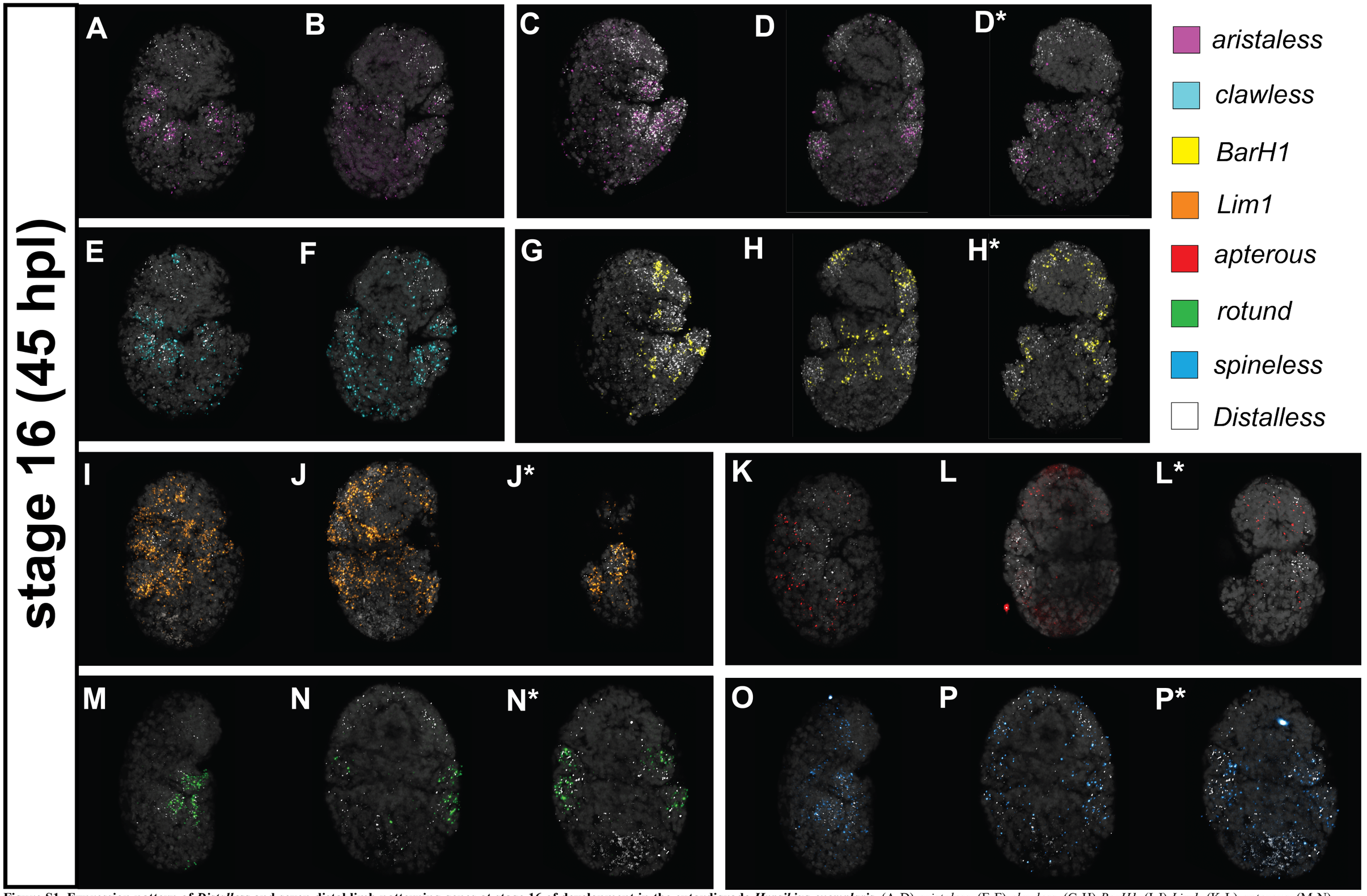


Figure S1. Expression pattern of *Distalless* and seven distal limb patterning genes at stage 16 of development in the eutardigrade *Hypsibius exemplaris*. (A-D) *aristaless*. (E-F) *clawless*. (G-H) *BarH1*. (I-J) *Lim1*. (K-L) *apterous*. (M-N) *rotund*. (O-P) *spineless*. Figures with the same letter indicates the same embryo viewed in similar optical sections; with asterisk (*) indicate the same embryo but viewed at different optical sections.

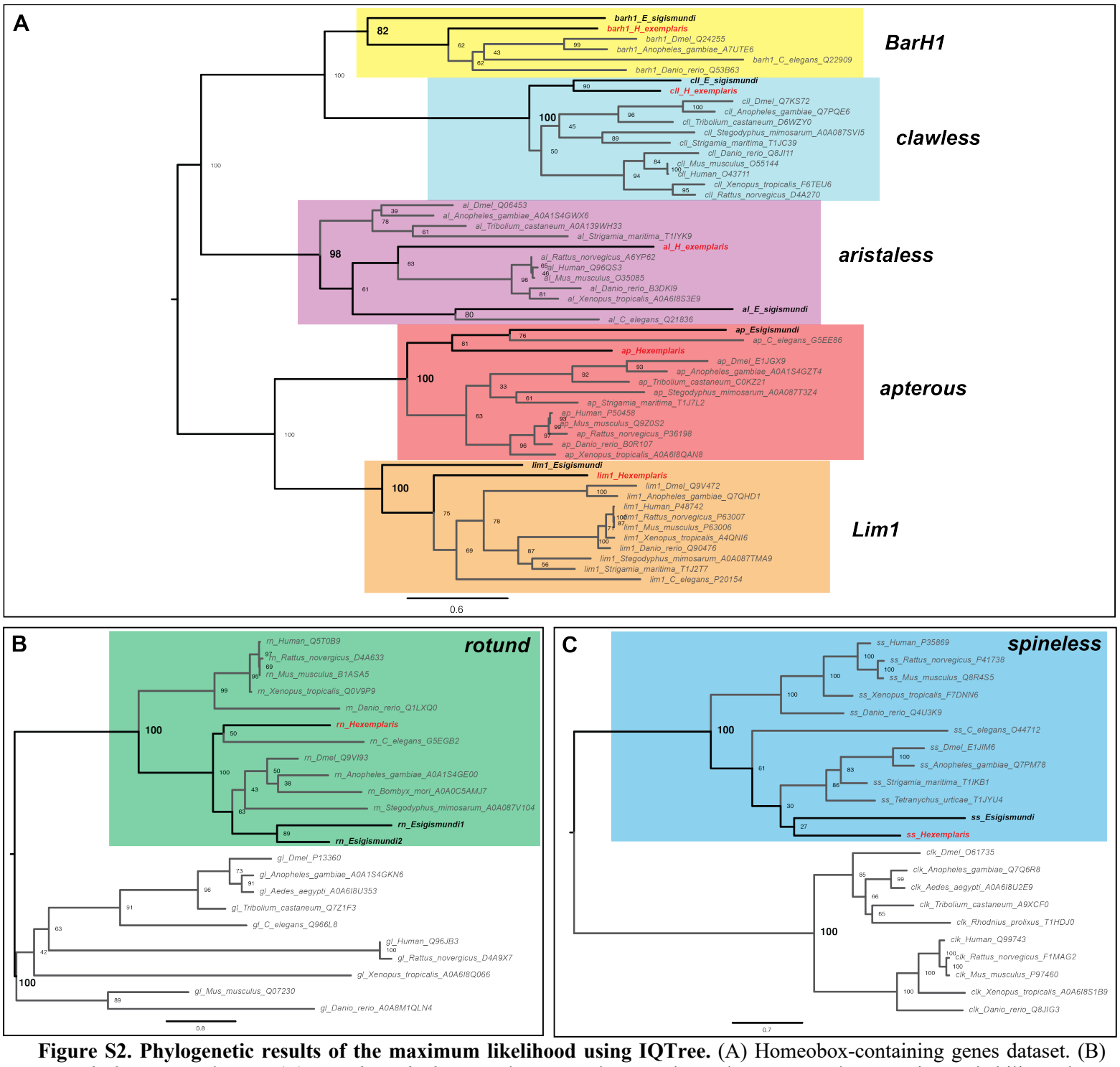


Figure S2. Phylogenetic results of the maximum likelihood using IQTree. (A) Homeobox-containing genes dataset. (B) *rotund-glass* genes dataset. (C) *spineless-clock* genes dataset. Values on the node represent the posterior probability values. Tardigrade taxa are highlighted in bold

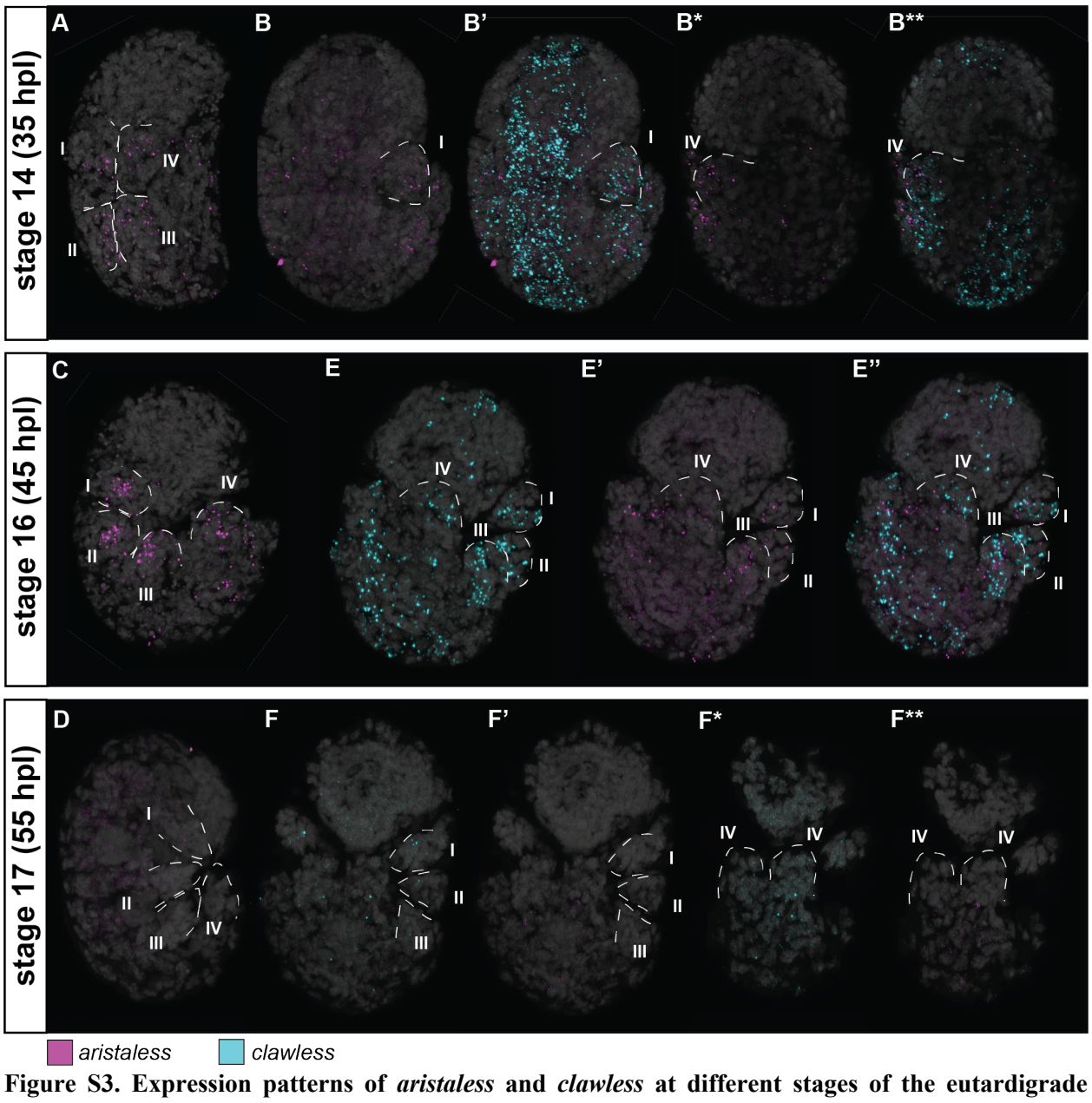


Figure S3. Expression patterns of *aristaless* and *clawless* at different stages of the eutardigrade *Hypsibius exemplaris* limb development. (A-B) Stage 14. (C,E) Stage 16. (D,F) Stage 17. (A,B,B*,C,D,E',F',F**) *al* expression. (E,F,F*) *cll* expression. (B',B**,E") *al* and *cll* expression. Figures with the same letter indicates the same embryo viewed in similar optical sections; with asterisk (*) indicate the same embryo but viewed at different optical sections. Figures with the same letters in the main figures represent the same embryos. Embryos are in dorsoventral mount in all panels, except for A,C, and D, which are in lateral view and facing right. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). Nuclei are labeled with DAPI (Gray).

