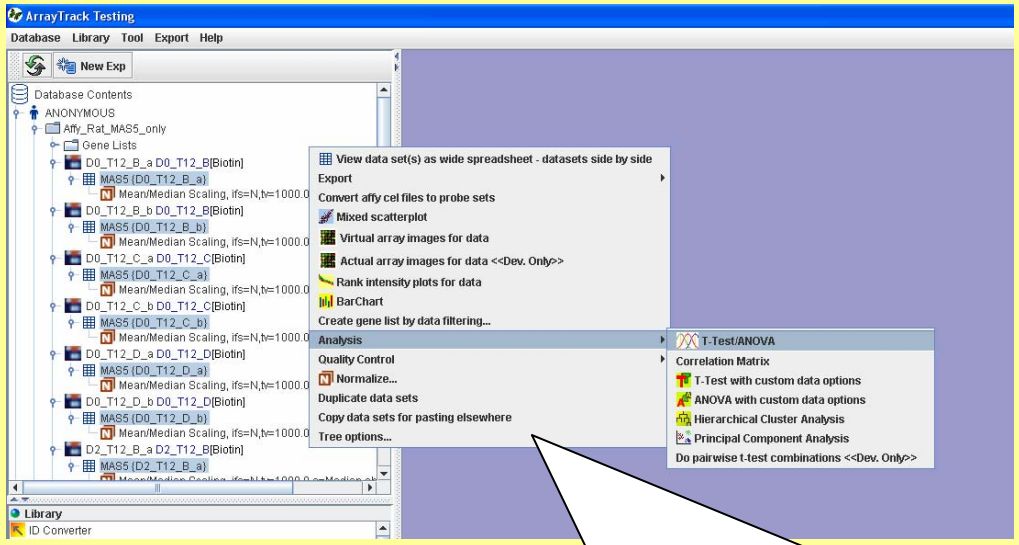
Array Track

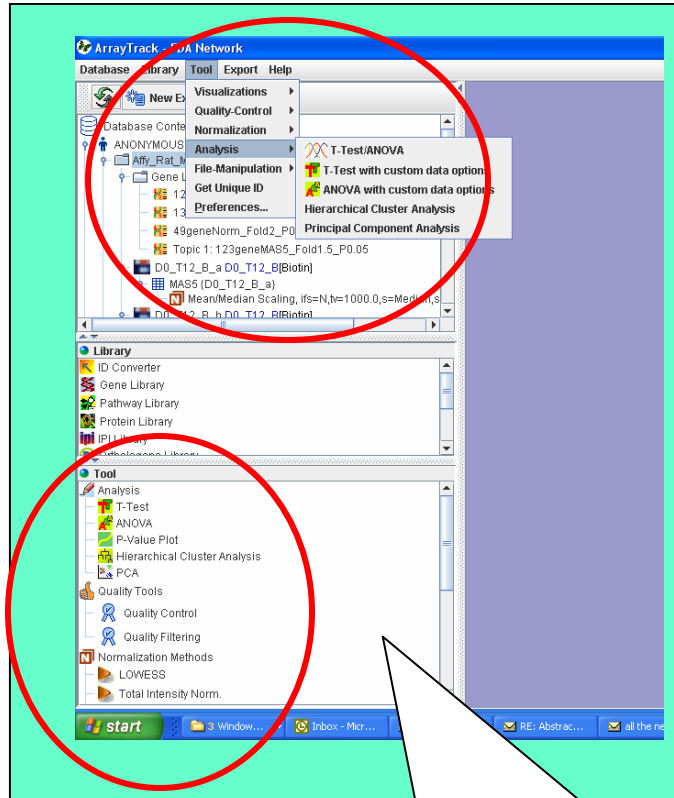
Tutorial 1:

Comparing two groups (e.g., treated vs control groups)

Useful Tips



Right-click on a (set of) selected dataset(s) under the Database Contents tree to access the applicable TOOL functions. ***This is one of the most frequently used functions.***



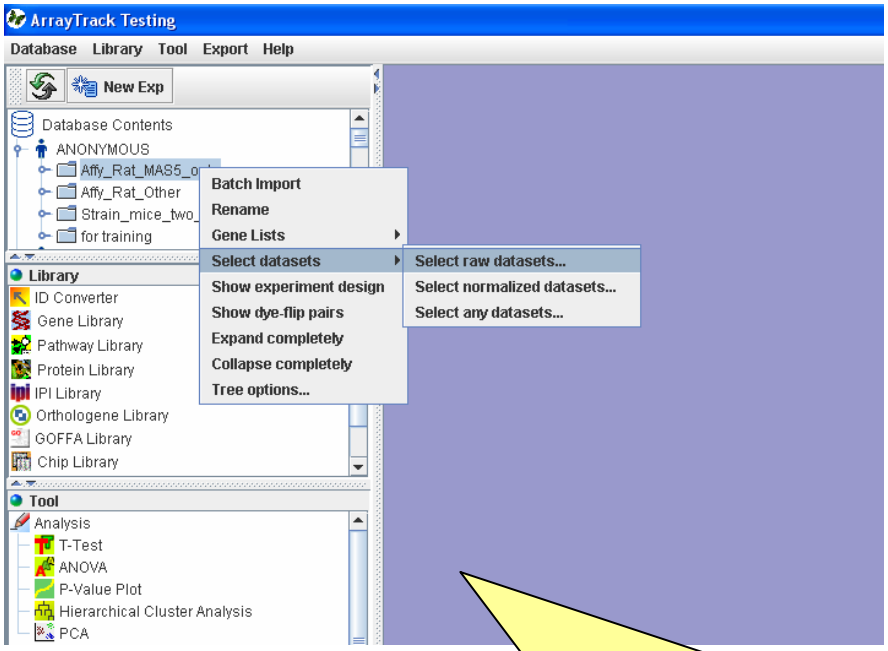
Many functions in ArrayTrack are accessible from multiple paths, for example, left-side window panels, pull down menus and right mouse-click options. (***Analyze the external datasets by accessing the tools from the left-window panel***)

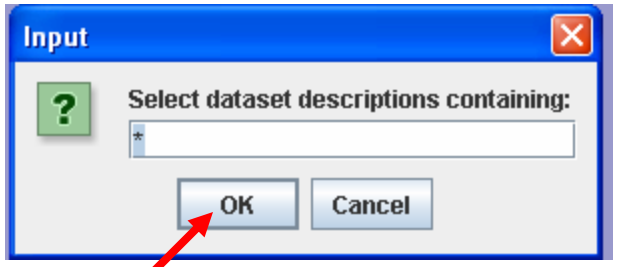
Bookmark the website for the convenience of accessing ArrayTrack (***Recommended***)

