

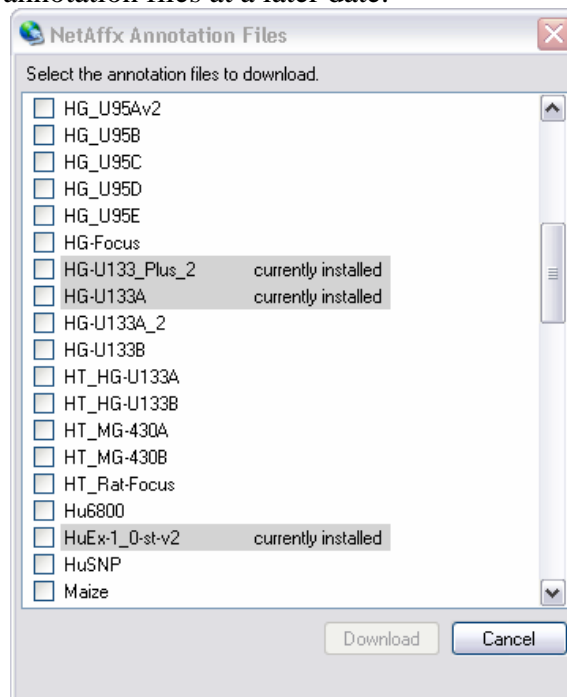
## How to Export Signal Values with Annotation Information

The purpose of the Expression Console™ software application is to enable probe set summarization and initial data quality examination for Affymetrix gene expression arrays. To aid in the analysis of expression data, a probe level summarization file can be generated by combining annotation information (contained in comma-separated files (CSV files)) with the signal values into a single tab-delimited file. This probe level summarization file can then be further analyzed using software applications from Affymetrix GeneChip Compatible partners to identify differentially expressed genes (<http://www.affymetrix.com/products/software/compatible/index.affx>).

Merging annotation information into a probe set results table is a one step process after a short setup procedure. The setup procedure consists of two steps: Step 1, download the annotation file corresponding to the array type being analyzed; Step 2, create an annotation merge file by selecting the annotation information of interest. To merge the annotations with the probe set results, one simply opens a study containing the CHP files of interest and selects **Export->Export Probe Set Results (pivot table) with Annotations to TXT** and uses the dialog box to select the appropriate annotation merge file.

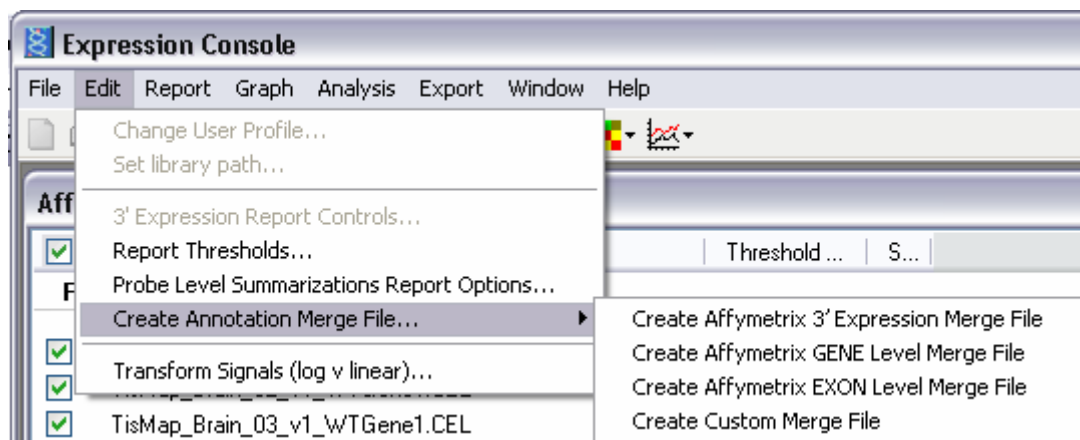
### Set-up

1. Download the necessary annotation files for the array type if they are not already in the library file directory.
  - a. Go to the **File** menu and select **Download Annotation Files**.
  - b. Enter your NetAffx email address and password. (Note: If you have not registered previously, you will first need to register at <https://www.affymetrix.com/site/terms.affx?buttons=on&dest=register>)
  - c. In the NetAffx Annotation File window, check all probe array types that you will be analyzing now or in the future and click on the **Download** button. You can always come back and add more annotation files at a later date.



