Microarray data was background corrected and normalized within and between arrays with R using the limma package. Using a python script, the normalized expression matrix was simplified to a trinary matrix of values 1, 0 and -1 (for normalized expression values above 0.5, below -0.5 and between those 2 values respectively). Genes were filtered according to their value in each array (supplementary table X que contiene las busquedas realizadas). The resulting gene lists were used as input for DAVID database in order to analyze pathway enrichment.