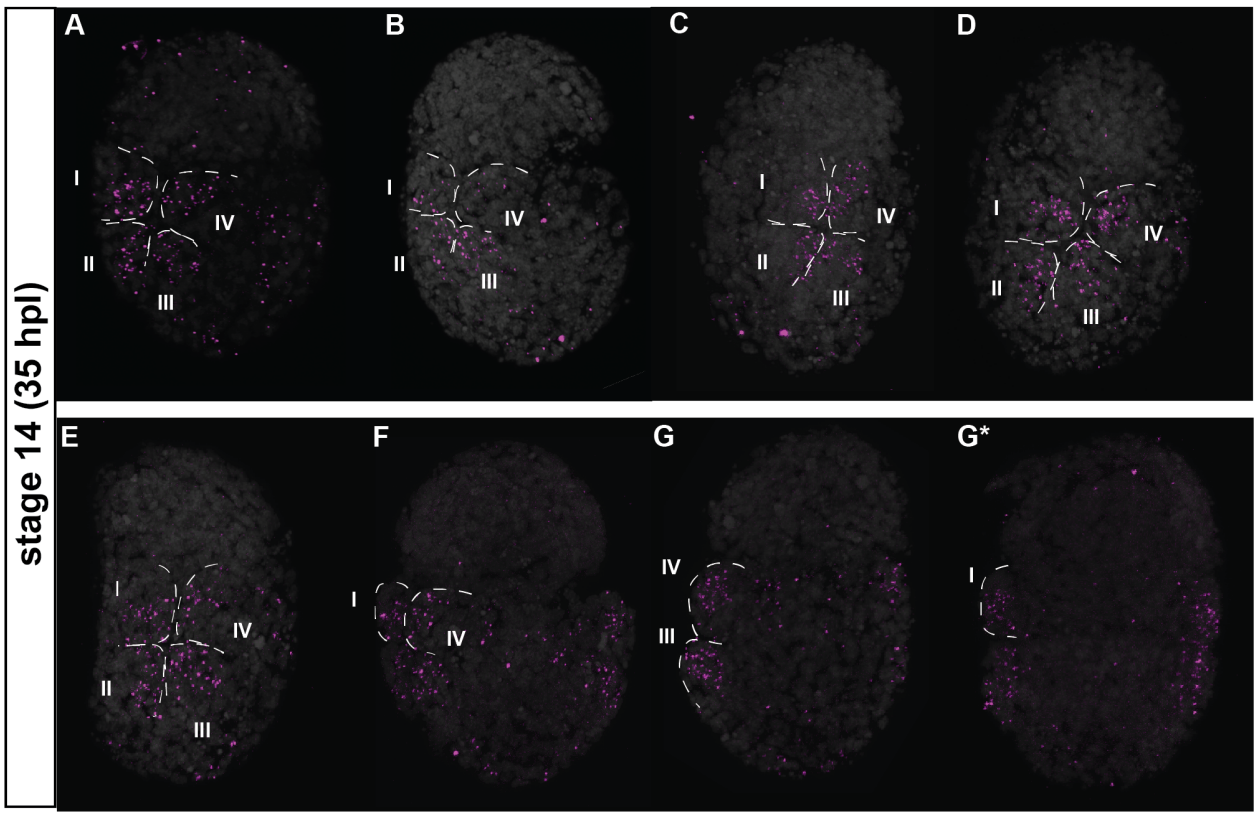


Figure S4. Expression patterns of *aristaless* at stage 14 of the eutardigrade *Hypsibius exemplaris* limb development. Embryos A-B viewed similar to all embryos in the paper. Embryos C-G were viewed with Olympus FV1000 Fluoview confocal microscope using 405 nm and 543 nm lasers to visualize DAPI and *aristaless*, respectively. Figures with the same letter and asterisk (*) indicate the same embryo but viewed at different optical sections. Embryos are in lateral view and facing right in all panels, except for G and G*, which are in dorsoventral mount. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). Nuclei are labeled with DAPI (Gray).

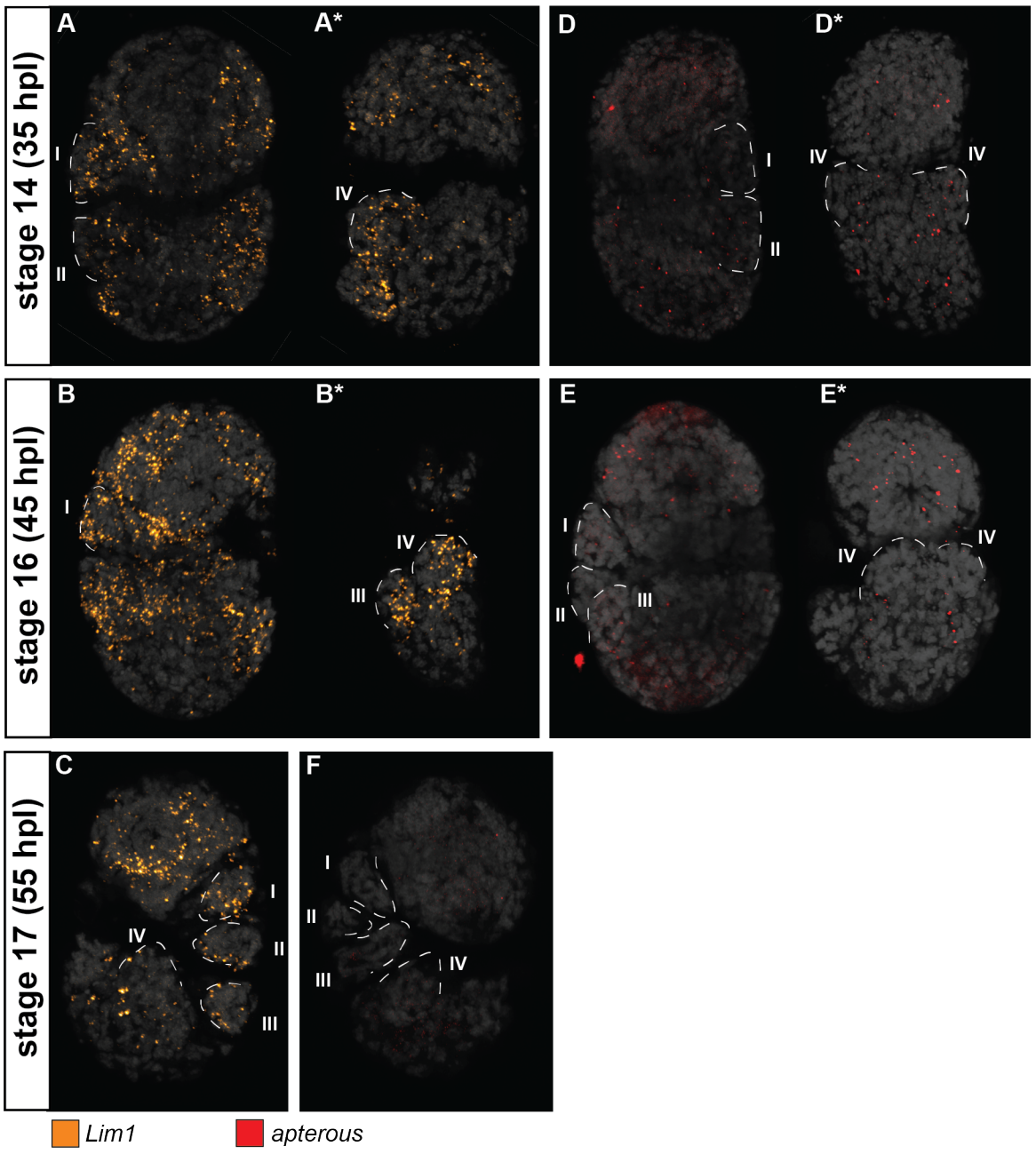


Figure S5. Expression patterns of *apterous* and *Lim1* at different stages of the eutardigrade *Hypsibius exemplaris* limb development. (A,D) Stage 14. (B,E) Stage 16. (C,F) Stage 17. (A-C) *Lim1* expression. (D-F) *ap* expression. Figures with the same letter indicates the same embryo viewed in similar optical sections; with asterisk (*) indicate the same embryo but viewed at different optical sections. Embryos are in dorsoventral mount in all panels, except for F, which is in a dorsolateral view. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). Nuclei are labeled with DAPI (Gray).

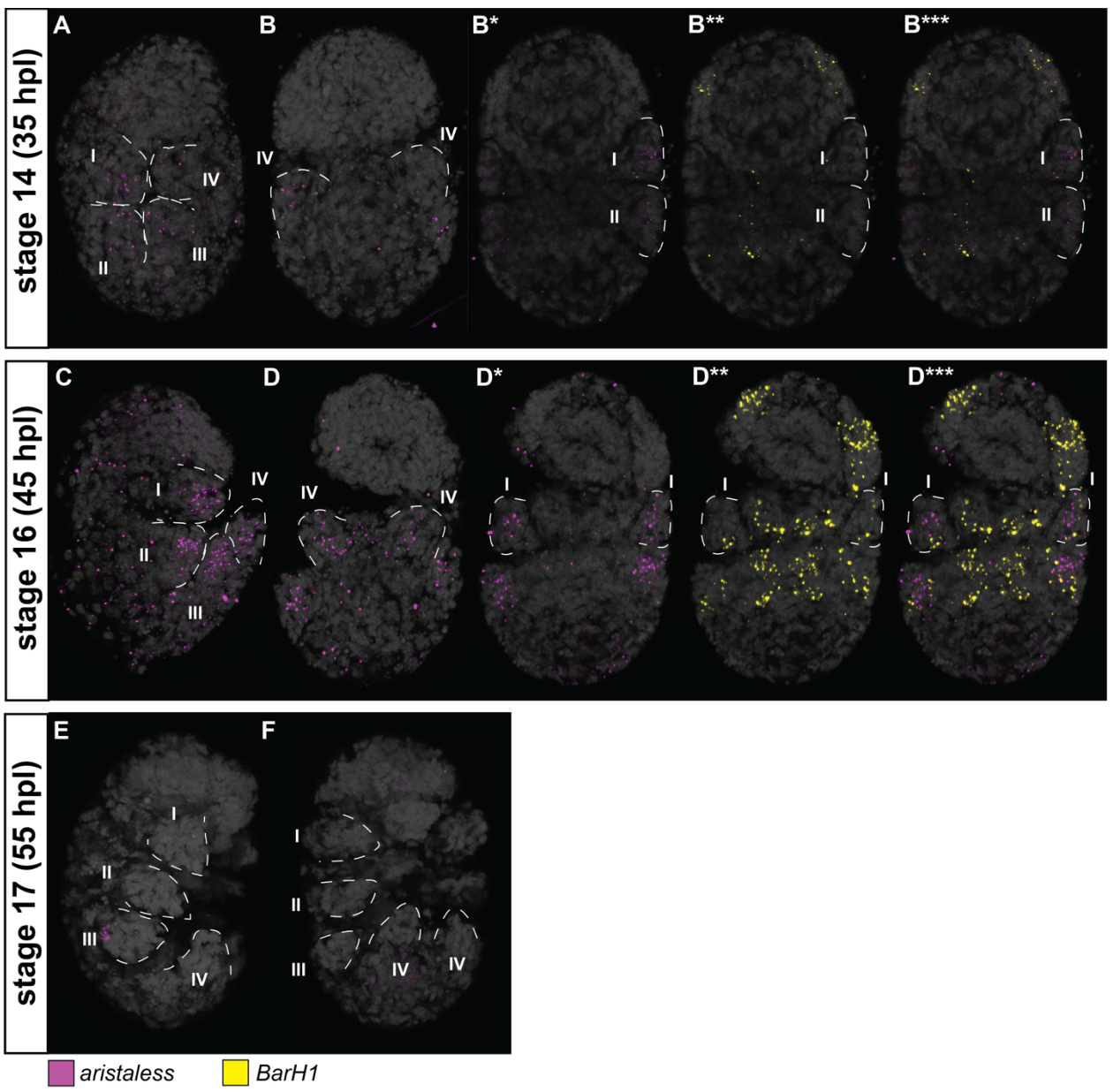


Figure S6. Expression patterns of *aristaless* and *BarH1* at different stages of the eutardigrade *Hypsibius exemplaris* limb development. (A-B) Stage 14. (C-D) Stage 16. (E-F) Stage 17. (A,B,B*,C,D,D*,E,F) *al* expression. (B**,D**) *BarH1* expression. (B***,D***) *al* and *BarH1* expression. Figures with the same letter indicates the same embryo viewed in similar optical sections; with asterisk (*) indicate the same embryo but viewed at different optical sections. Figures with the same letters in the main figures represent the same embryos. Embryos are in dorsoventral mount in all panels, except for A,C, and E, which are in lateral view and facing right. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). Nuclei are labeled with DAPI (Gray).

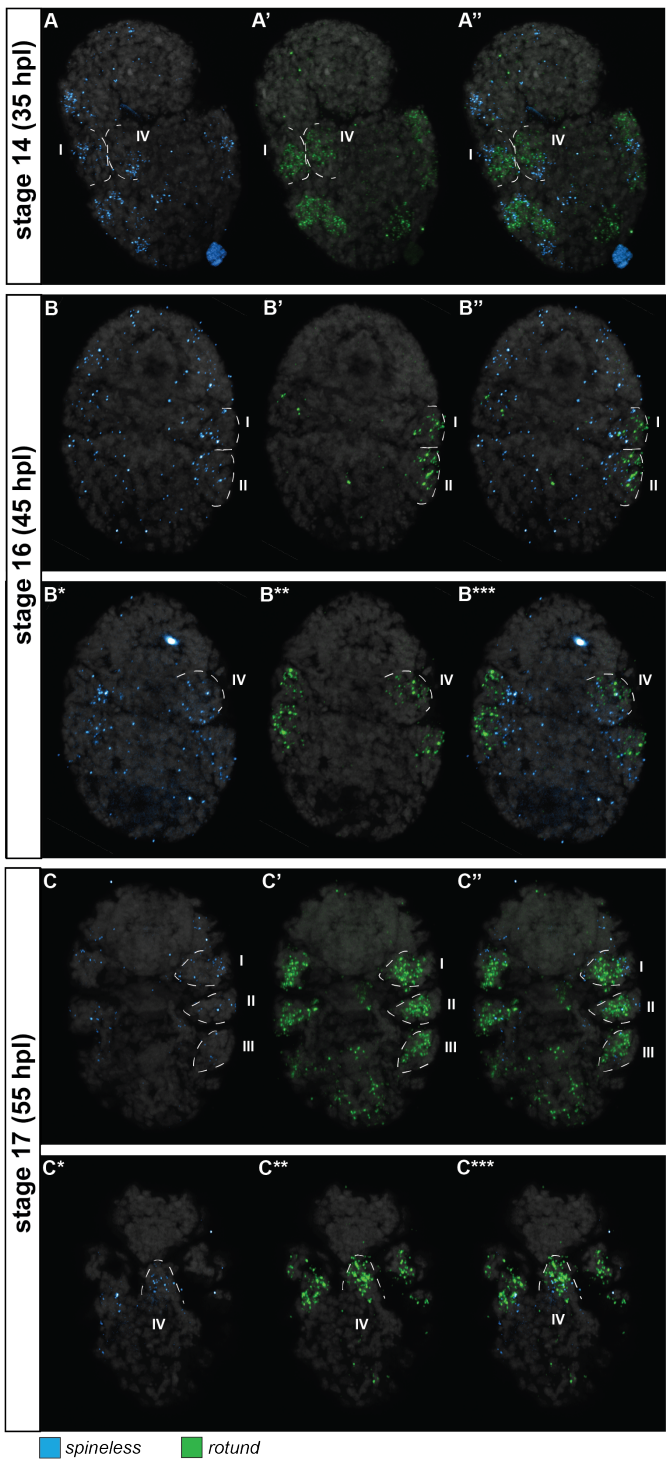


Figure S7. Expression patterns of *rotund* and *spineless* at different stages of the eutardigrade *Hypsibius exemplaris* limb development. (A) Stage 14. (B) Stage 16. (C) Stage 17. (A,B,B*,C,C*) *ss* expression. (A',B',B**,C',C**) *rn* expression. (A",B",B***,C",C***) *ss* and *rn* expression. Figures with the same letter indicates the same embryo viewed in similar optical sections; with asterisk (*) indicate the same embryo but viewed at different optical sections. Embryos are in dorsoventral mount in all panels. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). Nuclei are labeled with DAPI (Gray).

