Supplementary Files, Tables & Notes

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Pax3/7 duplicated and diverged independently in amphioxus, the basal chordate lineage

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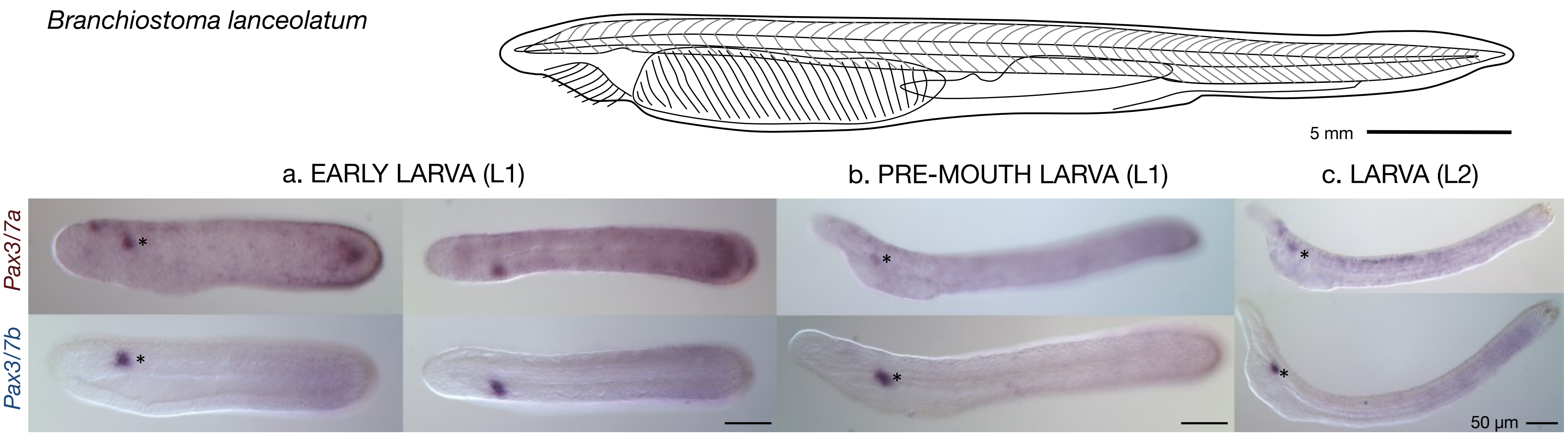
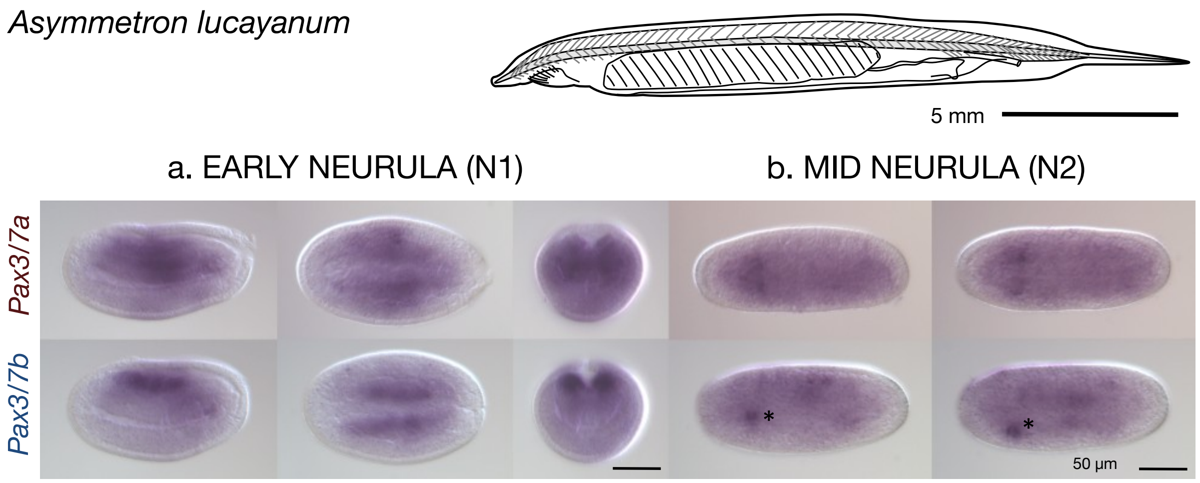
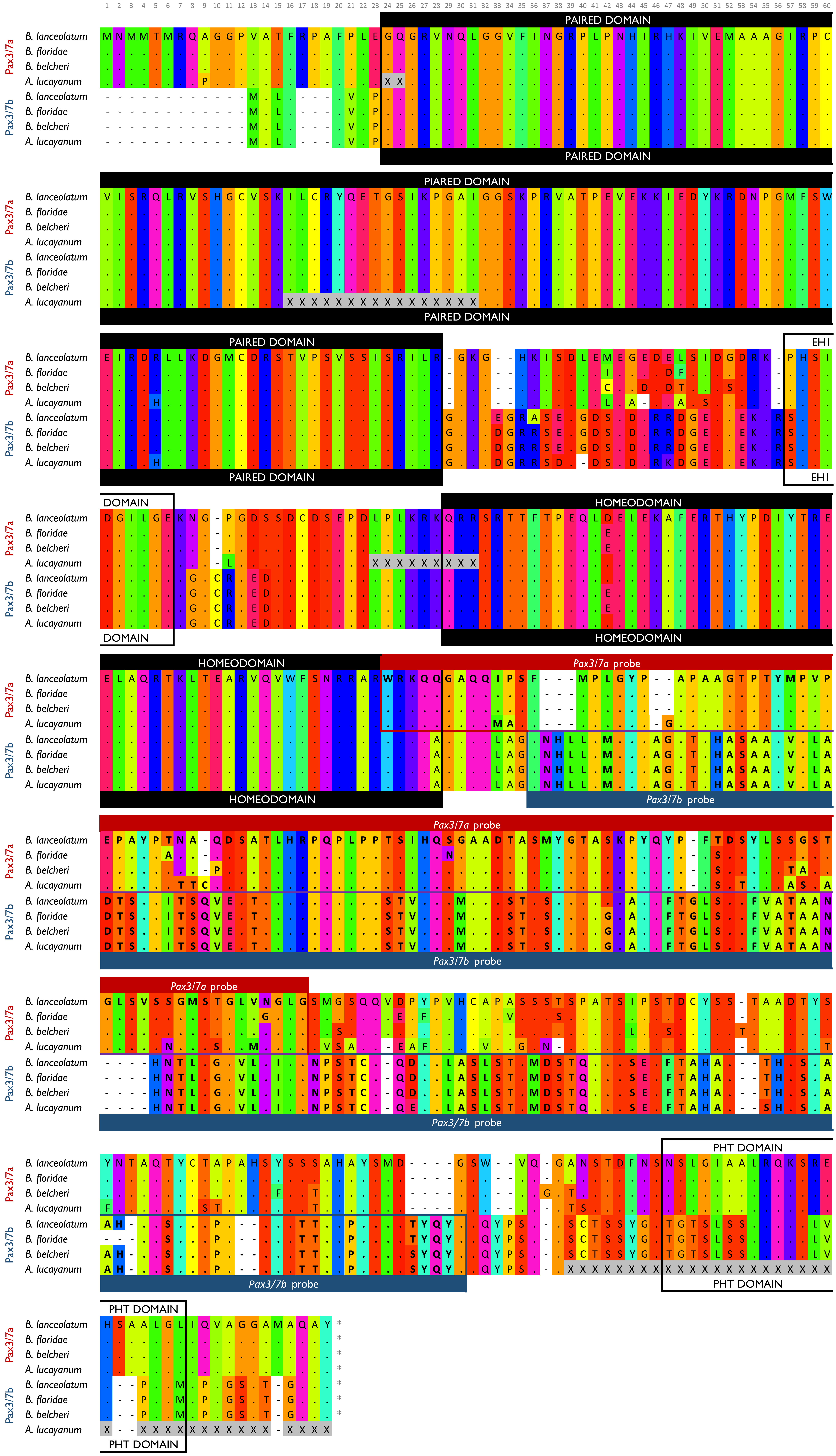


Supplementary figure S1: **Expression of Pax3/7a and Pax3/7b in a *B. lanceolatum* later developmental time course.** Top: Illustrative line drawing of adult B.*lanceolatum.* Scale bar ≈ 5 mm. Bottom: Whole mount *in situ* hybridization images of *Pax3/7a*-specific probe (top row of block) and *Pax3/7b*-specific probe (bottom row of block) in *B. lanceolatum* larvae. Views are presented in the left-to-right order: lateral (all) and dorsal (early larva only). All views are oriented with the anterior to the left. Asterisks mark to the immediate anterior the common sinistral domain of expression. (**a**) Early larva, L1, 30 hpf. (**b**) Pre-mouth neurula, L1, 36 hpf. (**c**) Larva, L2, 48 hpf. Scale bars = 50 micrometres.



