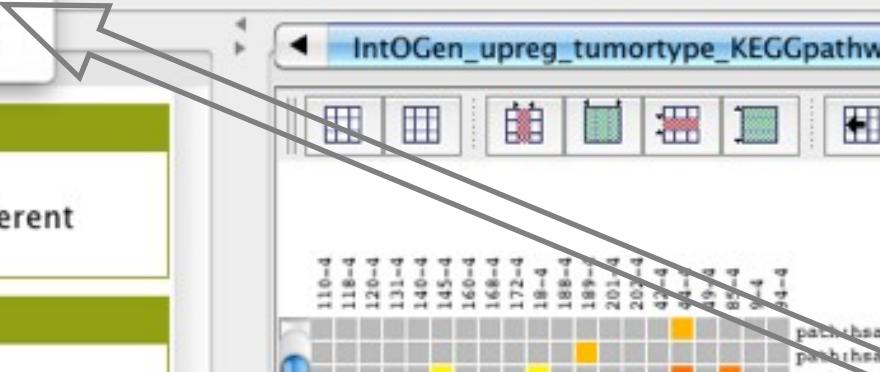


Tutorial 1.4: Explore results in a heatmap

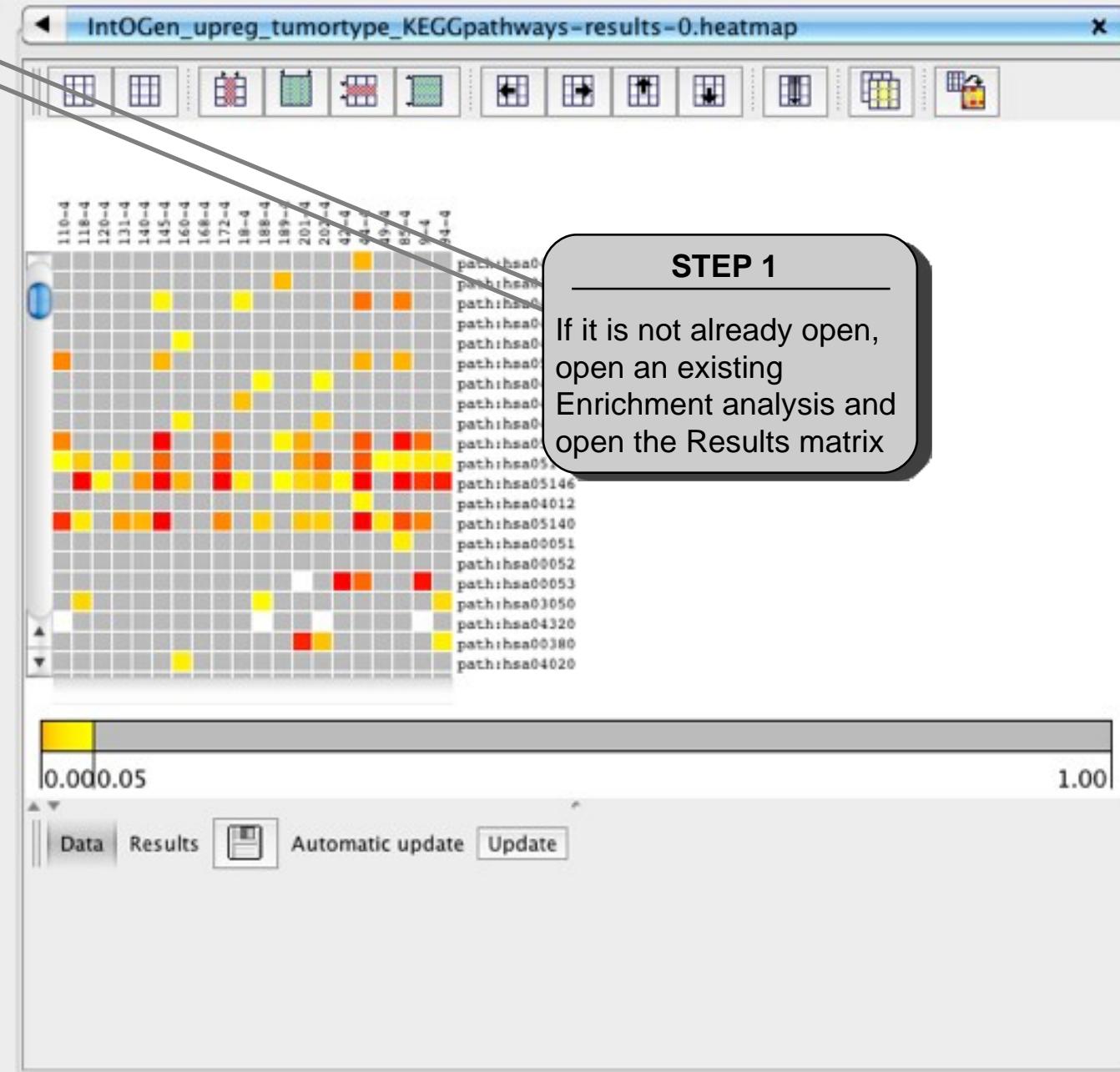
Explore the heatmap with the enrichment analysis results by sorting, filtering, searching, hiding and moving rows and columns

New ►
Open ► 
Save
Save As ...
Close
Import ►
Export ►
Exit

Rows 181

Analysis ...
Heatmap ...