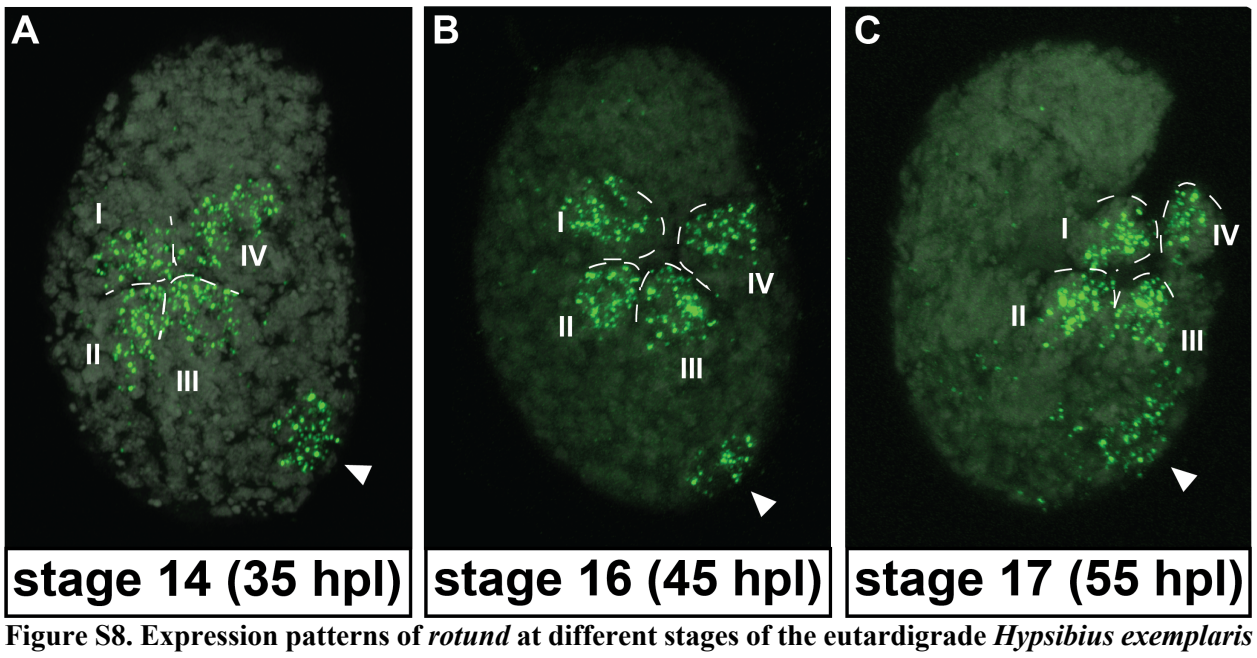


Figure S8. Expression patterns of *rotund* at different stages of the eutardigrade *Hypsibius exemplaris* limb development. (A) Stage 14. (B) Stage 16. (C) Stage 17. Embryos are in lateral view and facing right in all panels. Roman numeral number indicates leg number (e.g., I – 1st pair of legs). White arrowhead denotes the expression dorsal to the third leg. Nuclei are labeled with DAPI (Gray).

Figure S9. Expression patterns distal limb patterning genes in the first pair of walking legs of different panarthropods. Colored diagrams represent RNA expression, unless stated; Brown box represent the body wall; question mark (?) denotes unknown data. Stages when the illustrated expression patterns appeared are indicated. Hexapod and Chelicerata podomere abbreviations: cx – coxa, gn – gnathendite, tr – trochanter, fe – femur, pa – patella, ti – tibia, mt – metatarsus, ta – tarsus, pt – pretarsus, cc – claw cells. Malacostraca podomere abbreviations: cx – coxa, ba -basis, is – ischium, mr – merus, cp – carpus, pr – propodus, da – dactyl. Expression references: *H. exemplaris* (this study); *E. kanangrensis* (Oliveira et al 2014, Janssen 2017); *E. rowelli* (Treffkorn & Mayer 2019); *P. tepidariorum, P. opilio, L. atkinsoni, P. hawaiensis, O. fasciatus* (Setton et al 2017); *G. marginata* (Janssen 2017); *G. bimaculatus* (Miyawaki et al 2002); *T. castaneum* (Beermann & Schröder 2004, Toegel et al 2009, Beermann et al 2011, Grossman & Prpic 2012); *D. melanogaster* (Campbell et al 1993, Duncan et al 1998, Kojima et al 2000, Pueyo et al 2000, Kojima et al 2005, Natori et al 2012).

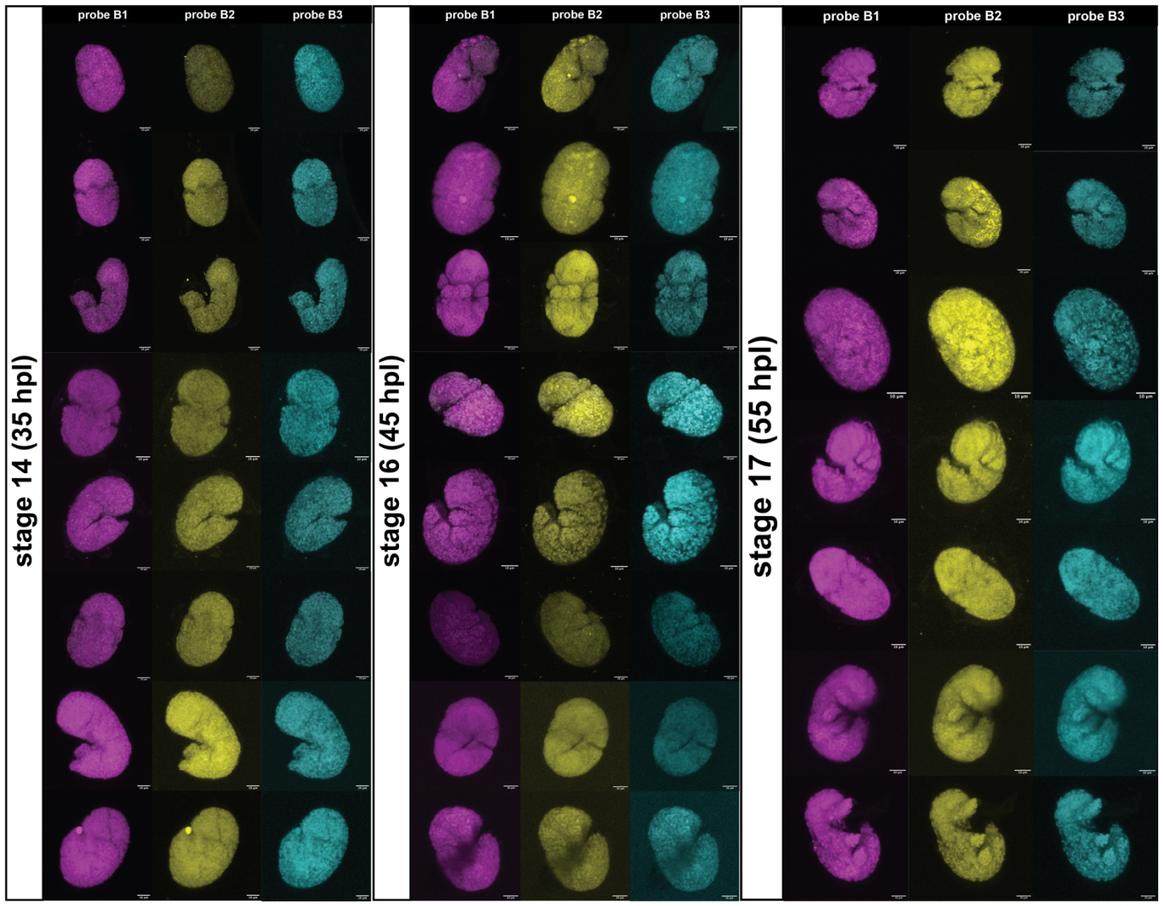


Figure S10. Negative controls for the different probes used in the *in situ* hybridization experiment in the eutardigrade *Hypsibius exemplaris*.
Gain and detector settings were increased until just below saturation. No patterns were detected. Nuclei are labeled with DAPI (Gray

Table S1. Amino acid sequences of *Drosophila melanogaster* distal limb patterning genes used for building profile HMMs

Protein	Flybase ID
aristaless-PA	FBpp0077713
clawless-PA	FBpp0083510
Lim1-PA	FBpp0071216
apterous-PA	FBpp0085394
BarH1-PA	FBpp0074204
rotund-PG	FBpp0303173
spineless-PC	FBpp0297168

Table S2. Coding sequences of *Hypsibius exemplaris* distal limb patterning gene homologs

Gene	Coding Sequence
aristaless	ATGGTCGGTCACGACGAGCGTCCTAAAAAGGAGAACGACTGTGTCGTGCCTGAACGAATATCCCCGAGCA TCGCTTCAGCCGGGAGTTTGGATGATAAAGAGTCCTTCGTCGATGACGACTCGGAGGACTCTGCGTCGTTC GGCGCCGGAGGCGGAGCAGGAGCCCGGAGTGGCGCCGGGTTGAGCAGCAAACAGCGCCGTTACCGAACT ACCTTCACGGCTTTCCAGCTGCAGGAGCTGGAAAAGTGCTTCGGGAAGACGCATTATCCAGACATTTTTAC CAGAGACGAGCTAGCGATGCGAATCCACCTGACCGAGGCGCGCATCCAAGTCTGGTTCCAGAATCGTCGT GCGAAATGGCGCAAGACCGAAAAGTCCTCCGCACCACATCCGATTTCGGGTGTCGAGCCCAGCCCAGCAG TCCAGTCCTTCAACACCACCCATCCCATCCCCAACAGCAACTGTTCCTTCTCCAAAGGTCACACCGACCCCT TCCTGCAGTCACCGCACGGTCCGTCATCCGCAGACTACAACGTCCGGATGAACCCCGGATGGCCGCTCATC CCGCCGTCCAATAAATACAGTCGCAGCAGTTTGACGCAGAATTTCTACCCGGAACAAGCAGCAGCAGCCG CAGCAGCAGCAGCCATGGCCGCCACTACCAACATGTGGAACCAACGCTGGCTCCAACAAATGGCCGTCAA TTCGCTCCTCCATCGGGATGTTCCGCCGTCCTGGACGACACAGACATCGGCCGGATCGGCCGTCTCGCCGG CGCATCATTTGACCTTCCATCCGGAGTTCCGACCGTTCTTCCATCCTCATCCCAATGGGACAACGACTGCTG GTCAGTTGACCGGTCCCAGCGCGACTGCTGCTCAGTGGACCGGTCCCGGCGTGACTGCTGACGCGATGCAG AAATACGGAGCGTTTCGATCGATCGCCAGGAATGACGGAGGTGGAGGTGGGCGCTGA
clawless	ATGATGGAGAACCCTCCGGCACGCAGTGTCTTCAAGGCACCCTCCTCCAGGTCGCCTGTTGCGGAGAAACC TCTGAAAAAGCGTACTCCCTTCAGTATCGACAGTATTCTCAGCACAGATACGGACACTTCGCCGAAGGAAG AGTGCTTCTCGCCGAGTTTATCCGAGACAAAATGCAGTAACAACGAGAATATCCACACGGCGATGGATGCT TATGCGGCGGCGGCGGCGGCTGCAACGACGGCCATGTATTCCTCATCGGGCTATTACTCGTCCCCCGCCGA CGCCTATAATTACGGATCGATGGTCAATTCACACGTCGTCAAGGTGCCGGCGCAGCGAGTCCAGCAGCAGC AGCAGCAGCAACACTTGGCGCCATGCGGTGGCGTCAGTCCTCATCCAGCCCTTTTCGGGATCGGACATCAC GTCGGCATGTCTGCCTACCAGTGGATGGACCCCGCCCGACGACTTTTGACAAGGAGAATTGGGCATCCCTA CCAGAATAGAACCCCTCCCAAACGGAAGAAGCCTCGCACTTCCTTCACACGGATTCAGATTTGCGAATTAG AGAAACGCTTTCACAGACAAAAATATCTAGCGTCGGCGGAGCGAGCCTCGCTGGCCAAGTCCTTGAAGAT GACGGATGCTCAGGTCAAAACTTGGTTTCAAAACCGACGGACAAAACACAGGCGGCAAACCAACGAAGA GCGGGAAGCGGACCGACAGGCCGCCAATCGGATGCTTTTGTCACAGCTGGCCGAAGTGACCAAGACCAGC GGAGCGTATGACAGCACCGACGCGTTATGCCTTAATAATGCTTCCCTTCACGCTCTTCACAATCTCCGACCG TGGGTCAATGCCGGCGACGGCGGTGGTTCCCTCTCCAACAATAATCATCATCCCCACATTATTACCTGTCCT CAGACAAACAGCTCTTCACCCAACAACAATAACACCAACAACAACTGCAGTAGCCGATGTAGCAGCAGCA GCGAAACAAGTCACGAGGAAGAGGACCGTGATGATGATGACAACCGGTCAGAGGTCTCATCAGATGAGG ATGCACTATCCGTCTAA
Lim1	ATGCCTGTCCGCCACCGTTATCTTCAGCAACATCCGCAGCCGCCGCCGCCACCATCATCCTCGTCCGGGCC GATAAGTGTCACGGCTGTGGAATGGTGATTTTGGATCCTTTTATCATGGCCATCGCCACTCCGACGGCCAG TCAGGTTTGGCATGCCGATTGTTTGCGCTGTTGTGAGTGCAAGTGCCCACTTCAGGAGCGGTGTTTCTGCAA TGGAGGACGCTTTTTTTGCCGCGAAGACTATTTCAGAGCTTTCGGTCAGCCGTGTAAGGGCTGCGGCGTCG GGATCGATCCGACGGAACTGGTGCGGCAGACGCAGCGCGGGAATTTTCATTTGAAATGTTTTATCTGCACG GCATGTCGGAAACAGCTGTCCACCGGGGAAGAATGCTACAACATCGGGGACTGCGAGTTCAACTGCAAGG ACGATTATGTCACCAGCAAACACGCCAAAGCCGCCTCCTCCACACTGCAATCATTTTCCTGCAAAGCAGAG CAATCGTCGCCGGGAGCTGCTACCTCACCCTGTCTGCTCGGCGGAGGCGGTCGCGACCTGTCCAGAAGCGA GTCTCTCAAACCTGACCAACACGATTGTTTATCAACAACGGGTCCTTCAGACGTGACGAACGGTGCGCCGA TGAATAACAACAACAGTAATACCGCAACCCCAATTATCGGCAGCGGGATCGGCCGGGCAATGGACGGTCA CCTTCTCCATCGCGGAGAGGATTGCGAGGACGACGACGAGGAAGACGAGGATGCCATGAAGTGCAGCGAG AGCGGTTCGCACGTGCCGGCCTCGGATCGGGATTGTTGTGACAAGGACGGGAAGAGCGTCAACGGCGACA ACACCAGCAGCATCGACGAGAGCGAACCGCGCAACGGCAACGACGAGAATGTCAGCACCAAACGCCGCG GCCCACGCACCACTATCAAAGCAAAACAACTCGAATTACTCAAAAACGCCTTCGCACAGACGCCCAAACC CACGCGCCATATCCGCGACCAGTTGTCGCAGGAAACCGGTCTCACTATGCGAGTCATTCAGGTTTGGTTTC AAAATCGCCGAAGCAAAGAACGCCGGATGAAACAGCAGAACATCATGGGGCCAGGTCGGCGATGCAATA TGTTTCGATCGCGTCGCTCGGGAGGACGATCGCTGCGGGAGTTCGACGGTGATTCCGGTGATATGGGAGTT CAGGGTCCACCCGGATTCGCTTATTTTCCAGATGGTCCCGGCAATCACGGCATGGACTTCTTTCCCGGACA GGTTTCTCCCCACGGCGGCCCACATGCCGGGCCACTCGGACATCCTCCGGGTATTTTTGAATTCGCCCACTA TCGACCGCCGCAGAACGCGGCGGAAGCAGCCGCCATGCAGGCGCATTTCAACGAAATGTCCCCCAACGCT CACGGCATGCCCGGAAACATCAATCACCCCGGCATGGATGGCCACTTTCGGCAGGAGATGCTGTCACAGA GTTCAACTCCAGAACGGACGCTAAACTCCTTGACACCGGACGGCTACGGGCATCCTGCTTTTGACACTTTA CCCCTCCATCCCGGCGGCAACGGCGGTATCGGGCCGGTTCCTGGCGGGATGAACGGCAGCAACTCACCCGT CTGGCAGAGCATGACGATGGCCCAATAG
apterous	ATGCCGATTCTGGAGCGGTCTAACAGCGGTCATAATGAGCAGGAGGAAGCCATCAATTCCCATGTTACCGC ACACGGGGAAGAGCCATCGTGTCTGCAGCTTGACCACGACCACGACCACGGACTATTACCCGGAAACGAG GACGTGGCCCATCCCCAACACCATGTCCAACACCCTGCTGCGGGATACTTCCCCGCGCTAATCTGCTCCGG CTGTCGGAATGGGATATCGGAGCAGTACTTCTTATCTGTTTCCAATTCGCAAGACTTTTATCACTGCCACTG TCTAAAGTGCAGTGTTTGTAGTGTAACTCTAGACCGACAAATGATCTGCTATTACAAGGACGGGATGATTC TTTGTAAAGAGGACTATTACAAGTACAAGAGTCGAAGGCTGAGCCCCGAAGGTTATCAAAATAGCCGCTG CCACGGCTGCAACTACCCGATCCGAGCGGACGAGTTTGTGATGCGCGTACGGGAGTTTGTCTTCCACGTCC CGTGTTTCCGCTGCCTGGCCTGCACCGCGACACTCCACACGGGGGATGAGTTTACGATGCGTGACGACGGC GCCATCCTCTGTCAACGTCATTTCCATCCCGCTGCAGCCGTCGCTCACGTCGGCGGCGGCGGCGGCGGCGG TGTCGGATCCTCGTCAAACCCCGCAAGTGACACTCTATCCTCGACAGCAGCACTACTGCCCCCACACAGCA GCCATGACTCCTTCTCGGCCGCCTCCTCCGACATCCCCACCACCACCGCCACCGCCGCATCCCTCCGTCTGC

