

Supplementary Figure 1 | Phylogenetic position of Rotifera and Chaetognatha based on recent large scale phylogenomic studies.

PG2: Hox2/Proboscipedia

10	20	30	40	50	60	70	
PRRLRTAYTNTQL	LELEKEFHFNKY	LCRPRRIEI	AASLDLTERQV	KVWFQNRRM	KHKRQTSVMK	DDDKDGVD	Chelicerata
					LGKQ	GG-DK-	Insecta
					NLGKG	AE-S-CNS	Onychophora
					-FGKGS	G-SP-AEC	Annelida/Polychaeta
					-YGKDG	4-ENSVSS	Nemertea
HN	FN		-SN-S		R-HK-	-RKALDNK	Rotifera/Monogononta
KK	S		-SL		-YLM-QD	PKLAEEFE	Rotifera/Bdelloida
SV		K	-SYN		-QRD-KG-		Cephalochordata
H 			-SM		IMKAA	/SGSPIP-	Hemichordata
	10 PRRIRTAYTNTQL	10 20 PERLETAYTNTQLLELEKEFHFNKY H	10 20 30 PRRIRTAYTNTQLLELEKEFHFNKYLCRPRRIEI 	10 20 30 40 PRRIRTAYTNTQLLELEKEFHFNKYLCRPRRIEIAASLDLTERQV H N N N N N N N N N N N N N N N N N N N	10 20 30 40 50 PRRIATAYINTQLLELEKEFHFNKYLCRPRRIEIAASLDLTEROVKVWFQNRRM 	10 20 30 40 50 60 PRRIATAYINTQLLELEKEFHFNMYLCRPRRIEIAASLDLTERQVKVWFQNRRMKHKRQTSVMKI 	10 20 30 40 50 60 70 PRRIATAYINTQLLELEKEFHFNKYLCRPRRIEIAASLDLTERQVKVWFQNRRMKHKRQTSVMKDDDKDGVD

PG3: Hox3

	10	20	30	40	50	60	70	
Cupiennius Hox3	AKRARTAYTSAQL	ELEKEFHFNRY	LCRPRRIEM	ANLLNLSERQI	KIWFQNRRMK	KKEQKSKGI	LYIQQSEK	Chelicerata
Tribolium Hox3	G	RHGK-	SQI	-EN]	HMN-VS	STPRS-PA	Insecta
Euperipatoides Hox3				-A		D	-SGKSDSP	Onychophora
Priapulus Hox3				-AMT	<u></u>			Priapulida
Capitella Hox3	S			-AT		DQ-N-	-MEK-YAG	Annelida/Polychaeta
Euprymna Hox3		Q		-A	R	FK-L-VI	MDKSGCG	Mollusca/Cephalopoda
Lingula Hox3	T			-AT]	HA-RNRKS	SCSKN-SN	Brachiopoda
Maculaura Hox3	PS			-A		DQ-N-	-MEKIHME	Nemertea
Brachionus Hox3	S	T	L	-SI-H-T	-			Rotifera/Monogononta
Adineta Hox3a	S	LY-K-	NL	-QA-S-TV				Rotifera/Bdelloida
Adineta Hox3b	S	LY-K-	NL	-QT-C-T]	DDG-NRTS	S-TNGCGM	Rotifera/Bdelloida
Branchiostoma Hox3	G		V	-AMT		V(GGSGGGSG	Cephalochordata
Saccoglossus Hox3	IMNFCT	RRRRRRR	QKQT-L	SSVT	-V]	FM-D	-VDPYQAG	Hemichordata

