

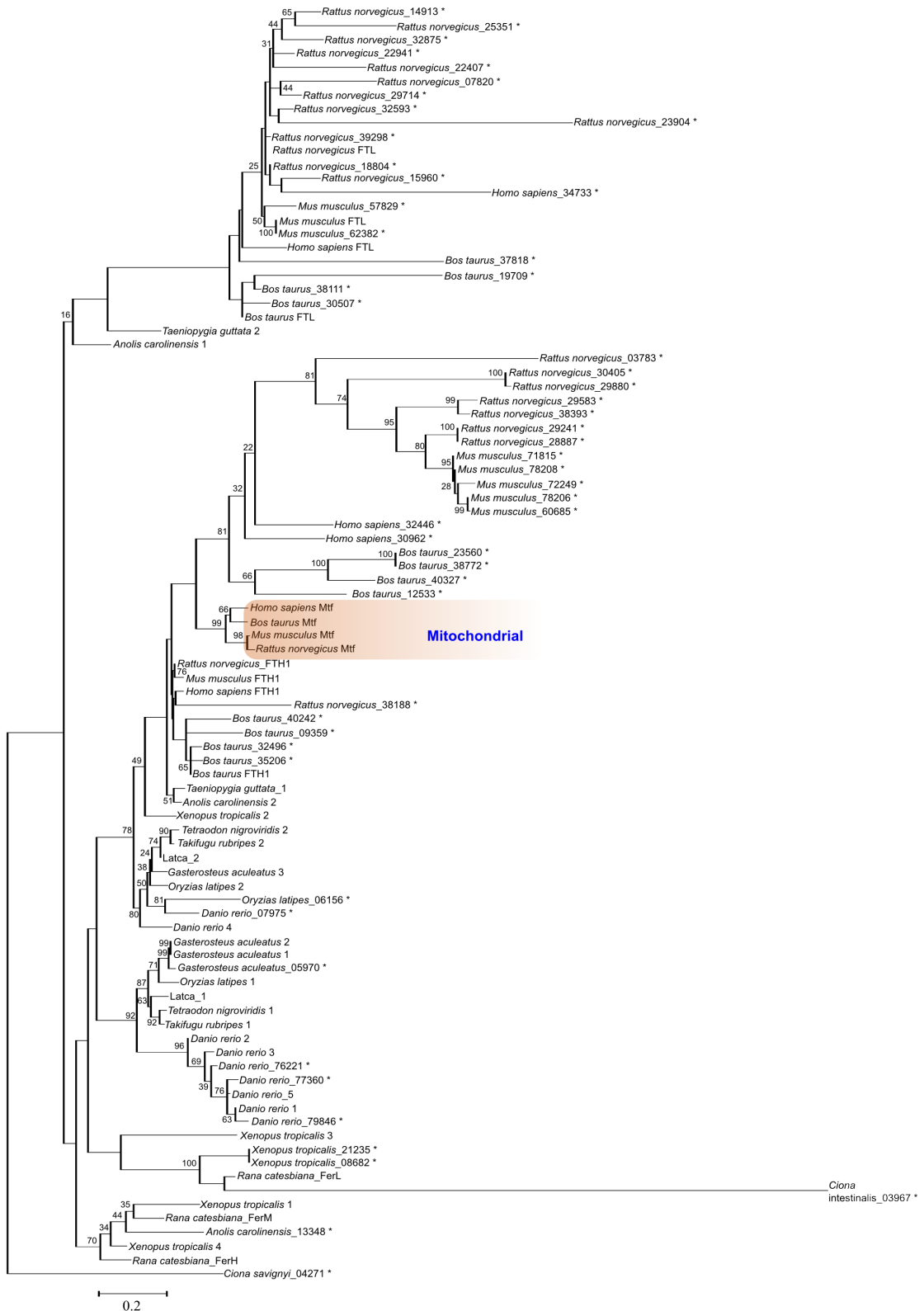
**Supplementary Figure 1. Results of a protein BLAST search against NCBI GenBank (2.2.26), excluding *L. calcarifer* (directs to this study) and *Salmo salar* (numerous identical entries). The red arrows indicate sequences that were non-specific on the subunit type or incorrectly annotated.**

