



1  GCAACACAAGAAGCCCCGAAGTCCCTGTTTCCCGTGTGGCAGTGGCGCTCGTCCCCTGAT 60
A T Q E A P K S L F P V W Q C G S S P D

61 GGTTTTGTCACTCTGGGCTGCGTCACCCGCGACTTGGCAACCCCTGATGGACTGAGCTAC 120
G F V T L G C V T R D L A T P D G L S Y

121 GTTTGAAGGATGCGAGCGGCACCGCGCTGACTACTAACGTTGTACAATACCCGGCGGTG 180
V W K D A S G T A L T T N V V Q Y P A V

181 ATCGAGGGCGAAAAGTACTCCTCAGTGAGTCAGGCGCGCTCAGTGCTAACGACTGGAAC 240
I E G G K Y S S V S Q A R V S A N D W N

241 GCGAACAAAGAAGTTCACCTTGCGAAGTCACTAATCCCCGGGGAACGAAAACGGCAGAGCTG 300
A N K K F T C E V T N P R G T K T A E L


301  AAAAAGCCAGTTGTGCCCGACATCCCTGCAAATCTCTGCTTCTAACAGCTCCGAGCCAA 360
K K P V V P D I P A K S L L L T A P S Q

361 ACAGAATTAGAAAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTACCTAAA 420
T E L E N G T A T F I C L A S E F S P K

421 ACGTCCACATTTAAGTGGACCCGTGGAGGAACAAGCATCGATAATAAGGCCAAAAGACCCC 480
T S T F K W T R G G T S I D N K A K D P

481 ATTTTAAATCGCGGGAAAACCTACTTACAGTTCCTTTAGTATTTTGGTACTCACTGCTGCC 540
I L I A G K P T Y S S F S I L V L T A A

541 GAATGGACTGGCTCAACTTCTCCAGTTAAGTGGCAGTTCAGCAGAAGTCACAGACTCTG 600
E W T G S T S P V K C E F Q Q K S Q T L


601  TCCAAGGAGGCAAGTTATCATTATGTGACCCGGGAGCAGCCAACAATTACAATAATCCCA 660
S K E A S Y H Y V T R E Q P T I T I I P


661 CCTTCCAACAATGACATGCTTATCAAAAGATCTGGCGACCTCGTGTGCAAGGCTGAAGGA 720
P S N N D M L I K R S G D L V C K A E G

721 CCATTGGGTTTCACTGGAATTAAGTGGGTTGCTAACGGTAAAGAGTTGTTTCCCTATCT 780
P L G F T G I K W V A N G K E V V S L S

781 GAAAAAGTTGTGTCTACGAAGGCAGCGATCTCACTCACCACCTCAATCTCTTACGAAGAG 840
E K V V S T K A A I S L T T S I S Y E E

841 TGGCATAAGGGCATGAAATTTACCTGTGAGGTGCATCATTCTCATTGCTCAGGGGTTT 900
W H K G M K F T C E V H H S S F A Q G F

901  ATAACAGAAGTCTACAAAAGAGAAAATATGCCTTAACATTTGTATTTCTCTCCTCATC 960
I T E V Y K R E N Y A L T F V F L F L I

961  ACCCTGTTCTACAGCATCGGGGTGACTGTTATCAAGGTGAAATGGGAAACAATAATGGA 1020
T L F Y S I G V T V I K V K W E T T N G

1021 ACGATTTTGATTTTCTCTCTGTTTTTTTTTCTTTCAGTATAAGTTGTTTGTGTTTTT 1080
T I L I F S L F F F S S V *

1081 TTTTATTTTAGTGTCTGAGTTACCCTTCTGTATCATCTAGAAGATCTCTACATCACGG 1140
1141 CAAATACTTTTGGACATTTAAATGTTGGACATTTTTCATGCATTTACTCAAATCTCAA 1200
1201 **ATAAA**TGCTTACAAAAGTATGCAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1260
1261 AAA 1263

Supplementary Fig. 1. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the bighead catfish (*Cm_mIgM* 1.1, GenBank accession number MN934742) and hybrid catfish (hybrid:*Cm_mIgM* 1.1, GenBank accession number MN934751). The sequence was consisted of three CH and two TM domains: C μ 1-C μ 2-C μ 3-TM1-TM2. The atypical polyadenylation signal (AATAAA) in the 3'-UTR was bold.

