Targeted germ line disruptions reveal general and species-specific roles for paralog group 1 hox genes in zebrafish

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Et al.
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Steven E Weicksel, Ankit Gupta, Denise A Zannino, Scot A Wolfe and Charles G Sagerström*

Abstract

Background: The developing vertebrate hindbrain is transiently segmented into rhombomeres by a process requiring Hox activity. Hox genes control specification of rhombomere fates, as well as the stereotypic differentiation of rhombomere-specific neuronal populations. Accordingly, germ line disruption of the paralog group 1 (PG1) Hox genes Hoxa1 and Hoxb1 causes defects in hindbrain segmentation and neuron formation in mice. However, antisense-mediated interference with zebrafish hoxb1a and hoxb1b (analogous to murine Hoxb1 and Hoxa1, respectively) produces phenotypes that are qualitatively and quantitatively distinct from those observed in the mouse. This suggests that PG1 Hox genes may have species-specific functions, or that anti-sense mediated interference may not completely inactivate Hox function in zebrafish.

Results: Using zinc finger and TALEN technologies, we disrupted hoxb1a and hoxb1b in the zebrafish germ line to establish mutant lines for each gene. We find that zebrafish hoxb1a germ line mutants have a more severe phenotype than reported for Hoxb1a antisense treatment. This phenotype is similar to that observed in Hoxb1 knock out mice, suggesting that Hoxb1/hoxb1a have the same function in both species. Zebrafish hoxb1b germ line mutants also have a more severe phenotype than reported for hoxb1b antisense treatment (e.g. in the effect on Mauthner neuron differentiation), but this phenotype differs from that observed in Hoxa1 knock out mice (e.g. in the specification of rhombomere 5 (r5) and r6), suggesting that Hoxa1/hoxb1b have species-specific activities. We also demonstrate that Hoxb1b regulates nucleosome organization at the hoxb1a promoter and that retinoic acid acts independently of hoxb1b to activate hoxb1a expression.

Conclusions: We generated several novel germ line mutants for zebrafish hoxb1a and hoxb1b. Our analyses indicate that Hoxb1 and hoxb1a have comparable functions in zebrafish and mouse, suggesting a conserved function for these genes. In contrast, while Hoxa1 and hoxb1b share functions in the formation of r3 and r4, they differ with regards to r5 and r6, where Hoxa1 appears to control formation of r5, but not r6, in the mouse, whereas hoxb1b regulates formation of r6, but not r5, in zebrafish. Lastly, our data reveal independent regulation of hoxb1a expression by retinoic acid and Hoxb1b in zebrafish.

Keywords: Zinc finger nuclease, TALEN nuclease, Retinoic acid signaling, Hindbrain, Nucleosome positioning, Gene expression
Background

Hox genes encode a conserved family of homeodomain-containing transcription factors essential for metazoan development [1-4]. As a result of duplication events, vertebrate genomes contain four clusters of Hox genes, with the exception of teleost fish that have undergone an additional genome duplication - for instance, the zebrafish genome contains seven Hox clusters [4]. In most cases, genes that occupy the same position in different clusters (known as paralogs) have similar expression patterns and functions, leading to redundancy of Hox function. During early development, Hox genes specify tissue identities along the anterior-posterior (AP) axis of the animal. The linear arrangement of Hox genes in the genomic clusters coincides with the timing and position of their expression along the AP axis, a characteristic termed colinearity [3,5,6]. The retinoic acid (RA) signaling pathway activates early Hox gene expression and is important in colinear regulation [7,8]. RA binds a heterodimeric complex of RA receptors (RARs) and retinoic X receptors (RXRs) that target cis-regulatory sites known as RA response elements (RAREs) in the Hox clusters [9-11]. RA promotes decondensation of Hox clusters from compact chromosomal chromatin in cells and embryos [12-14] and this process correlates with the progressive activation of Hox transcription along the genomic cluster. Once transcribed, Hox genes also regulate the expression of other Hox genes in auto- and cross-regulatory loops. The highly conserved process of Hox gene activation and regulation leads to an overlapping series of Hox expression domains along the AP axis, sometimes referred to as the “Hox code” [15].

