

SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure S1. Sequence alignments of Krox20 amino acid sequences from different vertebrate species. The comparison reveals a relatively good evolutionary conservation of a large N-terminal domain (up to position 311), an almost complete identity over a region including the DNA binding domain (positions 312 to 425) and very poor conservation in the C-terminal domain. The two acidic regions are overlined in red. The previously described HCF-1 binding motif (HBM) is indicated by a red box. The isoleucine within the R1 domain involved in the interaction with Nab factors is indicated by a blue box. Numbers above the sequences correspond to the N-terminal extremities of the deletions.

Supplementary Figure S2. Analysis of *Nab* and *Hcf* expression in the chick developing hindbrain. (A-D) Whole mounted (A-C) and flat-mounted (D) hindbrains were prepared from chick embryos *in situ* hybridized with a *Nab* probe at the indicated somite stage (ss). At 7 ss, the expression of *Nab* is restricted to r3, whereas later on the gene is expressed in both r3 and r5. (E-J) Analysis of the expression of the chick *HCF* gene by *in situ* hybridization. Whole mounted (E-G, lateral views) and flat-mounted (H-J) hindbrains from embryos at the indicated somite stage (ss) are shown. In (F-J) co-hybridization was performed with a *Krox20* probe (orange). *HCF* is expressed in a decreasing gradient from the midbrain to the posterior part of the hindbrain and overlaps with the *Krox20*-positive domains (r3 and r5).

