

Table 4. Number of CRE sites within 5 kb of the transcription start site of genes significantly regulated 2 h after cAMP treatment

Locus Link	Gene Name	Gene symbol	Fold 2h	2h wt	Fold 6h	6h wt	Fold 24h	24h wt	Conserved CRE sites
			wt	*P value	wt	*P value	wt	*P value	
73094	RIKEN cDNA 3110007P09 gene	3110007P09Rik	115.9	0.029	147.4	0.029	370.8	0.029	1
19735	regulator of G-protein signaling 2	Rgs2	43.7	0.029	21.8	0.029	27.0	0.029	1
94222	oligodendrocyte transcription factor 3	Olig3	19.0	0.029	22.4	0.029	57.4	0.029	1
19252	dual specificity phosphatase 1	Dusp1	16.3	0.029	11.5	0.029	8.1	0.029	2
12508	CD53 antigen	Cd53	15.9	0.029	27.5	0.029	29.6	0.029	1
17872	myeloid differentiation primary response gene 116	Myd116	14.2	0.029	4.4	0.029	4.4	0.029	1
68728	RIKEN cDNA 1110029F20 gene	1110029F20Rik	10.8	0.029	12.1	0.029	8.3	0.029	1
17133	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	Maff	8.4	0.029	1.2	0.057	-1.1	0.600	1
64213	suppression of tumorigenicity 7	St7	6.8	0.029	3.7	0.029	4.0	0.029	1
110521	human immunodeficiency virus type I enhancer binding protein 1	Hivep1	5.9	0.029	6.8	0.029	7.1	0.029	1
14605	delta sleep inducing peptide, immunoreactor	Dsip1	4.8	0.029	2.9	0.029	1.7	0.029	1
18626	period homolog 1 (Drosophila)	Per1	4.0	0.029	1.9	0.029	1.5	0.086	3
80976	synaptotagmin 13	Syt13	3.9	0.029	3.5	0.029	2.2	0.029	1
101497	expressed sequence AI194308	AI194308	3.8	0.029	6.5	0.029	5.3	0.029	1
67064	RIKEN cDNA 2810405I11 gene	2810405I11Rik	3.7	0.029	2.5	0.029	4.4	0.029	1
20848	signal transducer and activator of transcription 3	Stat3	3.7	0.029	2.4	0.029	2.5	0.029	2
19073	proteoglycan, secretory granule	Prg	3.6	0.029	6.6	0.029	15.9	0.029	1
212398	frequently rearranged in advanced T-cell lymphomas 2	Frat2	3.5	0.029	1.8	0.057	2.1	0.057	1
22764	zinc finger protein X-linked	Zfx	3.4	0.029	1.1	0.600	1.2	0.086	2
11502	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	Adam9	3.4	0.029	2.4	0.029	1.3	0.343	1
108954	protein phosphatase 1, regulatory (inhibitor) subunit 15b	Ppp1r15b	3.3	0.029	1.3	0.371	1.0	1.000	1
319162	histone 3, H2a	Hist3h2a	3.3	0.029	1.7	0.257	3.6	0.029	1
11605	galactosidase, alpha	Gla	3.1	0.029	2.1	0.029	1.2	0.571	1
50790	acyl-CoA synthetase long-chain family member 4	Acs14	3.1	0.029	3.8	0.029	2.1	0.029	1
12053	B-cell leukemia/lymphoma 6	Bcl6	3.0	0.029	2.5	0.029	-1.3	0.486	1
15205	hairy and enhancer of split 1 (Drosophila)	Hes1	2.9	0.029	2.2	0.029	2.5	0.029	1
74182	RIKEN cDNA 2310032D16 gene	2310032D16Rik	2.7	0.029	2.0	0.029	1.5	0.086	1
104318	casein kinase 1, delta	Csnk1d	2.7	0.029	1.7	0.029	1.3	0.114	1
66087	RIKEN cDNA 0610039A15 gene	0610039A15Rik	2.7	0.029	2.3	0.029	1.6	0.029	1
70561	RIKEN cDNA 5730420B22 gene	5730420B22Rik	2.7	0.029	3.9	0.029	3.8	0.029	1
53334	golgi SNAP receptor complex member 1	Gosr1	2.5	0.029	1.8	0.029	1.4	0.029	1
15936	immediate early response 2	Ier2	2.5	0.029	1.4	0.029	1.4	0.057	2
