Supplementary Figure 2

Comparison of gene expression levels measured by hybridization on macroarray and by quantitative PCR in a series of PTC and paired NT. Transcripts from six genes (C11ORF8, TIMP1, SDC4, PROS1, CHI3L1 and FN1) were assayed in PTC-ga(+) (n=17), PTC-ga(-) (n=6) and paired NT by quantitative PCR and compared to gene expression values obtained by macroarray on the same samples. Results are expressed as log2 values of tumor to NT ratio. Values deriving from PCR measurements and hybridization on macroarray are presented as squares and triangles, respectively. Symbols and horizontal bars represent the mean and SEM.