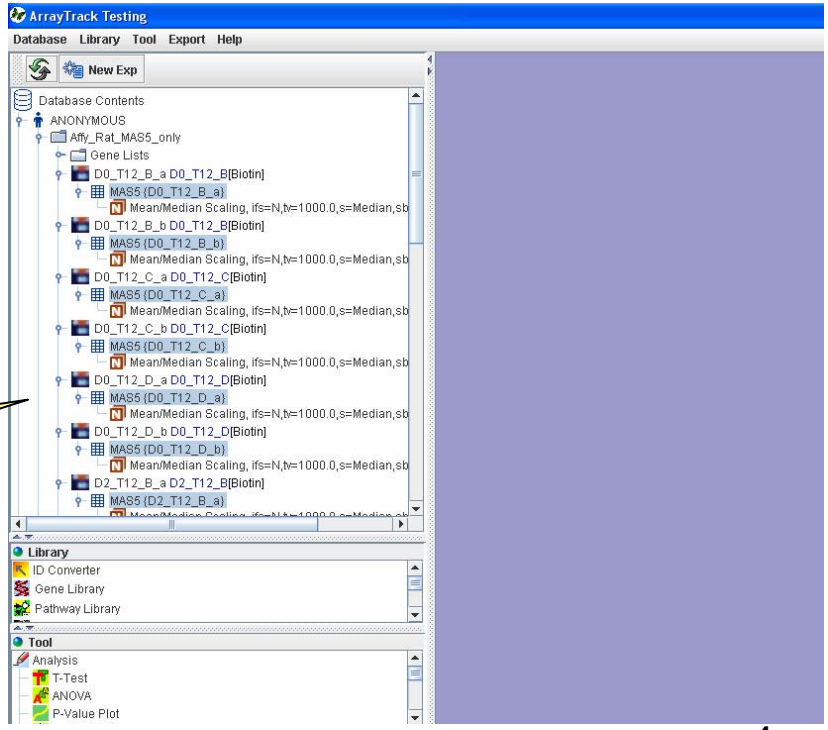
Other Tips

- Multiple sets of arrays can be selected by a combinations of mouse-click and SHIFT-CTRL keys.
- Most functions come with default parameter settings. If you do not know a better setting, use the default.
- All Spreadsheet viewers share similar functions, e.g. Copy/Paste of selected table content.
- You can find ArrayTrack websites by searching the keyword “ArrayTrack” in any web searching engine (e.g., Google)

Step 1 - Select “Dataset” for Analysis



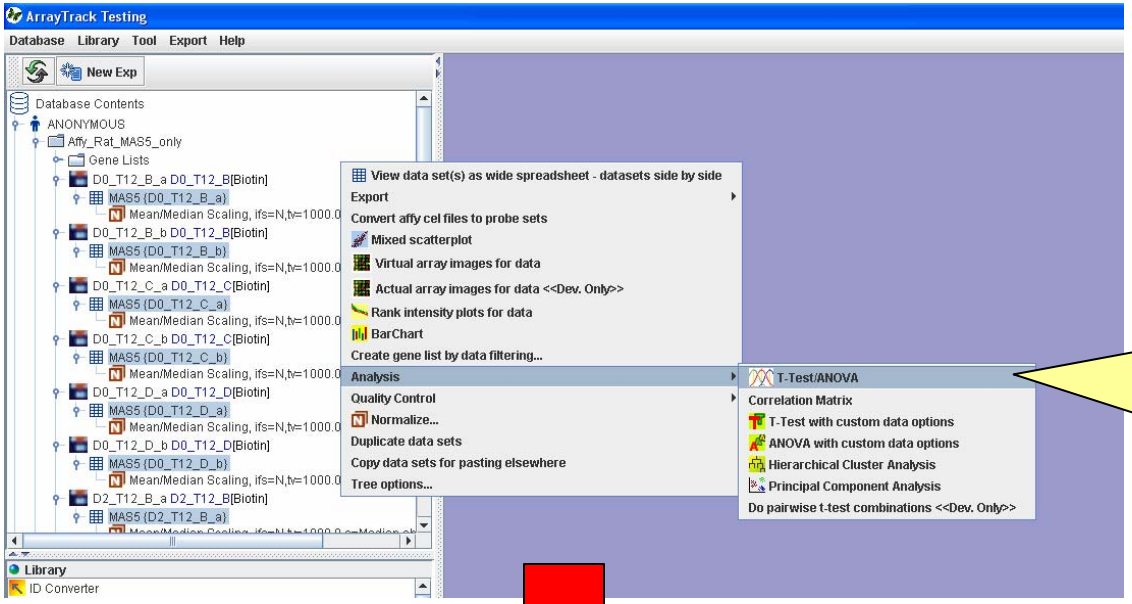




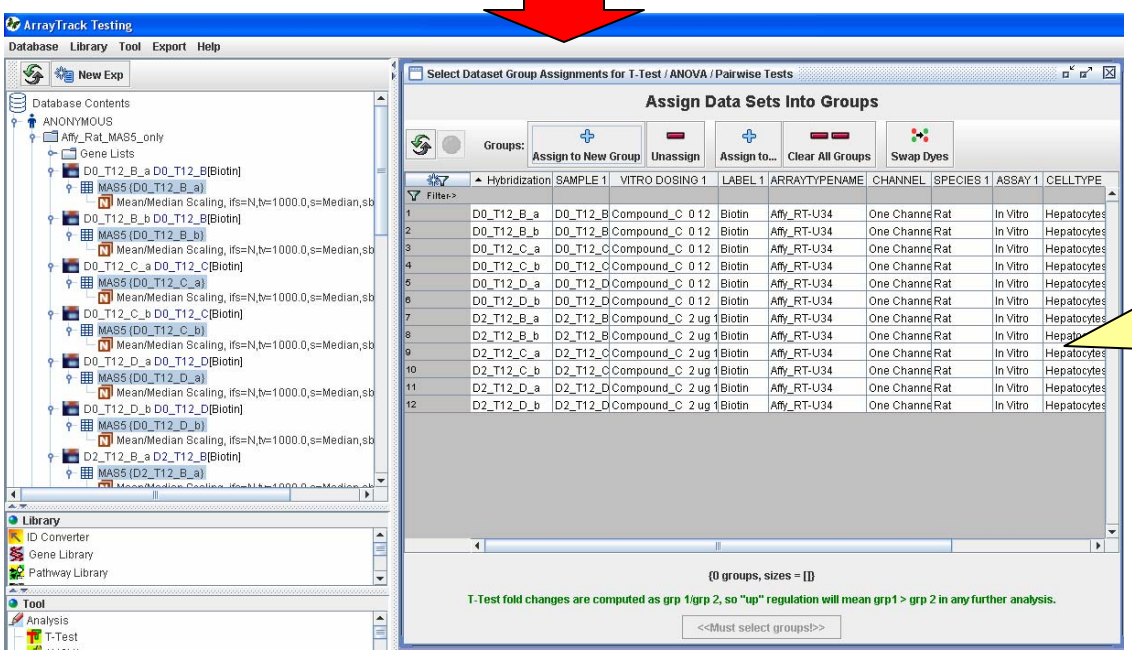
Right click the experiment “Affy_Rat_MAS5_Only” and select “select datasets” → “select raw dataset…”

- 12 arrays are highlighted.
- Move the mouse to any place of this panel (or window) and right click, the analysis options are shown in the next slide