56812	DnaJ (Hsp40) homolog, subfamily B, member 10	Dnajb10	2.4	0.029	2.5	0.029	2.2	0.057	1
231655	2'-5' oligoadenylate synthetase-like 1	Oasl1	2.4	0.029	1.8	0.029	1.4	0.229	1
231464	RIKEN cDNA 4932442K20 gene	4932442K20Rik	2.4	0.029	1.8	0.029	4.0	0.029	1
22644	ring finger protein 103	Rnf103	2.4	0.029	2.7	0.029	3.8	0.029	1
114716	sprouty protein with EVH-1 domain 2, related sequence	Spred2	2.4	0.029	1.7	0.029	1.4	0.086	1
72795	RIKEN cDNA 2810460C24 gene	2810460C24Rik	2.4	0.029	1.6	0.029	-1.0	0.657	1

Locus Link	Gene Name	Gene symbol	Fold 2h	2h wt	Fold 6h	6h wt	Fold 24h	24h wt	Conserved CRE sites
				*P value		*P value		*P value	
80795	selenoprotein K	Selk	2.4	0.029	2.6	0.029	1.4	0.029	1
20873	polo-like kinase 4 (Drosophila)	Plk4	2.3	0.057	1.0	0.971	-2.9	0.029	1
214597	cDNA sequence BC023957	BC023957	2.3	0.029	2.3	0.029	3.2	0.029	1
81703	Jun dimerization protein 2	Jundm2	2.2	0.029	1.8	0.057	1.9	0.029	1
12226	B-cell translocation gene 1, anti-proliferative	Btg1	2.2	0.029	2.2	0.029	4.3	0.029	1
66629	golgi phosphoprotein 3	Golph3	2.2	0.029	1.4	0.371	1.2	0.629	1
56516	RNA binding motif, single stranded interacting protein 2	Rbms2	2.2	0.029	2.9	0.029	1.7	0.057	1
27399	inositol hexaphosphate kinase 1	Ihpk1	2.2	0.029	2.0	0.029	3.3	0.029	1
229096	RIKEN cDNA 9130022A11 gene	9130022A11Rik	2.2	0.029	1.2	0.229	1.4	0.086	2
56212	ras homolog gene family, member G	Rhog	2.2	0.029	2.2	0.029	1.9	0.029	1
12227	B-cell translocation gene 2, anti-proliferative	Btg2	2.1	0.029	1.5	0.057	3.4	0.029	1
53892	protein phosphatase 1D magnesium-dependent, delta isoform	Ppm1d	2.1	0.029	1.2	0.057	1.2	0.143	1
17691	SNF1-like kinase	Snf1lk	2.1	0.029	1.7	0.057	2.0	0.029	3
230648	RIKEN cDNA 4732418C07 gene	4732418C07Rik	2.1	0.057	1.5	0.371	1.1	0.886	1
12189	breast cancer 1	Brca1	2.1	0.029	-1.2	0.543	-8.0	0.029	1
20658	Son cell proliferation protein	Son	2.1	0.057	1.1	0.457	-1.2	0.314	1
56389	syntaxin 5A	Stx5a	2.1	0.029	2.3	0.029	2.3	0.029	1
22057	transducer of ErbB-2.1	Tob1	2.1	0.029	1.5	0.171	2.5	0.029	1
20224	SAR1a gene homolog 1 (S. cerevisiae)	Sara1	2.1	0.029	1.8	0.029	-1.3	0.029	1
19820	ring finger protein 12	Rnf12	2.0	0.029	1.2	0.057	-1.1	0.200	1
18739	phosphatidylinositol membrane-associated	Pitpnm	2.0	0.029	3.0	0.029	3.0	0.029	1
18701	phosphatidylinositol glycan, class F	Pigf	2.0	0.029	2.0	0.029	-1.1	0.114	1
17966	neighbor of Brca1 gene 1	Nbr1	2.0	0.029	1.5	0.029	1.6	0.029	1
67121	microtubule associated serine/threonine kinase-like	Mastl	2.0	0.029	1.2	0.086	-2.7	0.057	1
22210	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	Ube2b	1.9	0.029	2.2	0.029	1.6	0.029	1
12177	BCL2/adenovirus E1B 19kDa-interacting protein 3-like	Bnip3l	1.9	0.029	2.4	0.029	2.4	0.029	1
68721	RIKEN cDNA 1110032A03 gene	1110032A03Rik	1.9	0.057	2.6	0.029	3.9	0.029	1
22284	ubiquitin specific protease 9, X chromosome	Usp9x	1.9	0.029	1.8	0.029	1.1	0.429	1
