

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., $I - 1^{st}$ 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., $I - 1^{st}$ 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).



spineless 🚺 rotund

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., $I - 1^{st}$ 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

T	Γ able S1. Amino acid sequences of <i>Drosophila melanogaster</i> distal limb patterning genes used for build
pi	profile HMMs
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pi	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
	TCGCTTCAGCCGGGAGTTTGGATGATGATGAAGAGTCCTTCGTCGATGACGACTCGGGAGGACTCTGCGTCGTTC
	CAGAGACGAGCTAGCGAATGCGAATCCACCTGACCGAGGCGCGCATCCAAGTCTGGTTCCAGAATCGTCGT
	GCGAAATGGCGCAAGACCGAAAAGTCCTCCGCACCACATCCGATTTCGGGTGTCGAGCCCAGCCAG
	TCCAGTCCTTCAACACCCACCCATCCCAACCAGCAACTGTTCCTTCTCCAAAGGTCACACCGACCCCT
	TCCTGCAGTCACCGCACGGTCCGTCATCCGCAGACTACAACGTCCGGATGAACCCCGGATGGCCGCTCATC
	CCGCCGTCCAATAAATACAGTCGCAGCAGTTTGACGCAGAATTTCTACCCGGAACAAGCAGCAGCAGCCG
	CAGCAGCAGCAGCCATGGCCGCCACTACCAACATGTGGACACCAACGCTGGCTCCAACAAAGGCCGTCAA
	CGCATCATCGGCGAGTCCGGCGTCCGGCGGCGCGCGCGGCGGCGGCGGCGGCGG
	GTCAGTTGACCGGTCCCAGCGCGACTGCTGCTCCGGTGGACCGGGCGTGACTGCTGACGCGATGCAG
	AAATACGGAGCGTTTCGATCGATCGCCAGGAATGACGGAGGTGGAGGTGGGCGCTGA
clawless	ATGATGGAGAACCCTCCGGCACGCAGTGTCTTCAAGGCACCCTCCTCCAGGTCGCCTGTTGCGGAGAAACC
	TCTGAAAAAGCGTACTCCCTTCAGTATCGACAGTATTCTCAGCACAGATACGGACACTTCGCCGAAGGAAG
	AGTGCTTCTCGCCGAGTTTATCCGAGACAAAATGCAGTAACAACGAGAATATCCACGGGCGATGGATG
	TATGCGGCGGCGGCGGCGGCTGCAACGACGGCCATGTATTCCTCATCGGGCTATTACTCGTCCCCGCCGA
	CGCCTATAATTACGGATCGATGGTCAATTCACACGTCGTCAAGGTGCCCGCGCGCG
	GTCGGCATGTCTGCCTACCAGTGGATGGATCCCCGCCCGACGACTTTTGACAAGGGAAATGGGCATCCCTA
	CCAGAATAGAACCCCTCCCAAACGGAAGAAGCCTCGCACTTCCTTC
	AGAAACGCTTTCACAGACAAAAATATCTAGCGTCGGCGGAGCGAGC
	GACGGATGCTCAGGTCAAAACTTGGTTTCAAAACCGACGGACAAAACACAGGCGGCAAACCAACGAAGA
	GCGGGAAGCGGACCGACAGGCCGCCAATCGGATGCTTTTGTCACAGCTGGCCGAAGTGACCAAGACCAGC
	GGAGCGTATGACAGCACCGACGCGTTATGCCTTAATAATGCTTCCCTTCACGCTCTTCACAATCTCCGACCG
	GCGAAACAAGCCCCCGAGGAGAGGACGACGATGATGACGACCAACAACCACCGGCCAGGGCCCCGACGACGACGA
	ATGCACTATCCGTCTAA
Liml	ATGCCTGTCCGCCACCGTTATCTTCAGCAACATCCGCAGCCGCCGCCACCATCATCCTCGTCCGGGCC
2000	GGAAGATTTCGAGAGCCACAACAACAGGAGGATTGTCTCGGGGAAGATGCAAAATCCCGGTGGGATGTAT
	GATAAGTGTCACGGCTGTGGAATGGTGATTTTGGATCCTTTTATCATGGCCATCGCCACTCCGACGGCCAG
	TCAGGTTTGGCATGCCGATTGTTGCGCTGTTGTGAGTGCAAGTGCCCACTTCAGGAGCGGTGTTTCTGCAA
	IGGAGGGCGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	GCATGETCGAAACAGCTGTCCACCGGGAAGAAGGCGGGGAATTTCATTGAAATOTTTAATTGTCAACG
	ACGATTATGTCACCAGCAAACACGCCAAAGCCGCCTCCTCCACACTGCAATCATTTTCCTGCAAAGCAGAG
	CAATCGTCGCCGGGAGCTGCTACCTCACCCTGTCTGCTCGGCGGAGGCGGTCGCGACCTGTCCAGAAGCGA
	GTCTCTCAAACCTGACCAACACGATTGTTTATCAACAACGGGTCCTTCAGACGTGACGAACGGTGCGCCGA
	TGAATAACAACAACAGTAATACCGCAACCCCAATTATCGGCAGCGGGATCGGCCGGGCAATGGACGGTCA
	CCTTCTCCATCGCGGAGAGGATTGCGAGGAGACGACGACGAGGAGGAGGATGCCATGAAGTGCCAGCGAG
	AGCAGGTEGGCACGTGCGGCGTCGGATCGGGATCGGGATGGTGTGGGACAGGGGAAGGAGGGGGAAGGGGGAAGAGCGCGACA
	CACGCGCCATATCCGCGACCAGTTGTCGCAGGAAACCGGTCTCACTATGCGAGTCATTCAGGTTGGCTTC
	AAAATCGCCGAAGCAAAGAACGCCGGATGAAACAGCAGAACATCATGGGGCCAGGTCGGCGATGCAATA
	TGTTTCGATCGCGTCGCTCGGGAGGACGATCGCTGCGGGAGTTCGACGGTGATTCCGGTGATATGGGAGTT
	CAGGGTCCACCCGGATTCGCTTATTTTCCAGATGGTCCCGGCAATCACGGCATGGACTTCTTTCCCGGACA
	GGTTTCTCCCCACGGCGCCCACATGCCGGGCCACTCGGACATCCTCCGGGTATTTTTGAATTCGCCCACTA
	IUGAUUGUUGUAGAAUGUGGUGGAAGUAGUUGUUATGUATG
	CAUGGCA I GCUUGGCAALATICAA I CAUUUGGCA I GGUIGGUCACI I I CUGUCAGGAGA I GUIGI CAUGAG GTTCAACTCCACA A ACCAUCATICAA I CAUUUGGCA I GGUIGGUCACCI A COGCUATOCTGCTTTTCACA COCU
	CTCCTCCATCCCGGCGCAACGGCATCGGCAGGCAGCCGGTCCTGGCGGGATCAACGCAACCCATCCCGT
	CTGGCAGAGCATGACGATGGCCCCAATAG
anterous	ATGCCGATTCTGGAGCGGTCTAACAGCGGTCATAATGAGCAGGAGGAAGCCATCAATTCCCATGTTACCGC
apierous	ACACGGGGAAGAGCCATCGTGTCTGCAGCTTGACCACGACCACGACCACGGACTATTACCCGGAAACGAG
	GACGTGGCCCATCCCCAACACCATGTCCAACACCCTGCTGCGGGATACTTCCCCGCGCTAATCTGCTCCGG
	CTGTCGGAATGGGATATCGGAGCAGTACTTCTTATCTGTTTCCAATTCGCAAGACTTTTATCACTGCCACTG
	TCTAAAGTGCAGTGTTTGTAGTGTAACTCTAGACCGACAAATGATCTGCTATTACAAGGACGGGATGATTC
	IIIGIAAAGAGGACTATTACAAGTACAAGAGTCGAAGGCIGAGCCCCGAAGGTTATCAAAATAGCCGCTG
	ULAUGU IGUAAU IAUUUA IUUGAGUGAGUGAUGAGI IIGIGA IGUGUGI AUGUGAGI IIGIU IIUUAUGUGACIUU CGTGTTTCCGCTGCCTGGCCTGCACCGCGACACTCCACACGGGGGCATGAGTTTACGATGCGTGACGGC
	GCCATCCTCTGTCAACGTCATTTCCATCCCGCTGCAGCCGCTCGCT
	TGTCGGATCCTCGTCAAACCCCGCAAGTGACACTCTATCCTCGACAGCAGCACTACTGCCCCCACACAGCA