Supplementary figure S2: **Expression of *Pax3/7a* and *Pax3/7b* in an *A. lucayanum* early developmental time course.** Top: Illustrative line drawing of adult *A. lucayanum*, adapted from Andrews, E.A. *An undescribed acraniate:* Asymmetron lucayanum (Baltimore, 1893). Scale bar ≈ 5 mm. Bottom: Whole mount *in situ* hybridisation images of *Pax3/7a*-specific probe (top row of block) and *Pax3/7b*-specific probe (bottom row of block) in *A. lucayanum* embryos. Views are presented in the right-to-left order: lateral, dorsal, and blastoporal (early neurula only). Lateral and dorsal views are oriented with the anterior to the left. **(a)** Early neurula, N1, 12 hpf. **(b)** Mid neurula, N2, 16 hpf. Asterisks mark to the immediate anterior the sinistral domain of expression found in both paralogues and in *A. lucayanum*. Scale bars = 50 micrometres.



Supplementary Figure S3: Annotated amino acid alignment of cephalochordate Pax3/7 sequences. Residues are coloured according to the Taylor colour scheme. Domains are highlighted in white and black boxes, and the region covered by the probes highlighted by a red box (*Pax3/7a* probe) and a blue box (*Pax3/7b* probe).

Assembly	Scaffold/contig	Modifications
Bl71nemr	Sc0000222	None
BRAFL v2	scaffold23 contig4522	None
	scaffold23 contig 4524	None
HapV3	scaffold5	Trimmed to bases 2035000-4035000
GCA_001663935.1_Asyluc0.1	LZCU01018971.1_scaffold1268824_cov58	None
	LZCU01148733.1_scaffold328746_cov58	None
	LZCU01080238.1_scaffold2528110_cov53	Reverse complement
	LZCU01117694.1_scaffold2608874_cov71	Reverse complement
	LZCU01137041.1_scaffold2697051_cov71	Reverse complement; padded 3' & 5' with 2,000 Ns to prevent VISTA alignment ignoring it
	LZCU01078009.1_scaffold2501631_cov61	None
	LZCU01058212.1_scaffold20007_cov45	Reverse complement; extended 3' with SRA data
	LZCU01078009.1_scaffold2501631_cov61	Extended 5' with SRA data
	LZCU01179060.1_scaffold612678_cov42	Reverse complement; split into two pieces to allow insertion of scaffold628499; assembly gaps in first half improved with SRA data
	LZCU01180542.1_scaffold628499_cov66	Reverse complement
	LZCU01040462.1_scaffold1632309_cov71	None
	LZCU01174809.1_scaffold568960_cov59	Reverse complement
	LZCU01210302.1_scaffold973465_cov59	None
	LZCU01048762.1_scaffold17933_cov44	Reverse complement
	LZCU01157810.1_scaffold40939_cov53_mid_whole	Gap partially filled with SRA data
	LZCU01012722.1_scaffold1175651_cov61	None
	LZCU01126896.1_scaffold2650035_cov73	None
	LZCU01085103.1_scaffold2534474_cov61	None

Supplementary Table S1: Details of cephalochordate genomic data used in Fig. 1A (mVISTA plot)

	5'	3'	AMPLICON (*B.lan*)	AMPLICON (*A.luc*)
Pax3/7a	CTGGAGGAAGCAGCAGGG	GCCCAGTCCGTTCACCAA	*CTGGAGGAAGCAGCAGGG*CGCCCAGCAGATACCGTCCTTCATGCCGCTGGGATACCCCGCTCCCGCCGCCGGGACACCCACCTACATGCCGGTCCCCGAGCCCGCATACCCAACTAGCGCTCAAGATTCGGCAACCCTGCACAGACCGCAGCCTTTGCCCCCCACCAGCATCCATCAGAGCGGGGCTGCAGACACGGCCAGCATGTACGGCACTGCCAGCAAACCTTACCAGTACCCTTTCACCGACTCCTACCTGTCCTCGGGATCCACCGGTCTGTCTGTCAGCAGTGGAATGTCGACTGG*GTTGGTGAACGGACTGGGC*	*CTGGAGGAAGCAGCAGGG*CGCCCAGCAGATACCGTCCTTCATGCCGCTGGGATACCCCGCTCCCGCCGCCGGGACACCCACCTACATGCCGGTCCCCGAGCCCGCATACCCAACTAGCGCTCAAGATTCGGCAACCCTGCACAGACCGCAGCCTTTGCCCCCCACCAGCATCCATCAGAGCGGGGCTGCAGACACGGCCAGCATGTACGGCACTGCCAGCAAACCTTACCAGTACCCTTTCACCGACTCCTACCTGTCCTCGGGATCCACCGGTCTGTCTGTCAGCAGTGGAATGTCGACTGG*GTTGGTGAACGGACTGGGC*
Pax3/7b	CTTCAACCACCTGCTACCCA	CCCGTACTGATAGGTGTCCATG	*CTTCAACCACCTGCTACCCA*TGGGCTACCCCGCCGGAGCCACTGCGCATGCGTCAGCAGCCTACGTCCCGCTGGCGGACACCAGTTATCCCATCACTTCACAAGTAGAATCGACCACCTTGCACCGACCGCAGCCCCTCCCCCCGTCTACGGTGCACCAGAGCATGGCGGCCGACTCCACGTCCTCGTACGGCACGGCCAGCAAGGCGTACCAGTTCACGGGCCTCTCCGACTCCTTCGTCGCCACCGCAGCCAACCACAACACGCTCTCTGGAGGGGTATTGAACATCCTAGGCAACCCCAGCACGTGCCAACAAGACTACCCTCTCGCCTCGCTCTCAACCTCCATGGACTCCACGCAAGCCACCAGCTCAGAAAGCTTCACGGCGCATGCGTCGACCCACGACAGCTACGCCGCGCATGCTCAGTCGTACTGCACCCCGCCTAGCTACTCGACCACCGCCCACCCGTACAG*CATGGACACCTATCAGTACGGG*	*CTTCAACCACCTGCTACCCA*TGGGCTACCCCGCCGGAGCCACTGCGCATGCGTCAGCAGCCTACGTCCCGCTGGCGGACACCAGTTATCCCATCACTTCACAAGTAGAATCGACCACGTTGCACCGACCACAGCCCCTCCCCCCGTCTACGGTGCACCAGAGCATGGCGGCCGACTCCACGTCCTCGTACGGCACGGCCAGCAAGGCGTACNAGTTCACGGGCCTCTCCGACTCCTTCGTCGCCACCGCAGCCAATCACAACACGCTCTCTGGAGGGGTGTTGAACATCCTCGGCAACCCCAGCACGTGCCAACAAGACTACCCTCTCGCCTCGCTCTCAACCTCCATGGACTCCACGCAAGCCACCAGCTCAGAAAGCTTCACGGCGCATGCGTCGACACACGACAGCTACGCCGCGCATGCTCAGTCGTACTGCACCCCGCCTAGCTACTCGACCACCGCCCACCCGTACAG*CATGGACACCTATCAGTACGGG*

Supplementary Table S2: Details of primers and amplicons used as probes in WM*IS*H experiment (Figs. 3, 4, S1)

Group/Species	**Accession details**		
VERTEBRATES	Pax3	Pax7	-
Homo sapiens	NP_852123.1	NP_001128726.1	-
Mus musculus	AAH48699.1	NP_035169.1	-
Gallus gallus	BAB85652.1	XP_015152318.1	-
Python bivitattus	XP_007425723.1	XP_007424290.1	-
Danio rerio (a)	AAC41253.1	CAM12909.1	-
Scyliorhinus torazame	BAM15710.1	BAM15711.1	-
Petromyzon marinus	-	AAL04156.1	-
CEPHALOCHORDATES	Pax3/7a	Pax3/7b	-
Branchiostoma lanceolatum	MF979121	MF979122	(new)
	ACE79721.1	-	(old)
Branchiostoma floridae	MF979123	MF979124	(new)
	EEN66816.1	-	(old)
Branchiostoma belcheri	MF979125	MF979126	(new)
	-	ABK54280.1	(old)
Asymmetron lucayanum	MF979127	MF979128	(new)
	-	-	(old)
OTHER DEUTEROSTOMES	Pax3/7	-	-
Halocynthia roretzi	BAA12289.1	-	-
Saccoglossus kowalevskii	XP_006823827.1	-	-
ARTHROPODS	paired	gooseberry	gooseberry-neuro
Tribolium castaneum	NP_001071090.1	EFA09269.2	EFA09140.1
OTHER PROTOSTOMES	Pax3/7	-	-
Crassostrea gigas	EKC41820.1		
Capitella teleta	ABC68267.1		

Supplementary Table S3: Details of accession numbers used in alignment/phylogenetic analyses

