

Additional file 4: *Target* promoter sequence analysis: all over- and under-represented regulatory elements

<i>Target</i> regulation	Representation (vs control)	Matrix in TRANSFAC	Transcription Factors	Hit numbers		Frequency		Odds ratio	Fisher exact test	
				<i>Target</i> set	Control set	<i>Target</i> set	Control set			
Up-regulated <i>target</i> promoters	Over-represented regulatory elements	V\$API_Q4	AP-1	18	78	14%	7%	2.08	0.0048	
		V\$E2F_Q2	E2F, E2F-1, E2F-2, E2F-3, E2F-4, E2F-5	11	37	8%	3%	2.68	0.0058	
		V\$E2F1DP1RB_01	Rb:E2F-1:DP-1	11	37	8%	3%	2.68	0.0058	
		V\$E2F_Q3	E2F	5	10	4%	1%	4.50	0.012	
		V\$E2F4DP1_01	E2F-4:DP-1	5	10	4%	1%	4.50	0.012	
		V\$E2F_Q3	E2F, E2F-1	8	29	6%	2%	2.48	0.02557	
		V\$MYOGNF1_01	NF-1, NF-1A1, NF-1B1, NF-1B2, NF-1C2, NF-1/L, NF-1/Red1, NF-1X	12	54	9%	5%	2.00	0.026	
		V\$E2F_Q4	E2F	15	75	11%	6%	1.80	0.0283	
		V\$HTF_Q1	HTF	2	1	2%	0%	18.00	0.031	
		V\$E2F_Q3_Q1	E2F, E2F+E4, E2F-1, E2F-3, E2F-4, DP-1	9	38	7%	3%	2.13	0.038	
		V\$E2F1_Q4_Q1	E2F, E2F+E4, E2F-1, E2F-3, E2F-4, DP-1	9	38	7%	3%	2.13	0.038	
		V\$E2A_Q2	E12, E47, ITF-1, MRF4, MyoD, myogenin	9	40	7%	3%	2.03	0.049	
		Under-represented regulatory elements	V\$MEF2_Q6_Q1	MEF-2, aMEF-2, MEF-2C, MEF-2DAB	2	68	2%	6%	0.26	0.021
			V\$COREBINDING_FACTOR_Q6	core-binding	3	72	2%	6%	0.38	0.0458
	V\$CREB_Q4_Q1		CREB, deltaCREB, CREMtau, CREMalpha, CREMbeta, CREMgamma, CREMtaualpha, CREMtau1, CREMtau2, CREBbeta	3	71	2%	6%	0.38	0.049	
V\$SELK1_Q1	Elk-1		2	58	2%	5%	0.31	0.049		
Down-regulated <i>target</i> promoters	Over-represented regulatory elements	V\$E2F1DP1_Q1	E2F-1:DP-1	22	55	9%	5%	1.99	0.0053	
		V\$E2F1_Q6	E2F-1	67	249	28%	21%	1.34	0.011	
		V\$SREBP1_Q1	SREBP-1a, SREBP-1b, SREBP-1c, SREBP-1	9	16	4%	1%	2.80	0.015	
		V\$E2F_Q6	E2F	48	169	20%	14%	1.41	0.015	
		V\$E2F1DP2_Q1	E2F-1:DP-2	17	45	7%	4%	1.88	0.021	
		V\$E2F4DP2_Q1	E2F-4:DP-2	17	45	7%	4%	1.88	0.021	
		V\$OCT1_Q6	POU2F1, POU2F1a	52	196	22%	16%	1.32	0.033	
		V\$PIT1_Q6	POU1F1, POU1F1a, POU1F1b, POU1F1c	18	52	8%	4%	1.72	0.034	
		V\$E2F1_Q6_Q1	E2F-1	20	60	8%	5%	1.66	0.034	
		V\$AR_Q1	AR	3	2	1%	0%	7.46	0.035	
		V\$USF_Q6	USF, USF1, USF-1, USF2, USF-1:USF-2	27	89	11%	7%	1.51	0.037	
		V\$HNF3B_Q1	HNF-3B	13	34	5%	3%	1.90	0.038	
		V\$PPARG_Q3	PPAR-gamma, PPAR-gamma1, PPAR-gamma2	22	70	9%	6%	1.56	0.043	
		V\$MMEF2_Q6	MEF-2	7	14	3%	1%	2.49	0.0477	
	Under-represented regulatory element	V\$CMYB_Q1	c-Myb	0	31	0%	3%	0.00	0.004	

TFExplorer predicted regulatory element database was used to map regulatory elements in promoters (from -1000 bp to +300 bp from transcription start site). We analyzed promoters of *target* genes (132 up-regulated gene promoters, 239 down-regulated gene promoters in TFExplorer database) and of a control set of promoters from genes randomly chosen among genes that were expressed in Min6 cells (1188 promoters). For each gene promoter set (up-regulated *target*, down-regulated *target* and control) we counted the number of genes (Hit numbers) for which a given regulatory element was present in the promoter. We calculated the frequencies for any given regulatory element, and evaluated the statistical significance of difference to control set by Fisher exact test. The tables present all results with p value < 0.05. Regulatory elements are referred to their matrix name in the TRANSFAC database.