1 →Cm_ighu1
 GCAACACAAGAAGCCCCGAAGTCCCTGTTTCCCGTGTGGCAGTGC GGCTCGTCCCCTGAT 60
 A T Q E A P K S L F P V W Q C G S S P D
 61 GGT TTTGTCACTCTGGGCTGCGTCACCCGCGACTTGGCAACCCCTGATGGACTGAGCTAC 120
 G F V T L G C V T R D L A T P D G L S Y
 121 G T T T G G A A G G A T G C G A G C G G C A C C G C G T G A C T A C T A A C G T T G T A C A A T A C C C G G C G G T G 180
 V W K D A S G T A L T T N V V Q Y P A V
 181 A T C G A G G G C G A A A G T A C T C C T C A G T G A G T C A G G C G C G T C A G T G C T A A C G A C T G G A A C 240
 I E G G K Y S S V S Q A R V S A N D W N
 241 G C G A A C A A G A A G T T C A C T T G C G A A G T C A C T A A T C C C C G G G A A C G A A A A C G G C A G A G A C T G 300
 A N K K F T C E V T N P R G T K T A E L
 301 →Cm_ighu2
 A A A A G C C A G T T G T G C C C G A C A T C C C T G C A A A A T C T C T G C T T C T A A C A G C T C C G A G C C A A 360
 K K P V V P D I P A K S L L L T A P S Q
 361 A C A G A A T T A G A A A A T G G A A C A G C T A C C T T C A T C T G C T T A G C T T C A G A A T T T T C A C C T A A A 420
 T E L E N G T A T F I C L A S E F S P K
 421 A C G T C C A C A T T T A A G T G G A C C C G T G G A G A A C A A G C A T C G A T A A T A A G C C A A A G A C C C C 480
 T S T F K W T R G G T S I D N K A K D P
 481 A T T T T A A T C G C G G G A A A A C C T A C T T A C A G T T C C T T T A G T A T T T T G G T A C T C A C T G C T G C C 540
 I L I A G K P T Y S S F S I L V L T A A
 541 G A A T G G A C T G G C T C A A C T T C C A G T T A A G T G C G A G T T C C A G C A G A A G T C A C A G A C T C T G 600
 E W T G S T S P V K C E F Q Q K S Q T L
 601 →Cm_ighu3
 T C C A A G G A G G C A A G T T A T C A T T A T G T G A C C C G G G A G C A G C C A A C A A T T A C A A T A A T C C C A 660
 S K E A S Y H Y V T R E Q P T I T I I P
 661 C C T T C C A A C A A T G A C A T G C T T A T C A A A A G A T C T G G C G A C C T C G T G T G C A A G G C T G A A G G A 720
 P S N N D M L I K R S G D L V C K A E G
 721 C C A T T G G G T T T C A C T G G A A T T A A G T G G G T T G C T A A C G G T A A A G A G G T T G T T T C C C T A T C T 780
 P L G F T G I K W V A N G K E V V S L S
 781 G A A A A A G T T G T G T C T A C G A A G G C A G C G A T C T C A C T C A C C A C C T C A A T C T C T T A C G A A G A G 840
 E K V V S T K A A I S L T T S I S Y E E
 841 T G G C A T A A G G C A T G A A A T T T A C C T G T G A G G T G C A T C A T T C C T C A T T G C T C A G G G G T T T 900
 W H K G M K F T C E V H H S S F A Q G F
 901 →Cm_ighutm1
 A T A A C A G A A G T C T A C A A A A G A G A A A A T T A T G C C T T A A C A T T T G T A T T T C T C T T C C T C A T C 960
 I T E V Y K R E N Y A L T F V F L F L I
 961 →Cm_ighutm2
 A C C C T G T T C T A C A G C A T C G G G G T G A C T G T T A T C A A G G T G A A A T G G G A A C A A C T A A T G G A 1020
 T L F Y S I G V T V I K V K W E T T N G
 1021 A C G A T T T T G A T T T T C T C T G T T T T T T T T T C T T C A G T A T A A G T T T G T T T G T T T T G T T T T 1080
 T I L I F S L F F F S S V *
 1081 T T T T A T T T T A G T G T T C T G A G T T A C C C T T T C T G T A T C A T C T A G A A G A T C T C T A C A T C A C G G 1140
 1141 C A A A T A C T T T T G G A C A T T T A A A T G T T G G A C A T T T T T T C A T G C A T T T A C T C A A A T C T C A A 1200
 1201 A T A A A T A T T T G A C A A A A A T A T G C A A T T A A A A G T C T A A T T G T T T T C T G T A T C T T T A T T T G A 1260
 1261 A T T A T A G T C A G C C T T A A A G T A T A G T G T T A T G T T A T T A G C T T A T A T T A C A T G T C T A T A T T 1320
 1321 T T A T T A G T T T T T A A T A A A T G T C T T A C A A A A A T A T G C G A 1380
 1381 A A A A A A A 1387