During early embryogenesis, the presumptive vertebrate hindbrain is transiently divided into seven to eight segments (rhombomeres) and Hox genes play a key role in formation of the more posterior rhombomeres [16]. Each rhombomere gives rise to unique cell populations from which segment-specific motor neurons and reticulospinal neurons differentiate. For motor neurons, this includes the trigeminal neurons in rhombomere 2 (r2) and r3, the facial motor neurons (FMNs) in r4, the abducens neurons in r5 and r6, and the vagal neurons in the caudal hindbrain. These neuronal pools form the motor neuron nuclei of the Vth, VIth, VIIth and Xth cranial nerves that innervate the face, head, and neck of the animal. Reticulospinal neurons also form in a rhombomere determinate manner and regulate breathing and circulation, as well as the coordination of locomotor signals between the spinal cord and the brain. For instance, the Mauthner neurons (MNs) form in r4 and extend axons contralaterally and posteriorly and function to control the escape response. Segmentation of the hindbrain starts with the formation of r4 followed by r1/r2, r3, r7, and r5/r6 [17]. Accordingly, the first Hox genes transcribed in the mouse, Hoxa1 and Hoxb1, are expressed in r4 [5,18,19]. A series of loss-of-function studies have determined that Hoxa1 and its downstream target Hoxb1 have separate functions. In particular, Hoxa1 mutant mouse embryos have segmentation defects while Hoxb1 mutants appear to have neuronal defects related to r4 specification. The segmentation defects observed in Hoxa1 mutants include an enlarged r3, a reduced r4, and a reduced or completely lost r5 [20-24]. Similar segmentation defects are also found in mice with mutations made to the retinoic acid response element (RARE) found in the downstream enhancer of Hoxa1 [25]. These segmentation defects are specific to the function of Hoxa1, as mouse Hoxb1 mutant embryos show no defects in hindbrain segmentation [26,27]. While hindbrain segments form normally in Hoxb1 mutants, r4-derived FMNs fail to migrate into r5 [23,26,28] and instead migrate away from the midline of r4, assuming lateral positions similar to trigeminal neurons in r3. FMN neurons in Hoxb1 mutants extend axons out through r4 into the second pharyngeal arch similar to the projection of wild type FMN axons. Loss-of-function studies for zebrafish hoxb1b and hoxb1a (functionally analogous to murine Hoxa1 and Hoxb1, respectively) have been accomplished using antisense morpholino oligos (MOs) to block translation of hoxb1b and hoxb1a. Embryos injected with hoxb1bMO have hindbrain segmentation defects with an expanded r3 and a reduced r4, r5 and r6, while hindbrain segmentation is unaffected in hoxb1aMO-injected embryos [29]. Furthermore, hoxb1aMO-injected embryos possess FMNs remaining in r4 that resemble the stalled FMNs observed in mouse Hoxb1 mutants. While these data indicate that the zebrafish hoxb1b and hoxb1a genes have roles similar to those of mouse Hoxa1 and Hoxb1, there are also differences between the defects observed in the mouse mutants versus MO-injected zebrafish. First, segmentation defects appear more severe in Hoxa1−/− and Hoxa1+/−;Hoxb1−/− mutants than in hoxb1bMO and hoxb1bMO;hoxb1aMO-injected zebrafish embryos. Specifically, the r5 domain in Hoxa1−/− mouse embryos is lost, while r5 is merely reduced in zebrafish hoxb1bMO-injected embryos. Hoxa1−/−;Hoxb1−/− mice also appear to have a stronger segmentation defect, with loss of both r4 and r5, while hoxb1bMO; hoxb1aMO-injected zebrafish embryos show only a 50% reduction in the size of r4. Second, unlike the Hoxa1−/− mice, hoxb1bMO-injected embryos have a reduced r6. Third, the hoxb1aMO shows no effect on the reticulospinal neurons in r4 although Hoxb1 mutant mice have a miss-specified r4. Indeed, even when hoxb1bMO and hoxb1aMO are co-injected, only incomplete formation of Mauthner neurons is observed in r4. These phenotypic differences suggest that either these genes function differently in mouse and zebrafish, or the MO phenotypes do not recapitulate true loss-of-function of hoxb1b and
Here we report the generation of $hoxb1a$ and $hoxb1b$ germ line mutations using zinc finger and TALE nucleases in zebrafish. We find that these germ line mutants have more severe phenotypes than those reported from antisense MO injections, suggesting that the MOs do not completely block Hox function. Our results demonstrate that $hoxb1a$ is required for specification of r4 and for the formation of r4-specific neurons. This is similar to the reported mouse phenotype, suggesting that $hoxb1a$ and $hoxb1b$ share conserved functions in r4 formation. Similarly, our results reveal that zebrafish $hoxb1b$ and mouse $Hoxa1$ share functions in the formation of r3 and r4, but their roles also differ, such that $Hoxa1$ is required in mouse r5 while $hoxb1b$ is required in zebrafish r6. Lastly, we demonstrate that $hoxb1b$ and retinoic acid act separately to activate $hoxb1a$ in zebrafish r6. Lastly, we demonstrate that $hoxb1b$ and $Hoxb1b$ share conserved functions in r4 formation.

**Results**

**Generation of $hoxb1a$ and $hoxb1b$ germ line mutants**

To investigate the roles of $hoxb1a$ and $hoxb1b$ in zebrafish hindbrain development, we generated $hoxb1a$ and $hoxb1b$ loss-of-function mutants using zinc finger nucleases (ZFNs) and TALE nucleases (TALENs). ZFNs and TALENs consist of the Fok1 endonuclease tethered to sequence-specific DNA-binding domains (zinc finger or TALE) that target the nuclease to a desired genomic location [30,31]. The use of obligate heterodimeric Fok1 nucleases increases target specificity by requiring that two complementary Fok1 nucleosome domains bind to adjacent genomic sequences for activity [32,33], thereby reducing, but not eliminating, the likelihood of off-target effects. Once activated through dimerization, the Fok1 nuclease introduces a double strand DNA break that is repaired through the non-homologous end joining (NHEJ) repair pathway. NHEJ is error prone and will introduce mutations at a low rate. While many of the resulting mutations do not affect protein function, we were particularly interested in identifying the small number of mutations that lead to shifts in the reading frame and introduce stop codons.

We initially employed ZFNs to target both $hoxb1a$ and $hoxb1b$ based on several criteria. First, nucleases were targeted to a site in the first exon of each gene in order to increase the likelihood that a frame shift would terminate translation upstream of known functional domains, particularly the homeodomain. Second, the spacing between the target sequences for each ZFN pair was set to either 5 bp or 6 bp based on previous reports indicating that these represent optimal spacing [34]. Third, we targeted regions containing a restriction site that could be used to screen for mutations. Based on these criteria, we designed several ZFNs to each gene using three separate ZFN “builds” (Table 1). The first and second builds were based on a modular library of single zinc finger proteins [35]. For build 1, we generated one ZFN targeting $hoxb1a$ (Zb1a-1) and one targeting $hoxb1b$ (Zb1b-1) where each ZFN contained three zinc fingers (ZF) assembled from the modular library. Build 2 (Zb1a-2 and Zb1b-2) employed the same modular library and targeted the same genomic sites as build 1, but each fusion protein contained four ZFs to increase specificity for the target sequence while decreasing the instances of off-target effects.

<table>
<thead>
<tr>
<th>TALEN/ZFN</th>
<th>Target coordinatea</th>
<th>Upstream TALEN/ZFN Target sequenceb</th>
<th>Downstream TALEN/ZFN Target sequenceb</th>
<th>Gapc</th>
<th>No. of unitsd</th>
<th>Embryos injectedf</th>
<th>Activityg</th>
<th>Diagnostic enzymeh</th>
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<td>2916</td>
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<td>15/16</td>
<td>50</td>
<td>NO</td>
<td>RsaI</td>
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</table>

*Target coordinate as defined by midpoint between the upstream and downstream nuclease recognition sites.

*Genomic sequence targeted by the upstream and downstream TALE and ZF nucleases.

*The number of ZF units used to assemble each nuclease.

*Target coordinate as defined by midpoint between the upstream and downstream nuclease recognition sites.

*The number of embryos injected to test activity and raise mutant families.

*Nucleases that disrupted the diagnostic restriction site were defined as active.

*The enzyme used to test activity of nucleases.
effects. For build 3, we designed two ZFNs to each gene (Zb1a-3, Zb1a-4, Zb1b-3 and Zb1b-4). Zb1b-3 and Zb1b-4 targeted the same genomic sequence as Zb1b-1 and Zb1b-2, although Zb1b-4 was offset 3 bp relative to Zb1b-3, while Zb1a-3 and Zb1a-4 targeted sites 60 bp and 125 bp, respectively, upstream of the site targeted by Zb1a-1 and Zb1a-2. The ZFNs designed in build 3 also used four ZFs each, but were assembled from an updated version of the ZF library that includes two-finger modules [36]. These two-finger modules were optimized for their ability to bind DNA efficiently in tandem to minimize the impact of context-dependent effects on recognition when fingers are assembled into arrays.

