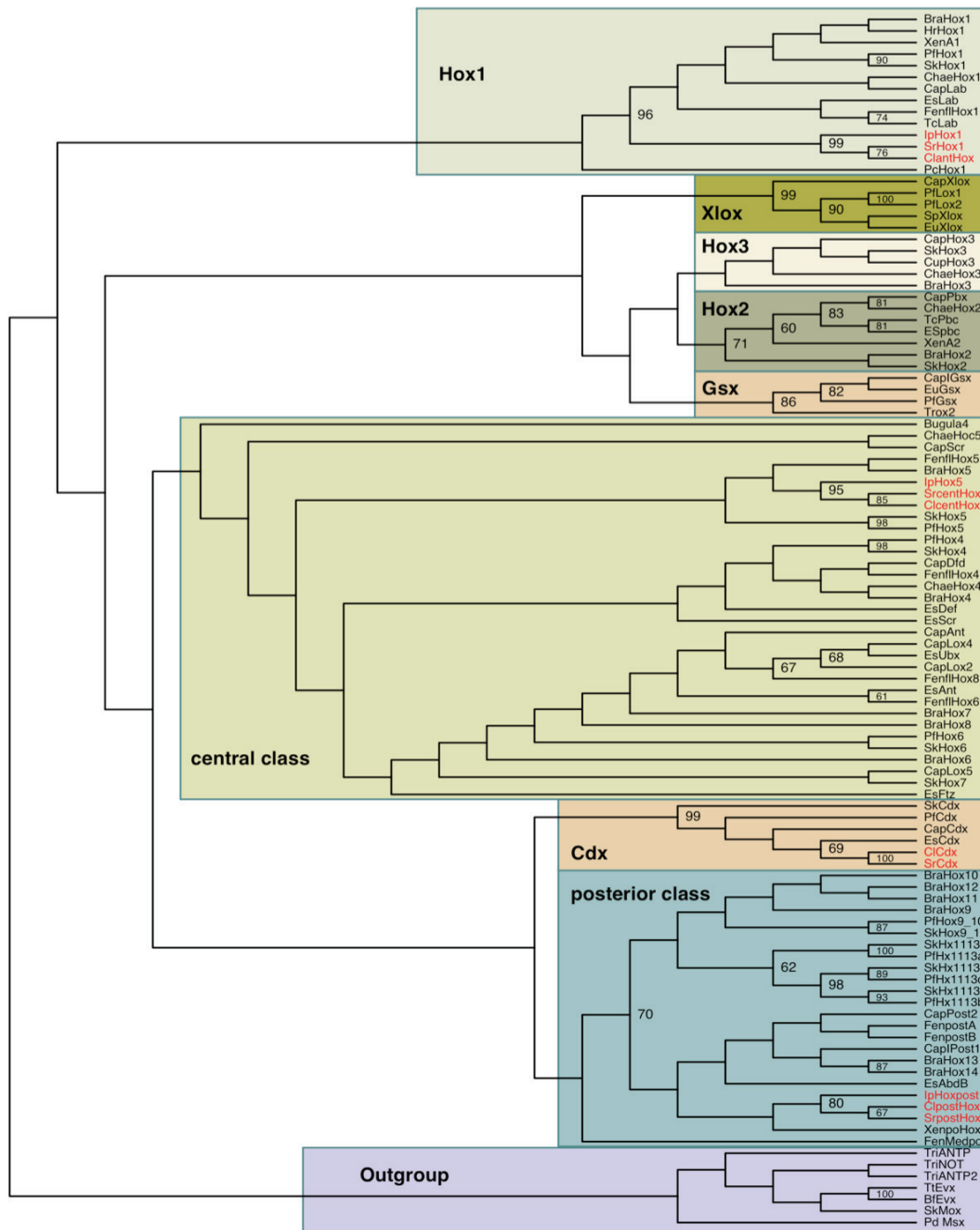
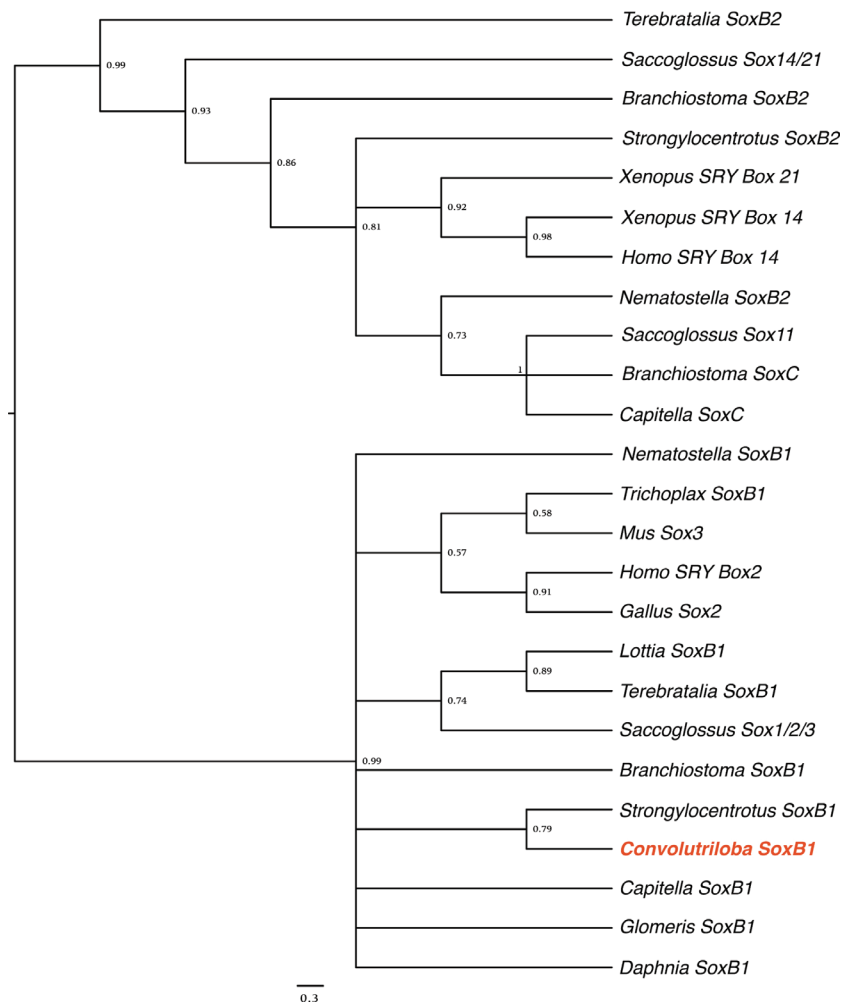