Accession	Description	Max score	Total score	Query coverage	E value	Max Ident
<a href="#">ADF80517.1</a>	ferritin M subunit [ <i>Sciaenops ocellatus</i> ]	<a href="#">357</a>	357	99%	9e-130	95%
<a href="#">ACY75476.1</a>	ferritin M subunit [ <i>Larimichthys crocea</i> ]	<a href="#">353</a>	353	99%	2e-128	94%
<a href="#">AEI87383.1</a>	ferritin middle subunit [ <i>Epinephelus bruneus</i> ]	<a href="#">352</a>	352	99%	1e-127	94%
<a href="#">ADI24354.1</a>	ferritin middle subunit [ <i>Scophthalmus maximus</i> ]	<a href="#">350</a>	350	99%	5e-127	93%
→ <a href="#">CAG02064.1</a>	unnamed protein product [ <i>Tetraodon nigroviridis</i> ]	<a href="#">344</a>	344	97%	1e-124	92%
<a href="#">ACQ37873.1</a>	Ferritin, middle subunit [ <i>Anoplopoma fimbria</i> ]	<a href="#">343</a>	343	99%	4e-124	91%
<a href="#">ACQ37862.1</a>	Ferritin, middle subunit [ <i>Anoplopoma fimbria</i> ]	<a href="#">342</a>	342	99%	5e-124	91%
<a href="#">ACO08179.1</a>	Ferritin, middle subunit [ <i>Oncorhynchus mykiss</i> ]	<a href="#">340</a>	340	99%	6e-123	89%
<a href="#">ACO10415.1</a>	Ferritin, middle subunit [ <i>Caligus rogercresseyi</i> ]	<a href="#">339</a>	339	99%	8e-123	89%
<a href="#">P83838.1</a>	RecName: Full=Ferritin, liver middle subunit; Short=Ferritin M	<a href="#">338</a>	338	99%	1e-122	88%
<a href="#">ACO07744.1</a>	Ferritin, middle subunit [ <i>Oncorhynchus mykiss</i> ]	<a href="#">338</a>	338	99%	3e-122	89%
<a href="#">P83839.1</a>	RecName: Full=Ferritin, middle subunit; Short=Ferritin M	<a href="#">337</a>	337	99%	7e-122	87%
→ <a href="#">NP_001118021.1</a>	ferritin H-3 [ <i>Oncorhynchus mykiss</i> ] >dbj BAA13148.1  ferritin H-3 [ <i>Oncorhynchus mykiss</i> ]	<a href="#">337</a>	337	99%	7e-122	89%
<a href="#">XP_003446437.1</a>	PREDICTED: ferritin, middle subunit-like [ <i>Oreochromis niloticus</i> ]	<a href="#">337</a>	337	99%	8e-122	89%
<a href="#">XP_003446470.1</a>	PREDICTED: ferritin, middle subunit-like isoform 1 [ <i>Oreochromis niloticus</i> ]	<a href="#">336</a>	336	99%	1e-121	89%
<a href="#">ACO08329.1</a>	Ferritin, middle subunit [ <i>Oncorhynchus mykiss</i> ]	<a href="#">336</a>	336	99%	1e-121	89%
→ <a href="#">NP_001118019.1</a>	ferritin H-1 [ <i>Oncorhynchus mykiss</i> ] >dbj BAA13146.1  ferritin H-1 [ <i>Oncorhynchus mykiss</i> ]	<a href="#">336</a>	336	99%	2e-121	89%
→ <a href="#">NP_001118020.1</a>	ferritin H-2 [ <i>Oncorhynchus mykiss</i> ] >dbj BAA13147.1  ferritin H-2 [ <i>Oncorhynchus mykiss</i> ]	<a href="#">335</a>	335	99%	5e-121	88%
<a href="#">P83839.1</a>	RecName: Full=Ferritin, spleen middle subunit; Short=Ferritin M	<a href="#">334</a>	334	99%	9e-121	86%
<a href="#">XP_003446471.1</a>	PREDICTED: ferritin, middle subunit-like isoform 2 [ <i>Oreochromis niloticus</i> ]	<a href="#">332</a>	332	99%	9e-120	89%
<a href="#">NP_001187208.1</a>	ferritin middle subunit [ <i>Ictalurus punctatus</i> ] >gb ADE09345.1  ferritin middle subunit [ <i>Ictalurus punctat</i>	<a href="#">330</a>	330	98%	3e-119	86%
<a href="#">ADO29006.1</a>	ferritin middle subunit [ <i>Ictalurus punctatus</i> ]	<a href="#">329</a>	329	98%	8e-119	86%
<a href="#">ACO09733.1</a>	Ferritin, middle subunit [ <i>Osmerus mordax</i> ]	<a href="#">327</a>	327	97%	6e-118	87%
<a href="#">ADO28388.1</a>	ferritin middle subunit [ <i>Ictalurus furcatus</i> ]	<a href="#">327</a>	327	98%	6e-118	86%
<a href="#">AEB71787.1</a>	ferritin M subunit [ <i>Cynoglossus semilaevis</i> ]	<a href="#">326</a>	326	99%	1e-117	88%
<a href="#">ADO28147.1</a>	ferritin middle subunit [ <i>Ictalurus furcatus</i> ]	<a href="#">320</a>	320	98%	6e-115	83%
<a href="#">AAG13315.1</a>	ferritin middle subunit [ <i>Gillichthys mirabilis</i> ]	<a href="#">316</a>	316	98%	2e-113	85%
<a href="#">ACO09242.1</a>	Ferritin, middle subunit [ <i>Osmerus mordax</i> ]	<a href="#">315</a>	315	97%	3e-113	85%
→ <a href="#">NP_001002378.1</a>	ferritin heavy chain [ <i>Danio rerio</i> ] >gb AAH75879.1  Zgc:92066 [ <i>Danio rerio</i> ]	<a href="#">304</a>	304	97%	5e-109	81%
→ <a href="#">ABY81252.1</a>	ferritin subunit [ <i>Acipenser sinensis</i> ]	<a href="#">304</a>	304	99%	9e-109	82%
→ <a href="#">ABV30907.1</a>	ferritin heavy chain [ <i>Pimephales promelas</i> ]	<a href="#">299</a>	299	96%	6e-107	80%
→ <a href="#">NP_001120325.1</a>	uncharacterized protein LOC100145388 [ <i>Xenopus (Silurana) tropicalis</i> ] >gb AAI54147.1  Zgc:109934 p1	<a href="#">299</a>	299	96%	8e-107	80%
→ <a href="#">AAY86952.1</a>	ferritin H-3 [ <i>Ictalurus punctatus</i> ]	<a href="#">298</a>	298	91%	2e-106	83%
→ <a href="#">P83838.1</a>	RecName: Full=Ferritin, heavy subunit; Short=Ferritin H	<a href="#">298</a>	298	97%	2e-106	75%
→ <a href="#">NP_001103324.1</a>	uncharacterized protein LOC100126128 [ <i>Danio rerio</i> ] >ref NP_001123766.1  uncharacterized protein LC	<a href="#">296</a>	296	96%	1e-105	79%
→ <a href="#">NP_001018367.1</a>	uncharacterized protein LOC553552 [ <i>Danio rerio</i> ] >gb AAH95061.1  Zgc:109934 [ <i>Danio rerio</i> ]	<a href="#">295</a>	295	96%	2e-105	79%
<a href="#">XP_001921731.1</a>	PREDICTED: ferritin, middle subunit-like [ <i>Danio rerio</i> ]	<a href="#">294</a>	294	96%	6e-105	79%
→ <a href="#">P83837.1</a>	RecName: Full=Ferritin, heavy subunit; Short=Ferritin H	<a href="#">292</a>	292	97%	3e-104	74%
<a href="#">XP_087173.1</a>	PREDICTED: ferritin, middle subunit-like [ <i>Danio rerio</i> ]	<a href="#">291</a>	291	95%	8e-104	78%
→ <a href="#">NP_001103175.1</a>	uncharacterized protein LOC559768 [ <i>Danio rerio</i> ] >ref NP_001120189.1  uncharacterized protein LOC10	<a href="#">288</a>	288	95%	1e-102	78%
→ <a href="#">ACO09911.1</a>	Ferritin, heavy subunit [ <i>Osmerus mordax</i> ]	<a href="#">287</a>	287	99%	4e-102	72%
→ <a href="#">AAI71692.1</a>	Wu:fj24c01 [ <i>Danio rerio</i> ]	<a href="#">286</a>	286	95%	9e-102	78%
→ <a href="#">NP_001107131.1</a>	uncharacterized protein LOC100006523 [ <i>Danio rerio</i> ] >gb AAI54747.1  Wu:fj24c01 protein [ <i>Danio rerio</i> ]	<a href="#">285</a>	285	95%	2e-101	77%
→ <a href="#">NP_001124139.1</a>	uncharacterized protein LOC100170833 [ <i>Danio rerio</i> ] >gb AAI62709.1  Zgc:194125 [ <i>Danio rerio</i> ] >gb A	<a href="#">285</a>	285	95%	3e-101	77%
→ <a href="#">CAR60080.1</a>	ferritin high chain [ <i>Notothenia coriiceps</i> ]	<a href="#">281</a>	281	99%	6e-100	71%
→ <a href="#">CAL92185.1</a>	ferritin heavy chain [ <i>Chionodraco rastrospinosus</i> ] >emb CAR66074.1  ferritin high chain [ <i>Chionodraco ha</i>	<a href="#">281</a>	281	99%	8e-100	71%
→ <a href="#">CAR66076.1</a>	ferritin high chain [ <i>Paracheilichthys charcoti</i> ] >emb CAR66077.1  ferritin high chain [ <i>Gymnodraco acutk</i>	<a href="#">281</a>	281	99%	1e-99	70%
→ <a href="#">NP_001187207.1</a>	ferritin heavy chain subunit [ <i>Ictalurus punctatus</i> ] >gb ADE09343.1  ferritin heavy chain subunit [ <i>Ictaluru</i>	<a href="#">280</a>	280	99%	3e-99	70%
→ <a href="#">ACN80998.1</a>	ferritin heavy polypeptide [ <i>Dicentrarchus labrax</i> ]	<a href="#">280</a>	280	99%	3e-99	70%
→ <a href="#">ACY75475.1</a>	ferritin H subunit [ <i>Larimichthys crocea</i> ]	<a href="#">280</a>	280	99%	4e-99	70%
→ <a href="#">CAR66078.1</a>	ferritin high chain [ <i>Trematomus bernacchii</i> ]	<a href="#">279</a>	279	99%	4e-99	70%
→ <a href="#">P07229.3</a>	RecName: Full=Ferritin, higher subunit; Short=Ferritin H >gb AAA49523.1  ferritin, higher subunit [ <i>Rana</i>	<a href="#">279</a>	279	99%	6e-99	74%
→ <a href="#">CAR66075.1</a>	ferritin high chain [ <i>Chaenocephalus aceratus</i> ]	<a href="#">279</a>	279	99%	6e-99	70%
→ <a href="#">ABO75379.1</a>	ferritin H [ <i>Bufo gargarizans</i> ]	<a href="#">278</a>	278	99%	1e-98	74%
→ <a href="#">AAA49532.1</a>	ferritin [ <i>Rana catesbeiana</i> ]	<a href="#">277</a>	277	99%	3e-98	73%

