

**CRTC1 mediates preferential transcription at neuronal activity-regulated
CRE/TATA promoters**

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Supplementary Table 1. Consensus CRE sites in the promoter regions of CREB target genes in *H. Sapiens*

Symbol	Gene Name	Accession	Chrom	Strand	Position	CRE Sites	Total CRE sites	Proximal CRE (-500b to 300b)	Distal CRE (-3Kb to -500b)	Proximal CRE TATA
<i>FOS</i>	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_005252	chr14	+	73735571	HT_-343 HT_-296 HT_-63 H_190	4	4	0	3
<i>DUSP1</i>	dual specificity phosphatase 1	NM_004417	chr5	-	172179126	h_97 ht_-102 FT_-113 HT_-163 ht_-1239	5	4	1	3
<i>NR4A1</i>	nuclear receptor subfamily 4, group A, member 1	NM_002135	chr12	+	50731457	ht_-1234 ht_-683 HT_-197 HT_-177 HT_-34 HT_-5	6	4	2	4
<i>NR4A2</i>	nuclear receptor subfamily 4, group A, member 2	NM_006186	chr2	-	157391745	HT_-71 HT_-81 FT_-163 h_-493 H_-1936 H_-2033 H_-2053	7	4	3	3
<i>PSEN1</i>	presenilin 1 Transcript variant 1	NM_000021	chr14	+	71593219	h_-166 h_-32	2	2	0	0
<i>PSEN1</i>	presenilin 1 Transcript variant 2	NM_007318	chr14	+	71593565	h_-512 h_-378	2	1	1	0
<i>PSEN2</i>	presenilin 2 (isoform 1)	NM_000447	chr1	+	224033590	-	0	-	-	-
<i>PSEN2</i>	presenilin 2 (isoform 2)	NM_012486	chr1	+	224033590	-	0	-	-	-
<i>PTGS2</i>	prostaglandin-endoperoxide synthase 2	NM_000963	chr1	-	183888548	h_29 ht_-53 ht_-564	3	2	1	1

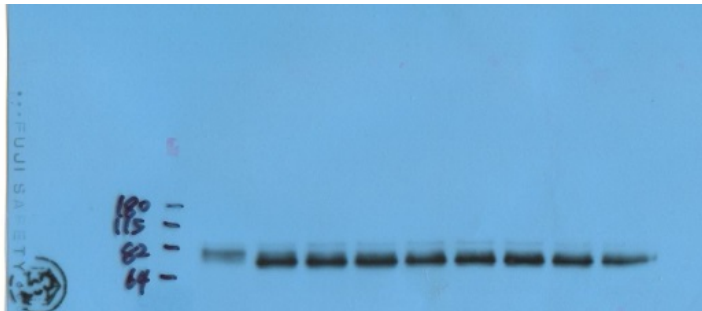
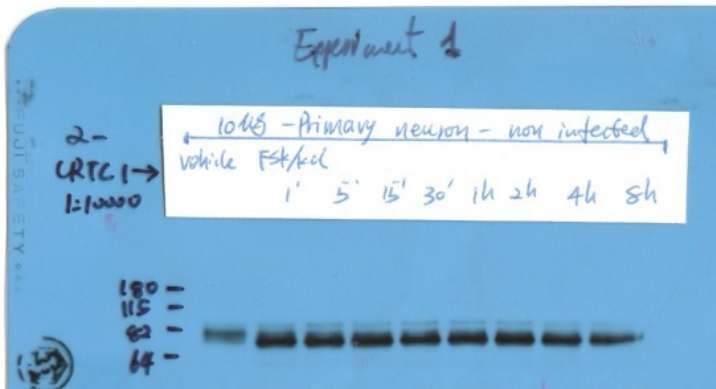
Promoter elements according to the CREB Target Gene database (<http://natural.salk.edu/CREB>)¹⁸. Number of CRE sites in gene promoters classified according to the distance to the transcription starting site as follows: total, proximal (-500 bp to 300 bp), distal (-3Kbp to -500bp) and proximal CRE/TATA (with TATA boxes < 300bp). The position of each CRE relative to the TSS is indicated following the underlined dash."FT_": conserved full CRE site (TGACGTCA/TGACGTCA) containing a downstream TATA box at less than 300 bp; "H_" or "HT_" mean a half CRE site (TGACG/CGTCA) conserved between species without (H) or with (HT) a TATA box less than 300 bp, respectively; "h_" or "ht_" mean a non-conserved half CRE site (TGACG/CGTCA) without (h) or with (ht) a TATA box less than 300 bp, respectively.

