Supplementary Material Brauchle et al.

Overview and legends

Supplementary Table S1 ……Pages 1- 5
Overview of family membership of all described homeodomain proteins. Also compare to supplementary fig. S4 for the actual alignments.

Supplementary Table S2 ……Page 6
Overview of class membership of all identified homeodomain proteins in 8 more Xenacoelomorpha spp. based on the Cannon et al., 2016 transcriptomes.

Supplementary Figure S3 ……Page 7
1 - ORF sequences of all identified homeodomain proteins of *I. pulchra*……7-14
and identified PFAM domains therein……14-16
2 - ORF sequences of all identified homeodomain proteins of *S. roscoffensis*……16-26
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Supplementary Figure S4……Page 93
Sequence alignment of all homeodomains relative to described family members of other species.

Supplementary Figure S5 ……Page 122
A phylogenetic tree indicates the family relationships of acoel ANTP genes (colors as in Fig. 1) relative to previously classified human ANTP sequences. The 3 *B. floridae* genes for *Bari*, *Rough* and *Abox* are included since these families are lacking in humans. This tree is rooted and Tale genes are used as an outgroup. All Hs genes are in black and Bf genes in dark red. Orange nodes represent a bootstrap value > 70%.

Supplementary Figure S6 ……Page 123
A phylogenetic tree indicates the family relationships of acoel non-ANTP genes (colors as in Fig. 1) relative to previously classified human non-ANTP sequences. *B. floridae Repo* is included so as to include a member of this family. For the zinc-finger proteins all homeodomains are listed, as well as for DUX proteins. Homeodomain sequences of proteins that are exactly the same are represented only by a single sequence. This tree is rooted and HoxA genes are used as an outgroup. Orange nodes represent a bootstrap value > 70%.

Supplementary Figure S7 ……Page 124
A phylogenetic tree indicating the family relationships of 5 different Xenacoelomorpha ANTP gene complements relative to previously classified ANTP homeobox sequences of 5 other species including *B. floridae, C. gigas, C. elegans, D. melanogaster* and *N. vectensis* (colors as in Fig.3). This tree is rooted and Tale genes are used as an outgroup. Orange nodes represent a bootstrap value > 70%.

Supplementary Figure S8 ……Page 125
A phylogenetic tree indicating the family relationships of 5 different Xenacoelomorpha non-ANTP gene complements relative to previously classified ANTP homeobox sequences of 5 other species including *B. floridae, C. gigas, C. elegans, D. melanogaster* and *N. vectensis* (colors as in Fig. 3). For the zinc-finger proteins all homeodomains are listed, as well as for DUX proteins. Homeodomain sequences of proteins that are exactly the same are represented only by a single sequence. This tree is rooted and HoxA genes are used as an outgroup. Orange nodes represent a bootstrap value > 70%.

Supplementary Figure S9 ……Page 126
Sequence alignment of human HNF1a and the identified Aq homolog. Domains are indicated in boxes.

Supplementary Figure S10 ……Page 127
Sequence alignment of human CERS and Aq Ip and Nv homologs. Domains are indicated in boxes.

Supplementary Table S11 ……Page 128-163
List of homeodomain sequences for the generation of Supplementary Figure S7 and S8

Supplementary Table S1:
Number of Xenacoelomorpha homeodomain genes by class and family in comparison to other selected species

	Hs	Bf	Dm	Ce	Cg	Ip	Sr	Hm	Nw	Xb	Nv
ANTP class											
HoxL subclass											
Cdx	3	1	1	1	1	1	1	1	1	1	1
Evx	2	2	1	1	2	1	1	1	2	1	1
Gbx	2	1	1	0	1	0	0	0	1	1	1
Gsx	2	1	1	0	1	1	1	1	0	1	1
Hox1 / antHox	3	1	1	1	1	1	1[a]	1	1	1	2
Hox2	2	1	1	0	1	0	0	0	0	0	3
Hox3	3	1	3	0	1	0	0	0	0	0	0
Hox4 / CentHox	4	1	1	0	1						0
Hox5 / CentHox	3	1	1	1	1	1[b]	1[b]	1[b]	0	3[b]	0
Hox6-8	8	3	4	1	3						0
Hox9-13/PostHox	16	7	1	3	2	1	1	1	2	1	0
Meox	2	1	1	0	1	1	0	0	1	1	4
Mnx/Exex	1	2	1	1	2	1	1	1	1	0	1
Pdx/Ipf	1	1	0	0	1	0	0	0	0	0	0
Rough	0	1	1	1	1	1	1	2	1	0	1
Total	52	25	19	10	20	9	8	9	10	10	15
NKL subclass											
Abox	0	1	1	1	0	1	1	1	0	0	0
Ankx	0	1	0	0	0	0	0	0	0	0	0
Barhl	2	1	2	2	3	1	1	1	0	1	0
Bari	0	1	1	0	0	1	1[c]	1	0	0	0
Barx	2	1	0	0	1	2	1	1	1	1	1
Bsx	1	1	1	1	1	1[d]	1	1	0	0	0
Dbx	2	1	1	0	1	0	0	0	2	0	0
Dlx	6	1	1	1	1	1	1	2	3	1	1
Emx	2	3	2	1	3	1	1	0	2	1	2
En	2	1	2	1	2	0	0	0	0	0	0
Hhex	1	1	1	1	1	0	0	0	0	1	1
Hlx	1	1	1	0	1	0	0	0	0	0	7
Hx	0	1	0	0	0	0	0	0	0	0	0
Lbx	2	1	2	0	1	0	0	0	0	0	1
Lcx	0	1	0	0	0	0	0	0	0	0	0
Msx	2	1	1	1	1	0	0	0	0	1	1
Msxlx	0	1	1	0	1	1	1	1	1	0	2
Nanog	1	0	0	0	0	0	0	0	0	0	0

Nedx CG13424	0	2	1	0	0	0	0	0	0	0	2
Nk1	2	2	1	1	1	1	1	0	0	1	1
Nk2.1	2	1	1	2	1	3	2	3	1	1	5
Nk2.2	2	1	1	1	1	1	1	1	1	1	
Nk3	2	1	1	0	1	1	1	1	0	0	1
Nk4	3	1	1	1	1	0	0	1	1	1	1
Nk5/Hmx	3	1	1	1	2	1	2	2	1	1	1
Nk6	3	1	1	1	1	1	1	1	1	1	1
Nk7	0	1	1	1	1	0	0	0	0	1	1
Noto/Emxlx	1	1	1	0	1	0	0	0	0	0	2
Tlx	3	1	1	0	2	1	1	1	1	1	2
Vax	2	1	0	1	1	2	2	1	2	0	2
Ventx	1	2	0	0	0	0	0	0	0	0	0
Unknown family				4	1	4	2	2	4	3	24
Total	48	35	28	22	31	23	20	21	21	17	59
PRD											
Alx	3	1	0	0	0	1	1	1	2	1	1
AprdA-E	0	5	0	0	0	0	0	0	0	0	0
Argfx	1	0	0	0	0	0	0	0	0	0	0
Arx/All	1	1	2	1	1	0	0	0	0	0	1
CG11294	0	0	1	0	0	0	0	0	0	0	0
Dmbx	1	1	0	1	1	0	0	0	0	0	6
Dprx	1	0	0	0	0	0	0	0	0	0	0
Drgx	1	1	1	0	1	0	0	0	0	1	0
Dux	24	0	0	0	0	0	0	0	0	0	3
Esx	1	0	0	0	0	0	0	0	0	0	0
Gsc	2	1	1	1	3	1	1	1	1	1	1
Hbn	0	0	1	0	1	0	0	0	0	1	1
Hesx/Anf	1	0	0	0	0	0	0	0	0	0	0
Hopx	1	1	0	0	1	0	0	0	0	0	0
Isx	1	1	0	0	0	0	0	0	0	0	0
Leutx	1	0	0	0	0	0	0	0	0	0	0
Mix	1	0	0	0	0	0	0	0	0	0	0
Nobox	1	0	0	0	0	0	0	0	0	0	0
Otp	1	1	1	0	1	1	1	1	1	1	1
Otx	3	1	1	3	1	1	1	2	1	1	3
Pax3/7	2	1	3	1	1	0	0	0	0	0	2
Pax4/6	2	1	4	2	2	2	2	2	2	2	2
Phox/Arix	2	1	1	1	0	0	0	0	0	0	0
Pitx/Ptx	3	1	1	1	1	2	2	2	1	1	1
Prop	1	1	1	1	1	1	1	1	0	1	0
Prrx	2	1	1	0	0	0	0	0	0	0	0

Repo	0	1	1	0	1	1	1	1	1	1	1
Rax/Rx	2	1	1	1	1	1	1	1	1	1	1
Rhox	3	0	0	0	0	0	0	0	0	0	0
Sebox	1	0	0	0	0	0	0	0	0	0	0
Shox	2	1	1	0	1	0	1	1	0	1	0
Tprx	1	0	0	0	0	0	0	0	0	0	0
Uncx	1	3	2	1	1	1	1	1	0	1	1
Vsx/Ceh10	2	1	2	2	2	2	2	2	1	1	1
Unknown family				1	9	2	1	3	2	2	7
Total	69	27	26	17	30	16	16	19	13	17	33
LIM class											
Ap/Lhx2/9	2	2	1	1	1	2	2	2	2	1	0
Islet	2	1	1	1	1	1	1	2	2	1	1
Lhx1/5	2	1	1	2	1	1	1	1	1	1	1
Lhx3/4	2	1	1	1	1	1	1	1	1	1	1
Lhx6/8	2	1	1	1	2	1	1	1	1	1	1
Lmx	2	1	2	1	2	1	1	1	6	1	0
Unknown family						1	1	1			
Total	12	7	7	7	8	8	8	9	13	6	4
POU class											
Hdx	1	1	0	0	0	0	0	0	0	0	0
Pou1	1	1	0	0	0	0	0	0	0	0	1
Pou2	3	1	2	1	1	2	1	1	0	1	0
Pou3	4	2	1	1	1	1	1	1	1	1	2
Pou4	3	1	1	1	1	1	1	1	1	0	1
Pou5	2	0	0	0	0	0	0	0	0	0	0
Pou6	2	1	1	0	1	0	0	1	1	1	1
Unknown family									1		
Total	16	7	5	3	4	4	3	4	4	3	5
HNF											
AhnF	0	1	0	0	0	0	0	0	0	0	0
Hmbox	1	2	0	1	0	1	1	1	1	1	0
Hnf	2	1	0	0	0	0	0	0	0	0	1
Total	3	4	0	1	0	1	1	1	1	1	1
SINE class											
Six1/2	2	1	1	2	1	1	1	1	0	1	1
Six3/6	2	1	1	1	1	1	1	1	2	2	1
Six4/5	2	1	1	1	1	1	1	1	0	1	2
Unknown family											1

Total	6	3	3	4	3	3	3	3	2	4	5
TALE											
Atale	0	1	0	0	0	0	0	0	0	0	0
Irx	6	3	3	1	4	4	4	3	5	2	1
Meis	3	1	1	1	1	1	1	2	0	2	1
Mkx	1	1	1	0	1	0	0	0	0	0	0
Pbx	4	1	1	3	1	1	1	1	3	1	1
Pknox	2	1	0	0	1	1	1	1	1	1	2
Tgif	4	1	2	0	1	1	1	1	0	1	1
Unknown family					14	1	1				
Total	20	9	8	5	23	9	9	8	9	7	6
CUT class											
Acut	0	1	0	0	0	0	0	0	0	0	0
Compass	0	1	1	1	2	0	0	0	0	0	0
Cux/Cutl	2	1	1	1	1	0	0	0	0	0	0
Onecut	3	1	1	6	1	2	2	1	1	1	1
Satb	2	0	0	0	0	0	0	0	0	0	0
Unknown family					2				2	2	
Total	7	4	3	8	6	2	2	1	3	3	1
ZF class											
Adnp	2	0	0	0	0	0	0	0	0	0	0
Azfh	0	1	0	0	0	0	0	0	0	0	0
Tshx	3	1	0	0	0	0	0	0	0	0	0
Zeb	2	1	1	1	1	0	0	0	0	0	0
Zfhx[d]	3	1	1	1	1	1[e]	1[e]	1[e]	1[e]	1[e]	0
Zhx/Homez	4	1	0	0	1	0	0	0	0	0	0
Unknown family					1	2	2	2			
Total	14	5	2	2	4	3	3	3	1	1	0
CERS class											
Lass	5	1	1	0	1	1	1	1	4	2	(1)
Total	5	1	1	0	1	1	1	1	4	2	1
PROS class											
Pros	2	1	1	1	1	1	1	1	2	1	0
Total	2	1	1	1	1	1	1	1	2	1	0
unknown class	6	3	0	23	3	3	3	1	3	2	4
	260	131	103	103	134	83	78	81	86	74	134

[a] This gene has not been identified in our dataset but was previously identified.

[b] Central Hox genes have uncertain family membership.

[c] This gene has a very different N-terminus. Possibly an assembling issue.

[d] Current sequence runs into a putative intron.

[e] Each Xenacoelomorpha protein has 4 HD's; the number of HD's can vary in other species.

Hs: *Homo sapiens*
Bf: *Branchiostoma floridae*
Dm: *Drosophila melanogaster*
Ce: *Caenorhabditis elegans*
Cg: *Crassostrea gigas*
Ip: *Isodiametra pulchra*
Sr: *Symsagittifera roscoffensis*
Hm: *Hofstenia miamia*
Nw: *Nemertoderma westbladi*
Xb: *Xenoturbella bocki*
Nv: *Nematostella vectensis*

also see supplementary fig. S4 for the actual alignments

Supplementary Table S2

Overview of class membership of all identified homeodomain proteins in 8 more Xenacoelomorpha spp. based on the Cannon et al., 2016 transcriptomes.

Species	#	ANTP	CUT	POU	HNF	LIM	PRD	ZF	CERS	TALE	PROS	SINE	Amb
Ascoparia sp	14	6					2			3			3
Childia submaculatum	52	16	2	3	1	5	10	1		6	1	4	3
Convolutriloba macropyga	76	31	3	4	1	8	16	1		6	1	3	2
Diopisthoporus gymnopharyngeus	49	17	2	1		6	9	2		6	1	2	3
Diopisthoporus longitubus	58	20	2	3		10	9	2	1	6		2	3
Eumecynostomum macrobursalium	11	2		1		2	2			2		1	1
Meara stichopi	67	18	1	4	1	8	15	1	3	8	1	3	4
Sterreria sp	1	1											

#: number of genes based on unique sequences
Amb: number of genes classified in more than 1 class (ambiguous)

Supplementary Figure S3

1 - *Isodiametra pulchra*

>IP_DN10641_ANTP_AMB
EEFKKDKYLSVSKRLELSVALSLTETQIKTWFQNRRTKWKKQVASRMKIAYRSFWTVPNSAGGHQPQFPLPNPFYALGNPLNPL
NPLYLQSVSGGGGFLGAAHSPLDDDDRELDQSDCFSPDDSDDPGNESPLRS
>IP_DN12279_ANTP_Evx
MQSSAFSISSIIDLPRPTQPGTGHVVENETPGESRSPSPDFPAGSQTAHQQQSTGSPPPRCLSPMSAAGMRRYRTAFSKHQQD
SLEMEFRKENYVSRPRRCELAASLNLPETTIKVWFQNRRMKEKRQRQAFTWPPYFDPYYYGYLISRGLIPAPVAQPSIPQMP
>IP_DN12334_PRD_Pax4/6
AVAAAAHCAAAVTDEQQQKKLEEAAGGGGCTGASEEARMQLKRKLQRNRTSFTPEQIDALEKQFEVTHYPDVFARERLAGKI
ALPEARIQVWFSNRRAKWRREEKLRTQKQQQQQQQQQQQQQQ
>IP_DN15610_ANTP_Nk5/Hmx
MQKPKFVSPFSISHILGHSPAAASEPAPAKQVEEQEATKHVIQSKEQLDLLLGIATNPVDSVEASTNRPNEAASPQAQQPKAKQ
NTEVSPSENISPCSVECDTSSDDEDGGDDGDKERRKKTRTVFSRNQVCQLESMFDMKRYLSSSERTGIARDLGLSEQQIKIWFQ
NRRNKLKRQIKTGLEMAGNISAGTVPPPNVNAALLGSFSSQQPSHHSQMLPFPSPTSMYHQLPGSTPNLSLKVDSNPASNFPH
LNFPAPNRTMAPSASQAATVSHTQGTPFSARPSQQNQPADLFSFHNFSMMRSLSGLV
>IP_DN18113_POU_AMB
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LLVLAPSTTTPVAKGPIRISNPQVTVACPVGFSPESPDSEKTRSGGVDSTEVNVVTKKFAPQPPAVDDSSILEELEAFAKDFRTRRI
KLGFTQADVGLSLGKMHGSDFSQTTISRFEALNLSFKNMINLKPFMEKWIDDAERHISMVKNDLTQLSDEDQRKLGLFINAGD
PLTNRKRKRRCVIDAHTKKTLEQSFRDKPHPSPDETNALAEALGLDRETVRIWFTNRRYRERRSETPNSTS
>IP_DN19265_PRD_Rax
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KHRRNRTTFTTFQLHELERAFEKSHYPDVYSREELAARVNLPEVRVQVWFQNRRAKWRRQEKLEQSQLKLNTDFPLATLRASA
AAAKFSALDPWGLGAAASAAFPFIPPTAFFHPYSGGQMTAAAAALSNPFFFGNPSQQSV
>IP_DN26203_ANTP_AMB
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VQAPSPPVHRLAPTPGDGEDSDKENIDPRGGSSPPIIRPFSSSPGHLASDAEQTGRSKRQGRTVFTKQQLEILNGHFNHRQYLSL
AERAQLSEQLCLSQKQVKIWFQNMRSKAKRVMNASSRTQPQDLAQKQSQEAFECAGNQVTSALDENHNVSRNESTGESSYF
YQPPTINSFLCPNPDSPECNGANGCHRTTDSDSPSNLVIDC
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HESNVLCKQHYLDLLEVPGKATTGSSSSSDKMADLVSNSGGDSSDGNSELDLSMGSPHKSKRSRTTFSEDQLKILQANFNLDSN
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>IP_DN31212_CUT_Onecut
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L
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WFQNRRAKWRKKEKTWGRAS
>IP_DN36044_ANTP_Barhl
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>IP_DN36933_CUT_Onecut
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YDSFESAFAYAAAGTATRQPAATAAVPNIYSSPKLKEECIFTSLATSTQPPSKPRNRNSSRQSGEKEMTMKEVGESGGSELDTRD
VAHRITAELKRYSIPQAVFAEKVLGRSQGTLSDLLRNPKPWGKLKSGRETFRKMEKWLEEPEFQRMSSLRVAACKKKELESLNP

GGLPAASAAAPVQNPGKPHQKKNRLVFTDIQRRTLFAIFRETKRPSKEMQLQISRQLGLEPTTVSNFFMNARRRCGDRWKDPS
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>IP_DN38710_PRD_Alx
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Protein domain identification

trinityID class	(homeoDB blast)	protein domains (Hmmer search)
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2 - *Symsagittifera roscoffensis*

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Protein domain identification

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3 - *Hofstenia miamia*

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Protein domain identification

trinityID class	(homeoDB blast)	protein domains (Hmmer search)
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DN12035_c0_g1_i1|m.3241	ANTP	CITED Homez
DN44693_c0_g1_i1|m.40284	ANTP	Homez
DN90735_c0_g1_i1|m.44111	ANTP	
DN104433_c0_g1_i1|m.45397	ANTP	DUF4476 Homez
DN58284_c0_g1_i1|m.41535	ANTP	Terminase_5
DN18872_c0_g1_i1|m.5077	ANTP	
DN3930_c0_g1_i1|m.1095	ANTP	
DN58320_c0_g1_i1|m.41539	ANTP	Homez
DN4748_c0_g1_i1|m.1255	ANTP	QLQ
DN12978_c0_g1_i1|m.3456	ANTP	Homez Oxidored-like
DN43016_c0_g2_i1|m.36485	ANTP	
DN36484_c0_g2_i1|m.17692	ANTP	
DN15813_c0_g1_i1|m.4392	ANTP	

DN34181_c0_g1_i1|m.14867	ANTP	HTH_28
DN20211_c0_g1_i1|m.5588	ANTP	Auxin_canalis Homez
DN29024_c0_g1_i1|m.10351	ANTP	
DN3061_c0_g2_i1|m.947	NTP	
DN24302_c0_g1_i1|m.7955	ANTP	
DN12216_c0_g1_i1|m.3286	ANTP	Homez
DN34160_c0_g1_i1|m.14868	LIM+ZF	DUF2180 DUF2321 SIR2 zf-C2H2 zf-C2H2_2 zf-C2H2_4 zf-C2H2_6 zf-C2H2_jaz zf-H2C2_2
DN8120_c0_g2_i1|m.2184	LIM+ZF+ANTP	DUF1319 DUF164 LIM
DN34694_c0_g1_i1|m.15382	PRD+LIM	SOBP

4 – *Nemertoderma westbladi*

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LDTRESSTTYRVNPNNGKTRTKDKYRVVYSDRQRAELESEFRCNQYITIKRKTELAGMVGLSERQVKIWFQNRR
AKERKVARKYTIGGK*
>Locus_48679.0_Transcript_3/0_Confidence_10_Length_1102
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LPETTIKVWFQNRRMKDKRQRQALLWPYLDPYYYAYLVSRGIIPVTSPPPGGLPGLPEVTPTIAEYRNKLPTQRLA
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>Locus_36518.0_Transcript_1/0_Confidence_4_Length_1293
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PAGGTLDLRQKTIHQSMTAPRIMLPSEPQMGELQAVFEFPSLHRDPISMMPAATAVPSSRDYLFTGFPGQSAPG
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>Locus_35873.0_Transcript_1/0_Confidence_5_Length_1977
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PNGYYPATPMDTYGVVDNDRPSEPAEYHVVPNARLFNADSLPVTNNNPTQLYHGNAPYESGSPDVKPFTDSYIN
GTTEPPHQVYSWMRLKRSQPNANKSHEFGYAGQTRGGRTNFTTKQLTELEKEFLYNKYLTRARRVEIAASLNLN
ENQVKIWFQNRRMKQKKLVKEGK*
>Locus_54694.0_Transcript_1/0_Confidence_0_Length_1248
MYTSTTVSEGMINSWPGIAPYYDTEPLGSVRYTNLDNRDSWLINSRSVAAVDPSSCNDEKSGTGLPRGGTAAATI
HYTTGYQNNYSQYGNNLYGNNEDAYNYSTSLFPQHHFTYAADTIDEAVKHSRTLPSYHGNSIDCTTGRDSVHQP
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TLCL*
>Locus_10725.0_Transcript_1/0_Confidence_0_Length_314
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FLFNVYITRERRSEISRSLNLTDRQVKIWFQ
>Locus_58015.0_Transcript_1/0_Confidence_0_Length_736
AEYMGDYCADGIPNSANFPFFSCENFSEINNNNIFNGSITAPSNDQFIALDTNCDSVWMEERNPPDQQPIPNCGI
QMVNVVNGVATATQFIYPVAITNRNLHVSDNLEYEDADDNENDAFNKRKDRTAFSKFQIEQLESEFETYNYLTRL
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>Locus_58481.0_Transcript_1/0_Confidence_0_Length_480
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SRPKRFEVATSLNLTETQVKIWFQNRRMKLKRSERILPHTNGSSK*
>Locus_6133.0_Transcript_1/0_Confidence_0_Length_867
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NQIETITPTVVQSIFTSVEKMCESAELSASRISNVDLLSHPTMQDIVLSNHSSFMRNHLSYIPTLHWRALVRPDNKN
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>Locus_44999.0_Transcript_2/0_Confidence_12_Length_1575
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CDYQSAYRNKKCRRTRTVFTELQMLGLEKRFDMQKYLSTPDRLGLSDSLGLTQLQVKTWYQNRRMKWKKEILIC
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>Locus_50937.0_Transcript_3/0_Confidence_47_Length_2589