In vitro transcribed mRNA encoding each ZFN pair was injected into early one-cell stage embryos and genomic DNA was prepared from pools of whole embryos collected 24 hours post fertilization (hpf; Figure 1A). ZFN activity was measured by amplifying the targeted region, followed by digest by digestion to estimate the fraction of genome with a disruption of the diagnostic restriction site. Notably, the ZFNs are likely to act after the first several cell divisions (due to the rapid cell cycle of zebrafish embryos, as well as due to the need for the ZFN mRNA to be translated) and it is therefore expected that mutations will be induced in only a subset of cells – rendering the embryos mosaic. Embryos injected with Zb1b-3 and Zb1b-4, but not Zb1b-2 or Zb1b-1 (Figure 1B) revealed a partial loss of the diagnostic restriction site, suggesting that these ZFNs are active. Based on the intensity of the uncut band in the diagnostic digest, the Zb1b-3 ZFN may be more active than Zb1b-4. Since ZFNs from all three builds failed to induce mutations at the hoxb1a locus, we turned to TALENs as an alternative method to disrupt the hoxb1a gene. To increase the likelihood of success, we generated three different hoxb1a TALENs that differ slightly in the length of their target sequences (Table 1) using Golden Gate TALEN assembly [31]. As with ZFNs, TALENs were designed to target regions in the first exon of hoxb1a that include a diagnostic restriction site. Notably, the TALENs were directed to sites 450 bp (Tb1a-1) or 430 bp (Tb1a-2 and Tb1a-3) upstream of the region targeted by hoxb1a ZFNs. Using the same mRNA microinjection strategy as for the ZFNs, we found that TALEN Tb1a-2 introduced mutations – as evidenced by loss of the diagnostic restriction site – but that Tb1a-1 and Tb1a-3 did not (Figure 1B).

Having identified functional ZFNs and TALENs, we raised injected embryos to establish an adult F0 founder population. As noted, fish in this F0 population will be mosaic and each individual fish may carry more than one mutant allele for the same gene (Figure 1A). Genotyping of pooled offspring identified 20 hoxb1a (out of 24 tested) and 15 hoxb1b (out of 35 tested) F0 founders that transmit mutations via their germ lines, suggesting mutagenesis rates of 83% and 43% for hoxb1a and hoxb1b, respectively. Sequencing of mutant alleles from each F0 founder revealed that two of the 20 hoxb1a (A2 and A20) and three of the 15 hoxb1b (B2, B11 and B15) F0 founders carry mutations that introduce frame shifts (Table 2), while the remaining F0 founders transmitted mutations that disrupt the diagnostic restriction site, but that do not create frame shifts (two representative examples are shown in Additional file 1: Table S1). The five F0 fish that carry mutations causing frame shifts were outcrossed to wild type fish and the resulting offspring raised to generate the F1 generation. Genotyping of F1 fish allowed us to determine the transmission rate of mutations from mosaic F0 fish. We find that the hoxb1b F0 founders transmit their mutations at a frequency of ~40% (45% for B2, 43% for B11 and 41% for B15), while the hoxb1a F0 fish transmit their mutations at ~10% (14% for A2 and 9% for A20). Notably, we also find that the three hoxb1b founders each transmitted only one mutant allele, while the two hoxb1a founders transmitted multiple mutant alleles each (four alleles from A2 and two alleles from A20). Thus, we have generated six hoxb1a (um189, um190, um191, um192, um193, um194) and three hoxb1b (um195, um196, um197) mutant lines (Table 2) that were used for further phenotypic analysis.

Closer analysis of the mutant sequences revealed that Zb1b-3 and Tb1a-2 generated both insertions and deletions (Figure 1C). In particular, the Zb1b-3 ZFN introduced deletions ranging from 1 bp to 8 bp, as well as a 19 bp insertion in the hoxb1b gene, while the Tb1a-2 TALEN introduced deletions ranging from 1 bp to 8 bp, as well as a 17 bp insertion, in the hoxb1a gene. We note that large insertions and deletions that interfere with the PCR reaction (e.g. by deleting a primer site) would not be detected by our experiments, suggesting that the sizes observed here may be somewhat biased to smaller deletions and insertions. Conceptual translation of each mutant allele confirmed a shift in the reading frame (Figure 1 and Additional file 2: Figure S1). As a result, hoxb1a mutant alleles go out of frame starting with residue 15 (um193), residue 16 (um190, um191 and um192) or residue 17 (um189 and um194) and hoxb1b mutants starting with residue 71 (um197), residue 74 (um195) or residue 75 (um196). While the out of frame sequences code for varying numbers of missense residues, all terminate in a premature stop codon and none of the mutant alleles is predicted to encode a homeodomain.

Lastly, we raised embryos from hoxb1a+/um191 x hoxb1a+/um192 and hoxb1b+/um197 x hoxb1b+/um197 crosses to adulthood and genotyped them. We find that hoxb1aum191/um192 animals do not survive to adulthood (0/23 genotyped adults were hoxb1aum191/um192), while hoxb1bum197/um197 embryos do – although their viability may be somewhat reduced (13/84 genotyped adults were
Figure 1 Generation of \textit{hoxb1a} and \textit{hoxb1b} germ line mutants using ZFN and TALEN technologies. A. Diagram outlining experimental strategy. Active ZFNs and TALENs were identified by their ability to disrupt the sequence of a diagnostic restriction site in genomic DNA. Embryos injected with active ZFNs and TALENs were then raised and screened for founders that transmit frameshift mutations via their germ line. B. Identification of active nucleases. Genomic DNA was prepared from pools of injected embryos and digested with a diagnostic restriction enzyme. The $Z_{b1b}^3$, $Z_{b1b}^4$ and $T_{b1a}^2$ injected pools contain undigested material (arrows), indicating that the diagnostic restriction site has been disrupted. C. Characterization of germ line transmitted \textit{hoxb1a} and \textit{hoxb1b} mutations. Six mutant \textit{hoxb1a} (top) and three mutant \textit{hoxb1b} (bottom) alleles were identified to cause frameshift mutations. Nucleotide and peptide sequences are indicated for each mutant allele. Gaps in the nucleotide sequence indicate deletions, while red nucleotides indicate insertions. Numbers to the right of each nucleotide sequence indicate the net size of insertions/deletions. For the peptide sequence, gray boxes indicate residues read out of frame prior to encountering a premature stop codon. Amino acid numbers below each peptide sequence indicate the residue affected by the frameshift mutation, while numbers to the right indicate the length of the mutant peptide. HD = homeodomain. Black wedge indicates site of single intron in each sequence.
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Table 2 Characteristics of hoxb1a and hoxb1b germ line mutant alleles