PG4: Hox4/Deformed

	10	20	30	40	50	60	70	
Cupiennius Dfd	PKRQRTAYTRHQIL	ELEKEFHFNR'	LTRRRRIE	AHALCLSERC	IKIWFQNRRM	KWKKDNKLPN	TKNVKKKQ	Chelicerata
Tribolium Dfd		Y		T-V				Insecta
Euperipatoides Dfd				T		H	PASSSS	Onychophora
Priapulus Dfd	V			ST				Priapulida
Capitella Dfd	ST					EH	TRLTDS	Annelida/Polychaeta
Bugula Hox4	A					EH	GKIPEI	Bryozoa
Maculaura Hox4	NT			T		EH	LRLPDA	Nemertea
Brachionus Hox4	SAV	K				H-I	S-SKLSEC	Rotifera/Monogononta
Adineta Hox4a	YIS	KK	N	-RT-M-T	V	HN	SKLIET	Rotifera/Bdelloida
Adineta Hox4b	TAV	SSK		S-V-T		H	SKLPET	Rotifera/Bdelloida
Adineta Hox4c	TAV	SK				H	SKLPD-	Rotifera/Bdelloida
Flaccisagitta Hox4	AV			T		HG	TSRA	Chaetognatha
Branchiostoma Hox4	TSQ-V			S-G-T		R <mark></mark>	TRSSSA	Cephalochordata
Saccoglossus Hox4	HTY-V			G-T		HN	TKSSTP	Hemichordata

PG6: Hox6/lox5

	10)	20	30	40	50	60	70	
Capitella Lox5	QKRTRQTYTF	TUTLELER	KEFHYNRYL'	TRRRRIEIAH	ALQLTERQIKI	WFQNRRMKYK	KENNISKLTG	PNGEL	Annelida/Polychaeta
Euprymna Lox5				8	6- <mark>6</mark>		<mark></mark>	-KSK	Mollusca/Cephalopoda
Lingula Lox5				F	l- <mark>G</mark>		P	-QK-	Brachiopoda
Bugula Lox5				I	-G		A		Bryozoa
Maculaura Lox5					G		Q	-TK-	Nemertea
Dugesia Lox5	N	H			3- <u>1</u>		HA	GSCD	Platyhelminthes/Tricladida
Brachionus Hox6	H	-H		9	6- <mark>G</mark>		KS-ND	-SVK-	Rotifera/Monogononta
Adineta Hox6a	H	H	T	S	5- <u>A</u>		FKS-ND	VK-	Rotifera/Bdelloida
Adineta Hox6b	N	-H	GS	5	S- <u>S</u>		-DFKS-ND	-HVK-	Rotifera/Bdelloida
Flaccisagitta Hox6		-Н			G		KS-ND	AKP-F	Chaetognatha
Branchiostoma Hox6	KG			I			K-PS-NA	FTINQ	Cephalochordata
Saccoglossus Hox6	G			T	C-G		QKTGGAPS	-KQFA	Hemichordata

Supplementary Figure 2 | Alignment of *Hox* gene homeodomains and 3' flanking regions of paralog group 2, 3, 4 and 6. Dashes represent identity with respective Hox paraloges from Cupiennius salei shown in the top line of each group. Ecdysozoan genes listed in red, platytrochozoan genes listed in blue and deuterostome genes listed in green respectively. The following Hox signatures are marked: Hox4/Dfd motif highlighted in orange, Lox5 parapeptide motif in blue and gnathiferan peptide in yellow. Residues diagnostic for different paralog groups shared by sequences recovered from Brachionus majavacas are highlighted in grey: dark grey boxes mark residues found in paralogs across bilaterians and residues boxed in light grey are found in protostomes only.

