Supplementary Figure 2. Phylogenetic footprinting of the known BMP-responsive enhancer (BRE) of msx1 and of the in silico predicted BREs of msx2 (A), gata2 and gata3 (B), vox, vent, bmpr2, tlx2 and tbx2 (C). Aligned are the currently available genomic sequences of Homo (h), Mus (m), Rattus (r), Canis (c), Gallus (g), Xenopus (x) Danio (d), Tetraodon (t) and Fugu (f). The SBE and bre7 motifs are highlighted in blue and red respectively. A BRE composed of GCCG and SBE motifs was reported in the proximal enhancer (PE; MacKenzie et al., 1997) of msx1 (Alvarez Martinez et al., 2002). Multispecies alignment demonstrates the evolutionary conservation of the enhancer and the SBE motif in it, but not of the GCCG element. However, a fully conserved bre7 motif is present close to the SBE instead. The same two elements, phylogenetically conserved and with similar spacing, are also found upstream of the msx2 gene. Therefore, we propose that BMP responsiveness of msx genes is due to a conserved cluster of SBE and bre7 motifs in their 5' flanking region. The observed similar organisation of the BMP-responsive enhancers of msx1 (experimentally proven) and msx2 (in silico predicted) is in line with their similar expression patterns and redundant functions. The predicted BRE of msx2 is located downstream of the recently published mouse msx2 Lef1/Smad-dependent enhancer (Hussein et al., 2003), which is not phylogenetically conserved (data not shown). For the mouse tlx2 promoter, a 1.6 kb fragment was found BMP-responsive (Tang et al., 1998) and the enhancer activity was recently mapped to the fragment -1443/-1072 (Xiao et al., 2003). This segment contains the in silico predicted BRE shown in panel C.

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