Supplemental figure legends

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

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

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

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

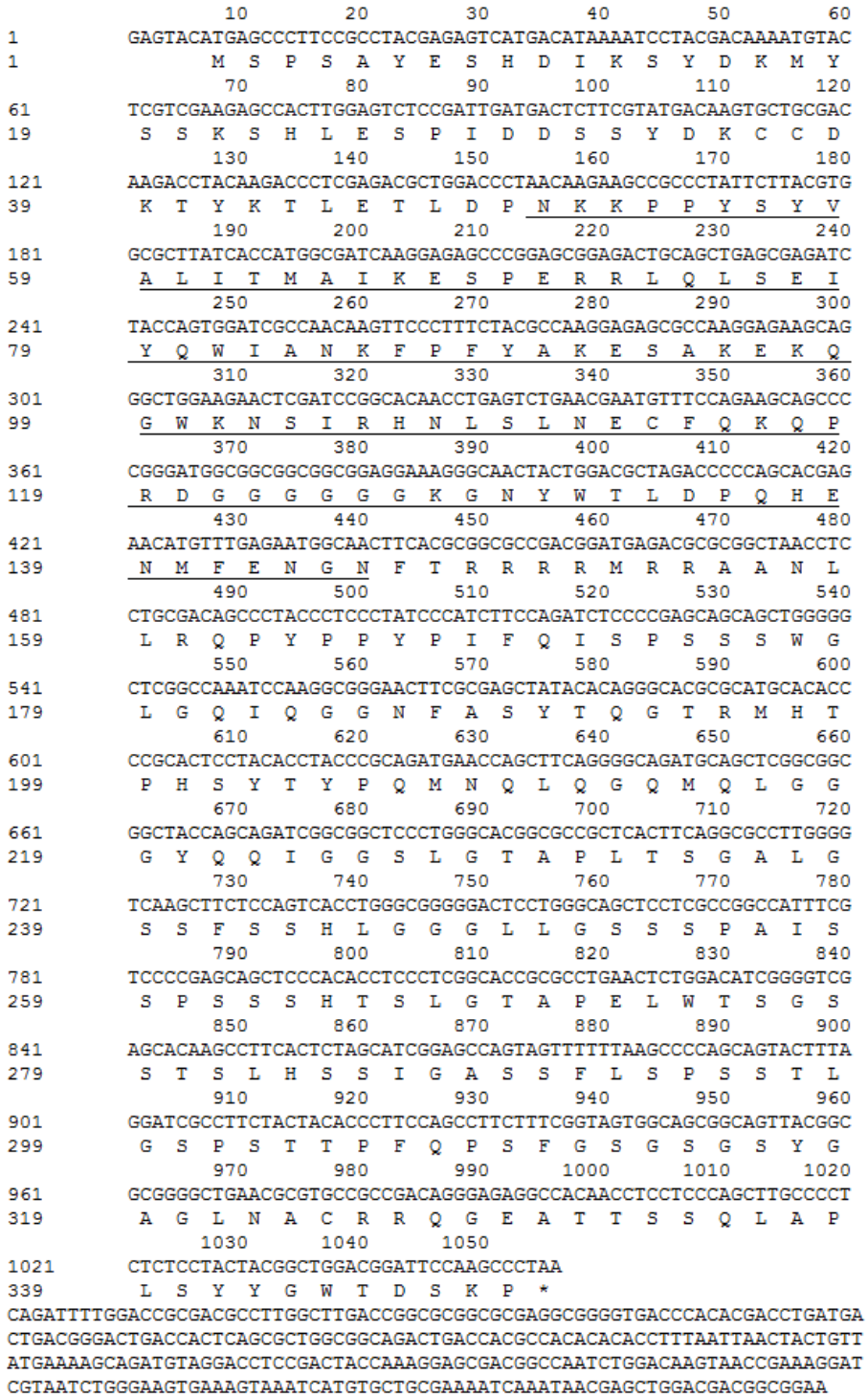
Supplemental Fig. S5. Phylogenetic analysis of Es-FTZ-F1 and other members of the NR5As subfamily. The phylogenetic tree was constructed using the neighbor-joining method in Mega 4.0 software. Numbers in the phylogram nodes indicate percent bootstrap, and the bar at the bottom indicates 10% amino acid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

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

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

Supplemental figures

Supplemental Fig. S1.