<table>
<thead>
<tr>
<th>Founder</th>
<th>Transmission frequency</th>
<th>Sequencea</th>
<th>Type of mutationb</th>
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<tr>
<td>A2</td>
<td>14%</td>
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<td>Deletion (−1 bp)</td>
<td>um189</td>
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<tr>
<td></td>
<td></td>
<td>TTTTGAACAGGCGCTACT</td>
<td>Insertion/deletion (+17 bp)</td>
<td>um190</td>
</tr>
<tr>
<td></td>
<td></td>
<td>TTTTGAACAGGCGCTACT</td>
<td>Insertion (−5 bp)</td>
<td>um191</td>
</tr>
<tr>
<td>A20</td>
<td>9%</td>
<td>TTGGAATGCGCTACT</td>
<td>Deletion (−8 bp)</td>
<td>um193</td>
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<tr>
<td>hoxb1b</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>B2</td>
<td>45%</td>
<td>ATCGCGAGCCTCCAACACCGCTACT</td>
<td>Deletion (−8 bp)</td>
<td>um194</td>
</tr>
<tr>
<td>B11</td>
<td>43%</td>
<td>ATCGCGAGCCTCCAACACCGCTACT</td>
<td>Insertion (−1 bp)</td>
<td>um196</td>
</tr>
<tr>
<td>B15</td>
<td>41%</td>
<td>TTTTGAACAGGCGCTACT</td>
<td>Insertion (−19 bp)</td>
<td>um197</td>
</tr>
</tbody>
</table>

aSequence of mutant alleles. Deletions are shown as gaps and insertions are italicized. Nucleotides in bold indicate target site for diagnostic restriction enzyme in wild type sequence.
bIndicates whether mutation results from insertion, deletion or both. Numbers in parenthesis indicate net gain/loss of nucleotides in mutant sequence.
cIdentifying designation for each mutant allele.

hoxb1bum197/um197). We note that this is in contrast to the situation in the mouse, where both Hoxa1Icre and Hoxb1Icre pups die shortly after birth [20,26].

**hoxb1b is required for zebrafish hindbrain segmentation**

Formation of the vertebrate hindbrain requires segmentation of the neural tube into rhombomere domains, as well as the specification of distinct cell fates and the differentiation of characteristic types of neurons in each rhombomere. Paralog group 1 (PG1) hox genes, such as hoxb1a and hoxb1b, are among the earliest genes expressed in the hindbrain primordium and hox function has been implicated in multiple aspects of hindbrain development (reviewed in [16]). We therefore made use of the hoxb1a and hoxb1b mutant lines to examine the role of these genes in development of the zebrafish hindbrain.

We first examined the expression of several rhombomere-restricted genes – pax2 (expressed at the midbrain-hindbrain boundary; MHB), krox20 (expressed in r3 and r5), hoxb1a (expressed in r4), hoxb3a (expressed in r5 and r6) and hoxd4a (expressed in r7 and r8). For this purpose, heterozygous hoxb1b^um197/um197^ F1 fish were in-crossed and the resulting embryos were assayed at 22hpf by in situ hybridization followed by genotyping. We find that homozygous hoxb1b^um197/um197^ mutant embryos express krox20 in r3 and r5, as well as hoxb1a in r4 (Figure 2C). However, the size of r3 is increased and the size of r4 is decreased in hoxb1b mutants relative to wild type (or heterozygous) embryos (Figure 2A; Additional file 3: Table S2). To address the possibility that the Zb1b-3 ZFN might have introduced off-target mutations in the hoxb1b^um197^ line that could contribute to this phenotype, we also examined in-crossoes of the hoxb1b^um196^ and hoxb1b^um195^ lines, as well as pair-wise inter-crosses among all three lines. We find that mutant embryos derived from all such crosses exhibit the same phenotype and that this phenotype segregates with the hoxb1b mutation (Additional file 3: Table S2 and Additional file 4: Figure S2), suggesting that it is due to disruption of the hoxb1b gene. Furthermore, the PROGNOS on-line tool [37] revealed five exonic sites in the top fifty potential off-target sites for Zb1b-3, but neither of these sites resides on the same chromosome as the hoxb1b gene, and they would therefore segregate independently of the hoxb1b mutation in our crosses. Further analysis of hoxb1b^um197/um197^ mutant embryos revealed expression of pax2, hoxb3a and hoxd4a in the expected domains (Figure 2G, O). In addition to the enlargement of r3 and the reduction of r4 noted above, this analysis also revealed an apparent reduction of r6 – as evidenced by a smaller gap between r5 krox20 staining and r7 hoxd4a staining (brackets in Figure 2E, G), as well as by a reduction in the size of the hoxb3a expression domain (brackets in Figure 2M, O) in mutant embryos relative to wild type embryos.

We next quantified the changes in rhombomere size by direct measurements (Figure 2P). We find that r3 is significantly enlarged (~94.4 μm in hoxb1b mutants versus 62.0 μm in wild type; p = 0.0003) and r4 significantly reduced (~18.5 μm in mutant versus 47.6 μm in wild type; p = 2.53E-12) in mutant embryos. Notably, we cannot distinguish whether this effect is due to some cells switching from an r4 to an r3 fate, or if r3 cells have a growth advantage in the absence of hoxb1b function. We also find that r6 (~26.5 μm in mutant versus 47.6 μm in wild type; p = 3.32E-09) and r1/r2 (~129 μm in mutant versus 139 μm in wild type; p = 0.007) are somewhat reduced, but r5 is unaffected, in hoxb1b mutants. Accordingly, measuring the length of the entire hindbrain reveals it to be significantly shorter in hoxb1b mutant embryos...
(306 μm in mutant versus 354 μm in wild type; p = 3.28E-05), presumably as a result of the reduced length of several rhombomeres.