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PHQPSPVGLGYGYHSQAPPNYPHSTLQPPHHPSSAYMATTVRDSLSISPDSKEDKLLHDPELRLSSKGKKLRKP
RTIYSSYQLSMLNKRFQGTQYLALPERAELAATLGLTQTQVKIWFQNRRSKFKKLLKADPDAMPSEAMQTLLDED
MAGVDDADENAESKPVKQEYLGGQQPQGWDQVLADSRTLETEKHYHGNPTQFPRGSPSLSGNHDNGGGPPS
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>Locus_54562.0_Transcript_1/0_Confidence_0_Length_921
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SFLDYSANQSSSYTPSSPGGQVCAYHPPNVPSMYGTMQPYQYHPHGNYRDAPHHPHYPSSAAPYQGSRHAIG
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>Locus_35817.0_Transcript_2/0_Confidence_6_Length_1968
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AAAHHMSQLFNSGQAGRQPVHSSSAGSAPPGLGYFNGAGEQYPNTMAMMNPYSPYSGSPTANQFTINHHPSQ
QRSGVLPSHHHPSQSSNLPPYHHGGPYPTPPSHGYHHQSLQGVHPASSNYLSPRDQMMDMKDEKLIDGELRQ
TGKGKKIRKPRTIYSSYQLSMLNKRFQGTQYLALPERAELAASLGLTQTQVKIWFQNRRSKFKKLMKADPNSLTS
EVMAKLMEEDRRTSQRDLTSVDSDNETSEESVKSVNIKQEPYAWNNSVLEHNNLDNKLTYQDNNLLPPIGELAN
NNASNSINPPIGTREDLRANINMSVTASTAVHSDNNSMLNYSHHAGISLVNSQQPGLSLGNSPMGGALSGFGQF
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>Locus_17210.0_Transcript_1/0_Confidence_1_Length_1444
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PTAGHHPVVHHPAVHYPAVSPSLPLPNFPMHQMSQLAANHHLQSSQLSHPNYHLLQSSLIGSPVYRHPILPSNN
MQCYSSAVNGSLGDLLHRKPKRIRTAFTSEQLQRLENEFTSNPYIVGEERRQFAASLRLSETQVKVWYQNRRTK
DKREIAKDEKGCEDEEDCEETGGEPRGENCGDIRGESCRDIGRENDRDGRETRELTGRDIQVQTSRDFRGENC
RDIREQNSRDESRDIDNAIDVVNGKYENNKELNVKSRKRLNSFTEDNNMKLYKISSYNELLYR*
>Locus_44961.0_Transcript_2/0_Confidence_9_Length_1683
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NLHTSYYQSQLAMSPLQLARYQSQLAAPPLQLANYQSMMTPHHPNATYIADLLHKPKRIRTAFTTEQLQRLEDEFI
ANPYIVGEERRRFAANLNLTETQVKVWYQNRRTKDKRETSREEKRENSGVENLGNIGEEKRGSWDGKRETVKIE
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>Locus_45472.0_Transcript_2/0_Confidence_5_Length_3205
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GMSQLSHPGMGSGCNGTTPSMNELGHYNPYTDPRSSYTGWYGASAAADPRISSEYWASMAGMNMGFSADYN
KILPSQQRRKRRVLFTQAQVYELERRFKQQKYLSAPEREQLAAMIHLTPTQVKIWFQNHRYKMKRQAKEKTPHD
GNQGQQQQNSPRRVAVPVLVKDGKPCTGGANSNTTTGNNNISTTSPTSSNRHQSITNIANNNTAIIPNYSSNFAV
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>Locus_20731.0_Transcript_1/0_Confidence_1_Length_661
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RRVLFSKQQTYELERRFRQQRYLSAPEREHLASIINLTPTQVKIWFQN
>Locus_36577.0_Transcript_2/0_Confidence_2_Length_1846
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SAFTPPVSTLPVHPLATHIPSGMASGLLGYQLGPLCPSWLACRGPPTVSLPTLLPPPQFVLPSSGNFGRSGEIVD
TSSGKLFPSSIPFAPNNESEIEGPNDELENKAESDDDELESIEEEVDISDKEDKLDDSKDSDQENKRSYRKKKTRT
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>Locus_41714.0_Transcript_1/0_Confidence_6_Length_1153
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DNKHRPQQPFPIPTFPLVSKNRLAGSYEYFSQLGVTVPSLNQSHINNIEGKKHTRPTFSGHQIFALEKTFEQTKYL
AGPERGRLAYTLGMSESQVKVWFQNRRTKWRKRAVQESKFKHRVGCGLTDDFAEETVIDDIHPITNNSIDIIEPP
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>Locus_33755.0_Transcript_1/0_Confidence_1_Length_2054
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>Locus_49354.0_Transcript_1/0_Confidence_14_Length_2077
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HSPNALLHQYRQGLPLLPPQNLPPIHGNTFLPKVAQNRATYQPHQLQAFNARMAFPASTIDSVSMEPPNKYLRH
DPSFYQGDNTLLYQTPRLPNNTITSPTTKHYETPQPKETERFIDNLKPNKPVSCDGYQTSGGVTTYNPSLLLGSV
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SAPGEIKEPRRIKITDSNGVIKEYVFPRGLDLDRPKRQRTSFTAEQLYILEKEFRRNQYMVGKDRGLLAESLDLTET
QVKVWFQNRRTKYKREKTRHEEYHQVNAESLAACNILKMLELPPPPVALIPPTGAPPAAASGISPLGGAISCSPP
RAADHYSKPIAAGAAANMFPR*
>Locus_4231.0_Transcript_1/0_Confidence_0_Length_1276
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LTNGYVDMMAQNSSNNGHASLTSSHNSYKKPALKFGIDRILAIEDSKDEVCSSRNSRFYNDSHEESTIDRSEPIKN
LELFLIRNPPECDYRMGPFEPAISPLLRDQHPESYLSSTSNNSQFNSRNDSDLLGLVSRQQQHPRDGVKHQSLL
GVDHTEKFQWLQCTRYSPPKIQRTKKYSERKRKLGRNPRVPFTQTQVDHLELKFREAKYLSSLDVADISTHLNLT
DTRVKIWFQNRRARERREKAAESAPPDNSEEIIDIVNIDDETSNHADIKPIDKHNSAKNIISDNFKLTKTVTNQKSTI
DLYKTGNSI*
>Locus_15302.1_Transcript_1/0_Confidence_1_Length_337
RKPRILFNHSQIFQLELRFKHQRYLTANDRRELSDQLNLTQNQIKIWFQNRRYKSKRQEINQSLASYYQHNKQLPT
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>Locus_20062.0_Transcript_4/0_Confidence_2_Length_1268
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TFCSGTPPQPVPVASLTHGIYYNTVGDEYRITDNITSSSNQVSPRTQLSEDVSSQTPSNSHTTTTTPCRTIPEGCE
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DTPIIGYRRKRTSFSSSQLRELEKHFNRKKYLSVPDRTLLANILHLTQPQIKVWFQNRRAKWKRIKAGSYQAATSG
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>Locus_49786.0_Transcript_4/0_Confidence_14_Length_1543
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LLYSPYGDLVEVSSYKGTSLGSMIVRNGPSPTHSTQSCAANSYELSNDNFTHDHNSRNNVSLFQSPMYCRTQPS
HPRSSYSKGFAHTANLHGNTNCTQSISNLKFSIRSILGPNVDDNHETSTLVVGNSSLNDLSEATVSHIPTVTAKNV
ASLADEDLSDLHFPLTHGVNPQPGLGMWNSRALPCTYDFLSTGNIIPSPYFPPTGGAYYWPFASRGKPRRGMLR
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>Locus_29958.0_Transcript_1/0_Confidence_2_Length_908
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MVKPPPFVFPFNRLSCSPFPRHTWVPPGLCFPGDAPCLQSDICMCYFHSRRNRGWNRVRTVFTNAQRLGLEEQ
FREQKYVSKPDRKELAGKLGLSDSQVKVWFQNRRMKWRNSLKLKAAARNGRRAITVEKDSNNVGIEEESESDD
NI*
>Locus_31941.1_Transcript_1/0_Confidence_3_Length_2634
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NYTVQTSTSAPVGTSVNALTTAASVAVSSVYDGSITSTTSEGSMLGSMRPPPPLVLHRNHSASSSNSAMGKVTP
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VFFQNLRARVRARTKQQVNDIPTRQTENIILSDGTLT*
>Locus_36321.0_Transcript_1/0_Confidence_7_Length_1157
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APPSGLFHSGYNDPAPVMLPAAPLMTAYPPITSQQPMLPAMLPPTMDPYSINRIQQHLPGVPSMTSPQFSNSYA
PVQPSIAIGQGFLHPSQTQSPLANTEFWLNSNRIALDVGLPNRMPPLGVYH*
>Locus_45900.0_Transcript_1/0_Confidence_5_Length_1608
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LFLCRSVLSFYGILALAGREFSKTSRLKTVWIGYPRHPISEAIYEFYMLEIAFYASQIITSLRHANKRGVKLEILYDSIIL
SMSIAAWVCNYHRMMCLILLAIDVGQPGRHLAKVFHYAHFDVPATFTYIVQLTIYAIFTVYAFSFHIFVTATISFTEIF
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>Locus_50700.0_Transcript_1/0_Confidence_27_Length_1758
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>Locus_20893.0_Transcript_2/0_Confidence_2_Length_1499
MICYAFMSKRDTFYNKSGSTSRGNGTPHRVQSPNRNADSHTRQIKYINKRSTQFQDQHNSSSYNQKNQHLYVQ
PALFQALKTTSHSTQSKQPQKGSQERHTSKNPLHCNIYSQVQQPKDQQSGTHTLQSHYPYNRAQQSNSQQTTS
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SPRPYIMGHCSAQLSHPSFPNIPSYGFPSGISHPSYSSPPPRVVYSSPPHSGSSYGFDPASSADGSDLQPRSAA
ASLVSQTSSIVDQLDKISDSRPGNQPETVLVKDVSDSRKRSLSVSETDRKEPKRILVTDSSGAVKEYVFPAALDLD
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>Locus_55290.0_Transcript_1/0_Confidence_1_Length_1438
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>Locus_40829.0_Transcript_1/0_Confidence_6_Length_1163
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DSPCYPTDFRTSSIAALRLKAREHQVAMGLFNPHGNAMAPTHTSHYAIS*
>Locus_40214.0_Transcript_2/0_Confidence_4_Length_1637
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VGELVSTQTGPGSRYEVPVGEPASRYGIPVAEGDNSDSYLSSDNGGEHHLDETEMVDVEI*
>Locus_53544.0_Transcript_15/0_Confidence_41_Length_3588
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DIRDESWLSRRHNEYQR*
>Locus_48073.0_Transcript_2/0_Confidence_17_Length_2165
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>Locus_49939.0_Transcript_2/0_Confidence_19_Length_2983
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>Locus_24274.0_Transcript_1/0_Confidence_4_Length_1313
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>Locus_27707.0_Transcript_1/0_Confidence_3_Length_1324
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>Locus_29086.0_Transcript_1/0_Confidence_4_Length_1565
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>Locus_21928.0_Transcript_1/0_Confidence_0_Length_1379
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DSSAVI*
>Locus_54213.0_Transcript_49/0_Confidence_50_Length_4112
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>Locus_47651.0_Transcript_2/0_Confidence_7_Length_269
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>Locus_54455.0_Transcript_1/0_Confidence_0_Length_772
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>Locus_51594.0_Transcript_4/0_Confidence_29_Length_2823
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>Locus_51594.0_Transcript_2/0_Confidence_12_Length_1330
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>Locus_45303.0_Transcript_4/0_Confidence_14_Length_1909
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>Locus_22501.1_Transcript_1/0_Confidence_1_Length_2011
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>Locus_61503.0_Transcript_1/0_Confidence_0_Length_420
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>Locus_38224.0_Transcript_1/0_Confidence_1_Length_1306
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>Locus_50222.0_Transcript_6/0_Confidence_13_Length_1916
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>Locus_14051.0_Transcript_1/0_Confidence_0_Length_1064
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ESRSNYSEVTSDEEETMSRRKTTKTKGVGRKRVILTHNQRRVLRAAFIVSQKPSRKVKEDLGGATQLPVRIVQV
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>Locus_48370.0_Transcript_1/0_Confidence_2_Length_1736
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>Locus_52392.0_Transcript_2/0_Confidence_13_Length_3474
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SEHDLLMENAGLMDDDDDLNMDAESLEDGGNGSNELSGYGLSDSPLPSFVPQQFPPSQLQTTTGTSPTTAGG
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>Locus_27996.0_Transcript_1/0_Confidence_2_Length_2302
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GLNYPIISYPSLPSNQYISSPTMSAKQPQNSAPMSSANSDINALTYNSSPM*
>Locus_9311.1_Transcript_1/0_Confidence_0_Length_709
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>Locus_52441.0_Transcript_6/0_Confidence_5_Length_1244
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>Locus_53834.0_Transcript_19/0_Confidence_35_Length_2674
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SESQETLRRRKRRTSLNPDVREKLEAHFEVNSRPGANQIFVISEHLSLDREVVRVWFCNRRQKIKRVNSSTAATR
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>Locus_48953.0_Transcript_27/0_Confidence_27_Length_1864
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>Locus_36924.0_Transcript_1/0_Confidence_0_Length_774
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>Locus_42137.0_Transcript_1/0_Confidence_3_Length_1922
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>Locus_28871.0_Transcript_1/0_Confidence_6_Length_1464
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>Locus_10005.0_Transcript_1/0_Confidence_0_Length_1138
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>Locus_26582.1_Transcript_1/0_Confidence_0_Length_1190
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>Locus_48316.0_Transcript_1/0_Confidence_8_Length_1528
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>Locus_52332.1_Transcript_9/0_Confidence_46_Length_2474
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>Locus_52332.1_Transcript_11/0_Confidence_46_Length_2489
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FLHMRASPEDNSSDPQLDRLNNMLRAEGVDGPEINPGTGGPGQPDNAIEHTDYRDKLQQIRMIYRQELDKYETA
CNEFTTHVMNLLREQSRTRPISSKEIDRMVEIIHKKFNTIQIQLKQSTCEAVMILRSRFLDARRKRRNFNKTATEVL
NEYFYSHLSNPYPSEEVKEDLAKKCNLSISQVSNWFGNKRIRYKKNIGKAQEEANLYAAKAAAQGIHEDDSPSRS
DSPISNHGSLRGYFVDNPYFQESPSDAFIAAHSQPQFSTVVPNGYSENQADNLRQMIQTPNYHDDSQSFDLQYA
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>Locus_52537.0_Transcript_2/0_Confidence_21_Length_3983
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MIYRQELEKYETACNEFTTHVMNLLREQSRTRPISGREIDRMVSIIHKKFNAIQIQLKQSTCEAVMILRSRFLDARR
KRRNFNKNATEFLNEYFYSHLNNPYPSEETKEELAKKCGLSISQVSNWFGNKRIRYKKNIGKAHEEASLYAAKAA
SHPLPGGTDSPTHSDSPHSTHGSLVGYFSDTRYLTDSPTDPFAPPPSTEGQMTIQSELYNIGAASNGYHENQAE
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>Locus_45317.0_Transcript_1/0_Confidence_7_Length_2004
MHSENLLRNDAFNNYGNPVQHAISPQEMQCHASLVGSSLPSPGNNQLIYQPVAMVSPPGSFQLHQSHGHAIHG
STPLSQIGVTQQQQQQQQPLQPSHLDPSMSINHQAMLMDHMLGGVGVDNCSMDPKKVSKRGILPKHATSVMR
SWLFQHIVHPYPTEDEKRQLAGQTGLTLLQVNNWFINARRRILQPMLEASNPESLPKPKKAKTAGRPAQQRFWP
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>Locus_46342.0_Transcript_1/0_Confidence_9_Length_2142

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>Locus_35933.0_Transcript_2/0_Confidence_4_Length_3307
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GGSELNIFPDDYNSDVGMANSLSPLPPIDDDYRVTIKPTCQSALPPSVITVEGTVDTCQLVDYIKELLHKNNIGQKL
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>Locus_ZFHX
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>Locus_51994.0_Transcript_4/0_Confidence_17_Length_2917
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>Locus_44536.0_Transcript_4/0_Confidence_10_Length_1995
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MVQLGYYLKEIPMHMKESRRKDNLIMFVHHVLTINLIAFSWLFDYVRIGLLIVVVHDVMDPVAYTAKVLHYAKLDYI
ARPLVYVLVAVFTVSRLYIFPYFVLYSTIFESLDTFDCYIPAVPESFQTPRSFRLPLISWWSLFNSQLLLLLVFSAVW
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>Locus_40648.1_Transcript_1/0_Confidence_2_Length_1479
YICIKEMAAISQWFWSERFWLPDNVTWADLKNDGTTTYPEASALLAALPLALLIYLIRVLSERLVFSNIGIMFGIRSS
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MFGCQIQSNHGYIYNLKVCWQDYPFLNVPYDVHMYYIVSLAFYCSLLISQFTDIRRKDFWVMFTHHIVTVFLISFS
WAANFIRIGCCIIVIHDSSDVLLELAKLLRYIKYMSFCNVAFGLFTATFFVTRLYFYPVYLVHSIHTSTAVVGFYQSW
YVFMALSVSLVFMHFYWSILILKVIYNIVIRSKTEDSRSDSESDLREAEEDDDREGSGNSNGSVPSGYN*
>Locus_62117.0_Transcript_1/0_Confidence_0_Length_466
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HT
>Locus_44308.0_Transcript_1/0_Confidence_11_Length_2316

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>Locus_51275.0_Transcript_2/0_Confidence_33_Length_3000
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LRINFPDVRFTRHINAQLIKWFSNFREYFYIQIEKFARQSVVDGAAIATDIVVNEDSALHRALNLHYNKANLLQIPKS
FVTAVTTTTQEFFFAVFHNKDRDPSWKKRIYKIITKLDCSIPLSFRSPNFMEELERSYQHEYTQ*
>Locus_53646.0_Transcript_1/0_Confidence_15_Length_4742
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VQHVRDCSPNGSLPTLLEGQPPSGVDKVLNLLNQPRPSPNAKRGFYHHAINLLDAAQENPGQKVKLIPVTSDKP
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>Locus_32393.0_Transcript_2/0_Confidence_5_Length_1036
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>Locus_44118.0_Transcript_2/0_Confidence_9_Length_1342
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AGGVSMRYPPWNSEAFYRNRIHRIVAKPSTAEMELSSHQLSVLESAYKLNKCPDTDELSILSEKANMSTSLVKTW
YENKLSEWRRREGLPARGSSVFDRFR*

	predicted class	PFAM domains
Locus_10725.0	ANTP	
Locus_15302.1	ANTP	DUF1374, Homez, RcbX,TUDOR
Locus_17210.0	ANTP	
Locus_20062.0	ANTP	
Locus_20731.0	ANTP	
Locus_20893.0	ANTP	

Locus_29958.0	ANTP	Homez
Locus_31941.1	ANTP	CUT
Locus_33755.0	ANTP	
Locus_35817.0	ANTP	BROMI
Locus_35873.0	ANTP	HTH_23
Locus_36321.0	ANTP	Homez
Locus_36518.0	ANTP	
Locus_36577.0	ANTP	Ax_dynein_light, CDC45, DUF2115
Locus_41714.0	ANTP	Luteo_P1-P2
Locus_4231.0	ANTP	Homez
Locus_44961.0	ANTP	Transpeptidase
Locus_44999.0	ANTP	DUF3078
Locus_45472.0	ANTP	
Locus_45900.0	ANTP	Homez
Locus_48679.0	ANTP	Death
Locus_49193.0	ANTP	Med3
Locus_49354.0	ANTP	
Locus_49786.0	ANTP	ARF7EP_C
Locus_50700.0	ANTP	Homez
Locus_50937.0	ANTP	
Locus_54562.0	ANTP	
Locus_54694.0	ANTP	HTH_23
Locus_58015.0	ANTP	C6; Homez
Locus_58481.0	ANTP	
Locus_6133.0	ANTP	DUF382, DUF3870, DUF4445, Imm7
Locus_18856.0	PRD	HA
Locus_21928.0	PRD	
Locus_24274.0	PRD	HTH_23, HTH_29, HTH_Tnp_IS1,PAX
Locus_27707.0	PRD	DUF1631, HTH_32, QLQ
Locus_29086.0	PRD	
Locus_40214.0	PRD	Adeno_PV
Locus_40829.0	PRD	OAR
Locus_47651.0	PRD	
Locus_48073.0	PRD	
Locus_49939.0	PRD	MRP-L20
Locus_53544.0	PRD	ActA, OAR
Locus_54213.0	PRD	
Locus_55290.0	PRD	OAR
Locus_10005.0	TALE	Homez
Locus_26582.1	TALE	Homez
Locus_28871.0	TALE	Homez
Locus_36182.0	TALE	Homez
Locus_45317.0	TALE	
Locus_48316.0	TALE	Homez, MRP-S32
Locus_52332.1	TALE	DUF1319, Homez, HTH_19, PBC
Locus_52537.0	TALE	DUF1319, Homez, HTH_19, PBC, HTH_23, HTH_26, HTH_3
Locus_14051.0	LIM	LIM
Locus_22501.1	LIM	LIM, RFXA_RFXANK_bdg
Locus_38224.0	LIM	DUF581, LIM
Locus_45303.0	LIM	LIM, RFXA_RFXANK_bdg, Treslin_N
Locus_48370.0	LIM	LIM, ORC5_C
Locus_50222.0	LIM	LIM
Locus_52392.0	LIM	LIM
Locus_54455.0	LIM	Homez

Locus_61503.0	LIM	CDC45, MmgE_PrpD, Orbi_VP3, RRN3, YL1
Locus_7973.0	LIM	LIM
Locus_49053.0	LIM	DUF164, LIM
Locus_27996.0	POU	HTH_31, Pou
Locus_35933.0	CUT	CUT, HTH_23, HTH_3, Med9, Terminase_5
Locus_46342.0	CUT	CDK2AP, CUT
Locus_36924.0	SINE	Homez, HTH_23, HTH_3
Locus_42137.0	SINE	
Locus_40648.1	CERS	TRAM_LAG1_CLN8
Locus_44536.0	CERS	TRAM_LAG1_CLN8, DBC1
Locus_51994.0	CERS	TRAM_LAG1_CLN8
Locus_44308.0	PROS	HPD
Locus_51275.0	PROS	HPD, RTX
Locus_48953.0	HNF	HNF-1_N, HTH_19
Locus_50181.0	ZF	Glycos_transf_N, HA, zf-C2H2, zf-C2H2_4, zf-C2H2_6
Locus_9311.1	PRD+ZF+ANTP	HTH_19, HTH_31, POU
Locus_62117.0	PRD+CERS	FKS1_dom1
Locus_53646.0	PRD+ANTP	CUT
Locus_53834.0	PRD+ANTP+POU	HTH_19, HTH_31, POU
Locus_52441.0	CUT+ANTP	HTH_31, Pou
Locus_51594.0	LIM+ZF	LIM, TNFR_c6, Homez
Locus_39214.0	PRD+ANTP	Homez
Locus_44118.0	LIM+ANTP+PRD	Homez
Locus_32393.0	PRD+ANTP	

5 – *Xenoturbella bocki*

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6- *Ascoparia sp.*

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11- *Eumecynostomum macrobursalium*

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12- *Meara stichopi*

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>Msti.rna.tri.17312.1|m.19074
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>Msti.rna.tri.17700.1|m.19381
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>Msti.rna.tri.1108.1|m.1029
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>Msti.rna.tri.14107.1|m.16124
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SSSESLTSLPDFAPS*
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>Msti.rna.tri.20507.1|m.21302
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13 – *Sterreria sp*

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PIPVHVNRVGATNSIQQAPSGPTTLHLSASHWSL*

Supplementary Figure S4

Generic homeobox Sequence:

```
             RKRGRQTYTRYQTLELEKEFHF----NRYLTRRRRIEIAHALC-----------LTERQIKIWFQNRRMKWKKEN
```

ANTP class HOXL subclass

Cdx family

```
CDX1       Hs KDKY.VV..DH.R........Y----S..I.I..KS.L.AN.G-----------.....V........A.ER.V. NP_001795
CDX2       Hs KDKY.VV..DH.R........Y----S..I.I..KA.L.AT.G-----------.S...V........A.ER.I. NP_001256
CDX4       Hs KEKY.VV..DH.R........C----...I.IQ.KS.L.VN.G-----------.S...V........A.ER.MI NP_005184
CDX        Bf KDKY.VVYSDH.R.......YS----NK.I.I.RKVQL.NE.G-----------.S...V........A.QR.MA
cad        Dm KDKY.VV..DF.R......YCT----S..I.I..KS.L.QT.S-----------.S...V........A.ER.Q. NP_476954
pal-1      Ce  DKY.MV.SDY.R.......HT----SPFI.SD.KSQLSTM.S-----------.....I........A.DRRDK
Cdx        Cg  DKY.VV.SDH.R........Y----S..I.I..KA.L.QN.A-----------.S...V........A.ER.
Cdx        Ip KDKY.VV..DR.RA...N..RS----AQ.I.I..KS.L.MQVG-----------.S...V........A.ER.VS DN44102_c0_g2_i1|m.23116
Cdx        Sr KDKY.VV..DR.RA...N..RS----AQ.I.I..KS.L.MQVG-----------.S...V........A.ER.VS DN125595_c2_g1_i1|m.86363
Cdx        Hm KDKY.VV..DR.RA...N..RS----.Q.I.I..KT.L.SLVG-----------.S...V........A.ER.VA DN14515_c0_g2_i1|m.3895
Cdx        Nw KDKY.VV.SDR.RA...S..RC----.Q.I.IK.KT.L.GMVG-----------.S...V........A.ER.VA 49193.0
Cdx        Xb KDKY.VV..DR.RA...N..RC----.Q.I.I..KT...G.IG-----------.S...V........A.ER.VA DN63819
NVHD065    Nv .S.A.TA..AS.Q.......LY----S..I..T..K.L.NT.D-----------.S.KH...........K..TD DQ301955
```

Evx family

```
EVX1       Hs MR.Y.TAF..E.IAR.....YR----EN.VS.P..C.L.A..N-----------.P.TT..V........D.RQK NP_001980
EVX2       Hs VR.Y.TAF..E.IAR.....YR----EN.VS.P..C.L.A..N-----------.P.TT..V........D.RQR AAA52414
EVXa       Bf VR.Y.TAF..E.LAR.....YR----EN.VS.P..C.L.AQ.N-----------.P.TT..V........D.RQR
EVXb       Bf VR.Y.TAFS.E.TAR.....HR----DN..S.P..C.L.A..N-----------.P.TT..V........E.RQR
eve        Dm VR.Y.TAF..D.LGR.....YK----EN.VS.P..C.L.AQ.N-----------.P.ST..V........D.RQR NP_523670
Vab-7      Ce MR.Y.TAFS.E.IGR..R..AK----EN.VS.KT.G.L.AE.N-----------.P.GT..V........D.RQR
Evx1       Cg  R.Y.TAF.KE.LNR.....LK----EN.VS.PK.C.L.AQ.N-----------.S.ST..V........D.R
Evx2       Cg  R.Y.TAF..E.IGR.....YK----EN.VS.P..C.L.KL.N-----------.P.NT..V........D.R
Evx        Ip MR.Y.TAFSKH.QDS..M..RK----EN.VS.P..C.L.AS.N-----------.P.TT..V........E.RQR DN12279_c0_g2_i1|m.4929
Evx        Sr IR.Y.TAFSKD.QDI..A..RK----EN.VS.P..C.M.A..N-----------.P.TT..V........E.RQK DN124972_c0_g3_i4|m.83074
Evx        Hm LR.Y.TAF.KE.QDK..A..KK----EN.IS.PK.C.I.SE.N-----------.P.TT..V........E.RQR DN58284_c0_g1_i1|m.41535
Evx a      Nw QR.Y.TAFS.Q.LQR..R.FVK----EN.VS.PK.C.L.SS.G-----------.P.TT..V........D.RQR 48679.0
Evx b      Nw QR.Y.TAFS.Q.LQR..R.FMK----EN.VS.PK.C.L.AT.G-----------.A.TT..V........D.RQR 36518.0
Evx        Xb                  K.YTR----EN.VS.P..C.L.AQ.N-----------LP.TT..V........D.RQR DN14752
EVX (109)  Nv TR.Y.TAF..E.LKR.....MR----EN.VS.T..C.L.N..N-----------.S.TT...........S.RRR DQ206338
```

Gbx family

```
GBX1       Hs SR.R.TAF.SE.L........C----KK..SLTE.SQ.....K-----------.S.V.V........A...RI
GBX2       Hs NR.R.TAF.SE.L........C----KK..SLTE.SQ.....K-----------.S.VQV........A...RVK
```

```
GBX        Bf TR.R.TAF.SE.L........S----KK..SLTE.SQ.....K-----------.S.V.V........A...RVK
Unpg       Dm SR.R.TAF.SE.L....R...A----KK..SLTE.SQ..TS.K-----------.S.V.V........A...RVK
Gbx        Cg  R.R.TAF.SE.L........S----KK..SLTE.SH...N.K-----------.S.V.V........A...R
Gbx        Nw YR.K.TSFSSS.LR....H.NR----KK..SVPD.TLL.NI.H-----------..QP...V......A...RIK 20062
Gbx        Xb SR.R.TAY.SE.L.Q..R...G----KK..SLTE.SH..KN.K-----------...G.V........A...RVK DN90720
GBX (018)  Nv .R.K.TAF.SK.L.Q..R...N----KK.VSLEE.SV..TN.N-----------...V.V........A...RVR DQ206305
```

Gsx family

```
GSH1       Hs S..M.TAF.ST.L....R..AS----.M..S.L......TY.N-----------.S.K.V........V.H...G NP_663632
GSH2       Hs G..M.TAF.ST.L....R..SS----.M..S.L......TY.N-----------.S.K.V........V.H...G NP_573574
GSX        Bf SR.M.TAFSST.L....R..AS----.M..S.L......TF.N-----------.S.K.V........V.H...A
ind        Dm S..I.TAF.ST.L....R..SH----.A..S.L......NR.R-----------.S.K.V........V.Q.KGG NP_996087
Gsx        Cg  K.I.TAF.ST.L....R..NS----.M..S.L......TY.N-----------.S.K.V........V.F..
Gsx        Ip SR.T.TAFSSS.LMC..S..ES----SN..T.I......NK.H-----------...K..........V.N..GA DN47321_c0_g1_i1
Gsx        Sr ER.S.TAFSSV.LIQ..R..DL----.N....M......NR.N-----------...K.V........V.C..QL DN87690_c0_g1_i1
Gsx        Hm AR.S.TAF.SN.LVM.....NN----SK....L...D..TS.K-----------...K..........V.D..TK DN24302_c0_g1_i1|m.7955
Gsx        Xb AK.T.TAFSST.L.N.....SR----.S....I....L.QS.D-----------.S.K.V........V.Q..LL DN115451
GSX (130)  Nv S..I.TA..SM.L.......SQ----....S.L...Q..AL.D-----------.S.K.V........V....DK AAD39349
```

antHox family (Hox1)

```
HOXA1      Hs PNAV.TNF.TK.LT........----.K....A..V...AS.Q-----------.N.T.V..........Q..RE NP_005513
HOXB1      Hs PSGL.TNF.TR.LT........----.K..S.A..V...AT.E-----------.N.T.V..........Q..RE NP_002135
HOXD1      Hs SSAI.TNFSTK.LT........----.K....A......NC.H-----------.NDT.V..........Q..RE NP_078777
HOX1       Bf PNN..TNF.TK.LT.......Y----.K....A..V...AA.N-----------.N.T.V..........Q..RE
lab        Dm NNS..TNF.NK.LT........----......A......NT.Q-----------.N.T.V..........Q..RV NP_476613
ceh-13     Ce NGTN.TNF.TH.LT.......T----AK.VN.T..T...SN.K-----------.Q.A.V..........E..RE
Hox1       Cg  NM..TNF.NK.LT........----.K....A......AA.G-----------.N.T.V..........Q..
antHox     Ip TRG..TNF.NK.LT........----......A......SS.N-----------.N.T.V..........Q..LV DN75362_c0_g1_i3|m.221830
antHox     Hm TRG..TNF.NK.LT........----......A......AS.N-----------.N.T.V..........Q..LL DN54918_c0_g1_i1|m.41056
antHox     Nw TRG..TNF.TK.LT......LY----.K....A..V...AS.N-----------.N.N.V..........Q..LV 35873.0
antHox     Xb SRG..TNF.NK.QT........----......A......AS.S-----------.N.T.V..........Q..LL (Hox 1) DN2325
anthox6_12 Nv SQKK.F.F.QR.LV........----SK....T......TT.K-----------...M.............R.F DQ206301
NVHD060    Nv SDKN.TI.STR.LV.......Y----....C.P......QS.E-----------...K.V............... DQ206321
```

centHox family (Hox4/5)

```
HOXA5      Hs G..A.TA..............----................-----------.S.................D. NP_061975
HOXB5      Hs G..A.TA..............----................-----------.S.................D. NP_002138
HOXC5      Hs G..S.TS..............----............NN..-----------.N................DS NP_061826
           Bf N..T.TA..............----................-----------...................
Scr        Dm T..Q.TS..............----................-----------...................H NP_996164
lin-39     Ce E..Q.TA...N.V........T----HK....K....V..S.M-----------.....V..........H....
```

```
HoxC5      Cg  ..S.TS...H.........Y----.K.............N----------...................  XP_011424787.1
centHox    Ip C..T.TA...F..........----............NL.A-----------.S................D. DN31614/17434
centHox    Sr C..T.TA...F..........----............NL.A-----------...................D. DN118344_c1_g1_i1|m.54580
centHox    Hm S..T.TA...H..........----............TL.S-----------.S................D. DN27605_c0_g1_i1|m.9399
centHox3   Xb S..T.TA...Q.V.......Y----.K..T.......N..L-----------................Y.... DN124767
centHox2   Xb R...................Y----.Q..........TG.G-----------................F.... (HoxM2) DN84275
centHox1   Xb CR.K.SS.D.L.C........----....SK...SQ.SKH.G-----------.....V.V........H..DR (HoxM1) DN76496
```

