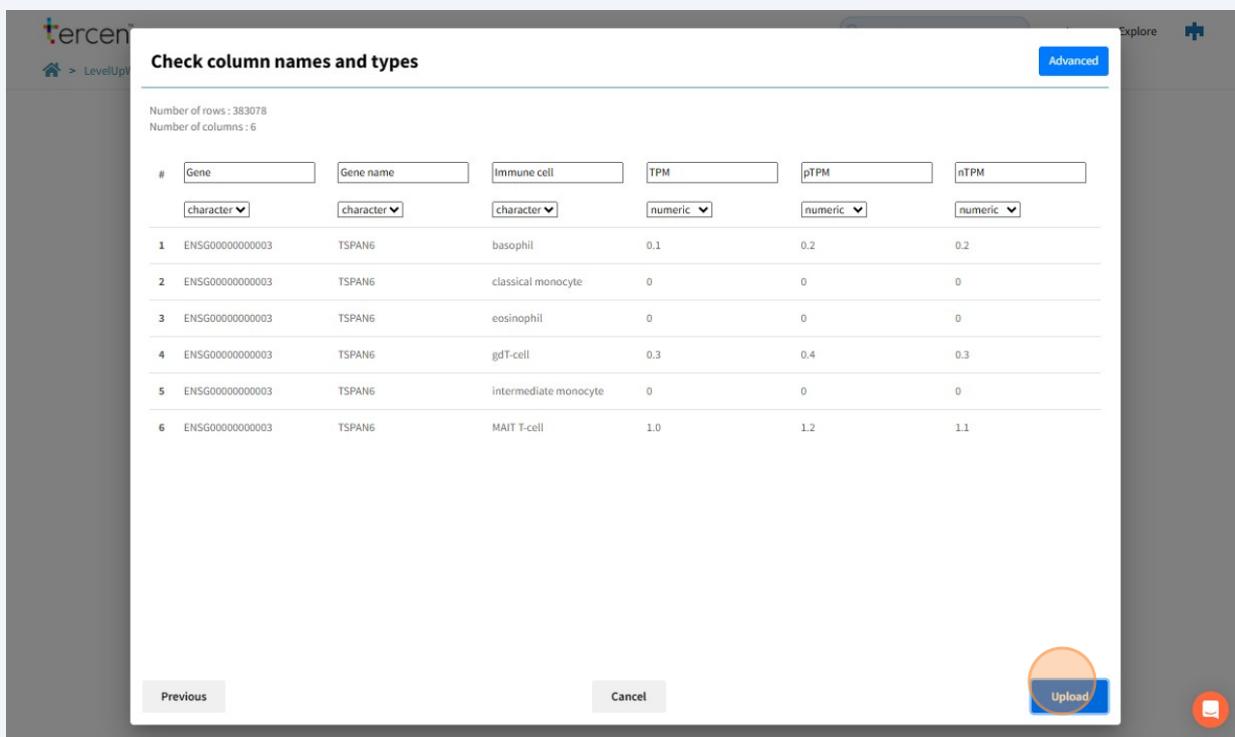
7 Click **Choose File** button.



8 Click "Next"



9 Click "Upload"



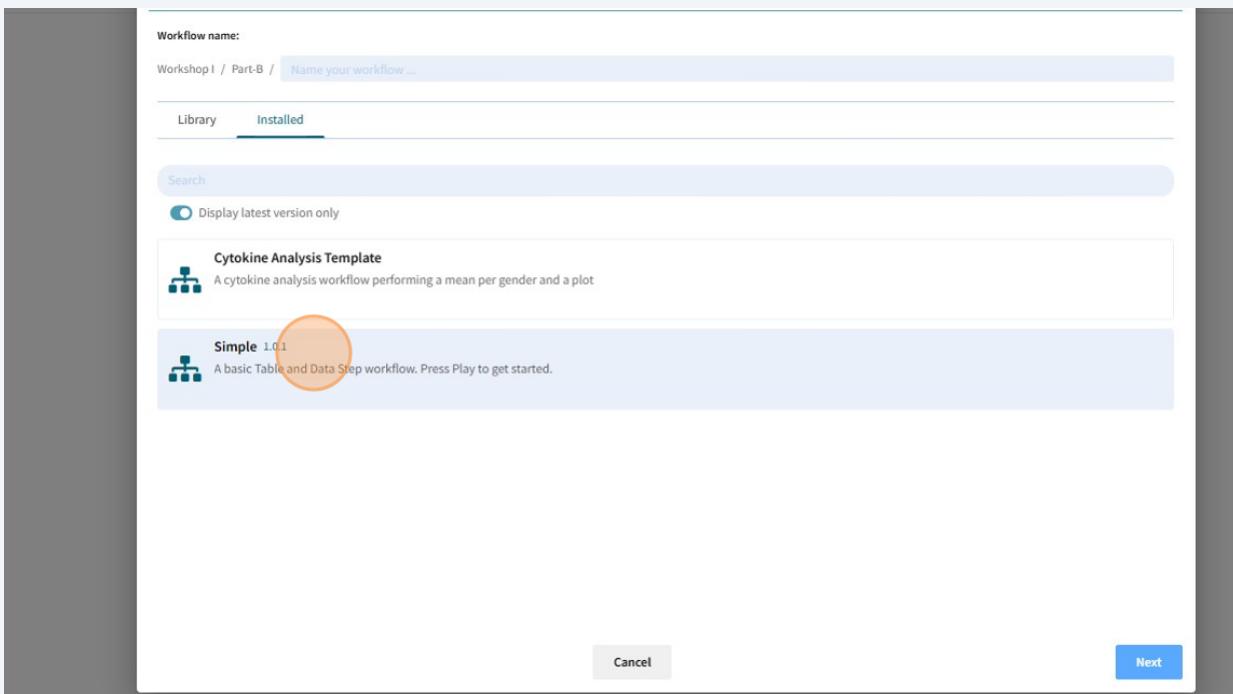
10 Click "New workflow"

The screenshot shows the 'LevelUpWorkshopsTeam' project page. At the top, there's a navigation bar with icons for home, user, and team. Below it is a header with the team name 'LevelUpWorkshopsTeam'. A sub-header indicates the project is 'Workshop I / Part-B'. The main content area shows a list of files: 'faris.naji updated workflow Simple', 'guides', 'grifols_cytokine_data.csv', 'donor_annotation.csv', and 'rna immune_cell.tsv'. At the top of this list is a toolbar with several buttons: 'New data set', 'New workflow' (which has an orange circle around it), 'New file', 'Upload file', 'Upload workflow', and 'Project settings'.