Step 2 – Select an analysis method

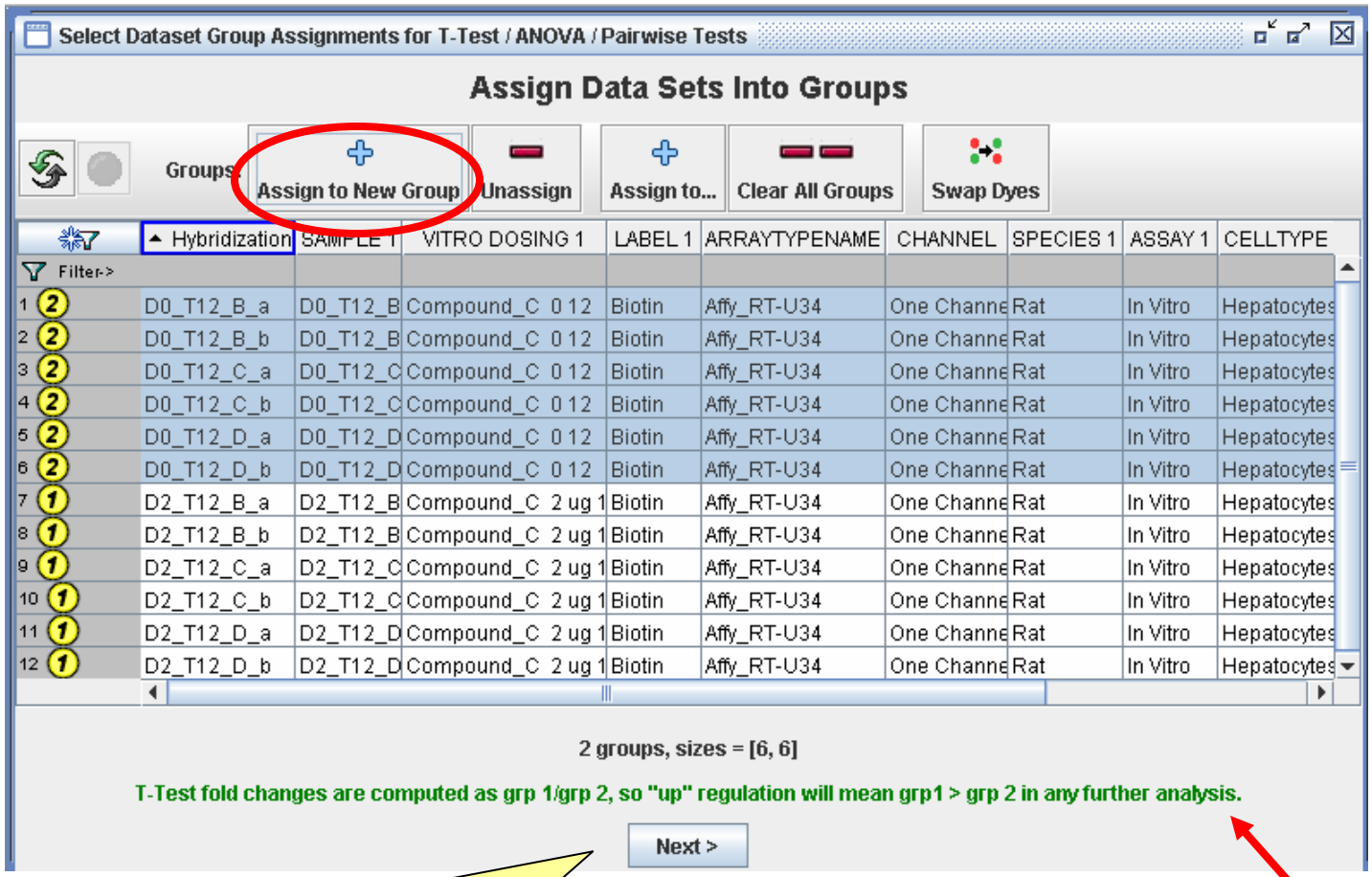


- Select “T-Test/ANOVA”
- Note: there are other analysis methods available in this menu.



A table is pop-up with the array on the row and the experimental description on the column.

Step 3 – Assign arrays into groups



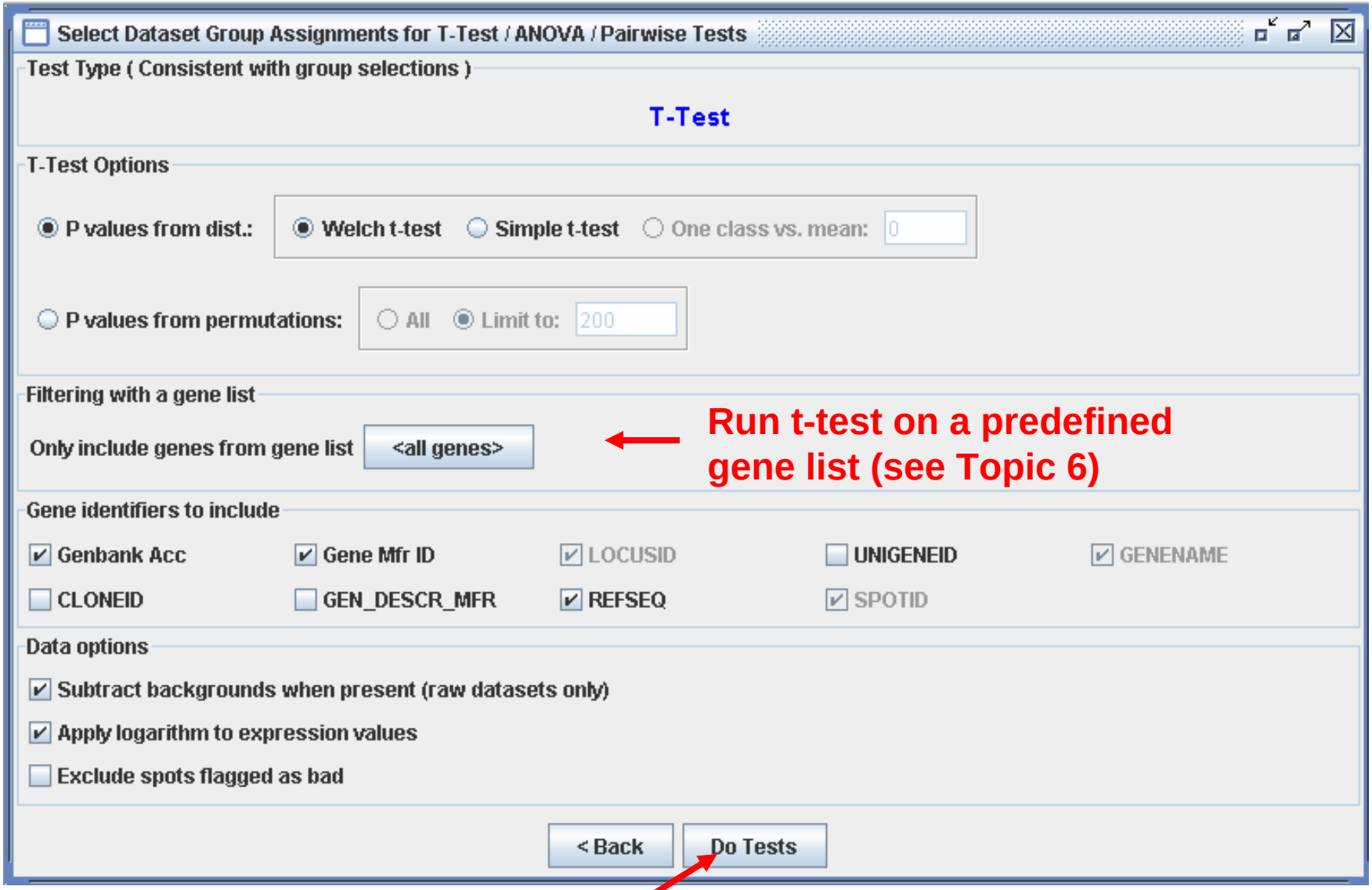
		Hybridization	SAMPLE 1	VITRO DOSING 1	LABEL 1	ARRAYTYPENAME	CHANNEL	SPECIES 1	ASSAY 1	CELLTYPE
1	2	D0_T12_B_a	D0_T12_B	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
2	2	D0_T12_B_b	D0_T12_B	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
3	2	D0_T12_C_a	D0_T12_C	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
4	2	D0_T12_C_b	D0_T12_C	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
5	2	D0_T12_D_a	D0_T12_D	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
6	2	D0_T12_D_b	D0_T12_D	Compound_C 0 12	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
7	1	D2_T12_B_a	D2_T12_B	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
8	1	D2_T12_B_b	D2_T12_B	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
9	1	D2_T12_C_a	D2_T12_C	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
10	1	D2_T12_C_b	D2_T12_C	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
11	1	D2_T12_D_a	D2_T12_D	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes
12	1	D2_T12_D_b	D2_T12_D	Compound_C 2 ug 1	Biotin	Affy_RT-U34	One Channe	Rat	In Vitro	Hepatocytes

There are total 12 arrays. The arrays whose name starting with D2 are the treated sample while those starting with D0 are the controls

- Select the arrays starting with D0 (treated samples, from 7 to 12) and click “Assign to New Group”
- Repeat the above process for the 1st 6 arrays