	CCATCCTCATGGCCGATCATGGCGCCCCGGTCTCGCCGCACTTTGCCCAACTTCAGAACCGCATCGTCCCGC
	GACATGACGACGGTGGTGACGGGAACGACGGTCGGAAAGACCTTTTCCACCATCACCACCAGACATC
	AGCATCATCCTCCGCGTCGTCGCGTATGAAAAGCCGGATTCGACGGACCAAGCGAAACTTGATTTCCTTCG
	ACGACGGGAGTGGCGGTGTAATTAACCAGCGCCACACTGCGGGGGGGG
	ACACGGIGAICCGGIGGGCCAGGCGGAGCIGIIGCAGCAGCAGCAAGCA
	GAGGAGIGHACCACCACHELECCAGIGCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	GCGCACTCACGCACTCACGGACTCATCCTCACCGCACACACA
	ATGAGAACCAGCTTCAAGCACCAACAACTTCGCTCCATGAAACAGTACCTTCGGTATCAATCA
	CGCAAAGGACCTCAAGCAGCTTGCACAGAAGACGGGCCTGACGAAGAGAGTCCTTCAGGTATGGTTCCAG
	AATGCCCGTGCAAAATATCGCCGTAGTCTCCTCAAGCAGGACCCCAATCGGGTGCTGGAAGCTAGCCCGAT
	CGCCAAAGCCCAGTCCAACTCCCCATCACCACGACCGGATTACGGTTTGCCGGACAATGCTTCAGCAAAGC
	AACACGACCTTAATCATTACCCAATGTCGAACGGAAGCAATTCTCAAGACAATGGCGCTGAGTACTACTAA
BarH1	AIGGATAGGGATAACGGGGAGGAGGGAGCAGTAGCAGTCGCCGTTGGATATGACTGCGCATCCTGCGCATC
	CCTGTCCATGCGACACTCCTCCTCATCAAGGACATCCTCAGTCAATCCGAGGCAAGCAGGAGGAG
	GTCGCAGTGGAGCAGGAGACGGAATGGGTGCTGGCACATTCCGCCCGGGAGTCAGGAGGAGGAGGAGCAG
	CGACGTCCAGAGTGAACTTTCCGATACAGAAAGCAAAGATGACCACGACGGGGCGGATTCAACCGCGACC
	AGCCGCAATAGTCCGAAAAGGCAAGAAATCCCCGGAAAGCCAGGACAGCGTTTACGGACAGCCAGTTACAGA
	CGCTGGAGAAACGCTTCGAGCGACAGAAATATCTCAGCGTACAGGACCGGATGGAATTAGCGGCCAGTTT
	GAGCCTGTCCGACGCGCAAGTTAAATGCTGGTTCCAAAATCGCCGAACCAAATGGAAGCGTCAGACGTCG
	GIGACGAICGAGIIGCIGGCCGAAGCGGCCAATIACGCGGCCAIGCAGCGGAIGCIGCAGIACIGGI
	ATGCAGGAGCTGTACTACCGAAGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCGAGTGGTGGACGAGTGG
	TCGGCGGACCAGGCGGCATACCGCAGAGCCGATGAATCCGGCGACGACGCGATTCTGGCCGACCCAGC
	CAACATGACCTTCCCCACGGGCAATTCCGCGCCCAATGTTCATCTCATCGCATCATCAACAGCGGTCGCCA
	CTCCCGCTGCTCCGGCTAGTCCGCCGTCACCGGTCCACCGGGATTAAAACCGGCAGCTCAATCAGACGATGGC
	ACCGATTAA
otund	ATGGCTGGAGCCCATGAGACCGCGGATGAGCTGAATCTAATGCAGCAGCAGCACCCGCAACGATTCACTC
	CCTGGAACCAAAACGCCATGGACTTCCAGAAGATTTTGAACCAGCAAGCGGCGGCCAACAGCCTCAATGG
	TGGTA ACCCCCA TCATCATCACCGA GCATCATGTCTGGCTTCATGCCCAACATCGGTGGACATA
	ACTTGCCAAAAACCCTCAGCGGACGCCAAATTCCCATGCAACATCAGGTGTTGGAGTCAAAGGC
	CGAGTTCCAGATGCACAATCAGTCGCACATGCGCGAACCCAAGCCCTACCGATGCTCGCAGTGTCCCAAAT
	CCTTTGCCAATTCCTCCTATCTCCCCAGCATATGCGCATTCATCTCGGCATTAAGCCCTACCACTGTGACA
	TCTGCAAGAAAAAGTTCACCCAACTCTCCCATCTGCAGCAGCACCATCCGCACCCATACAGGTGATAAGCCG
	TACCGTTGCCCTCAACCGACTTGCACAAAGGCCTTCTCCCAGTTGAGCAACCTGCAGAGTCATTCTCGGTGT
	CATCAACAGGACAAGCCCTTCAAATGCCAATCCTGTTACAAGTGTTTTTACGACGAACAATCTCTGCTGGA
	TCTCA ACCATATTA A A ACTGCCACACA I GOCCAACACAACAACAACAACAACAACAACAACAACAACAA
	TGAGCCAGGAGGATCTGTTCATGTACAGGGGGGGGCTATTACAGCGCCGCCAACTACGGTAACGCCCACCAC
	GCTGTTCATCCTTACGGCGCGGGCAGACATCTCCCGTTAACTATGACACCAGTAATAAGAACTCGGGATC
	AGCCTTCTCCATTCTTTCGGGAAGCAGCGGTCGGAACGTGATGGCTCATCCTCATGCGCATAACTACTACG
	ACTCGGCATTTGGATCTGGAGCGATGAAGAGTCAGAATGTCCTTTCTGACTCGATGGCCACTTCCAAGAAC
	GGTCCAATTTCGGTGGATCACTTTGCCGGTTTCACCAATCATCAGATGCCCGCTATGCGTAATCACTTTTCC
	GCAGGATTCGTCGGCAATAATGGAATGCCGACCATGCTGATGGGAGGAGGAGGAGGCGGCAGTACCGCTT
• 1	
spineless	
	CAACCCTAGCAAGCGTCACCGTGAACTCCGAACTAGAACGGATCGCCAGTTGCTTCCATTG
	AAGCGAATATCCTTTCCAAACTGGACAAGCTCTCCATACTGCGTCTTAGCGTTAGTTA
	AGTTATTTTCATGCCATTCAATTACGAGAGCAGACATACGGCGGATACGACGGTCCCGGTGGACATAAAAC
	GAGTGCCGATCATTTCCACGCCGATCCATCACTGACACGCACCGATTCAGTTCTCAAGGCATTGAATGGAT
	TTGTCCTGGTGTTGACCGTTCAAGGCGAAGTCTTTTTTGCTTCAAGCAACATCGAGGAGTTTTTAGGCTTCC
	ATCAGTCGGATGTTATTCATCAGAGCGGTTTACGAGCTGATTCACTCAGAGGACCGGGTCGAGCTGCAGAAG
	CACTTCCGGTTTTCTGCGACTGGAAATTCGCGGCCGCATCGGACTCTTCACCGCCAGAACTTCCACTCCA
	CCGGCGAGGCGCCGCCGGGTCTGTTGGCAATCTGCACGCCCTTCGGACCGGCCACACTGCCGGACAACCTG
	CCCAAGGAGTCCGTCTTCAAAAGTAAACTCAAGCTCGACCTGACCTATCATCAACATCGACACCAAAGGCA
	AGGATTTGTTGGGATGGGGTGGGGAAGAAAGTGGTTGTCGCTCCTTCTACAACGCCCTTCATCCAGACGAC
	GTTCTCTACGCAGCCAGTGCACACCGTGAACTGAGTAAGACAAATTCGTGTGTCATGTACGCTCATCGTAT
	GGCGCGGAAGGTCGTCCCGGGGACGGCGCTACAATGGCAATGGGTCCAGACGACCATGAAAATCATTCCG
	AAAAACGGAAAAACCTGACCATGTCTCCGCTGCTCACCGTCGGCGACGAAGAAGGGAAAGATCTGA
	IUAUAAAGCGIGUGIUUATUAUUAAATTATGCGACUTGGACTUTGACGCATCACTGGCCCTGGCCAACAGC
	₲₶₶₲₮₮₶₲₲₳₶₲₶₳₲₮₲₶₶₲₮₶₳₶₲₲₳₲₮₲₲₳₲₽₶₲₶₶₶₶₶₶₲₳₶₳₲₮₳₶₮₶₶₶₳₶₳₳₳₲ ₢₢₢₢₢₳₳₳₢₢₲₢₢₢₳₳₳₳₳₲₢₲₳₢₢₮₸₢₳₢₢₳₲₢₢₲₢₢₼₳₮₢₺₢₢₢₳₲₳₢₢₢₢₳₢₲₮₢₡₮₢₢₮₢₢₮₢₡
	ACCAGTAACAACATCAATAATACTTCTCACTACTCCGCCCAACCATCCTCCTTATCCAGCGGTTCCAGCTCC

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

Gene	Amino Acid Sequence
aristaless	MVGHDERPKKENDCVVPERISPSIASAGSLDDKESFVDDDSEDSASFGAGGGAGARSGAGLSSKQRRYRTTFTAFQ
	$\label{eq:lecost} LQELEKCFGKTHYPDIFTRDELAMRIHLTEARIQVWFQNRRAKWRKTEKSSAPHPISGVEPSPAVQSFNTTHPIPNS$
	NCSFSKGHTDPFLQSPHGPSSADYNVRMNPGWPLIPPSNKYSRSSLTQNFYPEQAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	WLQQMAVNSLLHRDVPPSWTTQTSAGSAVSPAHHLTFHPEFRPFFHPHPNGTTTAGQLTGPSATAAQWTGPGVT
	ADAMQKYGAFRSIARNDGGGGGR
clawless	${\tt MMENPPARSVFKAPSSRSPVAEKPLKKRTPFSIDSILSTDTDTSPKEECFSPSLSETKCSNNENIHTAMDAYAAAAA$
	AATTAMYSSSGYYSSPADAYNYGSMVNSHVVKVPAQRVQQQQQQHLAPCGGVSPHPALFGIGHHVGMSAYQ
	WMDPARRLLTRRIGHPYQNRTPPKRKKPRTSFTRIQICELEKRFHRQKYLASAERASLAKSLKMTDAQVKTWFQN
	RRTKHRRQTNEEREADRQAANRMLLSQLAEVTKTSGAYDSTDALCLNNASLHALHNLRPWVNAGDGGGSLSNN
	NHHPHIITCPQTNSSSPNNNNTNNNCSSRCSSSSETSHEEEDRDDDDNRSEVSSDEDALSV
Liml	MPVRHRYLQQHPQPPPPSSSSGPEDFESHNNRRIVSGKMQNPGGMYDKCHGCGMVILDPFIMAIATPTASQVWH
	eq:addlrcceckcplqercfcnggrffcredyfrafqqpckgcgvgidptelvrqtqrgnfhlkcfictacrkqlstg
	${\tt EECYNIGDCEFNCKDDYVTSKHAKAASSTLQSFSCKAEQSSPGAATSPCLLGGGGRDLSRSESLKPDQHDCLSTTG}$
	$\label{eq:source} PSDVTNGAPMNNNNSNTATPIIGSGIGRAMDGHLLHRGEDCEDDDEEDEDAMKCSESGSHVPASDRDCCDKDGK$
	${\it SVNGDNTSSIDESEPRNGNDENVSTKRRGPRTTIKAKQLELLKNAFAQTPKPTRHIRDQLSQETGLTMRVIQVWFQ}$
	NRRSKERRMKQQNIMGPGRRCNMFRSRRSGGRSLREFDGDSGDMGVQGPPGFAYFPDGPGNHGMDFFPGQVSPH
	${\tt GGPHAGPLGHPPGIFEFAHYRPPQNAAEAAAMQAHFNEMSPNAHGMPGNINHPGMDGHFRQEMLSQSSTPERTL}$
	NSLTPDGYGHPAFDTLPLHPGGNGGIGPVPGGMNGSNSPVWQSMTMAQ
apterous	MPILERSNSGHNEQEEAINSHVTAHGEEPSCLQLDHDHDHGLLPGNEDVAHPQHHVQHPAAGYFPALICSGCRNGI
1	SEQYFLSVSNSQDFYHCHCLKCSVCSVTLDRQMICYYKDGMILCKEDYYKYKSRRLSPEGYQNSRCHGCNYPIRA
	DEFVMRVREFVFHVPCFRCLACTATLHTGDEFTMRDDGAILCQRHFHPAAAVAHVGGGGGGGGVGSSSNPASDTL
	${\tt SSTAALLPPHSSHDSFSAASSDIPTTTATAASLRLPILMADHGAPVSPHFAQLQNRIVPRHDDGGDGNDGRKDLFHH}$
	${\tt HHHQTSASSSASSRMKSRIRRTKRNLISFDDGSGGVINQRHTAGGLNGSGGELHGDPVGQAELLQQRQAAAAMQL}$
	$\label{eq:constraint} EQQCYHHFSSAASPNAALPVQTAQQSSFTSSSEESSPSRLASSSPGLQMAHLTHSITDSSSPNNQQHQRTKRMRTSF$
	KHQQLRSMKQYFGINHNPDAKDLKQLAQKTGLTKRVLQVWFQNARAKYRRSLLKQDPNRVLEASPIAKAQSNSP
	SPRPDYGLPDNASAKQHDLNHYPMSNGSNSQDNGAEYY
BarH1	${\tt MDRDNGERSSSKSPLDMTAHPAHPQPLTSPSITSHVKVTSSNCAPQNLSMRHSFLIKDILSQVNPRQQESSRSGAGD}$
	GMGAGTFPPGSQEDGDSDVQSELSDTESKDDHDGADSTATSRNSPKGKKSRKARTAFTDSQLQTLEKRFERQKYL
	SVQDRMELAASLSLSDAQVKCWFQNRRTKWKRQTSVTIELLAEATGNYAAMQRMLQYWSCGGPAAMLAAPAA
	AYPAQNQLFQMQELYYRSLQQQQQQQQQGGRVVGGPGGIPQMPMNPVTTRFWPTPANMTFPTGNSAPNVHLI
	ASSTAVATPAAPASPPSRSTGIKTAAQSDDGTD
rotund	MAGAHETADELNLMQQQHPQRFTPWNQNAMDFQKILNQQAAANSLNGHAHSLQGKGPNFDMVSMEMDETGG
	GGVGAVSDLYGVQQATRAIQSVMVTPHHHHSSIMSGFMHQHHAGGHNLPRTLSGRKFPCKMCNQVLESKAEFQ
	MHNQSHMREPKPYRCSQCPKSFANSSYLSQHMRIHLGIKPYHCDUCKKKF1QLSHLQQHRIHIGDKPYRCPQP1C
	I KAFSQLSNLQSHSRCHQQDKPFRCQSC Y KCF Y DEQSLLDHIPKHRDSKHLK I HICICCCGKS Y I QE I Y LLRHMAK
	HNDKNEKQQKMSLNHIK IAI VDPY WPKQEMEGAHKMSQEDLIM Y SGGY Y SAAN Y GNAHHA VHPY GAGQISPV
	NY DISNKNSGSAFSILSGSSGKNVMAHPHAHNY YDSAFGSGAMKSQNVLSDSMAISKNGPISVDHFAGFINHQM
. 1	PAMKNHFSAUF VGNNGMP I MLMGGGGDGS I ASGMKKEHSNHNSSSKPGGK I
spineless	MYA I KKKKKSLKUSSSKICLSKSA YD I SHHUNSUUUUUGUNSSELKSNYSKKHKEKLNSELEKIASLLPPEANILSK I DVI SII DI SVSVI DIVSVEII A IO DEOLYD CONOCOCUWT SA DIWEII A DDSI TEDSVI V A I NCEVI W TVOCEVE
	LDKLSILKLSVSYLKIKSYFHAIQLKEQI I GGY DGPGGHKI SADHFHADPSLIKI DSVLKALNGYLVLI VQGEVF
	FASSNIEEFLGFRUSDVIRUSV I ELINSEDKVELUKULS WLGSPSAAAAHHPUSSKIINPHDAFSSDINPUHLEKSLI AK
	FRELEDINI SUFLELEIKUKIUVEHUUNFHSAUEAPPULLAICI PPUPA LEPDNEKESVFKSKLKLDETHINIDI KUKD LI CWCCEEECCECEVIA LUDDDVI VA AS AUDEL SVENSCVAWA UDA AD VVVDCTAT OVODVOTTAVUDDVIC
	LLOW OUDEDOUCRST I NALHEPD VLI AASAHKELSKI NSCYM I AHRMARKY V POTALQWQW VQI I MKHIPKNO VDNUVSAAUDDI SDECKDI MYZDASITVI ODI DCDASI ATANSAVSED SACUSUDS SOTVEDIY ADVDDIV DD
	KI DIAYAAANA ESDELOKDEN I KKASII KEEDEESDAALAANSA YSEKSAUIO YEDSESEI Y IFI KAPKFYKKK SDA AMUDDDYSSSSSTSINIINIYSEVS A DOSSI SGASSTDDDY GEGTENIITA DNGAGEIA A VSEDVIITEOSI IVG AG
	σε αλιτικώς εισσόσι συντινίνι τοπ ει σαγέσομοσοσι κκκικός σε τείν γι εακινόπομεία Α΄ τόσε τη Πεσόδια γι αγγ Ντυσταίει στα νέοςς εί ίρυς σουνιμότες α σε ύς το αι δυςσέχει ανας εισχνισκός τι εί το ευντί για αι αι νός αι α
	IN TH TATE IT A VEGOSIFT SOUTHING IS ANT ISTORE VSDSVES VASIIO VNOSTEEDKSTDET AAAAT (SSAAD) GEOGONT KNVVCGMDTVDENVVNTDESSEULISSA TVA AAANGWAASSEUDOSSU VWNNGSODDMOTG
	OLI SUUDI LENATI I KUMIDI I ESINYI INI DI ISOSII III IISOA I KAAAAAANG WIMASSIIIKUS VEV WINDONSKEDMSEU ETDETTETTESEVVOOGA ODVOA EETTA DESCED HANNIOVMSAOD SUDA ENNEVTNIGDDESCA SOGGI WAA ADI UOQU

