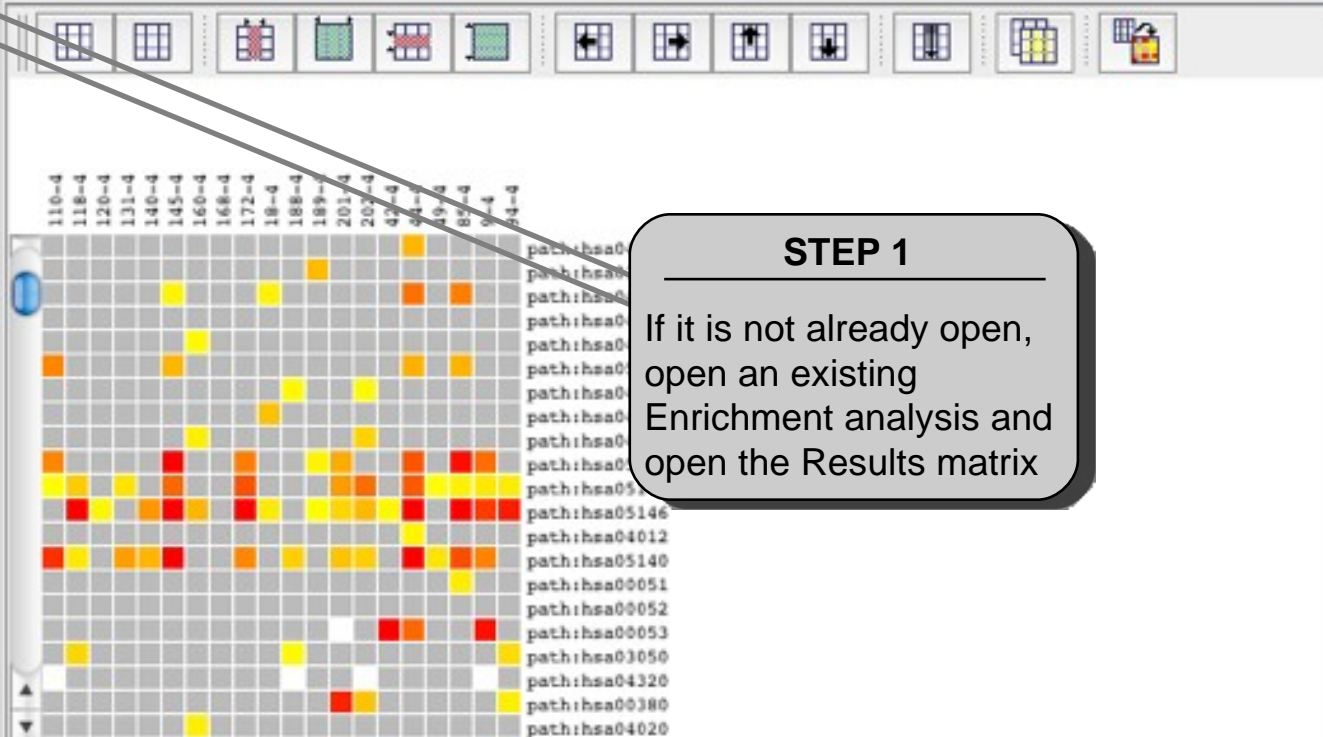




Tutorial 1.4: Explore results in a heatmap

Explore the heatmap with the enrichment analysis results by sorting, filtering, searching, hiding and moving rows and columns



If it is not already open,
open an existing
Enrichment analysis and
open the Results matrix