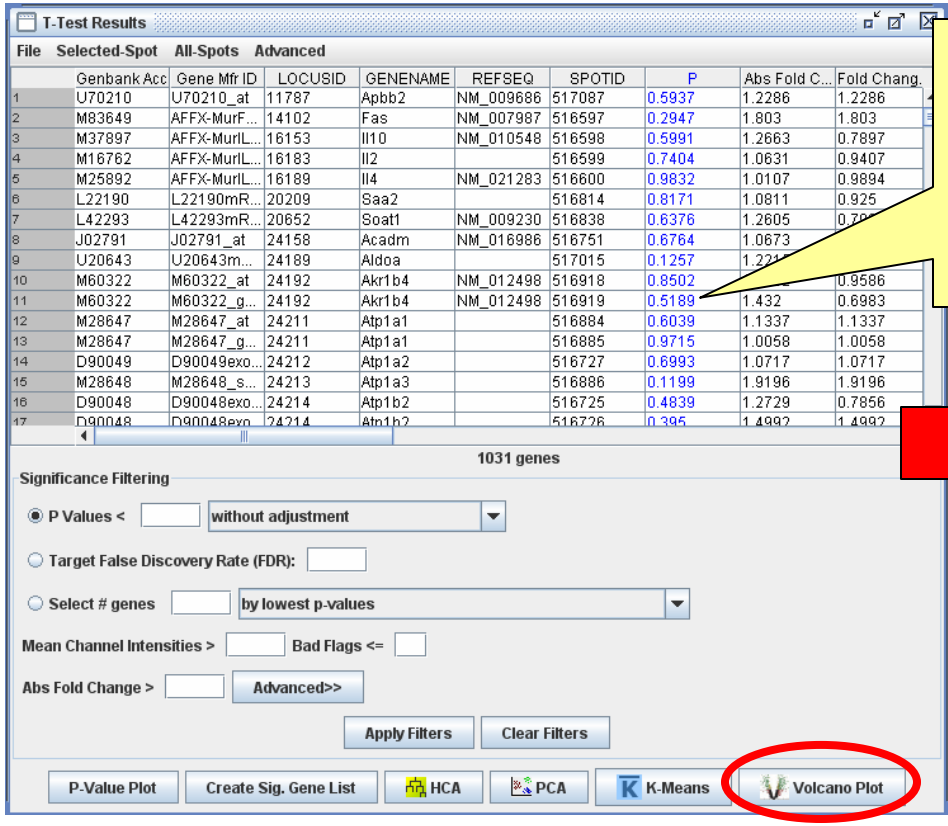
Pay attention on this statement and click “next”

Step 4 – Run "T-Test" with different options

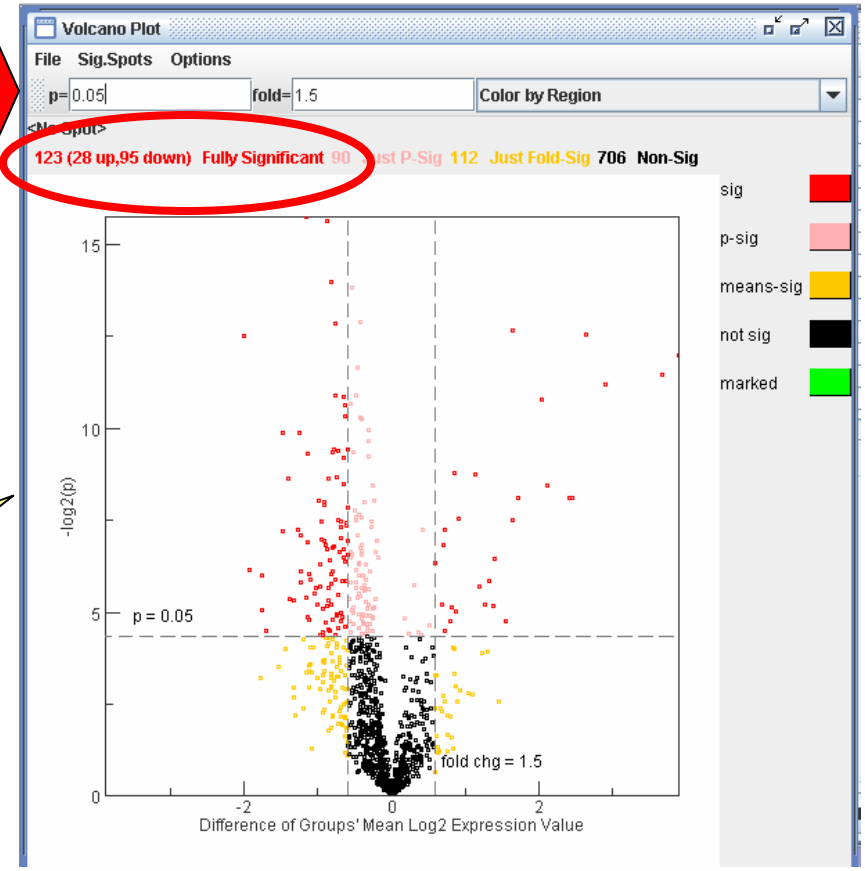


Select "Do Test" if you don't know which option should be used.

Step 5 – Determine differentially expressed genes

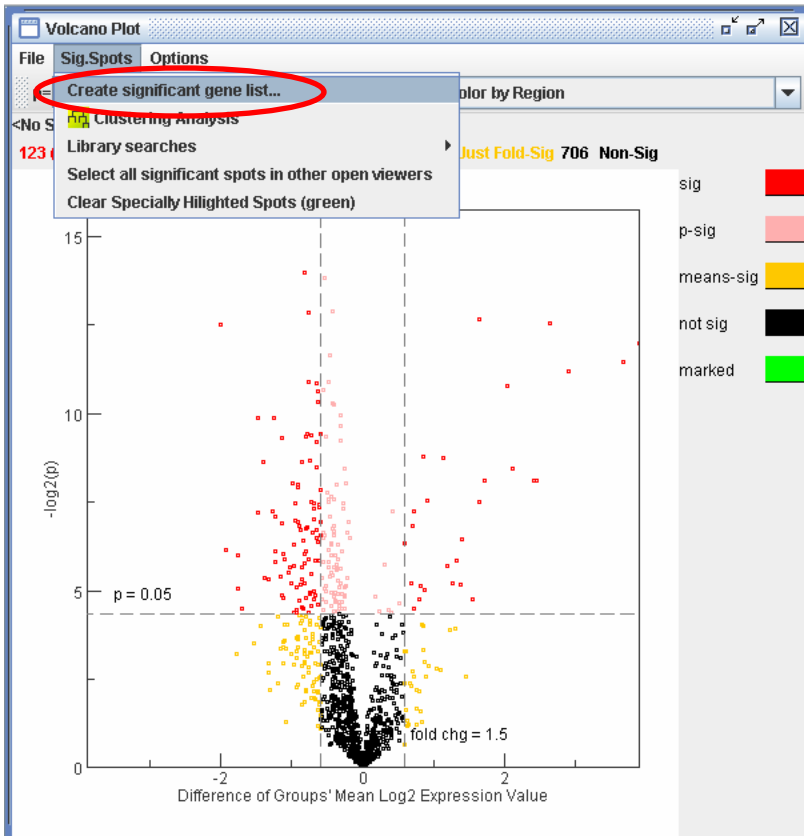


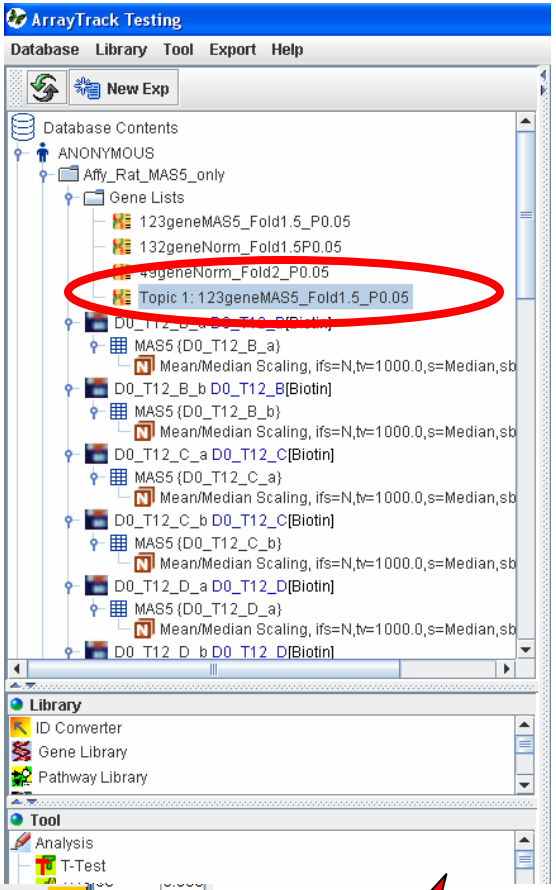
- T-test results with p-value is highlighted
- Many options are available under the table. We recommend to use “Volcano Plot”.