Gene	 BLAST H	it Summ	ary	
aristaless	BLAST Hit Summary			
un istatess	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
				0 10017 10
	Ptx1-PC	Dmel	92.0485	8.43247e-19
clawless	Ptx1-PC BLAST Hit Summary	Dmel	92.0485	8.43247e-19
clawless	PIX1-PC BLAST Hit Summary Description	Species	92.0485 Score	E value
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA	Species Dmel	92.0485 Score 199.904	E value 2.63135e-51
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA B-H1-PA B-H1-PA	Species Dmel Dmel	92.0485 Score 199.904 81.6481	E value 2.63135e-51 1.06197e-15
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE	Dmel Species Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777	E value 2.63135e-51 1.06197e-15 2.15834e-15
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PE Hmx-PC	Dmel Species Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15
clawless	Pbx1-PC BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC Hmx-PD	Dmel Species Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA	Dmel Species Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15 2.9636e-15
clawless	Ptx1-PC Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD	Dmel Species Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15 2.9636e-15 8.84131e-15
clawless	Ptx1-PC BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.75834e-15 2.7636e-15 2.9636e-15 8.84131e-15 8.84131e-15
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PC NK7.1-PC NK7.1-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15 2.9636e-15 8.84131e-15 8.84131e-15 8.84131e-15
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PB NK7.1-PB NK7.1-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15 2.72636e-15 8.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PB NK7.1-PA NK7.1-PA B-H2-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.72636e-15 2.9636e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.21796e-15
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PC NK7.1-PC NK7.1-PA B-H2-PA B-H2-PA bap-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666	8.432476-19 E value 2.631356-51 1.061976-15 2.158346-15 2.158346-15 2.158346-15 8.841316-15 8.841316-15 8.841316-15 9.217996-15 9.217996-15
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PD NK7.1-PB NK7.1-PA B-H2-PA bap-PA Ims-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.76536e-15 2.9636e-15 2.84131e-15 8.84131e-15 8.84131e-15 9.2952e-15 1.03601e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC Ibe-PA NK7.1-PD NK7.1-PB NK7.1-PB NK7.1-PA B-H2-PA bap-PA Ims-PC Ims-PC Ims-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.72636e-15 2.9636e-15 8.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.21796e-15 9.21796e-15 9.21796e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PA B-H2-PA B-H2-PA Dap-PA Ims-PE Ims-PB Dr-PA	Species Dmei Dmei Dmei Dmei Dmei Dmei Dmei Dmei	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666	8.432476-19 E value 2.631356-51 1.061976-15 2.158346-15 2.158346-15 2.158346-15 8.841316-15 8.841316-15 8.841316-15 9.217966-15 9.217966-15 9.219526-15 1.036016-14 1.116816-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PA Ims-PA Ims-PA Dap-PA Ims-PC Ims-PA Dap-PA Ims-PA Dr-PA Dr-PA bsh-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.1814 78.1814	8.432476-19 E value 2.631356-51 1.061976-15 2.158346-15 2.158346-15 2.158346-15 2.84336-15 8.841316-15 8.841316-15 8.841316-15 9.217966-15 9.217966-15 9.217966-15 1.036016-14 1.036016-14 1.265716-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PD NK7.1-PA B-H2-PA Ims-PA Ims-PC Ims-PC Description NK7.1-PD NK7.1-PD NK7.1-PA B-H2-PA Ims-PC Ims-PA Dr-PA Desh-PC Ims-PE Dr-PA Dr-PA Ims-PE	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.8666 78.8666 78.8666 78.81814 78.1814 78.1814	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.72636e-15 2.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.2952e-15 1.03601e-14 1.11681e-14 1.26571e-14 1.26571e-14
clawless	Pbt1-PC Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PB NK7.1-PB NK7.1-PB Ibe-PA Ibe-PA NK7.1-PB Ims-PC Ims-PC Ims-PC Ims-PC Ims-PC Ims-PC Ims-PC Ims-PC Ims-PC Ims-PB Dr-PA Ibi-PA Ibi-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.1814 78.1814 77.411 77.411	E value E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.72636e-15 2.9636e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.21796e-15 9.21796e-15 9.21796e-15 9.21796e-14 1.03601e-14 1.1681e-14 1.26571e-14 2.2571e-14 2.17706e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PC NK7.1-PC NK7.1-PA B-H2-PA bap-PA Ims-PE Ims-PC bap-PA Ims-PE Dr-PA bah-PC bah-PC bah-PB IbI-PA B-H2-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.814 78.1814 78.1814 77.411 77.411 77.411	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.15834e-15 2.2636e-15 2.2636e-15 2.2636e-15 8.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.21796e-15 9.21796e-15 9.2571e-14 1.26571e-14 1.26571e-14 1.26571e-14 1.26571e-14 1.26271e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PA Ims-PA Ims-PC Ims-PC Ims-PA Dr-PA Dr-PA B-H2-PA B-H2-PA B-H2-PA B-H2-PA B-PA Ims-PC Ims-PB Dr-PA B-H2-PA B-H2-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.8566 78.8566 78.8566 78.8566 78.1814 78.1814 78.1814 77.411 77.411 77.411 76.2554	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.15834e-15 2.15834e-15 2.84313e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.247296e-15 9.252e-15 1.03601e-14 1.03601e-14 1.26571e-14 1.26571e-14 2.42649e-14 4.76972e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PD Ibe-PA NK7.1-PD NK7.1-PC NK7.1-PC NK7.1-PB NK7.1-PB NK7.1-PA B-H2-PA bap-PA Ims-PC Ims-PC Ims-PB Dr-PA bh-PC bsh-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.8566 78.8566 78.8144 78.1814 78.1814 77.411 76.2554 76.2554	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.72636e-15 2.834e-15 2.72636e-15 8.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.2952e-15 1.03601e-14 1.26571e-14 1.26571e-14 1.26571e-14 2.42649e-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PD NK7.1-PB NK7.1-PA B-H2-PA bap-PA Ims-PB Dr-PA bah-PB bh-PB bh-PB bh-PB bh-PA B-H2-PB pb-PB bh-PC pb-PB bh-PC bh-PC bh-PB bh-PB bh-PB bh-PB bh-PB bh-PB bh-PC pb-PB pb-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.8666 78.8666 78.8666 78.8666 78.8666 78.81814 77.411 77.411 77.411 77.411 77.411 77.411 77.412 76.2554 76.2554 76.2554	8.432476-19 E value 2.631356-51 1.061976-15 2.158346-15 2.158346-15 2.158346-15 2.158346-15 2.8341316-15 8.841316-15 8.841316-15 8.841316-15 9.29526-15 1.036016-14 1.16816-14 1.2657716-14 2.177066-14 2.47696-14 5.05666-14 5.05666-14 5.05666-14 5.05666-14
clawless	BLAST Hit Summary Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC NK7.1-PD NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PA bap-PA Ims-PC Ims-PC Jms-PB Dr-PA bah-PC bah-PA bh-PA B-H2-PB pb-PA pb-PA B-H2-PB pb-PA pb-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.8144 78.1814 78.1814 77.411 77.411 77.411 77.411 76.2554 76.2554 76.2554	8.432476-19 E value 2.631356-51 1.061976-15 2.158346-15 2.158346-15 2.158346-15 2.168346-15 2.8346-15 2.8346-15 8.841316-15 8.841316-15 8.841316-15 9.217906-15 9.217906-15 9.217906-15 9.25226-15 1.036016-14 1.036016-14 1.265716-14 2.177006-14 2.177006-14 2.177056-14 5.05667-14
clawless	Pbt1-PC Description C15-PA B-H1-PA Hmx-PE Hmx-PC Hmx-PC Hmx-PC NK7.1-PC NK7.1-PD NK7.1-PC NK7.1-PC NK7.1-PC NK7.1-PC NK7.1-PC De-PA bap-PA Ims-PC Ims-PC Ims-PA bab-PA Ims-PC Ims-PC Ims-PB Dr-PA bsh-PC bsh-PC bsh-PB Ibl-PA B-H2-PB Dr-PA Dr-PA B-H2-PB Dr-PA B-H2-PB Dr-PA B-H2-PB Dr-PA B-H2-PB Dr-PC Dr-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	92.0485 Score 199.904 81.6481 80.8777 80.8777 80.4925 80.1073 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.1814 78.1814 78.1814 77.411 77.411 76.2554 76.2554 76.2554 76.2554 76.2554 76.2554	E value 2.63135e-51 1.06197e-15 2.15834e-15 2.15834e-15 2.15834e-5 2.215834e-5 2.215834e-15 2.843131e-15 8.84131e-15 8.84131e-15 8.84131e-15 8.84131e-15 9.2952e-15 1.03601e-14 1.03601e-14 1.03601e-14 1.26571e-14 2.2571e-14 2.42649e-14 2.42649e-14 4.76972e-14 5.0566e-14 5