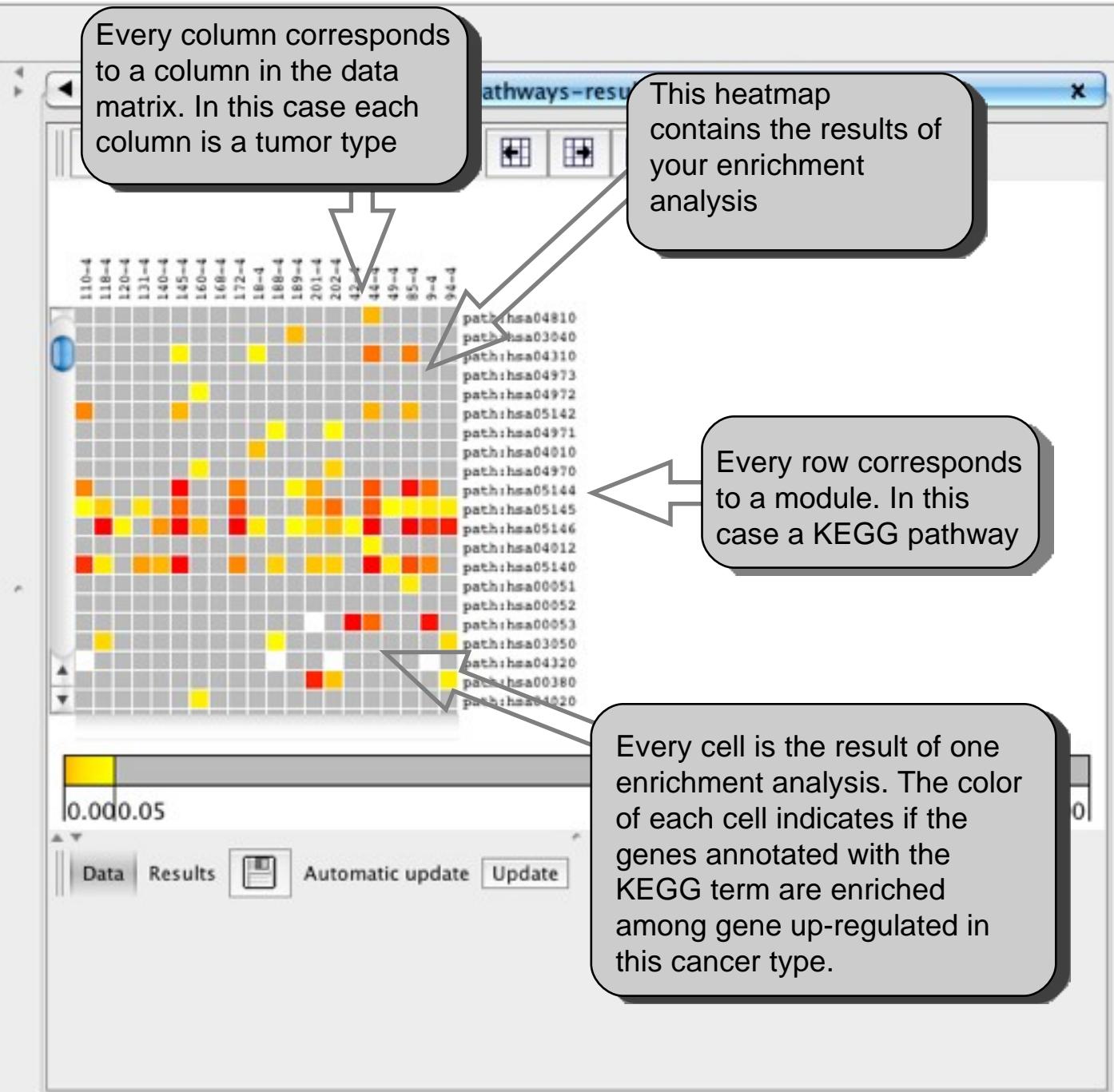
pathways in genes
regulated in different
(results)

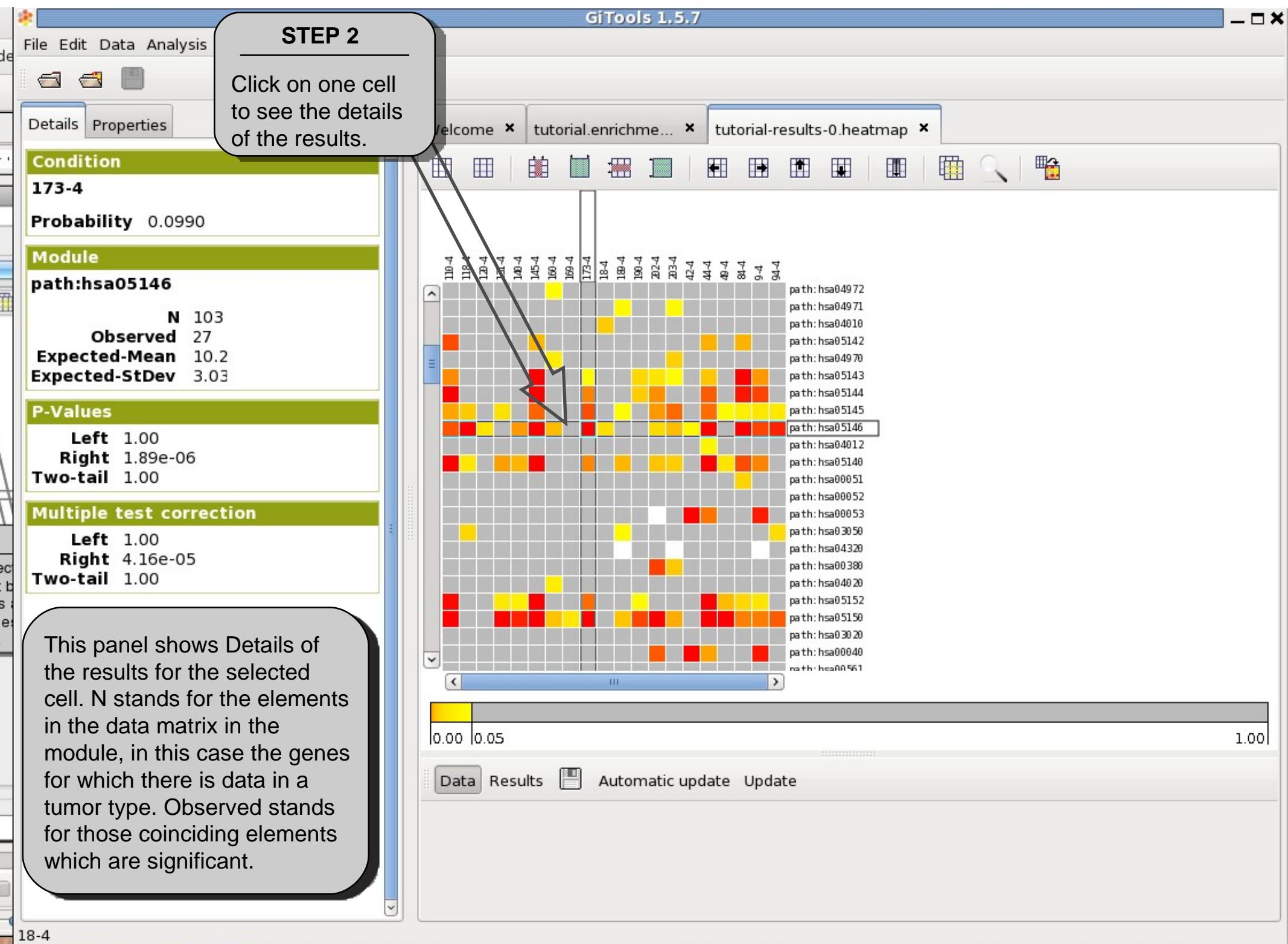


Details **Properties**

Title
EA of KEGG pathways in genes significantly upregulated in different tumour types (results)