SPECIES	ACCESSION	GENE	ISO-FORM	# EXONS	EXON LENGTHS, AA	PRD BOX POS'N	LEN ^	HOM. DOM. POS'N	LEN ^	Pax7 DOM. POS'N	LEN ^
Mus musculus	AAH48699.1	3	b	9	28|78|43|45|68|55|71|82|11*	34-159	*125*	222-275	*53*	347-391	*44*
Homo sapiens	NP_852124.1	3	3	8	28|78|43|45|68|55|71|89*	34-159	*125*	222-275	*53*	347-391	*44*
Gallus gallus	BAB85652.1	3	-	6	partial chromosome 47|68|55|71|82|11*	34-161	*195*	222-275	*53*	347-391	*44*
Alligator mississippiensis	XP_006266132.1	3	X2	9	28|78|43|45|68|55|71|82|11*	34-159	*193*	222-275	*53*	347-391	*44*
Danio rerio	NP_571352.1/AAC41253.1	3a	-	8	28|78|43|48|66|55|73|116*	34-159	*193*	223-276	*53*	350-394	*44*
Danio rerio	NP_001315326.1	3b	-	9	28|78|42|51|66|55|62|73|11*	34-158	*192*	225-278	*53*	346-385	*39*
Callorhinchus milii	XP_007887991.1	3	-	13	56|66|58|19|14|77|43|45|66|55|71|82|11*	220-346	*126*	405-458	*53*	543-574	*31*
Mus musculus	NP_035169.1	7	-	9	28|78|43|43|66|55|67|82|38*	34-159	*193*	218-271	*53*	345-383	*38*
Homo sapiens	NP_002575.1/CAA65522.1	7	1	8	28|78|43|45|66|55|67|136*	34-163	*197*	220-273	*53*	347-385	*38*
Gallus gallus	NP_990396.1	7	-	10	28|78|43|43|66|55|66|22|82|38*	34-159	*193*	218-271	*53*	352-382	*30*
Danio rerio	XP_009304561.1/CAM12909.1	7a	X1	9	28|78|43|43|66|55|65|83|38*	34-161	*195*	218-271	*53*	338-381	*43*
Danio rerio	NP_001139621.1	7b	-	9	28|78|52|43|65|55|65|83|38*	34-170	*204*	226-279	*53*	346-389	*43*
Callorhinchus milii	XP_007896063.1	7	-	9	28|78|43|43|67|55|58|82|38*	34-161	*195*	219-272	*53*	344-378	*34*
A.mississippiensis	XP_014457309.1	7	-	9	46|43|43|66|55|66|82|38*		*0*	157-210	*53*	283-321	*38*
Lethenteron japonicum	KE993866.1:1	7	-	9	18|79|43|49|69|54|68|90|39*	24-149	*173*	215-268	*53*	347-380	*33*
Saccoglossus kowalevski	XP_006823827.1	3B-I		6	16|162|66|55|51|90*	17-141	*158*	202-254	*52*		
B. lanceolatum	**MF979121**	**3/7a**		**7**	**23| 162 |65|49|60|79|42***	**24-151**	***175***	**207-260**	***53***	320-364	*44*
B. lanceolatum	**MF979122**	**3/7b**		**6**	**| 178 |62|54|59|79|39***	**9-136**	***143***	**197-250**	***53***	316-357	*41*
Ciona intestinalis	XP_018669403.1	3/7		10	15|55|49|38|75|75|85|95|96|39*	16-143	*127*	192-245	*53*		

Supplementary Table S4: Details of exon/intron structure for a selection of Pax3/7 homologues, showing the conserved exon structure