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

Limi		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	3.435828-18
		tup-PB	Dmel	90.1225	5.57444e-18
		Lmx1a-PC	Dmel	90.1225	6.21311e-18
		Lmx1a-PB	Dmel	90.1225	6.477798-18
		CG4328-PB	Dmei	81.6481	2.049946-15
			Dmel	70,8626	2.103/38-12
		Bx-FB Bx-PD	Dinei	70.0020	5.80032e-12
		BX-PC	Dmel	70.0922	7 172430.12
		BX-F C	Dillei	10.0322	7.172436-12
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	Dmei	90.5077	4.03204e-18
		LIM3-PB	Dmei	90.5077	4.03204e-18
		Lim3 PE	Dmel	90.3077	4.531646-16
		Lim3 PA	Dmel	90.3521	0.03300-10
			Dinei	87 8113	2 635300-17
			Dmol	97 9112	2.035356-17
		CG4328-PB	Dmel	82 0333	1.45820-15
		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
		67.1 B	1 5.110	00.0210	
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
		D-FIZ-PD	Dmel	130.272	1.02/968-32
		ims-PG	umei	91.0033	1.094210-18
		Ime_PR	Dmal		1.034218-10
		Ims-PB CG11085-PA	Dmel	90 5077	2 045860 19
		Ims-PB CG11085-PA NK7 1-PD	Dmel Dmel	90.5077	2.04586e-18
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC	Dmel Dmel Dmel	90.5077 87.4261 87.4261	2.04586e-18 1.82084e-17 1.82084e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PC	Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PB	Dmel Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261 87.4261	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Iba-DA	Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibe-PA DII-PB	Dmel Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.0409 85.8853	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibe-PA DI-PB DI-PB DI-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.0409 85.8853 85.5001	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibs-PA DII-PB DII-PA DII-PC	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.0409 85.8853 85.5001 85.5001	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.74812e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibe-PA DII-PB DII-PC bb-PC	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.8853 85.5001 85.5001	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.74812e-17 6.91917e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibe-PA DII-PB DII-PB DII-PC bsh-PC bsh-PB	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	90.5077 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.78131e-17 6.91917e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PB NK7.1-PB NK7.1-PA Ibe-PA DII-PA DII-PA DII-PA DII-PC bsh-PC bsh-PB slou-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4469 85.8653 85.5001 85.5001 85.5001 85.5001	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.74812e-17 6.91917e-17 6.91917e-17 9.90537e-17
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibs-PA DII-PB DII-PC bs-PC bs-PA slou-PB	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5003 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.51149 84.7297	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.74812e-17 6.74812e-17 6.91917e-17 9.90537e-17 1.20009e-16
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PA Ibe-PA DII-PB DII-PC bsh-PC bsh-PB slou-PA slou-PB C15-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.70000 85.70000 85.70000 85.700000 85.7000000000000000000000000000000000000	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 6.58131e-17 6.58131e-17 6.58131e-17 6.91917e-17 9.90537e-17 1.20009e-16 3.21222e-16
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB Ibe-PA DII-PB DII-PA DII-PC bsh-PC bsh-PB slou-PA Slou-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.302 85.301 85.302 85.30	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.58131e-17 6.58131re-17 9.90537e-17 1.20009e-16 3.21222e-16 4.12585e-16
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB Ibe-PA DII-PB DII-PC bsh-PC bsh-PC slou-PA slou-PB C15-PA exex-PA toe-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 84.7297 83.1889 82.8037	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 6.58131e-17 6.58131e-17 6.58131e-17 6.58131e-17 6.91917e-17 9.90537e-17 1.20009e-16 3.21222e-16 4.12585e-16
	V V	Ims-PB CG11085-PA NK7.1-PD NK7.1-PB NK7.1-PA Ibs-PA DII-PB DII-PC bs-PC bs-PA Slou-PB Slou-PA c15-PA exx-PA toe-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.2003 85.2003 82.8037 82.8037 82.0033 82.0033 82.0037 82.00577 82.00577 82.00577 82.00577 82.00577 82.00577 82.005	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.58131e-17 6.91917e-17 9.90537e-17 1.20009e-16 3.21222e-16 4.42761e-16 8.88974e-16
		Ims-PB CG11085-PA NK7.1-PD NK7.1-PC NK7.1-PB DII-PB DII-PA DII-PA DII-PA DII-PA C15-PA slou-PA Slou-PA C15-PA exxx-PA tos-PA Hmx-PE	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.3001 85.5001 85.3003 85.3005 85.3005 85.3005 85.3005 85.3005 85.3005 85.3005 85.	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43336e-17 6.58131e-17 6.58131e-17 6.58131e-17 6.51917e-17 6.51917e-17 9.90537e-17 1.2000e-16 3.21222e-16 4.12585e-16 4.42585e-16 8.88974e-16
	S S	Ims-PB CG11085-PA NK7.1-PD NK7.1-PB NK7.1-PB DII-PA DII-PA DII-PC bsh-PC bsh-PB Slou-PB C15-PA exxx-PA toe-PA Hmx-PE Hmx-PC Hmx-PC	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	91.5037 90.5077 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 87.4261 85.5001 85.7001 85.7001 85.7001 85.7001 85.7001 85.7001 85.7001 85.7001 85.7001 82.8037 82.8037 82.8033 82.0333 81.6481	2.04586e-18 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 1.82084e-17 2.43836e-17 5.80708e-17 6.58131e-17 6.58131e-17 6.58131e-17 9.90537e-17 1.20009e-16 3.21222e-16 4.44761e-16 8.88974e-16 8.88974e-16