0.000.05

1.00

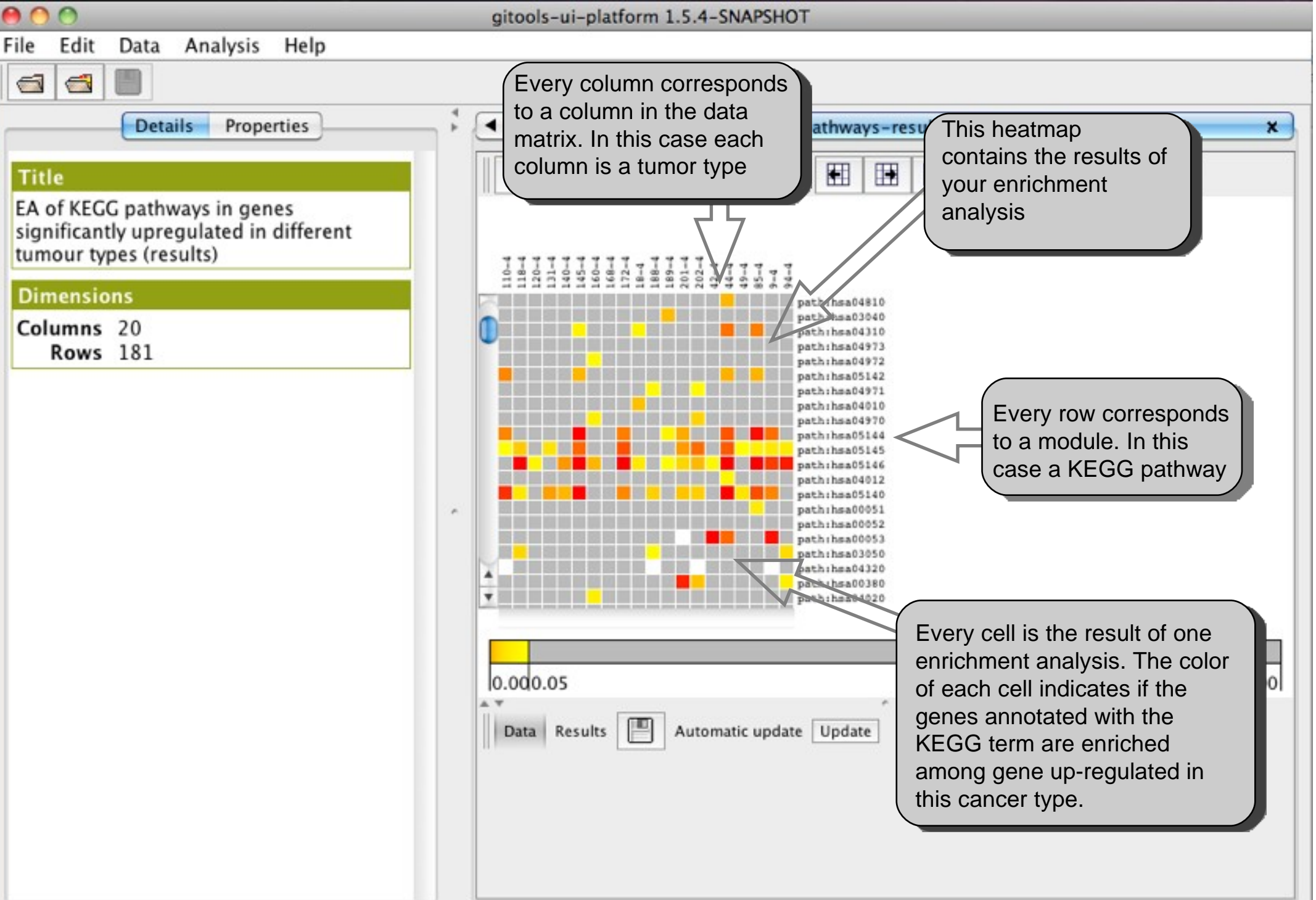
Data

Results



Automatic update

Update

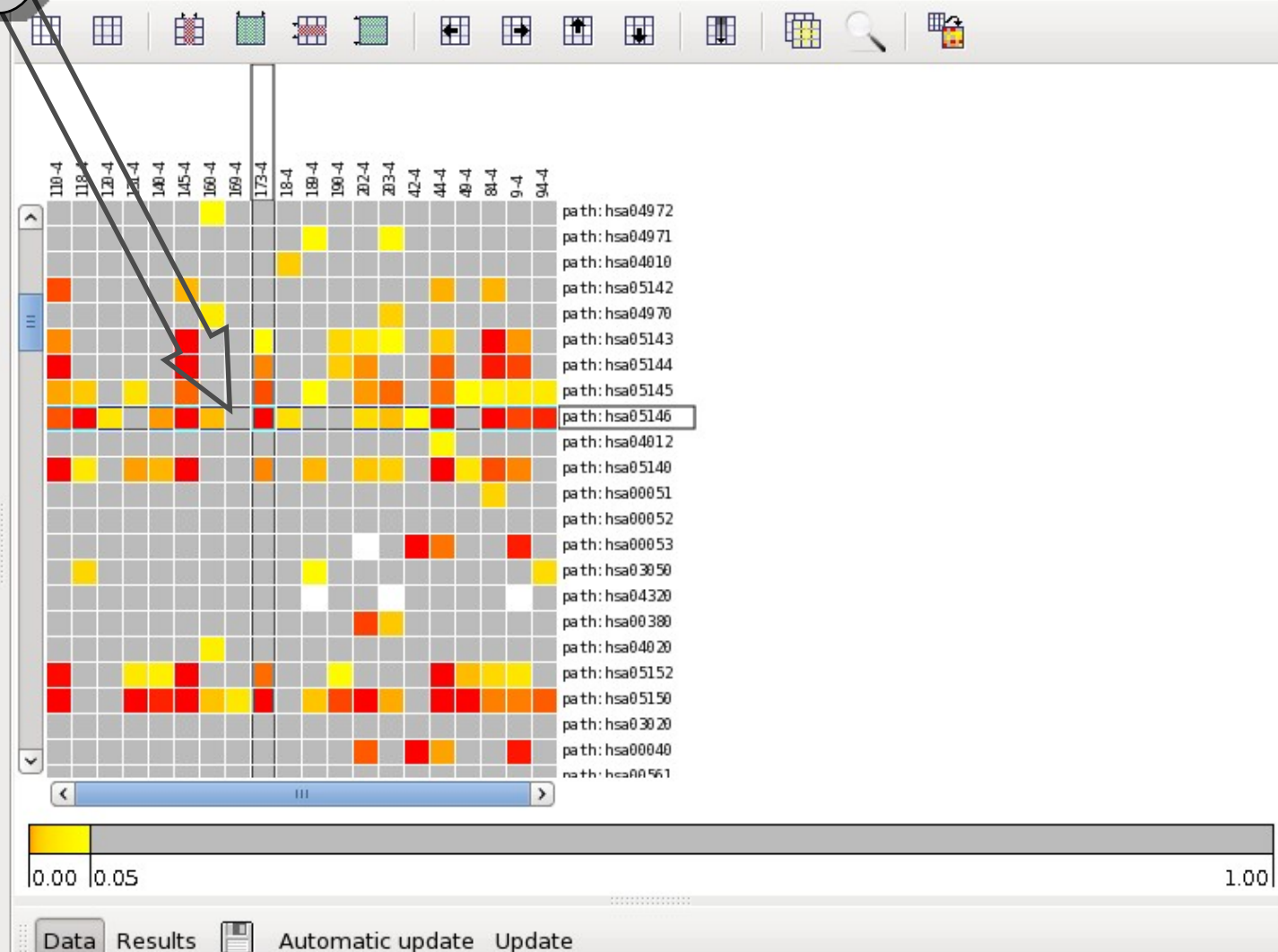


STEP 2

Click on one cell
to see the details
of the results.

Condition**173-4****Probability** 0.0990**Module****path:hsa05146****N** 103**Observed** 27**Expected-Mean** 10.2**Expected-StDev** 3.03**P-Values****Left** 1.00**Right** 1.89e-06**Two-tail** 1.00**Multiple test correction****Left** 1.00**Right** 4.16e-05**Two-tail** 1.00

This panel shows Details of the results for the selected cell. N stands for the elements in the data matrix in the module, in this case the genes for which there is data in a tumor type. Observed stands for those coinciding elements which are significant.



Details Properties

Condition

173-4

Links

[KEGG](#)
[NCBI Gen](#)
[AmiGO G](#)
[AmiGO T](#)
[NCBI Nuc](#)
[Ensembl](#)

STEP 3

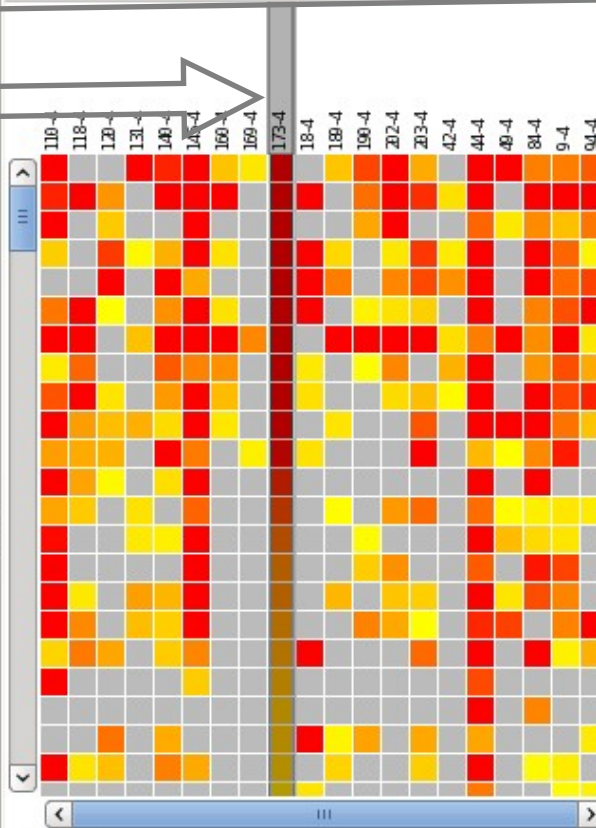
Select a column (=tumor type) and click the Sort button to sort the rows according to the values of the selected column.

STEP 4

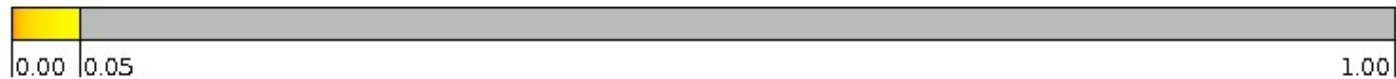
Click Properties tab to change properties of the matrix

In order to recognize the KEGG terms and the tumor types we want to use other annotations instead of IDs.

Welcome x tutorial.enrichme... x tutorial-results-0.heatmap x



The matrix has been rearranged so that on top we see the KEGG pathways more enriched among up-regulated genes in the tumor type selected.



Data Results Automatic update Update



Details Properties

Document Rows Columns Cells

Type of identifiers
Not specified

Annotations
pathways ensembl genes annotations.tsv
Load Import... Cle... Filt...

Headers
Text: ID
Add Remove E... Up Down
Size 80 Visible

Welcome tutorial.enrichme... tutorial-results-0.heatmap

Heatmap visualization with color scale from 0.00 to 1.00

path: hsa04110
path: hsa04510
path: hsa05322
path: hsa04974
path: hsa05146
path: hsa05323
path: hsa05219
path: hsa04060
path: hsa05145
path: hsa05152
path: hsa05144
path: hsa05140
path: hsa04145
path: hsa05200
path: hsa04380
path: hsa05217
path: hsa04114
path: hsa05164
path: hsa04135

Data Results

STEP 5

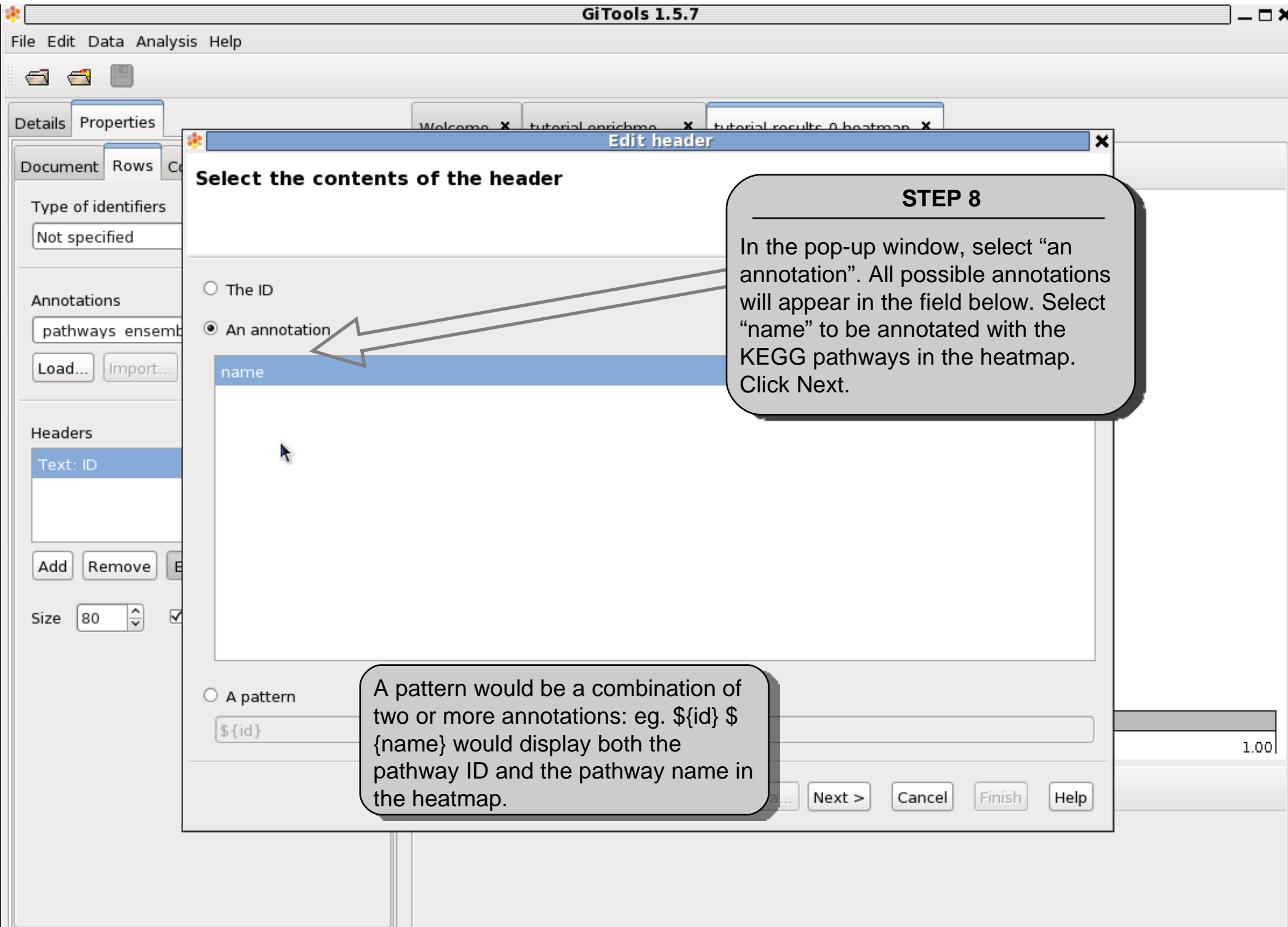
Select Rows tab to change Properties of the rows

STEP 6

Load the file that contains annotations for rows; KEGG terms in this case

STEP 7

Click on Edit to select the column of the annotation file to be used



Select the contents of the header

☐ The ID☒ An annotation

name

☐ A pattern

A pattern would be a combination of two or more annotations: eg. `${id} ${name}` would display both the pathway ID and the pathway name in the heatmap.