Analysis of hoxb1a mutant embryos (derived from an inter-cross of hoxb1aum191/+ and hoxb1aum192/+ carriers) revealed normal expression of krox20 in r3 and r5 of the hindbrain (Figure 2B, F, J, N). Furthermore, the size of the r4 domain is normal, but expression of hoxb1a is markedly reduced in r4 of hoxb1a mutants (Figure 2B; Additional file 3: Table S2). Examination of embryos derived from inter-crosses of the hoxb1aum189, hoxb1aum190, hoxb1aum193, and hoxb1aum194 alleles confirmed this phenotype and suggest that it results from mutation of hoxb1a rather than from off-target mutations introduced by the Tb1a-2 TALEN (Additional file 3: Table S2 and Additional file 5: Figure S3). Accordingly, the PROGNOS tool did not reveal any exonic sites among the top fifty potential off-target sites for the Tb1a-2 TALEN. Since hoxb1a regulates its own expression [38], the loss of hoxb1a transcript in hoxb1a mutants may be due to the loss of Hoxb1a protein, or, alternatively, to reduced stability of the mutant hoxb1a transcript. Accordingly, expression of fgf3, another r4-restricted gene dependent on hoxb1a for expression, is also markedly reduced in r4 of hoxb1a mutants at 14hpf (Figure 2J). Further analyses demonstrated normal expression of pax2, hoxd4a and hoxb3a (Figure 2F, N) and also revealed normal size of rhombomeres in hoxb1a mutant embryos. We conclude that hoxb1b is required for formation of appropriately sized rhombomere segments in the caudal hindbrain. In contrast, hoxb1a is essential in regulating expression of r4-restricted genes, indicating a role for hoxb1a in r4 specification.

hoxb1a is required for formation of r4-derived neurons

A key event in hindbrain development is the differentiation of unique complements of neurons in each rhombomere. In particular, motor neurons of the Vth (trigeminal) cranial nerve differentiate in r2 and r3, motor neurons of the VIth (abducens) cranial nerve form in r5 and r6 and motor neurons of the Xth (vagal) cranial nerve form in the caudal most region of the hindbrain. In addition, motor neurons of the VIIth (facial) cranial nerve form in r4, but subsequently migrate to r6 and r7 in zebrafish. In order to determine if neuronal differentiation is affected in hoxb1a and hoxb1b mutants, we analyzed cranial motor neuron formation. Wild type embryos displayed the expected stereotypical arrangement of cranial motor neurons at 48hpf (Figure 3A). Notably, this includes an almost complete lack of facial motor neurons (FMNs) in r4 as a result of these neurons having migrated caudally by this stage. In contrast, all hoxb1aum191/um192 mutant embryos revealed a large number of motor neurons in r4 and reduced numbers in r6 and r7 (Figure 3B). We
interpret this to mean that FMNs fail to migrate out of r4 and that the residual motor neurons in r5/r6 primarily represent abducens neurons. FMNs also remain in r4 of all \textit{hoxb1b} mutants, but the phenotype is more variable than what is observed in \textit{hoxb1a} mutants. Approximately half of the \textit{hoxb1b} mutants reveal significant retention of FMNs in r4 (Figure 3C), while the other half shows more extensive FMN migration (Figure 3D). In addition to impaired FMN migration from r4, the number of FMNs appears lower in \textit{hoxb1b} mutants and these are less well organized, with cells being less tightly grouped in r5-r7 and numerous cells found located outside the main clusters.

Similar to the cranial motor neurons, reticulospinal neurons also display rhombomere-specific differentiation in zebrafish. Specifically, bilaterally arranged Mauthner neurons form in r4 and project their axons across the midline down into the spinal cord at 36hpf (Figure 3F). Notably, differentiated Mauthner neurons are absent in \textit{hoxb1a} mutant embryos (Figure 3G). As observed for the cranial motor neurons, \textit{hoxb1b} mutants show a variable phenotype such that approximately half of the embryos retain one Mauthner neuron, while the other half fails to form both Mauthner neurons (Figure 3H, I). We conclude that \textit{hoxb1a} function is absolutely required for FMN migration and Mauthner neuron formation, but that \textit{hoxb1b} is only partially required for these processes.

\textit{hoxb1a} and \textit{hoxb1b} have separate functions in zebrafish hindbrain development

Since \textit{hoxb1a} and \textit{hoxb1b} are both required for normal r4 formation, we examined their functional relationship by analyzing \textit{hoxb1a}/\textit{hoxb1b} double mutant embryos (generated from a cross between \textit{hoxb1a}^{+/um193}; \textit{hoxb1b}^{+/um197} and \textit{hoxb1a}^{+/um194}; \textit{hoxb1b}^{+/um192} double heterozygotes). Using in situ hybridization, we find that double mutant embryos have hindbrain segmentation defects with an expansion of r3 and a reduction of r4 and r6 (Figure 2D, H; Additional file 3: Table S2). These changes in rhombomere size are indistinguishable from those observed in \textit{hoxb1b} mutant embryos (compare Figure 2G to H), further demonstrating that \textit{hoxb1a} does not play a role in zebrafish hindbrain segmentation. Furthermore, double mutant embryos lack \textit{hoxb1a} expression, while single mutants show a reduction either in the level (\textit{hoxb1a} mutants) or domain size (\textit{hoxb1b} mutants) of \textit{hoxb1a} expression (compare Figures 2B-D), indicating that both genes may play a role in \textit{hoxb1a} transcription.

Next we examined neuronal differentiation in double mutant embryos. We find that FMNs form in r4 of double mutants, but do not migrate caudally (Figure 3E), similar to the phenotype of \textit{hoxb1a} mutants (Figure 3B). We also note that the population of FMNs is smaller in double mutants (Figure 3E), similar to the phenotype of \textit{hoxb1b} mutants (Figure 3C, D). Lastly, double mutants completely lack Mauthner neuron formation in r4 (Figure 3J), identical to the \textit{hoxb1a} mutant phenotype. These findings are consistent with \textit{hoxb1b} being required for the size of r4 (and therefore the number of neurons formed in r4), while \textit{hoxb1a} is required for the migration of FMNs and the differentiation of Mauthner neurons. Notably, the abducens neuron population in r6 may be slightly smaller in double mutants, consistent with r6 being smaller in the absence of \textit{hoxb1b}, but this effect cannot be seen in \textit{hoxb1b} single mutants due to the residual migrating FMNs. We conclude that \textit{hoxb1a} and \textit{hoxb1b} have different functions in hindbrain development.
**hoxb1b and retinoic acid independently activate hoxb1a expression**

Although the size of r4 is reduced in hoxb1b mutant embryos, we note that hoxb1a expression persists. The expression of hoxb1a in the absence of hoxb1b is somewhat surprising since previous work suggested that early neural expression of hoxb1a depends on a Hoxb1b-regulated enhancer [29]. Since retinoic acid (RA) is known to activate hox gene transcription in many settings [13,25,28,39-43], we next investigated whether RA signaling activates hoxb1a transcription in the absence of hoxb1b.

