

Supplementary Information for

BMP controls dorsoventral and neural patterning in indirect developing hemichordates providing insight into a possible origin of chordates

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Supplementary Materials and Methods

Phylogenetic analysis

Complete protein sequences were aligned using ClustalW with default settings on MEGA ver. 6.06. The alignments were analyzed using Bayesian inference analysis (MrBayes ver. 3.2.6, CIPRES Science Gateway). The Markov chain Monte Carlo analyses were specified at 100,000 or 1,000,000 generations, and the other parameters were defaults. FigTree ver. 1.4.3 was used to illustrate the trees. GenBank accession numbers of the genes used for the phylogenetic analyses are listed in Table S2.

Larval culture and feeding experiments

P. flava and *S. purpuratus* larvae were cultured in 200 ml of filtered seawater with constant gentle stirring. The culture medium was replaced every other day with fresh filtered seawater containing *Rhodomonas* (1). Equal amount of *Rhodomonas* were added into control and mBMP4-treated samples.

In situ hybridization of the amphioxus onecut

The amphioxus *onecut* was cloned by RACE PCR with two nested forward primers (forward primer F743: 5'-AACGTTCAACGGTTATGCCAACCACC-3'; forward primer F1308: 5'-AAGCGGAAAGAAGAAGAAGCTGCG-3') and the 3' RACE primer provided in the FirstChoice RLM-RACE Kit (Thermo Fisher Scientific). *B. floridae* adults and embryos were cultured at room temperature and *in situ* hybridization was performed as described (2).

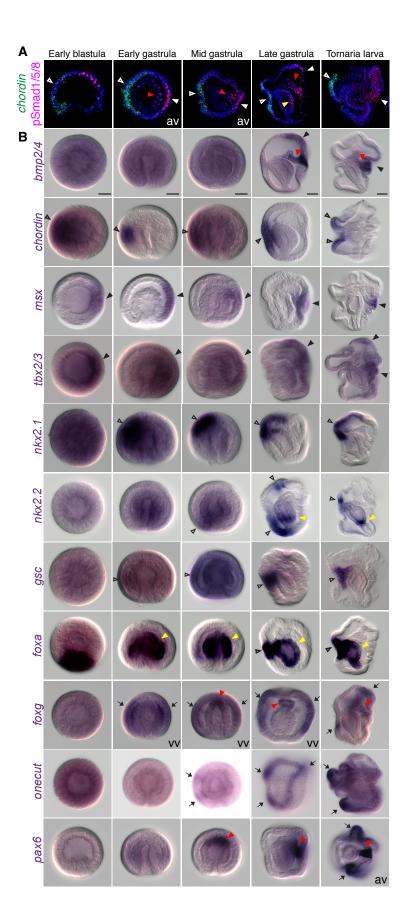


Fig. S1. Ectodermal gene expression patterns throughout embryogenesis of *P. flava*. (A) Double staining of *chordin* fluorescent *in situ* hybridization and immunostaining with an anti-pSmad1/5/8 antibody at various embryonic stages. (B) In situ hybridization of genes investigated in this study. Specific expression of bmp2/4 on the dorsal side was initiated at the late gastrula stage. Expression of *chordin* in the presumptive ventral ectoderm at the blastula stage possibly acts on ubiquitously distributed, maternal BMP ligands. Genes encoding Msx and Tbx2/3 transcription factors were expressed in the presumptive dorsal ectoderm, beginning at the blastula stage. Genes that showed specific expression in subdomains of the ventral ectoderm during gastrulation include *nkx2.1* and *nkx2.2* (near the animal and vegetal poles, respectively), and *gsc* and *foxa* (in the stomodeal region). The foxg, onecut, and pax6 genes were expressed in the lateral ectoderm, which marks the positions of future ciliary bands between the dorsal and ventral ectoderm. Except *pax6*, orthologs of these genes exhibit similar expression patterns in sea urchin embryos (3, 4), suggesting that the patterning mechanism and the deployment of the transcription factors for establishing the larval DV axis, including the ciliary band between the dorsal and ventral ectoderm, was present in the ambulacrarian ancestor. Scale bar is 30 µm. Empty arrowheads, black arrowheads, and arrows indicate the expression in the ventral ectoderm, dorsal ectoderm, and lateral ectoderm, respectively. Red and yellow arrowheads indicate the mesodermal and endodermal expression patterns, respectively. All images are side views unless otherwise indicated; av, apical view; vv, ventral view.