rotund		BLAST Hit Summary						
rouna		Description	Species	Score	E value			
		m-PF	Dmel	303.138	3.87162e-82			
		m-PE	Dmel	302.753	5.2719e-82			
		rn-PG	Dmel	302.368	5.82708e-82			
		m-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			
		gI-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			
	BLAST Hit Summary							
snineless		BLAST Hit Summary						
spineless		BLAST Hit Summary Description	Species	Score	E value			
spineless		BLAST Hit Summary Description ss-PD	Species Dmel	Score 371.703	E value 1.41622e-102			
spineless		BLAST Hit Summary Description ss-PD ss-PC	Species Dmel Dmel	Score 371.703 371.703	E value 1.41622e-102 1.41622e-102			
spineless	✓ ✓ ✓ ✓	BLAST Hit Summary Description ss-PC ss-PC ss-PA	Species Dmel Dmel Dmel	Score 371.703 371.703 371.703	E value 1.41622e-102 1.41622e-102 2.47694e-102			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA	Species Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC	Species Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22			
spineless		BLAST Hit Summary Description Ss-PD Ss-PC Ss-PA Sim-PA Sim-PC Sim-PD	Species Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.23683e-22			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PD sim-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.23683e-22 2.68753e-22			
spineless		BLAST Hit Summary Description ss-PO ss-PC ss-PA sim-PA sim-PC sim-PB th-PG th-PG	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 89.7373	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27604e-102 2.21824e-22 2.23683e-22 2.68753e-22 9.80667e-18			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PC sim-PC sim-PD sim-PB tth-PG sim-PD	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 89.7373 88.5817	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27501e-22 2.21824e-22 2.28683e-22 2.68753e-22 9.80667e-18 2.53873e-17			
spineless		BLAST Hit Summary Description Ss-PD Ss-PC Ss-PA Sim-PA Sim-PA Sim-PD Sim-PB th-PG Sim-PD th-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 89.7373 88.5817 88.5817	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.23683e-22 2.68753e-22 9.80667e-18 9.53873e-17 2.56e-17			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PD sim-PB th-PG sima-PD th-PC th-PC th-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 89.7373 88.5817 88.5817 88.1965	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.1824e-22 2.8363a-22 9.80667e-18 2.58673a-72 9.80667e-18 3.02492e-17			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PC sim-PB th-PG sima-PD th-PC th-PR sima-PD sima-PD th-PR sima-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 89.7373 88.5817 88.1965 88.1965	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27501e-22 2.23843e-22 2.23843e-22 2.86875a-22 9.80667e-18 2.53873e-17 2.568e-17 3.02492e-17 3.42822e-17			
spineless		BLAST Hit Summary Description \$s-PD \$s-PC \$s-PA \$im-PA \$im-PC \$im-PD \$im-PB th-PG \$ima-PD th-PC th-PC th-PG \$ima-PA \$ima-PA \$ima-PA \$ima-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.1965 82.4185	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.217824e-22 2.23824e-22 2.268753e-22 9.80667e-18 2.53873e-17 3.22492e-17 3.42822e-17 3.42822e-17			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PD sim-PB th-PG sima-PD th-PC th-PC dys/PB dys/PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 88.5817 88.5817 88.1965 88.1965 82.4185 82.0333	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.23863e-22 2.68753e-22 9.80667e-18 2.53873e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.39609e-15			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PD th-PG th-PC th-PC th-PC th-PB sima-PA dysf-PB dysf-PC dysf-PD	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 89.7373 88.5817 88.1965 82.4185 82.0333 81.6481	E value 1.4.1622e-102 1.4.1622e-102 2.47694e-102 2.27501e-22 2.23863a-22 2.86875a-22 2.86875a-22 2.86875a-22 2.86875a-22 3.8075a-17 2.56e-17 3.02492e-17 3.42822e-17 1.73054e-15 2.39609e-15 2.62642e-15			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PC sim-PC sim-PC sim-PB trh-PG sim-PD sim-PB trh-PG sim-PA dysf-PB dysf-PB dysf-PD sim-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 89.7373 88.5817 88.5817 88.1965 82.4185 82.4185 82.0333 81.6481 80.1073	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27501e-22 2.231824e-22 2.23838-22 2.86753e-22 9.80667e-18 2.53873e-17 3.02492e-17 1.73054e-15 2.3642e-15 7.77029e-15			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PD sim-PD sim-PD sim-PD sim-PD sim-PD sim-PB th-PC th-PC dysf-PB dysf-PB dysf-PD sima-PB Met-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 88.5817 88.5817 88.5817 88.1965 82.4185 82.0333 81.6481 80.1073 79.7221	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.286753e-22 9.80667e-18 2.53873e-17 3.02492e-17 3.02492e-17 3.02492e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.39609e-15 2.6242e-15 1.16949e-14			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PD sim-PB trh-PG sima-PD trh-PG sima-PD dyst-PB dyst-PB dyst-PB dyst-PB dyst-PB dyst-PC dyst-PD sima-PB Met-PB Met-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 89.7373 88.5817 88.5817 88.1965 82.4185 82.0333 81.6481 80.1073 79.7221	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.3685a-22 9.80667e-18 2.56873e-17 3.02492e-17 3.02492e-17 3.02492e-17 2.36609e-15 2.66242e-15 7.7702e-15 1.16949e-14 1.6949e-14			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PC sim-PC sim-PC sim-PC sim-PC sim-PB tth-PG sima-PD tth-PC tth-PC tth-PB sima-PA dysf-PB dysf-PD sima-PB Met-PB Met-PA goe-PE	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.1965 82.4185 80.1073 79.7221 79.7221 79.7221	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27501e-22 2.21824e-22 2.23838-22 2.868575a-22 9.80667e-18 2.53873e-17 2.56e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.39609e-15 7.77029e-15 1.16949e-14 1.16949e-14 1.6949e-14			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PC sim-PC sim-PC sim-PB th-PG th-PC th-PC dysf-PB dysf-PB dysf-PB dysf-PB ma-PB sima-PA dysf-PB dysf-PB dysf-PB dysf-PB dysf-PB gione-PB Met-P8 Met-PA gce-PE gce-PD	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.5817 88.5817 82.0333 81.6481 80.1073 79.7221 79.7221 71.2478	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.47694e-102 2.21824e-22 2.2883e-22 2.868753e-22 9.80667e-18 2.53873e-17 3.42822e-17 3.42822e-17 3.42822e-17 3.42822e-17 1.73054e-15 2.66642e-15 2.66642e-15 1.16949e-14 1.16949e-14 4.30067e-12			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PD sim-PD sim-PD th-PG sima-PD th-PC th-PC dysf-PB gce-PE gce-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 89.7373 88.5817 88.1965 88.1965 88.1965 88.1965 82.4185 82.4185 82.0333 81.6481 80.1073 79.7221 79.7221 71.2478	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.21824e-22 2.23853e-22 9.80667e-18 2.53873e-17 3.02492e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.8669e-15 2.86242e-15 7.77029e-15 1.16949e-14 4.30067e-12 4.30067e-12			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PC sim-PC sim-PC sim-PC sim-PC sim-PB tth-PG sima-PD tth-PG sima-PD sima-PD dysf-PB dysf-PC dysf-PD sima-PB Met-PA gce-PE gce-PC gce-PG	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 370.933 105.531 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.5817 88.5817 88.065 82.4185 82.033 81.6481 80.1073 79.7221 71.2478 71.2478 71.2478 71.2478	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.27501e-22 2.21824e-22 2.23838-22 2.868575a-22 2.86875a-22 2.86875a-22 2.86875a-22 2.86875a-22 2.86847a-17 3.02492e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.39609e-15 2.86242e-15 7.77029e-15 1.16949e-14 4.30067e-12 4.30067e-12			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PD sim-PB tth-PG sim-PA dysf-PB dysf-PB dysf-PB dysf-PB dysf-PB ges-PE gec-PE gec-PC gec-PG th-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.513 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.1965 82.4185 80.1073 79.7221 79.7221 79.7221 71.2478 71.2478 71.2478 71.2478 71.2478 70.8626	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.07501e-22 2.81824e-22 2.8683e-22 2.868753e-22 9.80667e-18 2.53873e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.36009e-15 2.62642e-16 7.77029e-15 1.16949e-14 1.6949e-14 4.30067e-12 4.30067e-12 4.30067e-12 4.30067e-12 5.478e-12			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PA sim-PC sim-PD sim-PB th-PG sima-PD th-PC dysf-PB dysf-PB dysf-PB dysf-PB dysf-PB dysf-PB dysf-PC dysf-PB dysf-PC gce-PB gce-PC gce-PC gce-PC gce-PG th-PE	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 88.5817 88.5817 88.5817 88.5817 82.4185 82.0333 81.6481 79.7221 79.7221 79.7221 71.2478 71.2478 71.2478 70.8626 70.4774	E value 1.41622e-102 1.41622e-102 2.47694e-102 2.47694e-102 2.21824-22 2.23883e-22 2.288753e-22 9.80667e-18 2.53873e-17 3.02492e-17 3.02492e-17 3.02492e-17 3.02492e-17 1.73054e-15 2.39609e-15 2.62642e-15 1.16949e-14 4.30067e-12 4.30067e-12 4.30067e-12 5.478e-12 5.478e-12 5.478e-12			
spineless		BLAST Hit Summary Description ss-PD ss-PC ss-PA sim-PC sim-PC sim-PC sim-PC sim-PC sim-PB th-PG sima-PD th-PG sima-PD dysf-PD dysf-PB dysf-PC dysf-PD sima-PB Met-PB Met-PA gce-PC gce-PC <	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 371.703 371.703 371.703 370.933 105.531 105.145 105.145 105.145 88.5817 88.5817 88.5817 88.5817 88.24185 82.4185 80.1073 79.7221 71.2478 71.2478 71.2478 71.2478 70.8626 70.4774	E value 1.4.1622e-102 1.4.1622e-102 2.47694e-102 2.47694e-102 2.27824e-22 2.23863a-22 2.86875a-22 2.86875a-22 2.86875a-22 2.8686-77 3.02492e-17 3.42822e-17 3.42822e-17 3.42822e-17 1.73054e-15 2.86242e-15 7.77029e-15 1.16949e-14 4.30067e-12 4.3006			

aristaless		
	Query seq.	
Drosophila		specific DNA binding site
melanogaster	Specific hits	Homeobox
	Superfamilies	homeodonain superfamily 048 sup
	Query seq.	
Hypsibius		specific DNR bank contacts A AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
exemplaris	Specific hits	Homeobox
	Supertanilies	Bomeodomin swarfanil 1 50 100 135
Echiniscoides	Query seq. specific DNA DNA	base contacts
cf. sigismundi	Spacific bits	
-j · · · g · · · · · · · ·	Superfamilies	Nomeodox horeodorain superfanil
clawless		
	Query seq.	
Drosonhila		specific DNR base contacts A A A A A
melanogaster	Specific hits	
	Superfamilies	C005576 honeodonain surerfanily
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1	Superfamilies	honeodonain superfanity
	Query seq.	
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cf. sigismundi	Specific hits	
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		1 75 150 225 300 375 450 565
	Query seq.	Zn binding site 📉 🛺 specific DNR base contects 👬 🔐
Drosophila	Zn bind:	ing site AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
melanogaster	Specific hits Superfamilies	LTMI_LINSI_LINS LTMI_LINS Homeobox
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cf. sigismundi		Zn binding site Annual DNN binding site Annual Annual
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apterous		
Drosonhila	Query seq.	1
Drosophila	Query seq.	75 150 225 360 375 450 460 2n binding site 2n binding site Abb Abb Mile binding site Abb
Drosophila melanogaster	Query seq. Specific hits	2n binding site A AMA A specific DNR base contacts A AMA DNR binding site A AMA A specific DNR base contacts A AMA A Specific DNR binding site A AMA A AMA A Specific DNR bindin
Drosophila melanogaster	Query seq. Specific hits Superfamilies	275 155 275 380 375 455 469 2n binding site 2n binding site Abba specific DWR base contacts Abba LTM_Linv2_Linv3 LTM2_Linv2_Linv3 Homeobox LTM superfamily Homeodorein supe
Drosophila melanogaster	Query seq. Specific hits Superfamilies	2n 2150 225 380 375 450 450 450 2n 2n 380 375 450 450 450 2n binding site Abb Abb Specific DN0 base contects Abb
Drosophila melanogaster Hypsibius	Query seq. Specific hits Superfamilies Query seq.	20 225 349 375 459 469 2n binding site 2n binding site 1192_1hx2_1hx9 1192_1hx2_1hx9 1192_1hx2_1hx9 1 75 159 225 369 375 459 469 2n binding site 1192_1hx2_1hx9 1192_1hx2_1hx9 1192_1hx2_1hx9 1192_1hx2_1hx9 1192_1hx2_1hx9 2n binding site 119 225 369 375 459 469 2n binding site 129 199 369 375 459 525 566 2n binding site 119 225 369 375 459 525 566 2n binding site 119 225 369 375 459 525 566
Drosophila melanogaster Hypsibius exemplaris	Query seq. Specific hits Superfamilies Query seq. Specific hits	20 225 240 375 460 490 2n binding site Attal specific DNR base contects Attal DNR binding site 2n binding site Attal specific DNR base contects Attal DNR binding site 2n binding site Attal Attal specific DNR base contects Attal 2n binding site Attal Attal specific DNR base contects Attal 2n binding site Attal Attal specific DNR base contects Attal 2n binding site Attal Attal Specific DNR base contects Attal 2n binding site Attal Attal Specific DNR base contects Attal 2n binding site Attal Attal Specific DNR base contects Attal 2n binding site Attal Attal Attal Attal Attal 2n binding site Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal Attal

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

Echiniscoides	Query seq.	2n binding site A specific DNA base contacts A
cf. sigismundi	Specific hits Superfamilies	An binding site
BarH1		
	Query seg.	75 159 225 300 300 375 450 525 54 -
Drosophila malanogastar	4001 9 0041	specific DNR binding site A Annual DNR binding site
meiunogusier	Specific hits S <mark>uperfamilies</mark>	Honeobox horeodorain super
Hypsibius	Query seq.	specific DNA base contacts A ANA DNA binding site A Anal
exemplaris	Specific hits	Ионеорок
Echiniscoides	Query seq.	NR base contacts
cf. sigismundi	Specific hits Superfamilies	Moneobox Koneodonalin super
rotund		
	Query seq.	1 125 259 275 599 625 779 875 946
Drosophila melanogaster		C202 2n finger 1 202 2n finger 2 202 2n finger 2 2n Zn finder 3 site 2 2n finder 3 site 2 2n finder 3 2n finde
	Specific hits Superfamilies	डाज्य ≠2012_8 ≠C ≠11
Hypsibius	Query seq.	125 28 975 492 C2H2 Zn finger C C2H2 Zn finger C C2H2 Zn finger C C2H2 Zn finger C C2H2 Zn finger CH2 C2H2 Zn finger CH2 Zn binding site A Zn binding site Zn binding site A Zn binding site Zn binding site A
exemplaris		2n binding site 📶 📶 2n binding site 📶
	Specific hits Superfamilies	9688 847 84-C 242_3 8-F
	gene 1	
	Query seq.	1 125 259 29 C202 2n Finger (C202 2n Finger (C)) C202 2n Finger (C) C202 2n Finger (C)
	putative nuc	C2R2 Dn Finnger C2R2 Dn Finneer C 2n blading site 2n blading site 2n blading site 2 2n blading site 2 2n blading site 2
Echiniscoides	putative nuc Specific hits Superfamilies	CRI2 Da Finger C 2002 Da Finger D Zh binding site A Da binding site A latic actid binding site A 2h binding site A Da binding site
Echiniscoides cf. sigismundi	putative nuc Specific hits Superfamilies gene 2	CORE On Finger Core 2n Fineter 2n binding site A Da binding site 2n binding site A Da b
Echiniscoides cf. sigismundi	putative mac Specific hits Superfamilies gene 2 Query seq. c2m2 2 c	CORE DA Finger Conception Concept
Echiniscoides cf. sigismundi	specific hits Superfanilies gene 2 Query seq. Care 2 Ch binding sic ecid binding si	CORE DA Finance Concession of the concession of
Echiniscoides cf. sigismundi	putative moc specific hits superfanilies gene 2 Query seq. CH2 2 Ch bindi Size acid binding si	CB2 Da Finger Da binding site Da binding site
Echiniscoides cf. sigismundi Spineless	putative more specific hits superfanilies gene 2 Query seq. COM2 o Dubindin Superfanilies	COG5048 COG
Echiniscoides cf. sigismundi Spineless Drosophila	putative nuc Specific hits Superfanilies gene 2 Query seq. Core 2 Core 2	CORE DA Finder COCESO48 Construction of the construction of the c