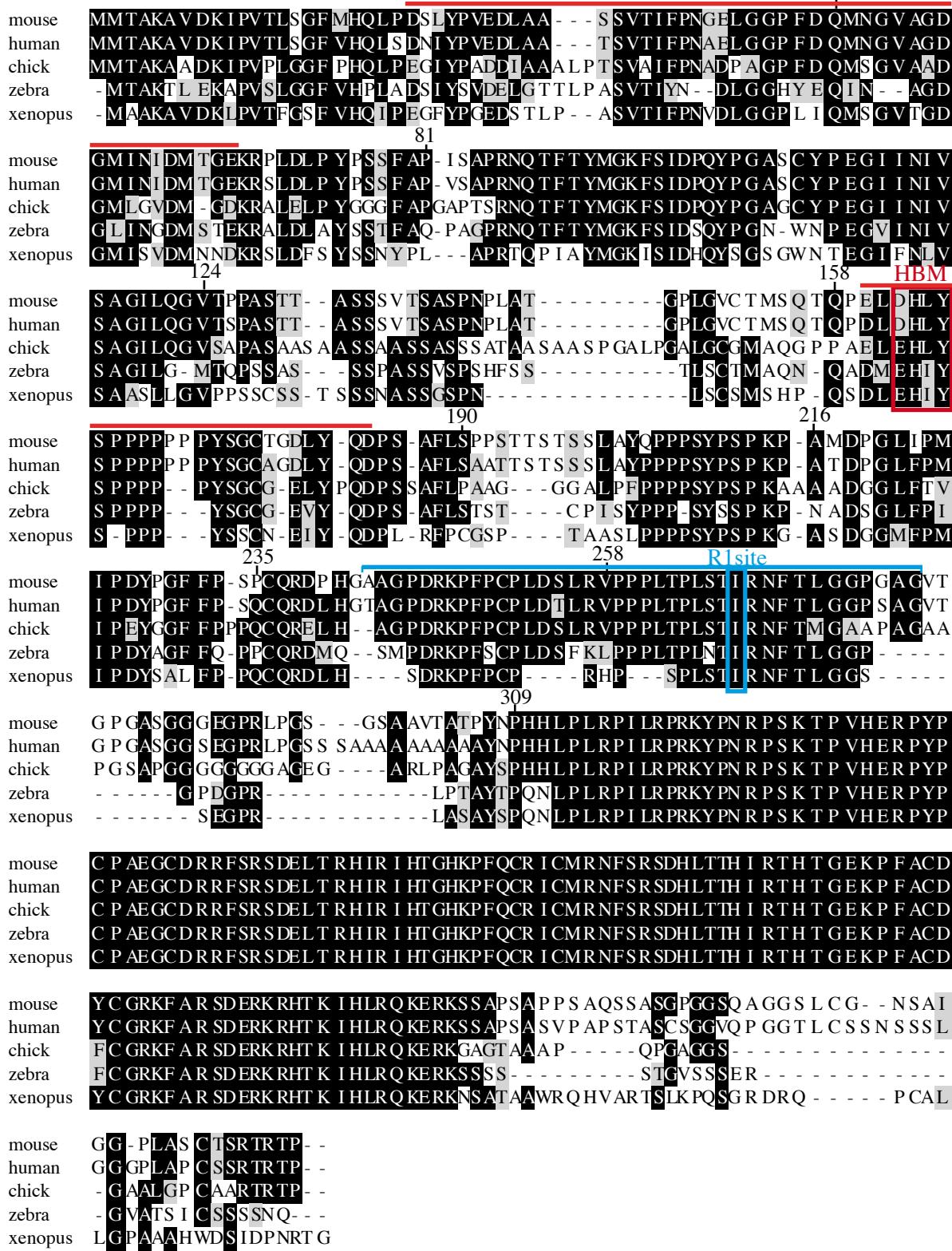


Figure S1

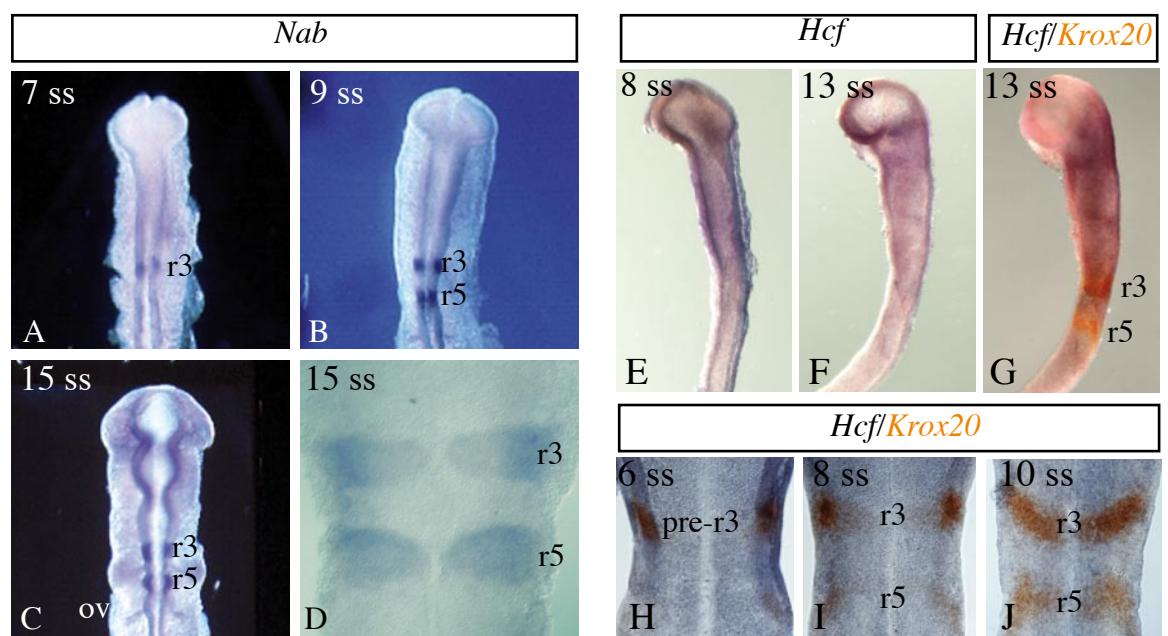


Figure S2