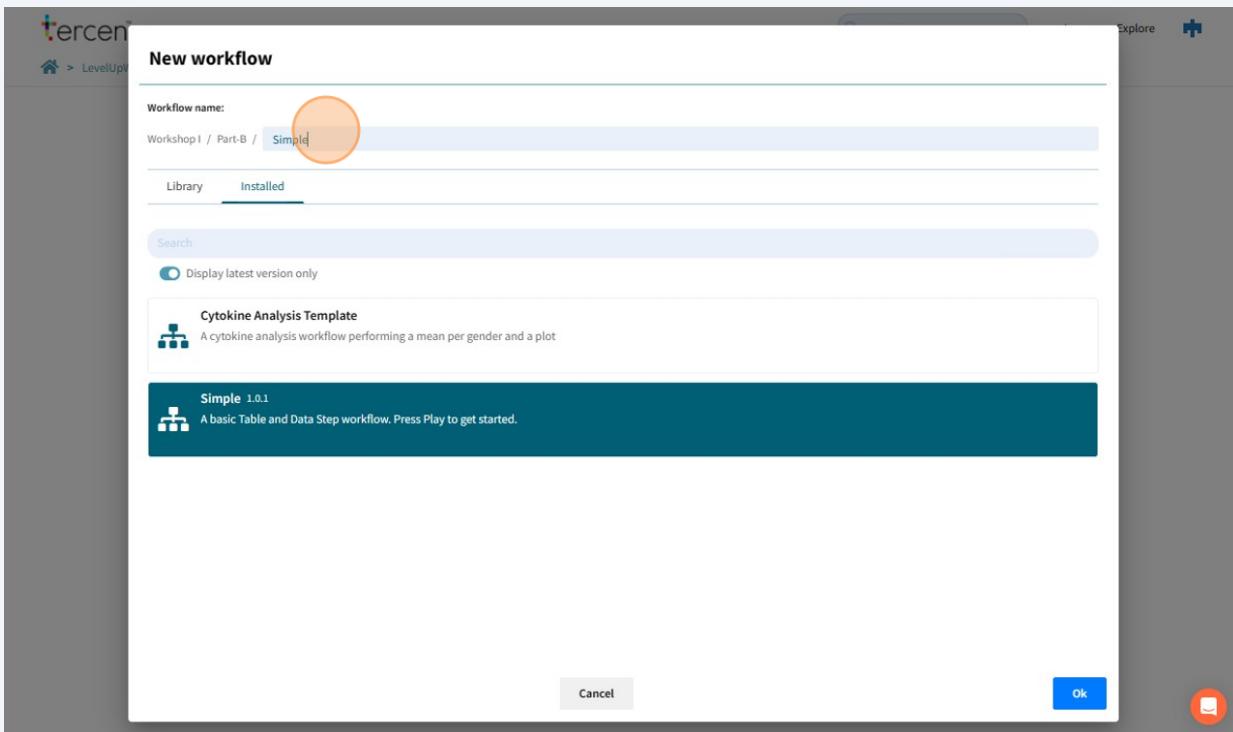
11 Click "Installed"

The screenshot shows a 'New workflow' dialog box. At the top, it says 'Workflow name:' followed by a placeholder 'Name your workflow ...'. Below this are two tabs: 'Library' (which is selected) and 'Installed' (which has an orange circle around it). There are also 'Search' and 'Display latest version only' buttons. Under the tabs, there's a 'Tag list' section with a 'Get Started with Flow Cytometry 0.0.4' entry. The main list contains three items: 'FlowJo Cluster Explorer - Quick View 0.0.7', 'FlowJo Cluster Explorer - Full 0.0.7', and 'Simple 1.0.1'. At the bottom right of the dialog is a 'Next' button.