Dimensions
Columns 20
Rows 181







Details Properties

Condition

173-4

STEP 3

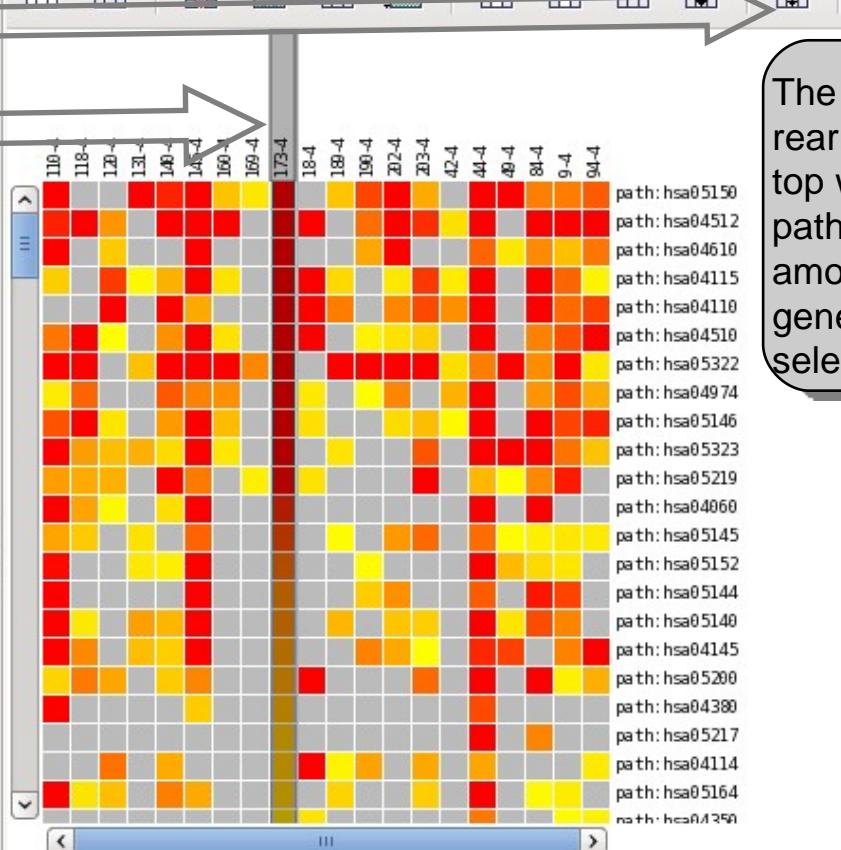
Select a column (=tumor type) and click the Sort button to sort the rows according to the values of the selected column.

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

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

The screenshot shows the GiTools 1.5.7 interface. On the left, a properties panel for a 'Rows' tab is open, showing settings like 'Type of identifiers' (set to 'Not specified'), 'Annotations' (loading 'pathways ensembl genes annotations.tsv'), and 'Headers' (set to 'Text: ID'). A 'Size' dropdown is set to 80. On the right, a heatmap titled 'tutorial-results-0.heatmap' is displayed, showing a grid of colored cells. A tooltip indicates that the 'Rows' tab is selected. Three callout boxes provide instructions: 'STEP 5' points to the 'Rows' tab in the properties panel; 'STEP 6' points to the 'Annotations' section in the properties panel; and 'STEP 7' points to the 'Edit' button in the 'Headers' section of the properties panel.



Details Properties

Document Rows C

Type of identifiers

Not specified

Annotations

pathways ensemble

Load...

Import...

Headers

Text: ID

Add

Remove

Size 80

Select the contents of the header

The ID
 An annotation

name

A pattern
{\$id}

Next > Cancel Finish Help

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.

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.



Details Properties

Document Rows Co

Type of identifiers

Not specified

Annotations

pathways ensemble

Load... Import...

Headers

Text: ID

Add Remove E

Size 80

Header configuration

Fo... Monospaced plain, 9

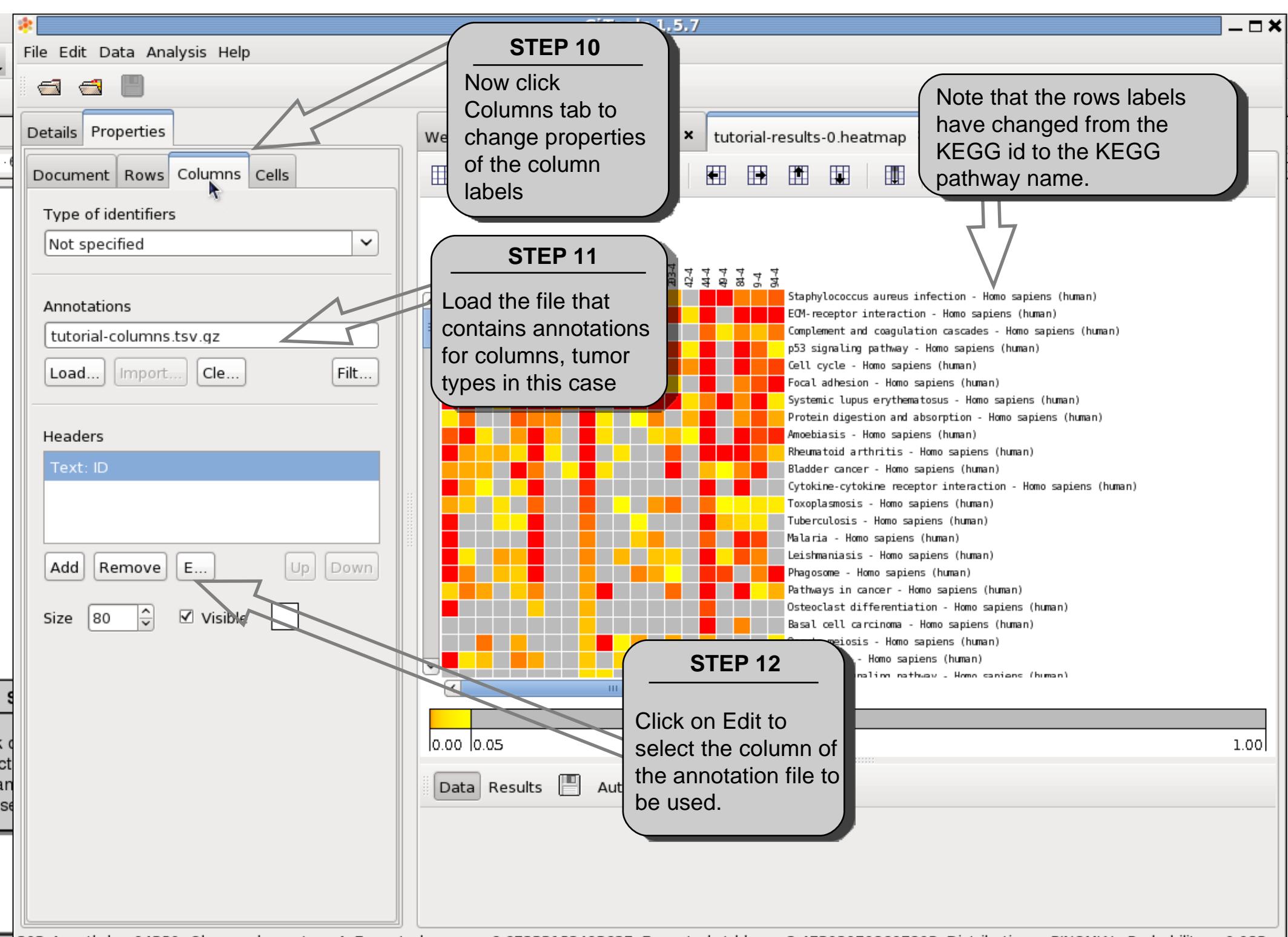
Col... [Color Swatch]

STEP 9

Select font type, size and color.
Click Finish.

< Ba... Next > Cancel Finish Help

1.00





Details Properties

Document Rows Co

Type of identifiers

Not specified

Annotations

tutorial-columns.ts

Load... Import...

