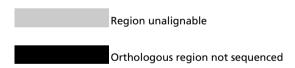
Table S1. Largest T-box binding site clusters and their conservation among fish species

Gene	Position in gene	Number of T-box sites in given species				
		Zebrafish	Fugu	Tetraodon Stickleback		Medaka
hhip	Intron 2	9	3	3		2
her7	Upstream	9			1	2
efnb2b	Upstream	8		2	2	3
hhip	Intron 3	8				
hhip	Intron 11	8	1	1		6
cdx4	Upstream	8	4		7	7
pcdh10b	Intron 3	8	1	4	6	2
aldh1a2	Intron 7	8			1	3
dld (Hans and Campos-Ortega, 2002)	Intron 2	7	7		6	5*
pcdh8	Upstream	7	9	9	9	
zgc:66052	Upstream	7	4		3	1
fbxw4	Intron 5	7				
aldh1a2	Upstream	7	0		0	0
pcdh10b	Upstream	7	1	3	5	4
pcdh10b	Upstream	7	3	3	5	1
cxcl12b	Intron 2	7				
mespa (Haraguchi et al., 2001)	Upstream	7	1	3		
tbx6 (Szeto and Kimelman, 2004)	Upstream	6				



* Intron not completely sequenced

Binding site scoring matrices identify Spt and Ntl binding motif clusters within putative target non-coding sequence. Loci with the highest number of Spt- and Ntl-binding motifs within a 500 bp window are listed. Each locus was aligned with the orthologous loci from other fish species. The number of T-box motifs found in the region that aligned with the zebrafish T-box cluster is shown (see example for the dld gene in Fig. S4). Clusters occurring in previously identified regulatory regions are indicated with a citation next to the gene name. The dld T-box site cluster is part of a 2.8 kb region known to drive gene expression in the tail bud (Hans and Campos-Ortega, 2002). The mespa T-box site cluster aligns with part of an early mesoderm regulatory element upstream of mouse Mesp1 (Haraguchi et al., 2001). The tbx6 T-box site cluster is part of an early mesoderm regulatory element (Szeto and Kimelman, 2004).

References

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