Developmental Studies on Eye Types and Pedipalps in *Parasteatoda tepidariorum*

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Submitted by

Christoph Schomburg

from Osterode am Harz

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Thesis Committee
Dr. Nikola-Michael Prpic-Schäper (advisor)
Department of Developmental Biology
Georg-August University Göttingen

Prof. Dr. André Fiala
Department of Molecular Neurobiology of Behaviour
Georg-August-University Göttingen

Prof. Dr. Tim Beißbarth
Department of Medical Statistics
University Medical Center Göttingen

Further members of the examination board
Prof. Dr. Ernst Wimmer
Department of Developmental Biology
Georg-August University Göttingen

Prof. Dr. Gregor Bucher
Department of Evolutionary Developmental Genetics
Georg-August University Göttingen

Dr. Roland Dosch
Department of Developmental Biochemistry
University Medical Center Göttingen

Date of oral examination: 21.07.2017

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Herewith I ensure, that the thesis “Developmental Studies on Eye Types and Pedipalps in *Parasteatoda tepidariorum*” has been written independently and with no other sources and aids than quoted. Apart from the publication below the thesis has not been published so far. I also declare that I have not previously applied for a doctoral degree at another university.

__________________________________ Göttingen, May 31st, 2017

Christoph Schomburg

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List of abbreviations

ALE – Anterior lateral eyes
DNA – Desoxyribonucleic acid
GO – Gene ontology
LE – Lateral eyes
ME – Median eyes
MLE – Median lateral eyes
PCR – Polymerase chain reaction
PLE – Posterior lateral eyes
RNA – Ribinucleic acid

Species names

A. queenslandica – Amphimedon queenslandica
B. floridae – Branchiostome floridae
C. gigas – Crassostrea gigas
C. intestinalis – Ciona intestinalis
C. owzarzaki – Capsaspora owzarzaki
C. salei – Cupiennius salei
D. melanogaster – Drosophila melanogaster
D. pulex – Daphnia pulex
D. rerio – Danio rerio
E. kanangrensis – Euperipatoides kanangrensis
E. multilocularis – Echinococcus multilocularis
G. marginata – Glomaris marginata
H. robusta – Helobdella robusta
L. anatina – Lingula anatina
L. polyphemus – Limulus Polyphemus
M. leidyi – Mnemiopsis leidyi
M. musculus – Mus musculus
N. vectensis – Nematostella vectensis
P. caudatus – Priapulus caudatus
P. dumerilii – Platynereis dumerilii
P. auricularia – Polycelis auricularia
P. mammillata – Phallusia mammillata
P. tepidariorum – Parasteatoda tepidariorum
S. purpuratus – Strongylocentrotus purpuratus
S. rosetta – Salpingoeca rosetta
T. castaneum – Tribolium castaneum
X. tropicalis – Xenopus tropicalis

Gene names

cnc – cap ‘n’ collar
col - collier
croc - crocodile
CtBP – C-terminal binding protein
da - daughterless
dac - dachshund
dl - dorsal
Dr - Drop
ds - dachsous
ems – empty spiracles
en - engrailed
exd - extradenticle
ey - eyeless
eya – eyes absent
E(z) – Enhancer of zeste
Fas2 – Fasciclin 2
gsb - gooseberry
hb - huinchback
hh - hedgehog
hkb - huckebein
HMGB1 – High Mobility Group B Member 1
hth - homothorax
klu - klumpfuss
Kr - Krüppel
lab - labial

lbe – ladybird early

maf-s -

Med - Medea

otd - orthodenticle

Pc - Polycomb

pho - pleiohomeotic

ph-p – polyhomeotic-proximal

prd - paired

repo – reversed polarity

sens - senseless

Sfmbt – Scm-related gene containing four mbt domains

slp – sloppy paired

so – sine oculis

tll - tailless

toy – twin of eyeless

trx - trithorax

Ubx - Ultrabithorax

vnd – ventral nervechord defective

vri - vrille

wg - wingless

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1 Summary

Arthropods are by far the most species rich phylum in the animal kingdom and their evolutionary success is at least in part rooted in their diverse morphology. Despite these morphological differences, arthropods share a common segmented body plan. These two factors make the arthropods an ideal group for comparative studies. Furthermore, arthropods, and especially chelicerates, show many lineage-specific evolutionary novelties. Parts of both these aspects were addressed in the spider *Parasteatoda tepidariorum* in the four parts of this thesis

Molecular characterization and embryonic origin of the eyes in *P tepidariorum*

Two visual systems are present in most arthropod groups: median and lateral eyes. Most of our current knowledge about the developmental and molecular mechanisms involved in eye formation in arthropods comes from research in the model system *Drosophila melanogaster*. By contrast, not much is known about the development of the up-to-eight eyes present in spiders. Therefore, the embryonic expression of core retinal determination genes in the common house spider *Parasteatoda tepidariorum* was analyzed. The anlagen of the median and lateral eyes in *P. tepidariorum* originate from different regions of the non-neurogenic ectoderm in the embryonic head. The median eyes are specified as two individual anlagen in an anterior median position in the developing head and subsequently move to their final position following extensive morphogenetic movements of the non-neurogenic ectoderm. The lateral eyes develop from a more lateral position. Using gene expression analyses, a unique combination of determination gene expression in the anlagen of the lateral and median eyes, respectively were identified.

Phylogenetic analysis of forkhead transcription factors

The forkhead family of transcription factors is present in the entire animal kingdom and has roles in various aspects of development and physiological processes. Although homologs of family members have been identified in almost all animals, the relationship between the different groups, especially arthropods and vertebrates is not entirely clear. Therefore, homologs of forkhead transcription factors were identified from the official gene sets of animals with sequenced genomes from all major phylogenetic groups available. This resulted in the categorization of forkhead domain genes into 25 different classes. The roles of these classes correlated with the evolutionary novelties of animal groups, sharing these genes. Moreover, the genomic organization of the forkhead genes was analyzed, adding further evidence to the presence of a conserved cluster from a subset of forkhead genes in different animal lineages.

Embryonic development of the pedipalp in *P. tepidariorum*

The pedipalp is the appendage of the tritocerebral segment in chelicerates. Its development is dependent on the Hox gene *labial*, which gives identity to this segment. Apart from that, the genetic framework, which leads to the development of this appendage and its specific morphology, different from the walking legs is unknown. Therefore, homologs of genes were identified and analyzed, which were known from *Drosophila* to be expressed in the tritocerebral segment, or which interact with *labial*, since they might have retained ancient functions in *P. tepidariorum*. None of the genes analyzed here showed exclusive expression in the pedipalps, or differential expression patterns between the pedipalps and the legs, but they gave insights into various aspects of shared and diverged developmental processes among arthropods.

Development of the bulbus organ in *P. tepidariorum*

The bulbus organ is a specialized outgrowth of the male spiders' pedipalp tarsus, which is used as a copulatory organ. It is developed between the last juvenile stage and the adult in a process called pediapalp metamorphosis. Nothing is known of the developmental processes and genetic basis during this process. Therefore, the transcriptomes of juvenile, subadult male, subadult female and adult male spiders were used to find genes, which might be involved in the development of this structure. The analysis resulted in a set of candidate genes, which showed a specific and high expression in the developing subadult male pedipalps. Apart from a large number of genes, which appeared to be specific to spiders, or even only *P. tepidariorum*, candidate genes included a set of transcription factors with known roles in appendage or sex-specific development.

2 General introduction

Over the course of evolution, the animal kingdom has produced a plethora of species with different morphologies and adaptations, which allowed animals to survive in almost all conditions and niches imaginable. Arguably, the most successful group of animals are the arthropods with over one million species described and 5-10 million species estimated (Ødegaard 2000). Arthropods, morphologically, can be divided into four major groups. The Chelicerata (e.g. spiders, scorpions, mites), the Myriapoda (millipedes and centipedes), the Crustacea (e.g. crabs, crayfish), and the Hexapoda (e.g. beetles, flies). Phylogenetic relationships among arthropods show the Chelicerata to be the most basally branching and sister group to the Mandibulata, which is comprised out of the Myriapoda and the Pancrustacea, containing Crustacea and Hexapoda, although molecular phylogenies argue for a paraphyletic relationship of Hexapoda and Crustacea (Regier et al. 2010) (Figure 1).

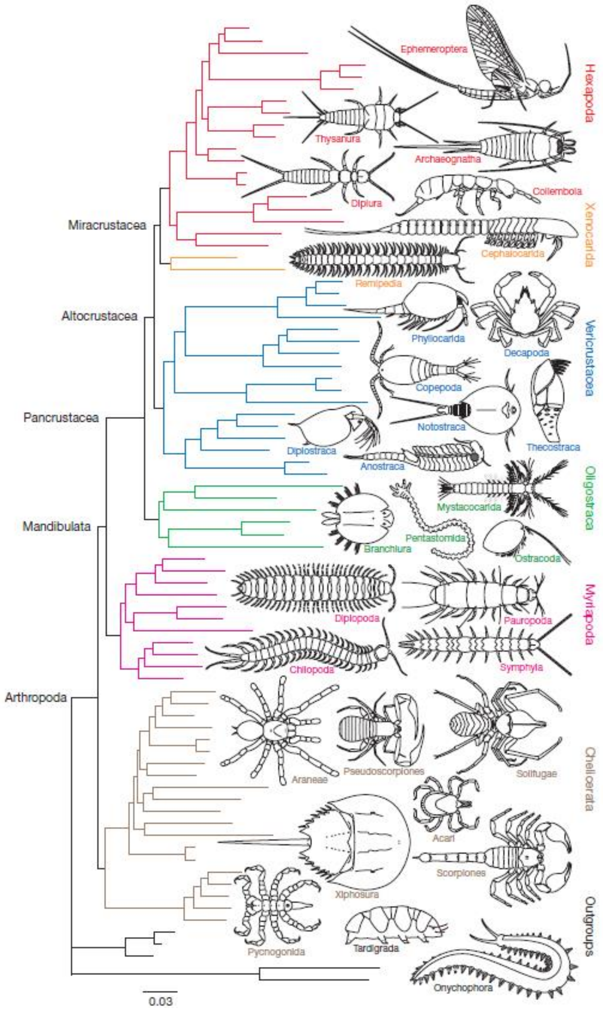

Figure 1 – Phylogenetic relationships among arthropods. Tardigrades and onychophorans are the sister group to the arthropods. The most basally branching group are the chelicerates, which are the sister group to the Mandibulata, consisting of Myriapoda and the Pancrustacea. In contrast to classical morphology based phylogenies, there is no distinction of Crustacea and Insecta. Instead, the Hexapoda together with the Xenocarida form a subphylum of the Pancrustacea, as in (from Regier et al. 2010)

Although arthropods show a large diversity in sizes and shapes, they share a segmented body plan with articulated appendages, which is believed to be one of the major causes for their evolutionary success (Angelini & Kaufman 2005). Based on the similarity of their bauplan and the diverse adaptations in different lineages (Figure 2), this group of animals is very well suited for comparative studies to better understand the evolutionary mechanisms, which shape the differences in the development of the bodyplan. Pioneer subjects of these studies were the Hox genes, the genetic basis of homeotic transformations first shown in *Drosophila melanogaster* (Lewis 1978) and their conservation in other metazoan animals (McGinnis et al. 1984). The study of conserved genes that are involved in the same developmental processes in diverse animals and the fact that these genes could also have different functions, ultimately lead to the emergence of a new field, the Evolutionary-Developmental Biology (Evo-Devo) (Müller 2007, Raff 2000), which in the beginning was dominated by the comparative studies on insects (Heffer & Pick 2013).

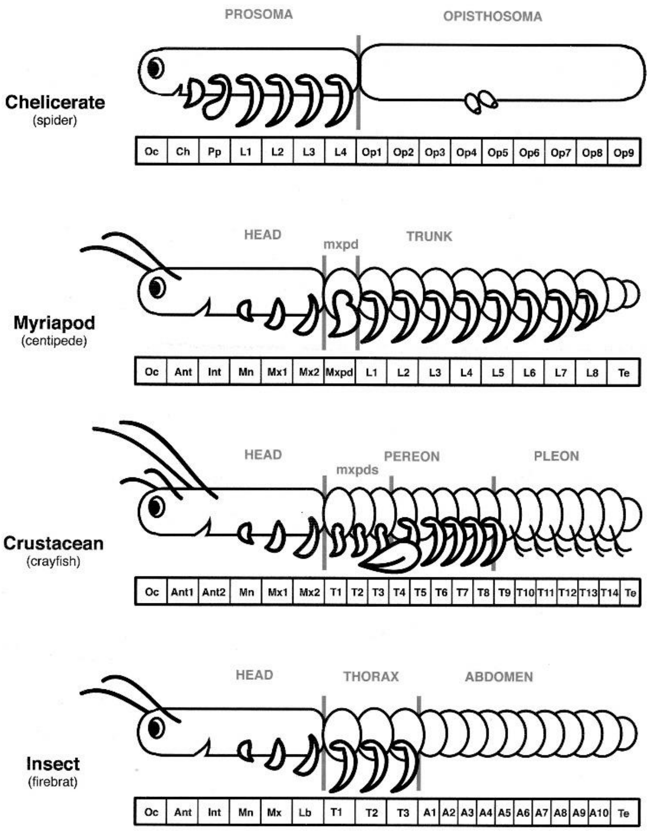

Figure 2 – Overview of arthropod body plans. Chelicerates are subdivided into prosoma and opisthosoma with the prosoma consisting of ocular, cheliceral, pedipalpal, and four leg-bearing segments and the opisthosoma comprised out of nine segments with the spinnerets developing on the opisthosomal segments 4 and 5. Myriapods are divided into a head consisting out of six segments and a variable number of leg-bearing trunk segments. In centipedes, head and trunk are separated by a maxillopod segment. Crustaceans have a large diversity of body plans, but can be subdivided into a head consisting out of six segments with the 2nd antennae as an appendage on the tritocerebral segment. The head is followed by a variable number of maxillopods, the pereon, which usually bears walkings legs and the pleon, which usually bears swimming legs. Insects show three different tagmata. A head consisting out of six segments, the three segment-spanning thorax, which bears the walking legs, and the limbless abdomen (modified from Hughes and Kaufman 2002)

Their position as basally branching arthropods make the chelicerates very good models for comparative studies with other arthropods to help understand the evolutionary history of this clade (McGregor et al. 2008). In recent years, chelicerates in general, and spiders particularly, have helped to broaden the knowledge of a variety of developmental processes. Studies have analyzed the development of appendages (Janssen et al. 2008, Pechmann & Prpic 2009, Prpic & Damen 2004, Prpic et al. 2003), segmentation (Damen et al. 1998, 2005; Janssen et al. 2011, Kanayama et al. 2011), or bodyplan evolution (Akiyama-Oda & Oda 2006, Khadjeh et al. 2012, Pechmann et al. 2015), or the evolution of new structures by gene duplication and subsequent neofunctionalization (Turetzek et al. 2016), and thus have shown conserved and derived aspects of many developmental processes.

Apart from the study of the conserved aspects among arthropods, spiders provide a chance to study a number of evolutionary novelties. Spiders have evolved toxins to capture prey, which show a high potential for therapeutic use in the development of new drugs (Lewis & Garcia 2003). Moreover, toxin genes provide a chance to study the molecular evolution and diversification of recently evolved genes, the selective forces involved in the selection of prey and toxin specificity, and the convergent evolution of the modular composition and physiological targeting of toxins among venomous animals (reviewed in Casewell et al. 2013).

Spiders have also evolved the ability to produce silk with interesting mechanical properties (Gosline et al. 1986) with various compositions depending on their purpose as e.g. drag line silk, or for cocoon building (Hayashi et al. 1999) from a number of conserved peptide subunits, which are assembled by a change in ionic composition in the silk glands (Gatesy et al. 2001, Hagn et al. 2010). Spider silk has also come to the attention of medical research, due to its suitability to act as a guide for nerve regrowth after injury and the ability to act as a scaffold for the growth of skin during the treatment of burn wounds (Allmeling et al. 2006, 2008; Radtke et al. 2011).

Several aspects of spider biology were addressed in this thesis through studies in the best-established spider model *Parasteatoda tepidariorum.* Firstly, the development of the visual systems in spiders was analyzed with respect to the expression of conserved retinal determination factors, as well as the embryonic origin of the two distinct eye types. Secondly, the recently sequenced *P. tepidariorum* genome (Schwager et al. 2017), along with the genomes from a variety of animals was used to investigate the phylogenetic history of the forkhead domain containing genes. Thirdly, with a candidate gene approach it was attempted to identify genes, which could potentially influence the morphology of the pedipalps during embryonic development. Lastly, the genetic basis for the development of the male specific bulb apparatus was investigated, by comparison of transcriptomes from different post-embryonic stages of *P. tepidariorum*.

3 Material & methods

3.1 Spider culture

Spider embryos and juvenile, subadult, and adult stages of *P. tepidariorum* were obtained from our Laboratory stock in Göttingen. The embryos were staged as previously published (Mittmann & Wolff 2012).

3.2 Molecular methods

3.2.1 RNA isolation

3.2.1.1 *RNA isolation for cDNA synthesis*

Total RNA for cDNA synthesis was isolated from a mixture of all embryonic stages of P. tepidariorum using TRIzol® (Life Technologies, Thermo Fisher Scientific, Carlsbad, CA, USA) according to the manufacturer's instructions.

3.2.1.2 *RNA isolation for next Illumina® sequencing*

Juvenile, subadult, and adult spiders were dissected on dry ice. Collected samples were snap frozen in liquid nitrogen and stored at -80°C until further use. Total RNA was extracted with the ZR Tissue & Insect RNA MicroPrep™ Kit (Zymo Research Group, Irvine, CA, USA) according to the manufacturer's instructions.

3.2.2 cDNA synthesis

cDNA for cloning purposes was synthesized using the SMARTer™ PCR cDNA Synthesis Kit (Clontech, Mountain View, CA, USA), according to the manufacturer's instructions.

3.2.3 Cloning

3.2.3.1 *PCR*

Primers for the PCR reaction to amplify fragments from cDNA were designed using Primer3 (Untergasser et al. 2012) (Table 1). PCRs were performed with the Taq DNA polymerase (Thermo Fisher Scientifc, Carlsbad, CA, USA).

Table 1 – List of used primers

Gene specific primers:	
Name:	**Sequence 5' →3':**
cnc_fwd	GTTCGTTTAGGTTCAACATCAGCC
cnc_rev	ACTTGATTGCCGGAATTTCTTGG
col2_fwd	TGGGACCAGTAACTTATGGCACTG
col2_rev	TCTGTGGGAGTTGTAGCTGTGC
croc_fwd	CCCTTTACGGTGAACATCATGGC
croc_rev	TGAAGTTCCGACGCCAAAGTTC
CtBP_fwd	CGCCCTGGTGCATTTCTAGTG
CtBP_rev	ATGAGGTGCTGGGATGGCTG

CTCF_fwd	TCAGGAACCAGGCCCAAGTG
CTCF_rev	GTGTCGCTTTCTCATGTGCCG
da_fwd	TCCCTCCAACCTCTACATTCCAC
da_rev	TGATGCTGCTTTTCTAGATGCGG
dac1_fwd	CCGGTGGTGTGCAATGTAGAGC
dac1_rev	TTCGTGATGGGGTTATTGTTGC
dac2_fwd	CGTCTTCCCAAACCGCCACGTG
dac2_rev	GTCTGCTCCGTCATTGTATGGTCC
dl1_fwd	GCACCACGGAGCCTTAGATTTAG
dl1-rev	GGGTGAAGTGGCGAAATTGGG
dl2-fwd	CGGGCCGCCTTATTTTCCAC
dl2-rev	AGTGTGAGTTTCCAATGCCAACC
dl3-fwd	ATTCAATCACCTGGTCCGCC
dl3-rev	ACAGAAAGGATGCCGAGATTTGG
Dr1_fwd	GATTGTTCACGAAGTCCAAGTCC
Dr1_rev	TCATTGAAGGAATGCAATACGG
Dr2_fwd	TAGCGTGGATATGGAAGAGTCG
Dr2_rev	GGGCACACAGTTGAAGATGAAG
Dr3_fwd	CGAATCATCACCAAACAAATCC
Dr3_rev	TAGGCGACGACGTATAGAATGG
ds_fwd	GAACAACGCGTTTCGTTTGTC
ds_rev	AATCGTGGCGCATTATCATTG
ems1_fwd	AGTCAGTCTTGTTCTTCAGTCT
ems1_rev	AAGCAAAATAAAGTTCGCTTCG
ems2_fwd	GGTCCGAACATCCTGTGGCTG
ems2_rev	TGGCCCACTCTCAATCTCAACC
ems3_fwd	ACAATGCTTCTCCGGTTTCTGTC
ems3_rev	CTTCGCACTTTTCATCACTGGTG
eya_fwd	CTATCCTTCGTCCTACTATAGCAGTATG
eya_rev	GCCAAAGTTGCCCAATTGTCAG
E(z)_fwd	CGCAATAAGAAACCCACCCGC
E(z)_rev	ACACCGACAGCCTGGAAATC
Fas2-1_fwd	CGAACCCACTCACCTACACTTG
Fas2-1_rev	ACTCCTTTCCACAGCTTTGTCC
Fas2-2_fwd	GGTCCTAAAGGTCCCATTGTTG
Fas2-2_rev	GTGATCCAAGGGAATTTTCAGC
Fas2-3_fwd	CAGCAGATGATGGAGGATTGCC
Fas2-3_rev	ACAACAGTCTCTCCTACTTCGCC
gsb_fwd	ACTGCTTTAGCTGGGAACTTCG
gsb_rev	ATAAGCCTAAGGCCCTGAATCC
hkb1_fwd	GGGGATTCCCTGAGAAAATCAG
hkb1_rev	GCATTCTCTGATGCGTTTTCAC
hkb2_fwd	AGTCACTCAGATTTCACTACGGC
hkb2_rev	CAGTTTTGGATATGGCATGCGC
HMGB1_fwd	CCATTCCGGCATCAGAATATG
HMGB1_rev	CAGCAGCAGCTCTCGCTTTAG

klu_fwd	`TTCCCCGTTTGTTCTCCGCAG`
klu_rev	`TCATTGTGGGTGGTGTCCGAG`
Kr1_fwd	`CGAGCAAAGTCGCCGTAACG`
Kr1_rev	`TTACGATGGTGGCGGAGGTC`
Kr2_fwd	`CCGACAGCACAGTGTCAAATGG`
Kr2_rev	`TCGCAACCTGAACAAACTGCC`
lbe_fwd	`AATTCCATCTCCGCCACCAG`
lbe_rev	`TTAGATGATCCAGTCACCTTTGC`
maf-s_fwd	`GGGTGACATGGATTTTGGGGAT`
maf-s_rev	`AGGAATGTCTAAGTCAGGAGGAA`
Med_fwd	`GCTCAACCACAGACTGATGCG`
Med_rev	`CCGACTGAATTTGGCCCTGG`
otd1_fwd	`CGCTGGTGTGAGGACATCGAC`
otd1_rev	`CTGAAGATTCCTTGGTGGTATG`
otd2_fwd	`CGGGTTCCTCCTGCGCTCC`
otd2_rev	`GGCAAATAGTCCATGTTCATG`
ovo_fwd	`GGCAAAAAGCTGAAGGTGGTAG`
ovo_rev	`TTATGCAATGCGGGACTAAGAG`
pax6.1_fwd	`CCGAGTATTGGACAACCCATGG`
pax6.1_rev	`TCATAACTCCTAGTCCCGCCAG`
pax6.2_fwd	`ACACCATCAACATCAGCTGACG`
pax6.2_rev	`TTTCAGACGCATTCGCATTTGG`
Pc_fwd	`TGGAGCTGTCATCTGTTGGTG`
Pc_rev	`TGTACTGCTAGGCGTGGATGG`
peropsin_fwd	`TCGGAAATGGTGCCGTACTCA`
peropsin_rev	`GCAGAGGAGGGTGGCAAGAAT`
pho1_fwd	`TCCTGGTCGGTATGCCTGTTG`
pho1_rev	`AACATAAGGTCTGTCGCCCG`
pho2_fwd	`TTGAGTGTGTTGATGGGCATCC`
pho2_rev	`TCCCGCATTCAGCACATACATG`
ph-p1_fwd	`ACAGTCACGCCGTCCTCATC`
ph-p1_rev	`TGCACGTCCCATTGTAAATCCC`
ph-p2_fwd	`TCAGCAACCGAATCAATGGAGG`
ph-p2_rev	`GAACACTCCACTTGGAAGGTGG`
prd_fwd	`TGTCCGTCCTTGCGTCATCAG`
prd_rev	`TAGGAAATGGTGCGGGGTTCC`
repo1_fwd	`ACCGACTCTTGATAGACAGCCC`
repo1_rev	`ACTCTCGCTTCACTGAGGTCC`
repo2_fwd	`ATGCTCGGTGGTATGACGCAG`
repo_2_rev	`AGGTGGAAGGGAAGTCAAGCG`
sens_fwd	`ACGGCGCAGAAAGAAGCAAG`
sens_rev	`TCCATGTGTCGCAGGAGGTC`
Sfmbt1_fwd	`TTGCTCTTTCCAATTGCTGGGA`
Sfmbt1_rev	`AGGTATTGTTTTAGCACCCACCA`
Sfmbt2_fwd	`TGTTGTCCTTCTACTCCCTGCTG`
Sfmbt2_rev	`CGGGACTTTCGCAATCACACC`

slp_fwd	`CCATCAGCAGCCTTATCAACG`
slp_rev	`CAGAACTGGACGTCGTGGAAC`
six3.1_fwd	`AAGATCGTGCCAAGGCATTC`
six3.1_rev	`TGCTCAGGAGGATGTAAGCTGC`
six3.2_fwd	`TAGGACACCTTCCTTTTCTATTTAC`
six3.2_rev	`TTAGTAGAGATGATATCTCGATCCG`
so1_fwd	`TGCGGATTGCAGGATAGAGAC`
so1_rev	`CTGGATGCGTGGGACTGA`
so2_fwd	`AACAACAATCTCCCGTCTTTCG`
tll_fwd	`GGCCACCACTGAGGAAATTATG`
tll_rev	`ATTTTCTCCAGCCTCACCAGTC`
trx_fwd	`CTGTCCCGTTTGCCACAAGTG`
trx_rev	`TGCCCACAGTACAACAATCGTCC`
vnd1_fwd	`ATTTGTCTGATGTGACGCTTCC`
vnd1_rev	`CCTCAGCTTGTTGCTTGTTCAG`
vnd2_fwd	`TTTCTGTGCGTGATATTTTGGAC`
vnd2_rev	`CAACGCTGCTGATGAAATAAATG`
vri_fwd	`CTCCAAATCCCTACCAGTCACC`
vri_rev	`GTTCTGCACCCATTCCTTTACC`
Standard primers:	
M13_fwd	`GTAAAACGACGGCCAG`
M13_rev	`CAGGAAACAGCTATGAC`
SP6	`GATTTAGGTGACACTATAGA`
T7	`GTAATACGACTCACTATAGGGCGAAT`

3.2.3.2 *Transformation*

After gel-electrophoresis, bands of the expected sizes were excised with a scalpel and extracted from the gel with the NucleoSpin® Gel and PCR Clean-Up kit (Macherey-Nagel, Düren, Germany) and were ligated into the pCR®II vector using the TA Cloning ® Kit Dual Promoter (Life Technologies, Thermo Fischer Scientific, Carlsbad, CA, USA). Chemically competent Escherichia coli DH5a cells were transformed with the ligated vectors and positive colonies were selected from LB-Agar plates containing 40 µl X-Gal (4% in DMF) after over-night incubation at 37°C. Positive colonies were picked and amplified over-night in 3 ml LB medium containing 1:2000 ampicillin.

3.2.3.3 *Plasmid preparation*

Plasmid DNA was extracted using either the Zyppy™ Plasmid Miniprep Kit (Zymo Research, Irvine, CA, USA), or the NucleoSpin® Plasmid Miniprep Kit (Macherey-Nagel, Düren, Germany). Clones were further tested by test digest with EcoRI (New England Biolabs, Ipswich, MA, USA) and clones with the correct insert size were send for Sanger sequencing to LGC Genomics (Berlin, Germany) or SeqLab (Göttingen, Germany).

Table 2 – List of clones used in this thesis

Name:	Accession Number:	Clone:	Reference:
cnc	-	own cloning	this work; sequence in appendix
col2	-	own cloning	this work; sequence in appendix
croc	-	own cloning	this work; sequence in appendix
CtBP	-	own cloning	this work; sequence in appendix
CTCF	-	own cloning	this work; sequence in appendix
da	-	own cloning	this work; sequence in appendix
dac1	FM945397.1	Dr. Matthias Pechmann	Pechmann et al. 2009
dac2	KP725072	Dr. Natascha Zhang	Schomburg et al. 2015
dl2	-	own cloning	this work; sequence in appendix
dl3	-	own cloning	this work; sequence in appendix
Dr1	-	own cloning	this work; sequence in appendix
Dr2	-	own cloning	this work; sequence in appendix
Dr3	-	own cloning	this work; sequence in appendix
ds	-	own cloning	this work; sequence in appendix
ems1	-	own cloning	this work; sequence in appendix
ems2	-	own cloning	this work; sequence in appendix
ems3	-	own cloning	this work; sequence in appendix
eya	KP725071	own cloning	Schomburg et al. 2015
E(z)	-	own cloning	this work; sequence in appendix
Fas2-1	-	own cloning	this work; sequence in appendix
Fas2-3	-	own cloning	this work; sequence in appendix
gsb	-	own cloning	this work; sequence in appendix
hkb1	-	own cloning	this work; sequence in appendix
HMGB1	-	own cloning	this work; sequence in appendix
klu	-	own cloning	this work; sequence in appendix
Kr1	-	own cloning	this work; sequence in appendix
maf-s	-	own cloning	this work; sequence in appendix
Med	-	own cloning	this work; sequence in appendix
otd1	AB096074.1	Dr. Matthias Pechmann	Akiyama-Oda and Oda 2003
otd2	KP725073	own cloning	Schomburg et al. 2015
ovo	-	own cloning	this work; sequence in appendix
pax6.1	FM945394.1	Dr. Matthias Pechmann	Pechmann et al. 2009
pax6.2	KP725068	own cloning	Schomburg et al. 2015
Pc	-	own cloning	this work; sequence in appendix
peropsin	KP725074	own cloning	Schomburg et al. 2015
pho1	-	own cloning	this work; sequence in appendix
pho2	-	own cloning	this work; sequence in appendix
ph-p2	-	own cloning	this work; sequence in appendix

prd	-	own cloning	this work; sequence in appendix
repo1	-	own cloning	this work; sequence in appendix
sfmbt1	-	own cloning	this work; sequence in appendix
slp	-	own cloning	this work; sequence in appendix
six3.1	AB605265.1		Kanayama et al. 2011
six3.2	AB605266.1		Kanayama et al. 2011
so1	KP725069	own cloning	Schomburg et al. 2015
so2	KP725070	own cloning	Schomburg et al. 2015
tll	-	own cloning	this work; sequence in appendix
trx	-	own cloning	this work; sequence in appendix
vnd1	-	own cloning	this work; sequence in appendix
vnd2	-	own cloning	this work; sequence in appendix

3.2.4 Whole mount in-situ hybridization

3.2.4.1 *RNA probe synthesis*

Antisense RNA probes were synthesized with 6 µl linearized DNA template, 1 µl 10x transcription buffer (Roche), 1 µl DIG RNA labeling mix (Roche), 1 µl RNase Inhibitor (Roche) and 1 µl SP6 or T7 RNA polymerase (depending on the orientation of the insert) were mixed and incubated for 2 h at 37°C. The RNA probes were precipitated by adding 80 µl H_2O, 20 µl NH_4Ac, and 500 µl 100% EtOH and storage at -20°C for one hour. After centrifugation (15,000g, 30 min, 4°C), the pellet was washed with 70% EtOH and centrifuged again. The resulting pellet was air-dried and resuspended in 40 µl resuspension buffer (50% Formamide, 5x SSC (pH 4.5), 0.1% Tween-20, 20µg/ml heparin).

3.2.4.2 *Embryo fixation*

P.tepidariorum embryos were fixated as previously described for *Cupiennus salei* (Prpic et al. 2008a).

3.2.4.3 *Staining*

Preparations and staining was performed as previously described (Prpic et al. 2008b). Additionally, embryos were counterstained with SYTOX Green (Life Technologies, Carlsbad, CA, USA) to mark nuclei.

3.2.5 Imaging

Images were taken with Leica M205 FA binocular (Leica Microsystems, Wetzlar, Germany) equipped with a QImaging MicroPublisher 5.0 RTV camera (QImaging, Surrey, Canada) and UV light. Stacks of nuclear SYTOX® stainings were taken with a Zeiss LSM 510 microscope (Zeiss, Oberkochen, Germany). Images were corrected for color values and brightness with Adobe Photoshop image processing software (version 12.0).

3.3 Bioinformatical methods

3.3.1 Phylogenetic analyses

3.3.1.1 *Identification of homologs*

Potential homologs were identified via BLAST search (version 2.4.0) of a given *D. melanogaster* protein sequence against the custom database of *P. tepidariorum* protein predictions (Camacho et al. 2009). The thus identified *P. tepidariorum* homologs were then back-blasted against the UniProtKB / Swiss-Prot and the Reference proteins database available at the NCBI BLAST homepage. For the identification of opsin homologs, opsin sequences from *D. melanogaster* were blasted against the *P. tepidariorum* protein predictions from the official transcriptome (Posnien et al. 2014), which were aligned with previously published opsin sequences (Delroisse et al. 2014, Feuda et al. 2014, Zopf et al. 2013)

3.3.1.2 *Alignments*

Alignments of the protein sequences were performed using the Clustal Omega algorithm (version 1.2) (Sievers et al. 2014) with automated settings.

3.3.1.3 *Fast Tree*

Alignments resulting from the blasts and back-blast to identify homologs of genes expressed in the intercalary segment in *D. melanogaster* or interaction partners of *labial* or *hoxb1* were phylogenetically analyzed using the FastTree algorithm (version 2.1.5) (Price et al. 2009), using the Jones-Taylor-Thorton model and optimized Gamma20 likelihood. Branch values in all FastTree figures are the FastTree support values and all trees are depicted as cladograms with relative branch lengths

3.3.1.4 *MrBayes*

The phylogenetic tree of opsin sequences was inferred using the parallel version of MrBayes (version 3.2.4) (Ronquist & Huelsenbeck 2003, Ronquist et al. 2012) with default settings for the likelihood model and the priors for the phylogenetic model. The amino acid substitution model was set to “Blosum”, as determined by the MrBayes to be best suited for the input data.

In all other cases Bayesian likelihood was inferred from a subset of the FastTree trees, containing the gene of interest and the closest phylogenetic group of genes. FastTree subsets were cleared from redundant isoforms manually and realigned with Clustal Omega before using MrBayes. The trees are depicted as unrooted trees with branch values indicating the posterior probability.

3.3.1.5 *RAxML*

To infer phylogenetic relationships of forkhead genes, the Randomized Axelarated Maximum Likelihood algorithm (RAxML) was used (version 8.2.1) (Stamatakis 2014). The amino acid substitution model was automatically determined by RAxML as “LG”. The tree depicted is the best scoring maximum likelihood tree out of 75 individual runs.

3.3.2 Domain search

The official gene sets from the NCBI genome database, the predicted protein data from *P. tepidariorum* (Schwager et al. 2017), and the protein predictions from the transcriptomes of *E. kanangrensis* and *G. marginata* (provided by Dr. Nico Posnien and Dr. Ralf Janssen) were scanned with the hmmscan algorithm from HMMER (version 3.1b2) (Eddy 2011) against the Pfam database (Finn et al. 2016).

3.3.3 Annotation of FOX genes

The genomic position of genes with a forkhead domain was visualized with Geneious (version 10.0.1) (Kearse et al. 2012) using the genomic annotation files from the NCBI genome database.

3.3.4 Illumina sequencing

Total RNA was quality checked and prepared for sequencing by the Microarray and Deep-Sequencing Core Facility (TAL) of the University Medicine Göttingen. Sequencing of cDNA from purified mRNA was done with 50 bp single end reads on a HiSeq4000 machine (Illumina, San Diego, CA, USA).

3.3.5 Read mapping

Reads were mapped to the mRNA predictions from the *P. tepidariorum* genome (Schwager et al. 2017) using Bowtie2 (version 2.2.9) (Langmead & Salzberg 2012). Mapping was done with the end-to-end option, allowing for one mismatch per sequence. Unmapped reads were mapped again against the *P. tepidariorum* genome sequence to account for possible genomic contamination. Reads that were still unmapped were mapped with Kraken (Wood & Salzberg 2014) to check for contamination by Bacteria, Archaea, viruses, Fungi, or human sequences (supplemental material 9.5.1).

3.3.6 Differential Expression Analysis

Differential expression analysis between the sequenced sample types was done, with DESeq2 (version 1.16.1) (Love et al. 2014), as outlined by the DESeq2 manual, using R (version 3.2.5) in RStudio Desktop (0.99b). The protein sequences of candidate genes from the *P. tepidariorum* genome (Schwager et al. 2017), which are shown throughout this thesis, were blasted against the NCBI reference sequence database to be able to assign them a name other than the Augustus identifier. In cases, where only one similar sequence was identified which was annotated to be an uncharacterized protein of the *P. tepidariorum* gene predictions from the original i5k genome sequencing with no homologues in other species, this annotation was carried over to the Augustus predictions. For a short description of the functions of identified genes (and in the combination of differential expression and clustering) in the results part, associated GO terms were used from the Gene Ontology Consortium (Ashburner et al. 2000, Blake et al. 2015).

3.3.7 GO term analysis

For GO term analysis *P. tepidariorum* genes were assigned GO terms in a database according to the instructions from the functional annotation and analysis suite Trinotate (version 3.0.1) (Haas et al. 2013). In short, mRNA and protein predictions from *P. tepidariorum* were blasted against the UniProt/Swiss-Prot database, protein predictions were scanned for conserved domains with HMMER (Eddy 2011), scanned for signal peptide cleavage sites with SignalIP 4.1 (Petersen et al. 2011), and scanned transmembrane regions with tmHMM (version 2.0c) (Krogh et al. 2001). Information retrieved from these analyses was written to a SQLite (version 3.13.0) database with the scripts provided by Trinotate from which an Excel file was extracted for further use.

Go term enrichment of lists of candidate genes was performed using GOSeq (Young et al. 2010) from Trinity version (version 2.2.0) (Haas et al. 2013).

3.3.8 Expression cluster analysis

Clustering of genes into clusters with the same profile was done using coseq (Rau & Maugis-Rabusseau 2017) with the settings suggested for the analysis of RNA sequencing data in the manual. The data was normalized with the “DESeq” method. Coseq was run with the “Poisson” model and no data transformation. The number of clusters was determined with “Djump” from a choice of 2 to 50 different clusters possible

4 Molecular characterization and embryonic origin of the eyes in the common house spider *Parasteatoda tepidariorum*

4.1 INTRODUCTION

Animal visual systems allow the perception of environmental information and are essential for basic behaviors like feeding, reproduction, and interaction with the environment. Bilaterians have evolved various organs to perceive visual cues ranging from simple light sensitive cells shielded by a pigment cell, for example, in the planarian *Polycelis auricularia* (Hesse 1897) or the trochophora larvae of the annelid *Platynereis* (Jékely et al. 2008) to sophisticated eyes like compound eyes in insects and lens eyes in vertebrates (Gehring 2014, Gehring & Ikeo 1999). In arthropods, two independent visual systems prepresent: lateral and median eyes (Paulus 1979) (*Figure 3*). It has been proposed that these two visual systems have evolved from one primordial visual organ more than 500 million years ago (Friedrich 2006a,b). The most comprehensive understanding of the processes involved in adult eye formation is available for insects, mainly from work performed in the fruit fly *Drosophila melanogaster*. There, the lateral compound eyes and the dorsal-median ocelli (*Figure 3*B) originate from a few cells of the visual anlage in the dorsal head neuroectoderm in the embryo (Green et al. 1993, Melzer & Paulus 2001, Younossi-Hartenstein et al. 1993). During the first larval instar, these cells are part of the eye-antennal imaginal disc that undergoes massive proliferation throughout larval and pupal development (Domínguez & Casares 2005). Within the eye-antennal imaginal disc, the two visual systems are determined in non-overlapping domains, implying that the anlagen of both visual systems develop largely independent of one another (Pichaud & Casares 2000, Royet & Finkelstein 1995). The retinal field (that is, the anlage of the lateral compound eyes) of the eye-antennal imaginal disc is determined on a molecular level by the action of a cascade of transcription factors that is known as the retinal determination gene network (RDGN). In summary, the *pax6* genes *eyeless* (*ey*) and *twin of eyeless* (*toy*) activate an auto-regulatory network of transcription factors involving *sine-oculis* (*so*), *eyes absent* (*eya*), and *dachshund* (*dac*) (Kumar 2009). The *Drosophila* ortholog of the *six3* gene, *optix*, is involved in eye morphogenesis in an *ey*-independent manner (Seimiya & Gehring 2000) and has been linked to differentiation processes within the retinal field (Li et al. 2013). The core of the RDGN not only determines the retinal field that gives rise to the lateral compound eyes but also operates in the dorsal median ocelli (Aguilar-Hidalgo et al. 2013). However, initial establishment of the ocellar primordium requires unique regulatory interactions between *engrailed* (*en*), *hedgehog* (*hh*), and *orthodenticle* (*otd*), which eventually lead to RDGN activation via *eya* in the ocelli anlagen (Aguilar-Hidalgo et al. 2013; Blanco et al. 2009, 2010; Royet & Finkelstein 1995). Additionally, the RDGN genes *ey* and *dac* are only present in the determination of the lateral compound eyes (Friedrich 2006a,b; Mardon et al. 1994). These data suggest that the molecular mechanisms underlying the determination of the lateral and median eyes represent a combination of shared and unique aspects. Intriguingly, comparative expression data accumulated over the last decades suggest that the core RDGN known from *Drosophila* might be conserved in the various different bilaterian eye types (Gehring 2001, 2014). For instance, members of the *pax* family genes are the most widely conserved eye selector genes and appear to initiate eye development in all animals. *pax6* orthologues are expressed during eye development, for example, in Cnidarians (Kozmik 2008, Kozmik et al. 2003, Plaza et al. 2003, Suga et al. 2010), the lancelet *Branchiostoma floridae* (Kozmik et al. 2007), the polychaete *Platynereis dumerilii* (Arendt et al. 2002), the ascidian *Phallusia mammillata* (Glardon et al. 1997), and the onychophoran *Euperipatoides kanangrensis* (Eriksson et al. 2013b). However, more detailed examination of expression and/or function of RDGN genes also revealed functional differences. For instance, in the flour beetle *Tribolium* and in *Drosophila*, the *pax6* orthologues *ey* and *toy* seem to play a more dominant role during larval eye development, rather than in the adult eyes (Yang et al. 2009). Similarly, in the American Horseshoe Crab, *Limulus polyphemus*, *pax6* does not seem to be expressed in the eye primordia during late embryogenesis, implying that it might not be involved in retinal determination (Blackburn et al. 2008).

Figure 3 - Eyes in spiders and insects. (A) Dorso-frontal view of the eyes of an adult specimen *of P. tepidariorum*. Adult spiders usually have eight eyes: a pair of median eyes (ME) and three pairs of lateral eyes (LE): the median (MLE), posterior (PLE) and anterior lateral eyes (ALE). Note that the PLE and ALE share a common socket in the carapace. (B) Dorsal view of the head of an adult specimen of *D. melanogaster*. Insects also have median and lateral eyes, but these differ in morphology from those of spiders. The median eyes are simple ocelli, whereas the lateral eyes are multi-facetted complex eyes.

In terms of visual system evolution, chelicerates represent an interesting arthropod group because various different eye types have evolved in this class. Horseshoe crabs (Xiphosura) possess large compound lateral eyes, but their median eyes are highly reduced (Fahrenbach 1975, Wald & Krainin 1963). Other chelicerate groups, for example, scorpions (Loria & Prendini 2014) and spiders (Land 1985) have a varying number of simple lateral eyes and one pair of simple median eyes (that may be reduced). In, for example, harvestmen (Opiliones), only a pair of simple median eyes are present, but lateral eyes are entirely missing (Shultz & Pinto-da-Rocha 2007). Mites (Acari) may have a pair of median eyes and one to three pairs of lateral eyes, but most Acari species are lacking eyes altogether (Thor 1931). Spiders usually have four pairs of eyes: (1) one pair of median eyes (ME), which lack a light-reflecting tapetum and usually are the largest eyes and thus the main optical system (Land 1985), and (2) three pairs of lateral eyes, which usually have a light-reflecting tapetum. In adult spiders, the innermost pair of lateral eyes is often situated directly behind the median eyes and they are therefore sometimes called posterior median eyes (Land 1985). However, we prefer the term median lateral eyes (MLE) to clearly denote them as lateral eyes. Depending on their location, the other two lateral eyes are called anterior lateral eyes (ALE) and posterior lateral eyes (PLE) (*Figure 3* A and Figure 4 D, E). The arthropod ground plan includes both median and lateral eyes as two separate visual systems. However, in extant arthropod groups, one of the two systems is usually the dominant visual system, strongly suggesting that a single visual system is largely sufficient. For instance, in insects, the main visual organs are the lateral eyes (compound eyes), whereas the median eyes are simple lens eyes (ocelli) with only poor visual capacities. The ocelli have instead acquired novel functions, for example, in flight stability control (Wilson 1978), or have been entirely reduced in many insect groups (Parry 1947). In contrast, in most spiders, the median eyes represent the main visual system, while the lateral eyes mostly visualize movement (Land 1985). Insects and spiders have thus used different evolutionary strategies for their visual systems. However, so far only little is known about eye development in spiders and the molecular genetic mechanisms that govern their formation. Therefore, we have isolated homologues of several retinal determination genes known from *Drosophila* in the spider *Parasteatoda tepidariorum* and present here an analysis of their expression patterns throughout head development.

4.2 RESULTS

4.2.1 Morphogenesis of the non-neurogenic ectoderm in the embryonic head

P. tepidariorum has one pair of median eyes and three pairs of lateral eyes (*Figure 3* A). Similar to several other members of the spider family Theridiidae, the anterior (ALE) and posterior lateral eyes (PLE) are located very close to each other (Agnarsson 2004), and in *P. tepidariorum* adults, they even share a common socket in the carapace (*Figure 3* A). In *P. tepidariorum*, the formation of the brain begins at stage 9 with the invagination of clusters of neuroblast precursors from the anterior neurogenic ectoderm (Mittmann & Wolff 2012, Stollewerk et al. 2003) (orange tissue in Figure 4 A to D). Shortly after the onset of neuroblast invagination, the first signs of brain differentiation are visible as deep grooves in the head neurogenic ectoderm near the anterior rim of the germ band (anterior furrow, AF in Figure 4 A to C) and oval pits near the lateral edge of the head lobes (lateral furrow, LF in Figure 4 A to C). The rim of the head lobes itself (shown in dark gray in Figure 4) comprises only non-neurogenic ectoderm and starts to overgrow the neurogenic ectoderm of the head at stage 11/12 (Figure 4 B, C). Until stage 13, the non-neurogenic ectoderm originating from the anterior and lateral rim of the head lobes has almost fully overgrown the neurogenic ectoderm and thus covers the developing brain almost completely (Figure 4 D). At stage 14, the brain primordium is fully covered by the non-neurogenic ectoderm (Figure 4 E). The first morphological signs of the lateral eye primordia can be detected as shallow grooves in the non-neurogenic ectoderm from stage 13 onwards (Figure 4 D, E and 19 A). The median eyes are morphologically only visible in postembryonic stages (Mittmann & Wolff 2012).

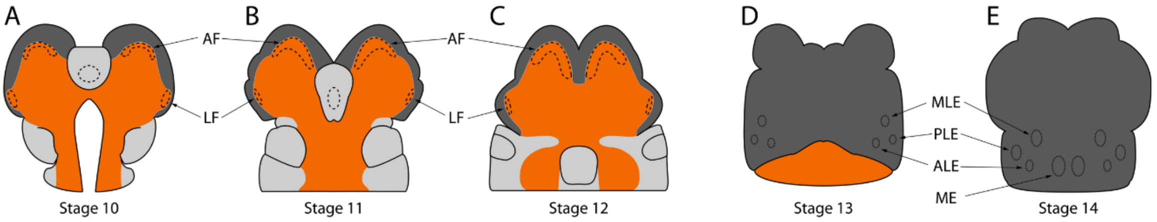

Figure 4 - Morphogenesis of the head region of *P. tepidariorum*. Schematic drawings of embryonic heads in ventral view at stage 10 (A), stage 11 (B), stage 12 (C), stage 13 (D), and stage 14 (E). Stages were defined after [57]. The non-neurogenic ectoderm is shown in gray; the neurogenic ectoderm is shown in orange. The non-neurogenic ectoderm at the anterior rim of the head lobes (dark gray) gradually overgrows the neurogenic ectoderm. The anterior (AF) and lateral furrow (LF) in the brain primordium are indicated. In the non-neurogenic head ectoderm, the primordia of the eyes are also indicated: ALE, anterior lateral eyes; PLE, posterior lateral eyes; MLE, median lateral eyes; ME, median eyes.

4.2.2 *Pt*-peropsin is expressed in all eye primordia at late embryonic stages

Since the eye primordia in *P. tepidariorum* are morphologically visible only late during embryonic and postembryonic development, we sought to identify a molecular marker that prefigures the eye primordia. We identified one homologue of the *peropsin* group and four homologues from the group of r-Opsins (Supplemental material 9.2.1). We cloned these five *opsins* and analyzed their expression throughout late embryonic development. *Pt-peropsin* is the only opsin homologue that is detectable at embryonic stages. It is expressed at stage 14 in three spots on either side of the prosomal shield (white arrowheads in Figure 5 B). These expression domains coincide morphologically with the indentations of the lateral eyes in the epidermal tissue (arrowheads in Figure 5 A). Additionally, *Pt-peropsin* is expressed in two spots in the anterior median region of the prosomal shield (black arrowheads in Figure 5 B). In this median position, the two median eyes will develop during first instar stages (Mittmann & Wolff 2012). In summary, we identify *Pt-peropsin* as embryonic molecular marker for developing eyes in the spider *P. tepidariorum*.

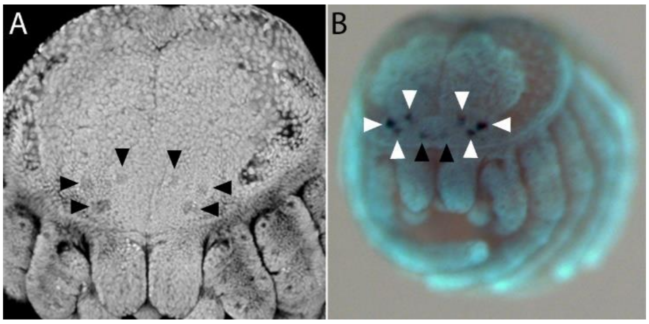

Figure 5 - Markers for eye primordia at the final embryonic stages. (A) Confocal microscopy image of nuclear SYTOX® staining of a stage 14 embryo in frontal view. The primordia of the lateral eyes are visible as shallow pits in the head region (arrowheads). (B) Expression of *Pt-peropsin* at stage 14 marks not only the lateral eye primordia (white arrowheads) but also the median eye primordia (black arrowheads).

4.2.3 Spider homologues of Drosophila retinal determination genes

We have isolated homologues of key components of the retinal determination gene network known from *Drosophila*, and have studied their expression in all eye primordia of *P. tepidariorum*. In the following, we give a detailed account of the expression of all studied genes during the developmental stages 10 to 14, which comprise the time span between the formation of the non-neurogenic ectoderm at the anterior and lateral rim of the head lobes, the overgrowth of the brain anlage, and the development of the primordia of the lateral and median eyes within the non-neurogenic ectoderm.

4.2.3.1 *Homologues of pax6*

We identified two *pax6* orthologues in the transcriptome of *P. tepidariorum* (Posnien et al. 2014, Samadi et al. 2015). At stages 10 and 11, *Pt-pax6.1* is expressed in a narrow domain in the neurogenic ectoderm directly adjacent to the anterior and lateral furrows (arrowheads in Figure 6 A, B). Throughout stages 12 to 14 while the non-neurogenic ectoderm overgrows the brain primordium, the *Pt-pax6.1* expression domains remain in the neurogenic ectoderm (Figure 6 C to E). From stage 13 onwards, *Pt-pax6.1* expression can only be detected as diffuse signal in the brain anlage that is already fully covered by the non-neurogenic ectoderm (Figure 6 D, E). *Pt-pax6.2* is expressed in a transversal stripe across the neurogenic ectoderm in the head lobes and a smaller domain, which surrounds the lateral furrow (arrowhead in Figure 6 F). At stages 11 and 12, the transversal domain condenses, while the expression surrounding the lateral furrow ceases (Figure 6 G, H). During non-neurogenic ectoderm overgrowth at stages 13 and 14, *Pt-pax6.2* shows a diffuse expression in the underlying brain anlagen (Figure 6 I, J). Note that the non-neurogenic ectoderm outside of the anterior and lateral furrows is free of *Pt-pax6.1* and *Pt-pax6.2* expression throughout the embryonic stages analyzed.

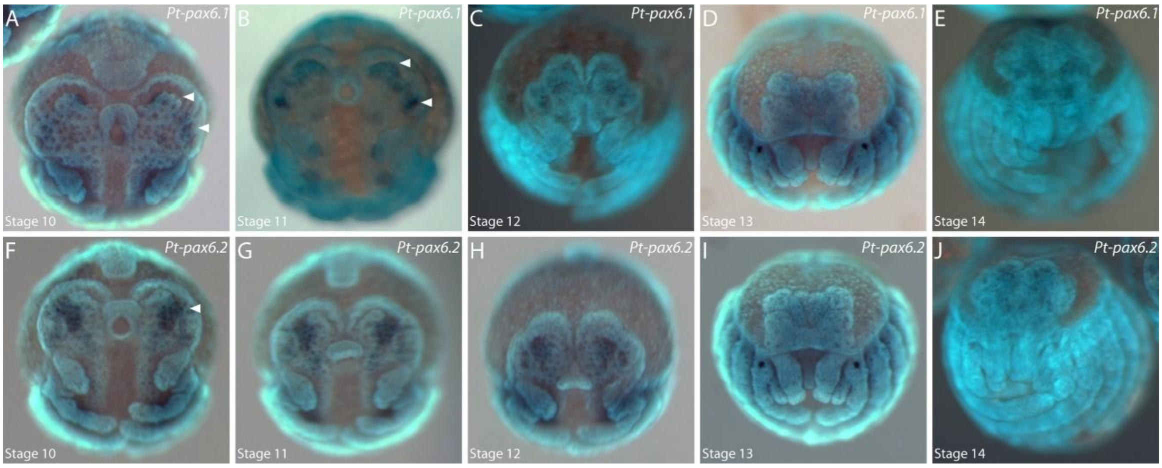

Figure 6 - Embryonic expression of *pax6* homologues in the head of *P. tepidariorum*. (A to E) Expression of *Pt-pax6.1* during head development. A large connected domain in the brain anlage is denoted by arrowheads in A and B. (F to J) Expression of *Pt-pax6.2* during head development. A transversal stripe of expression is denoted by the arrowhead in F. All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

4.2.3.2 *Homologues of six1/sine-oculis*

We identified two orthologues of the six1/so gene in the transcriptome of *P. tepidariorum* (Posnien et al. 2014, Samadi et al. 2015). In the head anlagen at stages 10 and 11, *Pt-so1* expression is observed in a region around the stomodeum and in two domains at the rim of the head lobes next to the anterior and lateral furrows, respectively (arrowheads in Figure 7 A, B; Figure 8 A to C). While the non-neurogenic ectoderm overgrows the neurogenic ectoderm of the head from stage 12 onwards, the anterior *Pt-so1* expression domain always remains at the leading edge of the non-neurogenic ectoderm throughout development (black arrowhead in Figure 7 C; asterisk in Figure 8 A to H; the leading edge is indicated by the dotted line). Thus, the domain is relocated from the anterior rim of the head lobe to the anterior rim of the prospective carapace (black arrowhead in Figure 7 D; asterisk in Figure 8 H), which is also the location where *Pt-peropsin* expression is observed in the primordia of the median eyes (compare Figure 7 D, E with Figure 5 B). When the non-neurogenic ectoderm has fully overgrown the brain anlage, *Pt-so1* is diffusely expressed in the primordia of the median eyes (black arrowhead in Figure 7 E; asterisk in Figure 8 I, J). By contrast, the lateral expression domain does not change its relative location and does not follow the leading edge of the overgrowing nonneural ectoderm (Figure 7 C to E; white arrowheads in Figure 8). In stage 12, this domain becomes slightly bipartite (Figure 8 D) and then splits into two separate domains at the transition between stage 12 and stage 13 (Figure 8 E). At early stage 13, the more posterior domain splits once more (Figure 8 F) and buds off another domain (Figure 8 G), which however stays in close vicinity to its parental domain (Figure 8 H to J). *Pt-so2* is expressed in the labrum at stage 10 (Figure 7 F), but is not expressed in the brain anlage or the non-neurogenic ectoderm during stages 10 to 12 (Figure 7 F to H). However, once the brain anlage is fully overgrown by the non-neurogenic ectoderm, a new expression domain of *Pt-so2* arises at stage 13 in the non-neurogenic ectoderm close to the posterior-lateral edge of the head lobes (arrowhead in Figure 7 I) and persists throughout stage 14 in the primordia of the anterior lateral eyes (arrowhead in Figure 7 J).

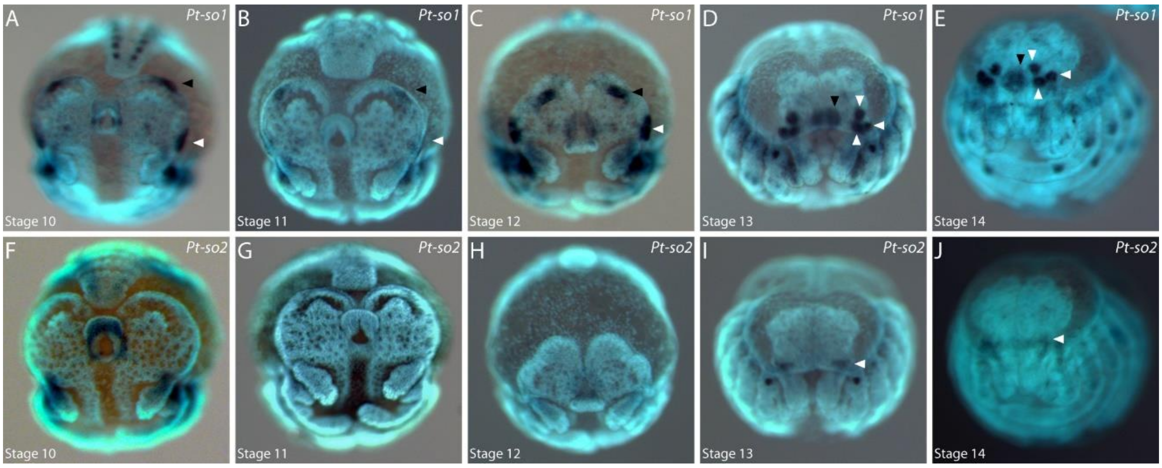

Figure 7 - Embryonic expression of *sine-oculis* homologues in the head of *P. tepidariorum*. (A to E) Expression of *Pt-so1* during head development. Two separate domains in the non-neurogenic ectoderm are denoted by arrowheads in A to C. Expression in the lateral eye primordia is indicated by arrowheads in D. (F to J) Expression of *Pt-so2* during head development. Late expression in the median eye primordia is denoted by an arrowhead in I and J. All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

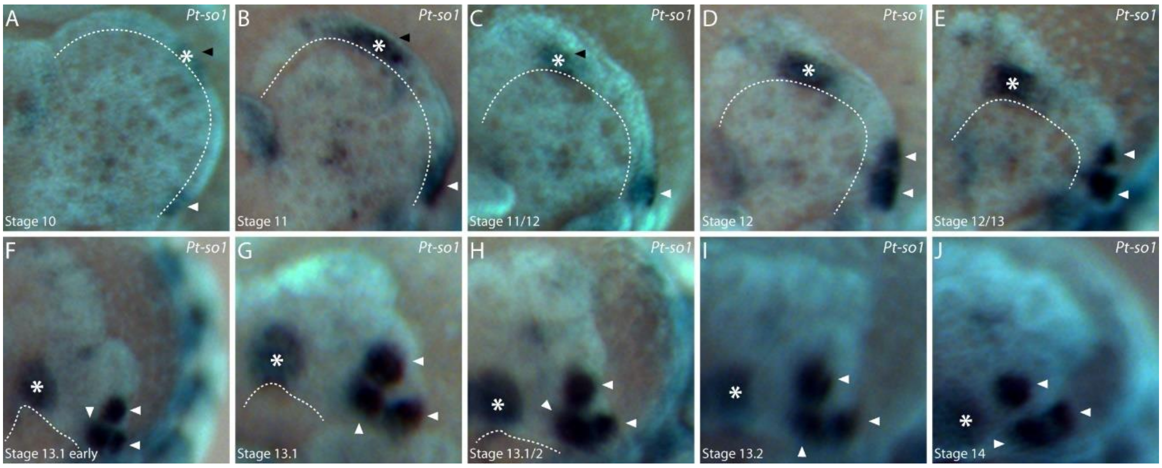

Figure 8 - Dynamics of *sine-oculis1* expression during brain overgrowth. All panels show the left half of the head lobes in frontal view (A to J). Expression in the primordia of the median eyes is denoted by the asterisk, expression in the lateral eye primordia is indicated by white arrowheads in all panels. The dotted line shows the leading edge of the non-neurogenic head ectoderm that overgrows the brain anlage. The developmental stage is indicated in each panel in the lower left corner.

4.2.3.3 *Homologues of eyes-absent*

For *eya*, we only found a single orthologue in the transcriptome (Posnien et al. 2014, Samadi et al. 2015). At stages 10 and 11, *Pt-eya* is expressed along the edge of the head lobes (red and white arrowheads in Figure 9 A, B). No expression is detected in the anterior and lateral furrows. Additional expression domains are present around the stomodeum (white arrow in Figure 9 A), in the developing labrum (black arrow in Figure 9 B) and in spots at the base of the chelicerae (black arrowhead in Figure 9 A, B). At stage 11, *Pt-eya* expression ceases at a lateral position thus dividing the expression along the rim into two separate domains (red and white arrowheads in Figure 9 B). When the non-neurogenic ectoderm starts to grow over the brain anlagen, *Pt-eya* expression at the rim of the leading edge becomes stronger (asterisk in Figure 9 C) and ends up in the primordia of the medial eyes (asterisk in Figure 9 D, E). The remaining anterior expression becomes patchy (red arrowhead in Figure 9 C) and then vanishes entirely in early stage 13 (Figure 9 D). The lateral portion of the rim domain increases in expression level (white arrowhead in Figure 9 C) and then separates first into two and finally into three pairs of dots in the primordia of the lateral eyes (white arrowheads in Figure 9 D, E).

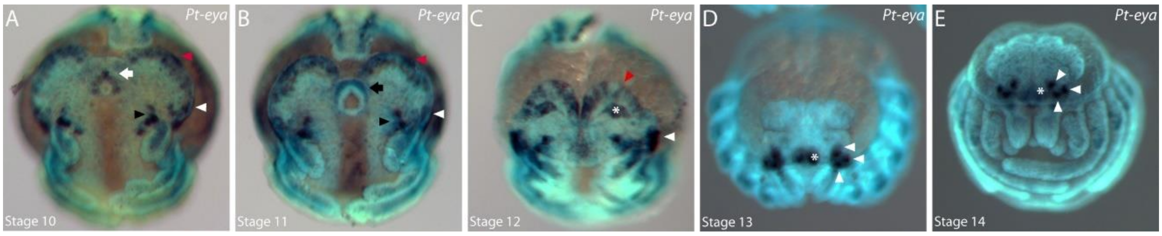

Figure 9 - Embryonic expression of the *eyes-absent* homologue in the head of *P. tepidariorum*. (A to E) Expression of *Pt-eya* during head development. A dynamic expression domain along the rim of the head lobes is denoted by arrowheads in A to C. Expression in the lateral eye primordia is indicated by white arrowheads in D and E. The black arrowheads in A and B point to expression at the base of the chelicerae. The arrows denote expression in the stomodeum (A) and in the labrum (B). All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

4.2.3.4 *Homologues of dachshund*

We found two orthologues of the *dac* gene in the transcriptome of *P. tepidariorum* (Pechmann et al. 2009, Posnien et al. 2014, Samadi et al. 2015). *Pt-dac1* shows a complex pattern in the neurogenic ectoderm of the head and all body segments that increases in complexity with the advancement of neural maturation. At stage 10, there are up to three distinguishable domains of *Pt-dac1* expression in the brain anlage (Figure 10 A). In addition, *Pt-dac1* is expressed at the posterior lateral edge of the head lobes (arrowhead in Figure 10 A to C). The expression pattern in the brain anlage becomes more complex in stage 11 (Figure 10 B) but then almost completely ceases at stage 12 (Figure 10 C).The lateral expression, however, remains strong and ends up in the primordia of the anterior lateral eyes and in cells at a lateral position on the developing carapace (arrowhead in Figure 10 D, E). *Pt-dac2* is not expressed in the head lobes before stage 12 (Figure 10 F, G). At stage 12, expression of *Pt-dac2* appears anterior to the labrum and in two distinct domains in the lateral head (Figure 10 H). During stages 13 and 14, all primordia of the lateral eyes express *Pt-dac2* very strongly (white arrowheads in Figure 10 I, J).

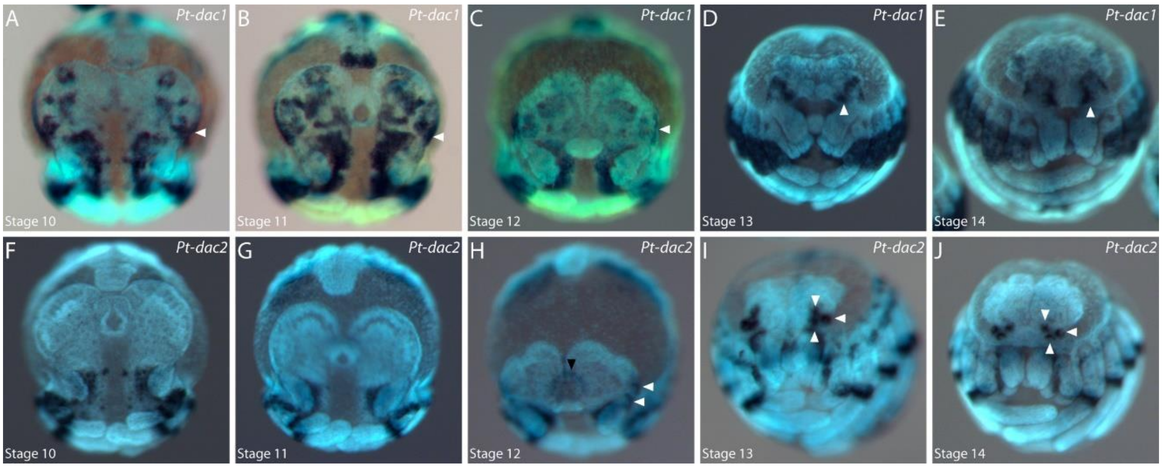

Figure 10 - Embryonic expression of *dachshund* homologues in the head of *P. tepidariorum*. (A to E) Expression of *Pt-dac1* during head development. The arrowhead in A to C points to expression at the lateral edge of the head lobes. The arrowhead in D and E points to expression in the primordia of the anterior lateral eyes. (F to J) Expression of *Pt-dac2* during head development. Expression in the lateral eye primordia is denoted by white arrowheads in H to J. The black arrowhead in H denotes expression anterior to the labrum. All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

4.2.3.5 *Homologues of six3/optix*

We identified two *optix/six3* orthologues in *P. tepidariorum* (Posnien et al. 2014, Samadi et al. 2015). At stage 10, *Pt-six3.1* is expressed in the labrum (white arrow in Figure 11 A), at the anterior rim of the head lobes (black arrow in Figure 11 A) and in an anterior (black arrowhead in Figure 11 A) and a lateral spot (white arrowhead in Figure 11 A) in the neurogenic ectoderm. The expression at the anterior rim of the head lobes vanishes during stage 11 (Figure 11 B). The other domains remain throughout stages 11 and 12 (arrowheads in Figure 11 B, C) and become covered by the non-neurogenic ectoderm. At stage 13, the *Pt-six3.1* expression in the neurogenic ectoderm is completely overgrown by the non-neurogenic ectoderm (Figure 11 D). The formerly lateral expression of *Pt-six3.1* becomes more complex during the stages 13 and 14 (white arrowheads in Figure 11 D, E). Thus, although *Pt-six3.1* shows a dynamic expression pattern in the neurogenic ectoderm, this gene is not expressed in the overlaying non-neurogenic ectoderm and not in the primordia of the eyes. At stages 10 and 11, *Pt-six3.2* is expressed in a wedge-shaped domain in the anterior median region of the head, in the labrum, and in the posterior stomodeum (Figure 11 F, G). The anterior median domain is fully overgrown by the non-neurogenic ectoderm during further development (Figure 11 H to J). Two expression domains appear de novo at the lateral edge of the head lobes (Figure 11 H and Figure 12 A), of which the posterior one splits into two domains (Figure 12 B) resulting in three distinct domains of *Pt-six3.2* expression (arrowheads in Figure 11 I, J; Figure 12 C to E). Thus, all primordia of the lateral eyes express *Pt-six3.2*. Note that the primordia of the median eyes do not express *Pt-six3.2*; the blurred staining in Figure 11 J at the position where the median eyes develop is located in the foregut primordium beneath the head tissue.

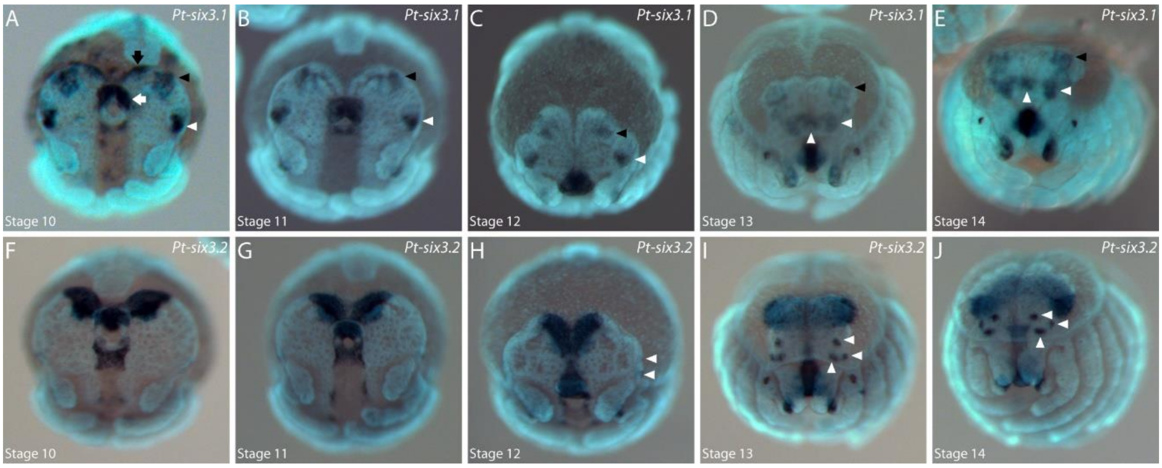

Figure 11 - Embryonic expression of *six3* homologues in the head of *P. tepidariorum*. (A to E) Expression of *Pt-six3.1* during head development. Two separate domains in the brain anlage are denoted by arrowheads in A to C. The black arrow in A denotes expression along the anterior end of the head lobes. Expression in the labrum is denoted by a white arrow in A. The white arrowheads in D and E point to the tripartite expression in the brain primordium that develops from the earlier lateral expression domains (white arrowheads in A to C). (F to J) Expression of *Pt-six3.2* during head development. Expression in the lateral eye primordia is denoted by arrowheads in H to J. All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

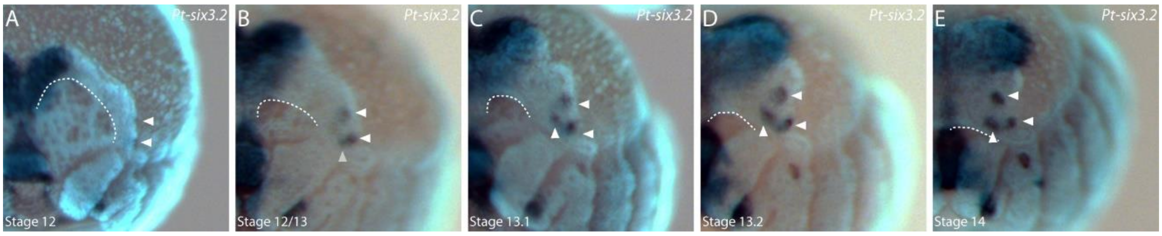

Figure 12 - Dynamics of *six3.2* expression during brain overgrowth (A to E). All panels show the left half of the head lobes in frontal view. Expression in the lateral eye primordia is indicated by arrowheads in all panels. The dotted line shows the leading edge of the non neurogenic head ectoderm that overgrows the brain anlage. The developmental stage is indicated in each panel in the lower left corner.

4.2.3.6 *Homologues of orthodenticle*

Two orthologues of the *otd* gene have been identified in *P. tepidariorum* (Akiyama-Oda 2003, Pechmann et al. 2009, Posnien et al. 2014, Samadi et al. 2015). *Pt-otd1* is expressed in two large, patchy domains in the developing brain on each side of the posterior head lobes throughout stages 10 to 12 (Figure 13 A to C). During stages 13 and 14, the non-neurogenic ectoderm grows over the *Pt-otd1*-positive cells, which end up in the center of the developing brain posterior to the median eye anlagen (arrowheads in Figure 13 D, E). At stages 10 and 11, *Pt-otd2* is expressed in a broad domain in the center of the developing brain and in two connected domains at the rim of the head lobes (white arrowheads in Figure 13 F, G). This entire expression is very dynamic during further development and finally covers most of the forming brain (Figure 13 H to J). Parts of the anterior rim domain move posteriorly with the overgrowing non-neurogenic ectoderm during stages 12 to 14 (white arrowheads in Figure 13 G to J), resulting in *Pt-otd2* expression in two small clusters of cells in the anterior-median non-neurogenic ectoderm that correspond to the median eye primordia (white arrowheads in Figure 13 J).

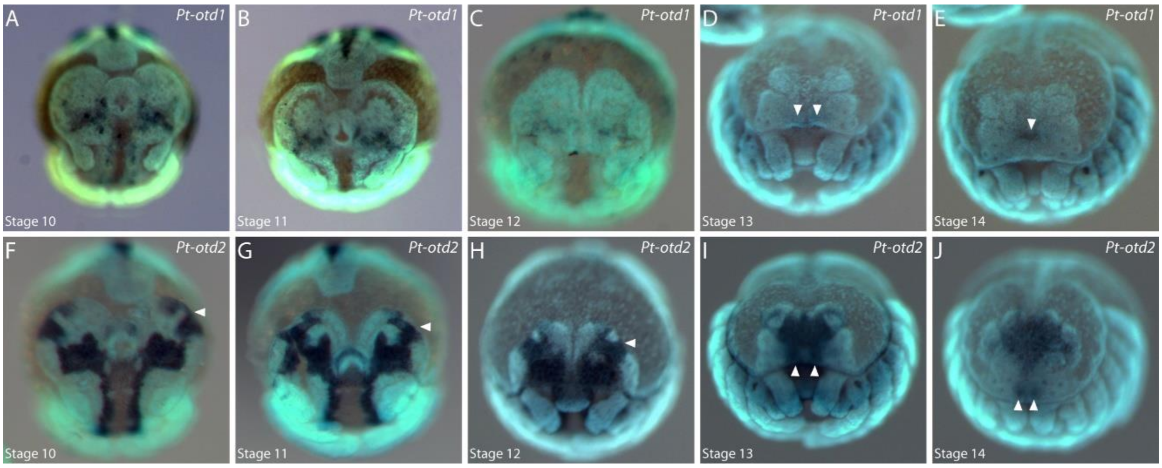

Figure 13- Embryonic expression of *orthodenticle* homologues in the head of *P. tepidariorum*. (A to E) Expression of *Pt-otd1* during head development. The arrowheads in D and E point to expression in the brain anlage underneath the non-neurogenic ectoderm. (F to J) Expression of *Pt-otd2* during head development. Arrowheads in F to J denote *Pt-otd2* expression in the non-neurogenic ectoderm, which ends up in the median eye anlagen. All embryos are shown in frontal aspect. The developmental stage is indicated in each panel in the lower left corner.

4.3 DISCUSSION

4.3.1 Embryonic origin of median and lateral eyes

Although the eyes become morphologically visible only in late embryonic stages (in the case of the lateral eyes) or even in postembryonic stages (in the case of the median eyes) (Mittmann & Wolff 2012), the primordia of all eyes can be identified much earlier based on their expression of conserved retinal determination genes. The primordia of the median eyes are defined in non-neurogenic tissue that is at first located at the anterior rim of the head lobes, but then moves with the leading edge of the overgrowing tissue and finally the median eyes are situated at the anterior rim of the developing carapace. This movement of the median eye primordia can be followed best using the expression of *Pt-so1* because this gene is expressed in the median eye primordia from their initial allocation at the anterior rim of the head lobe until their final location at the anterior rim of the carapace (Figure 8). The lateral eye primordia are also formed in non-neurogenic ectoderm, but at the lateral rim of the head lobes and they do not move with the leading edge of the overgrowing non-neural ectoderm. Intriguingly, our data suggest that at a molecular level all lateral eyes are initially specified as a single field of cells on each side of the head lobes. Differentiation into three separate lateral eyes then occurs later by splitting of the original uniform eye field. The first splitting gives rise to the median lateral eyes and the primordium of the posterior and anterior lateral eyes. In a second splitting event, the latter primordium then separates into the posterior and the anterior lateral eyes. It is tempting to speculate whether this composite lateral eye primordium is a remnant of a phylogenetically older complex lateral eye primordium (Bitsch & Bitsch 2005, Paulus 1979). Indeed, basal chelicerates (for example, *L. polyphemus*) have complex lateral eyes (Fahrenbach 1975), several fossil arthropod groups have complex lateral eyes (for example, Trilobites) (Clarkson et al. 2006), and multi-facetted complex eyes are widespread in the crustaceans and insects (Dohle 2001). This suggests that the formation of the lateral eyes via a common eye field that is subsequently subdivided into smaller eye units represents the plesiomorphic condition of the lateral visual system in the arthropods.

4.3.2 Every eye type expresses a unique combination of transcription factors

Our data show that most of the key genes of the retinal determination gene network known from *Drosophila* have a conserved expression in the eyes of *P. tepidariorum*. All eye primordia express *Pt-so1* and *Pt-eya*, and thus, these genes might be involved in specifying eye identity in general (Figure 14 A, B). This is in accordance with eye development in *Drosophila* where the transcription factor So and the co-activator Eya form a protein complex to activate downstream targets within the retinal determination network in the developing compound eyes (Pignoni et al. 1997) and in the ocelli (Blanco et al. 2010, Bonini et al. 1993, Cheyette et al. 1994). In the lateral compound eyes, the So/Eya complex activates the transcription factor *dac* that mediates eye specification (Mardon et al. 1994, Pignoni et al. 1997). However, ocelli development is not affected by loss of function mutants of *dac* (Mardon et al. 1994). Intriguingly, we find expression of both *dac* orthologues in *P. tepidariorum* exclusively in the lateral eyes (Figure 14 A, B), suggesting that the involvement of *dac* in eye determination might be specific to lateral eyes not only in *Drosophila* but also in arthropods in general. Similarly, *optix/six3* is involved in compound eye formation in *Drosophila* (Seimiya & Gehring 2000), while a potential function during ocelli formation remains to be elucidated. Of the two *six3* genes in *P. tepidariorum*, only *Pt-six3.2* is expressed in the anlagen of the lateral eyes (Figure 14 A, B). Therefore, expression of *Pt-dac2* and *Pt-six3.2* is specific to the lateral eyes and might specify lateral eye identity in general. The median eyes do not express these lateral eye factors, but express *Pt-otd2* as a unique marker for median eyes. Also in *Drosophila*, it has been shown that *otd* is essential to define the ocelli primordia (Blanco et al. 2009, 2010; Royet & Finkelstein 1995), while a function in the compound eyes is only evident during late differentiation stages (Tahayato et al. 2003, Vandendries et al. 1996). Not only the median and lateral eyes seem to be specified by different genetic mechanisms in the spider, but also among the lateral eyes developmental genetic differences exist. The anterior lateral eyes are specifically characterized by expression of *Pt-so2* and *Pt-dac1* (Figure 14 A, B), while we do not find gene expression that is specific to either the median or posterior lateral eyes. Of course, the latter two eyes could be further distinguished by the expression of genes that were not included in our present study. In summary, we find hints that a separation of the core eye determination network into two separate functional units governing median and lateral eye formation, respectively, might have been present already in the ancestral arthropod and thus may predate the split between chelicerates and insects. While in insects and spiders, the anlagen of median eyes are defined by the presence *otd* and a lack of So/Eya-mediated *dac* activation, lateral eye development relies on the action of Dac and Six3 in addition to the So/Eya complex that is necessary for the formation of all eyes (Figure 14 A, B). Additional molecular diversification of lateral eyes in spiders might be facilitated by the presence of paralogous eye determination genes.

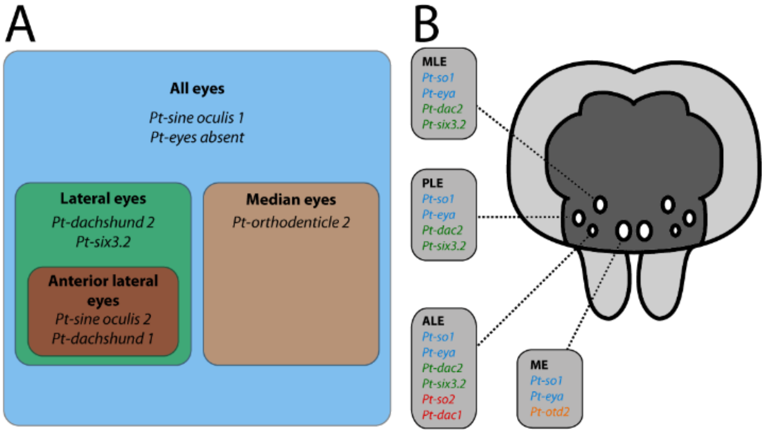

Figure 14 - Summary of the expression of eye patterning genes in eye primordia of *P. tepidariorum*. (A) The studied genes distinguish the different eyes. Apart from general eye genes (blue), other genes mark the median eyes (orange) and the lateral eyes (green) and even distinguish the anterior lateral eyes (red). (B)

The four eye pairs of spiders express their specific combinations of eye developmental genes. ALE, anterior lateral eyes; PLE, posterior lateral eyes; MLE, median lateral eyes; ME, median eyes.

4.3.3 The role of Pax6 during spider eye development

Intriguingly, we do not detect late expression of the two pax6 orthologues in any of the eye primordia of *P. tepidariorum*. A similar observation has been made in the American Horseshoe Crab *L. polyphemus* where late embryonic eye anlagen are free of *pax6* expression (Blackburn et al. 2008). This result is unexpected since Pax6 is required for eye development not only in insects but also, for example, in mammals (Hill et al. 1991, Ton et al. 1991, Walther & Gruss 1991). In *Limulus*, early *pax6* expression was not studied but qPCR results imply an activity prior to the analyzed late stages (Blackburn et al. 2008). Hence, it is likely that Pax6 is required early during anterior development to specify the future eye anlagen. This hypothesis is supported by *Pt-pax6.1* expression at the anterior rim of stage 6/7 germ disc embryos of *P. tepidariorum* (not shown), suggesting that this gene might be essential for the early specification of the non-neurogenic ectoderm at the anterior and lateral rim of the developing head lobes. Whether this early anterior expression of *Pt-pax6.1* is involved in the activation of further eye determination genes remains to be elucidated.

4.3.4 A potential role of peropsins during eye development

We identified a *peropsin* orthologue in *P. tepidariorum* that clusters with other chelicerate and vertebrate sequences (*Figure S 1*). Peropsins are expressed in the retina of several vertebrates (Sun et al. 1997, Tarttelin et al. 2003) and amphioxus (Koyanagi et al. 2002) where it is proposed to function as a retinal photoisomerase. Clear protostome *peropsin* orthologues have only been identified in spiders (Eriksson et al. 2013a, Nagata et al. 2009) and in the American horseshoe crab *L. polyphemus* (Battelle et al. 2015). We detect *Pt-peropsin* expression in the embryonic anlagen of lateral and median eyes, suggesting an early involvement in visual system development or function. Intriguingly, an early function during ocular development has been proposed for peropsins in mice and humans where expression can be detected already during early embryonic stages (Tarttelin et al. 2003). Hence, the accessibility of *P. tepidariorum* development and the availability of functional tools represents an excellent model to further investigate a potential role of *peropsins* in eye development.

4.3.5 Conclusions

The two eye types in spiders, lateral and median eyes, develop from two different areas in the non-neurogenic ectoderm. Although morphological signs of the eye primordia appear only in the final stages of embryogenesis or later, on the molecular level, the eyes are specified much earlier. Apart from factors that are expressed in all eyes, there are also factors that distinguish the lateral eyes and the median eyes. In addition, among the lateral eyes, the anterior ones are patterned differently from the remaining lateral eyes. The primordia of the median eyes are initially allocated at the anterior rim of the head lobes from where they move to their final location at the anterior rim of the carapace with the non-neural ectoderm that overgrows the underlying brain anlage. All lateral eyes on each side of the head develop from a common eye field, thus providing evidence for the notion that the individual lateral eyes in adult spiders are actually evolutionary remnants of a composite lateral eye. It will be interesting to study the formation and specification of the lateral eyes in spiders in more depth to compare it to the development of the facetted eyes in insects.

5 Phylogenetic analysis of forkhead transcription factors

5.1 INTRODUCTION

5.1.1 Forkhead transcription factors

Organismal diversity is achieved through changes in developmental programs. These processes are governed by genetic networks, which usually have transcription factors at the nodes inside these networks. For new genetic networks to arise, existing genes are either co-opted from other networks, or new functions are introduced by the expansion of existing gene families through duplication and subsequent neo-functionalization (Lynch 2000). One family of genes, that has been expanded in particular are the forkhead box genes (Fox genes). They were present with at least one family member found in the basal opisthokont lineage (Suga et al. 2013) to more than 40 members in mammals (Jackson et al. 2010).

The first forkhead domain gene to be identified was *forkhead* itself in *Drosophila* (Weigel et al. 1989), followed shortly by one of its homologs in the rat (Lai et al. 1990). Both genes were found to code for a similar helix-turn-helix motif DNA binding domain, which was termed winged-helix (Li & Tucker 1993). Subsequently it could be shown, that this 110 amino acid forkhead domain is widely conserved among different taxa (Kaufmann & Knöchel 1996) and that genes containing this domain are widespread throughout the animal kingdom. The identified forkhead genes have been shown to fulfill many diverse roles during embryonic development, cell fate decisions, morphogenesis, cell cycle control, metabolism, signal transduction, or the change of chromatin state (Carlsson & Mahlapuu 2002, Pohl & Knöchel 2004).

5.1.2 Homology of Fox family members

With the identification of more and more forkhead genes, it became apparent that many of these independently discovered genes represented homologous sequences between deuterostomes, lophotrochozoans, ecdysozoans and basal metazoans (Larroux et al. 2008, Magie et al. 2005, Mazet et al. 2003). This discovery led to the introduction of a unified nomenclature for forkhead genes of different families. Initially, from FoxA to FoxO (Kaestner et al. 2000), with new families added to FOXS. All Fox families can be roughly grouped into two clades, clade I with an intron inside the sequence of the forkhead box (A-I, L, Q, S), and clade II without an intron (J, K, M-P) (Shimeld et al. 2010a). However, the exact number of Fox families is still debated, ranging from 17 to 23 (Hannenhalli & Kaestner 2009, Larroux et al. 2008, Mazet et al. 2003, Shimeld et al. 2010a,b; Tu et al. 2006). Newly identified forkhead domain genes were usually compared to the Fox repertoire of well-studied model organisms, such as *Drosophila* or *Mus*. Thus, many genes which were not found to be homologs of any known Fox family were assigned an orphan state, for instance in the nematode *Caenorhabditis elegans* (Hope et al. 2003), the hemichordate *Saccoglossus kowalewskii*

(Fritzenwanker et al. 2014), and lophotrochozoans (Yang et al. 2014b) Other approaches concentrated on the Fox genes in a single lineage and identified forkhead homologs only in *Drosophila* (Lee & Frasch 2004), or among vertebrates (Kaestner et al. 2000). Several studies have tried to follow the phylogenetic history of forkhead genes and link their emergence to the introduction of evolutionary novelties (Larroux et al. 2008, Mazet et al. 2003, Shimeld et al. 2010a). These were all dependent on the correct initial identification of forkhead genes. Only genes which were thought to be members of an established forkhead gene class were used in the analyses (Figure 15). Thus, these studies potentially overlooked orphan genes, which might belong to a previously unidentified new family or derived members of an existing family, due to the lack of comparable sequences. With the ever-increasing availability of sequenced genomes from a wide variety of species it is now possible to compare the fox gene repertoire of many different taxa at the same time.

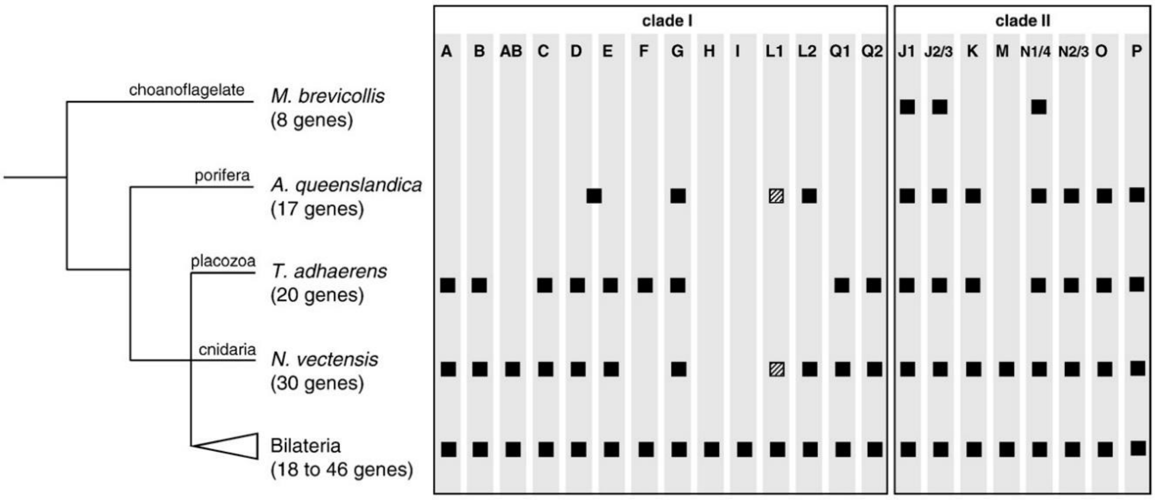

Figure 15 – Overview of Fox gene classes in different taxa. Only homologs of Fox genes in established classes are used to infer phylogenetic history of this gene family, while orphan genes are not considered. (modified from Shimeld et al. 2010b)

5.1.3 Clustered fox genes

The exsistence of clustered genes in a genome has been reported for several gene families. There are examples for clustering of GATA factors (He et al. 2007), *wnt* genes (Nusse 2001), *nkx* genes (Luke et al. 2003), but the most prominent example for clustered genes is the Hox cluster (Garcia-Fernàndez 2005, Lemons & McGinnis 2006). Clusters of genes of the same family are thought to arise via tandem duplication from one ancestral gene, and the cluster is maintained by selective pressures due to co-regulation by other factors (Shimeld et al. 2010a).

In the case of Fox genes, a close association had been observed for the two paralogs of *sloppy-paired / foxG* in *Drosophila* (Cadigan et al. 1994), but also for the homologs of *foxC* and *foxF* in *Drosophila*, humans, and *Mus* (Carlsson & Mahlapuu 2002). With the increasing number of sequenced genomes and their comparison, it was found that the homologs of *foxL1*, *foxC*, *foxF*, and *foxQ1* form a cluster in the genomes of many different lineages (Mazet et al. 2006, Shimeld et al. 2010a, Wotton et al. 2008, Yu et al. 2008b). This suggested that this cluster had evolved by tandem duplication of one gene and was already present in the basal bilaterian lineage (Mazet et al. 2006). Towards the vertebrate lineage, this cluster has been block-duplicated with subsequent loss of single genes from the new clusters, while protostomes had lost their homolog of *foxQ1* in their last common ancestor and the integrity of the cluster is dependent on the single lineages (Figure 16).

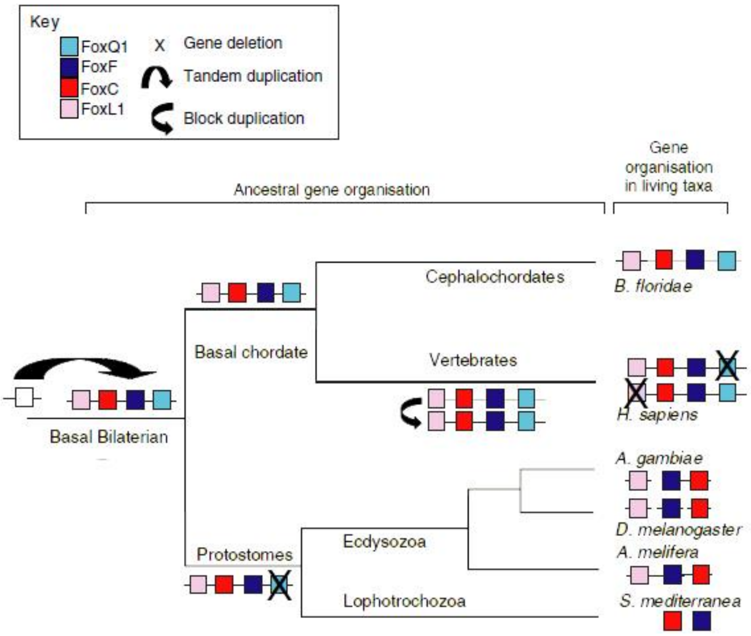

Figure 16 – Presence and evolution of the genetic cluster formed by FoxL1-FoxC-FoxF-FoxQ1. Already present in basal bilaterian lineages, the cluster was expanded by block duplication in the vertebrates with the subsequent loss of single members. In protostomes, the homolog of FoxQ1 was lost in the last common ancestor of ecdysozoans and lophotrochozoans, and the integrity of the rest of the cluster depends on the specific lineage. (modified from Mazet et al. 2006)

Traces of this cluster can be found throughout the bilaterian taxa, but the reason for its maintenance remains unknown. It has been proposed that the co-linearity of genomic arrangement and expression patterns may act as a selective force for the maintenance of such a cluster, as seen for the HOX genes (Monteiro & Ferrier 2006), or that their expression in the same tissue might explain their presence at the same chromosomal location, where they form a regulatory block of chromatin (Shimeld et al. 2010b).

Therefore, the aim was to first identify members of the forkhead family in members of different groups in the phylogenetic tree of the animal kingdom (Figure 17), assign them to their exact class and subsequently analyze their chromosomal location and identify possible clusters of fox genes in all the organisms. Thus, giving insights into the evolutionary history of this gene family.

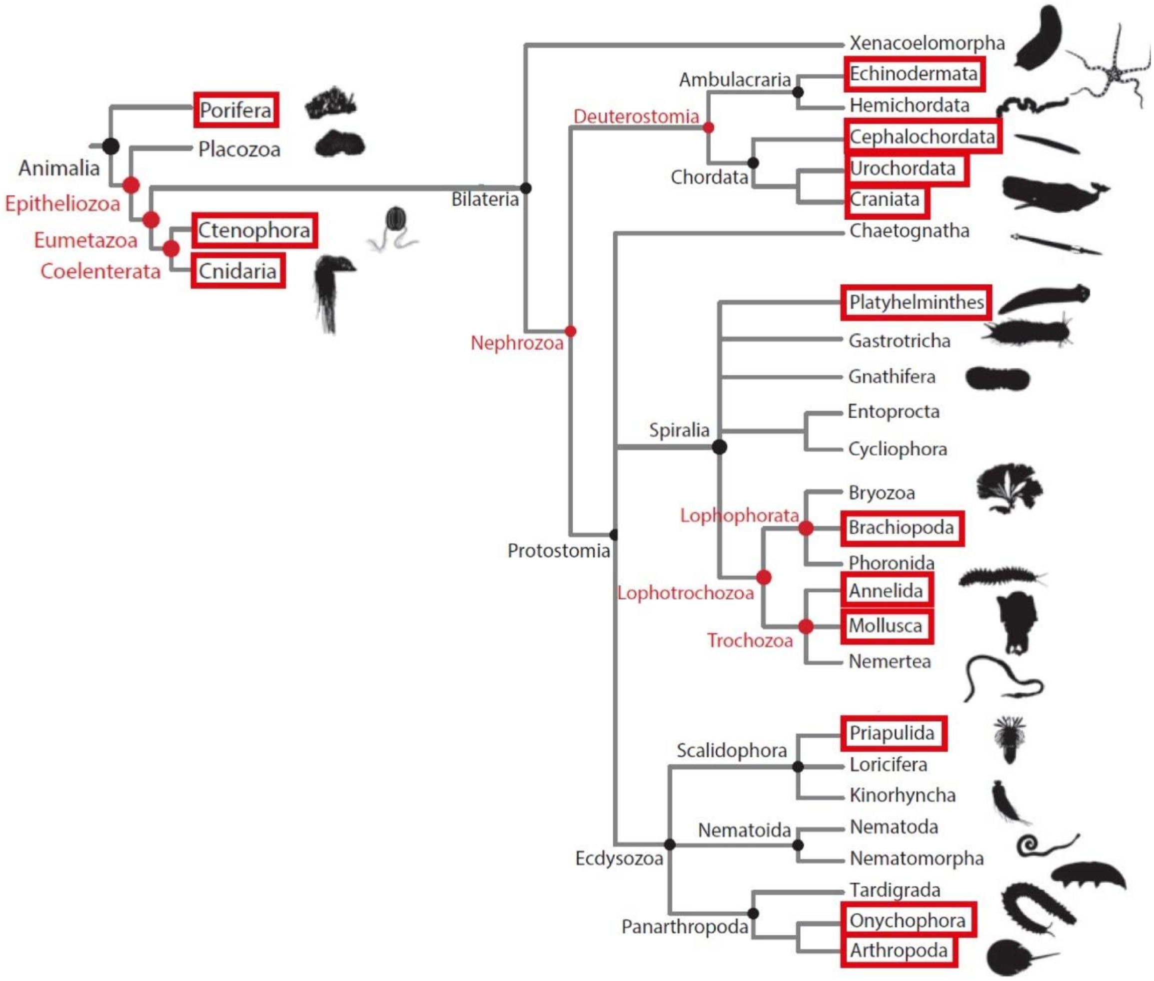

Figure 17 – Animal phylogeny, compiled across multiple studies (modified from Dunn et al. 2014). Black nodes show clades with broad consensus across studies. Red nodes indicate groups whose status is conflicting between studies and whose status is discussed. Animal groups from which available genomes were used to identify forkhead genes are marked with red boxes.

5.2 RESULTS

5.2.1 Identification of FOX domain genes

In order to get an unbiased and complete view of Forkhead domain containing genes, the official gene sets of specied with sequenced genomes, which represent interesting phylogenetic positions (Table 3) were scanned for forkhead domains. In addition to the publicly available gene sets, transcriptomic resources of the onychophoran *Euperipatoides kanangrensis* and the myriapod *Glomeris marginata* were used (for results of the initial scans see supplementary material 9.3.1.1 - 9.3.1.20).

Table 3 – Organisms analysed for the presence of Forkhead domain genes, their phylogenetic position (indicated by the taxon they belong to) and the type of gene set used for the analysis.

Name:	Phylogenetic position:	Type of gene set:
Capsaspora owczarzaki	Ichtyosporea	Genomic prediction
Salpingoeca rosetta	Choanoflagellida	Genomic prediction
Mnemiopsis leidyi	Ctenophora	Genomic prediction
Amphimedon queenslandica	Porifera	Genomic prediction
Nematostella vestensis	Cnidaria	Genomic prediction
Echinococcus multilocularis	Platyhelminthes	Genomic prediction
Helobdella robusta	Lophotrochozoa/Annelida	Genomic prediction
Lingula anatina	Lophotrochozoa/Brachiopoda	Genomic prediction
Crassostrea gigas	Lophotrochozoa/Mollusca	Genomic prediction
Priapulus caudatus	Ecdysozoa	Genomic prediction
Euperipatoides kanangrensis	Ecdysozoa/Onychophora	Transcriptome
Parasteatoda tepidariorum	Ecdysozoa/Arthropoda/Chelicerata	Genomic prediction
Glomeris marginata	Ecdysozoa/Arthropoda/Myriapoda	Transcriptome
Daphnia pulex	Ecdysozoa/Arthropoda/Crustacea	Genomic prediction
Tribolium castaneum	Ecdysozoa/Arthropoda/Insecta	Genomic prediction
Drosophila melanogaster	Ecdysozoa/Arthropoda/Insecta	Genomic prediction
Strongylocentrotus purpuratus	Echinodermata	Genomic prediction
Ciona intestinalis	Chordata/Tunicata	Genomic prediction
Branchiostoma floridae	Chordata/Cephalochordata	Genomic prediction
Danio rerio	Chordata/Vertebrata/Euteleostomi	Genomic prediction
Xenopus tropicalis	Chordata/Vertebrata/Amphibia	Genomic prediction
Mus musculus	Chordata/Vertebrata/Mammalia	Genomic prediction

5.2.2 Alignment / Tree

The identified genes were analysed for their position on their respective scaffolds, resulting in one isoform per genetic locus. This left 547 genes with an forkhead domain in the 22 species. From the singular loci identified in this way, the forkhead domains were excised and aligned using clustalOmega (Sievers et al. 2014) (Figure 18, see supplemental material 9.3.2 for full alignment)

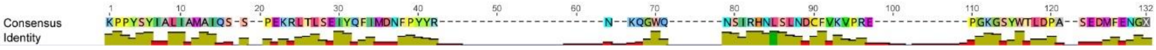

Figure 18 – Consensus alignment of forkhead domains from identified 547 genes in 22 species. For the full alignment see supplemental material 9.2.2.

The resulting alignment was used to infer phylogenetic relationships of the genes using the RaxML algorithm (Stamatakis 2014) (Figure 19, supplemental material 9.3.3.1 - 9.3.3.13). Within the tree, the forkhead domains were categorised into 25 subgroups (A, B, AB, C/S, D, E, F, G, H, I, J1, J2/3, K, L1, L2, M, N1/4, N2/3, O, P, Q1, Q2, R, Fd64a, Fd3F). FoxS was previously known to be an amniote specific subgroup of FoxC (Wotton & Shimeld 2006), and the vertebrate specific FoxR genes are a subtype of the FoxN1/4 group, sometimes called FoxN5 and FoxN6 (Katoh 2004). The phylogenetic tree shows close phylogenetic relationships of the insect specific Fd64a to the FoxG genes (Figure 19 ,supplemental material 9.3.3.7), as well as the group of Fd3F genes found only in panarthropods is located inside the group FoxN2/3 (Figure 19, supplemental material 9.3.3.11). Moreover, the Fd19b gene, which is only present in *Drosophila*, was found inside the group of FoxG (9.3.3.7). 12 genes, which showed a clear forkhead domain in their sequence, could not be attributed to any of the Fox classes. These genes were mostly in the basal species, *C. owzarzaki*, *S. rosetta*, *A. queenslandica*, *N. vectensis*, but also two in *H. robusta*, and one in *S. purpuratus* (Table 5).

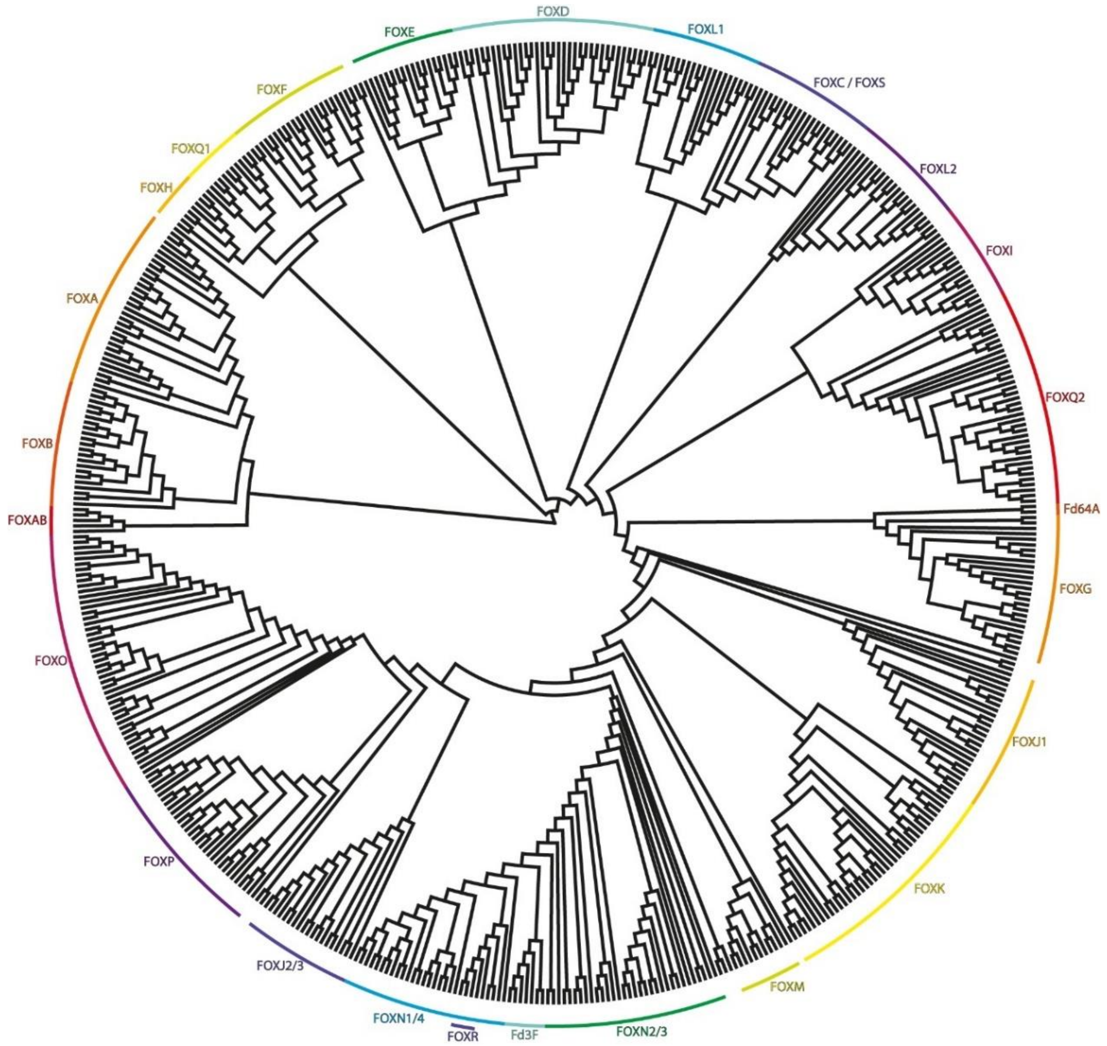

Figure 19 – Maximum likelihood tree resulting from the alignment of the identified forkhead domains. These sequences could be grouped into 25 classes of Fox genes.

5.2.3 Mapping of FOX genes to the tree of life

Two of the forkhead gene groups were present even in the basal opisthokont *C. owzarzaki* (*foxK*, *foxO*) (Figure 20, Table 4, Table 5). The choanoflagellate *S. rosetta* had the additional groups of Fox genes *foxJ1*, *foxN1/4*, and *foxP* present in its genome (Figure 20, Table 4, Table 5). At the base of the metazoans (*A. queenslandica* and the Eumetzoa) 5 new groups were present, namely *foxD*, *foxJ2/3*, *foxL1*, *foxL2*, and *foxN2/3* (Figure 20, Table 4, Table 5). The biggest addition of forkhead domain genes could be observed at the base of the Eumetazoan animals, where 9 new families appear (Figure 21, Table 4, Table 5). *foxA, foxB, foxAB, foxC, foxE*, *foxF*, *foxG, foxQ1*, and *foxQ2* are all present in the eumetazoan groups, but not in *A. queenslandica*. The only additions of new Forkhead genes in the eumetazoans happen in the bilaterian lineage (Figure 21, Table 4, Table 5). At the base of this clade *foxH* is present, which was found in most deuterostomes and the more basal ecdysozoans, while *foxM* could be found in deuterostomes, the basal ecdysozoans, and most lophotrochozoans (Figure 21, Table 4, Table 5). At least one copy of *foxI* is found to be present in all of the deuterostome species, while *foxR* is restricted to vertebrates and *foxS* is only found in *M. musculus* (Figure 21, Table 4, Table 5). There were two additions of Forkhead genes to the ecdysozoan clade. Homologs of the *fd3F* gene were present in the panarthropods, with the exception of *P. tepidariorum* and *G. marginata*, while *fd64A* could only be found in the two insect species (Figure 21, Table 4, Table 5). Not only the amount of different families of Fox genes was increased over the course of phylogenesis, but also the absolute amount of genes. While the unicellular organisms *C. owzarzaki* and *S. rosetta* showed 4 and 8 Forkhead domain genes, respectively, the basal multicellular organisms showed between 13 and 16 with the notable exception of *N. vectensis*, which appeared to have 36 Fox genes (Table 5). The different clades of the bilaterians start out with between 22 (*P. caudatus*) and 28 (*S. purpuratus*) forkhead transcription factors. In the lophotrochozoan species, *L. anatina* and *C. gigas* showed 25 genes each, the number in *H. robusta*, was slightly higher with 31 genes. In ecdysozoans, the number of forkhead genes start out with approximately 20 homologs (22 in *P. caudatus* and *P. tepidariorum*, 20 in *E. kanagrensis*) and are then reduced at the base of the mandibulata (16 in *G. marginata*), with subsequent addition of new or expanded families in pancrustaceans and insects. At the base of the deuterostome lineage, there are between 27 (*S. purpuratus*) and 30 (*B. floridae*) forkhead transcription factors present in the respective genomes (Table 5). In vertebrates, a large addition of Fox genes could be seen, which is largely due to the expansion of paralogs in existing groups, while only *foxR* and *foxS* appear as new additions of families in this lineage (Table 5).

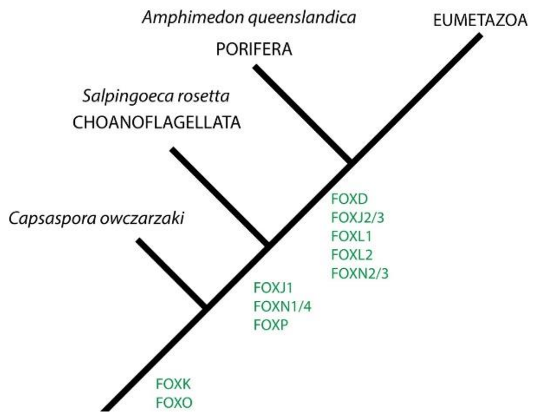

Figure 20 – Additions of Forkhead transcription factors at the base of the animal kingdom. Homologs of FOXK and FOXO were present even in the opisthokont *C. owczarzaki*. Choanoflagellates and Metazoans share FOXJ1, FOXN1/4, and FOXP as new additions. At the base of the metazoans FOXD, FOXJ2/3, FOXL1, FOXL2, and FOXN2/3 were introduced to the forkhead gene repertoire.

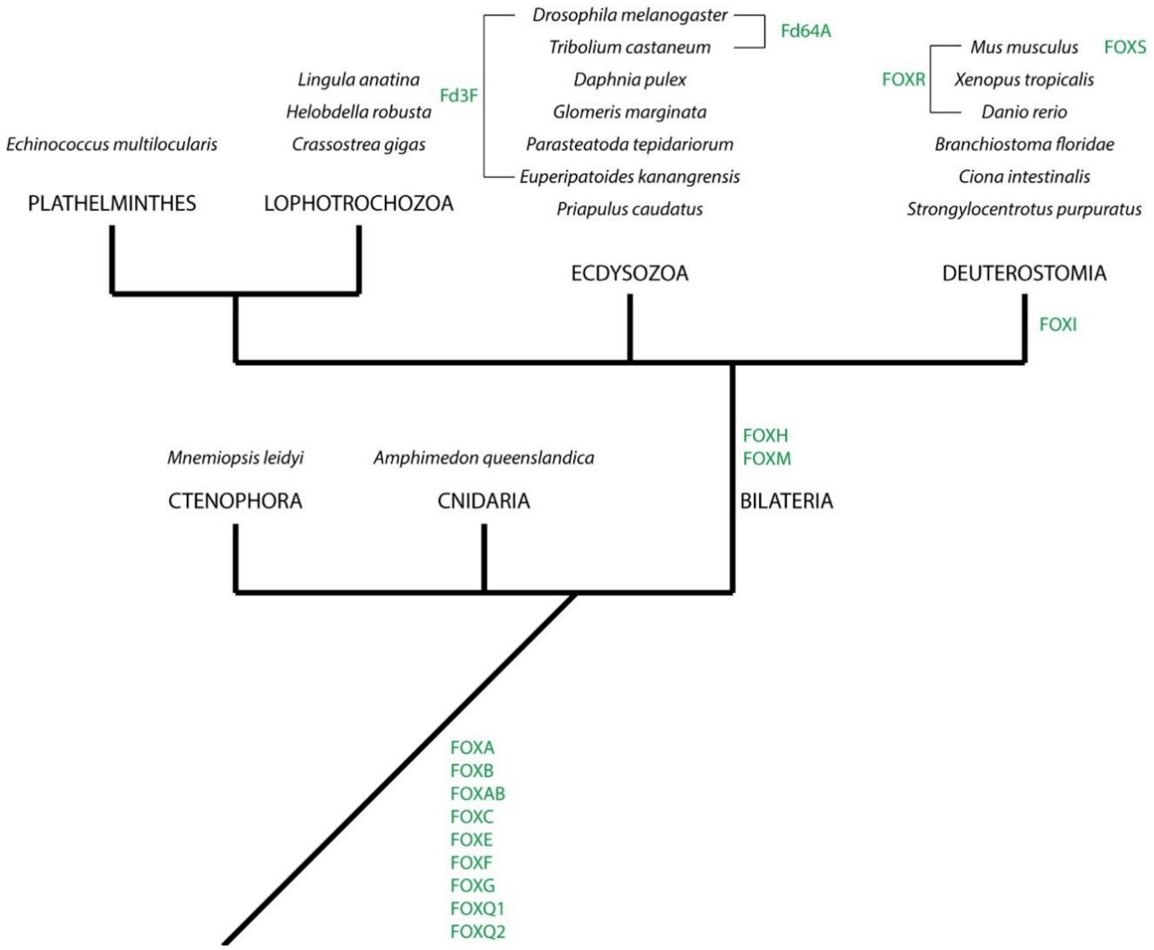

Figure 21 – Additions of Forkhead gene transcription factors in the eumetazoan lineage. At its' base this clade showed a large addition of Forkhead domain genes. FOXA, FOXB, FOXAB, FOXC, FOXE, FOXF, FOXG, FOXQ1, and FOXQ2 all appear here first. No addition of new FOX genes could be seen in Plathelminthes, Cnidarians, or Ctenophorans. In bilaterian animals, FOXH and FOXM are added to the repertoire. No new Forkhead gene classes were evident in the species of Lophotrochozoans. In Ecdysozoans, homologs of Fd3F were present in the panarthropods, and Fd64A was found in the two insect species. All deuterostomes share homologs of FOXI, while FOXR is specific to vertebrates, and FOXS was only found in the mammalian species.

The phylogenetic history of the forkhead genes did not only show the emergence of families of these genes, but also many instances of losses of family members. Many of these losses happened can be seen in the ecdysozoans, especially the insects. While none of the ecdysozoans showed a homolog of *foxAB*, a copy of *foxE* was present in *P. caudatus* (Table 4). The presence of *foxH* could be shown in *P. caudatus* and *E. kanagrensis*, but not in any of the arthropods (Table 4). *foxJ2/3* were present in the basal ecdysozoans, with the exception of *P. caudatus*, but not in pancrustaceans (Table 4). The same was true for homologs of *foxL1*, with the exception of it being present in *P. caudatus* (Table 4). A homolog of *foxM* was also only present in *P. caudatus*, but in no other ecdysozoan analysed (Table 5). A homolog of *foxQ1* could only be identified in *E. kanagrensis*, it was not present in any other ecdysozoan species (Table 5). Another strong reduction in the amount and variety of Fox genes could be seen in the plathelminth *E. multilocularis* (Table 4, Table 5). While 17 classes of forkhead genes could be seen in the cnidarian *N. vectensis*, the Lophotrochozoans, and the basal Ecdysozoans, only 12 were found in *E. multilocularis* (Table 4, Table 5). Moreover, the absolute number of Fox genes was reduced from around 30 in *N. vectensis* and Lophotrochozoans to 16 (Table 5). Similar observations could be made for the ctenophore *M. leidyi*, where only 6 Fox gene classes were present, totalling to 13 genes.

Table 4 – Presence and number of FOX genes in the species analyzed I.

Species	**Fox gene classes**														
	A	**B**	**AB**	**C**	**D**	**E**	**F**	**G**	**H**	**I**	**J1**	**J2/3**	**K**	**L1**	**L2**
Capsaspora owczarzaki													1		
Salpingoeca rosetta											1		1		
Amphimedon queenslandica					1						1	1	2	2	2
Nematostella vectensis	1	1	1	1	3	1		1			1	1	1		1
Mnemiopsis leidyi								2			2		1		
Echinococcus multilocularis	2			1	2		1				2	1	2	1	
Lingula anatina	1	1	1	1	1		1	1			1	1	2	2	1
Helobdella robusta	3	1		1	2		1	1			1	1	7		1
Crassostrea gigas	1	1	1	1	1	2	1	1			1	1	3	1	1
Priapulus caudatus	2	1		1	1	1	1	1	1		1		1	1	1
Euperipatoides kanangrensis	1	1		1	1		1	1	1		1	1	1	1	1
Parasteatoda tepidariorum	2	1		1	1		2	1			1	1	2	1	1
Glomeris marginata	1	1		1	1		1	1			1	1	1	1	1
Daphnia pulex	1	1		2	1		1	2			1		1		1
Tribolium castaneum	1	2		1	1		1	2			1		1		1
Drosophila melanogaster	1	2		1	1		1	3			1		1		
Strongylocentrotus purpuratus	1	1	1	1	1	1	1	1		1	1	2	2	1	1
Ciona intestinalis	2	1		1	2	1	1	1	2	4		1	2	1	1
Branchiostoma floridae	2		1		1	6	1	1		1	1	1	2	1	1
Danio rerio	4	3		2	5	2	3	4	1	4	2	2	3	2	3
Xenopus tropicalis	3	2		2	5	2	2	1	2	4	2	2	1	2	1
Mus musculus	3	2		2	4	2	2	1	1	3	1	2	2	2	1

Table 5 – Presence and number of FOX genes in the species analyzed II.

Species	Fox gene classes												
	M	N1/4	N2/3	O	P	Q1	Q2	R	S	Fd3F	Fd64A	unknown	Total
Capsaspora owczarzaki				1								2	4
Salpingoeca rosetta		3			1							2	8
Amphimedon queenslandica		2	1	1	1							1	15
Nematostella vectensis		1	1	8	1	1	5					2	32
Mnemiopsis leidyi			2		1		3					2	13
Echinococcus multilocularis			1	1	1		1						16
Lingula anatina	1	3	1	2			4						25
Helobdella robusta		1	3	3			3					2	31
Crassostrea gigas	1	1	2	1	1		3						25
Priapulus caudatus	1	1	1	3			3						22
Euperipatoides kanangrensis	1	1	1	1	1	1	1			1			20
Parasteatoda tepidariorum		1	1	2	3		1						22
Glomeris marginata		1	1	1	1		1						16
Daphnia pulex		1	1	1	1		1			1			17
Tribolium castaneum		1	1	1	1		1			1	1		18
Drosophila melanogaster		1	1	1	1		1			2	1		19
Strongylocentrotus purpuratus	1	1	1	1	1	1	4					1	27
Ciona intestinalis	1	2	1	1	1	1	1						28
Branchiostoma floridae	1	2	1	2	1	1	3						30
Danio rerio	1	2	5	7	6	4	1	1					67
Xenopus tropicalis	1	2	2	4	3	1		1					45
Mus musculus	1	2	2	4	4	1		2	1				45

5.2.4 Clustered Genes

All of the identified forkhead transcription factors were analysed for their genomic arrangement in all the species, where a genome was available. In this way, it was possible to check potentially conserved clusters of subgroups of the forkhead family members (For all annotations see supplementary material 9.3.4.1 - 9.3.4.20).

5.2.4.1 *FOXD – FOXE cluster*

In previous studies (Shimeld et al. 2010b) it could be shown, that there is a tight linkage between the *foxD* and *foxE* family members. In placozoans, cnidarians, and deuterostomes (Amphioxus and human) the linkage between these genes is less than 0.1% of their respective genomes. Here, tight linkage between *foxD* and *foxE* genes could be found in *N. vectensis*, *B. floridae*, *D. rerio*, *X. tropicalis*, and *M. musculus*. The distances between these genes shows the same magnitude (< 0.1% of the genomes), as in previous studies (Figure 22). In all cases, except *B. floridae*, the copies of *foxD* and *foxE* are oriented in the same direction. While in all clusters found, there is only one copy of *foxE* present, duplications and insertions of *foxD* genes are common. In *N. vectensis*, there is a tight linkage between the *foxE* and *foxD-2* genes, with an additional copy (*foxD-3*) in very close proximity. In *D. rerio*, there is a loosely linked *foxD* (*foxD-4*), which is separated by two *foxP* genes from the *foxD-foxE* cluster. In *X. tropicalis*, *foxD-3* is situated upstream of *foxE-3 – foxD-2* within less than 1% of the *X. tropicalis* genome. In *M. musculus*, an additional copy of *foxD* (*foxD*-3) can be found downstream of the *foxE-3 – foxD-2* cluster.

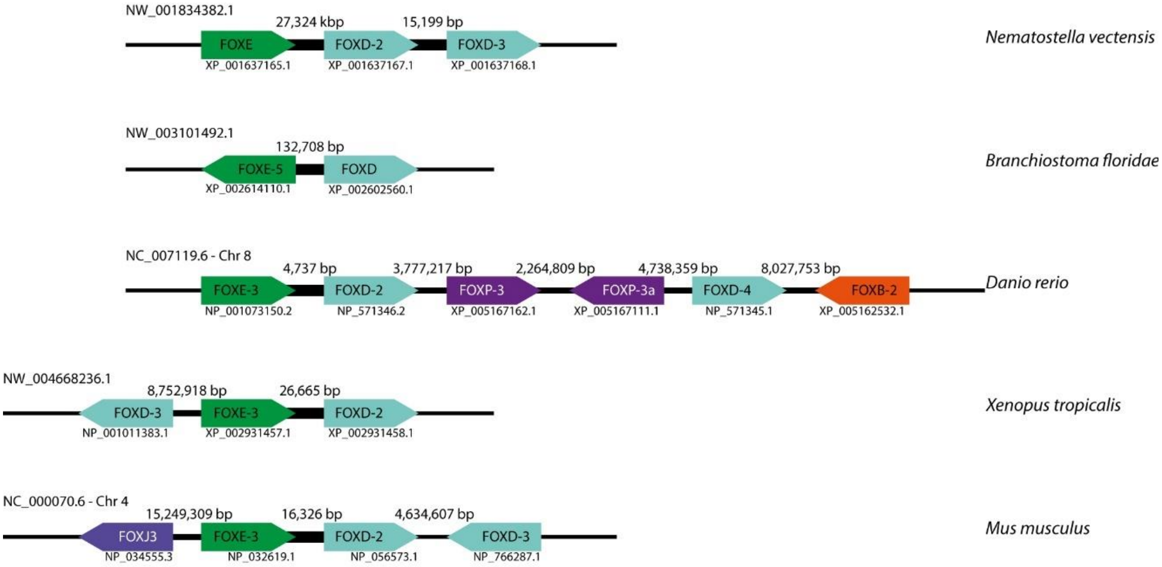

Figure 22 – Linkage between FOXD and FOXE genes. A linkage between FOXE and FOXD could be observed in *N. vectensis*, *B. floridae*, *D. rerio*, *X. tropicalis*, and *M. musculus*. In all cases, the distance between these genes was less than 0.1% of the respective genome size. In *N. vectensis*, the cluster of FOXE and FOXD-2 is followed by an additional paralog of FOXD-3. In *B. floridae*, The FOXE and FOXD homologs are not oriented in the same direction, in contrast to the instances of this linkage. In *D. rerio*, the FOXE-FOXD cluster is loosely associated with two homologs of FOXP, another paralog of FOXD-4, and FOXB-2. The cluster in *X. tropicalis* showed FOXD-3 to be within less than 1% of the genome length. In *M. musculus*, two other genes were loosely associated with the FOXE-FOXD cluster. Here, FOXJ3 and FOXD-5 surrounded the cluster within 1% of the genome size.

5.2.4.2 *FOXL1 – FOXC – FOXF – FOXQ1 cluster*

Another conservatively predicted cluster consists out of the genes *foxL1 – foxC – foxF – foxQ1*. This cluster had been found in placozoans, insects, lophotrochozoans, as well as deuterostomes (Mazet et al. 2006; Shimeld et al. 2010a,b; Wotton et al. 2008), although none of the arthropod and lophotrochophoran species possesses a homolog of *foxQ1* (Table 5). Here, we find closely linked genes of that cluster within the genomes of invertebrates (Figure 23) and deuterostomes (Figure 24). In *L. anatina*, there are two scaffolds, which show linkage between genes from this cluster. *fox1-1* is closely associated with *foxC*, while *foxL1-2* is tightly linked to *foxF*, suggesting that an original cluster of *foxL1 – foxC – foxF* has been broken in two parts. In *Crassostrea*, only *foxL1* and *foxC* can be found in close proximity on one scaffold. In Ecdysozoans, there is a close linkage between the *foxC* and *foxF* genes, namely in *P. caudatus*, *D. pulex*, and *T. castaneum*. In *P. tepidariorum*, the homolog of *foxL1* can be found in addition to *foxC* and *foxF*. In *D. melanogaster*, the homologs of *foxC* and *foxF* can be found on the same chromosome. However, the distance between these two is quite large and they are separated by the homolog of *foxK*.

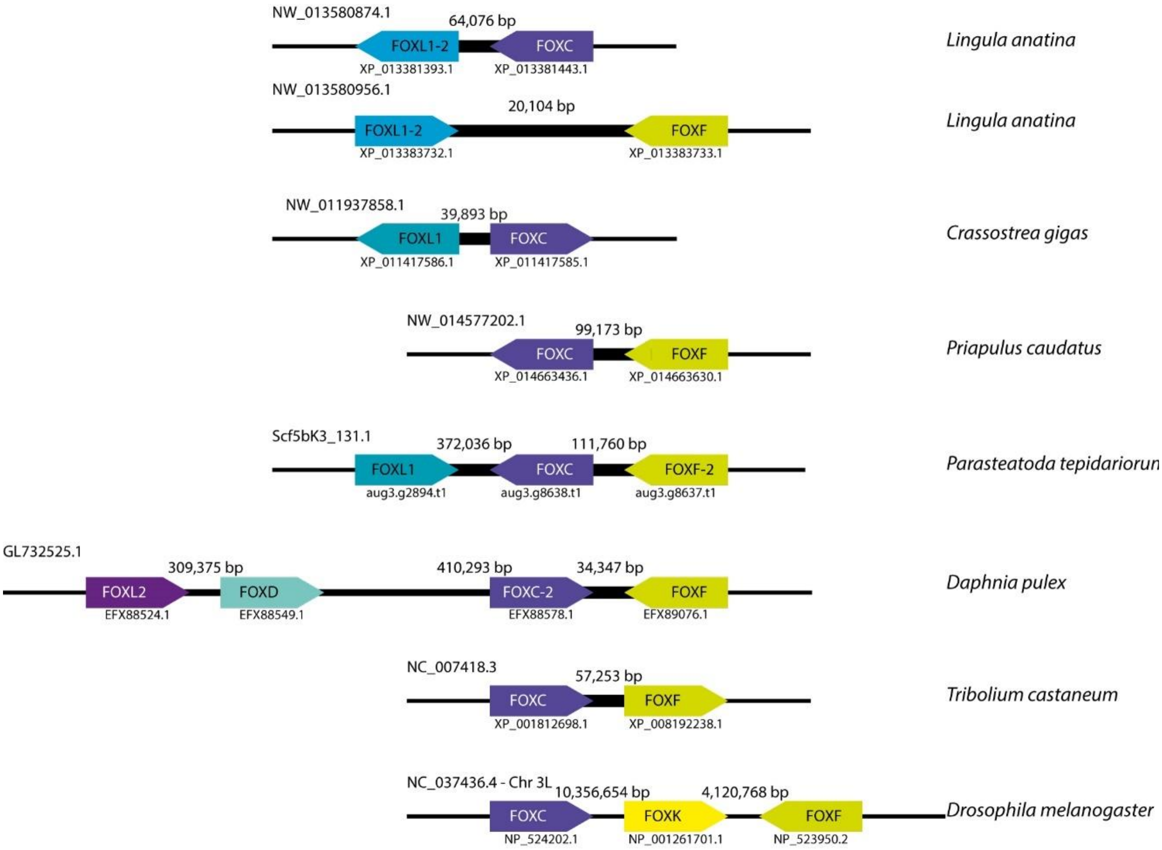

Figure 23 – FOXL1 – FOXC – FOXF – FOXQ1 cluster in invertebrates. *L. anatina* showed two scaffolds with genes of the proposed cluster in question. Homologs of FOXL1 and FOXC were closely associated in one of them, while the other showed close linkage of the paralog in FOXL1 and FOXF. In *C. gigas*, FOXL1 and FOXC were located within less than 0.1% of its genome size. FOXC and FOXF were also closely associated in *P. caudatus*, while in *P. tepidariorum* the homolog of FOXL1 was also present in close vicinity. *D. pulex* also showed FOXC and FOXF in close proximity to one another. Additionally, homologs of FOXD and FOXL2 were present within less than 1% of the genome size. In *T. castaneum*, only FOXC and FOXF were located very close together on the same scaffold. In *D. melanogaster*, while FOXC and FOXF were found to be on the chromosome, the distance between the two was about 15 Mbp and they were separated by the homolog of FOXK.

Analysis of the *foxL1* – *foxC* – *foxF* – *foxQ1* cluster in deuterostomes showed it to be more apparent (Figure 24). In *S. purpuratus*, the homologs of *foxL1*, *foxC*, and *foxF* form a tightly linked association. In *B. floridae*, *foxL1* and *foxF* are located in close proximity, while missing a copy of *foxC* between them. In vertebrates, there is more than one chromosome showing parts of the proposed original cluster. In *D. rerio*, chromosomes 2 and 20 show close association between copies of *foxC*, *foxF*, and *foxQ1*. On chromosome 18, *foxL1* and *foxF-1* are in moderate distance to one another, but lacking a copy of *foxC* between them. In *X. tropicalis*, one chromosome shows the cluster *foxC* – *foxF* – *foxQ1* as seen in *D. rerio*, while the other chromosome shows linkage between *foxL1* and *foxC*. In addition, this chromosome also has a homolog of *foxF* in association with *foxL1* and *foxC*. However, this gene is located upstream of *foxL1* and at a larger distance than other instances of this cluster. In *M. musculus*, the original cluster appears to have split up in two parts.

An anterior one comprised of *foxL1*, *foxC-2*, and *foxF-1* on chromosome 8, and a posterior part consisting of *foxC-1*, *foxF-1*, and *foxQ1*, the same as seen in *D. rerio* and *X. tropicalis*.

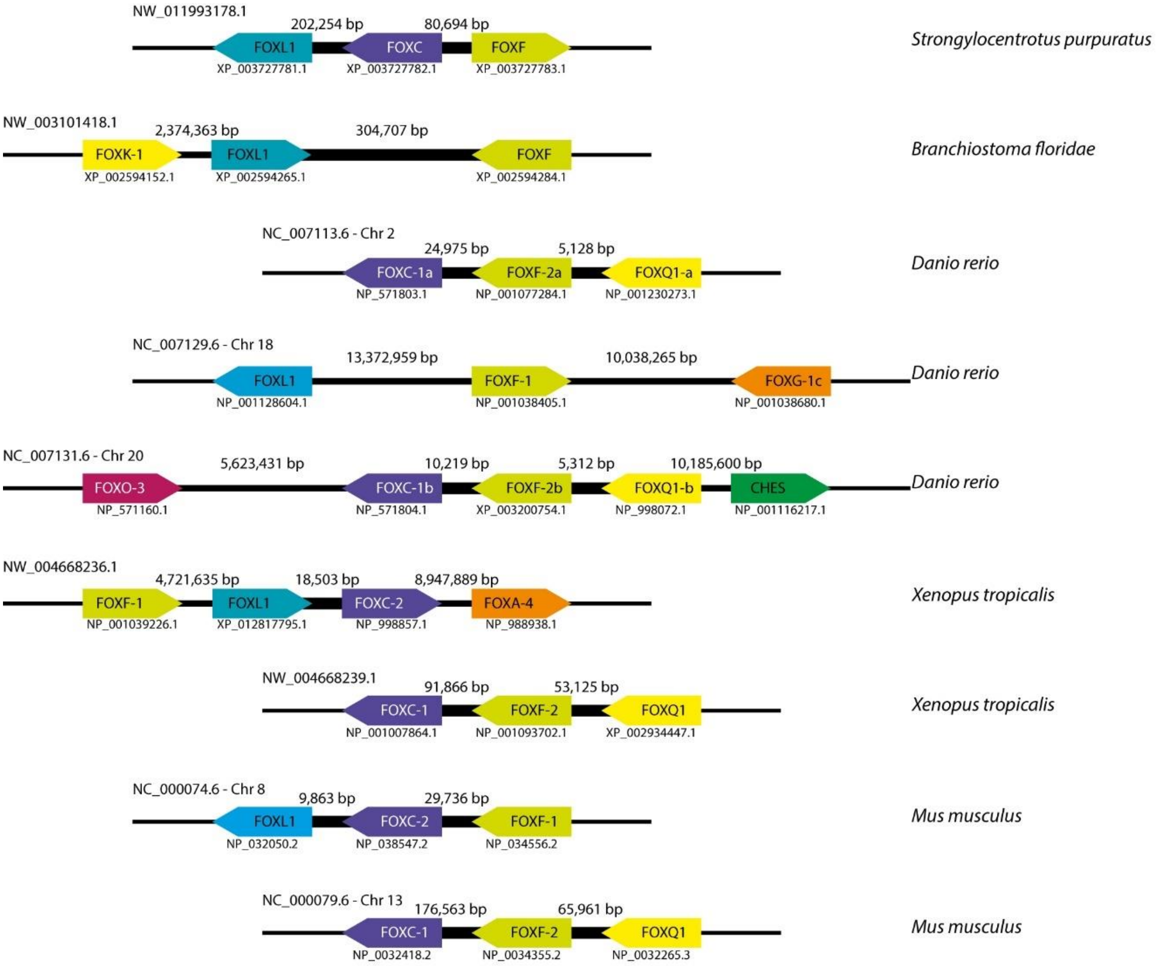

Figure 24 – FOXL1 – FOXC – FOXF – FOXQ1 cluster in deuterostomes. *S. purpuratus* showed the close association of FOXL1, FOXC, and FOXF together on the same scaffold. In *B. floridae*, FOXL1 and FOXF were located within less than 0.1% of the genome size, but without a homolog of FOXC in between them. Three chromosomes of *D. rerio* showed multiple genes of this cluster. FOXC-1a, FOXF-2a, and FOXQ1-a were together on chromosome 2. On chromosome 18, FOXL1 and FOXF-1 were present, but without a homolog of FOXC in between them. On chromosome 20, FOXC-1b, FOXF-2b, and FOXQ1-b were found in close proximity to one another and surrounded by homologs of FOXO and FON2/3 (CHES) at some distance. *X. tropicalis* showed members of this cluster to be present on two different scaffolds. FOXF-1, FOXL1, and FOXC-2 were located on the same scaffold, although in a different arrangement. The second scaffold in *X. tropicalis* showed the part of the cluster consisting of FOXC-1, FOXF-2, and FOXQ1. In *M. musculus* there were also two scaffolds with parts of the cluster present. Chromosome 8 showed FOXL1, FOXC-2, and FOXF-1, while FOXC-1, FOXF-2, and FOXQ1 were located on chromosome 13.

In contrast to the cluster of *foxD* and *foxE*, in which both genes were mostly oriented in the same direction, the conservation of gene orientation in this cluster appears not to be very strict. In vertebrates, all the genes share the reading direction with the exception of the incomplete instance in *D. rerio* on chromosome 18 (Figure 24). In the two other deuterostome species, *B. floridae* and

S. purpuratus, no conservation of orientation could be seen (Figure 24). In invertebrates, only two instances of the conservation in gene orientation could be found. Homologs of *foxC* and *foxF* in *P. caudatus* and *P. tepidariorum* had the same direction, as well as *foxC* and *foxF* in *D. pulex* and *D. melanogaster*, although in *D. melanogaster* they were interrupted by *foxK*, and in both cases the direction was different from the situation observed in *P. caudarus* and *P. tepidariorum* (Figure 23).

5.2.5 Other genes located closely together

In addition to the two proposed clusters of tight linkage among Fox genes, there are several other associations among different family members, which could be observed in more than one species. A relaxed linkage between *foxG* and *foxI* could be found in the two chordates *C. intestinalis* and *D. rerio* (supplementary material 9.3.4.4, 9.3.4.6). In both cases the distance between the two members of forkhead gene classes is less than 1% of their respective genomes. While in *D. rerio* both, *foxG-2* and *foxI-3,* are present as single copies, *C. intestinalis* shows three copies of *foxI* very closely linked to one another, possibly originating from tandem duplication events. The association between *foxG* and *foxI* was not present in any other of the analysed genomes. In *B. floridae*, as well as *X. tropicalis*, a relaxed linkage (< 1% genome size) can be found between the *foxI* and *foxM* genes (supplementary material 9.3.4.2, 9.3.4.20). However, while the genes in *X. tropicalis* are located in the same direction, in *B. floridae* they show different directions. Here as well, no other instance of linkage between *foxI* and *foxM* could be found in any of the genomes analysed here. In *T. castaneum* and *X. tropicalis*, the respective homologs of *foxK* and *foxJ1* could be observed to be located within less than 1% of the genome sizes (supplementary material 9.3.4.19, 9.3.4.20). Linkage of the homologs of *foxJ1* and *foxL1* could be shown in the sponge *A. queenslandica* and the flatworm *E. multilocularis* (supplementary material 9.3.4.1, 9.3.4.9).

5.3 DISCUSSION

5.3.1 Identification of Fox genes across the phylogenetic tree

Comparison of the forkhead genes identified in this thesis with previously published forkhead genes showed the same number of Fox genes in the two sequenced choanoflagellate species *S. rosetta* and *Monosiga brevicollis* (Shimeld et al. 2010b). In the sponge *A. queenslandica*, 17 genes were originally identified (Shimeld et al. 2010b). Only 15 of these initially annotated genes could be retrieved now, due to updated gene predictions between the first genome draft and the current draft sequence (Srivastava et al. 2010). Forkhead genes identified for cephalochordate *B. floridae* lacked homologs of *foxB*, *foxC*, *foxH*, and *foxM*. Sequences for *foxB* and *foxC* have been reported to be missing from the official gene predictions and were identified from cDNA with degenerate primers (Yu et al. 2008b). A similar situation might be expected for *foxH* and *foxM*, but is currently unclear. In the well-established model organisms *D. melanogaster* and *M. musculus* the method used here identified the predicted number of forkhead domain genes. In *D. melanogaster*, all 19 of the genes annotated to possess a forkhead domain on FlyBase, were also identified here and in *M. musculus* all members of the forkhead gene family were identified correctly (Jackson et al. 2010), with the addition of the recently automatically predicted *foxL1-like* gene. The identification of all of the annotated forkhead genes in the model organisms showed the unbiased identification approach used in this thesis to be reliable. However, in the non-model systems, the correctness of the identification is largely dependent on the quality of the existing gene predictions.

The phylogenetic analysis categorized the forkhead domains into 25 different family groups. There were, however, several genes which could not be attributed to one of the established categories. These were mostly found in the two single celled organisms and the basally branching metazoans. Uncategorized forkhead domain genes may have arisen from lineage specifc expansions of forkhead genes. Since most of these orphan genes are not shared between the taxa, they might indeed be diverged paralogs as proposed in other studies (Shimeld et al. 2010b). One exception to that is the clustering of three genes belonging to *C. owzarzaki*, *S. rosetta*, and *A. queenslandica*, respectively. These were found outside of the group of FoxN homologs and might represent an ancient class of forkhead gene, which was lost in the eumetazoan lineage. However, the analysis of the exact emergence and loss of forkhead genes in basally branching animals is hindered by the lack of sequenced organisms between these taxa. Three more orphan forkhead factors were found in the leech *H. robusta* and the sea urchin *S. purpuratus*. These were also not shared with other species and might represent lineage specific derived forkhead genes.

One of the largest debates about the forkhead family is the assignment of *D. melanogaster* genes to known classes and the relationships of forkhead genes among the bilaterians in general. Classically, the orphan genes from *D. melanogaster* are *fd3F*, *fd19B*, *fd64A*, *fd102C*, and *crg-1* (Lee & Frasch

2004). While *fd102C* has been shown to be a homologue of *foxQ2*, with possible functions in anterior patterning (Yu et al. 2003), the other genes remained unassigned. In the phylogenetic analysis here, *fd19B* appears as another homolog of *foxG* genes. *fd19B* is expressed in blastoderm stages of *D. melanogaster* embryos in a gap-like manner at the anterior pole (Tomancak et al. 2002, 2007), similar to the early expression of the *foxG* homolog *slp-1*. Therefore, according to its expression pattern and absence from other insects, such as *T. castaneum*, *fd19B* might represent a new paralog of *foxG* in *D. melanogaster*, involved in its derived mode of anterior patterning.

Homologs of *fd3F* were found in many members of the panarthropods (except for *P. tepidariorum* and *G. marginata*). The phylogenetic analysis showed them to be part of the *foxN* group, but their function remains largely unknown. The only exception is the *fd3F* gene in *D. melanogaster*, which has been shown to be involved in the formation of motile cilia (Newton et al. 2012). Interestingly, *D. melanogaster* appeared to have two paralogs, *fd3F* and *crg-1*. These two are located in close proximity to one another and share expression patterns (Tomancak et al. 2002, 2007), suggesting they might represent a very recent tandem duplication.

fd64A homologs were present in insects. Initially they had been characterized as members of the *foxL1* group, by comparison of *D. melanogaster* and human forkhead genes (Mazet et al. 2003), while other studies did not place them in any known forkhead category (Lee & Frasch 2004). The missing of clear homologs of *foxL1* in pancrustaceans and the presence of *fd64A* homologs in insects might indicate that *fd64A* is a very derived homolog of *foxL1* genes, especially since a recent study suggested that *fd64A* positive cells non-autonomously influence surrounding tissues similar to the *foxL1* homologs in mammalians (Hanlon & Andrew 2016).

5.3.2 FOX genes and their correlation with evolutionary novelties

5.3.2.1 *Opisthokonts*

Homologs of *foxK* were present in all the organisms analyzed. In vertebrates, it has been shown to promote the development of muscle tissue and its precursors (Golson & Kaestner 2016). Therefore, its presence in basal metazoans and unicellular eukaryotes was surprising. However, *foxK* acts by regulating autophagy in muscle precursors (Bowman et al. 2014) and is regulated by CDK-cyclin dependent complexes during the cell cycle (Marais et al. 2010). Additionally, *foxK* targets chromatin and attracts histone ubiquitinase complexes to remodel chromatin (Ji et al. 2014). In *D. melanogaster*, *foxK* is also involved in the defense against certain types of viruses (Panda et al. 2015). Thus, *foxK* appears to be involved in basic processes of the eukaryotic cell. The same is true for homologs of *foxO*, which were found in all organisms analyzed, with two exceptions (*S. rosetta* and *M. leidyi*). The lack of this forkhead gene class is in support of the theory that many genes seen in metazoans were already established in the opisthokont lineage, but were subsequently lost in choanoflagellates (Sebé-Pedrós et al. 2011, 2016), as well as the uncertain systematic position of ctenophores (Nosenko et al. 2013). Although paralogs of *foxO* in vertebrates are involved in neural and myeloid development (Golson & Kaestner 2016), the basic shared functions include DNA repair, cell cycle arrest, and energy homeostasis (Carter & Brunet 2007, Greer & Brunet 2005), as well as the resistance to oxidative stress and its regulation by the longevity factor SIRT1 (Brunet et al. 2004).

5.3.2.2 *Apoikozoa*

In the clade of Apoikozoa (Choanoflagellata and Metazoa), the forkhead gene repertoire was extended by three factors *foxJ1*, *foxN1/4*, and *foxP*. *foxJ1* has been identified as a master controller for the formation of motile cilia (Yu et al. 2008c). It acts in a concentration dependent manner in epithelial cells to in duce mono- or biciliated cells, and needs further factors to induce multicilliated cells (Stubbs et al. 2008). Expression of *foxJ1* homologs from different organisms were found to be expressed in ciliated tissues, and the conservation of the underlying ciliogenic program was shown through rescue experiments in the zebrafish *D. rerio* (Vij et al. 2012). In previous studies, it was found that *D. melanogaster* does not possess a homolog of *foxJ1* and is devoid of motile cilia (except for the case of bipolar sensory neurons, discussed below) (Vij et al. 2012). Here, *cg32006* was found in the *foxJ1* group. This gene showed a rather diverged sequence of the forkhead domain, which indicated that it might have lost its conserved role in this process. Members of the *foxN1/4* group have various roles in retinal, neural and thymus development (Golson & Kaestner 2016). The homolog of *foxN4* has been shown to be necessary for ciliogenesis, with similar phenotypes to those of *foxJ1*. Both, *foxJ1* and *foxN4* bind together to the promoters of genes involved in the development of multiciliated cells (Campell et al. 2016). Homologs of *foxP* are involved in the development of various cell types, such as cardiomyocytes, neurons, and regulatory T-cells (Golson & Kaestner 2016), as well as the acquisition of language in humans (Vargha-Khadem et al. 2005) and operant learning in *D. melanogaster* (Lawton et al. 2014). Another role for *foxP* homologs links them once again to the development of ciliated tissue, by promoting the cell fate of ciliated cell precursors (Ji et al. 2012).

5.3.2.3 *Metazoa*

At the base of the metazoans, new forkhead transcription factors are added to the repertoire, the functions of which correlate with evolutionary novelties of metazoans. *foxD* homologs have been shown to be involved in maintaining the pluripotency of embryonic stem cells (Hanna & Foreman 2002) and especially the induction of stem cells from differentiated tissue (Koga et al. 2014). *foxJ2/3* is involved in the response to shear stress (Cheng et al. 2014), as well as different stages of spermatogenesis (Granadino et al. 2000, Ni et al. 2016). *foxL2* regulates the estrogen production pathway and promotes the development of tissue in female-specific tissue (Ottolenghi et al. 2005, 2007; Wang et al. 2007). In contrast to unicellular eukaryotes, sponges produce gametes as specialized cells of reproduction. These cells are formed by de-differentiating choanocytes (Longo et al. 2012). Thus, there is a need for the control of de-differentiation and cues for the production of male and female gametes, possibly via nuclear receptors, which also evolved in early metazoans (Reitzel et al. 2011). Homologs of *foxN2/3* are another example for forkhead domain genes, which are involved in basic cellular processes. They are involved in the response to hypoxia (Lee et al. 2008) and can act as transcriptional repressors (Busygina et al. 2006, Scott & Plon 2005). They also help facilitating asymmetric cell divisions in different tissues (Ahmad et al. 2012) and are involved in the specification of germ layers (McCauley et al. 2010, 2012; Rho & McClay 2011). Although the most basal metazoans do not have germ layers in the classical definition of the words, they consist of the pinacoderm and the choanoderm as two differentiated tissues. The movement of cells leading to gastrulation in eumetazoans and the formation of tissues in Porifera, have been proposed to be homologous (Ereskovsky & Dondua 2006), therefore a portion of the genes involved might also be shared. Homologs of *foxL1* are known to be involved in very different processes in different clades. In vertebrates, they are involved in the cell positioning of endoderm derived tissues (Perreault et al. 2005, Takano-Maruyama et al. 2006), while the as *foxL1* annotated gene in *D. melanogaster* is expressed in the mesoderm and affects the behaviour of surrounding tissues (Häcker et al. 1992, Hanlon & Andrew 2016). Considering the difficult phylogenetic position of the *foxL1* / *fd64a* gene in *D. melanogaster* and the different expression in mandibulates compared to other arthropods (Dr. Ralf Janssen, personal communication), as well as the lack of functional studies in basal metazoans, no shared function of *foxL1* homologs can be concluded.

5.3.2.4 *Eumetazoa*

A great expansion of the forkhead transcription factor family could be seen in the eumetazoans, correlating with the increasing organismal complexity in this lineage. With the establishment of distinct germ layers, these need to be differentiated from one another and notably the expression of many of the newly introduced forkhead transcription factors is limited to one of the germ layers. *foxB* is expressed in the ectoderm and is required for its early patterning (Takebayashi-Suzuki et al. 2011), while *foxA* is restricted to endodermal tissues (Stainier 2002). Homologs of *foxC*, *foxE*, *foxF*, and *foxQ1* show mesodermal expression. *foxC* is expressed in the mesoderm in insects (Häcker et al. 1995) and divides the paraxial and intermediate mesoderm in vertebrates (Wilm et al. 2004). *foxE* is involved in the development of the mesodermally derived thyroid (Trueba et al. 2005). *foxF* promotes mesodermal cell fate in *D. melanogaster* (Zaffran et al. 2001) and mesodermal differentiation (Mahlapuu et al. 2001). Also, *foxQ1* is restricted to the mesoderm (Wotton et al. 2008), especially to the endostyl in chordates (Mazet et al. 2005). Interestingly, homologs of *foxC* and *foxE* are already present in *N. vectensis*, a cnidarian with only two germ layers and no functional data concerning the role of these genes in the absence of the mesoderm, although there is evidence, that cnidarians might have a triploblastic origin (Martindale 2004). Data on the role of *foxAB* is scarce, but it is reported to be expressed in the epidermis of bryozoans (Fuchs et al. 2011) and might have a role during gastrulation in *B. floridae*, since it is expressed specifically in the dorsal blastopore lip (Aldea et al. 2015). The rest of the forkhead genes introduced at this point reflect the establishment and patterning of axis in the eumetazoans. *foxG* is best known for its role in segmentation along the anterior-posterior axis in *D. melanogaster* (Cadigan et al. 1994) and *foxG* homologs in vertebrates show a patterning function in the developing brain (Hanashima et al. 2004, Martynoga et al. 2005). *foxQ2* is also largely involved in patterning processes. It distinguishes the vegetal from the animal pole in sea urchins (Yaguchi et al. 2008) and the oral from the aboral side in hydrozoans (Chevalier et al. 2006). It is involved in anterior-posterior patterning in Amphioxus (Yu et al. 2003) and is required for the anterior head development in *T. castaneum* (Kitzmann et al. 2016).

5.3.2.5 *Bilateria*

foxM and *foxH* first appear at the base of the bilaterians. *foxM* has effects on cell cycle progression and cytokinesis (Golson & Kaestner 2016, Laoukili et al. 2005). It also leads to severe heart defects in vertebrates (Laoukili et al. 2007), but there is no data in other groups. However, it is noteworthy that the appearance of *foxM* coincides with evolution of a dedicated circulatory system in bilaterians. Homologs of *foxH* have been shown to facilitate the left-right asymmetry in *D. rerio* (Pogoda et al. 2000, von Both et al. 2004), *X. tropicalis* (Kofron et al. 2004), and *M. musculus* (Hoodless et al. 2001, Norris et al. 2002). No data from other species is available yet, but the origin of a gene needed for the break of symmetry would very well agree with the origin of bilateral symmetry in the Bilateria.

5.3.2.6 *Deuterostomia*

Homologs of *foxI* first appear in the deuterostome lineage. This gene has been shown to be involved in the development of the otic placode and jaw in *D. rerio* (Nissen et al. 2003, Solomon et al. 2003) and it shows an expression restricted to placodes in *M. musculus* (Ohyama & Groves 2004). Placodes are precursors of elaborate sense organs, usually only found in chordates (Padanad & Riley 2011). However, homologous precursors have been found in all deuterostomes (Graham & Shimeld 2013). The deuterostome clade also sees the addition of *foxR* in vertebrates and *foxS* in mammals, but their specific roles have not yet been analyzed.

5.3.2.7 *Ecdysozoa*

Apart from *fd64A* in insects, which has been proposed to be a homolog of *foxL1* (discussed above), but rather represents a new forkhead domain family member in insects, the panarthropod lineage of the ecdysozoans shows the emergence of *fd3F*, which falls into the group of *foxN* homologs in the phylogenetic analysis. The function of this forkhead gene has been shown in the development of chordotonal neurons in *D. melanogaster* (Newton et al. 2012). These bipolar neurons possess mechanosensory motile cilia. As discussed above, the homolog of the master controller gene for motile cilia formation (*foxJ1*/*cg32006*) has a very diverged sequence in *D. melanogaster* and somatic cells in *D. melanogaster* do not possess motile cilia with the exception of bipolar sensory neurons. Therefore, the expression analysis of *fd3F* and its role in the development of cells with motile cilia suggests that functions of *foxJ1* have been taken over by *fd3F* in *D. melanogaster*.

While many members of the forkhead gene family possess derived roles in development, there are also a number of shared general functions. These common functions generally correlate with the evolutionary novelties of the taxa in which they have evolved. Genes, which are present in unicellular eukaryotes perform basic cell autonomous functions and are involved in cell cycle control, defense against viruses, or homeostasis. Later, new members are involved in sex-specific development and the patterning of germ layers and the differential development of newly evolved tissue types.

5.3.3 Existence and maintenance of FOX gene clusters

The presence of tightly linked homologs of *foxD* and *foxE* had been shown for the genomes of notochordata, cnidaria, and placozoans (Shimeld et al. 2010b). These findings could be verified for *N. vectensis*, *B. floridae*, and the analyzed vertebrate species. Previous studies also suggested the loss of *foxE* in the ecdysozoans, while here *foxE* could be shown to be present in *P. caudatus*, suggesting a loss of this forkhead family member in the panarthropod lineage. However, except for the five species in which homologs of both genes were present, a linkage between *foxD* and *foxE* could not be shown other lineages. The loss of the close association of these two genes had previously been shown for several lophotrochozoan species and the urochordate *C. intestinalis* (Shimeld et al. 2010a). The same situation was found here in another lophotrochozoan, *C. gigas*, and the deuterstome *S. purpuratus*. All of which indicated, that the linkage between *foxD* and *foxE* has been lost independently in several lineages.

A more expanded cluster of forkhead genes had been shown for homologs of *foxL1*, *foxC*, *foxF*, and *foxQ1*. Instances for a partial linkage of these genes had been proposed for as early as the basal bilaterian lineages (Mazet et al. 2006). A linkage of parts of these genes could be observed in members of all bilaterian lineages analyzed here. Especially in the vertebrates there was more than one instance of linkage in each of the species, probably resulting from incomplete block duplication of the original cluster during the genome evolution of these species. Also in the basally branching deuterostomes parts of the cluster could be seen, except for the tunicate *C. intestinalis*, which had previously been shown not to possess clustered forkhead genes and no association between *foxD* and *foxE* as well (Shimeld et al. 2010a). None of these deuterostomes had an associated *foxQ1* homolog on the same scaffolds as the other genes. In the case of *B. floridae* no homolog of *foxC* could be found in between *foxL1* and *foxF*, which can be explained by the lack of this gene's sequence from the predicted gene set (as mentioned above).

In the other bilaterian lineages, lophotrochozoa and ecdysozoa, clustering of a subset of the genes could also be shown. In no case was a homolog of *foxQ1* associated with the other genes. *foxQ1* has been proposed to be broken off from this cluster in lophotrochozoans (Mazet et al. 2006), and lost completely in the ecdysozoan lineage, although its presence in *E. kanangrensis* suggests that it was ancestrally present in the ecdysozoans. Instances of a grouping of the genes were present in *L. anatina* and *C. gigas*, with two partial clusters in *L. anatina* and only close association of *foxL1* and *foxC* in *C. gigas*. Among the ecdysozoans, only *P. tepidariorum* showed the three remaining genes, *foxL1*, *foxC*, and *foxF* to be present in close proximity to one another. In the members of the pancrustaceans, *D. pulex* and *T. castaneum* showed homologs of *foxC* and *foxF* closely associated, while in *D. melanogaster* the cluster seemed to be completely broken up with large distances and the insertion of another Fox gene between the two.

A shared regulation by the presence of regulatory genomic blocks has been proposed as the driving force for the maintenance of gene clusters in a genome (Shimeld et al. 2010b). In the case of the *foxL1*-*foxC*-*foxF*-*foxQ1*-cluster the genes are linked by their expression in mesoderm derived tissues (Mazet et al. 2006, Tu et al. 2006, Wotton et al. 2008). Thus, a shared regulation of these genes seems probable. Additionally, the expression of these genes appears sequentially after gastrulation in lophotrochozoans (Shimeld et al. 2010a). Therefore, a temporal component could be another driving force of cluster integrity, as has been proposed for the temporal co-linearity of the Hox genes (Garcia-Fernàndez 2005). Moreover, genes of this Fox cluster share an anterior, overlapping expression in tissue surrounding the foregut in lophotrochozoans and other organisms (Shimeld et al. 2010a). This spatially shared expression is another indicator for the organization as a genomic block with shared regulation and chromosomal compartmentalization. Interestingly, the organisms with broken-up Fox clusters also show incomplete Hox clusters. Both clusters are broken up or unusual in *D. melanogaster*, *C. intestinalis* (Mazet et al. 2006), as well as *S. purpuratus* (Lemons & McGinnis 2006), while in the vertebrates, *P. tepidariorum* (Schwager et al. 2017) and to some extend *T. castaneum* have both gene clusters present. This might be a side effect of elevated rates of genome evolution in these lineages and suggests that there are other mechanisms for the conservation of the roles of these genes in *D. melanogaster, C. intestinalis*, and *S. purpuratus*.

6 Embryonic development of the pedipalp of *Parasteatoda tepidariorum*

6.1 INTRODUCTION

6.1.1 Appendages in arthropods and serial homology

The evolutionary success of arthropods can in large parts be attributed to the manifold diversity of their appendages (Angelini & Kaufman 2005, Williams & Nagy 2001). The body plan of arthropods consists of serially homologous segments, which can bear appendages adapted for different purposes in different lineages (Figure 25). The evolution and development of different morphologies of serially homologous appendages is not yet well understood (Angelini & Kaufman 2005).

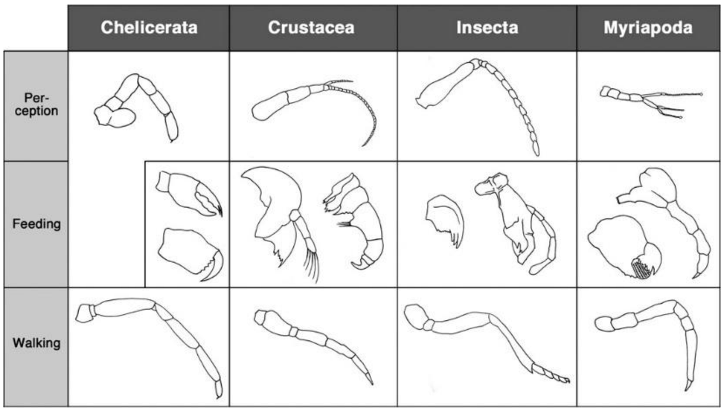

Figure 25 – Overview of the different morphologies of appendages in arthropods and their roles in behaviors. (from Prpic & Damen 2008)

Appendages across the arthropods share developmental features. They are regionalized by a distal domain of *Distal-less*, a median domain of *dachshund*, and a proximal co-expression of *homothorax* and *extradenticle*, a process that predates the evolution of the segmented arthropod leg, since regionalization through the same genes can be seen in onychophorans (Janssen et al. 2010a). Polarity among the anterior-posterior axis is derived from the expression of segment-polarity genes, which also act to set up the dorso-ventral axis, although this requires different genes in different arthropod groups (reviewed in Angelini & Kaufman 2005, Pechmann et al. 2010). It has been shown, that slight changes in the expression domains and interactions of these genes might account for some of the morphological differences of appendage types (Dong et al. 2000, 2001). However, one of the main reason for the development of different appendages is the positional information derived from the expression of Hox genes. For instance, the presence of *Antennapedia* discriminates between antennal and walking leg fate in *D. melanogaster* (Casares 2001), and the absence of *Ultrabithorax* in the crustacean *Parhyale hawaiensis* leads to the transformation of gnathopods into a second pair of maxillopods (Liubicich et al. 2009).

Recent studies have revealed more detailed aspects of how different morphologies have evolved. For instance, the development of leg differences in water striders is achieved by the interaction of Ubx and the Gamma interferoninducible thiol reductase (Gilt) as a new target gene, which leads to the morphological changes needed for the jumping escape reflex (Armisén et al. 2015) (Figure 26A). Moreover, morphological changes can be achieved through duplication of genes and subsequent neo-functionalization of its paralogs. In the case of *P. tepidariorum* it could be shown, that *dachshund-1* regionalizes the leg-like appendages as expected in arthropods, while *dachshund-2* is necessary for the development of the patella, a leg segment unique to chelicerates (Turetzek et al. 2016) (Figure 26 B).

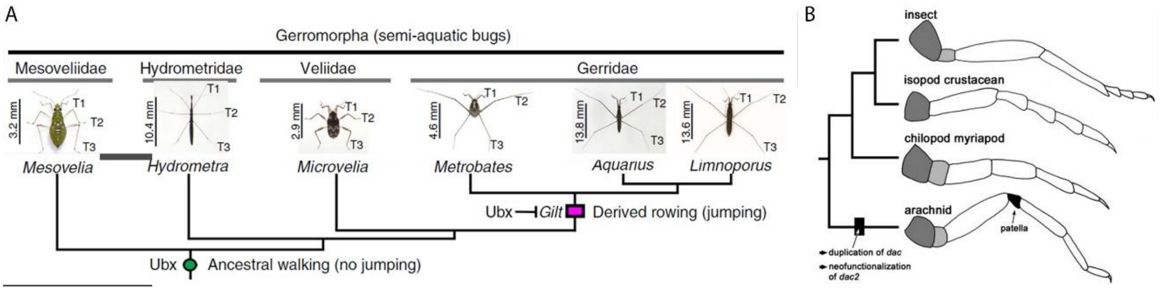

Figure 26 – Examples for the evolution of different morphologies. A new genetic interaction of Ubx with gilt lead to evolution of distinct morphology of the legs on the 2nd and 3rd thoracic segments of the Gerridae (modified from Armisén et al. 2015) (A). The duplication and subsequent neofunctionalization of *dachshund* in the arachnids lead to the evolution of the patella as a new leg segment in this clade (from Turetzek et al. 2016) (B).

6.1.2 Embryonic pedipalp development in *P. tepidariorum*

Spiders possess two types of appendages with a leg-like morphology, the pedipalps and the walking legs (Figure 25). While the lack of a median expression domain of *dac* is the difference, which might account for the special morphology of the chelicera (Prpic & Damen 2004), the expression of appendage patterning genes between pedipalps and walking legs is very similar (Pechmann et al. 2010). The positional information of the pedipalp segment in *P. tepidariorum* is provided by the anterior expression border of the Hox gene *labial* (Pechmann et al. 2015), which makes it homologous to the tritocerebral segment of other arthropods and to the segment bearing the slime papillae in onychophorans, the sister group of the arthropods (Janssen et al. 2014).

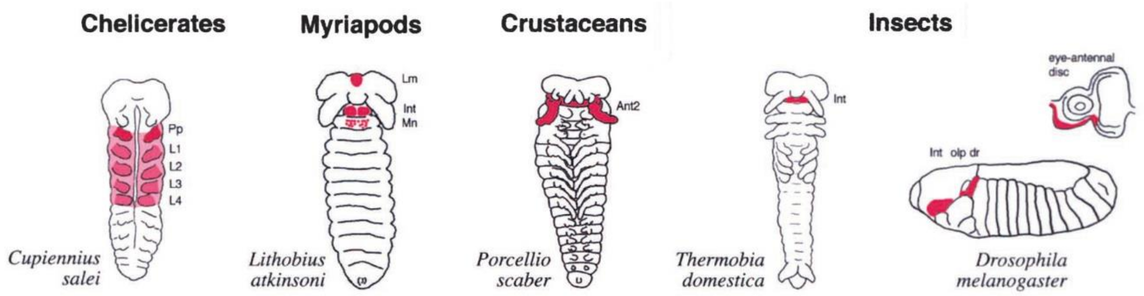

Figure 27 – Schematic representation of *labial* expression in different arthropods. In chelicerates, like *Cupiennius salei*, *labial* is expressed strongly in the pedipalp segment and shows weaker expression in the segments bearing the walking legs. In the myriapod *Lithobius atkinsoni*, *labial* is strongly expressed in the intercalary segment and the labrum and weakly in the mandibular segment. In crustaceans, such as the isopod *Porcellio scaber*, *labial* is expressed in the 2nd antennal segment and its appendages. In basal insects, such as *Thermobia domestica*, *labial* is expressed in the intercalary segment similar to its expression in higher insect, such as *Drosophila melanogaster*, where it has an additional expression domain in the eye-antennal imaginal disc.(modified from Hughes & Kaufman 2002a)

RNA interference with the *labial* gene in *P. tepidariorum* led to the loss of the pedipalps and an increase in cell death in the remaining tissue of the tritocerebral segment (Figure 28) (Pechmann et al. 2015). Thus, showing a conserved role for *labial* in the maintenance of anterior segments, especially the tritocerebral segment (Merrill et al. 1989, Schaeper et al. 2010). In *P. tepidariorum*, *labial* has the additional function of appendage initiation and development of the pedipalps, a function not present in insects, due to the appendage-less character of the tritocerebral segment.

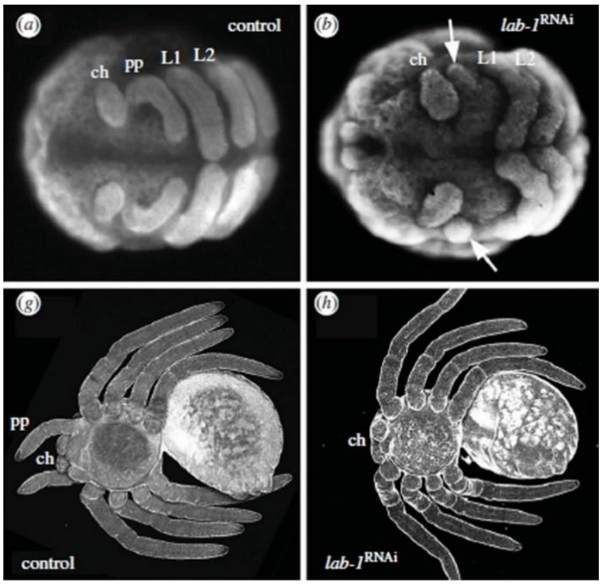

Figure 28 – Phenotype of *labial* RNAi in *P. tepidariorum*. Treated spiders lack the pedipalps in embryonic stages (b) and an increase in cell death results in a reduced tritocerebral segment after hatching (h), showing functions for segment maintenance and appendage initiation and development for *labial* in *P. tepidariorum*. (modified from Pechmann et al. 2015)

Since the tritocerebral segment of the well-studied model organism *D. melanogaster* does not have an appendage, an interesting question is whether genes, which are still expressed in the intercalary segment in *D. melanogaster* or interact on any level with *labial* might have a function in the development of the pedipalps in *P. tepidariorum*. Similar to the case of *labial* itself, which in insects does not have a role in appendage development, but is involved in tissue maintenance during development in both, *Drosophila* and *Parasteatoda* . Therefore, homologs of these genes from *D. melanogaster* were identified in *P. tepidariorum* and their expression in the stages of limb development (Figure *29*) was analyzed.

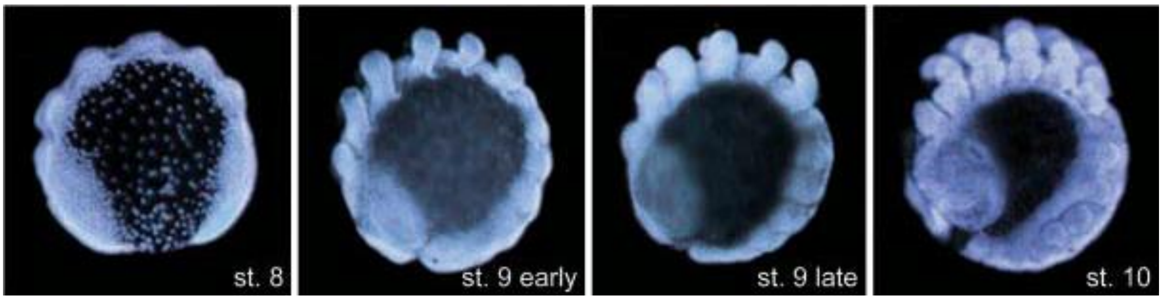

Figure 29 – Stages of appendage initiation and differentiation in *P. tepidariorum*. Limb buds can first be seen during stage 8. They grow in length in the following stage and become morphologically differentiated at stage 10. (modified from McGregor et al. 2008)

6.2 RESULTS

6.2.1 Homologs of genes with expression in the intercalary segment of Drosophila and interaction partners of labial / HOXB1

Although there is no homologous structure to the spider pedipalps in *D. melanogaster*, there are several genes annotated to be expressed during development in the intercalary segment on Flybase (Gramates et al. 2017). Moreover, the *labial* gene determines the identity of the appendage of the pedipalp segment in *P. tepidariorum* and is required for the correct development of the pedipalps itself (Pechmann et al. 2015). Therefore, homologs of interaction partners of the *D. melanogaster labial* gene might show conserved interactions with the labial homolog in spiders. Additionally, *labial* is the homolog of the vertebrate gene *hoxB1*, interaction partners of which might also have homologs in *P. tepidariorum*, that interact with *labial*. In order to see whether there is the possibility of conserved interactions between *labial* and other genes in the pedipalp segment of *P. tepidariorum* during development, homologs of genes, which were expressed in the intercalary segment of *D. melanogaster*, were known to interact with *labial* (from DroID (Murali et al. 2011, Yu et al. 2008a)), or the vertebrate homolog *hoxB1* (from BioGrid (Chatr-Aryamontri et al. 2017)) were identified in *P. tepidariorum* and checked for possible paralogs. Subsequently, the genes were cloned and their expression patterns were analyzed for the presence of transcripts in the pedipalps or any difference in the expression patterns between pedipalps and walking legs. Especially during stage 8 in which the limb buds are formed to see if pedipalps might be set up differently from the walking legs from the start, as well as the subsequent stages up to stage 11 in which the limbs are differentiated. 53 genes met the requirements mentioned above (Table 6).

Table 6 – List of genes expressed in the intercalary segment of *D. melanogaster* and known interaction partners of *labial/hoxB1*

Gene	Source	Already published in *Parasteatoda*
brinker	DroID	
buttonhead	Flybase	
C-terminal binding protein	DroID	
CTCF	DroID	
cap-n-collar	Flybase	
chinmo	DroID	
crocodile	Flybase	
dachshund	Flybase	Yes
dachsous	Flybase	
daughterless	DroID	
dorsal	DroID	
Drop	Flybase	
empty spiracles	Flybase	
Enhancer of zeste	DroID	
extradenticle	DroID / Interaction with *hoxB1*	Yes
eyeless / PAX6	Flybase / Interaction with *hoxB1*	Yes
Fasciclin 2	Flybase	
fussel	Flybase	
glial cells missing	Flybase	
gooseberry	Flybase	

HMGB1 / Dsp1	DroID / Interaction with *hoxB1*	
homothorax	DroID	Yes
huckebein	Flybase	
hunchback	Flybase	Yes
insensitive	DroID	
intermediate neuroblasts defective	Flybase	
klumpfuss	Flybase	
knot	Flybase	Yes
Kruppel	DroID	
labial	Flybase / DroID	Yes
ladybird early	Flybase	
lethal of scute	Flybase	
Maf-S	Flybase	
Medea	DroID	
NR3C1	Interaction with *hoxB1*	
oceliless	Flybase	Yes
ovo	Flybase	
paired	DroID	
pleiohomeotic	DroID	
polycomb	DroID	
polyhomeotic-proximal	DroID	
reversed polarity	Flybase	
senseless	DroID	
Sfmbt	DroID	
sloppy paired 1	Flybase	
sloppy paired 2	Flybase	
Tachykinin	Flybase	
tailless	Flybase	
trithorax	DroID	
twin of eyeless	Flybase	Yes
ventral nervous system defective	Flybase	
vrille	Flybase	
wingless	Flybase	Yes
zeste	DroID	

6.2.2 Verification of previously published genes

10 of the genes of interest had already been published in *P. tepidariorum*. The homologs of *eyeless*/*pax6*, *ocelliless*/*otd* were already analysed in the context of eye development and showed no expression in the pedipalps, or no difference in expression patterns between pedipalps and legs. Both homologs of the *dachshund* gene were analysed in a previous publication for their involvement in the development of legs, but they showed no differential expression patterns between the appendages (Turetzek et al. 2016). *labial* itself also has two homologs in *P. tepidariorum*. The first homolog was identified as an important regulator of pedipalp development, while its paralog showed no phenotype (Pechmann et al. 2015). Both, *extradenticle* and *homothorax* have two homologs each in *P. tepidariorum*. The homologs of *homothorax*, although both are expressed in the pedipalps, showed no difference in their expression between pedipalps and legs (Turtezek et al, in preparation). In the case of *extradenticle*, *extradenticle-1* showed diffuse expression at the distal tip of the pedipalp, but resulted in no phenotype after dsRNA injection.

extradenticle-2, on the other hand, was expressed in the same manner in all appendages (Zhang 2016).

Homologs of *hunchback*, *knot* (*collier*), and *wingless* were identified before transcriptomic or genomic resources were available in *P. tepidariorum*. None of these genes showed expression in the pedipalps different from expression in the legs. In order to determine any paralogs of these genes in *P. tepidariorum*, the transcriptome was surveyed for paralogs, which were not identified in the original publications.

6.2.2.1 *Hunchback*

hunchback (*hb*) expression in *P. tepidariorum* starts in the middle of the germ disc and an additional ring of expression at the circumference of the disc. After the break of radial symmetry, *hb* is expressed in alternating broad and narrow stripes along the embryo. Functionally, *hb* acts as a gap gene in *P. tepidariorum*. Parental RNAi leads to the loss of the first walking legs in milder phenotypes, while more severe phenotypes displayed the loss of the first two and fourth pair of walking legs, corresponding with the striped expression of this gene (Schwager et al. 2009). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed the originally identified homolog of *hb* to be the only one present (Figure 30).

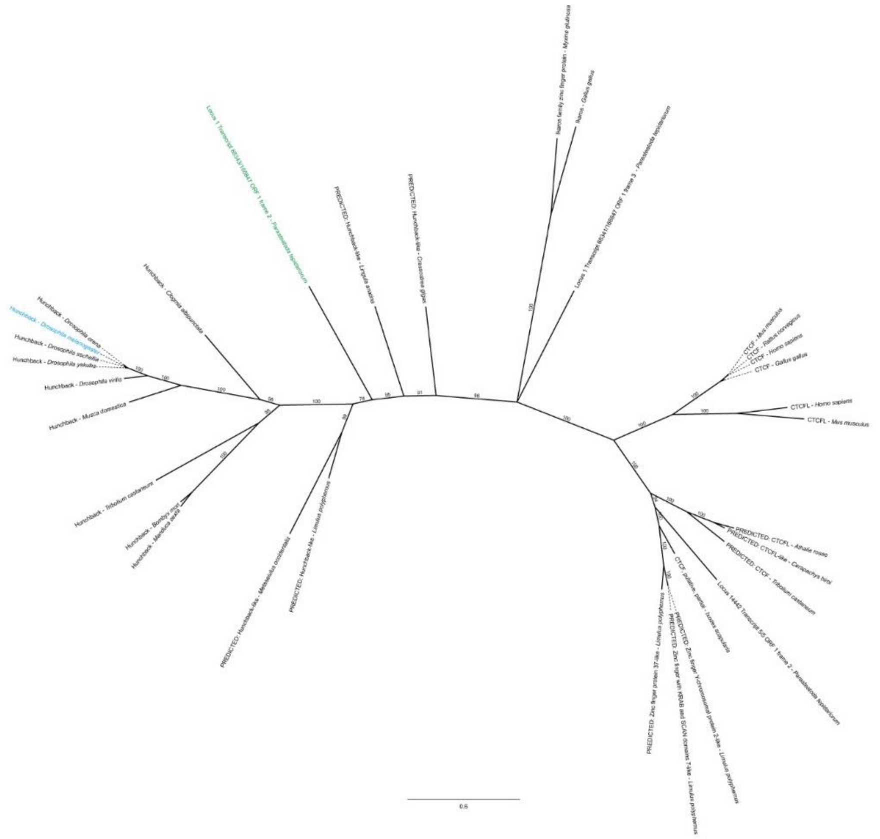

Figure 30 – Phylogenetic tree of *hb.* Branch values represent posterior probabilities of Bayesian likelihood (780 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.1). One homolog of the *D. melanogaster hb* (blue) could be identified (Locus 1 transcript 68343, green)

6.2.2.2 *Knot (collier)*

knot (*kn*) in *P. tepidariorum* first appears in the extended germ band and is restricted to the nervous system with additional spots of expression in the opisthosoma. There was no difference in the expression pattern between the segments (Schaeper et al. 2010). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed another paralog of *kn* (Locus 24497 (*col-2*)) (Figure 31).

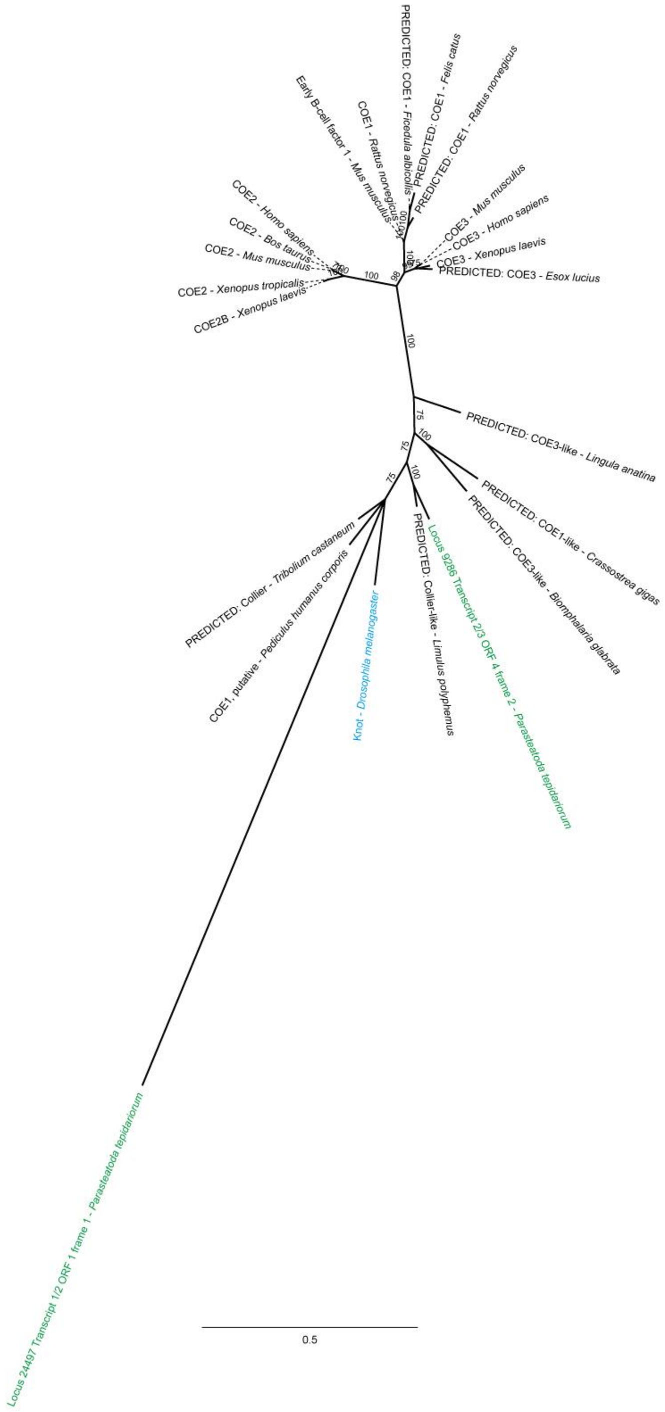

Figure 31 – Phylogenetic tree of *kn*. Branch values represent posterior probabilities of Bayesian likelihood (1152 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation. Two homolog of the *D. melanogaster kn* (blue) could be identified (Locus 9286 (*col-1*), Locus 24497 (*col-2*), both green).

No expression of *col-2* could be observed during embryogenesis prior to stage 12 (Figure 32 A, B, C, D). During stage 12 two spots of expression appear in the segments of the fourth walking legs and the first opisthosomal segment (black arrowheads in Figure 32 G, H).

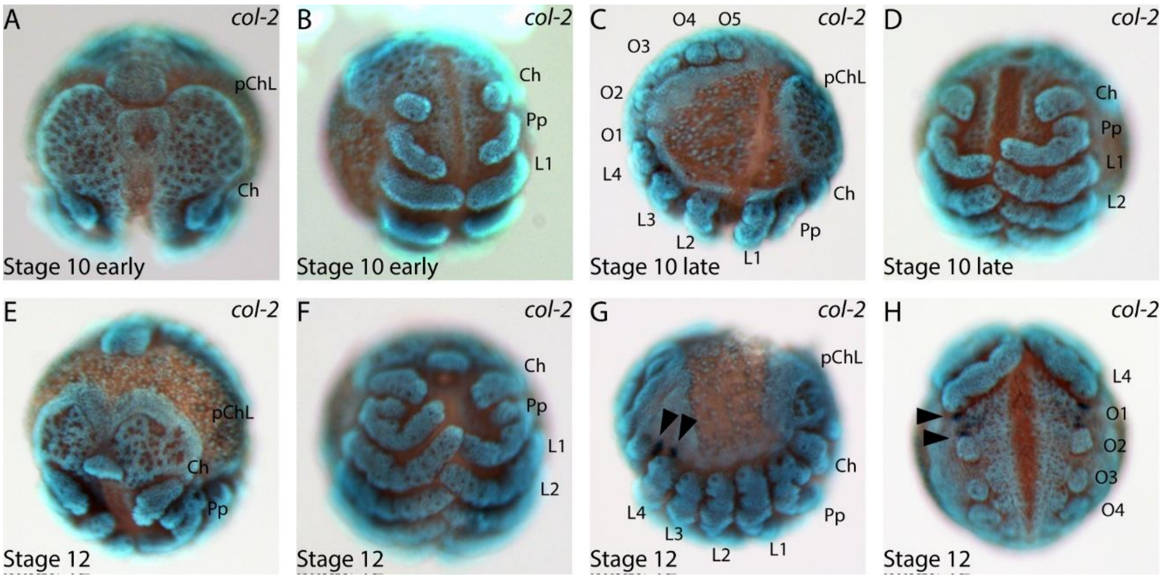

Figure 32 – Embryonic expression of *collier-2* in *P. tepidariorum*. No expression of *col-2* was observed in the earlier embryonic stages (A, B, C, D). At stage 12, no expression could be detected in the pre-cheliceral lobes (A, B), while two expression spots were visible in L4 and O1 (black arrowheads in G and H. A and E show embryos in frontal aspect. B, D, F, and H are ventral views with anterior to the top. C and G are lateral views with the anterior to the right.

6.2.2.3 *Wingless*

wingless (*wg*) was expressed in spots at the base of the prosomal limb buds at stage 8. Later during development, it is expressed along the proximo-distal axis of the prosomal limbs with additional expression domains in the opisthosomal appendages and the labrum (janssen et al 2010). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed no paralogs to the originally identified gene (Figure 33).

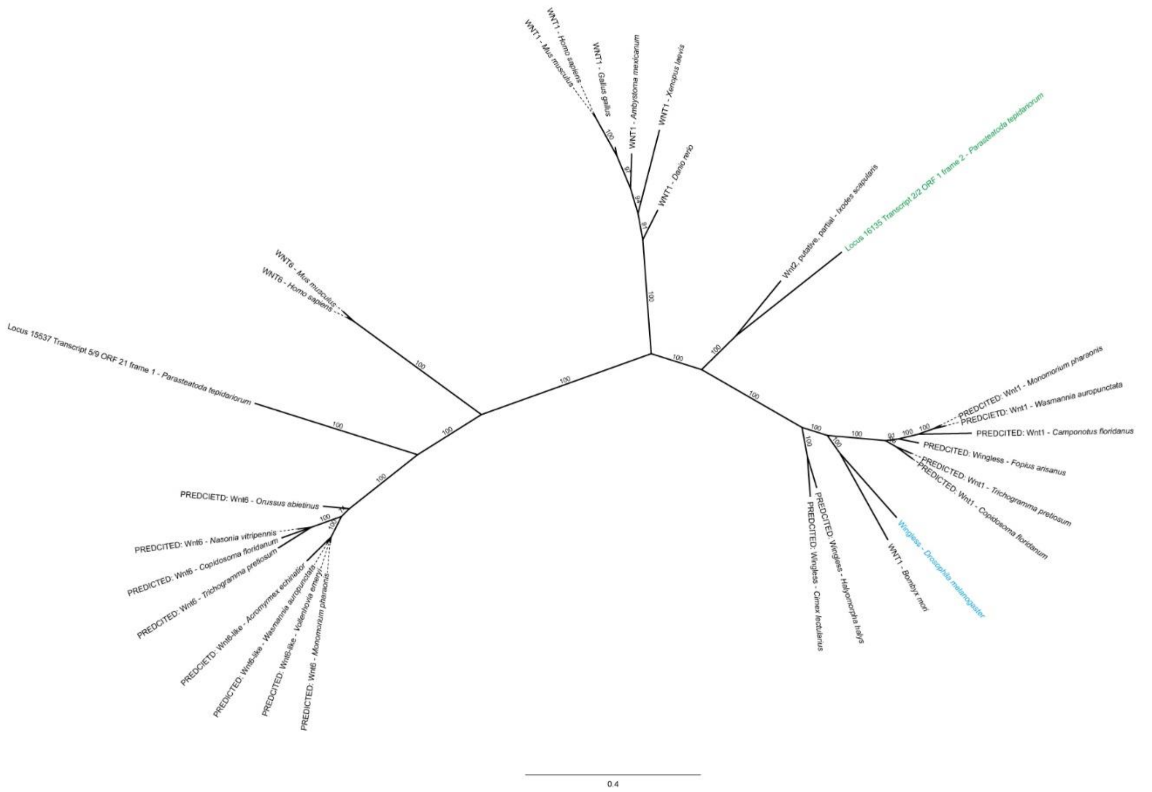

Figure 33 – Phylogenetic tree of *wg.* Branch values represent posterior probabilities of Bayesian likelihood (540 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.2). One homolog of the *D. melanogaster wg* (blue) could be identified (Locus 16135, green).

6.2.3 Identification and analysis of previously uncharacterized genes

Apart from the 10 previously analyzed genes, for their involvement in various aspects of spider development, 43 genes remained on the list of candidates, which were previously neither identified nor analyzed in *P. tepidariorum*.

6.2.3.1 *brinker*

brinker (brk) is a transcriptional repressor (Stöbe et al. 2009), which in *Drosophila* is involved in wing disc morphogenesis (Dworkin & Gibson 2006, Moser & Campbell 2005), and plays a role in the BMP and TGF-beta pathways (Affolter et al. 2001, Stronach & Perrimon 2001). Homologs have been identified in insects other than *Drosophila*, but not in other arthropods. Also in *P. tepidariorum* no homolog could be found, since the blast against the *P. tepidariorum* transcriptome resulted in no hits.

6.2.3.2 *buttonhead*

buttonhead (*btd*) is a member of the SP1/KLF transcription factor family, which acts as a head gap gene during *Drosophila* development (Jaeger 2011, Peel 2004, Wimmer et al. 1993), but is also involved in the morphogenesis of the legs (Estella & Mann 2010). Phylogenetic analysis of blasted sequences showed one homolog of the Sp1-4 and Sp5-9 in *P. tepidariorum*, respectively, but no homolog of the *Drosophila buttonhead* (Figure 34).

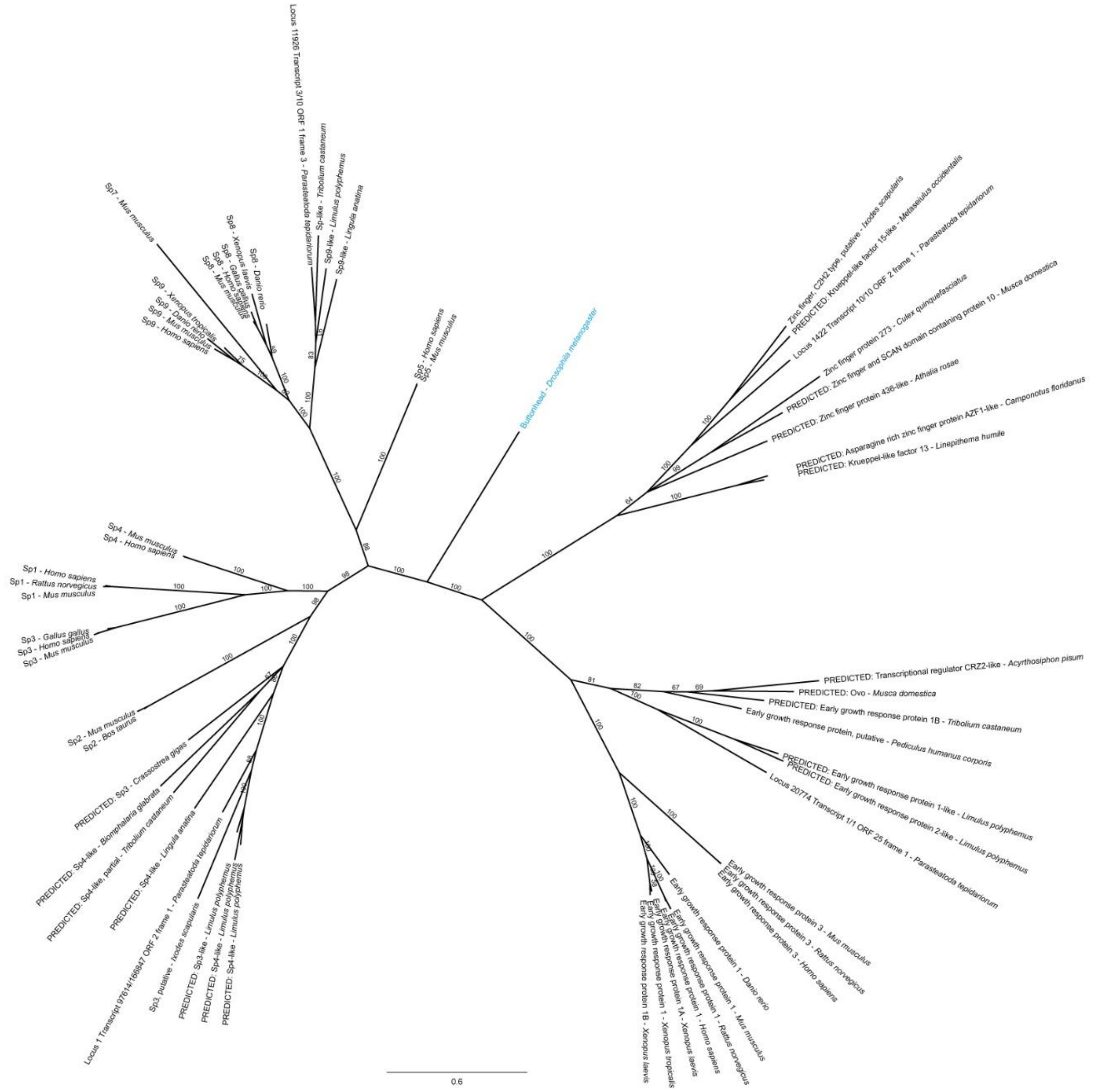

Figure 34 – Phylogenetic tree of *buttonhead*. Branch values represent posterior probablilities of Bayesian likelihood (1848 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.3). No homologous sequence could be found for Drosophila btd (blue).

6.2.3.3 *C-terminal binding protein*

The C-terminal binding protein is, depending on its context, a transcriptional co-activator, or co-repressor (Fang et al. 2006, Keller et al. 2000). It is involved in the Wnt signaling pathway

(Bhambhani et al. 2011, Fang et al. 2006), in the development of eye precursors via interaction with Eyeless and Dachshund (Hoang et al. 2010), controls the DNA binding of pleiohomeotic (Basu & Atchison 2010), and interacts with Hairy during *Drosophila* embryonic segmentation (Poortinga et al. 1998).

Phylogenetic analysis found one homolog of CtBP in the transcriptome of *P.tepidariorum* (Locus 1 transcript 460) (Figure 35). The analysis of this genes expression showed mild ubiquitous expression during embryogenesis (supplementary material 9.4.3.1).

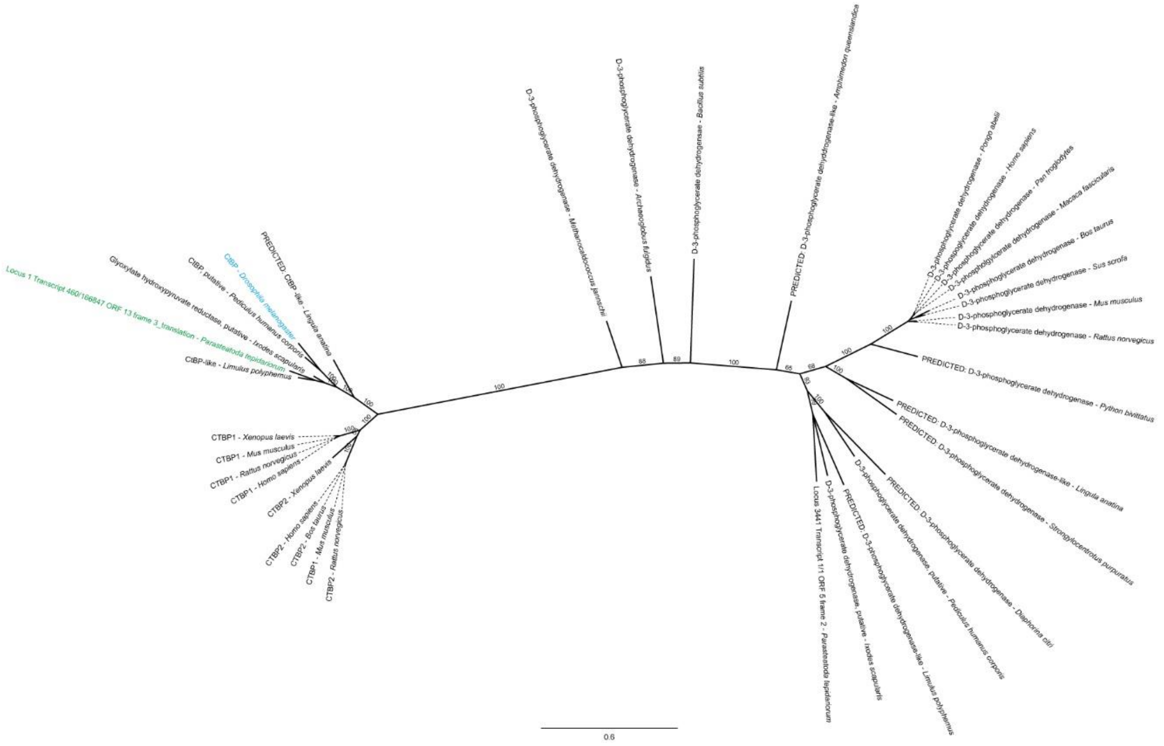

Figure 35 – Phylogenetic tree of *CtBP*. Branch values represent posterior probabilities of Bayesian likelihood (2010 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.4). One homolog to the CtBP of *D. melanogaster* (blue) could be identified (Locus 1 transcript 460, green).

6.2.3.4 *CTCF*

CTCF is a ubiquitous transcription factor, which is involved in the TGF-beta pathway, where it recruits Smad proteins to a subset of binding sites, as well as facilitating their redistribution in response to BMP signaling (Van Bortle et al. 2012).

Phylogenetic analysis in *P. tepidariorum* showed one CTCF homolog (Locus 14442) (Figure 36), the expression of which is ubiquitous during embryonic development (supplementary material 9.4.3.2).

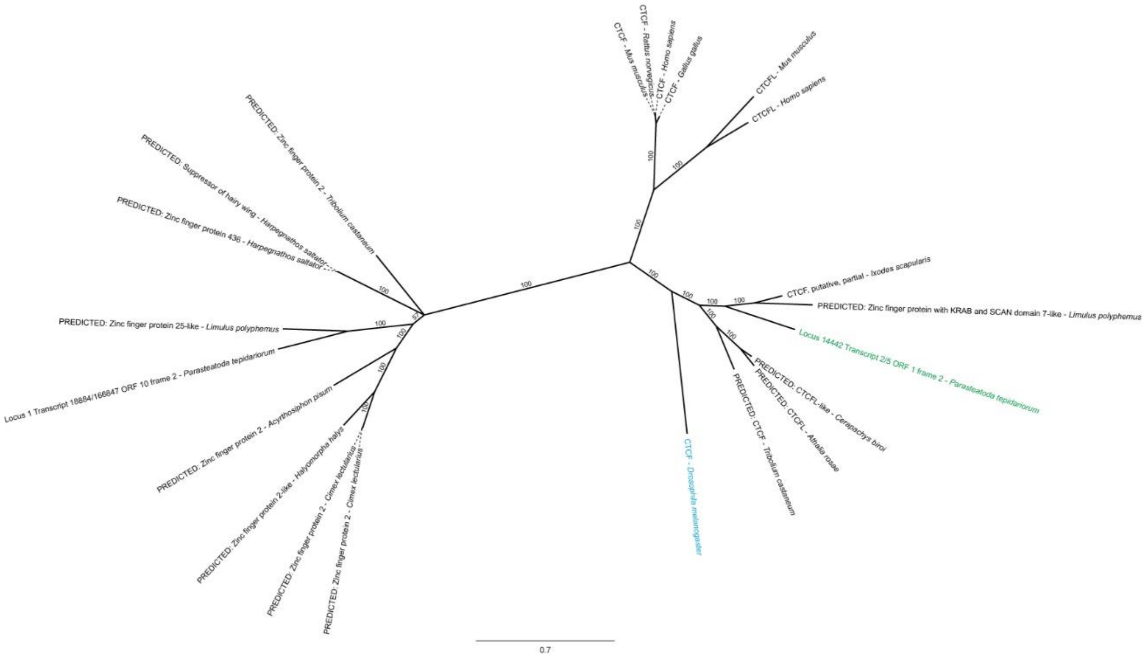

Figure 36 – Phylogenetic tree of CTCF. Branch values represent posterior probabilities of Bayesian likelihood (68 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.5). One homolog to the *D. melanogaster* CTCF sequence (blue) could be identified (Locus 14442, green).

6.2.3.5 *cap-n-collar*

cap-n-collar (*cnc*) is a transcription factor with a Basic leucine zipper domain, which is involved in the regulation of many diverse processes, such as growth and ecdysone response, aging, stress defense, or stem cell maintenance (Pitoniak & Bohmann 2015). It is best known for its role in the specification of head segments of insects during embryogenesis (Janssen et al. 2011, Kittelmann et al. 2013) and the suppression of Deformed Hox gene function (McGinnis et al. 1998, Veraksa et al. 2000).

Phylogenetic analysis showed one homolog of *cnc* to be present in the transcriptom of *P. tepidariorum* (Locus 1274) (Figure 37). The expression of this homolog is ubiquitous during the embryonic development *P. tepidariorum* (supplementary material 9.4.3.3). This finding is in concert with previously published data, stating that insect-typical expression pattern is restricted to the Mandibulata (Sharma et al. 2014).

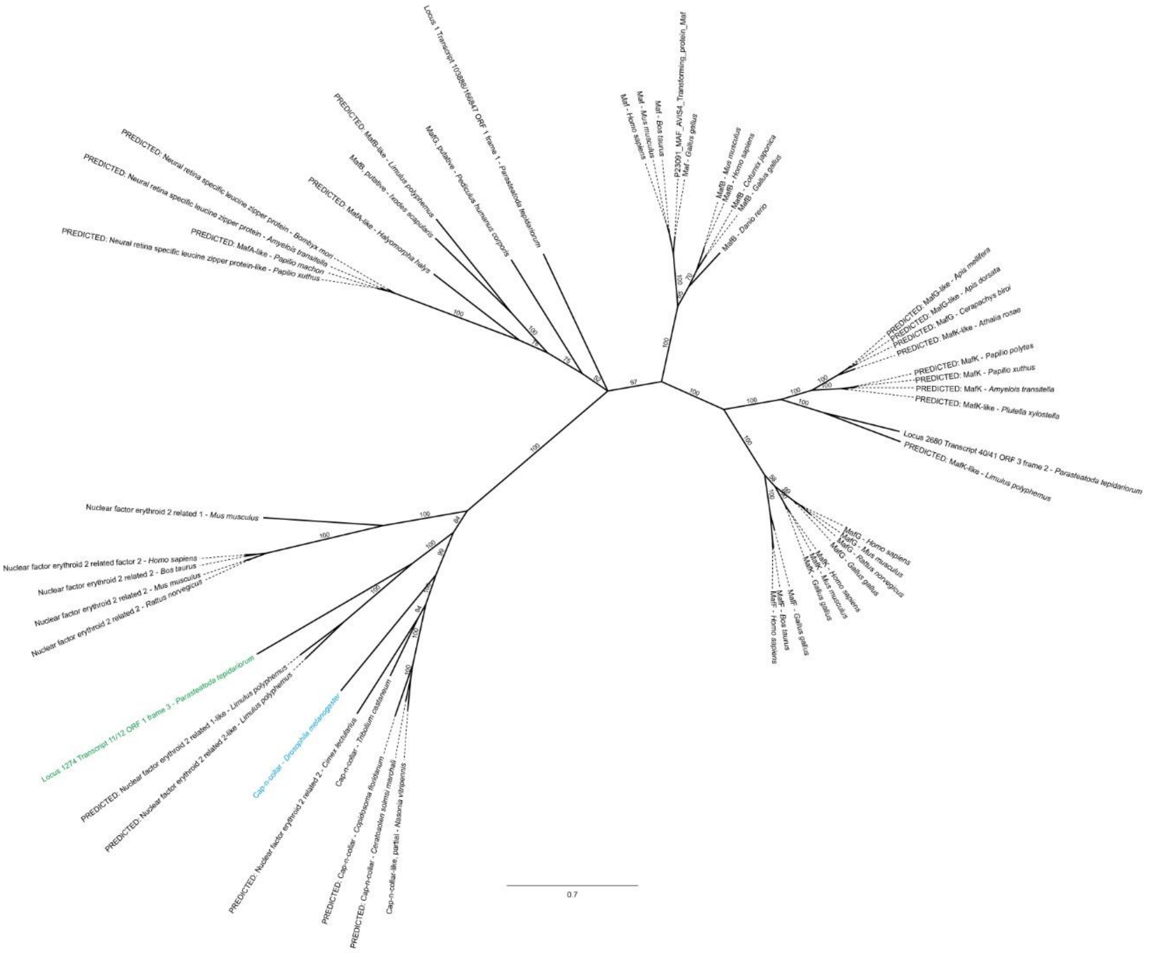

Figure 37 – Phylogenetic tree of cnc. Branch values represent posterior probabilities of Bayesian likelihood (474 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.6). One homolog of the *D. melanogaster* cnc (blue) could be found (Locus 1274, green).

6.2.3.6 *Chinmo (Chronologically inappropriate morphogenesis)*

Chinmo is a BTB-zinc finger transcription factor, which is involved in the morphogenesis of the *Drosophila* wing (Carreira et al. 2011), development of the mushroom bodies (Wu et al. 2012), and somatic sex determination in males (Ma et al. 2014, Zarkower 2014). Phylogenetic analysis showed no homolog of *chinmo* in *P. tepidariorum* (Figure 38).

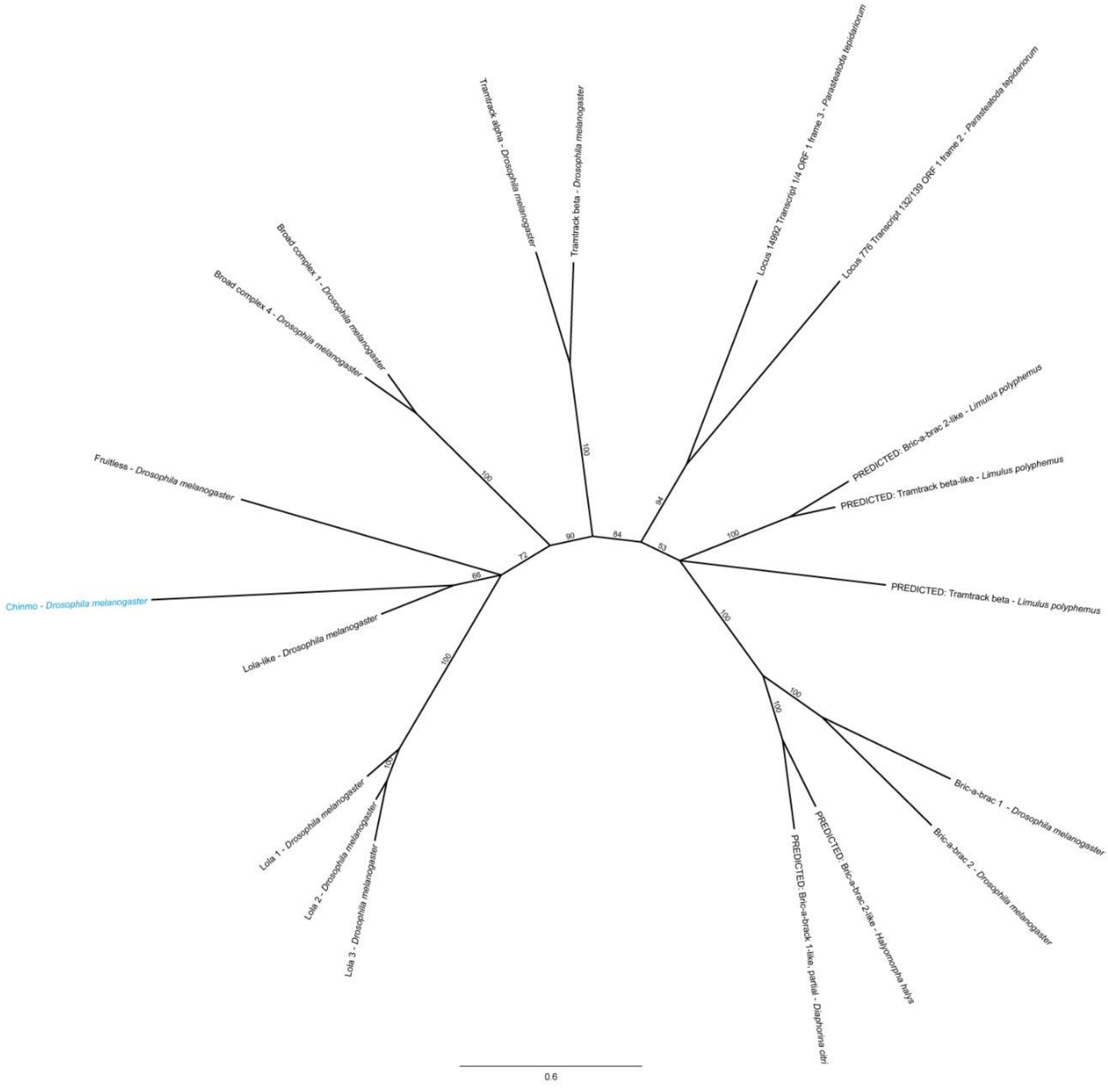

Figure 38 – Phylogenetic tree of *chinmo*. Branch values represent posterior probabilities of Bayesian likelihood (1032 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.7). No homolog of the *D. melanogaster* chinmo (blue) could be found.

6.2.3.7 *crocodile / FOXC*

crocodile (*croc*) is a member of the forkhead-domain transcription factor family, which is involved in the patterning and specification of the identity of head segments in holometabolous insects (Häcker et al. 1995, Kittelmann et al. 2013). Its expression suggests, that its role is conserved in hemimetabolous insects (Birkan et al. 2011, Economou & Telford 2009), as well as myriapods (Janssen et al. 2011). Phylogenetic analysis revealed one homolog in *P. tepidariorum* (part 5.2.2) .This gene shows expression in a V-shaped domain in the pre-cheliceral lobes, leaving out the anterior part of this tissue in stage 8. In later stages, this domain splits at the posterior end and surrounds the stomatodeum (black arrowheads in Figure 39 A, C, E, G). In addition, *croc* is expressed in a segmental fashion at the earlier stages 8 and 9 (white arrowheads in Figure 39 A, B). This expression vanishes by stage 10 (Figure 39 C, D).

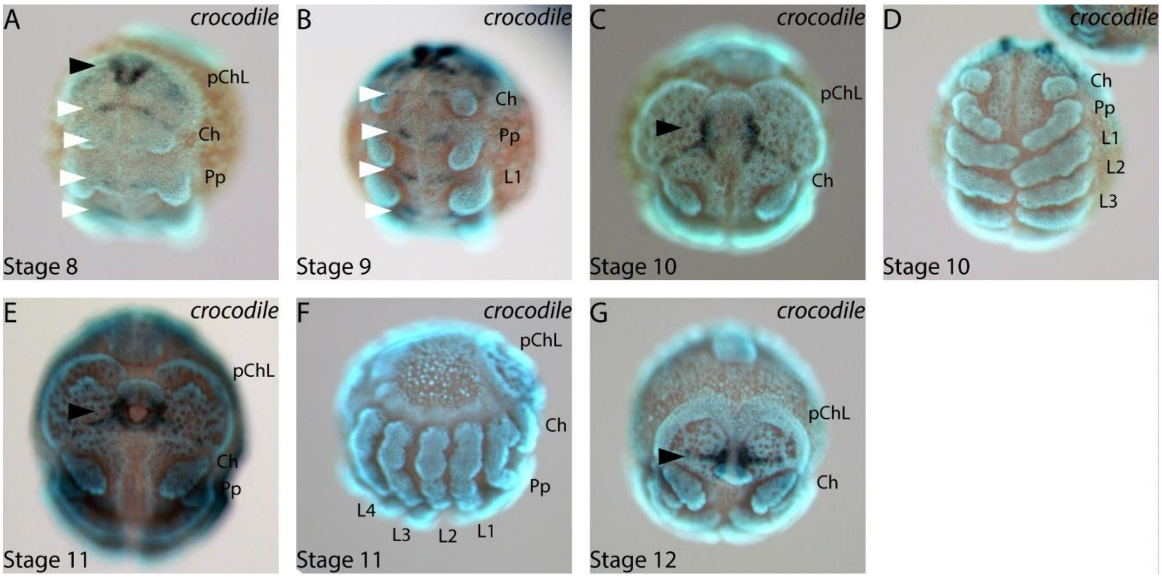

Figure 39 – Embryonic expression of crocodile/foxC in P. tepidariorum. croc is expressed in a v-shaped domain in the anterior part of the pre-cheliceral lobes (black arrowhead in A), followed by segmental stripes in the lobes and the posterior segments (white arrowheads in A and B), during stage 8 and 9. At stage 10, the v-shaped domain surrounds the presumptive stomodeum and is fused to the most anterior of the segmental stripes (arrowhead in C), while the rest of the segmental expression had vanished (D). The expression domain in the pre-cheliceral lobes stayed in pace during further development (E and G), while no other expression domains were visible in the rest of the embryo (F). A, C, E, and G show embryos in frontal aspect. B and D are ventral views with the anterior to the top. F is a lateral view with anterior to the right.

6.2.3.8 *Dachsous*

dachsous (*ds*) is cadherin-like cell adhesion molecule involved in imaginal disc morphogenesis in *Drosophila* (Clark et al. 1995). It controls left-right asymmetry through interaction with Myosin ID (González-Morales et al. 2015) and regulates morphogenesis through the Fat/Dachsous/Four-Jointed planar cell polarity pathway (Bosveld et al. 2012), for instance, dorso-ventral signaling in the *Drosophila* eye (Rawls et al. 2002). Phylogenetic analysis revealed one homolog of *ds* in *P. tepidariorum* (Locus 1 transcript 150321) (Figure 40).

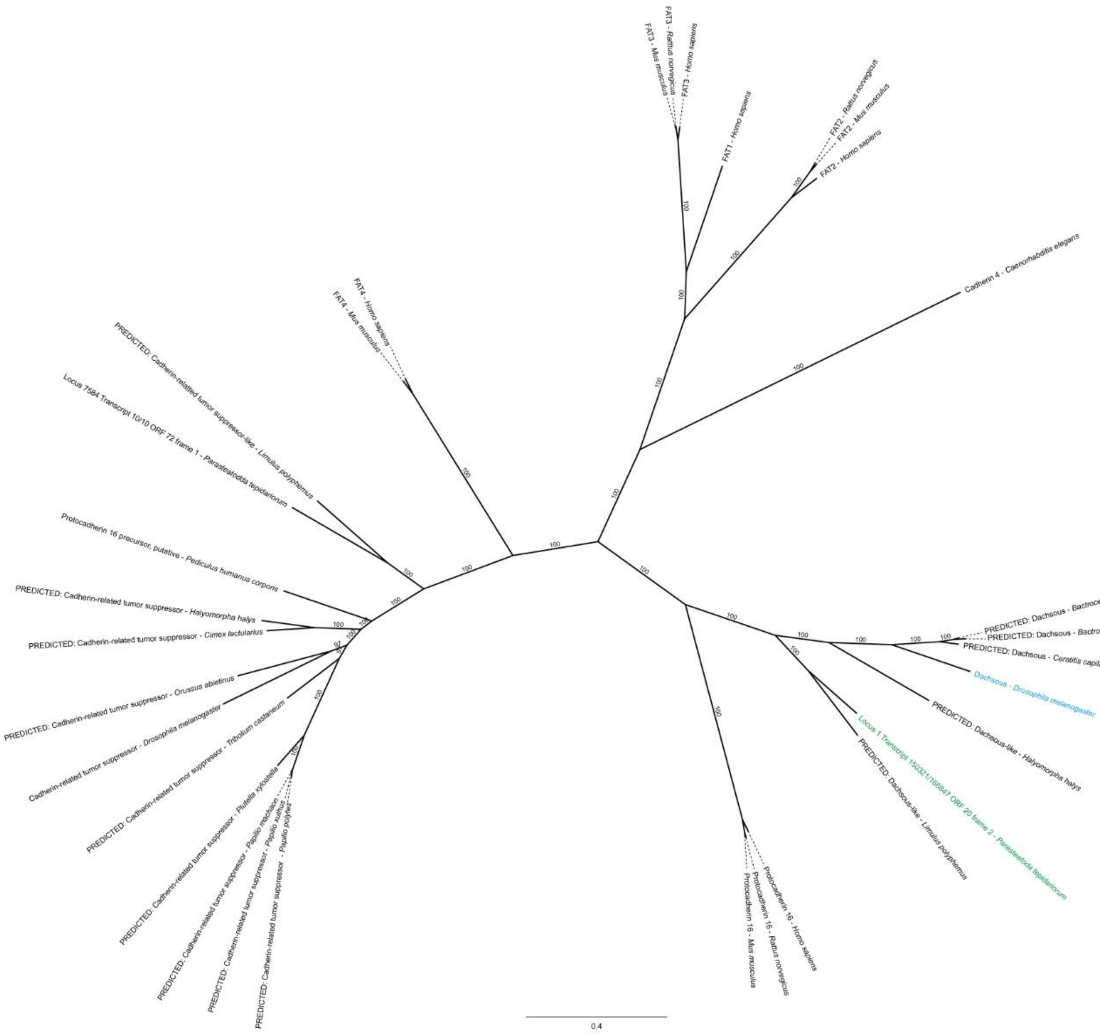

Figure 40 – Phylogenetic tree of *ds*. Branch values represent posterior probabilities of Bayesian likelihood (38 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.8). One homolog of the *D. melanogaster* ds (blue) could be found (Locus 1 transcript 150321, green)

The expression of the *P. tepidariorum ds* homolog is located to the proximal base of the prosomal limb buds in stages 8 and 9, while no expression is visible in the opisthosomal appendages (black arrowheads in Figure 41 A-F). At stage 10 a new ring-like expression domain appears in the distal part of the pedipalps and walking legs, while there is still no expression in opithosomal appendages (black arrowheads in Figure 41 H). Towards the end of embryogenesis, *ds* is still expressed in rings in the distal part of the appendages. In addition, new expression domains appear in the proximal parts of the of the legs, alternating with rings of no expression in the presumptive joints of pedipalps and walking legs (Figure 41 J).

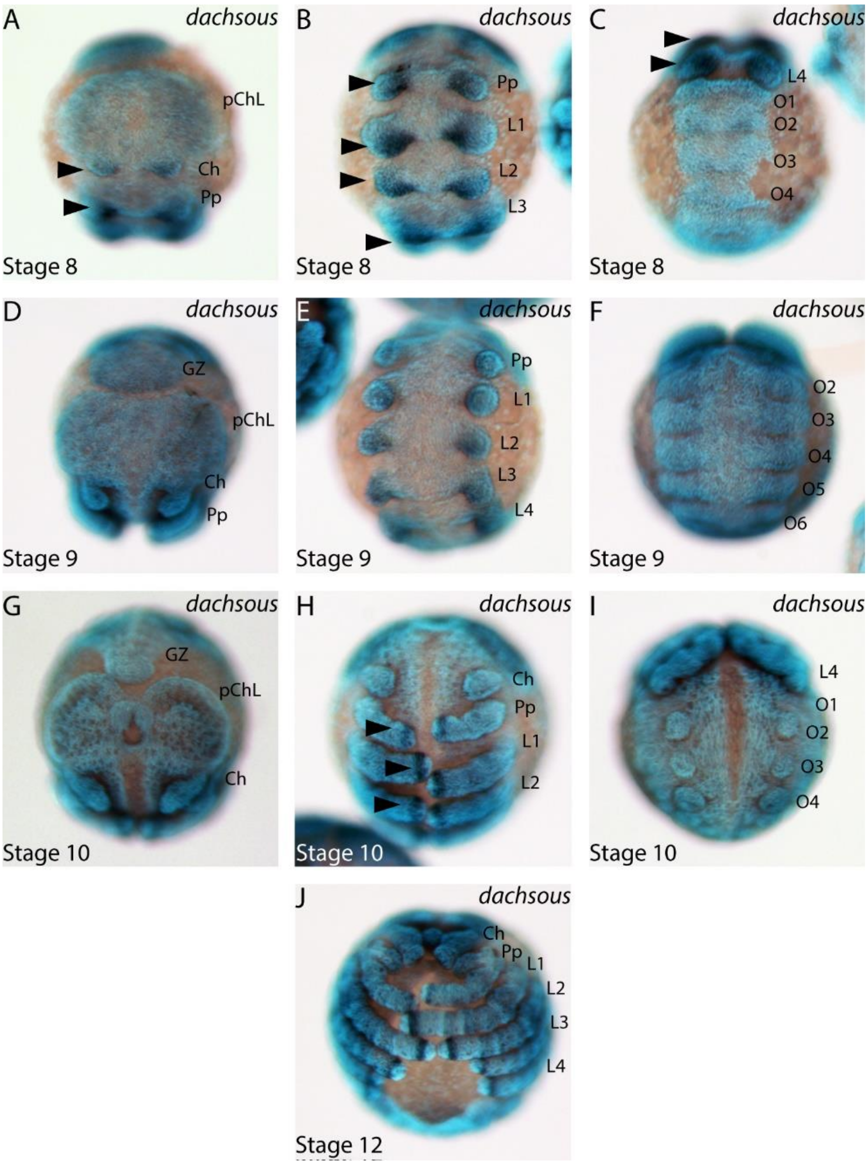

Figure 41 – Embryonic expression of *dachsous* in *P. tepidariorum*. Expression is first detected at the proximal base of the prosomal limb buds at stage 8 (arrowheads in A, B, C) and continues to be expressed there at stage 9 (E, F). At stage 10, *ds* expression appears in the distal part of the prosomal appendages, except the chelicerae (arrowheads in H), while there was still no expression in the pre-cheliceral lobes or the opisthosoma (G, I). At stage 12, new expression domains appear in the pedipalps and walking legs. They can be seen as weak expression domains in the appendage segements, while the joint regions are free of ds

expression (J). A, D, and G show embryos in frontal aspect. B, C, E, F, H, I, J are ventral views with anterior to the top.

6.2.3.9 *Daughterless*

daughterless (*da*) is transcription factor with a basic helix-loop-helix domain, which plays a role in sex-determination (Heng & Tan 2003, Younger-Shepherd et al. 1992) and dosage compensation (Schütt & Nöthiger 2000) in *D. melanogaster*. Phylogenetic analysis showed one homolog of *da* in *P. tepidariorum* (Locus 1 transcript 9632) (Figure 42). Expression analysis of this gene showed ubiquitous expression during embryogenesis in the spider (supplementary material 9.4.3.4).

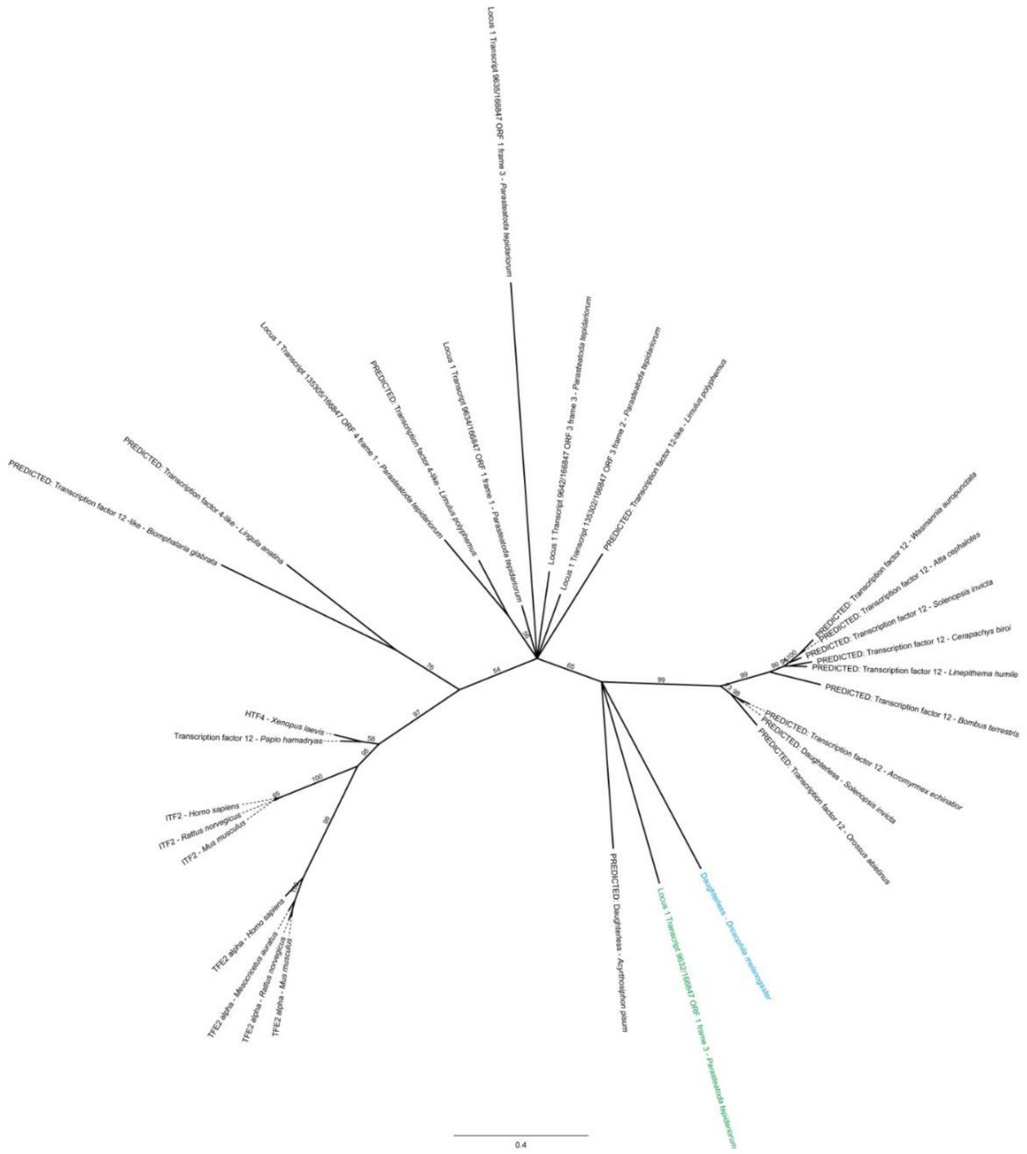

Figure 42 – Phylogenetic tree of *da*. Branch values represent posterior probabilities of Bayesian likelihood (9858 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.9). One homolog of the *D. melanogaster* da (blue) could be found (Locus 1 transcript 9632 , green).

6.2.3.10 *Dorsal*

dorsal (*dl*) is a transcription factor, which, in *Drosophila*, contributes to immune response (Lemaitre et al. 1995) and neural development in the peripheral nervous system (Ayyar et al. 2007)), but is best known for its role in dorso-ventral patterning of the early embryo (Janssens & Beyaert 2002). Phylogenetic analysis revealed three homologs of the Drosophila *dl* gene to be present in the transcriptome of *P. tepidariorum* (Locus 1 transcript 26288 (*dl-1*), Locus 15237 (*dl-2*), Locus 32713 (*dl-3*)) (Figure 43). Expression analysis of *dl-2* and *dl-3* showed ubiquitous expression during embryogenesis (supplementary material 9.4.3.5), while *dl-1* could not be cloned.

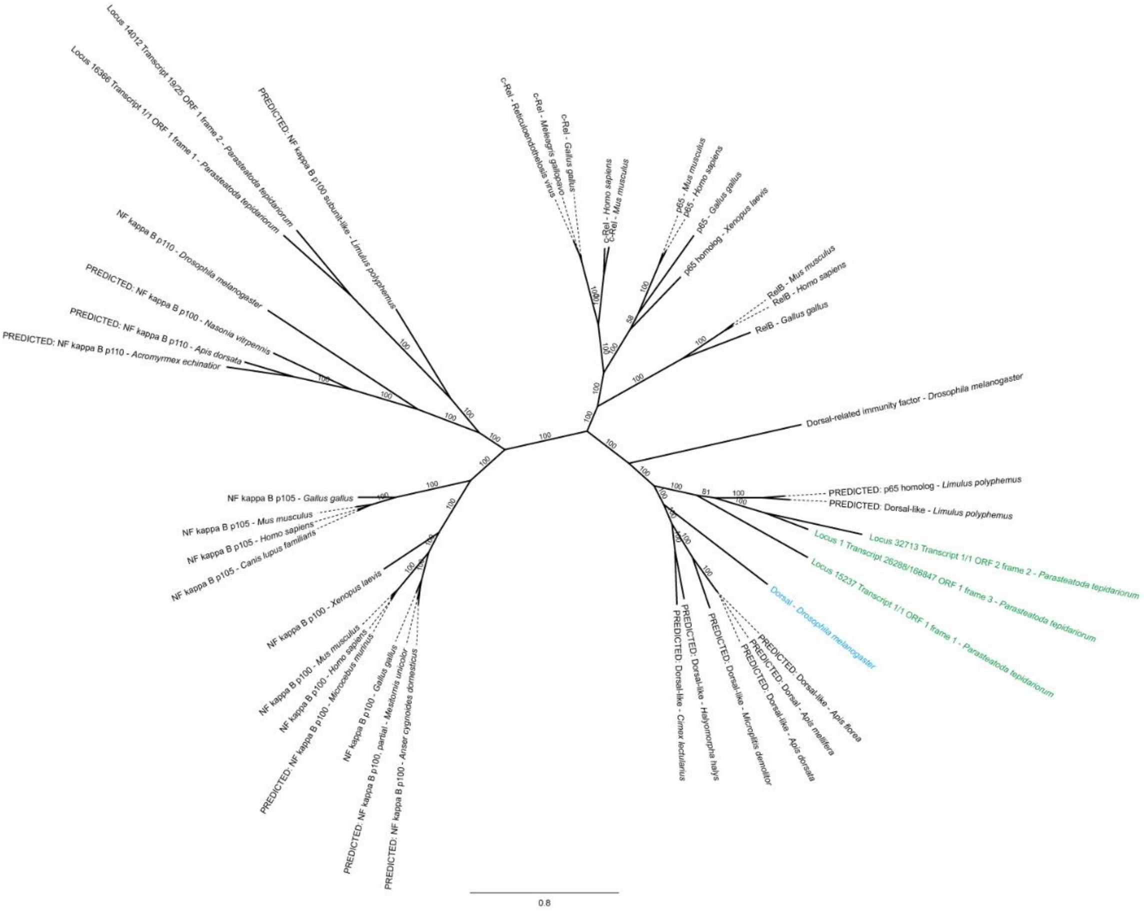

Figure 43 – Phylogenetic tree of *dl*. Branch values represent posterior probabilities of Bayesian likelihood (62 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.10). Three homologs of the *D. melanogaster* dl (blue) could be found (Locus 1 transcript 26288 (*dl-1*), Locus 15237 (*dl-2*), Locus 32713 (*dl-3*), all green).