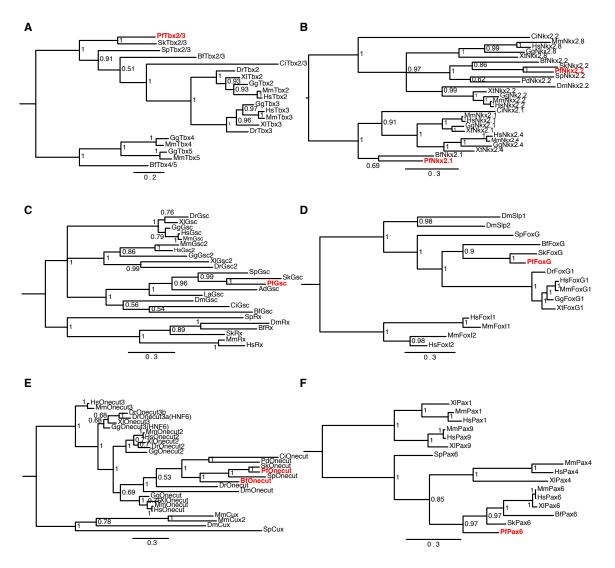


Fig. S2. Phylogenetic analyses of genes identified in this study. Complete protein sequences of (**A**) Tbx2/3, (**B**) Nk2.2, (**C**) Gsc, (**D**) FoxG, (**E**) Onecut, and (**F**) Pax6 from various species were aligned and analyzed using Bayesian inference analysis. The Markov chain Monte Carlo analysis was set to run for 100,000 (**a,c,f**) or 1,000,000 (**b,d,e**) generations. The outgroup sequences used in the analyses were (**A**) Tbx4/5, (**B**) Nk2.1/Nk2.4, (**C**) Rx, (**D**) FoxI, (**E**) Cux, and (**F**) Pax1/Pax9. The nodes indicate the posterior possibilities, and the scale bars are changes per site. GenBank accession numbers of the analyzed protein sequences are given in Table S2.

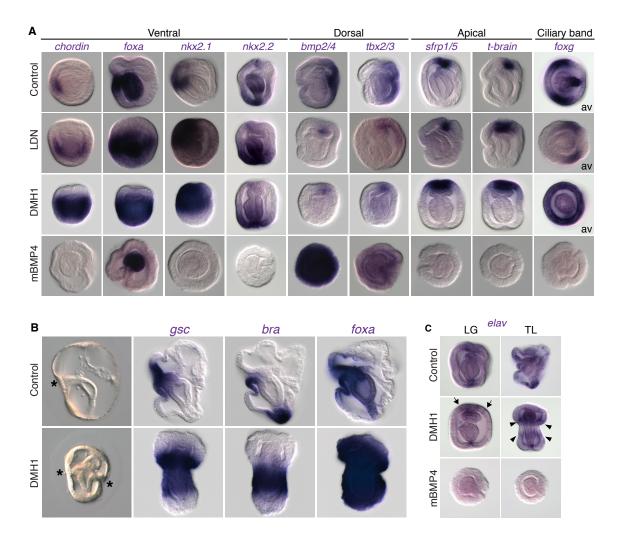


Fig. S3. BMP signaling controls DV patterning in *P. flava*. (A) Expression of ventral, dorsal, apical, and ciliary band marker genes in control gastrulae and embryos treated with 2 μ M LDN, 2 μ M DMH1, or 125 ng/ml mBMP4 after fertilization. (B) Expression of the stomodeal marker genes in control tornaria larvae and larvae treated with 2 μ M DMH1. Asterisks indicate mouth openings. (C) Expression of *elav* was detected in several domains, including the apical region, the ciliary band, cells around the blastopore, and some mesodermal cells. In DMH1-treated embryos, *elav* expression in the apical region (arrows) and ciliary band expanded (arrowheads). Exogenous mBMP4 abolished its expression. All images are side views unless otherwise indicated. av, apical view. The data presented represent the phenotypes of most samples (>95%).