67300	clathrin, heavy polypeptide (Hc)	Cltc	1.8	0.029	2.0	0.029	1.2	0.400	1
19084	protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	1.8	0.029	2.6	0.029	1.8	0.029	1
22151	tubulin, beta 2	Tubb2	1.8	0.029	2.0	0.029	2.8	0.029	1
66884	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Appbp2	1.8	0.029	1.3	0.057	-1.0	0.571	1
13139	diacylglycerol kinase, alpha	Dgka	1.8	0.029	3.5	0.029	9.5	0.029	1
14312	bromodomain containing 2	Brd2	1.8	0.029	1.1	0.114	-1.2	0.029	2
16911	LIM domain only 4	Lmo4	1.8	0.029	2.9	0.029	3.6	0.029	1
67296	suppressor of cytokine signaling 4	Socs4	1.8	0.029	-1.0	1.000	-2.1	0.029	1
20912	syntaxin binding protein 3	Stxbp3	1.8	0.029	1.6	0.029	1.4	0.114	1
14462	GATA binding protein 3	Gata3	1.8	0.029	2.3	0.029	3.4	0.029	1
14815	nuclear receptor subfamily 3, group C, member 1	Nr3c1	1.7	0.029	1.8	0.029	2.8	0.029	1
171508	cysteine-rich with EGF-like domains 1	Creld1	1.7	0.057	1.3	0.114	1.0	0.914	1
19255	protein tyrosine phosphatase, non-receptor type 2	Ptpn2	1.7	0.029	-1.1	0.457	-1.2	0.029	1
56724	RIKEN cDNA 1200020A08 gene	1200020A08Rik	1.7	0.029	1.8	0.029	1.5	0.029	1
71340	RIO kinase 1 (yeast)	Riok1	1.7	0.029	1.9	0.029	1.3	0.057	1

Locus Link	Gene Name	Gene symbol	Fold 2h	2h wt	Fold 6h	6h wt	Fold 24h	24h wt	Conserved CRE sites
				*P value		*P value		*P value	
22381	WW domain binding protein 5	Wbp5	1.7	0.029	2.1	0.029	1.5	0.029	1
83431	nuclear distribution gene E-like homolog 1 (<i>A. nidulans</i>)	Ndel1	1.7	0.029	1.3	0.057	1.3	0.029	1
69742	RIKEN cDNA 2410018G23 gene	2410018G23Rik	1.7	0.029	1.4	0.029	1.3	0.029	1
241296	leucine-rich repeat-containing 8	Lrrc8	1.7	0.029	1.4	0.029	1.1	0.286	1
14593	geranylgeranyl diphosphate synthase 1	Ggps1	1.7	0.029	1.1	0.514	1.0	0.686	1
19291	purine rich element binding protein B	Purb	1.7	0.029	1.7	0.029	-1.5	0.029	1
13371	deiodinase, iodothyronine, type II	Dio2	1.6	0.029	1.5	0.286	-1.0	0.914	1
67581	RIKEN cDNA 4930451A13 gene	4930451A13Rik	1.6	0.029	1.7	0.114	1.2	0.200	1
22682	zinc finger protein 216	Zfp216	1.6	0.029	1.1	0.371	1.1	0.429	1
73804	kinesin family member 2C	Kif2c	1.6	0.029	-1.1	0.629	-3.6	0.029	1
71770	adaptor-related protein complex 2, beta 1 subunit	Ap2b1	1.6	0.029	1.8	0.029	-1.1	0.457	1
28199	WD repeat domain 23	Wdr23	1.6	0.057	2.1	0.029	1.9	0.029	1
74375	golgi coiled coil 1	Gcc1	1.6	0.057	1.4	0.057	1.9	0.029	2
211556	cDNA sequence BC002199	BC002199	1.6	0.029	1.5	0.029	3.3	0.029	1
17261	myocyte enhancer factor 2D	Mef2d	1.6	0.029	1.3	0.057	1.2	0.057	1
56398	RIKEN cDNA 1500003O03 gene	1500003O03Rik	1.6	0.029	1.7	0.029	1.4	0.029	1
16451	Janus kinase 1	Jak1	1.6	0.029	2.0	0.029	3.4	0.029	1
12283	calcium binding protein 39	Cab39	1.6	0.029	1.3	0.114	1.2	0.229	1
21969	topoisomerase (DNA) I	Top1	1.6	0.057	1.2	0.314	-1.3	0.286	1
28146	DNA segment, Chr 3, University of California at Los Angeles 1	D3Ucla1	1.6	0.029	1.7	0.029	-1.2	0.057	1