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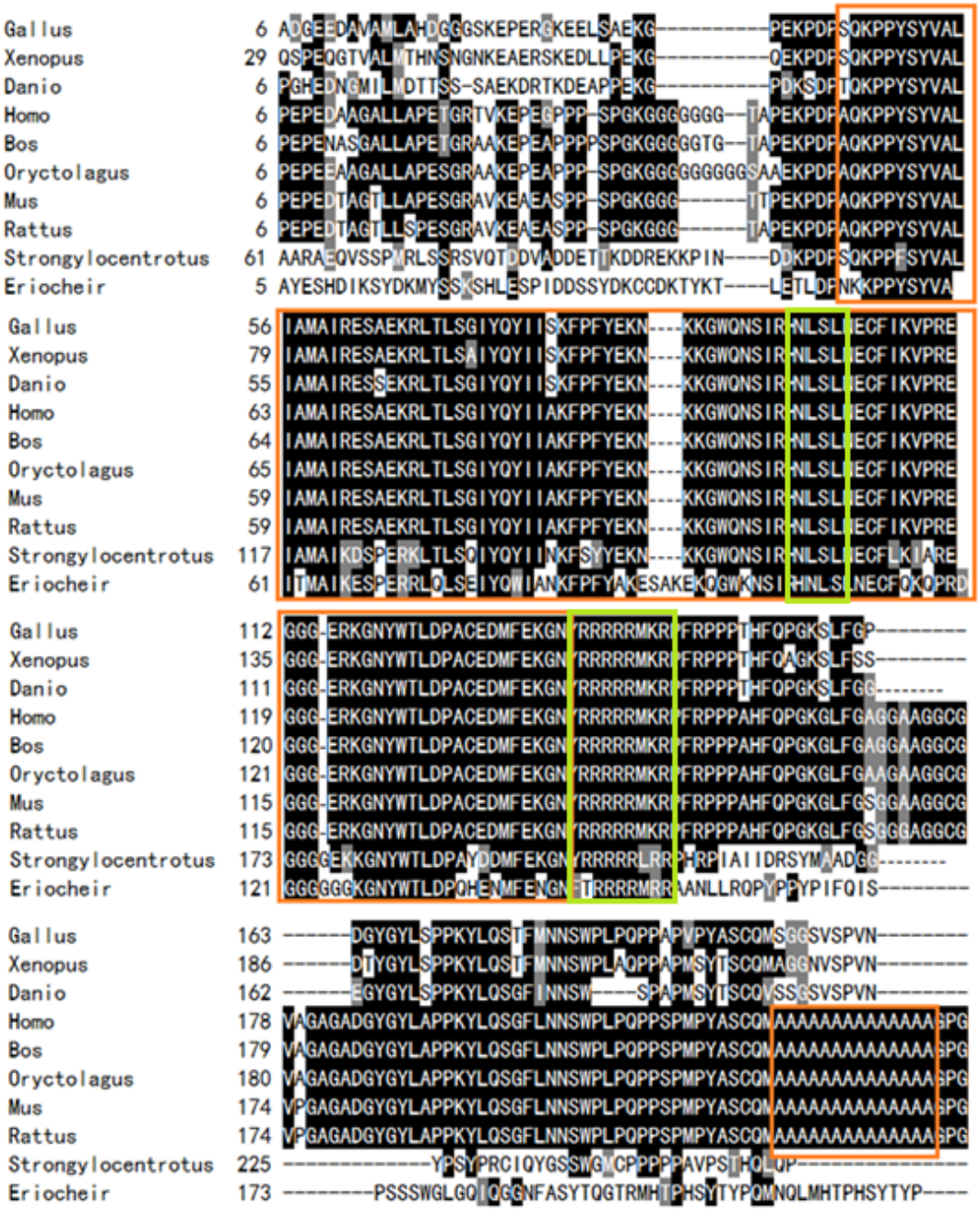