	Query seq.
Hypsibius	DNR binding site
exemplaris	Specific hits
	Superfamilies DHLF_SF av PRS_superf PRS_11
Echiniscoides	Query seq.
cf. sigismundi	Specific hits THE
	Superfamilies PAS superf PAS_11

Table S6. Amino acid sequences of <i>Echiniscoids cf. sigismundi</i> distal limb patterning gene homologs	

Gene	Amino Acid Sequence
aristaless	MSSITATNNISTASIFGYGNEDKLNQRKQRRYRTTFSSTQLDELERVFGETHYPDVFIREELALRINLTEARVQVWF
	QNRRAKHRKQDKNELQSIPINPVMNNFALLMQQQQQQQNEMQFHSGLQQQPQPQQQHQ
clawless	NNNNNVNEKSTSTSAFTPVIKHQQPQQQQNHHLNQHQQHQNALNSVLATHLAWNDPSIRRLGRRIGHPYQQR
	$\label{eq:templation} TPPKRKKPRTSFTRIQICELEKRFQRQKYLASAERATLAKSLKMTDAQVKTWFQNRRTKWRRQTAEEREAERQAA$
	${\tt SRMLLSLQAELAQKAPPMSAQPDPICMSNKSLYALHNLQPWASNMVQTTTTSPISSVYNDDKCNSSDVIDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD$
	LDDYDIID
Liml	MQVVKCCACDQLINDKFIMNVLDRTWHAECLRCCICSMILTDKCFSRHGKVYCRDHFYKAFGAKCCVCFEGINP
	DELVRRTVQGGVYHIKCFKCNECHKELTTGEQFYCIDESRFLCKSDFLMKQIPLTTSSNQVNNSWPKSIKSENDDE
	EIEQGSPQQQLYNTNNAHSNNCTTPNAHQSSSEKEEEFDDSDSTNKDNKIKHDNDSTHQPSGTKRRGPRTTIKQKQ
	LEQLKEIFDSQPKPKAIRDQLASKTGLSKRVIQVWFQNRRSKERRMKISQNLRGRNAYARHRNGGRSSSSGRPEL
	EQHAQGGPPPHIFGFY1DNGVPNGPPPPDMFGASPGNFYPNDPNNFNFNEAPPPPPPPPDVMNNNGGANGGGN
	LSAMSQHFPPSSISNESPVPPSLVINGIQPNESLNANNNNTNSQQQQKFNGTRDHFLPSPISIDGYQASNFQDPCSMQ
	FSGMRIQQQPPPAIQISPESAGLIN
apterous	LEPPMDLAEITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	LDCGvQLCeDDRSCFFNSGNVYCRQDYQKRFNQKQC1RCNV1FQS1DLVM1vPCeDLQNNSNSNN1P1LPSSLP
	QFH v DCFSCAICER V LASGELYR Y IPMPHN I LLCCEHLEWSNFKDDSGKLS I K VGRPKKRSSQDSSHS I CSGGNGG
	NNEHSMQRFRKMRTSFRHQIN VMRQFFISNQNPDARMLRTLSARTSLSRVLQVWFQNQRARFRKEHSKRQHQ
D 111	HQSVGMINGPDG1NPHGPDV1QLHIPP1VQSLPSVAS15FGG1V15KNINGINNNLGQQQQQQQQSL53D515
BarHI	QILINKLIM DDDSDDCEDTCDKTNKTTTTTNNNRQQUICHLESKRAKKPKTAFTERQEDVLESSQQQXTLSVQE
rotuna	
	DI TAAABKEMT KQQQQQQQQ I YQI TQIQIQIINI ASIDD YAQKSEASEEQSYA ALESAKSI I KQYATSYKKI IN ODMOXYSEETY OEHIOHVO A HMDEHY DVY CTOCDYTE ANGSYI TOHMDIHI GI DDVY CSOCEVIETOI SHKINOH
	ENTRESPETIQUE INQUE INTERPRETATION CONTRACTOR A LA CONCENTRA CONTRACTOR A LA CONTRACTÓRIA DE LA CONT
	GK SYAOFTYI TKHI SKHI PKOSDTOSFSFK SNI EVYNSKKI KKPATTEVI DSEKSFITNSSNNNTTNNMYVMI
	TKTFANSSYLSOHMRIHLGVRPYKCPSCDKRFTOLSHLOOHDRTHSGDKPYACKHPNCNKAFSOLSNLOSHSRCH
	OTNKPYKCNSCERSFEDEKSLLEHIPRHKESKHLKTHICEHCGKSYAOETYLOKHLNKHPHNLGGGCNKRNSNNG
	RGKCKRIOOOOOPOPOOHLOOOOOONTIW
snineless	YHSHHOHHLHOOOOOOLHNTHYNOFSNYPSTSDNACNRILTAGLGPOILSRESIMKALNGFLVIIOADGEVFYVSN
spinciess	TVEHFLGFHOSDVLHOSICDLIHSEDRIDFOKOLEWNSLRONSOPYSDFALADNPFMLERNFTARFRCLLDNTSGFL
	RLDVRGRLSLLPGQKTRSSSIALFALCSVFGPTQMIESVSRNCLFRSKHKMDLEVINFDAKGKINIDDKNDIEGEKL
	YNLVHSDDLQYIATGHAELLKTGTTGLLAYRLRFDSEQKWQWVQSNLRINYRSGRGEFITAIHRVLIDEEGIDLYS
	KRKISSAFSYLVDFTNSTQQQTNNNNNSLTTTDSSQQSSFTRPITN

Gene	BLAS	T Hit Summ	ary	
aristaless	BLAST Hit Summary	1		
	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	Dmol	01 2791	2 871840-19
	00112041 A	Dhiel	91.2701	2.071046-10
clawless	BLAST Hit Summary	Dinei	51.2701	2.071040-13
clawless	BLAST Hit Summary Description	Species	Score	E value
clawless	BLAST Hit Summary Description C15-PA	Species Dmel	Score 199.134	E value 2.88667e-51
clawless	BLAST Hit Summary Description C15-PA Hmx-PE	Species Dmel Dmel Dmel	Score 199.134 86.6557	E value 2.88667e-51 2.01947e-17
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC	Species Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557	E value 2.88667e-51 2.01947e-17 2.01947e-17
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD	Species Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA	Species Dmei Dmei Dmei Dmei Dmei Dmei	Score 199.134 86.6557 86.6557 86.2705 85.1149	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA	Species Dmei Dmei Dmei Dmei Dmei Dmei Dmei	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481	E value 2.88667e-51 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA B-H2-PA	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.3889e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC	Species Dmei Dmei Dmei Dmei Dmei Dmei Dmei Dmei	Score 199.134 86.6557 86.6557 86.6557 86.149 81.6481 81.6481 81.6481	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.13682e-16 6.3889e-16 6.55085e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481 81.2629	E value 2.88667e-51 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.35889e-16 6.55085e-16 7.06171e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PC	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629	E value 2.88667e-51 2.01947e-17 2.42637e-17 2.42637e-17 6.33582e-16 6.3889e-16 6.5805e-16 7.06171e-16 7.06171e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PE NK7.1-PB	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 85.2705 85.1149 81.6481 81.6481 81.6481 81.6481 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.35898e-16 6.55085e-16 7.06171e-16 7.06171e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PB NK7.1-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.35839e-16 6.55035e-16 7.06171e-16 7.06171e-16 7.06171e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PB NK7.1-PA B-H2-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 81.2629 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.42637e-17 2.42637e-17 6.32627e-17 6.33582e-18 6.38989e-16 6.55058e-18 7.06171e-16 7.06171e-16 8.55567e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PB Ims-PC	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 2.42637e-17 6.33582e-16 6.3585e-16 6.55058e-16 7.06171e-16 7.06171e-16 7.06171e-16 9.07025e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PA B-H2-PB Ims-PC Ims-PB	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 85.1149 81.6481 81.6481 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33852e-16 6.3889e-16 6.35898e-16 6.35898-16 7.06171e-16 7.06171e-16 7.06171e-16 8.55557e-16 9.07025e-16 9.07025e-16
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PD NK7.1-PB NK7.1-PB Ims-PC Ims-PC Ims-PB bap-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629 81.2629	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.32607e-17 6.33582e-16 6.35838e-16 6.55055e-16 7.06171e-16 7.06171e-16 8.55567e-16 9.07025e-16 3.56367e-15
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PB NK7.1-PB B-H2-PB Ims-PC Ims-PB bap-PA exex-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 86.1705 85.1149 81.6481 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 2.42637e-17 6.33582e-18 6.38989e-16 6.55058e-18 7.06171e-16 7.06171e-16 7.06171e-16 8.55567e-16 9.07025e-16 9.07025e-16 9.07025e-16 9.07025e-15 9.30286e-15
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PB NK7.1-PB NK7.1-PB NK7.1-PB NK7.1-PB NK7.1-PA B-H2-P8 Ims-PB bap-PA exex-PA Ibe-PA	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.6557 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 81.2629 81.2629 81.2629 81.2629 80.8777 78.9518 77.7962	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.3582e-16 6.35898e-16 6.55085e-16 7.06171e-16 7.06171e-16 7.06171e-16 8.55567e-16 9.07025e-16 9.07025e-16 9.30286e-15 9.30286e-15 2.77532e-14
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PD NK7.1-PB NK7.1-PA B-H2-PB Ims-PC Ims-PB bap-PA exex-PA Ibe-PA Dr-PA	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.8557 86.2705 85.1149 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.3589e-16 6.3589e-16 7.06171e-16 7.06171e-16 7.06171e-16 7.06171e-16 9.07025e-16 9.07025e-16 3.56367e-15 9.30226e-15 9.30226e-15 9.30226e-14 4.89465e-14
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PD NK7.1-PB NK7.1-PB Ims-PC Ims-PB bap-PA exex-PA Ibe-PA Dr-PA DI-PB	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 86.1705 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42837e-17 6.12607e-17 6.3382e-16 6.3889e-16 6.35835e-16 7.06171e-16 7.06171e-16 7.06171e-16 8.555567e-16 9.07025e-16 9.07025e-16 9.07025e-15 9.30286e-15 2.77532e-14 4.89465e-14 6.60956e-14
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PC NK7.1-PB NK7.1-PB NK7.1-PB NK7.1-PA B-H2-PB Ims-PC Ims-PA exex-PA Ibe-PA DII-PB DII-PC	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 86.2705 85.1149 81.6481 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.42637e-17 2.42637e-17 2.42637e-17 6.33582e-16 6.38989e-16 6.55055e-18 7.06171e-16 7.06171e-16 7.06171e-16 8.55567e-16 9.07025e-16 9.07025e-16 9.07025e-16 9.07025e-15 9.30286e-15 2.77532e-14 4.89465e-14 7.74501e-14
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PA B-H2-PB Ims-PC Ims-PC Ims-PA bap-PA exex-PA Iba-PA DI-PB DII-PA	Species Species Dmei Dmei Dmei Dmei Dmei Dmei Dmei Dmei	Score 199.134 86.6557 86.8557 86.2705 85.1149 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33852e-16 7.06171e-16 7.06171e-16 7.06171e-16 7.06171e-16 7.06171e-16 9.07025e-16 9.07025e-16 9.07025e-15 9.30286e-15 9.30286e-15 9.30286e-15 9.30286e-14 4.89465e-14 6.60956e-14 8.00786e-14
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PC Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PC NK7.1-PA B-H2-PA HGTX-PC NK7.1-PC NK7.1-PB NK7.1-PA B-H2-PB Ims-PC Ims-PC Ims-PA exex-PA bap-PA or-PA DII-PB DII-PA ibi-PC	Species Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 85.1149 81.6481 81.6481 81.2629 80.8777 78.9518 77.7962 74.7146 74.7146 74.3294	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42637e-17 6.12607e-17 6.33582e-16 6.3889e-16 6.55058e-16 7.06171e-16 7.06171e-16 7.06171e-16 9.07025e-16 9.07025e-16 9.07025e-16 3.56367e-15 9.07025e-15 2.77532e-14 4.89455e-14 6.60955e-14 7.7451e-14 8.00786e-14 1.00312e-13
clawless	BLAST Hit Summary Description C15-PA Hmx-PE Hmx-PD B-H1-PA HGTX-PA B-H2-PA HGTX-PC NK7.1-PD NK7.1-PC NK7.1-PB NK7.1-PB NK7.1-PB NK7.1-PA B-H2-P8 Ims-PC Ims-PA exex-PA Ibe-PA DI-PA DII-PB DII-PA IbJ-PA IbJ-PA	Species Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	Score 199.134 86.6557 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 86.2705 81.6481 81.6481 81.2629 8	E value 2.88667e-51 2.01947e-17 2.01947e-17 2.42837e-17 2.42837e-17 6.33582e-16 6.3889e-16 6.35035e-16 7.06171e-16 7.06171e-16 7.06171e-16 8.55557e-16 9.07025e-16 1.1805e-12 1.11805e-13 1.11805e-13