22214	ubiquitin-conjugating enzyme E2H	Ube2h	1.6	0.029	1.8	0.029	2.5	0.029	1
50753	F-box only protein 8	Fbxo8	1.5	0.029	1.0	0.857	-1.1	0.229	1
12566	cyclin-dependent kinase 2	Cdk2	1.5	0.029	1.1	0.400	-1.5	0.029	1
104360	insulin related protein 2 (islet 2)	Isl2	1.5	0.029	1.2	0.200	1.1	0.457	1
21372	transducin (beta)-like 1 X-linked	Tbl1x	1.5	0.057	1.3	0.057	-1.4	0.257	1
19687	replication factor C 1	Recc1	1.5	0.029	-1.1	0.171	-1.2	0.200	1
57439	RIKEN cDNA 1300007B12 gene	1300007B12Rik	1.5	0.029	1.2	0.086	-1.4	0.029	1
67849	RIKEN cDNA 2610036L13 gene	2610036L13Rik	1.5	0.029	-1.1	0.029	-4.1	0.029	1
52708	DNA segment, Chr 12, ERATO Doi 748, expressed	D12Erd748e	1.5	0.029	1.2	0.229	1.1	0.114	1
23806	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (<i>DrosoArih1</i>)		1.5	0.029	1.1	0.514	-1.1	0.457	1
66603	survivor of motor neuron protein interacting protein 1	Sip1	-1.6	0.057	-1.7	0.029	-2.9	0.029	1
21379	transforming growth factor beta regulated gene 4	Tbrg4	-1.6	0.029	-2.9	0.029	-2.6	0.029	1
233875	expressed sequence AI225782	AI225782	-1.6	0.029	-1.4	0.029	-1.7	0.029	1
12488	CD2-associated protein	Cd2ap	-1.6	0.057	-1.2	0.086	-1.1	0.457	1
67561	RIKEN cDNA 8430408H12 gene	8430408H12Rik	-1.6	0.029	1.1	0.143	-1.2	0.114	1
58220	par-6 (partitioning defective 6) homolog beta (<i>C. elegans</i>)	Pard6b	-1.6	0.029	-1.4	0.029	1.1	0.229	1
66587	Fas-activated serine/threonine kinase	Fastk	-1.6	0.029	-1.6	0.029	-1.4	0.029	1
70047	tRNA nucleotidyl transferase, CCA-adding, 1	Trnt1	-1.6	0.029	-1.9	0.029	-2.0	0.029	1
101612	glutamate-rich WD repeat containing 1	Grwd1	-1.6	0.057	-2.6	0.029	-3.2	0.029	1
14455	growth arrest specific 5	Gas5	-1.6	0.029	-4.2	0.029	-4.1	0.029	1
67095	RIKEN cDNA 2310001H13 gene	2310001H13Rik	-1.7	0.029	1.1	0.057	1.2	0.029	1
52906	Abelson helper integration site	Ahi1	-1.7	0.029	-1.6	0.029	-1.3	0.029	1
12499	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	-1.7	0.057	-1.5	0.086	1.2	0.200	1

Locus Link	Gene Name	Gene symbol	Fold 2h	2h wt	Fold 6h	6h wt	Fold 24h	24h wt	Conserved CRE sites
			wt	*P value	wt	*P value	wt	*P value	
74164	nuclear transcription factor, X-box binding 1	Nfx1	-1.7	0.029	-1.7	0.029	1.2	0.086	1
27643	ubiquitin-like 4	Ubl4	-1.7	0.029	-1.4	0.029	-1.3	0.029	1
20606	somatostatin receptor 2	Sstr2	-1.8	0.029	-1.6	0.029	-2.5	0.029	1
170719	oxidation resistance 1	Oxr1	-1.8	0.057	1.2	0.543	1.6	0.143	1
67870	RIKEN cDNA 2310057D15 gene	2310057D15Rik	-1.8	0.029	-2.2	0.029	-2.8	0.029	1
216549	RIKEN cDNA 9130023F12 gene	9130023F12Rik	-1.8	0.029	1.3	0.057	1.1	0.086	1
72400	PIN2/TRF1-interacting protein	Pinx1	-1.8	0.029	-2.5	0.029	-2.5	0.029	1
104662	expressed sequence AW550801	AW550801	-1.8	0.029	-2.5	0.029	-2.1	0.029	2
68449	RIKEN cDNA 1110003P22 gene	1110003P22Rik	-1.8	0.029	-1.9	0.029	-2.3	0.029	1
