

MeV – Affymetrix Loading and File Format

[MAS 5.0 and 5.1 text file creation]

For each array that you want to load into MeV, do the following in MAS:

- a Open the corresponding .chp file.
- b Select: File -> Save As (Illustration 1).

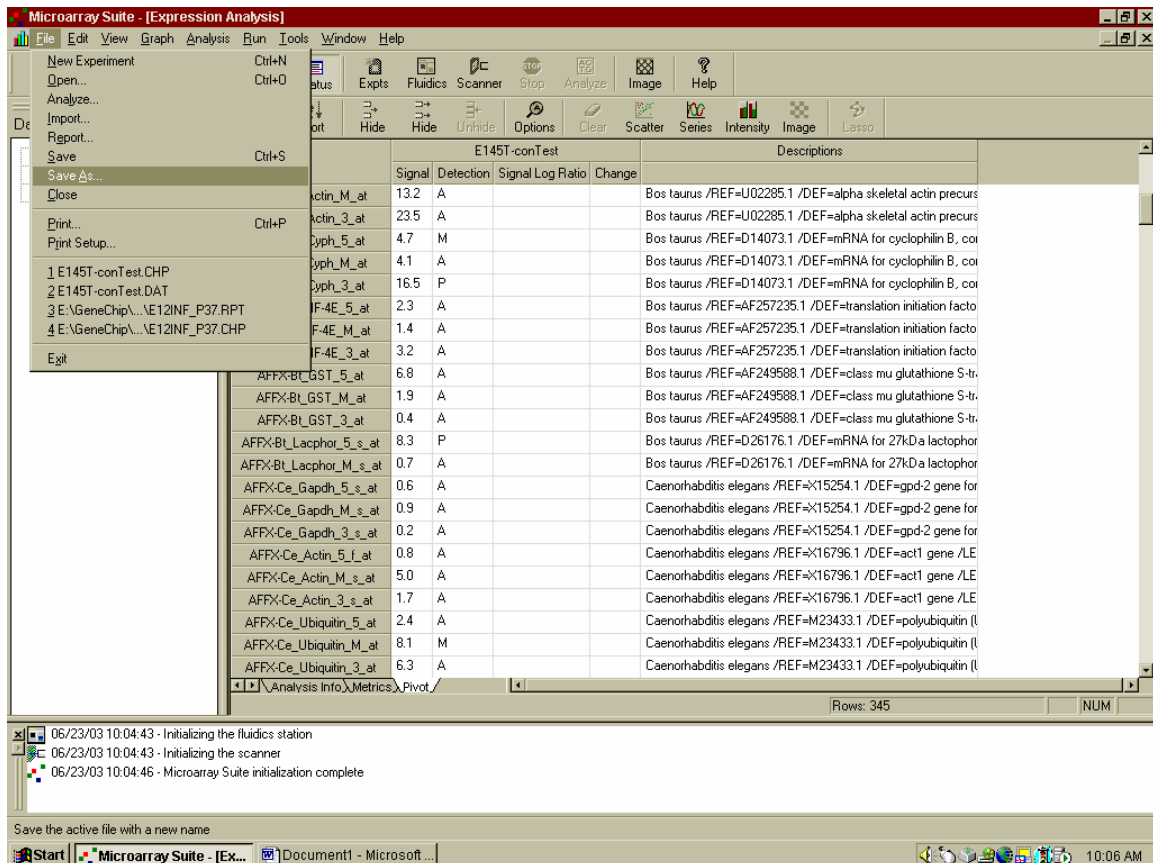


Illustration 1 Saving array data as a text file

- c Give the .txt file a name that describes the sample and differentiates it from other arrays that you will be loading.
- d You can check to see that the file was saved correctly by opening it in an editor such as Notepad. It should appear roughly as in figure 2.

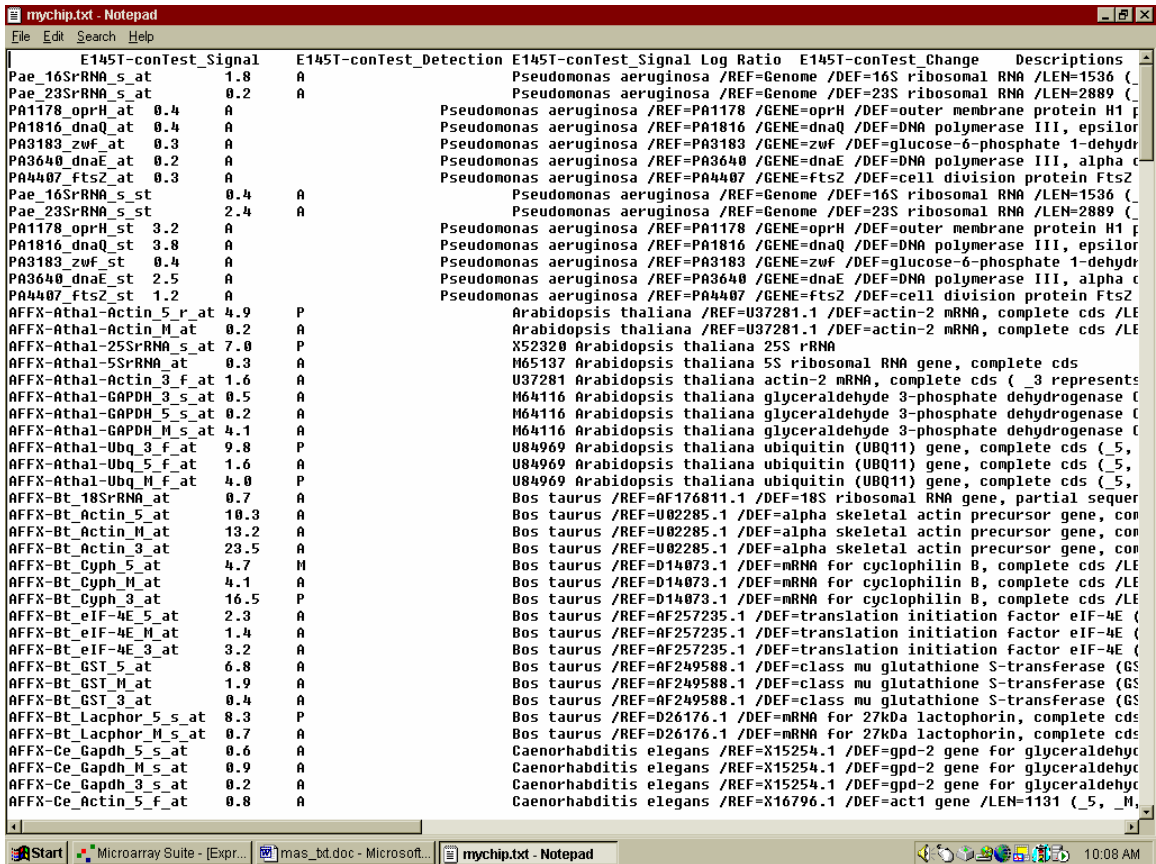


Illustration 2 Resulting text file that will be loaded into MeV

File Format:

Tab delimited file text file.

Affy probeset Identifier Signal Detection call Gene annotation