Original scans of Western blots

Figure 2

Figure 2A left panel: two different exposures of the same membrane are shown

pCRTC1 (upper band detected mainly in Vehicle treated neurons) and dephospho-CRTC1 (prominent lower band detected mainly at 1-8h):



GAPDH:

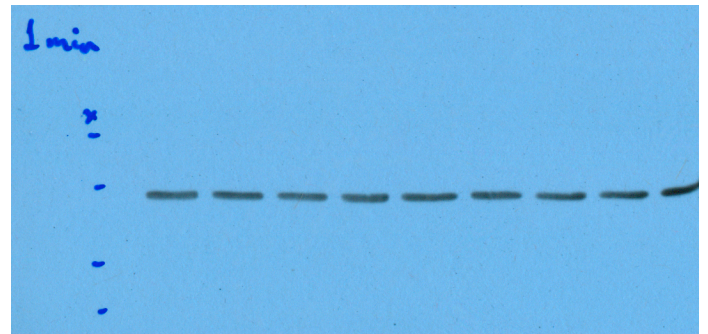
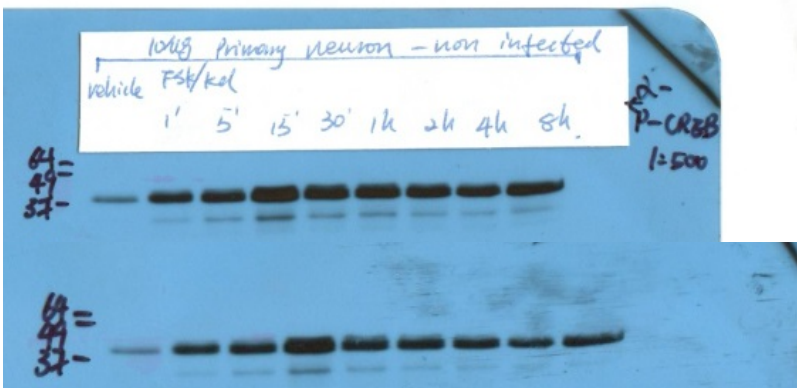
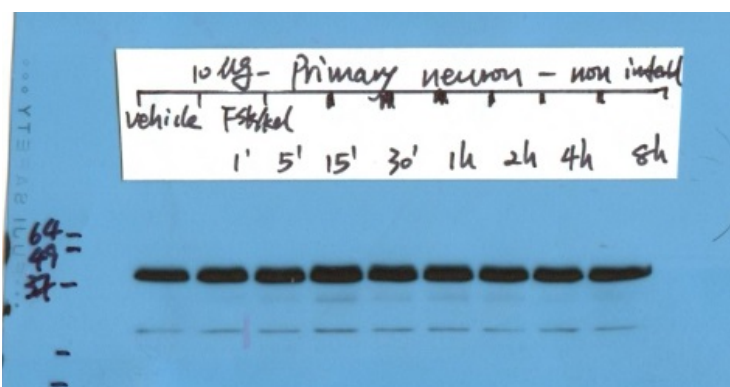


Figure 2A right panel:

pCREB (Ser133): Two different exposures are shown



CREB:



GAPDH:

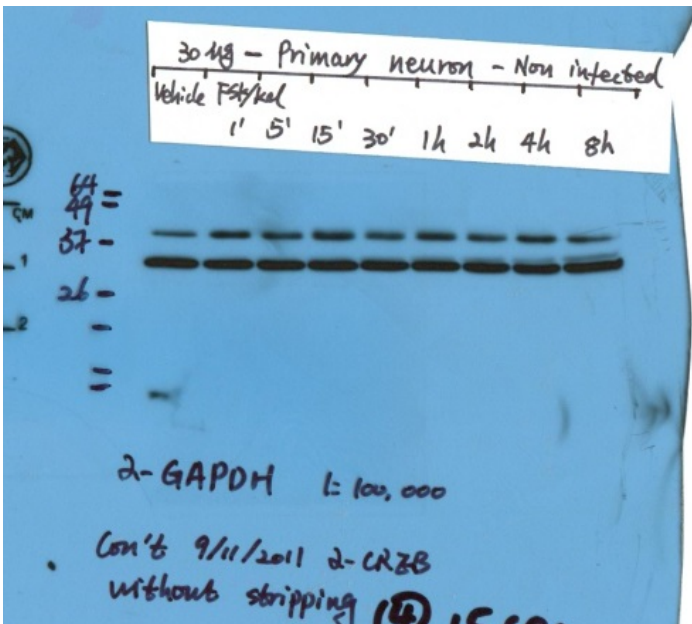
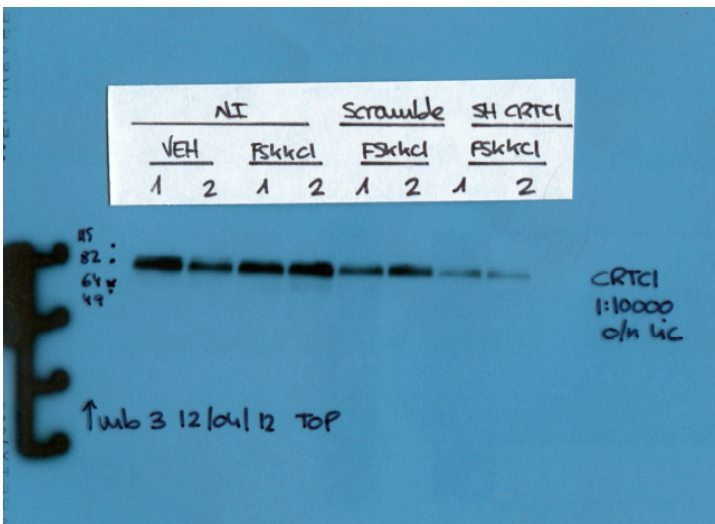


Figure 2D

CRTC1:



GAPDH:

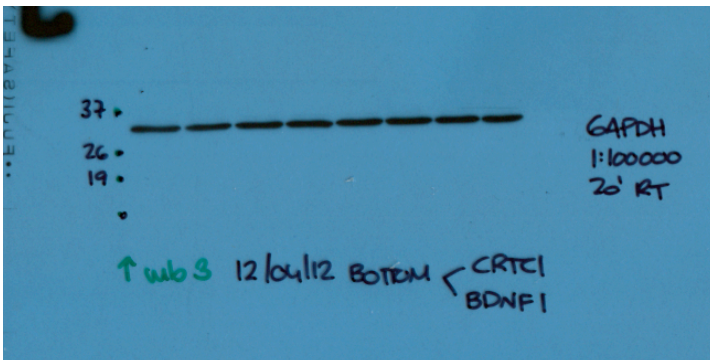
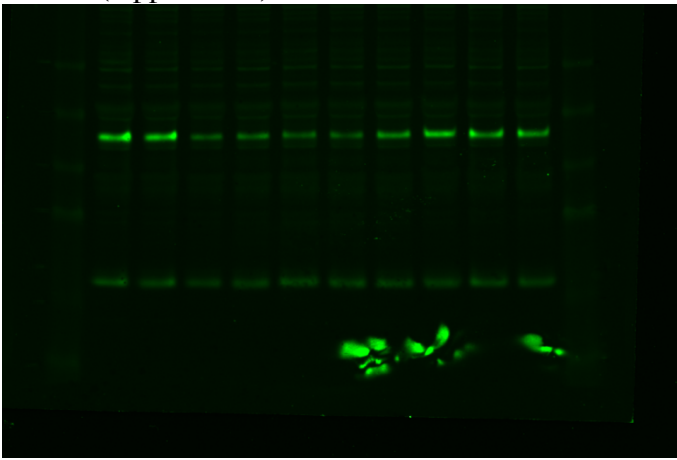