Supplementary File 2: FASTA format alignment of Bilaterian Pax3/7 genes

```
>Pax4/6__B._floridae_(ROOT)/1-483
------MPHKAWTLQRPADEHAQYS----PVQ-------------------ADPGHSGVNQLGGVFVGGRPLPDSTRRKIVELAHQGARP
CDISRLLQVSNGCVSKILGRYYETGSIRPRAIGGSKPR-VATPEVVAKIAQFKRECPSIFAWEIRDRLLSEGICTNENIPS-----VSSI
NRVLRNLA---SGEKNTLQS-LQSADPQMLEKLRLLNGNAWPHPGPWPYPPSTAGAPPPQTNGNVTTKKEGDGKLASQILTLHGYQDQGD
GSNDDSDEAQARLRLKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREEKLRN--QRRSQ-
DSDSSSP-----SRIP---------------------------------ISSS----FSTATMYQ-------------------------
-------------PIAPPSAPVMSR------------------------------------------SSHAGLTDSYSSLPPVPSFS---
------------------------------------------------------------------VPGNMAPMPSMQ------------
-------------------------QSRDQTSYSCMIPHSTAM----------------------------------------TPR---G
YDSLALGSY---NPTHAG-------------------------HHVTTTHPSHMQAPSMPGH--SHMSHANGGSAGL-ISPGVS------
-VPVQVPGAVTEEMT---------------SQPYWPRIQ

>PAX3__H._sapiens/1-484
---MTTLAGAVPRMMRPGPGQNYPR-SGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEEYKRENPGMFSWEIRDKLLKDAVCDRNTVPS-----VSSI
SRILRSKF---GKGEEEEAD-LERKEA---------------------------------EESEKKAKHSIDGILSERASA-----PQSD
E-G-SDIDSEPDLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LMAF-
-NHL-IP-----GGFP--------PTA-------------MPTLPTYQLSETS----YQPTSIPQAVSDPSS------------------
-------------TVHRPQPLPPST-VHQSTI---P------------SNPDSSSAYCLPSTR----HGFSSYTDSFVP-PSGPSNPMNP
TIGNGLSPQ----VMGLLT-----------------------------------------------NHGGVPHQPQTD------------
-------------------------YALSPL--TGGLEPTTTV----------------------------------SASC--SQR----
LDHMKSLDS---LPTSQSYCP------------------P---TYSTTG--YSMDP-V-TGY--QY-GQYGQSAFHY-LKPDIA------
---------------------------------------

>PAX3__M._musculus/1-484
---MTTLAGAVPRMMRPGPGQNYPR-SGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEEYKRENPGMFSWEIRDKLLKDAVCDRNTVPS-----VSSI
SRILRSKF---GKGEEEEAD-LERKEA---------------------------------EESEKKAKHSIDGILSERASA-----PQSD
E-G-SDIDSEPDLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LMAF-
-NHL-IP-----GGFP--------PTA-------------MPTLPTYQLSETS----YQPTSIPQAVSDPSS------------------
-------------TVHRPQPLPPST-VHQSTI---P------------SNADSSSAYCLPSTR----HGFSSYTDSFVP-PSGPSNPMNP
TIGNGLSPQ----VMGLLT-----------------------------------------------NHGGVPHQPQTD------------
-------------------------YALSPL--TGGLEPTTTV----------------------------------SASC--SQR----
LEHMKNVDS---LPTSQPYCP------------------P---TYSTAG--YSMDP-V-TGY--QY-GQYGQSAFHY-LKPDIA------
---------------------------------------

>PAX3__G._gallus/1-484
---MTTLAGAVPRMMRPGAGQSYPR-GGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEEYKRENAGMFSWEIRDRLLKDGVCDRNTVPS-----VSSI
SRILRSKF---GKGEEEEAE-LERKEA---------------------------------EEGDKKAKHSIDGILSERASA-----AQSD
E-G-SDIDSEPDLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LMAF-
-NHL-IP-----GGFP--------PSA-------------MPTLPTYQLSEPS----YQPTSIPQAVSDPSS------------------
-------------TVHRPQPLPPST-VHQSSL---P------------SNPESSSAYCLPSTR----HGFSSYTDSFVP-PSGPSNPMNP
AIGNGLSPQ----VMGLLT-----------------------------------------------NHGGVPHQPQTD------------
-------------------------YALSPL--TGGLEPTTTV----------------------------------SASC--SQR----
LDHMKSLDS---LPTSQSYCP------------------P---TYSTTG--YSMDP-V-TGY--QY-GQYGQSAFHY-LKPDIA------
---------------------------------------

>PAX3__P._bivittatus/1-484
---MTTLGGAVPRMMRPAPGQNYPR-SGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEEYKRENAGMFSWEIRDKLLKDGVCDRNTVPS-----VSSI
SRILRSKF---GKGEEEEGE-LERKEA---------------------------------EENEKKAKHSIDGILSERASA-----PQSD
E-G-SDIDSEPDLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LMAF-
-NHL-IP-----GGFP--------PTA-------------MPTLPTYQLSESS----YQPTSIPQAVSDPSS------------------
-------------TVHRPQPLPPST-VHQSSL---P------------SNPDSSSAYCLPSTR----HGFSSYTDSFVP-PSGPSNPMNP
AIGNGLSPQ----VMGLLT-----------------------------------------------NHGGVPHQPQTD------------
-------------------------YALSPL--TGGLEPTTTV----------------------------------SASC--SQR----
LDHMKSLDS---LPTSQSYCP------------------P---TYSTTG--YSMDP-V-PGY--QY-GQYGQSAFHY-LKPDIA------
---------------------------------------

>Pax3__D._rerio/1-509
---MTALAGGISRMMRPTPPQNYPR-GGYSLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQSTTPDVEKKIEEYKRENPGMFSWEIRDKLLKDGICDRNNVPS-----VSSI
SRMLRCKFGGNGDEDEDDDE-VEKREI---------------------------------EENERRAKHSIDGILGDRSS-------HSD
E-G-SDVDSEPGLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LMAF-
-NHL-IP-----GGFP--------PSA-------------MSSLQPYQLADSP----YPPSSISQ-VSEQPS------------------
-------------TVHRPQPLPPTS-VHQSGLGSGP------------GAQEGSSAYCLSSGR----HGFSGYSDGYVA-APGHANPVNP
SISNGLPSQ----VMGLL------------------------------------------------NPGAVPHQPQSD------------
-------------------------FALSPL--TGGLEPSTGM----------------------------------PASCHSSQR----
LEALPGLPSMPALPSSQSYCP------------------S---SYSSPG--YSVDH-V-ASY--QY-SQYGQSKVNTSTVTTVERLSRVY
PLKR----------ASFGLVE------------------

>Pax7__S._torazame/1-495
---MTSLTGTAPRMMRPSPGQSYSR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
```

```
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKKIEEYKRENPGMFSWEIRDKLLKDGICDRSSVPS-----VSSI
SRVLRAKF---GRRDDDE-E-MEKKD----------------------------------EDGVRKTKHSIDGILGEKGN-------RLD
D-GASDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PTG-------------MPTLPPYQLPEAS----YPGTTLSQ---DGGS------------------
-------------TVHRPQPLPPSS-MHQSGL----------------TSAAESGSYGLAPNR----HTFSSYPESFMN-ATGANNPMN-
--------Q----VMSILS-----------------------------------------------NPGAVPPQPQHD------------
-------------------------FSISPL--HGSLDTSNPL----------------------------------SASC--SQR----
SDSIKGVES---LPSSQSYCT------------------P---AYSTSG--YSMDP-V-PGY--QY-AQYGQSAVDY-LTKNVS------
-LSTQRRMKLSEHSAVLGLLQV----ET--GQAY-----

>PAX7__H._sapiens/1-505
---MAALPGTVPRMMRPAPGQNYPR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKKIEEYKRENPGMFSWEIRDRLLKDGHCDRSTVPSG---LVSSI
SRVLRIKF---GKKEEED-E-ADKKE----------------------------------DDGEKKAKHSIDGILGDKGN-------RLD
E-G-SDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PTG-------------MPTLPPYQLPDST----YPTTTISQ---DGGS------------------
-------------TVHRPQPLPPST-MHQGGLAAAA------------AAADTSSAYG---AR----HSFSSYSDSFMN-PAAPSNHMNP
-VSNGLSPQ----VMSILG-----------------------------------------------NPSAVPPQPQAD------------
-------------------------FSISPL--HGGLDSATSI----------------------------------SASC--SQR----
ADSIKPGDS---LPTSQAYCP------------------P---TYSTTG--YSVDP-V-AGY--QY-GQYGQTAVDY-LAKNVS------
-LSTQRRMKLGEHSAVLGLLPV----ET--GQAY-----

>PAX7__M._musculus/1-503
---MAALPGAVPRMMRPGPGQNYPR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKKIEEYKRENPGMFSWEIRDRLLKDGHCDRSTVPS-----VSSI
SRVLRIKF---GKKEDDE-E-GDKKE----------------------------------EDGEKKAKHSIDGILGDKGN-------RLD
E-G-SDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PTG-------------MPTLPPYQLPDST----YPTTTISQ---DGGS------------------
-------------TVHRPQPLPPST-MHQGGLAAAA------------AAADTSSAYG---AR----HSFSSYSDSFMN-PGAPSNHMNP
-VSNGLSPQ----VMSILS-----------------------------------------------NPSAVPPQPQAD------------
-------------------------FSISPL--HGGLDSASSI----------------------------------SASC--SQR----
ADSIKPGDS---LPTSQSYCP------------------P---TYSTTG--YSVDP-V-AGY--QY-SQYGQTAVDY-LAKNVS------
-LSTQRRMKLGEHSAVLGLLPV----ET--GQAY-----

>PAX7__G._gallus/1-502
---MAALPGTVPRMMRPAPGQNYPR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKKIEEYKRENPGMFSWEIRDRLLKDGHCDRSTVPS-----VSSI
SRVLRIKF---GKKEEEE-D-CDKKE----------------------------------EDGEKKAKHSIDGILGDKGN-------RLD
E-G-SDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PTG-------------MPTLPPYQLPDST----YPTTTISQ---DGGS------------------
-------------TVHRPQPLPPST-MHQGGL-AAA------------AAADSSSAYG---AR----HSFSSYSDSFMN-AAAPANHMNP
-VSNGLSPQ----VMSILS-----------------------------------------------NPSGVPPQPQAD------------
-------------------------FSISPL--HGGLDTTNSI----------------------------------SASC--SQR----
SDSIKSVDS---LPTSQSYCP------------------P---TYSTTS--YSVDP-V-AGY--QY-GQYGQTAVDY-LTKNVS------
-LSTQRRMKLGEHSAVLGLLPV----ET--GQAY-----

>PAX7__P._bivittatus/1-501
---MAALPGTVPRMMRPAPGQNYPR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKKIEEYKRENPGMFSWEIRDRLLKDGHCDRTTVPS-----VSSI
SRVLRIKF---GKKEEED-D-CEKKE----------------------------------EDCEKKAKHSIDGILGDKGS-------RLD
E-G-SDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PAG-------------MPTLPPYQLPDST----YPTTTLSQ---DGGS------------------
-------------TVHRPQPLPPST-MHQGGL--SA------------TTGDSNSAYG---AR----HGFSSYTDSFMN-PTAPANHMNP
-VSNGLSPQ----VMSILS-----------------------------------------------HPSGAPPPAPAD------------
-------------------------FSISPL--HGGLESTNSL----------------------------------SASC--SQR----
SESIKSVDS---LPTSQAYCP------------------P---TYTSTG--YSVDP-V-AGY--QY-GQYSQTAVDY-LTKNVS------
-LSTQRRMKLGEHSAVLGLLPV----ET--GQAY-----

>Pax7__D._rerio/1-507
---MATLPGTVPRMMRPAPGQNYPR-TGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVATPDVEKRIEEYKRENPGMFSWEIRDKLLKDGVCDRGTVPSGEASSVSSI
SRVLRARF---GKKDDDD-E-CDKKD----------------------------------EDGEKKTKHSIDGILGDKGN-------RTD
E-G-SDVESEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-LP-----GGFP--------PTG-------------MPTLPTYQLPEST----YPSTTLSQ---DGSS------------------
-------------TLHRPQPLPPSS-MHQGGL-----------------SADSGSAYGLSSNR----HTFSSYSETFMS-PTASSNHMNP
-VSNGLSPQ----VMSILS-----------------------------------------------NPSAVPSQPQHD------------
-------------------------FSISPL--HGGLEASNPI----------------------------------SASC--SQR----
SDPIKSVDS---LASTQSYCP------------------P---TYSATS--YSVDP-VTAGY--QY-SQYGQTAVDY-LAKNVS------
-LSTQRRMKLGDHSAVLGLLQV----ET--GQAY-----

>Pax3__S._torazame/1-506
---MSTLAGPLPRMMRPAPGQSYPRSSGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAHHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAT-GSKPRQMAIPDVEKKIEEYKKENPGMFSWEIRDKLLKDGMCDRNTIPS-----VSSI
SRILRSRF---GKKEDEEDD-CERKEY---------------------------------EEGEKKTKHSIDGILANKAN-------NSD
E-A-SDIDSEPDLPLKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQ---LLAF-
-NHL-IP-----GGFP--------PTA-------------MPALSPYQLSDAS----YPPTSIPQAISDPSN------------------
-------------TVHRPQPLPPTS-VHQSSL---P------------STPDSSSAYCLSTSR----HGFSGYTDSFVS-PTGSTNPMNP
```

```
TVSNGLSPQ----VMGLLA-----------------------------------------------NPGGVPHQPQTD------------
-------------------------YALSPL--TGGLEPSTSV----------------------------------SASC--SQR----
LDPMKPLDS---LPTTQSYCP------------------S---TYSSSG--YSMDS-V-AGY--QY-GQYGQSKCHVNLSNTFSYKNAYP
PHPSSICIKMCDSVYKL----------------------

>Pax7__P._marinus/1-505
-------------MMRPAPGQNYPR-SGFPLEVSTPL-----------------GQGRVNQLGGVFINGRPLPNHIRHKIVELAHHGVRP
CVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPRQVASTDVERKIEEYKRENPGMFSWEIRDRLLKDGVCDRASVPS-----VSSI
SRILRAKF---GKRDEEEEEGAEKKDF--------------------------------GDDGDKKAKHSIDGILGDKAG-------STV
E-DSSDVDSEPDLPLKRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGANQ---LAAF-
-NHL-IP-----GGFP--------PAS-------------MPGLPPYQLPEGP----YPGSGIPQ--VDTGT------------------
-------------TVHRPQPLPPSS-MHQGGG---L------------AGGDGAGAYGLSSNR----SGF--YSDSFMSAASAPSNHMAP
-MANGLSPQ----MMGILG-----------------------------------------------NPSAMPPQHGQE------------
-------------------------YSLSPLPSSGLVDHSSGL----------------------------------SASC--SQRGGGG
GDGMKHGDG---LPPP-GLLP------------------A---TYAAAG--YGLEP-MPAAY--QY-GQYGQTAADY-LAKNVG------
-LGGQRRLKLGEHSAVLGLLQV---AET--GQAY-----

>Pax3/7b__A._lucayanum/1-469
--------------------MALF----FVLP----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKXXXXXXXXXXXXXXXXGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDHLLKDGMCDRSTVPS-----VSSI
SRILRGGKGDGRRSDD-DSE-DERKDG---------------------------------EDGEKKRSHSIDGILGEKGG-------CRG
E-D-SDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQ---LAGF-
-NHL-LP-----MGYPAGATAHASAAY-------------VP------LADTS----YPITSQVE-----ST------------------
-------------TLHRPQPLPPST-VHQSMA------------------ADSTSSYGTAGKA----YQFTGLSDSFVATAAN-------
--HNTLSGG----VLNILG-----------------------------------------------NPST---CQ-QE------------
-------------------------YPLASLSTSMDSTQATSS---------------------------------ESFTAHAS------
-----SHDS-YAAH-AQSYCT------------------PP--SYSTTAHPYSMDS-YQYGS--QYPSQ-GXXXXXX-XXXXXX------
--XXXXXXXXXXX--XXXXXXX---XXXX-XXXX-----

>Pax3/7b__B._belcheri/1-470
--------------------MALF----FVLP----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILRGGKGDGRRSEDGDSE-DERRDG---------------------------------EDGEKKRSHSIDGILGEKGG-------CRG
E-D-SDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQ---LAGF-
-NHL-LP-----MGYPAGATAHASAAY-------------VP------LADTS----YPITSQVE-----ST------------------
-------------TLHRPQPLPPST-VHQSMA------------------ADSTSSYGTAGKA----YQFTGLSDSFVATAAN-------
--HNTLSGG----VLNILG-----------------------------------------------NPST---CQ-QD------------
-------------------------YPLASLSTSMDSTQATSS---------------------------------ESFTAHAS------
-----THDS-YAAH-AQSYCT------------------PP--SYSTTAHPYSMDS-YQYGS--QYPSQ-GSCTSSY-GSTGTS------
--LSSLRQKSLVH--PLGMIPV---GSGT-GQAY-----

>Pax3/7b__B._floridae/1-468
--------------------MALF----FVLP----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILRGGKGDGRRSEDGDSE-DERRDG---------------------------------EDGEKKRSHSIDGILGEKGG-------CRG
E-D-SDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQ---LAGF-
-NHL-LP-----MGYPAGATAHASAAY-------------VP------LADTS----YPITSQVE-----ST------------------
-------------TLHRPQPLPPST-VHQSMA------------------ADSTSSYGTAGKA----YQFTGLSDSFVATAAN-------
--HNTLSGG----VLNILG-----------------------------------------------NPST---CQ-QD------------
-------------------------YPLASLSTSMDSTQATSS---------------------------------ESFTAHAS------
-----THDS-YA---AQSYCT------------------PP--SYSTTAHPYSMDT-YQYGS--QYPSQ-GSCTSSY-GSTGTS------
--LSSLRQKSLVH--PLGMIPV---GSGT-GQAY-----

>Pax3/7b__B._lanceolatum/1-470
--------------------MALF----FVLP----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILRGGKGEGRASEDGDSE-DERRDG---------------------------------EDGEKKRSHSIDGILGEKGG-------CRG
E-D-SDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQ---LAGF-
-NHL-LP-----MGYPAGATAHASAAY-------------VP------LADTS----YPITSQVE-----ST------------------
-------------TLHRPQPLPPST-VHQSMA------------------ADSTSSYGTASKA----YQFTGLSDSFVATAAN-------
--HNTLSGG----VLNILG-----------------------------------------------NPST---CQ-QD------------
-------------------------YPLASLSTSMDSTQATSS---------------------------------ESFTAHAS------
-----THDS-YAAH-AQSYCT------------------PP--SYSTTAHPYSMDT-YQYGS--QYPSQ-GSCTSSY-GSTGTS------
--LSSLRQKSLVH--PLGMIPV---GSGT-GQAY-----

>Pax3/7a__A._lucayanum/1-478
--------MNMMTMRQPGGPVATFR-PAFPLE----------------------XXGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDHLLKDGMCDRSTVPS-----VSSI
SRILR---GKGHKISDLELE-A-DEAS---------------------------------SDGDRK-PHSIDGILGEKNG--------LG
D-S-SDCDSEPDXXXXXXXXXSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQ---MASF-
-----MP-----LGYP-GAPAAGTPTY-------------MP------VPEPA----YPTTTCQD-----SA------------------
-------------TLHRPQPLPPTS-IHQSGA------------------ADTASMYGTASKP----YQYP-FSDTYLSASSAGLS----
-VSNGMSSG----LMNGLG-----------------------------------------------SVSA---QQ-EA------------
-------------------------FPVHCVPAGSN-SPATSI---------------------------------PSTDCYSS-T----
-----AADT-YTFNTAQTYCS------------------TPAHSYSSTAHAYSMD-----GS--W--VQ-GTSSTDF-NSNSLG------
--IAALRQKSREHSAALGLIQV---AGGAMAQAY-----
```

