

1 **Supplemental figure legends**

2 **Supplemental Fig. S1.** Nucleotide sequence and deduced amino acid sequence of
3 FOXL2 in *E. sinensis* (Es-FOXL2). The underlined sequences indicate the forkhead
4 domain of the FOX family. The initiation and stop codons are in bold.

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6 **Supplemental Fig. S2.** Multiple alignment of FOXL2 amino acid sequences from *E.*
7 *sinensis* and other representative invertebrates and vertebrates. The sequence
8 alignment was performed with software ClustalX software. The forkhead domain and
9 the alanine polymer region are marked in red boxes. The green boxes indicate the
10 nuclear localization signal. The sequences were downloaded from NCBI with
11 following accession numbers: *Homo sapiens*: P58012, *Mus musculus*: Q2TVT7,
12 *Gallus gallus*: Q5J7N5, *Rattus norvegicus*: D4A0S1, *Bos Taurus*: Q6VFT7,
13 *Oryctolagus cuniculus*: Q6VFT5, *Xenopus tropicalis*: F7E8K4, *Danio rerio*:
14 NP_001038717.1, *Strongylocentrotus purpuratus*: ABB89483.1.

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16 **Supplemental Fig. S3.** Phylogenetic analysis of Es-FOXL2 and FOXL2 homologs
17 from other invertebrates and vertebrates. The phylogenetic tree was constructed using
18 the neighbor-joining method in Mega 4.0 software. Numbers in the phylogram nodes
19 indicate percent bootstrap, and the bar at the bottom indicates 5% amino acid
20 divergence in sequence.

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22 **Supplemental Fig. S4.** Nucleotide and deduced amino acid sequence of FTZ-F1 in *E.*
23 *sinensis* (Es-FTZ-F1). The DNA binding domain and the ligand binding domain are
24 shown in bold and italicized, respectively. The two zinc fingers (amino acid residues
25 33–53 for ZF1 and 69–88 for ZF2) are boxed. The underlined region is the FTZ-F1
26 box. The AF2 core is shown in a bold box.

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28 **Supplemental Fig. S5.** Phylogenetic analysis of Es-FTZ-F1 and other members of the
29 NR5As subfamily. The phylogenetic tree was constructed using the neighbor-joining
30 method in Mega 4.0 software. Numbers in the phylogram nodes indicate percent
31 bootstrap, and the bar at the bottom indicates 10% amino acid divergence in sequence.

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33 **Supplemental Fig. S6.** Particle Nucleotide and deduced amino acid sequence of
34 DDX20 in *E. sinensis*.

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36 **Supplemental Fig. S7.** Analysis of recombinant forkhead domain protein. (A)
37 Recombinant plasmid amplified by PCR; M, marker; RP, recombinant pET-32a-EsFH
38 plasmid; D, plasmid digested by *EcoRI* and *XhoI* restriction enzymes. The band at ~5
39 kb is the empty plasmid, and the lower band is the forkhead domain sequence (not
40 observed due to low concentration). (B) Recombinant forkhead domain protein
41 analysed by Coomassie Blue staining. M, marker; Un, lysates of BL21 cells with
42 recombinant pET-32a-EsFH plasmid; In, BL21 cells with recombinant pET-32a-EsFH
43 plasmid induced with IPTG. (C) Forkhead domain protein analysed by western blot.
44 FH, forkhead domain protein; EP, empty plasmid.