12 Click **Simple**, this will choose a workflow template called "Simple".

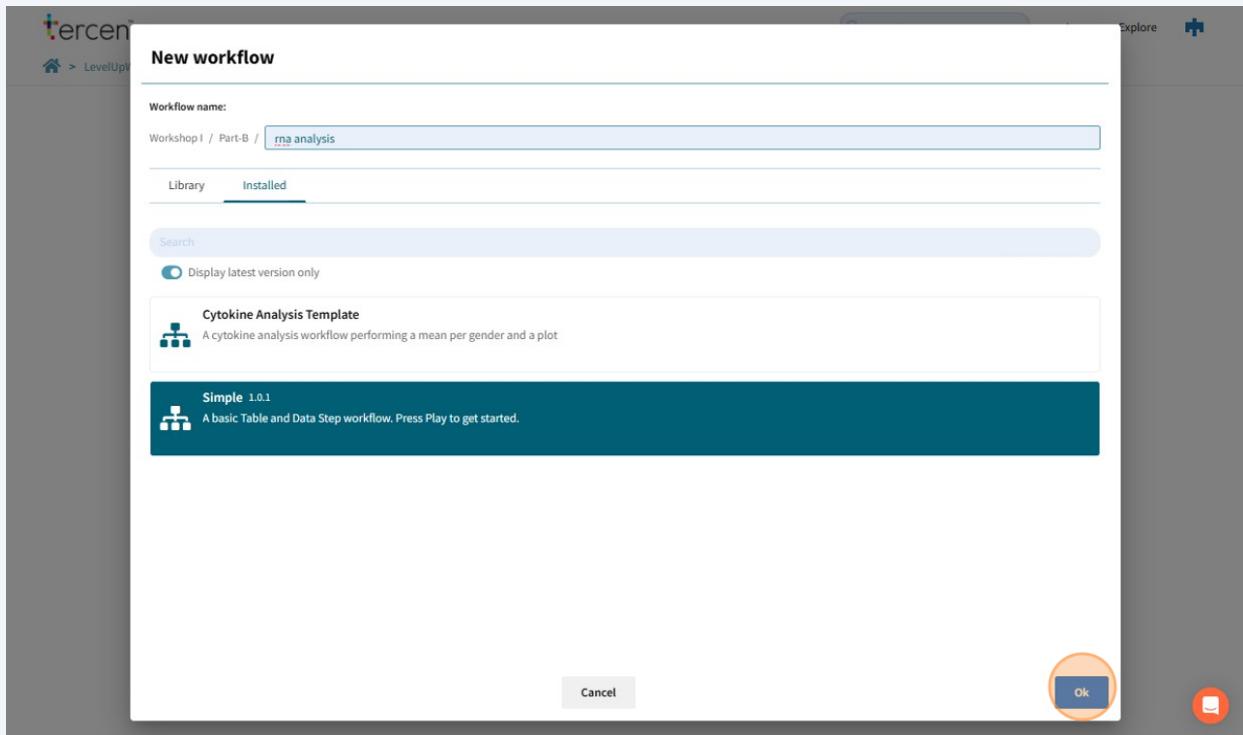


13 Click the "Name your workflow ..." field.

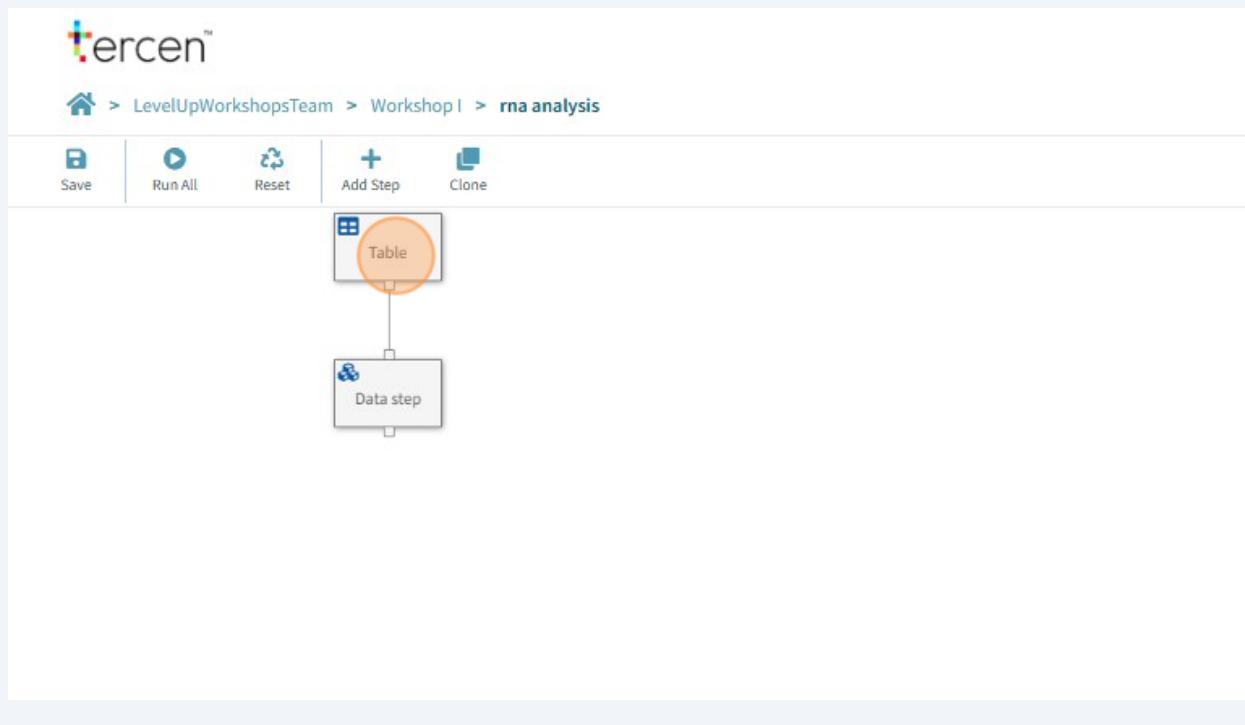


14 Type "rna analysis"

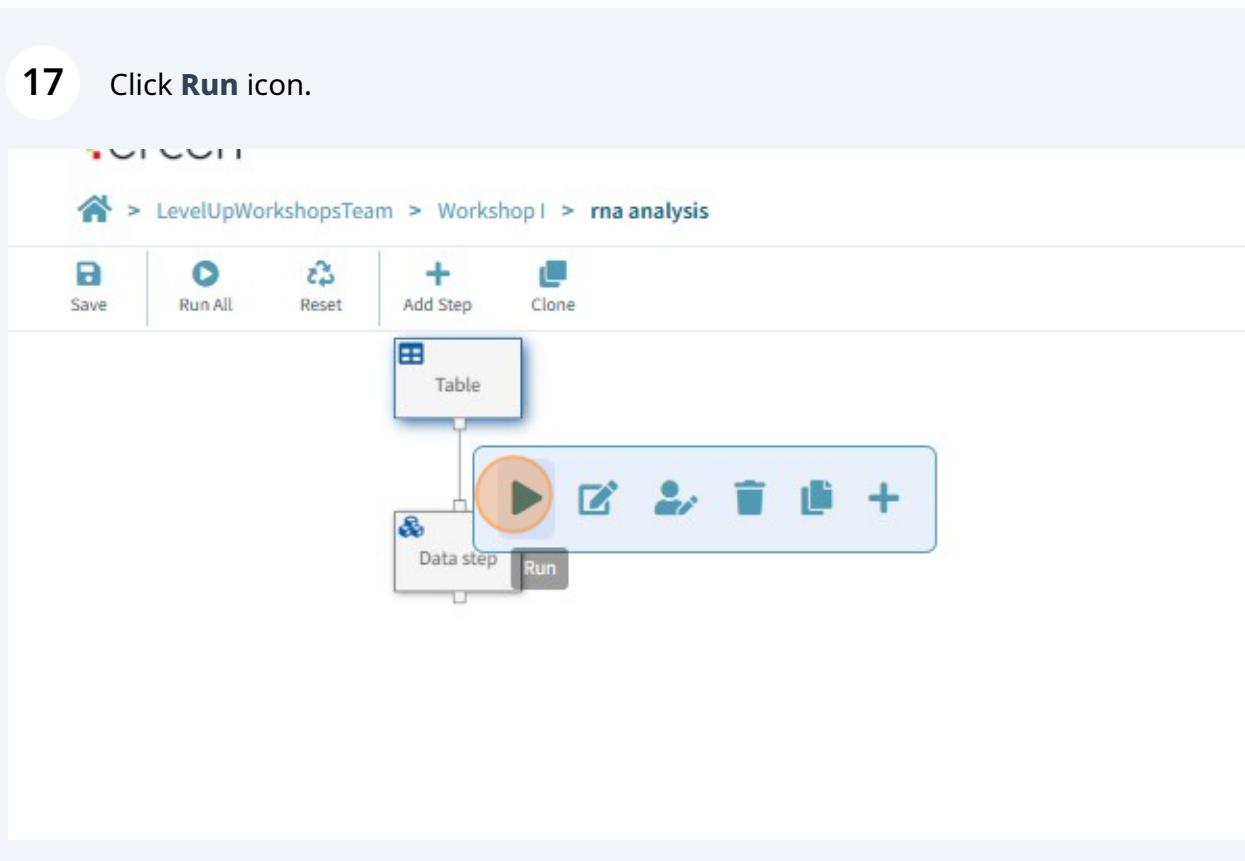
15 Click "Ok"



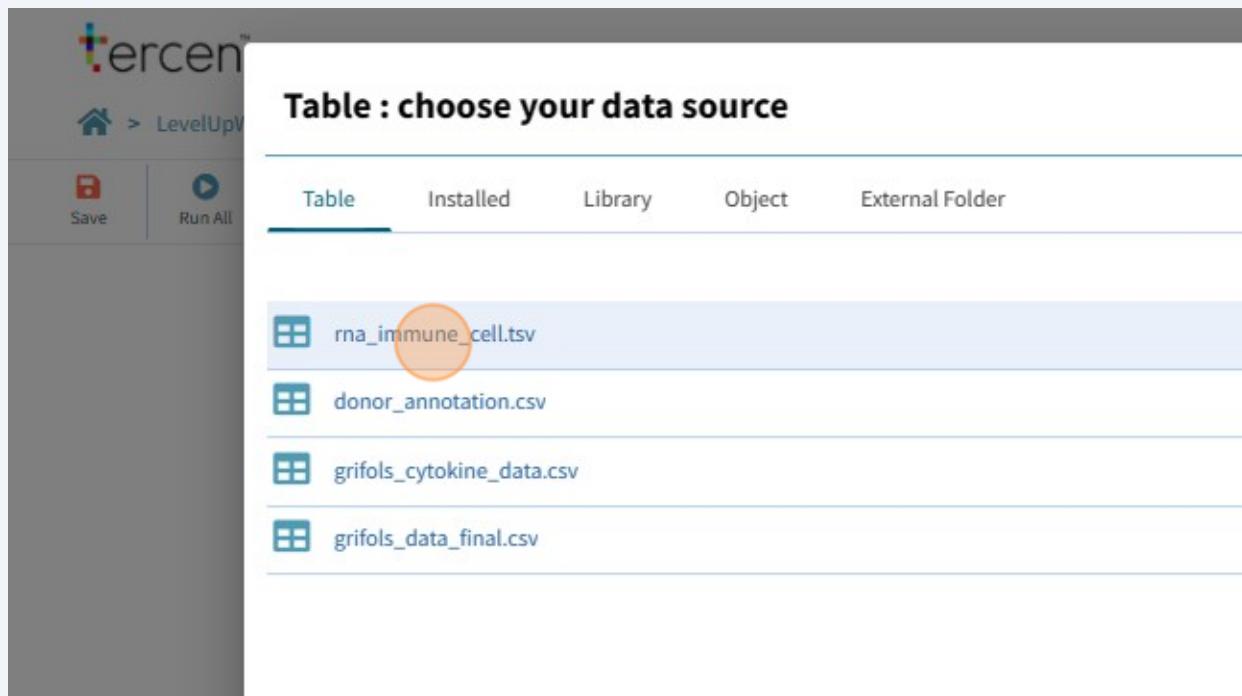
16 Click on the **Table** step.