STEP 8

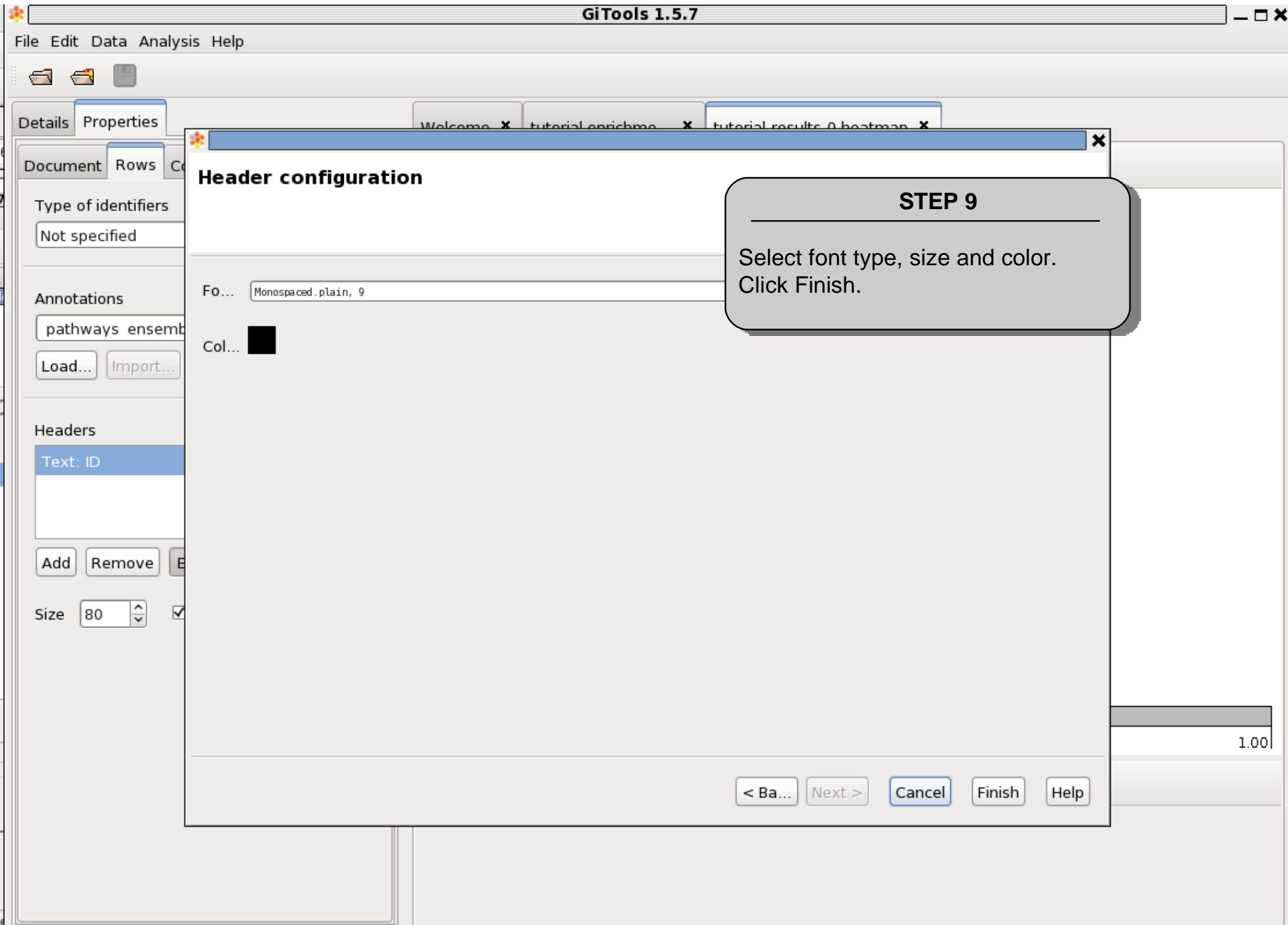
In the pop-up window, select "an annotation". All possible annotations will appear in the field below. Select "name" to be annotated with the KEGG pathways in the heatmap. Click Next.