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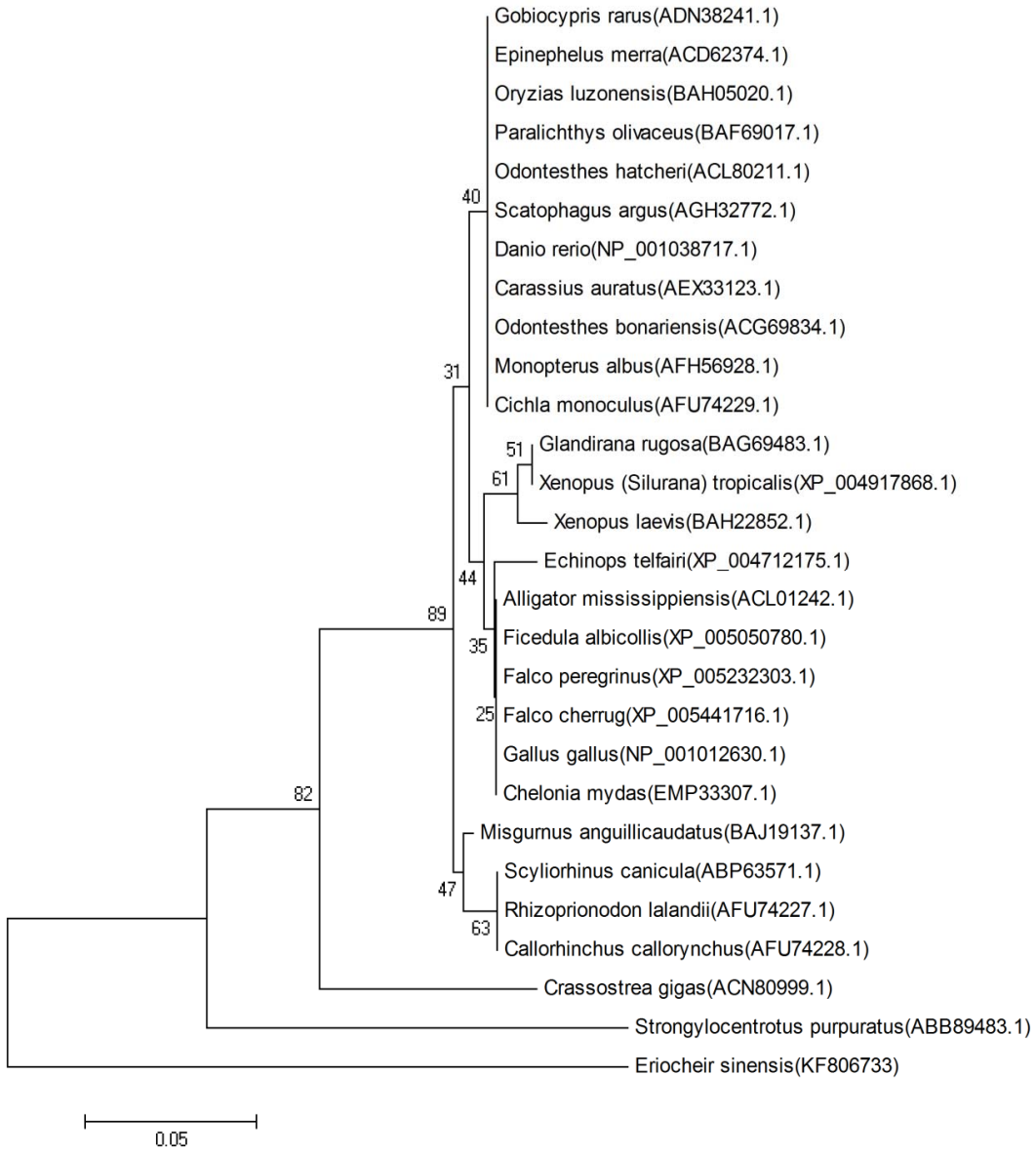