6.2.3.11 *Drop / muscle segment homeobox*

Drop (*Dr*) is a homeodomain transcription factor, which is involved in patterning of the *D. melanogaster* wing disc (Villa-Cuesta 2005), cell fate determination of neuroblasts (Skeath & Thor

2003), dorso-ventral pattern formation (Urbach & Technau 2003), and the development of muscles (Dworak & Sink 2002). In *P. tepidariorum*, phylogenetic analysis of transcriptomic sequences shows three homologs of *Dr* to be present (Locus 17634 (*Dr-1*), Locus 28432 (*Dr-2*), Locus 11933 (*Dr-3*)) (Figure 44).

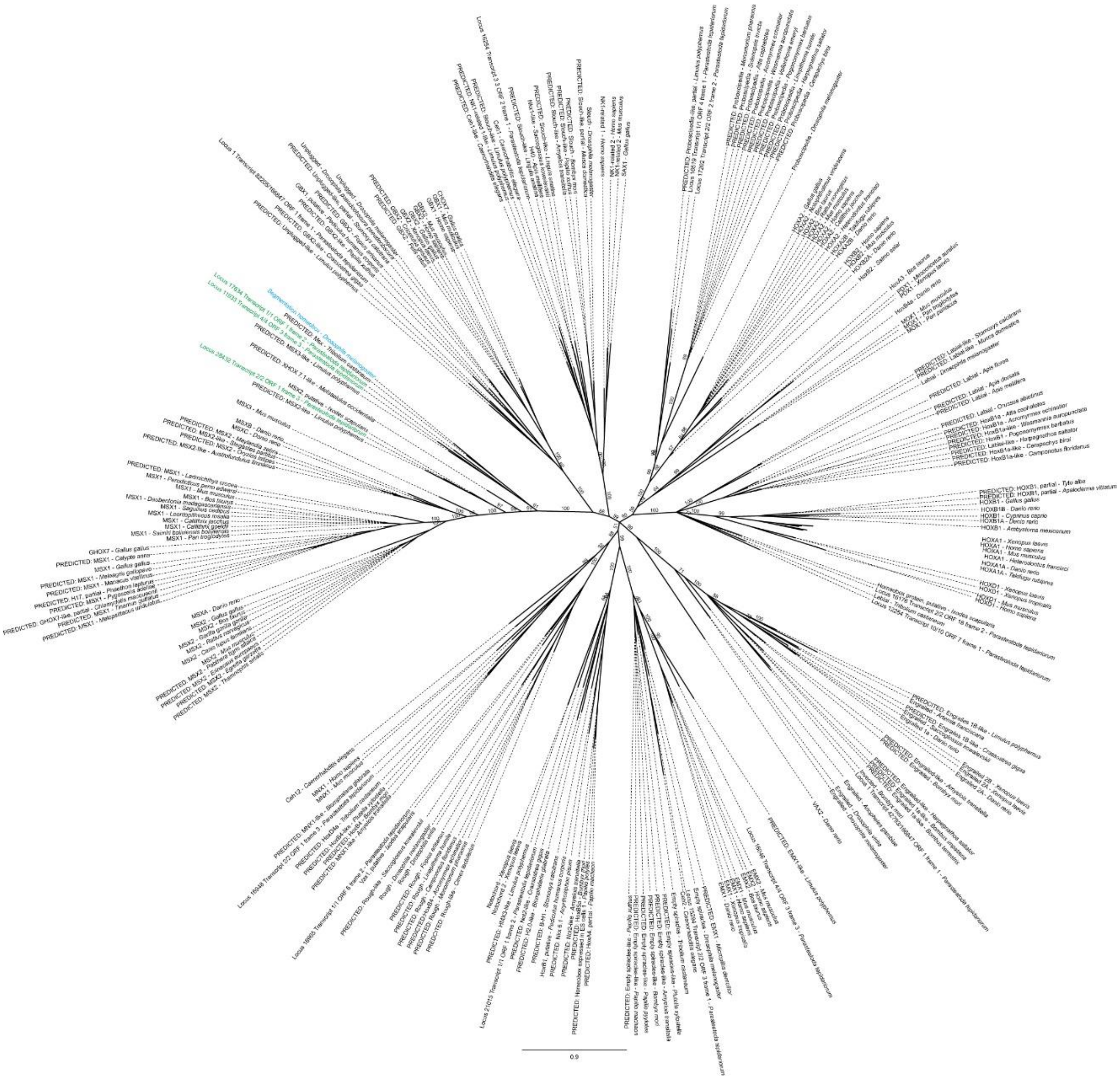

Figure 44 –Phylogenetic tree of *Dr*. Branch values represent posterior probabilities of Bayesian likelihood (39,548 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.11). Three homologs of the *D. melanogaster Dr* (blue) could be identified (Locus 17634 (*Dr-1*), Locus 28432 (*Dr-2*), Locus 11933 (*Dr-3*), all green).

While both, *Dr-1* and *Dr-2* showed no expression during embryogenesis in *P. tepidariorum* (supplementary material 9.4.3.6), *Dr-3* in expressed in a segmental fashion during stage 7 (Figure 45 A). After the formation of limb buds in stage 8, the expression of Dr-3 is restricted to the lateral part of the neuroectoderm, at an anterior-median position of each developing limb (black arrowheads in Figure 45 B, C). This expression pattern is kept throughout embryonic development (Figure 45 E, F, I, J, L, M). In the opisthosomal segments, *Dr-3* expression starts as continuous segmental stripes in the growth zone, which splits at the median sulcus as the segments mature (Figure 45 D, H, K). Eventually *Dr-3* in the opisthosomal segemtns shows the same expression pattern in the lateral neuroectoderm as seen in the prosomal segments. Additionally, opisthosomal expression retains stripe-like domains at the posterior end of each hemi-segment, which becomes weaker towards the posterior (Figure 45 D, G, H, J, K).

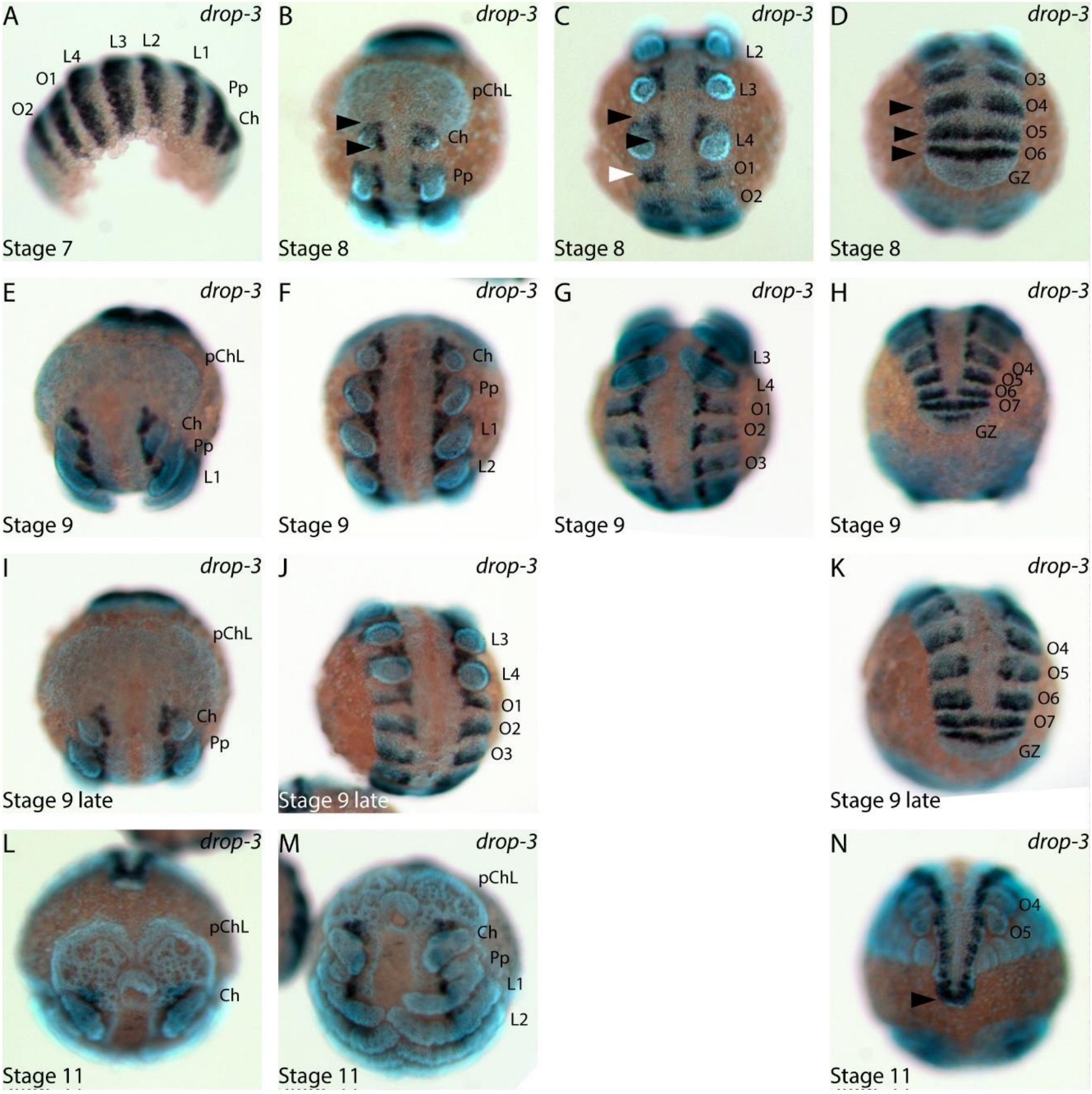

Figure 45 – Embryonic expression of *Drop-3* in *P. tepidariorum*. *Dr-3* is expressed in a segmental fashion in all established segments at stage 7 (A). After the development of limb buds at stage 8, *Dr-3* is expressed in the lateral neuro-ectoderm at an anterior and median position of each limb bud (B, C). This expression domain persists during further development (E, F, I, J, L, M). In the opisthosomal segments, *Dr-3* expression starts as segmental stripes in the growth zone and splits at the median sulcus as the segments mature (D, H, K). In older opsithosomal segments, the same expression domain appears in the lateral neuro-ectoderm as seen in the prosomal segments (G, H, J, K, N). The segmental expression in the opisthosoma is restricted to the posterior part of the segments, with weaker expression to the anterior (G, H, J, K) until at stage 11,

only the neuro-ectodermal domain is present (N). A is lateral view with anterior to the right. B, E, I, and L show embryos in frontal aspect. C, D, F, G, H, J K, M, and N are ventral view with anterior to the top.

6.2.3.12 *Empty spiracles / EMX*

empty spiracles (*ems*) is homeobox domain containing transcription factor, which in *Drosophila* is involved in multiple aspects of brain development (Hartmann et al. 2000, Hirth et al. 1995, Lichtneckert et al. 2007), development of the tracheal system (Ebner et al. 2002, Hu & Castelli-Gair 1999). It acts as a gap gene during the head development (Peel 2004), and has been shown to act with HOX genes, such as *labial* (Macías & Morata 1996) and *Abdominal-B* (Jones & McGinnis 1993). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed three homologs of *ems* (Locus 15791 (*ems-1*), Locus 16046 (*ems-2*), Locus 21143 (*ems-3*)) (Figure 46).

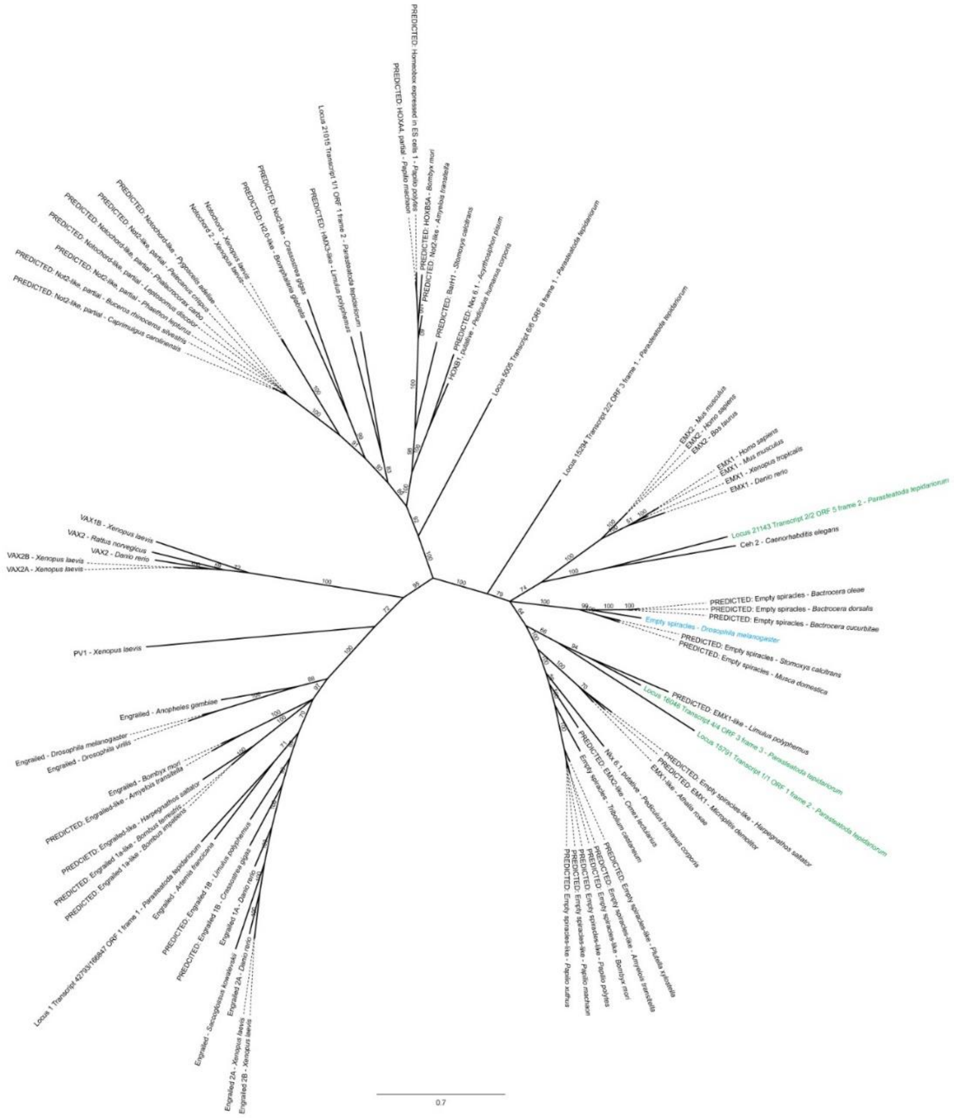

Figure 46 – Phylogenetic tree of *ems*. Branch values represent posterior probabilities of Bayesian likelihood (1764 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.12). Three homologs of the *D. melanogaster ems* (blue) could be identified (Locus 15791 (*ems-1*), Locus 16046 (*ems-2*), Locus 21143 (*ems-3*), all green).

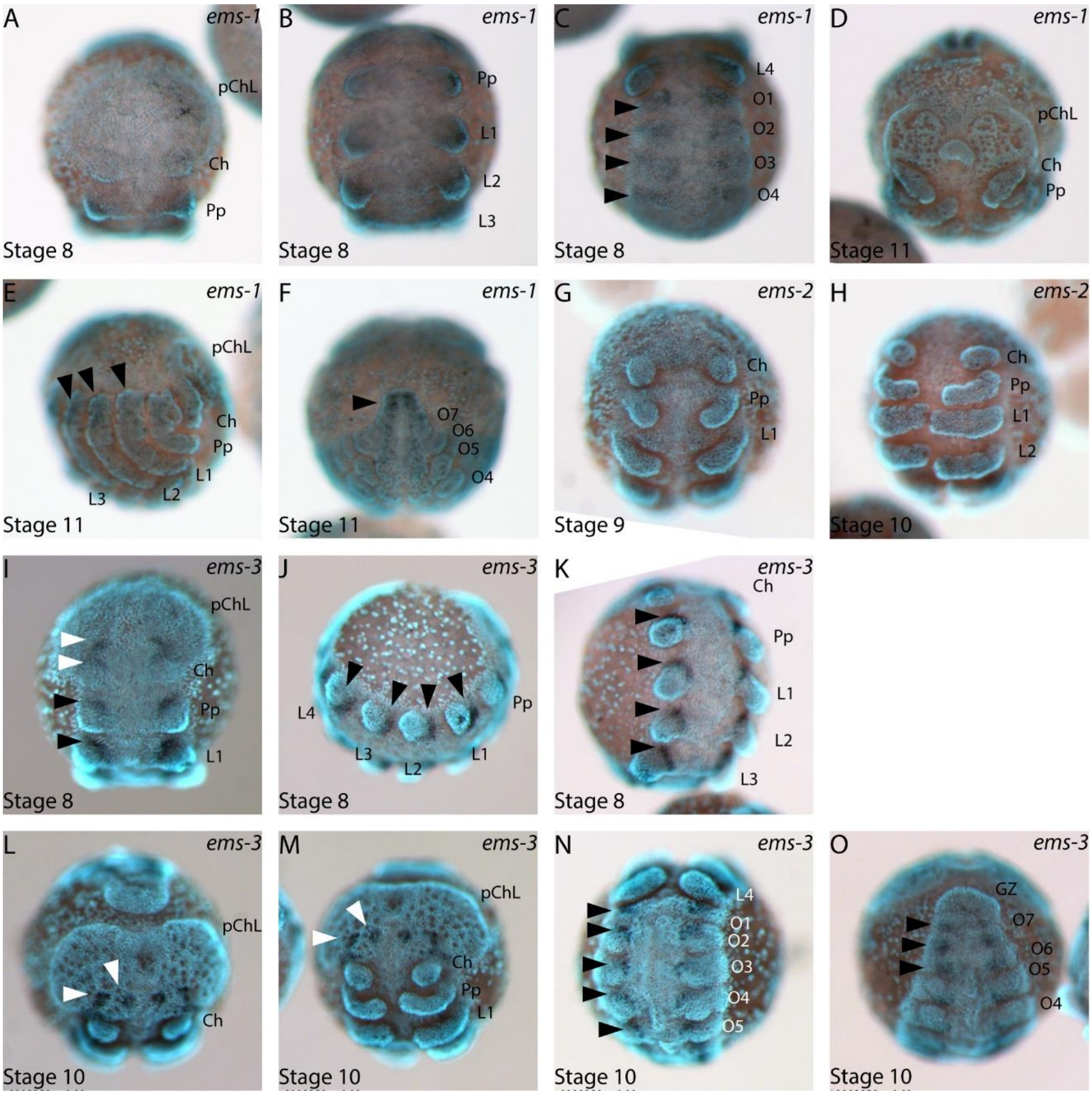

Figure 47 - Embryonic expression of *empty spiracles 1*, *empty spiracles 2*, and *empty spiracles 3* in *P. tepidariorum*. *ems-1* is expressed in ubiquitously in the prosoma during stage 8 (A, B), while diffuse segmental expression domains are visible in the opisthosomal segments (arrowheads in C). At stage 11, no expression of *ems-1* could be detected in the pre-cheliceral lobes (D), while faint expression appeared in the proximal part of the walking legs at a posterior position (arrowheads in E), and stronger expression was located in the most posterior tip of the embryo (arrowhead in F). *ems-2* showed no expression of transcript in the stages analyzed (G, H). *ems-3* is expressed in every segment in the lateral neuro-ectoderm at the base of the prosomal appendages (black arrowheads in I, J, K). Additionally, two expression domains were visible in the pre-cheliceral lobes (white arrowheads in I). At stage 10, the expression in the pre-cheliceral lobes form 4 spots in a straight row (L, M). In the opisthosoma *ems-3* is expressed in neural precursors in every segment (arrowheads in N), while it is expressed in the neuro-ectoderm in the younger opisthosomal segments (arrowheads in O). A, D, I, and L show embryos in frontal aspects., B, C, G, H, K, M, and N are ventral views with anterior to the top. E and J are lateral views with anterior to the right. F and O are ventral views of the opisthosoma with the posterior to the top.

The expression of *ems-1* in stage 8 showed a diffuse and ubiquitous pattern in the prosomal segments, while the opisthosomal segments showed expression in a segmental fashion (Figure 47 A, B and arrowheads in Figure 47 C). At stage 11, *ems-1* showed weak expression in the posterior part of the prosomal appendages, as well as in the growth zone of the embryo (Figure 47 E, F). *ems*-

2 showed no expression in the stages analysed here (Figure 47 G, H). The expression of *ems-3* appears in every segment in lateral part of the neuroectoderm, similar to the expression of *Dr-3*, at stage 8 (black arrowheads in Figure 47 I, J, K). Additionally, there is another expression domain in the precheliceral lobes during that stage (white arrowheads in Figure 47 I, L, M). In later stages, the cheliceral and pre-cheliceral domains of *ems-3* expression move relative to one another until they form a straight row in the posterior part of the pre-cheliceral lobes (arrowheads in Figure 47 L, M). The expression in the posterior segments is restricted to the sites of neural precursors, while it is expressed in the neuroectoderm in more recently formed segments (arrowheads in Figure 47 N, O)

6.2.3.13 *Enhancer of zeste*

Enhancer of zeste (*E(z)*) is a lysine methyltransferase, which is involved in the silencing of Polycomb target genes (Stepanik & Harte 2012), for instance, during muscle development (Parrish & Kim 2006), or neurogenesis (Bello et al. 2007). Phylogenetic analysis revealed one homolog of *E(z)* to be present in *P. tepidariorum* (Locus 81) (Figure 48). However, this gene appeared to be ubiquitously expressed (supplementary material 9.4.3.7).

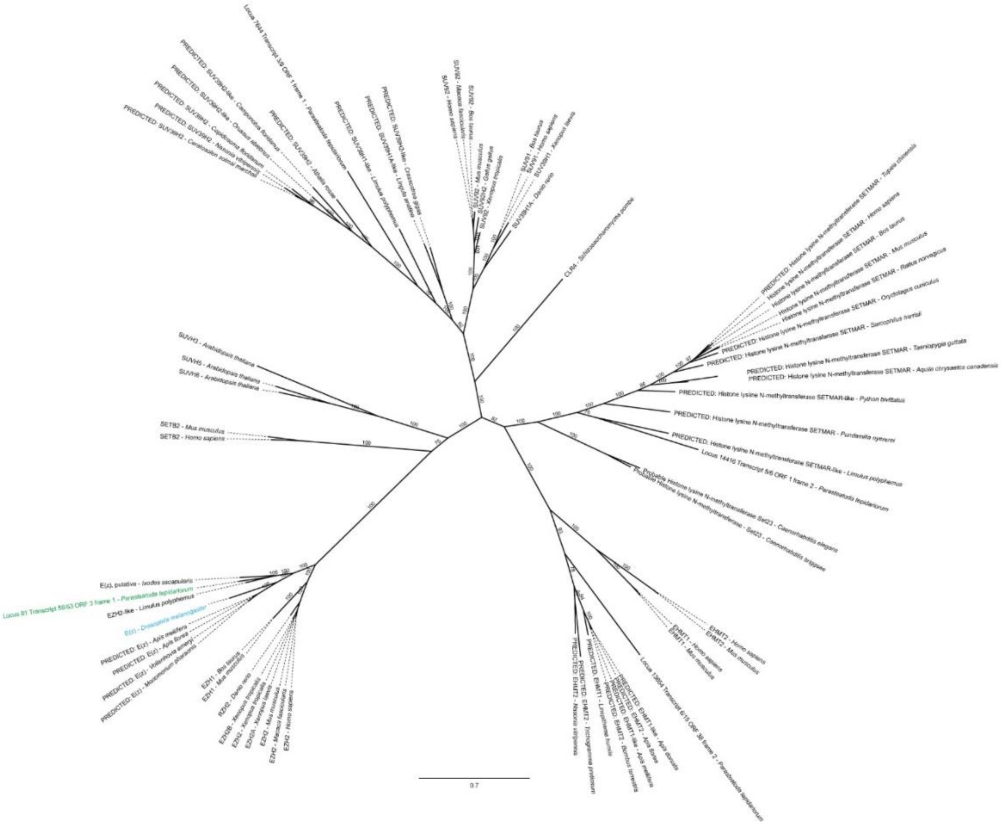

Figure 48 – Phylogenetic tree of *E(z)*. Branch values represent posterior probabilities of Bayesian likelihood (230 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.13). One homolog of the *D. melanogaster* E(z) (blue) could be identified (Locus 81, green)

6.2.3.14 *Fasciclin 2*

Fasciclin-2 (*Fas2*) is a neural cell adhesion molecule homolog, which is involved in axon guidance (Kristiansen et al. 2005, Zarin et al. 2014), but is also involved in the negative regulation of EgfR signaling (Mao & Freeman 2009), as well as the morphogenesis of the male genitalia in *D. melanogaster* (Adam 2003). Phylogenetic analysis showed three homologs of *Fas2* to be present in *P. tepidariorum* (Locus 1 transcript 35406 (*Fas2-1*), Locus 1 transcript 23671 (*Fas2-2*), Locus 1 transcript 23706 (*Fas2-3*)) (Figure 49).

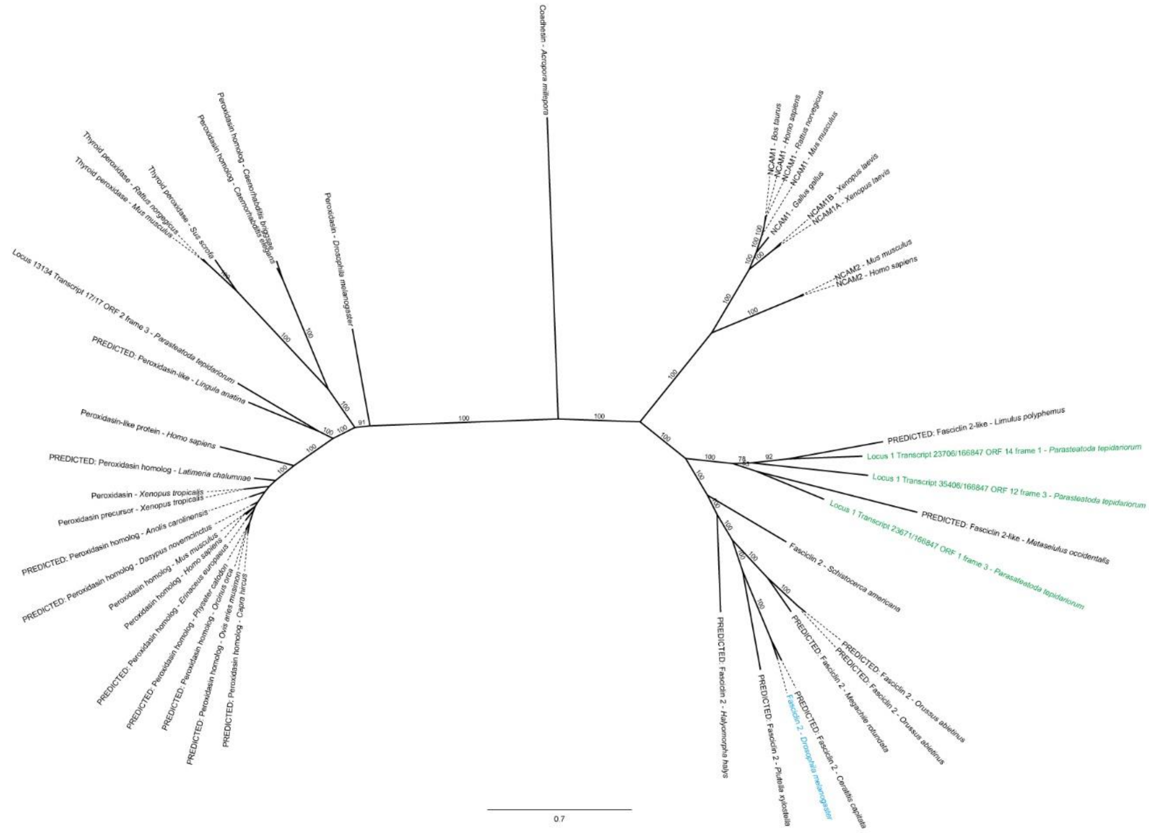

Figure 49 –Phylogenetic tree of *Fas2*. Branch values represent posterior probabilities of Bayesian likelihood (236 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.14). Three homologs to the *D. melanogaster* Fas2 (blue) could be found (Locus 1 transcript 35406 (*Fas2-1*), Locus 1 transcript 23671 (*Fas2-2*), Locus 1 transcript 23706 (*Fas2-3*), all green).

The expression of *Fas2-1* appears at stage 10, where it marks several neural precursor groups in the pre-cheliceral lobes (white arrowheads in Figure 50 B). Several other groups of neural precursors are marked in each segment in the neuroectoderm (black arrowheads in Figure 50 B, C). At stage 11, the expression domains in the pre-cheliceral lobes have moved to the anterior and lateral furrow, respectively (Figure 50 D), while the expression in the appendage-bearing and opithosomal segments remained unchanged (Figure 50 E). The expression of *Fas2-3* appears to be ubiquitous in the embryonic stages analysed (Figure 50 F, G, H).

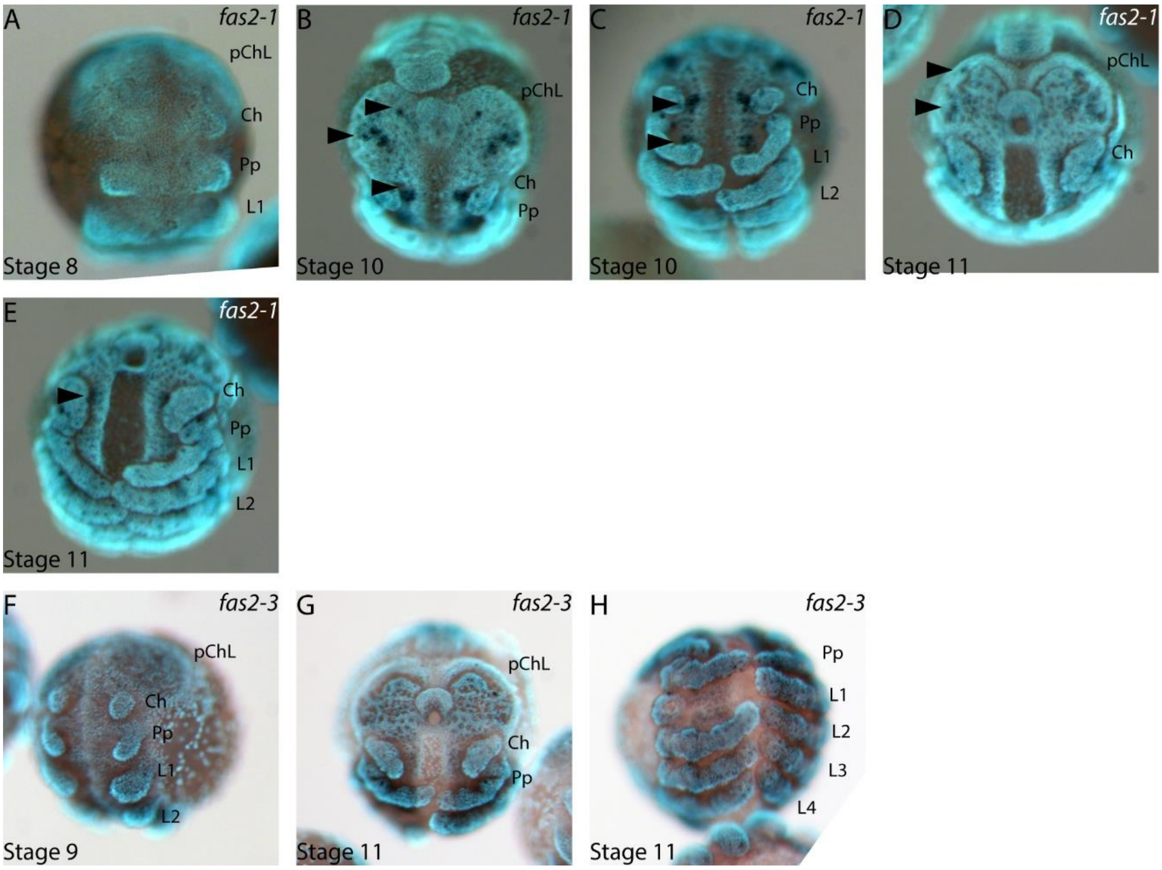

Figure 50 – Embryonic expression of *fasciclin2-1* and *fasciclin 2-3* in *P. tepidariorum*. No expression of fas2-1 could be observed at stage 8 (A). at stage 10, fas2-1 marked several neural precursors in the pre-cheliceral lobes and in every segment of the trunk (arrowheads in B, C). At stage 11, expression in the pre-cheliceral lobes had moved to the anterior and lateral furrows (arrowheads in D), while the expression in the trunk remained unchanged (arrowhead in E). fas2-3 showed ubiquitous expression throughout the stages analyzed (F, G, H). A, B, D, and G show embryos in frontal aspect. C e F and H are ventral views with the anterior to the top.

6.2.3.15 *Fussel*

Fussel (*fuss*) is a member of the Sno/Ski family of Smad binding protein, which acts as an antagonist to BMP signaling during *Drosophila* development (Fischer et al. 2012). Homologs of this have been suggested in other insects and crustaceans, but no similar sequence could be identified in the *P. tepidariorum* transcriptome.

6.2.3.16 *Glial cells missing*

glial cells missing (*gcm*) is a zinc finger transcription factor, which, in *Drosophila*, is involved in many aspects of neural tissue development (Chotard et al. 2005, Kammerer & Giangrande 2001, Stork et al. 2008), as well as segmentation of the posterior head (Stöbe et al. 2009). In *P. tepidariorum*, no homologs could be identified in the transcriptome.

6.2.3.17 *Gooseberry*

gooseberry (*gsb*) is a member of the paired homeobox family of transcription factors, which is involved in neurogenesis (Marie et al. 2010, Skeath & Thor 2003) and acts as a segment polarity gene (Davis & Patel 2003, He & Noll 2013). In *P. tepidariorum*, two sequences could be identified, which show sequence similarity with the *D. melanogaster gsb* (Figure 51). However, only one of these (Locus 17531) turned out to be the homolog of *gsb*, while the other sequences (Locus 13554) was the homolog of the closely related genes paired (see below). In the stages analysed, *gsb* showed no expression in *P. tepidariorum* (supplementary material 9.4.3.8).

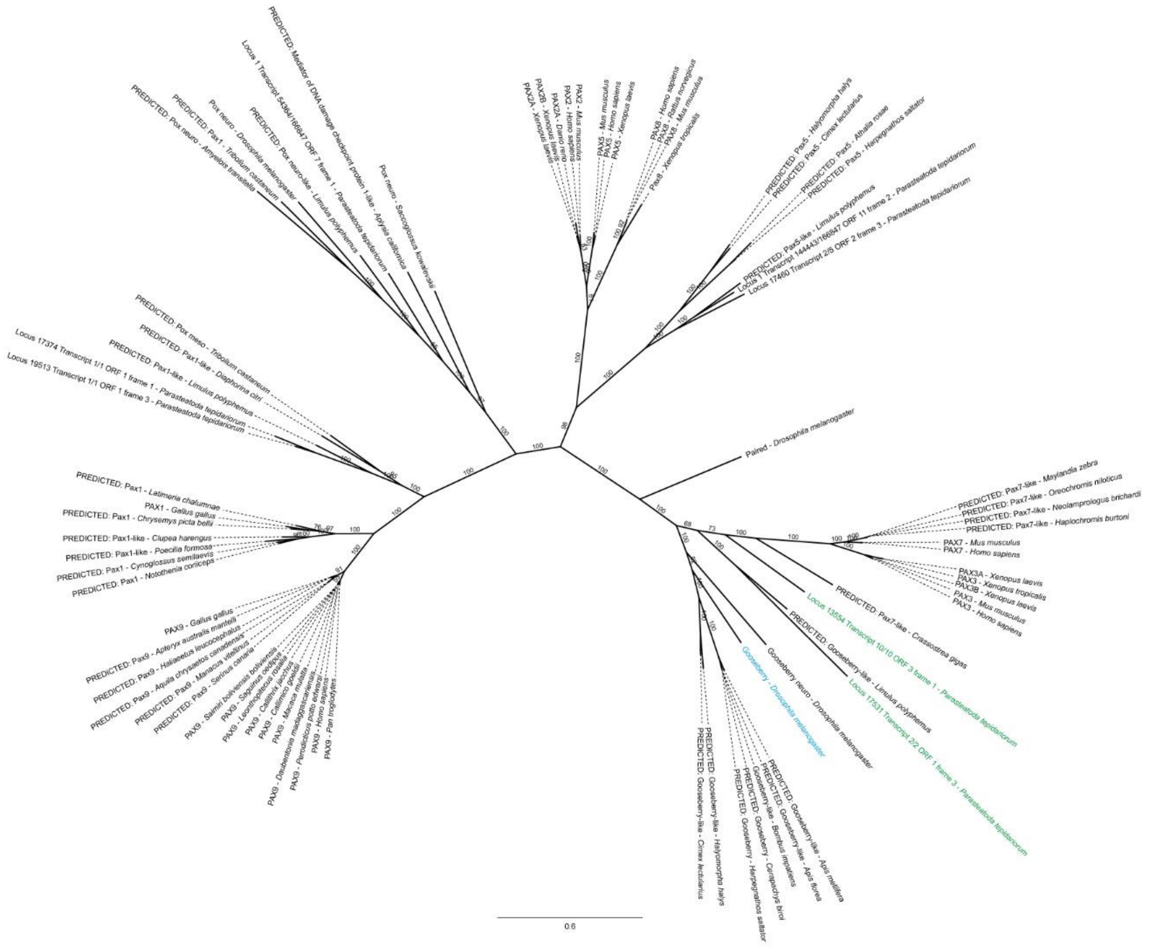

Figure 51 – Phylogenetic tree of *gsb.* Branch values represent posterior probabilities of Bayesian likelihood (1650 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.15). Two possible homologs of the *D. melanogaster* gsb (blue) could be identified (Locus 17531, Locus 13554, both green). Only Locus 17531 proved to be a homolog of gsb, while the other was a homolog of paired (see section below).

6.2.3.18 *HMGB1*

HMGB1 is a member of the high mobility group proteins, which are able to reversibly change the chromatin state in a huge variety of animals (Agresti & Bianchi 2003). Moreover, they have been shown to have control functions for a limited number of specific genes, such as a number of HOX genes (Decoville et al. 2001). Phylogenetic analysis of the *P. tepidariorum* transcriptome revealed one homolog (Locus 1 transcript 97552) (Figure 52), the expression of which was ubiquitous in the embryonic stages analysed (supplementary material 9.4.3.9).

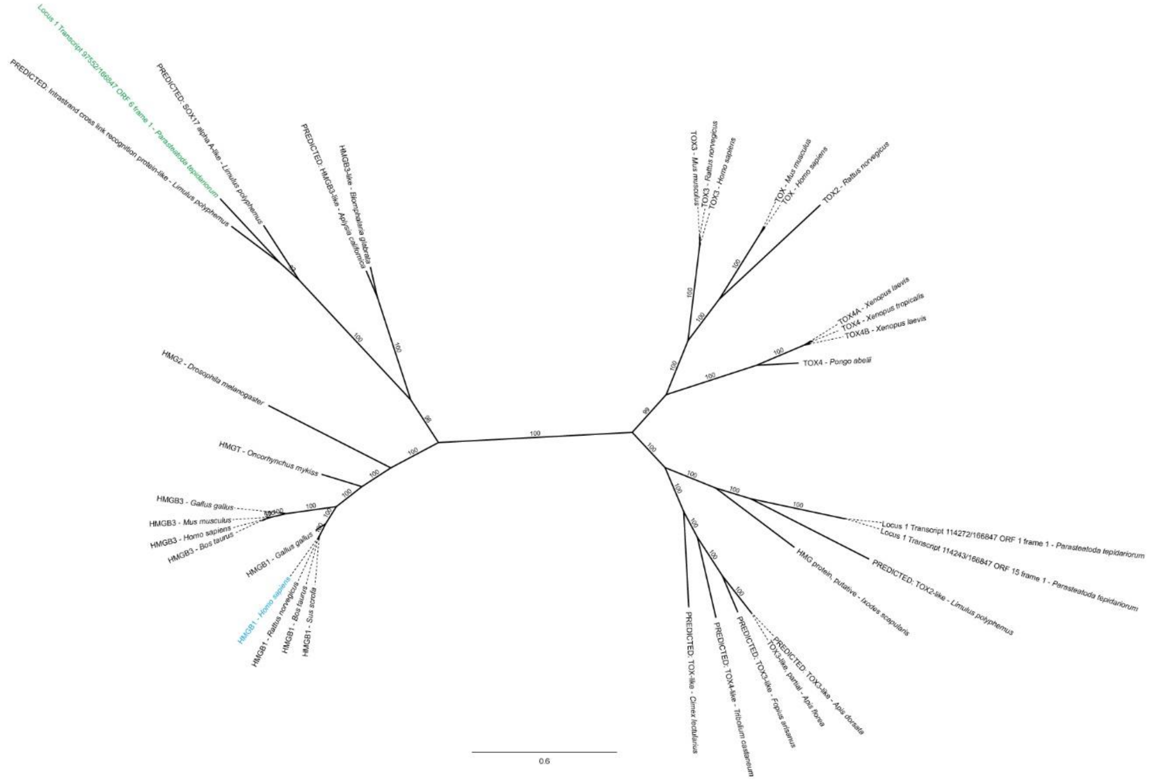

Figure 52 – Phylogenetic tree of HMGB1. Branch values represent posterior probabilities of Bayesian likelihood (170 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.16). One homolog of the *Homo sapiens* HMGB1 (blue) could be found (Locus 1 transcript 97552, green).

6.2.3.19 *Huckebein*

huckebein (*hkb*) is a transcription factor, which belongs to the SP1/KLF group of transcription factors. In *Drosophila*, it determines fate in a subset of neuroblast during neurogenesis (Skeath & Thor 2003) and as a terminal gap gene is involved in the anterior-posterior axis determination (Leptin 1999). Phylogenetic analysis showed two homologs of the *Drosophila hkb* in the transcriptome *of P. tepidariorum* (Locus 1422 (*hkb-1*), Locus 26294 (*hkb-2*)) (Figure 53).

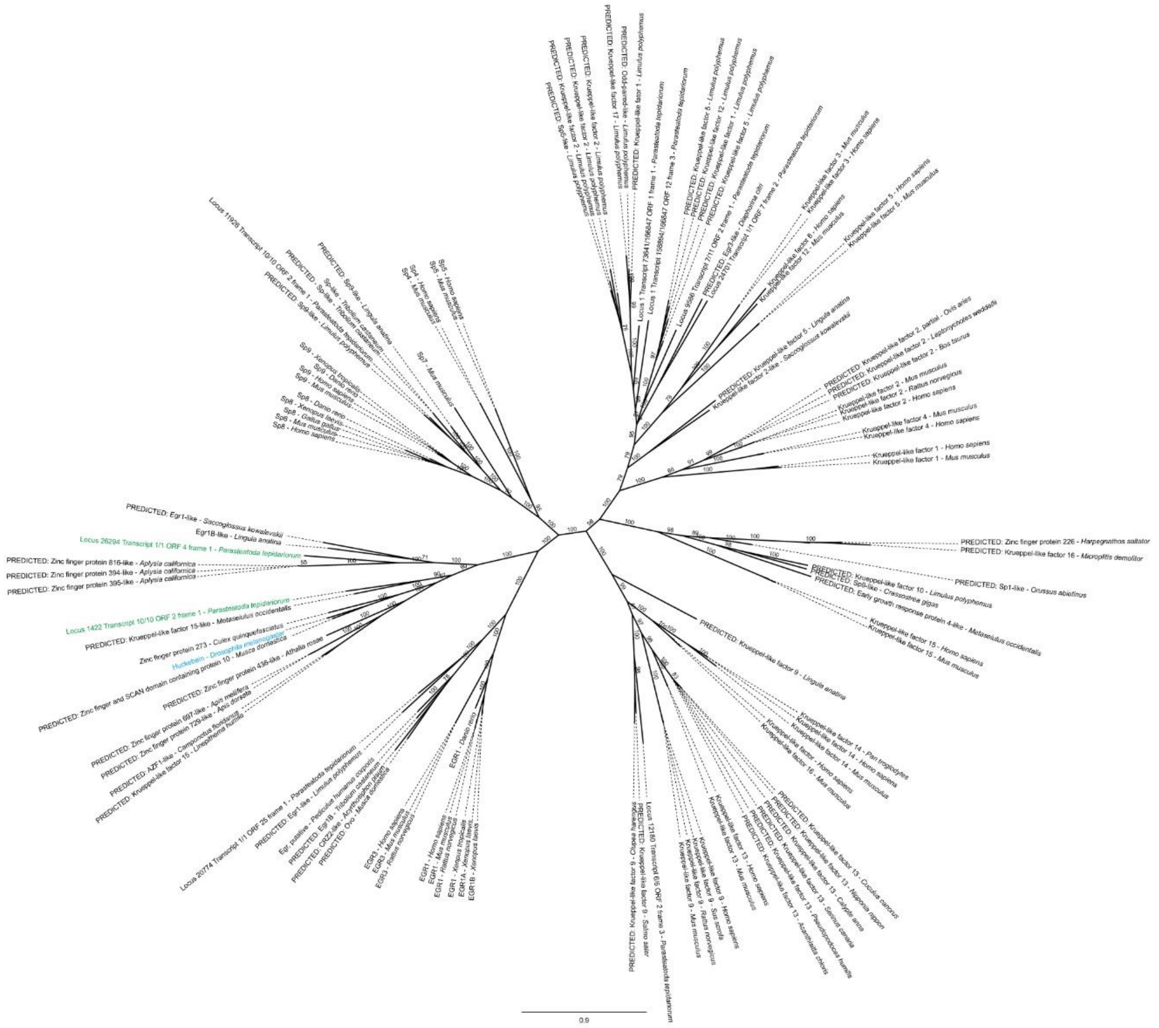

Figure 53 – Phylogenetic tree of *hkb*. Branch values represent posterior probabilities of Bayesian likelihood (3104 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.17). Two homologs of the *D. melanogaster* hkb (blue) could be identified (Locus 1422 (*hkb-1*), Locus 26294 (*hkb-2*), both green).

In *P. tepidariorum*, at stage 8, *hkb-1* is expressed in the ventral neuroectoderm at the base of each appendage (Figure 54 B). At stage 9, *hkb-1* expression marks a subset of neural precursor groups at position seen in the previous stage, and an additional domain of weaker expression anterior to that in every segment (Figure 54 D). At stage 11, the expression of *hkb-1* stays in the groups of cells building the neural precursors (Figure 54 E, F). *hkb-2* could not be cloned for expression analysis.

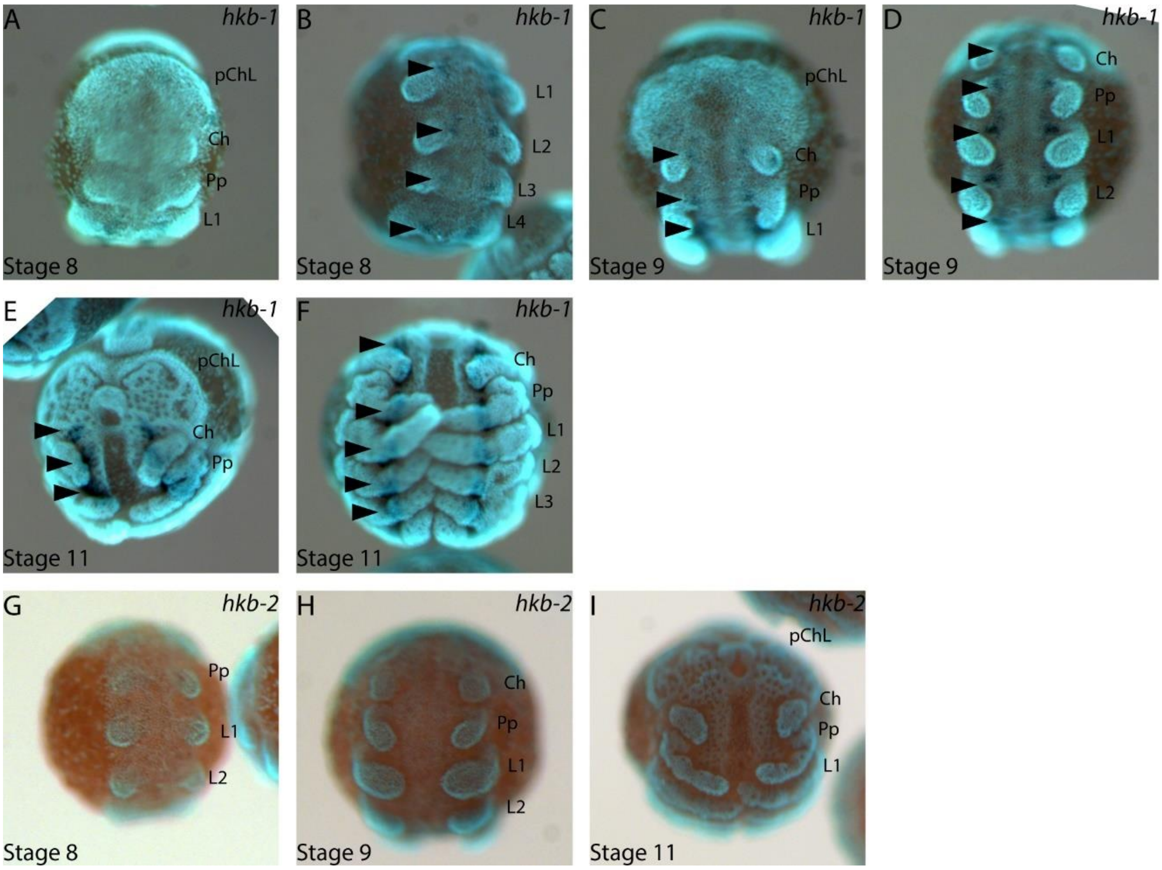

Figure 54 – Embryonic expression of *huckebein-1* in *P. tepidariorum*. No expression of *hkb-1* could be observed in the pre-cheliceral lobes at stage 8 (A), but it is expressed in the neural ectoderm of at the base of the appendages (arrowheads in B). These expression domains remained throughout all stages analyzed (arrowheads in C, D, E, F). A, C, and E show embryos in frontal aspect. B, D, and F are ventral views with the anterior to the top.

6.2.3.20 *Insensitive*

insensitive (*insv*) is a transcriptional corepressor involved in Notch signaling, via genetic interactions with Notch, Numb, and Suppressor of hairy (Duan et al. 2011). No homologous sequence could be found in the transcriptome of *P. tepidariorum*.

6.2.3.21 *Intermediate neuroblasts defective*

intermediate neuroblasts defective (*ind*) is a homeobox transcription factor, which play a role in the development of the nervous system in *Drosophila*, by the determination of neuroblast fate (Skeath & Thor 2003), and dorso-ventral pattern formation (Urbach & Technau 2003). Phylogenetic analysis showed no homologs of this *Drosophila* gene to be present in the transcriptome of *P. tepidariorum* (Figure 55).

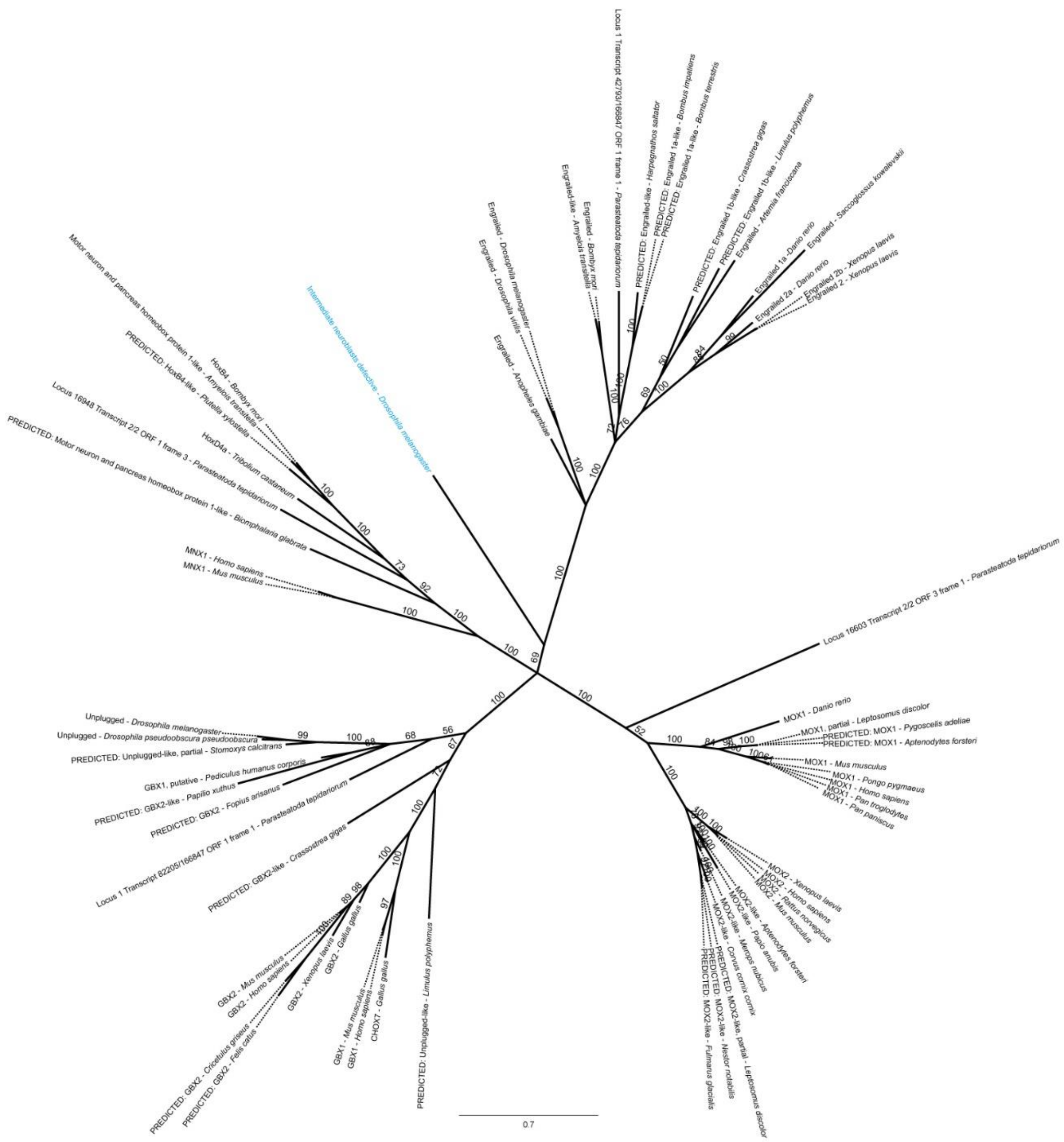

Figure 55 –Phylogenetic tree of *ind.* Branch values represent posterior probabilities of Bayesian likelihood (2976 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.18). No homolog of the *D. melanogaster ind* (blue) could be identified.

6.2.3.22 *Klumpfuss*

klumpfuss (*klu*), a zinc finger transcription factor, has been shown to affect leg development in *Drosophila* (Klein & Campos-Ortega 1997). It has further been implicated in the development of neuroblasts (Berger et al. 2012), the maintenance of neuronal stem cells (Xiao et al. 2012), and the determination of sensory precursors (Kaspar et al. 2008). Phylogenetic analysis of the *P. tepidariorum* transcriptome, showed one *klu* homolog (Locus 5949) (Figure 56).

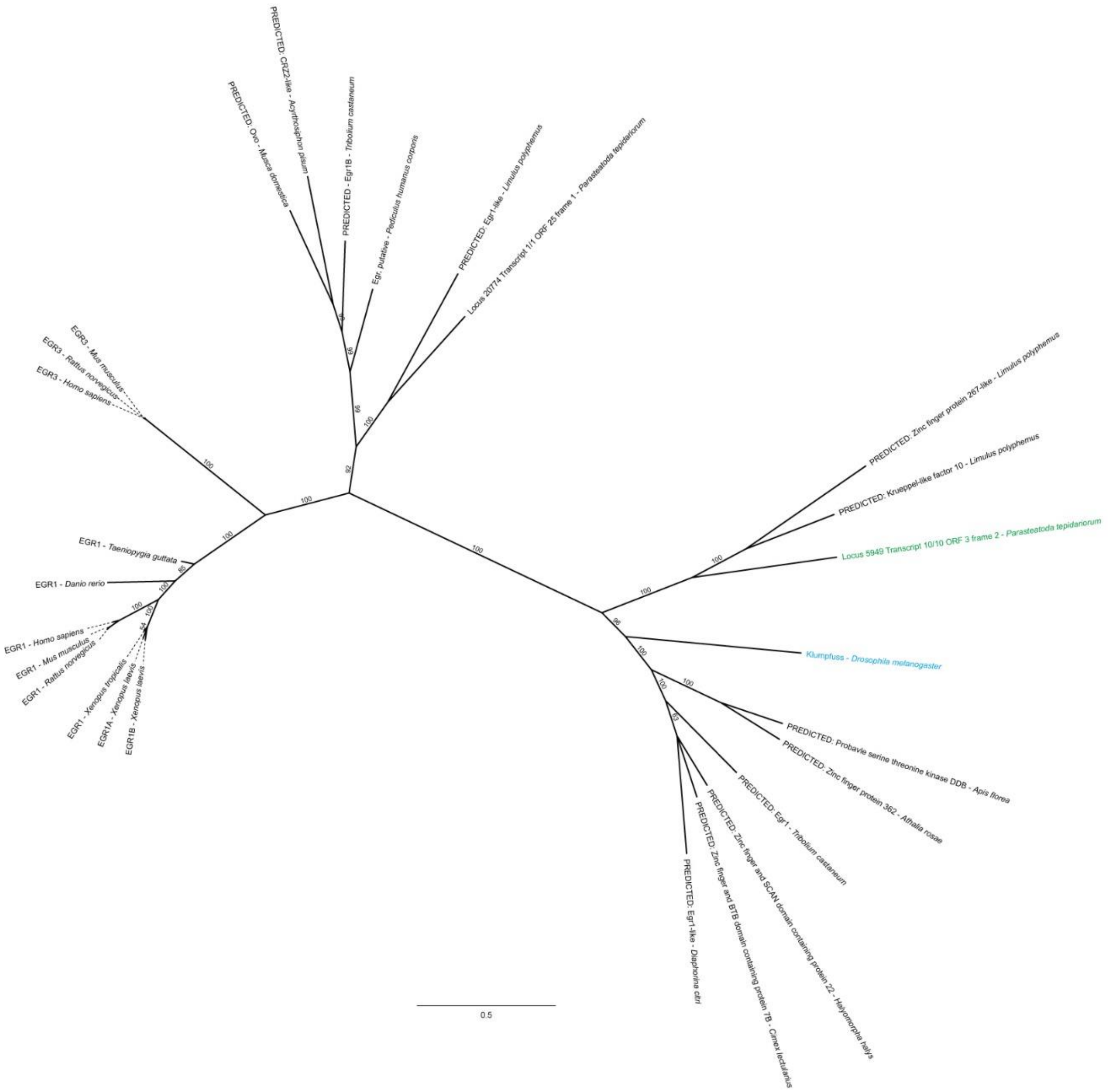

Figure 56 – Phylogenetic tree of *klu*. Branch values represent posterior probabilities of Bayesian likelihood (462 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.19). One homolog of the *D. melanogaster klu* (blue) could be identified (Locus 5949, green).

Expression analysis of this *klu* homolog showed no expression of its transcript at stage 8 of *P. tepidariorum* development (Figure 57 A, B). At stage 11, a weak expression could be observed in the majority of neural precursors in pre-cheliceral lobes, prosoma, as well as opisthosoma (Figure 57 C, D, E, F). Additional weak expression was present in the regions of the joints in the walking legs and sensory precursors at the tip of the legs during that stage (Figure 57 D, E, F).

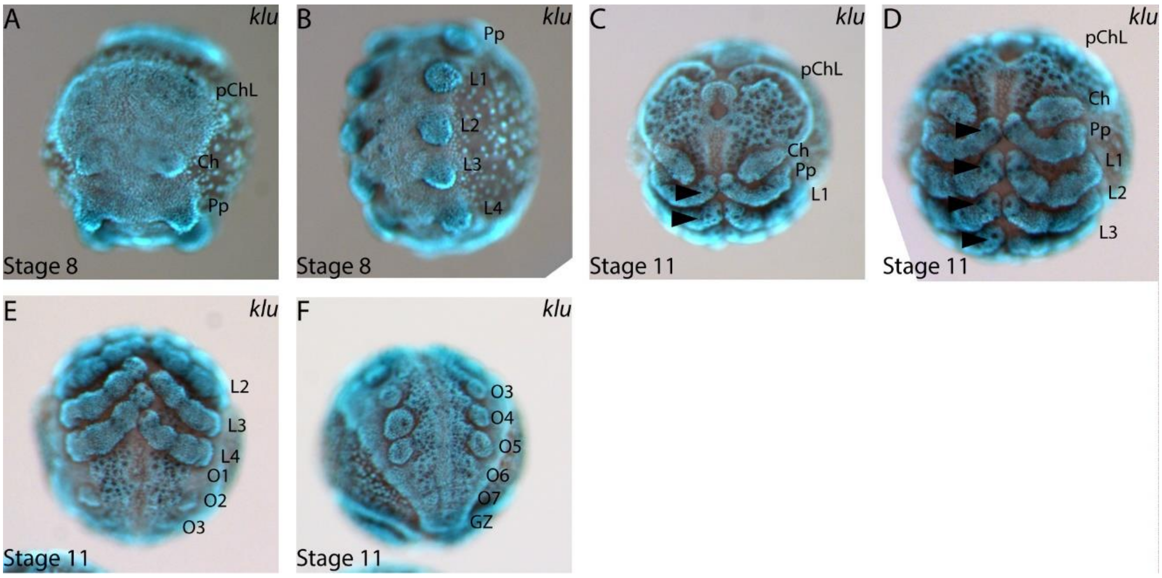

Figure 57 – Embryonic expression of *klumpfuss* in *P. tepidariorum*. No expression of *klu* was present at stage 8 (A, B). at stage 11 *klu* was expressed in most of the neural precursors in the pre-cheliceral lobes and the rest of the body (C, D, E, F). Additional expression could be observed in the prosomal appendages in the region of the joints (D, E and in sensory precursors at the tip of the appendages (black arrowheads in C, D). A and C show embryos in frontal aspect. B, D, E, and F are ventral views with the anterior to the top.

6.2.3.23 *Krüppel*

Krüppel (*Kr*) is zinc finger domain transcription factor, which acts as a gap gene in the thorax region during segmentation in *Drosophila* (Gaul & Jäckle 1987, Nüsslein-Volhard & Wieschaus 1980), but also determines the fate of neuroblasts during neurogenesis (Isshiki et al. 2001). Phylogenetic analysis of the transcriptome of *P. tepidariorum* showed two homologs of the *Drosophila Kr* (Locus 6712 (*Kr-1*), Locus 28965 (*Kr-2*)) (Figure 58).

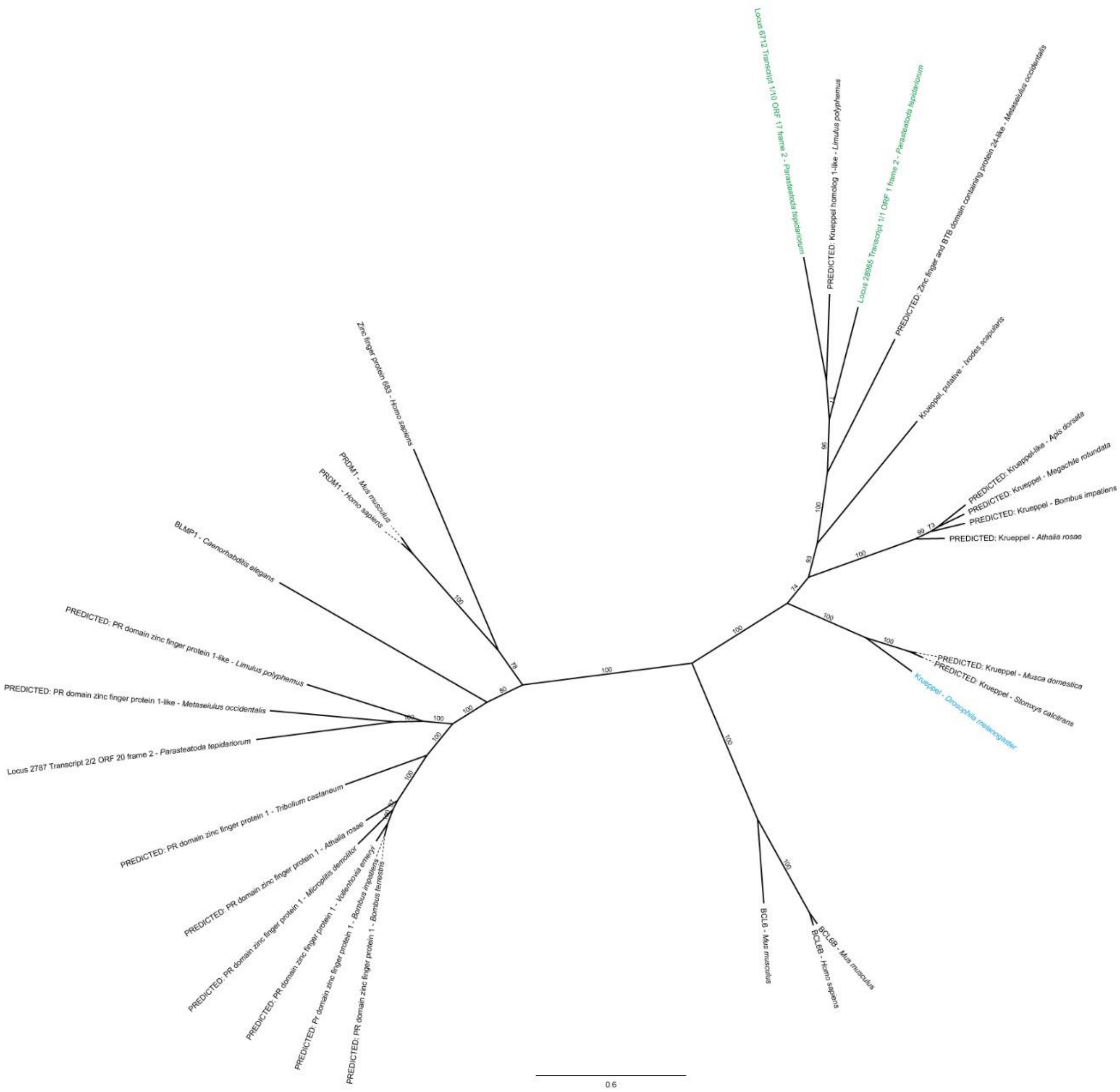

Figure 58 – Phylogenetic tree of *Kr*. Branch values represent posterior probabilities of Bayesian likelihood (384 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.20). Two homologs of the *Drosophila Kr* (blue) could be identified (Locus 6712 (*Kr-1*), Locus 28965 (*Kr-2*), both green).

Expression of *Kr-1* in *P. tepidariorum* is located in the prosomal appendages (except the cheliceres) at stage 8 and continues throughout the stages analysed (Figure 59 A, B, C, D, G, H). At stage 9, *Kr-1* is also expressed in a subset of neural precursors at the anterior end of the pre-cheliceral lobes, and in the ventral neuroectoderm of the leg-bearing segments and the opisthosoma (white arrowheads in Figure 59 C, D, E). During stage 10, more pro neural cluster are positive for *Kr-1*, namely in the posterior part of the pre-cheliceral lobes and the cheliceral and pedipalp segment

(Figure 59 F, G). The second homolog in *P. tepidariorum* could not be cloned for expression analysis.

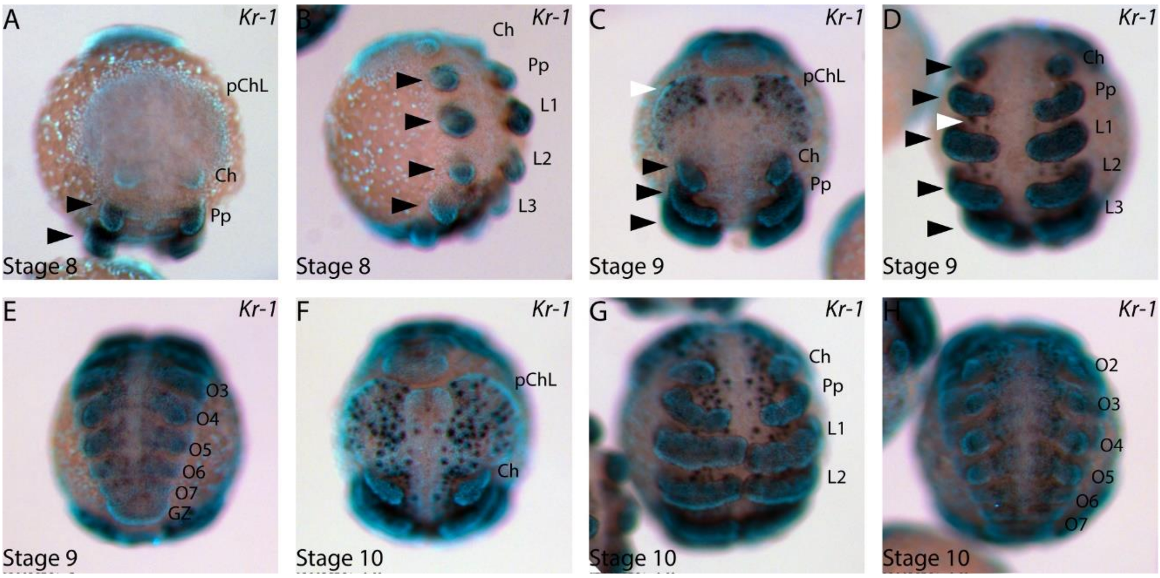

Figure 59 – Embryonic expression of *Krüppel-1* in *P. tepidariorum*. Expression of *Kr-1* was present in the prosomal limb buds, except the chelicerae, at stage 8 (black arrowheads in A and B). Expression in the appendages was still present at stage 9 (black arrowheads in C, D). Additional expression appeared in a subset of neural precursors in the pre-cheliceral lobes and along the body axis in the neurogenic ectoderm (white arrowheads in C, D, and E). In the subsequent stage, a larger subset of neural precursors showed expression of Kr-1 (F, G, H). A, C, and F show embryos in frontal aspect. B, D, E, G, and H are ventral views with the anterior to the top.

6.2.3.24 *Ladybird early*

ladybird early (*lbe*) is a homeobox domain containing transcription factor, which in *Drosophila*, is involved in the development of mesoderm derived tissues (Jagla et al. 2001, Junion et al. 2007, Parrish & Kim 2006), but also specification of neural cells (De Graeve et al. 2004), and the morphogenesis of leg and genital imaginal discs (Jagla et al. 1997, Maqbool et al. 2006). Phylogenetic analysis of the transcriptome of *P. tepidariorum* showed one homolog of *lbe* to be present (Locus 15017) (Figure 60), which could not be cloned for expression analysis.

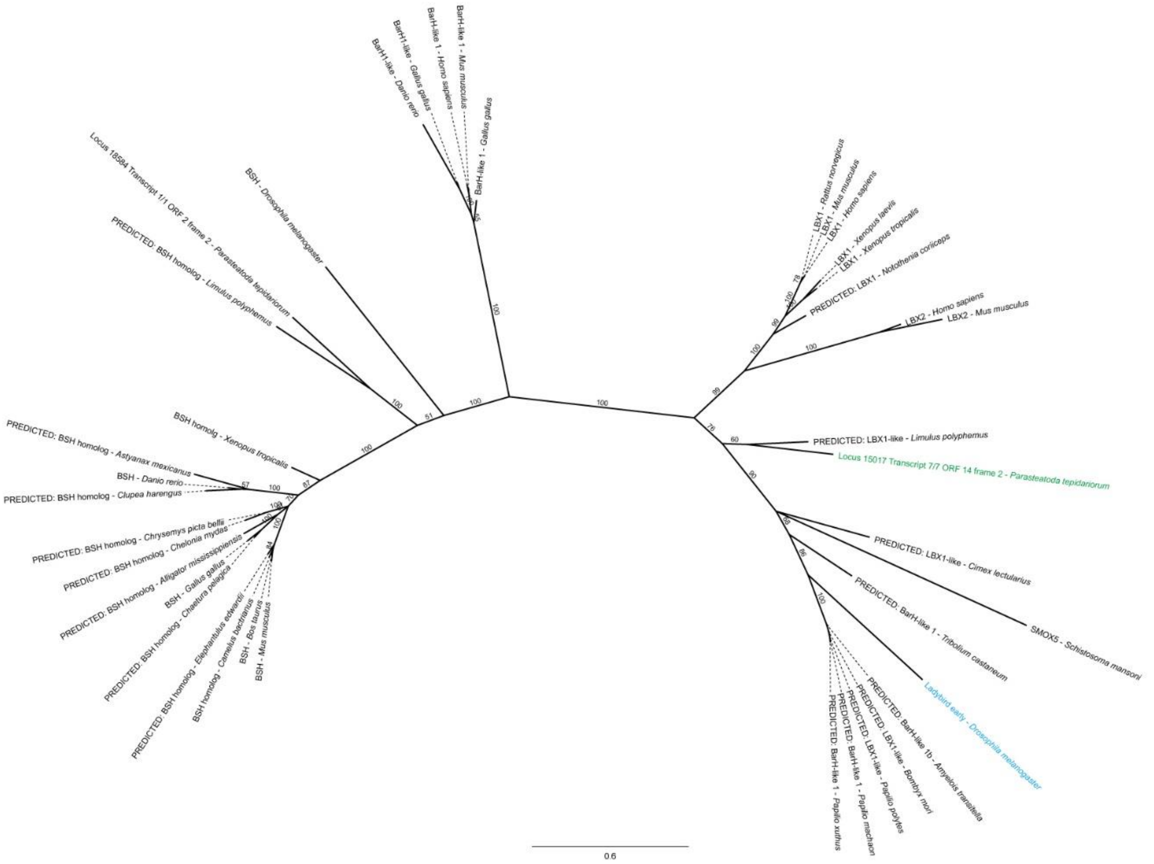

Figure 60 – Phylogenetic tree of *lbe*. Branch values represent posterior probabilities of Bayesian likelihood (1488 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.21). One homolog of the *Drosophila lbe* (blue) could be identified (Locus 15017, green).

6.2.3.25 *Lethal of scute*

lethal of scute (*l(1)sc*) is a achaete-scute transcription factor related protein, which is involved in the development of the nervous system in *Drosophila* (Neumüller et al. 2011, Skaer et al. 2002) via the determination of neuroblasts (Apitz & Salecker 2015, Skeath & Thor 2003). Phylogenetic analysis of the *P. tepidariorum* transcriptome revealed no homolog of this gene to be present in the spider (Figure 61).

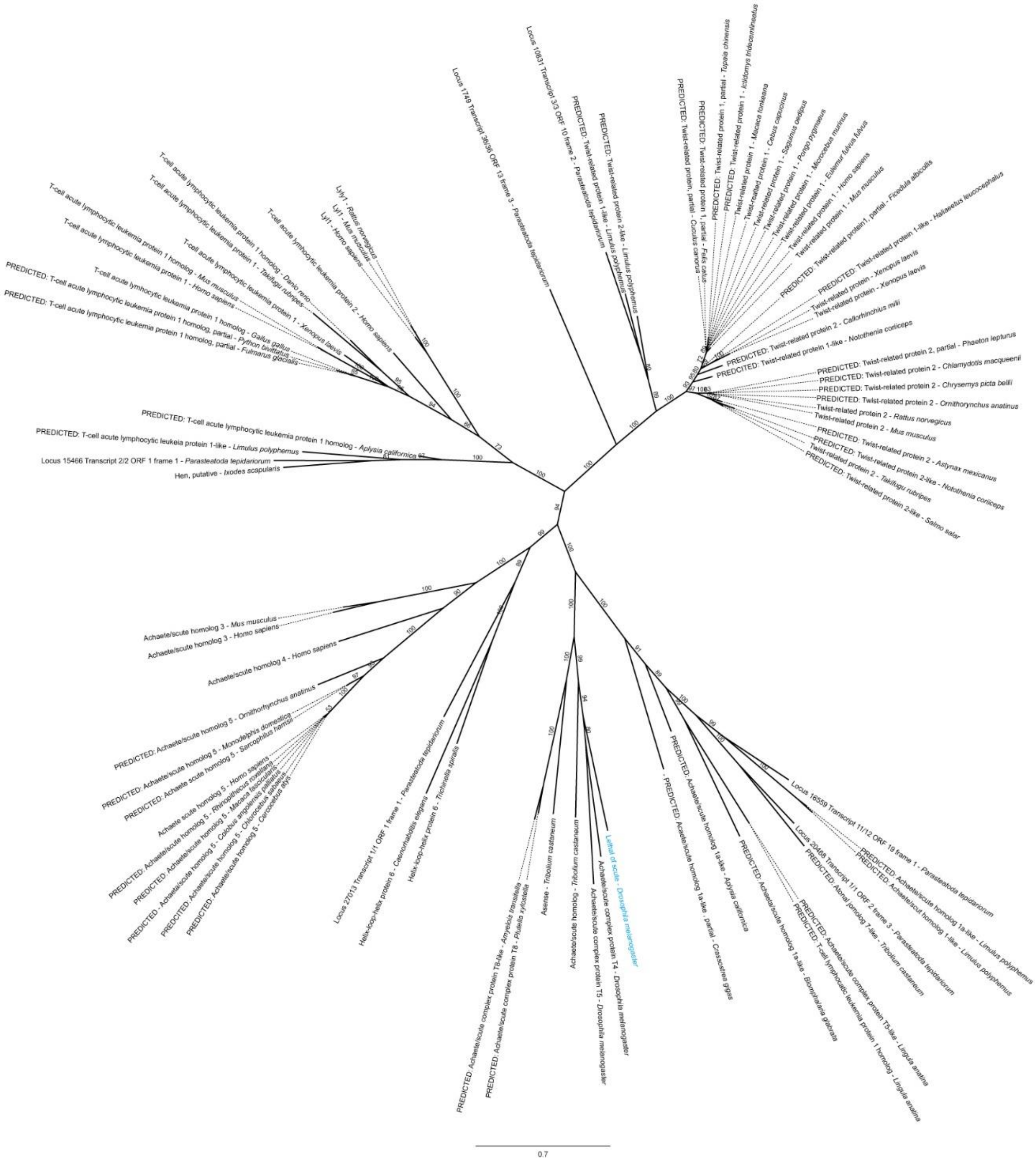

Figure 61 – Phylogenetic tree of *l(1)sc*. Branch values represent posterior probabilities of Bayesian likelihood (9974 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.22). No homolog of the *Drosophila l(1)sc* (blue) could be identified.

6.2.3.26 *Maf-S*

maf-s is a transcription factor with a basic leucine zipper domain, which is involved in *Drosophila* head development, where it can suppress homeotic functions through the interaction with *cnc* (Veraksa et al. 2000). Phylogenetic analysis showed one homolog of the maf family to be present in the transcriptome of *P. tepidariorum* (Locus 2680) (Figure 62). Expression analysis of this homolog showed ubiquitous presence of *maf-s* transcripts in the stages analysed (supplementary material 9.4.3.10).

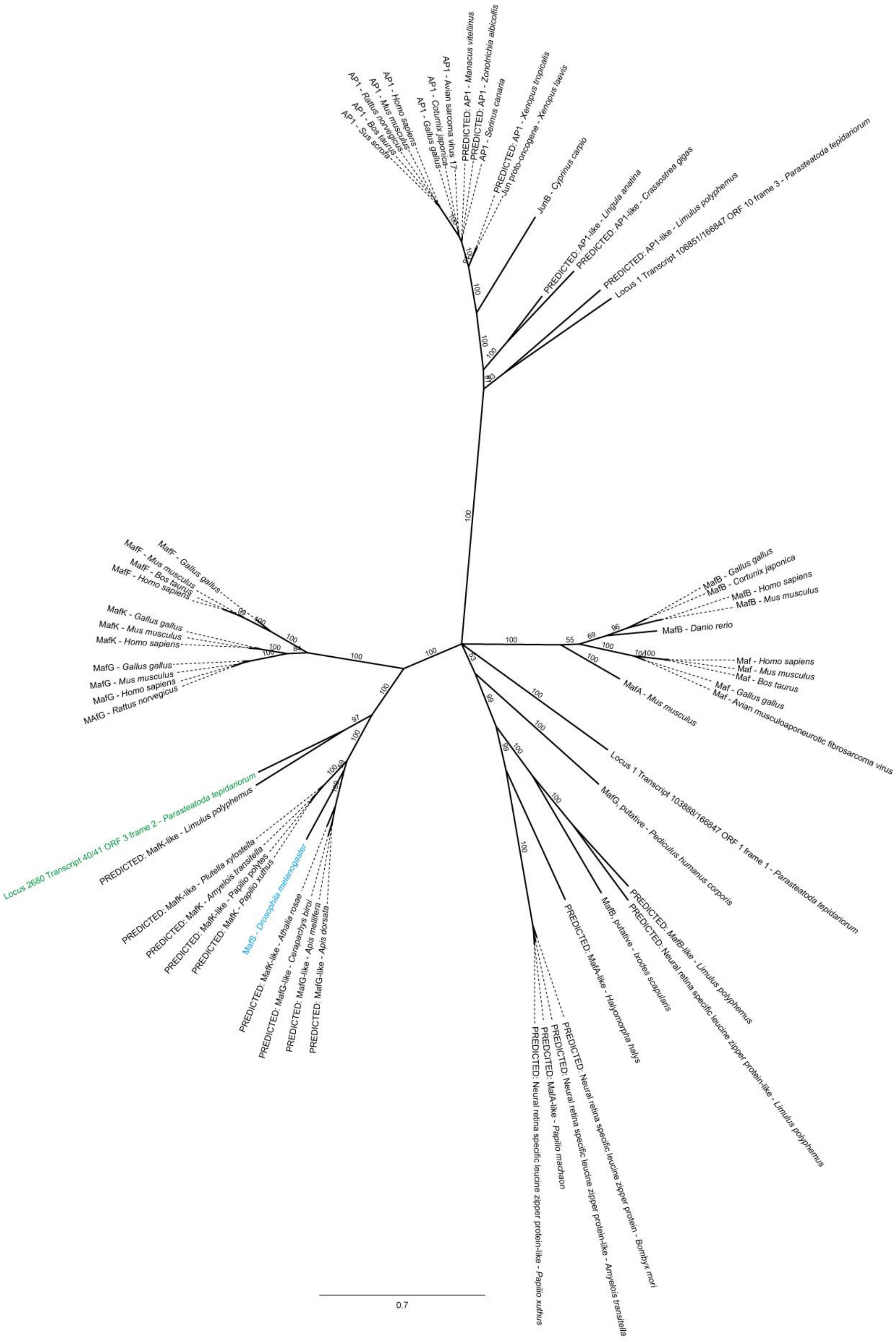

Figure 62 – Phylogenetic tree of *MafS*. Branch values represent posterior probabilities of Bayesian likelihood (1548 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.23). One homolog of the *Drosophila MafS* (blue) could be found (Locus 2680, green).

6.2.3.27 *Medea*

Medea (*Med*) is a member of the Smad family, which is involved in the establishment and specification of the dorso-ventral axis, via the TGF-beta signaling pathway (Hudson et al. 1998, Marquez et al. 2001, Wisotzkey et al. 1998). Phylogenetic analysis of the transcriptome *of P. tepidariorum* showed one *Med* homolog to be present (Locus 2495) (Figure 63). The expression of this gene appeared to be ubiquitous during the embryonic stages analysed (supplementary material 9.4.3.11).

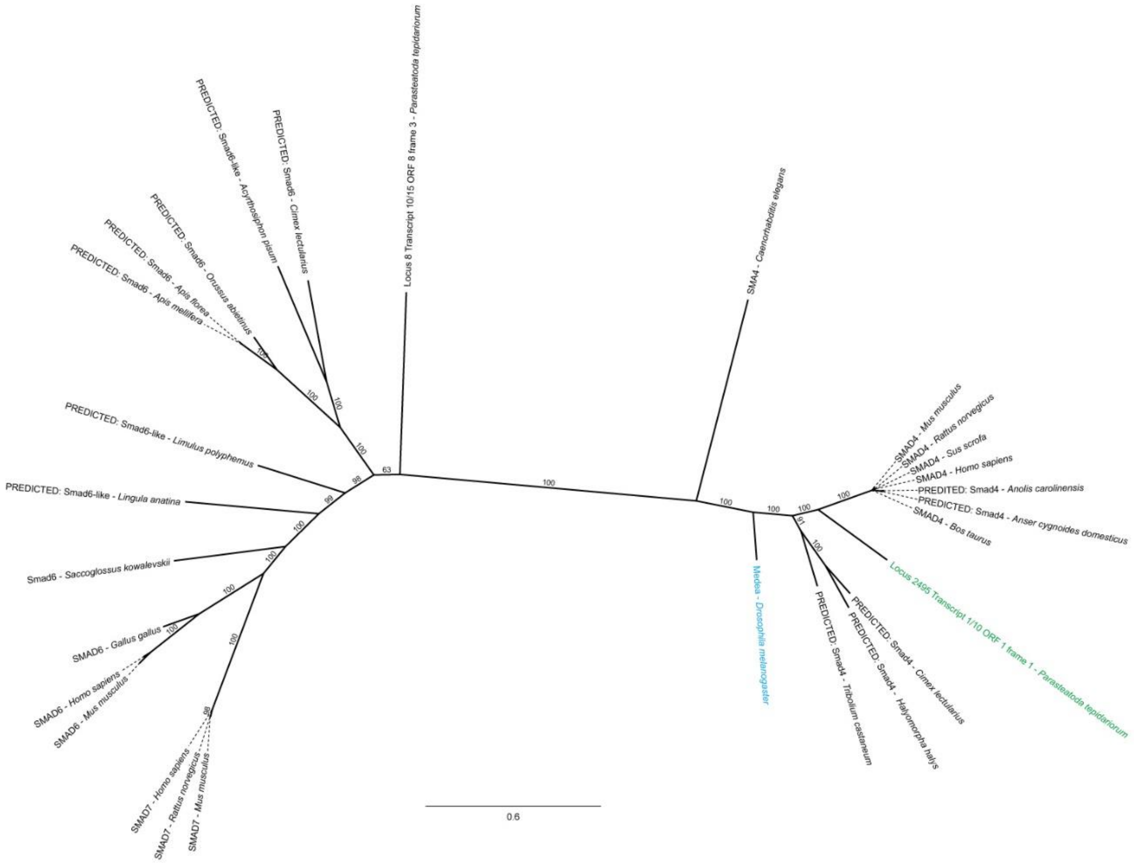

Figure 63 – Phylogenetic tree of *Med*. Branch values represent posterior probabilities of Bayesian likelihood (522 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.24). One homolog of the *Drosophila Med* (blue) could be found (Locus 2495, green).

6.2.3.28 *NR3C1*

NR3C1 (Nuclear receptor subfamily 3 group C member 1) mediates the transcription of target genes in response to glucocorticoid signals (Barnes 1998, Tronche et al. 2004). It acts through nuclear receptor signaling (Lu & Cidlowski 2005) and has been shown to interact with HOXB2 (Chatr-Aryamontri et al. 2017). No homolog of NR3C1 could be found in the transcriptome of *P. tepidariorum* (Figure 64).

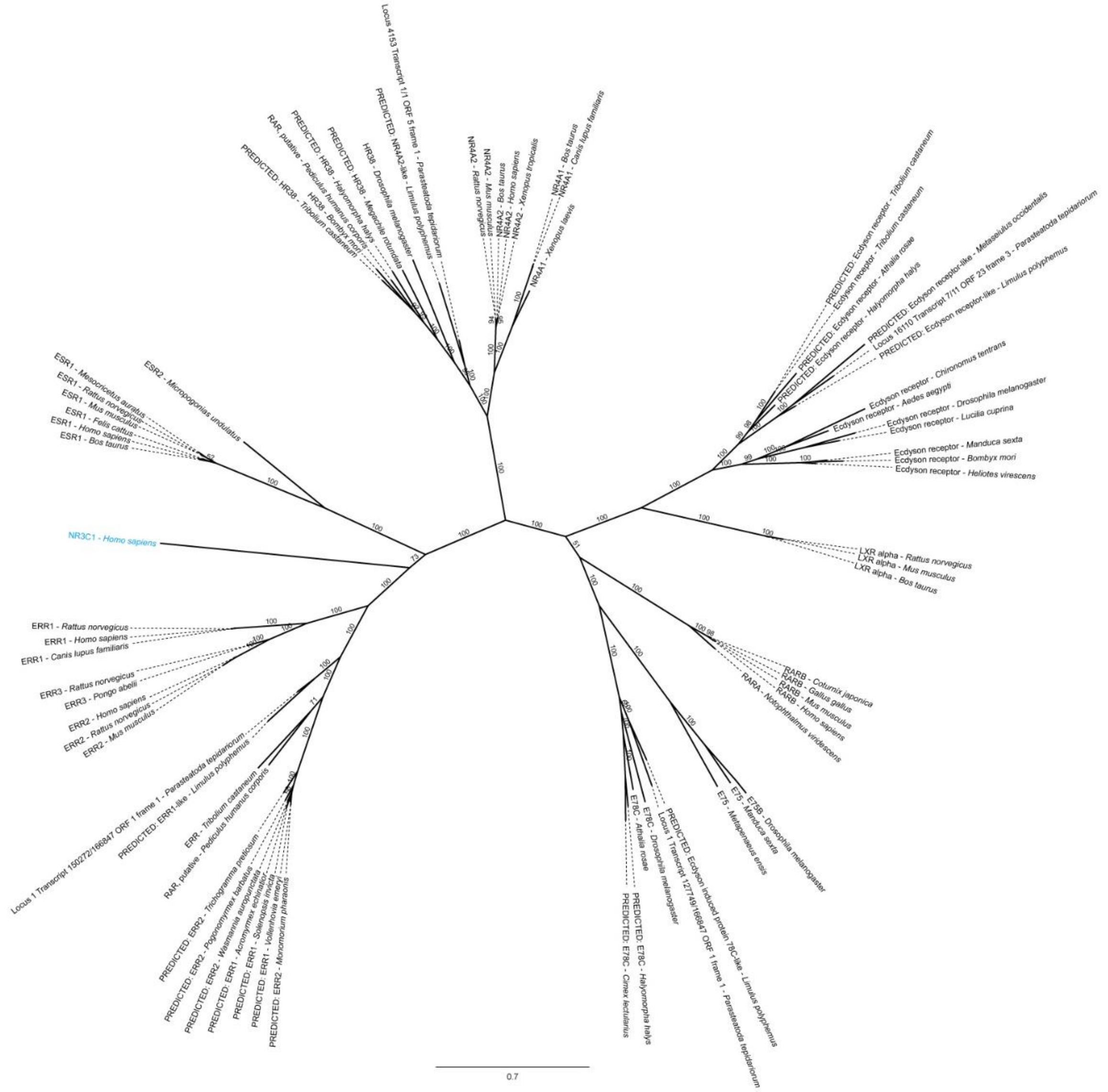

Figure 64 – Phylogenetic tree of *NR3C1*. Branch values represent posterior probabilities of Bayesian likelihood (194 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.25). No homolog to the *Homo sapiens NR3C1* (blue) could be identified.

6.2.3.29 *Ovo*

ovo (*shaven baby*) is a zinc finger transcription factor, which is involved in pattern formation in the cuticle (Chanut-Delalande et al. 2006), differentiation of epidermal cells (Payre et al. 1999), and it plays a role in the morphogenesis of leg joints in *Drosophila* (Pueyo & Couso 2011). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed one *ovo* homolog (Locus 13054) (Figure 65), which showed no expression in the embryonic stages analysed (supplementary material 9.4.3.12).

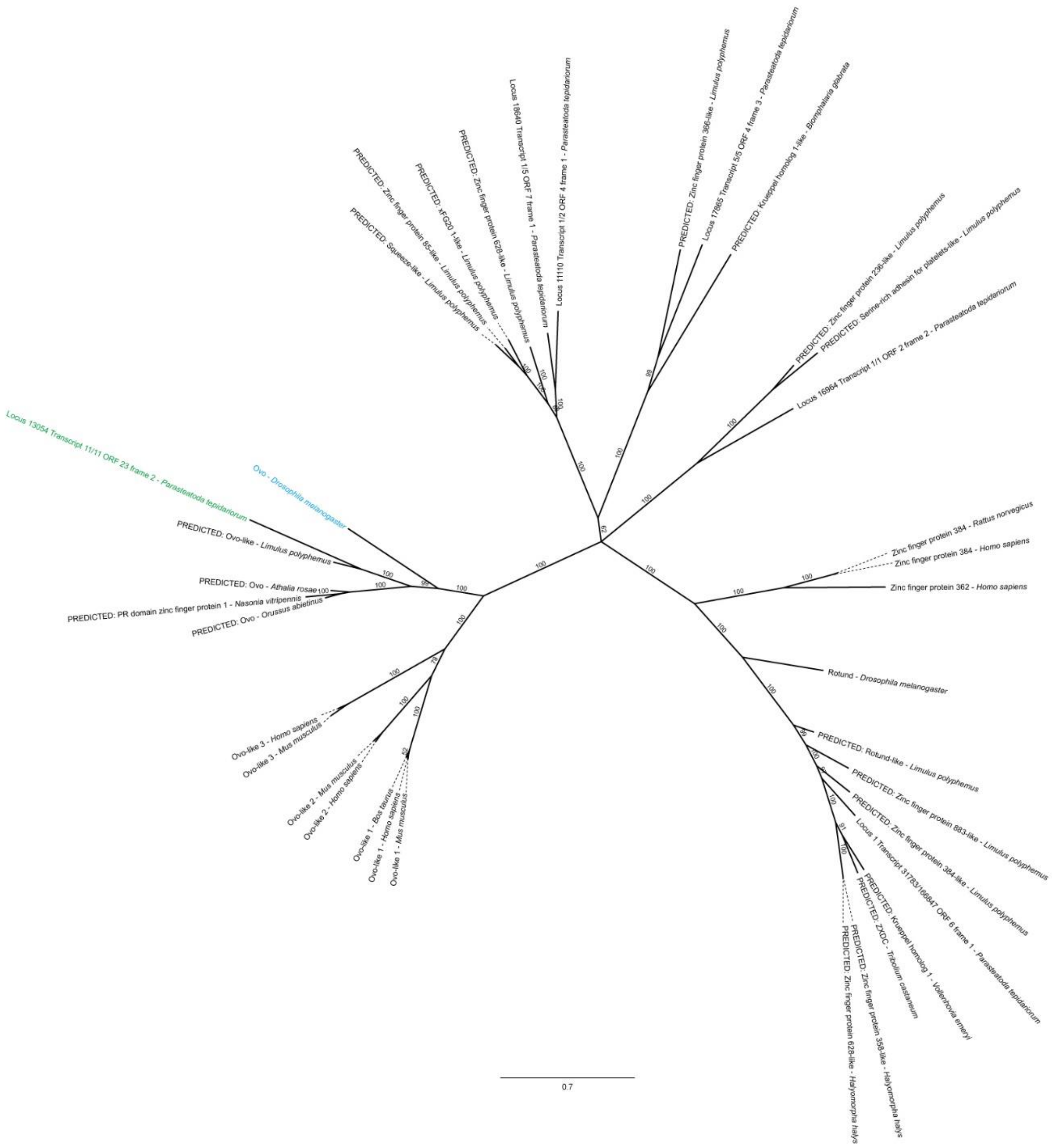

Figure 65 – Phylogenetic tree of *ovo*. Branch values represent posterior probabilities of Bayesian likelihood (368 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.26). One homolog of the *Drosophila ovo* (blue) could be found (Locus 13054, green).

6.2.3.30 *Paired*

paired (*prd*) is a transcription factor with both, paired and homeodomain, which belongs to the PAX3/7 group of proteins (Davis et al. 2005). In *Drosophila*, it acts as a pair-rule gene during embryonic development (Davis & Patel 2003, Peel 2004). Phylogenetic analysis of the *P. tepidariorum* transcriptome revealed two possible homologs of *prd* (Locus 17531, Locus 13554) (Figure 66). By the analysis of their expression, Locus 13554 was determined as the homolog of *prd*, while locus 17531 was assigned as the homolog of *gsb*, because of the phylogenetic tree resulting from the search for *gsb* homologs (see above).

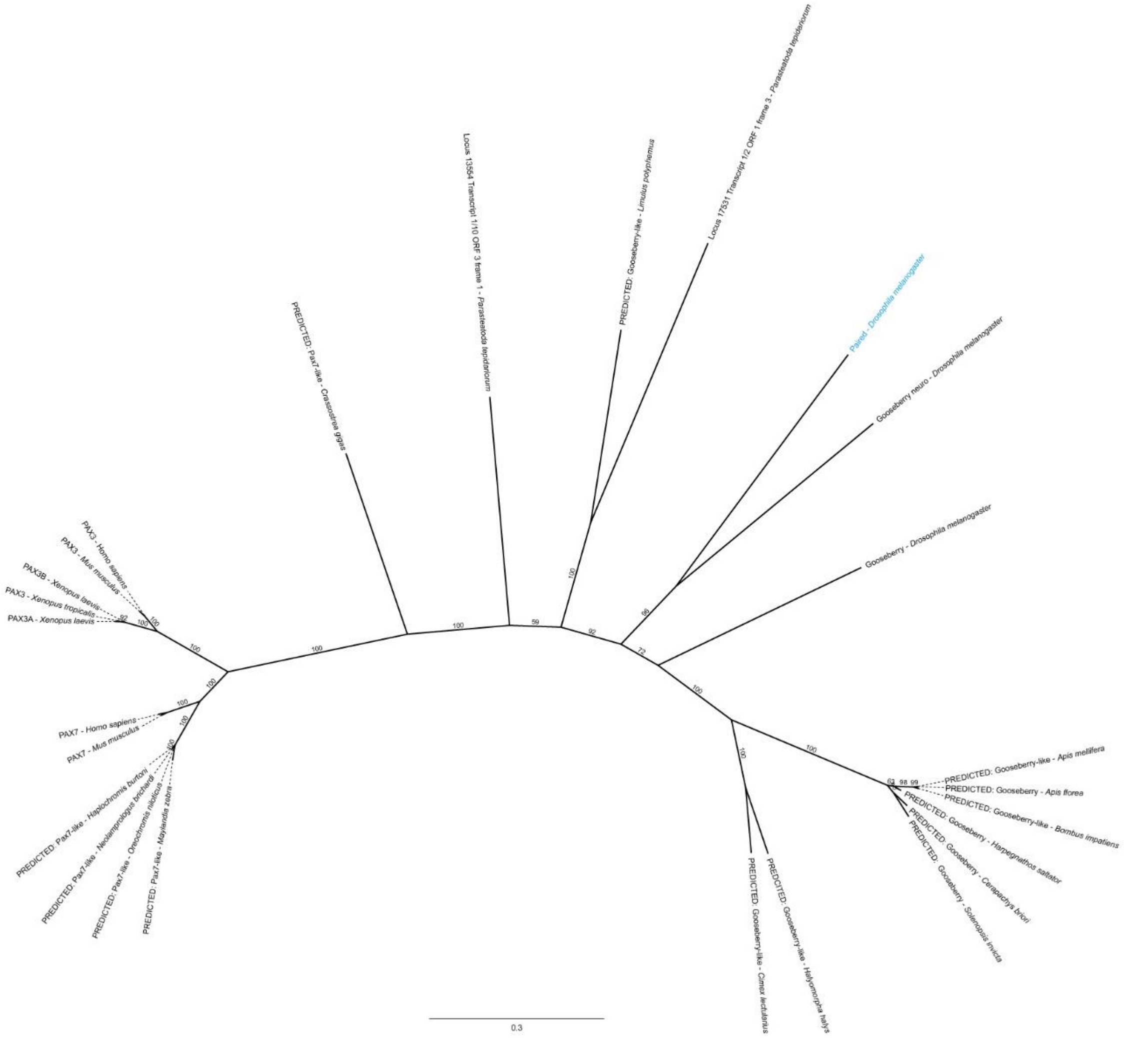

Figure 66 – Phylogenetic tree of *prd*. Branch values represent posterior probabilities of Bayesian likelihood (914 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.27).

The expression of *prd* first appears in the opisthosomal segments at stage 7 in a segmental fashion (black arrowheads in Figure 67 A, B). These expression domains loose intensity in the older segments, while a broader expression can be seen in the newly forming segments in the growth zone (white arrowhead in Figure 67 B). In later stages, *prd* is expressed in a segmental fashion in all segments from the chelicera to the growth zone (Figure 67 C, D, E, F, G).

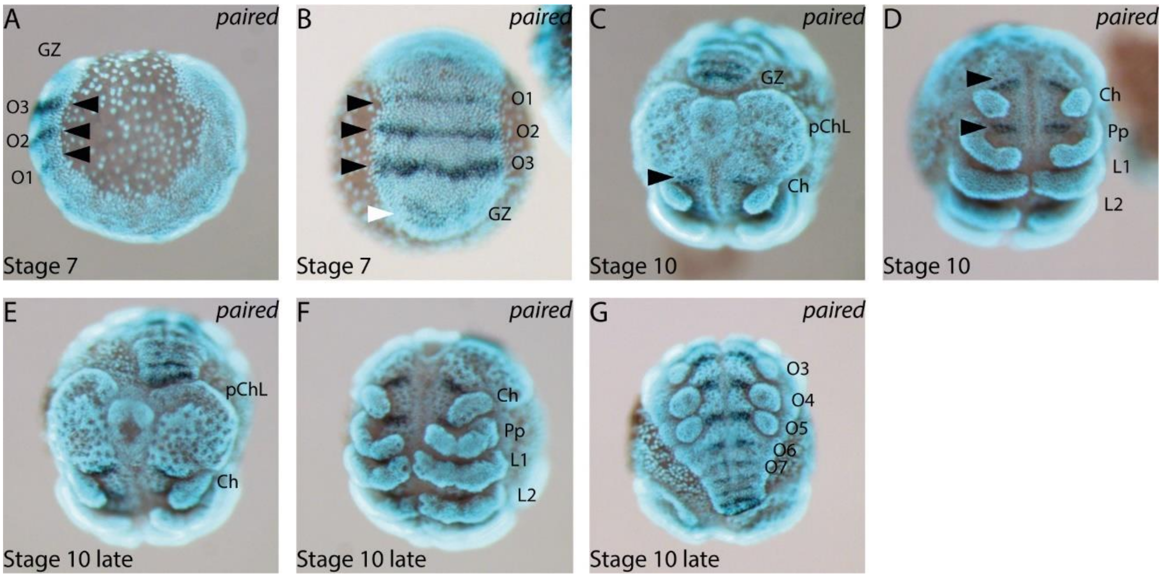

Figure 67 – Embryonic expression of *paired* in *P. tepidariorum*. *prd* expression first appears at stage 7 in segmental stripes in the opisthosomal segments (black arrowheads in A, B) and an additional stripe of expression in the growth zone (white arrowheads in B). At stage 10, all segments from the chelicerae to the growth zone show *prd* expression in a segmental fashion (C, D, E, F, G). A is a lateral view with the anterior to the right. B, D, F, and G are ventral views with the anterior to the top. C and E show embryos in frontal aspect.

6.2.3.31 *Pleiohomeotic*

pleiohomeotic (*pho*) is a zinc finger domain protein, which recruits Polycomb group protein complexes to the chromatin as a transcriptional repressor (Fritsch et al. 1999). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed two homologs of *pho* to be present (Locus 5955 (*pho-1*), Locus 10241 (*pho-2*)) (Figure 68). Both of the identified homologs showed ubiquitous expression during the embryonic stages analysed (supplementary material 9.4.3.13).

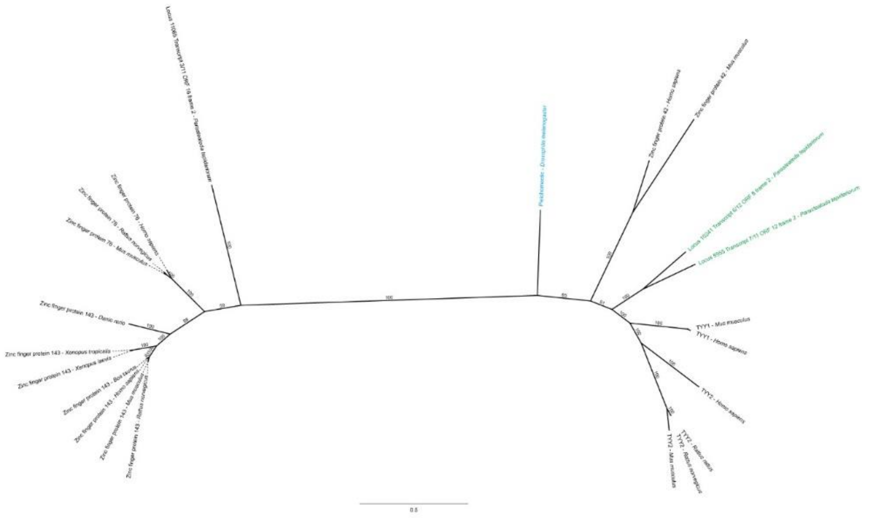

Figure 68 – Phylogenetic tree of *pho.* Branch values represent posterior probabilities of Bayesian likelihood (54 trees sampled, AA substitution model was Dayhoff, using sequences from an initial FastTree calculation

(supplementary material 9.4.1.28). Two homolog of the *Drosophila pho* (blue) could be identified (Locus 5955 (pho-1), Locus 10241 (pho-2), both green).

6.2.3.32 *Polycomb*

Polycomb (*Pc*) is a chromatin binding protein, which is involved in epigenetic silencing of developmental genes (Nègre et al. 2006, Roseman et al. 2001). Phylogenetic analysis showed one *Pc* homolog in the *P. tepidariorum* transcriptome (Locus 2368) (Figure 69). This homolog showed ubiquitous expression in the early embryonic stages analysed (supplementary material 9.4.3.14).

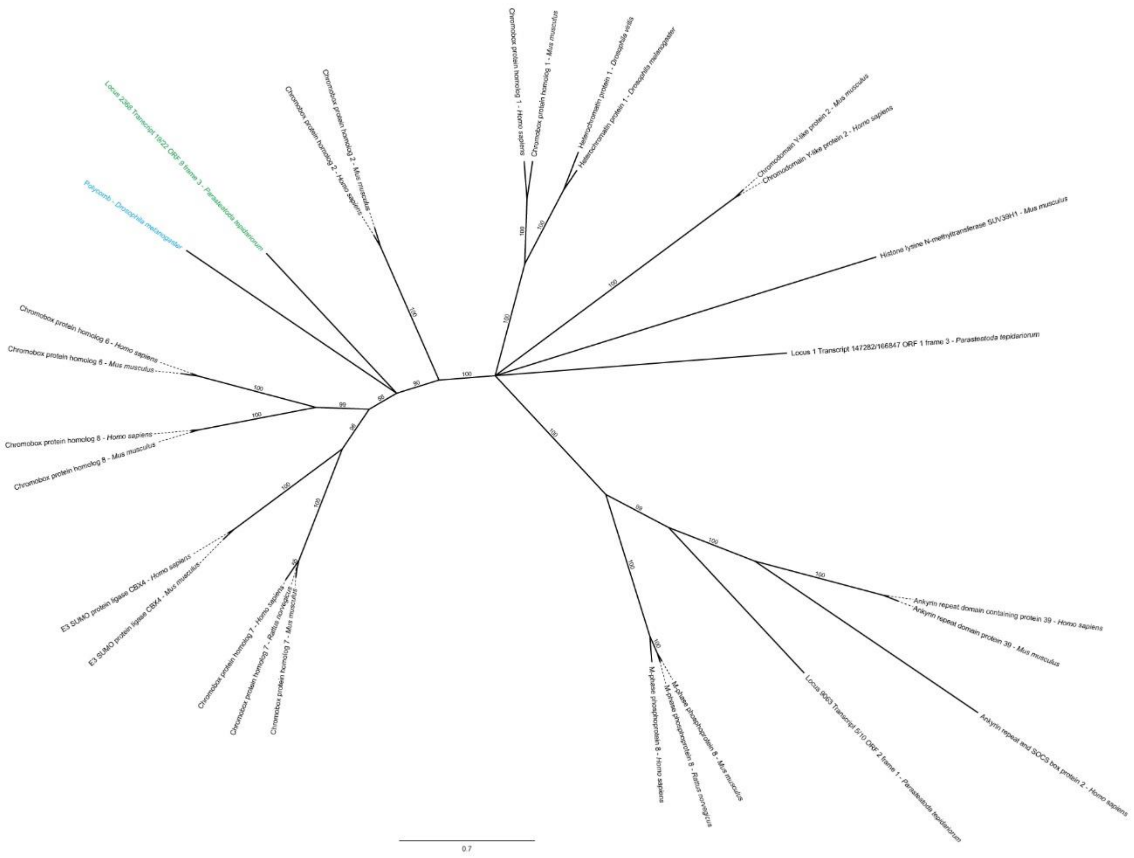

Figure 69 – Phylogenetic tree of *Pc*. Branch values represent posterior probabilities of Bayesian likelihood (1298 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.29). One homolog of the *Drosophila Pc* (blue) could be identified (Locus 2368, green).

6.2.3.33 *Polyhomeotic-proximal*

polyhomeotic-proximal (*ph-p*) is a zinc finger domain protein, which is a transcriptional silencer and part of the Polycomb repressive complex 1 (Nègre et al. 2006, Roseman et al. 2001). Phylogenetic analysis showed two homologs of *ph-p* in the transcriptome of *P. tepidariorum* (Locus

11157 (*ph-p-1*), Locus 17041 (*ph-p-2*)) (Figure 70). While *ph-p-1* could not be cloned for analysis, *ph-p-2* showed ubiquitous expression in the stages analysed (supplementary material 9.4.3.15).

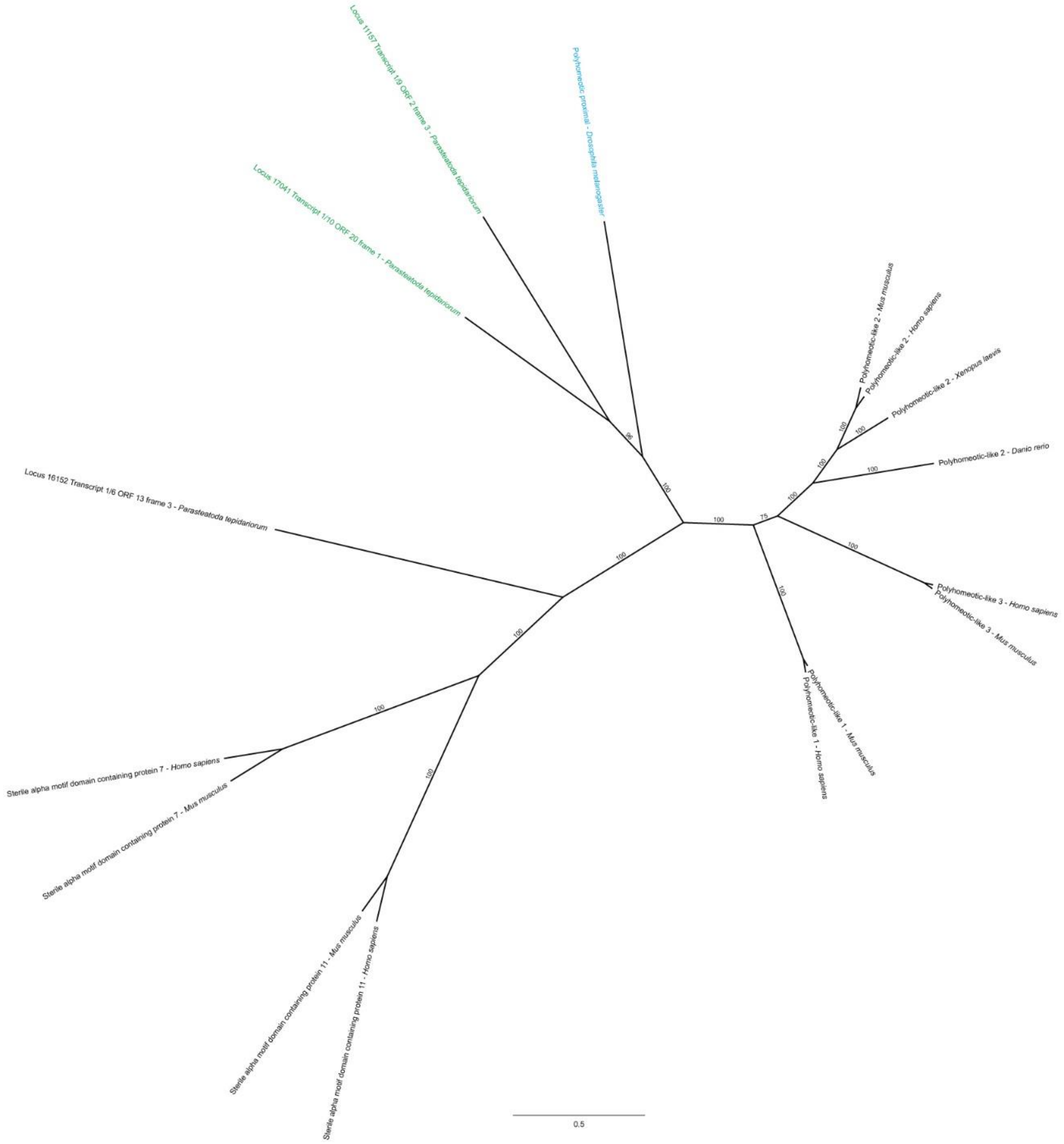

*Figure 70 – Phylogenetic tree of ph-p. Branch values represent posterior probabilities of Bayesian likelihood (24 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (*supplementary material 9.4.1.30*). Two homologs of the Drosophila ph-p (blue) could be identified (Locus 11157 (ph-p-1), Locus 17041 (ph-p-2), both green).*

6.2.3.34 *Reversed polarity*

reversed polarity (*repo*) is a homeodomain transcription factor, which is required for the differentiation of glial cell in the nervous system in *Drosophila* (Halter et al. 1995, Yuasa 2003).

Phylogenetic analysis of the transcriptome of *P. tepidariorum* revealed two homologs of *repo* to be present (Locus 16095 (*repo-1*), Locus 20045 (*repo-2*)) (Figure 71).

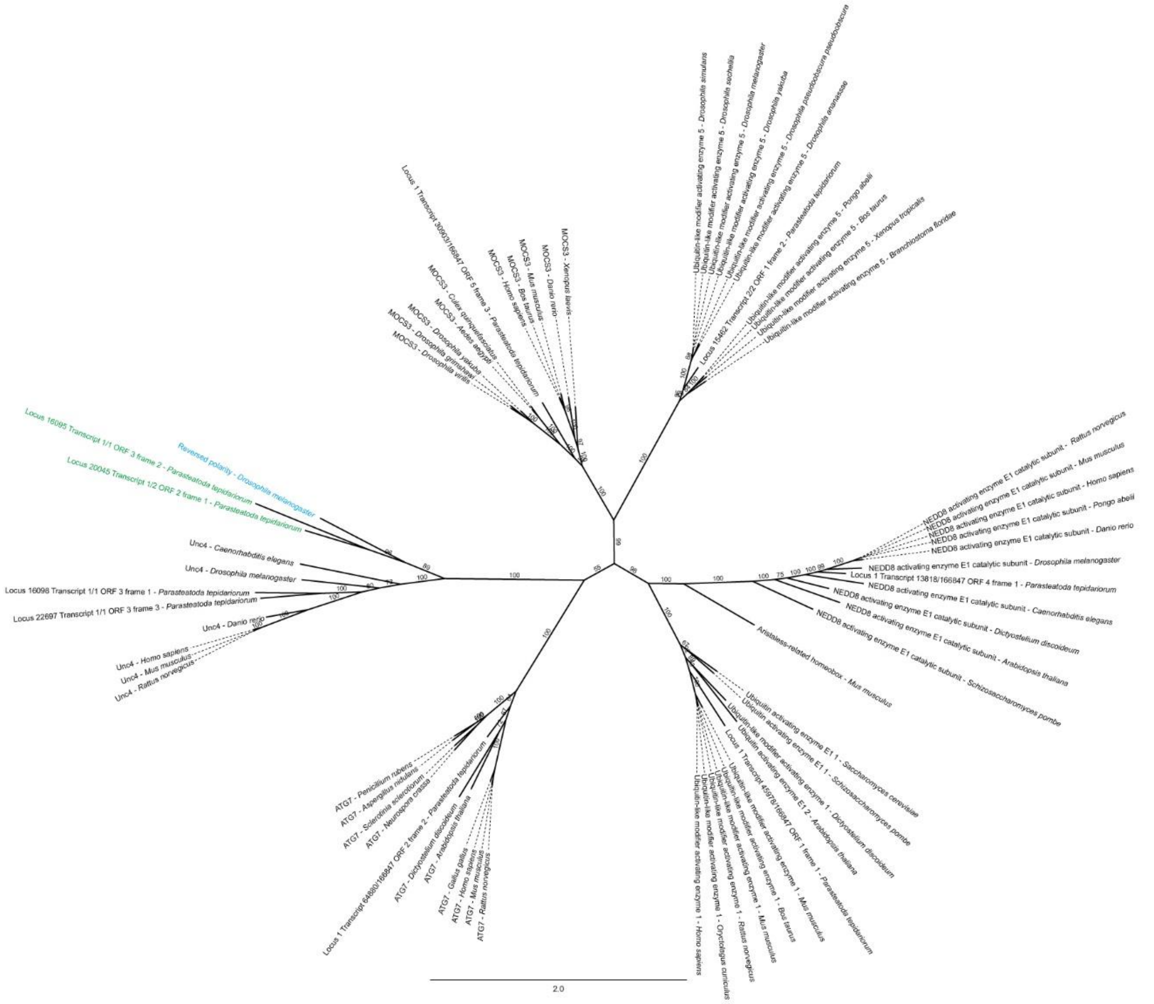

Figure 71 – Phylogenetic tree of *repo*. Branch values represent posterior probabilities of Bayesian likelihood (1484 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.31). Two homologs of the *Drosophila repo* (blue) could be identified (Locus 16095 (repo-1), Locus 20045 (repo-2), both green).

repo-1 showed expression in two domains in the anterior-lateral region of the pre-cheliceral head lobes (Figure 72 A). At later stages, these domains are located inside the anterior furrow of the pre-cheliceral lobes (Figure 72 B, C). *repo-2* could not be cloned for expression analysis.

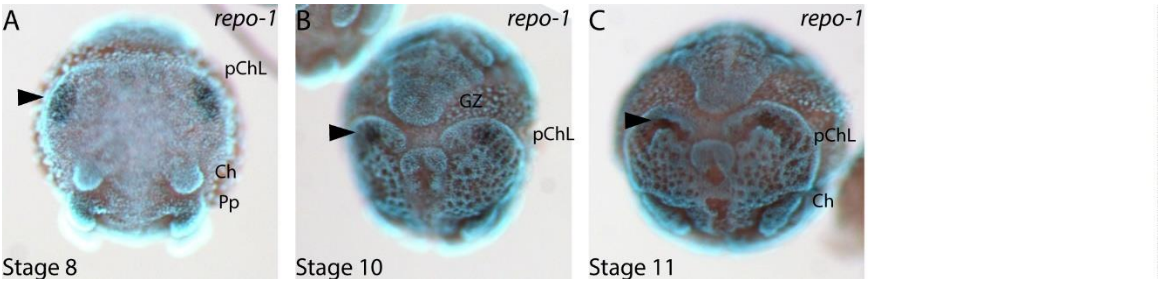

Figure 72 – Embryonic expression of *reversed polarity 1* in *P. tepidariorum*. *repo-1* expression appears first as two domains in a lateral anterior position in the pre-cheliceral lobes at stage 8 (arrowhead in A). This domain persists in the subsequent stages, where it is located in the anterior furrow (arrowheads in B, C). All pictures show embryos in frontal aspects.

6.2.3.35 *Senseless*

senseless (*sens*) is a zinc finger transcription factor, which is involved in sensory organ development (Jafar-Nejad 2006, Treisman 2004). One homolog of *sens* could be identified in the transcriptome of *P. tepidariorum* (Locus 25081) (Figure 73). This homolog could not be cloned for expression analysis.

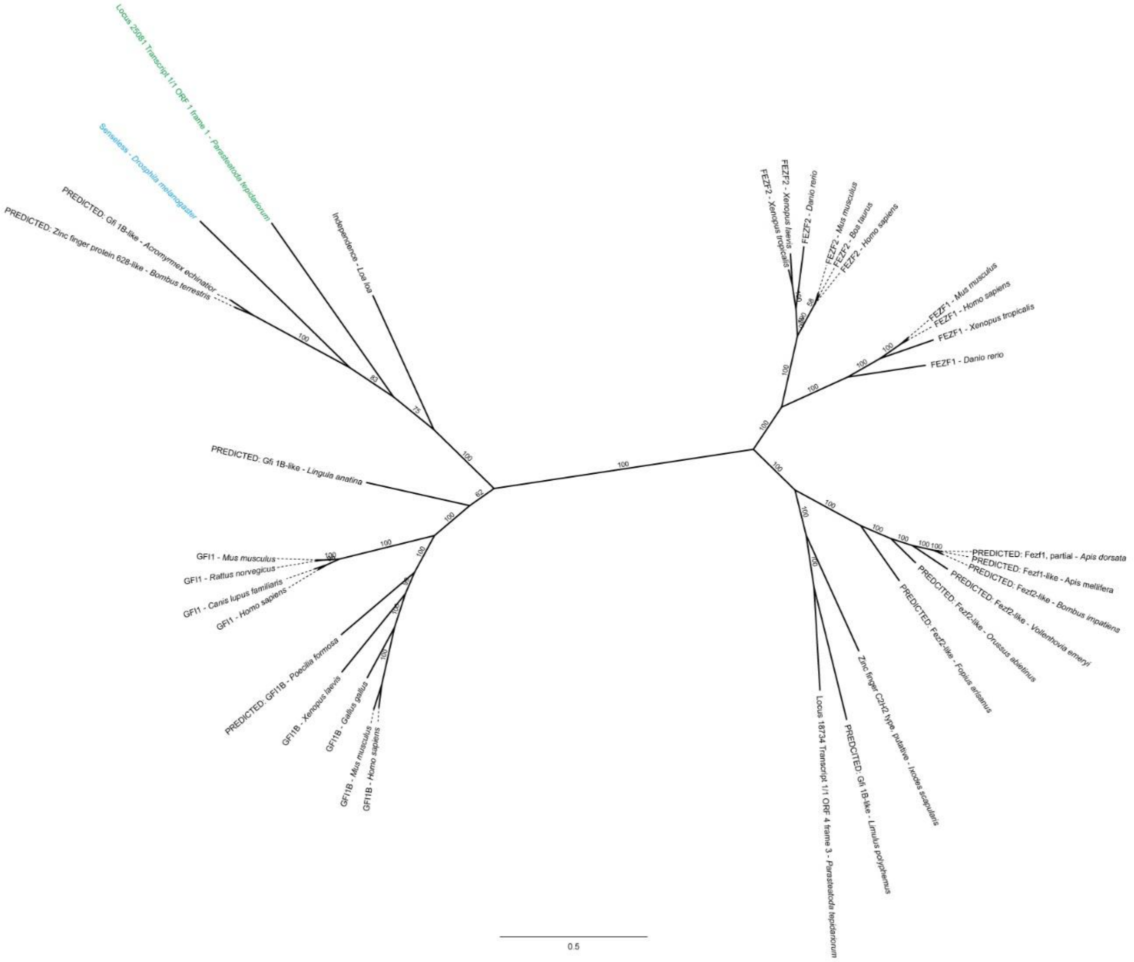

Figure 73 – Phylogenetic tree of *sens*. Branch values represent posterior probabilities of Bayesian likelihood (224 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation

(supplementary material 9.4.1.32). One homolog of the *Drosophila sens* (blue) could be identified (Locus 25081, green).

6.2.3.36 *Sfmbt (Scm-related gene containing four mbt domains)*

Sfmbt is zinc finger transcription factor, which binds to chromatin and silences genes as a part of the *pho* repressive complex (Grimm et al. 2009, Klymenko et al. 2006). Phylogenetic analysis of the *P. tepidariorum* transcriptome revealed two homologs of *Sfmbt* (Locus 1 transcript 107630 (*sfmbt-1*), Locus 3961 (*sfmbt-2*)) (Figure 74). *sfmbt-1* showed ubiquitous expression in the stages analysed (supplementary material 9.4.3.16), while *sfmbt-2* could not be cloned.

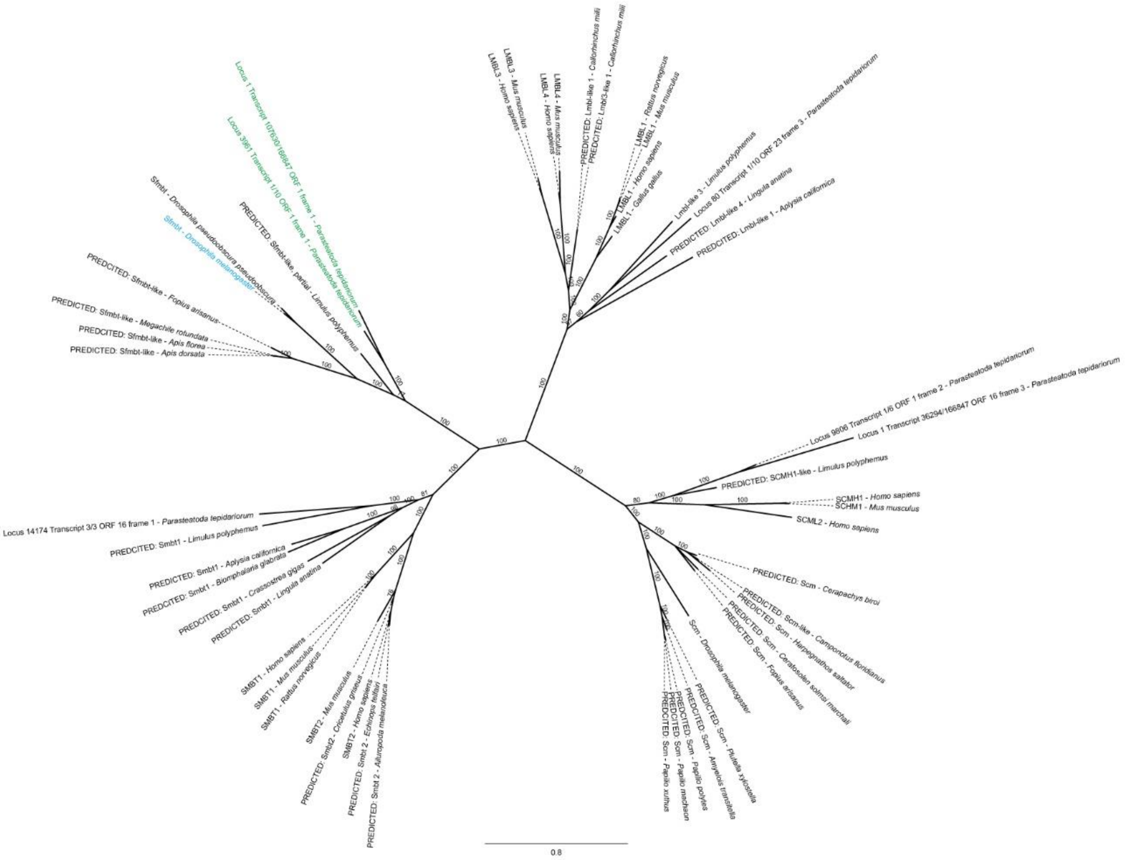

Figure 74 – Phylogenetic tree of *Sfmbt*. Branch values represent posterior probabilities of Bayesian likelihood (1484 trees sampled, AA substitution model was WAG, using sequences from an initial FastTree calculation (supplementary material 9.4.1.33). Two homologs of the *Drosophila Sfmbt* (blue) could be found (Locus 1 transcript 107630 (sfmbt-1), Locus 3961 (sfmbt-2), both green).

6.2.3.37 *Sloppy paired / FOXG*

sloppy paired (*slp*), is a forkhead domain transcription factor, is involved in the development of mesoderm derived tissue (Cripps & Olson 2002) and the specification of head segment identity through interactions with *bcd*, *dl*, *ems*, and *Kr*, among others (Grossniklaus et al. 1994). Phylogenetic analysis revealed one homolog of *slp* to be present in *P. tepidariorum* (part 5.2.2). *slp* is expressed in the pre-cheliceral head lobes in two domains on each side at stage 9. One domain in the lateral part of the neurogenic ectoderm and a smaller domain anterior of the median sulcus (white and red arrowhead, respectively in Figure 75 A). Further expression was present in segmental stripes in all prosomal and opithosomal segments (Figure 75 A, B, C). At stage 10, *slp* expression can be seen in both, the neurogenic ectoderm and the newly formed neural precursors along the anterio-posterior body axis (black arrowheads in Figure 75 D, E, F, G). In the pre-cheliceral lobes, the first domain is located in the lateral part of the anterior furrow, while the second domain is now in neural precursors at the same position as before (white and red arrowheads in Figure 75 D). At stage 12, *slp* expression in the head lobes appears in two domains in the neurogenic ectoderm, underneath the overgrowing non-neurogenic ectoderm (black arrowheads in Figure 75 H), while the segmental expression from previous stages is kept (Figure 75 I, J).

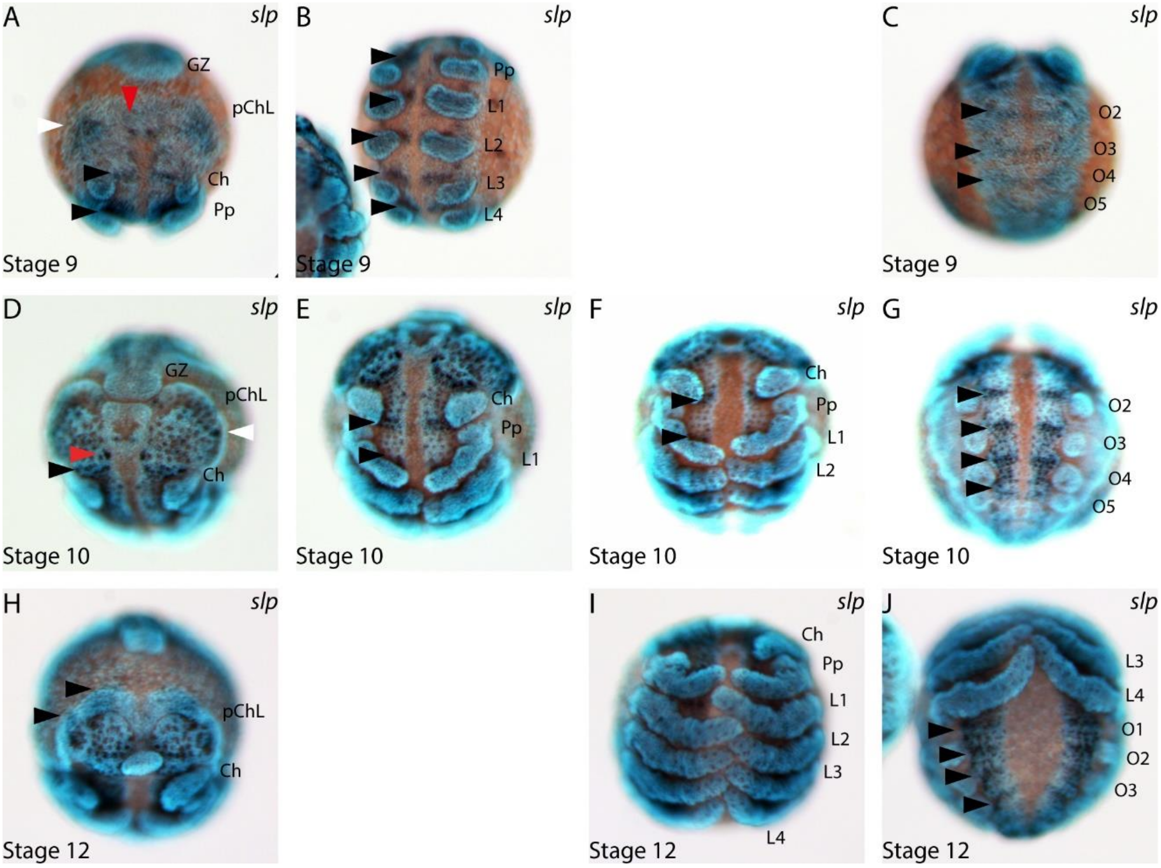

Figure 75 – Embryonic expression of *sloppy paired* in *P. tepidariorum*. *slp* is expressed in two large domains in the pre-cheliceral lobes at stage 9 (white arrowhead in A). Additional expression was present in two spots at the anterior tip of the median sulcus (red arrowhead in A) and in segmental stripes in the neuroectoderm along the body axis (black arrowheads in A, B, C). At stage 10, slp epression remains in segmental stripes and also in the newly formed neural precursors (arrowheads in D, E, F, G). The large expression domain in the pre-cheliceral lobes was located in the region of the anterior furrow. At stage 12, expression in the neural precursors is still visible (H, I, J), while the domain in the pre-cheliceral lobes is split into an anterior and a lateral part (arrowheads in in H). A, D, and H show embryos in frontal aspect. B, C, E, F, G, I, and J are ventral views with the anterior to the top.

6.2.3.38 *Tachykinin*

Tachykinin (*Tk*) is a neuropeptide hormone, which is involved in behavioural traits (Asahina et al. 2014, Winther et al. 2006), perception (Im et al. 2015, Shankar et al. 2015), and metabolic processes (Song et al. 2014). No similar sequence could be found in the transcriptome of *P. tepidariorum* via blast.

6.2.3.39 *Tailless*

tailless (*tll*) is a zinc finger transcription factor, which is involved in anterio-posterior axis formation, where it determines terminal regions via torso signaling (Leptin 1999, Strecker et al. 1991). One *tll* homolog could be identified in the transcriptome of *P. tepidariorum* (Locus 135) (Figure 76).

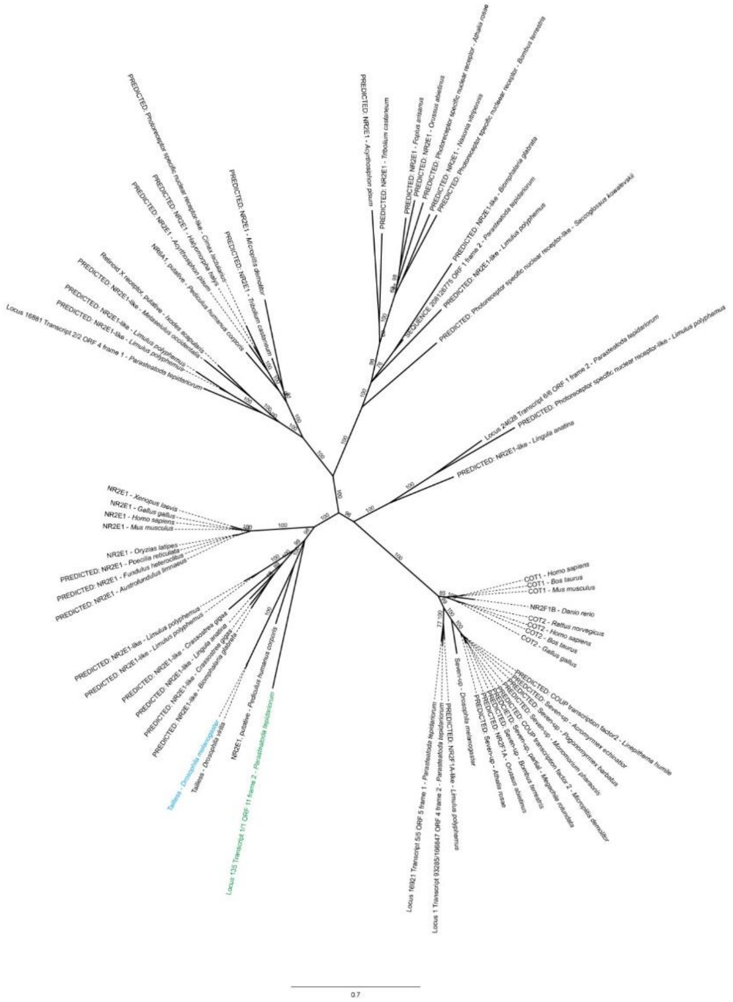

Figure 76 – Phylogenetic tree of *tll.* Branch values represent posterior probabilities of Bayesian likelihood (2934 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.34). One homolog of the *Drosophila tll* could be found (Locus 135, green).

Expression of *tll* in *P. tepidariorum* can first be seen in the pre-cheliceral lobes at stage 8 (Figure 77 A). At stage 10 and 11, *tll* is expressed on each side of the pre-cheliceral lobes in one domain at the anterior tip, next to the region of the developing stomodeum and labrum anlagen, as well as in the lateral furrow (arrowheads in Figure 77 B, C, E, F). *tll* is still expressed in the anterior region at stage 13 (Figure 77 D).

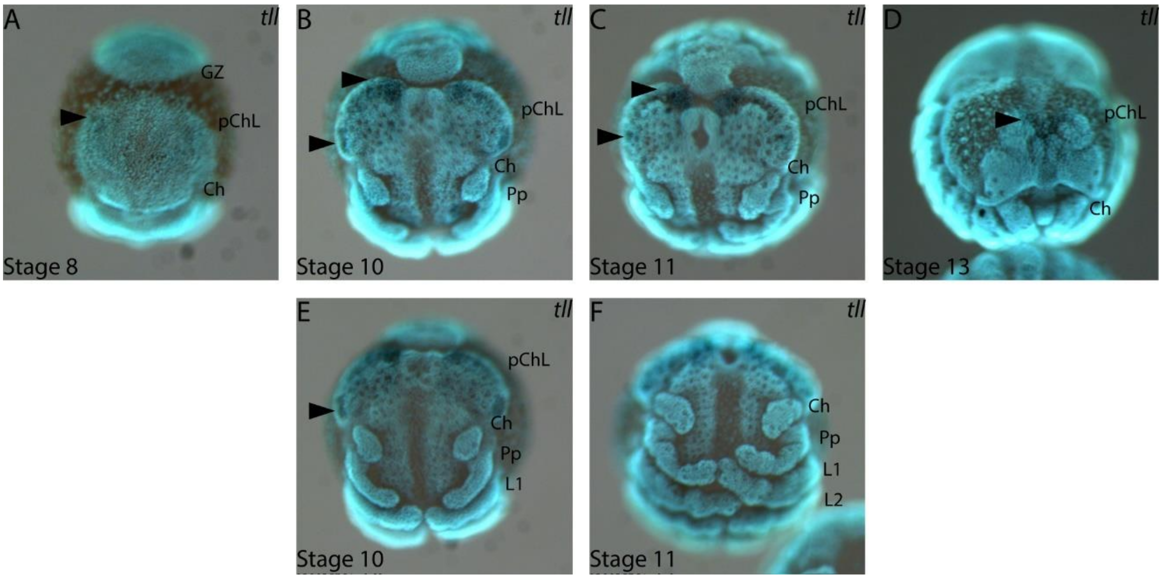

Figure 77 – Embryonic expression of *tailless* in *P. tepidariorum*. *tll* expression first appeared in two spots in the anterior pre-cheliceral lobes at stage 8 (arrowhead in A). At stage 10 and 11, expression is located at the anterior pre-cheliceral lobes adjacent to the labrum and in the lateral furrows (arrowheads in B, C, D, and E). tll is still expressed at the anterior tip of the head at stage 13 (arrowhead in D). A, B, C, and D show embryos in frontal aspect. E and F are ventral views with the anterior to the top.

6.2.3.40 *Trithorax*

trithorax (*trx*) is a methyltransferase, which acts as a transcriptional activator to maintain gene expression through histone modification (Czermin et al. 2002, Enderle et al. 2011, Petruk et al. 2006). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed one homolog of *trx* to be present (Locus 690) (Figure 78), which was ubiquitously expressed in the embryonic stages analysed (supplementary material 9.4.3.17).

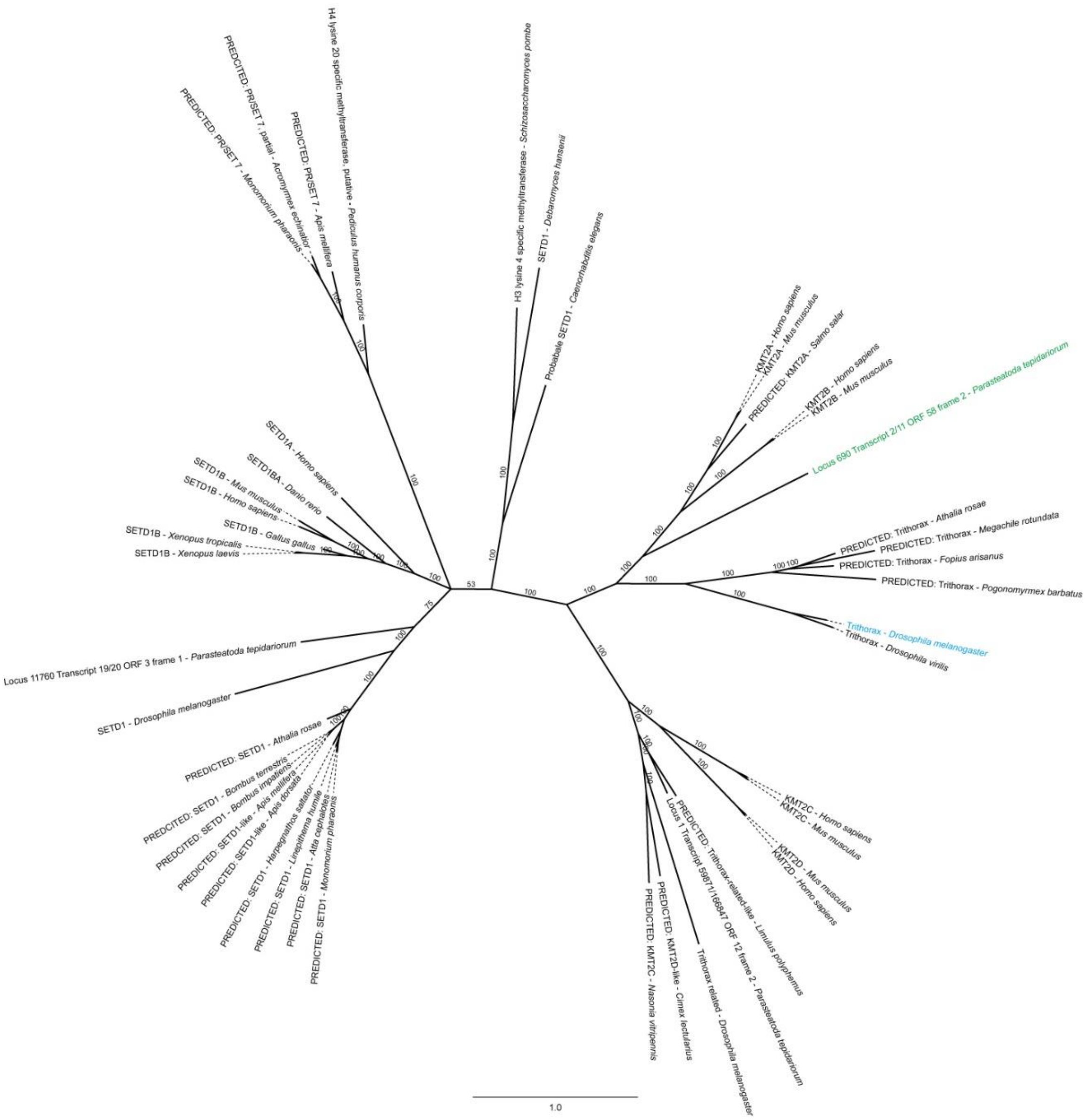

Figure 78 – Phylogenetic tree of *trx.* Branch values represent posterior probabilities of Bayesian likelihood (200 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.35). One homolog of the *Drosophila trx* (blue) could be identified (Locus 690, green)

6.2.3.41 *Ventral nervous system defective*

ventral nervous system defective (*vnd*) is a homeobox transcription factor, which is involved in the development of the central nervous system (Ball et al. 2004), determination of neuroblast fate (Skeath et al. 1994), and dorso-ventral patterning of the nervous system (Skeath & Thor 2003, Urbach & Technau 2003). Phylogenetic analysis of the *P. tepidariorum* transcriptome revealed two homologs of *vnd* in the spider (Locus 16018 (*vnd-1*), Locus 12534 (*vnd-2*)) (Figure 79).

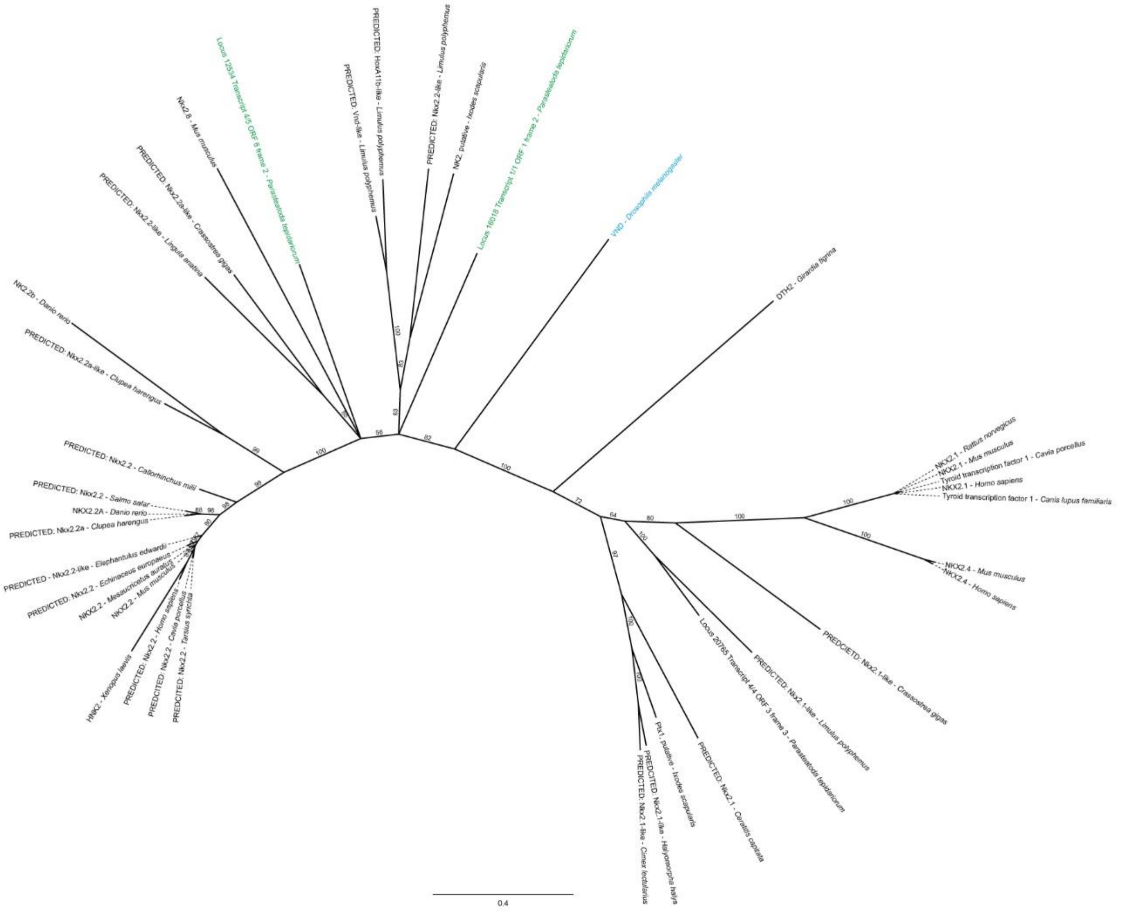

Figure 79 – Phylogenetic tree of *vnd*. Branch values represent posterior probabilities of Bayesian likelihood (4532 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.36). Two homologs of the *Drosophila vnd* (blue) could be identified (Locus 16018 (vnd-1), Locus 12534 (vnd-2), both green).

While the expression of *vnd-1* appeared to be ubiquitous in the embryonic stages analysed (Figure 80 A, B, C), the expression of *vnd-2* appears as a continuous stripe along the ventral midline and in two domains in the pre-cheliceral lobes at stage 8 (arrowheads in Figure 80 D, E). At stage 10, *vnd-2* is expressed on both sides of the median sulcus along the embryo, with commissural expression between the two stripes (Figure 80 F, G).

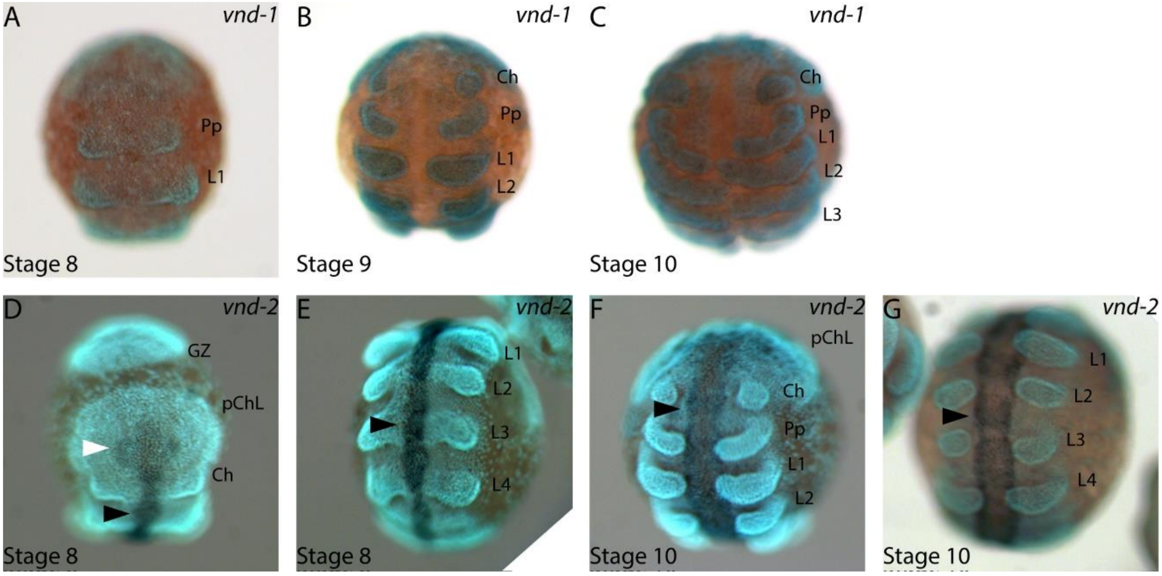

Figure 80 – Embryonic expression of *ventral nervous system defectice-1* and *ventral nervous system defective-2* in *P. tepidariorum*. *vnd-1* showed ubiquitous expression during stage 8, 9, and 10 (A, B, C). *vnd-2* is expressed in two spots in the pre-cheliceral lobes on either side of the midline (white arrowhead in D) and in one stripe along the length of the embryo (black arrowhead in D and E). At stage 10, *vnd-2* is expressed on both sides of the median sulcus (F) with commissural expression between the stripes (G). A, B, C, E, F, and G are ventral views with the anterior to the top. D is an embryo in frontal aspect.

6.2.3.42 *Vrille*

vrille (*vri*) is a transcription factor with a basic leucine zipper domain. It acts as an enhancer of *dpp* effects in embryos and wing discs of *Drosophila* (Szuplewski et al. 2003, 2010). Phylogenetic analysis of the *P. tepidariorum* transcriptome showed one homolog of *vri* in the spider (Locus 16266) (Figure 81). This homolog could not be cloned for expression analysis.

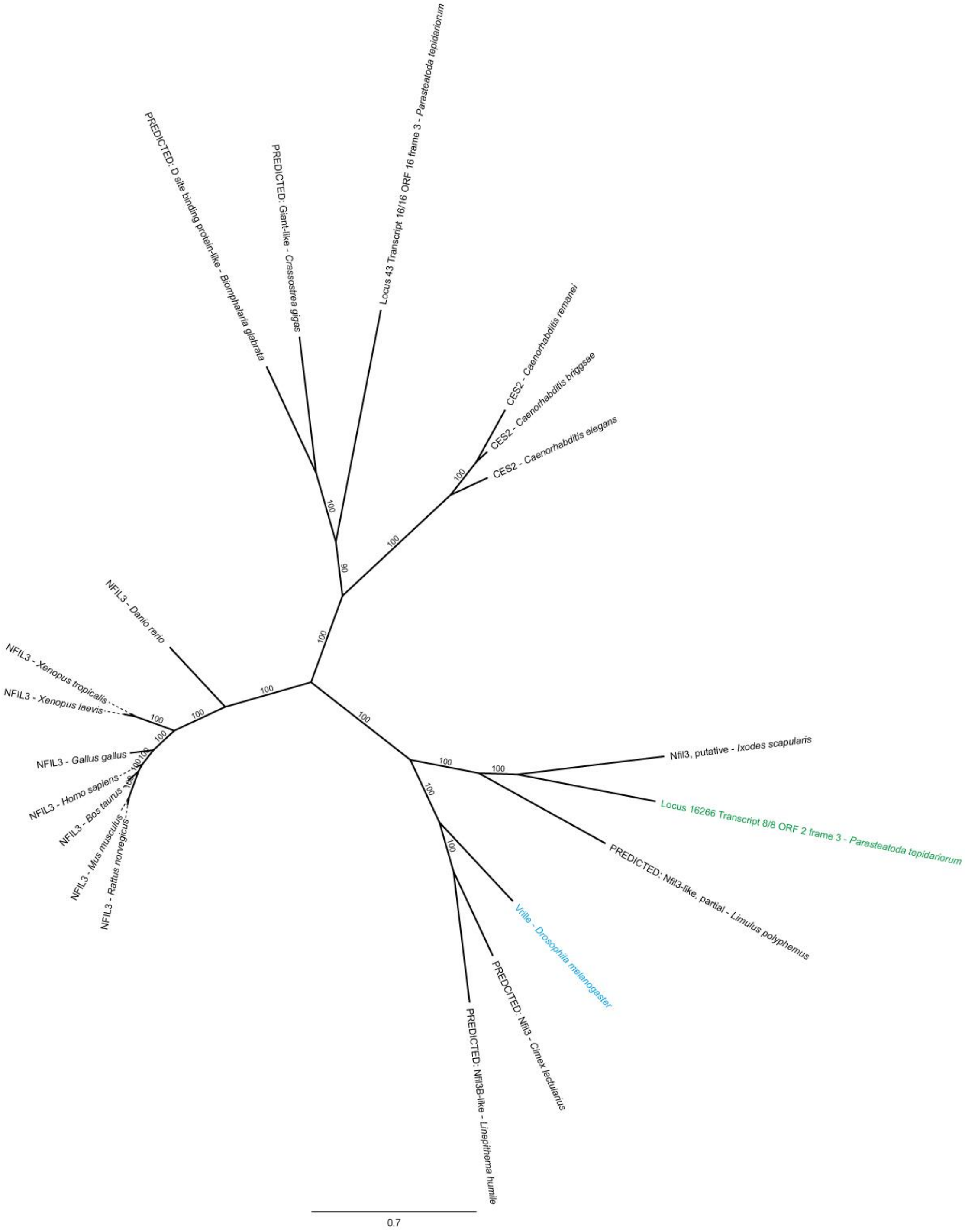

Figure 81 – Phylogenetic tree of *vri.* Branch values represent posterior probabilities of Bayesian likelihood (20 trees sampled, AA substitution model was Jones, using sequences from an initial FastTree calculation (supplementary material 9.4.1.37). One homolog of the *Drosophila vri* (blue) could be found (Locus 16266, green).

6.2.3.43 *Zeste*

zeste (*z*) is a DNA-binding protein, which is a member of Polycomb recruiters (Mulholland et al. 2003). No similar sequences could be found via blast in the transcriptome of *P. tepidariorum*.

6.3 DISCUSSION

The analysis of genes which were annotated to be expressed in the intercalary segment in Drosophila, or were known interaction partners of labial or its vertebrate homolog did not show any indication of a specific role in the pedipalps, which was different from that in the legs, based on their expression patterns (except for *extradenticle-1,* discussed below). The genes showed a similar expression in every segment in cases where specific domains were visible and most were expressed in the segment itself rather than the actual appendages. However, the genes analyzed here provided some insights into conserved and disparate aspects of the development in *Parasteatoda*.

6.3.1 Appendage patterning

Homologs of *extradenticle* and *homothorax* are involved in the patterning of limbs in the panarthropod clade (Janssen et al. 2010a). Their role in *Parasteatoda* has already been studied in detail (Zhang 2016). Both paralogs of *homothorax* and *extradenticle-2* showed no difference in expression between pedipalps and legs. Interestingly, *extradenticle-1* was differentially expressed in the two appendage types, showing a distal domain of expression in the pedipalps. The presence of this domain in *Parasteatoda* and other spiders indicated a new role for *extradenticle-2* in the development of the pedipalp. However, functional studies in *Parasteatoda* have so far failed to produce a visible phenotype for *extradenticle-1* and its specific role in the pedipalp remains unclear. Furthermore, due to the lack of expression analysis in other chelicerates, it is also unknown whether the special pedipalp expression is specific to spiders, or a general trait of chelicerates to differentiate the pedipalp from the walking legs.

6.3.2 Segmentation

A role of paired in segmentation appeared to be conserved in *Parasteatoda*, although paired is not expressed in a pair-rule pattern, but segmentally repeated. This difference has been shown for several pair-rule genes in spiders, especially members of the Pax group III (Damen et al. 2005, Schoppmeier & Damen 2005) and has been hypothesized to be the ancestral condition in arthropod segmentation (Peel et al. 2005). Arguing from the expression pattern in *Parasteatoda*, *paired* seems to have a function in the establishment of newly formed segments in the growth zone, as well as the maintenance of mature segments, indicated by the segmental expression in later stages.

tailless facilitates the determination of terminal structures in the *Drosophila* embryo (Casanova 1990, Morán & Jiménez 2006). This function is conserved among long-germ insects (Wratten et al. 2006), albeit with differences in the amount of effect at each pole and the genes needed to activate it (Lynch et al. 2006). *tailless* is also involved in the early patterning of the brain in the dorsal median region and in the optic lobes (Rudolph et al. 1997). In *Parasteatoda*, the expression in the pre-cheliceral lobes could be found in the lateral furrow, which could indicate a role for *tailless* in the early development of the optical system. Further expression was observed in the most anterior part of the pre-cheliceral lobes, at a region, which correlates with dorsal medial brain structures in later embryos. The possible involvement of *tll* in the development in terminal structures in *Parasteatoda* cannot be assumed, due to the different fate map, since *Parasteatoda* displays a short-germ mode of development (Mittmann & Wolff 2012), and also the lack of terminal expression at the posterior pole.

sloppy paired 1 in *Drosophila* is a pair-rule gene in trunk segmentation (Cadigan et al. 1994) and is also involved in the specification of head segments (Grossniklaus et al. 1994). A function in segmentation is conserved between *Drosophila* and *Tribolium*, however, *slp* in *Tribolium* is involved in the formation of even-numbered segments in contrast to *Drosophila* (Choe & Brown 2007, Choe et al. 2006). The segmental expression of *slp* in *Parasteatoda* suggests that a function in segmentation might be conserved, although *slp* seems to specify one at a time and not in a pair-rule fashion. Moreover, an expression in the neural precursors indicated a neural function and the expression in the neurogenic ectoderm in the pre-cheliceral lobes might indicate a function in the patterning of this tissue.

6.3.3 Segment identity

knot (*collier*) has been shown to fulfill several roles during development. It is involved in neuron differentiation in the peripheral nervous system (Crozatier et al. 2002, Jinushi-Nakao et al. 2007). The restriction of expression of one of the paralogs in *Parasteatoda* suggest, that this role might be conserved. *knot* has also been shown to be regulated by *labial* in the intercalary segment of *Drosophila*, where it activates the expression of segment polarity genes (Ntini & Wimmer 2011). This function in head development has been shown to be conserved in insects, but not in crustaceans and chelicerates (Schaeper et al. 2010). Since also the second, newly identified paralog of *knot* in *Parasteatoda* did not show any expression in the segment of the pedipalps, this adds to the evidence, that the role of *knot* in head development is insect-specific, and that it might be linked to the appendage-less nature of the intercalary segment.

cap ‘n’ collar is also known to be able to confer identity of head segments. It is involved in the pharyngeal development in *Drosophila* (Veraksa et al. 2000) and the development of the mandible in *Tribolium* (Coulcher & Telford 2012), in both cases through the repression of homeotic functions. A previous study proposed, that the specific expression domains of *cnc* have evolved in the mandibulata clade (Sharma et al. 2014). This is supported by the ubiquitous expression found here in *Parasteatoda* and the expression patterns from opiliones and scorpions (Sharma et al. 2014).

The forkhead gene *crocodile* has been shown to be involved in the development of head segments in insects. In *Drosophila*, lack of *crocodile* leads to various head defects (Häcker et al. 1995) and in *Tribolium* it is involved in the patterning of the anterior median region and is required for the correct formation of the stomodeum (Kittelmann et al. 2013). The anterior expression domains of crocodile are conserved among insects and myriapods (Birkan et al. 2011, Janssen et al. 2011). This indicates a conserved role for this gene in head development. The expression pattern in *Parasteatoda* indicated that also here crocodile is involved in the patterning of the stomodeal region. Interestingly, *crocodile* showed segmental expression in the mesoderm in the earlier stages, which had not been reported for other arthropods, but correlates to mesodermal expression in Drosophila (Tomancak et al. 2002, 2007).

empty spiracles acts as a gap gene during the head development of *Drosophila* and is involved in the development of the tracheal system, as well as the determination of neuroblast identity in various segments (Ebner et al. 2002, Urbach & Technau 2003). It is involved in the development of the antennae in *Tribolium* and the expression in the trunk was conserved (Schinko et al. 2008). Expression patterns in *Parasteatoda* suggested a conserved role for ems in neural development through its expression in neural precursor groups (*ems-3*), but did not seem to be involved in the anterior segment development different from other segments. Additionally, *ems* in *Parasteatoda* did not seem to be involved in the development of the trachea, which would have been an example of the convergent use of genes, since tracheae in spiders develop from the 3rd opithosomal segment only and are not homologous to the tracheal system in insects (Foelix 2011).

6.3.4 Adhesion

dachsous is a member of the cadherin family and is involved in morphogenesis of wings and legs in *Drosophila*, especially affecting tarsal segmentation (Clark et al. 1995). *dachsous* acts together with *fat*, *four-jointed*, and *dachs* via the planar cell polarity pathway along the proximo-distal axis (Cho & Irvine 2004, Matakatsu & Blair 2004). Strong expression in the distal part of the appendages in *Parasteatoda* might indicate a conserved role in patterning of this region between *Drosophila* and *Parasteatoda*.

fasciclin 2 is another cell adhesion molecule, which has been shown to be involved in the morphogenesis of the male genital structures in *Drosophila* (Adám et al. 2003). Expression of *fasciclin 2* homologs in *Parasteatoda* suggest, that it might be involved in general adhesion processes (*fas2-3*) and that it also marks certain groups of neural precursors in the developing nervous system (*fas2-1*), as in *Drosophila* (Urbach & Technau 2003).

6.3.5 Similarities in neurogenesis of spiders and insects

Neuroblasts in *Drosophila* develop from a field of cells in the neuroectoderm, which expresses several pro-neural genes, such as *achaete*, *scute*, and *lethal of scute* (Skeath & Thor 2003). While the establishment of neural precursors by *achaete-scute* genes and the subsequent lateral inhibition in these groups by Delta / Notch signalling is regarded to be generally conserved in spiders (Stollewerk 2002, Stollewerk et al. 2003), the exact mechanisms of providing pro-neural identity appear to be different since a homolog of *lethal of scute* is missing in *Parasteatoda*. Moreover, the mechanisms of separating neural precursors are different. While in *Drosophila* single neuroblasts delaminate from the neuro-ectoderm, there are several rounds of delamination of a larger group of cells, called neural progenitor groups (Stollewerk 2002). The expression pattern of *hkb-1* in *Parasteatoda* neural precursor groups suggests a conserved role for *hkb-1* in the determination of neural precursors in the neuroectoderm. The expression domains of *wingless* (Janssen et al. 2010b) correlating with early *hkb-1* expression suggest that at least part of its regulation is conserved (McDonald & Doe 1997), since no expression of the *gsb* homolog was observed in a segment polarity fashion in *Parasteatoda*. The homolog of *sloppy paired* in *Parasteatoda* showed great similarity to the *Drosophila* homologs. *slp* was expressed in segmental stripes in every segment during stage 9, where anterior expression was stronger than in the posterior part of the embryo. This correlated with the temporal gradient of segment establishment in *Parasteatoda* and indicates a role for slp in the maintenance of segment boundaries as in *Drosophila* (Cadigan et al. 1994). Moreover, *slp* expression in later stages is not seen in segmental stripes, but in cells of the nervous system as in *Drosophila* (Tomancak et al. 2002, 2007).

Neuroblast identity along the dorso-ventral axis in *Drosophila* is achieved through the expression of the columnar genes *vnd*, *ind*, and *Drop* (Skeath 1999). While the expression of *vnd* and *Drop-3* in *Parasteatoda* appeared to be conserved between insects and spiders, and the analysis of *Drop* in *Cupiennius salei* suggest functional conservation (Döffinger & Stollewerk 2010), the lack of a homolog of *ind* indicates differences in the establishment of dorso-ventral identity among neuroblasts in contrast to neural precursor groups.

Neuroblasts in *Drosophila* display a well defined temporal cascade, in which *hb*, *Kr*, *Pdm*, and *castor* are expressed in this exact order and only transiently to provide their progeny with unique identities (Isshiki et al. 2001). While the expression patterns of *pdm* and *castor* in *Parasteatoda* are unknown, the homolog of *hunchback* is expressed in the nervous system like in other arthropods (Schwager et al. 2009). Additionally, the expression pattern of *Kr-1* in *Parasteatoda* displayed temporal dynamics, showing an anterio-posterior gradient, with the exception of a small subset of neural precursors in the leg-bearing segments that were established early on. The timing and dynamics of *Kr-1* expression after the establishment of neural precursors in early stage 9 (Mittmann & Wolff 2012) suggests the presence of a mechanism for temporal identity in the neural precursor groups.

The expression of the *klu* homolog also suggested conserved functions of this gene between *Parasteatoda* and *Drosophila*. *Klu*, in *Drosophila*, provides identity to a subset of neuroblast lineages (Yang et al. 1997) and also in *Parasteatoda* it is expressed in a subset of neural precursor groups. Additionally, *klu* plays a role in bristle and leg development in *Drosophila*, where it is involved in the differentiation of sensory organ mother cells and the formation of legs joints (Klein

& Campos-Ortega 1997). In *Parasteatoda* it was also expressed in the invagination sites of sensory precursors in the legs, as well as in faint rings in the developing leg joints.

A difference between the developments of *Drosophila* and *Parasteatoda* nervous systems could also be observed in the establishment of glia cells. In *Drosophila*, the gene *glia cells missing* acts as a switch to determine glia fate instead of neuronal fate (Hosoya et al. 1995, Jones et al. 1995). *gcm* subsequently activates the pan-neural glia marker *repo* (Granderath & Klämbt 1999, Lee & Jones 2005). Since a homolog of *gcm* is missing in *Parasteatoda*, the determination of glial fate must be initiated differently. Additionally, the expression of the one cloned repo homolog showed expression in specific areas of the pre-cheliceral lobes. Whether its paralog is conserved as a marker for glia development needs to be determined.

While the earlier aspects of neurogenesis appear to be conserved among most bilaterian lineages, the exact mechanisms leading to diversity among neural precursors are understudied in arthropods other than *Drosophila* (Hartenstein & Stollewerk 2015). Based on the analysis of the expression patterns here, many of the genes involved in this process appear to be conserved in spiders. Homologs of *empty spiracles*, *hunchback*, *sloppy-paired*, *huckebein*, *Drop*, *dachshund*, *fasciclin-2*, and *klumpfuss* all mark groups of neural precursor groups in the nervous system of *Drosophila*. However, *otd*, *tailless*, *gooseberry*, *vnd*, and the *pax6* homologs do not. Whether this partly shared expression in neuroblasts and neural precursor groups represents a synapomorphy of the arthropods, or is a plesiomorphic tracing from non-arthropod ancestors, or is even the result of convergent evolution by which the same developmental genes were co-opted during neurogenesis independently in different arthropod groups, is currently not certain, especially for lack of comparison between neuroblasts in *Drosophila* and neural precursor groups in *Parasteatoda*.

6.3.6 Ubiquitously expressed genes / genes with no expression

All the homologs of genes, which in other organisms are involved in chromatin remodeling or the assignment of a certain transcriptional state (*CtBP*, *E(z)*, *hmgb1*, *Pc*, *ph-p*, *pho*, *sfmbt*, *trx*) (Courey & Jia 2001, Schuettengruber et al. 2007) were ubiquitously expressed in *Parasteatoda*. Since these proteins are parts of complexes, which facilitate the respective functions (Cao et al. 2002, Czermin et al. 2002), they are all known to be expressed ubiquitously and depend on their recruitment by DNA binding proteins, which bind to *Polycomb*- or *trithorax*-responsive elements on the genome (Schuettengruber et al. 2007). The same was true for transcriptional repressor CTCF, which confers the blocking of enhancers through insulator elements (Mohan et al. 2007, Moon et al. 2005). Also, the homolog of *Medea* showed ubiquitous expression, as was shown for *Drosophila* (Tomancak et al. 2002, 2007) and expected for a gene, which is involved in the transduction of TGF-beta-like signals (Das et al. 1998, Marquez et al. 2001), that rely on the correct spatio-temporal activation by factors from the outside rather than the specific expression of effectors themselves.

daughterless is involved in the sex-specific development in *Drosophila* by interpreting the ratio of gonosomes to autosomes (Schütt & Nöthiger 2000). As in *Drosophila* (Cronmiller & Cummings 1993), *daughterless* was expressed ubiquitously in *Parasteatoda*. However, since the molecular mechanisms of the sex-determination system in chelicerates are unknown, no conclusion can be drawn on the role of *daughterless* in *Parasteatoda*.

dorsal homologs were also found to be ubiquitously expressed in *Parasteatoda*. In *Drosophila*, it establishes dorso-ventral patterning of body axis through a nuclear concentration gradient of the protein (Lall & Patel 2001), and is also involved in the immune response after injury (Lemaitre et al. 1995). While the specification of the dorso-ventral axis in *Parasteatoda* has been shown to be facilitated by the migration of cells of the cumulus (Akiyama-Oda & Oda 2006), and thus by a mechanism apparently not dependent on dorsal function, an immune-specific role of dorsal might be conserved.

The zinc finger domain gene *ovo/shaven-baby* is involved in many aspects of *Drosophila* development, such as the sex-determination in the germ-line (Oliver et al. 1990, Williamson & Lehmann 1996), the control of cell shape of epidermal tissues (Chanut-Delalande et al. 2006), and the formation of joints in the legs (Pueyo & Couso 2011). The homolog in *Parasteatoda* did not seem to be involved in these processes for lack of expression during embryogenesis.

6.3.7 Other conserved factors

The role of the homologs of *pax6* and *otd* in the development of eyes has already been discussed above. Both factors were involved in the differentiation of the eye types and did not show any expression, which would indicate that they are involved in making the pedipalps different from other appendages.

In summary, based on the expression patterns presented in this work, there seems to be no evidence that *Drosophila* has retained ancient features of a specific expression or interaction of genes from ancestors with appendages on the intercalary segment. Moreover, the duplication of genes in *Parasteatoda*, which are expressed in the intercalary segment in *Drosophila* did not show any specification to the pedipalp in the spider. The major part of the genes identified appeared to be involved in processes such as segmentation and the development of the nervous system, which are the only features retained in the intercalary segment in insects.

7 Development of the bulbus organ of adult males in *Parasteatoda tepidariorum*

7.1 INTRODUCTION

7.1.1 Pedipalps

Pedipalps are the appendages of the tritocerebral segment of all extant chelicerates (Dunlop & Lamsdell 2016). They have a leg-like morphology, but lack one podomere, the metatarsus, and in spiders the coxa posses a shovel-like outgrowth, the gnathendite, which is used during feeding (Prpic & Damen 2008) (Figure 82). Apart from this role in feeding behavior, the pedipalp is also one of the spiders' main structure for sensory perception. Chemosensitive hairs are used for food recognition, mechano-sensitive sensilla detect vibration, trichobothria are used to pick up air movements, and a specialized organ in the tarsal segment is used to perceive humidity and temperature (summarized in Barth 2001). Moreover, the pedipalps are heavily involved in mating behavior. In some species, acoustic signals produced by the pedipalps (Uetz & Stratton 1983), as well as waving movements are used to attract mating partners (Foelix 2011). Other examples include males following a pheromone trail, which is sensed with the pedipalps (Foelix 2011).

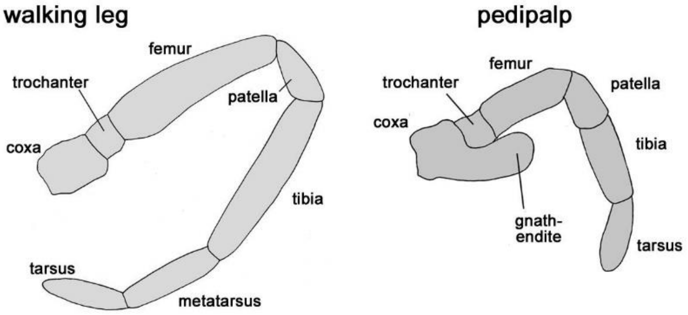

Figure 82 – Schematic depictions of walking leg and pedipalp morphologies in spiders. The walking legs consist out of 7 segments: coxa, trochanter, femur, the chelicerate specific patella, tibia, metatarsus, and tarsus. In contrast, the pedipalp lack the metatarsus and have an additional outgrowth at the base of the coxa, the ganthendite. (modified from Pechmann et al. 2010)

7.1.2 Pedipalp adaptations

Pedipalps of the chelicerates show a large variety of specialized adaptations. While the pedipalps in hooded tickspider (Ricinulei) and micro-whip scorpions (Palpigradi) function as an additional pair of walking legs (Talarico et al. 2008), scorpions, whip scorpions (Uropygi), and whip spiders (Amblypygi) use their pedipalps for prey capture and immobilization with chelae and cuticular spikes (Polis 1990; Weygoldt 1971, 1996). A special function of the pedipalps can be seen in the camel spiders (Solifugae), which have evolved an adhesive organ at the tip of the tarsus, which is used in prey capture (Klann et al. 2008, Willemart et al. 2011). A great diversity of pedipalp morphologies is present in the group of harvestmen (Opiliones), where they can have leg-like characteristics, are used for prey capture with spines or sticky secretions (Wolff et al. 2016), and pedipalps are even used in male-male aggressive behavior (Willemart et al. 2006).

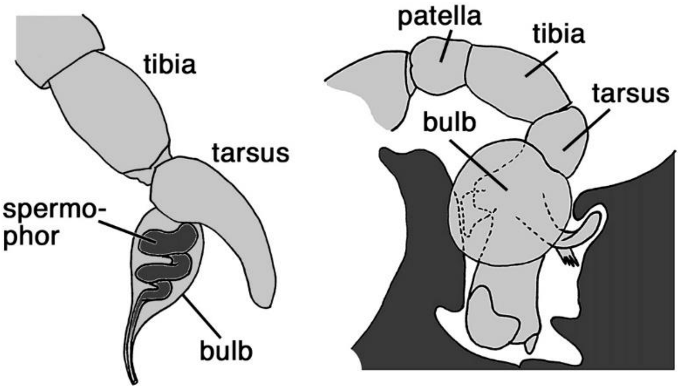

Figure 83 – Schematic depiction of the bulbus organ of spiders. Left: the bulb apparatus is an outgrowth of the tarsus, which contains the spermophore in which sperm can be taken up and stored. Right: Interaction of parts of the bulb apparatus with the female genital opening (dark grey). An example for the lock-and-key fitting mechanism during copulation. (modified from Pechmann et al. 2010)

One of the most elaborate adaptations of the pedipalp can be seen in spiders. Here, the male spider uses its pedipalp as a copulatory organ. While most other male chelicerates produce a spermatophore, which has to be taken up by the female (Proctor 1998), or even have a mode of external fertilization, like Limulus polyphemus (brockmann 1990), the male spider pedipalp shows a structure adapted for this purpose. The tarsus possesses an outgrowth called the bulb apparatus (Figure 83). In its simplest form, the bulb apparatus is a fleshy pipette-like structure, which is used to aspirate sperm fluid, store it and discharge it into the female genital opening. In most species however, the bulb apparatus is surrounded by a number of sclerites (Figure 84), which species-specifically fit the female structures and aid during copulation. In the resting state, the structure is collapsed so that the embolus is protected from damage, but in preparation for copulation, the bulb apparatus expands and the sclerites project from the rest of the palp. For instance, the median apophysis hooks onto a process of the female epigynum and through an increase in hemolymph pressure the tegulum and conductor rotate and open the epigyne for the embolus.

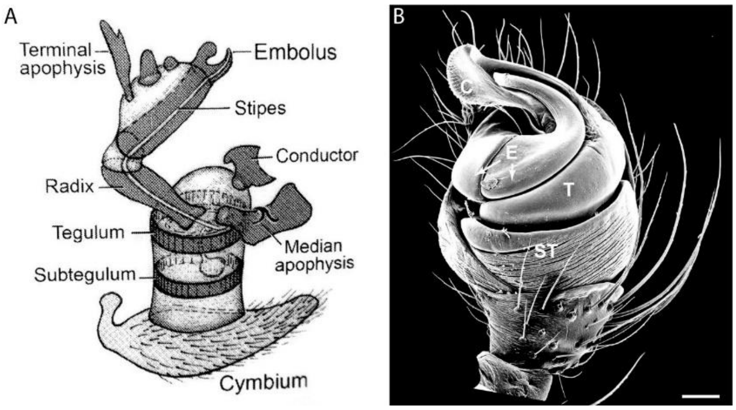

Figure 84 – Parts of the bulb apparatus. A - Schematic representation of the sclerites of the bulb apparatus located on the inflatable soft hematodocha (Foelix 2011). B – Scanning electron microscopy of the bulb apparatus of *P. tepidariorum* in its resting position locken in the cymbium, showing the subtegulum (ST), tegulum (T), embolus (E), and conductor (C) (modified from Agnarsson et al. 2007).

7.1.3 Metamorphosis

The male specific structures of the adult pedipalp do not appear during embryogenesis, or develop progressively throughout the nymphal stages, but results from a metamorphosis-like event in the last nymphal (subadult) and adult stage. The first evidence of the bulb apparatus can be seen in the subadult males, in which the distal part of the pedipalp thickens (Figure 84 B), until after the final molt the functional structure is everted. The underlying developmental processes have only been studied morphologically in a few cases (Coddington 1990). The development is started by invaginating cells at the distal tip of the tarsus, which then undergo a phase of differential growth, establishing the primordia of the single elements of the bulb apparatus. This process is reminiscent of the role of imaginal cells during the metamorphosis of holometabolous insects. However, it is not known if this is a superficial resemblance, or if there are more mechanistic similarities is unknown, especially since no studies have been undertaken to identify genes, which might be involved in the process of bulb apparatus development. For instance, is there patterning of precursor cells before the establishment of the actual structure like in the imaginal discs in *Drosophila* or is there a growth in undifferentiated tissue first with subsequent patterning.

Figure 85 – Developmental stages of the male pedipalp in *P. tepidariorum*. A – juvenile pedipalp with no difference to the female morphology. B – Subadult male pedipalp with thickened distal structure. C – Adult male pedipalp with fully developed sclerites.

7.1.4 Aim

To identify genes, which are involved in the development of the male pedipalp, the transcriptomes of opisthosomas, legs, and pedipalps of juvenile spiders, subadult males, age-matched females, and adult males were generated. The differential expression of genes was analyzed between the pedipalps and other tissues among the different samples to investigate genes, which might be involved in the differentiation of the pedipalps from the legs and opisthosoma. The differential expression of genes was also analyzed between the different pedipalp samples, in order to identify genes, which might be responsible for the male specific development of the pedipalp from juvenile to adult male and the sex-specific development of male and female pedipalps (Figure 86). Moreover, the expression profiles of genes among the male samples was analyzed in order to establish a more detailed view of the temporal activity of genes and processes involved in the post embryonic development of the male spiders.

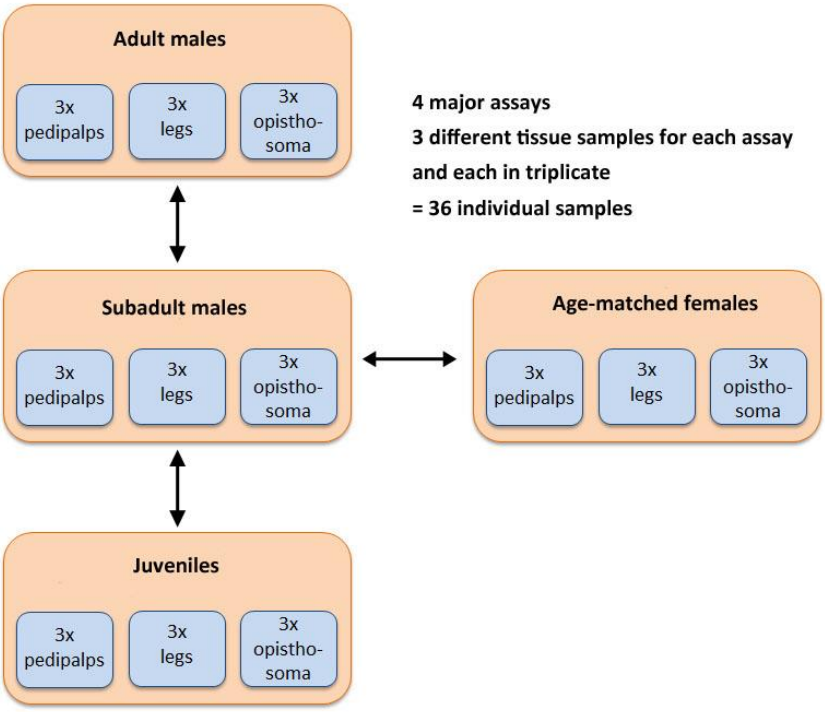

Figure 86 – Overview over samples for sequencing.Pedipalps, legs, and opisthosomas were sampled in triplicates from juvenile spiders, subadult males, subadult females and adult males. The resulting transcriptomes were analyzed for differentially expressed genes between the pedipalps and the other tissues of the respective samples, and the pedipalps of the different stages and sexes.

7.2 RESULTS

7.2.1 Differentially expressed genes

7.2.1.1 *Juveniles*

Analysis of differentially expressed genes among the tissues of juvenile spiders showed comparably large differences between the appendages and the opisthosoma. 15,819 genes were differentially expressed between the juvenile pedipalps and the opisthosoma (6812 up-regulated, 9007 down-regulated) (Figure 87 A). 14,819 genes were differentially expressed between the legs and the opisthosoma (6073 up-regulated, 8746 down-regulated) (Figure 87 C). A smaller number of 2206 genes were differentially expressed between the two appendage types, pedipalps and legs. (780 up-regulated, 1426 down-regulated) (Figure 87 B).

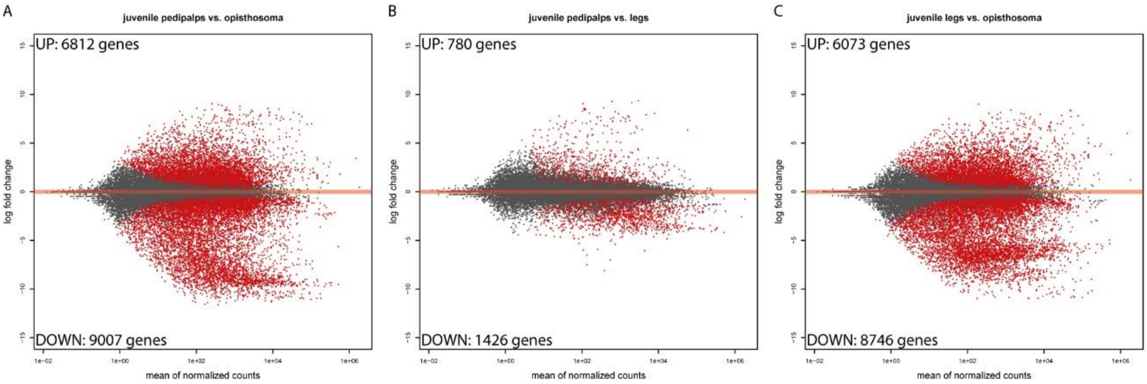

Figure 87 -Differentially expressed genes between the juvenile tissues. 15,819 genes were differentially expressed between the juvenile pedipalps and the opisthosoma (6812 up-regulated, 9007 down-regulated) (A). 2206 genes were differentially expressed between the pedipalps and the legs (780 up-regulated, 1426 down-regulated) (B). 14,819 genes were differentially expressed between the legs and the opisthosoma (6073 up-regulated, 8746 down-regulated) (C). Red dots in A, B, and C represent significantly differentially expressed genes with p-adjusted below 0.05. The log fold change refers to the ratio of a gene's normalized expression values in the two conditions on a log2 scale.

In order to get a more specific insight into the differentially expressed genes in the different tissues at the juvenile stage, the differentially expressed genes were analysed for their presence in different comparisons (Figure 88). 9936 genes (3767 up-regulated, 6169 down-regulated) were differentially expressed between the appendages (legs and pedipalps) and the opisthosoma, without being differentially expressed between pedipalps and legs as well, showing these genes to be appendage specific. 338 genes (222 up-regulated, 116 down-regulated) were differentially expressed in both comparisons of the pedipalps with the other two tissues, without being differentially expressed between the legs and the opisthosoma as well, making them pedipalp-specific differentially expressed genes.

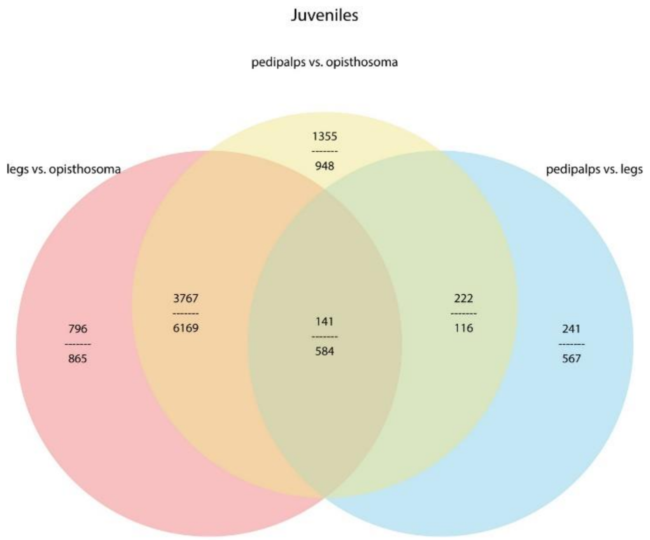

Figure 88 – Venn diagram showing the overlap of genes differentially expressed in juveniles among the different comparisons. Numbers above the fraction bar indicate the amount of genes that were up-regulated in the single or shared comparisons, while number below the fraction bar in dicate the amount of down-regulated genes.

The lists of appendage- and pedipalp-specific genes were analysed for the enrichment of GO-terms in order to get a better picture of the processes, which are happening in the juvenile stage (Table 7, **Fehler! Verweisquelle konnte nicht gefunden werden.**). The appendage-specifically up-regulated genes were enriched for metabolic processes, as well as morphogenesis and development of anatomical structures, adhedion, and regulation. The pedipalp-specific genes mainly showed enrichment for terms related to the activity of ion channels (Table 7).

Table 7 – GO terms enriched in genes up-regulated in juvenile appendages and pedipalps.

Up-regulated in juvenile appendages			
category	**over-represented pvalue**	**term**	**ontology**
GO:0044767	9.32E-68	single-organism developmental process	BP
GO:0032501	9.65E-67	multicellular organismal process	BP
GO:0044707	3.10E-66	single-multicellular organism process	BP
GO:0032502	5.29E-48	developmental process	BP
GO:0048856	3.65E-45	anatomical structure development	BP
GO:0009653	2.22E-43	anatomical structure morphogenesis	BP
GO:0022610	9.64E-43	biological adhesion	BP
GO:0007155	6.52E-42	cell adhesion	BP
GO:0048869	1.71E-39	cellular developmental process	BP
GO:0065007	3.86E-39	biological regulation	BP
GO:0050789	1.64E-37	regulation of biological process	BP
GO:0050794	3.66E-37	regulation of cellular process	BP
GO:0022836	1.06E-32	gated channel activity	MF
GO:0007610	1.66E-32	behavior	BP

GO:0003008	2.27E-31	system process	BP
Up-regulated in juvenile pedipalps			
category	**over-represented pvalue**	**term**	**ontology**
GO:0006887	6.31E-11	exocytosis	BP
GO:0015280	1.34E-10	ligand-gated sodium channel activity	MF
GO:0015081	5.67E-10	sodium ion transmembrane transporter activity	MF
GO:0032940	6.29E-09	secretion by cell	BP
GO:0005272	9.55E-09	sodium channel activity	MF
GO:0046903	7.88E-08	secretion	BP
GO:0015276	3.33E-07	ligand-gated ion channel activity	MF
GO:0022834	3.33E-07	ligand-gated channel activity	MF
GO:0080019	3.47E-07	fatty-acyl-CoA reductase (alcohol-forming) activity	MF
GO:0006968	1.18E-06	cellular defense response	BP
GO:0005216	2.14E-06	ion channel activity	MF
GO:0035725	2.25E-06	sodium ion transmembrane transport	BP
GO:0022836	2.31E-06	gated channel activity	MF
GO:0004317	2.72E-06	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity	MF
GO:0004319	2.72E-06	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity	MF

Genes that were specifically down-regulated in the appendages were enriched for metabolic enzyme activities and transport activities, while genes specifically down-regulated in the juvenile pedipalps were enriched for terms related to the development of muscle tissue (supplementary material 9.5.2.1).

7.2.1.2 *Subadult females*

Analysis of differentially expressed genes between the sequenced tissues of subadult females showed large differences between the appendage types and the opisthosoma (Figure 89). 17,985 genes (8383 up-regulated, 9602 down-regulated) were differentially expressed between the subadult female pedipalps and the opisthosoma (Figure 89 A). A comparable number of genes were differentially expressed between the legs and the opisthosoma (7491 up-regulated, 9090 down-regulated, 16581 total) (Figure 89 C). With 5005, the number of genes differentially expressed between pedipalps and legs was again smaller than in the other tissues comparisons (2538 up-regulated, 2467 down-regulated) (Figure 89 B).

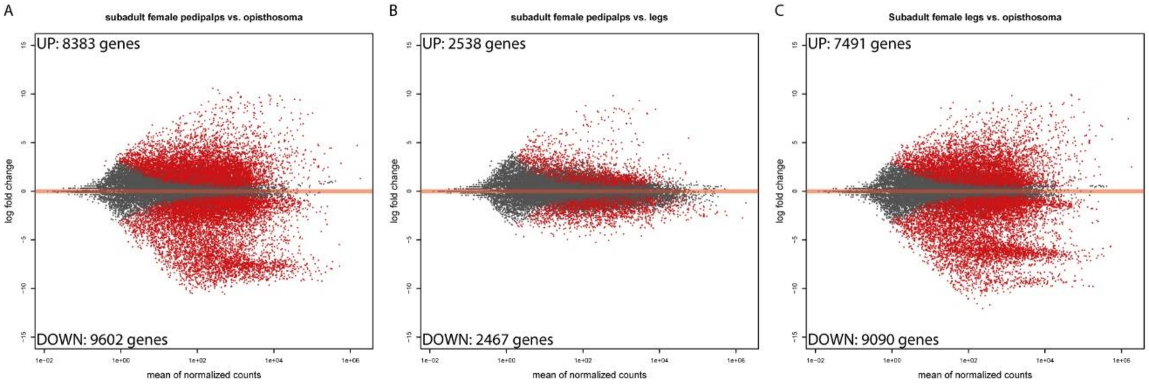

Figure 89 – Differentially expressed genes between the subadult female tissues. 17,985 genes were differentially expressed between the subadult female pedipalps and the opisthosoma (8383 up-regulated, 9602 down-regulated) (A). 5005 genes were differentially expressed between the pedipalps and the legs (2538 up-regulated, 2467 down-regulated) (B). 16,581 genes were differentially expressed between the legs and the opithosoma (7491 up-regulated, 9090 down-regulated) (C). Red dots in A, B, and C represent significantly differentially expressed genes with p-adjusted below 0.05. The log fold change refers to the ratio of a gene’s normalized expression values in the two conditions on a log2 scale.

Of these differentially expressed genes, 11,029 were specific to the appendages. 4497 genes up-regulated and 6532 genes down-regulated, shared for pedipalps and legs compared to the opisthosoma, without being differentially expressed between the appendages themselves (Figure 90). In the subadult females, 1242 differentially expressed genes were shared by the comparisons of pedipalps with legs and opisthosoma, without being differentially expressed between legs and opisthosoma, making them pedipalp specific genes (Figure 90).

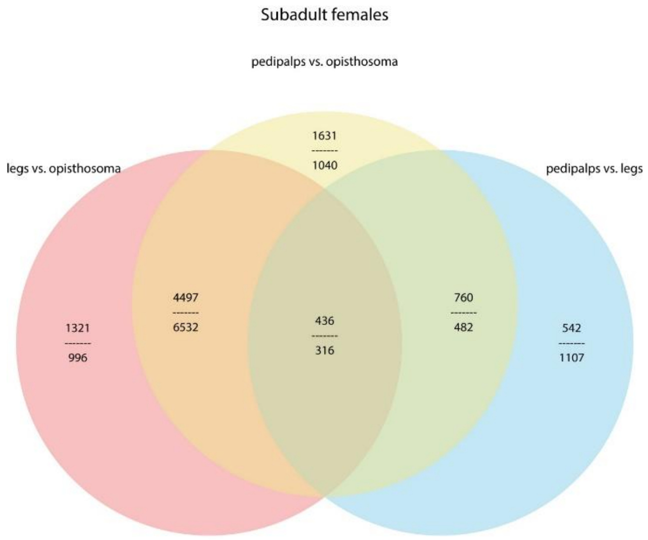

Figure 90 – Venn diagram showing the overlap of genes differentially expressed in subadult females among the different comparisons. Numbers above the fraction bar indicate the amount of genes that were up-regulated in the single or shared comparisons, while number below the fraction bar in dicate the amount of down-regulated genes.

Genes that were specifically up-regulated in the subadult female appendages, showed enrichment for GO-terms associated with the activity of membrane channels and adhesion. The enrichment in terms related to the activity of channels was shared by the pedipalp specific genes at this stage. Additionally, this set showed enrichment for exocytosis and secretion (Table 8).

Table 8 – GO terms enriched in up-regulated genes of appendages and pedipalps of subadult females.

Up-regulated in subadult female appendages			
category	**over represented pvalue**	**term**	**ontology**
GO:0032501	3.24E-50	multicellular organismal process	BP
GO:0044707	4.93E-50	single-multicellular organism process	BP
GO:0044767	4.94E-37	single-organism developmental process	BP
GO:0022836	5.59E-31	gated channel activity	MF
GO:0048856	4.59E-29	anatomical structure development	BP
GO:0005216	4.46E-27	ion channel activity	MF
GO:0022610	1.87E-26	biological adhesion	BP
GO:0022838	1.91E-26	substrate-specific channel activity	MF
GO:0007155	3.85E-26	cell adhesion	BP
GO:0015267	4.14E-26	channel activity	MF
GO:0022803	4.14E-26	passive transmembrane transporter activity	MF
GO:0032502	6.85E-26	developmental process	BP
GO:0007610	6.97E-26	behavior	BP
GO:0007165	5.63E-24	signal transduction	BP
GO:0060089	9.17E-24	molecular transducer activity	MF
Up-regulated in subadult female pedipalps			
category	**over represented pvalue**	**term**	**ontology**
GO:0006887	6.31E-11	exocytosis	BP
GO:0015280	1.34E-10	ligand-gated sodium channel activity	MF
GO:0015081	5.67E-10	sodium ion transmembrane transporter activity	MF
GO:0032940	6.29E-09	secretion by cell	BP
GO:0005272	9.55E-09	sodium channel activity	MF
GO:0046903	7.88E-08	secretion	BP
GO:0015276	3.33E-07	ligand-gated ion channel activity	MF
GO:0022834	3.33E-07	ligand-gated channel activity	MF
GO:0080019	3.47E-07	fatty-acyl-CoA reductase (alcohol-forming) activity	MF
GO:0006968	1.18E-06	cellular defense response	BP
GO:0005216	2.14E-06	ion channel activity	MF
GO:0035725	2.25E-06	sodium ion transmembrane transport	BP
GO:0022836	2.31E-06	gated channel activity	MF
GO:0004317	2.72E-06	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity	MF
GO:0004319	2.72E-06	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity	MF

Down-regulated genes in the subadult female appendages were enriched for GO-terms with transporter activity and enzymatic activity. The genes specifically down-regulated in the pedipalps showed enrichment for posttranscriptional regulation of gene expression and terms involving peroxisomal processes (supplementary material 9.5.2.2).

7.2.1.3 *Subadult males*

In the subadult male tissues a large number of genes was differentially expressed between the pedipalps and the opisthosoma (7226 up-regulated, 9315 down-regulated, 16,541 total) (Figure 91 A). A comparable amount of genes was differentially expressed in the comparison of legs and opisthosoma at this stage (6669 up-reguated, 9294 down-regulated, 15,963 total) (Figure 91 C). In contrast to the the other stages amalysed, a larger number of genes was also differentially expressed between the pediapalps and the legs. 10,189 genes were differentially expressed between the two appendage types, with 4582 genes up-regulated in the pedipalps and 5607 genes down-regulated (Figure 91 B).

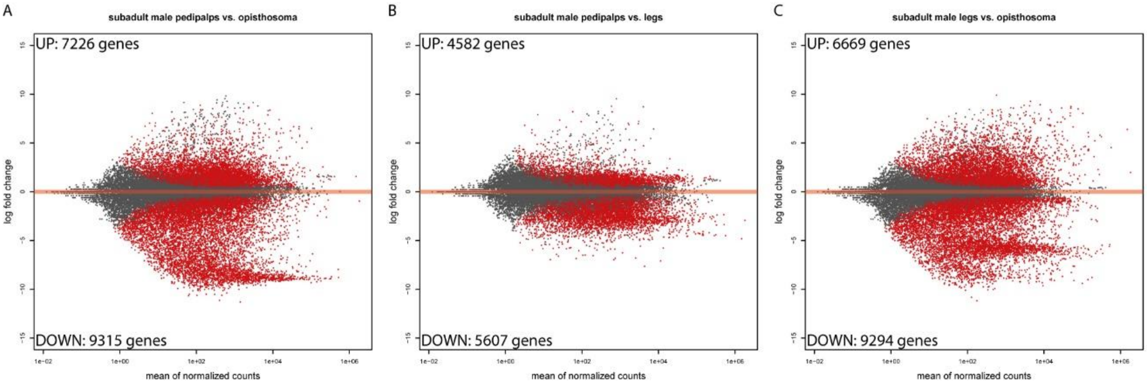

Figure 91 – Differentially expressed genes between the different tissues in subadult males. 16,541 genes were differentially expressed between subadult male peidpalps and opisthosoma (7226 up-regulated, 9315 down-regulated) (A). 10,189 genes were differentially expressed between pedipalps and legs (4582 up-regulated, 5607 down-regualted) (B). 15,963 genes were differentially expressed between the legs and the opisthosoma (6669 up-regulated, 9294 down-regulated) (C). Red dots in A, B, and C represent significantly differentially expressed genes with p-adjusted below 0.05. The log fold change refers to the ratio of a gene's normalized expression values in the two conditions on a log2 scale.

Of the differentially expressed genes, 7883 were shared in the comparisons between both appendage types and the opithosoma (2671 up-regulated, 5212 down-regulated), making them appendage-specific (Figure 92). In terms of pedipalp-specific genes, 1959 genes were shared in the comparison between pedipalps and the other two tissues (1121 up-regulated, 838 down-regulated) (Figure 90).

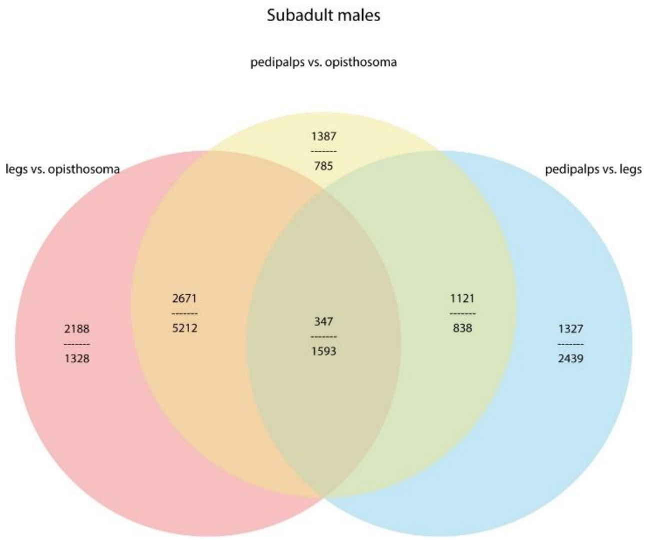

Figure 92 – Venn diagram showing the overlap of genes differentially expressed in subadult males among the different comparisons. Numbers above the fraction bar indicate the amount of genes that were up-regulated in the single or shared comparisons, while number below the fraction bar in dicate the amount of down-regulated genes.

In the subadult male samples, genes, which were up-regulated in the appendages, showed enrichment for GO terms involved in the morphogenesis and development of anatomical structures, adhesion, as well as neurological processes. Genes, which were differentially expressed in the pedipalps specifically, were enriched for GO terms associated with RNA metabolism and processing (Table 9).

Table 9 – GO terms enriched in up-regulated genes in appendages and pedipalps of subadult males.

Up-regulated in subadult male appendages			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0044707	4.07E-45	single-multicellular organism process	BP
GO:0032501	2.78E-43	multicellular organismal process	BP
GO:0044767	1.41E-36	single-organism developmental process	BP
GO:0048856	5.91E-28	anatomical structure development	BP
GO:0032502	8.23E-26	developmental process	BP
GO:0050877	6.22E-21	neurological system process	BP
GO:0003008	1.50E-20	system process	BP
GO:0009653	8.31E-20	anatomical structure morphogenesis	BP
GO:0022610	1.81E-17	biological adhesion	BP
GO:0050789	1.92E-17	regulation of biological process	BP
GO:0004872	2.87E-17	receptor activity	MF
GO:0007155	5.12E-17	cell adhesion	BP
GO:0007600	7.05E-17	sensory perception	BP
GO:0050794	1.24E-16	regulation of cellular process	BP
GO:0007610	5.21E-16	behavior	BP
Up-regulated in subadult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0016070	4.80E-54	RNA metabolic process	BP

GO:0003723	1.85E-47	RNA binding	MF
GO:0006396	6.38E-46	RNA processing	BP
GO:0006397	3.91E-41	mRNA processing	BP
GO:0090304	6.35E-41	nucleic acid metabolic process	BP
GO:0008380	1.34E-39	RNA splicing	BP
GO:0016071	3.46E-38	mRNA metabolic process	BP
GO:0006139	1.19E-35	nucleobase-containing compound metabolic process	BP
GO:0003676	4.77E-35	nucleic acid binding	MF
GO:0000377	5.66E-33	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP
GO:0000398	5.66E-33	mRNA splicing, via spliceosome	BP
GO:0000375	4.08E-32	RNA splicing, via transesterification reactions	BP
GO:0044822	9.40E-32	poly(A) RNA binding	MF
GO:0006725	1.24E-31	cellular aromatic compound metabolic process	BP
GO:0046483	4.68E-31	heterocycle metabolic process	BP

Appendage-specific genes, which were down-regulated in the subadult males showed enrichment mainly for GO terms concerning the activity of transporter proteins. The genes specifically down-regulated in the pedipalps were enriched for GO terms associated with cyclic nucleotides and cytoskeleton (supplementary material 9.5.2.3).

7.2.1.4 *Adult males*

In adult male tissue, a large number of genes was differentially between the pedipalps and the opithosoma (6240 up-regulated, 7145 down-regulated, 13,385 total) (Figure 93 A). Also 12,775 genes were differentially expressed in the legs compared to the opisthosoma (5763 up-regulated, 7012 down-regulated) (Figure 93 C). A significantly smaller number was differentially expressed in the comparison of the pedipalps with the legs (1529 up-regulated, 1656 down-regulated, 3185 total) (Figure 93 B).

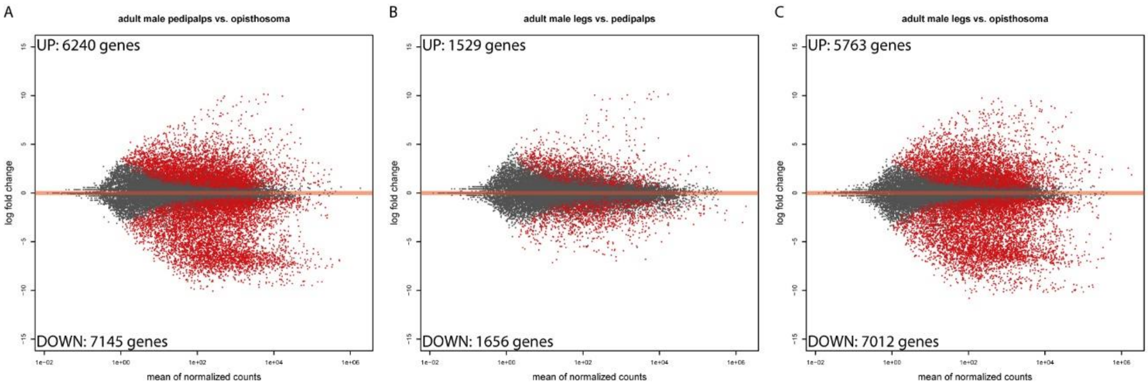

Figure 93 – Differentially expressed genes between the different tissues in adult males. 13,385 genes were differentially expressed between subadult male pediapls nd opisthosoma (6240 up-regulated, 7145 down-regulated) (A). 3185 genes were differentially expressed between pediaplps and legs (1529 up-regulated, 1656 down-regulated) (B). 12,775 genes were differentially expressed between legs and opisthosoma (5763

up-regulated, 7012 down-regulated) (C). Red dots in A, B, and C represent significantly differentially expressed genes with p-adjusted below 0.05. The log fold change refers to the ratio of a gene's normalized expression values in the two conditions on a log2 scale.

Of the differentially expressed genes, 8037 were shared by the comparison of pedipalps and legs to the appendages (2958 up-regulated, 5079 down-regulated), while not being differentially expressed between the two appendage types. The number of pedipalp specific genes was 844 (680 up-regulated, 164 down-regulated) (Figure 94).

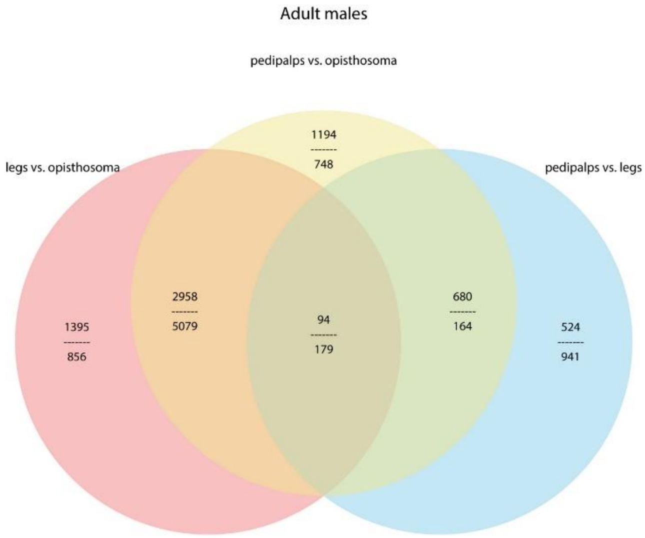

Figure 94 – Venn diagram showing the overlap of genes differentially expressed in adult males among the different comparisons. Numbers above the fraction bar indicate the amount of genes that were up-regulated in the single or shared comparisons, while number below the fraction bar in dicate the amount of down-regulated genes.

Up-regulated genes in the appendages of adult males were enriched for GO terms for adhesion, as well as some associated with the organisation of synapses. The up-regulated genes in the pedipalps were enriched with GO terms concerning DNA replication and DNA polymerase activity and the activity of transferases (Table 10).

Table 10 – GO terms enriched in genes up-regulated in appendages and pedipalps of adult males.

Up-regulated in adult male appendages			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0022610	9.25E-57	biological adhesion	BP
GO:0007155	3.46E-56	cell adhesion	BP
GO:0098742	9.08E-42	cell-cell adhesion via plasma-membrane adhesion molecules	BP
GO:0032501	9.07E-41	multicellular organismal process	BP
GO:0098609	1.52E-40	cell-cell adhesion	BP

GO:0007156	2.72E-40	homophilic cell adhesion via plasma membrane adhesion molecules	BP
GO:0044707	4.87E-39	single-multicellular organism process	BP
GO:0044767	6.42E-39	single-organism developmental process	BP
GO:0050808	5.52E-35	synapse organization	BP
GO:0022836	8.14E-30	gated channel activity	MF
GO:0007416	2.55E-28	synapse assembly	BP
GO:0048856	3.50E-28	anatomical structure development	BP
GO:0032502	1.71E-27	developmental process	BP
GO:0048869	2.16E-27	cellular developmental process	BP
GO:0005509	4.55E-27	calcium ion binding	MF
Up-regulated in adult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0016788	1.76E-08	hydrolase activity, acting on ester bonds	MF
GO:0034061	1.84E-06	DNA polymerase activity	MF
GO:0004518	3.81E-06	nuclease activity	MF
GO:0004035	8.94E-06	alkaline phosphatase activity	MF
GO:0006260	1.22E-05	DNA replication	BP
GO:0003887	1.27E-05	DNA-directed DNA polymerase activity	MF
GO:0032877	6.20E-05	positive regulation of DNA endoreduplication	BP
GO:0003677	6.38E-05	DNA binding	MF
GO:0016779	9.49E-05	nucleotidyltransferase activity	MF
GO:0033033	0.000127	negative regulation of myeloid cell apoptotic process	BP
GO:0016028	0.000136	rhabdomere	CC
GO:0060718	0.00014	chorionic trophoblast cell differentiation	BP
GO:0016744	0.000158	transferase activity, transferring aldehyde or ketonic groups	MF
GO:0016740	0.000158	transferase activity	MF
GO:0070365	0.00017	hepatocyte differentiation	BP

In terms of down-regulated genes in the appendages, adult males show enrichment of certain metabolic processes and transporter activities. The pedipalp specific down-regulated genes show enrichment of GO terms associated with transcription, specification, and determination of tissues (supplementary material 9.5.2.4).

7.2.2 Differentially expressed genes between the different pedipalp samples

After the different sequenced stages were analysed for differences in in gene expression profiles in the different tissues at each stage, the gene expression differences associated with the development of the pedipalp in males was analysed. To this end, the transcriptomes of juvenile pedipalps was compared to that of subadult male pedipalps showing the developmental differences associated with the development of the bulbus organ. To elucidate the genes involved in the actual formation of the bulbus organ the transcriptome of subadult male pedipalps was compared to that of age-matched female pedipalps, finding the sex specific differences during that stage. Finally, the transcriptomes of adult and subadult male pedipalps were compared, in order to see the expression profile remains after the development of the bulb apparatus has finished.

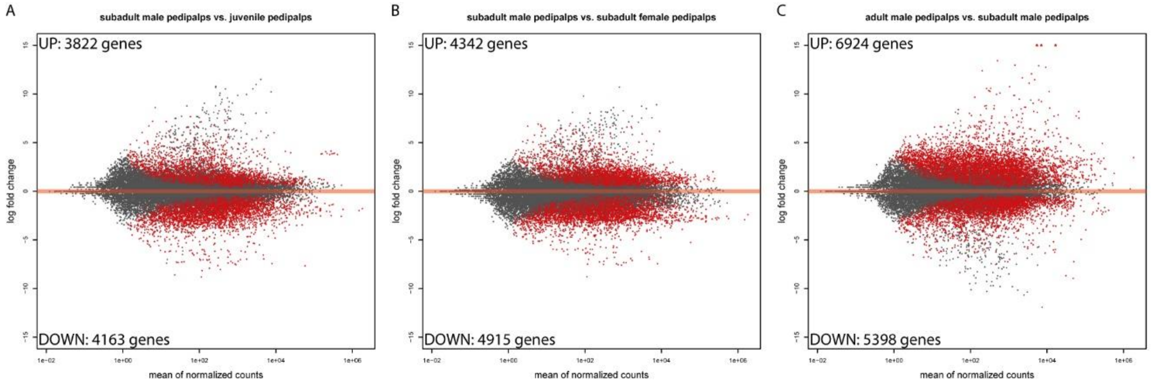

Figure 95 – Differentially expressed genes between the pedipalps of subadult males and juvenile, subadult males and subadult females, and adult males and subadult males. 7985 genes were differentially expressed between subadult males pedipalps and juvenile pedipalps (3822 up-regulated, 4163 genes down-regulated) (A). 9257 genes were differentially expressed between subadult male pedipalps and suadult female pedipalps (4342 up-regulatedm 4915 down-regulated) (B). 12,322 genes were differentially expressed between adult male peidpalps and subadult male pedipalps (6924 up-regulated, 5398 down-regulated) (C). Red dots in A, B, and C represent significantly differentially expressed genes with p-adjusted below 0.05. The log fold change refers to the ratio of a gene's normalized expression values in the two conditions on a log2 scale.

7.2.2.1 *Differentially expressed genes between subadult male and juvenile pedipalps*

The developmental comparison showed 7985 genes to be differentially expressed between the pedipalps of subadult males and juveniles (3822 up-regulated, 4163 down-regulated) (Figure 95 A). To get an overview of the processes involved in this transition, the GO terms of the differentially expressed genes were analysed. The genes up-regulated in this comparison showed enrichment for GO terms associated with the processing and binding of RNA, as well as mitotic cell cycle progression (Table 11).

Table 11 – GO terms enriched in genes differentially expressed between subadult male pedipalps and juvenile pedipalps.

Up-regulated in subadult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0003723	6.49691415872639e-43	RNA binding	MF
GO:0044822	9.1042445968719e-41	poly(A) RNA binding	MF
GO:0016070	8.0243964878503e-25	RNA metabolic process	BP
GO:0008380	1.07702950749377e-23	RNA splicing	BP
GO:0006396	1.74772598828576e-22	RNA processing	BP
GO:0006397	4.77802200985204e-22	mRNA processing	BP
GO:0016071	4.09714330134903e-21	mRNA metabolic process	BP
GO:0000377	4.94822544147737e-20	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP
GO:0000398	4.94822544147737e-20	mRNA splicing, via spliceosome	BP
GO:0000375	6.55222814292237e-20	RNA splicing, via transesterification reactions	BP
GO:0022402	7.81356372261603e-20	cell cycle process	BP
GO:0022618	2.09462896358411e-18	ribonucleoprotein complex assembly	BP
GO:0034660	2.90993700843587e-18	ncRNA metabolic process	BP
GO:0043933	6.39875688838997e-18	macromolecular complex subunit organization	BP
GO:1903047	8.50088143663808e-18	mitotic cell cycle process	BP

Down-regulated in subadult male pedipalps in subadult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0005215	1.12240959572936e-55	transporter activity	MF
GO:0005216	6.88033082281767e-47	ion channel activity	MF
GO:0015267	7.75647376308528e-46	channel activity	MF
GO:0022803	7.75647376308528e-46	passive transmembrane transporter activity	MF
GO:0022857	8.32119003321481e-46	transmembrane transporter activity	MF
GO:0022838	9.3132865518423e-46	substrate-specific channel activity	MF
GO:0022836	1.30717971972032e-45	gated channel activity	MF
GO:0015075	3.45176822388421e-44	ion transmembrane transporter activity	MF
GO:0022891	1.46622867359445e-43	substrate-specific transmembrane transporter activity	MF
GO:0022892	3.48018496560148e-40	substrate-specific transporter activity	MF
GO:0006811	1.25799405686442e-35	ion transport	BP
GO:0046873	2.04934728156438e-34	metal ion transmembrane transporter activity	MF
GO:0005261	5.97950138168034e-34	cation channel activity	MF
GO:0044765	1.06203420466237e-29	single-organism transport	BP
GO:0015276	2.96069124090026e-29	ligand-gated ion channel activity	MF

Since the genes identified as differentially expressed could also be involved in other processes, interesting candidates should be specific to the pedipalps. Therefore, genes were considered, which were differentially expressed between juvenile and subadult pedipalps with a log2FoldChange of more than 1 (for up-regulated genes), or below 1 (for down-regulated genes), which where also differentially expressed berween the pedipalps and the legs in subadult males. This step reduced the amount of candidate genes from 7958 genes to 3453 genes (1281 up-regulated, 2172 down-regulated). Interestingly, the attempt to further reduce this number by only taking genes into account, which are also differentially expressed between the subadult male pedipalps and the subadult male opisthosoma resulted in the same amount of candidates.

The top differentially expressed genes in the transition from juvenile to subadult male pedipalps involve, next to uncharacterized proteins (genes, which show no blast homologies to genes from other organisms, or only other chelicerates, but have no conserved domain), the homologs of known transcription factors, FOXL2, Pax1-like and Homeobox protein 2-like, as well as Hornerin-like and Skeletor, both involved in cell structure (Table 12).

Among the most down-regulated genes in this list there are several genes involved in neurological processes, such as endothelin-converting enzyme 2-like and Transient receptor potential proteins, also Lachesin, which may play a role in neuronal differentiation and axon guidance (Table 12).

Table 12 – Top 15 genes differentially expressed between subadult male pedipalps and juvenie pedipalps.

Up-regulated in subadult male pedipalps		
Augustus ID	**Log2 fold change**	**Blast annotation**
aug3.g7640.t1	8.60175199	FOXL2
aug3.g750.t1	7.66771758	uncharacterized protein
aug3.g8968.t2	7.19371604	Pax1-like

aug3.g12235.t1	7.16789117	hypothetical protein
aug3.g25812.t1	7.14249464	uncharacterized protein
aug3.g11261.t1	7.01072179	Cuticle protein 10.9-like
aug3.g23740.t1	6.75537645	uncharacterized protein
aug3.g26610.t1	6.71174494	Hornerin-like
aug3.g21291.t1	6.55391681	1,4-beta-xylanase
aug3.g23880.t1	6.40575468	Transposable element Tcb2 transposase
aug3.g27943.t1	6.36052313	Homeobox protein 2-like
aug3.g7019.t1	6.16059544	uncharacterized protein
aug3.g5361.t3	6.10603443	Skeletor
aug3.g16431.t1	6.01302119	Beta-hexosaminidase subunit beta-like
aug3.g6268.t1	5.988710884	Abhydrolase domain-containing protein 11
Down-regulated in subadult male pedipalps		
Augustus ID	**Log2 fold change**	**Blast annotation**
aug3.g20518.t1	-6.78080842	Endothelin-converting enzyme 2-like
aug3.g11055.t1	-6.67176541	hypothetical protein
aug3.g9144.t2	-6.1999266	Transient receptor potential-gamma protein-like
aug3.g7596.t1	-6.1468576	Transient receptor potential-like protein
aug3.g17535.t1	-5.69773942	hypothetical protein
aug3.g23808.t1	-5.59945718	uncharacterized protein
aug3.g9014.t1	-5.17414293	Lachesin-like
aug3.g5424.t1	-5.0528174	hypothetical protein
aug3.g15969.t1	-4.85333428	uncharacterized protein
aug3.g3342.t1	-4.81255824	-
aug3.g2254.t1	-4.7556404	Chymotrypsin-1-like
aug3.g4168.t1	-4.70141969	hypothetical protein
aug3.g16309.t1	-4.68818562	uncharacterized protein
aug3.g9504.t1	-4.6724945	Prolactin-releasing peptide receptor-like
aug3.g13460.t1	-4.63946934	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase

7.2.2.2 *Differentially expressed genes between male and female subadult pedipalps*

The comparison of the subadult male pedipalps and the subadult female pedipalps resulted in 9257 differentially expressed between these two tissues (4342 up-regulated, 4915 down-regulated) (Figure 95 B). Analysis of the GO terms associated with the up- and down-regulated genes showed terms involved in the production and processing of RNA to be enriched in up-regulated genes in adult male pedipalps. Moreover, among this set of genes, terms associated with the regulation of gene expression and the regulation of biosynthetic processes were also enriched (Table 13). In the genes downregulated between these two tissues there was an enrichment of terms for the activity of ion channels and transporter proteins (Table 13).

Table 13 – GO enriched in genes differentially expressed between subadult males pedipalps and subadult female pedipalps

Up-regulated in subadult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0044822	9.0083936062369e-74	poly(A) RNA binding	MF
GO:0003723	5.96058661355127e-71	RNA binding	MF
GO:0016070	5.1046681846626e-45	RNA metabolic process	BP
GO:0043933	1.06212466550486e-37	macromolecular complex subunit organization	BP
GO:0010468	1.87169587699904e-34	regulation of gene expression	BP
GO:0006396	3.4396835747909e-34	RNA processing	BP
GO:0016071	9.27538399984782e-34	mRNA metabolic process	BP

GO:0006397	1.36068226819114e-32	mRNA processing	BP
GO:0010556	1.92357502101414e-32	regulation of macromolecule biosynthetic process	BP
GO:0008380	3.61830593053063e-31	RNA splicing	BP
GO:2000112	5.12189744040738e-31	regulation of cellular macromolecule biosynthetic process	BP
GO:1903047	2.17579614680991e-30	mitotic cell cycle process	BP
GO:0031326	6.00256202796456e-29	regulation of cellular biosynthetic process	BP
GO:0060255	9.09608877431525e-29	regulation of macromolecule metabolic process	BP
GO:0009889	1.14011622695196e-28	regulation of biosynthetic process	BP
Down-regulated in subadult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0005215	2.05401250863909e-51	transporter activity	MF
GO:0022857	4.06373699530778e-41	transmembrane transporter activity	MF
GO:0015075	4.77574893648353e-40	ion transmembrane transporter activity	MF
GO:0022891	1.05614328132267e-39	substrate-specific transmembrane transporter activity	MF
GO:0006811	3.56906110652321e-39	ion transport	BP
GO:0022836	1.76700184616624e-37	gated channel activity	MF
GO:0005216	1.87370338114327e-37	ion channel activity	MF
GO:0022892	1.89664316838185e-37	substrate-specific transporter activity	MF
GO:0015267	4.28029182732644e-37	channel activity	MF
GO:0022803	4.28029182732644e-37	passive transmembrane transporter activity	MF
GO:0022838	8.34993462751829e-37	substrate-specific channel activity	MF
GO:0046873	2.28340795263618e-31	metal ion transmembrane transporter activity	MF
GO:0044765	4.29833670877785e-31	single-organism transport	BP
GO:1902578	3.36587629849126e-29	single-organism localization	BP
GO:0005261	6.9718762135255e-29	cation channel activity	MF

In order to reduce this gene set more towards specificity, only genes were considered, which were not only differentially expressed between the male and female subadult pedipalps, but which also showed difference in the expression between the subadult male pedipalps and legs. Thus, the amount of differentially expressed genes was reduced from 9257 to 3935 (1489 up-regulated, 2446 down-regulated). An attempt to reduce the number of candidate genes further by including only genes, which were also differentially expressed between the subadult male pedipalps and opisthosoma resulted in exactly the same amount of genes as in the reduction before.

Analysis of the most differentially expressed genes, showed that both FOXL2 and Pax-1-like are highly up-regulated between the subadult male and female pedipalps, as seen between the juvenile and subadult male pedipalps. Another transcription factor, which was highly expressed in subadult male pedipalps was crocodile, another member of the forkhead domain transcription factor family (Table 14). The genes most down-regulated in this comparison included neural related genes like the endothelin-converting enzyme 2-like, GABA receptor subunit beta, and the neural cell adhesion molecule 2-like. In addition, the homolog of unc-89, involved in muscle fiber assembly, was found (Table 14).

Table 14 – Top 15 differentially expressed genes between subadult male pedipalps and subadult female pedipalps

Up-regulated in subadult male pedipalps		
Augustus ID	**Log2 Fold Change**	**Blast annotation**
aug3.g23880.t1	10.70549368	Transposable element Tcb2 transposase
aug3.g8968.t2	6.895747268	Pax-1-like
aug3.g23740.t1	6.87584794	uncharacterized protein
aug3.g7640.t1	6.807557491	FOXL2
aug3.g23385.t1	6.660109221	Decaprenyl-diphosphate synthase subunit 2-like
aug3.g16857.t1	6.647472288	uncharacterized protein
aug3.g8638.t1	6.553250052	Crocodile
aug3.g20490.t1	6.509828365	uncharacterized protein
aug3.g23819.t1	6.407736856	uncharacterized protein
aug3.g6268.t1	6.346751634	Abhydrolase domain-containing protein 11
aug3.g23405.t1	6.318206929	Kinesin-like protein KIF11-B
aug3.g16431.t1	6.149565525	Beta-hexosaminidase subunit beta-like
aug3.g26870.t1	6.140921051	Extensin-like
aug3.g750.t1	6.093054916	uncharacterized protein
aug3.g14955.t1	6.08503554	uncharacterized protein
Down-regulated in subadult male pedipalps		
Augustus ID	**Log2 FoldChange**	**Blast Annotation**
aug3.g20518.t1	-6.298990654	Endothelin-converting enzyme 2-like
aug3.g17907.t1	-5.870593003	uncharacterized protein
aug3.g24709.t1	-5.775444699	hypothetical protein
aug3.g15969.t1	-5.281066313	uncharacterized protein
aug3.g12025.t1	-5.159341234	Cyclin-dependent kinase 14-like
aug3.g6552.t1	-5.13716398	uncharacterized protein
aug3.g3483.t1	-5.1302889	Gamma-aminobutyric acid receptor subunit beta-like
aug3.g21755.t1	-4.994420565	uncharacterized protein
aug3.g16032.t1	-4.916483366	uncharacterized protein
aug3.g20277.t1	-4.912546113	Protein ABHD11-like
aug3.g712.t1	-4.8177192	neural cell adhesion molecule 2-like
aug3.g13460.t1	-4.704984002	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase
aug3.g24871.t1	-4.68738366	Muscle M-line assembly protein unc-89
aug3.g24157.t1	-4.643250701	uncharacterized protein
aug3.g13791.t1	-4.631919868	Glucose dehydrogenase [FAD, quinone]-like

7.2.2.3 *Differentially expressed genes between adult and subadult male pedipalps*

In contrast to the comparisons in terms of male development and sex-specific differences, the analysis of differential expressed genes between the adult male pedipalps and subadult male pedipalps showed a larger number of genes to be involved in this transition. 12,322 genes were differentially expressed (6924 up-regulated, 5398 down-regulated) (Figure 95 C). The enriched GO terms for the up- and down-regulated genes in this comparison showed an exactly opposite trend as compared to the previous analyses. Here, the up-regulated genes showed enrichment of terms associated with ion transport, while the down-regulated genes were enriched for GO terms associated with the production and processing of RNAs (Table 15).

Table 15 – GO terms enriched in genes differentially expressed between adult male pedipalps and subadult male pedipalps.