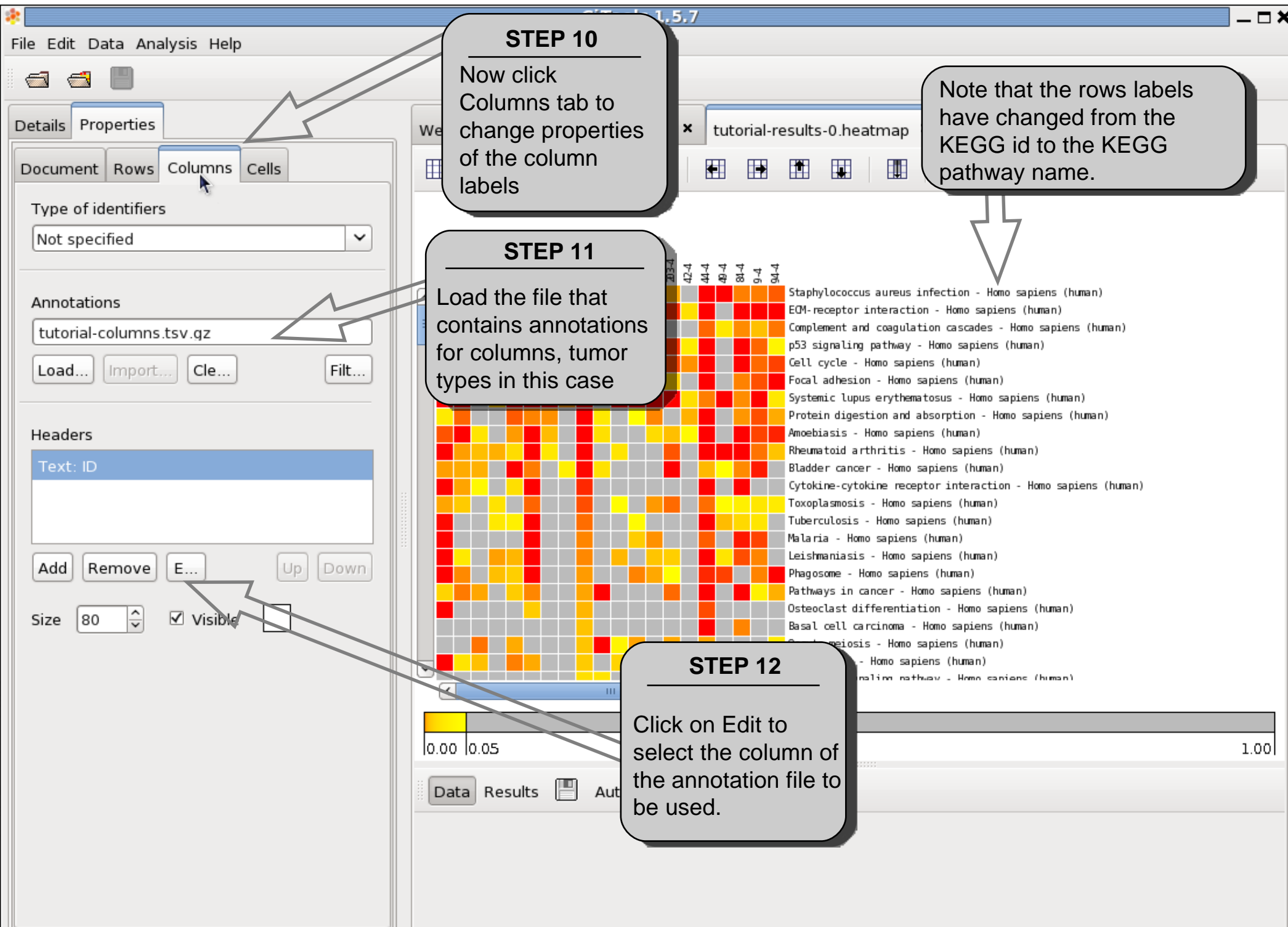
Next >

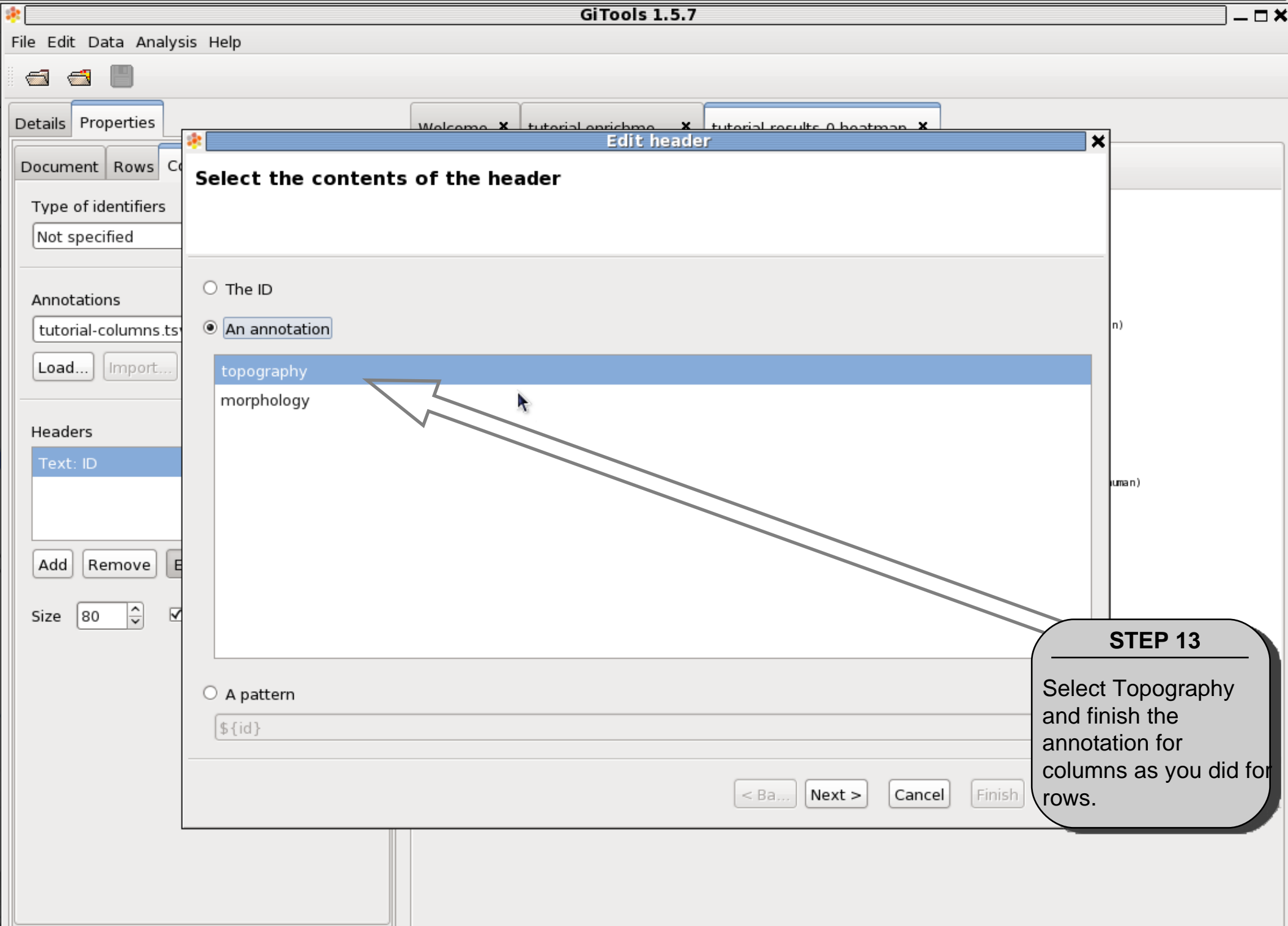
Cancel

Finish

Help







STEP 13

Select Topography and finish the annotation for columns as you did for rows.



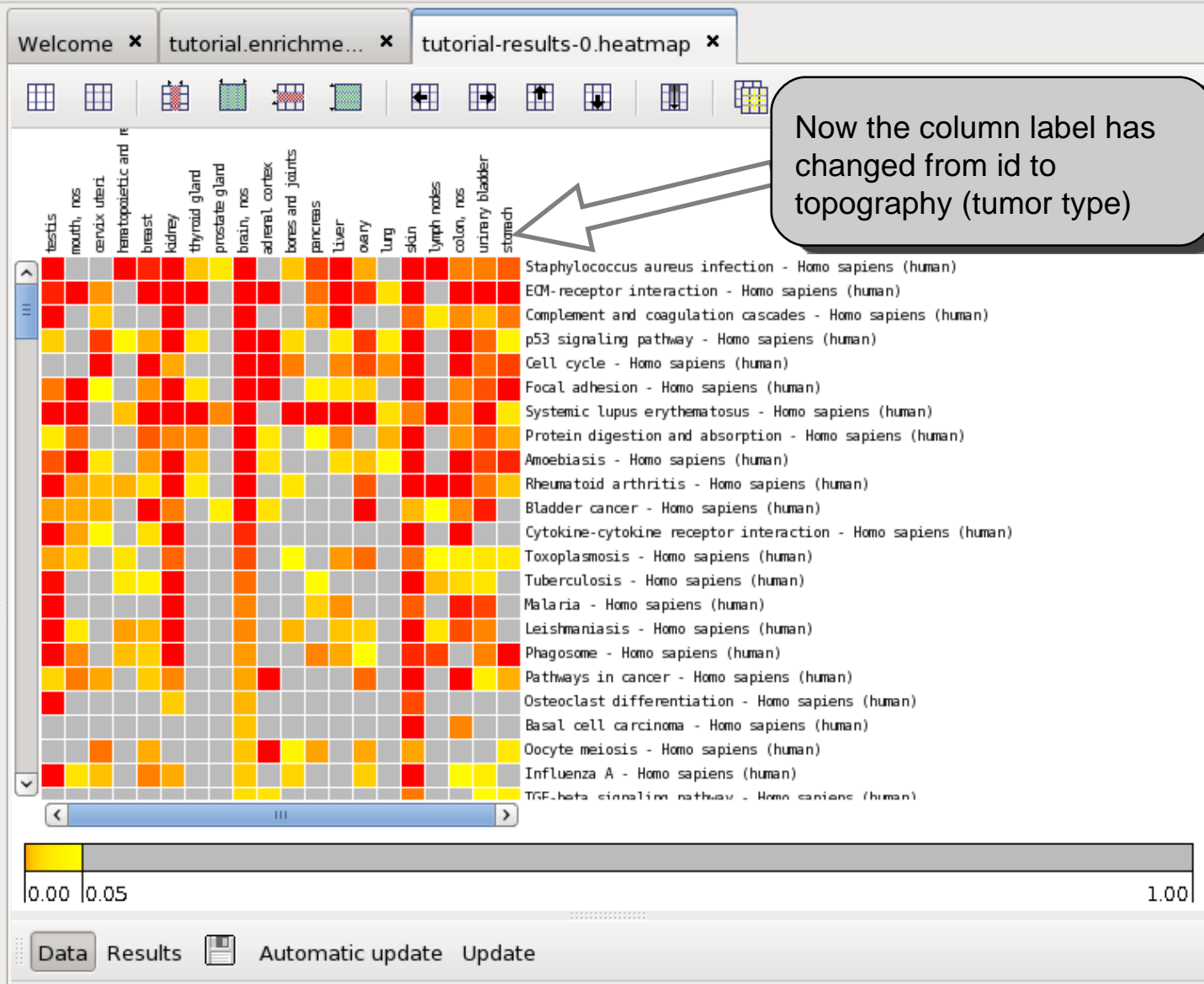
Details Properties

Document Rows Columns Cells

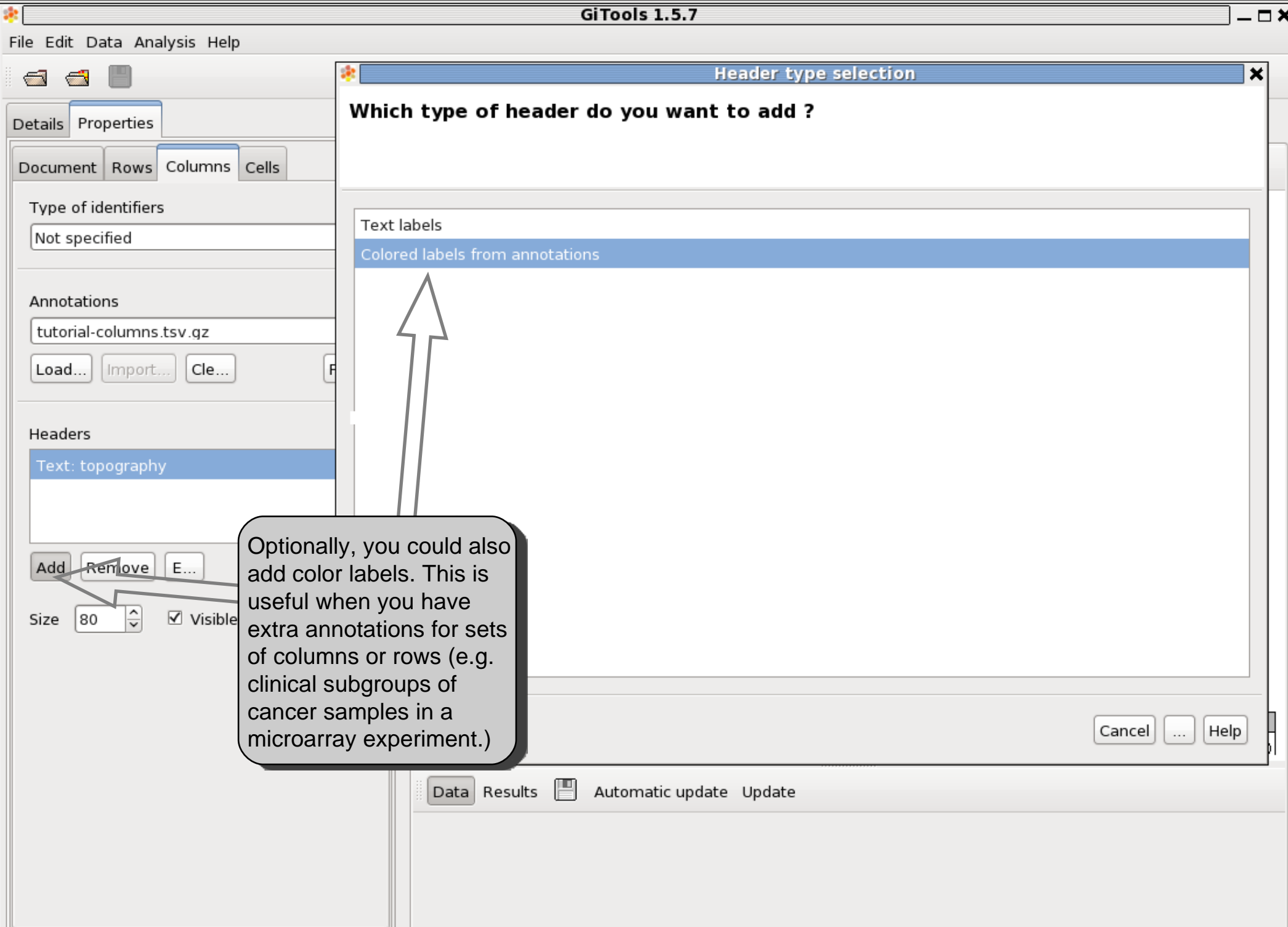
Type of identifiers
Not specified

Annotations
tutorial-columns.tsv.gz
Load... Import... Clear... Filter...