	CCATCCTCATGGCCGATCATGGCGCCCCGGTCTCGCCGCACTTTGCCCAACTTCAGAACCGCATCGTCCCGC GACATGACGACGGTGGTGACGGGAACGACGGTCGGAAAGACCTTTTCCACCATCACCACCACCAGACATC AGCATCATCCTCCGCGTCGTCGCGTATGAAAAGCCGGATTCGACGGACCAAGCGAAACTTGATTTCCTTCG ACGACGGGAGTGGCGGTGTAATTAACCAGCGCCACACTGCGGGTGGGTTGAATGGAAGCGGTGGGGAGTT ACACGGTGATCCGGTGGGGCAGGCGGAGCTGTTGCAGCAGCGGCAAGCAGCAGCCGCGATGCAACTGGAG CAGCAGTGTTACCACCACTTCTCCAGTGCCGCCTCGCCGAACGCGGCTCTTCCGGTGCAAACTGCGCAGCA GTCGTCTTTTACATCTAGCTCAGAGGAATCGTCCCCGTCCCGATTAGCCAGTTCCAGTCCCGGCTTGCAGAT GGCGCACCTCACGCACTCCATCACGGACTCATCCTCACCGAACAACCAACAACACCAGCGCACCAAGCGC ATGAGAACCAGCTTCAAGCACCAACAACTTCGCTCCATGAAACAGTACTTCGGTATCAATCACAATCCTGA CGCAAAGGACCTCAAGCAGCTTGCACAGAAGACGGGCCTGACGAAGAGAGTCCTTCAGGTATGGTTCCAG AATGCCCGTGCAAAATATCGCCGTAGTCTCCTCAAGCAGGACCCCAATCGGGTGCTGGAAGCTAGCCCGAT CGCCAAAGCCCAGTCCAACTCCCCATCACCACGACCGGATTACGGTTTGCCGGACAATGCTTCAGCAAAGC AACACGACCTTAATCATTACCCAATGTCGAACGGAAGCAATTCTCAAGACAATGGCGCTGAGTACTACTAA
BarH1	ATGGATAGGGATAACGGGGAGAGGAGCAGTAGCAAGTCGCCGTTGGATATGACTGCGCATCCTGCGCATC CGCAGCCGTTGACCAGTCCCAGTATCACCAGCCATGTAAAGGTCACGTCGAGTAACTGCGCACCGCAGAA CCTGTCCATGCGACACTCCTTCCTCATCAAGGACATCCTCAGTCAGGTCAATCCGAGGCAGCAGGAGAGCA GTCGCAGTGGAGCAGGAGACGGAATGGGTGCTGGCACATTTCCGCCCGGGAGTCAGGAGGATGGAGACAG CGACGTCCAGAGTGAACTTTCCGATACAGAAAGCAAAGATGACCACGACGGGGCGGATTCAACCGCGACC AGCCGCAATAGTCCGAAAGGCAAGAAATCCCGGAAAGCCAGGACAGCGTTTACGGACAGCCAGTTACAGA CGCTGGAGAAACGCTTCGAGCGACAGAAATATCTCAGCGTACAGGACCGGATGGAATTAGCGGCCAGTTT GAGCCTGTCCGACGCGCAAGTTAAATGCTGGTTCCAAAATCGCCGAACCAAATGGAAGCGTCAGACGTCG GTGACGATCGAGTTGCTGGCCGAAGCGACGGGCAATTACGCGGCCATGCAGCGGATGCTGCAGTACTGGT CGTGCGGCGGTCCGGCAGCCATGCTGGCCGCACCAGCCGCGGCCTATCCCGCGCAGAACCAGCTCTTTCAG ATGCAGGAGCTGTACTACCGAAGTCTCCAGCAGCAGCAGCAGCAGCAGCAGGTTGGTGGACGAGTGG TCGGCGGACCAGGCGGCATACCGCAGATGCCGATGAATCCGGTGACGACGCGATTCTGGCCGACTCCGGC CAACATGACCTTCCCCACGGGCAATTCCGCGCCCAATGTTCATCTCATCGCATCATCAACAGCGGTCGCCA CTCCCGCTGCTCCGGCTAGTCCGCCGTCACGGTCCACCGGGATTAAAACGGCAGCTCAATCAGACGATGGC ACCGATTAA
rotund	ATGGCTGGAGCCCATGAGACCGCGGATGAGCTGAATCTAATGCAGCAGCAGCACCCGCAACGATTCACTC CCTGGAACCAAAACGCCATGGACTTCCAGAAGATTTTGAACCAGCAAGCGGCGGCCAACAGCCTCAATGG TCATGCCCATTCTCTCCAAGGCAAAGGGCCCAACTTCGACATGGTCTCAATGGAGATGGACGAGACGGGA GGAGGAGGAGTAGGAGCCGTGAGTGACCTTTATGGAGTACAACAGGCAACAAGAGCCATACAATCGGTGA TGGTAACTCCTCATCATCATCACTCGAGCATCATGTCTGGCTTCATGCACCAACATCATGCTGGTGGACATA ACTTGCCAAAAACCCTCAGCGGACGCAAATTCCCATGCAAAATGTGCAATCAGGTGTTGGAGTCAAAGGC CGAGTTCCAGATGCACAATCAGTCGCACATGCGCGAACCCAAGCCCTACCGATGCTCGCAGTGTCCCAAAT CCTTTGCCAATTCCTCCTATCTCTCCCAGCATATGCGCATTCATCTCGGCATTAAGCCCTACCACTGTGACA TCTGCAAGAAAAAGTTCACCCAACTCTCCCATCTGCAGCAGCACATCCGCACCCATACAGGTGATAAGCCG TACCGTTGCCCTCAACCGACTTGCACAAAGGCCTTCTCCCAGTTGAGCAACCTGCAGAGTCATTCTCGGTGT CATCAACAGGACAAGCCCTTCAAATGCCAATCCTGTTACAAGTGTTTTTACGACGAACAATCTCTGCTGGA TCACATTCCCAAGCATAAGGACAGCAAGCATCTCAAGACTCACATCTGTACCTGCTGCGGCAAGTCCTACA CCCAGGAGACTTACCTACTGCGACACATGGCCAAGCACAACGACAAAAACGAAAAGCAGCAGCGGATGTC TCTCAACCATATTAAAACTGCCACAGTGGACCCGTATTGGCCTAAGCAAGAAATGGAAGGTGCCCACCGTA TGAGCCAGGAGGATCTGTTCATGTACAGCGGTGGCTATTACAGCGCCGCCAACTACGGTAACGCCCACCAC GCTGTTCATCCTTACGGCGCGGGGCAGACATCTCCCGTTAACTATGACACCAGTAATAAGAACTCGGGATC AGCCTTCTCCATTCTTTCGGGAAGCAGCGGTCGGAACGTGATGGCTCATCCTCATGCGCATAACTACTACG ACTCGGCATTTGGATCTGGAGCGATGAAGAGTCAGAATGTCCTTTCTGACTCGATGGCCACTTCCAAGAAC GGTCCAATTTCGGTGGATCACTTTGCCGGTTTCACCAATCATCAGATGCCCGCTATGCGTAATCACTTTTCC GCAGGATTCGTCGGCAATAATGGAATGCCGACCATGCTGATGGGAGGAGGAGGAGACGGCAGTACCGCTT CCGGTATGCGCAAGGAGCACAGCAACCATAACAGCAGCAGCAAGCCGGGAGGACGCTACTGA
spineless	ATGTATGCCACCAAACGACGCCGCCGTTCCCTGAAAGGAAGCAGCAGCAAAATTTGCCTATCTAAAAGTG CGTACGACACCAGCCACCACGGGAACAGCGGCGGCGGTTGCGGTGGCGGAAACTCTTCTTCCCTCAAAAG CAACCCTAGCAAGCGTCACCGTGAACGGTTGAATTCCGAACTAGAACGGATCGCCAGTTTGCTTCCATTTG AAGCGAATATCCTTTCCAAACTGGACAAGCTCTCCATACTGCGTCTTAGCGTTAGTTACCTCCGAATCAAA AGTTATTTTCATGCCATTCAATTACGAGAGCAGACATACGGCGGATACGACGGTCCCGGTGGACATAAAAC GAGTGCCGATCATTTCCACGCCGATCCATCACTGACACGCACCGATTCAGTTCTCAAGGCATTGAATGGAT TTGTCCTGGTGTTGACCGTTCAAGGCGAAGTCTTTTTTGCTTCAAGCAACATCGAGGAGTTTTTAGGCTTCC ATCAGTCGGATGTTATTCATCAGAGCGTTTACGAGCTGATTCACTCAGAGGACCGGGTCGAGCTGCAGAAG CAGCTCTCTTGGCTGGGGAGCCCTTCCGCCGCTGCGGCGCATCATCCCGGCTCGAGGATGAATCCGCACGA CGCCTTTTCGTCGGACAATTTTCAACATTTGGAGCGCAGTCTGACGGCCCGGTTTCGTTGCCTGCTTGATAA CACTTCCGGTTTTCTGCGACTGGAAATTCGCGGCCGCATCGGAGTTCTTCACGGGCAGAACTTCCACTCGG CCGGCGAGGCGCCGCCGGGTCTGTTGGCAATCTGCACGCCCTTCGGACCGGCCACACTGCCGGACAACCTG CCCAAGGAGTCCGTCTTCAAAAGTAAACTCAAGCTCGACCTGACTATCATCAACATCGACACCAAAGGCA AGGATTTGTTGGGATGGGGTGGGGAAGAAAGTGGTTGTCGCTCCTTCTACAACGCCCTTCATCCAGACGAC GTTCTCTACGCAGCCAGTGCACACCGTGAACTGAGTAAGACAAATTCGTGTGTCATGTACGCTCATCGTAT GGCGCGGAAGGTCGTCCCGGGGACGGCGCTACAATGGCAATGGGTCCAGACGACCATGAAAATCATTCCG AAAAACGGAAAACCTGACCATGTCTCCGCTGCTCACCGTCCGTTGAGCGACGAAGAAGGGAAAGATCTGA TGACAAAGCGTGCGTCCATCACCAAATTATGCGACCTGGACTCTGACGCATCACTGGCCCTGGCCAACAGC GCCGTATCGGAACGCAGTGCCGGTCACGGAGTGGAAGACAGCCTCTCCTGCACAGTAACTCCCACAAAAG CCCCCAAACCGCCCAAAAAGCGACCTTCACCAGCGGCCAATCACCGAGACCCCACGTCATCCTCCTCCTCA ACCAGTAACAACATCAATAATACTTCTCACTACTCCGCCCAACCATCCTCCTTATCCAGCGGTTCCAGCTCC

