Supporting Information

Gehrke et al. 10.1073/pnas.1420208112

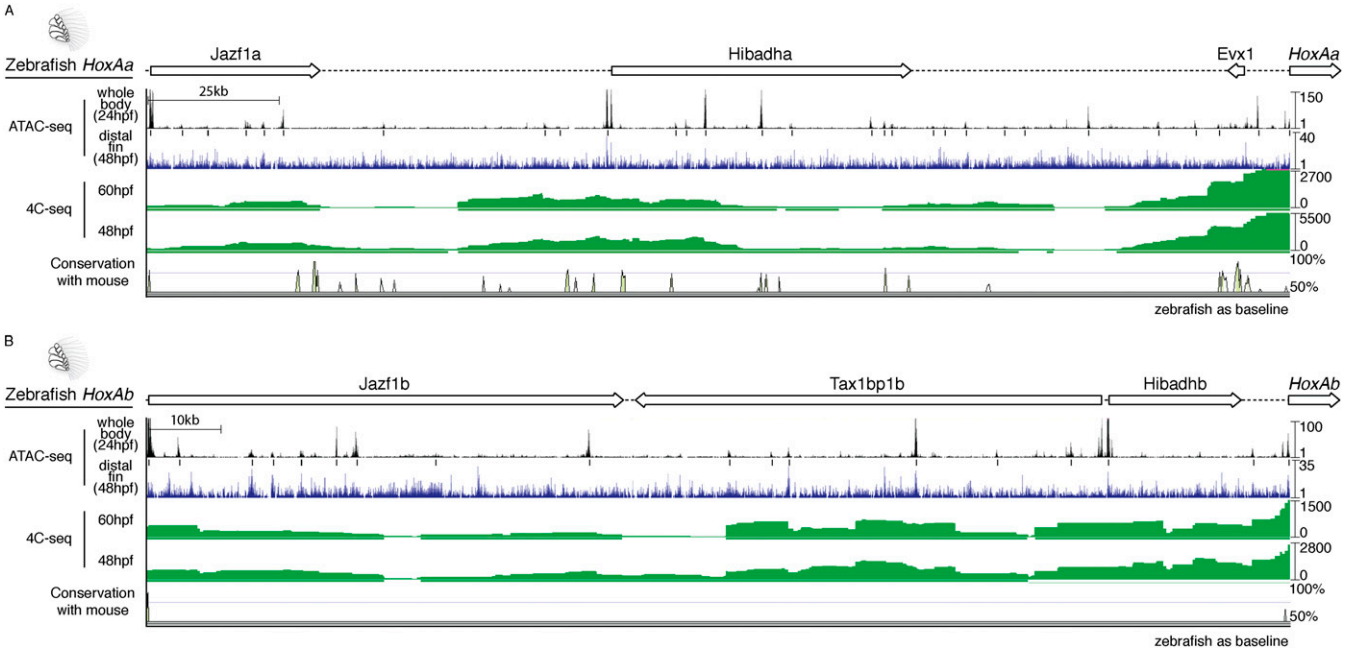

Fig. S1. Epigenetic profiling and sequence conservation of the zebrafish *hoxAa* (*A*) and *hoxAb* clusters (*B*). Schematic representations of the zebrafish *hoxA* clusters are shown at the top. ATAC-seq for both whole-body and distal fin are shown, combined with 4C-seq data to reveal areas of interaction with the *hoxa13a* and *hoxa13b* genes.