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>Pax3/7a__B._belcheri/1-481
--------MNMMTMRQAGGPVATFR-PAFPLE----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILR---GKGHKISDLECE-GDDDTS---------------------------------IDSDRK-PHSIDGILGEKNG--------PG
D-S-SDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQ---IPSF-
-----MP-----LGYP--APAAGTPTY-------------MP------VPEPA----YPTNA-PD-----SA------------------
-------------TLHRPQPLPPTS-IHQSGA------------------ADTASMYGTASKP----YQYP-FSDSYLSTASTGLS----
-VSSGMSTG----LVNGLG-----------------------------------------------SMSS---QQVDP------------
-------------------------YPVHCAPASSSTSPATSL---------------------------------PSSDCYSSTT----
-----AADT-YSYNTAQTYCT------------------APAHSFSSTAHAYSMD-----GS--W--VQGGTNSTDF-NSNSLG------
--IAALRQKSREHSAALGLIQV---AGGAMAQAY-----

>Pax3/7a__B._floridae/1-479
--------MNMMTMRQAGGPVATFR-PAFPLE----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILR---GKGHKISDLEIE-GEDDFS---------------------------------IDGDRK-PHSIDGILGEKNG--------PG
D-S-SDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQ---IPSF-
-----MP-----LGYP--APAAGTPTY-------------MP------VPEPA----YPANA-QD-----SA------------------
-------------TLHRPQPLPPTS-IHQNGA------------------ADTASMYGTASKP----YQYP-FSDSYLSSGSTGLS----
-VSSGMSTG----LVGGLG-----------------------------------------------SMGS---QQVEP------------
-------------------------FPVHCAPVSSSSSPATSI---------------------------------PSTDCYSS-T----
-----AADT-YSYNTAQTYCT------------------APAHSYSSSAHAYSMD-----GS--W--VQ-GANSTDF-NSNSLG------
--IAALRQKSREHSAALGLIQV---AGGAMAQAY-----

>Pax3/7a__B._lanceolatum/1-479
--------MNMMTMRQAGGPVATFR-PAFPLE----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPR-VATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPS-----VSSI
SRILR---GKGHKISDLEME-GEDELS---------------------------------IDGDRK-PHSIDGILGEKNG--------PG
D-S-SDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQ---IPSF-
-----MP-----LGYP--APAAGTPTY-------------MP------VPEPA----YPTNA-QD-----SA------------------
-------------TLHRPQPLPPTS-IHQSGA------------------ADTASMYGTASKP----YQYP-FTDSYLSSGSTGLS----
-VSSGMSTG----LVNGLG-----------------------------------------------SMGS---QQVDP------------
-------------------------YPVHCAPASSSTSPATSI---------------------------------PSTDCYSS-T----
-----AADT-YSYNTAQTYCT------------------APAHSYSSSAHAYSMD-----GS--W--VQ-GANSTDF-NSNSLG------
--IAALRQKSREHSAALGLIQV---AGGAMAQAY-----

>Pax3/7__H._roretzi/1-704
-------------MMHRP---GTFR-PAFPLE----------------------GQGRVNQLGGVFINGRPLPNHIRHKIVEMAAHGIRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPK-VTNSEIESKIEQYKKDSPSMFSWEIRDQLIKEGLCDRSSAPT-----VSAI
SRILR------SKGCDTSNE-SAEDP----------------------------------ENGNTNSDTSSNGATGER---------EAD
E-GDSDCDSEPELPLKRKQRRSRTTFSADQLEELERCFERTHYPDIYTREELAQRTRLTEARVQVWFSNRRARWRKQMAAQQ---LPAIH
PHHT-HPHLPHHLGAYHQTIAAAGMSAHNYMLQAAAAAQHQPPPSSNPLAQNG----HSSHYAAHHPSAHGHLPTTPTAASAGTSVCGPI
ESSFASPTAHDLGSVHRHTHHPLSSPLHHAHPYSQAGMRYDGSHDAALNVAAVAAGYGLVGAS----AAAARYSAQFPS-TAFGDGY---
HQHHSLSPE--SSIFGVNGSVHSHAPGAADLTVSDYGPRQTESSHVRQHQSSAAVGGSTTRTSENHSPSSSSPRQQHQTQGGISHDSVSG
NGRRSESSAGSHDNHPRNGVSNSTSSPVTTSESHVSGMPES-VYNQRPSNAPMHLQQQSHQHSAAHLQHLRGGPSVDHTSCNGNQMIQSS
QYSLMHRSNVPEHSSIQSAAAYSAGFGVTAD--------P---SMATAAHQYHTTHNPFASC--QY-SGYGQAASDY-ENAGIT------
----ALRMKSREHSAALGLISVGAGGATSMQPAY-----

