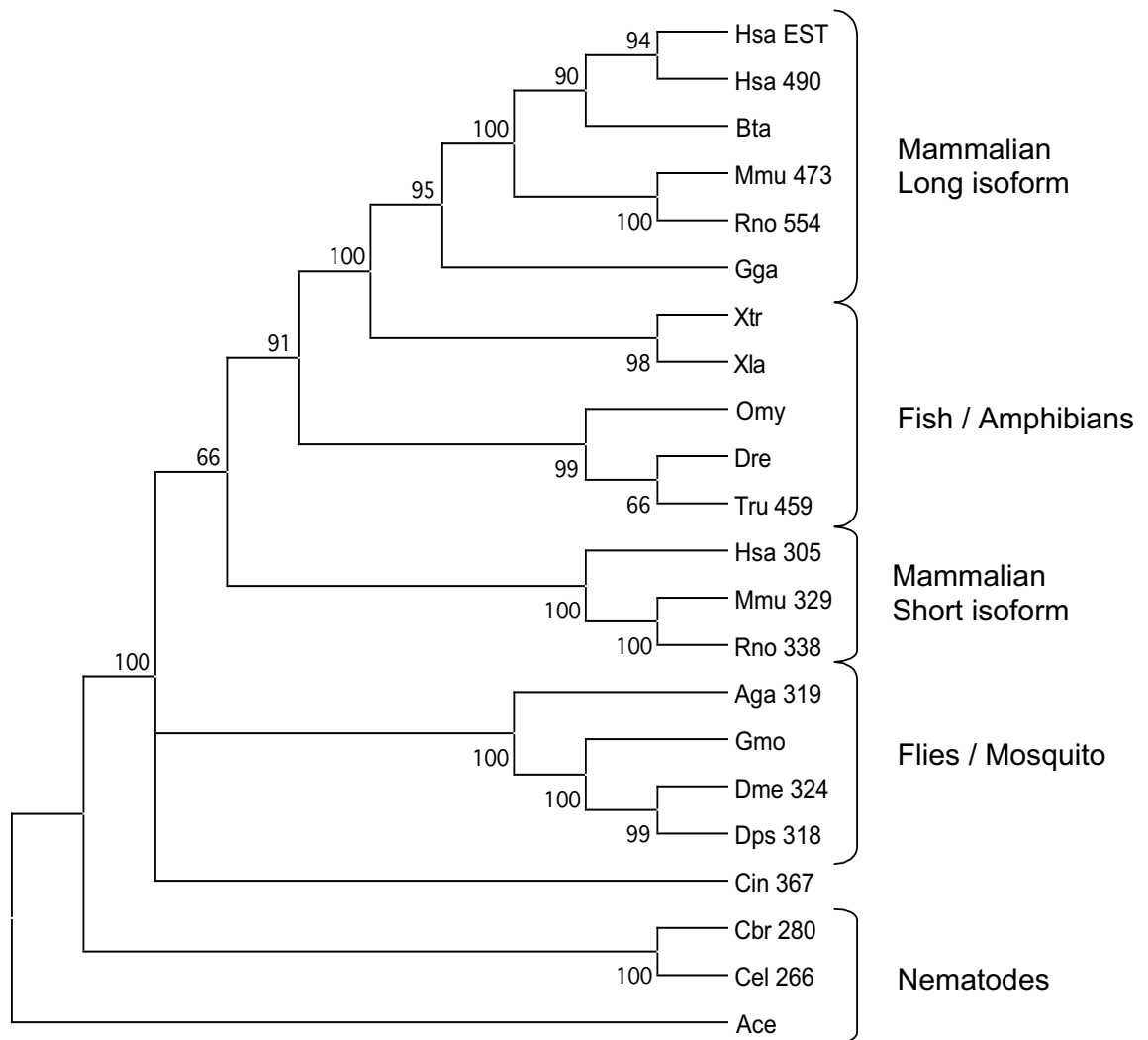


Table S1

<i>Accession No</i>	<i>Organism</i>	<i>Abbreviation</i>	<i>Sequence</i>	<i>Length</i>
CA389381	H. sapiens	Hsa	Partial EST	-
BC030555	H. sapiens	Hsa	cDNA	490
P07106	B. taurus	Bta	Protein	533
XM_237252	R. norvegus	Rno	cDNA	554
AK005001	M. musculus	Mmu	cDNA	473
TC28717	G. gallus ¹	Gga	EST	-
CF216920	S. tropicalis	Str	EST	-
BG409523	X. laevis	Xla	EST	-
CA354989	O. mykiss	Omy	EST	-
AW422493	D. renio	Dre	EST	-
SINFRUG00000122689	T. rubripes ²	Tru	Pred. ORF	398
BC029164	H. sapiens	Hsa	cDNA	305
BC048371	M. musculus	Mmu	cDNA	329
XM_221005	R. norvegus	Rno	Protein	338
TC13206	A. gambie ¹	Aga	Protein	319
BX550023	G. morsitans	Gmo	Partial EST	-
NM_134885	D. melanogaster	Dme	cDNA	324
Contig4092_Contig573	D. pseudoobscura ³	Dps	Pred. ORF	318
AK112135	C. intestinalis	Cin	cDNA	367
CBG13297	C. briggsae	Cbr	Pred. ORF	280
NM_067130	C. elegans	Cel	cDNA	266
CB175137	A. ceylanium	Ace	Partial EST	-

All the BLAST searches were conducted using non-redundant nucleotide or protein databases, EST databases, contig databases from the following sites: NCBI (<http://www.ncbi.nlm.nih.gov/BLAST/>), 1) The Institute for Genomic Research (TIGR) (<http://tigrblast.tigr.org/tgi/>), 2) The Sanger Institute, (<http://www.sanger.ac.uk/DataSearch/>), 3) Human Genome Sequencing Center, Baylor College of Medicine, (<http://www.hgsc.bcm.tmc.edu/>).

Figure S1



Methods

Alignments: The sequences used for phylogenetic analysis were aligned using CLUSTALX v. 1.82. The protein alignments were conducted with the Gonnet matrix.

Construction of the phylogenetic trees: Rooted neighbour-joining phylogenetic tree was constructed using the MEGA software package. The nematode *A. ceylanium* was chosen as outgroup. The numbers indicated at each branch node is the bootstrap support value based on 1000 bootstrap replications.