45 **Supplemental figures**

46 **Supplemental Fig. S1.**

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10      20      30      40      50      60
1      GAGTACATGAGCCCTTCCGCCTACGAGAGTCAATGACATAAAATCCTACGACAAAATGTAC
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70      80      90      100     110     120
61     TCGTCGAAGAGCCACTTGGAGTCTCCGATTGATGACTCTTCGTATGACAAGTGTGCGAC
19     S S K S H L E S P I D D S S Y D K C C D
130     140     150     160     170     180
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730     740     750     760     770     780
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259    S P S S S H T S L G T A P E L W T S G S
850     860     870     880     890     900
841    AGCACAAGCCTTCACTCTAGCATCGGAGCCAGTAGTTTTTAAAGCCCAGCAGTACTTTA
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910     920     930     940     950     960
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970     980     990     1000    1010    1020
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1030    1040    1050
1021   CTCTCTACTACGGCTGGACGGATTCCAAGCCCTAA
339   L S Y Y G W T D S K P *
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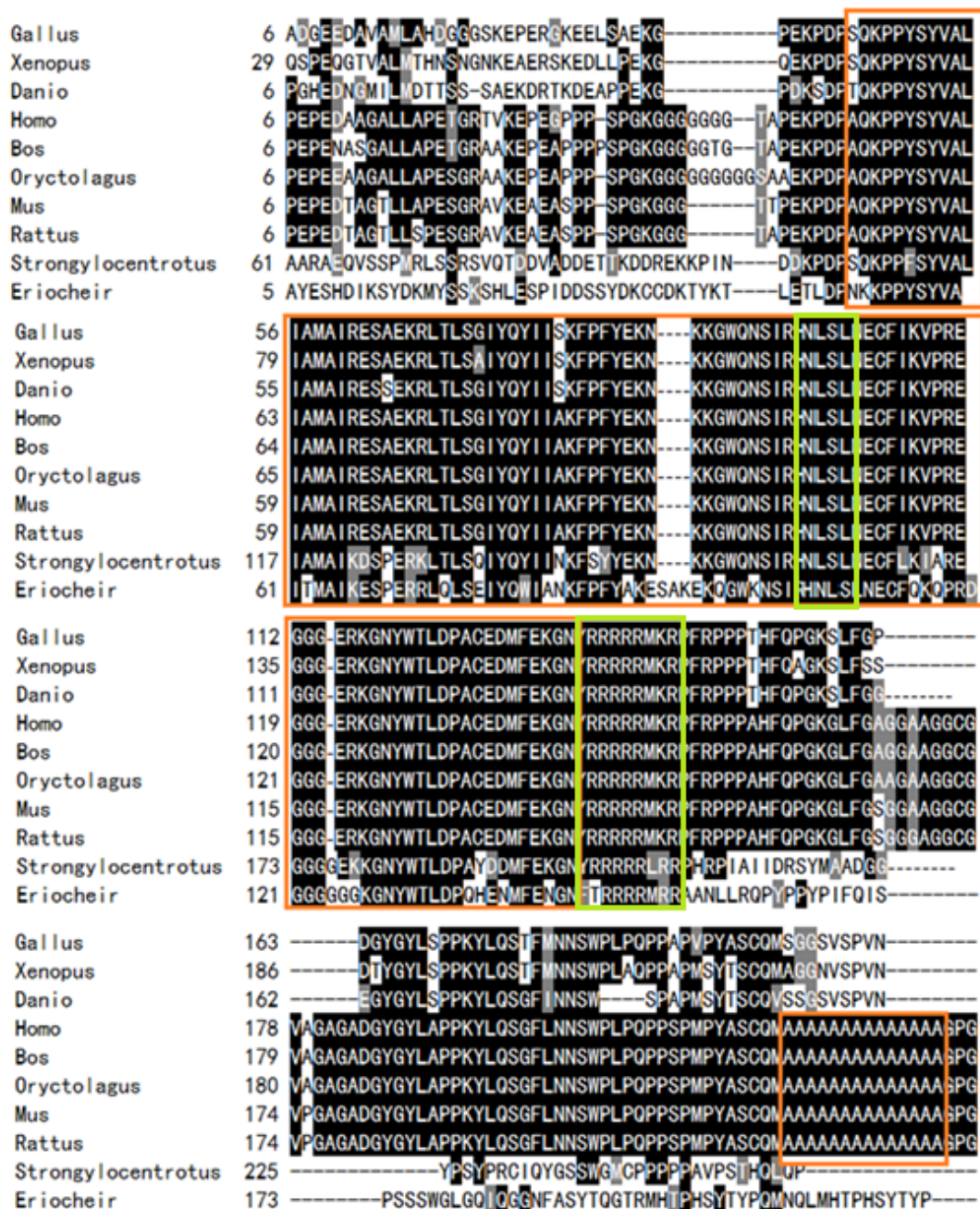
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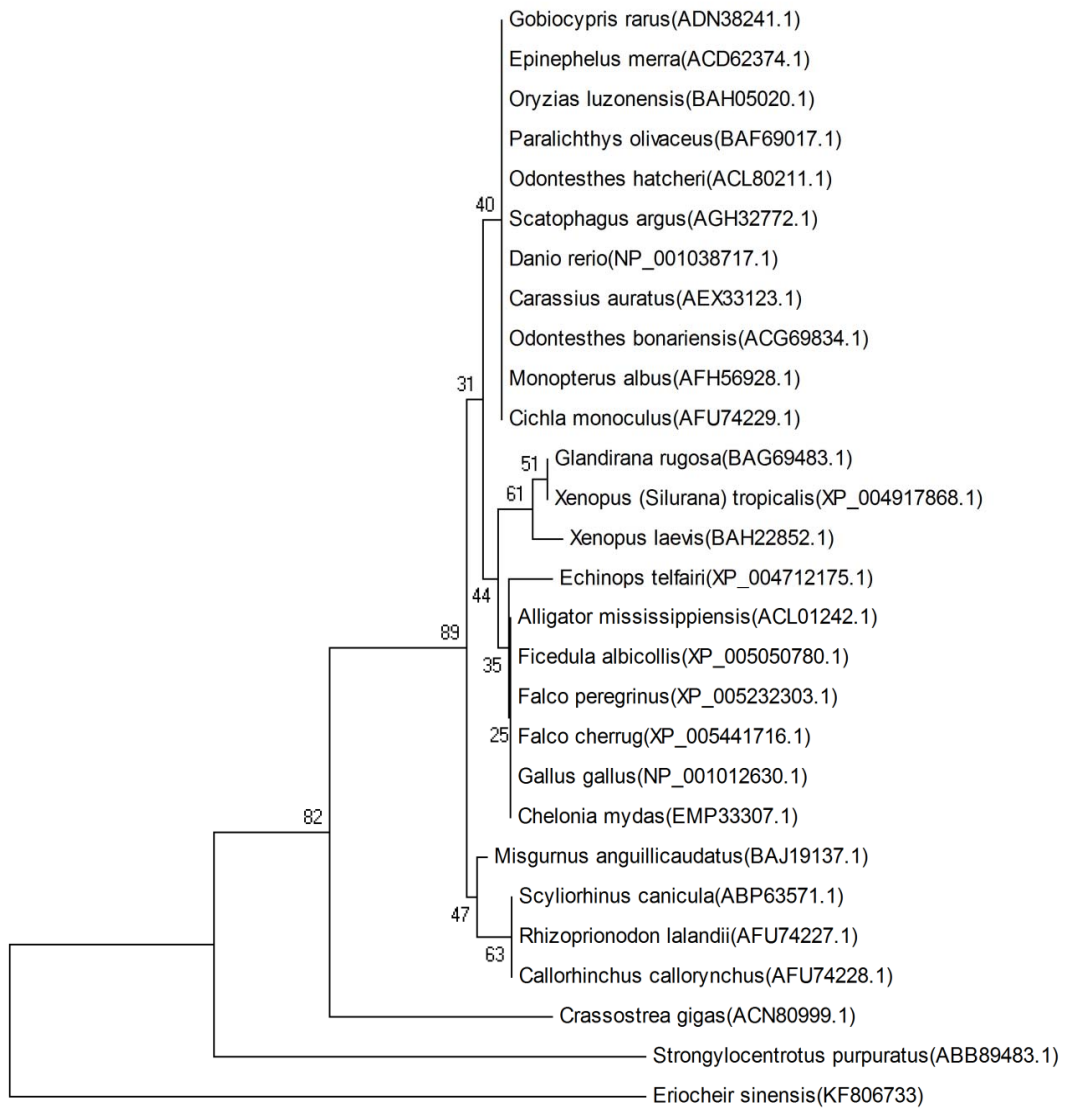