To this end, embryos were treated with 10uM diethylaminobenzaldehyde (DEAB; a small molecule inhibitor of the RALDH enzyme involved in RA synthesis), or with 100nM exogenous retinoic acid, from 1hpf to 19hpf (Figure 4). We find that, in wild type embryos, 10uM DEAB blocks krox20 expression in r5, though not in r3 (that instead appears to be expanded), but does not affect hoxb1a expression in r4 (Figure 4C). Treatment of wild type embryos with RA produces a distinct phenotype such that hoxb1a expression is expanded, while krox20 expression is lost in r3 and reduced in r5 (Figure 4E). These results indicate that RA supports krox20 expression in r5 while it inhibits it in r3, consistent with previous reports that RA promotes posterior fates [44,45]. Furthermore, while hoxb1a expression in wild type embryos is enhanced by exogenous RA, it is not lost upon treatment with 10uM DEAB.

In hoxb1b<sup>um197/um197</sup> mutants, DEAB treatment blocks r5 krox20 expression – similar to the effect in wild type embryos – while r3 size is reduced somewhat (Figure 4D). However, while DEAB treatment has no effect on hoxb1a expression in wild type embryos, it blocks expression in hoxb1b mutants (Figure 4D). In contrast, RA treatment has the same effect in hoxb1b mutants as in wild type embryos, in that krox20 expression is lost in r3 and reduced in r5, while hoxb1a expression is expanded (Figure 4F). Taken together, our results reveal that hoxb1a expression is abolished upon simultaneous removal of hoxb1b and RA, but not when either factor is removed by itself, suggesting that RA and hoxb1b independently activate hoxb1a expression in zebrafish r4.

**hoxb1b affects nucleosome positioning at the promoter of hoxb1a**

We recently found that nucleosome positioning at the promoter regions of zebrafish hox genes is a progressive process that occurs over several stages of embryogenesis independent of RA signaling [46]. Since Hoxb1b regulates hoxb1a expression, at least in part, we wanted to test if Hoxb1b plays a role in nucleosome positioning at the hoxb1a promoter. We took advantage of the fact that hoxb1b<sup>um197/um197</sup> mutant fish are viable and mapped nucleosomes at the hoxb1a promoter of WT and hoxb1b mutant embryos using a modified nucleosome scanning approach (Figure 5A; [47]).

We detected three well-positioned nucleosomes at approximately 360 bp, 180 bp and 35 bp upstream of the transcription start site (TSS; -3, -2, and -1 nucleosomes; Figure 5B), as well as two less well-defined nucleosomes at 50 bp and 200 bp downstream of the TSS (+1 and +2 nucleosomes) at 4hpf – a stage when Hoxb1b protein is not yet expressed and cannot yet be detected at the hoxb1a promoter [48]. The nucleosome profile at 9hpf – when Hoxb1b is present at the hoxb1a promoter [48] – is similar...
to that at 4hpf, but there are some notable differences (Figure 5B). In particular, there is reduced nucleosome density surrounding the TSS from approximately position -200 bp to position +200 bp, indicating that changes in nucleosome density occur at the hoxb1a promoter at developmental time points when Hoxb1b is bound at the promoter.

To determine if the change in nucleosome arrangement between 4hpf and 9hpf is driven by Hoxb1b, we compared the nucleosome profile of hoxb1b mutant embryos at 9hpf to that of wild type embryos at 4hpf (Figure 5C). If Hoxb1b is solely responsible for promoting changes in nucleosome arrangement, the two profiles should be similar. Indeed, the 9hpf hoxb1b mutant and 4hpf wild type profiles are more similar to each other than are the wild type 9hpf and wild type 4hpf profiles, with the exception of a region centered at approximately +120 bp downstream of the TSS (Site 2; red arrow). This finding suggests that Hoxb1b is responsible for affecting nucleosome organization at the TSS and immediately upstream, but not further downstream at Site 2. Such a scenario is consistent with the fact that Hoxb1b is known to bind regulatory elements located 250-150 bp upstream of the hoxb1a TSS.

Accordingly, when we compare the nucleosome profile of 9hpf hoxb1b mutants to that of 9hpf wild type embryos, we find that the region around +120 bp (Site 2) is relatively unaffected, again consistent with nucleosomes in this region being organized independently of Hoxb1b (Figure 5D). As expected, there remains a significant difference upstream of the TSS (Site 1, green arrow) between 9hpf wild type and 9hpf mutant embryos, confirming that nucleosome occupancy in this region is likely dependent on Hoxb1b binding. Together, these data identify two regions where nucleosome organization is affected at the hoxb1a promoter. The first, ~120 bp upstream of the hoxb1a TSS (Site 1), near the known Hoxb1b binding site appears to be directly affected by Hoxb1b binding, while the second, ~120 bp downstream of the TSS (Site 2), appears to be independent of Hoxb1b binding.

**Discussion**

The phenotypes of mouse Hoxa1 and Hoxb1 germ line mutants, as well as the phenotypes of anti-sense mediated knock-down of zebrafish hoxb1b and hoxb1a have been characterized [20-24,26-29,43]. Differences between the zebrafish and mouse phenotypes suggest that these genes may play different roles in different species, or, possibly, that zebrafish phenotypes induced by anti-sense morpholinos (MOs) may not represent complete loss of function. To clarify these differences we created targeted germ line mutations for zebrafish hoxb1b and hoxb1a with ZFN and TALEN systems, respectively. Our findings indicate that Hoxa1 and hoxb1b share roles in hindbrain segmentation and that Hoxb1 and hoxb1a have similar roles in facial motor neuron migration. Comparing the phenotypes of our germ line mutants to those of MO loss-of-function suggests that the MO phenotypes do not represent complete loss of function in all respects, although we cannot completely rule out the
possibility that differences in genetic backgrounds may also affect the observed differences. Our experiments also reveal that hoxb1 and hoxb1a have species-specific functions. In addition, we report that hoxb1a transcription is independently regulated by both RA and Hoxb1b. Lastly, we demonstrate that Hoxb1b mediates its effect on hoxb1a expression, at least in part, by affecting nucleosome positioning at the hoxb1a promoter.