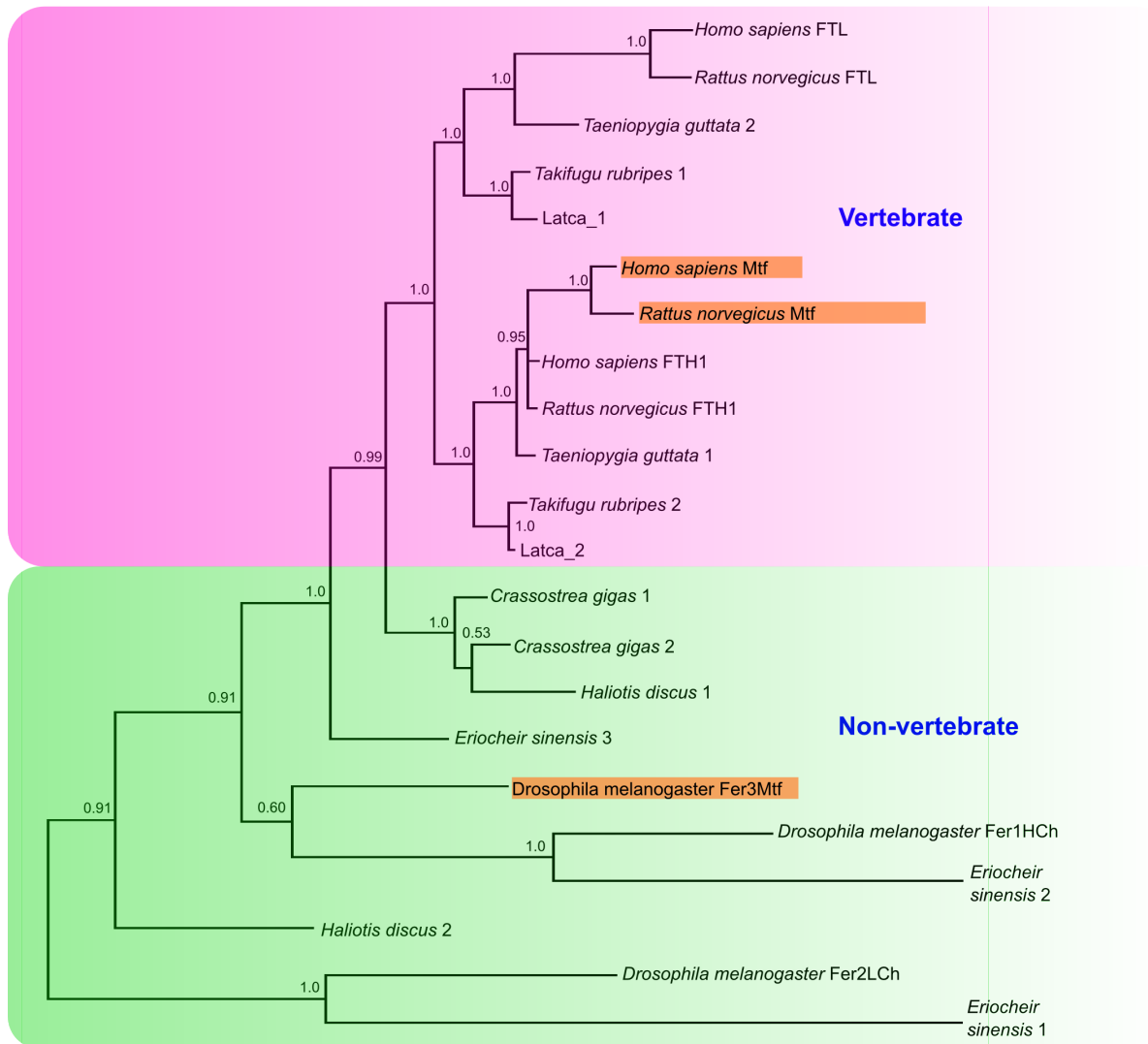
**Supplementary Figure 2. Multiple sequence alignment showing the conserved ferroxidase centres (green) and nucleation sites (yellow) in selected vertebrate sequences.** Latca\_1, Dre2, Tru1, Tni1, Xtr4, HsaFTL, and MmuFTL represent putative middle/light-chain sequences while Latca\_2, Dre4, Tru2, Tni2, Xtr2, HsaFTH1 and MmuFTH1 represent putative H-chains. The teleost M-chains appear to possess all of the conserved ferroxidase sites found in vertebrate H-chains.