Up-regulated in adult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0006811	2.13022427933535e-30	ion transport	BP
GO:0005215	3.35878660306895e-28	transporter activity	MF
GO:0022857	1.30551321560388e-25	transmembrane transporter activity	MF
GO:0022891	1.5217043484643e-23	substrate-specific transmembrane transporter activity	MF
GO:0044765	1.4890555669831e-22	single-organism transport	BP
GO:0007155	2.37069876368207e-22	cell adhesion	BP
GO:0015075	3.91004763853663e-22	ion transmembrane transporter activity	MF
GO:0022610	1.33442532449494e-20	biological adhesion	BP
GO:1902578	1.98373251798402e-20	single-organism localization	BP
GO:0022892	3.6416635188741e-20	substrate-specific transporter activity	MF
GO:0005509	1.31617146343297e-18	calcium ion binding	MF
GO:0007156	1.45418210280869e-17	homophilic cell adhesion via plasma membrane adhesion molecules	BP
GO:0032501	7.29762286815066e-17	multicellular organismal process	BP
GO:0006820	6.33350444582926e-16	anion transport	BP
GO:0030001	9.14528699062851e-16	metal ion transport	BP
Down-regulated in adult male pedipalps			
category	**over_represented_pvalue**	**term**	**ontology**
GO:0003723	1.05700339200215e-93	RNA binding	MF
GO:0016070	1.18181769177951e-84	RNA metabolic process	BP
GO:0044822	2.81332183544697e-79	poly(A) RNA binding	MF
GO:0006396	6.83612333620987e-57	RNA processing	BP
GO:0016071	4.79370959850884e-51	mRNA metabolic process	BP
GO:0006397	7.85217174415912e-50	mRNA processing	BP
GO:0034470	1.3170180485502e-48	ncRNA processing	BP
GO:0034660	2.07381396298056e-48	ncRNA metabolic process	BP
GO:0044260	8.64340667466023e-45	cellular macromolecule metabolic process	BP
GO:0008380	9.92213480950084e-44	RNA splicing	BP
GO:0043170	4.60675399028059e-42	macromolecule metabolic process	BP
GO:0043933	9.17866613842693e-41	macromolecular complex subunit organization	BP
GO:0090304	1.25942731558089e-39	nucleic acid metabolic process	BP
GO:0009059	7.19072169696907e-38	macromolecule biosynthetic process	BP
GO:0034645	2.82031706742068e-37	cellular macromolecule biosynthetic process	BP

This list of genes, as in the previous comparisons, was made more pedipalp specific, by only taking genes into account, which apart from being differential expressed between the adult and subadult male pedipalps, also show differences between the adult male pedipalps and legs. This resulted in a significant reduction of genes from 12,322 to 927 (809 up-regulated, 118 down-regulated). However, as seen in the analysis of sex-specific genes, the incorporation of genes, which are also differentially expressed between the adult male pedipalps and legs did not reduce the amount of genes.

Among the genes most highly up-regulated in the adult male pedipalps were a large number Cathepsin and serpin homologs (Table 16). The down-regulated genes, on the other hand, contained a number of cuticle proteins, as well as genes involved in the differentiation and development of neural tissues, the homologs of TLX-3 and Achaete-scute 1a (Table 16).

Table 16 – Top 15 genes differentially expressed between adult male pedipalps and subadult male pedipalps.

Up-regulated in adult male pedipalps		
Augustus ID	**Log2 Fold Change**	**Blast annotation**
aug3.g4403.t1	15.99340159	uncharacterized protein
aug3.g6434.t1	13.42093605	Cathepsin L1-like
aug3.g1496.t1	12.96659399	Basic proline-rich protein-like
aug3.g1495.t1	12.89743459	hypothetical protein
aug3.g17976.t1	12.74202588	carboxypeptidase inhibitor SmCI-like
aug3.g4896.t1	12.38391869	Toxin-like protein 14
aug3.g13759.t1	12.07358706	uncharacterized protein
aug3.g9346.t1	11.66153349	Phospholipase D LbSicTox-betaIA1a-like
aug3.g20259.t1	11.46147287	Papilin-like
aug3.g18605.t1	11.10274081	Serpin B3-like
aug3.g6437.t1	10.74544603	Cathepsin S-like
aug3.g24368.t1	10.57862076	Serpin B8-like
aug3.g6433.t1	10.34624361	Cathepsin K-like
aug3.g1554.t1	10.26541059	Clotting factor B-like
aug3.g20807.t1	9.962377807	Serpin B8-like
Down-regulated in adult male pedipalps		
Augustus ID	**Log2 Fold Change**	**Blast annotation**
aug3.g10755.t1	-4.952528267	uncharacterized protein
aug3.g4167.t1	-4.195317826	T-cell leukemia homeobox protein 3-like
aug3.g27326.t1	-4.12803612	uncharacterized protein
aug3.g13014.t1	-4.107810036	Adult-specific rigid cuticular protein 15.7-like
aug3.g24065.t1	-3.970293105	uncharacterized protein
aug3.g10915.t1	-3.863390245	uncharacterized protein
aug3.g50.t1	-3.797300505	RNA-directed DNA polymerase from mobile element jockey
aug3.g1904.t1	-3.770973578	Tubulin alpha-1D chain-like
aug3.g22098.t1	-3.766744153	Tubulin alpha-1-chain-like
aug3.g16167.t1	-3.738064512	High mobility group protein HMG-I/HMG-Y-like
aug3.g10760.t1	-3.73618323	uncharacterized protein
aug3.g10844.t1	-3.699530059	uncharacterized protein
aug3.g26796.t1	-3.564537527	Transposable element Tc1 transposase
aug3.g15679.t1	-3.558649276	Achaete-scute homolog 1a-like
aug3.g11655.t1	-3.501098352	Cuticle protein 16.8-like

7.2.3 Expression profiles in the different tissues

In another approach to identify processes during the post embryonic development of male spiders, genes with similar relative expression profiles were grouped into clusters using the coseq algorithm (Rau & Maugis-Rabusseau 2017). Expression profiles were grouped for the legs, the opisthosoma, and the pedipalps of juveniles and the two male samples. Thus, the aim is to identify different developmental processes, which take place at specific time points during the development.

7.2.3.1 *Legs*

The analysis of gene expression patterns in male legs showed 12 clusters, which could be grouped into five categories. One cluster showed higher expression in juvenile and subadult legs, which receeded in the adult stage. Three cluster showed highest expression in the subadult stage and only low or almost no expression in juvenile and adult legs. Five clusters had their highest expression in the adult legs, while only little expression was apparent in the earlier stages. One cluster showed rising expression, while two clusters showed only little change of expression throughout development.

7.2.3.1.1 Active in juvenile and subadult legs

Cluster 7 showed medium expression of its 1132 genes in the juvenile and subadult stage, while expression dropped at the adult stage (Figure 96). The GO terms of genes in this cluster were enriched for endopeptidase activities, organization of collagen structures, and base-excision repair (supplemental material 9.5.3.1.1).

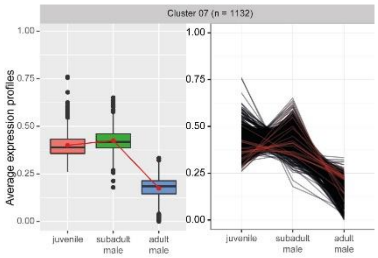

Figure 96 – Expression cluster 7 in legs. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.3.2 *Active in subadult legs*

Three clusters showed their peaks of expression in the subadult stage, while little or no expression was present in juvenile and adult stages. Cluster 1 showed relatively low expression in the juvenile stage and even less in the adult, while peaking in the subadult stage (Figure *97* A). This cluster was enriched for GO terms for cuticle and chitin binding, as well as the binding of ions, apolipoproten receptors and the localization of proteins to the cell surface (supplemental material 9.5.3.1.2). Cluster 2 showed an even higher difference of expression between juvenile and adult compared to the subadult stage (Figure 97 B). This cluster showed high enrichment in GO terms related to cuticle and chitin (supplemental material 9.5.3.1.2). Cluster 4 showed a smaller difference between the relative expression levels of the subadult stage than compared to the other two stages (Figure 97 C). Enriched GO terms in this cluster included oxidation-reduction processes, and the development of anatomical structures (supplemental material 9.5.3.1.2).

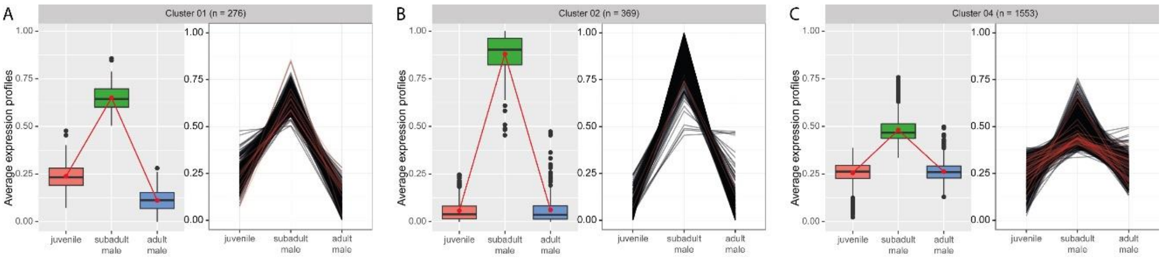

Figure 97 – Expression clusters 01 (A), 02 (B), and 04 (C) in legs, showing highest relative expression in the subadult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.3.3 *Active in adult legs*

Five of the identified clusters showed the highest expression of their genes in the adult stage. Cluster 3 showed low expression in juvenile and aubadult stages, while the expression profile rose towards the adult leg tissue (Figure 98 A). This cluster showed high enrichment of GO terms for membrane components, as well as the cell-cell adhesion and the assembly of synapses (supplemental material 9.5.3.1.3). Cluster 6 showed a very specific expression peak in the adult legs (Figure *98* B). GO terms in this cluster were mostly associated with the metabolism of lipids and triglycerides (supplemental material 9.5.3.1.3). Cluster 10 showed an expression profile with a slight rise from the juvenile legs to the subadult stage (Figure 98 C). GO terms in this cluster included several metabolic and catabolic precesses, next to ligase activities and cell migration (supplemental material 9.5.3.1.3). Cluster 11 and 12 showed a higher difference between the adult and the younger stages (Figure 98 D, E). GO terms associated with cluster 11 showed enrichment in protein localisation and catchol biosynthesis, as well as the transition of mitotic phases during the cell cycle (supplemental material 9.5.3.1.3). Cluster 12 showed enrichment of GO terms associated with neuronal terms, such as synaptic transmission, neurotransmitter binding, and ion channel activity (supplemental material 9.5.3.1.3).

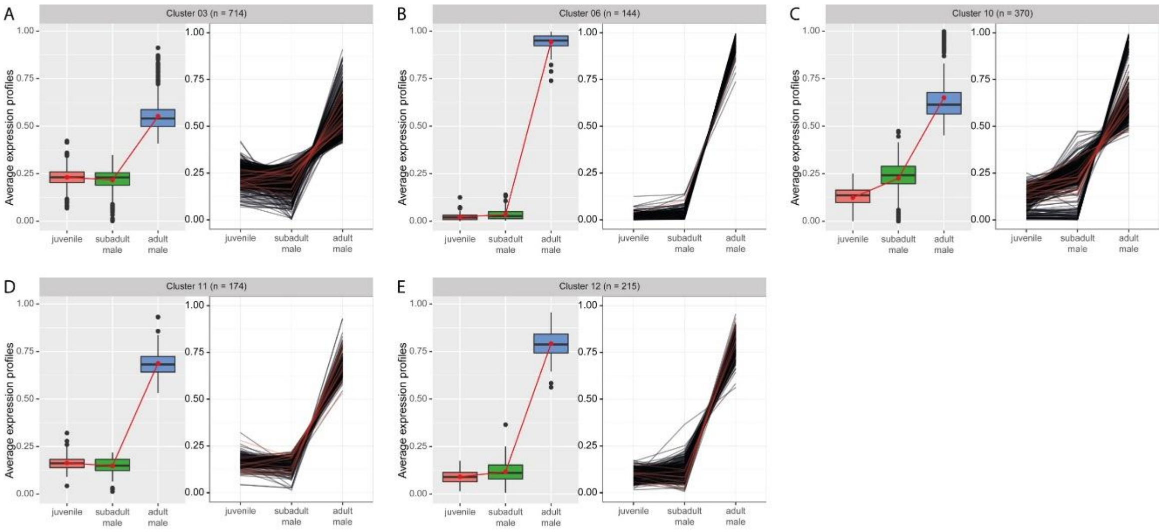

Figure 98 - Expression clusters 03 (A), 06 (B), 10 (C), 11 (D), and 12 (E) in legs, showing highest relative expression in the adult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.3.4 *Increasing expression through development*

Cluster 8 was identified to have a steady increase of expression from the juvenile to the adult legs (Figure 99). Genes in this cluster showed enrichment in GO terms associated with localization and cell junctions (supplemental material 9.5.3.1.4).

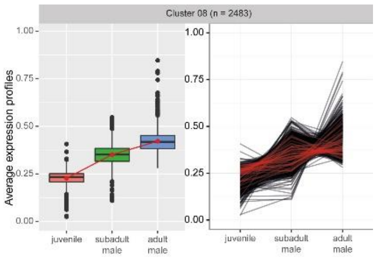

Figure 99 – Expression cluster 8 in legs. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.3.5 *Continuous expression*

Clusters 5 and 9 showed a relatively stable profile of continuous expression throughout the three stages (Figure 100). Both clusters showed enrichment in GO terms for RNA metabolism and processing. The terms for cluster 5 also included the regulation of gene expression (supplemental material 9.5.3.1.5), while cluster 9 was enriched for terms involved in translation (supplemental material 9.5.3.1.5).

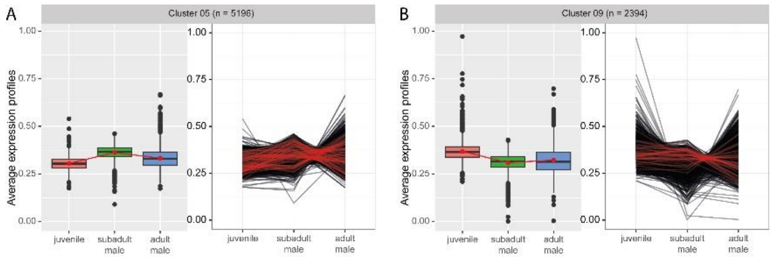

Figure 100 - Expression clusters 05 (A)and 09 (B) in legs, showing continuous expression. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4 Opisthosoma

The analysis of gene expression profiles in the male opithosomas identified 18 clusters, which could be grouped into 5 different types of profile. Genes, that are mainly expressed in the juvenile stages, with less expression in the older stages. 3 Clusters, which showed genes to be prominently active in juvenile and subadult opisthosomas. One cluster each, which showed high expression in the subadult stage, or subadult and adult stage, respectively. Three clusters, which showed the down-regulation of genes in the subadult opisthosomas. And finally, seven clusters of genes, which showed the highest expression in the adult stage.

7.2.4.1 *Active in juvenile opisthosomas*

Cluster 4, 14, and 16 showed the highest expression in the juvenile male opisthosoma. The expression profile of cluster 4 showed a steep decrease in expression from the juvenile stage to the subadult stage, and an even further decrease towards the adult stage (Figure 101 A). In cluster 14, genes expression was also highest in the juvenile tissue, and decreased towards medium levels in the subadult and adult opisthosomas (Figure 101 B). The most specific expression in the juvenile stages was found in cluster 16, which showed almost no expression in the older stages (Figure 101 C). The GO terms associated with cluster 4 contained mostly the activity of peptidases and phosphatases, along with the negative regulation killer cells (supplemental material 9.5.3.2.1). Cluster 14 showed enrichment of GO terms related to the production and processing of RNA, as well as translational terms (supplemental material 9.5.3.2.1). In cluster 16, only one GO term was enriched for the genes in this cluster, the activity of phospholipase A2 (supplemental material 9.5.3.2.1).

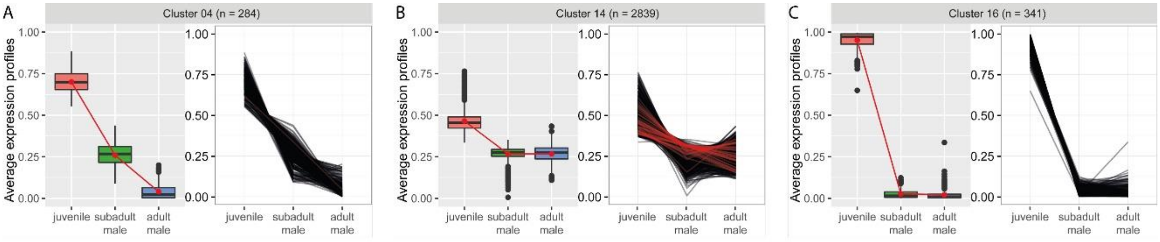

Figure 101 - Expression clusters 04 (A), 14 (B), and 16 (C) in opisthosomas, showing highest relative expression in the juvenile stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4.2 *Active in juvenile and subadult males*

Three clusters identified by the expression of male opisthosoma genes showed higher expression in the juvenile and subadult stages, than in the adults. While there was only a small difference in the relative expression between the younger stages and the adult in cluster 3 (Figure 102 A), the difference between the younger and adult stage was more prominent in clusters 8 (Figure 102 B) and 10 (Figure 102 C). GO terms associated with cluster 3 were enrichrd for metabolic processes, the establishment of protein localization, and the regulation of gene expression (supplemental material 9.5.3.2.2). Cluster 8 showed high enrichment for GO terms associated with the mitotic cell cycle and nuclear division (supplemental material 9.5.3.2.2). Enriched GO terms for cluster 10 contained mainly the activity of peptidases, but also the binding of collagen fibrils (supplemental material 9.5.3.2.2).

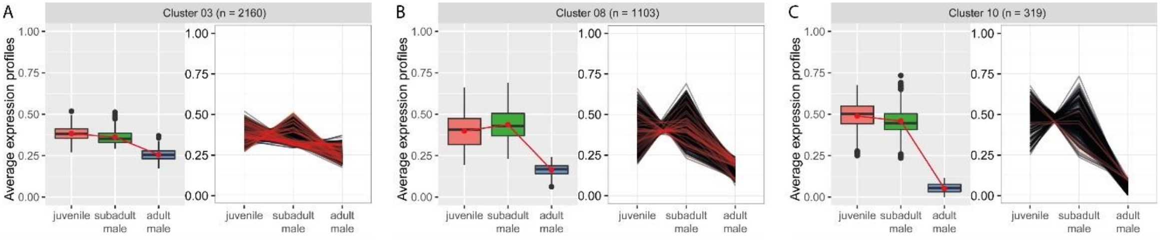

Figure 102 - Expression clusters 03 (A), 08 (B), and 10 (C) in opisthosomas, showing highest relative expression in the juvenile and subadult stages. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4.3 *Active in subadult opisthosoma*

Cluster 11 showed a peak of expression in the subadult opisthosoma (Figure 103). The GO terms associated with this cluster of genes contained terms linked to the cytoskeleton, but also nuclear division and the meiotic cell cycle (9.5.3.2.3).

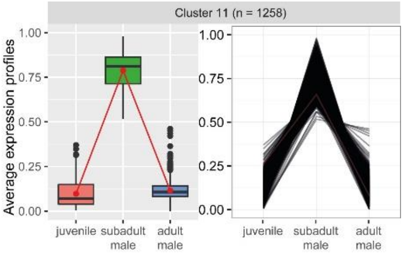

Figure 103 – Expression cluster 11 in the opisthosoma. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4.4 *Active in subadult and adult opisthosomas*

Cluster 12 showed an expression profile with relatively few changes, but with a trend towards lower expression in the juvenile stage, followed by slightly higher expression in the subadult and adult stage (Figure 104). The genes in this cluster were enriched in terms associated with the regulation and localisation of biological and cellular processes, as well as the signal transduction and transport (supplemental material 9.5.3.2.4).

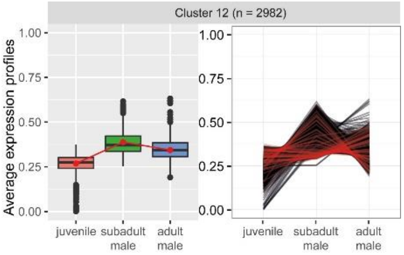

Figure 104 – Expression cluster 12 in the opisthosoma. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4.5 *Low activity in subadult opisthosomas*

Three of the identified clusters showed a profile with the lowest expression in the subadult stage. Cluster 2, which showed a decrease in relative expression levels from the juvenile to the subadult stage, while showing a peak expression in the adult stage (Figure 105 A). The GO terms in this cluster were mainly enriched for the activity of transporters (supplemental material 9.5.3.2.5). Cluster 9 showed only a relatively small difference between the stages, but still a recognisable drop in expression levels in the subadult stage (Figure 105 B). In this cluster, the enriched GO terms contained enzymatic activities, catabolic processes, localisation, and the initiation of transcription (supplemental material 9.5.3.2.5). In cluster 15, the profile showed a reduction in expression levels from the juvenile to the subadult stage, while rising at the adult stage (Figure 105 C). GO terms enriched in this cluster were associated with transmembrane transport, the metabolism of peroxides, and enzymes, which are associated with tetrahydrofolate (supplemental material 9.5.3.2.5).

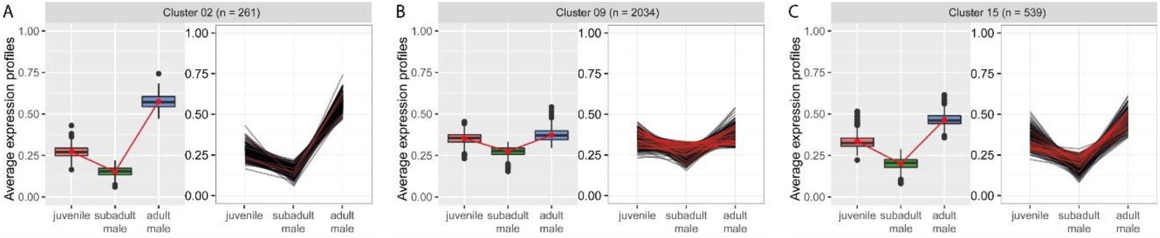

Figure 105 - Expression clusters 02 (A), 09 (B), and 15 (C) in opisthosomas, showing lowest relative expression in the subadult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.4.6 *Active in the adult opisthosoma*

The expression profiles of genes in 7 clusters showed little or no expression in the juvenile and subadult, but had a peak of expression in the adult opisthosomal tissues. Cluster 1 showed a relatively low expression in the juvenile and the subadult stage, while rising strongly in the adult stage (Figure 106 A). This cluster showed high enrichment of GO terms associated in hatching and the activity of inositol hexakisphosphate kinase (supplemental material 9.5.3.2.6). Cluster 5 showed virtually no expression in the younger stages and high relative expression in the adult stage (Figure 106 B). GO terms in this cluster were highly enriched in the activity of peptidases and triglyceride lipase (supplemental material 9.5.3.2.6). Cluster 6 showed an intermediate expression of its genes in the juveniles and subadults, while slightly rising towards the adult stage (Figure 106 C). GO terms enrichd in this cluster contained the organisation of actin and myosin, and the organisation of extracellular space (supplemental material 9.5.3.2.6). Cluster 7, again, showed a high increase in expression levels in the adult tissue, compared to the younger stages (Figure 106 D). This cluster was enriched for GO terms like the activity of growth factors and the metabolism of peroxides and the reduction of reactive oxygen species (supplemental material 9.5.3.2.6). Cluster 13 showed a realtively low expression in the first two stages, while expression levels increased in the adult tissue (Figure 106 E). This cluster was enriched in terms of transmembrane and ion transport (supplemental material 9.5.3.2.6). Cluster 17 showed a similar expression profile as cluster 13, while expression levels were realtively higher in the adult opisthosomas (Figure 106 F). This cluster was enriched in terms of actinin binding ans well as collagen metabolic processes (supplemental material 9.5.3.2.6). Finally, cluster 18 showed almost no expression in the juvenile and subadult stages and a relatively high expression in the adult stage (Figure 106 G). This cluster was enriched in GO terms of peptidase activity and the negative regulation of retina development (supplemental material 9.5.3.2.6).

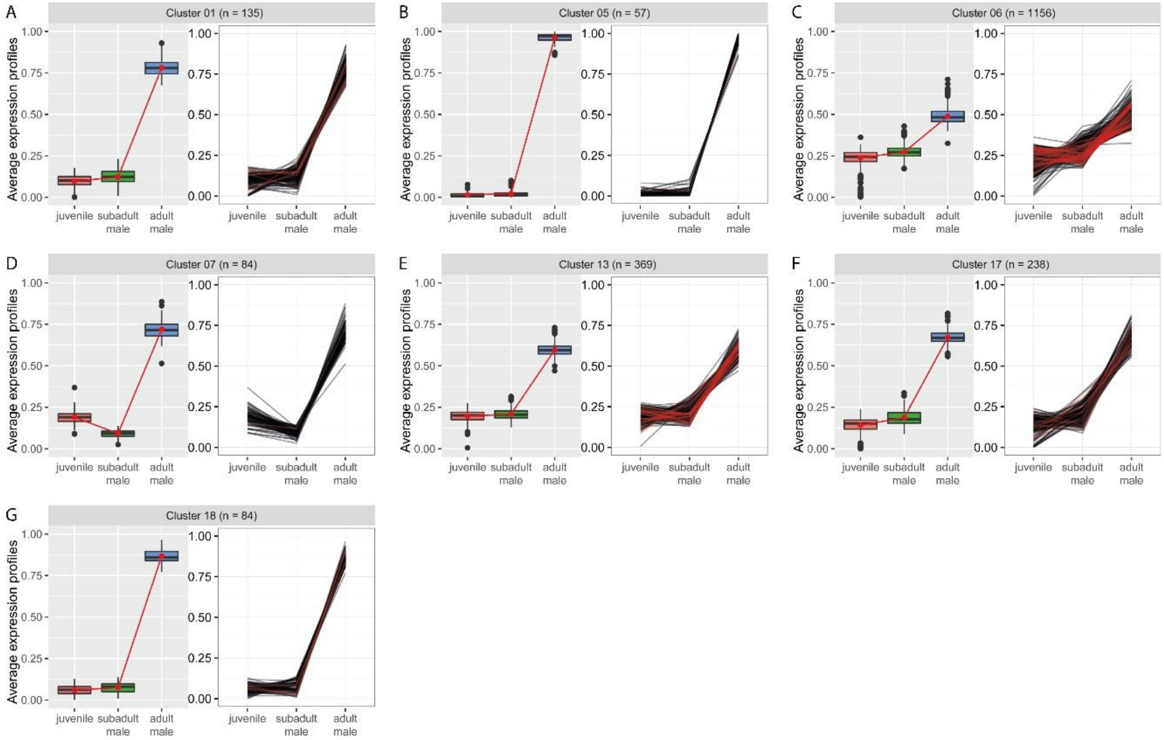

Figure 106 - Expression clusters 01 (A), 05 (B), 06 (C), 07 (D), 13 (E), 17 (F), and 18 (G) in opisthosomas, showing highest relative expression in the adult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.5 Pedipalps

The clustering of expression profiles in the juvenile and male pedipalps resulted in 18 clusters, which could be grouped into six different types. One cluster contained genes, which were mainly active in juvenile pedipalps, four clusters showed a peak of expression in the subadult pedipalps, while another four clusters were down-regulated during this stage. Seven clusters had the main expression during the adult stage, while there was one cluster, respectively, which showed expression profiles rising throughout development, or continuous expression.

7.2.5.1 *Active in juvenile pedipalps*

Cluster 7 showed an expression profile, which was mostly active during the juvenile stage, while showing less expression in subadult and adult male pedipalps (Figure 107). This cluster showed enrichment in GO terms associated with the regulation of coagulation, hemostasis, or platelet activation (supplemental material 9.5.3.3.1).

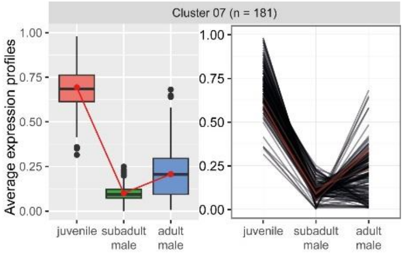

Figure 107 – Expression cluster 7 in pedipalps. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.5.2 *Active in subadult male pedipalps*

Cluster 1 showed almost no expression in the juvenile and adult male pedipalps, while the genes in this cluster were highly expressed in the subadult stage (Figure 108 A). The only GO term enriched in this cluster was the regulation of chemokine production (supplemental material 9.5.3.3.2). Cluster 3 showed a medium relative expression in juveniles and adults with a higher expression in the subadults (Figure 108 B). The genes in this cluster were enriched in GO terms associated with the processing and metabolism of RNAs (supplemental material 9.5.3.3.2). Cluster 5, again, showed an expression profile specific to the subadult male pedipalps (Figure 108 C), and was enriched for the GO terms chitin binding and structural constituent of cuticle (supplemental material 9.5.3.3.2). Cluster 17 showed an expression profile with lowest expression in the juvenile pedipalps, peak expression in the subadult males, and lower expression in the adults (Figure 108 D). This cluster, again, showed enrichment in GO terms of cuticle and chitin binding, as well as the activity of peptidases (supplemental material 9.5.3.3.2).

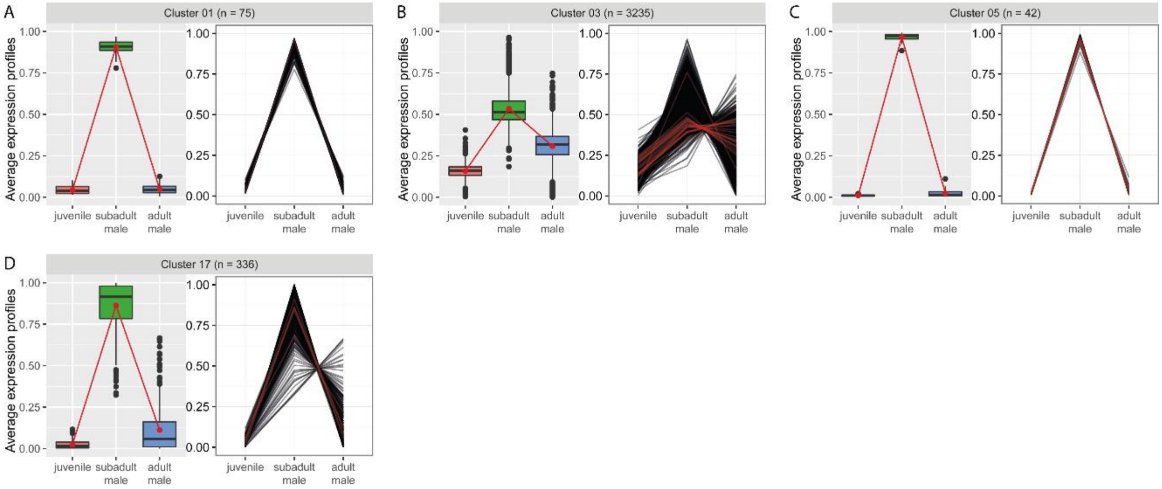

Figure 108 - Expression clusters 01 (A), 03 (B), 05 (C), and 17 (D) in pedipalps, showing highest relative expression in the subadult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq.

7.2.5.3 *Low activity in subadult pedipalps*

Four clusters had expression profiles with the lowest expression in the subadult male pedipalps. Cluster 13 showed intermediate expression levels in juveniles and adults, while being strongly reduced during the subadult stage (Figure 109 A). Enriched GO terms in this cluster were associated with different binding activities (heme, tetrapyrrole, lipids, iron ions) and the activity of oxidoreductase (supplemental material 9.5.3.3.3). The expression profile of cluster 14 showed an intermediate expression in the juvenile stage, followed by almost no expression during the subadults, while expression levels peaked at the adult stage (Figure 109 B). The GO terms enriched in this cluster were mainly associated with the detection of external stimuli (supplemental material 9.5.3.3.3). Cluster 15 showed a similar expression profile, with slightly higher expression levels in the subadult tissue (Figure 109 C). The enriched GO terms in this cluster were associated with the synapse organisation, transmembrane transport and the regulation cGMP (supplemental material 9.5.3.3.3). Cluster 16 mainly showed intermediate expression levels in the juvenile peidpalps, lowest expression in the subadult male pedipalps and rising expression in the adult pedpalps (Figure 109 D). This cluster was enriched in GO terms associated with the metabolism of lipids and acyl-CoA metabolism (supplemental material 9.5.3.3.3).

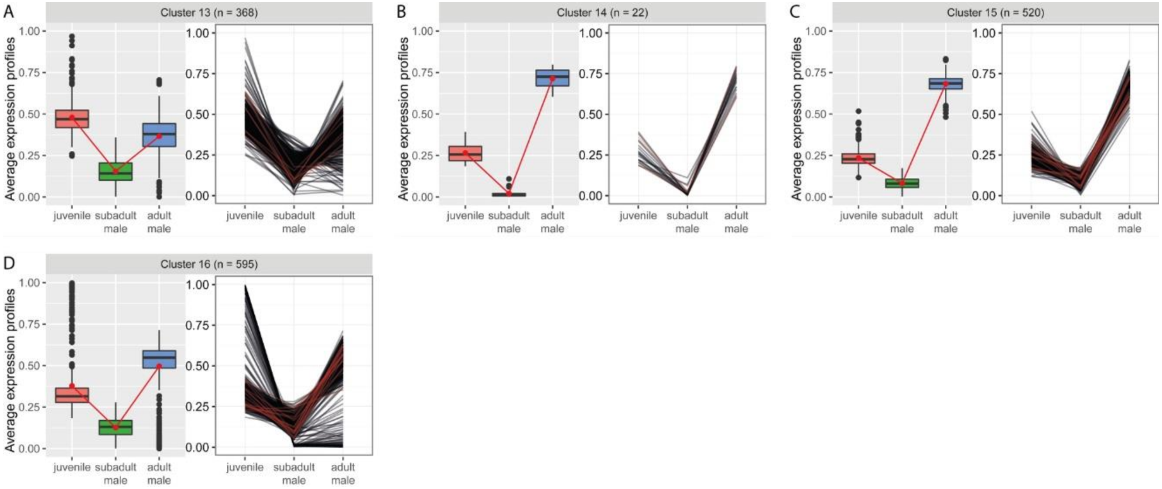

Figure 109 - Expression clusters 13 (A), 14 (B), 15 (C), and 16 (D) in pedipalps, showing lowest relative expression in the subadult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq

7.2.5.4 *Active in adult male pedipalps*

Genes in seven clusters showed their highest expression in the adult male pedipalps, while no or little expression could be seen in the earlier stages. Cluster 2 showed a very specific expression only in the adult male pedipalps (Figure 110 A). The GO terms found to be enriched in this cluster associated with the inhibition of enzymatic activity, especially that of endopeptidases, as well as the coagulation of hemolymph and the disassembly of the basement membrane (supplemental material 9.5.3.3.4). Cluster 4 showed low to intermediate expression in the juvenile and subadult male pedipalps and a high relative expression in the adult male pedipalps (Figure 110 B). GO terms in this cluster were enriched for the activity of ligases, as well as the regulation of peptidases (supplemental material 9.5.3.3.4). Cluster 6 showed an expression profile, again very specific in the adult tissue (Figure 110 C). This cluster also showed an enrichment in GO terms for the regulation of peptidase activities, as well as the binding of kringle domains and insulin-like growth factors (supplemental material 9.5.3.3.4). Cluster 10 showed very low expression of its genes in the juvenile stage, even less expression in the subadult male pedipalps, followed by peak expression in the adult tissue (Figure 110 D). GO terms associated with this cluster were enriched for ion channels and cell-substrate junctions (supplemental material 9.5.3.3.4). Cluster 11 showed an expression profile similar to cluster 10 with low expression in juvenile and subadult male pedipalps and high expression in adults (Figure 110 E). The GO terms enriched in this set of genes were related to various kinds of transport activities (supplemental material 9.5.3.3.4). Cluster 12 showed relatively low expression levels in juvenile and subadult male pedipalps, while rising to higher levels in adult tissue (Figure 110 F). Genes in this cluster showed an enrichment in GO terms for biological regulation, as well as organelle fusion, signal transduction, and protein binding (supplemental material 9.5.3.3.4). Cluster 18 showed very specific expression in the adult male pedipalps, while expression levels in the earlier stages were at a minimum (Figure 110 G). GO terms found to be enriched in the metabolism of glycerol and ethers (supplemental material 9.5.3.3.4).

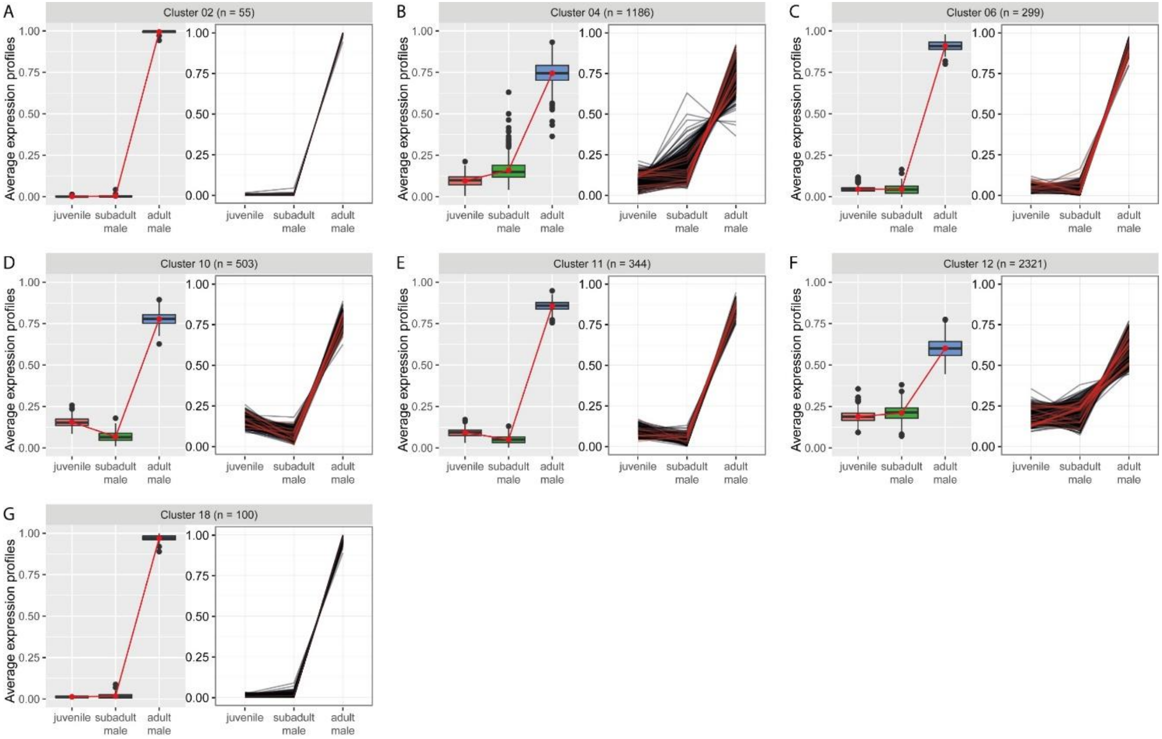

Figure 110 - Expression clusters 02 (A), 04 (B), 06 (C), 10 (D), 11 (E), 12 (F), and 18 (G) in pedipalps, showing highest relative expression in the adult stage. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq

7.2.5.5 *Increasing expression over develoment*

The expression profile of cluster 9 showed a continuous increase in relative expression from juvenile to adult male pedipalps (Figure 111). This cluster showed enrichment in GO terms associated with the regulation of gene expression and metabolic processes and protein localisation (supplemental material 9.5.3.3.5).

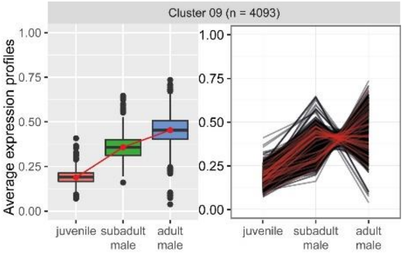

Figure 111 – Expression cluster 9 in peidpalps. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq

7.2.5.6 *Continous expression during development*

Cluster 12 showed an expression profile, which was relatively continuous throughout the developemtnal stages analysed (Figure 112). The GO terms enriched in this set of genes were associated with the organisation of cilia, activity of inositol hexakisphosphate kinase, as well as butyryl-CoA dehydrogenase activity and forebrain development (supplemental material 9.5.3.3.6).

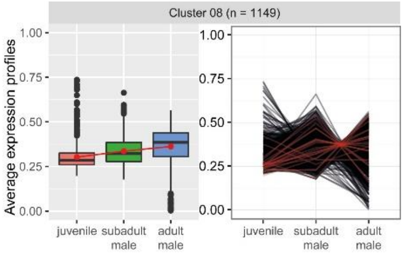

Figure 112 – Expression cluster 8 in pedipalps. Left: Box plots with the general progression of the expression profile from juvenile to adult. Right: Graph showing the relative expression profiles of all genes assigned to this cluster. Y-axis shows the relative expression levels of clustered genes as calculated by coseq

7.2.6 Combination of differential expression and specific timing of activity

The metamorphosis of the bulbus organ of the male pedipalps appears to happen very specifically during the subadult stage (Coddington 1990). Therefore, genes which are involved in the development of this structure should not only be differentially expressed between the male and female pedipalps at this stage, but should also show a peak of expression in subadult male pedipalps. The list of genes, which are present in both approaches should be highly specific in promoting the metamorphosis of immature male pedipalps into the adult structure. On the other hand, there should be genes, which are needed for the normal development of an appendage structure, or the female specific development of the pedipalps. These genes should be differentially expressed between the subadult male and female pedipalps, while their expression profile should be at a minimum in the subadult male pedipalps. For a short description of the gene functions in this part, associated GO terms from the GO database were used (Ashburner et al. 2000, Blake et al. 2015).

7.2.6.1 *Male-specific genes with activity in the subadult stage*

There were 136 genes, which specifically up-regulated in the male subadult pedipalps, compared to the female subadults, and which were included in clusters, that showed specific activity in the male subadult pedipalps. 46 of these genes showed no similarities with other genes, or were annotated as uncharacterized protein via blast. 28 genes were involved in various aspects of cell cycle progression, RNA processing, or are constituents of cellular structures (Table 17). Histone H2A and the two HMG protein are part of the nucleosomes, while Lamin and the nuclear pore membrane glycoproteins are constituents of the nuclear membrane. Skeletor, the targeting protein for Xklp2, ERCC-6-like, and the spindle associated and abnormal spindle-like protein are involved in the assembly of the mitotic spindle apparatus, while the homologs of Geminin, Cdc-20, Cdk-1, MAD2A-like, and Cyclin-B are involved in the transition of cell cycle phases. 4 homologs of kinesins and anilin-like are involved in the progression of cytokinesis. Finally, the genes associated with transcription and translation are a subunit of the ribonucleoprotein complex, which is involved in ribosome biogenesis and two Serine/arginine repetitive matrix proteins, as well as the nucleolar protein 14, which are involved in splicing.

Table 17 – Male spefifc genes associated with cell cycle.

Augustus ID	Blast annotation	Function
aug3.g3249.t1	Protein regulator of cytokinesis 1-like	cytokinesis
aug3.g3831.t1	Kinesin-like protein KIF23	cytokinesis
aug3.g4059.t1	Nucleolar protein 14 homolog	splicing
aug3.g4311.t1	Carboxy-terminal kinesin 2-like	cytokinesis
aug3.g5361.t3	Skeletor	Mitotic spindle
aug3.g7148.t1	Lamin Dm0-like	Nucleus part
aug3.g7252.t1	Geminin	Cylce transition
aug3.g7601.t1	Histone H2A-like	nucleosome
aug3.g8469.t1	G2/mitotic-specific cyclin-B-like	Cycle transition
aug3.g8839.t1	Serine/arginine repetitive matrix protein 1-like	splicing
aug3.g9690.t1	Mitotic spindle assembly checkpoint protein MAD2A-like	Cycle transition
aug3.g11601.t1	Cyclin-dependent kinase 1-like	Cycle transition
aug3.g12249.t1	H/ACA ribonucleoprotein complex subunit 4-like	Ribosome biogenesis
aug3.g14278.t1	G2/mitotic-specific cyclin-B3-like	Cycle transition
aug3.g15794.t1	Abnormal spindle-like microcephaly-associated protein homolog	Mitotic spindle
aug3.g16167.t1	High mobility group protein HMG-I/HMG-Y-like	nucleosome
aug3.g17615.t1	Kinesin-like protein KIF20B	cytokinesis
aug3.g18726.t1	DNA excision repair protein ERCC-6-like	Mitotic spindle
aug3.g19167.t1	Nuclear pore membrane glycoprotein 210-like	Nucleus part
aug3.g19893.t1	Kinesin-like protein KIF11-B	cytokinesis
aug3.g20612.t1	Nuclear pore membrane glycoprotein 210-like	Nucleus part
aug3.g20875.t1	Cell division cycle protein 20 homolog	Cycle transition
aug3.g23896.t1	Targeting protein for Xklp2-like	Mitotic spindles
aug3.g24664.t1	High mobility group protein HMG-I/HMG-Y-like	nucleosome
aug3.g24980.t1	Nucleolar and spindle-associated protein 1-like	Mitotic spindle
aug3.g25352.t1	Structural maintenance of chromosomes protein 2-like	Cycle transition
aug3.g26302.t1	Serine/arginine repetitive matrix protein 2-like	splicing
aug3.g27287.t1	Actin binding protein anilin-like	cytokinesis

8 genes were contituents of cuticle, or the adult-specific rigid cuticle. This list also contained the homologs of a chitinase and a beta-hexosaminidase, involved in the decomposition of chitin (Table 18). 5 genes are genes associated with structure (Table 18). Three of them were glycine-rich proteins, while Restin is involved in regulation of the microtubule cytoskeleton, and hornerin in the keratinization of epidermal tissue. 3 of the genes were associated with adhesion (Table 18). Four-jointed is a kinase, which acts on cadherins, such as Fat and Ds, and is also involved in the establishment of planar cell polarity. Starry night (Stan) is itself a cadherin, which not only controls planar cell polarity, but is also involved in dendrite morphogenesis and axon guidance, while Chaoptin is a component of the plasma membrane, which facilitates homophylic cell adhesion.

Table 18 – Male specific genes associated with structure.

Augustus ID	Blast annotation	Function
aug3.g581.t1	Four-jointed-like	Cell adhesion
aug3.g797.t1	Cuticle protein 6-like	Constituent of cuticle
aug3.g4085.t1	Glycine-rich cell wall structural protein 1.8-like	-
aug3.g6274.t1	Cuticle protein 16.8-like	Constituent of cuticle
aug3.g11261.t1	Cuticle protein 10.9-like	Constituent of cuticle
aug3.g11423.t1	Glycine-rich cell wall structural protein 1.8-like	-
aug3.g14123.t1	Cuticle protein 10.9-like	Constituent of cuticle
aug3.g15160.t1	Starry night	Cell adhesion
aug3.g16431.t1	Beta-hexosaminidase	Chitin decomposition
aug3.g18218.t1	Adult-specific rigid cuticular protein 15.7-like	Constituent of cuticle
aug3.g19089.t1	Glycine-rich protein-like	-
aug3.g19101.t1	Adult-specific rigid cuticular protein 15.7-like	Constituent of cuticle
aug3.g21266.t1	Acidic mamalian chitinase-like	Chitin decomposition
aug3.g22816.t1	Cuticle protein 10.9-like	-
aug3.g24987.t1	Restin homolog	Microtubule cytoskeleton
aug3.g26610.t1	Hornerin-like	Keratinization of epidermal tissue
aug3.g26906.t1	Chaoptin-like	Component of plasma membrane

5 genes are involved in transporter or channel activity (Table 19), such as the transporters for monocarboxylate, zinc, and inorganic phosphate, as well as a member of the major facilitator superfamily domain-containing protein, and the homolog of Annexin A7, which can form channels through membranes.

Table 19 – Male specific genes associated with transporter activity.

Augustus ID	Blast annotation	Function
aug3.g7424.t1	Sodium-coupled monocarboxylate transporter 2-like	Transporter
aug3.g10764.t1	Annexin A7-like	Channel
aug3.g16026.t1	Major facilitator superfamily domain-containing protein 6-like	Transporter
aug3.g18010.t1	Zinc transporter SLC39A7	Transporter
aug3.g19984.t1	Sialin-like (putative inorganic phosphate cotransporter)	Transporter

13 enzymes were found to be specifically up-regulated in the male subadult pedipalps. 9 of these could not be assigned to any specific pathway. However, the TTK-like kinase is involved in cell proliferation and both, the short-chain specific acyl-CoA dehydrogenase and L-threonine 3-dehydrogenase are metaolic enzymes in mitochondria.

Table 20 – Male specific enzymes

Augustus ID	Blast annotation	Function
aug3.g226.t1	NADPH oxidase 4-like	Redox signalling
aug3.g3587.t1	Dual specificity protein kinase TTK-like	Phosphorylase (cell proliferation)
aug3.g4432.t1	Lysosomal acid Phosphatase-like	Phosphatase
aug3.g6268.t1	Alpha/beta hydrolase	Hydrolase

aug3.g9237.t1	Nose resistant to fluoxetine protein 6-like	Acyl-transferase
aug3.g10728.t1	Ectonucleotide pyrophosphatase/phosphodiesterase 6-like	Esterase
aug3.g12063.t1	Peroxisomal (S)-2-hydroxy-acid oxidase GL03-like	Oxidoreductase
aug3.g12644.t2	Serine protease 27-like	peptidase
aug3.g14576.t1	Short-chain specific acyl-CoA dehydrogenase, mitochondrial-like	Dehydrogenase (fatty acid metabolism)
aug3.g16696.t1	Peroxidase-like	peroxidase
aug3.g23385.t1	Decraprenyl-diphosphate synthase subunit 2-like	Synthase
aug3.g23526.t1	L-threonine 3-dehydrogenase, mitochondrial-like	Dehydrogenase (Amino acid metabolism)
aug3.g24467.t1	Aldehyde dehydrogenase, mitochondrial-like	Dehydrogenase

11 genes were identified, which are transcription factors (Table 21). Among these were three forkhead domain genes (FoxL2, Croc, Slp), the two homeodomain transcription factors engrailed and LBX1-like (ladybird-early), the homolog of the T-box transcription factor TBX20, SOX-14-like, the paired box gene Pax-1-like, and Doublesex- and mab 3-related factor 1B-like, which play roles in sex determination, as well as the homolog of homeobox protein 2.

Table 21 – Male specific transcription factors.

Augustus ID	Blast annotation	Domain
aug3.g558.t2	Doublesex- and mab-3-related transcription factor 1B-like	DM domain
aug3.g2665.t1	SOX-14-like	HMG-box
aug3.g7640.t1	FOXL2	Forkhead
aug3.g8638.t1	Crocodile	Forkhead
aug3.g8837.t1	T-box transcription factor TBX20-like	T-box
aug3.g8968.t2	Pax-1-like	Paired-box
aug3.g13322.t1	Zinc finger protein 358-like	Zinc finger
aug3.g15983.t1	Engrailed	homeobox
aug3.g16867.t1	LBX-1like	homeobox
aug3.g23979.t1	Sloppy paired	forkhead
aug3.g27943.t1	Homeobox protein 2-like	-

15 genes were specifically up-regulated in the subadult male pedipalps for which no specific function was annotated, or which fit none of the above categories. Two Mucin homologs were identified, which are involved in anti-microbial defense. Homologs of Calumenin, Peroxidasin, 5-Formyltetrahydrofolate cyclo-ligase were contained in these genes, which are involved in metabolic processes of amino acids, peroxides, and folic acid, respectively. Other genes are involved in the formation of gap junctions between cells (Innexin 2-like), act as chaperones in protein folding (lethal(2)essential for life-like), intracellular signalling (Ca(2+)/calmodulin-responsive adenylate cyclase), phagocytosis (Multiple epidermal growth factor-like domains protin 10). Or immune response (Somatomedin-B anf Thrombospondin type-I domain containing protein-like).

Table 22 – Other male specific genes.

Augustus ID	Blast annotation	Function
aug3.g1913.t1	Mucin-7-like	Anti microbial
aug3.g4731.t1	Calumenin-like	Amino acid carboxylation
aug3.g5634.t1	Ankyrin repeat and BTB/POZ domain-containing protein 2-like	-

aug3.g10448.t1	Innexin 2-like	Gap junctions
aug3.g10619.t1	Matrix metalloproteinase 2-like	-
aug3.g11038.t1	Rho GTPase-activating protein 19-like	-
aug3.g13280.t2	EMI domain-containing protein 1-like (Collagen alpha-1 chain-like)	-
aug3.g14129.t1	Protein lethal(2)essential for life-like (Heat shock protein beta-2)	Protein folding
aug3.g14327.t1	Mucin-5AC-like	Anti microbial
aug3.g20742.t1	Peroxidasin homolog	Peroxide metabolism
aug3.g23791.t1	Ca(2+)/calmodulin-responsive adenylate cyclase-like	Intracellular signalling
aug3.g23881.t1	Multiple epidermal growth factor-like domains protein 10	phagocytosis
aug3.g24883.t1	5-Formyltetrahydrofolate cyclo-ligase-like	Folic acid metabolism
aug3.g26353.t1	Histidine-rich protein PFHRP-II-like	-
aug3.g26535.t1	Somatomedin-B and Thrombospondin type-I domain-containing protein-like	Immune response

7.2.6.2 *Genes specifically down-regulated in subadult males*

224 genes were both down-regulated in subadult male pedipalps in comparison to their female counterparts and were contained in cluster with an expression profile showing a minimum in the subadult male pedipalps. 97 of these genes showed either no homology with other proteins in a blast search, or were annotated as uncharacterized proteins. 33 of these genes were involved in neuronal or transport activities (Table 23). 15 of these form or control channels through membranes, another 11 were annotated as transport molecules. There was one alkaloid and one octopamine receptor each, as well as three genes involved in vesicle maturation and endocytosis. The G-protein coupled receptor and the homolog of turtle are both involved in the organization of synapses. The homolog of the acetylcholinesterase, synaptosomal-associated protein 25, and kainite-1 are associated with neurotransmitters, while the BAI1-associated protein 3-like, IDLSRF-like peptide, and the neuroendocrine protein 7B2-like are involved in signalling.

Table 23 – Male specifically down-regulated genes associated with neural functions.

Agustus ID	Blast annotation	Function
aug3.g235.t1	BAI1-associated protein 3-like	Signal transduction
aug3.g672.t1	Protein unc-13 homolog A	Vesicle maturation
aug3.g735.t1	Annexin A7-like	Channel
aug3.g1472.t1	Probable G-protein coupled receptor No18	Octopamine receptor activity
aug3.g1512.t1	Adhesion G protein-coupled receptor L3-like	Glutamatergic synapses
aug3.g2810.t1	Monocarboxylate transporter 10-like	Transporter
aug3.g2811.t1	Monocarboxylate transporter 10-like	Transporter
aug3.g3883.t1	neural cell adhesion molecule 2-like	olfaction
aug3.g4418.t1	Acetylcholinesterase-like	Neurotransmitter
aug3.g4981.t1	Sodium- and chloride-dependent glycine transporter 2-like	Transporter
aug3.g5618.t1	Acid-sensing ion channel 2-like	Channel
aug3.g7422.t1	Putative sodium-dependent multivitamin transporter	Transporter
aug3.g7521.t1	Neuroendocrine protein 7B2-like	Neuropeptide signalling
aug3.g7522.t1	Anoctamin-7-like	Channel
aug3.g9003.t1	Amiloride-sensitive sodium channel subunit beta-like	Channel
aug3.g10776.t1	Adenosine 3'-phospho 5'-phosphosulfate transporter 1-like	Transporter
aug3.g12976.t1	5-hydroxytryptamine receptor 1-like	Alkaloid receptor

aug3.g13687.t1	Sodium/potassium-transporting ARPase subunit alpha-B-like	transporter
aug3.g13972.t1	H(+)/Cl(-) exchange transporter 5-like	transporter
aug3.g14675.t1	IDLSRF-like peptide	Neuropeptide signaling
aug3.g15211.t1	Synaptosomal-associated protein 25-like	Neurotransmitter
aug3.g15866.t1	EF-hand calcium-binding domain-containing protein 1-like	Channel
aug3.g16668.t1	Vesicular glutamate transporter 1-like	Transporter
aug3.g18431.t2	Acid-sensing ion channel 1-like	Channel
aug3.g18643.t2	Sodium- and chloride-dependent glycine transporter 2-like	Transporter
aug3.g21367.t1	Degenerin mec-10-like	Channel
aug3.g21368.t1	Acid-sensing ion channel 4-like	Channel
aug3.g23687.t1	Clavesin-2-like	Transporter
aug3.g25661.t1	Putative inorganic phosphate cotransporter	Transporter
aug3.g25690.t1	Protein turtle-like	Synapse organization
aug3.g26220.t1	Polycystic kidney disease 2-like 1 protein	Channel
aug3.g26968.t1	SCY1-like protein 2	Endocytosis
aug3.g27535.t1	Glutamate receptor ionotropic, kainate 1-like	Neurotransmitter

17 genes were associated with various aspects of lipid synthesis and metabolism (Table 24). 6 enzymes, which are involved in fatty acid or lipid metabolism. 4 SEC14-like proteins, which bind lipids and three homologs of the Nose resistant to fluoxetine protein 6, which transport lipids. Among this list was also the Long-chain-fatty-acid—CoA ligase 1-like, which activates fatty acids and three endocytosis related genes, which are involved in the uptake of HDLs, VLDLs, or LDL receptors. 6 genes in this list were associated with motor activity (Table 25). Three of these were constitiuents of dynein, or involed in its assembly. Two of these genes were Nephrin homologs, which bind myosin, and one was the homolg of the Kyphoscoliosis peptidase, wich is involved in sarcomere formation.

Table 24 – male specifically down-regulated genes associated with lipids.

Augustus ID	Blast annotation	Function
aug3.g403.t1	Low density lipoprotein receptor adapter protein 1-B-like	Endocytosis of LDL receptor
aug3.g1809.t1	Long-chain-fatty-acid--CoA ligase 1-like	Activation of fatty acids
aug3.g3267.t1	SEC14-like protein 3	Lipid binding
aug3.g3895.t1	Fatty acyl-CoA reductase 1-like	Fatty acid metabolism
aug3.g4485.t1	Phospholipase A2 Scol/Pla-like	Fatty acid metabolism
aug3.g4786.t1	Patanin-like phospholipase domain-containing protein	Lipid metabolism
aug3.g6770.t1	Nose resistant to fluoxetine protein 6-like	Lipid transport
aug3.g6074.t1	Elongation of very long chain fatty acids protein AAEL008004	Fatty acid metabolism
aug3.g8491.t2	SEC14-like protein 2	Lipid binding
aug3.g9796.t1	Low-density lipoprotein receptor-related protein 2-like	HDL endocytosis
aug3.g10901.t1	Nose resistant to fluoxetine protein 6-like	Lipid transport
aug3.g13299.t1	SEC14-like protein	Lipid binding
aug3.g16555.t1	SEC14-like protein 3	Lipid binding
aug3.g16570.t1	Stearoyl-CoA desaturase 5-like	Fatty acid metabolism
aug3.g19230.t1	Fatty-acid synthase-like	Fatty acid metabolism
aug3.g19695.t1	Very low-density lipoprotein receptor-like	VLDL endocytosis
aug3.g20583.t1	Nose resistant to fluoxetine protein 6-like	Lipid transport

Table 25 – Male specifically down-regulated genes associated with muscles.

Augustus ID	Blast Annotation
aug3.g2526.t6	Dynein heavy chain 2, axonemal-like
aug3.g4279.t1	Dynein asssembly factor 1, axonemal homolog
aug3.g4728.t1	Dynein heavy chain 7, axonemal-like
aug3.g6721.t1	Nephrin-like
aug3.g11972.t1	Kyphoscoliosis peptidase-like
aug3.g15010.t1	Nephrin-like

7 of the genes in this list were involved in homophilic or heterophilic cell adhesion (Table 26). 6 other genes were associated with aspects of structure (Table 27). Fillagrin-2 is involved in the establishment of the skin barrier as a structural molecule, while the homolog of CG42247 binds to microtubules and is involved in locomotory behavior.

Table 26 – Male specifically down-regulated genes associated with adhesion.

Augustus ID	Blast annotation	Function
aug3.g6887.t1	Chaoptin-like	Homophilic cell adhesion
aug3.g15394.t1	P-selectin	Heterophilic cell adhesion
aug3.g17018.t1	Dscam	Homophilic cell adhesion
aug3.g17083.t1	FRAS1-related extracellular matrix protein 2-like	Cell adhesion
aug3.g17489.t1	Dscam2	Homophilic cell adhesion
aug3.g27356.t1	Chaoptin-like	Homophilic cell adhesion
aug3.g27791.t2	Dscam2	Homophilic cell adhesion

Table 27 – Male specifically down-regulated genes associated with structure.

Augustus ID	Blast annotation
aug3.g5323.t1	Glycine-rich cell wall structural protein-like
aug3.g5743.t1	Filaggrin-2-like
aug3.g11987.t1	Echinoderm microtubule-associated protein-like CG42247
aug3.g16966.t1	small proline-rich protein 2H-like
aug3.g17740.t1	Cuticle collagen 2-like
aug3.g21830.t1	Collagen alpha-1(I) chain-like

11 genes, which were specifically down-regulated in subadult male pedipalps were associated with signaling in several pathways (Table 28). Dorsalin1-like and CD109 antigen-like are involved in signaling with TGF-beta. RTK signaling was represented by the homologs of a Leucine-rich repeats and immunoglobulin-like domains protein, Diaglycerol kinase theta, the Receptor-type tyrosine-protein phosphatase T, and a Phosphodiesterase. Arrestin-like and the adhesion G-protein coupled receptor D1-like are involved in GPC signaling, while the Corticotropin-releasing factor-binding protein-like, the Calcium/calmodulin-dependent phosphodiesterase 1C-like and the Granulins-like protein are associated with general signal transduction activities.

Table 28 – Male specifically down-regulated genes associated with signaling.

Augustus ID	Blast annotation	Pathway
aug3.g540.t1	Dorsalin-1-like	TGF-beta signalling
aug3.g1777.t1	Corticotropin-releasing factor-binding protein-like	Intracellular signaling, response to hormones
aug3.g2192.t1	Leucine-rich repeats and immunoglobulin-like domains protein	RTK signaling
aug3.g2288.t1	CD109 antigen-like	TGF-beta signalling
aug3.g4649.t1	Diaglycerol kinase theta-like	RTK signalling
aug3.g11520.t1	Arrestin, lateral eye-like	GPC signalling
aug3.g15741.t2	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C-like	Signal transduction
aug3.g15923.t1	Receptor-type tyrosine-protein phosphatase T-like	RTK signalling
aug3.g16161.t1	Adhesion G-protein coupled receptor D1-like	GPC signalling
aug3.g18550.t1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase	RTK signalling
aug3.g21854.t1	Granulins-like	Signal transduction

6 genes were associated with activities in transcription. TATA-binding protein-associated factor 2N-like is involved in the start of general transcription. The Guanine nucleotide-binding protein subunit beta 2-like negatively regulates the progression of the cell cycle, while the homologs of Scratch-2, NF-X1, and the member of the AfsR family are all known to negatively regulate transcription in general.

Table 29 – Male specifically down-regulted genes associated with transcription.

Augustus ID	Blast annotation
aug3.g2608.t1	TATA-binding protein-associated factor 2N-like
aug3.g8096.t1	Guanine nucleotide-binding protein subunit beta-2-like
aug3.g8916.t1	Transcriptional repressor scratch 2-like
aug3.g15673.t1	Zinc finger protein 41-like
aug3.g17708.t1	Transcriptional repressor NF-X1
aug3.g18215.t1	AfsR family transcriptional regulator

18 genes, which were specifically down-regulated in the subadult male pedipalps were associated with toxins (Table 30). 9 of these were homologs of Alpha and Delta latrotoxins, in addition to 3 Latrotoxin associated proteins. Moreover, this list contained two homologs of venom peptides, as well as 3 other toxin genes and a gene annotated as the Crustacean hyperglycemic hormone 6-like.

Table 30 – Male specifically down-regulated genes associated with toxins.

Augustus ID	Blast annotation
aug3.g427.t1	U8-agatoxin-Ao1a-like
aug3.g1194.t1	Alpha-latrotoxin-Lh1a-like
aug3.g5236.t1	Alpha-latrocrustotoxin-Lt1a-like
aug3.g5430.t1	U9-ctenotoxin-Pr1a-like
aug3.g7397.t1	Alpha-latrotoxin associated low molecular weight protein SVG150-311-like
aug3.g7398.t1	Crustacean hyperglycemic hormone 6-like

aug3.g7399.t1	Alpha-latrotrotoxin associated low molecular weight protein SVG150-311-like
aug3.g10236.t1	Toxin CSTX-10-like
aug3.g11807.t1	Alpha-latrotoxin associated low molecular weight protein 2
aug3.g14215.t1	Delta-latroinsectotoxin-Lt1a-like
aug3.g14217.t1	Delta-latroinsectotoxin-Lt1a-like
aug3.g14218.t1	Delta-latroinsectotoxin_Lt1a-like
aug3.g16830.t1	Alpha-latrocrustotoxin-Lt1a-like
aug3.g18022.t1	Delta-latroinsectotoxin-Lt1a-like
aug3.g21759.t1	Venom peptideSjAPI-like
aug3.g25578.t1	Delta-latroinsectotoxin_Lt1a-like
aug3.g26326.t1	Delta-latroinsectotoxin-Lt1a-like
aug3.g27022.t1	Venom protein 164-like

23 genes were identified in this approach, which did not fit any of the above categories (Table 31). 4 genes were enzymes with peptidase (Equistatin-like, Membrane metallo-endopeptidase-like 1) or hydrolase (ABHD11-like, Histidine triad nucleotide-binding protein 3-like) activities. The homologs of Hemicentin-1, KIF13B are involved in aspects of cell-cycle progression. Other genes carry out transport functions (Cytochrome P450 3A19-like and 3A2-like, Transport and Golgi organizing protein 2, Translocon-associated protein subunit beta-like).

Table 31 – Other genes specifically down-regulated in subadult male pedipalps.

Augustus ID	Blast annotation	Function
aug3.g792.t1	Equistatin-like	Endopeptidase
aug3.g5487.t1	Hemicentin-1-like	cleavage
aug3.g7542.t1	Transport and Golgi organizing protein 2 homolog	Golgi apparatus
aug3.g10069.t1	Serine-rich adhesin for platelets-like	Pathogenesis
aug3.g10533.t2	Stathmin domain-containing protein 1-like	Cell cycle regualtion
aug3.g12555.t1	DUF4876 domain-containing protein	-
aug3.g13904.t1	BTB/POZ domain-containing protein 6-like	Protein metabolism
aug3.g14726.t1	Cytochrome P450 3A19-like	Electron transport
aug3.g16252.t1	Meiotic recombination protein DMC/LIM15 homolog	Meiosis
aug3.g17093.t1	Chymotrypsin inhibitor-like	Digestion
aug3.g17736.t1	Collagen and Calcium-binding EGF domain-containing protein 1-like	Angiogenesis
aug3.g18496.t1	Kinesin-like protein KIF13B	Cytokinesis
aug3.g18747.t1	Cytochrome P450 3A2-like	Electron transport
aug3.g19900.t1	Neprilysin-2-like	Olfaction
aug3.g20785.t1	Membrane metallo-endopeptidase-like 1	Peptidase
aug3.g21924.t1	Putative phosphoenolpyruvate synthase	Transferase
aug3.g23741.t1	Multiple coagulation factor deficienca protein 2 homolog	Secretion
aug3.g23997.t1	Parathymosin-like	Immune response
aug3.g24001.t1	SPRY domain-containing SOCS box protein 3-like	Ubiquitination
aug3.g24842.t1	Translocon-associated protein subunit beta-like	Transport to ER
aug3.g25284.t1	Protein ABHD11-like	Hydrolase
aug3.g26555.t2	Histidine triad nucleotide-binding protein 3-like	Hydrolase
aug3.g27758.t1	Coiled-coil domain containing protein CG32809-like	Protein dimerization

7.3 DISCUSSION

7.3.1 Subadult male pedipalps show high amounts of differentially expressed genes in relation to legs

In the comparisons of the different tissue samples of juveniles, subadults, and adults among one another, the main differences could be seen between the two appendage types in contrast to the opisthosoma. The number of differentially expressed genes between the pedipalps and the legs was considerably lower in juveniles and adult males. This reduced diversity of gene expression between these two tissues reflects the fact that they are both types of appendages, which share more features than the appendages share with the opisthosoma. In contrast to this general trend, the number of differentially expressed genes between the subadult pedipalps and the corresponding legs was higher than compared to the other stages. While in subadult female pedipalps more than 5000 genes were differentially expressed, the number in the subadult males was highest with more than 10,000, indicating, that there is sex-specific development in both these tissues, with the need for more differentially expressed genes in subadult males pedipalps in which the bulbus organ develops at this time (Coddington 1990), in contrast to the legs.

7.3.2 The development of male pedipalps is different from other appendages

7.3.2.1 *Juvenile appendages and pedipalps*

In the juvenile stage, 9936 genes were differentially expressed between the appendages and the opisthosoma and 338 were specifically differentially expressed in the pedipalps of juveniles. The genes up-regulated in the appendages showed enrichment for GO terms associated in the development and morphogenesis of anatomical structures, while the down-regulated genes showed enrichment of terms concerning the activity of transporters and metabolic processes. On the other hand, genes, which were specifically involved in the difference of the juvenile pedipalps were enriched for GO terms of exocytosis and channel activity, while terms for the development of muscle tissue were associated with down-regulated genes. Although the number of genes differentially expressed between the legs and pedipalps in the juvenile stage was relatively low, the difference in the associated GO terms between the appendage-specific genes and the pedipalp-specific genes was clearly evident. While there was a number of developmental processes happening in the appendages in general, which indicates changes in the appendages between the different juvenile stages, the enriched terms for behavior and regulation, show that these tissues also need to be functioning in the juvenile spiders. The GO terms in the down-regulated genes showed a high enrichment for several metabolic processes, which also indicated the developing nature of the juvenile legs. The enrichment of genes associated channel activity and secretion in the genes specifically up-regulated in juvenile pedipalps is coherent with the special role of the pedipalps as a main source of sensory information. The enrichment of GO terms related to the development of muscles shows this process to be involved in the legs and opisthosoma at this stage, rather than the pedipalps.

7.3.2.2 *Subadult female appendages and pedipalps*

In subadult females, 11,029 genes were differentially expressed in the appendages compared to the opisthosoma and 1242 genes were differentially expressed specifically in the pedipalps. Up-regulated genes in the appendages were enriched for GO terms for the activity of channels, developmental processes, as well as adhesion, while catabolic processes, but also the activity of channels and transporters were among the enriched GO terms in the down-regulated genes. The GO terms associated with the up-regulated genes in subadult female pedipalps showed also a high enrichment in the activity of channels and exocytosis. The down-regulated genes in the pedipalps were enriched for GO terms for the regulation of metabolic processes and also the regulation of gene expression and apoptotic processes. Interestingly, there was virtually no difference between the enriched GO terms of the appendages between the juvenile sand the subadult females. This shows, that the subadult female appendages are still under the influence of developmental processes, and have not yet reached their final stage. The pedipalps in the subadult females were enriched with similar GO terms in the up-regulated genes as seen in the juveniles, indicating no difference between these two. Notably, the down-regulated genes were not enriched for GO terms associated with muscle development, but rather the regulation of metabolic and other processes. Since regulation in this case can mean either up- or down-regulation, it is not clear if the associated GO terms mean, for instance, an increase of apoptotic processes, or their decrease.

7.3.2.3 *Subadult male appendages and pedipapls*

In the subadult males, the number of differentially expressed genes specific to the appendages was with 7883 slightly less than the numbers seen in the previous stages. Notably, the number of genes, which were differentially expressed specifically in the pedipalps (1959) was comparable to the amount seen in the subadult female pedipalps. The amount of genes differentially expressed between the pedipalps and opisthosoma, and especially the pedipalps and legs showed large differences between the two subadult stages. The GO terms enriched in up- and down-regulated genes were consistent with the observations in the juvenile and subadult females. In the genes specifically differentially expressed in the subadult male pedipalps, GO terms which are associated with the processing of RNA, and specifically mRNA, were enriched in genes up-regulated here, indicating, that this tissue is occupied with the expression and regulation of the expression of genes. The down-regulated genes in the subadult male pedipalps, were enriched with GO terms associated with the cytoskeleton. Therefore, the developmental processes in the subadult male pedipalps are presumably involved in the specification of newly forming tissue, through the continuing heightened levels of gene expression, rather than maintenance of established structures.

7.3.2.4 *Adult male appendages and pedipalps*

In the adult males, 8037 genes were differentially expressed in the appendages. Up-regulated genes were highly enriched for GO terms involved in cell adhesion. Moreover, terms for developmental processes and structure development were still enriched. Metabolic processes and transporter activities were enriched in the genes down-regulated in the adult male appendages. In the genes differentially expressed in the pedipalps (844), GO terms associated with the activity of DNA polymerase and DNA replication and the action of transferases were enriched, while processes of specification and cell fate determination were found in the down-regulated genes. This change in associated GO terms suggests, that the developmental processes in the male pedipalps were finished and the transferase activity might indicate the involvement of regulatory complexes, such as Polycomb or Trithorax, which imprint expressional profiles in fully committed tissues (Schuettengruber et al. 2007). However, the activity of the DNA replication machinery indicates, that the tissue in the pedipalps might still be growing to its final size, while all necessary structures are already present, or that there is secretory tissue in the adult male pedipalps, which is needed for sperm storage. Such tissues are often associated with polyploid cells , especially since there were no GO terms associated with cytokinesis.

7.3.2.5 *Across development*

GO term enrichment among the genes differentially expressed in the appendages in contrast to the opisthosoma was very similar throughout the post-embryonic stages. The respective gene sets were enriched with terms associated with general developmental processes and the development of anatomical structures in the juvenile, both the subadult, and the adult appendages. The down-regulated genes showed a similar context as well. The activity of channels, transporters, and metabolic processes was enriched in these genes, reflecting that these structures are still developing, even in the adult stage, in contrast to the opisthosoma. More diversity in GO terms patterns could be seen in the genes specifically involved in the pedipalps. Genes associated in GO terms concerning exocytosis and channel activities were up-regulated in both, juvenile and subadult female pedipalps, showing a different trend as seen in the appendages in general. The depletion of genes associated with developmental processes and the regulation of gene expression indicates, that no major developmental processes are ongoing in this tissue. The male pedipalps, on the other hand, show ongoing developmental processes. Up-regulation of RNA metabolism and processing, and down-regulation of the actin cytoskeleton indicate the establishment of a new structure in this tissue at the subadult stage, while up-regulation of replication processes and down-regulation of specification related terms suggest the finalization of the development of this structure. In summary, the identified differences in the GO terms associated with the differentially expressed genes in the pedipalps compared to the appendages in general supports the assumption that a specific development in the male pedipalps (i.e. the bulbus organ) in the subadult stage and is finished in the adults.

7.3.3 Developmental differences in male pedipalps

7.3.3.1 *Juvenile to subadult*

In addition to showing the differences among the three tissue types in their own stage, the post-embryonic development of the male pedipalps was also investigated in this tissue type among the different stages. The transition of development from the juvenile pedipalps to the subadult male pedipalps confirmed the GO terms enriched in the differentially expressed genes that were identified before in the genes that were exclusively differentially expressed in the pedipalps. Up-regulated genes here were associated with the processing of RNA molecules, while down-regulated genes were associated with channel and transport activities. In contrast to the similar GO terms identified, the transition from juveniles to subadults showed the up-regulation of cell cycle associated genes. These terms come up as a difference between the juvenile and subadult pedipalps, but not between these in relation to other tissues of the same stage in the analysis above. This suggests the rate of cell division and thus tissue growth are similar between the tissues of the same stage and therefore can only be seen by the direct comparison between two stages. The identified GO terms were also reflected in the most differentially expressed genes. The terms in the up-regulated genes were very generic and only indicate a elevated transcriptional activity, which can only relate to the up-regulated genes in general. However, considering the GO terms identified for up-regulated genes in the subadult male appendages, the transcription factors like FOXL2 and Pax1-like fit the general developmental terms, while the homologs of Cuticle protein 10.9, Hornerin, and Skeletor account for the structure associated terms. In case of the top down-regulated genes Transient receptor potential homologs corresponded directly to the channel activities in the GO terms.

7.3.3.2 *Subadult males and females*

The most obvious comparison to find genes responsible for the male specific development of the pedipalps was to look into the differences of male and female structures at the stage when the differences are first visible, namely, the subadult male and female pedipalps (Coddington 1990). GO terms enriched in genes with male bias, again, showed RNA processing, but also the regulation of gene expression and biosynthetic processes, which relates to the still highly expressed transcription factors Pax-1-like and FOXL2, as well Crocodile, which was added to the top genes here. Genes with a female bias were enriched for GO terms were enriched for transporter and channel activities. The presence of the GABA receptor subunit beta in the top differentially expressed genes accounted for this. In addition, the gene, which was expressed the highest in subadult female pedipalps, compared to the males was Endothelin-converting enzyme 2-like, which plays a role in vasoconstriction, however there were no terms highly enriched in this, or related processes in the GO term analysis.

7.3.3.3 *Subadult to adult pedipalps*

The comparison between adult and subadult male pedipalps, showed the same trend as seen in the comparisons of subadult male and juvenile or female subadult pedipalps. Subadult male pedipalps were enriched for GO terms associated with RNA metabolism and processing, as well as biosynthetic processes, while the genes more strongly expressed in the adult pedipalps were enriched in terms of transport and cell adhesion. Similar terms as were found to be enriched in the genes up-regulated in the adult male pedipalps when compared to the adult tissues. The top up-regulated genes in the adult male pedipalps included a large number of Cathepsin and Serpin homologs. While Cathepsins are proteases and Serpins are protease inhibitors (Joyce & Hanahan 2004, Law et al. 2006), they both have roles in structural development. Cathepsins are involved in the degradation of the extracellular matrix and basal lamina (Wang & Shuaib 2007), while Serpins act as chaperones during the folding of collagen subunits and there is evidence that they can act as chromatin remodeling molecules (Grigoryev et al. 1999). While these processes were not enriched in the GO terms in the direct comparison of adult and subadult male pedipalps, they correspond to the structural developmental terms identified in the adult appendages compared to the opisthosoma. The GO terms associated with the genes higher enriched in the subadult male pedipalps showed the enrichment of RNA processing and biosynthetic processes, which were found in all the comparisons of this tissue with any other. From the point of view of the most differentially expressed genes, the subadult tissue also showed the presence of structural genes, such as Tubulin and cuticle proteins, as well as two genes involved in the development of neural tissue, the homolog of TLX3 and Achaete-scute homolog 1a. As supported by the GO term enrichment in the previous analyses, both tissues display developmental processes. In the subadult these appear to be concerned with intracellular structures and neural development, while in the adults there is structural development and rearrangement of tissue.

7.3.3.4 *Specificity of the identified gene sets*

The specificity of the genes and therefore in the associated GO terms, which were differentially expressed in the pedipalps was achieved in different ways. In the first approach the pedipalps were compared to the other tissues of the same age. Subsequently, comparing the processes in appendages in general and pedipalps specifically among the different stages and sexes. In the second approach, the pedipalps were first compared among the different samples. Therefore, the identified differentially expressed genes were not only specific to the pedipalps, but also contained the genes necessary for appendage development. More specificity was achieved by only considering genes, which were not only differentially expressed between the pedipalps themselves, but also between the different tissues. This attempt of showed that there were genes, which were shared between pedipalps and legs. Interestingly, all genes which were differentially expressed between the pedipalps in the different stages and between pedipalps and legs at the same stage were also differentially expressed between the pedipalps and opisthosoma at each stage. Thus, showing that the development of the male pedipalps is very distinct from other developmental processes.

7.3.3.5 *Novel genes in pedipalp development*

The genes identified to be most differentially expressed between the different stages of male pedipalp development contained a large number of previously uncharacterized genes. These have in common that they do not have any conserved domains in their amino acid sequence and that there are no homologous sequences to be found in other organisms, except for members of the chelicerate clade. The involvement of these genes in the development of the male pedipalp and their uniqueness to a group of animals, which possess these structures indicates male bulbus development to be a special adaptation of this clade, which does not seem to rely heavily on the co-option of evolutionarily conserved pathways.

7.3.4 Changes in GO terms between the different samples

Both analyses of pedipalp-specific gene expression single out the subadult male pedipalps as a tissue very different from other subadult male tissues and the other pedipalp tissues. RNA metabolism and processing are higher in this tissue than in any other, indicating an increase of transcriptional activity. This observation is also supported by the fact that there was a high increase of differentially expressed genes between the similar appendages pedipalps and legs at this stage (summarized in Figure 113).

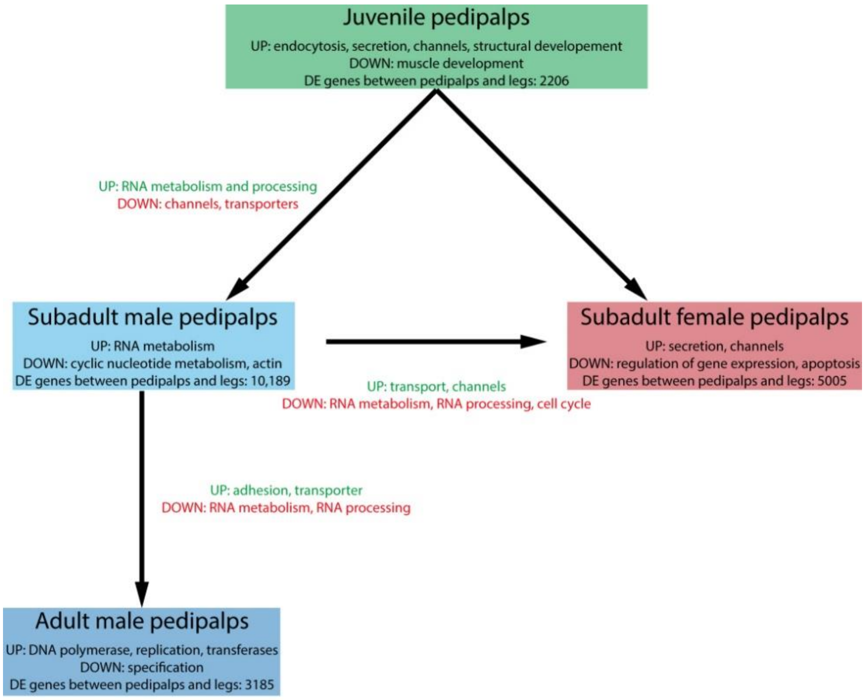

Figure 113 – Summary of enriched GO terms in pedipalps among tissues from the same stages and across development.

7.3.5 Clusters

The analysis of enriched GO terms in differentially expressed genes suggested, that the development of the bulbus organ in male pedipalps is a process that happens in the subadult stage. Therefore, all the expressed genes in all male spider tissues were clustered by their expression profile, thus identifying processes, which are stage specific by the analysis of enriched GO terms in all the clusters identified.

The 12 identified clusters with different expression profiles in the male legs showed the activity of genes with terms for collagen, histone dephosphorylation, and the binding of snoRNAs enriched in the juvenile and subadult legs, while their expression was reduced in the adult tissue. The subadult legs showed heightened or exclusive expression of genes involved in structural processes, such as cuticle constituents, chitin binding, but also oxygen transport and to a smaller extent oxidation and metabolism. Processes restricted to the adult legs were the progression of the cell cycle, lipid metabolism, but also cell adhesion and synaptic processes. Over the course of the development, there was an increase of the activity of adherens junctions, while the processing of RNAs, regulation of gene expression and translation remained constant over all stages.

In the male opisthosomas, the activity of a number of phosphatases and peptidases was restricted to juvenile stage, but also genes associated with GO terms of RNA metabolism, processing, and translation were relatively higher expressed in juvenile, compared to the later stages. In contrast, genes involved the regulation of biological processes, localization, and signal transduction were less expressed in the juveniles, indicating a change from developmental processes toward maintenance. In the subadult opisthosomas, genes were active, which are associated with terms of the cytoskeleton and meiotic cell division, while transporter activities were specifically down-regulated. Thus, suggesting high activity in the gonads and confirms the finding that subadult spiders show all stages of spermatogenesis (Michalik & Uhl 2005). In the adult opisthosomas, genes were active, which were associated with GO terms for transporter activity, and the motor functions, such as actin and myosin. On the other hand, protein metabolism, the regulation of gene expression, and cell division were associated with genes, which showed the lowest expression in that stage. Therefore, tissue growth and the metabolic energy needed for cell division was lower in the adult structure.

In the pedipalps, the juvenile tissue showed high expression of genes with GO terms for activities in the hemolymph, such as platelet activation, or blood coagulation. In the subadult male pedipalps, genes associated with the production of chemokines, RNA processing, and chitin and cuticle were much higher expressed than compared to the other stages, while the opposite was true for genes involved in binding and transporter activities, lipid metabolism, locomotion, and perception. This corresponded to the terms identified for the legs at this stage, which were also connected to cuticle and chitin binding, as well as the terms from the analysis identified for the differentially expressed genes in the pedipalps, associated with RNA metabolism and processing. In the adult tissue, genes were highly expressed, which were associated with the activity of channels, transport, the regulation of biological processes, certain peptidases, or terms relating to hemolymph. Thus, the GO terms reflect the role of the adult pedipalp as one of the main sources of perception and the involvement of the hemolymph for the functionality of the bulbus organ (Foelix 2011).

7.3.6 Combination

The previous analyses have shown, that the development of the adult male structure of the pedipalps is set up in the subadult stage, because of the high activity of transcription, large amounts of differentially expressed genes between the pedipalps and legs, as well as between the pedipalps of different stages.

The analysis of differentially expressed genes has no indication of a specific timing of gene expression in comparison to other stages, while clustering the genes by their expression profiles does not necessarily answer the question of differential expression.

Additionally, the GO terms analyzed above had to be highly enriched in the respective sets of genes in order to be considered. Thus, only showing the general trend of processes, which were happening over the course of post-embryonic development. Therefore, both approaches were combined to find genes, which might play a specific role in the pedipalps at the subadult stage. Firstly, genes which showed specific activity in the subadult male pedipalps and were up-regulated compared to the subadult female pedipalps, were considered important for male specific development. Secondly, genes which were lowered in their activity in the subadult male pedipalps and down-regulated in males compared to females were considered to be involved in the female specific-development.

135 genes were identified for the male-specific development. 46 of them were previously uncharacterized genes, which again showed this developmental process to involve a large number of spider or chelicerate specific genes. As much as 28 genes were involved in various aspects of cell cycle progression, or were parts of structures important for this process. Together with the genes involved in cell adhesion and the enrichment of GO terms associated with RNA metabolism and processing, this indicates a structure in which is growing and developing. The adult structures of the male pedipalps are supposed to be developing inside the expanded subadult tissue (Coddington 1990), which explains the presence of a set of cuticular genes in this list.

A number of transcription factors was present among the genes specifically active in the subadult male pedipalps. Two of these are homologs of genes with prominent roles during segmentation. Engrailed has been shown to be a major factor during segmentation in a plethora of animals (Patel et al. 1989, Tautz 2004) and its function in segmental patterning appeared largely conserved between invertebrated and vertebrates (Hanks et al. 1998). In vertebrates, however, Engrailed homologs are also involved in the patterning of the distal part of limbs (Loomis et al. 1996, Wurst et al. 1994), a function which cannot be substituted by the *Drosophila* protein in mice (Hanks et al. 1998). In *Drosophila*, Engrailed has also an effect on the growth rates in imaginal wing discs (Hidalgo 1994). Patterning of the distal limb and growth control in tissue are making Engrailed a promising candidate for bulbus development in *Parasteatoda*. The other gene primarily known for segmentation was the homolog of Sloppy paired/FoxG. In *Drosophila*, homologs of *sloppy paired* maintain the polarity of established segments (Cadigan et al. 1994) and are required for the identity of head segments (Grossniklaus et al. 1994). In vertebrates, the homolog, FoxG1, is involved in the development of the brain (Hanashima et al. 2004, Martynoga et al. 2005). Moreover, FoxG1 is involved in the regulation of the mammalian androgen receptor (Obendorf et al. 2007), thus, implicating a possible sex-specific role in spiders as well.

Like Sloppy paired, Crocodile/FoxC is involved in the establishment of head segment identity in *Drosophila* (Häcker et al. 1995), while in vertebrates FoxC is involved in the formation of mesoderm derived structures, such as the cardio-vascular system and somites (Kume et al. 2001, Seo et al. 2006). Homologs of FoxC have also been shown to regulate the expression of chemokine receptors in mice (Hayashi & Kume 2008), which correlates with the specific activity in chemokine related genes in the subadult male pedipalps in the expression cluster analysis.

Ladybird has a well documented role in the formation of appendicular muscles in vertebrates and invertebrates (Gross et al. 2000, Jagla et al. 1998, Maqbool et al. 2006). Additionally, the vertebrate homolog *lbx1* has been shown to interact with pax genes during this process (Mennerich et al. 1998), suggesting that this might be a conserved function in *Parasteatoda*.

Members of the T-box family of transcription factors have been shown to be involved in the outgrowth and identity of limbs in vertebrates (Rodriguez-Esteban et al. 1999). TBX20 specifically, determines ventral fate in limbs (Meins et al. 2000), a function conserved in the closely related H15 gene in *Drosophila* (Svendsen et al. 2009).

Three of the transcription factors are involved in sexual differentiation. The zinc finger protein 358 homolog Clamp is involved in the process of dosage compensation in *Drosophila* (Soruco et al. 2013). A process very little understood in spiders, which is nevertheless responsible for many sexual polymorphisms. Homologs of SOX14 have been shown to be very conserved throughout evolution (Popovic & Stevanovic 2009). Like Engrailed, SOX14 exhibits very different functions in vertebrates and invertebrates. In vertebrates, it is a candidate gene for the Möbius syndrome, which leads to limb defects (Wilmore et al. 2000), while in *Drosophila* it is required for the response to ecdysone at the beginning of metamorphosis(Ritter & Beckstead 2010).

The Doublesex-and-mab-3-related transcription factor 1B (Dmrt1b) has been shown to be involved in the sex determination and establishment of sexual dimorphisms in a large variety of species (Guan et al. 2000, Ottolenghi et al. 2002, Smith et al. 2009, Zhu et al. 2000), where it promotes a male-specific fate. Dmrt1b has also been shown to work antagonistically to Foxl2 (Alam et al. 2008). Foxl2 in vertebrates, promotes female-specific development and is involved in the formation of ovarys (Batista et al. 2007, Uda et al. 2004) through the regulation of aromatase activity, which is part of the hormone production pathway (Govoroun et al. 2004; Wang et al. 2007, 2010). This regulation might not be conserved in *Parasteatoda*, since Foxl2 is highly expressed in the subadult male pedipalps and the noticeable drop in aromatase activity at this stage could be seen.

224 genes were specifically down-regulated in the subadult male pedipalps, including as much as 97 spider specific uncharacterized proteins. Among the other 128, was a large number (33) of genes associated with neural functions, such as transporter and channel activities, olfaction, or signaling. This reflects the finding, that the subadult male pedipalps showed down-regulation of genes associated with these terms in comparison to all other tissues. Together with the findings, that lipid metabolism and genes involved in the adhesion of tissues were also specifically down-regulated in subadult male pedipalps, this is in support of the assumption that metabolic, and homeostatic processes are down-regulated in favor of developmental processes.

A number of genes were involved in signaling cascades, such as Receptor tyrosine kinase, or Transforming growth factor. Both are known to have many roles in intra- and extra-cellular signaling (Christensen et al. 2011, Kingsley 1994, Schlessinger 2000). TGF-beta has been shown to be involved in the regulation of the lipid metabolism (Yang et al. 2014a), which would account for the number of lipid-related genes in this list.

The list of genes specifically down-regulated in the subadult male pedipalp contained also a larger number of toxins and venom peptides. The identification and composition of the toxin repertoire in spiders is usually analyzed by the expression profile and protein composition of venom glands themselves (Fernandes-pedrosa et al. 2008, Gremski et al. 2010). Because of the focus of the analysis and the lack of post-embryonic transcriptomes and available genome predictions, the presence of toxin transcripts in tissues other than the venom glands or the chelicerae had not been observed. Here, the presence of such transcripts was only observed because they were specifically down-regulated in the developing male pedipalp in contrast to the female in which no major developmental processes are ongoing. This could indicate a potential role of the spider toxins as protection against predators. Since spider toxins are highly specific in terms of which organisms they affect (Bende et al. 2014), there would be no need for a protective mechanism against the own toxin.

Genes, which were associated with transcriptional activities in this list were either involved in transcription in general, or were transcriptional repressors, indicating that the development of the male pedipalp needs the active expression of factors in order to change it from the ground state, which would lead to female development. This also reflects the fact, that the bulbus organ is a novel trait for sperm transfer in male spiders in contrast to other chelicerates, which produce spermatophors, such as scorpions or whip spiders (Alexander 1956, Alexander 1962, Tallarovic et al. 2000), that have to be taken up by the females, or the mating mode of Xiphosurans, in which the male fertilizes eggs already laid by the female (Brockmann 1990). Only the homolog of the zinc finger protein 41-like was contained in this list as a transcription factor. This factor was identified in humans, due to its role in X-chromosome inactivation (Rosati et al. 1999, Shoichet et al. 2003).

In summary, the analysis of differentially expressed genes in the pedipalps of subadult males of *Parasteatoda*, together with the temporal specification of genes, which are active at this stage, produced a list of promising transcription factors, which might be involved in the male specific development of the pedipalp. Many of these genes are known to be involved in the development of appendages, or other morphological structures in other species, or are involved in the establishment of sex-specific traits. Now, these candidates need to be tested functionally in order to determine their specific role in the development of the pedipalps in *Parasteatoda*.

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9 Supplemental material

9.1 Cloned sequences

9.1.1.1 *cap n collar*

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9.1.1.2 *collier-2*

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9.1.1.3 *crocodile*

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9.1.1.4 *CtBP*

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9.1.1.5 *CTCF*

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9.1.1.6 *dachsous*

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9.1.1.7 *daughterless*

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9.1.1.8 *dorsal2*

NNCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCGGGCCGCCTTATTTTCCACATCC
TCACAATTTAGTTGGCAAAACTTGTGCTAATGGAGTGTGCTACAAGACAATTAATTCTCCTGATATGGTTTGCAGTTTTG
CCAATCTGGGAATACAATGTGTGAAAAAAAAAGATATCAAAGAATCTCTATCGCACAGGGAAGCAATTCAAGTTGATCCA
TTTGGGACTGGTTTCTCTCATCATCTTGAACCAGGAAAGGTTAATCTGAATTGTTTAAGGCTCTGCTTCCAAGTCTTCTT
ACCTAATGAAACCGGTAAAATGTGCATCCCTCTTTCACCTGTTGTAAGCAATGCAATTTATGATAATAAAACAGTATCTG
ATCTCACCATTACGAAGTTGAGTCATTCTTCTGCTCCAGTTACAGGTGGTCAAGAAGTTATTTTGTTATGTGATCAAGTG
AGTAAGGATGATATTCAGATATTATTTTATGAAGAAGTAAACAATAAAATAATTTGGTGTGCCAATGGAAAGTTTGCTCC
TCATCATGTTCATCGCAAAGCAGCGATATCTTTTCAAACTCCTGCCTACAGAGATGTAACTGTTCCCCAAGGTGTTGATT
GTTTTGTTCAGTTGCGCAGACCTTCAGATGGAGCTGTTGGTAAACCTAGGACATTTTGTTTTATCCCATTAAAACAAGAT
CCTGAGGGTCTGGCTAGGAAGCGTAATAAATTTGAGGCACTAAGGCTTAGTCAAATACTTCAACCAAGTAATTTGCCTTC
GAGTAGTAATAATGCTGAGCCATTAGCTACACCTAGGGTTATTAAACAAGCTGTTAGATCGAAAACCAGTCCAACTAATG
GCTTGGTGAATAATTTTACCAGCAATATTGTGTCTTCGACTAACTATCAGTTAAACCCAAATCTTTCTGGCAGTGATTTC
AAACAGAAAAGAASTGTTCAAATGCTTAGTCAAGANAAGTGTCATATATCTGAAAGCAGATCAACTTACAACACTGCTTT
ACTAGAATCTCGTCAAAAGGTAGATGATATTTTAGCTATTGCAAAAGATCAGGTTGGCATTGGAAACTCMMMCT

9.1.1.9 *dorsal3*

ATTCAATCACCTGGTCCGCCTTAGAGGAAGTGATGAAAAAGGCACAATTAATGGATCCACCATATGTTCGTATAGTAGAA
CAACCATCTCCAAGCAACTTTAGGTTTCGCTATGAGCGAGAATATGAAGATCGATGTGGTTGCATTGGTAACCTAGTTGG
TATTAACTCGACATACGAAAAAAGAACTTTTCCTAAAATACAGGTCATGAACTGCAAAGGCTCTTTTGCTGTAGTCGTAT
CTTGTGTGACTAAAGATGGACCTCCGTATCGGCCTCATCCTAATAAAATAGTAGAGAACCTTAAGAAAGAAGCTTATCAT
AAATTAGAAGACGAAGAAAGAAGAGGGATATATTGTAAAATTATAAAAAACTCTACCATGACATGCAGTTTTCCAAATCT
CGGCATCC

9.1.1.10 *Drop1*

TATTGTTCACGAAGTCCAAGTCCTGCGTTAAAAAATGTGGATACCAAGAGTGAAATATTAATGGGACCCACTAAAAGAGA
AACATCGGAATTAATCTCGAATTTCTCGGTAGCTTCTCTACTCTCAGATTCTAAGACAAACTCACCAAGACCTACTCTTT
GGAGTCCTACTGAATTTTATTTGGGTCATACTACAGGACATGATGCCAATTTTAGACCCAAACTAAAAACTGCAGACGAC
ATATCCGGACCAGAATTTTTTTTAATGGATCGAATTTTGGATGACCGCCGTTTCATGACTCCACATCACTCAAGACTACC
ACAACCTAATGTATGGTCTTCTCACATGACAACCGGTCAAAGGGCTCTTGTACAACCACAGTGGAATTCTGCTATTGCTC
TGCAAGCTGCAAATGGACAAGGAGCGGATGGATCTTCATCAAAGCCTCTTACTTGTCACTTAAGAAGACACAAAAGTAAT
AGGAAACCCAGGACTCCTTTTACAACACAACAATTATTAGCCTTAGAACGAAAATTTCGTTCCAAGCAATATTTATCAAT
AGCAGAAAGAGCTGAGTTTTCATCTTCTTTAAGTCTTACGGAAACTCAAGTAAAAATTTGGTTTCAAAATCGAAGAGCAA
AAGAAAAACGACTTAAAGAAGCTGAAATAGAAAAATTACGCATGGCATCTAGACCTTATCCTCCACATCCAAGTCACATT
GCTGGTTTACCTTCTACCTTTTTTTCCCCCATTGTGTCTTTACCGAATCTACCGTATTGCATTCCTTCAATGA

9.1.1.11 *Drop2*

GGGCACACAGTTGAAGATGAAGAGTATATAGGATAAGGTGCCATCAGAGGTCCTAATATTGGTCTATTGAAATGGCTTTG
CAAGAAATGCATACCAAATCCAAAGGACGGCAATATAGGGCGCGTTGCCATACGCAATTTTTCCATTTCAGCTTCTTTCA
ATCGTTTCTCTTTTGCTCGACGATTCTGAAACCAAATTTTTACTTGTGTTTCTGTTAGATTTAAAGAAGATGAGAACTCT
GCTCTCTCAGCGATGGACAAATATTGTTTCGAGCGGAATTTTCTTTCTAGTGCCAACAGCTGTTGAGTTGTAAAAGGAGT
TCGAGGCTTTCTGTTACTTTTATGTTTCCTCAACTGGCATTTCATGGCTGGCAGCTTTGCTCCTTCCACGGGTTTGGGAG
ATCTAGGAATCCAAGAAAATGTTGATTCAAGAGGATGTGACCAACAAGGAGTATCAATTGAGGGTCCCGGCAATCGTTCT
TCTAAAATTCTGTCCACTGAGAATTGTTTTGGAATATGTGTTTTTCTAGTATCTGCTAATAAATAGTCCACAGAAAAAGA
TATACACGATTTCGACTCTTCCATATCCACGCTA

9.1.1.12 *Drop3*

CGAATCATCACCAAACAAATCCATTGAATACCAACGGACTTCTCCAGGACTTTTAACTTCACATTTGACTATGCCCGCCA
GGTATCAACACAGTTCGAGATCCCCCTCCAAAAGTCCGGAAATCGTCGAGGCCAAGATATCCTCCAAGACCCCCAAAGGG

ATATCTTTTTTCGGTCGAATCCTTGCTTTCTGAAGATTGCAGTAAAAGATCTTCCTCCAGTCCTGATTTCAAGGTACCAA
GTCCTGAAGAAATTAAAGAAATCAATGGTTCCTCTAGTCGGCATGATGTATCTGAGCTGCTTTCAAGGAGGTTCTGTGTA
GATCGGTTATTAGATCATCATGGACTTAAATTAACCGGACTTCCACCCACCTACTTACCACCAACGTCAGCAGTTAAAAC
TTTGGTACATCATCCGGATACGAACTTAAGTTCTCCTACAATGTCCTGGAATTCACCTCTTAGTGTGGGTGTACCTTGGT
TCCAAGTGTCCAGGTCAATATCTCCCGTTCACAAACCAGGAGAAATGCCTAAACTACCCATGAAATGCCAACTGAGGAAG
CACAAAAGCAACCGCAAGCCTCGAACTCCTTTTACAACCCAACAGTTACTATCTCTGGAAAGAAAGTTCCGATCCAAGCA
GTACCTGTCTATAGCAGAAAGAACCGAGTTTTCCTCATCACTGAACCTAACCGAAACTCAGGTTAAAATTTGGTTTCAGA
ACAGGCGTGCCAAAGAAAAACGACTAAAAGAGGCCGAATTGGAAAAGTTGAGGATAGCCACGTCTAGGCCTATGCTATCT
ACTTTTGCATTTGGTGGACCTGGTTTCCTGGCTGGCTTACCGCCACCAGCACATATAGGACCCAATGCCAGTCCCAGACC
CTTCCTAGGTAGCTATCCTTATCCATTCTATACGTCGTCGCC

9.1.1.13 *empty spiracles 1*

AAGCAAAATAAAGTTCGCTTCGTTAACTATCATATTTGAATGTTTGAGGTGACTGTGAACGGATGTAATTTGAATTTGAT
GCCATAGGATTCCATAAAGTTTCCCTTTTAAGGTAAGAAGAATCAAAAGTTTCTTCTGGAGTAGATAATGTTCTATCTGG
AACGGGAGGACTAGATTTTTCTGAGACCGATTCTTCTTCATCAGAGGAACTACACTGATCAGCGGAATCAAAGAAGTCTT
TATTTTTAAGATCGCAACTTTGGTCATCCTGTTTCTGTCGTTTGTGTTTTGTCCTCCGATTTTGAAACCACACTTTAACC
TGTGTTTCAGAGAGGTTAAGATTTTGAGCAAGTTCTCGCCTCTCGCTTCCAACAACGTAATGATTCTTTTCGAACGCGTG
CTCCAATTGAAGAAGTTGATTTGGTGAAAAAGCAGTTCGAATACGTTTTGGCTTGCGGAAGGGATGAAAAAAGAACGCTG
ATGCACCTTGCCATTTATGAGGTAAGACTCTTAGATCCCTATTCAAGAGCCATGGGAACATCATCTGCGAATCTCTTGTC
ACTGCTAACGGTAACGTTGGTCGAACAGGCTCACAACCATTCAGTAAAGAGTATTTTGGTCTACCAAAACCAAAAAAATC
AACTTCAGGTTCAGGAGAATGGTAAATTGGATATGCTTGAGAGTATAGTTCTGGGACTCTTGGCATCAAAACATGAGATT
TTTCTAAATTTGCATGATGGATATTAGAATCGTAGGAGTCTTTTTTAATTATTAAATTTTCAGGTGTCCTCTGATGGGTA
ATAGGAGACGGTGATTTATCACTTTTACCAACTAGTTCTTCAATAGAGAAACCTATTTTAGGTCGTGTTGGTTTTGGAAT
AGCAATTGAAGAAACTTTATGGAAATCTGCCAAAGCCATGGTCAAAATTTAGTATCGGCACTTTTAATAACTTTTTTTCA
AATTTCCCACATTTCTTTCAAACAACAATACTTGAATACTATTTCAGTTTTAATAATTGGTTTAAAAATTAAAAAATCTG
AM

9.1.1.14 *empty spiracles 2*

TGGCCCACTCTCAATCTCAACCATTGAGCCGTCATCAGACAAAGGTGACGATGGCATTTCATCGCCATTTTGCCATGCAT
GTTTGTTAGAATATTCATGGCCACCGGTGTGAGGATGATGATTCTTCGATTCACTGGATGCATTTGAAGACGAGGATTTG
TGATCAGATTGGCGAGTACTTTGTTCTTCTTCCTGCTTCTGTCGTTTGTGTTTCGTCCGTCTGTTTTGAAACCAAACTTT
CACTTGTGTTTCTGTGAGGCTTAAACTTTGTGCCAACTGTTTTCTTTCAGCTCCAACAACATAATGGTTTTTTCGAATGC
GTGCTCCAATTTCAAAAGCTGTGAAGGTGAAAATGCAGTTCGTATTCTTTTTGGCTTTCTAAAAGGATGTAAAAGAAAAC
CGGCTCCGTCGGGACCCGGTAGCCTATGAGCCAGGAACCTTGGGTGCCGGGCCAGAAGCCAGGGATACAAAGGATAAGTC
TCTCTCCCTAGGAAAAAGGGTGATACCGGGGCGCACGCCCCAGGTATTGCTGCATAGCCCCCAGGGTGTTCATGTTGATG
ATGATGCGGTGGGTATAGCACACCGCCTCCCGTTCTACTGCCGCACAGAGAGTCCAGAAAAGCCGCATTAGCTGCCGCTG
CTACCAGGCTGCCGGACGCCCCCGGTACACCCCCGGGCGCAGTAGCAGGGAAAGTGGCTACTGGTGCAGCCACAGGATGT
TCGGACC

9.1.1.15 *empty spiracles 3*

TGCTTCTCCGGTTTCTGTCAAAGACTTTAGTATAAATAAATTTCACACAGAAGAAATCCCGAAGTCACATTCTCCTTTAA
ATGTTCCTGTGCCACCGAAGCCTTCCGTACTTGTTCCTATTCCTACGTTTCCCGGCGGGCTTACCGGGACTTCACCGACT
CTTAGAACTGTAGTCGGTAGTCGAGAGAGAGCCGGTCTTTTCAACGCAGCTTTGTATCAACATACTTTGCCTCATGTTTC
TGCCGCAGGTATGGACCATTCTTTAGCCGGTATGATTTTACCTGGTGAGGCGTTGCACGGTTATCCATGGTATTTTCATC
GGCAAAGATTTCTACATAGATTTCCAGGTCCAGATATATCTGGTTATCTGCTTCCTCCATTTCGAAAAGCTAAAAGAATA
CGAACTGCTTTTTCAGCATCTCAACTCATGAAATTAGAAAGTGCGTTTGATAAAAATCATTATGTTACAGGAAATGAAAG
AAAACAACTTGCAGAAGGTTTAGGCTTAACTGAAACTCAGGTTAAAGTGTGGTTCCAAAATCGTCGAACAAAGCAAAAAC
GACAGGTTTTGGAAGATAAAGAAAGAAGCGAAAAGACCCAACGTTTGTCTGTTAATAAAGGAAGTGAACACGAAACTAAT
GAAATCAATCATATATCTCTTTCCTGCAGAACTGAAAACCTCAATTTTTATGAAGATGAAGAAAGTAATTCATCTTTCAC
CAGTGATGAAAAGTGCG

9.1.1.16 *Enhancer of zeste*

CGCAATAAGAAACCCACCCGCACACCATCATGGACTGCGCCAAGTACTTCACCTCATGAAAAGCAACCTATTCCTGAACA
ATATGACATTATATTTGCTGCCATATCAGCTGTATTTCCAGACAAGGGTGCTCCTGAACAACTTAAACAAAGATATCGTG
AACTTGTGGATAAAAAAGATTCTAATTCATCATTGCCTGAATGTACACCCAATTTGGATGGACCTGGCGCTCAGTCCGTT
ATAAGAGAGCAGAGCATGCATTCCTTTCACACTTTGTTTTGTCGGAGATGTTTCAAATATGATTGTTTTCCACATCCTTT

TCATCCATCACCAAGTCAATTCAAACATAAAAAATGTGATATGAAACCAGATTCCCAGCCATGTGGATATCAATGTTATC
TTCATTTGGATATGGTGCAGGAAAAACTTCGAGAAAAATTGCGTGAGGAAAAAGAACAGAATGAGCGTCGCAAGATGATG
AAACAAATGTCTGTTGATAGTGGTAATGAAGCTAGCAGTGAAGATAGTAATGACAGCTTGAGGAGCTCAAGGAAAAGAAT
CATTCCTGAACGTGAAAATAATGAAGGAAACTTCAATATCCTTAACCACACCATATCAAGTAAATCAAATTTAAAGGATC
TTGAAACAACTTGGTCTGGAGCTGAACAATCATTGTTTAGAGTTCTATGGAAAGTTTTTATAGGCAATTATTGCGCTATT
GCCCAAATGCTACGAGATAAGACCTGTGCTCAGACTTATGCTTTTGCTCAGAAAGAGCTTGCTGATTACCACCCAGAAGA
AAACACTTTAGATAATACACCACCTCGAAAGAAGAAGAAGAAACAGAGACTGTGGTCGATGCATTGCCGTAAAATACATT
TTAAAAAGGACTCTTCTTCTAACCATGTATATAATTACACCCCATGTGATCATCCTGGTCAACCTTGTGATTTGTCATGT
CCATGTGTTATGGCTCAGAATTTTTGTGAAAAATTTTGCCATTGTAGCTCTGATTGCCAGCAAAGATTTCCAGGCTGTCG
GTGT

9.1.1.17 *Fasciclin 2-1*

ACTCCTTTCCACAGCTTTGTCCATCTGTACCCAGCCTTTGATGTCTCTCTCAACCTTGAAGAATCTGATTTCAAAATGGT
TGATGGGTTCTCCGTTATCATTTGGCACATCCCACCTCACTTCAAATCTGTCTGGGTAACTGGACACAGTTTCTTGTTCT
GTGCCGATAATGGGAGGTTCAGGCACTGTTTCTTCAGGCATTATGTACTCTGTTGTTTTCTCAGGTCCCTCACCAACAAC
ATTGCGAGCTGTTACTCTGAACTGGTACTTTGCACGAGGTTTTAAATCACTCAGAATATATGGAGCATCTTTAATCCATT
CAACAGTGGTTGTAGTATGATCTGGTTCATTGGCATTCTTGTATTTCATGATGTAATGAGTGATAGGTAATCCTCCTGTG
TTGCCCGGTCCCATCAGCCTGAATGTTATTGTTGTGGATGTCACTTTATCAAACACTATTTGGGTTACTTGACCAGGGGC
AGTGGCTTCTTCTAAGTTAATATTTGTAAAATTATCTCCTAAGCCATTTTTAGCTTCACAAGTATAAACTCCAAATACAT
CATATTGTGCCCTGTTTTCTGTTAGGACCAGAAGACTACTGTAGGATACAGTTCCTTGAATTTGGAATCTGTCATCTCCA
ATTTCAATAGGTTCATTTTGGAATTTCCACGTGATTGTTGCGTTTGGATTAGCTTGGGCTATGCAAGAAAGATTTGCTGG
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TTTCGGTTTCACCTGCTGCATTTGAAGCTTTGCAAAAGTATAGCCCATCATCTTGACGTTTCACATTGATGATGCGAACT
CTCAATATTCTGTATTCTCCTGCGTCCAGTTCTTCGATTTCTATTCGGTCATCTTCTCCATCTTGTAAAGGATGATAAGC
ATTGTCTTTCCTGATTGTCAGAGATGGCACTGGAACACCGTCAGCTTTACATTCTATTGTCGCCACTTTTCCCTCCTCCT
TGGTCAGATTGTCAAGTTGCACAATACTTGGTCGAACTTGTACAGTTAAAACCACAGATGCCTCATCTTCGTCAGCAGGA
TTTTTGACTTTACATTTGTATTCTCCACCAGCGTGTCTGTCAACTCGTAAAATGGTCAACATTCCTTCGTTTACTCTAAA
ACCTTCGACTGTGCTCAAATCTCGTAGTTGCGGATCTAGCCAAGTGTAGGTGAGTGGGTTCG

9.1.1.18 *Fasciclin 2-3*

CAGCAGATGATGGAGGATTGCCAATTCGTGCCTATGTTGTCAAATACCATGAAGAAAATGAGCCTTATGATGCTCCTGCA
GTTCAAGAATGGAGTGAAGGATTCCCATATGTACTTGAGAATCTCAAACCTCGCACTACATACAAGTTTCAATTTGCTGC
CAGAAATGAAGTCGGTGTTGGTGAATATAGTGATGAAAGAAGAATAGAAATGCCTGCAGAATCAGCTCCTGAACCGCCTA
AATTCATTACTCCTGGAGGAAAAGTTAGCACATATCCAGATCGGTTCTCCATTCGATGGACTGTCCCTCTCGATAATGGC
AGAAAAATTGATTATTTTGAACTTCGTTATTTTGAAGCAGAAAAAAAGAATGGTGCTTGGCGAAGTAGGAGAGACTGTTG
T

9.1.1.19 *gooseberry*

ACTGCTTTAGCTGGGAACTTCGCCAAAGGATCTCCAAAGAATCAAATTATGAACATAAAGTAAACCAAAATGCAATAGCA
CAACTTCTGAACACTGCATTAAGTACAAATAAACTTGATAAAACTGAGGACTTAAACCAAAAAGGTACCGGTGGTCATAA
ACACACAATTGATGGCATTCTGGCTTCAAAAAAGTCATCAAGCGGCGAAGAAGGAGGCTCAGATTGTGATTCAGAACCGG
GTCTTACTTTAAAAAGGAAGCAAAGGCGATCTCGAACTACTTTCACCGCTACTCAACTAGAGGAATTAGAGAAAGCATTC
GAAAAATCCCAATATCCGGATATATATTCGAGAGAAGAGCTTGCTCAGAAGACGAGTCTCACCGAAGCCAGGGTACAGGT
TTGGTTCAGTAATAGGCGAGCTCGTTGGAGGAAGCAAGTTGGCAGCCAAAACTACAGTCATTATAATTCTCCAGTAAACT
ACAGCTATCCAAATGCTTATCTAGTCCCCGATGCTGCCGCATACTCCGCTCATACAGACTCTTCACCATTACAGACGGGA
CCCAGCGTATCGTTACATCACCATCACTTGCATGCATCATCAACAGAGCCTCGATCATCTCTAGCCTATAACTCCATAGC
AGAGTGCAATCCTGCTATACCATCTACGGTAATGTCCATGCTGCATCAATCCGTCCCATCCTCAGCCGGAGCAGTTGATT
ATACTCACCATCAACATGGAGTTGGCAGCTCCACAGCTGCCGCAATGGCAACGGCATCTTCCGGCGAGGAATGCTGGAAC
GCGGCAGCCAGAGCAAACTTCAACGGCTGGACAGCAGCGGCTGCCGCTCAGCAAAATTCTGCCAGTTCCTCGTCTGCTGC
GGATGCTACAGCGGCTGCATTCGCTAGCGAACATCACATAGCCGGAAGCGACGCTTATTCAGGGTTTAATACTATGGCTC
ATCATCATCATCATTACCCTGATATAAAACCGCCCTTTTATTATACAGGGCAATATCCTACCGGATTCAGGGCCTTAGGC
TTAT

9.1.1.20 *huckebein 1*

AGTCACTCAGATTTCACTACGGCTAAATACAATTTGTCCAGTGAGAATGTAGAAAACAGAGGAAAGACTGAAATCTGGAG
GCCATTCGAGACTCAGCATTTATCCATAAATAAACTCAATCATTCAACCTCATCAGTGTTCGTCCCAGTTAAGAAGAAGT
TTTGTTCGAAATGTTCAGCTGTATTTTACAGTAATTTGCAGCTAATTGCTCATATGCAAGTACATACAGGTTCAAAACCC
TTTGCATGTGACGATCCAAATTGCTCCAAGTCTTTCGCCAGAAATGAAGAATTAACAAGGCATCGAAGAATTCATAGTGG

TTATAAACCGCACCATTGTAATTCATGTGGAAAATGTTTTGGACGCAAAGATCATTTAAGCAAACATCTAAAAACTCATC
TTCAAGTCTCTGAAAAAAAAGTATATGTGTGTCGTATGTGTGGACATCGTTATACAAGATCTGATGCTTTAACTCGACAT
AGAAGTAATGCGCATGCCATATCCAAAACT

9.1.1.21 *HMGB1*

CCATTCCGGCATCAGAATATGTCACTCTCTACTGAATATGATTATCAACAGGCCATGGCACAGCATGCTGCAGCTGTCAA
TGCAGCGAACAGTCCATCTTTACATTCTGTTATGGCTCAAATTCCATCACTTCCAGCTGCTTTAAATCTTAGTGTGAACT
CAGTGAATCAAGGCTATTCCTCTTCTGGTTTAGGTTCATCTTTAGGCAACAATAATGCTGCCTACCATTATTCATATGGG
TCTCTGGGATCTTCAGGTGGTGGTAGTGGTAATAGTGTTGTCGGACAACATCATGTAGGACATGTTGGACACCACCATGC
TGGTGGTGGAAAATCAAAAAAGAAATATAAACTAAATAAAGATGGTATTCCTCCTCCTAAAAGGGCAACTACTGCTTATA
TACATTTCACTCAGTGGTATAGGGAAGAATTAAAAAGGAGTGGTCGTGAAATTCCTAAAATTGGAGAGTTTGGCAAAGAA
TGTGCTGCAAAATGGAATGCCATGAATGAAGAACAAAAGGAACCATTTTTGGAGTCTGCAGGCAGGGACAGAGGACGATA
CAAGCGTGAGATGTCAATATACAAACCAGCTAGGGATGCAAATAAACCAAAACGACCTGGAACTGCATTTATGATATTCA
TGGCTGATTTCAGGAAAGAAATGGCTGGCAAAGAACCTGAAGGTGGTGTTGCAGCTATGGCAAAACTAGGTGGTGAAAGG
TGGAGAGGTATGACCGATGATGATAAACAGCCTTATGTAGAACAGCAATTAGAAGCAAAACTTCGATATGAGCACTCCAT
GGAAGAATATAGGAGAACTCAAAATTTAGAAGCTCAAGCTCAGGCAGCTAAAGCGAGAGCTGCTGCTG

9.1.1.22 *klumpfuss*

TTCCCCGTTTGTTCTCCGCAGAAAAAAGTTCCGTTCGCACACACAATGAGAGAAAGCTGCAGGTCTCCCACAGGTATCTG
TACCCCCCTGGTAAGGGGGTCGGGTGTTGAGACACCCCCCAAGGAGGAAGATATAGAAGGAGATGATGACGCTTTCAGTT
CGCCTTCAGGCAACAGGCTGTCAAGTAATCGCCCTACTCCGCTCCAGATATTGCCATATCCACCGGGACTCTTACAGCCA
CCTCCTCGTCTTTCGCATCCCATCGTGATCTCGCATCATCCTTACTCCGGAGAACACCCCGTTGTCATGGGCAACGGGGC
ATCGGTGGGGAACACCGCTCTTTCGCATCACCTCAACACTAGTATCCCGAGTTTTCCCATCTGTGATTGCCATCTTTGCC
GAAGATTGGCCGTTCAGCCACCGGGCCATCCTTTTGATTGGGACTTCGACCAACAGCGTGCTCTTTTTCACAAGATGATG
GCCACTGGTAGTCCGATGACTCCCGTGTCTCCTATCACCCCTCCCTATTCTGCCCTGTTGCAGAACAAGTTAGAACTGTA
TTATCGCAGAAGAAGCCATTCAGATTCGGACTTAAAACAATGGTTAGCCGATTCTGGAGTAACTGGATCTGGTGGAGATG
CATCGAGCCATCCTCACCTTGGCTTACACCCCGCGATGCCACCTCCGCCTCCCAGAGAATCTCAGACGGAAAGTTTTAAC
TTTACCGCTCGTAATGGAAGGCCAAAACCTTTGAACATACCACANAAAGGAGGAAGTTTGGACTCTGATAATAGCTCAAC
TCCTCAAGATTCACCGTTAGACTTGTCAGTGAAATCAAATACTCCGGCTAGTTCTGATTCGACGGCATCATCGACAACAT
GCTTCCNCCTCTCACCATTAGCGARNNRNTTTTTCGAGCGAATCCCAAGGAAGCCCAARAGGTTCTT

9.1.1.23 *Krüppel 1*

GGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGGCTTCGAGCAAAGTCGCCGTAA
CGGCGTGGCCGAGGTGGCTGTGGACATCAACGCCCTGCCTGTTGGCGGCACCTTAATCACAGACGCCGCCAGCACCAATG
GAGACAGCGACAAAACCAAAAACGGTGTCCCAAAGAACGGCGAGAAGCAGTTCTTCTGCAGGATCTGTAACCGAAGCTTC
GGTTACAAGCATGTCTTGCAAAACCATGAACGTACACATACAGGCGAAAAACCATTTGAGTGTCCTGAGTGCCACAAACG
GTTTACGCGGGATCACCACCTCAAGACTCACATGCGTTTGCACACGGGTGAAAAGCCATATCAATGTTCCCACTGCGATC
GCCACTTTGTGCAAGTTGCTAACCTCAGGCGACATCTTCGTGTGCACACGGGTGAGCGGCCTTATGCTTGCCAAATGTGT
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GTGCCTGGGACGATTCCGTCGCAGACATCACCTGATTCATCACAAATGCCCTAAAGATGAATCCAACTTGGGCAAGTCCA
GGAAAGGCAGGCGACCCAAAGTTTACGAGCAAATCCATACTTCCGACCATGAAGATCACGAAGATCTTGATGGTGAACTT
CTGCCTGACATTTCGGATAACGAGGAGAACATGGTTGACACCAACAACTCCTCATCAGAAGCTGAGCAACCATCTCCTCC
GTCTGTTCATCCAGTAGAAACTATTATCCACCACAATAATCATCACAACAATCATCACAATGAGATAATGGTAATAACCA
ATGGCGTTACCAATGGCACACACGGCATCAACGGTACAAACGGAACCAATGGTACCAACGGTAATCGAAGAAAACCAAGT
AGAACCATTCGCATTTTAACTCCCCNANCACGCGAGCTTTTTATTCGAGACAAATTAACCATGCAAACGCAAGCTATAGA
CATGAGGTTGTCTCCGTCCTCTGTCGAGGTGCAACCAGTGACAGTTATTGTTCCCAATAGGTTTCTCTCGACTGTC

9.1.1.24 *maf-s*

GGGTGACATGGATTTTGGGGATTTTTCCTCTTCCAATGGCACAGAAATAACTGATGATGAACTTGTGTCTCTCACAGTTC
GGGATCTCAATCGTCTTTTGAAGACGTCGGGTTTAAGCCGGTCAGAAATACAACGCATAAAACAAAGGAGAAGAACATTG
AAAAACCGTGGATATGCTGCAAGCTGTAGAAACAAAAGACTGGAACAAAAAGATGAATTGCAAGTAGAACGATCCTCCAT
TTTAGGTGACATTAATAGCCTTAAGGAAGAAAATAGAATGATAGAAAATCAAATTGAGGAATTTAAAAATCGATATGAGA
ATTTAAGAAAATTTGCTCTTCAAAATAATATTTTCATTCCTCCTGACTTAGACATTCCT

9.1.1.25 *Medea*

CCGACTGAATTTGGCCCTGGAATATGACCAGCTACTGCTGCAGCTTGAGCAACAGCTGCATCTTGGGCTGTCAATGCTTG
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CTGGTGCTCTTCCTGCTTCCCGATCCAGATAGTAACTCTGCACAAAGACACTGTAATCGCTAAGGCATCTCAGCCACACA
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TTAGAGAGAGTGCCCTGCTGTAAAGCTACATCAGCATGCAATTGCTGATGTCCCCAGAAGTTAGTTCCTTGTGGACGCAG
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TAYGCAGAATACTTTGKKA

9.1.1.26 *ovo*

TTTATGCAATGCGGGACTAAGAGGATGATTTAACTTCAAATGCATGTAATGAACTTCTGGTTCAGTTGTAGTATGTCCAC
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GATTCTAAAGAACATCTTTGAGTGAAAGACTTCTCACACATATTGCATTTATATGGGCGCACACCTTCCAGCTTCAGACT
CAGAAATTCCTGGAAGAATTTCTTGGCAAGGAGGGGTTATTTGAGTTAATTCTTGTCCAGTAGCAGAATGTCTATGATTT
CTTTGCAGAAGGGGATTTTTAATGCCATGTCCTCCATTTACGAACTCAATAGGAGTATCAGTCGGAAGTCCAAGTGTTAA
GGAAGACATCACTATTTTCTCTCCTCTTTCATCCAAGCTCTCTGGAGAGCGTGAAGAATTACTATCACTATCACCAGGAG
AACTGGGACGCATTCCTATGGAGTAGCTATCAGAATGGGAATCATCTTGAGAGTCTGACATCGGCAAGCAAGGTCTCGTG
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GCAGAATCATCTCTGCTATCAGGTTTGAATGAAACTCTACTAGAAAATGTGGTTACAGGAACTTCATTGGTATCTGTGTT
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ACCTTCAGCTTTTTGCC

9.1.1.27 *pleiohomeotic 1*

AACATAAGGTCTGTCGCCCGTATGAATACGCACATGAGTACGGAGATTAAAGTCCAAAGAAAATCTTTTCCCGCATCCTT
CAAAAGTACATTGAAACGGTTTTTCTCCAGTATGCACTAACTGATGTCGTTTAAGTTTTGAGCTTTCCACAAATGCTTTA
CCACATTCAGCACACACATGCACTCTAGGACCGTGAGTATGCAGGTGCTTCCTCATAGCAGAATTATCTCTAAACATTTT
GTTGCAACCTTTATGAGGGCAGGCAATTGTCCTAGCAATGTCATCATTCTGTTTACGAGGCTTCATTTTGGCAAATTCCG
CTAACTGCTTTGGATCACTTAAATCTACACCTGGTATACCACCAGGTAAAGATTTTTTTCCCGTCATGTATTCGGTATAA
TCTGGATCAGGTTCAGGATTAGTGGAATCATCTACAGATATACCTTTTTTATTGTCATCATCACTACCAGAGGCCCATAC
AGTAACAGAAAACTCTCCTTCAAGTGTTTTGATTTGAACTTGTTTACGATCCCATTTGCGGGCAGCTCGTTTATTTTCCG
TGAGTTGTTCACCGGTAAGTTTGTTTTTACCAACAAGTTTTTTACTTTTTCTGCCTCGTTTGCTTGTGGGACCAGCACTG
GTATCTAGCATTACATCAGTCGCCGACACAGGTATCTGTTCGTAAGCAGACAAACCTTCCGATTCCGAATCAGCACCGAC
TATTTCCTCTTGAGGTTGAAGAATAATACCTTGGCTAGTAGCATCCAGTAACGGTTGCAAAGATATAAGGGGTTGCTCTT
CGGAGACGTCACCAGAAGCACTTACAGTTAATTGGGTTTCAACAGGCATACCGACCAGGA

9.1.1.28 *pleiohomeotic 2*

TTGAGTGTGTTGATGGGCATCCTATAATATCATTACAAACATTGGATTCAAATAGCCCAGAAATTATATTACAAACTCAA
GAAGAAATAGTAGTTGATGTGGATGATTCCGAAATGCTTGCATCTTACAATAATTTAACAATACCACATGAAGTCCTTTT
TGAAACGAATCCAGGAACTTCTAAGCGAACTAAAAAAAATAAAAAAAGTAGCAAAGTGAAAATTGAAAATGAACTTTCCT
ATGAAATGGAAAGAAGTTCTCGAAAGTGGGAACAAAAACAAGTTCAAATAAAAACTCTTGAAGGTGAATTTTCTGTCACT
ATGTGGGCGTCGGGAATAGATGAGGATGAAGCAACTGTTCCTGAGCCTGATCCAGATTATACGGAATATATGACTGGTAA
AAAGATATCAGCTGATGATCTTCCTGGTGTGGATCTCAGTGATCCCAAGCAATTAGCAGAATTTACCAAAATGAAGCCTA
GAAAATTATCTGATGATCTGTCCAGAACAATTGCCTGCCCTCATAAGGGTTGCATTAAAATGTTTCGTGATAATTCCGCT
ATGCGGAAACATCTTCATACACATGGACCCAGAGTTCATGTATGTGCTGAATGCGGGA

9.1.1.29 *Polycomb*

TGTACTGCTAGGCGTGGATGGGCTAACATCCCAAGAGCCATCAGTAGATTGTGAGTTAGCAAGCTTTGGCACTTTAGCTA
GTGGTTGAGAATCTTCTGATGAAGTTTCAGCTTGAGCAAGATGATTATCAGCAACTTTTTCTCTACTTATGCCTTTACTA
CTAGGTAAATCAGTTATTGATTCGTCAAGAGAATTGGTAGAACTCTCTTCAGGTAAAACTTGACTATCAATCTGTGTGGG
CACAGAGTTATGTGATGACGTTTCTTGTATTGAATGCTTTCTTTTTCCTTTTGGTCCTCTTTTGGCAGGAGTGTGTTCTT
TACTTTGACTTGCTTCAAAGGCTTCAAACAACCTTACATCTAAGATGTTTTCTTCTGGCTCCCAAGTATTATACCGACTA
CTCCAACCTTTCCATTTAACCAAGTATTCAACTTTGCCTCTGCGAATACGCTTTTTCTGAATATATTCGGCATCAAACAC
TCTTTCACCAACAGATGACAGCTCCA

9.1.1.30 *polyhomeotic-proximal 2*

TCAGCAACCGAATCAATGGAGGGGTCGGAGGTTTTTATGCCTCTTCATGCTGAGAGTATGGAAACATCTGTAGAGAAAGA
TACTTTAAAGCTGCAAGATTCCATGAAAAAGACTTCTTTGAATTCTGCTAAAGATAAACAACCGCAGAAAGCTATTGTAA
AACCTCAAGTTTTGACTCATGTTATTGAAGGTTTTCTTATCCAGGAAGGCCCAGAACCTTTTCCGGTAAGGTCTTCACTC
TTTGATTCTCCTTGCCGAAGTACAACGTTAGAAAGAGCAGATGTCATTGATAAAAGAAAAGAATCACCCACGGCTTCAAG
CCCAGAAAAGAAGATAAAAATTCACAGAGGCCGAGGTCCTGGTCGAAGAAAAAAGATGGGCAGAGGTAGAAAAGGATTCC
GCAAATTACCCCAAATTGAAGAGAATGAGTTGTCTACCGTACAAGAACAAGAAAATAATGTTAGTATTCCTGATGATGAA
TCATCTCTTTCAAATAGAACAGAAGAAAGTTCAGAAATTCAGGAAATGAGTGTTATTTCTCCTTCTCAGAAACCACCTTC
CAAGTGGAGTGTTC

9.1.1.31 *paired*

CCGTCCTTGCGTCATCAGTCGACAGTTGAGAGTATCTCATGGATGTGTGTCCAAAATCTTAAATAGATATCAGGAAACAG
GTAGTATTAGACCTGGTGTGATTGGAGGAAGCAAACCACGTGTTGCCACTCCTGAAGTTGAAAAGAAAATTGAGGAATAT
AAAAGAGATAATCCTGGTATTTTCAGCTGGGAAATCAAAGACAGACTAGTCAAGGATGGTATCTGTGATAAAGAATCAGT
TCCGAGTGTCAGTTCCATCAGTCGTGTGCTCCGTGGTTCACGCCTTGGTTCAAGTGAATCAGGTGATTCATGTGACGGAA
GCAAAAAGGCCGATCACAGCATCGATGGTATTTTGGGAGGTCGCTTAGGCAACGATGAATCTGACTGTGAATCAGAACCG
GGCATTCCTTTAAAACGAAAACAGCGCAGATCTAGAACAACCTTCAGTGCAGAACAAGTGGAAGAACTGGAAAGGGCATT
TGAAAGGACTCAATATCCCGATATCTACACCAGAGAAGAACTAGCTTTGAGAACAGGCCTCACTGAAGCACGAGTTCAAG
TATGGTTTAGCAACCGTCGTGCTCGATGGAGAAAGCAAGTTGGAGGCCAACACTTGACTGCTGCTTTTTCTGCAGCACCA
ACTGTTCCGTTGGGTTACTCAGCCAATCCTCACTGCTATGAAGCAAATGCTCACCCTGATGCCAGTACATGGCATCGAGC
ACAAGCCCTGAGTGGTACTACATCTACATCAGGATTTCAACCTTCTTTCTCCTCAAGTCATTCCACAGCTTATTCACAAC
TACCTCCTGAACCATGCGTCAATCCAGCTCCACTAGCCCAACAGGTGTTCTCTATTTTGGGAAACTCAGTCAATACTAAC
TCCCAAGTGTCTTCTACTTCTGAATTCCATCTACCACCAACAAACAGCGAGGATGGGATGGAACTCCGCAAACATGCAAC
CTCGACCCGACACTACATCTTCGTGGAACCCCGCACCATTTCCTAAATTCCAGCMMACTG

9.1.1.32 *reversed polarity 1*

ACCGACTCTTGATAGACAGCCCAGTAGATTCTCACTGTATAGTATCGAAAGACTTCTGAATGTAGGCAGAGACGTTGTGC
GTCGTCCCAATCTAATTGACATTCAAGAAGTTGGTGAACCAAGAGGTAAACCAGATGGAGCCATTGATTTTAGTGTCCAT
ACCAGAGATCCGACTGCTGCTCTACGAGACACGCTTTCAAGGCTTGTACAGAGACAGGAGCGCTCTTCCTTATCCGATTT
GGGAGTGATGGGTGAAGAGAATCCTTCAACTCCATCAGAGCAGACAGATCAACAGAATCGGGGCCCACACCACCCTCTAG
ATTCCACAGATGATGGGGAGACCACTAATGGAAGTGGACCTGACAAACCTAGGAAGATTCGAAGGAGTCGAACAACTTTC
ACTACCTATCAGCTGCATCAGCTGGAGAGGGCTTTCGAGAAAACACAGTACCCAGATGTATTTACAAGAGAAGAATTGGC
AATGAGGCTGGACCTCAGTGAAGCGAGAGT

9.1.1.33 *sfmbt 1*

AGGTATTGTTTTAGCACCCACCATTTTCTTTAACAAGTAACTTGACCAAGAGTCAACTAAGTTTTCAAGACTTTTTGGGG
GCACAAGAGGTTTTCTGTGTTTTGCACACCAGCCAATGGGATGAATATGAGGATGCGTACATAGGTTAACCCATTTATCA
CGTAAGTGGTTGTATCTTACAGTAAAGTCCTCTGCACCTACATAGCGTAACAGGCCCCAATAGCCAGACACTTTAACAAC
TGATGCTATCCAATAAGAGCAAGGTGTAGTCGTGCAGCAAGTTTTGCAGTCAGGGCTTCTAACTTCCACCATTACTCCAG
CGACTATCCGATCCCAGCAATTGGAAAGAGCAA

9.1.1.34 *sloppy paired*

CCATCAGCAGCCTTATCAACGGCGGCGAGGACGACGATAATGTTCCGGCGACTGCCGCGGCGGTCGTCACTCCACCACCT
CCCGCGGTCGAATGCCCCCGGGACTTCAGTAATCGGCGAAATAACATTGATGGAGTTTCCACACYTCCAGATTCCGATAC
GAAATCGGACGCGACTACCCCGATCACTTCTTCGCCTCCTTCTCCAAGCAAAGTTGCTCAAGACAAATCTAGCAACAAAG
CAAAAAAACTCATCCGATGACAAAAAATCTACCTTTGAAAAGCCACCGTTCAGTTATAATGCACTTATTATGATGGCCAT
CCGCCAAAGTCCAGAAAAGAGACTGACCCTAAACGGAATTTATGAGTTCATCATGAAAAACTTTCCTTATTATCGAGAAA
ATAAACAAGGTTGGCAAAATTCCATTAGACATAACTTAAGTCTTAACAAGTGTTTTGTCAAAGTTCCACGGCATTATGAT
GATCCAGGAAAAGGAAACTATTGGATGCTCGATCCAAGTTCAGATGACGTATTCATTGGTGGTACAACCGGTAAACTACG
CAGGAGAACTACCGCAGCATCCAGAAGCAGACTTGCTGCTTTCAAACGGGCAGGAGCCCCCATGTTCCATGCAGGACTCA
ATCCAGCATTTCATCATCACGACAAATCAACTCTGGGCTGGTCCCTTGCTGGTTATGGTGGTTTTCACACGCCTGGTGGT
CTCTTGTCTTTCAAATACCCATATTCTAGCTTAACAACGAATATGGCAGCTTTACAAAGTCCCAAGCCAACAGGCTTCAG
TGTAGATAGACTAATAGGGGCAGAAACTGCCGCAAATCTTCATAATCCTTTGTGGTCAAGTCTGGGATGCCCTCCTGGCT
GTTCTCCTCTAGGATTAGGTAGTCCTCAAGGTTATTCAGCTATGCCTGGTTGTGGGTACTTACTATCATCTCTAGTCGCT

CCTGGACAAGCTCTTTATGATCTCCAAGCCCTAAGGACAGTTTCTGCAATGAATTGCCAAGCTGGACAGGCGAGGAATGC
CAGTCAAAGTTCCACGACGTCCAGTTCTG

9.1.1.35 *tailless*

ATTTTCTCCAGCCTCACCAGTCCGACTGTTTTGCTGAAGAAGAGTTTGTGGATTTGATCGCTGGTGATGGTGCGGAGGCA
GGCCGGTATTTGGTGCATCCGAACCACCCTCAGTTGCTGGTTGGGATAGTAGAGCTCTAAATGTCGCATCAGGATCACCT
GCACGTGATCGTGAACCGCTGCAACAGTGCTAACTTCTTTGAGGTCTTTAATGGAAGGGGGAGCTCCTGGAAAATCTTTC
TTGAAAAGCGTGATGAGCCTCAGGTAATGATACTCATAAGCATCCAGATTGAGCTCTTTGATCTGAGACATGATTCTCTG
AAAGGCGATCATCGAAGCCTTGATTGCACTCTCTCGTTCAGGAGTCATCTCACAATCCTCACTCAGACCTGTAGCACAGC
GTAAGAATTCTTCATCGACTGGCAGATTGCATTGGGCTGCTGAAAGAACAAACAATTCACTCGATGCTTCTTCCAGAAGA
ATTTCCTGATCTCTTATTGGTAGAGTCATGAACTCGGGTACGCCTCTTACTAAGCTCCGATTCCAGATCAGAACTTGGGC
GGCTAATTCAGCTGCATCAGCTTCCGCTTTAGGTGAAACGTTATTTCTCCCCGCAAAAGCAGTGGCGTAAGTAGCGTAGG
AGTGATATTGGGGCAGTGGTTGAAGAATGGGTGCTGTTGTAGAGCCCATTCTCATGAGCCTCATGTGGGTCAATGGAAGA
TTCGGGGAGGACAGTGGACTGGCAATGAAGGAGGGATCTCGAAGGGGACGATTGGCAAAAAATCCACTCCCATCAGCTGG
CAATGAAAATCCTCCAGGTGATGCCTGATGATGAAACAAGGAGGGAGAGATCGATCCCTGATTCCAGGAATCTCGAATTA
TCATCGCAGCATGTCGCTGTCTTGTGGAGTTGCGAGGACCTCTCTCGTGTTGGACAGCTTCTTTGTTCATGCCAGCTTCT
TGGCACTTTTTGAGTCTGCAGTGCCTGCACTGATTTCTGTGAACTTTGTCGATCGGGCAATTTCCAGTCGCACCGTTCTT
TCCTTTACAGACATAGTTTCGAGCTCTACGAATCGATCTTTTAAAAAAGCCAGCACACCCATCACAAGAATAAATTCCGT
AGTGTTTTCCGGAAGAAAAATCTCTGCACACTTTACACTTTACATCAGTTAGAATGCGATTTGAGGGTGGACGTTTAATC
ATAATTTCCTCAGTGGTGGCCGCTTCTTCAAACTCTAAACCAAATACTGATTTCATGTGA

9.1.1.36 *trithorax*

CTGTCCCGTTTGCCACAAGTGCTATGAAGAGAATGACTATGAATCTGAAATGGTGCAATGTTTTGACTGTCTTCGATGGG
TTCATGCTGCTTGTGGTAACATAAGCGCTGAAGGATATGAAATTCTCTCTTGTCTTCCTGATAGTGTTGTTTACACTTGT
ATTAATTGTACTGATGAAGTTGTTCCAACATGGCGCAAAGCAATTAAAGAATATCTGAAGCATGGTTTAAAGAATGTTCT
TAACACTCTCATGGCATCAAGATGTGCAAATCATCTAATTAATCTTGATCAATCTTATCAAAAACGTAAAATTCCTGATT
ACATGATGGCTAAGCAAGCTGAATCTGTGTCGAGAGATGAGCCTTCCAATAGAAAAGAGGACGATAGAAACCCCTTTTTC
ATTGATGAAGTGGCTGATAGCACTGATTCAACCGACGTTAAGAGAACCATTTCTGCCATCGTGAAATCAGTTGATGATGT
CTCAGCTTGTATGAAAAATATGTTGAATAAGTGTGAGGAAAGCAGTTCTTCAAAGCATCTCAATGAATGTTCTCCCACAA
CTGTTGATAATGTTGTCCAATCTGCTCCCAAAGAGCGATCTGAGGAGAAAAATGTGCTATTTAAAAAAAAAAAAGAGTTC
ACTGGATTTATCTGTAATCAGGTTTAATCTTGATAAGGGAAAATATTCAAACATTGCTTCTTTTTTCGAAGATGTATTGT
ATGTAATTGATGCCAATAGTAACATGGGTAAAAAACATAATGCCAATGCAGCCAAAGTACTTCTAACTAAGCAAACAGAA
AAAATATTTCCTTGGTTTAAAATTCCAACTTCAAAAGTATGGACTTCAAAAAGTGATCTTCCAGAAGGGATGCTCCCAAA
TGCAGTTATTCCACCTTACGTTGATCATACTTATTCTCAATATTTGGARRAGAAGAGATTATTTCCCCAAAATTAAAAAT
GAAGTTTTGCCTGATGCTAGATTCYG

9.1.1.37 *ventral nervechord defective 1*

ATTTGTCTGATGTGACGCTTCCAGCGTTGTGTTACAGCAGTTTTTGTCCTGACACTTCTTATTCGCGGTGGTTGGCATCA
GAAATTATTCCAGCCTATGCAGCTTTACCTTTTGCACACATGGGTCTTGATCCTTGCCTAACAGGAGCCGAACCTGGATT
CCTCGCAAGCCATGAACTCACTCGTAGCACTGATGAGAGGGACGAAATGGACGAAGAGGATGATCTTGAGGATGAAGAAG
ATGAAATAGTTGATGACGATAGTGCTCTCGAGGACCTTCCGGTTGTGTCAAGCCCTGGTGCGGGGATGCCTACGGGTGCC
ACCGGTGGGGTTTCCGTCATCACTCGGCACCGAAGAGGGGATGATTCCGATTCAGATGAAGTCACTTCATCGCAACAGCC
ATCAACAAGTATTTTGAACTGCAGTACTAATAATAACAATAACACTAGTGGGTGTAATAACAATAATACACCAACGAGTT
CCACGTCTGGAGACGCTGGAAATCCTCCTTTGAAAAAAAGAAAAAGAAGAGTTTTATTTTCAAAAGCCCAAACATATGAA
CTAGAAAGAAGGTTTCGACAACAGAGGTACCTGTCAGCCCCAGAAAGAGAGCACTTGGCAAGTATAATCCGGTTAACGCC
TACGCAAGTAAAAATCTGGTTTCAGAACCACAGATACGAAACTAAGCGAGCCAGACAGGAAAAAGGTCTGGATGTGAACC
CGTTACCTTCACCGCGGAGAGTAGCTGTACCCGTTTTAGTTCGCGATGGCAAGCCATGCCAACCAGCAAGTTCTGCTCTG
AACAAGCAACAAGCTGAGG

9.1.1.38 *ventral nervechord defective 2*

CAACGCTGCTGATGAAATAAATGCGGATTATAACTTGGCATCATATTATTCATGTTATAGGAACTAATATATGAGTTCGT
GACACAGTTATTGGTGGCAGCTGTTAATGAAGTTATGGAAGGCAAATCATTACGAGGTAATCCAATGGACTGTGCTTCTT
GTGGCATTGATGGTTGACAAGGTTTGCCATCTCGTACTAATACAGGCACAGCAACTCTTCTTGGCGATTGGAAGTTTATA
TCCACCCTATCTGCTCTCGCTCTCTTATGCTTATAGCGATGGTTTTGAAACCAAATCTTTACTTGAGTTGGTGTCAATCT
TATAATGCTGGCCAGATGTTCTCTTTCTGGTGCTGACAGATACCGCTGTTGTCGGAATCGTCGTTCCAGTTCAAAAGTTT
GACTTTTTGAAAACAATACTCGTCGTTTTCGTTTTTTCTGCGCGCTATCGGAATCACTTCCAGAAACATTTTGCATAGGC

GCTGGTTCATCTCCTTTTTCAACAATGCTTTCTTCTGATGATGAAGAATATTCTTGATTCAAAGTAGTGTTAATGGATAT
AGATGGAGATGAAAAATTTTCTGGTACCTCTCCTCCAGAACTCACGTCAATTGGAAGATTGAAATTTGTTGTTGCGTCTG
TTGGAAGATATCTTGAAAAGTGATCAAGTCCACCATAATTAGAATTTTCTTCTACTTCATTGCTTGATGGAAAACTAGAA
GGAGATTTAGTTTCAGATAAGTCCAAAATATCACGCACAGAAA

9.2 Molecular characterization and embryonic origin of the eyes in the common house spider *Parasteatoda tepidariorum*

9.2.1 Maximum likelihood tree of Opsin sequences

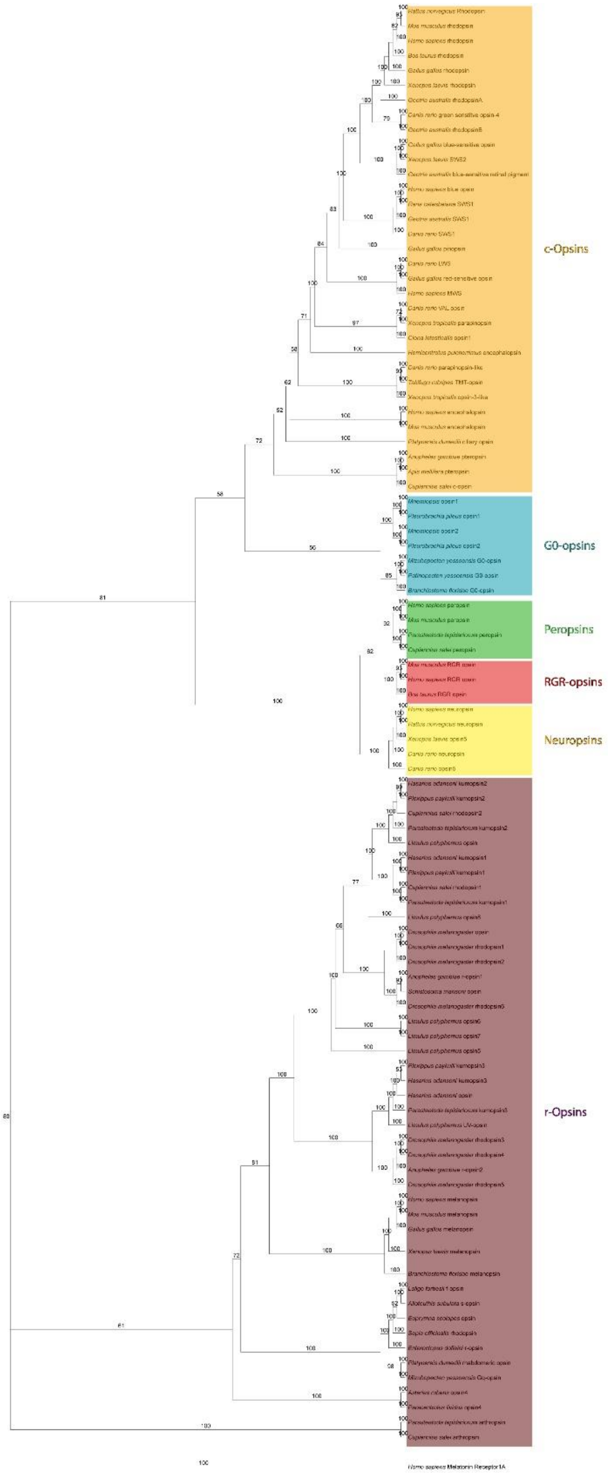

Figure S 1 – Phylogenetic tree of Opsin sequences with the human Melatonin receptor 1A as outgroup. Sequences were obtained from published literature. The tree was built using amino acid sequences. Branch values are the posterior probabilities of Bayesian likelihood. The *P. tepidariorum* Peropsin sequence clusters to the Peropsin group with the vertebrates and *C. salei*, while the other *P. tepidariorum* sequences analyzed cluster with the r-Opsin group

9.2.2 Accession numbers of Opsin genes

Accession number	Organism	Gene
Q17094	*Allotheutis subulata*	s-opsin
XM312503	*Anopheles gambiae*	Pteropsin
XP001238567	*Anopheles gambiae*	r-opsin1
XP556823	*Anopheles gambiae*	r-opsin2
NP_001035057.1	*Apis mellifera*	pteropsin
KM249890	*Asterias rubens*	opsin4
NP786969	*Bos taurus*	RGR opsin
NP_001014890.1	*Bos taurus*	rhodopsin
ABO50606	*Branchiostoma floridae*	G0-opsin
Q4R1I4.1	*Branchiostoma floridae*	Melanopsin
NP_001027727.1	*Ciona intestinalis*	opsin1
CCO61973	*Cupiennius salei*	rhodopsin 1
CCO61974	*Cupiennius salei*	rhodopsin 2
CCP46949	*Cupiennius salei*	peropsin
CCP46950	*Cupiennius salei*	c-opsin
CCP46951	*Cupiennius salei*	arthropsin
AAH76120.1	*Danio rerio*	LWS opsin
NP_571329.1	*Danio rerio*	MWS opsin
BX088599	*Danio rerio*	neuropsin
XP698118.5	*Danio rerio*	opsin5
XP_002666709.2	*Danio rerio*	parapinopsin
NP_571394.1	*Danio rerio*	SWS opsin
NP_571661.1	*Danio rerio*	VAL opsin
AAA28734	*Drosophila melanogaster*	rhosopsin 2
AAA28735	*Drosophila melanogaster*	opsin
AAA28854	*Drosophila melanogaster*	rhodopsin 3
AAA28856	*Drosophila melanogaster*	rhodopsin 4
AAC47426	*Drosophila melanogaster*	rhosopsin 5
AAF55712	*Drosophila melanogaster*	rhosopsin 1
O01668.1	*Drosophila melanogaster*	rhodopsin6
P09241	*Enteroctopus dofleini*	r-opsin
ACB05672	*Euprymna scolopes*	opsin
NP_990848.1	*Gallus gallus*	SWS opsin
NP001038118	*Gallus gallus*	melanopsin
U15762	*Gallus gallus*	pinopsin
NP_990771.1	*Gallus gallus*	LWS opsin
NP001025777	*Gallus gallus*	rhodopsin
AAR14682	*Geotria australis*	rhodopsinA
AAR14683	*Geotria australis*	rhodopsinB
AAR14684	*Geotria australis*	SWS1-opsin
AAR14681	*Geotria australis*	SWS2-opsin
BAG14330	*Hasarius adansoni*	kumopsin 1
BAG14331	*Hasarius adansoni*	kumopsin 2
BAG14332	*Hasarius adansoni*	kumopsin 3
BAO73879	*Hasarius adansoni*	opsin
BAH28806.1	*Hemicentrotus pulcherrimus*	Opsin1
M13299	*Homo sapiens*	SWS opsin
NP055137	*Homo sapiens*	encephalopsin
AF147788	*Homo sapiens*	melanopsin
AAH74946.1	*Homo sapiens*	melatonin receptor1A
NP_000504.1	*Homo sapiens*	MWS opsin
AY377391	*Homo sapiens*	neuropsin
NP006574	*Homo sapiens*	peropsin
P47804	*Homo sapiens*	RGR opsin
NP000530	*Homo sapiens*	rhodopsin
AAA02498	*Limulus polyphemus*	opsin
ACO05013	*Limulus polyphemus*	opsin 5

AEL29244	*Limulus polyphemus*	UV opsin
AIT75830	*Limulus polyphemus*	opsin 6
AIT75831	*Limulus polyphemus*	opsin 7
AIT75832	*Limulus polyphemus*	opsin 8
P24603	*Loligo forbesii*	f-opsin
O15974.1	*Mizuhopecten yessoensis*	G0-opsin
Mnemiopsis_opsin1_13055	*Mnemiopsis*	opsin 1
Mnemiopsis_opsin2_12047	*Mnemiopsis*	opsin 2
Mnemiopsis_opsin3_215412	*Mnemiopsis*	opsin 3
NP_034228.1	*Mus musculus*	encephalopsin
NP_033128.1	*Mus musculus*	peropsin
AAC69836.1	*Mus musculus*	GRG opsin
NP663358	*Mus musculus*	rhodopsin
KM249889	*Paracentrotus lividus*	opsin4
Locus 16558 transcript 1/1	*Parasteatoda tepidariorum*	arthropsin
KP725074	*Parasteatoda tepidariorum*	peropsin
Locus 20849 transcript 1/1	*Parasteatoda tepidariorum*	kumopsin 1
Locus 26929 transcript 4/5	*Parasteatoda tepidariorum*	kumopsin 2
Locus 35644 transcript 3/3	*Parasteatoda tepidariorum*	kumopsin 3
AB006455	*Patinopecten yessoensis*	G0-opsin
AAV63834.1	*Platynereis dumerilii*	c-opsin
CAC86665.1	*Platynereis dumerilii*	r-opsin
CU419614	*Pleurobrachia pileus*	opsin1
FQ011385	*Pleurobrachia pileus*	opsin2
BAG14333	*Plexippus paykulli*	kumopsin 1
BAG14334	*Plexippus paykulli*	kumopsin 2
BAG14335	*Plexippus paykulli*	kumopsin 3
BAA96828	*Rana catesbeiana*	SWS1 opsin
EDM18681.1	*Rattus norvegicus*	neuropsin
NP_254276.1	*Rattus norvegicus*	rodopsin
AAF73286	*Schistosoma mansoni*	opsin
AAC26329.1	*Sepia officinalis*	rhodopsin
opsin_AAL83430.1	*Takifugu rubipes*	TMT opsin
AAO38746	*Xenopus laevis*	MWS opsin
AAC41235.1	*Xenopus laevis*	melanopsin
NP_001182522.1	*Xenopus laevis*	opsin5
P29403	*Xenopus laevis*	opsin
XP_002933418.2	*Xenopus tropicalis*	opsin3
AB159672	*Xenopus tropicalis*	parapinopsin

9.3 Phylogenetic analysis of forkhead transcription factors

9.3.1 HMMER scans

9.3.1.1 *Amphimedon queenslandica*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_003383008.2       -              1e-31   96.4   0.4   1.9e-31   95.6   0.4
Forkhead             PF00250.14 XP_003383135.1       -            5.7e-06   13.9   0.1   9.5e-06   13.2   0.1
Forkhead             PF00250.14 XP_003384249.1       -            2.6e-06   15.0   0.0   4.4e-06   14.3   0.0
Forkhead             PF00250.14 XP_003384287.1       -            1.5e-05   12.5   1.6    0.0003    8.4   0.5
Forkhead             PF00250.14 XP_003384421.1       -            4.1e-39  120.2   0.1   9.6e-39  119.0   0.1
Forkhead             PF00250.14 XP_003384534.2       -              3e-37  114.1   0.2   6.2e-37  113.2   0.2
Forkhead             PF00250.14 XP_003384559.1       -            1.6e-39  121.5   0.0   2.3e-39  120.9   0.0
Forkhead             PF00250.14 XP_003385351.1       -            6.9e-41  125.8   0.2   1.3e-40  125.0   0.2
Forkhead             PF00250.14 XP_003386176.1       -            1.7e-32   98.9   0.1   5.1e-32   97.4   0.1
Forkhead             PF00250.14 XP_003386177.1       -            1.2e-33  102.6   0.1   2.4e-33  101.7   0.1
Forkhead             PF00250.14 XP_003386405.1       -            2.3e-39  120.9   0.2   3.8e-39  120.2   0.2
Forkhead             PF00250.14 XP_003387169.1       -            2.1e-42  130.7   0.0   3.8e-42  129.9   0.0
Forkhead             PF00250.14 XP_003387576.1       -            2.6e-34  104.7   0.7   4.5e-34  104.0   0.7
Forkhead             PF00250.14 XP_003387810.2       -            1.6e-30   92.6   0.5   3.1e-30   91.7   0.5
Forkhead             PF00250.14 XP_003390089.1       -            7.2e-40  122.6   0.1   1.3e-39  121.7   0.1
Forkhead             PF00250.14 XP_003392087.1       -            3.8e-39  120.3   0.1     5e-39  119.9   0.1
Forkhead             PF00250.14 XP_011402861.1       -            5.6e-31   94.1   0.1   9.4e-31   93.4   0.1
Forkhead             PF00250.14 XP_011405015.1       -            3.1e-28   85.3   0.1   5.1e-28   84.6   0.1
Forkhead             PF00250.14 XP_011407693.1       -            5.8e-44  135.7   0.0   8.6e-44  135.1   0.0
Forkhead             PF00250.14 XP_011408626.1       -            1.1e-05   13.0   0.9    0.0015    6.2   0.0
```

9.3.1.2 *Branchiostoma floridae*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_002590110.1       -              1e-38  118.9   0.1   1.6e-38  118.3   0.1
Forkhead             PF00250.14 XP_002591636.1       -            7.1e-38  116.2   0.2   8.1e-38  116.0   0.2
Forkhead             PF00250.14 XP_002591873.1       -            2.4e-37  114.5   0.0   4.2e-37  113.7   0.0
Forkhead             PF00250.14 XP_002594152.1       -            5.8e-14   39.5   0.0   1.5e-13   38.2   0.0
Forkhead             PF00250.14 XP_002594265.1       -            3.6e-35  107.5   0.4   5.9e-35  106.8   0.4
Forkhead             PF00250.14 XP_002594284.1       -            1.1e-41  128.4   0.0   3.5e-41  126.8   0.0
Forkhead             PF00250.14 XP_002594291.1       -            1.7e-36  111.7   0.0   3.1e-36  110.9   0.0
Forkhead             PF00250.14 XP_002595677.1       -            1.4e-05   12.7   0.0   1.5e-05   12.6   0.0
Forkhead             PF00250.14 XP_002597064.1       -              3e-38  117.4   0.0   3.3e-38  117.2   0.0
Forkhead             PF00250.14 XP_002597237.1       -            1.4e-38  118.4   0.1     2e-38  117.9   0.1
Forkhead             PF00250.14 XP_002599263.1       -            2.8e-44  136.7   0.2     5e-44  135.9   0.2
Forkhead             PF00250.14 XP_002599776.1       -            5.7e-06   13.9   0.0   0.00018    9.1   0.0
Forkhead             PF00250.14 XP_002601441.1       -            2.5e-15   43.9   0.0     4e-15   43.3   0.0
Forkhead             PF00250.14 XP_002602031.1       -            6.1e-39  119.6   0.0   8.1e-39  119.2   0.0
Forkhead             PF00250.14 XP_002602294.1       -            5.3e-41  126.2   0.0   6.1e-41  126.0   0.0
Forkhead             PF00250.14 XP_002602296.1       -            3.7e-41  126.7   0.0   4.3e-41  126.5   0.0
Forkhead             PF00250.14 XP_002602547.1       -              2e-42  130.7   0.0   3.7e-42  129.9   0.0
Forkhead             PF00250.14 XP_002602560.1       -            7.2e-41  125.8   0.0   1.1e-40  125.2   0.0
Forkhead             PF00250.14 XP_002603103.1       -            6.5e-07   16.9   0.2   1.8e-05   12.3   0.0
Forkhead             PF00250.14 XP_002604185.1       -            2.6e-15   43.9   0.0     4e-15   43.3   0.0
Forkhead             PF00250.14 XP_002604922.1       -            1.7e-34  105.3   0.0     2e-34  105.1   0.0
Forkhead             PF00250.14 XP_002605066.1       -            1.7e-43  134.2   0.4     3e-43  133.4   0.4
Forkhead             PF00250.14 XP_002606556.1       -            1.9e-36  111.6   0.0   2.5e-36  111.2   0.0
Forkhead             PF00250.14 XP_002607158.1       -            1.9e-39  121.2   0.6   3.2e-39  120.5   0.6
Forkhead             PF00250.14 XP_002608285.1       -              4e-43  133.0   0.0   6.6e-43  132.3   0.0
Forkhead             PF00250.14 XP_002608493.1       -            1.2e-31   96.3   0.4   1.5e-31   95.9   0.4
Forkhead             PF00250.14 XP_002610230.1       -            2.2e-42  130.6   0.2   5.1e-42  129.5   0.0
Forkhead             PF00250.14 XP_002612405.1       -            2.2e-31   95.4   0.1   7.2e-31   93.7   0.1
Forkhead             PF00250.14 XP_002613158.1       -            2.8e-40  123.9   0.2   6.5e-40  122.7   0.2
Forkhead             PF00250.14 XP_002613160.1       -            2.1e-40  124.2   0.1     4e-40  123.4   0.1
Forkhead             PF00250.14 XP_002613659.1       -            1.9e-34  105.2   0.5     2e-34  105.1   0.5
Forkhead             PF00250.14 XP_002613661.1       -              6e-38  116.4   0.0   7.2e-38  116.2   0.0
Forkhead             PF00250.14 XP_002614110.1       -            3.7e-41  126.7   0.0   4.3e-41  126.5   0.0
Forkhead             PF00250.14 XP_002614112.1       -            5.7e-40  122.9   0.0   9.1e-40  122.2   0.0
Forkhead             PF00250.14 XP_002614113.1       -            3.7e-41  126.7   0.0   4.3e-41  126.5   0.0
```

9.3.1.3 *Capsaspora owzarzaki*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_004343293.2       -              4e-32   97.7   0.1   9.6e-32   96.5   0.1
Forkhead             PF00250.14 XP_004346423.1       -            2.7e-39  120.7   0.0   4.7e-39  119.9   0.0
Forkhead             PF00250.14 XP_004364634.2       -            5.7e-37  113.3   0.3   1.9e-36  111.6   0.3
Forkhead             PF00250.14 XP_004365808.1       -            2.9e-39  120.6   0.3   2.9e-39  120.6   0.3
```

9.3.1.4 *Ciona intestinalis*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001027695.1       -            1.5e-39  121.5   0.8   4.2e-39  120.1   0.0
Forkhead             PF00250.14 NP_001027769.1       -            9.7e-42  128.6   0.0   1.6e-41  127.9   0.0
Forkhead             PF00250.14 NP_001027947.1       -            2.2e-41  127.4   0.0   4.5e-41  126.4   0.0
Forkhead             PF00250.14 NP_001071708.1       -            4.2e-44  136.1   0.2   8.4e-44  135.2   0.2
Forkhead             PF00250.14 NP_001071709.1       -            8.1e-41  125.6   0.0   1.7e-40  124.5   0.0
Forkhead             PF00250.14 NP_001071710.1       -            2.4e-41  127.3   0.0     5e-41  126.3   0.0
Forkhead             PF00250.14 NP_001071711.1       -            7.2e-40  122.6   0.1   1.5e-39  121.6   0.1
Forkhead             PF00250.14 NP_001071712.1       -            2.9e-41  127.0   0.1     5e-41  126.3   0.1
Forkhead             PF00250.14 NP_001071713.1       -            8.9e-43  131.9   0.1   1.6e-42  131.1   0.1
Forkhead             PF00250.14 NP_001071714.1       -            8.8e-40  122.3   2.2   3.5e-39  120.3   0.2
Forkhead             PF00250.14 NP_001071715.1       -            1.1e-42  131.6   0.6   1.9e-42  130.8   0.6
```

```
Forkhead             PF00250.14 NP_001071716.1       -            1.4e-34  105.6   0.1   3.2e-34  104.5   0.1
Forkhead             PF00250.14 NP_001071717.1       -              9e-30   90.2   2.7   1.6e-28   86.2   0.2
Forkhead             PF00250.14 NP_001071718.1       -            1.6e-36  111.8   0.0   3.1e-36  110.9   0.0
Forkhead             PF00250.14 NP_001071787.1       -            2.8e-22   66.2   2.7   1.2e-21   64.2   0.3
Forkhead             PF00250.14 NP_001071788.1       -            2.3e-23   69.7   0.6   2.3e-23   69.7   0.6
Forkhead             PF00250.14 NP_001071789.1       -            3.1e-33  101.3   0.1   7.6e-33  100.1   0.1
Forkhead             PF00250.14 NP_001071790.1       -              4e-34  104.1   0.8   1.1e-33  102.7   0.0
Forkhead             PF00250.14 NP_001071939.1       -            2.2e-32   98.6   0.4   2.2e-32   98.6   0.4
Forkhead             PF00250.14 NP_001071991.1       -            4.3e-41  126.5   0.2     1e-40  125.3   0.2
Forkhead             PF00250.14 NP_001071992.1       -            1.4e-29   89.6   0.1   2.7e-29   88.7   0.1
Forkhead             PF00250.14 NP_001071993.1       -            7.7e-33  100.0   1.0   2.6e-32   98.3   1.0
Forkhead             PF00250.14 XP_002121210.1       -            3.3e-07   17.9   0.0   5.4e-07   17.2   0.0
Forkhead             PF00250.14 XP_002124993.3       -            2.8e-41  127.1   0.7   6.1e-41  126.0   0.7
Forkhead             PF00250.14 XP_004227156.1       -            1.2e-28   86.6   0.1   2.1e-28   85.8   0.1
Forkhead             PF00250.14 XP_009858520.1       -            1.7e-41  127.8   0.0   3.2e-41  126.9   0.0
Forkhead             PF00250.14 XP_009858528.1       -            3.3e-33  101.2   0.1   8.4e-33   99.9   0.1
Forkhead             PF00250.14 XP_009859457.1       -            7.5e-41  125.7   0.0   1.6e-40  124.6   0.0
Forkhead             PF00250.14 XP_009860051.1       -            1.6e-37  115.0   0.2   3.8e-37  113.8   0.2
Forkhead             PF00250.14 XP_009860182.1       -            1.9e-39  121.2   0.1   3.5e-39  120.4   0.1
Forkhead             PF00250.14 XP_009861074.1       -              8e-40  122.4   2.4   3.1e-39  120.5   0.2
Forkhead             PF00250.14 XP_009861272.1       -            2.3e-23   69.7   0.6   2.3e-23   69.7   0.6
Forkhead             PF00250.14 XP_009861630.1       -            3.1e-30   91.7   0.2   7.2e-30   90.5   0.2
```

9.3.1.5 *Crassostrea gigas*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_011412452.1       -            1.1e-26   80.3   0.2   2.3e-26   79.3   0.2
Forkhead             PF00250.14 XP_011413445.1       -            3.9e-41  126.6   0.2   1.2e-40  125.1   0.1
Forkhead             PF00250.14 XP_011414359.1       -            4.6e-30   91.1   0.1   1.2e-29   89.7   0.1
Forkhead             PF00250.14 XP_011415497.1       -            9.1e-44  135.1   0.4   7.1e-42  129.0   0.0
Forkhead             PF00250.14 XP_011416099.1       -              1e-42  131.7   0.2   1.7e-42  131.0   0.2
Forkhead             PF00250.14 XP_011416100.1       -              1e-42  131.7   0.2   1.7e-42  131.0   0.2
Forkhead             PF00250.14 XP_011417585.1       -            7.3e-43  132.2   0.1   1.4e-42  131.3   0.1
Forkhead             PF00250.14 XP_011417586.1       -            5.1e-44  135.9   0.1     8e-44  135.2   0.1
Forkhead             PF00250.14 XP_011419330.1       -            2.1e-32   98.6   0.6   4.9e-32   97.5   0.6
Forkhead             PF00250.14 XP_011419331.1       -            1.6e-32   99.0   0.6   3.8e-32   97.8   0.6
Forkhead             PF00250.14 XP_011419332.1       -            1.6e-32   99.0   0.6   3.8e-32   97.8   0.6
Forkhead             PF00250.14 XP_011419333.1       -            1.6e-32   99.0   0.6   3.8e-32   97.8   0.6
Forkhead             PF00250.14 XP_011419335.1       -            1.6e-32   99.0   0.6   3.8e-32   97.8   0.6
Forkhead             PF00250.14 XP_011419336.1       -            1.6e-32   99.0   0.6   3.8e-32   97.8   0.6
Forkhead             PF00250.14 XP_011421891.1       -            1.8e-15   44.3   0.1   4.1e-15   43.2   0.1
Forkhead             PF00250.14 XP_011422959.1       -            5.8e-40  122.9   0.2   1.2e-39  121.9   0.2
Forkhead             PF00250.14 XP_011425762.1       -            5.6e-38  116.5   0.0   1.4e-37  115.2   0.0
Forkhead             PF00250.14 XP_011426090.1       -            3.6e-36  110.7   0.0   7.7e-36  109.6   0.0
Forkhead             PF00250.14 XP_011427689.1       -            9.2e-42  128.6   0.0   1.9e-41  127.6   0.0
Forkhead             PF00250.14 XP_011434081.1       -            1.4e-32   99.2   0.9   3.3e-32   98.0   0.9
Forkhead             PF00250.14 XP_011434585.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011434586.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011434587.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011434588.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011434589.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011434590.1       -              1e-37  115.7   0.0   2.1e-37  114.6   0.0
Forkhead             PF00250.14 XP_011435457.1       -            5.5e-37  113.3   0.0     1e-36  112.4   0.0
Forkhead             PF00250.14 XP_011439389.1       -            5.2e-36  110.2   0.1   1.1e-35  109.1   0.1
Forkhead             PF00250.14 XP_011441298.1       -            8.9e-40  122.3   0.0   1.4e-39  121.6   0.0
Forkhead             PF00250.14 XP_011444080.1       -            1.3e-16   48.0   0.1   3.8e-16   46.5   0.1
Forkhead             PF00250.14 XP_011444776.1       -            2.4e-37  114.5   0.0     4e-37  113.8   0.0
Forkhead             PF00250.14 XP_011445234.1       -            3.2e-39  120.5   0.4   5.3e-39  119.8   0.4
Forkhead             PF00250.14 XP_011445235.1       -            3.2e-39  120.5   0.4   5.3e-39  119.8   0.4
Forkhead             PF00250.14 XP_011445317.1       -              5e-41  126.3   0.0   1.2e-40  125.1   0.0
Forkhead             PF00250.14 XP_011445364.1       -            2.3e-39  120.9   0.4   1.6e-38  118.2   0.0
Forkhead             PF00250.14 XP_011446328.1       -              9e-41  125.5   0.0   2.1e-40  124.3   0.0
Forkhead             PF00250.14 XP_011447418.1       -            1.8e-05   12.3   0.0   2.5e-05   11.8   0.0
Forkhead             PF00250.14 XP_011447567.1       -            1.3e-20   60.9   0.3   2.3e-20   60.1   0.3
Forkhead             PF00250.14 XP_011455622.1       -            2.4e-37  114.5   0.0     4e-37  113.8   0.0
```

9.3.1.6 *Danio rerio*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001008648.1       -            8.1e-40  122.4   1.4   1.3e-39  121.7   0.3
Forkhead             PF00250.14 NP_001009988.1       -              8e-31   93.6   0.0   1.6e-30   92.6   0.0
Forkhead             PF00250.14 NP_001017555.1       -              6e-36  110.0   0.0   9.8e-36  109.3   0.0
Forkhead             PF00250.14 NP_001025253.1       -            2.6e-32   98.3   0.5   6.7e-32   97.0   0.5
Forkhead             PF00250.14 NP_001034726.1       -            9.5e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 NP_001038244.1       -            2.8e-17   50.1   0.0     1e-16   48.3   0.0
Forkhead             PF00250.14 NP_001038405.1       -            7.1e-18   52.1   0.0   2.5e-17   50.3   0.0
Forkhead             PF00250.14 NP_001038680.1       -              2e-41  127.6   0.0   4.7e-41  126.4   0.0
Forkhead             PF00250.14 NP_001038717.1       -            9.4e-43  131.8   0.1   1.5e-42  131.2   0.1
Forkhead             PF00250.14 NP_001038728.1       -            1.9e-38  118.0   0.6   5.4e-38  116.6   0.1
Forkhead             PF00250.14 NP_001070174.2       -            4.2e-39  120.1   0.3   7.4e-39  119.3   0.3
Forkhead             PF00250.14 NP_001070725.2       -            3.4e-30   91.5   0.1   6.4e-30   90.7   0.1
Forkhead             PF00250.14 NP_001071032.2       -            4.1e-33  100.9   0.2   9.9e-33   99.7   0.2
Forkhead             PF00250.14 NP_001073150.2       -            2.1e-42  130.7   0.0   3.4e-42  130.0   0.0
Forkhead             PF00250.14 NP_001073655.1       -            3.6e-42  129.9   0.0   6.5e-42  129.1   0.0
Forkhead             PF00250.14 NP_001076326.1       -            1.9e-30   92.4   0.1   3.6e-30   91.5   0.1
Forkhead             PF00250.14 NP_001076343.1       -            1.3e-17   51.2   0.5   3.9e-17   49.7   0.5
Forkhead             PF00250.14 NP_001077284.1       -            1.1e-39  122.0   0.0   1.8e-39  121.3   0.0
Forkhead             PF00250.14 NP_001082957.1       -            5.5e-41  126.1   0.0   9.5e-41  125.4   0.0
Forkhead             PF00250.14 NP_001096594.1       -              5e-28   84.6   0.0   8.7e-28   83.8   0.0
Forkhead             PF00250.14 NP_001098411.1       -            2.1e-37  114.6   0.1   3.3e-37  114.0   0.1
Forkhead             PF00250.14 NP_001116096.1       -            6.2e-42  129.2   0.0     1e-41  128.5   0.0
Forkhead             PF00250.14 NP_001116217.1       -            4.5e-37  113.6   0.0   8.8e-37  112.7   0.0
Forkhead             PF00250.14 NP_001122282.1       -            2.5e-42  130.4   0.2   3.7e-42  129.9   0.2
Forkhead             PF00250.14 NP_001128604.1       -            1.9e-28   85.9   0.0   4.2e-28   84.8   0.0
Forkhead             PF00250.14 NP_001182055.1       -            2.7e-40  123.9   0.1     5e-40  123.1   0.1
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Forkhead             PF00250.14 NP_001184186.1       -              3e-42  130.2   0.2   4.9e-42  129.5   0.2
Forkhead             PF00250.14 NP_001186420.1       -              3e-32   98.2   0.1   8.8e-32   96.6   0.1
Forkhead             PF00250.14 NP_001230273.1       -            3.8e-36  110.6   0.0   5.6e-36  110.1   0.0
Forkhead             PF00250.14 NP_571024.1          -            2.4e-41  127.3   0.2   4.7e-41  126.4   0.2
Forkhead             PF00250.14 NP_571142.1          -            1.7e-42  131.0   0.0   5.5e-42  129.3   0.0
Forkhead             PF00250.14 NP_571160.1          -              1e-29   90.0   0.0   2.2e-29   88.9   0.0
Forkhead             PF00250.14 NP_571174.1          -            6.4e-37  113.1   0.2   1.2e-36  112.2   0.2
Forkhead             PF00250.14 NP_571345.1          -            5.6e-41  126.1   0.0   1.1e-40  125.2   0.0
Forkhead             PF00250.14 NP_571346.2          -            4.9e-42  129.5   0.0   7.9e-42  128.8   0.0
Forkhead             PF00250.14 NP_571357.1          -            2.1e-41  127.5   0.1   4.7e-41  126.4   0.1
Forkhead             PF00250.14 NP_571358.1          -            7.6e-39  119.3   0.0   1.3e-38  118.6   0.0
Forkhead             PF00250.14 NP_571359.1          -            1.2e-41  128.2   0.4   2.2e-41  127.4   0.4
Forkhead             PF00250.14 NP_571360.1          -            2.6e-39  120.8   0.0     4e-39  120.2   0.0
Forkhead             PF00250.14 NP_571365.1          -            5.6e-42  129.3   0.0   9.1e-42  128.6   0.0
Forkhead             PF00250.14 NP_571374.1          -            4.7e-41  126.4   0.6   9.2e-41  125.4   0.6
Forkhead             PF00250.14 NP_571577.1          -            3.7e-32   97.8   0.0   6.6e-32   97.0   0.0
Forkhead             PF00250.14 NP_571803.1          -            3.2e-44  136.5   0.1   7.8e-44  135.3   0.1
Forkhead             PF00250.14 NP_571804.1          -            1.1e-43  134.8   0.1   2.1e-43  133.9   0.1
Forkhead             PF00250.14 NP_859424.1          -            7.6e-43  132.1   0.1   7.6e-43  132.1   0.1
Forkhead             PF00250.14 NP_944598.2          -            4.6e-43  132.8   0.1   7.8e-43  132.1   0.1
Forkhead             PF00250.14 NP_944599.2          -            1.9e-41  127.6   0.0     3e-41  127.0   0.0
Forkhead             PF00250.14 NP_944600.1          -            6.5e-42  129.1   0.0   9.3e-42  128.6   0.0
Forkhead             PF00250.14 NP_956196.1          -            2.1e-43  133.9   0.2   3.6e-43  133.1   0.2
Forkhead             PF00250.14 NP_956672.1          -            1.2e-05   12.8   0.0   4.3e-05   11.1   0.0
Forkhead             PF00250.14 NP_957278.1          -            3.2e-43  133.3   0.0   5.7e-43  132.5   0.0
Forkhead             PF00250.14 NP_957391.1          -              3e-34  104.5   0.4   5.1e-34  103.8   0.4
Forkhead             PF00250.14 NP_997738.1          -            2.6e-35  107.9   0.1   5.1e-35  107.0   0.1
Forkhead             PF00250.14 NP_998072.1          -            1.4e-36  112.0   0.0   3.2e-36  110.9   0.0
Forkhead             PF00250.14 NP_998078.1          -            6.6e-42  129.1   0.0   9.8e-42  128.5   0.0
Forkhead             PF00250.14 NP_998079.2          -              3e-42  130.2   0.0   4.9e-42  129.5   0.0
Forkhead             PF00250.14 XP_001922273.1       -            4.7e-41  126.4   0.2   1.5e-40  124.7   0.2
Forkhead             PF00250.14 XP_001922856.1       -            5.7e-43  132.5   0.1   9.8e-43  131.7   0.1
Forkhead             PF00250.14 XP_001923743.3       -              1e-34  106.1   0.0   1.7e-34  105.3   0.0
Forkhead             PF00250.14 XP_002667360.3       -            2.7e-36  111.1   0.0   4.5e-36  110.4   0.0
Forkhead             PF00250.14 XP_003200754.1       -            1.2e-41  128.3   0.0   2.6e-41  127.2   0.0
Forkhead             PF00250.14 XP_005156137.1       -            3.7e-32   97.8   0.0   6.6e-32   97.0   0.0
Forkhead             PF00250.14 XP_005156261.1       -            3.9e-36  110.6   0.1   6.4e-36  109.9   0.1
Forkhead             PF00250.14 XP_005157520.1       -            9.4e-43  131.8   0.1   1.5e-42  131.2   0.1
Forkhead             PF00250.14 XP_005158808.1       -            1.7e-42  130.9   0.0   5.5e-42  129.3   0.0
Forkhead             PF00250.14 XP_005159967.1       -            8.9e-42  128.7   0.0   1.9e-41  127.6   0.0
Forkhead             PF00250.14 XP_005160476.1       -            4.5e-37  113.6   0.0   8.7e-37  112.7   0.0
Forkhead             PF00250.14 XP_005162016.1       -              4e-33  100.9   0.2   9.9e-33   99.7   0.2
Forkhead             PF00250.14 XP_005162017.1       -            3.4e-33  101.2   0.2     8e-33  100.0   0.2
Forkhead             PF00250.14 XP_005162532.1       -              2e-38  117.9   0.0   3.2e-38  117.3   0.0
Forkhead             PF00250.14 XP_005164564.1       -            2.2e-34  105.0   0.3   3.7e-34  104.3   0.3
Forkhead             PF00250.14 XP_005165156.1       -            6.4e-37  113.1   0.2   1.2e-36  112.2   0.2
Forkhead             PF00250.14 XP_005165157.1       -            6.3e-37  113.1   0.2   1.2e-36  112.2   0.2
Forkhead             PF00250.14 XP_005166112.1       -            9.2e-30   90.2   0.0   2.7e-29   88.7   0.0
Forkhead             PF00250.14 XP_005166114.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_005166115.1       -            9.5e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_005167111.1       -            1.8e-32   98.9   0.4   4.9e-32   97.5   0.4
Forkhead             PF00250.14 XP_005167112.1       -            1.8e-32   98.9   0.4   4.9e-32   97.5   0.4
Forkhead             PF00250.14 XP_005167142.1       -            3.3e-29   88.4   0.2     8e-29   87.2   0.2
Forkhead             PF00250.14 XP_005169480.1       -            2.9e-32   98.2   0.1   4.8e-32   97.5   0.1
Forkhead             PF00250.14 XP_005169895.1       -            4.1e-38  116.9   0.7   9.6e-38  115.8   0.1
Forkhead             PF00250.14 XP_005169896.1       -            4.1e-38  116.9   0.7   9.6e-38  115.8   0.1
Forkhead             PF00250.14 XP_005171882.1       -            6.6e-42  129.1   0.0   9.8e-42  128.5   0.0
Forkhead             PF00250.14 XP_009289443.1       -            8.8e-30   90.2   0.2   1.7e-29   89.3   0.2
Forkhead             PF00250.14 XP_009289702.1       -            3.4e-30   91.5   0.1   6.4e-30   90.7   0.1
Forkhead             PF00250.14 XP_009289890.1       -            2.6e-35  107.9   0.1   5.1e-35  107.0   0.1
Forkhead             PF00250.14 XP_009289891.1       -            2.6e-35  107.9   0.1   5.1e-35  107.0   0.1
Forkhead             PF00250.14 XP_009291171.1       -            4.1e-38  116.9   0.7   9.6e-38  115.8   0.1
Forkhead             PF00250.14 XP_009291172.1       -            4.1e-38  116.9   0.7   9.6e-38  115.8   0.1
Forkhead             PF00250.14 XP_009294941.1       -            3.4e-33  101.2   0.2     8e-33  100.0   0.2
Forkhead             PF00250.14 XP_009297230.1       -            8.3e-43  132.0   0.0   1.5e-42  131.1   0.0
Forkhead             PF00250.14 XP_009299558.1       -            4.3e-37  113.7   0.2   7.7e-37  112.9   0.2
Forkhead             PF00250.14 XP_009300829.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300830.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300831.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300832.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300833.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300835.1       -            9.4e-33   99.7   0.2   2.7e-32   98.3   0.2
Forkhead             PF00250.14 XP_009300836.1       -            6.5e-33  100.3   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_009302271.1       -            1.8e-32   98.9   0.4   4.9e-32   97.5   0.4
Forkhead             PF00250.14 XP_009302272.1       -            1.8e-32   98.9   0.4   4.9e-32   97.5   0.4
Forkhead             PF00250.14 XP_009304271.1       -              3e-32   98.1   0.1   8.9e-32   96.6   0.1
Forkhead             PF00250.14 XP_009304339.1       -            4.8e-41  126.3   0.2   1.5e-40  124.7   0.2
Forkhead             PF00250.14 XP_009304629.1       -              3e-42  130.2   0.2   4.9e-42  129.5   0.2
Forkhead             PF00250.14 XP_009304887.1       -            8.2e-40  122.4   1.4   1.3e-39  121.7   0.3
Forkhead             PF00250.14 XP_686801.4          -            2.2e-37  114.6   0.0     4e-37  113.8   0.0
Forkhead             PF00250.14 XP_690041.2          -              5e-29   87.8   0.1   9.3e-29   87.0   0.1
```

9.3.1.7 *Daphnia pulex*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 EFX63453.1           -            4.2e-32   97.7   0.3   1.2e-31   96.2   0.3
Forkhead             PF00250.14 EFX65742.1           -            6.2e-43  132.4   0.2   9.5e-43  131.8   0.2
Forkhead             PF00250.14 EFX66763.1           -            2.6e-35  108.0   0.1     3e-35  107.7   0.1
Forkhead             PF00250.14 EFX69677.1           -            1.4e-41  128.0   0.0   1.6e-41  127.9   0.0
Forkhead             PF00250.14 EFX71322.1           -            5.6e-43  132.5   0.0   6.2e-43  132.4   0.0
Forkhead             PF00250.14 EFX72776.1           -            4.9e-39  119.9   0.1   6.2e-39  119.6   0.1
Forkhead             PF00250.14 EFX73364.1           -              1e-40  125.3   0.1   1.7e-40  124.6   0.1
Forkhead             PF00250.14 EFX74320.1           -            9.8e-11   29.2   1.6     1e-10   29.1   0.0
Forkhead             PF00250.14 EFX75590.1           -            3.1e-14   40.4   2.6   3.6e-14   40.2   1.8
Forkhead             PF00250.14 EFX76422.1           -            1.4e-39  121.7   0.4   1.5e-39  121.5   0.4
Forkhead             PF00250.14 EFX80260.1           -            5.7e-35  106.9   0.0     7e-35  106.6   0.0
Forkhead             PF00250.14 EFX81480.1           -            2.5e-37  114.4   0.0   2.9e-37  114.2   0.0
Forkhead             PF00250.14 EFX86713.1           -            4.5e-27   81.5   0.2   4.8e-27   81.5   0.2
Forkhead             PF00250.14 EFX88524.1           -            4.7e-45  139.2   0.5   5.2e-45  139.0   0.5
```

```
Forkhead             PF00250.14 EFX88549.1           -            3.2e-42  130.1   0.0   3.6e-42  129.9   0.0
Forkhead             PF00250.14 EFX88578.1           -            1.2e-43  134.7   0.1   1.4e-43  134.4   0.1
Forkhead             PF00250.14 EFX89076.1           -            7.9e-43  132.1   0.0     9e-43  131.9   0.0
```

9.3.1.8 *Drosophila melanogaster*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001097726.1       -            3.4e-33  101.2   0.2   3.9e-32   97.8   0.3
Forkhead             PF00250.14 NP_001163762.1       -            4.5e-40  123.2   0.1   8.3e-40  122.4   0.1
Forkhead             PF00250.14 NP_001246609.1       -            2.4e-42  130.5   0.1     4e-42  129.8   0.1
Forkhead             PF00250.14 NP_001247011.1       -            1.4e-30   92.8   0.1   1.3e-29   89.6   0.2
Forkhead             PF00250.14 NP_001259311.1       -            3.9e-36  110.6   0.2   9.9e-36  109.3   0.2
Forkhead             PF00250.14 NP_001259312.1       -            3.9e-36  110.6   0.2   9.9e-36  109.3   0.2
Forkhead             PF00250.14 NP_001261701.1       -            2.5e-41  127.3   0.2   2.5e-41  127.3   0.2
Forkhead             PF00250.14 NP_001261702.1       -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_001261703.1       -            9.2e-42  128.6   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_001262557.1       -            2.4e-29   88.8   0.1   2.4e-29   88.8   0.1
Forkhead             PF00250.14 NP_001263038.1       -            3.9e-40  123.4   0.1   1.3e-39  121.7   0.1
Forkhead             PF00250.14 NP_001287516.1       -            2.8e-38  117.5   0.1   4.5e-38  116.8   0.1
Forkhead             PF00250.14 NP_001287574.1       -            4.5e-40  123.2   0.1   8.3e-40  122.4   0.1
Forkhead             PF00250.14 NP_001303426.1       -            2.4e-29   88.9   0.1   2.4e-29   88.9   0.1
Forkhead             PF00250.14 NP_001303461.1       -            4.6e-40  123.2   0.1   8.5e-40  122.3   0.1
Forkhead             PF00250.14 NP_001303501.1       -              3e-19   56.5   0.1   4.2e-18   52.8   0.2
Forkhead             PF00250.14 NP_476730.1          -            2.6e-40  124.0   0.1   4.5e-40  123.2   0.1
Forkhead             PF00250.14 NP_476834.1          -              3e-41  127.0   0.1   5.3e-41  126.2   0.1
Forkhead             PF00250.14 NP_511071.3          -            3.9e-36  110.6   0.2   9.9e-36  109.3   0.2
Forkhead             PF00250.14 NP_523814.1          -            1.4e-40  124.8   0.0   2.3e-40  124.2   0.0
Forkhead             PF00250.14 NP_523912.1          -            2.4e-42  130.5   0.1     4e-42  129.8   0.1
Forkhead             PF00250.14 NP_523950.2          -            8.2e-36  109.6   0.0   1.4e-35  108.8   0.0
Forkhead             PF00250.14 NP_524202.1          -            3.9e-43  133.0   0.1   8.1e-43  132.0   0.1
Forkhead             PF00250.14 NP_524302.1          -            3.5e-34  104.3   0.0   6.7e-34  103.4   0.0
Forkhead             PF00250.14 NP_524495.1          -            2.8e-38  117.5   0.1   4.5e-38  116.8   0.1
Forkhead             PF00250.14 NP_524496.1          -            1.1e-37  115.6   0.1     2e-37  114.7   0.1
Forkhead             PF00250.14 NP_524542.1          -            4.5e-40  123.2   0.1   8.3e-40  122.4   0.1
Forkhead             PF00250.14 NP_608369.1          -            1.5e-36  112.0   1.1   4.1e-36  110.5   0.0
Forkhead             PF00250.14 NP_648440.2          -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_650330.3          -            2.4e-29   88.8   0.1   2.4e-29   88.8   0.1
Forkhead             PF00250.14 NP_651951.1          -            2.5e-36  111.2   0.0   5.8e-36  110.0   0.0
Forkhead             PF00250.14 NP_726538.1          -            4.6e-26   78.3   1.7   8.3e-26   77.5   0.1
Forkhead             PF00250.14 NP_726887.1          -            1.9e-09   25.1   0.0   3.3e-09   24.3   0.0
Forkhead             PF00250.14 NP_726889.3          -            4.9e-28   84.6   0.0   1.4e-27   83.2   0.0
Forkhead             PF00250.14 NP_729672.1          -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_729673.2          -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_729674.2          -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_729675.2          -            2.4e-41  127.3   0.2   2.4e-41  127.3   0.2
Forkhead             PF00250.14 NP_996204.1          -            2.3e-29   88.9   0.1   2.3e-29   88.9   0.1
Forkhead             PF00250.14 NP_996205.1          -            2.3e-29   88.9   0.1   2.3e-29   88.9   0.1
Forkhead             PF00250.14 NP_996362.2          -            3.9e-36  110.6   0.2   9.9e-36  109.3   0.2
```

9.3.1.9 *Echinococcus multilocularis*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 CDI97793.1           -            2.9e-39  120.6   0.1   6.9e-39  119.4   0.1
Forkhead             PF00250.14 CDI97856.1           -            5.1e-37  113.4   0.0   7.1e-37  113.0   0.0
Forkhead             PF00250.14 CDI97973.1           -            6.4e-29   87.5   0.8   1.3e-28   86.5   0.8
Forkhead             PF00250.14 CDI98329.1           -              1e-37  115.7   0.1     1e-37  115.7   0.1
Forkhead             PF00250.14 CDS36201.1           -            2.6e-29   88.7   0.1   5.5e-29   87.7   0.1
Forkhead             PF00250.14 CDS36650.1           -            1.7e-38  118.2   0.0     3e-38  117.3   0.0
Forkhead             PF00250.14 CDS37227.1           -            2.9e-41  127.0   0.0   5.4e-41  126.2   0.0
Forkhead             PF00250.14 CDS37735.1           -            3.8e-37  113.9   0.6   8.2e-37  112.8   0.6
Forkhead             PF00250.14 CDS39410.1           -            4.1e-39  120.1   0.0   8.8e-39  119.1   0.0
Forkhead             PF00250.14 CDS40344.1           -            7.8e-34  103.2   0.0     2e-33  101.9   0.0
Forkhead             PF00250.14 CDS43635.1           -            1.6e-41  127.9   0.1   2.8e-41  127.1   0.1
Forkhead             PF00250.14 CDS43663.1           -              5e-23   68.6   0.0   1.2e-22   67.4   0.0
Forkhead             PF00250.14 CUT99136.1           -            1.8e-42  130.9   0.0   2.6e-42  130.4   0.0
Forkhead             PF00250.14 CUT99217.1           -            8.9e-42  128.7   0.1   3.1e-41  126.9   0.0
Forkhead             PF00250.14 CUT99233.1           -            6.8e-40  122.6   0.1   1.2e-39  121.8   0.1
Forkhead             PF00250.14 CUT99502.1           -            5.2e-35  107.0   0.0   1.2e-34  105.9   0.0
```

9.3.1.10 *Helobdella robusta*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_009009422.1       -            6.3e-39  119.5   0.1   1.6e-38  118.3   0.1
Forkhead             PF00250.14 XP_009013544.1       -            1.2e-42  131.4   0.5   1.7e-42  131.0   0.5
Forkhead             PF00250.14 XP_009013735.1       -            1.1e-44  138.0   0.2   1.3e-44  137.8   0.2
Forkhead             PF00250.14 XP_009013997.1       -            7.2e-37  112.9   0.0   8.1e-37  112.8   0.0
Forkhead             PF00250.14 XP_009014923.1       -            6.1e-41  126.0   0.1   6.9e-41  125.8   0.1
Forkhead             PF00250.14 XP_009014932.1       -            2.1e-41  127.5   0.1   2.7e-41  127.1   0.1
Forkhead             PF00250.14 XP_009015132.1       -            1.1e-13   38.6   0.1   7.5e-13   36.0   0.1
Forkhead             PF00250.14 XP_009015142.1       -            1.1e-38  118.7   0.4   1.4e-38  118.4   0.4
Forkhead             PF00250.14 XP_009015510.1       -            1.8e-29   89.2   0.2   1.8e-29   89.2   0.2
Forkhead             PF00250.14 XP_009016381.1       -            1.1e-41  128.3   0.1   1.6e-41  127.8   0.1
Forkhead             PF00250.14 XP_009018807.1       -              5e-42  129.5   0.0     5e-42  129.5   0.0
Forkhead             PF00250.14 XP_009019388.1       -            2.4e-41  127.3   0.3   2.8e-41  127.1   0.3
Forkhead             PF00250.14 XP_009020254.1       -            4.2e-33  100.9   0.2   4.4e-33  100.8   0.2
Forkhead             PF00250.14 XP_009020647.1       -            6.6e-31   93.8   0.5     9e-31   93.4   0.5
Forkhead             PF00250.14 XP_009020863.1       -            8.5e-26   77.5   1.4     2e-24   73.0   1.4
Forkhead             PF00250.14 XP_009022719.1       -            5.6e-24   71.6   0.2   5.6e-24   71.6   0.2
Forkhead             PF00250.14 XP_009022888.1       -            5.2e-40  123.0   0.0   5.9e-40  122.8   0.0
Forkhead             PF00250.14 XP_009022991.1       -            1.3e-13   38.4   6.1   6.4e-13   36.2   0.4
Forkhead             PF00250.14 XP_009022992.1       -            1.6e-13   38.1   6.1   6.3e-13   36.2   0.4
Forkhead             PF00250.14 XP_009023719.1       -            4.6e-38  116.8   0.0   5.3e-38  116.6   0.0
Forkhead             PF00250.14 XP_009024266.1       -            1.8e-24   73.2   0.0     2e-24   73.1   0.0
```

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Forkhead             PF00250.14 XP_009024770.1       -            5.3e-15   42.9   0.1   5.3e-15   42.9   0.1
Forkhead             PF00250.14 XP_009026623.1       -            7.9e-33  100.0   2.0   9.9e-33   99.7   2.0
Forkhead             PF00250.14 XP_009026840.1       -            1.2e-34  105.8   0.1   1.7e-34  105.3   0.1
Forkhead             PF00250.14 XP_009027458.1       -            7.6e-41  125.7   0.1   7.6e-41  125.7   0.1
Forkhead             PF00250.14 XP_009028926.1       -            2.3e-32   98.5   0.2   2.4e-32   98.4   0.2
Forkhead             PF00250.14 XP_009029398.1       -              2e-40  124.3   0.4   2.3e-40  124.1   0.4
Forkhead             PF00250.14 XP_009029677.1       -            4.8e-42  129.5   0.0   5.5e-42  129.3   0.0
Forkhead             PF00250.14 XP_009029822.1       -              7e-33  100.2   0.1   1.1e-32   99.5   0.1
Forkhead             PF00250.14 XP_009030794.1       -            3.4e-30   91.6   0.5   3.6e-30   91.5   0.5
Forkhead             PF00250.14 XP_009032024.1       -            3.5e-33  101.1   0.8   3.6e-33  101.1   0.8
```

9.3.1.11 *Lingula anatina*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias    E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_013381393.1       -            8.2e-44  135.2   0.1   1.5e-43  134.4   0.1
Forkhead             PF00250.14 XP_013381443.1       -            3.2e-42  130.1   0.1   6.4e-42  129.1   0.1
Forkhead             PF00250.14 XP_013383732.1       -            8.3e-44  135.2   0.1   1.5e-43  134.4   0.1
Forkhead             PF00250.14 XP_013383733.1       -            4.2e-41  126.5   0.0     1e-40  125.3   0.0
Forkhead             PF00250.14 XP_013386606.1       -            1.1e-40  125.2   0.1   1.9e-40  124.4   0.1
Forkhead             PF00250.14 XP_013389343.1       -            7.1e-41  125.8   0.0   1.4e-40  124.9   0.0
Forkhead             PF00250.14 XP_013393783.1       -            1.1e-16   48.3   0.0     2e-16   47.4   0.0
Forkhead             PF00250.14 XP_013395178.1       -            7.9e-37  112.8   0.0   2.2e-36  111.4   0.0
Forkhead             PF00250.14 XP_013395187.1       -            7.9e-37  112.8   0.0   2.2e-36  111.4   0.0
Forkhead             PF00250.14 XP_013395191.1       -            1.7e-28   86.1   0.1   1.4e-27   83.2   0.2
Forkhead             PF00250.14 XP_013395192.1       -            1.8e-28   86.1   0.1   1.4e-27   83.2   0.2
Forkhead             PF00250.14 XP_013395193.1       -            2.4e-31   95.2   0.2   2.2e-30   92.2   0.4
Forkhead             PF00250.14 XP_013395195.1       -            1.7e-32   98.9   0.3   1.6e-31   95.8   0.6
Forkhead             PF00250.14 XP_013395578.1       -            3.2e-39  120.5   0.3   5.1e-39  119.8   0.3
Forkhead             PF00250.14 XP_013396976.1       -            3.4e-35  107.6   1.1   4.6e-35  107.2   0.0
Forkhead             PF00250.14 XP_013397016.1       -              2e-22   66.7   1.6   4.9e-22   65.4   1.5
Forkhead             PF00250.14 XP_013397763.1       -            1.1e-38  118.7   0.0   1.7e-38  118.1   0.0
Forkhead             PF00250.14 XP_013398094.1       -              3e-37  114.1   0.2   5.1e-37  113.4   0.2
Forkhead             PF00250.14 XP_013398404.1       -            2.4e-42  130.5   0.0   4.4e-42  129.7   0.0
Forkhead             PF00250.14 XP_013399208.1       -            3.7e-43  133.1   0.2   6.5e-43  132.3   0.2
Forkhead             PF00250.14 XP_013399209.1       -            3.5e-43  133.2   0.2   6.5e-43  132.3   0.2
Forkhead             PF00250.14 XP_013401340.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401341.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401342.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401344.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401345.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401346.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401347.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401348.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401349.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401350.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401351.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401352.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401353.1       -            2.2e-38  117.8   0.1   4.1e-38  116.9   0.1
Forkhead             PF00250.14 XP_013401354.1       -            2.1e-38  117.9   0.1   3.9e-38  117.0   0.1
Forkhead             PF00250.14 XP_013401532.1       -            3.6e-12   33.8   0.3   2.8e-11   30.9   0.1
Forkhead             PF00250.14 XP_013404097.1       -            3.5e-40  123.6   0.1   6.4e-40  122.7   0.1
Forkhead             PF00250.14 XP_013404303.1       -            6.9e-33  100.2   2.4   1.1e-32   99.5   1.2
Forkhead             PF00250.14 XP_013404304.1       -            6.3e-33  100.3   2.5   9.9e-33   99.7   1.2
Forkhead             PF00250.14 XP_013410597.1       -            6.3e-20   58.6   0.7   1.5e-19   57.4   0.7
Forkhead             PF00250.14 XP_013410984.1       -            5.4e-35  106.9   1.2   6.3e-35  106.7   0.0
Forkhead             PF00250.14 XP_013410985.1       -            5.4e-35  106.9   1.2   6.3e-35  106.7   0.0
Forkhead             PF00250.14 XP_013410986.1       -              4e-35  107.3   1.0   5.5e-35  106.9   0.0
Forkhead             PF00250.14 XP_013413481.1       -            9.6e-41  125.4   0.1   2.6e-40  124.0   0.0
Forkhead             PF00250.14 XP_013416328.1       -            5.8e-40  122.9   0.2   5.8e-40  122.9   0.2
Forkhead             PF00250.14 XP_013416330.1       -            5.2e-40  123.0   0.2   5.2e-40  123.0   0.2
Forkhead             PF00250.14 XP_013416331.1       -            4.9e-40  123.1   0.2   4.9e-40  123.1   0.2
Forkhead             PF00250.14 XP_013416332.1       -            4.4e-40  123.3   0.2   4.4e-40  123.3   0.2
Forkhead             PF00250.14 XP_013421812.1       -            4.1e-36  110.5   0.0   7.1e-36  109.8   0.0
```

9.3.1.12 *Mnemiopsis leidyi*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias    E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 ML025018a            -            3.7e-42  129.9   0.3   6.4e-42  129.1   0.3
Forkhead             PF00250.14 ML03251a             -            2.5e-17   50.3   0.6   1.7e-15   44.4   0.2
Forkhead             PF00250.14 ML048612a            -            2.2e-12   34.5   0.7   2.4e-11   31.2   0.2
Forkhead             PF00250.14 ML06159a             -            5.7e-44  135.7   0.0   1.3e-43  134.5   0.0
Forkhead             PF00250.14 ML061510a            -            3.5e-43  133.2   0.0   5.3e-43  132.6   0.0
Forkhead             PF00250.14 ML077613a            -            1.2e-36  112.2   0.0   2.4e-36  111.3   0.0
Forkhead             PF00250.14 ML09683a             -            1.3e-05   12.8   0.1   2.5e-05   11.9   0.1
Forkhead             PF00250.14 ML11501a             -            1.4e-15   44.7   0.0   3.6e-15   43.4   0.0
Forkhead             PF00250.14 ML12315a             -             0.0013    6.3  10.7    0.0011    6.6   0.5
Forkhead             PF00250.14 ML12521a             -            1.9e-18   53.9   0.7   4.6e-18   52.7   0.7
Forkhead             PF00250.14 ML154122a            -            5.2e-42  129.4   0.1   3.3e-41  126.9   0.1
Forkhead             PF00250.14 ML154527a            -            1.2e-39  121.9   0.1     2e-39  121.1   0.1
Forkhead             PF00250.14 ML216314a            -            1.7e-36  111.8   0.0   3.6e-36  110.7   0.0
Forkhead             PF00250.14 ML23712a             -            1.3e-39  121.7   1.6   2.3e-39  120.9   0.1
Forkhead             PF00250.14 ML46085a             -            1.9e-34  105.2   0.0   3.4e-34  104.4   0.0
```

9.3.1.13 *Mus musculus*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias    E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001028641.1       -            3.4e-09   24.2   0.0   6.3e-09   23.4   0.0
Forkhead             PF00250.14 NP_001030066.1       -            3.8e-28   85.0   0.0   6.5e-28   84.3   0.0
Forkhead             PF00250.14 NP_001074401.2       -            2.2e-43  133.9   0.2   3.3e-43  133.3   0.2
Forkhead             PF00250.14 NP_001094934.1       -            1.3e-42  131.3   0.0   1.9e-42  130.8   0.0
Forkhead             PF00250.14 NP_001104294.1       -            1.3e-32   99.3   0.1   3.5e-32   97.9   0.1
Forkhead             PF00250.14 NP_001104295.1       -            1.2e-32   99.4   0.1   3.4e-32   98.0   0.1
Forkhead             PF00250.14 NP_001153584.1       -            3.2e-42  130.1   0.0   6.9e-42  129.0   0.0
Forkhead             PF00250.14 NP_001182057.1       -            1.1e-38  118.8   0.0   2.9e-38  117.4   0.0
Forkhead             PF00250.14 NP_001184250.1       -            8.3e-33   99.9   0.2   2.1e-32   98.6   0.2
```

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Forkhead             PF00250.14 NP_001184251.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 NP_001186276.1      -          1.3e-30   92.9   0.4   2.2e-30   92.1   0.4
Forkhead             PF00250.14 NP_001186277.1      -          1.3e-30   92.9   0.4   2.2e-30   92.1   0.4
Forkhead             PF00250.14 NP_001264219.1      -          5.2e-36  110.2   0.2   8.5e-36  109.5   0.2
Forkhead             PF00250.14 NP_001273536.1      -          6.7e-33  100.2   0.4   2.5e-32   98.4   0.4
Forkhead             PF00250.14 NP_001277625.1      -          7.3e-41  125.7   0.2   1.5e-40  124.7   0.2
Forkhead             PF00250.14 NP_001277994.1      -          2.2e-41  127.4   0.2   3.4e-41  126.8   0.2
Forkhead             PF00250.14 NP_001277996.1      -          1.9e-41  127.6   0.2     3e-41  127.0   0.2
Forkhead             PF00250.14 NP_032015.1         -            1e-28   86.8   0.0     2e-28   85.9   0.0
Forkhead             PF00250.14 NP_032047.4         -          5.1e-34  103.8   0.7   9.9e-34  102.9   0.7
Forkhead             PF00250.14 NP_032048.1         -          2.5e-40  124.0   0.0   3.8e-40  123.5   0.0
Forkhead             PF00250.14 NP_032049.1         -          1.8e-38  118.1   0.0   2.6e-38  117.6   0.0
Forkhead             PF00250.14 NP_032223.2         -          8.5e-07   16.6   0.4   1.4e-06   15.8   0.4
Forkhead             PF00250.14 NP_032264.1         -          5.2e-36  110.2   0.2   8.5e-36  109.5   0.2
Forkhead             PF00250.14 NP_032265.3         -          1.3e-35  108.9   0.0   1.8e-35  108.5   0.0
Forkhead             PF00250.14 NP_032266.3         -            5e-39  119.9   0.1   7.2e-39  119.4   0.1
Forkhead             PF00250.14 NP_032267.1         -          3.2e-42  130.1   0.0   6.9e-42  129.0   0.0
Forkhead             PF00250.14 NP_032268.2         -          8.9e-42  128.7   0.0   1.2e-41  128.3   0.0
Forkhead             PF00250.14 NP_032285.2         -            2e-41  127.5   0.3   3.4e-41  126.8   0.3
Forkhead             PF00250.14 NP_032286.1         -          5.1e-41  126.2   0.2   7.8e-41  125.7   0.2
Forkhead             PF00250.14 NP_032618.2         -          1.5e-43  134.4   0.1   2.5e-43  133.7   0.1
Forkhead             PF00250.14 NP_032619.1         -          2.9e-41  127.0   0.0   3.9e-41  126.6   0.0
Forkhead             PF00250.14 NP_034355.2         -          7.9e-42  128.8   0.0   1.2e-41  128.3   0.0
Forkhead             PF00250.14 NP_034356.1         -          2.1e-41  127.5   0.0   2.8e-41  127.1   0.0
Forkhead             PF00250.14 NP_034555.3         -          8.8e-42  128.7   0.0   1.4e-41  128.1   0.0
Forkhead             PF00250.14 NP_034556.2         -          5.1e-42  129.5   0.0   9.1e-42  128.7   0.0
Forkhead             PF00250.14 NP_034576.2         -          2.1e-41  127.5   0.2   3.4e-41  126.8   0.2
Forkhead             PF00250.14 NP_036150.1         -          3.1e-42  130.1   0.0   4.5e-42  129.6   0.0
Forkhead             PF00250.14 NP_038547.2         -          1.3e-43  134.5   0.1   2.2e-43  133.8   0.1
Forkhead             PF00250.14 NP_056573.1         -          3.8e-39  120.2   0.0     5e-39  119.9   0.0
Forkhead             PF00250.14 NP_061259.1         -          4.5e-30   91.2   0.1   7.7e-30   90.4   0.1
Forkhead             PF00250.14 NP_062713.2         -          6.9e-30   90.6   0.1   1.4e-29   89.6   0.1
Forkhead             PF00250.14 NP_062714.1         -          3.8e-29   88.2   0.0   7.1e-29   87.3   0.0
Forkhead             PF00250.14 NP_068699.1         -          1.1e-38  118.8   1.7   1.7e-38  118.1   0.3
Forkhead             PF00250.14 NP_071773.2         -          5.5e-40  122.9   0.0     8e-40  122.4   0.0
Forkhead             PF00250.14 NP_076396.3         -          4.9e-42  129.5   0.0   7.9e-42  128.8   0.0
Forkhead             PF00250.14 NP_083043.2         -          1.2e-32   99.4   0.1   3.4e-32   98.0   0.1
Forkhead             PF00250.14 NP_444432.1         -          7.3e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 NP_444472.2         -          2.6e-32   98.3   0.4   2.6e-32   98.3   0.4
Forkhead             PF00250.14 NP_473380.1         -          1.3e-30   92.9   0.4   2.2e-30   92.1   0.4
Forkhead             PF00250.14 NP_683737.2         -          1.3e-35  108.9   0.1   2.1e-35  108.3   0.1
Forkhead             PF00250.14 NP_766287.1         -          7.8e-41  125.7   0.2   1.6e-40  124.6   0.2
Forkhead             PF00250.14 NP_851305.2         -          8.2e-38  116.0   0.1     2e-37  114.8   0.1
Forkhead             PF00250.14 NP_899009.2         -            3e-38  117.4   0.1   5.5e-38  116.5   0.1
Forkhead             PF00250.14 NP_899016.1         -          6.7e-42  129.1   0.0   9.2e-42  128.6   0.0
Forkhead             PF00250.14 NP_899121.1         -            2e-40  124.3   0.0   2.7e-40  123.9   0.0
Forkhead             PF00250.14 NP_918949.1         -            3e-29   88.5   0.0   5.1e-29   87.8   0.0
Forkhead             PF00250.14 NP_951031.2         -          1.2e-43  134.7   0.2   1.8e-43  134.1   0.2
Forkhead             PF00250.14 NP_997600.1         -          2.6e-32   98.3   0.4   2.6e-32   98.3   0.4
Forkhead             PF00250.14 XP_006503080.1      -          7.8e-41  125.7   0.2   1.6e-40  124.6   0.2
Forkhead             PF00250.14 XP_006504717.1      -          8.1e-44  135.2   0.2   1.2e-43  134.7   0.2
Forkhead             PF00250.14 XP_006504780.1      -          1.5e-38  118.3   0.0   2.6e-38  117.6   0.0
Forkhead             PF00250.14 XP_006505371.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505373.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505374.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505375.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505376.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505377.1      -          7.2e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505378.1      -          6.9e-33  100.2   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505379.1      -          6.9e-33  100.2   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505380.1      -          6.9e-33  100.2   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_006505381.1      -          5.3e-33  100.5   0.2   1.8e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505382.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505383.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505384.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505385.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505386.1      -          6.9e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_006505387.1      -          1.1e-29   90.0   0.0   3.3e-29   88.4   0.0
Forkhead             PF00250.14 XP_006509944.1      -          1.6e-05   12.5   0.1   0.00026    8.6   0.0
Forkhead             PF00250.14 XP_006509945.1      -          1.6e-05   12.5   0.1   0.00026    8.6   0.0
Forkhead             PF00250.14 XP_006512869.1      -          3.8e-29   88.2   0.0   7.1e-29   87.3   0.0
Forkhead             PF00250.14 XP_006515542.1      -            2e-41  127.5   0.3   3.4e-41  126.8   0.3
Forkhead             PF00250.14 XP_006515543.1      -            2e-41  127.5   0.3   3.4e-41  126.8   0.3
Forkhead             PF00250.14 XP_006515544.1      -            2e-41  127.5   0.3   3.4e-41  126.8   0.3
Forkhead             PF00250.14 XP_006515546.1      -            2e-41  127.5   0.3   3.4e-41  126.8   0.3
Forkhead             PF00250.14 XP_006516295.1      -          3.3e-38  117.3   0.1   5.9e-38  116.4   0.1
Forkhead             PF00250.14 XP_006516296.1      -          3.3e-38  117.3   0.1   5.9e-38  116.4   0.1
Forkhead             PF00250.14 XP_006516297.1      -          3.3e-38  117.3   0.1   5.9e-38  116.4   0.1
Forkhead             PF00250.14 XP_006516299.1      -          3.3e-38  117.3   0.1   5.9e-38  116.4   0.1
Forkhead             PF00250.14 XP_006516301.1      -          3.2e-38  117.3   0.1   5.9e-38  116.4   0.1
Forkhead             PF00250.14 XP_006516302.1      -            3e-38  117.4   0.1   5.5e-38  116.5   0.1
Forkhead             PF00250.14 XP_006516303.1      -            3e-38  117.4   0.1   5.5e-38  116.5   0.1
Forkhead             PF00250.14 XP_006519853.2      -          6.2e-06   13.8   2.3   0.00061    7.4   0.2
Forkhead             PF00250.14 XP_006519855.1      -          5.9e-06   13.9   2.3   0.00059    7.4   0.2
Forkhead             PF00250.14 XP_006519857.1      -          5.7e-06   13.9   2.5   0.00049    7.7   0.2
Forkhead             PF00250.14 XP_006519976.2      -          1.5e-06   15.8   2.3   0.00036    8.1   0.1
Forkhead             PF00250.14 XP_006520499.1      -          1.3e-24   73.7   0.0   2.5e-24   72.7   0.0
Forkhead             PF00250.14 XP_006523714.1      -          8.2e-38  116.0   0.1     2e-37  114.8   0.1
Forkhead             PF00250.14 XP_006523715.1      -          8.2e-38  116.0   0.1     2e-37  114.8   0.1
Forkhead             PF00250.14 XP_006523716.1      -          8.2e-38  116.0   0.1     2e-37  114.8   0.1
Forkhead             PF00250.14 XP_006523717.1      -          8.2e-38  116.0   0.1     2e-37  114.8   0.1
Forkhead             PF00250.14 XP_006523718.1      -          7.8e-38  116.0   0.1   1.8e-37  114.9   0.1
Forkhead             PF00250.14 XP_006525079.1      -          1.3e-32   99.3   0.1   3.5e-32   97.9   0.1
Forkhead             PF00250.14 XP_006525080.1      -          1.3e-32   99.3   0.1   3.5e-32   97.9   0.1
Forkhead             PF00250.14 XP_006528202.1      -            9e-16   45.3   0.0   1.3e-15   44.9   0.0
Forkhead             PF00250.14 XP_006530184.1      -          1.3e-35  108.9   0.1   2.1e-35  108.3   0.1
Forkhead             PF00250.14 XP_006530185.1      -          1.1e-35  109.1   0.1   1.7e-35  108.5   0.1
Forkhead             PF00250.14 XP_006532327.2      -          5.2e-36  110.2   0.2   8.5e-36  109.5   0.2
Forkhead             PF00250.14 XP_006532328.1      -          5.8e-36  110.1   0.2   9.6e-36  109.3   0.2
Forkhead             PF00250.14 XP_006532329.1      -          5.2e-36  110.2   0.2   8.5e-36  109.5   0.2
Forkhead             PF00250.14 XP_006532330.1      -          5.2e-36  110.2   0.2   8.5e-36  109.5   0.2
Forkhead             PF00250.14 XP_006532331.2      -          3.5e-36  110.7   0.2   5.6e-36  110.1   0.2
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Forkhead             PF00250.14 XP_006532332.1       -              5e-39  119.9   0.1   7.2e-39  119.4   0.1
Forkhead             PF00250.14 XP_006534145.1       -            1.8e-43  134.1   0.2   2.8e-43  133.5   0.2
Forkhead             PF00250.14 XP_011238799.1       -            7.3e-41  125.7   0.2   1.5e-40  124.7   0.2
Forkhead             PF00250.14 XP_011238860.1       -            8.6e-11   29.4   0.0   1.5e-10   28.6   0.0
Forkhead             PF00250.14 XP_011239340.1       -            2.7e-32   98.3   0.4   2.7e-32   98.3   0.4
Forkhead             PF00250.14 XP_011239423.1       -            7.3e-33  100.1   0.2   2.2e-32   98.5   0.2
Forkhead             PF00250.14 XP_011239424.1       -            8.2e-33  100.0   0.2   2.1e-32   98.6   0.2
Forkhead             PF00250.14 XP_011239425.1       -            7.8e-33  100.0   0.2   2.1e-32   98.6   0.2
Forkhead             PF00250.14 XP_011239426.1       -              7e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_011239427.1       -              7e-33  100.2   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_011239428.1       -              7e-33  100.2   0.2   1.7e-32   99.0   0.2
Forkhead             PF00250.14 XP_011243577.1       -            6.3e-06   13.8   2.3   0.00061    7.4   0.2
Forkhead             PF00250.14 XP_011243578.1       -            5.9e-06   13.9   2.3   0.00059    7.4   0.2
Forkhead             PF00250.14 XP_011243579.1       -            8.4e-06   13.4   1.5   0.00051    7.7   0.2
Forkhead             PF00250.14 XP_011246142.1       -            3.8e-28   85.0   0.0   6.5e-28   84.3   0.0
Forkhead             PF00250.14 XP_011246143.1       -            3.8e-28   85.0   0.0   6.5e-28   84.3   0.0
Forkhead             PF00250.14 XP_011246461.1       -            1.3e-35  108.9   0.1   2.1e-35  108.3   0.1
Forkhead             PF00250.14 XP_011246462.1       -            1.1e-35  109.1   0.1   1.7e-35  108.5   0.1
Forkhead             PF00250.14 XP_011247520.1       -            2.3e-43  133.8   0.2   3.6e-43  133.1   0.2
Forkhead             PF00250.14 XP_011247521.1       -            2.3e-43  133.8   0.2   3.6e-43  133.1   0.2
Forkhead             PF00250.14 XP_011247522.1       -              2e-43  134.0   0.2   3.1e-43  133.4   0.2
Forkhead             PF00250.14 XP_011247523.1       -              2e-43  134.0   0.2   3.1e-43  133.4   0.2
```

9.3.1.14 *Nematostella vectensis*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_001619310.1       -            3.7e-05   11.3  17.5    0.0045    4.6   0.0
Forkhead             PF00250.14 XP_001619589.1       -              3e-13   37.3   0.1   3.6e-13   37.0   0.1
Forkhead             PF00250.14 XP_001623177.1       -            3.2e-22   66.0   1.0     4e-22   65.7   1.0
Forkhead             PF00250.14 XP_001624096.1       -            1.1e-23   70.7   0.1   1.3e-23   70.5   0.1
Forkhead             PF00250.14 XP_001624144.1       -            1.7e-09   25.3   0.0   3.6e-09   24.2   0.0
Forkhead             PF00250.14 XP_001624739.1       -            2.7e-36  111.1   0.9   2.9e-36  111.0   0.9
Forkhead             PF00250.14 XP_001626000.1       -            1.9e-43  134.0   0.1   3.8e-43  133.1   0.1
Forkhead             PF00250.14 XP_001626709.1       -            1.2e-38  118.7   0.2   1.3e-38  118.5   0.2
Forkhead             PF00250.14 XP_001627122.1       -            5.8e-42  129.3   0.5   1.1e-41  128.4   0.5
Forkhead             PF00250.14 XP_001627564.1       -            6.6e-06   13.7   0.0   7.2e-06   13.6   0.0
Forkhead             PF00250.14 XP_001627679.1       -            1.8e-23   70.0   0.2   3.7e-23   69.0   0.2
Forkhead             PF00250.14 XP_001627842.1       -              2e-35  108.3   0.0   2.8e-35  107.9   0.0
Forkhead             PF00250.14 XP_001628369.1       -            1.4e-37  115.3   0.5     2e-37  114.7   0.5
Forkhead             PF00250.14 XP_001629014.1       -            6.2e-45  138.8   0.1   7.1e-45  138.6   0.1
Forkhead             PF00250.14 XP_001630317.1       -            2.1e-32   98.6   0.0   2.3e-32   98.5   0.0
Forkhead             PF00250.14 XP_001630413.1       -            9.6e-18   51.7   0.0   1.4e-17   51.1   0.0
Forkhead             PF00250.14 XP_001630565.1       -            1.8e-37  114.9   0.0   2.1e-37  114.7   0.0
Forkhead             PF00250.14 XP_001631592.1       -            6.1e-41  126.0   0.1   7.1e-41  125.8   0.1
Forkhead             PF00250.14 XP_001631625.1       -            1.2e-39  121.8   0.0   1.9e-39  121.2   0.0
Forkhead             PF00250.14 XP_001634161.1       -            9.1e-34  103.0   0.0   1.6e-33  102.2   0.0
Forkhead             PF00250.14 XP_001634555.1       -            3.1e-42  130.2   0.1   5.4e-42  129.4   0.1
Forkhead             PF00250.14 XP_001634563.1       -             0.0046    4.6  16.8    0.0013    6.4   2.2
Forkhead             PF00250.14 XP_001634717.1       -            1.3e-43  134.6   0.1   1.4e-43  134.5   0.1
Forkhead             PF00250.14 XP_001636048.1       -            3.3e-32   98.0   0.0   3.6e-32   97.9   0.0
Forkhead             PF00250.14 XP_001636939.1       -              3e-40  123.8   0.0   3.3e-40  123.6   0.0
Forkhead             PF00250.14 XP_001637106.1       -            1.3e-37  115.4   0.1   1.4e-37  115.2   0.1
Forkhead             PF00250.14 XP_001637165.1       -            2.7e-40  123.9   0.0   3.9e-40  123.4   0.0
Forkhead             PF00250.14 XP_001637167.1       -              5e-38  116.7   0.0   5.6e-38  116.5   0.0
Forkhead             PF00250.14 XP_001637168.1       -              2e-42  130.8   0.0   2.2e-42  130.6   0.0
Forkhead             PF00250.14 XP_001637690.1       -              2e-06   15.4   0.0   2.2e-06   15.3   0.0
Forkhead             PF00250.14 XP_001638070.1       -            1.2e-34  105.8   0.1   2.1e-34  105.0   0.1
Forkhead             PF00250.14 XP_001638529.1       -            1.3e-32   99.3   0.0   2.2e-32   98.6   0.0
Forkhead             PF00250.14 XP_001638662.1       -            4.4e-23   68.8   0.4   7.7e-23   68.0   0.4
Forkhead             PF00250.14 XP_001638891.1       -            5.7e-42  129.3   0.0   6.7e-42  129.1   0.0
Forkhead             PF00250.14 XP_001638960.1       -            1.7e-32   98.9   0.1   3.6e-32   97.9   0.1
Forkhead             PF00250.14 XP_001639875.1       -            1.2e-44  137.9   0.1   1.4e-44  137.7   0.1
Forkhead             PF00250.14 XP_001639907.1       -            3.9e-24   72.1   0.4   4.2e-24   72.0   0.4
Forkhead             PF00250.14 XP_001641147.1       -            8.2e-40  122.4   0.0   9.5e-40  122.2   0.0
Forkhead             PF00250.14 XP_001642015.1       -            3.4e-06   14.6   1.2   5.3e-05   10.8   0.1
```

9.3.1.15 *Parasteatoda tepidariorum*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 aug3.g244.t1         -            3.9e-18   52.9   1.0   2.2e-17   50.5   0.2
Forkhead             PF00250.14 aug3.g1967.t1        -            1.7e-32   98.9   1.9   1.3e-17   51.3   0.3
Forkhead             PF00250.14 aug3.g1967.t2        -            5.5e-38  116.5   0.3   1.2e-37  115.5   0.3
Forkhead             PF00250.14 aug3.g2894.t1        -            3.4e-42  130.0   0.0   7.1e-42  129.0   0.0
Forkhead             PF00250.14 aug3.g2974.t1        -            8.1e-31   93.6   0.3   2.3e-30   92.1   0.3
Forkhead             PF00250.14 aug3.g4586.t1        -            9.6e-37  112.5   0.3   1.7e-36  111.7   0.0
Forkhead             PF00250.14 aug3.g6985.t1        -            3.2e-40  123.7   0.1   7.3e-40  122.5   0.1
Forkhead             PF00250.14 aug3.g7591.t1        -            1.5e-31   95.9   4.6   2.4e-31   95.2   0.4
Forkhead             PF00250.14 aug3.g7640.t1        -            6.8e-37  113.0   0.4   2.4e-36  111.3   0.0
Forkhead             PF00250.14 aug3.g7640.t2        -            8.8e-37  112.7   0.3   2.9e-36  111.0   0.0
Forkhead             PF00250.14 aug3.g8637.t1        -            2.2e-38  117.8   0.0   4.7e-38  116.8   0.0
Forkhead             PF00250.14 aug3.g8638.t1        -            4.4e-43  132.8   0.1   9.4e-43  131.8   0.1
Forkhead             PF00250.14 aug3.g9968.t1        -            1.3e-39  121.7   0.2   2.2e-39  121.0   0.2
Forkhead             PF00250.14 aug3.g11575.t1       -            3.4e-07   17.8   0.4    0.0004    8.0   0.0
Forkhead             PF00250.14 aug3.g13018.t1       -              6e-06   13.8   0.5    0.0024    5.5   0.0
Forkhead             PF00250.14 aug3.g13311.t1       -            1.7e-39  121.3   0.3   3.8e-39  120.2   0.3
Forkhead             PF00250.14 aug3.g14391.t1       -            7.3e-06   13.6   0.7   1.2e-05   12.9   0.7
Forkhead             PF00250.14 aug3.g15476.t1       -            3.2e-42  130.1   0.4     6e-42  129.2   0.4
Forkhead             PF00250.14 aug3.g19184.t1       -            6.7e-36  109.9   0.0   1.5e-35  108.7   0.0
Forkhead             PF00250.14 aug3.g19520.t1       -              3e-41  127.0   0.0     5e-41  126.3   0.0
Forkhead             PF00250.14 aug3.g19784.t1       -            1.2e-36  112.2   0.3   2.7e-36  111.1   0.3
Forkhead             PF00250.14 aug3.g22782.t1       -            3.9e-23   68.9   1.1     5e-23   68.6   0.5
Forkhead             PF00250.14 aug3.g23979.t1       -            2.6e-42  130.4   0.0   4.9e-42  129.5   0.0
Forkhead             PF00250.14 aug3.g25060.t1       -            3.1e-39  120.5   0.0   5.1e-39  119.8   0.0
Forkhead             PF00250.14 aug3.g25746.t1       -              2e-41  127.6   0.1   3.9e-41  126.6   0.1
Forkhead             PF00250.14 aug3.g25746.t2       -              2e-41  127.6   0.1   3.9e-41  126.6   0.1
Forkhead             PF00250.14 aug3.g26292.t1       -              2e-31   95.5   0.3     2e-31   95.5   0.3
Forkhead             PF00250.14 aug3.g26292.t2       -              2e-31   95.5   0.3     2e-31   95.5   0.3
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Forkhead             PF00250.14 aug3.g26292.t3       -              2e-31   95.5   0.3     2e-31   95.5   0.3
Forkhead             PF00250.14 aug3.g26292.t4       -            2.1e-31   95.4   0.3   2.1e-31   95.4   0.3
Forkhead             PF00250.14 aug3.g26293.t1       -            2.6e-32   98.3   0.2   6.2e-32   97.1   0.2
Forkhead             PF00250.14 aug3.g27823.t1       -            2.9e-42  130.2   0.2   5.5e-42  129.4   0.2
```

9.3.1.16 *Priapulus caudatus*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_014663430.1       -            1.7e-41  127.8   0.0   2.2e-41  127.4   0.0
Forkhead             PF00250.14 XP_014663436.1       -            3.6e-42  129.9   0.1   9.1e-42  128.6   0.1
Forkhead             PF00250.14 XP_014663541.1       -            1.2e-39  121.9   0.1   2.2e-39  121.0   0.1
Forkhead             PF00250.14 XP_014663542.1       -            6.4e-40  122.7   0.1   1.4e-39  121.6   0.1
Forkhead             PF00250.14 XP_014665528.1       -            5.9e-30   90.8   0.4   1.2e-29   89.8   0.2
Forkhead             PF00250.14 XP_014667461.1       -            1.4e-42  131.3   0.0   3.4e-42  130.0   0.0
Forkhead             PF00250.14 XP_014667886.1       -            7.5e-40  122.5   0.2   1.2e-39  121.9   0.2
Forkhead             PF00250.14 XP_014668251.1       -            2.5e-40  124.0   0.0   3.8e-40  123.4   0.0
Forkhead             PF00250.14 XP_014670001.1       -            3.5e-39  120.4   0.0   5.9e-39  119.6   0.0
Forkhead             PF00250.14 XP_014670340.1       -            8.7e-42  128.7   0.1   2.2e-41  127.4   0.1
Forkhead             PF00250.14 XP_014670342.1       -            8.7e-42  128.7   0.1   2.2e-41  127.4   0.1
Forkhead             PF00250.14 XP_014674743.1       -            1.8e-35  108.5   0.1   2.9e-35  107.8   0.1
Forkhead             PF00250.14 XP_014675728.1       -            3.8e-29   88.2   0.4   7.3e-29   87.3   0.1
Forkhead             PF00250.14 XP_014675729.1       -            3.8e-29   88.2   0.4   7.3e-29   87.3   0.1
Forkhead             PF00250.14 XP_014675730.1       -            3.8e-29   88.2   0.4   7.3e-29   87.3   0.1
Forkhead             PF00250.14 XP_014675731.1       -            3.8e-29   88.2   0.4   7.3e-29   87.3   0.1
Forkhead             PF00250.14 XP_014676297.1       -            3.1e-34  104.5   0.1   4.8e-34  103.9   0.1
Forkhead             PF00250.14 XP_014677184.1       -            3.2e-43  133.3   0.2   6.9e-43  132.2   0.2
Forkhead             PF00250.14 XP_014677185.1       -            3.2e-43  133.3   0.2   6.9e-43  132.2   0.2
Forkhead             PF00250.14 XP_014677186.1       -            3.2e-43  133.3   0.2   6.7e-43  132.3   0.2
Forkhead             PF00250.14 XP_014677554.1       -            2.7e-30   91.9   0.0   4.6e-30   91.1   0.0
Forkhead             PF00250.14 XP_014678926.1       -            5.4e-44  135.8   0.1   5.3e-43  132.6   0.1
Forkhead             PF00250.14 XP_014679728.1       -            7.6e-15   42.4   0.0   1.1e-14   41.8   0.0
Forkhead             PF00250.14 XP_014679887.1       -            4.5e-12   33.5   0.4   8.3e-12   32.6   0.4
Forkhead             PF00250.14 XP_014680181.1       -            3.1e-34  104.5   0.0   5.6e-34  103.7   0.0
Forkhead             PF00250.14 XP_014681484.1       -            1.6e-36  111.9   0.0   4.2e-36  110.5   0.0
Forkhead             PF00250.14 XP_014681485.1       -            1.5e-36  111.9   0.0   4.1e-36  110.5   0.0
Forkhead             PF00250.14 XP_014681615.1       -            6.8e-32   97.0   0.0   1.2e-31   96.2   0.0
Forkhead             PF00250.14 XP_014681653.1       -            4.5e-37  113.6   0.0   7.2e-37  112.9   0.0
```

