Appendix 8: Statistically over-represented TREs derived from the PAINT analysis of the rat promoter regions.

Represented for each TRE identified in the promoter sequences is the cluster in which the TRE was determined to be enriched, the TRANSFAC identifier and the p-value of the TRE in both gene sets.

Cluster/Group	TRE	p-values	
		Undifferentiated	Differentiated
Cluster 1: TREs significantly over-represented in Undifferentiated cluster (p-value<0.1)	HFH-1/V$HFH1_01	0.00263	0.11634
	GATA-1/V$GATA1_03	0.01239	1
	GATA-1/V$GATA1_05	0.03937	1
	Elk-1/V$ELK1_01	0.04491	1
	HES1/V$HES1_Q2	0.05137	1
	GCM/V$GCM_Q2	0.05655	1
	Oct-1/V$OCT1_B	0.05655	0.13804
	SRF/V$SRF_Q5_01	0.06236	1
	CHOP:C/EBPalpha/V$CHOP_01	0.06267	0.4391
	E2F/V$E2F_02	0.07436	1
	Rb:E2F-1:DP-1/V$E2F1DP1RB_01	0.07436	1
	IRF-7/V$IRF7_01	0.09129	0.48078
	Nkx2-5/V$NKX25_02	0.09129	1
Cluster 2: TREs significantly over-represented in Differentiated cluster (p-value<0.1)	Barbie Box/V$BARBIE_01	1	0.00089
	Cdc5/V$CDC5_01	0.75032	0.01424
	Sox-5/V$SOX5_01	1	0.02435
	alpha-CP1/V$ALPHACP1_01	1	0.02435
	Pax-3/V$PAX3_B	0.31787	0.06699
	E47/V$E47_01	1	0.0714
	AP-1/V$AP1_Q2	0.60571	0.08865
	NF-muE1/V$NFMUE1_Q6	1	0.09413