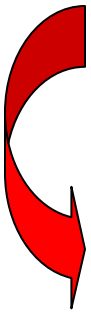


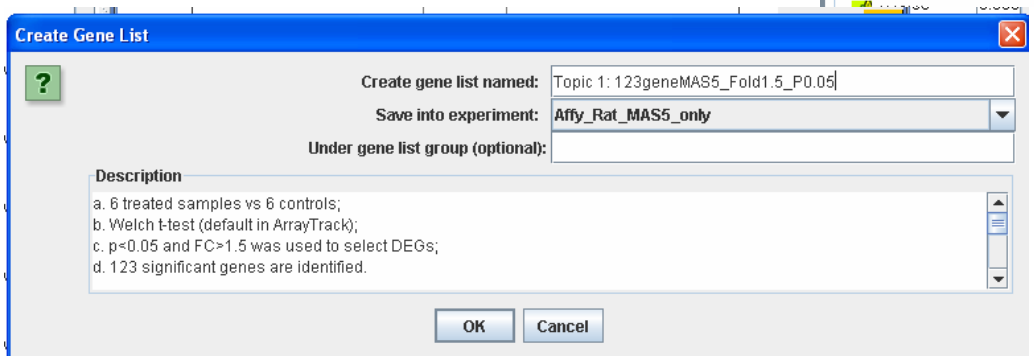
- Volcano plot results
- 123 genes have p<0.05 and Fold Change >1.5

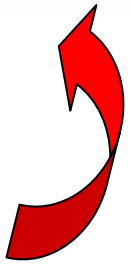
Step 6 – Save the significant gene list (recommended)











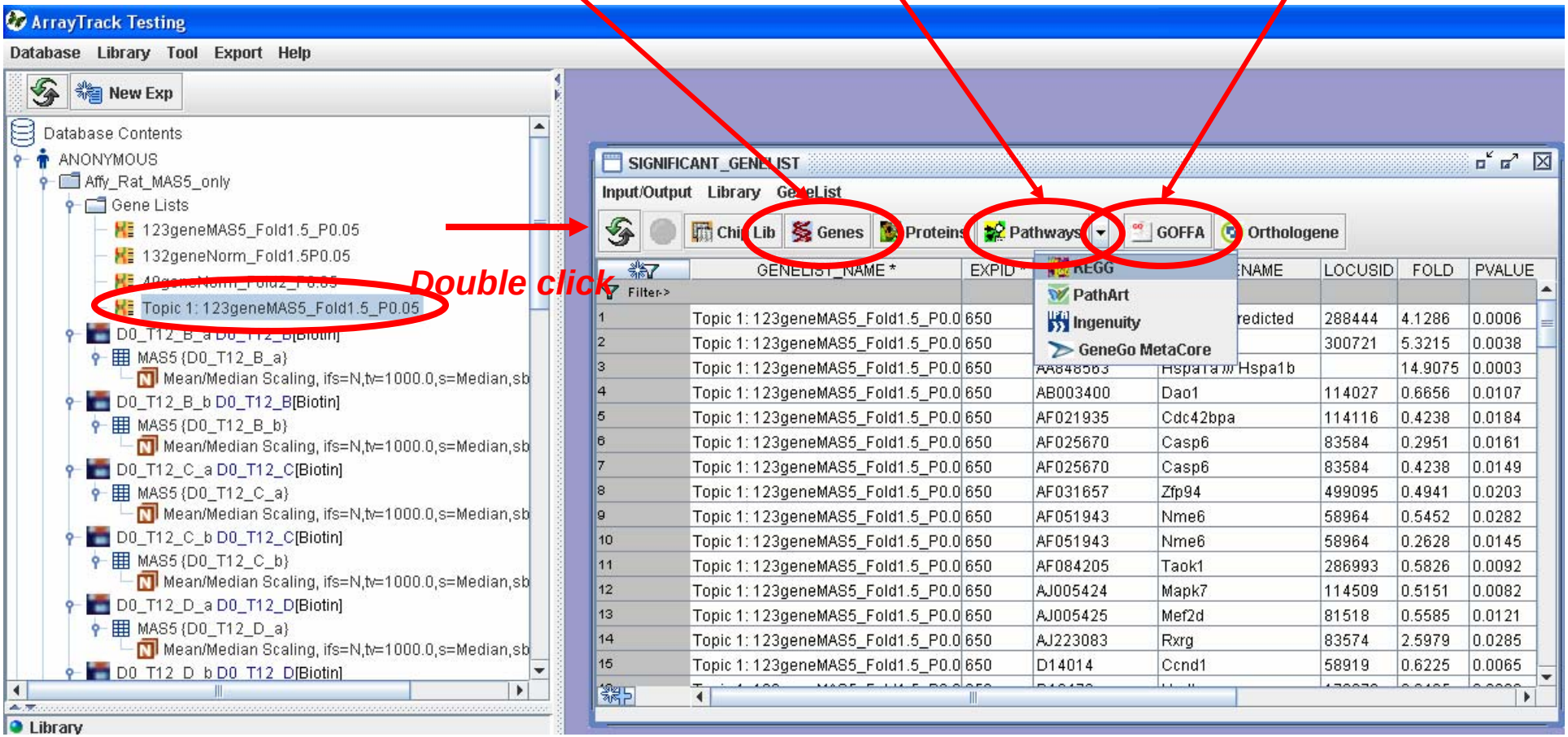
Step 7 – Biological interpretation using ArrayTrack pathway, GO and other tools

Clicking the three buttons in red circle will direct you to step 8, 9, 10 correspondingly, see the next three slides

