Supplementary Materials

Supplementary Text

1. Full-length cDNA and bioinformatics of *LcHif-1α*

The full-length cDNA of *LcHif-1α* (GenBank accession number: MZ197829) was 3 647 bp, including a 272 bp 5’ non-coding region, 1 091 bp 3’ non-coding region, and 2 256 bp open reading frame (ORF), encoding a total of 751 amino acids (aa) (Figure S1). The predicted molecular weight of the *Lc*Hif-1α protein was 84.19 kDa. The *Lc*Hif-1α protein contained a basic helix-loop-helix domain (bHLH, 12–82 aa), PAS domain (88–151 aa), PAS_3 domain (251–338 aa), Hif-1 domain (548–578 aa), and carboxy-terminal transcription activation domain (C-TAD, 714–750 aa) (Figure S2).

Multiple sequence comparison of *Lc*Hif-1α with Hif-1α proteins from other species is shown in Figure S3. *Lc*Hif-1α shared 99.3%, 72.4%, 50.8%, 59.8%, 53.9%, 51.5%, 51.4%, 50.2%, and 50.2% homology with the Hif-1α of *Collichthys lucidus*, *Oryzias latipes*, *Mustelus canis*, *Danio rerio*, *Gallus gallus*, *Homo sapiens*, *Sus scrofa*, *Mus musculus*, and *Xenopus tropicalis*, respectively. The homology of the functional bHLH, PAS, PAS-3, Hif-1, and C-TAD domains among the Hif-1α proteins of the above species was extremely high, suggesting that the Hif-1α protein is relatively conserved among species.

The phylogenetic tree of *Lc*Hif-1α with homologous Hif-1α proteins from other species is shown in Figure S4. *Lc*Hif-1α was evolutionarily closer to the Hif-1α protein of bony fish, such as *C. lucidus*, *Micropogonias undulatus*, *Epinephelus coioides*, *Oryzias latipes*, and *Danio rerio*, and more evolutionarily distant from the Hif-1α protein of cartilaginous fish, mollusks, amphibians, and mammals.

2. Full-length cDNA and bioinformatics of *LcHsp70*

The full-length cDNA of *LcHsp70* (GenBank accession number: MZ197830) was 2 205 bp, including a 142 bp 5' non-coding region, 146 bp 3' non-coding region, and 1 917 bp ORF, encoding a total of 638 aa (Figure S5). The predicted molecular weight of the *Lc*Hsp70 protein was 70.29 kDa. The *Lc*Hsp70 protein contained a DNA binding domain (NBD, 3–387 aa), substrate binding domain (SBD, 395–510 aa), and carboxy-terminal (C-terminal) variable region (VH, 511–634 aa). The nuclear localization signal (NLS, 247–274 aa) was located within the NBD. In addition, 4 aa at the C-terminus (EEVD) were cytoplasm-specific regulatory motifs (Figure S6).

Multiple sequence alignment of *Lc*Hsp70 with homologous Hsp70 proteins from other species is shown in Figure S7. *Lc*Hsp70 shared 99.7%, 70.8%, 89.5%, 84.7%, 85.0%, 85.0%, 83.4%, 82.4%, and 79.1% homology with the Hsp70 of *Drosophila melanogaster*, *Danio rerio*, *H. sapiens*, *X. tropicalis*, *G. gallus*, *Pelodiscus sinensis*, *Procambarus clarkii*, and *Octopus tankahkeei*, respectively, suggesting that the Hsp70 protein is highly conserved among species.

The phylogenetic tree of *Lc*Hsp70 with s Hsp70 proteins from other species is shown in Figure S8. *Lc*Hsp70 was evolutionarily closer to the Hsp70 protein of bony fish, such as *Miichthys miiuy*, *Micropterus salmoides*, *O. mykiss*, and *D. rerio*, and relatively evolutionarily distant from the Hsp70 protein of invertebrates, such as *D. melanogaster* and *Bombyx mori*.