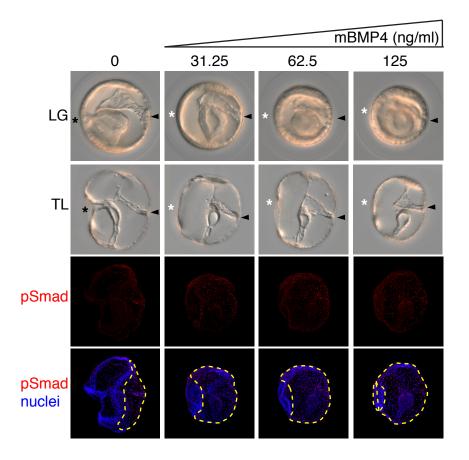


Fig. S4. To vary the level of the BMP signaling, embryos were treated with different concentrations of mBMP4 for 4 hrs during early gastrulation (from 24 to 28 hrs post fertilization). The phenotypes were observed at the late gastrula (LG) and the tornaria larval (TL) stages. To examine regions that receive BMP signaling, the TL-stage samples were stained with an anti-phospho-Smad1/5/8 (pSmad) antibody. When mBMP4 concentrations were increased, the pSmad-positive regions expanded (yellow dashed regions), while the pSmad-negative regions became smaller. The black asterisks and arrowheads indicate the mouth and the hydropore openings, respectively. The white asterisks denote the disappearance of the mouth. All images are side views (ventral to the left). The data presented represent the phenotypes of most samples (>95%).

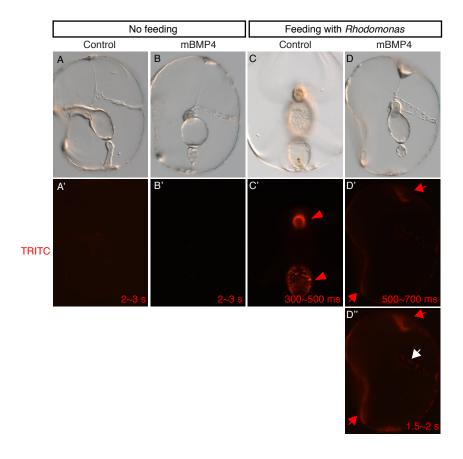


Fig. S5. Feeding experiments for control and mouthless tornaria larvae. (**A-B**) Eight-day-old control tornaria and mouthless larvae (mBMP4 treatment from 24 to 28 hpf) cultured in filtered seawater without feeding. (**C-D**) Eight-day-old control and mouthless larvae (mBMP4) fed with *Rhodomonas* (feeding started from 3 dpf). A TRITC filter was used to detect fluorescent signals emitted from *Rhodomonas*. The exposure time for the fluorescent images is indicated at the bottom-right corner. The arrowheads (**C**') denote the presence of *Rhodomonas* in the digestive tract. The red and white arrows (**D**' and **D**'') indicate fluorescent signals in the ectoderm and mesoderm, respectively. Fluorescent signals were not detected in the mouthless larva without feeding (**B**'), suggesting that the mouthless larva may be able to take-up *Rhodomonas* or its debris from seawater. (**A**), (**B**), and (**D**) are side views (ventral to the left) and (**C**) is viewed from the ventral side.

	No feeding		Feeding with Rhodomonas	
	Control	mBMP4+SB	Control	mBMP4+SB
	A	B	c	D
	A'	B'	C'	D'
TRITC		1 s	100~200 ms	1 s
TRITC	A" 3~4 s	B" 3~4 s		D"

Fig. S6. Feeding experiments for control and mouthless sea urchin pluteus larvae. (**A-B**) Sevenday-old control and mouthless sea urchin larvae (mBMP4+SB treatment from 24 to 28 hpf) cultured in filtered seawater without feeding. (**C-D**) Seven-day-old control and mouthless larvae (mBMP4+SB) fed with *Rhodomonas* (feeding started from 3 dpf). A TRITC filter was used to detect *Rhodomonas*. The exposure time for the fluorescent images is indicated at the bottom-right corner. The arrowheads (**C'**) denote the presence of *Rhodomonas* in the digestive tract. The red arrows (**B''** and **D''**) indicate fluorescent signals in some mesodermal cells. The mesodermal fluorescent signals were detected in the mouthless larvae regardless of feeding, demonstrating that the fluorescence was not due to the presence of algae. All images are side views (ventral to the left).

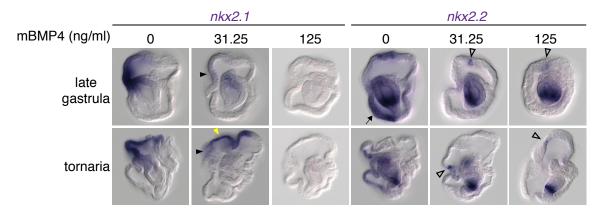


Fig. S7. Transient over-activation of BMP signals affects ectodermal expression of nkx2.1 and nkx2.2. In situ hybridization of nkx2.1 and nkx2.2 was performed in control and mBMP4-treated (treatment from 24 to 28 hpf) *P. flava* embryos. At the late gastrula stage, the anterior-ventral ectodermal expression of nkx2.1 (arrowhead) was decreased at a lower concentration of mBMP4 (31.25 ng/ml) and completely disappeared at a high level of mBMP4 (125 ng/ml). Its anterior ectodermal expression was detected at the tornaria stage (yellow arrowhead). Upon treatment, the posterior-ventral ectodermal expression of nkx2.2 (arrow) disappeared, and only a few nkx2.2-positive cells remained in the ventral ectoderm (empty arrowheads). All images are side views (ventral to the left).