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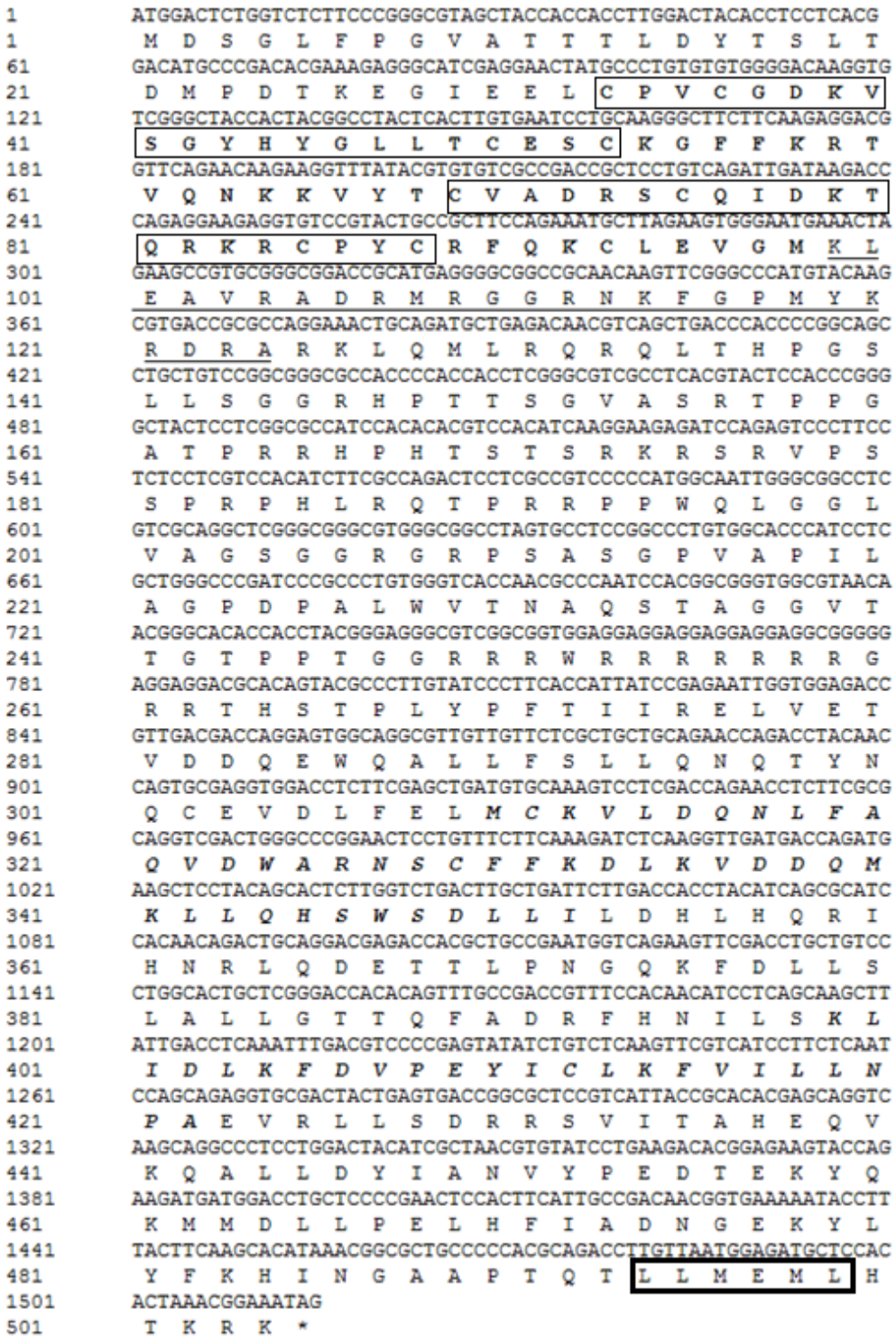