Supplementary Figures

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1       AGCGTGGCACTGTCTTTGAAGAAGAGGAAGAGTACAGACGAGTGGGCTGTGCGTGTGTTTTTTTGTTAGCGGATTAAAAGGCTCGGCTTTTCTTTTCTT
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199     TTCATTTCCTCGACGGGCCCGGATACAGCTCGATAACCCAGAGAGAGACTCAACTCAGGTCCTTTCGTCCTGACATGGACACAGGAATTGTACCAGAAA
1                                                                                  M  D  T  G  I  V  P  E
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9       K  K  R  V  S  S  E  R  R  K  E  K  S  R  D  A  A  R  C  R  R  G  K  E  S  E  V  F  Y  E  L  A  Q
397     AGCTGCCCCTGCCCCACAGCGTCAGCTCCAGCCTGGACAAGGCCTCAATAATGAGGCTCACAATCAGCTACCTGCGCATGAGGAAACTGCTCAGCACTG
42      E  L  P  L  P  H  S  V  S  S  S  L  D  K  A  S  I  M  R  L  T  I  S  Y  L  R  M  R  K  L  L  S  T
496     ATGAGCCAATCGCAGAGGAGGAGACAGATCTTGATTTCCAGCTCAATGGCTCCTACCTAAAGGCTCTGGACGGCTTTTTCATGGTGCTGTCTGAAGACG
75      D  E  P  I  A  E  E  E  T  D  L  D  F  Q  L  N  G  S  Y  L  K  A  L  D  G  F  F  M  V  L  S  E  D
595     GAGATATGATCTATCTGTCGGAGAACATCAACAAGTGCCTCGGGCTGGCACAGTTTGATCTGACCGGACACAGCGTGTTTGACTTCACGCATCCCTGTG
108     G  D  M  I  Y  L  S  E  N  I  N  K  C  L  G  L  A  Q  F  D  L  T  G  H  S  V  F  D  F  T  H  P  C
694     ACCACGAGGAGCTGAGGGAGATGCTGATCCACAAAACAGGCTCCAAAAAGGCCAAGGAACCAAACACAGAGCGCAACTTCTTCATCCGGATGAAGTGCA
141     D  H  E  E  L  R  E  M  L  I  H  K  T  G  S  K  K  A  K  E  P  N  T  E  R  N  F  F  I  R  M  K  C
793     CTCTCACAAGCCGCGGCCGCACCGTCAATGTCAAATCAGCTACATGGAAGGTGCTCCACTGCTCAGGTCATGTCCGTGTCAGTGACAACCGCACCGAGC
174     T  L  T  S  R  G  R  T  V  N  V  K  S  A  T  W  K  V  L  H  C  S  G  H  V  R  V  S  D  N  R  T  E
892     AGACAAACGGGCAAAAGGAACCACCCGTCCCCTACCTGGTTTTAATCTGTGATCCCATCCCACACCCCTCCAACATCGAGGTCCCTCTGGACACCAAGA
207     Q  T  N  G  Q  K  E  P  P  V  P  Y  L  V  L  I  C  D  P  I  P  H  P  S  N  I  E  V  P  L  D  T  K
991     CCTTCCTCAGCCGCCATACAATGGACATGAAGTTCACATATTGTGACGAGAGGATCACCGAGCTCATGGGTTATGATCCAGATGACCTGTTGAATCGTT
240     T  F  L  S  R  H  T  M  D  M  K  F  T  Y  C  D  E  R  I  T  E  L  M  G  Y  D  P  D  D  L  L  N  R
1090    CTGTGTACGAGTACTATCACGCTCAGGACTCAGACCATCTCACCAAGACTCACCACAACTTGTTTGCAAAGGGCCAGGTCTGCACAGGCCAGTACAGGA
273     S  V  Y  E  Y  Y  H  A  Q  D  S  D  H  L  T  K  T  H  H  N  L  F  A  K  G  Q  V  C  T  G  Q  Y  R
1189    TGTTGGCCAAGAGAGGAGGCTTTGTGTGGGTGGAAACCCAAGCCACTGTCATCTACAACAACAAGAACTCTCAGCCACAGTGTGTCGTCTGTGTCAACT