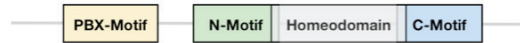
Additional Data



Supplementary Figure 1: Maximum Likelihood Phylogenetic without cnidarian *Hox* orthologs. *Hox* and *ParaHox* genes of acoels indicated in red. Bootstraps (3000) above 60 are indicated in percentage.



Supplementary Figure 2: Bayesian phylogenetic orthology assignment of the C/SoxB1.



Hox/paraHox Class	Species	PBX-Motif	presence	distance from Homeodomain	N-Motif	N-Name	C-Motif	C-Name
Hox1	<i>C. longifissura</i>	QFAWMK	✓	38	PGVQTRGGRTNFTNK	Na	KLLKEGKLS--	-
	<i>I. pulchra</i>	--SWMK	✓	28	PGSQTRGGRTNFTNK	Na	KLVKEGKLA--	-
	<i>S. roscoffensis</i>	PFSWMK	✓	37	PGVQTRGGRTNFTNK	Na	KLLKEGKLS--	-
	<i>S. kowalewski</i>	MYNWMK	✓	17	FTGSPANGRTNFTNK	Na	KQKKRFKDGPS	-
	<i>Capitella lab</i>	TYKWMT	✓	21	FAGQPNMGRTNFTNK	Na	KRLKENTSTTP	-
Hox2	<i>S. kowalewski</i>	MYNWMK	✓	20	EAGHHRRVRTAFNT	Nb	RQIMKAAVSGS	-
	<i>Capitella pb</i>	EYPWMR	✓	55	ASNHPRLRTAYTNT	Nb	RQTGKSGNSP	-
Hox3	<i>S. kowalewski Hox3</i>	MYAWMT	✓	25	GRSPIKRMRTNFCTA	Nb	KDKGLVDPYQA	-
	<i>Capitella Hox3</i>	IYPWMR	✓	40	VGQPSKRARTAYTSA	Nb	KQKQKQNLMEK	-
central Hox	<i>C. longifissura</i>	MFAWMS	✓	3	PPTDCKRTRTAYTRF	Nb	KDNNLKSMSQV	Ca
	<i>I. pulchra</i>	?	?	?	?	?	KDNNLKSMSQV	Ca
	<i>S. roscoffensis</i>	VFAWMS	✓	3	PPTDCKRTRTAYTRF	Nb	KDNNLKSMSQI	Ca
	<i>S. kowalewski Hox4</i>	MYPWMK	✓	15	NGAEHKRTRTAYTRY	Nb	KDHNLPNTKT	Ca
	<i>S. kowalewski Hox5</i>	VYPWMR	✓	10	NGMEAKRSRTAYTRY	Nb	KEHNKVSISQI	Ca1
	<i>Capitella dfd</i>	IYPWMK	✓	14	FVGDSKRTRTAYTRH	Nb	KEHKLPTNKT	Ca
	<i>Capitella scr</i>	IYPWMK	✓	7	SNADNKRTRTSYTRH	Nb	KEHKLHLAKS	Ca1
	<i>S. kowalewski Hox6</i>	IYPWMR	✓	5	CGSDQRRGRQTYTRY	Nb	KEQKTGGASP	Ca
	<i>S. kowalewski Hox7</i>	LYPWVN	✓	5	PEVPKKRCRQTYTRY	Nb	KESKKDDGENS	Ca
	<i>Capitella lox5</i>	IYPWMR	✓	8	FGYEQKRTRQTYTRY	Nb	KENNISKLTGP	Ca
	<i>Capitella antp</i>	?	-	?	AGPERKGRQTYTRY	Nb	KENRQIEVLRLQ	Ca
posterior Hox	<i>C. longifissura</i>	SPGWL	reduced	3	VRNVSRRKKRRPYTKN	Nbx	KQHSGGPGLGP	-
	<i>I. pulchra</i>	-MGWIA	reduced	3	ARNVSRRKKRRPYTKT	Nbx	KQMNGGTPQTM	-
	<i>S. roscoffensis</i>	GMAWMA	✓	3	ARNVSRRKKRRPYTKN	Nbx	KQHSGGPGMGP	-
