

## Supplemental Figure 1

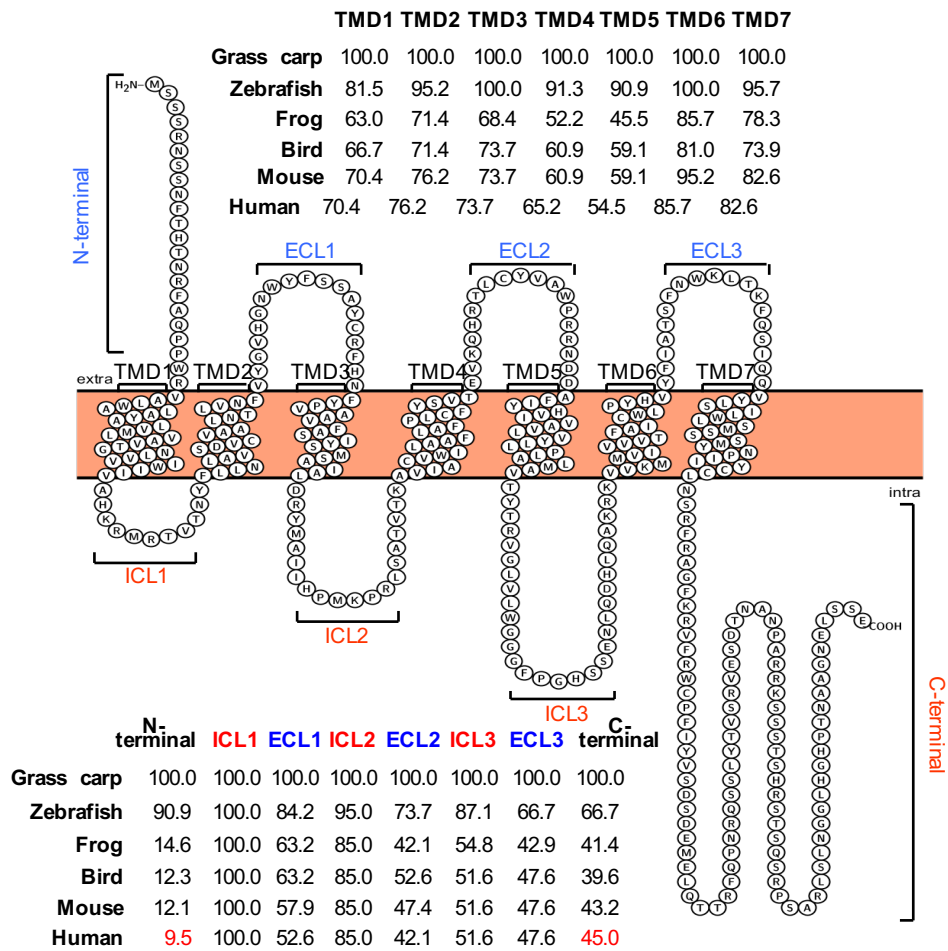
```

1      cacacacacacacacagacagacagacagacagcagggtgtcttctgagagaatc
52  ATGTCCTCATCAAGAACTCCTCAAACCTCACC CATAACC AACAGGTTTCGCGCAGCCTCCA 20
    M S S S R N S S N F T H T N R F A Q P P
112 TGGCGCGTCGCGCTCTGGGCGCTCGCGTACGCGCTGGTTATGCTGTGGCCGTGACGGGA 40
    W R V A L W A L A Y A L V M L V A V T G
172 AACCTGGTCGTCATCTGGATCATCGTTGCGCAC AAGAGGATGAGA ACCGTCACCAACTAC 60
    N L V V I W I I V A H K R M R T V T N Y
232 TTTCGTGCTCAACCTCGCGGTGTCTGACGTGTGCGTGGCCGCGCTCAACACGCTGGTGAAC 80
    F L L N L A V S D V C V A A L N T L V N
292 TTCGTGTACGGCGTGCACGGGAACTGGTACTTC AGCAGCGCGTAC TGCCGCTTCCAC AAC 100
    F V Y G V H G N W Y F S S A Y C R F H N
352 TTCTACCGGTGGCGCGGTGTTCGCGAGCATCTACTCCATGAGCGCCATCGCCTTAGAC 120
    F Y P V A A V F A S I Y S M S A I A L D
412 AGGTACATGGCGATCATCCACCGATGAAGCCC CGCCTCTCAGCGACGGTCACCAAGCT 140
    R Y M A I I H P M K P R L S A T V T K A
472 GTGATCGCATGTGTGGGATTCTGGCCGCAATTCTGGCCTTTCCACTCTGCTTTTACTCC 160
    V I A C V W I L A A F L A F P L C F Y S
532 GTAACGGAAGTGAAGCAGCACAGGACGCTCTGCTATGTGGCCTGGCCGCGCGCAACGAC 180
    V T E V K Q H R T L C Y V A W P R R N D
592 GACGCCTTCATATATACGTCGTCGTCGGCGGTGCTGGTA TATCTCTGCGCTCTGGCATG 200
    D A F I Y H V I V A V L V Y L L P L A L
652 ATGGCCGTACCTACACAGGTTGGGACTCGTGCTGTGGGGCGGTGGATTC CCGGACAC 220
    M A V T Y T R V G L V L W G G G F P G H
712 TCCTCGGAAACTTACAGGATCATCTGCAGGCC AAGAGA AAGGTTGTGAAGATGATGTTG 240
    S S E N L Q D H L Q A K R K V V K M M V
772 ATCGTGGTAGTAACATTGTCATCTCTGGCTCCATATCATGTGTATTTCATCGCGACG 260
    I V V V T F A I C W L P Y H V Y F I A T
832 AGCTTCAACTGGAAGCTGACAAAATTCAGTCGATCCAGCAGGTGTATCTGTCGATCTG 280
    S F N W K L T K F Q S I Q Q V Y L S I L
892 TGGCTCTCCATGAGCTCTCCATGTACAACCCCATCATCTACTGCTGCGCTCAACAGCAGG 300
    W L S M S S S M Y N P I I Y C C L N S R
952 TTCCGCGCGGCTTCAAGCGGGTGTTCGCTGGTGTCCC TTCAATTATGTGTGCGACTCT 320
    F R A G F K R V F R W C P F I Y V S D S