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339     F  V  L  S  G  I  Q  D  E  K  L  I  L  S  L  E  Q  T  E  D  V  K  P  V  K  E  E  L  Q  L  E  E  E
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1783    CTAGCTCCTCAGAGGCTGACAGTCCACTGGACTTTTGTTTCCCCATGGACTCAGATATGAGTTCAGATTTCAAACTCGACTTGGTGGAGAAGCTGTTTG
504     A  S  S  S  E  A  D  S  P  L  D  F  C  F  P  M  D  S  D  M  S  S  D  F  K  L  D  L  V  E  K  L  F
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537     A  I  D  T  E  P  K  T  P  F  T  T  Q  A  V  E  D  L  D  L  E  M  L  A  P  Y  I  P  M  D  D  D  F
1981    AGCTACGCAGTCTGCCCCAAGAAGAGCCTCTATCTTGTGGACCAGTCAAATCCCTTGACAGTTCTCCAGTCTGTGTCACTAAGGACATCCAGAGCTATC
570     Q  L  R  S  L  P  Q  E  E  P  L  S  C  G  P  V  K  S  L  D  S  S  P  V  C  V  T  K  D  I  Q  S  Y
2080    CCAGCTCCCCATTCAGCTCACCAGGCAGCCGCACGGCGTCCCCAGCACCACCGGAGCCAGTTAACACCTCTCATCTTGCCACCATCCTTGCTATGAGGA
603     P  S  S  P  F  S  S  P  G  S  R  T  A  S  P  A  P  P  E  P  V  N  T  S  H  L  A  T  I  L  A  M  R
2179    CCACACAGCTGGGCAACGAAGTCTCGCTTCGGACTTTGGCAGCGCAGAACTCGCAGCGCAAAAGAAAATTATGTGACATAAAAGAGATGATTGGACAGG
636     T  T  Q  L  G  N  E  V  S  L  R  T  L  A  A  Q  N  S  Q  R  K  R  K  L  C  D  I  K  E  M  I  G  Q
2278    GAACTCTGCGCCAGGAAGAGCTGGAACAAGGCAAAAAGCTGAAGGCTTCAGAGTCAGGAACAACGACCATACTGTTGCTGCCTTCAGATTTGGCGAGTC
669     G  T  L  R  Q  E  E  L  E  Q  G  K  K  L  K  A  S  E  S  G  T  T  T  I  L  L  L  P  S  D  L  A  S
2377    GTCTGCTGGGAAGCACGTCAGAGAACACCAGTTCCCTCTTCACACTGCCGCAGCTCACCCGCGACGACTGCGAGGTCAACGCCCCCTTGCAGGGTCGTC
702     R  L  L  G  S  T  S  E  N  T  S  S  L  F  T  L  P  Q  L  T  R  D  D  C  E  V  N  A  P  L  Q  G  R
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735     Q  Y  L  L  Q  G  E  E  L  L  R  A  L  D  H  V  I  *
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2674    GTTTGTGCACATCAAGTGATATCTGCAGCATTCCACCGTGACAAACGCCATAGCAGCATCTGGGGTTTTTTTTGGTGCAAGGGATTCAGGCATCATGAG
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3466    GTCATCAATAGTATCATTCGTGAGTTGTCAAACTTGTTTGCTCATTTAATGGTAGTCGGTTTAATACCATTGTTGGGTCTCATGCTTCTTGTTGCTGTC
3565    TAACATTAAATGGCTTTAATAAAGTGTAGAAAAAAAAAAAAAAAAAAAAAAAAAA
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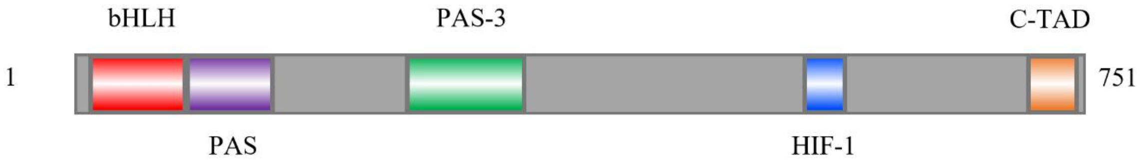
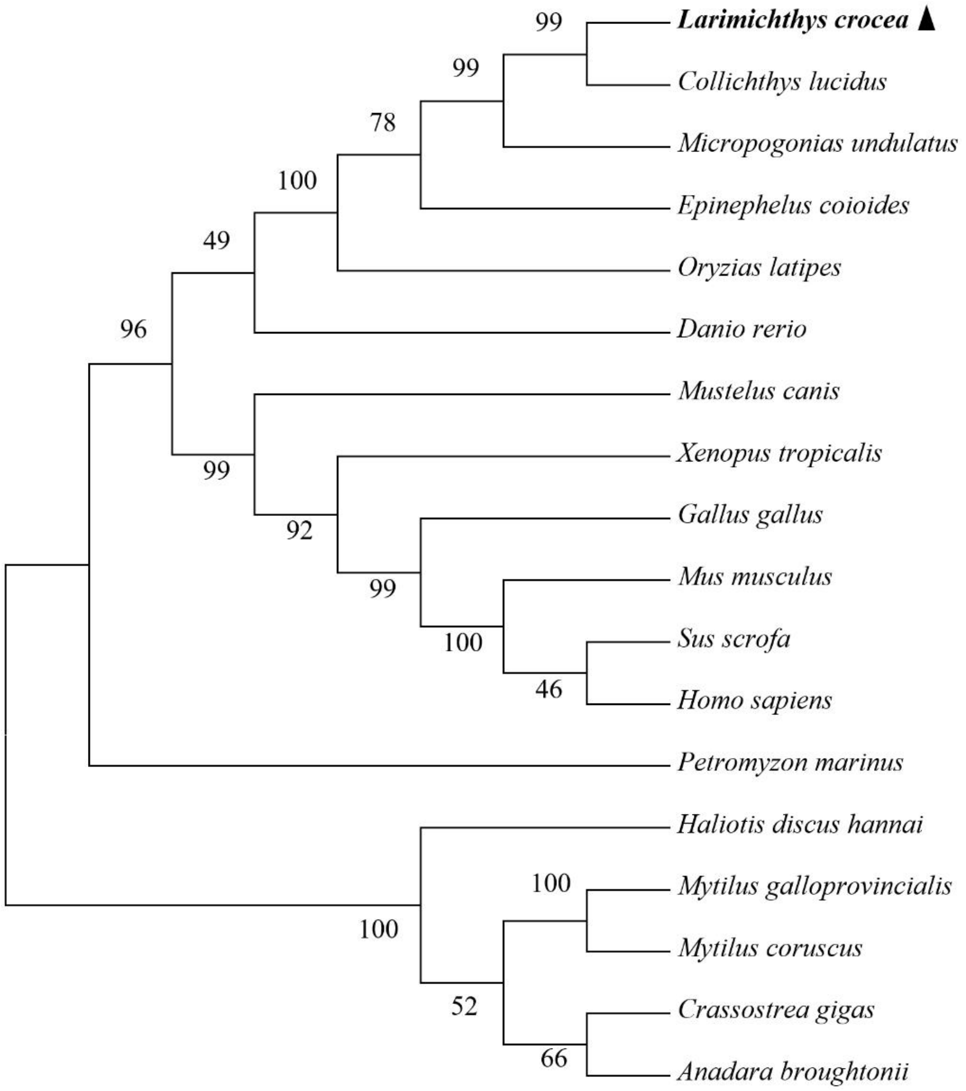
Supplementary Figure S1 Full-length *LcHif-1α* cDNA and predicted *Lc*Hif-1α protein. Green letters represent corresponding amino acid sequences. Bold red letters show start and stop codons. Bold black letters show polyadenylate tail (Poly A) signals.