	ACCCGTCGACGGAAATCTTTCTCCACGGAGAATGTCATCACCGCCAGAAATGGACACGGCGAGATTGCGG
	CGTACTCTTCACCCTACCACACGGAGAGTTCCCTCAACTACTGCGCTCAGAATACCTACCCGACTGCCATTT
	TTCTTCCAACGGCCGTGGAACAGTGTTCGCTGATTCCCTACTCCGGACAGTATCATCACGGTACATCGGCC
	GGATTTTACTCGACGGGAGCTTTGCCTGTCTCGGATTCGGTCCTTTCAGTCGCCTCGCACGGGGTCAATGGA
	TCGACTTTGTTAGACCGATCATACGACTTGTACGCAGCGGCTGCATATGGCTCCGCGGCTGACGGTCTACC
	CTCTCAAGGGGATTACCTGAAGAACTATTACAAAGGCATGGACACCTACCCGAGCAATGTCTACAACACG
	GATCACTCCTCCAGCCATCACCATTCATCAGCGACCAAGGCCGCCGCTGCAGCAAACGGTTGGATGGCATC
	TTCCCACCACAGGCAAAGCGTGCTTGTGTGGAACAACGGTAACTCCCGGCCAGACATGAGTCTAGGCTTCA
	CTCCTTCCACGCGAACTACCTCAGGAGTGTATTCCCAAGGAGCGCCACCTGTGTCGGCTTTCTCAACCACA
	GCTGACTCTTCTTCCCGCCACGCAAATAATCAAGTTATGTCCGCACAACGTTCGCACGACGCTGAAAACAA
	TAAGGTCACCAACGGAGATGACTCTTCAGGAGCTTCAGGCATCGGCCTAATCAAGACTGCTGCCCCGTTAC
	ATCAAAGCCATAACTTCTCCATCTGTGAGGCGACCAATACCATGCTCGAATCTGCTGGATAA

Table S3. Amino acid sequences of *Hypsibius exemplaris* distal limb patterning gene homologs

Gene	Amino Acid Sequence
aristaless	MVGHDERPKKENDCVVPERISPSIASAGSLDDKESFVDDDSEDSASFGAGGGAGARSGAGLSSKQRRYRTTFTAFQ LQELEKCFGKTHYPDIFTRDELAMRIHLTEARIQVWFQNRRAKWRKTEKSSAPHPISGVEPSPAVQSFNTTHPIPNS NCSFSKGHTDPFLQSPHGPSSADYNVRMNPGWPLIPPSNKYSRSSLTQNFYPEQAAAAAAAAAMAATTNMWNQR WLQQMAVNSLLHRDVPPSWTTQTSAGSAVSPAHHLTFHPEFRPFFHPHPNGTTTAGQLTGPSATAAQWTGPGVT ADAMQKYGAFRSIARNDGGGGGR
clawless	MMENPPARSVFKAPSSRSPVAEKPLKKRTPFSIDSILSTDTDTSPKEECFSPSLSETKCSNNENIHTAMDAYAAAAA AATTAMYSSSGYYSSPADAYNYGSMVNSHVVKVPAQRVQQQQQQQHLAPCGGVSPHPALFGIGHHVGMSAYQ WMDPARRLLTRRIGHPYQNRTPPKRKKPRTSFTRIQICELEKRFHRQKYLASAERASLAKSLKMTDAQVKTWFQN RRTKHRRQTNEEREADRQAANRMLLSQLAEVTKTSGAYDSTDALCLNNASLHALHNLRPWVNAGDGGGSLSNN NHHPHIITCPQTNSSSPNNNNTNNNCSSRCSSSSETSHEEEDRDDDDNRSEVSSDEDALSV
Lim1	MPVRHRYLQQHPQPPPPPSSSSGPEDFESHNNRRIVSGKMQNPGGMYDKCHGCGMVILDPFIMAIATPTASQVWH ADCLRCCECKCPLQERCFCNGGRFFCREDYFRAFGQPCKGCGVGIDPTELVRQTQRGNFHLKCFICTACRKQLSTG EECYNIGDCEFNCKDDYVTSKHAKAASSTLQSFSCKAEQSSPGAATSPCLLGGGGRDLSRSESLKPDQHDCLSTTG PSDVTNGAPMNNNNSNTATPIIGSGIGRAMDGHLLHRGEDCEDDDEEDEDAMKCSESGSHVPASDRDCCDKDGK SVNGDNTSSIDESEPRNGNDENVSTKRRGPRTTIKAKQLELLKNAFAQTPKPTRHIRDQLSQETGLTMRVIQVWFQ NRRSKERRMKQQNIMGPGRRCNMFRSRRSGGRSLREFDGDSGDMGVQGPPGFAYFPDGPGNHGMDFFPGQVSPH GGPHAGPLGHPPGIFEFAHYRPPQNAAEAAAMQAHFNEMSPNAHGMPGNINHPGMDGHFRQEMLSQSSTPERTL NSLTPDGYGHPAFDTLPLHPGGNGGIGPVPGGMNGSNSPVWQSMTMAQ
apterous	MPILERSNSGHNEQEEAINSHVTAHGEEPSCLQLDHDHDHGLLPGNEDVAHPQHHVQHPAAGYFPALICSGCRNGI SEQYFLSVSNSQDFYHCHCLKCSVCSVTLDRQMICYYKDGMILCKEDYYKYKSRRLSPEGYQNSRCHGCNYPIRA DEFVMRVREFVFHVPCFRCLACTATLHTGDEFTMRDDGAILCQRHFHPAAAVAHVGGGGGGGVGSSSNPASDTL SSTAALLPPHSSHDSFSAASSDIPTTTATAASLRLPILMADHGAPVSPHFAQLQNRIVPRHDDGGDGNDGRKDLFHH HHHQTSASSSASSRMKSRIRRTKRNLISFDDGSGGVINQRHTAGGLNGSGGELHGDPVGQAELLQQRQAAAAMQL EQQCYHHFSSAASPNAALPVQTAQQSSFTSSSEESSPSRLASSSPGLQMAHLTHSITDSSSPNNQQHQRTKRMRTSF KHQQLRSMKQYFGINHNPDAKDLKQLAQKTGLTKRVLQVWFQNARAKYRRSLLKQDPNRVLEASPIAKAQSNSP SPRPDYGLPDNASAKQHDLNHYPMSNGSNSQDNGAEYY
BarH1	MDRDNGERSSSKSPLDMTAHPAHPQPLTSPSITSHVKVTSSNCAPQNLSMRHSFLIKDILSQVNPRQQESSRSGAGD GMGAGTFPPGSQEDGDSDVQSELSDTESKDDHDGADSTATSRNSPKGKKSRKARTAFTDSQLQTLEKRFERQKYL SVQDRMELAASLSLSDAQVKCWFQNRRTKWKRQTSVTIELLAEATGNYAAMQRMLQYWSCGGPAAMLAAPAA AYPAQNQLFQMQELYYRSLQQQQQQQQQVGGRVVGGPGGIPQMPMNPVTTRFWPTPANMTFPTGNSAPNVHLI ASSTAVATPAAPASPPSRSTGIKTAAQSDDGTD
rotund	MAGAHETADELNLMQQQHPQRFTPWNQNAMDFQKILNQQAAANSLNGHAHSLQGKGPNFDMVSMEMDETGG GGVGAVSDLYGVQQATRAIQSVMVTPHHHHSSIMSGFMHQHHAGGHNLPKTLSGRKFPCKMCNQVLESKAEFQ MHNQSHMREPKPYRCSQCPKSFANSSYLSQHMRIHLGIKPYHCDICKKKFTQLSHLQQHIRTHTGDKPYRCPQPTC TKAFSQLSNLQSHSRCHQQDKPFKCQSCYKCFYDEQSLLDHIPKHKDSKHLKTHICTCCGKSYTQETYLLRHMAK HNDKNEKQQRMSLNHIKTATVDPYWPKQEMEGAHRMSQEDLFMYSGGYYSAANYGNAHHAVHPYGAGQTSPV NYDTSNKNSGSAFSILSGSSGRNVMAHPHAHNYYDSAFGSGAMKSQNVLSDSMATSKNGPISVDHFAGFTNHQM PAMRNHFSAGFVGNNGMPTMLMGGGGDGSTASGMRKEHSNHNSSSKPGGRY
spineless	MYATKRRRRSLKGSSSKICLSKSAYDTSHHGNSGGGCGGGNSSSLKSNPSKRHRERLNSELERIASLLPFEANILSK LDKLSILRLSVSYLRIKSYFHAIQLREQTYGGYDGPGGHKTSADHFHADPSLTRTDSVLKALNGFVLVLTVQGEVF FASSNIEEFLGFHQSDVIHQSVYELIHSEDRVELQKQLSWLGSPSAAAAHHPGSRMNPHDAFSSDNFQHLERSLTAR FRCLLDNTSGFLRLEIRGRIGVLHGQNFHSAGEAPPGLLAICTPFGPATLPDNLPKESVFKSKLKLDLTIINIDTKGKD LLGWGGEESGCRSFYNALHPDDVLYAASAHRELSKTNSCVMYAHRMARKVVPGTALQWQWVQTTMKIIPKNG KPDHVSAAHRPLSDEEGKDLMTKRASITKLCDLDSDASLALANSAVSERSAGHGVEDSLSCTVTPTKAPKPPKKRP SPAANHRDPTSSSSSTSNNINNTSHYSAQPSSLSSGSSSTRRRKSFSTENVITARNGHGEIAAYSSPYHTESSLNYCAQ NTYPTAIFLPTAVEQCSLIPYSGQYHHGTSAGFYSTGALPVSDSVLSVASHGVNGSTLLDRSYDLYAAAAYGSAAD GLPSQGDYLKNYYKGMDTYPSNVYNTDHSSSHHHSSATKAAAAANGWMASSHHRQSVLVWNNGNSRPDMSLG FTPSTRTTSGVYSQGAPPVSAFSTTADSSSRHANNQVMSAQRSHDAENNKVTNGDDSSGASGIGLIKTAAPLHQSH NFSICEATNTMLESAG

Table S4. Blastp result against the Flybase database using *Hypsibius exemplaris* distal limb patterning gene homologs as query

aristaless

BLAST Hit Summary

Description	Species	Score	E value
al-PA	Dmel	122.094	6.02387e-28
Pph13-PA	Dmel	114.39	1.225e-25
hbn-PA	Dmel	111.309	1.34315e-24
Drgx-PF	Dmel	109.383	4.35569e-24
Drgx-PE	Dmel	109.383	4.35569e-24
Rx-PB	Dmel	109.383	4.39219e-24
PHDP-PA	Dmel	106.686	3.17311e-23
prd-PA	Dmel	99.7525	3.3102e-21
prd-PB	Dmel	99.7525	3.45122e-21
CG9876-PA	Dmel	98.2117	1.12858e-20
CG32532-PD	Dmel	95.5153	6.9002e-20
CG34367-PC	Dmel	94.7449	1.08278e-19
CG34367-PB	Dmel	94.3597	1.36773e-19
CG32532-PB	Dmel	94.3597	1.39075e-19
CG32532-PC	Dmel	94.3597	1.44999e-19
CG11294-PB	Dmel	94.3597	1.68497e-19
CG11294-PA	Dmel	94.3597	1.68497e-19
otp-PK	Dmel	93.2041	3.25731e-19
otp-PJ	Dmel	93.2041	3.69159e-19
otp-PF	Dmel	92.8189	4.43541e-19
otp-PC	Dmel	92.8189	4.66311e-19
Ptx1-PE	Dmel	92.0485	6.73157e-19
Ptx1-PA	Dmel	92.0485	7.50281e-19
ey-PB	Dmel	92.0485	8.29292e-19
Ptx1-PC	Dmel	92.0485	8.43247e-19

clawless

BLAST Hit Summary

Description	Species	Score	E value
C15-PA	Dmel	199.904	2.63135e-51
B-H1-PA	Dmel	81.6481	1.06197e-15
Hmx-PE	Dmel	80.8777	2.15834e-15
Hmx-PC	Dmel	80.8777	2.15834e-15
Hmx-PD	Dmel	80.4925	2.72636e-15
lbe-PA	Dmel	80.1073	2.9636e-15
NK7.1-PD	Dmel	78.5666	8.84131e-15
NK7.1-PC	Dmel	78.5666	8.84131e-15
NK7.1-PB	Dmel	78.5666	8.84131e-15
NK7.1-PA	Dmel	78.5666	8.84131e-15
B-H2-PA	Dmel	78.5666	9.21796e-15
bap-PA	Dmel	78.5666	9.2952e-15
lms-PC	Dmel	78.5666	1.03601e-14
lms-PB	Dmel	78.5666	1.03601e-14
Dr-PA	Dmel	78.1814	1.11681e-14
bsh-PC	Dmel	78.1814	1.26571e-14
bsh-PB	Dmel	78.1814	1.26571e-14
lbl-PA	Dmel	77.411	2.17706e-14
B-H2-PB	Dmel	77.411	2.42649e-14
pb-PD	Dmel	76.2554	4.76972e-14
pb-PC	Dmel	76.2554	5.0566e-14
pb-PB	Dmel	76.2554	5.0566e-14
pb-PA	Dmel	76.2554	5.0566e-14
Dll-PC	Dmel	74.7146	1.23478e-13
Dll-PB	Dmel	74.7146	1.24512e-13