17 Click **Run** icon.



18 Click **rna_immune_cell.tsv**

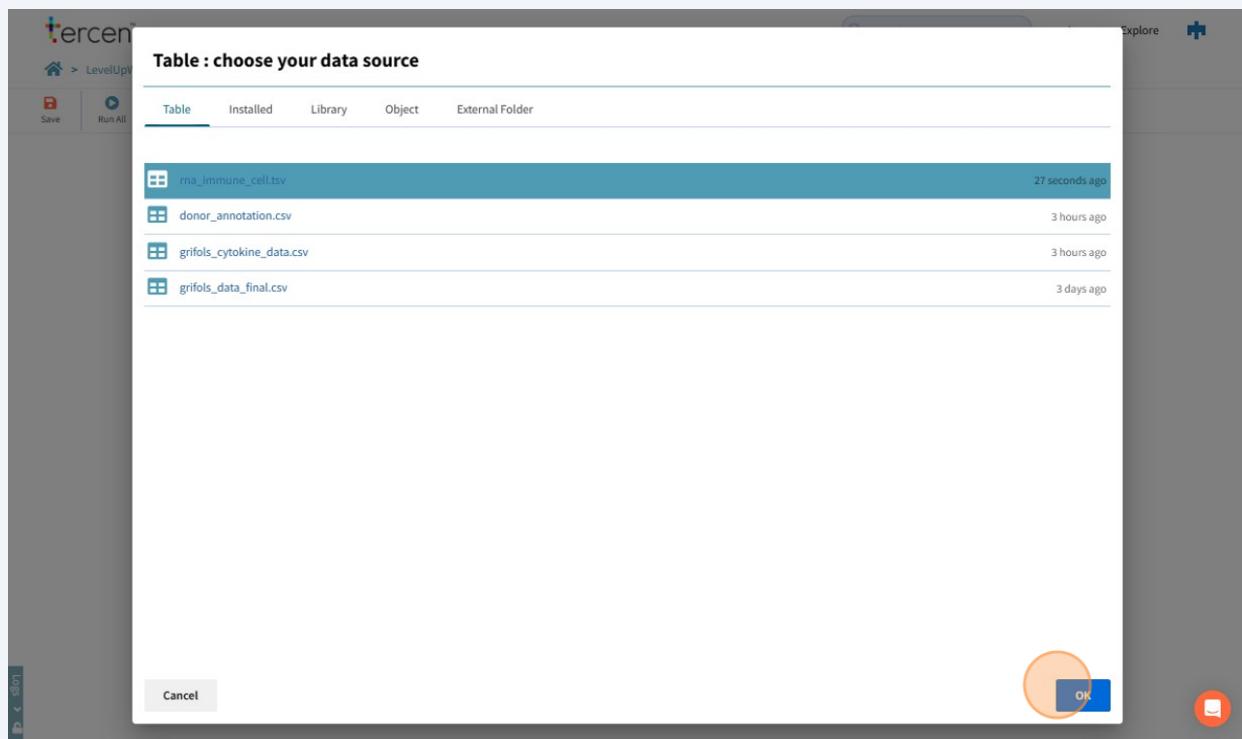


The screenshot shows the tercen software interface with the title "Table : choose your data source". There are five tabs at the top: "Table" (which is selected), "Installed", "Library", "Object", and "External Folder". Below the tabs is a list of four files:

- rna_immune_cell.tsv
- donor_annotation.csv
- grifols_cytokine_data.csv
- grifols_data_final.csv

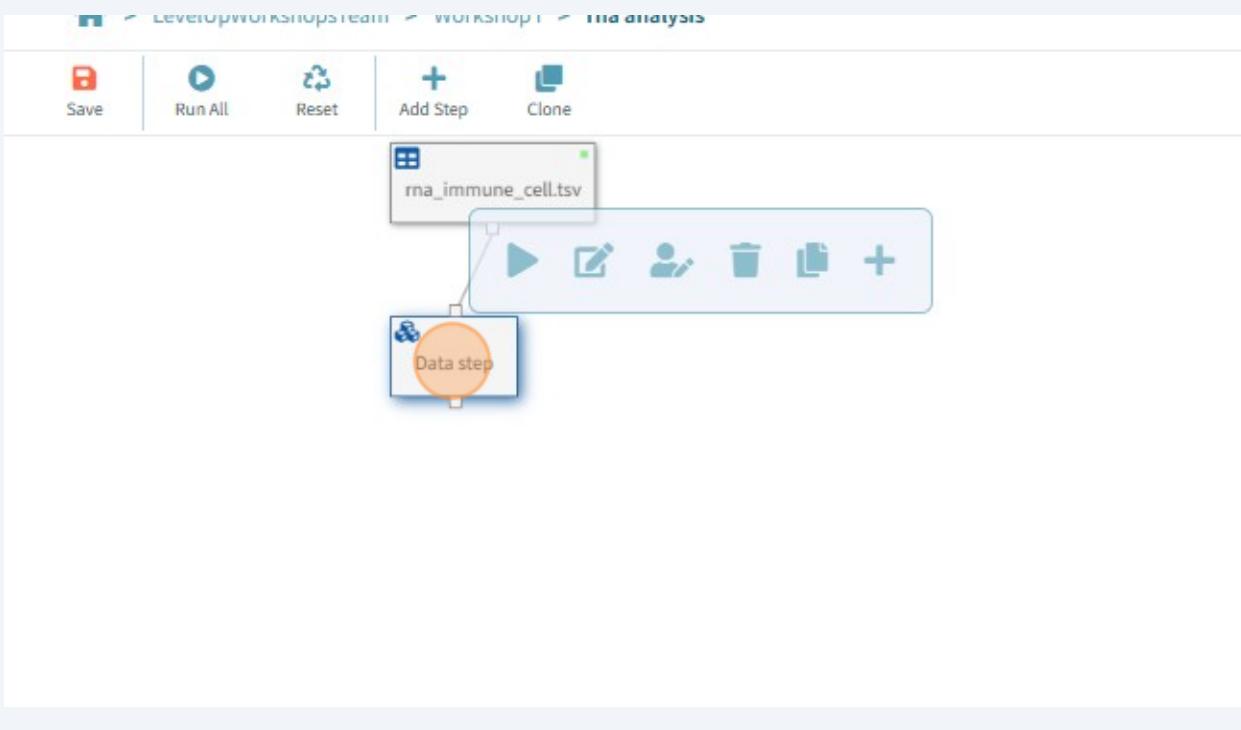
The first file, "rna_immune_cell.tsv", is highlighted with an orange circle.

19 Click "OK"

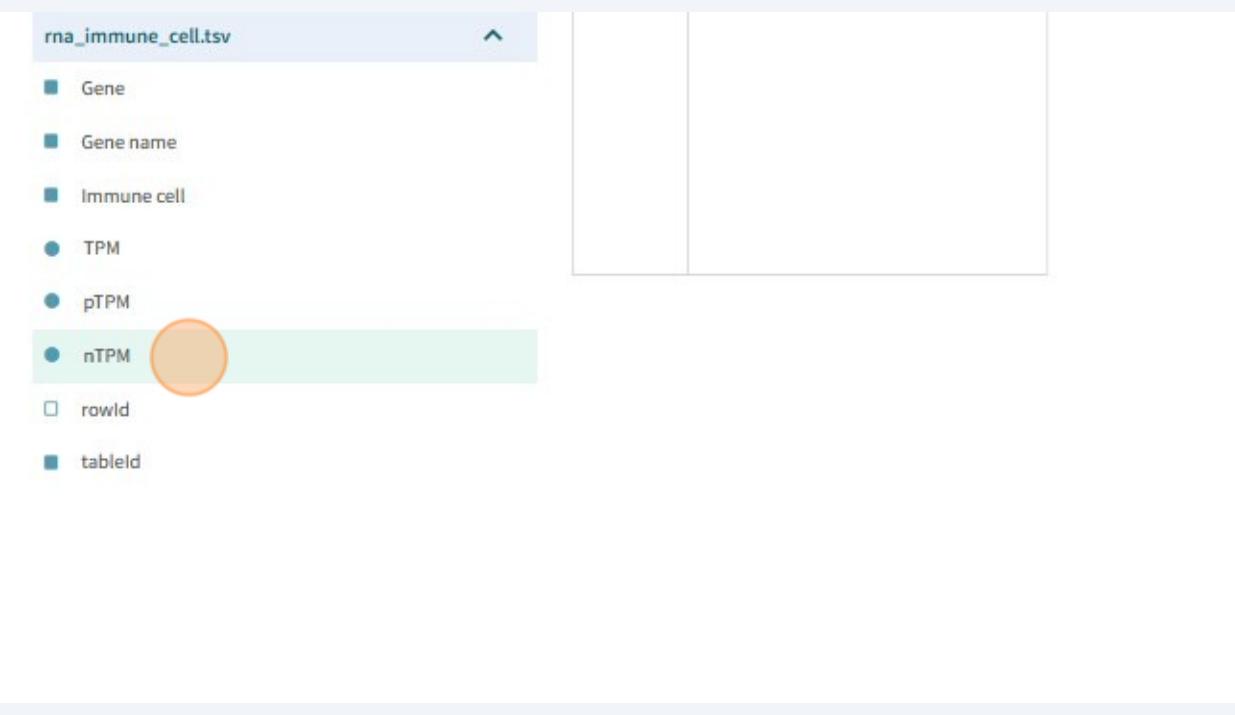


The screenshot shows the tercen software interface with the title "Table : choose your data source". The "rna_immune_cell.tsv" file is selected, indicated by a blue background. The other files are listed below it with their last modified times: "donor_annotation.csv" (3 hours ago), "grifols_cytokine_data.csv" (3 hours ago), and "grifols_data_final.csv" (3 days ago). At the bottom left is a "Cancel" button, and at the bottom right is an "OK" button, which is highlighted with an orange circle.