PG8: Hox8/Lox4/Lox2/AbdA/Ubx

		10	20	30	40	50	60 70	
Capitella Lox4	RRRGRC	TYSR	YQTLELEKEFQFNHY	LTRKRRI	EIAHALCLTERQIK	IWFQNRRMKLKK	ERQQIKDLNGLDGK	Annelida/Polychaeta
Euprymna Lox4			FY-N-		-VN-SV-		-KREMACRS	Mollusca/Cephalopoda
Maculaura Lox4				R	S		EDSTKD	Nemertea
Lingula Lox4			F <mark>-</mark>		-V		EI-DTLK-	Brachiopoda
Cupiennius AbdA		T-	FH	R			-MRAV-EI-EQARM	Chelicerata
Tribolium AbdA		T-	FH	R			-LRAV-EI-EQARR	Insecta
Euperipatoides AbdA		T-	H	R	V		-LRAV-EI-EQARL	Onychophora
<i>Cupiennius</i> Ubx		T-	HT	R	-M		-I-AEEQERQ	Chelicerata
Tribolium Ubx		T-	HT	R	-М		-I-AEEQEKQ	Tribolium
Euperipatoides Ubx	-K	T-	HT	R	-М		-M-TEQEK-	Onychophora
Priapulus Ubx		T-	RR	R	-MSQ		-T-AL-EM-AHAKA	Priapulida
Capitella Lox2		T-	KR-	R	-LS-M	E	-I-AEEKEKT	Annelida/Polychaeta
Helobdella Lox2		T-	KR-	R	-LS-T-Y	E	-V-A-REEIEKT	Annelida/Hirudinea
Urechis Lox2		T-	KR- <mark>-</mark>	R	-LS-M			Annelida/Echiurida
Gibbula Lox2		T-	FDKR-	R	-LS-M	E	-L-AESPRAP	Mollusca/Gastropoda
Brachionus MedPost	K-KH	V	HFYCYSK-	V	GSIKV-	E-R	-VGKQSH-I-SI-M	Rotifera/Monogononta
A <i>dineta</i> MedPost	KH	V-T-	AFYR-SQ-	S	G-VQ-SDV-	E-R	-NLKFNSAVSTSKQ	Rotifera/Bdelloida
Flaccisagitta MedPost	H-ER	T-	HAR-YVT-R-	R	SQS-H-S	E-R	-KDHVTSPRKNK	Chaetognatha
<i>Spadella</i> MedPost	H-KR		QAR-YVS-R-	R	SQH-D-S	ERR	-KDHPATTTTSPR-	Chaetognatha
Branchiostoma Hox7	-K	T-	HK- <mark>-</mark>	R		WW	-NKLESLKQQPAES	Cephalochordata
Branchiostoma Hox8			HK	R	G		-AAMLCPPKAETET	Cephalochordata
Saccoglossus Hox7	KK-C	T-	HY_R_	R	-1.S-1G	Y	-SKKDDGE-SNODN	Hemichordata