9.3.1.17 *Salpingoeca rosetta*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 XP_004988709.1       -            1.4e-35  108.8   0.0   1.4e-35  108.8   0.0
Forkhead             PF00250.14 XP_004988980.1       -            3.6e-06   14.5   0.0   8.3e-06   13.4   0.0
Forkhead             PF00250.14 XP_004992236.1       -            1.3e-16   48.1   0.0   2.9e-16   46.9   0.0
Forkhead             PF00250.14 XP_004996643.1       -            4.3e-33  100.8   0.0     9e-33   99.8   0.0
Forkhead             PF00250.14 XP_004996805.1       -            6.8e-30   90.6   0.0     2e-29   89.1   0.0
Forkhead             PF00250.14 XP_004996854.1       -            5.5e-22   65.2   0.0   5.5e-22   65.2   0.0
Forkhead             PF00250.14 XP_004998378.1       -            2.4e-32   98.4   0.0   7.3e-32   96.9   0.0
Forkhead             PF00250.14 XP_004998409.1       -              3e-38  117.4   1.9   3.4e-38  117.2   0.1
Forkhead             PF00250.14 XP_004998851.1       -            3.3e-31   94.8   0.0   5.4e-31   94.1   0.0
```

9.3.1.18 *Strongylocentrotus purpuratus*

```
#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001073010.1       -            3.5e-40  123.6   0.1   5.9e-40  122.8   0.1
Forkhead             PF00250.14 NP_001073013.1       -            2.6e-39  120.8   0.8   2.6e-39  120.8   0.8
Forkhead             PF00250.14 NP_001073018.1       -            2.8e-36  111.0   0.0   4.5e-36  110.4   0.0
Forkhead             PF00250.14 NP_001073025.1       -            8.8e-23   67.8   0.6   1.8e-22   66.8   0.1
Forkhead             PF00250.14 NP_001123284.1       -            3.5e-42  130.0   0.0   6.9e-42  129.0   0.0
Forkhead             PF00250.14 NP_999797.1          -            8.4e-39  119.1   0.1   1.9e-38  118.0   0.1
Forkhead             PF00250.14 XP_001176798.2       -              1e-41  128.5   0.5   2.9e-41  127.0   0.5
Forkhead             PF00250.14 XP_001200755.1       -            9.8e-41  125.3   0.1   1.6e-40  124.6   0.1
Forkhead             PF00250.14 XP_003724544.1       -            9.5e-41  125.4   0.0   1.5e-40  124.8   0.0
Forkhead             PF00250.14 XP_003725384.1       -            2.9e-36  111.0   0.0   4.6e-36  110.4   0.0
Forkhead             PF00250.14 XP_003725385.1       -            2.8e-36  111.0   0.0   4.5e-36  110.4   0.0
Forkhead             PF00250.14 XP_003726009.1       -            7.9e-29   87.2   0.0   1.6e-28   86.2   0.0
Forkhead             PF00250.14 XP_003727486.1       -            1.1e-34  105.9   0.0     2e-34  105.1   0.0
Forkhead             PF00250.14 XP_003727487.1       -            1.1e-34  105.9   0.0     2e-34  105.1   0.0
Forkhead             PF00250.14 XP_003727565.1       -            3.9e-41  126.6   0.0   1.2e-40  125.0   0.0
Forkhead             PF00250.14 XP_003727781.1       -            2.1e-42  130.7   0.0   4.5e-42  129.6   0.0
Forkhead             PF00250.14 XP_003727782.1       -            4.5e-42  129.6   0.1   7.7e-42  128.9   0.1
Forkhead             PF00250.14 XP_003727783.1       -            7.8e-42  128.9   0.0   1.3e-41  128.1   0.0
Forkhead             PF00250.14 XP_003728863.2       -            7.1e-13   36.0   0.2   1.7e-12   34.8   0.2
Forkhead             PF00250.14 XP_003729928.2       -            1.5e-35  108.7   0.0   2.8e-35  107.8   0.0
Forkhead             PF00250.14 XP_003731560.1       -            2.8e-36  111.0   0.0   4.5e-36  110.4   0.0
Forkhead             PF00250.14 XP_011661759.1       -            7.5e-38  116.1   0.4   9.9e-38  115.7   0.4
Forkhead             PF00250.14 XP_011668162.1       -            3.1e-28   85.3   0.1     6e-28   84.4   0.1
Forkhead             PF00250.14 XP_011676224.1       -            3.9e-43  133.0   0.0   1.1e-42  131.6   0.0
Forkhead             PF00250.14 XP_011682692.1       -            1.1e-34  105.9   0.0     2e-34  105.1   0.0
Forkhead             PF00250.14 XP_011683767.1       -            6.6e-31   93.8   0.1   1.6e-30   92.6   0.1
Forkhead             PF00250.14 XP_011683768.1       -            6.6e-31   93.8   0.1   1.6e-30   92.6   0.1
Forkhead             PF00250.14 XP_011683769.1       -            6.5e-31   93.9   0.1   1.6e-30   92.6   0.1
Forkhead             PF00250.14 XP_011683770.1       -            6.3e-31   93.9   0.1   1.6e-30   92.6   0.1
Forkhead             PF00250.14 XP_011683771.1       -            6.5e-31   93.9   0.1   1.5e-30   92.7   0.1
Forkhead             PF00250.14 XP_011683772.1       -            6.1e-31   94.0   0.1   1.5e-30   92.7   0.1
Forkhead             PF00250.14 XP_789327.2          -            2.1e-36  111.5   0.4   5.8e-36  110.0   0.1
Forkhead             PF00250.14 XP_789411.2          -            6.4e-29   87.5   0.0   1.4e-28   86.4   0.0
Forkhead             PF00250.14 XP_793339.3          -            1.4e-42  131.2   0.2   2.3e-42  130.6   0.2
Forkhead             PF00250.14 XP_795496.2          -            1.1e-34  105.9   0.0     2e-34  105.1   0.0
Forkhead             PF00250.14 XP_797015.2          -            9.8e-32   96.5   0.0   2.4e-31   95.3   0.0
```

9.3.1.19 *Tribolium castaneum*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001034503.2       -            5.3e-41  126.2   0.1   1.3e-40  124.9   0.1
Forkhead             PF00250.14 NP_001071091.1       -              5e-43  132.7   0.0   7.4e-43  132.1   0.0
Forkhead             PF00250.14 XP_001812698.1       -            1.9e-44  137.3   0.1     4e-44  136.2   0.1
Forkhead             PF00250.14 XP_008191760.1       -            4.1e-38  116.9   0.1   9.1e-38  115.8   0.1
Forkhead             PF00250.14 XP_008191761.1       -            4.1e-38  116.9   0.1   9.1e-38  115.8   0.1
Forkhead             PF00250.14 XP_008191763.1       -            4.1e-38  116.9   0.1   9.1e-38  115.8   0.1
Forkhead             PF00250.14 XP_008191764.1       -            4.1e-38  116.9   0.1     9e-38  115.8   0.1
Forkhead             PF00250.14 XP_008192238.1       -            1.1e-42  131.6   0.4   1.8e-41  127.7   0.0
Forkhead             PF00250.14 XP_008193755.1       -            7.7e-43  132.1   0.1   1.2e-42  131.5   0.1
Forkhead             PF00250.14 XP_008196646.1       -            1.9e-06   15.5   0.4   5.4e-06   14.0   0.4
Forkhead             PF00250.14 XP_008196647.1       -            2.2e-06   15.2   0.6   6.4e-06   13.8   0.6
Forkhead             PF00250.14 XP_008196648.1       -            2.2e-06   15.2   0.6   6.4e-06   13.8   0.6
Forkhead             PF00250.14 XP_008196921.1       -            2.6e-34  104.7   0.2   4.7e-34  103.9   0.2
Forkhead             PF00250.14 XP_008198974.1       -            5.1e-44  135.9   0.3     1e-43  134.9   0.0
Forkhead             PF00250.14 XP_008199360.2       -            1.1e-31   96.3   1.2   4.5e-31   94.4   0.3
Forkhead             PF00250.14 XP_008200175.1       -            5.4e-41  126.2   0.0   1.1e-40  125.2   0.0
Forkhead             PF00250.14 XP_008200691.1       -            1.7e-37  114.9   0.0   2.6e-37  114.4   0.0
Forkhead             PF00250.14 XP_008200692.1       -            1.3e-37  115.3   0.0   1.9e-37  114.8   0.0
Forkhead             PF00250.14 XP_008201201.1       -              1e-31   96.4   0.1   2.2e-31   95.4   0.1
Forkhead             PF00250.14 XP_008201697.1       -            8.8e-31   93.4   0.3   1.9e-30   92.4   0.3
Forkhead             PF00250.14 XP_008201698.1       -            1.9e-30   92.4   1.1   3.8e-30   91.4   1.1
Forkhead             PF00250.14 XP_008201699.1       -            6.4e-31   93.9   0.3   1.3e-30   92.9   0.3
Forkhead             PF00250.14 XP_008201700.1       -            6.4e-31   93.9   0.3   1.3e-30   92.9   0.3
Forkhead             PF00250.14 XP_015834592.1       -            4.1e-38  116.9   0.1   9.1e-38  115.8   0.1
Forkhead             PF00250.14 XP_015836118.1       -            3.2e-29   88.4   1.0   1.5e-28   86.2   0.2
Forkhead             PF00250.14 XP_015836123.1       -            3.1e-29   88.5   0.9   1.5e-28   86.2   0.2
Forkhead             PF00250.14 XP_015836124.1       -              3e-29   88.5   0.9   1.5e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836132.1       -            1.1e-31   96.3   1.2   4.5e-31   94.4   0.3
Forkhead             PF00250.14 XP_015836134.1       -              3e-29   88.5   0.9   1.5e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836137.1       -            4.4e-29   88.0   1.4   1.5e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836139.1       -            4.6e-29   87.9   1.5   1.5e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836144.1       -            4.6e-29   87.9   1.5   1.5e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836146.1       -              6e-29   87.6   0.2   1.4e-28   86.3   0.2
Forkhead             PF00250.14 XP_015836148.1       -            5.5e-29   87.7   0.2   1.4e-28   86.4   0.2
Forkhead             PF00250.14 XP_015836151.1       -            5.5e-29   87.7   0.2   1.4e-28   86.4   0.2
Forkhead             PF00250.14 XP_015836154.1       -            5.3e-29   87.7   0.2   1.3e-28   86.5   0.2
Forkhead             PF00250.14 XP_015836159.1       -            1.1e-31   96.4   1.2   4.5e-31   94.4   0.3
Forkhead             PF00250.14 XP_015836876.1       -            2.4e-38  117.7   0.1   4.2e-38  116.9   0.1
Forkhead             PF00250.14 XP_015838010.1       -              2e-06   15.4   0.5   5.9e-06   13.9   0.5
Forkhead             PF00250.14 XP_015838011.1       -              2e-06   15.4   0.5   5.9e-06   13.9   0.5
Forkhead             PF00250.14 XP_015838185.1       -            2.6e-34  104.7   0.2   4.7e-34  103.9   0.2
Forkhead             PF00250.14 XP_015840687.1       -            8.8e-31   93.4   0.3   1.9e-30   92.4   0.3
Forkhead             PF00250.14 XP_015840688.1       -            8.5e-31   93.5   0.3   1.8e-30   92.4   0.3
Forkhead             PF00250.14 XP_015840689.1       -            6.4e-31   93.9   0.3   1.3e-30   92.9   0.3
Forkhead             PF00250.14 XP_968056.1          -              1e-38  118.9   0.1   1.6e-38  118.3   0.1
Forkhead             PF00250.14 XP_968211.1          -            2.2e-38  117.8   0.1   3.7e-38  117.1   0.1
Forkhead             PF00250.14 XP_969282.1          -            7.8e-36  109.6   0.1   1.6e-35  108.6   0.1
Forkhead             PF00250.14 XP_969795.2          -            4.2e-44  136.1   0.4   6.6e-44  135.5   0.4
Forkhead             PF00250.14 XP_973691.3          -            2.3e-42  130.5   0.1   4.2e-42  129.7   0.1
Forkhead             PF00250.14 XP_974828.2          -            7.5e-43  132.1   0.1   1.2e-42  131.5   0.1
Forkhead             PF00250.14 XP_975200.2          -            1.4e-31   96.0   0.1   2.9e-31   95.0   0.1
Forkhead             PF00250.14 XP_976315.1          -            1.9e-06   15.5   0.4   5.4e-06   14.0   0.4
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9.3.1.20 *Xenopus tropicalis*

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#                                                               --- full sequence ---- --- best 1 domain ----
# target name        accession  query name           accession    E-value  score  bias   E-value  score  bias
#------------------- ---------- -------------------- ---------- --------- ------ ----- --------- ------ -----
Forkhead             PF00250.14 NP_001005675.2       -            6.1e-39  119.6   0.1   1.2e-38  118.6   0.1
Forkhead             PF00250.14 NP_001007864.1       -            1.1e-43  134.8   0.1     2e-43  134.0   0.1
Forkhead             PF00250.14 NP_001008016.1       -            2.5e-30   92.0   0.1   4.9e-30   91.1   0.1
Forkhead             PF00250.14 NP_001008143.1       -            4.8e-40  123.1   0.1   8.8e-40  122.3   0.1
Forkhead             PF00250.14 NP_001008148.1       -            4.1e-42  129.7   0.0   6.4e-42  129.1   0.0
Forkhead             PF00250.14 NP_001011367.1       -              1e-39  122.0   0.5   2.9e-39  120.6   0.1
Forkhead             PF00250.14 NP_001011383.1       -            5.4e-42  129.4   0.0     9e-42  128.7   0.0
Forkhead             PF00250.14 NP_001016300.2       -              3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 NP_001016544.1       -            5.9e-43  132.5   0.6   1.2e-42  131.5   0.1
Forkhead             PF00250.14 NP_001016787.1       -            1.2e-43  134.7   0.0   2.5e-43  133.6   0.0
Forkhead             PF00250.14 NP_001016928.1       -            1.8e-41  127.7   0.0   3.2e-41  126.9   0.0
Forkhead             PF00250.14 NP_001017017.1       -            9.5e-37  112.6   0.1   2.2e-36  111.4   0.1
Forkhead             PF00250.14 NP_001017084.1       -            5.1e-30   91.0   0.0   9.8e-30   90.1   0.0
Forkhead             PF00250.14 NP_001037918.1       -              2e-27   82.7   0.0   3.4e-27   81.9   0.0
Forkhead             PF00250.14 NP_001039226.1       -            3.3e-42  130.0   0.0   6.3e-42  129.2   0.0
Forkhead             PF00250.14 NP_001070655.1       -            2.7e-32   98.3   0.1   8.4e-32   96.7   0.1
Forkhead             PF00250.14 NP_001093702.1       -            6.3e-42  129.2   0.0   1.1e-41  128.4   0.0
Forkhead             PF00250.14 NP_001093722.1       -              2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 NP_001096332.1       -              8e-37  112.8   0.1   1.4e-36  112.0   0.1
Forkhead             PF00250.14 NP_001096419.1       -              6e-30   90.8   0.1   1.8e-29   89.3   0.1
Forkhead             PF00250.14 NP_001103516.1       -            4.9e-41  126.3   0.3   1.5e-40  124.7   0.3
Forkhead             PF00250.14 NP_001107970.1       -            8.4e-40  122.3   0.1   1.3e-39  121.7   0.1
Forkhead             PF00250.14 NP_001116933.1       -            2.7e-42  130.4   0.0   5.8e-42  129.3   0.0
Forkhead             PF00250.14 NP_001120586.1       -            4.2e-06   14.3   0.2   8.6e-06   13.3   0.2
Forkhead             PF00250.14 NP_001135634.1       -            1.7e-43  134.2   0.2   3.3e-43  133.3   0.2
Forkhead             PF00250.14 NP_988938.1          -            1.3e-41  128.2   0.5   2.2e-41  127.4   0.5
Forkhead             PF00250.14 NP_988949.1          -            2.7e-42  130.4   0.0   4.4e-42  129.7   0.0
Forkhead             PF00250.14 NP_989265.1          -            1.1e-42  131.5   0.1   1.8e-42  130.9   0.1
Forkhead             PF00250.14 NP_989419.1          -            1.5e-40  124.7   0.3   3.8e-40  123.4   0.3
Forkhead             PF00250.14 NP_989423.1          -            1.5e-41  128.0   0.2   3.1e-41  127.0   0.2
Forkhead             PF00250.14 NP_998857.1          -            8.1e-44  135.2   0.1   1.6e-43  134.3   0.1
Forkhead             PF00250.14 XP_002931457.1       -            1.7e-42  131.0   0.0   3.2e-42  130.1   0.0
Forkhead             PF00250.14 XP_002931458.1       -            4.7e-42  129.6   0.0   7.1e-42  129.0   0.0
Forkhead             PF00250.14 XP_002932017.1       -            7.7e-40  122.5   0.1   1.7e-39  121.4   0.1
Forkhead             PF00250.14 XP_002934447.1       -            1.5e-36  111.9   0.0   2.7e-36  111.1   0.0
Forkhead             PF00250.14 XP_002934931.1       -            7.1e-31   93.7   0.3   1.2e-30   93.0   0.3
Forkhead             PF00250.14 XP_002935635.1       -            1.8e-40  124.5   0.0   3.6e-40  123.5   0.0
Forkhead             PF00250.14 XP_002936729.1       -            3.1e-41  126.9   0.0   5.7e-41  126.1   0.0
Forkhead             PF00250.14 XP_002939401.1       -            3.8e-29   88.2   0.0   8.9e-29   87.0   0.0
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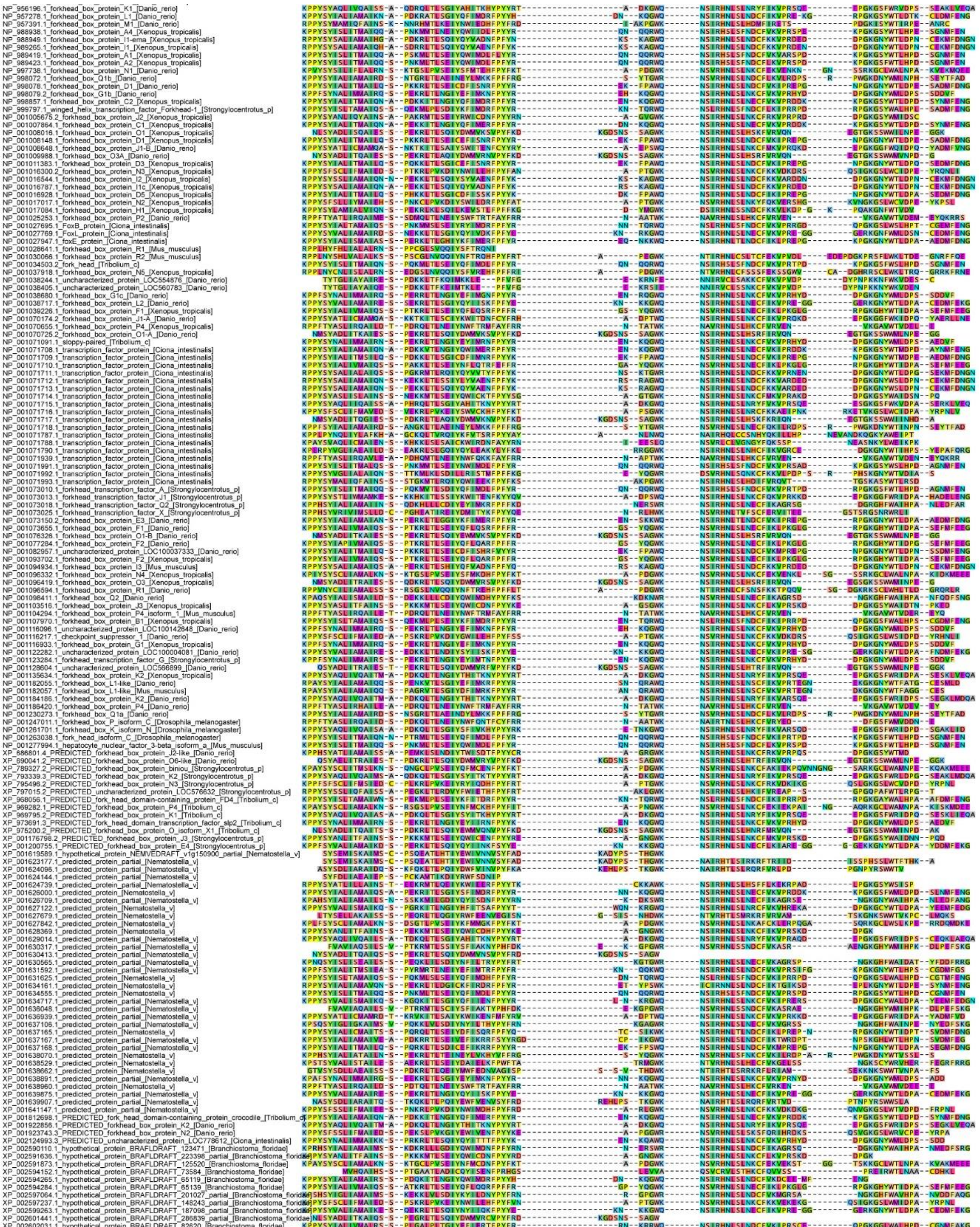
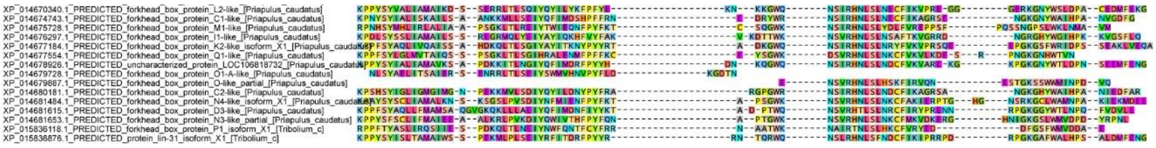
Forkhead             PF00250.14 XP_002941428.1       -             1.6e-34  105.5   0.5   3.5e-34  104.3   0.5
Forkhead             PF00250.14 XP_004912791.1       -             1.6e-34  105.5   0.5   3.5e-34  104.3   0.5
Forkhead             PF00250.14 XP_004913691.1       -             5.6e-43  132.5   0.0   8.9e-43  131.9   0.0
Forkhead             PF00250.14 XP_004916879.1       -               7e-31   93.8   0.3   1.2e-30   93.0   0.3
Forkhead             PF00250.14 XP_004917868.1       -             2.7e-42  130.3   0.1   4.7e-42  129.6   0.1
Forkhead             PF00250.14 XP_004921500.1       -             1.7e-39  121.3   0.0   2.7e-39  120.7   0.0
Forkhead             PF00250.14 XP_012809373.1       -             5.1e-30   91.0   0.0   9.8e-30   90.1   0.0
Forkhead             PF00250.14 XP_012809375.1       -             5.1e-30   91.0   0.0   9.8e-30   90.1   0.0
Forkhead             PF00250.14 XP_012810735.1       -             3.5e-14   40.2   0.0   5.8e-14   39.5   0.0
Forkhead             PF00250.14 XP_012813757.1       -             1.5e-36  111.9   1.5   7.4e-36  109.7   0.2
Forkhead             PF00250.14 XP_012813833.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813834.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813835.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813836.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813837.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813838.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813839.1       -               2e-32   98.7   0.2     2e-32   98.7   0.2
Forkhead             PF00250.14 XP_012813840.1       -             1.9e-32   98.8   0.2   1.9e-32   98.8   0.2
Forkhead             PF00250.14 XP_012813841.1       -             1.9e-32   98.8   0.2   1.9e-32   98.8   0.2
Forkhead             PF00250.14 XP_012813842.1       -             1.9e-32   98.8   0.2   1.9e-32   98.8   0.2
Forkhead             PF00250.14 XP_012813843.1       -             1.9e-32   98.8   0.2   1.9e-32   98.8   0.2
Forkhead             PF00250.14 XP_012813844.1       -             1.7e-32   98.9   0.2   1.7e-32   98.9   0.2
Forkhead             PF00250.14 XP_012813845.1       -             5.1e-33  100.6   0.2   1.6e-32   99.0   0.2
Forkhead             PF00250.14 XP_012815104.1       -             1.6e-34  105.4   0.5   3.5e-34  104.3   0.5
Forkhead             PF00250.14 XP_012817795.1       -               6e-43  132.4   0.0   9.5e-43  131.8   0.0
Forkhead             PF00250.14 XP_012818282.1       -             1.2e-43  134.6   0.0   2.8e-43  133.5   0.0
Forkhead             PF00250.14 XP_012820066.1       -             2.7e-32   98.3   0.1   8.4e-32   96.7   0.1
Forkhead             PF00250.14 XP_012820069.1       -             2.7e-32   98.3   0.1   8.4e-32   96.7   0.1
Forkhead             PF00250.14 XP_012820074.1       -             2.8e-32   98.2   0.1   8.3e-32   96.7   0.1
Forkhead             PF00250.14 XP_012823837.1       -               3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 XP_012823838.1       -               3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 XP_012823840.1       -               3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 XP_012823841.1       -               3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 XP_012823842.1       -               3e-38  117.4   0.1   5.7e-38  116.5   0.1
Forkhead             PF00250.14 XP_012823843.1       -             2.7e-38  117.5   0.1   5.3e-38  116.6   0.1
Forkhead             PF00250.14 XP_012823844.1       -             2.7e-38  117.5   0.1   5.3e-38  116.6   0.1
Forkhead             PF00250.14 XP_012825183.1       -             1.3e-29   89.6   1.5   1.7e-29   89.3   0.3
Forkhead             PF00250.14 XP_012825449.1       -             8.4e-40  122.3   0.1   1.3e-39  121.7   0.1
Forkhead             PF00250.14 XP_012825801.1       -             2.7e-37  114.3   0.1   4.9e-37  113.5   0.1
Forkhead             PF00250.14 XP_012826963.1       -             4.8e-41  126.3   0.3   1.5e-40  124.8   0.3
Forkhead             PF00250.14 XP_012827170.1       -             1.5e-39  121.6   0.5   3.9e-39  120.2   0.1
```