1012 GATGAGATGGAATCCAGACCCCGATTCCAGCCAAACCGCAGAGCAGCCTGTACACG 340
    D E M E L Q T T R F Q P N R Q S S L Y T
1072 GTCTCACGTGTGGAGTCCGACCAACGCCAACCCGCGAGAGCGAAGAGCTCCAGCACC 360
    V S R V E S D T N A N P A R R K S S S T
1132 AGCCACCGCAGCACCACCAATCACGACCTCTGCCCGCTGTCACTCAATGGTGGTCTC 380
    S H R S T S Q S R P S A R L S L N G G L
1192 CATGGACCCCTACGAACGCCGCGGTAATGAACTCAGTCTCAGAGTAGGtcgcaaaacac 395
    H G H P T N A A G N E L S S E *
1252 taagctgcagaaatgacaggaaattcaccttcaggagctgctgaatgccagcctcagtc 400
1312 accagcttcactttgacctctcttcaattccaacatat taaaaataactcaccacaca 410
1372 tatgaaaaatgaacacttctgaggacatacacacgggtctgttgacgaagattgttaaca 420
1432 gggttacactgtgtcctaaccagacacatacaaa taagat tccagcgacaagaagtttatc 430
1492 tgtccacaccagacgcgactacaagatgccaca aaatca atcgcaaatcacagccaa tca 440
1552 taagagcatgtggcgaggagtctctctgcaggcc cactac actcgc aacctaatcaatcca 450
1612 aaatcgctgcacgcactgcactcactaccaaatt ggataa gcacaaatcaaatcattcaaa 460
1672 tatcacaccattttaacattattaaaaaacgt actgagttactgaaacaa tctttgtca 470
1732 tagaatacacttacttgttcacagcacgaaaaa aaaaaa aaaa

```

**Supplemental Figure 1.** Molecular cloning of grass carp TACR3. Nucleotide and deduced amino acid sequences of the grass carp TACR3. Numbering of the deduced amino acid sequences begins with the first methionine of the ORF to the right of each line. Nucleotide numbers are to the left of each line. The start and stop codons are shaded in gray. Predicted transmembrane domains (TMD1-TMD7) are boxed.

Supplemental Figure 2



**Supplemental Fig. 2.** Sequence analysis of grass carp TACR3. Snake diagram of grass carp TACR3 with Protter program. The seven transmembrane domains, three intracellular domains and three extracellular domains are labeled as TMD1-7, ICL1-3 and ECL1-3, respectively. Sequence identities of transmembrane domains (TMD1-7) and extracellular domains (ECL1-3), intracellular domains (ICL1-3), N-terminal and C-terminal between grass carp and other vertebrates were showed in the table.