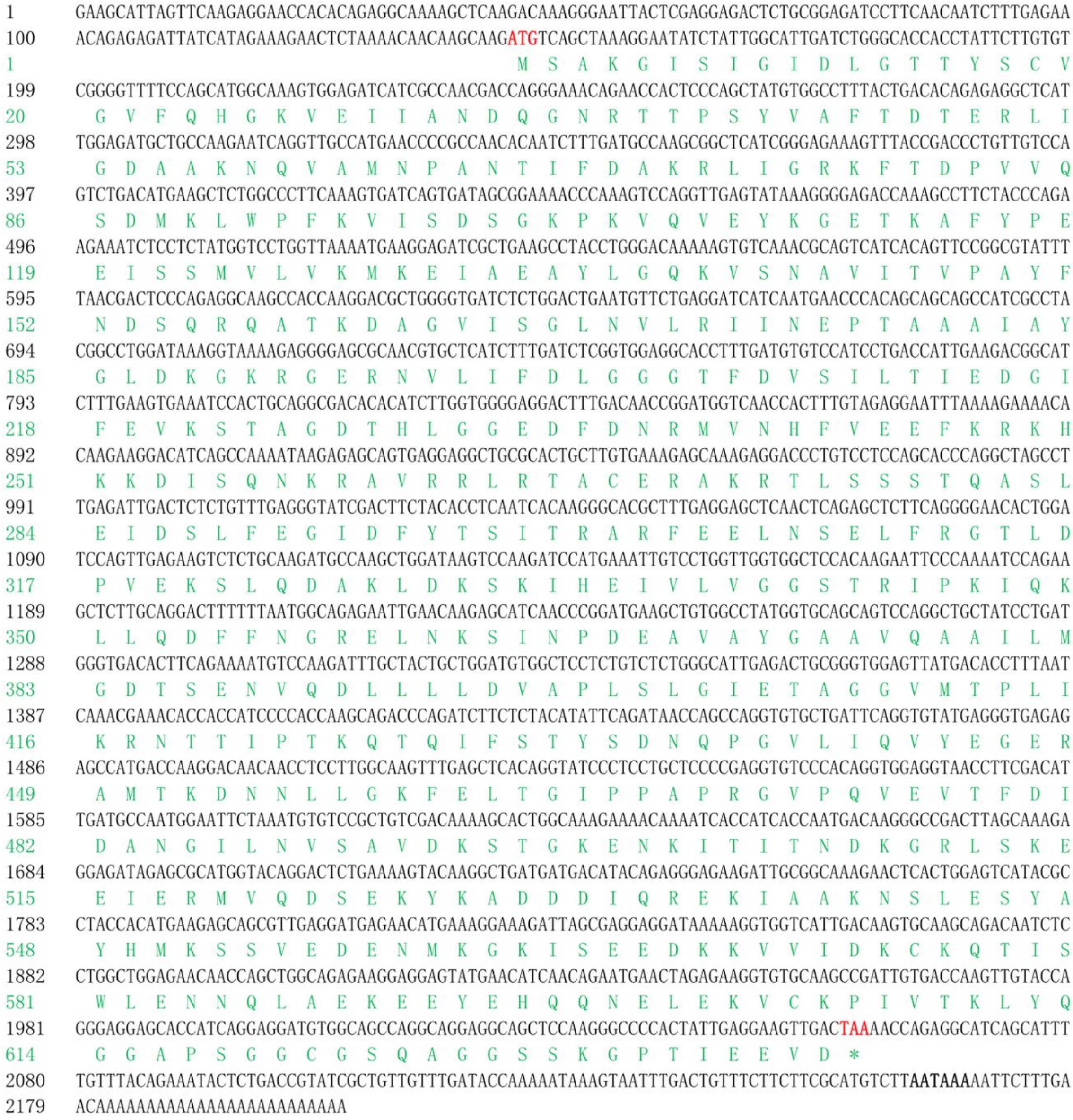
Supplementary Figure S2 Predicted structural domains of *Lc*Hif-1α protein. Red module shows basic helix-loop-helix (bHLH, 12–82 aa), purple module shows PAS domain (88~151 aa), green module shows PAS_3 domain (251–338 aa), blue module shows Hif-1α domain (548–578 aa) and orange module shows C terminal transactivation domain (C-TAD, 714–750 aa).