9.3.2 Forkhead domain alignment





```
XP_014670340.1_PREDICTED_forkhead_box_protein_L2-like_[Priapulus_caudatus] KPPYSYVALIAMAIKD-S--SERRLTLSQIYQYILYKFPFYE-------------------KN---KKGWQ-------NSIRHNLSLNECFIKVPRE-GG--------GERKGNYWSLDPA--CEDMFEKG
XP_014674743.1_PREDICTED_forkhead_box_protein_C1-like_[Priapulus_caudatus] KPNYSYIALISKAILS-A--ANKKMLLSEIYQFIMDSHPFFRN--------------------E--DRYWR-------NSIRHNLSLNECFIKAGRSE-----------NGKGNYWAIHPA--NVGDFG
XP_014675728.1_PREDICTED_forkhead_box_protein_M1-like_[Priapulus_caudatus] RPNHSYMHLIRLALIA-A--PSGKLTLREIYTWIEQNFPYFKT--------------------C--SQGWK-------NSIRHNLSLYDLFVREPPSF--------PQSSNGPSLWKLNMA--VM
XP_014676297.1_PREDICTED_forkhead_box_protein_I1-like_[Priapulus_caudatus] KPDLSYSSLIAMAILS-S--REGRMQLYEIYAYIQKHFVYFAK--------------------V-KDTTWK-------NSVRHNLSLNSAFTKVGRRD-----------NGRGHYWGIHPK--KVGSFLQ
XP_014677184.1_PREDICTED_forkhead_box_protein_K2-like_isoform_X1_[Priapulus_caudatus] K[illegible]PFSYAQLIVQAISS-A--HDKQLTLSGIYAYITKNYPYYRT--------------------A--DKGWQ-------NSIRHNLSLNRYFVKVPRSQE---------EPGKGSFWRIDPS--SEAKLVEQA
XP_014677554.1_PREDICTED_forkhead_box_protein_Q1-like_[Priapulus_caudatus] KPPFSYLGLMVTAIQS-S--PSGKLTLSGIHRALENMFPFFKC--------------------E--YSGWK-------DSVRHNLSLNKCFVKVLKDE-S---R----PNGKGNHWTVN
XP_014678926.1_PREDICTED_uncharacterized_protein_LOC106818732_[Priapulus_caudatus] KPPYSYIALIAMAVKS-A--PDKKITLNGIYQFIMDRFPYYH-------------------DN---KQGWQ-------NSIRHNLSLNDCFVKVARE-KG--------KPGKGNYWTLDPN--SEEMFENG
XP_014679728.1_PREDICTED_forkhead_box_protein_O1-A-like_[Priapulus_caudatus]   NLSYAELITSAIER-S--ENRRLTLSEIYSWMVHNVPYFLD---------------KGDTN
XP_014679887.1_PREDICTED_forkhead_box_protein_O-like_partial_[Priapulus_caudatus]                                                                       E-------NSVRHNLSLHSKFIRVQN-----------ESTGKSSWAMINPD--VQ
XP_014680181.1_PREDICTED_forkhead_box_protein_C2-like_[Priapulus_caudatus] KPSHSYIGLIGMGIMG-N--PEKKMVLSDIYQYILDNYPYFRA----------------------RGPGWR-------NSIRHNLSLNDCFIKAGRSA-----------NGKGHYWAIHPA--NIEDFAR
XP_014681484.1_PREDICTED_forkhead_box_protein_N4-like_isoform_X1_[Priapulus_caudatus] K[illegible]AYSYSCLIAMALKN-S--KSGSLPVSDIYNFMIENFPYFKT--------------------A--PSGWK-------NSVRHNLSLNKCFAKIERPTG---HG----NSRKGCLWAMNPA--KIEKMDEE
XP_014681615.1_PREDICTED_forkhead_box_protein_D3-like_[Priapulus_caudatus] KPPFSYAQLLFMAMSA-QGVGKQKLLLAEIYQFIMDNFIYYKT--------------------A-D-PTWQ-------NSVRHTLSLNRCFIRYPRENN---------RPGKGGYWTLNPQ--FVDVLE
XP_014681653.1_PREDICTED_forkhead_box_protein_N3-like_partial_[Priapulus_caudatus] KPPYSFSCLIFMAIEE-A--ALKRLPVKDIYQWIVTHFPYFQN--------------------A--PTGWK-------NSVRHNLSLNKCFMKVDKERG--------HNIGKGSLWMVDPD--YRPNL
XP_015836118.1_PREDICTED_forkhead_box_protein_P1_isoform_X1_[Tribolium_c] RPPFTYASLIRQSIIE-S--PDKQLTLNEIYNWFQNTFCYFRR--------------------N--AATWK-------NAIRTNLSLHKCFVRYED--------------DFGSFWMVDDA--E
XP_015836876.1_PREDICTED_protein_lin-31_isoform_X1_[Tribolium_c] KPPYSYISLTAMAIWS-S--PEKMLPLSEIYRFIITDRFPYYR-------------------RN--TQRWQ-------NSLRHNLSFNDCFIKIPRRPD---------RPGKGAFWALHPS--ALDMFENG
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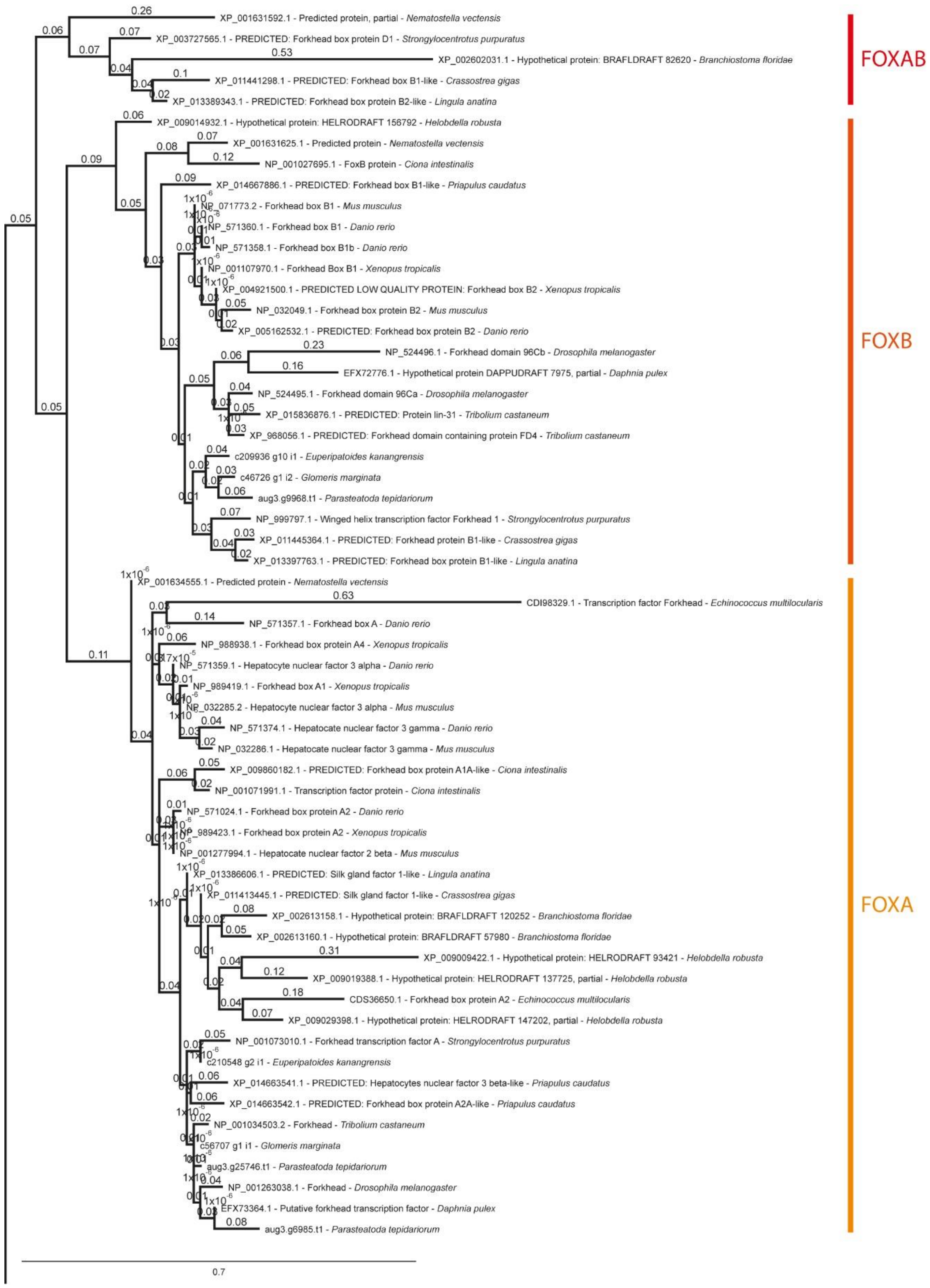
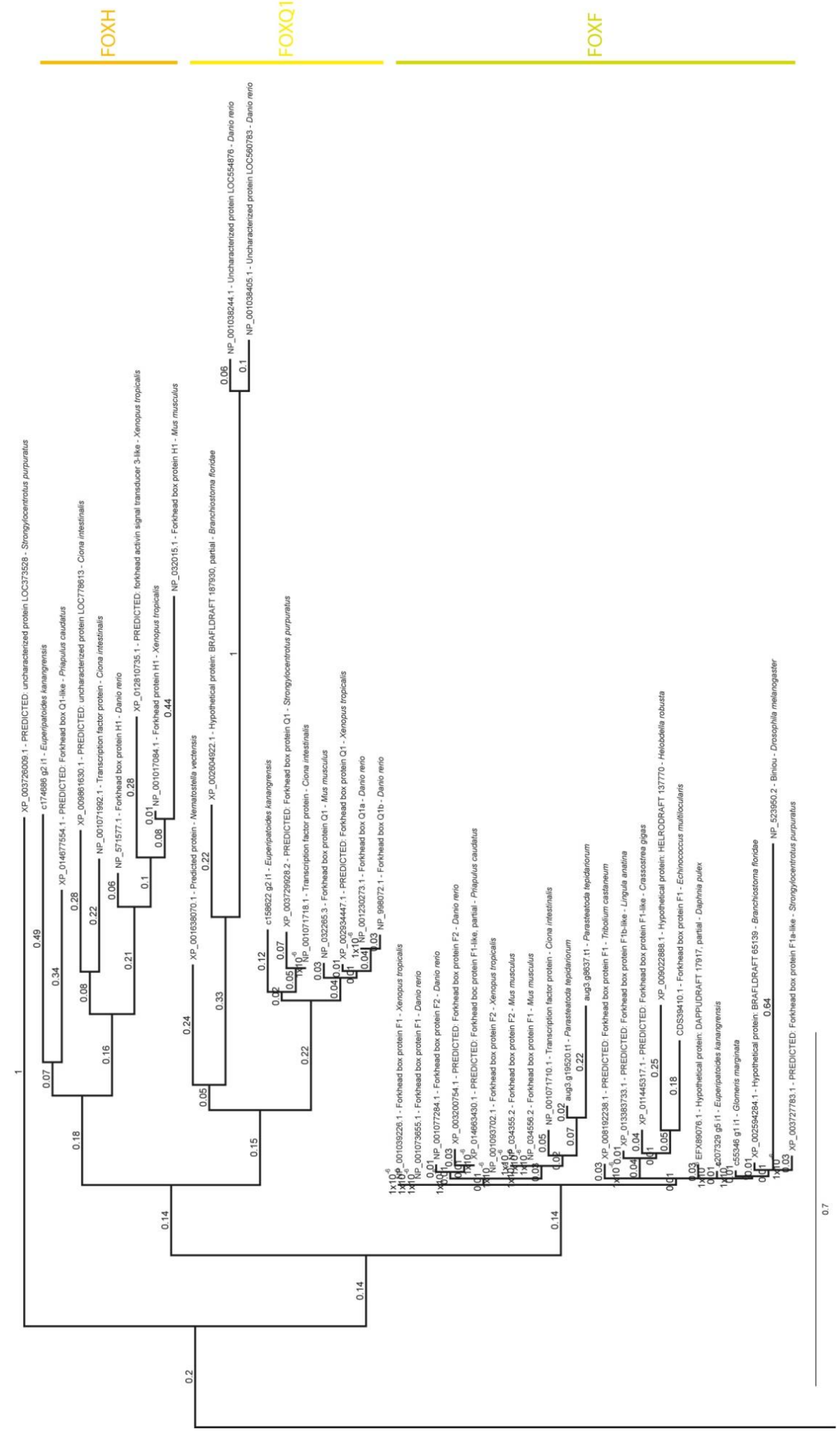
9.3.3 Maximum likelihood tree of forkhead domains

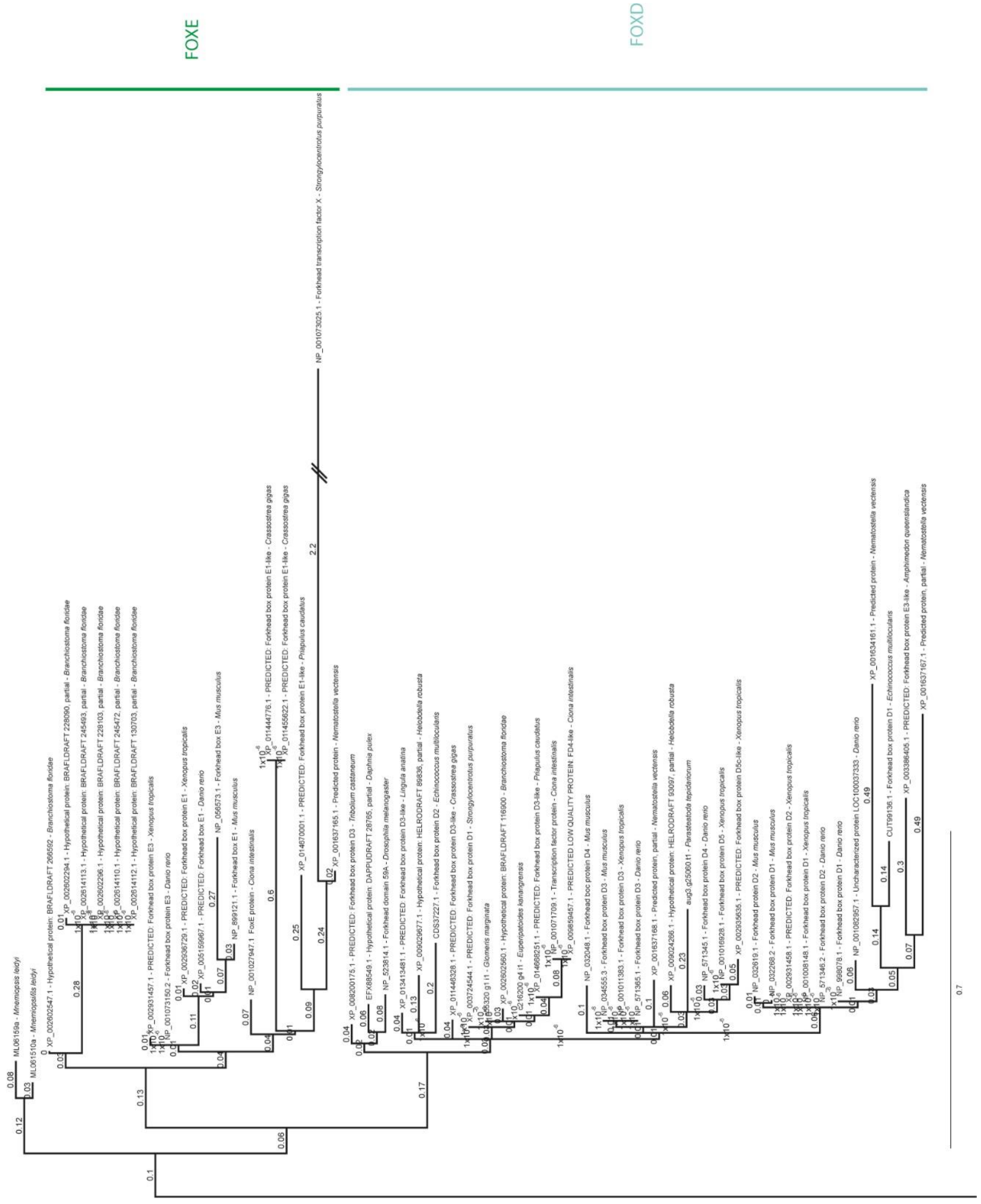
9.3.3.1 *FOXAB FOXB FOXA*



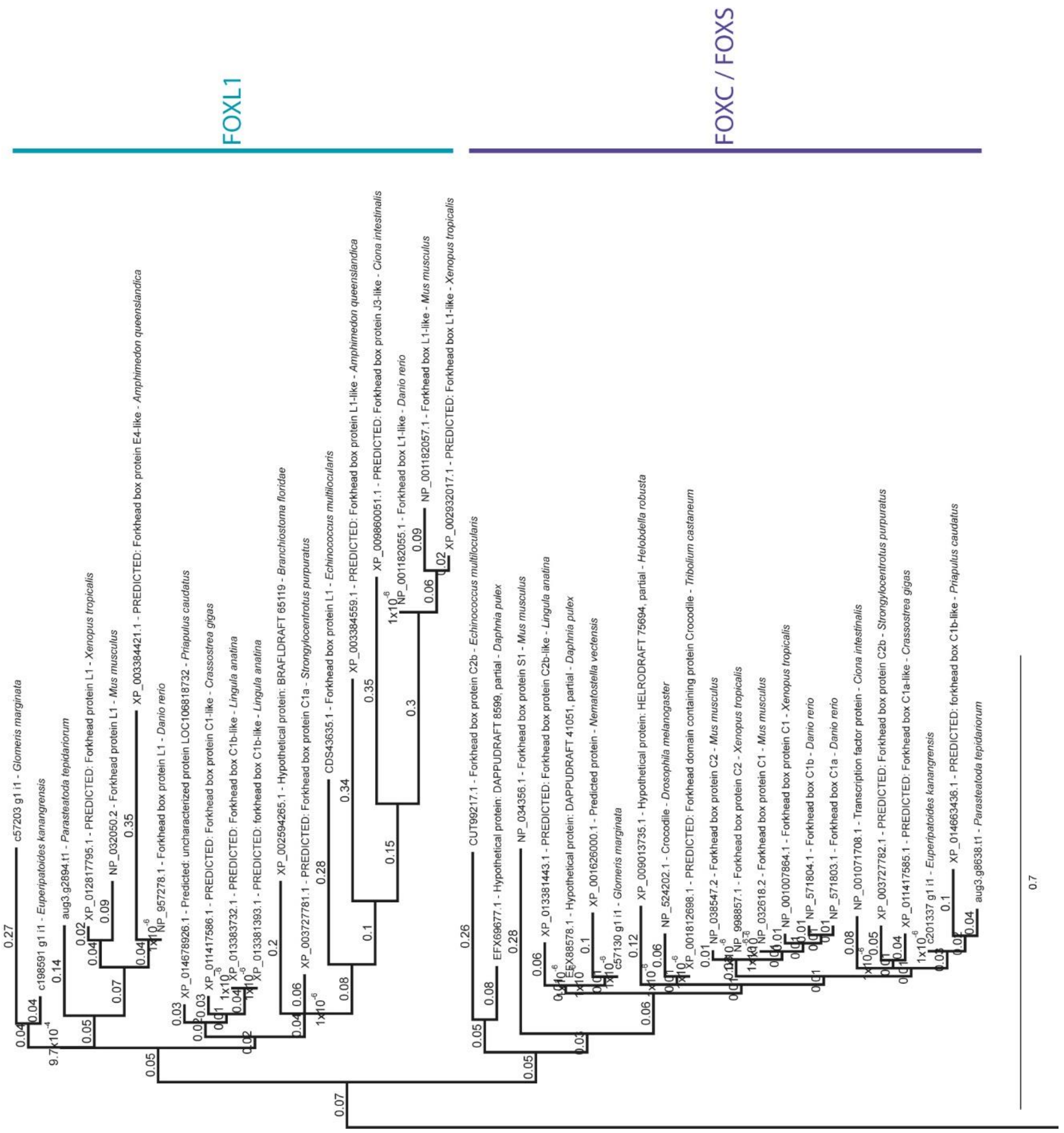
9.3.3.2 *FOXH FOXQ1 FOXF*



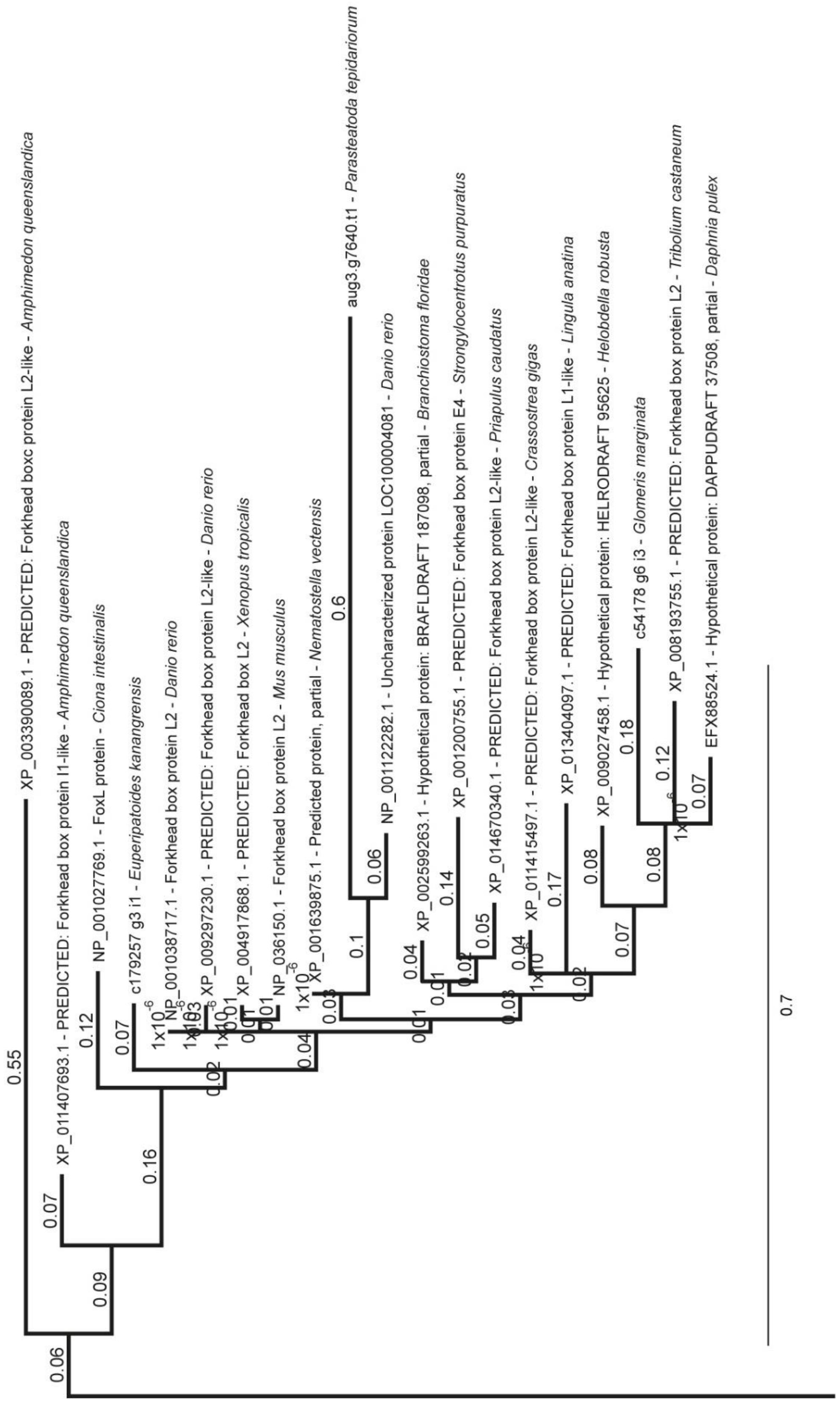
9.3.3.3 *FOXE FOXD*



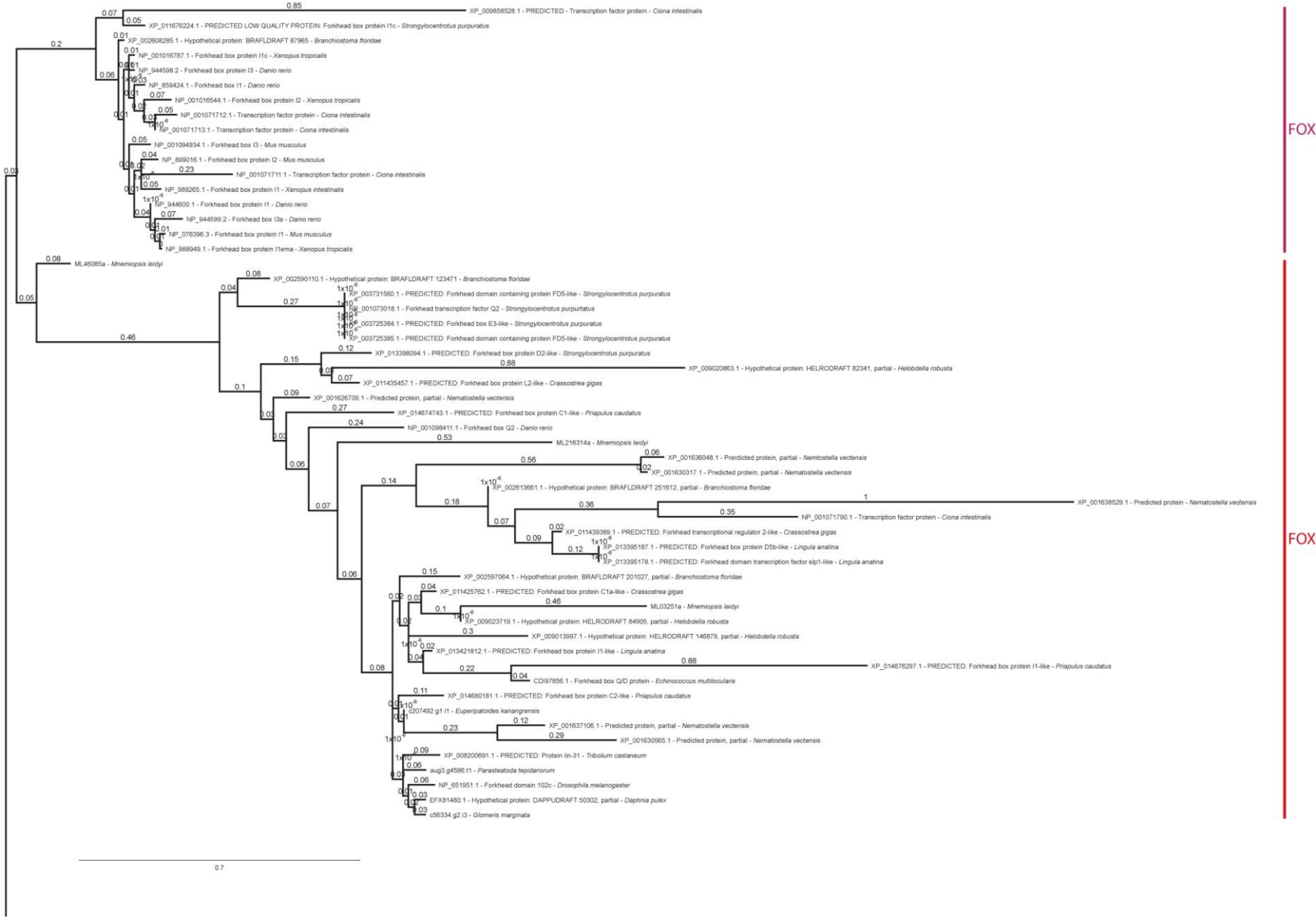
9.3.3.4 *FOXL1 FOXC/FOXS*



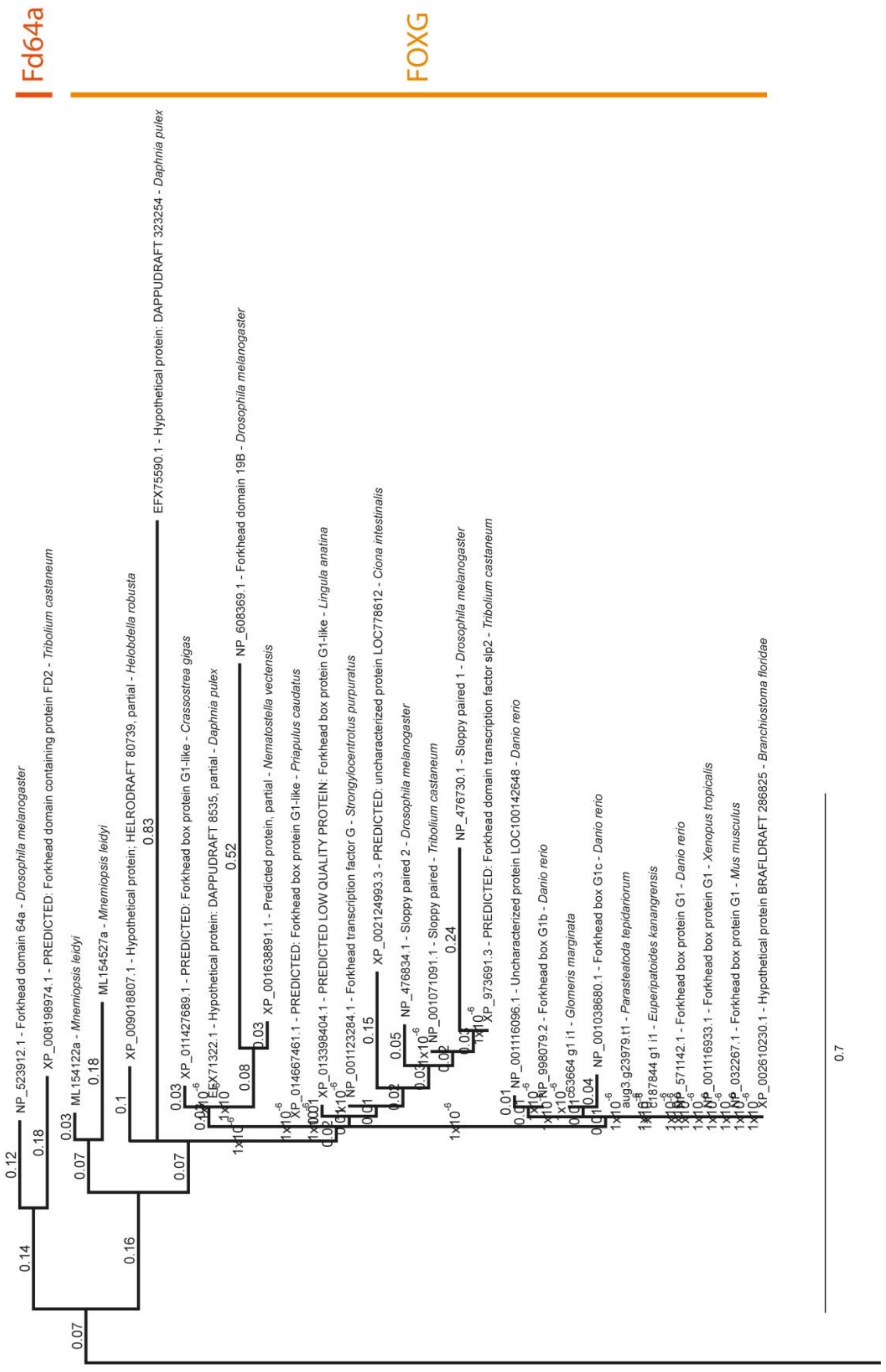
9.3.3.5 *FOXL2*


XP_003390089.1 - PREDICTED: Forkhead boxc protein L2-like - Amphimedon queenslandica
XP_011407693.1 - PREDICTED: Forkhead box protein I1-like - Amphimedon queenslandica
NP_001027769.1 - FoxL protein - Ciona intestinalis
c179257 g3 i1 - Euperipatoides kanangrensis
NP_001038717.1 - Forkhead box protein L2 - Danio rerio
XP_009297230.1 - PREDICTED: Forkhead box protein L2-like - Danio rerio
XP_004917868.1 - PREDICTED: Forkhead box L2 - Xenopus tropicalis
NP_036150.1 - Forkhead box protein L2 - Mus musculus
XP_001639875.1 - Predicted protein, partial - Nematostella vectensis
aug3.g7640.t1 - Parasteatoda tepidariorum
NP_001122282.1 - Uncharacterized protein LOC100004081 - Danio rerio
XP_002599263.1 - Hypothetical protein: BRAFLDRAFT 187098, partial - Branchiostoma floridae
XP_001200755.1 - PREDICTED: Forkhead box protein E4 - Strongylocentrotus purpuratus
XP_014670340.1 - PREDICTED: Forkhead box protein L2-like - Priapulus caudatus
XP_011415497.1 - PREDICTED: Forkhead box protein L2-like - Crassostrea gigas
XP_013404097.1 - PREDICTED: Forkhead box protein L1-like - Lingula anatina
XP_009027458.1 - Hypothetical protein: HELRODRAFT 95625 - Helobdella robusta
c54178 g6 i3 - Glomeris marginata
XP_008193755.1 - PREDICTED: Forkhead box protein L2 - Tribolium castaneum
EFX88524.1 - Hypothetical protein: DAPPUDRAFT 37508, partial - Daphnia pulex
0.55
0.07
0.09
0.06
0.12
0.16
0.07
1x10^-6
1x10^-6
0.03
1x10^-6
0.01
0.02
0.01
0.01
1x10^-6
0.04
0.6
0.1
0.06
0.03
0.04
0.01
0.01
0.14
0.02
0.05
0.03
0.04
1x10^-6
0.17
0.02
0.08
0.07
0.18
0.08
0.12
1x10^-6
0.07
0.7

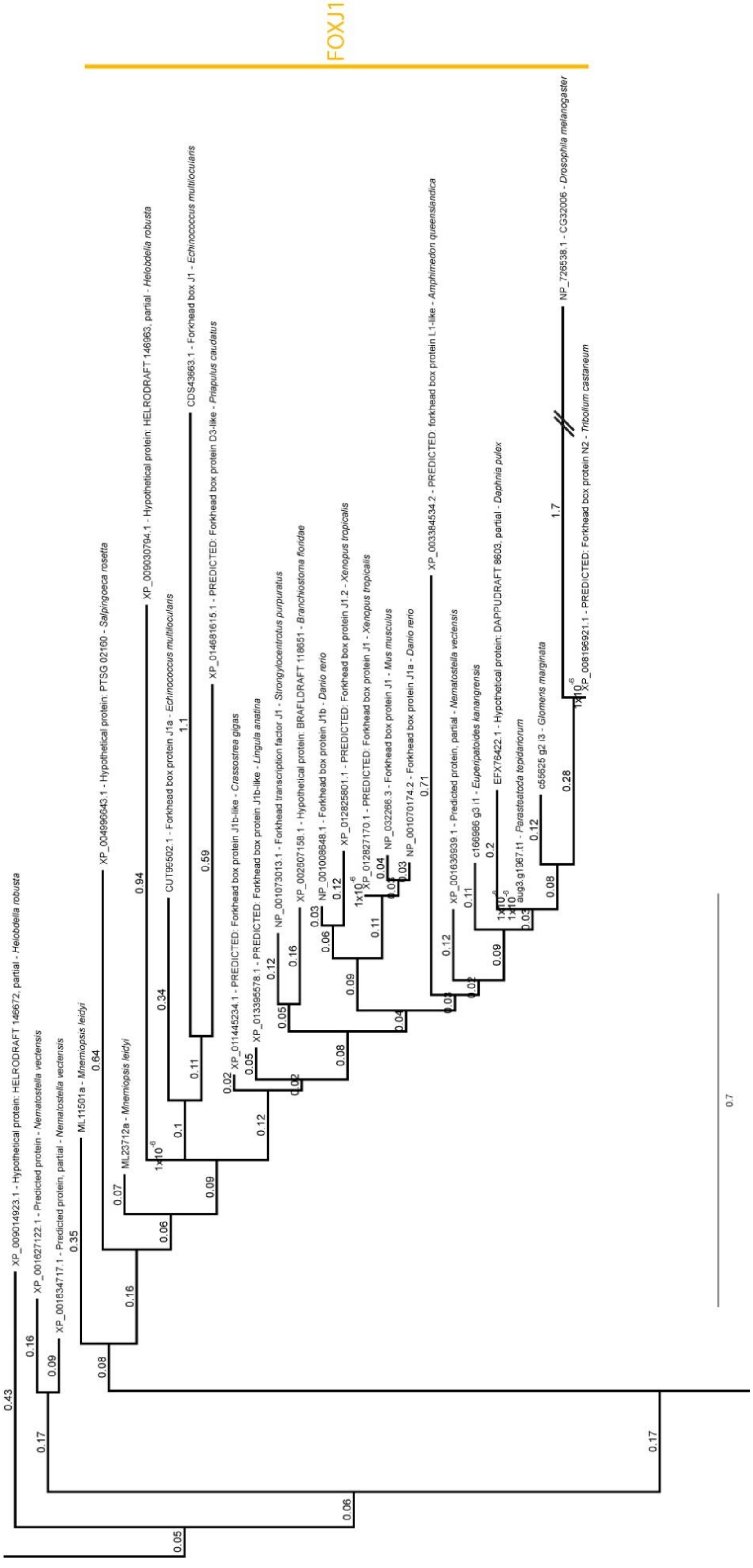
9.3.3.6 *FOXI FOXQ2*



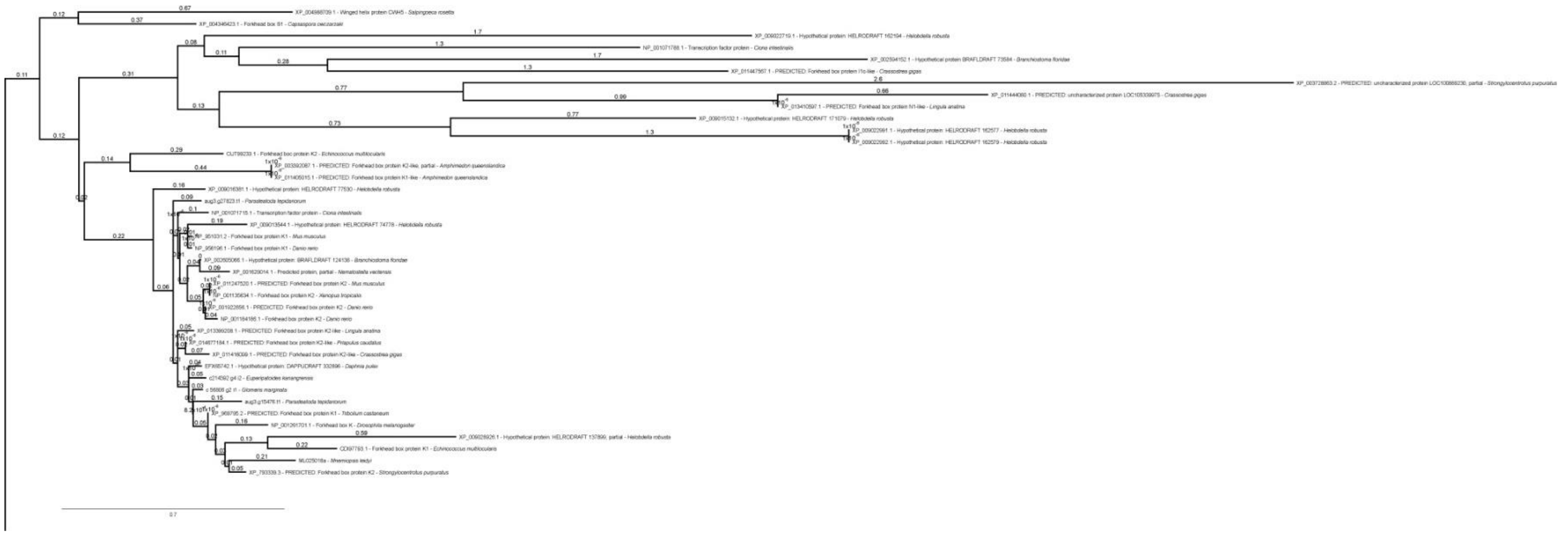
9.3.3.7 *Fd64A FOXG*



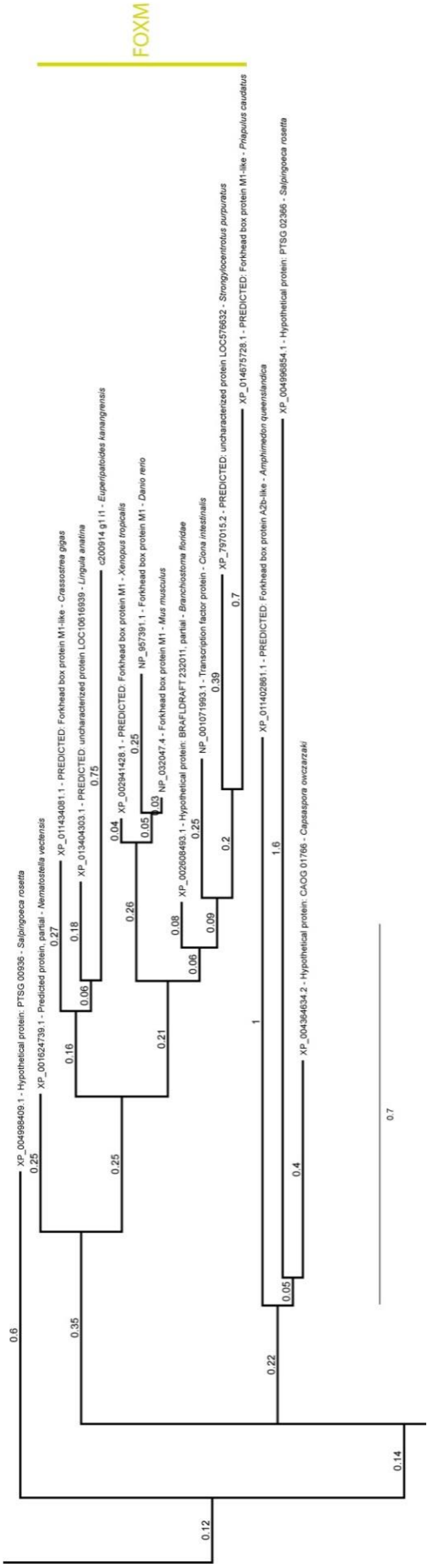
9.3.3.8 *FOXJ1*


FOXJ1
XP_090014923.1 - Hypothetical protein: HELRODRAFT 146672, partial - Helobdella robusta
XP_001627122.1 - Predicted protein - Nematostella vectensis
XP_001634717.1 - Predicted protein, partial - Nematostella vectensis
ML11501a - Mnemiopsis leidyi
ML23712a - Mnemiopsis leidyi
XP_004996643.1 - Hypothetical protein: PTSG 02160 - Salpingoeca rosetta
XP_009030794.1 - Hypothetical protein: HELRODRAFT 146963, partial - Helobdella robusta
CUT99502.1 - Forkhead box protein J1a - Echinococcus multilocularis
CDS43663.1 - Forkhead box J1 - Echinococcus multilocularis
XP_014681615.1 - PREDICTED: Forkhead box protein D3-like - Priapulus caudatus
XP_011445234.1 - PREDICTED: Forkhead box protein J1b-like - Crassostrea gigas
XP_013395578.1 - PREDICTED: Forkhead box protein J1b-like - Lingula anatina
NP_001073013.1 - Forkhead transcription factor J1 - Strongylocentrotus purpuratus
XP_002607158.1 - Hypothetical protein: BRAFLDRAFT 118651 - Branchiostoma floridae
NP_001008648.1 - Forkhead box protein J1b - Danio rerio
XP_012825801.1 - PREDICTED: Forkhead box protein J1.2 - Xenopus tropicalis
XP_012827170.1 - PREDICTED: Forkhead box protein J1 - Xenopus tropicalis
NP_032266.3 - Forkhead box protein J1 - Mus musculus
NP_001070174.2 - Forkhead box protein J1a - Danio rerio
XP_003384534.2 - PREDICTED: forkhead box protein L1-like - Amphimedon queenslandica
XP_001636939.1 - Predicted protein, partial - Nematostella vectensis
c166986 g3 i1 - Euperipatoides kanangrensis
EFX76422.1 - Hypothetical protein: DAPPUDRAFT 8603, partial - Daphnia pulex
aug3.g1967.t1 - Parasteatoda tepidariorum
c55625 g2 i3 - Glomeris marginata
NP_726538.1 - CG32006 - Drosophila melanogaster
XP_008196921.1 - PREDICTED: Forkhead box protein N2 - Tribolium castaneum
0.43
0.16
0.09
0.35
0.64
0.07
0.94
0.34
1.1
0.59
0.12
0.16
0.71
1.7
0.28
0.17
0.06
0.05
0.7

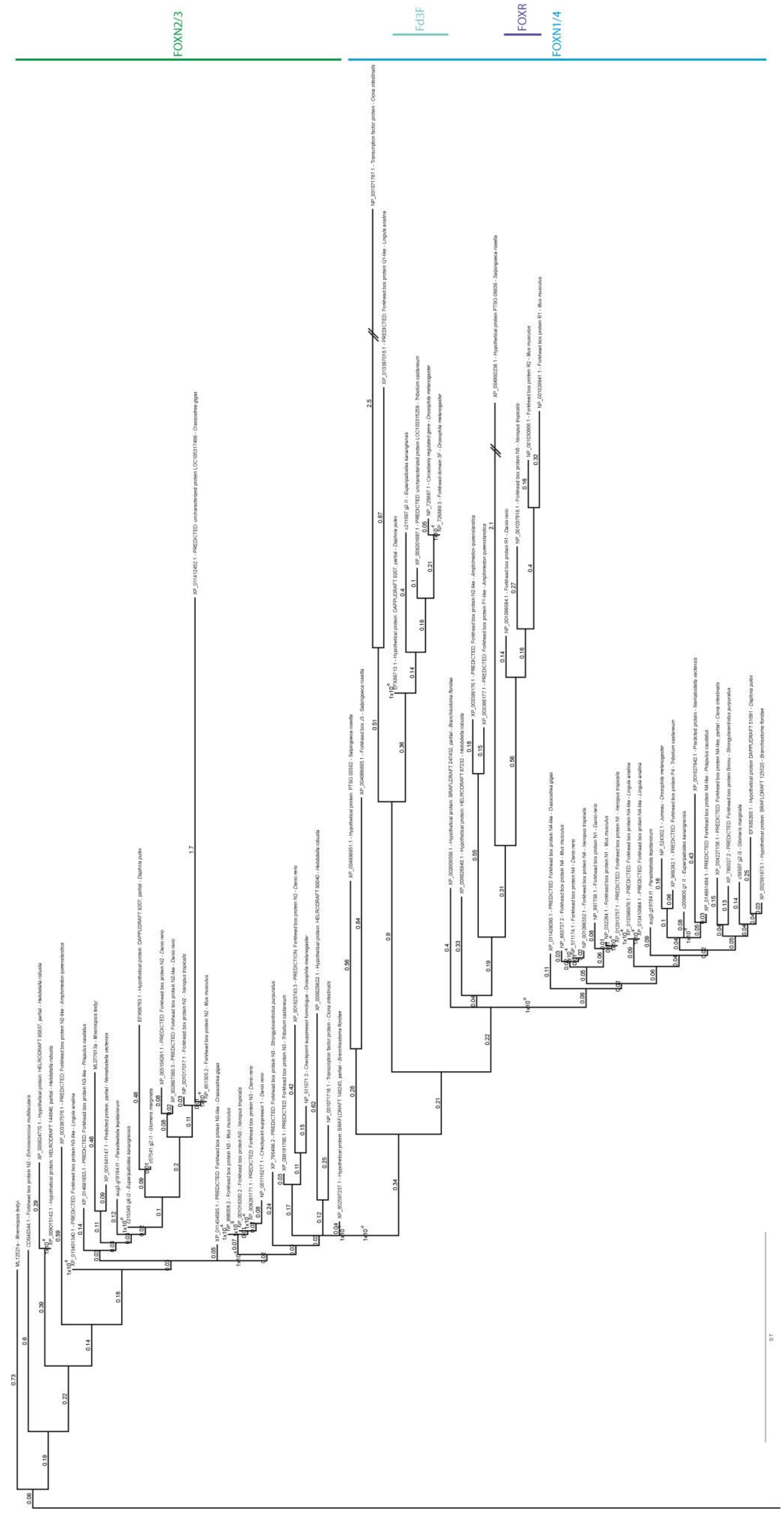
9.3.3.9 *FOXK*


XP_004988709.1 - Winged helix protein CWH5 - Salpingoeca rosetta
XP_004346423.1 - Forkhead box I1 - Capsaspora owczarzaki
XP_009022719.1 - Hypothetical protein: HELRODRAFT 162194 - Helobdella robusta
NP_001071788.1 - Transcription factor protein - Ciona intestinalis
XP_002594152.1 - Hypothetical protein BRAFLDRAFT 73584 - Branchiostoma floridae
XP_011447567.1 - PREDICTED: Forkhead box protein I1c-like - Crassostrea gigas
XP_003728863.2 - PREDICTED: uncharacterized protein LOC100889230, partial - Strongylocentrotus purpuratus
XP_011444080.1 - PREDICTED: uncharacterized protein LOC105339975 - Crassostrea gigas
XP_013410597.1 - PREDICTED: Forkhead box protein N1-like - Lingula anatina
XP_009015132.1 - Hypothetical protein: HELRODRAFT 171079 - Helobdella robusta
XP_009022981.1 - Hypothetical protein: HELRODRAFT 162577 - Helobdella robusta
XP_009022982.1 - Hypothetical protein: HELRODRAFT 162579 - Helobdella robusta
CUT99233.1 - Forkhead boc protein K2 - Echinococcus multilocularis
XP_003392087.1 - PREDICTED: Forkhead box protein K2-like, partial - Amphimedon queenslandica
XP_011405015.1 - PREDICTED: Forkhead box protein K1-like - Amphimedon queenslandica
XP_009016381.1 - Hypothetical protein: HELRODRAFT 77530 - Helobdella robusta
aug3.g27823.t1 - Parasteatoda tepidariorum
NP_001071715.1 - Transcription factor protein - Ciona intestinalis
XP_009013544.1 - Hypothetical protein: HELRODRAFT 74778 - Helobdella robusta
NP_951031.2 - Forkhead box protein K1 - Mus musculus
NP_956196.1 - Forkhead box protein K1 - Danio rerio
XP_002605066.1 - Hypothetical protein: BRAFLDRAFT 124136 - Branchiostoma floridae
XP_001629014.1 - Predicted protein, partial - Nematostella vectensis
XP_011247520.1 - PREDICTED: Forkhead box protein K2 - Mus musculus
NP_001135634.1 - Forkhead box protein K2 - Xenopus tropicalis
XP_001922656.1 - PREDICTED: Forkhead box protein K2 - Danio rerio
NP_001164186.1 - Forkhead box protein K2 - Danio rerio
XP_013396208.1 - PREDICTED: Forkhead box protein K2-like - Lingula anatina
XP_014677184.1 - PREDICTED: Forkhead box protein K2-like - Priapulus caudatus
XP_011418099.1 - PREDICTED: Forkhead box protein K2-like - Crassostrea gigas
EFX68742.1 - Hypothetical protein: DAPPUDRAFT 332896 - Daphnia pulex
c214392 g4 i2 - Euperipatoides kanangrensis
c 56808 g2 i1 - Glomeris marginata
aug3.g15476.t1 - Parasteatoda tepidariorum
XP_968795.2 - PREDICTED: Forkhead box protein K1 - Tribolium castaneum
NP_001261701.1 - Forkhead box K - Drosophila melanogaster
XP_009028926.1 - Hypothetical protein: HELRODRAFT 137899, partial - Helobdella robusta
CDI97763.1 - Forkhead box protein K1 - Echinococcus multilocularis
ML025018a - Mnemiopsis leidyi
XP_793339.3 - PREDICTED: Forkhead box protein K2 - Strongylocentrotus purpuratus
0.7

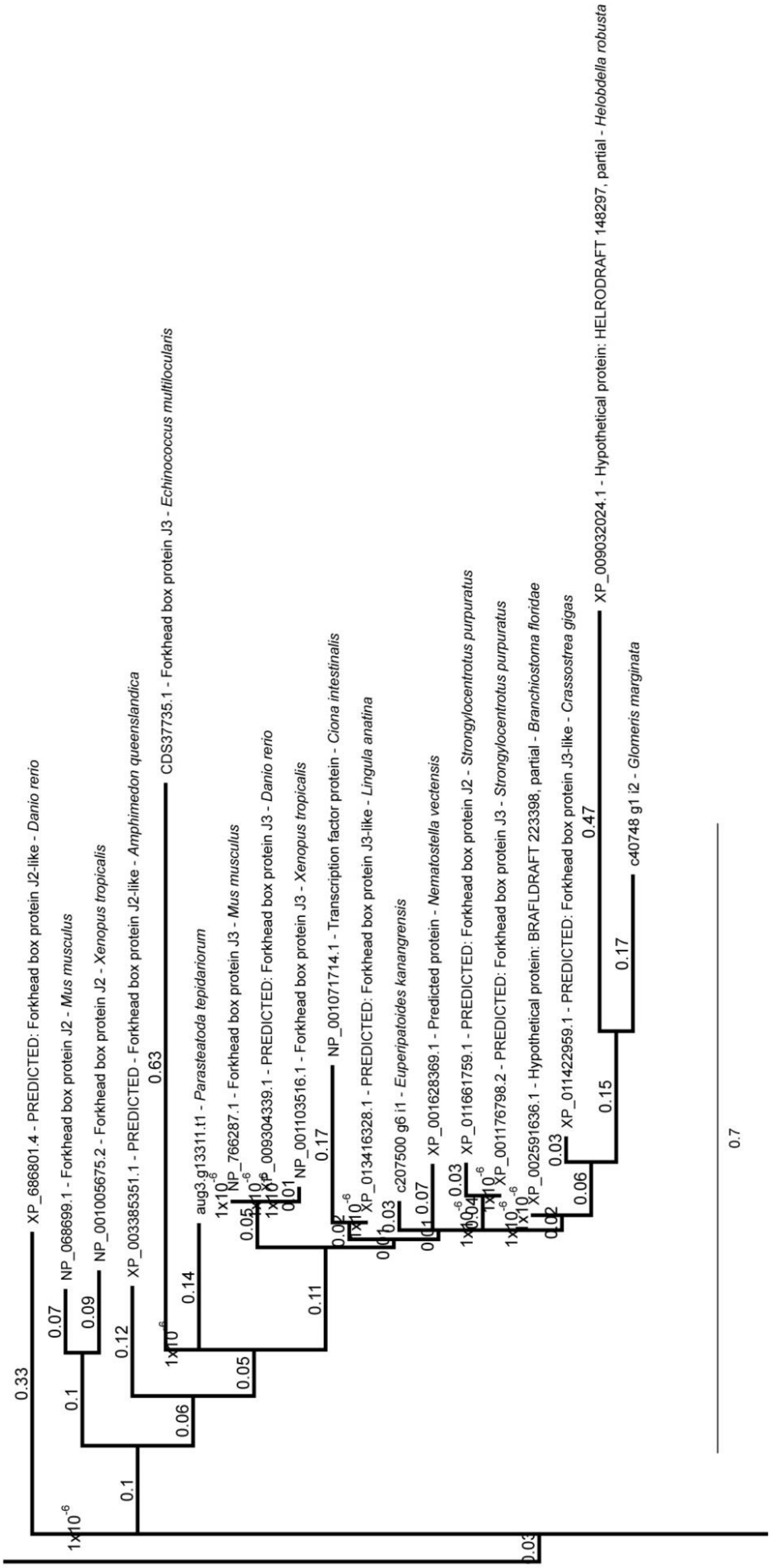
9.3.3.10 *FOXM*


FOXM
0.6
XP_004998409.1 - Hypothetical protein: PTSG 00936 - *Salpingoeca rosetta*
0.25
XP_001624739.1 - Predicted protein, partial - *Nematostella vectensis*
0.27
XP_011434081.1 - PREDICTED: Forkhead box protein M1-like - *Crassostrea gigas*
0.18
XP_013404303.1 - PREDICTED: uncharacterized protein LOC10616939 - *Lingula anatina*
0.75
c200914 g1 i1 - *Euperipatoides kanangrensis*
0.04
XP_002941428.1 - PREDICTED: Forkhead box protein M1 - *Xenopus tropicalis*
0.25
NP_957391.1 - Forkhead box protein M1 - *Danio rerio*
0.03
NP_032047.4 - Forkhead box protein M1 - *Mus musculus*
0.08
XP_002608493.1 - Hypothetical protein: BRAFLDRAFT 232011, partial - *Branchiostoma floridae*
0.25
NP_001071993.1 - Transcription factor protein - *Ciona intestinalis*
0.39
XP_797015.2 - PREDICTED: uncharacterized protein LOC576632 - *Strongylocentrotus purpuratus*
0.7
XP_014675728.1 - PREDICTED: Forkhead box protein M1-like - *Priapulus caudatus*
1
XP_011402861.1 - PREDICTED: Forkhead box protein A2b-like - *Amphimedon queenslandica*
1.6
XP_004996854.1 - Hypothetical protein: PTSG 02366 - *Salpingoeca rosetta*
0.4
XP_004364634.2 - Hypothetical protein: CAOG 01766 - *Capsaspora owczarzaki*
0.35
0.16
0.06
0.25
0.26
0.05
0.21
0.06
0.09
0.2
0.22
0.05
0.12
0.14
0.7

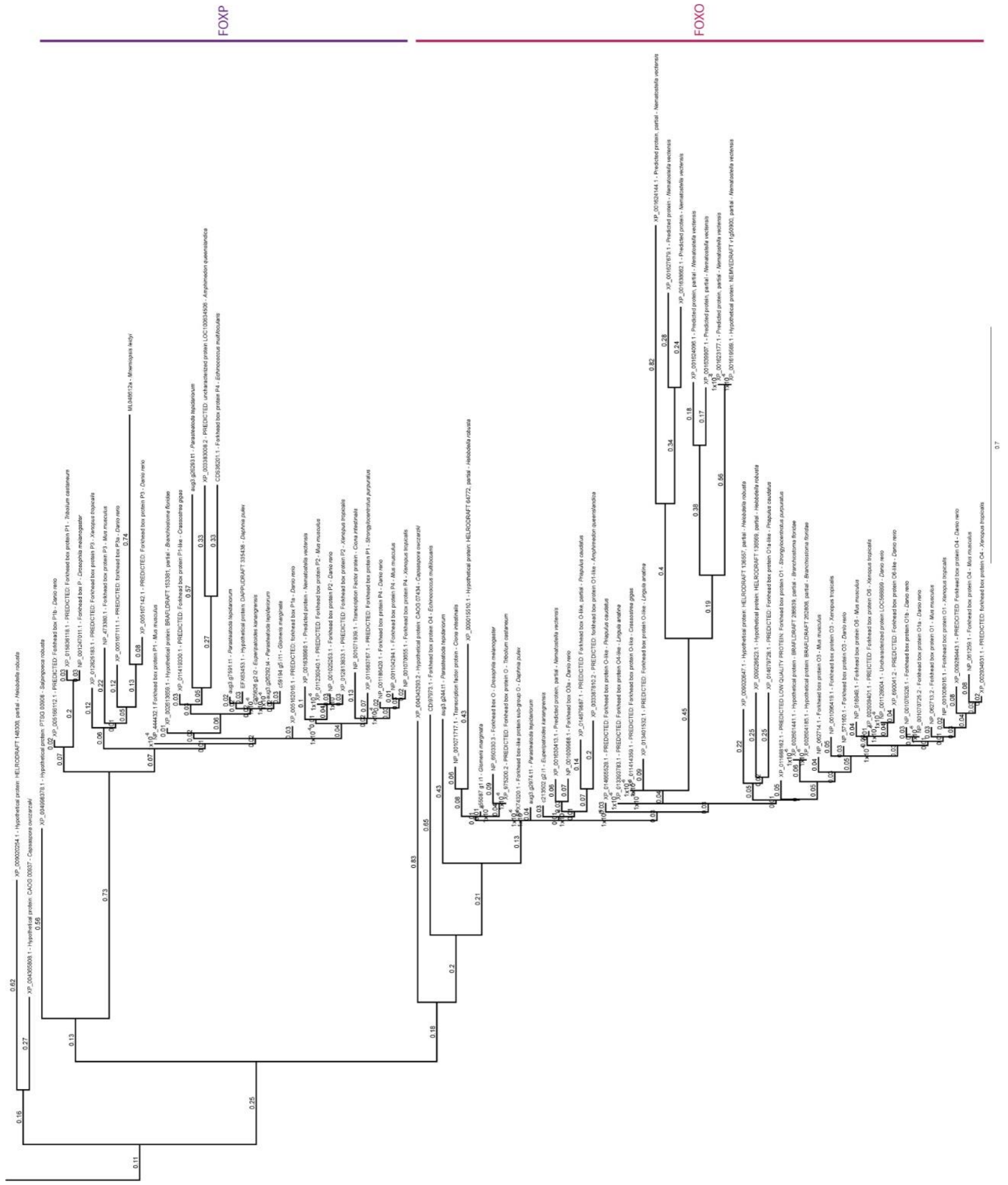
9.3.3.11 *FOXN1/4 FOXN2/3 FOXR Fd3F*



9.3.3.12 *FOXJ2/3*

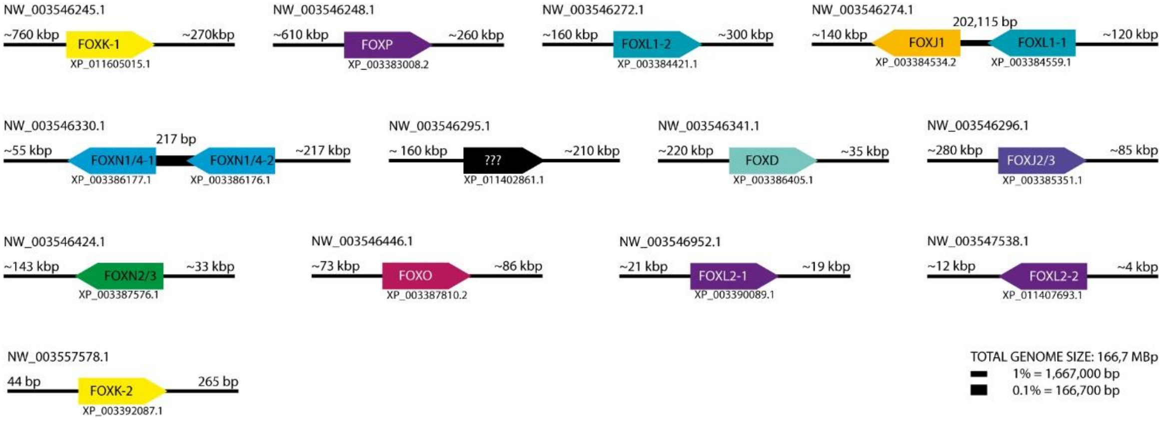


9.3.3.13 *FOXP FOXO*

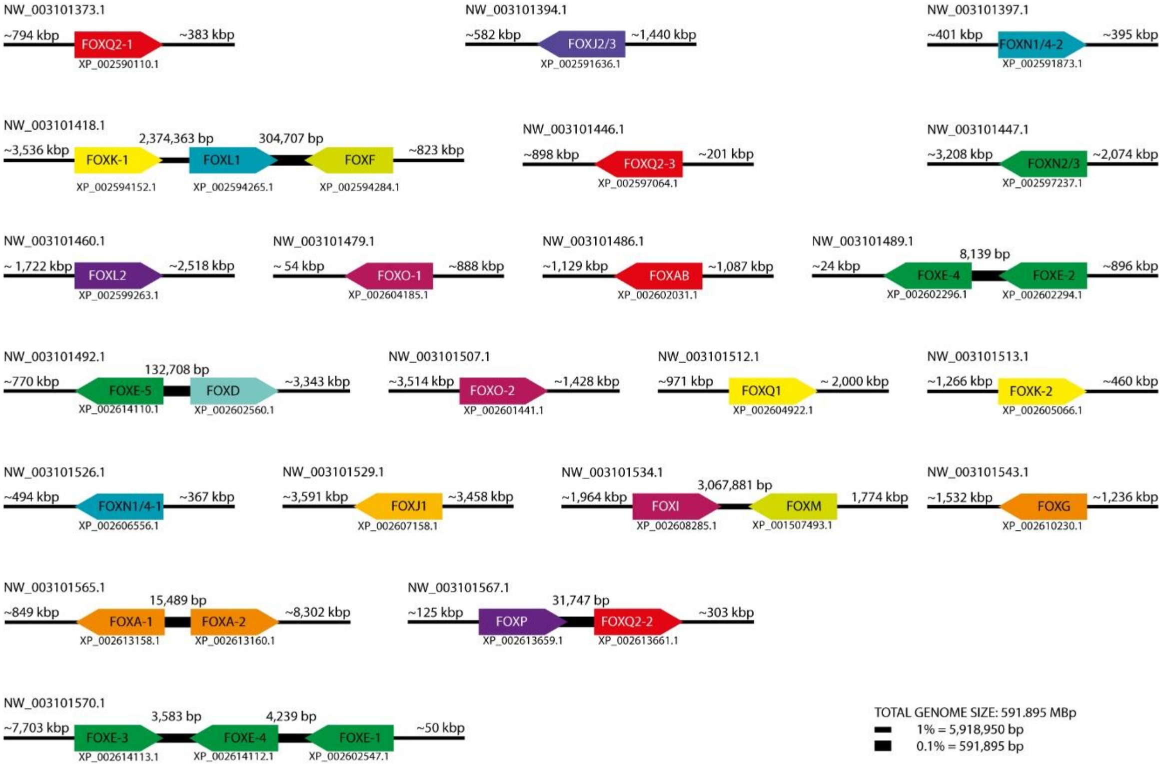


9.3.4 Genomic organization of forkhead genes

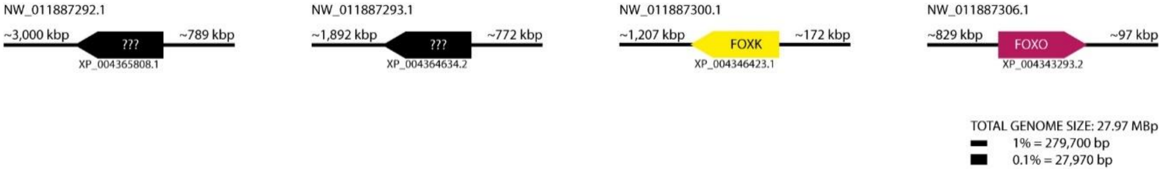
9.3.4.1 *Amphimedon queenslandica*



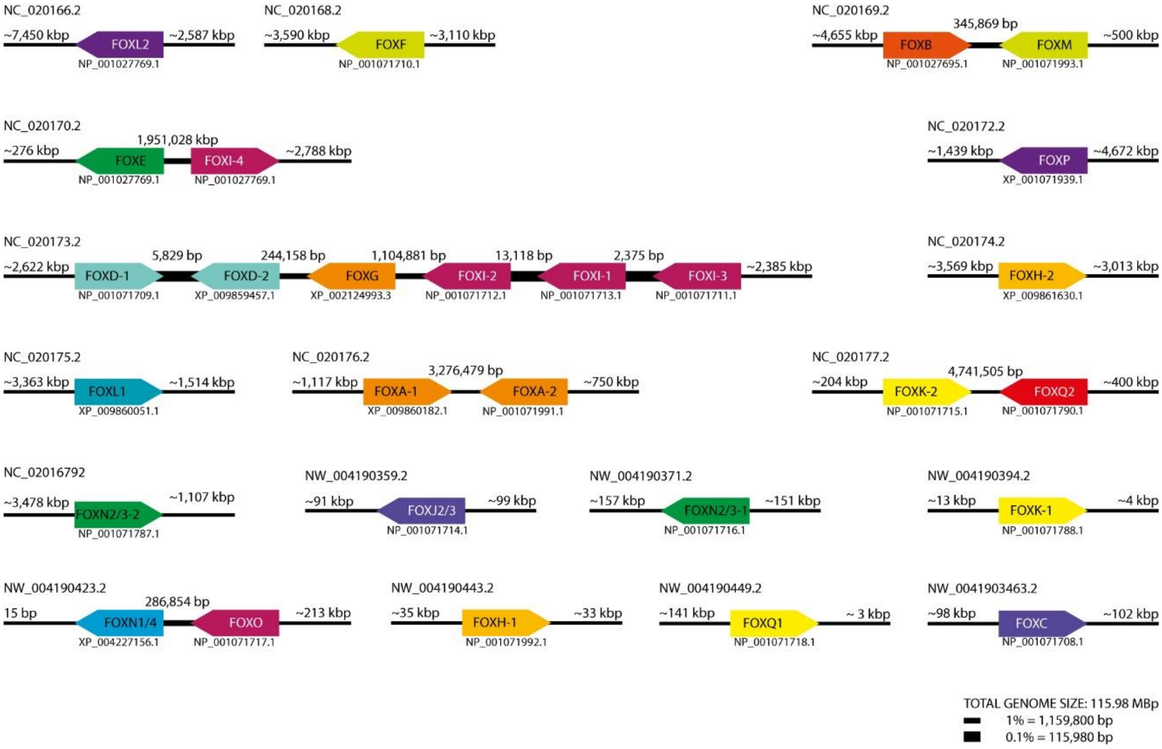
9.3.4.2 *Branchiostoma floridae*



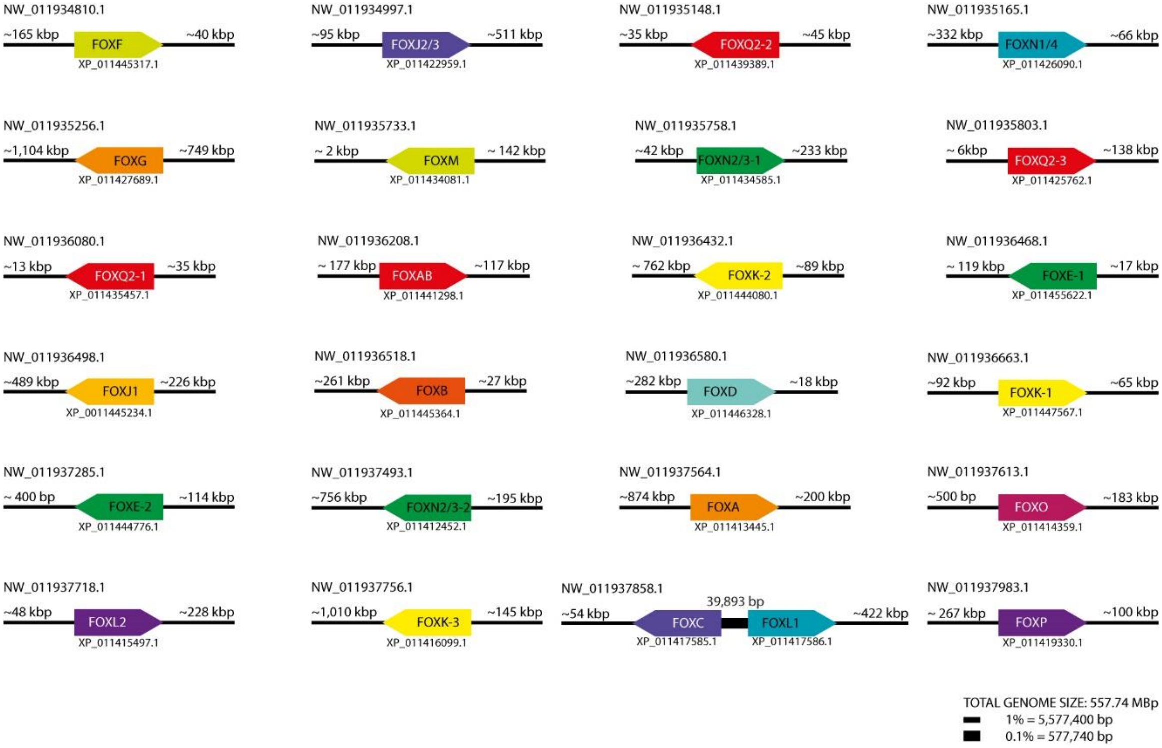
9.3.4.3 *Capsaspora owzarzaki*



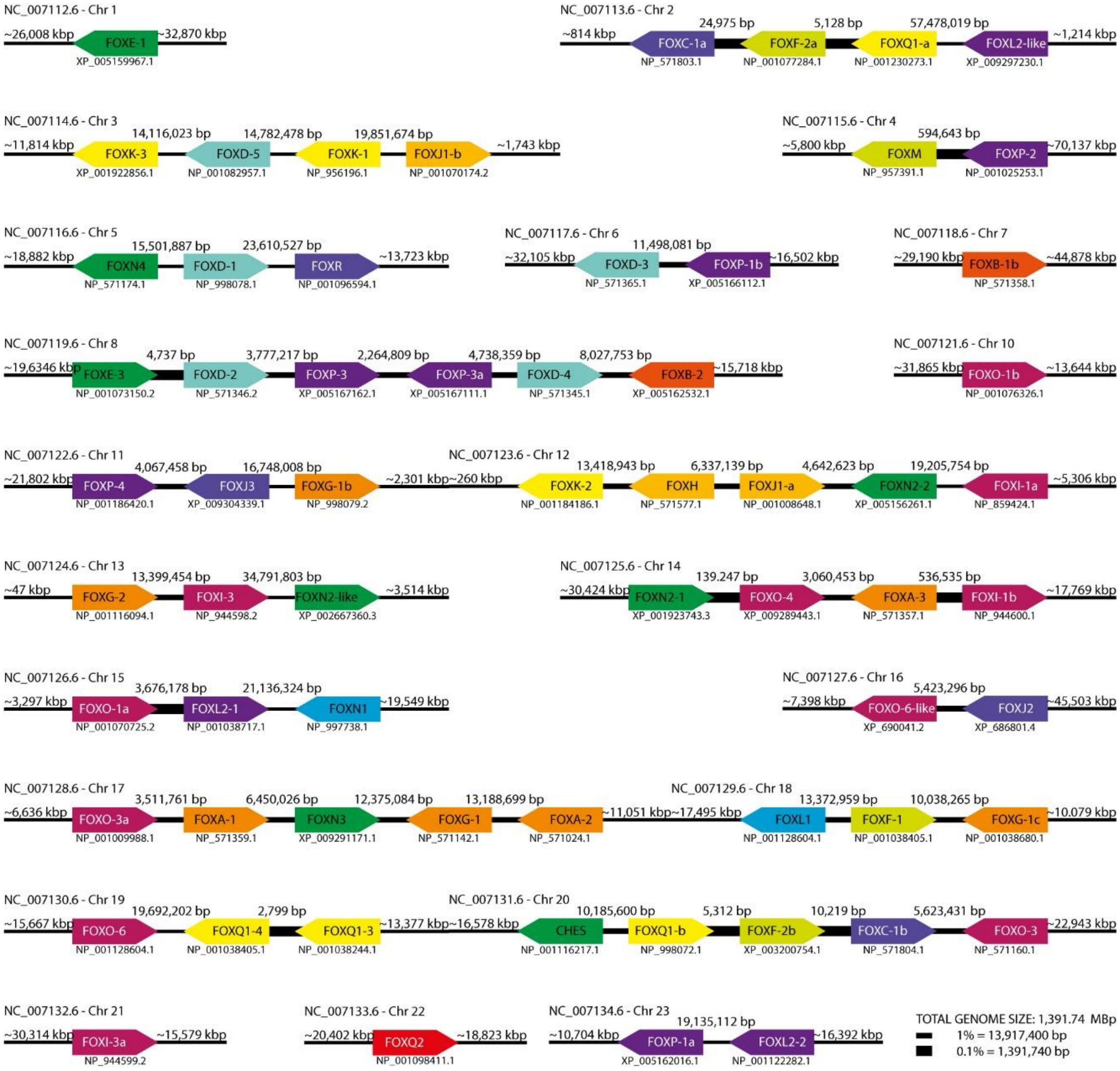
9.3.4.4 *Ciona intestinalis*



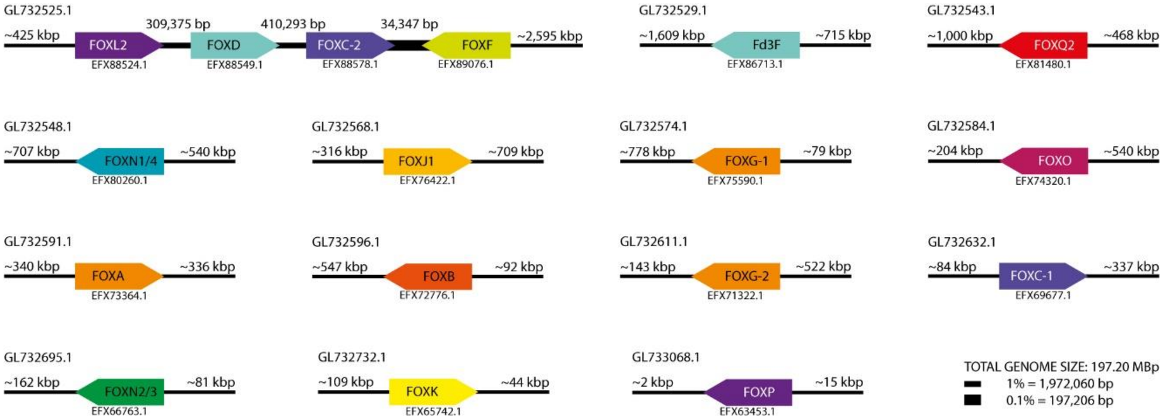
9.3.4.5 *Crassostrea gigas*



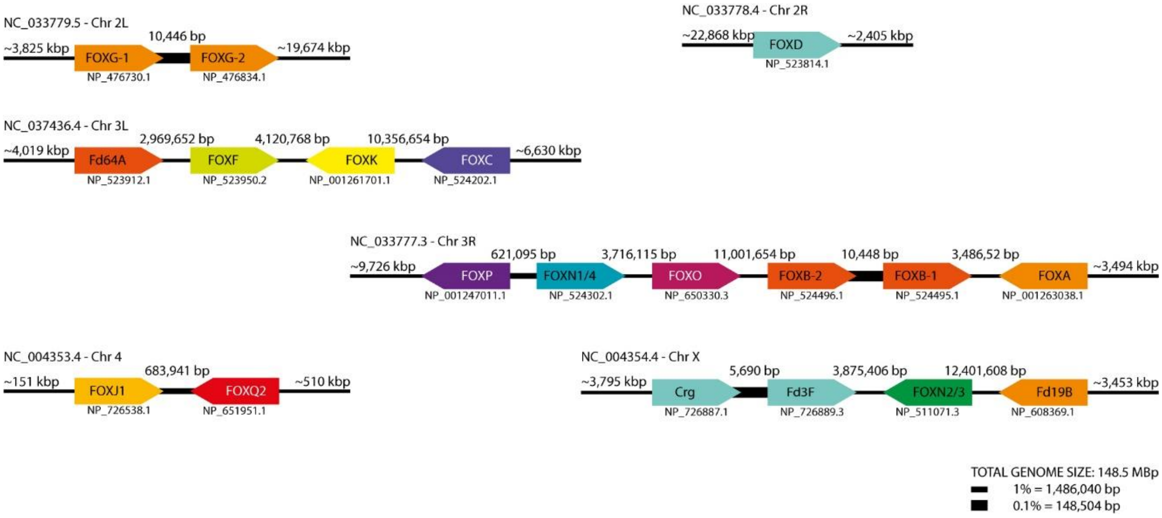
9.3.4.6 *Danio rerio*



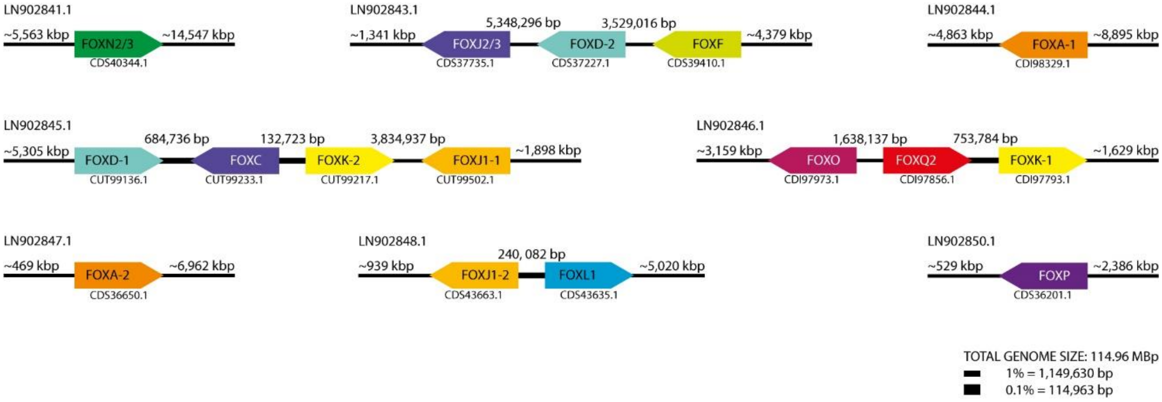
9.3.4.7 *Daphnia pulex*



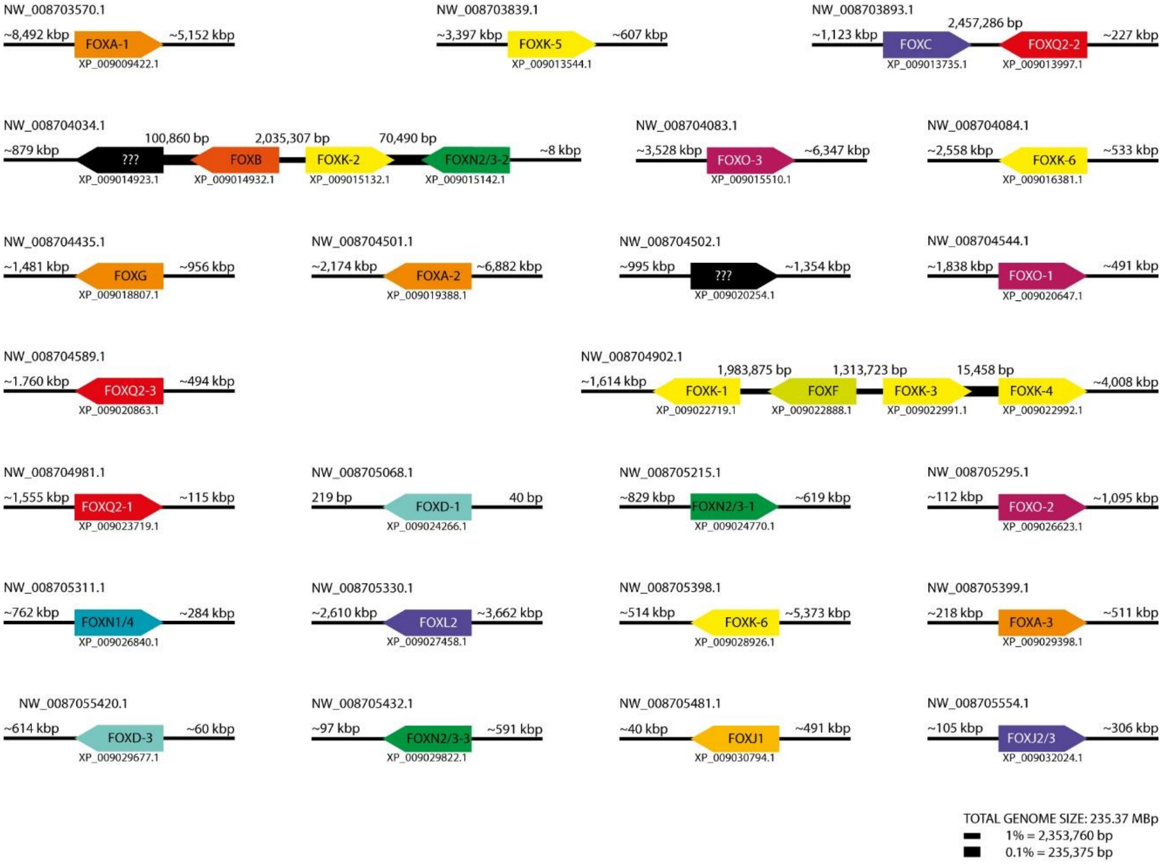
9.3.4.8 *Drosophila melanogaster*



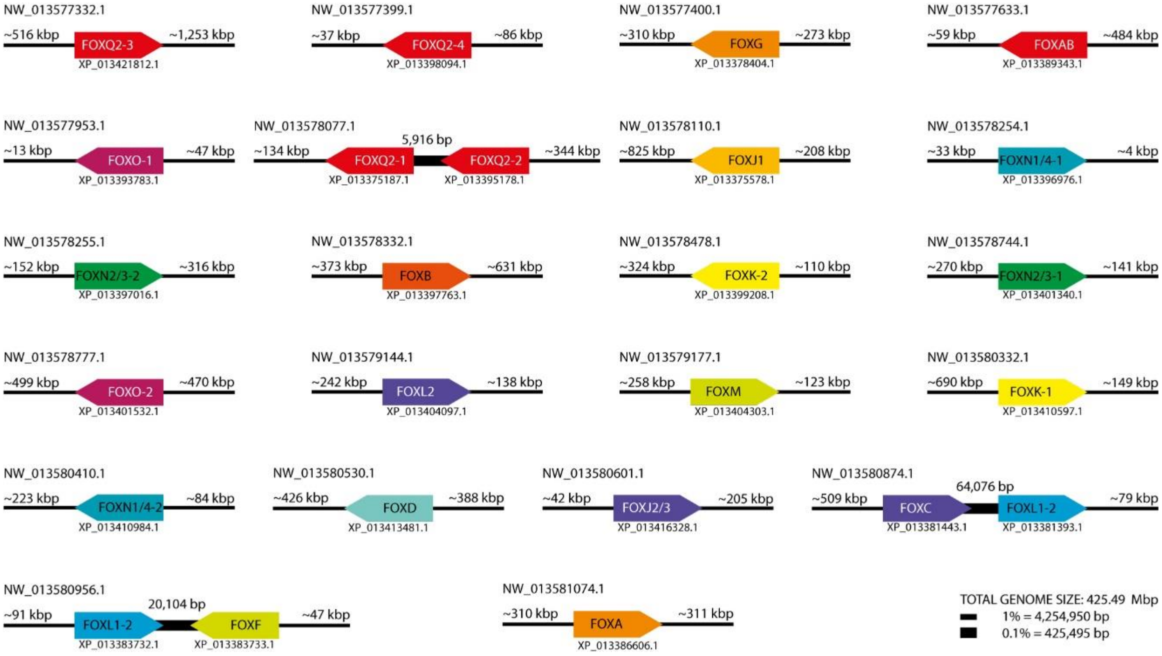
9.3.4.9 *Echinococcus multilocularis*



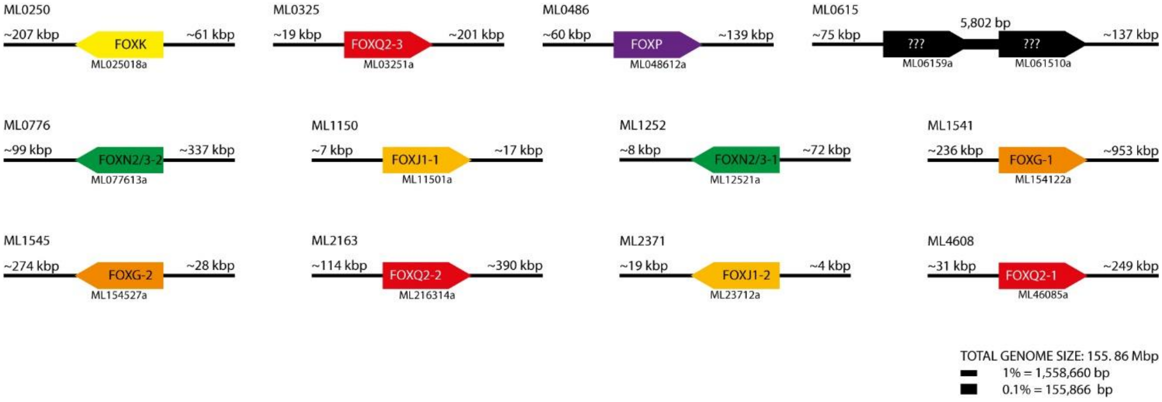
9.3.4.10 *Helobdella robusta*



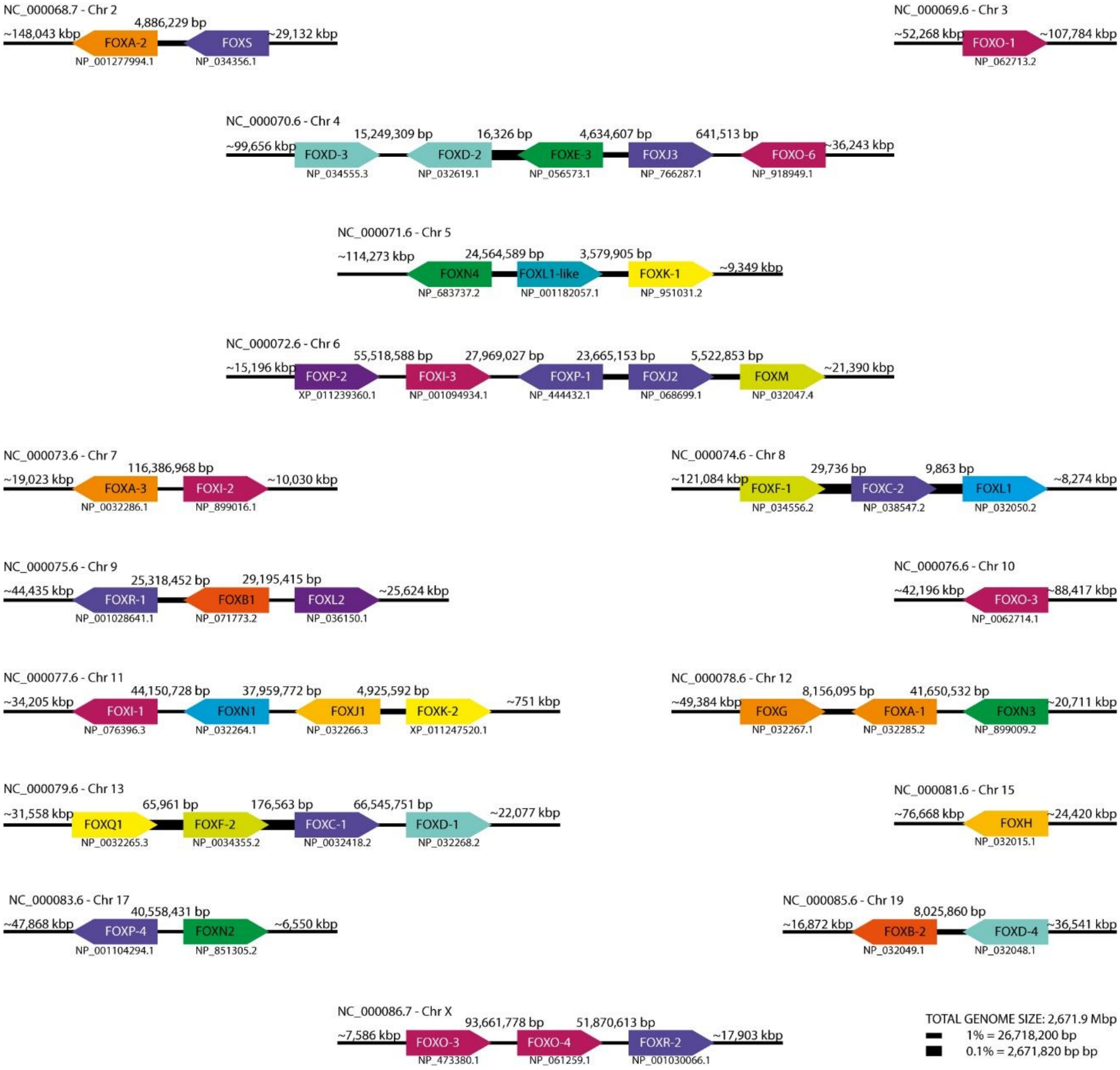
9.3.4.11 *Lingula anatine*



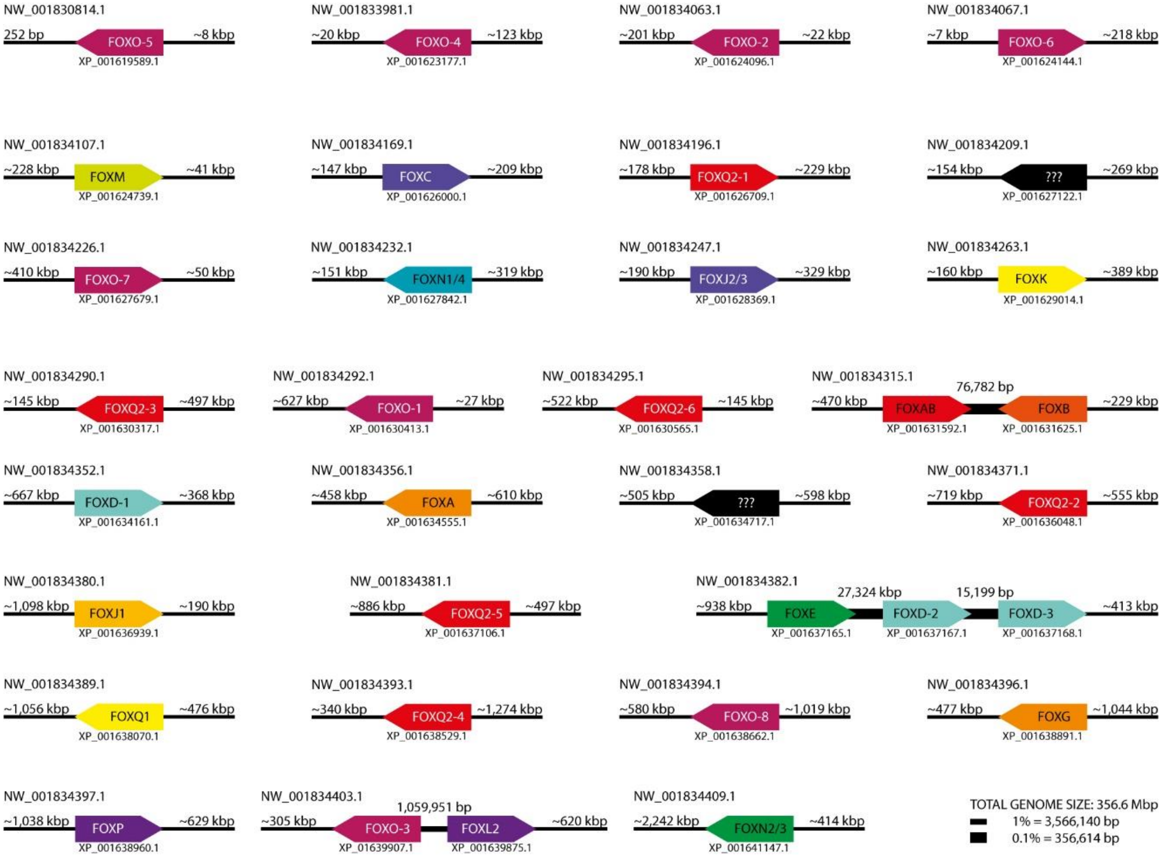
9.3.4.12 *Mnemiopsis leidyi*



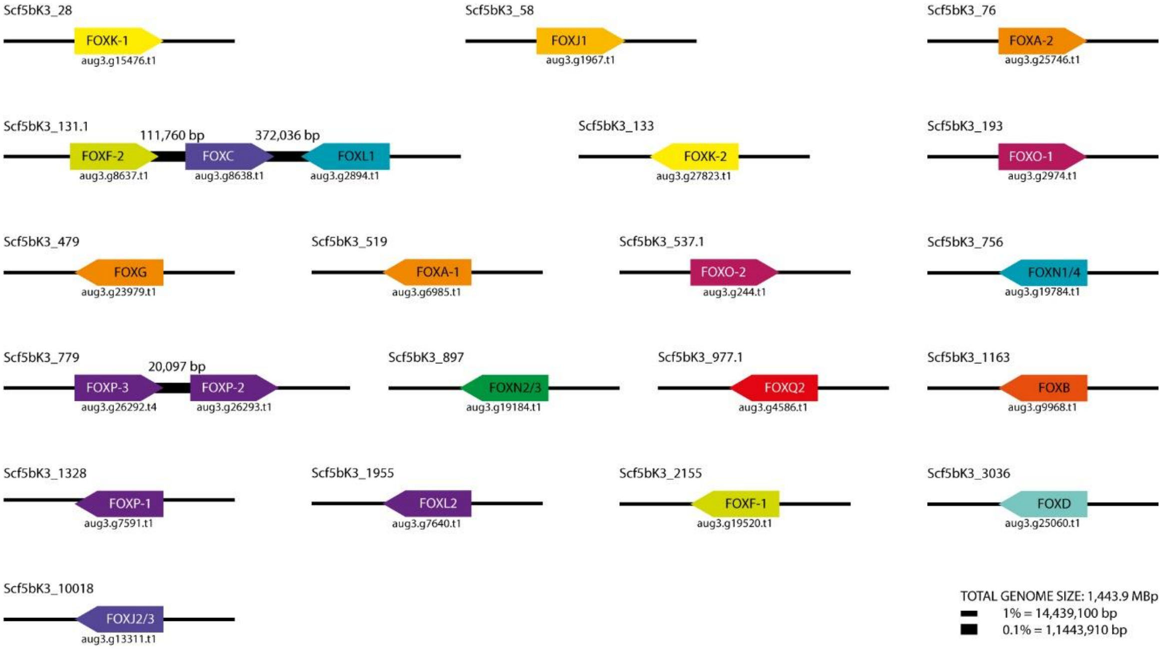
9.3.4.13 *Mus musculus*



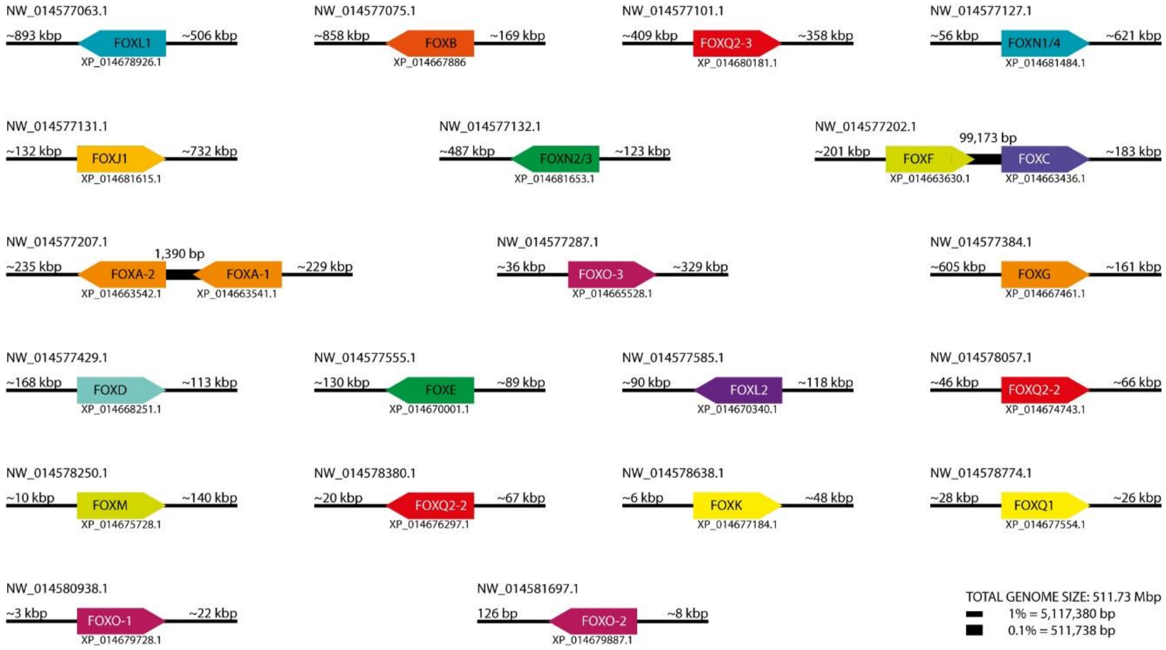
9.3.4.14 *Nematostella vectensis*



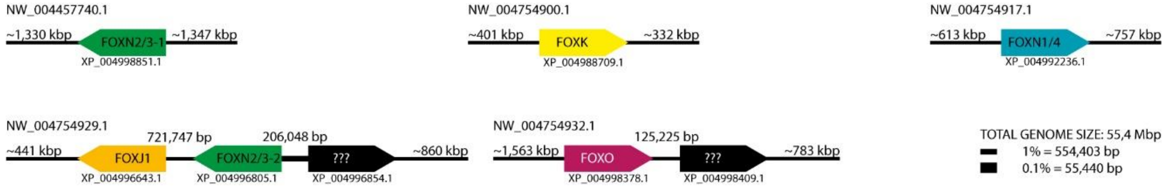
9.3.4.15 *Parasteatoda tepidariorum*



9.3.4.16 *Priapulus caudatus*

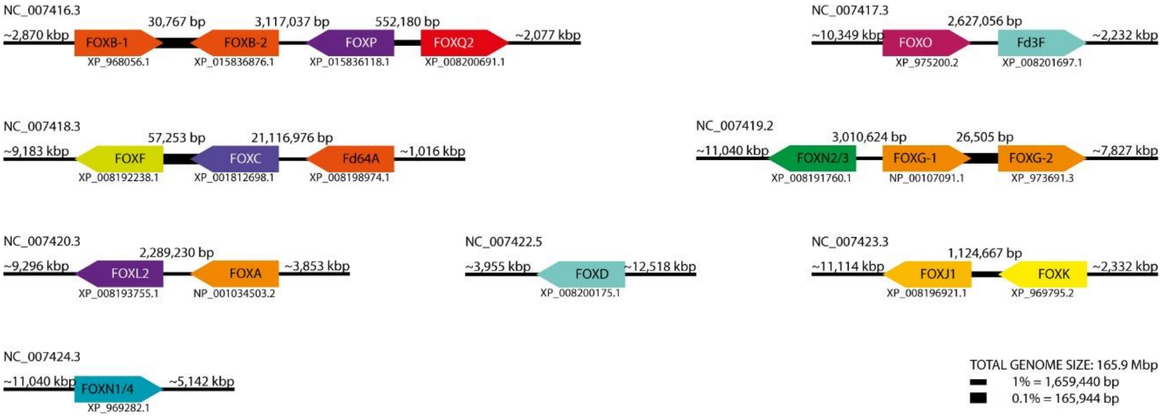


9.3.4.17 *Salpingoeca rosetta*

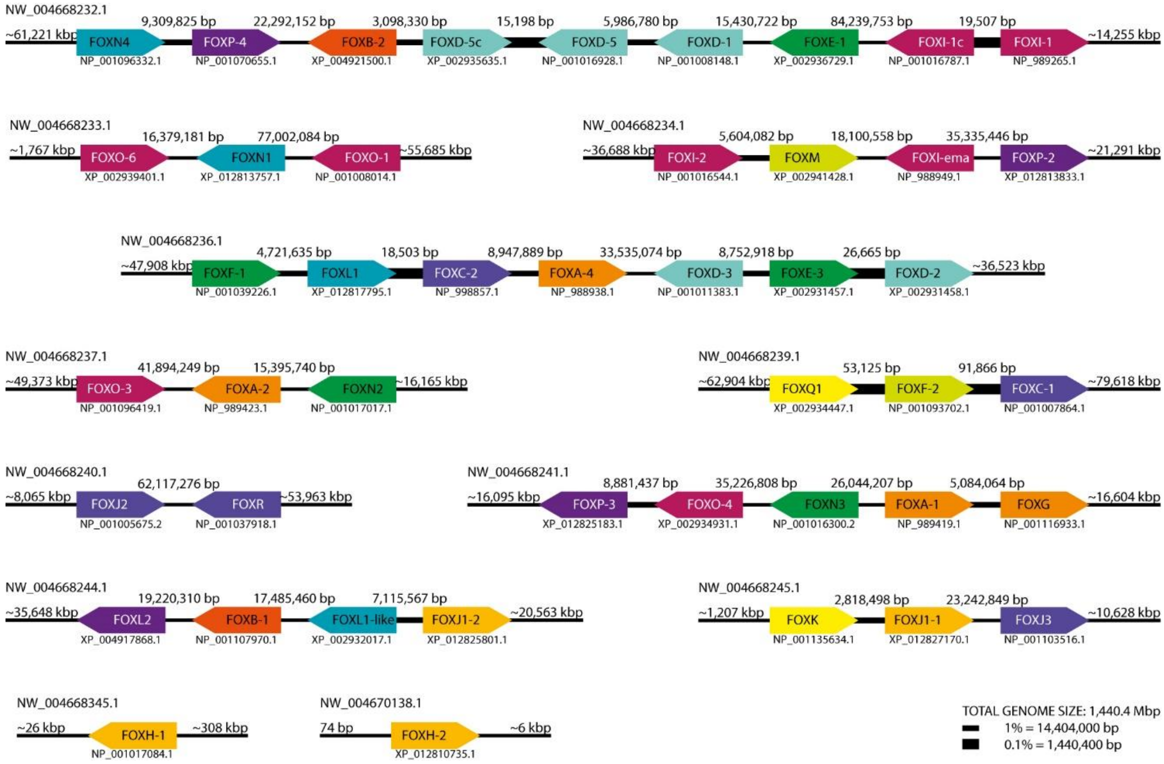


9.3.4.18 *Strongylocentrotus purpuratus*

9.3.4.19 *Tribolium castaneum*



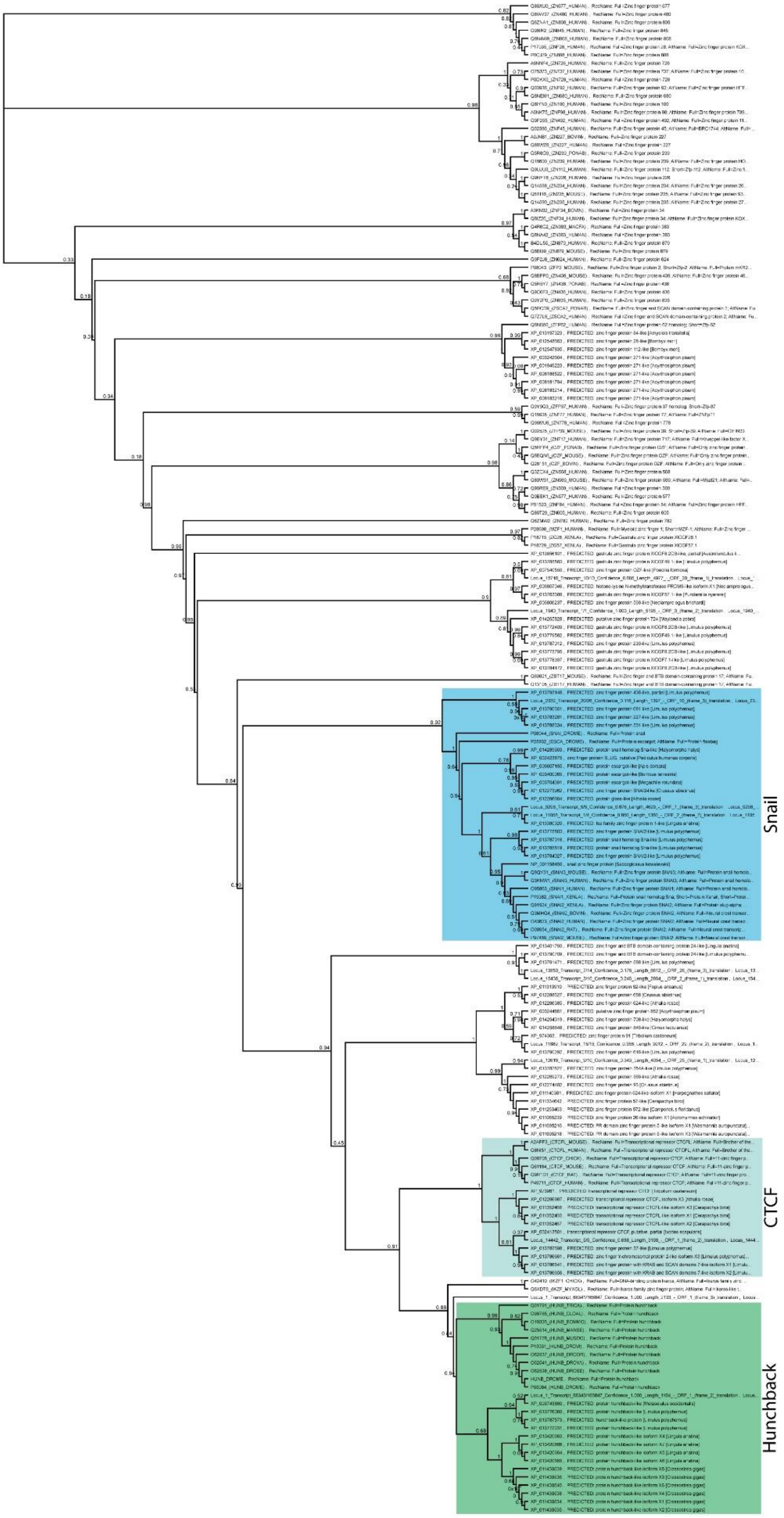
9.3.4.20 *Xenopus tropicalis*



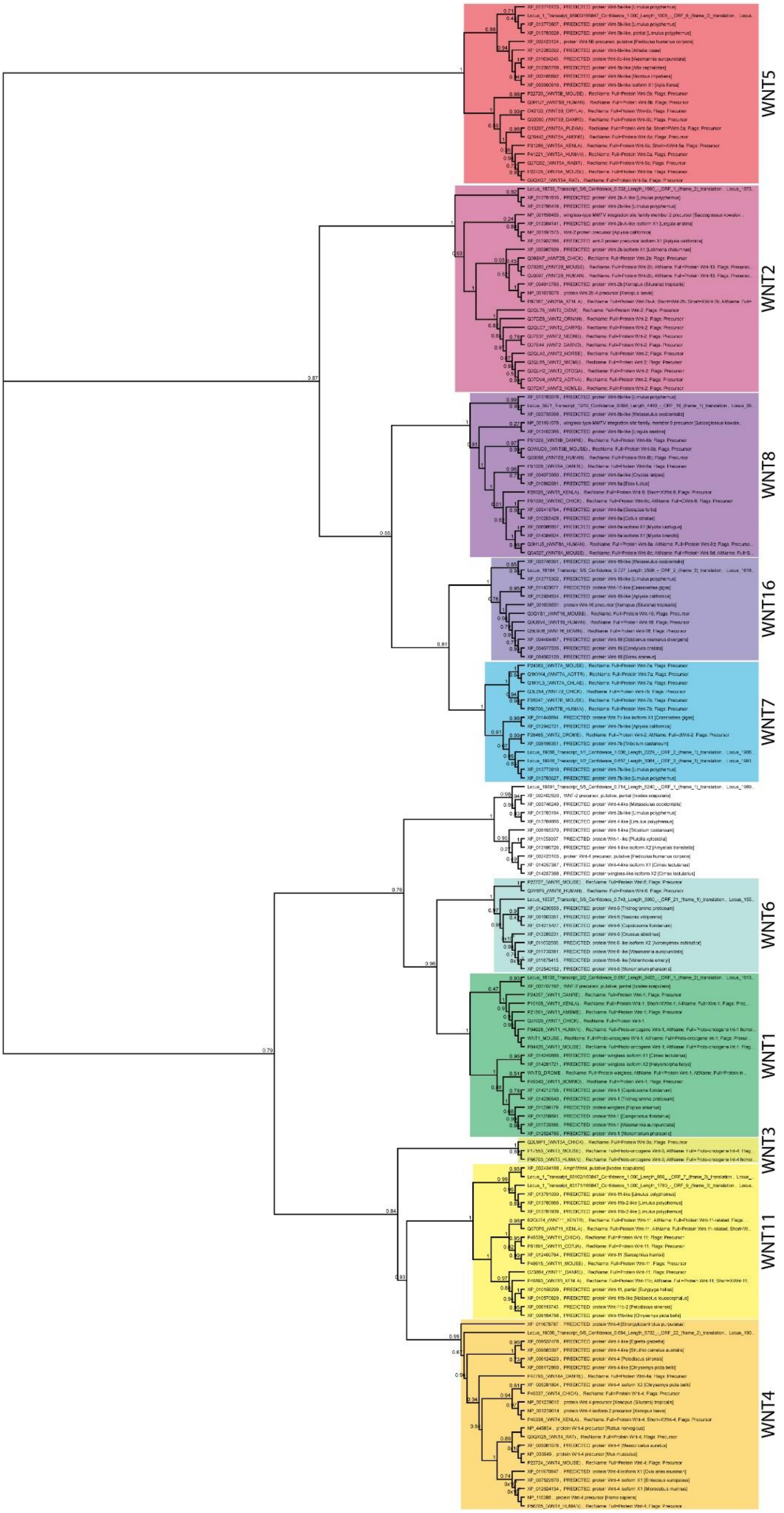
9.4 Embryonic development of the pedipalp of *Parasteatoda tepidariorum*

9.4.1 Phylogenetic trees

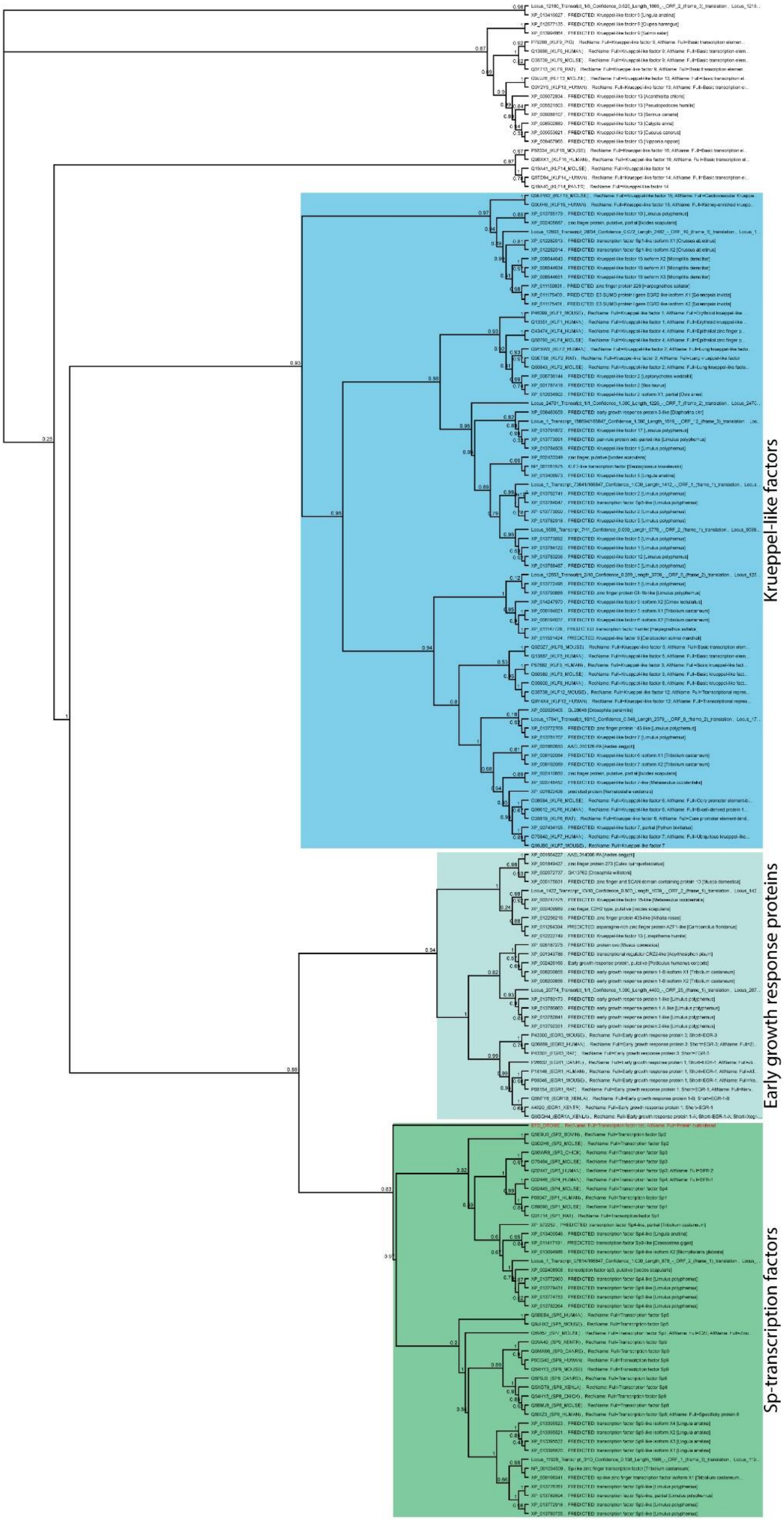
9.4.1.1 *Hunchback*



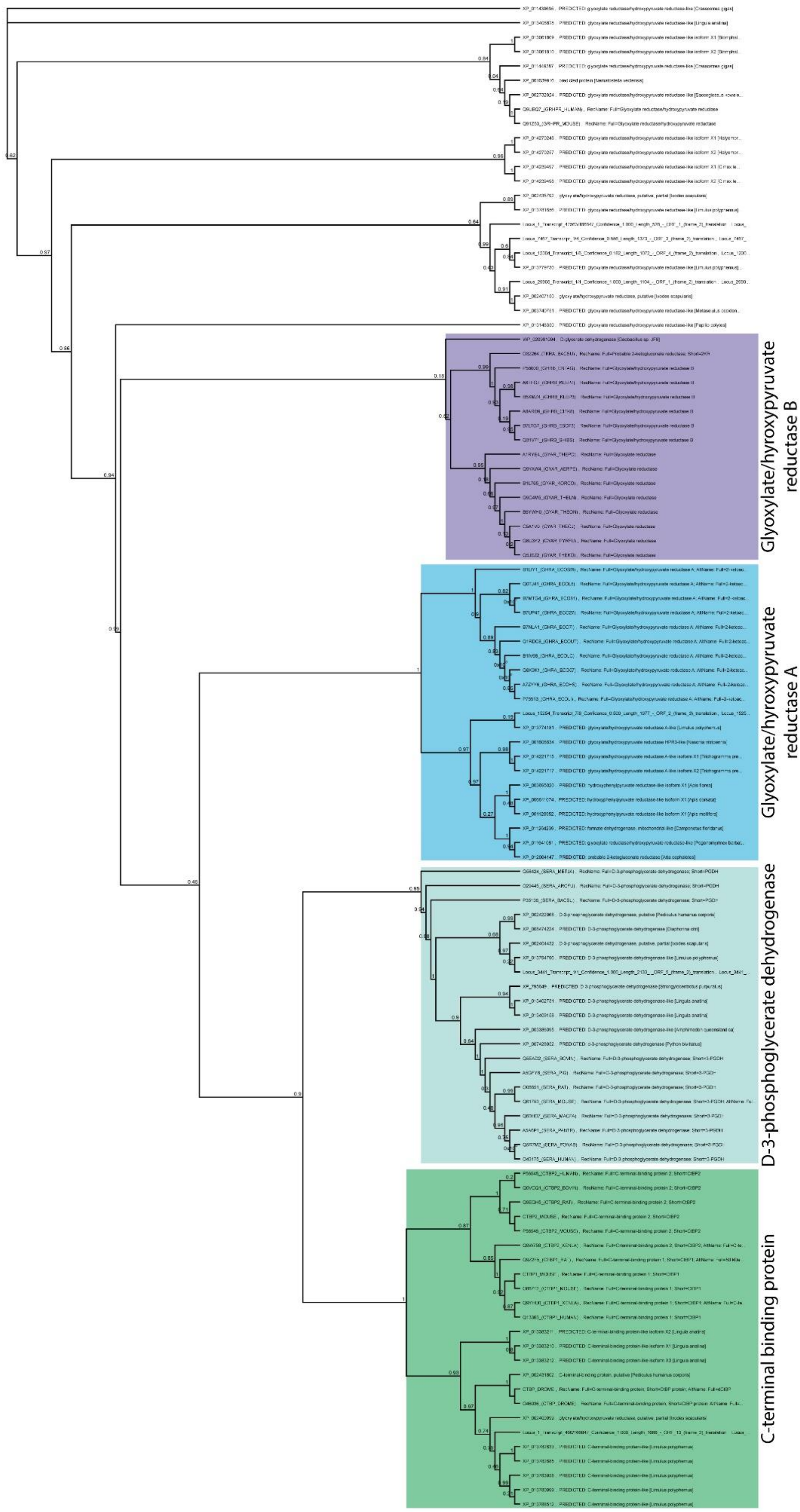
9.4.1.2 *Wingless*



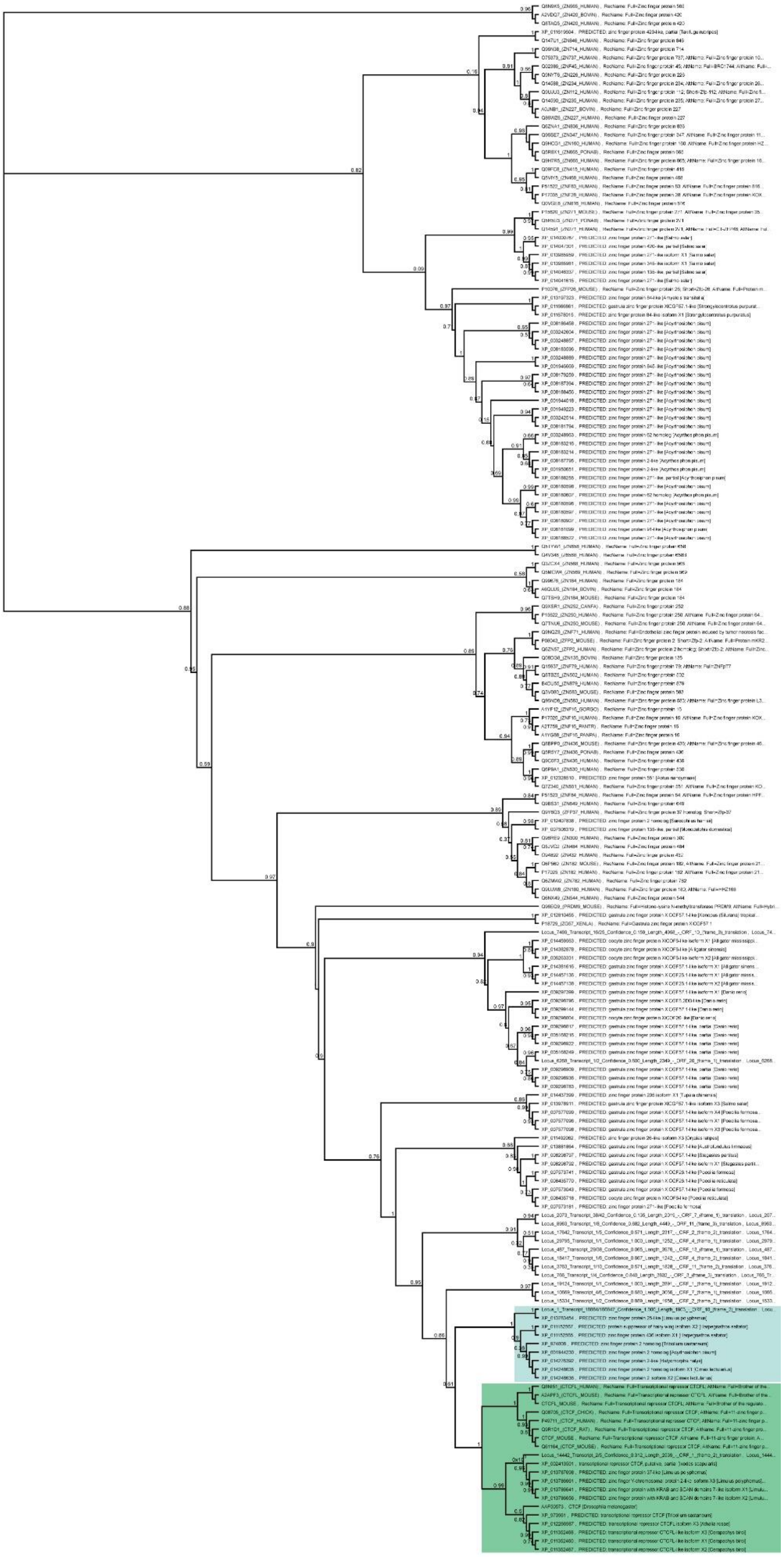
9.4.1.3 *Buttonhead*



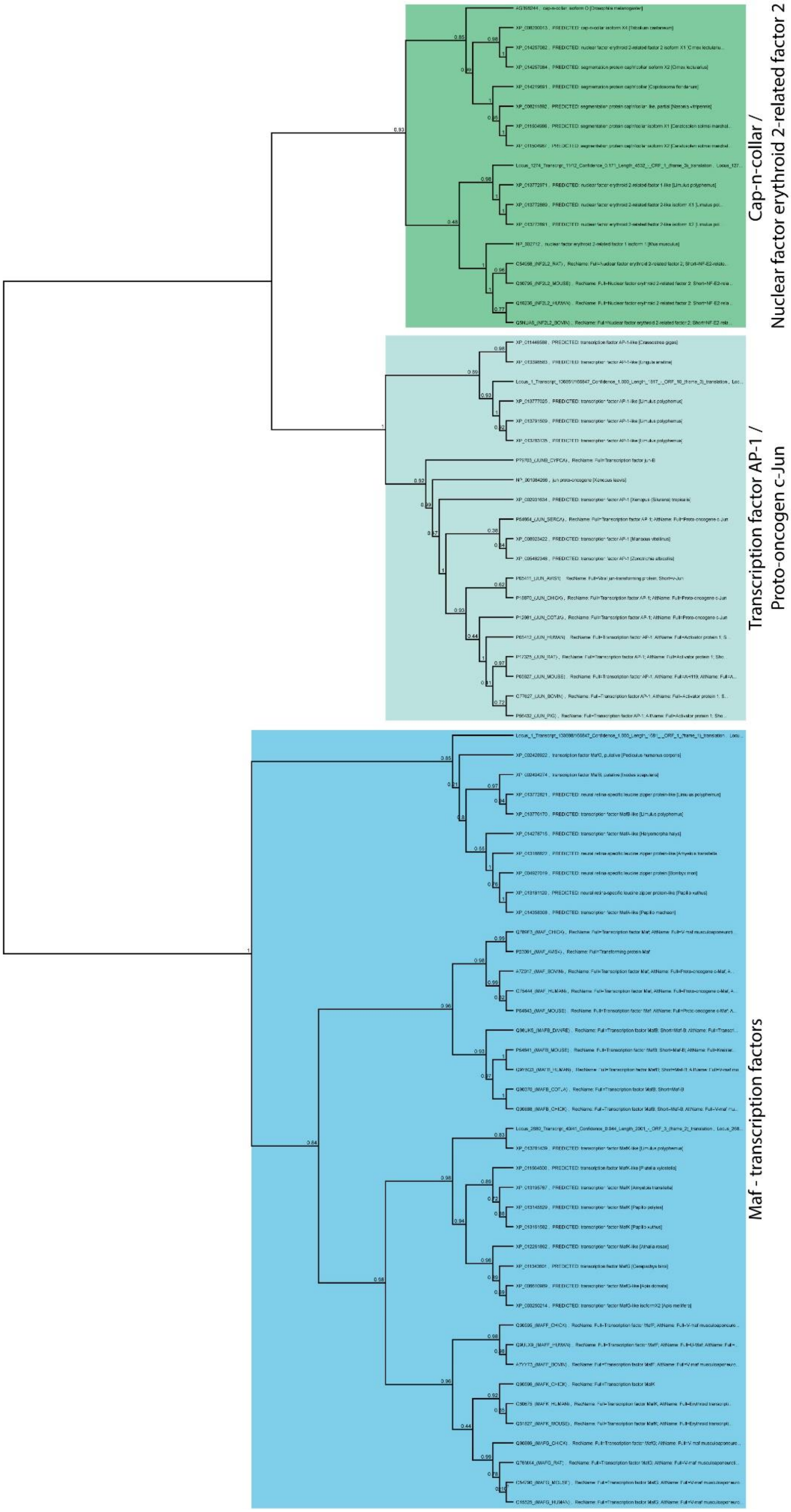
9.4.1.4 *CtBP*


Glyoxylate/hyroxypyruvate reductase B
Glyoxylate/hyroxypyruvate reductase A
D-3-phosphoglycerate dehydrogenase
C-terminal binding protein

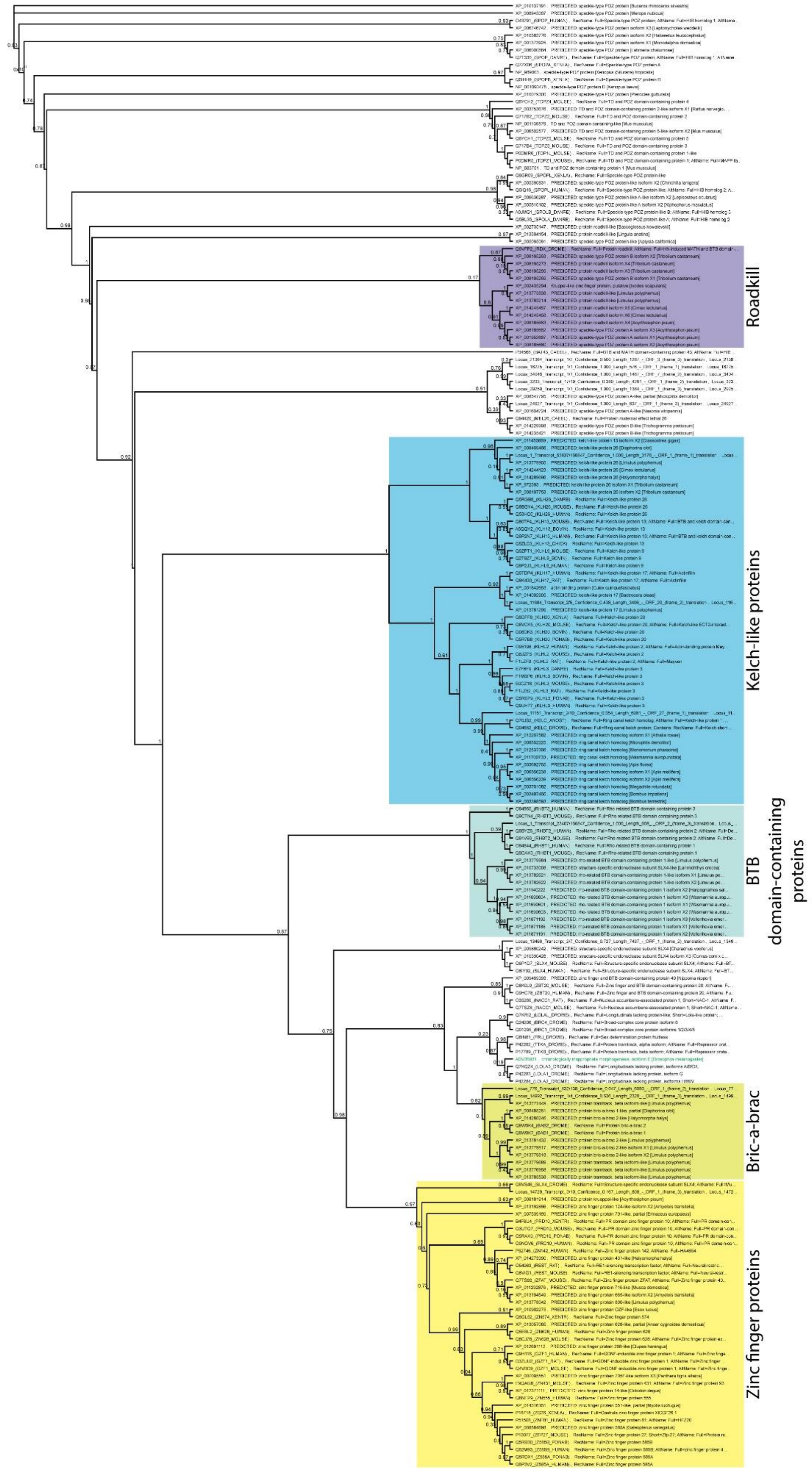
9.4.1.5 *CTCF*



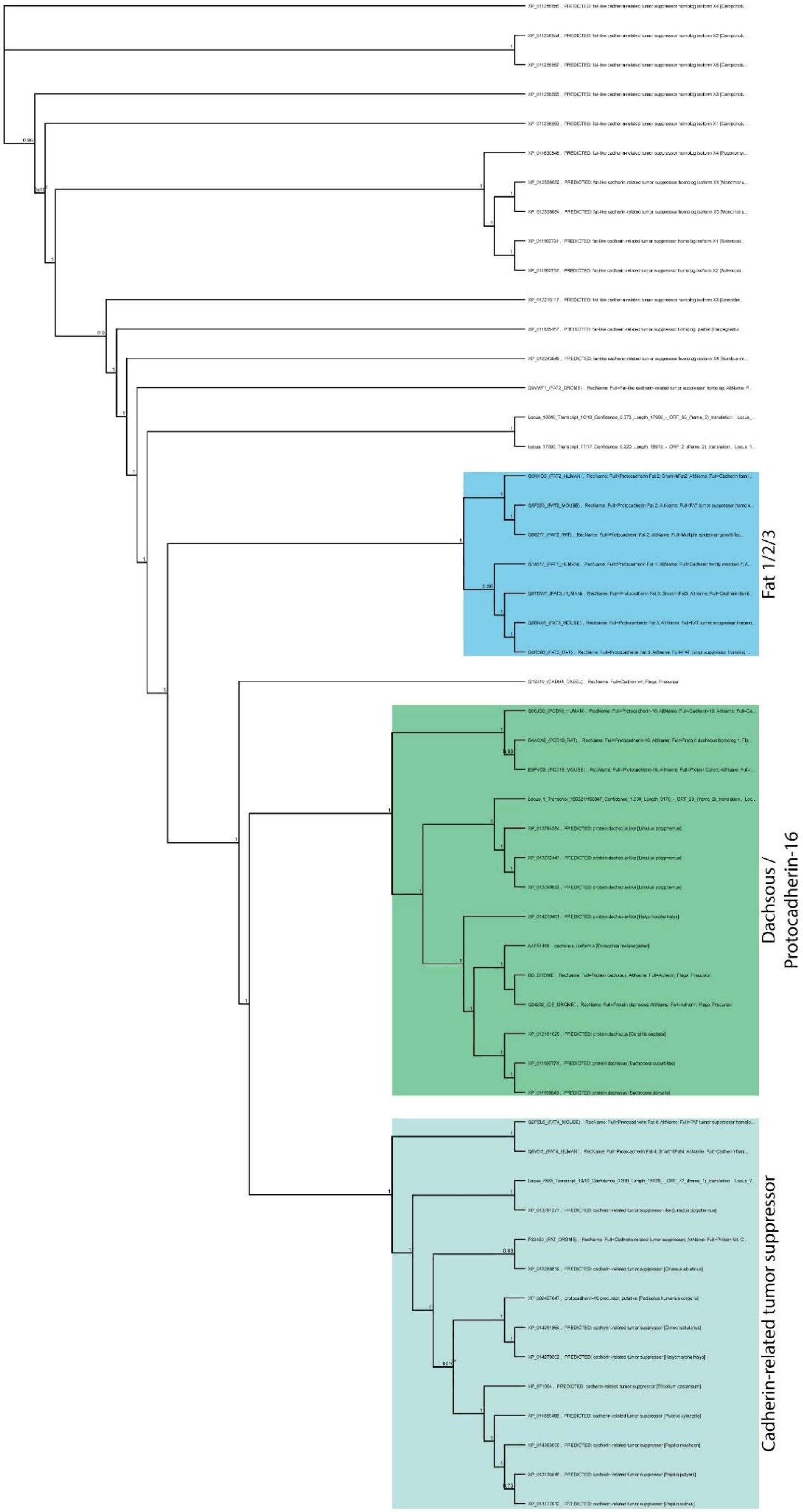
9.4.1.6 *Cap-n-Collar*



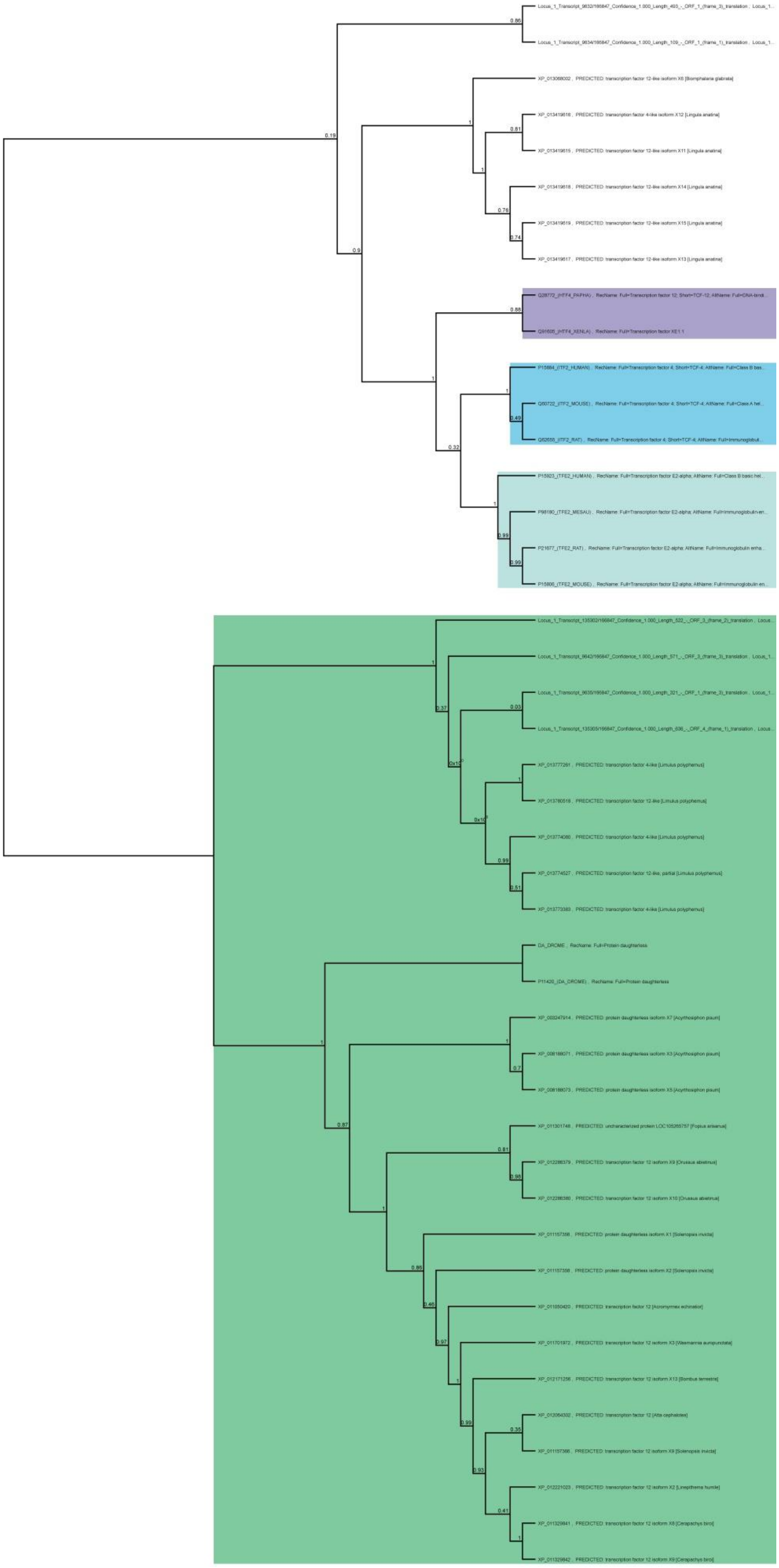
9.4.1.7 *Chinmo*


Roadkill
Kelch-like proteins
BTB domain-containing proteins
Bric-a-brac
Zinc finger proteins

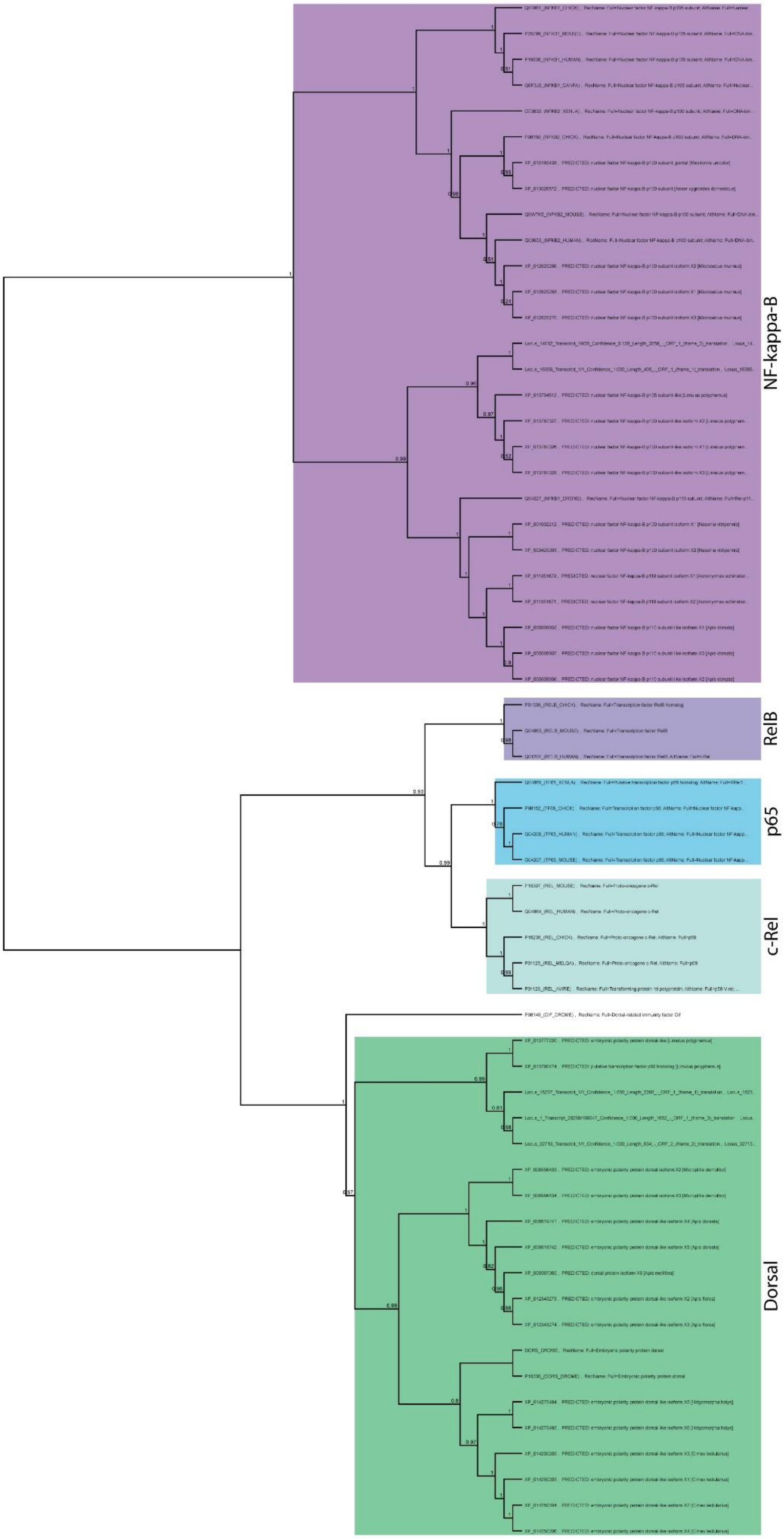
9.4.1.8 *Dachsous*



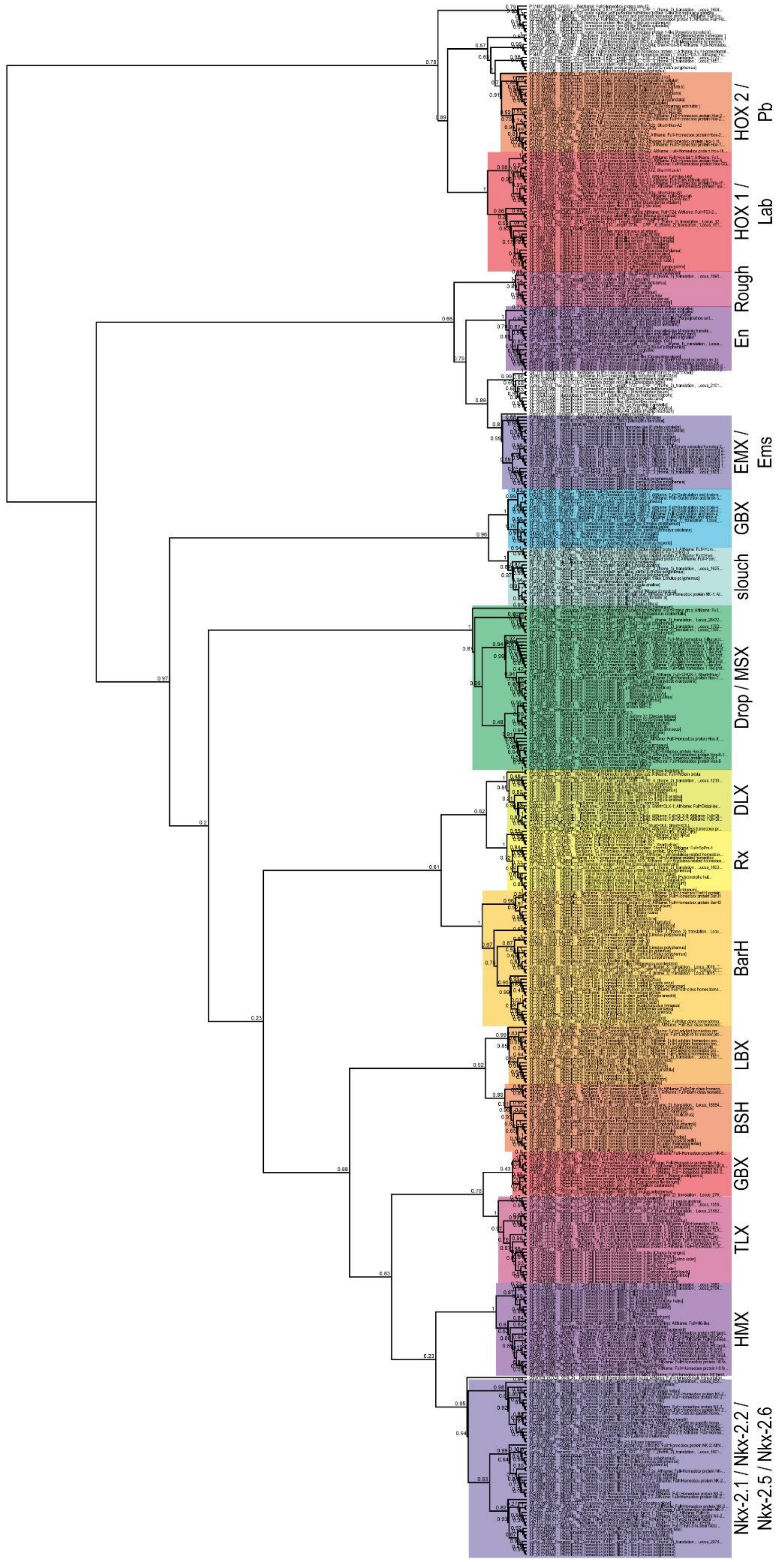
9.4.1.9 *Daughterless*



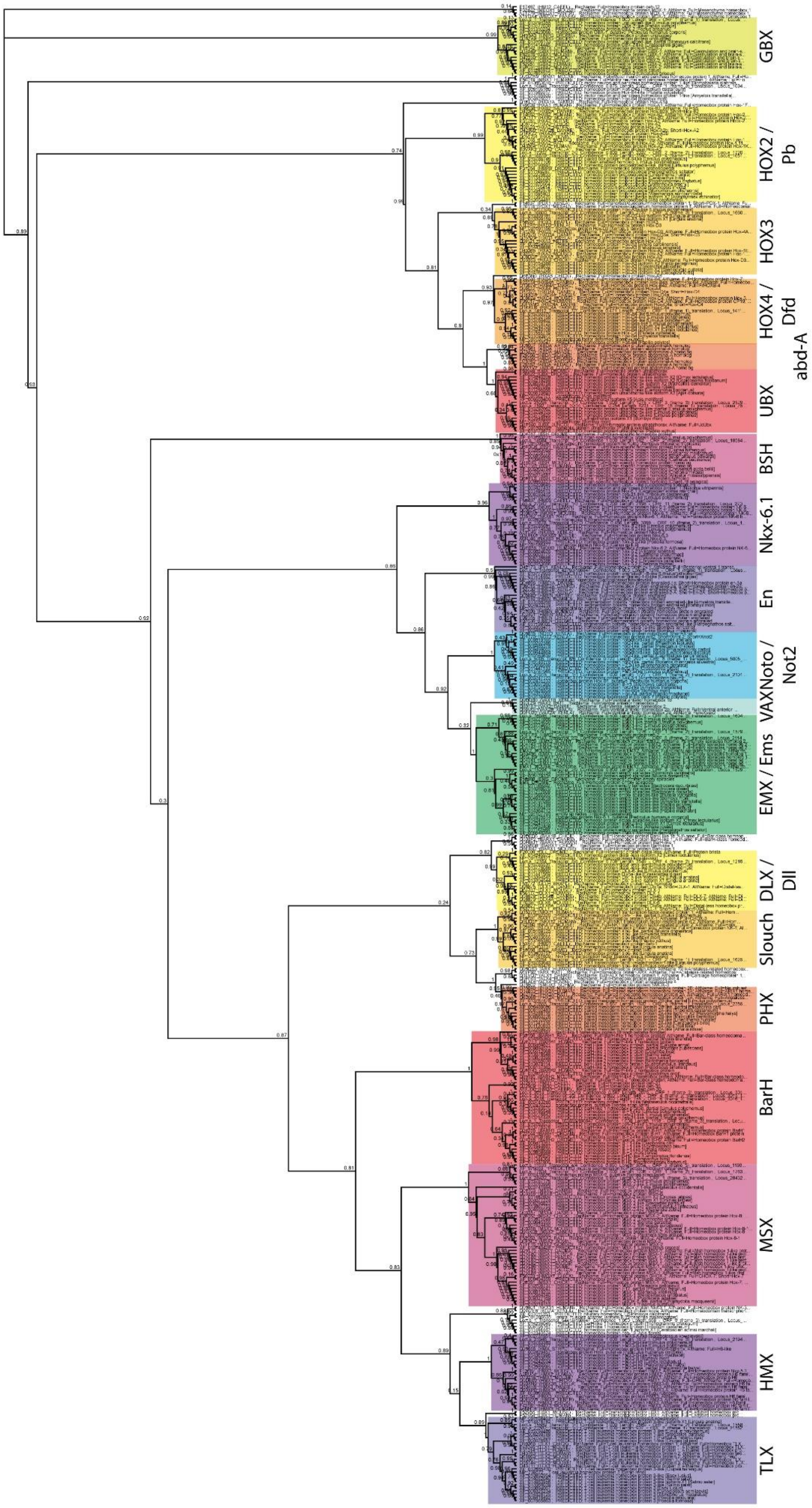
9.4.1.10 *Dorsal*



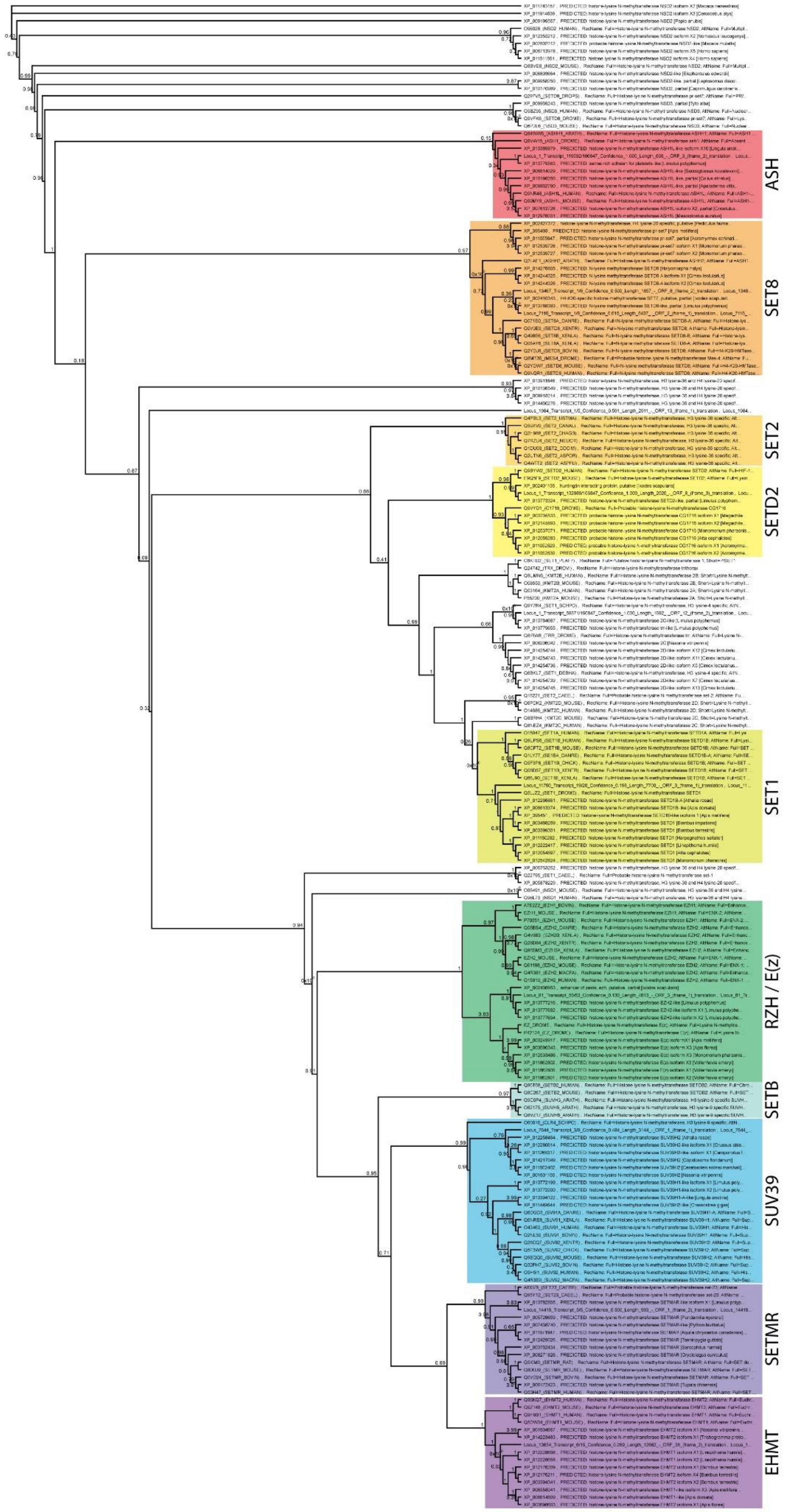
9.4.1.11 *Drop*


HOX 2 / Pb
HOX 1 / Lab
Rough
En
EMX / Ems
GBX
slouch
Drop / MSX
DLX
Rx
BarH
LBX
BSH
GBX
TLX
HMX
Nkx-2.1 / Nkx-2.2 / Nkx-2.5 / Nkx-2.6

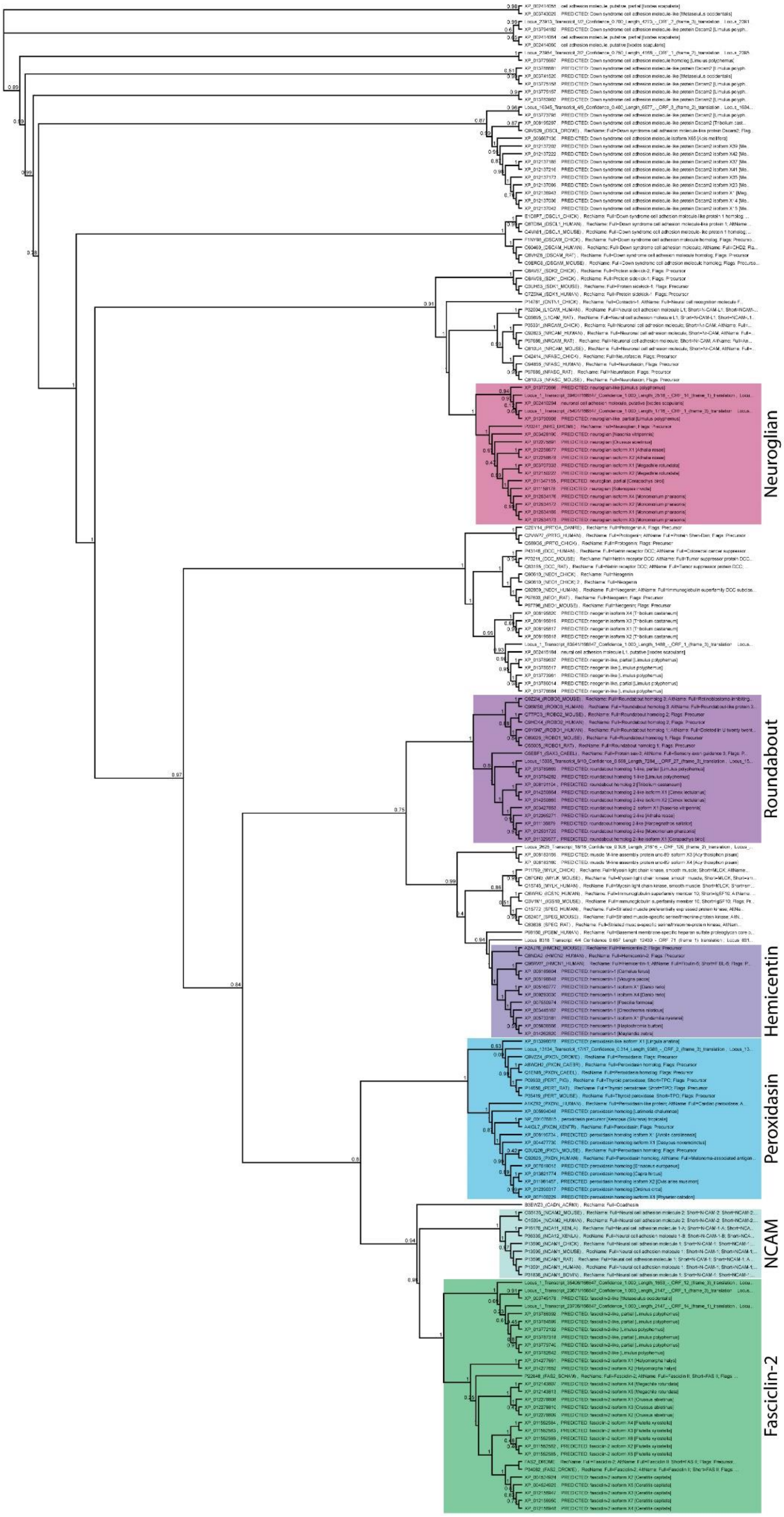
9.4.1.12 *Empty spiracles*



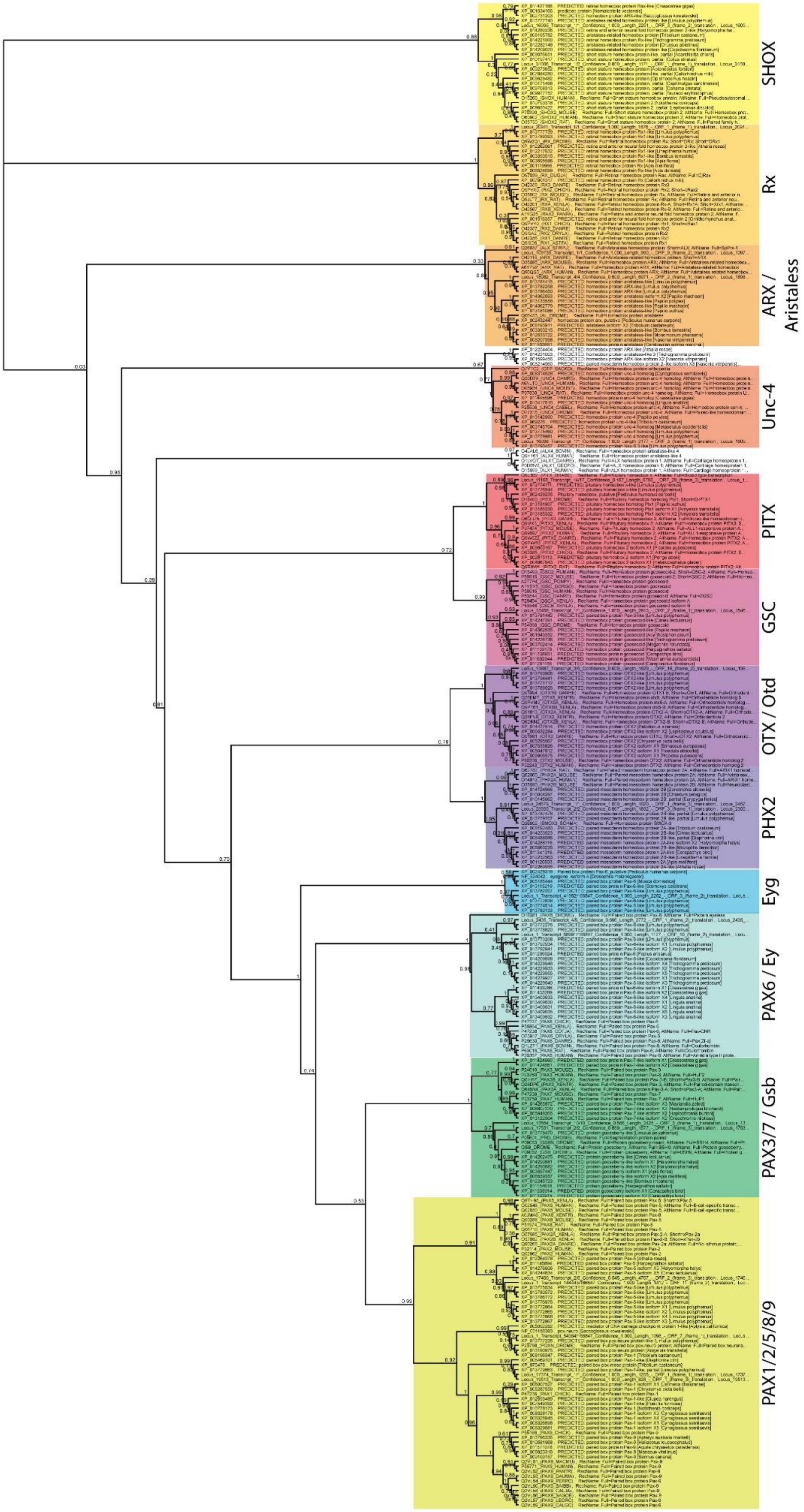
9.4.1.13 *Enhancer of zeste*



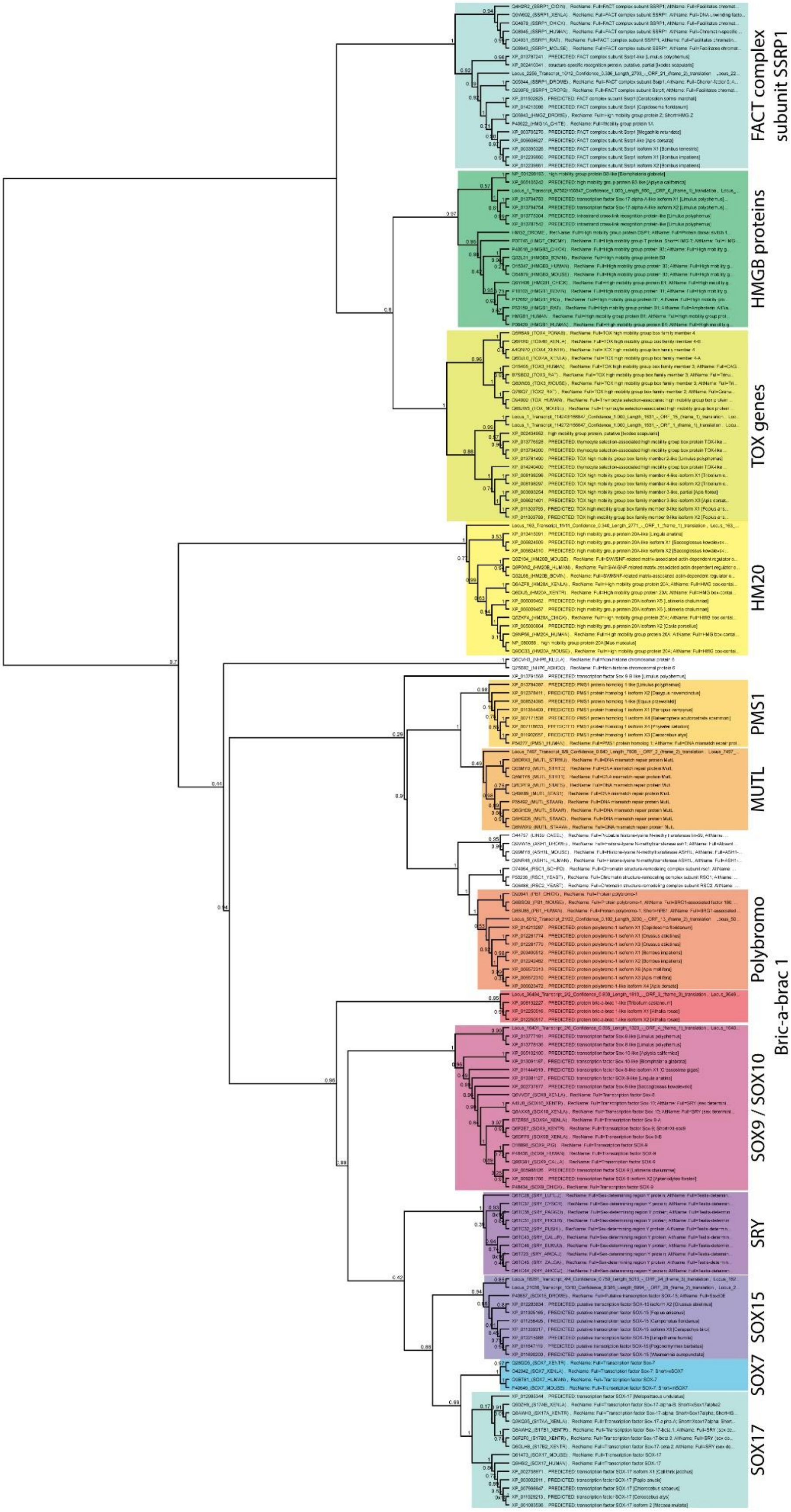
9.4.1.14 *Fasciclin 2*



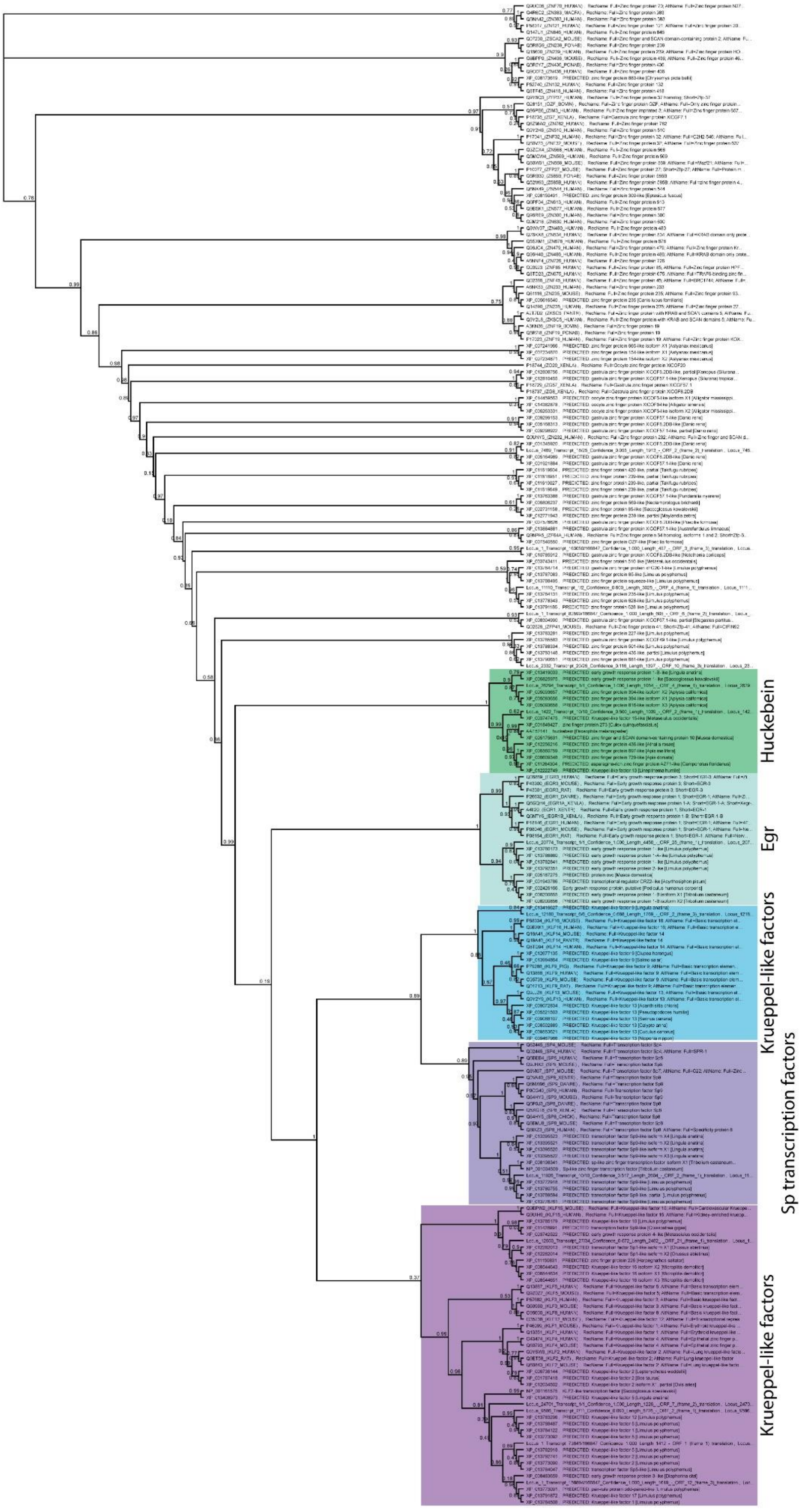
9.4.1.15 *Gooseberry*



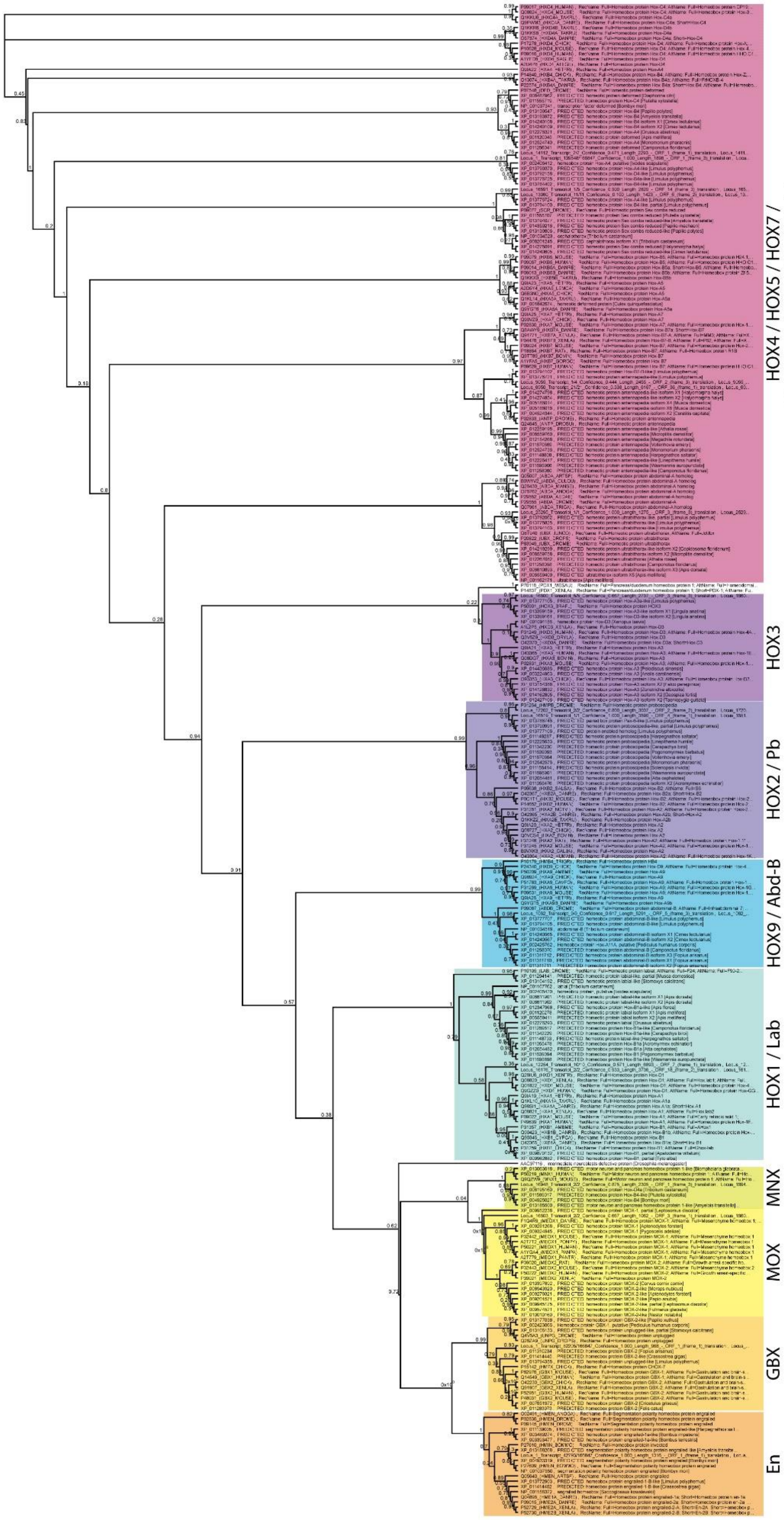
9.4.1.16 *HMGB1*


FACT complex subunit SSRP1
HMGB proteins
TOX genes
HM20
PMS1
MUTL
Polybromo
Bric-a-brac 1
SOX9 / SOX10
SRY
SOX15
SOX7
SOX17

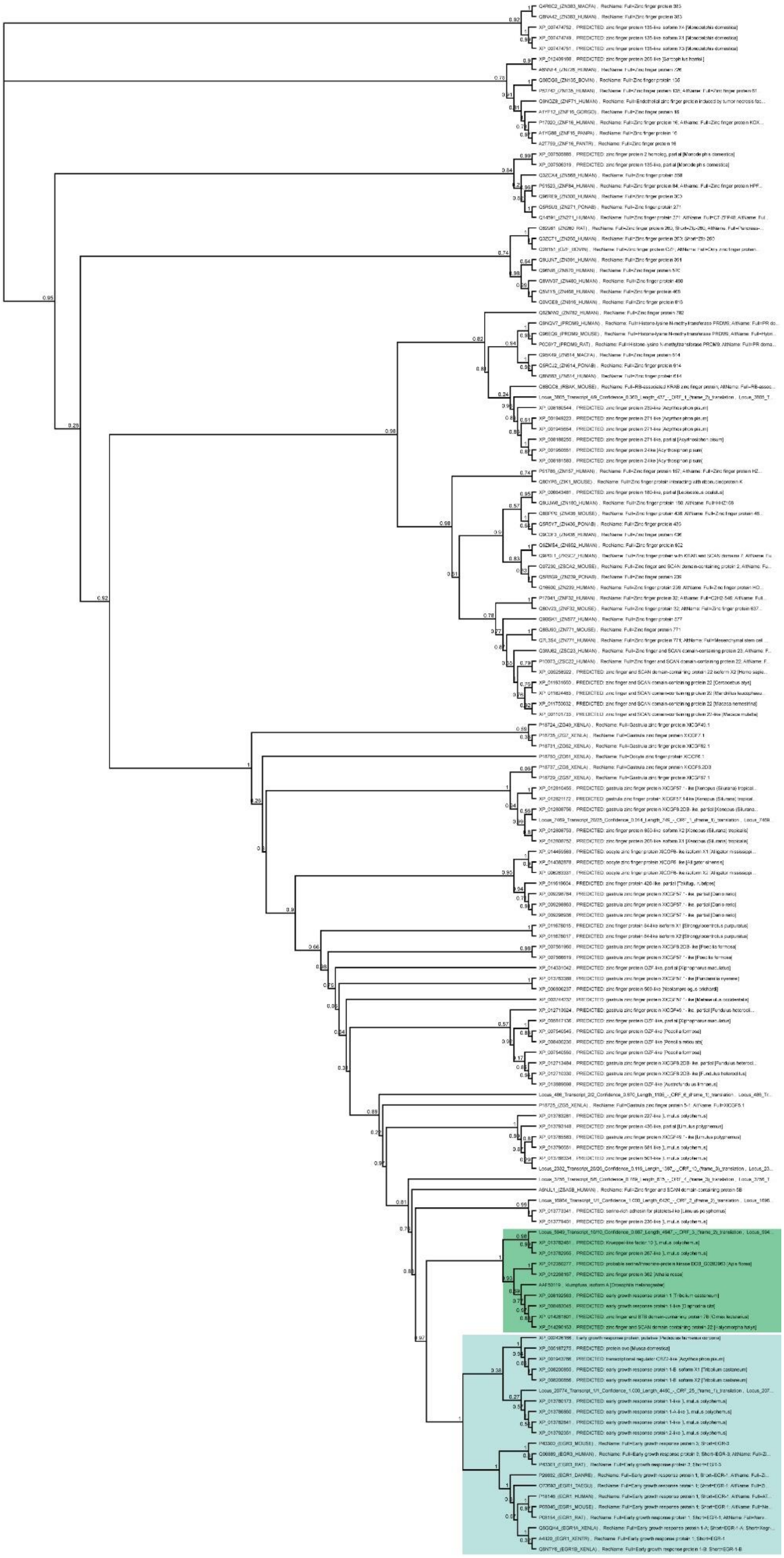
9.4.1.17 *Huckebein*



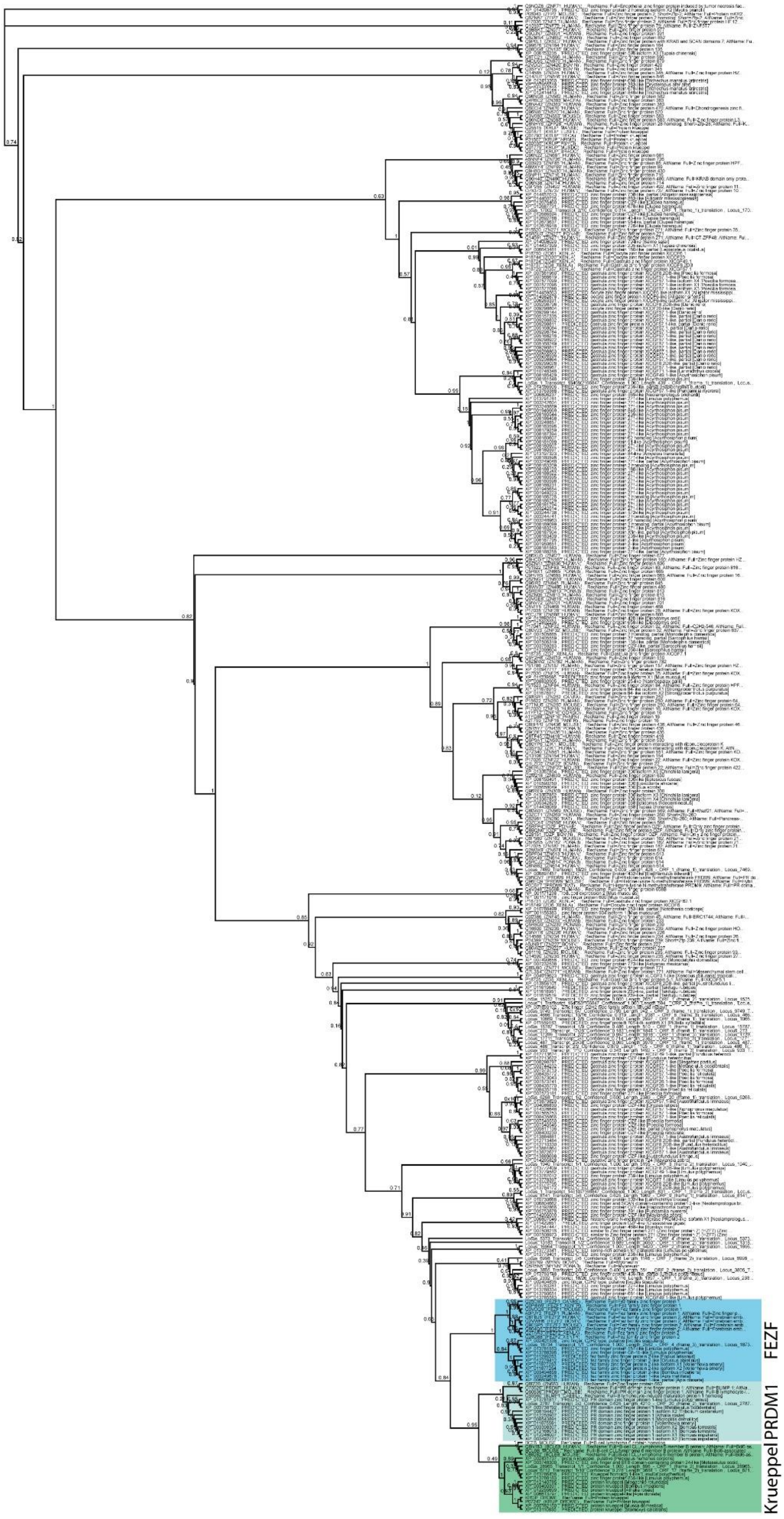
9.4.1.18 *Intermediate neuroblasts defective*



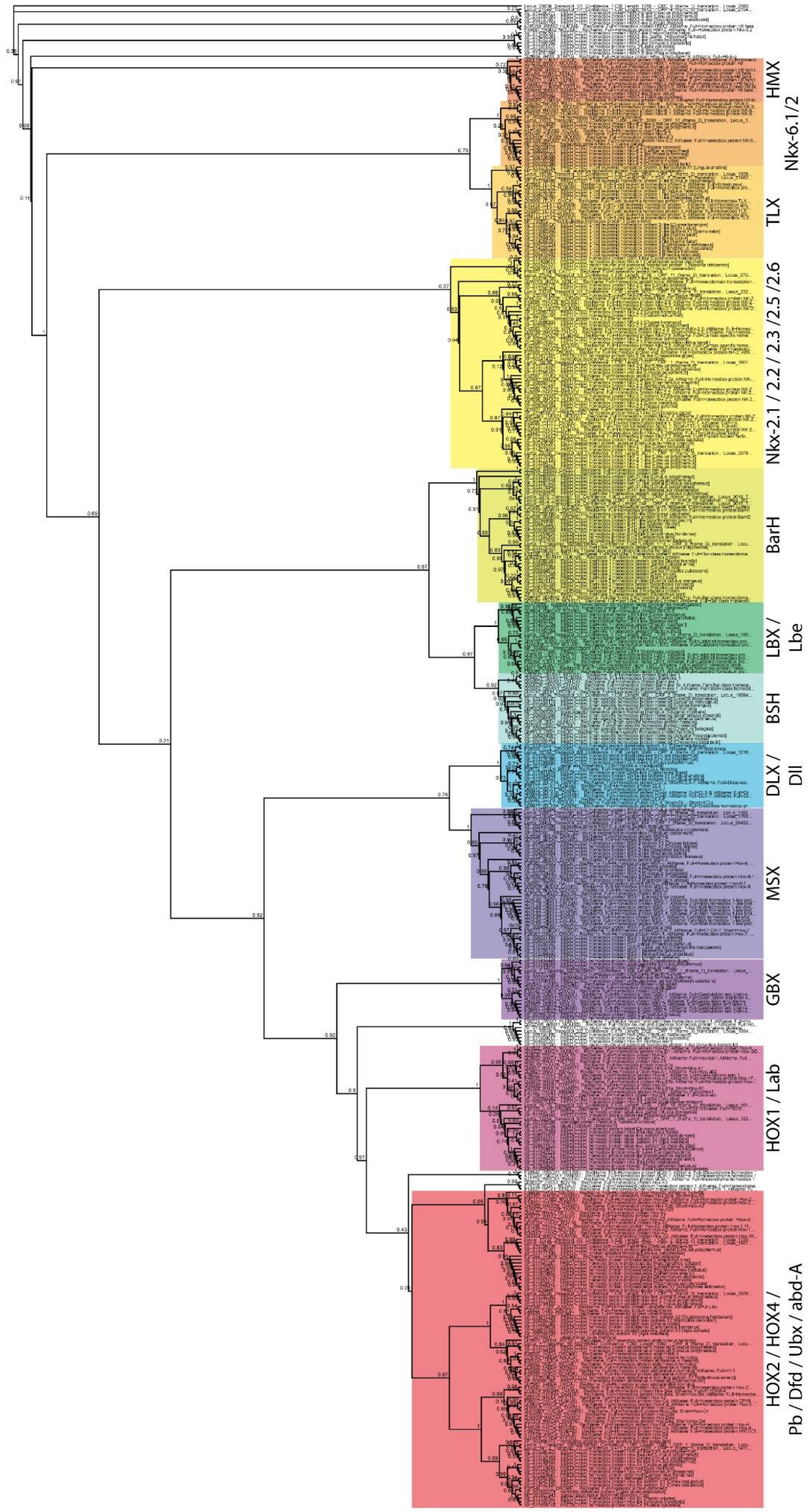
9.4.1.19 *Klumpfuss*



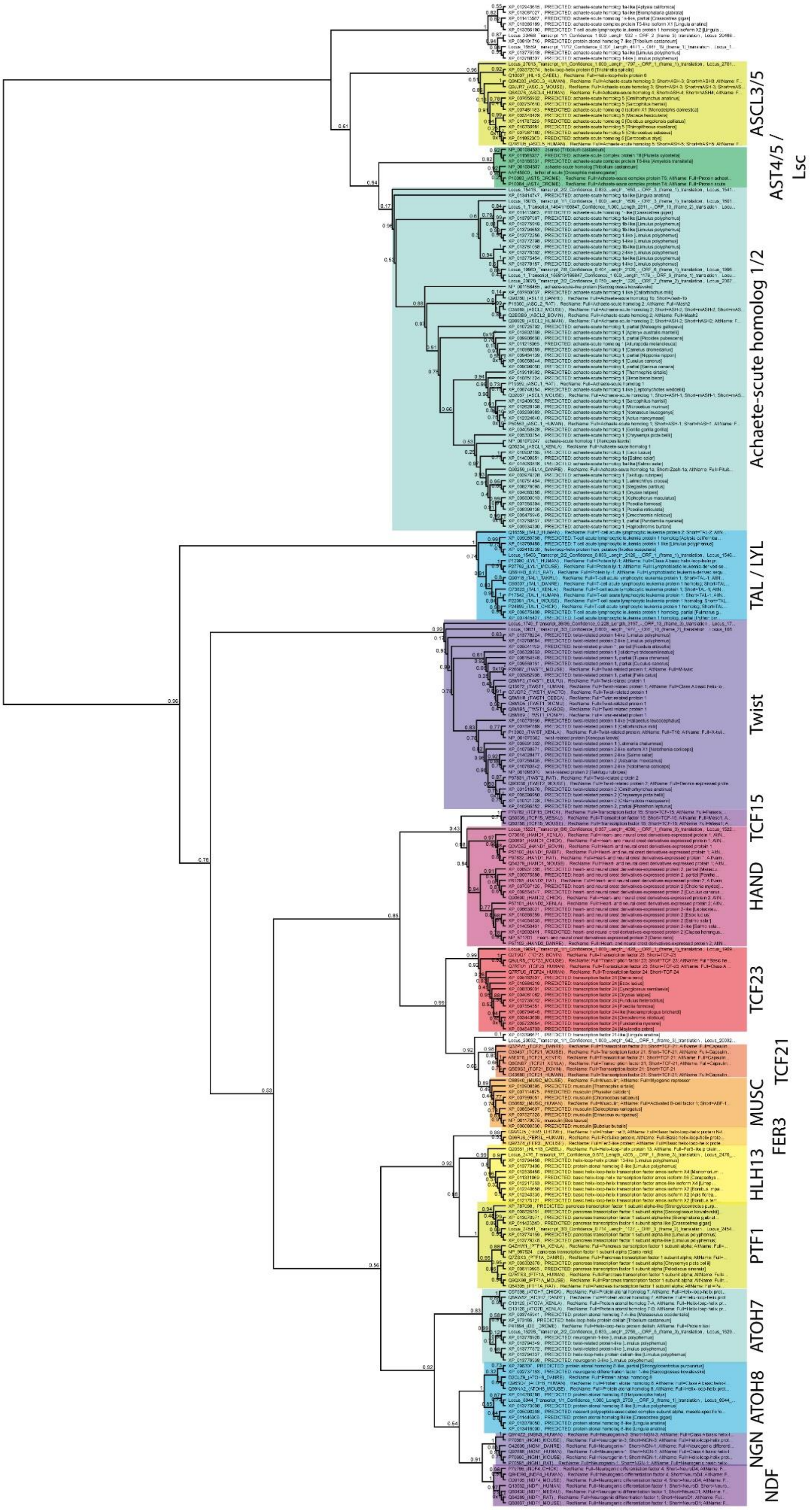
9.4.1.20 *Krüppel*



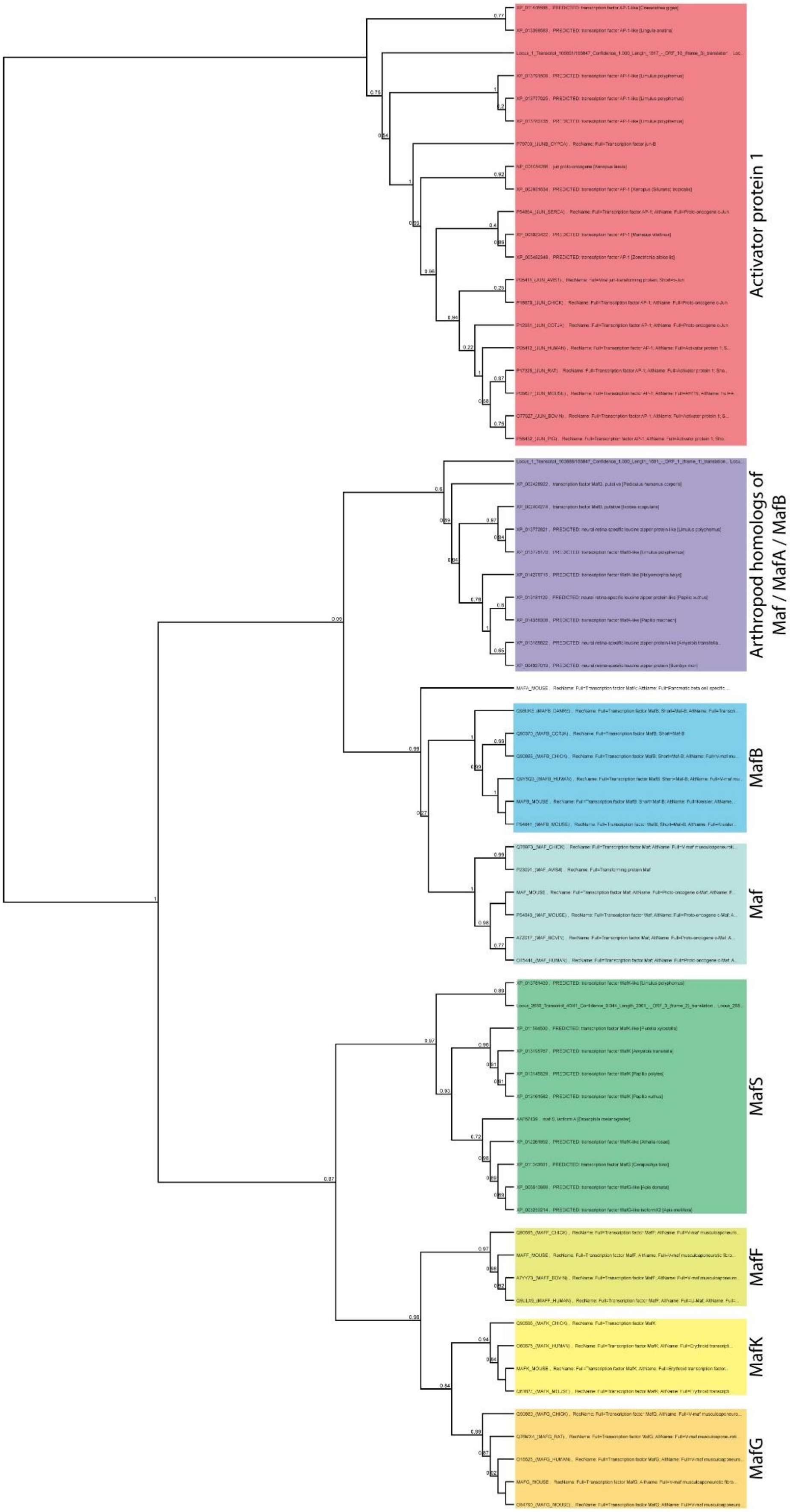
9.4.1.21 *Ladybird early*



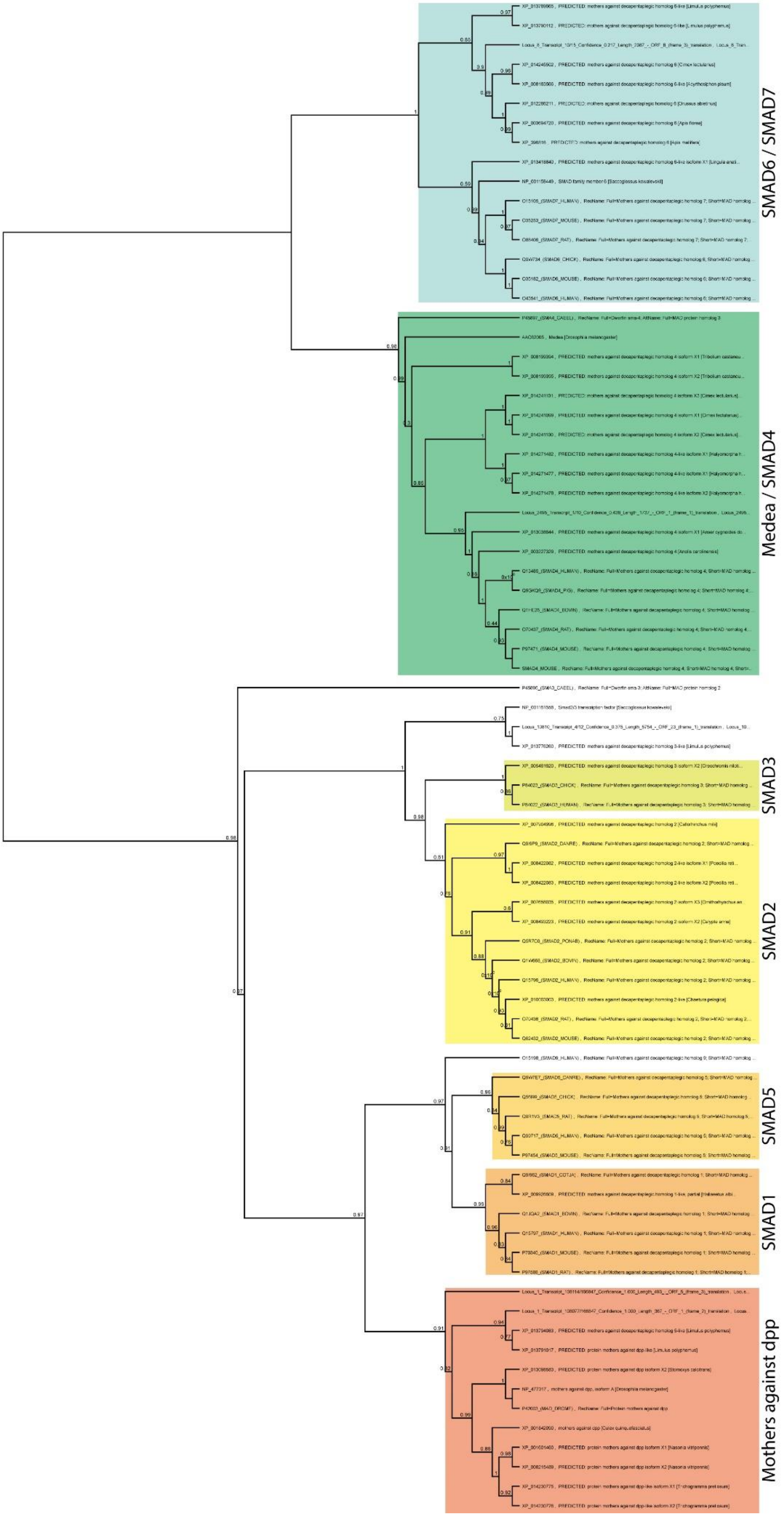
9.4.1.22 *Lethal of scute*



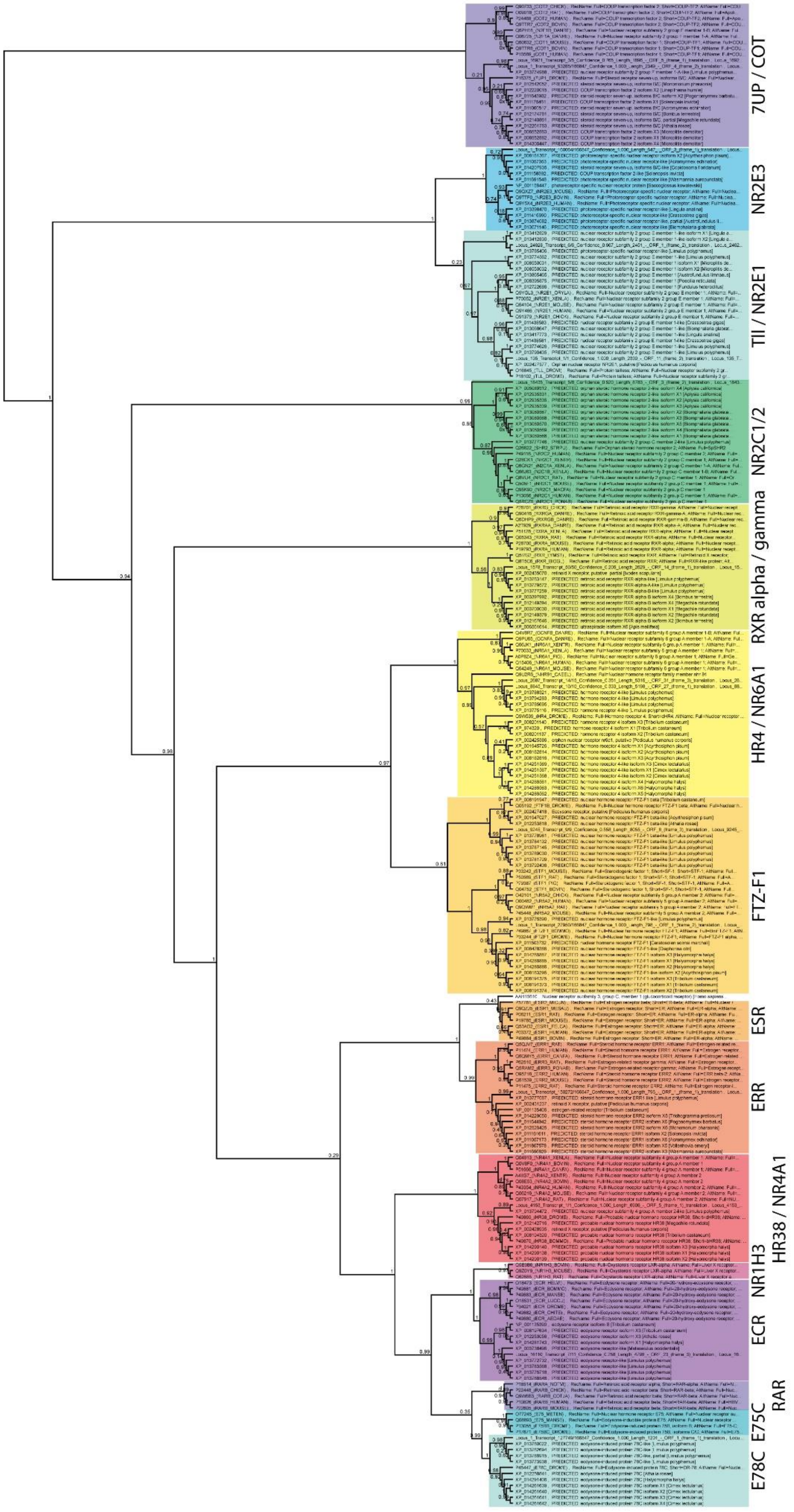
9.4.1.23 *MafS*


Activator protein 1
Arthropod homologs of Maf / MafA / MafB
MafB
Maf
MafS
MafF
MafK
MafG

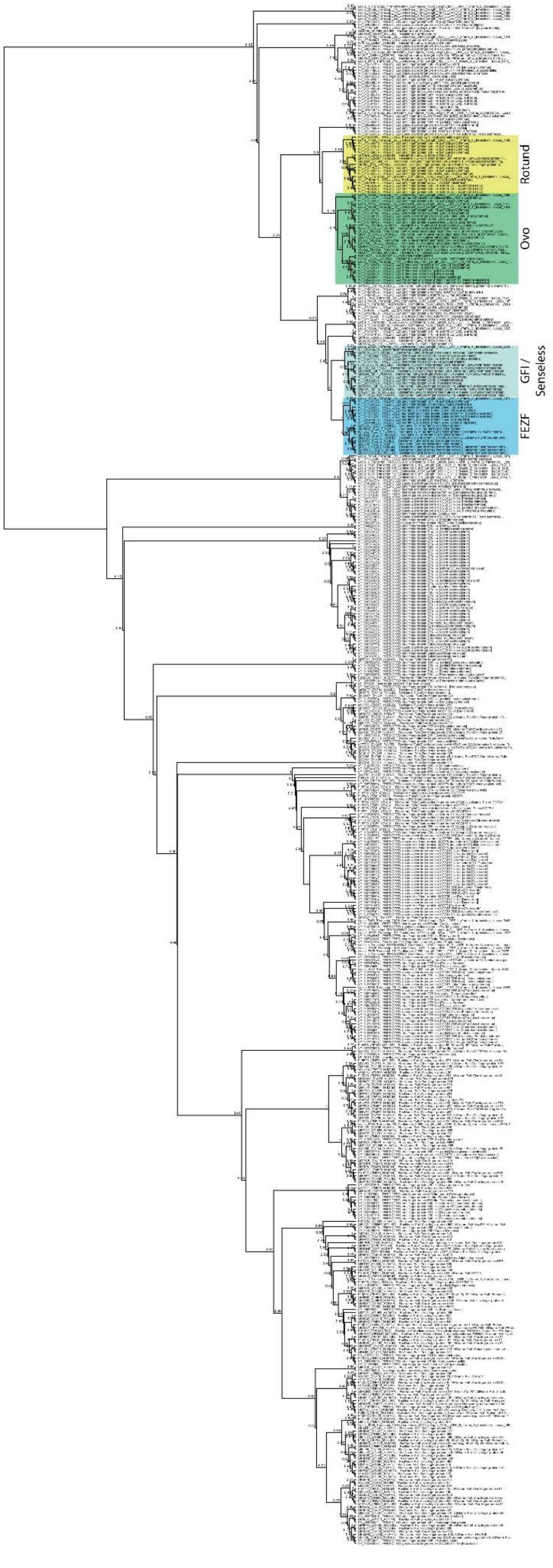
9.4.1.24 *Medea*


SMAD6 / SMAD7
Medea / SMAD4
SMAD3
SMAD2
SMAD5
SMAD1
Mothers against dpp

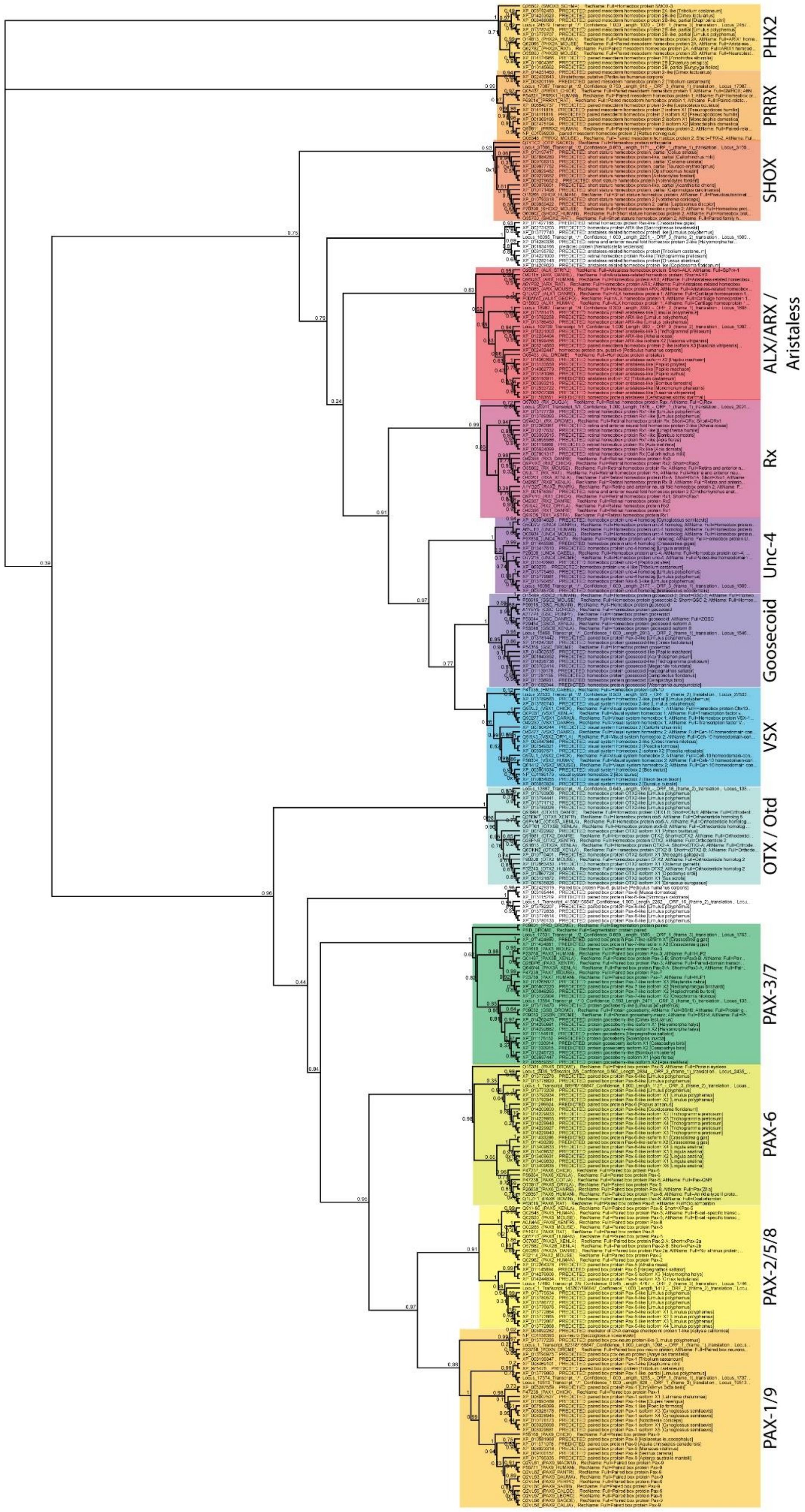
9.4.1.25 *NR3C1*


7UP / COT
NR2E3
Tll / NR2E1
NR2C1/2
RXR alpha / gamma
HR4 / NR6A1
FTZ-F1
ESR
ERR
HR38 / NR4A1
NR1H3
ECR
RAR
E75C
E78C

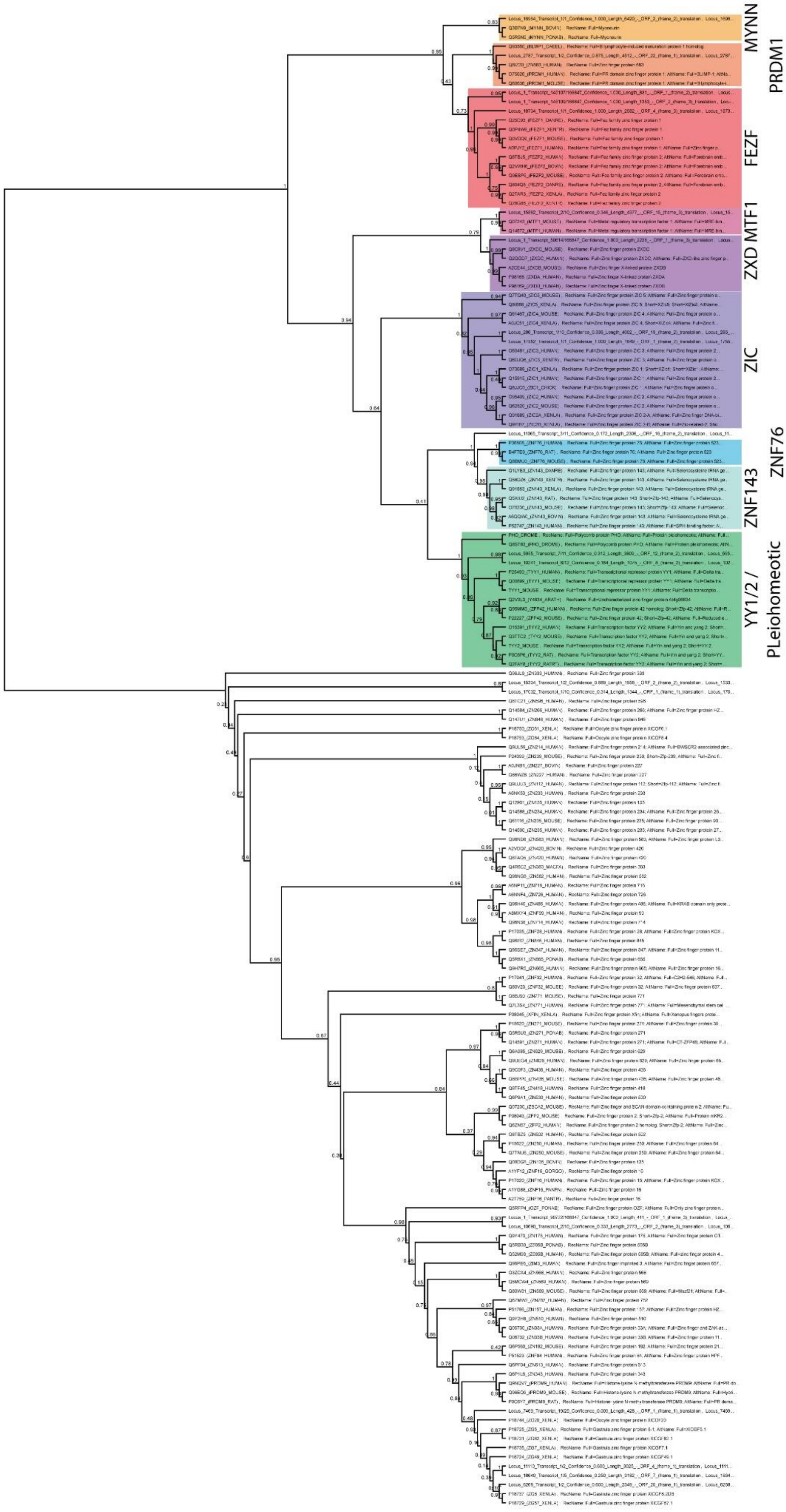
9.4.1.26 *Ovo / Shaven baby*



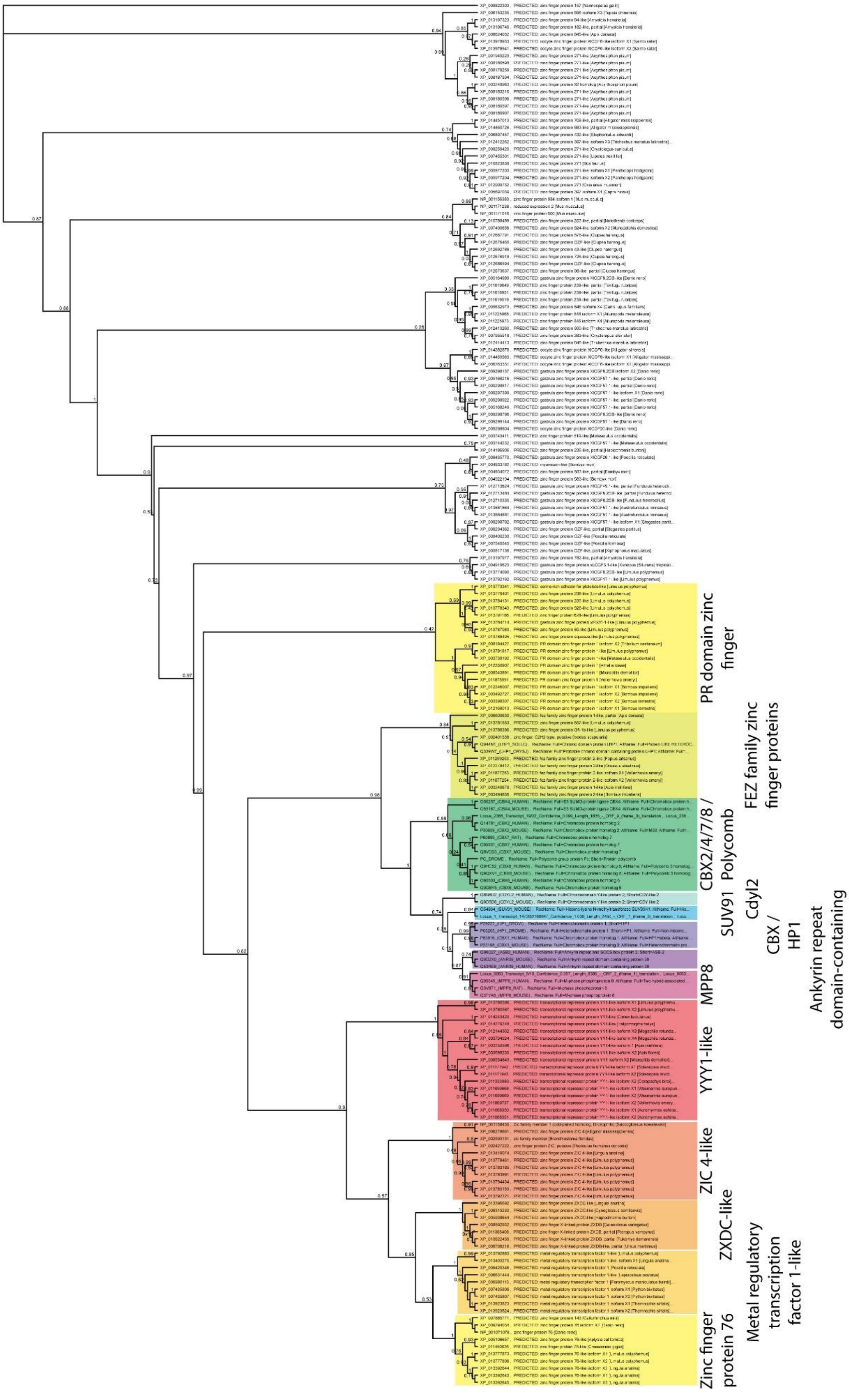
9.4.1.27 *Paired*



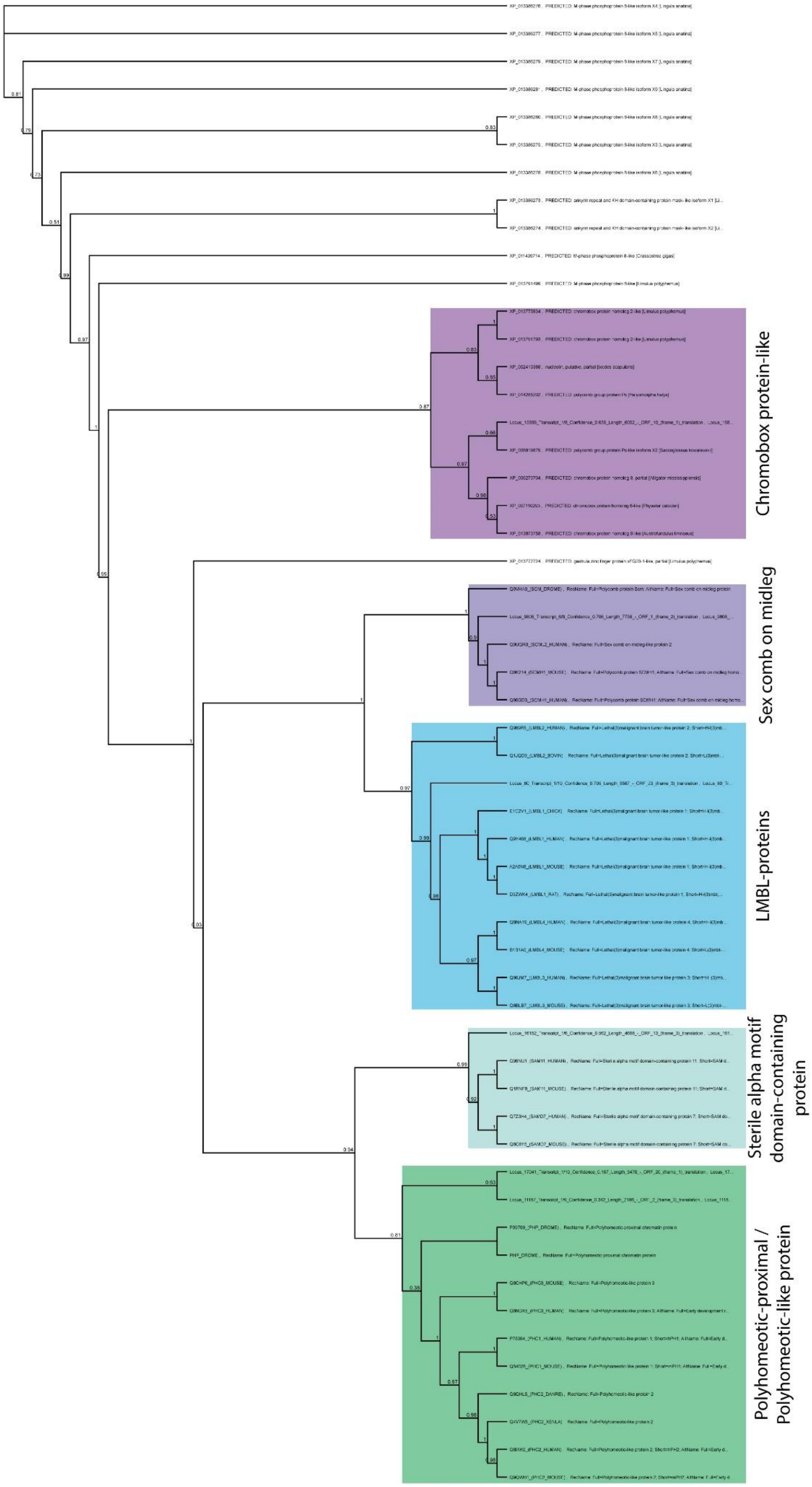
9.4.1.28 *Pleiohomeotic*



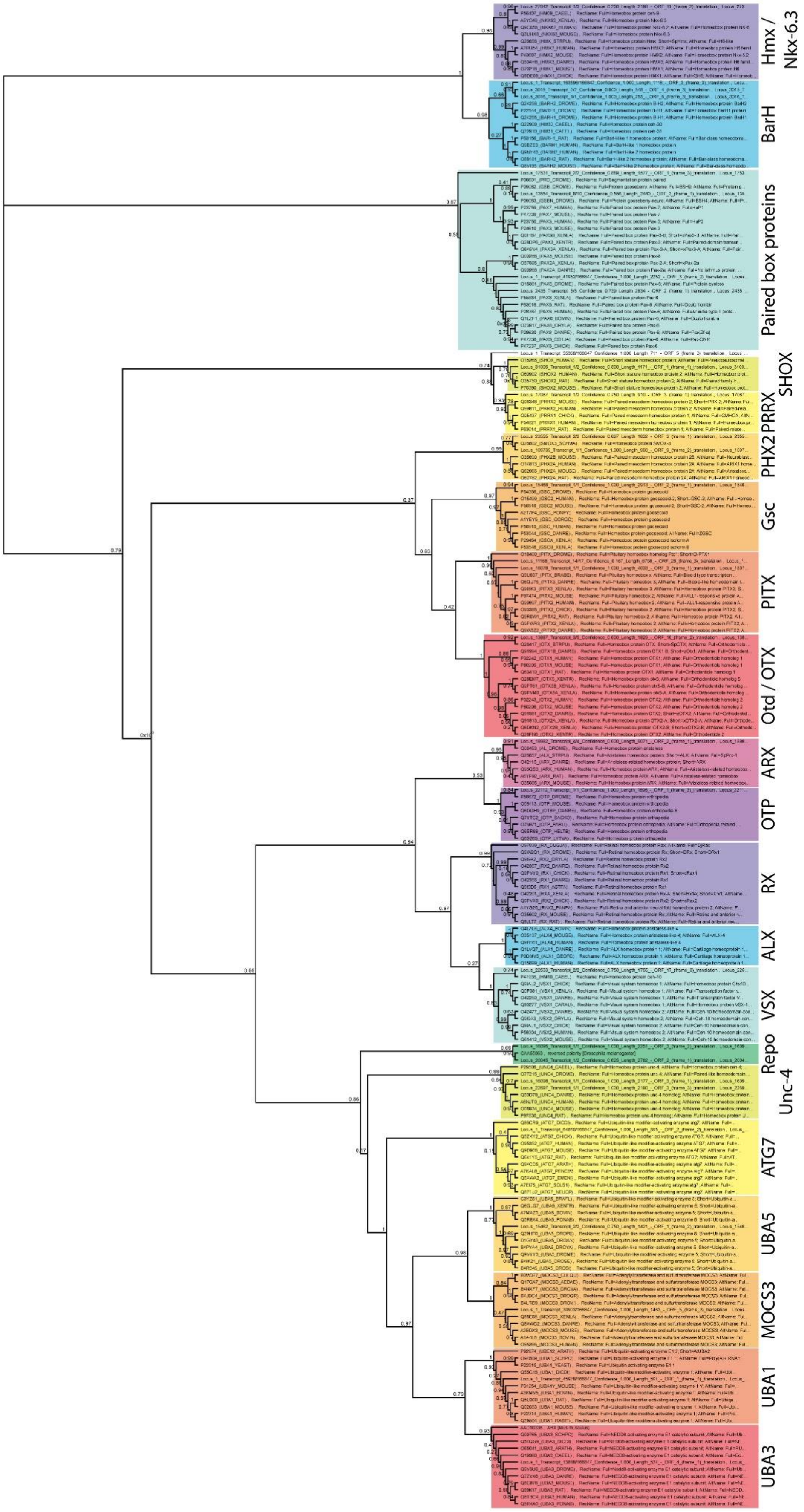
9.4.1.29 *Polycomb*



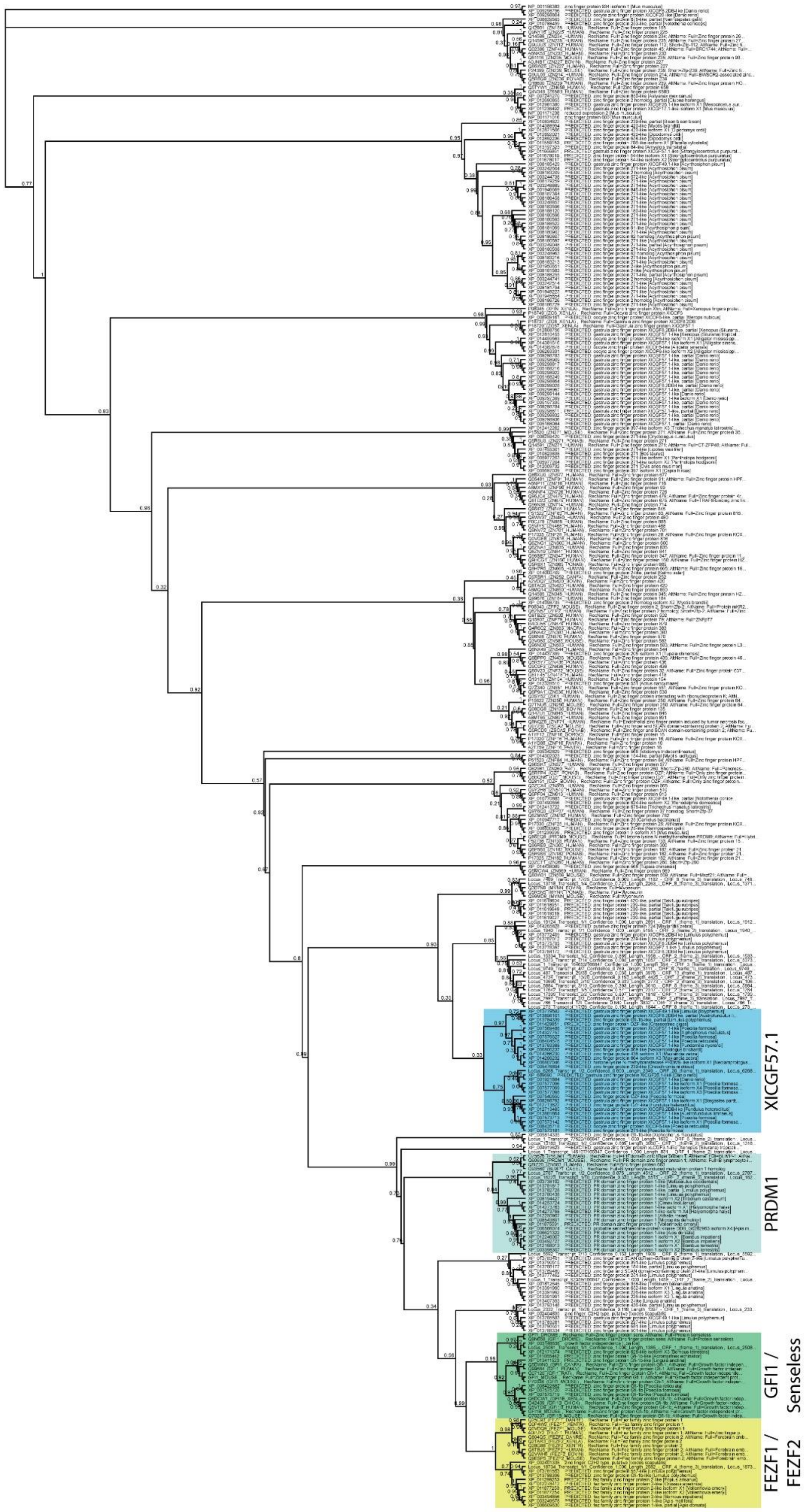
9.4.1.30 *Polyhomeotic proximal*



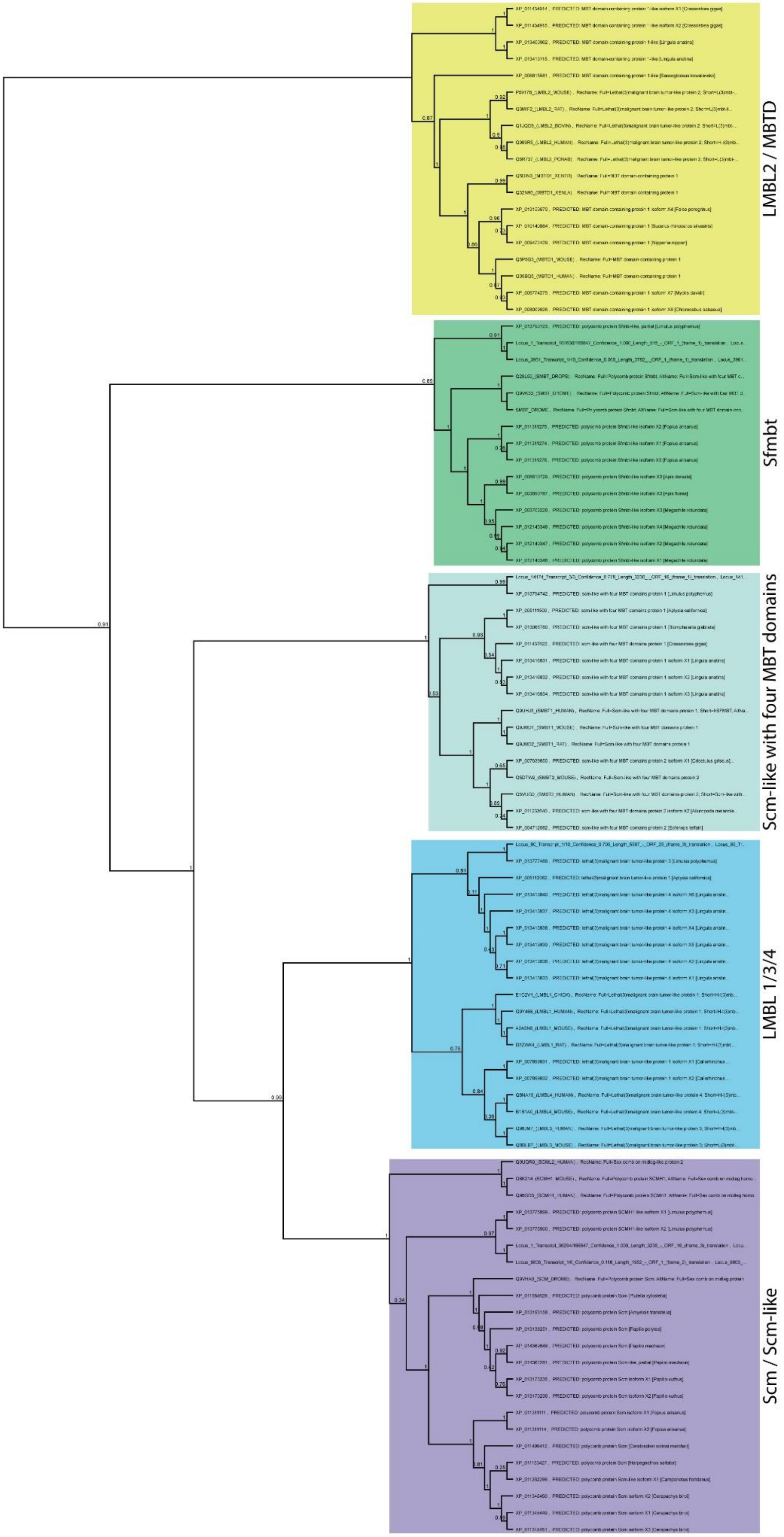
9.4.1.31 *Reversed polarity*



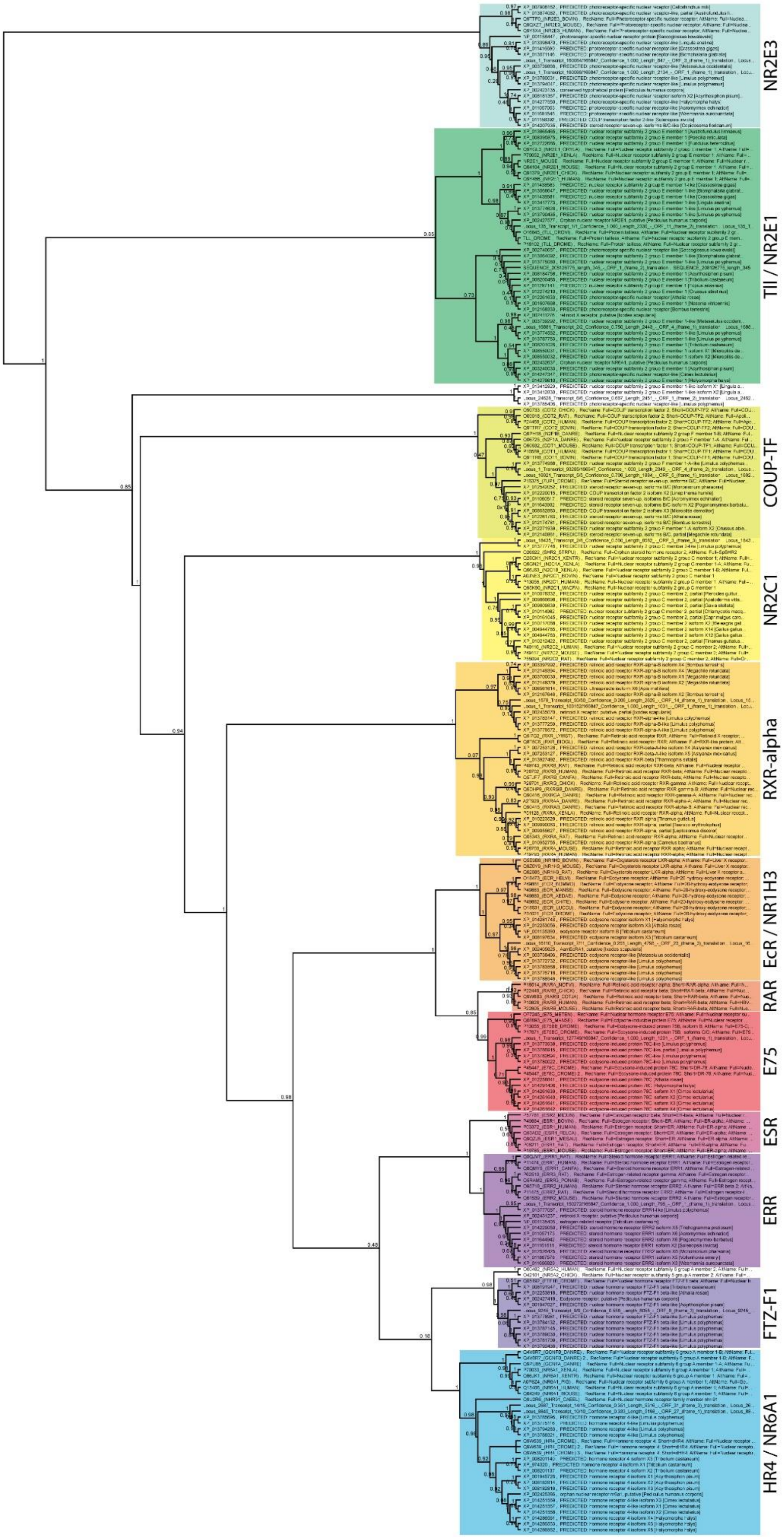
9.4.1.32 *Senseless*



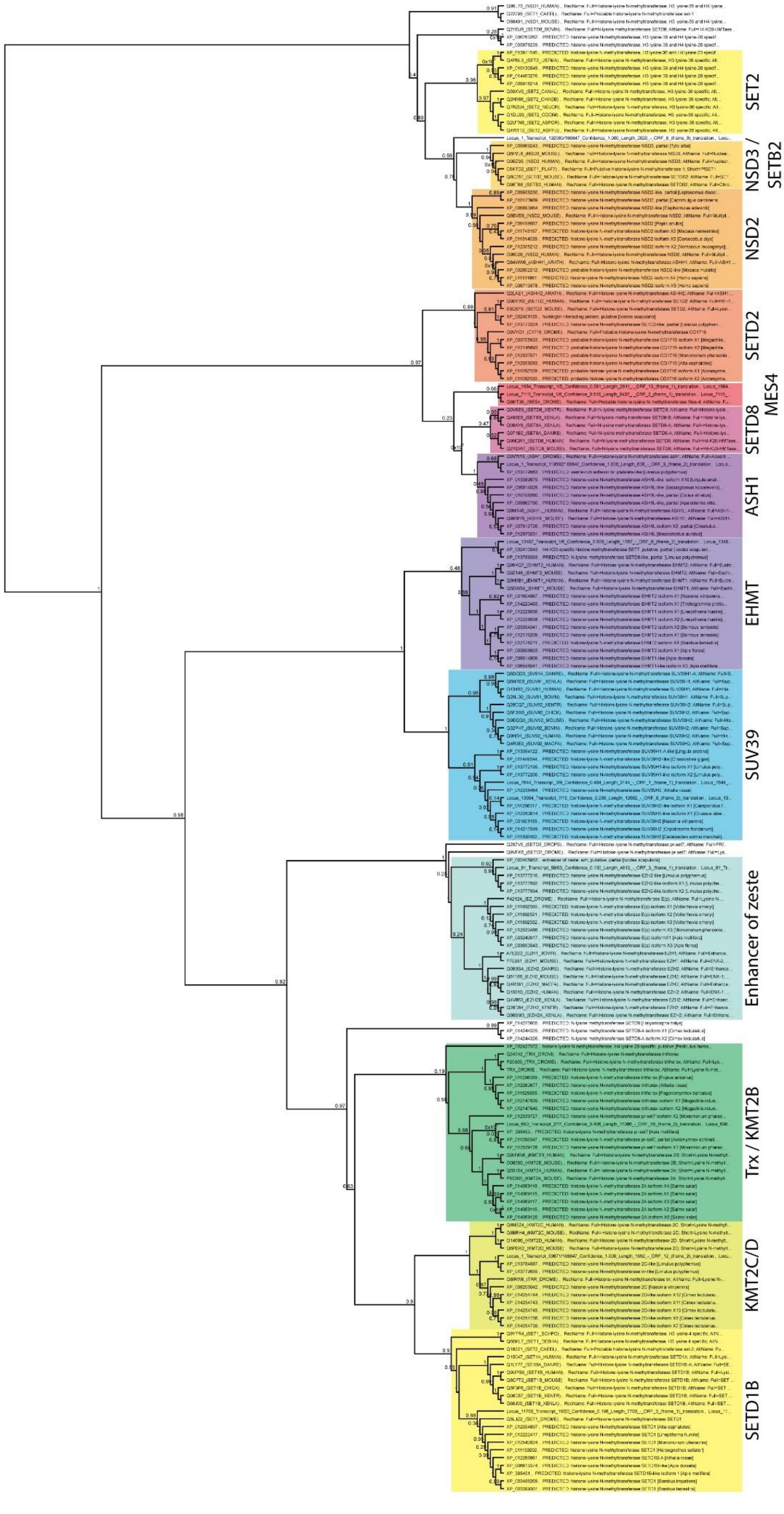
9.4.1.33 *Sfmbt*


LMBL2 / MBTD
Sfmbt
Scm-like with four MBT domains
LMBL 1/3/4
Scm / Scm-like

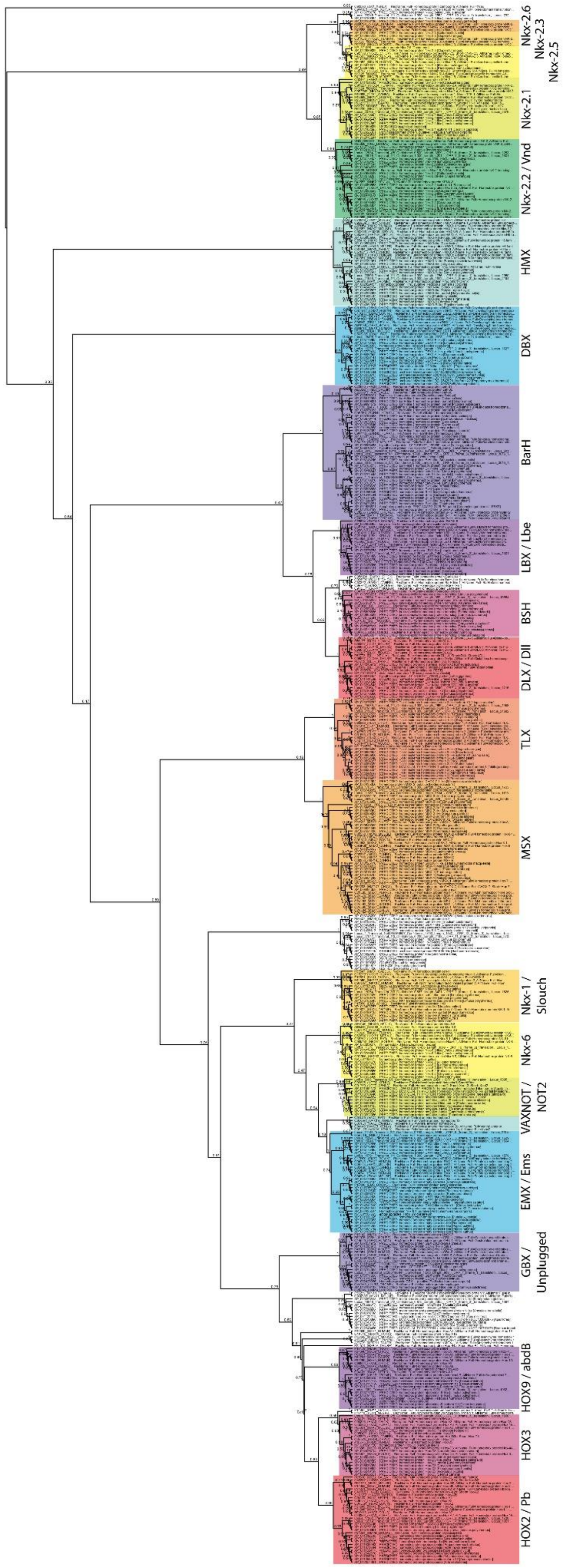
9.4.1.34 *Tailless*



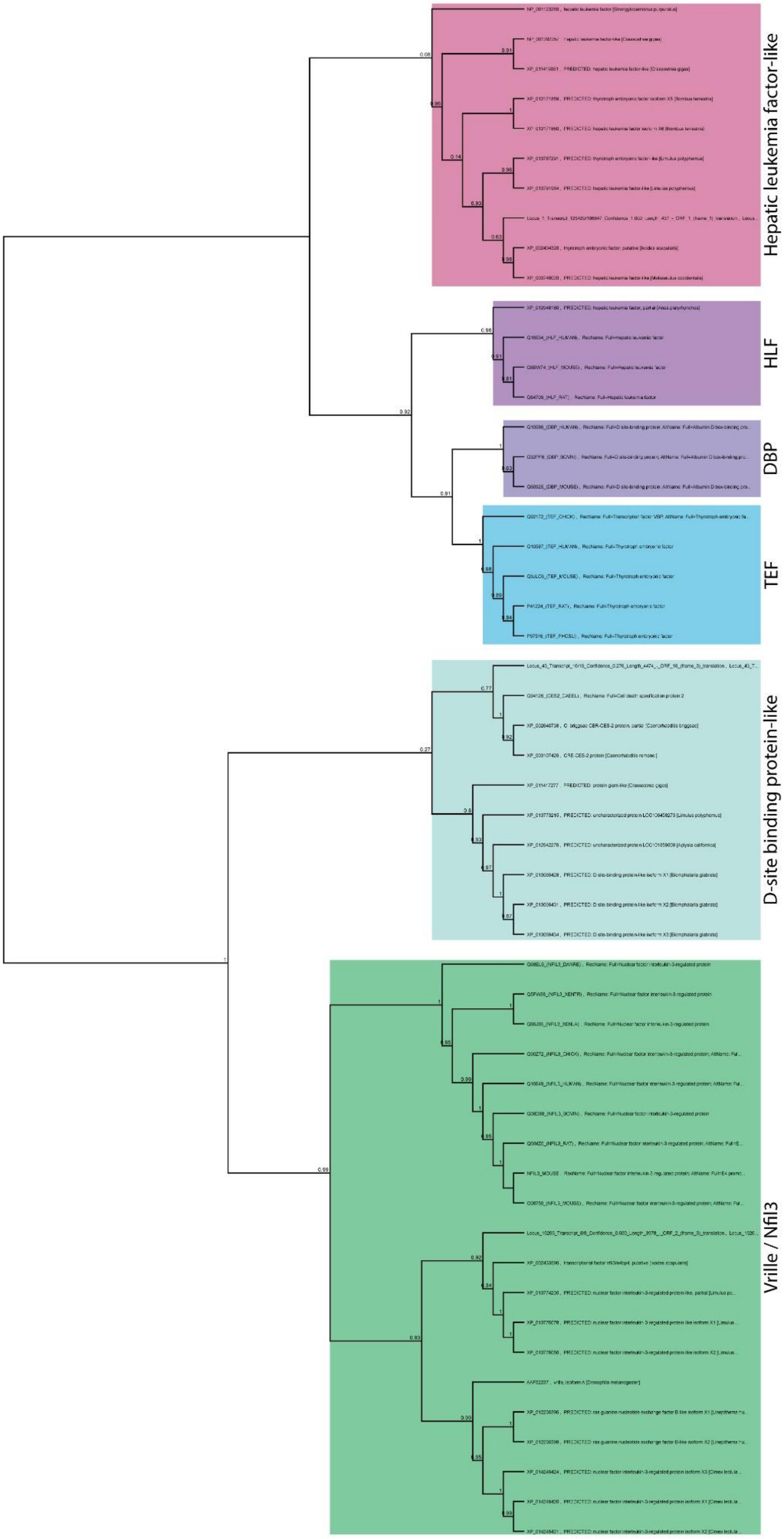
9.4.1.35 *Trithorax*



9.4.1.36 *Ventral nervchord defective*



9.4.1.37 *Vrille*



9.4.2 Accession numbers used in phylogenetic trees

9.4.2.1 *Hunchback*

Name	Description
A0JNB1 (ZN227_BOVIN)	RecName: Full=Zinc finger protein 227
A2APF3 (CTCFL_MOUSE)	RecName: Full=Transcriptional repressor CTCFL; AltName: Full=Brother of the regulator of imprinted sites; AltName: Full=CCCTC-binding factor; AltName: Full=CTCF paralog; AltName: Full=CTCF-like protein
A3KN32 (ZNF34_BOVIN)	RecName: Full=Zinc finger protein 34
A6NK75 (ZNF98_HUMAN)	RecName: Full=Zinc finger protein 98; AltName: Full=Zinc finger protein 739; AltName: Full=Zinc finger protein F7175
A6NNF4 (ZN726_HUMAN)	RecName: Full=Zinc finger protein 726
B4DU55 (ZN879_HUMAN)	RecName: Full=Zinc finger protein 879
HUNB_DROME	RecName: Full=Protein hunchback
Locus_1_Transcript_68341/166847_Confidence_1.000_Length_2133 - ORF 1 (frame 3) translation	Locus_1_Transcript_68341/166847_Confidence_1.000_Length_2133
Locus_1_Transcript_68343/166847_Confidence_1.000_Length_1164 - ORF 1 (frame 2) translation	Locus_1_Transcript_68343/166847_Confidence_1.000_Length_1164
Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195 - ORF 3 (frame 2) translation	Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195
Locus_2332_Transcript_20/26_Confidence_0.116_Length_1397 - ORF 10 (frame 3) translation	Locus_2332_Transcript_20/26_Confidence_0.116_Length_1397
Locus_9298_Transcript_9/9_Confidence_0.676_Length_4629 - ORF 1 (frame 3) translation	Locus_9298_Transcript_9/9_Confidence_0.676_Length_4629
Locus_11058_Transcript_1/4_Confidence_0.850_Length_1360 - ORF 2 (frame 2) translation	Locus_11058_Transcript_1/4_Confidence_0.850_Length_1360
Locus_11889_Transcript_15/15_Confidence_0.356_Length_9012 - ORF 29 (frame 2) translation	Locus_11889_Transcript_15/15_Confidence_0.356_Length_9012
Locus_12619_Transcript_9/10_Confidence_0.343_Length_4054 - ORF 25 (frame 1) translation	Locus_12619_Transcript_9/10_Confidence_0.343_Length_4054
Locus_13853_Transcript_7/14_Confidence_0.176_Length_6612 - ORF 26 (frame 3) translation	Locus_13853_Transcript_7/14_Confidence_0.176_Length_6612
Locus_14442_Transcript_5/5_Confidence_0.688_Length_3106 - ORF 1 (frame 2) translation	Locus_14442_Transcript_5/5_Confidence_0.688_Length_3106
Locus_15436_Transcript_3/10_Confidence_0.246_Length_2864 - ORF 2 (frame 1) translation	Locus_15436_Transcript_3/10_Confidence_0.246_Length_2864
Locus_15710_Transcript_10/10_Confidence_0.685_Length_4977 - ORF 20 (frame 1) translation	Locus_15710_Transcript_10/10_Confidence_0.685_Length_4977
NP_001158460	snail zinc finger protein [Saccoglossus kowalevskii]
O08954 (SNAI2_RAT)	RecName: Full=Zinc finger protein SNAI2; AltName: Full=Neural crest transcription factor Slug; AltName: Full=Protein snail homolog 2
O18326 (HUNB_BOMMO)	RecName: Full=Protein hunchback
O42410 (IKZF1_CHICK)	RecName: Full=DNA-binding protein Ikaros; AltName: Full=Ikaros family zinc finger protein 1
O43623 (SNAI2_HUMAN)	RecName: Full=Zinc finger protein SNAI2; AltName: Full=Neural crest transcription factor Slug; AltName: Full=Protein snail homolog 2
O62537 (HUNB_DROOR)	RecName: Full=Protein hunchback
O62538 (HUNB_DROSE)	RecName: Full=Protein hunchback
O62541 (HUNB_DROYA)	RecName: Full=Protein hunchback
O75373 (ZN737_HUMAN)	RecName: Full=Zinc finger protein 737; AltName: Full=Zinc finger protein 102
O95863 (SNAI1_HUMAN)	RecName: Full=Zinc finger protein SNAI1; AltName: Full=Protein snail homolog 1; Short=Protein sna
O96785 (HUNB_CLOAL)	RecName: Full=Protein hunchback
P0CJ79 (ZN888_HUMAN)	RecName: Full=Zinc finger protein 888
P0DKX0 (ZN728_HUMAN)	RecName: Full=Zinc finger protein 728
P05084 (HUNB_DROME)	RecName: Full=Protein hunchback
P08043 (ZFP2_MOUSE)	RecName: Full=Zinc finger protein 2; Short=Zfp-2; AltName: Full=Protein mKR2
P08044 (SNAI_DROME)	RecName: Full=Protein snail
P13361 (HUNB_DROVI)	RecName: Full=Protein hunchback
P17035 (ZNF28_HUMAN)	RecName: Full=Zinc finger protein 28; AltName: Full=Zinc finger protein KOX24
P18715 (ZG26_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF26.1
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P19382 (SNAI1_XENLA)	RecName: Full=Protein snail homolog Sna; Short=Protein Xsnail; Short=Protein xSna
P25932 (ESCA_DROME)	RecName: Full=Protein escargot; AltName: Full=Protein fleabag
P28698 (MZF1_HUMAN)	RecName: Full=Myeloid zinc finger 1; Short=MZF-1; AltName: Full=Zinc finger and SCAN domain-containing protein 6; AltName: Full=Zinc finger protein 42
P49711 (CTCF_HUMAN)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
P97469 (SNAI2_MOUSE)	RecName: Full=Zinc finger protein SNAI2; AltName: Full=Neural crest transcription factor Slug; AltName: Full=Protein snail homolog 2
Q3KNW1 (SNAI3_HUMAN)	RecName: Full=Zinc finger protein SNAI3; AltName: Full=Protein snail homolog 3; AltName: Full=Zinc finger protein 293
Q3MHQ4 (SNAI2_BOVIN)	RecName: Full=Zinc finger protein SNAI2; AltName: Full=Neural crest transcription factor Slug; AltName: Full=Protein snail homolog 2
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4R6C2 (ZN383_MACFA)	RecName: Full=Zinc finger protein 383
Q5R5Y7 (ZN436_PONAB)	RecName: Full=Zinc finger protein 436
Q5R8G9 (ZN239_PONAB)	RecName: Full=Zinc finger protein 239
Q5RCD9 (ZSCA2_PONAB)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29 homolog; Short=Zfp-29

Q5RFP4 (OZF_PONAB)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q6XDT6 (IKZF_MYXGL)	RecName: Full=Ikaros family zinc finger protein; AltName: Full=Ikaros-like transcription factor; Short=HIL
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q6ZNA1 (ZN836_HUMAN)	RecName: Full=Zinc finger protein 836
Q7Z7L9 (ZSCA2_HUMAN)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29 homolog; Short=Zfp-29; AltName: Full=Zinc finger protein 854
Q8BI99 (ZN879_MOUSE)	RecName: Full=Zinc finger protein 879
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q8BQN6 (OZF_MOUSE)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q8IYN0 (ZN100_HUMAN)	RecName: Full=Zinc finger protein 100
Q8IZ26 (ZNF34_HUMAN)	RecName: Full=Zinc finger protein 34; AltName: Full=Zinc finger protein KOX32
Q8N4W9 (ZN808_HUMAN)	RecName: Full=Zinc finger protein 808
Q8NA42 (ZN383_HUMAN)	RecName: Full=Zinc finger protein 383
Q8NB50 (ZFP62_HUMAN)	RecName: Full=Zinc finger protein 62 homolog; Short=Zfp-62
Q8NEM1 (ZN680_HUMAN)	RecName: Full=Zinc finger protein 680
Q8NI51 (CTCFL_HUMAN)	RecName: Full=Transcriptional repressor CTCFL; AltName: Full=Brother of the regulator of imprinted sites; AltName: Full=CCCTC-binding factor; AltName: Full=CTCF paralog; AltName: Full=CTCF-like protein; AltName: Full=Cancer/testis antigen 27; Short=CT27; AltName: Full=Zinc finger protein CTCF-T
Q8WV37 (ZN480_HUMAN)	RecName: Full=Zinc finger protein 480
Q9BSK1 (ZN577_HUMAN)	RecName: Full=Zinc finger protein 577
Q9BY31 (ZN717_HUMAN)	RecName: Full=Zinc finger protein 717; AltName: Full=Krueppel-like factor X17
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q9NYT6 (ZN226_HUMAN)	RecName: Full=Zinc finger protein 226
Q9P2J8 (ZN624_HUMAN)	RecName: Full=Zinc finger protein 624
Q9P255 (ZN492_HUMAN)	RecName: Full=Zinc finger protein 492; AltName: Full=Zinc finger protein 115
Q9QY31 (SNAI3_MOUSE)	RecName: Full=Zinc finger protein SNAI3; AltName: Full=Protein snail homolog 3; AltName: Full=Snail-related gene from muscle cells; AltName: Full=Zinc finger protein 293
Q9R1D1 (CTCF_RAT)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
Q9UJU3 (ZN112_HUMAN)	RecName: Full=Zinc finger protein 112; Short=Zfp-112; AltName: Full=Zinc finger protein 228
Q9Y2P0 (ZN835_HUMAN)	RecName: Full=Zinc finger protein 835
Q9Y6Q3 (ZFP37_HUMAN)	RecName: Full=Zinc finger protein 37 homolog; Short=Zfp-37
Q80W31 (ZN569_MOUSE)	RecName: Full=Zinc finger protein 569; AltName: Full=Mszf21; AltName: Full=Zinc finger protein 74; Short=Zfp-74
Q86T29 (ZN605_HUMAN)	RecName: Full=Zinc finger protein 605
Q86WZ6 (ZN227_HUMAN)	RecName: Full=Zinc finger protein 227
Q86XU0 (ZN677_HUMAN)	RecName: Full=Zinc finger protein 677
Q96IR2 (ZN845_HUMAN)	RecName: Full=Zinc finger protein 845
Q96MU6 (ZN778_HUMAN)	RecName: Full=Zinc finger protein 778
Q96RE9 (ZN300_HUMAN)	RecName: Full=Zinc finger protein 300
Q01778 (HUNB_MUSDO)	RecName: Full=Protein hunchback
Q01791 (HUNB_TRICA)	RecName: Full=Protein hunchback
Q02386 (ZNF45_HUMAN)	RecName: Full=Zinc finger protein 45; AltName: Full=BRC1744; AltName: Full=Zinc finger protein 13; AltName: Full=Zinc finger protein KOX5
Q02525 (ZFP39_MOUSE)	RecName: Full=Zinc finger protein 39; Short=Zfp-39; AltName: Full=CtFIN33
Q03936 (ZNF92_HUMAN)	RecName: Full=Zinc finger protein 92; AltName: Full=Zinc finger protein HTF12
Q08705 (CTCF_CHICK)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
Q13105 (ZBT17_HUMAN)	RecName: Full=Zinc finger and BTB domain-containing protein 17; AltName: Full=Myc-interacting zinc finger protein 1; Short=Miz-1; AltName: Full=Zinc finger protein 151; AltName: Full=Zinc finger protein 60
Q14588 (ZN234_HUMAN)	RecName: Full=Zinc finger protein 234; AltName: Full=Zinc finger protein 269; AltName: Full=Zinc finger protein HZF4
Q14590 (ZN235_HUMAN)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 270; AltName: Full=Zinc finger protein 93 homolog; Short=Zfp-93; AltName: Full=Zinc finger protein HZF6
Q15935 (ZNF77_HUMAN)	RecName: Full=Zinc finger protein 77; AltName: Full=ZNFpT1
Q16600 (ZN239_HUMAN)	RecName: Full=Zinc finger protein 239; AltName: Full=Zinc finger protein HOK-2; AltName: Full=Zinc finger protein MOK-2
Q25514 (HUNB_MANSE)	RecName: Full=Protein hunchback
Q28151 (OZF_BOVIN)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q60821 (ZBT17_MOUSE)	RecName: Full=Zinc finger and BTB domain-containing protein 17; AltName: Full=LP-1; AltName: Full=Polyomavirus late initiator promoter-binding protein; AltName: Full=Zinc finger protein 100; Short=Zfp-100; AltName: Full=Zinc finger protein 151; AltName: Full=Zinc finger protein Z13
Q61116 (ZN235_MOUSE)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 93; Short=Zfp-93
Q61164 (CTCF_MOUSE)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog

Q91924 (SNAI2_XENLA)	RecName: Full=Zinc finger protein SNAI2; AltName: Full=Protein slug-alpha; AltName: Full=Protein snail homolog 2; AltName: Full=Snail protein homolog Slug; Short=xSlu
XP_973961	PREDICTED: transcriptional repressor CTCF [Tribolium castaneum]
XP_974363	PREDICTED: zinc finger protein 91 [Tribolium castaneum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_002413501	transcriptional repressor CTCF, putative, partial [Ixodes scapularis]
XP_002423875	zinc finger protein SLUG, putative [Pediculus humanus corporis]
XP_003242604	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003244861	PREDICTED: putative zinc finger protein 852 [Acyrthosiphon pisum]
XP_003400065	PREDICTED: protein escargot-like [Bombus terrestris]
XP_003704391	PREDICTED: protein escargot-like [Megachile rotundata]
XP_003743860	PREDICTED: protein hunchback-like [Metaseiulus occidentalis]
XP_006607165	PREDICTED: protein escargot-like [Apis dorsata]
XP_006806237	PREDICTED: zinc finger protein 569-like [Neolamprologus brichardi]
XP_006807046	PREDICTED: histone-lysine N-methyltransferase PRDM9-like isoform X1 [Neolamprologus brichardi]
XP_007540550	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_008181794	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183214	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183216	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008188522	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_011065239	PREDICTED: zinc finger protein 26-like isoform X1 [Acromyrmex echinatior]
XP_011140381	PREDICTED: zinc finger protein 624-like isoform X1 [Harpegnathos saltator]
XP_011263463	PREDICTED: zinc finger protein 572-like [Camponotus floridanus]
XP_011313910	PREDICTED: zinc finger protein 62-like [Fopius arisanus]
XP_011334642	PREDICTED: zinc finger protein 57-like [Cerapachys biroi]
XP_011352460	PREDICTED: transcriptional repressor CTCFL-like isoform X1 [Cerapachys biroi]
XP_011352467	PREDICTED: transcriptional repressor CTCFL-like isoform X2 [Cerapachys biroi]
XP_011352468	PREDICTED: transcriptional repressor CTCFL-like isoform X3 [Cerapachys biroi]
XP_011430534	PREDICTED: protein hunchback-like isoform X1 [Crassostrea gigas]
XP_011430535	PREDICTED: protein hunchback-like isoform X2 [Crassostrea gigas]
XP_011430536	PREDICTED: protein hunchback-like isoform X3 [Crassostrea gigas]
XP_011430538	PREDICTED: protein hunchback-like isoform X4 [Crassostrea gigas]
XP_011430539	PREDICTED: protein hunchback-like isoform X5 [Crassostrea gigas]
XP_011430540	PREDICTED: protein hunchback-like isoform X6 [Crassostrea gigas]
XP_011695216	PREDICTED: PR domain zinc finger protein 5-like isoform X1 [Wasmannia auropunctata]
XP_011695218	PREDICTED: PR domain zinc finger protein 5-like isoform X3 [Wasmannia auropunctata]
XP_012266385	PREDICTED: zinc finger protein 624-like [Athalia rosae]
XP_012266664	PREDICTED: protein glass-like [Athalia rosae]
XP_012266987	PREDICTED: transcriptional repressor CTCFL isoform X3 [Athalia rosae]
XP_012269273	PREDICTED: zinc finger protein 569-like [Athalia rosae]
XP_012273962	PREDICTED: zinc finger protein SNAI2-like [Orussus abietinus]
XP_012274482	PREDICTED: zinc finger protein 93 [Orussus abietinus]
XP_012288627	PREDICTED: zinc finger protein 658 [Orussus abietinus]
XP_012547835	PREDICTED: zinc finger protein 112-like [Bombyx mori]
XP_012548663	PREDICTED: zinc finger protein 28-like [Bombyx mori]
XP_013197323	PREDICTED: zinc finger protein 84-like [Amyelois transitella]
XP_013380320	PREDICTED: fez family zinc finger protein 1-like [Lingula anatina]
XP_013401760	PREDICTED: zinc finger and BTB domain-containing protein 24-like [Lingula anatina]
XP_013420663	PREDICTED: protein hunchback-like isoform X4 [Lingula anatina]
XP_013420664	PREDICTED: protein hunchback-like isoform X5 [Lingula anatina]
XP_013420665	PREDICTED: protein hunchback-like isoform X6 [Lingula anatina]
XP_013420666	PREDICTED: protein hunchback-like isoform X7 [Lingula anatina]
XP_013763388	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Pundamilia nyererei]
XP_013772231	PREDICTED: protein hunchback-like [Limulus polyphemus]
XP_013772409	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013775795	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013775803	PREDICTED: zinc finger protein SNAI2-like [Limulus polyphemus]
XP_013776060	PREDICTED: protein hunchback-like [Limulus polyphemus]
XP_013778397	PREDICTED: gastrula zinc finger protein XlCGF7.1-like [Limulus polyphemus]
XP_013779582	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013782827	PREDICTED: zinc finger protein 354A-like [Limulus polyphemus]
XP_013783281	PREDICTED: zinc finger protein 227-like [Limulus polyphemus]
XP_013784027	PREDICTED: zinc finger protein SNAI2-like [Limulus polyphemus]
XP_013784172	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013785583	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013785819	PREDICTED: protein snail homolog Sna-like [Limulus polyphemus]
XP_013786641	PREDICTED: zinc finger protein with KRAB and SCAN domains 7-like isoform X1 [Limulus polyphemus]
XP_013786656	PREDICTED: zinc finger protein with KRAB and SCAN domains 7-like isoform X2 [Limulus polyphemus]
XP_013786661	PREDICTED: zinc finger Y-chromosomal protein 2-like isoform X3 [Limulus polyphemus]

XP_013787012	PREDICTED: zinc finger protein 239-like [Limulus polyphemus]
XP_013787016	PREDICTED: protein snail homolog Sna-like [Limulus polyphemus]
XP_013787573	PREDICTED: hunchback-like protein [Limulus polyphemus]
XP_013787698	PREDICTED: zinc finger protein 37-like [Limulus polyphemus]
XP_013788334	PREDICTED: zinc finger protein 501-like [Limulus polyphemus]
XP_013790292	PREDICTED: zinc finger protein 616-like [Limulus polyphemus]
XP_013790651	PREDICTED: zinc finger protein 681-like [Limulus polyphemus]
XP_013790709	PREDICTED: zinc finger and BTB domain-containing protein 24-like [Limulus polyphemus]
XP_013791471	PREDICTED: zinc finger protein 888-like [Limulus polyphemus]
XP_013793148	PREDICTED: zinc finger protein 436-like, partial [Limulus polyphemus]
XP_013856101	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Austrofundulus limnaeus]
XP_014258648	PREDICTED: zinc finger protein 845-like [Cimex lectularius]
XP_014265828	PREDICTED: putative zinc finger protein 724 [Maylandia zebra]
XP_014289603	PREDICTED: protein snail homolog Sna-like [Halyomorpha halys]
XP_014294319	PREDICTED: zinc finger protein 708-like [Halyomorpha halys]

9.4.2.2 *Wingless*

Name	Description
B2GUT4 (WNT11_XENTR)	RecName: Full=Protein Wnt-11; AltName: Full=Protein Wnt-11-related; Flags: Precursor
Locus_1_Transcript_68102/166847_Confidence_1.000_Length_869 - ORF 7 (frame 3) translation	Locus_1_Transcript_68102/166847_Confidence_1.000_Length_869
Locus_1_Transcript_83171/166847_Confidence_1.000_Length_1780 - ORF 9 (frame 3) translation	Locus_1_Transcript_83171/166847_Confidence_1.000_Length_1780
Locus_1_Transcript_98900/166847_Confidence_1.000_Length_1008 - ORF 6 (frame 2) translation	Locus_1_Transcript_98900/166847_Confidence_1.000_Length_1008
Locus_3571_Transcript_10/10_Confidence_0.658_Length_4480 - ORF 19 (frame 1) translation	Locus_3571_Transcript_10/10_Confidence_0.658_Length_4480
Locus_15537_Transcript_5/9_Confidence_0.743_Length_3990 - ORF 21 (frame 1) translation	Locus_15537_Transcript_5/9_Confidence_0.743_Length_3990
Locus_16135_Transcript_2/2_Confidence_0.857_Length_3405 - ORF 1 (frame 2) translation	Locus_16135_Transcript_2/2_Confidence_0.857_Length_3405
Locus_16184_Transcript_5/5_Confidence_0.727_Length_2556 - ORF 2 (frame 3) translation	Locus_16184_Transcript_5/5_Confidence_0.727_Length_2556
Locus_18733_Transcript_5/6_Confidence_0.333_Length_1590 - ORF 1 (frame 2) translation	Locus_18733_Transcript_5/6_Confidence_0.333_Length_1590
Locus_19006_Transcript_6/6_Confidence_0.684_Length_5732 - ORF 22 (frame 2) translation	Locus_19006_Transcript_6/6_Confidence_0.684_Length_5732
Locus_19066_Transcript_1/1_Confidence_1.000_Length_2229 - ORF 2 (frame 1) translation	Locus_19066_Transcript_1/1_Confidence_1.000_Length_2229
Locus_19891_Transcript_5/5_Confidence_0.714_Length_5240 - ORF 1 (frame 1) translation	Locus_19891_Transcript_5/5_Confidence_0.714_Length_5240
Locus_19916_Transcript_1/2_Confidence_0.667_Length_3064 - ORF 3 (frame 3) translation	Locus_19916_Transcript_1/2_Confidence_0.667_Length_3064
NP_033549	protein Wnt-4 precursor [Mus musculus]
NP_110388	protein Wnt-4 precursor [Homo sapiens]
NP_445854	protein Wnt-4 precursor [Rattus norvegicus]
NP_001079279	protein Wnt-2b-A precursor [Xenopus laevis]
NP_001096551	protein Wnt-16 precursor [Xenopus (Silurana) tropicalis]
NP_001158455	wingless-type MMTV integration site family member 2 precursor [Saccoglossus kowalevskii]
NP_001161678	wingless-type MMTV integration site family, member 8 precursor [Saccoglossus kowalevskii]
NP_001191573	Wnt-2 protein precursor [Aplysia californica]
NP_001239014	protein Wnt-4 isoform 2 precursor [Xenopus laevis]
NP_001239015	protein Wnt-4 precursor [Xenopus (Silurana) tropicalis]
O13267 (WNT5A_PLEWA)	RecName: Full=Protein Wnt-5a; Short=PWnt-5a; Flags: Precursor
O42122 (WNT5B_ORYLA)	RecName: Full=Protein Wnt-5b; Flags: Precursor
O70283 (WNT2B_MOUSE)	RecName: Full=Protein Wnt-2b; AltName: Full=Protein Wnt-13; Flags: Precursor
O73864 (WNT11_DANRE)	RecName: Full=Protein Wnt-11; Flags: Precursor
P04426 (WNT1_MOUSE)	RecName: Full=Proto-oncogene Wnt-1; AltName: Full=Proto-oncogene Int-1; Flags: Precursor
P04628 (WNT1_HUMAN)	RecName: Full=Proto-oncogene Wnt-1; AltName: Full=Proto-oncogene Int-1 homolog; Flags: Precursor
P10108 (WNT1_XENLA)	RecName: Full=Protein Wnt-1; Short=XWnt-1; AltName: Full=XInt-1; Flags: Precursor
P17553 (WNT3_MOUSE)	RecName: Full=Proto-oncogene Wnt-3; AltName: Full=Proto-oncogene Int-4; Flags: Precursor
P21551 (WNT1_AMBME)	RecName: Full=Protein Wnt-1; Flags: Precursor
P22724 (WNT4_MOUSE)	RecName: Full=Protein Wnt-4; Flags: Precursor
P22725 (WNT5A_MOUSE)	RecName: Full=Protein Wnt-5a; Flags: Precursor
P22726 (WNT5B_MOUSE)	RecName: Full=Protein Wnt-5b; Flags: Precursor
P22727 (WNT6_MOUSE)	RecName: Full=Protein Wnt-6; Flags: Precursor
P24257 (WNT1_DANRE)	RecName: Full=Protein Wnt-1; Flags: Precursor
P24383 (WNT7A_MOUSE)	RecName: Full=Protein Wnt-7a; Flags: Precursor
P28026 (WNT8_XENLA)	RecName: Full=Protein Wnt-8; Short=XWnt-8; Flags: Precursor
P28047 (WNT7B_MOUSE)	RecName: Full=Protein Wnt-7b; Flags: Precursor
P28465 (WNT2_DROME)	RecName: Full=Protein Wnt-2; AltName: Full=dWnt-2; Flags: Precursor
P31286 (WNT5A_XENLA)	RecName: Full=Protein Wnt-5a; Short=XWnt-5a; Flags: Precursor
P41221 (WNT5A_HUMAN)	RecName: Full=Protein Wnt-5a; Flags: Precursor
P47793 (WNT4A_DANRE)	RecName: Full=Protein Wnt-4a; Flags: Precursor
P48615 (WNT11_MOUSE)	RecName: Full=Protein Wnt-11; Flags: Precursor
P49337 (WNT4_CHICK)	RecName: Full=Protein Wnt-4; Flags: Precursor
P49338 (WNT4_XENLA)	RecName: Full=Protein Wnt-4; Short=XWnt-4; Flags: Precursor

P49339 (WNT11_CHICK)	RecName: Full=Protein Wnt-11; Flags: Precursor
P49340 (WNT1_BOMMO)	RecName: Full=Protein Wnt-1; Flags: Precursor
P49893 (WN11B_XENLA)	RecName: Full=Protein Wnt-11b; AltName: Full=Protein Wnt-11; Short=XWnt-11; Flags: Precursor
P51028 (WNT8A_DANRE)	RecName: Full=Protein Wnt-8a; Flags: Precursor
P51029 (WNT8B_DANRE)	RecName: Full=Protein Wnt-8b; Flags: Precursor
P51030 (WNT8C_CHICK)	RecName: Full=Protein Wnt-8c; AltName: Full=CWnt-8; Flags: Precursor
P51891 (WNT11_COTJA)	RecName: Full=Protein Wnt-11; Flags: Precursor
P56703 (WNT3_HUMAN)	RecName: Full=Proto-oncogene Wnt-3; AltName: Full=Proto-oncogene Int-4 homolog; Flags: Precursor
P56705 (WNT4_HUMAN)	RecName: Full=Protein Wnt-4; Flags: Precursor
P56706 (WNT7B_HUMAN)	RecName: Full=Protein Wnt-7b; Flags: Precursor
P87387 (WN2BA_XENLA)	RecName: Full=Protein Wnt-2b-A; Short=Wnt-2b; Short=XWnt-2b; AltName: Full=XWnt-2; Flags: Precursor
Q1KYK4 (WNT7A_AOTTR)	RecName: Full=Protein Wnt-7a; Flags: Precursor
Q1KYL3 (WNT7A_CHLAE)	RecName: Full=Protein Wnt-7a; Flags: Precursor
Q2LMP1 (WNT3A_CHICK)	RecName: Full=Protein Wnt-3a; Flags: Precursor
Q2QL76 (WNT2_DIDVI)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q2QL85 (WNT2_MICMU)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q2QLA5 (WNT2_HORSE)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q2QLC7 (WNT2_CARPS)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q2QLH2 (WNT2_OTOGA)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q3L254 (WNT7B_CHICK)	RecName: Full=Protein Wnt-7b; Flags: Precursor
Q5E9U6 (WNT16_BOVIN)	RecName: Full=Protein Wnt-16; Flags: Precursor
Q07DV4 (WNT2_AOTNA)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q07DX7 (WNT2_NOMLE)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q07DZ8 (WNT2_ORNAN)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q07E31 (WNT2_NEONE)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q07E44 (WNT2_DASNO)	RecName: Full=Protein Wnt-2; Flags: Precursor
Q9H1J5 (WNT8A_HUMAN)	RecName: Full=Protein Wnt-8a; AltName: Full=Protein Wnt-8d; Flags: Precursor
Q9H1J7 (WNT5B_HUMAN)	RecName: Full=Protein Wnt-5b; Flags: Precursor
Q9QXQ5 (WNT4_RAT)	RecName: Full=Protein Wnt-4; Flags: Precursor
Q9QXQ7 (WNT5A_RAT)	RecName: Full=Protein Wnt-5a; Flags: Precursor
Q9QYS1 (WNT16_MOUSE)	RecName: Full=Protein Wnt-16; Flags: Precursor
Q9UBV4 (WNT16_HUMAN)	RecName: Full=Protein Wnt-16; Flags: Precursor
Q9WUD6 (WNT8B_MOUSE)	RecName: Full=Protein Wnt-8b; Flags: Precursor
Q9Y6F9 (WNT6_HUMAN)	RecName: Full=Protein Wnt-6; Flags: Precursor
Q27Q52 (WNT5A_RABIT)	RecName: Full=Protein Wnt-5a; Flags: Precursor
Q98SN7 (WNT2B_CHICK)	RecName: Full=Protein Wnt-2b; Flags: Precursor
Q670P5 (WNT11_XENLA)	RecName: Full=Protein Wnt-11; AltName: Full=Protein Wnt-11-related; Short=Wnt11-R; Short=Wnt11r; Flags: Precursor
Q06442 (WNT5A_AMBME)	RecName: Full=Protein Wnt-5a; Flags: Precursor
Q64527 (WNT8A_MOUSE)	RecName: Full=Protein Wnt-8a; AltName: Full=Protein Wnt-8d; AltName: Full=Stimulated by retinoic acid gene 11 protein; Flags: Precursor
Q91029 (WNT1_CHICK)	RecName: Full=Protein Wnt-1
Q92050 (WNT5B_DANRE)	RecName: Full=Protein Wnt-5b; Flags: Precursor
Q93097 (WNT2B_HUMAN)	RecName: Full=Protein Wnt-2b; AltName: Full=Protein Wnt-13; Flags: Precursor
Q93098 (WNT8B_HUMAN)	RecName: Full=Protein Wnt-8b; Flags: Precursor
WNT1_MOUSE	RecName: Full=Proto-oncogene Wnt-1; AltName: Full=Proto-oncogene Int-1; Flags: Precursor
WNTG_DROME	RecName: Full=Protein wingless; AltName: Full=Protein Wnt-1; AltName: Full=Protein int-1; AltName: Full=dInt-1; AltName: Full=dWnt-1; Flags: Precursor
XP_001603351	PREDICTED: protein Wnt-6 [Nasonia vitripennis]
XP_002402520	WNT-2 precursor, putative, partial [Ixodes scapularis]
XP_002407192	WNT-2 precursor, putative, partial [Ixodes scapularis]
XP_002423103	protein Wnt-4 precursor, putative [Pediculus humanus corporis]
XP_002423124	protein Wnt-5B precursor, putative [Pediculus humanus corporis]
XP_002434188	AmphiWnt4, putative [Ixodes scapularis]
XP_003488892	PREDICTED: protein Wnt-5b-like [Bombus impatiens]
XP_003690619	PREDICTED: protein Wnt-5b-like isoform X1 [Apis florea]
XP_003738399	PREDICTED: protein Wnt-8b-like [Metaseiulus occidentalis]
XP_003746249	PREDICTED: protein Wnt-4-like [Metaseiulus occidentalis]
XP_003746391	PREDICTED: protein Wnt-16-like [Metaseiulus occidentalis]
XP_004073580	PREDICTED: protein Wnt-8a-like [Oryzias latipes]
XP_004404467	PREDICTED: protein Wnt-16 [Odobenus rosmarus divergens]
XP_004602120	PREDICTED: protein Wnt-16 [Sorex araneus]
XP_004677035	PREDICTED: protein Wnt-16 [Condylura cristata]
XP_004910783	PREDICTED: protein Wnt-2b [Xenopus (Silurana) tropicalis]
XP_005081076	PREDICTED: protein Wnt-4 [Mesocricetus auratus]
XP_005281804	PREDICTED: protein Wnt-4 isoform X2 [Chrysemys picta bellii]
XP_005418764	PREDICTED: protein Wnt-8a [Geospiza fortis]
XP_005987699	PREDICTED: protein Wnt-2b isoform X1 [Latimeria chalumnae]
XP_006086607	PREDICTED: protein Wnt-8a isoform X1 [Myotis lucifugus]
XP_006113743	PREDICTED: protein Wnt-11b-2 [Pelodiscus sinensis]
XP_006124223	PREDICTED: protein Wnt-4 [Pelodiscus sinensis]
XP_007522670	PREDICTED: protein Wnt-4 isoform X1 [Erinaceus europaeus]
XP_008164756	PREDICTED: protein Wnt-11b-like [Chrysemys picta bellii]
XP_008172860	PREDICTED: protein Wnt-4-like [Chrysemys picta bellii]
XP_008195370	PREDICTED: protein Wnt-1-like [Tribolium castaneum]
XP_008196351	PREDICTED: protein Wnt-7b [Tribolium castaneum]
XP_009637478	PREDICTED: protein Wnt-4-like [Egretta garzetta]
XP_009683397	PREDICTED: protein Wnt-4-like [Struthio camelus australis]
XP_010156299	PREDICTED: protein Wnt-11, partial [Eurypyga helias]
XP_010205428	PREDICTED: protein Wnt-8a [Colius striatus]
XP_010570829	PREDICTED: protein Wnt-11b-like [Haliaeetus leucocephalus]
XP_010892681	PREDICTED: protein Wnt-8a [Esox lucius]
XP_011062506	PREDICTED: protein Wnt-6-like isoform X2 [Acromyrmex echinatior]
XP_011268891	PREDICTED: protein Wnt-1 [Camponotus floridanus]
XP_011299179	PREDICTED: protein wingless [Fopius arisanus]

XP_011423677	PREDICTED: protein Wnt-16-like [Crassostrea gigas]
XP_011440894	PREDICTED: protein Wnt-7b-like isoform X1 [Crassostrea gigas]
XP_011553397	PREDICTED: protein Wnt-1-like [Plutella xylostella]
XP_011678787	PREDICTED: protein Wnt-4 [Strongylocentrotus purpuratus]
XP_011694243	PREDICTED: protein Wnt-5b-like [Wasmannia auropunctata]
XP_011703368	PREDICTED: protein Wnt-1 [Wasmannia auropunctata]
XP_011703381	PREDICTED: protein Wnt-6-like [Wasmannia auropunctata]
XP_011875415	PREDICTED: protein Wnt-6-like [Vollenhovia emeryi]
XP_011970847	PREDICTED: protein Wnt-4 isoform X1 [Ovis aries musimon]
XP_012055758	PREDICTED: protein Wnt-5b-like [Atta cephalotes]
XP_012263292	PREDICTED: protein Wnt-5b-like [Athalia rosae]
XP_012289231	PREDICTED: protein Wnt-6 [Orussus abietinus]
XP_012400784	PREDICTED: protein Wnt-11 [Sarcophilus harrisii]
XP_012524785	PREDICTED: protein Wnt-1 [Monomorium pharaonis]
XP_012540152	PREDICTED: protein Wnt-6 [Monomorium pharaonis]
XP_012624134	PREDICTED: protein Wnt-4 isoform X1 [Microcebus murinus]
XP_012934624	PREDICTED: protein Wnt-16-like [Aplysia californica]
XP_012937266	PREDICTED: wnt-2 protein precursor isoform X1 [Aplysia californica]
XP_012942721	PREDICTED: protein Wnt-7b-like [Aplysia californica]
XP_013186726	PREDICTED: protein Wnt-1-like isoform X2 [Amyelois transitella]
XP_013384141	PREDICTED: protein Wnt-2b-A-like isoform X1 [Lingula anatina]
XP_013402385	PREDICTED: protein Wnt-8b-like [Lingula anatina]
XP_013773807	PREDICTED: protein Wnt-5b-like [Limulus polyphemus]
XP_013773810	PREDICTED: protein Wnt-7b-like [Limulus polyphemus]
XP_013775302	PREDICTED: protein Wnt-16-like [Limulus polyphemus]
XP_013778123	PREDICTED: protein Wnt-5a-like [Limulus polyphemus]
XP_013780966	PREDICTED: protein Wnt-11b-2-like [Limulus polyphemus]
XP_013781816	PREDICTED: protein Wnt-2b-A-like [Limulus polyphemus]
XP_013781939	PREDICTED: protein Wnt-11b-2-like [Limulus polyphemus]
XP_013783076	PREDICTED: protein Wnt-8b-like [Limulus polyphemus]
XP_013783194	PREDICTED: protein Wnt-2b-like [Limulus polyphemus]
XP_013783627	PREDICTED: protein Wnt-7b-like [Limulus polyphemus]
XP_013783628	PREDICTED: protein Wnt-5b-like, partial [Limulus polyphemus]
XP_013784866	PREDICTED: protein Wnt-4-like [Limulus polyphemus]
XP_013786418	PREDICTED: protein Wnt-2b-like [Limulus polyphemus]
XP_013791039	PREDICTED: protein Wnt-11-like [Limulus polyphemus]
XP_014212755	PREDICTED: protein Wnt-1 [Copidosoma floridanum]
XP_014215427	PREDICTED: protein Wnt-6 [Copidosoma floridanum]
XP_014236540	PREDICTED: protein Wnt-1 [Trichogramma pretiosum]
XP_014236555	PREDICTED: protein Wnt-6 [Trichogramma pretiosum]
XP_014249666	PREDICTED: protein wingless isoform X1 [Cimex lectularius]
XP_014257387	PREDICTED: protein Wnt-4-like isoform X1 [Cimex lectularius]
XP_014257388	PREDICTED: protein wingless-like isoform X2 [Cimex lectularius]
XP_014281721	PREDICTED: protein wingless isoform X2 [Halyomorpha halys]
XP_014384624	PREDICTED: protein Wnt-8a isoform X1 [Myotis brandtii]

9.4.2.3 *Buttonhead*

Name	**Description**
A4II20 (EGR1_XENTR)	RecName: Full=Early growth response protein 1; Short=EGR-1
BTD_DROME	RecName: Full=Transcription factor btd; AltName: Full=Protein buttonhead
Locus_1_Transcript_158894/166847_Confidence_1.000_Length_1619 - ORF 12 (frame 3) translation	Locus_1_Transcript_158894/166847_Confidence_1.000_Length_1619
Locus_1_Transcript_73641/166847_Confidence_1.000_Length_1412 - ORF 1 (frame 1) translation	Locus_1_Transcript_73641/166847_Confidence_1.000_Length_1412
Locus_1_Transcript_97614/166847_Confidence_1.000_Length_878 - ORF 2 (frame 1) translation	Locus_1_Transcript_97614/166847_Confidence_1.000_Length_878
Locus_11926_Transcript_3/10_Confidence_0.138_Length_1586 - ORF 1 (frame 3) translation	Locus_11926_Transcript_3/10_Confidence_0.138_Length_1586
Locus_12180_Transcript_1/6_Confidence_0.625_Length_1666 - ORF 2 (frame 3) translation	Locus_12180_Transcript_1/6_Confidence_0.625_Length_1666
Locus_12603_Transcript_28/34_Confidence_0.072_Length_2482 - ORF 10 (frame 1) translation	Locus_12603_Transcript_28/34_Confidence_0.072_Length_2482
Locus_12853_Transcript_2/10_Confidence_0.289_Length_3709 - ORF 6 (frame 2) translation	Locus_12853_Transcript_2/10_Confidence_0.289_Length_3709
Locus_1422_Transcript_10/10_Confidence_0.500_Length_1039 - ORF 2 (frame 1) translation	Locus_1422_Transcript_10/10_Confidence_0.500_Length_1039
Locus_17841_Transcript_10/10_Confidence_0.346_Length_2379 - ORF 8 (frame 2) translation	Locus_17841_Transcript_10/10_Confidence_0.346_Length_2379
Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450 - ORF 25 (frame 1) translation	Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450
Locus_24701_Transcript_1/1_Confidence_1.000_Length_1226 - ORF 7 (frame 2) translation	Locus_24701_Transcript_1/1_Confidence_1.000_Length_1226
Locus_9586_Transcript_7/11_Confidence_0.090_Length_5776 - ORF 2 (frame 1) translation	Locus_9586_Transcript_7/11_Confidence_0.090_Length_5776
NP_001034509	Sp-like zinc finger transcription factor [Tribolium castaneum]
NP_001161575	KLF2-like transcription factor [Saccoglossus kowalevskii]
O08584 (KLF6_MOUSE)	RecName: Full=Krueppel-like factor 6; AltName: Full=Core promoter element-binding protein
O35738 (KLF12_MOUSE)	RecName: Full=Krueppel-like factor 12; AltName: Full=Transcriptional repressor AP-2rep
O35739 (KLF9_MOUSE)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1; AltName: Full=GC-box-binding protein 1; AltName: Full=Transcription factor BTEB1
O35819 (KLF6_RAT)	RecName: Full=Krueppel-like factor 6; AltName: Full=Core promoter element-binding protein; AltName: Full=Transcription factor Zf9

O43474 (KLF4_HUMAN)	RecName: Full=Krueppel-like factor 4; AltName: Full=Epithelial zinc finger protein EZF; AltName: Full=Gut-enriched krueppel-like factor
O70494 (SP3_MOUSE)	RecName: Full=Transcription factor Sp3
O75840 (KLF7_HUMAN)	RecName: Full=Krueppel-like factor 7; AltName: Full=Ubiquitous krueppel-like factor
O89090 (SP1_MOUSE)	RecName: Full=Transcription factor Sp1
O95600 (KLF8_HUMAN)	RecName: Full=Krueppel-like factor 8; AltName: Full=Basic krueppel-like factor 3; AltName: Full=Zinc finger protein 741
P08046 (EGR1_MOUSE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein Krox-24
P08047 (SP1_HUMAN)	RecName: Full=Transcription factor Sp1
P08154 (EGR1_RAT)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein Krox-24
P0CG40 (SP9_HUMAN)	RecName: Full=Transcription factor Sp9
P18146 (EGR1_HUMAN)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=AT225; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor ETR103; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein 225; AltName: Full=Zinc finger protein Krox-24
P26632 (EGR1_DANRE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Zinc finger protein Krox-24
P43300 (EGR3_MOUSE)	RecName: Full=Early growth response 3; Short=EGR-3
P43301 (EGR3_RAT)	RecName: Full=Early growth response 3; Short=EGR-3
P46099 (KLF1_MOUSE)	RecName: Full=Krueppel-like factor 1; AltName: Full=Erythroid krueppel-like transcription factor; Short=EKLF
P57682 (KLF3_HUMAN)	RecName: Full=Krueppel-like factor 3; AltName: Full=Basic krueppel-like factor; AltName: Full=CACCC-box-binding protein BKLF; AltName: Full=TEF-2
P58334 (KLF16_MOUSE)	RecName: Full=Krueppel-like factor 16; AltName: Full=Basic transcription element-binding protein 4; Short=BTE-binding protein 4; AltName: Full=Dopamine receptor-regulating factor; AltName: Full=Transcription factor BTEB4
P79288 (KLF9_PIG)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1; AltName: Full=GC-box-binding protein 1; AltName: Full=Transcription factor BTEB1
Q01713 (KLF9_RAT)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1; AltName: Full=GC-box-binding protein 1; AltName: Full=Transcription factor BTEB1
Q01714 (SP1_RAT)	RecName: Full=Transcription factor Sp1
Q02446 (SP4_HUMAN)	RecName: Full=Transcription factor Sp4; AltName: Full=SPR-1
Q02447 (SP3_HUMAN)	RecName: Full=Transcription factor Sp3; AltName: Full=SPR-2
Q06889 (EGR3_HUMAN)	RecName: Full=Early growth response protein 3; Short=EGR-3; AltName: Full=Zinc finger protein pilot
Q0VA40 (SP9_XENTR)	RecName: Full=Transcription factor Sp9
Q13351 (KLF1_HUMAN)	RecName: Full=Krueppel-like factor 1; AltName: Full=Erythroid krueppel-like transcription factor; Short=EKLF
Q13886 (KLF9_HUMAN)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1; AltName: Full=GC-box-binding protein 1; AltName: Full=Transcription factor BTEB1
Q13887 (KLF5_HUMAN)	RecName: Full=Krueppel-like factor 5; AltName: Full=Basic transcription element-binding protein 2; Short=BTE-binding protein 2; AltName: Full=Colon krueppel-like factor; AltName: Full=GC-box-binding protein 2; AltName: Full=Intestinal-enriched krueppel-like factor; AltName: Full=Transcription factor BTEB2
Q19A40 (KLF14_PANTR)	RecName: Full=Krueppel-like factor 14
Q19A41 (KLF14_MOUSE)	RecName: Full=Krueppel-like factor 14
Q5E9U0 (SP2_BOVIN)	RecName: Full=Transcription factor Sp2
Q5XGT8 (SP8_XENLA)	RecName: Full=Transcription factor Sp8
Q60793 (KLF4_MOUSE)	RecName: Full=Krueppel-like factor 4; AltName: Full=Epithelial zinc finger protein EZF; AltName: Full=Gut-enriched krueppel-like factor
Q60843 (KLF2_MOUSE)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q60980 (KLF3_MOUSE)	RecName: Full=Krueppel-like factor 3; AltName: Full=Basic krueppel-like factor; AltName: Full=CACCC-box-binding protein BKLF; AltName: Full=TEF-2
Q62445 (SP4_MOUSE)	RecName: Full=Transcription factor Sp4
Q64HY3 (SP9_MOUSE)	RecName: Full=Transcription factor Sp9
Q64HY5 (SP8_CHICK)	RecName: Full=Transcription factor Sp8
Q6BEB4 (SP5_HUMAN)	RecName: Full=Transcription factor Sp5
Q6GQH4 (EGR1A_XENLA)	RecName: Full=Early growth response protein 1-A; Short=EGR-1-A; Short=Xegr-1
Q6NTY6 (EGR1B_XENLA)	RecName: Full=Early growth response protein 1-B; Short=EGR-1-B
Q6NW96 (SP9_DANRE)	RecName: Full=Transcription factor Sp9
Q6P0J3 (SP8_DANRE)	RecName: Full=Transcription factor Sp8
Q8BMJ8 (SP8_MOUSE)	RecName: Full=Transcription factor Sp8
Q8IXZ3 (SP8_HUMAN)	RecName: Full=Transcription factor Sp8; AltName: Full=Specificity protein 8
Q8TD94 (KLF14_HUMAN)	RecName: Full=Krueppel-like factor 14; AltName: Full=Basic transcription element-binding protein 5; Short=BTE-binding protein 5; AltName: Full=Transcription factor BTEB5
Q8VI67 (SP7_MOUSE)	RecName: Full=Transcription factor Sp7; AltName: Full=C22; AltName: Full=Zinc finger protein osterix
Q90WR8 (SP3_CHICK)	RecName: Full=Transcription factor Sp3
Q99612 (KLF6_HUMAN)	RecName: Full=Krueppel-like factor 6; AltName: Full=B-cell-derived protein 1; AltName: Full=Core promoter element-binding protein;

	AltName: Full=GC-rich sites-binding factor GBF; AltName: Full=Proto-oncogene BCD1; AltName: Full=Suppressor of tumorigenicity 12 protein; AltName: Full=Transcription factor Zf9
Q99JB0 (KLF7_MOUSE)	RecName: Full=Krueppel-like factor 7
Q9BXK1 (KLF16_HUMAN)	RecName: Full=Krueppel-like factor 16; AltName: Full=Basic transcription element-binding protein 4; Short=BTE-binding protein 4; AltName: Full=Novel Sp1-like zinc finger transcription factor 2; AltName: Full=Transcription factor BTEB4; AltName: Full=Transcription factor NSLP2
Q9D2H6 (SP2_MOUSE)	RecName: Full=Transcription factor Sp2
Q9EPW2 (KLF15_MOUSE)	RecName: Full=Krueppel-like factor 15; AltName: Full=Cardiovascular Krueppel-like factor
Q9ET58 (KLF2_RAT)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q9JHX2 (SP5_MOUSE)	RecName: Full=Transcription factor Sp5
Q9JJZ6 (KLF13_MOUSE)	RecName: Full=Krueppel-like factor 13; AltName: Full=Basic transcription element-binding protein 3; Short=BTE-binding protein 3; AltName: Full=Erythroid transcription factor FKLF-2; AltName: Full=RANTES factor of late activated T-lymphocytes 1; Short=RFLAT-1; AltName: Full=Transcription factor BTEB3
Q9UIH9 (KLF15_HUMAN)	RecName: Full=Krueppel-like factor 15; AltName: Full=Kidney-enriched krueppel-like factor
Q9Y2Y9 (KLF13_HUMAN)	RecName: Full=Krueppel-like factor 13; AltName: Full=Basic transcription element-binding protein 3; Short=BTE-binding protein 3; AltName: Full=Novel Sp1-like zinc finger transcription factor 1; AltName: Full=RANTES factor of late activated T-lymphocytes 1; Short=RFLAT-1; AltName: Full=Transcription factor BTEB3; AltName: Full=Transcription factor NSLP1
Q9Y4X4 (KLF12_HUMAN)	RecName: Full=Krueppel-like factor 12; AltName: Full=Transcriptional repressor AP-2rep
Q9Y5W3 (KLF2_HUMAN)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q9Z0Z7 (KLF5_MOUSE)	RecName: Full=Krueppel-like factor 5; AltName: Full=Basic transcription element-binding protein 2; Short=BTE-binding protein 2; AltName: Full=Intestinal-enriched krueppel-like factor; AltName: Full=Transcription factor BTEB2
XP_001622426	predicted protein [Nematostella vectensis]
XP_001660650	AAEL010126-PA [Aedes aegypti]
XP_001664227	AAEL014006-PA [Aedes aegypti]
XP_001787418	PREDICTED: Krueppel-like factor 2 [Bos taurus]
XP_001849427	zinc finger protein 273 [Culex quinquefasciatus]
XP_001943786	PREDICTED: transcriptional regulator CRZ2-like [Acyrthosiphon pisum]
XP_002026405	GL20646 [Drosophila persimilis]
XP_002072737	GK13762 [Drosophila willistoni]
XP_002405687	zinc finger protein, putative, partial [Ixodes scapularis]
XP_002408908	transcription factor sp3, putative [Ixodes scapularis]
XP_002409989	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_002410850	zinc finger protein, putative, partial [Ixodes scapularis]
XP_002426166	Early growth response protein, putative [Pediculus humanus corporis]
XP_002433349	zinc finger, putative [Ixodes scapularis]
XP_003747475	PREDICTED: Krueppel-like factor 15-like [Metaseiulus occidentalis]
XP_003748452	PREDICTED: Krueppel-like factor 7-like [Metaseiulus occidentalis]
XP_005175631	PREDICTED: zinc finger and SCAN domain-containing protein 10 [Musca domestica]
XP_005187275	PREDICTED: protein ovo [Musca domestica]
XP_005521503	PREDICTED: Krueppel-like factor 13 [Pseudopodoces humilis]
XP_006736144	PREDICTED: Krueppel-like factor 2 [Leptonychotes weddellii]
XP_007434195	PREDICTED: Krueppel-like factor 7, partial [Python bivittatus]
XP_008192084	PREDICTED: Krueppel-like factor 6 isoform X1 [Tribolium castaneum]
XP_008192089	PREDICTED: Krueppel-like factor 7 isoform X2 [Tribolium castaneum]
XP_008194021	PREDICTED: Krueppel-like factor 5 isoform X1 [Tribolium castaneum]
XP_008194027	PREDICTED: Krueppel-like factor 6 isoform X2 [Tribolium castaneum]
XP_008198341	PREDICTED: sp-like zinc finger transcription factor isoform X1 [Tribolium castaneum]
XP_008200855	PREDICTED: early growth response protein 1-B isoform X1 [Tribolium castaneum]
XP_008200856	PREDICTED: early growth response protein 1-B isoform X2 [Tribolium castaneum]
XP_008483659	PREDICTED: early growth response protein 3-like [Diaphorina citri]
XP_008502889	PREDICTED: Krueppel-like factor 13 [Calypte anna]
XP_008544634	PREDICTED: Krueppel-like factor 16 isoform X1 [Microplitis demolitor]
XP_008544643	PREDICTED: Krueppel-like factor 16 isoform X2 [Microplitis demolitor]
XP_008544651	PREDICTED: Krueppel-like factor 16 isoform X3 [Microplitis demolitor]
XP_009072834	PREDICTED: Krueppel-like factor 13 [Acanthisitta chloris]
XP_009088107	PREDICTED: Krueppel-like factor 13 [Serinus canaria]
XP_009467966	PREDICTED: Krueppel-like factor 13 [Nipponia nippon]
XP_009553621	PREDICTED: Krueppel-like factor 13 [Cuculus canorus]
XP_011147728	PREDICTED: transcription factor hamlet [Harpegnathos saltator]
XP_011150831	PREDICTED: zinc finger protein 226 [Harpegnathos saltator]
XP_011175400	PREDICTED: E3 SUMO-protein ligase EGR2-like isoform X1 [Solenopsis invicta]
XP_011175401	PREDICTED: E3 SUMO-protein ligase EGR2-like isoform X2 [Solenopsis invicta]
XP_011264304	PREDICTED: asparagine-rich zinc finger protein AZF1-like [Camponotus floridanus]
XP_011417101	PREDICTED: transcription factor Sp3-like [Crassostrea gigas]
XP_011501424	PREDICTED: Krueppel-like factor 5 [Ceratosolen solmsi marchali]
XP_012034502	PREDICTED: Krueppel-like factor 2 isoform X1, partial [Ovis aries]
XP_012222749	PREDICTED: Krueppel-like factor 13 [Linepithema humile]
XP_012256216	PREDICTED: zinc finger protein 436-like [Athalia rosae]

XP_012282013	PREDICTED: transcription factor Sp1-like isoform X1 [Orussus abietinus]
XP_012282014	PREDICTED: transcription factor Sp1-like isoform X2 [Orussus abietinus]
XP_012677135	PREDICTED: Krueppel-like factor 9 [Clupea harengus]
XP_013094986	PREDICTED: transcription factor Sp4-like isoform X2 [Biomphalaria glabrata]
XP_013395520	PREDICTED: transcription factor Sp9-like isoform X1 [Lingula anatina]
XP_013395521	PREDICTED: transcription factor Sp9-like isoform X2 [Lingula anatina]
XP_013395522	PREDICTED: transcription factor Sp9-like isoform X3 [Lingula anatina]
XP_013395523	PREDICTED: transcription factor Sp9-like isoform X4 [Lingula anatina]
XP_013400546	PREDICTED: transcription factor Sp4-like [Lingula anatina]
XP_013408973	PREDICTED: Krueppel-like factor 5 [Lingula anatina]
XP_013416627	PREDICTED: Krueppel-like factor 9 [Lingula anatina]
XP_013772496	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013772769	PREDICTED: zinc finger protein 143-like [Limulus polyphemus]
XP_013772918	PREDICTED: transcription factor Sp9-like [Limulus polyphemus]
XP_013772960	PREDICTED: transcription factor Sp4-like [Limulus polyphemus]
XP_013773090	PREDICTED: Krueppel-like factor 2 [Limulus polyphemus]
XP_013773091	PREDICTED: pair-rule protein odd-paired-like [Limulus polyphemus]
XP_013773092	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013774753	PREDICTED: transcription factor Sp3-like [Limulus polyphemus]
XP_013776761	PREDICTED: transcription factor Sp9-like [Limulus polyphemus]
XP_013779431	PREDICTED: transcription factor Sp4-like [Limulus polyphemus]
XP_013780173	PREDICTED: early growth response protein 1-like [Limulus polyphemus]
XP_013780755	PREDICTED: transcription factor Sp9-like [Limulus polyphemus]
XP_013781707	PREDICTED: Krueppel-like factor 7 [Limulus polyphemus]
XP_013782264	PREDICTED: transcription factor Sp4-like [Limulus polyphemus]
XP_013782841	PREDICTED: early growth response protein 1-like [Limulus polyphemus]
XP_013782918	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013783296	PREDICTED: Krueppel-like factor 12 [Limulus polyphemus]
XP_013784047	PREDICTED: transcription factor Sp5-like [Limulus polyphemus]
XP_013784122	PREDICTED: Krueppel-like factor 1 [Limulus polyphemus]
XP_013784508	PREDICTED: Krueppel-like factor 1 [Limulus polyphemus]
XP_013785179	PREDICTED: Krueppel-like factor 10 [Limulus polyphemus]
XP_013786860	PREDICTED: early growth response protein 1-A-like [Limulus polyphemus]
XP_013788487	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013789594	PREDICTED: transcription factor Sp9-like, partial [Limulus polyphemus]
XP_013790888	PREDICTED: zinc finger protein Gfi-1b-like [Limulus polyphemus]
XP_013791872	PREDICTED: Krueppel-like factor 17 [Limulus polyphemus]
XP_013792351	PREDICTED: early growth response protein 2-like [Limulus polyphemus]
XP_013792741	PREDICTED: Krueppel-like factor 2 [Limulus polyphemus]
XP_013994864	PREDICTED: Krueppel-like factor 9 [Salmo salar]
XP_014247970	PREDICTED: Krueppel-like factor 9 isoform X2 [Cimex lectularius]
XP_972252	PREDICTED: transcription factor Sp4-like, partial [Tribolium castaneum]

9.4.2.4 *CtBP*

Name	**Description**
A1RYE4 (GYAR_THEPD)	RecName: Full=Glyoxylate reductase
A5A6P1 (SERA_PANTR)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
A5GFY8 (SERA_PIG)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
A6TFG7 (GHRB_KLEP7)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
A7ZYY6 (GHRA_ECOHS)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
A8ARD9 (GHRB_CITK8)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
B1IV68 (GHRA_ECOLC)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
B1L765 (GYAR_KORCO)	RecName: Full=Glyoxylate reductase
B1LIY1 (GHRA_ECOSM)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
B5XMZ4 (GHRB_KLEP3)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
B6YWH0 (GYAR_THEON)	RecName: Full=Glyoxylate reductase
B7LTG7 (GHRB_ESCF3)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
B7MTG4 (GHRA_ECO81)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
B7NLA1 (GHRA_ECO7I)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
B7UP47 (GHRA_ECO27)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
C5A1V0 (GYAR_THEGJ)	RecName: Full=Glyoxylate reductase
CTBP1_MOUSE	RecName: Full=C-terminal-binding protein 1; Short=CtBP1
CTBP2_MOUSE	RecName: Full=C-terminal-binding protein 2; Short=CtBP2
CTBP_DROME	RecName: Full=C-terminal-binding protein; Short=CtBP protein; AltName: Full=dCtBP
Locus_1_Transcript_460/166847_Confidence_1.000_Length_1666 - ORF 13 (frame 3) translation	Locus_1_Transcript_460/166847_Confidence_1.000_Length_1666
Locus_1_Transcript_47563/166847_Confidence_1.000_Length_528 - ORF 1 (frame 3) translation	Locus_1_Transcript_47563/166847_Confidence_1.000_Length_528

Locus_3441_Transcript_1/1_Confidence_1.000_Length_2133 - ORF 5 (frame 2) translation	Locus_3441_Transcript_1/1_Confidence_1.000_Length_2133
Locus_7467_Transcript_1/4_Confidence_0.556_Length_1373 - ORF 3 (frame 2) translation	Locus_7467_Transcript_1/4_Confidence_0.556_Length_1373
Locus_12304_Transcript_1/6_Confidence_0.182_Length_1072 - ORF 4 (frame 2) translation	Locus_12304_Transcript_1/6_Confidence_0.182_Length_1072
Locus_15254_Transcript_7/8_Confidence_0.500_Length_1977 - ORF 2 (frame 3) translation	Locus_15254_Transcript_7/8_Confidence_0.500_Length_1977
Locus_29905_Transcript_1/1_Confidence_1.000_Length_1104 - ORF 1 (frame 2) translation	Locus_29905_Transcript_1/1_Confidence_1.000_Length_1104
O08651 (SERA_RAT)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
O29445 (SERA_ARCFU)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=PGDH
O32264 (TKRA_BACSU)	RecName: Full=Probable 2-ketogluconate reductase; Short=2KR
O43175 (SERA_HUMAN)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
O46036 (CTBP_DROME)	RecName: Full=C-terminal-binding protein; Short=CtBP protein; AltName: Full=dCtBP
O88712 (CTBP1_MOUSE)	RecName: Full=C-terminal-binding protein 1; Short=CtBP1
P35136 (SERA_BACSU)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=PGDH
P56545 (CTBP2_HUMAN)	RecName: Full=C-terminal-binding protein 2; Short=CtBP2
P56546 (CTBP2_MOUSE)	RecName: Full=C-terminal-binding protein 2; Short=CtBP2
P58000 (GHRB_ENTAG)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
P75913 (GHRA_ECOLI)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
Q0TJ41 (GHRA_ECOL5)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
Q0VCQ1 (CTBP2_BOVIN)	RecName: Full=C-terminal-binding protein 2; Short=CtBP2
Q1RDC8 (GHRA_ECOUT)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
Q5EAD2 (SERA_BOVIN)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
Q5JEZ2 (GYAR_THEKO)	RecName: Full=Glyoxylate reductase
Q5R7M2 (SERA_PONAB)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
Q8U3Y2 (GYAR_PYRFU)	RecName: Full=Glyoxylate reductase
Q8X9K1 (GHRA_ECO57)	RecName: Full=Glyoxylate/hydroxypyruvate reductase A; AltName: Full=2-ketoacid reductase
Q9C4M5 (GYAR_THELN)	RecName: Full=Glyoxylate reductase
Q9EQH5 (CTBP2_RAT)	RecName: Full=C-terminal-binding protein 2; Short=CtBP2
Q9UBQ7 (GRHPR_HUMAN)	RecName: Full=Glyoxylate reductase/hydroxypyruvate reductase
Q9W758 (CTBP2_XENLA)	RecName: Full=C-terminal-binding protein 2; Short=CtBP2; AltName: Full=C-terminal-binding protein B; AltName: Full=TCF-3 corepressor CtBP; AltName: Full=XCtBP
Q9YAW4 (GYAR_AERPE)	RecName: Full=Glyoxylate reductase
Q9YHU0 (CTBP1_XENLA)	RecName: Full=C-terminal-binding protein 1; Short=CtBP1; AltName: Full=C-terminal-binding protein A
Q9Z2F5 (CTBP1_RAT)	RecName: Full=C-terminal-binding protein 1; Short=CtBP1; AltName: Full=50 kDa BFA-dependent ADP-ribosylation substrate; AltName: Full=BARS-50; AltName: Full=C-terminal-binding protein 3; Short=CtBP3
Q31V71 (GHRB_SHIBS)	RecName: Full=Glyoxylate/hydroxypyruvate reductase B
Q60HD7 (SERA_MACFA)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH
Q91Z53 (GRHPR_MOUSE)	RecName: Full=Glyoxylate reductase/hydroxypyruvate reductase
Q13363 (CTBP1_HUMAN)	RecName: Full=C-terminal-binding protein 1; Short=CtBP1
Q58424 (SERA_METJA)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=PGDH
Q61753 (SERA_MOUSE)	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=3-PGDH; AltName: Full=A10
WP_020961094	D-glycerate dehydrogenase [Geobacillus sp. JF8]
XP_795649	PREDICTED: D-3-phosphoglycerate dehydrogenase [Strongylocentrotus purpuratus]
XP_001120952	PREDICTED: hydroxyphenylpyruvate reductase-like isoform X1 [Apis mellifera]
XP_001606634	PREDICTED: glyoxylate/hydroxypyruvate reductase HPR3-like [Nasonia vitripennis]
XP_001639916	predicted protein [Nematostella vectensis]
XP_002400999	glyoxylate/hydroxypyruvate reductase, putative, partial [Ixodes scapularis]
XP_002404432	D-3-phosphoglycerate dehydrogenase, putative, partial [Ixodes scapularis]
XP_002407150	glyoxylate/hydroxypyruvate reductase, putative [Ixodes scapularis]
XP_002422968	D-3-phosphoglycerate dehydrogenase, putative [Pediculus humanus corporis]
XP_002431802	C-terminal-binding protein, putative [Pediculus humanus corporis]
XP_002435792	glyoxylate/hydroxypyruvate reductase, putative, partial [Ixodes scapularis]
XP_002732924	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Saccoglossus kowalevskii]
XP_003386095	PREDICTED: D-3-phosphoglycerate dehydrogenase-like [Amphimedon queenslandica]
XP_003695020	PREDICTED: hydroxyphenylpyruvate reductase-like isoform X1 [Apis florea]
XP_003740751	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Metaseiulus occidentalis]
XP_006611074	PREDICTED: hydroxyphenylpyruvate reductase-like isoform X1 [Apis dorsata]
XP_007428952	PREDICTED: d-3-phosphoglycerate dehydrogenase [Python bivittatus]
XP_008474224	PREDICTED: D-3-phosphoglycerate dehydrogenase [Diaphorina citri]

XP_011264239	PREDICTED: formate dehydrogenase, mitochondrial-like [Camponotus floridanus]
XP_011439665	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Crassostrea gigas]
XP_011449387	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Crassostrea gigas]
XP_011641081	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Pogonomyrmex barbatus]
XP_012064147	PREDICTED: probable 2-ketogluconate reductase [Atta cephalotes]
XP_013061809	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X1 [Biomphalaria glabrata]
XP_013061810	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X2 [Biomphalaria glabrata]
XP_013148350	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Papilio polytes]
XP_013383210	PREDICTED: C-terminal-binding protein-like isoform X1 [Lingula anatina]
XP_013383211	PREDICTED: C-terminal-binding protein-like isoform X2 [Lingula anatina]
XP_013383212	PREDICTED: C-terminal-binding protein-like isoform X3 [Lingula anatina]
XP_013402731	PREDICTED: D-3-phosphoglycerate dehydrogenase-like [Lingula anatina]
XP_013408878	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Lingula anatina]
XP_013409158	PREDICTED: D-3-phosphoglycerate dehydrogenase-like [Lingula anatina]
XP_013774181	PREDICTED: glyoxylate/hydroxypyruvate reductase A-like [Limulus polyphemus]
XP_013779730	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Limulus polyphemus]
XP_013780999	PREDICTED: C-terminal-binding protein-like [Limulus polyphemus]
XP_013781656	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like [Limulus polyphemus]
XP_013782633	PREDICTED: C-terminal-binding protein-like [Limulus polyphemus]
XP_013782685	PREDICTED: C-terminal-binding protein-like [Limulus polyphemus]
XP_013783958	PREDICTED: C-terminal-binding protein-like [Limulus polyphemus]
XP_013788512	PREDICTED: C-terminal-binding protein-like [Limulus polyphemus]
XP_013794796	PREDICTED: D-3-phosphoglycerate dehydrogenase-like [Limulus polyphemus]
XP_014221715	PREDICTED: glyoxylate/hydroxypyruvate reductase A-like isoform X1 [Trichogramma pretiosum]
XP_014221717	PREDICTED: glyoxylate/hydroxypyruvate reductase A-like isoform X2 [Trichogramma pretiosum]
XP_014239497	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X1 [Cimex lectularius]
XP_014239498	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X2 [Cimex lectularius]
XP_014270248	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X1 [Halyomorpha halys]
XP_014270257	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform X2 [Halyomorpha halys]

9.4.2.5 *CTCF*

Name	Description
A0JNB1 (ZN227_BOVIN)	RecName: Full=Zinc finger protein 227
A1YF12 (ZNF16_GORGO)	RecName: Full=Zinc finger protein 16
A1YG88 (ZNF16_PANPA)	RecName: Full=Zinc finger protein 16
A2APF3 (CTCFL_MOUSE)	RecName: Full=Transcriptional repressor CTCFL; AltName: Full=Brother of the regulator of imprinted sites; AltName: Full=CCCTC-binding factor; AltName: Full=CTCF paralog; AltName: Full=CTCF-like protein
A2T759 (ZNF16_PANTR)	RecName: Full=Zinc finger protein 16
A2VDQ7 (ZN420_BOVIN)	RecName: Full=Zinc finger protein 420
A6QLU5 (ZN184_BOVIN)	RecName: Full=Zinc finger protein 184
AAF50573	CTCF [Drosophila melanogaster]
B4DU55 (ZN879_HUMAN)	RecName: Full=Zinc finger protein 879
CTCF_MOUSE	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
CTCFL_MOUSE	RecName: Full=Transcriptional repressor CTCFL; AltName: Full=Brother of the regulator of imprinted sites; AltName: Full=CCCTC-binding factor; AltName: Full=CTCF paralog; AltName: Full=CTCF-like protein
Locus_1_Transcript_18884/166847_Confidence_1.000_Length_1903 - ORF 10 (frame 2) translation	Locus_1_Transcript_18884/166847_Confidence_1.000_Length_1903
Locus_487_Transcript_29/38_Confidence_0.065_Length_3976 - ORF 13 (frame 1) translation	Locus_487_Transcript_29/38_Confidence_0.065_Length_3976
Locus_766_Transcript_1/4_Confidence_0.840_Length_3832 - ORF 3 (frame 3) translation	Locus_766_Transcript_1/4_Confidence_0.840_Length_3832
Locus_2073_Transcript_38/42_Confidence_0.135_Length_2019 - ORF 7 (frame 1) translation	Locus_2073_Transcript_38/42_Confidence_0.135_Length_2019
Locus_3763_Transcript_1/10_Confidence_0.571_Length_1828 - ORF 11 (frame 2) translation	Locus_3763_Transcript_1/10_Confidence_0.571_Length_1828
Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349 - ORF 20 (frame 1) translation	Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349
Locus_7469_Transcript_16/25_Confidence_0.159_Length_4958 - ORF 10 (frame 3) translation	Locus_7469_Transcript_16/25_Confidence_0.159_Length_4958

Locus_8963_Transcript_1/8_Confidence_0.682_Length_4449 - ORF 11 (frame 3) translation	Locus_8963_Transcript_1/8_Confidence_0.682_Length_4449
Locus_10669_Transcript_4/6_Confidence_0.680_Length_3066 - ORF 7 (frame 1) translation	Locus_10669_Transcript_4/6_Confidence_0.680_Length_3066
Locus_14442_Transcript_2/5_Confidence_0.312_Length_2539 - ORF 1 (frame 2) translation	Locus_14442_Transcript_2/5_Confidence_0.312_Length_2539
Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958 - ORF 2 (frame 2) translation	Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958
Locus_17642_Transcript_1/5_Confidence_0.571_Length_2317 - ORF 2 (frame 2) translation	Locus_17642_Transcript_1/5_Confidence_0.571_Length_2317
Locus_18417_Transcript_1/6_Confidence_0.667_Length_1242 - ORF 4 (frame 2) translation	Locus_18417_Transcript_1/6_Confidence_0.667_Length_1242
Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891 - ORF 1 (frame 1) translation	Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891
Locus_29795_Transcript_1/1_Confidence_1.000_Length_1252 - ORF 4 (frame 1) translation	Locus_29795_Transcript_1/1_Confidence_1.000_Length_1252
O75373 (ZN737_HUMAN)	RecName: Full=Zinc finger protein 737; AltName: Full=Zinc finger protein 102
O94892 (ZN432_HUMAN)	RecName: Full=Zinc finger protein 432
P08043 (ZFP2_MOUSE)	RecName: Full=Zinc finger protein 2; Short=Zfp-2; AltName: Full=Protein mKR2
P10076 (ZFP26_MOUSE)	RecName: Full=Zinc finger protein 26; Short=Zfp-26; AltName: Full=Protein mKR3
P15620 (ZN271_MOUSE)	RecName: Full=Zinc finger protein 271; AltName: Full=Zinc finger protein 35; Short=Zfp-35
P15622 (ZN250_HUMAN)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
P17020 (ZNF16_HUMAN)	RecName: Full=Zinc finger protein 16; AltName: Full=Zinc finger protein KOX9
P17025 (ZN182_HUMAN)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21; AltName: Full=Zinc finger protein KOX14
P17035 (ZNF28_HUMAN)	RecName: Full=Zinc finger protein 28; AltName: Full=Zinc finger protein KOX24
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P49711 (CTCF_HUMAN)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
P51522 (ZNF83_HUMAN)	RecName: Full=Zinc finger protein 83; AltName: Full=Zinc finger protein 816B; AltName: Full=Zinc finger protein HPF1
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
Q0VGE8 (ZN816_HUMAN)	RecName: Full=Zinc finger protein 816
Q3V080 (ZN583_MOUSE)	RecName: Full=Zinc finger protein 583
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4V348 (Z658B_HUMAN)	RecName: Full=Zinc finger protein 658B
Q5JVG2 (ZN484_HUMAN)	RecName: Full=Zinc finger protein 484
Q5MCW4 (ZN569_HUMAN)	RecName: Full=Zinc finger protein 569
Q5R5U3 (ZN271_PONAB)	RecName: Full=Zinc finger protein 271
Q5R5Y7 (ZN436_PONAB)	RecName: Full=Zinc finger protein 436
Q5R8X1 (ZN665_PONAB)	RecName: Full=Zinc finger protein 665
Q5TYW1 (ZN658_HUMAN)	RecName: Full=Zinc finger protein 658
Q5VIY5 (ZN468_HUMAN)	RecName: Full=Zinc finger protein 468
Q6NX49 (ZN544_HUMAN)	RecName: Full=Zinc finger protein 544
Q6P9A1 (ZN530_HUMAN)	RecName: Full=Zinc finger protein 530
Q6P560 (ZN182_MOUSE)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q6ZN57 (ZFP2_HUMAN)	RecName: Full=Zinc finger protein 2 homolog; Short=Zfp-2; AltName: Full=Zinc finger protein 751
Q6ZNA1 (ZN836_HUMAN)	RecName: Full=Zinc finger protein 836
Q7TNU6 (ZN250_MOUSE)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
Q7TSH9 (ZN184_MOUSE)	RecName: Full=Zinc finger protein 184
Q7Z340 (ZN551_HUMAN)	RecName: Full=Zinc finger protein 551; AltName: Full=Zinc finger protein KOX23
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q08DG8 (ZN135_BOVIN)	RecName: Full=Zinc finger protein 135
Q8N9K5 (ZN565_HUMAN)	RecName: Full=Zinc finger protein 565
Q8NI51 (CTCFL_HUMAN)	RecName: Full=Transcriptional repressor CTCFL; AltName: Full=Brother of the regulator of imprinted sites; AltName: Full=CCCTC-binding factor; AltName: Full=CTCF paralog; AltName: Full=CTCF-like protein; AltName: Full=Cancer/testis antigen 27; Short=CT27; AltName: Full=Zinc finger protein CTCF-T
Q8TAQ5 (ZN420_HUMAN)	RecName: Full=Zinc finger protein 420
Q8TBZ5 (ZN502_HUMAN)	RecName: Full=Zinc finger protein 502
Q9BS31 (ZN649_HUMAN)	RecName: Full=Zinc finger protein 649
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q09FC8 (ZN415_HUMAN)	RecName: Full=Zinc finger protein 415
Q9H7R5 (ZN665_HUMAN)	RecName: Full=Zinc finger protein 665; AltName: Full=Zinc finger protein 160-like
Q9HCG1 (ZN160_HUMAN)	RecName: Full=Zinc finger protein 160; AltName: Full=Zinc finger protein HZF5; AltName: Full=Zinc finger protein Kr18; Short=HKr18
Q9NQZ8 (ZNF71_HUMAN)	RecName: Full=Endothelial zinc finger protein induced by tumor necrosis factor alpha; AltName: Full=Zinc finger protein 71
Q9NYT6 (ZN226_HUMAN)	RecName: Full=Zinc finger protein 226
Q9R1D1 (CTCF_RAT)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
Q9UJU3 (ZN112_HUMAN)	RecName: Full=Zinc finger protein 112; Short=Zfp-112; AltName: Full=Zinc finger protein 228

Q9UJW8 (ZN180_HUMAN)	RecName: Full=Zinc finger protein 180; AltName: Full=HHZ168
Q9XSR1 (ZN252_CANFA)	RecName: Full=Zinc finger protein 252
Q9Y6Q3 (ZFP37_HUMAN)	RecName: Full=Zinc finger protein 37 homolog; Short=Zfp-37
Q86WZ6 (ZN227_HUMAN)	RecName: Full=Zinc finger protein 227
Q96EQ9 (PRDM9_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=Hybrid sterility protein 1; AltName: Full=Meiosis-induced factor containing a PR/SET domain and zinc-finger motif; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q96N38 (ZN714_HUMAN)	RecName: Full=Zinc finger protein 714
Q96ND8 (ZN583_HUMAN)	RecName: Full=Zinc finger protein 583; AltName: Full=Zinc finger protein L3-5
Q96RE9 (ZN300_HUMAN)	RecName: Full=Zinc finger protein 300
Q96SE7 (ZN347_HUMAN)	RecName: Full=Zinc finger protein 347; AltName: Full=Zinc finger protein 1111
Q147U1 (ZN846_HUMAN)	RecName: Full=Zinc finger protein 846
Q02386 (ZNF45_HUMAN)	RecName: Full=Zinc finger protein 45; AltName: Full=BRC1744; AltName: Full=Zinc finger protein 13; AltName: Full=Zinc finger protein KOX5
Q08705 (CTCF_CHICK)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
Q14588 (ZN234_HUMAN)	RecName: Full=Zinc finger protein 234; AltName: Full=Zinc finger protein 269; AltName: Full=Zinc finger protein HZF4
Q14590 (ZN235_HUMAN)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 270; AltName: Full=Zinc finger protein 93 homolog; Short=Zfp-93; AltName: Full=Zinc finger protein HZF6
Q14591 (ZN271_HUMAN)	RecName: Full=Zinc finger protein 271; AltName: Full=CT-ZFP48; AltName: Full=Epstein-Barr virus-induced zinc finger protein; Short=EBV-induced zinc finger protein; Short=ZNF-EB; AltName: Full=Zinc finger protein HZF7; AltName: Full=Zinc finger protein ZNFphex133; AltName: Full=Zinc finger protein dp; Short=ZNF-dp
Q15937 (ZNF79_HUMAN)	RecName: Full=Zinc finger protein 79; AltName: Full=ZNFpT7
Q61164 (CTCF_MOUSE)	RecName: Full=Transcriptional repressor CTCF; AltName: Full=11-zinc finger protein; AltName: Full=CCCTC-binding factor; AltName: Full=CTCFL paralog
Q99676 (ZN184_HUMAN)	RecName: Full=Zinc finger protein 184
XP_973961	PREDICTED: transcriptional repressor CTCF [Tribolium castaneum]
XP_974808	PREDICTED: zinc finger protein 2 homolog [Tribolium castaneum]
XP_001944018	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001944230	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_001946669	PREDICTED: zinc finger protein 845-like [Acyrthosiphon pisum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001950651	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_002413501	transcriptional repressor CTCF, putative, partial [Ixodes scapularis]
XP_003242514	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003242604	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248857	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248889	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248963	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_005168216	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168249	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_006263331	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Alligator mississippiensis]
XP_007506319	PREDICTED: zinc finger protein 135-like, partial [Monodelphis domestica]
XP_007573043	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007573181	PREDICTED: zinc finger protein 271-like [Poecilia formosa]
XP_007573741	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Poecilia formosa]
XP_007577096	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Poecilia formosa]
XP_007577098	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X3 [Poecilia formosa]
XP_007577099	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X4 [Poecilia formosa]
XP_008179259	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180597	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180598	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180607	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_008180907	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008181099	PREDICTED: zinc finger protein 91-like [Acyrthosiphon pisum]
XP_008181794	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183214	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183216	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008186458	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187394	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187795	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_008188255	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_008188456	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008188522	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008298792	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Stegastes partitus]
XP_008298797	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Stegastes partitus]

XP_008435718	PREDICTED: oocyte zinc finger protein XlCOF6-like [Poecilia reticulata]
XP_008435770	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Poecilia reticulata]
XP_009297399	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Danio rerio]
XP_009298783	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298796	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Danio rerio]
XP_009298804	PREDICTED: oocyte zinc finger protein XlCOF20-like [Danio rerio]
XP_009298817	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298909	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298922	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298936	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009299144	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_011152565	PREDICTED: zinc finger protein 436 isoform X1 [Harpegnathos saltator]
XP_011152567	PREDICTED: protein suppressor of hairy wing isoform X2 [Harpegnathos saltator]
XP_011352460	PREDICTED: transcriptional repressor CTCFL-like isoform X1 [Cerapachys biroi]
XP_011352467	PREDICTED: transcriptional repressor CTCFL-like isoform X2 [Cerapachys biroi]
XP_011352468	PREDICTED: transcriptional repressor CTCFL-like isoform X3 [Cerapachys biroi]
XP_011492062	PREDICTED: zinc finger protein 26-like isoform X3 [Oryzias latipes]
XP_011619604	PREDICTED: zinc finger protein 420-like, partial [Takifugu rubripes]
XP_011666861	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Strongylocentrotus purpuratus]
XP_011678015	PREDICTED: zinc finger protein 84-like isoform X1 [Strongylocentrotus purpuratus]
XP_012266987	PREDICTED: transcriptional repressor CTCFL isoform X3 [Athalia rosae]
XP_012328510	PREDICTED: zinc finger protein 551 [Aotus nancymaae]
XP_012407838	PREDICTED: zinc finger protein 2 homolog [Sarcophilus harrisii]
XP_012810455	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_013197323	PREDICTED: zinc finger protein 84-like [Amyelois transitella]
XP_013783454	PREDICTED: zinc finger protein 25-like [Limulus polyphemus]
XP_013786641	PREDICTED: zinc finger protein with KRAB and SCAN domains 7-like isoform X1 [Limulus polyphemus]
XP_013786656	PREDICTED: zinc finger protein with KRAB and SCAN domains 7-like isoform X2 [Limulus polyphemus]
XP_013786661	PREDICTED: zinc finger Y-chromosomal protein 2-like isoform X3 [Limulus polyphemus]
XP_013787698	PREDICTED: zinc finger protein 37-like [Limulus polyphemus]
XP_013881864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013978911	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X3 [Salmo salar]
XP_013985959	PREDICTED: zinc finger protein 271-like isoform X1 [Salmo salar]
XP_013985961	PREDICTED: zinc finger protein 345-like isoform X1 [Salmo salar]
XP_014000767	PREDICTED: zinc finger protein 271-like [Salmo salar]
XP_014041615	PREDICTED: zinc finger protein 271-like [Salmo salar]
XP_014046337	PREDICTED: zinc finger protein 135-like, partial [Salmo salar]
XP_014047301	PREDICTED: zinc finger protein 420-like, partial [Salmo salar]
XP_014248635	PREDICTED: zinc finger protein 2 homolog isoform X1 [Cimex lectularius]
XP_014248636	PREDICTED: zinc finger protein 2 isoform X2 [Cimex lectularius]
XP_014276392	PREDICTED: zinc finger protein 2-like [Halyomorpha halys]
XP_014381616	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Alligator sinensis]
XP_014382878	PREDICTED: oocyte zinc finger protein XlCOF6-like [Alligator sinensis]
XP_014437399	PREDICTED: zinc finger protein 205 isoform X1 [Tupaia chinensis]
XP_014457136	PREDICTED: gastrula zinc finger protein XlCGF26.1-like isoform X1 [Alligator mississippiensis]
XP_014457138	PREDICTED: gastrula zinc finger protein XlCGF26.1-like isoform X2 [Alligator mississippiensis]
XP_014459563	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Alligator mississippiensis]

9.4.2.6 *Cap n collar*

Name	Description
A7YY73 (MAFF_BOVIN)	RecName: Full=Transcription factor MafF; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
A7Z017 (MAF_BOVIN)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
AGB96244	cap-n-collar, isoform O [Drosophila melanogaster]
Locus_1_Transcript_103888/166847_Confidence_1.000_Length_1681 - ORF 1 (frame 1) translation	Locus_1_Transcript_103888/166847_Confidence_1.000_Length_1681
Locus_1_Transcript_106851/166847_Confidence_1.000_Length_1817 - ORF 10 (frame 3) translation	Locus_1_Transcript_106851/166847_Confidence_1.000_Length_1817

Locus_1274_Transcript_11/12_Confidence_0.171_Length_4532 - ORF 1 (frame 3) translation	Locus_1274_Transcript_11/12_Confidence_0.171_Length_4532
Locus_2680_Transcript_40/41_Confidence_0.044_Length_2001 - ORF 3 (frame 2) translation	Locus_2680_Transcript_40/41_Confidence_0.044_Length_2001
NP_032712	nuclear factor erythroid 2-related factor 1 isoform 1 [Mus musculus]
NP_001084266	jun proto-oncogene [Xenopus laevis]
O15525 (MAFG_HUMAN)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G; AltName: Full=hMAF
O54790 (MAFG_MOUSE)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
O54968 (NF2L2_RAT)	RecName: Full=Nuclear factor erythroid 2-related factor 2; Short=NF-E2-related factor 2; Short=NFE2-related factor 2; AltName: Full=Nuclear factor, erythroid derived 2, like 2
O60675 (MAFK_HUMAN)	RecName: Full=Transcription factor MafK; AltName: Full=Erythroid transcription factor NF-E2 p18 subunit
O75444 (MAF_HUMAN)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
O77627 (JUN_BOVIN)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P05411 (JUN_AVIS1)	RecName: Full=Viral jun-transforming protein; Short=v-Jun
P05412 (JUN_HUMAN)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog; AltName: Full=p39
P05627 (JUN_MOUSE)	RecName: Full=Transcription factor AP-1; AltName: Full=AH119; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog; Short=Jun A
P12981 (JUN_COTJA)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P17325 (JUN_RAT)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P18870 (JUN_CHICK)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P23091 (MAF_AVIS4)	RecName: Full=Transforming protein Maf
P54841 (MAFB_MOUSE)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=Kreisler; AltName: Full=Segmentation protein Kr; AltName: Full=Transcription factor Maf-1; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
P54843 (MAF_MOUSE)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
P54864 (JUN_SERCA)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P56432 (JUN_PIG)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P79703 (JUNB_CYPCA)	RecName: Full=Transcription factor jun-B
Q5NUA6 (NF2L2_BOVIN)	RecName: Full=Nuclear factor erythroid 2-related factor 2; Short=NF-E2-related factor 2; Short=NFE2-related factor 2; AltName: Full=Nuclear factor, erythroid derived 2, like 2
Q9ULX9 (MAFF_HUMAN)	RecName: Full=Transcription factor MafF; AltName: Full=U-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
Q9Y5Q3 (MAFB_HUMAN)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
Q76MX4 (MAFG_RAT)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
Q98UK5 (MAFB_DANRE)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=Transcription factor Val; AltName: Full=Valentino
Q789F3 (MAF_CHICK)	RecName: Full=Transcription factor Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
Q16236 (NF2L2_HUMAN)	RecName: Full=Nuclear factor erythroid 2-related factor 2; Short=NF-E2-related factor 2; Short=NFE2-related factor 2; AltName: Full=HEBP1; AltName: Full=Nuclear factor, erythroid derived 2, like 2
Q60795 (NF2L2_MOUSE)	RecName: Full=Nuclear factor erythroid 2-related factor 2; Short=NF-E2-related factor 2; Short=NFE2-related factor 2; AltName: Full=Nuclear factor, erythroid derived 2, like 2
Q61827 (MAFK_MOUSE)	RecName: Full=Transcription factor MafK; AltName: Full=Erythroid transcription factor NF-E2 p18 subunit
Q90370 (MAFB_COTJA)	RecName: Full=Transcription factor MafB; Short=Maf-B
Q90595 (MAFF_CHICK)	RecName: Full=Transcription factor MafF; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
Q90596 (MAFK_CHICK)	RecName: Full=Transcription factor MafK
Q90888 (MAFB_CHICK)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
Q90889 (MAFG_CHICK)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
XP_002404274	transcription factor MafB, putative [Ixodes scapularis]
XP_002428922	transcription factor MafG, putative [Pediculus humanus corporis]
XP_002931634	PREDICTED: transcription factor AP-1 [Xenopus (Silurana) tropicalis]
XP_003250214	PREDICTED: transcription factor MafG-like isoformX2 [Apis mellifera]
XP_004927019	PREDICTED: neural retina-specific leucine zipper protein [Bombyx mori]
XP_005482348	PREDICTED: transcription factor AP-1 [Zonotrichia albicollis]
XP_006610989	PREDICTED: transcription factor MafG-like [Apis dorsata]
XP_008200013	PREDICTED: cap-n-collar isoform X4 [Tribolium castaneum]

XP_008211892	PREDICTED: segmentation protein cap'n'collar-like, partial [Nasonia vitripennis]
XP_008923422	PREDICTED: transcription factor AP-1 [Manacus vitellinus]
XP_011343601	PREDICTED: transcription factor MafG [Cerapachys biroi]
XP_011446588	PREDICTED: transcription factor AP-1-like [Crassostrea gigas]
XP_011504986	PREDICTED: segmentation protein cap'n'collar isoform X1 [Ceratosolen solmsi marchali]
XP_011504987	PREDICTED: segmentation protein cap'n'collar isoform X2 [Ceratosolen solmsi marchali]
XP_011564500	PREDICTED: transcription factor MafK-like [Plutella xylostella]
XP_012261892	PREDICTED: transcription factor MafK-like [Athalia rosae]
XP_013145529	PREDICTED: transcription factor MafK [Papilio polytes]
XP_013161582	PREDICTED: transcription factor MafK [Papilio xuthus]
XP_013181120	PREDICTED: neural retina-specific leucine zipper protein-like [Papilio xuthus]
XP_013188822	PREDICTED: neural retina-specific leucine zipper protein-like [Amyelois transitella]
XP_013195767	PREDICTED: transcription factor MafK [Amyelois transitella]
XP_013398583	PREDICTED: transcription factor AP-1-like [Lingula anatina]
XP_013772821	PREDICTED: neural retina-specific leucine zipper protein-like [Limulus polyphemus]
XP_013772889	PREDICTED: nuclear factor erythroid 2-related factor 2-like isoform X1 [Limulus polyphemus]
XP_013772891	PREDICTED: nuclear factor erythroid 2-related factor 2-like isoform X2 [Limulus polyphemus]
XP_013772971	PREDICTED: nuclear factor erythroid 2-related factor 1-like [Limulus polyphemus]
XP_013776170	PREDICTED: transcription factor MafB-like [Limulus polyphemus]
XP_013777025	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_013781439	PREDICTED: transcription factor MafK-like [Limulus polyphemus]
XP_013783135	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_013791509	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_014219691	PREDICTED: segmentation protein cap'n'collar [Copidosoma floridanum]
XP_014257082	PREDICTED: nuclear factor erythroid 2-related factor 2 isoform X1 [Cimex lectularius]
XP_014257084	PREDICTED: segmentation protein cap'n'collar isoform X2 [Cimex lectularius]
XP_014278715	PREDICTED: transcription factor MafA-like [Halyomorpha halys]
XP_014358308	PREDICTED: transcription factor MafA-like [Papilio machaon]

9.4.2.7 *Chinmo*

Name	Description
A0JMG1 (SPOLB_DANRE)	RecName: Full=Speckle-type POZ protein-like B; AltName: Full=HIB homolog 3
A6QQY2 (KLH13_BOVIN)	RecName: Full=Kelch-like protein 13
ADV36931	chronologically inappropriate morphogenesis, isoform E [Drosophila melanogaster]
B4F6U4 (PRD10_XENTR)	RecName: Full=PR domain zinc finger protein 10; AltName: Full=PR domain-containing protein 10
D3ZUU2 (GZF1_RAT)	RecName: Full=GDNF-inducible zinc finger protein 1; AltName: Full=Zinc finger protein 336
E0CZ16 (KLHL3_MOUSE)	RecName: Full=Kelch-like protein 3
E7F6F9 (KLHL3_DANRE)	RecName: Full=Kelch-like protein 3
E9QAG8 (ZN431_MOUSE)	RecName: Full=Zinc finger protein 431; AltName: Full=Zinc finger protein 932
F1LZ52 (KLHL3_RAT)	RecName: Full=Kelch-like protein 3
F1LZF0 (KLHL2_RAT)	RecName: Full=Kelch-like protein 2; AltName: Full=Mayven
F1MBP6 (KLHL3_BOVIN)	RecName: Full=Kelch-like protein 3
Locus_1_Transcript_23407/166847_Confidence_1.000_Length_608 - ORF 2 (frame 3) translation	Locus_1_Transcript_23407/166847_Confidence_1.000_Length_608
Locus_1_Transcript_53837/166847_Confidence_1.000_Length_3176 - ORF 1 (frame 1) translation	Locus_1_Transcript_53837/166847_Confidence_1.000_Length_3176
Locus_776_Transcript_132/139_Confidence_0.047_Length_6093 - ORF 1 (frame 2) translation	Locus_776_Transcript_132/139_Confidence_0.047_Length_6093
Locus_3233_Transcript_17/19_Confidence_0.380_Length_4261 - ORF 1 (frame 2) translation	Locus_3233_Transcript_17/19_Confidence_0.380_Length_4261
Locus_11151_Transcript_2/10_Confidence_0.354_Length_6081 - ORF 27 (frame 1) translation	Locus_11151_Transcript_2/10_Confidence_0.354_Length_6081
Locus_11684_Transcript_2/5_Confidence_0.438_Length_3406 - ORF 20 (frame 2) translation	Locus_11684_Transcript_2/5_Confidence_0.438_Length_3406
Locus_13466_Transcript_2/7_Confidence_0.727_Length_7437 - ORF 1 (frame 2) translation	Locus_13466_Transcript_2/7_Confidence_0.727_Length_7437
Locus_14729_Transcript_3/10_Confidence_0.167_Length_808 - ORF 1 (frame 3) translation	Locus_14729_Transcript_3/10_Confidence_0.167_Length_808
Locus_14992_Transcript_1/4_Confidence_0.636_Length_2328 - ORF 1 (frame 3) translation	Locus_14992_Transcript_1/4_Confidence_0.636_Length_2328
Locus_16225_Transcript_1/1_Confidence_1.000_Length_576 - ORF 1 (frame 1) translation	Locus_16225_Transcript_1/1_Confidence_1.000_Length_576
Locus_21364_Transcript_1/2_Confidence_0.500_Length_1287 - ORF 3 (frame 3) translation	Locus_21364_Transcript_1/2_Confidence_0.500_Length_1287
Locus_24927_Transcript_1/1_Confidence_1.000_Length_637 - ORF 1 (frame 3) translation	Locus_24927_Transcript_1/1_Confidence_1.000_Length_637
Locus_29259_Transcript_1/1_Confidence_1.000_Length_1384 - ORF 1 (frame 3) translation	Locus_29259_Transcript_1/1_Confidence_1.000_Length_1384
Locus_34046_Transcript_1/1_Confidence_1.000_Length_1487 - ORF 7 (frame 2) translation	Locus_34046_Transcript_1/1_Confidence_1.000_Length_1487
NP_683751	TD and POZ domain-containing protein 1 [Mus musculus]

NP_989003	speckle-type POZ protein [Xenopus (Silurana) tropicalis]
NP_001090478	speckle-type POZ protein B [Xenopus laevis]
NP_001139579	TD and POZ domain containing-like [Mus musculus]
O35260 (NACC1_RAT)	RecName: Full=Nucleus accumbens-associated protein 1; Short=NAC-1; AltName: Full=BTB/POZ domain-containing protein 14B
O43791 (SPOP_HUMAN)	RecName: Full=Speckle-type POZ protein; AltName: Full=HIB homolog 1; AltName: Full=Roadkill homolog 1
O54963 (REST_RAT)	RecName: Full=RE1-silencing transcription factor; AltName: Full=Neural-restrictive silencer factor
O94844 (RHBT1_HUMAN)	RecName: Full=Rho-related BTB domain-containing protein 1
O94955 (RHBT3_HUMAN)	RecName: Full=Rho-related BTB domain-containing protein 3
O95198 (KLHL2_HUMAN)	RecName: Full=Kelch-like protein 2; AltName: Full=Actin-binding protein Mayven
P0DMR5 (TDPZ1_MOUSE)	RecName: Full=TD and POZ domain-containing protein 1; AltName: Full=MAPP family protein 2
P0DMR6 (TDP1L_MOUSE)	RecName: Full=TD and POZ domain-containing protein 1-like
P10077 (ZFP27_MOUSE)	RecName: Full=Zinc finger protein 27; Short=Zfp-27; AltName: Full=Protein mKR4
P17789 (TTKB_DROME)	RecName: Full=Protein tramtrack, beta isoform; AltName: Full=Repressor protein fushi tarazu; AltName: Full=Tramtrack p69
P18715 (ZG26_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF26.1
P34568 (BAT43_CAEEL)	RecName: Full=BTB and MATH domain-containing protein 43; AltName: Full=HIB homolog
P42282 (TTKA_DROME)	RecName: Full=Protein tramtrack, alpha isoform; AltName: Full=Repressor protein fushi tarazu; AltName: Full=Tramtrack p88
P42283 (LOLA1_DROME)	RecName: Full=Longitudinals lacking protein, isoform G
P42284 (LOLA2_DROME)	RecName: Full=Longitudinals lacking protein, isoforms H/M/V
P51508 (ZNF81_HUMAN)	RecName: Full=Zinc finger protein 81; AltName: Full=HFZ20
P52746 (ZN142_HUMAN)	RecName: Full=Zinc finger protein 142; AltName: Full=HA4654
Q0IHH9 (SPOPB_XENLA)	RecName: Full=Speckle-type POZ protein B
Q2T9Z7 (KLHL9_BOVIN)	RecName: Full=Kelch-like protein 9
Q3UTQ7 (PRD10_MOUSE)	RecName: Full=PR domain zinc finger protein 10; AltName: Full=PR domain-containing protein 10; AltName: Full=Tristanin
Q4VBD9 (GZF1_MOUSE)	RecName: Full=GDNF-inducible zinc finger protein 1; AltName: Full=Zinc finger protein 336
Q5BL35 (SPOLA_DANRE)	RecName: Full=Speckle-type POZ protein-like A; AltName: Full=HIB homolog 2
Q5EBL2 (ZN628_HUMAN)	RecName: Full=Zinc finger protein 628
Q5R7B8 (KLH20_PONAB)	RecName: Full=Kelch-like protein 20
Q5RAX9 (PRD10_PONAB)	RecName: Full=PR domain zinc finger protein 10; AltName: Full=PR domain-containing protein 10
Q5RB30 (Z585B_PONAB)	RecName: Full=Zinc finger protein 585B
Q5RDX1 (Z585A_PONAB)	RecName: Full=Zinc finger protein 585A
Q5REP9 (KLHL3_PONAB)	RecName: Full=Kelch-like protein 3
Q5RGB8 (KLH26_DANRE)	RecName: Full=Kelch-like protein 26
Q5ZLD3 (KLH13_CHICK)	RecName: Full=Kelch-like protein 13
Q6DFF6 (KLH20_XENLA)	RecName: Full=Kelch-like protein 20
Q6GL52 (ZN574_XENTR)	RecName: Full=Zinc finger protein 574
Q6GR09 (SPOPL_XENLA)	RecName: Full=Speckle-type POZ protein-like
Q6IQ16 (SPOPL_HUMAN)	RecName: Full=Speckle-type POZ protein-like; AltName: Full=HIB homolog 2; AltName: Full=Roadkill homolog 2
Q6P1D7 (SLX4_MOUSE)	RecName: Full=Structure-specific endonuclease subunit SLX4; AltName: Full=BTB/POZ domain-containing protein 12
Q6P3V2 (Z585A_HUMAN)	RecName: Full=Zinc finger protein 585A
Q6TDP4 (KLH17_HUMAN)	RecName: Full=Kelch-like protein 17; AltName: Full=Actinfilin
Q6YCH1 (TDPZ5_MOUSE)	RecName: Full=TD and POZ domain-containing protein 5
Q6YCH2 (TDPZ4_MOUSE)	RecName: Full=TD and POZ domain-containing protein 4
Q6ZPT1 (KLHL9_MOUSE)	RecName: Full=Kelch-like protein 9
Q7KQZ4 (LOLA3_DROME)	RecName: Full=Longitudinals lacking protein, isoforms A/B/D/L
Q7KRI2 (LOLAL_DROME)	RecName: Full=Longitudinals lacking protein-like; Short=Lola-like protein; AltName: Full=Protein Batman
Q7T330 (SPOP_DANRE)	RecName: Full=Speckle-type POZ protein; AltName: Full=HIB homolog 1; AltName: Full=SPOP1
Q7TS63 (ZFAT_MOUSE)	RecName: Full=Zinc finger protein ZFAT; AltName: Full=Zinc finger protein 406
Q7TSZ8 (NACC1_MOUSE)	RecName: Full=Nucleus accumbens-associated protein 1; Short=NAC-1; AltName: Full=BTB/POZ domain-containing protein 14B
Q7ZX06 (SPOPA_XENLA)	RecName: Full=Speckle-type POZ protein A
Q8BGY4 (KLH26_MOUSE)	RecName: Full=Kelch-like protein 26
Q8CJ78 (ZN628_MOUSE)	RecName: Full=Zinc finger protein 628; AltName: Full=Zinc finger protein expressed in embryonal cells and certain adult organs
Q08DK3 (KLH20_BOVIN)	RecName: Full=Kelch-like protein 20
Q8IN81 (FRU_DROME)	RecName: Full=Sex determination protein fruitless
Q8IY92 (SLX4_HUMAN)	RecName: Full=Structure-specific endonuclease subunit SLX4; AltName: Full=BTB/POZ domain-containing protein 12
Q8JZP3 (KLHL2_MOUSE)	RecName: Full=Kelch-like protein 2
Q8K0L9 (ZBT20_MOUSE)	RecName: Full=Zinc finger and BTB domain-containing protein 20; AltName: Full=BTB/POZ domain zinc finger factor HOF; AltName: Full=Zinc finger protein 288
Q8K430 (KLH17_RAT)	RecName: Full=Kelch-like protein 17; AltName: Full=Actinfilin
Q8NEP9 (ZN555_HUMAN)	RecName: Full=Zinc finger protein 555
Q8VCK5 (KLH20_MOUSE)	RecName: Full=Kelch-like protein 20; AltName: Full=Kelch-like ECT2-interacting protein
Q8VIG1 (REST_MOUSE)	RecName: Full=RE1-silencing transcription factor; AltName: Full=Neural-restrictive silencer factor
Q9BYZ6 (RHBT2_HUMAN)	RecName: Full=Rho-related BTB domain-containing protein 2; AltName: Full=Deleted in breast cancer 2 gene protein; AltName: Full=p83

Q9CTN4 (RHBT3_MOUSE)	RecName: Full=Rho-related BTB domain-containing protein 3
Q9DAK3 (RHBT1_MOUSE)	RecName: Full=Rho-related BTB domain-containing protein 1
Q9H116 (GZF1_HUMAN)	RecName: Full=GDNF-inducible zinc finger protein 1; AltName: Full=Zinc finger and BTB domain-containing protein 23; AltName: Full=Zinc finger protein 336
Q9HC78 (ZBT20_HUMAN)	RecName: Full=Zinc finger and BTB domain-containing protein 20; AltName: Full=Dendritic-derived BTB/POZ zinc finger protein; AltName: Full=Zinc finger protein 288
Q9NQV6 (PRD10_HUMAN)	RecName: Full=PR domain zinc finger protein 10; AltName: Full=PR domain-containing protein 10; AltName: Full=Tristanin
Q9P2J3 (KLHL9_HUMAN)	RecName: Full=Kelch-like protein 9
Q9P2N7 (KLH13_HUMAN)	RecName: Full=Kelch-like protein 13; AltName: Full=BTB and kelch domain-containing protein 2
Q9UH77 (KLHL3_HUMAN)	RecName: Full=Kelch-like protein 3
Q9VFP2 (RDX_DROME)	RecName: Full=Protein roadkill; AltName: Full=Hh-induced MATH and BTB domain-containing protein
Q9VS48 (SLX4_DROME)	RecName: Full=Structure-specific endonuclease subunit SLX4; AltName: Full=Mutagen-sensitive protein 312
Q9W0K4 (BAB2_DROME)	RecName: Full=Protein bric-a-brac 2
Q9W0K7 (BAB1_DROME)	RecName: Full=Protein bric-a-brac 1
Q52M93 (Z585B_HUMAN)	RecName: Full=Zinc finger protein 585B; AltName: Full=zinc finger protein 41-like protein
Q53HC5 (KLH26_HUMAN)	RecName: Full=Kelch-like protein 26
Q70JS2 (KELC_ANOST)	RecName: Full=Ring canal kelch homolog; AltName: Full=Kelch-like protein 1; Contains: RecName: Full=Kelch short protein
Q80TF4 (KLH13_MOUSE)	RecName: Full=Kelch-like protein 13; AltName: Full=BTB and kelch domain-containing protein 2
Q91V93 (RHBT2_MOUSE)	RecName: Full=Rho-related BTB domain-containing protein 2; AltName: Full=Deleted in breast cancer 2 gene protein homolog
Q717B2 (TDPZ2_MOUSE)	RecName: Full=TD and POZ domain-containing protein 2
Q717B4 (TDPZ3_MOUSE)	RecName: Full=TD and POZ domain-containing protein 3
Q01295 (BRC1_DROME)	RecName: Full=Broad-complex core protein isoforms 1/2/3/4/5
Q04652 (KELC_DROME)	RecName: Full=Ring canal kelch protein; Contains: RecName: Full=Kelch short protein
Q24206 (BRC4_DROME)	RecName: Full=Broad-complex core protein isoform 6
Q94420 (MEL26_CAEEL)	RecName: Full=Protein maternal effect lethal 26
XP_972393	PREDICTED: kelch-like protein 26 isoform X1 [Tribolium castaneum]
XP_001373925	PREDICTED: speckle-type POZ protein isoform X1 [Monodelphis domestica]
XP_001604724	PREDICTED: speckle-type POZ protein A-like [Nasonia vitripennis]
XP_001842653	actin binding protein [Culex quinquefasciatus]
XP_001952667	PREDICTED: speckle-type POZ protein A isoform X1 [Acyrthosiphon pisum]
XP_002435294	Kruppel-like zinc finger protein, putative [Ixodes scapularis]
XP_002735147	PREDICTED: protein roadkill-like [Saccoglossus kowalevskii]
XP_003398593	PREDICTED: ring canal kelch homolog [Bombus terrestris]
XP_003487466	PREDICTED: ring canal kelch homolog [Bombus impatiens]
XP_003692755	PREDICTED: ring canal kelch homolog [Apis florea]
XP_003701082	PREDICTED: ring canal kelch homolog [Megachile rotundata]
XP_003753676	PREDICTED: TD and POZ domain-containing protein 2-like isoform X1 [Rattus norvegicus]
XP_005095091	PREDICTED: speckle-type POZ protein-like [Aplysia californica]
XP_005390831	PREDICTED: speckle-type POZ protein-like isoform X2 [Chinchilla lanigera]
XP_005810102	PREDICTED: speckle-type POZ protein-like A isoform X2 [Xiphophorus maculatus]
XP_006000884	PREDICTED: speckle-type POZ protein [Latimeria chalumnae]
XP_006502577	PREDICTED: TD and POZ domain-containing protein 5-like isoform X2 [Mus musculus]
XP_006566238	PREDICTED: ring canal kelch homolog isoform X1 [Apis mellifera]
XP_006566239	PREDICTED: ring canal kelch homolog isoform X2 [Apis mellifera]
XP_006636287	PREDICTED: speckle-type POZ protein-like A-like isoform X2 [Lepisosteus oculatus]
XP_006746742	PREDICTED: speckle-type POZ protein isoform X3 [Leptonychotes weddellii]
XP_007095551	PREDICTED: zinc finger protein 705F-like isoform X3 [Panthera tigris altaica]
XP_007539169	PREDICTED: zinc finger protein 791-like, partial [Erinaceus europaeus]
XP_008181914	PREDICTED: protein krueppel-like [Acyrthosiphon pisum]
XP_008185660	PREDICTED: speckle-type POZ protein A isoform X2 [Acyrthosiphon pisum]
XP_008185662	PREDICTED: speckle-type POZ protein A isoform X3 [Acyrthosiphon pisum]
XP_008185663	PREDICTED: protein roadkill isoform X4 [Acyrthosiphon pisum]
XP_008195259	PREDICTED: speckle-type POZ protein B isoform X1 [Tribolium castaneum]
XP_008195263	PREDICTED: speckle-type POZ protein B isoform X2 [Tribolium castaneum]
XP_008195269	PREDICTED: protein roadkill isoform X3 [Tribolium castaneum]
XP_008195273	PREDICTED: protein roadkill isoform X4 [Tribolium castaneum]
XP_008197753	PREDICTED: kelch-like protein 26 isoform X2 [Tribolium castaneum]
XP_008469466	PREDICTED: kelch-like protein 26 [Diaphorina citri]
XP_008485251	PREDICTED: protein bric-a-brac 1-like, partial [Diaphorina citri]
XP_008547795	PREDICTED: speckle-type POZ protein A-like, partial [Microplitis demolitor]
XP_008552225	PREDICTED: ring canal kelch homolog [Microplitis demolitor]
XP_008584898	PREDICTED: zinc finger protein 585A [Galeopterus variegatus]
XP_008945067	PREDICTED: speckle-type POZ protein [Merops nubicus]

XP_009469393	PREDICTED: zinc finger and BTB domain-containing protein 49 [Nipponia nippon]
XP_009880242	PREDICTED: structure-specific endonuclease subunit SLX4 [Charadrius vociferus]
XP_010079300	PREDICTED: speckle-type POZ protein [Pterocles gutturalis]
XP_010137191	PREDICTED: speckle-type POZ protein [Buceros rhinoceros silvestris]
XP_010390428	PREDICTED: structure-specific endonuclease subunit SLX4 isoform X3 [Corvus cornix cornix]
XP_010583776	PREDICTED: speckle-type POZ protein isoform X2 [Haliaeetus leucocephalus]
XP_010733008	PREDICTED: structure-specific endonuclease subunit SLX4-like [Larimichthys crocea]
XP_010902275	PREDICTED: zinc finger protein OZF-like [Esox lucius]
XP_011140222	PREDICTED: rho-related BTB domain-containing protein 1 isoform X2 [Harpegnathos saltator]
XP_011292876	PREDICTED: zinc finger protein 716-like [Musca domestica]
XP_011450889	PREDICTED: kelch-like protein 13 isoform X2 [Crassostrea gigas]
XP_011690601	PREDICTED: rho-related BTB domain-containing protein 1 isoform X1 [Wasmannia auropunctata]
XP_011690603	PREDICTED: rho-related BTB domain-containing protein 1 isoform X2 [Wasmannia auropunctata]
XP_011690604	PREDICTED: rho-related BTB domain-containing protein 1 isoform X3 [Wasmannia auropunctata]
XP_011700730	PREDICTED: ring canal kelch homolog [Wasmannia auropunctata]
XP_011871188	PREDICTED: rho-related BTB domain-containing protein 1 isoform X1 [Vollenhovia emeryi]
XP_011871191	PREDICTED: rho-related BTB domain-containing protein 1 isoform X2 [Vollenhovia emeryi]
XP_011871192	PREDICTED: rho-related BTB domain-containing protein 1 isoform X3 [Vollenhovia emeryi]
XP_012267582	PREDICTED: ring canal kelch homolog isoform X1 [Athalia rosae]
XP_012371111	PREDICTED: zinc finger protein 14-like [Octodon degus]
XP_012537366	PREDICTED: ring canal kelch homolog [Monomorium pharaonis]
XP_012691112	PREDICTED: zinc finger protein 208-like [Clupea harengus]
XP_013057085	PREDICTED: zinc finger protein 628-like, partial [Anser cygnoides domesticus]
XP_013192866	PREDICTED: zinc finger protein 124-like isoform X2 [Amyelois transitella]
XP_013194549	PREDICTED: zinc finger protein 665-like isoform X2 [Amyelois transitella]
XP_013394154	PREDICTED: protein roadkill-like [Lingula anatina]
XP_013775838	PREDICTED: protein roadkill-like [Limulus polyphemus]
XP_013776958	PREDICTED: protein tramtrack, beta isoform-like [Limulus polyphemus]
XP_013777449	PREDICTED: protein tramtrack, beta isoform-like [Limulus polyphemus]
XP_013778042	PREDICTED: zinc finger protein 800-like [Limulus polyphemus]
XP_013779689	PREDICTED: protein tramtrack, beta isoform-like [Limulus polyphemus]
XP_013779817	PREDICTED: protein bric-a-brac 2-like isoform X1 [Limulus polyphemus]
XP_013779818	PREDICTED: protein bric-a-brac 2-like isoform X2 [Limulus polyphemus]
XP_013779905	PREDICTED: kelch-like protein 26 [Limulus polyphemus]
XP_013779984	PREDICTED: rho-related BTB domain-containing protein 1-like [Limulus polyphemus]
XP_013781299	PREDICTED: kelch-like protein 17 [Limulus polyphemus]
XP_013781432	PREDICTED: protein bric-a-brac 2-like [Limulus polyphemus]
XP_013782621	PREDICTED: rho-related BTB domain-containing protein 1-like isoform X1 [Limulus polyphemus]
XP_013782622	PREDICTED: rho-related BTB domain-containing protein 1-like isoform X2 [Limulus polyphemus]
XP_013783214	PREDICTED: protein roadkill-like [Limulus polyphemus]
XP_013785538	PREDICTED: protein tramtrack, beta isoform-like [Limulus polyphemus]
XP_014092905	PREDICTED: kelch-like protein 17 [Bactrocera oleae]
XP_014229998	PREDICTED: speckle-type POZ protein B-like [Trichogramma pretiosum]
XP_014235421	PREDICTED: speckle-type POZ protein B-like [Trichogramma pretiosum]
XP_014244123	PREDICTED: kelch-like protein 26 [Cimex lectularius]
XP_014245457	PREDICTED: protein roadkill isoform X5 [Cimex lectularius]
XP_014245458	PREDICTED: protein roadkill isoform X6 [Cimex lectularius]
XP_014273390	PREDICTED: zinc finger protein 431-like [Halyomorpha halys]
XP_014288246	PREDICTED: protein bric-a-brac 2-like [Halyomorpha halys]
XP_014289696	PREDICTED: kelch-like protein 26 [Halyomorpha halys]
XP_014316161	PREDICTED: zinc finger protein 551-like, partial [Myotis lucifugus]

9.4.2.8 *Dachsous*

Name	**Description**
AAF51468	dachsous, isoform A [Drosophila melanogaster]
D4ACX8 (PCD16_RAT)	RecName: Full=Protocadherin-16; AltName: Full=Protein dachsous homolog 1; Flags: Precursor
DS_DROME	RecName: Full=Protein dachsous; AltName: Full=Adherin; Flags: Precursor
E9PVD3 (PCD16_MOUSE)	RecName: Full=Protocadherin-16; AltName: Full=Protein Dchs1; AltName: Full=Protein dachsous homolog 1; Flags: Precursor

Locus_1_Transcript_150321/166847_Confidence_1.000_Length_3170 - ORF 20 (frame 2) translation	Locus_1_Transcript_150321/166847_Confidence_1.000_Length_3170
Locus_7584_Transcript_10/10_Confidence_0.318_Length_16126 - ORF 72 (frame 1) translation	Locus_7584_Transcript_10/10_Confidence_0.318_Length_16126
Locus_10049_Transcript_10/10_Confidence_0.373_Length_17969 - ORF 65 (frame 2) translation	Locus_10049_Transcript_10/10_Confidence_0.373_Length_17969
Locus_17090_Transcript_17/17_Confidence_0.220_Length_16919 - ORF 2 (frame 2) translation	Locus_17090_Transcript_17/17_Confidence_0.220_Length_16919
O88277 (FAT2_RAT)	RecName: Full=Protocadherin Fat 2; AltName: Full=Multiple epidermal growth factor-like domains protein 1; Short=Multiple EGF-like domains protein 1; Flags: Precursor
P33450 (FAT_DROME)	RecName: Full=Cadherin-related tumor suppressor; AltName: Full=Protein fat; Contains: RecName: Full=Ft-mito; Flags: Precursor
Q2PZL6 (FAT4_MOUSE)	RecName: Full=Protocadherin Fat 4; AltName: Full=FAT tumor suppressor homolog 4; AltName: Full=Fat-like cadherin protein FAT-J; Flags: Precursor
Q5F226 (FAT2_MOUSE)	RecName: Full=Protocadherin Fat 2; AltName: Full=FAT tumor suppressor homolog 2; Flags: Precursor
Q6V0I7 (FAT4_HUMAN)	RecName: Full=Protocadherin Fat 4; Short=hFat4; AltName: Full=Cadherin family member 14; AltName: Full=FAT tumor suppressor homolog 4; AltName: Full=Fat-like cadherin protein FAT-J; Flags: Precursor
Q8BNA6 (FAT3_MOUSE)	RecName: Full=Protocadherin Fat 3; AltName: Full=FAT tumor suppressor homolog 3; Flags: Precursor
Q8R508 (FAT3_RAT)	RecName: Full=Protocadherin Fat 3; AltName: Full=FAT tumor suppressor homolog 3; Flags: Precursor
Q8TDW7 (FAT3_HUMAN)	RecName: Full=Protocadherin Fat 3; Short=hFat3; AltName: Full=Cadherin family member 15; AltName: Full=FAT tumor suppressor homolog 3; Flags: Precursor
Q9NYQ8 (FAT2_HUMAN)	RecName: Full=Protocadherin Fat 2; Short=hFat2; AltName: Full=Cadherin family member 8; AltName: Full=Multiple epidermal growth factor-like domains protein 1; Short=Multiple EGF-like domains protein 1; Flags: Precursor
Q9VW71 (FAT2_DROME)	RecName: Full=Fat-like cadherin-related tumor suppressor homolog; AltName: Full=Protein kugelei; Flags: Precursor
Q96JQ0 (PCD16_HUMAN)	RecName: Full=Protocadherin-16; AltName: Full=Cadherin-19; AltName: Full=Cadherin-25; AltName: Full=Fibroblast cadherin-1; AltName: Full=Protein dachsous homolog 1; Flags: Precursor
Q14517 (FAT1_HUMAN)	RecName: Full=Protocadherin Fat 1; AltName: Full=Cadherin family member 7; AltName: Full=Cadherin-related tumor suppressor homolog; AltName: Full=Protein fat homolog; Contains: RecName: Full=Protocadherin Fat 1, nuclear form; Flags: Precursor
Q19319 (CADH4_CAEEL)	RecName: Full=Cadherin-4; Flags: Precursor
Q24292 (DS_DROME)	RecName: Full=Protein dachsous; AltName: Full=Adherin; Flags: Precursor
XP_971084	PREDICTED: cadherin-related tumor suppressor [Tribolium castaneum]
XP_002427847	protocadherin-16 precursor, putative [Pediculus humanus corporis]
XP_011135487	PREDICTED: fat-like cadherin-related tumor suppressor homolog, partial [Harpegnathos saltator]
XP_011160731	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X1 [Solenopsis invicta]
XP_011160732	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X2 [Solenopsis invicta]
XP_011186774	PREDICTED: protein dachsous [Bactrocera cucurbitae]
XP_011199649	PREDICTED: protein dachsous [Bactrocera dorsalis]
XP_011256853	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X1 [Camponotus floridanus]
XP_011256854	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X2 [Camponotus floridanus]
XP_011256855	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X3 [Camponotus floridanus]
XP_011256856	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X4 [Camponotus floridanus]
XP_011256857	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X5 [Camponotus floridanus]
XP_011559498	PREDICTED: cadherin-related tumor suppressor [Plutella xylostella]
XP_011630848	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X4 [Pogonomyrmex barbatus]
XP_012161625	PREDICTED: protein dachsous [Ceratitis capitata]
XP_012216117	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X3 [Linepithema humile]
XP_012243646	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X4 [Bombus impatiens]
XP_012288619	PREDICTED: cadherin-related tumor suppressor [Orussus abietinus]
XP_012538682	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X1 [Monomorium pharaonis]
XP_012538684	PREDICTED: fat-like cadherin-related tumor suppressor homolog isoform X3 [Monomorium pharaonis]
XP_013136845	PREDICTED: cadherin-related tumor suppressor [Papilio polytes]
XP_013177912	PREDICTED: cadherin-related tumor suppressor [Papilio xuthus]
XP_013772447	PREDICTED: protein dachsous-like [Limulus polyphemus]
XP_013781277	PREDICTED: cadherin-related tumor suppressor-like [Limulus polyphemus]
XP_013790823	PREDICTED: protein dachsous-like [Limulus polyphemus]
XP_013794584	PREDICTED: protein dachsous-like [Limulus polyphemus]
XP_014251864	PREDICTED: cadherin-related tumor suppressor [Cimex lectularius]
XP_014270302	PREDICTED: cadherin-related tumor suppressor [Halyomorpha halys]
XP_014270461	PREDICTED: protein dachsous-like [Halyomorpha halys]
XP_014363600	PREDICTED: cadherin-related tumor suppressor [Papilio machaon]

9.4.2.9 *Daughterless*

Name	Description
DA_DROME	RecName: Full=Protein daughterless
Locus_1_Transcript_9632/166847_Confidence_1.000_Length_493 - ORF 1 (frame 3) translation	Locus_1_Transcript_9632/166847_Confidence_1.000_Length_493
Locus_1_Transcript_9634/166847_Confidence_1.000_Length_109 - ORF 1 (frame 1) translation	Locus_1_Transcript_9634/166847_Confidence_1.000_Length_109
Locus_1_Transcript_9635/166847_Confidence_1.000_Length_321 - ORF 1 (frame 3) translation	Locus_1_Transcript_9635/166847_Confidence_1.000_Length_321
Locus_1_Transcript_9642/166847_Confidence_1.000_Length_571 - ORF 3 (frame 3) translation	Locus_1_Transcript_9642/166847_Confidence_1.000_Length_571
Locus_1_Transcript_135302/166847_Confidence_1.000_Length_522 - ORF 3 (frame 2) translation	Locus_1_Transcript_135302/166847_Confidence_1.000_Length_522
Locus_1_Transcript_135305/166847_Confidence_1.000_Length_636 - ORF 4 (frame 1) translation	Locus_1_Transcript_135305/166847_Confidence_1.000_Length_636
P11420 (DA_DROME)	RecName: Full=Protein daughterless
P15806 (TFE2_MOUSE)	RecName: Full=Transcription factor E2-alpha; AltName: Full=Immunoglobulin enhancer-binding factor E12/E47; AltName: Full=Transcription factor 3; Short=TCF-3; AltName: Full=Transcription factor A1
P15884 (ITF2_HUMAN)	RecName: Full=Transcription factor 4; Short=TCF-4; AltName: Full=Class B basic helix-loop-helix protein 19; Short=bHLHb19; AltName: Full=Immunoglobulin transcription factor 2; Short=ITF-2; AltName: Full=SL3-3 enhancer factor 2; Short=SEF-2
P15923 (TFE2_HUMAN)	RecName: Full=Transcription factor E2-alpha; AltName: Full=Class B basic helix-loop-helix protein 21; Short=bHLHb21; AltName: Full=Immunoglobulin enhancer-binding factor E12/E47; AltName: Full=Immunoglobulin transcription factor 1; AltName: Full=Kappa-E2-binding factor; AltName: Full=Transcription factor 3; Short=TCF-3; AltName: Full=Transcription factor ITF-1
P21677 (TFE2_RAT)	RecName: Full=Transcription factor E2-alpha; AltName: Full=Immunoglobulin enhancer-binding factor E12/E47; AltName: Full=Pancreas specific transcription factor 1c; AltName: Full=Transcription factor 3; Short=TCF-3; AltName: Full=Transcription regulator Pan
P98180 (TFE2_MESAU)	RecName: Full=Transcription factor E2-alpha; AltName: Full=Immunoglobulin-enhancer-binding factor E12/E47; AltName: Full=Transcription factor 3; Short=TCF-3; AltName: Full=Transcription regulator Pan
Q28772 (HTF4_PAPHA)	RecName: Full=Transcription factor 12; Short=TCF-12; AltName: Full=DNA-binding protein HTF4; AltName: Full=E-box-binding protein; AltName: Full=Transcription factor HTF-4
Q60722 (ITF2_MOUSE)	RecName: Full=Transcription factor 4; Short=TCF-4; AltName: Full=Class A helix-loop-helix transcription factor ME2; AltName: Full=Immunoglobulin transcription factor 2; Short=ITF-2; Short=MITF-2; AltName: Full=SL3-3 enhancer factor 2; Short=SEF-2
Q62655 (ITF2_RAT)	RecName: Full=Transcription factor 4; Short=TCF-4; AltName: Full=Immunoglobulin transcription factor 2; Short=ITF-2; Short=RITF-2; AltName: Full=R8f DNA-binding protein; AltName: Full=SL3-3 enhancer factor 2; Short=SEF-2
Q91605 (HTF4_XENLA)	RecName: Full=Transcription factor XE1.1
XP_003247914	PREDICTED: protein daughterless isoform X7 [Acyrthosiphon pisum]
XP_008188071	PREDICTED: protein daughterless isoform X3 [Acyrthosiphon pisum]
XP_008188073	PREDICTED: protein daughterless isoform X5 [Acyrthosiphon pisum]
XP_011050420	PREDICTED: transcription factor 12 [Acromyrmex echinatior]
XP_011157356	PREDICTED: protein daughterless isoform X1 [Solenopsis invicta]
XP_011157358	PREDICTED: protein daughterless isoform X2 [Solenopsis invicta]
XP_011157366	PREDICTED: transcription factor 12 isoform X9 [Solenopsis invicta]
XP_011301748	PREDICTED: uncharacterized protein LOC105265757 [Fopius arisanus]
XP_011329841	PREDICTED: transcription factor 12 isoform X8 [Cerapachys biroi]
XP_011329842	PREDICTED: transcription factor 12 isoform X9 [Cerapachys biroi]
XP_011701972	PREDICTED: transcription factor 12 isoform X3 [Wasmannia auropunctata]
XP_012064302	PREDICTED: transcription factor 12 [Atta cephalotes]
XP_012171256	PREDICTED: transcription factor 12 isoform X13 [Bombus terrestris]
XP_012221023	PREDICTED: transcription factor 12 isoform X2 [Linepithema humile]
XP_012286379	PREDICTED: transcription factor 12 isoform X9 [Orussus abietinus]
XP_012286380	PREDICTED: transcription factor 12 isoform X10 [Orussus abietinus]
XP_013068002	PREDICTED: transcription factor 12-like isoform X6 [Biomphalaria glabrata]
XP_013419615	PREDICTED: transcription factor 12-like isoform X11 [Lingula anatina]
XP_013419616	PREDICTED: transcription factor 4-like isoform X12 [Lingula anatina]
XP_013419617	PREDICTED: transcription factor 12-like isoform X13 [Lingula anatina]
XP_013419618	PREDICTED: transcription factor 12-like isoform X14 [Lingula anatina]
XP_013419619	PREDICTED: transcription factor 12-like isoform X15 [Lingula anatina]
XP_013773383	PREDICTED: transcription factor 4-like [Limulus polyphemus]
XP_013774080	PREDICTED: transcription factor 4-like [Limulus polyphemus]
XP_013774527	PREDICTED: transcription factor 12-like, partial [Limulus polyphemus]
XP_013777261	PREDICTED: transcription factor 4-like [Limulus polyphemus]
XP_013780518	PREDICTED: transcription factor 12-like [Limulus polyphemus]

9.4.2.10 *Dorsal*

Name	Description
DORS_DROME	RecName: Full=Embryonic polarity protein dorsal

Locus_1_Transcript_26288/166847_Confidence_1.000_Length_1652 - ORF 1 (frame 3) translation	Locus_1_Transcript_26288/166847_Confidence_1.000_Length_1652
Locus_14012_Transcript_19/25_Confidence_0.128_Length_3558 - ORF 1 (frame 2) translation	Locus_14012_Transcript_19/25_Confidence_0.128_Length_3558
Locus_15237_Transcript_1/1_Confidence_1.000_Length_2268 - ORF 1 (frame 1) translation	Locus_15237_Transcript_1/1_Confidence_1.000_Length_2268
Locus_16366_Transcript_1/1_Confidence_1.000_Length_405 - ORF 1 (frame 1) translation	Locus_16366_Transcript_1/1_Confidence_1.000_Length_405
Locus_32713_Transcript_1/1_Confidence_1.000_Length_634 - ORF 2 (frame 2) translation	Locus_32713_Transcript_1/1_Confidence_1.000_Length_634
O73630 (NFKB2_XENLA)	RecName: Full=Nuclear factor NF-kappa-B p100 subunit; AltName: Full=DNA-binding factor KBF2; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2; Contains: RecName: Full=Nuclear factor NF-kappa-B p52 subunit
P01125 (REL_MELGA)	RecName: Full=Proto-oncogene c-Rel; AltName: Full=p68
P01126 (REL_AVIRE)	RecName: Full=Transforming protein rel polyprotein; AltName: Full=p58 V-rel; Contains: RecName: Full=Env polyprotein N-terminal; Contains: RecName: Full=Transforming protein rel; Contains: RecName: Full=Env polyprotein C-terminal
P15307 (REL_MOUSE)	RecName: Full=Proto-oncogene c-Rel
P15330 (DORS_DROME)	RecName: Full=Embryonic polarity protein dorsal
P16236 (REL_CHICK)	RecName: Full=Proto-oncogene c-Rel; AltName: Full=p68
P19838 (NFKB1_HUMAN)	RecName: Full=Nuclear factor NF-kappa-B p105 subunit; AltName: Full=DNA-binding factor KBF1; AltName: Full=EBP-1; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; Contains: RecName: Full=Nuclear factor NF-kappa-B p50 subunit
P25799 (NFKB1_MOUSE)	RecName: Full=Nuclear factor NF-kappa-B p105 subunit; AltName: Full=DNA-binding factor KBF1; AltName: Full=EBP-1; AltName: Full=NF-kappa-B1 p84/NF-kappa-B1 p98; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; Contains: RecName: Full=Nuclear factor NF-kappa-B p50 subunit
P51509 (RELB_CHICK)	RecName: Full=Transcription factor RelB homolog
P98149 (DIF_DROME)	RecName: Full=Dorsal-related immunity factor Dif
P98150 (NFKB2_CHICK)	RecName: Full=Nuclear factor NF-kappa-B p100 subunit; AltName: Full=DNA-binding factor KBF2; AltName: Full=Lyt-10; AltName: Full=Nuclear factor NF-kappa-B p97 subunit; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2; Contains: RecName: Full=Nuclear factor NF-kappa-B p52 subunit; AltName: Full=Nuclear factor NF-kappa-B p50B subunit
P98152 (TF65_CHICK)	RecName: Full=Transcription factor p65; AltName: Full=Nuclear factor NF-kappa-B p65 subunit
Q6F3J0 (NFKB1_CANFA)	RecName: Full=Nuclear factor NF-kappa-B p105 subunit; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; Contains: RecName: Full=Nuclear factor NF-kappa-B p50 subunit
Q9WTK5 (NFKB2_MOUSE)	RecName: Full=Nuclear factor NF-kappa-B p100 subunit; AltName: Full=DNA-binding factor KBF2; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2; Contains: RecName: Full=Nuclear factor NF-kappa-B p52 subunit
Q00653 (NFKB2_HUMAN)	RecName: Full=Nuclear factor NF-kappa-B p100 subunit; AltName: Full=DNA-binding factor KBF2; AltName: Full=H2TF1; AltName: Full=Lymphocyte translocation chromosome 10 protein; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2; AltName: Full=Oncogene Lyt-10; Short=Lyt10; Contains: RecName: Full=Nuclear factor NF-kappa-B p52 subunit
Q01201 (RELB_HUMAN)	RecName: Full=Transcription factor RelB; AltName: Full=I-Rel
Q04206 (TF65_HUMAN)	RecName: Full=Transcription factor p65; AltName: Full=Nuclear factor NF-kappa-B p65 subunit; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 3
Q04207 (TF65_MOUSE)	RecName: Full=Transcription factor p65; AltName: Full=Nuclear factor NF-kappa-B p65 subunit; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 3
Q04861 (NFKB1_CHICK)	RecName: Full=Nuclear factor NF-kappa-B p105 subunit; AltName: Full=Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; Contains: RecName: Full=Nuclear factor NF-kappa-B p50 subunit
Q04863 (RELB_MOUSE)	RecName: Full=Transcription factor RelB
Q04864 (REL_HUMAN)	RecName: Full=Proto-oncogene c-Rel
Q04865 (TF65_XENLA)	RecName: Full=Putative transcription factor p65 homolog; AltName: Full=XRel1
Q94527 (NFKB1_DROME)	RecName: Full=Nuclear factor NF-kappa-B p110 subunit; AltName: Full=Rel-p110; AltName: Full=Relish protein; Contains: RecName: Full=Nuclear factor NF-kappa-B p68 subunit; AltName: Full=Rel-p68; Contains: RecName: Full=Nuclear factor NF-kappa-B p49 subunit; AltName: Full=Rel-p49
XP_001602212	PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X1 [Nasonia vitripennis]
XP_003425093	PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X2 [Nasonia vitripennis]
XP_006567065	PREDICTED: dorsal protein isoform X6 [Apis mellifera]
XP_006608935	PREDICTED: nuclear factor NF-kappa-B p110 subunit-like isoform X1 [Apis dorsata]
XP_006608936	PREDICTED: nuclear factor NF-kappa-B p110 subunit-like isoform X2 [Apis dorsata]
XP_006608937	PREDICTED: nuclear factor NF-kappa-B p110 subunit-like isoform X3 [Apis dorsata]
XP_006619741	PREDICTED: embryonic polarity protein dorsal-like isoform X4 [Apis dorsata]
XP_006619742	PREDICTED: embryonic polarity protein dorsal-like isoform X5 [Apis dorsata]

XP_008556433	PREDICTED: embryonic polarity protein dorsal isoform X2 [Microplitis demolitor]
XP_008556434	PREDICTED: embryonic polarity protein dorsal isoform X3 [Microplitis demolitor]
XP_010185438	PREDICTED: nuclear factor NF-kappa-B p100 subunit, partial [Mesitornis unicolor]
XP_011051670	PREDICTED: nuclear factor NF-kappa-B p110 subunit isoform X1 [Acromyrmex echinatior]
XP_011051671	PREDICTED: nuclear factor NF-kappa-B p110 subunit isoform X2 [Acromyrmex echinatior]
XP_012343273	PREDICTED: embryonic polarity protein dorsal-like isoform X2 [Apis florea]
XP_012343274	PREDICTED: embryonic polarity protein dorsal-like isoform X3 [Apis florea]
XP_012625258	PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X1 [Microcebus murinus]
XP_012625266	PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X2 [Microcebus murinus]
XP_012625270	PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X3 [Microcebus murinus]
XP_013026572	PREDICTED: nuclear factor NF-kappa-B p100 subunit [Anser cygnoides domesticus]
XP_013777220	PREDICTED: embryonic polarity protein dorsal-like [Limulus polyphemus]
XP_013787326	PREDICTED: nuclear factor NF-kappa-B p100 subunit-like isoform X1 [Limulus polyphemus]
XP_013787327	PREDICTED: nuclear factor NF-kappa-B p100 subunit-like isoform X2 [Limulus polyphemus]
XP_013787328	PREDICTED: nuclear factor NF-kappa-B p100 subunit-like isoform X3 [Limulus polyphemus]
XP_013790474	PREDICTED: putative transcription factor p65 homolog [Limulus polyphemus]
XP_013794512	PREDICTED: nuclear factor NF-kappa-B p105 subunit-like [Limulus polyphemus]
XP_014250203	PREDICTED: embryonic polarity protein dorsal-like isoform X1 [Cimex lectularius]
XP_014250204	PREDICTED: embryonic polarity protein dorsal-like isoform X2 [Cimex lectularius]
XP_014250205	PREDICTED: embryonic polarity protein dorsal-like isoform X3 [Cimex lectularius]
XP_014250206	PREDICTED: embryonic polarity protein dorsal-like isoform X4 [Cimex lectularius]
XP_014275494	PREDICTED: embryonic polarity protein dorsal-like isoform X5 [Halyomorpha halys]
XP_014275495	PREDICTED: embryonic polarity protein dorsal-like isoform X6 [Halyomorpha halys]

9.4.2.11 *Drop*

Name	Description
A1YF16_(MSX2_GORGO)	RecName: Full=Homeobox protein MSX-2
A1YGA4_(MEOX1_PANPA)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2T779_(MEOX1_PANTR)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
B0VXK3_(HXA2_CALJA)	RecName: Full=Homeobox protein Hox-A2
G5ECT8_(HM02_CAEEL)	RecName: Full=Homeobox protein ceh-2
HMSH_DROME	RecName: Full=Muscle segmentation homeobox; AltName: Full=Protein drop; AltName: Full=Protein msh
Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316_-_ORF_1_(frame_1)_translation	Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316
Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968_-_ORF_1_(frame_1)_translation	Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968
Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534_-_ORF_3_(frame_3)_translation	Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534
Locus_12254_Transcript_10/10_Confidence_0.571_Length_6893_-_ORF_7_(frame_1)_translation	Locus_12254_Transcript_10/10_Confidence_0.571_Length_6893
Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327_-_ORF_3_(frame_1)_translation	Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327
Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973_-_ORF_3_(frame_3)_translation	Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973
Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736_-_ORF_18_(frame_2)_translation	Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736
Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421_-_ORF_2_(frame_1)_translation	Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421
Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590_-_ORF_4_(frame_1)_translation	Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590
Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305_-_ORF_1_(frame_3)_translation	Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305
Locus_16965_Transcript_1/1_Confidence_1.000_Length_2357_-_ORF_6_(frame_2)_translation	Locus_16965_Transcript_1/1_Confidence_1.000_Length_2357
Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037_-_ORF_2_(frame_2)_translation	Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037
Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236_-_ORF_1_(frame_2)_translation	Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236
Locus_21015_Transcript_1/1_Confidence_1.000_Length_1727_-_ORF_1_(frame_2)_translation	Locus_21015_Transcript_1/1_Confidence_1.000_Length_1727
Locus_28432_Transcript_2/2_Confidence_0.667_Length_824_-_ORF_1_(frame_3)_translation	Locus_28432_Transcript_2/2_Confidence_0.667_Length_824

MSX1_MOUSE	RecName: Full=Homeobox protein MSX-1; AltName: Full=Homeobox protein Hox-7; AltName: Full=Hox-7.1; AltName: Full=Msh homeobox 1
MSX2_MOUSE	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
MSX3_MOUSE	RecName: Full=Homeobox protein MSX-3
NP_034966	homeobox protein MSX-3 [Mus musculus]
NP_001037550	segmentation polarity homeobox protein engrailed [Bombyx mori]
NP_001107762	labial [Tribolium castaneum]
NP_001107793	empty spiracles [Tribolium castaneum]
NP_001158372	engrailed homeobox [Saccoglossus kowalevskii]
NP_001161609	Nkx1-like transcription factor [Saccoglossus kowalevskii]
O02491_(HMEN_ANOGA)	RecName: Full=Segmentation polarity homeobox protein engrailed
O02786_(MSX1_BOVIN)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
O42230_(GBX2_CHICK)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
O42365_(HXA2B_DANRE)	RecName: Full=Homeobox protein Hox-A2b; Short=Hox-A2
O42366_(HXB1A_DANRE)	RecName: Full=Homeobox protein Hox-B1a; Short=Hox-B1
O42367_(HXB2A_DANRE)	RecName: Full=Homeobox protein Hox-B2a; Short=Hox-B2
O43364_(HXA2_HUMAN)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1K
P0C1T1_(HXB2_MOUSE)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8
P02836_(HMEN_DROME)	RecName: Full=Segmentation polarity homeobox protein engrailed
P09015_(HME2A_DANRE)	RecName: Full=Homeobox protein engrailed-2a; Short=Homeobox protein en-2a; AltName: Full=Zf-En-2
P09022_(HXA1_MOUSE)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Early retinoic acid 1; AltName: Full=Homeobox protein Hox-1.6; AltName: Fu
P09145_(HMEN_DROVI)	RecName: Full=Segmentation polarity homeobox protein engrailed
P09638_(HXB2_SALSA)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=S6
P10105_(LAB_DROME)	RecName: Full=Homeotic protein labial; AltName: Full=F24; AltName: Full=F90-2
P10181_(ROUGH_DROME)	RecName: Full=Homeobox protein rough
P14652_(HXB2_HUMAN)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8; AltName: Full=Homeobox protein Hox-2H; AltName:
P14837_(PDX1_XENLA)	RecName: Full=Pancreas/duodenum homeobox protein 1; Short=PDX-1; AltName: Full=Homeobox protein 8; Short=XlHbox-8
P15142_(HM7X_CHICK)	RecName: Full=Homeobox protein CHOX-7
P15858_(EMS_APIME)	RecName: Full=Homeobox protein H40
P17487_(HM12_CAEEL)	RecName: Full=Homeobox protein ceh-12
P18264_(ROUGH_DROVI)	RecName: Full=Homeobox protein rough
P18488_(EMS_DROME)	RecName: Full=Homeotic protein empty spiracles
P19601_(SAX1_CHICK)	RecName: Full=Homeobox protein SAX-1; AltName: Full=CHOX-3
P22574_(HXB4A_DANRE)	RecName: Full=Homeobox protein Hox-B4a; Short=Hox-B4; AltName: Full=Homeobox protein Zf-13
P22807_(SLOU_DROME)	RecName: Full=Homeobox protein slou; AltName: Full=Homeobox protein NK-1; AltName: Full=Protein slouch; AltName: Full=S59/2
P27609_(HMEN_BOMMO)	RecName: Full=Segmentation polarity homeobox protein engrailed
P27610_(HMIN_BOMMO)	RecName: Full=Homeobox protein invected
P28361_(MSX1_CHICK)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Homeobox protein Hox-7; Short=CHOX-7; AltName: Full=Msh homeobox 1-like pro
P28362_(MSX2_CHICK)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8; Short=CHOX-8; Short=GHox-8
P31245_(HXA2_MOUSE)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11; Short=Hox1.11
P31246_(HXA2_RAT)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11
P31259_(HXB1_CHICK)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=Ghox-lab
P31261_(HXA2_NOTVI)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hbox-2.8; Short=NvHbox-2.8
P31264_(HMPB_DROME)	RecName: Full=Homeotic protein proboscipedia
P31357_(HXB1_AMBME)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=AHox1
P32442_(MEOX1_MOUSE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P42580_(NKX12_MOUSE)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
P48031_(GBX2_MOUSE)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=Stimulate
P49639_(HXA1_HUMAN)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Homeobox protein Hox-1F
P50219_(MNX1_HUMAN)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
P50223_(HMGX7_CHICK)	RecName: Full=Homeobox protein GHOX-7; AltName: Full=CHOX-7; Short=Hox-7
P52729_(HME2A_XENLA)	RecName: Full=Homeobox protein engrailed-2-A; Short=En-2A; Short=Homeobox protein en-2-A; AltName: Full=En2 1.4
P52730_(HME2B_XENLA)	RecName: Full=Homeobox protein engrailed-2-B; Short=En-2B; Short=Homeobox protein en-2-B; AltName: Full=En2 MABEN
P52951_(GBX2_HUMAN)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
P52953_(MSX2_RAT)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
P53547_(HM01_CAEEL)	RecName: Full=Homeobox protein ceh-1
P70118_(PDX1_MESAU)	RecName: Full=Pancreas/duodenum homeobox protein 1; AltName: Full=Homeodomain protein PDX1; AltName: Full=Insulin promoter fact

P82976_(GBX1_MOUSE)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q0P5C3_(MSX2_BOVIN)	RecName: Full=Homeobox protein MSX-2
Q0VCS4_(HXA2_BOVIN)	RecName: Full=Homeobox protein Hox-A2
Q1KKZ2_(HXA2B_TAKRU)	RecName: Full=Homeobox protein Hox-A2b
Q1KL10_(HXA1A_TAKRU)	RecName: Full=Homeobox protein Hox-A1a
Q2VL79_(MSX1_DAUMA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL80_(MSX1_PERPO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL82_(MSX1_SAGOE)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL83_(MSX1_LEORO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL84_(MSX1_CALJA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL85_(MSX1_CALGO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL86_(MSX1_SAIBB)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL88_(MSX1_PANTR)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q4V5A3_(UNPG_DROME)	RecName: Full=Homeobox protein unplugged
Q6GLB9_(EMX1_XENTR)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q08DG7_(HXA3_BOVIN)	RecName: Full=Homeobox protein Hox-A3
Q9GK08_(MSX2_CANFA)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8
Q9GZZ0_(HXD1_HUMAN)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-GG
Q9IA19_(HXA1_HETFR)	RecName: Full=Homeobox protein Hox-A1
Q9IA20_(HXA2_HETFR)	RecName: Full=Homeobox protein Hox-A2
Q9QZW9_(MNX1_MOUSE)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
Q9UD57_(NKX12_HUMAN)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
Q17R00_(EMX2_BOVIN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q28IU6_(HXD1_XENTR)	RecName: Full=Homeobox protein Hox-D1
Q28ZA9_(UNPG_DROPS)	RecName: Full=Homeobox protein unplugged
Q98SI1_(HXA1A_DANRE)	RecName: Full=Homeobox protein Hox-A1a; Short=Hox-A1
Q801E1_(VAX2_DANRE)	RecName: Full=Ventral anterior homeobox 2
Q804S6_(EMX1_DANRE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q01703_(MSXC_DANRE)	RecName: Full=Homeobox protein MSH-C
Q01822_(HXD1_MOUSE)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-4.9
Q03356_(MSXB_DANRE)	RecName: Full=Homeobox protein MSH-B
Q03357_(MSXA_DANRE)	RecName: Full=Homeobox protein MSH-A
Q03358_(MSX2_MOUSE)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
Q04741_(EMX1_HUMAN)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04742_(EMX1_MOUSE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04743_(EMX2_HUMAN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04744_(EMX2_MOUSE)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04896_(HME1A_DANRE)	RecName: Full=Homeobox protein engrailed-1a; Short=Homeobox protein en-1a
Q05640_(HMEN_ARTSF)	RecName: Full=Homeobox protein engrailed
Q06615_(NOTO_XENLA)	RecName: Full=Homeobox protein notochord; Short=Xnot
Q08727_(HXA2_CHICK)	RecName: Full=Homeobox protein Hox-A2
Q08820_(HXD1_XENLA)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Hox.lab1; AltName: Full=Labial protein; Short=Xlab
Q08821_(HXA1_XENLA)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Hox.lab2
Q14549_(GBX1_HUMAN)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q15270_(NKX11_HUMAN)	RecName: Full=NK1 transcription factor-related protein 1; AltName: Full=Homeobox protein 153; Short=HPX-153; AltName: Full=Home
Q90346_(HXB1_CYPCA)	RecName: Full=Homeobox protein Hox-B1
Q90423_(HXB1B_DANRE)	RecName: Full=Homeobox protein Hox-B1b; AltName: Full=Homeobox protein Hox-A1
Q91770_(NOT2_XENLA)	RecName: Full=Homeobox protein not2; Short=Xnot-2; Short=Xnot2
Q91907_(GBX2_XENLA)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=XGBX-2
XP_975059	PREDICTED: muscle segmentation homeobox [Tribolium castaneum]
XP_001120278	PREDICTED: homeotic protein labial isoform X1 [Apis mellifera]
XP_002402803	Vax1 transcription factor, putative [Ixodes scapularis]
XP_002406420	homeobox protein, putative [Ixodes scapularis]
XP_002423066	Homeobox protein GBX-1, putative [Pediculus humanus corporis]
XP_002431233	Homeobox protein Hox-B1, putative [Pediculus humanus corporis]
XP_002435656	homeobox protein MSX-2, putative [Ixodes scapularis]
XP_003247173	PREDICTED: homeobox protein Nkx-6.1 [Acyrthosiphon pisum]
XP_003393477	PREDICTED: homeobox protein engrailed-1a-like [Bombus terrestris]
XP_003489274	PREDICTED: homeobox protein engrailed-1a-like [Bombus impatiens]
XP_003741994	PREDICTED: homeobox protein XHOX-7.1-like [Metaseiulus occidentalis]

XP_004077224	PREDICTED: homeobox protein MSX-2 isoform X1 [Oryzias latipes]
XP_004555954	PREDICTED: homeobox protein MSX-2-like [Maylandia zebra]
XP_004925027	PREDICTED: homeobox protein Hox-B4 [Bombyx mori]
XP_004926504	PREDICTED: homeobox protein Hox-B5a [Bombyx mori]
XP_004933018	PREDICTED: homeotic protein empty spiracles-like [Bombyx mori]
XP_004933055	PREDICTED: homeobox protein slou [Bombyx mori]
XP_004933319	PREDICTED: segmentation polarity homeobox protein engrailed [Bombyx mori]
XP_005189125	PREDICTED: homeobox protein slou-like, partial [Musca domestica]
XP_006559411	PREDICTED: homeotic protein labial isoform X2 [Apis mellifera]
XP_006611901	PREDICTED: homeotic protein labial-like isoform X1 [Apis dorsata]
XP_006611902	PREDICTED: homeotic protein labial-like isoform X2 [Apis dorsata]
XP_006821574	PREDICTED: homeobox protein rough-like [Saccoglossus kowalevskii]
XP_007085565	PREDICTED: homeobox protein MSX-2 [Panthera tigris altaica]
XP_007524430	PREDICTED: homeobox protein MSX-2 [Erinaceus europaeus]
XP_007651972	PREDICTED: homeobox protein GBX-2 [Cricetulus griseus]
XP_008195160	PREDICTED: homeobox protein Hox-D4a [Tribolium castaneum]
XP_008295823	PREDICTED: homeobox protein MSX-2-like [Stegastes partitus]
XP_008494359	PREDICTED: homeobox protein MSX-1 [Calypte anna]
XP_008548384	PREDICTED: homeobox protein EMX1 [Microplitis demolitor]
XP_008919202	PREDICTED: homeobox protein MSX-1 [Manacus vitellinus]
XP_009327169	PREDICTED: homeobox protein MSX-1 [Pygoscelis adeliae]
XP_009645359	PREDICTED: homeobox protein MSX-2 [Egretta garzetta]
XP_009870132	PREDICTED: homeobox protein Hox-B1, partial [Apaloderma vittatum]
XP_009962682	PREDICTED: homeobox protein Hox-B1, partial [Tyto alba]
XP_010125476	PREDICTED: homeobox protein GHOX-7-like, partial [Chlamydotis macqueenii]
XP_010218153	PREDICTED: homeobox protein MSX-1 [Tinamus guttatus]
XP_010295047	PREDICTED: homeobox protein H17, partial [Phaethon lepturus]
XP_010708737	PREDICTED: homeobox protein MSX-1 [Meleagris gallopavo]
XP_010740428	PREDICTED: homeobox protein MSX-1 [Larimichthys crocea]
XP_011055476	PREDICTED: homeotic protein proboscipedia isoform X2 [Acromyrmex echinatior]
XP_011055478	PREDICTED: homeobox protein Hox-B1a [Acromyrmex echinatior]
XP_011066082	PREDICTED: homeobox protein Hox-B4 [Acromyrmex echinatior]
XP_011139005	PREDICTED: segmentation polarity homeobox protein engrailed-like [Harpegnathos saltator]
XP_011148733	PREDICTED: homeotic protein labial-like [Harpegnathos saltator]
XP_011149287	PREDICTED: homeotic protein proboscipedia [Harpegnathos saltator]
XP_011155414	PREDICTED: homeotic protein proboscipedia [Solenopsis invicta]
XP_011250565	PREDICTED: homeobox protein rough [Camponotus floridanus]
XP_011269817	PREDICTED: homeobox protein Hox-B1a-like [Camponotus floridanus]
XP_011283973	PREDICTED: homeobox protein GBX-2 [Felis catus]
XP_011294141	PREDICTED: homeotic protein labial-like, partial [Musca domestica]
XP_011304204	PREDICTED: homeobox protein rough [Fopius arisanus]
XP_011310234	PREDICTED: homeobox protein GBX-2 [Fopius arisanus]
XP_011342229	PREDICTED: homeobox protein Hox-B1a-like [Cerapachys biroi]
XP_011342230	PREDICTED: homeotic protein proboscipedia [Cerapachys biroi]
XP_011414445	PREDICTED: homeobox protein GBX-2-like [Crassostrea gigas]
XP_011414452	PREDICTED: homeobox protein engrailed-1-B-like [Crassostrea gigas]
XP_011447133	PREDICTED: homeobox protein not2-like [Crassostrea gigas]
XP_011482809	PREDICTED: homeobox protein MSX-2 isoform X2 [Oryzias latipes]
XP_011569017	PREDICTED: homeobox protein Hox-B4-like [Plutella xylostella]
XP_011569355	PREDICTED: homeotic protein empty spiracles-like [Plutella xylostella]
XP_011639093	PREDICTED: homeotic protein proboscipedia [Pogonomyrmex barbatus]
XP_011639094	PREDICTED: homeobox protein Hox-B1 [Pogonomyrmex barbatus]
XP_011695898	PREDICTED: homeobox protein Hox-B1a-like [Wasmannia auropunctata]
XP_011695901	PREDICTED: homeotic protein proboscipedia [Wasmannia auropunctata]
XP_011870664	PREDICTED: homeotic protein proboscipedia [Vollenhovia emeryi]
XP_012054481	PREDICTED: homeotic protein proboscipedia [Atta cephalotes]
XP_012054482	PREDICTED: homeobox protein Hox-B1a [Atta cephalotes]
XP_012219471	PREDICTED: homeobox protein rough [Linepithema humile]
XP_012225633	PREDICTED: homeotic protein proboscipedia [Linepithema humile]
XP_012276293	PREDICTED: homeotic protein labial [Orussus abietinus]
XP_012347968	PREDICTED: homeobox protein Hox-B1a-like [Apis florea]
XP_012534491	PREDICTED: homeobox protein rough [Monomorium pharaonis]
XP_012542576	PREDICTED: homeotic protein proboscipedia [Monomorium pharaonis]
XP_012984340	PREDICTED: homeobox protein MSX-1 [Melopsittacus undulatus]
XP_013063618	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Biomphalaria glabrata]
XP_013096599	PREDICTED: homeobox protein H2.0-like [Biomphalaria glabrata]
XP_013097260	PREDICTED: homeobox protein B-H1 [Stomoxys calcitrans]
XP_013104192	PREDICTED: homeotic protein labial-like [Stomoxys calcitrans]
XP_013106133	PREDICTED: homeobox protein unplugged-like, partial [Stomoxys calcitrans]
XP_013138469	PREDICTED: homeobox expressed in ES cells 1 [Papilio polytes]
XP_013141799	PREDICTED: homeotic protein empty spiracles-like [Papilio polytes]
XP_013165380	PREDICTED: homeobox protein slou-like [Papilio xuthus]
XP_013165415	PREDICTED: homeotic protein empty spiracles-like [Papilio xuthus]
XP_013177038	PREDICTED: homeobox protein GBX-2-like [Papilio xuthus]
XP_013185500	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Amyelois transitella]

XP_013188077	PREDICTED: homeobox protein slou-like [Amyelois transitella]
XP_013188268	PREDICTED: segmentation polarity homeobox protein engrailed-like [Amyelois transitella]
XP_013191083	PREDICTED: homeobox protein not2-like [Amyelois transitella]
XP_013197085	PREDICTED: homeotic protein empty spiracles-like [Amyelois transitella]
XP_013403731	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013403757	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013772903	PREDICTED: homeobox protein engrailed-1-B-like [Limulus polyphemus]
XP_013774650	PREDICTED: homeobox protein EMX1-like, partial [Limulus polyphemus]
XP_013774651	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013775485	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013777866	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013780476	PREDICTED: homeobox protein slou-like [Limulus polyphemus]
XP_013783643	PREDICTED: NK1 transcription factor-related protein 1-like [Limulus polyphemus]
XP_013783998	PREDICTED: homeobox protein MSX-2-like [Limulus polyphemus]
XP_013787176	PREDICTED: homeobox protein MSX-3-like [Limulus polyphemus]
XP_013787965	PREDICTED: homeobox protein HMX3-like [Limulus polyphemus]
XP_013790991	PREDICTED: homeotic protein proboscipedia-like, partial [Limulus polyphemus]
XP_013792320	PREDICTED: homeobox protein ceh-1-like, partial [Limulus polyphemus]
XP_013794355	PREDICTED: homeobox protein unplugged-like [Limulus polyphemus]
XP_013867753	PREDICTED: homeobox protein MSX-2-like [Austrofundulus limnaeus]
XP_013921049	PREDICTED: homeobox protein MSX-2 [Thamnophis sirtalis]
XP_014257192	PREDICTED: homeobox protein rough-like [Cimex lectularius]
XP_014357065	PREDICTED: homeobox protein Hox-A4, partial [Papilio machaon]
XP_014364712	PREDICTED: homeotic protein empty spiracles-like [Papilio machaon]

9.4.2.12 *Empty spiracles*

Name	**Description**
A1L2P5 (HXD3_XENLA)	RecName: Full=Homeobox protein Hox-D3
A1YF16 (MSX2_GORGO)	RecName: Full=Homeobox protein MSX-2
A1YGA4 (MEOX1_PANPA)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2RU54 (HMX2_HUMAN)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein H6 family member 2
A2T779 (MEOX1_PANTR)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A5YC49 (NKX63_XENLA)	RecName: Full=Homeobox protein Nkx-6.3
A6NHT5 (HMX3_HUMAN)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
A6NJ46 (NKX63_HUMAN)	RecName: Full=Homeobox protein Nkx-6.3
A6YP92 (ARX_RAT)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
A8XJD0 (HM30_CAEBR)	RecName: Full=Homeobox protein ceh-30
B0VXK3 (HXA2_CALJA)	RecName: Full=Homeobox protein Hox-A2
B0W1V2 (ABDA_CULQU)	RecName: Full=Homeobox protein abdominal-A homolog
EMS_DROME	RecName: Full=Homeotic protein empty spiracles
EMX1_MOUSE	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
EMX2_MOUSE	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
G5ECT8 (HM02_CAEEL)	RecName: Full=Homeobox protein ceh-2
Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316 - ORF 1 (frame 1) translation	Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316
Locus_1_Transcript_54418/166847_Confidence_1.000_Length_958 - ORF 9 (frame 3) translation	Locus_1_Transcript_54418/166847_Confidence_1.000_Length_958
Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968 - ORF 1 (frame 1) translation	Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968
Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118 - ORF 3 (frame 3) translation	Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118
Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075 - ORF 1 (frame 3) translation	Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075
Locus_3015_Transcript_2/2_Confidence_0.800_Length_548 - ORF 4 (frame 3) translation	Locus_3015_Transcript_2/2_Confidence_0.800_Length_548
Locus_3016_Transcript_1/1_Confidence_1.000_Length_755 - ORF 6 (frame 3) translation	Locus_3016_Transcript_1/1_Confidence_1.000_Length_755
Locus_5005_Transcript_6/6_Confidence_0.722_Length_2921 - ORF 8 (frame 1) translation	Locus_5005_Transcript_6/6_Confidence_0.722_Length_2921
Locus_7592_Transcript_10/14_Confidence_0.254_Length_4231 - ORF 18 (frame 1) translation	Locus_7592_Transcript_10/14_Confidence_0.254_Length_4231
Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099 - ORF 10 (frame 2) translation	Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099
Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534 - ORF 3 (frame 3) translation	Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534
Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549 - ORF 4 (frame 2) translation	Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549
Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293 - ORF 1 (frame 1) translation	Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293
Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327 - ORF 3 (frame 1) translation	Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327

Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869 - ORF 2 (frame 2) translation	Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869
Locus_15791_Transcript_1/1_Confidence_1.000_Length_1276 - ORF 1 (frame 2) translation	Locus_15791_Transcript_1/1_Confidence_1.000_Length_1276
Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973 - ORF 3 (frame 3) translation	Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973
Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421 - ORF 2 (frame 1) translation	Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421
Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590 - ORF 4 (frame 1) translation	Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590
Locus_16600_Transcript_5/5_Confidence_0.667_Length_2737 - ORF 3 (frame 3) translation	Locus_16600_Transcript_5/5_Confidence_0.667_Length_2737
Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305 - ORF 1 (frame 3) translation	Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305
Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037 - ORF 2 (frame 2) translation	Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037
Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236 - ORF 1 (frame 2) translation	Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236
Locus_18584_Transcript_1/1_Confidence_1.000_Length_982 - ORF 2 (frame 2) translation	Locus_18584_Transcript_1/1_Confidence_1.000_Length_982
Locus_21015_Transcript_1/1_Confidence_1.000_Length_1727 - ORF 1 (frame 2) translation	Locus_21015_Transcript_1/1_Confidence_1.000_Length_1727
Locus_21143_Transcript_2/2_Confidence_0.750_Length_1655 - ORF 5 (frame 2) translation	Locus_21143_Transcript_2/2_Confidence_0.750_Length_1655
Locus_21582_Transcript_1/1_Confidence_1.000_Length_907 - ORF 2 (frame 1) translation	Locus_21582_Transcript_1/1_Confidence_1.000_Length_907
Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612 - ORF 4 (frame 3) translation	Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612
Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832 - ORF 3 (frame 1) translation	Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832
Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275 - ORF 3 (frame 3) translation	Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275
Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198 - ORF 11 (frame 2) translation	Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198
Locus_28432_Transcript_2/2_Confidence_0.667_Length_824 - ORF 1 (frame 3) translation	Locus_28432_Transcript_2/2_Confidence_0.667_Length_824
NP_739572	T-cell leukemia homeobox protein 3 [Danio rerio]
NP_001037341	transcription factor deformed [Bombyx mori]
NP_001037550	segmentation polarity homeobox protein engrailed [Bombyx mori]
NP_001091156	homeobox protein Hox-D3 [Xenopus laevis]
NP_001095280	brain-specific homeobox protein homolog [Xenopus (Silurana) tropicalis]
NP_001107632	ultrabithorax [Bombyx mori]
NP_001107793	empty spiracles [Tribolium castaneum]
NP_001158371	distal-less homeobox 1 [Saccoglossus kowalevskii]
NP_001158372	engrailed homeobox [Saccoglossus kowalevskii]
NP_001158453	T-cell leukemia homeobox protein [Saccoglossus kowalevskii]
NP_001161609	Nkx1-like transcription factor [Saccoglossus kowalevskii]
NP_001162171	ultrabithorax [Apis mellifera]
NP_001186477	homeobox protein Nkx-6.2 [Gallus gallus]
NP_001286635	lateral muscles scarcer, isoform B [Drosophila melanogaster]
NP_001303599	homeotic protein ultrabithorax [Plutella xylostella]
O02491 (HMEN_ANOGA)	RecName: Full=Segmentation polarity homeobox protein engrailed
O13074 (HXB4A_TAKRU)	RecName: Full=Homeobox protein Hox-B4a; AltName: Full=FrHOXB-4
O14813 (PHX2A_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
O35690 (PHX2B_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2B; AltName: Full=Neuroblastoma Phox; Short=NBPhox; AltName: Full=PHOX2B homeodomain protein; AltName: Full=Paired-like homeobox 2B
O35762 (NKX61_RAT)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
O42173 (PV1_XENLA)	RecName: Full=Homeobox protein pv.1; AltName: Full=Posterior-ventral 1 transcription factor
O42230 (GBX2_CHICK)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
O42365 (HXA2B_DANRE)	RecName: Full=Homeobox protein Hox-A2b; Short=Hox-A2
O42367 (HXB2A_DANRE)	RecName: Full=Homeobox protein Hox-B2a; Short=Hox-B2
O42370 (HXD3A_DANRE)	RecName: Full=Homeobox protein Hox-D3a; Short=Hox-D3
O43364 (HXA2_HUMAN)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1K
O43365 (HXA3_HUMAN)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1E
O43711 (TLX3_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox protein Hox-11L2
O43763 (TLX2_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Neural crest homeobox protein
O55144 (TLX3_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2; AltName: Full=Respiratory neuron homeobox protein
O57374 (HXD4A_DANRE)	RecName: Full=Homeobox protein Hox-D4a; Short=Hox-D4
O57601 (HMX3_CHICK)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=cNkx5-1
O70218 (HMX1_MOUSE)	RecName: Full=Homeobox protein HMX1; AltName: Full=Homeobox protein H6
O76762 (ABDA_ANOGA)	RecName: Full=Homeobox protein abdominal-A homolog
O88181 (BARH2_RAT)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1

O93353 (HXA3_CHICK)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-D3
O93366 (TLX1_CHICK)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
O93367 (TLX3_CHICK)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2
P0C1T1 (HXB2_MOUSE)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8
P02831 (HXA3_MOUSE)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1.5; AltName: Full=Homeobox protein MO-10
P02836 (HMEN_DROME)	RecName: Full=Segmentation polarity homeobox protein engrailed
P09015 (HME2A_DANRE)	RecName: Full=Homeobox protein engrailed-2a; Short=Homeobox protein en-2a; AltName: Full=Zf-En-2
P09017 (HXC4_HUMAN)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein CP19; AltName: Full=Homeobox protein Hox-3E
P09145 (HMEN_DROVI)	RecName: Full=Segmentation polarity homeobox protein engrailed
P09638 (HXB2_SALSA)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=S6
P14652 (HXB2_HUMAN)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8; AltName: Full=Homeobox protein Hox-2H; AltName: Full=K8
P14837 (PDX1_XENLA)	RecName: Full=Pancreas/duodenum homeobox protein 1; Short=PDX-1; AltName: Full=Homeobox protein 8; Short=XlHbox-8
P14840 (HXB4_CHICK)	RecName: Full=Homeobox protein Hox-B4; AltName: Full=Homeobox protein Hox-Z; Short=Chox-Z
P15142 (HM7X_CHICK)	RecName: Full=Homeobox protein CHOX-7
P15858 (EMS_APIME)	RecName: Full=Homeobox protein H40
P17487 (HM12_CAEEL)	RecName: Full=Homeobox protein ceh-12
P18488 (EMS_DROME)	RecName: Full=Homeotic protein empty spiracles
P19601 (SAX1_CHICK)	RecName: Full=Homeobox protein SAX-1; AltName: Full=CHOX-3
P20009 (DLL_DROME)	RecName: Full=Homeotic protein distal-less; AltName: Full=Protein brista
P20822 (UBX_DROPS)	RecName: Full=Homeotic protein ultrabithorax
P22544 (BARH1_DROAN)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox BarH1 protein
P22574 (HXB4A_DANRE)	RecName: Full=Homeobox protein Hox-B4a; Short=Hox-B4; AltName: Full=Homeobox protein Zf-13
P22807 (SLOU_DROME)	RecName: Full=Homeobox protein slou; AltName: Full=Homeobox protein NK-1; AltName: Full=Protein slouch; AltName: Full=S59/2
P27609 (HMEN_BOMMO)	RecName: Full=Segmentation polarity homeobox protein engrailed
P27610 (HMIN_BOMMO)	RecName: Full=Homeobox protein invected
P28361 (MSX1_CHICK)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Homeobox protein Hox-7; Short=CHOX-7; AltName: Full=Msh homeobox 1-like protein
P28362 (MSX2_CHICK)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8; Short=CHOX-8; Short=GHox-8
P29552 (ABDA_AEDAE)	RecName: Full=Homeobox protein abdominal-A homolog
P29555 (ABDA_DROME)	RecName: Full=Homeobox protein abdominal-A
P29556 (ABDA_SCHGR)	RecName: Full=Homeobox protein abdominal-A homolog
P31245 (HXA2_MOUSE)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11; Short=Hox1.11
P31246 (HXA2_RAT)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11
P31249 (HXD3_HUMAN)	RecName: Full=Homeobox protein Hox-D3; AltName: Full=Homeobox protein Hox-4A
P31261 (HXA2_NOTVI)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hbox-2.8; Short=NvHbox-2.8
P31264 (HMPB_DROME)	RecName: Full=Homeotic protein proboscipedia
P31314 (TLX1_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox protein Hox-11; AltName: Full=Proto-oncogene TCL-3; AltName: Full=T-cell leukemia/lymphoma protein 3
P32442 (MEOX1_MOUSE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P42580 (NKX12_MOUSE)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
P42581 (HMX3_MOUSE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
P43345 (TLX1_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
P43687 (HMX2_MOUSE)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein Nkx-5.2
P48031 (GBX2_MOUSE)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=Stimulated by retinoic acid gene 7 protein
P49639 (HXA1_HUMAN)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Homeobox protein Hox-1F
P50219 (MNX1_HUMAN)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
P50223 (HMGX7_CHICK)	RecName: Full=Homeobox protein GHOX-7; AltName: Full=CHOX-7; Short=Hox-7
P50901 (HOX3_BRAFL)	RecName: Full=Homeobox protein HOX3
P52729 (HME2A_XENLA)	RecName: Full=Homeobox protein engrailed-2-A; Short=En-2A; Short=Homeobox protein en-2-A; AltName: Full=En2 1.4
P52730 (HME2B_XENLA)	RecName: Full=Homeobox protein engrailed-2-B; Short=En-2B; Short=Homeobox protein en-2-B; AltName: Full=En2 MABEN
P52951 (GBX2_HUMAN)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
P52953 (MSX2_RAT)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
P52954 (LBX1_HUMAN)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1

P52955 (LBX1_MOUSE)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
P53547 (HM01_CAEEL)	RecName: Full=Homeobox protein ceh-1
P53772 (DLLH_BRAFL)	RecName: Full=Homeobox protein DLL homolog
P53773 (DLL1_XENLA)	RecName: Full=Homeobox protein DLL-1; Short=DLL; Short=XDLL
P56177 (DLX1_HUMAN)	RecName: Full=Homeobox protein DLX-1
P56407 (HM09_CAEEL)	RecName: Full=Homeobox protein ceh-9
P63156 (BARH1_RAT)	RecName: Full=BarH-like 1 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH2; AltName: Full=BarH-related homeobox protein 1
P70118 (PDX1_MESAU)	RecName: Full=Pancreas/duodenum homeobox protein 1; AltName: Full=Homeodomain protein PDX1; AltName: Full=Insulin promoter factor 1; Short=IPF-1
P70397 (DLX6_MOUSE)	RecName: Full=Homeobox protein DLX-6
P78426 (NKX61_HUMAN)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
P82976 (GBX1_MOUSE)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
P83949 (UBX_DROME)	RecName: Full=Homeotic protein ultrabithorax
Q0P4W6 (HMX3_XENTR)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q0P5C3 (MSX2_BOVIN)	RecName: Full=Homeobox protein MSX-2
Q0VCS4 (HXA2_BOVIN)	RecName: Full=Homeobox protein Hox-A2
Q1KKS8 (HXD4A_TAKRU)	RecName: Full=Homeobox protein Hox-D4a
Q1KKU6 (HXC4A_TAKRU)	RecName: Full=Homeobox protein Hox-C4a
Q1KKZ2 (HXA2B_TAKRU)	RecName: Full=Homeobox protein Hox-A2b
Q1KL10 (HXA1A_TAKRU)	RecName: Full=Homeobox protein Hox-A1a
Q1LVQ7 (ALX1_DANRE)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q2VL79 (MSX1_DAUMA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL80 (MSX1_PERPO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL82 (MSX1_SAGOE)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL83 (MSX1_LEORO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL84 (MSX1_CALJA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL85 (MSX1_CALGO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL86 (MSX1_SAIBB)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL88 (MSX1_PANTR)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q3C1V8 (BSH_HUMAN)	RecName: Full=Brain-specific homeobox protein homolog
Q3UHX8 (NKX63_MOUSE)	RecName: Full=Homeobox protein Nkx-6.3
Q3V5Z9 (HXD3_ORYLA)	RecName: Full=Homeobox protein Hox-D3
Q4LAL6 (ALX4_BOVIN)	RecName: Full=Homeobox protein aristaless-like 4
Q4V5A3 (UNPG_DROME)	RecName: Full=Homeobox protein unplugged
Q6B3N0 (HXA5_CHICK)	RecName: Full=Homeobox protein Hox-A5
Q6GLB9 (EMX1_XENTR)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q6R3Q6 (BSH_DANRE)	RecName: Full=Brain-specific homeobox protein homolog
Q6RFL5 (BSH_CHICK)	RecName: Full=Brain-specific homeobox protein homolog
Q08DG7 (HXA3_BOVIN)	RecName: Full=Homeobox protein Hox-A3
Q8JJ64 (HMX3_XENLA)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=X-nkx-5.1
Q8T940 (UBX_JUNCO)	RecName: Full=Homeotic protein ultrabithorax; AltName: Full=JcUbx
Q8VIB5 (BARH2_MOUSE)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
Q9BZE3 (BARH1_HUMAN)	RecName: Full=BarH-like 1 homeobox protein
Q9C056 (NKX62_HUMAN)	RecName: Full=Homeobox protein Nkx-6.2; AltName: Full=Homeobox protein NK-6 homolog B
Q9DDB0 (VAX1B_XENLA)	RecName: Full=Ventral anterior homeobox 1b
Q9DE09 (HMX1_CHICK)	RecName: Full=Homeobox protein HMX1; AltName: Full=GH6; AltName: Full=Homeobox protein H6
Q9DED6 (BAX1B_CHICK)	RecName: Full=Homeobox protein BarH-like 1b; AltName: Full=Bar class homeoprotein Barx1b
Q9ER42 (BARX1_MOUSE)	RecName: Full=Homeobox protein BarH-like 1
Q9GK08 (MSX2_CANFA)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8
Q9H161 (ALX4_HUMAN)	RecName: Full=Homeobox protein aristaless-like 4
Q9HBU1 (BARX1_HUMAN)	RecName: Full=Homeobox protein BarH-like 1
Q9IA20 (HXA2_HETFR)	RecName: Full=Homeobox protein Hox-A2
Q9IA21 (HXA3_HETFR)	RecName: Full=Homeobox protein Hox-A3
Q9IA22 (HXA4_HETFR)	RecName: Full=Homeobox protein Hox-A4
Q9IAX9 (VAX2B_XENLA)	RecName: Full=Ventral anterior homeobox 2b; AltName: Full=Ventral anterior homeobox 3
Q9JLZ9 (VAX2_RAT)	RecName: Full=Ventral anterior homeobox 2
Q9NY43 (BARH2_HUMAN)	RecName: Full=BarH-like 2 homeobox protein
Q9PU20 (VAX2A_XENLA)	RecName: Full=Ventral anterior homeobox 2a; AltName: Full=Xvax2
Q9PWM3 (HXC4A_DANRE)	RecName: Full=Homeobox protein Hox-C4a; Short=Hox-C4
Q9QZW9 (MNX1_MOUSE)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
Q9UD57 (NKX12_HUMAN)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
Q9W6D8 (BARX1_CHICK)	RecName: Full=Homeobox protein BarH-like 1

Q9W7E8 (KOZA_XENLA)	RecName: Full=Homeobox protein koza; AltName: Full=Homeodomain transcription factor koza
Q17R00 (EMX2_BOVIN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q28ZA9 (UNPG_DROPS)	RecName: Full=Homeobox protein unplugged
Q90XN9 (HMX3B_ORYLA)	RecName: Full=Homeobox protein HMX3-B; AltName: Full=Homeobox protein H6 family member 3-B; AltName: Full=Homeobox protein Nkx-5.1.2; AltName: Full=OlNkx-5.1.2
Q90XP0 (HMX3A_ORYLA)	RecName: Full=Homeobox protein HMX3-A; AltName: Full=Homeobox protein H6 family member 3-A; AltName: Full=Homeobox protein Nkx-5.1.1; AltName: Full=OlNkx-5.1.1
Q96QS3 (ARX_HUMAN)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
Q99MA9 (NKX61_MOUSE)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q503F2 (BARX1_DANRE)	RecName: Full=Homeobox protein BarH-like 1; AltName: Full=BarH-class homeodomain transcription factor 4
Q504H8 (HMX3_DANRE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q801E1 (VAX2_DANRE)	RecName: Full=Ventral anterior homeobox 2
Q804S6 (EMX1_DANRE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q810B3 (BSH_MOUSE)	RecName: Full=Brain-specific homeobox protein homolog
Q01703 (MSXC_DANRE)	RecName: Full=Homeobox protein MSH-C
Q03356 (MSXB_DANRE)	RecName: Full=Homeobox protein MSH-B
Q03357 (MSXA_DANRE)	RecName: Full=Homeobox protein MSH-A
Q03358 (MSX2_MOUSE)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
Q04741 (EMX1_HUMAN)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04742 (EMX1_MOUSE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04743 (EMX2_HUMAN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04744 (EMX2_MOUSE)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04787 (BSH_DROME)	RecName: Full=Brain-specific homeobox protein
Q04896 (HME1A_DANRE)	RecName: Full=Homeobox protein engrailed-1a; Short=Homeobox protein en-1a
Q05007 (ABDA_ARTSF)	RecName: Full=Homeobox protein abdominal-A homolog
Q05640 (HMEN_ARTSF)	RecName: Full=Homeobox protein engrailed
Q06615 (NOTO_XENLA)	RecName: Full=Homeobox protein notochord; Short=Xnot
Q07961 (ABDA_TRICA)	RecName: Full=Homeobox protein abdominal-A homolog
Q08624 (HXC4_MOUSE)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein Hox-3.5
Q08727 (HXA2_CHICK)	RecName: Full=Homeobox protein Hox-A2
Q14549 (GBX1_HUMAN)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q15270 (NKX11_HUMAN)	RecName: Full=NK1 transcription factor-related protein 1; AltName: Full=Homeobox protein 153; Short=HPX-153; AltName: Full=Homeobox protein SAX-2; AltName: Full=NKX-1.1
Q22909 (HM30_CAEEL)	RecName: Full=Homeobox protein ceh-30
Q22910 (HM31_CAEEL)	RecName: Full=Homeobox protein ceh-31
Q24255 (BARH1_DROME)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox protein BarH1
Q24256 (BARH2_DROME)	RecName: Full=Homeobox protein B-H2; AltName: Full=Homeobox protein BarH2
Q26430 (ABDA_MANSE)	RecName: Full=Homeobox protein abdominal-A homolog
Q26602 (SMOX3_SCHMA)	RecName: Full=Homeobox protein SMOX-3
Q26656 (HMX_STRPU)	RecName: Full=Homeobox protein Hmx; Short=SpHmx; AltName: Full=H6-like
Q60554 (NKX61_MESAU)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q61663 (TLX2_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Enteric neuron homeobox protein; AltName: Full=Homeobox TLX-2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Hox11L.1; AltName: Full=PMUR10F
Q62066 (PHX2A_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=PHOX2A homeodomain protein; AltName: Full=Paired-like homeobox 2A
Q62782 (PHX2A_RAT)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
Q64317 (DLX1_MOUSE)	RecName: Full=Homeobox protein DLX-1
Q91770 (NOT2_XENLA)	RecName: Full=Homeobox protein not2; Short=Xnot-2; Short=Xnot2
Q91907 (GBX2_XENLA)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=XGBX-2
Q98875 (DLX1A_DANRE)	RecName: Full=Homeobox protein Dlx1a; Short=DLX-1; AltName: Full=Distal-less homeobox gene 1a
Q98877 (DLX6A_DANRE)	RecName: Full=Homeobox protein Dlx6a; AltName: Full=Distal-less homeobox protein 6a; Short=DLX-6
Q98878 (DLX4B_DANRE)	RecName: Full=Homeobox protein Dlx4b; AltName: Full=DLX-7; AltName: Full=Distal-less homeobox protein 4b
Q98879 (DLX4A_DANRE)	RecName: Full=Homeobox protein Dlx4a; AltName: Full=DLX-8; AltName: Full=Distal-less homeobox protein 4a
Q99801 (NKX31_HUMAN)	RecName: Full=Homeobox protein Nkx-3.1; AltName: Full=Homeobox protein NK-3 homolog A
XP_975059	PREDICTED: muscle segmentation homeobox [Tribolium castaneum]
XP_001120833	PREDICTED: paired mesoderm homeobox protein 2A [Apis mellifera]
XP_001944887	PREDICTED: homeobox protein B-H1-like [Acyrthosiphon pisum]

XP_002423066	Homeobox protein GBX-1, putative [Pediculus humanus corporis]
XP_002425514	Homeobox protein Nkx-6.1, putative [Pediculus humanus corporis]
XP_002429457	Homeobox protein Hmx, putative [Pediculus humanus corporis]
XP_002431233	Homeobox protein Hox-B1, putative [Pediculus humanus corporis]
XP_002435656	homeobox protein MSX-2, putative [Ixodes scapularis]
XP_002436223	homeobox protein, putative [Ixodes scapularis]
XP_002596391	BarH-like 1 homeobox protein [Branchiostoma floridae]
XP_002609070	nk homeobox 6 [Branchiostoma floridae]
XP_002731951	PREDICTED: homeobox protein HMX3-A-like [Saccoglossus kowalevskii]
XP_003224963	PREDICTED: homeobox protein Hox-A3 [Anolis carolinensis]
XP_003247173	PREDICTED: homeobox protein Nkx-6.1 [Acyrthosiphon pisum]
XP_003393477	PREDICTED: homeobox protein engrailed-1a-like [Bombus terrestris]
XP_003427431	PREDICTED: motor neuron and pancreas homeobox protein 1 [Nasonia vitripennis]
XP_003489274	PREDICTED: homeobox protein engrailed-1a-like [Bombus impatiens]
XP_003698568	PREDICTED: homeobox protein B-H2 [Apis florea]
XP_003741994	PREDICTED: homeobox protein XHOX-7.1-like [Metaseiulus occidentalis]
XP_003743246	PREDICTED: homeobox protein B-H1-like [Metaseiulus occidentalis]
XP_003963996	PREDICTED: homeobox protein HMX3-A [Takifugu rubripes]
XP_004076957	PREDICTED: T-cell leukemia homeobox protein 1-like [Oryzias latipes]
XP_004077224	PREDICTED: homeobox protein MSX-2 isoform X1 [Oryzias latipes]
XP_004555954	PREDICTED: homeobox protein MSX-2-like [Maylandia zebra]
XP_004925027	PREDICTED: homeobox protein Hox-B4 [Bombyx mori]
XP_004926504	PREDICTED: homeobox protein Hox-B5a [Bombyx mori]
XP_004933018	PREDICTED: homeotic protein empty spiracles-like [Bombyx mori]
XP_004933035	PREDICTED: homeobox protein HMX3-B [Bombyx mori]
XP_004933055	PREDICTED: homeobox protein slou [Bombyx mori]
XP_004933319	PREDICTED: segmentation polarity homeobox protein engrailed [Bombyx mori]
XP_005179335	PREDICTED: homeotic protein empty spiracles [Musca domestica]
XP_005189125	PREDICTED: homeobox protein slou-like, partial [Musca domestica]
XP_005303794	PREDICTED: brain-specific homeobox protein homolog [Chrysemys picta bellii]
XP_005305386	PREDICTED: homeobox protein Nkx-6.2 [Chrysemys picta bellii]
XP_005512968	PREDICTED: barH-like 1 homeobox protein [Columba livia]
XP_006003775	PREDICTED: homeobox protein Nkx-6.2 [Latimeria chalumnae]
XP_006024676	PREDICTED: homeobox protein Nkx-6.2 [Alligator sinensis]
XP_006136686	PREDICTED: homeobox protein Nkx-6.2 [Pelodiscus sinensis]
XP_006137362	PREDICTED: barH-like 2 homeobox protein [Pelodiscus sinensis]
XP_006274581	PREDICTED: brain-specific homeobox protein homolog [Alligator mississippiensis]
XP_006559409	PREDICTED: ultrabithorax isoform X5 [Apis mellifera]
XP_006610893	PREDICTED: homeotic protein ultrabithorax-like isoform X3 [Apis dorsata]
XP_006895666	PREDICTED: brain-specific homeobox protein homolog [Elephantulus edwardii]
XP_007053086	PREDICTED: homeobox protein Nkx-6.2 [Chelonia mydas]
XP_007067023	PREDICTED: brain-specific homeobox protein homolog [Chelonia mydas]
XP_007085565	PREDICTED: homeobox protein MSX-2 [Panthera tigris altaica]
XP_007258178	PREDICTED: brain-specific homeobox protein homolog [Astyanax mexicanus]
XP_007524430	PREDICTED: homeobox protein MSX-2 [Erinaceus europaeus]
XP_007565863	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia formosa]
XP_007566853	PREDICTED: homeobox protein Nkx-6.2-like [Poecilia formosa]
XP_007651972	PREDICTED: homeobox protein GBX-2 [Cricetulus griseus]
XP_008192483	PREDICTED: paired mesoderm homeobox protein 2A-like [Tribolium castaneum]
XP_008193415	PREDICTED: homeobox protein ceh-31-like [Tribolium castaneum]
XP_008195160	PREDICTED: homeobox protein Hox-D4a [Tribolium castaneum]
XP_008195161	PREDICTED: barH-like 1 homeobox protein [Tribolium castaneum]
XP_008295823	PREDICTED: homeobox protein MSX-2-like [Stegastes partitus]
XP_008299788	PREDICTED: T-cell leukemia homeobox protein 1-like [Stegastes partitus]
XP_008325234	PREDICTED: T-cell leukemia homeobox protein 3 [Cynoglossus semilaevis]
XP_008418492	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia reticulata]
XP_008473261	PREDICTED: homeobox protein B-H1-like [Diaphorina citri]
XP_008488086	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Diaphorina citri]
XP_008489821	PREDICTED: barH-like 1 homeobox protein, partial [Calypte anna]
XP_008494359	PREDICTED: homeobox protein MSX-1 [Calypte anna]
XP_008548384	PREDICTED: homeobox protein EMX1 [Microplitis demolitor]
XP_008559758	PREDICTED: homeotic protein ultrabithorax isoform X2 [Microplitis demolitor]
XP_008560226	PREDICTED: paired mesoderm homeobox protein 2B-like [Microplitis demolitor]
XP_008919202	PREDICTED: homeobox protein MSX-1 [Manacus vitellinus]
XP_009319165	PREDICTED: homeobox protein notochord-like [Pygoscelis adeliae]
XP_009327169	PREDICTED: homeobox protein MSX-1 [Pygoscelis adeliae]
XP_009485378	PREDICTED: homeobox protein not2-like, partial [Pelecanus crispus]
XP_009499002	PREDICTED: homeobox protein notochord-like, partial [Phalacrocorax carbo]
XP_009645359	PREDICTED: homeobox protein MSX-2 [Egretta garzetta]
XP_009894572	PREDICTED: barH-like 1 homeobox protein, partial [Picoides pubescens]
XP_009944864	PREDICTED: homeobox protein notochord-like, partial [Leptosomus discolor]

XP_009993327	PREDICTED: brain-specific homeobox protein homolog [Chaetura pelagica]
XP_010125476	PREDICTED: homeobox protein GHOX-7-like, partial [Chlamydotis macqueenii]
XP_010140778	PREDICTED: homeobox protein not2-like, partial [Buceros rhinoceros silvestris]
XP_010160639	PREDICTED: homeobox protein not2-like, partial [Caprimulgus carolinensis]
XP_010218153	PREDICTED: homeobox protein MSX-1 [Tinamus guttatus]
XP_010292386	PREDICTED: homeobox protein not2-like, partial [Phaethon lepturus]
XP_010295047	PREDICTED: homeobox protein H17, partial [Phaethon lepturus]
XP_010708737	PREDICTED: homeobox protein MSX-1 [Meleagris gallopavo]
XP_010740428	PREDICTED: homeobox protein MSX-1 [Larimichthys crocea]
XP_010765038	PREDICTED: barH-like 2 homeobox protein [Notothenia coriiceps]
XP_010870399	PREDICTED: barH-like 2 homeobox protein [Esox lucius]
XP_010892954	PREDICTED: T-cell leukemia homeobox protein 3-like [Esox lucius]
XP_010894067	PREDICTED: T-cell leukemia homeobox protein 3 [Esox lucius]
XP_010965528	PREDICTED: brain-specific homeobox protein homolog [Camelus bactrianus]
XP_011055476	PREDICTED: homeotic protein proboscipedia isoform X2 [Acromyrmex echinatior]
XP_011139005	PREDICTED: segmentation polarity homeobox protein engrailed-like [Harpegnathos saltator]
XP_011142568	PREDICTED: homeotic protein empty spiracles-like [Harpegnathos saltator]
XP_011149287	PREDICTED: homeotic protein proboscipedia [Harpegnathos saltator]
XP_011155414	PREDICTED: homeotic protein proboscipedia [Solenopsis invicta]
XP_011185992	PREDICTED: homeotic protein empty spiracles [Bactrocera cucurbitae]
XP_011212609	PREDICTED: homeotic protein empty spiracles [Bactrocera dorsalis]
XP_011256835	PREDICTED: homeobox protein B-H2-like [Camponotus floridanus]
XP_011258058	PREDICTED: homeotic protein ultrabithorax [Camponotus floridanus]
XP_011283973	PREDICTED: homeobox protein GBX-2 [Felis catus]
XP_011310234	PREDICTED: homeobox protein GBX-2 [Fopius arisanus]
XP_011341316	PREDICTED: paired mesoderm homeobox protein 2A-like [Cerapachys biroi]
XP_011342230	PREDICTED: homeotic protein proboscipedia [Cerapachys biroi]
XP_011344364	PREDICTED: homeobox protein B-H2 [Cerapachys biroi]
XP_011414445	PREDICTED: homeobox protein GBX-2-like [Crassostrea gigas]
XP_011414452	PREDICTED: homeobox protein engrailed-1-B-like [Crassostrea gigas]
XP_011441569	PREDICTED: homeobox protein Dlx6a-like [Crassostrea gigas]
XP_011447133	PREDICTED: homeobox protein not2-like [Crassostrea gigas]
XP_011482809	PREDICTED: homeobox protein MSX-2 isoform X2 [Oryzias latipes]
XP_011494442	PREDICTED: homeobox protein ceh-1 isoform X1 [Ceratosolen solmsi marchali]
XP_011495613	PREDICTED: homeobox protein Nkx-6.1 [Ceratosolen solmsi marchali]
XP_011555719	PREDICTED: homeobox protein Hox-C4 [Plutella xylostella]
XP_011569017	PREDICTED: homeobox protein Hox-B4-like [Plutella xylostella]
XP_011569355	PREDICTED: homeotic protein empty spiracles-like [Plutella xylostella]
XP_011637906	PREDICTED: homeobox protein B-H2 [Pogonomyrmex barbatus]
XP_011639093	PREDICTED: homeotic protein proboscipedia [Pogonomyrmex barbatus]
XP_011695901	PREDICTED: homeotic protein proboscipedia [Wasmannia auropunctata]
XP_011870664	PREDICTED: homeotic protein proboscipedia [Vollenhovia emeryi]
XP_012054481	PREDICTED: homeotic protein proboscipedia [Atta cephalotes]
XP_012225633	PREDICTED: homeotic protein proboscipedia [Linepithema humile]
XP_012232563	PREDICTED: paired mesoderm homeobox protein 2B-like [Linepithema humile]
XP_012252406	PREDICTED: homeobox protein EMX1-like [Athalia rosae]
XP_012267082	PREDICTED: homeotic protein ultrabithorax [Athalia rosae]
XP_012268630	PREDICTED: homeobox protein B-H1-like [Athalia rosae]
XP_012269935	PREDICTED: paired mesoderm homeobox protein 2A-like [Athalia rosae]
XP_012340524	PREDICTED: homeobox protein ceh-19 [Apis florea]
XP_012427106	PREDICTED: homeobox protein Hox-A3 isoform X2 [Taeniopygia guttata]
XP_012542576	PREDICTED: homeotic protein proboscipedia [Monomorium pharaonis]
XP_012549555	PREDICTED: ultrabithorax isoform X1 [Bombyx mori]
XP_012683084	PREDICTED: brain-specific homeobox protein homolog [Clupea harengus]
XP_012685430	PREDICTED: T-cell leukemia homeobox protein 3-like [Clupea harengus]
XP_012707525	PREDICTED: T-cell leukemia homeobox protein 1 [Fundulus heteroclitus]
XP_012873727	PREDICTED: barH-like 2 homeobox protein [Dipodomys ordii]
XP_012984340	PREDICTED: homeobox protein MSX-1 [Melopsittacus undulatus]
XP_013063618	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Biomphalaria glabrata]
XP_013096599	PREDICTED: homeobox protein H2.0-like [Biomphalaria glabrata]
XP_013097260	PREDICTED: homeobox protein B-H1 [Stomoxys calcitrans]
XP_013103134	PREDICTED: homeotic protein empty spiracles [Stomoxys calcitrans]
XP_013106133	PREDICTED: homeobox protein unplugged-like, partial [Stomoxys calcitrans]
XP_013108189	PREDICTED: homeobox protein B-H2-like [Stomoxys calcitrans]
XP_013111263	PREDICTED: pituitary homeobox 1 [Stomoxys calcitrans]
XP_013138469	PREDICTED: homeobox expressed in ES cells 1 [Papilio polytes]
XP_013139547	PREDICTED: homeobox protein Hox-B4 [Papilio polytes]
XP_013141799	PREDICTED: homeotic protein empty spiracles-like [Papilio polytes]
XP_013154388	PREDICTED: homeobox protein Hox-A3 isoform X2 [Falco peregrinus]

XP_013165380	PREDICTED: homeobox protein slou-like [Papilio xuthus]
XP_013165415	PREDICTED: homeotic protein empty spiracles-like [Papilio xuthus]
XP_013173873	PREDICTED: homeotic protein ultrabithorax [Papilio xuthus]
XP_013177038	PREDICTED: homeobox protein GBX-2-like [Papilio xuthus]
XP_013185500	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Amyelois transitella]
XP_013188077	PREDICTED: homeobox protein slou-like [Amyelois transitella]
XP_013188268	PREDICTED: segmentation polarity homeobox protein engrailed-like [Amyelois transitella]
XP_013191083	PREDICTED: homeobox protein not2-like [Amyelois transitella]
XP_013193972	PREDICTED: homeobox protein Hox-B4 [Amyelois transitella]
XP_013197085	PREDICTED: homeotic protein empty spiracles-like [Amyelois transitella]
XP_013378782	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Lingula anatina]
XP_013394544	PREDICTED: homeobox protein Dlx1a-like isoform X1 [Lingula anatina]
XP_013394545	PREDICTED: homeobox protein Dlx1a-like isoform X2 [Lingula anatina]
XP_013399159	PREDICTED: homeobox protein Hox-A3-like isoform X1 [Lingula anatina]
XP_013399161	PREDICTED: homeobox protein Hox-D3-like isoform X2 [Lingula anatina]
XP_013403731	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013403757	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013772903	PREDICTED: homeobox protein engrailed-1-B-like [Limulus polyphemus]
XP_013774538	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013774650	PREDICTED: homeobox protein EMX1-like, partial [Limulus polyphemus]
XP_013774651	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013775485	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013775825	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013776086	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013776376	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]
XP_013776725	PREDICTED: homeobox protein Hox-B4a-like [Limulus polyphemus]
XP_013776843	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]
XP_013777105	PREDICTED: homeobox protein Hox-A3a-like [Limulus polyphemus]
XP_013777106	PREDICTED: protein enabled homolog [Limulus polyphemus]
XP_013777866	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013780476	PREDICTED: homeobox protein slou-like [Limulus polyphemus]
XP_013780477	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783221	PREDICTED: brain-specific homeobox protein homolog [Limulus polyphemus]
XP_013783383	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783573	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]
XP_013783575	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]
XP_013783643	PREDICTED: NK1 transcription factor-related protein 1-like [Limulus polyphemus]
XP_013783998	PREDICTED: homeobox protein MSX-2-like [Limulus polyphemus]
XP_013784402	PREDICTED: homeobox protein Hox-B4-like [Limulus polyphemus]
XP_013785537	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013785548	PREDICTED: homeobox protein B-H1-like [Limulus polyphemus]
XP_013785691	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013786746	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013787176	PREDICTED: homeobox protein MSX-3-like [Limulus polyphemus]
XP_013787478	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Limulus polyphemus]
XP_013787965	PREDICTED: homeobox protein HMX3-like [Limulus polyphemus]
XP_013788660	PREDICTED: homeobox protein DLX-6-like [Limulus polyphemus]
XP_013790370	PREDICTED: homeobox protein Hox-A4-like [Limulus polyphemus]
XP_013790705	PREDICTED: homeobox protein HMX3-like [Limulus polyphemus]
XP_013790991	PREDICTED: homeotic protein proboscipedia-like, partial [Limulus polyphemus]
XP_013791445	PREDICTED: homeobox protein ceh-31-like, partial [Limulus polyphemus]
XP_013792062	PREDICTED: homeotic protein ultrabithorax-like, partial [Limulus polyphemus]
XP_013792158	PREDICTED: homeobox protein Hox-D4-like [Limulus polyphemus]
XP_013792320	PREDICTED: homeobox protein ceh-1-like, partial [Limulus polyphemus]
XP_013794103	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013794355	PREDICTED: homeobox protein unplugged-like [Limulus polyphemus]
XP_013794488	PREDICTED: T-cell leukemia homeobox protein 3-like [Limulus polyphemus]
XP_013867753	PREDICTED: homeobox protein MSX-2-like [Austrofundulus limnaeus]
XP_013879114	PREDICTED: barH-like 2 homeobox protein [Austrofundulus limnaeus]
XP_013921049	PREDICTED: homeobox protein MSX-2 [Thamnophis sirtalis]
XP_013978546	PREDICTED: barH-like 2 homeobox protein [Salmo salar]
XP_013983956	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Salmo salar]
XP_014052040	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014068039	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014088070	PREDICTED: homeotic protein empty spiracles [Bactrocera oleae]
XP_014128632	PREDICTED: homeobox protein Hox-A3 [Zonotrichia albicollis]
XP_014162805	PREDICTED: homeobox protein Hox-A3 isoform X2 [Geospiza fortis]
XP_014209645	PREDICTED: homeobox protein GBX-1-like [Copidosoma floridanum]

XP_014219299	PREDICTED: homeotic protein ultrabithorax-like isoform X2 [Copidosoma floridanum]
XP_014236045	PREDICTED: barH-like 1 homeobox protein [Trichogramma pretiosum]
XP_014240108	PREDICTED: homeobox protein Hox-B4 isoform X1 [Cimex lectularius]
XP_014240109	PREDICTED: homeobox protein Hox-B4 isoform X2 [Cimex lectularius]
XP_014240209	PREDICTED: homeotic protein ultrabithorax-like isoform X2 [Cimex lectularius]
XP_014241910	PREDICTED: homeobox protein EMX2-like isoform X1 [Cimex lectularius]
XP_014241911	PREDICTED: homeotic protein empty spiracles-like isoform X2 [Cimex lectularius]
XP_014242034	PREDICTED: homeobox protein HMX3-like [Cimex lectularius]
XP_014245972	PREDICTED: homeotic protein distal-less isoform X2 [Cimex lectularius]
XP_014280507	PREDICTED: homeobox protein HMX3-like [Halyomorpha halys]
XP_014288116	PREDICTED: paired mesoderm homeobox protein 2A-like isoform X2 [Halyomorpha halys]
XP_014293083	PREDICTED: homeobox protein HMX3-like, partial [Halyomorpha halys]
XP_014328725	PREDICTED: T-cell leukemia homeobox protein 3 [Xiphophorus maculatus]
XP_014357065	PREDICTED: homeobox protein Hox-A4, partial [Papilio machaon]
XP_014361996	PREDICTED: homeobox protein HMX3-B-like [Papilio machaon]
XP_014364712	PREDICTED: homeotic protein empty spiracles-like [Papilio machaon]
XP_014385363	PREDICTED: barH-like 1 homeobox protein, partial [Myotis brandtii]
XP_014436686	PREDICTED: homeobox protein Hox-A3 [Pelodiscus sinensis]

9.4.2.13 *Enhancer of zeste*

Name	Description
A7E2Z2 (EZH1_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase EZH1; AltName: Full=Enhancer of zeste homolog 1
A8XI75 (SET23_CAEBR)	RecName: Full=Probable histone-lysine N-methyltransferase set-23; AltName: Full=SET-domain containing protein 23
C6KTD2 (SET1_PLAF7)	RecName: Full=Putative histone-lysine N-methyltransferase 1; Short=PfSET1
E9Q5F9 (SETD2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETD2; AltName: Full=Lysine N-methyltransferase 3A; AltName: Full=SET domain-containing protein 2
EZ_DROME	RecName: Full=Histone-lysine N-methyltransferase E(z); AltName: Full=Lysine N-methyltransferase 6; AltName: Full=Protein enhancer of zeste
EZH1_MOUSE	RecName: Full=Histone-lysine N-methyltransferase EZH1; AltName: Full=ENX-2; AltName: Full=Enhancer of zeste homolog 1
EZH2_MOUSE	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=ENX-1; AltName: Full=Enhancer of zeste homolog 2
Locus_1_Transcript_59871/166847_Confidence_1.000_Length_1692 - ORF 12 (frame 2) translation	Locus_1_Transcript_59871/166847_Confidence_1.000_Length_1692
Locus_1_Transcript_119592/166847_Confidence_1.000_Length_638 - ORF 3 (frame 2) translation	Locus_1_Transcript_119592/166847_Confidence_1.000_Length_638
Locus_1_Transcript_132989/166847_Confidence_1.000_Length_2020 - ORF 8 (frame 3) translation	Locus_1_Transcript_132989/166847_Confidence_1.000_Length_2020
Locus_81_Transcript_58/63_Confidence_0.130_Length_4613 - ORF 3 (frame 1) translation	Locus_81_Transcript_58/63_Confidence_0.130_Length_4613
Locus_1984_Transcript_1/5_Confidence_0.591_Length_2911 - ORF 13 (frame 1) translation	Locus_1984_Transcript_1/5_Confidence_0.591_Length_2911
Locus_7116_Transcript_1/8_Confidence_0.615_Length_8437 - ORF 2 (frame 1) translation	Locus_7116_Transcript_1/8_Confidence_0.615_Length_8437
Locus_7644_Transcript_3/9_Confidence_0.484_Length_3144 - ORF 1 (frame 1) translation	Locus_7644_Transcript_3/9_Confidence_0.484_Length_3144
Locus_11760_Transcript_19/20_Confidence_0.198_Length_7700 - ORF 3 (frame 1) translation	Locus_11760_Transcript_19/20_Confidence_0.198_Length_7700
Locus_13467_Transcript_1/6_Confidence_0.500_Length_1857 - ORF 8 (frame 2) translation	Locus_13467_Transcript_1/6_Confidence_0.500_Length_1857
Locus_13654_Transcript_6/15_Confidence_0.269_Length_12662 - ORF 38 (frame 2) translation	Locus_13654_Transcript_6/15_Confidence_0.269_Length_12662
