Appendix 6: Statistically over-represented TREs derived from the PAINT analysis of the mouse 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)	POU1F1/V$POU1F1_Q6	0.00943	0.51764
	STATx/V$STAT_01	0.01922	1
	FOXJ2/V$FOXJ2_02	0.01924	1
	IRF-7/V$IRF7_01	0.03846	0.15221
	Pax-6/V$PAX6_01	0.03846	1
	Nrf-1/V$NRF1_Q6	0.05189	0.13325
	Poly A/V$LDSPOLYA_B	0.06713	0.67458
	Cdx-2/V$CDX2_Q5	0.06797	0.73687
	AR/V$AR_01	0.07865	1
	IRF/V$IRF_Q6	0.07865	1
	POU3F2/V$POU3F2_01	0.07865	1
	Hand1:E47/V$HAND1E47_01	0.0866	0.49313
	Cdc5/V$CDC5_01	0.09003	0.98341
	CDP CR3+HD/V$CDPCR3HD_01	0.09852	1
Cluster 2: TREs significantly over-represented in Differentiated cluster (p-value<0.1)	Barbie Box/V$BARBIE_01	0.59748	0.03502
	TFE/V$TFE_Q6	0.2012	0.04568
	E2F-1/V$E2F1_Q3_01	0.30284	0.05517
	Sox-5/V$SOX5_01	1	0.05544
	HIF-1/V$HIF1_Q5	1	0.08207