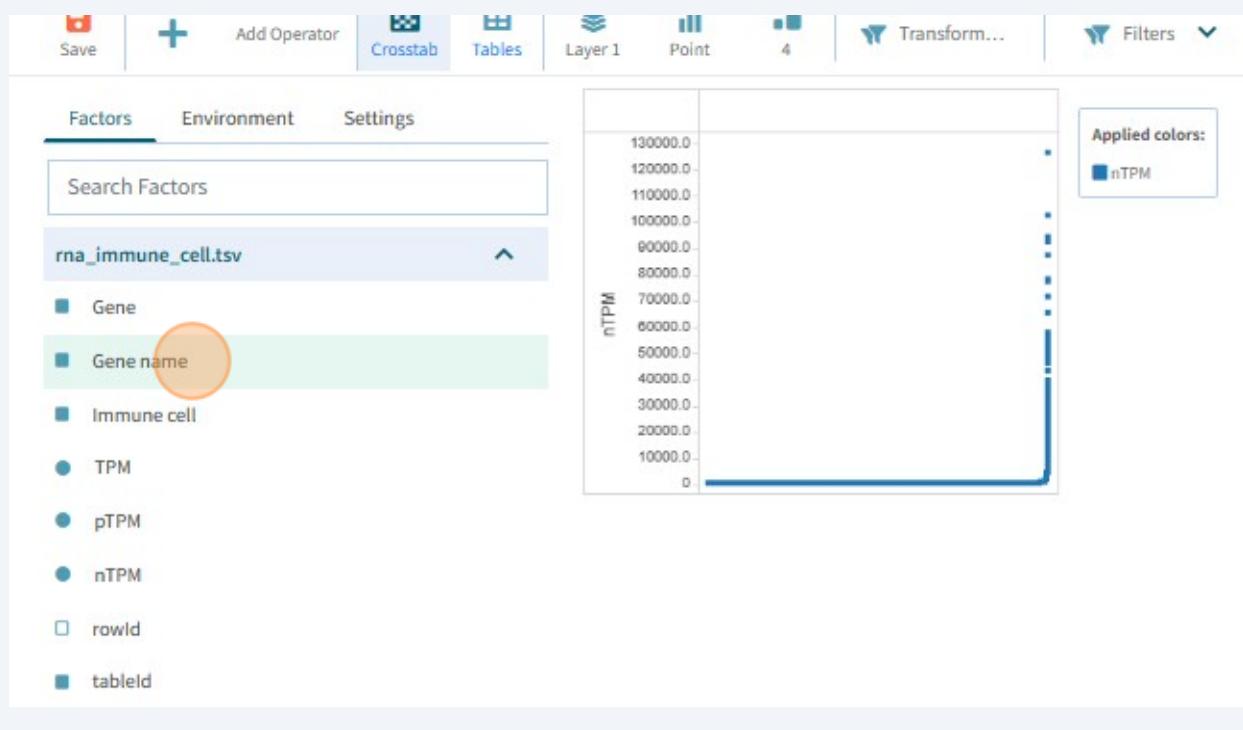
20 Click **Data step**.



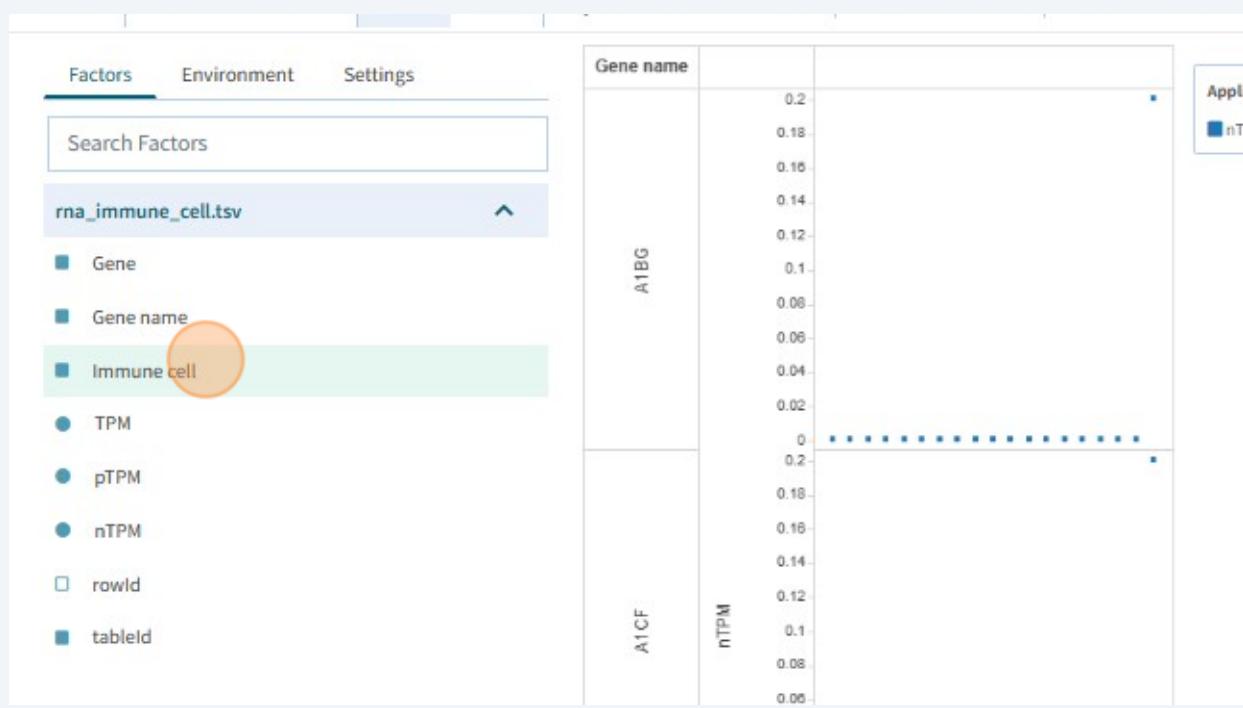
21 Drag the **nTPM** factor and drop onto the **Y-Axis**.



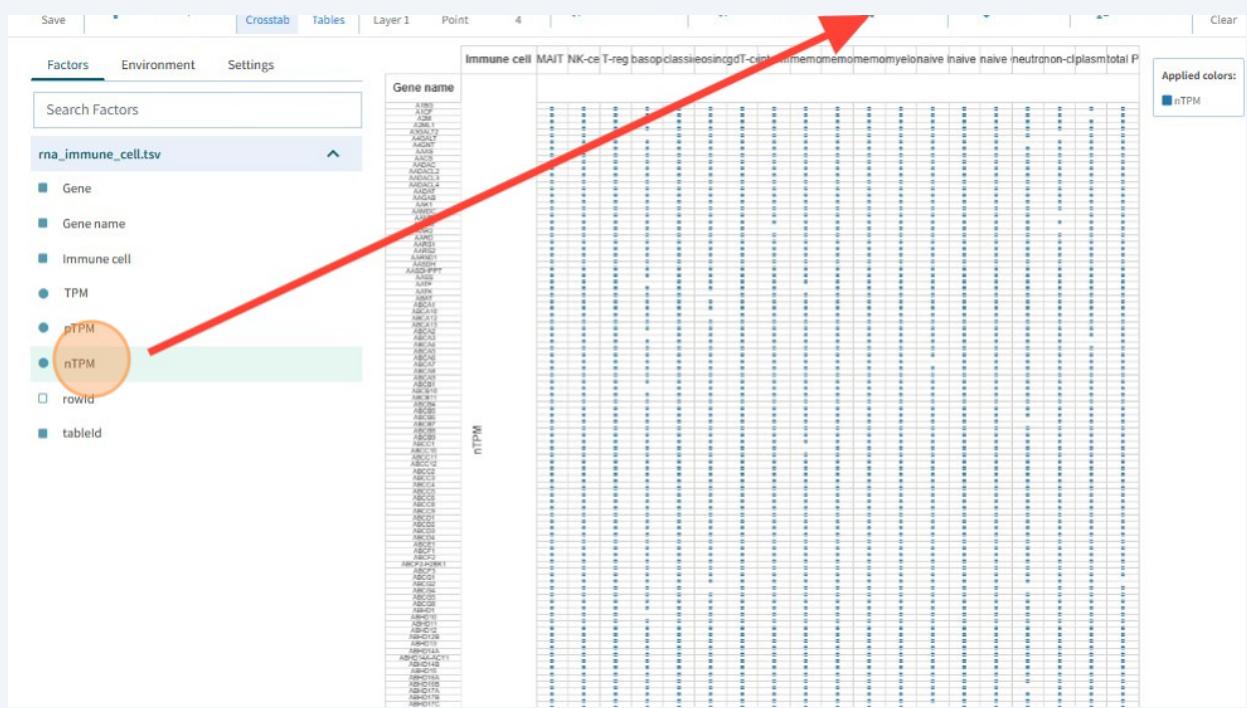
22 Drag the **Gene name** to the **Rows**.