>Pax3/7__C._intestinalis/1-625
-------------MMHPG---SNFR-PAFPLE----------------------GQGRVNQLGGMFINGRPLPSHVRHKIVEMAAHGVRP
CVISRQLRVSHGCVSKILCRYQETGSIKPGAIGGSKPK-VATADVDNKIEEYKKENPGIFSWEIRERLIKEGICDRSNVPS-----VSSI
SRTLR------AKGCDVENE-SESSA----------------------------------RLDPGNRSSSSGG--------------EPN
EVGGSDSESEPDLPLKRKQRRSRTTFSAEQLDELERCFERTHYPDIYTREELAQRTRLTEARVQVWFSNRRARWRKQMAAQQFHGIPAHH
PHHL-SP----HLGYPHTMPGSVGQAAHNYMLQTSGAHH----------VQSM----HESF--AHTASSHDH----------GS------
-------------SLHRPHASVLTSPVHHA---SQA-IRYDTTD--PLNQSA-AAAYGLMGASAAAAAAAARYS-QYPSAAAFGDAYPIH
YHHHSTSPPSGSSIFGFPSHTRQTATNPVELT--------TGNPHSGPNSSPIDVG----------SPGEAGNHPLHQ-----QHFVLAQ
SARRAHQASNQRNHHNQHHSGETTTAPSTSPASNGDGHPTTGIESQ--SRAYSALAGQQHHNTDLH----------SSTSVAGQQSTAML
SSSVDHSSNVFAGQE-RGAPSSRAGYGVGPSGFATGEVLP---TSSAASHQ------SYASC--QY-SPYGQASGDY-GSAGIA------
----ALRMKSREHSASIGLIPV--GGGPSVQHAY-----

>Pax3/7__S._kowalevskii/1-438
-------------MIQPG---RSFAAPGFPLE----------------------GQGRMNQLGGLFINGRPLPNHIRYKIVEMAHQGIRP
CQISRTLRVSHGCVSKILCRYQETGSIRPGTIGGSKPK-VATVEVEKRIEDYRKDNEGIFSWEIRERLLNEKICDQQNVPS-----ISSI
SRILRHGN---GRHKTNEHEKVCRADG---------------------------------NAERAKNSHSIEGILN-----------KRD
EEPDYEPELQPDLPLKHKQRRCRTTFTCEQLEQLEKAFDRTHYPDIYTREELAQRTGLTEARVQVWFSNRRARWRKQASFLP---LNGY-
-----SP------WYPMATTGSVMPVSAGPPCVLPDTMHSFPSQDFSFLPPSHPSRLYQNSFYTQYNPPTFSLPSMP-------------
-------------DLSTGSKSVVSGPVHQ--------------------------------------HVYQGQPEYVQSSLCKNPIVMNR
PIIPPVSKSPVCSLPMIVN-----------------------------------------------------------------------
-------------------------HPMTPTVTNTPCQPFPSP-----------------------------------------------
---------------------------------------PWVHTMPAGGQEPY-----------QQVSQFSPKHGLYSSFM---------
---------------------------------------

>Gsb__T._castaneum/1-399
--------------MAPYF-------TGYPFQ----------------------GQGRVNQLGGVFINGRPLPNHIRLKIVEMAAAGIRP
CVISRQLRVSHGCVSKILNRYQETGSIRPGVIGGSKPR-VATLEVEARIEQLKKEEPQIFSWEIRDRLIKEGICDKNSAPS-----VSSI
SRLLRG-----G--RKE--------------------------------------------DPD-RKNHSIEGILGPNSS-------CD-
---ESDTESEPGIPLKRKQRRSRTTFTGEQLEALERAFGRTQYPDVYTREELAQKTKLTEARVQVWFSNRRARLRKQLNSQQ---LNAF-
```

```
-NSMSLP-----SAFP------------------------V----QHQYGDPA----FNQSTWAQQSYASAALSSGALPHSALTTGGAST
-------------SVASSTPNTL----YNSY-----------------------NSAATLDQNNQFGYNMAQVSPNQHSVSP-----AAH
QQSAVWSRQNNKVAENL----------------------------------------------------SSWHENYSL------------
------------------------------------------------------------------------------------------
---------------------------------------FAGSHYGAHSPSEAKSGYPYLGTMDMCASRVH-------------------
---------------------------------------

>Gsb-n__T._castaneum/1-338
------------MDMRPIF-------GGYPFQ----------------------GQGRVNQLGGVFINGRPLPNHIRLKIVEMAAAGVRP
CVISRQLRVSHGCVSKILNRYQETGSIRPGVIGGSKPR-VATPEIETRIEQMKKENPTIFSWEIRERLIKEGVTD---PPS-----VSSI
SRLLRG-----GGRRDG---------------------------------------------DPDGKKDYTIDGILGGRE---------E-
---ESDTESEPGIPLKRKQRRSRTTFSGEQLEALERAFSRTQYPDVYTREELAQQTGLTEARIQVWFSNRRARLRKHVGNSN---ALAF-
-PLANMP-----CQYP------------------------AESAHQHDWRNAQ----FTNYNMFQQ-----------------------T
-------------SYTNPQENRD----Y----------------------------SAIFDAN--YATLMAQ------------------
-------KNKESDAKNLGG-----------------------------------------------NPGTSW-ANFQD------------
------------------------------------------------------------------------------------------
---------------------------------------FSGDQY---APKNYWA-----------------------------------
---------------------------------------

>Prd__T._castaneum/1-414
-MTVTGNLGIM----HRHC-------FGYPFQGTTYKYTGCSDNDGFLP-----GQGRVNQLGGVFINGRPLPNHIRLKIVEMAANGIRP
CVISRQLRVSHGCVSKILNRYQETGSIRPGVIGGSKPR-VATPEVENRIEQYKRENPSIFSWEIRDRLVKEGICDRSTAPS-----VSAI
SRLLRGK----GGECDEITIQAILEFS--------------------------------VTN--PTIKEDFCAVLWKDKS-------TDN
EG-VSDCDSEPGIPLKRKQRRSRTTFTAHQLDELEKAFERTQYPDIYTREELAQRTKLTEARIQVWFSNRRARLRKQITSAA---TPLV-
-RSY-AP-----ERYP------------------------P----------------------LAQGVNDDAF----------------N
-------------SVATPTPTSVMTELYPSPV-------------------PGHSTSPNL----PLTHNIAH---------------NPY
PSHSIYPSSNLMPLNNI-Q-----------------------------------------------NLSQS-GINYKD------------
------------------------------------------------------------------------------------------
---------------------------------------TNDNNVSAV----TTQH---QGYPTNTVTILGPNSGNT-PKI---------
------------------LLQI-----------------

>Pax3/7__C._gigas/1-466
MFGFVNGFGVYLINEERLI-------VRYPTAMFSYHLAAL----GLMPSFQMEGQGRVNQLGGVFINGRPLPNHIRLKIVELAAQGVRP
CVISRQLRVSHGCVSKILQRYQETGSIRPGVIGGSKPR-VATPEVEKKIEQYKRENPGIFSWEIRDRLLKEGICDRSSVPS-----VSSI
SRVLRSKFQNIGSDSEDEEPRPSDDIS--------------------------------VNDNEKSSKYSIDGLLADDKS-------EKS
EDEESDCDSEPGLSVKRKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQMGSNQ---ISAL-
-NSI-L----------------------------------H----------------------LPQGGASSYL----------------L
-------------HETTPS--------YPLP-----------------------SVSDTLWHRNSMTHHLQNFSSLKTNDSAYAGLMENY
LSHA-------SQMHNL-T-----------------------------------------------NPTDSLASNWCS------------
------------------------------------------------------------------------------------------
---------------------------------------PVTSSVSALAYQTTTNHFNPHGYGDVTKSTLHPYNSHI-ASVSSAERCAID
ESLVALRMKSREHSAALSLMQVTDNKMSASF--------

>Pax3/7__C._teleta/1-416
-------------MLQRL----------FPLG-----------LPPLLPTYGLDGQGRVNQLGGVFINGRPLPNHIRLKIIEMASQGVRP
CVISRTLRVSHGCVSKILQRYQETGSIRPGSIGGSKPR-VATPDVEDRIHDLKKENPGIFSWEIRDRLLKDGVCDRSSVPS-----VSSI
SRVLRSHL---REGDEDKIDDEDEEES--------------------------------KDD-------------------------DDD
DDDSESLTSEPGLSLSRKQRRSRTTFSADQLEHLEKAFDRTHYPDIYTREELAQRSGLTEARVQVWFSNRRARWRKQMGSGQ---LASSF
NSLLSAA-----SGYS---------------------------------STPS----YTPSLNQDHP-----------------------
-------------ALPHPTPSVPAPPIKAESL-------------------------------------PPAFSDPFRQHSHLPYPF---
------------------------------------------------------------------LPGPTPHHPVSQ------------
------------------------------------------------------------------------------------------
----------------------------------------SLMTSVASSWNSAMSSLRSSACLPPYPSPYPPSSMQHPFHYHTSFNAGHE
AGSYPYPSGKVHAPTPIGLGSFGAMAPPSHIVSGL----
```

Supplementary File 3: FASTA format alignment of cephalochordate Pax3/7 genes

