Supplementary Figure 1

Relationship between transcript levels measured by hybridization on macroarray and by RT-QPCR in individual samples. Analyses of FN1, PROS1 or CHI3L1 transcripts were performed on 34 separate samples corresponding to i) 16 PTC-ga(+), 12 with \( BRAFT^{T1799A} \) (black squares) and 4 with \( RET/PTC \) rearrangement (grey squares), ii) 6 PTC-ga(-) (open squares) and iii) 12 NT (open triangles). Data from real-time PCR (y-axis) and macroarray (x-axis) were subjected to log2 transformation. Dotted lines representing regression lines were calculated by the least square method. The correlation coefficient (r) is given for each gene.