Supplementary Fig. 2. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the bighead catfish (*Cm_mIgM* 1.2, GenBank accession number MN934743). The sequence was consisted of three CH and two TM domains: C_μ1-C_μ2-C_μ3-TM1-TM2. The atypical polyadenylation signal (AATTTAA) in the 3'-UTR was bold.

→ *Cm_ighu1*
1 | GCAACACAAGAAGCCCCGAAGTCCCTGTTTCCCGTGTGGCAGTGCGGCTCGTCCCCTGAT 60
| A T Q E A P K S L F P V W Q C G S S P D
61 | GGTTTTGTCACTCTGGGCTGCGTCACCCGCGACTTGGCAACCCCTGATGGACTGAGCTAC 120
| G F V T L G C V T R D L A T P D G L S Y
121 | GTTTGGAAAGGATGCGAGCGGCACCGCGCTGACTACTAACGTTGTACAATACCCGGCGGTG 180
| V W K D A S G T A L T T N V V Q Y P A V
181 | ATCGAGGGCGGAAAGTACTCCTCAGTGAGTCAGGCGCGCTCAGTGCTAACGACTGGAAC 240
| I E G G K Y S S V S Q A R V S A N D W N
241 | GCGAACAAGAAGTTCACTTGCGAAGTCACATAATCCCCGGGGAACGAAAACGGCAGAGCTG 300
| A N K K F T C E V T N P R G T K T A E L
301 | AAAAAGCCAGTTGTGCCCCGACATCCCTGCAAAATCTCTGCTTCTAACAGCTCCGAGCCAA 360
| K K P V V P D I P A K S L L L T A P S Q
→ *Cm_ighu2*
361 | ACAGAATTAGAAAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTCACCTAAA 420
| T E L E N G T A T F I C L A S E F S P K
421 | ACGTCCACATTTAAGTGGACCCGTGGAGGAACAAGCATCGATAATAAGGCCAAAGACCCC 480
| T S T F K W T R G G T S I D N K A K D P
481 | ATTTTAAATCGCGGGAAAACCTACTTACAGTTCCTTTAGTATTTTGGTACTCACTGCTGCC 540
| I L I A G K P T Y S S F S I L V L T A A
541 | GAATGGACTGGCTCAACTTCTCCAGTTAAGTGCAGTTCAGCAGAAGTCACAGACTCTG 600
| E W T G S T S P V K C E F Q Q K S Q T L
601 | TCCAAGGAGCAAGTTATCATTATGTGACCCGGGAGCAGCCAACAATTACAATAATCCCA 660
| S K E A S Y H Y V T R E Q P T I T I I P
→ *Cm_ighu3*
661 | CCTTCCAACAATGACATGCTTATCAAAAGATCTGGCGACCTCGTGTGCAAGGCTGAAGGA 720
| P S N N D M L I K R S G D L V C K A E G
721 | CCATTGGGTTTCACTGGAATTAAGTGGGTTGCTAACGGTAAAAGAGGTTGTTTCCCTATCT 780
| P L G F T G I K W V A N G K E V V S L S
781 | GAAAAAGTTGTGTCTACGAAGGCAGCGATCTCACTCACCACTCAATCTCTTACGAAGAG 840
| E K V V S T K A A I S L T T S I S Y E E
841 | TGGCATAAGGGCATGAAATTTACCTGTGAGGTGCATCATTCTCATTGCTCAGGGGTTT 900
| W H K G M K F T C E V H H S S F A Q G F
901 | ATAACAGAAGTCTACAAAAGAGAAAATTTATGCCTTAACATTTGTATTTCTCTCTCATC 960