Headers

Text: ID

Add Remove E

Size 80

Select the contents of the header The ID An annotation

topography

morphology

 A pattern

{\$id}

< Ba... Next > Cancel Finish

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... Cle... Filt...

Headers

Text: topography

Add Remove E... Up Down

Size 80 Visible

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



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



Data Results Automatic update Update

Details Properties

Document Rows Columns Cells

Type of identifiers
Not specified

Annotations
tutorial-columns.tsv.gz

Load... Import... Cle... F...

Headers
Text: topography

Add Remove E... Size 80 ▲ ▼ Visible

Header type selection

Which type of header do you want to add ?

Text labels

Colored labels from annotations

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.)

Cancel ... Help

Data Results Automatic update Update



Details Properties

Document Rows Columns Cells

Type of identifiers

Not specified

Annotations

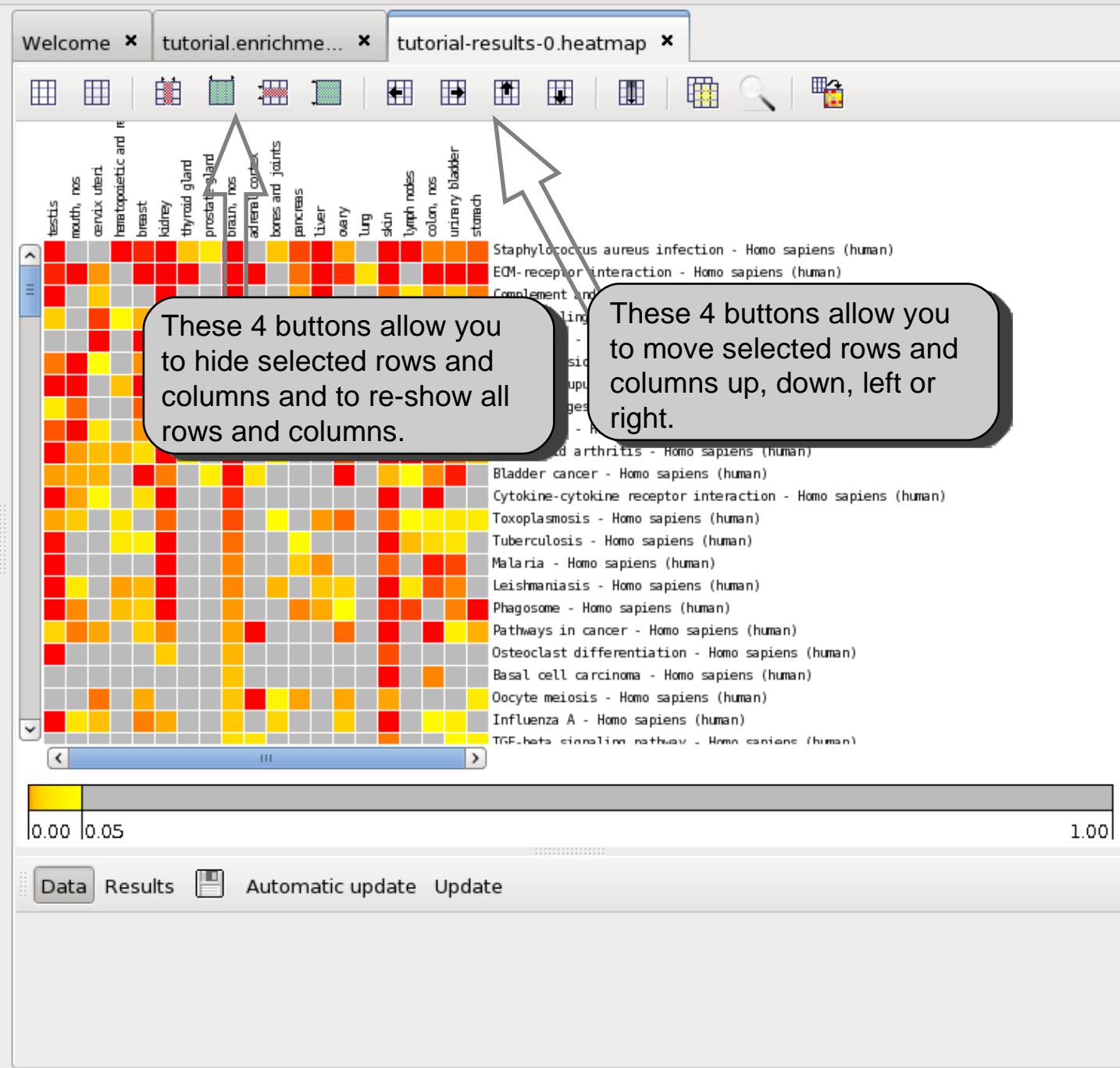
tutorial-columns.tsv.gz

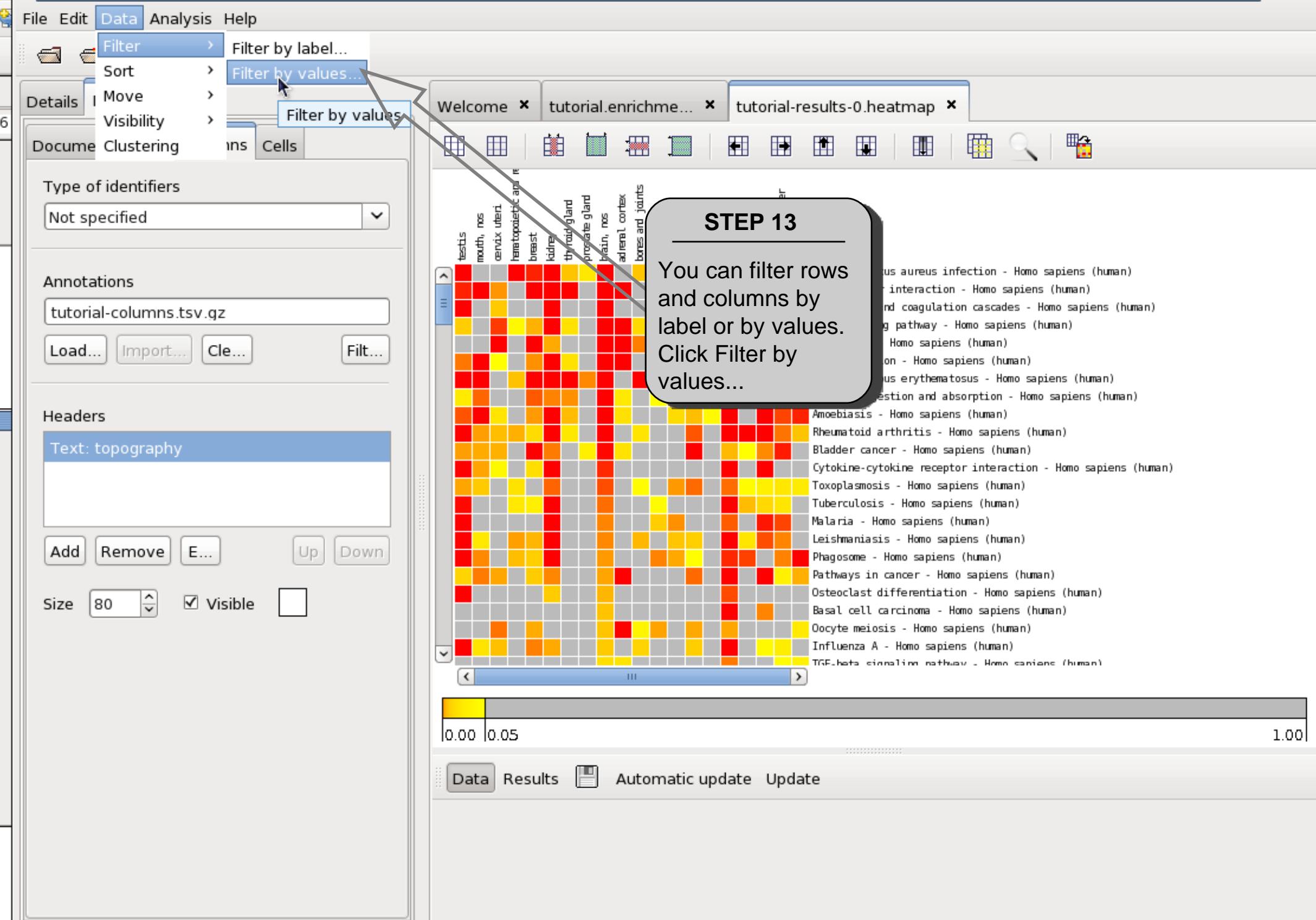
Load... Import... Cle... Filt...

