Appendix 10: Statistically over-represented TREs derived from the PAINT analysis of the chicken 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)	Nkx2-2/V$NKX22_01	0.00758	0.26684
	Lentiviral Poly A/V$LPOLYA_B	0.02888	0.58639
	Oct-1/V$OCT1_02	0.03682	1
	RFX1/V$RFX1_01	0.03682	1
	E47/V$E47_02	0.05188	1
	NF-kappaB/V$NFKB_Q6	0.06845	0.29205
	TCF-4/V$TCF4_Q5	0.0985	0.50668
Cluster 2: TREs significantly over-represented in Differentiated cluster (p-value<0.1)	XFD-2/V$XFD2_01	0.52693	0.01973
	HNF-4/V$HNF4_01	0.97017	0.02364
	Nkx2-5/V$NKX25_01	0.83068	0.04751
	COMP1/V$COMP1_01	0.48357	0.05066
	Poly A/V$LDSPOLYA_B	0.84538	0.07571
	TFE/V$TFE_Q6	0.97146	0.08191
	MyoD/V$MYOD_01	1	0.08487
	GATA-1/V$GATA1_06	0.27304	0.09749
	NF-muE1/V$NFMUE1_Q6	0.27304	0.09749