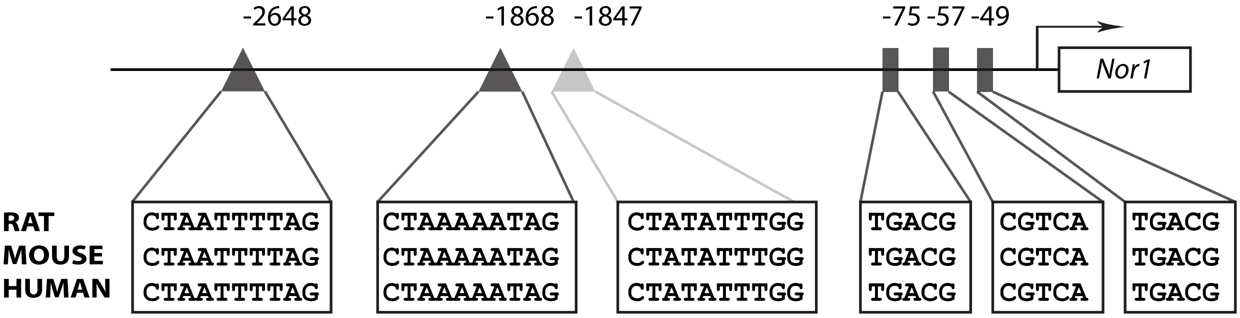
Supplementary Table 1 List of qPCR primers used in this study.

Gene	Forward Primer (5’ - 3’)	Reverse Primer (5’ - 3’)
Gapdh	AAACCCATCACCATCTTCCA	GTGGTTCACACCCATCACAA
c-fos	AGAATCCGAAGGGAAAGGAA	ATTGAGAAGAGGCAGGGTGA
Nur77	GGCATGGTGAAGGAAGTTGT	AAAGGCGGACTCTAGCAACA
Nor1	CCCCTCTATCCTTCCTCCAG	TCTGCAAGGTTTCTGGCTTT
Egr1	TGCACCCACCTTTCCTACTC	AGGTCTCCCTGTTGTTGTGG
Egr2	CTGGAGATGGCATGATCAACA	GGGAGCGAAGCTACTCGGATA
Arc	TGAGACCAGTTCCACTGCTG	CTCCAGGGTCTCCCTAGTCC
Human *c-fos*	CAAGCGGAGACAGACCAACT	AGTCAGATCAAGGGAAGCCA
Human α-globin	TGGACAAGTTCCTGGCTTCT	CCGCCCACTCAGACTTTATT



Supplementary Figure 1 The organisation of the rat *Nor1* promoter.
The *Nor1* promoter consists of 3 half CRE sites at -49, -57, -75 bp upstream of the transcription start site (TSS). There are 2 putative MREs at positions -1868 and -2648 that are conserved in the rat, mouse and human genes. A conserved MRE-like sequence CTATATTTGG was also found at -1847 bp upstream of the TSS. Sequences of 5000 bp upstream and 200 bp downstream of the TSS of the *Nor1* gene from *Rattus Norvegicus* (accession no.: NC_005104.2), *Mus Musculus* (accession no.: NC000070.4) and *Homo Sapiens* (accession no.: NC_000009.10) were retrieved from Genbank and aligned using Clustalw (available from EMBL-European Bioinformatics Institute, http://www.ebi.ac.uk). The sequences were scanned for the presence of CREs using the consensus sequence for a full CRE TGACGTCA or half CREs TGACG and CGTCA. The MRE consensus sequence CTAWWWWTAR was used to search for putative MEF2 binding sites.