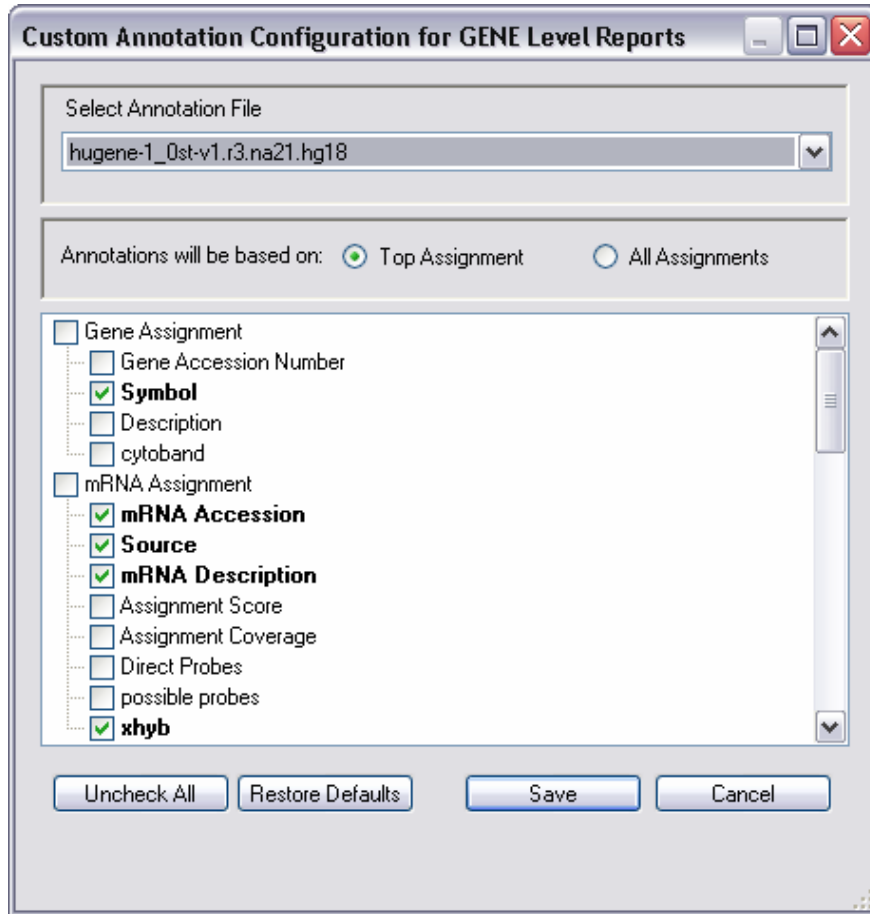
## How To Export Signal Values With Annotation

2. Create an annotation merge file containing the fields from the CSV file you want to have available in the exported probe set results file.
  - a. From the **Edit** menu, select **Create Annotation Merge File** and then select one of the types of annotation merge file to create.



