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Alternative splicing of genes during neuronal differentiation of NT2 pluripotential human embryonal carcinoma cells

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Abstract

We analyzed the mRNA diversity of genes after inducing neuronal differentiation in human NT2 teratocarcinoma cells using all-trans retinoic acid (RA). DNA microarray analyses of cells treated with RA for 0, 1, 2 and 7 days identified 358 RA-responsive genes. mRNA diversity analysis revealed that 274 genes (~77% of the selected genes) produced multiple protein-coding transcripts by alternative splicing (AS). Among these 274 genes, we chose 26 genes that showed AS in their C-terminus and 12 transcription factor genes for further analysis. By using transcript-specific primers, we performed quantitative real-time PCR analysis to examine the expression profiles of all the protein-coding transcripts. Consequently, we identified genes which showed different RA-induced changes in the expression of their protein-coding transcripts.

Keywords: Alternative splicing, Neuronal differentiation, mRNA diversity, Transcription factor, Expression profile, Multiple protein-coding transcript