Hierarchical clustering of samples from Giordano et al., 2005 according to Affymetrix microarray expression data (Giordano et al., 2005) corresponding to the 51 genes dys-regulated in PTC-ga(+) or PTC-ga(-) (see Figure 2). Data deriving from 51 PTC (classified in 4 subgroups according to their mutational status: PTC with the BRAF1799A mutation (n=26), PTC with a RET/PTC rearrangement (n=10), PTC with a RAS mutation (n=5) and PTC with no mutation (n=10)) and 4NT were subjected to treatment by Cluster and Treeview softwares. Samples are identified by a number and the PTC subgroup or NT. Genes identified by their gene symbol appear on the right side of the figure. Each column gives the gene expression profile of a sample and each line indicates the variations in the level of expression of a given gene among tissue samples. Red and green colors indicate transcript levels above and below the median values, respectively.