330836	expressed sequence AI643885	AI643885	-1.8	0.029	-1.5	0.029	-1.5	0.057	1
68092	nuclear cap binding protein subunit 2	Ncbp2	-1.9	0.029	-1.5	0.057	-1.2	0.143	1
101612	glutamate-rich WD repeat containing 1	Grwd1	-1.9	0.029	-4.0	0.029	-4.7	0.029	1
68040	RIKEN cDNA 3110024A21 gene	3110024A21Rik	-1.9	0.057	-2.0	0.029	-1.5	0.314	1
22632	YY1 transcription factor	Yy1	-1.9	0.029	-1.1	0.629	1.1	0.143	1
13684	eukaryotic translation initiation factor 4E	Eif4e	-2.0	0.029	-2.2	0.029	-2.5	0.029	1
66973	mitochondrial ribosomal protein S18B	Mrps18b	-2.0	0.029	-2.3	0.029	-2.7	0.029	1
19206	patched homolog 1	Ptch1	-2.0	0.057	-1.0	0.943	-1.4	0.086	1
50926	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	-2.0	0.029	-3.2	0.029	-2.7	0.029	1
67053	ribonuclease P 14kDa subunit (human)	Rpp14	-2.1	0.029	-2.0	0.029	-1.9	0.057	1
103737	peroxisomal biogenesis factor 12	Pex12	-2.2	0.029	-1.5	0.057	-1.0	0.971	1
13537	dual specificity phosphatase 2	Dusp2	-2.2	0.029	-1.1	0.686	1.4	0.171	1
108673	DNA segment, Chr 19, ERATO Doi 678, expressed	D19Erd678e	-2.3	0.029	-3.3	0.029	-3.6	0.029	1
56207	ubiquitin carboxyl-terminal esterase L5	Uchl5	-2.3	0.029	-3.1	0.029	-5.1	0.029	1
20383	splicing factor, arginine/serine-rich 3 (SRp20)	Sfrs3	-2.4	0.029	-2.6	0.029	-2.9	0.029	1
12068	blocked early in transport 1 homolog (<i>S. cerevisiae</i>)	Bet1	-2.5	0.057	1.6	0.200	1.2	0.343	1
19272	protein tyrosine phosphatase, receptor type, K	Ptprk	-2.5	0.029	-3.9	0.029	-3.6	0.029	1
67712	mitochondrial solute carrier protein	Mscp	-2.7	0.029	-2.0	0.029	-1.6	0.029	1
58208	B-cell leukemia/lymphoma 11B	Bcl11b	-3.9	0.029	-3.1	0.029	-2.1	0.029	1

**P* value, permuted *P* value.

Locus Link IDs were used to determine the genomic loci of all genes on our microarray. Five-kb upstream regions from each mouse transcriptional start along with orthologous human sequence were extracted from the whole genome alignment of rat, mouse, and human (1). CRE sites were determined with the rVista program (2) based on TRANSFAC Professional 7.4 library (3) to identify CRE (TRANSFAC matrix ID-V\$CREB_01) sites in each of the aligned sequences, and determined which of the predicted sites are aligned and conserved between the species in the alignment. Conserved-total number of CRE sites aligned between human and mouse within 21-bp window of >80% conservation (2).

1. Zambon, A. C., McDearmon, E. L., Salomonis, N., Vranizan, K. M., Johansen, K. L., Adey, D., Takahashi, J. S., Schambelan, M. & Conklin, B. R. (2003) *Genome Biol.* **4**, R61.
2. Conkright, M. D., Guzman, E., Flechner, L., Su, A. I., Hogenesch, J. B. & Montminy, M. (2003) *Mol. Cell.* **11**, 1101-1108.
3. Joshi-Tope, G., Vastrik, I., Gopinathrao, G., Matthews, L., Schmidt, E., Gillespie, M., D'Eustachio, P., Jassal, B., Lewis, S., Wu, G., *et al.* (2003) *Cold Spring Harbor Symp. Quant. Biol.* **68**, 237-243.