postHox family (Hox9-13(15))

```
HOXA9      Hs TRKK.CP..KH........L.----.M....D..Y.V.RL.N-----------.....V..........M..I. NP_002133
HOXB9      Hs SRKK.CP..K.........L.----.M....D..H.V.RL.N-----------.S...V..........M..M. NP_076922
HOXC9      Hs TRKK.CP..K.........L.----.M....D..Y.V.RV.N-----------.....V..........M..M. NP_008828
HOXD9      Hs TRKK.CP..K.........L.----.M....D..Y.V.RI.N-----------.....V..........M..MS NP_055028
HOXA10     Hs GRKK.CP..KH........L.----.M....E..L..SRSVH-----------..D..V..........L..M. NP_061824
HOXC10     Hs GRKK.CP..KH........L.----.M....E..L..SKTIN-----------..D..V..........L..M. NP_059105
HOXD10     Hs GRKK.CP..KH........L.----.M....E..L..SKSVN-----------..D..V..........L..MS NP_002139
HOXA11     Hs TRKK.CP..K..IR...R..F.----SV.INKEK.LQLSRM.N-----------..D..V..........E..I. NP_005514
HOXC11     Hs TRKK.CP.SKF.IR...R..F.----.V.INKEK.LQLSRM.N-----------..D..V..........E..L. NP_055027
HOXD11     Hs SRKK.CP..K..IR...R..F.----.V.INKEK.LQLSRM.N-----------..D..V..........E..LN NP_067015
HOXC12     Hs SRKK.KP.SKL.LA...G..LV----.EFI..Q..R.LSDR.N-----------.SDQ.V..........K.RLL NP_776272
HOXD12     Hs ARKK.KP..KQ.IA...N..LV----.EFIN.QK.K.LSNR.N-----------.SDQ.V..........K.RVV NP_067016
HOXA13     Hs GRKK.VP..KV.LK...R.YAT----.KFI.KDK.RR.SATTN-----------.S...VT.......V.E..VI NP_000513
HOXB13     Hs GRKK.IP.SKG.LR...R.YAA----.KFI.KDK.RK.SA.TS-----------.S....T.......V.E..VL NP_006352
HOXC13     Hs GRKK.VP..KV.LK.....YAA----SKFI.KEK.RR.SATTN-----------.S...VT.......V.E..VV NP_059106
HOXD13     Hs GRKK.VP..KL.LK...N.YAI----.KFINKDK.RR.SA.TN-----------.S...VT.......V.D..IV NP_000514
Hox9       Bf SRKK.CP...F.........LY----.M....E..Y..SQHVN-----------.....V..........M..MS
Hox10      Bf GRKK.CP..K..I.......L.----.M.VS.E..Q..SRHVN-----------.SD..V..........M.RM.
Hox11      Bf TRKK.CP..K.........L.----.MFV..E..Q...RQ.N-----------..D..V..........M.RMK
Hox12      Bf SRKK.CP.SKV.L.......LY----.M.I..EQ.G...RKVN-----------..D..V..........M.RMK
Hox13      Bf GRKK.CP..K..LSV..Q.YIQ----.R.VS.ET.L.LSQR.N-----------..D..V..........Q.RLE
Hox14      Bf VRPK.RP.SK..LN...N.YVQ----.Q.IS.DK.LQLSQK.N-----------.....V........I.Q..LD
Hox15      Bf TRKK.RP.SKP.LAL..D.YAS----QKF..KEK.K..SESSS-----------.S...VM.........E..LA
Abd-B      Dm VRKK.KP.SKF.........L.----.A.VSKQK.W.L.RN.Q-----------.....V..........N..NS NP_996220
egl-5      Ce S.K.....Q....SV..AK.QQ----SS.VSKKQ.E.LRLQTQ-----------..D..I..........A...K
nob-1      Ce  .KK..P.KKD.ISR..Y.YSV----.Q...NK..S.LSAQ.M-----------.D.K.V.V........D..LR
php-3      Ce MRKK.KP..KA.........LY----.T.VSKQK.W.L.KY.H-----------.....V..........D..QK
Post1      Cg  RKR.RPYSKF.IA...R.YNN----ST.ISKS..W.LSQLIN-----------.S............IKA..
Post2      Cg -RKK.KP......MV..N..LN----SS.I..Q..W.ISCK.Q-----------.S...V.V........R..
postHox    Ip SRKK.RP..KT.........LY----.T.I..E..L...RS.S-----------..D..V..........N..QM DN66164_c4_g4_i4|m.87486
postHox    Sr SRKK.RP..KN.........L.----.T.I..E..L...RS.N-----------..D..V..........N..QH DN123370_c1_g1_i1|m.74729
```

```
postHox     Hm TRKK.RP..KT.........LY----.T.I..E..LQ..KS.N-----------..D..V.........M..I. DN3061_c0_g2_i1|m.947
postHox2    Nw SRKK.RP..K.........L.----.T.I..E..S..SR..N-----------.SD..V.........M..MT 54694.0
postHox1    Nw  RKK.RP..K.........L.----.V.I..E..S..SRS.N-----------..D..V....           10725.0
postHox     Xb  RKK.RP..KF........L.----.T.I..E..LEISR..N-----------..D..V.........M..M. (HoxP) DN3733
```

Meox/Mox family

```
MEOX1       Hs ARKE.TAF.KE.LR...A..AH----HN....L..Y...VN.D-----------.S...V.V..........RVK
MEOX2       Hs PRKE.TAF.KE.IR...A..AH----HN....L..Y...VN.D-----------.....V.V..........RVK
            Bf PRKE.TAF.KQ.IM...N..RH----HN....L..Y...VK.D-----------.....V.V..........RTK
Btn         Dm NRKE.TAFSKT.LKQ..A..CY----SN....L..Y...V..E-----------.....V.V........C.RIK
Meox        Cg  RKE.TAF.KH.IR......AV----HN....L..Y...V..D-----------.....VKV..........R
Mox         Ip    E.TAF.KF.VHA.....TL----HN.VN.P..QL..RK.C-----------.S...V.V..........RTK DN54162_c1_g1_i1
Mox         Nw KRKD.TAFSKF.IEQ..S..ET----YN....L..F.LSKK.S-----------.S...V.V..........RVK 58015.0
Mox         Xb PRKE.TAF.KH.IR...R..TK----HN....L..Y...VS.E-----------.S...V.V..........RVK DN86948
MOXa (034)  Nv KRKE.TAF.TH.LR...N..TR----.N....L..Y...VS.D-----------.....V.V..........RVK DQ206313
MOXb (110)  Nv KRKE.TAF.KH.IQ...N..QR----.N....L..Y...VS.D-----------.....V.V..........RVK DQ206339
MOXc (019)  Nv KRKE.TAFSKH.LQ...N..IR----.N....L..Y...VS.D-----------.....V.V..........RVK DQ206306
MOXd (119)  Nv KRKE.TVFSK..LT...R..CR----.N....L..Y...VS.D-----------.G...V.V..........RGR DQ206342
```

Mnx / HlxB9 family

```
MNX/HLXB9   Hs CR.P.TAF.SQ.L....HQ.K.----.K..S.PK.F.V.TS.M-----------...T.V...........RSK NP_005506
Mnxa        Bf TR.P.TAF.SQ.L.....Y.KE----.K..S.PK.F.V.TA.M-----------...T.V...........RSK
Mnxb        Bf TR.P.TAF.SQ.L.....H.KE----.K..S.PK.F.V.TS.M-----------...T.V...........RSK
exex        Dm TR.P.TAF.SQ.L.....Q.KQ----.K..S.PK.F.V.SG.M-----------.S.T.V...........RSK NP_648164
ceh-12      Ce MR.P.TAFSSE.LVQ...Q.SD----....S.P..YQL.QQ.S-----------.S.T............N.RCP
Mnx1        Cg                      M----.K..S.PK.F.V.TS.M-----------...T.V...........R
Mnx         Ip SR.P.TAF.                     .S.PK.F.V.TK.L-----------...T.V...........RSK DN98046/DN86741
Mnx         Sr CR.P.TAF.SQ.L....NQ.RK----.K..S.PK.F.V.TK.M-----------...T.V...........RAK DN123752_c0_g1_i1|m.76614
Mnx         Hm SR.P.TAF.SQ.L....NQ.KR----.K..S.PK.F.V.TK.M-----------...T.V...........RAR DN4748_c0_g1_i1|m.1255
Mnx         Nw SR.P.TSYSSK.IKI..EH.VL----....S.PK.F.V.TS.N-----------...T.V..........L.RSE 58481.0
HLXB9-069   Nv HR.P.TAFSSH.L.A..RQ.QL----HK....PQ.Y.L.TS.M-----------...T.V...........RC. DQ206324
```

Ro family

```
ro          Bf QR.Q.T.F.TE..MK..L.YNR----TE.I..P..F.L.EM.N-----------.S.T..........A.D.RIE
ro          Dm QR.Q.T.FSTE...R..V...R----.E.IS.S..F.L.ET.R-----------...T..........A.D.RIE NP_733173
R06F6.6     Ce SR.K.T.FSPE.ATR..A.YIG----DS.MA.EK.HLL.QS.K-----------.S.N.V.T......A.D.RDR
Ro          Cg  R.Q.T.FSSD..VK..I.YSR----TE.I..S..Y.LAEL.C-----------...N..........A.E.R
Ro          Ip SR.Q.TSF.PD...Q..LQYER----SE.I..SK.F.L.ES.G-----------.S.G.....Y....A.D.RIE DN62850_c0_g1_i3|m.66453
Ro          Sr GR.Q.TSFSAE..IK..L..QM----.E.I..S..F.L.DT.G-----------.S.N.....Y....A.D.RIE DN119820_c0_g1_i1|m.59912
Ro a        Hm NR.E.T.F.SD.SVK..I.YQR----SE.I..S..FTL.EM.K-----------MS.N..........A.D.RIE DN18872_c0_g1_i1|m.5077
Ro b        Hm ER.Q.T.F.TK.ANI..S.YQR----RE..SKQQ.QAL.TS.Q-----------.S.T..........A.D.RTG DN12978_c0_g1_i1|m.3456
```

```
Ro          Nw NR.Q.T.FSSE...S..V..QR----SE.IS.SK.Y...EH.H-----------...N.V........A.D.RME 6133.0
RO (126)    Nv PR.Q.T.F.SE...K..L...Q----.E.I..S..F.L.AC.N-----------...T.V........A.D.RLE DQ206293
```

ANTP class NKL subclass

Abox family

```
ABOX        Bf DRKP..A.SSR.LER..E..KK----DK..SVSK.V.L.ES.E-----------...I.V.T......T....QT
CG34031     Dm DRKP..A.SAS.LER..N..NL----DK..SVSK.V.LSKS.S-----------...V.V.T......T....QL
ceh-19      Ce ERKP..A.SAR.LDR..T..QT----DK..SVNK.IQLSQT.N-----------...T...T......T....QL
Abox        Ip                  E..KK----DK..SVSK.L.LSV..S-----------...T...T......T....QV DN10641_c0_g1_i1|m.4062
Abox        Hm ERKP..A.STK.LEK..E..KK----DK..SVS..L.LSV..E-----------...T...T......T....QM DN29024_c0_g1_i1|m.10351
Abox        Sr DRKP..AYSAK.LEK..E..KN----DK..SVSK.L.LSV..N-----------.S.T...T......T....QL DN112643_c0_g1_i1|m.40300
```

Barhl family

```
BARHL1      Hs PRKA.TAF.DH.LAQ..RS.ER----QK..SVQD.M.L.AS.N-----------..DT.V.T.Y....T...RQT NP_064448
BARHL2      Hs PRKA.TAFSDH.LNQ..RS.ER----QK..SVQD.MDL.A..N-----------..DT.V.T.Y....T...RQT NP_064447
Barh        Bf PRKA.TAF.DH.LAQ..RS.ER----QK..SVQD.M.L.AS.N-----------..DT.V.T.Y....T...RQN
B-H1        Dm QRKA.TAF.DH.LQT...S.ER----QK..SVQE.Q.L..K.D-----------.SDC.V.T.Y....T...RQT NP_523387
B-H2        Dm QRKA.TAF.DH.LQT...S.ER----QK..SVQD.M.L.NK.E-----------.SDC.V.T.Y....T...RQT NP_523386
Ceh-30      Ce ARKA.TIF.DK.LQ...NT.EK----QK..SVQD.MDL..RMG-----------..DT.V.T.Y....T...RQA
Ceh-31      Ce ARKA.TIF.DK.LQ...NT.EK----QK..SVQD.M.L..RMG-----------..DT.V.T.Y....T...RQA
BarH1       Cg  RKA.TAF.DH.LNS...S.ER----QK..SVQD.M.L.SK.N-----------..DTQV.T.Y....T...R
BarH2       Cg  RKA.TAF.DH.LNC...S.ER----QK..SVQD.M.L.AK.N-----------..DT.V.T.Y...SHDLLK
BarH3       Cg  RKA.TAF.DQ.LNN...H.AR----QK..SVQD.M.L.AK.G-----------.SDT.V.T.Y....T...R
BarHl       Ip MRKA.TAF.DE.LVK..QN.ER----HK..SVQD.LDL.A..D-----------..DT.V.T.Y....T...RQA DN36044_c0_g2_i1|m.16521
BarHl       Sr HRKA.TAF.DE.LAQ..QN.ER----HK..SVQD.LDL.AS.Q-----------.SDT.V.T.Y....T...RQT DN152752_c0_g1_i1|m.134562
BarHl       Hm TRKA.TAF.EE.LSK..AS.ER----QK..SVQD.LDL.SS.D-----------.SDT.V.T.Y....T...RQA DN68850_c0_g1_i1|m.42447
BarHl       Xb PRKA.TAF.DD.LAR..TS.ER----QK..SVQD.MDL.AN.N-----------..DT.V.T.Y... T...RQT DN44680
```

Bari family

```
Bari        Bf QR.R.TVF.QS.LRA..RK.RC----QK..SVSE.A.V.R..G-----------.S.T...T.Y....T...R.T
CG11085     Dm PR.R.TAF.HA.LAY..RK.RC----QK..SVAD.SDV.ET.N-----------.S.T.V.T.Y....T...RQN
Bari        Ip TR.R.TAF.QA.LNF..RK.RC----QK..SVAD.SDV.EM.R-----------.S.T.V.T.Y....T...RQT DN60676_c0_g1_i2|m.56432
Bari        Sr SVS.SISVPPSSSIPSPLALQN----FLNKKN...SDV.EL..-----------.S.T.V.T.Y....T...RQT DN100159_c0_g1_i1
Bari        Hm PR.R.TAF.QA.LNF..RK.RC----QK..SVAD.N.V.TQ.A-----------.S.T.V.T.Y....T...RQT DN83548_c0_g1_i1|m.43646
```

Barx family

```
BARX1       Hs GR.S.TVF.EL.LMG...R.EK----QK..STPD..DL.ES.G-----------.SQL.V.T.Y.........IV NP_067545
BARX2       Hs PR.S.TIF.EL.LMG...K.QK----QK..STPD.LDL.QS.G-----------..QL.V.T.Y.........MV NP_003649
            Bf CR.S.TVF.EL.L.G...R.EK----QK..STPD.VEL.ES.G-----------.SQL.V.T.Y.........MV
Barx        Cg  R.S.TVF.EL.LIG...R.ES----QK..STPD..DL.ES.G-----------.SQV.V.T.Y.........
Barx a      Ip YR.N.SVFSEK.LAD...W.VA----EK..TASL.VK..SQCG-----------...M.V.T.Y.........QM DN76364_c0_g1_i1|m.230241
```

```
Barx b     Ip CR.S.TVF.EA.LAN...Q.GN----TK..STAQ.SR..KSSG-----------..QM.V.T.Y.........QL DN67947_c0_g2_i1|m.104238
Barx       Sr CR.S.TVFSDQ.LKG...N.CS----TK...TMQ.NRL.KESG-----------..QM.V.T.Y.........QL DN80548_c0_g1_i1|m.15026
Barx       Hm CR.S.TVF.DS.LIG.D.S.KH----SK..NTPE.NRL.KH.G-----------..QT.V.T.Y.........QL DN34181_c0_g1_i1|m.14867
Barx       Nw CR.T.TVF.EL.M.G...R.DM----QK..STPD.LGLSDS.G-----------..QL.V.T.Y.........EI 44999.0
Barx       Xb CR.S.TVF.ES.LVG..RR.AD----QK..STPD..TL.DQ.R-----------.SQI.V.T.Y.........QV DN81549
041        Nv FR.I.TVF..D.LQK..DR.KH----DK..STQD.N.F.RS.Q-----------..PL.L.T.Y.........DM (this study)
```

Bsh/Bsx family

```
LOC390259  Hs .RKA.TVFSDS.LSG...R.EI----Q...STPE.V.L.T..S-----------.S.T.V.T........H..QL XP_372433
bsx        Bf .RKA.TVFSDS.LNG...R.ES----QK..STPE.MDL.A..N-----------...T.V.T........H..LQ
bsh        Dm .RKA.TVFSDP.LSG...R.EG----Q...STPE.V.L.T..G-----------.S.T.V.T........H..QL NP_995728
tab-1      Ce .RKA.TVFSDQ.LQG..RR.ES----Q...STPE...L.N..N-----------.S.T.V.T........H..VV
Bsx        Cg  RKA.TVFSDQ.LNG...R.EA----Q...STPE.V.L.NQ.S-----------.S.T.V.T........H..
Bsx        Ip .RKA.TVFSDG.LHG..RR.ES----Q...STPE..DV.S.FN-----------...T.V-intron         DN57889_c1_g2_i1
Bsx        Sr .RKA.TVFSDG.LHG..RK.QQ----Q...STPE.....TQYN-----------...T.V.T........Q..IF DN106437_c0_g1_i1|m.31009
Bsx        Hm .RKA.TVFSDS.LQG..ER.KD----QK..STPE...M.TL..-----------...T.V.T........D..CC DN1275_c0_g1_i1|m.391
```

Dbx family

```
DBX1       Hs GMLR.AVFSDV.RKA...M.QK----QK.ISKPD.KKL.AK.G-----------.KDS.V...........RNSK
DBX2       Hs GILR.AVFSED.RKA...M.QK----QK.ISKTD.KKL.IN.G-----------.K.S.V...........RNSK
DBX        Bf GMLR.AVFSDF.RKS...M.QK----QK.ISKQD.RKL.EK.G-----------.KDS.V...........RNSK
CG12361    Dm GMMR.AVFSDS.RKG...R.QQ----QK.ISKPD.KKL.ER.G-----------.KDS.V...........RNSK
Dbx        Cg  MLR.AVFSDM.RKG...M.QK----QK.ISKPD.KKL.AK.G-----------.KDS.V...........RN
Dbx        Nw GMLR.AVFSDA.RRG..RK.RE----LK.ISKPD.K.L.NK.D-----------.RDS.V...........RNSK 49786
Dbx        Nw WN.V.TVF.NA.R.G..EQ.RE----QK.VSKPD.K.L.GK.G-----------.SDS.V.V.........RNSL 29958.0
```

Dlx family

```
DLX1       Hs IRKP.TI.SSL.LQA.NRR.QQ----TQ..ALPE.A.L.AS.G-----------..QT.V......K.S.F..LM NP_835221
DLX2       Hs VRKP.TI.SSF.LAA.QRR.QK----TQ..ALPE.A.L.AS.G-----------..QT.V........S.F..MW NP_004396
DLX3       Hs VRKP.TI.SS..LAA.QRR.QK----AQ..ALPE.A.L.AQ.G-----------..QT.V........S.F..LY NP_005211
DLX4       Hs LRKP.TI.SSL.LQH.NQR.QH----TQ..ALPE.AQL.AQ.G-----------..QT.V......K.S.Y..LL NP_001925
DLX5       Hs VRKP.TI.SSF.LAA.QRR.QK----TQ..ALPE.A.L.AS.G-----------..QT.V......K.S.I..IM NP_005212
DLX6       Hs IRKP.TI.SSL.LQA.NHR.QQ----TQ..ALPE.A.L.AS.G-----------..QT.V......K.S.F..LL XP_376652
           Bf MRKP.TI.TSF.LQQ.NRR.QR----TQ..ALPE.A.L.AQ.G-----------..QT.V........S.Y..LM
Dll        Dm MRKP.TI.SSL.LQQ.NRR.QR----TQ..ALPE.A.L.AS.G-----------..QT.V........S.Y..MM NP_523857
Ceh-43     Ce MRKP.TI.NSS.LQM.Q.K.QK----TQ..ALPD.AAL..E.G-----------.SQT.V........S.Q..QK
Dll        Cg   KP.TI.SSL.LQQ.NRR.QR----TQ..ALPE.A.L.AS.G-----------..QT.V........S.A..   Cgi_10016653
Dlx        Ip LRKP.TI.STV.IQQ.TRR.QR----TQ..ALPE.A.L.A..G-----------..QT.V......K.S.M..II DN61228_c2_g1_i1|m.58904
Dlx        Sr MRKP.TI.STI.IQQ.TRR.QR----TQ..ALPE.A.L.A..G-----------..QT.V......K.S.M..LM DN123563_c1_g2_i1|m.75836
Dlx a      Hm IRKP.TI.STM.LQQ.NRR.QR----TQ..ALPE.A.L.A..G-----------..QT.V......K.S.V..IL DN12216_c0_g1_i1|m.3286
Dlx b      Hm IRKP.TI.SST.LQQ.NRRYNT----TQ..ALPE.ADL.AT.G-----------..QT.V......K.S.M..IM DN12035_c0_g1_i1|m.3241
```

```
Dlx a      Nw LRKP.TIYSS..LSM.N.R.QG----TQ..ALPE.A.L.AT.G-----------..QT.V........S.F..LL 50937.0
Dlx b      Nw MRKP.TIYSSL.LQI.N.R.QQ----TQ..ALPE.A.L.AS.G-----------..QT.V..               54562.0
Dlx c      Nw IRKP.TIYSS..LSM.N.R.QG----TQ..ALPE.A.L.AS.G-----------..QT.V........S.F..LM 35817.0
Dlx        Xb MRKP.TI..SL.LQQ.N.R.AR----TQ..ALPE.A.L.AS.G-----------..QT.V........S.Y..VL DN90457
DLX 095    Nv IRKP.TI.SSF.LR..N.R.IK----TQ..ALPE.ADL.AY.G-----------..QT.V........S.F..TL DQ206283
```

Emx family

```
EMX1       Hs P..I.TAFSPS.L.R..RA.EK----.H.VVGAE.KQL.GS.S-----------.S.T.V.V......T.Y.RQK NP_004088
EMX2       Hs P..I.TAFSPS.L.R..HA.EK----.H.VVGAE.KQL..S.S-----------...T.V.V......T.F.RQK NP_004089
Emxa       Bf P..V.TAF.PT.L.R..HA.EK----.H.VVGQE.KQL.QQ.T-----------.S.T.V.V......T.Y.RDQ
Emxb       Bf P..I.TAF.PS.L.R..HA.EK----.H.VVGQE.KHL.QS.S-----------...T.V.V......T.H.REQ
Emxc       Bf P..I.TAF.PS.L.R..HA.EK----.H.VVGQE.KHL.QS.S-----------...T.V.V......T.Y.RDQ
ems        Dm P..I.TAFSPS.L.K..HA.ES----.Q.VVGAE.KAL.QN.N-----------.S.T.V.V......T.H.RMQ NP_731868
E5         Dm P..V.TAFSPT.L.K..HA.EG----.H.VVGAE.KQL.QG.S-----------...T.V.V......T.H.RMQ NP_524825
ceh-2      Ce N..I.TAFSAS.LIQ...A.EG----.H.VVGNE.KQL.AK.S-----------...T.V.V......T.H.RVR
Emx1       Cg  ..I.TAFSPT.L.Q..HA.EK----.H.VVGQE.K.L.LK.G-----------.S.T.V.V......T.Y.R
Emx2       Cg  ..I.TAFSPS.L.K...V.ER----.H.VVGQE.KDL.TN.N-----------.S.T.V.V......T.Y.R
Emx3       Cg  ..I.TAFSPS.L.Q...A.EK----SH.VVGQE.KDL.SE.Q-----------...T.V.V......T.H.R
Emx        Ip C..V.TAF.AT.LAM..RH.LQ----SP.VVGSQ.RKLSSD.G-----------.S.T.V.V......T.A.RCI DN43104_c0_g1_i1|m.22332
Emx        Sr S..I.TAF.PA.LAK..TQ.AR----SP.VVGHQ.RQ.SEE.G-----------...T.V.V......T.E.RVL DN118899_c0_g1_i1|m.56533
Emx a      Nw P..I.TAF.SE.LQR..N..TS----.P.IVGEE.RQF.AS.R-----------.S.T.V.V.Y....T.D.R.I 17210.0
Emx b      Nw P..I.TAF.TE.LQR..D..IA----.P.IVGEE.RRF.AN.N-----------...T.V.V.Y....T.D.R.T 44961.0
Emx        Xb P..V.TAFSPSQL.R..H..EK----NH.VVGEE.KQL.NV.N-----------.S.T.V.V......T.Y.RQK DN105712
EMXa 013   Nv P..I.TAF.PT.L.H..NA.EK----.H.IVGTE.KQL.SY.N-----------.S.T...V......T...RQQ DQ206302
EMXb 104   Nv VR.V.TAF.PF.L.C..TS.DK----.H.VVGTE.KQL.SY.K-----------.S.T.V.V......T...RQA DQ206286
```

Hhex family

```
Hhex       Hs R.G.QVRFSND..I....K.ET----QK..SPPE.KRL.KM.Q-----------.S..QV.T......A..RRLK
Hhex       Bf R.G.QVRFSND...E...K.ES----QK..SPPE.KRL.KS.Q-----------.....V.T......A..RRLK
Hhex       Dm R.G.QIRF.SQ..KN..AR.AS----SK..SPEE.RHL.LQ.K-----------..D.QV.T......A..RRAN
Pha-2      Ce R.G.QIRF.NE..DA..HK.DS----HK..SPQE.KKL.KS.S-----------.S..QV.T......A..RRVR
Hhex       Cg  .G.QVRFSND..V....K.ES----HK..SPPE.KRL.KT.Q-----------....QV.T......A..RR
Hhex       Xb R.G.QVRFSNE...K...T..K----QK..SPSE.KKI.KS.Q-----------.....V.T......A..RRLE DN94983
Hhex 048   Nv K.G.QVRFSNE..M....I.ET----QK..SPPE.KQLSKV.G-----------.S...V.T......A..RRFK DQ206317
```

Msx family

```
MSX1       Hs NRKP.TPF.TA.L.A..RK.RQ----KQ..SIAE.A.FSSS.S-----------...T.V........A.A.RLQ NP_002439
MSX2       Hs NRKP.TPF.TS.L.A..RK.RQ----KQ..SIAE.A.FSSS.N-----------...T.V.......SA.A.RLQ NP_002440
Msx        Bf NRKP.TPF.TQ.L.A..RK.RQ----KQ..SIAE.A.FSAS.N-----------...T.V........A.A.RLQ
Dr         Dm NRKP.TPF.TQ.L.S...K.RE----KQ..SIAE.A.FSSS.R-----------...T.V........A.A.RLQ NP_477324
Vab-15     Ce NRKP.TPFSTQ.LIS..RK.QS----KQ..SIAE.A.FSAS.Q-----------...T.V........A.S.RLQ
```

```
Msx         Cg  RKP.TPF.TS.L.A..RK.RQ----KQ..SIAE.A.FSAS.N-----------...T.V........A.A.R
Msx         Xb NRKP.TPF.TS.L.A..RK.RH----KQ..SIAE.A.FSSS.S-----------...T.V........A.A.RLQ DN63160
MSX (142)   Nv NRKP.TPF.TS.L.A..RK.RQ----KQ..SIAE.A.FSAS.N-----------...T.V........A.A.RLH DQ206296
```

Msxlx family

```
MSX1        Bf GRNP.VPFSAH.VAT..SK.RR----TH..SSVDVS.LSV..N-----------.S.NRV........ARERR.R
CG15696     Dm GRLP.IPF.PQ.LQA..NAYKE----SN..SAEDANKL.DS.E-----------..NTRV........ARERR.K
Msxlx       Cg   NP.VPF.QH.VAV..HK.RR----TH..SSMDVA.LST..S-----------...NRVSSVSA            (end ?)
Msxlx       Ip GRNP.VPFSST.VAV..QKYQH----KQ..SSIDVA.LSSL.N-----------.NDSRV........A.A.K.Q DN65413_c0_g2_i2|m.82199
Msxlx       Sr GRNP.VPFSSA.VAI..QKYQV----KQ..SSIDVA.LSTM.S-----------.NDSRV........ARAR..Q DN124792_c0_g1_i1|m.82241
Msxlx       Hm SRNP.IPF.SN.VAL..QT.QK----KQ..SSMDVSDLSNS.R-----------.SDTR.........ARARRDG DN104433_c0_g1_i1|m.45397
Msxlx       Nw GRNP.VPF.QT.VDH..LK.RE----AK..SSLDVAD.STH.N-----------..DTRV........ARERREK 4231
MSXLXa046   Nv SGNP.VPFSTS.LM...HKYVE----T...SGPEVA.L.NG.R-----------.S.HRV........ARE..AK DQ206269
MSXLXb066   Nv DRNP.IPFSAS.LAA..AK.LD----TH..SSVEVRDLSSS.S-----------V..HRV........ARE..TK DQ206275
```