Locus_14416_Transcript_5/6_Confidence_0.500_Length_993 - ORF 1 (frame 2) translation	Locus_14416_Transcript_5/6_Confidence_0.500_Length_993
O08550 (KMT2B_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2B; Short=Lysine N-methyltransferase 2B; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 4 homolog; AltName: Full=Trithorax homolog 2; AltName: Full=WW domain-binding protein 7; Short=WBP-7
O14686 (KMT2D_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2D; Short=Lysine N-methyltransferase 2D; AltName: Full=ALL1-related protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 2
O15047 (SET1A_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD1A; AltName: Full=Lysine N-methyltransferase 2F; AltName: Full=SET domain-containing protein 1A; Short=hSET1A; AltName: Full=Set1/Ash2 histone methyltransferase complex subunit SET1
O43463 (SUV91_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Histone H3-K9 methyltransferase 1; Short=H3-K9-HMTase 1; AltName: Full=Lysine N-methyltransferase 1A; AltName: Full=Position-effect variegation 3-9 homolog; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
O60016 (CLR4_SCHPO)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-9 specific; AltName: Full=Cryptic loci regulator 4; AltName: Full=Histone H3-K9 methyltransferase; Short=H3-K9-HMTase; AltName: Full=Lysine N-methyltransferase 1

O82175 (SUVH5_ARATH)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5; AltName: Full=Histone H3-K9 methyltransferase 5; Short=H3-K9-HMTase 5; AltName: Full=Protein SET DOMAIN GROUP 9; AltName: Full=Suppressor of variegation 3-9 homolog protein 5; Short=Su(var)3-9 homolog protein 5
O88491 (NSD1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific; AltName: Full=H3-K36-HMTase; AltName: Full=H4-K20-HMTase; AltName: Full=Nuclear receptor-binding SET domain-containing protein 1; Short=NR-binding SET domain-containing protein
O96028 (NSD2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase NSD2; AltName: Full=Multiple myeloma SET domain-containing protein; Short=MMSET; AltName: Full=Nuclear SET domain-containing protein 2; Short=NSD2; AltName: Full=Protein trithorax-5; AltName: Full=Wolf-Hirschhorn syndrome candidate 1 protein; Short=WHSC1
P42124 (EZ_DROME)	RecName: Full=Histone-lysine N-methyltransferase E(z); AltName: Full=Lysine N-methyltransferase 6; AltName: Full=Protein enhancer of zeste
P55200 (KMT2A_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2A; Short=Lysine N-methyltransferase 2A; AltName: Full=ALL-1; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 1; AltName: Full=Zinc finger protein HRX; Contains: RecName: Full=MLL cleavage product N320; AltName: Full=N-terminal cleavage product of 320 kDa; Short=p320; Contains: RecName: Full=MLL cleavage product C180; AltName: Full=C-terminal cleavage product of 180 kDa; Short=p180
P70351 (EZH1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EZH1; AltName: Full=ENX-2; AltName: Full=Enhancer of zeste homolog 1
Q0V9E9 (SETD8_XENTR)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=SET domain-containing protein 8
Q0VD24 (SETMR_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase SETMAR; AltName: Full=SET domain and mariner transposase fusion protein homolog
Q1DU03 (SET2_COCIM)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q1LY77 (SE1BA_DANRE)	RecName: Full=Histone-lysine N-methyltransferase SETD1B-A; AltName: Full=SET domain-containing protein 1B-A
Q2H988 (SET2_CHAGB)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q2LAE1 (ASHH2_ARATH)	RecName: Full=Histone-lysine N-methyltransferase ASHH2; AltName: Full=ASH1 homolog 2; AltName: Full=H3-K4-HMTase; AltName: Full=Histone H3-K36 methyltransferase 8; Short=H3-K36-HMTase 8; AltName: Full=Protein EARLY FLOWERING IN SHORT DAYS; AltName: Full=Protein LAZARUS 2; AltName: Full=Protein SET DOMAIN GROUP 8
Q2NL30 (SUV91_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
Q2UTN6 (SET2_ASPOR)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q2YDJ8 (SETD8_BOVIN)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q2YDW7 (SETD8_MOUSE)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q4PBL3 (SET2_USTMA)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q4R3E0 (SUV92_MACFA)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q4R381 (EZH2_MACFA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2
Q4V863 (EZH2B_XENLA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2-B
Q4WTT2 (SET2_ASPFU)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q5DW34 (EHMT1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EHMT1; AltName: Full=Euchromatic histone-lysine N-methyltransferase 1; Short=Eu-HMTase1; AltName: Full=G9a-like protein 1; Short=GLP; Short=GLP1; AltName: Full=Lysine N-methyltransferase 1D
Q5F3P8 (SET1B_CHICK)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q5F3W5 (SUV92_CHICK)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q5I0M0 (SETMR_RAT)	RecName: Full=Histone-lysine N-methyltransferase SETMAR; AltName: Full=SET domain and mariner transposase fusion protein homolog
Q5LJZ2 (SET1_DROME)	RecName: Full=Histone-lysine N-methyltransferase SETD1
Q6BKL7 (SET1_DEBHA)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-4 specific; AltName: Full=COMPASS component SET1; AltName: Full=SET domain-containing protein 1
Q6DGD3 (SV91A_DANRE)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1-A; AltName: Full=Suppressor of variegation 3-9 homolog 1-A; Short=Su(var)3-9 homolog 1-A

Q6NRE8 (SUV91_XENLA)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
Q6P2L6 (NSD3_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase NSD3; AltName: Full=Nuclear SET domain-containing protein 3; AltName: Full=Wolf-Hirschhorn syndrome candidate 1-like protein 1 homolog; Short=WHSC1-like protein 1
Q6PDK2 (KMT2D_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2D; Short=Lysine N-methyltransferase 2D; AltName: Full=ALL1-related protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 2
Q7RZU4 (SET2_NEUCR)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q08AY6 (SET8A_XENLA)	RecName: Full=N-lysine methyltransferase SETD8-A; AltName: Full=Histone-lysine N-methyltransferase SETD8-A; AltName: Full=SET domain-containing protein 8-A
Q8BRH4 (KMT2C_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2C; Short=Lysine N-methyltransferase 2C; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog
Q08BS4 (EZH2_DANRE)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2
Q8BVE8 (NSD2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase NSD2; AltName: Full=Multiple myeloma SET domain-containing protein; Short=MMSET; AltName: Full=Nuclear SET domain-containing protein 2; Short=NSD2; AltName: Full=Wolf-Hirschhorn syndrome candidate 1 protein homolog; Short=WHSC1
Q8C267 (SETB2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETDB2; AltName: Full=SET domain bifurcated 2
Q8CFT2 (SET1B_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q08D57 (SET1B_XENTR)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q8IRW8 (TRR_DROME)	RecName: Full=Histone-lysine N-methyltransferase trr; AltName: Full=Lysine N-methyltransferase 2C; AltName: Full=Trithorax-related protein
Q8MT36 (MES4_DROME)	RecName: Full=Probable histone-lysine N-methyltransferase Mes-4; AltName: Full=Maternal-effect sterile 4 homolog
Q8NEZ4 (KMT2C_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2C; Short=Lysine N-methyltransferase 2C; AltName: Full=Homologous to ALR protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 3
Q8VZ17 (SUVH6_ARATH)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6; AltName: Full=Histone H3-K9 methyltransferase 6; Short=H3-K9-HMTase 6; AltName: Full=Protein SET DOMAIN GROUP 23; AltName: Full=Suppressor of variegation 3-9 homolog protein 6; Short=Su(var)3-9 homolog protein 6
Q9BYW2 (SETD2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD2; AltName: Full=HIF-1; AltName: Full=Huntingtin yeast partner B; AltName: Full=Huntingtin-interacting protein 1; Short=HIP-1; AltName: Full=Huntingtin-interacting protein B; AltName: Full=Lysine N-methyltransferase 3A; AltName: Full=SET domain-containing protein 2; Short=hSET2; AltName: Full=p231HBP
Q9BZ95 (NSD3_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase NSD3; AltName: Full=Nuclear SET domain-containing protein 3; AltName: Full=Protein whistle; AltName: Full=WHSC1-like 1 isoform 9 with methyltransferase activity to lysine; AltName: Full=Wolf-Hirschhorn syndrome candidate 1-like protein 1; Short=WHSC1-like protein 1
Q9C5P4 (SUVH3_ARATH)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Protein SET DOMAIN GROUP 19; AltName: Full=Suppressor of variegation 3-9 homolog protein 3; Short=Su(var)3-9 homolog protein 3
Q9EQQ0 (SUV92_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Histone H3-K9 methyltransferase 2; Short=H3-K9-HMTase 2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q9H5I1 (SUV92_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Histone H3-K9 methyltransferase 2; Short=H3-K9-HMTase 2; AltName: Full=Lysine N-methyltransferase 1B; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q9H9B1 (EHMT1_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EHMT1; AltName: Full=Euchromatic histone-lysine N-methyltransferase 1; Short=Eu-HMTase1; AltName: Full=G9a-like protein 1; Short=GLP; Short=GLP1; AltName: Full=Histone H3-K9 methyltransferase 5; Short=H3-K9-HMTase 5; AltName: Full=Lysine N-methyltransferase 1D
Q9NQR1 (SETD8_HUMAN)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=Lysine N-methyltransferase 5A; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q9NR48 (ASH1L_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; Short=huASH1; AltName: Full=Absent small and homeotic disks protein 1 homolog; AltName: Full=Lysine N-methyltransferase 2H
Q9UMN6 (KMT2B_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2B; Short=Lysine N-methyltransferase 2B; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 4; AltName: Full=Trithorax homolog 2; AltName: Full=WW domain-binding protein 7; Short=WBP-7
Q9UPS6 (SET1B_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=Lysine N-methyltransferase 2G; AltName: Full=SET domain-containing protein 1B; Short=hSET1B

Q9VFK6 (SETD8_DROME)	RecName: Full=Histone-lysine N-methyltransferase pr-set7; AltName: Full=Lysine N-methyltransferase 5A; AltName: Full=PR/SET domain-containing protein 07; AltName: Full=dSET8
Q9VW15 (ASH1_DROME)	RecName: Full=Histone-lysine N-methyltransferase ash1; AltName: Full=Absent small and homeotic disks protein 1; AltName: Full=Lysine N-methyltransferase 2H
Q9VYD1 (C1716_DROME)	RecName: Full=Probable histone-lysine N-methyltransferase CG1716
Q9Y7R4 (SET1_SCHPO)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-4 specific; AltName: Full=COMPASS component set1; AltName: Full=Lysine N-methyltransferase 2; AltName: Full=SET domain-containing protein 1; AltName: Full=Set1 complex component set1; Short=Set1C component set1; AltName: Full=Spset1
Q9Z148 (EHMT2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EHMT2; AltName: Full=Euchromatic histone-lysine N-methyltransferase 2; AltName: Full=HLA-B-associated transcript 8; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Protein G9a
Q28CQ7 (SUV92_XENTR)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q28D84 (EZH2_XENTR)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2
Q32PH7 (SUV92_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q53H47 (SETMR_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETMAR; AltName: Full=SET domain and mariner transposase fusion protein; Short=Metnase; Includes: RecName: Full=Histone-lysine N-methyltransferase; Includes: RecName: Full=Transposon Hsmar1 transposase
Q59XV0 (SET2_CANAL)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q66J90 (SET1B_XENLA)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q071E0 (SET8A_DANRE)	RecName: Full=N-lysine methyltransferase SETD8-A; AltName: Full=Histone-lysine N-methyltransferase SETD8-A; AltName: Full=SET domain-containing protein 8-A
Q80UJ9 (SETMR_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETMAR; AltName: Full=SET domain without mariner transposase fusion protein
Q84WW6 (ASHH1_ARATH)	RecName: Full=Histone-lysine N-methyltransferase ASHH1; AltName: Full=ASH1 homolog 1; AltName: Full=Protein SET DOMAIN GROUP 26
Q95Y12 (SET23_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase set-23; AltName: Full=SET-domain containing protein 23
Q96KQ7 (EHMT2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EHMT2; AltName: Full=Euchromatic histone-lysine N-methyltransferase 2; AltName: Full=HLA-B-associated transcript 8; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Lysine N-methyltransferase 1C; AltName: Full=Protein G9a
Q96L73 (NSD1_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific; AltName: Full=Androgen receptor coactivator 267 kDa protein; AltName: Full=Androgen receptor-associated protein of 267 kDa; AltName: Full=H3-K36-HMTase; AltName: Full=H4-K20-HMTase; AltName: Full=Lysine N-methyltransferase 3B; AltName: Full=Nuclear receptor-binding SET domain-containing protein 1; Short=NR-binding SET domain-containing protein
Q96T68 (SETB2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETDB2; AltName: Full=Chronic lymphocytic leukemia deletion region gene 8 protein; AltName: Full=Lysine N-methyltransferase 1F; AltName: Full=SET domain bifurcated 2
Q98SM3 (EZH2A_XENLA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2-A
Q99MY8 (ASH1L_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; AltName: Full=Absent small and homeotic disks protein 1 homolog
Q297V5 (SETD8_DROPS)	RecName: Full=Histone-lysine N-methyltransferase pr-set7; AltName: Full=PR/SET domain-containing protein 07
Q498E6 (SET8B_XENLA)	RecName: Full=N-lysine methyltransferase SETD8-B; AltName: Full=Histone-lysine N-methyltransferase SETD8-B; AltName: Full=Mitotic phosphoprotein 36; AltName: Full=SET domain-containing protein 8-B
Q03164 (KMT2A_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2A; Short=Lysine N-methyltransferase 2A; AltName: Full=ALL-1; AltName: Full=CXXC-type zinc finger protein 7; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 1; AltName: Full=Trithorax-like protein; AltName: Full=Zinc finger protein HRX; Contains: RecName: Full=MLL cleavage product N320; AltName: Full=N-terminal cleavage product of 320 kDa; Short=p320; Contains: RecName: Full=MLL cleavage product C180; AltName: Full=C-terminal cleavage product of 180 kDa; Short=p180
Q15910 (EZH2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=ENX-1; AltName: Full=Enhancer of zeste homolog 2; AltName: Full=Lysine N-methyltransferase 6
Q18221 (SET2_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase set-2; AltName: Full=SET domain-containing protein 2
Q22795 (SET1_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase set-1
Q24742 (TRX_DROVI)	RecName: Full=Histone-lysine N-methyltransferase trithorax
Q61188 (EZH2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=ENX-1; AltName: Full=Enhancer of zeste homolog 2
XP_395451	PREDICTED: histone-lysine N-methyltransferase SETD1B-like isoform 1 [Apis mellifera]

XP_395493	PREDICTED: histone-lysine N-methyltransferase pr-set7 [Apis mellifera]
XP_001601155	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Nasonia vitripennis]
XP_001604667	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Nasonia vitripennis]
XP_002401135	huntingtin interacting protein, putative [Ixodes scapularis]
XP_002408953	enhancer of zeste, ezh, putative, partial [Ixodes scapularis]
XP_002410343	H4-K20-specific histone methyltransferase SET7, putative, partial [Ixodes scapularis]
XP_002427372	histone-lysine N-methyltransferase, H4 lysine-20 specific, putative [Pediculus humanus corporis]
XP_002802212	PREDICTED: probable histone-lysine N-methyltransferase NSD2-like [Macaca mulatta]
XP_003249917	PREDICTED: histone-lysine N-methyltransferase E(z) isoformX1 [Apis mellifera]
XP_003394341	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X2 [Bombus terrestris]
XP_003399301	PREDICTED: histone-lysine N-methyltransferase SETD1 [Bombus terrestris]
XP_003488269	PREDICTED: histone-lysine N-methyltransferase SETD1 [Bombus impatiens]
XP_003690343	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Apis florea]
XP_003698603	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Apis florea]
XP_003705533	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X1 [Megachile rotundata]
XP_003762434	PREDICTED: histone-lysine N-methyltransferase SETMAR [Sarcophilus harrisii]
XP_005726659	PREDICTED: histone-lysine N-methyltransferase SETMAR [Pundamilia nyererei]
XP_005878229	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific [Myotis brandtii]
XP_006172423	PREDICTED: histone-lysine N-methyltransferase SETMAR [Tupaia chinensis]
XP_006558041	PREDICTED: histone-lysine N-methyltransferase EHMT1-like isoform X3 [Apis mellifera]
XP_006613374	PREDICTED: histone-lysine N-methyltransferase SETD1B-like [Apis dorsata]
XP_006614809	PREDICTED: histone-lysine N-methyltransferase EHMT1-like [Apis dorsata]
XP_006713978	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X5 [Homo sapiens]
XP_006763262	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like [Myotis davidii]
XP_006814029	PREDICTED: histone-lysine N-methyltransferase ASH1L-like [Saccoglossus kowalevskii]
XP_006893664	PREDICTED: histone-lysine N-methyltransferase NSD2-like [Elephantulus edwardii]
XP_007438740	PREDICTED: histone-lysine N-methyltransferase SETMAR-like [Python bivittatus]
XP_007612726	PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X2, partial [Cricetulus griseus]
XP_008206042	PREDICTED: histone-lysine N-methyltransferase 2C [Nasonia vitripennis]
XP_008271826	PREDICTED: histone-lysine N-methyltransferase SETMAR [Oryctolagus cuniculus]
XP_009199567	PREDICTED: histone-lysine N-methyltransferase NSD2 [Papio anubis]
XP_009862790	PREDICTED: histone-lysine N-methyltransferase ASH1L-like, partial [Apaloderma vittatum]
XP_009918214	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like [Haliaeetus albicilla]
XP_009958250	PREDICTED: histone-lysine N-methyltransferase NSD2-like, partial [Leptosomus discolor]
XP_009969243	PREDICTED: histone-lysine N-methyltransferase NSD3, partial [Tyto alba]
XP_010136549	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like, partial [Buceros rhinoceros silvestris]
XP_010170989	PREDICTED: histone-lysine N-methyltransferase NSD2, partial [Caprimulgus carolinensis]
XP_010198260	PREDICTED: histone-lysine N-methyltransferase ASH1L-like, partial [Colius striatus]
XP_011052529	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X1 [Acromyrmex echinatior]
XP_011052530	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X2 [Acromyrmex echinatior]
XP_011055947	PREDICTED: histone-lysine N-methyltransferase pr-set7, partial [Acromyrmex echinatior]
XP_011150292	PREDICTED: histone-lysine N-methyltransferase SETD1 [Harpegnathos saltator]
XP_011266317	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like isoform X1 [Camponotus floridanus]
XP_011449544	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like [Crassostrea gigas]
XP_011502402	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Ceratosolen solmsi marchali]
XP_011511861	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X4 [Homo sapiens]
XP_011571947	PREDICTED: histone-lysine N-methyltransferase SETMAR [Aquila chrysaetos canadensis]

XP_011743157	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X2 [Macaca nemestrina]
XP_011862500	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X1 [Vollenhovia emeryi]
XP_011862501	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X2 [Vollenhovia emeryi]
XP_011862502	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Vollenhovia emeryi]
XP_011914639	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X3 [Cercocebus atys]
XP_012054897	PREDICTED: histone-lysine N-methyltransferase SETD1 [Atta cephalotes]
XP_012059283	PREDICTED: probable histone-lysine N-methyltransferase CG1716 [Atta cephalotes]
XP_012145893	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X2 [Megachile rotundata]
XP_012176209	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Bombus terrestris]
XP_012176211	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X4 [Bombus terrestris]
XP_012222417	PREDICTED: histone-lysine N-methyltransferase SETD1 [Linepithema humile]
XP_012228656	PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X1 [Linepithema humile]
XP_012228658	PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X2 [Linepithema humile]
XP_012258464	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Athalia rosae]
XP_012266861	PREDICTED: histone-lysine N-methyltransferase SETD1B-A [Athalia rosae]
XP_012280614	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like isoform X1 [Orussus abietinus]
XP_012355212	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X2 [Nomascus leucogenys]
XP_012429026	PREDICTED: histone-lysine N-methyltransferase SETMAR [Taeniopygia guttata]
XP_012533486	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Monomorium pharaonis]
XP_012537071	PREDICTED: probable histone-lysine N-methyltransferase CG1716 [Monomorium pharaonis]
XP_012539726	PREDICTED: histone-lysine N-methyltransferase pr-set7 isoform X1 [Monomorium pharaonis]
XP_012539727	PREDICTED: histone-lysine N-methyltransferase pr-set7 isoform X2 [Monomorium pharaonis]
XP_012542824	PREDICTED: histone-lysine N-methyltransferase SETD1 [Monomorium pharaonis]
XP_012976031	PREDICTED: histone-lysine N-methyltransferase ASH1L [Mesocricetus auratus]
XP_013389879	PREDICTED: histone-lysine N-methyltransferase ASH1L-like isoform X10 [Lingula anatina]
XP_013394122	PREDICTED: histone-lysine N-methyltransferase SUV39H1-A-like [Lingula anatina]
XP_013772199	PREDICTED: histone-lysine N-methyltransferase SUV39H1-like isoform X1 [Limulus polyphemus]
XP_013772200	PREDICTED: histone-lysine N-methyltransferase SUV39H1-like isoform X2 [Limulus polyphemus]
XP_013773324	PREDICTED: histone-lysine N-methyltransferase SETD2-like, partial [Limulus polyphemus]
XP_013777216	PREDICTED: histone-lysine N-methyltransferase EZH2-like [Limulus polyphemus]
XP_013777692	PREDICTED: histone-lysine N-methyltransferase EZH2-like isoform X1 [Limulus polyphemus]
XP_013777694	PREDICTED: histone-lysine N-methyltransferase EZH2-like isoform X2 [Limulus polyphemus]
XP_013779563	PREDICTED: serine-rich adhesin for platelets-like [Limulus polyphemus]
XP_013779655	PREDICTED: histone-lysine N-methyltransferase trr-like [Limulus polyphemus]
XP_013782805	PREDICTED: histone-lysine N-methyltransferase SETMAR-like isoform X1 [Limulus polyphemus]
XP_013784687	PREDICTED: histone-lysine N-methyltransferase 2C-like [Limulus polyphemus]
XP_013788393	PREDICTED: N-lysine methyltransferase SETD8-like, partial [Limulus polyphemus]
XP_013911646	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific [Thamnophis sirtalis]
XP_014217049	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Copidosoma floridanum]
XP_014223483	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Trichogramma pretiosum]
XP_014244325	PREDICTED: N-lysine methyltransferase SETD8-A isoform X1 [Cimex lectularius]
XP_014244326	PREDICTED: N-lysine methyltransferase SETD8-A isoform X2 [Cimex lectularius]
XP_014254736	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X5 [Cimex lectularius]
XP_014254739	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X7 [Cimex lectularius]
XP_014254743	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X11 [Cimex lectularius]
XP_014254744	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X12 [Cimex lectularius]

XP_014254745	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X13 [Cimex lectularius]
XP_014276805	PREDICTED: N-lysine methyltransferase SETD8 [Halyomorpha halys]
XP_014460276	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific, partial [Alligator mississippiensis]

9.4.2.14 *Fasciclin 2*

Name	Description
A1KZ92 (PXDNL_HUMAN)	RecName: Full=Peroxidasin-like protein; AltName: Full=Cardiac peroxidase; AltName: Full=Vascular peroxidase 2; AltName: Full=polysomal ribonuclease 1; Short=PRM1; Flags: Precursor
A2AJ76 (HMCN2_MOUSE)	RecName: Full=Hemicentin-2; Flags: Precursor
A4IGL7 (PXDN_XENTR)	RecName: Full=Peroxidasin; Flags: Precursor
A8WQH2 (PXDN_CAEBR)	RecName: Full=Peroxidasin homolog; Flags: Precursor
B3EWZ3 (CADN_ACRMI)	RecName: Full=Coadhesin
E1C8P7 (DSCL1_CHICK)	RecName: Full=Down syndrome cell adhesion molecule-like protein 1 homolog; Flags: Precursor
F1NY98 (DSCAM_CHICK)	RecName: Full=Down syndrome cell adhesion molecule homolog; Flags: Precursor
FAS2_DROME	RecName: Full=Fasciclin-2; AltName: Full=Fasciclin II; Short=FAS II; Flags: Precursor
G5EBF1 (SAX3_CAEEL)	RecName: Full=Protein sax-3; AltName: Full=Sensory axon guidance 3; Flags: Precursor
Locus_1_Transcript_23671/166847_Confidence_1.000_Length_2147 - ORF 1 (frame 3) translation	Locus_1_Transcript_23671/166847_Confidence_1.000_Length_2147
Locus_1_Transcript_23706/166847_Confidence_1.000_Length_2147 - ORF 14 (frame 1) translation	Locus_1_Transcript_23706/166847_Confidence_1.000_Length_2147
Locus_1_Transcript_35406/166847_Confidence_1.000_Length_1653 - ORF 12 (frame 3) translation	Locus_1_Transcript_35406/166847_Confidence_1.000_Length_1653
Locus_1_Transcript_39407/166847_Confidence_1.000_Length_2518 - ORF 14 (frame 1) translation	Locus_1_Transcript_39407/166847_Confidence_1.000_Length_2518
Locus_1_Transcript_75401/166847_Confidence_1.000_Length_1716 - ORF 1 (frame 3) translation	Locus_1_Transcript_75401/166847_Confidence_1.000_Length_1716
Locus_1_Transcript_83541/166847_Confidence_1.000_Length_1488 - ORF 1 (frame 3) translation	Locus_1_Transcript_83541/166847_Confidence_1.000_Length_1488
Locus_2625_Transcript_18/18_Confidence_0.306_Length_21616 - ORF 120 (frame 2) translation	Locus_2625_Transcript_18/18_Confidence_0.306_Length_21616
Locus_8318_Transcript_4/4_Confidence_0.667_Length_12430 - ORF 71 (frame 1) translation	Locus_8318_Transcript_4/4_Confidence_0.667_Length_12430
Locus_13134_Transcript_17/17_Confidence_0.314_Length_9388 - ORF 2 (frame 3) translation	Locus_13134_Transcript_17/17_Confidence_0.314_Length_9388
Locus_15035_Transcript_9/10_Confidence_0.588_Length_7284 - ORF 27 (frame 3) translation	Locus_15035_Transcript_9/10_Confidence_0.588_Length_7284
Locus_16345_Transcript_4/9_Confidence_0.400_Length_6577 - ORF 3 (frame 2) translation	Locus_16345_Transcript_4/9_Confidence_0.400_Length_6577
Locus_23913_Transcript_1/2_Confidence_0.700_Length_4273 - ORF 2 (frame 3) translation	Locus_23913_Transcript_1/2_Confidence_0.700_Length_4273
Locus_23954_Transcript_2/2_Confidence_0.750_Length_4168 - ORF 1 (frame 2) translation	Locus_23954_Transcript_2/2_Confidence_0.750_Length_4168
NP_001076815	peroxidasin precursor [Xenopus (Silurana) tropicalis]
O15394 (NCAM2_HUMAN)	RecName: Full=Neural cell adhesion molecule 2; Short=N-CAM-2; Short=NCAM-2; Flags: Precursor
O35136 (NCAM2_MOUSE)	RecName: Full=Neural cell adhesion molecule 2; Short=N-CAM-2; Short=NCAM-2; AltName: Full=Neural cell adhesion molecule RB-8; AltName: Full=R4B12; Flags: Precursor
O42414 (NFASC_CHICK)	RecName: Full=Neurofascin; Flags: Precursor
O55005 (ROBO1_RAT)	RecName: Full=Roundabout homolog 1; Flags: Precursor
O60469 (DSCAM_HUMAN)	RecName: Full=Down syndrome cell adhesion molecule; AltName: Full=CHD2; Flags: Precursor
O89026 (ROBO1_MOUSE)	RecName: Full=Roundabout homolog 1; Flags: Precursor
O94856 (NFASC_HUMAN)	RecName: Full=Neurofascin; Flags: Precursor
P09933 (PERT_PIG)	RecName: Full=Thyroid peroxidase; Short=TPO; Flags: Precursor
P11799 (MYLK_CHICK)	RecName: Full=Myosin light chain kinase, smooth muscle; Short=MLCK; AltName: Full=Telokin; Contains: RecName: Full=Myosin light chain kinase, smooth muscle, deglutamylated form
P13590 (NCAM1_CHICK)	RecName: Full=Neural cell adhesion molecule 1; Short=N-CAM-1; Short=NCAM-1; Flags: Precursor
P13591 (NCAM1_HUMAN)	RecName: Full=Neural cell adhesion molecule 1; Short=N-CAM-1; Short=NCAM-1; AltName: CD_antigen=CD56; Flags: Precursor
P13595 (NCAM1_MOUSE)	RecName: Full=Neural cell adhesion molecule 1; Short=N-CAM-1; Short=NCAM-1; AltName: CD_antigen=CD56; Flags: Precursor
P13596 (NCAM1_RAT)	RecName: Full=Neural cell adhesion molecule 1; Short=N-CAM-1; Short=NCAM-1; AltName: CD_antigen=CD56; Flags: Precursor
P14650 (PERT_RAT)	RecName: Full=Thyroid peroxidase; Short=TPO; Flags: Precursor
P14781 (CNTN1_CHICK)	RecName: Full=Contactin-1; AltName: Full=Neural cell recognition molecule F11; Flags: Precursor
P16170 (NCA11_XENLA)	RecName: Full=Neural cell adhesion molecule 1-A; Short=N-CAM-1-A; Short=NCAM-1-A; Flags: Precursor
P20241 (NRG_DROME)	RecName: Full=Neuroglian; Flags: Precursor
P22648 (FAS2_SCHAM)	RecName: Full=Fasciclin-2; AltName: Full=Fasciclin II; Short=FAS II; Flags: Precursor
P31836 (NCAM1_BOVIN)	RecName: Full=Neural cell adhesion molecule 1; Short=N-CAM-1; Short=NCAM-1; Flags: Precursor
P32004 (L1CAM_HUMAN)	RecName: Full=Neural cell adhesion molecule L1; Short=N-CAM-L1; Short=NCAM-L1; AltName: CD_antigen=CD171; Flags: Precursor
P34082 (FAS2_DROME)	RecName: Full=Fasciclin-2; AltName: Full=Fasciclin II; Short=FAS II; Flags: Precursor

P35331 (NRCAM_CHICK)	RecName: Full=Neuronal cell adhesion molecule; Short=Nr-CAM; AltName: Full=Neuronal surface protein Bravo; Short=gBravo; AltName: Full=NgCAM-related cell adhesion molecule; Short=Ng-CAM-related; Flags: Precursor
P35419 (PERT_MOUSE)	RecName: Full=Thyroid peroxidase; Short=TPO; Flags: Precursor
P36335 (NCA12_XENLA)	RecName: Full=Neural cell adhesion molecule 1-B; Short=N-CAM-1-B; Short=NCAM-1-B; Flags: Precursor
P43146 (DCC_HUMAN)	RecName: Full=Netrin receptor DCC; AltName: Full=Colorectal cancer suppressor; AltName: Full=Immunoglobulin superfamily DCC subclass member 1; AltName: Full=Tumor suppressor protein DCC; Flags: Precursor
P70211 (DCC_MOUSE)	RecName: Full=Netrin receptor DCC; AltName: Full=Tumor suppressor protein DCC; Flags: Precursor
P97603 (NEO1_RAT)	RecName: Full=Neogenin; Flags: Precursor
P97685 (NFASC_RAT)	RecName: Full=Neurofascin; Flags: Precursor
P97686 (NRCAM_RAT)	RecName: Full=Neuronal cell adhesion molecule; Short=Nr-CAM; AltName: Full=Ankyrin-binding cell adhesion molecule NrCAM; AltName: Full=Neuronal surface protein Bravo; Short=rBravo; AltName: Full=NgCAM-related cell adhesion molecule; Short=Ng-CAM-related; Flags: Precursor
P97798 (NEO1_MOUSE)	RecName: Full=Neogenin; Flags: Precursor
P98160 (PGBM_HUMAN)	RecName: Full=Basement membrane-specific heparan sulfate proteoglycan core protein; Short=HSPG; AltName: Full=Perlecan; Short=PLC; Contains: RecName: Full=Endorepellin; Contains: RecName: Full=LG3 peptide; Flags: Precursor
Q1ENI8 (PXDN_CAEEL)	RecName: Full=Peroxidasin homolog; Flags: Precursor
Q2EY14 (PRTGA_DANRE)	RecName: Full=Protogenin A; Flags: Precursor
Q2VWP7 (PRTG_HUMAN)	RecName: Full=Protogenin; AltName: Full=Protein Shen-Dan; Flags: Precursor
Q3UH53 (SDK1_MOUSE)	RecName: Full=Protein sidekick-1; Flags: Precursor
Q3UQ28 (PXDN_MOUSE)	RecName: Full=Peroxidasin homolog; Flags: Precursor
Q3V1M1 (IGS10_MOUSE)	RecName: Full=Immunoglobulin superfamily member 10; Short=IgSF10; Flags: Precursor
Q4VA61 (DSCL1_MOUSE)	RecName: Full=Down syndrome cell adhesion molecule-like protein 1 homolog; Flags: Precursor
Q6PDN3 (MYLK_MOUSE)	RecName: Full=Myosin light chain kinase, smooth muscle; Short=MLCK; Short=smMLCK; AltName: Full=Kinase-related protein; Short=KRP; AltName: Full=Telokin; Contains: RecName: Full=Myosin light chain kinase, smooth muscle, deglutamylated form
Q6WRI0 (IGS10_HUMAN)	RecName: Full=Immunoglobulin superfamily member 10; Short=IgSF10; AltName: Full=Calvaria mechanical force protein 608; Short=CMF608; Flags: Precursor
Q7TPD3 (ROBO2_MOUSE)	RecName: Full=Roundabout homolog 2; Flags: Precursor
Q7Z5N4 (SDK1_HUMAN)	RecName: Full=Protein sidekick-1; Flags: Precursor
Q8AV57 (SDK2_CHICK)	RecName: Full=Protein sidekick-2; Flags: Precursor
Q8AV58 (SDK1_CHICK)	RecName: Full=Protein sidekick-1; Flags: Precursor
Q8NDA2 (HMCN2_HUMAN)	RecName: Full=Hemicentin-2; Flags: Precursor
Q8TD84 (DSCL1_HUMAN)	RecName: Full=Down syndrome cell adhesion molecule-like protein 1; AltName: Full=Down syndrome cell adhesion molecule 2; Flags: Precursor
Q8VHZ8 (DSCAM_RAT)	RecName: Full=Down syndrome cell adhesion molecule homolog; Flags: Precursor
Q9ERC8 (DSCAM_MOUSE)	RecName: Full=Down syndrome cell adhesion molecule homolog; Flags: Precursor
Q9HCK4 (ROBO2_HUMAN)	RecName: Full=Roundabout homolog 2; Flags: Precursor
Q9VS29 (DSCL_DROME)	RecName: Full=Down syndrome cell adhesion molecule-like protein Dscam2; Flags: Precursor
Q9VZZ4 (PXDN_DROME)	RecName: Full=Peroxidasin; Flags: Precursor
Q9Y6N7 (ROBO1_HUMAN)	RecName: Full=Roundabout homolog 1; AltName: Full=Deleted in U twenty twenty; AltName: Full=H-Robo-1; Flags: Precursor
Q9Z2I4 (ROBO3_MOUSE)	RecName: Full=Roundabout homolog 3; AltName: Full=Retinoblastoma-inhibiting gene 1 protein; Short=Rig-1; Flags: Precursor
Q96MS0 (ROBO3_HUMAN)	RecName: Full=Roundabout homolog 3; AltName: Full=Roundabout-like protein 3; Flags: Precursor
Q96RW7 (HMCN1_HUMAN)	RecName: Full=Hemicentin-1; AltName: Full=Fibulin-6; Short=FIBL-6; Flags: Precursor
Q589G5 (PRTG_CHICK)	RecName: Full=Protogenin; Flags: Precursor
Q810U3 (NFASC_MOUSE)	RecName: Full=Neurofascin; Flags: Precursor
Q810U4 (NRCAM_MOUSE)	RecName: Full=Neuronal cell adhesion molecule; Short=Nr-CAM; AltName: Full=Neuronal surface protein Bravo; Short=mBravo; AltName: Full=NgCAM-related cell adhesion molecule; Short=Ng-CAM-related; Flags: Precursor
Q05695 (L1CAM_RAT)	RecName: Full=Neural cell adhesion molecule L1; Short=N-CAM-L1; Short=NCAM-L1; AltName: Full=Nerve-growth factor-inducible large external glycoprotein; Short=NILE; AltName: CD_antigen=CD171; Flags: Precursor
Q15746 (MYLK_HUMAN)	RecName: Full=Myosin light chain kinase, smooth muscle; Short=MLCK; Short=smMLCK; AltName: Full=Kinase-related protein; Short=KRP; AltName: Full=Telokin; Contains: RecName: Full=Myosin light chain kinase, smooth muscle, deglutamylated form
Q15772 (SPEG_HUMAN)	RecName: Full=Striated muscle preferentially expressed protein kinase; AltName: Full=Aortic preferentially expressed protein 1; Short=APEG-1
Q62407 (SPEG_MOUSE)	RecName: Full=Striated muscle-specific serine/threonine-protein kinase; AltName: Full=Aortic preferentially expressed protein 1; Short=APEG-1
Q63155 (DCC_RAT)	RecName: Full=Netrin receptor DCC; AltName: Full=Tumor suppressor protein DCC; Flags: Precursor
Q63638 (SPEG_RAT)	RecName: Full=Striated muscle-specific serine/threonine-protein kinase; AltName: Full=Aortic preferentially expressed protein 1; Short=APEG-1

Q90610 (NEO1_CHICK)	RecName: Full=Neogenin
Q90610 (NEO1_CHICK)	RecName: Full=Neogenin
Q92626 (PXDN_HUMAN)	RecName: Full=Peroxidasin homolog; AltName: Full=Melanoma-associated antigen MG50; AltName: Full=Vascular peroxidase 1; AltName: Full=p53-responsive gene 2 protein; Flags: Precursor
Q92823 (NRCAM_HUMAN)	RecName: Full=Neuronal cell adhesion molecule; Short=Nr-CAM; AltName: Full=Neuronal surface protein Bravo; Short=hBravo; AltName: Full=NgCAM-related cell adhesion molecule; Short=Ng-CAM-related; Flags: Precursor
Q92859 (NEO1_HUMAN)	RecName: Full=Neogenin; AltName: Full=Immunoglobulin superfamily DCC subclass member 2; Flags: Precursor
XP_002410294	neuronal cell adhesion molecule, putative [Ixodes scapularis]
XP_002414055	cell adhesion molecule, putative, partial [Ixodes scapularis]
XP_002414060	cell adhesion molecule, putative [Ixodes scapularis]
XP_002414064	cell adhesion molecule, putative, partial [Ixodes scapularis]
XP_002415184	neural cell adhesion molecule L1, putative [Ixodes scapularis]
XP_003427853	PREDICTED: roundabout homolog 2 isoform X1 [Nasonia vitripennis]
XP_003428190	PREDICTED: neuroglian [Nasonia vitripennis]
XP_003445167	PREDICTED: hemicentin-1 [Oreochromis niloticus]
XP_003707333	PREDICTED: neuroglian isoform X1 [Megachile rotundata]
XP_003741520	PREDICTED: Down syndrome cell adhesion molecule-like [Metaseiulus occidentalis]
XP_003743029	PREDICTED: Down syndrome cell adhesion molecule-like [Metaseiulus occidentalis]
XP_003745178	PREDICTED: fasciclin-2-like [Metaseiulus occidentalis]
XP_004477730	PREDICTED: peroxidasin homolog isoform X1 [Dasypus novemcinctus]
XP_004524924	PREDICTED: fasciclin-2 isoform X2 [Ceratitis capitata]
XP_004524925	PREDICTED: fasciclin-2 isoform X5 [Ceratitis capitata]
XP_005160777	PREDICTED: hemicentin-1 isoform X1 [Danio rerio]
XP_005733181	PREDICTED: hemicentin-1 isoform X1 [Pundamilia nyererei]
XP_005938566	PREDICTED: hemicentin-1 [Haplochromis burtoni]
XP_005994048	PREDICTED: peroxidasin homolog [Latimeria chalumnae]
XP_006185604	PREDICTED: hemicentin-1 [Camelus ferus]
XP_006198848	PREDICTED: hemicentin-1 [Vicugna pacos]
XP_006567130	PREDICTED: Down syndrome cell adhesion molecule isoform X65 [Apis mellifera]
XP_007100229	PREDICTED: peroxidasin homolog isoform X1 [Physeter catodon]
XP_007519015	PREDICTED: peroxidasin homolog [Erinaceus europaeus]
XP_007550974	PREDICTED: hemicentin-1 [Poecilia formosa]
XP_008116734	PREDICTED: peroxidasin homolog isoform X1 [Anolis carolinensis]
XP_008183159	PREDICTED: muscle M-line assembly protein unc-89 isoform X3 [Acyrthosiphon pisum]
XP_008183160	PREDICTED: muscle M-line assembly protein unc-89 isoform X4 [Acyrthosiphon pisum]
XP_008191104	PREDICTED: roundabout homolog 2 [Tribolium castaneum]
XP_008195297	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Tribolium castaneum]
XP_008195817	PREDICTED: neogenin isoform X1 [Tribolium castaneum]
XP_008195818	PREDICTED: neogenin isoform X2 [Tribolium castaneum]
XP_008195819	PREDICTED: neogenin isoform X3 [Tribolium castaneum]
XP_008195820	PREDICTED: neogenin isoform X4 [Tribolium castaneum]
XP_009293030	PREDICTED: hemicentin-1 isoform X4 [Danio rerio]
XP_011136879	PREDICTED: roundabout homolog 2-like [Harpegnathos saltator]
XP_011158178	PREDICTED: neuroglian [Solenopsis invicta]
XP_011329577	PREDICTED: roundabout homolog 2-like isoform X1 [Cerapachys biroi]
XP_011347155	PREDICTED: neuroglian, partial [Cerapachys biroi]
XP_011552582	PREDICTED: fasciclin-2 isoform X2 [Plutella xylostella]
XP_011552583	PREDICTED: fasciclin-2 isoform X3 [Plutella xylostella]
XP_011552584	PREDICTED: fasciclin-2 isoform X4 [Plutella xylostella]
XP_011552585	PREDICTED: fasciclin-2 isoform X5 [Plutella xylostella]
XP_011552586	PREDICTED: fasciclin-2 isoform X6 [Plutella xylostella]
XP_011981457	PREDICTED: peroxidasin homolog isoform X2 [Ovis aries musimon]
XP_012136943	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X1 [Megachile rotundata]
XP_012137036	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X14 [Megachile rotundata]
XP_012137042	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X15 [Megachile rotundata]
XP_012137099	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X23 [Megachile rotundata]
XP_012137173	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X35 [Megachile rotundata]
XP_012137185	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X37 [Megachile rotundata]
XP_012137202	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X39 [Megachile rotundata]
XP_012137216	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X41 [Megachile rotundata]
XP_012137222	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 isoform X42 [Megachile rotundata]
XP_012143807	PREDICTED: fasciclin-2 isoform X4 [Megachile rotundata]
XP_012143813	PREDICTED: fasciclin-2 isoform X5 [Megachile rotundata]
XP_012150222	PREDICTED: neuroglian isoform X2 [Megachile rotundata]
XP_012156947	PREDICTED: fasciclin-2 isoform X3 [Ceratitis capitata]
XP_012156948	PREDICTED: fasciclin-2 isoform X4 [Ceratitis capitata]
XP_012156950	PREDICTED: fasciclin-2 isoform X7 [Ceratitis capitata]
XP_012258677	PREDICTED: neuroglian isoform X1 [Athalia rosae]
XP_012258678	PREDICTED: neuroglian isoform X2 [Athalia rosae]

XP_012265271	PREDICTED: roundabout homolog 2-like [Athalia rosae]
XP_012275891	PREDICTED: neuroglian [Orussus abietinus]
XP_012278808	PREDICTED: fasciclin-2 isoform X1 [Orussus abietinus]
XP_012278809	PREDICTED: fasciclin-2 isoform X2 [Orussus abietinus]
XP_012278810	PREDICTED: fasciclin-2 isoform X3 [Orussus abietinus]
XP_012390317	PREDICTED: peroxidasin homolog [Orcinus orca]
XP_012531725	PREDICTED: roundabout homolog 2-like [Monomorium pharaonis]
XP_012534169	PREDICTED: neuroglian isoform X1 [Monomorium pharaonis]
XP_012534172	PREDICTED: neuroglian isoform X2 [Monomorium pharaonis]
XP_012534173	PREDICTED: neuroglian isoform X3 [Monomorium pharaonis]
XP_012534176	PREDICTED: neuroglian isoform X4 [Monomorium pharaonis]
XP_013398078	PREDICTED: peroxidasin-like isoform X1 [Lingula anatina]
XP_013772132	PREDICTED: fasciclin-2-like [Limulus polyphemus]
XP_013772666	PREDICTED: neuroglian-like [Limulus polyphemus]
XP_013773795	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013773961	PREDICTED: neogenin-like [Limulus polyphemus]
XP_013775157	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013775158	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013775667	PREDICTED: Down syndrome cell adhesion molecule homolog [Limulus polyphemus]
XP_013776684	PREDICTED: neogenin-like [Limulus polyphemus]
XP_013779740	PREDICTED: fasciclin-2-like, partial [Limulus polyphemus]
XP_013782642	PREDICTED: fasciclin-2-like [Limulus polyphemus]
XP_013783902	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013784282	PREDICTED: roundabout homolog 1-like [Limulus polyphemus]
XP_013784599	PREDICTED: fasciclin-2-like, partial [Limulus polyphemus]
XP_013786014	PREDICTED: neogenin-like, partial [Limulus polyphemus]
XP_013786392	PREDICTED: fasciclin-2-like, partial [Limulus polyphemus]
XP_013786517	PREDICTED: neogenin-like [Limulus polyphemus]
XP_013786681	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013787318	PREDICTED: fasciclin-2-like, partial [Limulus polyphemus]
XP_013789637	PREDICTED: neogenin-like, partial [Limulus polyphemus]
XP_013789869	PREDICTED: roundabout homolog 1-like, partial [Limulus polyphemus]
XP_013790908	PREDICTED: neuroglian-like, partial [Limulus polyphemus]
XP_013794182	PREDICTED: Down syndrome cell adhesion molecule-like protein Dscam2 [Limulus polyphemus]
XP_013821774	PREDICTED: peroxidasin homolog [Capra hircus]
XP_014250864	PREDICTED: roundabout homolog 2-like isoform X1 [Cimex lectularius]
XP_014250865	PREDICTED: roundabout homolog 2-like isoform X2 [Cimex lectularius]
XP_014262820	PREDICTED: hemicentin-1 [Maylandia zebra]
XP_014277651	PREDICTED: fasciclin-2 isoform X1 [Halyomorpha halys]
XP_014277652	PREDICTED: fasciclin-2 isoform X2 [Halyomorpha halys]

9.4.2.15 *Gooseberry*

Name	Description
A0JMA6 (PAX8_XENTR)	RecName: Full=Paired box protein Pax-8
A1YEY5 (GSC_GORGO)	RecName: Full=Homeobox protein goosecoid
A1YG25 (RAX2_PANPA)	RecName: Full=Retina and anterior neural fold homeobox protein 2; AltName: Full=Retina and anterior neural fold homeobox-like protein 1
A2T7P4 (GSC_PONPY)	RecName: Full=Homeobox protein goosecoid
A6NJT0 (UNC4_HUMAN)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
A6YP92 (ARX_RAT)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
GSB_DROME	RecName: Full=Protein gooseberry; AltName: Full=BSH9; AltName: Full=Protein gooseberry distal
Locus_1_Transcript_41952/166847_Confidence_1.000_Length_2252 - ORF 3 (frame 2) translation	Locus_1_Transcript_41952/166847_Confidence_1.000_Length_2252
Locus_1_Transcript_54364/166847_Confidence_1.000_Length_1098 - ORF 7 (frame 1) translation	Locus_1_Transcript_54364/166847_Confidence_1.000_Length_1098
Locus_1_Transcript_68991/166847_Confidence_1.000_Length_1127 - ORF 10 (frame 2) translation	Locus_1_Transcript_68991/166847_Confidence_1.000_Length_1127
Locus_1_Transcript_144443/166847_Confidence_1.000_Length_1412 - ORF 11 (frame 2) translation	Locus_1_Transcript_144443/166847_Confidence_1.000_Length_1412
Locus_2435_Transcript_4/5_Confidence_0.696_Length_2772 - ORF 1 (frame 2) translation	Locus_2435_Transcript_4/5_Confidence_0.696_Length_2772
Locus_11168_Transcript_14/17_Confidence_0.167_Length_6758 - ORF 28 (frame 3) translation	Locus_11168_Transcript_14/17_Confidence_0.167_Length_6758
Locus_13554_Transcript_10/10_Confidence_0.556_Length_2425 - ORF 3 (frame 1) translation	Locus_13554_Transcript_10/10_Confidence_0.556_Length_2425
Locus_13887_Transcript_3/5_Confidence_0.600_Length_1829 - ORF 16 (frame 2) translation	Locus_13887_Transcript_3/5_Confidence_0.600_Length_1829
Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913 - ORF 2 (frame 1) translation	Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913
Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251 - ORF 3 (frame 2) translation	Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251
Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177 - ORF 3 (frame 1) translation	Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177

Locus_17374_Transcript_1/1_Confidence_1.000_Length_1255 - ORF 1 (frame 1) translation	Locus_17374_Transcript_1/1_Confidence_1.000_Length_1255
Locus_17460_Transcript_2/5_Confidence_0.545_Length_4767 - ORF 2 (frame 3) translation	Locus_17460_Transcript_2/5_Confidence_0.545_Length_4767
Locus_17531_Transcript_2/2_Confidence_0.889_Length_1577 - ORF 1 (frame 3) translation	Locus_17531_Transcript_2/2_Confidence_0.889_Length_1577
Locus_18982_Transcript_4/4_Confidence_0.600_Length_6071 - ORF 2 (frame 1) translation	Locus_18982_Transcript_4/4_Confidence_0.600_Length_6071
Locus_19513_Transcript_1/1_Confidence_1.000_Length_828 - ORF 1 (frame 3) translation	Locus_19513_Transcript_1/1_Confidence_1.000_Length_828
Locus_20911_Transcript_1/1_Confidence_1.000_Length_1876 - ORF 1 (frame 1) translation	Locus_20911_Transcript_1/1_Confidence_1.000_Length_1876
Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832 - ORF 3 (frame 1) translation	Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832
Locus_24579_Transcript_1/1_Confidence_1.000_Length_1020 - ORF 1 (frame 3) translation	Locus_24579_Transcript_1/1_Confidence_1.000_Length_1020
Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171 - ORF 1 (frame 1) translation	Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171
Locus_109739_Transcript_1/1_Confidence_1.000_Length_990 - ORF 9 (frame 2) translation	Locus_109739_Transcript_1/1_Confidence_1.000_Length_990
NP_524042	eyegone, isoform A [Drosophila melanogaster]
NP_001158393	pox-neuro [Saccoglossus kowalevskii]
O08934 (UNC4_MOUSE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
O14813 (PHX2A_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
O15266 (SHOX_HUMAN)	RecName: Full=Short stature homeobox protein; AltName: Full=Pseudoautosomal homeobox-containing osteogenic protein; AltName: Full=Short stature homeobox-containing protein
O15499 (GSC2_HUMAN)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
O18381 (PAX6_DROME)	RecName: Full=Paired box protein Pax-6; AltName: Full=Protein eyeless
O18400 (PITX_DROME)	RecName: Full=Pituitary homeobox homolog Ptx1; Short=D-PTX1
O35085 (ARX_MOUSE)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
O35602 (RX_MOUSE)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
O35690 (PHX2B_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2B; AltName: Full=Neuroblastoma Phox; Short=NBPhox; AltName: Full=PHOX2B homeodomain protein; AltName: Full=Paired-like homeobox 2B
O35750 (SHOX2_RAT)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Paired family homeodomain protein Prx3
O42115 (ARX_DANRE)	RecName: Full=Aristaless-related homeobox protein; Short=ARX
O42201 (RXA_XENLA)	RecName: Full=Retinal homeobox protein Rx-A; Short=Rx1A; Short=Xrx1; AltName: Full=Retina and anterior neural fold homeobox protein A
O42356 (RX1_DANRE)	RecName: Full=Retinal homeobox protein Rx1
O42357 (RX2_DANRE)	RecName: Full=Retinal homeobox protein Rx2
O42358 (RX3_DANRE)	RecName: Full=Retinal homeobox protein Rx3
O42567 (RXB_XENLA)	RecName: Full=Retinal homeobox protein Rx-B; AltName: Full=Retina and anterior neural fold homeobox protein B; AltName: Full=Rx2A; Short=Xrx2
O57682 (PAX2B_XENLA)	RecName: Full=Paired box protein Pax-2-B; Short=xPax-2b
O57685 (PAX2A_XENLA)	RecName: Full=Paired box protein Pax-2-A; Short=xPax-2a
O60902 (SHOX2_HUMAN)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; AltName: Full=Paired-related homeobox protein SHOT
O73917 (PAX6_ORYLA)	RecName: Full=Paired box protein Pax-6
O77215 (UNC4_DROME)	RecName: Full=Homeobox protein unc-4; AltName: Full=Paired-like homeodomain protein unc-4; Short=DPHD-1
O93385 (PITX2_CHICK)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; Short=cPITX2; AltName: Full=Paired-like homeodomain transcription factor 2
O97039 (RX_DUGJA)	RecName: Full=Retinal homeobox protein Rax; AltName: Full=DjRax
P0DMV5 (ALX1_GEOFO)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
P06601 (PRD_DROME)	RecName: Full=Segmentation protein paired
P09082 (GSB_DROME)	RecName: Full=Protein gooseberry; AltName: Full=BSH9; AltName: Full=Protein gooseberry distal
P09083 (GSBN_DROME)	RecName: Full=Protein gooseberry-neuro; AltName: Full=BSH4; AltName: Full=Protein gooseberry proximal
P23758 (POXN_DROME)	RecName: Full=Paired box pox-neuro protein; AltName: Full=Paired box neuronal protein
P23759 (PAX7_HUMAN)	RecName: Full=Paired box protein Pax-7; AltName: Full=HuP1
P23760 (PAX3_HUMAN)	RecName: Full=Paired box protein Pax-3; AltName: Full=HuP2
P24610 (PAX3_MOUSE)	RecName: Full=Paired box protein Pax-3
P26367 (PAX6_HUMAN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Oculorhombin
P26630 (PAX6_DANRE)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax[Zf-a]
P29454 (GSCA_XENLA)	RecName: Full=Homeobox protein goosecoid isoform A
P29506 (UNC4_CAEEL)	RecName: Full=Homeobox protein unc-4; AltName: Full=Homeobox protein ceh-4; AltName: Full=Uncoordinated protein 4
P32114 (PAX2_MOUSE)	RecName: Full=Paired box protein Pax-2
P32243 (OTX2_HUMAN)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P47236 (PAX1_CHICK)	RecName: Full=Paired box protein Pax-1
P47237 (PAX6_CHICK)	RecName: Full=Paired box protein Pax-6
P47238 (PAX6_COTJA)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax-QNR
P47239 (PAX7_MOUSE)	RecName: Full=Paired box protein Pax-7

P51974 (PAX8_RAT)	RecName: Full=Paired box protein Pax-8
P53544 (GSC_DANRE)	RecName: Full=Homeobox protein goosecoid; AltName: Full=ZGSC
P53546 (GSCB_XENLA)	RecName: Full=Homeobox protein goosecoid isoform B
P54366 (GSC_DROME)	RecName: Full=Homeobox protein goosecoid
P55166 (PAX9_CHICK)	RecName: Full=Paired box protein Pax-9
P55771 (PAX9_HUMAN)	RecName: Full=Paired box protein Pax-9
P55864 (PAX6_XENLA)	RecName: Full=Paired box protein Pax-6
P56915 (GSC_HUMAN)	RecName: Full=Homeobox protein goosecoid
P56916 (GSC2_MOUSE)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
P63016 (PAX6_RAT)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
P70390 (SHOX2_MOUSE)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; Short=OG-12; AltName: Full=Paired family homeodomain protein Prx3
P80206 (OTX2_MOUSE)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P97474 (PITX2_MOUSE)	RecName: Full=Pituitary homeobox 2; AltName: Full=ALL1-responsive protein ARP1; AltName: Full=BRX1 homeoprotein; AltName: Full=Homeobox protein PITX2; AltName: Full=Orthodenticle-like homeobox 2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=Paired-like homeodomain transcription factor Munc 30; AltName: Full=Solurshin
P97830 (UNC4_RAT)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1; AltName: Full=Paired-type homeodomain transcription factor 1
Q0IH87 (PAX3B_XENLA)	RecName: Full=Paired box protein Pax-3-B; Short=xPax3-B; AltName: Full=Paired-domain transcription factor Pax3-B
Q1LVQ7 (ALX1_DANRE)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q1LZF1 (PAX6_BOVIN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
Q2VL53 (PAX9_DAUMA)	RecName: Full=Paired box protein Pax-9
Q2VL54 (PAX9_PERPO)	RecName: Full=Paired box protein Pax-9
Q2VL56 (PAX9_SAGOE)	RecName: Full=Paired box protein Pax-9
Q2VL57 (PAX9_LEORO)	RecName: Full=Paired box protein Pax-9
Q2VL58 (PAX9_CALJA)	RecName: Full=Paired box protein Pax-9
Q2VL59 (PAX9_CALGO)	RecName: Full=Paired box protein Pax-9
Q2VL60 (PAX9_SAIBB)	RecName: Full=Paired box protein Pax-9
Q2VL61 (PAX9_MACMU)	RecName: Full=Paired box protein Pax-9
Q2VL62 (PAX9_PANTR)	RecName: Full=Paired box protein Pax-9
Q4LAL6 (ALX4_BOVIN)	RecName: Full=Homeobox protein aristaless-like 4
Q6DKN2 (OTX2B_XENLA)	RecName: Full=Homeobox protein OTX2-B; Short=xOTX2-B; AltName: Full=Orthodenticle 2-B; AltName: Full=Orthodenticle-A-like protein B
Q6QU75 (PITX3_DANRE)	RecName: Full=Pituitary homeobox 3; AltName: Full=Bicoid-like homeodomain transcription factor Pitx3; AltName: Full=Homeobox protein PITX3; AltName: Full=Paired-like homeodomain transcription factor 3
Q7YTC2 (OTP_SACKO)	RecName: Full=Homeobox protein orthopedia
Q9H161 (ALX4_HUMAN)	RecName: Full=Homeobox protein aristaless-like 4
Q9I8K3 (PITX3_XENLA)	RecName: Full=Pituitary homeobox 3; AltName: Full=Homeobox protein PITX3; Short=XPitx-3; Short=xPitx3; AltName: Full=Paired-like homeodomain transcription factor 3
Q9I9A2 (RX2_ORYLA)	RecName: Full=Retinal homeobox protein Rx2
Q9I9D5 (RX1_ASTFA)	RecName: Full=Retinal homeobox protein Rx1
Q9JLT7 (RX_RAT)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
Q9PT61 (OTX5B_XENLA)	RecName: Full=Homeobox protein otx5-B; AltName: Full=Orthodenticle homolog 5-B; AltName: Full=XOtx5b
Q9PVM0 (OTX5A_XENLA)	RecName: Full=Homeobox protein otx5-A; AltName: Full=Orthodenticle homolog 5-A; AltName: Full=Xotx5
Q9PVX0 (RX2_CHICK)	RecName: Full=Retinal homeobox protein Rx2; Short=cRax2
Q9PVY0 (RX1_CHICK)	RecName: Full=Retinal homeobox protein Rx1; Short=cRax1
Q9PWR3 (PITX2_XENLA)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=xPtx2
Q9R0W1 (PITX2_RAT)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=rPtx2
Q9U637 (PITX_BRABE)	RecName: Full=Pituitary homeobox x; AltName: Full=Bicoid type transcription factor Pitx; Short=BbPtx; AltName: Full=Homeobox protein Ptx; AltName: Full=Paired-like homeodomain transcription factor x
Q9W2Q1 (RX_DROME)	RecName: Full=Retinal homeobox protein Rx; Short=DRx; Short=DRx1
Q9W5Z2 (PITX2_DANRE)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2
Q9YH95 (PAX5_XENLA)	RecName: Full=Paired box protein Pax-5; Short=XPax-5
Q28DP6 (PAX3_XENTR)	RecName: Full=Paired box protein Pax-3; AltName: Full=Paired-domain transcription factor Pax3
Q28EM7 (OTX5_XENTR)	RecName: Full=Homeobox protein otx5; AltName: Full=Orthodenticle homolog 5
Q28FN6 (OTX2_XENTR)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle 2
Q50D79 (UNC4_DANRE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
Q96QS3 (ARX_HUMAN)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
Q00288 (PAX8_MOUSE)	RecName: Full=Paired box protein Pax-8
Q645N4 (PAX3A_XENLA)	RecName: Full=Paired box protein Pax-3-A; Short=xPax3-A; AltName: Full=Paired-domain transcription factor Pax3-A

Q02548 (PAX5_HUMAN)	RecName: Full=Paired box protein Pax-5; AltName: Full=B-cell-specific transcription factor; Short=BSAP
Q02650 (PAX5_MOUSE)	RecName: Full=Paired box protein Pax-5; AltName: Full=B-cell-specific transcription factor; Short=BSAP
Q02962 (PAX2_HUMAN)	RecName: Full=Paired box protein Pax-2
Q06453 (AL_DROME)	RecName: Full=Homeobox protein aristaless
Q06710 (PAX8_HUMAN)	RecName: Full=Paired box protein Pax-8
Q15699 (ALX1_HUMAN)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q26602 (SMOX3_SCHMA)	RecName: Full=Homeobox protein SMOX-3
Q26657 (ALX_STRPU)	RecName: Full=Aristaless homeobox protein; Short=ALX; AltName: Full=SpPrx-1
Q62066 (PHX2A_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=PHOX2A homeodomain protein; AltName: Full=Paired-like homeobox 2A
Q62782 (PHX2A_RAT)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
Q90268 (PAX2A_DANRE)	RecName: Full=Paired box protein Pax-2a; AltName: Full=No isthmus protein; AltName: Full=Pax[Zf-b]
Q91813 (OTX2A_XENLA)	RecName: Full=Homeobox protein OTX2-A; Short=xOTX2-A; AltName: Full=Orthodenticle 2-A; AltName: Full=Orthodenticle-A-like protein A
Q91981 (OTX2_DANRE)	RecName: Full=Homeobox protein OTX2; Short=zOTX2; AltName: Full=Orthodenticle homolog 2
Q91994 (OTX1B_DANRE)	RecName: Full=Homeobox protein OTX1 B; Short=zOtx1; AltName: Full=Orthodenticle homolog 1 B
Q99697 (PITX2_HUMAN)	RecName: Full=Pituitary homeobox 2; AltName: Full=ALL1-responsive protein ARP1; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=RIEG bicoid-related homeobox transcription factor; AltName: Full=Solurshin
XP_969276	PREDICTED: homeobox protein unc-4-like [Tribolium castaneum]
XP_975478	PREDICTED: paired box pox-meso protein [Tribolium castaneum]
XP_001119966	PREDICTED: retinal homeobox protein Rx [Apis mellifera]
XP_001120833	PREDICTED: paired mesoderm homeobox protein 2A [Apis mellifera]
XP_001516357	PREDICTED: retina and anterior neural fold homeobox protein 2 [Ornithorhynchus anatinus]
XP_001599456	PREDICTED: homeobox protein ARX-like isoform X2 [Nasonia vitripennis]
XP_001634166	predicted protein [Nematostella vectensis]
XP_001943352	PREDICTED: homeobox protein goosecoid [Acyrthosiphon pisum]
XP_002429235	Pituitary homeobox, putative [Pediculus humanus corporis]
XP_002429319	Paired box protein Pax-6, putative [Pediculus humanus corporis]
XP_002432447	homeobox protein arx, putative [Pediculus humanus corporis]
XP_002731203	PREDICTED: homeobox protein ARX-like [Saccoglossus kowalevskii]
XP_002815113	PREDICTED: pituitary homeobox 2 isoform X1 [Pongo abelii]
XP_003393215	PREDICTED: homeobox protein aristaless-like [Bombus terrestris]
XP_003393515	PREDICTED: retinal homeobox protein Rx1-like [Bombus terrestris]
XP_003695586	PREDICTED: retinal homeobox protein Rx1-like [Apis florea]
XP_003697447	PREDICTED: protein gooseberry isoform X1 [Apis florea]
XP_003702414	PREDICTED: homeobox protein goosecoid [Megachile rotundata]
XP_003745704	PREDICTED: homeobox protein unc-4 homolog [Metaseiulus occidentalis]
XP_004867643	PREDICTED: pituitary homeobox 2 isoform X1 [Heterocephalus glaber]
XP_005047812	PREDICTED: homeobox protein OTX2 isoform X1 [Ficedula albicollis]
XP_005092282	PREDICTED: mediator of DNA damage checkpoint protein 1-like [Aplysia californica]
XP_005185444	PREDICTED: paired box protein Pax-6 [Musca domestica]
XP_005287559	PREDICTED: paired box protein Pax-1 [Chrysemys picta bellii]
XP_005295567	PREDICTED: homeobox protein OTX2 [Chrysemys picta bellii]
XP_005948265	PREDICTED: paired box protein Pax-7-like isoform X2 [Haplochromis burtoni]
XP_006007527	PREDICTED: paired box protein Pax-1 isoform X1 [Latimeria chalumnae]
XP_006559357	PREDICTED: protein gooseberry-like isoform X2 [Apis mellifera]
XP_006624099	PREDICTED: retinal homeobox protein Rx-like [Apis dorsata]
XP_006632284	PREDICTED: homeobox protein OTX2-like isoform X2 [Lepisosteus oculatus]
XP_006807220	PREDICTED: paired box protein Pax-7-like isoform X2 [Neolamprologus brichardi]
XP_007535826	PREDICTED: homeobox protein OTX2 isoform X1 [Erinaceus europaeus]
XP_007549399	PREDICTED: paired box protein Pax-1-like [Poecilia formosa]
XP_007884280	PREDICTED: short stature homeobox protein-like, partial [Callorhinchus milii]
XP_007901317	PREDICTED: retinal homeobox protein Rx [Callorhinchus milii]
XP_008192483	PREDICTED: paired mesoderm homeobox protein 2A-like [Tribolium castaneum]
XP_008193911	PREDICTED: aristaless isoform X2 [Tribolium castaneum]
XP_008195782	PREDICTED: aristaless-related homeobox protein [Tribolium castaneum]
XP_008196347	PREDICTED: paired box protein Pax-1 [Tribolium castaneum]
XP_008207398	PREDICTED: homeobox protein aristaless-like [Nasonia vitripennis]
XP_008214560	PREDICTED: paired mesoderm homeobox protein 2-like isoform X3 [Nasonia vitripennis]
XP_008314528	PREDICTED: homeobox protein unc-4 homolog [Cynoglossus semilaevis]
XP_008326698	PREDICTED: paired box protein Pax-1 isoform X1 [Cynoglossus semilaevis]
XP_008328178	PREDICTED: paired box protein Pax-1 isoform X3 [Cynoglossus semilaevis]

XP_008328945	PREDICTED: paired box protein Pax-1 isoform X4 [Cynoglossus semilaevis]
XP_008329681	PREDICTED: paired box protein Pax-1 isoform X5 [Cynoglossus semilaevis]
XP_008469101	PREDICTED: paired box protein Pax-1-like [Diaphorina citri]
XP_008488086	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Diaphorina citri]
XP_008560226	PREDICTED: paired mesoderm homeobox protein 2B-like [Microplitis demolitor]
XP_008923318	PREDICTED: paired box protein Pax-9 [Manacus vitellinus]
XP_009076651	PREDICTED: short stature homeobox protein-like, partial [Acanthisitta chloris]
XP_009100157	PREDICTED: paired box protein Pax-9 [Serinus canaria]
XP_009279652	PREDICTED: short stature homeobox protein [Aptenodytes forsteri]
XP_009708313	PREDICTED: short stature homeobox protein, partial [Cariama cristata]
XP_009903167	PREDICTED: pituitary homeobox 2 isoform X1 [Picoides pubescens]
XP_009906575	PREDICTED: homeobox protein OTX2 isoform X1 [Picoides pubescens]
XP_009929482	PREDICTED: short stature homeobox protein [Opisthocomus hoazin]
XP_009950422	PREDICTED: short stature homeobox protein 2, partial [Leptosomus discolor]
XP_009977752	PREDICTED: short stature homeobox protein, partial [Tauraco erythrolophus]
XP_010004397	PREDICTED: paired mesoderm homeobox protein 2B [Chaetura pelagica]
XP_010145662	PREDICTED: paired mesoderm homeobox protein 2B, partial [Eurypyga helias]
XP_010171498	PREDICTED: short stature homeobox protein, partial [Caprimulgus carolinensis]
XP_010197417	PREDICTED: short stature homeobox protein, partial [Colius striatus]
XP_010581968	PREDICTED: paired box protein Pax-9 [Haliaeetus leucocephalus]
XP_010778173	PREDICTED: paired box protein Pax-1 [Notothenia coriiceps]
XP_010793318	PREDICTED: short stature homeobox protein 2 [Notothenia coriiceps]
XP_011139178	PREDICTED: homeobox protein goosecoid [Harpegnathos saltator]
XP_011145894	PREDICTED: paired box protein Pax-5 [Harpegnathos saltator]
XP_011154618	PREDICTED: protein gooseberry [Harpegnathos saltator]
XP_011261155	PREDICTED: homeobox protein goosecoid [Camponotus floridanus]
XP_011299924	PREDICTED: paired box protein Pax-6 [Fopius arisanus]
XP_011333914	PREDICTED: protein gooseberry isoform X1 [Cerapachys biroi]
XP_011333915	PREDICTED: protein gooseberry isoform X2 [Cerapachys biroi]
XP_011338931	PREDICTED: homeobox protein goosecoid [Cerapachys biroi]
XP_011341316	PREDICTED: paired mesoderm homeobox protein 2A-like [Cerapachys biroi]
XP_011424860	PREDICTED: paired box protein Pax-7-like isoform X1 [Crassostrea gigas]
XP_011424861	PREDICTED: paired box protein Pax-7-like isoform X2 [Crassostrea gigas]
XP_011427188	PREDICTED: retinal homeobox protein Rax-like [Crassostrea gigas]
XP_011433286	PREDICTED: paired box protein Pax-6-like isoform X1 [Crassostrea gigas]
XP_011433289	PREDICTED: paired box protein Pax-6-like isoform X2 [Crassostrea gigas]
XP_011445596	PREDICTED: homeobox protein unc-4 homolog [Crassostrea gigas]
XP_011503661	PREDICTED: homeobox protein aristaless [Ceratosolen solmsi marchali]
XP_011571078	PREDICTED: paired box protein Pax-9 [Aquila chrysaetos canadensis]
XP_011692944	PREDICTED: homeobox protein goosecoid [Wasmannia auropunctata]
XP_012217632	PREDICTED: retinal homeobox protein Rx1-like [Linepithema humile]
XP_012232563	PREDICTED: paired mesoderm homeobox protein 2B-like [Linepithema humile]
XP_012245723	PREDICTED: protein gooseberry-like [Bombus impatiens]
XP_012254404	PREDICTED: homeobox protein ARX-like [Athalia rosae]
XP_012262061	PREDICTED: retina and anterior neural fold homeobox protein 2-like [Athalia rosae]
XP_012264378	PREDICTED: paired box protein Pax-5 [Athalia rosae]
XP_012269935	PREDICTED: paired mesoderm homeobox protein 2A-like [Athalia rosae]
XP_012282148	PREDICTED: aristaless-related homeobox protein [Orussus abietinus]
XP_012533722	PREDICTED: homeobox protein aristaless-like [Monomorium pharaonis]
XP_012693489	PREDICTED: paired box protein Pax-1-like [Clupea harengus]
XP_013115219	PREDICTED: paired box protein Pax-6-like [Stomoxys calcitrans]
XP_013122904	PREDICTED: paired box protein Pax-7-like isoform X2 [Oreochromis niloticus]
XP_013133558	PREDICTED: homeobox protein aristaless-like [Papilio polytes]
XP_013142990	PREDICTED: homeobox protein unc-4 [Papilio polytes]
XP_013181086	PREDICTED: homeobox protein aristaless-like [Papilio xuthus]
XP_013181607	PREDICTED: pituitary homeobox homolog Ptx1 [Papilio xuthus]
XP_013185330	PREDICTED: pituitary homeobox homolog Ptx1 isoform X1 [Amyelois transitella]
XP_013185332	PREDICTED: pituitary homeobox homolog Ptx1 isoform X2 [Amyelois transitella]
XP_013190975	PREDICTED: paired box pox-neuro protein [Amyelois transitella]
XP_013409630	PREDICTED: paired box protein Pax-6-like isoform X1 [Lingula anatina]
XP_013409631	PREDICTED: paired box protein Pax-6-like isoform X2 [Lingula anatina]
XP_013409632	PREDICTED: paired box protein Pax-6-like isoform X3 [Lingula anatina]
XP_013409633	PREDICTED: paired box protein Pax-6-like isoform X4 [Lingula anatina]
XP_013409635	PREDICTED: paired box protein Pax-6-like isoform X6 [Lingula anatina]
XP_013417610	PREDICTED: homeobox protein unc-4 homolog [Lingula anatina]
XP_013771712	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]

XP_013772276	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013772838	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013772864	PREDICTED: paired box protein Pax-5-like isoform X1 [Limulus polyphemus]
XP_013772865	PREDICTED: paired box protein Pax-5-like isoform X2 [Limulus polyphemus]
XP_013772867	PREDICTED: paired box protein Pax-5-like isoform X3 [Limulus polyphemus]
XP_013772868	PREDICTED: paired box protein Pax-5-like isoform X4 [Limulus polyphemus]
XP_013773208	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013774111	PREDICTED: pituitary homeobox x-like [Limulus polyphemus]
XP_013774514	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013775460	PREDICTED: homeobox protein unc-4 homolog [Limulus polyphemus]
XP_013775534	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013776544	PREDICTED: pituitary homeobox x-like [Limulus polyphemus]
XP_013776976	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013777226	PREDICTED: paired box pox-neuro protein-like [Limulus polyphemus]
XP_013777739	PREDICTED: retinal homeobox protein Rx1-like [Limulus polyphemus]
XP_013777740	PREDICTED: aristaless-related homeobox protein-like [Limulus polyphemus]
XP_013778470	PREDICTED: protein gooseberry-like [Limulus polyphemus]
XP_013778820	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013779707	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Limulus polyphemus]
XP_013779863	PREDICTED: paired box protein Pax-1-like, partial [Limulus polyphemus]
XP_013779981	PREDICTED: homeobox protein unc-4 homolog [Limulus polyphemus]
XP_013780133	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013780572	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013781415	PREDICTED: homeobox protein aristaless-like [Limulus polyphemus]
XP_013781442	PREDICTED: paired box protein Pax-3-like [Limulus polyphemus]
XP_013782207	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013782258	PREDICTED: homeobox protein ARX-like [Limulus polyphemus]
XP_013786450	PREDICTED: homeobox protein ARX-like [Limulus polyphemus]
XP_013786772	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013787478	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Limulus polyphemus]
XP_013789026	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013789393	PREDICTED: retinal homeobox protein Rx1-like [Limulus polyphemus]
XP_013790457	PREDICTED: homeobox protein Nkx-6.3-like [Limulus polyphemus]
XP_013792934	PREDICTED: paired box protein Pax-6-like isoform X1 [Limulus polyphemus]
XP_013792941	PREDICTED: paired box protein Pax-6-like isoform X2 [Limulus polyphemus]
XP_013793906	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013794441	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013796335	PREDICTED: paired box protein Pax-9 [Apteryx australis mantelli]
XP_014124966	PREDICTED: paired mesoderm homeobox protein 2B [Zonotrichia albicollis]
XP_014209020	PREDICTED: aristaless-related homeobox protein-like [Copidosoma floridanum]
XP_014209699	PREDICTED: paired box protein Pax-6-like [Copidosoma floridanum]
XP_014221000	PREDICTED: retinal homeobox protein Rx-like [Trichogramma pretiosum]
XP_014221003	PREDICTED: homeobox protein aristaless-like 3 [Trichogramma pretiosum]
XP_014226736	PREDICTED: homeobox protein goosecoid-like [Trichogramma pretiosum]
XP_014229927	PREDICTED: paired box protein Pax-6-like isoform X1 [Trichogramma pretiosum]
XP_014229933	PREDICTED: paired box protein Pax-6-like isoform X2 [Trichogramma pretiosum]
XP_014229940	PREDICTED: paired box protein Pax-6-like isoform X3 [Trichogramma pretiosum]
XP_014229948	PREDICTED: paired box protein Pax-6-like isoform X4 [Trichogramma pretiosum]
XP_014229955	PREDICTED: paired box protein Pax-6-like isoform X5 [Trichogramma pretiosum]
XP_014244834	PREDICTED: paired box protein Pax-5 isoform X5 [Cimex lectularius]
XP_014247391	PREDICTED: homeobox protein goosecoid-like [Cimex lectularius]
XP_014253523	PREDICTED: paired mesoderm homeobox protein 2B-like [Cimex lectularius]
XP_014262476	PREDICTED: protein gooseberry-like [Cimex lectularius]
XP_014265872	PREDICTED: paired box protein Pax-7-like isoform X3 [Maylandia zebra]
XP_014276606	PREDICTED: paired box protein Pax-5 isoform X3 [Halyomorpha halys]
XP_014280336	PREDICTED: retina and anterior neural fold homeobox protein 2-like [Halyomorpha halys]
XP_014288116	PREDICTED: paired mesoderm homeobox protein 2A-like isoform X2 [Halyomorpha halys]
XP_014290681	PREDICTED: protein gooseberry-like isoform X1 [Halyomorpha halys]
XP_014290682	PREDICTED: protein gooseberry-like isoform X2 [Halyomorpha halys]
XP_014362535	PREDICTED: homeobox protein goosecoid-like [Papilio machaon]
XP_014362693	PREDICTED: homeobox protein aristaless isoform X2 [Papilio machaon]
XP_014362779	PREDICTED: homeobox protein aristaless-like [Papilio machaon]
XP_014427514	PREDICTED: homeobox protein OTX2 [Pelodiscus sinensis]

9.4.2.16 *HMGB1*

Name	Description
A4IIJ8 (SOX10_XENTR)	RecName: Full=Transcription factor Sox-10; AltName: Full=SRY (sex determining region Y)-box 10
A4QNP0 (TOX4_XENTR)	RecName: Full=TOX high mobility group box family member 4
B7SBD2 (TOX3_RAT)	RecName: Full=TOX high mobility group box family member 3; AltName: Full=Trinucleotide repeat-containing gene 9 protein
B7ZR65 (SOX9A_XENLA)	RecName: Full=Transcription factor Sox-9-A
HMG2_DROME	RecName: Full=High mobility group protein DSP1; AltName: Full=Protein dorsal switch 1
HMGB1_HUMAN	RecName: Full=High mobility group protein B1; AltName: Full=High mobility group protein 1; Short=HMG-1
Locus_1_Transcript_97552/166847_Confidence_1.000_Length_950 - ORF 6 (frame 1) translation	Locus_1_Transcript_97552/166847_Confidence_1.000_Length_950
Locus_1_Transcript_114243/166847_Confidence_1.000_Length_1631 - ORF 15 (frame 1) translation	Locus_1_Transcript_114243/166847_Confidence_1.000_Length_1631
Locus_1_Transcript_114272/166847_Confidence_1.000_Length_1631 - ORF 1 (frame 1) translation	Locus_1_Transcript_114272/166847_Confidence_1.000_Length_1631
Locus_163_Transcript_11/11_Confidence_0.340_Length_2771 - ORF 1 (frame 1) translation	Locus_163_Transcript_11/11_Confidence_0.340_Length_2771
Locus_2256_Transcript_10/12_Confidence_0.306_Length_2793 - ORF 21 (frame 2) translation	Locus_2256_Transcript_10/12_Confidence_0.306_Length_2793
Locus_5012_Transcript_21/22_Confidence_0.102_Length_3230 - ORF 13 (frame 2) translation	Locus_5012_Transcript_21/22_Confidence_0.102_Length_3230
Locus_7497_Transcript_9/9_Confidence_0.640_Length_7908 - ORF 2 (frame 2) translation	Locus_7497_Transcript_9/9_Confidence_0.640_Length_7908
Locus_16401_Transcript_2/6_Confidence_0.385_Length_1323 - ORF 4 (frame 1) translation	Locus_16401_Transcript_2/6_Confidence_0.385_Length_1323
Locus_18281_Transcript_4/4_Confidence_0.750_Length_5013 - ORF 24 (frame 3) translation	Locus_18281_Transcript_4/4_Confidence_0.750_Length_5013
Locus_21036_Transcript_10/10_Confidence_0.386_Length_6994 - ORF 28 (frame 2) translation	Locus_21036_Transcript_10/10_Confidence_0.386_Length_6994
Locus_36494_Transcript_2/2_Confidence_0.800_Length_1810 - ORF 3 (frame 3) translation	Locus_36494_Transcript_2/2_Confidence_0.800_Length_1810
NP_080088	high mobility group protein 20A [Mus musculus]
NP_001298193	high mobility group protein B3-like [Biomphalaria glabrata]
O15347 (HMGB3_HUMAN)	RecName: Full=High mobility group protein B3; AltName: Full=High mobility group protein 2a; Short=HMG-2a; AltName: Full=High mobility group protein 4; Short=HMG-4
O15405 (TOX3_HUMAN)	RecName: Full=TOX high mobility group box family member 3; AltName: Full=CAG trinucleotide repeat-containing gene F9 protein; AltName: Full=Trinucleotide repeat-containing gene 9 protein
O18896 (SOX9_PIG)	RecName: Full=Transcription factor SOX-9
O42342 (SOX7_XENLA)	RecName: Full=Transcription factor Sox-7; Short=xSOX7
O44757 (LIN59_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase lin-59; AltName: Full=Abnormal cell lineage protein 59
O54879 (HMGB3_MOUSE)	RecName: Full=High mobility group protein B3; AltName: Full=High mobility group protein 2a; Short=HMG-2a; AltName: Full=High mobility group protein 4; Short=HMG-4
O74964 (RSC1_SCHPO)	RecName: Full=Chromatin structure-remodeling complex subunit rsc1; AltName: Full=RSC complex subunit rsc1; AltName: Full=Remodel the structure of chromatin complex subunit 1
O94900 (TOX_HUMAN)	RecName: Full=Thymocyte selection-associated high mobility group box protein TOX; AltName: Full=Thymus high mobility group box protein TOX
P07746 (HMGT_ONCMY)	RecName: Full=High mobility group-T protein; Short=HMG-T; AltName: Full=HMG-T1; Short=HMG-1
P09429 (HMGB1_HUMAN)	RecName: Full=High mobility group protein B1; AltName: Full=High mobility group protein 1; Short=HMG-1
P10103 (HMGB1_BOVIN)	RecName: Full=High mobility group protein B1; AltName: Full=High mobility group protein 1; Short=HMG-1
P12682 (HMGB1_PIG)	RecName: Full=High mobility group protein B1; AltName: Full=High mobility group protein 1; Short=HMG-1
P40618 (HMGB3_CHICK)	RecName: Full=High mobility group protein B3; AltName: Full=High mobility group protein 2a; Short=HMG-2a; AltName: Full=High mobility group protein 4; Short=HMG-4
P40622 (HMG1A_CHITE)	RecName: Full=Mobility group protein 1A
P40646 (SOX7_MOUSE)	RecName: Full=Transcription factor SOX-7; Short=mSOX7
P40657 (SOX15_DROME)	RecName: Full=Putative transcription factor SOX-15; AltName: Full=Sox50E
P48434 (SOX9_CHICK)	RecName: Full=Transcription factor SOX-9
P48436 (SOX9_HUMAN)	RecName: Full=Transcription factor SOX-9
P53236 (RSC1_YEAST)	RecName: Full=Chromatin structure-remodeling complex subunit RSC1; AltName: Full=RSC complex subunit RSC1; AltName: Full=Remodel the structure of chromatin complex subunit 1
P54277 (PMS1_HUMAN)	RecName: Full=PMS1 protein homolog 1; AltName: Full=DNA mismatch repair protein PMS1
P63159 (HMGB1_RAT)	RecName: Full=High mobility group protein B1; AltName: Full=Amphoterin; AltName: Full=Heparin-binding protein p30; AltName: Full=High mobility group protein 1; Short=HMG-1
P65492 (MUTL_STAAN)	RecName: Full=DNA mismatch repair protein MutL
Q3KQ35 (S17AA_XENLA)	RecName: Full=Transcription factor Sox-17-alpha-A; Short=Xsox17alpha; Short=xSox17alpha1
Q03MY0 (MUTL_STRTD)	RecName: Full=DNA mismatch repair protein MutL
Q4H2R2 (SSRP1_CIOIN)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Structure-specific recognition protein 1
Q5HGD5 (MUTL_STAAC)	RecName: Full=DNA mismatch repair protein MutL
Q5M1Y6 (MUTL_STRT1)	RecName: Full=DNA mismatch repair protein MutL
Q5R6A9 (TOX4_PONAB)	RecName: Full=TOX high mobility group box family member 4

Q5ZKF4 (HM20A_CHICK)	RecName: Full=High mobility group protein 20A; AltName: Full=HMG box-containing protein 20A
Q6AZF8 (HM20A_XENLA)	RecName: Full=High mobility group protein 20A; AltName: Full=HMG box-containing protein 20A
Q6CVH3 (NHP6_KLULA)	RecName: Full=Non-histone chromosomal protein 6
Q6DFF5 (SOX9B_XENLA)	RecName: Full=Transcription factor Sox-9-B
Q6DIJ5 (HM20A_XENTR)	RecName: Full=High mobility group protein 20A; AltName: Full=HMG box-containing protein 20A
Q6DJL0 (TOX4A_XENLA)	RecName: Full=TOX high mobility group box family member 4-A
Q6F2E7 (SOX9_XENTR)	RecName: Full=Transcription factor Sox-9; Short=Xt-sox9
Q6F2F0 (S17B3_XENTR)	RecName: Full=Transcription factor Sox-17-beta.3; AltName: Full=SRY (sex determining region Y)-box 17-beta.3
Q6GHD9 (MUTL_STAAR)	RecName: Full=DNA mismatch repair protein MutL
Q6GLH8 (S17B2_XENTR)	RecName: Full=Transcription factor Sox-17-beta.2; AltName: Full=SRY (sex determining region Y)-box 17-beta.2
Q6IRR0 (TOX4B_XENLA)	RecName: Full=TOX high mobility group box family member 4-B
Q6T723 (SRY_ARCAU)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC28 (SRY_LUTLU)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC31 (SRY_PHOLR)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC32 (SRY_PUSHI)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC36 (SRY_PAGGO)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC37 (SRY_CYSCR)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC43 (SRY_CALUR)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC44 (SRY_ARCGZ)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC45 (SRY_ZALCA)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6TC46 (SRY_EUMJU)	RecName: Full=Sex-determining region Y protein; AltName: Full=Testis-determining factor
Q6VVD7 (SOX8_XENLA)	RecName: Full=Transcription factor Sox-8
Q8AWH2 (S17B1_XENTR)	RecName: Full=Transcription factor Sox-17-beta.1; AltName: Full=SRY (sex determining region Y)-box 17-beta.1; Short=tSox17beta
Q8AWH3 (SX17A_XENTR)	RecName: Full=Transcription factor Sox-17-alpha; Short=Sox17alpha; Short=tSox17alpha
Q8AXX8 (SOX10_XENLA)	RecName: Full=Transcription factor Sox-10; AltName: Full=SRY (sex determining region Y)-box 10
Q8BSQ9 (PB1_MOUSE)	RecName: Full=Protein polybromo-1; AltName: Full=BRG1-associated factor 180; Short=BAF180
Q8CPE9 (MUTL_STAES)	RecName: Full=DNA mismatch repair protein MutL
Q8DRX0 (MUTL_STRMU)	RecName: Full=DNA mismatch repair protein MutL
Q8NWX9 (MUTL_STAAW)	RecName: Full=DNA mismatch repair protein MutL
Q9BG91 (SOX9_CALJA)	RecName: Full=Transcription factor SOX-9
Q9BT81 (SOX7_HUMAN)	RecName: Full=Transcription factor SOX-7
Q9DC33 (HM20A_MOUSE)	RecName: Full=High mobility group protein 20A; AltName: Full=HMG box-containing protein 20A; AltName: Full=HMG domain-containing protein HMGX1; AltName: Full=Inhibitor of BRAF35; Short=iBRAF
Q9H6I2 (SOX17_HUMAN)	RecName: Full=Transcription factor SOX-17
Q9NP66 (HM20A_HUMAN)	RecName: Full=High mobility group protein 20A; AltName: Full=HMG box-containing protein 20A; AltName: Full=HMG domain-containing protein 1; AltName: Full=HMG domain-containing protein HMGX1
Q9NR48 (ASH1L_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; Short=huASH1; AltName: Full=Absent small and homeotic disks protein 1 homolog; AltName: Full=Lysine N-methyltransferase 2H
Q9P0W2 (HM20B_HUMAN)	RecName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related; Short=SMARCE1-related protein; AltName: Full=BRCA2-associated factor 35; AltName: Full=HMG box-containing protein 20B; AltName: Full=HMG domain-containing protein 2; AltName: Full=HMG domain-containing protein HMGX2; AltName: Full=Sox-like transcriptional factor; AltName: Full=Structural DNA-binding protein BRAF35
Q9VW15 (ASH1_DROME)	RecName: Full=Histone-lysine N-methyltransferase ash1; AltName: Full=Absent small and homeotic disks protein 1; AltName: Full=Lysine N-methyltransferase 2H
Q9W602 (SSRP1_XENLA)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=DNA unwinding factor 87 kDa subunit; Short=DUF87; AltName: Full=Facilitates chromatin transcription complex subunit ssrp1; AltName: Full=Structure-specific recognition protein 1
Q9YH06 (HMGB1_CHICK)	RecName: Full=High mobility group protein B1; AltName: Full=High mobility group protein 1; Short=HMG-1
Q9Z104 (HM20B_MOUSE)	RecName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related; Short=SMARCE1-related protein; AltName: Full=BRCA2-associated factor 35; AltName: Full=HMG box-containing protein 20B; AltName: Full=Structural DNA-binding protein BRAF35
Q28GD5 (SOX7_XENTR)	RecName: Full=Transcription factor Sox-7
Q32L31 (HMGB3_BOVIN)	RecName: Full=High mobility group protein B3
Q32L68 (HM20B_BOVIN)	RecName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related; Short=SMARCE1-related protein; AltName: Full=HMG box-containing protein 20B
Q49X89 (MUTL_STAS1)	RecName: Full=DNA mismatch repair protein MutL
Q66JW3 (TOX_MOUSE)	RecName: Full=Thymocyte selection-associated high mobility group box protein TOX; AltName: Full=Thymus high mobility group box protein TOX

Q75B82 (NHP6_ASHGO)	RecName: Full=Non-histone chromosomal protein 6
Q76IQ7 (TOX2_RAT)	RecName: Full=TOX high mobility group box family member 2; AltName: Full=Granulosa cell HMG box protein 1; Short=GCX-1
Q80W03 (TOX3_MOUSE)	RecName: Full=TOX high mobility group box family member 3; AltName: Full=Trinucleotide repeat-containing gene 9 protein
Q86U86 (PB1_HUMAN)	RecName: Full=Protein polybromo-1; Short=hPB1; AltName: Full=BRG1-associated factor 180; Short=BAF180; AltName: Full=Polybromo-1D
Q90ZH9 (S17AB_XENLA)	RecName: Full=Transcription factor Sox-17-alpha-B; Short=xSox17alpha2
Q99MY8 (ASH1L_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; AltName: Full=Absent small and homeotic disks protein 1 homolog
Q293F6 (SSRP1_DROPS)	RecName: Full=FACT complex subunit Ssrp1; AltName: Full=Facilitates chromatin transcription complex subunit Ssrp1; AltName: Full=Recombination signal sequence recognition protein; AltName: Full=Single-strand recognition protein
Q04678 (SSRP1_CHICK)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Recombination signal sequence recognition protein 1; AltName: Full=Structure-specific recognition protein 1; AltName: Full=T160
Q04931 (SSRP1_RAT)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Recombination signal sequence recognition protein 1; AltName: Full=Structure-specific recognition protein 1; AltName: Full=T160
Q05344 (SSRP1_DROME)	RecName: Full=FACT complex subunit Ssrp1; AltName: Full=Chorion-factor 5; AltName: Full=Facilitates chromatin transcription complex subunit Ssrp1; AltName: Full=Recombination signal sequence recognition protein; AltName: Full=Single-strand recognition protein; AltName: Full=dSSRP1
Q06488 (RSC2_YEAST)	RecName: Full=Chromatin structure-remodeling complex subunit RSC2; AltName: Full=RSC complex subunit RSC2; AltName: Full=Remodel the structure of chromatin complex subunit 2
Q06943 (HMGZ_DROME)	RecName: Full=High mobility group protein Z; Short=HMG-Z
Q08943 (SSRP1_MOUSE)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Recombination signal sequence recognition protein 1; AltName: Full=Structure-specific recognition protein 1; AltName: Full=T160
Q08945 (SSRP1_HUMAN)	RecName: Full=FACT complex subunit SSRP1; AltName: Full=Chromatin-specific transcription elongation factor 80 kDa subunit; AltName: Full=Facilitates chromatin transcription complex 80 kDa subunit; Short=FACT 80 kDa subunit; Short=FACTp80; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Recombination signal sequence recognition protein 1; AltName: Full=Structure-specific recognition protein 1; Short=hSSRP1; AltName: Full=T160
Q61473 (SOX17_MOUSE)	RecName: Full=Transcription factor SOX-17
Q90941 (PB1_CHICK)	RecName: Full=Protein polybromo-1
XP_001083536	PREDICTED: transcription factor SOX-17 isoform 2 [Macaca mulatta]
XP_002410341	structure-specific recognition protein, putative, partial [Ixodes scapularis]
XP_002434952	high mobility group protein, putative [Ixodes scapularis]
XP_002737877	PREDICTED: transcription factor Sox-9-like [Saccoglossus kowalevskii]
XP_002758971	PREDICTED: transcription factor SOX-17 isoform X1 [Callithrix jacchus]
XP_003395326	PREDICTED: FACT complex subunit Ssrp1 isoform X1 [Bombus terrestris]
XP_003490512	PREDICTED: protein polybromo-1 isoform X1 [Bombus impatiens]
XP_003693254	PREDICTED: TOX high mobility group box family member 3-like, partial [Apis florea]
XP_003705276	PREDICTED: FACT complex subunit Ssrp1 [Megachile rotundata]
XP_003902811	PREDICTED: transcription factor SOX-17 [Papio anubis]
XP_005000864	PREDICTED: high mobility group protein 20A isoform X2 [Cavia porcellus]
XP_005102100	PREDICTED: transcription factor Sox-10-like [Aplysia californica]
XP_005105242	PREDICTED: high mobility group protein B3-like [Aplysia californica]
XP_005988126	PREDICTED: transcription factor SOX-9 [Latimeria chalumnae]
XP_006009452	PREDICTED: high mobility group protein 20A isoform X5 [Latimeria chalumnae]
XP_006009457	PREDICTED: high mobility group protein 20A isoform X6 [Latimeria chalumnae]
XP_006572310	PREDICTED: protein polybromo-1 isoform X3 [Apis mellifera]
XP_006572313	PREDICTED: protein polybromo-1 isoform X6 [Apis mellifera]
XP_006608627	PREDICTED: FACT complex subunit Ssrp1-like [Apis dorsata]
XP_006621401	PREDICTED: TOX high mobility group box family member 3-like isoform X3 [Apis dorsata]
XP_006623472	PREDICTED: protein polybromo-1-like isoform X4 [Apis dorsata]
XP_006824509	PREDICTED: high mobility group protein 20A-like isoform X1 [Saccoglossus kowalevskii]
XP_006824510	PREDICTED: high mobility group protein 20A-like isoform X2 [Saccoglossus kowalevskii]
XP_007116633	PREDICTED: PMS1 protein homolog 1 isoform X4 [Physeter catodon]
XP_007171538	PREDICTED: PMS1 protein homolog 1 isoform X4 [Balaenoptera acutorostrata scammoni]
XP_007998847	PREDICTED: transcription factor SOX-17 [Chlorocebus sabaeus]
XP_008192227	PREDICTED: protein bric-a-brac 1-like [Tribolium castaneum]
XP_008198296	PREDICTED: TOX high mobility group box family member 4-like isoform X1 [Tribolium castaneum]
XP_008198297	PREDICTED: TOX high mobility group box family member 4-like isoform X2 [Tribolium castaneum]

XP_008524395	PREDICTED: PMS1 protein homolog 1-like [Equus przewalskii]
XP_009281766	PREDICTED: transcription factor SOX-9 isoform X2 [Aptenodytes forsteri]
XP_011256495	PREDICTED: putative transcription factor SOX-15 [Camponotus floridanus]
XP_011303765	PREDICTED: TOX high mobility group box family member 3-like isoform X1 [Fopius arisanus]
XP_011303766	PREDICTED: TOX high mobility group box family member 3-like isoform X2 [Fopius arisanus]
XP_011305165	PREDICTED: putative transcription factor SOX-15 [Fopius arisanus]
XP_011339317	PREDICTED: putative transcription factor SOX-15 isoform X3 [Cerapachys biroi]
XP_011354400	PREDICTED: PMS1 protein homolog 1 isoform X1 [Pteropus vampyrus]
XP_011444919	PREDICTED: transcription factor Sox-8-like isoform X1 [Crassostrea gigas]
XP_011502825	PREDICTED: FACT complex subunit Ssrp1 [Ceratosolen solmsi marchali]
XP_011647119	PREDICTED: putative transcription factor SOX-15 [Pogonomyrmex barbatus]
XP_011690200	PREDICTED: putative transcription factor SOX-15 [Wasmannia auropunctata]
XP_011902657	PREDICTED: PMS1 protein homolog 1 isoform X3 [Cercocebus atys]
XP_011929213	PREDICTED: transcription factor SOX-17 [Cercocebus atys]
XP_012215988	PREDICTED: putative transcription factor SOX-15 [Linepithema humile]
XP_012239860	PREDICTED: FACT complex subunit Ssrp1 isoform X1 [Bombus impatiens]
XP_012239861	PREDICTED: FACT complex subunit Ssrp1 isoform X2 [Bombus impatiens]
XP_012242462	PREDICTED: protein polybromo-1 isoform X2 [Bombus impatiens]
XP_012250516	PREDICTED: protein bric-a-brac 1-like isoform X1 [Athalia rosae]
XP_012250517	PREDICTED: protein bric-a-brac 1-like isoform X2 [Athalia rosae]
XP_012281774	PREDICTED: protein polybromo-1 isoform X1 [Orussus abietinus]
XP_012281779	PREDICTED: protein polybromo-1 isoform X3 [Orussus abietinus]
XP_012283834	PREDICTED: putative transcription factor SOX-15 isoform X2 [Orussus abietinus]
XP_012378411	PREDICTED: PMS1 protein homolog 1 isoform X2 [Dasypus novemcinctus]
XP_012985344	PREDICTED: transcription factor SOX-17 [Melopsittacus undulatus]
XP_013091187	PREDICTED: transcription factor Sox-10-like [Biomphalaria glabrata]
XP_013381127	PREDICTED: transcription factor SOX-9-like [Lingula anatina]
XP_013415091	PREDICTED: high mobility group protein 20A-like [Lingula anatina]
XP_013775304	PREDICTED: intrastrand cross-link recognition protein-like [Limulus polyphemus]
XP_013776528	PREDICTED: thymocyte selection-associated high mobility group box protein TOX-like [Limulus polyphemus]
XP_013777181	PREDICTED: transcription factor Sox-8-like [Limulus polyphemus]
XP_013778136	PREDICTED: transcription factor Sox-8-like [Limulus polyphemus]
XP_013781490	PREDICTED: TOX high mobility group box family member 2-like [Limulus polyphemus]
XP_013787241	PREDICTED: FACT complex subunit Ssrp1-like [Limulus polyphemus]
XP_013787542	PREDICTED: intrastrand cross-link recognition protein-like [Limulus polyphemus]
XP_013791568	PREDICTED: transcription factor Sox-9-B-like [Limulus polyphemus]
XP_013794200	PREDICTED: thymocyte selection-associated high mobility group box protein TOX-like [Limulus polyphemus]
XP_013794397	PREDICTED: PMS1 protein homolog 1-like [Limulus polyphemus]
XP_013794753	PREDICTED: transcription factor Sox-17-alpha-A-like isoform X1 [Limulus polyphemus]
XP_013794754	PREDICTED: transcription factor Sox-17-alpha-A-like isoform X2 [Limulus polyphemus]
XP_014213086	PREDICTED: FACT complex subunit Ssrp1 [Copidosoma floridanum]
XP_014213287	PREDICTED: protein polybromo-1 isoform X1 [Copidosoma floridanum]
XP_014240400	PREDICTED: thymocyte selection-associated high mobility group box protein TOX-like isoform X2 [Cimex lectularius]

9.4.2.17 *Huckebein*

Name	Description
A4II20_(EGR1_XENTR)	RecName: Full=Early growth response protein 1; Short=EGR-1
AAF52141	huckebein [Drosophila melanogaster]
Locus_1_Transcript_73641/166847_Confidence_1.000_Length_1412_-_ORF_1_(frame_1)_translation	Locus_1_Transcript_73641/166847_Confidence_1.000_Length_1412
Locus_1_Transcript_158894/166847_Confidence_1.000_Length_1619_-_ORF_12_(frame_3)_translation	Locus_1_Transcript_158894/166847_Confidence_1.000_Length_1619
Locus_1422_Transcript_10/10_Confidence_0.500_Length_1039_-_ORF_2_(frame_1)_translation	Locus_1422_Transcript_10/10_Confidence_0.500_Length_1039
Locus_9586_Transcript_7/11_Confidence_0.090_Length_5776_-_ORF_2_(frame_1)_translation	Locus_9586_Transcript_7/11_Confidence_0.090_Length_5776
Locus_11926_Transcript_10/10_Confidence_0.517_Length_2604_-_ORF_2_(frame_1)_translation	Locus_11926_Transcript_10/10_Confidence_0.517_Length_2604
Locus_12180_Transcript_6/6_Confidence_0.688_Length_1769_-_ORF_2_(frame_3)_translation	Locus_12180_Transcript_6/6_Confidence_0.688_Length_1769
Locus_12603_Transcript_27/34_Confidence_0.072_Length_2482_-_ORF_21_(frame_1)_translation	Locus_12603_Transcript_27/34_Confidence_0.072_Length_2482
Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450_-_ORF_25_(frame_1)_translation	Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450

Locus_24701_Transcript_1/1_Confidence_1.000_Length_1226_-_ORF_7_(frame_2)_translation	Locus_24701_Transcript_1/1_Confidence_1.000_Length_1226
Locus_26294_Transcript_1/1_Confidence_1.000_Length_1064_-_ORF_4_(frame_1)_translation	Locus_26294_Transcript_1/1_Confidence_1.000_Length_1064
NP_001034509	Sp-like zinc finger transcription factor [Tribolium castaneum]
NP_001161575	KLF2-like transcription factor [Saccoglossus kowalevskii]
O35738_(KLF12_MOUSE)	RecName: Full=Krueppel-like factor 12; AltName: Full=Transcriptional repressor AP-2rep
O35739_(KLF9_MOUSE)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1;
O43474_(KLF4_HUMAN)	RecName: Full=Krueppel-like factor 4; AltName: Full=Epithelial zinc finger protein EZF; AltName: Full=Gut-enriched krueppel-lik
O95600_(KLF8_HUMAN)	RecName: Full=Krueppel-like factor 8; AltName: Full=Basic krueppel-like factor 3; AltName: Full=Zinc finger protein 741
P0CG40_(SP9_HUMAN)	RecName: Full=Transcription factor Sp9
P08046_(EGR1_MOUSE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A;
P08154_(EGR1_RAT)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A;
P18146_(EGR1_HUMAN)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=AT225; AltName: Full=Nerve growth factor-induced prot
P26632_(EGR1_DANRE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Zinc finger protein Krox-24
P43300_(EGR3_MOUSE)	RecName: Full=Early growth response protein 3; Short=EGR-3
P43301_(EGR3_RAT)	RecName: Full=Early growth response protein 3; Short=EGR-3
P46099_(KLF1_MOUSE)	RecName: Full=Krueppel-like factor 1; AltName: Full=Erythroid krueppel-like transcription factor; Short=EKLF
P57682_(KLF3_HUMAN)	RecName: Full=Krueppel-like factor 3; AltName: Full=Basic krueppel-like factor; AltName: Full=CACCC-box-binding protein BKLF; A
P58334_(KLF16_MOUSE)	RecName: Full=Krueppel-like factor 16; AltName: Full=Basic transcription element-binding protein 4; Short=BTE-binding protein 4
P79288_(KLF9_PIG)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1;
Q0VA40_(SP9_XENTR)	RecName: Full=Transcription factor Sp9
Q5XGT8_(SP8_XENLA)	RecName: Full=Transcription factor Sp8
Q6BEB4_(SP5_HUMAN)	RecName: Full=Transcription factor Sp5
Q6GQH4_(EGR1A_XENLA)	RecName: Full=Early growth response protein 1-A; Short=EGR-1-A; Short=Xegr-1
Q6NTY6_(EGR1B_XENLA)	RecName: Full=Early growth response protein 1-B; Short=EGR-1-B
Q6NW96_(SP9_DANRE)	RecName: Full=Transcription factor Sp9
Q6P0J3_(SP8_DANRE)	RecName: Full=Transcription factor Sp8
Q8BMJ8_(SP8_MOUSE)	RecName: Full=Transcription factor Sp8
Q8IXZ3_(SP8_HUMAN)	RecName: Full=Transcription factor Sp8; AltName: Full=Specificity protein 8
Q8TD94_(KLF14_HUMAN)	RecName: Full=Krueppel-like factor 14; AltName: Full=Basic transcription element-binding protein 5; Short=BTE-binding protein 5
Q8VI67_(SP7_MOUSE)	RecName: Full=Transcription factor Sp7; AltName: Full=C22; AltName: Full=Zinc finger protein osterix
Q9BXK1_(KLF16_HUMAN)	RecName: Full=Krueppel-like factor 16; AltName: Full=Basic transcription element-binding protein 4; Short=BTE-binding protein 4
Q9EPW2_(KLF15_MOUSE)	RecName: Full=Krueppel-like factor 15; AltName: Full=Cardiovascular Krueppel-like factor
Q9ET58_(KLF2_RAT)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q9JHX2_(SP5_MOUSE)	RecName: Full=Transcription factor Sp5
Q9JJZ6_(KLF13_MOUSE)	RecName: Full=Krueppel-like factor 13; AltName: Full=Basic transcription element-binding protein 3; Short=BTE-binding protein 3
Q9UIH9_(KLF15_HUMAN)	RecName: Full=Krueppel-like factor 15; AltName: Full=Kidney-enriched krueppel-like factor
Q9Y2Y9_(KLF13_HUMAN)	RecName: Full=Krueppel-like factor 13; AltName: Full=Basic transcription element-binding protein 3; Short=BTE-binding protein 3
Q9Y5W3_(KLF2_HUMAN)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q9Z0Z7_(KLF5_MOUSE)	RecName: Full=Krueppel-like factor 5; AltName: Full=Basic transcription element-binding protein 2; Short=BTE-binding protein 2;
Q19A40_(KLF14_PANTR)	RecName: Full=Krueppel-like factor 14
Q19A41_(KLF14_MOUSE)	RecName: Full=Krueppel-like factor 14
Q64HY3_(SP9_MOUSE)	RecName: Full=Transcription factor Sp9
Q64HY5_(SP8_CHICK)	RecName: Full=Transcription factor Sp8
Q01713_(KLF9_RAT)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1;
Q02446_(SP4_HUMAN)	RecName: Full=Transcription factor Sp4; AltName: Full=SPR-1
Q06889_(EGR3_HUMAN)	RecName: Full=Early growth response protein 3; Short=EGR-3; AltName: Full=Zinc finger protein pilot
Q13351_(KLF1_HUMAN)	RecName: Full=Krueppel-like factor 1; AltName: Full=Erythroid krueppel-like transcription factor; Short=EKLF
Q13886_(KLF9_HUMAN)	RecName: Full=Krueppel-like factor 9; AltName: Full=Basic transcription element-binding protein 1; Short=BTE-binding protein 1;
Q13887_(KLF5_HUMAN)	RecName: Full=Krueppel-like factor 5; AltName: Full=Basic transcription element-binding protein 2; Short=BTE-binding protein 2;
Q60793_(KLF4_MOUSE)	RecName: Full=Krueppel-like factor 4; AltName: Full=Epithelial zinc finger protein EZF; AltName: Full=Gut-enriched krueppel-lik
Q60843_(KLF2_MOUSE)	RecName: Full=Krueppel-like factor 2; AltName: Full=Lung krueppel-like factor
Q60980_(KLF3_MOUSE)	RecName: Full=Krueppel-like factor 3; AltName: Full=Basic krueppel-like factor; AltName: Full=CACCC-box-binding protein BKLF; A
Q62445_(SP4_MOUSE)	RecName: Full=Transcription factor Sp4
XP_001787418	PREDICTED: Krueppel-like factor 2 [Bos taurus]
XP_001849427	zinc finger protein 273 [Culex quinquefasciatus]
XP_001943786	PREDICTED: transcriptional regulator CRZ2-like [Acyrthosiphon pisum]

XP_002426166	Early growth response protein, putative [Pediculus humanus corporis]
XP_003742522	PREDICTED: early growth response protein 4-like [Metaseiulus occidentalis]
XP_003747475	PREDICTED: Krueppel-like factor 15-like [Metaseiulus occidentalis]
XP_005093656	PREDICTED: zinc finger protein 394-like isoform X1 [Aplysia californica]
XP_005093657	PREDICTED: zinc finger protein 394-like isoform X2 [Aplysia californica]
XP_005093658	PREDICTED: zinc finger protein 816-like isoform X3 [Aplysia californica]
XP_005175631	PREDICTED: zinc finger and SCAN domain-containing protein 10 [Musca domestica]
XP_005187275	PREDICTED: protein ovo [Musca domestica]
XP_005521503	PREDICTED: Krueppel-like factor 13 [Pseudopodoces humilis]
XP_006560759	PREDICTED: zinc finger protein 697-like [Apis mellifera]
XP_006609348	PREDICTED: zinc finger protein 729-like [Apis dorsata]
XP_006736144	PREDICTED: Krueppel-like factor 2 [Leptonychotes weddellii]
XP_006825975	PREDICTED: early growth response protein 1-like [Saccoglossus kowalevskii]
XP_008198341	PREDICTED: sp-like zinc finger transcription factor isoform X1 [Tribolium castaneum]
XP_008200855	PREDICTED: early growth response protein 1-B isoform X1 [Tribolium castaneum]
XP_008483659	PREDICTED: early growth response protein 3-like [Diaphorina citri]
XP_008502889	PREDICTED: Krueppel-like factor 13 [Calypte anna]
XP_008544634	PREDICTED: Krueppel-like factor 16 isoform X1 [Microplitis demolitor]
XP_009072834	PREDICTED: Krueppel-like factor 13 [Acanthisitta chloris]
XP_009088107	PREDICTED: Krueppel-like factor 13 [Serinus canaria]
XP_009467966	PREDICTED: Krueppel-like factor 13 [Nipponia nippon]
XP_009553621	PREDICTED: Krueppel-like factor 13 [Cuculus canorus]
XP_011150831	PREDICTED: zinc finger protein 226 [Harpegnathos saltator]
XP_011264304	PREDICTED: asparagine-rich zinc finger protein AZF1-like [Camponotus floridanus]
XP_011428991	PREDICTED: transcription factor Sp9-like [Crassostrea gigas]
XP_012034502	PREDICTED: Krueppel-like factor 2 isoform X1, partial [Ovis aries]
XP_012222749	PREDICTED: Krueppel-like factor 13 [Linepithema humile]
XP_012256216	PREDICTED: zinc finger protein 436-like [Athalia rosae]
XP_012282013	PREDICTED: transcription factor Sp1-like isoform X1 [Orussus abietinus]
XP_012677135	PREDICTED: Krueppel-like factor 9 [Clupea harengus]
XP_013395520	PREDICTED: transcription factor Sp9-like isoform X1 [Lingula anatina]
XP_013408973	PREDICTED: Krueppel-like factor 5 [Lingula anatina]
XP_013416627	PREDICTED: Krueppel-like factor 9 [Lingula anatina]
XP_013419033	PREDICTED: early growth response protein 1-B-like [Lingula anatina]
XP_013772918	PREDICTED: transcription factor Sp9-like [Limulus polyphemus]
XP_013773090	PREDICTED: Krueppel-like factor 2 [Limulus polyphemus]
XP_013773091	PREDICTED: pair-rule protein odd-paired-like [Limulus polyphemus]
XP_013773092	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013782841	PREDICTED: early growth response protein 1-like [Limulus polyphemus]
XP_013782918	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013783296	PREDICTED: Krueppel-like factor 12 [Limulus polyphemus]
XP_013784047	PREDICTED: transcription factor Sp5-like [Limulus polyphemus]
XP_013784122	PREDICTED: Krueppel-like factor 1 [Limulus polyphemus]
XP_013784508	PREDICTED: Krueppel-like factor 1 [Limulus polyphemus]
XP_013785179	PREDICTED: Krueppel-like factor 10 [Limulus polyphemus]
XP_013788487	PREDICTED: Krueppel-like factor 5 [Limulus polyphemus]
XP_013791872	PREDICTED: Krueppel-like factor 17 [Limulus polyphemus]
XP_013792741	PREDICTED: Krueppel-like factor 2 [Limulus polyphemus]
XP_013994864	PREDICTED: Krueppel-like factor 9 [Salmo salar]

9.4.2.18 *Intermediate neuroblasts defective*

Name	Description
A1L2P5 (HXD3_XENLA)	RecName: Full=Homeobox protein Hox-D3
A1YFA5 (HXB7_GORGO)	RecName: Full=Homeobox protein Hox-B7
A1YFD8 (HXD4_SAGLB)	RecName: Full=Homeobox protein Hox-D4
A1YGA4 (MEOX1_PANPA)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2D4P8 (HXD4_ATEGE)	RecName: Full=Homeobox protein Hox-D4
A2D5Y4 (HXA5_LEMCA)	RecName: Full=Homeobox protein Hox-A5
A2T7T2 (MEOX1_PONPY)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2T779 (MEOX1_PANTR)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
AAC97116	intermediate neuroblasts defective protein [Drosophila melanogaster]
B0VXK3 (HXA2_CALJA)	RecName: Full=Homeobox protein Hox-A2
B0W1V2 (ABDA_CULQU)	RecName: Full=Homeobox protein abdominal-A homolog
F1Q4R9 (MEOX1_DANRE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1; AltName: Full=Protein choker
Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316 - ORF 1 (frame 1) translation	Locus_1_Transcript_42793/166847_Confidence_1.000_Length_1316
Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968 - ORF 1 (frame 1) translation	Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968
Locus_1_Transcript_139848/166847_Confidence_1.000_Length_1898 - ORF 1 (frame 3) translation	Locus_1_Transcript_139848/166847_Confidence_1.000_Length_1898

Locus_1062_Transcript_9/9_Confidence_0.617_Length_5291 - ORF 5 (frame 3) translation	Locus_1062_Transcript_9/9_Confidence_0.617_Length_5291
Locus_6950_Transcript_21/21_Confidence_0.338_Length_6167 - ORF 36 (frame 1) translation	Locus_6950_Transcript_21/21_Confidence_0.338_Length_6167
Locus_9055_Transcript_1/4_Confidence_0.444_Length_2455 - ORF 2 (frame 3) translation	Locus_9055_Transcript_1/4_Confidence_0.444_Length_2455
Locus_12254_Transcript_10/10_Confidence_0.571_Length_6893 - ORF 7 (frame 1) translation	Locus_12254_Transcript_10/10_Confidence_0.571_Length_6893
Locus_13060_Transcript_11/11_Confidence_0.100_Length_1423 - ORF 6 (frame 2) translation	Locus_13060_Transcript_11/11_Confidence_0.100_Length_1423
Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293 - ORF 1 (frame 1) translation	Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293
Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736 - ORF 18 (frame 2) translation	Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736
Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590 - ORF 4 (frame 1) translation	Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590
Locus_16591_Transcript_1/5_Confidence_0.500_Length_2820 - ORF 14 (frame 3) translation	Locus_16591_Transcript_1/5_Confidence_0.500_Length_2820
Locus_16600_Transcript_5/5_Confidence_0.667_Length_2737 - ORF 3 (frame 3) translation	Locus_16600_Transcript_5/5_Confidence_0.667_Length_2737
Locus_16603_Transcript_2/2_Confidence_0.667_Length_1062 - ORF 3 (frame 1) translation	Locus_16603_Transcript_2/2_Confidence_0.667_Length_1062
Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305 - ORF 1 (frame 3) translation	Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305
Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037 - ORF 2 (frame 2) translation	Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037
Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275 - ORF 3 (frame 3) translation	Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275
NP_001034519	abdominal-B [Tribolium castaneum]
NP_001034523	cephalothorax [Tribolium castaneum]
NP_001037341	transcription factor deformed [Bombyx mori]
NP_001037550	segmentation polarity homeobox protein engrailed [Bombyx mori]
NP_001091156	homeobox protein Hox-D3 [Xenopus laevis]
NP_001107762	labial [Tribolium castaneum]
NP_001158372	engrailed homeobox [Saccoglossus kowalevskii]
NP_001162171	ultrabithorax [Apis mellifera]
O02491 (HMEN_ANOGA)	RecName: Full=Segmentation polarity homeobox protein engrailed
O13074 (HXB4A_TAKRU)	RecName: Full=Homeobox protein Hox-B4a; AltName: Full=FrHOXB-4
O42230 (GBX2_CHICK)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
O42365 (HXA2B_DANRE)	RecName: Full=Homeobox protein Hox-A2b; Short=Hox-A2
O42366 (HXB1A_DANRE)	RecName: Full=Homeobox protein Hox-B1a; Short=Hox-B1
O42367 (HXB2A_DANRE)	RecName: Full=Homeobox protein Hox-B2a; Short=Hox-B2
O42370 (HXD3A_DANRE)	RecName: Full=Homeobox protein Hox-D3a; Short=Hox-D3
O43364 (HXA2_HUMAN)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1K
O43365 (HXA3_HUMAN)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1E
O57374 (HXD4A_DANRE)	RecName: Full=Homeobox protein Hox-D4a; Short=Hox-D4
O76762 (ABDA_ANOGA)	RecName: Full=Homeobox protein abdominal-A homolog
O93353 (HXA3_CHICK)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-D3
P0C1T1 (HXB2_MOUSE)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8
P02830 (HXA7_MOUSE)	RecName: Full=Homeobox protein Hox-A7; AltName: Full=Homeobox protein Hox-1.1; AltName: Full=Homeobox protein M6-12; Short=M6
P02831 (HXA3_MOUSE)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1.5; AltName: Full=Homeobox protein MO-10
P02833 (ANTP_DROME)	RecName: Full=Homeotic protein antennapedia
P02836 (HMEN_DROME)	RecName: Full=Segmentation polarity homeobox protein engrailed
P04476 (HXB7B_XENLA)	RecName: Full=Homeobox protein Hox-B7-B; AltName: Full=P52; AltName: Full=XlHbox-2 B
P07548 (DFD_DROME)	RecName: Full=Homeotic protein deformed
P09013 (HXB5B_DANRE)	RecName: Full=Homeobox protein Hox-B5b; AltName: Full=Homeobox protein Zf-54; AltName: Full=Hox-B5-like
P09014 (HXB5A_DANRE)	RecName: Full=Homeobox protein Hox-B5a; Short=Hox-B5; AltName: Full=Homeobox protein Zf-21
P09015 (HME2A_DANRE)	RecName: Full=Homeobox protein engrailed-2a; Short=Homeobox protein en-2a; AltName: Full=Zf-En-2
P09016 (HXD4_HUMAN)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein HHO.C13; AltName: Full=Homeobox protein Hox-4B; AltName: Full=Homeobox protein Hox-5.1
P09017 (HXC4_HUMAN)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein CP19; AltName: Full=Homeobox protein Hox-3E
P09022 (HXA1_MOUSE)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Early retinoic acid 1; AltName: Full=Homeobox protein Hox-1.6; AltName: Full=Homeoboxless protein ERA-1-399; AltName: Full=Homeotic protein ERA-1-993
P09024 (HXB7_MOUSE)	RecName: Full=Homeobox protein Hox-B7; AltName: Full=Homeobox protein Hox-2.3; AltName: Full=Homeobox protein MH-22B; AltName: Full=Homeobox protein MuB1
P09067 (HXB5_HUMAN)	RecName: Full=Homeobox protein Hox-B5; AltName: Full=Homeobox protein HHO.C10; AltName: Full=Homeobox protein Hox-2A; AltName: Full=Homeobox protein Hu-1
P09077 (SCR_DROME)	RecName: Full=Homeotic protein Sex combs reduced
P09079 (HXB5_MOUSE)	RecName: Full=Homeobox protein Hox-B5; AltName: Full=Homeobox protein H24.1; AltName: Full=Homeobox protein Hox-2.1; AltName: Full=Homeobox protein Mu-1
P09087 (ABDB_DROME)	RecName: Full=Homeobox protein abdominal-B; AltName: Full=Infraabdominal 7; Short=IAB-7; AltName: Full=P3; AltName: Full=PH189

P09145 (HMEN_DROVI)	RecName: Full=Segmentation polarity homeobox protein engrailed
P09629 (HXB7_HUMAN)	RecName: Full=Homeobox protein Hox-B7; AltName: Full=Homeobox protein HHO.C1; AltName: Full=Homeobox protein Hox-2C
P09631 (HXA9_MOUSE)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1.7
P09638 (HXB2_SALSA)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=S6
P10105 (LAB_DROME)	RecName: Full=Homeotic protein labial; AltName: Full=F24; AltName: Full=F90-2
P10179 (HMB4_TRIGR)	RecName: Full=Homeobox protein HB4
P10628 (HXD4_MOUSE)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein Hox-4.2; AltName: Full=Homeobox protein Hox-5.1
P14652 (HXB2_HUMAN)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8; AltName: Full=Homeobox protein Hox-2H; AltName: Full=K8
P14837 (PDX1_XENLA)	RecName: Full=Pancreas/duodenum homeobox protein 1; Short=PDX-1; AltName: Full=Homeobox protein 8; Short=XlHbox-8
P14840 (HXB4_CHICK)	RecName: Full=Homeobox protein Hox-B4; AltName: Full=Homeobox protein Hox-Z; Short=Chox-Z
P15142 (HM7X_CHICK)	RecName: Full=Homeobox protein CHOX-7
P17278 (HXD4_CHICK)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein Hox-A; Short=Chox-A
P18864 (HXB7_RAT)	RecName: Full=Homeobox protein Hox-B7; AltName: Full=Homeobox protein R1B
P20822 (UBX_DROPS)	RecName: Full=Homeotic protein ultrabithorax
P22574 (HXB4A_DANRE)	RecName: Full=Homeobox protein Hox-B4a; Short=Hox-B4; AltName: Full=Homeobox protein Zf-13
P24340 (HXD9_CHICK)	RecName: Full=Homeobox protein Hox-D9; AltName: Full=Homeobox protein Hox-4.4; Short=Chox-4.4
P27609 (HMEN_BOMMO)	RecName: Full=Segmentation polarity homeobox protein engrailed
P27610 (HMIN_BOMMO)	RecName: Full=Homeobox protein invected
P29552 (ABDA_AEDAE)	RecName: Full=Homeobox protein abdominal-A homolog
P29555 (ABDA_DROME)	RecName: Full=Homeobox protein abdominal-A
P31245 (HXA2_MOUSE)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11; Short=Hox1.11
P31246 (HXA2_RAT)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11
P31249 (HXD3_HUMAN)	RecName: Full=Homeobox protein Hox-D3; AltName: Full=Homeobox protein Hox-4A
P31259 (HXB1_CHICK)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=Ghox-lab
P31261 (HXA2_NOTVI)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hbox-2.8; Short=NvHbox-2.8
P31264 (HMPB_DROME)	RecName: Full=Homeotic protein proboscipedia
P31269 (HXA9_HUMAN)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1G
P31357 (HXB1_AMBME)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=AHox1
P32442 (MEOX1_MOUSE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P32443 (MEOX2_MOUSE)	RecName: Full=Homeobox protein MOX-2; AltName: Full=Mesenchyme homeobox 2
P39020 (MEOX2_RAT)	RecName: Full=Homeobox protein MOX-2; AltName: Full=Growth arrest-specific homeobox; AltName: Full=Mesenchyme homeobox 2
P39021 (MEOX2_XENLA)	RecName: Full=Homeobox protein MOX-2
P48031 (GBX2_MOUSE)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=Stimulated by retinoic acid gene 7 protein
P49639 (HXA1_HUMAN)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Homeobox protein Hox-1F
P50209 (HXA9_AMBME)	RecName: Full=Homeobox protein Hox-A9
P50219 (MNX1_HUMAN)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
P50221 (MEOX1_HUMAN)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P50222 (MEOX2_HUMAN)	RecName: Full=Homeobox protein MOX-2; AltName: Full=Growth arrest-specific homeobox; AltName: Full=Mesenchyme homeobox 2
P50901 (HOX3_BRAFL)	RecName: Full=Homeobox protein HOX3
P51783 (HXA9_CAVPO)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1.7
P52729 (HME2A_XENLA)	RecName: Full=Homeobox protein engrailed-2-A; Short=En-2A; Short=Homeobox protein en-2-A; AltName: Full=En2 1.4
P52730 (HME2B_XENLA)	RecName: Full=Homeobox protein engrailed-2-B; Short=En-2B; Short=Homeobox protein en-2-B; AltName: Full=En2 MABEN
P52951 (GBX2_HUMAN)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
P70118 (PDX1_MESAU)	RecName: Full=Pancreas/duodenum homeobox protein 1; AltName: Full=Homeodomain protein PDX1; AltName: Full=Insulin promoter factor 1; Short=IPF-1
P82976 (GBX1_MOUSE)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
P83949 (UBX_DROME)	RecName: Full=Homeotic protein ultrabithorax
Q0VCS4 (HXA2_BOVIN)	RecName: Full=Homeobox protein Hox-A2
Q1KKR6 (HXD4B_TAKRU)	RecName: Full=Homeobox protein Hox-D4b
Q1KKS8 (HXD4A_TAKRU)	RecName: Full=Homeobox protein Hox-D4a
Q1KKU6 (HXC4A_TAKRU)	RecName: Full=Homeobox protein Hox-C4a
Q1KKX0 (HXB5B_TAKRU)	RecName: Full=Homeobox protein Hox-B5b
Q1KKZ2 (HXA2B_TAKRU)	RecName: Full=Homeobox protein Hox-A2b
Q1KL10 (HXA1A_TAKRU)	RecName: Full=Homeobox protein Hox-A1a
Q1KL14 (HXA5A_TAKRU)	RecName: Full=Homeobox protein Hox-A5a
Q3V5Z9 (HXD3_ORYLA)	RecName: Full=Homeobox protein Hox-D3
Q4V5A3 (UNPG_DROME)	RecName: Full=Homeobox protein unplugged
Q6B3N0 (HXA5_CHICK)	RecName: Full=Homeobox protein Hox-A5
Q8AWY9 (HXB7A_DANRE)	RecName: Full=Homeobox protein Hox-B7a; Short=Hox-B7

Q08DG7 (HXA3_BOVIN)	RecName: Full=Homeobox protein Hox-A3
Q8T940 (UBX_JUNCO)	RecName: Full=Homeotic protein ultrabithorax; AltName: Full=JcUbx
Q9GZZ0 (HXD1_HUMAN)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-GG
Q9IA19 (HXA1_HETFR)	RecName: Full=Homeobox protein Hox-A1
Q9IA20 (HXA2_HETFR)	RecName: Full=Homeobox protein Hox-A2
Q9IA21 (HXA3_HETFR)	RecName: Full=Homeobox protein Hox-A3
Q9IA22 (HXA4_HETFR)	RecName: Full=Homeobox protein Hox-A4
Q9IA23 (HXA5_HETFR)	RecName: Full=Homeobox protein Hox-A5
Q9IA25 (HXA7_HETFR)	RecName: Full=Homeobox protein Hox-A7
Q9IA26 (HXA9_HETFR)	RecName: Full=Homeobox protein Hox-A9
Q9PWM3 (HXC4A_DANRE)	RecName: Full=Homeobox protein Hox-C4a; Short=Hox-C4
Q9QZW9 (MNX1_MOUSE)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
Q9TT89 (HXB7_BOVIN)	RecName: Full=Homeobox protein Hox-B7
Q9YGT5 (HXA9B_DANRE)	RecName: Full=Homeobox protein Hox-A9b
Q9YGT6 (HXA5A_DANRE)	RecName: Full=Homeobox protein Hox-A5a
Q28IU6 (HXD1_XENTR)	RecName: Full=Homeobox protein Hox-D1
Q28ZA9 (UNPG_DROPS)	RecName: Full=Homeobox protein unplugged
Q90VZ9 (HXA7_CHICK)	RecName: Full=Homeobox protein Hox-A7
Q98SI1 (HXA1A_DANRE)	RecName: Full=Homeobox protein Hox-A1a; Short=Hox-A1
Q01822 (HXD1_MOUSE)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-4.9
Q04896 (HME1A_DANRE)	RecName: Full=Homeobox protein engrailed-1a; Short=Homeobox protein en-1a
Q05007 (ABDA_ARTSF)	RecName: Full=Homeobox protein abdominal-A homolog
Q05640 (HMEN_ARTSF)	RecName: Full=Homeobox protein engrailed
Q07961 (ABDA_TRICA)	RecName: Full=Homeobox protein abdominal-A homolog
Q08624 (HXC4_MOUSE)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein Hox-3.5
Q08727 (HXA2_CHICK)	RecName: Full=Homeobox protein Hox-A2
Q08820 (HXD1_XENLA)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Hox.lab1; AltName: Full=Labial protein; Short=Xlab
Q08821 (HXA1_XENLA)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Hox.lab2
Q14549 (GBX1_HUMAN)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q24645 (ANTP_DROSU)	RecName: Full=Homeotic protein antennapedia
Q26430 (ABDA_MANSE)	RecName: Full=Homeobox protein abdominal-A homolog
Q90346 (HXB1_CYPCA)	RecName: Full=Homeobox protein Hox-B1
Q90423 (HXB1B_DANRE)	RecName: Full=Homeobox protein Hox-B1b; AltName: Full=Homeobox protein Hox-A1
Q91771 (HXB7A_XENLA)	RecName: Full=Homeobox protein Hox-B7-A; AltName: Full=MM3; AltName: Full=XlHbox-2 A
Q91907 (GBX2_XENLA)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=XGBX-2
Q98924 (HXA9_CHICK)	RecName: Full=Homeobox protein Hox-A9
XP_001120045	PREDICTED: homeotic protein deformed [Apis mellifera]
XP_001120278	PREDICTED: homeotic protein labial isoform X1 [Apis mellifera]
XP_001842674	homeotic deformed protein [Culex quinquefasciatus]
XP_002406412	homeobox protein Hox-A4, putative [Ixodes scapularis]
XP_002406420	homeobox protein, putative [Ixodes scapularis]
XP_002423066	Homeobox protein GBX-1, putative [Pediculus humanus corporis]
XP_002425762	Homeobox protein Hox-A11A, putative [Pediculus humanus corporis]
XP_003224963	PREDICTED: homeobox protein Hox-A3 [Anolis carolinensis]
XP_003393477	PREDICTED: homeobox protein engrailed-1a-like [Bombus terrestris]
XP_003489274	PREDICTED: homeobox protein engrailed-1a-like [Bombus impatiens]
XP_004524344	PREDICTED: homeotic protein antennapedia isoform X2 [Ceratitis capitata]
XP_004925027	PREDICTED: homeobox protein Hox-B4 [Bombyx mori]
XP_004933319	PREDICTED: segmentation polarity homeobox protein engrailed [Bombyx mori]
XP_005186014	PREDICTED: homeotic protein antennapedia isoform X4 [Musca domestica]
XP_005186016	PREDICTED: homeotic protein antennapedia isoform X6 [Musca domestica]
XP_006559409	PREDICTED: ultrabithorax isoform X5 [Apis mellifera]
XP_006559411	PREDICTED: homeotic protein labial isoform X2 [Apis mellifera]
XP_006610893	PREDICTED: homeotic protein ultrabithorax-like isoform X3 [Apis dorsata]
XP_006611901	PREDICTED: homeotic protein labial-like isoform X1 [Apis dorsata]
XP_006611902	PREDICTED: homeotic protein labial-like isoform X2 [Apis dorsata]
XP_007651972	PREDICTED: homeobox protein GBX-2 [Cricetulus griseus]
XP_008195160	PREDICTED: homeobox protein Hox-D4a [Tribolium castaneum]
XP_008201245	PREDICTED: cephalothorax isoform X1 [Tribolium castaneum]
XP_008487962	PREDICTED: homeotic protein deformed [Diaphorina citri]
XP_008559758	PREDICTED: homeotic protein ultrabithorax isoform X2 [Microplitis demolitor]
XP_008559760	PREDICTED: homeotic protein antennapedia [Microplitis demolitor]
XP_008943920	PREDICTED: homeobox protein MOX-2-like [Merops nubicus]
XP_009201571	PREDICTED: homeobox protein MOX-2-like [Papio anubis]
XP_009279321	PREDICTED: homeobox protein MOX-2-like [Aptenodytes forsteri]
XP_009281268	PREDICTED: homeobox protein MOX-1 [Aptenodytes forsteri]
XP_009324945	PREDICTED: homeobox protein MOX-1 [Pygoscelis adeliae]
XP_009574521	PREDICTED: homeobox protein MOX-2-like [Fulmarus glacialis]
XP_009870132	PREDICTED: homeobox protein Hox-B1, partial [Apaloderma vittatum]
XP_009945175	PREDICTED: homeobox protein MOX-2-like, partial [Leptosomus discolor]
XP_009952238	PREDICTED: homeobox protein MOX-1, partial [Leptosomus discolor]
XP_009962682	PREDICTED: homeobox protein Hox-B1, partial [Tyto alba]
XP_010010160	PREDICTED: homeobox protein MOX-2-like [Nestor notabilis]

XP_010397692	PREDICTED: homeobox protein MOX-2 [Corvus cornix cornix]
XP_011055476	PREDICTED: homeotic protein proboscipedia isoform X2 [Acromyrmex echinatior]
XP_011055478	PREDICTED: homeobox protein Hox-B1a [Acromyrmex echinatior]
XP_011139005	PREDICTED: segmentation polarity homeobox protein engrailed-like [Harpegnathos saltator]
XP_011148733	PREDICTED: homeotic protein labial-like [Harpegnathos saltator]
XP_011148808	PREDICTED: homeotic protein antennapedia [Harpegnathos saltator]
XP_011149287	PREDICTED: homeotic protein proboscipedia [Harpegnathos saltator]
XP_011155414	PREDICTED: homeotic protein proboscipedia [Solenopsis invicta]
XP_011256041	PREDICTED: homeotic protein deformed [Camponotus floridanus]
XP_011258058	PREDICTED: homeotic protein ultrabithorax [Camponotus floridanus]
XP_011258060	PREDICTED: homeotic protein antennapedia-like [Camponotus floridanus]
XP_011258070	PREDICTED: homeobox protein abdominal-B [Camponotus floridanus]
XP_011269817	PREDICTED: homeobox protein Hox-B1a-like [Camponotus floridanus]
XP_011283973	PREDICTED: homeobox protein GBX-2 [Felis catus]
XP_011294141	PREDICTED: homeotic protein labial-like, partial [Musca domestica]
XP_011310234	PREDICTED: homeobox protein GBX-2 [Fopius arisanus]
XP_011311710	PREDICTED: homeobox protein abdominal-B isoform X1 [Fopius arisanus]
XP_011311711	PREDICTED: homeobox protein abdominal-B isoform X2 [Fopius arisanus]
XP_011311712	PREDICTED: homeobox protein abdominal-B isoform X3 [Fopius arisanus]
XP_011342229	PREDICTED: homeobox protein Hox-B1a-like [Cerapachys biroi]
XP_011342230	PREDICTED: homeotic protein proboscipedia [Cerapachys biroi]
XP_011414445	PREDICTED: homeobox protein GBX-2-like [Crassostrea gigas]
XP_011414452	PREDICTED: homeobox protein engrailed-1-B-like [Crassostrea gigas]
XP_011555707	PREDICTED: homeotic protein Sex combs reduced [Plutella xylostella]
XP_011555719	PREDICTED: homeobox protein Hox-C4 [Plutella xylostella]
XP_011569017	PREDICTED: homeobox protein Hox-B4-like [Plutella xylostella]
XP_011639093	PREDICTED: homeotic protein proboscipedia [Pogonomyrmex barbatus]
XP_011639094	PREDICTED: homeobox protein Hox-B1 [Pogonomyrmex barbatus]
XP_011695898	PREDICTED: homeobox protein Hox-B1a-like [Wasmannia auropunctata]
XP_011695901	PREDICTED: homeotic protein proboscipedia [Wasmannia auropunctata]
XP_011695906	PREDICTED: homeotic protein antennapedia [Wasmannia auropunctata]
XP_011870664	PREDICTED: homeotic protein proboscipedia [Vollenhovia emeryi]
XP_011870669	PREDICTED: homeotic protein antennapedia [Vollenhovia emeryi]
XP_012054481	PREDICTED: homeotic protein proboscipedia [Atta cephalotes]
XP_012054482	PREDICTED: homeobox protein Hox-B1a [Atta cephalotes]
XP_012154268	PREDICTED: homeotic protein antennapedia [Megachile rotundata]
XP_012225633	PREDICTED: homeotic protein proboscipedia [Linepithema humile]
XP_012226417	PREDICTED: homeotic protein antennapedia-like [Linepithema humile]
XP_012259195	PREDICTED: homeotic protein antennapedia-like [Athalia rosae]
XP_012267082	PREDICTED: homeotic protein ultrabithorax [Athalia rosae]
XP_012276293	PREDICTED: homeotic protein labial [Orussus abietinus]
XP_012276321	PREDICTED: homeobox protein Hox-A4 [Orussus abietinus]
XP_012347968	PREDICTED: homeobox protein Hox-B1a-like [Apis florea]
XP_012427106	PREDICTED: homeobox protein Hox-A3 isoform X2 [Taeniopygia guttata]
XP_012524736	PREDICTED: homeotic protein antennapedia [Monomorium pharaonis]
XP_012524740	PREDICTED: homeobox protein Hox-A4 [Monomorium pharaonis]
XP_012542576	PREDICTED: homeotic protein proboscipedia [Monomorium pharaonis]
XP_013063618	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Biomphalaria glabrata]
XP_013104192	PREDICTED: homeotic protein labial-like [Stomoxys calcitrans]
XP_013106133	PREDICTED: homeobox protein unplugged-like, partial [Stomoxys calcitrans]
XP_013139547	PREDICTED: homeobox protein Hox-B4 [Papilio polytes]
XP_013139806	PREDICTED: homeotic protein Sex combs reduced-like [Papilio polytes]
XP_013154388	PREDICTED: homeobox protein Hox-A3 isoform X2 [Falco peregrinus]
XP_013177038	PREDICTED: homeobox protein GBX-2-like [Papilio xuthus]
XP_013185500	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Amyelois transitella]
XP_013188268	PREDICTED: segmentation polarity homeobox protein engrailed-like [Amyelois transitella]
XP_013193972	PREDICTED: homeobox protein Hox-B4 [Amyelois transitella]
XP_013194077	PREDICTED: homeotic protein Sex combs reduced-like [Amyelois transitella]
XP_013399159	PREDICTED: homeobox protein Hox-A3-like isoform X1 [Lingula anatina]
XP_013399161	PREDICTED: homeobox protein Hox-D3-like isoform X2 [Lingula anatina]
XP_013772903	PREDICTED: homeobox protein engrailed-1-B-like [Limulus polyphemus]
XP_013775825	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013776721	PREDICTED: homeotic protein antennapedia-like [Limulus polyphemus]
XP_013776724	PREDICTED: homeobox protein Hox-A4-like [Limulus polyphemus]
XP_013776725	PREDICTED: homeobox protein Hox-B4a-like [Limulus polyphemus]

XP_013777105	PREDICTED: homeobox protein Hox-A3a-like [Limulus polyphemus]
XP_013777106	PREDICTED: protein enabled homolog [Limulus polyphemus]
XP_013777707	PREDICTED: homeobox protein abdominal-B-like [Limulus polyphemus]
XP_013784402	PREDICTED: homeobox protein Hox-B4-like [Limulus polyphemus]
XP_013786746	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013790370	PREDICTED: homeobox protein Hox-A4-like [Limulus polyphemus]
XP_013790991	PREDICTED: homeotic protein proboscipedia-like, partial [Limulus polyphemus]
XP_013792062	PREDICTED: homeotic protein ultrabithorax-like, partial [Limulus polyphemus]
XP_013792158	PREDICTED: homeobox protein Hox-D4-like [Limulus polyphemus]
XP_013794100	PREDICTED: homeobox protein Hox-B4-like, partial [Limulus polyphemus]
XP_013794102	PREDICTED: homeobox protein Hox-B7-B-like [Limulus polyphemus]
XP_013794103	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013794105	PREDICTED: homeobox protein abdominal-B-like [Limulus polyphemus]
XP_013794355	PREDICTED: homeobox protein unplugged-like [Limulus polyphemus]
XP_014128632	PREDICTED: homeobox protein Hox-A3 [Zonotrichia albicollis]
XP_014162805	PREDICTED: homeobox protein Hox-A3 isoform X2 [Geospiza fortis]
XP_014219299	PREDICTED: homeotic protein ultrabithorax-like isoform X2 [Copidosoma floridanum]
XP_014240108	PREDICTED: homeobox protein Hox-B4 isoform X1 [Cimex lectularius]
XP_014240109	PREDICTED: homeobox protein Hox-B4 isoform X2 [Cimex lectularius]
XP_014240565	PREDICTED: homeobox protein abdominal-B isoform X1 [Cimex lectularius]
XP_014240567	PREDICTED: homeobox protein abdominal-B isoform X2 [Cimex lectularius]
XP_014240605	PREDICTED: homeotic protein Sex combs reduced-like [Cimex lectularius]
XP_014274798	PREDICTED: homeotic protein antennapedia-like isoform X1 [Halyomorpha halys]
XP_014274854	PREDICTED: homeotic protein antennapedia-like isoform X2 [Halyomorpha halys]
XP_014275091	PREDICTED: homeotic protein Sex combs reduced [Halyomorpha halys]
XP_014359216	PREDICTED: homeotic protein Sex combs reduced [Papilio machaon]
XP_014436686	PREDICTED: homeobox protein Hox-A3 [Pelodiscus sinensis]

9.4.2.19 *Klumpfuss*

Name	**Description**
A1YF12 (ZNF16_GORGO)	RecName: Full=Zinc finger protein 16
A1YG88 (ZNF16_PANPA)	RecName: Full=Zinc finger protein 16
A2T759 (ZNF16_PANTR)	RecName: Full=Zinc finger protein 16
A4II20 (EGR1_XENTR)	RecName: Full=Early growth response protein 1; Short=EGR-1
A6NJL1 (ZSA5B_HUMAN)	RecName: Full=Zinc finger and SCAN domain-containing protein 5B
A6NNF4 (ZN726_HUMAN)	RecName: Full=Zinc finger protein 726
AAF50119	klumpfuss, isoform A [Drosophila melanogaster]
Locus_486_Transcript_2/2_Confidence_0.870_Length_1105 - ORF 6 (frame 1) translation	Locus_486_Transcript_2/2_Confidence_0.870_Length_1105
Locus_2332_Transcript_20/26_Confidence_0.116_Length_1397 - ORF 10 (frame 3) translation	Locus_2332_Transcript_20/26_Confidence_0.116_Length_1397
Locus_3756_Transcript_6/6_Confidence_0.789_Length_615 - ORF 4 (frame 3) translation	Locus_3756_Transcript_6/6_Confidence_0.789_Length_615
Locus_3805_Transcript_4/9_Confidence_0.360_Length_437 - ORF 1 (frame 2) translation	Locus_3805_Transcript_4/9_Confidence_0.360_Length_437
Locus_5949_Transcript_10/10_Confidence_0.667_Length_4947 - ORF 3 (frame 2) translation	Locus_5949_Transcript_10/10_Confidence_0.667_Length_4947
Locus_7469_Transcript_20/25_Confidence_0.014_Length_749 - ORF 1 (frame 1) translation	Locus_7469_Transcript_20/25_Confidence_0.014_Length_749
Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420 - ORF 2 (frame 2) translation	Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420
Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450 - ORF 25 (frame 1) translation	Locus_20774_Transcript_1/1_Confidence_1.000_Length_4450
O73693 (EGR1_TAEGU)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Zinc finger protein ZENK
P0C6Y7 (PRDM9_RAT)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
P08046 (EGR1_MOUSE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein Krox-24
P08154 (EGR1_RAT)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein Krox-24
P10073 (ZSC22_HUMAN)	RecName: Full=Zinc finger and SCAN domain-containing protein 22; AltName: Full=Krueppel-related zinc finger protein 2; AltName: Full=Protein HKR2; AltName: Full=Zinc finger protein 50
P17020 (ZNF16_HUMAN)	RecName: Full=Zinc finger protein 16; AltName: Full=Zinc finger protein KOX9
P17041 (ZNF32_HUMAN)	RecName: Full=Zinc finger protein 32; AltName: Full=C2H2-546; AltName: Full=Zinc finger protein KOX30

P18146 (EGR1_HUMAN)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=AT225; AltName: Full=Nerve growth factor-induced protein A; Short=NGFI-A; AltName: Full=Transcription factor ETR103; AltName: Full=Transcription factor Zif268; AltName: Full=Zinc finger protein 225; AltName: Full=Zinc finger protein Krox-24
P18724 (ZG49_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF49.1
P18725 (ZG5_XENLA)	RecName: Full=Gastrula zinc finger protein 5-1; AltName: Full=XlCGF5.1
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P18731 (ZG62_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF62.1
P18735 (ZG7_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF7.1
P18737 (ZG8_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF8.2DB
P18750 (ZO61_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF6.1
P26632 (EGR1_DANRE)	RecName: Full=Early growth response protein 1; Short=EGR-1; AltName: Full=Zinc finger protein Krox-24
P43300 (EGR3_MOUSE)	RecName: Full=Early growth response protein 3; Short=EGR-3
P43301 (EGR3_RAT)	RecName: Full=Early growth response protein 3; Short=EGR-3
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
P51786 (ZN157_HUMAN)	RecName: Full=Zinc finger protein 157; AltName: Full=Zinc finger protein HZF22
P52742 (ZN135_HUMAN)	RecName: Full=Zinc finger protein 135; AltName: Full=Zinc finger protein 61; AltName: Full=Zinc finger protein 78-like 1
Q0VGE8 (ZN816_HUMAN)	RecName: Full=Zinc finger protein 816
Q3MJ62 (ZSC23_HUMAN)	RecName: Full=Zinc finger and SCAN domain-containing protein 23; AltName: Full=Zinc finger protein 390; AltName: Full=Zinc finger protein 453
Q3ZCT1 (ZN260_HUMAN)	RecName: Full=Zinc finger protein 260; Short=Zfp-260
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4R6C2 (ZN383_MACFA)	RecName: Full=Zinc finger protein 383
Q5R5U3 (ZN271_PONAB)	RecName: Full=Zinc finger protein 271
Q5R5Y7 (ZN436_PONAB)	RecName: Full=Zinc finger protein 436
Q5R8G9 (ZN239_PONAB)	RecName: Full=Zinc finger protein 239
Q5RCJ2 (ZN614_PONAB)	RecName: Full=Zinc finger protein 614
Q5VIY5 (ZN468_HUMAN)	RecName: Full=Zinc finger protein 468
Q6GQH4 (EGR1A_XENLA)	RecName: Full=Early growth response protein 1-A; Short=EGR-1-A; Short=Xegr-1
Q6NTY6 (EGR1B_XENLA)	RecName: Full=Early growth response protein 1-B; Short=EGR-1-B
Q6ZMS4 (ZN852_HUMAN)	RecName: Full=Zinc finger protein 852
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q7L3S4 (ZN771_HUMAN)	RecName: Full=Zinc finger protein 771; AltName: Full=Mesenchymal stem cell protein DSC43
Q8BJ90 (ZN771_MOUSE)	RecName: Full=Zinc finger protein 771
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q8BQC8 (RBAK_MOUSE)	RecName: Full=RB-associated KRAB zinc finger protein; AltName: Full=RB-associated KRAB repressor; AltName: Full=Zinc finger protein 769
Q08DG8 (ZN135_BOVIN)	RecName: Full=Zinc finger protein 135
Q8N883 (ZN614_HUMAN)	RecName: Full=Zinc finger protein 614
Q8NA42 (ZN383_HUMAN)	RecName: Full=Zinc finger protein 383
Q8WV37 (ZN480_HUMAN)	RecName: Full=Zinc finger protein 480
Q9BSK1 (ZN577_HUMAN)	RecName: Full=Zinc finger protein 577
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q9NQV7 (PRDM9_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q9NQZ8 (ZNF71_HUMAN)	RecName: Full=Endothelial zinc finger protein induced by tumor necrosis factor alpha; AltName: Full=Zinc finger protein 71
Q9P0L1 (ZKSC7_HUMAN)	RecName: Full=Zinc finger protein with KRAB and SCAN domains 7; AltName: Full=Zinc finger protein 167; AltName: Full=Zinc finger protein 448; AltName: Full=Zinc finger protein 64
Q9UJN7 (ZN391_HUMAN)	RecName: Full=Zinc finger protein 391
Q9UJW8 (ZN180_HUMAN)	RecName: Full=Zinc finger protein 180; AltName: Full=HHZ168
Q80V23 (ZNF32_MOUSE)	RecName: Full=Zinc finger protein 32; AltName: Full=Zinc finger protein 637
Q80YP6 (ZIK1_MOUSE)	RecName: Full=Zinc finger protein interacting with ribonucleoprotein K
Q95K49 (ZN614_MACFA)	RecName: Full=Zinc finger protein 614
Q96EQ9 (PRDM9_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=Hybrid sterility protein 1; AltName: Full=Meiosis-induced factor containing a PR/SET domain and zinc-finger motif; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q96NI8 (ZN570_HUMAN)	RecName: Full=Zinc finger protein 570
Q96RE9 (ZN300_HUMAN)	RecName: Full=Zinc finger protein 300
Q06889 (EGR3_HUMAN)	RecName: Full=Early growth response protein 3; Short=EGR-3; AltName: Full=Zinc finger protein pilot
Q07230 (ZSCA2_MOUSE)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29; Short=Zfp-29
Q14591 (ZN271_HUMAN)	RecName: Full=Zinc finger protein 271; AltName: Full=CT-ZFP48; AltName: Full=Epstein-Barr virus-induced zinc finger protein; Short=EBV-induced zinc finger protein; Short=ZNF-EB; AltName: Full=Zinc finger protein HZF7; AltName: Full=Zinc finger protein ZNFphex133; AltName: Full=Zinc finger protein dp; Short=ZNF-dp

Q16600 (ZN239_HUMAN)	RecName: Full=Zinc finger protein 239; AltName: Full=Zinc finger protein HOK-2; AltName: Full=Zinc finger protein MOK-2
Q28151 (OZF_BOVIN)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q62981 (ZN260_RAT)	RecName: Full=Zinc finger protein 260; Short=Zfp-260; AltName: Full=Pancreas-only zinc finger protein 1; Short=POZF-1
XP_001101733	PREDICTED: zinc finger and SCAN domain-containing protein 22-like [Macaca mulatta]
XP_001943786	PREDICTED: transcriptional regulator CRZ2-like [Acyrthosiphon pisum]
XP_001945654	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001950651	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_002426166	Early growth response protein, putative [Pediculus humanus corporis]
XP_003744232	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Metaseiulus occidentalis]
XP_005187275	PREDICTED: protein ovo [Musca domestica]
XP_005258922	PREDICTED: zinc finger and SCAN domain-containing protein 22 isoform X2 [Homo sapiens]
XP_005817136	PREDICTED: zinc finger protein OZF-like, partial [Xiphophorus maculatus]
XP_006263331	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Alligator mississippiensis]
XP_006643481	PREDICTED: zinc finger protein 180-like, partial [Lepisosteus oculatus]
XP_006806237	PREDICTED: zinc finger protein 569-like [Neolamprologus brichardi]
XP_007474749	PREDICTED: zinc finger protein 135-like isoform X1 [Monodelphis domestica]
XP_007474751	PREDICTED: zinc finger protein 135-like isoform X3 [Monodelphis domestica]
XP_007474752	PREDICTED: zinc finger protein 135-like isoform X4 [Monodelphis domestica]
XP_007505885	PREDICTED: zinc finger protein 2 homolog, partial [Monodelphis domestica]
XP_007506319	PREDICTED: zinc finger protein 135-like, partial [Monodelphis domestica]
XP_007540545	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007540550	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007561960	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Poecilia formosa]
XP_007566619	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_008180544	PREDICTED: zinc finger protein 239-like [Acyrthosiphon pisum]
XP_008181583	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_008188255	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_008192563	PREDICTED: early growth response protein 1 [Tribolium castaneum]
XP_008200855	PREDICTED: early growth response protein 1-B isoform X1 [Tribolium castaneum]
XP_008200856	PREDICTED: early growth response protein 1-B isoform X2 [Tribolium castaneum]
XP_008400230	PREDICTED: zinc finger protein OZF-like [Poecilia reticulata]
XP_008483045	PREDICTED: early growth response protein 1-like [Diaphorina citri]
XP_009298784	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298863	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298936	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_011619604	PREDICTED: zinc finger protein 420-like, partial [Takifugu rubripes]
XP_011678015	PREDICTED: zinc finger protein 84-like isoform X1 [Strongylocentrotus purpuratus]
XP_011678017	PREDICTED: zinc finger protein 84-like isoform X2 [Strongylocentrotus purpuratus]
XP_011750032	PREDICTED: zinc finger and SCAN domain-containing protein 22 [Macaca nemestrina]
XP_011824483	PREDICTED: zinc finger and SCAN domain-containing protein 22 [Mandrillus leucophaeus]
XP_011931660	PREDICTED: zinc finger and SCAN domain-containing protein 22 [Cercocebus atys]
XP_012268167	PREDICTED: zinc finger protein 362 [Athalia rosae]
XP_012350277	PREDICTED: probable serine/threonine-protein kinase DDB_G0282963 [Apis florea]
XP_012409188	PREDICTED: zinc finger protein 208-like [Sarcophilus harrisii]
XP_012710330	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012713484	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Fundulus heteroclitus]
XP_012713624	PREDICTED: gastrula zinc finger protein XlCGF49.1-like, partial [Fundulus heteroclitus]
XP_012808752	PREDICTED: zinc finger protein 208-like isoform X1 [Xenopus (Silurana) tropicalis]
XP_012808753	PREDICTED: zinc finger protein 850-like isoform X2 [Xenopus (Silurana) tropicalis]

XP_012808756	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Xenopus (Silurana) tropicalis]
XP_012810455	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_012821172	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_013763388	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Pundamilia nyererei]
XP_013773341	PREDICTED: serine-rich adhesin for platelets-like [Limulus polyphemus]
XP_013779401	PREDICTED: zinc finger protein 236-like [Limulus polyphemus]
XP_013780173	PREDICTED: early growth response protein 1-like [Limulus polyphemus]
XP_013782461	PREDICTED: Krueppel-like factor 10 [Limulus polyphemus]
XP_013782841	PREDICTED: early growth response protein 1-like [Limulus polyphemus]
XP_013782955	PREDICTED: zinc finger protein 267-like [Limulus polyphemus]
XP_013783281	PREDICTED: zinc finger protein 227-like [Limulus polyphemus]
XP_013785583	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013786860	PREDICTED: early growth response protein 1-A-like [Limulus polyphemus]
XP_013788334	PREDICTED: zinc finger protein 501-like [Limulus polyphemus]
XP_013790651	PREDICTED: zinc finger protein 681-like [Limulus polyphemus]
XP_013792351	PREDICTED: early growth response protein 2-like [Limulus polyphemus]
XP_013793148	PREDICTED: zinc finger protein 436-like, partial [Limulus polyphemus]
XP_013889698	PREDICTED: zinc finger protein OZF-like [Austrofundulus limnaeus]
XP_014261801	PREDICTED: zinc finger and BTB domain-containing protein 7B [Cimex lectularius]
XP_014290163	PREDICTED: zinc finger and SCAN domain-containing protein 22 [Halyomorpha halys]
XP_014331042	PREDICTED: zinc finger protein OZF-like, partial [Xiphophorus maculatus]
XP_014382878	PREDICTED: oocyte zinc finger protein XlCOF6-like [Alligator sinensis]
XP_014459563	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Alligator mississippiensis]

9.4.2.20 *Krüppel*

Name	**Description**
A0JNB1 (ZN227_BOVIN)	RecName: Full=Zinc finger protein 227
A0PJY2 (FEZF1_HUMAN)	RecName: Full=Fez family zinc finger protein 1; AltName: Full=Zinc finger protein 312B
A1YF12 (ZNF16_GORGO)	RecName: Full=Zinc finger protein 16
A1YG88 (ZNF16_PANPA)	RecName: Full=Zinc finger protein 16
A2T759 (ZNF16_PANTR)	RecName: Full=Zinc finger protein 16
A2VDQ7 (ZN420_BOVIN)	RecName: Full=Zinc finger protein 420
A6NK53 (ZN233_HUMAN)	RecName: Full=Zinc finger protein 233
A6NNF4 (ZN726_HUMAN)	RecName: Full=Zinc finger protein 726
A6NP11 (ZN716_HUMAN)	RecName: Full=Zinc finger protein 716
A8MXY4 (ZNF99_HUMAN)	RecName: Full=Zinc finger protein 99
B4DU55 (ZN879_HUMAN)	RecName: Full=Zinc finger protein 879
BCL6_MOUSE	RecName: Full=B-cell lymphoma 6 protein homolog
BCL6B_MOUSE	RecName: Full=B-cell CLL/lymphoma 6 member B protein; AltName: Full=Bcl6-associated zinc finger protein
KRUP_DROME	RecName: Full=Protein krueppel
Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831 - ORF 1 (frame 2) translation	Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831
Locus_1_Transcript_164650/166847_Confidence_1.000_Length_439 - ORF 1 (frame 1) translation	Locus_1_Transcript_164650/166847_Confidence_1.000_Length_439
Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594 - ORF 3 (frame 1) translation	Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594
Locus_273_Transcript_17/26_Confidence_0.183_Length_1844 - ORF 8 (frame 1) translation	Locus_273_Transcript_17/26_Confidence_0.183_Length_1844
Locus_486_Transcript_2/2_Confidence_0.870_Length_1105 - ORF 6 (frame 1) translation	Locus_486_Transcript_2/2_Confidence_0.870_Length_1105
Locus_487_Transcript_29/38_Confidence_0.065_Length_3976 - ORF 13 (frame 1) translation	Locus_487_Transcript_29/38_Confidence_0.065_Length_3976
Locus_933_Transcript_1/10_Confidence_0.343_Length_1492 - ORF 2 (frame 3) translation	Locus_933_Transcript_1/10_Confidence_0.343_Length_1492
Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195 - ORF 3 (frame 2) translation	Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195
Locus_2332_Transcript_18/26_Confidence_0.116_Length_1397 - ORF 1 (frame 3) translation	Locus_2332_Transcript_18/26_Confidence_0.116_Length_1397
Locus_2787_Transcript_2/2_Confidence_0.625_Length_4210 - ORF 20 (frame 2) translation	Locus_2787_Transcript_2/2_Confidence_0.625_Length_4210
Locus_3805_Transcript_2/9_Confidence_0.400_Length_551 - ORF 2 (frame 2) translation	Locus_3805_Transcript_2/9_Confidence_0.400_Length_551
Locus_4666_Transcript_13/16_Confidence_0.319_Length_2381 - ORF 8 (frame 3) translation	Locus_4666_Transcript_13/16_Confidence_0.319_Length_2381
Locus_5373_Transcript_7/14_Confidence_0.085_Length_1057 - ORF 4 (frame 3) translation	Locus_5373_Transcript_7/14_Confidence_0.085_Length_1057
Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349 - ORF 20 (frame 1) translation	Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349

Locus_6712_Transcript_1/10_Confidence_0.278_Length_3684 - ORF 17 (frame 2) translation	Locus_6712_Transcript_1/10_Confidence_0.278_Length_3684
Locus_6998_Transcript_2/8_Confidence_0.408_Length_1146 - ORF 7 (frame 2) translation	Locus_6998_Transcript_2/8_Confidence_0.408_Length_1146
Locus_7469_Transcript_19/25_Confidence_0.009_Length_428 - ORF 1 (frame 1) translation	Locus_7469_Transcript_19/25_Confidence_0.009_Length_428
Locus_8141_Transcript_3/8_Confidence_0.625_Length_1969 - ORF 9 (frame 1) translation	Locus_8141_Transcript_3/8_Confidence_0.625_Length_1969
Locus_9749_Transcript_6/7_Confidence_0.769_Length_942 - ORF 3 (frame 1) translation	Locus_9749_Transcript_6/7_Confidence_0.769_Length_942
Locus_10669_Transcript_2/6_Confidence_0.600_Length_2997 - ORF 6 (frame 1) translation	Locus_10669_Transcript_2/6_Confidence_0.600_Length_2997
Locus_13183_Transcript_1/2_Confidence_0.889_Length_3060 - ORF 1 (frame 2) translation	Locus_13183_Transcript_1/2_Confidence_0.889_Length_3060
Locus_15252_Transcript_1/2_Confidence_0.800_Length_2057 - ORF 1 (frame 2) translation	Locus_15252_Transcript_1/2_Confidence_0.800_Length_2057
Locus_15787_Transcript_1/9_Confidence_0.486_Length_510 - ORF 1 (frame 1) translation	Locus_15787_Transcript_1/9_Confidence_0.486_Length_510
Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420 - ORF 2 (frame 2) translation	Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420
Locus_17002_Transcript_2/10_Confidence_0.314_Length_1340 - ORF 1 (frame 1) translation	Locus_17002_Transcript_2/10_Confidence_0.314_Length_1340
Locus_17399_Transcript_2/2_Confidence_0.897_Length_1818 - ORF 1 (frame 3) translation	Locus_17399_Transcript_2/2_Confidence_0.897_Length_1818
Locus_17711_Transcript_2/3_Confidence_0.714_Length_2362 - ORF 6 (frame 3) translation	Locus_17711_Transcript_2/3_Confidence_0.714_Length_2362
Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582 - ORF 4 (frame 3) translation	Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582
Locus_28965_Transcript_1/1_Confidence_1.000_Length_896 - ORF 1 (frame 2) translation	Locus_28965_Transcript_1/1_Confidence_1.000_Length_896
NP_001156383	zinc finger protein 934 isoform 1 [Mus musculus]
NP_001171016	zinc finger protein 600 [Mus musculus]
NP_001171238	reduced expression 2 [Mus musculus]
O75373 (ZN737_HUMAN)	RecName: Full=Zinc finger protein 737; AltName: Full=Zinc finger protein 102
O75626 (PRDM1_HUMAN)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=BLIMP-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1; AltName: Full=Positive regulatory domain I-binding factor 1; Short=PRDI-BF1; Short=PRDI-binding factor 1
O88282 (BCL6B_MOUSE)	RecName: Full=B-cell CLL/lymphoma 6 member B protein; AltName: Full=Bcl6-associated zinc finger protein
P0C6Y7 (PRDM9_RAT)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
P0CJ79 (ZN888_HUMAN)	RecName: Full=Zinc finger protein 888
P07247 (KRUP_DROME)	RecName: Full=Protein krueppel
P08043 (ZFP2_MOUSE)	RecName: Full=Zinc finger protein 2; Short=Zfp-2; AltName: Full=Protein mKR2
P15620 (ZN271_MOUSE)	RecName: Full=Zinc finger protein 271; AltName: Full=Zinc finger protein 35; Short=Zfp-35
P15622 (ZN250_HUMAN)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
P17020 (ZNF16_HUMAN)	RecName: Full=Zinc finger protein 16; AltName: Full=Zinc finger protein KOX9
P17025 (ZN182_HUMAN)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21; AltName: Full=Zinc finger protein KOX14
P17026 (ZNF22_HUMAN)	RecName: Full=Zinc finger protein 22; AltName: Full=Zinc finger protein KOX15; AltName: Full=Zinc finger protein Krox-26
P17030 (ZNF25_HUMAN)	RecName: Full=Zinc finger protein 25; AltName: Full=Zinc finger protein KOX19
P17035 (ZNF28_HUMAN)	RecName: Full=Zinc finger protein 28; AltName: Full=Zinc finger protein KOX24
P17036 (ZNF3_HUMAN)	RecName: Full=Zinc finger protein 3; AltName: Full=Zinc finger protein HF.12; AltName: Full=Zinc finger protein HZF3.1; AltName: Full=Zinc finger protein KOX25
P17041 (ZNF32_HUMAN)	RecName: Full=Zinc finger protein 32; AltName: Full=C2H2-546; AltName: Full=Zinc finger protein KOX30
P18724 (ZG49_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF49.1
P18725 (ZG5_XENLA)	RecName: Full=Gastrula zinc finger protein 5-1; AltName: Full=XlCGF5.1
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P18731 (ZG62_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF62.1
P18735 (ZG7_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF7.1
P18737 (ZG8_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF8.2DB
P18744 (ZO20_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF20
P18749 (ZO6_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF6
P18750 (ZO61_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF6.1
P24399 (ZN239_MOUSE)	RecName: Full=Zinc finger protein 239; Short=Zfp-239; AltName: Full=Zinc finger protein MOK-2
P31507 (KRUP_APIME)	RecName: Full=Protein krueppel
P51522 (ZNF83_HUMAN)	RecName: Full=Zinc finger protein 83; AltName: Full=Zinc finger protein 816B; AltName: Full=Zinc finger protein HPF1
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
P51786 (ZN157_HUMAN)	RecName: Full=Zinc finger protein 157; AltName: Full=Zinc finger protein HZF22
Q0P4W9 (FEZF1_XENTR)	RecName: Full=Fez family zinc finger protein 1
Q0VDQ9 (FEZF1_MOUSE)	RecName: Full=Fez family zinc finger protein 1
Q0VGE8 (ZN816_HUMAN)	RecName: Full=Zinc finger protein 816
Q1LZC0 (ZNF22_BOVIN)	RecName: Full=Zinc finger protein 22

Q2M3X9 (ZN674_HUMAN)	RecName: Full=Zinc finger protein 674
Q2M218 (ZN630_HUMAN)	RecName: Full=Zinc finger protein 630
Q2TAR3 (FEZF2_XENLA)	RecName: Full=Fez family zinc finger protein 2
Q2VWH6 (FEZF2_BOVIN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q3B7N9 (MYNN_BOVIN)	RecName: Full=Myoneurin
Q3SY52 (ZIK1_HUMAN)	RecName: Full=Zinc finger protein interacting with ribonucleoprotein K; AltName: Full=Zinc finger protein 762
Q3SYV7 (ZN345_BOVIN)	RecName: Full=Zinc finger protein 345
Q3V080 (ZN583_MOUSE)	RecName: Full=Zinc finger protein 583
Q3ZCT1 (ZN260_HUMAN)	RecName: Full=Zinc finger protein 260; Short=Zfp-260
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4R6C2 (ZN383_MACFA)	RecName: Full=Zinc finger protein 383
Q4V348 (Z658B_HUMAN)	RecName: Full=Zinc finger protein 658B
Q5R5N5 (MYNN_PONAB)	RecName: Full=Myoneurin
Q5R5U3 (ZN271_PONAB)	RecName: Full=Zinc finger protein 271
Q5R5Y7 (ZN436_PONAB)	RecName: Full=Zinc finger protein 436
Q5R8G9 (ZN239_PONAB)	RecName: Full=Zinc finger protein 239
Q5R8X1 (ZN665_PONAB)	RecName: Full=Zinc finger protein 665
Q5R9S5 (ZN182_PONAB)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q5RCJ2 (ZN614_PONAB)	RecName: Full=Zinc finger protein 614
Q5RER9 (ZN813_PONAB)	RecName: Full=Zinc finger protein 813
Q5RFP4 (OZF_PONAB)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q5VIY5 (ZN468_HUMAN)	RecName: Full=Zinc finger protein 468
Q6ECI4 (ZN470_HUMAN)	RecName: Full=Zinc finger protein 470; AltName: Full=Chondrogenesis zinc finger protein 1; Short=CZF-1
Q6P9A1 (ZN530_HUMAN)	RecName: Full=Zinc finger protein 530
Q6P560 (ZN182_MOUSE)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q6PF04 (ZN613_HUMAN)	RecName: Full=Zinc finger protein 613
Q6ZMS4 (ZN852_HUMAN)	RecName: Full=Zinc finger protein 852
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q6ZN06 (ZN813_HUMAN)	RecName: Full=Zinc finger protein 813
Q6ZN57 (ZFP2_HUMAN)	RecName: Full=Zinc finger protein 2 homolog; Short=Zfp-2; AltName: Full=Zinc finger protein 751
Q6ZNA1 (ZN836_HUMAN)	RecName: Full=Zinc finger protein 836
Q6ZNG1 (ZN600_HUMAN)	RecName: Full=Zinc finger protein 600
Q7L3S4 (ZN771_HUMAN)	RecName: Full=Zinc finger protein 771; AltName: Full=Mesenchymal stem cell protein DSC43
Q7TNU6 (ZN250_MOUSE)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
Q7Z340 (ZN551_HUMAN)	RecName: Full=Zinc finger protein 551; AltName: Full=Zinc finger protein KOX23
Q8BJ90 (ZN771_MOUSE)	RecName: Full=Zinc finger protein 771
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q8BQN6 (OZF_MOUSE)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q08DG8 (ZN135_BOVIN)	RecName: Full=Zinc finger protein 135
Q8IZ20 (ZN683_HUMAN)	RecName: Full=Zinc finger protein 683
Q8N143 (BCL6B_HUMAN)	RecName: Full=B-cell CLL/lymphoma 6 member B protein; AltName: Full=Bcl6-associated zinc finger protein; AltName: Full=Zinc finger protein 62
Q8N883 (ZN614_HUMAN)	RecName: Full=Zinc finger protein 614
Q8NA42 (ZN383_HUMAN)	RecName: Full=Zinc finger protein 383
Q8NHY6 (ZFP28_HUMAN)	RecName: Full=Zinc finger protein 28 homolog; Short=Zfp-28; AltName: Full=Krueppel-like zinc finger factor X6
Q8TBJ5 (FEZF2_HUMAN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q8TC21 (ZN596_HUMAN)	RecName: Full=Zinc finger protein 596
Q8TF45 (ZN418_HUMAN)	RecName: Full=Zinc finger protein 418
Q8WV37 (ZN480_HUMAN)	RecName: Full=Zinc finger protein 480
Q9BSK1 (ZN577_HUMAN)	RecName: Full=Zinc finger protein 577
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q9ERU3 (ZNF22_MOUSE)	RecName: Full=Zinc finger protein 22; AltName: Full=Zinc finger protein 422; AltName: Full=Zinc finger protein Krox-25; AltName: Full=Zinc finger protein Krox-26
Q9ESP5 (FEZF2_MOUSE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q9H7R5 (ZN665_HUMAN)	RecName: Full=Zinc finger protein 665; AltName: Full=Zinc finger protein 160-like
Q9H8G1 (ZN430_HUMAN)	RecName: Full=Zinc finger protein 430
Q9HCG1 (ZN160_HUMAN)	RecName: Full=Zinc finger protein 160; AltName: Full=Zinc finger protein HZF5; AltName: Full=Zinc finger protein Kr18; Short=HKr18
Q9NQV7 (PRDM9_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q9NQZ8 (ZNF71_HUMAN)	RecName: Full=Endothelial zinc finger protein induced by tumor necrosis factor alpha; AltName: Full=Zinc finger protein 71
Q9NV72 (ZN701_HUMAN)	RecName: Full=Zinc finger protein 701
Q9NYT6 (ZN226_HUMAN)	RecName: Full=Zinc finger protein 226

Q9P0L1 (ZKSC7_HUMAN)	RecName: Full=Zinc finger protein with KRAB and SCAN domains 7; AltName: Full=Zinc finger protein 167; AltName: Full=Zinc finger protein 448; AltName: Full=Zinc finger protein 64
Q9P255 (ZN492_HUMAN)	RecName: Full=Zinc finger protein 492; AltName: Full=Zinc finger protein 115
Q9UJN7 (ZN391_HUMAN)	RecName: Full=Zinc finger protein 391
Q9XSR1 (ZN252_CANFA)	RecName: Full=Zinc finger protein 252
Q9Y2H8 (ZN510_HUMAN)	RecName: Full=Zinc finger protein 510
Q25C93 (FEZF1_DANRE)	RecName: Full=Fez family zinc finger protein 1
Q28G88 (FEZF2_XENTR)	RecName: Full=Fez family zinc finger protein 2
Q80V23 (ZNF32_MOUSE)	RecName: Full=Zinc finger protein 32; AltName: Full=Zinc finger protein 637
Q80W31 (ZN569_MOUSE)	RecName: Full=Zinc finger protein 569; AltName: Full=Mszf21; AltName: Full=Zinc finger protein 74; Short=Zfp-74
Q80YP6 (ZIK1_MOUSE)	RecName: Full=Zinc finger protein interacting with ribonucleoprotein K
Q86WZ6 (ZN227_HUMAN)	RecName: Full=Zinc finger protein 227
Q86XU0 (ZN677_HUMAN)	RecName: Full=Zinc finger protein 677
Q95K49 (ZN614_MACFA)	RecName: Full=Zinc finger protein 614
Q96EQ9 (PRDM9_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=Hybrid sterility protein 1; AltName: Full=Meiosis-induced factor containing a PR/SET domain and zinc-finger motif; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q96H40 (ZN486_HUMAN)	RecName: Full=Zinc finger protein 486; AltName: Full=KRAB domain only protein 2
Q96IR2 (ZN845_HUMAN)	RecName: Full=Zinc finger protein 845
Q96N22 (ZN681_HUMAN)	RecName: Full=Zinc finger protein 681
Q96N38 (ZN714_HUMAN)	RecName: Full=Zinc finger protein 714
Q96ND8 (ZN583_HUMAN)	RecName: Full=Zinc finger protein 583; AltName: Full=Zinc finger protein L3-5
Q96NG8 (ZN582_HUMAN)	RecName: Full=Zinc finger protein 582
Q96NI8 (ZN570_HUMAN)	RecName: Full=Zinc finger protein 570
Q96RE9 (ZN300_HUMAN)	RecName: Full=Zinc finger protein 300
Q147U1 (ZN846_HUMAN)	RecName: Full=Zinc finger protein 846
Q804Q5 (FEZF2_DANRE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Foreheadin protein; AltName: Full=Zinc finger protein Fez-like
Q01779 (KRUP_MUSDO)	RecName: Full=Protein krueppel
Q01792 (KRUP_BRACO)	RecName: Full=Protein krueppel
Q01793 (KRUP_TRICA)	RecName: Full=Protein krueppel
Q01871 (KRUP_EUSPL)	RecName: Full=Protein krueppel
Q02035 (KRUP_PSYCI)	RecName: Full=Protein krueppel
Q02386 (ZNF45_HUMAN)	RecName: Full=Zinc finger protein 45; AltName: Full=BRC1744; AltName: Full=Zinc finger protein 13; AltName: Full=Zinc finger protein KOX5
Q03923 (ZNF85_HUMAN)	RecName: Full=Zinc finger protein 85; AltName: Full=Zinc finger protein HPF4; AltName: Full=Zinc finger protein HTF1
Q13106 (ZN154_HUMAN)	RecName: Full=Zinc finger protein 154
Q14585 (ZN345_HUMAN)	RecName: Full=Zinc finger protein 345; AltName: Full=Zinc finger protein HZF10
Q14588 (ZN234_HUMAN)	RecName: Full=Zinc finger protein 234; AltName: Full=Zinc finger protein 269; AltName: Full=Zinc finger protein HZF4
Q14590 (ZN235_HUMAN)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 270; AltName: Full=Zinc finger protein 93 homolog; Short=Zfp-93; AltName: Full=Zinc finger protein HZF6
Q14591 (ZN271_HUMAN)	RecName: Full=Zinc finger protein 271; AltName: Full=CT-ZFP48; AltName: Full=Epstein-Barr virus-induced zinc finger protein; Short=EBV-induced zinc finger protein; Short=ZNF-EB; AltName: Full=Zinc finger protein HZF7; AltName: Full=Zinc finger protein ZNFphex133; AltName: Full=Zinc finger protein dp; Short=ZNF-dp
Q15937 (ZNF79_HUMAN)	RecName: Full=Zinc finger protein 79; AltName: Full=ZNFpT7
Q16600 (ZN239_HUMAN)	RecName: Full=Zinc finger protein 239; AltName: Full=Zinc finger protein HOK-2; AltName: Full=Zinc finger protein MOK-2
Q25515 (KRUP_MANSE)	RecName: Full=Protein krueppel
Q28151 (OZF_BOVIN)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q60636 (PRDM1_MOUSE)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=B lymphocyte-induced maturation protein 1; Short=Blimp-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1
Q61116 (ZN235_MOUSE)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 93; Short=Zfp-93
Q62981 (ZN260_RAT)	RecName: Full=Zinc finger protein 260; Short=Zfp-260; AltName: Full=Pancreas-only zinc finger protein 1; Short=POZF-1
Q93560 (BLMP1_CAEEL)	RecName: Full=B lymphocyte-induced maturation protein 1 homolog
Q99676 (ZN184_HUMAN)	RecName: Full=Zinc finger protein 184
XP_001893102	Zinc finger, C2H2 type family protein [Brugia malayi]
XP_001945654	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001946669	PREDICTED: zinc finger protein 845-like [Acyrthosiphon pisum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001950651	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_002401338	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_002404835	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_002431737	protein krueppel, putative [Pediculus humanus corporis]
XP_003242514	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003242604	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003244738	PREDICTED: zinc finger protein 572-like [Acyrthosiphon pisum]
XP_003244741	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_003248857	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248889	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]

XP_003248963	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_003249048	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_003249678	PREDICTED: fez family zinc finger protein 1-like [Apis mellifera]
XP_003398307	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus terrestris]
XP_003490397	PREDICTED: protein krueppel [Bombus impatiens]
XP_003492727	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus impatiens]
XP_003494856	PREDICTED: fez family zinc finger protein 2-like [Bombus impatiens]
XP_003738192	PREDICTED: PR domain zinc finger protein 1-like [Metaseiulus occidentalis]
XP_003744232	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Metaseiulus occidentalis]
XP_003748300	PREDICTED: zinc finger and BTB domain-containing protein 24-like [Metaseiulus occidentalis]
XP_003759283	PREDICTED: zinc finger protein OZF-like, partial [Sarcophilus harrisii]
XP_004086830	PREDICTED: zinc finger protein OZF-like [Oryzias latipes]
XP_004919623	PREDICTED: gastrula zinc finger protein xLCGF3.1-like [Xenopus (Silurana) tropicalis]
XP_005157335	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168084	PREDICTED: gastrula zinc finger protein XlCGF57.1, partial [Danio rerio]
XP_005168216	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168249	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005182150	PREDICTED: protein krueppel [Musca domestica]
XP_005342829	PREDICTED: zinc finger protein 568 [Ictidomys tridecemlineatus]
XP_005658049	PREDICTED: zinc finger protein 300 [Sus scrofa]
XP_005753878	PREDICTED: zinc finger protein 391-like [Pundamilia nyererei]
XP_005817136	PREDICTED: zinc finger protein OZF-like, partial [Xiphophorus maculatus]
XP_006153235	PREDICTED: zinc finger protein 596 isoform X3 [Tupaia chinensis]
XP_006263331	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Alligator mississippiensis]
XP_006609630	PREDICTED: fez family zinc finger protein 1-like, partial [Apis dorsata]
XP_006613797	PREDICTED: protein krueppel-like [Apis dorsata]
XP_006643481	PREDICTED: zinc finger protein 180-like, partial [Lepisosteus oculatus]
XP_006804662	PREDICTED: zinc finger and SCAN domain-containing protein 2-like [Neolamprologus brichardi]
XP_006806237	PREDICTED: zinc finger protein 569-like [Neolamprologus brichardi]
XP_006807046	PREDICTED: histone-lysine N-methyltransferase PRDM9-like isoform X1 [Neolamprologus brichardi]
XP_006897457	PREDICTED: zinc finger protein 432-like [Elephantulus edwardii]
XP_007232538	PREDICTED: zinc finger protein 773-like [Astyanax mexicanus]
XP_007490656	PREDICTED: zinc finger protein 624-like isoform X2 [Monodelphis domestica]
XP_007505885	PREDICTED: zinc finger protein 2 homolog, partial [Monodelphis domestica]
XP_007506319	PREDICTED: zinc finger protein 135-like, partial [Monodelphis domestica]
XP_007508216	PREDICTED: similar to Zinc finger protein 271 (Zinc finger protein 7) (HZF7) (Zinc finger protein ZNFphex133) (Epstein-Barr virus-induced zinc finger protein) (ZNF-EB) (CT-ZFP48) (Zinc finger protein [Bathycoccus prasinos]
XP_007508973	PREDICTED: similar to Zinc finger protein 271 (Zinc finger protein 7) (HZF7) (Zinc finger protein ZNFphex133) (Epstein-Barr virus-induced zinc finger protein) (ZNF-EB) (CT-ZFP48) (Zinc finger protein [Bathycoccus prasinos]
XP_007540545	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007540550	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007561960	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Poecilia formosa]
XP_007565253	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007566619	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007573043	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007573181	PREDICTED: zinc finger protein 271-like [Poecilia formosa]
XP_007573713	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007573741	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Poecilia formosa]
XP_007577096	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Poecilia formosa]
XP_007577098	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X3 [Poecilia formosa]
XP_007577099	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X4 [Poecilia formosa]
XP_007955518	PREDICTED: zinc finger protein 383-like [Orycteropus afer afer]
XP_008150491	PREDICTED: zinc finger protein 300-like [Eptesicus fuscus]
XP_008179259	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180544	PREDICTED: zinc finger protein 239-like [Acyrthosiphon pisum]
XP_008180595	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180597	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180598	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]

XP_008180607	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_008180907	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008181099	PREDICTED: zinc finger protein 91-like [Acyrthosiphon pisum]
XP_008181548	PREDICTED: zinc finger protein 239-like [Acyrthosiphon pisum]
XP_008181583	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_008181794	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183209	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_008183216	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183439	PREDICTED: zinc finger protein 239-like [Acyrthosiphon pisum]
XP_008183596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008185429	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Acyrthosiphon pisum]
XP_008186458	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008186726	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_008186729	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187394	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187795	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_008187904	PREDICTED: zinc finger protein Xfin-like, partial [Acyrthosiphon pisum]
XP_008188120	PREDICTED: zinc finger protein 180-like [Acyrthosiphon pisum]
XP_008188231	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008188255	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_008188522	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008189099	PREDICTED: zinc finger protein 2 homolog, partial [Acyrthosiphon pisum]
XP_008194427	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Tribolium castaneum]
XP_008298797	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Stegastes partitus]
XP_008400230	PREDICTED: zinc finger protein OZF-like [Poecilia reticulata]
XP_008435718	PREDICTED: oocyte zinc finger protein XlCOF6-like [Poecilia reticulata]
XP_008435770	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Poecilia reticulata]
XP_008435772	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia reticulata]
XP_008435866	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia reticulata]
XP_008543891	PREDICTED: PR domain zinc finger protein 1 [Microplitis demolitor]
XP_008830905	PREDICTED: zinc finger protein 25-like [Nannospalax galili]
XP_009298784	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298796	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Danio rerio]
XP_009298804	PREDICTED: oocyte zinc finger protein XlCOF20-like [Danio rerio]
XP_009298811	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298817	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298832	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298863	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298922	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298936	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298967	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009299028	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Danio rerio]
XP_009299144	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_010590250	PREDICTED: zinc finger protein 300 [Loxodonta africana]
XP_010730666	PREDICTED: zinc finger protein 502-like [Larimichthys crocea]
XP_010748348	PREDICTED: gastrula zinc finger protein XlCGF71.1-like [Larimichthys crocea]
XP_010788499	PREDICTED: zinc finger protein 253-like, partial [Notothenia coriiceps]
XP_010947717	PREDICTED: zinc finger protein 25 [Camelus bactrianus]
XP_011239595	PREDICTED: zinc finger protein 9 isoform X1 [Mus musculus]
XP_011299253	PREDICTED: fez family zinc finger protein 2-like [Fopius arisanus]
XP_011429851	PREDICTED: zinc finger protein OZF-like [Crassostrea gigas]
XP_011559153	PREDICTED: zinc finger protein 708-like isoform X1 [Plutella xylostella]
XP_011618951	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619519	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619649	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011678015	PREDICTED: zinc finger protein 84-like isoform X1 [Strongylocentrotus purpuratus]
XP_011678017	PREDICTED: zinc finger protein 84-like isoform X2 [Strongylocentrotus purpuratus]
XP_011875591	PREDICTED: PR domain zinc finger protein 1 [Vollenhovia emeryi]
XP_011877253	PREDICTED: fez family zinc finger protein 2-like isoform X1 [Vollenhovia emeryi]
XP_011877254	PREDICTED: fez family zinc finger protein 2-like isoform X2 [Vollenhovia emeryi]
XP_012140785	PREDICTED: protein krueppel [Megachile rotundata]

XP_012168013	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus terrestris]
XP_012246007	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus impatiens]
XP_012250907	PREDICTED: PR domain zinc finger protein 1 [Athalia rosae]
XP_012255699	PREDICTED: protein krueppel [Athalia rosae]
XP_012278412	PREDICTED: fez family zinc finger protein 2-like [Orussus abietinus]
XP_012399604	PREDICTED: zinc finger protein 260-like [Sarcophilus harrisii]
XP_012405559	PREDICTED: zinc finger protein 37 homolog, partial [Sarcophilus harrisii]
XP_012413260	PREDICTED: zinc finger protein 699-like [Trichechus manatus latirostris]
XP_012413722	PREDICTED: zinc finger protein 678-like [Trichechus manatus latirostris]
XP_012414413	PREDICTED: zinc finger protein 846-like [Trichechus manatus latirostris]
XP_012547447	PREDICTED: zinc finger protein 468-like [Bombyx mori]
XP_012673637	PREDICTED: zinc finger protein 98-like, partial [Clupea harengus]
XP_012676460	PREDICTED: zinc finger protein OZF-like [Clupea harengus]
XP_012676918	PREDICTED: zinc finger protein 726-like [Clupea harengus]
XP_012686594	PREDICTED: zinc finger protein OZF-like [Clupea harengus]
XP_012687791	PREDICTED: zinc finger protein 678-like [Clupea harengus]
XP_012692788	PREDICTED: zinc finger protein 43-like [Clupea harengus]
XP_012710330	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012713484	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Fundulus heteroclitus]
XP_012713622	PREDICTED: zinc finger protein OZF-like [Fundulus heteroclitus]
XP_012713624	PREDICTED: gastrula zinc finger protein XlCGF49.1-like, partial [Fundulus heteroclitus]
XP_012892021	PREDICTED: zinc finger protein 420-like [Dipodomys ordii]
XP_012892236	PREDICTED: zinc finger protein 658-like [Dipodomys ordii]
XP_013110835	PREDICTED: protein krueppel [Stomoxys calcitrans]
XP_013197323	PREDICTED: zinc finger protein 84-like [Amyelois transitella]
XP_013367852	PREDICTED: zinc finger protein 300 isoform X3 [Chinchilla lanigera]
XP_013367853	PREDICTED: zinc finger protein 300 isoform X4 [Chinchilla lanigera]
XP_013367854	PREDICTED: zinc finger protein 300 isoform X5 [Chinchilla lanigera]
XP_013763388	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Pundamilia nyererei]
XP_013772409	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013773341	PREDICTED: serine-rich adhesin for platelets-like [Limulus polyphemus]
XP_013775795	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013778397	PREDICTED: gastrula zinc finger protein XlCGF7.1-like [Limulus polyphemus]
XP_013779401	PREDICTED: zinc finger protein 236-like [Limulus polyphemus]
XP_013779582	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013781553	PREDICTED: zinc finger protein 557-like [Limulus polyphemus]
XP_013781817	PREDICTED: PR domain zinc finger protein 1-like [Limulus polyphemus]
XP_013783281	PREDICTED: zinc finger protein 227-like [Limulus polyphemus]
XP_013784172	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013785583	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013786436	PREDICTED: Krueppel homolog 1-like [Limulus polyphemus]
XP_013787012	PREDICTED: zinc finger protein 239-like [Limulus polyphemus]
XP_013788183	PREDICTED: zinc finger protein 835-like [Limulus polyphemus]
XP_013788334	PREDICTED: zinc finger protein 501-like [Limulus polyphemus]
XP_013788396	PREDICTED: zinc finger protein Gfi-1b-like [Limulus polyphemus]
XP_013790651	PREDICTED: zinc finger protein 681-like [Limulus polyphemus]
XP_013791781	PREDICTED: zinc finger protein 271-like [Limulus polyphemus]
XP_013793148	PREDICTED: zinc finger protein 436-like, partial [Limulus polyphemus]
XP_013856101	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Austrofundulus limnaeus]
XP_013872677	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013879820	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013881864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013884881	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013889698	PREDICTED: zinc finger protein OZF-like [Austrofundulus limnaeus]
XP_014008020	PREDICTED: zinc finger protein 79-like [Salmo salar]
XP_014186906	PREDICTED: zinc finger protein 239-like, partial [Haplochromis burtoni]
XP_014192866	PREDICTED: zinc finger protein OZF-like [Haplochromis burtoni]
XP_014265828	PREDICTED: putative zinc finger protein 724 [Maylandia zebra]
XP_014266000	PREDICTED: zinc finger protein OZF-like [Maylandia zebra]
XP_014326648	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xiphophorus maculatus]
XP_014382878	PREDICTED: oocyte zinc finger protein XlCOF6-like [Alligator sinensis]
XP_014398735	PREDICTED: zinc finger protein 2 homolog isoform X2 [Myotis brandtii]
XP_014437399	PREDICTED: zinc finger protein 205 isoform X1 [Tupaia chinensis]

XP_014438089	PREDICTED: zinc finger protein 568 [Tupaia chinensis]
XP_014457013	PREDICTED: zinc finger protein 708-like, partial [Alligator mississippiensis]
XP_014459563	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Alligator mississippiensis]
XP_014460726	PREDICTED: zinc finger protein 883-like [Alligator mississippiensis]

9.4.2.21 *Ladybird early*

Name	Description
A1YF16 (MSX2_GORGO)	RecName: Full=Homeobox protein MSX-2
A1YFD8 (HXD4_SAGLB)	RecName: Full=Homeobox protein Hox-D4
A1YGA4 (MEOX1_PANPA)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2D4P8 (HXD4_ATEGE)	RecName: Full=Homeobox protein Hox-D4
A2RU54 (HMX2_HUMAN)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein H6 family member 2
A2T779 (MEOX1_PANTR)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A5YC49 (NKX63_XENLA)	RecName: Full=Homeobox protein Nkx-6.3
A6NCS4 (NKX26_HUMAN)	RecName: Full=Homeobox protein Nkx-2.6; AltName: Full=Homeobox protein NK-2 homolog F
A6NHT5 (HMX3_HUMAN)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
A6NJ46 (NKX63_HUMAN)	RecName: Full=Homeobox protein Nkx-6.3
B0VXK3 (HXA2_CALJA)	RecName: Full=Homeobox protein Hox-A2
B0W1V2 (ABDA_CULQU)	RecName: Full=Homeobox protein abdominal-A homolog
CAA70056	ladybird early homeodomain transcription factor [Drosophila melanogaster]
LBX1_MOUSE	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968 - ORF 1 (frame 1) translation	Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968
Locus_1_Transcript_139848/166847_Confidence_1.000_Length_1898 - ORF 1 (frame 3) translation	Locus_1_Transcript_139848/166847_Confidence_1.000_Length_1898
Locus_1_Transcript_161802/166847_Confidence_1.000_Length_3902 - ORF 8 (frame 2) translation	Locus_1_Transcript_161802/166847_Confidence_1.000_Length_3902
Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118 - ORF 3 (frame 3) translation	Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118
Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075 - ORF 1 (frame 3) translation	Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075
Locus_3015_Transcript_2/2_Confidence_0.800_Length_548 - ORF 4 (frame 3) translation	Locus_3015_Transcript_2/2_Confidence_0.800_Length_548
Locus_3016_Transcript_1/1_Confidence_1.000_Length_755 - ORF 6 (frame 3) translation	Locus_3016_Transcript_1/1_Confidence_1.000_Length_755
Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099 - ORF 10 (frame 2) translation	Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099
Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534 - ORF 3 (frame 3) translation	Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534
Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549 - ORF 4 (frame 2) translation	Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549
Locus_12254_Transcript_5/10_Confidence_0.556_Length_6877 - ORF 7 (frame 1) translation	Locus_12254_Transcript_5/10_Confidence_0.556_Length_6877
Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293 - ORF 1 (frame 1) translation	Locus_14112_Transcript_7/7_Confidence_0.471_Length_2293
Locus_15017_Transcript_7/7_Confidence_0.742_Length_5840 - ORF 14 (frame 2) translation	Locus_15017_Transcript_7/7_Confidence_0.742_Length_5840
Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869 - ORF 2 (frame 2) translation	Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869
Locus_16018_Transcript_1/1_Confidence_1.000_Length_4201 - ORF 1 (frame 2) translation	Locus_16018_Transcript_1/1_Confidence_1.000_Length_4201
Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736 - ORF 18 (frame 2) translation	Locus_16176_Transcript_2/2_Confidence_0.933_Length_3736
Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590 - ORF 4 (frame 1) translation	Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590
Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305 - ORF 1 (frame 3) translation	Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305
Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037 - ORF 2 (frame 2) translation	Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037
Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236 - ORF 1 (frame 2) translation	Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236
Locus_18584_Transcript_1/1_Confidence_1.000_Length_982 - ORF 2 (frame 2) translation	Locus_18584_Transcript_1/1_Confidence_1.000_Length_982
Locus_20765_Transcript_4/4_Confidence_0.843_Length_3077 - ORF 3 (frame 3) translation	Locus_20765_Transcript_4/4_Confidence_0.843_Length_3077
Locus_20809_Transcript_1/1_Confidence_1.000_Length_1766 - ORF 9 (frame 1) translation	Locus_20809_Transcript_1/1_Confidence_1.000_Length_1766
Locus_21582_Transcript_1/1_Confidence_1.000_Length_907 - ORF 2 (frame 1) translation	Locus_21582_Transcript_1/1_Confidence_1.000_Length_907
Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612 - ORF 4 (frame 3) translation	Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612
Locus_23245_Transcript_1/1_Confidence_1.000_Length_2652 - ORF 19 (frame 1) translation	Locus_23245_Transcript_1/1_Confidence_1.000_Length_2652
Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275 - ORF 3 (frame 3) translation	Locus_25295_Transcript_1/1_Confidence_1.000_Length_1275
Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198 - ORF 11 (frame 2) translation	Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198

Locus_28432_Transcript_2/2_Confidence_0.667_Length_824 - ORF 1 (frame 3) translation	Locus_28432_Transcript_2/2_Confidence_0.667_Length_824
NP_034822	transcription factor LBX2 [Mus musculus]
NP_571496	homeobox protein Nkx-2.5 [Danio rerio]
NP_739572	T-cell leukemia homeobox protein 3 [Danio rerio]
NP_001037341	transcription factor deformed [Bombyx mori]
NP_001095280	brain-specific homeobox protein homolog [Xenopus (Silurana) tropicalis]
NP_001107762	labial [Tribolium castaneum]
NP_001158371	distal-less homeobox 1 [Saccoglossus kowalevskii]
NP_001158453	T-cell leukemia homeobox protein [Saccoglossus kowalevskii]
NP_001162171	ultrabithorax [Apis mellifera]
NP_001186477	homeobox protein Nkx-6.2 [Gallus gallus]
O13074 (HXB4A_TAKRU)	RecName: Full=Homeobox protein Hox-B4a; AltName: Full=FrHOXB-4
O35762 (NKX61_RAT)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
O35767 (NKX25_RAT)	RecName: Full=Homeobox protein Nkx-2.5; Short=rNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
O42230 (GBX2_CHICK)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
O42365 (HXA2B_DANRE)	RecName: Full=Homeobox protein Hox-A2b; Short=Hox-A2
O42366 (HXB1A_DANRE)	RecName: Full=Homeobox protein Hox-B1a; Short=Hox-B1
O42367 (HXB2A_DANRE)	RecName: Full=Homeobox protein Hox-B2a; Short=Hox-B2
O43364 (HXA2_HUMAN)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1K
O43711 (TLX3_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox protein Hox-11L2
O43763 (TLX2_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Neural crest homeobox protein
O55144 (TLX3_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2; AltName: Full=Respiratory neuron homeobox protein
O57374 (HXD4A_DANRE)	RecName: Full=Homeobox protein Hox-D4a; Short=Hox-D4
O57601 (HMX3_CHICK)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=cNkx5-1
O70218 (HMX1_MOUSE)	RecName: Full=Homeobox protein HMX1; AltName: Full=Homeobox protein H6
O76762 (ABDA_ANOGA)	RecName: Full=Homeobox protein abdominal-A homolog
O88181 (BARH2_RAT)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
O93366 (TLX1_CHICK)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
O93367 (TLX3_CHICK)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2
O95096 (NKX22_HUMAN)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P0C1T1 (HXB2_MOUSE)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8
P07548 (DFD_DROME)	RecName: Full=Homeotic protein deformed
P09016 (HXD4_HUMAN)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein HHO.C13; AltName: Full=Homeobox protein Hox-4B; AltName: Full=Homeobox protein Hox-5.1
P09017 (HXC4_HUMAN)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein CP19; AltName: Full=Homeobox protein Hox-3E
P09022 (HXA1_MOUSE)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Early retinoic acid 1; AltName: Full=Homeobox protein Hox-1.6; AltName: Full=Homeoboxless protein ERA-1-399; AltName: Full=Homeotic protein ERA-1-993
P09638 (HXB2_SALSA)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=S6
P10105 (LAB_DROME)	RecName: Full=Homeotic protein labial; AltName: Full=F24; AltName: Full=F90-2
P10628 (HXD4_MOUSE)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein Hox-4.2; AltName: Full=Homeobox protein Hox-5.1
P14652 (HXB2_HUMAN)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8; AltName: Full=Homeobox protein Hox-2H; AltName: Full=K8
P14837 (PDX1_XENLA)	RecName: Full=Pancreas/duodenum homeobox protein 1; Short=PDX-1; AltName: Full=Homeobox protein 8; Short=XlHbox-8
P14840 (HXB4_CHICK)	RecName: Full=Homeobox protein Hox-B4; AltName: Full=Homeobox protein Hox-Z; Short=Chox-Z
P15142 (HM7X_CHICK)	RecName: Full=Homeobox protein CHOX-7
P15856 (ABDA_APIME)	RecName: Full=Homeobox protein abdominal-A homolog; AltName: Full=H15
P17278 (HXD4_CHICK)	RecName: Full=Homeobox protein Hox-D4; AltName: Full=Homeobox protein Hox-A; Short=Chox-A
P20009 (DLL_DROME)	RecName: Full=Homeotic protein distal-less; AltName: Full=Protein brista
P20822 (UBX_DROPS)	RecName: Full=Homeotic protein ultrabithorax
P22544 (BARH1_DROAN)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox BarH1 protein
P22574 (HXB4A_DANRE)	RecName: Full=Homeobox protein Hox-B4a; Short=Hox-B4; AltName: Full=Homeobox protein Zf-13
P22808 (VND_DROME)	RecName: Full=Homeobox protein vnd; AltName: Full=Homeobox protein NK-2; AltName: Full=Protein ventral nervous system defective
P23441 (NKX21_RAT)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1

P28361 (MSX1_CHICK)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Homeobox protein Hox-7; Short=CHOX-7; AltName: Full=Msh homeobox 1-like protein
P28362 (MSX2_CHICK)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8; Short=CHOX-8; Short=GHox-8
P29552 (ABDA_AEDAE)	RecName: Full=Homeobox protein abdominal-A homolog
P29555 (ABDA_DROME)	RecName: Full=Homeobox protein abdominal-A
P29556 (ABDA_SCHGR)	RecName: Full=Homeobox protein abdominal-A homolog
P31245 (HXA2_MOUSE)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11; Short=Hox1.11
P31246 (HXA2_RAT)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11
P31259 (HXB1_CHICK)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=Ghox-lab
P31261 (HXA2_NOTVI)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hbox-2.8; Short=NvHbox-2.8
P31264 (HMPB_DROME)	RecName: Full=Homeotic protein proboscipedia
P31314 (TLX1_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox protein Hox-11; AltName: Full=Proto-oncogene TCL-3; AltName: Full=T-cell leukemia/lymphoma protein 3
P31357 (HXB1_AMBME)	RecName: Full=Homeobox protein Hox-B1; AltName: Full=AHox1
P32442 (MEOX1_MOUSE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P42581 (HMX3_MOUSE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
P42582 (NKX25_MOUSE)	RecName: Full=Homeobox protein Nkx-2.5; AltName: Full=Cardiac-specific homeobox; AltName: Full=Homeobox protein CSX; AltName: Full=Homeobox protein NK-2 homolog E
P42583 (NKX25_XENLA)	RecName: Full=Homeobox protein Nkx-2.5; Short=xNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
P42586 (NKX22_MOUSE)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P42587 (HNK2_XENLA)	RecName: Full=Homeobox protein XENK-2
P43345 (TLX1_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
P43687 (HMX2_MOUSE)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein Nkx-5.2
P43688 (NKX26_MOUSE)	RecName: Full=Homeobox protein Nkx-2.6; AltName: Full=Homeobox protein NK-2 homolog F
P43697 (NKX22_MESAU)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P43698 (TITF1_CANFA)	RecName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1
P43699 (NKX21_HUMAN)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Homeobox protein NK-2 homolog A; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Thyroid-specific enhancer-binding protein; Short=T/EBP
P48031 (GBX2_MOUSE)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=Stimulated by retinoic acid gene 7 protein
P49639 (HXA1_HUMAN)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Homeobox protein Hox-1F
P50219 (MNX1_HUMAN)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
P50220 (NKX21_MOUSE)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Thyroid-specific enhancer-binding protein; Short=T/EBP
P50223 (HMGX7_CHICK)	RecName: Full=Homeobox protein GHOX-7; AltName: Full=CHOX-7; Short=Hox-7
P52951 (GBX2_HUMAN)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
P52952 (NKX25_HUMAN)	RecName: Full=Homeobox protein Nkx-2.5; AltName: Full=Cardiac-specific homeobox; AltName: Full=Homeobox protein CSX; AltName: Full=Homeobox protein NK-2 homolog E
P52953 (MSX2_RAT)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
P52954 (LBX1_HUMAN)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
P52955 (LBX1_MOUSE)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
P53772 (DLLH_BRAFL)	RecName: Full=Homeobox protein DLL homolog
P53773 (DLL1_XENLA)	RecName: Full=Homeobox protein DLL-1; Short=DLL; Short=XDLL
P56177 (DLX1_HUMAN)	RecName: Full=Homeobox protein DLX-1
P56407 (HM09_CAEEL)	RecName: Full=Homeobox protein ceh-9
P63156 (BARH1_RAT)	RecName: Full=BarH-like 1 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH2; AltName: Full=BarH-related homeobox protein 1
P70118 (PDX1_MESAU)	RecName: Full=Pancreas/duodenum homeobox protein 1; AltName: Full=Homeodomain protein PDX1; AltName: Full=Insulin promoter factor 1; Short=IPF-1
P70397 (DLX6_MOUSE)	RecName: Full=Homeobox protein DLX-6
P78426 (NKX61_HUMAN)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
P82976 (GBX1_MOUSE)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
P83949 (UBX_DROME)	RecName: Full=Homeotic protein ultrabithorax
P97273 (TITF1_CAVPO)	RecName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1

P97334 (NKX23_MOUSE)	RecName: Full=Homeobox protein Nkx-2.3; AltName: Full=Homeobox protein NK-2 homolog 3; AltName: Full=Homeobox protein NK-2 homolog C; AltName: Full=Nkx2-C
Q0P4H6 (LBX1_XENTR)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q0P4W6 (HMX3_XENTR)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q0P5C3 (MSX2_BOVIN)	RecName: Full=Homeobox protein MSX-2
Q0VCS4 (HXA2_BOVIN)	RecName: Full=Homeobox protein Hox-A2
Q1KKR6 (HXD4B_TAKRU)	RecName: Full=Homeobox protein Hox-D4b
Q1KKS8 (HXD4A_TAKRU)	RecName: Full=Homeobox protein Hox-D4a
Q1KKU6 (HXC4A_TAKRU)	RecName: Full=Homeobox protein Hox-C4a
Q1KKZ2 (HXA2B_TAKRU)	RecName: Full=Homeobox protein Hox-A2b
Q1KL10 (HXA1A_TAKRU)	RecName: Full=Homeobox protein Hox-A1a
Q1XID0 (LBX1_RAT)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q2PYN8 (LBX1_XENLA)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q2VL79 (MSX1_DAUMA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL80 (MSX1_PERPO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL82 (MSX1_SAGOE)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL83 (MSX1_LEORO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL84 (MSX1_CALJA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL85 (MSX1_CALGO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL86 (MSX1_SAIBB)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL88 (MSX1_PANTR)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q3C1V8 (BSH_HUMAN)	RecName: Full=Brain-specific homeobox protein homolog
Q3UHX8 (NKX63_MOUSE)	RecName: Full=Homeobox protein Nkx-6.3
Q4V5A3 (UNPG_DROME)	RecName: Full=Homeobox protein unplugged
Q6R3Q6 (BSH_DANRE)	RecName: Full=Brain-specific homeobox protein homolog
Q6RFL5 (BSH_CHICK)	RecName: Full=Brain-specific homeobox protein homolog
Q6XYB7 (LBX2_HUMAN)	RecName: Full=Transcription factor LBX2; AltName: Full=Ladybird homeobox protein homolog 2
Q08DG7 (HXA3_BOVIN)	RecName: Full=Homeobox protein Hox-A3
Q8JJ64 (HMX3_XENLA)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=X-nkx-5.1
Q8T940 (UBX_JUNCO)	RecName: Full=Homeotic protein ultrabithorax; AltName: Full=JcUbx
Q8TAU0 (NKX23_HUMAN)	RecName: Full=Homeobox protein Nkx-2.3; AltName: Full=Homeobox protein NK-2 homolog C
Q8VIB5 (BARH2_MOUSE)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
Q9BZE3 (BARH1_HUMAN)	RecName: Full=BarH-like 1 homeobox protein
Q9C056 (NKX62_HUMAN)	RecName: Full=Homeobox protein Nkx-6.2; AltName: Full=Homeobox protein NK-6 homolog B
Q9DE09 (HMX1_CHICK)	RecName: Full=Homeobox protein HMX1; AltName: Full=GH6; AltName: Full=Homeobox protein H6
Q9DED6 (BAX1B_CHICK)	RecName: Full=Homeobox protein BarH-like 1b; AltName: Full=Bar class homeoprotein Barx1b
Q9EQM3 (NKX24_MOUSE)	RecName: Full=Homeobox protein Nkx-2.4; AltName: Full=Homeobox protein NK-2 homolog D
Q9ER42 (BARX1_MOUSE)	RecName: Full=Homeobox protein BarH-like 1
Q9GK08 (MSX2_CANFA)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8
Q9GZZ0 (HXD1_HUMAN)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-GG
Q9H2Z4 (NKX24_HUMAN)	RecName: Full=Homeobox protein Nkx-2.4; AltName: Full=Homeobox protein NK-2 homolog D
Q9HBU1 (BARX1_HUMAN)	RecName: Full=Homeobox protein BarH-like 1
Q9IA19 (HXA1_HETFR)	RecName: Full=Homeobox protein Hox-A1
Q9IA20 (HXA2_HETFR)	RecName: Full=Homeobox protein Hox-A2
Q9IA22 (HXA4_HETFR)	RecName: Full=Homeobox protein Hox-A4
Q9NY43 (BARH2_HUMAN)	RecName: Full=BarH-like 2 homeobox protein
Q9PWM3 (HXC4A_DANRE)	RecName: Full=Homeobox protein Hox-C4a; Short=Hox-C4
Q9QZW9 (MNX1_MOUSE)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
Q9W6D8 (BARX1_CHICK)	RecName: Full=Homeobox protein BarH-like 1
Q9W7E8 (KOZA_XENLA)	RecName: Full=Homeobox protein koza; AltName: Full=Homeodomain transcription factor koza
Q9WUN8 (LBX2_MOUSE)	RecName: Full=Transcription factor LBX2; AltName: Full=Ladybird homeobox protein homolog 2
Q28IU6 (HXD1_XENTR)	RecName: Full=Homeobox protein Hox-D1
Q28ZA9 (UNPG_DROPS)	RecName: Full=Homeobox protein unplugged
Q90XN9 (HMX3B_ORYLA)	RecName: Full=Homeobox protein HMX3-B; AltName: Full=Homeobox protein H6 family member 3-B; AltName: Full=Homeobox protein Nkx-5.1.2; AltName: Full=OlNkx-5.1.2
Q90XP0 (HMX3A_ORYLA)	RecName: Full=Homeobox protein HMX3-A; AltName: Full=Homeobox protein H6 family member 3-A; AltName: Full=Homeobox protein Nkx-5.1.1; AltName: Full=OlNkx-5.1.1
Q98SI1 (HXA1A_DANRE)	RecName: Full=Homeobox protein Hox-A1a; Short=Hox-A1

Q99MA9 (NKX61_MOUSE)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q00401 (HMH2_GIRTI)	RecName: Full=Homeobox protein DTH-2
Q503F2 (BARX1_DANRE)	RecName: Full=Homeobox protein BarH-like 1; AltName: Full=BarH-class homeodomain transcription factor 4
Q504H8 (HMX3_DANRE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q810B3 (BSH_MOUSE)	RecName: Full=Brain-specific homeobox protein homolog
Q01703 (MSXC_DANRE)	RecName: Full=Homeobox protein MSH-C
Q01822 (HXD1_MOUSE)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Homeobox protein Hox-4.9
Q03356 (MSXB_DANRE)	RecName: Full=Homeobox protein MSH-B
Q03357 (MSXA_DANRE)	RecName: Full=Homeobox protein MSH-A
Q03358 (MSX2_MOUSE)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
Q04787 (BSH_DROME)	RecName: Full=Brain-specific homeobox protein
Q05007 (ABDA_ARTSF)	RecName: Full=Homeobox protein abdominal-A homolog
Q07961 (ABDA_TRICA)	RecName: Full=Homeobox protein abdominal-A homolog
Q08624 (HXC4_MOUSE)	RecName: Full=Homeobox protein Hox-C4; AltName: Full=Homeobox protein Hox-3.5
Q08727 (HXA2_CHICK)	RecName: Full=Homeobox protein Hox-A2
Q08820 (HXD1_XENLA)	RecName: Full=Homeobox protein Hox-D1; AltName: Full=Hox.lab1; AltName: Full=Labial protein; Short=Xlab
Q08821 (HXA1_XENLA)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Hox.lab2
Q14549 (GBX1_HUMAN)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q22909 (HM30_CAEEL)	RecName: Full=Homeobox protein ceh-30
Q22910 (HM31_CAEEL)	RecName: Full=Homeobox protein ceh-31
Q24255 (BARH1_DROME)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox protein BarH1
Q24256 (BARH2_DROME)	RecName: Full=Homeobox protein B-H2; AltName: Full=Homeobox protein BarH2
Q26430 (ABDA_MANSE)	RecName: Full=Homeobox protein abdominal-A homolog
Q26604 (SMOX5_SCHMA)	RecName: Full=Homeobox protein SMOX-5
Q26656 (HMX_STRPU)	RecName: Full=Homeobox protein Hmx; Short=SpHmx; AltName: Full=H6-like
Q60554 (NKX61_MESAU)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q61663 (TLX2_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Enteric neuron homeobox protein; AltName: Full=Homeobox TLX-2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Hox11L.1; AltName: Full=PMUR10F
Q64317 (DLX1_MOUSE)	RecName: Full=Homeobox protein DLX-1
Q90346 (HXB1_CYPCA)	RecName: Full=Homeobox protein Hox-B1
Q90423 (HXB1B_DANRE)	RecName: Full=Homeobox protein Hox-B1b; AltName: Full=Homeobox protein Hox-A1
Q90481 (NX22A_DANRE)	RecName: Full=Homeobox protein Nkx-2.2a; AltName: Full=Homeobox protein NK-2 homolog B-A
Q90788 (NKX25_CHICK)	RecName: Full=Homeobox protein Nkx-2.5; Short=cNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
Q91907 (GBX2_XENLA)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=XGBX-2
Q98875 (DLX1A_DANRE)	RecName: Full=Homeobox protein Dlx1a; Short=DLX-1; AltName: Full=Distal-less homeobox gene 1a
Q98877 (DLX6A_DANRE)	RecName: Full=Homeobox protein Dlx6a; AltName: Full=Distal-less homeobox protein 6a; Short=DLX-6
Q98878 (DLX4B_DANRE)	RecName: Full=Homeobox protein Dlx4b; AltName: Full=DLX-7; AltName: Full=Distal-less homeobox protein 4b
Q98879 (DLX4A_DANRE)	RecName: Full=Homeobox protein Dlx4a; AltName: Full=DLX-8; AltName: Full=Distal-less homeobox protein 4a
XP_975006	PREDICTED: homeobox protein BarH-like 1 [Tribolium castaneum]
XP_975059	PREDICTED: muscle segmentation homeobox [Tribolium castaneum]
XP_001120045	PREDICTED: homeotic protein deformed [Apis mellifera]
XP_001120278	PREDICTED: homeotic protein labial isoform X1 [Apis mellifera]
XP_001842674	homeotic deformed protein [Culex quinquefasciatus]
XP_001944887	PREDICTED: homeobox protein B-H1-like [Acyrthosiphon pisum]
XP_002406412	homeobox protein Hox-A4, putative [Ixodes scapularis]
XP_002414321	homeobox protein NK-2, putative [Ixodes scapularis]
XP_002423066	Homeobox protein GBX-1, putative [Pediculus humanus corporis]
XP_002426081	Ptx1 homeodomain protein, putative [Pediculus humanus corporis]