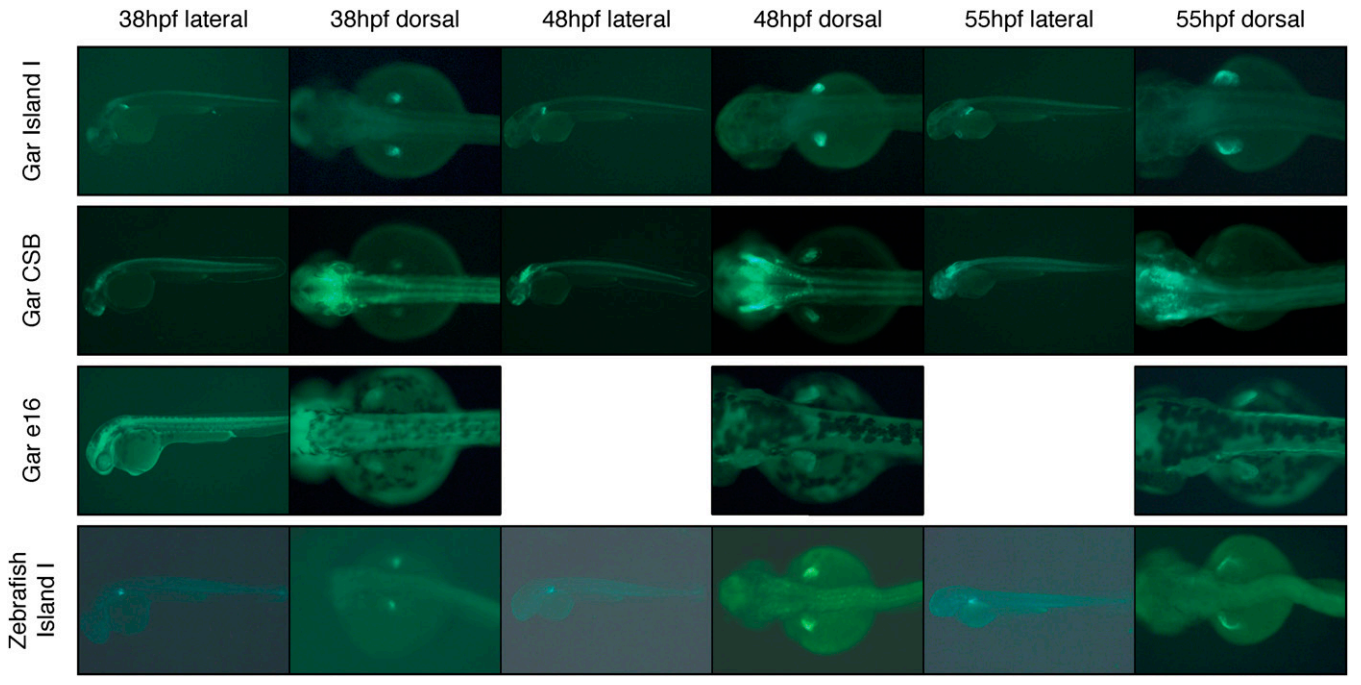

Fig. S2. Whole-body views of transgenic zebrafish. Lateral and dorsal views are shown for transgenic animals at 38, 48, and 55 hpf.