	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
	10	20	30	40	50	60	
Latca_1	MESQVRQNYH	RDCEAAVNRM	VNMEMFASYT	YTSMAFYFSR	DDVALPGFSH	FFK <b>ENSD</b> EEER	
Dre2	MDSQVRQNYD	RDCEALINKM	INLELYAGYT	YTSMAFYFDR	DDVALPGFAK	FFK <b>KNS</b> EEER	
Tru1	MESQVRQNYH	RDCEAAINKM	INMELYASYT	YTSMAFFFSR	DDVALPGFAH	FFK <b>ENSD</b> EEER	
Tni1	MESQVRQNYH	RDCEAAINKM	INMELYASYT	YTSMAFYFSR	DDVALPGFAH	FFK <b>ENSE</b> EEER	
Xtr4	MQSQVRQNFN	SDCEAAINRM	VNMELYASYV	YLSMSYYFDR	DDVALHHVAK	FFK <b>EQS</b> HEER	
HsaFTL	MSSQIRQNYH	TDVEAAVNSL	VNLYLQASYT	YLSLGFYFDR	DDVALEGVSH	FF <b>RELA</b> EEER	
MmuFTL	MTSQIRQNYH	TEVEAAVNRH	VNLHLRASVT	YLSLGFYFDR	DDVALEGVGH	FF <b>RELA</b> EEER	
Latca_2	-SSQVRQNFH	QDCEAAINRQ	INLELYASYV	YLSMAYYFDR	DDQALHNFAK	FFR <b>HQS</b> HEER	
Dre4	-SSQVRQNFH	EACEAAVNRQ	INMELYASYV	YLSMSYYFDR	DDQALHNFAK	FFR <b>HQS</b> HEER	
Tru2	MSSQVRQNFH	QDCEAAINRQ	INLELYASYV	YLSMAYYFDR	DDQALHNFAK	FFR <b>HQS</b> HEER	
Tni2	-SSQVRQNFH	QDCEAAINRQ	INLELYASYV	YLSMAYYFDR	DDQALHNFAK	FFR <b>HQS</b> HEER	
Xtr2	MNSQVRQNYH	QECEAAINRQ	VNMELYASYV	YLSMAYYFDR	DDVALKNFSK	YFL <b>HQS</b> HEER	
HsaFTH1	MTSQVRQNYH	QDSEAAINRQ	INLELYASYV	YLSMSYYFDR	DDVALKNFAK	YFL <b>HQS</b> HEER	
MmuFTH1	MPSQVRQNYH	QDAEAAINRQ	INLELYASYV	YLSMSCYFDR	DDVALKNFAK	YFL <b>HQS</b> HEER	
	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
	70	80	90	100	110	120	
Latca_1	<b>E</b> HAEKLLSFQ	NKRGGHIFLQ	DIKKPERDEW	GSGLEAMQCA	LQLE <b>K</b> KNVNQA	LLDLHKLASD	
Dre2	<b>E</b> HAEKFMFEFQ	NKRGGRIVLQ	DIKKPERDEW	DNGLTAMQCA	LQLE <b>K</b> KNVNQA	LLDLHKVASQ	
Tru1	<b>E</b> HAEKLLSFQ	NKRGGRIFLQ	DIKKPERDEW	GSGLEAMQCA	LQLE <b>K</b> KKNVNQA	LLDLHKLASD	
Tni1	<b>E</b> HADKLLSFQ	NKRGGRIFLQ	DIKKPERDEW	GSGLEAMQCA	LQLE <b>K</b> KKNVNQA	LLDLHKLASD	
Xtr4	<b>E</b> HAEKFLKYQ	NKRGGRAVLQ	DIKKPERDEW	GNTLEAMQAA	LQLE <b>K</b> KTVNQA	LLDLHKLASD	
HsaFTL	<b>E</b> GYERLLKMQ	NQRGGRALFQ	DIKKPAEDEW	GKTPDAMKAA	MALEKKNLQA	LLDLHALGSA	
MmuFTL	<b>E</b> GAERLLEFQ	NDRGGRALFQ	DVQKPSQDEW	GKTQEAMEAA	LAMEKKNLQA	LLDLHALGSA	
Latca_2	<b>E</b> HAEKLMKLQ	NQRGGRIFLQ	DVRKPDRDEW	GSGVEALECA	LQLE <b>K</b> SVNQS	LLDLHKLCSQ	
Dre4	<b>E</b> HAEKLMKFQ	NQRGGRIFLQ	DVKKPEKDEW	GSGVEALECA	LQLE <b>K</b> SVNHS	LLELHKLASQ	
Tru2	<b>E</b> HAEKLMKMQ	NQRGGRIFLQ	DVRKPERDEW	GSGMEALECA	LQLE <b>K</b> SVNQS	LLDLHKMCSQ	
Tni2	<b>E</b> HAEKLMKMQ	NQRGGRIFLQ	DVRKPERDEW	GSGTEALECA	LQLE <b>K</b> SVNQS	LLDMHKMCSQ	
Xtr2	<b>E</b> HAEKLMKMQ	NQRGGRIFLQ	DVKKPDREW	ANGLEALECS	LQLE <b>K</b> SVNQS	LLELHKLSTD	
HsaFTH1	<b>E</b> HAEKLMKLQ	NQRGGRIFLQ	DIKKPDCDDW	ESGLNAMECA	LHLE <b>K</b> KNVNQS	LLELHKLATD	
MmuFTH1	<b>E</b> HAEKLMKLQ	NQRGGRIFLQ	DIKKPDRDDW	ESGLNAMECA	LHLE <b>K</b> SVNQS	LLELHKLATD	
	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
	130	140	150	160	170		
Latca_1	HGDPHLCDFL	ETHYLNEQVE	AIKKLGDYIS	NLSRMDAQKN	KMAEYLFDKH	SLGGK	
Dre2	KGDPHLCDFL	ESHYLNEQVE	AIKKLGDHIT	NLSKMDAGNN	RMAEYLFDKH	TLDS-	
Tru1	HVDPHLCDFL	ESHYLNEQVE	AIKKLGDYIT	NLSRMDAQNN	KMAEYLFDKH	TLGSK	
Tni1	HVDPHLCDFL	ETHYLNEQVE	AIKKLGDYIT	NLSRMDAQNN	KLAEYLFDKH	TLGSK	
Xtr4	KTDPHLCDFL	ESEYLEEQVK	AMKELGDYIT	NLKRLGVPQN	GMGEYLFDKH	TLGES	
HsaFTL	RTDPHLCDFL	ETHFLDEEVK	LIKKMGDHLT	NLHRL---EA	GLGEYLFERL	TLKHD	
MmuFTL	RADPHLCDFL	ESHYLDKEVK	LIKKMGNHLT	NLRRVGAPQG	SLGEYLFERL	TLKHD	
Latca_2	HNDPHLCDFI	ETHYLDEQVK	SIKELADWVT	NLRRMGAPQN	GMAEYLFDKH	TLGKE	
Dre4	HNDPHMCDFI	ETHYLDEQVK	SIKELGDHVT	NLRRMGAPQN	GMAEYMFDKL	TLGKE	
Tru2	HNDPHLCDFI	ETHFLDEQVK	SIKELADWVT	NLRRMGAPQN	GMAEYLFDKH	TLGKV	
Tni2	HNDPHMCDFI	ETHFLDEQVK	SIKELADWVA	NLRRMGAPQN	GMAEYLFDKH	TLGKE	
Xtr2	HNDPHLCDFL	ESHYLDKEQVK	SMKELGDHIT	NLRRMGAPSN	GMAEYLFDKH	TLGEH	
HsaFTH1	KNDPHLCDFI	ETHYLNEQVK	AIKELGDHVT	NLRKMGAPES	GLAEYLFDKH	TLGDS	
MmuFTH1	KNDPHLCDFI	ETYYLSEQVK	SIKELGDHVT	NLRKMGAPEA	GMAEYLFDKH	TLGHG	