NK-1/slouch family

```
NKX1-1      Hs PR.A.TAF.YE.LVA..NK.KA----T...SVCE.LNL.LS.S-----------...T.V........T....Q.
NKX1-2      Hs PR.A.TAF.YE.LVA..NK.RA----T...SVCE.LNL.LS.S-----------...T.V........T....Q. XP_372331
Nkx1a       Bf PR.A.TAF.YE.LVA..NK.KQ----T...SVCE.LNL.LS.S-----------...T.V........T....Q.
Nkx1b       Bf PR.V.TAF.YE.LVA..NK.KQ----T...SVCE.LNL.LS.S-----------...T.V........T....Q.
slou        Dm PR.A.TAF.YE.LVS..NK.KT----T...SVCE.LNL.LS.S-----------...T.V........T....Q. NP_476657
ceh-1       Ce MR.A.TAF.YE.LVA..NK.KT----S...SVVE.LNL.IQ.Q-----------.S.T.V........T....H.
Nk1         Cg  R.A.TAF.YE.LVA..NK.KT----T...SVCE.LNL.LS.N-----------...T.V........T....
NK1         Ip .R.S.TAF.YE.LVA..NK.RA----S...SVCE.LN..L..N-----------...T.V........T.F..Q. DN40909_c0_g1_i1|m.20738
NK1         Sr   .S.TAF.YE.LVA..NK.RC----S...SVCE.LN..L..N-----------...T.V........T.F..Q. DN56103_c0_g1_i1|m.8196
NK1         Xb                 ..NK.KL----T...SVCE.LNL.LS.S-----------...N.V........T....   DN131037
SLOU (091)  Nv PR.A.TAF.YE.LVA..NK.KS----T...SVCE.LNL.LS.G-----------...T.V........TNGRSRT DQ206255
```

NK-2.1 family

```
NKX2-1      Hs .RKR.VLFSQA.VY...RR.KQ----QK..SAPE.EHL.SMIH-----------..PT.V......H.Y.M.RQA NP_003308
NKX2-4      Hs .RKR.VLFSQA.VY...RR.KQ----QK..SAPE.EHL.SMIH-----------..PT.V......H.Y.M.RQA
Nkx2-1      Bf .RKR.VLFSQA.VY...RR.KQ----QK..SAPE.EHL.QLIN-----------..PT.V......H.Y.C.RQD
scro        Dm .RKR.VLF.QA.VY...RR.KQ----QR..SAPE.EHL.SLIH-----------..PT.V......H.Y.C.RQA
ceh-24      Ce .RKR.VLFSQA.VY...RR.KQ----AK..TAPE.EQL.NSIR-----------..PT.V......H.Y.C.RQE
ceh-27      Ce .RKR.VLFSPQ.VHV..RK.QI----....SAAD.ENL.KSIN----- -----.SAT.V......Q.Y.C.RQE
Nkx2_1      Cg .RKR.VLFSQA.VY...RR.KQ----QK..SAPE.EHL.SMIN-----------..PT.V......H.Y.C.R
Nkx2.1 a    Ip .RKR.VLF.QA.IY...RR.KQ----QK...AAE.ENL..VIN-----------.SPT.V......H.Y.T..SK DN64840_c0_g1_i1|m.78270
Nkx2.1 a    Sr .RKR.VLF.QA.IH...RR.KQ----QK...AAE.ESL..LIN-----------.SPT.V......H.Y.T..SK DN122139_c1_g1_i1|m.69070
Nkx2.1 b    Ip  RKR.VLF.QA.VY...RR.KA----QK..SAPE.ETL..SIG-----------..PT.V.....          DN66164_c5_g1_i1|m.87491
Nkx2.1 c    Ip .RKR.VLF.QA.VY...RR.KT----QK..SAPE.ETL...IN-----------..PT.V......H.Y.C.RAS DN66164_c5_g2_i1|m.87495
Nkx2.1 b    Sr .RKR.VLF.QA.VY...RR.KQ----QK..SAPE.EAL.QGIN-----------..PT.V......H.Y.C.RAS DN126831_c2_g4_i1|m.94319
```

```
Nkx2.1 a   Hm .RKR.VLF.QA.VY...RR.KQ----Q...SAPE.ENL.QLIN-----------..PT.V......H.Y.Y.RAS DN44693_c0_g1_i1|m.40284
Nkx2.1 b   Hm .RKR.VLF.QA.VY...RR.KQ----Q...SAPE.ETL..LIN-----------..PT.V......H.Y.C.RAS DN15813_c0_g1_i1|m.4392
Nkx2.1 c   Hm PRKR.ILF.QA.VY...RR.KM----QK..NAPE.ESL.QLIN-----------..PT.V......H.Y.C.RAA DN36484_c0_g2_i1|m.17692
Nkx2.1     Nw .RKR.VLF.QA.VY...RR.KQ----QK..SAPE.EQL.AMIH-----------..PT.V......H.Y.M.RQA 45472.0
Nkx2.1     Xb KRKR.VLF.QA.VY...RR.KQ----QK..SAPE.EHL.SLIN-----------..PT.V......H.Y.C.RAA 93010
```

Nk-2.2 family

```
NKX2-2     Hs KRKR.VLFSKA..Y...RR.RQ----Q...SAPE.EHL.SLIR-----------..PT.V......H.Y.M.RAR NP_002500
NKX2-8     Hs ..KR.VLFSKA......RR.RQ----Q...SAPE.EQL.SL.R-----------..PT.V......H.Y.L.RAR NP_055175
Nkx2-2     Bf KRKR.VLFSKA..Y...RR.RQ----Q...SAPE.EHL.RLIR-----------..PT.V......H.Y.C.RAQ
vnd        Dm KRKR.VLF.KA..Y...RR.RQ----Q...SAPE.EHL.SLIR-----------..PT.V......H.Y.T.RAQ NP_476786
ceh-22     Ce KRKR.VLF.KA..Y...RR.RS----QK..SAPE.EAL.MQIR-----------..PT.V......H.Y.T..SH
Nk2_2      Cg  RKR.VLFSKA..Y...RR.RQ----Q...SAPE.EHL.SIIR-----------..PV.V......H.Y.L.R
Nkx2.2     Ip KRKR.VLF.KN..Y...RR.RQ----Q...SAPE.EAL.AMID-----------..PG.V......H.Y.C..S. DN66907_c1_g1_i2|m.94022
Nkx2.2     Sr KRKR.VLFSKS..FQ..SR.RQ----Q...SAPE.EQL.N.IN-----------..PG.V......H.Y.C..SS DN89648_c0_g1_i2|m.18777
Nkx2.2     Hm KRKR.VLFSKA.TF...RR.RQ----Q...SAPE.EHL.NLIK-----------..PT.V......H.Y.C..NH DN90735_c0_g1_i1|m.44111
Nkx2.2     Nw KRKR.VLFSKQ..Y...RR.RQ----Q...SAPE.EHL.SIIN-----------..PT.V...... 20731.0
Nkx2.2     Xb            ..Y...RR.RQ----Q...SAPE.EHL.SIIR-----------.SPT.VEV....H.Y.L.RSR DN101095

NK2c (051) Nv KRKR.ILF.KS.IY...RR.RY----Q...SAPE.EQLGRMIN-----------..PT.V......H.Y.H..QA DQ206270
NK2d (103) Nv KRKR.VLF.KA..Y...RR.RQ----Q...SAPE.EQL.RIIN-----------..PT.V......H.Y.F..Q. DQ206285
NK2a (057) Nv KRKR.ILF.KA..FI..RR.TQ----Q...SAPE.E.L.RIAN-----------..PA.V......H.Y.YR.QM DQ206320
NK2b (025) Nv K.KR.ILF.KS.IF...RR.RQ----QK..SANE.EQL.RIID-----------..PT.V......H.Y.F..QI DQ206262
NK2e (026) Nv KRKQ.VLFSKV.RKQ...K.LE----KP..SYTE.DQL.R.VN-----------..AK.V.V....K.Y.T.ERE DQ206310
```

Nk-3 family

```
NKX3-1     Hs Q..S.AAFSHT.VI...RK.SH----QK..SAPE.AHL.KN.K-----------...T.V........Y.T.RKQ NP_006158
NKX3-2     Hs K..S.AAFSHA.VF...RR.NH----Q...SGPE.ADL.AS.K-----------...T.V........Y.T.RRQ NP_001180
Nkx3       Bf K..S.AAFSHA.VF...RR.SH----Q...SGPE.ADL.A..K-----------...T.V........Y.T.RRQ
bap        Dm K..S.AAFSHA.VF...RR.AQ----Q...SGPE.S.M.KS.R-----------...T.V........Y.T.RKQ NP_732637
Nk3        Cg  ..S.AAFSHA.VF...RR.RH----Q...SGPE.ADL.N..K-----------...T.I........Y.T.R
Nk3        Ip   .T.AAFSHA.VF...RR.AQ----QK..SGPE.ADL.N..K-----------...T..........Y.T.RKQ DN64224_c0_g1_i1
Nk3        Sr K..T.AAFSHA.VF...RR.AQ----QK..SGPE.S.L.S..K-----------...T..........Y.T.RKQ DN121921_c0_g2_i1|m.68018
Nk3        Hm K..T.AAFSHA.VF...RR.TQ----Q...SGPE.S.V.SN.K-----------...T.V........Y.T.RKQ DN79735_c0_g1_i1|m.43259
NK3 (098)  Nv ...S.AAFSHQ.VF...RR.SH----QK..SGPE.ADL.A..K-----------...T.V........Y.T.RRQ DQ206336
```

Nk-4 family

```
NKX2-3     Hs .RKP.VLFSQA.VF...RR.KQ----Q...SAPE.EHL.SS.K-----------..ST.V........Y.C.RQR
NKX2-5     Hs .RKP.VLFSQA.VY...RR.KQ----Q...SAPE.DQL.SV.K-----------..ST.V........Y.C.RQR
NKX2-6     Hs .RKP.VLFSQA.VLA..RR.KQ----Q...SAPE.EHL.S..Q-----------..ST.V........Y.C.RQR
csx        Bf .RKP.VLFSQA.VF...RR.KQ----Q...SAPE.EQL.QM.K-----------..ST.V........Y.C.RQR
```

```
Tin         Dm KRKP.VLFSQA.VL...CR.RL----KK...GAE.EI..QK.N-----------.SAT.V........Y.S.RGD
ceh-28      Ce KRKP.VLF.QH.VN...ER.KK----Q..V.ATE.E.L.QC.G-----------..AT.V........Y.C.RLA
Nk4         Cg  RKP.VLFSQA.VF...RR.KQ----Q...SAPE.EQL.NL.K-----------..ST.V........Y.C.R
Nk4         Hm ..KQ.ILFHHR.IEQ..DF.AA----QP.ISAIE.QCLSQKTG-----------..NN.V........Y.E.RLK DN91365_c0_g1_i1|m.44211
Nk4         Nw  RKP.ILFNHS.IFQ..LR.KH----Q....AND.R.LSDQ.N-----------..QN..........Y.S.RQE 15302
Nk4         Xb .RKP.VLF.QA.VY...RR.KQ----Q...SAPE.EHL.HL.K-----------LSST.V........Y.C.RQR DN50727
NK4         Nv .RKP.VLFSQA.VY...RR.KG----QK..SAPE.DHL.SL.K-----------..PN.V......K.Y.C..QA Q0N4L5
```

Nk5/Hmx family

```
HMX1        Hs K.KT.TVFS.S.VFQ..ST.DL----K...STAE.AGL.AS.Q-----------...T.V........N...RHV NP_061815
HMX2        Hs K.KT.TVFS.S.VYQ..ST.DM----K...SSSE.ACL.SS.Q-----------...T.V.T......N...RQL NP_005510
LOC340784   Hs K.KT.TVFS.S.VFQ..ST.DM----K...SSSE.AGL.AS.H-----------...T.V........N...RQL XP_291716
Hmx         Bf K.KT.TVFS.Q.VFQ..ST.DM----K...SSSE.AGL.AS.H-----------...T.V........N...RQL
hmx         Dm K.KT.TVFS.A.VFQ..ST.DL----K...SSSE.AGL.AS.R-----------...T.V........N...RQL NP_524951
mls-2       Ce K.KT.TVFS.S.VSQ..MM.EC----K...SSQE.SNL.QK.H-----------...T.V........N.F.RQA
Hmx1/nk5    Cg  .KT.TVFS.H.IFY..SA.DA----K...SSTE.S...ST.N-----------...T.V.V......N...S
Hmx2/nk5    Cg  .KT.TVFS.S.VFQ..ST.DM----K...SSSE.AGL.AS.Q-----------...T.V........N...R
Nk5         Ip R.KT.TVFS.N.VCQ..SM.DM----K...SSSE.TGI.RD.G-----------.S.Q.I........N.L.RQI DN15610_c0_g1_i1|m.6431
Nk5 a       Sr K.KT.TVFS.T.VCQ..NM.DL----K...SSSE.ATL.RD.T-----------.S.Q.I........N.L.RQI DN110321_c0_g1_i1|m.36339
Nk5 a       Hm K.KS.TVFS.S.VCQ..GT.DQ----K...SSAE.STL.RS.K-----------...T.V........N.L.RQI DN8401_c0_g1_i1|m.2232
Nk5 b       Sr K.KT.TVFS.S.VFQ..ST.DV----K...SSSE.ANL.NS.H-----------...T.V........N...RQI DN123682_c0_g2_i1|m.76247
Nk5 b       Hm K.KT.TVFS.N.VFQ..TT.DL----K...SSSE.ASL.AT.S-----------...T.V........N...RQL DN43016_c0_g2_i1|m.36485
Nk5         Nw K.KT.TVFS.H.VYQ..TM.DC----KK..SSSE.AGL.AT.H-----------...T.V........N.L.RQF 36577.0
Nk5         Xb K.KT.TVFS.S.VFQ..ST.DM----KR..SSSE.AGL.AS.H-----------...T.V........N...RQL DN92869
HMX (116)   Nv K.KT.TVFS.S.VYQ..ST.DM----K...SSSE.AGL.SQ.H-----------...T.V........N...RQI DQ206341
```

Nk-6 family

```
NKX6-1      Hs ..HT.P.FSGQ.IFA...T.EQ----TK..AGPE.ARL.YS.G-----------M..S.V.V......T..R.KH NP_006159
NKX6-2      Hs K.HS.P.FSGQ.IFA...T.EQ----TK..AGPE.ARL.YS.G-----------M..S.V.V......T..R.RH NP_796374
NKX6-3      Hs K.HT.P.FTGH.IFA...T.EQ----TK..AGPE.ARL.YS.G-----------M..S.V.V......T..R.KS
Nkx6        Bf ..HT.P.FSGQ.IFA...T.EQ----TK..AGPE.ARL.YS.G-----------M..S.V.V......T..R.KH
HGTX        Dm K.HT.P.FSGQ.IFA...T.EQ----TK..AGPE.AKL.Y..G-----------MS.S.V.V......T..R.RH NP_652614
Cog-1       Ce K.QS.P.FTGH.IYQ..RK.EQ----TK..AGAD.AQL.QE.N-----------MS.S.V.V......T..R.KE
Nk6         Cg  .HT.P.FSGQ.IFA...T.EQ----TK..AGPE.ARL.Y..G-----------MS.S.V.V......T..R.
Nk6         Ip K.HT.P.FSGH.IFA...T.EQ----TK..AGPE.ARL.F..G-----------MS.S.V.V......T..R.KH DN69723_c1_g1_i4|m.125267
Nk6         Sr K.HT.P.FSGH.IFA...T.EQ----TK..AGPE.ARL.F..G-----------M..S.V.V......T..R.KH DN130725_c3_g1_i1|m.123269
Nk6         Hm K.HT.P.FSGH.IFA...T.EQ----TK..AGPE.ARL.Y..G-----------MS.S.V.V......T..R.KH DN10228_c0_g1_i1|m.2704
Nk6         Nw K.HT.P.FSGH.IFA...T.EQ----TK..AGPE.GRL.YT.G-----------MS.S.V.V......T..R.RA 41714.0
Nk6         Xb ..HT.P.FSGH.IFA...T.EQ----TK..AGPE.RRL.FS.G-----------M..S.V.V......T..R.KH DN75963
NK6 (112)   Nv ..HT.P.FSGH.IFA...T.EQ----TK..AGPE.ARL.YS.G-----------M..S.V.V......T..R.RH DQ206340
```

Nk7 family

```
           Bf K.KA.T.F.GR.IF....Q.EV----KK..SASE.ADL.AL.N-----------VTDT.V.......T....QD
Nk7.1      Dm K.KA.T.F.GR.IF....M.EN----KK..SASE.T.M.KL.M-----------V..T.V.......T....QD
ceh-9      Ce R.KA.T.FSGK.VF....Q.EA----KK..SSSD.S.L.KR.D-----------V..T.V.......T....IE
Nk7        Cg  .KA.T.F.GR.IF....Q.EQ----KK..SSAE.A.M.TL.N-----------V..T.V.......T....
Nk7        Xb R.KA.TVF.GR.IF...RQ.EA----KK..SAHE.A.M.AL.N-----------V.DQ.V.......T...RLD DN94680
NK7 (070)  Nv K.KA.T.F.GR.IF....Q.EA----KK...ATE.SDM.SL.N-----------V..T.V.......T....QE DQ206276
```

Tlx family

```
TCL3       Hs K.KP.TSF..L.IC....R..R----QK..ASAE.AAL.K..K-----------M.DA.V.T......T..RRQT NP_005512
TLX2       Hs ..KP.TSFS.S.V....RR.LR----QK..ASAE.AAL.K..R-----------M.DA.V.T......T..RRQT NP_001525
TLX3       Hs ..KP.TSFS.V.IC....R..R----QK..ASAE.AAL.KS.K-----------M.DA.V.T......T..RRQT NP_066305
           Bf ..KP.TSF..L.IC....R..K----QK..ASAE.AQL.TQ.K-----------M.DA.V.T......T..RRQT
C15        Dm ..KP.TSF..I.VA....R..K----QK..ASAE.AAL.RG.K-----------M.DA.V.T......T..RRQT NP_476873
Tlx1       Cg  .KP.TSFS.MTII....R.DR----QK..ASSE.TSL.KS.K-----------ISDS.V.T......T..RR
Tlx2       Cg  .KP.TSFS.L.IM....R..R----QK..ASAE.STL.K..K-----------M.DA.V.T......T..RR
Tlx        Ip ..KP.TSF..L.IC....R..Q----QK..ASGE.ATL.SR.N-----------M.DS.V.T......T..RRQS DN68209_c2_g2_i2|m.107169
Tlx        Sr ..KP.TSF..L.IC....R.HQ----QK..ASGE.ATL.SK.N-----------M.DS.V.T......T..RRQS DN74225_c0_g2_i1|m.12757
Tlx        Hm ..KP.TSF..L.IC....R..L----QK..ASTE.ASL.KS.K-----------M.DA.V.T......T..RRQT DN40476_c0_g2_i2|m.25716
Tlx        Nw ..KP.TSF..V.VG....R.IV----QK..ASAE.NSL.KG.G-----------M.DA.V.T......T..RRQT 33755.0
Tlx        Xb  .KP.TSF..L.IM....R..K----QK..ASAE.SSL.KD.K-----------M.DA.V.T......T..RR DN135951
NVHD004    Nv K.KP.TAF.ES.IS....R.QS----QK..GSKE.S.L.GT.G-----------..DT.V                DQ206223
NVHD024    Nv A.KP.TAF.ES.IS....R.QV----TEIPREQE.S.L.GT.G-----------..DT.V.T.......L.RQR
```

Vax family

```
VAX1       Hs P..T.TSF.AE.LYR..M..QR----CQ.VVG.E.T.L.RQ.N-----------.S.T.V.V......T.Q..DQ
VAX2       Hs P..T.TSF.AE.LYR..M..QR----CQ.VVG.E.T.L.RQ.N-----------.S.T.V.V......T.Q..DQ NP_036608
           Bf P..A.TAF.AD.LKD..RAFQG----SQ.VVGQD.T.L.RQ.R-----------...T.V.V......T.Y.R.K
Ceh-5      Ce P..P.TVF.DE.LEK..ESFNT----SG..SGST.AKL.ES.G-----------.SDN.V.V......T.Q..ID
Vax        Cg  ..A.TTFSPE.LYQ.....QR----.Q..VGKE.T.L.KL.K-----------.S.T.NNITFE
Vax a      Ip P..E.TSF.PE.LFR.....RA----.Q.MVG.D.GDL.AS.G-----------.S.T.V.V......T.Y.R.K DN60553_c0_g2_i1|m.55905
Vax a      Sr P..E.TSF.PE.LFR.....SL----.Q.MVG.D.GQL.TC.G-----------...T.V.V......T.Y.R.K DN116214_c0_g1_i1|m.48271
Vax        Hm P..E.TSF.PQ.LYQ......K----.Q.MIG.D.A.L.VL.K-----------...T.V.V......T.Y.R.K DN58320_c0_g1_i1|m.41539
Vax b      Ip P..E.TSF.AQ.LFL..E..LK----AQ..VG.D.T.L.KK.N-----------.S.T...V......T.H.R.K DN89774_c0_g1_i1|m.233752
Vax b      Sr P..E.TCFSAE.LFL..E..T.----GQ.MVG.D.TLL.GR.G-----------...T...V......T.Q.R.S DN109741_c1_g1_i1|m.35411
Vax a      Nw P..Q.TSF.AE.LYI.....RR----.Q.MVGKD.GLL.ES.D-----------...T.V.V......T.Y.R.K 49354.0
Vax b      Nw  ..Q.TCFSAE.LYV..QE.IK----NQ.MVGKD.TLL.QS.T-----------.S.T.V*                20893.0
VAX (072)  Nv P..S.TSF.PA.LDR..D..RV----DM.VVGLK.MKL.ND.N-----------.S...V.V.......Y.R.R DQ206277
NVHD010    Nv ...A.TAFSAE.LKK...R.QA----.H.IVGEE.QK..KD.D-----------.S.A.V.V......T.F.RDQ DQ206300
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Novel Xenacoelomorpha family

```
           Ip K.KN.TAF.PG.IF....R.RV----Q...SASE.G.F.SH.N-----------..DT...T.......HKRQQ DN56009_c0_g1_i5|m.42659
           Sr ..KN.TAF.PH.IY....R.RS----QK..SASE.G.F.LS.K-----------..DT...T.......H.RQQ DN126921_c0_g1_i2|m.94661
           Hm K.KN.TAF.PG.IC...NR.RL----QQ..STTE.G.F.SR.K-----------..DT.V.T.......L.RQQ DN3930_c0_g1_i1|m.1095
           Ip S.KQ.TAF.PD.VY...RR.SQ----QK..SASE.A.F.SK.Q-----------.SDT...T.......R.RQQ DN60800_c0_g1_i2|m.56990
           Sr C.KQ.TAF.PD.IH...RR.AQ----QK..SASE.ADF.NK.K-----------.SDT...T.......R.RQQ DN130717_c3_g1_i1|m.123804
           Hm K.KQ.TAF.PE.VF....R.QI----QK...ASE.SDFSDS.K-----------.SDT.V.T.......H.RQQ DN20211_c0_g1_i1|m.5588
50700.0    Nw N.KS.TSF.AC.VVK..QK.QS----QK..AAVE.GEF.EK.G-----------.SDT.V.T.......H.RVQ
36321.0    Nw G.KS.TSF.PV.V.K..HK.QT----QK..AAVE.GEF.EK.G-----------..DT.V.T.......H.RVQ
DN122354   Xb K.KT.TAFSPS.IY....R.RL----QK..AASE.GEF.DK.S-----------..DT.V.T.......Y.RQH
```

ANTP CLASS Novel/ambiguous family membership

```
           Ip                                .A......SS.N-----------.N.T.V.........Q..LV DN65240_c0_g1_i5
           Ip KRQG.TVF.KQ.LEI.NGH.NH----RQ..SLAE.AQLSEQ.C-----------.SQK.V.....M.S.A.RVM DN26203_c0_g1_i1|m.10708
           Nw  SHQDHVENQGYQPI..SK.AI----NN.ISGSEVE.LSNR.G-----------I.DI..RD..A...RRGQFSQ 45900.0
           Nw LRIRTPITG.HRASMFQHFLTK----SQ...PVDCSNMSCN.G-----------IP.PA.RVFF..LRARVRAR  31941.1
           Xb G..M.TVF.YK.LQK...V.QD----QQ.MVGED.CRL.DS.G-----------.S.T.VRV......I..R..T DN41925
           Xb S..R.TSFSQE.IRL...K.EE----KQ...AKE.DD..CD.D-----------.KAS.VIT....K.S.IRR.T DN69228
```

PRD CLASS

Alx 3/4 (CART1) family

```
ALX1/CART1 Hs KR.H.T.F.SL.LE....V.QK----TH.PDVYV.EQL.LRTE-----------...ARVQV......A..R.RE NP_008913
ALX3       Hs KR.N.T.FSTF.LE....V.QK----TH.PDVYA.EQL.LRTD-----------...ARVQV......A..R.RE NP_006483
ALX4       Hs KR.N.T.F.S..LE....V.QK----TH.PDVYA.EQL.MRTD-----------...ARVQV......A..R.RE NP_068745
           Bf KR.N.T.F.SF.LE.M.RV.QK----TH.PDVYM.EQL.LRAD-----------...ARVQV......A..R.KE
Alx        Hm KR.N.T.F.NL.LE.M.KI.QK----TH.PDVYV.EQL.NRCE-----------...ARVQV......A..R.RE DN38072_c0_g2_i1|m.20141
Alx        Sr KR.N.T.F.QG.LE.M.RI.QK----TH.PDVYV.EQL.LKCD-----------...ARVQV......A..R.KE DN122029_c0_g1_i1|m.68599
Alx        Ip KR.N.T.F.QA.LE.M.RI.QK----TH.PDVYV.EQL.VKCD-----------...ARVQV......A..R.KE DN38710_c0_g1_i2|m.18965
Alx a      Nw KR.N.T.F.S..LD...RI.QK----TH.PDVYC.EQL.ARCN-----------...ARVQV......A..R.KE 55290.0
Alx b      Nw KR.N.T.F.S..LD...RI.QK----TH.PDVYC.EQL.VRCT-----------...ARVQV......A..R.KE 40829.0
Alx        Xb KR.N.T.F.SF.LD...RV.QK----TH.PDVYL.EQL.LRAD-----------...ARVQV......A..R.KE DN84186
CART1 120  Nv KR.N.T.F.A..LE.M.RV.QK----TH.PDVYT.EQL.LRCA-----------...ARVQV......A..R.RE DQ206256
```

Drgx family

```
DRGX       Hs QR.N.T.F.LQ.LEA..AV.AQ----TH.PDVFT.E.L.MKIN-----------...ARVQV......A..R.TE
Drgx       Bf QR.N.T.F.LH.LEQ..AV.AQ----TH.PDVFT.E.L.MKIN-----------...ARVQV......A..R.QE
CG34340    Dm QR.N.T.F.LQ.LEE..TA.AQ----TH.PDVFT.EDL.MKIN-----------...ARVQV......A..R.AE
Drgx       Cg  R.N.T.F.LQ.LEE..KA.AQ----TH.PDVFT.EDL.MRIN-----------...ARVQV......A..R.
DRGX       Xb QR.N.T.F.LH.LEQ..TA.AQ----TH.PDVFT.E.L.LKIN-----------...ARVQV......A..R.HE DN102158
```

Gsc family

```
GSC        Hs KR.H.TIF.DE.LEA..NL.QE----TK.PDVGT.EQL.RKVH-----------.R.EKVEV..K...A..RRQK NP_776248
GSCL       Hs TR.H.TIFSEE.LQA..AL.VQ----.Q.PDVST.ERL.GRIR-----------.R.ERVEV..K...A..RHQK NP_005306
Gsc        Bf KR.H.TIF.EE.LEL..KT.EK----TH.PDVLL.E.L.MKVE-----------.K.ERVEV..K...A..R.QQ
Gsc        Dm KR.H.TIF.EE.LEQ..AT.DK----TH.PDVVL.EQL.LKVD-----------.K.ERVEV..K...A..R.QK NP_476949
Ceh-45     Ce KR.H.TIFSEE.LNI..TT.ST----TH.PDATT.E.L.VQCS-----------.K.ERVEV..K...A.ER.QK
Gsc1       Cg                                ML.E.L.MKVD-----------.K.ERVEV..K...A..R.
Gsc2       Cg  R.H.TIF.EE.LE....T.NK----TH.PDVLL.E.L.MKID-----------.K.ERVEV..K...A..R.
GSC        Ip KR.H.TIF.EE.LA...AV.VR----SH.PDVLA.EKV.TS.G-----------.K.ERVEV..K...A..R.QK DN67235_c0_g4_i4
GSC        Sr KR.H.TIFSEE.LK...EA.LK----CH.PDVVT.EGV.QK.S-----------.K.ERVEV..K...A..R.QK DN120054_c0_g1_i1|m.60873
GSC        Hm TR.H.TIF.EE.LE...KT.SL----TH.PDVQT.EQL.AKAD-----------.K.ERVEV..K...A..R.QK DN27253_c0_g1_i2|m.9227
GSC        Nw KR.H.TIFSEE.LD...TT.AK----TH.PDVLL.EQL.LRVE-----------.K.ERVEV..K...A..R.YK 40214.0
GSC        Xb KR.H.TIF.EE.LE...RT.EK----TH.PDVLL.EQL.VKVD-----------.KEERVEV..K...A..R.QK DN48278
GSC (068)  Nv KR.H.TIF.EE.-....TT.QK----TH.PDVLL.E.L.MKVD-----------.K.ERVEV..K...A..R.QK DQ206230
```

Hbn family