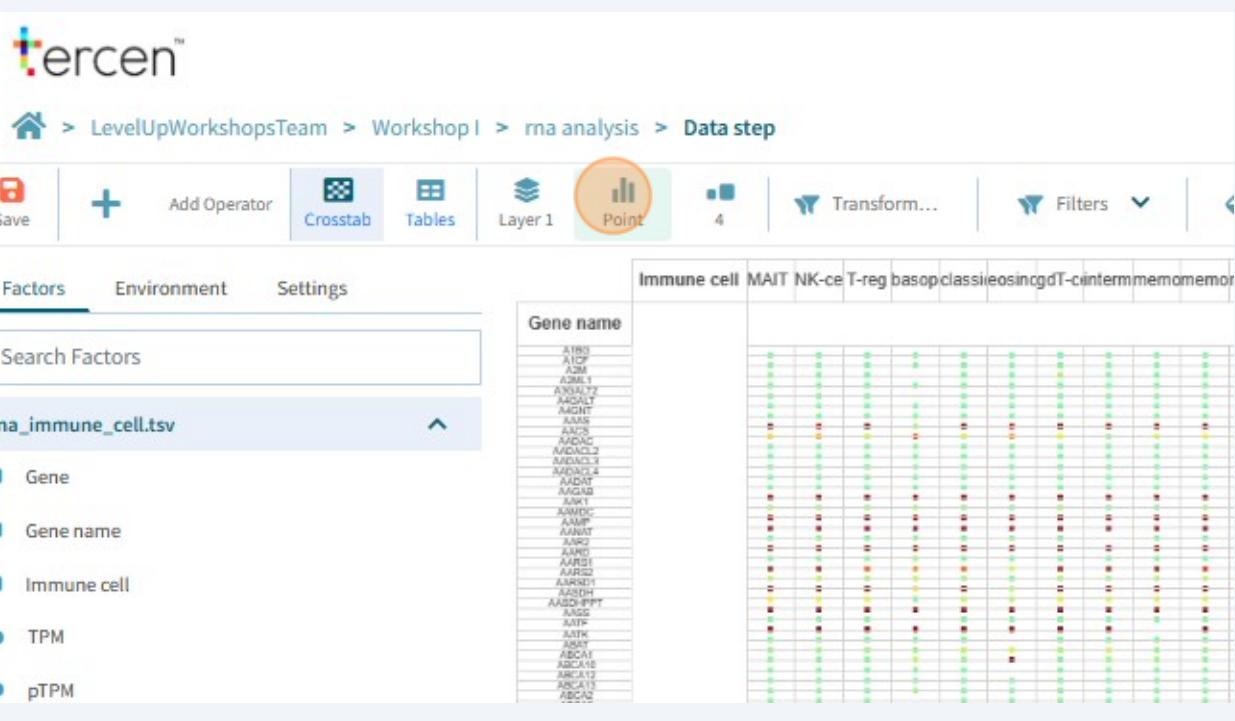
23 Drag **immune cell** to **Columns**



24 Drag nTPM actor to Color .



25 Click on the Style



26 Select "heatmap" as the style.

The screenshot shows the KNIME Data step interface. The top navigation bar includes 'Add Operator', 'Crosstab', 'Tables', 'Layer 1', 'Point' (selected), '4', 'Transform...', 'Filters', and a 'Color palette'. Below the navigation is a toolbar with 'Factors', 'Environment', and 'Settings'. A search bar contains 'Search Factors' and 'rna_immune_cell.tsv'. On the left, a sidebar lists factors: 'Gene', 'Gene name', 'Immune cell', 'TPM', 'pTPM', and 'nTPM'. A dropdown menu under 'Point' shows options: 'point', 'line', 'bar', 'heatmap' (circled in orange), 'h-grid', and 'v-grid'. The main workspace displays a heatmap grid with rows labeled by immune cell types and columns labeled by gene names.

27 Drag the Gene name to Filter

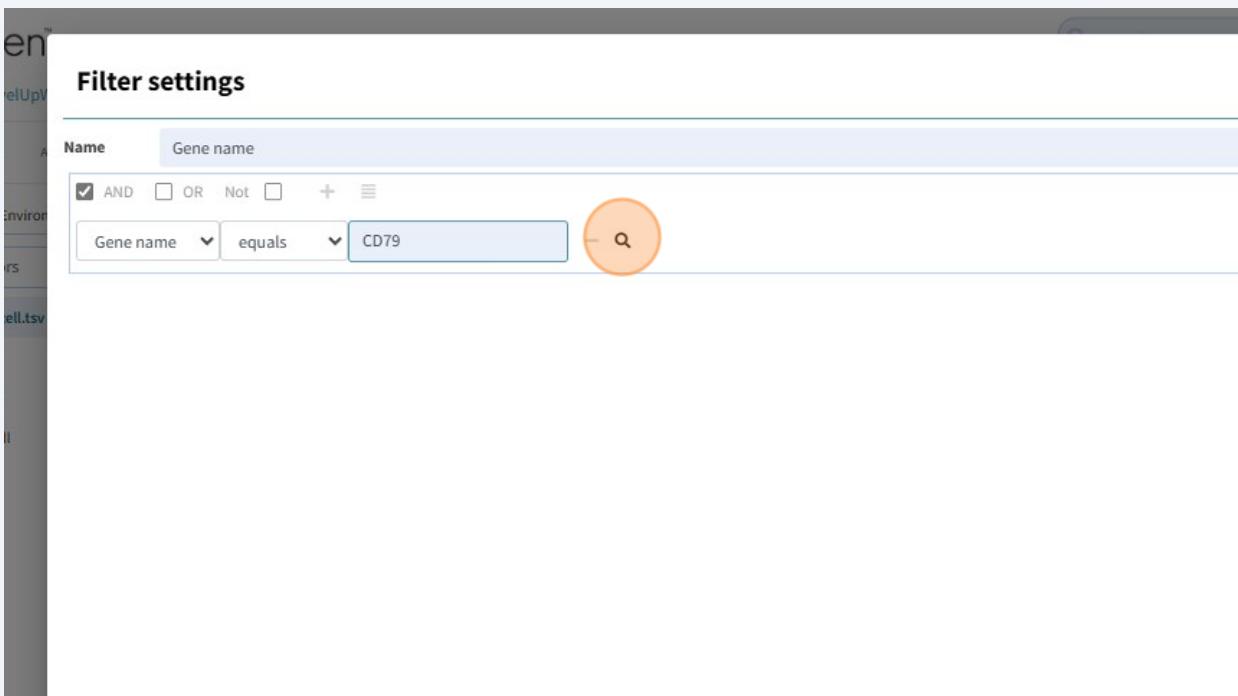
The screenshot shows the KNIME Data step interface with a heatmap visualization. A red arrow points from the 'Gene name' factor in the sidebar to the 'Filters' button in the top toolbar. The sidebar also shows 'Gene', 'Immune cell', 'TPM', 'pTPM', 'nTPM', 'rowId', and 'tableId'. The top toolbar includes 'Save', 'Add Operator', 'Crosstab', 'Tables', 'Layer 1', 'Heatmap' (selected), '4', 'Transform...', 'Filters' (with a dropdown arrow), 'Colors', and 'Labels'. The main workspace is a heatmap showing gene expression levels across different immune cell types.