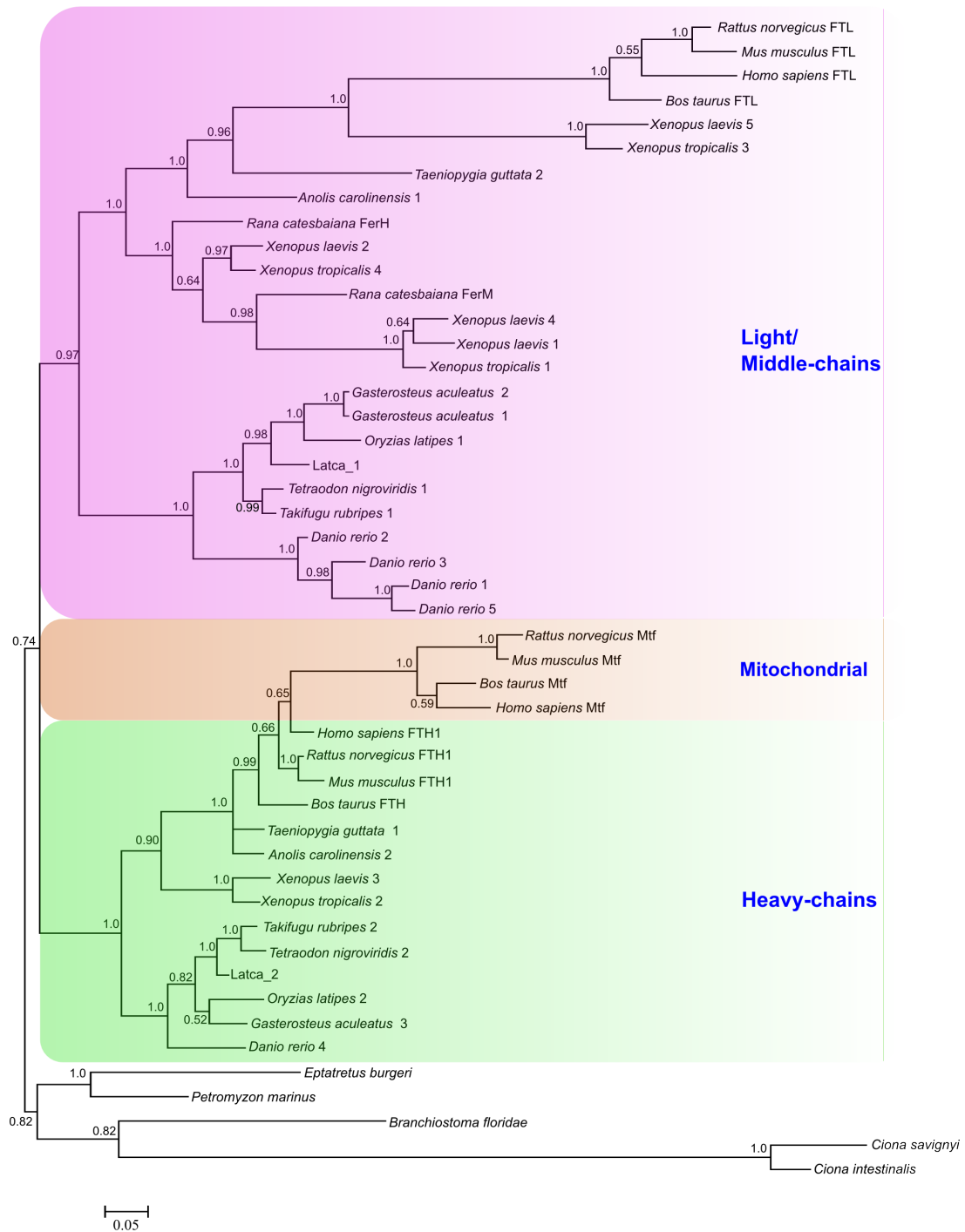
**Supplementary Figure 3. Initial Maximum Likelihood analysis conducted using all sequences mined from Ensembl and the three annotated Rana sequences, with *C. savignyi* as the outgroup.** No clear pattern of grouping was observed other than the clustering of the mammalian mitochondrial sequences and many branches lacked bootstrap support (values indicated at branches). Sequences that are indicated with \* were removed from subsequent analysis.