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

T · 1				
Liml	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
	L my1a-PC	Dmol	92.0485	9.81649e-19
		Dillei		
	CG4328-PB	Dmel	89.3521	5.52142e-18
	CG4328-PB Lim3-PA	Dmel Dmel	89.3521 87.0409	5.52142e-18 3.02882e-17
	CGA328-PB C Lim3-PA Lim3-PF	Dmel Dmel Dmel	89.3521 87.0409 85.5001	5.52142e-18 3.02882e-17 8.31256e-17
	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PF Lim3-PD	Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17
	CG4328-PB Lim3-PA Lim3-PF Lim3-PF Lim3-PD Lim3-PC	Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17
	CG4328-PB Lim3-PA Lim3-PF Lim3-PF Lim3-PC Lim3-PB	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17
	CG4328-PB Lim3-PA Lim3-PF Lim3-PF Lim3-PC Lim3-PB Lim3-PB Lim3-PE	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.88636e-17
	CG4328-PB C Lim3-PF Lim3-PD Lim3-PD Lim3-PD Lim3-PD Lim3-PD Lim3-PE Lim3-PE Lim3-PE Lim3-PE Lim3-PG	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.88636e-17 9.98746e-17
	CG4328-PB C Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PC Lim3-PB Lim3-PB Lim3-PG Lim3-PG C CG5708-PC	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.88636e-17 9.98746e-17 9.19328e-15
	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PC Lim3-PC Lim3-PB Lim3-PB Lim3-PB Lim3-PC Lim3-PC CG5708-PC CG5708-PB	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.88636e-17 9.98746e-17 9.19328e-15 9.19328e-15
	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PB Lim3-PB Lim3-PB Lim3-PB Lim3-PB Lim3-PB Lim3-PB Lim3-PB Lim3-PB CG5708-PC CG5708-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.88636e-17 9.98746e-17 9.19328e-15 9.19328e-15
	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PB Lim3-PG Lim3-PE CG5708-PG CG5708-PA	Dmel Dmel Dmel Dmel Dmel Dmel Dmel Dmel	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 63.929	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.38636e-17 9.98746e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10
D III	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PB Lim3-PG Lim3-PG CG5708-PC CG5708-PA CG5708-PA CG9876-PA	Difference of the second secon	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 63.929	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.98746e-17 9.98746e-15 9.19328e-15 9.19328e-15 2.34327e-10
BarH1	CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PC Lim3-PB Lim3-PB Lim3-PG Lim3-PG Lim3-PG CG5708-PC CG5708-PA CG5708-PA CG5708-PA ELAST Hit Summary	Difference of the second secon	89.3521 87.0409 85.5001 85.50000 85.5000 85.50000 85.50000 85.50000 85.50000000000	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10
BarH1	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PD Lim3-PC Lim3-PB Lim3-PE Lim3-PE Lim3-PE CG5708-PC CG5708-PA CG5708-PA CG59708-PA CG9876-PA ELAST Hit Summary Description	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 63.929 Score	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value
BarH1	CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PD Lim3-PC Lim3-PG Lim3-PE Lim3-PG Lim3-PG Lim3-PG Lim3-PG CG5708-PC CG5708-PA CG5708-PA CG5708-PA BLAST Hit Summary B-H1-PA P	Difference of the second secon	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 929 Score 100.908	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.38636e-17 9.98746e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.23327e-10
BarH1	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PC Lim3-PB Lim3-PB Lim3-PG Lim3-PG CG5708-PC CG5708-PC CG5708-PA CG5708-PA CG5708-PA CG5708-PA BLAST Hit Summary B-H1-PA B-H2-PA Description	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 83.929 Score 100.908 97.4413 95.602	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21
BarH1	▲ C64328-PB ✓ C64328-PB ✓ Lim3-PA ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ C65708-PE ✓ C65708-PA ✓ C65708-PA ✓ C69876-PA ✓ C69876-PA ✓ B-H1-PA ✓ B-H2-PA ✓ B-H2-PA ✓ B-H2-PA ✓ B-H2-PA ✓ B-H2-PA	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.50000 85.50000 85.50000 85.50000000000	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20
BarH1	▲ CG4328-PB ✓ CG4328-PB ✓ Lim3-PA ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PB ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ CG5708-PG ✓ CG5708-PG ✓ CG5708-PA ✓ CG4708-PA ✓ CG5708-PA ✓ CG4708-PA ✓ CG4708-PA ✓ B-H1-PA ✓ B-H2-PB ✓ CH2PB ✓ CH2PD	Difference of the second secon	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.101 85.1149 78.5666 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.6732	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.99544e-16 8.9776-21
BarH1	▲ CG4328-PB ✓ CG4328-PB ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PC ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PG ✓ CG5708-PC ✓ CG5708-PA	Difference of the second secon	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 99.78.5666 99.74413 95.1301 82.0333 80.1073	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 8.24568-17 1.96544e-16 6.8708e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 8.24568-17 1.96544e-16 1.965644e-16 1.965446464e-16 1.96
BarH1	▲ C64328-PB ✓ C64328-PB ✓ Lim3-PF ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PB ✓ Lim3-PE ✓ Lim3-PG ✓ Lim3-PG ✓ C65708-PG ✓ C65708-PA ✓ C65708-PA ✓ C69708-PA ✓ C9970-PA ✓ B-H1-PA ✓ B-H2-PA ✓ B-H2-PA ✓ B-H2-PA ✓ B-H2-PA	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5666 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16
BarH1	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PD Lim3-PC Lim3-PE Lim3-PG Lim3-PG CG5708-PG CG5708-PA CG5708-PA CG5708-PA CG5708-PA CG5708-PA CG9876-PA B-H1-PA B-H2-PA B-H2-PB OB-H2-PB DII-PB DII-PB DII-PA DII-PA	Difference of the second secon	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073 79.7221	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16
BarH1	■ □	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 97.4413 95.1301 82.0333 80.1073 95.1301 82.0333 80.1073 79.7221 78.1814 70.651	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 9.43421e-16 9.43421e-16
BarH1	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PD Lim3-PC Lim3-PG Lim3-PG Lim3-PG CG5708-PC CG5708-PA CG5708-PA CG5708-PA CG5708-PA CG5708-PA CG5708-PA CG9876-PA B-H1-PA B-H2-PB B-H2-PB OB-H2-PB OB-H2-PA DII-PC DII-PA C15-PA	Difference of the second secon	89.3521 87.0409 85.5001 85.500	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 9.43421e-16 9.43421e-16 2.677708e-15 2.7213e-15
BarH1	▲ C64328-PB ✓ C64328-PB ✓ Lim3-PA ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ C65708-PC ✓ C65708-PA ✓ C65708-PA ✓ C69876-PA ✓ C69876-PA ✓ C69876-PA ✓ B-H1-PA ✓ B-H2-PB ✓ B-H2-PA ✓ B-H2-PA ✓ DII-PA ✓ DII-PA ✓ DII-PA ✓ DII-PA ✓ C15-PA ✓ C1-PA ✓ C1-PA	Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.033 80.1073 79.7221 78.1814 78.1814 76.2554	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-17 9.19326e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 2.67708e-15 2.72213e-15 1.00884e-14
BarH1	CG4328-PB CG4328-PB Lim3-PA Lim3-PF Lim3-PD Lim3-PD Lim3-PB Lim3-PG Lim3-PG Lim3-PG CG5708-PG CG5708-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073 79.7221 78.1814 78.1814 78.8702	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 2.67708e-15 2.72213e-15 1.00884e-14 1.13384e-14
BarH1	▲ CG4328-PB ✓ CG4328-PB ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ CG5708-PC ✓ CG5708-PA ✓ B-H2-PB ✓ B-H2-PB ✓ B-H2-PA ✓ DI-PC ✓ DI-PA ✓ CI19-PA <	Dimei Di Dimei Dimei Dimei Dimei Dimei Dimei Dimei Di	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 97.8566 97.4413 95.1301 82.0333 80.1073 80.1073 80.1073 79.7221 78.1814 76.2554 75.8702 75.8702	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 2.72213e-15 1.0884e-14 1.13384e-14 1.1384e-14 1.13384e-14
BarH1	■ ■ Q ■	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 79.7221 78.8144 78.1814 78.1814 76.2554 75.8702 75.8702	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.870&e-16 9.43421e-16 6.870&e-16 9.43421e-16 1.13384e-14 1.13384e-14 1.1384e-14 1.13824e-14
BarH1	CG4328-PB Q CG4328-PB Q Lim3-PA Q Lim3-PF Q Lim3-PD Q Lim3-PB Q Lim3-PG Q Lim3-PG Q Lim3-PG Q Lim3-PG Q CG5708-PG Q CG5708-PA Q B-H1-PA Q B-H2-PB Q B-H2-PB Q DI-PA Q DI-PA Q DI-PA Q DI-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073 80.1073 79.7221 78.1814 76.2554 75.8702 75.8702 75.8702	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.3189e-22 3.37877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 2.67708e-15 1.00884e-14 1.13364e-14 1.13364e-14 1.19205e-14
BarH1	▲ CG4328-PB ✓ CG4328-PB ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PB ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ Lim3-PG ✓ CG5708-PG ✓ CG5708-PA ✓ B-H12-PA ✓ B-H12-PA ✓ B-H12-PA ✓ DI-PA ✓ DI-PA ✓ DI-PA ✓ CG11085-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 78.5666 97.8566 97.4413 95.1301 82.0333 80.1073 95.1301 82.0333 80.1073 79.7221 78.1814 78.1814 78.1814 75.8702 75.8702 75.8702	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 2.67708e-15 2.72213e-15 2.72213e-15 1.0384e-14 1.13205e-14 1.13205e-14 1.99988e-14 2.21026e-14 2.21026e-14
BarH1	▲ CG4328-PB ✓ CG4328-PB ✓ Lim3-PA ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PG ✓ Lim3-PG ✓ CG5708-PG ✓ CG5708-PA ✓ B-H1-PA ✓ B-H2-PA ✓ DI-PC ✓ DI-PA ✓ DI-PA ✓ CG15-PA <td>Dimei Dimei</td> <td>89.3521 87.0409 85.5001 85.5002 85.500</td> <td>5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 1.13384e-14 1.13205e-14 1.13205e-14 1.99058e-14 2.21026e-14 2.21026e-14</td>	Dimei Dimei	89.3521 87.0409 85.5001 85.5002 85.500	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 1.13384e-14 1.13205e-14 1.13205e-14 1.99058e-14 2.21026e-14 2.21026e-14
BarH1	CG4328-PB Q CG4328-PB Q Lim3-PA Q Lim3-PF Q Lim3-PD Q Lim3-PE Q Lim3-PG Q Lim3-PG Q Lim3-PG Q Lim3-PG Q CG5708-PC Q CG5708-PA Q B-H1-PA Q B-H2-PB Q B-H2-PA Q B-H2-PA Q DII-PA Q DII-PA Q DII-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 63.929 Score 100.908 97.4413 95.1301 80.1073 95.1301 80.1073 95.1301 80.1073 79.7221 78.1814 76.2554 75.8702 75.8702 75.0998 75.0998 74.3294	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 9.43421e-16 2.67708e-15 2.72213e-15 1.00884e-14 1.13205e-14 1.13205e-14 1.19205e-14 1.19205e-14 1.19205e-14 1.19205e-14 1.19205e-14 1.221026e-14 2.21026e-14 2.21026e-14 4.03038e-14
BarH1	■ ■ Q ■ Q ■ Lim3-PF ■ Q ■<	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073 80.1073 79.7221 78.1814 78.1814 78.8702 75.8702 75.8702 75.0998 75.0998 75.0998	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.13256e-17 9.13226e-17 9.13226e-15 9.13328e-15 9.13328e-15 2.34327e-10 7.13228e-15 2.34327e-10 7.34508e-16 8.87038e-16 7.34508e-16 8.87038e-16 9.43421e-16 2.67708e-15 1.00884e-14 1.13205e-14 1.13205e-14 1.19205e-14 1.19205e-14 1.19205e-14 2.21026e-14 2.21026e-14 2.21026e-14 2.21026e-14 1.2026e-14 1.2026e-14 1.61017e-13
BarH1	■ C64328-PB ✓ C64328-PB ✓ Lim3-PA ✓ Lim3-PF ✓ Lim3-PD ✓ Lim3-PE ✓ Lim3-PE ✓ Lim3-PG ✓ Lim3-PG ✓ C65708-PC ✓ C65708-PA ✓ C69708-PA ✓ D1-PA ✓ D1-PA ✓ C15-PA ✓ D1-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 97.85666 63.929 97.4413 95.1301 82.0333 80.107	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.24291e-20 E value 3.37897e-21 2.24291e-20 1.96544e-16 6.8708e-16 7.34508e-16 2.72213e-15 1.00848e-14 1.19205e-14 1.19205e-14 1.99968e-14 2.21026e-14 2.21026e-14 2.21026e-14 2.21026e-14 1.61017e-13 1.72131e-13
BarH1	■ ■ Q ■ Q ■ Lim3-PA ■ Q ■ Lim3-PD ■ Q ■ Lim3-PD ■ Q ■ Lim3-PE ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ Q ■ CGS708-PA ■ Q ■ B-H1-PA ■ Q ■ B-H2-PB ■ Q	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.1149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 79.7221 78.1814 76.2554 75.8702 75.8702 75.8702 75.8702 75.9998 75.0998 74.3294 72.0182 72.0182 72.0182	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19326e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 9.43421e-16 6.8708e-16 9.43421e-16 1.13384e-14 1.13384e-14 1.13205e-14 1.19205e-14
BarH1	CG4328-PB Q CG4328-PB Q Lim3-PF Q Lim3-PD Q Lim3-PB Q Lim3-PG Q Lim3-PG Q Lim3-PG Q Lim3-PG Q CG5708-PG Q CG5708-PA Q B-H1-PA Q B-H2-PB Q DI-PA Q DI-PA Q DI-PA Q DI-PA Q DI-PA	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 80.1073 80.1073 80.1073 79.7221 78.1814 76.2554 75.8702 75.8702 75.8702 75.9998 75.0998 75.0998 74.3294 72.0182 72.0182 71.2478	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.13256e-17 9.13226e-17 9.13328e-15 9.13328e-15 9.13328e-15 9.13328e-15 2.34327e-10 7.34528e-15 2.34327e-10 7.34528e-16 9.43421e-16 2.67708e-15 1.00884e-14 1.13205e-14 1.1320
BarH1	■ CG4328-PB Q Lim3-PA Q Lim3-PF Q Lim3-PD Q Lim3-PB Q Lim3-PG Q Lim3-PG Q Lim3-PG Q Lim3-PG Q CG5708-PG Q CG5708-PA Q B-H1-PA Q B-H2-PB Q B-H2-PA Q DI-PC Q DI-PA Q CG11085-PA Q CG1085-PA Q CG34031-PC	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5666 63.929 78.5666 63.929 97.4413 95.1301 82.0333 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 80.1073 75.8702 75.8702 75.9998 75.0998 75.0998 75.0998 75.0998 75.0998 74.3294 72.0182 72.0182 72.0182 72.0182 72.0182	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.98746e-17 9.98746e-17 9.98746e-17 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 E value 3.37897e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 2.72213e-15 1.0084e-14 1.19205e-14
BarH1	■ ■ Q ■ C64328-PB ■ Q ■ Lim3-PF ■ Q	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 78.5666 63.929 78.5666 63.929 78.5666 63.929 97.4413 95.1301 82.0333 80.1073 79.7221 70.908 75.0998 75.0998 75.0998 75.0998 75.0998 75.0998 75.0998 75.0998 75.0998 74.3224 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182 72.0182	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.24216-20 1.96544e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 9.43421e-16 1.19205e-14 1.19205e-14 1.19205e-14 1.19205e-14 1.19205e-14 1.221026e-14 2.21026e-14 2.21026e-14 1.61017e-13 3.08685e-13 7.53781e-13
BarH1	CG4328-PB Q CG4328-PB Q Lim3-PA Q Lim3-PF Q Lim3-PD Q Lim3-PG Q Lim3-PG Q Lim3-PG Q Lim3-PG Q CG5708-PC Q CG5708-PA Q B-H2-PA Q B-H2-PA Q B-H2-PA Q DI-PA Q DI-PA Q DI-PA <trtr></trtr>	Dimei Dimei	89.3521 87.0409 85.5001 85.5001 85.5001 85.5001 85.5001 85.5001 85.149 78.5666 63.929 Score 100.908 97.4413 95.1301 82.0333 80.1073 95.1301 82.0333 80.1073 97.7221 78.1814 76.2554 75.8702 75.8702 75.9998 75.0998 74.3294 72.0182 72.0182 72.0182 71.2478 71.2478 70.0922 70.0922 70.0922	5.52142e-18 3.02882e-17 8.31256e-17 8.31256e-17 8.31256e-17 8.31256e-17 9.19328e-15 9.19328e-15 9.19328e-15 9.19328e-15 2.34327e-10 E value 3.3189e-22 3.57877e-21 2.22491e-20 1.96544e-16 6.8708e-16 7.34508e-16 9.43421e-16 2.67708e-15 2.72213e-15 1.00884e-14 1.13384e-14 1.13384e-14 1.13384e-14 1.13205e-14 1.19205e-14 1.9958e-14 2.21026e-14 2.21026e-14 2.21026e-14 1.9958e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9058e-14 1.9205e-14 1.92

