

Appendix 30: Criteria table for transcription response element inclusion in gene promoter region regulatory network models

Represented for each TRE identified in the promoter regions of each gene are the TRANSFAC identifier name, the p-value, the ECF (evolutionary conservation factor), and the FR (frequency ratio) as defined in Materials and Methods. TREs included in this table are those with p-value <0.1, ECF =2, and FR >3.

TRE	p-value	Evolutionary Conservation Factor	Frequency Ratio
Upregulated			
<i>E2F-1/V\$E2F1_Q3_01</i>	0.00095	2	3.725
<i>Oct-1/V\$OCT1_02</i>	0.00801	3	4.25
<i>SREBP-1/V\$SREBP1_Q6</i>	0.03498	1	1.34
<i>E4F1/V\$E4F1_Q6</i>	0.04207	1	5.375
<i>Evi-1/V\$EVI1_05</i>	0.04207	1	18.625
<i>LEF1TCF1/V\$LEF1TCF1_Q4</i>	0.05185	1	3.37
<i>Nkx2-5/V\$NKX25_02</i>	0.05404	2	2.3
<i>TFIIA/V\$TFIIA_Q6</i>	0.06491	1	1.46
<i>Poly A/V\$LDSPOLYA_B</i>	0.07291	2	2.16
<i>AML/V\$AML_Q6</i>	0.08969	1	10.5
<i>AREB6/V\$AREB6_01</i>	0.08969	1	10.5
<i>IRF/V\$IRF_Q6_01</i>	0.08969	2	2.33
<i>MAF/V\$MAF_Q6</i>	0.08969	1	10.5
<i>SREBP/V\$SREBP_Q3</i>	0.08969	1	1.34
<i>TGIF/V\$TGIF_01</i>	0.08969	1	10.5
<i>SOX/V\$SOX_Q6</i>	0.0936	1	3.91
<i>TTF1/V\$TTF1_Q3</i>	0.09443	1	2.24
<i>Evi-1/V\$EVI1_04</i>	0.09494	1	18.625
Down-regulated			
<i>Hand1:E47/V\$HAND1E47_01</i>	0.01479	1	2.68
<i>VDR, CAR, PXR/V\$DR3_Q4</i>	0.0148	1	
<i>COMP1/V\$COMP1_01</i>	0.03569	2	2.52
<i>HEB/V\$HEB_Q6</i>	0.06901	1	2.13
<i>PEBP/V\$PEBP_Q6</i>	0.07282	1	4.29
<i>HFH-3/V\$HFH3_01</i>	0.08118	1	4.16
<i>RFX1 (EF-C)/V\$EFC_Q6</i>	0.08983	1	3.91