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21     D M P D T K E G I E E L C P V C G D K V
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401    I D L K F D V P E Y I C L K F V I L L N
1261   CCAGCAGAGGTGCGACTACTGAGTGACCGGCGCTCCGTCATTACCGCACACGAGCAGGTC
421    P A E V R L L S D R R S V I T A H E Q V
1321   AAGCAGGCCCTCCTGGACTACATCGCTAACGTGTATCCTGAAGACACGGAGAAGTACCAG
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461    K M M D L L P E L H F I A D N G E K Y L
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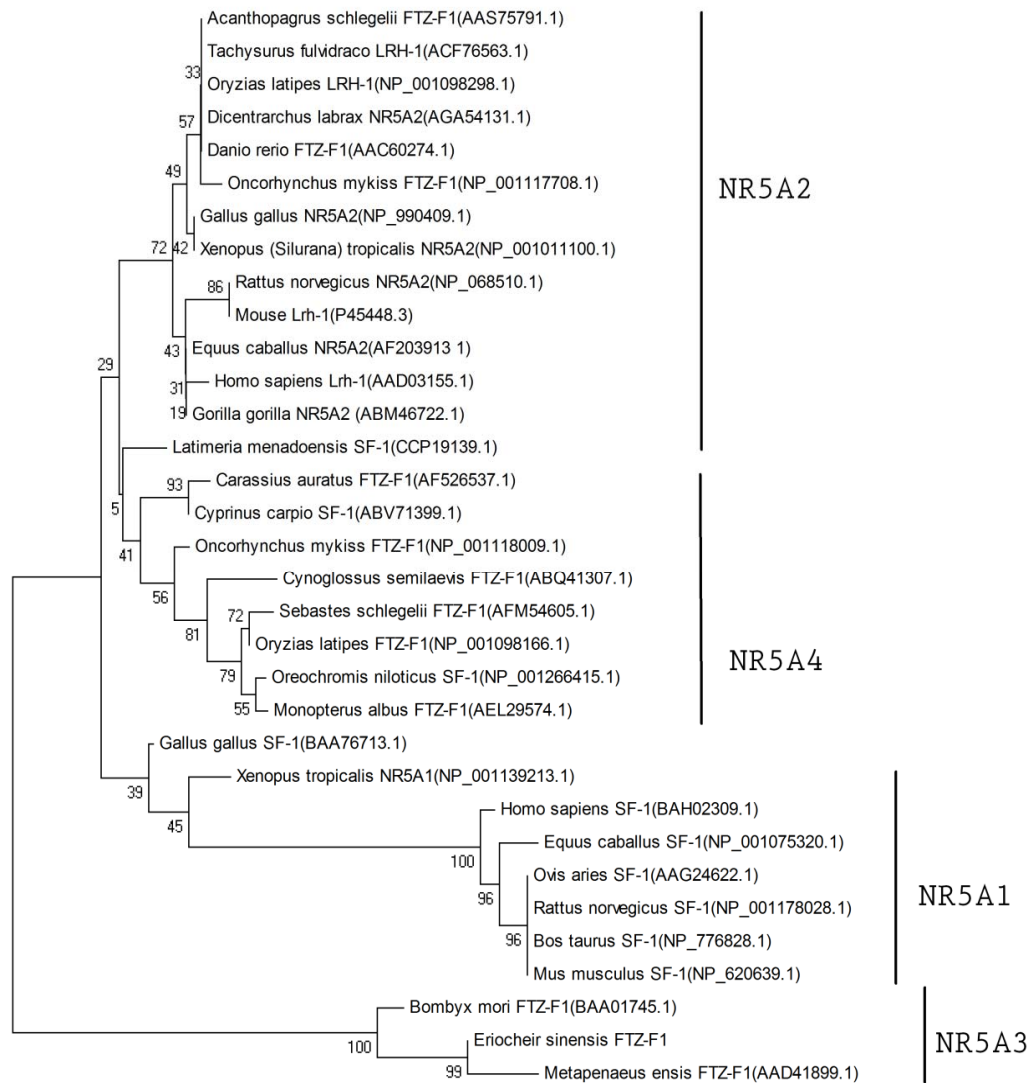
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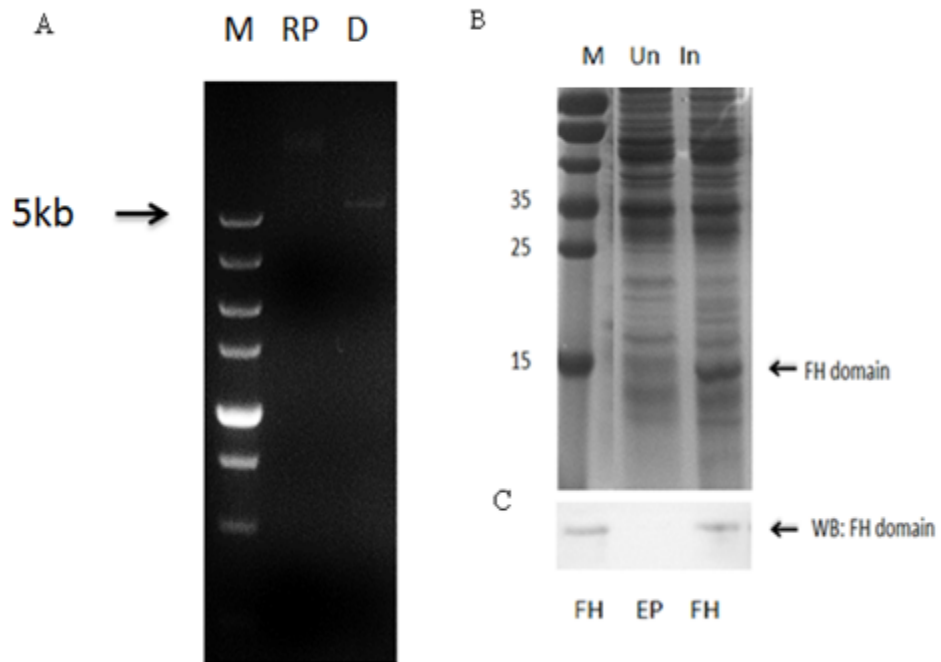