Headers

Text: topography

Add Remove E... Up Down

Size 80 Visible 





Details Properties

Document Rows Columns Cells

Type of identifiers

Not specified

Annotations

tutorial-columns.tsv.gz

Load...

Import...

Cle...

Headers

Text: topography

Add

Remove

E...

Up

Size 80

Visible

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

Apply to:

- rows
 columns
 rows and columns

0.00 0.05

Data Results Automatic update Update

OK

Cancel

Filter criteria

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

Add

Remove

Load...

Save...



omo sapiens (human)
iens (human)
- Homo sapiens (human)
s (human)

n)

sapiens (human)
Homo sapiens (human)

STEP 14

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

File Edit Data Analysis Help

Filter > Filter by label...

Sort > Filter by values...

Move >

Visibility >

Document Clustering >

Cells

Type of identifiers

Not specified

Annotations

tutorial-columns.tsv.gz

Load...

Import...

Cle...

Filt...

Headers

Text: topography

Add

Remove

E...

Up Down

Size

80

Visible

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



STEP 15

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

Staphylococcus aureus infection - Homo sapiens (human)
Protein interaction - Homo sapiens (human)
Coagulation cascades - Homo sapiens (human)
Pathway - Homo sapiens (human)
Homo sapiens (human)
Infection - Homo sapiens (human)
Systemic lupus erythematosus - Homo sapiens (human)
Protein digestion and absorption - Homo sapiens (human)
Amoebiasis - Homo sapiens (human)
Rheumatoid 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)



Data Results Automatic update Update

STEP 16

Select if you want to filter rows or columns.

Filter by value
 Rows

id

STEP 17

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

Change...

 Columns

id

Change...

Labels to include:

ECM-receptor interaction - Homo sapiens (human)
 Complement and coagulation cascades - Homo sapiens (human)
 p53 signaling pathway - Homo sapiens (human)
 Cell cycle - Homo sapiens (human)
 Focal adhesion - Homo sapiens (human)
 TGF-beta signaling pathway - Homo sapiens (human)
 Cell adhesion molecules (CAMs) - Homo sapiens (human)
 Drug metabolism - cytochrome P450 - Homo sapiens (human)

Load...

Save...

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 (...)

Cancel

...

Help



Details Properties

Document Rows Columns Cells

Type of identifiers

Not specified

Annotations

pathways ensembl genes annotations.tsv

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

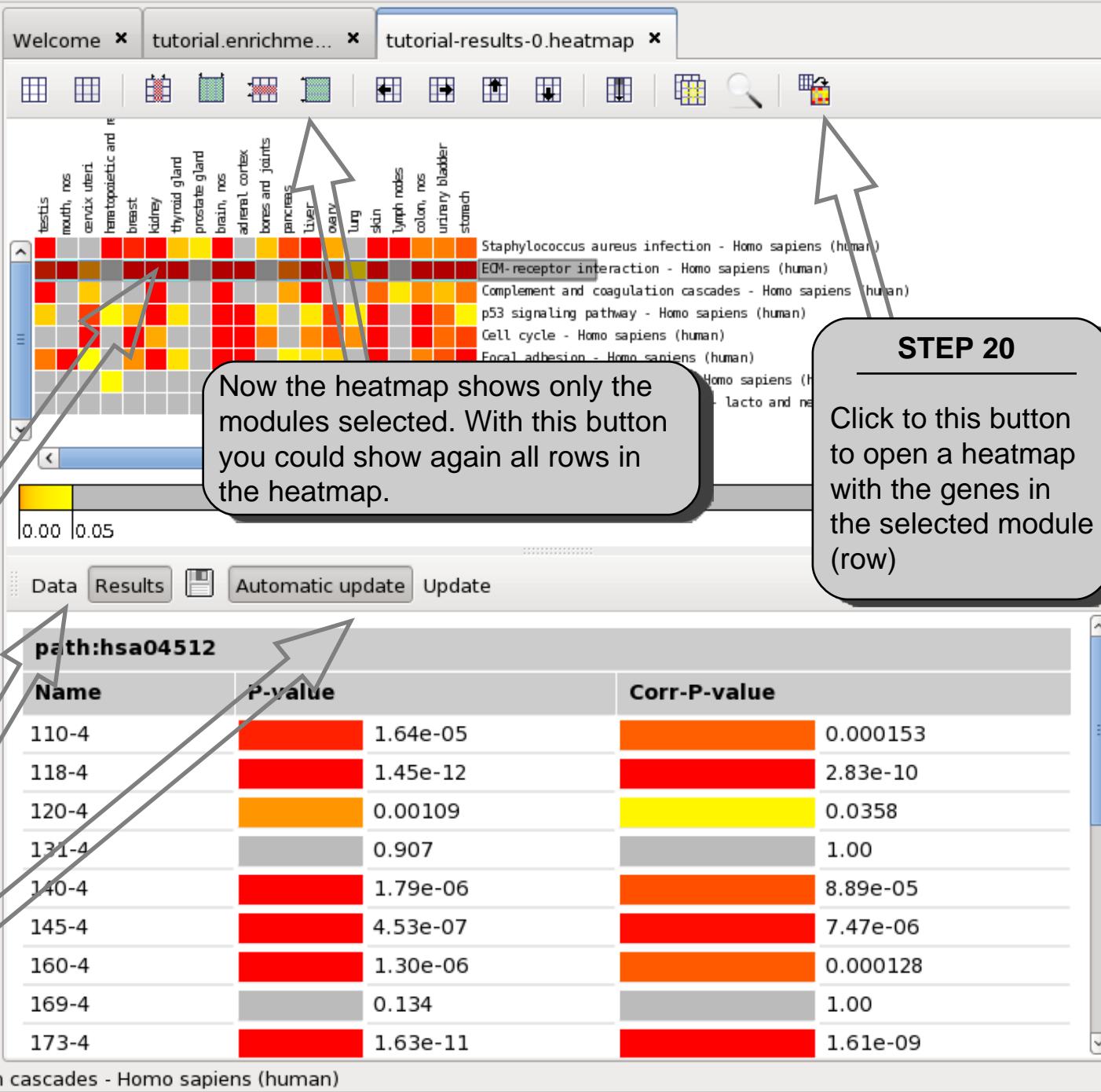
Headers

Text: name

Add Remove E... Up Down

Size 80 Visible **STEP 19**

In the lower part of the tab, click Update or Automatic Update to show more details from the original Data or from the Results of a selected row or column.