PG9-15: Hox9-15/Post1/Post2/AbdB

30 40 50 60 VRKKRKPYSKFQTLELEKEFLFNAYVSKQKRWELARNLNLTERQVKIWFQNRRMKSKKTSQRNAENNQNNTN Chelicerata Cupiennius AbdB Tribolium AbdB ----Q-AQQ---N-Insecta _____N___ Euperipatoides AbdB Onychophora ----T-Y-----T-----T------Priapulus AbdB -----KOROHOS Priapulida --S-----Q-IVD----YKV-P-ITR-R-F-M-H--G-S--------T--HLLTLRV Priapulus HB4 Priapulida PK------I-NDATIST IT-AR-K-Y-M-H-G-S----I-HLLIKV PK-----P-VSA--N-YSTST-IT-AR-K-V-E-D----I--Y---I-E-IATKR-KVQSDLFM L--R-R---Y-IA---R-YALST-I--SR----SQL--S---I-----I-A--LQK-DETLKTQTP-M-----Y-IA---R-YVS-T-I-P----SQR-Q-S------IA--LNE-AKSLIKDHEP Q-----TRY--MV-N-IN-S-ITR----ISCK-H-S----V-----R--LNE-AKSLIKDHEP G------TRY--MV-N-N-SS-ITR----ISCK-Q-----V-----R-LNE-AKSLIKDHEP Capitella Post1 Annelida/Polychaeta Euprymna Post1 Mollusca/Cephalopoda Lingula Post1 Brachiopoda Annelida/Polychaeta Capitella Post2 Mollusca/Cephalopoda Euprymna Post2 Lingula Post2 ----TRY--MV--N---N---ITR-----ISCK-H-S----V----R--LNE-AKALFKSEDI Brachiopoda S-----TRY--MV--T--IN-S-ITR----ISCR-R-----V----R--LND-AKNAOLTVOO Bugula Post2 Bryozoa S------R-LND-ARIAQUIVQ0 T------R-LND-ARVKSEVENT K--H-QV--RH--F-----YCYSK-LTRKR-V-I-GSIK------V----E-REVGKQSHLIGSIGM R--H-QV-TRA--F----YR-SQ-LTRKR-S-I-GAVQ-SD-----E-RENLKFNSAVSTSKQ Maculaura Post2 Nemertea Brachionus MedPost Rotifera/Monogononta Adineta MedPost Rotifera/Bdelloida H = ER-QT-TRH-A--R-YVT-R-LTRRR-I-ISQS-H-S--I--E-REKDHVTSPRK-K H-R-QT--RQ-A--R-YVS-R-LTRRR-I-ISQH-D-S--I--E-REKDHP-TTTTSPRK S---R-P-N----T-ITRRR-L-I-S---D---N-QHSGGPGMGPPIPG Flaccisagitta MedPost Chaetognatha Spadella MedPost Symsagittifera Post Chaetognatha Acoela S----C--TR-----Y-M-LTRER-Y-ISQHV--S------PPP Cephalochordata Branchiostoma Hox9 G----C--T-Y-I----M---RER-Q-IS-HV--SD--T----C--T-Y------MF-TRER-Q-I--Q----D----C--T-Y-I-----M---RER-Q-IS-HV--SD--------M-RMNKAREE-IR-HQE Branchiostoma Hox10 Cephalochordata Branchiostoma Hox11 -----M-RMK--AMQ-LMEEKQ Cephalochordata Branchiostoma Hox12 Cephalochordata Branchiostoma Hox13 Cephalochordata Cephalochordata Branchiostoma Hox14 Branchiostoma Hox15 Cephalochordata Saccoglossus Hox9/10 Hemichordata Saccoglossus Hox1113a Hemichordata Saccoglossus Hox1113b Hemichordata R-T--R---L-IF-----QQ-M-LTRDR-SR-SQA-----I---MTD-ERNEQDMMQQ Saccoglossus Hox1113c Hemichordata

Summary

Brachionus MedPost Adineta MedPost Flaccisagitta MedPost Spadella MedPost

	10	20	30	40	50	60	70	
:	KR <mark>K</mark> HR <mark>Q</mark> VYS <mark>R</mark> HQTFI	ELEKE <mark>Y</mark> CYSK	Y <mark>LTRKRRV</mark> EI.	AGSIKLTERQ	VKIWFQNRRM	KEKR <mark>E</mark> VGK(SHLIGSIGM	Rotifera/Monogononta
	RR <mark>K</mark> HR <mark>Q</mark> VYT <mark>R</mark> AQTFI	ELEKE <mark>Y</mark> RFSQ	Y <mark>LTRKRRS</mark> EI.	AGAVQLSDRQ	VKIWFQNRRM	KEKR <mark>E</mark> NLKI	NSAVSTSKQ	Rotifera/Bdelloida
Post	HRERR <mark>QTYT</mark> RHQTAI	ELEREYVTNR'	Y <mark>LTRRRRI</mark> EI:	SQSLHLSERQ	IKIWFQNRRM	kekr <mark>e</mark> kdhv	TSPRKNK	Chaetognatha
	HRKRRQTYS <mark>R</mark> QQTAI	ELEREYVSNR'	Y <mark>LTRRRRI</mark> EI.	SQHLDLSERQ	IKIWFQNRRMI	ker <mark>re</mark> kdhi	PATTTTSPRK	Chaetognatha