bHLH
PAS
PAS-3
HIF-1
CTAD
Larimichthys crocea
Collichthys lucidus
Oryzias latipes
Danio rerio
Gallus gallus
Homo sapiens
Sus scrofa
Mus musculus
Xenopus tropicalis
Mustelus canis
Consensus

Supplementary Figure S3 Multiple sequence comparisons of homologous Hif-1α proteins. Red boxes show functional domains of bHLH, PAS, PAS_3, Hif-1, and C-TAD shared by Hif-1α protein. Homology of *Lc*Hif-1α to Hif-1α of *Collichthys lucidus*, *Oryzias latipes*, *Mustelus canis*, *Danio rerio*, *Gallus gallus*, *Homo sapiens*, *Sus scrofa*, *Mus musculus*, and *Xenopus tropicalis* (99.3%, 72.4%, 50.8%, 59.8%, 53.9%, 51.5%, 51.4%, 50.2% and 52.2%, respectively).



Supplementary Figure S4 Phylogenetic tree of homologous Hif-1α proteins. Constructed using MEGA v5.1 software and neighbor-joining method. Same below.



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1                                                 M  S  A  K  G  I  S  I  G  I  D  L  G  T  T  Y  S  C  V
199   CGGGGTTTTCCAGCATGGCAAAGTGGAGATCATCGCCAACGACCAGGGAAACAGAACCACTCCCAGCTATGTGGCCTTTACTGACACAGAGAGGCTCAT
20      G  V  F  Q  H  G  K  V  E  I  I  A  N  D  Q  G  N  R  T  T  P  S  Y  V  A  F  T  D  T  E  R  L  I
298   TGGAGATGCTGCCAAGAATCAGGTTGCCATGAACCCCGCCAACACAATCTTTGATGCCAAGCGGCTCATCGGGAGAAAGTTTACCGACCCTGTTGTCCA
53      G  D  A  A  K  N  Q  V  A  M  N  P  A  N  T  I  F  D  A  K  R  L  I  G  R  K  F  T  D  P  V  V  Q
397   GTCTGACATGAAGCTCTGGCCCTTCAAAGTGATCAGTGATAGCGGAAAACCCAAAGTCCAGGTTGAGTATAAAGGGGAGACCAAAGCCTTCTACCCAGA
86      S  D  M  K  L  W  P  F  K  V  I  S  D  S  G  K  P  K  V  Q  V  E  Y  K  G  E  T  K  A  F  Y  P  E
496   AGAAATCTCCTCTATGGTCCTGGTTAAAATGAAGGAGATCGCTGAAGCCTACCTGGGACAAAAAGTGTCAAACGCAGTCATCACAGTTCCGGCGTATTT
