

Supplementary Figure

Fig. S1 The full cDNA sequence and deduced amino acid sequence of *Trachinotus ovatus* IRF1. The full-length of cDNA was 1,763 bp, and 299 residues were deduced. The bold underlined letters indicated the start codon (ATG) and the stop codon (TGA). The letters in the box and italic represented the polyadenylation single sequence (AATAAA) and mRNA degradation motifs (ATTTA), respectively. The yellow indicates the DBD domain (aa 1-113), which contains six conserved tryptophan residues.

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1 ACTTCTGTCTCAGACTGTCTCTAGGTGGATAACACAAAGCCGAGGAGAAGTCTCTCTAGAGCAAACGAAA 70
71 TCCAAGCGGATTATTTTTGTGCATTTTCTCTTAAGGATCATTGAACAAACAAAGCCCGCAAACatgcc 140
1 M P 2
141 tgtgtctcggatgaggatgaggccgtggctggagaagatgatcagtcacaacaccatctcgggacctgatg 210
3 V S R M R M R P W L E K M I E S N T I S G L M 25
211 tgggtggacaaggagaagaccatgttctcaattccctggaagcatgcagctcgacacggctgggagctgg 280
26 W V D K E K T M F S I P W K H A A R H G W E L D 49
281 acaaggatgcatgtctgttcaaacagtggccatccacacagggaaatacgttgagggccagaactgtga 350
50 K D A C L F K Q W A I H T G K Y V E G Q N C D 72
351 cccaaagacgtgaaagccaacttccgctgtgcatgaattcactgctgacatagaggaggtgaaagac 420
73 P K T W K A N F R C A M N S L P D I E E V K D 95
421 aagagcatcaacaagggccaccaagccatgcgtgtgttcaggatgctgctgccacccccaaaaactagag 490
96 K S I N K G H Q A M R V F R M L P A T P K T R D 119
491 ataaacgaagcaaaggaaaggaagcaaagttaaggaggaaggaccaatggtaaagatggaggaagacat 560
120 K R S K G K E A K L R R K D P M V K M E E D M 142
561 ggactacagtgatactcagctctcctcggatgcatcactgccggatgagacaactcaggaaaacacagtg 630
143 D Y S D T Q S P S D A S L P D E T T Q E N T V 165
631 gacagtacagtgcacacagagcagcgagatttcatgtgcgtggcttcatctgaggttctcagtggtctc 700
166 D S T V H T E Q R D F M C V A S S E V P E W S H 189
701 attcagttgagattgggtctgagacctctcaaggagcttctacgagagatttgaagtttcacctgagca 770
190 S V E I G S E T F S R S F Y E R F E V S P E H 212
771 cagcttcgacggcagctataccgacgacattgttgagatctgcgagcagctggagagagactcacaattt 840
213 S F D G S Y T D D I V E I C E Q L E R D S Q F 235
841 cagtggatgtcaagcagtgtagatggcagggggttctcagcaatgaacctgcaccagtccagagagcc 910
236 Q W M S S S V D G R G F L S N E P C T S P E S R 259
911 ggtggagtgactcctcctcagtcgacgaattagacgacatgcccaagttacacaacactgggctcagactt 980
260 W S D S S S V D E L D D M P S Y T T L G S D F 282
981 tacaattccacagacgaaatctggaacaccttttgccaaccatacctccaactgaGAGCCTCAGGACGGA 1050
283 T N S T D E I W N T F C Q P Y L H * 299
1051 CAGGACAGGACAATGCTTTGACATTTGGACTAAAAAGCTGTTTCTGCCACCGTCTCCCCCATCTTT 1120
1121 TCAGCTGAGTACCCATCATCACCCCTCCAGTCTGTGACAGGCAGTGTCCACAATTTAAGCTAAAACACT 1190
1191 GCCCTCAACTGCGTCTACTGTGCGTCTGACTCTGTACCAGTTGGAGAGCTTTCCTCATTCCCTCAAC 1260
1261 CTTTATGTGAAGTTATGAAGAGAAGATATGAAGTGCCTGCTGTTAAAGGACATTCTGTTCAATTGTCTCT 1330
1331 GTTTTTGGCTGGTTCAAGGCATTGTGGTGTCTCAGTTTTTTGTCATGTTTAGTTCTAATTGGATAGAACTG 1400
1401 TGTTTTGCTCAGGAAGGTATTTACATGGTCATACTCAGCTATGAATACATAAAGCTAGTCAACACTTA 1470
1471 ACCATAAAGTGCAAATAGGCTCACATTCAGTGCTCTCACATTTGATAGTAAGTCAGTAATTGTAGTGTC 1540
1541 AAATAGTTATCACATAAATCATTTATTTTCCGTTATGTGTACCCATCAATTCTAGTTAAAGGGATTATA 1610
1611 AGACATTTGTCAAATTAATCTTCTTAACCTCAACTTCTGGTAAAAGCGCTACTTCATTATCTGAGTTT 1680
1681 TCTTACTTCCGGAAATTGTAGAAAGTTTCTGTAAATAGTTGTGTCTGTCTGTGTTTTTATAAAATAAA 1750
1751 AAAAAAAAAAAAAA 1763
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1 **Supplementary Table**