Supplementary Figure 3 | Alignment of *Hox* gene homeodomains and 3' flanking regions of paralog group 8 and 9-15 in comparison with the MedPost sequence recovered from *Brachionus manjavacas*. Dashes represent identity with respective *Hox* paraloges from *Capitella teleta* and *Cupiennius salei* shown in the top line of each group. Ecdysozoan genes listed in red, lophotrochozoan genes listed in blue and deuterostome genes listed in green respectively. Residues diagnostic for central class *Hox* genes shared by sequences recovered from *Brachionus majavacas* are highlighted in dark yellow and those representing residues diagnostic for posterior class *Hox* genes are enclosed in green boxes. In the summary residues recovered in rotifers or chaetognaths only are marked in lighter colors respectively.



Supplementary Figure 4 | Orthology assignments for *Brachionus plicatilis Hox* genes. Alignments of the 60 amino acid homeodomain and the 12 amino-acids 3' of the homeodomain of representative bilaterian Hox genes were used to conduct a Bayesian phylogenetic analysis based on 400,000 trees from 40,000,000 stationary generations. Bayesian posterior probabilities are shown above the branches. Sequences used for this been isolated from the following species: Saccoglossus kowalevskii analysis had (Hemichordata) and Branchiostoma floridae (Chordata), Cupiennius salei (Chelicerata), Tribolium castaneum (Insecta), Euperipatoides kanangrensis (Onychophora) and Priapulus caudatus (Priapulida), Capitella teleta (Annelida/Polychaeta), Helobdella robusta (Annelida/Echiurida), (Annelida/Hirudinea), Urechis unicinctus Euprymna scolopes (Mollusca/Cephalopoda), Gibbula varia (Mollusca/Gastropoda), Maculaura alaskensis (Nemertea), Lingula anatina (Brachiopoda), Bugula turrita (Bryozoa) and Dugesia japonica (Platyhelminthes), Symsagittifera roscoffensis (Xenacoelomorpha), Flaccisagitta enflata and Spadella cephaloptera (Chaetognatha) and Brachionus manjavacas and Adineta vaga (monogont and bdelloid rotifers respectively). Sequences from *B. manjavacas* are shown underlined and in bold. B. manjavacas possesses orthologs from Hox paralogy groups (PG) 2, 3, 4 and 6 and an ortholog of *MedPost*.



Supplementary Figure 5 | Orthology assignments for *Brachionus manjavacas Hox* genes. Alignments of the 60 amino acid homeodomain and the 12 amino-acids 3' of the homeodomain of representative bilaterian Hox genes were used to conduct an maximumlikelihood analysis with RAxML-HPC V8.2.9 under the LG+ Γ +I model. Bootstrap support values >50 from 1000 iterations are shown above the branches. Sequences used for this analysis had been isolated from the following species: Saccoglossus kowalevskii (Hemichordata) and Branchiostoma floridae (Chordata), Cupiennius salei (Chelicerata), Tribolium castaneum (Insecta), Euperipatoides kanangrensis (Onychophora) and Priapulus caudatus (Priapulida). Capitella teleta (Annelida/Polychaeta). Helobdella robusta (Annelida/Hirudinea), (Annelida/Echiurida), Urechis unicinctus Euprymna scolopes (Mollusca/Cephalopoda), Gibbula varia (Mollusca/Gastropoda), Maculaura alaskensis (Nemertea), Lingula anatina (Brachiopoda), Bugula turrita (Bryozoa) and Dugesia japonica (Platyhelminthes), Symsagittifera roscoffensis (Xenacoelomorpha), Flaccisagitta enflata and Spadella cephaloptera (Chaetognatha) and Brachionus manjavacas and Adineta vaga (monogonont and bdelloid rotifers respectively). Sequences from B. manjavacas are shown underlined and in bold. B. manjavacas possesses orthologs from Hox paralogy groups 2, 3, 4 and 6 and an ortholog of MedPost.



