SUPPLEMENTARY FIGURES

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

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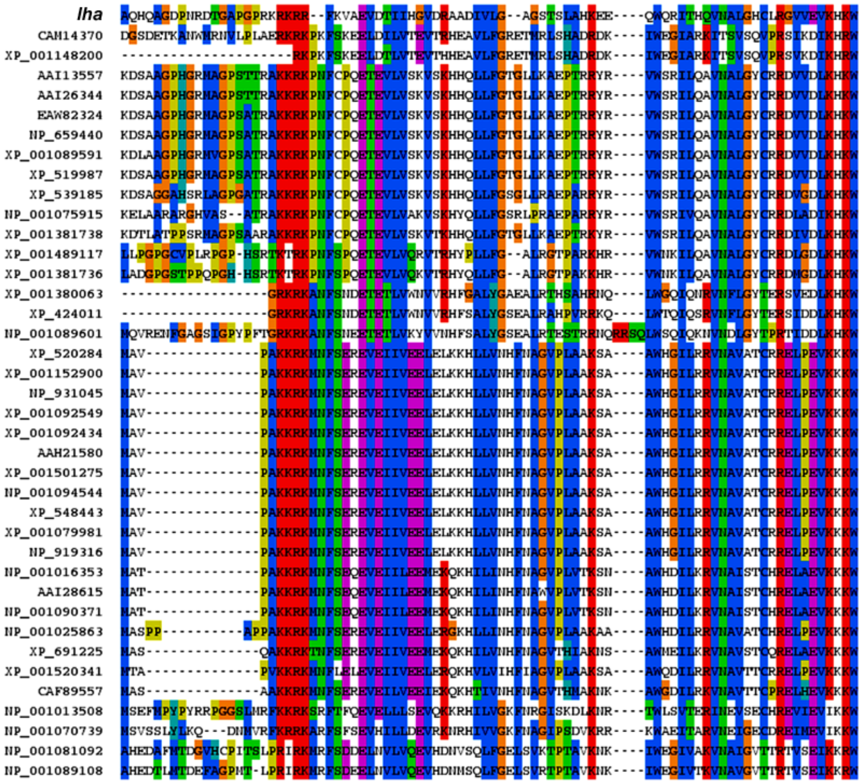
Supplementary Figure S1 - Amino acid alignment of *lha*-like proteins – The amino acid sequence of *lha* shares sequence similarity with several vertebrate proteins, but is not overtly similar to any particular group of sequences. The alignment includes all vertebrate blast hits to the predicted *lha*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



lha
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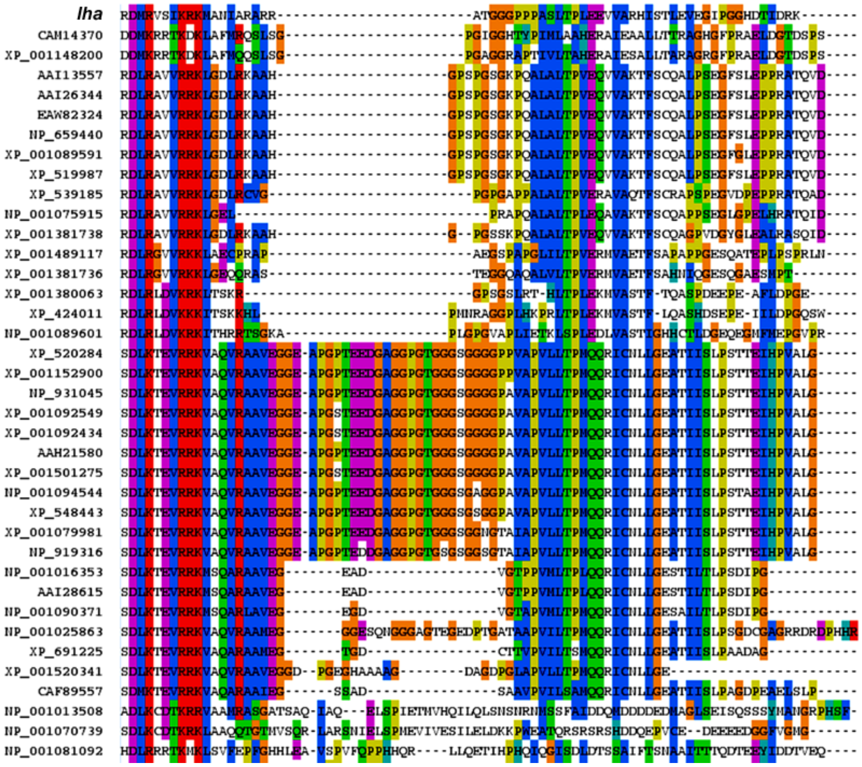