28 Click this text field.

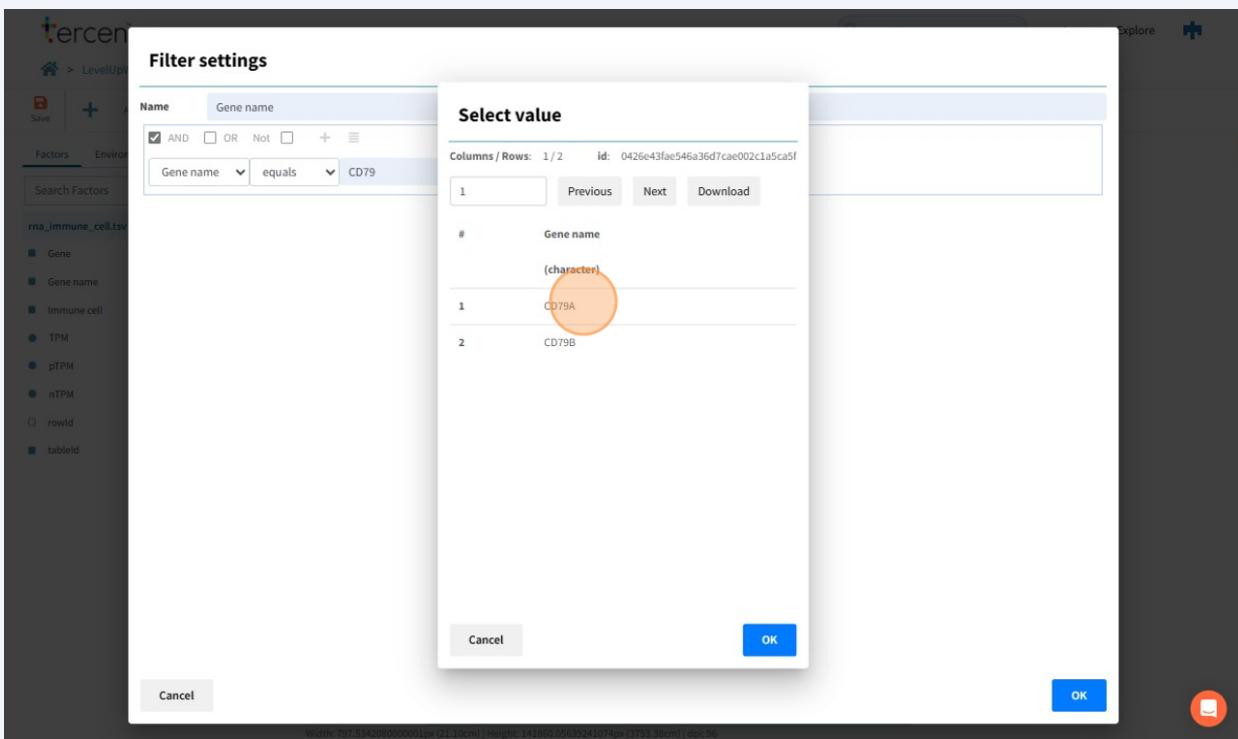
The screenshot shows the 'Filter settings' dialog in the tercen software. The 'Name' dropdown is set to 'Gene name'. The 'equals' dropdown is selected. The search input field contains 'NaN' and is highlighted with an orange circle. The background shows a sidebar with 'Factors' and 'Environ' tabs, and a list of files including 'rna immune cell.tsv'.

29 Type " CD79"

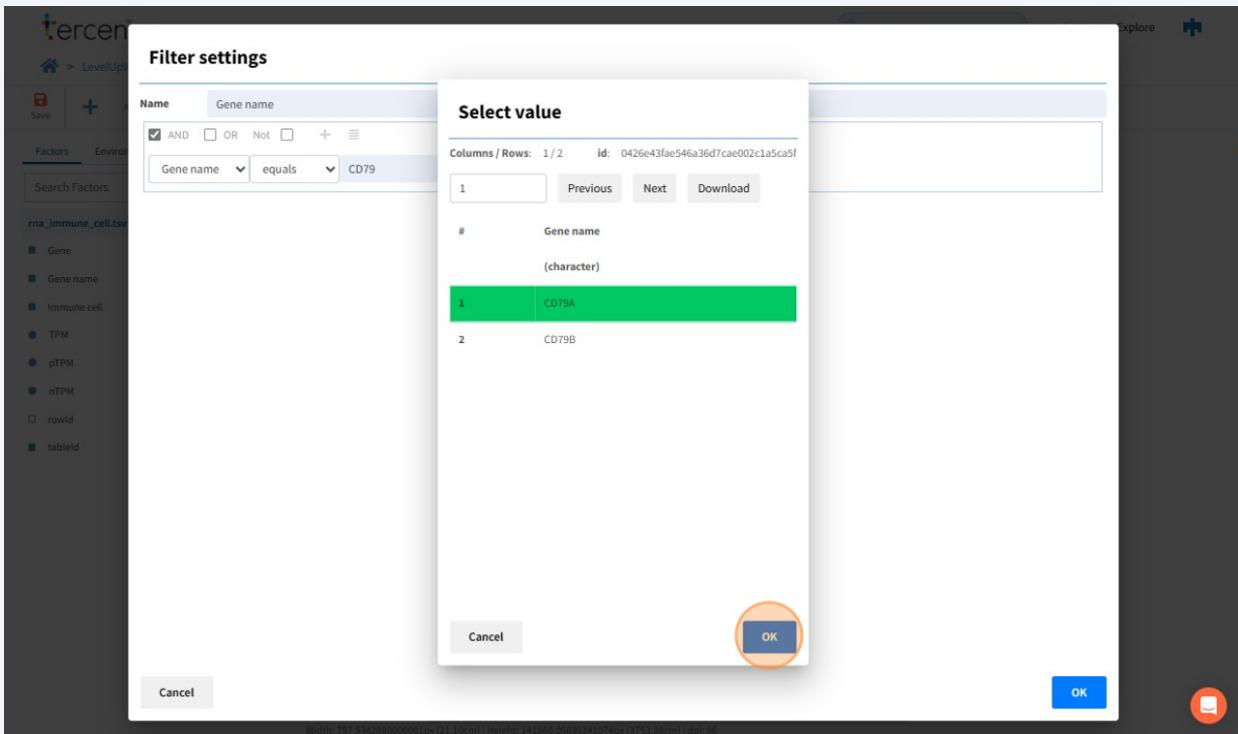
30 Click here.