```
>Pax3/7a__B._lanceolatum/1-479
MNMMTMRQAGGPVATFRPAFPLEGQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRPCVISRQLRVSHGCVSKILCRYQETGSIKPGAIGG
SKPRVATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPSVSSISRILR---GKGHKISDLEMEGEDELSIDGDRK-PHSIDGILGE
KNG-PGDSSDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQIPSF---
MPLGYP--APAAGTPTYMPVPEPAYPTNA-QDSATLHRPQPLPPTSIHQSGAADTASMYGTASKPYQYP-FTDSYLSSGSTGLSVSSGMSTGL
VNGLGSMGSQQVDPYPVHCAPASSSTSPATSIPSTDCYSS-TAADTYSYNTAQTYCTAPAHSYSSSAHAYSMD----GSW--VQ-GANSTDFN
SNSLGIAALRQKSREHSAALGLIQVAGGAMAQAY

>Pax3/7a__B._floridae/1-479
MNMMTMRQAGGPVATFRPAFPLEGQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRPCVISRQLRVSHGCVSKILCRYQETGSIKPGAIGG
SKPRVATPEVEKKIEDYKRDNPGMFSWEIRDRLLKDGMCDRSTVPSVSSISRILR---GKGHKISDLEIEGEDDFSIDGDRK-PHSIDGILGE
KNG-PGDSSDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQIPSF---
MPLGYP--APAAGTPTYMPVPEPAYPANA-QDSATLHRPQPLPPTSIHQNGAADTASMYGTASKPYQYP-FSDSYLSSGSTGLSVSSGMSTGL
VGGLGSMGSQQVEPFPVHCAPVSSSSSPATSIPSTDCYSS-TAADTYSYNTAQTYCTAPAHSYSSSAHAYSMD----GSW--VQ-GANSTDFN
SNSLGIAALRQKSREHSAALGLIQVAGGAMAQAY

>Pax3/7a__B._belcheri/1-481
MNMMTMRQAGGPVATFRPAFPLEGQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRPCVISRQLRVSHGCVSKILCRYQETGSIKPGAIGG
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KNG-PGDSSDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQIPSF---
MPLGYP--APAAGTPTYMPVPEPAYPTNA-PDSATLHRPQPLPPTSIHQSGAADTASMYGTASKPYQYP-FSDSYLSTASTGLSVSSGMSTGL
VNGLGSMSSQQVDPYPVHCAPASSSTSPATSLPSSDCYSSTTAADTYSYNTAQTYCTAPAHSFSSTAHAYSMD----GSW--VQGGTNSTDFN
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>Pax3/7a__A._lucayanum/1-478
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KNG-LGDSSDCDSEPDXXXXXXXXXSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQQGAQQMASF---
MPLGYP-GAPAAGTPTYMPVPEPAYPTTTCQDSATLHRPQPLPPTSIHQSGAADTASMYGTASKPYQYP-FSDTYLSASSAGLSVSNGMSSGL
MNGLGSVSAQQ-EAFPVHCVPAGSN-SPATSIPSTDCYSS-TAADTYTFNTAQTYCSTPAHSYSSTAHAYSMD----GSW--VQ-GTSSTDFN
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>Pax3/7b__B._lanceolatum/1-470
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KGGCRGEDSDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQLAGFNHL
LPMGYPAGATAHASAAYVPLADTSYPITSQVESTTLHRPQPLPPSTVHQSMAADSTSSYGTASKAYQFTGLSDSFVATAAN----HNTLSGGV
LNILGNPSTCQ-QDYPLASLSTSMDSTQATSSESFTAHAS--THDSYAAH-AQSYCTPP--SYSTTAHPYSMDTYQYGSQYPSQ-GSCTSSYG
STGTSLSSLRQKSLVH--PLGMIPVGSGT-GQAY

>Pax3/7b__B._floridae/1-468
------------MALF---
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DNPGMFSWEIRDRLLKDGMCDRSTVPSVSSISRILRGGKGDGRRSEDGDSEDERRDGEDGEKKRSHSIDGILGEKGGCRGEDSDCDSEPDLPL
KRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQLAGFNHLLPMGYPAGATAHASAAYVP
LADTSYPITSQVESTTLHRPQPLPPSTVHQSMAADSTSSYGTAGKAYQFTGLSDSFVATAAN----HNTLSGGVLNILGNPSTCQ-QDYPLAS
LSTSMDSTQATSSESFTAHAS--THDSYA---AQSYCTPP--SYSTTAHPYSMDTYQYGSQYPSQ-GSCTSSYGSTGTSLSSLRQKSLVH--
PLGMIPVGSGT-GQAY

>Pax3/7b__B._belcheri/1-470
------------MALF---FVLPGQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRPCVISRQLRVSHGCVSKILCRYQETGSIKPGAIGG
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KGGCRGEDSDCDSEPDLPLKRKQRRSRTTFTPEQLEELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQLAGFNHL
LPMGYPAGATAHASAAYVPLADTSYPITSQVESTTLHRPQPLPPSTVHQSMAADSTSSYGTAGKAYQFTGLSDSFVATAAN----HNTLSGGV
LNILGNPSTCQ-QDYPLASLSTSMDSTQATSSESFTAHAS--THDSYAAH-AQSYCTPP--SYSTTAHPYSMDSYQYGSQYPSQ-GSCTSSYG
STGTSLSSLRQKSLVH--PLGMIPVGSGT-GQAY

>Pax3/7b__A._lucayanum/1-469
------------MALF---FVLPGQGRVNQLGGVFINGRPLPNHIRHKIVEMAAAGIRPCVISRQLRVSHGCVSKXXXXXXXXXXXXXXXXGG
SKPRVATPEVEKKIEDYKRDNPGMFSWEIRDHLLKDGMCDRSTVPSVSSISRILRGGKGDGRRSDD-DSEDERKDGEDGEKKRSHSIDGILGE
KGGCRGEDSDCDSEPDLPLKRKQRRSRTTFTPEQLDELEKAFERTHYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQAGAQQLAGFNHL
LPMGYPAGATAHASAAYVPLADTSYPITSQVESTTLHRPQPLPPSTVHQSMAADSTSSYGTAGKAYQFTGLSDSFVATAAN----HNTLSGGV
LNILGNPSTCQ-QEYPLASLSTSMDSTQATSSESFTAHAS--SHDSYAAH-AQSYCTPP--SYSTTAHPYSMDSYQYGSQYPSQ-GXXXXXXX
XXXXXXXXXXXXXXXX--XXXXXXXXXXX-XXXX
```

Supplementary File 4: Python script to map equivalent support values between unadorned .nwk format trees

```
import re
from collections import OrderedDict
from math import log10, floor

try:
    import pyperclip
except ImportError:
    pyper = False
else:
    pyper = True

from comparatordata import *

""" FORMAT TREE FUNCS """

def makespecieslist(speciesstring):
    """ Makes comma-deliniated species string into species list """
    specieslist = speciesstring.split(",")
    specieslist2 = []
    for item in specieslist:
        specieslist2.append(item.replace(" ", ""))
    return specieslist2

def curatespecieslist(specieslist, replacedict):
    """ Removes colons, replaces digits with placeholders, adds inverted commas if missing
"""
    curatedspeciesdict = {}
    for item in specieslist:
        rplace = item.replace(":", "")
        for key in replacedict:
            rplace = rplace.replace(key, replacedict[key])
        rplace = "\'" + rplace + "\'"
        rplace = rplace.replace("\'\'", "\'")
        curatedspeciesdict[item] = rplace
    return curatedspeciesdict

def curatetreespecies(tree, curatedspeciesdict):
    """ Replaces the species names in a tree with the curated species names """
    edited = tree
    for find, replace in curatedspeciesdict.iteritems():
        edited = re.sub(find, replace, edited, 1)
    return edited

def curatetreelist(treelist, curatedspeciesdict):
    """ Replaces the species names in the trees in their list with the curated species names
"""
    curatedtreelist = []
    for tree in treelist:
        edited = curatetreespecies(tree, curatedspeciesdict)
        curatedtreelist.append(edited)
    return curatedtreelist

def curatetrees(specieslistSTR, replacedict, treelist):
    """ Marshals the above funcs into order. """
    specieslist = makespecieslist(specieslistSTR)
    curatedspeciesdict = curatespecieslist(specieslist, replacedict)
    curatedtreelist = curatetreelist(treelist, curatedspeciesdict)
    return curatedtreelist

def uncuratetrees(semifinaltree, replacedict):
    """ Marshals the above funcs to undo curatetrees() and replace the placeholders with
digits"""
    replacedict2 = dict((v, k) for k, v in replacedict.iteritems())
    specieslist = makespecieslist(specieslistSTR)
    curatedspeciesdict = curatespecieslist(specieslist, replacedict)
    uncuratedspeciesdict = dict((v, "\'{}\'".format(k)) for k, v in
curatedspeciesdict.iteritems())
    finaltree = curatetreespecies(semifinaltree, uncuratedspeciesdict)
    return finaltree