Individual gene annotation and analysis

Pathway analysis

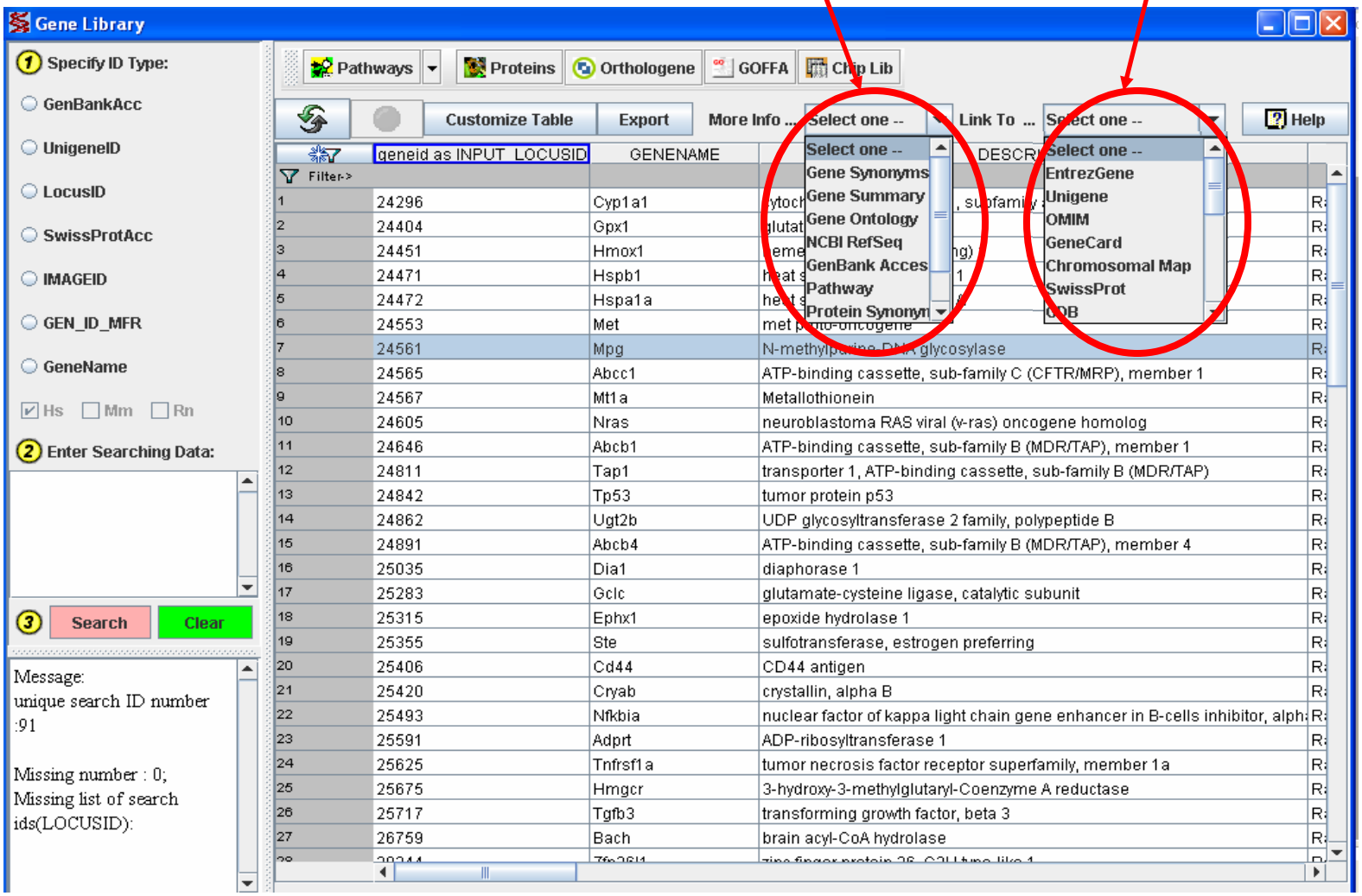
GO-based functional analysis



Step 8 – Individual gene annotation and analysis using GeneLib

Summary info for the highlighted gene

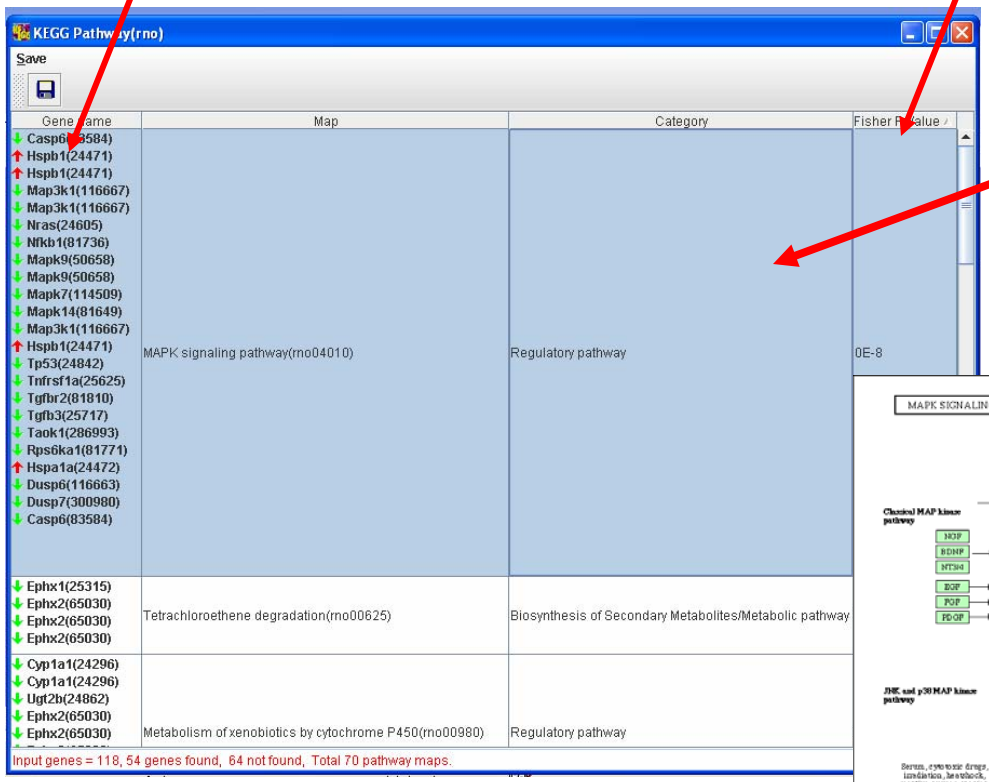
Link to other pub databases for the highlighted gene