| I T E V Y K R E N Y A L T F V F L F L I
→ *Cm_ighutm1*
→ *Cm_ighutm2*
961 | ACCCTGTTCTACAGCATCGGGGTGACTGTTATCAAGGTGAAATGGGAAACAATAATGGA 1020
| T L F Y S I G V T V I K V K W E T T N G
1021 | ACGATTTGATTTTCTCTCTGTTTTTTTTTCTTTCAGTATAAGTTTGTGTTTGTGTTTT 1080
| T I L I F S L F F F S S V *
1081 | TTTTATTTTGTGTTCTGAGTTACCCTTTCTGTATCATCTAGAAGATCTCTACATCACGG 1140
1141 | CAAATACTTTTGGACATTTAAATGTTGGACATTTTTTTTCATGCATTTACTCAAATCTCAA 1200
1201 | ATAAATATTTGACAAAAATATGCAATTAAGTCTAATGTTTCTGTATCTTTATTTGA 1260
1261 | ATTATAGTCAGCCTTAAAGTATAGTGTATTATGTTATTAGCTTATATTACATGTCTATATT 1320
1321 | TTATTAGTTTTTAATAAAATTAATAAGACGTTTCGATGACAGTAGTGTTCCTCAGTTT 1380
1381 | GCTGTTGAAACATAGTAAACTATTGAGTTATATTATTTATTTGATCTTTTTAGCTAATAG 1440
1441 | ATGTAGAGATCCTGGTGTGACCAACCTTTCTACAATGAGACAGAAGTTGATGATGACA 1500
1501 | ACGTGGCAACCACTGCCTTAACATTTGTATTTCTCTTCTCATCACCTGTCTACAGCA 1560
1561 | TCGGGGTGACTGTTATCAAGGTGAAATGAGAAAC**AATAAA**TGCAATTAAGTCAAAAAA 1620
1621 | AAAAAAAAAAAAAAAAAAAAAA 1641

Supplementary Fig. 3. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the bighead catfish (*Cm_mIgM* 1.3, GenBank accession number MN934744). The sequence was consisted of three CH and two TM domains: C_μ1-C_μ2-C_μ3-TM1-TM2. The atypical polyadenylation signal (AATTTAA) in the 3'-UTR was bold.

1 *Cm_ighu1*
GCAACACAAGAAGCCCGAAGTCCCTGTTTCCCGTGTGGCAGTGC GGCTCGTCCCCTGAT 60
A T Q E A P K S L F P V W Q C G S S P D

61
GGTTTTGTCACTCTGGGCTGCGTCACCCGCGACTTGGCAACCCCTGATGGACTGAGCTAC 120
G F V T L G C V T R D L A T P D G L S Y

121
GTTTGAAGGATGCGAGCGGCACCCGCGTACTACTAACGTTGTACAATACCCGGCGGTG 180
V W K D A S G T A L T T N V V Q Y P A V

181
ATCGAGGGCGGAAAGTACTCCTCAGTGTAGTACAGGCGCGCTCAGTGTAAACGACTGGAAC 240
I E G G K Y S S V S Q A R V S A N D W N

241
GCGAACAAGAAGTTCAC'TGCGAAGTCACTAATCCCCGGGAACGAAACGGCAGAGCTG 300
A N K K F T C E V T N P R G T K T A E L

301 *Cm_ighu2*
AAAAAGCCAGTTGTGCCCCGACATCCCTGCAAAATCTCTGCTTCTAACAGCTCCGAGCCAA 360
K K P V V P D I P A K S L L L T A P S Q

361
ACAGAATTAGAAAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTCACCTAAA 420
T E L E N G T A T F I C L A S E F S P K