Headers
Text: topography
Add Remove Edit Up Down
Size 80 Visible



Now the column label has changed from id to topography (tumor type)



Header type selection

Which type of header do you want to add ?

Text labels

Colored labels from annotations

Cancel

...

Help

Optionally, you could also add color labels. This is useful when you have extra annotations for sets of columns or rows (e.g. clinical subgroups of cancer samples in a microarray experiment.)



Details Properties

Document Rows Columns Cells

Type of identifiers
Not specified

Annotations
tutorial-columns.tsv.gz
Load... Import... Clear... Filter...

Headers
Text: topography
Add Remove Edit Up Down
Size 80 Visible

Welcome tutorial.enrichme... tutorial-results-0.heatmap

Grid icons

These 4 buttons allow you to hide selected rows and columns and to re-show all rows and columns.

These 4 buttons allow you to move selected rows and columns up, down, left or right.

testis	mouth, nos	cervix uteri	pancreatic and re	breast	kidney	thyroid gland	prostate gland	brain, nos	adrenal cortex	bones and joints	pancreas	liver	ovary	lung	skin	lymph nodes	colon, nos	urinary bladder	stomach	
																				Staphylococcus aureus infection - Homo sapiens (human)
																				EGF-receptor interaction - Homo sapiens (human)
																				Complement and
																				lin
																				sid
																				upu
																				ges
																				- H
																				ad arthritis - Homo sapiens (human)
																				Bladder cancer - Homo sapiens (human)
																				Cytokine-cytokine receptor interaction - Homo sapiens (human)
																				Toxoplasmosis - Homo sapiens (human)
																				Tuberculosis - Homo sapiens (human)
																				Malaria - Homo sapiens (human)
																				Leishmaniasis - Homo sapiens (human)
																				Phagosome - Homo sapiens (human)
																				Pathways in cancer - Homo sapiens (human)
																				Osteoclast differentiation - Homo sapiens (human)
																				Basal cell carcinoma - Homo sapiens (human)
																				Oocyte meiosis - Homo sapiens (human)
																				Influenza A - Homo sapiens (human)
																				TGF-beta signaling pathway - Homo sapiens (human)

0.00 0.05 1.00

Data Results Automatic update Update

Not specified

tutorial-columns.tsv.gz

Load... Import... Cle... Filt...

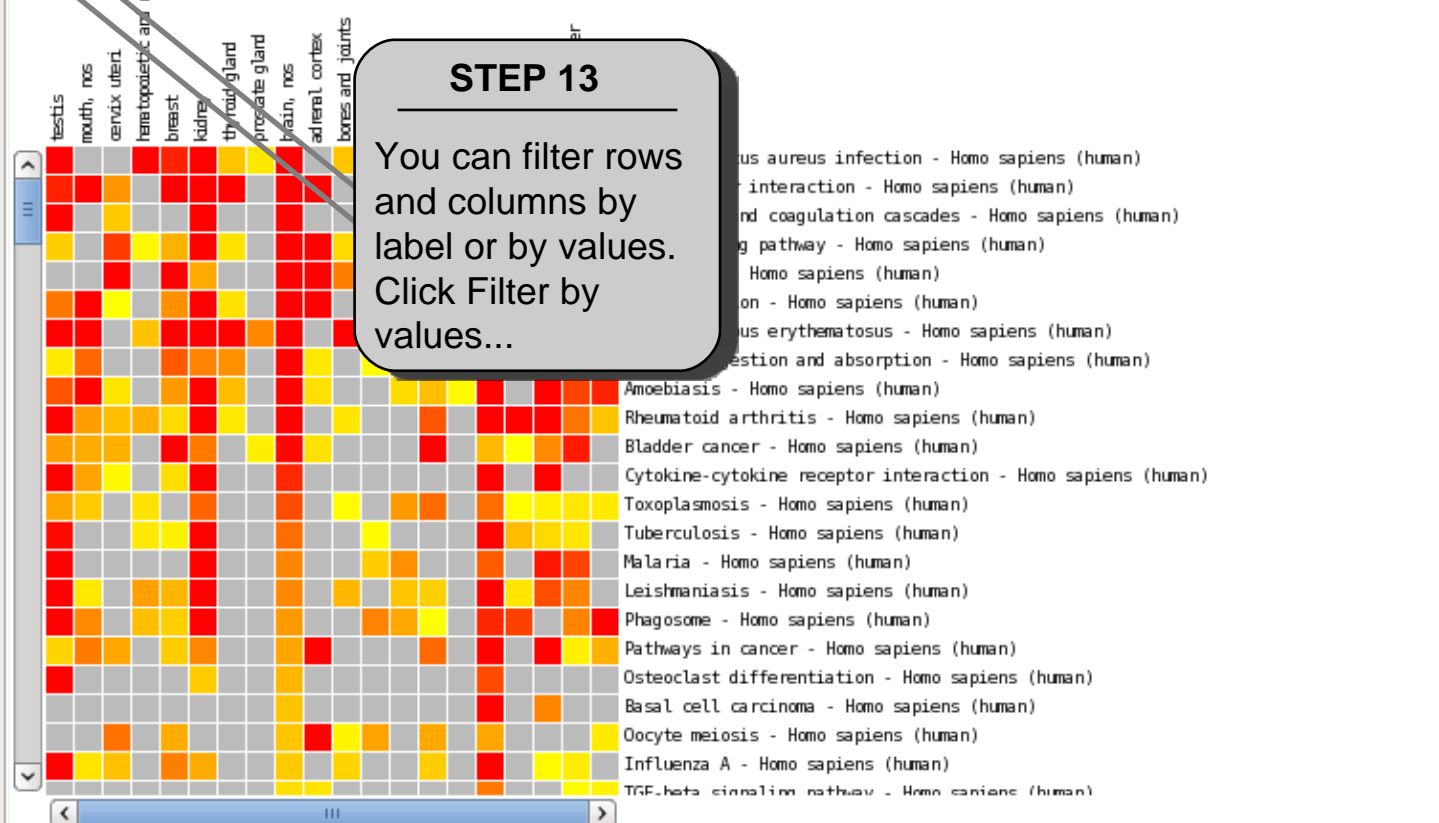
Text: topography

Add Remove E... Up Down

Size 80 ☒ Visible

Welcome x tutorial.enrichme... x tutorial-results-0.heatmap x

You can filter rows and columns by label or by values. Click Filter by values...



Data Results Automatic update Update

Type of identifiers

Not specified

Annotations

tutorial-columns.tsv.gz

Load...

Import...

Cle...

Headers

Text: topography

Add

Remove

E...

Up

Size

80

Visible

☒☐

Filter criteria

Attribute	Condition	Value
Observed events	>	10.0
Corrected right P-Value	<	0.01

Add

Remove

Load...

Save...

- ☐ All criteria should match
- ☐ All elements should match
- ☐ Invert criteria when filtering

Apply to:

- ☒ rows
- ☐ columns
- ☐ rows and columns

OK

Cancel

STEP 14

Add the criteria you want to use to filter rows and/or columns

0.00 0.05

1.00

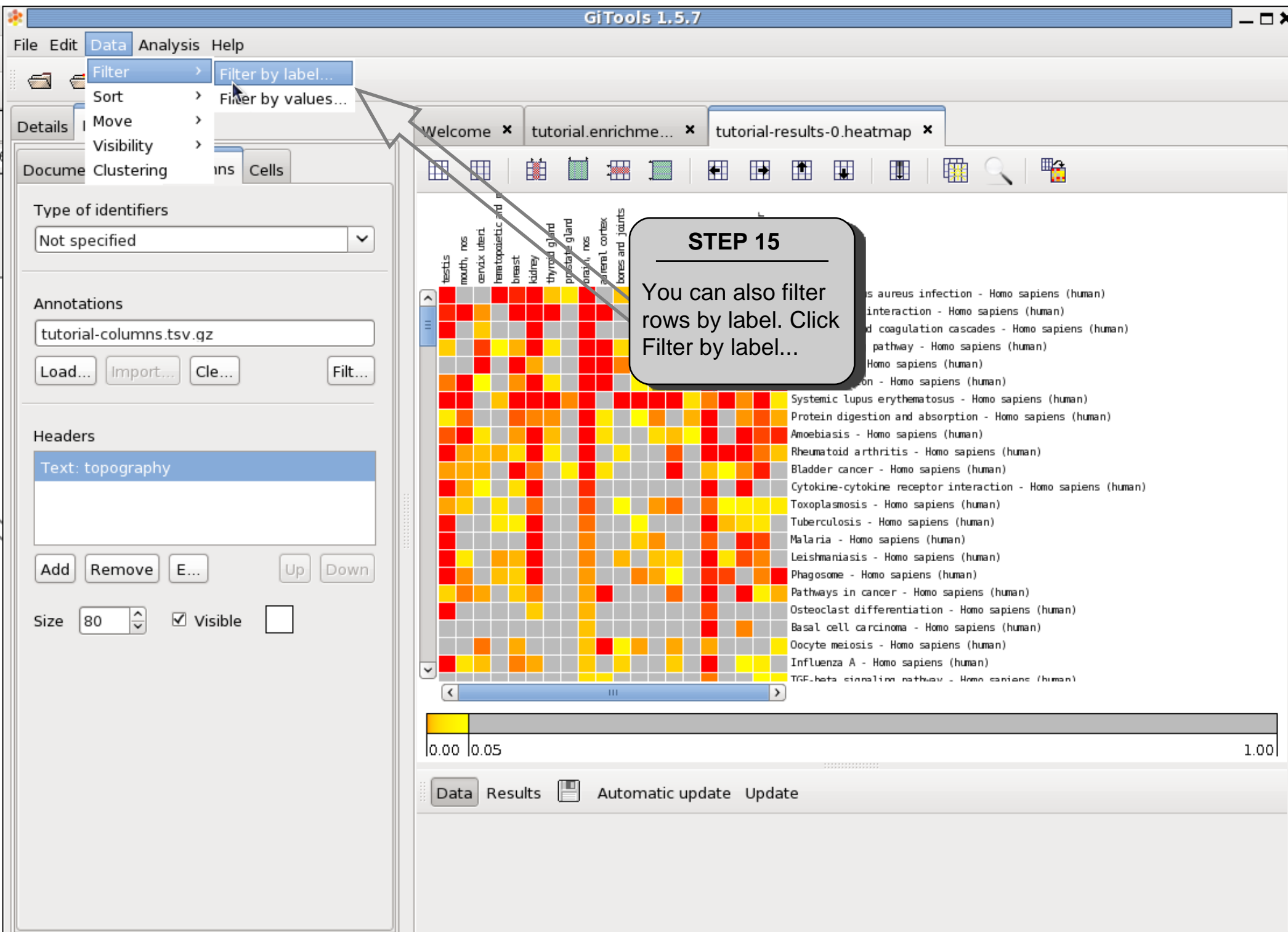
Data

Results



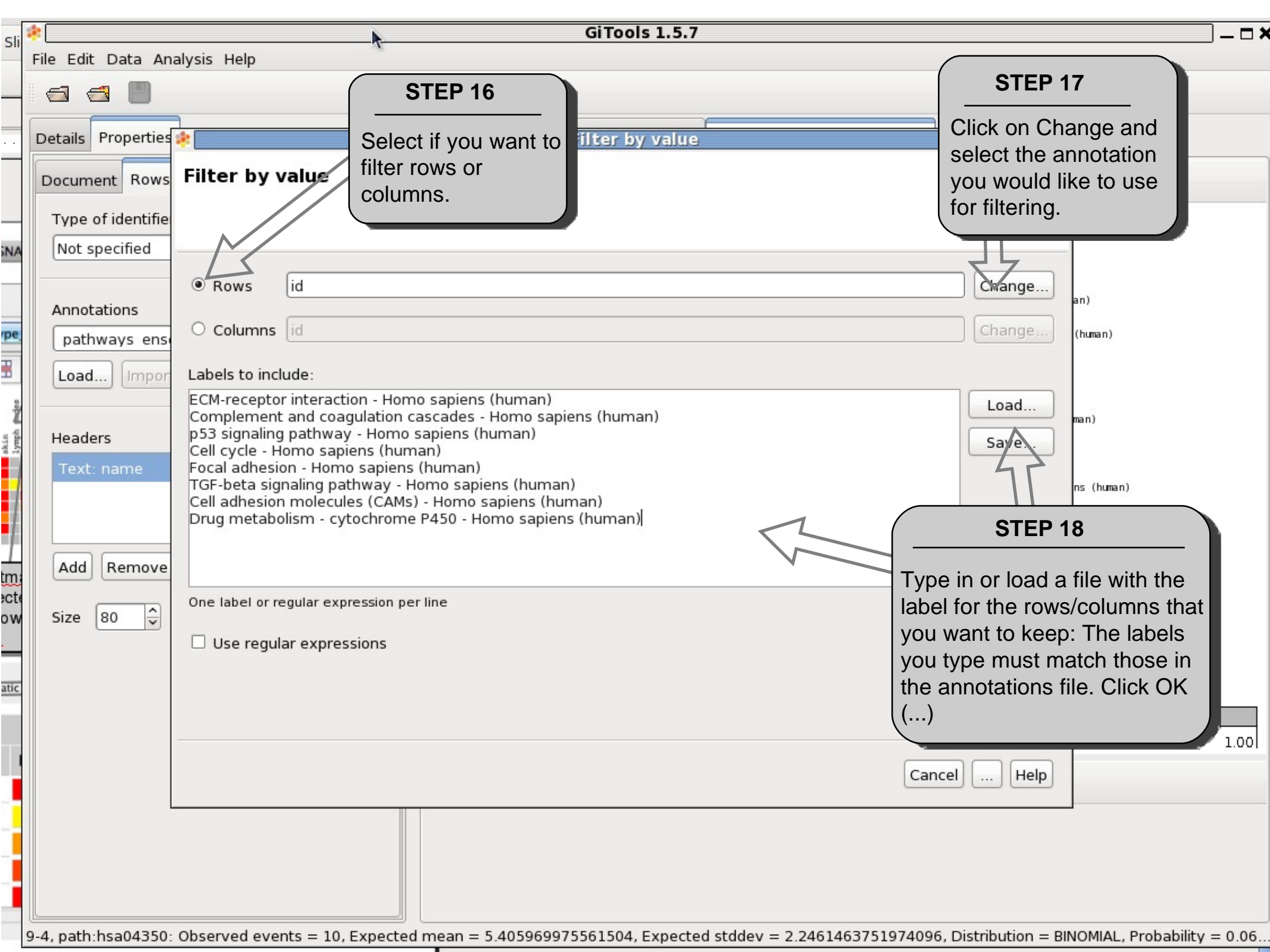
Automatic update

Update



STEP 15

You can also filter rows by label. Click Filter by label...



STEP 16

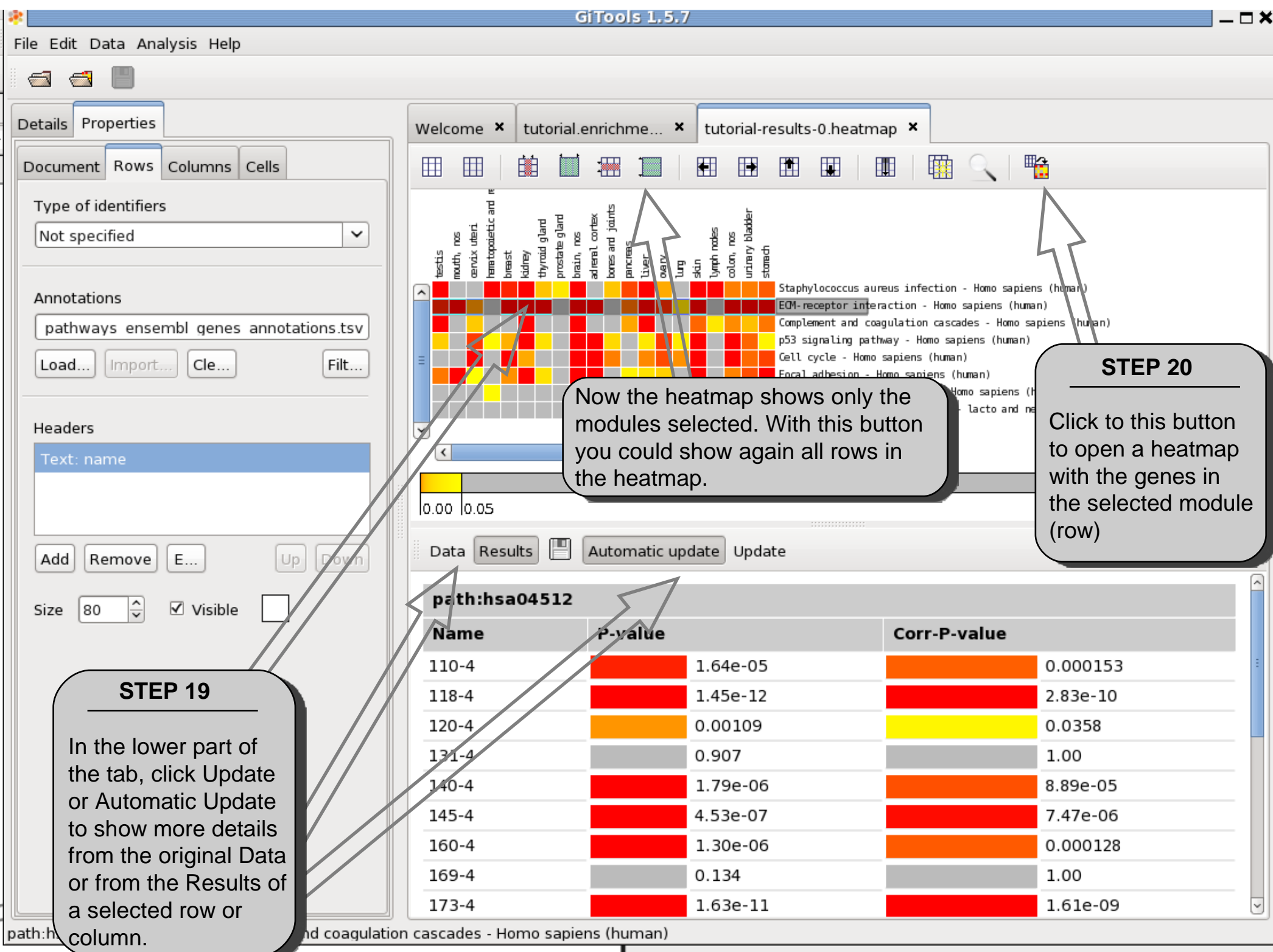
Select if you want to filter rows or columns.