119     E  I  S  S  M  V  L  V  K  M  K  E  I  A  E  A  Y  L  G  Q  K  V  S  N  A  V  I  T  V  P  A  Y  F
595   TAACGACTCCCAGAGGCAAGCCACCAAGGACGCTGGGGTGATCTCTGGACTGAATGTTCTGAGGATCATCAATGAACCCACAGCAGCAGCCATCGCCTA
152     N  D  S  Q  R  Q  A  T  K  D  A  G  V  I  S  G  L  N  V  L  R  I  I  N  E  P  T  A  A  A  I  A  Y
694   CGGCCTGGATAAAGGTAAAAGAGGGGAGCGCAACGTGCTCATCTTTGATCTCGGTGGAGGCACCTTTGATGTGTCCATCCTGACCATTGAAGACGGCAT
185     G  L  D  K  G  K  R  G  E  R  N  V  L  I  F  D  L  G  G  G  T  F  D  V  S  I  L  T  I  E  D  G  I
793   CTTTGAAGTGAAATCCACTGCAGGCGACACACATCTTGGTGGGGAGGACTTTGACAACCGGATGGTCAACCACTTTGTAGAGGAATTTAAAAGAAAACA
218     F  E  V  K  S  T  A  G  D  T  H  L  G  G  E  D  F  D  N  R  M  V  N  H  F  V  E  E  F  K  R  K  H
892   CAAGAAGGACATCAGCCAAAATAAGAGAGCAGTGAGGAGGCTGCGCACTGCTTGTGAAAGAGCAAAGAGGACCCTGTCCTCCAGCACCCAGGCTAGCCT
251     K  K  D  I  S  Q  N  K  R  A  V  R  R  L  R  T  A  C  E  R  A  K  R  T  L  S  S  S  T  Q  A  S  L
991   TGAGATTGACTCTCTGTTTGAGGGTATCGACTTCTACACCTCAATCACAAGGGCACGCTTTGAGGAGCTCAACTCAGAGCTCTTCAGGGGAACACTGGA
284     E  I  D  S  L  F  E  G  I  D  F  Y  T  S  I  T  R  A  R  F  E  E  L  N  S  E  L  F  R  G  T  L  D
1090  TCCAGTTGAGAAGTCTCTGCAAGATGCCAAGCTGGATAAGTCCAAGATCCATGAAATTGTCCTGGTTGGTGGCTCCACAAGAATTCCCAAAATCCAGAA
317     P  V  E  K  S  L  Q  D  A  K  L  D  K  S  K  I  H  E  I  V  L  V  G  G  S  T  R  I  P  K  I  Q  K
1189  GCTCTTGCAGGACTTTTTTAATGGCAGAGAATTGAACAAGAGCATCAACCCGGATGAAGCTGTGGCCTATGGTGCAGCAGTCCAGGCTGCTATCCTGAT
350     L  L  Q  D  F  F  N  G  R  E  L  N  K  S  I  N  P  D  E  A  V  A  Y  G  A  A  V  Q  A  A  I  L  M
1288  GGGTGACACTTCAGAAAATGTCCAAGATTTGCTACTGCTGGATGTGGCTCCTCTGTCTCTGGGCATTGAGACTGCGGGTGGAGTTATGACACCTTTAAT
383     G  D  T  S  E  N  V  Q  D  L  L  L  L  D  V  A  P  L  S  L  G  I  E  T  A  G  G  V  M  T  P  L  I