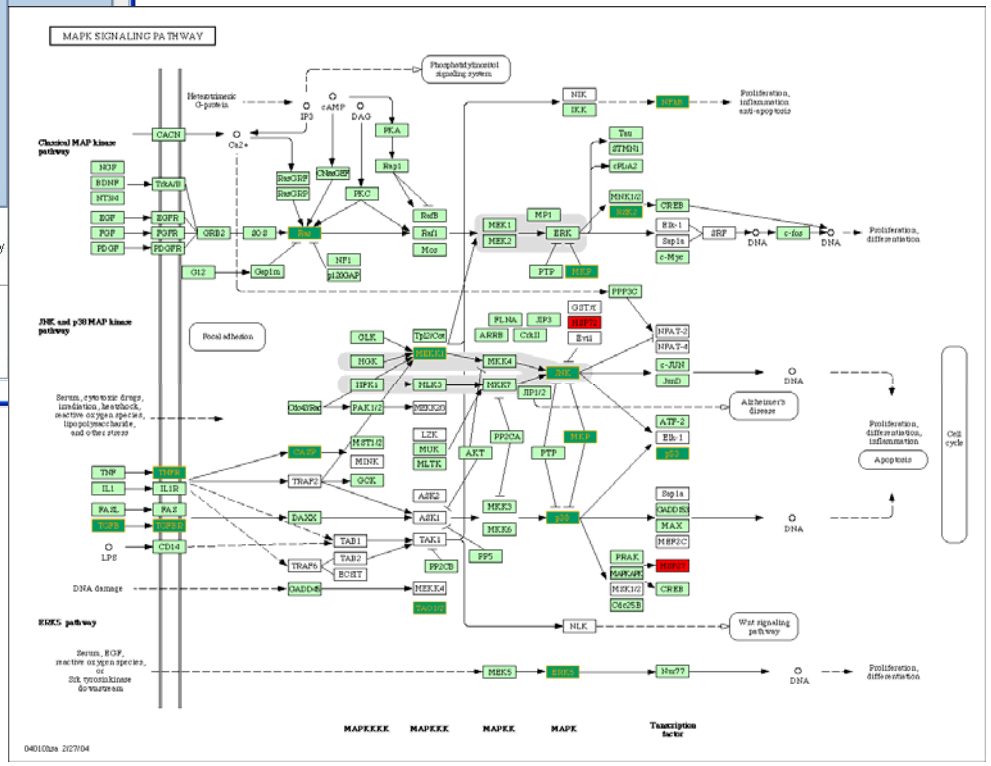
Step 9 – Pathway analysis using KEGG

the up- and down-regulated genes
that involves the same pathways

Statistical significance

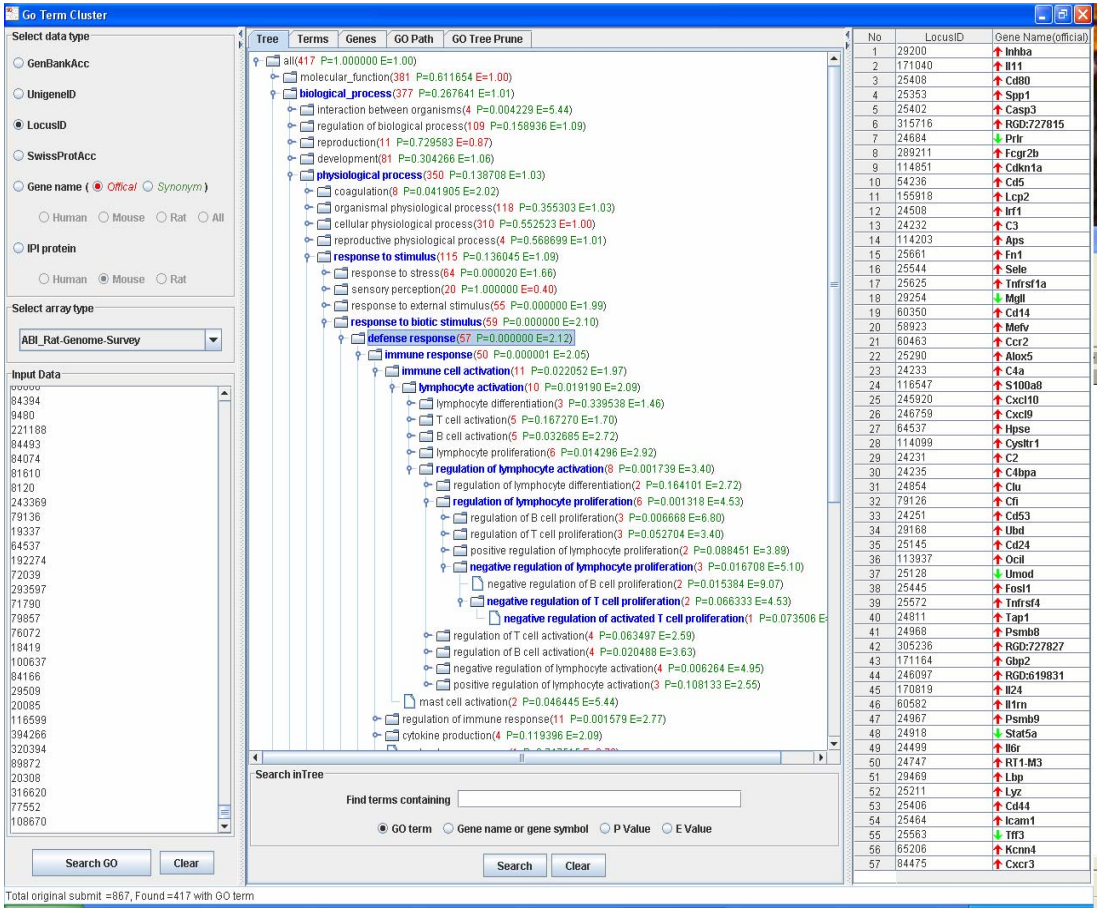


Double click the pathway



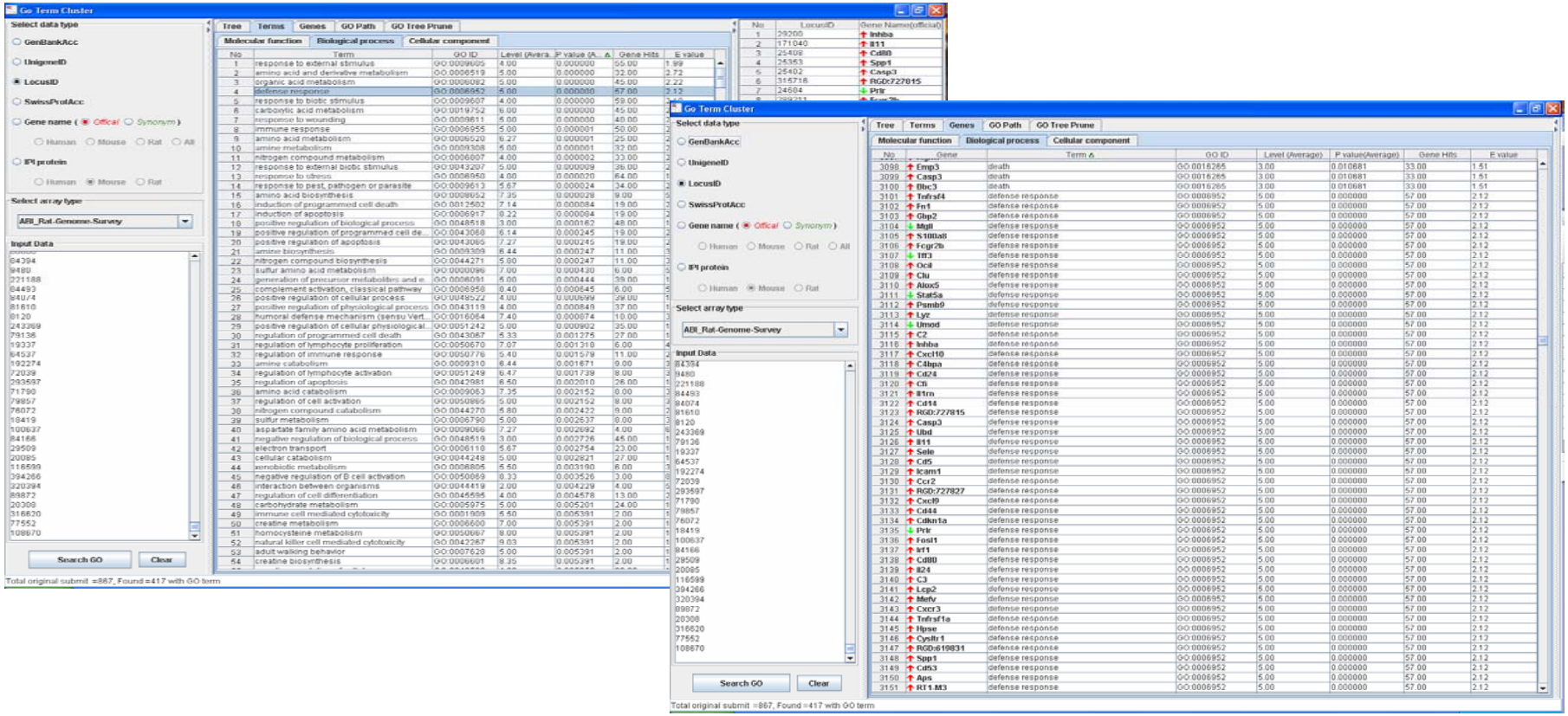
MKP	Down-regulation
HSP72	Up-regulation

Step 10 – GO-based analysis using GOFFA



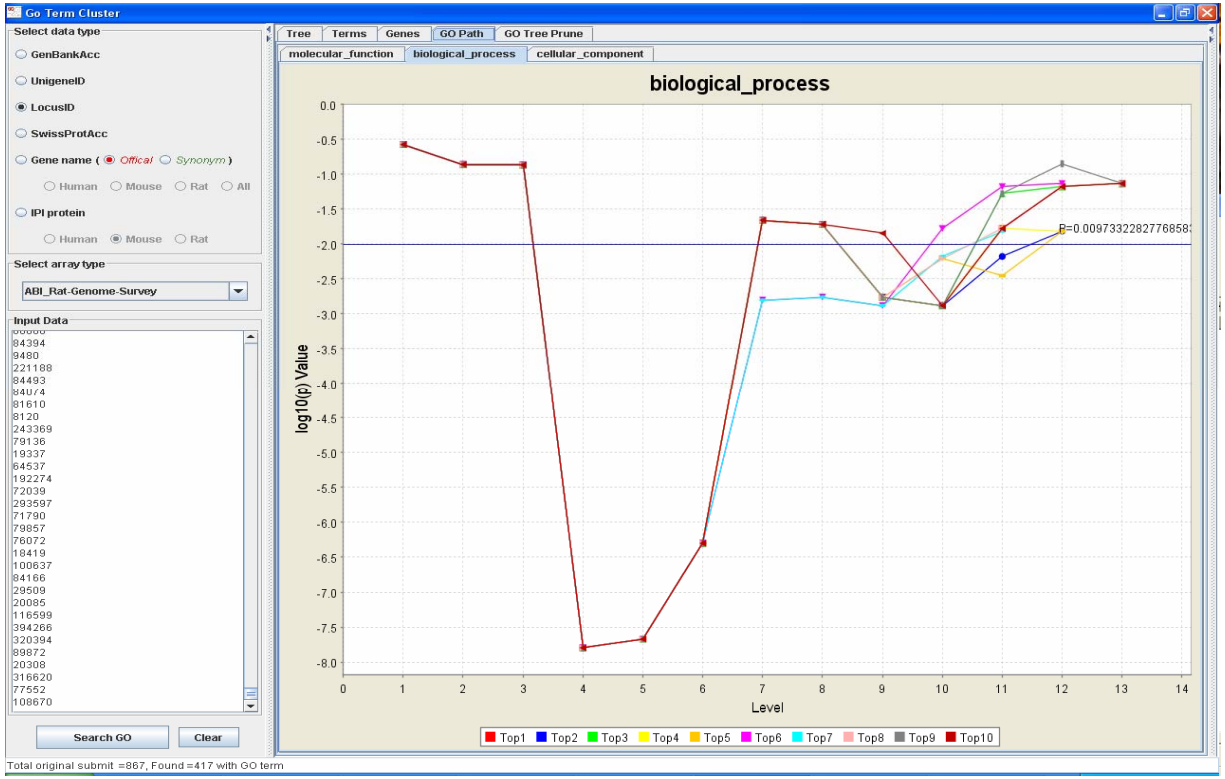
Tree Window – This is the default view of GOFFA, which enables the hierarchical display of the GO terms in a tree-like format; p- and E-values as well as the number of genes are also displayed for each GO term. E-values >1 are shown in green and those <1 in red, respectively denoting greater or lesser prevalence of the GO term in DEG's rather than in the overall experimental platform. The user can query the tree by GO term, gene name/symbol, p-value and E-value with functions below the view. The query-matched GO terms are highlighted as blue.

Step 10 – GO-based analysis using GOFFA (cont.)



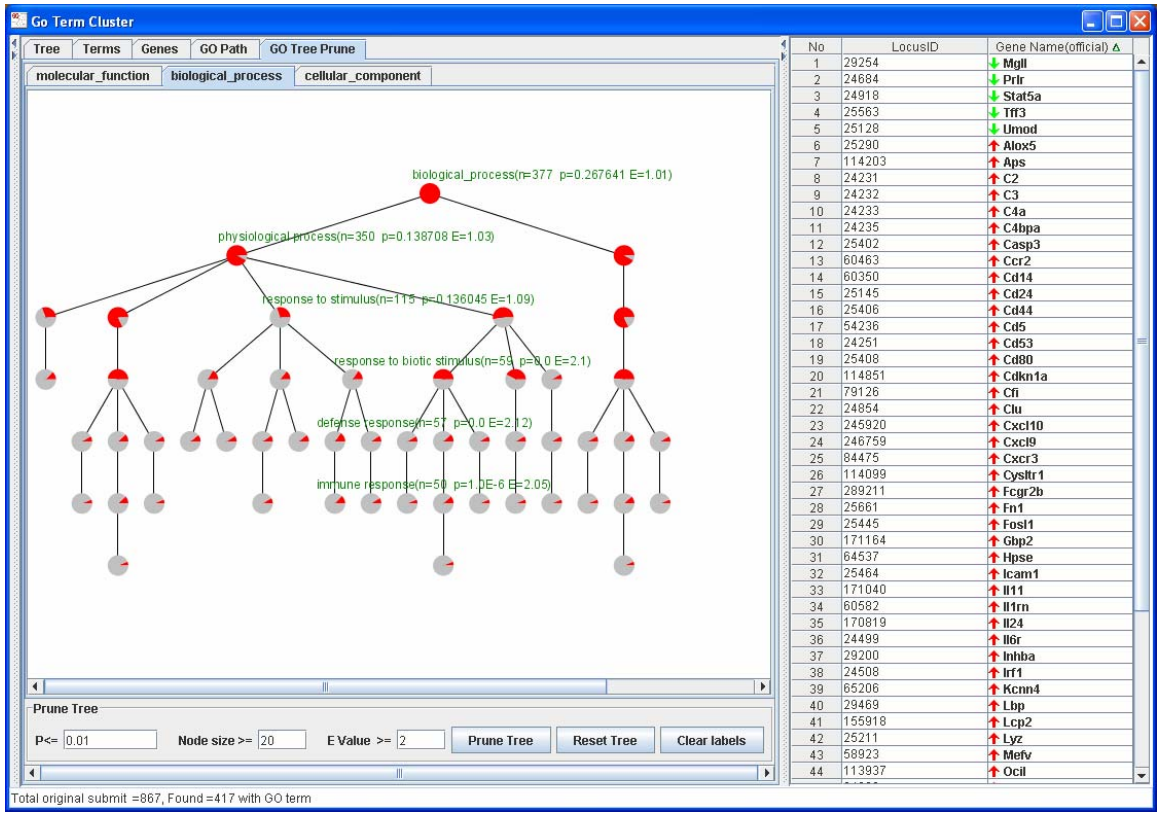
Terms and Genes Windows – The Terms Window (A) and Genes Window (B) summarize the findings associated with GO terms and genes respectively in a table format along with various statistical parameters (e.g., p- and E-values). Each View contains three tabs corresponding to three categories of GO (molecular functions, biological processes and cellular components). The table can be sorted in every column by clicking on the column header. Sorting on multiple columns is also supported (pressing Ctrl key while clicking on the second column header for sorting). Both copy/paste and export functions are available to transfer data to external software.

