

## DESCRIPTION OF AFFYMETRIX FILE TYPES

- .dat file**      This is the image file of the scanned array corresponding to the sample indicated, and can be considered as “raw hybridization data”. This file can only be analyzed by Affymetrix software. No processing of data is done on this file, and no scaling factors or normalization is embedded.
- .chp file**      This contains the processed and normalized analysis of the image file. This provides an absolute analysis of the expression levels of each gene on the array. This file can only be analyzed by Affymetrix software. All .chp files include a normalization of target intensity to 800. Researchers using this data with a normalization other than the value of 800 may wish to re-process the .dat file with a different target intensity in order to make comparisons to their own expression profiles.
- .cel file**      This file describes the intensities determined for every feature on a chip, without providing information about which probes correspond to which probe sets (such information provided by the CDF or 1LQ file). This format is not a fixed standard.