SUPPLEMENTARY FIGURES

A living fossil in the genome of a living fossil: Harbinger transposons in the coelacanth genome

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Supplementary Figure S1 - Amino acid alignment of *lha***-like proteins** – The amino acid sequence of *lha* shares sequence similarity with several vertebrate proteins, but is not overtly similar to any particular group of sequences. The alignment includes all vertebrate blast hits to the predicted *lha* gene from *Latimeria* and covers 141 conserved amino acids from *lha*. All sequences aligning to *lha* are labeled by their GenBank identifiers.

lha	AQHQAGDPIIRDTGAPGPRKRKRR FKVAEVDTIIHGVDRAADIVIG AGSTSLAHKEE QWQRTTHQVNALGHCLRGVVEVKHKV
CAM14370	DOSDETKAIMHRIVLPLAERKRKPKFSKEELDLINTEVTRHEAVLPGRETHRLSHADRDKIWEGIARRTTSVSQVPRSIKDINHR
XP_001148200	REPERSION OF THE AVERAGE AND A A A A A A A A A A A A A A A A A A
AAI13557	KDSAAGPHGKNAGPSTIKAKKKK PHYCPO251EV LVSKVSKHHQLLDYGIGLLKAEPTRIYR WSRILQAVHALGYCRKDVDLFHK KDSAAGPHGPHAGPSTIKAKKKK PHYCPO251EV LVSKVSKHHQLLDYGIGLLKAEPTRIYR WSRILQAVHALGYCRKDVDLFHK
EAW82324	KDSAAGPHGRHAGPSATRAKKRK PNFCPOETEVLWSKVSKHHOLLFGTGLLKAEPTRYR WSRILOAVHALGYCRRDWDLKHW
NP_659440	KDSAA <mark>gphgrhagpsatrakkrkphfcpqetevly</mark> skyskhhq <mark>llfgtgllkaeptryrvwsrtlqavhalgycrdvvdlahr</mark> y
XP_001089591	KDLAA <mark>GPHGRNVGPSATRAKKRKPNFC</mark> PQ <mark>ETEVLV</mark> SKVSKHHQ <mark>LLF</mark> GTGLLKAEPTREYRVWSRILQAVNALGYCRRDVVDLKHK
XP_519987	KDSAAGPHGRNAGPSATRAKKER PNFCPQETEV LVSKVSKHHQLLFGTGLLKAEPTREYRVWSRLLQAVHALGYCRHDVDLKHW
NP 001075915	KUSA GGARSKI AG PORTRAKKEN DIFC POETEV IN SKUSKHYOLLING SGULKEPPER I R WSRTD QAVIALIG I LED VID JAHAV KELAARARGHVAS ATRAKKEN DIFC POETEV IN AKVSKHYOLLING SRLPRAEPAREY R WSRTD QAVIALIG Y CREDIADIKHY
XP_001381738	KUTLATPPSRHAGPSAARA <mark>KKRKPHFCPQETEVLV</mark> SKVTKHHQ <mark>LLP</mark> GTGLLKAEPTRFYR VWSRTLQAVHALGYTRRDIVDLKHRV
XP_001489117	LLPGPGCVPLRPGP-HSRTWTRKPNFSPQETEVLVQRVTRHYPLLFGALRGTPARKHRWHKTLQAWHALGYCRHDLGDLKHK
XP_001381736	LADGPGSTPPQPGH - HSRTWTRE PNFSPQETEVLVQKWTRHYQLLFG - ALRGTPAKKHR WNIKILQAWNALGYGREDHGDLAHK
XP 424011	GREEKALI SUDSTEELIIVAUVERISALIYA LINA URA SALIYA SALIYA SALIYA SUDSTEELIIVAUVERISALIYA SALIYA SALIYA SUDSTEELIIVAUVERISALIYA SALIYA SALIY
NP_001089601	NOVRETIP <mark>GAGSIGPYP</mark> FT <mark>GRKRKANFS</mark> TIESTETLIVKYVVITHFSALYGSEALRTESTRETO <mark>RRSQLN</mark> SQLOKTVIDLGYTPRTIDDLKHKV
XP_520284	NAVP <mark>akkrknifsereveliveel</mark> elkkh <mark>llv</mark> ihfnagvplaaksaanhgiirrvnavatorrelpevkkky
XP_001152900	NAVP <mark>AKKRKNIFSEREVEI IVEEL</mark> ELKKH LLN IHFNAGVPLAARSAAWHGI LREVNAVAT (RRELPEVKKK)
NP_931045	HAV