Lim1

BLAST Hit Summary			
Description	Species	Score	E value
Lim1-PA	Dmel	251.136	2.15928e-66
Lim1-PB	Dmel	138.272	1.87657e-32
Lim3-PG	Dmel	128.257	1.89394e-29
Lim3-PF	Dmel	127.872	2.43263e-29
Lim3-PD	Dmel	127.872	2.43263e-29
Lim3-PC	Dmel	127.872	2.43263e-29
Lim3-PB	Dmel	127.872	2.43263e-29
Lim3-PE	Dmel	126.716	5.69754e-29
Lim3-PA	Dmel	126.331	6.84554e-29
Awh-PC	Dmel	96.6709	7.09635e-20
Awh-PB	Dmel	95.9005	1.0159e-19
Awh-PD	Dmel	95.5153	1.25154e-19
Awh-PA	Dmel	92.8189	8.45781e-19
ap-PA	Dmel	92.8189	8.892e-19
ap-PC	Dmel	92.8189	9.04163e-19
tup-PC	Dmel	90.8929	3.43582e-18
tup-PA	Dmel	90.8929	3.43582e-18
tup-PB	Dmel	90.1225	5.57444e-18
Lmx1a-PC	Dmel	90.1225	6.21311e-18
Lmx1a-PB	Dmel	90.1225	6.47779e-18
CG4328-PB	Dmel	81.6481	2.04994e-15
Bx-PF	Dmel	71.633	2.10373e-12
Bx-PB	Dmel	70.8626	3.96632e-12
Bx-PD	Dmel	70.0922	5.82204e-12
Bx-PC	Dmel	70.0922	7.17243e-12

apterous

BLAST Hit Summary			
Description	Species	Score	E value
ap-PA	Dmel	126.331	6.97109e-29
ap-PC	Dmel	126.331	7.02949e-29
ap-PE	Dmel	125.176	1.61916e-28
ap-PB	Dmel	125.176	1.61916e-28
tup-PC	Dmel	100.908	3.64471e-21
tup-PA	Dmel	100.908	3.64471e-21
tup-PB	Dmel	99.7525	7.53218e-21
Awh-PC	Dmel	94.7449	2.65593e-19
Awh-PB	Dmel	93.5893	4.60657e-19
Awh-PD	Dmel	93.2041	6.27266e-19
Awh-PA	Dmel	91.2781	2.48515e-18
Lim3-PF	Dmel	90.5077	4.03204e-18
Lim3-PD	Dmel	90.5077	4.03204e-18
Lim3-PC	Dmel	90.5077	4.03204e-18
Lim3-PB	Dmel	90.5077	4.03204e-18
Lim3-PG	Dmel	90.5077	4.53164e-18
Lim3-PE	Dmel	89.3521	8.8338e-18
Lim3-PA	Dmel	89.3521	8.8338e-18
Lmx1a-PC	Dmel	87.8113	2.63539e-17
Lmx1a-PB	Dmel	87.8113	2.67974e-17
CG4328-PB	Dmel	82.0333	1.4582e-15
Lim1-PA	Dmel	73.559	5.9271e-13
Bx-PF	Dmel	69.707	7.24328e-12
Bx-PD	Dmel	69.3218	9.94567e-12
Bx-PB	Dmel	69.3218	1.16542e-11

BarH1

BLAST Hit Summary			
Description	Species	Score	E value
B-H1-PA	Dmel	143.665	2.28872e-34
B-H2-PA	Dmel	139.813	3.59249e-33
B-H2-PB	Dmel	138.272	1.02796e-32
lms-PC	Dmel	91.6633	1.09421e-18
lms-PB	Dmel	91.6633	1.09421e-18
CG11085-PA	Dmel	90.5077	2.04586e-18
NK7.1-PD	Dmel	87.4261	1.82084e-17
NK7.1-PC	Dmel	87.4261	1.82084e-17
NK7.1-PB	Dmel	87.4261	1.82084e-17
NK7.1-PA	Dmel	87.4261	1.82084e-17
lbe-PA	Dmel	87.0409	2.43836e-17
Dll-PB	Dmel	85.8853	5.80708e-17
Dll-PA	Dmel	85.5001	6.58131e-17
Dll-PC	Dmel	85.5001	6.74812e-17
bsh-PC	Dmel	85.5001	6.91917e-17
bsh-PB	Dmel	85.5001	6.91917e-17
slou-PA	Dmel	85.1149	9.90537e-17
slou-PB	Dmel	84.7297	1.20009e-16
C15-PA	Dmel	83.1889	3.21222e-16
exex-PA	Dmel	82.8037	4.12585e-16
toe-PA	Dmel	82.8037	4.44761e-16
Hmx-PE	Dmel	82.0333	8.88974e-16
Hmx-PC	Dmel	82.0333	8.88974e-16
Hmx-PD	Dmel	81.6481	1.10434e-15
lbl-PA	Dmel	80.4925	2.50162e-15

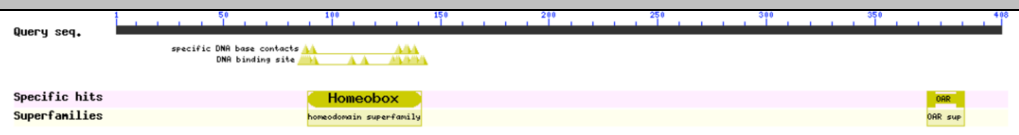
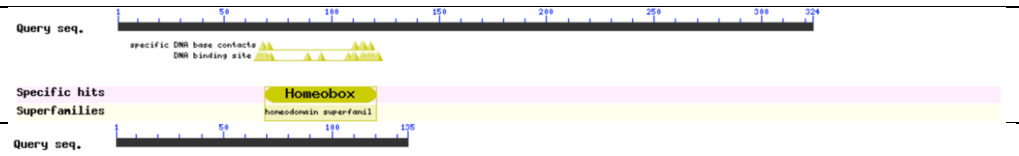
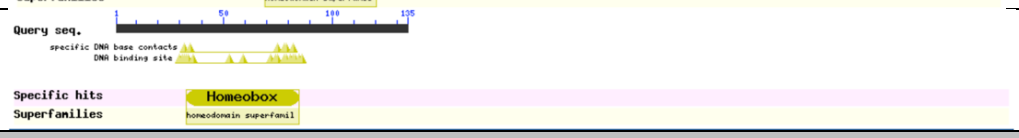
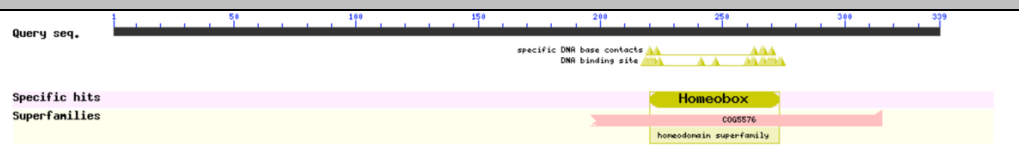
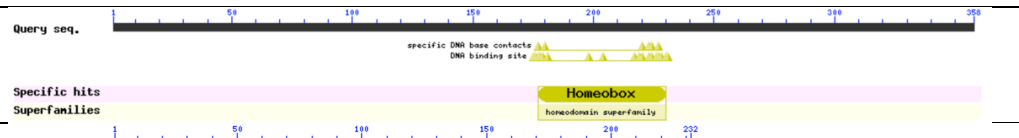
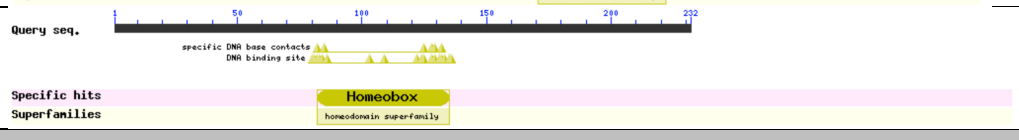
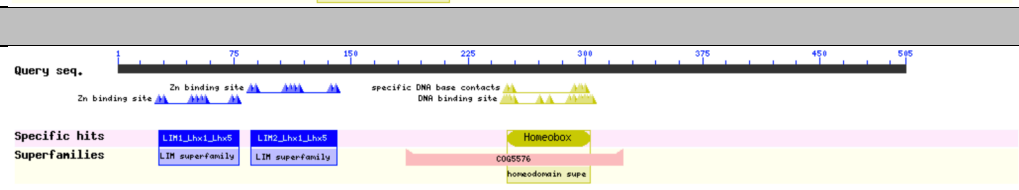
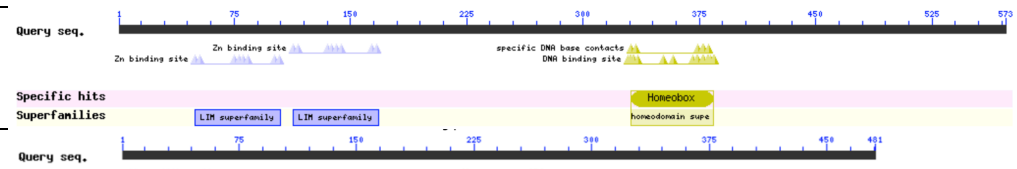
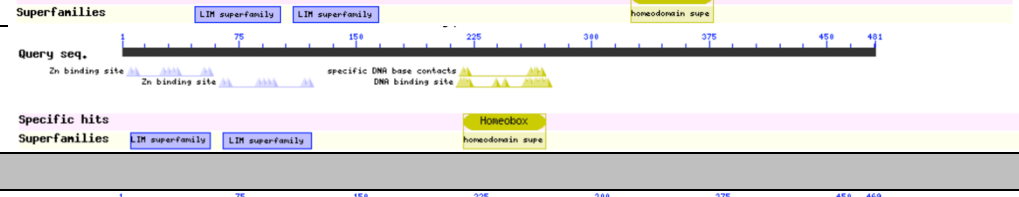
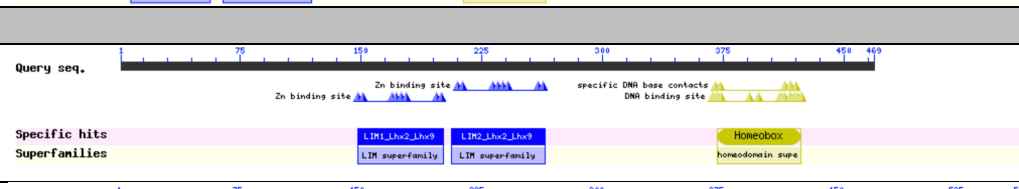
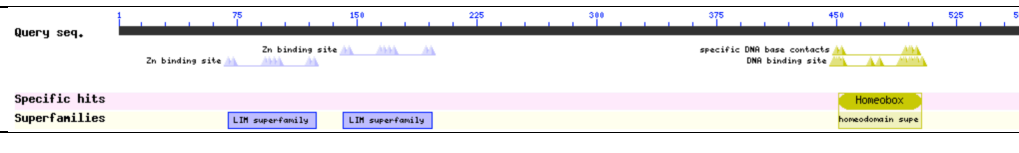
rotund

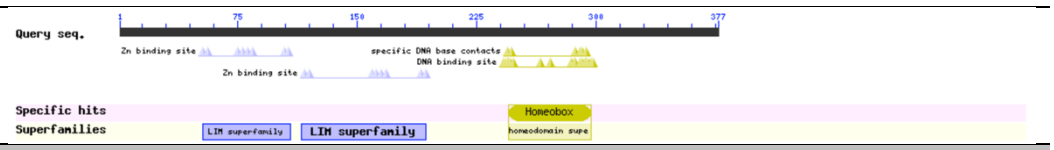
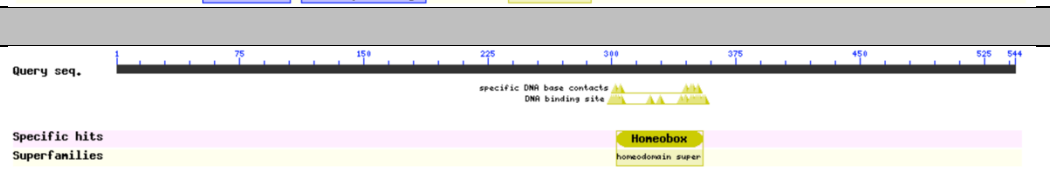
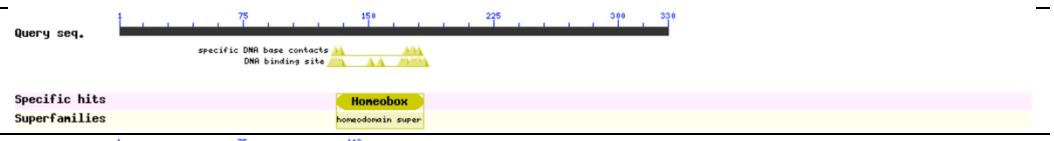
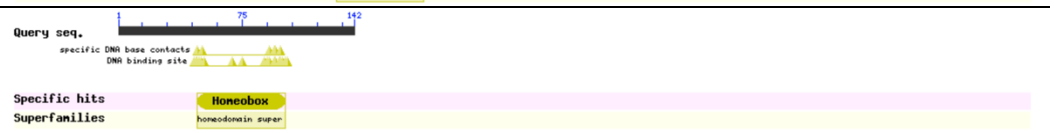
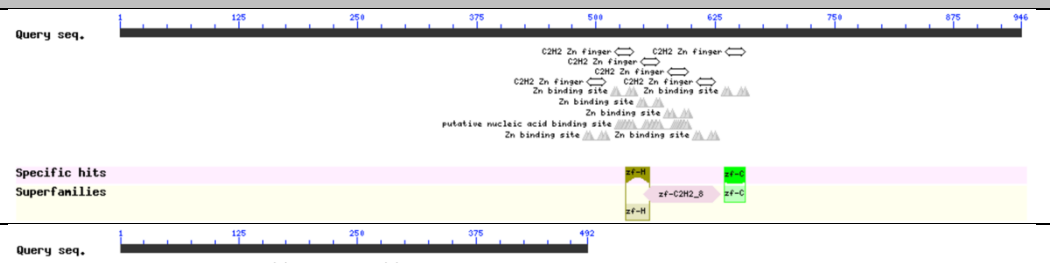
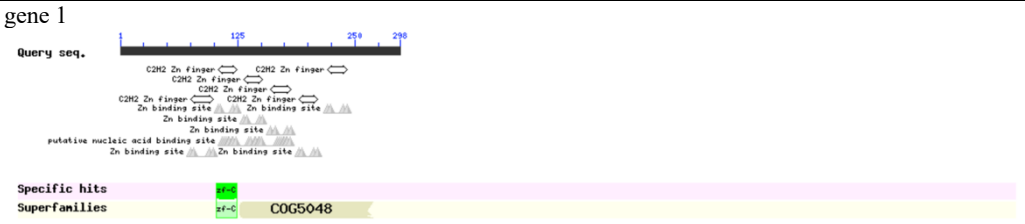
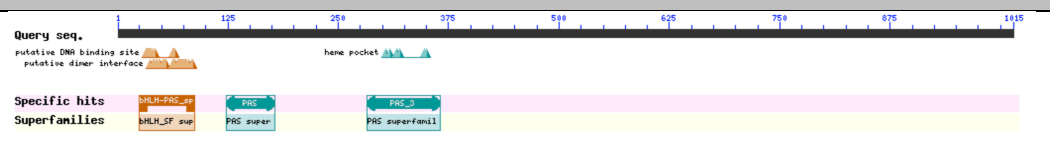
BLAST Hit Summary			
Description	Species	Score	E value
rn-PF	Dmel	303.138	3.87162e-82
rn-PE	Dmel	302.753	5.2719e-82
rn-PG	Dmel	302.368	5.82708e-82
rn-PC	Dmel	287.345	2.3113e-77
sqz-PA	Dmel	263.462	2.95001e-70
Kr-h1-PA	Dmel	134.806	1.73459e-31
Kr-h1-PB	Dmel	134.806	1.79346e-31
dati-PA	Dmel	125.561	9.52077e-29
dati-PC	Dmel	125.561	9.52077e-29
dati-PD	Dmel	125.176	1.29642e-28
dati-PB	Dmel	124.79	1.90298e-28
gl-PA	Dmel	118.242	1.50739e-26
gl-PC	Dmel	118.242	1.55854e-26
crol-PG	Dmel	118.242	1.61144e-26
Meics-PA	Dmel	117.472	3.06361e-26
Meics-PB	Dmel	117.087	3.47207e-26
Clamp-PA	Dmel	115.161	1.6119e-25
Kr-PB	Dmel	114.775	1.98578e-25
Kr-PA	Dmel	114.775	1.98578e-25
CG12299-PA	Dmel	114.39	2.38589e-25
Clamp-PB	Dmel	114.39	2.5935e-25
CG17385-PB	Dmel	114.005	3.22182e-25
CG17385-PA	Dmel	114.005	3.22182e-25
crol-PD	Dmel	113.62	3.90342e-25
gl-PB	Dmel	113.62	4.06971e-25