Supplementary Figure 6 | Morphological features of the nervous system of the monogonont rotifer *Brachionus manjavacas* revealed by immunohistochemical staining on adult females. Red staining: labeling of neurons with anti-FRMFamide, green staining: labelling of neurons with anti-5HT. Blue staining: labelling of nuclei with Hoechst 33342. Anterior to the top. Ventral views except for an anteroventral view in b. br, brain; cg, caudal ganglion; cn, caudal nerves; con, coronal nerve; gvl, germovitellarial nerve loop; lan, lateral nerves; mg, mastax ganglion; mn, mastax nerve; tr, trophi; ven, ventrolateral nerves.

Supplementary Table 1 | Primers used for isolation of *Hox* gene sequences of *Brachionus* manjavacas.

Primer	Sequence 5'->3'	
ELEKEF	GAR YTN GAR AAR GAR TT	universal forward Hox primer
WFQNRR	CKN CKR TTY TGR AAC CA	universal reverse Hox primer
KLARTAYT	AAG CTT GCC MGN ACN GCN TAY AC	PG1-3 Hox primer
AQLVELEKE	GCB CAR YTN GTH GAR YTV GAR AAR G	PG3 primer
RGRQTY	MGN GGN MGN CAR ACN TA	PG4-8 Hox primer
BmHox2_RACEfw	TGT GTC GGC CTA GAC GTG TTG AAA TAG CGT CC	Brachionus Hox23'RACE-primer
BmHox2_RACErev	CAA ATT GGA CGC TAT TTC AAC ACG TCT AGG CCG AC	Brachionus Hox25'RACE-primer
BmHox3_RACEfw	CTT TAC CGC CTA CTT GTG CAG ACC GCG CCG CAT C	Brachionus Hox33'RACE-primer
BmHox3_RACErev	TAG TTC GAT GCG GCG CGG TCT GCA CAA GTA GC	Brachionus Hox35'RACE-primer
BmHox4_RACEfw	CAC CAG GTC CTG GAG CTG GAA AAA GAG TTC CAC	Brachionus Hox43'RACE-primer
BmHox4_RACErev	GCC TCT CGG ACA AAC TGA GTG TGT GCG CGA TCT C	Brachionus Hox45'RACE-primer
BmHox6_RACEfw	TGA CTA GAA AGA GGC GAG TTG AAA TTG CCG GAA GC	Brachionus Hox63'RACE-primer
BmHox6_RACErev	TGC TTC CGG CAA TTT CAA CTC GCC TCT TTC TAG TC	Brachionus Hox65'RACE-primer
BmMedPost_RACEfw	GCG CCG AAT TGA GAT AGC GCA CTC GTT GGG	Brachionus MedPost3'RACE-primer
BmMedPost_RACErev	ATC TTG ATC TGA CGC TCA GTC AAA CCC AAC GAG TGC	Brachionus MedPost 5'RACE-primer

Supplementary Table 2 | Genome accession numbers of *Adineta vaga* genes and Genbank accession numbers of all remaining sequences used in this study.