XP_001092434	NAVP <mark>AKKKKIIIFSEREVEIIVEEL</mark> ELKKH <mark>LLV</mark> IIIFNAGVPLAAKSAAWHGILREVNAVATCREELPEVKKK
AAH21580	NAVP <mark>akkrkini Fs</mark> erevei i veelelkkillivii finagv <mark>plaan</mark> sa awh <mark>gi lrrvnav</mark> at crrelpevkkky
XP_001501275	NAVP <mark>AKKKKNIJFSEREVEI IVEEL</mark> ELKKH LLV IHFNAGVPLAAKSAAWHGI LREVNAVATCRRELPEVKKV
NP_001094544 XP 548443	HAVPAKKRKILIFSEREVELTVEELELKKHLLVIIHTIAGVPLAAKSAAWHGILREVHAVATCRRELPEVKKV
XP_001079981	NAV
NP_919316	NAVP <mark>akkrknips</mark> ereveliveelelkkhliviihtilagvplaaksa <mark>anhgilreviav</mark> at <mark>creelpevkky</mark>
NP_001016353	NATP <mark>akkrkunfsb</mark> oevelileenen och ilinfnag vplvtysnawhotekevnatstchrelaevekrv
AAI28615	NATPAKKRKINIFSEQEVELILEENENQKHILLINHFNAAVPLVTNSIIAWHOILKEVNAISTCHRELAEVKKK
NP_001025863	NASPPAPPAKKKHINFSEREVELIVEELERGKHLLTIHFIJAGVPLAALAAAWHDILRRVIAVATCHRELPEVKKY
XP691225	HASQ <mark>akkrythfsereveliveenen</mark> Qkh <mark>ilv</mark> hhfnagvthlakhsawnetlk <mark>evnav</mark> sto <mark>crelaeve</mark> kry
XP_001520341	MTAP <mark>VKRKHIFLELEVEIIVEELEN</mark> QKH <mark>VIN</mark> IHFIAGV <mark>PLAA</mark> KSA <mark>A</mark> WQDILR <mark>VNAV</mark> ITCRRELPEVKKK
CAF89557	ASAAKKRKINFSEREVEI LVEETEN OKHTI VIIHFIJAGVTHIAKIIKAWGDI LRAVIJAVITOPRELHEVKKV
NP_001013508	NOEPHTIPICKPOOS DIR FARRA SKETPOOVEDDUSEOVERED VARRED VARRED VARRED VARRED VAR TIKO SKETVARVIET TRANSFORMET VAR
NP_001081092	AHEDA FHTD <mark>GVHCP ITSLPH I RKHRFSDDELHVLVQEV</mark> HDHVSQLFGELSVKTPTAVHHK INE <mark>C IVAKVHAIG</mark> VTTPTVSEIKKR
NP_001089108	AHEDTLATTDEFAGPAT - LPHIRKARFSDEELAVLVQEVHDAASQLFGELSVRTPTAVKAK IMEGIVAVNAVGVTTRAVSEIKKR
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Supplementary Figure S2 - Structure of the pPAC-GFP-1054-RFP-iTol2-Kan PAC clone – This clone was used for generating the *Tg (pPAC-GFP-1054-RFP-iTol2-Kan) B6C3* mouse transgenic line.



Supplementary Figure S3 - Southern hybridizations of *lha* gene. – M = Low Range PFG Marker (NEB #N0350S), marker labels are in kilobases. D, E, and H represent *Lm* genomic heart DNA digested with *DraI*, *Eco*RI and *Hin*dIII respectively. Left panel is the ethidium bromide-stained gel and the right panel is the subsequent Southern blothybridization with the *lha probe*.



Supplementary Figure S4 - Hybridization of *lha* gene to a high-density filter of the *Lm* BAC library. – The *Lm* BAC library was spotted onto 22 cm² nylon filters in a 4 x 4 grid pattern (18,432 individual clones per filter) for hybridization screening (Danke et al. 2004). This region of a high density filter represents ~400 clones from the library spotted in duplicate.



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