Table 1. GO functional classification of 358 genes selected from DNA microarray analysis.

Functional category (GO : Molecular function)		Number of matched genes			
		Selected genes		RefSeq	
		(358 genes)	%	(24,210 cDNAs)	%
Binding	Nucleic acid binding	25	(14.4)	706	(8.9)
	Nucleotide binding	20	(11.5)	1,047	(13.2)
	Ion binding	12	(6.9)	245	(3.1)
	Protein binding	9	(5.2)	450	(5.7)
	Other bindings	3	(1.7)	304	(3.8)
Catalytic activity	Transferase activity	19	(10.9)	808	(10.2)
	Hydrolase activity	15	(8.6)	902	(11.3)
	Ligase activity	9	(5.2)	107	(1.3)
	Other catalytic activity	11	(6.3)	653	(8.2)
Transcription regulator activity		18	(10.3)	364	(4.6)
Signal transducer activity		12	(6.9)	879	(11.0)
Transporter activity		11	(6.3)	997	(12.5)
Structural molecule activity		4	(2.3)	163	(2.0)
Enzyme regulator activity		3	(1.7)	142	(1.8)
Others		3	(1.7)	193	(2.4)
Total		174		7,960	

Total refers to the number of cDNAs used for the classification of molecular function. We categorized each cDNA used for identifying the genomic regions of extracted 423 probes. Results obtained using the cDNAs transcribed from the same genomic region were merged. We categorized 24,210 human RefSeq and identified 20,072 protein-coding genes. Results obtained using the human RefSeq transcribed from the same genomic region were also merged. If an encoded protein was predicted to belong to two or more categories, it was counted every time.

Table 2. Quantitative evaluation of 12 transcription factors by real-time PCR.

AS pattern	Gene symbol	cDNA name	Change in expression level compared to the 0-day sample			Expression pattern
			1-day	2- day	7- day	
Alt. N-terminus	ETV1	NM_004956.3	±	↓	±	Differ
		FLJ50494	±	±	↓	
	ETV4	NM_001986.1	±	↓	↓	Same
		BC007242.1	±	↓	↓	
	ETV5	NM_004454.1	↓	↓	↓	Differ
		FLJ56169	±	↓	↓	
	HOXA3	NM_030661.3	↑↑	↑↑↑	↑↑↑	Differ
		NM_153632.1	±	↑	↑	
	PAX6	NM_000280.2	↑	↑	↑↑	Same
		FLJ36930	↑	↑	↑↑	
	POU5F1	NM_002701.3	±	±	↓	Differ
		NM_203289.3	±	↓	↓	
	RARB	NM_000965.2	↑	↑↑	↑↑	Differ
		FLJ56241	↑	↑	↑	
Alt. C-terminus	HNF1B	NM_000458.1	↑	↑↑	↑↑	Same
		NM_006481.1	↑	↑↑	↑↑	
	HOXA2	NM_006735.3	↑↑↑	↑↑↑	↑↑↑	Differ
		FLJ39423	↑↑	↑↑	↑↑↑	
	PEG3	NM_006210.1	±	±	↑	Differ
		NM_015363.3	±	±	±	
	ZNF483	NM_133464.1	±	↓	↓	Differ
		FLJ35492	±	±	↓	
Alt. cassette-exon	RFX2	NM_000635.2	±	↑	↑	Same
		FLJ53376	±	↑	↑	

Out of the 18 transcription factors, 6 transcription factors – namely GATA6 (NM_005257.3), GBX2 (NM_001485.2), HESX1 (NM_003865.1), HOXB2 (NM_002145.2), HOXB4 (NM_024015.3) and HOXC4 (NM_014620.2) - produced only single protein-coding transcripts. They are not shown in this table. Symbols used to indicate Differences of mean averages of log2 ratios between the control (0-day) and experimental samples (1-day, 2-day and 7-day): "±", >1/2 but <twofold; "↓", > 1/100 but ≤ 1/2; "↑", ≥ twofold but < 100-fold; "↑↑", ≥ 100-fold but < 1000-fold; and "↑↑↑", ≥ 1000-fold