

Supplementary Figure 1. (A) Phylogenetic footprinting of the previously known *id1* BMP-responsive enhancer (Katagiri *et al.*, 2002; Korchynskiy and ten Dijke, 2002; Lopez-Rovira *et al.*, 2002). The SBE and *bre7* motifs are highlighted in blue and red respectively. The SBE and the GC-rich (containing *bre7*) elements were found important for BMP-inducibility. These two elements plus the CREB/ATF motif were shown to mediate repression of *id1* by TGF- β (Kang *et al.*, 2003). The presence of the same three motifs within the BREs of *id2* and *id3* (Fig. 7A) may explain both their induction by BMP and their repression by TGF- β , similar to *id1* (Kang *et al.*, 2003; Locklin *et al.*, 2001). Aligned are the currently available genomic sequences of *Homo* (h), *Mus* (m), *Rattus* (r), *Canis* (c), *Gallus* (g), *Danio* (d), *Tetraodon* (t) and *Fugu* (f). Genomic sequences were extracted from the public databases, using the whole-genome shotgun data and the annotation browsers of NCBI (<http://www.ncbi.nih.gov>) and the Sanger Centre (<http://www.ensembl.org>). Sequence analyses were performed with the integrated bioinformatic package HUSAR (<http://genome.dkfz-heidelberg.de>). Multiple sequence alignments were created with the programs ClustalW (<http://www.ch.embnet.org/software/ClustalW.html>) and BoxShade (http://www.ch.embnet.org/software/BOX_form.html). Putative transcription factor binding sites were predicted using the program MatInspector (Genomatix; <http://www.genomatix.de/>). (B) Schematic map of the *id1-4* genes: the exons are in blue, the known *id1* BRE is in green and the novel, *in silico* discovered BREs are shown in red colour. (C) Nucleotide sequences of the BRE segments cloned and tested in Fig. 7C. Shown is the length of each segment, its position within human genomic contigs and the conserved part depicted in Fig. 7A,B or Supplementary Fig. 1A is highlighted. The length of each enhancer segment to be cloned was selected according to the *Homo/Mus* sequence conservation (not shown).

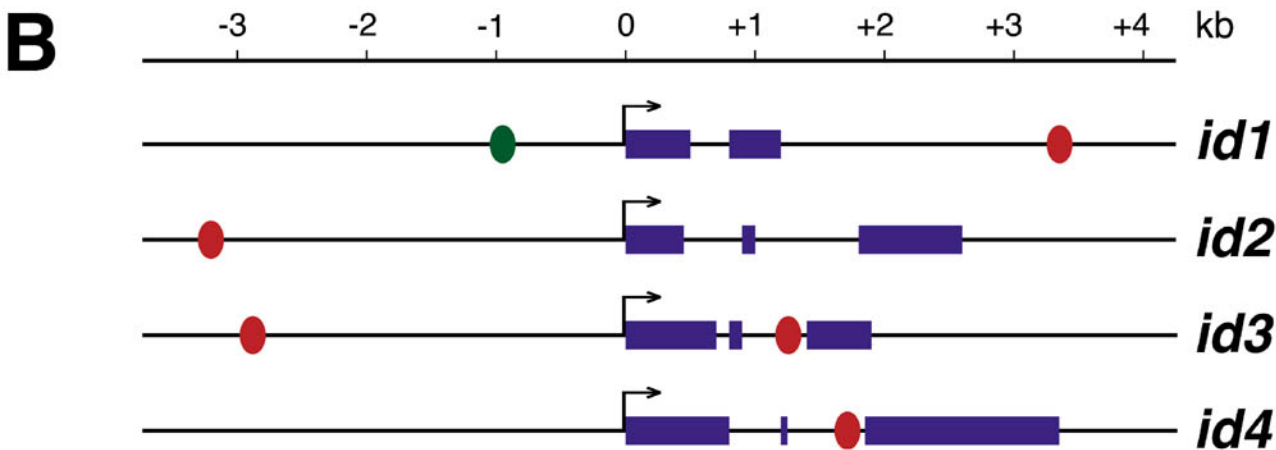
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C

id1 (-1.0 kb), 180 bp, NT_028392.4 (388163 - 388342):
GGGGAGCACGGGAAGTACTAGCTAGACCAGTTTGTCTGCTCCATGGCGACCGCCCGCGGGGCCAGCCTGAC
AGTCCGTCGGGTTTATGAATGGGTGACGTCACAGGCCTGGCGTCTAACGGTCTGAGCCGCTGGTTACG
ACGCTGACACAGACCGGCCCGGGAAGGGAGGGGGGAGACT

id1 (+3.3 kb), 171 bp, NT_028392.4 (392419 - 392589):
CCAGACCCAGCCCATCTGGAGGCCGGCTCCCGCGGGCCTGGGAGCGTTTTCCATCAGCTGGGCCCCGAGGA
ATGCGGAGCTATTTAACTGAGCATCCCCAGGTGTACGGAGGGCGCTGGCTGTCTGGGGCCCCGAGCCTT
TGGCACAGCCGCTAGACAAACAGCGCGCC

id2 (-3.2 kb), 153 bp, NT_005334.14 (3653089 - 3653241):
AGGCATTGATCAGCTGGGCGCGCGCTGAGTGACGGCGCGGTTGCCATGGCAGCCGCCTGAGCGGGCGCC
CGGAGGACAAGCTGCAGGGCGCGTGAATGGGCGGCGTACGCGCCTGGCGCCAGAGAGTCTGCTCCGG
GGCTCCGGCTCCG

id3 (-2.9 kb), 191 bp, NT_004610.16 (4692256 - 4692066):
GGAAAGGTTGCTGGGACACGCATCCCTGTGTGAACGCATGACGTCACCCACCTGGCGCCAGGCTGTCTGG
GGCTGAGTCTTAGATCAACACAGCTGTGGGACCGGGACCCACAGCTGGGCAAAGGAGCGGATTCTCAAC
AAAAATAGGATTGTGAGAAAAGTTCTGAAACAAAAACAGCGCAGACAAAA

id3 (+1.3 kb), 153 bp, NT_004610.16 (4688331 - 4688179):
CTCCGCTGTGGTCTTTGGCGCCAACTGGGTGGGGGCGAGCTGGGGCGCGGAGTTATCAGCTGGAGGTAC
AGACCAAGTTTCTCCCTGGCGCCGGCCAGTCTGCGGACGGCCCCCGCCTCGGCACGCTCGGCGGAAACT
GACTGCTCCTTGG

id4 (+1.7 kb), 161 bp, NT_007592.13 (10697561 - 10697721):
GGGCGGGTGTGTCTGACCTGGTGGTTTTGTTTTGGGTTGTTGATCAAGCATGTCTTGAGTTTTGGTGGTGG
GCGCCAGTTAGTCTGCAGCGAGAAGGTTACACACCCCCTCTATTCACTTCTTCCACAGGTGTGCGGC
CGCCTGAGCCCCGAGCCAGGAG