	<i>Branchiostoma Hox9</i>	QPGWMN	✓	3	NNHSSRRKKRCPYTRF	Nbx	KMSKQRQEQQQ	-
	<i>Ptychodera 9/10</i>	PPNWMT	✓	3	TSASGRKKRCPYTKF	Nbx	KQNHRTNCTMI	-
	<i>Strongylocentrotus 11/13</i>	TPSWMF	✓	3	AALPRRTKRRPYTKL	Nbx	KQKKMNEREKR	-
	<i>Capitella Post1</i>	-----	-	-	SDVNPKKRKPYSKP	Nbx	KEKKIATKRAK	-
	<i>Capitella Post2</i>	-----	-	-	DAPKQKKRKPYPYTRY	Nbx	KRKKLNERAKS	-
	<i>Capitella</i>	-----	-	-	SSDAVKRMRTAFSST	Nb	KEGAAHGSRDH	-
Gsx	<i>Ptychodera</i>	-----	-	-	NLQSSKRIRTAFTST	Nb	KRRKTRVRDCR	-
	<i>Capitella</i>	HFPWMK	✓	21	TFSENKRTRTAYTRA	Nb	KDVKKKRPQQS	-
Xlox	<i>Strongylocentrotus</i>	QFPWMK	✓	21	DFDENKRTRTAYTRA	Nb	KEEAKRKPLKQ	-
Cdx	<i>C. longifissura</i>	-----	-	-	KTRTKDKYRVVYTDR	-	KVSRKVPGGGN	-
	<i>S. roscoffensis</i>	-----	-	-	KTRTKDKYRVVYTDR	-	KVSRKVPGGGN	-
	<i>S. kowalewski</i>	PYAWMR	✓	13	KTRTKDKYRVVYTDH	-	KERKQNKKKVM	-
	<i>Capitella</i>	PYDWMK	✓	14	KTRTKDKYRIVYSEY	-	KQKRKMEALS	-
Nv Anthox1	postHox	-----	-	-	KQPFKHKRMAYTRI	-	KDNKPIPTSR	-
Nv Anthox1a	postHox	DAPWHY	✓	3	KQPFKHKRMAYTRI	-	KDNKPIPTSR	-
Nv Anthox2	gsx?	-----	-	-	GNSRSKRIRTAYTSM	Nb	KDKKAAQHGTT	-
Nv Anthox7	hox2	IYPWMR	✓	11	GGKHTKRYRTSYTNR	Nb	KDEKQKEDGPS	-
Nv Anthox6	hox1	-----	-	-	NPSPSQKKRFTFTQR	-	REFKDSLQKPA	-
Nv Anthox6a	(HDV060)	IYPWMT	✓	14	ECTSDKNRTIYSTRQ	-	KENKLVEKAIE	-
Nv Anthox8	hox2?	IYPWMK	✓	12	FVRESKRHRYSYTNK	-	-	-
Nv Anthox8b	Hox2?	IYPWMK	✓	12	FVRESKRHRYSYTNK	-	KDEKQKTEDCY	-
Nv HD065	(Cdx/Xlox)	-----	-	-	SAQVRSRARTAYTAS	-	KTDSNGAFEGV	-
Nv Anthox9	(HDV117)	VYPWMV	✓	21	SSTS NHAPRSAFTTV	-	REAKNVEEVLH	-
Che9-14A	pHox?	YFPWNC	✓	4	CFTDGRKRRTSYTRR	-	REKPTSTKNEN	-
Che9-14B	pHox?	-----	-	-	DSNGHRRKRRTAYSRA	-	-	-
Che9-14C	pHox?	AGPWIC	✓	4	RDIDTKRKRMTYSRK	-	KECNKKKTGAV	-
CheHox1	pHox?	NYQWMN	✓	59	ATGEQGGKKRIFCSQK	-	REMKGKRFQLR	-
CheCdx	cdx?	-----	-	-	SQDPTMRSRPFSSH	-	KQKKISGEVIE	-
CheGsx	gsx?	-----	-	-	GGSKSKRIRTAYSI	Nb	KDKKSGFNNSY	-
TurrPdx	xlox?	-----	-	-	SAKVKKRNRTTYTRV	-	RDEEDALRNEN	-

Supplementary Table 1: Motif comparison of the acoel *Hox* genes with that of bilaterian and cnidarian sequences.