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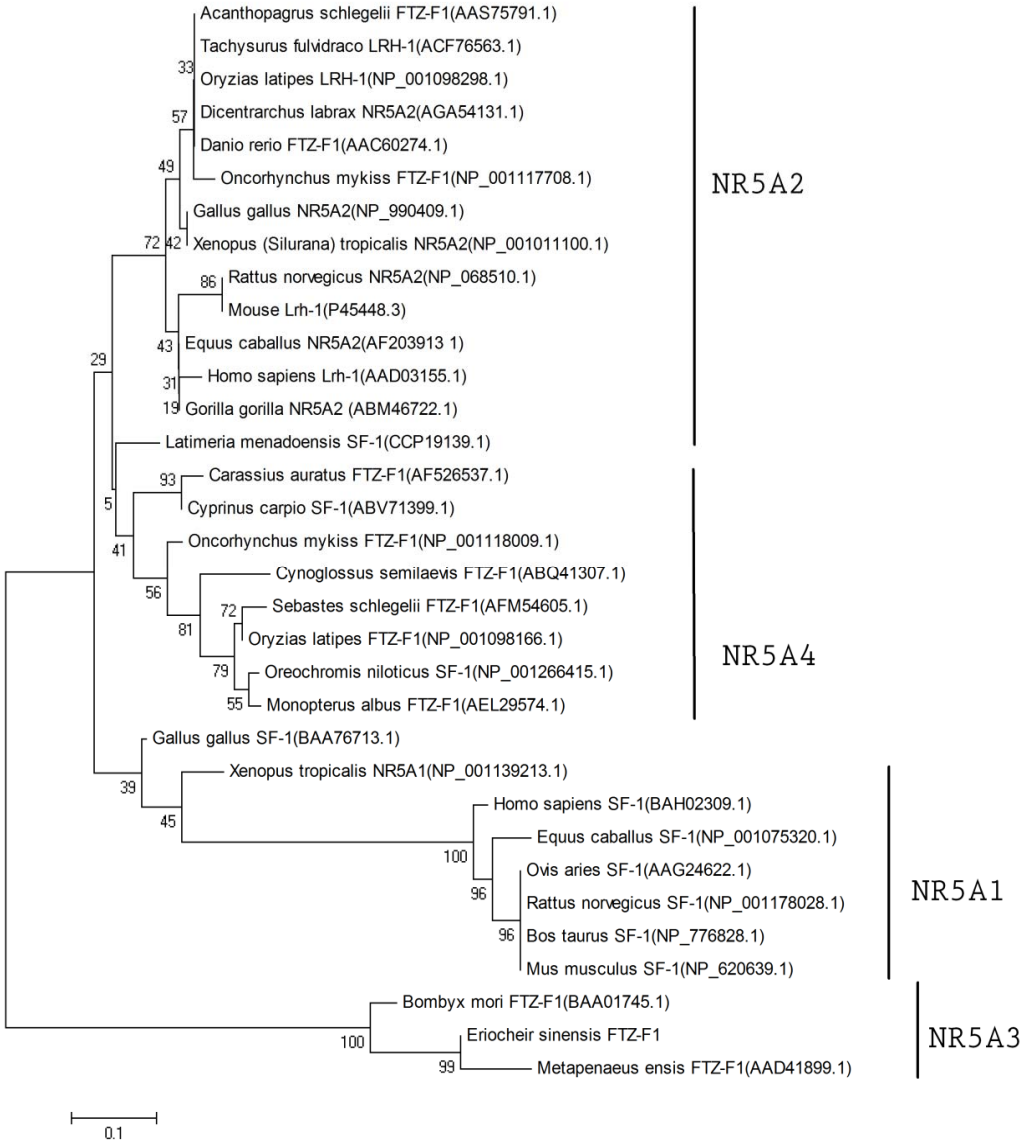