```
Hbn        Dm VR.S.T.F.TF.LHQ..RA.EK----TQ.PDVFT.EDL.MR.D-----------.S.ARVQV......A..R.RE
Hbn        Cg  R.S.T.F.T..LHQ..RA.EK----TQ.PDVFT.E.L.MR.D-----------.S.ARVQV......A..R.
HBN        Xb VR.S.T.F.TF.LHH..RA.EK----SH.PDVFT.E.L.AS.H-----------.S.ARVQV......A..RKTE DN83632
HBN (079)  Nv VR.S.T.F.T..LHQ..RA.EK----TQ.PDVFT.E.L.LR.D-----------.S.ARVQV......A..R.RE DQ206231
```

Otp family

```
OTP        Hs Q..H.TRF.PA.LN...RS.AK----TH.PDIFM.E.L.LRIG-----------...SRVQV......A....RK NP_115485
           Bf Q..H.TRF.PA.LQ...RS.SK----TH.PDIFM.E.L.LRIG-----------...SRVQV......A....RK
otp        Dm Q..H.TRF.PA.LN...RC.SK----TH.PDIFM.E...MRIG-----------...SRVQV......A....RK NP_995909
Otp        Cg  ..H.TRF.PA.LN...RS.AK----TH.PDIFM.E.L.LRIG-----------...SRVQV......A....
OTP        Ip A..H.TRF.PA.LN...RC.NK----TH.PDIFM.E.L.MRIA-----------...SRVQV......A....RK DN57662_c0_g1_i1|m.46698
OTP        Sr P..H.TRF.PA.LN...RC.NK----TH.PDIFM.E.L.MRIA-----------...SRVQV......A....RK DN116171_c0_g1_i2|m.48160
OTP        Hm P..H.TRFSPN.LN...RC.GK----TH.PDIFM.E.M.LRIG-----------...SRVQV......A....RK DN10420_c0_g1_i1|m.2841
OTP        Nw P..H.TRF.PA.LN...RC.TK----TH.PDIFM.E.L.VRIG-----------...SRVQV......A....RK 53544.0
OTP        Xb P..H.TRF.PA.LN...RS.NK----TH.PDIFM.E.L.MRIG-----------...SRVQV......A....RK DN86933
OTP (047)  Nv Q..H.TRF.PA.LN...RC.AR----TH.PDVFM.E.L.ARIG-----------...SRVQV......A....RK DQ206247
```

Otx family

```
OTX1       Hs QR.E.T.F..S.LDV..AL.AK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQQQ NP_055377
OTX2       Hs QR.E.T.F..A.LDV..AL.AK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQQQ NP_068374
CRX        Hs QR.E.T.F..S.LE...AL.AK----TQ.PDVYA.E.V.LKIN-----------.P.SRVQV..K...A.CRQQR NP_000545
otx        Bf QR.E.T.F..A.LDV..AL.AK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQQA
oc         Dm QR.E.T.F..A.LDV..AL.GK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQQL NP_511091
ceh-36     Ce GR.E.TSFN.G.LDQ...V.RE----TQ.PDVHR.EAL.K.IN--------LPDGRVQV.TV..K...A.DRNNK
ceh-37     Ce NR.E.T.YS.Q.LEI..TL.NE----TQ.PDVFA.ERV.DQIR-----------.Q.SR.QV..K...A.YRLQE
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```
ttx-1       Ce QR.E.T.F..N.LEI..SY.VK----T..PDIFM.EDM.HKIQ-----------.P.SRVQV..K...A.ARQQK
Otx         Cg  R.E.T.F..A.LDI..SL.QK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQ
OTX         Ip QR.E.T.F..T.LEI..QL.SK----T..PDIFM.E.V.NRIN-----------.P.SRVQV..K...A.CRQQQ DN73075_c6_g1_i5|m.177200
OTX         Sr QR.E.T.F..T.LEI..AL.SK----T..PDIFM.E.V.NRIN-----------.P.SRVQV..K...A.CRQQQ DN123029_c0_g3_i3|m.73095
OTX a       Hm QR.E.T.F..A.LEI..SL.SK----T..PDIFM.E.V.MKIN-----------.P.SRVQV..K...A.CRQQQ DN24659_c0_g2_i1|m.8154
OTX b       Hm PR.E.T.FSKN.VLY..EL.TK----T..PDVFM.Q...DK.H-----------...SRVQV..K...A.SRQQT DN56217_c0_g1_i1|m.41307
OTX         Nw QR.E.T.F..A.LEV..SL.TK----T..PDIFM.E.V.MKIN-----------.P.SRVQV..K...A.CRQQQ 48073.0
OTX         Xb QR.E.T.F..A.LEV..AL.SK----T..PDIFM.E.V.LKIN-----------.P.SRVQV..K...A.CRQQA DN55770
OTXa 114    Nv QR.E.T.F.KN.LEV..EL.AK----T..PDIFM.E.V.IKIN-----------.P.SRVQV..K...A.TRQLE DQ206236
OTXb 123    Nv QR.E.T.F.KN.LEI..EL.AK----T..PDIFM.E.V.IKIN-----------.P.SRVQV..K...A.ARQQA DQ206257
OTXc 078    Nv QR.E.T.F.KN.LEI..EL.AK----T..PDIFM.E.V.IKIN-----------.P.SRVQV..K...A.LRQLS DQ206252
```

Pax 4/6 family

```
PAX4        Hs GH.N.TIFSPS.AEA.....QR----GQ.PDSVA.GKL.T.TS-----------.P.DTVRV..S...A..RRQE NP_006184
PAX6        Hs LQ.N.TSF.QE.IEA.....ER----TH.PDVFA.ERL.AKID-----------.P.AR.QV..S...A..RR.E NP_001595
            Bf LQ.N.TSF.QE.IEA.....ER----TH.PDVFA.ERL.AKID-----------.P.ARIQV..S...A..RR.E
eyg         Dm FR.N.T.FSPE.LE......DK----SH.PCVST.ERLSSRTS-----------.S.ARVQV..S...A..RRH NP_524042
toe         Dm FR.N.T.FSPE.LD......DK----SH.PCVNT.EKL.ARTA-----------.S.ARVQV..S...A..RRHQ NP_524041
toy         Dm LQ.N.TSFSNE.IDS.....ER----TH.PDVFA.ERL.DKIG-----------.P.AR.QV..S...A..RR.E NP_524638
ey          Dm LQ.N.TSF.ND.IDS.....ER----TH.PDVFA.ERL.GKIG-----------.P.AR.QV..S...A..RR.E NP_726607
vab-3       Ce LQ.N.TSF.QV.IES.....ER----TH.PDVFA.ERL.QKIQ-----------.P.AR.QV..S...A..RR.E
eyg-1       Ce .RLS.STF.NE.LQS..EV.LR----DP.PSPNE.ADLVKRTN-----------.P.AR.QV..S...A..R.TN
Pax4_6      Cg  R.NRTTF.SQ.LDL..QS.QK----AH.PGVQT.E.L.TKTN-----------.S.ARVQV..S...A..RR
Pax6        Cg  Q.N.TSF.AA.IEA.....ER----TH.PDVFA.ERLSQKID-----------.P.AR.QV..S...A..RR
Pax4/6 a    Ip NQ.N.TAYSQN.LEL.....EK----SH.PDVYA.ERLSEATD-----------IP.SK.Q...S...A.HRR.E DN54186_c0_g1_i2|m.38019
Pax4/6 a    Sr SQ.N.TA..SE.VDA.....EK----SH.PDVYA.ERLSTLTG-----------IP.TK.Q...S...A.HRR.E DN127496_c0_g2_i1|m.98660
Pax4/6 a    Hm FQ.N.TSF.QS.IDA.....ER----TH.PDVYA.ERLSESTS-----------.A.NK.QV..S...A..RR.E DN37527
Pax4/6 b    Ip LQ.N.TSF.PE.IDA...Q.EV----TH.PDVFA.ERL.GKIA-----------.P.AR.QV..S...A..RR.E DN12334_c0_g1_i1|m.4957
Pax4/6 b    Sr LQ.N.TSF.PE.IEA...Q.EV----TH.PDVFA.ERL.GKIN-----------.P.AR.QV..S...A..RR.E DN116853_c0_g1_i1|m.50040
Pax4/6 b    Hm LQ.N.TSF.QE.IDN..L..DR----TH.PDIFA.EKLSEKIK-----------.A.AR.QV..S...A..RR.E DN15356_c0_g1_i1|m.4176
PAX4/6 a    Nw LQ.N.TSFSVE.IDA..ST.NE----SH.PDSNE.ERL.EKVG-----------IP.AK.QV..S...AR.RR.D 24274.0
PAX4/6 b    Nw LQ.N.TSF.PE.IDA.....ER----TH.PDVFA.EKL.EKIG-----------.P.AR.QV..S...A..RR.E 49939.0 also 46535.0
PAX4/6 a    Xb LQ.N.TSF.PE.IDS.....ER----TH.PDVFA.ERL.KDID-----------.P.AR.QV..S...A..RR.E DN77439
PAX4/6 b    Xb LQ.N.TSF.PE.LES.....ER----TH.PDVFA.ERL.AKID-----------.P.AR.QV..S...A..RR.E DN86691
PAX4/6 022  Nv LR.N.T.F.PD.LEM.....EK----SH.PDVAT.E.L.NKID-----------MS.ARVQV..S...A..RRHQ DQ206243
NVHD148     Nv SR.Q.TNF.DE.IEK...V.EK----TH.PDVFT.E.L.QQVN-----------.S.AR.QV.YS...A..R.EG DQ206260
```

Pitx family

```
PITX1       Hs QR.Q.THF.SQ.LQ...AT.QR----...PDMSM.E...VWTN-----------...PRVRV..K...A..R.RE NP_002644
PITX2       Hs QR.Q.THF.SQ.LQQ..AT.QR----...PDMST.E...VWTN-----------...ARVRV..K...A..R.RE NP_000316
PITX3       Hs QR.Q.THF.SQ.LQ...AT.QR----...PDMST.E...VWTN-----------...ARVRV..K...A..R.RE NP_005020
```

```
pitx        Bf QR.Q.THF.SQ.LQ...AS.AR----...PDMAT.E...AWTN-----------...ARVRV..K...A..R.RE
ptx1        Dm QR.Q.THF.SQ.LQ...HT.SR----...PDMST.E...MWTN-----------...ARVRV..K...A..R.RE NP_996314
unc-30      Ce  R.Q.THF.SH.LT...NW.SR----...PDMAC.E...VWIS-----------...PRVRV..K...A..R.RE
Pitx        Cg  R.Q.THF.SQ.LQ...AT.AR----...PDMAT.E...AWTN-----------...ARVRV..K...A..R.
Pitx a      Ip AR.Q.THF.SQ.LQ...TL.SR----...PDMAT.E..SAWTN-----------.P.AKVR...K...A..R.KE DN51842_c2_g1_i1|m.33653
Pitx a      Sr TR.Q.THF.SQ.LQ...TL.AR----...PDMAT.E..SAWTN-----------.P.AKVR...K...A..R.KE DN122619_c1_g1_i1|m.71282
Pitx a      Hm QR.Q.THF.SQ.LT...TL.SR----...PDMAT.ED.SAYIL-----------.P.SKVR...K...A..R.KE DN26989_c0_g2_i1|m.9094
Pitx b      Ip ER.Q.TQF.SH.LR...SM.AR----...PDMAT.ERLSAWVQ-----------.S.TKVR...K...A..R.KE DN68900_c3_g1_i2|m.114481
Pitx b      Sr ER.Q.TQF.SH.LR...SM.AR----...PDMAT.ERLSAWIS-----------.S.TKVR...K...A..R.KE DN126115_c0_g4_i7|m.89715
Pitx b      Hm ER.Q.TQF.SH.LR...TM.AR----...PDMAS.ERLSAWIS-----------.S.SKVR...K...A..R.KR DN29252_c0_g1_i2|m.10492
Pitx        Nw PR.Q.THF.SQ.LQ...SM.TR----...PDMAT.E...AWTG-----------...SRVRV..K...A..R.KE 27707.0
Pitx        Xb QR.Q.THF.SQ.LQ...AT.AR----...PDMAT.E..SVWTN-----------...ARVRV..K...A..R.KE DN49217
PTX (105)   Nv QR.Q.THF.SF.LQQ..GT.GR----...PDMQM.E...LYTN-----------...ARVRV..K...A..R.KE DQ206235
```

Prop family

```
PROP1       Hs .R.H.T.FSPV.LEQ..SA.GR----.Q.PDIWA.ESL.RDTG-----------.S.AR.QV......A.QR.QE NP_006252 1
            Bf .R.H.T.F.QE.LAQ..EA.SK----SH.PDIYV.E.L.RATK-----------.N.AR.QV......A.YR.QE
CG32532     Dm .R.H.T.F.QE.LA...AA.AK----SH.PDIYC.E.L.RTTK-----------.N.AR.QV......A.YR.QE NP_608318
unc-42      Ce .R.H.T.F.QE.LQ..DAA.QK----SH.PDIYV.E.L.RITK-----------.N.AR.QV......A.HR.HE
Prop        Cg  R.H.T.F.QE.LQ...NA.AK----SH.PDIYC.E.L.RITK-----------.N.AR.QV......A.YR.
Prop        Ip .R.H.T.F.QE.LN...AA.AK----SH.PDIYV.E.L.RITK-----------.N.AR.QV......A.YR.QE DN60252_c0_g2_i3|m.55039
Prop        Sr .R.H.T.F.QD.LN...AA.SK----SH.PDIYV.E.L.RITK-----------.N.AR.QV......A.YR.QE DN118878_c0_g1_i4|m.56464
Prop        Hm .R.H.T.FNQD.LN...AA.SK----SH.PDIYV.E.L.RITK-----------.N.AR.QV......A.YR.HE DN23062_c0_g1_i1|m.7235
Prop        Xb .R.H.T.F.QE.LN...AA.AK----SH.PDIYV.E.L.RITK-----------.N.AR.QV......A.YR.QE DN88387
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Repo family

```
            Bf KT.Y.T.FST..LE...KA.ER----AP.PDVFA.E.L.MR.N-----------.S.ARVQV......A..R.RE
repo        Dm K.KT.T.F.A..LE...RA.ER----AP.PDVFA.E.L.IK.N-----------.S.SRVQV......A..R.HE NP_477026
Repo        Cg  P.H.T.FSPF.LK.M.KA.RK----AP.PDVMT.E.L.RR.A-----------.N.SRVQ.......A..R.
Repo        Ip KS.Y.T.FSAE.LEQM.RA.QL----AP.PDVFT.E.L.ARVG-----------...ARVQV......AR.R..R DN64595_c0_g1_i1|m.76632
Repo        Sr KS.Y.T.F.SE.LDQM.RA.EC----AP.PDVFT.E.L.NRIK-----------...ARVQV......AR.R..R DN108331_c0_g1_i2|m.33300
Repo        Hm KS.Y.T.F.VF.LES..KA.ER----AA.PDVFA.E.L.RRIN-----------.S.AR.QV......A..R.DK DN41482_c1_g1_i2|m.28797
Repo        Nw KP.H.T.F.SW.LQ.M.RA.ER----AP.PDSPM.EQL.INIG-----------..DARVQV......A..R.QT 18856.0
Repo        Xb KT.Y.T.F.AW.LE.M.RA.ER----AP.PDVFQ.E.L.MKIS-----------.S.ARVQV......A..R.LK DN70414
REPO118     Nv KT.Y.T.FSQ..IE...RA.DK----AP.PDVFA.E.L.AK.G-----------...AR.QV......A..R.RE DQ206237
```

Rax family

```
RX/RAX      Hs HR.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.GKVN-----------.P.VRVQV......A..RRQE NP_038463
MGC15631    Hs HR.N.T.F.T..LHQ..RA.EA----SH.PDVYS.E.L.AKVH-----------.P.VRVQV......A..RRQE NP_116142
rax         Bf HR.N.T.F.TF.LH...RA.EK----SH.PDVYS.E.L.MKIN-----------.P.VRVQV......A..RRQE
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```
Rx          Dm HR.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.MKVN-----------.P.VRVQV......A..RRQE NP_726006
Ceh-8       Ce QR.N.T.F.TF.LHA..AA.DK----TH.PDVYA.ETL.AKVQ-----------.P.VRVQV......A.FRRQE
Rax         Cg  R.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.MKID-----------.P.VRVQV......A..RR
Rax         Ip HR.N.T.F.TF.LH...RA.EK----SH.PDVYS.E.L.ARVN-----------.P.VRVQV......A..RRQE DN19265_c0_g1_i1|m.7660
Rax         Sr HR.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.SRVN-----------.P.VRVQV......A..RRQE DN126115_c0_g3_i1|m.89710
Rax         Hm HR.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.TRVQ-----------.P.VRVQV......A..RRQE DN20170_c0_g1_i1|m.5558
Rax         Nw HR.N.T.F.T..LH...RA.EK----SH.PDVYA.E.I.LKIN-----------.P.VRVQV......A..RRQE 29086.0 also 43623.0
Rx          Xb HR.N.T.F.T..LH...RA.EK----SH.PDVYS.E.L.MKVA-----------.P.VRVQV......A..RRQE DN67189 (end from DN56207)
RX (129)    Nv LR.N.T.F.TF.LH...RA.EK----SH.PDVYT.E.L.LKIS-----------.P.VRVQV......A..RRQE DQ206258
```

Shox (OG12) family

```
SHOX        Hs QR.S.TNF.LE.LN...RL.DE----TH.PDAFM.E.LSQR.G-----------.S.ARVQV......A.CR.QE NP_000442
SHOX20.61   Hs QR.S.TNF.LE.LN...RL.DE----TH.PDAFM.E.LSQR.G-----------.S.ARVQV......A.CR.QE NP_003021
shox        Bf QR.S.TNF.LE.LQ...RL.DE----TH.PDAFM.E.LSQR.G-----------.S.ARVQV......A.CR.QE
CG34367     Dm QR.S.TNF.LD.LN...RL.EE----TH.PDAFM.E.LSQR.G-----------.S.ARVQV......A.CR.HE
Shox        Cg  R.S.TNF.LE.LN...RL.DE----TH.PDAFM.E.LSQR.G-----------.S.ARVQV......A.CR.
Shox        Hm C..N.TQFSTF.IKR..KL.EE----TH.PDSYM.E.LGKR.N-----------.S.SR.QV......A.CR.YD DN27245_c0_g1_i1|m.9220
Shox        Sr Y..T.TQFSED.ICA...L.EE----SH.PDSSA.N.LVA.TG-----------..DSK.QV......A.AR..K DN120882_c0_g2_i7|m.63873
Shox        Xb QR.T.TNF.LE.LE....L.DE----TH.PDAFM.E.LSS.LG-----------.SEARVQV......A.C     DN14020
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Uncx family

```
UNCX        Hs .R.T.TNFTGW.LE....A.NE----SH.PDVFM.EAL.LR.D-----------.V.SRVQV......A..R.KE
uncxA       Bf .R.T.TNFNSW.LE...RA.QE----SH.PDVFM.EAL.LR.D-----------.V.SRVQV......A..R.KE
uncxB       Bf QR.S.ANYSQW.LE...KA.ET----TQ.PDIFM.EAL.LR.D-----------.I.ARVQV......A.LRRQL
uncxC       Bf .M.V.TNFTSW.LEA..RA.ET----TH.PDIFM.EAL.LR.D-----------.M.SRVQV......A..RKQE
unc-4       Dm .R.S.TNFNSW.LE...RA.SA----SH.PDIFM.EAL.MR.D-----------.K.SRVAV......A.VR.RE NP_573242
OdsH        Dm KR...TNFNSW.LR...RV.QG----SH.PDIFM.EAL.TK.D-----------.M.GR.AV......A..R.QE NP_523389
unc-4       Ce .R.T.TNFSGW.LE...SA.EA----SH.PDVFM.EAL.MR.D-----------.L.SRVQV......A..R.RE
Uncx        Cg. R.T.TNF.GW.LE...RA.QD----SH.PDVFM.EAL.LR.D-----------.V.SRVQV......A..R.
Uncx        Ip .R.T.TNF.NW.LEQ..LA.HR----TH.PDVFV.ETL.LQ.N-----------.M.SRVQV......A..R    DN58162_c0_g1_i2|m.48062
Uncx        Sr .R.T.TNF.NW.LEQ..MA.HR----TH.PDVFV.ETL.MQ.N-----------.M.SRVQV......A..R.ME DN113036_c0_g1_i1|m.41100
Uncx        Hm .R.T.TNF.SL.LE...RA.AA----SH.PDVFM.ESLGQR.S-----------.L.SRVQV......A..R.IE DN31526_c0_g1_i1|m.12245
Uncx        Xb .R.T.TNFNSW.LE....A.LV----SH.PDIFM.EAL.MR.D-----------.I.SRVQV......A..R.KE DN12917
UNC4 059    Nv .M.V.TNFSPW.LE...HA.ET----TH.PDVFM.EAL.MR.D-----------...ARVQV......A..R.RE DQ206229
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Vsx/Chx10 family

```
CHX10       Hs KR.H.TVF.AH.LE....A.SE----AH.PDVYA.EML.VKTE-----------.P.DR.QV......A..R.RE NP_878314
VSX1        Hs KR.H.TIF.AH.LE....A.SE----AH.PDVYA.EML.VKTE-----------.P.DR.QV......A..R.RE NP_055403
vsx         Bf KR.H.TIF.S..LE....A.NE----AH.PDVYA.EML.MKTD-----------.P.DR.QV......A..R.KE
4136/vsx1   Dm .RH..TIF.SS.LE....A.KE----AH.PDVSA.ELLSMKTG-----------.A.DR.QV.Y....A..R.TE NP_572232
15782/vsx2  Dm .RHS.TIF.S..LEK..EA.KE----AH.PDVYA.EMLSLKTE-----------.P.DR.QV......A..R.TE NP_572230
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ceh-10      Ce KR.H.TIF.Q..ID....A.QD----SH.PDIYA.EVL.GKTE-----------.Q.DR.QV......A..R.TE
dsc-1       Ce .R.F.TNF.EL.STF..DS.KE----SH.PDHKA.KYM.DF.K-----------IP.DR.TV......A..RRKE
Vsx1        Cg  R.H.TIF.S..VE....T.KE----AH.PDLYA.EVL.LKID-----------.P.DR.QV......A..R.
Vsx2        Cg  R.H.TIF.S..LE....A.KD----AH.PDVYA.EVL.LKTS-----------.P.DR.QV......A..R.
Vsx a       Ip .R.H.TIF.S..IE....A.KE----AH.PDVYA.ELLSIKTD-----------.P.DR.QV......A..R.KE DN31321_c0_g1_i1|m.13615
Vsx b       Ip .R.H.TIF.NS.VE....A.EE----AH.PDVYQ.EILSLKTD-----------.P.DR.QV......A..R.KE DN66046_c0_g1_i4|m.86993
Vsx a       Sr .R.H.TIF.S..IE....A.GD----AH.PDVYA.EMLSLKTD-----------.P.DR.QV......A..R.KE DN98097_c0_g1_i1|m.23524
Vsx b       Sr .R.H.TIFSVS.VE...RA.ED----AH.PDVVQ.ETLSNKTE----------.P.DR.QV......A..R.KE DN111202_c0_g2_i1|m.37759
Vsx a       Hm .R.H.TIF.SL.ID....A.SE----AH.PDVYA.EMLSLKTD-----------.P.DR.QV......A..R.KE DN7688_c0_g1_i1|m.2075
Vsx b       Hm .R.H.TIF.NE.VD....I.QT----AH.PDVNA.EMLSLKTE-----------.P.DR.QV......A..R.KE DN80881_c0_g1_i1|m.43410
Vsx         Nw KR.H.TIF.AL.LE...AA.GD----AH.PDVYA.ELLSIKTD-----------.P.DR.QV......A..R.KE 21928.0
Vsx         Xb RR.H.TIF.S..LEQ...A.TE----AH.PDVYA.EMLSLKTD-----------.P.DR.QV......A..R.KE DN86983
CEH10085    Nv KR.H.TIF.N..LE....A.KE----SH.PDVYA.ENLSLKID-----------.P.DR.QV......A..R.KE DQ206232
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PRD CLASS / Family membership ambiguous

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            Ip PQILPLHMLTDAEKT..RS.MR----DHNPADYMYEIMAEEIG-----------WNLN.VKQ.YDRKKAT.RSNE DN73593_c0_g2_i3
            Ip PR.S.T.F.AF.LHQ..SI.LS----N..PDVA..DQL.AM.G-----------...SR.QV......A.RR.AE DN71583_c0_g1_i1|m.152092
            Sr CR.S.T...PW.LHQ..SS.ED----.P.PDVGQ.DYL.GVMG-----------V..SR.QV......A.RR.LA DN112801_c0_g1_i2|m.40593
            Hm KP.V.TFF.SD.LRN..KA.SE----NA.PDVKM.A..CSR.K-----------.R.S.VL.....K.ARN..LK DN35675_c0_g1_i1|m.16721
HD1         Hm                      K----DQFPSKESKKTLSKK.N-----------.DYSSVDV....K.ARTNSKI DN34694_c0_g1_i1|m.15382
HD2         Hm GRKA.TSITPF.QDQ..AA.RL----.PFPLWSDKDY..SE.D-----------.D.SVVQV......ARS.RKL DN34694_c0_g1_i1|m.15382
            Hm QR.N.T.F.NY.LNT..CA.RK----TH.PDVFT.E.L.KKVE-----------...ARVQV......A..R.GE DN36971_c0_g1_i2|m.18384
            Nw K.REKKVFDPM.IAL..HNYME----IR.PDLQ..K.L.AVVG-----------ID.KR.QV......ARTRRKH 54213.0
            Nw K..VKKVFEPG.IAL..HNYIL----.Q.PSPQG.KALSNEVG-----------ID.KRIQV......ARTR.KH 47651.0
            Xb  R.N.MSFQPE.RAI..EAYRV----.K.PDILH.AWISQMTN-----------IPDLR.Q......A.SR.RE DN122491
            Xb QR.N.T.F.PQ.LE...QL.SK----TH.PDIFV.EDL.MRIN-----------.S.ARVQV... DN122218
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LIM CLASS

Apterous / Lhx2/9 family

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LHX2        Hs T..M.TSFKHH.LRTMKSY.AI----.HNPDAKDLKQL.QKTG-----------..K.VLQV....A.A.FRRNL NP_004780
LHX9        Hs T..M.TSFKHH.LRTMKSY.AI----.HNPDAKDLKQL.QKTG-----------..K.VLQV....A.A.FRRNL NP_001014434
Lhx2/9a     Bf T..I.TSFKHH.LRT.KSY.AI----.HNPDSKDLQQL.QKTG-----------..K.VLQV....A.A.HRRNA
Lhx2/9b     Bf Q..M.TSFKHH.LRAMKSY.AL----.HNPDAKDLKQL.QKTG-----------..K.VLQV....A.A.YRRNL
ap          Dm T..M.TSFKHH.LRTMKSY.AI----.HNPDAKDLKQLSQKTG-----------.PK.VLQV....A.A..RRMM NP_724428
ttx-3       Ce S..M.TSFKHH.LRAMKTY.AL----.HNPDAKDLKQL.AKTN-----------..K.VLQV....A.A.YRREL
Lhx2_9      Cg  ..V.TSFKHH.LRTMKSY.AL----.HNPDAKDLKQL.QKTG-----------.SK.VLQV....A.A.YRR
Lhx2/9 a    Ip A..V.TSFKNH.LRV.KQY.QL----.HNPDAKELKQLSQKTG-----------.SK.VLQV....A.A.YRRMM DN67846_c0_g1_i1 .2
Lhx2/9 a    Sr T..V.TSFKNH.LRV.KQY.QL----.HNPDAKELKQLSQKTG-----------.SK.VLQV....A.A.YRRLM DN125451_c0_g1_i1|m.85840
Lhx2/9 a    Hm N..V.TSFKNH.LRV.KQY.QL----.HNPDAKELKQLSQKTG-----------.SK.VLQV....A.A.YRRNV DN36226_c0_g1_i1|m.17408
Lhx2/9 b    Ip S..M.TSFKHH.LQAMKVY.NA----.HNPDAKDLKQL.TKTG-----------..K.VLQV....A.A.FRRNL DN67846_c0_g4_i1|m.102863 .1
Lhx2/9 b    Sr S..M.TSFKHH.LQAMKQY.NA----.HNPDAKDLKSL.QKTG-----------..K.VLQV....A.A.FRRNL DN128068_c1_g1_i1|m.102330
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Lhx2/9 b    Hm S..M.TSFKNN.LVQMKQY.TM----.HNPDAKDLKQLSHKTG-----------..K.VLQV....S.A.YRRNM DN9855_c0_g2_i1|m.2527
Lhx2/9 a    Nw T..V.TSFKHH.LRTMKSY.NL----.HNPDAKDLKQLSQKTC-----------.SK.VLQV....A.A.YRRLM 51594.0
Lhx2/9 b    Nw T..V.TSFKNP.LRVLKQY.QL----.HNPDAKELKQLSQKTS-----------.SK.VLQV....A.A.YRRQV 54455.0
Lhx2/9      Xb Q..M.TSFKHH.LRAMKSY.SI----.HNPDAKDLKQL.QKTG-----------..K.VLQV....A.A.FRRNM DN63074
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Islet family

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ISL1        Hs TT.V.TVLNEK.LHT.RTCYAA----.PRPDALMKEQLVEMTG-----------.SP.V.RV....K.C.D..RS NP_002193
ISL2        Hs TT.V.TVLNEK.LHT.RTCYAA----.PRPDALMKEQLVEMTS-----------.SP.V.RV....K.C.D..KS NP_665804
isl         Bf PT.V.TVLNEK.LHT.RTCYAA----.PRPDALMKEQLVEMTG-----------.SP.V.RV....K.C.D..KS
tup         Dm PT.V.TVLNEK.LHT.RTCYNA----.PRPDALMKEQLVEMTS-----------.SP.V.RV....K.C.D..KT NP_476774
lim-7       Ce AT.V.TVLNEN.LKI.RDCYSI----.SRPDATLKERLVEMTG-----------.SA.V.RV....K.C.D..RQ
Islet       Cg  T.V.TVLNEK.LHT.RTCYNA----.PRPDALMKEQLVEMTG-----------.SP.V.RV....K.C.D..
Islet       Ip PT.I.TVLNEK.LHT.RTCYNA----.PRPDALM.EQLVEMTG-----------.SP.V.RV....K.C.D..RS DN56056_c0_g1_i1|m.42738
Islet       Sr PT.I.TVLNEK.LHT.RTCYNA----.PRPDALM.EQLVEMTG-----------.SP.V.RV....K.C.D..RS DN125302_c3_g2_i1|m.85233
Islet a     Hm PT.V.TVLNEK.LHT.RTCYNA----.PRPDALMKEQLTEMTA-----------.SP.V.RV....K.C.D..RS DN27964_c0_g1_i1|m.9540
Islet b     Hm SG.V.TVLNEK.LST.RAYYHA----.PRPDAPM.EQLVEMTS-----------.SH.V.RV....K.C.D..RQ DN14479_c0_g1_i1|m.3858
Islet a     Nw PT.V.TVLNEK.LST.RTCYAA----.ARPDALM.EQLSDMTG-----------.SG.V.RV....K.C.D..RS 45303.0
Islet b     Nw PT.V.TVLNEK.LQT.RQCYAA----.SRPDALM.EQLSDMTS-----------.SG.V.RV....K.C.D..RS 22501.1
Islet       Xb TT.V.TVLNEK.LHT.RTCYAA----NPRPDALMKEQLVEMTA-----------.SP.V.RV....K.C.D..KS DN91806
ISL (028)   Nv PT.V.TVLNEK.LHT.RTCYNA----.PRPDAMMKEQLVEMTG-----------.SP.V.RV....K.C.D..KA DQ206225
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Lhx 1/5 family