rotund (gene 1)

BLAST Hit Summary			
Description	Species	Score	E value
m-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				
 	m-PF	Dmel	228.409	2.59572e-60				
✓	m-PE	Dmel	227.639	3.74713e-60				
 	m-PG	Dmel	227.639	4.00578e-60				
✓	sqz-PA	Dmel	223.787	6.44705e-59				
✓	dati-PA	Dmel	112.849	1.64339e-25				
 Image: A start of the start of	dati-PC	Dmel	112.849	1.64339e-25				
✓	dati-PD	Dmel	112.849	1.72776e-25				
 	dati-PB	Dmel	111.309	4.7024e-25				
✓	gI-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				
\checkmark	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

spineless		,			
1		Description	Species	Score	E value
	\checkmark	ss-PD	Dmel	266.929	1.79906e-71
	✓	ss-PC	Dmel	266.929	1.79906e-71
	 Image: A set of the set of the	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
	\checkmark	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
	 Image: A set of the set of the	tgo-PA	Dmel	46.595	3.98431e-05
	\checkmark	sima-PD	Dmel	45.0542	0.000132482

Gene groups for phylogenetic analyses	Coding Sequence
aristaless-apterous-BarH1-clawless-Lim1	al_Dmel_Q06453
1	al_Anopheles_gambiae_A0A1S4GWX6
	al_Tribolium_castaneum_A0A139WH33
	al_Strigamia_maritima_TTIYK9
	al_C_elegans_Q21836
	al Danio rerio B3DK19
	al Human 0960S3
	al Mus musculus O35085
	al_Xenopus_tropicalis_A0A6I8S3E9
	ap_Dmel_E1JGX9
	ap_Human_P50458
	ap_Rattus_norvegicus_P36198
	ap_Mus_musculus_Q92082
	ap_Achopus_hopicans_AOA010QAN6 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
	barh 1_C_elegans_Q22909 barh 1_Dania_reria_Q53B63
	cll Dmel 07KS72
	cll Anopheles gambiae O7POE6
	cll Tribolium castaneum D6WZY0
	cll_Stegodyphus_mimosarum_A0A087SVI5
	cll_Strigamia_maritima_T1JC39
	cll_Danio_rerio_Q8JI11
	cll_Xenopus_tropicalis_F6TEU6
	cll_Mus_musculus_055144
	cll Pottus porvegious D4A270
	lim1 Dmel O9V472
	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_Q/QHD1 lim1_Stagedumbug_mimogerum_A0A087TMA0
	lim1_Stegodyphus_himosarum_A0A0671MA9
rotund-alass	rn Dmel O9VI93
Totuna-glass	rn Human Q5T0B9
	rn_Rattus_novergicus_D4A633
	rn_Mus_musculus_B1ASA5
	rn_Xenopus_tropicalis_Q0V9P9
	rn_Danio_rerio_Q1LXQ0
	rn_C_elegans_G5EGB2
	m_Anopheles_gamblae_A0A154GE00
	rn Bombyy mori A0A0C5AMI7
	gl Dmel P13360
	gl Human Q96JB3
	gl_Rattus_novergicus_D4A9X7
	gl_Mus_musculus_Q07230
	gl_Xenopus_tropicalis_A0A6I8Q066
	gl_Danio_rerio_A0A8M1QLN4
	gI_U_elegans_Q966L8
	gl_Anopheles_gamblae_AUA154UKN0 gl_Tribalium_castaneum_0771F3
	gl_ritosium_casancum_q/2113
	<u>B_110005_005</u> 990_110/10100333

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

spineless-clock	ss Dmel E1JIM6	
spineress ereen	ss Human P35869	
	ss_Rattus_norvegicus_P41738	
	ss Mus musculus Q8R4S5	
	ss Xenopus tropicalis F7DNN6	
	ss Danio rerio Q4U3K9	
	ss C elegans 044712	
	ss Anopheles gambiae Q7PM78	
	ss Tetranychus urticae T1JYU4	
	ss Strigamia maritima T1IKB1	
	clk_Dmel_061735	
	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	