**Hoxa1 and hoxb1b have universal as well as species-specific roles in hindbrain segmentation**

Comparison of the previously reported hindbrain phenotypes of mouse Hoxa1 (produced by targeted germ line disruption) and zebrafish hoxb1b (produced by antisense MO) loss-of-function studies reveal several similarities. In particular, r3 is expanded while r4 and r5 are reduced in both species [20-22,24,28,29]. However, there are differences in the segmentation defects observed. In particular, the r5 segmentation defect in mouse Hoxa1−/− mutants is more severe, with some embryos losing r5 entirely [22], while hoxb1bMO zebrafish embryos display a reduction, but not a loss, of r5 [29]. In hoxb1bMO embryos r6 is also reduced, a phenotype not observed in Hoxa1−/− mice. The hoxb1b germ line mutants presented here have an expanded r3 and a reduced r4, similar to mouse Hoxa1 mutants and hoxb1bMO embryos, indicating that Hoxa1 and hoxb1b share universal roles in the formation of these rhombomeres. However, germ line disruption of hoxb1b produces a more severe phenotype than MO injection – e.g. Mauthner neurons are affected in the germ line mutant, but not by Hoxb1b MO – suggesting that the Hoxb1b MO does not completely block Hoxb1b function. Lastly, we observe a fully formed r5 and a reduced r6 in hoxb1b germ line mutants, distinct from mouse Hoxa1 mutants, suggesting that the loss of r5 in Hoxa1−/− mice is species specific and that hoxb1b has a species-specific role in r6 of zebrafish. We note that a zebrafish hoxb1b TILLING mutant was recently published [49]. While the effects on anteroposterior patterning were not characterized in detail for this mutant, Mauthner neuron formation was affected and it appears that r4 may be reduced in size – consistent with the phenotype of our hoxb1b ZFN alleles.

**Hoxb1 and hoxb1a are required for r4 specification**

Previous reports indicate that mouse Hoxb1 and zebrafish hoxb1a share functions important for the migration of facial motor neurons (FMNs) from r4 during vertebrate hindbrain development [26,27,29] and we confirm this function in the hoxb1a germ line mutants reported here. However, it has not been clear if hoxb1a is absolutely required for r4 specification in zebrafish. In particular, r4 specification can be tested further in zebrafish by assaying the formation of Mauthner neurons. In previous work, embryos injected with hoxb1aMO were found to have normal Mauthner neurons (McClintock et al., 2002) – suggesting either that hoxb1a is not absolutely required in r4, or that the MO-injections do not produce a complete null phenotype. Strikingly, we find that Mauthner neurons fail to form in hoxb1a germ line mutant embryos, indicating that the hoxb1aMO does not completely eliminate hoxb1a activity. It is not clear what step in Mauthner neuron differentiation is affected by loss of hoxb1a function, but the absence of Mauthner neurons was accompanied by the appearance of smaller neurons at the equivalent position in embryos co-injected with hoxb1aMO and hoxb1bMO [29], potentially suggesting a fate change or a failure to differentiate. Since our hoxb1a germ line mutant embryos also lack expression of the r4-specific fgf3 gene, we conclude that hoxb1a is required for r4-specific gene expression and neuronal differentiation in zebrafish.

**Regulation of hoxb1a transcription by RA and Hoxb1b**

Initiation of Hoxb1/hoxb1a transcription can be mediated by Hoxa1/Hoxb1 binding with Pbx and Meis/Prep cofactors at a Pbx/Prep/Hox responsive element (r4-regulatory element) located upstream of the Hoxb1/hoxb1a TSS [38,50-56]. In addition, expression of mouse Hoxb1 depends on a RA response element (RARE) located 3’ of the gene [43,57], but it is unclear if such an element is functional at the zebrafish hoxb1a locus [29,58], suggesting that hoxb1a might instead be highly dependent on hoxb1b for its expression in zebrafish. While we find that the hoxb1a expression domain is smaller in hoxb1b mutants, the level of expression does not appear noticeably affected, demonstrating that hoxb1a expression can be activated independently of Hoxb1b in zebrafish. Treatment with DEAB revealed that the hoxb1a expression observed in hoxb1b mutants requires RA signaling. Hence, our data suggest that Hoxb1b and RA can act independently to activate hoxb1a expression and that they are the predominant factors involved in this process – since simultaneous removal of both factors abolishes hoxb1a transcription. However, it remains possible that some aspects of hoxb1a expression require cooperation of RA and hoxb1b – e.g. RA induces hoxb1a more broadly in wild type than in hoxb1b mutant embryos. Since a functional RARE has not been identified at the hoxb1a locus, it is not clear whether RA acts directly, or if it acts indirectly via an intermediate factor.

As discussed, Hoxb1b regulates hoxb1a transcription by forming a complex with Pbx and Prep/Meis factors at the r4 regulatory element upstream of the hoxb1a TSS [48,54]. We recently demonstrated that nucleosome positioning around the promoters of hox genes is influenced by DNA-binding factors during early embryogenesis, but that RA signaling does not appear to affect this process.
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plasmids containing completed ZFNs and TALENs were following previously published protocols [31, 60]. pCS2
[35, 36]. TALENs were constructed using the Golden Gate
were completed using previously published protocols
recognition [36]. Nuclease assemblies for all three builds
were constructed from a single finger modular archive
matings and staged using morphological criteria as de-
Ekkwill (EK) embryos were collected through natural

Methods

Fish care
Ekkwill (EK) embryos were collected through natural
matings and staged using morphological criteria as de-
defined previously [59].

Identification of germ line mutations
Genomic DNA (gDNA) was prepared from a pool of 50
injected embryos at 24hpf. A fragment overlapping the
nuclease target site (a 200 bp fragment carrying a BtgI
restriction site from exon one of hoxb1a and a 300 bp
fragment carrying a Bsll restriction site from exon one
of hoxb1b; see Additional file 6: Table S3 for primer
sequences) was amplified and digested to determine if
the diagnostic restriction site had been disrupted, indicating
an active nuclease. Embryos injected with active TALENs
and ZFNs were raised to adulthood. These mosaic foun-
ders (F0) were outcrossed to wild type fish and pools of
50 embryos were genotyped as above to identify germ
line transmission. An F1 generation was raised from each
germ line positive founder and F1 carriers were identified
by genotyping of gDNA isolated from fin clips [61]. Indi-
vidual F1 carriers were then sequenced to determine if a
frameshift had occurred. Carriers with frameshift muta-
tions were used for phenotypic analysis.