```
LIM1/LHX1   Hs .RGP.T.IKAK.LET.KAA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK NP_005559
LHX5        Hs .RGP.T.IKAK.LET.KAA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK NP_071758
Lhx1/5      Bf .RGP.T.IKAK.LET.KAA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK
lim1        Dm .RGP.T.IKAK.LEV.KTA.NQ----TPKP..HI.EQL.KETG-----------.PM.V.QV....K.S.ERRMK NP_572505
lin-11      Ce .RGP.T.IKAK.LET.KNA.AA----TPKPT.HI.EQL.AETG-----------.NM.V.QV......S.ERRMK
mec-3       Ce .RGP.T.IKQN.LDV.NEM.SN----TPKPSKHA.AKL.LETG-----------.SM.V.QV......S.ERRLK
Lhx1/5      Cg  RGP.T.IKAK.LET.KAA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERR
Lhx1/5      Ip .RGP.T.IKAK.LET.KSA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK DN68178_c0_g1_i3|m.106476
Lhx1/5      Sr .RGP.T.IKAK.LET.KSA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK DN118733_c0_g2_i1|m.55910
Lhx1/5      Hm .RGP.T.IKAK.LET.KTA.MN----TPKP..HI.EQL.METG-----------.NM.V.QV......S.ERRMK DN30383_c0_g1_i1|m.11355
Lhx1/5      Nw RRGP.T.IKAK.LDT.KAA.DA----TPKP..HI.EQL.QDTG-----------.NM.V.QV......S.ERRMT 61503.0
Lhx1/5      Xb RRGP.T.IKAK.LET.KAA.AA----TPKP..HI.EQL.QETG-----------.NM.V.QV......S.ERRMK DN95395
LHX1/5 127  Nv .RGP.T.IKAK.LEA.KST.AA----TPKPS.NI.EKL.QETG-----------.NM.V.QV......S.ERRLK DQ206345
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Lhx 3/4 family

```
LHX3        Hs A..P.T.I.AK.LET.KSAYNT----SPKPA.HV.EQLSSETG-----------.DM.VVQV......A.E.RLK NP_055379
LHX4        Hs A..P.T.I.AK.LET.KNAYKN----SPKPA.HV.EQLSSETG-----------.DM.VVQV......A.E.RLK NP_071758
Lhx3/4      Bf Q..P.T.I.AK.LET.KQAYQN----SPKPA.HV.EQLSQETG-----------.DM.VVQV......A.E.RLK
Lim3        Dm N..P.T.I.AK.LET.KTAYNN----SPKPA.HV.EQLSQDTG-----------.DM.VVQV......A.E.RLK NP_572505
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Ceh-14      Ce N..P.T.ISAKSLET.KQAYQT----SSKPA.HV.EQL.SETG-----------.DM.VVQV......A.E.RLK
Lhx3/4      Cg  ..P.T.I.AK.LEA.KRAYNE----SPKPA.HV.EQLSAETG-----------.DM.VVQV......A.E.R
Lhx3/4      Ip N..P.T.I.AK.LEI.KNAYKS----SSKPA.HI.EQLSKDTG-----------.DM.VVQV......A.E.RLK DN49678_c0_g2_i1|m.29979
Lhx3/4      Sr N..P.T.I.AK.LEV.KSAYKN----SSKPA.HI.EQLSKDTG-----------.DM.VVQV......A.E.RLK DN124757_c1_g2_i2|m.82144
Lhx3/4      Hm N..P.T.INNK.LDV.REAYSK----SAKPA.HI.EDLSKKTD-----------.DM.VVQV......A.E.RLK DN28959_c0_g1_i1|m.10298
Lhx3/4      Nw Q..P.T.I.AK.LET.KTAYSN----SPKPA.HI.EQLSHDTG-----------.DM.VVQV......A.E.RLK 38224.0
Lhx3/4      Xb S..P.T.I.AK.LET.KNAYSN----SPKPA.HV.EQLSNETG-----------.DM.VVQV......A.E.RLK DN11429
055         Nv S..A.TFISND.LAF.KVAYAS----SPKT.L.D.ER..KETG-----------.DM.VVQV......A.D.RLS DQ206345 (newly assigned)
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Lhx 6/8 family

```
LHX6        Hs A..A.TSF.AE.LQVMQAQ.AQ----DNNPDAQTLQKL.DMTG-----------.SR.V.QV....C.ARH..HT NP_055183
LHX8        Hs A..A.TSF.AD.LQVMQAQ.AQ----DNNPDAQTLQKL.ERTG-----------.SR.V.QV....C.ARH..HV NP_001001933
Lhx6/8      Bf P..V.T.F.EE.LRV.QAN.NI----DSNPDGQDLER..QITG-----------.SK.VTQV....S.ARQ..YG
awh         Dm T..V.T.F.EE.LQV.QAN.QI----DSNPDGQDLER..SVTG-----------.SK.VTQV....S.ARQ..HI NP_523907
lim-4       Ce T..V.T.FAED.LSV.QTY.NR----DSNPDGADLEK..SMTG-----------.SK.VTQV....S.ARQ..WH
Awh1        Cg  ..V.SSF.EE.LQI.QAN.RI----ESNPDSQELNR..ITAG-----------VSR.VAQV....A.ARQ..
Awh2        Cg  ..V.T.F.ED.LQV.QAN.QL----DSNPDGQDLER..QITG-----------.SK.VTQV....S.ARQ..
Lhx6/8      Ip S..S.T.FSED.LKI.QAN.NL----DSNPDGQDLER..QQTG-----------.SK.V.QV....A.SRQ..HM DN27657_c1_g1_i1|m.11322
Lhx6/8      Sr S..S.T.FSED.LKV.QAN.NM----DSNPDGQDLER..SQTG-----------.SK.V.QV....A.SRQ..HL DN123001_c0_g1_i1|m.72616
Lhx6/8      Hm T..S.T.FSEE.LKV.QAN.SL----DSNPDGQDLER..QMTG-----------.SK.V.QV....A.SRQ..HL DN1193_c0_g1_i1|m.357
Lhx6/8      Nw KR.H.TMFHRY.LEQ.KES.KT----.SNPSSIDVEYI.KSVN-----------S.K.IIQV....A.S.QQRRL 51594.0/1
Lhx6/8      Xb A..V.T.F.EE.LQI.QAN.NL----DSNPDGQDLER..QLTG-----------.SK.VTQV....S.ARQ..NN DN81776
LHX6/8 044 Nv A..V.T.F.ED.LQI.QAN.NI----DSNPDGQDLER..QLTG-----------.SK.VTQV....S.ARQ..YG DQ206316
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Lmx family

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LMX1A       Hs P..P.TIL.TQ.RRAFKAS.EV----SSKPC.KV.ETL.AETG-----------.SV.VVQV....Q.A.M..LA
LMX1B       Hs P..P.TIL.TQ.RRAFKAS.EV----SSKPC.KV.ETL.AETG-----------.SV.VVQV....Q.A.M..LA NP_002307
            Bf P..P.TIL.TQ.RREFKAL.EV----SPKPC.KV.ETL.AETG-----------.SV.VVQV....Q.A.M..LA
CG32105     Dm P..P.TIL.SQ.RKQFKAS.DQ----SPKPC.KV.EAL.KDTG-----------.SV.VVQV....Q.A.M..IQ NP_729801
CG4328      Dm P..P.TILNTQ.RRAFKAS.EV----SPKPC.KV.ENL.KDTG-----------.SL.IVQV....Q.A.V..IQ NP_648567
lim-6       Ce P..P.TILNAQ.RRQFKTA.ER----SSKPS.KV.EQL.NETG-----------.SV.VVQV....Q.A.I..L.
Lmx1        Cg  ..P.TIL.TS.RRKFKQA.EA----.PKPC.KV.EQL.AETG-----------.TI.VVQV....Q.A.V..
Lmx2        Cg  ..P.TIL.TS.RRKFKSA.EL----.PKPC.KV.EQL.AETG-----------.SV.VVQV....Q.A.V..
Lmx         Ip PC.K.VIL.TQ.RRAFKAA.DL----SSKPC.KV.EQL.RETG-----------.SV.VVQV....E.A.V..LA DN72227_c0_g9_i2|m.162480
Lmx         Hm PC.K.VIL.TQ.RRAFKAA.DV----SSKPC.KV.EQL.RDTG-----------.SV.VVQV....E.A.V..LA DN41603_c0_g1_i1|m.29404
Lmx         Sr PC.K.VIL.TQ.RRAFKAA.DL----SSKPC.KV.EQL.RDTG-----------.SV.VVQV....E.A.V..IG DN127948_c0_g1_i1|m.101565
Lmx a       Nw  RSK.VIL.TT.RRIFRTA.DV----SQKPS.KVKERL.DETG-----------.PV.IVQV....E.A.G..LA 50222.0
Lmx b       Nw VG.K.VIL.HN.RRVLRAA.IV----SQKPS.KVKEDLGGATQ-----------.PV.IVQV....E.A.V..LA 14051.0
Lmx c       Nw  G.K.VLL.NP.RRIFRSA.TI----SDKPC.RVKEGL.MMTQ-----------.PI.IVQV....E.A.MR.LS 7973.0
Lmx d       Nw HNNK.VNLNNM.RHILLAAYET----SHKPT.SMKETL.EQTG-----------.PM.IVQV....E.A.C..MA 48370.0
Lmx e       Nw GS.K.VVL.PE.RKIFQQA.DM----SPKPS.KV.EQL.SECT-----------VSM.FIQV....Q.A.M..LA 52392.0
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Lmx f      Nw GS.K.VVLSPE.RKIFQLA.DA----SAKPS.KV.EDL.NKCS-----------VSM.FIQV....Q.A.M..LA 49053.0
Lmx        Xb PC.K.IIL.TQ.RRIFKAA.EV----SSKPC.KV.ESL.AETG-----------.SV.VVQV....Q.A.V..LA DN87622
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LIM CLASS / family membership ambiguous

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           Ip NNNT.KPLKREIAEH.RAY.DK----.SKP.KPE.E.L.NQLG-----------ITE.V.QI......S.DRRVA DN68501_c2_g1_i1|m.110831
           Sr KRGPGNHLKGP.ADY.RSYYLT----.QKPSKEE.DA..AEIG-----------VEAKT.AT......S.E.IRR DN123163_c0_g1_i1|m.73968
           Hm KA.K.TVFTQQ.LAV.QSR.AI----KQILS.QEYANL.DEIG-----------VKIPIVRV....Y.QRS.TNS DN8120_c0_g2_i1|m.2184
```

POU CLASS

Pou2 family

```
POU2F1     Hs .RKK.TSIETNIRVA...S.LE----.QKP.SEEITM..DQ.N-----------MEKEV.RV..C...Q.E.RIN NP_002688
POU2F2     Hs .RKK.TSIETNVRFA...S.LA----.QKP.SEEILL..EQ.H-----------MEKEV.RV..C...Q.E.RIN NP_002689
POU2F3     Hs KRKK.TSIETNIR.T...R.QD----.PKPSSEEISM..EQ.S-----------MEKEVVRV..C...Q.E.RIN NP_055167
           Bf .RKK.TSIETNVRVA...A.IQ----.PKP.SEEIGI..EQ.G-----------MEKEVVRV..C...Q.E.RIN
Nub        Dm .RKK.TSIETTIRGA...A.LA----.QKP.SEEITQL.DR.S-----------MEKEVVRV..C...Q.E.RIN NP_476659
pdm2       Dm .RKK.TSIETTVRTT...A.LM----.CKP.SEEISQLSER.N-----------MDKEV.RV..C...Q.E.RIN NP_723763
ceh-18     Ce .R.K.TNLDMN.RNA.DTF.AL----.PRPDHDKMTD..NS.E-----------.DRDVVRV..C...Q.MRRVD
Pou2       Cg  RKK.TSIETNIRVA...S.QQ----.PKPSSEEITSV.DQ.S-----------MEKEVVRV..C...Q.Q.R
Pou2 a     Ip KRKK.SCIDSNCRET..QL.DQ----.NHP.PDEIVKYSE..N-----------MEPET.R...S...Q.Q.RLA DN55409_c0_g2_i1|m.41119
Pou2 b     Ip KRKR.CVIDAHTKKT..QS.RD----KPHPSPDETNAL.E..G-----------.DRETVR...T...YRERRSE DN18113_c0_g1_i1|m.7284
Pou2       Sr .RKR.TCIDVKTKKA..QFYND----KPHP.HEECCA..E..N-----------QDRNT.R...G...QRD.RLM DN116892_c2_g1_i1|m.50278
Pou2       Hm .RKK.ASIETKSK.A...S.SL----.SKP.AEQINLL.DQ.I-----------MERETVRV..C...Q.E.RVP DN43708_c0_g1_i1|m.40060
Pou2       Xb  RKK.TSIETNVRVA...A.LS----.PKP.SEEIQML.ES.C-----------MEKEVVRV..C...Q.E.R DN87006
```

Pou3 family

```
POU3F1     Hs KRKK.TSIEVGVKGA..SH.LK----CPKPSAHEITGL.DS.Q-----------.EKEVVRV..C...Q.E.RMT NP_002690
POU3F2     Hs KRKK.TSIEVSVKGA..SH.LK----CPKPSAQEITSL.DS.Q-----------.EKEVVRV..C...Q.E.RMT NP_005595
POU3F3     Hs KRKK.TSIEVSVKGA..SH.LK----CPKPSAQEITNL.DS.Q-----------.EKEVVRV..C...Q.E.RMT NP_006227
POU3F4     Hs KRKK.TSIEVSVKGV..TH.LK----CPKPAAQEISSL.DS.Q-----------.EKEVVRV..C...Q.E.RMT NP_000298
POU3       Bf KRKK.TSIEVTVKGA..SH.LK----QPKPSAQEIAQL.DS.Q-----------.EKEVVRV..C...Q.E.RMT
POU3L      Bf KRKK.TSIEVSVKGA..TF.YK----QPKPSAIEISQLSEG.N-----------.DKEVVRV..C...Q.ERRMS
vvl        Dm KRKK.TSIEVSVKGA..QH..K----QPKPSAQEITSL.DS.Q-----------.EKEVVRV..C...Q.E.RMT NP_523948
ceh-6      Ce KRKK.TSIEVNVKSR..FH.QS----.QKPNAQEITQV.ME.Q-----------.EKEVVRV..C...Q.E.RIA
Pou3       Cg  RKK.TSIEVTVKGA..NH.MK----QPKPAAQEISQL.EQ.Q-----------.EKEVVRV..C...Q.E.R
Pou3       Hm KRKK.TSIEVGIKGA..NH..L----QPKPAAPEITGL.DS.Q-----------.EKEVVRV..C...Q.E.RMN DN20967_c0_g1_i1
Pou3       Sr KRKK.TSIEVSIKNA..HN..I----QPKPSAHEISAL.NS.Q-----------.EKEVVRV..C...Q.E.RMT DN123138_c1_g2_i1|m.73697
Pou3       Ip KRKK.TSIEVTIKGA..QH..L----H                                                 DN88733_c0_g1_i1
Pou3       Nw KRKK.TSIEMSVKGA..NH.MK----QAKPCAPEIQAL.DS.Q-----------.DKEVVRV..C...Q.E.RMT 27996.0
Pou3       Xb KRKK.TSIEVTVKGV..SH.QK----QPKPSAQDITNL.ES.Q-----------.EKEVVRV..C...Q. DN83679
POU3a125   Nv KRKK.TSIEVAVKGA..NH.CK----SPKP.AQEISAL.EN.G-----------.DKEVVRV..C...Q.E.RMT DQ206344
```

```
POU3b075   Nv KRKR.TIIEKNVKGV..NH.EK----MPRPSTSDISSL.ES.G-----------.DREVVRV..C...Q.ERRVS DQ206327
```

Pou4 family

```
POU4F1     Hs K..K.TSIAAPEKRS..AY.AV----QPRPSSEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RMK NP_006228
POU4F2     Hs K..K.TSIAAPEKRS..AY.AI----QPRPSSEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RMK NP_004566
POU4F3     Hs ...K.TSIAAPEKRS..AY.AI----QPRPSSEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RMK NP_002691
POU4       Bf K..K.TSIAAPEKRS..AY.AV----QPRPSSEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RMK
acj6       Dm K..K.TSIAAPEKRS..AY.AV----QPRPSGEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RIV NP_727845
unc-86     Ce K..K.TSIAAPEKRE..QF.KQ----QPRPSGERIAS..DR.D-----------.KKNVVRV..C.Q.Q.Q.RDF
Pou4       Cg  ..K.TSIAAPEKRS..AY.AV----QPRPSGEKIAQ..EK.D-----------.KKNVVRV..C.Q.Q.Q.R
Pou4       Ip K..K.TSIAAPEKRS..AY.TV----QPRPSGEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RLK DN75504_c0_g2_i7|m.225572
Pou4       Sr K..K.TSIAAPEKRS..AY.TV----QPRPSGEKISA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RLK DN125354_c0_g1_i1|m.85350
Pou4       Hm K..K.TSIAAPEKRS..AY.AV----QPRPSGEKIAA..EK.D-----------.KKNVVRV..C.Q.Q.Q.RLK DN7261_c0_g1_i1|m.1968
Pou4       Nw R..K.TSIASPEKRS..AY.AV----QPRPSSEKIGQ..DK.D-----------.KKNVVRV..C.Q.Q.Q.RLK 9311.1
POU4(124)  Nv K..K.TSIGAAEKRS..AY.AM----.PRPSSDKIAS..EK.D-----------.SKNVVRV..C.Q.Q.K.RMK DQ206292
```

Pou6 family

```
POU6F1     Hs KRKR.TSF.PQAIEA.NAY.EK----.PLP.GQEIT...KE.N-----------YDREVVRV..C...QTL.NTS NP_002693
POU6F2     Hs KRKR.TSF.PQALEI.NAH.EK----.THPSGQEMT...EK.N-----------YDREVVRV..C.K.QAL.NTI NP_009183
           Bf KRKR.TSF.PQALEV.NAH.EK----.THPSGAEMTAL.EK.N-----------YDREV.RV..C.K.QAL.NTI
pdm3
/CG11641   Dm KRKR.TSF.PQALEL.NAH.ER----.THPSGTEITGL..Q.G-----------YEREV.R...C.K.QAL.NTV NP_610377
Pou6       Cg  RKR.TSF.PQALEV.NNF.ER----.THPSGAEMTELSDK.N-----------YDREV.RV..C.K.QAL.N
Pou6       Hm SRKK.TQFSAET.IF.NDY.EK----ITHPRGFQINE..NT.Q-----------.DREVVRV..C.K.QLM.SKD DN37913_c0_g2_i2|m.19890
Pou6       Nw KRKR.TSFPPAAIDI.NSY.LK----.SHPSGHEFTQLSRL.E-----------HDREV.RV..C.K.QAMRHYA 52441.0
Pou6       Xb  RKR.TSF.PAALEI.NVH.EK----.THPSGSEMTE..SK.N-----------YDREVVRV..C.K.QAL. DN93613
NVHD084    Nv KRKR.TSFSNEA.RL.ISH.EQ----.PKPSSSEIAQ..SK.G-----------.EPVTVRV..C..KQML.RMA DQ206280
```

Pou family amb

```
           Nw .RKR.TSLNPDVREK.EAH.EV----.SRPGANQIFV.SEH.S-----------.DREVVRV..C.RRQ.I.RVN 53834.0
                                                                                          46372 added aa in end
```

HNF CLASS

Hmbox family

```
HMBOX1     Hs    .RGS.F.WRKECLAVM.SY.NE.Q.PDEAK.E...N.CN-----AVIQKPGKKLSDLERV.SLKVYN..A...KEI.RRA
HMBOX1A    Bf    .RGH.FNWPEACITIM..Y.EE.Q.PDEKK.E..TN.CN-----SVIQKPGVELPAQMLVNSARVYN..A...KDV.RRH
HMBOX1B    Bf    .RGSKFHWPPSAVMIV..Y.QQ.P.P.EGE.D...N.CN-----SVLQKPGEDLPSYKLVSPVRVQT..I...REA.IKQ
Hmbx-1     Ce    QR.E.YVFRPILIRM..SF.TQTPFPDLP..V...N.CN---HVLKMDKKGVGLMPKEVVSPQVVSN..A.K.KELRRR
Hmbox      Ip    K..D.FVWKENCVAL...YYEA.P.PDDT..E...A.CN------QLNGNSGSGQEERVV.AVKVYN..A...KEV.RK. DN65023_c0_g1_i1|m.79542
Hmbox      Sr    K..D.FVWKESCVCL...FY.V.P.PDDAK.E...Q.CN------QLIDSTGQGHDEKLV.AVKVYN..A...KEI.RKN DN121592_c0_g1_i4|m.66335
```

```
Hmbox       Hm    K..D.FVWKDSCVSI..QFYQE.S.PDDLK.E...Q.CN-----NALELQGQFLNDEKLV.SVKVYN..A...KEI.RKQ DN37226_c0_g1_i1|m.18864
Hmbox       Nw       E.FVWREECMPV.DKF.NENQYPDDRKREDIASACN-GVLEAPGVHIPGERLVTPAKVPAKVYN..V...NSY.IKM 48953.0
Hmbox       Xb        RS.INWDPSAVNI.EHH.NTK--------..FPNAFE.ET..ANINGACHSKGRKV.AHH.QT..N...N.RTGVS DN90583 (Hnf?)
```

SINE CLASS

Six 1/2 family

```
SIX1        Hs GEETSYCFKEKSRGV.REWYAH----.P.PSP.EKR.L.E.TG-----------..TT.VSN..K...QRDRAAE NP_005973
SIX2        Hs GEETSYCFKEKSRSV.REWYAH----.P.PSP.EKR.LTE.TG-----------..TT.VSN..K...QRDRAAE NP_058628
SIX1/2      Bf GEETSYCFKEKSRGV.REWYAH----.P.PSP.EKR.L.E.TG-----------..TT.VSN..K...QRDRAAE
so          Dm GEETSYCFKEKSRSV.RDWYSH----.P.PSP.EKRDL.E.TG-----------..TT.VSN..K...QRDRAAE NP_476733
ceh-33      Ce GEETSYCFRDKSRVL.RDWYCR----.S.PSP.EKR.L.EKTH-----------..VT.VSN..K...QRDRAGV
ceh-34      Ce GEETNYCFKSKSRNV.RDAYKK----CQ.PSVEDKRRL.QQTE-----------.SII.VSN..K.K.QRERAAG
Six1_2      Cg  EETSYCFKEKSRTI.REWYQH----.P.PSP.EKREL.EATG-----------..TT.VSN..K...QRDRA
Six1/2      Ip GEETSYCFKEKSRNM.RDYYGH----.P.PSP.EKRDL.EATD-----------.SIT.VSN..K...QRDRALE DN45560_c0_g1_i1|m.24666
Six1/2      Sr GEETSYCFKEKSRNM.REYYQH----.P.PSP.EKRDL.ENTD-----------.SVT.VSN..K...QRDRALE DN87552_c0_g1_i1|m.17761
Six1/2      Hm GEETSYCFKEKSRNV.RDYYLH----.P.PSP.EKRDL.EATD-----------..II.VSN..K...QRDRALE DN32866_c0_g1_i1|m.13539
Six1/2      Xb GEETSYCFKEKSRTV.REWYSH----.P.PSP.EKRELSDGTG-----------..VT.VSN..K...QRDRAAE DN63639
SIX1/2073   Nv GEETSYCFKEKSRNI.REWYSH----.P.PSP.EKR.L.EGTG-----------..TT.VSN..K...QRDRAAE DQ206326
```

Six 3/6 family

```
SIX3        Hs GEQKTHCFKERTRSL.REWYLQ----DP.PNPSKKR.L.Q.TG-----------..PT.VGN..K...QRDRAAA NP_005404
SIX6        Hs GEQKTHCFKERTRNL.REWYLQ----DP.PNPSKKR.L.Q.TG-----------..PT.VGN..K...QRDRAAA NP_031400
Six3/6      Bf GEQKTHCFKERTRSL.REWYLQ----DP.PNPQKKR.L.Q.TG-----------..PT.VGN..K...QRDRAAA
optix       Dm GEQKTHCFKERTRSL.REWYLQ----DP.PNPTKKR.L.K.TG-----------.NPT.VGN..K...QRDRAAA NP_524695
ceh-32      Ce GEQKTHCFKERTRSL.REWYLK----DP.PNPPKKK.L.N.TG-----------..QM.VGN..K...QRDRAAA
Six3_6      Cg  EQKTHCFKERTRNL.REWYLQ----DP.PNPTKKR.L.S.TG-----------..PT.VGN..K...QRDRA
Six3/6      Ip GEQKTHCFKERTRGL.REYYLT----DP.PNPNKKK.L.QLTG-----------..PT.VGN..K...QRDRAAA DN62049_c0_g2_i3|m.62452
SixX3/6     Sr GEQKTHCFKERTRGL.REYYLT----DP.PNPNKKK.L.QLTG-----------..PT.VGN..K...QRDRAAA DN126162_c1_g1_i3|m.89990
Six3/6      Hm GEQKTHCFKERTRGL.REWYLQ----DP.PNPAKKR.L...TG-----------..PT.VGN..K...QRDRAAA DN28007_c0_g1_i1|m.9588
Six3/6 a    Nw GEQKTHCFKERTRNL.REWYLQ----DP.PNPQKKR.L.A.TG-----------..PT.VGN..K...QRDRAAA 36924.0
Six3/6 b    Nw GEQKTHCFKERTRNL.REWYLQ----DP.PNPQKKR.L.G.TG-----------..PT.VGN..K...QRDRAAA 42137.0
Six3/6 a    Xb GEQKTHCFKERTRSL.REWYLQ----DP.PNPTKKR.L.Q.TG-----------..PT.VGN..K...QRDRAAA DN23152
Six3/6 b    Xb EAQTTRLFQKNTLSV.KDFYQS----DP.PNLNKIKDL.R.TR-----------.SPI.IRT..K...QRDRIAA DN97213
SIX3/6128   Nv GEQKTHCFKERTRSL.REWYLQ----DP.PNPTKKR.L.Q.TG-----------..PT.VGN..K...QRDRAAA DQ206294
```

Six 4/5 family