Details Properties

Document Rows Columns Cells

Title

Significantly upregulated in different tumor types

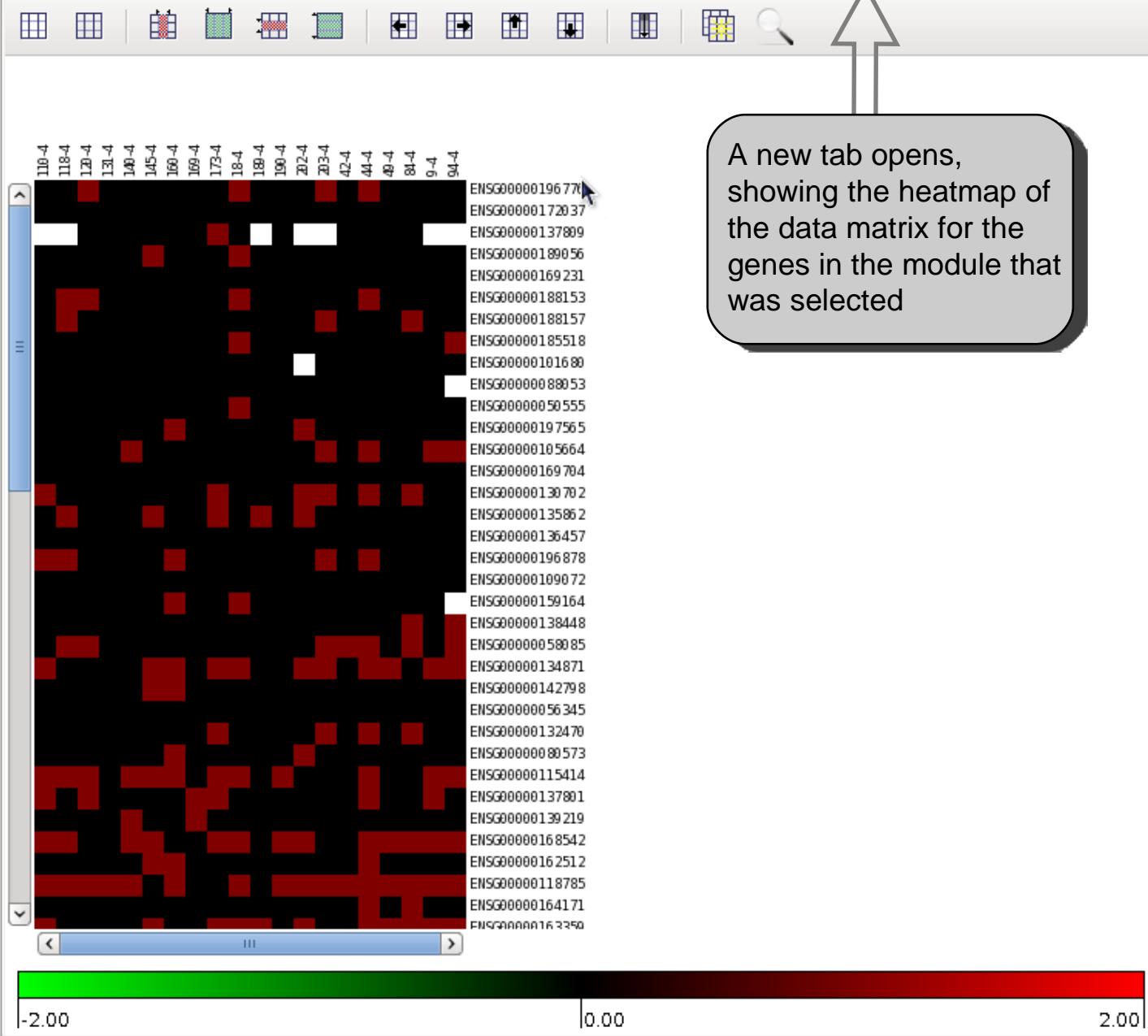
Description

Annotated elements for modules:
path:hsa04512

STEP 21

Open the Document tab to view the description of the heat map

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



A new tab opens, showing the heatmap of the data matrix for the genes in the module that was selected

File Edit Data Analysis Help

Details Properties

Document Rows Columns Cells

Type of identifiers
Not specified

Annotations
tutorial-rows.tsv.gz
Load... **Import...** **Cle...**

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

STEP 22
Click Rows tab to change properties of the rows

STEP 23
Load the file that contains annotations for rows (genes).