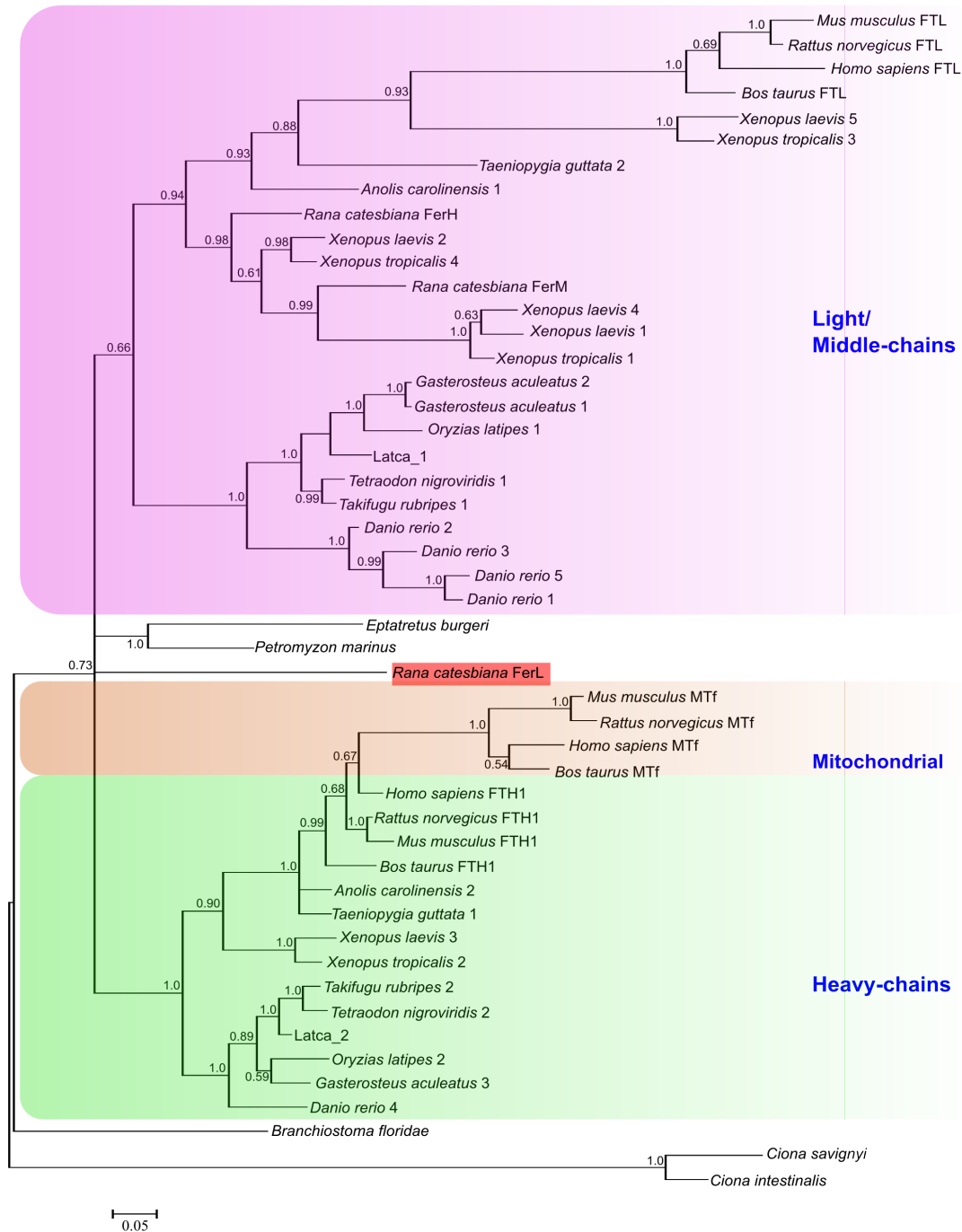
**Supplementary Figure 4. Bayesian tree constructed from the amino acid sequences of metazoan ferritins.** The mammalian (*H. sapiens*, *M. musculus*) and non-vertebrate (*D. melanogaster*) mitochondria sequences are highlighted in brown and clustered separately. Values at branches indicate the posterior probabilities.