```
SIX4        Hs GEETVYCFKEKSRNA.KELYKQ----...PSPAEKRHL.KITG-----------.SLT.VSN..K...QRDRNPS NP_059116
SIX5        Hs GEETVYCFKERSRAA.KACYRG----...P.PDEKRRL.TLTG-----------.SLT.VSN..K...QRDRTGA NP_787071
SIX4/5      Bf GEETVYCFKEKARQA.KEMYNN----...P.PDEKRNL.KKTG-----------..LT.VSN..K...QRDRTPS
six4        Dm GEETVYCFKEKSRNA.KDCYLT----...P.PDEKKTL.KKTG-----------..LT.VSN..K...QRDRTPQ NP_649256
unc-39      Ce GEEIVYSFKDSSRKF.KQFFRN---VSE.P.QEQKR..SRATG-----------.KIV.ISN..K...QRDKSN
```

```
Six4_5      Cg  EETIYCFKEKSRQS.KECYKN----.R.P.PDEKRNL.KKTG-----------..LT.VSN..K...QRDRT
Six4/5      Ip GEETVYCFKEKSRAK.KDSYRR----.K.PSPEEKRSL.KSSG-----------..LT.VSN..K...QRDRTPH DN26501_c1_g1_i1
Six4/5      Sr GEETIYCFKEKSRNK.KESYKK----.K.P.PEEKKAL.KNSG-----------..LT.VSN..K...QRDRTPH DN118860_c2_g1_i2|m.56407
Six4/5      Hm GEETVYCFKEKARRK.KESYKK----.K.P.PEEKKSL.KASG-----------..LT.VSN..K...QRDRAPT DN66848_c0_g1_i1|m.42105
Six4/5      Xb  EETVYCFKEKSRQA.KECYRR----.R.P.PEEKRSL.KMTG-----------..LT.VSN..K...QRDRAPK DN120045
SIX4/5a030 Nv GEETVYCFKEKARAA.KDCYEQ----.K.P.PQEKRL..KQTN-----------..LK.VSN..K...QRGRIPS DQ206264
SIX4/5b061 Nv GEKTIYFFKEKVRTV.KECYEH----KK.P.LKEKRV..TQTN-----------..L..VRN..R...HRDRISS DQ206322
```

TALE CLASS

Irx family

```
IRX1        Hs DPGRPKNA.RES.ST.KAWLNEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_077313
IRX2        Hs DPAY.KNA..DA.AT.KAWLNEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_150366
IRX3        Hs DPSRPKNA.RES.ST.KAWLNEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_077312
IRX4        Hs SGTR.KNA..ET.ST.KAWLQEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_057442
IRX5        Hs DPAY.KNA.RDA.AT.KAWLNEHRK-...P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_005844
IRX6        Hs GAGR.KNA..ET.ST.KAWLNEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_077311
IRXA        Bf DGAR.KNA..ET.AT.KAWLMEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL....
IRXB1       Bf DGTR.KNA..DA.ST.KAWLNEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL....
IRXB2       Bf DGTP.KNA..DA.ST.KAWLNEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL....
ara         Dm LAAR.KNA..ES.AT.KAWLNEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_524045
caup        Dm LAAR.KNA..ES.AT.KAWLSEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_524046
mirr        Dm NGAR.KNA..ET.ST.KAWLNEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... NP_524047
irx-1       Ce DGIKKRNA..EA.AP.KDWLHSHRK-.P.PSKADKVML.VGTG-----------M.LT.VST..A.A.RRL....
Irx1        Cg  AARRKNA..ET.SA.KAWLYEHRK-.PYP.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL..
Irx2        Cg  NARRKNA..ET.NT.KAWLYEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL..
Irx3        Cg  GGRRKNA..ET.AP.KAWLKEHMK-.P.P.KAEKVML.IVTK-----------M.LT.IST..A.A.RRL..
Irx4        Cg  AARRKNA..ET.NT.KAWLYEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL..
Irx a       Ip SSIR.KNAS.ET.AA.KAWLYEHRN-.P.P.KGEK.ML.IITK-----------M.LT..ST..A.A.RRL.... DN44510_c0_g1_i1|m.23508
Irx a       Sr SSMR.KNAS.ET.AA.KTWLFEHRK-.P.P.KGEK.ML.IITK-----------MSLT..ST..A.A.RRL.... DN126498_c0_g1_i4|m.91973
Irx a       Hm CNIR.KNTS.ET.AA.KSWLYEHRN-.P.P.KGEKVML.IITK-----------M.LT.VST..A.A.RRL.... DN21447_c0_g3_i1|m.6190
Irx a       Nw SGMRRKNSS.ET.QY.KSWLKHHQK-.P.P.KGEK.ML.ILTK-----------M.LT.VST..A.S.RRI.     26582.1
Irx a       Xb GMMRKKSA..ET.NA.KAWLREHRR-.P.P.KSEK.ML.IITK-----------M.LT.VST..A.A.RRL. DN63799
Irx b       Ip MITR.KNA..ET.SA.KAWLNDHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... DN66612_c1_g4_i2|m.91737
Irx b       Sr MITR.KNA..ET.SA.KAWLSEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... DN127996_c1_g1_i3|m.101906
Irx b       Hm GIAR.KNA..ET.SA.KAWLSEHKK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL.... DN36375_c0_g1_i1
            (sequencing issue, remove one A from a polyA stretch)
Irx c       Ip SSPASPSAVKES.YP.RVWMEENRA-.P.P.KNQKLIL.LVTK-----------..LT.VST..A.A.RRL...R DN73792_c1_g1_i1
Irx c       Sr SSPNSATAVKEN.YP.RVWLEENRD-.P.P.KSEKLMLSIVTK-----------M.LT.VST..A.A.RRL...R DN123214_c0_g1_i1
Irx d       Sr ALGR.KNA..ET.AA.KSWLQDHLK-.P.P.KGEKVML.IITK-----------MSLT.VST..A.A.RRL...G DN126207_c1_g2_i3|m.90240
Irx d       Hm PLAR.KNA..ET.AA.KTWLNDHLK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL...G DN24763_c0_g1_i1|m.8213
Irx d       Ip                           .P.P.KGEKVML.IITK-----------MSLT.VST..A.A.RRL...G DN71570_c5_g7_i5
```

```
Irx b       Nw VGCRRKNA..ET.SA.KTWLADHRK-.P.P.KAEK.ML.VITK-----------M.LT.VST..A.A.RRL. 10005.0
Irx b       Xb  GVARRKNA.ET.SA.KAWLHEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL. DN84998
Irx c       Nw LGLRRKNA..ET.SP.KAWLYEHRK-.P.P.KAEK.ML.IITK-----------M.LT.VST..A.A.RRL. 28871.0
Irx d       Nw NGIRRKNA..ET.ST.KAWLYEHRK-.P.P.KGEK.ML.VITK-----------M.LT.VST..A.A.RRL. 36182.0
Irx e       Nw PGIRRKNA..ET.ST.KAWLYEHRK-.P.P.KGEK.ML.IITK-----------M.LT.VST..A.A.RRL. 48316.0
IRX (108)   Nv AGAR.KNA..ET.ST.KAWLFEHRK-.P.P.KGEK.ML.ILTK-----------M.LT.VST..A.A.RRL.... DQ206288
```

Meis family

```
MEIS1       Hs .HKK.GIFPKVA.NIMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM NP_002389
MEIS2       Hs .QKK.GIFPKVA.NIMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM NP_002390
MEIS3       Hs .NKK.GIFPKVA.NIMRAWLFQHLS-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM NP_001009813
Meis        Bf .QKK.GIFPKVA.NIMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM
hth         Dm NQKK.GIFPKVA.NI.RAWLFQHLT-HP.PSEDQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM NP_476577
unc-62      Ce KSRG.GIFPKQA.NR.RQWLFQNLT-HP.PSEEQKKQL.KETG-----------..IL.VNN..I.A.RRIVQPM
Meis        Cg                IMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQ
Meis        Ip PQKK.GIFPKTA.NIMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.V                DN70650_c1_g5_i7
ext above   Ip                             P.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM DN69333_c0_g4_i5
Meis        Sr PQKK.GIFPKTA.NIMRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM DN129314_c1_g2_i3|m.111748
Meis a      Hm PQKK.GIFPKAA.NIMRTWLFTNLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM DN34684_c0_g1_i2|m.15334
Meis b      Hm PQKK.GIFPKAA.NIMRSWLFTNLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIVQPM DN37189_c0_g1_i1|m.18754
Meis a      Xb HQKK.GIFPKSA.NVMRAWLFQHLS-HP.PSEEQKKQL.QETG-----------..IL.VNN..I.A.RRIV    DN64910
Meis b      Xb YQKK.GIFPKSA.NILRAWLFQHLT-HP.PSEEQKKQL.QDTG-----------..IL.VNN..I.A.RRIV    DN79707
MEIS (107)  Nv SQKK.GIFPKAA.NIMKAWLFQHLT-HP.PSEEQKRSL.QETG-----------..IL.VNN..I.A.RRIVQPM DQ206227
```

Pbx family

```
PBX1        Hs AR.K.RNFNKQA.EI.NEY.YSHLS-.P.PSEEAKE.L.KKCG-----------I.VS.VSN..G.K.IRY..NI NP_002576
PBX2        Hs AR.K.RNFSKQA.EV.NEY.YSHLS-.P.PSEEAKE.L.KKCG-----------I.VS.VSN..G.K.IRY..NI NP_002577
PBX3        Hs AR.K.RNFSKQA.EI.NEY.YSHLS-.P.PSEEAKE.L.KKCS-----------I.VS.VSN..G.K.IRY..NI NP_006186
PBX4        Hs AR.K.RNFSKQA.EV.NEY.YSHLN-.P.PSEEAKE.L.RKGG-----------..IS.VSN..G.K.IRY..NM NP_079521
PBX         Bf NR.K.RNFSKQA.EV.NEY.YSHLS-.P.PSEEAKE.L.RKCG-----------I.VS.VSN..G.K.IRF..NI
exd         Dm AR.K.RNFSKQASEI.NEY.YSHLS-.P.PSEEAKE.L.RKCG-----------I.VS.VSN..G.K.IRY..NI NP_523360
Ceh-20      Ce AR.K.RNFSKQA.EV.NEY.YGHLS-.P.PSEEAKEDL.RQCN-----------I.VS.VSN..G.K.IRY..NM
Ceh-40      Ce AR.K.RNFSKTS.EI.NEY.LANIN-HP.PSEEVKQAL.MQCN-----------ISVA.VSN..G.K.IRY..TM
Ceh-60      Ce QG.K.RNFDKNT.DI.QNW..DHRQ-.P.PSDQEKA.L.KQCN-----------IKIS.VNN..G.Q.IRT.QQA
Pbx         Cg  R.K.RNFSKQA.EL.NEY.YSHLS-.P.PSEEAKE.L.RKCG-----------I.VSQVSN..G.K.IRY..
Pbx         Ip AR.K.RNFSKQASEI.NEY.YSHLN-.P.PSEEVKE.L.KKCC-----------.SVS..SN..G.K.IRY..NI DN70276_c2_g3_i3|m.132878
Pbx         Sr AR.K.RNFSKQASEI.NEY.YSHLN-.P.PSEEVKE.L.KKCG-----------.SVS..SN..G.K.IRY..NI DN127821_c2_g3_i2|m.101192
Pbx         Hm AR.K.RNFSKQASEI.NEY.YSHLC-.P.PSEEVKE.L.KKCC-----------.SVS..SN..G.K.IRY..NI DN21081_c0_g1_i1|m.5973
Pbx a       Nw AR.K.RNFNKTA.EV.NEY.YSHLS-.P.PSEEVKEDL.KKCN-----------LSIS.VSN..G.K.IRY..NI 52332.1 A
Pbx b       Nw AR.K.RNFNKTA.EV.NEY.YSHLS-.P.PSEEVKEDL.KKCG-----------LSIS.VSN..G.K.IRY. 52332.1 B
Pbx c       Nw AR.K.RNFNKNA.EF.NEY.YSHLN-.P.PSEETKE.L.KKCG-----------LSIS.VSN..G.K.IRY. 52537.0
```

```
Pbx        Xb AR.K.RNFNTNA.QI.NEY.YSHLS-.P.PSEEVKE.L.RKCG-----------..VS..SN..G.K.IRY. DN68543
PBX (040)  Nv YR.K.RNFSKQA.EI.NEY.YSHLS-.P.PSEEAKE.L.RKCN-----------ISVA..SN..G.K.IRY..NI DQ206245
```

Pknox family

```
PKNOX1     Hs S.NK.GVLPKHA.NVMRSWLFQHIG-HP.P.EDEKKQ..AQTN-----------..LL.VNN..I.A.RRILQPM NP_004562
PKNOX2     Hs S.NK.GVLPKHA.NIMRSWLFQHLM-HP.P.EDEKRQ..AQTN-----------..LL.VNN..I.A.RRILQPM
PKNOX      Bf .NGK.GILPKQA.DVMRSWLFQHIV-HP.P.EDEKRA..NQTN-----------..LL.VNN..I.A.RRILQPM
Pknox      Cg  .SK.GVLPKHA.QVMKSWLFQHIV-HP.P.EDEKRQ..NQTN-----------..LL.VNN..I.A.RRILQ
Pknox      Ip K.TK.GVLPKHA.QIMRQWLFQHIV-HP.P.EDEKRQ..VQTN-----------..LL.VNN..I.A.RRILQPM DN69528_c1_g2_i3|m.122462
Pknox      Hm K.TK.GVLPKQA.QIMRSWLFQHIV-HP.P.EDEKRQL.QQTS-----------..LL.VNN..I.A.RRILQPM DN37578_c0_g1_i2|m.19358
Pknox      Sr K.TK.GVLPKHA.QIMRQWLFQHIV-HP.P.EDEKRQ..VQTN-----------..LL.VNN..I.A.RRILQPM DN128964_c2_g7_i4|m.109271
Pknox      Nw KVSK.GILPKHA.SVMRSWLFQHIV-HP.P.EDEKRQL.GQTG-----------..LL.VNN..I.A.RRILQPM 45317.0 added aa
Pknox      Xb    K.GVLPKQA.NIMRSWLFQHIV-HP.P.EDEKRQ..VQTN-----------..LL.VNN..I.A.RRILQPM DN74939
NVHD036    Nv R.SK.GVLPKQA.SIM.TWL.QHIM-HP.P.EDEKRS..QQTN-----------..IL.VNN..I.A.RRILQPM DQ301954
NVHD143    Nv ARKR.GKLPESARTR.MTWLFAHSN-RP.P.EEEKSNL.TITG-----------..PI..NN..S.A.RRIL.KA DQ301952
```

Tgif family

```
TGIF1      Hs KR.R.GNLPKESVQI.RDWLYEHRY-.A.PSEQEKALLSQQTH-----------.STL.VCN..I.A.RRLLPDM NP_003235
TGIF2      Hs KRKR.GNLPKESVKI.RDWLYLHRY-.A.PSEQEKLSLSGQTN-----------.SVL..CN..I.A.RRLLPDM
TGIF2LX    Hs K.KRKGNLPAESVKI.RDWMYKHRF-KA.PSEEEKQMLSEKTN-----------.SLL..SN..I.A.RRILPDM
TGIF2LY    Hs K.KRKGNLPAESVKI.RDWMYKHRF-KA.PSEEEKQMLSEKTN-----------.SLLR.SN..I.A.RRILPDM
TGIF       Bf ARKR.GNLPKEAVQI.RAWLYDHRY-.A.P.DAEKLDL.REAG-----------.TVL.VCN..I.A.RRILPDM
achi       Dm LRKR.GNLPKTSVKI.KRWLYEHRY-.A.PSDAEKFTLSQEAN-----------..VL.VCN..I.A.RRILP.M NP_725182
vis        Dm LRKR.GNLPKSSVKI.KRWLYHRY.-.A.PSDAEKFTLSQEAN-----------..VL.VCN..I.A.RRILP.M NP_523714
Tgif       Cg  R.R.GNLPKEAVRI.KTWLYEHRY-.A.PSDQEKVYLSS.TN-----------..VL.VCN..I.A.RRILP
Tgif       Ip E.KK.GSLPKEAICIMRSWLEQHRY-HA.P.EQEKLSL.QQTN-----------..PL.VCN..I.A.RRVLPEI DN71480_c1_g4_i4
Tgif       Sr L.KQ.GTLPKEAVDILRSWLELHRY-HA.P.EQEK.SLSE.TN-----------..PL.VCN..I.A.RRILPAL DN142180_c0_g1_i1|m.133360
Tgif       Hm M.KK.GNLPKESVEVMK.WLNEHRY-.A.PNETEKNQL.EKAN-----------..VL.VCN..I.A.RRILPEM DN12757_c0_g1_i1|m.3416
Tgif       Xb  ..R.GNLPKDAVNV.RLWLYEHRF-.A.P.EQEKVELSEKAS-----------.SVL.VCN..I.A.RRILPDM DN45414
TGIF (149) Nv P..R.GNLPKDSVNV.RLWLWEHRF-.A.PSEAEKQYLSK.AN-----------.SVL.VCN..I.A.RRILPDM DQ206298
```

TALE CLASS / Family membership ambiguous

```
           Sr SEARSASFNDNALEV.KEWLEGHLD-HP.IE.SDILK.QTRTS-----------.SRK..MG.CT.I.RRRLTII DN106703_c0_g1_i2
           Ip SR.RSKDQIEED.VPLRHWLLLHSG-HPFP..VEKKRL.RECG-----------.QLK.VED..L.T.RRIL.HH DN68679_c0_g2_i1
```

CUT CLASS

Onecut family

```
ONECUT1    Hs P.KP.LVF.DV.RRT.HAI.KE----.KRPSKELQ.T.SQQ..-----------.ELSTVSNF.M.A.RRSLDKW NP_004489
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ONECUT2     Hs Q.KS.LVF.DL.RRT.FAI.KE----.KRPSKEMQ.T.SQQ.G-----------.ELTTVSNF.M.A.RRSLEKW NP_004843
Loc390874   Hs P.KQ.LVF.DL.RRT.IAI.KE----.KRPSKEMQVT.SQQ.G-----------.ELNTVSNF.M.A.RRCMNRW XP_372702
ONECUT      Bf P.KP.LVF.DL.RRT.HAI.KE----.KRPSKEMQAQ.AKQ.G-----------.DLSTVCNF.M.A.RRSQDKW
onecut      Dm P.KP.LVF.DL.RRT.QAI.KE----TKRPSKEMQVT..RQ.G-----------.EPTTVGNF.M.A.RRSMDKW NP_524842
ceh-21      Ce V.VI.LTF.ET.LKS.QKS.QQ----.HRPT.EMRQKLSAT.E-----------.DFSTVGNF.M.S.RRLRIDQ
ceh-38      Ce S.RP.LVF.DI.KRT.QAI.KE----TQRPS.EMQQT.AEH.R-----------.DLSTVANF.M.A.RRSRLGG
ceh-39      Ce  RIR.FTF.QT.LDS.HTV.QQ----QDRPN.EMQQALSAT.K-----------.NRSTVGNF.M.A.RRLPKAA
ceh-41      Ce P.KTKSPF.EHEIAVMMAL.EI----.KSPNHEEVQKLAVQ.N-----------.GYRSVANF.M.K.A.ER.KL
ceh-48      Ce P.KT.LVFSDI.RRT.QAI.RE----TKRPS.EMQIT.SQQ.N-----------.DPTTVANF.M.A.RRGHDLK
ceh-49      Ce TP.A.CLLSQD.KSQ.SIF.ET----.PRPDSLEMKQLGST.N-----------.CKSTIINY.T.M.RRKATSS
Onecut      Cg  .KP.LVF.DI.RRT.HAI.KE----TKRPSKEMQAT.AQQ.G-----------.EVTTVANF.M.A.RRSLD
Onecut a    Ip Q.KN.LVF.DI.RRT.FAI.RE----TKRPSKEMQLQ.SRQ.G-----------.EPTTVSNF.M.A.RRCGDRW DN36933_c0_g1_i1|m.17321
Onecut b    Ip M.KS.LVF.DL.RRT.RAI.QE----SQRPSKESQAQ..KQ.G-----------.EVTTVSNF.M.A.RRCGDRW DN31212_c0_g1_i1|m.13546
Onecut a    Sr T.KN.LVF.DL.RRT.FAI.RE----TKRPSKEMQ.T.SRQ.G-----------.EQSTVSNF.M.A.RRCSDRW DN125608_c1_g1_i1|m.86741
Onecut b    Sr S.KS.LVF.DI.RRT.RAI.QE----TQRPSKESQVQ.GKQ.G-----------.EVSTVSNF.M.A.RRCGDRW DN117560_c0_g1_i1|m.52153
Onecut      Hm P.KI.LVF.DI.RRT.YAI.RE----TKRPSKEMQQT.GQQ.G-----------.DPTTVSNF.M.A.RRCMGDR DN40002_c0_g1_i1|m.24477
Onecut      Nw   KQ.LVF.DL.RRT.HAI.KE----TQRPSKEMQLQ..SQ.G-----------.QLTTVSNF.M.A.RRSVDKW 46342.0
Onecut      Xb                      RE----TKRPSKEMQMT..QQ.G-----------.ELSTVSNF.M.A.RRSLDKW DN97994
            Nv S.KI.RQF.ET.KRT.FAI.KE----TKKPTKDMQKAV.EE.G-----------.DLNSVANF.M.A.RRHTDA  XP_001637067.1
```

CUT class ambiguous

```
            Nw S..L.YSLDDDSKRFLLSVYQH----VTHPSQDTISRL.TH.N-----------MQPATVYN......QRF.VKD 35933
            Nw LRARTVISQKDRAIMFQHFLTR----.Q...ANELLHLSRS.D-----------IPQPT.R.F...LRARIRART 53646.0
            Xb N.IRRINL.TREKNR.LEAYNN----EP.PSPQTIEGL.QELG-----------IRQTTVNN..H.H.SRS.RTK DN95119
            Xb RR.RTTLSDHAKRVMTTYFMTT----SR.LSADA.MAFSQQLG-----------.S.ETVR.F.K.L.ANT.NM  DN91240
```

ZF CLASS

Zfhx family

```
ZFHX2 I     Hs .RFS.TKF.EF..QA.QSF.ET----SA.PKDGEVERL.SL.G-----------LAS.VVVV....A.Q.AR.NA
ZFHX2 II    Hs D..L.T.ILPE.LEI.YRWYMQ----DSNP..KMLDC.SEEVG-----------.KK.VVQV....T.ARER.GQ
ZFHX2 III   Hs QR.Y.TQMSSL.LKIMKACYEA----Y.TP.MQECEVLGEEIG-----------.PK.V.QV....A.A.E..AK NP_207646
ZFHX3 I     Hs N..P.TRI.DD.LRV.RQY.DI----.NSPSEEQIK.M.DKSG-----------.PQKV..H..R.TLF.ERQR.
ZFHX3 II    Hs KRSS.TRF.D..LRV.QDF.DA----.A.PKDDEFEQLSNL.N-----------.PT.V.VV....A.Q.AR.NY
ZFHX3 III   Hs D..L.T.I.PE.LEI.YQKYLL----DSNP..KMLDH...EVG-----------.KK.VVQV....T.ARER.GQ
ZFHX3 IV    Hs Q..F.TQM.NL.LKV.KSC.ND----Y.TP.MLECEVLGNDIG-----------.PK.VVQV....A.A.E..SK
ZFHX4 I     Hs F..P.TRI.DD.LKI.RAY.DI----.NSPSEEQIQ.M.EKSG-----------.SQKV..H..R.TLF.ERQR.
ZFHX4 II    Hs KRSS.TRF.D..LRV.QDF.DT----.A.PKDDEIEQLSTV.N-----------.PT.V.VV....A.Q.AR.SY
ZFHX4 III   Hs D..L.T.I.PE.LEI.YEKYLL----DSNP..KMLDHI.REVG-----------.KK.VVQV....T.ARER.GQ
ZFHX4 IV    Hs H..F.TQMSNL.LKV.KAC.SD----Y.TP.MQECEMLGNEIG-----------.PK.VVQV....A.A.E..FK
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ZFHX I      Bf G..P.TRI.DE.LKI.RAH.DI----.NSPSEDQIL.MSEKSG-----------.PTKV..H..R.TLF.ERQRN
ZFHX II     Bf RRAG.TRF.DY.IKV.QEF.EQ----.A.PKDDDLEHLSKI.N-----------.SP.V.VV....A.Q.AR.SF
ZFHX III    Bf N..L.T.I.PE.LEI.YQKYQI----DCNP..KMLDL..REVG-----------.KK.VVQV....T.ARER.GQ
ZFHX IV     Bf G..Y.TQMSNL.LKM.KSA.TE----YKTP.MQECEILGNEIG-----------.PK.VVQV....A.A.D..SK
zfh2 I      Dm N..L.T.ILPE.LNF.YECYQS----ESNPS.KMLE..SKKVN-----------.KK.VVQV....S.A.D..SR NP_524623
zfh2 II     Dm KRAN.TRF.D..IKV.QEF.EN----.S.PKDSDLEYLSKL.L-----------.SP.V.VV....A.QKQR.IY
zfh2 III    Dm N..L.T.ILPE.LNF.YECYQS----ESNPS.KMLE..SKKVN-----------.KK.VVQV....S.A.DK.SR
ZC123.3 I   Ce A..A.TRI.DD.LKV.RQY.NI----.NSPSEAQIKEMSQKAS-----------.P.KV..H..R.TLFKERQRD
ZC123.3 II  Ce RRAN.TRF.DF.LRT.QQF.DK----QAYPKDDDLEALSKK.Q-----------.SP.V.VV....A.Q.AR.IY
ZC123.3 3   Ce N..F.THL.PM.VQMMKSV.NE----YKTPSMAECELLGKEVG-----------.HK.VVQV....A.A.ER.TR
Zfhx        Cg Q..A.TRINDE.LKI.RAH.DI----.NSPSEEQINAMSEQSG-----------.PQKV.KH..R.TLF.ERQRN
            Cg KRAN.TRF.DY.IKV.QEY.EQ----.A.PKDDELDHLSQM.N-----------.SP.V.VV....A.Q.AR.IY
            Cg D..L.T.ILPE.LDY.YQKYQI----DCNPS.KQLETISAEVG-----------.KK.VVQV....T.ARER.GQ
            Cg G..Y.TQM.SL.VRIMKSI.ID----YKTP.MAECEMLGREIG-----------.PK.VVQV....A.A.E..AK
3550-3700   Ip SKQP.TKISDE.LAI.KQN.DI----SNSPSEEQYLAISVQTG-----------.PMKV..H..R.TLF.ERQKD DN75125_c1_g6_i2|m.217565
3950-4050   Ip KRAT.TRF.DH.IKA.QDF.DQ----.P.PRDDDLETLSKN.N-----------.SP.VVVV....Q.Q.ARRSL DN75125_c1_g6_i2|m.217565
4750-4940   Ip FR.M.T.ISPD.LEV.YEKYGE----.SNPS.SEMEA.SA.VG-----------.SR.VVQV.Y..T.ARQRRGQ DN75125_c1_g6_i2|m.217565
5540-5620   Ip ...H.TNLSML.IKT.KSI.AE----YKTP.MTECET.GSE.N-----------.SK.VVQV....A.S.E..IQ DN75125_c1_g6_i2|m.217565
4784-4963   Sr QKQP.TKISEP.LEI.KQN.DI----SNLPSEEKY.ALSQQTG-----------.PVKV..H..R.TLF.ERQKD DN127982_c1_g1_i6|m.101793
5225-5404   Sr KRAT.TRF.DH.IKS.QDF.DQ----.P.PRDDDLENLSKS.S-----------.SP.VVVV....Q.Q.ARRSM DN127982_c1_g1_i6|m.101793
6167-6346   Sr FR.M.T.ISPD.LEI.YTKYGE----.SNPS.TEMET.ASSVG-----------.SR.VVQV.Y..T.ARQRRGQ DN127982_c1_g1_i6|m.101793
6977-7156   Sr K..H.THLSNV.VRT.KAM.LD----FKTPSMGECEQ.G.E.G-----------.SK.VVQV....A.S.E..GK DN127982_c1_g1_i6|m.101793
2704-2883   Hm QK.P.TRISDE.LKI.KDH.DL----SNSPTDSEVDQ..IKTG-----------.QGKV..H..R.TLF.ERQK. DN33495_c0_g1_i4|m.14054
3046-3225   Hm .RAS.TRFSDF.LKS.QEF.ER----.A.PRDEDLEKLSKS.N-----------.SP.VVVV....Q.Q.ARRNI DN33495_c0_g1_i4|m.14054
3628-3807   Hm DKRI.TTISPA.LEV.YSSYQE----DSNPS.QMLE..CAKVG-----------.KR.VVQV....T.ARQR.GA DN33495_c0_g1_i4|m.14054
4459-4638   Hm .R.Y.THLSVT.IKIFKVI.AD----YKTPTMSDCEVLGSQ.D-----------.PK.VVQV....A.S.E..AR DN33495_c0_g1_i4|m.14054
I           Nw  K.P.TRITDD.LKV.RTH.DI----.NSPNDDQIAN.SQETV-----------.PVKV.KH..R.TLF.ERQRN 60532.0
II          Nw KRAG.TRFTDW.IQK.QEF.EI----.A.PKDDDLDTLSKDLS-----------.NP.V.VV....Q.Q.AR.SF 64721.0
III         Nw DR.L.TSITPK.LNT.YKW.KE----.SNPS.KMLEI.SVDVS-----------.KK.VVQV....T.ARQR.AS 50181.0
IV          Nw D..Y.TQLSHL.IRV.KACYVD----YKTPTMNECE.LGKTIG-----------.AK.VVQV....A.A.D..SK 50181.0 is one protein.
I           Xb TK.P.TRITDE.LKI.RAY.DI----.NSPSEEQII.MSEKSG-----------.PQKV.KH..R.TLF.ERQRN DN93733
II          Xb RRAG.TRFTDF.IKR.QEF.DT----.AYPKDDDLDRLSKELN-----------.NP.V.VV....A.Q.AR.SF DN93733
III         Xb DR.L.TTITPE.LEI.YEKYQE----.SNPS..MLDI.SREVG-----------.KK.VVQV....T.ARQR.GQ DN93733
IV          Xb G..F.TQMSNT.LKV.KHC.TE----Y.TPTMQECELLGSCIG-----------.QK.VVQV....A.A.E..SK DN93733
```

ZF CLASS / Family membership ambiguous