Select the contents of the header

The ID
 An annotation

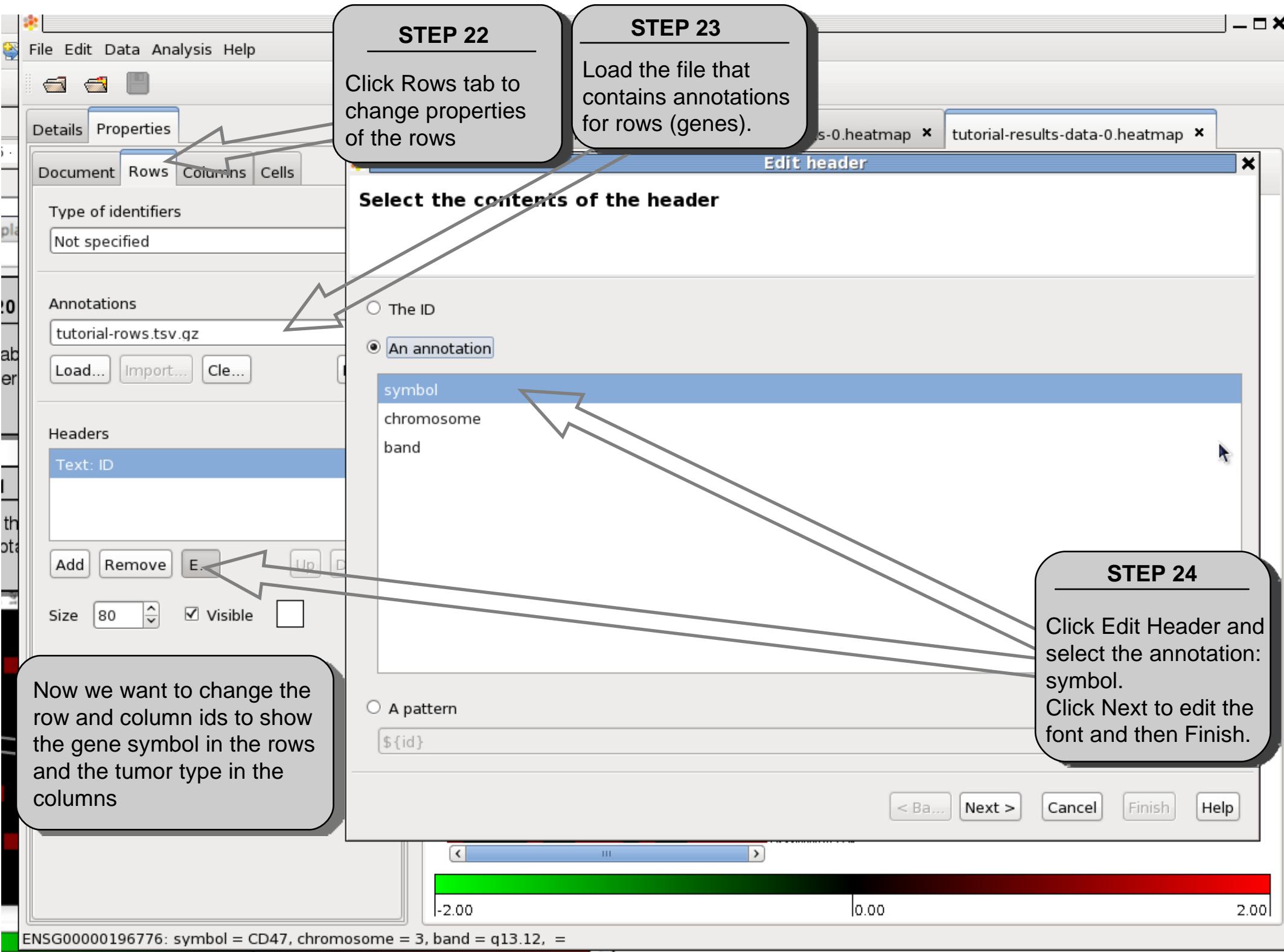
symbol
chromosome
band

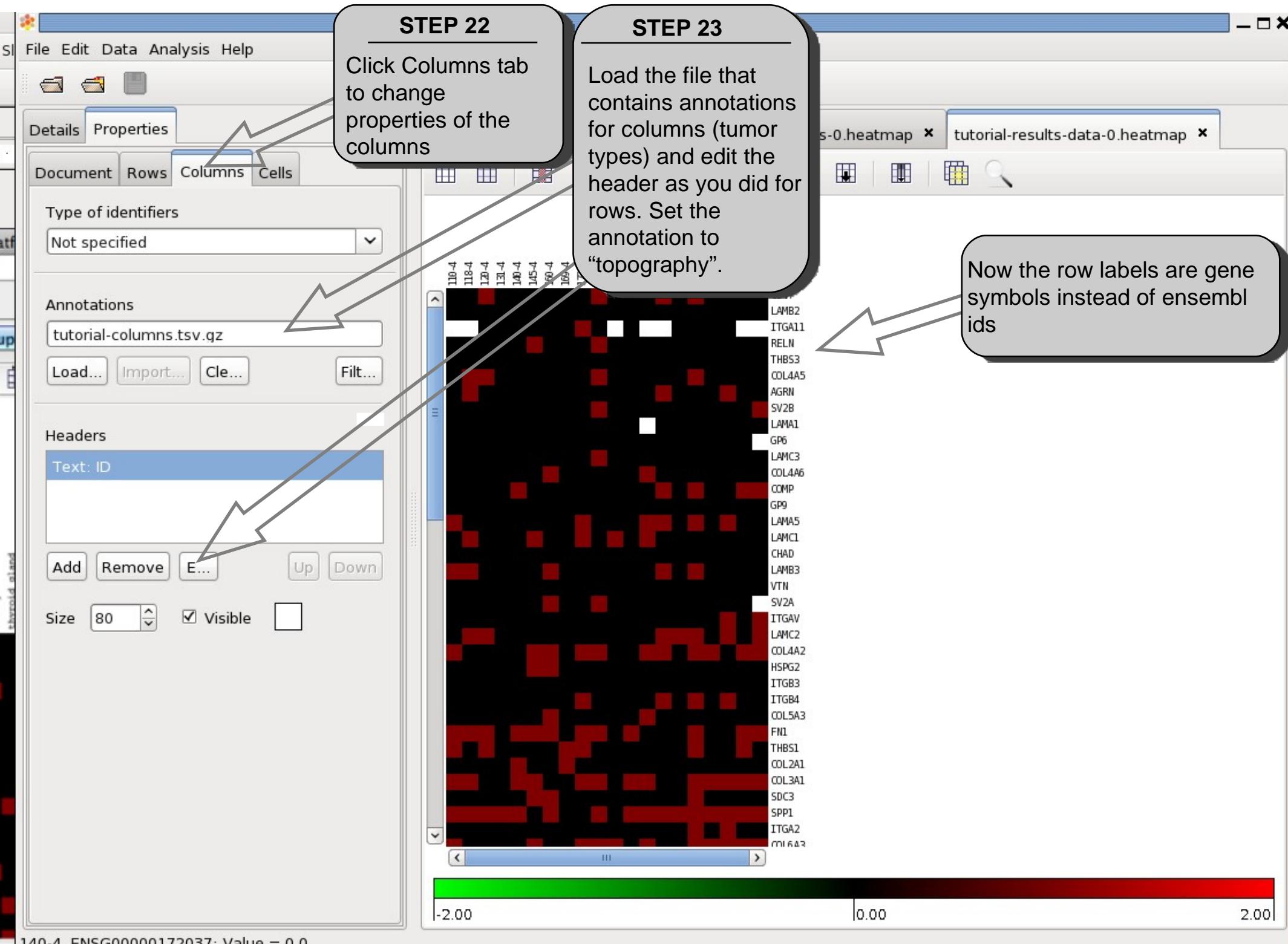
A pattern
\${id}

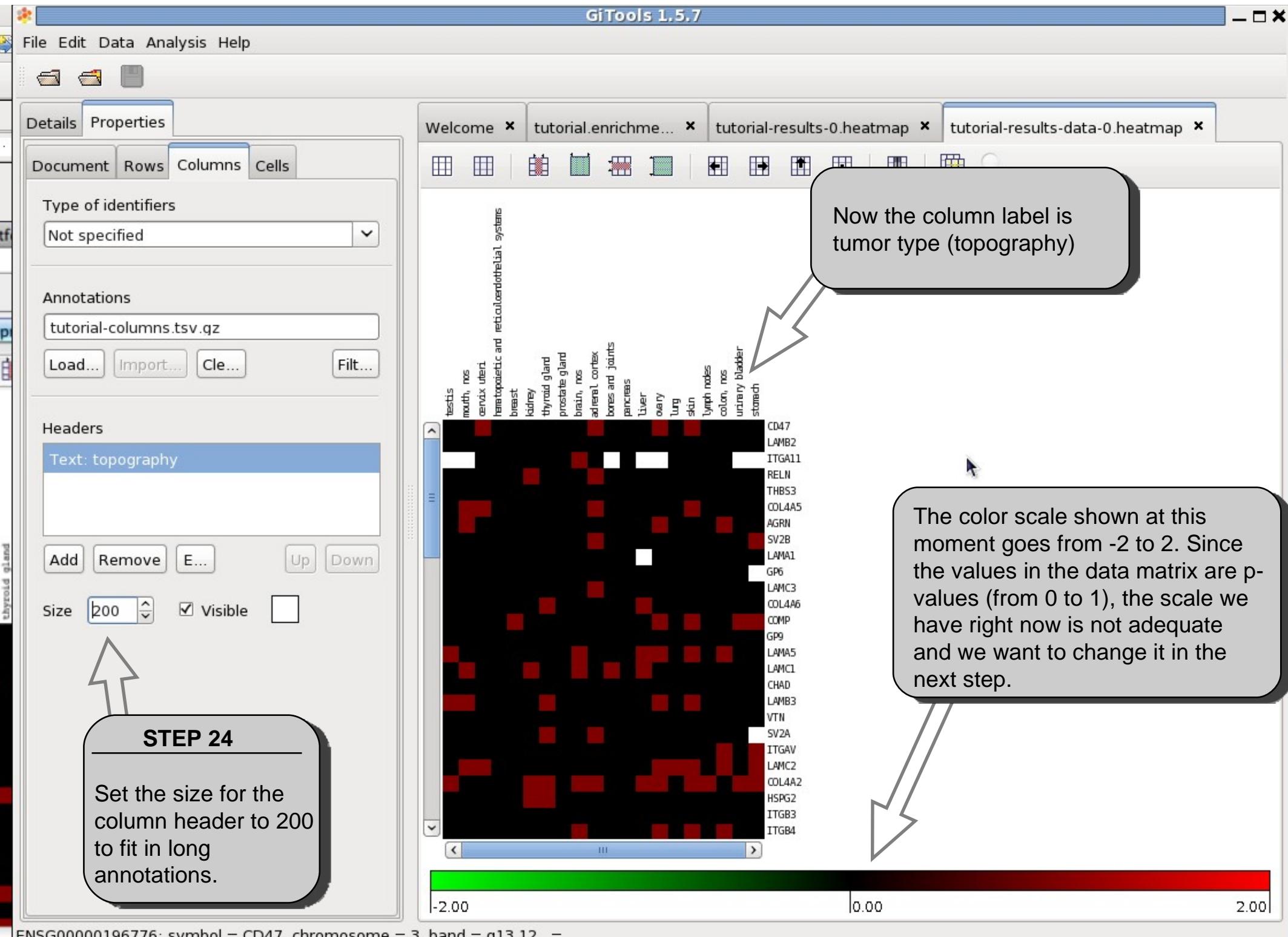
< Ba... **Next >** Cancel **Finish** Help