Adineta vaga Adineta Hox1 AV 303240 Eupryma scolopes Eupryma Post1 AL25811 Adineta vaga Adineta Hox2 AV 36830 Raccisagitta enflata Raccisagitta Hox1 ABS18809 Adineta vaga Adineta Hox2 AV 36830 Raccisagitta enflata Raccisagitta Hox3 ABS18810 Adineta vaga Adineta Hox4 AV 436320 Raccisagitta enflata Raccisagitta Hox4 ABS18811 Adineta vaga Adineta Hox5 AV 294680 Raccisagitta enflata Raccisagitta (Hox5)Hox6* ABS18812 Adineta vaga Adineta Hox6 AV 170420 Raccisagitta enflata Raccisagitta Hox6 AS170 Adineta vaga Adineta Mox6 AV 170420 Raccisagitta enflata Raccisagitta Hox6 AS1812 Adineta vaga Adineta Medpost AV 586970 Raccisagitta enflata Raccisagitta hox8 ABS18811 Adineta vaga Brachionus Hox2 K1989539 Raccisagitta enflata Raccisagitta postA ABS18816 Brachionus majavacas Brachionus Hox2 K1989540 Raccisagitta enflata Raccisagitta postA ABS18816 Brachionus majavacas Brachionus Hox4 K1989541 </th
Adineta vagaAdineta Hox2Av346430Flaccisagitta enflataFlaccisagitta Hox1ABS18809Adineta vagaAdineta Hox3Av567830Flaccisagitta enflataFlaccisagitta Hox3ABS18810Adineta vagaAdineta Hox4Av36520Flaccisagitta enflataFlaccisagitta Hox3ABS18811Adineta vagaAdineta Hox4Av36520Flaccisagitta enflataFlaccisagitta Hox4ABS18811Adineta vagaAdineta Hox6Av170420Flaccisagitta enflataFlaccisagitta (Hox5)Hox6*ABS18812Adineta vagaAdineta Hox6Av170420Flaccisagitta enflataFlaccisagitta (Hox6)Hox7*ABS18813Adineta vagaAdineta MedpostAv566970Flaccisagitta enflataFlaccisagitta MedPostABS18814Brachionus manjavacasBrachionus Hox3K1989539Flaccisagitta enflataFlaccisagitta MedPostABS18815Brachionus manjavacasBrachionus Hox3K1989540Flaccisagitta enflataFlaccisagitta postAABS18816Brachionus manjavacasBrachionus Hox4K1989542Helodela robustaHelodela Lox2CAA78665Brachionus manjavacasBrachionus Hox4K17989542Helodela robustaHelodela Lox2CAA78665Brachionus manjavacasBrachionus Mar4AC174382Lingula anatinaLingula LoxAAD45587Branchiostoma IanceolatumBranchiostoma Hox4AC174381Lingula anatinaLingula AntipAAD455891Branchiostoma IanceolatumBranchiostoma Hox4AC174384Lingula anatinaLingula AntipA
Adineta vaga Adineta Hox3 Av 567830 Flaccisagitta enflata Flaccisagitta Hox3 ABS18810 Adineta vaga Adineta Hox4 Av 436520 Av 117920 Av 117920 Av 117920 Adineta vaga Adineta Hox5 Av 294680 Flaccisagitta enflata Flaccisagitta (Hox5)Hox6* ABS18812 Adineta vaga Adineta Hox5 Av 294680 Flaccisagitta enflata Flaccisagitta (Hox5)Hox6* ABS18812 Adineta vaga Adineta Hox6 Av 170420 Flaccisagitta enflata Flaccisagitta (Hox6)Hox7* ABS18813 Adineta vaga Adineta Medpost Av 586970 Flaccisagitta enflata Flaccisagitta MedPost ABS18814 Brachionus majavacas Brachionus Hox2 K1999539 Flaccisagitta enflata Flaccisagitta postB ABS18816 Brachionus majavacas Brachionus Hox4 K1999540 Flaccisagitta enflata Flaccisagitta postB ABS18816 Brachionus majavacas Brachionus MePost K1999542 Lingula anatina Lingula Lab ADJ18238 Branchiostoma lanceolatum Branchiostoma Hox2 ACJ74382 Lingula anatina Lingula Antina Lingula Antina Lingula Antina Lingula Anti
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* Matus et al. (2007)¹⁰ isolated *Flaccisagitta enflata* orthologs of Hox6 and Hox7 genes as shown in Fig.3 and Fig.4 of that publication. The sequences

however were submitted to Genbank as *Hox5* and *Hox6* respectively even though a *Flaccisagitta Hox5* had not been isolated. All of our phylogenetic analyses identify these genes as the original *Hox6* and *Hox7* orthologs. The assignments shown in this study reflect the original assignments.

Supplementary References

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