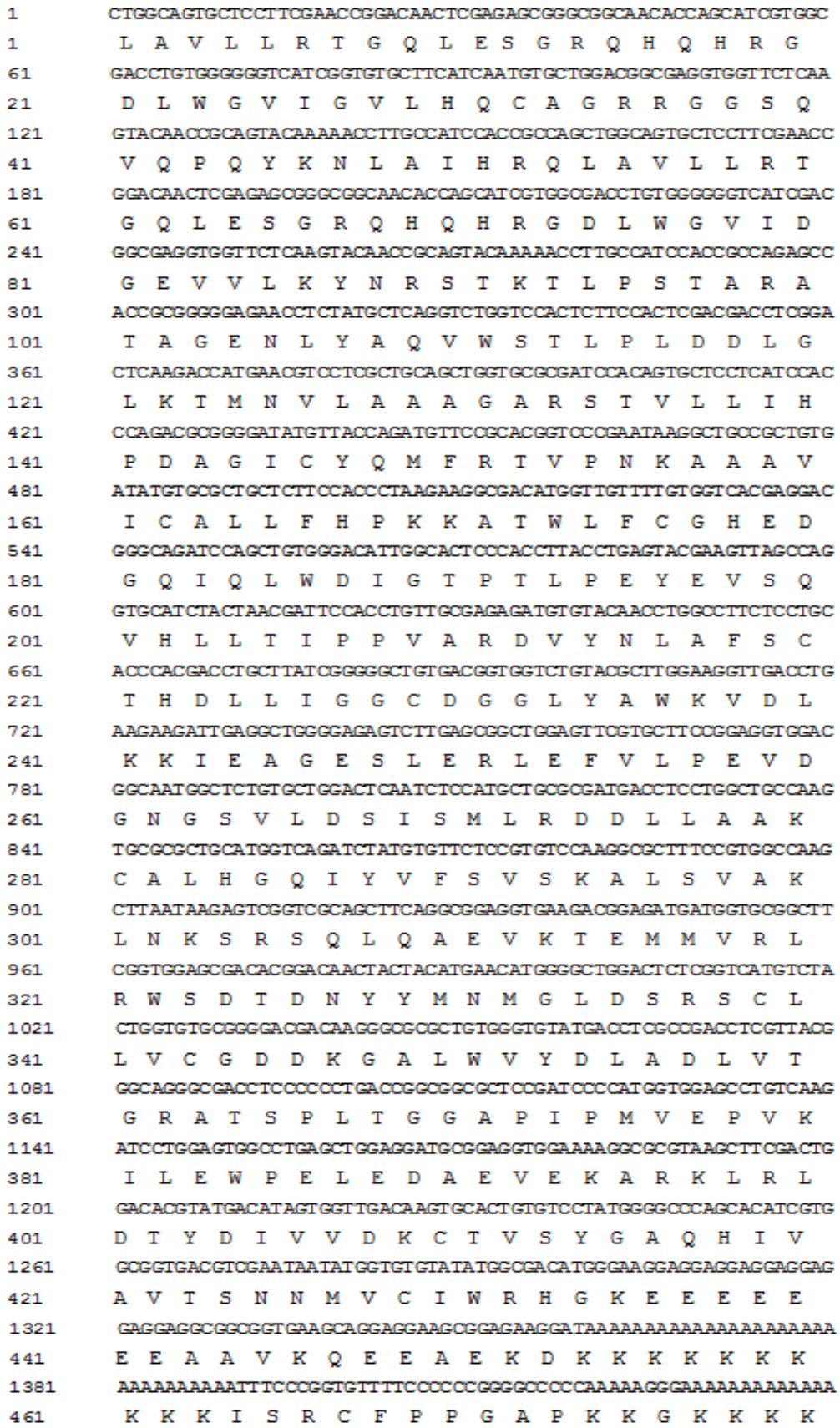


Supplemental Fig. S6.



Supplemental Fig. S7.