1387  CAAACGAAACACCACCATCCCCACCAAGCAGACCCAGATCTTCTCTACATATTCAGATAACCAGCCAGGTGTGCTGATTCAGGTGTATGAGGGTGAGAG
416     K  R  N  T  T  I  P  T  K  Q  T  Q  I  F  S  T  Y  S  D  N  Q  P  G  V  L  I  Q  V  Y  E  G  E  R
1486  AGCCATGACCAAGGACAACAACCTCCTTGGCAAGTTTGAGCTCACAGGTATCCCTCCTGCTCCCCGAGGTGTCCCACAGGTGGAGGTAACCTTCGACAT
449     A  M  T  K  D  N  N  L  L  G  K  F  E  L  T  G  I  P  P  A  P  R  G  V  P  Q  V  E  V  T  F  D  I
1585  TGATGCCAATGGAATTCTAAATGTGTCCGCTGTCGACAAAAGCACTGGCAAAGAAAACAAAATCACCATCACCAATGACAAGGGCCGACTTAGCAAAGA
482     D  A  N  G  I  L  N  V  S  A  V  D  K  S  T  G  K  E  N  K  I  T  I  T  N  D  K  G  R  L  S  K  E
1684  GGAGATAGAGCGCATGGTACAGGACTCTGAAAAGTACAAGGCTGATGATGACATACAGAGGGAGAAGATTGCGGCAAAGAACTCACTGGAGTCATACGC
515     E  I  E  R  M  V  Q  D  S  E  K  Y  K  A  D  D  D  I  Q  R  E  K  I  A  A  K  N  S  L  E  S  Y  A
1783  CTACCACATGAAGAGCAGCGTTGAGGATGAGAACATGAAAGGAAAGATTAGCGAGGAGGATAAAAAGGTGGTCATTGACAAGTGCAAGCAGACAATCTC
548     Y  H  M  K  S  S  V  E  D  E  N  M  K  G  K  I  S  E  E  D  K  K  V  V  I  D  K  C  K  Q  T  I  S
1882  CTGGCTGGAGAACAACCAGCTGGCAGAGAAGGAGGAGTATGAACATCAACAGAATGAACTAGAGAAGGTGTGCAAGCCGATTGTGACCAAGTTGTACCA
581     W  L  E  N  N  Q  L  A  E  K  E  E  Y  E  H  Q  Q  N  E  L  E  K  V  C  K  P  I  V  T  K  L  Y  Q
1981  GGGAGGAGCACCATCAGGAGGATGTGGCAGCCAGGCAGGAGGCAGCTCCAAGGGCCCCACTATTGAGGAAGTTGACTAAAACCAGAGGCATCAGCATTT
614     G  G  A  P  S  G  G  C  G  S  Q  A  G  G  S  S  K  G  P  T  I  E  E  V  D  *
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2179  ACAAAAAAAAAAAAAAAAAAAAAAAA
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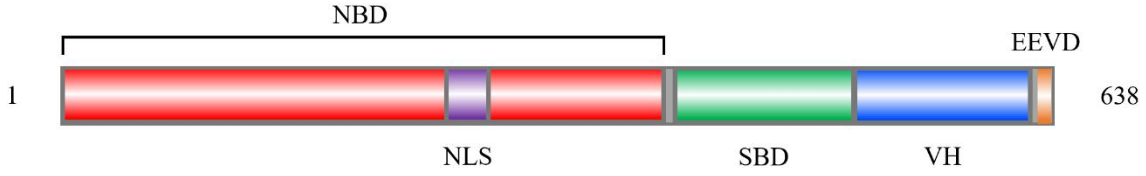
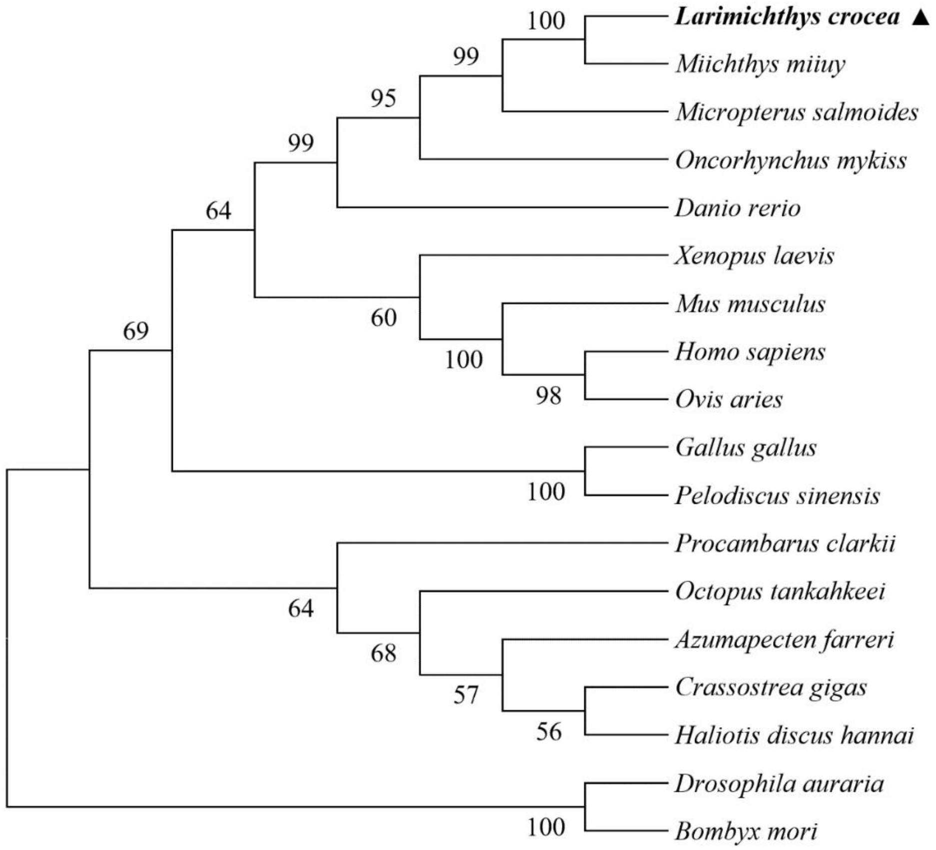
Supplementary Figure S5 Full-length *LcHsp70* cDNA and predicted *Lc*Hsp70 protein.