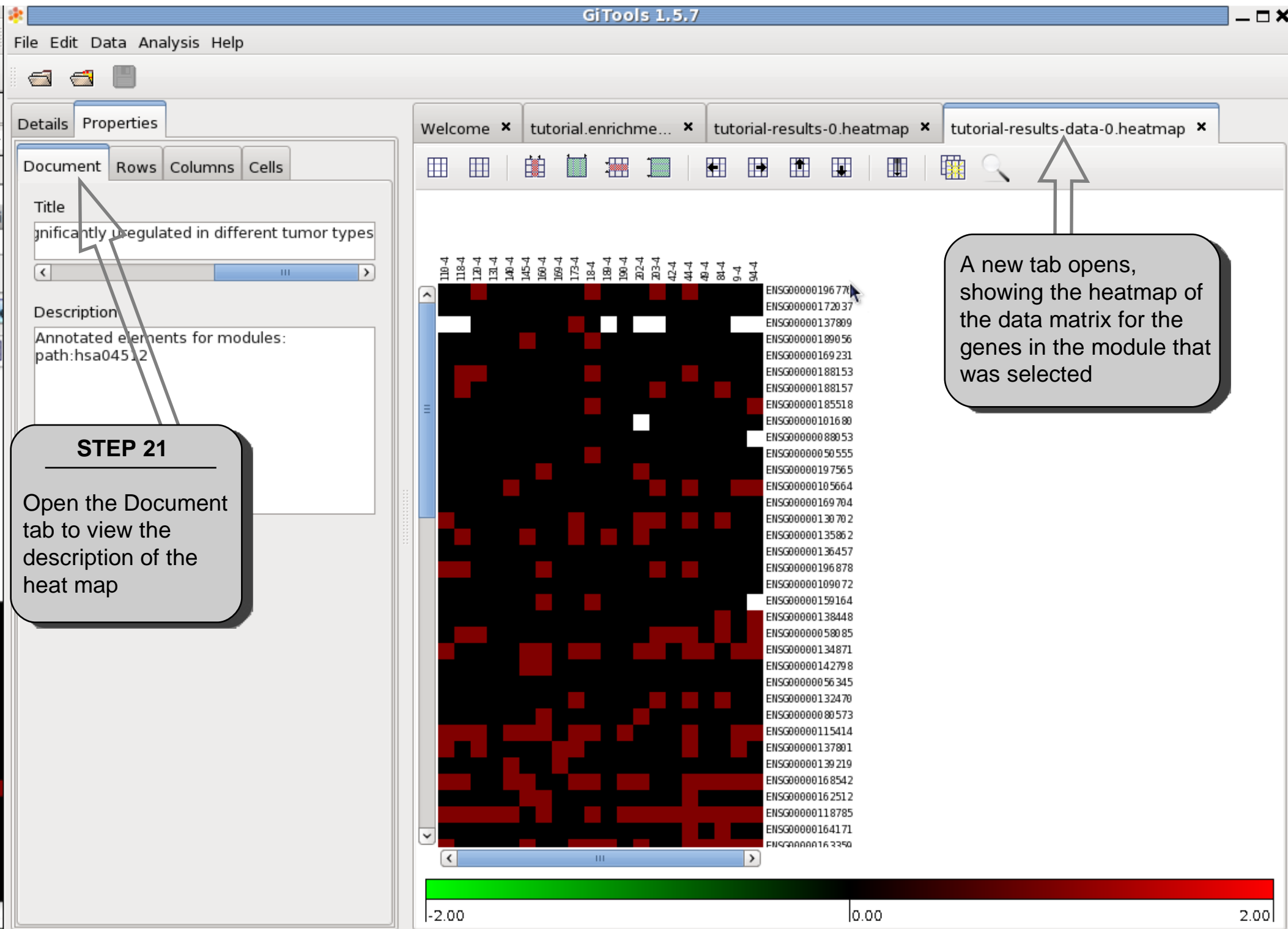
STEP 17

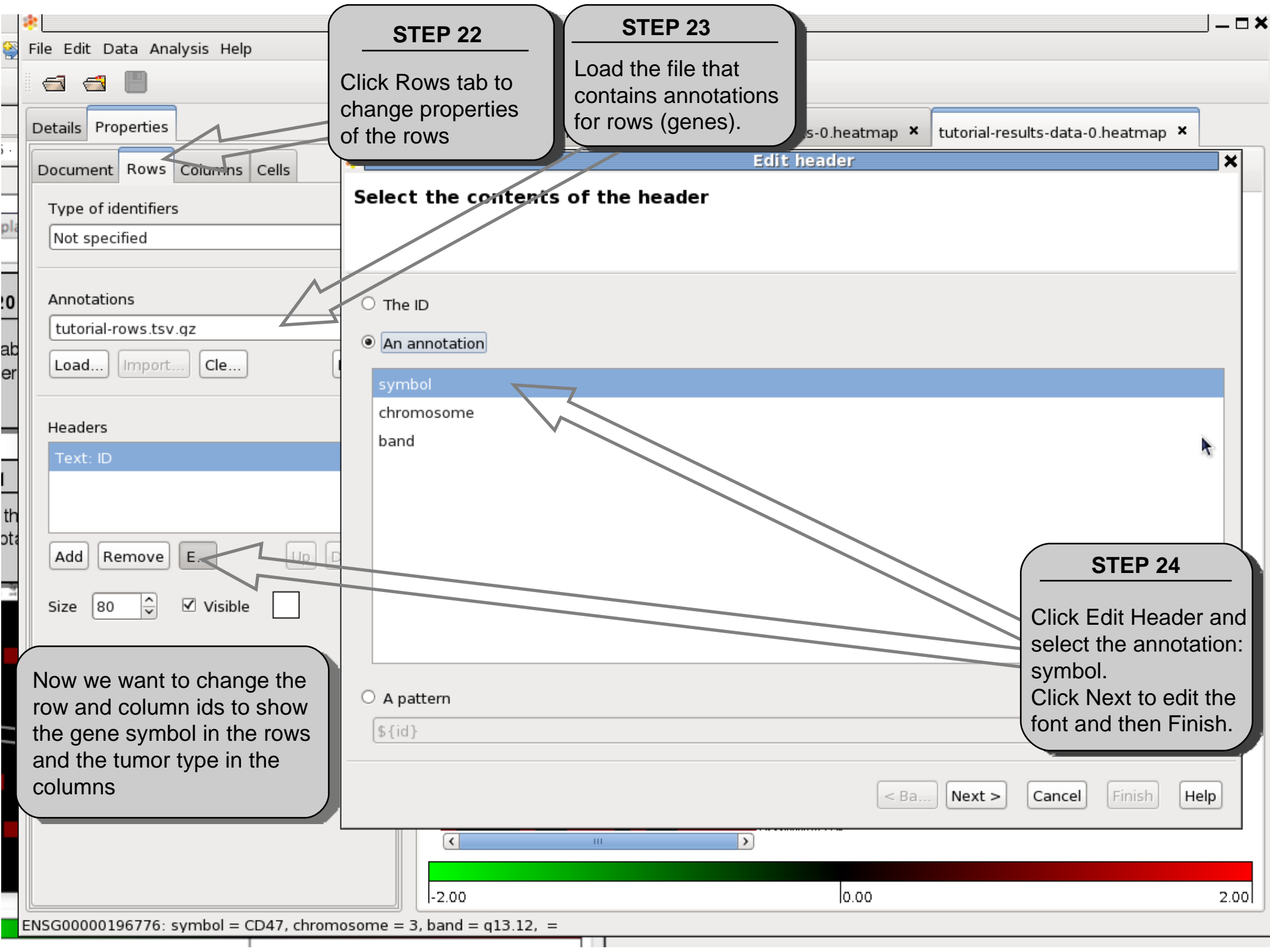
Click on Change and select the annotation you would like to use for filtering.