2 **Table S1.** IRF1 proteins used in multiple alignment.

Species	Abbreviation	Protein name	Total AA identity %	DBD domain identity %	No.
<i>Trachinotus ovatus</i>	Tov	IRF1	100	100	MN244166
<i>Gasterosteus aculeatus</i>	Gga	IRF1	65.42	84.07	ENSGACT00000027655.1
<i>Takifugu rubripes</i>	Tru	IRF1	57.75	81.42	ENSTRUT00000010295.3
<i>Oreochromis niloticus</i>	Oni	IRF1	71.72	92.92	ENSONIT00000069535.1
<i>Oryzias latipes</i>	Ola	IRF1	65.12	85.71	ENSORLT00020035606.1
<i>Poecilia formosa</i>	Pfo	IRF1	68.47	95.58	ENSPFOT00000032009.1
<i>Xiphophorus maculatus</i>	Xma	IRF1	67.80	92.92	ENSXMAT00000011129.2
<i>Danio rerio</i>	Dre	IRF1	55.74	85.09	ENSDART00000158742.2
<i>Astyanax mexicanus</i>	Ame	IRF1	55.41	83.04	ENSAMXT00005051691.1
<i>Xenopus tropicalis</i>	Xtr	IRF1	43.87	69.03	ENSXETT00000030538.1
<i>Gallus gallus</i>	Gga	IRF1	46.27	74.34	ENSGALT00000002244.6
<i>Homo sapiens</i>	Hsa	IRF1	42.72	70.80	ENST00000245414.9
<i>Mus musculus</i>	Msu	IRF1	44.88	70.80	ENSMUST00000108920.8

Table S2. Lengths of exons (bp) and introns (bp) of each *IRF1* gene.

Species	E1	I1	E2	I2	E3	I3	E4	I4	E5	I5	E6	I6	E7	I7	E8
<i>Trachinotus ovatus</i>	87	755	100	105	168	191	41	255	127	175	117	140	29	184	124
<i>Gasterosteus aculeatus</i>	87	376	100	84	168	103	41	147	127	101	117	127	29	121	118
<i>Takifugu rubripes</i>	87	86	100	74	168	105	38	108	133	91	117	111	26	151	121
<i>Oreochromis niloticus</i>	87	480	100	98	168	143	41	220	127	98	102	130	29	188	124
<i>Oryzias latipes</i>	87	148	100	83	168	134	38	172	133	100	117	107	29	195	91
<i>Poecilia formosa</i>	87	92	100	113	168	116	41	154	133	111	114	125	29	174	115
<i>Xiphophorus maculatus</i>	87	86	100	93	168	114	41	182	133	108	114	129	29	178	115
<i>Danio rerio</i>	87	88	100	250	209	-	-	603	100	137	102	531	29	162	124
<i>Astyanax mexicanus</i>	87	123	100	102	212	-	-	126	121	111	117	130	29	153	133
<i>Xenopus tropicalis</i>	87	599	100	379	177	206	47	110	115	510	120	1223	41	113	127
<i>Gallus gallus</i>	87	871	100	175	177	241	50	126	136	191	126	468	32	615	136
<i>Homo sapiens</i>	87	1366	100	795	177	109	50	108	130	183	123	534	50	1169	136
<i>Mus musculus</i>	87	1463	100	717	177	93	50	86	133	151	123	585	50	814	136

