

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
<i>hhip</i>	Intron 2	9	3	3		2
<i>her7</i>	Upstream	9			1	2
<i>efnb2b</i>	Upstream	8		2	2	3
<i>hhip</i>	Intron 3	8				
<i>hhip</i>	Intron 11	8	1	1		6
<i>cdx4</i>	Upstream	8	4		7	7
<i>pcdh10b</i>	Intron 3	8	1	4	6	2
<i>aldh1a2</i>	Intron 7	8			1	3
<i>dld</i> (Hans and Campos-Ortega, 2002)	Intron 2	7	7		6	5*
<i>pcdh8</i>	Upstream	7	9	9	9	
<i>zgc:66052</i>	Upstream	7	4		3	1
<i>fbxw4</i>	Intron 5	7				
<i>aldh1a2</i>	Upstream	7	0		0	0
<i>pcdh10b</i>	Upstream	7	1	3	5	4
<i>pcdh10b</i>	Upstream	7	3	3	5	1
<i>cxcl12b</i>	Intron 2	7				
<i>mespa</i> (Haraguchi et al., 2001)	Upstream	7	1	3		
<i>tbx6</i> (Szeto and Kimelman, 2004)	Upstream	6				

 Region unalignable

 Orthologous region not sequenced

* 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

- Hans, S. and Campos-Ortega, J. A. (2002). On the organization of the regulatory region of the zebrafish *deltaD* gene. *Development* **129**, 4773-4784.
- Haraguchi, S., Kitajima, S., Takagi, A., Takeda, H., Inoue, T. and Saga, Y. (2001). Transcriptional regulation of *Mesp1* and *Mesp2* genes: differential usage of enhancers during development. *Mech. Dev.* **108**, 59-69.
- Szeto, D. P. and Kimelman, D. (2004). Combinatorial gene regulation by BMP and Wnt in zebrafish posterior mesoderm formation. *Development* **131**, 3751-3760.