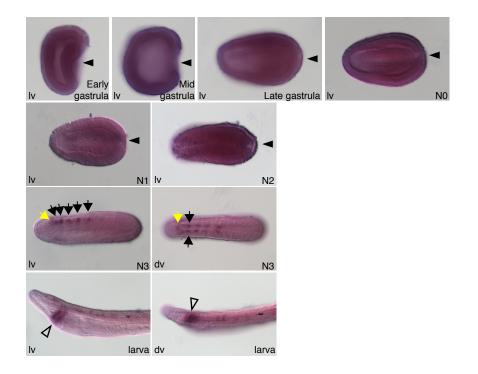


Fig. S8. Expression of the amphioxus *onecut* gene during embryogenesis. The *Branchiostoma floridae* homolog of *onecut* was cloned (Fig. S2) and *in situ* hybridization was performed at various developmental stages, beginning from early and mid-gastrula, extending to different neurula (N0-N3) stages, and finally to the larval stage. Developmental stages are indicated at the bottom-right corner. Views of the samples are indicated at the bottom-left corner (lv, lateral view; dv, dorsal view). Anterior is to the left and the arrowheads indicate the blastopores. No specific expression is detected before the N2 stage. At the N3 stage, *onecut* transcript is detected in the posterior part of the cerebral vesicle (yellow arrow) and in five pairs of neurons in the neural tube (black arrows; only one pair of neurons is indicated in the dorsal-view N3 embryo). At the larval stage (only the anterior part of the larva is shown), strong expression in the endostyle (empty arrowheads) is observed.

Gene Name	primer direction	Sequence
Goosecoid (gsc)	F	TCACGTCGCGTCACGTCAAAGTCAC
	R	CCCAACATTCGAGCAATCGTTCACTC
tbx2/3	F	ACAGCGTTAGACTGCCACCTGTGGTC
	R	CGCTAAGATGTGTGTGTGAACGACTTC
foxg	F	ACACACGCGCGCACATCCGTACATC
	R	CCGTTCGTAAGTCCTGCAAAAGTTGTC
pax6	F	CGCCTTCTGAACGGCCAGACAT
	R	TTGCGATGAGTGGGTGTCTGCC
onecut	F	GAGCAATGTGAGCGGTAGTTTTAC
	R	GCATGTGGCCAGTCGAATTATAAC

Table S1. Primers used for cloning *P. flava* genes

F: forward; R: reverse.

Gene	Species	Accession Number	Abbreviation in figures
Gsc	Ciona intestinalis	BAE06479.1	CiGsc
Gsc	Danio rerio	AAH81381.1	DrGsc
Gsc	Branchiostoma floridae	AAF97935.1	BfGsc
Gsc	Strongylocentrotus purpuratus	NP_999663.1	SpGsc
Gsc	Gallus gallus	NP_990662.1	GgGsc
Gsc	Xenopus laevis	XP_018087379.1	XlGsc
Gsc	Homo sapiens	EAW81594.1	HsGsc
Gsc	Mus musculus	EDL18791.1	MmGsc
Gsc	Drosophila melanogaster	AAB17948.1	DmGsc
Gsc	Lingula anatina	XP_013379052.1	LaGsc
Gsc	Acropora digitifera	BAQ19108.1	AdGsc
Gsc	Saccoglossus kowalevskii	NP_001161560.1	SkGsc
Gsc	Ptychodera flava	MH782152	PfGsc
Gsc2	Mus musculus	AAI25357.1	MmGsc2
Gsc2	Xenopus laevis	XP_018099595.1	XlGsc2
Gsc2	Gallus gallus	XP_025011442.1	GgGsc2
Gsc2	Homo sapiens	NP_005306.1	HsGsc2
Gsc2	Danio rerio	XP_021332017.1	DrGsc2
FoxG1	Danio rerio	AAH92710.1	DrFoxG1
FoxG1	Homo sapiens	AAH50072.1	HsFoxG1
FoxG1	Xenopus tropicalis	NP_001116933.1	XtFoxG1
FoxG	Branchiostoma floridae	AAC18392.1	BfFoxG
FoxG	Saccoglossus kowalevskii	XP_002735197.2	SkFoxG
FoxG	Strongylocentrotus purpuratus	NP_001123284.1	SpFoxG
FoxG	Ptychodera flava	MH782154	PfFoxG
Slp 1	Drosophila melanogaster	NP_476730.1	DmSlp1
Slp2	Drosophila melanogaster	NP_476834.1	DmSlp2
FoxI1	Homo sapiens	AAH29778.2	HsFoxI1
FoxI1	Mus musculus	AAH07475.2	MmFoxI1
FoxI2	Homo sapiens	NP_997309.2	HsFoxI2
FoxI2	Mus musculus	AAH96623.1	MmFoxI2
FoxG1	Mus musculus	NP_001153584.1	MmFoxG1
FoxG1	Gallus gallus	NP_990524.1	GgFoxG1
Pax1	Mus musculus	AAK01146.1	MmPax1
Pax4	Mus musculus	BAA24517.1	MmPax4
Pax6	Mus musculus	AAH36957.1	MmPax6
Pax9	Mus musculus	NP 035171.1	MmPax9
Pax1	Xenopus laevis		XlPax1
Pax4	Xenopus laevis	XP 017948145.1	XlPax4