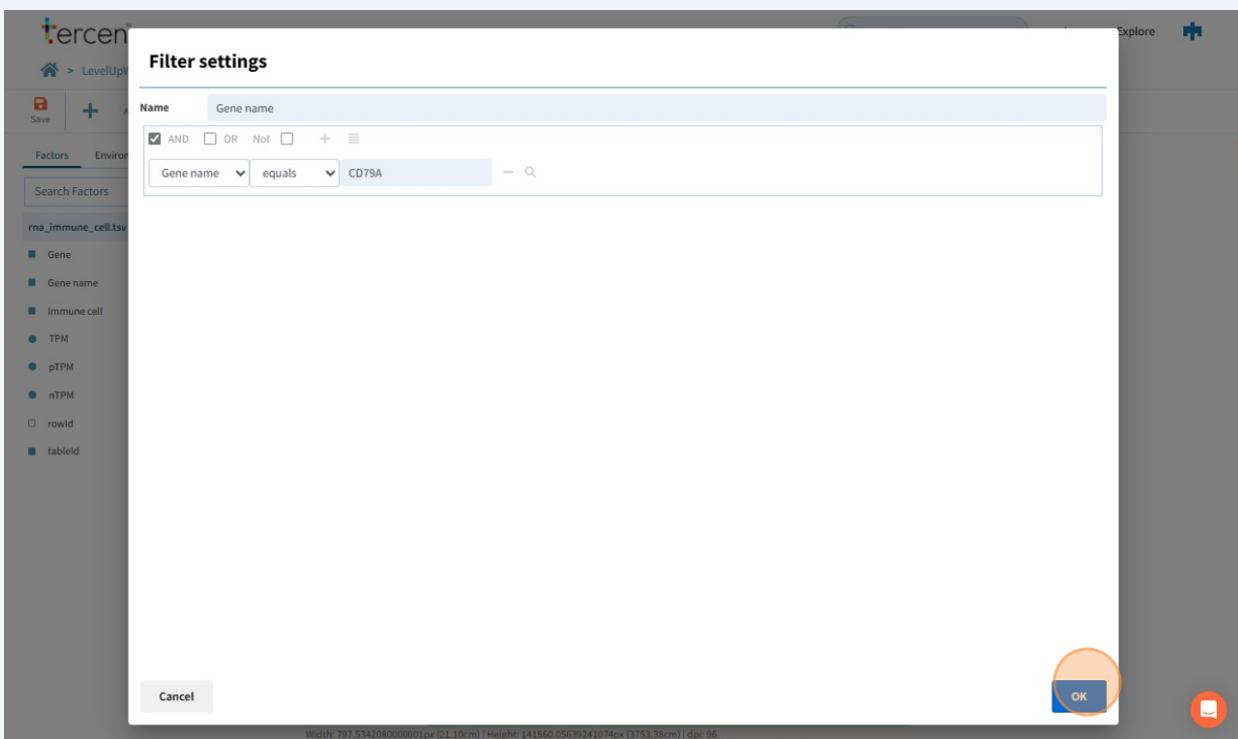
31 Click "CD79A"



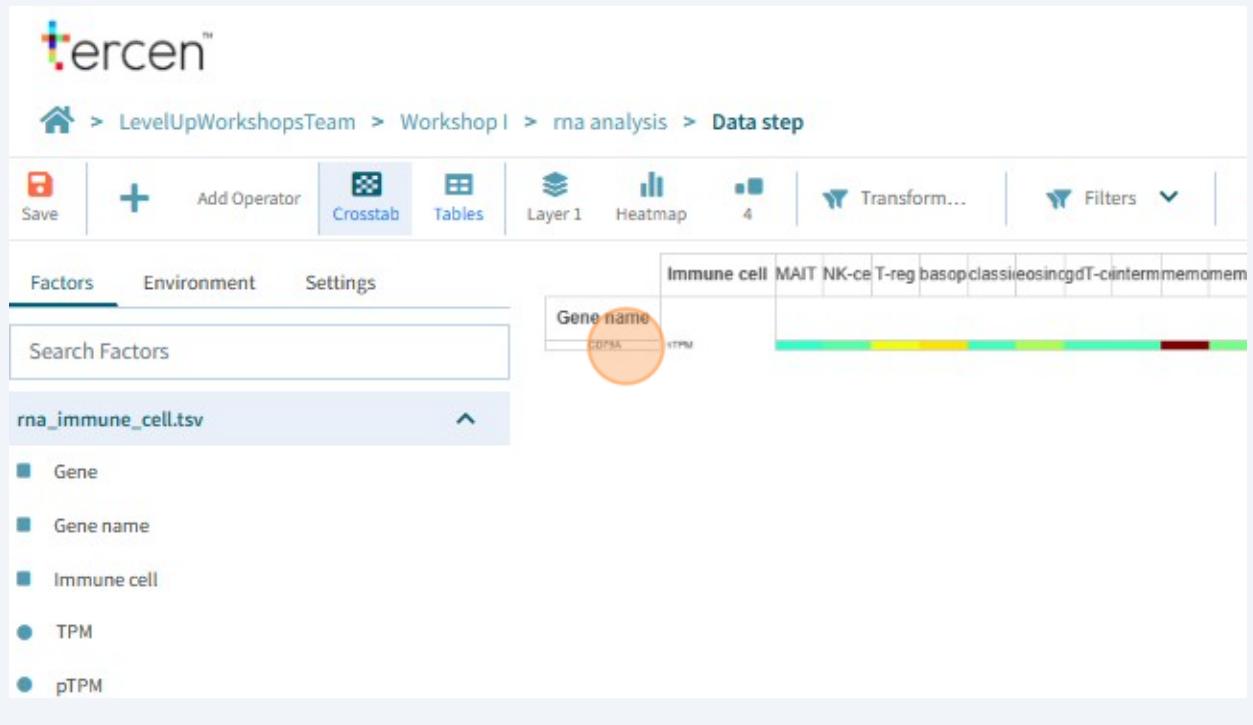
32 Click "OK"



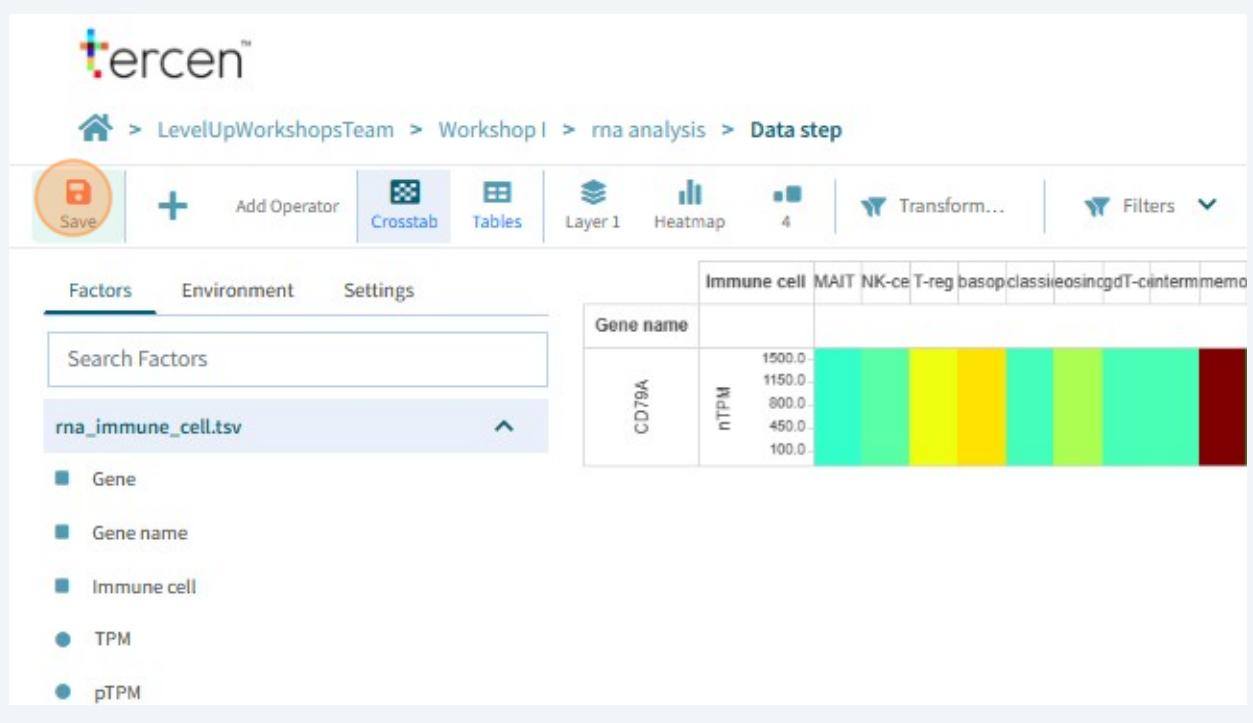
33 Click "OK"



34 Drag the last line of the column line to the bottom to expand the view vertically.



35 Click on **Save** icon.



36

Well done!

If you have uploaded an RNA transcription dataset and look at a specific gene transcription value across immune cells.