

Fig 1

Fig 1. Comparison of gene expression profiles of control and RA-induced NT2 cells.

Gene expression profiles of RA-treated cell data after filtering out the control cell data as described under Materials and methods. (A) 1-day, (B) 2-day and (C) 7-day samples, included 40, 106, 340 probes respectively. (Lists of genes are shown in Supplementary Table 1). Columns and rows indicate RA time point samples and genes, respectively. Genes and samples are aligned in the order defined by the results of the clustering analysis. The color bar represents the grades of the relative expression levels: increase, red; decrease, blue.

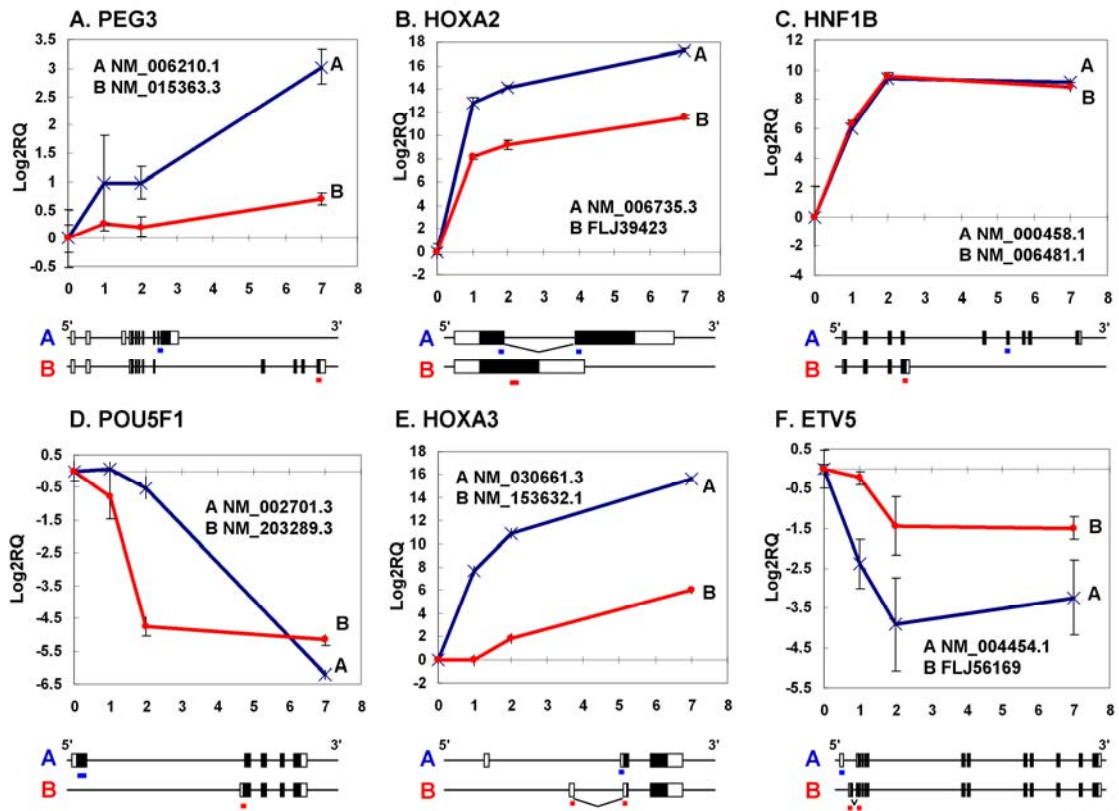


Fig 2

Fig 2. Quantitative evaluation of selected 6 transcription factors by real-time PCR.

Expression levels of two transcripts produced by AS from each gene were analyzed by real-time PCR, and were represented in log<sub>2</sub> base. The data were normalized with respect to that of the human GAPDH.

Name of the genes: (A) PEG3, (B) HOXA2, (C) HNF1B, (D) POU5F1, (E) HOXA3, (F) ETV5  
 Schematic views of selected genes: boxes, exons; gray lines, introns; black boxes, coding regions; white boxes, untranslated regions; red or navy bars, amplified regions by real-time PCR.