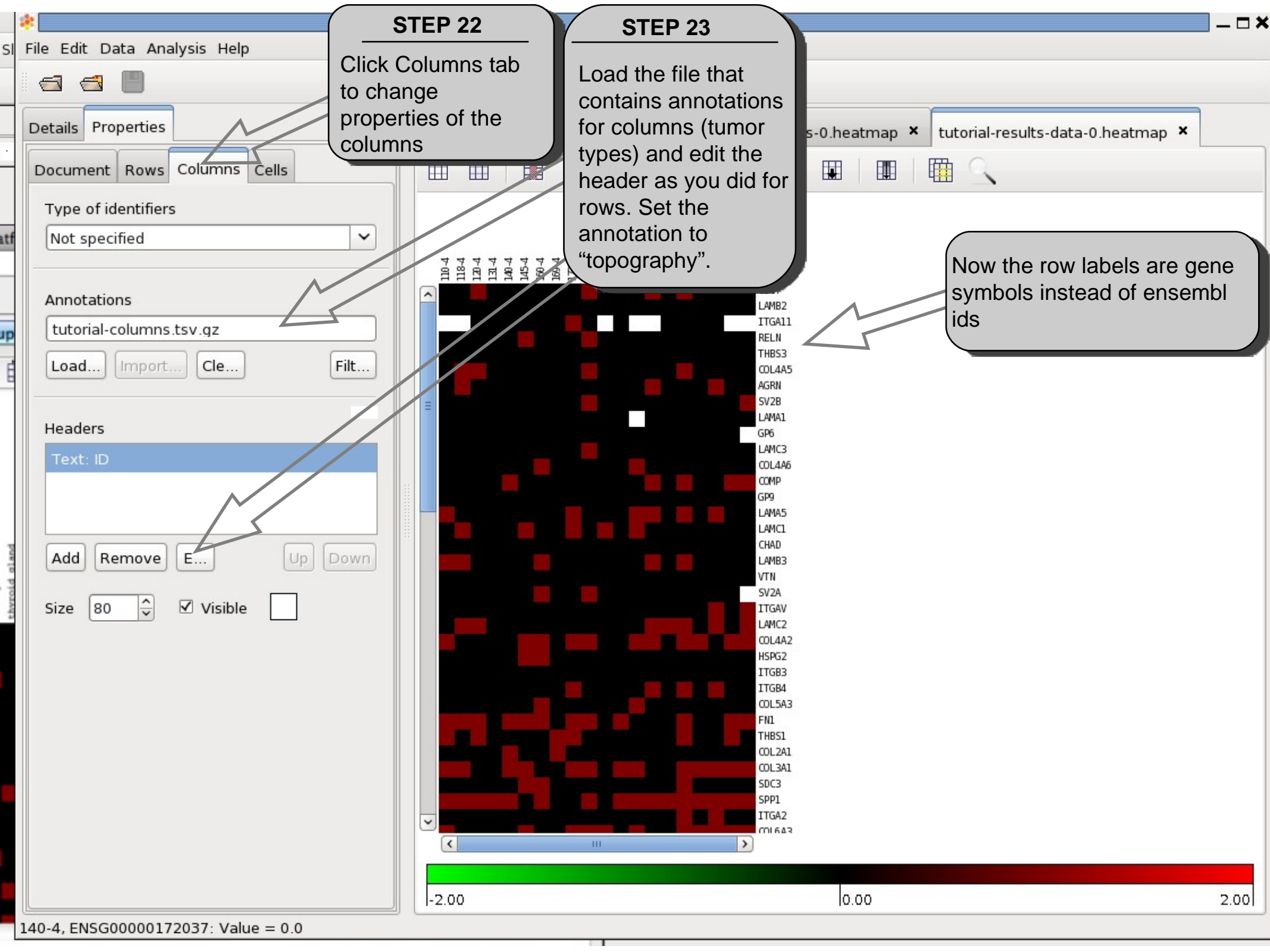
STEP 18

Type in or load a file with the label for the rows/columns that you want to keep: The labels you type must match those in the annotations file. Click OK (...)









Details Properties

Document Rows Columns Cells

Type of identifiers

Not specified

Annotations

tutorial-columns.tsv.gz

Load...

Import...

Cle...

Filt...

Headers

Text: topography

Add

Remove

E...

Up

Down

Size 200

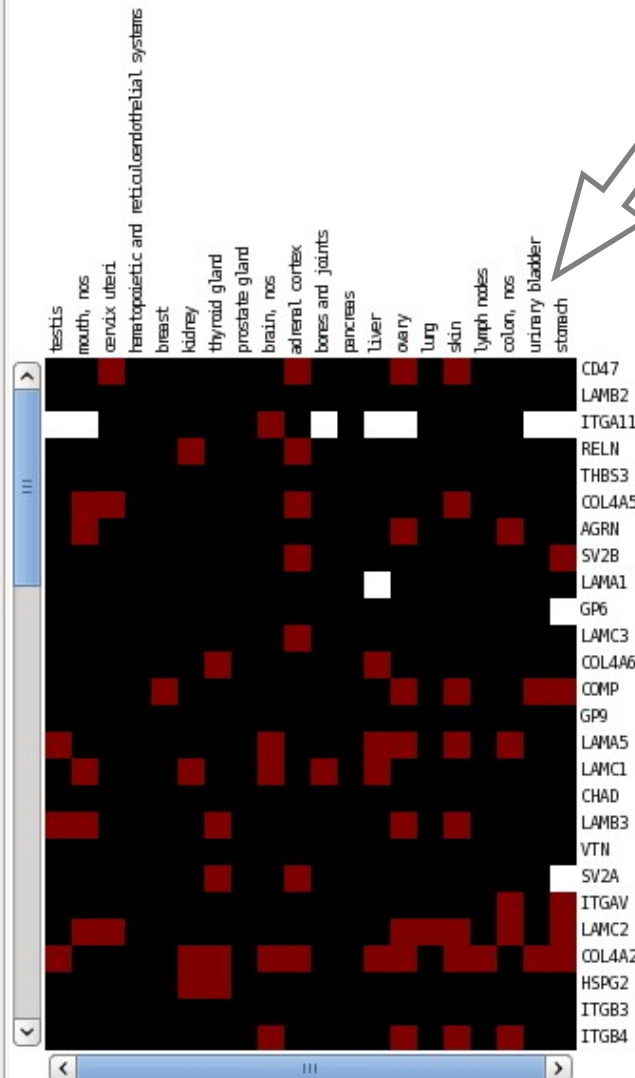
☒ Visible**STEP 24**

Set the size for the column header to 200 to fit in long annotations.

Welcome x tutorial.enrichme... x tutorial-results-0.heatmap x tutorial-results-data-0.heatmap x



Now the column label is tumor type (topography)

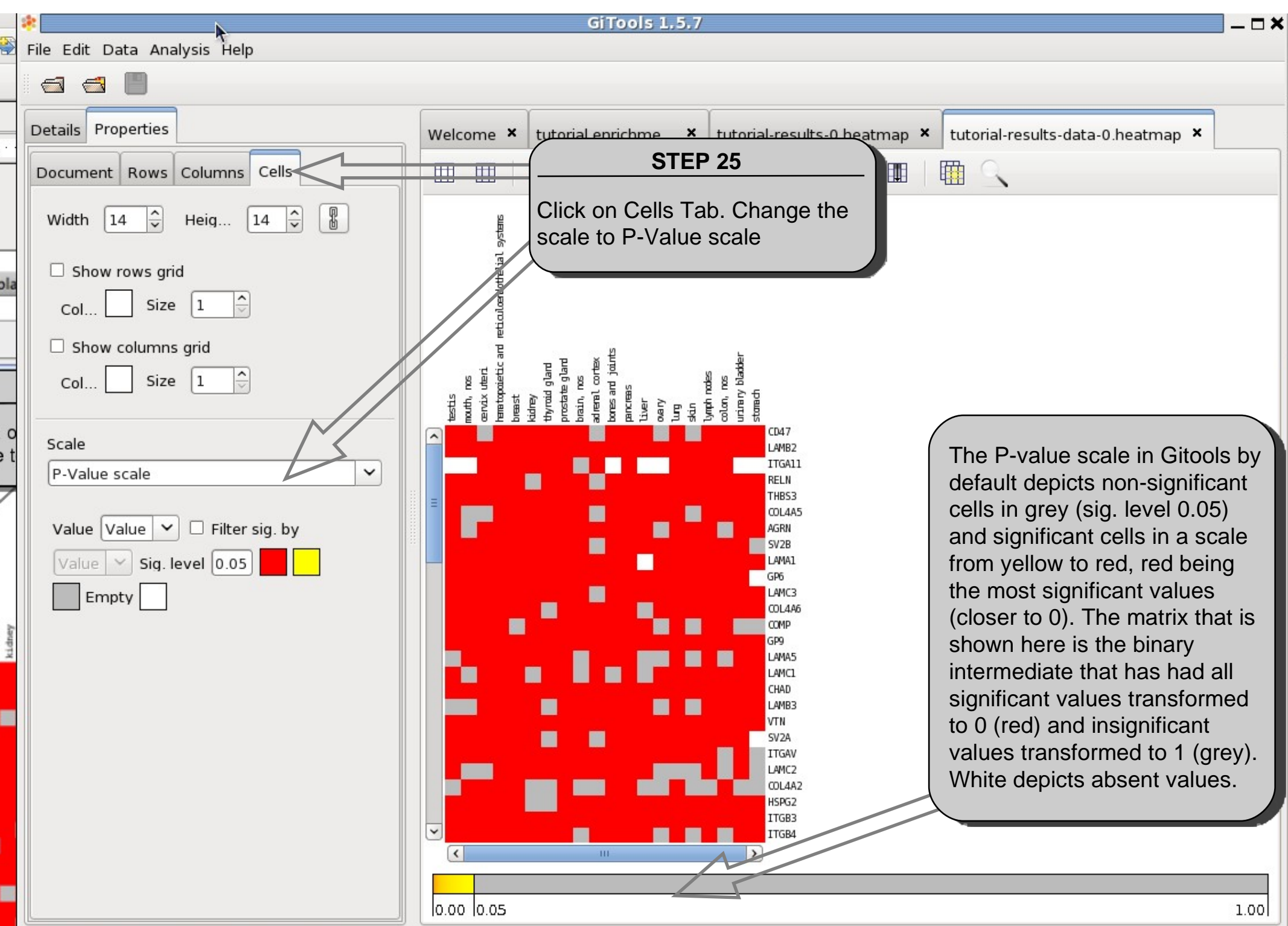


The color scale shown at this moment goes from -2 to 2. Since the values in the data matrix are p-values (from 0 to 1), the scale we have right now is not adequate and we want to change it in the next step.

-2.00

0.00

2.00





THANKS FOR USING GITTOOLS

<http://www.gittools.org>