421
ACGTCCACATTTAAGTGGACCCGTGGAGGAACAAGCATCGATAATAAGGCCAAAGACCCC 480
T S T F K W T R G G T S I D N K A K D P

481
ATTTTAATCGGGGAAAACCTACTTACAGTTCCTTTAGTATTTTGGTACTCACTGCTGCC 540
I L I A G K P T Y S S F S I L V L T A A

541
GAATGGACTGGCTCAACTTCTCCAGTTAAGTGCAGATTCCAGCAGAAGTACAGACTCTG 600
E W T G S T S P V K C E F Q Q K S Q T L

601 *Cm_ighu3*
TCCAAGGAGCAAGTTATCATTATGTGACCCGGGAGCAGCCAACAATTACAATAATCCCA 660
S K E A S Y H Y V T R E Q P T I T I I P

661
CCTTCCAACAATGACATGCTTATCAAAAGATCTGGCGACCTCGTGTGCAAGGCTGAAGGA 720
P S N N D M L I K R S G D L V C K A E G

721
CCATFGGGTTTCACTGGAATTAAGTGGTTGCTAACGGTAAAGAGGTTGTTTCCCTATCT 780
P L G F T G I K W V A N G K E V V S L S

781
GAAAAGTGTGTCTACGAAGGCAGCATCTCACTACCACCTCAATCTCTTACGAAGAG 840
E K V V S T K A A I S L T T S I S Y E E

841
TGGCATAAGGGCATGAAATTTACCTGTGAGGTGCATCATTCTCATTGCTCAGGGGTTT 900
W H K G M K F T C E V H H S S F A Q G F

901 *Cm_ighu4*
ATAACAGAAGTCTACAAAAGAGAAAATGGCCGAAACGCTAACAGCCAGGGGTTTCTTG 960
I T E V Y K R E N G R T P N C P G V F L

961
CTCCCGCCACCAGAGAGCTCAAATGGGGATTTGAAGACCCTGACTTGCTATATAAAAAAC 1020
L P P P E S S N G D L K T L T C Y I K N

1021
TTTTACCCTAAGGAGGTTGCTGTGCTTTGGCTTATTGGTGATAAAACAAGTGGACAATGAG 1080
F Y P K E V A V S W L I G D K Q V D N E

1081
AGCATCACTAAAGTTATTGAGAAAAATGGCAACTTTTTCAGCATAACAGTACAGTGTGTC 1140
S I T K V I E K N G N F S A Y S Q L I V

1141
AATCAGGACTCCTGGGAAATGGCACAGAGTTACCTGCAATGTTTATCATGAGTCCATC 1200
N Q D S W G N G T E F T C N V Y H E S I

1201
ATGGATAATCTTCGCCACCTTTCCAGAACCATTACTGGCACTTCAATCCACCCTCCATA 1260
M D N L R H L S R T I T G T S N P P S I

1261 *Cm_ighutm1*
GTGAATCTCAGCCTAAATGTTCCCCAAAACCTGCCAAATCTGGTCTGTATGCCTTAACA 1320
V N L S L N V P Q N C P N P G L Y A L T

1321 *Cm_ighutm2*
TTTGTATTTCTCTCTCCTCATCACCTGTTCTACAGCATCGGGGTGACTGTTATCAAGGTG 1380
F V F L F L I T L F Y S I G V T V I K V