spineless

BLAST Hit Summary			
Description	Species	Score	E value
ss-PD	Dmel	371.703	1.41622e-102
ss-PC	Dmel	371.703	1.41622e-102
ss-PA	Dmel	370.933	2.47694e-102
sim-PA	Dmel	105.531	2.07501e-22
sim-PC	Dmel	105.145	2.21824e-22
sim-PD	Dmel	105.145	2.23683e-22
sim-PB	Dmel	105.145	2.68753e-22
trh-PG	Dmel	89.7373	9.80667e-18
sima-PD	Dmel	88.5817	2.53873e-17
trh-PC	Dmel	88.5817	2.56e-17
trh-PB	Dmel	88.1965	3.02492e-17
sima-PA	Dmel	88.1965	3.42822e-17
dysf-PB	Dmel	82.4185	1.73054e-15
dysf-PC	Dmel	82.0333	2.39609e-15
dysf-PD	Dmel	81.6481	2.62642e-15
sima-PB	Dmel	80.1073	7.77029e-15
Met-PB	Dmel	79.7221	1.16949e-14
Met-PA	Dmel	79.7221	1.16949e-14
gce-PE	Dmel	71.2478	4.30067e-12
gce-PD	Dmel	71.2478	4.30067e-12
gce-PC	Dmel	71.2478	4.30067e-12
gce-PG	Dmel	71.2478	4.30067e-12
trh-PA	Dmel	70.8626	5.478e-12
trh-PE	Dmel	70.4774	6.31283e-12
trh-PD	Dmel	70.4774	6.36572e-12

Table S5. Protein domains of *Drosophila melanogaster, Hypsibius exemplaris,* and *Echiniscoides cf. sigimundi* distal limb patterning genes

aristaless	
Drosophila melanogaster	
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	
clawless	
Drosophila melanogaster	
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	
Lim1	
Drosophila melanogaster	
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	
apterous	
Drosophila melanogaster	
Hypsibius exemplaris	

Echiniscoides cf. sigismundi	
BarH1	
Drosophila melanogaster	
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	
rotund	
Drosophila melanogaster	
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	gene 1  gene 2 
Spineless	
Drosophila melanogaster	

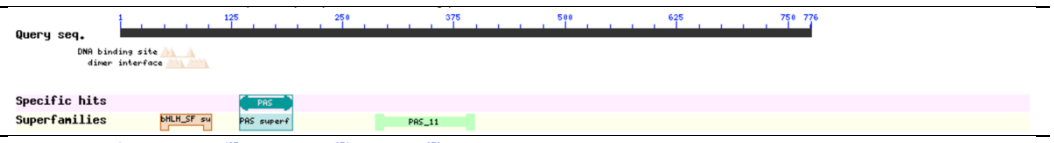
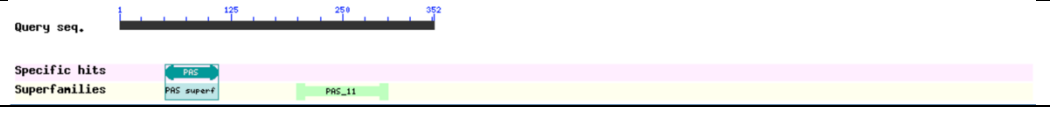
Hypsibius exemplaris	
Echiniscoides cf. sigismundi	

Table S6. Amino acid sequences of *Echiniscoids cf. sigismundi* distal limb patterning gene homologs

Gene	Amino Acid Sequence
aristaless	MSSITATNNISTASIFGYGNEDKLNQRKQRRYRTTFSSTQLDELERVFGETHYPDVFIREELALRINLTEARVQVWF QNRRAKHRKQDKNELQSIPINPVMNNFALLMQQQQQQQNEMQFHSGLQQQPQPQQQHQ
clawless	NNNNNNVNEKSTSTSAFTPVIKHQQPQQQQQNHHLNQHQQHQNALNSVLATHLAWNDPSIRRLGRRIGHPYQQR TPPKRKKPRTSFTRIQICELEKRFQRQKYLASAERATLAKSLKMTDAQVKTWFQNRRTKWRRQTAEEREAERQAA SRMLLSLQAELAQKAPPMSAQPDPICMSNKSLYALHNLQPWASNMVQTTTTSPISSVYNDDKCNSSDVIDDDDDD LDDYDIID
Lim1	MQVVKCCACDQLINDKFIMNVLDRTWHAECLRCCICSMILTDKCFSRHGKVYCRDHFYKAFGAKCCVCFEGINP DELVRRTVQGGVYHIKCFKCNECHKELTTGEQFYCIDESRFLCKSDFLMKQIPLTTSSNQVNNSWPKSIKSENDDE EIEQGSPQQQLYNTNNAHSNNCTTPNAHQSSSEKEEEFDDSDSTNKDNKIKHDNDSTHQPSGTKRRGPRTTIKQKQ LEQLKEIFDSQPKPPKAIRDQLASKTGLSKRVIQVWFQNRRSKERRMKTSQNLRGRNAYARHRNGGRSSSSGRPEL EQHAQGGPPPHIFGFYTDNGVPNGPPPPDMFGASPGNFYPNDPNNFNFNLAPPPPPPPPDVMNNNNGGANGGGN LSAMSQHFPPSSISNESPVPPSLVINGIQPNESLNANNNNTNSQQQQKFNGTRDHFLPSPTSIDGYQASNFQDPCSMQ FSGMRIQQQQPPPATQISPESAGLIN
apterous	ILFPMDLNEEITTTTTTATTIAPPLINISSSSVENINTPAITETQSLSTSDICNACFLPIQERYLLMLGDSLLYHSHCLKC LDCGVQLCEDDRSCFFNSGNVYCRQDYQKRFNQRQCTRCNVTFQSTDLVMTVPCEDLQNNSNSNNTPTLPSSLPI QFHVDCFSCAICERVLASGELYRYIPMPHNTLLCCEHLEWSNFKDDSGKLSTKVGRPRKRKSQDSSHSTCSGGNGG NNEHSMQRPKRMRTSFKHPQIKVMKQFFISNQNPDAKMLKTLSARTSLSKRVLQVWFQNQRAKFRREHSKRQHQ HQSVGMNGPDGYNPHGPDVYQLHIPPTVQSLPSVASYSPGGTVTSRNNGNNNNLGQQQQQQQQQKPSDSYS
BarH1	QTLNKLHYDDDSDDCEDYCDKTNKTTTTTHNNNKQQNLHLLSKKARKPRTAFTEHQLDVLEKSFQGQKYLSVQE RLELAAKLCLTDAQVKCWFQNRRTKWKRTMEAEQFNQALYNVYNGHHHLHHNNLLIGNTTQQQQQQQQ
rotund	(gene 1) FDPTAAAERLMYRQQQQQQQQQPVVQPTQHQFQHNTASIDDVAQRSLASLEQSVAQLSAKSTPRQVATSVRRYN CRMCSKSFETKQEHHQHVQAHMREHKPYKCTQCPKTFANSSYLTQHMRIHLGLRPYKCSQCEKNFTQLSHKNQH ERTHSGKKPYLCPQPGCGKYFSQLSNLQSHSRCHQSHKAFKCQSCHKCFDDEESLLEHIPKHIESKHLKKHICRYC GKSYAQETYLTKHLSKHLPKQSDTDSESEKSNLEVTNSKKLKKPATTEKLDSIEKSEITNSSNNNTTNNMYYML (gene 2) TKTFANSSYLSQHMRIHLGVRPYKCPSCDKRFTQLSHLQQHDRTHSGDKPYACKHPNCNKAFSQLSNLQSHSRCH QTNKPYKCNSCFRSFEDEKSLLEHIPRHKESKHLKTHICEHCGKSYAQETYLQKHLNKHPHNLGGGCNKRNSNNG RGKCKRIQQQQQPQPQQHLQQQQQQNTIW
spineless	YHSHHQHHLHQQQQQQLHNTHYNQFSNYPSTSDNACNRILTAGLGPQILSRESIMKALNGFLVIIQADGEVFYVSN TVEHFLGFHQSDVLHQSICDLIHSEDRIDFQKQLEWNSLRQNSQPYSDFALADNPFMLERNFTARFRCLLDNTSGFL RLDVRGRLSLLPGQKTRSSSIALFALCSVFGPTQMIESVSRNCLFRSKHKMDLEVINFDAKGKINIDDKNDIEGEKL YNLVHSDDLQYIATGHAELLKTGTTGLLAYRLRFDSEQKWQWVQSNLRINYRSGRGEFITAIHRVLIDEEGIDLYS KRKISSAFSYLVDFTNSTQQQTNNNNNSLTTTDSSQQSSFTRPITN

Table S7. Blastp result against the Flybase database using *Echiniscoides cf. sigismundi* distal limb patterning gene homologs as query

aristaless

BLAST Hit Summary

Description	Species	Score	E value
al-PA	Dmel	122.865	8.19371e-29
Pph13-PA	Dmel	110.923	3.16876e-25
Drgx-PF	Dmel	103.219	7.06335e-23
Drgx-PE	Dmel	103.219	7.06335e-23
PHDP-PA	Dmel	102.834	8.92221e-23
prd-PA	Dmel	100.908	3.01665e-22
prd-PB	Dmel	100.908	3.27915e-22
Rx-PB	Dmel	98.9821	1.22545e-21
oc-PE	Dmel	98.5969	1.50969e-21
oc-PD	Dmel	98.2117	1.82908e-21
oc-PG	Dmel	98.2117	1.82908e-21
oc-PC	Dmel	98.2117	1.82908e-21
oc-PF	Dmel	98.2117	1.8444e-21
oc-PH	Dmel	97.8265	2.61848e-21
CG9876-PA	Dmel	97.0561	4.8551e-21
hbn-PA	Dmel	95.9005	9.78553e-21
CG34367-PB	Dmel	95.9005	1.09067e-20
gsb-PA	Dmel	94.3597	2.89507e-20
otp-PJ	Dmel	92.0485	1.47322e-19
otp-PF	Dmel	92.0485	1.54886e-19
OdsH-PA	Dmel	91.6633	1.86093e-19
otp-PC	Dmel	91.6633	1.9081e-19
CG32532-PD	Dmel	91.2781	2.55523e-19
CG11294-PB	Dmel	91.2781	2.87184e-19
CG11294-PA	Dmel	91.2781	2.87184e-19

clawless

BLAST Hit Summary

Description	Species	Score	E value
C15-PA	Dmel	199.134	2.88667e-51
Hmx-PE	Dmel	86.6557	2.01947e-17
Hmx-PC	Dmel	86.6557	2.01947e-17
Hmx-PD	Dmel	86.2705	2.42637e-17
B-H1-PA	Dmel	85.1149	6.12607e-17
HGTX-PA	Dmel	81.6481	6.33582e-16
B-H2-PA	Dmel	81.6481	6.3889e-16
HGTX-PC	Dmel	81.6481	6.55085e-16
NK7.1-PD	Dmel	81.2629	7.06171e-16
NK7.1-PC	Dmel	81.2629	7.06171e-16
NK7.1-PB	Dmel	81.2629	7.06171e-16
NK7.1-PA	Dmel	81.2629	7.06171e-16
B-H2-PB	Dmel	81.2629	8.55567e-16
lms-PC	Dmel	80.8777	9.07025e-16
lms-PB	Dmel	80.8777	9.07025e-16
bap-PA	Dmel	78.9518	3.56367e-15
exex-PA	Dmel	77.7962	9.30286e-15
lbe-PA	Dmel	76.2554	2.77532e-14
Dr-PA	Dmel	75.485	4.89465e-14
Dll-PB	Dmel	74.7146	6.60956e-14
Dll-PC	Dmel	74.7146	7.74501e-14
Dll-PA	Dmel	74.7146	8.00786e-14
lbl-PC	Dmel	74.3294	1.00312e-13
lbl-PA	Dmel	73.9442	1.11805e-13
CG18599-PA	Dmel	73.9442	1.11805e-13