XP_002426656	predicted protein [Pediculus humanus corporis]
XP_002429457	Homeobox protein Hmx, putative [Pediculus humanus corporis]
XP_002435656	homeobox protein MSX-2, putative [Ixodes scapularis]
XP_002596391	BarH-like 1 homeobox protein [Branchiostoma floridae]
XP_002609070	nk homeobox 6 [Branchiostoma floridae]
XP_002731951	PREDICTED: homeobox protein HMX3-A-like [Saccoglossus kowalevskii]
XP_003427431	PREDICTED: motor neuron and pancreas homeobox protein 1 [Nasonia vitripennis]
XP_003476493	PREDICTED: homeobox protein Nkx-2.2 [Cavia porcellus]
XP_003698568	PREDICTED: homeobox protein B-H2 [Apis florea]
XP_003741994	PREDICTED: homeobox protein XHOX-7.1-like [Metaseiulus occidentalis]
XP_003743246	PREDICTED: homeobox protein B-H1-like [Metaseiulus occidentalis]
XP_003963996	PREDICTED: homeobox protein HMX3-A [Takifugu rubripes]
XP_004076957	PREDICTED: T-cell leukemia homeobox protein 1-like [Oryzias latipes]
XP_004077224	PREDICTED: homeobox protein MSX-2 isoform X1 [Oryzias latipes]
XP_004555954	PREDICTED: homeobox protein MSX-2-like [Maylandia zebra]
XP_004925027	PREDICTED: homeobox protein Hox-B4 [Bombyx mori]

XP_004933035	PREDICTED: homeobox protein HMX3-B [Bombyx mori]
XP_004933121	PREDICTED: transcription factor LBX1-like [Bombyx mori]
XP_005303794	PREDICTED: brain-specific homeobox protein homolog [Chrysemys picta bellii]
XP_005305386	PREDICTED: homeobox protein Nkx-6.2 [Chrysemys picta bellii]
XP_005349079	PREDICTED: homeobox protein Nkx-2.5 [Microtus ochrogaster]
XP_005512968	PREDICTED: barH-like 1 homeobox protein [Columba livia]
XP_005992571	PREDICTED: homeobox protein Nkx-2.5 [Latimeria chalumnae]
XP_006003775	PREDICTED: homeobox protein Nkx-6.2 [Latimeria chalumnae]
XP_006024676	PREDICTED: homeobox protein Nkx-6.2 [Alligator sinensis]
XP_006136686	PREDICTED: homeobox protein Nkx-6.2 [Pelodiscus sinensis]
XP_006137362	PREDICTED: barH-like 2 homeobox protein [Pelodiscus sinensis]
XP_006274581	PREDICTED: brain-specific homeobox protein homolog [Alligator mississippiensis]
XP_006559409	PREDICTED: ultrabithorax isoform X5 [Apis mellifera]
XP_006559411	PREDICTED: homeotic protein labial isoform X2 [Apis mellifera]
XP_006610893	PREDICTED: homeotic protein ultrabithorax-like isoform X3 [Apis dorsata]
XP_006611901	PREDICTED: homeotic protein labial-like isoform X1 [Apis dorsata]
XP_006611902	PREDICTED: homeotic protein labial-like isoform X2 [Apis dorsata]
XP_006723629	PREDICTED: homeobox protein Nkx-2.2 isoform X2 [Homo sapiens]
XP_006895666	PREDICTED: brain-specific homeobox protein homolog [Elephantulus edwardii]
XP_006895718	PREDICTED: homeobox protein Nkx-2.2-like [Elephantulus edwardii]
XP_006978927	PREDICTED: homeobox protein Nkx-2.5 [Peromyscus maniculatus bairdii]
XP_007053086	PREDICTED: homeobox protein Nkx-6.2 [Chelonia mydas]
XP_007067023	PREDICTED: brain-specific homeobox protein homolog [Chelonia mydas]
XP_007085565	PREDICTED: homeobox protein MSX-2 [Panthera tigris altaica]
XP_007258178	PREDICTED: brain-specific homeobox protein homolog [Astyanax mexicanus]
XP_007524430	PREDICTED: homeobox protein MSX-2 [Erinaceus europaeus]
XP_007525491	PREDICTED: homeobox protein Nkx-2.2 [Erinaceus europaeus]
XP_007565863	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia formosa]
XP_007566853	PREDICTED: homeobox protein Nkx-6.2-like [Poecilia formosa]
XP_007651972	PREDICTED: homeobox protein GBX-2 [Cricetulus griseus]
XP_007907293	PREDICTED: homeobox protein Nkx-2.3 [Callorhinchus milii]
XP_008068304	PREDICTED: homeobox protein Nkx-2.2 [Tarsius syrichta]
XP_008193415	PREDICTED: homeobox protein ceh-31-like [Tribolium castaneum]
XP_008195160	PREDICTED: homeobox protein Hox-D4a [Tribolium castaneum]
XP_008295823	PREDICTED: homeobox protein MSX-2-like [Stegastes partitus]
XP_008299788	PREDICTED: T-cell leukemia homeobox protein 1-like [Stegastes partitus]
XP_008325234	PREDICTED: T-cell leukemia homeobox protein 3 [Cynoglossus semilaevis]
XP_008418492	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia reticulata]
XP_008473261	PREDICTED: homeobox protein B-H1-like [Diaphorina citri]
XP_008481092	PREDICTED: homeobox protein abdominal-A homolog [Diaphorina citri]
XP_008487962	PREDICTED: homeotic protein deformed [Diaphorina citri]
XP_008489821	PREDICTED: barH-like 1 homeobox protein, partial [Calypte anna]
XP_008494359	PREDICTED: homeobox protein MSX-1 [Calypte anna]
XP_008559758	PREDICTED: homeotic protein ultrabithorax isoform X2 [Microplitis demolitor]
XP_008919202	PREDICTED: homeobox protein MSX-1 [Manacus vitellinus]
XP_009327169	PREDICTED: homeobox protein MSX-1 [Pygoscelis adeliae]
XP_009645359	PREDICTED: homeobox protein MSX-2 [Egretta garzetta]
XP_009870132	PREDICTED: homeobox protein Hox-B1, partial [Apaloderma vittatum]
XP_009894572	PREDICTED: barH-like 1 homeobox protein, partial [Picoides pubescens]
XP_009962682	PREDICTED: homeobox protein Hox-B1, partial [Tyto alba]
XP_009993327	PREDICTED: brain-specific homeobox protein homolog [Chaetura pelagica]
XP_010125476	PREDICTED: homeobox protein GHOX-7-like, partial [Chlamydotis macqueenii]
XP_010158126	PREDICTED: homeobox protein Nkx-2.6-like, partial [Eurypyga helias]
XP_010218153	PREDICTED: homeobox protein MSX-1 [Tinamus guttatus]
XP_010295047	PREDICTED: homeobox protein H17, partial [Phaethon lepturus]
XP_010708737	PREDICTED: homeobox protein MSX-1 [Meleagris gallopavo]
XP_010740428	PREDICTED: homeobox protein MSX-1 [Larimichthys crocea]
XP_010765038	PREDICTED: barH-like 2 homeobox protein [Notothenia coriiceps]
XP_010771400	PREDICTED: transcription factor LBX1 [Notothenia coriiceps]
XP_010868231	PREDICTED: homeobox protein HMX3-like [Esox lucius]
XP_010870399	PREDICTED: barH-like 2 homeobox protein [Esox lucius]
XP_010892954	PREDICTED: T-cell leukemia homeobox protein 3-like [Esox lucius]
XP_010894067	PREDICTED: T-cell leukemia homeobox protein 3 [Esox lucius]
XP_010965528	PREDICTED: brain-specific homeobox protein homolog [Camelus bactrianus]
XP_011055476	PREDICTED: homeotic protein proboscipedia isoform X2 [Acromyrmex echinatior]
XP_011055478	PREDICTED: homeobox protein Hox-B1a [Acromyrmex echinatior]
XP_011148733	PREDICTED: homeotic protein labial-like [Harpegnathos saltator]
XP_011149287	PREDICTED: homeotic protein proboscipedia [Harpegnathos saltator]
XP_011155414	PREDICTED: homeotic protein proboscipedia [Solenopsis invicta]
XP_011256041	PREDICTED: homeotic protein deformed [Camponotus floridanus]
XP_011256835	PREDICTED: homeobox protein B-H2-like [Camponotus floridanus]
XP_011258058	PREDICTED: homeotic protein ultrabithorax [Camponotus floridanus]
XP_011269817	PREDICTED: homeobox protein Hox-B1a-like [Camponotus floridanus]
XP_011283973	PREDICTED: homeobox protein GBX-2 [Felis catus]

XP_011294141	PREDICTED: homeotic protein labial-like, partial [Musca domestica]
XP_011310234	PREDICTED: homeobox protein GBX-2 [Fopius arisanus]
XP_011342229	PREDICTED: homeobox protein Hox-B1a-like [Cerapachys biroi]
XP_011342230	PREDICTED: homeotic protein proboscipedia [Cerapachys biroi]
XP_011344364	PREDICTED: homeobox protein B-H2 [Cerapachys biroi]
XP_011414445	PREDICTED: homeobox protein GBX-2-like [Crassostrea gigas]
XP_011437391	PREDICTED: homeobox protein Nkx-2.2a-like [Crassostrea gigas]
XP_011441569	PREDICTED: homeobox protein Dlx6a-like [Crassostrea gigas]
XP_011451803	PREDICTED: homeobox protein Nkx-2.1-like [Crassostrea gigas]
XP_011482809	PREDICTED: homeobox protein MSX-2 isoform X2 [Oryzias latipes]
XP_011495613	PREDICTED: homeobox protein Nkx-6.1 [Ceratosolen solmsi marchali]
XP_011555719	PREDICTED: homeobox protein Hox-C4 [Plutella xylostella]
XP_011561507	PREDICTED: homeobox protein Hmx [Plutella xylostella]
XP_011569017	PREDICTED: homeobox protein Hox-B4-like [Plutella xylostella]
XP_011637906	PREDICTED: homeobox protein B-H2 [Pogonomyrmex barbatus]
XP_011639093	PREDICTED: homeotic protein proboscipedia [Pogonomyrmex barbatus]
XP_011639094	PREDICTED: homeobox protein Hox-B1 [Pogonomyrmex barbatus]
XP_011695898	PREDICTED: homeobox protein Hox-B1a-like [Wasmannia auropunctata]
XP_011695901	PREDICTED: homeotic protein proboscipedia [Wasmannia auropunctata]
XP_011870664	PREDICTED: homeotic protein proboscipedia [Vollenhovia emeryi]
XP_011870678	PREDICTED: homeobox protein abdominal-A homolog isoform X1 [Vollenhovia emeryi]
XP_012054481	PREDICTED: homeotic protein proboscipedia [Atta cephalotes]
XP_012054482	PREDICTED: homeobox protein Hox-B1a [Atta cephalotes]
XP_012162595	PREDICTED: homeobox protein Nkx-2.1 isoform X1 [Ceratitis capitata]
XP_012225633	PREDICTED: homeotic protein proboscipedia [Linepithema humile]
XP_012267082	PREDICTED: homeotic protein ultrabithorax [Athalia rosae]
XP_012268630	PREDICTED: homeobox protein B-H1-like [Athalia rosae]
XP_012276293	PREDICTED: homeotic protein labial [Orussus abietinus]
XP_012276321	PREDICTED: homeobox protein Hox-A4 [Orussus abietinus]
XP_012347968	PREDICTED: homeobox protein Hox-B1a-like [Apis florea]
XP_012524740	PREDICTED: homeobox protein Hox-A4 [Monomorium pharaonis]
XP_012542576	PREDICTED: homeotic protein proboscipedia [Monomorium pharaonis]
XP_012683084	PREDICTED: brain-specific homeobox protein homolog [Clupea harengus]
XP_012685430	PREDICTED: T-cell leukemia homeobox protein 3-like [Clupea harengus]
XP_012686839	PREDICTED: homeobox protein Nkx-2.5 [Clupea harengus]
XP_012687703	PREDICTED: homeobox protein Nkx-2.3 [Clupea harengus]
XP_012707525	PREDICTED: T-cell leukemia homeobox protein 1 [Fundulus heteroclitus]
XP_012873727	PREDICTED: barH-like 2 homeobox protein [Dipodomys ordii]
XP_012984340	PREDICTED: homeobox protein MSX-1 [Melopsittacus undulatus]
XP_013063618	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Biomphalaria glabrata]
XP_013104192	PREDICTED: homeotic protein labial-like [Stomoxys calcitrans]
XP_013106133	PREDICTED: homeobox protein unplugged-like, partial [Stomoxys calcitrans]
XP_013108189	PREDICTED: homeobox protein B-H2-like [Stomoxys calcitrans]
XP_013138028	PREDICTED: transcription factor LBX1-like [Papilio polytes]
XP_013139547	PREDICTED: homeobox protein Hox-B4 [Papilio polytes]
XP_013165384	PREDICTED: barH-like 1 homeobox protein [Papilio xuthus]
XP_013177038	PREDICTED: homeobox protein GBX-2-like [Papilio xuthus]
XP_013185056	PREDICTED: homeobox protein BarH-like 1b [Amyelois transitella]
XP_013185500	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Amyelois transitella]
XP_013188056	PREDICTED: homeobox protein HMX3-like [Amyelois transitella]
XP_013193972	PREDICTED: homeobox protein Hox-B4 [Amyelois transitella]
XP_013378776	PREDICTED: homeobox protein Nkx-2.5-like [Lingula anatina]
XP_013378782	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Lingula anatina]
XP_013394544	PREDICTED: homeobox protein Dlx1a-like isoform X1 [Lingula anatina]
XP_013394545	PREDICTED: homeobox protein Dlx1a-like isoform X2 [Lingula anatina]
XP_013403758	PREDICTED: homeobox protein HMX3-like [Lingula anatina]
XP_013772635	PREDICTED: homeobox protein Nkx-2.2-like [Limulus polyphemus]
XP_013774538	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013775139	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013775457	PREDICTED: homeobox protein Hox-A11b-like [Limulus polyphemus]
XP_013775825	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013775826	PREDICTED: homeobox protein abdominal-A homolog [Limulus polyphemus]
XP_013776086	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013776376	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]
XP_013776587	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013776725	PREDICTED: homeobox protein Hox-B4a-like [Limulus polyphemus]
XP_013776843	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]
XP_013777106	PREDICTED: protein enabled homolog [Limulus polyphemus]
XP_013780477	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783221	PREDICTED: brain-specific homeobox protein homolog [Limulus polyphemus]
XP_013783383	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783573	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]
XP_013783575	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]

XP_013783998	PREDICTED: homeobox protein MSX-2-like [Limulus polyphemus]
XP_013784402	PREDICTED: homeobox protein Hox-B4-like [Limulus polyphemus]
XP_013785537	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013785548	PREDICTED: homeobox protein B-H1-like [Limulus polyphemus]
XP_013785691	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013786467	PREDICTED: homeobox protein vnd-like [Limulus polyphemus]
XP_013786746	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013787176	PREDICTED: homeobox protein MSX-3-like [Limulus polyphemus]
XP_013788660	PREDICTED: homeobox protein DLX-6-like [Limulus polyphemus]
XP_013789064	PREDICTED: homeobox protein Nkx-2.5-like [Limulus polyphemus]
XP_013789774	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013790370	PREDICTED: homeobox protein Hox-A4-like [Limulus polyphemus]
XP_013790705	PREDICTED: homeobox protein HMX3-like [Limulus polyphemus]
XP_013790991	PREDICTED: homeotic protein proboscipedia-like, partial [Limulus polyphemus]
XP_013791445	PREDICTED: homeobox protein ceh-31-like, partial [Limulus polyphemus]
XP_013792062	PREDICTED: homeotic protein ultrabithorax-like, partial [Limulus polyphemus]
XP_013792158	PREDICTED: homeobox protein Hox-D4-like [Limulus polyphemus]
XP_013794103	PREDICTED: homeotic protein ultrabithorax-like [Limulus polyphemus]
XP_013794104	PREDICTED: homeobox protein abdominal-A homolog [Limulus polyphemus]
XP_013794355	PREDICTED: homeobox protein unplugged-like [Limulus polyphemus]
XP_013794488	PREDICTED: T-cell leukemia homeobox protein 3-like [Limulus polyphemus]
XP_013794489	PREDICTED: transcription factor LBX1-like [Limulus polyphemus]
XP_013794562	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013867753	PREDICTED: homeobox protein MSX-2-like [Austrofundulus limnaeus]
XP_013879114	PREDICTED: barH-like 2 homeobox protein [Austrofundulus limnaeus]
XP_013921049	PREDICTED: homeobox protein MSX-2 [Thamnophis sirtalis]
XP_013978546	PREDICTED: barH-like 2 homeobox protein [Salmo salar]
XP_013983956	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Salmo salar]
XP_014052040	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014068039	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014209645	PREDICTED: homeobox protein GBX-1-like [Copidosoma floridanum]
XP_014219299	PREDICTED: homeotic protein ultrabithorax-like isoform X2 [Copidosoma floridanum]
XP_014240108	PREDICTED: homeobox protein Hox-B4 isoform X1 [Cimex lectularius]
XP_014240109	PREDICTED: homeobox protein Hox-B4 isoform X2 [Cimex lectularius]
XP_014242016	PREDICTED: transcription factor LBX1-like [Cimex lectularius]
XP_014242034	PREDICTED: homeobox protein HMX3-like [Cimex lectularius]
XP_014245972	PREDICTED: homeotic protein distal-less isoform X2 [Cimex lectularius]
XP_014249513	PREDICTED: homeobox protein Nkx-2.1-like [Cimex lectularius]
XP_014274437	PREDICTED: homeobox protein Nkx-2.1-like [Halyomorpha halys]
XP_014280507	PREDICTED: homeobox protein HMX3-like [Halyomorpha halys]
XP_014293083	PREDICTED: homeobox protein HMX3-like, partial [Halyomorpha halys]
XP_014328725	PREDICTED: T-cell leukemia homeobox protein 3 [Xiphophorus maculatus]
XP_014361996	PREDICTED: homeobox protein HMX3-B-like [Papilio machaon]
XP_014370704	PREDICTED: barH-like 1 homeobox protein [Papilio machaon]
XP_014385363	PREDICTED: barH-like 1 homeobox protein, partial [Myotis brandtii]

9.4.2.22 *Lethal of scute*

Name	**Description**
A8E5T6 (TCF21_XENTR)	RecName: Full=Transcription factor 21; Short=TCF-21; AltName: Full=Capsulin; AltName: Full=Epicardin; AltName: Full=Podocyte-expressed 1; Short=Pod 1; Short=Pod-1
AAF45500	lethal of scute [Drosophila melanogaster]
D2CLZ9 (ATOH8_DANRE)	RecName: Full=Protein atonal homolog 8
Locus_1_Transcript_14641/166847_Confidence_1.000_Length_2311 - ORF 13 (frame 2) translation	Locus_1_Transcript_14641/166847_Confidence_1.000_Length_2311
Locus_1_Transcript_156819/166847_Confidence_1.000_Length_1176 - ORF 9 (frame 1) translation	Locus_1_Transcript_156819/166847_Confidence_1.000_Length_1176
Locus_1749_Transcript_36/36_Confidence_0.228_Length_3197 - ORF 13 (frame 3) translation	Locus_1749_Transcript_36/36_Confidence_0.228_Length_3197
Locus_2476_Transcript_7/7_Confidence_0.675_Length_4505 - ORF 1 (frame 3) translation	Locus_2476_Transcript_7/7_Confidence_0.675_Length_4505
Locus_8944_Transcript_1/1_Confidence_1.000_Length_2758 - ORF 3 (frame 1) translation	Locus_8944_Transcript_1/1_Confidence_1.000_Length_2758
Locus_10831_Transcript_3/3_Confidence_0.600_Length_1977 - ORF 10 (frame 2) translation	Locus_10831_Transcript_3/3_Confidence_0.600_Length_1977
Locus_15221_Transcript_6/6_Confidence_0.357_Length_4080 - ORF 1 (frame 3) translation	Locus_15221_Transcript_6/6_Confidence_0.357_Length_4080
Locus_15416_Transcript_2/2_Confidence_0.833_Length_1653 - ORF 3 (frame 1) translation	Locus_15416_Transcript_2/2_Confidence_0.833_Length_1653
Locus_15466_Transcript_2/2_Confidence_0.833_Length_2126 - ORF 1 (frame 1) translation	Locus_15466_Transcript_2/2_Confidence_0.833_Length_2126
Locus_16016_Transcript_1/1_Confidence_1.000_Length_1609 - ORF 3 (frame 1) translation	Locus_16016_Transcript_1/1_Confidence_1.000_Length_1609
Locus_16298_Transcript_2/2_Confidence_0.833_Length_2759 - ORF 5 (frame 3) translation	Locus_16298_Transcript_2/2_Confidence_0.833_Length_2759
Locus_16559_Transcript_11/12_Confidence_0.301_Length_4471 - ORF 19 (frame 1) translation	Locus_16559_Transcript_11/12_Confidence_0.301_Length_4471
Locus_19091_Transcript_1/1_Confidence_1.000_Length_1428 - ORF 1 (frame 1) translation	Locus_19091_Transcript_1/1_Confidence_1.000_Length_1428

Locus_19960_Transcript_7/8_Confidence_0.404_Length_2120 - ORF 6 (frame 1) translation	Locus_19960_Transcript_7/8_Confidence_0.404_Length_2120
Locus_20032_Transcript_1/1_Confidence_1.000_Length_942 - ORF 1 (frame 3) translation	Locus_20032_Transcript_1/1_Confidence_1.000_Length_942
Locus_20078_Transcript_2/2_Confidence_0.750_Length_1220 - ORF 7 (frame 2) translation	Locus_20078_Transcript_2/2_Confidence_0.750_Length_1220
Locus_20468_Transcript_1/1_Confidence_1.000_Length_932 - ORF 2 (frame 3) translation	Locus_20468_Transcript_1/1_Confidence_1.000_Length_932
Locus_24541_Transcript_3/3_Confidence_0.714_Length_1127 - ORF 3 (frame 2) translation	Locus_24541_Transcript_3/3_Confidence_0.714_Length_1127
Locus_27013_Transcript_1/1_Confidence_1.000_Length_1797 - ORF 1 (frame 1) translation	Locus_27013_Transcript_1/1_Confidence_1.000_Length_1797
NP_571701	heart- and neural crest derivatives-expressed protein 2 [Danio rerio]
NP_997524	pancreas transcription factor 1 subunit alpha [Danio rerio]
NP_001034533	asense [Tribolium castaneum]
NP_001034537	achaete-scute homolog [Tribolium castaneum]
NP_001079247	achaete-scute homolog 1 [Xenopus laevis]
NP_001079352	twist-related protein [Xenopus laevis]
NP_001098070	twist-related protein 2 [Takifugu rubripes]
NP_001158485	achaete-scute-like protein [Saccoglossus kowalevskii]
NP_001179075	musculin [Bos taurus]
O09105 (NDF4_MOUSE)	RecName: Full=Neurogenic differentiation factor 4; Short=NeuroD4; AltName: Full=Helix-loop-helix protein mATH-3; Short=mATH3; AltName: Full=Protein atonal homolog 3
O13125 (ATO7A_XENLA)	RecName: Full=Protein atonal homolog 7-A; AltName: Full=Helix-loop-helix protein xATH-5-A; AltName: Full=Protein atonal homolog 5-A; Short=xAth5-A
O13126 (ATO7B_XENLA)	RecName: Full=Protein atonal homolog 7-B; AltName: Full=Helix-loop-helix protein xATH-5-B; AltName: Full=Protein atonal homolog 5-B; Short=xAth5-B
O35437 (TCF21_MOUSE)	RecName: Full=Transcription factor 21; Short=TCF-21; AltName: Full=Capsulin; AltName: Full=Epicardin; AltName: Full=Podocyte-expressed 1; Short=Pod-1
O35885 (ASCL2_MOUSE)	RecName: Full=Achaete-scute homolog 2; Short=ASH-2; Short=mASH-2; Short=mASH2
O42606 (NGN1_DANRE)	RecName: Full=Neurogenin-1; Short=NGN-1; AltName: Full=Neurogenic differentiation factor 3; Short=NeuroD3; AltName: Full=Neurogenin-related protein 1
O43680 (TCF21_HUMAN)	RecName: Full=Transcription factor 21; Short=TCF-21; AltName: Full=Capsulin; AltName: Full=Class A basic helix-loop-helix protein 23; Short=bHLHa23; AltName: Full=Epicardin; AltName: Full=Podocyte-expressed 1; Short=Pod-1
O57598 (ATOH7_CHICK)	RecName: Full=Protein atonal homolog 7; AltName: Full=Helix-loop-helix protein cATH-5; Short=cATH5; AltName: Full=Protein atonal homolog 5
O60682 (MUSC_HUMAN)	RecName: Full=Musculin; AltName: Full=Activated B-cell factor 1; Short=ABF-1; AltName: Full=Class A basic helix-loop-helix protein 22; Short=bHLHa22
O73615 (HAND1_XENLA)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1; AltName: Full=Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1; Short=eHAND
O73823 (TAL1_XENLA)	RecName: Full=T-cell acute lymphocytic leukemia protein 1; Short=TAL-1; AltName: Full=Stem cell leukemia protein SCL; Short=xSCL
O88940 (MUSC_MOUSE)	RecName: Full=Musculin; AltName: Full=Myogenic repressor
O93507 (TAL1_DANRE)	RecName: Full=T-cell acute lymphocytic leukemia protein 1 homolog; Short=TAL-1; AltName: Full=Stem cell protein; Short=zSCL
P10083 (AST5_DROME)	RecName: Full=Achaete-scute complex protein T5; AltName: Full=Protein achaete
P10084 (AST4_DROME)	RecName: Full=Achaete-scute complex protein T4; AltName: Full=Protein scute
P12980 (LYL1_HUMAN)	RecName: Full=Protein lyl-1; AltName: Full=Class A basic helix-loop-helix protein 18; Short=bHLHa18; AltName: Full=Lymphoblastic leukemia-derived sequence 1
P13903 (TWIST_XENLA)	RecName: Full=Twist-related protein; AltName: Full=T18; AltName: Full=X-twist
P17542 (TAL1_HUMAN)	RecName: Full=T-cell acute lymphocytic leukemia protein 1; Short=TAL-1; AltName: Full=Class A basic helix-loop-helix protein 17; Short=bHLHa17; AltName: Full=Stem cell protein; AltName: Full=T-cell leukemia/lymphoma protein 5
P19359 (ASCL1_RAT)	RecName: Full=Achaete-scute homolog 1
P19360 (ASCL2_RAT)	RecName: Full=Achaete-scute homolog 2; AltName: Full=Mash2
P22091 (TAL1_MOUSE)	RecName: Full=T-cell acute lymphocytic leukemia protein 1 homolog; Short=TAL-1; AltName: Full=Stem cell protein
P24899 (TAL1_CHICK)	RecName: Full=T-cell acute lymphocytic leukemia protein 1 homolog; Short=TAL-1; AltName: Full=Stem cell protein
P26687 (TWST1_MOUSE)	RecName: Full=Twist-related protein 1; AltName: Full=M-twist
P27792 (LYL1_MOUSE)	RecName: Full=Protein lyl-1; AltName: Full=Lymphoblastic leukemia-derived sequence 1
P41894 (DEI_DROME)	RecName: Full=Helix-loop-helix protein delilah; AltName: Full=Protein taxi
P50553 (ASCL1_HUMAN)	RecName: Full=Achaete-scute homolog 1; Short=ASH-1; Short=hASH1; AltName: Full=Class A basic helix-loop-helix protein 46; Short=bHLHa46
P57100 (HAND1_RABIT)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1; AltName: Full=Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1; Short=eHAND
P57101 (HAND2_XENLA)	RecName: Full=Heart- and neural crest derivatives-expressed protein 2; AltName: Full=Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2; Short=dHAND

P57102 (HAND2_DANRE)	RecName: Full=Heart- and neural crest derivatives-expressed protein 2; AltName: Full=Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2; Short=dHAND
P61295 (HAND2_RAT)	RecName: Full=Heart- and neural crest derivatives-expressed protein 2; AltName: Full=Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2; Short=dHAND
P70595 (NGN1_RAT)	RecName: Full=Neurogenin-1; Short=NGN-1; AltName: Full=Neurogenic basic-helix-loop-helix protein; AltName: Full=Neurogenic differentiation factor 3; Short=NeuroD3
P70660 (NGN1_MOUSE)	RecName: Full=Neurogenin-1; Short=NGN-1; AltName: Full=Helix-loop-helix protein mATH-4C; Short=mATH4C; AltName: Full=Neurogenic basic-helix-loop-helix protein; AltName: Full=Neurogenic differentiation factor 3; Short=NeuroD3
P70661 (NGN3_MOUSE)	RecName: Full=Neurogenin-3; Short=NGN-3; AltName: Full=Helix-loop-helix protein mATH-4B; Short=mATH4B; AltName: Full=Protein atonal homolog 5
P79766 (NDF4_CHICK)	RecName: Full=Neurogenic differentiation factor 4; Short=NeuroD4; AltName: Full=NeuroM
P79782 (TCF15_CHICK)	RecName: Full=Transcription factor 15; Short=TCF-15; AltName: Full=Paraxis; AltName: Full=Protein bHLH-EC2
P97831 (TWST2_RAT)	RecName: Full=Twist-related protein 2
P97832 (HAND1_RAT)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1; AltName: Full=Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1; Short=eHAND
Q0VCE2 (HAND1_BOVIN)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1
Q2EGB9 (ASCL2_BOVIN)	RecName: Full=Achaete-scute homolog 2; AltName: Full=Mash2
Q2T9Q7 (TCF23_BOVIN)	RecName: Full=Transcription factor 23; Short=TCF-23
Q4ZHW1 (PTF1A_XENLA)	RecName: Full=Pancreas transcription factor 1 subunit alpha; AltName: Full=Pancreas-specific transcription factor 1a; AltName: Full=Transcription factor Ptf1a/p48
Q5E9S3 (TCF21_BOVIN)	RecName: Full=Transcription factor 21; Short=TCF-21
Q6GNB7 (TCF21_XENLA)	RecName: Full=Transcription factor 21; Short=TCF-21; AltName: Full=Capsulin; AltName: Full=Epicardin; AltName: Full=Podocyte-expressed 1; Short=Pod 1; Short=Pod-1
Q6XD76 (ASCL4_HUMAN)	RecName: Full=Achaete-scute homolog 4; Short=ASH-4; Short=hASH4; AltName: Full=Achaete-scute-like protein 4; AltName: Full=Class A basic helix-loop-helix protein 44; Short=bHLHa44
Q7JGP2 (TWST1_MACTO)	RecName: Full=Twist-related protein 1
Q7RTS3 (PTF1A_HUMAN)	RecName: Full=Pancreas transcription factor 1 subunit alpha; AltName: Full=Class A basic helix-loop-helix protein 29; Short=bHLHa29; AltName: Full=Pancreas-specific transcription factor 1a; AltName: Full=bHLH transcription factor p48; AltName: Full=p48 DNA-binding subunit of transcription factor PTF1; Short=PTF1-p48
Q7RTU0 (TCF24_HUMAN)	RecName: Full=Transcription factor 24; Short=TCF-24
Q7RTU1 (TCF23_HUMAN)	RecName: Full=Transcription factor 23; Short=TCF-23; AltName: Full=Class A basic helix-loop-helix protein 24; Short=bHLHa24
Q7RTU5 (ASCL5_HUMAN)	RecName: Full=Achaete-scute homolog 5; Short=ASH-5; Short=hASH5; AltName: Full=Class A basic helix-loop-helix protein 47; Short=bHLHa47
Q7ZSX3 (PTF1A_DANRE)	RecName: Full=Pancreas transcription factor 1 subunit alpha; AltName: Full=Pancreas-specific transcription factor 1a; AltName: Full=bHLH transcription factor p48
Q8AW52 (ATOH7_DANRE)	RecName: Full=Protein atonal homolog 7; AltName: Full=Helix-loop-helix protein zATH-5; Short=zATH5; AltName: Full=Protein atonal homolog 5; AltName: Full=Protein lakritz
Q8MIB5 (TWST1_SAGOE)	RecName: Full=Twist-related protein 1
Q8MIB9 (TWST1_PONPY)	RecName: Full=Twist-related protein 1
Q8MID5 (TWST1_MICMU)	RecName: Full=Twist-related protein 1
Q8MIF3 (TWST1_EULFU)	RecName: Full=Twist-related protein 1
Q8MIH8 (TWST1_CEBCA)	RecName: Full=Twist-related protein 1
Q9D030 (TWST2_MOUSE)	RecName: Full=Twist-related protein 2; AltName: Full=Dermis-expressed protein 1; Short=Dermo-1
Q9HD90 (NDF4_HUMAN)	RecName: Full=Neurogenic differentiation factor 4; Short=NeuroD4; AltName: Full=Class A basic helix-loop-helix protein 4; Short=bHLHa4; AltName: Full=Protein atonal homolog 3; Short=ATH-3; Short=Atoh3
Q9JJR7 (ASCL3_MOUSE)	RecName: Full=Achaete-scute homolog 3; Short=ASH-3; Short=mASH-3; Short=mASH3; AltName: Full=bHLH transcriptional regulator Sgn-1
Q9JLR5 (TCF23_MOUSE)	RecName: Full=Transcription factor 23; Short=TCF-23; AltName: Full=Basic helix-loop-helix transcription factor OUT; AltName: Full=Ovary, uterus and testis protein
Q9NQ33 (ASCL3_HUMAN)	RecName: Full=Achaete-scute homolog 3; Short=ASH-3; Short=hASH3; AltName: Full=Class A basic helix-loop-helix protein 42; Short=bHLHa42; AltName: Full=bHLH transcriptional regulator Sgn-1
Q9QX98 (PTF1A_MOUSE)	RecName: Full=Pancreas transcription factor 1 subunit alpha; AltName: Full=Pancreas-specific transcription factor 1a; AltName: Full=bHLH transcription factor p48; AltName: Full=p48 DNA-binding subunit of transcription factor PTF1; Short=PTF1-p48
Q9VGJ5 (FER3_DROME)	RecName: Full=Protein Fer3; AltName: Full=Basic helix-loop-helix protein N-twist; AltName: Full=Nephew of atonal 3; AltName: Full=Neuronal twist
Q9Y4Z2 (NGN3_HUMAN)	RecName: Full=Neurogenin-3; Short=NGN-3; AltName: Full=Class A basic helix-loop-helix protein 7; Short=bHLHa7; AltName: Full=Protein atonal homolog 5
Q32PV5 (TCF21_DANRE)	RecName: Full=Transcription factor 21; Short=TCF-21; AltName: Full=Capsulin; AltName: Full=Epicardin; AltName: Full=MyoRa2
Q66HH3 (LYL1_RAT)	RecName: Full=Protein lyl-1; AltName: Full=Lymphoblastic leukemia-derived sequence 1
Q90YI8 (TAL1_TAKRU)	RecName: Full=T-cell acute lymphocytic leukemia protein 1; Short=TAL-1; AltName: Full=FrSCL; AltName: Full=Stem cell protein

Q96RJ6 (FER3L_HUMAN)	RecName: Full=Fer3-like protein; AltName: Full=Basic helix-loop-helix protein N-twist; AltName: Full=Class A basic helix-loop-helix protein 31; Short=bHLHa31; AltName: Full=Nephew of atonal 3; AltName: Full=Neuronal twist
Q96SQ7 (ATOH8_HUMAN)	RecName: Full=Protein atonal homolog 8; AltName: Full=Class A basic helix-loop-helix protein 21; Short=bHLHa21; AltName: Full=Helix-loop-helix protein hATH-6; Short=hATH6
Q99NA2 (ATOH8_MOUSE)	RecName: Full=Protein atonal homolog 8; AltName: Full=Helix-loop-helix protein mATH-6; Short=mATH6; AltName: Full=Okadin
Q923Z4 (FER3L_MOUSE)	RecName: Full=Fer3-like protein; AltName: Full=Basic helix-loop-helix protein N-twist; AltName: Full=Nephew of atonal 3; AltName: Full=Neuronal twist
Q02067 (ASCL1_MOUSE)	RecName: Full=Achaete-scute homolog 1; Short=ASH-1; Short=mASH-1; Short=mASH1
Q06234 (ASCL1_XENLA)	RecName: Full=Achaete-scute homolog 1
Q10007 (HLH6_CAEEL)	RecName: Full=Helix-loop-helix protein 6
Q13562 (NDF1_HUMAN)	RecName: Full=Neurogenic differentiation factor 1; Short=NeuroD; Short=NeuroD1; AltName: Full=Class A basic helix-loop-helix protein 3; Short=bHLHa3
Q15672 (TWST1_HUMAN)	RecName: Full=Twist-related protein 1; AltName: Full=Class A basic helix-loop-helix protein 38; Short=bHLHa38; AltName: Full=H-twist
Q16559 (TAL2_HUMAN)	RecName: Full=T-cell acute lymphocytic leukemia protein 2; Short=TAL-2; AltName: Full=Class A basic helix-loop-helix protein 19; Short=bHLHa19
Q20561 (HLH13_CAEEL)	RecName: Full=Helix-loop-helix protein 13; AltName: Full=Fer3-like protein; AltName: Full=Nephew of atonal 3
Q60430 (NDF1_MESAU)	RecName: Full=Neurogenic differentiation factor 1; Short=NeuroD1; AltName: Full=Beta-cell E-box transcriptional activator 2; Short=Beta2
Q60539 (TCF15_MESAU)	RecName: Full=Transcription factor 15; Short=TCF-15; AltName: Full=Meso1; AltName: Full=Paraxis; AltName: Full=Protein bHLH-EC2
Q60756 (TCF15_MOUSE)	RecName: Full=Transcription factor 15; Short=TCF-15; AltName: Full=Meso1; AltName: Full=Paraxis; AltName: Full=Protein bHLH-EC2
Q60867 (NDF1_MOUSE)	RecName: Full=Neurogenic differentiation factor 1; Short=NeuroD1; AltName: Full=Beta-cell E-box transcriptional activator 2; Short=Beta2
Q64279 (HAND1_MOUSE)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1; AltName: Full=Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1; Short=eHAND; AltName: Full=Helix-loop-helix transcription factor expressed in extraembryonic mesoderm and trophoblast; AltName: Full=Thing-1; Short=Th1
Q64289 (NDF1_RAT)	RecName: Full=Neurogenic differentiation factor 1; Short=NeuroD1; AltName: Full=Basic helix-loop-helix factor 1; Short=BHF-1
Q64305 (PTF1A_RAT)	RecName: Full=Pancreas transcription factor 1 subunit alpha; AltName: Full=Pancreas-specific transcription factor 1a; AltName: Full=bHLH transcription factor p48; AltName: Full=p48 DNA-binding subunit of transcription factor PTF1; Short=PTF1-p48
Q90259 (ASL1A_DANRE)	RecName: Full=Achaete-scute homolog 1a; Short=Zash-1a; AltName: Full=Pituitary-absent protein
Q90260 (ASL1B_DANRE)	RecName: Full=Achaete-scute homolog 1b; Short=Zash-1b
Q90690 (HAND2_CHICK)	RecName: Full=Heart- and neural crest derivatives-expressed protein 2; AltName: Full=Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2; Short=dHAND
Q90691 (HAND1_CHICK)	RecName: Full=Heart- and neural crest derivatives-expressed protein 1; AltName: Full=Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1; Short=eHAND
Q92886 (NGN1_HUMAN)	RecName: Full=Neurogenin-1; Short=NGN-1; AltName: Full=Class A basic helix-loop-helix protein 6; Short=bHLHa6; AltName: Full=Neurogenic basic-helix-loop-helix protein; AltName: Full=Neurogenic differentiation factor 3; Short=NeuroD3
Q99929 (ASCL2_HUMAN)	RecName: Full=Achaete-scute homolog 2; Short=ASH-2; Short=hASH2; AltName: Full=Class A basic helix-loop-helix protein 45; Short=bHLHa45; AltName: Full=Mash2
XP_787068	PREDICTED: pancreas transcription factor 1 subunit alpha-like [Strongylocentrotus purpuratus]
XP_796307	PREDICTED: protein atonal homolog 8-like, partial [Strongylocentrotus purpuratus]
XP_973186	PREDICTED: helix-loop-helix protein delilah [Tribolium castaneum]
XP_001510876	PREDICTED: twist-related protein 2 [Ornithorhynchus anatinus]
XP_002410238	helix-loop-helix protein hen, putative [Ixodes scapularis]
XP_002737163	PREDICTED: neurogenic differentiation factor 1-like [Saccoglossus kowalevskii]
XP_003269983	PREDICTED: achaete-scute homolog 1 [Nomascus leucogenys]
XP_003372074	helix-loop-helix protein 6 [Trichinella spiralis]
XP_003443609	PREDICTED: transcription factor 24 [Oreochromis niloticus]
XP_003745941	PREDICTED: protein atonal homolog 7-A-like [Metaseiulus occidentalis]
XP_003767610	PREDICTED: achaete-scute homolog 5 [Sarcophilus harrisii]
XP_003979728	PREDICTED: achaete-scute homolog 1 [Takifugu rubripes]
XP_003982906	PREDICTED: twist-related protein 1, partial [Felis catus]
XP_004053828	PREDICTED: achaete-scute homolog 1 [Gorilla gorilla gorilla]
XP_004081082	PREDICTED: transcription factor 24 [Oryzias latipes]
XP_004083256	PREDICTED: achaete-scute homolog 1 [Oryzias latipes]
XP_004546703	PREDICTED: transcription factor 24 [Maylandia zebra]
XP_005041199	PREDICTED: twist-related protein 1, partial [Ficedula albicollis]
XP_005089768	PREDICTED: T-cell acute lymphocytic leukemia protein 1 homolog [Aplysia californica]
XP_005090266	PREDICTED: nascent polypeptide-associated complex subunit alpha, muscle-specific form-like [Aplysia californica]
XP_005162807	PREDICTED: transcription factor 24 [Danio rerio]
XP_005299958	PREDICTED: twist-related protein 2 [Chrysemys picta bellii]

XP_005302876	PREDICTED: pancreas transcription factor 1 subunit alpha [Chrysemys picta bellii]
XP_005303754	PREDICTED: achaete-scute homolog 1 [Chrysemys picta bellii]
XP_005328863	PREDICTED: twist-related protein 1 [Ictidomys tridecemlineatus]
XP_005475946	PREDICTED: achaete-scute homolog 1 [Oreochromis niloticus]
XP_005540429	PREDICTED: achaete-scute homolog 5 [Macaca fascicularis]
XP_005722654	PREDICTED: transcription factor 24 [Pundamilia nyererei]
XP_005800013	PREDICTED: achaete-scute homolog 1 [Xiphophorus maculatus]
XP_005934300	PREDICTED: achaete-scute homolog 1 [Haplochromis burtoni]
XP_005975888	PREDICTED: heart- and neural crest derivatives-expressed protein 2, partial [Pantholops hodgsonii]
XP_005991332	PREDICTED: twist-related protein 1 [Latimeria chalumnae]
XP_006080530	PREDICTED: musculin [Bubalus bubalis]
XP_006119596	PREDICTED: pancreas transcription factor 1 subunit alpha [Pelodiscus sinensis]
XP_006154546	PREDICTED: twist-related protein 1, partial [Tupaia chinensis]
XP_006630021	PREDICTED: heart- and neural crest derivatives-expressed protein 2-like [Lepisosteus oculatus]
XP_006748254	PREDICTED: achaete-scute homolog 1-like [Leptonychotes weddellii]
XP_006794646	PREDICTED: transcription factor 24-like [Neolamprologus brichardi]
XP_006825561	PREDICTED: pancreas transcription factor 1 subunit alpha [Saccoglossus kowalevskii]
XP_007067125	PREDICTED: heart- and neural crest derivatives-expressed protein 2 [Chelonia mydas]
XP_007114875	PREDICTED: musculin [Physeter catodon]
XP_007256435	PREDICTED: twist-related protein 2 [Astyanax mexicanus]
XP_007445427	PREDICTED: T-cell acute lymphocytic leukemia protein 1 homolog, partial [Python bivittatus]
XP_007481183	PREDICTED: achaete-scute homolog 5 isoform X1 [Monodelphis domestica]
XP_007527325	PREDICTED: musculin [Erinaceus europaeus]
XP_007554551	PREDICTED: transcription factor 24 [Poecilia formosa]
XP_007555394	PREDICTED: achaete-scute homolog 1 [Poecilia formosa]
XP_007655932	PREDICTED: achaete-scute homolog 5 [Ornithorhynchus anatinus]
XP_007897889	PREDICTED: twist-related protein 1 [Callorhinchus milii]
XP_007903037	PREDICTED: achaete-scute homolog 1-like [Callorhinchus milii]
XP_007987180	PREDICTED: achaete-scute homolog 5 [Chlorocebus sabaeus]
XP_007999051	PREDICTED: musculin [Chlorocebus sabaeus]
XP_008191716	PREDICTED: protein atonal homolog 7-like [Tribolium castaneum]
XP_008279095	PREDICTED: achaete-scute homolog 1 [Stegastes partitus]
XP_008306001	PREDICTED: transcription factor 24 [Cynoglossus semilaevis]
XP_008399136	PREDICTED: achaete-scute homolog 1 [Poecilia reticulata]
XP_008564697	PREDICTED: musculin [Galeopterus variegatus]
XP_008931366	PREDICTED: heart- and neural crest derivatives-expressed protein 2, partial [Manacus vitellinus]
XP_009099060	PREDICTED: achaete-scute homolog 1, partial [Serinus canaria]
XP_009464139	PREDICTED: achaete-scute homolog 1, partial [Nipponia nippon]
XP_009558844	PREDICTED: achaete-scute homolog 1 [Cuculus canorus]
XP_009564547	PREDICTED: heart- and neural crest derivatives-expressed protein 2 [Cuculus canorus]
XP_009569161	PREDICTED: twist-related protein 1, partial [Cuculus canorus]
XP_009575408	PREDICTED: T-cell acute lymphocytic leukemia protein 1 homolog, partial [Fulmarus glacialis]
XP_009906660	PREDICTED: achaete-scute homolog 1, partial [Picoides pubescens]
XP_010121728	PREDICTED: twist-related protein 2 [Chlamydotis macqueenii]
XP_010286552	PREDICTED: twist-related protein 2, partial [Phaethon lepturus]
XP_010360981	PREDICTED: achaete-scute homolog 5 [Rhinopithecus roxellana]
XP_010575966	PREDICTED: twist-related protein 1-like [Haliaeetus leucocephalus]
XP_010725792	PREDICTED: achaete-scute homolog 1, partial [Meleagris gallopavo]
XP_010751464	PREDICTED: achaete-scute homolog 1 [Larimichthys crocea]
XP_010768871	PREDICTED: twist-related protein 2-like isoform X1 [Notothenia coriiceps]
XP_010783842	PREDICTED: twist-related protein 2-like [Notothenia coriiceps]
XP_010851724	PREDICTED: achaete-scute homolog 1 [Bison bison bison]
XP_010884216	PREDICTED: transcription factor 24 [Esox lucius]
XP_010886559	PREDICTED: heart- and neural crest derivatives-expressed protein 2 [Esox lucius]
XP_010902165	PREDICTED: achaete-scute homolog 1 [Esox lucius]
XP_010988359	PREDICTED: achaete-scute homolog 1 [Camelus dromedarius]
XP_011218366	PREDICTED: achaete-scute homolog 1 [Ailuropoda melanoleuca]
XP_011331069	PREDICTED: basic helix-loop-helix transcription factor amos isoform X6 [Cerapachys biroi]
XP_011413563	PREDICTED: achaete-scute homolog 1-like [Crassostrea gigas]
XP_011413587	PREDICTED: achaete-scute homolog 1a-like, partial [Crassostrea gigas]
XP_011423240	PREDICTED: pancreas transcription factor 1 subunit alpha-like [Crassostrea gigas]
XP_011446306	PREDICTED: protein atonal homolog 8-like [Crassostrea gigas]
XP_011568337	PREDICTED: achaete-scute complex protein T8 [Plutella xylostella]
XP_011787226	PREDICTED: achaete-scute homolog 5 [Colobus angolensis palliatus]
XP_011892300	PREDICTED: achaete-scute homolog 5 [Cercocebus atys]
XP_012175121	PREDICTED: basic helix-loop-helix transcription factor amos isoform X2 [Bombus terrestris]
XP_012217263	PREDICTED: basic helix-loop-helix transcription factor amos-like isoform X4 [Linepithema humile]
XP_012240658	PREDICTED: basic helix-loop-helix transcription factor amos isoform X2 [Bombus impatiens]
XP_012324640	PREDICTED: achaete-scute homolog 1 [Aotus nancymaae]
XP_012340335	PREDICTED: basic helix-loop-helix transcription factor amos isoform X2 [Apis florea]
XP_012406052	PREDICTED: achaete-scute homolog 1 [Sarcophilus harrisii]

XP_012536456	PREDICTED: basic helix-loop-helix transcription factor amos isoform X4 [Monomorium pharaonis]
XP_012628138	PREDICTED: achaete-scute homolog 1 [Microcebus murinus]
XP_012692411	PREDICTED: heart- and neural crest derivatives-expressed protein 2 [Clupea harengus]
XP_012735012	PREDICTED: transcription factor 24 [Fundulus heteroclitus]
XP_012943615	PREDICTED: achaete-scute homolog 1a-like [Aplysia californica]
XP_013070971	PREDICTED: pancreas transcription factor 1 subunit alpha-like [Biomphalaria glabrata]
XP_013087027	PREDICTED: achaete-scute homolog 1a-like [Biomphalaria glabrata]
XP_013185531	PREDICTED: achaete-scute complex protein T8-like [Amyelois transitella]
XP_013379050	PREDICTED: protein atonal homolog 8-like [Lingula anatina]
XP_013385189	PREDICTED: achaete-scute complex protein T5-like isoform X1 [Lingula anatina]
XP_013385190	PREDICTED: T-cell acute lymphocytic leukemia protein 1 homolog isoform X2 [Lingula anatina]
XP_013396671	PREDICTED: transcription factor 21-like [Lingula anatina]
XP_013414747	PREDICTED: achaete-scute homolog 1a-like [Lingula anatina]
XP_013416000	PREDICTED: protein atonal homolog 8-like [Lingula anatina]
XP_013769837	PREDICTED: achaete-scute homolog 1, partial [Pundamilia nyererei]
XP_013772256	PREDICTED: achaete-scute homolog 1-like [Limulus polyphemus]
XP_013772798	PREDICTED: achaete-scute homolog 1-like [Limulus polyphemus]
XP_013773008	PREDICTED: protein atonal homolog 8-like [Limulus polyphemus]
XP_013773406	PREDICTED: protein atonal homolog 8-like [Limulus polyphemus]
XP_013774169	PREDICTED: pancreas transcription factor 1 subunit alpha-like [Limulus polyphemus]
XP_013775454	PREDICTED: achaete-scute homolog 1a-like [Limulus polyphemus]
XP_013775918	PREDICTED: achaete-scute homolog 1a-like [Limulus polyphemus]
XP_013775919	PREDICTED: achaete-scute homolog 1b-like [Limulus polyphemus]
XP_013776562	PREDICTED: achaete-scute homolog 2-like [Limulus polyphemus]
XP_013776926	PREDICTED: neurogenin-1-like [Limulus polyphemus]
XP_013776938	PREDICTED: neurogenin-3-like [Limulus polyphemus]
XP_013777872	PREDICTED: twist-related protein-like [Limulus polyphemus]
XP_013778157	PREDICTED: achaete-scute homolog 1-like [Limulus polyphemus]
XP_013778224	PREDICTED: twist-related protein 1-like [Limulus polyphemus]
XP_013779246	PREDICTED: pancreas transcription factor 1 subunit alpha-like [Limulus polyphemus]
XP_013781068	PREDICTED: achaete-scute homolog 1b-like [Limulus polyphemus]
XP_013787987	PREDICTED: achaete-scute homolog 1a-like [Limulus polyphemus]
XP_013788489	PREDICTED: T-cell acute lymphocytic leukemia protein 1-like [Limulus polyphemus]
XP_013788507	PREDICTED: achaete-scute homolog 1-like [Limulus polyphemus]
XP_013788684	PREDICTED: twist-related protein 2-like [Limulus polyphemus]
XP_013794337	PREDICTED: helix-loop-helix protein delilah-like [Limulus polyphemus]
XP_013794349	PREDICTED: twist-related protein-like [Limulus polyphemus]
XP_013794458	PREDICTED: helix-loop-helix protein 13-like [Limulus polyphemus]
XP_013794653	PREDICTED: achaete-scute homolog 1b-like [Limulus polyphemus]
XP_013802568	PREDICTED: achaete-scute homolog 1 [Apteryx australis mantelli]
XP_013908595	PREDICTED: musculin [Thamnophis sirtalis]
XP_013918992	PREDICTED: achaete-scute homolog 1 [Thamnophis sirtalis]
XP_014008851	PREDICTED: achaete-scute homolog 1a [Salmo salar]
XP_014028477	PREDICTED: twist-related protein 2-like [Salmo salar]
XP_014050461	PREDICTED: heart- and neural crest derivatives-expressed protein 2-like [Salmo salar]
XP_014063816	PREDICTED: achaete-scute homolog 1a-like [Salmo salar]
XP_014064835	PREDICTED: heart- and neural crest derivatives-expressed protein 2 [Salmo salar]
XP_014280288	PREDICTED: protein atonal homolog 8 [Halyomorpha halys]

9.4.2.23 *MafS*

Name	**Description**
A7YY73 (MAFF_BOVIN)	RecName: Full=Transcription factor MafF; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
A7Z017 (MAF_BOVIN)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
AAF57439	maf-S, isoform A [Drosophila melanogaster]
Locus_1_Transcript_103888/166847_Confidence_1.000_Length_1681 - ORF 1 (frame 1) translation	Locus_1_Transcript_103888/166847_Confidence_1.000_Length_1681
Locus_1_Transcript_106851/166847_Confidence_1.000_Length_1817 - ORF 10 (frame 3) translation	Locus_1_Transcript_106851/166847_Confidence_1.000_Length_1817
Locus_2680_Transcript_40/41_Confidence_0.044_Length_2001 - ORF 3 (frame 2) translation	Locus_2680_Transcript_40/41_Confidence_0.044_Length_2001
MAF_MOUSE	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
MAFA_MOUSE	RecName: Full=Transcription factor MafA; AltName: Full=Pancreatic beta-cell-specific transcriptional activator; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog A
MAFB_MOUSE	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=Kreisler; AltName: Full=Segmentation protein Kr; AltName: Full=Transcription factor Maf-1; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
MAFF_MOUSE	RecName: Full=Transcription factor MafF; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
MAFG_MOUSE	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G

MAFK_MOUSE	RecName: Full=Transcription factor MafK; AltName: Full=Erythroid transcription factor NF-E2 p18 subunit
NP_001084266	jun proto-oncogene [Xenopus laevis]
O15525 (MAFG_HUMAN)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G; AltName: Full=hMAF
O54790 (MAFG_MOUSE)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
O60675 (MAFK_HUMAN)	RecName: Full=Transcription factor MafK; AltName: Full=Erythroid transcription factor NF-E2 p18 subunit
O75444 (MAF_HUMAN)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
O77627 (JUN_BOVIN)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P05411 (JUN_AVIS1)	RecName: Full=Viral jun-transforming protein; Short=v-Jun
P05412 (JUN_HUMAN)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog; AltName: Full=p39
P05627 (JUN_MOUSE)	RecName: Full=Transcription factor AP-1; AltName: Full=AH119; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog; Short=Jun A
P12981 (JUN_COTJA)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P17325 (JUN_RAT)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P18870 (JUN_CHICK)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P23091 (MAF_AVIS4)	RecName: Full=Transforming protein Maf
P54841 (MAFB_MOUSE)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=Kreisler; AltName: Full=Segmentation protein Kr; AltName: Full=Transcription factor Maf-1; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
P54843 (MAF_MOUSE)	RecName: Full=Transcription factor Maf; AltName: Full=Proto-oncogene c-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
P54864 (JUN_SERCA)	RecName: Full=Transcription factor AP-1; AltName: Full=Proto-oncogene c-Jun
P56432 (JUN_PIG)	RecName: Full=Transcription factor AP-1; AltName: Full=Activator protein 1; Short=AP1; AltName: Full=Proto-oncogene c-Jun; AltName: Full=V-jun avian sarcoma virus 17 oncogene homolog
P79703 (JUNB_CYPCA)	RecName: Full=Transcription factor jun-B
Q9ULX9 (MAFF_HUMAN)	RecName: Full=Transcription factor MafF; AltName: Full=U-Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
Q9Y5Q3 (MAFB_HUMAN)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
Q76MX4 (MAFG_RAT)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
Q98UK5 (MAFB_DANRE)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=Transcription factor Val; AltName: Full=Valentino
Q789F3 (MAF_CHICK)	RecName: Full=Transcription factor Maf; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog
Q61827 (MAFK_MOUSE)	RecName: Full=Transcription factor MafK; AltName: Full=Erythroid transcription factor NF-E2 p18 subunit
Q90370 (MAFB_COTJA)	RecName: Full=Transcription factor MafB; Short=Maf-B
Q90595 (MAFF_CHICK)	RecName: Full=Transcription factor MafF; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog F
Q90596 (MAFK_CHICK)	RecName: Full=Transcription factor MafK
Q90888 (MAFB_CHICK)	RecName: Full=Transcription factor MafB; Short=Maf-B; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog B
Q90889 (MAFG_CHICK)	RecName: Full=Transcription factor MafG; AltName: Full=V-maf musculoaponeurotic fibrosarcoma oncogene homolog G
XP_002404274	transcription factor MafB, putative [Ixodes scapularis]
XP_002428922	transcription factor MafG, putative [Pediculus humanus corporis]
XP_002931634	PREDICTED: transcription factor AP-1 [Xenopus (Silurana) tropicalis]
XP_003250214	PREDICTED: transcription factor MafG-like isoformX2 [Apis mellifera]
XP_004927019	PREDICTED: neural retina-specific leucine zipper protein [Bombyx mori]
XP_005482348	PREDICTED: transcription factor AP-1 [Zonotrichia albicollis]
XP_006610989	PREDICTED: transcription factor MafG-like [Apis dorsata]
XP_008923422	PREDICTED: transcription factor AP-1 [Manacus vitellinus]
XP_011343601	PREDICTED: transcription factor MafG [Cerapachys biroi]
XP_011446588	PREDICTED: transcription factor AP-1-like [Crassostrea gigas]
XP_011564500	PREDICTED: transcription factor MafK-like [Plutella xylostella]
XP_012261892	PREDICTED: transcription factor MafK-like [Athalia rosae]
XP_013145529	PREDICTED: transcription factor MafK [Papilio polytes]
XP_013161582	PREDICTED: transcription factor MafK [Papilio xuthus]
XP_013181120	PREDICTED: neural retina-specific leucine zipper protein-like [Papilio xuthus]
XP_013188822	PREDICTED: neural retina-specific leucine zipper protein-like [Amyelois transitella]
XP_013195767	PREDICTED: transcription factor MafK [Amyelois transitella]
XP_013398583	PREDICTED: transcription factor AP-1-like [Lingula anatina]
XP_013772821	PREDICTED: neural retina-specific leucine zipper protein-like [Limulus polyphemus]
XP_013776170	PREDICTED: transcription factor MafB-like [Limulus polyphemus]

XP_013777025	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_013781439	PREDICTED: transcription factor MafK-like [Limulus polyphemus]
XP_013783135	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_013791509	PREDICTED: transcription factor AP-1-like [Limulus polyphemus]
XP_014278715	PREDICTED: transcription factor MafA-like [Halyomorpha halys]
XP_014358308	PREDICTED: transcription factor MafA-like [Papilio machaon]

9.4.2.24 *Medea*

Name	Description
AAC62005	Medea [Drosophila melanogaster]
Locus_1_Transcript_108077/166847_Confidence_1.000_Length_367 - ORF 1 (frame 2) translation	Locus_1_Transcript_108077/166847_Confidence_1.000_Length_367
Locus_1_Transcript_108114/166847_Confidence_1.000_Length_493 - ORF 5 (frame 3) translation	Locus_1_Transcript_108114/166847_Confidence_1.000_Length_493
Locus_8_Transcript_10/15_Confidence_0.217_Length_2087 - ORF 8 (frame 3) translation	Locus_8_Transcript_10/15_Confidence_0.217_Length_2087
Locus_2495_Transcript_1/10_Confidence_0.438_Length_1737 - ORF 1 (frame 1) translation	Locus_2495_Transcript_1/10_Confidence_0.438_Length_1737
Locus_10810_Transcript_4/12_Confidence_0.375_Length_5754 - ORF 23 (frame 1) translation	Locus_10810_Transcript_4/12_Confidence_0.375_Length_5754
NP_477017	mothers against dpp, isoform A [Drosophila melanogaster]
NP_001158449	SMAD family member 6 [Saccoglossus kowalevskii]
NP_001161658	Smad2/3 transcription factor [Saccoglossus kowalevskii]
O15105 (SMAD7_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 7; Short=MAD homolog 7; Short=Mothers against DPP homolog 7; AltName: Full=Mothers against decapentaplegic homolog 8; Short=MAD homolog 8; Short=Mothers against DPP homolog 8; AltName: Full=SMAD family member 7; Short=SMAD 7; Short=Smad7; Short=hSMAD7
O15198 (SMAD9_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 9; Short=MAD homolog 9; Short=Mothers against DPP homolog 9; AltName: Full=Madh6; AltName: Full=SMAD family member 9; Short=SMAD 9; Short=Smad9
O35182 (SMAD6_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 6; Short=MAD homolog 6; Short=Mothers against DPP homolog 6; AltName: Full=Mad homolog 7; AltName: Full=SMAD family member 6; Short=SMAD 6; Short=Smad6
O35253 (SMAD7_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 7; Short=MAD homolog 7; Short=Mothers against DPP homolog 7; AltName: Full=Mothers against decapentaplegic homolog 8; Short=MAD homolog 8; Short=Mothers against DPP homolog 8; AltName: Full=SMAD family member 7; Short=SMAD 7; Short=Smad7
O43541 (SMAD6_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 6; Short=MAD homolog 6; Short=Mothers against DPP homolog 6; AltName: Full=SMAD family member 6; Short=SMAD 6; Short=Smad6; Short=hSMAD6
O70436 (SMAD2_RAT)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=Mad-related protein 2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2
O70437 (SMAD4_RAT)	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4
O88406 (SMAD7_RAT)	RecName: Full=Mothers against decapentaplegic homolog 7; Short=MAD homolog 7; Short=Mothers against DPP homolog 7; AltName: Full=SMAD family member 7; Short=SMAD 7; Short=Smad7
P42003 (MAD_DROME)	RecName: Full=Protein mothers against dpp
P45896 (SMA3_CAEEL)	RecName: Full=Dwarfin sma-3; AltName: Full=MAD protein homolog 2
P45897 (SMA4_CAEEL)	RecName: Full=Dwarfin sma-4; AltName: Full=MAD protein homolog 3
P70340 (SMAD1_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 1; Short=MAD homolog 1; Short=Mothers against DPP homolog 1; AltName: Full=Dwarfin-A; Short=Dwf-A; AltName: Full=Mothers-against-DPP-related 1; Short=Mad-related protein 1; Short=mMad1; AltName: Full=SMAD family member 1; Short=SMAD 1; Short=Smad1
P84022 (SMAD3_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 3; Short=MAD homolog 3; Short=Mad3; Short=Mothers against DPP homolog 3; Short=hMAD-3; AltName: Full=JV15-2; AltName: Full=SMAD family member 3; Short=SMAD 3; Short=Smad3; Short=hSMAD3
P84023 (SMAD3_CHICK)	RecName: Full=Mothers against decapentaplegic homolog 3; Short=MAD homolog 3; Short=Mad3; Short=Mothers against DPP homolog 3; AltName: Full=SMAD family member 3; Short=SMAD 3; Short=Smad3
P97454 (SMAD5_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 5; Short=MAD homolog 5; Short=Mothers against DPP homolog 5; AltName: Full=Dwarfin-C; Short=Dwf-C; AltName: Full=SMAD family member 5; Short=SMAD 5; Short=Smad5; Short=mSmad5
P97471 (SMAD4_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=Deletion target in pancreatic carcinoma 4 homolog; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4

P97588 (SMAD1_RAT)	RecName: Full=Mothers against decapentaplegic homolog 1; Short=MAD homolog 1; Short=Mothers against DPP homolog 1; AltName: Full=SMAD family member 1; Short=SMAD 1; Short=Smad1
Q1HE26 (SMAD4_BOVIN)	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4
Q1JQA2 (SMAD1_BOVIN)	RecName: Full=Mothers against decapentaplegic homolog 1; Short=MAD homolog 1; Short=Mothers against DPP homolog 1; AltName: Full=SMAD family member 1; Short=SMAD 1; Short=Smad1
Q1W668 (SMAD2_BOVIN)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2
Q5R7C0 (SMAD2_PONAB)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2
Q9GKQ9 (SMAD4_PIG)	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4
Q9I9P9 (SMAD2_DANRE)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2
Q9I962 (SMAD1_COTJA)	RecName: Full=Mothers against decapentaplegic homolog 1; Short=MAD homolog 1; Short=Mothers against DPP homolog 1; AltName: Full=Mad-related protein 1; AltName: Full=SMAD family member 1; Short=SMAD 1; Short=Smad1
Q9R1V3 (SMAD5_RAT)	RecName: Full=Mothers against decapentaplegic homolog 5; Short=MAD homolog 5; Short=Mothers against DPP homolog 5; AltName: Full=SMAD family member 5; Short=SMAD 5; Short=Smad5
Q9W7E7 (SMAD5_DANRE)	RecName: Full=Mothers against decapentaplegic homolog 5; Short=MAD homolog 5; Short=Mothers against DPP homolog 5; AltName: Full=Protein somitabun; AltName: Full=SMAD family member 5; Short=SMAD 5; Short=Smad5
Q9W734 (SMAD6_CHICK)	RecName: Full=Mothers against decapentaplegic homolog 6; Short=MAD homolog 6; Short=Mothers against DPP homolog 6; AltName: Full=SMAD family member 6; Short=SMAD 6; Short=Smad6
Q56I99 (SMAD5_CHICK)	RecName: Full=Mothers against decapentaplegic homolog 5; Short=MAD homolog 5; Short=Mothers against DPP homolog 5; AltName: Full=SMAD family member 5; Short=SMAD 5; Short=Smad5
Q13485 (SMAD4_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=Deletion target in pancreatic carcinoma 4; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4; Short=hSMAD4
Q15796 (SMAD2_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=JV18-1; AltName: Full=Mad-related protein 2; Short=hMAD-2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2; Short=hSMAD2
Q15797 (SMAD1_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 1; Short=MAD homolog 1; Short=Mothers against DPP homolog 1; AltName: Full=JV4-1; AltName: Full=Mad-related protein 1; AltName: Full=SMAD family member 1; Short=SMAD 1; Short=Smad1; Short=hSMAD1; AltName: Full=Transforming growth factor-beta-signaling protein 1; Short=BSP-1
Q62432 (SMAD2_MOUSE)	RecName: Full=Mothers against decapentaplegic homolog 2; Short=MAD homolog 2; Short=Mothers against DPP homolog 2; AltName: Full=Mad-related protein 2; Short=mMad2; AltName: Full=SMAD family member 2; Short=SMAD 2; Short=Smad2
Q99717 (SMAD5_HUMAN)	RecName: Full=Mothers against decapentaplegic homolog 5; Short=MAD homolog 5; Short=Mothers against DPP homolog 5; AltName: Full=JV5-1; AltName: Full=SMAD family member 5; Short=SMAD 5; Short=Smad5; Short=hSmad5
SMAD4_MOUSE	RecName: Full=Mothers against decapentaplegic homolog 4; Short=MAD homolog 4; Short=Mothers against DPP homolog 4; AltName: Full=Deletion target in pancreatic carcinoma 4 homolog; AltName: Full=SMAD family member 4; Short=SMAD 4; Short=Smad4
XP_396816	PREDICTED: mothers against decapentaplegic homolog 6 [Apis mellifera]
XP_001601460	PREDICTED: protein mothers against dpp isoform X1 [Nasonia vitripennis]
XP_001842090	mothers against dpp [Culex quinquefasciatus]
XP_003227329	PREDICTED: mothers against decapentaplegic homolog 4 [Anolis carolinensis]
XP_003694720	PREDICTED: mothers against decapentaplegic homolog 6 [Apis florea]
XP_005461620	PREDICTED: mothers against decapentaplegic homolog 3 isoform X2 [Oreochromis niloticus]
XP_007658035	PREDICTED: mothers against decapentaplegic homolog 2 isoform X3 [Ornithorhynchus anatinus]
XP_007904996	PREDICTED: mothers against decapentaplegic homolog 2 [Callorhinchus milii]

XP_008183566	PREDICTED: mothers against decapentaplegic homolog 6-like [Acyrthosiphon pisum]
XP_008199394	PREDICTED: mothers against decapentaplegic homolog 4 isoform X1 [Tribolium castaneum]
XP_008199395	PREDICTED: mothers against decapentaplegic homolog 4 isoform X2 [Tribolium castaneum]
XP_008215489	PREDICTED: protein mothers against dpp isoform X2 [Nasonia vitripennis]
XP_008422082	PREDICTED: mothers against decapentaplegic homolog 2-like isoform X1 [Poecilia reticulata]
XP_008422083	PREDICTED: mothers against decapentaplegic homolog 2-like isoform X2 [Poecilia reticulata]
XP_008493223	PREDICTED: mothers against decapentaplegic homolog 2 isoform X2 [Calypte anna]
XP_009926609	PREDICTED: mothers against decapentaplegic homolog 1-like, partial [Haliaeetus albicilla]
XP_010003003	PREDICTED: mothers against decapentaplegic homolog 2-like [Chaetura pelagica]
XP_012286211	PREDICTED: mothers against decapentaplegic homolog 6 [Orussus abietinus]
XP_013038644	PREDICTED: mothers against decapentaplegic homolog 4 isoform X1 [Anser cygnoides domesticus]
XP_013098583	PREDICTED: protein mothers against dpp isoform X2 [Stomoxys calcitrans]
XP_013418840	PREDICTED: mothers against decapentaplegic homolog 6-like isoform X1 [Lingula anatina]
XP_013776260	PREDICTED: mothers against decapentaplegic homolog 3-like [Limulus polyphemus]
XP_013789665	PREDICTED: mothers against decapentaplegic homolog 6-like [Limulus polyphemus]
XP_013790112	PREDICTED: mothers against decapentaplegic homolog 6-like [Limulus polyphemus]
XP_013791017	PREDICTED: protein mothers against dpp-like [Limulus polyphemus]
XP_013794083	PREDICTED: mothers against decapentaplegic homolog 5-like [Limulus polyphemus]
XP_014230775	PREDICTED: protein mothers against dpp-like isoform X1 [Trichogramma pretiosum]
XP_014230776	PREDICTED: protein mothers against dpp-like isoform X2 [Trichogramma pretiosum]
XP_014241099	PREDICTED: mothers against decapentaplegic homolog 4 isoform X1 [Cimex lectularius]
XP_014241100	PREDICTED: mothers against decapentaplegic homolog 4 isoform X2 [Cimex lectularius]
XP_014241101	PREDICTED: mothers against decapentaplegic homolog 4 isoform X3 [Cimex lectularius]
XP_014245502	PREDICTED: mothers against decapentaplegic homolog 6 [Cimex lectularius]
XP_014271477	PREDICTED: mothers against decapentaplegic homolog 4-like isoform X1 [Halyomorpha halys]
XP_014271478	PREDICTED: mothers against decapentaplegic homolog 4-like isoform X2 [Halyomorpha halys]
XP_014271482	PREDICTED: mothers against decapentaplegic homolog 4-like isoform X1 [Halyomorpha halys]

9.4.2.25 *NR3C1*

Name	Description
A0P8Z4 (NR6A1_PIG)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF
A2T929 (RXRAA_DANRE)	RecName: Full=Retinoic acid receptor RXR-alpha-A; AltName: Full=Nuclear receptor subfamily 2 group B member 1-A; AltName: Full=RXRalpha-B; AltName: Full=Retinoid X receptor alpha-A
A4IIG7 (NR4A2_XENTR)	RecName: Full=Nuclear receptor subfamily 4 group A member 2
AAH15610	Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) [Homo sapiens]
Locus_1_Transcript_27950/166847_Confidence_1.000_Length_798 - ORF 1 (frame 2) translation	Locus_1_Transcript_27950/166847_Confidence_1.000_Length_798
Locus_1_Transcript_93285/166847_Confidence_1.000_Length_2349 - ORF 4 (frame 2) translation	Locus_1_Transcript_93285/166847_Confidence_1.000_Length_2349
Locus_1_Transcript_127749/166847_Confidence_1.000_Length_1201 - ORF 1 (frame 1) translation	Locus_1_Transcript_127749/166847_Confidence_1.000_Length_1201
Locus_1_Transcript_150272/166847_Confidence_1.000_Length_796 - ORF 1 (frame 1) translation	Locus_1_Transcript_150272/166847_Confidence_1.000_Length_796
Locus_1_Transcript_160064/166847_Confidence_1.000_Length_647 - ORF 3 (frame 1) translation	Locus_1_Transcript_160064/166847_Confidence_1.000_Length_647
Locus_135_Transcript_1/1_Confidence_1.000_Length_2330 - ORF 11 (frame 2) translation	Locus_135_Transcript_1/1_Confidence_1.000_Length_2330
Locus_1578_Transcript_50/50_Confidence_0.206_Length_2629 - ORF 14 (frame 1) translation	Locus_1578_Transcript_50/50_Confidence_0.206_Length_2629
Locus_2687_Transcript_14/15_Confidence_0.351_Length_5316 - ORF 31 (frame 3) translation	Locus_2687_Transcript_14/15_Confidence_0.351_Length_5316
Locus_4153_Transcript_1/1_Confidence_1.000_Length_6906 - ORF 5 (frame 1) translation	Locus_4153_Transcript_1/1_Confidence_1.000_Length_6906
Locus_8845_Transcript_10/10_Confidence_0.333_Length_5198 - ORF 27 (frame 1) translation	Locus_8845_Transcript_10/10_Confidence_0.333_Length_5198
Locus_9245_Transcript_9/9_Confidence_0.558_Length_8055 - ORF 8 (frame 3) translation	Locus_9245_Transcript_9/9_Confidence_0.558_Length_8055
Locus_16110_Transcript_7/11_Confidence_0.258_Length_4798 - ORF 23 (frame 3) translation	Locus_16110_Transcript_7/11_Confidence_0.258_Length_4798

Locus_16921_Transcript_3/5_Confidence_0.765_Length_1896 - ORF 5 (frame 1) translation	Locus_16921_Transcript_3/5_Confidence_0.765_Length_1896
Locus_18435_Transcript_5/8_Confidence_0.520_Length_8783 - ORF 3 (frame 2) translation	Locus_18435_Transcript_5/8_Confidence_0.520_Length_8783
Locus_24628_Transcript_6/6_Confidence_0.667_Length_2451 - ORF 1 (frame 2) translation	Locus_24628_Transcript_6/6_Confidence_0.667_Length_2451
NP_001135390	ecdysone receptor isoform B [Tribolium castaneum]
NP_001135406	estrogen-related receptor [Tribolium castaneum]
NP_001158447	photoreceptor-specific nuclear receptor protein [Saccoglossus kowalevskii]
O00482 (NR5A2_HUMAN)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=Alpha-1-fetoprotein transcription factor; AltName: Full=B1-binding factor; Short=hB1F; AltName: Full=CYP7A promoter-binding factor; AltName: Full=Hepatocytic transcription factor; AltName: Full=Liver receptor homolog 1; Short=LRH-1
O09018 (COT2_RAT)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=Apolipoprotein A-I regulatory protein 1; Short=ARP-1; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=COUPb; AltName: Full=Nuclear receptor subfamily 2 group F member 2; AltName: Full=Ovalbumin upstream promoter beta nuclear receptor
O16845 (TLL_DROVI)	RecName: Full=Protein tailless; AltName: Full=Nuclear receptor subfamily 2 group E member 2
O18473 (ECR_HELVI)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=HvEcR; AltName: Full=Nuclear receptor subfamily 1 group H member 1
O18531 (ECR_LUCCU)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
O42101 (NR5A2_CHICK)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=FTF/LRH-1; AltName: Full=OR2.0
O77245 (E75_METEN)	RecName: Full=Nuclear hormone receptor E75; AltName: Full=Nuclear receptor subfamily 1 group D member 3
O95718 (ERR2_HUMAN)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=ERR beta-2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
P03372 (ESR1_HUMAN)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P06211 (ESR1_RAT)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P10589 (COT1_HUMAN)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1; AltName: Full=V-erbA-related protein 3; Short=EAR-3
P10826 (RARB_HUMAN)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=HBV-activated protein; AltName: Full=Nuclear receptor subfamily 1 group B member 2; AltName: Full=RAR-epsilon
P11474 (ERR1_HUMAN)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen receptor-like 1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1
P11475 (ERR2_RAT)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
P13055 (E75BB_DROME)	RecName: Full=Ecdysone-induced protein 75B, isoform B; AltName: Full=E75-C; AltName: Full=Nuclear receptor subfamily 1 group D member 3, isoform B
P13056 (NR2C1_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2
P16375 (7UP1_DROME)	RecName: Full=Steroid receptor seven-up, isoforms B/C; AltName: Full=Nuclear receptor subfamily 2 group F member 3, isoforms B/C
P17671 (E75BC_DROME)	RecName: Full=Ecdysone-induced protein 75B, isoforms C/D; AltName: Full=E75-A; AltName: Full=Nuclear receptor subfamily 1 group D member 3, isoforms C/D
P18102 (TLL_DROME)	RecName: Full=Protein tailless; AltName: Full=Nuclear receptor subfamily 2 group E member 2
P18514 (RARA_NOTVI)	RecName: Full=Retinoic acid receptor alpha; Short=RAR-alpha; AltName: Full=Nuclear receptor subfamily 1 group B member 1
P19785 (ESR1_MOUSE)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P19793 (RXRA_HUMAN)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
P22448 (RARB_CHICK)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
P22605 (RARB_MOUSE)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
P24468 (COT2_HUMAN)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=Apolipoprotein A-I regulatory protein 1; Short=ARP-1; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
P28700 (RXRA_MOUSE)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha

P28701 (RXRG_CHICK)	RecName: Full=Retinoic acid receptor RXR-gamma; AltName: Full=Nuclear receptor subfamily 2 group B member 3; AltName: Full=Retinoid X receptor gamma
P33242 (STF1_MOUSE)	RecName: Full=Steroidogenic factor 1; Short=SF-1; Short=STF-1; AltName: Full=Adrenal 4-binding protein; AltName: Full=Embryonal LTR-binding protein; Short=ELP; AltName: Full=Embryonal long terminal repeat-binding protein; AltName: Full=Fushi tarazu factor homolog 1; AltName: Full=Nuclear receptor subfamily 5 group A member 1; AltName: Full=Steroid hormone receptor Ad4BP; AltName: Full=Steroid hydroxylase positive regulator
P33244 (FTZF1_DROME)	RecName: Full=Nuclear hormone receptor FTZ-F1; AltName: Full=FTZ-F1 alpha; AltName: Full=Nuclear receptor subfamily 5 group A member 3
P34021 (ECR_DROME)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P43354 (NR4A2_HUMAN)	RecName: Full=Nuclear receptor subfamily 4 group A member 2; AltName: Full=Immediate-early response protein NOT; AltName: Full=Orphan nuclear receptor NURR1; AltName: Full=Transcriptionally-inducible nuclear receptor
P45447 (E78C_DROME)	RecName: Full=Ecdysone-induced protein 78C; Short=DR-78; AltName: Full=Nuclear receptor subfamily 1 group E member 1
P45448 (NR5A2_MOUSE)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=Liver receptor homolog 1; Short=LRH-1
P49116 (NR2C2_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group C member 2; AltName: Full=Orphan nuclear receptor TAK1; AltName: Full=Orphan nuclear receptor TR4; AltName: Full=Testicular receptor 4
P49867 (FTZF1_BOMMO)	RecName: Full=Nuclear hormone receptor FTZ-F1; AltName: Full=BmFTZ-F1; AltName: Full=Nuclear receptor subfamily 5 group A member 3
P49869 (HR38_DROME)	RecName: Full=Probable nuclear hormone receptor HR38; Short=dHR38; AltName: Full=Nuclear receptor subfamily 4 group A member 4
P49870 (HR38_BOMMO)	RecName: Full=Probable nuclear hormone receptor HR38; Short=bHR38; AltName: Full=Nuclear receptor subfamily 4 group A member 4
P49880 (ECR_AEDAE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; Short=AaEcR; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49881 (ECR_BOMMO)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49882 (ECR_CHITE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49883 (ECR_MANSE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49884 (ESR1_BOVIN)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P50569 (STF1_RAT)	RecName: Full=Steroidogenic factor 1; Short=SF-1; Short=STF-1; AltName: Full=Adrenal 4-binding protein; AltName: Full=Fushi tarazu factor homolog 1; AltName: Full=Nuclear receptor subfamily 5 group A member 1; AltName: Full=Steroid hormone receptor Ad4BP
P51128 (RXRA_XENLA)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
P51666 (NR4A1_CANFA)	RecName: Full=Nuclear receptor subfamily 4 group A member 1; AltName: Full=Orphan nuclear receptor HMR; AltName: Full=Orphan nuclear receptor NGFI-B
P57781 (ESR2_MICUN)	RecName: Full=Estrogen receptor beta; Short=ER-beta; AltName: Full=Nuclear receptor subfamily 3 group A member 2
P62510 (ERR3_RAT)	RecName: Full=Estrogen-related receptor gamma; AltName: Full=Estrogen receptor-related protein 3; AltName: Full=Nuclear receptor subfamily 3 group B member 3
P70033 (NR6A1_XENLA)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=xGCNF
P70052 (NR2E1_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=xTLL
P79387 (STF1_PIG)	RecName: Full=Steroidogenic factor 1; Short=SF-1; Short=STF-1; AltName: Full=Adrenal 4-binding protein; AltName: Full=Fushi tarazu factor homolog 1; AltName: Full=Nuclear receptor subfamily 5 group A member 1; AltName: Full=Steroid hormone receptor Ad4BP
Q0V8F0 (NR4A1_BOVIN)	RecName: Full=Nuclear receptor subfamily 4 group A member 1
Q4V8R7 (GCNFB_DANRE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1-B; AltName: Full=Germ cell nuclear factor B; Short=GCNF-B
Q5E9B6 (NR1H3_BOVIN)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3
Q5I7G2 (RXR_LYMST)	RecName: Full=Retinoic acid receptor RXR; AltName: Full=Retinoid X receptor; Short=LymRXR
Q5QJV7 (ERR1_RAT)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1

Q5RAM2 (ERR3_PONAB)	RecName: Full=Estrogen-related receptor gamma; AltName: Full=Estrogen receptor-related protein 3; AltName: Full=Nuclear receptor subfamily 3 group B member 3
Q5RCZ5 (NR2C1_PONAB)	RecName: Full=Nuclear receptor subfamily 2 group C member 1
Q6DHP9 (RXRGB_DANRE)	RecName: Full=Retinoic acid receptor RXR-gamma-B; AltName: Full=Nuclear receptor subfamily 2 group B member 3-B; AltName: Full=Retinoid X receptor gamma-B
Q6GN21 (N2C1A_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1-A; AltName: Full=Developmental orphan receptor 2-A; Short=DOR2-A; Short=xDOR2-A; AltName: Full=Orphan nuclear receptor TR2-A; AltName: Full=Testicular receptor 2-A
Q6PH18 (N2F1B_DANRE)	RecName: Full=Nuclear receptor subfamily 2 group F member 1-B; AltName: Full=COUP transcription factor 1-B; Short=COUP-TFalpha-B
Q6QMY5 (ERR1_CANFA)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1
Q08E53 (NR4A2_BOVIN)	RecName: Full=Nuclear receptor subfamily 4 group A member 2
Q8T5C6 (RXR_BIOGL)	RecName: Full=Retinoic acid receptor RXR; AltName: Full=RXR-like protein; AltName: Full=Retinoid X receptor; Short=BgRXR
Q8VIJ4 (NR2C1_RAT)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2
Q9PU65 (GCNFA_DANRE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1-A; AltName: Full=Germ cell nuclear factor A; Short=GCNF-A; Short=zfGCNF
Q9QWM1 (NR5A2_RAT)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=FTZ-F1 beta; AltName: Full=Liver receptor homolog 1; Short=LRH-1
Q9QXZ7 (NR2E3_MOUSE)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor
Q9QZJ5 (ESR1_MESAU)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
Q9TTF0 (NR2E3_BOVIN)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor
Q9TTR7 (COT2_BOVIN)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
Q9TTR8 (COT1_BOVIN)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1
Q9U2R6 (NHR91_CAEEL)	RecName: Full=Nuclear hormone receptor family member nhr-91
Q9W6B3 (RARB_COTJA)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
Q9W539 (HR4_DROME)	RecName: Full=Hormone receptor 4; Short=dHR4; AltName: Full=Nuclear receptor subfamily 6 group A member 2
Q9Y5X4 (NR2E3_HUMAN)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor
Q9Y466 (NR2E1_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=hTll
Q9YGL3 (NR2E1_ORYLA)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll
Q9Z0Y9 (NR1H3_MOUSE)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3
Q28CK1 (NR2C1_XENTR)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Developmental orphan receptor 2; Short=DOR2; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2
Q53AD2 (ESR1_FELCA)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
Q66J63 (N2C1B_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1-B; AltName: Full=Developmental orphan receptor 2-B; Short=DOR2-B; Short=xDOR2-B; AltName: Full=Orphan nuclear receptor TR2-B; AltName: Full=Testicular receptor 2-B
Q66JK1 (NR6A1_XENTR)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF
Q95K90 (NR2C1_MACFA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1
Q505F1 (NR2C1_MOUSE)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2; Short=mTR2
Q04752 (STF1_BOVIN)	RecName: Full=Steroidogenic factor 1; Short=SF-1; Short=STF-1; AltName: Full=Adrenal 4-binding protein; AltName: Full=Fushi tarazu factor homolog 1; AltName: Full=Nuclear receptor subfamily 5 group A member 1; AltName: Full=Steroid hormone receptor Ad4BP
Q04913 (NR4A1_XENLA)	RecName: Full=Nuclear receptor subfamily 4 group A member 1; AltName: Full=Nerve growth factor-induced protein I-B homolog
Q05192 (FTF1B_DROME)	RecName: Full=Nuclear hormone receptor FTZ-F1 beta; AltName: Full=Nuclear hormone receptor HR39; Short=dHR39; AltName: Full=Nuclear receptor subfamily 5 group B member 1
Q05343 (RXRA_RAT)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
Q06219 (NR4A2_MOUSE)	RecName: Full=Nuclear receptor subfamily 4 group A member 2; AltName: Full=NUR-related factor 1; AltName: Full=Orphan nuclear receptor NURR1

Q06725 (N2F1A_DANRE)	RecName: Full=Nuclear receptor subfamily 2 group F member 1-A; AltName: Full=COUP transcription factor 1-A; Short=COUP-TFalpha-A; Short=zCOUP-TFI; AltName: Full=Seven-up related 44; Short=Svp[44]; Short=zSvp[44]; AltName: Full=Steroid receptor homolog SVP 44
Q07917 (NR4A2_RAT)	RecName: Full=Nuclear receptor subfamily 4 group A member 2; AltName: Full=NUR-related factor 1; AltName: Full=Nuclear orphan receptor HZF-3; AltName: Full=Orphan nuclear receptor NURR1; AltName: Full=Regenerating liver nuclear receptor 1; Short=RNR-1; AltName: Full=SL-322
Q08893 (E75_MANSE)	RecName: Full=Ecdysone-inducible protein E75; AltName: Full=Nuclear receptor subfamily 1 group D member 3
Q15406 (NR6A1_HUMAN)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=hGCNF; AltName: Full=Retinoid receptor-related testis-specific receptor; Short=RTR; Short=hRTR
Q26622 (SHR2_STRPU)	RecName: Full=Orphan steroid hormone receptor 2; AltName: Full=SpSHR2
Q60632 (COT1_MOUSE)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1; AltName: Full=V-erbA-related protein 3; Short=EAR-3
Q61539 (ERR2_MOUSE)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
Q62685 (NR1H3_RAT)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3; AltName: Full=RLD-1
Q64104 (NR2E1_MOUSE)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=mTll
Q64249 (NR6A1_MOUSE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=mGCNF; AltName: Full=Retinoid receptor-related testis-specific receptor; Short=RTR
Q90416 (RXRGA_DANRE)	RecName: Full=Retinoic acid receptor RXR-gamma-A; AltName: Full=Nuclear receptor subfamily 2 group B member 3-A; AltName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Retinoid X receptor alpha; AltName: Full=Retinoid X receptor gamma-A
Q90733 (COT2_CHICK)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
Q91379 (NR2E1_CHICK)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll
XP_974320	PREDICTED: hormone receptor 4 isoform X1 [Tribolium castaneum]
XP_001945726	PREDICTED: hormone receptor 4 isoform X1 [Acyrthosiphon pisum]
XP_001947027	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Acyrthosiphon pisum]
XP_002425386	orphan nuclear receptor nr6a1, putative [Pediculus humanus corporis]
XP_002427418	Ecdysone receptor, putative [Pediculus humanus corporis]
XP_002427577	Orphan nuclear receptor NR2E1, putative [Pediculus humanus corporis]
XP_002428935	retinoid X receptor, putative [Pediculus humanus corporis]
XP_002431237	retinoid X receptor, putative [Pediculus humanus corporis]
XP_002435070	retinoid X receptor, putative, partial [Ixodes scapularis]
XP_003397992	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X4 [Bombus terrestris]
XP_003700030	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X1 [Megachile rotundata]
XP_003738496	PREDICTED: ecdysone receptor-like [Metaseiulus occidentalis]
XP_005089312	PREDICTED: orphan steroid hormone receptor 2-like isoform X4 [Aplysia californica]
XP_006561614	PREDICTED: ultraspiracle isoform X6 [Apis mellifera]
XP_008181367	PREDICTED: photoreceptor-specific nuclear receptor isoform X2 [Acyrthosiphon pisum]
XP_008182814	PREDICTED: hormone receptor 4 isoform X2 [Acyrthosiphon pisum]
XP_008182816	PREDICTED: hormone receptor 4 isoform X3 [Acyrthosiphon pisum]
XP_008183295	PREDICTED: nuclear hormone receptor FTZ-F1-like isoform X2 [Acyrthosiphon pisum]
XP_008191373	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X1 [Tribolium castaneum]
XP_008191374	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X2 [Tribolium castaneum]
XP_008191375	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X3 [Tribolium castaneum]
XP_008191947	PREDICTED: nuclear hormone receptor FTZ-F1 beta [Tribolium castaneum]
XP_008194320	PREDICTED: probable nuclear hormone receptor HR38 [Tribolium castaneum]
XP_008197634	PREDICTED: ecdysone receptor isoform X3 [Tribolium castaneum]
XP_008201137	PREDICTED: hormone receptor 4 isoform X2 [Tribolium castaneum]
XP_008201140	PREDICTED: hormone receptor 4 isoform X3 [Tribolium castaneum]
XP_008395875	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Poecilia reticulata]
XP_008478386	PREDICTED: nuclear hormone receptor FTZ-F1-like [Diaphorina citri]
XP_008550031	PREDICTED: nuclear receptor subfamily 2 group E member 1 isoform X1 [Microplitis demolitor]
XP_008550032	PREDICTED: nuclear receptor subfamily 2 group E member 1 isoform X2 [Microplitis demolitor]

XP_008552882	PREDICTED: COUP transcription factor 2 isoform X1 [Microplitis demolitor]
XP_008552883	PREDICTED: COUP transcription factor 2 isoform X3 [Microplitis demolitor]
XP_011057053	PREDICTED: photoreceptor-specific nuclear receptor-like [Acromyrmex echinatior]
XP_011057173	PREDICTED: steroid hormone receptor ERR1 isoform X6 [Acromyrmex echinatior]
XP_011060517	PREDICTED: steroid receptor seven-up, isoforms B/C [Acromyrmex echinatior]
XP_011158392	PREDICTED: COUP transcription factor 2-like [Solenopsis invicta]
XP_011161611	PREDICTED: steroid hormone receptor ERR1 isoform X2 [Solenopsis invicta]
XP_011175461	PREDICTED: COUP transcription factor 2 isoform X1 [Solenopsis invicta]
XP_011416690	PREDICTED: photoreceptor-specific nuclear receptor-like [Crassostrea gigas]
XP_011438581	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Crassostrea gigas]
XP_011438583	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Crassostrea gigas]
XP_011503732	PREDICTED: nuclear hormone receptor FTZ-F1 [Ceratosolen solmsi marchali]
XP_011643932	PREDICTED: steroid receptor seven-up, isoforms B/C isoform X2 [Pogonomyrmex barbatus]
XP_011644942	PREDICTED: steroid hormone receptor ERR2 isoform X6 [Pogonomyrmex barbatus]
XP_011691548	PREDICTED: photoreceptor-specific nuclear receptor-like [Wasmannia auropunctata]
XP_011696829	PREDICTED: steroid hormone receptor ERR2 isoform X3 [Wasmannia auropunctata]
XP_011867578	PREDICTED: steroid hormone receptor ERR1 isoform X5 [Vollenhovia emeryi]
XP_012140861	PREDICTED: steroid receptor seven-up, isoforms B/C, partial [Megachile rotundata]
XP_012142716	PREDICTED: probable nuclear hormone receptor HR38 [Megachile rotundata]
XP_012149379	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X2 [Megachile rotundata]
XP_012149394	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X4 [Megachile rotundata]
XP_012167646	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X2 [Bombus terrestris]
XP_012174781	PREDICTED: steroid receptor seven-up, isoforms B/C [Bombus terrestris]
XP_012220015	PREDICTED: COUP transcription factor 2 isoform X2 [Linepithema humile]
XP_012253056	PREDICTED: ecdysone receptor isoform X3 [Athalia rosae]
XP_012253818	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Athalia rosae]
XP_012258841	PREDICTED: ecdysone-induced protein 78C [Athalia rosae]
XP_012261783	PREDICTED: steroid receptor seven-up, isoforms B/C [Athalia rosae]
XP_012526425	PREDICTED: steroid hormone receptor ERR2 isoform X6 [Monomorium pharaonis]
XP_012542052	PREDICTED: steroid receptor seven-up, isoforms B/C [Monomorium pharaonis]
XP_012722686	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Fundulus heteroclitus]
XP_012935331	PREDICTED: orphan steroid hormone receptor 2-like isoform X1 [Aplysia californica]
XP_012935335	PREDICTED: orphan steroid hormone receptor 2-like isoform X2 [Aplysia californica]
XP_012935339	PREDICTED: orphan steroid hormone receptor 2-like isoform X3 [Aplysia californica]
XP_013068647	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Biomphalaria glabrata]
XP_013071146	PREDICTED: photoreceptor-specific nuclear receptor-like [Biomphalaria glabrata]
XP_013080566	PREDICTED: orphan steroid hormone receptor 2-like isoform X1 [Biomphalaria glabrata]
XP_013080567	PREDICTED: orphan steroid hormone receptor 2-like isoform X2 [Biomphalaria glabrata]
XP_013080568	PREDICTED: orphan steroid hormone receptor 2-like isoform X3 [Biomphalaria glabrata]
XP_013080569	PREDICTED: orphan steroid hormone receptor 2-like isoform X4 [Biomphalaria glabrata]
XP_013080570	PREDICTED: orphan steroid hormone receptor 2-like isoform X5 [Biomphalaria glabrata]
XP_013398470	PREDICTED: photoreceptor-specific nuclear receptor-like [Lingula anatina]
XP_013412829	PREDICTED: nuclear receptor subfamily 2 group E member 1-like isoform X1 [Lingula anatina]
XP_013412830	PREDICTED: nuclear receptor subfamily 2 group E member 1-like isoform X2 [Lingula anatina]
XP_013417773	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Lingula anatina]
XP_013772732	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013773938	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013774562	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]

XP_013774626	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013774988	PREDICTED: nuclear receptor subfamily 2 group F member 1-A-like [Limulus polyphemus]
XP_013775116	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013776390	PREDICTED: nuclear hormone receptor FTZ-F1-like [Limulus polyphemus]
XP_013776718	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013777087	PREDICTED: steroid hormone receptor ERR1-like [Limulus polyphemus]
XP_013777259	PREDICTED: retinoic acid receptor RXR-alpha-B-like [Limulus polyphemus]
XP_013777746	PREDICTED: nuclear receptor subfamily 2 group C member 2-like [Limulus polyphemus]
XP_013778961	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013779572	PREDICTED: retinoic acid receptor RXR-alpha-A-like [Limulus polyphemus]
XP_013780022	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013781709	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013782694	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013783147	PREDICTED: retinoic acid receptor RXR-alpha-like [Limulus polyphemus]
XP_013783568	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013784132	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013785406	PREDICTED: photoreceptor-specific nuclear receptor-like [Limulus polyphemus]
XP_013785695	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013786915	PREDICTED: ecdysone-induced protein 78C-like, partial [Limulus polyphemus]
XP_013787145	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013788321	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013788546	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013789030	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013790435	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013792436	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013794283	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013794472	PREDICTED: nuclear receptor subfamily 4 group A member 2-like [Limulus polyphemus]
XP_013865465	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Austrofundulus limnaeus]
XP_013874082	PREDICTED: photoreceptor-specific nuclear receptor-like, partial [Austrofundulus limnaeus]
XP_014207935	PREDICTED: steroid receptor seven-up, isoforms B/C-like [Copidosoma floridanum]
XP_014229050	PREDICTED: steroid hormone receptor ERR2 isoform X5 [Trichogramma pretiosum]
XP_014251567	PREDICTED: hormone receptor 4-like isoform X1 [Cimex lectularius]
XP_014251568	PREDICTED: hormone receptor 4-like isoform X2 [Cimex lectularius]
XP_014251569	PREDICTED: hormone receptor 4-like isoform X3 [Cimex lectularius]
XP_014261639	PREDICTED: ecdysone-induced protein 78C isoform X1 [Cimex lectularius]
XP_014261640	PREDICTED: ecdysone-induced protein 78C isoform X2 [Cimex lectularius]
XP_014261641	PREDICTED: ecdysone-induced protein 78C isoform X3 [Cimex lectularius]
XP_014261642	PREDICTED: ecdysone-induced protein 78C isoform X4 [Cimex lectularius]
XP_014281743	PREDICTED: ecdysone receptor isoform X1 [Halyomorpha halys]
XP_014286561	PREDICTED: hormone receptor 4 isoform X4 [Halyomorpha halys]
XP_014286562	PREDICTED: hormone receptor 4 isoform X5 [Halyomorpha halys]
XP_014286563	PREDICTED: hormone receptor 4 isoform X6 [Halyomorpha halys]
XP_014286885	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X1 [Halyomorpha halys]
XP_014286886	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X2 [Halyomorpha halys]
XP_014286887	PREDICTED: nuclear hormone receptor FTZ-F1 isoform X3 [Halyomorpha halys]
XP_014290138	PREDICTED: probable nuclear hormone receptor HR38 isoform X1 [Halyomorpha halys]
XP_014290139	PREDICTED: probable nuclear hormone receptor HR38 isoform X2 [Halyomorpha halys]
XP_014290140	PREDICTED: probable nuclear hormone receptor HR38 isoform X3 [Halyomorpha halys]
XP_014291406	PREDICTED: ecdysone-induced protein 78C [Halyomorpha halys]
XP_014300447	PREDICTED: COUP transcription factor 2 isoform X4 [Microplitis demolitor]

9.4.2.26 *Ovo / Shaven baby*

Name	**Description**
AAB50918	TFIIIA-like zinc finger transcription factor type M1 isoform, partial [Drosophila sp.]

AAB60216	Ovo-1028aa [Drosophila melanogaster]
AAF68526 (AF252743_1)	ovo protein, partial [Drosophila simulans]
AAF68527 (AF252744_1)	ovo protein, partial [Drosophila simulans]
AAF68533 (AF252750_1)	ovo protein, partial [Drosophila simulans]
ABO38687	ovo, partial [Drosophila orena]
ABO38688	ovo, partial [Drosophila simulans]
ABW92503	ovo protein, partial [Drosophila simulans]
ABW92504	ovo protein, partial [Drosophila melanogaster]
ABW92506	ovo protein, partial [Drosophila melanogaster]
ABW92511	ovo protein, partial [Drosophila melanogaster]
AHA80507	PRDM9, partial [Mus musculus castaneus]
AHA80523	PRDM9, partial [Mus musculus domesticus]
AHA80589	PRDM9, partial [Mus musculus musculus]
CAB36921	ovo protein [Drosophila melanogaster]
CAD23206	shavenbaby, partial [Drosophila melanogaster]
CAD23207	ovoA protein, partial [Drosophila melanogaster]
CAF91396	unnamed protein product, partial [Tetraodon nigroviridis]
CAJ82437	novel protein, partial [Xenopus (Silurana) tropicalis]
CDP94067	Protein BM-PAG-3, isoform c [Brugia malayi]
EFO12437	zinc finger protein [Loa loa]
KDR14571	Protein ovo [Zootermopsis nevadensis]
KFM57884	Zinc finger protein 732, partial [Stegodyphus mimosarum]
KFM58456	Zinc finger protein 782, partial [Stegodyphus mimosarum]
KFM59717	Zinc finger protein 583, partial [Stegodyphus mimosarum]
KFM59825	Zinc finger protein 85, partial [Stegodyphus mimosarum]
KFM60411	Zinc finger protein 84, partial [Stegodyphus mimosarum]
KFM60415	Zinc finger protein 84, partial [Stegodyphus mimosarum]
KFM60594	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM62177	Zinc finger protein 732, partial [Stegodyphus mimosarum]
KFM62882	putative zinc finger protein 735, partial [Stegodyphus mimosarum]
KFM63149	Zinc finger protein 84, partial [Stegodyphus mimosarum]
KFM63381	Zinc finger protein 420, partial [Stegodyphus mimosarum]
KFM63684	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM64059	Zinc finger protein 91, partial [Stegodyphus mimosarum]
KFM64279	Zinc finger protein 84, partial [Stegodyphus mimosarum]
KFM66767	Histone-lysine N-methyltransferase PRDM9, partial [Stegodyphus mimosarum]
KFM66768	Histone-lysine N-methyltransferase PRDM9, partial [Stegodyphus mimosarum]
KFM68906	Histone-lysine N-methyltransferase PRDM9, partial [Stegodyphus mimosarum]
KFM69154	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM69229	Zinc finger protein 681, partial [Stegodyphus mimosarum]
KFM69324	Zinc finger protein, partial [Stegodyphus mimosarum]
KFM69326	Zinc finger protein Gfi-1b, partial [Stegodyphus mimosarum]
KFM71430	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM71439	Zinc finger protein 726, partial [Stegodyphus mimosarum]
KFM71723	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM72658	Zinc finger protein 431, partial [Stegodyphus mimosarum]
KFM73312	Zinc finger protein 91, partial [Stegodyphus mimosarum]
KFM73610	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM74204	Zinc finger protein 91, partial [Stegodyphus mimosarum]
KFM74304	Zinc finger protein 98, partial [Stegodyphus mimosarum]
KFM75946	Zinc finger protein 235, partial [Stegodyphus mimosarum]
KFM76924	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM78567	Zinc finger protein 226, partial [Stegodyphus mimosarum]
KFM79009	PR domain zinc finger protein 1, partial [Stegodyphus mimosarum]
KFM79698	Zinc finger protein 271, partial [Stegodyphus mimosarum]
KFM80422	Histone-lysine N-methyltransferase PRDM9, partial [Stegodyphus mimosarum]
KFM80951	Zinc finger protein 484, partial [Stegodyphus mimosarum]
KFM80952	Zinc finger protein 420, partial [Stegodyphus mimosarum]
KFM80953	Zinc finger protein 569, partial [Stegodyphus mimosarum]
KFM81642	Zinc finger protein 583, partial [Stegodyphus mimosarum]
KFM82111	Protein ovo, partial [Stegodyphus mimosarum]
KFM83203	Zinc finger protein 85, partial [Stegodyphus mimosarum]
KFM83351	Zinc finger protein 26, partial [Stegodyphus mimosarum]
KFM83374	Zinc finger protein 91, partial [Stegodyphus mimosarum]
KKF11497	Zinc finger protein 665 [Larimichthys crocea]
KMZ08232	uncharacterized protein Dsimw501_GD16717, partial [Drosophila simulans]
KMZ08233	uncharacterized protein Dsimw501_GD24377 [Drosophila simulans]
Locus_1_Transcript_81644/166847_Confidence_1.000_Length_1812 - ORF 1 (frame 3) translation	Locus_1_Transcript_81644/166847_Confidence_1.000_Length_1812
Locus_1_Transcript_89368/166847_Confidence_1.000_Length_959 - ORF 5 (frame 1) translation	Locus_1_Transcript_89368/166847_Confidence_1.000_Length_959
Locus_1_Transcript_90581/166847_Confidence_1.000_Length_335 - ORF 1 (frame 2) translation	Locus_1_Transcript_90581/166847_Confidence_1.000_Length_335
Locus_1_Transcript_106668/166847_Confidence_1.000_Length_920 - ORF 3 (frame 3) translation	Locus_1_Transcript_106668/166847_Confidence_1.000_Length_920
Locus_1_Transcript_112175/166847_Confidence_1.000_Length_257 - ORF 1 (frame 3) translation	Locus_1_Transcript_112175/166847_Confidence_1.000_Length_257
Locus_1_Transcript_112611/166847_Confidence_1.000_Length_864 - ORF 3 (frame 3) translation	Locus_1_Transcript_112611/166847_Confidence_1.000_Length_864
Locus_1_Transcript_164650/166847_Confidence_1.000_Length_439 - ORF 1 (frame 1) translation	Locus_1_Transcript_164650/166847_Confidence_1.000_Length_439
Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594 - ORF 3 (frame 1) translation	Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594
Locus_1439_Transcript_1/4_Confidence_0.636_Length_2076 - ORF 1 (frame 2) translation	Locus_1439_Transcript_1/4_Confidence_0.636_Length_2076

Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195 - ORF 3 (frame 2) translation	Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195
Locus_5796_Transcript_3/10_Confidence_0.154_Length_899 - ORF 1 (frame 1) translation	Locus_5796_Transcript_3/10_Confidence_0.154_Length_899
Locus_6910_Transcript_3/10_Confidence_0.127_Length_480 - ORF 1 (frame 3) translation	Locus_6910_Transcript_3/10_Confidence_0.127_Length_480
Locus_7469_Transcript_20/25_Confidence_0.014_Length_749 - ORF 1 (frame 1) translation	Locus_7469_Transcript_20/25_Confidence_0.014_Length_749
Locus_8930_Transcript_1/2_Confidence_0.857_Length_1099 - ORF 2 (frame 2) translation	Locus_8930_Transcript_1/2_Confidence_0.857_Length_1099
Locus_9749_Transcript_6/7_Confidence_0.769_Length_942 - ORF 3 (frame 1) translation	Locus_9749_Transcript_6/7_Confidence_0.769_Length_942
Locus_13054_Transcript_8/11_Confidence_0.361_Length_5031 - ORF 5 (frame 2) translation	Locus_13054_Transcript_8/11_Confidence_0.361_Length_5031
Locus_15825_Transcript_1/1_Confidence_1.000_Length_1901 - ORF 1 (frame 3) translation	Locus_15825_Transcript_1/1_Confidence_1.000_Length_1901
Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891 - ORF 1 (frame 1) translation	Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891
Locus_25081_Transcript_1/1_Confidence_1.000_Length_1385 - ORF 1 (frame 1) translation	Locus_25081_Transcript_1/1_Confidence_1.000_Length_1385
NP_525077	ovo, isoform A [Drosophila melanogaster]
NP_726972	ovo, isoform C [Drosophila melanogaster]
NP_001033831	ovo, isoform D [Drosophila melanogaster]
NP_001088360	zinc finger protein 268 [Xenopus laevis]
OVO_DROME	RecName: Full=Protein ovo; AltName: Full=Protein shaven baby
P18714 (ZG20_XENLA)	RecName: Full=Gastrula zinc finger protein xFG20-1; AltName: Full=XlCGF20.1
XP_001945654	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001950651	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_002405934	zinc finger protein, putative [Ixodes scapularis]
XP_002415970	zinc finger protein, putative [Ixodes scapularis]
XP_003151632	zinc finger protein [Loa loa]
XP_003242514	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003242604	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003244738	PREDICTED: zinc finger protein 572-like [Acyrthosiphon pisum]
XP_003244741	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_003248857	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003249048	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_003759283	PREDICTED: zinc finger protein OZF-like, partial [Sarcophilus harrisii]
XP_004527391	PREDICTED: protein ovo isoform X1 [Ceratitis capitata]
XP_004527393	PREDICTED: protein ovo isoform X2 [Ceratitis capitata]
XP_004565243	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Maylandia zebra]
XP_005179980	PREDICTED: protein ovo-like isoform X3 [Musca domestica]
XP_005743428	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Pundamilia nyererei]
XP_005805452	PREDICTED: zinc finger protein 235-like [Xiphophorus maculatus]
XP_005814335	PREDICTED: zinc finger protein Gfi-1b-like [Xiphophorus maculatus]
XP_005932238	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Haplochromis burtoni]
XP_006793328	PREDICTED: zinc finger protein 271-like [Neolamprologus brichardi]
XP_006898045	PREDICTED: zinc finger protein 91-like [Elephantulus edwardii]
XP_007506319	PREDICTED: zinc finger protein 135-like, partial [Monodelphis domestica]
XP_007566505	PREDICTED: zinc finger protein 37-like isoform X1 [Poecilia formosa]
XP_007566506	PREDICTED: gastrula zinc finger protein XlCGF52.1-like isoform X2 [Poecilia formosa]
XP_007576654	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007957395	PREDICTED: zinc finger protein 420-like [Orycteropus afer afer]
XP_008179259	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180595	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180607	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_008181548	PREDICTED: zinc finger protein 239-like [Acyrthosiphon pisum]
XP_008181794	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008185429	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Acyrthosiphon pisum]
XP_008186726	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_008186729	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008188120	PREDICTED: zinc finger protein 180-like [Acyrthosiphon pisum]
XP_008203536	PREDICTED: PR domain zinc finger protein 1 isoform X3 [Nasonia vitripennis]
XP_008203537	PREDICTED: PR domain zinc finger protein 1 isoform X4 [Nasonia vitripennis]
XP_008285370	PREDICTED: gastrula zinc finger protein XlCGF71.1-like, partial [Stegastes partitus]
XP_008302764	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Stegastes partitus]
XP_008303030	PREDICTED: zinc finger protein OZF-like [Stegastes partitus]
XP_008307421	PREDICTED: zinc finger protein 708-like [Cynoglossus semilaevis]
XP_008335353	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Cynoglossus semilaevis]
XP_008404661	PREDICTED: zinc finger protein OZF-like [Poecilia reticulata]
XP_008420492	PREDICTED: zinc finger protein OZF-like [Poecilia reticulata]
XP_008468698	PREDICTED: zinc finger protein 239-like [Diaphorina citri]
XP_009293180	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_009298947	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_010587799	PREDICTED: zinc finger protein 420-like [Loxodonta africana]

XP_010600617	PREDICTED: zinc finger protein 345-like isoform X1 [Loxodonta africana]
XP_010600618	PREDICTED: zinc finger protein 345-like isoform X2 [Loxodonta africana]
XP_010749266	PREDICTED: zinc finger protein 32-like [Larimichthys crocea]
XP_010767458	PREDICTED: zinc finger protein 607-like, partial [Notothenia coriiceps]
XP_010902037	PREDICTED: gastrula zinc finger protein XlCGF28.1-like [Esox lucius]
XP_011065442	PREDICTED: zinc finger protein Gfi-1b-like [Acromyrmex echinatior]
XP_011181680	PREDICTED: protein ovo isoform X2 [Bactrocera cucurbitae]
XP_011214039	PREDICTED: protein ovo isoform X1 [Bactrocera dorsalis]
XP_011214040	PREDICTED: protein ovo isoform X2 [Bactrocera dorsalis]
XP_011214041	PREDICTED: protein ovo isoform X3 [Bactrocera dorsalis]
XP_011214042	PREDICTED: protein ovo isoform X4 [Bactrocera dorsalis]
XP_011429851	PREDICTED: zinc finger protein OZF-like [Crassostrea gigas]
XP_012158339	PREDICTED: protein ovo isoform X3 [Ceratitis capitata]
XP_012171374	PREDICTED: zinc finger protein 628-like isoform X3 [Bombus terrestris]
XP_012265037	PREDICTED: protein ovo isoform X2 [Athalia rosae]
XP_012397464	PREDICTED: zinc finger protein 501-like [Sarcophilus harrisii]
XP_012411644	PREDICTED: zinc finger protein 883-like [Trichechus manatus latirostris]
XP_012547447	PREDICTED: zinc finger protein 468-like [Bombyx mori]
XP_012713485	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012713624	PREDICTED: gastrula zinc finger protein XlCGF49.1-like, partial [Fundulus heteroclitus]
XP_012715333	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012808756	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Xenopus (Silurana) tropicalis]
XP_012810455	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_012821172	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_012892021	PREDICTED: zinc finger protein 420-like [Dipodomys ordii]
XP_013082078	PREDICTED: zinc finger protein 235-like, partial [Biomphalaria glabrata]
XP_013098416	PREDICTED: protein ovo isoform X3 [Stomoxys calcitrans]
XP_013772409	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013775795	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013778397	PREDICTED: gastrula zinc finger protein XlCGF7.1-like [Limulus polyphemus]
XP_013779582	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013780913	PREDICTED: protein ovo-like isoform X1 [Limulus polyphemus]
XP_013780914	PREDICTED: protein ovo-like isoform X2 [Limulus polyphemus]
XP_013784172	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013784339	PREDICTED: zinc finger protein Gfi-1b-like, partial [Limulus polyphemus]
XP_013787012	PREDICTED: zinc finger protein 239-like [Limulus polyphemus]
XP_013856101	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Austrofundulus limnaeus]
XP_013860411	PREDICTED: zinc finger protein OZF-like [Austrofundulus limnaeus]
XP_013868404	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Austrofundulus limnaeus]

9.4.2.27 *Paired*

Name	Description
A0JMA6 (PAX8_XENTR)	RecName: Full=Paired box protein Pax-8
A1YEY5 (GSC_GORGO)	RecName: Full=Homeobox protein goosecoid
A1YG25 (RAX2_PANPA)	RecName: Full=Retina and anterior neural fold homeobox protein 2; AltName: Full=Retina and anterior neural fold homeobox-like protein 1
A2T7P4 (GSC_PONPY)	RecName: Full=Homeobox protein goosecoid
A6NJT0 (UNC4_HUMAN)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
A6YP92 (ARX_RAT)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
Locus_1_Transcript_41866/166847_Confidence_1.000_Length_2252 - ORF 16 (frame 2) translation	Locus_1_Transcript_41866/166847_Confidence_1.000_Length_2252
Locus_1_Transcript_52318/166847_Confidence_1.000_Length_1098 - ORF 1 (frame 1) translation	Locus_1_Transcript_52318/166847_Confidence_1.000_Length_1098
Locus_1_Transcript_68976/166847_Confidence_1.000_Length_1127 - ORF 3 (frame 2) translation	Locus_1_Transcript_68976/166847_Confidence_1.000_Length_1127
Locus_1_Transcript_143207/166847_Confidence_1.000_Length_1412 - ORF 2 (frame 2) translation	Locus_1_Transcript_143207/166847_Confidence_1.000_Length_1412
Locus_2435_Transcript_2/5_Confidence_0.565_Length_2834 - ORF 2 (frame 1) translation	Locus_2435_Transcript_2/5_Confidence_0.565_Length_2834
Locus_13554_Transcript_1/10_Confidence_0.583_Length_2471 - ORF 3 (frame 1) translation	Locus_13554_Transcript_1/10_Confidence_0.583_Length_2471
Locus_13887_Transcript_1/5_Confidence_0.640_Length_1959 - ORF 18 (frame 2) translation	Locus_13887_Transcript_1/5_Confidence_0.640_Length_1959
Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913 - ORF 2 (frame 1) translation	Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913

Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251 - ORF 3 (frame 2) translation	Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251
Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177 - ORF 3 (frame 1) translation	Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177
Locus_17087_Transcript_1/2_Confidence_0.750_Length_910 - ORF 3 (frame 1) translation	Locus_17087_Transcript_1/2_Confidence_0.750_Length_910
Locus_17374_Transcript_1/1_Confidence_1.000_Length_1255 - ORF 1 (frame 1) translation	Locus_17374_Transcript_1/1_Confidence_1.000_Length_1255
Locus_17460_Transcript_2/5_Confidence_0.545_Length_4767 - ORF 2 (frame 3) translation	Locus_17460_Transcript_2/5_Confidence_0.545_Length_4767
Locus_17531_Transcript_1/2_Confidence_0.889_Length_1586 - ORF 1 (frame 3) translation	Locus_17531_Transcript_1/2_Confidence_0.889_Length_1586
Locus_18982_Transcript_1/4_Confidence_0.300_Length_3390 - ORF 2 (frame 1) translation	Locus_18982_Transcript_1/4_Confidence_0.300_Length_3390
Locus_19513_Transcript_1/1_Confidence_1.000_Length_828 - ORF 1 (frame 3) translation	Locus_19513_Transcript_1/1_Confidence_1.000_Length_828
Locus_20911_Transcript_1/1_Confidence_1.000_Length_1876 - ORF 1 (frame 1) translation	Locus_20911_Transcript_1/1_Confidence_1.000_Length_1876
Locus_22533_Transcript_1/2_Confidence_0.500_Length_923 - ORF 9 (frame 2) translation	Locus_22533_Transcript_1/2_Confidence_0.500_Length_923
Locus_24579_Transcript_1/1_Confidence_1.000_Length_1020 - ORF 1 (frame 3) translation	Locus_24579_Transcript_1/1_Confidence_1.000_Length_1020
Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171 - ORF 1 (frame 1) translation	Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171
Locus_109739_Transcript_1/1_Confidence_1.000_Length_990 - ORF 9 (frame 2) translation	Locus_109739_Transcript_1/1_Confidence_1.000_Length_990
NP_001099209	paired mesoderm homeobox protein 2 [Rattus norvegicus]
NP_001158393	pox-neuro [Saccoglossus kowalevskii]
NP_001180179	visual system homeobox 2 [Bos taurus]
O08934 (UNC4_MOUSE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
O14813 (PHX2A_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
O15266 (SHOX_HUMAN)	RecName: Full=Short stature homeobox protein; AltName: Full=Pseudoautosomal homeobox-containing osteogenic protein; AltName: Full=Short stature homeobox-containing protein
O15499 (GSC2_HUMAN)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
O18381 (PAX6_DROME)	RecName: Full=Paired box protein Pax-6; AltName: Full=Protein eyeless
O35085 (ARX_MOUSE)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
O35602 (RX_MOUSE)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
O35690 (PHX2B_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2B; AltName: Full=Neuroblastoma Phox; Short=NBPhox; AltName: Full=PHOX2B homeodomain protein; AltName: Full=Paired-like homeobox 2B
O35750 (SHOX2_RAT)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Paired family homeodomain protein Prx3
O42115 (ARX_DANRE)	RecName: Full=Aristaless-related homeobox protein; Short=ARX
O42201 (RXA_XENLA)	RecName: Full=Retinal homeobox protein Rx-A; Short=Rx1A; Short=Xrx1; AltName: Full=Retina and anterior neural fold homeobox protein A
O42250 (VSX1_DANRE)	RecName: Full=Visual system homeobox 1; AltName: Full=Transcription factor VSX1
O42356 (RX1_DANRE)	RecName: Full=Retinal homeobox protein Rx1
O42357 (RX2_DANRE)	RecName: Full=Retinal homeobox protein Rx2
O42358 (RX3_DANRE)	RecName: Full=Retinal homeobox protein Rx3
O42477 (VSX2_DANRE)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein ALX; AltName: Full=Homeobox protein CHX10; AltName: Full=Transcription factor VSX2
O42567 (RXB_XENLA)	RecName: Full=Retinal homeobox protein Rx-B; AltName: Full=Retina and anterior neural fold homeobox protein B; AltName: Full=Rx2A; Short=Xrx2
O57682 (PAX2B_XENLA)	RecName: Full=Paired box protein Pax-2-B; Short=xPax-2b
O57685 (PAX2A_XENLA)	RecName: Full=Paired box protein Pax-2-A; Short=xPax-2a
O60902 (SHOX2_HUMAN)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; AltName: Full=Paired-related homeobox protein SHOT
O73917 (PAX6_ORYLA)	RecName: Full=Paired box protein Pax-6
O77215 (UNC4_DROME)	RecName: Full=Homeobox protein unc-4; AltName: Full=Paired-like homeodomain protein unc-4; Short=DPHD-1
O97039 (RX_DUGJA)	RecName: Full=Retinal homeobox protein Rax; AltName: Full=DjRax
P0DMV5 (ALX1_GEOFO)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
P06601 (PRD_DROME)	RecName: Full=Segmentation protein paired
P09082 (GSB_DROME)	RecName: Full=Protein gooseberry; AltName: Full=BSH9; AltName: Full=Protein gooseberry distal
P09083 (GSBN_DROME)	RecName: Full=Protein gooseberry-neuro; AltName: Full=BSH4; AltName: Full=Protein gooseberry proximal
P23758 (POXN_DROME)	RecName: Full=Paired box pox-neuro protein; AltName: Full=Paired box neuronal protein
P23759 (PAX7_HUMAN)	RecName: Full=Paired box protein Pax-7; AltName: Full=HuP1
P23760 (PAX3_HUMAN)	RecName: Full=Paired box protein Pax-3; AltName: Full=HuP2
P24610 (PAX3_MOUSE)	RecName: Full=Paired box protein Pax-3
P26367 (PAX6_HUMAN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Oculorhombin
P26630 (PAX6_DANRE)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax[Zf-a]
P29454 (GSCA_XENLA)	RecName: Full=Homeobox protein goosecoid isoform A

P29506 (UNC4_CAEEL)	RecName: Full=Homeobox protein unc-4; AltName: Full=Homeobox protein ceh-4; AltName: Full=Uncoordinated protein 4
P32114 (PAX2_MOUSE)	RecName: Full=Paired box protein Pax-2
P32243 (OTX2_HUMAN)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P41935 (HM10_CAEEL)	RecName: Full=Homeobox protein ceh-10
P47236 (PAX1_CHICK)	RecName: Full=Paired box protein Pax-1
P47237 (PAX6_CHICK)	RecName: Full=Paired box protein Pax-6
P47238 (PAX6_COTJA)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax-QNR
P47239 (PAX7_MOUSE)	RecName: Full=Paired box protein Pax-7
P51974 (PAX8_RAT)	RecName: Full=Paired box protein Pax-8
P53544 (GSC_DANRE)	RecName: Full=Homeobox protein goosecoid; AltName: Full=ZGSC
P53546 (GSCB_XENLA)	RecName: Full=Homeobox protein goosecoid isoform B
P54366 (GSC_DROME)	RecName: Full=Homeobox protein goosecoid
P54821 (PRRX1_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=Homeobox protein PHOX1; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1
P55166 (PAX9_CHICK)	RecName: Full=Paired box protein Pax-9
P55771 (PAX9_HUMAN)	RecName: Full=Paired box protein Pax-9
P55864 (PAX6_XENLA)	RecName: Full=Paired box protein Pax-6
P56915 (GSC_HUMAN)	RecName: Full=Homeobox protein goosecoid
P56916 (GSC2_MOUSE)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
P58304 (VSX2_HUMAN)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
P63014 (PRRX1_RAT)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1; Short=rHox
P63016 (PAX6_RAT)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
P70390 (SHOX2_MOUSE)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; Short=OG-12; AltName: Full=Paired family homeodomain protein Prx3
P80206 (OTX2_MOUSE)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P97830 (UNC4_RAT)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1; AltName: Full=Paired-type homeodomain transcription factor 1
PRD_DROME	RecName: Full=Segmentation protein paired
Q0IH87 (PAX3B_XENLA)	RecName: Full=Paired box protein Pax-3-B; Short=xPax3-B; AltName: Full=Paired-domain transcription factor Pax3-B
Q0P031 (VSX1_XENLA)	RecName: Full=Visual system homeobox 1; AltName: Full=Transcription factor vsx1; AltName: Full=Xvsx1
Q1LVQ7 (ALX1_DANRE)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q1LZF1 (PAX6_BOVIN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
Q2VL53 (PAX9_DAUMA)	RecName: Full=Paired box protein Pax-9
Q2VL54 (PAX9_PERPO)	RecName: Full=Paired box protein Pax-9
Q2VL56 (PAX9_SAGOE)	RecName: Full=Paired box protein Pax-9
Q2VL57 (PAX9_LEORO)	RecName: Full=Paired box protein Pax-9
Q2VL58 (PAX9_CALJA)	RecName: Full=Paired box protein Pax-9
Q2VL59 (PAX9_CALGO)	RecName: Full=Paired box protein Pax-9
Q2VL60 (PAX9_SAIBB)	RecName: Full=Paired box protein Pax-9
Q2VL61 (PAX9_MACMU)	RecName: Full=Paired box protein Pax-9
Q2VL62 (PAX9_PANTR)	RecName: Full=Paired box protein Pax-9
Q6DKN2 (OTX2B_XENLA)	RecName: Full=Homeobox protein OTX2-B; Short=xOTX2-B; AltName: Full=Orthodenticle 2-B; AltName: Full=Orthodenticle-A-like protein B
Q7YTC2 (OTP_SACKO)	RecName: Full=Homeobox protein orthopedia
Q9I9A2 (RX2_ORYLA)	RecName: Full=Retinal homeobox protein Rx2
Q9I9A3 (VSX2_ORYLA)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10; AltName: Full=Transcription factor VSX2
Q9I9D5 (RX1_ASTFA)	RecName: Full=Retinal homeobox protein Rx1
Q9IAL1 (VSX2_CHICK)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
Q9IAL2 (VSX1_CHICK)	RecName: Full=Visual system homeobox 1; AltName: Full=Homeobox protein Chx10-1; AltName: Full=Transcription factor VSX1
Q9JLT7 (RX_RAT)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
Q9PT61 (OTX5B_XENLA)	RecName: Full=Homeobox protein otx5-B; AltName: Full=Orthodenticle homolog 5-B; AltName: Full=XOtx5b
Q9PVM0 (OTX5A_XENLA)	RecName: Full=Homeobox protein otx5-A; AltName: Full=Orthodenticle homolog 5-A; AltName: Full=Xotx5
Q9PVX0 (RX2_CHICK)	RecName: Full=Retinal homeobox protein Rx2; Short=cRax2
Q9PVY0 (RX1_CHICK)	RecName: Full=Retinal homeobox protein Rx1; Short=cRax1
Q9W2Q1 (RX_DROME)	RecName: Full=Retinal homeobox protein Rx; Short=DRx; Short=DRx1
Q9YH95 (PAX5_XENLA)	RecName: Full=Paired box protein Pax-5; Short=XPax-5
Q28DP6 (PAX3_XENTR)	RecName: Full=Paired box protein Pax-3; AltName: Full=Paired-domain transcription factor Pax3
Q28EM7 (OTX5_XENTR)	RecName: Full=Homeobox protein otx5; AltName: Full=Orthodenticle homolog 5
Q28FN6 (OTX2_XENTR)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle 2
Q50D79 (UNC4_DANRE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
Q96QS3 (ARX_HUMAN)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
Q00288 (PAX8_MOUSE)	RecName: Full=Paired box protein Pax-8

Q645N4 (PAX3A_XENLA)	RecName: Full=Paired box protein Pax-3-A; Short=xPax3-A; AltName: Full=Paired-domain transcription factor Pax3-A
Q02548 (PAX5_HUMAN)	RecName: Full=Paired box protein Pax-5; AltName: Full=B-cell-specific transcription factor; Short=BSAP
Q02650 (PAX5_MOUSE)	RecName: Full=Paired box protein Pax-5; AltName: Full=B-cell-specific transcription factor; Short=BSAP
Q02962 (PAX2_HUMAN)	RecName: Full=Paired box protein Pax-2
Q05437 (PRRX1_CHICK)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=GMHOX; AltName: Full=Homeobox protein MHOX; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1
Q06348 (PRRX2_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2; Short=PRX-2; AltName: Full=Homeobox protein S8
Q06453 (AL_DROME)	RecName: Full=Homeobox protein aristaless
Q06710 (PAX8_HUMAN)	RecName: Full=Paired box protein Pax-8
Q15699 (ALX1_HUMAN)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q26602 (SMOX3_SCHMA)	RecName: Full=Homeobox protein SMOX-3
Q26657 (ALX_STRPU)	RecName: Full=Aristaless homeobox protein; Short=ALX; AltName: Full=SpPrx-1
Q61412 (VSX2_MOUSE)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
Q62066 (PHX2A_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=PHOX2A homeodomain protein; AltName: Full=Paired-like homeobox 2A
Q62782 (PHX2A_RAT)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
Q90268 (PAX2A_DANRE)	RecName: Full=Paired box protein Pax-2a; AltName: Full=No isthmus protein; AltName: Full=Pax[Zf-b]
Q90277 (VSX1_CARAU)	RecName: Full=Visual system homeobox 1; AltName: Full=Homeobox protein VSX-1; AltName: Full=Transcription factor VSX1
Q91813 (OTX2A_XENLA)	RecName: Full=Homeobox protein OTX2-A; Short=xOTX2-A; AltName: Full=Orthodenticle 2-A; AltName: Full=Orthodenticle-A-like protein A
Q91981 (OTX2_DANRE)	RecName: Full=Homeobox protein OTX2; Short=zOTX2; AltName: Full=Orthodenticle homolog 2
Q91994 (OTX1B_DANRE)	RecName: Full=Homeobox protein OTX1 B; Short=zOtx1; AltName: Full=Orthodenticle homolog 1 B
Q99811 (PRRX2_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2; AltName: Full=Paired-related homeobox protein 2; Short=PRX-2
XP_969276	PREDICTED: homeobox protein unc-4-like [Tribolium castaneum]
XP_975478	PREDICTED: paired box pox-meso protein [Tribolium castaneum]
XP_001119966	PREDICTED: retinal homeobox protein Rx [Apis mellifera]
XP_001369196	PREDICTED: paired mesoderm homeobox protein 2 isoform X1 [Monodelphis domestica]
XP_001516357	PREDICTED: retina and anterior neural fold homeobox protein 2 [Ornithorhynchus anatinus]
XP_001599456	PREDICTED: homeobox protein ARX-like isoform X2 [Nasonia vitripennis]
XP_001634166	predicted protein [Nematostella vectensis]
XP_001943352	PREDICTED: homeobox protein goosecoid [Acyrthosiphon pisum]
XP_002429319	Paired box protein Pax-6, putative [Pediculus humanus corporis]
XP_002430643	Ultrabithorax, putative [Pediculus humanus corporis]
XP_002432447	homeobox protein arx, putative [Pediculus humanus corporis]
XP_002731203	PREDICTED: homeobox protein ARX-like [Saccoglossus kowalevskii]
XP_003121872	PREDICTED: homeobox protein OTX2 isoform X1 [Sus scrofa]
XP_003393215	PREDICTED: homeobox protein aristaless-like [Bombus terrestris]
XP_003393515	PREDICTED: retinal homeobox protein Rx1-like [Bombus terrestris]
XP_003447846	PREDICTED: visual system homeobox 2-like [Oreochromis niloticus]
XP_003695586	PREDICTED: retinal homeobox protein Rx1-like [Apis florea]
XP_003697447	PREDICTED: protein gooseberry isoform X1 [Apis florea]
XP_003702414	PREDICTED: homeobox protein goosecoid [Megachile rotundata]
XP_003745704	PREDICTED: homeobox protein unc-4 homolog [Metaseiulus occidentalis]
XP_005092282	PREDICTED: mediator of DNA damage checkpoint protein 1-like [Aplysia californica]
XP_005185444	PREDICTED: paired box protein Pax-6 [Musca domestica]
XP_005287559	PREDICTED: paired box protein Pax-1 [Chrysemys picta bellii]
XP_005901034	PREDICTED: visual system homeobox 2 [Bos mutus]
XP_005948265	PREDICTED: paired box protein Pax-7-like isoform X2 [Haplochromis burtoni]
XP_006007527	PREDICTED: paired box protein Pax-1 isoform X1 [Latimeria chalumnae]
XP_006053924	PREDICTED: visual system homeobox 2 [Bubalus bubalis]
XP_006559357	PREDICTED: protein gooseberry-like isoform X2 [Apis mellifera]
XP_006624099	PREDICTED: retinal homeobox protein Rx-like [Apis dorsata]
XP_006640737	PREDICTED: paired mesoderm homeobox protein 2-like [Lepisosteus oculatus]
XP_006807220	PREDICTED: paired box protein Pax-7-like isoform X2 [Neolamprologus brichardi]
XP_007422992	PREDICTED: homeobox protein OTX2 isoform X1 [Python bivittatus]
XP_007475194	PREDICTED: paired mesoderm homeobox protein 2 isoform X2 [Monodelphis domestica]
XP_007535826	PREDICTED: homeobox protein OTX2 isoform X1 [Erinaceus europaeus]
XP_007549321	PREDICTED: visual system homeobox 2 [Poecilia formosa]
XP_007549399	PREDICTED: paired box protein Pax-1-like [Poecilia formosa]
XP_007884280	PREDICTED: short stature homeobox protein-like, partial [Callorhinchus milii]
XP_007901317	PREDICTED: retinal homeobox protein Rx [Callorhinchus milii]
XP_007904244	PREDICTED: visual system homeobox 2 [Callorhinchus milii]

XP_008192483	PREDICTED: paired mesoderm homeobox protein 2A-like [Tribolium castaneum]
XP_008193911	PREDICTED: aristaless isoform X2 [Tribolium castaneum]
XP_008195782	PREDICTED: aristaless-related homeobox protein [Tribolium castaneum]
XP_008196347	PREDICTED: paired box protein Pax-1 [Tribolium castaneum]
XP_008201169	PREDICTED: paired mesoderm homeobox protein 2 [Tribolium castaneum]
XP_008207398	PREDICTED: homeobox protein aristaless-like [Nasonia vitripennis]
XP_008214560	PREDICTED: paired mesoderm homeobox protein 2-like isoform X3 [Nasonia vitripennis]
XP_008314528	PREDICTED: homeobox protein unc-4 homolog [Cynoglossus semilaevis]
XP_008326698	PREDICTED: paired box protein Pax-1 isoform X1 [Cynoglossus semilaevis]
XP_008328178	PREDICTED: paired box protein Pax-1 isoform X3 [Cynoglossus semilaevis]
XP_008328945	PREDICTED: paired box protein Pax-1 isoform X4 [Cynoglossus semilaevis]
XP_008329681	PREDICTED: paired box protein Pax-1 isoform X5 [Cynoglossus semilaevis]
XP_008397571	PREDICTED: visual system homeobox 2 isoform X2 [Poecilia reticulata]
XP_008469101	PREDICTED: paired box protein Pax-1-like [Diaphorina citri]
XP_008488086	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Diaphorina citri]
XP_008923318	PREDICTED: paired box protein Pax-9 [Manacus vitellinus]
XP_009076651	PREDICTED: short stature homeobox protein-like, partial [Acanthisitta chloris]
XP_009100157	PREDICTED: paired box protein Pax-9 [Serinus canaria]
XP_009279652	PREDICTED: short stature homeobox protein [Aptenodytes forsteri]
XP_009279652	PREDICTED: short stature homeobox protein [Aptenodytes forsteri]
XP_009708313	PREDICTED: short stature homeobox protein, partial [Cariama cristata]
XP_009929482	PREDICTED: short stature homeobox protein [Opisthocomus hoazin]
XP_009950422	PREDICTED: short stature homeobox protein 2, partial [Leptosomus discolor]
XP_009977752	PREDICTED: short stature homeobox protein, partial [Tauraco erythrolophus]
XP_010004397	PREDICTED: paired mesoderm homeobox protein 2B [Chaetura pelagica]
XP_010145662	PREDICTED: paired mesoderm homeobox protein 2B, partial [Eurypyga helias]
XP_010171498	PREDICTED: short stature homeobox protein, partial [Caprimulgus carolinensis]
XP_010197417	PREDICTED: short stature homeobox protein, partial [Colius striatus]
XP_010581968	PREDICTED: paired box protein Pax-9 [Haliaeetus leucocephalus]
XP_010710401	PREDICTED: homeobox protein OTX2 isoform X1 [Meleagris gallopavo]
XP_010778173	PREDICTED: paired box protein Pax-1 [Notothenia coriiceps]
XP_010793318	PREDICTED: short stature homeobox protein 2 [Notothenia coriiceps]
XP_010854055	PREDICTED: visual system homeobox 2 [Bison bison bison]
XP_011139178	PREDICTED: homeobox protein goosecoid [Harpegnathos saltator]
XP_011145894	PREDICTED: paired box protein Pax-5 [Harpegnathos saltator]
XP_011154618	PREDICTED: protein gooseberry [Harpegnathos saltator]
XP_011175152	PREDICTED: protein gooseberry [Solenopsis invicta]
XP_011261155	PREDICTED: homeobox protein goosecoid [Camponotus floridanus]
XP_011299924	PREDICTED: paired box protein Pax-6 [Fopius arisanus]
XP_011333914	PREDICTED: protein gooseberry isoform X1 [Cerapachys biroi]
XP_011333915	PREDICTED: protein gooseberry isoform X2 [Cerapachys biroi]
XP_011338931	PREDICTED: homeobox protein goosecoid [Cerapachys biroi]
XP_011424860	PREDICTED: paired box protein Pax-7-like isoform X1 [Crassostrea gigas]
XP_011424861	PREDICTED: paired box protein Pax-7-like isoform X2 [Crassostrea gigas]
XP_011427188	PREDICTED: retinal homeobox protein Rax-like [Crassostrea gigas]
XP_011433286	PREDICTED: paired box protein Pax-6-like isoform X1 [Crassostrea gigas]
XP_011433289	PREDICTED: paired box protein Pax-6-like isoform X2 [Crassostrea gigas]
XP_011445596	PREDICTED: homeobox protein unc-4 homolog [Crassostrea gigas]
XP_011503661	PREDICTED: homeobox protein aristaless [Ceratosolen solmsi marchali]
XP_011571078	PREDICTED: paired box protein Pax-9 [Aquila chrysaetos canadensis]
XP_011692944	PREDICTED: homeobox protein goosecoid [Wasmannia auropunctata]
XP_012217632	PREDICTED: retinal homeobox protein Rx1-like [Linepithema humile]
XP_012245723	PREDICTED: protein gooseberry-like [Bombus impatiens]
XP_012254404	PREDICTED: homeobox protein ARX-like [Athalia rosae]
XP_012262061	PREDICTED: retina and anterior neural fold homeobox protein 2-like [Athalia rosae]
XP_012264378	PREDICTED: paired box protein Pax-5 [Athalia rosae]
XP_012282148	PREDICTED: aristaless-related homeobox protein [Orussus abietinus]
XP_012533722	PREDICTED: homeobox protein aristaless-like [Monomorium pharaonis]
XP_012663430	PREDICTED: homeobox protein OTX2 isoform X1 [Otolemur garnettii]
XP_012693489	PREDICTED: paired box protein Pax-1-like [Clupea harengus]
XP_012867728	PREDICTED: homeobox protein OTX2 isoform X1 [Dipodomys ordii]
XP_013115219	PREDICTED: paired box protein Pax-6-like [Stomoxys calcitrans]
XP_013122904	PREDICTED: paired box protein Pax-7-like isoform X2 [Oreochromis niloticus]
XP_013133558	PREDICTED: homeobox protein aristaless-like [Papilio polytes]

XP_013142990	PREDICTED: homeobox protein unc-4 [Papilio polytes]
XP_013181086	PREDICTED: homeobox protein aristaless-like [Papilio xuthus]
XP_013190975	PREDICTED: paired box pox-neuro protein [Amyelois transitella]
XP_013409630	PREDICTED: paired box protein Pax-6-like isoform X1 [Lingula anatina]
XP_013409631	PREDICTED: paired box protein Pax-6-like isoform X2 [Lingula anatina]
XP_013409632	PREDICTED: paired box protein Pax-6-like isoform X3 [Lingula anatina]
XP_013409633	PREDICTED: paired box protein Pax-6-like isoform X4 [Lingula anatina]
XP_013409635	PREDICTED: paired box protein Pax-6-like isoform X6 [Lingula anatina]
XP_013417610	PREDICTED: homeobox protein unc-4 homolog [Lingula anatina]
XP_013771712	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013772276	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013772838	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013772864	PREDICTED: paired box protein Pax-5-like isoform X1 [Limulus polyphemus]
XP_013772865	PREDICTED: paired box protein Pax-5-like isoform X2 [Limulus polyphemus]
XP_013772867	PREDICTED: paired box protein Pax-5-like isoform X3 [Limulus polyphemus]
XP_013772868	PREDICTED: paired box protein Pax-5-like isoform X4 [Limulus polyphemus]
XP_013773208	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013774514	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013775460	PREDICTED: homeobox protein unc-4 homolog [Limulus polyphemus]
XP_013775534	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013776976	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013777226	PREDICTED: paired box pox-neuro protein-like [Limulus polyphemus]
XP_013777739	PREDICTED: retinal homeobox protein Rx1-like [Limulus polyphemus]
XP_013777740	PREDICTED: aristaless-related homeobox protein-like [Limulus polyphemus]
XP_013778470	PREDICTED: protein gooseberry-like [Limulus polyphemus]
XP_013778820	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013779707	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Limulus polyphemus]
XP_013779863	PREDICTED: paired box protein Pax-1-like, partial [Limulus polyphemus]
XP_013779981	PREDICTED: homeobox protein unc-4 homolog [Limulus polyphemus]
XP_013780133	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013780572	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013780740	PREDICTED: visual system homeobox 2-like [Limulus polyphemus]
XP_013781415	PREDICTED: homeobox protein aristaless-like [Limulus polyphemus]
XP_013781442	PREDICTED: paired box protein Pax-3-like [Limulus polyphemus]
XP_013782207	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013782258	PREDICTED: homeobox protein ARX-like [Limulus polyphemus]
XP_013786450	PREDICTED: homeobox protein ARX-like [Limulus polyphemus]
XP_013786772	PREDICTED: paired box protein Pax-5-like [Limulus polyphemus]
XP_013787478	PREDICTED: paired mesoderm homeobox protein 2B-like, partial [Limulus polyphemus]
XP_013789026	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013789393	PREDICTED: retinal homeobox protein Rx1-like [Limulus polyphemus]
XP_013789583	PREDICTED: visual system homeobox 2-like, partial [Limulus polyphemus]
XP_013790457	PREDICTED: homeobox protein Nkx-6.3-like [Limulus polyphemus]
XP_013792934	PREDICTED: paired box protein Pax-6-like isoform X1 [Limulus polyphemus]
XP_013792941	PREDICTED: paired box protein Pax-6-like isoform X2 [Limulus polyphemus]
XP_013793906	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013794441	PREDICTED: homeobox protein OTX2-like [Limulus polyphemus]
XP_013796335	PREDICTED: paired box protein Pax-9 [Apteryx australis mantelli]
XP_014111815	PREDICTED: paired mesoderm homeobox protein 2 isoform X1 [Pseudopodoces humilis]
XP_014111816	PREDICTED: paired mesoderm homeobox protein 2 isoform X2 [Pseudopodoces humilis]
XP_014124966	PREDICTED: paired mesoderm homeobox protein 2B [Zonotrichia albicollis]
XP_014209020	PREDICTED: aristaless-related homeobox protein-like [Copidosoma floridanum]
XP_014209699	PREDICTED: paired box protein Pax-6-like [Copidosoma floridanum]
XP_014221000	PREDICTED: retinal homeobox protein Rx-like [Trichogramma pretiosum]
XP_014221003	PREDICTED: homeobox protein aristaless-like 3 [Trichogramma pretiosum]
XP_014226736	PREDICTED: homeobox protein goosecoid-like [Trichogramma pretiosum]
XP_014229927	PREDICTED: paired box protein Pax-6-like isoform X1 [Trichogramma pretiosum]
XP_014229933	PREDICTED: paired box protein Pax-6-like isoform X2 [Trichogramma pretiosum]
XP_014229940	PREDICTED: paired box protein Pax-6-like isoform X3 [Trichogramma pretiosum]
XP_014229948	PREDICTED: paired box protein Pax-6-like isoform X4 [Trichogramma pretiosum]
XP_014229955	PREDICTED: paired box protein Pax-6-like isoform X5 [Trichogramma pretiosum]
XP_014244834	PREDICTED: paired box protein Pax-5 isoform X5 [Cimex lectularius]
XP_014247391	PREDICTED: homeobox protein goosecoid-like [Cimex lectularius]
XP_014251460	PREDICTED: paired mesoderm homeobox protein 2-like [Cimex lectularius]
XP_014253523	PREDICTED: paired mesoderm homeobox protein 2B-like [Cimex lectularius]

XP_014262476	PREDICTED: protein gooseberry-like [Cimex lectularius]
XP_014265872	PREDICTED: paired box protein Pax-7-like isoform X3 [Maylandia zebra]
XP_014276606	PREDICTED: paired box protein Pax-5 isoform X3 [Halyomorpha halys]
XP_014280336	PREDICTED: retina and anterior neural fold homeobox protein 2-like [Halyomorpha halys]
XP_014290681	PREDICTED: protein gooseberry-like isoform X1 [Halyomorpha halys]
XP_014290682	PREDICTED: protein gooseberry-like isoform X2 [Halyomorpha halys]
XP_014362535	PREDICTED: homeobox protein goosecoid-like [Papilio machaon]
XP_014362693	PREDICTED: homeobox protein aristaless isoform X2 [Papilio machaon]
XP_014362779	PREDICTED: homeobox protein aristaless-like [Papilio machaon]

9.4.2.28 *Pleiohomeotic*

Name	Description
A0JC51 (ZIC4_XENLA)	RecName: Full=Zinc finger protein ZIC 4; Short=XlZic4; AltName: Full=Zinc finger protein of the cerebellum 4
A0JNB1 (ZN227_BOVIN)	RecName: Full=Zinc finger protein 227
A0PJY2 (FEZF1_HUMAN)	RecName: Full=Fez family zinc finger protein 1; AltName: Full=Zinc finger protein 312B
A1YF12 (ZNF16_GORGO)	RecName: Full=Zinc finger protein 16
A1YG88 (ZNF16_PANPA)	RecName: Full=Zinc finger protein 16
A2CE44 (ZXDB_MOUSE)	RecName: Full=Zinc finger X-linked protein ZXDB
A2T759 (ZNF16_PANTR)	RecName: Full=Zinc finger protein 16
A2VDQ7 (ZN420_BOVIN)	RecName: Full=Zinc finger protein 420
A6NK53 (ZN233_HUMAN)	RecName: Full=Zinc finger protein 233
A6NNF4 (ZN726_HUMAN)	RecName: Full=Zinc finger protein 726
A6NP11 (ZN716_HUMAN)	RecName: Full=Zinc finger protein 716
A6QQW0 (ZN143_BOVIN)	RecName: Full=Zinc finger protein 143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor
A8MXY4 (ZNF99_HUMAN)	RecName: Full=Zinc finger protein 99
B4F7E9 (ZNF76_RAT)	RecName: Full=Zinc finger protein 76; AltName: Full=Zinc finger protein 523
Locus_1_Transcript_50614/166847_Confidence_1.000_Length_2228 - ORF 1 (frame 3) translation	Locus_1_Transcript_50614/166847_Confidence_1.000_Length_2228
Locus_1_Transcript_90722/166847_Confidence_1.000_Length_411 - ORF 1 (frame 3) translation	Locus_1_Transcript_90722/166847_Confidence_1.000_Length_411
Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831 - ORF 1 (frame 2) translation	Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831
Locus_1_Transcript_145109/166847_Confidence_1.000_Length_1353 - ORF 2 (frame 3) translation	Locus_1_Transcript_145109/166847_Confidence_1.000_Length_1353
Locus_286_Transcript_1/10_Confidence_0.336_Length_4002 - ORF 19 (frame 2) translation	Locus_286_Transcript_1/10_Confidence_0.336_Length_4002
Locus_2787_Transcript_1/2_Confidence_0.875_Length_4512 - ORF 22 (frame 1) translation	Locus_2787_Transcript_1/2_Confidence_0.875_Length_4512
Locus_5955_Transcript_7/11_Confidence_0.312_Length_3809 - ORF 12 (frame 2) translation	Locus_5955_Transcript_7/11_Confidence_0.312_Length_3809
Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349 - ORF 20 (frame 1) translation	Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349
Locus_7469_Transcript_19/25_Confidence_0.009_Length_428 - ORF 1 (frame 1) translation	Locus_7469_Transcript_19/25_Confidence_0.009_Length_428
Locus_10241_Transcript_6/12_Confidence_0.164_Length_1075 - ORF 8 (frame 2) translation	Locus_10241_Transcript_6/12_Confidence_0.164_Length_1075
Locus_10690_Transcript_2/10_Confidence_0.333_Length_2773 - ORF 2 (frame 3) translation	Locus_10690_Transcript_2/10_Confidence_0.333_Length_2773
Locus_11065_Transcript_3/11_Confidence_0.172_Length_2306 - ORF 16 (frame 2) translation	Locus_11065_Transcript_3/11_Confidence_0.172_Length_2306
Locus_11110_Transcript_1/2_Confidence_0.600_Length_3025 - ORF 4 (frame 1) translation	Locus_11110_Transcript_1/2_Confidence_0.600_Length_3025
Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958 - ORF 2 (frame 2) translation	Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958
Locus_15882_Transcript_2/10_Confidence_0.346_Length_4377 - ORF 15 (frame 3) translation	Locus_15882_Transcript_2/10_Confidence_0.346_Length_4377
Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420 - ORF 2 (frame 2) translation	Locus_16964_Transcript_1/1_Confidence_1.000_Length_6420
Locus_17002_Transcript_1/10_Confidence_0.314_Length_1344 - ORF 1 (frame 1) translation	Locus_17002_Transcript_1/10_Confidence_0.314_Length_1344
Locus_17552_Transcript_1/1_Confidence_1.000_Length_1849 - ORF 1 (frame 2) translation	Locus_17552_Transcript_1/1_Confidence_1.000_Length_1849
Locus_18640_Transcript_1/5_Confidence_0.250_Length_3182 - ORF 7 (frame 1) translation	Locus_18640_Transcript_1/5_Confidence_0.250_Length_3182
Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582 - ORF 4 (frame 3) translation	Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582
O15391 (TYY2_HUMAN)	RecName: Full=Transcription factor YY2; AltName: Full=Yin and yang 2; Short=YY-2; AltName: Full=Zinc finger protein 631
O60481 (ZIC3_HUMAN)	RecName: Full=Zinc finger protein ZIC 3; AltName: Full=Zinc finger protein 203; AltName: Full=Zinc finger protein of the cerebellum 3
O70230 (ZN143_MOUSE)	RecName: Full=Zinc finger protein 143; Short=Zfp-143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor; Short=mStaf
O73689 (ZIC1_XENLA)	RecName: Full=Zinc finger protein ZIC 1; Short=XZic1; Short=XlZic1; AltName: Full=ODD-paired-like; Short=Xopl; AltName: Full=ZIC-related protein 1; Short=ZIC-r1; AltName: Full=Zinc finger protein of the cerebellum 1
O75626 (PRDM1_HUMAN)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=BLIMP-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1;

	AltName: Full=Positive regulatory domain I-binding factor 1; Short=PRDI-BF1; Short=PRDI-binding factor 1
O95409 (ZIC2_HUMAN)	RecName: Full=Zinc finger protein ZIC 2; AltName: Full=Zinc finger protein of the cerebellum 2
P0C6P6 (TYY2_RAT)	RecName: Full=Transcription factor YY2; AltName: Full=Yin and yang 2; Short=YY-2
P0C6Y7 (PRDM9_RAT)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
P08043 (ZFP2_MOUSE)	RecName: Full=Zinc finger protein 2; Short=Zfp-2; AltName: Full=Protein mKR2
P08045 (XFIN_XENLA)	RecName: Full=Zinc finger protein Xfin; AltName: Full=Xenopus fingers protein; Short=Xfin
P15620 (ZN271_MOUSE)	RecName: Full=Zinc finger protein 271; AltName: Full=Zinc finger protein 35; Short=Zfp-35
P15622 (ZN250_HUMAN)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
P17020 (ZNF16_HUMAN)	RecName: Full=Zinc finger protein 16; AltName: Full=Zinc finger protein KOX9
P17035 (ZNF28_HUMAN)	RecName: Full=Zinc finger protein 28; AltName: Full=Zinc finger protein KOX24
P17041 (ZNF32_HUMAN)	RecName: Full=Zinc finger protein 32; AltName: Full=C2H2-546; AltName: Full=Zinc finger protein KOX30
P18724 (ZG49_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF49.1
P18725 (ZG5_XENLA)	RecName: Full=Gastrula zinc finger protein 5-1; AltName: Full=XlCGF5.1
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P18731 (ZG62_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF62.1
P18735 (ZG7_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF7.1
P18737 (ZG8_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF8.2DB
P18744 (ZO20_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF20
P18750 (ZO61_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF6.1
P18753 (ZO84_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF8.4
P22227 (ZFP42_MOUSE)	RecName: Full=Zinc finger protein 42; Short=Zfp-42; AltName: Full=Reduced expression protein 1; Short=REX-1; Short=mREX-1
P24399 (ZN239_MOUSE)	RecName: Full=Zinc finger protein 239; Short=Zfp-239; AltName: Full=Zinc finger protein MOK-2
P25490 (TYY1_HUMAN)	RecName: Full=Transcriptional repressor protein YY1; AltName: Full=Delta transcription factor; AltName: Full=INO80 complex subunit S; AltName: Full=NF-E1; AltName: Full=Yin and yang 1; Short=YY-1
P36508 (ZNF76_HUMAN)	RecName: Full=Zinc finger protein 76; AltName: Full=Zinc finger protein 523
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
P51786 (ZN157_HUMAN)	RecName: Full=Zinc finger protein 157; AltName: Full=Zinc finger protein HZF22
P52747 (ZN143_HUMAN)	RecName: Full=Zinc finger protein 143; AltName: Full=SPH-binding factor; AltName: Full=Selenocysteine tRNA gene transcription-activating factor; Short=hStaf
P98168 (ZXDA_HUMAN)	RecName: Full=Zinc finger X-linked protein ZXDA
P98169 (ZXDB_HUMAN)	RecName: Full=Zinc finger X-linked protein ZXDB
PHO_DROME	RecName: Full=Polycomb protein PHO; AltName: Full=Protein pleiohomeotic; AltName: Full=Transcription factor YY1 homolog
Q0P4W9 (FEZF1_XENTR)	RecName: Full=Fez family zinc finger protein 1
Q0VDQ9 (FEZF1_MOUSE)	RecName: Full=Fez family zinc finger protein 1
Q1LYE3 (ZN143_DANRE)	RecName: Full=Zinc finger protein 143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor
Q2FAY8 (TYY2_RATRT)	RecName: Full=Transcription factor YY2; AltName: Full=Yin and yang 2; Short=YY-2
Q2QGD7 (ZXDC_HUMAN)	RecName: Full=Zinc finger protein ZXDC; AltName: Full=ZXD-like zinc finger protein
Q2TAR3 (FEZF2_XENLA)	RecName: Full=Fez family zinc finger protein 2
Q2V3L3 (Y4634_ARATH)	RecName: Full=Uncharacterized zinc finger protein At4g06634
Q2VWH6 (FEZF2_BOVIN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q3B7N9 (MYNN_BOVIN)	RecName: Full=Myoneurin
Q3TTC2 (TYY2_MOUSE)	RecName: Full=Transcription factor YY2; AltName: Full=Yin and yang 2; Short=YY-2
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4R6C2 (ZN383_MACFA)	RecName: Full=Zinc finger protein 383
Q5MCW4 (ZN569_HUMAN)	RecName: Full=Zinc finger protein 569
Q5R5N5 (MYNN_PONAB)	RecName: Full=Myoneurin
Q5R5U3 (ZN271_PONAB)	RecName: Full=Zinc finger protein 271
Q5R8X1 (ZN665_PONAB)	RecName: Full=Zinc finger protein 665
Q5RB30 (Z585B_PONAB)	RecName: Full=Zinc finger protein 585B
Q5RFP4 (OZF_PONAB)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q5XIU2 (ZN143_RAT)	RecName: Full=Zinc finger protein 143; Short=Zfp-143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor
Q6A085 (ZN629_MOUSE)	RecName: Full=Zinc finger protein 629
Q6DJQ6 (ZIC3_XENTR)	RecName: Full=Zinc finger protein ZIC 3; AltName: Full=Zinc finger protein of the cerebellum 3
Q6P1L6 (ZN343_HUMAN)	RecName: Full=Zinc finger protein 343
Q6P9A1 (ZN530_HUMAN)	RecName: Full=Zinc finger protein 530
Q6P560 (ZN182_MOUSE)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q6PF04 (ZN613_HUMAN)	RecName: Full=Zinc finger protein 613
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q6ZN57 (ZFP2_HUMAN)	RecName: Full=Zinc finger protein 2 homolog; Short=Zfp-2; AltName: Full=Zinc finger protein 751

Q7L3S4 (ZN771_HUMAN)	RecName: Full=Zinc finger protein 771; AltName: Full=Mesenchymal stem cell protein DSC43
Q7TNU6 (ZN250_MOUSE)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
Q7TQ40 (ZIC5_MOUSE)	RecName: Full=Zinc finger protein ZIC 5; AltName: Full=Zinc finger protein of the cerebellum 5
Q8BJ90 (ZN771_MOUSE)	RecName: Full=Zinc finger protein 771
Q8BMU0 (ZNF76_MOUSE)	RecName: Full=Zinc finger protein 76; AltName: Full=Zinc finger protein 523
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q8C8V1 (ZXDC_MOUSE)	RecName: Full=Zinc finger protein ZXDC
Q08DG8 (ZN135_BOVIN)	RecName: Full=Zinc finger protein 135
Q8IZ20 (ZN683_HUMAN)	RecName: Full=Zinc finger protein 683
Q8JJC0 (ZIC1_CHICK)	RecName: Full=Zinc finger protein ZIC 1; AltName: Full=Zinc finger protein of the cerebellum 1
Q8ST83 (PHO_DROME)	RecName: Full=Polycomb protein PHO; AltName: Full=Protein pleiohomeotic; AltName: Full=Transcription factor YY1 homolog
Q8TAQ5 (ZN420_HUMAN)	RecName: Full=Zinc finger protein 420
Q8TBJ5 (FEZF2_HUMAN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q8TBZ5 (ZN502_HUMAN)	RecName: Full=Zinc finger protein 502
Q8TC21 (ZN596_HUMAN)	RecName: Full=Zinc finger protein 596
Q8TF45 (ZN418_HUMAN)	RecName: Full=Zinc finger protein 418
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q9ESP5 (FEZF2_MOUSE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q9H7R5 (ZN665_HUMAN)	RecName: Full=Zinc finger protein 665; AltName: Full=Zinc finger protein 160-like
Q9IB89 (ZIC5_XENLA)	RecName: Full=Zinc finger protein ZIC 5; Short=XZic5; Short=XlZic5; AltName: Full=Zinc finger protein of the cerebellum 5
Q9NQV7 (PRDM9_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q9UEG4 (ZN629_HUMAN)	RecName: Full=Zinc finger protein 629; AltName: Full=Zinc finger protein 65
Q9UJU3 (ZN112_HUMAN)	RecName: Full=Zinc finger protein 112; Short=Zfp-112; AltName: Full=Zinc finger protein 228
Q9UL59 (ZN214_HUMAN)	RecName: Full=Zinc finger protein 214; AltName: Full=BWSCR2-associated zinc finger protein 1; Short=BAZ-1
Q9Y2H8 (ZN510_HUMAN)	RecName: Full=Zinc finger protein 510
Q9Y473 (ZN175_HUMAN)	RecName: Full=Zinc finger protein 175; AltName: Full=Zinc finger protein OTK18
Q9YIB7 (ZIC2B_XENLA)	RecName: Full=Zinc finger protein ZIC 2-B; AltName: Full=Zic-related-2; Short=ZIC-R2; AltName: Full=Zinc finger protein of the cerebellum 2-B
Q25C93 (FEZF1_DANRE)	RecName: Full=Fez family zinc finger protein 1
Q28G88 (FEZF2_XENTR)	RecName: Full=Fez family zinc finger protein 2
Q52M93 (Z585B_HUMAN)	RecName: Full=Zinc finger protein 585B; AltName: Full=zinc finger protein 41-like protein
Q58DZ6 (ZN143_XENTR)	RecName: Full=Zinc finger protein 143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor
Q80V23 (ZNF32_MOUSE)	RecName: Full=Zinc finger protein 32; AltName: Full=Zinc finger protein 637
Q80W31 (ZN569_MOUSE)	RecName: Full=Zinc finger protein 569; AltName: Full=Mszf21; AltName: Full=Zinc finger protein 74; Short=Zfp-74
Q86WZ6 (ZN227_HUMAN)	RecName: Full=Zinc finger protein 227
Q96EQ9 (PRDM9_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=Hybrid sterility protein 1; AltName: Full=Meiosis-induced factor containing a PR/SET domain and zinc-finger motif; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q96H40 (ZN486_HUMAN)	RecName: Full=Zinc finger protein 486; AltName: Full=KRAB domain only protein 2
Q96IR2 (ZN845_HUMAN)	RecName: Full=Zinc finger protein 845
Q96JL9 (ZN333_HUMAN)	RecName: Full=Zinc finger protein 333
Q96MM3 (ZFP42_HUMAN)	RecName: Full=Zinc finger protein 42 homolog; Short=Zfp-42; AltName: Full=Reduced expression protein 1; Short=REX-1; Short=hREX-1; AltName: Full=Zinc finger protein 754
Q96N38 (ZN714_HUMAN)	RecName: Full=Zinc finger protein 714
Q96ND8 (ZN583_HUMAN)	RecName: Full=Zinc finger protein 583; AltName: Full=Zinc finger protein L3-5
Q96NG8 (ZN582_HUMAN)	RecName: Full=Zinc finger protein 582
Q96PE6 (ZIM3_HUMAN)	RecName: Full=Zinc finger imprinted 3; AltName: Full=Zinc finger protein 657
Q96SE7 (ZN347_HUMAN)	RecName: Full=Zinc finger protein 347; AltName: Full=Zinc finger protein 1111
Q147U1 (ZN846_HUMAN)	RecName: Full=Zinc finger protein 846
Q804Q5 (FEZF2_DANRE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Foreheadin protein; AltName: Full=Zinc finger protein Fez-like
Q00899 (TYY1_MOUSE)	RecName: Full=Transcriptional repressor protein YY1; AltName: Full=Delta transcription factor; AltName: Full=NF-E1; AltName: Full=UCR-motif DNA-binding protein; AltName: Full=Yin and yang 1; Short=YY-1
Q06730 (ZN33A_HUMAN)	RecName: Full=Zinc finger protein 33A; AltName: Full=Zinc finger and ZAK-associated protein with KRAB domain; Short=ZZaPK; AltName: Full=Zinc finger protein 11A; AltName: Full=Zinc finger protein KOX31

Q06732 (ZN33B_HUMAN)	RecName: Full=Zinc finger protein 33B; AltName: Full=Zinc finger protein 11B; AltName: Full=Zinc finger protein KOX2
Q07230 (ZSCA2_MOUSE)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29; Short=Zfp-29
Q07243 (MTF1_MOUSE)	RecName: Full=Metal regulatory transcription factor 1; AltName: Full=MRE-binding transcription factor; AltName: Full=Transcription factor MTF-1
Q12901 (ZN155_HUMAN)	RecName: Full=Zinc finger protein 155
Q14584 (ZN266_HUMAN)	RecName: Full=Zinc finger protein 266; AltName: Full=Zinc finger protein HZF1
Q14588 (ZN234_HUMAN)	RecName: Full=Zinc finger protein 234; AltName: Full=Zinc finger protein 269; AltName: Full=Zinc finger protein HZF4
Q14590 (ZN235_HUMAN)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 270; AltName: Full=Zinc finger protein 93 homolog; Short=Zfp-93; AltName: Full=Zinc finger protein HZF6
Q14591 (ZN271_HUMAN)	RecName: Full=Zinc finger protein 271; AltName: Full=CT-ZFP48; AltName: Full=Epstein-Barr virus-induced zinc finger protein; Short=EBV-induced zinc finger protein; Short=ZNF-EB; AltName: Full=Zinc finger protein HZF7; AltName: Full=Zinc finger protein ZNFphex133; AltName: Full=Zinc finger protein dp; Short=ZNF-dp
Q14872 (MTF1_HUMAN)	RecName: Full=Metal regulatory transcription factor 1; AltName: Full=MRE-binding transcription factor; AltName: Full=Transcription factor MTF-1
Q15915 (ZIC1_HUMAN)	RecName: Full=Zinc finger protein ZIC 1; AltName: Full=Zinc finger protein 201; AltName: Full=Zinc finger protein of the cerebellum 1
Q60636 (PRDM1_MOUSE)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=B lymphocyte-induced maturation protein 1; Short=Blimp-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1
Q61116 (ZN235_MOUSE)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 93; Short=Zfp-93
Q61467 (ZIC4_MOUSE)	RecName: Full=Zinc finger protein ZIC 4; AltName: Full=Zinc finger protein of the cerebellum 4
Q62520 (ZIC2_MOUSE)	RecName: Full=Zinc finger protein ZIC 2; AltName: Full=Zinc finger protein of the cerebellum 2
Q91689 (ZIC2A_XENLA)	RecName: Full=Zinc finger protein ZIC 2-A; AltName: Full=Zinc finger DNA-binding protein fZic; AltName: Full=Zinc finger protein ZIC 2; Short=XlZic2; Short=xZic2; AltName: Full=Zinc finger protein of the cerebellum 2-A
Q91853 (ZN143_XENLA)	RecName: Full=Zinc finger protein 143; AltName: Full=Selenocysteine tRNA gene transcription-activating factor
Q93560 (BLMP1_CAEEL)	RecName: Full=B lymphocyte-induced maturation protein 1 homolog
TYY1_MOUSE	RecName: Full=Transcriptional repressor protein YY1; AltName: Full=Delta transcription factor; AltName: Full=NF-E1; AltName: Full=UCR-motif DNA-binding protein; AltName: Full=Yin and yang 1; Short=YY-1
TYY2_MOUSE	RecName: Full=Transcription factor YY2; AltName: Full=Yin and yang 2; Short=YY-2

9.4.2.29 *Polycomb*

Name	**Description**
G3V8T1 (MPP8_RAT)	RecName: Full=M-phase phosphoprotein 8
Locus_1_Transcript_147282/166847_Confidence_1.000_Length_2450 - ORF 1 (frame 3) translation	Locus_1_Transcript_147282/166847_Confidence_1.000_Length_2450
Locus_2368_Transcript_19/22_Confidence_0.099_Length_1836 - ORF 9 (frame 3) translation	Locus_2368_Transcript_19/22_Confidence_0.099_Length_1836
Locus_9063_Transcript_5/10_Confidence_0.357_Length_8389 - ORF 2 (frame 1) translation	Locus_9063_Transcript_5/10_Confidence_0.357_Length_8389
NP_001071078	zinc finger protein 76 [Danio rerio]
NP_001156383	zinc finger protein 934 isoform 1 [Mus musculus]
NP_001158430	Zic family member 1 (odd-paired homolog, Drosophila) [Saccoglossus kowalevskii]
NP_001171016	zinc finger protein 600 [Mus musculus]
NP_001171238	reduced expression 2 [Mus musculus]
O00257 (CBX4_HUMAN)	RecName: Full=E3 SUMO-protein ligase CBX4; AltName: Full=Chromobox protein homolog 4; AltName: Full=Polycomb 2 homolog; Short=Pc2; Short=hPc2
O54864 (SUV91_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Histone H3-K9 methyltransferase 1; Short=H3-K9-HMTase 1; AltName: Full=Position-effect variegation 3-9 homolog; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
O55187 (CBX4_MOUSE)	RecName: Full=E3 SUMO-protein ligase CBX4; AltName: Full=Chromobox protein homolog 4; AltName: Full=Polycomb 2 homolog; Short=Pc2; Short=mPc2
O95503 (CBX6_HUMAN)	RecName: Full=Chromobox protein homolog 6
O95931 (CBX7_HUMAN)	RecName: Full=Chromobox protein homolog 7
P05205 (HP1_DROME)	RecName: Full=Heterochromatin protein 1; Short=HP1; AltName: Full=Non-histone chromosomal protein C1A9 antigen
P23198 (CBX3_MOUSE)	RecName: Full=Chromobox protein homolog 3; AltName: Full=Heterochromatin protein 1 homolog gamma; Short=HP1 gamma; AltName: Full=M32; AltName: Full=Modifier 2 protein
P29227 (HP1_DROVI)	RecName: Full=Heterochromatin protein 1; Short=HP1
P30658 (CBX2_MOUSE)	RecName: Full=Chromobox protein homolog 2; AltName: Full=M33; AltName: Full=Modifier 3 protein
P60889 (CBX7_RAT)	RecName: Full=Chromobox protein homolog 7
P83916 (CBX1_HUMAN)	RecName: Full=Chromobox protein homolog 1; AltName: Full=HP1Hsbeta; AltName: Full=Heterochromatin protein 1 homolog beta; Short=HP1 beta; AltName: Full=Heterochromatin protein p25;

	AltName: Full=M31; AltName: Full=Modifier 1 protein; AltName: Full=p25beta
PC_DROME	RecName: Full=Polycomb group protein Pc; Short=Protein polycomb
Q3TYA6 (MPP8_MOUSE)	RecName: Full=M-phase phosphoprotein 8
Q8N8U2 (CDYL2_HUMAN)	RecName: Full=Chromodomain Y-like protein 2; Short=CDY-like 2
Q8VDS3 (CBX7_MOUSE)	RecName: Full=Chromobox protein homolog 7
Q9D2X0 (ANR39_MOUSE)	RecName: Full=Ankyrin repeat domain-containing protein 39
Q9D5D8 (CDYL2_MOUSE)	RecName: Full=Chromodomain Y-like protein 2; Short=CDY-like 2
Q9DBY5 (CBX6_MOUSE)	RecName: Full=Chromobox protein homolog 6
Q9HC52 (CBX8_HUMAN)	RecName: Full=Chromobox protein homolog 8; AltName: Full=Polycomb 3 homolog; Short=Pc3; Short=hPc3; AltName: Full=Rectachrome 1
Q9QXV1 (CBX8_MOUSE)	RecName: Full=Chromobox protein homolog 8; AltName: Full=Polycomb 3 homolog; Short=Pc3; Short=mPc3
Q53RE8 (ANR39_HUMAN)	RecName: Full=Ankyrin repeat domain-containing protein 39
Q96Q27 (ASB2_HUMAN)	RecName: Full=Ankyrin repeat and SOCS box protein 2; Short=ASB-2
Q339W7 (LHP1_ORYSJ)	RecName: Full=Probable chromo domain-containing protein LHP1; AltName: Full=Protein LIKE HETEROCHROMATIN PROTEIN 1
Q944N1 (LHP1_SOLLC)	RecName: Full=Chromo domain protein LHP1; AltName: Full=Protein LIKE HETEROCHROMATIN PROTEIN 1; AltName: Full=Sl LHP1
Q14781 (CBX2_HUMAN)	RecName: Full=Chromobox protein homolog 2
Q99549 (MPP8_HUMAN)	RecName: Full=M-phase phosphoprotein 8; AltName: Full=Two hybrid-associated protein 3 with RanBPM; Short=Twa3
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_002401338	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_002427222	zinc finger protein ZIC, putative [Pediculus humanus corporis]
XP_002593131	zic family member [Branchiostoma floridae]
XP_003248963	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_003249678	PREDICTED: fez family zinc finger protein 1-like [Apis mellifera]
XP_003250596	PREDICTED: transcriptional repressor protein YY1-like isoform 1 [Apis mellifera]
XP_003398307	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus terrestris]
XP_003492727	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus impatiens]
XP_003494856	PREDICTED: fez family zinc finger protein 2-like [Bombus impatiens]
XP_003698235	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Apis florea]
XP_003704924	PREDICTED: transcriptional repressor protein YY1-like isoform X4 [Megachile rotundata]
XP_003738192	PREDICTED: PR domain zinc finger protein 1-like [Metaseiulus occidentalis]
XP_003743411	PREDICTED: zinc finger protein 510-like [Metaseiulus occidentalis]
XP_003744232	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Metaseiulus occidentalis]
XP_004919623	PREDICTED: gastrula zinc finger protein xLCGF3.1-like [Xenopus (Silurana) tropicalis]
XP_004922194	PREDICTED: zinc finger protein 583-like [Bombyx mori]
XP_004933782	PREDICTED: myoneurin-like [Bombyx mori]
XP_004934072	PREDICTED: zinc finger protein 583-like, partial [Bombyx mori]
XP_005106657	PREDICTED: zinc finger protein 76-like [Aplysia californica]
XP_005164989	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Danio rerio]
XP_005168216	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168249	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005632973	PREDICTED: zinc finger protein 846 isoform X4 [Canis lupus familiaris]
XP_005697039	PREDICTED: zinc finger protein 397 isoform X1 [Capra hircus]
XP_005817136	PREDICTED: zinc finger protein OZF-like, partial [Xiphophorus maculatus]
XP_005938654	PREDICTED: zinc finger protein ZXDC-like [Haplochromis burtoni]
XP_005977203	PREDICTED: zinc finger protein 271-like isoform X1 [Pantholops hodgsonii]
XP_005977204	PREDICTED: zinc finger protein 271-like isoform X2 [Pantholops hodgsonii]
XP_006153235	PREDICTED: zinc finger protein 596 isoform X3 [Tupaia chinensis]
XP_006263331	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Alligator mississippiensis]
XP_006278661	PREDICTED: zinc finger protein ZIC 4 [Alligator mississippiensis]
XP_006609630	PREDICTED: fez family zinc finger protein 1-like, partial [Apis dorsata]
XP_006624032	PREDICTED: zinc finger protein 845-like [Apis dorsata]
XP_006631444	PREDICTED: metal regulatory transcription factor 1-like [Lepisosteus oculatus]
XP_006897457	PREDICTED: zinc finger protein 432-like [Elephantulus edwardii]
XP_006980113	PREDICTED: metal regulatory transcription factor 1 [Peromyscus maniculatus bairdii]
XP_007435806	PREDICTED: metal regulatory transcription factor 1 isoform X1 [Python bivittatus]
XP_007435807	PREDICTED: metal regulatory transcription factor 1 isoform X2 [Python bivittatus]
XP_007455301	PREDICTED: zinc finger protein 271-like [Lipotes vexillifer]
XP_007490656	PREDICTED: zinc finger protein 624-like isoform X2 [Monodelphis domestica]
XP_007540545	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007885771	PREDICTED: zinc finger protein 143 [Callorhinchus milii]
XP_007955518	PREDICTED: zinc finger protein 383-like [Orycteropus afer afer]
XP_008179259	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180597	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180598	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]

XP_008180907	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183216	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187394	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008194427	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Tribolium castaneum]
XP_008259420	PREDICTED: zinc finger protein 271-like [Oryctolagus cuniculus]
XP_008294362	PREDICTED: zinc finger protein OZF-like, partial [Stegastes partitus]
XP_008298792	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Stegastes partitus]
XP_008319230	PREDICTED: zinc finger protein ZXDC-like [Cynoglossus semilaevis]
XP_008400230	PREDICTED: zinc finger protein OZF-like [Poecilia reticulata]
XP_008429346	PREDICTED: metal regulatory transcription factor 1 [Poecilia reticulata]
XP_008435770	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Poecilia reticulata]
XP_008543891	PREDICTED: PR domain zinc finger protein 1 [Microplitis demolitor]
XP_008554849	PREDICTED: transcriptional repressor protein YY1 isoform X2 [Microplitis demolitor]
XP_008592932	PREDICTED: zinc finger X-linked protein ZXDB [Galeopterus variegatus]
XP_008708216	PREDICTED: zinc finger X-linked protein ZXDB-like, partial [Ursus maritimus]
XP_008822303	PREDICTED: zinc finger protein 157 [Nannospalax galili]
XP_009294034	PREDICTED: zinc finger protein 76 isoform X2 [Danio rerio]
XP_009297399	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Danio rerio]
XP_009298137	PREDICTED: gastrula zinc finger protein XlCGF8.2DB isoform X2 [Danio rerio]
XP_009298796	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Danio rerio]
XP_009298804	PREDICTED: oocyte zinc finger protein XlCOF20-like [Danio rerio]
XP_009298817	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298922	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009299144	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_010622459	PREDICTED: zinc finger X-linked protein ZXDB, partial [Fukomys damarensis]
XP_010788499	PREDICTED: zinc finger protein 253-like, partial [Notothenia coriiceps]
XP_010823838	PREDICTED: zinc finger protein 271 [Bos taurus]
XP_011068350	PREDICTED: transcriptional repressor protein YY1-like isoform X1 [Acromyrmex echinatior]
XP_011068351	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Acromyrmex echinatior]
XP_011171942	PREDICTED: transcriptional repressor protein YY1-like isoform X1 [Solenopsis invicta]
XP_011171943	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Solenopsis invicta]
XP_011225968	PREDICTED: zinc finger protein 846 isoform X1 [Ailuropoda melanoleuca]
XP_011225973	PREDICTED: zinc finger protein 846 isoform X4 [Ailuropoda melanoleuca]
XP_011299253	PREDICTED: fez family zinc finger protein 2-like [Fopius arisanus]
XP_011333980	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Cerapachys biroi]
XP_011385408	PREDICTED: zinc finger X-linked protein ZXDB, partial [Pteropus vampyrus]
XP_011450026	PREDICTED: zinc finger protein 76-like [Crassostrea gigas]
XP_011618951	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619519	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619649	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011699668	PREDICTED: transcriptional repressor protein YY1-like isoform X1 [Wasmannia auropunctata]
XP_011699669	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Wasmannia auropunctata]
XP_011869737	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Vollenhovia emeryi]
XP_011875591	PREDICTED: PR domain zinc finger protein 1 [Vollenhovia emeryi]
XP_011877253	PREDICTED: fez family zinc finger protein 2-like isoform X1 [Vollenhovia emeryi]
XP_011877254	PREDICTED: fez family zinc finger protein 2-like isoform X2 [Vollenhovia emeryi]
XP_012009732	PREDICTED: zinc finger protein 271 [Ovis aries musimon]
XP_012144362	PREDICTED: transcriptional repressor protein YY1-like isoform X3 [Megachile rotundata]
XP_012168013	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus terrestris]
XP_012246007	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus impatiens]
XP_012250907	PREDICTED: PR domain zinc finger protein 1 [Athalia rosae]
XP_012278412	PREDICTED: fez family zinc finger protein 2-like [Orussus abietinus]
XP_012412262	PREDICTED: zinc finger protein 397-like isoform X3 [Trichechus manatus latirostris]
XP_012413260	PREDICTED: zinc finger protein 699-like [Trichechus manatus latirostris]
XP_012414413	PREDICTED: zinc finger protein 846-like [Trichechus manatus latirostris]
XP_012673637	PREDICTED: zinc finger protein 98-like, partial [Clupea harengus]
XP_012676460	PREDICTED: zinc finger protein OZF-like [Clupea harengus]
XP_012676918	PREDICTED: zinc finger protein 726-like [Clupea harengus]
XP_012686594	PREDICTED: zinc finger protein OZF-like [Clupea harengus]
XP_012687791	PREDICTED: zinc finger protein 678-like [Clupea harengus]

XP_012692788	PREDICTED: zinc finger protein 43-like [Clupea harengus]
XP_012710330	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012713484	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Fundulus heteroclitus]
XP_012713624	PREDICTED: gastrula zinc finger protein XlCGF49.1-like, partial [Fundulus heteroclitus]
XP_013196746	PREDICTED: zinc finger protein 182-like, partial [Amyelois transitella]
XP_013197323	PREDICTED: zinc finger protein 84-like [Amyelois transitella]
XP_013197977	PREDICTED: zinc finger protein 782-like, partial [Amyelois transitella]
XP_013392643	PREDICTED: zinc finger protein 76-like isoform X1 [Lingula anatina]
XP_013392644	PREDICTED: zinc finger protein 76-like isoform X2 [Lingula anatina]
XP_013392645	PREDICTED: zinc finger protein 76-like isoform X3 [Lingula anatina]
XP_013396692	PREDICTED: zinc finger protein ZXDC-like [Lingula anatina]
XP_013403275	PREDICTED: metal regulatory transcription factor 1-like isoform X1 [Lingula anatina]
XP_013419074	PREDICTED: zinc finger protein ZIC 4-like [Lingula anatina]
XP_013773341	PREDICTED: serine-rich adhesin for platelets-like [Limulus polyphemus]
XP_013774090	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013777873	PREDICTED: zinc finger protein 76-like isoform X1 [Limulus polyphemus]
XP_013777896	PREDICTED: zinc finger protein 76-like isoform X2 [Limulus polyphemus]
XP_013778343	PREDICTED: zinc finger protein 628-like [Limulus polyphemus]
XP_013778461	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013779401	PREDICTED: zinc finger protein 236-like [Limulus polyphemus]
XP_013780586	PREDICTED: transcriptional repressor protein YY1-like isoform X1 [Limulus polyphemus]
XP_013780587	PREDICTED: transcriptional repressor protein YY1-like isoform X2 [Limulus polyphemus]
XP_013781553	PREDICTED: zinc finger protein 557-like [Limulus polyphemus]
XP_013781817	PREDICTED: PR domain zinc finger protein 1-like [Limulus polyphemus]
XP_013783159	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013783185	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013784131	PREDICTED: zinc finger protein 235-like [Limulus polyphemus]
XP_013784714	PREDICTED: gastrula zinc finger protein xFG20-1-like [Limulus polyphemus]
XP_013787083	PREDICTED: zinc finger protein 85-like [Limulus polyphemus]
XP_013788396	PREDICTED: zinc finger protein Gfi-1b-like [Limulus polyphemus]
XP_013788495	PREDICTED: zinc finger protein squeeze-like [Limulus polyphemus]
XP_013791186	PREDICTED: zinc finger protein 628-like [Limulus polyphemus]
XP_013792192	PREDICTED: gastrula zinc finger protein XlCGF17.1-like [Limulus polyphemus]
XP_013792221	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013792883	PREDICTED: metal regulatory transcription factor 1-like [Limulus polyphemus]
XP_013793991	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013794434	PREDICTED: zinc finger protein ZIC 4-like [Limulus polyphemus]
XP_013881864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013884881	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_013923823	PREDICTED: metal regulatory transcription factor 1 isoform X1 [Thamnophis sirtalis]
XP_013923824	PREDICTED: metal regulatory transcription factor 1 isoform X2 [Thamnophis sirtalis]
XP_013978933	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Salmo salar]
XP_013978941	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Salmo salar]
XP_014186906	PREDICTED: zinc finger protein 239-like, partial [Haplochromis burtoni]
XP_014243420	PREDICTED: transcriptional repressor protein YY1-like [Cimex lectularius]
XP_014279248	PREDICTED: transcriptional repressor protein YY1-like [Halyomorpha halys]
XP_014382878	PREDICTED: oocyte zinc finger protein XlCOF6-like [Alligator sinensis]
XP_014457013	PREDICTED: zinc finger protein 708-like, partial [Alligator mississippiensis]
XP_014459563	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Alligator mississippiensis]
XP_014460726	PREDICTED: zinc finger protein 883-like [Alligator mississippiensis]

9.4.2.30 *Polyhomeotic proximal*

Name	**Description**
A2A5N8 (LMBL1_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog
B1B1A0 (LMBL4_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 4; Short=L(3)mbt-like protein 4
D3ZWK4 (LMBL1_RAT)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog

E1C2V1 (LMBL1_CHICK)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog
Locus_80_Transcript_1/10_Confidence_0.705_Length_5587 - ORF 23 (frame 3) translation	Locus_80_Transcript_1/10_Confidence_0.705_Length_5587
Locus_9806_Transcript_6/6_Confidence_0.706_Length_7758 - ORF 1 (frame 2) translation	Locus_9806_Transcript_6/6_Confidence_0.706_Length_7758
Locus_11157_Transcript_1/9_Confidence_0.342_Length_2186 - ORF 2 (frame 3) translation	Locus_11157_Transcript_1/9_Confidence_0.342_Length_2186
Locus_15856_Transcript_1/8_Confidence_0.656_Length_6052 - ORF 10 (frame 1) translation	Locus_15856_Transcript_1/8_Confidence_0.656_Length_6052
Locus_16152_Transcript_1/6_Confidence_0.562_Length_4668 - ORF 13 (frame 3) translation	Locus_16152_Transcript_1/6_Confidence_0.562_Length_4668
Locus_17041_Transcript_1/10_Confidence_0.167_Length_3470 - ORF 20 (frame 1) translation	Locus_17041_Transcript_1/10_Confidence_0.167_Length_3470
P39769 (PHP_DROME)	RecName: Full=Polyhomeotic-proximal chromatin protein
P78364 (PHC1_HUMAN)	RecName: Full=Polyhomeotic-like protein 1; Short=hPH1; AltName: Full=Early development regulatory protein 1
PHP_DROME	RecName: Full=Polyhomeotic-proximal chromatin protein
Q1JQD9 (LMBL2_BOVIN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=L(3)mbt-like protein 2
Q1RNF8 (SAM11_MOUSE)	RecName: Full=Sterile alpha motif domain-containing protein 11; Short=SAM domain-containing protein 11; AltName: Full=Major retinal SAM domain-containing protein; Short=Mr-s
Q4V7W5 (PHC2_XENLA)	RecName: Full=Polyhomeotic-like protein 2
Q7Z3H4 (SAMD7_HUMAN)	RecName: Full=Sterile alpha motif domain-containing protein 7; Short=SAM domain-containing protein 7
Q8BLB7 (LMBL3_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 3; Short=L(3)mbt-like protein 3; AltName: Full=MBT-1
Q8C8Y5 (SAMD7_MOUSE)	RecName: Full=Sterile alpha motif domain-containing protein 7; Short=SAM domain-containing protein 7
Q8CHP6 (PHC3_MOUSE)	RecName: Full=Polyhomeotic-like protein 3
Q8IXK0 (PHC2_HUMAN)	RecName: Full=Polyhomeotic-like protein 2; Short=hPH2; AltName: Full=Early development regulatory protein 2
Q8K214 (SCMH1_MOUSE)	RecName: Full=Polycomb protein SCMH1; AltName: Full=Sex comb on midleg homolog 1
Q8NA19 (LMBL4_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 4; Short=H-l(3)mbt-like protein 4; Short=L(3)mbt-like protein 4
Q8NDX5 (PHC3_HUMAN)	RecName: Full=Polyhomeotic-like protein 3; AltName: Full=Early development regulatory protein 3; AltName: Full=Homolog of polyhomeotic 3; Short=hPH3
Q8QHL5 (PHC2_DANRE)	RecName: Full=Polyhomeotic-like protein 2
Q9QWH1 (PHC2_MOUSE)	RecName: Full=Polyhomeotic-like protein 2; Short=mPH2; AltName: Full=Early development regulatory protein 2; AltName: Full=p36
Q9UQR0 (SCML2_HUMAN)	RecName: Full=Sex comb on midleg-like protein 2
Q9VHA0 (SCM_DROME)	RecName: Full=Polycomb protein Scm; AltName: Full=Sex comb on midleg protein
Q9Y468 (LMBL1_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog; AltName: Full=L3MBTL1
Q96GD3 (SCMH1_HUMAN)	RecName: Full=Polycomb protein SCMH1; AltName: Full=Sex comb on midleg homolog 1
Q96JM7 (LMBL3_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 3; Short=H-l(3)mbt-like protein 3; Short=L(3)mbt-like protein 3; AltName: Full=MBT-1
Q96NU1 (SAM11_HUMAN)	RecName: Full=Sterile alpha motif domain-containing protein 11; Short=SAM domain-containing protein 11
Q969R5 (LMBL2_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=H-l(3)mbt-like protein 2; Short=L(3)mbt-like protein 2
Q64028 (PHC1_MOUSE)	RecName: Full=Polyhomeotic-like protein 1; Short=mPH1; AltName: Full=Early development regulatory protein 1; AltName: Full=RAE-28
XP_002413388	nucleolin, putative, partial [Ixodes scapularis]
XP_006270704	PREDICTED: chromobox protein homolog 8, partial [Alligator mississippiensis]
XP_006819879	PREDICTED: polycomb group protein Pc-like isoform X2 [Saccoglossus kowalevskii]
XP_007110293	PREDICTED: chromobox protein homolog 6-like [Physeter catodon]
XP_011439714	PREDICTED: M-phase phosphoprotein 8-like [Crassostrea gigas]
XP_013386273	PREDICTED: ankyrin repeat and KH domain-containing protein mask-like isoform X1 [Lingula anatina]
XP_013386274	PREDICTED: ankyrin repeat and KH domain-containing protein mask-like isoform X2 [Lingula anatina]
XP_013386275	PREDICTED: M-phase phosphoprotein 8-like isoform X3 [Lingula anatina]
XP_013386276	PREDICTED: M-phase phosphoprotein 8-like isoform X4 [Lingula anatina]
XP_013386277	PREDICTED: M-phase phosphoprotein 8-like isoform X5 [Lingula anatina]
XP_013386278	PREDICTED: M-phase phosphoprotein 8-like isoform X6 [Lingula anatina]
XP_013386279	PREDICTED: M-phase phosphoprotein 8-like isoform X7 [Lingula anatina]
XP_013386280	PREDICTED: M-phase phosphoprotein 8-like isoform X8 [Lingula anatina]
XP_013386281	PREDICTED: M-phase phosphoprotein 8-like isoform X9 [Lingula anatina]
XP_013772724	PREDICTED: gastrula zinc finger protein xFG20-1-like, partial [Limulus polyphemus]

XP_013775834	PREDICTED: chromobox protein homolog 2-like [Limulus polyphemus]
XP_013791499	PREDICTED: M-phase phosphoprotein 8-like [Limulus polyphemus]
XP_013791793	PREDICTED: chromobox protein homolog 2-like [Limulus polyphemus]
XP_013873758	PREDICTED: chromobox protein homolog 8-like [Austrofundulus limnaeus]
XP_014285202	PREDICTED: polycomb group protein Pc [Halyomorpha halys]

9.4.2.31 *Repo*

Name	Description
A1A4L8 (MOCS3_BOVIN)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
A1YEY5 (GSC_GORGO)	RecName: Full=Homeobox protein goosecoid
A1YG25 (RAX2_PANPA)	RecName: Full=Retina and anterior neural fold homeobox protein 2; AltName: Full=Retina and anterior neural fold homeobox-like protein 1
A2BDX3 (MOCS3_MOUSE)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
A2RU54 (HMX2_HUMAN)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein H6 family member 2
A2T7P4 (GSC_PONPY)	RecName: Full=Homeobox protein goosecoid
A3KMV5 (UBA1_BOVIN)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Ubiquitin-activating enzyme E1
A5YC49 (NKX63_XENLA)	RecName: Full=Homeobox protein Nkx-6.3
A6NJT0 (UNC4_HUMAN)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
A6YP92 (ARX_RAT)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
A7EI75 (ATG7_SCLS1)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7
A7KAL8 (ATG7_PENCW)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7
A7MAZ3 (UBA5_BOVIN)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5; AltName: Full=UFM1-activating enzyme; AltName: Full=Ubiquitin-activating enzyme E1 domain-containing protein 1
AAD10338	ARX [Mus musculus]
B0W377 (MOCS3_CULQU)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
B4IK21 (UBA5_DROSE)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
B4JBC4 (MOCS3_DROGR)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
B4LRB9 (MOCS3_DROVI)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
B4NXF7 (MOCS3_DROYA)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
B4PYA4 (UBA5_DROYA)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5

B4R345 (UBA5_DROSI)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
C3YZ51 (UBA5_BRAFL)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
CAA55063	reversed polarity [Drosophila melanogaster]
D1GY43 (UBA5_DROAN)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
Locus_1_Transcript_13818/166847_Confidence_1.000_Length_524 - ORF 4 (frame 1) translation	Locus_1_Transcript_13818/166847_Confidence_1.000_Length_524
Locus_1_Transcript_30903/166847_Confidence_1.000_Length_1463 - ORF 5 (frame 3) translation	Locus_1_Transcript_30903/166847_Confidence_1.000_Length_1463
Locus_1_Transcript_41952/166847_Confidence_1.000_Length_2252 - ORF 3 (frame 2) translation	Locus_1_Transcript_41952/166847_Confidence_1.000_Length_2252
Locus_1_Transcript_45978/166847_Confidence_1.000_Length_591 - ORF 1 (frame 1) translation	Locus_1_Transcript_45978/166847_Confidence_1.000_Length_591
Locus_1_Transcript_55368/166847_Confidence_1.000_Length_711 - ORF 5 (frame 3) translation	Locus_1_Transcript_55368/166847_Confidence_1.000_Length_711
Locus_1_Transcript_64880/166847_Confidence_1.000_Length_595 - ORF 2 (frame 2) translation	Locus_1_Transcript_64880/166847_Confidence_1.000_Length_595
Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118 - ORF 3 (frame 3) translation	Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118
Locus_2435_Transcript_5/5_Confidence_0.739_Length_2834 - ORF 2 (frame 1) translation	Locus_2435_Transcript_5/5_Confidence_0.739_Length_2834
Locus_3015_Transcript_2/2_Confidence_0.800_Length_548 - ORF 4 (frame 3) translation	Locus_3015_Transcript_2/2_Confidence_0.800_Length_548
Locus_3016_Transcript_1/1_Confidence_1.000_Length_755 - ORF 6 (frame 3) translation	Locus_3016_Transcript_1/1_Confidence_1.000_Length_755
Locus_11168_Transcript_14/17_Confidence_0.167_Length_6758 - ORF 28 (frame 3) translation	Locus_11168_Transcript_14/17_Confidence_0.167_Length_6758
Locus_13554_Transcript_8/10_Confidence_0.556_Length_2440 - ORF 3 (frame 1) translation	Locus_13554_Transcript_8/10_Confidence_0.556_Length_2440
Locus_13887_Transcript_3/5_Confidence_0.600_Length_1829 - ORF 16 (frame 2) translation	Locus_13887_Transcript_3/5_Confidence_0.600_Length_1829
Locus_15462_Transcript_2/2_Confidence_0.750_Length_1421 - ORF 1 (frame 2) translation	Locus_15462_Transcript_2/2_Confidence_0.750_Length_1421
Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913 - ORF 2 (frame 1) translation	Locus_15468_Transcript_1/1_Confidence_1.000_Length_2913
Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251 - ORF 3 (frame 2) translation	Locus_16095_Transcript_1/1_Confidence_1.000_Length_2251
Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177 - ORF 3 (frame 1) translation	Locus_16098_Transcript_1/1_Confidence_1.000_Length_2177
Locus_17087_Transcript_1/2_Confidence_0.750_Length_910 - ORF 3 (frame 1) translation	Locus_17087_Transcript_1/2_Confidence_0.750_Length_910
Locus_17531_Transcript_2/2_Confidence_0.889_Length_1577 - ORF 1 (frame 3) translation	Locus_17531_Transcript_2/2_Confidence_0.889_Length_1577
Locus_18078_Transcript_1/1_Confidence_1.000_Length_4033 - ORF 3 (frame 1) translation	Locus_18078_Transcript_1/1_Confidence_1.000_Length_4033
Locus_18982_Transcript_4/4_Confidence_0.600_Length_6071 - ORF 2 (frame 1) translation	Locus_18982_Transcript_4/4_Confidence_0.600_Length_6071
Locus_20045_Transcript_1/2_Confidence_0.625_Length_2782 - ORF 2 (frame 1) translation	Locus_20045_Transcript_1/2_Confidence_0.625_Length_2782
Locus_22112_Transcript_1/1_Confidence_1.000_Length_1696 - ORF 1 (frame 3) translation	Locus_22112_Transcript_1/1_Confidence_1.000_Length_1696
Locus_22533_Transcript_2/2_Confidence_0.750_Length_1755 - ORF 17 (frame 3) translation	Locus_22533_Transcript_2/2_Confidence_0.750_Length_1755
Locus_22697_Transcript_1/1_Confidence_1.000_Length_2190 - ORF 3 (frame 3) translation	Locus_22697_Transcript_1/1_Confidence_1.000_Length_2190
Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832 - ORF 3 (frame 1) translation	Locus_23555_Transcript_2/2_Confidence_0.667_Length_1832
Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198 - ORF 11 (frame 2) translation	Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198
Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171 - ORF 1 (frame 1) translation	Locus_31006_Transcript_1/2_Confidence_0.800_Length_1171
Locus_109739_Transcript_1/1_Confidence_1.000_Length_990 - ORF 9 (frame 2) translation	Locus_109739_Transcript_1/1_Confidence_1.000_Length_990
O08934 (UNC4_MOUSE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
O09113 (OTP_MOUSE)	RecName: Full=Homeobox protein orthopedia
O14813 (PHX2A_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
O15266 (SHOX_HUMAN)	RecName: Full=Short stature homeobox protein; AltName: Full=Pseudoautosomal homeobox-containing osteogenic protein; AltName: Full=Short stature homeobox-containing protein
O15499 (GSC2_HUMAN)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
O18381 (PAX6_DROME)	RecName: Full=Paired box protein Pax-6; AltName: Full=Protein eyeless
O18400 (PITX_DROME)	RecName: Full=Pituitary homeobox homolog Ptx1; Short=D-PTX1
O35085 (ARX_MOUSE)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox
O35137 (ALX4_MOUSE)	RecName: Full=Homeobox protein aristaless-like 4; AltName: Full=ALX-4
O35602 (RX_MOUSE)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
O35690 (PHX2B_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2B; AltName: Full=Neuroblastoma Phox; Short=NBPhox; AltName: Full=PHOX2B homeodomain protein; AltName: Full=Paired-like homeobox 2B
O35750 (SHOX2_RAT)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Paired family homeodomain protein Prx3
O42115 (ARX_DANRE)	RecName: Full=Aristaless-related homeobox protein; Short=ARX

O42201 (RXA_XENLA)	RecName: Full=Retinal homeobox protein Rx-A; Short=Rx1A; Short=Xrx1; AltName: Full=Retina and anterior neural fold homeobox protein A
O42250 (VSX1_DANRE)	RecName: Full=Visual system homeobox 1; AltName: Full=Transcription factor VSX1
O42356 (RX1_DANRE)	RecName: Full=Retinal homeobox protein Rx1
O42357 (RX2_DANRE)	RecName: Full=Retinal homeobox protein Rx2
O42477 (VSX2_DANRE)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein ALX; AltName: Full=Homeobox protein CHX10; AltName: Full=Transcription factor VSX2
O57685 (PAX2A_XENLA)	RecName: Full=Paired box protein Pax-2-A; Short=xPax-2a
O60902 (SHOX2_HUMAN)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; AltName: Full=Paired-related homeobox protein SHOT
O65041 (UBA3_ARATH)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=RUB-activating enzyme; AltName: Full=Ubiquitin-activating enzyme E1-like protein
O70218 (HMX1_MOUSE)	RecName: Full=Homeobox protein HMX1; AltName: Full=Homeobox protein H6
O73917 (PAX6_ORYLA)	RecName: Full=Paired box protein Pax-6
O76971 (OTP_PARLI)	RecName: Full=Homeobox protein orthopedia; AltName: Full=Orthopedia-related; AltName: Full=PlOtp
O77215 (UNC4_DROME)	RecName: Full=Homeobox protein unc-4; AltName: Full=Paired-like homeodomain protein unc-4; Short=DPHD-1
O88181 (BARH2_RAT)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
O93385 (PITX2_CHICK)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; Short=cPITX2; AltName: Full=Paired-like homeodomain transcription factor 2
O94609 (UBA1_SCHPO)	RecName: Full=Ubiquitin-activating enzyme E1 1; AltName: Full=Poly(A)+ RNA transport protein 3
O95352 (ATG7_HUMAN)	RecName: Full=Ubiquitin-like modifier-activating enzyme ATG7; AltName: Full=ATG12-activating enzyme E1 ATG7; AltName: Full=Autophagy-related protein 7; Short=APG7-like; Short=hAGP7; AltName: Full=Ubiquitin-activating enzyme E1-like protein
O95396 (MOCS3_HUMAN)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; AltName: Full=Molybdopterin synthase sulfurylase; Short=MPT synthase sulfurylase; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
O97039 (RX_DUGJA)	RecName: Full=Retinal homeobox protein Rax; AltName: Full=DjRax
P0DMV5 (ALX1_GEOFO)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
P06601 (PRD_DROME)	RecName: Full=Segmentation protein paired
P09082 (GSB_DROME)	RecName: Full=Protein gooseberry; AltName: Full=BSH9; AltName: Full=Protein gooseberry distal
P09083 (GSBN_DROME)	RecName: Full=Protein gooseberry-neuro; AltName: Full=BSH4; AltName: Full=Protein gooseberry proximal
P22314 (UBA1_HUMAN)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Protein A1S9; AltName: Full=Ubiquitin-activating enzyme E1
P22515 (UBA1_YEAST)	RecName: Full=Ubiquitin-activating enzyme E1 1
P22544 (BARH1_DROAN)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox BarH1 protein
P23759 (PAX7_HUMAN)	RecName: Full=Paired box protein Pax-7; AltName: Full=HuP1
P23760 (PAX3_HUMAN)	RecName: Full=Paired box protein Pax-3; AltName: Full=HuP2
P24610 (PAX3_MOUSE)	RecName: Full=Paired box protein Pax-3
P26367 (PAX6_HUMAN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Oculorhombin
P26630 (PAX6_DANRE)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax[Zf-a]
P29454 (GSCA_XENLA)	RecName: Full=Homeobox protein goosecoid isoform A
P29506 (UNC4_CAEEL)	RecName: Full=Homeobox protein unc-4; AltName: Full=Homeobox protein ceh-4; AltName: Full=Uncoordinated protein 4
P31254 (UBA1Y_MOUSE)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1 Y; AltName: Full=Ubiquitin-activating enzyme E1; AltName: Full=Ubiquitin-activating enzyme E1 Y
P32242 (OTX1_HUMAN)	RecName: Full=Homeobox protein OTX1; AltName: Full=Orthodenticle homolog 1
P32243 (OTX2_HUMAN)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P41935 (HM10_CAEEL)	RecName: Full=Homeobox protein ceh-10
P43687 (HMX2_MOUSE)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein Nkx-5.2
P47237 (PAX6_CHICK)	RecName: Full=Paired box protein Pax-6
P47238 (PAX6_COTJA)	RecName: Full=Paired box protein Pax-6; AltName: Full=Pax-QNR
P47239 (PAX7_MOUSE)	RecName: Full=Paired box protein Pax-7
P53544 (GSC_DANRE)	RecName: Full=Homeobox protein goosecoid; AltName: Full=ZGSC
P53546 (GSCB_XENLA)	RecName: Full=Homeobox protein goosecoid isoform B
P54366 (GSC_DROME)	RecName: Full=Homeobox protein goosecoid
P54821 (PRRX1_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=Homeobox protein PHOX1; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1
P55864 (PAX6_XENLA)	RecName: Full=Paired box protein Pax-6
P56407 (HM09_CAEEL)	RecName: Full=Homeobox protein ceh-9
P56672 (OTP_DROME)	RecName: Full=Homeobox protein orthopedia
P56915 (GSC_HUMAN)	RecName: Full=Homeobox protein goosecoid

P56916 (GSC2_MOUSE)	RecName: Full=Homeobox protein goosecoid-2; Short=GSC-2; AltName: Full=Homeobox protein goosecoid-like; Short=GSC-L
P58304 (VSX2_HUMAN)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
P63014 (PRRX1_RAT)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1; Short=rHox
P63016 (PAX6_RAT)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
P63156 (BARH1_RAT)	RecName: Full=BarH-like 1 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH2; AltName: Full=BarH-related homeobox protein 1
P70390 (SHOX2_MOUSE)	RecName: Full=Short stature homeobox protein 2; AltName: Full=Homeobox protein Og12X; Short=OG-12; AltName: Full=Paired family homeodomain protein Prx3
P80205 (OTX1_MOUSE)	RecName: Full=Homeobox protein OTX1; AltName: Full=Orthodenticle homolog 1
P80206 (OTX2_MOUSE)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle homolog 2
P92974 (UBE12_ARATH)	RecName: Full=Ubiquitin-activating enzyme E1 2; Short=AtUBA2
P97474 (PITX2_MOUSE)	RecName: Full=Pituitary homeobox 2; AltName: Full=ALL1-responsive protein ARP1; AltName: Full=BRX1 homeoprotein; AltName: Full=Homeobox protein PITX2; AltName: Full=Orthodenticle-like homeobox 2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=Paired-like homeodomain transcription factor Munc 30; AltName: Full=Solurshin
P97830 (UNC4_RAT)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1; AltName: Full=Paired-type homeodomain transcription factor 1
Q0IH87 (PAX3B_XENLA)	RecName: Full=Paired box protein Pax-3-B; Short=xPax3-B; AltName: Full=Paired-domain transcription factor Pax3-B
Q0P031 (VSX1_XENLA)	RecName: Full=Visual system homeobox 1; AltName: Full=Transcription factor vsx1; AltName: Full=Xvsx1
Q1LVQ7 (ALX1_DANRE)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q1LZF1 (PAX6_BOVIN)	RecName: Full=Paired box protein Pax-6; AltName: Full=Oculorhombin
Q3UHX8 (NKX63_MOUSE)	RecName: Full=Homeobox protein Nkx-6.3
Q4LAL6 (ALX4_BOVIN)	RecName: Full=Homeobox protein aristaless-like 4
Q5AWA2 (ATG7_EMENI)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7
Q5R4A0 (UBA3_PONAB)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q5R8X4 (UBA5_PONAB)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5; AltName: Full=UFM1-activating enzyme; AltName: Full=Ubiquitin-activating enzyme E1 domain-containing protein 1
Q5U300 (UBA1_RAT)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Ubiquitin-activating enzyme E1
Q5ZKY2 (ATG7_CHICK)	RecName: Full=Ubiquitin-like modifier-activating enzyme ATG7; AltName: Full=ATG12-activating enzyme E1 ATG7; AltName: Full=Autophagy-related protein 7; Short=APG7-like
Q6DGH9 (OTBP_DANRE)	RecName: Full=Homeobox protein orthopedia B
Q6DKN2 (OTX2B_XENLA)	RecName: Full=Homeobox protein OTX2-B; Short=xOTX2-B; AltName: Full=Orthodenticle 2-B; AltName: Full=Orthodenticle-A-like protein B
Q6GLG7 (UBA5_XENTR)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5; AltName: Full=UFM1-activating enzyme; AltName: Full=Ubiquitin-activating enzyme E1 domain-containing protein 1
Q6QU75 (PITX3_DANRE)	RecName: Full=Pituitary homeobox 3; AltName: Full=Bicoid-like homeodomain transcription factor Pitx3; AltName: Full=Homeobox protein PITX3; AltName: Full=Paired-like homeodomain transcription factor 3
Q6SR68 (OTP_HELTB)	RecName: Full=Homeobox protein orthopedia
Q6SZ65 (OTP_LYTVA)	RecName: Full=Homeobox protein orthopedia
Q7YTC2 (OTP_SACKO)	RecName: Full=Homeobox protein orthopedia
Q7ZVX6 (UBA3_DANRE)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q8AWD2 (MOCS3_DANRE)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
Q8C878 (UBA3_MOUSE)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q8TBC4 (UBA3_HUMAN)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q8VIB5 (BARH2_MOUSE)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1

Q9BZE3 (BARH1_HUMAN)	RecName: Full=BarH-like 1 homeobox protein
Q9C056 (NKX62_HUMAN)	RecName: Full=Homeobox protein Nkx-6.2; AltName: Full=Homeobox protein NK-6 homolog B
Q9D906 (ATG7_MOUSE)	RecName: Full=Ubiquitin-like modifier-activating enzyme ATG7; AltName: Full=ATG12-activating enzyme E1 ATG7; AltName: Full=Autophagy-related protein 7; Short=APG7-like; Short=mAGP7; AltName: Full=Ubiquitin-activating enzyme E1-like protein
Q9DE09 (HMX1_CHICK)	RecName: Full=Homeobox protein HMX1; AltName: Full=GH6; AltName: Full=Homeobox protein H6
Q9H161 (ALX4_HUMAN)	RecName: Full=Homeobox protein aristaless-like 4
Q9I8K3 (PITX3_XENLA)	RecName: Full=Pituitary homeobox 3; AltName: Full=Homeobox protein PITX3; Short=XPitx-3; Short=xPitx3; AltName: Full=Paired-like homeodomain transcription factor 3
Q9I9A2 (RX2_ORYLA)	RecName: Full=Retinal homeobox protein Rx2
Q9I9A3 (VSX2_ORYLA)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10; AltName: Full=Transcription factor VSX2
Q9I9D5 (RX1_ASTFA)	RecName: Full=Retinal homeobox protein Rx1
Q9IAL1 (VSX2_CHICK)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
Q9IAL2 (VSX1_CHICK)	RecName: Full=Visual system homeobox 1; AltName: Full=Homeobox protein Chx10-1; AltName: Full=Transcription factor VSX1
Q9JLT7 (RX_RAT)	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeobox protein
Q9NY43 (BARH2_HUMAN)	RecName: Full=BarH-like 2 homeobox protein
Q9PT61 (OTX5B_XENLA)	RecName: Full=Homeobox protein otx5-B; AltName: Full=Orthodenticle homolog 5-B; AltName: Full=XOtx5b
Q9PVM0 (OTX5A_XENLA)	RecName: Full=Homeobox protein otx5-A; AltName: Full=Orthodenticle homolog 5-A; AltName: Full=Xotx5
Q9PVX0 (RX2_CHICK)	RecName: Full=Retinal homeobox protein Rx2; Short=cRax2
Q9PVY0 (RX1_CHICK)	RecName: Full=Retinal homeobox protein Rx1; Short=cRax1
Q9PWR3 (PITX2_XENLA)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=xPtx2
Q9R0W1 (PITX2_RAT)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=rPtx2
Q9U637 (PITX_BRABE)	RecName: Full=Pituitary homeobox x; AltName: Full=Bicoid type transcription factor Pitx; Short=BbPtx; AltName: Full=Homeobox protein Ptx; AltName: Full=Paired-like homeodomain transcription factor x
Q9V6U8 (UBA3_DROME)	RecName: Full=Nedd8-activating enzyme E1 catalytic subunit; AltName: Full=Ubiquitin-activating enzyme 3 homolog
Q9VYY3 (UBA5_DROME)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
Q9W2Q1 (RX_DROME)	RecName: Full=Retinal homeobox protein Rx; Short=DRx; Short=DRx1
Q9W5Z2 (PITX2_DANRE)	RecName: Full=Pituitary homeobox 2; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2
Q17CA7 (MOCS3_AEDAE)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
Q28DP6 (PAX3_XENTR)	RecName: Full=Paired box protein Pax-3; AltName: Full=Paired-domain transcription factor Pax3
Q28EM7 (OTX5_XENTR)	RecName: Full=Homeobox protein otx5; AltName: Full=Orthodenticle homolog 5
Q28FN6 (OTX2_XENTR)	RecName: Full=Homeobox protein OTX2; AltName: Full=Orthodenticle 2
Q29HT0 (UBA5_DROPS)	RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5
Q50D79 (UNC4_DANRE)	RecName: Full=Homeobox protein unc-4 homolog; AltName: Full=Homeobox protein Uncx4.1
Q54QG9 (UBA3_DICDI)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q55C16 (UBA1_DICDI)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Ubiquitin-activating enzyme E1
Q58E95 (MOCS3_XENLA)	RecName: Full=Adenylyltransferase and sulfurtransferase MOCS3; AltName: Full=Molybdenum cofactor synthesis protein 3; Includes: RecName: Full=Molybdopterin-synthase adenylyltransferase; AltName: Full=Adenylyltransferase MOCS3; AltName: Full=Sulfur carrier protein MOCS2A adenylyltransferase; Includes: RecName: Full=Molybdopterin-synthase sulfurtransferase; AltName: Full=Sulfur carrier protein MOCS2A sulfurtransferase; AltName: Full=Sulfurtransferase MOCS3
Q86CR9 (ATG7_DICDI)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7
Q94CD5 (ATG7_ARATH)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7; Short=AtAPG7; AltName: Full=Protein PEROXISOME UNUSUAL POSITIONING 4
Q96QS3 (ARX_HUMAN)	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox

Q99MI7 (UBA3_RAT)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=NEDD8-activating enzyme E1C; AltName: Full=Ubiquitin-activating enzyme E1C; AltName: Full=Ubiquitin-like modifier-activating enzyme 3; Short=Ubiquitin-activating enzyme 3
Q00288 (PAX8_MOUSE)	RecName: Full=Paired box protein Pax-8
Q504H8 (HMX3_DANRE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q641Y5 (ATG7_RAT)	RecName: Full=Ubiquitin-like modifier-activating enzyme ATG7; AltName: Full=ATG12-activating enzyme E1 ATG7; AltName: Full=Autophagy-related protein 7; Short=APG7-like
Q645N4 (PAX3A_XENLA)	RecName: Full=Paired box protein Pax-3-A; Short=xPax3-A; AltName: Full=Paired-domain transcription factor Pax3-A
Q871U2 (ATG7_NEUCR)	RecName: Full=Ubiquitin-like modifier-activating enzyme atg7; AltName: Full=ATG12-activating enzyme E1 atg7; AltName: Full=Autophagy-related protein 7
Q02053 (UBA1_MOUSE)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Ubiquitin-activating enzyme E1; AltName: Full=Ubiquitin-activating enzyme E1 X; AltName: Full=Ubiquitin-like modifier-activating enzyme 1 X
Q05437 (PRRX1_CHICK)	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=GMHOX; AltName: Full=Homeobox protein MHOX; AltName: Full=Paired-related homeobox protein 1; Short=PRX-1
Q06348 (PRRX2_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2; Short=PRX-2; AltName: Full=Homeobox protein S8
Q06453 (AL_DROME)	RecName: Full=Homeobox protein aristaless
Q09765 (UBA3_SCHPO)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=Ubiquitin-activating enzyme E1 3
Q15699 (ALX1_HUMAN)	RecName: Full=ALX homeobox protein 1; AltName: Full=Cartilage homeoprotein 1; Short=CART-1
Q19360 (UBA3_CAEEL)	RecName: Full=NEDD8-activating enzyme E1 catalytic subunit; AltName: Full=Ectopic membrane ruffles in embryo protein 1; AltName: Full=Ubiquitin-activating enzyme 3 homolog
Q22909 (HM30_CAEEL)	RecName: Full=Homeobox protein ceh-30
Q22910 (HM31_CAEEL)	RecName: Full=Homeobox protein ceh-31
Q24255 (BARH1_DROME)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox protein BarH1
Q24256 (BARH2_DROME)	RecName: Full=Homeobox protein B-H2; AltName: Full=Homeobox protein BarH2
Q26417 (OTX_STRPU)	RecName: Full=Homeobox protein OTX; Short=SpOTX; AltName: Full=Orthodenticle homolog
Q26602 (SMOX3_SCHMA)	RecName: Full=Homeobox protein SMOX-3
Q26656 (HMX_STRPU)	RecName: Full=Homeobox protein Hmx; Short=SpHmx; AltName: Full=H6-like
Q26657 (ALX_STRPU)	RecName: Full=Aristaless homeobox protein; Short=ALX; AltName: Full=SpPrx-1
Q29504 (UBA1_RABIT)	RecName: Full=Ubiquitin-like modifier-activating enzyme 1; AltName: Full=Ubiquitin-activating enzyme E1
Q61412 (VSX2_MOUSE)	RecName: Full=Visual system homeobox 2; AltName: Full=Ceh-10 homeodomain-containing homolog; AltName: Full=Homeobox protein CHX10
Q62066 (PHX2A_MOUSE)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=PHOX2A homeodomain protein; AltName: Full=Paired-like homeobox 2A
Q62782 (PHX2A_RAT)	RecName: Full=Paired mesoderm homeobox protein 2A; AltName: Full=ARIX1 homeodomain protein; AltName: Full=Aristaless homeobox protein homolog; AltName: Full=Paired-like homeobox 2A
Q63410 (OTX1_RAT)	RecName: Full=Homeobox protein OTX1; AltName: Full=Orthodenticle homolog 1
Q90268 (PAX2A_DANRE)	RecName: Full=Paired box protein Pax-2a; AltName: Full=No isthmus protein; AltName: Full=Pax[Zf-b]
Q90277 (VSX1_CARAU)	RecName: Full=Visual system homeobox 1; AltName: Full=Homeobox protein VSX-1; AltName: Full=Transcription factor VSX1