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1      L A V L L R T G Q L E S G R Q H Q H R G
61     GACCTGTGGGGGTTCATCGGTGTGCTTCAATCAATGTGCTGGACGGCGAGGTGTTCTCAA
21     D L W G V I G V L H Q C A G R R G G S Q
121    GTACAACCGCAGTACAAAAACCTTGCCATCCACCGCCAGCTGGCAGTGTCTCCTTGAACC
41     V Q P Q Y K N L A I H R Q L A V L L R T
181    GGACAACCTCGAGAGCGGGCCGCAACACCAGCATCGTGGCGACCTGTGGGGGTTCATCGAC
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301    ACCGGGGGGGAGAACCTCTATGCTCAGGTCTGGTCCACTCTTCCACTCGACGACCTCGGA
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201    V H L L T I P P V A R D V Y N L A F S C
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221    T H D L L I G G C D G G L Y A W K V D L
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781    GGCAATGGCTCTGTGCTGGACTCAATCTCCATGCTGGCGATGAOCTCCTGGCTGCCAAG
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1021   CTGGTGTGCGGGGACGACAAGGGCGCTGTGGGTGTATGACCTCGCGACCTCGTITACG
341    L V C G D D K G A L W V Y D L A D L V T
1081   GGCAGGGCGACCTCCCCCTGACCGGGCGGCGCTCCGATCCCATGGTGGAGCCTGTCAAG
361    G R A T S P L T G G A P I P M V E P V K
1141   ATCCTGGAGTGGCTGAGCTGGAGGATGCGGAGGTGGAAAAGGCCTAAGCTTCCACTG
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1201   GACACGTATGACATAGTGGTTGACAAGTGCCTGTGTCCTATGGGGCCAGCACATCGTG
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1261   GCGGTGACGTGAATAATATGGTGTGTATATGGCGACATGGGAAGGAGGAGGAGGAGG
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