Appendix 2: Statistically over-represented TREs derived from the PAINT analysis of the human 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.

Group/Cluster	TRE	p-values	
		Undifferentiated	Differentiated
Cluster 1: TREs significantly over-represented in Undifferentiated cluster (p-value<0.1)	E2F-1/V$E2F1_Q3_01	0.00108	0.44669
	Oct-1/V$OCT1_02	0.00866	1
	E4F1/V$E4F1_Q6	0.04378	1
	Evi-1/V$EVI1_05	0.04378	1
	SREBP-1/V$SREBP1_Q6	0.047	0.20271
	LEF1TCF1/V$LEF1TCF1_Q4	0.05473	1
	Nkx2-5/V$NKX25_02	0.05844	0.14679
	IRF-7/V$IRF7_01	0.06142	1
	TFIIA/V$TFIIA_Q6	0.07685	0.97704
	Poly A/V$LDSPOLYA_B	0.0786	0.53885
	AML/V$AML_Q6	0.0916	1
	AREB6/V$AREB6_01	0.0916	1
	IRF/V$IRF_Q6_01	0.0916	1
	MAF/V$MAF_Q6	0.0916	1
	SREBP/V$SREBP_Q3	0.0916	1
	TGIF/V$TGIF_01	0.0916	1
	SOX/V$SOX_Q6	0.09716	1
Cluster 2: TREs significantly over-represented in Differentiated cluster (p-value<0.1)	Hand1:E47/V$HAND1E47_01	0.75097	0.01479
	VDR, CAR, PXR/V$DR3_Q4	0.49165	0.0148
	COMP1/V$COMP1_01	0.96719	0.03569
	HEB/V$HEB_Q6	0.79571	0.06901
	PEBP/V$PEBP_Q6	0.44022	0.07282
	HFH-3/V$HFH3_01	0.80986	0.08118
	RFX1 (EF-C)/V$EFC_Q6	0.50385	0.08983