Q91813 (OTX2A_XENLA)	RecName: Full=Homeobox protein OTX2-A; Short=xOTX2-A; AltName: Full=Orthodenticle 2-A; AltName: Full=Orthodenticle-A-like protein A
Q91981 (OTX2_DANRE)	RecName: Full=Homeobox protein OTX2; Short=zOTX2; AltName: Full=Orthodenticle homolog 2
Q91994 (OTX1B_DANRE)	RecName: Full=Homeobox protein OTX1 B; Short=zOtx1; AltName: Full=Orthodenticle homolog 1 B
Q99697 (PITX2_HUMAN)	RecName: Full=Pituitary homeobox 2; AltName: Full=ALL1-responsive protein ARP1; AltName: Full=Homeobox protein PITX2; AltName: Full=Paired-like homeodomain transcription factor 2; AltName: Full=RIEG bicoid-related homeobox transcription factor; AltName: Full=Solurshin
Q99811 (PRRX2_HUMAN)	RecName: Full=Paired mesoderm homeobox protein 2; AltName: Full=Paired-related homeobox protein 2; Short=PRX-2

9.4.2.32 *Senseless*

Name	Description
A0JNB1 (ZN227_BOVIN)	RecName: Full=Zinc finger protein 227
A0PJY2 (FEZF1_HUMAN)	RecName: Full=Fez family zinc finger protein 1; AltName: Full=Zinc finger protein 312B
A1YF12 (ZNF16_GORGO)	RecName: Full=Zinc finger protein 16
A1YG88 (ZNF16_PANPA)	RecName: Full=Zinc finger protein 16
A2T759 (ZNF16_PANTR)	RecName: Full=Zinc finger protein 16
A2VDQ7 (ZN420_BOVIN)	RecName: Full=Zinc finger protein 420
A6NK53 (ZN233_HUMAN)	RecName: Full=Zinc finger protein 233
A6NNF4 (ZN726_HUMAN)	RecName: Full=Zinc finger protein 726
A6NP11 (ZN716_HUMAN)	RecName: Full=Zinc finger protein 716

A8MQ14 (ZN850_HUMAN)	RecName: Full=Zinc finger protein 850
A8MT65 (ZN891_HUMAN)	RecName: Full=Zinc finger protein 891
A8MXY4 (ZNF99_HUMAN)	RecName: Full=Zinc finger protein 99
B4DU55 (ZN879_HUMAN)	RecName: Full=Zinc finger protein 879
GFI1_DROME	RecName: Full=Zinc finger protein sens; AltName: Full=Protein senseless
GFI1_MOUSE	RecName: Full=Zinc finger protein Gfi-1; AltName: Full=Growth factor independent protein 1
GFI1B_MOUSE	RecName: Full=Zinc finger protein Gfi-1b; AltName: Full=Growth factor independent protein 1B
Locus_1_Transcript_77522/166847_Confidence_1.000_Length_1632 - ORF 6 (frame 2) translation	Locus_1_Transcript_77522/166847_Confidence_1.000_Length_1632
Locus_1_Transcript_92359/166847_Confidence_1.000_Length_1459 - ORF 7 (frame 2) translation	Locus_1_Transcript_92359/166847_Confidence_1.000_Length_1459
Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831 - ORF 1 (frame 2) translation	Locus_1_Transcript_145107/166847_Confidence_1.000_Length_831
Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594 - ORF 3 (frame 1) translation	Locus_1_Transcript_164653/166847_Confidence_1.000_Length_594
Locus_273_Transcript_17/26_Confidence_0.183_Length_1844 - ORF 8 (frame 1) translation	Locus_273_Transcript_17/26_Confidence_0.183_Length_1844
Locus_487_Transcript_29/38_Confidence_0.065_Length_3976 - ORF 13 (frame 1) translation	Locus_487_Transcript_29/38_Confidence_0.065_Length_3976
Locus_766_Transcript_1/4_Confidence_0.840_Length_3832 - ORF 3 (frame 3) translation	Locus_766_Transcript_1/4_Confidence_0.840_Length_3832
Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195 - ORF 3 (frame 2) translation	Locus_1940_Transcript_1/1_Confidence_1.000_Length_5195
Locus_2332_Transcript_18/26_Confidence_0.116_Length_1397 - ORF 1 (frame 3) translation	Locus_2332_Transcript_18/26_Confidence_0.116_Length_1397
Locus_2787_Transcript_1/2_Confidence_0.875_Length_4512 - ORF 22 (frame 1) translation	Locus_2787_Transcript_1/2_Confidence_0.875_Length_4512
Locus_4734_Transcript_13/20_Confidence_0.193_Length_4425 - ORF 2 (frame 2) translation	Locus_4734_Transcript_13/20_Confidence_0.193_Length_4425
Locus_5373_Transcript_7/14_Confidence_0.085_Length_1057 - ORF 4 (frame 3) translation	Locus_5373_Transcript_7/14_Confidence_0.085_Length_1057
Locus_5592_Transcript_7/13_Confidence_0.163_Length_1909 - ORF 6 (frame 1) translation	Locus_5592_Transcript_7/13_Confidence_0.163_Length_1909
Locus_5884_Transcript_3/10_Confidence_0.393_Length_3610 - ORF 5 (frame 3) translation	Locus_5884_Transcript_3/10_Confidence_0.393_Length_3610
Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349 - ORF 20 (frame 1) translation	Locus_6268_Transcript_1/2_Confidence_0.600_Length_2349
Locus_7469_Transcript_17/25_Confidence_0.009_Length_1182 - ORF 6 (frame 3) translation	Locus_7469_Transcript_17/25_Confidence_0.009_Length_1182
Locus_7997_Transcript_2/2_Confidence_0.812_Length_688 - ORF 2 (frame 3) translation	Locus_7997_Transcript_2/2_Confidence_0.812_Length_688
Locus_9749_Transcript_4/7_Confidence_0.769_Length_3111 - ORF 8 (frame 1) translation	Locus_9749_Transcript_4/7_Confidence_0.769_Length_3111
Locus_10690_Transcript_2/10_Confidence_0.333_Length_2773 - ORF 2 (frame 3) translation	Locus_10690_Transcript_2/10_Confidence_0.333_Length_2773
Locus_13183_Transcript_1/2_Confidence_0.889_Length_3060 - ORF 1 (frame 2) translation	Locus_13183_Transcript_1/2_Confidence_0.889_Length_3060
Locus_13718_Transcript_1/4_Confidence_0.727_Length_2263 - ORF 8 (frame 3) translation	Locus_13718_Transcript_1/4_Confidence_0.727_Length_2263
Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958 - ORF 2 (frame 2) translation	Locus_15334_Transcript_1/2_Confidence_0.889_Length_1958
Locus_16223_Transcript_1/10_Confidence_0.333_Length_5515 - ORF 2 (frame 3) translation	Locus_16223_Transcript_1/10_Confidence_0.333_Length_5515
Locus_17399_Transcript_2/2_Confidence_0.897_Length_1818 - ORF 1 (frame 3) translation	Locus_17399_Transcript_2/2_Confidence_0.897_Length_1818
Locus_17642_Transcript_1/5_Confidence_0.571_Length_2317 - ORF 2 (frame 2) translation	Locus_17642_Transcript_1/5_Confidence_0.571_Length_2317
Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582 - ORF 4 (frame 3) translation	Locus_18734_Transcript_1/1_Confidence_1.000_Length_2582
Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891 - ORF 1 (frame 1) translation	Locus_19124_Transcript_1/1_Confidence_1.000_Length_2891
Locus_25081_Transcript_1/1_Confidence_1.000_Length_1385 - ORF 1 (frame 1) translation	Locus_25081_Transcript_1/1_Confidence_1.000_Length_1385
NP_001156383	zinc finger protein 934 isoform 1 [Mus musculus]
NP_001171016	zinc finger protein 600 [Mus musculus]
NP_001171238	reduced expression 2 [Mus musculus]
O42409 (GFI1B_CHICK)	RecName: Full=Zinc finger protein Gfi-1b; AltName: Full=Growth factor-independent protein 1B
O70237 (GFI1B_MOUSE)	RecName: Full=Zinc finger protein Gfi-1b; AltName: Full=Growth factor independent protein 1B
O75626 (PRDM1_HUMAN)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=BLIMP-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1; AltName: Full=Positive regulatory domain I-binding factor 1; Short=PRDI-BF1; Short=PRDI-binding factor 1
P0CJ79 (ZN888_HUMAN)	RecName: Full=Zinc finger protein 888
P08043 (ZFP2_MOUSE)	RecName: Full=Zinc finger protein 2; Short=Zfp-2; AltName: Full=Protein mKR2
P08045 (XFIN_XENLA)	RecName: Full=Zinc finger protein Xfin; AltName: Full=Xenopus fingers protein; Short=Xfin
P15620 (ZN271_MOUSE)	RecName: Full=Zinc finger protein 271; AltName: Full=Zinc finger protein 35; Short=Zfp-35
P15622 (ZN250_HUMAN)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
P17020 (ZNF16_HUMAN)	RecName: Full=Zinc finger protein 16; AltName: Full=Zinc finger protein KOX9
P17025 (ZN182_HUMAN)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21; AltName: Full=Zinc finger protein KOX14

P17030 (ZNF25_HUMAN)	RecName: Full=Zinc finger protein 25; AltName: Full=Zinc finger protein KOX19
P17035 (ZNF28_HUMAN)	RecName: Full=Zinc finger protein 28; AltName: Full=Zinc finger protein KOX24
P18729 (ZG57_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF57.1
P18737 (ZG8_XENLA)	RecName: Full=Gastrula zinc finger protein XlCGF8.2DB
P18749 (ZO6_XENLA)	RecName: Full=Oocyte zinc finger protein XlCOF6
P24399 (ZN239_MOUSE)	RecName: Full=Zinc finger protein 239; Short=Zfp-239; AltName: Full=Zinc finger protein MOK-2
P51522 (ZNF83_HUMAN)	RecName: Full=Zinc finger protein 83; AltName: Full=Zinc finger protein 816B; AltName: Full=Zinc finger protein HPF1
P51523 (ZNF84_HUMAN)	RecName: Full=Zinc finger protein 84; AltName: Full=Zinc finger protein HPF2
P52736 (ZN133_HUMAN)	RecName: Full=Zinc finger protein 133; AltName: Full=Zinc finger protein 150
P70338 (GFI1_MOUSE)	RecName: Full=Zinc finger protein Gfi-1; AltName: Full=Growth factor independent protein 1
Q0P4W9 (FEZF1_XENTR)	RecName: Full=Fez family zinc finger protein 1
Q0VDQ9 (FEZF1_MOUSE)	RecName: Full=Fez family zinc finger protein 1
Q0VGE8 (ZN816_HUMAN)	RecName: Full=Zinc finger protein 816
Q2TAR3 (FEZF2_XENLA)	RecName: Full=Fez family zinc finger protein 2
Q2VWH6 (FEZF2_BOVIN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q3B7N9 (MYNN_BOVIN)	RecName: Full=Myoneurin
Q3SY52 (ZIK1_HUMAN)	RecName: Full=Zinc finger protein interacting with ribonucleoprotein K; AltName: Full=Zinc finger protein 762
Q3V080 (ZN583_MOUSE)	RecName: Full=Zinc finger protein 583
Q3ZCT1 (ZN260_HUMAN)	RecName: Full=Zinc finger protein 260; Short=Zfp-260
Q3ZCX4 (ZN568_HUMAN)	RecName: Full=Zinc finger protein 568
Q4R6C2 (ZN383_MACFA)	RecName: Full=Zinc finger protein 383
Q4V348 (Z658B_HUMAN)	RecName: Full=Zinc finger protein 658B
Q5DWN0 (GFI1_CANFA)	RecName: Full=Zinc finger protein Gfi-1; AltName: Full=Growth factor independence 1
Q5MCW4 (ZN569_HUMAN)	RecName: Full=Zinc finger protein 569
Q5R5N5 (MYNN_PONAB)	RecName: Full=Myoneurin
Q5R5U3 (ZN271_PONAB)	RecName: Full=Zinc finger protein 271
Q5R5Y7 (ZN436_PONAB)	RecName: Full=Zinc finger protein 436
Q5R8G9 (ZN239_PONAB)	RecName: Full=Zinc finger protein 239
Q5R8X1 (ZN665_PONAB)	RecName: Full=Zinc finger protein 665
Q5R9S5 (ZN182_PONAB)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q5RCD9 (ZSCA2_PONAB)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29 homolog; Short=Zfp-29
Q5RFP4 (OZF_PONAB)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q5TYW1 (ZN658_HUMAN)	RecName: Full=Zinc finger protein 658
Q5VIY5 (ZN468_HUMAN)	RecName: Full=Zinc finger protein 468
Q5VTD9 (GFI1B_HUMAN)	RecName: Full=Zinc finger protein Gfi-1b; AltName: Full=Growth factor independent protein 1B; AltName: Full=Potential regulator of CDKN1A translocated in CML
Q6DCW1 (GFI1B_XENLA)	RecName: Full=Zinc finger protein Gfi-1b; AltName: Full=Growth factor independent protein 1B
Q6NX49 (ZN544_HUMAN)	RecName: Full=Zinc finger protein 544
Q6P9A1 (ZN530_HUMAN)	RecName: Full=Zinc finger protein 530
Q6P560 (ZN182_MOUSE)	RecName: Full=Zinc finger protein 182; AltName: Full=Zinc finger protein 21
Q6PF04 (ZN613_HUMAN)	RecName: Full=Zinc finger protein 613
Q6ZMW2 (ZN782_HUMAN)	RecName: Full=Zinc finger protein 782
Q6ZN19 (ZN841_HUMAN)	RecName: Full=Zinc finger protein 841
Q6ZN57 (ZFP2_HUMAN)	RecName: Full=Zinc finger protein 2 homolog; Short=Zfp-2; AltName: Full=Zinc finger protein 751
Q6ZNA1 (ZN836_HUMAN)	RecName: Full=Zinc finger protein 836
Q6ZNG1 (ZN600_HUMAN)	RecName: Full=Zinc finger protein 600
Q7TNU6 (ZN250_MOUSE)	RecName: Full=Zinc finger protein 250; AltName: Full=Zinc finger protein 647
Q7Z340 (ZN551_HUMAN)	RecName: Full=Zinc finger protein 551; AltName: Full=Zinc finger protein KOX23
Q8BPP0 (ZN436_MOUSE)	RecName: Full=Zinc finger protein 436; AltName: Full=Zinc finger protein 46; Short=Zfp-46; AltName: Full=Zinc finger protein MLZ-4
Q8BQN6 (OZF_MOUSE)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q08DG8 (ZN135_BOVIN)	RecName: Full=Zinc finger protein 135
Q8IZ20 (ZN683_HUMAN)	RecName: Full=Zinc finger protein 683
Q8NA42 (ZN383_HUMAN)	RecName: Full=Zinc finger protein 383
Q8TAQ5 (ZN420_HUMAN)	RecName: Full=Zinc finger protein 420
Q8TBJ5 (FEZF2_HUMAN)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q8TBZ5 (ZN502_HUMAN)	RecName: Full=Zinc finger protein 502
Q8TD23 (ZN675_HUMAN)	RecName: Full=Zinc finger protein 675; AltName: Full=TRAF6-binding zinc finger protein; AltName: Full=TRAF6-inhibitory zinc finger protein
Q8TF45 (ZN418_HUMAN)	RecName: Full=Zinc finger protein 418
Q8WV37 (ZN480_HUMAN)	RecName: Full=Zinc finger protein 480
Q9BSK1 (ZN577_HUMAN)	RecName: Full=Zinc finger protein 577
Q9C0F3 (ZN436_HUMAN)	RecName: Full=Zinc finger protein 436
Q9ESP5 (FEZF2_MOUSE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName:

	Full=Zinc finger protein 312; AltName: Full=Zinc finger protein Fez-like
Q9H7R5 (ZN665_HUMAN)	RecName: Full=Zinc finger protein 665; AltName: Full=Zinc finger protein 160-like
Q9HCG1 (ZN160_HUMAN)	RecName: Full=Zinc finger protein 160; AltName: Full=Zinc finger protein HZF5; AltName: Full=Zinc finger protein Kr18; Short=HKr18
Q9N658 (GFI1_DROME)	RecName: Full=Zinc finger protein sens; AltName: Full=Protein senseless
Q9NQZ8 (ZNF71_HUMAN)	RecName: Full=Endothelial zinc finger protein induced by tumor necrosis factor alpha; AltName: Full=Zinc finger protein 71
Q9NV72 (ZN701_HUMAN)	RecName: Full=Zinc finger protein 701
Q9NYT6 (ZN226_HUMAN)	RecName: Full=Zinc finger protein 226
Q9UJU3 (ZN112_HUMAN)	RecName: Full=Zinc finger protein 112; Short=Zfp-112; AltName: Full=Zinc finger protein 228
Q9UL59 (ZN214_HUMAN)	RecName: Full=Zinc finger protein 214; AltName: Full=BWSCR2-associated zinc finger protein 1; Short=BAZ-1
Q9XSR1 (ZN252_CANFA)	RecName: Full=Zinc finger protein 252
Q9Y2H8 (ZN510_HUMAN)	RecName: Full=Zinc finger protein 510
Q9Y6Q3 (ZFP37_HUMAN)	RecName: Full=Zinc finger protein 37 homolog; Short=Zfp-37
Q25C93 (FEZF1_DANRE)	RecName: Full=Fez family zinc finger protein 1
Q28G88 (FEZF2_XENTR)	RecName: Full=Fez family zinc finger protein 2
Q80V23 (ZNF32_MOUSE)	RecName: Full=Zinc finger protein 32; AltName: Full=Zinc finger protein 637
Q80W31 (ZN569_MOUSE)	RecName: Full=Zinc finger protein 569; AltName: Full=Mszf21; AltName: Full=Zinc finger protein 74; Short=Zfp-74
Q86WZ6 (ZN227_HUMAN)	RecName: Full=Zinc finger protein 227
Q86XU0 (ZN677_HUMAN)	RecName: Full=Zinc finger protein 677
Q96EQ9 (PRDM9_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase PRDM9; AltName: Full=Hybrid sterility protein 1; AltName: Full=Meiosis-induced factor containing a PR/SET domain and zinc-finger motif; AltName: Full=PR domain zinc finger protein 9; AltName: Full=PR domain-containing protein 9
Q96IR2 (ZN845_HUMAN)	RecName: Full=Zinc finger protein 845
Q96JC4 (ZN479_HUMAN)	RecName: Full=Zinc finger protein 479; AltName: Full=Zinc finger protein Kr19; Short=HKr19
Q96N38 (ZN714_HUMAN)	RecName: Full=Zinc finger protein 714
Q96ND8 (ZN583_HUMAN)	RecName: Full=Zinc finger protein 583; AltName: Full=Zinc finger protein L3-5
Q96NI8 (ZN570_HUMAN)	RecName: Full=Zinc finger protein 570
Q96RE9 (ZN300_HUMAN)	RecName: Full=Zinc finger protein 300
Q96SE7 (ZN347_HUMAN)	RecName: Full=Zinc finger protein 347; AltName: Full=Zinc finger protein 1111
Q99MD8 (MYNN_MOUSE)	RecName: Full=Myoneurin
Q147U1 (ZN846_HUMAN)	RecName: Full=Zinc finger protein 846
Q804Q5 (FEZF2_DANRE)	RecName: Full=Fez family zinc finger protein 2; AltName: Full=Forebrain embryonic zinc finger-like protein 2; AltName: Full=Foreheadin protein; AltName: Full=Zinc finger protein Fez-like
Q02386 (ZNF45_HUMAN)	RecName: Full=Zinc finger protein 45; AltName: Full=BRC1744; AltName: Full=Zinc finger protein 13; AltName: Full=Zinc finger protein KOX5
Q05481 (ZNF91_HUMAN)	RecName: Full=Zinc finger protein 91; AltName: Full=Zinc finger protein HPF7; AltName: Full=Zinc finger protein HTF10
Q07120 (GFI1_RAT)	RecName: Full=Zinc finger protein Gfi-1; AltName: Full=Growth factor independent protein 1
Q07230 (ZSCA2_MOUSE)	RecName: Full=Zinc finger and SCAN domain-containing protein 2; AltName: Full=Zinc finger protein 29; Short=Zfp-29
Q12901 (ZN155_HUMAN)	RecName: Full=Zinc finger protein 155
Q13106 (ZN154_HUMAN)	RecName: Full=Zinc finger protein 154
Q14585 (ZN345_HUMAN)	RecName: Full=Zinc finger protein 345; AltName: Full=Zinc finger protein HZF10
Q14588 (ZN234_HUMAN)	RecName: Full=Zinc finger protein 234; AltName: Full=Zinc finger protein 269; AltName: Full=Zinc finger protein HZF4
Q14590 (ZN235_HUMAN)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 270; AltName: Full=Zinc finger protein 93 homolog; Short=Zfp-93; AltName: Full=Zinc finger protein HZF6
Q14591 (ZN271_HUMAN)	RecName: Full=Zinc finger protein 271; AltName: Full=CT-ZFP48; AltName: Full=Epstein-Barr virus-induced zinc finger protein; Short=EBV-induced zinc finger protein; Short=ZNF-EB; AltName: Full=Zinc finger protein HZF7; AltName: Full=Zinc finger protein ZNFphex133; AltName: Full=Zinc finger protein dp; Short=ZNF-dp
Q15937 (ZNF79_HUMAN)	RecName: Full=Zinc finger protein 79; AltName: Full=ZNFpT7
Q16600 (ZN239_HUMAN)	RecName: Full=Zinc finger protein 239; AltName: Full=Zinc finger protein HOK-2; AltName: Full=Zinc finger protein MOK-2
Q28151 (OZF_BOVIN)	RecName: Full=Zinc finger protein OZF; AltName: Full=Only zinc finger protein; AltName: Full=Zinc finger protein 146
Q60636 (PRDM1_MOUSE)	RecName: Full=PR domain zinc finger protein 1; AltName: Full=B lymphocyte-induced maturation protein 1; Short=Blimp-1; AltName: Full=Beta-interferon gene positive regulatory domain I-binding factor; AltName: Full=PR domain-containing protein 1
Q61116 (ZN235_MOUSE)	RecName: Full=Zinc finger protein 235; AltName: Full=Zinc finger protein 93; Short=Zfp-93
Q62981 (ZN260_RAT)	RecName: Full=Zinc finger protein 260; Short=Zfp-260; AltName: Full=Pancreas-only zinc finger protein 1; Short=POZF-1
Q93560 (BLMP1_CAEEL)	RecName: Full=B lymphocyte-induced maturation protein 1 homolog
Q99676 (ZN184_HUMAN)	RecName: Full=Zinc finger protein 184
Q99684 (GFI1_HUMAN)	RecName: Full=Zinc finger protein Gfi-1; AltName: Full=Growth factor independent protein 1; AltName: Full=Zinc finger protein 163
XP_689690	PREDICTED: gastrula zinc finger protein XlCGF26.1-like [Danio rerio]
XP_001812645	PREDICTED: zinc finger protein 358-like [Tribolium castaneum]
XP_001921884	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_001945654	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]

XP_001946669	PREDICTED: zinc finger protein 845-like [Acyrthosiphon pisum]
XP_001949223	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_001950651	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_002401338	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_002404835	zinc finger, C2H2 type, putative [Ixodes scapularis]
XP_003148638	growth factor independence [Loa loa]
XP_003242514	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003242604	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003244738	PREDICTED: zinc finger protein 572-like [Acyrthosiphon pisum]
XP_003244741	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_003248857	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248889	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_003248963	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_003249048	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_003249678	PREDICTED: fez family zinc finger protein 1-like [Apis mellifera]
XP_003398307	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus terrestris]
XP_003492727	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Bombus impatiens]
XP_003494856	PREDICTED: fez family zinc finger protein 2-like [Bombus impatiens]
XP_003738192	PREDICTED: PR domain zinc finger protein 1-like [Metaseiulus occidentalis]
XP_004919623	PREDICTED: gastrula zinc finger protein xLCGF3.1-like [Xenopus (Silurana) tropicalis]
XP_005157335	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168084	PREDICTED: gastrula zinc finger protein XlCGF57.1, partial [Danio rerio]
XP_005168216	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005168249	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_005342829	PREDICTED: zinc finger protein 568 [Ictidomys tridecemlineatus]
XP_005476894	PREDICTED: zinc finger protein 239-like [Oreochromis niloticus]
XP_005697039	PREDICTED: zinc finger protein 397 isoform X1 [Capra hircus]
XP_005814335	PREDICTED: zinc finger protein Gfi-1b-like [Xiphophorus maculatus]
XP_005977203	PREDICTED: zinc finger protein 271-like isoform X1 [Pantholops hodgsonii]
XP_005977204	PREDICTED: zinc finger protein 271-like isoform X2 [Pantholops hodgsonii]
XP_006263331	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X2 [Alligator mississippiensis]
XP_006566074	PREDICTED: probable serine/threonine-protein kinase DDB_G0282963 isoform X4 [Apis mellifera]
XP_006609630	PREDICTED: fez family zinc finger protein 1-like, partial [Apis dorsata]
XP_006621322	PREDICTED: PR domain zinc finger protein 1-like [Apis dorsata]
XP_006806237	PREDICTED: zinc finger protein 569-like [Neolamprologus brichardi]
XP_006807046	PREDICTED: histone-lysine N-methyltransferase PRDM9-like isoform X1 [Neolamprologus brichardi]
XP_007241270	PREDICTED: zinc finger protein 850-like [Astyanax mexicanus]
XP_007455301	PREDICTED: zinc finger protein 271-like [Lipotes vexillifer]
XP_007490656	PREDICTED: zinc finger protein 624-like isoform X2 [Monodelphis domestica]
XP_007540550	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
XP_007569488	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007573142	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Poecilia formosa]
XP_007573181	PREDICTED: zinc finger protein 271-like [Poecilia formosa]
XP_007573713	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007575719	PREDICTED: zinc finger protein Gfi-1b-like [Poecilia formosa]
XP_007575720	PREDICTED: zinc finger protein Gfi-1b [Poecilia formosa]
XP_007576627	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia formosa]
XP_007577096	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Poecilia formosa]
XP_007577098	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X3 [Poecilia formosa]
XP_007577099	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X4 [Poecilia formosa]
XP_008179259	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180595	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180597	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180598	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008180607	PREDICTED: zinc finger protein 62 homolog [Acyrthosiphon pisum]
XP_008180907	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008181099	PREDICTED: zinc finger protein 91-like [Acyrthosiphon pisum]
XP_008181583	PREDICTED: zinc finger protein 2-like [Acyrthosiphon pisum]
XP_008181794	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183209	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]
XP_008183213	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183216	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008183596	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008185429	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Acyrthosiphon pisum]
XP_008186458	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008186726	PREDICTED: zinc finger protein 2 homolog [Acyrthosiphon pisum]

XP_008186729	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008187394	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008188120	PREDICTED: zinc finger protein 180-like [Acyrthosiphon pisum]
XP_008188255	PREDICTED: zinc finger protein 271-like, partial [Acyrthosiphon pisum]
XP_008188522	PREDICTED: zinc finger protein 271-like [Acyrthosiphon pisum]
XP_008194427	PREDICTED: PR domain zinc finger protein 1 isoform X2 [Tribolium castaneum]
XP_008259420	PREDICTED: zinc finger protein 271-like [Oryctolagus cuniculus]
XP_008298792	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Stegastes partitus]
XP_008404678	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Poecilia reticulata]
XP_008422882	PREDICTED: zinc finger protein Gfi-1b [Poecilia reticulata]
XP_008435718	PREDICTED: oocyte zinc finger protein XlCOF6-like [Poecilia reticulata]
XP_008543891	PREDICTED: PR domain zinc finger protein 1 [Microplitis demolitor]
XP_008830905	PREDICTED: zinc finger protein 25-like [Nannospalax galili]
XP_008839595	PREDICTED: zinc finger protein 678-like, partial [Nannospalax galili]
XP_008939161	PREDICTED: oocyte zinc finger protein XlCOF6-like, partial [Merops nubicus]
XP_009297399	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Danio rerio]
XP_009298783	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298784	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298796	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Danio rerio]
XP_009298804	PREDICTED: oocyte zinc finger protein XlCOF20-like [Danio rerio]
XP_009298811	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298817	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298832	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298909	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298922	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298936	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009298967	PREDICTED: gastrula zinc finger protein XlCGF57.1-like, partial [Danio rerio]
XP_009299028	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Danio rerio]
XP_009299144	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]
XP_010770885	PREDICTED: gastrula zinc finger protein XlCGF49.1-like, partial [Notothenia coriiceps]
XP_010788499	PREDICTED: zinc finger protein 253-like, partial [Notothenia coriiceps]
XP_010823838	PREDICTED: zinc finger protein 271 [Bos taurus]
XP_010834622	PREDICTED: zinc finger protein 239-like, partial [Bison bison bison]
XP_010947717	PREDICTED: zinc finger protein 25 [Camelus bactrianus]
XP_011065442	PREDICTED: zinc finger protein Gfi-1b-like [Acromyrmex echinatior]
XP_011236492	PREDICTED: gastrula zinc finger protein XlCGF17.1-like isoform X1 [Mus musculus]
XP_011239595	PREDICTED: zinc finger protein 9 isoform X1 [Mus musculus]
XP_011299253	PREDICTED: fez family zinc finger protein 2-like [Fopius arisanus]
XP_011429851	PREDICTED: zinc finger protein OZF-like [Crassostrea gigas]
XP_011559153	PREDICTED: zinc finger protein 708-like isoform X1 [Plutella xylostella]
XP_011618951	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619027	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619519	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011619604	PREDICTED: zinc finger protein 420-like, partial [Takifugu rubripes]
XP_011619649	PREDICTED: zinc finger protein 239-like, partial [Takifugu rubripes]
XP_011666861	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Strongylocentrotus purpuratus]
XP_011678015	PREDICTED: zinc finger protein 84-like isoform X1 [Strongylocentrotus purpuratus]
XP_011678017	PREDICTED: zinc finger protein 84-like isoform X2 [Strongylocentrotus purpuratus]
XP_011875591	PREDICTED: PR domain zinc finger protein 1 [Vollenhovia emeryi]
XP_011877253	PREDICTED: fez family zinc finger protein 2-like isoform X1 [Vollenhovia emeryi]
XP_011877254	PREDICTED: fez family zinc finger protein 2-like isoform X2 [Vollenhovia emeryi]
XP_012009732	PREDICTED: zinc finger protein 271 [Ovis aries musimon]
XP_012168013	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus terrestris]
XP_012171374	PREDICTED: zinc finger protein 628-like isoform X3 [Bombus terrestris]
XP_012246007	PREDICTED: PR domain zinc finger protein 1 isoform X1 [Bombus impatiens]
XP_012250907	PREDICTED: PR domain zinc finger protein 1 [Athalia rosae]
XP_012278412	PREDICTED: fez family zinc finger protein 2-like [Orussus abietinus]
XP_012328510	PREDICTED: zinc finger protein 551 [Aotus nancymaae]

XP_012412262	PREDICTED: zinc finger protein 397-like isoform X3 [Trichechus manatus latirostris]
XP_012413722	PREDICTED: zinc finger protein 678-like [Trichechus manatus latirostris]
XP_012690855	PREDICTED: zinc finger protein 2 homolog, partial [Clupea harengus]
XP_012713485	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Fundulus heteroclitus]
XP_012713622	PREDICTED: zinc finger protein OZF-like [Fundulus heteroclitus]
XP_012808756	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Xenopus (Silurana) tropicalis]
XP_012810455	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xenopus (Silurana) tropicalis]
XP_012871506	PREDICTED: zinc finger protein 420-like isoform X1 [Dipodomys ordii]
XP_012892021	PREDICTED: zinc finger protein 420-like [Dipodomys ordii]
XP_012892236	PREDICTED: zinc finger protein 658-like [Dipodomys ordii]
XP_012981380	PREDICTED: gastrula zinc finger protein XlCGF26.1-like isoform X1 [Mesocricetus auratus]
XP_013197323	PREDICTED: zinc finger protein 84-like [Amyelois transitella]
XP_013391990	PREDICTED: zinc finger protein 652-like isoform X1 [Lingula anatina]
XP_013391991	PREDICTED: zinc finger protein 226-like isoform X2 [Lingula anatina]
XP_013391992	PREDICTED: zinc finger protein 226-like isoform X3 [Lingula anatina]
XP_013407393	PREDICTED: zinc finger protein 2-like [Lingula anatina]
XP_013411523	PREDICTED: zinc finger protein Gfi-1b-like [Lingula anatina]
XP_013763388	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Pundamilia nyererei]
XP_013772409	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013775795	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013777462	PREDICTED: zinc finger protein 251-like [Limulus polyphemus]
XP_013778397	PREDICTED: gastrula zinc finger protein XlCGF7.1-like [Limulus polyphemus]
XP_013779582	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013780438	PREDICTED: PR domain zinc finger protein 1-like [Limulus polyphemus]
XP_013781553	PREDICTED: zinc finger protein 557-like [Limulus polyphemus]
XP_013781817	PREDICTED: PR domain zinc finger protein 1-like [Limulus polyphemus]
XP_013782728	PREDICTED: PR domain zinc finger protein 1-like, partial [Limulus polyphemus]
XP_013783281	PREDICTED: zinc finger protein 227-like [Limulus polyphemus]
XP_013783401	PREDICTED: zinc finger and SCAN domain-containing protein 2-like [Limulus polyphemus]
XP_013784172	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like [Limulus polyphemus]
XP_013784339	PREDICTED: zinc finger protein Gfi-1b-like, partial [Limulus polyphemus]
XP_013785583	PREDICTED: gastrula zinc finger protein XlCGF49.1-like [Limulus polyphemus]
XP_013787012	PREDICTED: zinc finger protein 239-like [Limulus polyphemus]
XP_013788177	PREDICTED: zinc finger protein 184-like, partial [Limulus polyphemus]
XP_013788334	PREDICTED: zinc finger protein 501-like [Limulus polyphemus]
XP_013788396	PREDICTED: zinc finger protein Gfi-1b-like [Limulus polyphemus]
XP_013789480	PREDICTED: zinc finger and SCAN domain-containing protein 21-like [Limulus polyphemus]
XP_013790515	PREDICTED: zinc finger protein 391-like [Limulus polyphemus]
XP_013790651	PREDICTED: zinc finger protein 681-like [Limulus polyphemus]
XP_013793148	PREDICTED: zinc finger protein 436-like, partial [Limulus polyphemus]
XP_013856101	PREDICTED: gastrula zinc finger protein XlCGF8.2DB-like, partial [Austrofundulus limnaeus]
XP_013881864	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Austrofundulus limnaeus]
XP_014000709	PREDICTED: zinc finger protein 2-like, partial [Salmo salar]
XP_014253724	PREDICTED: PR domain zinc finger protein 1 [Cimex lectularius]
XP_014265828	PREDICTED: putative zinc finger protein 724 [Maylandia zebra]
XP_014266230	PREDICTED: zinc finger protein 436 isoform X1 [Maylandia zebra]
XP_014266232	PREDICTED: zinc finger protein 664 isoform X3 [Maylandia zebra]
XP_014273763	PREDICTED: PR domain zinc finger protein 1-like isoform X1 [Halyomorpha halys]
XP_014273768	PREDICTED: PR domain zinc finger protein 1-like isoform X4 [Halyomorpha halys]
XP_014302023	PREDICTED: zinc finger protein 154-like, partial [Myotis lucifugus]
XP_014327757	PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Xiphophorus maculatus]
XP_014381616	PREDICTED: gastrula zinc finger protein XlCGF57.1-like isoform X1 [Alligator sinensis]
XP_014382878	PREDICTED: oocyte zinc finger protein XlCOF6-like [Alligator sinensis]
XP_014388994	PREDICTED: zinc finger protein 420-like [Myotis brandtii]
XP_014398735	PREDICTED: zinc finger protein 2 homolog isoform X2 [Myotis brandtii]
XP_014437399	PREDICTED: zinc finger protein 205 isoform X1 [Tupaia chinensis]
XP_014438089	PREDICTED: zinc finger protein 568 [Tupaia chinensis]
XP_014459563	PREDICTED: oocyte zinc finger protein XlCOF6-like isoform X1 [Alligator mississippiensis]

9.4.2.33 *Sfmbt*

Name	Description
A2A5N8 (LMBL1_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog
B1B1A0 (LMBL4_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 4; Short=L(3)mbt-like protein 4
D3ZWK4 (LMBL1_RAT)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog
E1C2V1 (LMBL1_CHICK)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog
Locus_1_Transcript_36294/166847_Confidence_1.000_Length_3235 - ORF 16 (frame 3) translation	Locus_1_Transcript_36294/166847_Confidence_1.000_Length_3235
Locus_1_Transcript_107630/166847_Confidence_1.000_Length_515 - ORF 1 (frame 1) translation	Locus_1_Transcript_107630/166847_Confidence_1.000_Length_515
Locus_80_Transcript_1/10_Confidence_0.705_Length_5587 - ORF 23 (frame 3) translation	Locus_80_Transcript_1/10_Confidence_0.705_Length_5587
Locus_3961_Transcript_1/10_Confidence_0.560_Length_3782 - ORF 1 (frame 1) translation	Locus_3961_Transcript_1/10_Confidence_0.560_Length_3782
Locus_9806_Transcript_1/6_Confidence_0.118_Length_1952 - ORF 1 (frame 2) translation	Locus_9806_Transcript_1/6_Confidence_0.118_Length_1952
Locus_14174_Transcript_3/3_Confidence_0.778_Length_3230 - ORF 16 (frame 1) translation	Locus_14174_Transcript_3/3_Confidence_0.778_Length_3230
P59178 (LMBL2_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=L(3)mbt-like protein 2
Q1JQD9 (LMBL2_BOVIN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=L(3)mbt-like protein 2
Q3MIF2 (LMBL2_RAT)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=L(3)mbt-like protein 2
Q05BQ5 (MBTD1_HUMAN)	RecName: Full=MBT domain-containing protein 1
Q5DTW2 (SMBT2_MOUSE)	RecName: Full=Scm-like with four MBT domains protein 2
Q5R737 (LMBL2_PONAB)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=L(3)mbt-like protein 2
Q5VUG0 (SMBT2_HUMAN)	RecName: Full=Scm-like with four MBT domains protein 2; Short=Scm-like with 4 MBT domains protein 2
Q6DIN3 (MBTD1_XENTR)	RecName: Full=MBT domain-containing protein 1
Q6P5G3 (MBTD1_MOUSE)	RecName: Full=MBT domain-containing protein 1
Q8BLB7 (LMBL3_MOUSE)	RecName: Full=Lethal(3)malignant brain tumor-like protein 3; Short=L(3)mbt-like protein 3; AltName: Full=MBT-1
Q8K214 (SCMH1_MOUSE)	RecName: Full=Polycomb protein SCMH1; AltName: Full=Sex comb on midleg homolog 1
Q8NA19 (LMBL4_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 4; Short=H-l(3)mbt-like protein 4; Short=L(3)mbt-like protein 4
Q9JMD1 (SMBT1_MOUSE)	RecName: Full=Scm-like with four MBT domains protein 1
Q9JMD2 (SMBT1_RAT)	RecName: Full=Scm-like with four MBT domains protein 1
Q9UHJ3 (SMBT1_HUMAN)	RecName: Full=Scm-like with four MBT domains protein 1; Short=hSFMBT; AltName: Full=Renal ubiquitous protein 1
Q9UQR0 (SCML2_HUMAN)	RecName: Full=Sex comb on midleg-like protein 2
Q9VHA0 (SCM_DROME)	RecName: Full=Polycomb protein Scm; AltName: Full=Sex comb on midleg protein
Q9VK33 (SMBT_DROME)	RecName: Full=Polycomb protein Sfmbt; AltName: Full=Scm-like with four MBT domain-containing protein 1; AltName: Full=dSfmbt
Q9Y468 (LMBL1_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 1; Short=H-l(3)mbt; Short=H-l(3)mbt protein; Short=L(3)mbt-like; AltName: Full=L(3)mbt protein homolog; AltName: Full=L3MBTL1
Q29L50 (SMBT_DROPS)	RecName: Full=Polycomb protein Sfmbt; AltName: Full=Scm-like with four MBT domain-containing protein 1
Q32N90 (MBTD1_XENLA)	RecName: Full=MBT domain-containing protein 1
Q96GD3 (SCMH1_HUMAN)	RecName: Full=Polycomb protein SCMH1; AltName: Full=Sex comb on midleg homolog 1
Q96JM7 (LMBL3_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 3; Short=H-l(3)mbt-like protein 3; Short=L(3)mbt-like protein 3; AltName: Full=MBT-1
Q969R5 (LMBL2_HUMAN)	RecName: Full=Lethal(3)malignant brain tumor-like protein 2; Short=H-l(3)mbt-like protein 2; Short=L(3)mbt-like protein 2
SMBT_DROME	RecName: Full=Polycomb protein Sfmbt; AltName: Full=Scm-like with four MBT domain-containing protein 1; AltName: Full=dSfmbt
XP_003690787	PREDICTED: polycomb protein Sfmbt-like isoform X3 [Apis florea]
XP_003703228	PREDICTED: polycomb protein Sfmbt-like isoform X3 [Megachile rotundata]
XP_004712682	PREDICTED: scm-like with four MBT domains protein 2 [Echinops telfairi]
XP_005111500	PREDICTED: scm-like with four MBT domains protein 1 [Aplysia californica]
XP_005112062	PREDICTED: lethal(3)malignant brain tumor-like protein 1 [Aplysia californica]

XP_006610729	PREDICTED: polycomb protein Sfmbt-like isoform X3 [Apis dorsata]
XP_006774275	PREDICTED: MBT domain-containing protein 1 isoform X7 [Myotis davidii]
XP_006815581	PREDICTED: MBT domain-containing protein 1-like [Saccoglossus kowalevskii]
XP_007639850	PREDICTED: scm-like with four MBT domains protein 2 isoform X1 [Cricetulus griseus]
XP_007899831	PREDICTED: lethal(3)malignant brain tumor-like protein 1 isoform X1 [Callorhinchus milii]
XP_007899832	PREDICTED: lethal(3)malignant brain tumor-like protein 1 isoform X2 [Callorhinchus milii]
XP_008009626	PREDICTED: MBT domain-containing protein 1 isoform X8 [Chlorocebus sabaeus]
XP_009472429	PREDICTED: MBT domain-containing protein 1 [Nipponia nippon]
XP_010140884	PREDICTED: MBT domain-containing protein 1 [Buceros rhinoceros silvestris]
XP_011153427	PREDICTED: polycomb protein Scm [Harpegnathos saltator]
XP_011233640	PREDICTED: scm-like with four MBT domains protein 2 isoform X2 [Ailuropoda melanoleuca]
XP_011262299	PREDICTED: polycomb protein Scm-like isoform X1 [Camponotus floridanus]
XP_011311111	PREDICTED: polycomb protein Scm isoform X1 [Fopius arisanus]
XP_011311114	PREDICTED: polycomb protein Scm isoform X2 [Fopius arisanus]
XP_011311274	PREDICTED: polycomb protein Sfmbt-like isoform X1 [Fopius arisanus]
XP_011311275	PREDICTED: polycomb protein Sfmbt-like isoform X2 [Fopius arisanus]
XP_011311276	PREDICTED: polycomb protein Sfmbt-like isoform X3 [Fopius arisanus]
XP_011345449	PREDICTED: polycomb protein Scm isoform X1 [Cerapachys biroi]
XP_011345450	PREDICTED: polycomb protein Scm isoform X2 [Cerapachys biroi]
XP_011345451	PREDICTED: polycomb protein Scm isoform X3 [Cerapachys biroi]
XP_011434914	PREDICTED: MBT domain-containing protein 1-like isoform X1 [Crassostrea gigas]
XP_011434915	PREDICTED: MBT domain-containing protein 1-like isoform X2 [Crassostrea gigas]
XP_011437622	PREDICTED: scm-like with four MBT domains protein 1 [Crassostrea gigas]
XP_011499412	PREDICTED: polycomb protein Scm [Ceratosolen solmsi marchali]
XP_011555628	PREDICTED: polycomb protein Scm [Plutella xylostella]
XP_012140346	PREDICTED: polycomb protein Sfmbt-like isoform X1 [Megachile rotundata]
XP_012140347	PREDICTED: polycomb protein Sfmbt-like isoform X2 [Megachile rotundata]
XP_012140348	PREDICTED: polycomb protein Sfmbt-like isoform X4 [Megachile rotundata]
XP_013068780	PREDICTED: scm-like with four MBT domains protein 1 [Biomphalaria glabrata]
XP_013138251	PREDICTED: polycomb protein Scm [Papilio polytes]
XP_013159670	PREDICTED: MBT domain-containing protein 1 isoform X4 [Falco peregrinus]
XP_013173235	PREDICTED: polycomb protein Scm isoform X1 [Papilio xuthus]
XP_013173236	PREDICTED: polycomb protein Scm isoform X2 [Papilio xuthus]
XP_013193158	PREDICTED: polycomb protein Scm [Amyelois transitella]
XP_013400962	PREDICTED: MBT domain-containing protein 1-like [Lingula anatina]
XP_013413115	PREDICTED: MBT domain-containing protein 1-like [Lingula anatina]
XP_013413833	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X1 [Lingula anatina]
XP_013413836	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X2 [Lingula anatina]
XP_013413837	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X3 [Lingula anatina]
XP_013413838	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X4 [Lingula anatina]
XP_013413839	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X5 [Lingula anatina]
XP_013413840	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X6 [Lingula anatina]
XP_013416831	PREDICTED: scm-like with four MBT domains protein 1 isoform X1 [Lingula anatina]
XP_013416832	PREDICTED: scm-like with four MBT domains protein 1 isoform X2 [Lingula anatina]
XP_013416834	PREDICTED: scm-like with four MBT domains protein 1 isoform X3 [Lingula anatina]
XP_013775899	PREDICTED: polycomb protein SCMH1-like isoform X1 [Limulus polyphemus]
XP_013775900	PREDICTED: polycomb protein SCMH1-like isoform X2 [Limulus polyphemus]

XP_013777489	PREDICTED: lethal(3)malignant brain tumor-like protein 3 [Limulus polyphemus]
XP_013790123	PREDICTED: polycomb protein Sfmbt-like, partial [Limulus polyphemus]
XP_013794742	PREDICTED: scm-like with four MBT domains protein 1 [Limulus polyphemus]
XP_014362281	PREDICTED: polycomb protein Scm-like, partial [Papilio machaon]
XP_014369648	PREDICTED: polycomb protein Scm [Papilio machaon]

9.4.2.34 *Tailless*

Name	Description
A0JNE3 (NR2C1_BOVIN)	RecName: Full=Nuclear receptor subfamily 2 group C member 1
A0P8Z4 (NR6A1_PIG)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF
A2T929 (RXRAA_DANRE)	RecName: Full=Retinoic acid receptor RXR-alpha-A; AltName: Full=Nuclear receptor subfamily 2 group B member 1-A; AltName: Full=RXRalpha-B; AltName: Full=Retinoid X receptor alpha-A
Locus_1_Transcript_93285/166847_Confidence_1.000_Length_2349 - ORF 4 (frame 2) translation	Locus_1_Transcript_93285/166847_Confidence_1.000_Length_2349
Locus_1_Transcript_103152/166847_Confidence_1.000_Length_1031 - ORF 1 (frame 1) translation	Locus_1_Transcript_103152/166847_Confidence_1.000_Length_1031
Locus_1_Transcript_127749/166847_Confidence_1.000_Length_1201 - ORF 1 (frame 1) translation	Locus_1_Transcript_127749/166847_Confidence_1.000_Length_1201
Locus_1_Transcript_150272/166847_Confidence_1.000_Length_796 - ORF 1 (frame 1) translation	Locus_1_Transcript_150272/166847_Confidence_1.000_Length_796
Locus_1_Transcript_160064/166847_Confidence_1.000_Length_647 - ORF 3 (frame 1) translation	Locus_1_Transcript_160064/166847_Confidence_1.000_Length_647
Locus_1_Transcript_160066/166847_Confidence_1.000_Length_2134 - ORF 1 (frame 1) translation	Locus_1_Transcript_160066/166847_Confidence_1.000_Length_2134
Locus_135_Transcript_1/1_Confidence_1.000_Length_2330 - ORF 11 (frame 2) translation	Locus_135_Transcript_1/1_Confidence_1.000_Length_2330
Locus_1578_Transcript_50/50_Confidence_0.206_Length_2629 - ORF 14 (frame 1) translation	Locus_1578_Transcript_50/50_Confidence_0.206_Length_2629
Locus_2687_Transcript_14/15_Confidence_0.351_Length_5316 - ORF 31 (frame 3) translation	Locus_2687_Transcript_14/15_Confidence_0.351_Length_5316
Locus_8845_Transcript_10/10_Confidence_0.333_Length_5198 - ORF 27 (frame 1) translation	Locus_8845_Transcript_10/10_Confidence_0.333_Length_5198
Locus_9245_Transcript_9/9_Confidence_0.558_Length_8055 - ORF 8 (frame 3) translation	Locus_9245_Transcript_9/9_Confidence_0.558_Length_8055
Locus_16110_Transcript_7/11_Confidence_0.258_Length_4798 - ORF 23 (frame 3) translation	Locus_16110_Transcript_7/11_Confidence_0.258_Length_4798
Locus_16881_Transcript_2/2_Confidence_0.750_Length_2443 - ORF 4 (frame 1) translation	Locus_16881_Transcript_2/2_Confidence_0.750_Length_2443
Locus_16921_Transcript_5/5_Confidence_0.706_Length_1884 - ORF 5 (frame 1) translation	Locus_16921_Transcript_5/5_Confidence_0.706_Length_1884
Locus_18435_Transcript_2/8_Confidence_0.560_Length_8582 - ORF 3 (frame 3) translation	Locus_18435_Transcript_2/8_Confidence_0.560_Length_8582
Locus_24628_Transcript_6/6_Confidence_0.667_Length_2451 - ORF 1 (frame 2) translation	Locus_24628_Transcript_6/6_Confidence_0.667_Length_2451
NP_001135390	ecdysone receptor isoform B [Tribolium castaneum]
NP_001135406	estrogen-related receptor [Tribolium castaneum]
NP_001158447	photoreceptor-specific nuclear receptor protein [Saccoglossus kowalevskii]
NR2E1_MOUSE	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=mTll
O00482 (NR5A2_HUMAN)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=Alpha-1-fetoprotein transcription factor; AltName: Full=B1-binding factor; Short=hB1F; AltName: Full=CYP7A promoter-binding factor; AltName: Full=Hepatocytic transcription factor; AltName: Full=Liver receptor homolog 1; Short=LRH-1
O09018 (COT2_RAT)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=Apolipoprotein A-I regulatory protein 1; Short=ARP-1; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=COUPb; AltName: Full=Nuclear receptor subfamily 2 group F member 2; AltName: Full=Ovalbumin upstream promoter beta nuclear receptor
O16845 (TLL_DROVI)	RecName: Full=Protein tailless; AltName: Full=Nuclear receptor subfamily 2 group E member 2
O18473 (ECR_HELVI)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=HvEcR; AltName: Full=Nuclear receptor subfamily 1 group H member 1
O18531 (ECR_LUCCU)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1

O42101 (NR5A2_CHICK)	RecName: Full=Nuclear receptor subfamily 5 group A member 2; AltName: Full=FTF/LRH-1; AltName: Full=OR2.0
O77245 (E75_METEN)	RecName: Full=Nuclear hormone receptor E75; AltName: Full=Nuclear receptor subfamily 1 group D member 3
O95718 (ERR2_HUMAN)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=ERR beta-2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
P03372 (ESR1_HUMAN)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P06211 (ESR1_RAT)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P10589 (COT1_HUMAN)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1; AltName: Full=V-erbA-related protein 3; Short=EAR-3
P10826 (RARB_HUMAN)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=HBV-activated protein; AltName: Full=Nuclear receptor subfamily 1 group B member 2; AltName: Full=RAR-epsilon
P11474 (ERR1_HUMAN)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen receptor-like 1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1
P11475 (ERR2_RAT)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
P13055 (E75BB_DROME)	RecName: Full=Ecdysone-induced protein 75B, isoform B; AltName: Full=E75-C; AltName: Full=Nuclear receptor subfamily 1 group D member 3, isoform B
P13056 (NR2C1_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2
P16375 (7UP1_DROME)	RecName: Full=Steroid receptor seven-up, isoforms B/C; AltName: Full=Nuclear receptor subfamily 2 group F member 3, isoforms B/C
P17671 (E75BC_DROME)	RecName: Full=Ecdysone-induced protein 75B, isoforms C/D; AltName: Full=E75-A; AltName: Full=Nuclear receptor subfamily 1 group D member 3, isoforms C/D
P18102 (TLL_DROME)	RecName: Full=Protein tailless; AltName: Full=Nuclear receptor subfamily 2 group E member 2
P18514 (RARA_NOTVI)	RecName: Full=Retinoic acid receptor alpha; Short=RAR-alpha; AltName: Full=Nuclear receptor subfamily 1 group B member 1
P19785 (ESR1_MOUSE)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P19793 (RXRA_HUMAN)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
P22448 (RARB_CHICK)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
P22605 (RARB_MOUSE)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
P24468 (COT2_HUMAN)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=Apolipoprotein A-I regulatory protein 1; Short=ARP-1; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
P28700 (RXRA_MOUSE)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
P28701 (RXRG_CHICK)	RecName: Full=Retinoic acid receptor RXR-gamma; AltName: Full=Nuclear receptor subfamily 2 group B member 3; AltName: Full=Retinoid X receptor gamma
P28702 (RXRB_HUMAN)	RecName: Full=Retinoic acid receptor RXR-beta; AltName: Full=Nuclear receptor subfamily 2 group B member 2; AltName: Full=Retinoid X receptor beta
P34021 (ECR_DROME)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P45447 (E78C_DROME)	RecName: Full=Ecdysone-induced protein 78C; Short=DR-78; AltName: Full=Nuclear receptor subfamily 1 group E member 1
P45447 (E78C_DROME)	RecName: Full=Ecdysone-induced protein 78C; Short=DR-78; AltName: Full=Nuclear receptor subfamily 1 group E member 1
P49116 (NR2C2_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group C member 2; AltName: Full=Orphan nuclear receptor TAK1; AltName: Full=Orphan nuclear receptor TR4; AltName: Full=Testicular receptor 4

P49117 (NR2C2_MOUSE)	RecName: Full=Nuclear receptor subfamily 2 group C member 2; AltName: Full=Orphan nuclear receptor TAK1; AltName: Full=Orphan nuclear receptor TR4; AltName: Full=Testicular receptor 4
P49743 (RXRB_RAT)	RecName: Full=Retinoic acid receptor RXR-beta; AltName: Full=Nuclear receptor coregulator 1; AltName: Full=Nuclear receptor subfamily 2 group B member 2; AltName: Full=Retinoid X receptor beta
P49880 (ECR_AEDAE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; Short=AaEcR; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49881 (ECR_BOMMO)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49882 (ECR_CHITE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49883 (ECR_MANSE)	RecName: Full=Ecdysone receptor; AltName: Full=20-hydroxy-ecdysone receptor; Short=20E receptor; AltName: Full=EcRH; AltName: Full=Ecdysteroid receptor; AltName: Full=Nuclear receptor subfamily 1 group H member 1
P49884 (ESR1_BOVIN)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
P51128 (RXRA_XENLA)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
P55094 (NR2C2_RAT)	RecName: Full=Nuclear receptor subfamily 2 group C member 2; AltName: Full=Orphan nuclear receptor TR4; AltName: Full=Testicular receptor 4
P57781 (ESR2_MICUN)	RecName: Full=Estrogen receptor beta; Short=ER-beta; AltName: Full=Nuclear receptor subfamily 3 group A member 2
P62510 (ERR3_RAT)	RecName: Full=Estrogen-related receptor gamma; AltName: Full=Estrogen receptor-related protein 3; AltName: Full=Nuclear receptor subfamily 3 group B member 3
P70033 (NR6A1_XENLA)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=xGCNF
P70052 (NR2E1_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=xTLL
Q4V8R7 (GCNFB_DANRE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1-B; AltName: Full=Germ cell nuclear factor B; Short=GCNF-B
Q4V8R7 (GCNFB_DANRE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1-B; AltName: Full=Germ cell nuclear factor B; Short=GCNF-B
Q5E9B6 (NR1H3_BOVIN)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3
Q5I7G2 (RXR_LYMST)	RecName: Full=Retinoic acid receptor RXR; AltName: Full=Retinoid X receptor; Short=LymRXR
Q5QJV7 (ERR1_RAT)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1
Q5RAM2 (ERR3_PONAB)	RecName: Full=Estrogen-related receptor gamma; AltName: Full=Estrogen receptor-related protein 3; AltName: Full=Nuclear receptor subfamily 3 group B member 3
Q5TJF7 (RXRB_CANFA)	RecName: Full=Retinoic acid receptor RXR-beta; AltName: Full=Nuclear receptor subfamily 2 group B member 2; AltName: Full=Retinoid X receptor beta
Q6DHP9 (RXRGB_DANRE)	RecName: Full=Retinoic acid receptor RXR-gamma-B; AltName: Full=Nuclear receptor subfamily 2 group B member 3-B; AltName: Full=Retinoid X receptor gamma-B
Q6GN21 (N2C1A_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1-A; AltName: Full=Developmental orphan receptor 2-A; Short=DOR2-A; Short=xDOR2-A; AltName: Full=Orphan nuclear receptor TR2-A; AltName: Full=Testicular receptor 2-A
Q6PH18 (N2F1B_DANRE)	RecName: Full=Nuclear receptor subfamily 2 group F member 1-B; AltName: Full=COUP transcription factor 1-B; Short=COUP-TFalpha-B
Q6QMY5 (ERR1_CANFA)	RecName: Full=Steroid hormone receptor ERR1; AltName: Full=Estrogen-related receptor alpha; Short=ERR-alpha; AltName: Full=Nuclear receptor subfamily 3 group B member 1
Q8T5C6 (RXR_BIOGL)	RecName: Full=Retinoic acid receptor RXR; AltName: Full=RXR-like protein; AltName: Full=Retinoid X receptor; Short=BgRXR
Q9PU65 (GCNFA_DANRE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1-A; AltName: Full=Germ cell nuclear factor A; Short=GCNF-A; Short=zfGCNF
Q9QXZ7 (NR2E3_MOUSE)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor

Q9QZJ5 (ESR1_MESAU)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
Q9TTF0 (NR2E3_BOVIN)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor
Q9TTR7 (COT2_BOVIN)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
Q9TTR8 (COT1_BOVIN)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1
Q9U2R6 (NHR91_CAEEL)	RecName: Full=Nuclear hormone receptor family member nhr-91
Q9W6B3 (RARB_COTJA)	RecName: Full=Retinoic acid receptor beta; Short=RAR-beta; AltName: Full=Nuclear receptor subfamily 1 group B member 2
Q9W539 (HR4_DROME)	RecName: Full=Hormone receptor 4; Short=dHR4; AltName: Full=Nuclear receptor subfamily 6 group A member 2
Q9W539 (HR4_DROME)	RecName: Full=Hormone receptor 4; Short=dHR4; AltName: Full=Nuclear receptor subfamily 6 group A member 2
Q9W539 (HR4_DROME)	RecName: Full=Hormone receptor 4; Short=dHR4; AltName: Full=Nuclear receptor subfamily 6 group A member 2
Q9Y5X4 (NR2E3_HUMAN)	RecName: Full=Photoreceptor-specific nuclear receptor; AltName: Full=Nuclear receptor subfamily 2 group E member 3; AltName: Full=Retina-specific nuclear receptor
Q9Y466 (NR2E1_HUMAN)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=hTll
Q9YGL3 (NR2E1_ORYLA)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll
Q9Z0Y9 (NR1H3_MOUSE)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3
Q28CK1 (NR2C1_XENTR)	RecName: Full=Nuclear receptor subfamily 2 group C member 1; AltName: Full=Developmental orphan receptor 2; Short=DOR2; AltName: Full=Orphan nuclear receptor TR2; AltName: Full=Testicular receptor 2
Q53AD2 (ESR1_FELCA)	RecName: Full=Estrogen receptor; Short=ER; AltName: Full=ER-alpha; AltName: Full=Estradiol receptor; AltName: Full=Nuclear receptor subfamily 3 group A member 1
Q66J63 (N2C1B_XENLA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1-B; AltName: Full=Developmental orphan receptor 2-B; Short=DOR2-B; Short=xDOR2-B; AltName: Full=Orphan nuclear receptor TR2-B; AltName: Full=Testicular receptor 2-B
Q66JK1 (NR6A1_XENTR)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF
Q95K90 (NR2C1_MACFA)	RecName: Full=Nuclear receptor subfamily 2 group C member 1
Q05192 (FTF1B_DROME)	RecName: Full=Nuclear hormone receptor FTZ-F1 beta; AltName: Full=Nuclear hormone receptor HR39; Short=dHR39; AltName: Full=Nuclear receptor subfamily 5 group B member 1
Q05343 (RXRA_RAT)	RecName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Nuclear receptor subfamily 2 group B member 1; AltName: Full=Retinoid X receptor alpha
Q06725 (N2F1A_DANRE)	RecName: Full=Nuclear receptor subfamily 2 group F member 1-A; AltName: Full=COUP transcription factor 1-A; Short=COUP-TFalpha-A; Short=zCOUP-TFI; AltName: Full=Seven-up related 44; Short=Svp[44]; Short=zSvp[44]; AltName: Full=Steroid receptor homolog SVP 44
Q08893 (E75_MANSE)	RecName: Full=Ecdysone-inducible protein E75; AltName: Full=Nuclear receptor subfamily 1 group D member 3
Q15406 (NR6A1_HUMAN)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=hGCNF; AltName: Full=Retinoid receptor-related testis-specific receptor; Short=RTR; Short=hRTR
Q26622 (SHR2_STRPU)	RecName: Full=Orphan steroid hormone receptor 2; AltName: Full=SpSHR2
Q60632 (COT1_MOUSE)	RecName: Full=COUP transcription factor 1; Short=COUP-TF1; AltName: Full=COUP transcription factor I; Short=COUP-TF I; AltName: Full=Nuclear receptor subfamily 2 group F member 1; AltName: Full=V-erbA-related protein 3; Short=EAR-3
Q61539 (ERR2_MOUSE)	RecName: Full=Steroid hormone receptor ERR2; AltName: Full=Estrogen receptor-like 2; AltName: Full=Estrogen-related receptor beta; Short=ERR-beta; AltName: Full=Nuclear receptor subfamily 3 group B member 2
Q62685 (NR1H3_RAT)	RecName: Full=Oxysterols receptor LXR-alpha; AltName: Full=Liver X receptor alpha; AltName: Full=Nuclear receptor subfamily 1 group H member 3; AltName: Full=RLD-1
Q64104 (NR2E1_MOUSE)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll; Short=mTll

Q64249 (NR6A1_MOUSE)	RecName: Full=Nuclear receptor subfamily 6 group A member 1; AltName: Full=Germ cell nuclear factor; Short=GCNF; Short=mGCNF; AltName: Full=Retinoid receptor-related testis-specific receptor; Short=RTR
Q90415 (RXRAB_DANRE)	RecName: Full=Retinoic acid receptor RXR-alpha-B; AltName: Full=Nuclear receptor subfamily 2 group B member 1-B; AltName: Full=Retinoid X receptor alpha-B
Q90416 (RXRGA_DANRE)	RecName: Full=Retinoic acid receptor RXR-gamma-A; AltName: Full=Nuclear receptor subfamily 2 group B member 3-A; AltName: Full=Retinoic acid receptor RXR-alpha; AltName: Full=Retinoid X receptor alpha; AltName: Full=Retinoid X receptor gamma-A
Q90733 (COT2_CHICK)	RecName: Full=COUP transcription factor 2; Short=COUP-TF2; AltName: Full=COUP transcription factor II; Short=COUP-TF II; AltName: Full=Nuclear receptor subfamily 2 group F member 2
Q91379 (NR2E1_CHICK)	RecName: Full=Nuclear receptor subfamily 2 group E member 1; AltName: Full=Nuclear receptor TLX; AltName: Full=Protein tailless homolog; Short=Tll
SEQUENCE_208126775_length_345 - ORF 1 (frame 2) translation	SEQUENCE_208126775_length_345
TLL_DROME	RecName: Full=Protein tailless; AltName: Full=Nuclear receptor subfamily 2 group E member 2
XP_974320	PREDICTED: hormone receptor 4 isoform X1 [Tribolium castaneum]
XP_001607668	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Nasonia vitripennis]
XP_001945726	PREDICTED: hormone receptor 4 isoform X1 [Acyrthosiphon pisum]
XP_001947027	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Acyrthosiphon pisum]
XP_002405625	AamEcRA1, putative [Ixodes scapularis]
XP_002411276	retinoid X receptor, putative [Ixodes scapularis]
XP_002423135	conserved hypothetical protein [Pediculus humanus corporis]
XP_002425386	orphan nuclear receptor nr6a1, putative [Pediculus humanus corporis]
XP_002427418	Ecdysone receptor, putative [Pediculus humanus corporis]
XP_002427577	Orphan nuclear receptor NR2E1, putative [Pediculus humanus corporis]
XP_002431237	retinoid X receptor, putative [Pediculus humanus corporis]
XP_002432637	Orphan nuclear receptor NR6A1, putative [Pediculus humanus corporis]
XP_002435070	retinoid X receptor, putative, partial [Ixodes scapularis]
XP_002740657	PREDICTED: photoreceptor-specific nuclear receptor-like [Saccoglossus kowalevskii]
XP_003240033	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Acyrthosiphon pisum]
XP_003397992	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X4 [Bombus terrestris]
XP_003700030	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X1 [Megachile rotundata]
XP_003738496	PREDICTED: ecdysone receptor-like [Metaseiulus occidentalis]
XP_003739292	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Metaseiulus occidentalis]
XP_003739866	PREDICTED: photoreceptor-specific nuclear receptor-like [Metaseiulus occidentalis]
XP_004944783	PREDICTED: nuclear receptor subfamily 2 group C member 2 isoform X12 [Gallus gallus]
XP_004944785	PREDICTED: nuclear receptor subfamily 2 group C member 2 isoform X14 [Gallus gallus]
XP_006561614	PREDICTED: ultraspiracle isoform X6 [Apis mellifera]
XP_007253126	PREDICTED: retinoic acid receptor RXR-beta-A-like isoform X4 [Astyanax mexicanus]
XP_007253127	PREDICTED: retinoic acid receptor RXR-beta-A-like isoform X5 [Astyanax mexicanus]
XP_007908162	PREDICTED: photoreceptor-specific nuclear receptor [Callorhinchus milii]
XP_008181367	PREDICTED: photoreceptor-specific nuclear receptor isoform X2 [Acyrthosiphon pisum]
XP_008182814	PREDICTED: hormone receptor 4 isoform X2 [Acyrthosiphon pisum]
XP_008182816	PREDICTED: hormone receptor 4 isoform X3 [Acyrthosiphon pisum]
XP_008184758	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Acyrthosiphon pisum]
XP_008191947	PREDICTED: nuclear hormone receptor FTZ-F1 beta [Tribolium castaneum]
XP_008197634	PREDICTED: ecdysone receptor isoform X3 [Tribolium castaneum]
XP_008200485	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Tribolium castaneum]
XP_008201026	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Tribolium castaneum]
XP_008201137	PREDICTED: hormone receptor 4 isoform X2 [Tribolium castaneum]
XP_008201140	PREDICTED: hormone receptor 4 isoform X3 [Tribolium castaneum]
XP_008395875	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Poecilia reticulata]

XP_008550031	PREDICTED: nuclear receptor subfamily 2 group E member 1 isoform X1 [Microplitis demolitor]
XP_008550032	PREDICTED: nuclear receptor subfamily 2 group E member 1 isoform X2 [Microplitis demolitor]
XP_008552883	PREDICTED: COUP transcription factor 2 isoform X3 [Microplitis demolitor]
XP_009809839	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Gavia stellata]
XP_009866698	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Apaloderma vittatum]
XP_009955627	PREDICTED: retinoic acid receptor RXR-alpha, partial [Leptosomus discolor]
XP_009990063	PREDICTED: retinoic acid receptor RXR-alpha, partial [Tauraco erythrolophus]
XP_010078332	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Pterocles gutturalis]
XP_010114982	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Chlamydotis macqueenii]
XP_010161045	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Caprimulgus carolinensis]
XP_010212422	PREDICTED: nuclear receptor subfamily 2 group C member 2, partial [Tinamus guttatus]
XP_010223528	PREDICTED: retinoic acid receptor RXR-alpha [Tinamus guttatus]
XP_010717088	PREDICTED: nuclear receptor subfamily 2 group C member 2 isoform X2 [Meleagris gallopavo]
XP_010952755	PREDICTED: retinoic acid receptor RXR-alpha [Camelus bactrianus]
XP_011057053	PREDICTED: photoreceptor-specific nuclear receptor-like [Acromyrmex echinatior]
XP_011057173	PREDICTED: steroid hormone receptor ERR1 isoform X6 [Acromyrmex echinatior]
XP_011060517	PREDICTED: steroid receptor seven-up, isoforms B/C [Acromyrmex echinatior]
XP_011158392	PREDICTED: COUP transcription factor 2-like [Solenopsis invicta]
XP_011161611	PREDICTED: steroid hormone receptor ERR1 isoform X2 [Solenopsis invicta]
XP_011297141	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Fopius arisanus]
XP_011416690	PREDICTED: photoreceptor-specific nuclear receptor-like [Crassostrea gigas]
XP_011438581	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Crassostrea gigas]
XP_011438583	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Crassostrea gigas]
XP_011643932	PREDICTED: steroid receptor seven-up, isoforms B/C isoform X2 [Pogonomyrmex barbatus]
XP_011644942	PREDICTED: steroid hormone receptor ERR2 isoform X6 [Pogonomyrmex barbatus]
XP_011691548	PREDICTED: photoreceptor-specific nuclear receptor-like [Wasmannia auropunctata]
XP_011696829	PREDICTED: steroid hormone receptor ERR2 isoform X3 [Wasmannia auropunctata]
XP_011867578	PREDICTED: steroid hormone receptor ERR1 isoform X5 [Vollenhovia emeryi]
XP_012140861	PREDICTED: steroid receptor seven-up, isoforms B/C, partial [Megachile rotundata]
XP_012149379	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X2 [Megachile rotundata]
XP_012149394	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X4 [Megachile rotundata]
XP_012167646	PREDICTED: retinoic acid receptor RXR-alpha-B isoform X2 [Bombus terrestris]
XP_012168333	PREDICTED: photoreceptor-specific nuclear receptor [Bombus terrestris]
XP_012174781	PREDICTED: steroid receptor seven-up, isoforms B/C [Bombus terrestris]
XP_012220015	PREDICTED: COUP transcription factor 2 isoform X2 [Linepithema humile]
XP_012253056	PREDICTED: ecdysone receptor isoform X3 [Athalia rosae]
XP_012253818	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Athalia rosae]
XP_012258841	PREDICTED: ecdysone-induced protein 78C [Athalia rosae]
XP_012261633	PREDICTED: photoreceptor-specific nuclear receptor [Athalia rosae]
XP_012261783	PREDICTED: steroid receptor seven-up, isoforms B/C [Athalia rosae]
XP_012271939	PREDICTED: nuclear receptor subfamily 2 group F member 1-A isoform X2 [Orussus abietinus]
XP_012274210	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Orussus abietinus]
XP_012526425	PREDICTED: steroid hormone receptor ERR2 isoform X6 [Monomorium pharaonis]

XP_012542052	PREDICTED: steroid receptor seven-up, isoforms B/C [Monomorium pharaonis]
XP_012722686	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Fundulus heteroclitus]
XP_013064092	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Biomphalaria glabrata]
XP_013068647	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Biomphalaria glabrata]
XP_013071146	PREDICTED: photoreceptor-specific nuclear receptor-like [Biomphalaria glabrata]
XP_013398470	PREDICTED: photoreceptor-specific nuclear receptor-like [Lingula anatina]
XP_013412829	PREDICTED: nuclear receptor subfamily 2 group E member 1-like isoform X1 [Lingula anatina]
XP_013412830	PREDICTED: nuclear receptor subfamily 2 group E member 1-like isoform X2 [Lingula anatina]
XP_013417773	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Lingula anatina]
XP_013772732	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013773938	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013774562	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013774626	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013774988	PREDICTED: nuclear receptor subfamily 2 group F member 1-A-like [Limulus polyphemus]
XP_013775080	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013775116	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013776718	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013777087	PREDICTED: steroid hormone receptor ERR1-like [Limulus polyphemus]
XP_013777259	PREDICTED: retinoic acid receptor RXR-alpha-B-like [Limulus polyphemus]
XP_013777746	PREDICTED: nuclear receptor subfamily 2 group C member 2-like [Limulus polyphemus]
XP_013778961	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013779572	PREDICTED: retinoic acid receptor RXR-alpha-A-like [Limulus polyphemus]
XP_013780022	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013780031	PREDICTED: photoreceptor-specific nuclear receptor-like [Limulus polyphemus]
XP_013781709	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013782694	PREDICTED: ecdysone-induced protein 78C-like [Limulus polyphemus]
XP_013783147	PREDICTED: retinoic acid receptor RXR-alpha-like [Limulus polyphemus]
XP_013783568	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013784132	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013785406	PREDICTED: photoreceptor-specific nuclear receptor-like [Limulus polyphemus]
XP_013785695	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013786915	PREDICTED: ecdysone-induced protein 78C-like, partial [Limulus polyphemus]
XP_013787145	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013787753	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013788321	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013788546	PREDICTED: ecdysone receptor-like [Limulus polyphemus]
XP_013789030	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013790435	PREDICTED: nuclear receptor subfamily 2 group E member 1-like [Limulus polyphemus]
XP_013792436	PREDICTED: nuclear hormone receptor FTZ-F1 beta-like [Limulus polyphemus]
XP_013794047	PREDICTED: photoreceptor-specific nuclear receptor-like [Limulus polyphemus]
XP_013794283	PREDICTED: hormone receptor 4-like [Limulus polyphemus]
XP_013865465	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Austrofundulus limnaeus]
XP_013874082	PREDICTED: photoreceptor-specific nuclear receptor-like, partial [Austrofundulus limnaeus]
XP_013927492	PREDICTED: retinoic acid receptor RXR-beta [Thamnophis sirtalis]
XP_014207935	PREDICTED: steroid receptor seven-up, isoforms B/C-like [Copidosoma floridanum]

XP_014229050	PREDICTED: steroid hormone receptor ERR2 isoform X5 [Trichogramma pretiosum]
XP_014247347	PREDICTED: photoreceptor-specific nuclear receptor-like [Cimex lectularius]
XP_014251567	PREDICTED: hormone receptor 4-like isoform X1 [Cimex lectularius]
XP_014251568	PREDICTED: hormone receptor 4-like isoform X2 [Cimex lectularius]
XP_014251569	PREDICTED: hormone receptor 4-like isoform X3 [Cimex lectularius]
XP_014261639	PREDICTED: ecdysone-induced protein 78C isoform X1 [Cimex lectularius]
XP_014261640	PREDICTED: ecdysone-induced protein 78C isoform X2 [Cimex lectularius]
XP_014261641	PREDICTED: ecdysone-induced protein 78C isoform X3 [Cimex lectularius]
XP_014261642	PREDICTED: ecdysone-induced protein 78C isoform X4 [Cimex lectularius]
XP_014276610	PREDICTED: nuclear receptor subfamily 2 group E member 1 [Halyomorpha halys]
XP_014277550	PREDICTED: photoreceptor-specific nuclear receptor-like [Halyomorpha halys]
XP_014281743	PREDICTED: ecdysone receptor isoform X1 [Halyomorpha halys]
XP_014286561	PREDICTED: hormone receptor 4 isoform X4 [Halyomorpha halys]
XP_014286562	PREDICTED: hormone receptor 4 isoform X5 [Halyomorpha halys]
XP_014286563	PREDICTED: hormone receptor 4 isoform X6 [Halyomorpha halys]
XP_014291406	PREDICTED: ecdysone-induced protein 78C [Halyomorpha halys]

9.4.2.35 *Trithorax*

Name	Description
A7E2Z2 (EZH1_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase EZH1; AltName: Full=Enhancer of zeste homolog 1
C6KTD2 (SET1_PLAF7)	RecName: Full=Putative histone-lysine N-methyltransferase 1; Short=PfSET1
E9Q5F9 (SETD2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETD2; AltName: Full=Lysine N-methyltransferase 3A; AltName: Full=SET domain-containing protein 2
Locus_1_Transcript_59871/166847_Confidence_1.000_Length_1692 - ORF 12 (frame 2) translation	Locus_1_Transcript_59871/166847_Confidence_1.000_Length_1692
Locus_1_Transcript_119592/166847_Confidence_1.000_Length_638 - ORF 3 (frame 2) translation	Locus_1_Transcript_119592/166847_Confidence_1.000_Length_638
Locus_1_Transcript_132989/166847_Confidence_1.000_Length_2020 - ORF 8 (frame 3) translation	Locus_1_Transcript_132989/166847_Confidence_1.000_Length_2020
Locus_81_Transcript_58/63_Confidence_0.130_Length_4613 - ORF 3 (frame 1) translation	Locus_81_Transcript_58/63_Confidence_0.130_Length_4613
Locus_690_Transcript_2/11_Confidence_0.406_Length_11086 - ORF 58 (frame 2) translation	Locus_690_Transcript_2/11_Confidence_0.406_Length_11086
Locus_1984_Transcript_1/5_Confidence_0.591_Length_2911 - ORF 13 (frame 1) translation	Locus_1984_Transcript_1/5_Confidence_0.591_Length_2911
Locus_7116_Transcript_1/8_Confidence_0.615_Length_8437 - ORF 2 (frame 1) translation	Locus_7116_Transcript_1/8_Confidence_0.615_Length_8437
Locus_7644_Transcript_3/9_Confidence_0.484_Length_3144 - ORF 1 (frame 1) translation	Locus_7644_Transcript_3/9_Confidence_0.484_Length_3144
Locus_11760_Transcript_19/20_Confidence_0.198_Length_7700 - ORF 3 (frame 1) translation	Locus_11760_Transcript_19/20_Confidence_0.198_Length_7700
Locus_13467_Transcript_1/6_Confidence_0.500_Length_1857 - ORF 8 (frame 2) translation	Locus_13467_Transcript_1/6_Confidence_0.500_Length_1857
Locus_13654_Transcript_7/15_Confidence_0.269_Length_12662 - ORF 8 (frame 2) translation	Locus_13654_Transcript_7/15_Confidence_0.269_Length_12662
O08550 (KMT2B_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2B; Short=Lysine N-methyltransferase 2B; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 4 homolog; AltName: Full=Trithorax homolog 2; AltName: Full=WW domain-binding protein 7; Short=WBP-7
O14686 (KMT2D_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2D; Short=Lysine N-methyltransferase 2D; AltName: Full=ALL1-related protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 2
O15047 (SET1A_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD1A; AltName: Full=Lysine N-methyltransferase 2F; AltName: Full=SET domain-containing protein 1A; Short=hSET1A; AltName: Full=Set1/Ash2 histone methyltransferase complex subunit SET1
O43463 (SUV91_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Histone H3-K9 methyltransferase 1; Short=H3-K9-HMTase 1; AltName: Full=Lysine N-methyltransferase 1A; AltName: Full=Position-effect variegation 3-9 homolog; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
O88491 (NSD1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific; AltName: Full=H3-K36-HMTase; AltName: Full=H4-K20-HMTase; AltName: Full=Nuclear receptor-binding SET domain-containing protein 1; Short=NR-binding SET domain-containing protein
O96028 (NSD2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase NSD2; AltName: Full=Multiple myeloma SET domain-containing protein; Short=MMSET; AltName: Full=Nuclear SET domain-containing protein 2; Short=NSD2; AltName: Full=Protein trithorax-5; AltName: Full=Wolf-Hirschhorn syndrome candidate 1 protein; Short=WHSC1

P20659 (TRX_DROME)	RecName: Full=Histone-lysine N-methyltransferase trithorax; AltName: Full=Lysine N-methyltransferase 2A
P42124 (EZ_DROME)	RecName: Full=Histone-lysine N-methyltransferase E(z); AltName: Full=Lysine N-methyltransferase 6; AltName: Full=Protein enhancer of zeste
P55200 (KMT2A_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2A; Short=Lysine N-methyltransferase 2A; AltName: Full=ALL-1; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 1; AltName: Full=Zinc finger protein HRX; Contains: RecName: Full=MLL cleavage product N320; AltName: Full=N-terminal cleavage product of 320 kDa; Short=p320; Contains: RecName: Full=MLL cleavage product C180; AltName: Full=C-terminal cleavage product of 180 kDa; Short=p180
P70351 (EZH1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EZH1; AltName: Full=ENX-2; AltName: Full=Enhancer of zeste homolog 1
Q0V9E9 (SETD8_XENTR)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=SET domain-containing protein 8
Q1DU03 (SET2_COCIM)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q1LY77 (SE1BA_DANRE)	RecName: Full=Histone-lysine N-methyltransferase SETD1B-A; AltName: Full=SET domain-containing protein 1B-A
Q2H988 (SET2_CHAGB)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q2LAE1 (ASHH2_ARATH)	RecName: Full=Histone-lysine N-methyltransferase ASHH2; AltName: Full=ASH1 homolog 2; AltName: Full=H3-K4-HMTase; AltName: Full=Histone H3-K36 methyltransferase 8; Short=H3-K36-HMTase 8; AltName: Full=Protein EARLY FLOWERING IN SHORT DAYS; AltName: Full=Protein LAZARUS 2; AltName: Full=Protein SET DOMAIN GROUP 8
Q2NL30 (SUV91_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
Q2UTN6 (SET2_ASPOR)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q2YDJ8 (SETD8_BOVIN)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q2YDW7 (SETD8_MOUSE)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q4PBL3 (SET2_USTMA)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q4R3E0 (SUV92_MACFA)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q4R381 (EZH2_MACFA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2
Q4V863 (EZH2B_XENLA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2-B
Q4WTT2 (SET2_ASPFU)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q5DW34 (EHMT1_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EHMT1; AltName: Full=Euchromatic histone-lysine N-methyltransferase 1; Short=Eu-HMTase1; AltName: Full=G9a-like protein 1; Short=GLP; Short=GLP1; AltName: Full=Lysine N-methyltransferase 1D
Q5F3P8 (SET1B_CHICK)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q5F3W5 (SUV92_CHICK)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q5LJZ2 (SET1_DROME)	RecName: Full=Histone-lysine N-methyltransferase SETD1
Q6BKL7 (SET1_DEBHA)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-4 specific; AltName: Full=COMPASS component SET1; AltName: Full=SET domain-containing protein 1
Q6DGD3 (SV91A_DANRE)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1-A; AltName: Full=Suppressor of variegation 3-9 homolog 1-A; Short=Su(var)3-9 homolog 1-A
Q6NRE8 (SUV91_XENLA)	RecName: Full=Histone-lysine N-methyltransferase SUV39H1; AltName: Full=Suppressor of variegation 3-9 homolog 1; Short=Su(var)3-9 homolog 1
Q6P2L6 (NSD3_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase NSD3; AltName: Full=Nuclear SET domain-containing protein 3; AltName: Full=Wolf-Hirschhorn syndrome candidate 1-like protein 1 homolog; Short=WHSC1-like protein 1
Q6PDK2 (KMT2D_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2D; Short=Lysine N-methyltransferase 2D; AltName: Full=ALL1-related protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 2
Q7RZU4 (SET2_NEUCR)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q08AY6 (SET8A_XENLA)	RecName: Full=N-lysine methyltransferase SETD8-A; AltName: Full=Histone-lysine N-methyltransferase SETD8-A; AltName: Full=SET domain-containing protein 8-A
Q8BRH4 (KMT2C_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase 2C; Short=Lysine N-methyltransferase 2C; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog
Q08BS4 (EZH2_DANRE)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2

Q8BVE8 (NSD2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase NSD2; AltName: Full=Multiple myeloma SET domain-containing protein; Short=MMSET; AltName: Full=Nuclear SET domain-containing protein 2; Short=NSD2; AltName: Full=Wolf-Hirschhorn syndrome candidate 1 protein homolog; Short=WHSC1
Q8C267 (SETB2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETDB2; AltName: Full=SET domain bifurcated 2
Q8CFT2 (SET1B_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q08D57 (SET1B_XENTR)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q8IRW8 (TRR_DROME)	RecName: Full=Histone-lysine N-methyltransferase trr; AltName: Full=Lysine N-methyltransferase 2C; AltName: Full=Trithorax-related protein
Q8MT36 (MES4_DROME)	RecName: Full=Probable histone-lysine N-methyltransferase Mes-4; AltName: Full=Maternal-effect sterile 4 homolog
Q8NEZ4 (KMT2C_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2C; Short=Lysine N-methyltransferase 2C; AltName: Full=Homologous to ALR protein; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 3
Q9BYW2 (SETD2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD2; AltName: Full=HIF-1; AltName: Full=Huntingtin yeast partner B; AltName: Full=Huntingtin-interacting protein 1; Short=HIP-1; AltName: Full=Huntingtin-interacting protein B; AltName: Full=Lysine N-methyltransferase 3A; AltName: Full=SET domain-containing protein 2; Short=hSET2; AltName: Full=p231HBP
Q9BZ95 (NSD3_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase NSD3; AltName: Full=Nuclear SET domain-containing protein 3; AltName: Full=Protein whistle; AltName: Full=WHSC1-like 1 isoform 9 with methyltransferase activity to lysine; AltName: Full=Wolf-Hirschhorn syndrome candidate 1-like protein 1; Short=WHSC1-like protein 1
Q9EQQ0 (SUV92_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Histone H3-K9 methyltransferase 2; Short=H3-K9-HMTase 2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q9H5I1 (SUV92_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Histone H3-K9 methyltransferase 2; Short=H3-K9-HMTase 2; AltName: Full=Lysine N-methyltransferase 1B; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q9H9B1 (EHMT1_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EHMT1; AltName: Full=Euchromatic histone-lysine N-methyltransferase 1; Short=Eu-HMTase1; AltName: Full=G9a-like protein 1; Short=GLP; Short=GLP1; AltName: Full=Histone H3-K9 methyltransferase 5; Short=H3-K9-HMTase 5; AltName: Full=Lysine N-methyltransferase 1D
Q9NQR1 (SETD8_HUMAN)	RecName: Full=N-lysine methyltransferase SETD8; AltName: Full=H4-K20-HMTase SETD8; AltName: Full=Histone-lysine N-methyltransferase SETD8; AltName: Full=Lysine N-methyltransferase 5A; AltName: Full=PR/SET domain-containing protein 07; Short=PR-Set7; Short=PR/SET07; AltName: Full=SET domain-containing protein 8
Q9NR48 (ASH1L_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; Short=huASH1; AltName: Full=Absent small and homeotic disks protein 1 homolog; AltName: Full=Lysine N-methyltransferase 2H
Q9UMN6 (KMT2B_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2B; Short=Lysine N-methyltransferase 2B; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 4; AltName: Full=Trithorax homolog 2; AltName: Full=WW domain-binding protein 7; Short=WBP-7
Q9UPS6 (SET1B_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=Lysine N-methyltransferase 2G; AltName: Full=SET domain-containing protein 1B; Short=hSET1B
Q9VFK6 (SETD8_DROME)	RecName: Full=Histone-lysine N-methyltransferase pr-set7; AltName: Full=Lysine N-methyltransferase 5A; AltName: Full=PR/SET domain-containing protein 07; AltName: Full=dSET8
Q9VW15 (ASH1_DROME)	RecName: Full=Histone-lysine N-methyltransferase ash1; AltName: Full=Absent small and homeotic disks protein 1; AltName: Full=Lysine N-methyltransferase 2H
Q9VYD1 (C1716_DROME)	RecName: Full=Probable histone-lysine N-methyltransferase CG1716
Q9Y7R4 (SET1_SCHPO)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-4 specific; AltName: Full=COMPASS component set1; AltName: Full=Lysine N-methyltransferase 2; AltName: Full=SET domain-containing protein 1; AltName: Full=Set1 complex component set1; Short=Set1C component set1; AltName: Full=Spset1
Q9Z148 (EHMT2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EHMT2; AltName: Full=Euchromatic histone-lysine N-methyltransferase 2; AltName: Full=HLA-B-associated transcript 8; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Protein G9a
Q28CQ7 (SUV92_XENTR)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q28D84 (EZH2_XENTR)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2
Q32PH7 (SUV92_BOVIN)	RecName: Full=Histone-lysine N-methyltransferase SUV39H2; AltName: Full=Suppressor of variegation 3-9 homolog 2; Short=Su(var)3-9 homolog 2
Q59XV0 (SET2_CANAL)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 specific; AltName: Full=SET domain-containing protein 2
Q66J90 (SET1B_XENLA)	RecName: Full=Histone-lysine N-methyltransferase SETD1B; AltName: Full=SET domain-containing protein 1B
Q071E0 (SET8A_DANRE)	RecName: Full=N-lysine methyltransferase SETD8-A; AltName: Full=Histone-lysine N-methyltransferase SETD8-A; AltName: Full=SET domain-containing protein 8-A

Q84WW6 (ASHH1_ARATH)	RecName: Full=Histone-lysine N-methyltransferase ASHH1; AltName: Full=ASH1 homolog 1; AltName: Full=Protein SET DOMAIN GROUP 26
Q96KQ7 (EHMT2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EHMT2; AltName: Full=Euchromatic histone-lysine N-methyltransferase 2; AltName: Full=HLA-B-associated transcript 8; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Lysine N-methyltransferase 1C; AltName: Full=Protein G9a
Q96L73 (NSD1_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific; AltName: Full=Androgen receptor coactivator 267 kDa protein; AltName: Full=Androgen receptor-associated protein of 267 kDa; AltName: Full=H3-K36-HMTase; AltName: Full=H4-K20-HMTase; AltName: Full=Lysine N-methyltransferase 3B; AltName: Full=Nuclear receptor-binding SET domain-containing protein 1; Short=NR-binding SET domain-containing protein
Q96T68 (SETB2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase SETDB2; AltName: Full=Chronic lymphocytic leukemia deletion region gene 8 protein; AltName: Full=Lysine N-methyltransferase 1F; AltName: Full=SET domain bifurcated 2
Q98SM3 (EZH2A_XENLA)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=Enhancer of zeste homolog 2-A
Q99MY8 (ASH1L_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase ASH1L; AltName: Full=ASH1-like protein; AltName: Full=Absent small and homeotic disks protein 1 homolog
Q297V5 (SETD8_DROPS)	RecName: Full=Histone-lysine N-methyltransferase pr-set7; AltName: Full=PR/SET domain-containing protein 07
Q498E6 (SET8B_XENLA)	RecName: Full=N-lysine methyltransferase SETD8-B; AltName: Full=Histone-lysine N-methyltransferase SETD8-B; AltName: Full=Mitotic phosphoprotein 36; AltName: Full=SET domain-containing protein 8-B
Q03164 (KMT2A_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase 2A; Short=Lysine N-methyltransferase 2A; AltName: Full=ALL-1; AltName: Full=CXXC-type zinc finger protein 7; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia; AltName: Full=Myeloid/lymphoid or mixed-lineage leukemia protein 1; AltName: Full=Trithorax-like protein; AltName: Full=Zinc finger protein HRX; Contains: RecName: Full=MLL cleavage product N320; AltName: Full=N-terminal cleavage product of 320 kDa; Short=p320; Contains: RecName: Full=MLL cleavage product C180; AltName: Full=C-terminal cleavage product of 180 kDa; Short=p180
Q15910 (EZH2_HUMAN)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=ENX-1; AltName: Full=Enhancer of zeste homolog 2; AltName: Full=Lysine N-methyltransferase 6
Q18221 (SET2_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase set-2; AltName: Full=SET domain-containing protein 2
Q22795 (SET1_CAEEL)	RecName: Full=Probable histone-lysine N-methyltransferase set-1
Q24742 (TRX_DROVI)	RecName: Full=Histone-lysine N-methyltransferase trithorax
Q61188 (EZH2_MOUSE)	RecName: Full=Histone-lysine N-methyltransferase EZH2; AltName: Full=ENX-1; AltName: Full=Enhancer of zeste homolog 2
TRX_DROME	RecName: Full=Histone-lysine N-methyltransferase trithorax; AltName: Full=Lysine N-methyltransferase 2A
XP_395451	PREDICTED: histone-lysine N-methyltransferase SETD1B-like isoform 1 [Apis mellifera]
XP_395493	PREDICTED: histone-lysine N-methyltransferase pr-set7 [Apis mellifera]
XP_001601155	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Nasonia vitripennis]
XP_001604667	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Nasonia vitripennis]
XP_002401135	huntingtin interacting protein, putative [Ixodes scapularis]
XP_002408953	enhancer of zeste, ezh, putative, partial [Ixodes scapularis]
XP_002410343	H4-K20-specific histone methyltransferase SET7, putative, partial [Ixodes scapularis]
XP_002427372	histone-lysine N-methyltransferase, H4 lysine-20 specific, putative [Pediculus humanus corporis]
XP_002802212	PREDICTED: probable histone-lysine N-methyltransferase NSD2-like [Macaca mulatta]
XP_003249917	PREDICTED: histone-lysine N-methyltransferase E(z) isoformX1 [Apis mellifera]
XP_003394341	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X2 [Bombus terrestris]
XP_003399301	PREDICTED: histone-lysine N-methyltransferase SETD1 [Bombus terrestris]
XP_003488269	PREDICTED: histone-lysine N-methyltransferase SETD1 [Bombus impatiens]
XP_003690343	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Apis florea]
XP_003698603	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Apis florea]
XP_003705533	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X1 [Megachile rotundata]
XP_005878229	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific [Myotis brandtii]
XP_006558041	PREDICTED: histone-lysine N-methyltransferase EHMT1-like isoform X3 [Apis mellifera]
XP_006613374	PREDICTED: histone-lysine N-methyltransferase SETD1B-like [Apis dorsata]
XP_006614809	PREDICTED: histone-lysine N-methyltransferase EHMT1-like [Apis dorsata]
XP_006713978	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X5 [Homo sapiens]
XP_006763262	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like [Myotis davidii]

XP_006814029	PREDICTED: histone-lysine N-methyltransferase ASH1L-like [Saccoglossus kowalevskii]
XP_006893664	PREDICTED: histone-lysine N-methyltransferase NSD2-like [Elephantulus edwardii]
XP_007612726	PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X2, partial [Cricetulus griseus]
XP_008206042	PREDICTED: histone-lysine N-methyltransferase 2C [Nasonia vitripennis]
XP_009199567	PREDICTED: histone-lysine N-methyltransferase NSD2 [Papio anubis]
XP_009862790	PREDICTED: histone-lysine N-methyltransferase ASH1L-like, partial [Apaloderma vittatum]
XP_009918214	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like [Haliaeetus albicilla]
XP_009958250	PREDICTED: histone-lysine N-methyltransferase NSD2-like, partial [Leptosomus discolor]
XP_009969243	PREDICTED: histone-lysine N-methyltransferase NSD3, partial [Tyto alba]
XP_010136549	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like, partial [Buceros rhinoceros silvestris]
XP_010170989	PREDICTED: histone-lysine N-methyltransferase NSD2, partial [Caprimulgus carolinensis]
XP_010198260	PREDICTED: histone-lysine N-methyltransferase ASH1L-like, partial [Colius striatus]
XP_011052529	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X1 [Acromyrmex echinatior]
XP_011052530	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X2 [Acromyrmex echinatior]
XP_011055947	PREDICTED: histone-lysine N-methyltransferase pr-set7, partial [Acromyrmex echinatior]
XP_011150292	PREDICTED: histone-lysine N-methyltransferase SETD1 [Harpegnathos saltator]
XP_011266317	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like isoform X1 [Camponotus floridanus]
XP_011298309	PREDICTED: histone-lysine N-methyltransferase trithorax [Fopius arisanus]
XP_011449544	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like [Crassostrea gigas]
XP_011502402	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Ceratosolen solmsi marchali]
XP_011511861	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X4 [Homo sapiens]
XP_011629655	PREDICTED: histone-lysine N-methyltransferase trithorax [Pogonomyrmex barbatus]
XP_011743157	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X2 [Macaca nemestrina]
XP_011862500	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X1 [Vollenhovia emeryi]
XP_011862501	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X2 [Vollenhovia emeryi]
XP_011862502	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Vollenhovia emeryi]
XP_011914639	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X3 [Cercocebus atys]
XP_012054897	PREDICTED: histone-lysine N-methyltransferase SETD1 [Atta cephalotes]
XP_012059283	PREDICTED: probable histone-lysine N-methyltransferase CG1716 [Atta cephalotes]
XP_012145893	PREDICTED: probable histone-lysine N-methyltransferase CG1716 isoform X2 [Megachile rotundata]
XP_012147639	PREDICTED: histone-lysine N-methyltransferase trithorax isoform X1 [Megachile rotundata]
XP_012147640	PREDICTED: histone-lysine N-methyltransferase trithorax isoform X2 [Megachile rotundata]
XP_012176209	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Bombus terrestris]
XP_012176211	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X4 [Bombus terrestris]
XP_012222417	PREDICTED: histone-lysine N-methyltransferase SETD1 [Linepithema humile]
XP_012228656	PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X1 [Linepithema humile]
XP_012228658	PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X2 [Linepithema humile]
XP_012258464	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Athalia rosae]
XP_012260877	PREDICTED: histone-lysine N-methyltransferase trithorax [Athalia rosae]
XP_012266861	PREDICTED: histone-lysine N-methyltransferase SETD1B-A [Athalia rosae]
XP_012280614	PREDICTED: histone-lysine N-methyltransferase SUV39H2-like isoform X1 [Orussus abietinus]
XP_012355212	PREDICTED: histone-lysine N-methyltransferase NSD2 isoform X2 [Nomascus leucogenys]
XP_012533486	PREDICTED: histone-lysine N-methyltransferase E(z) isoform X3 [Monomorium pharaonis]
XP_012537071	PREDICTED: probable histone-lysine N-methyltransferase CG1716 [Monomorium pharaonis]
XP_012539726	PREDICTED: histone-lysine N-methyltransferase pr-set7 isoform X1 [Monomorium pharaonis]
XP_012539727	PREDICTED: histone-lysine N-methyltransferase pr-set7 isoform X2 [Monomorium pharaonis]

XP_012542824	PREDICTED: histone-lysine N-methyltransferase SETD1 [Monomorium pharaonis]
XP_012976031	PREDICTED: histone-lysine N-methyltransferase ASH1L [Mesocricetus auratus]
XP_013389879	PREDICTED: histone-lysine N-methyltransferase ASH1L-like isoform X10 [Lingula anatina]
XP_013394122	PREDICTED: histone-lysine N-methyltransferase SUV39H1-A-like [Lingula anatina]
XP_013772199	PREDICTED: histone-lysine N-methyltransferase SUV39H1-like isoform X1 [Limulus polyphemus]
XP_013772200	PREDICTED: histone-lysine N-methyltransferase SUV39H1-like isoform X2 [Limulus polyphemus]
XP_013773324	PREDICTED: histone-lysine N-methyltransferase SETD2-like, partial [Limulus polyphemus]
XP_013777216	PREDICTED: histone-lysine N-methyltransferase EZH2-like [Limulus polyphemus]
XP_013777692	PREDICTED: histone-lysine N-methyltransferase EZH2-like isoform X1 [Limulus polyphemus]
XP_013777694	PREDICTED: histone-lysine N-methyltransferase EZH2-like isoform X2 [Limulus polyphemus]
XP_013779563	PREDICTED: serine-rich adhesin for platelets-like [Limulus polyphemus]
XP_013779655	PREDICTED: histone-lysine N-methyltransferase trr-like [Limulus polyphemus]
XP_013784687	PREDICTED: histone-lysine N-methyltransferase 2C-like [Limulus polyphemus]
XP_013788393	PREDICTED: N-lysine methyltransferase SETD8-like, partial [Limulus polyphemus]
XP_013911646	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific [Thamnophis sirtalis]
XP_014069115	PREDICTED: histone-lysine N-methyltransferase 2A isoform X1 [Salmo salar]
XP_014069116	PREDICTED: histone-lysine N-methyltransferase 2A isoform X2 [Salmo salar]
XP_014069117	PREDICTED: histone-lysine N-methyltransferase 2A isoform X3 [Salmo salar]
XP_014069118	PREDICTED: histone-lysine N-methyltransferase 2A isoform X4 [Salmo salar]
XP_014069120	PREDICTED: histone-lysine N-methyltransferase 2A isoform X5 [Salmo salar]
XP_014217049	PREDICTED: histone-lysine N-methyltransferase SUV39H2 [Copidosoma floridanum]
XP_014223483	PREDICTED: histone-lysine N-methyltransferase EHMT2 isoform X1 [Trichogramma pretiosum]
XP_014244325	PREDICTED: N-lysine methyltransferase SETD8-A isoform X1 [Cimex lectularius]
XP_014244326	PREDICTED: N-lysine methyltransferase SETD8-A isoform X2 [Cimex lectularius]
XP_014254736	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X5 [Cimex lectularius]
XP_014254739	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X7 [Cimex lectularius]
XP_014254743	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X11 [Cimex lectularius]
XP_014254744	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X12 [Cimex lectularius]
XP_014254745	PREDICTED: histone-lysine N-methyltransferase 2D-like isoform X13 [Cimex lectularius]
XP_014276805	PREDICTED: N-lysine methyltransferase SETD8 [Halyomorpha halys]
XP_014460276	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific, partial [Alligator mississippiensis]

9.4.2.36 *Ventral nervechord defective*

Name	Description
A1L2P5 (HXD3_XENLA)	RecName: Full=Homeobox protein Hox-D3
A1YF16 (MSX2_GORGO)	RecName: Full=Homeobox protein MSX-2
A1YGA4 (MEOX1_PANPA)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A2RU54 (HMX2_HUMAN)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein H6 family member 2
A2T779 (MEOX1_PANTR)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
A5PKG8 (DBX1_BOVIN)	RecName: Full=Homeobox protein DBX1; AltName: Full=Developing brain homeobox protein 1
A5YC49 (NKX63_XENLA)	RecName: Full=Homeobox protein Nkx-6.3
A6NCS4 (NKX26_HUMAN)	RecName: Full=Homeobox protein Nkx-2.6; AltName: Full=Homeobox protein NK-2 homolog F
A6NHT5 (HMX3_HUMAN)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
A6NJ46 (NKX63_HUMAN)	RecName: Full=Homeobox protein Nkx-6.3
A6NMT0 (DBX1_HUMAN)	RecName: Full=Homeobox protein DBX1; AltName: Full=Developing brain homeobox protein 1
A8XJD0 (HM30_CAEBR)	RecName: Full=Homeobox protein ceh-30
B0VXK3 (HXA2_CALJA)	RecName: Full=Homeobox protein Hox-A2
G5ECT8 (HM02_CAEEL)	RecName: Full=Homeobox protein ceh-2
Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968 - ORF 1 (frame 1) translation	Locus_1_Transcript_82205/166847_Confidence_1.000_Length_968

Locus_1_Transcript_144485/166847_Confidence_1.000_Length_1540 - ORF 13 (frame 3) translation	Locus_1_Transcript_144485/166847_Confidence_1.000_Length_1540
Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118 - ORF 3 (frame 3) translation	Locus_1_Transcript_163596/166847_Confidence_1.000_Length_1118
Locus_1062_Transcript_9/9_Confidence_0.617_Length_5291 - ORF 5 (frame 3) translation	Locus_1062_Transcript_9/9_Confidence_0.617_Length_5291
Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075 - ORF 1 (frame 3) translation	Locus_3013_Transcript_10/10_Confidence_0.587_Length_2075
Locus_3015_Transcript_2/2_Confidence_0.800_Length_548 - ORF 4 (frame 3) translation	Locus_3015_Transcript_2/2_Confidence_0.800_Length_548
Locus_3016_Transcript_1/1_Confidence_1.000_Length_755 - ORF 6 (frame 3) translation	Locus_3016_Transcript_1/1_Confidence_1.000_Length_755
Locus_5005_Transcript_6/6_Confidence_0.722_Length_2921 - ORF 8 (frame 1) translation	Locus_5005_Transcript_6/6_Confidence_0.722_Length_2921
Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099 - ORF 10 (frame 2) translation	Locus_11678_Transcript_10/10_Confidence_0.456_Length_3099
Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534 - ORF 3 (frame 3) translation	Locus_11933_Transcript_4/4_Confidence_0.850_Length_3534
Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549 - ORF 4 (frame 2) translation	Locus_12164_Transcript_8/8_Confidence_0.708_Length_3549
Locus_12534_Transcript_4/5_Confidence_0.500_Length_3699 - ORF 6 (frame 2) translation	Locus_12534_Transcript_4/5_Confidence_0.500_Length_3699
Locus_15017_Transcript_1/7_Confidence_0.097_Length_1492 - ORF 8 (frame 2) translation	Locus_15017_Transcript_1/7_Confidence_0.097_Length_1492
Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327 - ORF 3 (frame 1) translation	Locus_15294_Transcript_2/2_Confidence_0.800_Length_2327
Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869 - ORF 2 (frame 2) translation	Locus_15589_Transcript_1/1_Confidence_1.000_Length_2869
Locus_15791_Transcript_1/1_Confidence_1.000_Length_1276 - ORF 1 (frame 2) translation	Locus_15791_Transcript_1/1_Confidence_1.000_Length_1276
Locus_16018_Transcript_1/1_Confidence_1.000_Length_4201 - ORF 1 (frame 2) translation	Locus_16018_Transcript_1/1_Confidence_1.000_Length_4201
Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973 - ORF 3 (frame 3) translation	Locus_16046_Transcript_4/4_Confidence_0.500_Length_2973
Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421 - ORF 2 (frame 1) translation	Locus_16254_Transcript_3/3_Confidence_0.667_Length_3421
Locus_16275_Transcript_1/2_Confidence_0.600_Length_1330 - ORF 2 (frame 3) translation	Locus_16275_Transcript_1/2_Confidence_0.600_Length_1330
Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590 - ORF 4 (frame 1) translation	Locus_16519_Transcript_1/1_Confidence_1.000_Length_3590
Locus_16600_Transcript_2/5_Confidence_0.167_Length_2020 - ORF 1 (frame 3) translation	Locus_16600_Transcript_2/5_Confidence_0.167_Length_2020
Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305 - ORF 1 (frame 3) translation	Locus_16948_Transcript_2/2_Confidence_0.875_Length_2305
Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037 - ORF 2 (frame 2) translation	Locus_17202_Transcript_2/2_Confidence_0.800_Length_3037
Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236 - ORF 1 (frame 2) translation	Locus_17634_Transcript_1/1_Confidence_1.000_Length_1236
Locus_18495_Transcript_2/2_Confidence_0.833_Length_2978 - ORF 18 (frame 2) translation	Locus_18495_Transcript_2/2_Confidence_0.833_Length_2978
Locus_18584_Transcript_1/1_Confidence_1.000_Length_982 - ORF 2 (frame 2) translation	Locus_18584_Transcript_1/1_Confidence_1.000_Length_982
Locus_20765_Transcript_4/4_Confidence_0.843_Length_3077 - ORF 3 (frame 3) translation	Locus_20765_Transcript_4/4_Confidence_0.843_Length_3077
Locus_20809_Transcript_1/1_Confidence_1.000_Length_1766 - ORF 9 (frame 1) translation	Locus_20809_Transcript_1/1_Confidence_1.000_Length_1766
Locus_21143_Transcript_2/2_Confidence_0.750_Length_1655 - ORF 5 (frame 2) translation	Locus_21143_Transcript_2/2_Confidence_0.750_Length_1655
Locus_21582_Transcript_1/1_Confidence_1.000_Length_907 - ORF 2 (frame 1) translation	Locus_21582_Transcript_1/1_Confidence_1.000_Length_907
Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612 - ORF 4 (frame 3) translation	Locus_21946_Transcript_1/1_Confidence_1.000_Length_1612
Locus_23245_Transcript_1/1_Confidence_1.000_Length_2652 - ORF 19 (frame 1) translation	Locus_23245_Transcript_1/1_Confidence_1.000_Length_2652
Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198 - ORF 11 (frame 2) translation	Locus_27042_Transcript_1/3_Confidence_0.200_Length_2198
Locus_28432_Transcript_2/2_Confidence_0.667_Length_824 - ORF 1 (frame 3) translation	Locus_28432_Transcript_2/2_Confidence_0.667_Length_824
NKX21_MOUSE	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Thyroid-specific enhancer-binding protein; Short=T/EBP
NKX22_MOUSE	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
NKX23_MOUSE	RecName: Full=Homeobox protein Nkx-2.3; AltName: Full=Homeobox protein NK-2 homolog 3; AltName: Full=Homeobox protein NK-2 homolog C; AltName: Full=Nkx2-C
NKX24_MOUSE	RecName: Full=Homeobox protein Nkx-2.4; AltName: Full=Homeobox protein NK-2 homolog D
NKX25_MOUSE	RecName: Full=Homeobox protein Nkx-2.5; AltName: Full=Cardiac-specific homeobox; AltName: Full=Homeobox protein CSX; AltName: Full=Homeobox protein NK-2 homolog E
NKX26_MOUSE	RecName: Full=Homeobox protein Nkx-2.6; AltName: Full=Homeobox protein NK-2 homolog F
NKX28_MOUSE	RecName: Full=Homeobox protein Nkx-2.8; AltName: Full=Homeobox protein NK-2 homolog H; AltName: Full=Homeobox protein Nkx-2.9
NP_571496	homeobox protein Nkx-2.5 [Danio rerio]
NP_739572	T-cell leukemia homeobox protein 3 [Danio rerio]
NP_001007783	NK2 homeobox 2b [Danio rerio]
NP_001034519	abdominal-B [Tribolium castaneum]
NP_001091156	homeobox protein Hox-D3 [Xenopus laevis]

NP_001095280	brain-specific homeobox protein homolog [Xenopus (Silurana) tropicalis]
NP_001107793	empty spiracles [Tribolium castaneum]
NP_001154858	uncharacterized protein LOC100301951 [Xenopus laevis]
NP_001158371	distal-less homeobox 1 [Saccoglossus kowalevskii]
NP_001158453	T-cell leukemia homeobox protein [Saccoglossus kowalevskii]
NP_001161609	Nkx1-like transcription factor [Saccoglossus kowalevskii]
NP_001186477	homeobox protein Nkx-6.2 [Gallus gallus]
O35762 (NKX61_RAT)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
O35767 (NKX25_RAT)	RecName: Full=Homeobox protein Nkx-2.5; Short=rNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
O42230 (GBX2_CHICK)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
O42365 (HXA2B_DANRE)	RecName: Full=Homeobox protein Hox-A2b; Short=Hox-A2
O42367 (HXB2A_DANRE)	RecName: Full=Homeobox protein Hox-B2a; Short=Hox-B2
O42370 (HXD3A_DANRE)	RecName: Full=Homeobox protein Hox-D3a; Short=Hox-D3
O43364 (HXA2_HUMAN)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1K
O43365 (HXA3_HUMAN)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1E
O43711 (TLX3_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox protein Hox-11L2
O43763 (TLX2_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Neural crest homeobox protein
O55144 (TLX3_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2; AltName: Full=Respiratory neuron homeobox protein
O57601 (HMX3_CHICK)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=cNkx5-1
O70218 (HMX1_MOUSE)	RecName: Full=Homeobox protein HMX1; AltName: Full=Homeobox protein H6
O88181 (BARH2_RAT)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
O93353 (HXA3_CHICK)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-D3
O93366 (TLX1_CHICK)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
O93367 (TLX3_CHICK)	RecName: Full=T-cell leukemia homeobox protein 3; AltName: Full=Homeobox TLX-3; AltName: Full=Homeobox protein Hox-11L2
O93590 (ZAX_XENLA)	RecName: Full=Homeobox protein zampogna; AltName: Full=Xzax
O95096 (NKX22_HUMAN)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P0C1T1 (HXB2_MOUSE)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8
P02831 (HXA3_MOUSE)	RecName: Full=Homeobox protein Hox-A3; AltName: Full=Homeobox protein Hox-1.5; AltName: Full=Homeobox protein MO-10
P09027 (HXD3_MOUSE)	RecName: Full=Homeobox protein Hox-D3; AltName: Full=Homeobox protein Hox-4.1; AltName: Full=Homeobox protein MH-19
P09087 (ABDB_DROME)	RecName: Full=Homeobox protein abdominal-B; AltName: Full=Infraabdominal 7; Short=IAB-7; AltName: Full=P3; AltName: Full=PH189
P09631 (HXA9_MOUSE)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1.7
P09638 (HXB2_SALSA)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=S6
P10179 (HMB4_TRIGR)	RecName: Full=Homeobox protein HB4
P14652 (HXB2_HUMAN)	RecName: Full=Homeobox protein Hox-B2; AltName: Full=Homeobox protein Hox-2.8; AltName: Full=Homeobox protein Hox-2H; AltName: Full=K8
P14837 (PDX1_XENLA)	RecName: Full=Pancreas/duodenum homeobox protein 1; Short=PDX-1; AltName: Full=Homeobox protein 8; Short=XlHbox-8
P15142 (HM7X_CHICK)	RecName: Full=Homeobox protein CHOX-7
P15858 (EMS_APIME)	RecName: Full=Homeobox protein H40
P18488 (EMS_DROME)	RecName: Full=Homeotic protein empty spiracles
P19601 (SAX1_CHICK)	RecName: Full=Homeobox protein SAX-1; AltName: Full=CHOX-3
P20009 (DLL_DROME)	RecName: Full=Homeotic protein distal-less; AltName: Full=Protein brista
P22544 (BARH1_DROAN)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox BarH1 protein
P22574 (HXB4A_DANRE)	RecName: Full=Homeobox protein Hox-B4a; Short=Hox-B4; AltName: Full=Homeobox protein Zf-13
P22807 (SLOU_DROME)	RecName: Full=Homeobox protein slou; AltName: Full=Homeobox protein NK-1; AltName: Full=Protein slouch; AltName: Full=S59/2
P22808 (VND_DROME)	RecName: Full=Homeobox protein vnd; AltName: Full=Homeobox protein NK-2; AltName: Full=Protein ventral nervous system defective
P23441 (NKX21_RAT)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1
P24340 (HXD9_CHICK)	RecName: Full=Homeobox protein Hox-D9; AltName: Full=Homeobox protein Hox-4.4; Short=Chox-4.4
P28361 (MSX1_CHICK)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Homeobox protein Hox-7; Short=CHOX-7; AltName: Full=Msh homeobox 1-like protein
P28362 (MSX2_CHICK)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8; Short=CHOX-8; Short=GHox-8
P31245 (HXA2_MOUSE)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11; Short=Hox1.11

P31246 (HXA2_RAT)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hox-1.11
P31249 (HXD3_HUMAN)	RecName: Full=Homeobox protein Hox-D3; AltName: Full=Homeobox protein Hox-4A
P31261 (HXA2_NOTVI)	RecName: Full=Homeobox protein Hox-A2; AltName: Full=Homeobox protein Hbox-2.8; Short=NvHbox-2.8
P31264 (HMPB_DROME)	RecName: Full=Homeotic protein proboscipedia
P31269 (HXA9_HUMAN)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1G
P31314 (TLX1_HUMAN)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox protein Hox-11; AltName: Full=Proto-oncogene TCL-3; AltName: Full=T-cell leukemia/lymphoma protein 3
P32442 (MEOX1_MOUSE)	RecName: Full=Homeobox protein MOX-1; AltName: Full=Mesenchyme homeobox 1
P42580 (NKX12_MOUSE)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
P42581 (HMX3_MOUSE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
P42582 (NKX25_MOUSE)	RecName: Full=Homeobox protein Nkx-2.5; AltName: Full=Cardiac-specific homeobox; AltName: Full=Homeobox protein CSX; AltName: Full=Homeobox protein NK-2 homolog E
P42583 (NKX25_XENLA)	RecName: Full=Homeobox protein Nkx-2.5; Short=xNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
P42586 (NKX22_MOUSE)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P42587 (HNK2_XENLA)	RecName: Full=Homeobox protein XENK-2
P43345 (TLX1_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 1; AltName: Full=Homeobox TLX-1; AltName: Full=Homeobox protein Hox-11
P43687 (HMX2_MOUSE)	RecName: Full=Homeobox protein HMX2; AltName: Full=Homeobox protein Nkx-5.2
P43688 (NKX26_MOUSE)	RecName: Full=Homeobox protein Nkx-2.6; AltName: Full=Homeobox protein NK-2 homolog F
P43697 (NKX22_MESAU)	RecName: Full=Homeobox protein Nkx-2.2; AltName: Full=Homeobox protein NK-2 homolog B
P43698 (TITF1_CANFA)	RecName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1
P43699 (NKX21_HUMAN)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Homeobox protein NK-2 homolog A; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Thyroid-specific enhancer-binding protein; Short=T/EBP
P48031 (GBX2_MOUSE)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=Stimulated by retinoic acid gene 7 protein
P49639 (HXA1_HUMAN)	RecName: Full=Homeobox protein Hox-A1; AltName: Full=Homeobox protein Hox-1F
P50209 (HXA9_AMBME)	RecName: Full=Homeobox protein Hox-A9
P50219 (MNX1_HUMAN)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
P50220 (NKX21_MOUSE)	RecName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1; AltName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Thyroid-specific enhancer-binding protein; Short=T/EBP
P50223 (HMGX7_CHICK)	RecName: Full=Homeobox protein GHOX-7; AltName: Full=CHOX-7; Short=Hox-7
P51783 (HXA9_CAVPO)	RecName: Full=Homeobox protein Hox-A9; AltName: Full=Homeobox protein Hox-1.7
P52950 (DBX1_MOUSE)	RecName: Full=Homeobox protein DBX1; AltName: Full=Developing brain homeobox protein 1
P52951 (GBX2_HUMAN)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2
P52952 (NKX25_HUMAN)	RecName: Full=Homeobox protein Nkx-2.5; AltName: Full=Cardiac-specific homeobox; AltName: Full=Homeobox protein CSX; AltName: Full=Homeobox protein NK-2 homolog E
P52953 (MSX2_RAT)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
P52954 (LBX1_HUMAN)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
P52955 (LBX1_MOUSE)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
P53547 (HM01_CAEEL)	RecName: Full=Homeobox protein ceh-1
P53772 (DLLH_BRAFL)	RecName: Full=Homeobox protein DLL homolog
P53773 (DLL1_XENLA)	RecName: Full=Homeobox protein DLL-1; Short=DLL; Short=XDLL
P56177 (DLX1_HUMAN)	RecName: Full=Homeobox protein DLX-1
P56407 (HM09_CAEEL)	RecName: Full=Homeobox protein ceh-9
P63156 (BARH1_RAT)	RecName: Full=BarH-like 1 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH2; AltName: Full=BarH-related homeobox protein 1
P70118 (PDX1_MESAU)	RecName: Full=Pancreas/duodenum homeobox protein 1; AltName: Full=Homeodomain protein PDX1; AltName: Full=Insulin promoter factor 1; Short=IPF-1
P70397 (DLX6_MOUSE)	RecName: Full=Homeobox protein DLX-6
P78426 (NKX61_HUMAN)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
P82976 (GBX1_MOUSE)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
P97273 (TITF1_CAVPO)	RecName: Full=Thyroid transcription factor 1; Short=TTF-1; AltName: Full=Homeobox protein Nkx-2.1; AltName: Full=Thyroid nuclear factor 1

P97334 (NKX23_MOUSE)	RecName: Full=Homeobox protein Nkx-2.3; AltName: Full=Homeobox protein NK-2 homolog 3; AltName: Full=Homeobox protein NK-2 homolog C; AltName: Full=Nkx2-C
Q0P4H6 (LBX1_XENTR)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q0P4W6 (HMX3_XENTR)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q0P5C3 (MSX2_BOVIN)	RecName: Full=Homeobox protein MSX-2
Q0VCS4 (HXA2_BOVIN)	RecName: Full=Homeobox protein Hox-A2
Q1KKZ2 (HXA2B_TAKRU)	RecName: Full=Homeobox protein Hox-A2b
Q1KL10 (HXA1A_TAKRU)	RecName: Full=Homeobox protein Hox-A1a
Q1XID0 (LBX1_RAT)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q2PYN8 (LBX1_XENLA)	RecName: Full=Transcription factor LBX1; AltName: Full=Ladybird homeobox protein homolog 1
Q2VL79 (MSX1_DAUMA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL80 (MSX1_PERPO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL82 (MSX1_SAGOE)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL83 (MSX1_LEORO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL84 (MSX1_CALJA)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL85 (MSX1_CALGO)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL86 (MSX1_SAIBB)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q2VL88 (MSX1_PANTR)	RecName: Full=Homeobox protein MSX-1; AltName: Full=Msh homeobox 1-like protein
Q3C1V8 (BSH_HUMAN)	RecName: Full=Brain-specific homeobox protein homolog
Q3UHX8 (NKX63_MOUSE)	RecName: Full=Homeobox protein Nkx-6.3
Q3V5Z9 (HXD3_ORYLA)	RecName: Full=Homeobox protein Hox-D3
Q4V5A3 (UNPG_DROME)	RecName: Full=Homeobox protein unplugged
Q5NSW5 (DBX1_RAT)	RecName: Full=Homeobox protein DBX1; AltName: Full=Developing brain homeobox protein 1
Q6GLB9 (EMX1_XENTR)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q6R3Q6 (BSH_DANRE)	RecName: Full=Brain-specific homeobox protein homolog
Q6RFL5 (BSH_CHICK)	RecName: Full=Brain-specific homeobox protein homolog
Q6XYB7 (LBX2_HUMAN)	RecName: Full=Transcription factor LBX2; AltName: Full=Ladybird homeobox protein homolog 2
Q6ZNG2 (DBX2_HUMAN)	RecName: Full=Homeobox protein DBX2; AltName: Full=Developing brain homeobox protein 2
Q08DG7 (HXA3_BOVIN)	RecName: Full=Homeobox protein Hox-A3
Q8JJ64 (HMX3_XENLA)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1; Short=X-nkx-5.1
Q8TAU0 (NKX23_HUMAN)	RecName: Full=Homeobox protein Nkx-2.3; AltName: Full=Homeobox protein NK-2 homolog C
Q8VIB5 (BARH2_MOUSE)	RecName: Full=BarH-like 2 homeobox protein; AltName: Full=Bar-class homeodomain protein MBH1; AltName: Full=Homeobox protein B-H1
Q9BZE3 (BARH1_HUMAN)	RecName: Full=BarH-like 1 homeobox protein
Q9C056 (NKX62_HUMAN)	RecName: Full=Homeobox protein Nkx-6.2; AltName: Full=Homeobox protein NK-6 homolog B
Q9DDB0 (VAX1B_XENLA)	RecName: Full=Ventral anterior homeobox 1b
Q9DE09 (HMX1_CHICK)	RecName: Full=Homeobox protein HMX1; AltName: Full=GH6; AltName: Full=Homeobox protein H6
Q9DED6 (BAX1B_CHICK)	RecName: Full=Homeobox protein BarH-like 1b; AltName: Full=Bar class homeoprotein Barx1b
Q9EQM3 (NKX24_MOUSE)	RecName: Full=Homeobox protein Nkx-2.4; AltName: Full=Homeobox protein NK-2 homolog D
Q9ER42 (BARX1_MOUSE)	RecName: Full=Homeobox protein BarH-like 1
Q9GK08 (MSX2_CANFA)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8
Q9H2Z4 (NKX24_HUMAN)	RecName: Full=Homeobox protein Nkx-2.4; AltName: Full=Homeobox protein NK-2 homolog D
Q9HBU1 (BARX1_HUMAN)	RecName: Full=Homeobox protein BarH-like 1
Q9I9H2 (DBX1_XENLA)	RecName: Full=Homeobox protein DBX1; AltName: Full=Developing brain homeobox protein 1; AltName: Full=Xdbx
Q9IA20 (HXA2_HETFR)	RecName: Full=Homeobox protein Hox-A2
Q9IA21 (HXA3_HETFR)	RecName: Full=Homeobox protein Hox-A3
Q9IA26 (HXA9_HETFR)	RecName: Full=Homeobox protein Hox-A9
Q9IAX9 (VAX2B_XENLA)	RecName: Full=Ventral anterior homeobox 2b; AltName: Full=Ventral anterior homeobox 3
Q9JLZ9 (VAX2_RAT)	RecName: Full=Ventral anterior homeobox 2
Q9NY43 (BARH2_HUMAN)	RecName: Full=BarH-like 2 homeobox protein
Q9PTU0 (DBX1B_DANRE)	RecName: Full=Homeobox protein DBX1-B; AltName: Full=Developing brain homeobox protein 1-B; AltName: Full=Homeobox protein hlx2
Q9PTU1 (DBX1A_DANRE)	RecName: Full=Homeobox protein DBX1-A; AltName: Full=Developing brain homeobox protein 1-A; AltName: Full=Homeobox protein hlx1
Q9PU20 (VAX2A_XENLA)	RecName: Full=Ventral anterior homeobox 2a; AltName: Full=Xvax2
Q9QZW9 (MNX1_MOUSE)	RecName: Full=Motor neuron and pancreas homeobox protein 1; AltName: Full=Homeobox protein HB9
Q9UD57 (NKX12_HUMAN)	RecName: Full=NK1 transcription factor-related protein 2; AltName: Full=Homeobox protein SAX-1; AltName: Full=NKX-1.1
Q9VEI9 (HMX_DROME)	RecName: Full=Homeobox protein Hmx; Short=DHmx
Q9W6D8 (BARX1_CHICK)	RecName: Full=Homeobox protein BarH-like 1

Q9W7E8 (KOZA_XENLA)	RecName: Full=Homeobox protein koza; AltName: Full=Homeodomain transcription factor koza
Q9WUN8 (LBX2_MOUSE)	RecName: Full=Transcription factor LBX2; AltName: Full=Ladybird homeobox protein homolog 2
Q9YGT5 (HXA9B_DANRE)	RecName: Full=Homeobox protein Hox-A9b
Q17QR5 (DBX2_BOVIN)	RecName: Full=Homeobox protein DBX2; AltName: Full=Developing brain homeobox protein 2
Q17R00 (EMX2_BOVIN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q28ZA9 (UNPG_DROPS)	RecName: Full=Homeobox protein unplugged
Q90XN9 (HMX3B_ORYLA)	RecName: Full=Homeobox protein HMX3-B; AltName: Full=Homeobox protein H6 family member 3-B; AltName: Full=Homeobox protein Nkx-5.1.2; AltName: Full=OlNkx-5.1.2
Q90XP0 (HMX3A_ORYLA)	RecName: Full=Homeobox protein HMX3-A; AltName: Full=Homeobox protein H6 family member 3-A; AltName: Full=Homeobox protein Nkx-5.1.1; AltName: Full=OlNkx-5.1.1
Q99MA9 (NKX61_MOUSE)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q00401 (HMH2_GIRTI)	RecName: Full=Homeobox protein DTH-2
Q503F2 (BARX1_DANRE)	RecName: Full=Homeobox protein BarH-like 1; AltName: Full=BarH-class homeodomain transcription factor 4
Q504H8 (HMX3_DANRE)	RecName: Full=Homeobox protein HMX3; AltName: Full=Homeobox protein H6 family member 3; AltName: Full=Homeobox protein Nkx-5.1
Q801E1 (VAX2_DANRE)	RecName: Full=Ventral anterior homeobox 2
Q804S6 (EMX1_DANRE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q810B3 (BSH_MOUSE)	RecName: Full=Brain-specific homeobox protein homolog
Q01703 (MSXC_DANRE)	RecName: Full=Homeobox protein MSH-C
Q03356 (MSXB_DANRE)	RecName: Full=Homeobox protein MSH-B
Q03357 (MSXA_DANRE)	RecName: Full=Homeobox protein MSH-A
Q03358 (MSX2_MOUSE)	RecName: Full=Homeobox protein MSX-2; AltName: Full=Homeobox protein Hox-8-1
Q04741 (EMX1_HUMAN)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04742 (EMX1_MOUSE)	RecName: Full=Homeobox protein EMX1; AltName: Full=Empty spiracles homolog 1; AltName: Full=Empty spiracles-like protein 1
Q04743 (EMX2_HUMAN)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04744 (EMX2_MOUSE)	RecName: Full=Homeobox protein EMX2; AltName: Full=Empty spiracles homolog 2; AltName: Full=Empty spiracles-like protein 2
Q04787 (BSH_DROME)	RecName: Full=Brain-specific homeobox protein
Q06615 (NOTO_XENLA)	RecName: Full=Homeobox protein notochord; Short=Xnot
Q08727 (HXA2_CHICK)	RecName: Full=Homeobox protein Hox-A2
Q14549 (GBX1_HUMAN)	RecName: Full=Homeobox protein GBX-1; AltName: Full=Gastrulation and brain-specific homeobox protein 1
Q15270 (NKX11_HUMAN)	RecName: Full=NK1 transcription factor-related protein 1; AltName: Full=Homeobox protein 153; Short=HPX-153; AltName: Full=Homeobox protein SAX-2; AltName: Full=NKX-1.1
Q22909 (HM30_CAEEL)	RecName: Full=Homeobox protein ceh-30
Q22910 (HM31_CAEEL)	RecName: Full=Homeobox protein ceh-31
Q24255 (BARH1_DROME)	RecName: Full=Homeobox protein B-H1; AltName: Full=Homeobox protein BarH1
Q24256 (BARH2_DROME)	RecName: Full=Homeobox protein B-H2; AltName: Full=Homeobox protein BarH2
Q26604 (SMOX5_SCHMA)	RecName: Full=Homeobox protein SMOX-5
Q26656 (HMX_STRPU)	RecName: Full=Homeobox protein Hmx; Short=SpHmx; AltName: Full=H6-like
Q60554 (NKX61_MESAU)	RecName: Full=Homeobox protein Nkx-6.1; AltName: Full=Homeobox protein NK-6 homolog A
Q61663 (TLX2_MOUSE)	RecName: Full=T-cell leukemia homeobox protein 2; AltName: Full=Enteric neuron homeobox protein; AltName: Full=Homeobox TLX-2; AltName: Full=Homeobox protein Hox-11L1; AltName: Full=Hox11L.1; AltName: Full=PMUR10F
Q64317 (DLX1_MOUSE)	RecName: Full=Homeobox protein DLX-1
Q90481 (NX22A_DANRE)	RecName: Full=Homeobox protein Nkx-2.2a; AltName: Full=Homeobox protein NK-2 homolog B-A
Q90788 (NKX25_CHICK)	RecName: Full=Homeobox protein Nkx-2.5; Short=cNKx-2.5; AltName: Full=Homeobox protein NK-2 homolog E
Q91770 (NOT2_XENLA)	RecName: Full=Homeobox protein not2; Short=Xnot-2; Short=Xnot2
Q91907 (GBX2_XENLA)	RecName: Full=Homeobox protein GBX-2; AltName: Full=Gastrulation and brain-specific homeobox protein 2; AltName: Full=XGBX-2
Q91975 (DBX2_CHICK)	RecName: Full=Homeobox protein DBX2; AltName: Full=Developing brain homeobox protein 2; AltName: Full=Homeobox protein CHox-E
Q98875 (DLX1A_DANRE)	RecName: Full=Homeobox protein Dlx1a; Short=DLX-1; AltName: Full=Distal-less homeobox gene 1a
Q98877 (DLX6A_DANRE)	RecName: Full=Homeobox protein Dlx6a; AltName: Full=Distal-less homeobox protein 6a; Short=DLX-6
Q98878 (DLX4B_DANRE)	RecName: Full=Homeobox protein Dlx4b; AltName: Full=DLX-7; AltName: Full=Distal-less homeobox protein 4b
Q98879 (DLX4A_DANRE)	RecName: Full=Homeobox protein Dlx4a; AltName: Full=DLX-8; AltName: Full=Distal-less homeobox protein 4a
Q98924 (HXA9_CHICK)	RecName: Full=Homeobox protein Hox-A9
VND_DROME	RecName: Full=Homeobox protein vnd; AltName: Full=Homeobox protein NK-2; AltName: Full=Protein ventral nervous system defective
XP_308706	AGAP007058-PA [Anopheles gambiae str. PEST]
XP_975006	PREDICTED: homeobox protein BarH-like 1 [Tribolium castaneum]
XP_975059	PREDICTED: muscle segmentation homeobox [Tribolium castaneum]
XP_001122113	PREDICTED: uncharacterized protein LOC726370 isoform X1 [Apis mellifera]

XP_001688571	Anopheles gambiae str. PEST AGAP012428-PA, partial [Anopheles gambiae str. PEST]
XP_001944887	PREDICTED: homeobox protein B-H1-like [Acyrthosiphon pisum]
XP_001952902	GF17487 [Drosophila ananassae]
XP_001965829	GF20558 [Drosophila ananassae]
XP_001994877	GH13706 [Drosophila grimshawi]
XP_001999938	GI24810 [Drosophila mojavensis]
XP_002054436	GJ24455 [Drosophila virilis]
XP_002070606	GK12153 [Drosophila willistoni]
XP_002400053	homeobox protein dbx, putative [Ixodes scapularis]
XP_002414321	homeobox protein NK-2, putative [Ixodes scapularis]
XP_002423066	Homeobox protein GBX-1, putative [Pediculus humanus corporis]
XP_002425514	Homeobox protein Nkx-6.1, putative [Pediculus humanus corporis]
XP_002425762	Homeobox protein Hox-A11A, putative [Pediculus humanus corporis]
XP_002426081	Ptx1 homeodomain protein, putative [Pediculus humanus corporis]
XP_002428141	Homeobox protein CHOX-E, putative [Pediculus humanus corporis]
XP_002429457	Homeobox protein Hmx, putative [Pediculus humanus corporis]
XP_002435656	homeobox protein MSX-2, putative [Ixodes scapularis]
XP_002436223	homeobox protein, putative [Ixodes scapularis]
XP_002596391	BarH-like 1 homeobox protein [Branchiostoma floridae]
XP_002609065	ladybird-like homeobox protein [Branchiostoma floridae]
XP_002609070	nk homeobox 6 [Branchiostoma floridae]
XP_002731951	PREDICTED: homeobox protein HMX3-A-like [Saccoglossus kowalevskii]
XP_003400164	PREDICTED: uncharacterized protein LOC100651894 [Bombus terrestris]
XP_003427431	PREDICTED: motor neuron and pancreas homeobox protein 1 [Nasonia vitripennis]
XP_003476493	PREDICTED: homeobox protein Nkx-2.2 [Cavia porcellus]
XP_003698568	PREDICTED: homeobox protein B-H2 [Apis florea]
XP_003740832	PREDICTED: uncharacterized protein LOC100900625 [Metaseiulus occidentalis]
XP_003741994	PREDICTED: homeobox protein XHOX-7.1-like [Metaseiulus occidentalis]
XP_003743246	PREDICTED: homeobox protein B-H1-like [Metaseiulus occidentalis]
XP_003748200	PREDICTED: uncharacterized protein LOC100906611 [Metaseiulus occidentalis]
XP_003963996	PREDICTED: homeobox protein HMX3-A [Takifugu rubripes]
XP_003970367	PREDICTED: LOW QUALITY PROTEIN: T-cell leukemia homeobox protein 3 [Takifugu rubripes]
XP_004076957	PREDICTED: T-cell leukemia homeobox protein 1-like [Oryzias latipes]
XP_004077224	PREDICTED: homeobox protein MSX-2 isoform X1 [Oryzias latipes]
XP_004426714	PREDICTED: homeobox protein Hox-D3 [Ceratotherium simum simum]
XP_004555954	PREDICTED: homeobox protein MSX-2-like [Maylandia zebra]
XP_004925027	PREDICTED: homeobox protein Hox-B4 [Bombyx mori]
XP_004933018	PREDICTED: homeotic protein empty spiracles-like [Bombyx mori]
XP_004933035	PREDICTED: homeobox protein HMX3-B [Bombyx mori]
XP_004933055	PREDICTED: homeobox protein slou [Bombyx mori]
XP_004933121	PREDICTED: transcription factor LBX1-like [Bombyx mori]
XP_005049129	PREDICTED: homeobox protein Hox-D3 [Ficedula albicollis]
XP_005179335	PREDICTED: homeotic protein empty spiracles [Musca domestica]
XP_005189125	PREDICTED: homeobox protein slou-like, partial [Musca domestica]
XP_005303794	PREDICTED: brain-specific homeobox protein homolog [Chrysemys picta bellii]
XP_005305386	PREDICTED: homeobox protein Nkx-6.2 [Chrysemys picta bellii]
XP_005349079	PREDICTED: homeobox protein Nkx-2.5 [Microtus ochrogaster]
XP_005512968	PREDICTED: barH-like 1 homeobox protein [Columba livia]
XP_005519892	PREDICTED: homeobox protein Hox-D3 [Pseudopodoces humilis]
XP_005979335	PREDICTED: homeobox protein Hox-A3 [Pantholops hodgsonii]
XP_005992571	PREDICTED: homeobox protein Nkx-2.5 [Latimeria chalumnae]
XP_006003775	PREDICTED: homeobox protein Nkx-6.2 [Latimeria chalumnae]
XP_006024676	PREDICTED: homeobox protein Nkx-6.2 [Alligator sinensis]
XP_006136686	PREDICTED: homeobox protein Nkx-6.2 [Pelodiscus sinensis]
XP_006137362	PREDICTED: barH-like 2 homeobox protein [Pelodiscus sinensis]
XP_006274581	PREDICTED: brain-specific homeobox protein homolog [Alligator mississippiensis]
XP_006723629	PREDICTED: homeobox protein Nkx-2.2 isoform X2 [Homo sapiens]
XP_006895666	PREDICTED: brain-specific homeobox protein homolog [Elephantulus edwardii]
XP_006895718	PREDICTED: homeobox protein Nkx-2.2-like [Elephantulus edwardii]
XP_006978927	PREDICTED: homeobox protein Nkx-2.5 [Peromyscus maniculatus bairdii]
XP_007053086	PREDICTED: homeobox protein Nkx-6.2 [Chelonia mydas]
XP_007067023	PREDICTED: brain-specific homeobox protein homolog [Chelonia mydas]
XP_007085565	PREDICTED: homeobox protein MSX-2 [Panthera tigris altaica]
XP_007258178	PREDICTED: brain-specific homeobox protein homolog [Astyanax mexicanus]
XP_007524430	PREDICTED: homeobox protein MSX-2 [Erinaceus europaeus]
XP_007525491	PREDICTED: homeobox protein Nkx-2.2 [Erinaceus europaeus]
XP_007565863	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia formosa]
XP_007566853	PREDICTED: homeobox protein Nkx-6.2-like [Poecilia formosa]
XP_007651972	PREDICTED: homeobox protein GBX-2 [Cricetulus griseus]
XP_007896539	PREDICTED: homeobox protein Nkx-2.2 [Callorhinchus milii]
XP_007907293	PREDICTED: homeobox protein Nkx-2.3 [Callorhinchus milii]
XP_008068304	PREDICTED: homeobox protein Nkx-2.2 [Tarsius syrichta]
XP_008193415	PREDICTED: homeobox protein ceh-31-like [Tribolium castaneum]
XP_008195160	PREDICTED: homeobox protein Hox-D4a [Tribolium castaneum]
XP_008295823	PREDICTED: homeobox protein MSX-2-like [Stegastes partitus]

XP_008299788	PREDICTED: T-cell leukemia homeobox protein 1-like [Stegastes partitus]
XP_008325234	PREDICTED: T-cell leukemia homeobox protein 3 [Cynoglossus semilaevis]
XP_008418492	PREDICTED: T-cell leukemia homeobox protein 3 [Poecilia reticulata]
XP_008473261	PREDICTED: homeobox protein B-H1-like [Diaphorina citri]
XP_008487559	PREDICTED: homeobox protein DBX1-A-like [Diaphorina citri]
XP_008489821	PREDICTED: barH-like 1 homeobox protein, partial [Calypte anna]
XP_008494359	PREDICTED: homeobox protein MSX-1 [Calypte anna]
XP_008548384	PREDICTED: homeobox protein EMX1 [Microplitis demolitor]
XP_008633065	PREDICTED: homeobox protein Hox-D3 [Corvus brachyrhynchos]
XP_008919202	PREDICTED: homeobox protein MSX-1 [Manacus vitellinus]
XP_009012574	hypothetical protein HELRODRAFT_152036, partial [Helobdella robusta]
XP_009046454	hypothetical protein LOTGIDRAFT_72890, partial [Lottia gigantea]
XP_009055779	hypothetical protein LOTGIDRAFT_119124 [Lottia gigantea]
XP_009056433	hypothetical protein LOTGIDRAFT_120090, partial [Lottia gigantea]
XP_009086561	PREDICTED: homeobox protein Hox-D3 [Serinus canaria]
XP_009276955	PREDICTED: homeobox protein Hox-D3, partial [Aptenodytes forsteri]
XP_009319165	PREDICTED: homeobox protein notochord-like [Pygoscelis adeliae]
XP_009327169	PREDICTED: homeobox protein MSX-1 [Pygoscelis adeliae]
XP_009485378	PREDICTED: homeobox protein not2-like, partial [Pelecanus crispus]
XP_009499002	PREDICTED: homeobox protein notochord-like, partial [Phalacrocorax carbo]
XP_009511207	PREDICTED: LOW QUALITY PROTEIN: barH-like 2 homeobox protein, partial [Phalacrocorax carbo]
XP_009645359	PREDICTED: homeobox protein MSX-2 [Egretta garzetta]
XP_009894572	PREDICTED: barH-like 1 homeobox protein, partial [Picoides pubescens]
XP_009944864	PREDICTED: homeobox protein notochord-like, partial [Leptosomus discolor]
XP_009958515	PREDICTED: homeobox protein Hox-B3, partial [Leptosomus discolor]
XP_009993327	PREDICTED: brain-specific homeobox protein homolog [Chaetura pelagica]
XP_010125476	PREDICTED: homeobox protein GHOX-7-like, partial [Chlamydotis macqueenii]
XP_010140778	PREDICTED: homeobox protein not2-like, partial [Buceros rhinoceros silvestris]
XP_010158126	PREDICTED: homeobox protein Nkx-2.6-like, partial [Eurypyga helias]
XP_010160639	PREDICTED: homeobox protein not2-like, partial [Caprimulgus carolinensis]
XP_010183846	PREDICTED: LOW QUALITY PROTEIN: homeobox protein notochord-like, partial [Mesitornis unicolor]
XP_010218153	PREDICTED: homeobox protein MSX-1 [Tinamus guttatus]
XP_010292386	PREDICTED: homeobox protein not2-like, partial [Phaethon lepturus]
XP_010295047	PREDICTED: homeobox protein H17, partial [Phaethon lepturus]
XP_010708737	PREDICTED: homeobox protein MSX-1 [Meleagris gallopavo]
XP_010708946	PREDICTED: LOW QUALITY PROTEIN: homeobox protein not2-like [Meleagris gallopavo]
XP_010726324	PREDICTED: homeobox protein Hox-D3-like, partial [Meleagris gallopavo]
XP_010740428	PREDICTED: homeobox protein MSX-1 [Larimichthys crocea]
XP_010765038	PREDICTED: barH-like 2 homeobox protein [Notothenia coriiceps]
XP_010868231	PREDICTED: homeobox protein HMX3-like [Esox lucius]
XP_010870399	PREDICTED: barH-like 2 homeobox protein [Esox lucius]
XP_010892954	PREDICTED: T-cell leukemia homeobox protein 3-like [Esox lucius]
XP_010894067	PREDICTED: T-cell leukemia homeobox protein 3 [Esox lucius]
XP_010965528	PREDICTED: brain-specific homeobox protein homolog [Camelus bactrianus]
XP_011055476	PREDICTED: homeotic protein proboscipedia isoform X2 [Acromyrmex echinatior]
XP_011142568	PREDICTED: homeotic protein empty spiracles-like [Harpegnathos saltator]
XP_011149287	PREDICTED: homeotic protein proboscipedia [Harpegnathos saltator]
XP_011155414	PREDICTED: homeotic protein proboscipedia [Solenopsis invicta]
XP_011182688	PREDICTED: ras guanine nucleotide exchange factor K [Bactrocera cucurbitae]
XP_011185992	PREDICTED: homeotic protein empty spiracles [Bactrocera cucurbitae]
XP_011212609	PREDICTED: homeotic protein empty spiracles [Bactrocera dorsalis]
XP_011214245	PREDICTED: uncharacterized protein PB18E9.04c [Bactrocera dorsalis]
XP_011256835	PREDICTED: homeobox protein B-H2-like [Camponotus floridanus]
XP_011258070	PREDICTED: homeobox protein abdominal-B [Camponotus floridanus]
XP_011283973	PREDICTED: homeobox protein GBX-2 [Felis catus]
XP_011310234	PREDICTED: homeobox protein GBX-2 [Fopius arisanus]
XP_011310733	PREDICTED: homeobox protein H2.0-like isoform X1 [Fopius arisanus]
XP_011311710	PREDICTED: homeobox protein abdominal-B isoform X1 [Fopius arisanus]
XP_011311711	PREDICTED: homeobox protein abdominal-B isoform X2 [Fopius arisanus]
XP_011311712	PREDICTED: homeobox protein abdominal-B isoform X3 [Fopius arisanus]
XP_011342230	PREDICTED: homeotic protein proboscipedia [Cerapachys biroi]
XP_011344364	PREDICTED: homeobox protein B-H2 [Cerapachys biroi]
XP_011345364	PREDICTED: uncharacterized protein LOC105283926 [Cerapachys biroi]
XP_011414445	PREDICTED: homeobox protein GBX-2-like [Crassostrea gigas]
XP_011437391	PREDICTED: homeobox protein Nkx-2.2a-like [Crassostrea gigas]
XP_011441569	PREDICTED: homeobox protein Dlx6a-like [Crassostrea gigas]
XP_011445831	PREDICTED: transcription factor LBX1-like [Crassostrea gigas]
XP_011451803	PREDICTED: homeobox protein Nkx-2.1-like [Crassostrea gigas]

XP_011482809	PREDICTED: homeobox protein MSX-2 isoform X2 [Oryzias latipes]
XP_011495613	PREDICTED: homeobox protein Nkx-6.1 [Ceratosolen solmsi marchali]
XP_011561507	PREDICTED: homeobox protein Hmx [Plutella xylostella]
XP_011569017	PREDICTED: homeobox protein Hox-B4-like [Plutella xylostella]
XP_011569355	PREDICTED: homeotic protein empty spiracles-like [Plutella xylostella]
XP_011587172	PREDICTED: LOW QUALITY PROTEIN: homeobox protein notochord-like, partial [Aquila chrysaetos canadensis]
XP_011637906	PREDICTED: homeobox protein B-H2 [Pogonomyrmex barbatus]
XP_011639093	PREDICTED: homeotic protein proboscipedia [Pogonomyrmex barbatus]
XP_011640429	PREDICTED: uncharacterized protein LOC105429261 isoform X2 [Pogonomyrmex barbatus]
XP_011695901	PREDICTED: homeotic protein proboscipedia [Wasmannia auropunctata]
XP_011866947	PREDICTED: uncharacterized protein LOC105561511 [Vollenhovia emeryi]
XP_011870664	PREDICTED: homeotic protein proboscipedia [Vollenhovia emeryi]
XP_012054481	PREDICTED: homeotic protein proboscipedia [Atta cephalotes]
XP_012060611	PREDICTED: uncharacterized protein LOC105623848 [Atta cephalotes]
XP_012143108	PREDICTED: uncharacterized protein LOC100882296 [Megachile rotundata]
XP_012162595	PREDICTED: homeobox protein Nkx-2.1 isoform X1 [Ceratitis capitata]
XP_012225633	PREDICTED: homeotic protein proboscipedia [Linepithema humile]
XP_012230217	PREDICTED: uncharacterized protein LOC105676703 [Linepithema humile]
XP_012248486	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100750176 [Bombus impatiens]
XP_012252406	PREDICTED: homeobox protein EMX1-like [Athalia rosae]
XP_012268630	PREDICTED: homeobox protein B-H1-like [Athalia rosae]
XP_012343890	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100866975 [Apis florea]
XP_012542576	PREDICTED: homeotic protein proboscipedia [Monomorium pharaonis]
XP_012679297	PREDICTED: homeobox protein Nkx-2.2a-like [Clupea harengus]
XP_012683084	PREDICTED: brain-specific homeobox protein homolog [Clupea harengus]
XP_012685430	PREDICTED: T-cell leukemia homeobox protein 3-like [Clupea harengus]
XP_012686839	PREDICTED: homeobox protein Nkx-2.5 [Clupea harengus]
XP_012687703	PREDICTED: homeobox protein Nkx-2.3 [Clupea harengus]
XP_012693523	PREDICTED: homeobox protein Nkx-2.2a [Clupea harengus]
XP_012707525	PREDICTED: T-cell leukemia homeobox protein 1 [Fundulus heteroclitus]
XP_012873727	PREDICTED: barH-like 2 homeobox protein [Dipodomys ordii]
XP_012984340	PREDICTED: homeobox protein MSX-1 [Melopsittacus undulatus]
XP_013063618	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Biomphalaria glabrata]
XP_013103134	PREDICTED: homeotic protein empty spiracles [Stomoxys calcitrans]
XP_013106133	PREDICTED: homeobox protein unplugged-like, partial [Stomoxys calcitrans]
XP_013106527	PREDICTED: serine-rich adhesin for platelets [Stomoxys calcitrans]
XP_013108189	PREDICTED: homeobox protein B-H2-like [Stomoxys calcitrans]
XP_013141799	PREDICTED: homeotic protein empty spiracles-like [Papilio polytes]
XP_013165380	PREDICTED: homeobox protein slou-like [Papilio xuthus]
XP_013165384	PREDICTED: barH-like 1 homeobox protein [Papilio xuthus]
XP_013165415	PREDICTED: homeotic protein empty spiracles-like [Papilio xuthus]
XP_013177038	PREDICTED: homeobox protein GBX-2-like [Papilio xuthus]
XP_013185056	PREDICTED: homeobox protein BarH-like 1b [Amyelois transitella]
XP_013185500	PREDICTED: motor neuron and pancreas homeobox protein 1-like [Amyelois transitella]
XP_013188056	PREDICTED: homeobox protein HMX3-like [Amyelois transitella]
XP_013188077	PREDICTED: homeobox protein slou-like [Amyelois transitella]
XP_013197085	PREDICTED: homeotic protein empty spiracles-like [Amyelois transitella]
XP_013378776	PREDICTED: homeobox protein Nkx-2.5-like [Lingula anatina]
XP_013378782	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Lingula anatina]
XP_013378788	PREDICTED: transcription factor LBX1-like [Lingula anatina]
XP_013394544	PREDICTED: homeobox protein Dlx1a-like isoform X1 [Lingula anatina]
XP_013394545	PREDICTED: homeobox protein Dlx1a-like isoform X2 [Lingula anatina]
XP_013403731	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013403757	PREDICTED: homeobox protein slou-like [Lingula anatina]
XP_013403758	PREDICTED: homeobox protein HMX3-like [Lingula anatina]
XP_013404623	PREDICTED: homeobox protein Nkx-2.2-like [Lingula anatina]
XP_013772635	PREDICTED: homeobox protein Nkx-2.2-like [Limulus polyphemus]
XP_013773695	PREDICTED: homeobox protein DBX1-B-like [Limulus polyphemus]
XP_013774538	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013774650	PREDICTED: homeobox protein EMX1-like, partial [Limulus polyphemus]
XP_013774651	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013775139	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013775457	PREDICTED: homeobox protein Hox-A11b-like [Limulus polyphemus]
XP_013775485	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013776086	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013776376	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]
XP_013776441	PREDICTED: homeobox protein lin-39-like [Limulus polyphemus]
XP_013776459	PREDICTED: homeobox protein DBX1-A-like [Limulus polyphemus]
XP_013776587	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013776843	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]

XP_013777106	PREDICTED: protein enabled homolog [Limulus polyphemus]
XP_013777707	PREDICTED: homeobox protein abdominal-B-like [Limulus polyphemus]
XP_013777866	PREDICTED: homeobox protein EMX1-like [Limulus polyphemus]
XP_013780476	PREDICTED: homeobox protein slou-like [Limulus polyphemus]
XP_013780477	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783221	PREDICTED: brain-specific homeobox protein homolog [Limulus polyphemus]
XP_013783383	PREDICTED: homeobox protein HMX3-B-like [Limulus polyphemus]
XP_013783573	PREDICTED: homeobox protein ceh-31-like [Limulus polyphemus]
XP_013783575	PREDICTED: barH-like 1 homeobox protein, partial [Limulus polyphemus]
XP_013783643	PREDICTED: NK1 transcription factor-related protein 1-like [Limulus polyphemus]
XP_013783998	PREDICTED: homeobox protein MSX-2-like [Limulus polyphemus]
XP_013785537	PREDICTED: homeotic protein distal-less-like [Limulus polyphemus]
XP_013785548	PREDICTED: homeobox protein B-H1-like [Limulus polyphemus]
XP_013785691	PREDICTED: homeobox protein Nkx-6.2-like [Limulus polyphemus]
XP_013786467	PREDICTED: homeobox protein vnd-like [Limulus polyphemus]
XP_013786746	PREDICTED: paired box protein Pax-6-like [Limulus polyphemus]
XP_013787176	PREDICTED: homeobox protein MSX-3-like [Limulus polyphemus]
XP_013788660	PREDICTED: homeobox protein DLX-6-like [Limulus polyphemus]
XP_013789064	PREDICTED: homeobox protein Nkx-2.5-like [Limulus polyphemus]
XP_013789774	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013790705	PREDICTED: homeobox protein HMX3-like [Limulus polyphemus]
XP_013790991	PREDICTED: homeotic protein proboscipedia-like, partial [Limulus polyphemus]
XP_013791445	PREDICTED: homeobox protein ceh-31-like, partial [Limulus polyphemus]
XP_013792320	PREDICTED: homeobox protein ceh-1-like, partial [Limulus polyphemus]
XP_013792414	PREDICTED: homeobox protein DBX1-A-like, partial [Limulus polyphemus]
XP_013794105	PREDICTED: homeobox protein abdominal-B-like [Limulus polyphemus]
XP_013794355	PREDICTED: homeobox protein unplugged-like [Limulus polyphemus]
XP_013794488	PREDICTED: T-cell leukemia homeobox protein 3-like [Limulus polyphemus]
XP_013794489	PREDICTED: transcription factor LBX1-like [Limulus polyphemus]
XP_013794562	PREDICTED: homeobox protein Nkx-2.1-like [Limulus polyphemus]
XP_013867753	PREDICTED: homeobox protein MSX-2-like [Austrofundulus limnaeus]
XP_013879114	PREDICTED: barH-like 2 homeobox protein [Austrofundulus limnaeus]
XP_013921049	PREDICTED: homeobox protein MSX-2 [Thamnophis sirtalis]
XP_013978546	PREDICTED: barH-like 2 homeobox protein [Salmo salar]
XP_013983956	PREDICTED: T-cell leukemia homeobox protein 3-like isoform X1 [Salmo salar]
XP_014052040	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014065863	PREDICTED: homeobox protein Nkx-2.2 isoform X1 [Salmo salar]
XP_014068039	PREDICTED: T-cell leukemia homeobox protein 3-like [Salmo salar]
XP_014088070	PREDICTED: homeotic protein empty spiracles [Bactrocera oleae]
XP_014092007	PREDICTED: homeobox protein slou [Bactrocera oleae]
XP_014209645	PREDICTED: homeobox protein GBX-1-like [Copidosoma floridanum]
XP_014235722	PREDICTED: homeotic protein antennapedia [Trichogramma pretiosum]
XP_014240565	PREDICTED: homeobox protein abdominal-B isoform X1 [Cimex lectularius]
XP_014240567	PREDICTED: homeobox protein abdominal-B isoform X2 [Cimex lectularius]
XP_014241910	PREDICTED: homeobox protein EMX2-like isoform X1 [Cimex lectularius]
XP_014241911	PREDICTED: homeotic protein empty spiracles-like isoform X2 [Cimex lectularius]
XP_014242016	PREDICTED: transcription factor LBX1-like [Cimex lectularius]
XP_014242034	PREDICTED: homeobox protein HMX3-like [Cimex lectularius]
XP_014245972	PREDICTED: homeotic protein distal-less isoform X2 [Cimex lectularius]
XP_014249513	PREDICTED: homeobox protein Nkx-2.1-like [Cimex lectularius]
XP_014258841	PREDICTED: homeobox protein DBX1-A [Cimex lectularius]
XP_014274437	PREDICTED: homeobox protein Nkx-2.1-like [Halyomorpha halys]
XP_014280507	PREDICTED: homeobox protein HMX3-like [Halyomorpha halys]
XP_014283662	PREDICTED: homeobox protein DBX1-A-like [Halyomorpha halys]
XP_014293083	PREDICTED: homeobox protein HMX3-like, partial [Halyomorpha halys]
XP_014328725	PREDICTED: T-cell leukemia homeobox protein 3 [Xiphophorus maculatus]
XP_014361996	PREDICTED: homeobox protein HMX3-B-like [Papilio machaon]
XP_014364712	PREDICTED: homeotic protein empty spiracles-like [Papilio machaon]
XP_014370704	PREDICTED: barH-like 1 homeobox protein [Papilio machaon]
XP_014385363	PREDICTED: barH-like 1 homeobox protein, partial [Myotis brandtii]

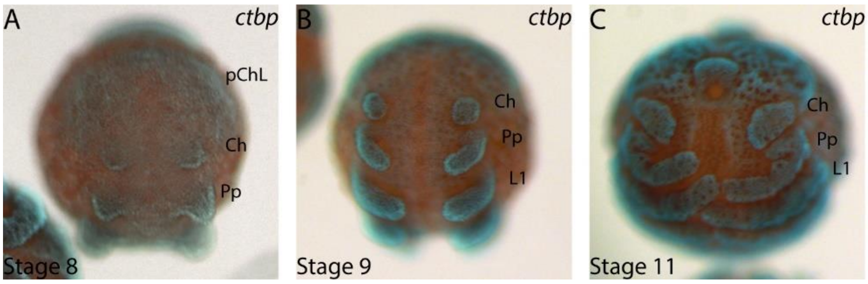
9.4.2.37 *Vrille*

Name	Description
AAF52237	vrille, isoform A [Drosophila melanogaster]
Locus_1_Transcript_125429/166847_Confidence_1.000_Length_437 - ORF 1 (frame 1) translation	Locus_1_Transcript_125429/166847_Confidence_1.000_Length_437
Locus_43_Transcript_16/16_Confidence_0.276_Length_4474 - ORF 16 (frame 3) translation	Locus_43_Transcript_16/16_Confidence_0.276_Length_4474

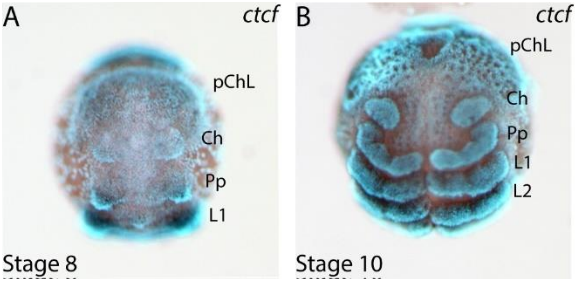
Locus_16266_Transcript_8/8_Confidence_0.600_Length_3978 - ORF 2 (frame 3) translation	Locus_16266_Transcript_8/8_Confidence_0.600_Length_3978
NFIL3_MOUSE	RecName: Full=Nuclear factor interleukin-3-regulated protein; AltName: Full=E4 promoter-binding protein 4; AltName: Full=Embryo implantation-related NFIL3/E4BP4-like transcription factor
NP_001123286	hepatic leukemia factor [Strongylocentrotus purpuratus]
NP_001292257	hepatic leukemia factor-like [Crassostrea gigas]
O08750 (NFIL3_MOUSE)	RecName: Full=Nuclear factor interleukin-3-regulated protein; AltName: Full=E4 promoter-binding protein 4; AltName: Full=Embryo implantation-related NFIL3/E4BP4-like transcription factor
P41224 (TEF_RAT)	RecName: Full=Thyrotroph embryonic factor
P97516 (TEF_PHOSU)	RecName: Full=Thyrotroph embryonic factor
Q5FW38 (NFIL3_XENTR)	RecName: Full=Nuclear factor interleukin-3-regulated protein
Q6IMZ0 (NFIL3_RAT)	RecName: Full=Nuclear factor interleukin-3-regulated protein; AltName: Full=E4 promoter-binding protein 4
Q8BW74 (HLF_MOUSE)	RecName: Full=Hepatic leukemia factor
Q08D88 (NFIL3_BOVIN)	RecName: Full=Nuclear factor interleukin-3-regulated protein
Q9JLC6 (TEF_MOUSE)	RecName: Full=Thyrotroph embryonic factor
Q32PF6 (DBP_BOVIN)	RecName: Full=D site-binding protein; AltName: Full=Albumin D box-binding protein; AltName: Full=Albumin D-element-binding protein
Q66J36 (NFIL3_XENLA)	RecName: Full=Nuclear factor interleukin-3-regulated protein
Q68EL6 (NFIL3_DANRE)	RecName: Full=Nuclear factor interleukin-3-regulated protein
Q90Z72 (NFIL3_CHICK)	RecName: Full=Nuclear factor interleukin-3-regulated protein; AltName: Full=E4 promoter-binding protein 4; Short=cE4BP4 protein; AltName: Full=bZIP protein E4BP4
Q10586 (DBP_HUMAN)	RecName: Full=D site-binding protein; AltName: Full=Albumin D box-binding protein; AltName: Full=Albumin D-element-binding protein; AltName: Full=Tax-responsive enhancer element-binding protein 302; Short=TaxREB302
Q10587 (TEF_HUMAN)	RecName: Full=Thyrotroph embryonic factor
Q16534 (HLF_HUMAN)	RecName: Full=Hepatic leukemia factor
Q16649 (NFIL3_HUMAN)	RecName: Full=Nuclear factor interleukin-3-regulated protein; AltName: Full=E4 promoter-binding protein 4; AltName: Full=Interleukin-3 promoter transcriptional activator; AltName: Full=Interleukin-3-binding protein 1; AltName: Full=Transcriptional activator NF-IL3A
Q60925 (DBP_MOUSE)	RecName: Full=D site-binding protein; AltName: Full=Albumin D box-binding protein; AltName: Full=Albumin D-element-binding protein
Q64709 (HLF_RAT)	RecName: Full=Hepatic leukemia factor
Q92172 (TEF_CHICK)	RecName: Full=Transcription factor VBP; AltName: Full=Thyrotroph embryonic factor homolog; AltName: Full=Vitellogenin gene-binding protein
Q94126 (CES2_CAEEL)	RecName: Full=Cell death specification protein 2
XP_002404320	thyrotroph embryonic factor, putative [Ixodes scapularis]
XP_002433590	transcriptional factor nfil3/e4bp4, putative [Ixodes scapularis]
XP_002640738	C. briggsae CBR-CES-2 protein, partial [Caenorhabditis briggsae]
XP_003107426	CRE-CES-2 protein [Caenorhabditis remanei]
XP_003746003	PREDICTED: hepatic leukemia factor-like [Metaseiulus occidentalis]
XP_011417277	PREDICTED: protein giant-like [Crassostrea gigas]
XP_011419051	PREDICTED: hepatic leukemia factor-like [Crassostrea gigas]
XP_012171859	PREDICTED: thyrotroph embryonic factor isoform X5 [Bombus terrestris]
XP_012171860	PREDICTED: hepatic leukemia factor isoform X6 [Bombus terrestris]
XP_012230396	PREDICTED: ras guanine nucleotide exchange factor B-like isoform X1 [Linepithema humile]
XP_012230399	PREDICTED: ras guanine nucleotide exchange factor B-like isoform X2 [Linepithema humile]
XP_012942276	PREDICTED: uncharacterized protein LOC101859809 [Aplysia californica]
XP_012948180	PREDICTED: hepatic leukemia factor, partial [Anas platyrhynchos]
XP_013069428	PREDICTED: D site-binding protein-like isoform X1 [Biomphalaria glabrata]
XP_013069431	PREDICTED: D site-binding protein-like isoform X2 [Biomphalaria glabrata]
XP_013069434	PREDICTED: D site-binding protein-like isoform X3 [Biomphalaria glabrata]
XP_013773215	PREDICTED: uncharacterized protein LOC106458273 [Limulus polyphemus]
XP_013774205	PREDICTED: nuclear factor interleukin-3-regulated protein-like, partial [Limulus polyphemus]
XP_013776078	PREDICTED: nuclear factor interleukin-3-regulated protein-like isoform X1 [Limulus polyphemus]
XP_013776080	PREDICTED: nuclear factor interleukin-3-regulated protein-like isoform X2 [Limulus polyphemus]
XP_013787291	PREDICTED: thyrotroph embryonic factor-like [Limulus polyphemus]
XP_013791984	PREDICTED: hepatic leukemia factor-like [Limulus polyphemus]
XP_014249420	PREDICTED: nuclear factor interleukin-3-regulated protein isoform X1 [Cimex lectularius]
XP_014249421	PREDICTED: nuclear factor interleukin-3-regulated protein isoform X2 [Cimex lectularius]
XP_014249424	PREDICTED: nuclear factor interleukin-3-regulated protein isoform X3 [Cimex lectularius]

9.4.3 In situ pictures

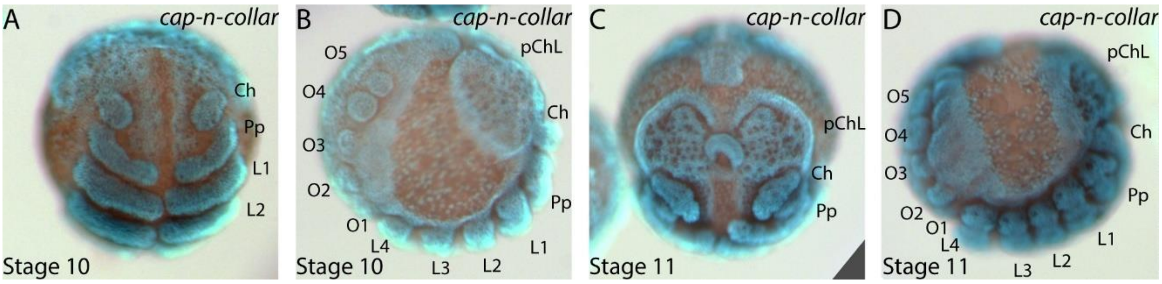
9.4.3.1 *CtBP*



9.4.3.2 *CTCF*

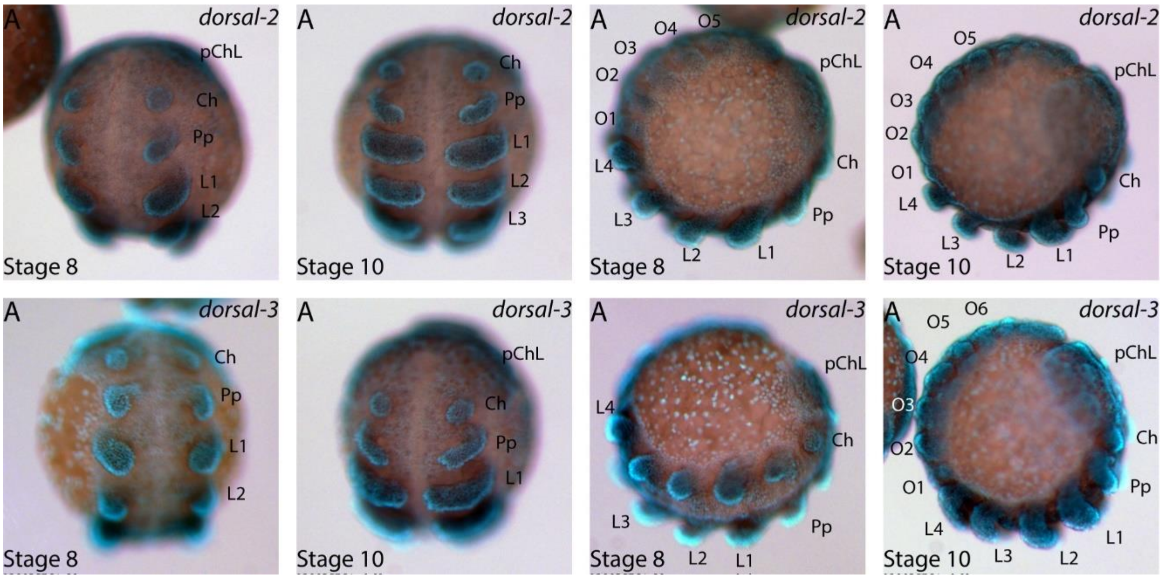


9.4.3.3 *Cap n collar*

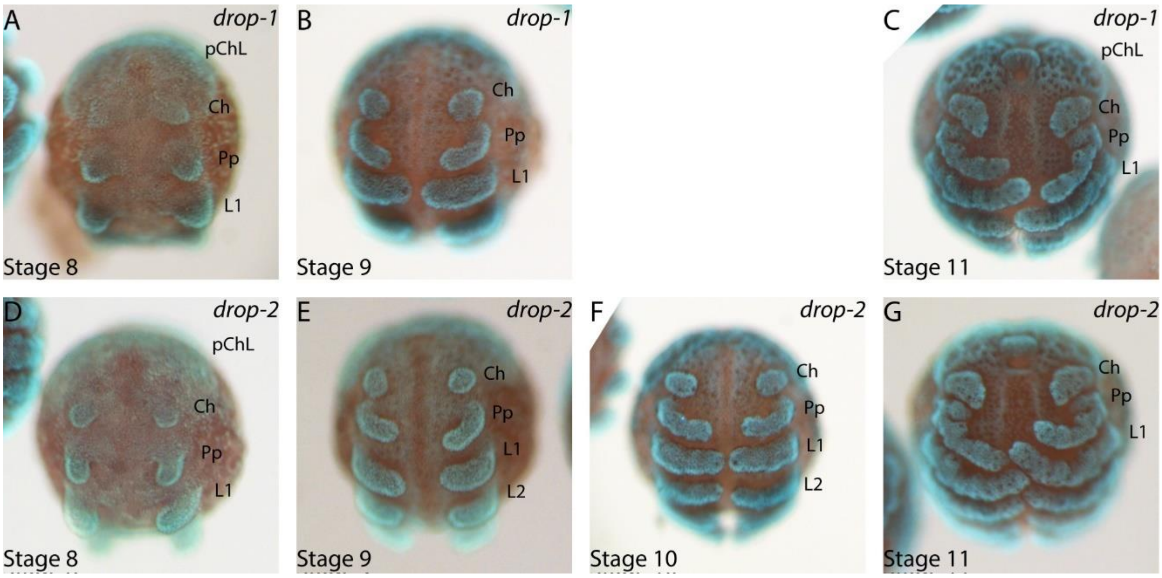


9.4.3.4 *Daughterless*

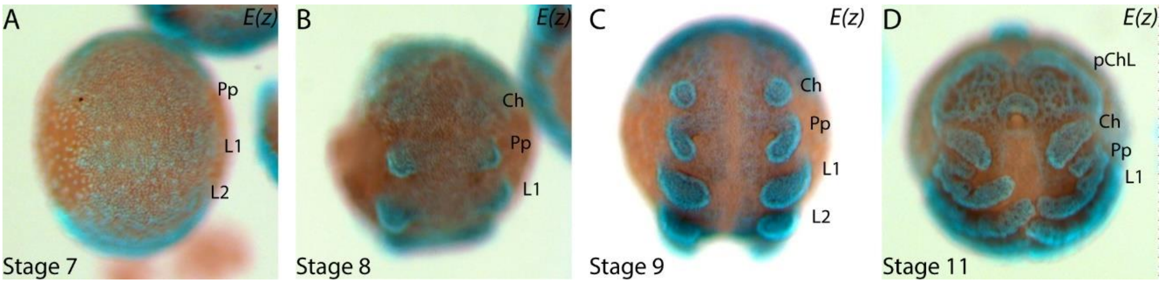
9.4.3.5 *Dorsal*



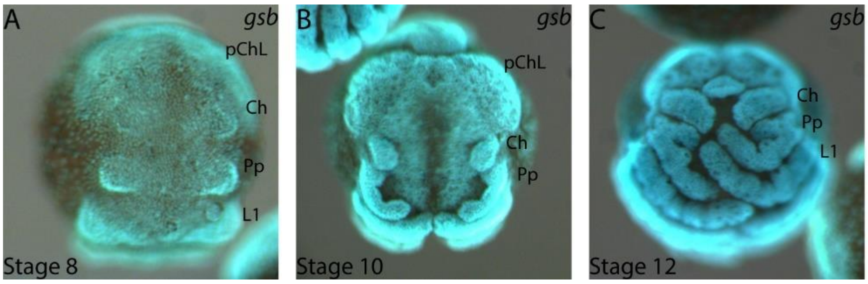
9.4.3.6 *Drop 1 and 2*



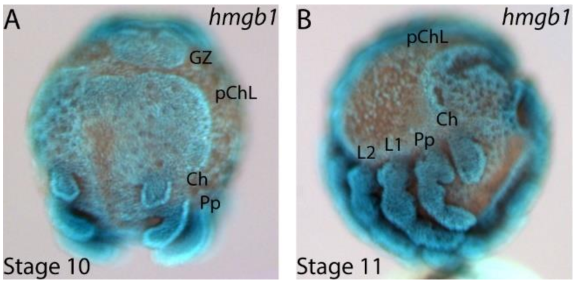
9.4.3.7 *Enhancer of zeste*



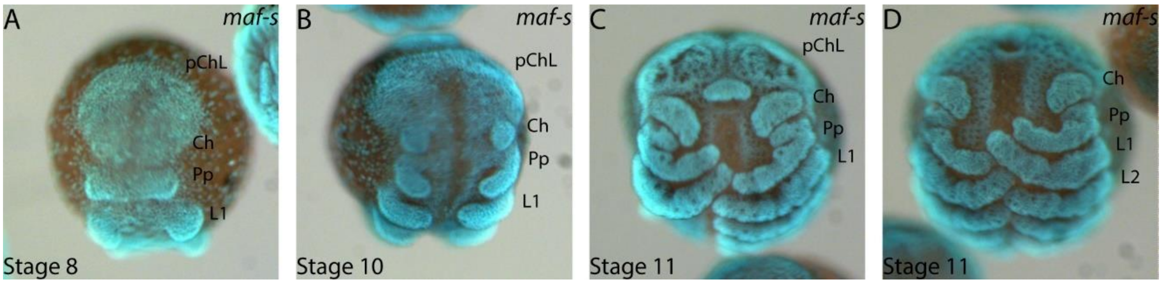
9.4.3.8 *Gooseberry*



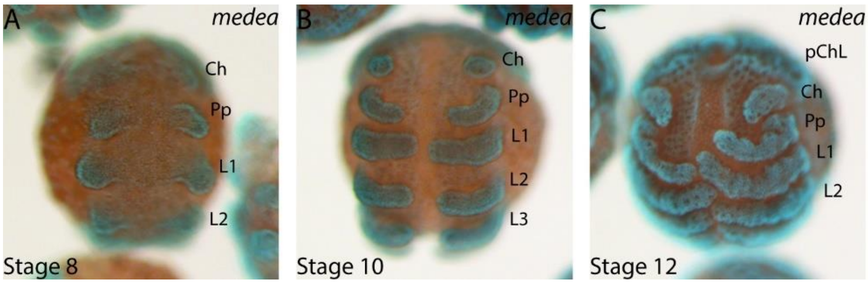
9.4.3.9 *HMGB1*



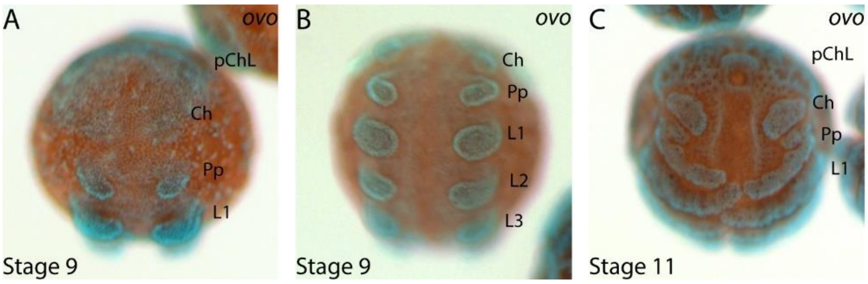
9.4.3.10 *MafS*



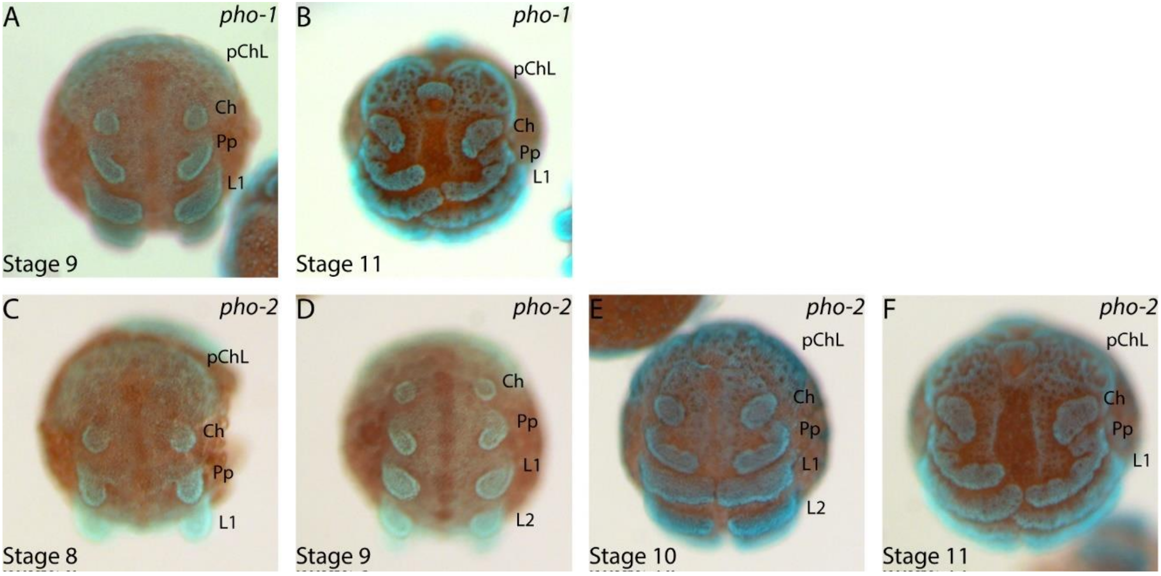
9.4.3.11 *Medea*



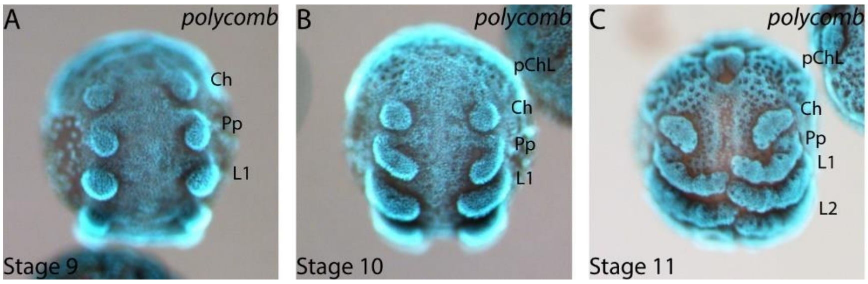
9.4.3.12 *Ovo / Shaven baby*



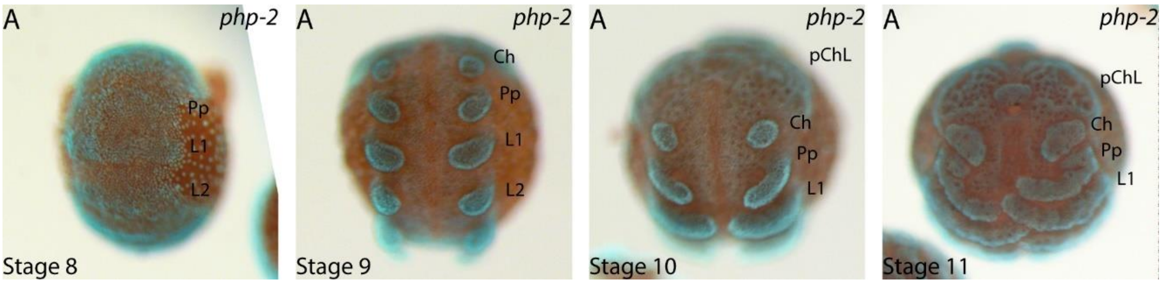
9.4.3.13 *Pleiohomeotic*



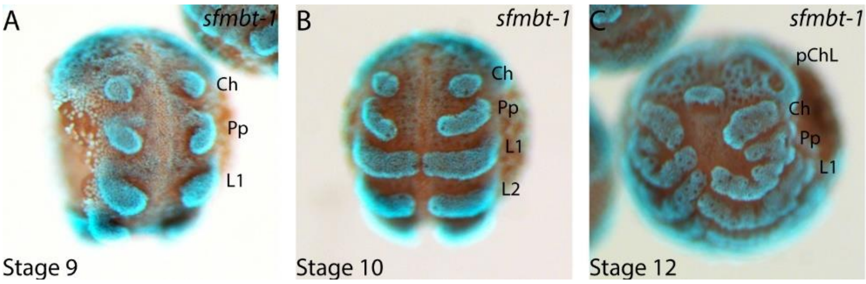
9.4.3.14 *Polycomb*



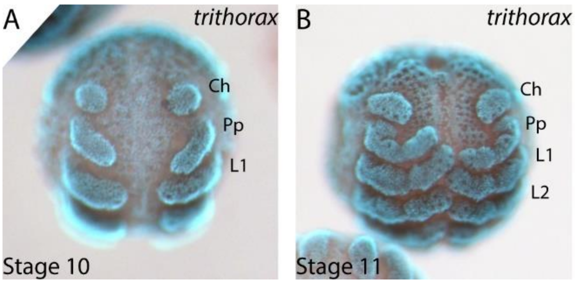
9.4.3.15 *Polyhomeotic proximal*



9.4.3.16 *Sfmbt*



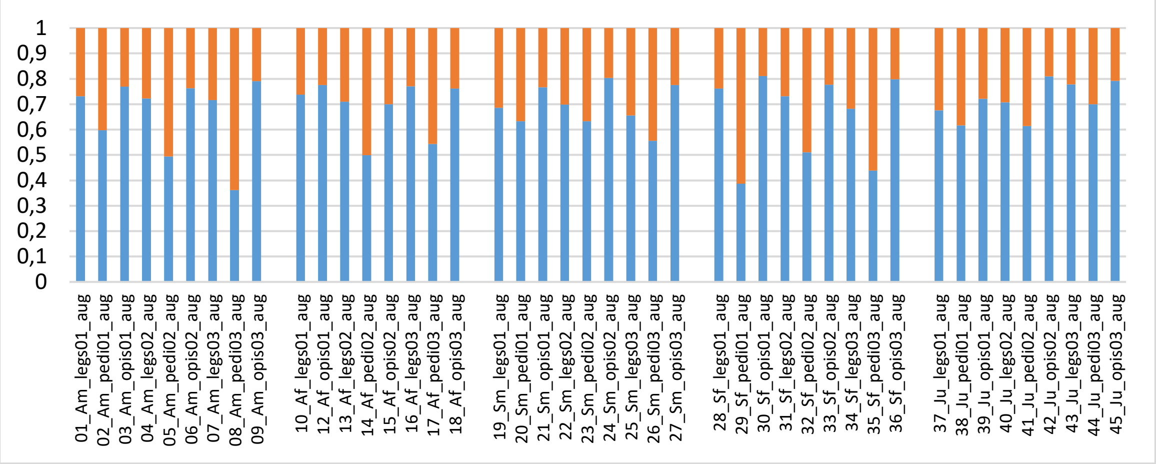
9.4.3.17 *Trithorax*



9.5 Development of the bulbus organ of adult males in *Parasteatoda tepidariorum*

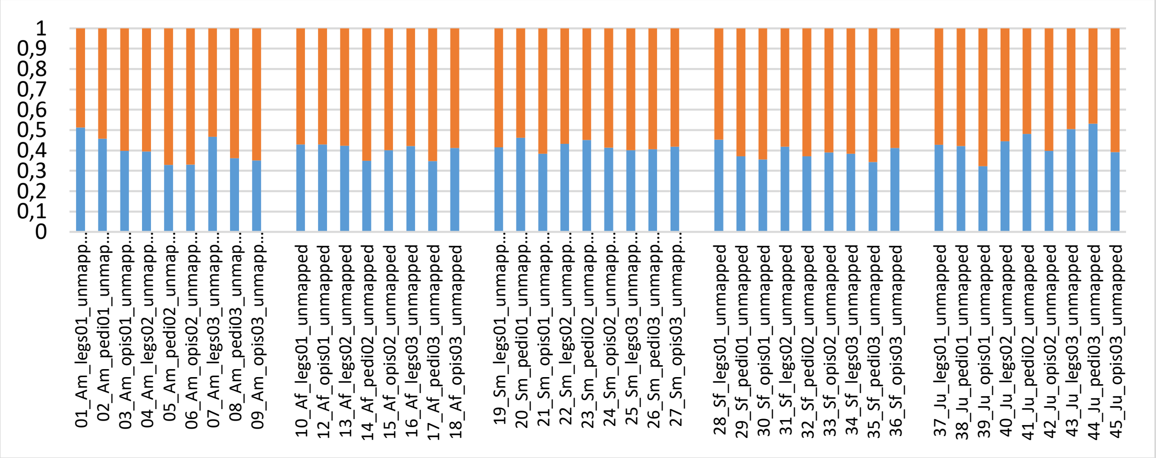
9.5.1 Mapping statistics

9.5.1.1 *Initial mapping to aug mRNA predictions*



Proportion of reads mapped to the mRNA predictions. Blue = mapped, orange = unmapped

9.5.1.2 *Mapping of unmapped reads to the Parasteatoda genome*



Proportion of reads, which did not map to the mRNA predictions, mapped to the genome sequence, showing, that approximately half of the reads, which did not map to the mRNA predictions were genomic contamination. Blue = mapped, orange = unmapped. Reads, which were still unmapped were combined into one file and analysed with Kraken, to identify contaminations from other organisms, which was the case for 47.9% of these sequences. The remaining reads are likely unmapped, due to allelic sequences, caused by lower inbreeding in the spider culture.

9.5.2 GO terms associated with down-regulated genes in appendages and pedipalps

9.5.2.1 *Juveniles*

Down-regulated in juvenile appendage			
category	**over-represented pvalue**	**term**	**ontology**
GO:0015293	3.89E-38	symporter activity	MF
GO:0044281	5.98E-33	small molecule metabolic process	BP
GO:0015291	4.36E-30	secondary active transmembrane transporter activity	MF
GO:0022804	8.60E-30	active transmembrane transporter activity	MF
GO:0004497	1.58E-26	monooxygenase activity	MF
GO:0016491	1.70E-26	oxidoreductase activity	MF
GO:0046906	3.08E-26	tetrapyrrole binding	MF
GO:0019752	7.28E-26	carboxylic acid metabolic process	BP
GO:0006082	8.41E-26	organic acid metabolic process	BP
GO:0043436	1.52E-25	oxoacid metabolic process	BP
GO:0006629	1.30E-23	lipid metabolic process	BP
GO:0016705	9.60E-23	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF
GO:0071702	1.58E-21	organic substance transport	BP
GO:0032787	5.19E-21	monocarboxylic acid metabolic process	BP
GO:0030163	5.29E-21	protein catabolic process	BP

Down-regulated in juvenile pedipalps			
category	**over-represented pvalue**	**term**	**ontology**
GO:0071689	1.44E-09	muscle thin filament assembly	BP
GO:0060361	2.35E-09	flight	BP
GO:0045214	3.34E-09	sarcomere organization	BP
GO:0007527	1.23E-08	adult somatic muscle development	BP
GO:0030898	1.19E-07	actin-dependent ATPase activity	MF
GO:0031032	6.83E-07	actomyosin structure organization	BP
GO:0007427	1.32E-06	epithelial cell migration, open tracheal system	BP
GO:0004614	1.65E-06	phosphoglucomutase activity	MF
GO:0030239	5.10E-06	myofibril assembly	BP
GO:0030241	5.22E-06	skeletal muscle myosin thick filament assembly	BP
GO:0071688	7.02E-06	striated muscle myosin thick filament assembly	BP
GO:0007525	8.87E-06	somatic muscle development	BP
GO:0043236	9.23E-06	laminin binding	MF
GO:0008307	1.07E-05	structural constituent of muscle	MF
GO:0031033	1.12E-05	myosin filament organization	BP

9.5.2.2 *Subadult females*

Down-regulated in subadult female appendages			
category	over_represented_pvalue	term	ontology
GO:0071702	6.20E-29	organic substance transport	BP
GO:0015293	1.51E-25	symporter activity	MF
GO:0030163	3.18E-22	protein catabolic process	BP
GO:0044281	5.52E-22	small molecule metabolic process	BP
GO:0004497	3.64E-21	monooxygenase activity	MF
GO:0046906	1.61E-20	tetrapyrrole binding	MF
GO:0006629	5.20E-20	lipid metabolic process	BP
GO:0015291	7.84E-20	secondary active transmembrane transporter activity	MF
GO:0008237	7.73E-19	metallopeptidase activity	MF
GO:0070330	2.58E-18	aromatase activity	MF
GO:0010498	6.31E-18	proteasomal protein catabolic process	BP
GO:1901575	1.25E-17	organic substance catabolic process	BP
GO:0006575	1.32E-17	cellular modified amino acid metabolic process	BP
GO:0043161	1.74E-17	proteasome-mediated ubiquitin-dependent protein catabolic process	BP
GO:0016491	2.60E-17	oxidoreductase activity	MF

Down-regulated in subadult female pedipalps			
category	over_represented_pvalue	term	ontology
GO:0010608	1.18E-10	posttranscriptional regulation of gene expression	BP
GO:0000268	3.68E-10	peroxisome targeting sequence binding	MF
GO:0005052	8.79E-10	peroxisome matrix targeting signal-1 binding	MF
GO:0005048	1.62E-09	signal sequence binding	MF
GO:0016560	5.21E-09	protein import into peroxisome matrix, docking	BP
GO:0051246	3.81E-08	regulation of protein metabolic process	BP
GO:0032268	9.61E-08	regulation of cellular protein metabolic process	BP
GO:0022615	2.08E-07	protein to membrane docking	BP

GO:0033034	2.81E-07	positive regulation of myeloid cell apoptotic process	BP
GO:2000111	2.81E-07	positive regulation of macrophage apoptotic process	BP
GO:0042277	3.54E-07	peptide binding	MF
GO:1902580	4.33E-07	single-organism cellular localization	BP
GO:0045346	8.33E-07	regulation of MHC class II biosynthetic process	BP
GO:2000109	8.33E-07	regulation of macrophage apoptotic process	BP
GO:0016561	8.36E-07	protein import into peroxisome matrix, translocation	BP

9.5.2.3 *Subadult males*

Down-regulted in subadult male appendages			
category	over_represented_pvalue	term	ontology
GO:0015293	3.44E-43	symporter activity	MF
GO:0015291	5.37E-36	secondary active transmembrane transporter activity	MF
GO:0022804	5.67E-33	active transmembrane transporter activity	MF
GO:0044281	3.13E-32	small molecule metabolic process	BP
GO:0044765	3.34E-30	single-organism transport	BP
GO:0046906	1.21E-29	tetrapyrrole binding	MF
GO:0006629	2.77E-28	lipid metabolic process	BP
GO:0006811	3.42E-26	ion transport	BP
GO:1902578	3.86E-26	single-organism localization	BP
GO:0004497	5.07E-26	monooxygenase activity	MF
GO:0006082	1.01E-25	organic acid metabolic process	BP
GO:0005215	5.03E-25	transporter activity	MF
GO:0006820	2.01E-24	anion transport	BP
GO:0043436	2.02E-24	oxoacid metabolic process	BP
GO:0006810	3.97E-24	transport	BP
Down-regulated in subadult male pedipalps			
category	over_represented_pvalue	term	ontology
GO:0042578	2.29E-13	phosphoric ester hydrolase activity	MF
GO:0046058	1.59E-12	cAMP metabolic process	BP
GO:0009187	1.44E-11	cyclic nucleotide metabolic process	BP
GO:0031032	3.11E-11	actomyosin structure organization	BP
GO:0004112	2.26E-09	cyclic-nucleotide phosphodiesterase activity	MF
GO:0030036	2.86E-09	actin cytoskeleton organization	BP
GO:0019935	5.16E-09	cyclic-nucleotide-mediated signaling	BP
GO:0065007	5.95E-09	biological regulation	BP
GO:0004114	8.44E-09	3',5'-cyclic-nucleotide phosphodiesterase activity	MF
GO:0048856	1.58E-08	anatomical structure development	BP
GO:0009214	1.64E-08	cyclic nucleotide catabolic process	BP
GO:0030029	2.31E-08	actin filament-based process	BP
GO:1902578	3.92E-08	single-organism localization	BP
GO:0035848	4.14E-08	oviduct morphogenesis	BP
GO:0019933	4.73E-08	cAMP-mediated signaling	BP

9.5.2.4 *Adult males*

Down-regulated in adult male appendages			
category	over_represented_pvalue	term	ontology
GO:0044281	1.68E-52	small molecule metabolic process	BP
GO:0006082	8.33E-45	organic acid metabolic process	BP
GO:0043436	1.84E-44	oxoacid metabolic process	BP
GO:0019752	9.99E-43	carboxylic acid metabolic process	BP
GO:0016491	7.64E-42	oxidoreductase activity	MF
GO:0015293	2.95E-39	symporter activity	MF
GO:0044282	6.41E-39	small molecule catabolic process	BP
GO:0004497	2.46E-37	monooxygenase activity	MF
GO:0015291	1.23E-35	secondary active transmembrane transporter activity	MF
GO:0022804	1.88E-35	active transmembrane transporter activity	MF
GO:0006629	8.33E-33	lipid metabolic process	BP
GO:0046906	2.50E-31	tetrapyrrole binding	MF
GO:0044712	6.41E-30	single-organism catabolic process	BP
GO:0016054	1.76E-29	organic acid catabolic process	BP
GO:0046395	1.76E-29	carboxylic acid catabolic process	BP
Down-regulated in adult male peidpalps			
category	over_represented_pvalue	term	ontology
GO:0004614	5.23E-06	phosphoglucomutase activity	MF
GO:0001667	1.80E-05	ameboidal-type cell migration	BP
GO:0021903	2.35E-05	rostrocaudal neural tube patterning	BP
GO:0048866	2.35E-05	stem cell fate specification	BP
GO:0060214	2.35E-05	endocardium formation	BP

GO:0060796	2.35E-05	regulation of transcription involved in primary germ layer cell fate commitment	BP
GO:0060807	2.35E-05	regulation of transcription from RNA polymerase II promoter involved in definitive endodermal cell fate specification	BP
GO:0001828	4.95E-05	inner cell mass cellular morphogenesis	BP
GO:0042662	5.83E-05	negative regulation of mesodermal cell fate specification	BP
GO:0003307	7.31E-05	regulation of Wnt signaling pathway involved in heart development	BP
GO:0003308	7.31E-05	negative regulation of Wnt signaling pathway involved in heart development	BP
GO:0007493	7.56E-05	endodermal cell fate determination	BP
GO:0005201	7.87E-05	extracellular matrix structural constituent	MF
GO:0003142	8.20E-05	cardiogenic plate morphogenesis	BP
GO:0061010	8.38E-05	gall bladder development	BP

9.5.3 GO terms associated with expression clusters

9.5.3.1 *Legs*

9.5.3.1.1 Active in juveniles and subadults

Cluster 7			
category	over_represented_pvalue	term	ontology
GO:0004222	5.9701562912167e-15	metalloendopeptidase activity	MF
GO:0030515	1.65400389304484e-11	snoRNA binding	MF
GO:0008237	3.04836991452373e-10	metallopeptidase activity	MF
GO:0016576	5.09031120532028e-07	histone dephosphorylation	BP
GO:0098633	6.25194434547295e-07	collagen fibril binding	MF
GO:1904027	6.25194434547295e-07	negative regulation of collagen fibril organization	BP
GO:0061135	6.75830598437043e-07	endopeptidase regulator activity	MF
GO:0006285	8.99108896790456e-07	base-excision repair, AP site formation	BP
GO:0003338	9.67166889167093e-07	metanephros morphogenesis	BP
GO:0004866	1.49668029774823e-06	endopeptidase inhibitor activity	MF

9.5.3.1.2 Active in subadult legs

Cluster 1			
category	over_represented_pvalue	term	ontology
GO:0005344	1.35284485871226e-14	oxygen transporter activity	MF
GO:0031404	2.97400716056415e-14	chloride ion binding	MF
GO:0042302	5.34449014105078e-14	structural constituent of cuticle	MF
GO:0005507	2.7552180914713e-09	copper ion binding	MF
GO:0008061	3.73534704815564e-09	chitin binding	MF
GO:0034191	1.05965683422006e-05	apolipoprotein A-I receptor binding	MF
GO:0018198	1.44627141594582e-05	peptidyl-cysteine modification	BP
GO:2000010	1.54192290451306e-05	positive regulation of protein localization to cell surface	BP
GO:0034190	1.9061597166163e-05	apolipoprotein receptor binding	MF
GO:0003774	2.70834791598532e-05	motor activity	MF

Cluster 2			
category	over_represented_pvalue	term	ontology
GO:0042302	2.46584273755907e-58	structural constituent of cuticle	MF
GO:0008061	5.28369906070216e-28	chitin binding	MF
GO:0005198	9.23353506329494e-20	structural molecule activity	MF
GO:0006032	8.07148295422068e-12	chitin catabolic process	BP
GO:1901072	3.40607092340137e-11	glucosamine-containing compound catabolic process	BP
GO:0004568	6.56447617838417e-11	chitinase activity	MF
GO:0046348	1.40641854133338e-10	amino sugar catabolic process	BP
GO:0006030	1.74610022754698e-09	chitin metabolic process	BP
GO:0060102	5.00891736874309e-09	collagen and cuticulin-based cuticle extracellular matrix	CC
GO:0051017	1.03925869470625e-08	actin filament bundle assembly	BP

Cluster 4			
category	over_represented_pvalue	term	ontology
GO:0016491	6.60268482362917e-14	oxidoreductase activity	MF
GO:0044281	3.89658143128955e-13	small molecule metabolic process	BP
GO:0055114	9.9247354257278e-13	oxidation-reduction process	BP
GO:0006091	2.64496132972638e-12	generation of precursor metabolites and energy	BP
GO:0048856	9.46342833982346e-12	anatomical structure development	BP
GO:0005201	1.10284755076269e-11	extracellular matrix structural constituent	MF
GO:0007298	4.56395275082602e-11	border follicle cell migration	BP
GO:0010631	2.7596269479317e-10	epithelial cell migration	BP
GO:0044723	3.40739595550272e-10	single-organism carbohydrate metabolic process	BP
GO:0003824	3.53015659708801e-10	catalytic activity	MF

9.5.3.1.3 Active in adult legs

Cluster 3			
category	over_represented_pvalue	term	ontology
GO:0016021	2.25656614898186e-15	integral component of membrane	CC
GO:0031224	2.91886746402889e-15	intrinsic component of membrane	CC
GO:0007156	5.33563750574274e-14	homophilic cell adhesion via plasma membrane adhesion molecules	BP
GO:0044425	1.40704580453967e-13	membrane part	CC

GO:0098742	4.40634358340320e-13	cell-cell adhesion via plasma-membrane adhesion molecules	BP
GO:0098609	1.39574007705639e-12	cell-cell adhesion	BP
GO:0007416	6.64294099036174e-12	synapse assembly	BP
GO:0005576	2.97427787013864e-11	extracellular region	CC
GO:0050808	4.01218904941069e-11	synapse organization	BP
GO:0007155	2.48853090629122e-10	cell adhesion	BP

Cluster 6			
category	over_represented_pvalue	term	ontology
GO:0004806	6.17437344436217e-13	triglyceride lipase activity	MF
GO:0016298	4.03787487548808e-09	lipase activity	MF
GO:0052689	6.14839551781875e-09	carboxylic ester hydrolase activity	MF
GO:0016042	5.17827609596307e-08	lipid catabolic process	BP
GO:0033387	1.41490571612338e-06	putrescine biosynthetic process from ornithine	BP
GO:0004586	2.41745863992805e-06	ornithine decarboxylase activity	MF
GO:0047714	2.92217387422228e-06	galactolipase activity	MF
GO:0019376	3.41563438514747e-06	galactolipid catabolic process	BP
GO:0019374	7.31033893154199e-06	galactolipid metabolic process	BP
GO:0047372	7.91273446700539e-06	acylglycerol lipase activity	MF

Cluster 10			
category	over_represented_pvalue	term	ontology
GO:0016877	1.65480999978722e-06	ligase activity, forming carbon-sulfur bonds	MF
GO:0003943	1.99087708290009e-06	N-acetylgalactosamine-4-sulfatase activity	MF
GO:0061580	1.99087708290009e-06	colon epithelial cell migration	BP
GO:0030207	2.85248393962357e-06	chondroitin sulfate catabolic process	BP
GO:0061582	4.09230975972302e-06	intestinal epithelial cell migration	BP
GO:0044273	8.95045914703018e-06	sulfur compound catabolic process	BP
GO:0016878	1.34249350071703e-05	acid-thiol ligase activity	MF
GO:0015889	1.50673673689197e-05	cobalamin transport	BP
GO:0006082	1.84565043522063e-05	organic acid metabolic process	BP

Cluster 11			
category	over_represented_pvalue	term	ontology
GO:0044795	8.69254752095463e-07	trans-Golgi network to recycling endosome transport	BP
GO:1902463	8.69254752095463e-07	protein localization to cell leading edge	BP
GO:0097368	1.40794613767979e-06	establishment of Sertoli cell barrier	BP
GO:0010737	2.35236474777771e-06	protein kinase A signaling	BP
GO:0042423	2.53735538273728e-06	catecholamine biosynthetic process	BP
GO:0009713	2.88223915177167e-06	catechol-containing compound biosynthetic process	BP
GO:0045842	1.035752911257e-05	positive regulation of mitotic metaphase/anaphase transition	BP
GO:1902101	1.035752911257e-05	positive regulation of metaphase/anaphase transition of cell cycle	BP
GO:0048265	1.11391175578705e-05	response to pain	BP
GO:0042417	1.24298469811331e-05	dopamine metabolic process	BP

Cluster 12			
category	over_represented_pvalue	term	ontology
GO:0036143	5.24958749471372e-09	kringle domain binding	MF
GO:0005520	1.78124083074719e-08	insulin-like growth factor binding	MF
GO:0007271	2.55527396376416e-08	synaptic transmission, cholinergic	BP
GO:0005231	3.9417340802626e-08	excitatory extracellular ligand-gated ion channel activity	MF
GO:0050997	9.2192038651201e-08	quaternary ammonium group binding	MF
GO:0042166	1.23279295476393e-07	acetylcholine binding	MF
GO:0005230	1.62815146257195e-07	extracellular ligand-gated ion channel activity	MF
GO:0042165	9.66075156607814e-07	neurotransmitter binding	MF
GO:0070405	2.05960820930212e-06	ammonium ion binding	MF
GO:0004889	4.51250366760511e-06	acetylcholine-activated cation-selective channel activity	MF

9.5.3.1.4 Increasing expression through development

Cluster 8			
category	over_represented_pvalue	term	ontology
GO:0003756	6.75254329117028e-14	protein disulfide isomerase activity	MF
GO:0016864	6.75254329117028e-14	intramolecular oxidoreductase activity, transposing S-S bonds	MF
GO:0034333	2.95986043782721e-13	adherens junction assembly	BP
GO:0007045	4.3154371100248e-12	cell-substrate adherens junction assembly	BP
GO:0048041	4.3154371100248e-12	focal adhesion assembly	BP
GO:0051234	1.49022170704119e-11	establishment of localization	BP

GO:0051179	2.75425304476313e-11	localization	BP
GO:0007044	5.78560728225989e-11	cell-substrate junction assembly	BP
GO:0006810	1.00531787613585e-10	transport	BP
GO:0019725	1.07949067044078e-10	cellular homeostasis	BP

9.5.3.1.5 Continuous expression

Cluster 5			
category	over_represented_pvalue	term	ontology
GO:0019222	3.59997386221609e-33	regulation of metabolic process	BP
GO:0016070	2.73880529423409e-31	RNA metabolic process	BP
GO:0044822	2.41464961112845e-30	poly(A) RNA binding	MF
GO:0046907	8.51046801807279e-30	intracellular transport	BP
GO:0016071	1.14830970468661e-29	mRNA metabolic process	BP
GO:1902582	3.46957885855445e-29	single-organism intracellular transport	BP
GO:0050789	4.9766738003713e-28	regulation of biological process	BP
GO:0006396	3.53657183332937e-27	RNA processing	BP
GO:0010468	1.17036771198873e-25	regulation of gene expression	BP
GO:0060255	3.52691997333443e-25	regulation of macromolecule metabolic process	BP

Cluster 9			
category	over_represented_pvalue	term	ontology
GO:0044822	2.05934340470232e-23	poly(A) RNA binding	MF
GO:0003723	7.42904386584599e-21	RNA binding	MF
GO:0006415	2.02713215092223e-14	translational termination	BP
GO:0006412	4.87107880701252e-14	translation	BP
GO:0016070	3.93384318037636e-13	RNA metabolic process	BP
GO:0003735	4.58818834399883e-13	structural constituent of ribosome	MF
GO:0016072	5.33028230928074e-13	rRNA metabolic process	BP
GO:0006364	5.68711349125128e-13	rRNA processing	BP
GO:0044085	5.69588469763898e-12	cellular component biogenesis	BP
GO:0006413	6.081031838099e-12	translational initiation	BP

9.5.3.2 *Opisthosoma*

9.5.3.2.1 Active in juveniles

Cluster 4			
category	over_represented_pvalue	term	ontology
GO:0003993	1.56244175953984e-22	acid phosphatase activity	MF
GO:0004866	1.79115033025617e-07	endopeptidase inhibitor activity	MF
GO:0004867	2.09374225325103e-07	serine-type endopeptidase inhibitor activity	MF
GO:0061135	2.30748274865294e-07	endopeptidase regulator activity	MF
GO:0030414	3.68807783080752e-07	peptidase inhibitor activity	MF
GO:0016791	1.54595275575886e-06	phosphatase activity	MF
GO:0061134	1.71457614076192e-06	peptidase regulator activity	MF
GO:0002716	4.68847442785549e-06	negative regulation of natural killer cell mediated immunity	BP
GO:0042270	4.68847442785549e-06	protection from natural killer cell mediated cytotoxicity	BP
GO:0045953	4.68847442785549e-06	negative regulation of natural killer cell mediated cytotoxicity	BP

Cluster 14			
category	over_represented_pvalue	term	ontology
GO:0003723	1.40009413041974e-86	RNA binding	MF
GO:0044822	1.43573285795952e-66	poly(A) RNA binding	MF
GO:0003735	3.21810404400925e-53	structural constituent of ribosome	MF
GO:0006412	1.65554127176679e-49	translation	BP
GO:0016070	1.1357838450711e-46	RNA metabolic process	BP
GO:0034470	7.53512902646327e-38	ncRNA processing	BP
GO:0006396	2.79089342665084e-37	RNA processing	BP
GO:0016071	3.83111837028898e-37	mRNA metabolic process	BP
GO:0006397	2.33084924777641e-33	mRNA processing	BP
GO:0034660	1.3347499167974e-31	ncRNA metabolic process	BP

Cluster 16			
category	over_represented_pvalue	term	ontology
GO:0004623	1.64448616900473e-07	phospholipase A2 activity	MF

9.5.3.2.2 Active in juveniles and subadults

Cluster 3			
category	over_represented_pvalue	term	ontology
GO:0019538	2.98249394075572e-13	protein metabolic process	BP
GO:0045184	3.14979888748254e-11	establishment of protein localization	BP
GO:0015031	5.49784684500359e-11	protein transport	BP
GO:0044267	6.09960403673787e-11	cellular protein metabolic process	BP
GO:0060255	2.64001433015821e-10	regulation of macromolecule metabolic process	BP
GO:0006511	4.24548527557714e-10	ubiquitin-dependent protein catabolic process	BP
GO:0010468	6.18805796825433e-10	regulation of gene expression	BP
GO:0019222	6.97429254483664e-10	regulation of metabolic process	BP
GO:0019941	8.81832466929149e-10	modification-dependent protein catabolic process	BP
GO:0051603	1.2666944750037e-09	proteolysis involved in cellular protein catabolic process	BP

Cluster 8			
category	over_represented_pvalue	term	ontology
GO:0022402	2.96857598361244e-08	cell cycle process	BP
GO:1903047	3.64531750078938e-08	mitotic cell cycle process	BP
GO:0007067	1.15536546512685e-07	mitotic nuclear division	BP
GO:0000280	3.06073589537682e-07	nuclear division	BP
GO:0051301	4.29366518386773e-07	cell division	BP
GO:0048285	8.24146500620267e-07	organelle fission	BP
GO:0015774	8.71082946114115e-07	polysaccharide transport	BP
GO:0051028	2.03754651462804e-06	mRNA transport	BP
GO:0061669	4.67170898762624e-06	spontaneous neurotransmitter secretion	BP
GO:0000278	5.75286395354661e-06	mitotic cell cycle	BP

Cluster 10			
category	over_represented_pvalue	term	ontology
GO:0004222	2.50371427263149e-19	metalloendopeptidase activity	MF
GO:0008237	5.42313511798132e-18	metallopeptidase activity	MF
GO:0004866	5.31664751126501e-12	endopeptidase inhibitor activity	MF
GO:0061135	7.79594494363614e-12	endopeptidase regulator activity	MF
GO:0030414	1.59357521614052e-11	peptidase inhibitor activity	MF
GO:0004175	4.74131409169649e-11	endopeptidase activity	MF
GO:0070011	1.18826052776993e-10	peptidase activity, acting on L-amino acid peptides	MF
GO:0061134	1.62950367324868e-10	peptidase regulator activity	MF
GO:0008233	3.37307951640274e-10	peptidase activity	MF
GO:0098633	5.08903715530377e-10	collagen fibril binding	MF

9.5.3.2.3 Active in subadults

Cluster 11			
category	over_represented_pvalue	term	ontology
GO:0007018	5.92622255791938e-19	microtubule-based movement	BP
GO:0007017	4.42470131900762e-16	microtubule-based process	BP
GO:0003341	4.66918210986339e-16	cilium movement	BP
GO:0000280	1.42890608529204e-14	nuclear division	BP
GO:0048285	6.9679038116893e-14	organelle fission	BP
GO:0070192	1.41487698745992e-10	chromosome organization involved in meiotic cell cycle	BP
GO:0070286	2.22118396736957e-10	axonemal dynein complex assembly	BP
GO:0044782	2.8350338473746e-10	cilium organization	BP
GO:0042384	1.38783081170878e-09	cilium assembly	BP
GO:0007126	1.75086283130882e-09	meiotic nuclear division	BP

9.5.3.2.4 Active in subadults and adults

Cluster 12			
category	over_represented_pvalue	term	ontology
GO:0050789	3.67845261817838e-19	regulation of biological process	BP
GO:0065007	8.42167124482432e-19	biological regulation	BP
GO:0050794	1.17003390824903e-17	regulation of cellular process	BP
GO:0051179	1.22530669171658e-17	localization	BP
GO:0005515	8.09033175442424e-17	protein binding	MF
GO:0051234	1.793714005057e-16	establishment of localization	BP
GO:0007165	9.98444708797432e-16	signal transduction	BP
GO:0006810	1.72049843368291e-14	transport	BP
GO:0032535	2.27221139216281e-13	regulation of cellular component size	BP
GO:0048518	5.41307062719096e-13	positive regulation of biological process	BP

9.5.3.2.5 Not active in subadults

Cluster 2			
category	over_represented_pvalue	term	ontology
GO:0015293	6.50528966578848e-08	symporter activity	MF
GO:0005215	1.0896573079739e-07	transporter activity	MF
GO:0006820	3.61053403530996e-07	anion transport	BP
GO:0008933	6.87344941058902e-07	lytic transglycosylase activity	MF
GO:0016998	1.23692296489934e-06	cell wall macromolecule catabolic process	BP
GO:0015370	1.43347061586866e-06	solute:sodium symporter activity	MF
GO:0034196	1.48304875796608e-06	acylglycerol transport	BP
GO:0034197	1.48304875796608e-06	triglyceride transport	BP
GO:0015711	1.61716789466536e-06	organic anion transport	BP
GO:0015296	1.92772382886497e-06	anion:cation symporter activity	MF

Cluster 9			
category	over_represented_pvalue	term	ontology
GO:0004298	5.15626023235048e-12	threonine-type endopeptidase activity	MF
GO:0070003	5.15626023235048e-12	threonine-type peptidase activity	MF
GO:0044248	1.46045474037566e-11	cellular catabolic process	BP
GO:0071702	3.94534588330681e-09	organic substance transport	BP
GO:0045184	8.23002321880879e-09	establishment of protein localization	BP
GO:0033036	8.73349738779693e-09	macromolecule localization	BP
GO:0060261	8.81093149913867e-09	positive regulation of transcription initiation from RNA polymerase II promoter	BP
GO:0016491	9.99825914218992e-09	oxidoreductase activity	MF
GO:0009056	1.08638387008829e-08	catabolic process	BP
GO:0015031	1.89754925171633e-08	protein transport	BP

Cluster 15			
category	over_represented_pvalue	term	ontology
GO:0015293	4.52298949865162e-09	symporter activity	MF
GO:0047066	4.2169045039573e-08	phospholipid-hydroperoxide glutathione peroxidase activity	MF
GO:0004601	8.43503518351211e-08	peroxidase activity	MF
GO:0016684	9.1950052491649e-08	oxidoreductase activity, acting on peroxide as acceptor	MF
GO:0015291	1.12875792203943e-07	secondary active transmembrane transporter activity	MF
GO:0004329	2.94575659582763e-07	formate-tetrahydrofolate ligase activity	MF
GO:2000359	4.3389673999092e-07	regulation of binding of sperm to zona pellucida	BP
GO:0015114	4.4854199348539e-07	phosphate ion transmembrane transporter activity	MF
GO:0004477	4.9087576480805e-07	methenyltetrahydrofolate cyclohydrolase activity	MF
GO:0004488	4.9087576480805e-07	methylenetetrahydrofolate dehydrogenase (NADP+) activity	MF

9.5.3.2.6 Active in adults

Cluster 1			
category	over_represented_pvalue	term	ontology
GO:0001835	3.67836414420482e-08	blastocyst hatching	BP
GO:0035188	5.28660071481679e-08	hatching	BP
GO:0071684	5.28660071481679e-08	organism emergence from protective structure	BP
GO:0000828	6.47854190082301e-07	inositol hexakisphosphate kinase activity	MF
GO:0000832	6.47854190082301e-07	inositol hexakisphosphate 5-kinase activity	MF
GO:0052723	6.47854190082301e-07	inositol hexakisphosphate 1-kinase activity	MF
GO:0052724	6.47854190082301e-07	inositol hexakisphosphate 3-kinase activity	MF
GO:0008440	5.02252405977197e-06	inositol-1,4,5-trisphosphate 3-kinase activity	MF
GO:0051766	8.24714754335619e-06	inositol trisphosphate kinase activity	MF

Cluster 5			
category	over_represented_pvalue	term	ontology
GO:0004222	0	metalloendopeptidase activity	MF
GO:0008237	2.89917065563984e-10	metallopeptidase activity	MF
GO:0004806	6.95374424510005e-06	triglyceride lipase activity	MF
GO:0070011	9.64553050932935e-06	peptidase activity, acting on L-amino acid peptides	MF
GO:0008233	1.34528884118684e-05	peptidase activity	MF
GO:0004175	1.71832971390877e-05	endopeptidase activity	MF

Cluster 6			
category	over_represented_pvalue	term	ontology

GO:0043062	1.03643592026439e-10	extracellular structure organization	BP
GO:0030029	2.90620659060437e-09	actin filament-based process	BP
GO:0030198	3.45217715530204e-09	extracellular matrix organization	BP
GO:0030036	6.84898018466841e-09	actin cytoskeleton organization	BP
GO:0031033	2.09583068904706e-08	myosin filament organization	BP
GO:0031034	2.09583068904706e-08	myosin filament assembly	BP
GO:0031032	3.91800613827636e-08	actomyosin structure organization	BP
GO:0016054	5.56744195922974e-08	organic acid catabolic process	BP
GO:0046395	5.56744195922974e-08	carboxylic acid catabolic process	BP
GO:0005509	9.20049694321544e-08	calcium ion binding	MF

Cluster 7			
category	over_represented_pvalue	term	ontology
GO:0008083	1.39951052212858e-08	growth factor activity	MF
GO:0007306	1.66085666545489e-07	eggshell chorion assembly	BP
GO:0042744	7.58388721736175e-07	hydrogen peroxide catabolic process	BP
GO:0042743	1.19810415950648e-06	hydrogen peroxide metabolic process	BP
GO:0004601	4.69642468289351e-06	peroxidase activity	MF
GO:0016684	4.87227129509128e-06	oxidoreductase activity, acting on peroxide as acceptor	MF
GO:0098869	9.00642955565825e-06	cellular oxidant detoxification	BP
GO:0016209	1.56041230196044e-05	antioxidant activity	MF
GO:0072593	2.7644527810038e-05	reactive oxygen species metabolic process	BP
GO:0043491	2.94245162457527e-05	protein kinase B signaling	BP

Cluster 13			
category	over_represented_pvalue	term	ontology
GO:0022857	1.76350452290112e-10	transmembrane transporter activity	MF
GO:0005215	4.62864042711856e-10	transporter activity	MF
GO:0008514	6.26295320433106e-10	organic anion transmembrane transporter activity	MF
GO:0022891	6.7466093486632e-10	substrate-specific transmembrane transporter activity	MF
GO:0008509	3.79761657102219e-09	anion transmembrane transporter activity	MF
GO:0072349	6.3317131016316e-09	modified amino acid transmembrane transporter activity	MF
GO:0005342	1.09683249888276e-08	organic acid transmembrane transporter activity	MF
GO:0046943	1.09683249888276e-08	carboxylic acid transmembrane transporter activity	MF
GO:0022892	1.80783020829654e-08	substrate-specific transporter activity	MF
GO:0006811	1.81137032695904e-08	ion transport	BP

Cluster 17			
category	over_represented_pvalue	term	ontology
GO:0015993	2.3607024586217e-07	molecular hydrogen transport	BP
GO:0047988	2.3607024586217e-07	hydroxyacid-oxoacid transhydrogenase activity	MF
GO:0004371	9.98411417982349e-07	glycerone kinase activity	MF
GO:0051371	1.21371833917195e-06	muscle alpha-actinin binding	MF
GO:0051393	3.35014883317863e-06	alpha-actinin binding	MF
GO:0042805	4.53264749775365e-06	actinin binding	MF
GO:0015651	4.86769080040637e-06	quaternary ammonium group transmembrane transporter activity	MF
GO:0032963	5.50922984641428e-06	collagen metabolic process	BP
GO:0071711	7.90047191082039e-06	basement membrane organization	BP
GO:0044259	9.65943153130704e-06	multicellular organismal macromolecule metabolic process	BP

Cluster 18			
category	over_represented_pvalue	term	ontology
GO:0070011	4.30565732809793e-08	peptidase activity, acting on L-amino acid peptides	MF
GO:0008233	7.09738582904499e-08	peptidase activity	MF
GO:0008234	9.65194608905442e-08	cysteine-type peptidase activity	MF
GO:0007566	8.21055133851358e-06	embryo implantation	BP
GO:0060220	1.09468818360806e-05	camera-type eye photoreceptor cell fate commitment	BP
GO:0060223	1.09468818360806e-05	retinal rod cell fate commitment	BP
GO:0060226	1.09468818360806e-05	negative regulation of retinal cone cell fate commitment	BP
GO:0061076	1.09468818360806e-05	negative regulation of neural retina development	BP
GO:1902867	1.09468818360806e-05	negative regulation of retina development in camera-type eye	BP
GO:1902869	1.09468818360806e-05	regulation of amacrine cell differentiation	BP

9.5.3.3 *Pedipalps*

9.5.3.3.1 Active in juveniles

Cluster 7			
category	over_represented_pvalue	term	ontology
GO:0010572	1.20671103139814e-08	positive regulation of platelet activation	BP
GO:0042806	1.14033114680923e-07	fucose binding	MF
GO:0070492	2.0084518013583e-07	oligosaccharide binding	MF
GO:0050901	6.61452695803023e-07	leukocyte tethering or rolling	BP
GO:0033623	8.28602859041643e-07	regulation of integrin activation	BP
GO:0030194	9.55433726144894e-07	positive regulation of blood coagulation	BP
GO:0050820	9.55433726144894e-07	positive regulation of coagulation	BP
GO:1900048	9.55433726144894e-07	positive regulation of hemostasis	BP
GO:0010543	2.02493725830969e-06	regulation of platelet activation	BP
GO:0002691	2.3509785426942e-06	regulation of cellular extravasation	BP

9.5.3.3.2 Active in subadults

Cluster 1			
category	over_represented_pvalue	term	ontology
GO:0032642	2.16037104198427e-07	regulation of chemokine production	BP

Cluster 3			
category	over_represented_pvalue	term	ontology
GO:0003723	1.09589056477987e-116	RNA binding	MF
GO:0044822	1.57194780591677e-104	poly(A) RNA binding	MF
GO:0016070	2.30143723880551e-73	RNA metabolic process	BP
GO:0006396	1.72459715720635e-59	RNA processing	BP
GO:0034660	1.84422650897495e-57	ncRNA metabolic process	BP
GO:0016071	5.0640488562428e-57	mRNA metabolic process	BP
GO:0006397	2.25848978055581e-55	mRNA processing	BP
GO:0034470	1.67479054425303e-53	ncRNA processing	BP
GO:0008380	9.67952370592894e-47	RNA splicing	BP
GO:0044260	3.47573994902179e-45	cellular macromolecule metabolic process	BP

Cluster 5			
category	over_represented_pvalue	term	ontology
GO:0008061	1.26934950639115e-08	chitin binding	MF
GO:0042302	2.76034334285268e-08	structural constituent of cuticle	MF

Cluster 17			
category	over_represented_pvalue	term	ontology
GO:0042302	4.16294802910089e-50	structural constituent of cuticle	MF
GO:0008061	3.90103043578189e-26	chitin binding	MF
GO:0005198	3.64989752599311e-20	structural molecule activity	MF
GO:0004252	3.83521874423939e-08	serine-type endopeptidase activity	MF
GO:0008236	2.19806640894449e-07	serine-type peptidase activity	MF
GO:0017171	2.19806640894449e-07	serine hydrolase activity	MF
GO:0044548	5.41522806616854e-06	S100 protein binding	MF
GO:0019826	2.01862996683362e-05	oxygen sensor activity	MF
GO:0006030	2.0660905852159e-05	chitin metabolic process	BP

9.5.3.3.3 Not active in subadults

Cluster 13			
category	over_represented_pvalue	term	ontology
GO:0020037	5.75697523361935e-10	heme binding	MF
GO:0070330	7.46853865061585e-10	aromatase activity	MF
GO:0004497	1.79032447845791e-09	monooxygenase activity	MF
GO:0016712	3.53904665047302e-09	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	MF
GO:0046906	6.18570661826956e-09	tetrapyrrole binding	MF
GO:0008289	2.20345184298092e-08	lipid binding	MF

GO:0016705	2.31154006646988e-08	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF
GO:0005215	3.30997417752848e-07	transporter activity	MF
GO:0005506	3.94476503676212e-07	iron ion binding	MF
GO:0016491	3.91609193799756e-06	oxidoreductase activity	MF

Cluster 14			
category	over_represented_pvalue	term	ontology
GO:0007601	1.42737685428722e-08	visual perception	BP
GO:0050953	1.60344366600392e-08	sensory perception of light stimulus	BP
GO:0009583	4.21733296465149e-08	detection of light stimulus	BP
GO:0015279	6.22745869076726e-07	store-operated calcium channel activity	MF
GO:0009581	1.00482142837831e-06	detection of external stimulus	BP
GO:0009582	1.05459342969005e-06	detection of abiotic stimulus	BP
GO:0006828	1.70429055042723e-06	manganese ion transport	BP
GO:0050908	1.96835965388158e-06	detection of light stimulus involved in visual perception	BP
GO:0050962	1.96835965388158e-06	detection of light stimulus involved in sensory perception	BP
GO:0000146	2.33337155939411e-06	microfilament motor activity	MF

Cluster 15			
category	over_represented_pvalue	term	ontology
GO:0050808	5.70199683665353e-08	synapse organization	BP
GO:0015171	6.13481959141716e-08	amino acid transmembrane transporter activity	MF
GO:0032501	3.75589623190201e-07	multicellular organismal process	BP
GO:0043090	5.79928601634859e-07	amino acid import	BP
GO:0008345	1.75712306283608e-06	larval locomotory behavior	BP
GO:0044707	1.78785120534709e-06	single-multicellular organism process	BP
GO:0030825	2.64470827145016e-06	positive regulation of cGMP metabolic process	BP
GO:0030828	2.64470827145016e-06	positive regulation of cGMP biosynthetic process	BP
GO:0098656	3.99693380211266e-06	anion transmembrane transport	BP
GO:0016188	4.80686242130397e-06	synaptic vesicle maturation	BP

Cluster 16			
category	over_represented_pvalue	term	ontology
GO:0004620	2.7348016427833e-12	phospholipase activity	MF
GO:0016298	1.30003101441596e-11	lipase activity	MF
GO:0006629	3.31733810065972e-11	lipid metabolic process	BP
GO:0046949	3.06750770230133e-10	fatty-acyl-CoA biosynthetic process	BP
GO:0044765	1.00484632112075e-09	single-organism transport	BP
GO:0035384	2.93875877099292e-09	thioester biosynthetic process	BP
GO:0071616	2.93875877099292e-09	acyl-CoA biosynthetic process	BP
GO:0046903	7.99356210877876e-09	secretion	BP
GO:0004629	8.28527264583214e-09	phospholipase C activity	MF
GO:0016491	9.06012475389273e-09	oxidoreductase activity	MF

9.5.3.3.4 Active in adults

Cluster 2			
category	over_represented_pvalue	term	ontology
GO:0004867	4.03628251716216e-10	serine-type endopeptidase inhibitor activity	MF
GO:0042381	5.91367420030883e-09	hemolymph coagulation	BP
GO:0004866	7.37137489103666e-09	endopeptidase inhibitor activity	MF
GO:0061135	8.79003221001327e-09	endopeptidase regulator activity	MF
GO:0030414	1.17577485189796e-08	peptidase inhibitor activity	MF
GO:0061134	3.4346167907401e-08	peptidase regulator activity	MF
GO:0034769	9.91757375878613e-08	basement membrane disassembly	BP
GO:0004857	5.89626871339693e-07	enzyme inhibitor activity	MF
GO:0004175	1.85962253953432e-06	endopeptidase activity	MF
GO:0006955	4.38248630718301e-06	immune response	BP

Cluster 4			
category	over_represented_pvalue	term	ontology
GO:0004356	5.38638939655996e-08	glutamate-ammonia ligase activity	MF
GO:1901565	8.54743611580215e-08	organonitrogen compound catabolic process	BP
GO:0016211	3.25124624250852e-07	ammonia ligase activity	MF
GO:0006542	8.42701962028427e-07	glutamine biosynthetic process	BP
GO:2000359	3.3145860863397e-06	regulation of binding of sperm to zona pellucida	BP
GO:0016880	5.33571721011022e-06	acid-ammonia (or amide) ligase activity	MF
GO:0061134	6.42210401886561e-06	peptidase regulator activity	MF

GO:0006538	1.28463575439552e-05	glutamate catabolic process	BP
GO:0004866	1.3973720658085e-05	endopeptidase inhibitor activity	MF
GO:0006656	1.56736533324519e-05	phosphatidylcholine biosynthetic process	BP

Cluster 6			
category	over_represented_pvalue	term	ontology
GO:0036143	1.9761913632646e-08	kringle domain binding	MF
GO:0004164	1.23853083721751e-07	diphthine synthase activity	MF
GO:0030414	9.94324571576463e-07	peptidase inhibitor activity	MF
GO:1901678	2.92145870146999e-06	iron coordination entity transport	BP
GO:0004866	3.20166582218989e-06	endopeptidase inhibitor activity	MF
GO:0061135	4.0348678468478e-06	endopeptidase regulator activity	MF
GO:0004867	4.28882088706976e-06	serine-type endopeptidase inhibitor activity	MF
GO:0061134	4.55058694611877e-06	peptidase regulator activity	MF
GO:0005520	5.43842433808555e-06	insulin-like growth factor binding	MF
GO:0033387	1.19173841886024e-05	putrescine biosynthetic process from ornithine	BP

Cluster 10			
category	over_represented_pvalue	term	ontology
GO:0007044	6.16757620912106e-13	cell-substrate junction assembly	BP
GO:0043149	1.30532378724609e-11	stress fiber assembly	BP
GO:0045725	2.22439733676023e-11	positive regulation of glycogen biosynthetic process	BP
GO:0005231	5.37070140430755e-11	excitatory extracellular ligand-gated ion channel activity	MF
GO:0005230	8.00238131758415e-11	extracellular ligand-gated ion channel activity	MF
GO:0035206	8.88191411732456e-11	regulation of hemocyte proliferation	BP
GO:0007045	1.73883172470176e-10	cell-substrate adherens junction assembly	BP
GO:0048041	1.73883172470176e-10	focal adhesion assembly	BP
GO:0015276	1.97174668626632e-10	ligand-gated ion channel activity	MF
GO:0022834	1.97174668626632e-10	ligand-gated channel activity	MF

Cluster 11			
category	over_represented_pvalue	term	ontology
GO:0005215	1.17010337627622e-11	transporter activity	MF
GO:0055085	1.60380471641145e-10	transmembrane transport	BP
GO:0044765	2.12598231468978e-10	single-organism transport	BP
GO:0022857	8.78346462693093e-10	transmembrane transporter activity	MF
GO:0015075	1.53150687231017e-09	ion transmembrane transporter activity	MF
GO:0022891	2.06511515654108e-09	substrate-specific transmembrane transporter activity	MF
GO:1902578	5.2893579360804e-09	single-organism localization	BP
GO:0015293	7.83126240797084e-09	symporter activity	MF
GO:0022892	1.77534608828448e-08	substrate-specific transporter activity	MF
GO:0006811	2.5456719659511e-08	ion transport	BP

Cluster 12			
category	over_represented_pvalue	term	ontology
GO:0065007	3.94803327712331e-17	biological regulation	BP
GO:0050789	1.88058485382897e-16	regulation of biological process	BP
GO:0050794	3.15723222694831e-14	regulation of cellular process	BP
GO:0051179	7.76027493900808e-14	localization	BP
GO:0065009	1.11088442166797e-13	regulation of molecular function	BP
GO:0048284	1.29175895232024e-13	organelle fusion	BP
GO:0090174	1.50100256481382e-13	organelle membrane fusion	BP
GO:0050790	4.34845499724382e-13	regulation of catalytic activity	BP
GO:0035556	4.49740691479984e-13	intracellular signal transduction	BP
GO:0005515	5.32480938215359e-13	protein binding	MF

Cluster 18			
category	over_represented_pvalue	term	ontology
GO:0046485	9.30033212923814e-07	ether lipid metabolic process	BP
GO:0004806	1.84812285611865e-06	triglyceride lipase activity	MF
GO:0047408	4.92012481884003e-06	alkenylglycerophosphocholine hydrolase activity	MF
GO:0047409	4.92012481884003e-06	alkenylglycerophosphoethanolamine hydrolase activity	MF
GO:0006662	9.35393499282163e-06	glycerol ether metabolic process	BP
GO:0018904	1.17018404855969e-05	ether metabolic process	BP
GO:0004035	1.28939464083791e-05	alkaline phosphatase activity	MF
GO:0016714	1.94284345148534e-05	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,	MF

		reduced pteridine as one donor, and incorporation of one atom of oxygen	
GO:0033280	2.40356446066162e-05	response to vitamin D	BP

9.5.3.3.5 Increasing through development

Cluster 9			
category	over_represented_pvalue	term	ontology
GO:0010468	3.68588378096505e-19	regulation of gene expression	BP
GO:0019222	1.56232451777434e-18	regulation of metabolic process	BP
GO:0060255	2.6156751196647e-17	regulation of macromolecule metabolic process	BP
GO:0016070	6.68530448161304e-17	RNA metabolic process	BP
GO:0043933	7.49402355216669e-17	macromolecular complex subunit organization	BP
GO:0033036	6.42539277338233e-16	macromolecule localization	BP
GO:0008104	9.83243789799477e-16	protein localization	BP
GO:0046907	1.9453656129034e-15	intracellular transport	BP
GO:0045184	3.58726938246412e-15	establishment of protein localization	BP
GO:0031323	5.00771991752078e-15	regulation of cellular metabolic process	BP

9.5.3.3.6 Continuous expression

Cluster 8			
category	over_represented_pvalue	term	ontology
GO:0004085	4.69722614036468e-09	butyryl-CoA dehydrogenase activity	MF
GO:0044782	2.59528999652962e-07	cilium organization	BP
GO:0021897	6.77498514065186e-07	forebrain astrocyte development	BP
GO:0048853	9.56776506976965e-07	forebrain morphogenesis	BP
GO:1902017	1.01192559957813e-06	regulation of cilium assembly	BP
GO:0000828	1.16573042630706e-06	inositol hexakisphosphate kinase activity	MF
GO:0000832	1.16573042630706e-06	inositol hexakisphosphate 5-kinase activity	MF
GO:0052723	1.16573042630706e-06	inositol hexakisphosphate 1-kinase activity	MF
GO:0052724	1.16573042630706e-06	inositol hexakisphosphate 3-kinase activity	MF
GO:0042384	1.20572025969596e-06	cilium assembly	BP

10 Curriculum vitae

Personal Data:

Name:	Christoph Schomburg
Date of birth:	23.10.1985
Place of birth:	Osterode am Harz, Germany
Home address:	Zimmermannstraße 64 37075 Göttingen
Work address:	Georg-August-Universität Göttingen Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie Abteilung Entwicklungsbiologie GZMB Ernst-Caspari-Haus Justus-von-Liebig-Weg 11 37077 Göttingen
E-mail:	cschomb@gwdg.de

Education:

2010-2013	Master program "Developmental, Neural and Behavioral Biology" at the Georg-August-University Göttingen, Final grade: "very good" 1.3 Master Thesis: "Identification of enhancer elements" at the Institute for Zoology and Anthropology, Department of Developmental Biology in the laboratory of Prof. Dr. Bucher Thesis evaluation: "very good" 1.3
2007-2010	Bachelor of Science in Biology at the Georg-August-University Göttingen. Final grade: "good" 1.6 Bachelor Thesis: "Establishment of the "Brainbow"-system in *Tribolium castaneum*" at the Institute for Zoology and Anthropology, Department of Developmental Biology in the laboratory of Prof. Dr. Bucher Thesis evaluation: "good" 1.7
2002-2005	Secondary school "Ernst-Moritz-Arndt Gymnasium Herzberg"
1998-2002	Secondary school "Kooperative Gesamtschule Bad Lauterberg"

Work Experience:

2013-present	PhD student of the GGNB (Göttingen Graduate School for Neurosciences and Molecular Biosciences), PhD program: “Genes and Development”, Georg-August-University, Department of Developmental Biology in the laboratory of Dr. Nikola-Michael Prpic-Schäper Doctoral Thesis Project: “Developmental Studies on Eye Types and Pedipalps in *Parasteatoda tepidariorum*”
2014	Co-Organizer “Size and shape – Integration of Morphometrics, mathematical modelling, Developmental and Evolutionary Biology
2013	Student Assistant at the GZMB, Department Developmental Biology (Prof. Dr. Wimmer) in the laboratory of Prof. Dr. Bucher

Teaching activities:

2015	Supervision of Lab rotation Melissa Jüds
2015	Bachelor Thesis supervision of Carolin Schilling “Identification and annotation of eye determination and differentiation genes in the common house spider *Parasteatoda tepidariorum*”
2014	Bachelor Thesis supervision of Magdalena Ines Schacht “*Pax6*, *eyegone* und *reduced ocelli* während der Augenentwicklung in der Gewächshausspinne *Parasteatoda tepidariorum*”
since 2013	Teaching assistant in the key competence module “Evolutionary Developmental Biology“, in the Master program Developmental, Neural and Behavioral Biology

Languages:

German (native)

English (fluent, spoken and written)

List of publications:

Schomburg, C., Turetzek, N., Schacht, M. I., Schneider, J., Kirfel, P., Prpic, N. M., & Posnien, N. (2015). Molecular characterization and embryonic origin of the eyes in the common house spider Parasteatoda tepidariorum. *Evodevo*, *6*(1), 15.

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Kanagaraj, P., Gautier-Stein, A., Riedel, D., Schomburg, C., Cerdà, J., Vollack, N., & Dosch, R. (2014). Souffle/Spastizin controls secretory vesicle maturation during zebrafish oogenesis. *PLoS Genet*, *10*(6), e1004449.

Schwager, E. E., Sharma, P. P., Clarke, T., Leite, D. J., Wierschin, T., Pechmann, M., ... & Buffry, A. D. (2017). The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. *bioRxiv*, 106385.