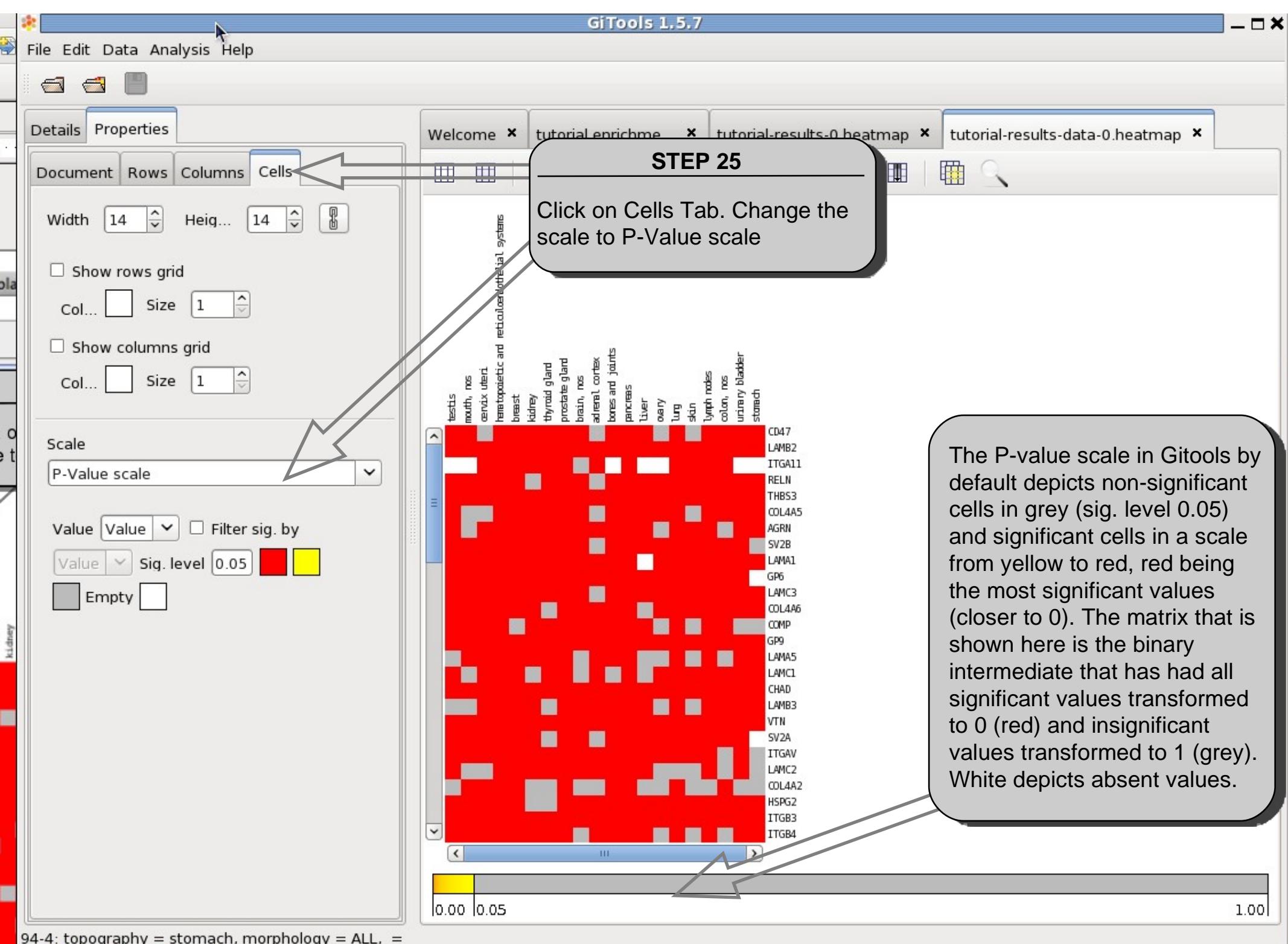
STEP 24
Click Edit Header and select the annotation: symbol.
Click Next to edit the font and then Finish.

ENSG00000196776: symbol = CD47, chromosome = 3, band = q13.12, =











THANKS FOR USING GITOOLS

<http://www.gitools.org>