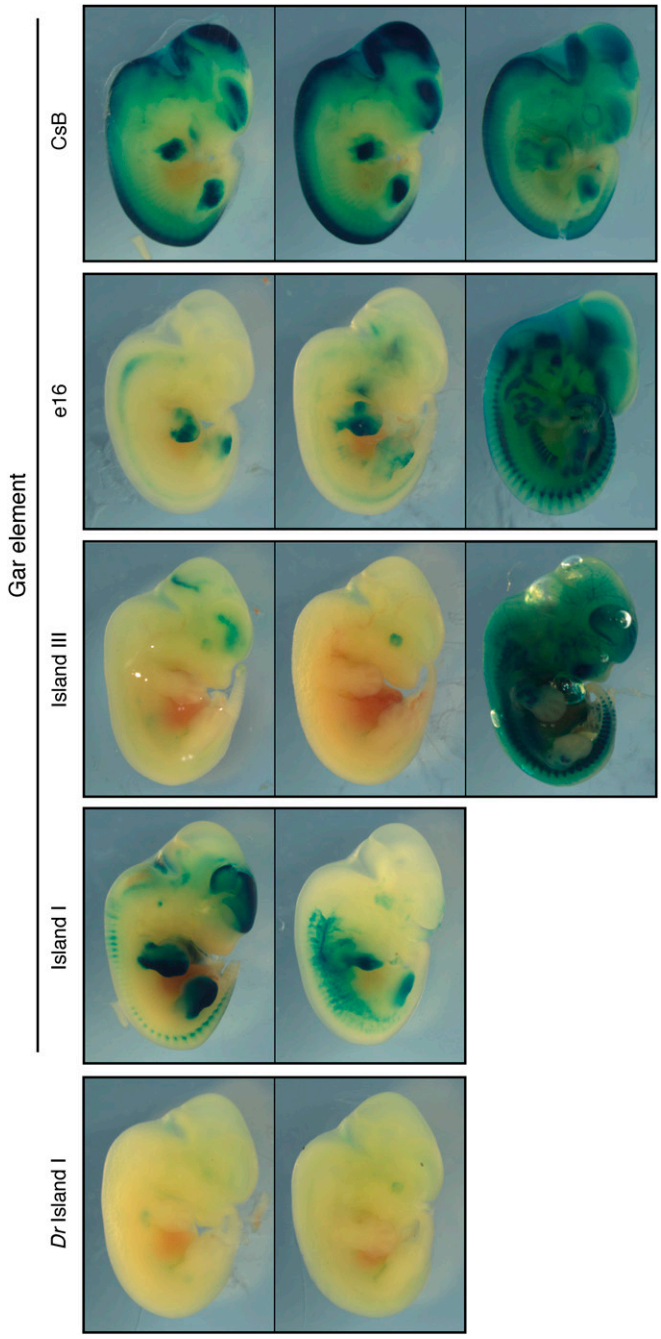

Fig. S3. Summary of mouse injections. All injected mouse embryos that were positive for LacZ staining are provided at stage e12.5.

Table S1. Comparisons between mouse and zebrafish ATAC-seq and previously published reports

Animal	Overlap with ATAC-seq
Mouse	
Peaks	
H3K4Me1 (LICR ENCODE)	26,210/52,705 (49.7)
H3K27ac (1)	18,082/25,861 (69.9)
Vista Enhancer Database (limb)	54/67 (80.6)
Vista Enhancer Database (all)	138/250 (55.2)
Zebrafish	
Peaks	
H3K27ac (2)	20,387/21,839 (93.3)

Values are number (percentage).

1. Cotney J, et al. (2012) Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. *Genome Res* 22(6):1069–1080.
2. Bogdanovic O, et al. (2012) Dynamics of enhancer chromatin signatures mark the transition from pluripotency to cell specification during embryogenesis. *Genome Res* 22(10): 2043–2053.

Table S2. Summary of zebrafish injections

Genomic region	No. injected	Stage screened (hpf)	No. fin positive	No. fin negative	% w/fin signal	Raise for line?
Lo CsB	172	48	66	106	62.2	Yes
Lo Island I	152	48	21	131	13.8	Yes
Lo e16	183	48	26	157	14.2	Yes
Lo Island II	160	48	4	156	2.5	No
Lo Island III	186	36, 48	12	174	6.4	No
Lo Island IV.1	171	48	6	165	3.4	No
Lo Island IV.2	168	48	4	164	2.4	No
Dr Island I	136	48	3	133	2.2	Yes

Table S3. List of primers used

Name	Locus	Sequence
Zebrafish		
Dr_Island_I_F	Zebrafish Island I	AGCAACGCATGTCTTTCAACA
Dr_Island_I_R	Zebrafish Island I	ATAACGTTGTGTGCCTGCTG
Gar		
Lo_Island_I_F	Gar Island I	TGGCCTACAACACCAGTGAA
Lo_Island_I_R	Gar Island I	CAGATTTTGTGCGTTTCTCCT
Lo_CsB_F	Gar CsB	GGAGTCTCCCACAAGGTGAA
Lo_CsB_R	Gar CsB	CGAAGGCTCTGCACTACTCA
Lo_Island_II_F2	Genomic "area" of mouse Island II	GAGGTTGTGGGCTGTCCAAA
Lo_Island_II_R2	Genomic "area" of mouse Island II	CCACATTTGTGGAAATTCCTG
Lo_Island_IV_F2	Genomic "area" of mouse Island IV part 1	GCTTGAAAGCAACTGCATC
I4_Split_R	Genomic "area" of mouse Island IV part 1	GAGATGGCAACGCCTTATGT
I4_Split_F	Genomic "area" of mouse Island IV part 2	CCGTGTGATCCAAAGCAATA
Lo_Island_IV_R	Genomic "area" of mouse Island IV part 2	TTGGGCTGACCTGCTTTTAT
Lo_e16_R	HoxA enhancer e16	GTGATTTTCTCGGCATTTGG
Lo_e16_F	HoxA enhancer e16	CACCGACTTTGCTGTGTCAT
Gar Island III	Lo_Island_III_Long_F	GTGAGCCATGAGATGTACCG
Gar Island III	Lo_Island_III_Long_F	GTAAAACACTCCGGCACCTT
Mouse		
Tg1_F	Mouse Island I	TTCAGACTAGGCCCTCCAGA
Tg1_R	Mouse Island I	GACAGTGGGGACAACCCTAA
Tg2_F	Mouse Island II	GTGTGTGCGCTAGGGATTCT
Tg2_R	Mouse Island II	AGAGAGGGCTCGTCACTCAA
Tg4_F	Mouse Island IV	GAGTTAGCCACTCAGCCATGT
Tg4_R	Mouse Island IV	TGGTGTCTTTCCTCCATTCTG