Step 10 – GO-based analysis using GOFFA (cont.)



GO Path – GO Path is sorted by descending statistical significance based on an inverse Chi-Squared test and the GOFFA Tree Paths (i.e., linked GO terms) that are displayed from high to low at each hierarchical level. GO Path plots the top ten paths with solid circles representing the GO terms on the path. The number in X-axis represents the hierarchical level to which the GO term belongs and the Y-axis (log p) indicates the statistical significance of the term. A colored legend for the top 10 paths is located beneath the plot. Clicking any circle in a path in the plot or its corresponding color key launches a Tree View with the selected path highlighted in blue. Other features are also available from a popup menu by right clicking the plot, including zoom in/out, export figure, etc.

Step 10 – GO-based analysis using GOFFA (cont.)



GO TreePrune - This function allows the user to filter out nodes and thus reduce the complexity of a tree by specifying the p- and E-value as well as the user-defined number of genes at the end node. A GO term is represented by a sectored pie, where the red sector shows the percentage of DEGs associated with the term. The individual genes associated with each term are displayed in the right panel by single clicking the term. The annotation of a term can be turned on or off by double clicking the term. Each term (red circle) is movable by mouse dragging, which is convenient when working on a dense tree or with many annotations. The tree diagram can be zoomed or moved by dragging with the right or left mouse button held down.