Figure 5

Figure 5A: Primary cortical neurons

CREB (Upper band):



β -tubulin:

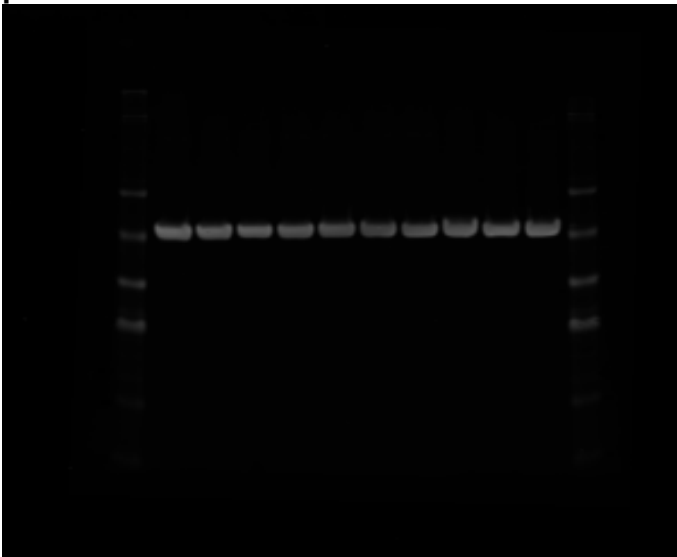
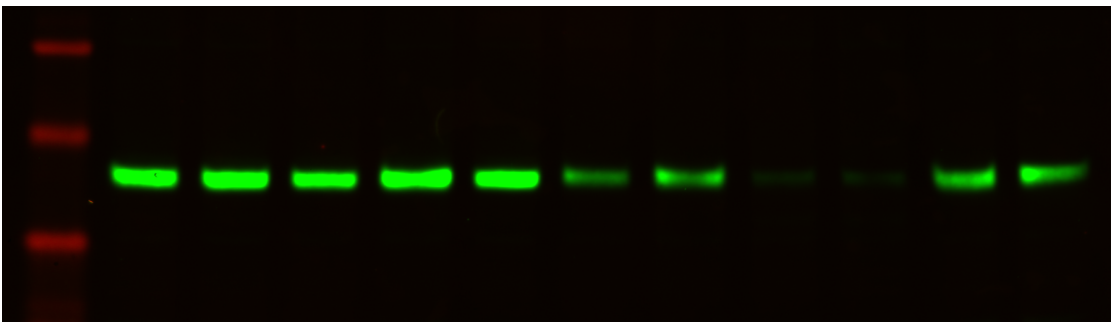


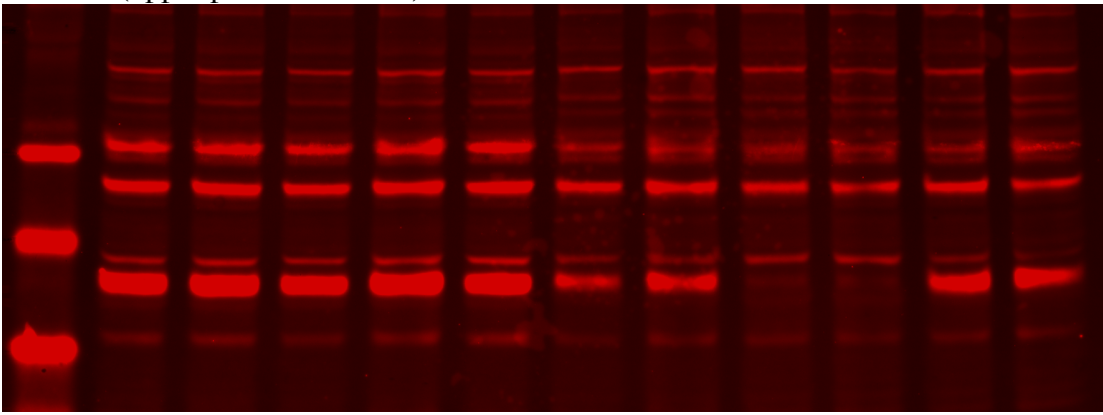
Figure 5C: HEK293 cells

Sequential blotting of the same membrane with the following antibodies:

CREB:



NURR1 (upper prominent band):



PS1 CTF (bottom band):

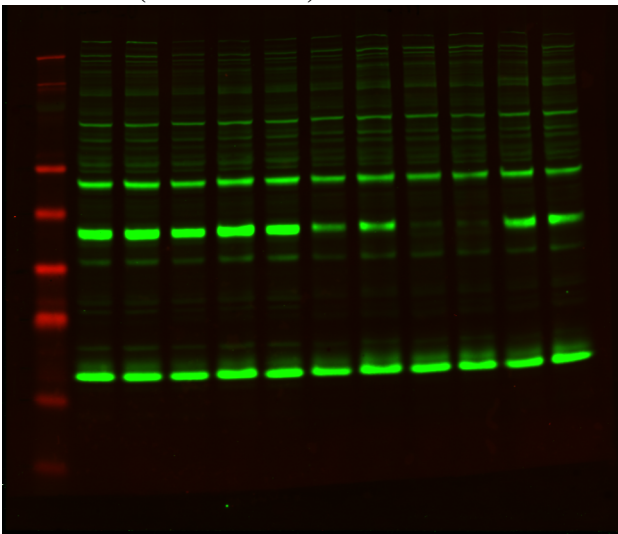
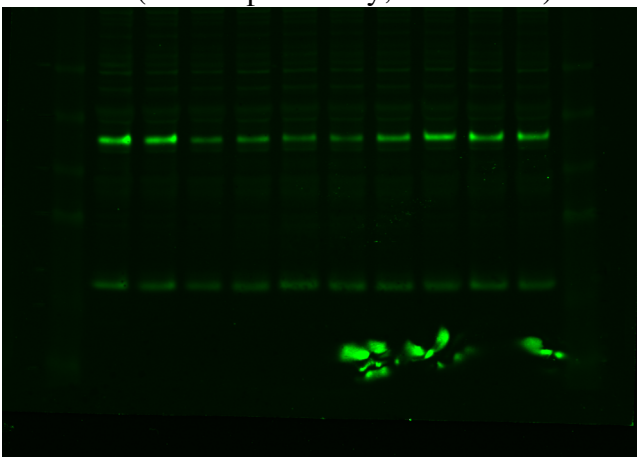


Figure 5D:

Same membrane than Figure 5A.

PS1 CTF (PS1 loop antibody; lower band)



β -tubulin:

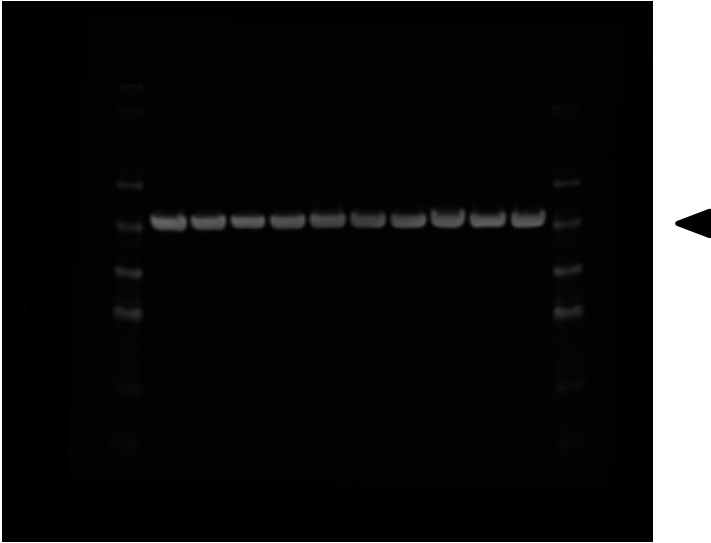


Figure 6

Figure 6A:

pCRTC1/CRTC1 : top (long exposure) and middle (short exposure) membranes and phosphorylated Ser133 CREB (pCREB; bottom membrane)