Lim1

BLAST Hit Summary

Description	Species	Score	E value
Lim1-PA	Dmel	233.417	3.61509e-61
Lim3-PF	Dmel	137.117	3.1635e-32
Lim3-PD	Dmel	137.117	3.1635e-32
Lim3-PC	Dmel	137.117	3.1635e-32
Lim3-PB	Dmel	137.117	3.1635e-32
Lim3-PG	Dmel	137.117	3.46759e-32
ap-PA	Dmel	136.346	5.72067e-32
ap-PC	Dmel	136.346	5.7686e-32
Lim3-PE	Dmel	135.961	7.28673e-32
Lim3-PA	Dmel	135.961	8.25824e-32
tup-PC	Dmel	116.701	4.97279e-26
tup-PA	Dmel	116.701	4.97279e-26
tup-PB	Dmel	115.931	8.20388e-26
Awh-PC	Dmel	113.235	5.78032e-25
Awh-PB	Dmel	112.464	1.01097e-24
Lmx1a-PC	Dmel	112.079	1.08981e-24
Lmx1a-PB	Dmel	112.079	1.10814e-24
Awh-PD	Dmel	111.694	1.37661e-24
Awh-PA	Dmel	108.997	1.07208e-23
Lim1-PB	Dmel	102.449	8.49214e-22
CG4328-PB	Dmel	92.8189	7.43732e-19
ap-PE	Dmel	78.1814	1.81824e-14
ap-PB	Dmel	78.1814	1.81824e-14
Bx-PF	Dmel	77.411	3.12743e-14
jub-PC	Dmel	77.411	3.15363e-14

apterous

BLAST Hit Summary

Description	Species	Score	E value
ap-PC	Dmel	137.502	1.90583e-32
ap-PA	Dmel	137.502	1.98702e-32
Awh-PB	Dmel	112.464	6.96035e-25
Awh-PC	Dmel	112.079	7.7578e-25
Awh-PA	Dmel	111.309	1.35682e-24
Awh-PD	Dmel	111.309	1.49971e-24
tup-PC	Dmel	96.2857	4.26055e-20
tup-PA	Dmel	96.2857	4.26055e-20
tup-PB	Dmel	95.9005	7.20701e-20
ap-PE	Dmel	95.5153	8.23633e-20
ap-PB	Dmel	95.5153	8.23633e-20
Lmx1a-PB	Dmel	92.0485	9.25956e-19
Lmx1a-PC	Dmel	92.0485	9.81649e-19
CG4328-PB	Dmel	89.3521	5.52142e-18
Lim3-PA	Dmel	87.0409	3.02882e-17
Lim3-PF	Dmel	85.5001	8.31256e-17
Lim3-PD	Dmel	85.5001	8.31256e-17
Lim3-PC	Dmel	85.5001	8.31256e-17
Lim3-PB	Dmel	85.5001	8.31256e-17
Lim3-PE	Dmel	85.5001	8.88636e-17
Lim3-PG	Dmel	85.1149	9.98746e-17
CG5708-PC	Dmel	78.5666	9.19328e-15
CG5708-PB	Dmel	78.5666	9.19328e-15
CG5708-PA	Dmel	78.5666	9.19328e-15
CG9876-PA	Dmel	63.929	2.34327e-10

BarH1

BLAST Hit Summary

Description	Species	Score	E value
B-H1-PA	Dmel	100.908	3.3189e-22
B-H2-PA	Dmel	97.4413	3.57877e-21
B-H2-PB	Dmel	95.1301	2.22491e-20
exex-PA	Dmel	82.0333	1.96544e-16
Dll-PB	Dmel	80.1073	6.8708e-16
Dll-PC	Dmel	80.1073	7.34508e-16
Dll-PA	Dmel	79.7221	9.43421e-16
C15-PA	Dmel	78.1814	2.67708e-15
Dr-PA	Dmel	78.1814	2.72213e-15
CG11085-PA	Dmel	76.2554	1.00884e-14
lbe-PA	Dmel	75.8702	1.13384e-14
lms-PC	Dmel	75.8702	1.19205e-14
lms-PB	Dmel	75.8702	1.19205e-14
CG34031-PC	Dmel	75.0998	1.99968e-14
Hmx-PE	Dmel	75.0998	2.21026e-14
Hmx-PC	Dmel	75.0998	2.21026e-14
Hmx-PD	Dmel	74.3294	4.03038e-14
lbl-PC	Dmel	72.0182	1.61017e-13
lbl-PA	Dmel	72.0182	1.72131e-13
slou-PA	Dmel	71.2478	2.91172e-13
slou-PB	Dmel	71.2478	3.08685e-13
pb-PB	Dmel	70.0922	7.16974e-13
Scr-PB	Dmel	70.0922	7.53781e-13
Scr-PA	Dmel	70.0922	7.53781e-13
bsh-PC	Dmel	69.707	7.85893e-13

rotund (gene 1)

BLAST Hit Summary				
	Description	Species	Score	E value
☑	rn-PF	Dmel	262.307	3.51091e-70
☑	rn-PG	Dmel	261.536	5.602e-70
☑	rn-PE	Dmel	261.536	6.50982e-70
☑	rn-PC	Dmel	249.98	1.89572e-66
☑	sqz-PA	Dmel	218.779	4.16418e-57
☑	Kr-h1-PB	Dmel	128.642	5.85968e-30
☑	Kr-h1-PA	Dmel	128.257	7.52634e-30
☑	dati-PA	Dmel	114.39	1.19231e-25
☑	dati-PC	Dmel	114.39	1.19231e-25
☑	dati-PD	Dmel	114.39	1.2023e-25
☑	dati-PB	Dmel	113.62	2.17415e-25
☑	Clamp-PA	Dmel	113.62	2.19237e-25
☑	Clamp-PB	Dmel	112.079	6.11818e-25
☑	CG17385-PB	Dmel	110.923	1.24346e-24
☑	CG17385-PA	Dmel	110.923	1.24346e-24
☑	gl-PC	Dmel	110.538	1.72169e-24
☑	gl-PA	Dmel	110.538	1.8715e-24
☑	Meics-PA	Dmel	109.768	2.77014e-24
☑	Meics-PB	Dmel	109.768	3.35618e-24
☑	CG32772-PE	Dmel	109.768	3.47008e-24
☑	CG32772-PC	Dmel	109.768	3.47008e-24
☑	Paris-PA	Dmel	107.071	2.12164e-23
☑	CG5245-PA	Dmel	105.145	7.29408e-23
☑	CG15269-PA	Dmel	104.76	9.93219e-23
☑	jim-PI	Dmel	104.375	1.36378e-22

(gene 2)

BLAST Hit Summary				
	Description	Species	Score	E value
☑	rn-PC	Dmel	228.409	2.51052e-60
☑	rn-PF	Dmel	228.409	2.59572e-60
☑	rn-PE	Dmel	227.639	3.74713e-60
☑	rn-PG	Dmel	227.639	4.00578e-60
☑	sqz-PA	Dmel	223.787	6.44705e-59
☑	dati-PA	Dmel	112.849	1.64339e-25
☑	dati-PC	Dmel	112.849	1.64339e-25
☑	dati-PD	Dmel	112.849	1.72776e-25
☑	dati-PB	Dmel	111.309	4.7024e-25
☑	gl-PA	Dmel	107.071	8.22678e-24
☑	gl-PC	Dmel	106.686	9.64004e-24
☑	Clamp-PA	Dmel	103.99	6.35364e-23
☑	Clamp-PB	Dmel	103.99	6.84913e-23
☑	gl-PB	Dmel	103.605	9.64284e-23
☑	Kr-h1-PA	Dmel	102.449	2.00949e-22
☑	Kr-h1-PB	Dmel	102.449	2.18435e-22
☑	CG5245-PA	Dmel	98.9821	2.22175e-21
☑	CG12299-PA	Dmel	97.0561	9.02542e-21
☑	Meics-PA	Dmel	95.5153	2.27873e-20
☑	Meics-PB	Dmel	95.5153	2.49777e-20
☑	Paris-PA	Dmel	95.1301	3.40116e-20
☑	CG32772-PF	Dmel	93.2041	1.10296e-19
☑	CG32772-PD	Dmel	93.2041	1.10296e-19
☑	CG32772-PE	Dmel	93.2041	1.12152e-19
☑	CG32772-PC	Dmel	93.2041	1.12152e-19

spineless

BLAST Hit Summary				
	Description	Species	Score	E value
☑	ss-PD	Dmel	266.929	1.79906e-71
☑	ss-PC	Dmel	266.929	1.79906e-71
☑	ss-PA	Dmel	266.929	2.00517e-71
☑	sim-PA	Dmel	86.6557	3.36023e-17
☑	sim-PB	Dmel	86.6557	3.7766e-17
☑	sim-PC	Dmel	86.2705	4.6139e-17
☑	sim-PD	Dmel	82.4185	7.00448e-16
☑	dysf-PC	Dmel	62.7734	5.28357e-10
☑	dysf-PD	Dmel	62.7734	5.37248e-10
☑	dysf-PB	Dmel	62.7734	5.69561e-10
☑	Clk-PF	Dmel	55.8398	6.56741e-08
☑	Clk-PA	Dmel	55.8398	7.50538e-08
☑	Clk-PD	Dmel	55.4546	8.8684e-08
☑	trh-PG	Dmel	54.299	1.78744e-07
☑	trh-PE	Dmel	47.7506	1.60463e-05
☑	trh-PA	Dmel	47.7506	1.63164e-05
☑	trh-PB	Dmel	47.7506	1.70115e-05
☑	trh-PC	Dmel	47.7506	1.75888e-05
☑	trh-PD	Dmel	47.7506	1.77362e-05
☑	Clk-PH	Dmel	47.7506	1.78848e-05
☑	Clk-PG	Dmel	47.7506	1.78848e-05
☑	trh-PF	Dmel	47.7506	1.83381e-05
☑	tgo-PB	Dmel	46.595	3.98431e-05
☑	tgo-PA	Dmel	46.595	3.98431e-05
☑	sima-PD	Dmel	45.0542	0.000132482

Table S8. Taxa used for the phylogenetic analyses with their accession numbers in Flybase or OrthoDB

Gene groups for phylogenetic analyses	Coding Sequence
aristaless-apterous-BarH1-clawless-Lim1	al_Dmel_Q06453 al_Anopheles_gambiae_A0A1S4GWX6 al_Tribolium_castaneum_A0A139WH33 al_Strigamia_maritima_T1IYK9 al_C_elegans_Q21836 al_Rattus_norvegicus_A6YP62 al_Danio_rerio_B3DKI9 al_Human_Q96QS3 al_Mus_musculus_O35085 al_Xenopus_tropicalis_A0A6I8S3E9 ap_Dmel_E1JGX9 ap_Human_P50458 ap_Rattus_norvegicus_P36198 ap_Mus_musculus_Q9Z0S2 ap_Xenopus_tropicalis_A0A6I8QAN8 ap_Danio_rerio_B0R107 ap_C_elegans_G5EE86 ap_Anopheles_gambiae_A0A1S4GZT4 ap_Stegodyphus_mimosarum_A0A087T3Z4 ap_Strigamia_maritima_T1J7L2 ap_Tribolium_castaneum_C0KZ21 barh1_Dmel_Q24255 barh1_Anopheles_gambiae_A7UTE6 barh1_C_elegans_Q22909 barh1_Danio_rerio_Q53B63 cll_Dmel_Q7KS72 cll_Anopheles_gambiae_Q7PQE6 cll_Tribolium_castaneum_D6WZY0 cll_Stegodyphus_mimosarum_A0A087SVI5 cll_Strigamia_maritima_T1JC39 cll_Danio_rerio_Q8JI11 cll_Xenopus_tropicalis_F6TEU6 cll_Mus_musculus_O55144 cll_Human_O43711 cll_Rattus_norvegicus_D4A270 lim1_Dmel_Q9V472 lim1_Human_P48742 lim1_Rattus_norvegicus_P63007 lim1_Mus_musculus_P63006 lim1_Xenopus_tropicalis_A4QNI6 lim1_Danio_rerio_Q90476 lim1_C_elegans_P20154 lim1_Anopheles_gambiae_Q7QHD1 lim1_Stegodyphus_mimosarum_A0A087TMA9 lim1_Strigamia_maritima_T1J2T7
rotund-glass	rn_Dmel_Q9VI93 rn_Human_Q5T0B9 rn_Rattus_novergicus_D4A633 rn_Mus_musculus_B1ASA5 rn_Xenopus_tropicalis_Q0V9P9 rn_Danio_rerio_Q1LXQ0 rn_C_elegans_G5EGB2 rn_Anopheles_gambiae_A0A1S4GE00 rn_Stegodyphus_mimosarum_A0A087V104 rn_Bombyx_mori_A0A0C5AMJ7 gl_Dmel_P13360 gl_Human_Q96JB3 gl_Rattus_novergicus_D4A9X7 gl_Mus_musculus_Q07230 gl_Xenopus_tropicalis_A0A6I8Q066 gl_Danio_rerio_A0A8M1QLN4 gl_C_elegans_Q966L8 gl_Anopheles_gambiae_A0A1S4GKN6 gl_Tribolium_castaneum_Q7Z1F3 gl_Aedes_aegypti_A0A6I8U353

spineless-clock	ss_Dmel_E1JIM6 ss_Human_P35869 ss_Rattus_norvegicus_P41738 ss_Mus_musculus_Q8R4S5 ss_Xenopus_tropicalis_F7DNN6 ss_Danio_rerio_Q4U3K9 ss_C_elegans_O44712 ss_Anopheles_gambiae_Q7PM78 ss_Tetranychus_urticae_T1JYU4 ss_Strigamia_maritima_T1IKB1 clk_Dmel_O61735 clk_Human_Q99743 clk_Rattus_norvegicus_F1MAG2 clk_Mus_musculus_P97460 clk_Danio_rerio_Q8JIG3 clk_Xenopus_tropicalis_A0A6I8S1B9 clk_Anopheles_gambiae_Q7Q6R8 clk_Tribolium_castaneum_A9XCF0 clk_Aedes_aegypti_A0A6I8U2E9 clk_Rhodnius_prolixus_T1HDJ0