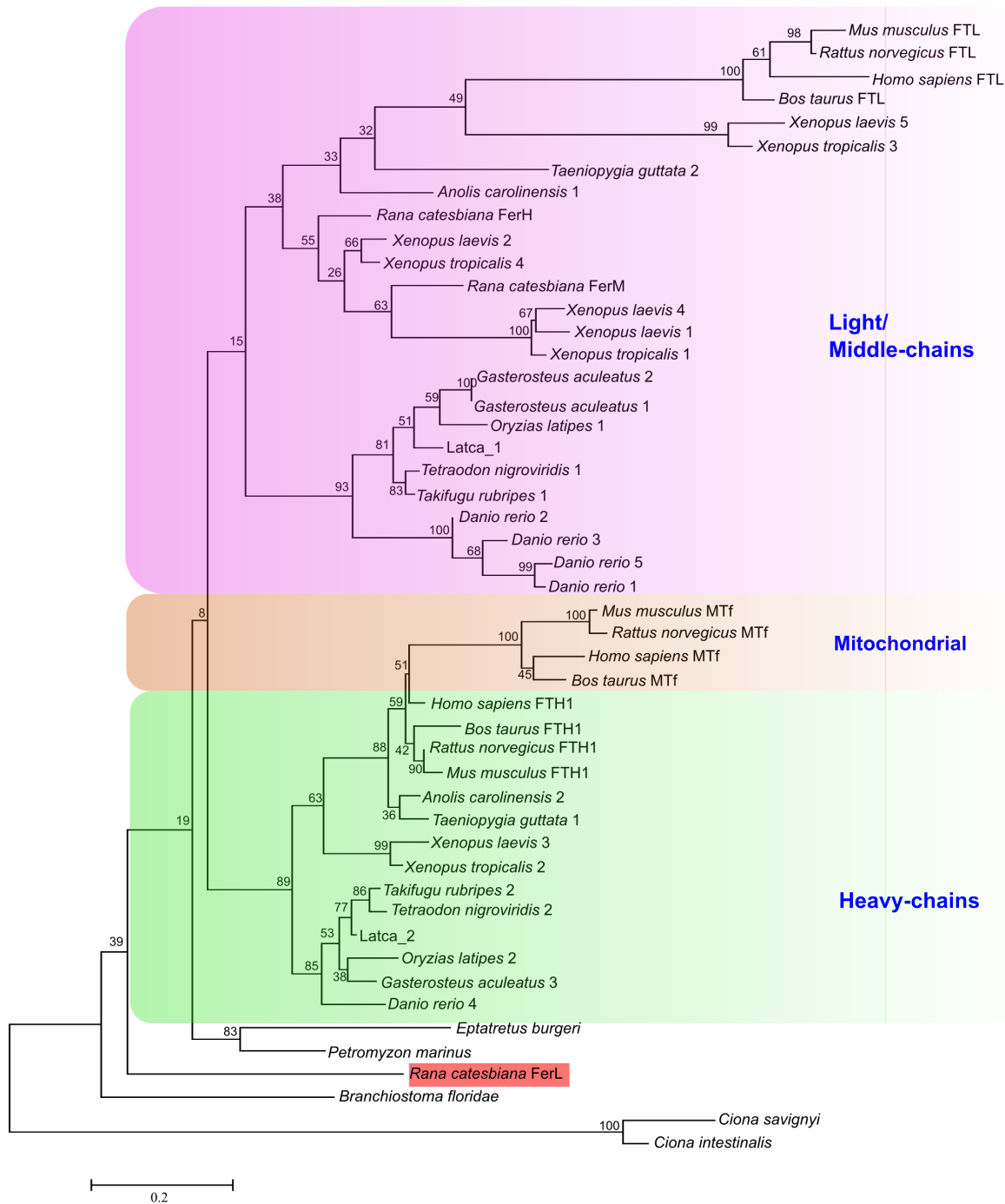
**Supplementary Figure 5. Bayesian tree constructed from amino acid sequences of vertebrates ferritins.** Values at branches indicate the posterior probabilities.



**Supplementary Figure 6. Maximum Likelihood tree constructed from the amino acid sequences of vertebrate ferritin, including the annotated *R. catesbiana* L-chain.** The inclusion of *R. catesbiana* L-chain (highlighted in red), clustered with the ancestral vertebrate sequences and decreases the bootstrap values (1000 replications; indicated at the branches).



**Supplementary Figure 7. Bayesian tree constructed from the amino acid sequences of vertebrate ferritin, including the annotated *R. catesbiana* L-chain.** The position of *R. catesbiana* L-chain in the tree was unresolved. Values at branches indicate the posterior probabilities.



**Supplementary Table 1: Primers used to generate the complete putative cDNA sequences.**

<b>Primer</b>	<b>Sequence</b>
FerM-F	5'-GAGCCTGGTTGACGTTCTTCTCC
FerM-R	5'-TCCTCCAGGACATCAAGAAACCG
FerH-F	5'-AGGCGTACAGCTCCAGGTTGATCTG
FerH-R	5'-GCAGATCAACCTGGAGCTGTACGC



**Supplementary Table 2: Sequences used in the study.**

Sequences marked with \* were subsequently discarded after the initial analysis.