Genotyping

Sequencing of F1 fish carrying frame shift mutations re-
vealed the introduction of a BtgI restriction site in the
hoxb1b\textsuperscript{um195} and hoxb1b\textsuperscript{um196} lines that was used for
subsequent genotyping. Further, hoxb1b\textsuperscript{um197} contains
an insertion that was used for subsequent genotyping by
employing an insertion-specific primer. See Additional
file 6: Table S3 for primer information.

In situ probes and antibody labeling

In situ protocols were as previous published [62]. Embryos
were fixed in 4% paraformaldehyde (pfa) and
stored in 100% methanol at −20°C. In situ probes for the
following genes were used: hoxb1a [63], krox20 [64], pax2
[65], hoxb3a [66], fgf3 [67], and hoxd4a [68]. Visualization
was completed using colorimetric reaction using NBT/ BCIP
or INT/BCIP in 10% polyvinyl alcohol. Embryos were
dissected from the yolk and flat mounted in 70%
glycerol for imaging on bridged coverslips as described
(Zannino and Appel, 2009). Images were captured using
a Nikon Eclipse E600 microscope equipped with Spot
RT Color camera (model 2.2.1). Antibody labeling with
mouse anti-Isl (39.4D5, 1:100; Developmental Studies
Hybridoma Bank (DSHB)) and mouse anti-3A10 (1:100;
DSHB) was visualized using the Alexa Fluro secondary
antibody 488 goat anti-mouse (1:200; Molecular Probes).
Embryos were fixed in 4% AB fix (4% paraformaldehyde,
8% sucrose, 1x PBS) for 2 hours at room temperature
(RT) or overnight at 4°C. Whole-mount fluorescent labeling

Generation of zinc finger and Tale nucleases

Zinc finger nucleases (ZFNs) in build 1 and 2 (Table 1)
were constructed from a single finger modular archive
[35]. ZFNs for build 3 were designed from a library con-
taining optimized two-finger modules for improved DNA
recognition [36]. Nuclease assemblies for all three builds
were completed using previously published protocols
[35, 36]. TALENs were constructed using the Golden Gate
TALEN assembly kit (addgene: TALEN Kit #10000000024)
following previously published protocols [31, 60]. pCS2
plasmids containing completed ZFNs and TALENs were
linearized and in vitro transcription was performed with the
T7 mMachine ultra kit (Ambion: AMB1345). 50-100 pg of mRNA encoding ZFNs or TALENs was then
injected into wild type embryos at the one cell stage.

Conclusions

We generated several novel germ line mutants for zebra-
fish hoxb1a and hoxb1b. Our analyses indicate that
mouse Hoxb1 and zebrafish hoxb1a have comparable
functions, suggesting a conserved role for these genes. In
contrast, while mouse Hoxa1 and zebrafish hoxb1b share
functions in the formation of r3 and r4, they differ with
regards to r5 and r6, where Hoxa1 appears to control for-
mation of r5, but not r6, in the mouse, whereas hoxb1b
regulates formation of r6, but not r5, in zebrafish. Lastly,
our data reveal independent regulation of hoxb1a expres-
sion by retinoic acid and Hoxb1b in zebrafish.
was performed as described [69]. Embryos were imaged by an upright Zeiss Imager.M2 equipped with a 20x water immersion objective (numerical aperture (NA) = 1.0), mounted on a Nano-Drive, and a Perkin Elmer Ultraview system. Images were imported into Adobe Photoshop and adjustments were limited to contrast, levels, and cropping and were applied to the entire image.

Micrococcal nuclease digestions and nucleosome identification

Micrococcal nuclease (MNase) digestions, isolation of mono-nucleosome fragments, and amplification of purified DNA was performed on 4 and 9 hour post fertilization embryos as previously published [46]. Nucleosomes were mapped to the hoxb1a promoter using a reported nucleosome scanning protocol [47]. Briefly, chromatin was isolated from embryos at 4hpf and 9hpf and digested with MNase. Mono-nucleosome sized fragments were purified and amplified by quantitative polymerase chain reaction (qPCR) using tiled primers spaced ~50 bp apart (See Additional file 6: Table S3 for primer sequences) from ~450 bp upstream to ~230 bp downstream of the hoxb1a TSS. qPCR was done using the Qiagen QuantiFast SYBR Green PCR Kit (Qiagen: 204054) on the ABI 7900HT Sequence detection system in a 384 well format and analyzed using SDS software v2.3. The signal from three biological replicates was averaged and values were expressed as a log2 ratio of the MNase sample to a control sample consisting of gDNA digested with MNase. Mono-nucleosome sized fragments were mapped to the entire image.

Additional file 6: Table S3. Primers used for genotyping and nucleosome scanning.

Competing interests

The authors declare that they have no competing interests.

Authors’ contributions

SEW participated in the design of the study, generated the germ-line mutants, analyzed their phenotype and drafted the manuscript. AG participated in the design of the ZFNs and TALENs and assisted in the assessment of their activity. DAZ participated in the phenotypic analysis of the mutants. SAW participated in the design of the study, the design of the ZFNs and TALENs and the assessment of their function. CGS conceived of the study, participated in its design, coordinated the study and finalized the manuscript. All authors read, revised and approved the final manuscript.

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References


Additional files

Additional file 1: Table S1. Sequences of two alleles with in-frame mutations.
Additional file 2: Figure S1. Alignment of mutant Hoxb1a and Hoxb1b proteins. Peptide alignment based on conceptual translation of mutant hoxb1a (A) and hoxb1b (B) alleles. Red residues represent missense residues caused by the frameshift mutation prior to encountering a premature stop codon. Blue indicates homeodomain.
Additional file 3: Table S2. Gene expression analysis of hoxb1a and hoxb1b mutants.
Additional file 4: Figure S2. Crosses of multiple hoxb1b mutant alleles reveal a consistent hindbrain specification phenotype. 22hpf wild type (A, C, E, G, I, K) and hoxb1b−/− (B, D, F, H, J, L) embryos were assayed by in situ hybridization for expression of hoxb1a in r4 (blue stain in panels A-L) and krox20 in r3/r5 (red stain in panels A-L). All embryos are flat mounted in dorsal view with anterior to the top.
Additional file 5: Figure S3. Crosses of multiple hoxb1a mutant alleles reveal a consistent hindbrain specification phenotype. 22hpf wild type (A, C, E) and hoxb1a−/− (B, D, F) embryos were assayed by in situ hybridization for expression of hoxb1a in r4 (blue stain in panels A-F) and krox20 in r3/r5 (red stain in panels A-F). All embryos are flat mounted in dorsal view with anterior to the top.


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