- i. For 3' Expression arrays, select “**Create Affymetrix 3' Expression Merge File**”
- ii. For Gene or transcript level analysis from the Exon and Gene Arrays, select “**Create Affymetrix Gene Level Merge File**”.
- iii. For Exon level analysis, select “**Create Affymetrix Exon Level Merge File**”.
- iv. To use your own comma-separated annotation file, select “**Create Custom Merge File**”. (Note: the first column of the custom CSV file must contain the probe set identifiers to be used to match-up the records during the merge)

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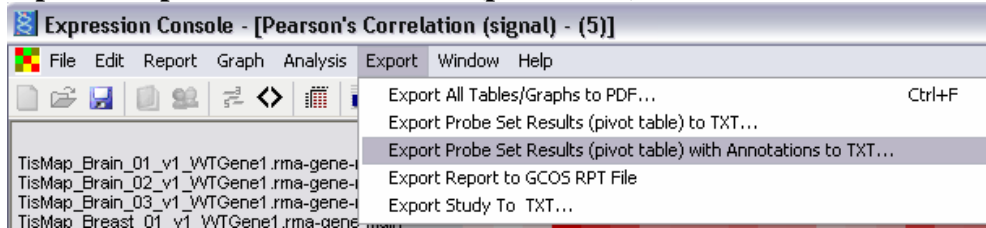



- b. Select the annotation file from the drop-down list at the top of the dialog box.
- c. Select the level of the annotations to be used in the merge file. (This is only supported for Affymetrix Supplied Annotation files).
  - i. Top Assignment: Annotations will be based on the **single** transcript to which the probe set best aligns. Selecting this option results in a single value for the annotation fields at the expense of information.
  - ii. All assignments: The annotation will be based on all of the transcripts contained in the annotation file.
- d. Select the annotation fields of interest
  - i. Bold indicates the default selections (This is only supported for Affymetrix Supplied Annotation files).
  - ii. The selected fields will each appear in their own column in the probe set summarization results table.
- e. Select **Save** to save the annotation merge file.
- f. Enter a name for the annotation merge file when prompted. The name of the CSV file used to create the merge file will automatically be appended to the name you enter.
- g. Depending on the size of the CSV file and the number of probe sets in the file several minutes may be required for processing. Once processing is complete the newly created annotation merge file is available by selecting **Export->Export Probe Set Results (pivot table) with Annotations to TXT**.

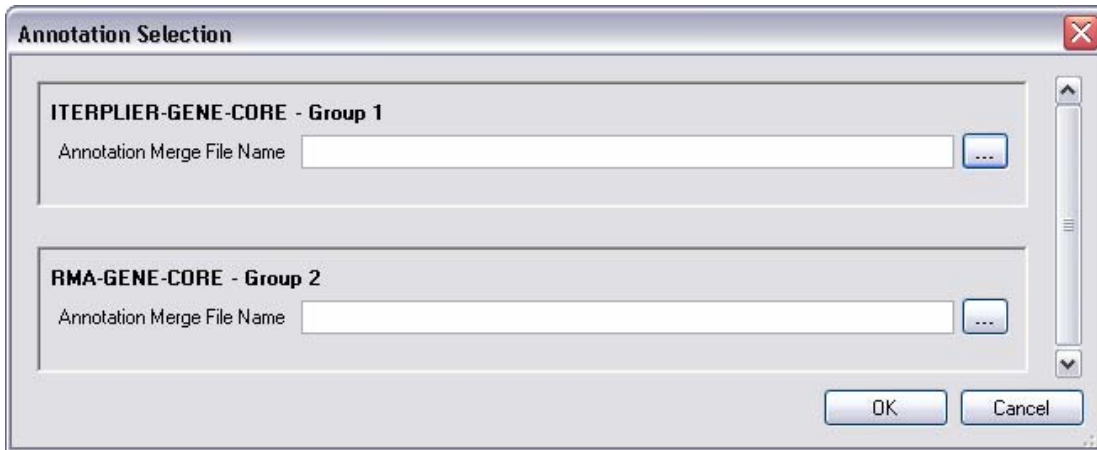
## Merging Annotation

Note: This functionality is only enabled if a study containing CHP files is open.

1. Select **Export->Export Probe Set Results (pivot table) with Annotations to TXT.**



2. Browse to select the Annotation Merge file to use for each group of CHP files by selecting the  button.



3. Select the output folder and enter a name for the file. If files from more than one group are selected the group number will be appended to the name entered.
4. Select OK