""" TOPOLOGY ANALYSIS FUNCS """
```

```
def parenthetic_contents(string):
    """ Generate parenthesized contents in string as pairs (level, contents)."""
    """ Borrowed and modified from Gareth Rees, stackoverflow.com/questions/4284991 """
    """ Takes tree string and returns list of the contents of each node, brackets & commas in
place """
    stack = []
    for i, c in enumerate(string):
        if c == '(':
            stack.append(i)
        elif c == ')' and stack:
            start = stack.pop()
            yield (string[start + 1: i])

def getlistofsupports(string):
    """ Takes tree string and returns list of support values in order - assuming\
    no numbers in seq names. Removes all :###s and then returns all other ###s """
    string2 = re.sub(r':\d+(?:\.\d+)?', '', string)
    return re.findall(r'\d+(?:\.\d+)?', string2)

def splittolists(list1):
    """Takes items in messy list from parenthetic_contents(), cuts out brackets, and\
     makes each item its own sublist of sequence names """
    list12 = []
    for item in list1:
        itemy = str(item)
        itemy2 = itemy.replace("(","").replace(")","")
        itemy3 = itemy2.split(",")
        itemy3.sort()
        list12.append(itemy3)
    return list12

def removeallnumbers(string):
    """ Removes all numbers and numbers preceded with a colon """
    string2 = re.sub(r':?\d+(?:\.\d+)?', '', string)
    return string2

def tuplifyalist(list1):
    """ Takes a list and returns a tuple - necessary to use as dict keys """
    return tuple(tuple(l) for l in list1)

def makeadict(tupley, listy):
    """ Takes a tuple of tuples and a list of lists and makes an ordered dict\
     where each tuple in the tuple is a key for the corresponding sublist """
    dictionary = OrderedDict()
    for n, item in enumerate(tupley):
        if n < len(listy):
            dictionary[item] = listy[n]
    return dictionary

def gofrominputtorightdict(string):
    """ Uses the above functs to go from input string to support value dictionary """
    string2 = removeallnumbers(string)
    listofsupports = getlistofsupports(string)
    list1 = list(parenthetic_contents(string2))
    list2 = splittolists(list1)
    tupleyboy = tuplifyalist(list2)
    dictyboy = makeadict(tupleyboy, listofsupports)
    return dictyboy

def maketreedicts(treelist):
    """ For each tree in the treelist, makes a support value dictionary above using above
funcs """
    dictlist = []
    for tree in treelist:
        treedict = gofrominputtorightdict(tree)
        dictlist.append(treedict)
    return dictlist

def formatsupportvalue(support):
    support2 = float(support)
    if support2 < 0:
        print support2, 'help'
    elif support2 > 0:
        if str(support2)[0:3] != "0.0":
            support2 = round(support2, n-int(floor(log10(float(support2))))-1)
        else:
            support2 = round(support2, n-int(floor(log10(float(support2))))-2)
```

```
    else:
        support2 = "0." + "0"*n
    support2 = str(support2)
    support2 = support2[1:] if support2[0] == "0" else support2
    if len(support) > n+2:
        support2 = support2.ljust(n+1, '0')
    return support2

def makelistofappendedsupports(treedictlist, delinchar, nocladechar, mastertree):
    """ Take list of dictionaries of clades:supports and makes a list of appended supports
"""
    listofappendedsupports = []
    for clade in treedictlist[mastertree]:
        working = []
        for treedict in treedictlist:
            support = treedict[clade] if clade in treedict else nocladechar
            if support != nocladechar:
                support = formatsupportvalue(support)
            working.append(support)
        listofappendedsupports.append(delinchar.join(working))
    return listofappendedsupports

def replacewithappendedsupports(appendedsupports, mastertree):
    """ Takes the master tree and replaces the support values (###:) with the appended
supports in quotations"""
    mastertreeeditlist = []
    edited = mastertree
    for item in appendedsupports:
        edited2 = re.sub(r'\d+(?:\.\d+)?:', '\"{}\"#:'.format(item), edited, 1)
        edited = edited2
        mastertreeeditlist.append(edited2)
    return mastertreeeditlist[-1].replace("#", "")

def formatoutput(finaltree, specieslisttstr):
    specieslist = makespecieslist(specieslisttstr)
    output = "#NEXUS\nbegin taxa;\n\tdimensions
ntax={0};\n\ttaxlabels".format(len(specieslist))
    for species in specieslist:
        output += "\n\t\'{0}\'".format(species)
    output += "\n;\nend;\n\nbegin trees;\n\ttree mastertree_with_all_supports =
{0}\nend;".format(finaltree)
    return output

def __treecomparator__():
    """ Puts all above function together into core program """
    curatedtreelist = curatetrees(specieslisttstr, replacedict, treelist)
    treedictlist = maketreedicts(curatedtreelist)
 #   print treedictlist
    appendedsupports = makelistofappendedsupports(treedictlist, delinchar, nocladechar,
mastertree)
    semifinaltree = replacewithappendedsupports(appendedsupports,
curatedtreelist[mastertree])
    finaltree = uncuratetrees(semifinaltree, replacedict)
    if pyper == True:
        outputty = formatoutput(finaltree, specieslisttstr)
        pyperclip.copy(outputty)
        print "Formatted tree copied to clipboard"
    else:
        print finaltree

if __name__ == "__main__":
    __treecomparator__()
```

Supplementary Note: Settings for the phylogenetic analyses

PHYLIP (changes from defaults)

seqboot:

`How many replicates?`	`1000`

protdist:

`Gamma distribution of rates among positions?`	`Yes`
`Analyze multiple data sets?`	`Yes, 1000 data sets`
`Coefficient of variation of substitution rate among positions`	`1.360827635 (= 1 / sqrt(0.54))`

neighbor:

`Outgroup root?`	`Yes, at species 1`
`Randomize input order of species?`	`Yes (random number seed =192837465)`
`Analyze multiple data sets?`	`Yes, 1000 sets`

consense:

`Trees to be treated as Rooted:`	`Yes`

MEGA-CC (complete contents of the .mao file)

```
    ; Please do not edit this file! If this file is modified, results are unpredictable.
    ; Instead of modifying this file, simply create a new MEGA Analysis Options file by using the MEGA Prototyper.
    [ MEGAinfo ]
    ver                                   = 7170509-x86_64 Mac OS
    [ DataSettings ]
    datatype                              = snProtein
    MissingBaseSymbol                     = ?
    IdenticalBaseSymbol                   = .
    GapSymbol                             = -
    [ ProcessTypes ]
    ppInfer                               = true
    ppML                                  = true
    [ AnalysisSettings ]
    Analysis                              = Phylogeny Reconstruction
    Statistical Method                    = Maximum Likelihood
    Phylogeny Test                        = ====================
    Test of Phylogeny                     = Bootstrap method
    No. of Bootstrap Replications         = 1000
    Substitution Model                    = ====================
    Substitutions Type                    = Amino acid
    Model/Method                          = JTT with Freqs. (+F) model
    Rates and Patterns                    = ====================
    Rates among Sites                     = Gamma Distributed (G)
    No of Discrete Gamma Categories       = 4
    Data Subset to Use                    = ====================
    Gaps/Missing Data Treatment           = Partial deletion
    Site Coverage Cutoff (%)              = 15
    Tree Inference Options                = ====================
    ML Heuristic Method                   = Nearest-Neighbor-Interchange (NNI)
    Initial Tree for ML                   = Make initial tree automatically (Default -
```

```
NJ/BioNJ)
    Branch Swap Filter                      = None
    System Resource Usage                   = ====================
    Number of Threads                       = 4
    Has Time Limit                          = False
    Maximum Execution Time                  = -1
```

MrBayes (changes from defaults made in CIPRES interface)

Maximum Hours to Run:	168
My Data Type is:	protein
Specify (only) one outgroup:	6_Bf
Set the model for among-site rate variation (Rates=)	gamma
Set number of rate categories for gamma distribution (Ngammacat=)	4
Set the Rate Matrix for Amino Acids (Aamodelpr=)	Jones
State Frequencies (Statefreqpr=)	fixed (empirical)
Number of Generations (Ngen=)	500000000
Stop early if the convergence diagnostic falls below the stop value?	Yes
Please enter the stop value	0.01

The following parameters entered into the command line version should produce an equivalent analysis (untested)

```
prset aamodelpr=fixed(jones) statefreqpr=fixed(empirical)
outgroup 6_Bf
lset rates=gamma ngammacat=4
mcmc ngen=500000000 stoprule=YES stopval=0.01 samplefreq=100 printfreq=100 diagnfreq=1000
```