```
            Sr ERKK.TV..DK.LET.REYYVK----QPNPNSDDIEK..NNIG-----------..KRNVQV....K.ARD..NP DN130571_c0_g1_i2|m.121942
            Ip ERKK.TV..DQ.LDT.KEYYIR----QPNP.SDDIER..SVIG-----------..K.NVQV....K.ARD..NP DN55547_c0_g2_i6|m.41438
            Hm QRKK.TVF.DF.QKM.RELYKI----.SSPTSEEISKL.DNIG-----------.SKRSIQV....K.ARD..SR DN34160_c0_g1_i1|m.14868

            Ip .H.T.TKLPAAELAL.K.IYET----.PSPSKKQFA.L.RRTS-----------.PIKVLKV....T.RLTRNTC DN61481_c0_g1_i1|m.60009
```

```
          Sr .H.T.TKL.QSEVVL.KSIYEN----TPSPSK.QFE.L.NSTG-----------.PTKVL.V....T.RLRRNTC DN108290_c0_g1_i1|m.33236
          Hm .H.V.TRL.AQDL.Y.HNMYRR----TANPS.RLLA..SNHIG-----------.PL.V.QV....T.RLM.NTC DN42050_c0_g2_i1|m.31057
```

Cers CLASS

```
LASS2      Hs NIKEKTRLRAPPNAT..HFYLTS---GKQPKQVEVELLSRQSG-----------.SG..VER..RR..NQDRPSL NM_022075
LASS3      Hs FGIKETVRKVTPNTV..NF.KHS---T.QPLQTDIYGL.KKCN-----------.....VER..RS..NQERPSR NP_849164
LASS4      Hs GVRDQTRRQVKPNAT...H.LTE---GHRPKEPQLSLL.AQCG-----------..LQ.TQR..RR..NQDRPQL
LASS5      Hs GIEDSGP.QAQPNAI...V.ISI---TK.PDKK.LEGLSKQ.D-----------WNV.K.QC..RH..NQD.PPT NP_671723
LASS6      Hs NIQANGPQIAPPNAI...V.TAI---TKHPDEK.LEGLSKQ.D-----------WDVRSIQR..RQ..NQE.PST
CERS       Bf LGIPGERKYAEPNAI...V.TSI---TKNPDEK.LQGL.KQ.D-----------WS...VQR..RR..NQDRPTL
Lag1/schlk Dm GI.SSRPKKAANVPI...TYAK----STR.DKKKLVPLSKQTD-----------MS..E.ER.WRL..AQD.PST NP_652526
Cers       Cg   IKDGRPKTVQPISALENSYRI---KKFPSEDTVKGLEKQTD-----------M..RE.QR..RM..NQERP
Cers       Ip GISP.GPRKPVHNAI..RV.HTI---TQKPDEK.LKGLEKQ.D-----------WSPY..RQ..AR..AQIRPTK DN63567_c1_g1_i1|m.70349
Cers       Sr GICP.GARKPYPNAI.ERV.LTI---TQRPDEKHLKGLEKQ.DC----------WNQYKIKQ..AL..AQLRPSK DN124898_c2_g4_i2
Cers       Hm VLPST.QP.PQPNAI.DKVYTSI---ARDPDAV.LAGL.KQ.D-----------WSIR.VQV..IA..ALDRPSH DN30308_c0_g1_i1|m.11388
Cers a     Nw IRSSSNQLRPIDNLV.ERVYLSV---SRTPDDS.LKGLSKQ.D-----------WS.KQVEA..HL..AQDRAS  51994.0
Cers b     Nw  IKAKKPSNGGLINPVLEEAYGK---CTRPNREAIKGM.KKAD-----------MEADRVER..RR..QQDQP   44536.0
Cers c     Nw   RSSNHLRAVDNLV.ERVYASV---SRNPDGN.IKGLSKQ.D-----------WN.KQVQA..HL..AQDRSS  40648.1
Cers d     Nw  QIKPKQRNSKSIHP.LEQVYKD---KSSPPDKVIE.L.KK.D-----------SEPPK.RR..SR.HRHDQP   62117.0
Cers a     Xb       RLRAPPNAT.EHFYLTS---GKQPKQVEVELLSRQSG-----------LSGRQVER..RR..NQDRPSL DN112933
Cers b     Xb GLKIPARH.PEDNTI.EKVYRSV---SKQPDAK.IEGL.KQ.D-----------WSERQVQR..RR..NSDRPS  DN87293
           Nv  GVKDKKINFTPNPFCEKVYQTI---.KFPPSD.ILGLSKQIG-----------W.T.EVER..RH...QS.PSL XP_001635937.1
```

Pros Class

```
PROX1      Hs GSAMQEGLSPNHLKKAKLM.FY----T..PSSNMLKTYFSDVKFNR--------CITS.LIK..S.F.EFYYIQM NP_002754
PROX2      Hs LVHIQEGLNPGHLKKAKLM.FF----T..PSSNLLKVYFPDVQFNR--------CITS.MIK..S.F.EFYYIQM
PROX       Bf SPPHPGSL.PTHLKKAKLM.FY----T..PSSSTLKQHFPDVKFNR--------CITS.LIK..S.F.EFYYIQM
Pros       Dm TPLHSSTL.PMHLRKAKLM.FW----V..PSSAVLKMYFPDIKFNK--------NNTA.LVK..S.F.EFYYIQM FBpp0293145
Ceh-26     Ce GGGSSSML.PMHLRKAKLM.FY----T..PNSNLLKSYFPDIRFNK--------NNTA.LVK..S.F.EFYYNQM
Pros X1    Cg LDHWNGTL.PMHLRKAKLM.FY----V..PSSAILKVYFPDVKFNK--------NNTA.LVK..S.F.EFYYIQM
Prox       Ip AVGSTDNL.ANHLRKAKLM.FF----Q..P.SSTLRQYFTDVKFNR--------HNNA.LIK..S.F.EYYYIQI DN52339_c0_g1_i2
Prox       Hm HSLAAE.L.ANHLKKAKLI.FY----Q..PNPSTLRMYFPDVRFNR--------QNNG.LIK..S.F.EYFYNQI DN24356_c0_g1_i1
Prox       Sr VVQMTENL.ANHLRKAKLM.FY----Q..PNSAILRQFFVDVKFNR--------SNNA.LIK..S.F.EYYYIQI DN113132_c0_g1_i1
Prox a     Nw NQGWATNL.PNHLKKAKLM.FY----T..PSSAVLRLHFPDVRFSR--------HNNA.LIK..S.F.EFFYLQI 44308.0
Prox b     Nw ASFWTSNL.PEHLKKAKLM.FY----T..P.SAMLRINFPDVRFTR--------HINA.LIK..S.F.EYFYIQI 51275.0
Prox       Xb SSGWNTNL.PSHLKKAKLM.FY----V..PNSATLRQHFPDVKFTR--------HNNA.LIK..S.F.EYFYIQI DN88028
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Ambiguous class membership

```
Sr MR.RTTISRSAKQVMF.WYLSN----G....ADG.SLLSSH.G-----------...ENVRVF.K.L.RLE..CE DN122932_c0_g2_i2|m.72688
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Hm IR.RTTIPKFAKKVMIDWYLGN----G....TEG.QLL.SQ.Q-----------...ENVRVF.            DN36591_c0_g1_i1|m.17917

Sr SS.H.CLFNSH.INL.KSL.EV----.AFPKKAELSIL.NH.R-----------KDRESLRK..DK..LNFRRQG DN113631_c0_g1_i3|m.42241
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Sr A..RKHILKFE.VSI..NYFHI----DSSWKMATVEKA.AE.G-----------.PVKKVYK.GYD.KHVSRNLG DN132449_c0_g1_i1|m.132246
Ip ...A.KSF.LQ.KSV.ST..SA----.QRPS.H.ISQL.SE.N-----------..SASVANF.A.S.QRN.HIS DN66473_c2_g1_i2|m.89822
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Xb KR.LRTVFSDT.INT..QA.RF----SP.IN.EV.VKLSEITG-----------.SDNA.Q.......ARQR.TG DN95135
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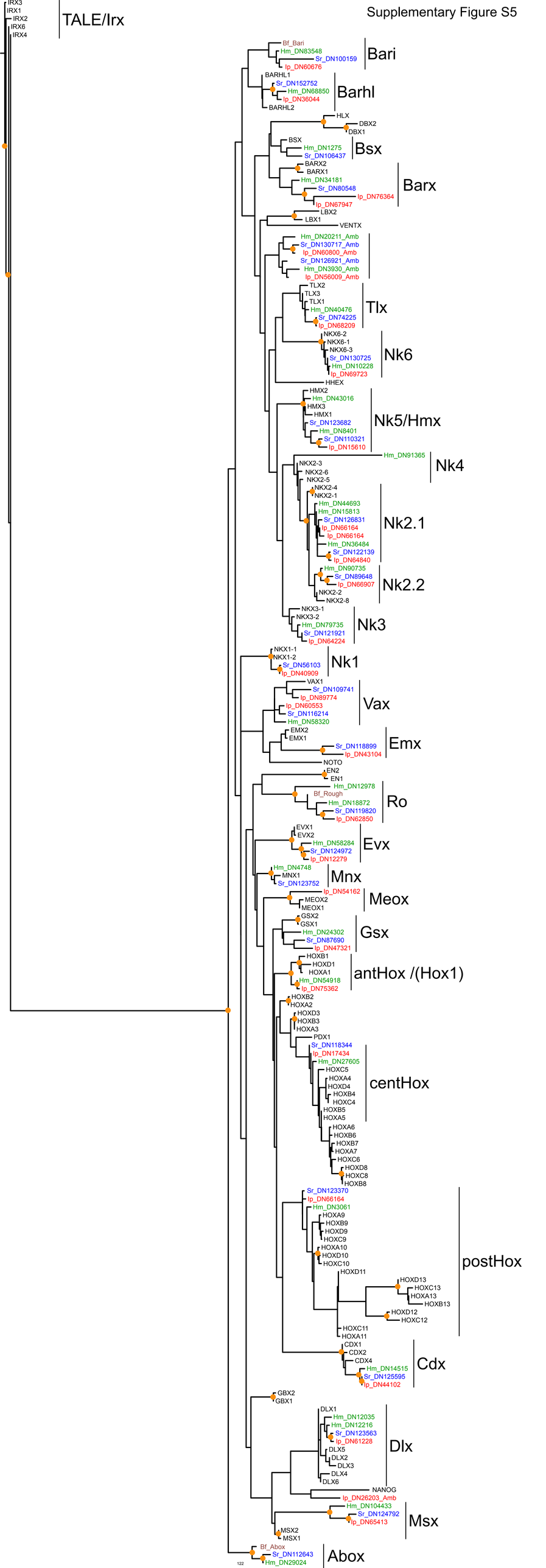
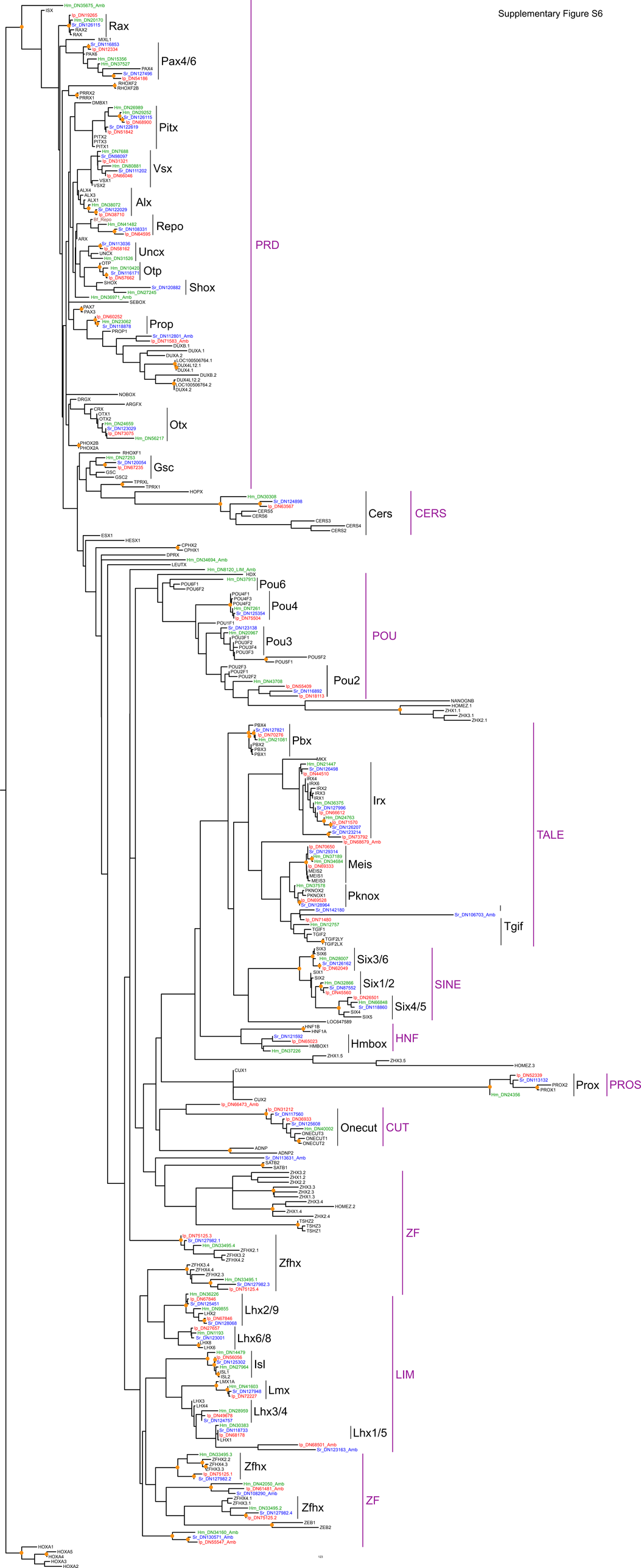
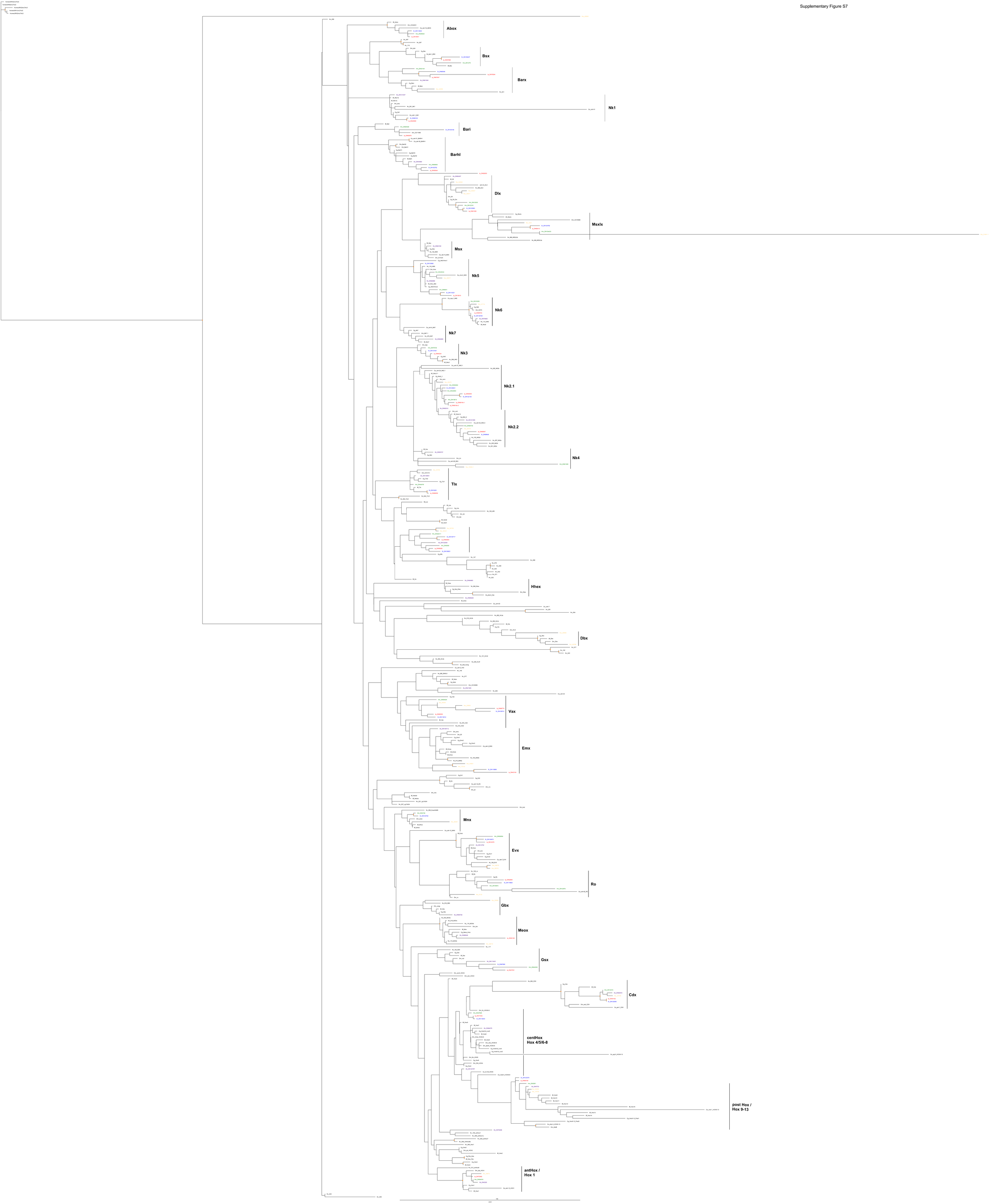
Supplementary Figure S5



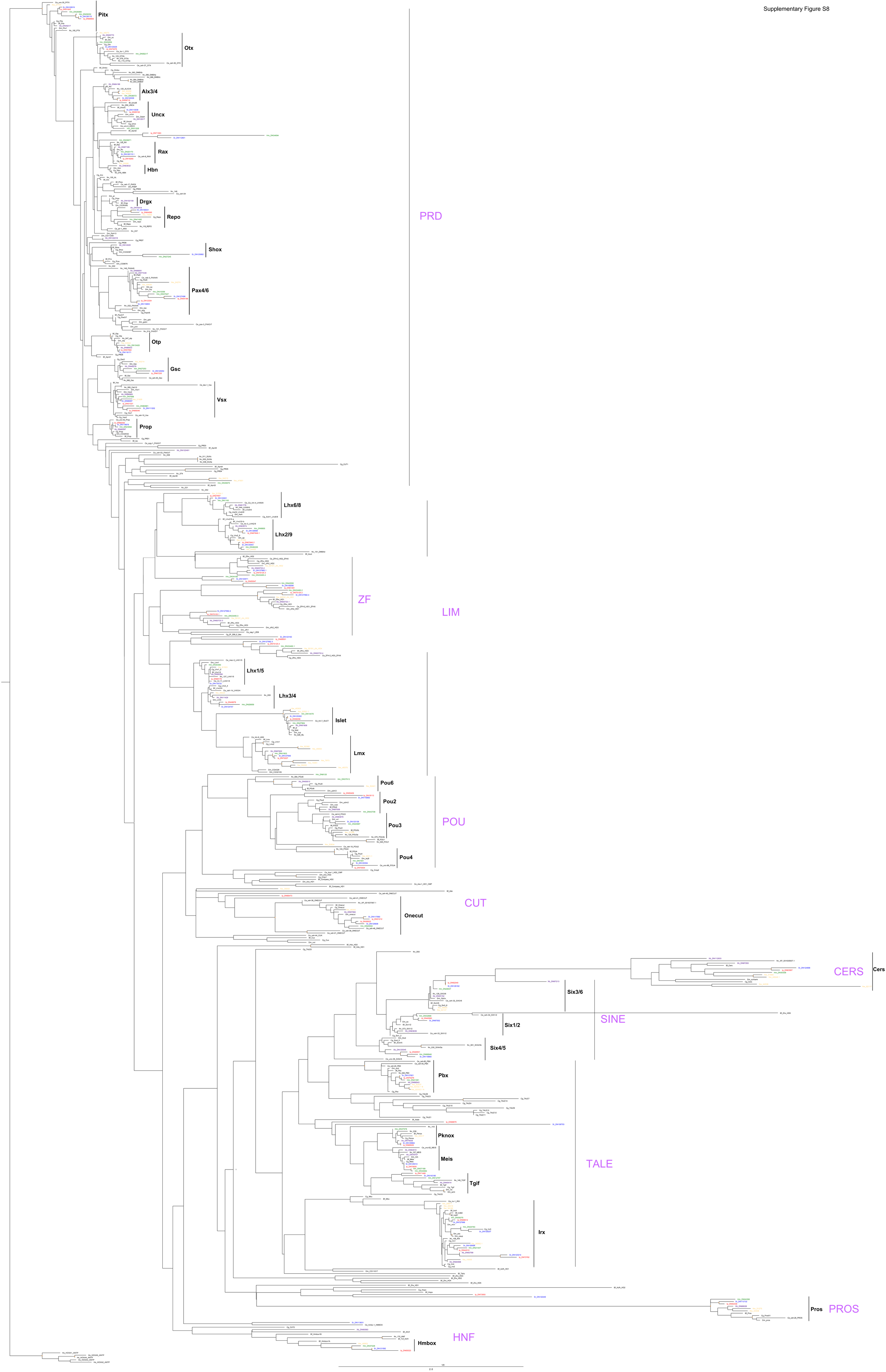
Supplementary Figure S6



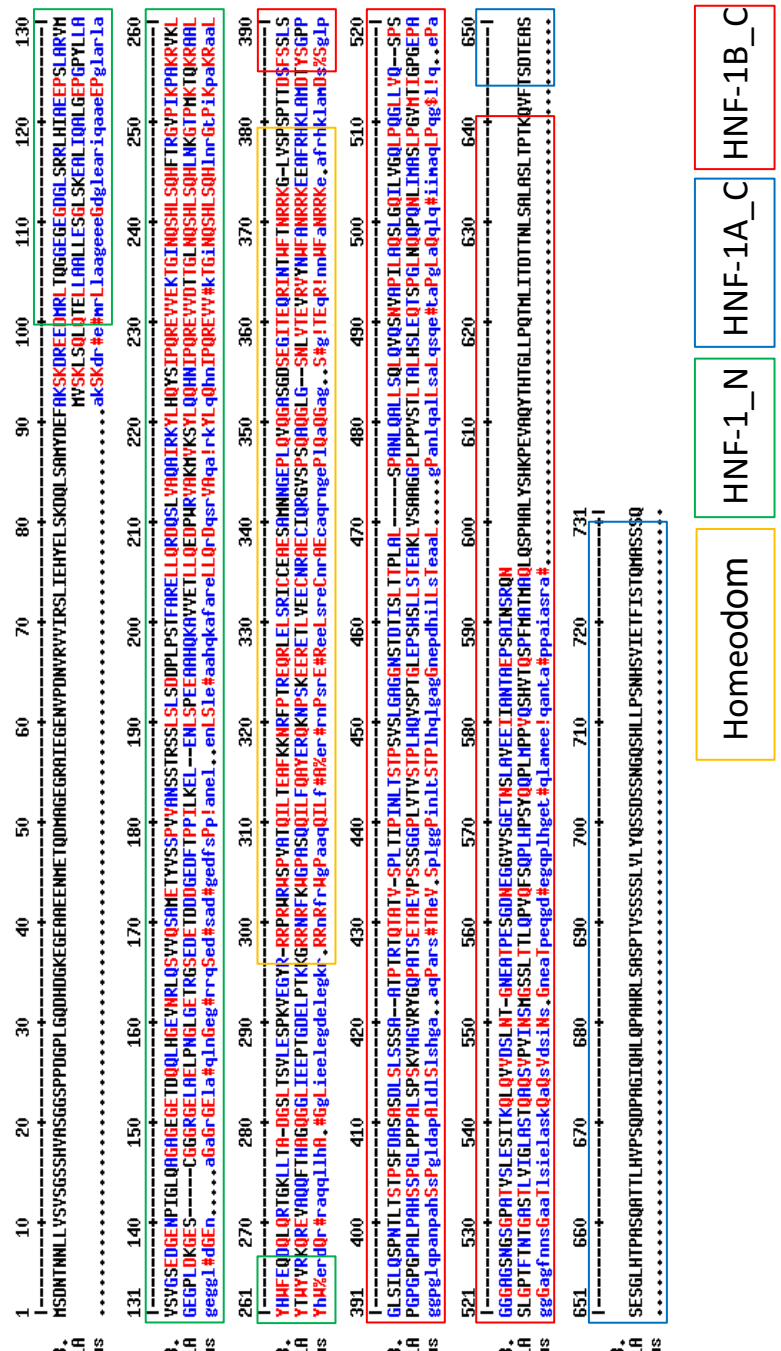
Supplementary Figure S7



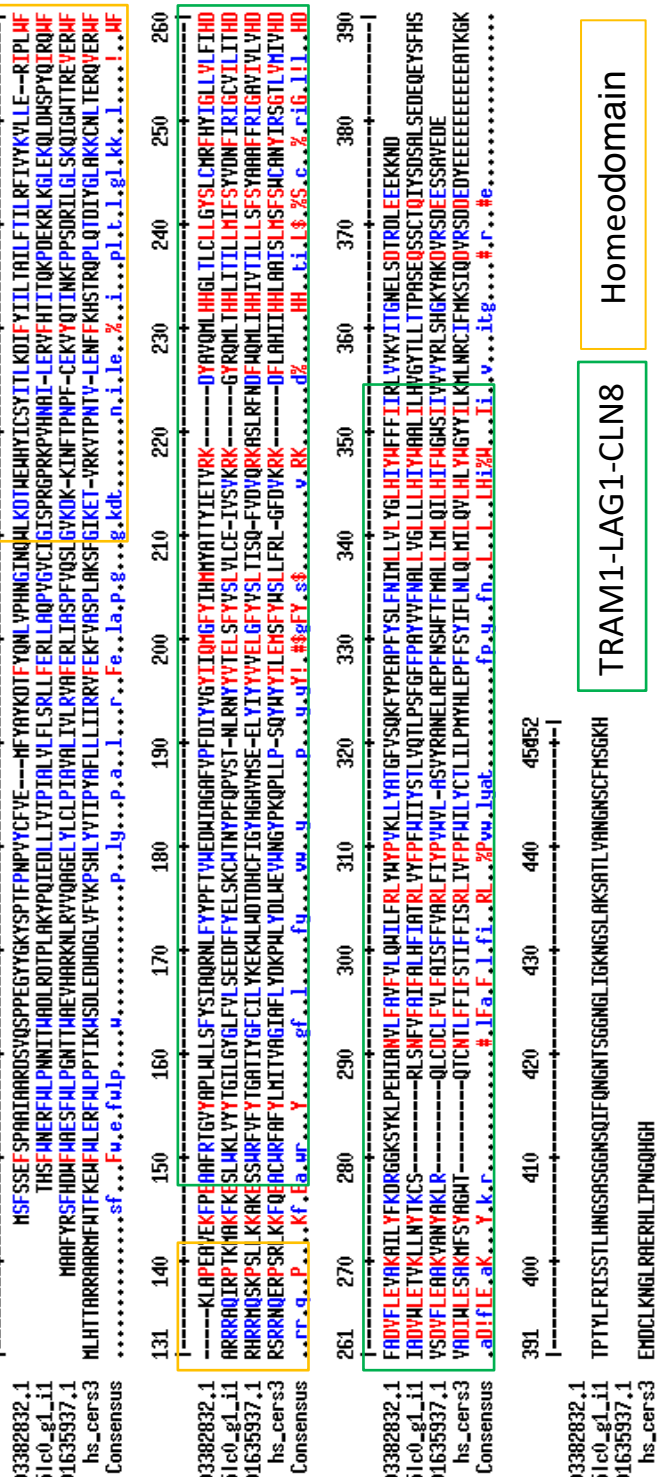
Supplementary Figure S8



Suppl. Figure S9: Human HNF1A vs Aq XP_003390473.1



Suppl. Figure S10: CERS class genes of Aq, Ip, Nv, Hs



Supplementary Table S11

ANTP HD sequences

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