Appendix 3: Statistically over-represented TREs derived from the PAINT analysis of the human first intron regions.

Represented for each TRE identified in the first intron 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)	HNF-4alpha/V$HNF4ALPHA_Q6	0	1
	MAF/V$MAF_Q6	0	1
	Tal-1alpha:E47/V$TAL1ALPHAE47_01	0	1
	Tal-1beta:E47/V$TAL1BETAE47_01	0	1
	VDR, CAR, PXR/V$DR3_Q4	0	1
	ZID/V$ZID_01	0	1
	Evi-1/V$EVI1_05	0.00004	1
	VBP/V$VBP_01	0.00004	0.08875
	COMP1/V$COMP1_01	0.00035	0.81981
	GR/V$GRE_C	0.00048	1
	NERF1a/V$NERF_Q2	0.00048	1
	Oct-1/V$OCT1_02	0.00049	1
	aMEF-2/V$AMEF2_Q6	0.00084	1
	SMAD-3/V$SMAD3_Q6	0.00086	0.18791
	IPF1/V$IPF1_Q4_01	0.00106	0.49877
	Muscle TATA box/V$MTATA_B	0.00108	0.57834
	myogenin / NF-1/V$MYOGNF1_01	0.00118	0.32972
	C/EBPdelta/V$CEBPDELTA_Q6	0.00151	0.72583
	RFX1/V$RFX1_02	0.00182	1
	c-Ets-2/V$ETS2_B	0.00182	1
	MEF-2/V$MMEF2_Q6	0.00267	1
	v-Myb/V$VMYB_01	0.00352	1
	HNF-4 direct repeat 1/V$HNF4_DR1_Q3	0.00368	0.20439
	GATA-3/V$GATA3_03	0.00405	0.39113
	TCF-4/V$TCF4_Q5	0.00412	0.32899
	HP1 site factor/V$HP1SITEFACTOR_Q6	0.00429	1
	core-binding factor/V$COREBINDINGFACTOR_Q6	0.00506	0.56198
	FOXP3/V$FOXP3_Q4	0.00523	1
	Gfi-1/V$GFI1_01	0.00628	1
	Pax-6/V$PAX6_01	0.00646	0.51093
	AP-1/V$AP1_Q2	0.00666	0.0931
	ATF6/V$ATF6_01	0.00782	1
	CRE-BP1/V$CREBP1_01	0.0081	0.00686
	TATA/V$TATA_C	0.0081	1
	CCAAT box/V$CAAT_01	0.00944	1
	HNF-1/V$HNF1_01	0.01019	0.00619
	SMAD-4/V$SMAD4_Q6	0.01104	1
	Hand1:E47/V$HAND1E47_01	0.013	1
	C/EBP/V$CEBP_C	0.01339	1
	FOXJ2/V$FOXJ2_02	0.01384	0.71135
	GATA-1/V$GATA1_02	0.01633	1
	NF-Y/V$NFY_Q6_01	0.01633	1
	NF-kappaB/V$NFKB_Q6_01	0.01784	0.3472
	NF-kappaB (p50)/V$NFKAPPAB50_01	0.01789	1
	POU3F2/V$POU3F2_02	0.01789	1
	OCT-x/V$OCT_C	0.01982	1
	Nrf2/V$NRF2_Q4	0.02017	1
	AP-1/V$AP1_C	0.02023	1
	Barbie Box/V$BARBIE_01	0.02023	1
	GCM/V$GCM_Q2	0.02023	1
	TFIIA/V$TFIIA_Q6	0.02389	0.5109
	Pax-3/V$PAX3_B	0.02535	0.53153
	MAZR/V$MAZR_01	0.02546	1
	XFD-2/V$XFD2_01	0.02866	1
	SREBP-1/V$SREBP1_Q6	0.0287	0.91575
	Oct-1/V$OCT1_05	0.03396	1
	c-Ets-1/V$ETS1_B	0.03396	1
	NKX3A/V$NKX3A_01	0.03511	1
	Nkx2-5/V$NKX25_02	0.03511	0.43376
	LEF1TCF1/V$LEF1TCF1_Q4	0.03868	0.20841
	c-Myb/V$CMYB_01	0.03868	1
	HFH-3/V$HFH3_01	0.03943	1
	AP-1/V$AP1_Q4	0.0412	0.18433
	MyoD/V$MYOD_01	0.04813	1
	HLF/V$HLF_01	0.05118	0.56773

	C/EBPgamma/V$CEBPGAMMA_Q6	0.0515	0.51588
	Brn-2/V$BRN2_01	0.05374	1
	XFD-3/V$XFD3_01	0.05374	0.10978
	SF-1/V$SF1_Q6	0.06176	0.38175
	TTF1/V$TITF1_Q3	0.06723	0.37628
	CREB/V$CREB_Q2	0.07655	1
	Lhx3/V$LHX3_01	0.07783	1
	AML/V$AML_Q6	0.08015	1
	AR/V$AR_03	0.08015	1
	AREB6/V$AREB6_01	0.08015	1
	ATATA/V$ATATA_B	0.08015	1
	AhR:Arnt/V$AHRARNT_01	0.08015	1
	Hox-1.3/V$HOX13_01	0.08015	1
	PPARalpha:RXR-alpha/V$PPARA_02	0.08015	1
	TGIF/V$TGIF_01	0.08015	1
	Tax/CREB/V$TAXCREB_02	0.08015	1
	Pax/V$PAX_Q6	0.08483	0.13386
	c-Rel/V$CREL_01	0.09076	1
	CHOP:C/EBPalpha/V$CHOP_01	0.09192	0.15451
	HNF-3beta/V$HNF3B_01	0.09764	0.21383
Cluster 2: TREs significantly over-represented in Differentiated cluster (p-value<0.1)	FOXO4/V$FOXO4_01	1	0
	HNF-1/V$HNF1_01	0.01019	0.00619
	CRE-BP1/V$CREBP1_01	0.0081	0.00686
	IRF/V$IRF_Q6_01	1	0.0229
	SREBP-1/V$SREBP1_02	1	0.0229
	GATA-2/V$GATA2_03	1	0.04532
	HTF/V$HTF_01	1	0.04532
	PTF1-beta/V$PTF1BETA_Q6	1	0.04532
	Bach2/V$BACH2_01	0.64607	0.05457
	TFE/V$TFE_Q6	0.10771	0.06333
	SOX-9/V$SOX9_B1	0.45989	0.06623
	CDP/V$CDP_01	1	0.06727
	VBP/V$VBP_01	0.00004	0.08875
	AP-1/V$AP1_Q2	0.00666	0.0931