Table. S2. I	List of genes	used in the	phylogeneti	c analyses.

Pax6	Xenopus laevis	AAB36683.1	XlPax6
Pax9	Xenopus laevis	NP 001167485.1	XlPax9
Paxl	Branchiostoma floridae	XP 002210646.1	BfPax1
Pax6	Branchiostoma floridae	CAA11368.1	BfPax6
Pax1	Strongylocentrotus purpuratus	SPU 006683.1	SpPax1
Pax6	Strongylocentrotus purpuratus	SPU 006786.1	SpP ax6
Pax1	Ptychodera flava	BAA78380.1	PfPax1
Pax6	Ptychodera flava	MH782156	PfPax6
Pax1	Saccoglossus kowalevskii	NP_001158408.1	SkPax1
Pax6	Saccoglossus kowalevskii	NP 001158383.1	SkPax6
Pax1	Homo sapiens	NP 006183.2	HsPax1
Pax4	Homo sapiens	NP 006184.2	HsPax4
Pax6	Homo sapiens	NP_001121084.1	HsPax6
Pax9	Homo sapiens	NP 006185.1	HsPax9
Nkx2.2	Mus musculus	AAI38160.1	MmNkx2.2
Nkx2.8	Mus musculus Mus musculus	NP 032727.2	MmNkx2.8
Nkx2.2	Homo sapiens	NP 002500.1	HsNkx2.2
Nkx2.8	Homo sapiens	NP 055175.2	HsNkx2.2
Nkx2.2	Gallus gallus	NP 001264647.1	GgNkx2.2
Nkx2.2 Nkx2.8	Gallus gallus	XP 003641408.3	GgNkx2.2 GgNkx2.8
Nkx2.2	Xenopus tropicalis	XP 002939477.1	XtNkx2.2
Nkx2.2 Nkx2.8	Xenopus tropicalis	NP 988951.1	XtNkx2.8
Nkx2.2	Branchiostoma floridae	XP_002589199.1	BfNkx2.2
Nkx2.2	Saccoglossus kowalevskii	NP 001158404.1	SkNkx2.2
Nkx2.2	Strongylocentrotus purpuratus	AAS58444.1	SpNkx2.2
Nkx2.2	Platynereis dumerilii	ABO93209.1	PdNkx2.2
vnd	Drosophila melanogaster	CAA60619.1	DmNkx2.2(vnd)
Nkx2.2	Ciona intestinalis	NP_001071957.1	CiNkx2.2
Nkx2.1	Ciona intestinalis	NP 001027667.1	CiNkx2.1
Nkx2.1	Mus musculus	AAH57607.1	MmNkx2.1
Nkx2.1	Homo sapiens	NP 001073136.1	HsNkx2.1
Nkx2.1	Gallus gallus	CAA11493.1	GgNkx2.1
Nkx2.1	Xenopus laevis	AAG17405.1	XlNkx2.1
Nkx2.1	Branchiostoma floridae	AAC35350.1	BfNkx2.1
Nkx2.4	Homo sapiens	NP_149416.1	HsNkx2.4
Nkx2.4	Gallus gallus	XP 015138916.1	GgNkx2.4
Nkx2.4	Mus musculus	NP 075993.1	MmNkx2.4
Nkx2.4	Xenopus laevis	AAI69924.1	XlNkx2.4
Nkx2.1	Ptychodera flava	AAM93268.1	PfNkx2.1
Nkx2.2	Ptychodera flava	MH782155	PfNkx2.2
Onecut	Mus musculus	NP 032288.1	MmOnecut
Onecut	Ciona intestinalis	NP 001071994.1	CiOnecut
			01010000