Supplementary Figure S6 Predicted structural domains of *Lc*Hsp70 protein. Red module shows DNA binding domain (NBD, 3–387 aa), green module shows substrate binding domain (SBD, 395–510 aa), blue module shows carboxy-terminal variable region (VH, 511–634 aa), purple module shows nuclear localization signal (NLS, 247–274 aa), and orange module shows EEVD cytoplasm-specific regulatory motifs.


NBD
SBD
Larimichthys crocea
Miichthys miiuy
Drosophila auraria
Danio rerio
Homo sapiens
Xenopus laevis
Gallus gallus
Pelodiscus sinensis
Procambarus clarkii
Octopus tankahkeei
Consensus
1
70
71
140
141
210
211
280
281
350
351
420
421
490
491
560
561
630
631
660

Supplementary Figure S7 Multiple sequence comparisons of homologous Hsp70 proteins. Red and black boxes show NBD and SBD functional domains shared by Hsp70 proteins, respectively. Homology of *Lc*Hsp70 to Hsp70 of *Miichthys miiuy*, *Drosophila auraria*, *Danio rerio*, *Xenopus tropicalis*, *Gallus gallus*, *Pelodiscus sinensis*, *Procambarus clarkii*, and *Octopus tankahkeei* (99.7%, 70.8%, 89.5%, 84.7%, 85.0%, 85.0%, 83.4%, 83.4%, 83.1%, and 79.1%, respectively).



Supplementary Figure S8 Phylogenetic tree of homologous Hsp70 proteins.

Supplementary Table S1 Primer sequences and siRNA information in this study.

Names	Sequences (5'-3')	Application
LcHif-1α-R1	AGTGATATCTGCAGCATTCCACCGTG	5' RACE
LcHif-1α-R2	GGTAGTCGGTTTAATACCATTGTTGGG	5' RACE
LcHif-1α-F1	AGTGATATCTGCAGCATTCCACCGTG	3' RACE
LcHif-1α-F2	GGTAGTCGGTTTAATACCATTGTTGGG	3' RACE
LcHsp70-R1	CGCATGGTACAGGACTCTGAA	5' RACE
LcHsp70-R2	GAGAAGGTGTGCAAGCCGATT	5' RACE
LcHsp70-F1	CGCATGGTACAGGACTCTGAA	3' RACE
LcHsp70-F2	GAGAAGGTGTGCAAGCCGATT	3' RACE
LcHif-1α-F3	CCTCTCATCTTGCCACCATCC	RT-qPCR
LcHif-1α-R3	GTTCCCTGTCCAATCATCTCTTTTA	RT-qPCR
LcHsf1-F1	TGATTGGACGGACGCAGGA	RT-qPCR
LcHsf1-R1	GAAAGTGGTGGGGGAAAGGG	RT-qPCR
LcHsp70-F3	CTCTGCGGAGATCCTTCAACA	RT-qPCR
LcHsp70-R3	ACAAGAATAGGTGGTGCCCAG	RT-qPCR
LcBax-F	CGCACTATTCTACTTTGCCTGTCG	RT-qPCR
LcBax-R	GCGAATGACTATGACAGTGGTGAGA	RT-qPCR
LcBcl-2-F	TCCACCGACTTTAGTCCGCC	RT-qPCR
LcBcl-2-R	AACAGTTCGTCTATCACCTCGGC	RT-qPCR
LcCaspase-3-F	CAGTTCTGAAATAGCATCAAAGGCA	RT-qPCR
LcCaspase-3-R	AAATGAACATAGGTCACTTCTGCCC	RT-qPCR
Lcβ-actin-F	CTGTCCCTGTATGCCTCTGGTC	RT-qPCR
Lcβ-actin-R	CTTGATGTCACGCACGATTTCC	RT-qPCR
LcHsp70-F3	ATGTCAGCTAAAGGAATATCTATTGG	Antibody preparation
LcHsp70-R3	CTGAATCAGCACACCTGGCT	Antibody preparation
si*LcHsp70*	F: CGGCCUGGAUAAAGGUAAATT R: UUUACCUUUAUCCAGGCCGTT	RNAi
si*LcHif-1α*	F: CGCACCGUCAAUGUCAAAUTT R: AUUUGACAUUGACGGUGCGTT	RNAi
siNC	F: UUCUCCGAACGUGUCAGGUTT R: ACGUGACACGUUCGGAGAATT	RNAi
LcHif-1α-F4	CGGGATCCATGGACACAGGAATTGTAC	Overexpression
LcHif-1α-R4	CCGCTCGAGAATGACGTGGTCCAGAG	Overexpression
LcHsp70-F4	CCCAAGCTTATGTCAGCTAAAGGAATATCTATTGG	Overexpression
LcHsp70-R4	CCGCTCGAGGTCAACTTCCTCAATAGTGGGGC	Overexpression
LcHsf1-F2	ACGGAATTCATGGAGTATCCCG	Overexpression
LcHsf1-R2	ACCGCTCGAGTCAGAGGTCAGAGTC	Overexpression
LcHsf1-F3	ACCGCTCGAGAAAGGTCACACGTCACCGCG	Luciferase reporter
LcHsf1-R3	ACCCAAGCTTGAGAGAGACACAAATCAAAC	Luciferase reporter

	ACTCCAA	
LcHsp70-F5	ACGGGGTACCAGACTCTGCGGAGATCCTTCAACA	Luciferase reporter
LcHsp70-R5	ACCGCTCGAGTCAGACACATGTTAGCAGTTCAGTTCA	Luciferase reporter