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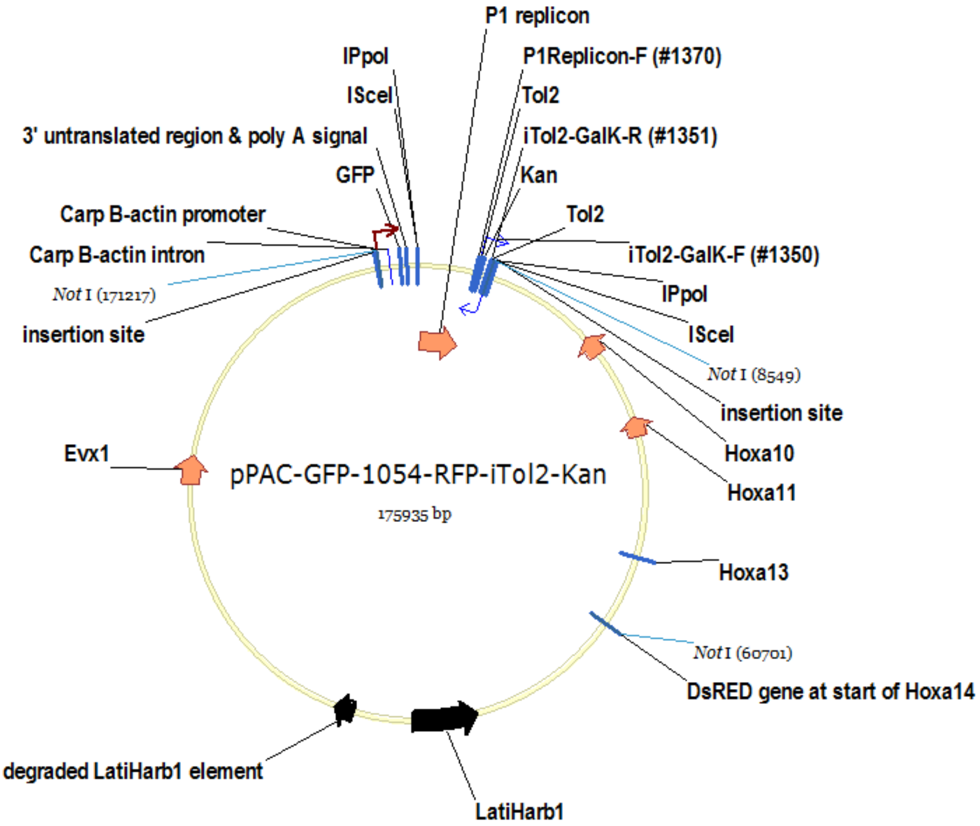
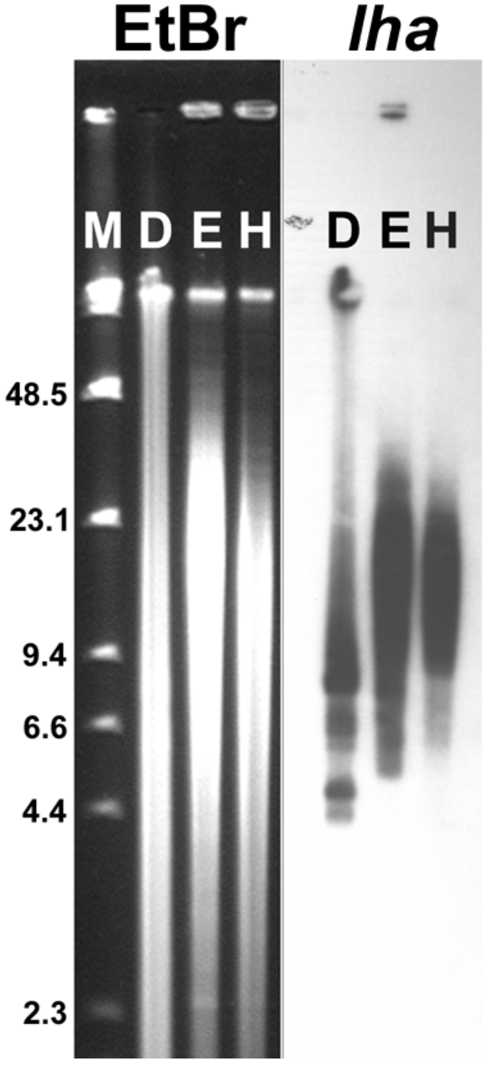
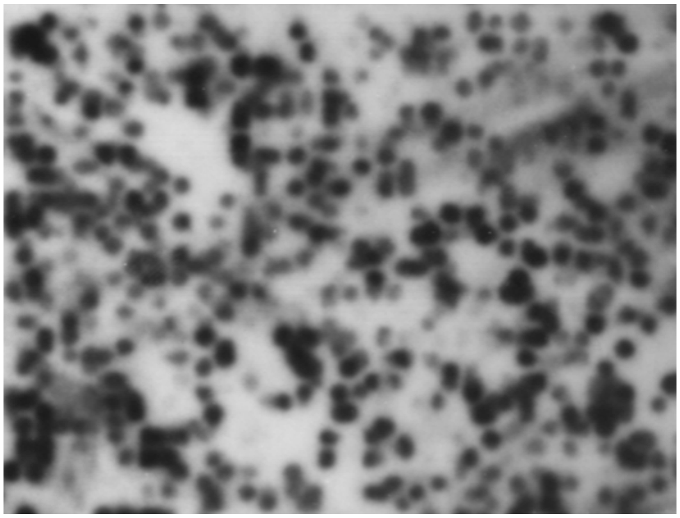
Supplementary Figure S2 - Structure of the pPAC-GFP-1054-RFP-iTol2-Kan PAC clone – This clone was used for generating the *Tg (pPAC-GFP-1054-RFP-iTol2-Kan) B6C3* mouse transgenic line.



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 *Dra*I, *Eco*RI and *Hin*dIII respectively. Left panel is the ethidium bromide-stained gel and the right panel is the subsequent Southern blot-hybridization 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 cm^2 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.



Literature Cited

Danke J, Miyake T, Powers T, Schein J, Shin H, Bosdet I, Erdmann M, Caldwell R, Amemiya CT. 2004. Genome resource for the Indonesian coelacanth, Latimeria menadoensis. J Exp Zoolog A Comp Exp Biol 301:228-234.

Higgins DG, Sharp PM. 1988. CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. Gene 73:237-244.

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876-4882.