Onecut	Saccoglossus kowalevskii	NP 001161619.1	SkOnecut
Onecut	Drosophila melanogaster	NP 524842.2	DmOnecut
Onecut	Platynereis dumerilii		PdOnecut
Onecut	Danio rerio	AAL02365.1	DrOnecut
Onecut	Strongylocentrotus purpuratus	AAR28054.1	SpOnecut
Onecut	Gallus gallus	XP 015147374.1	GgOnecut
Onecut	Xenopus tropicalis	NP_001093730.1	XtOnecut
Onecut	Homo sapiens	NP 004489.1	HsOnecut
Onecut	Ptychodera flava		PfOnecut
Onecut	Branchiostoma floridae	MK679618	BfOnecut
Onecut2	Mus musculus	AAI03669.1	MmOnecut2
Onecut2	Homo sapiens	NP 004843.2	HsOnecut2
Onecut2	Xenopus tropicalis	XP_004910425.1	XtOnecut2
Onecut2	Danio rerio	XP_001920308.3	DrOnecut2
Onecut2	Gallus gallus	XP_003642951.1	GgOnecut2
Cux	Mus musculus	CAA52922.1	MmCux
Cux2	Mus musculus	NP 001299837.1	MmCux2
Cux	Drosophila melanogaster	NP 524764.1	DmCux
Cux	Strongylocentrotus purpuratus	XP_011671723.1	SpCux
Hnf6	Danio rerio	XP 694209.1	DrOnecut3a(Hnf6)
Onecut3b	Danio rerio	XP_017207968.2	DrOnecut3b
Onecut3	Xenopus tropicalis	XP_002938867.1	XtOnecut3
Hnf6	Gallus gallus	XP_003642905.1	GgOnecut3(Hnf6)
Onecut3	Homo sapiens	NP_001073957.1	HsOnecut3
Onecut3	Mus musculus	AAL86921.1	MmOnecut3
Tbx2	Danio rerio	AAF59835.1	DrTbx2
Tbx2	Gallus gallus	XP_001235321.4	GgTbx2
Tbx2	Xenopus laevis	BAA93081.1	XlTbx2
Tbx2	Homo sapiens	AAA73861.1	HsTbx2
Tbx2	Mus musculus	AAC52697.1	MmTbx2
Tbx3	Gallus gallus	NP_001257807.1	GgTbx3
Tbx3	Xenopus laevis	AAH77254.1	X1Tbx3
Tbx3	Homo sapiens	AAD50989.2	HsTbx3
Tbx3	Mus musculus	AAH96551.1	MmTbx3
Tbx3	Danio rerio	NP_001095140.2	DrTbx3
<i>Tbx2/3</i>	Ciona intestinalis	NP_001027620.1	CiTbx2/3
<i>Tbx2/3</i>	Ptychodera flava	MH782153	PfTbx2/3
<i>Tbx2/3</i>	Branchiostoma floridae	XP_002598922.1	BfTbx2/3
<i>Tbx2/3</i>	Strongylocentrotus purpuratus	NP_001123280.1	SpTbx2/3
<i>Tbx2/3</i>	Saccoglossus kowalevskii	NP_001158392.1	SkTbx2/3
Tbx4/5	Branchiostoma floridae	ABU50779.1	BfTbx4/5
Tbx4	Gallus gallus	NP_001025708.1	GgTbx4

Tbx5	Gallus gallus	NP_989504.1	GgTbx5
Tbx4	Mus musculus	NP_035666.2	MmTbx4
Tbx5	Mus musculus	NP_035667.1	MmTbx5
Rx	Strongylocentrotus purpuratus	XP_003726050.1	SpRx
Rx	Drosophila melanogaster	NP_726006.3	DmRx
Rx	Mus musculus	NP_038861	MmRx
Rx	Branchiostoma floridae	AFQ55891	BfRx
Rx	Saccoglossus kowalevskii	NP_001158375	SkRx
Rx	Homo sapiens	AAH51901	HsRx

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