<b>Species</b>	<b>Sequence name</b>	<b>Ascension number</b>
<i>Danio rerio</i>	Dre1	ENSDARG00000079938
	Dre2	ENSDARG00000031776
	Dre3	ENSDARG00000078342
	Dre4	ENSDARG00000015551
	Dre5	ENSDARG00000073936
	Dre_79846*	ENSDARG00000079846
	Dre_77360*	ENSDARG00000077360
	Dre_76621*	ENSDARG00000076221
	Dre_07975*	ENSDARG00000007975
<i>Takifugu rubripes</i>	Tru1	ENSTRUG00000014292
	Tru2	ENSTRUG00000017266
<i>Oryzias latipes</i>	Ola1	ENSORLG00000016761
	Ola2	ENSORLG00000005872
	Ola_06156*	ENSORLG00000006156
<i>Tetraodon nigroviridis</i>	Tni1	ENSTNIP00000014079
	Tni2	ENSTNIP00000006889
<i>Gasterosteus aculeatus</i>	Gac1	ENSGACG00000005975
	Gac2	ENSGACG00000005990
	Gac3	ENSGACG00000015484
	Gac_05970*	ENSGACG00000005970
<i>Xenopus tropicalis</i>	Xtr1	ENSXETG00000021234
	Xtr2	ENSXETG00000006737
	Xtr3	ENSXETG00000021237
	Xtr4	ENSXETG00000021236
	Xtr_21235*	ENSXETG00000021235
	Xtr_08682*	ENSXETG00000008682
<i>Anolis carolinensis</i>	Aca1	ENSACAG00000004685
	Aca2	ENSACAG00000017578
	Aca_13348*	ENSACAG00000013348

<i>Taeniopygia guttata</i>	Tgu1	ENSTGUG00000005949
	Tgu2	ENSTGUG00000015659
<i>Homo sapiens</i>	HsaFTH1	ENSG00000167996
	HsaFTMtf	ENSG00000181867
	HsaFTL	ENSG00000087086
	Hsa_30962*	ENSG00000130962
	Hsa_32446*	ENSG00000132446
	Hsa_34733*	ENSG00000234733
<i>Mus musculus</i>	MmuFTH1	ENSMUSG00000024661
	MmuFTMtf	ENSMUSG00000024510
	MmuFTL	ENSMUSG00000050708
	Mmu_57829*	ENSMUSG00000057829
	Mmu_78208*	ENSMUSG00000078208
	Mmu_71815*	ENSMUSG00000071815
	Mmu_72249*	ENSMUSG00000072249
	Mmu_60685*	ENSMUSG00000060685
	Mmu_62382*	ENSMUSG00000062382
	Mmu_78206*	ENSMUSG00000078206
<i>Rattus norvegicus</i>	RnoFTH1	ENSRNOG00000022619
	RnoFTMtf	ENSRNOG00000014988
	RnoFTL	ENSRNOG00000020843
	Rno_28887*	ENSRNOG00000028887
	Rno_29241*	ENSRNOG00000029241
	Rno_38393*	ENSRNOG00000038393
	Rno_29583*	ENSRNOG00000029583
	Rno_39298*	ENSRNOG00000039298
	Rno_29880*	ENSRNOG00000029880
	Rno_30405*	ENSRNOG00000030405
	Rno_38188*	ENSRNOG00000038188
	Rno_29714*	ENSRNOG00000029714
	Rno_25351*	ENSRNOG00000025351
	Rno_32875*	ENSRNOG00000032875
	Rno_32593*	ENSRNOG00000032593
	Rno_18804*	ENSRNOG00000018804
	Rno_14913*	ENSRNOG00000014913

	Rno_07820*	ENSRNOG00000007820
	Rno_23094*	ENSRNOG00000023094
	Rno_22941*	ENSRNOG00000022941
	Rno_15960*	ENSRNOG00000015960
	Rno_22407*	ENSRNOG00000022407
	Rno_03783*	ENSRNOG00000003783
<i>Bos taurus</i>	BtaFTH1	ENSBTAG00000011184
	BtaFTMtf	ENSBTAG00000005779
	BtaFTL	ENSBTAG00000013343
	Bta_12533*	ENSBTAG00000012533
	Bta_32496*	ENSBTAG00000032496
	Bta_35206*	ENSBTAG00000035206
	Bta_40242*	ENSBTAG00000040242
	Bta_40327*	ENSBTAG00000040327
	Bta_38772*	ENSBTAG00000038772
	Bta_23560*	ENSBTAG00000023560
	Bta_09359*	ENSBTAG00000009359
	Bta_38111*	ENSBTAG00000038111
	Bta_30507*	ENSBTAG00000030507
	Bta_19709*	ENSBTAG00000019709
	Bta_37818*	ENSBTAG00000037818
<i>Rana catesbiana</i>	RcaFerH	M15655.1/P07229
	RcaFerM	J02724.1/P07798
	RcaFerL	J02725.1/P07797
<i>Drosophila melanogaster</i>	DmeFer1HCh	Fbgn0015222/FBpp0084995
	DmeFer2LCh	Fbgn0015221/FBpp0084986
	DmeFer3Mtf	Fbgn0030449/FBpp0073576
<i>Eriocheir sinensis</i>	Esi1	GU002544.1/ADF87490.1
	Esi2	GU002545.1/ADF87491.1
	Esi3	GU475115.2/ADD17345.1
<i>Crassostrea gigas</i>	CgiGF1	AY321299.1/Q7YZR9
	CgiGF2	AY321300.1/Q7YZR8
<i>Haliotis discus</i>	Hdi1	DQ821493.1
	Hdi2	DQ821494.1

<i>Branchiostoma floridae</i>	Bfl	BW844971.1
<i>Ciona intestinalis</i>	Cin	BW450247.1
	Cin_06943*	ENSCING00000006943
<i>Ciona savignyi</i>	Csa [contig]	BW577874.1; BW520036.1
	Csa_04271*	ENSCSAVG00000004271
<i>Eptatretus burgeri</i>	Ebu [contig]	BJ655837.1; BJ667150.1