1381
AAATGGGAAAACAATAATGGAACGATTTTGATTTTCTCTGTTTTTTTTTCTTTCAGTA 1440
K W E T T N G T I L I F S L F F F S S V

1441
TAAGTTGTTGTTTGTGTTTTTTTTTATTTTAGTGTCTGAGTTACCCCTTCTGTATCATC 1500
*

1501
TAGAAGATCTCTACATCACGGCAAATACTTTTGGACATTTAAATGTTGGACATTTTCTTTC 1560

1561
ATGCATTTACTCAAATCTCAAATAAATATTTGACAAAAATATGCAATTAAGTCTAATT 1620

1621
GTTTTCTGTATCTTTATTTGAATTATAGTCAGCCTTAAAGTATAGTGTATGTTATTAG 1680

1681
CTTATATTACATGTCTATATTTTATTAGTTTTTAATAAAATTAATTAAGACGTTTCGATGA 1740

1741
CAGTAGTGTCTCTCAGTTTGTGTTGAAACATAGTAAACTATTGAGTTATATTATTT 1800

1801
ATTGATCTTTTTAGCTAATAGATGTAGAGATCCTGGTGTGACCAACCTTTTCTACAATG 1860

1861
AGACAGAACCTTGATGATGACAACCTGGCAACCACTGCCTTAACATTTGATTTCTCTTCC 1920

1921
TCATCACCTGTTCTACAGCATCGGGGTGACTGTTATCAAGTGAAATGAGAAACAATTA 1980

1981
ATGCAATTAAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2022

Supplementary Fig. 4. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the bighead catfish (*Cm_mIgM 2*, GenBank accession number MN934745). The sequence was consisted of three CH and two TM domains: C μ 1-C μ 2-C μ 3-C μ 4-TM1-TM2. The atypical polyadenylation signal (AATTTAA) in the 3'-UTR was bold.

1 →Cm_ighu1
GCAACACAAGAACCCGAGTCCCTGTTCCCGTGTGGCAGTCGGGCTCGTCCCTGAT 60
A T Q E A P K S L F P V W Q C G S S P D

61 GGTTTGTCACTCTGGGCTGGCTACCCGGGACTTGGCAACCCCTGATGACTGAGCTAC 120
G F V T L G C V T R D L A T P D G L S Y

121 GTTTGGAAGGATGCGAGCGCACCCGGCTGACTACTAAGTGTACAATACCCGGGCTG 180
V W K D A S G T A L T T N V V Q Y P A V

181 ATCGAGGGCGAAAGTACTCCTCAGTGTAGTCAGGCGGCGTCACTGCTAACGACTGGAAC 240
I E G G K Y S S V S Q A R V S A N D W N

241 GCGAACAAGAAGTCTACTTGGCAAGTCACTAATCCCGGGGAACGAAACGGCAGAGCTG 300
A N K K F T C E V T N P R G T K T A E L

301 AAAAAAGCAAGTGAATGTGACTTCGCCAGCATCAGCATCAGCACAAGCTTCGACACA 360
K K F E V N V T S P S I S I S T S F D T

361 ACAACTAACGATACTAATCTGATTGCTGGTGGATGTTTACGCCCTAAAGCGATTAA 420
T T N D T N L I C W L D G F S P K A I N

421 GTTACTTGGGAGCGGTAAAGAAAGGACTGAGAGAAAATTCAAAAATGAGAAAATAAA 480
V T W G A G K K G T E R K F K N E E N K

481 AAGTTTGCATCTGAGCAAAATCAGCATAAATGCGAGCAATGGAAGAAGGCAAGAG 540
K F A M L S Q I S I N A E Q W K E G K E

541 TTCACCTGCAGCGCACACAAGTCAAACCTACAGTCAAACATGGAGCATTTGTAAA 600
F T C S A T H K S K T Y S Q T W S I C K

601 GGCCATCAAATCTGAACACGGATACGCTGGAGAACTGCTCTCAGTCCATATTG 660
G H L N S E P R I R L E K P A L R S I L

661 ACAGATACAGTGTACAGTCTCCTGTGTTGTAAGTGTGTTCCAGCCTAAAGTTTTA 720
T D T R V T V S C V V E T V F Q P K V L

721 TGGCTGTAGATGGAAGCACAATACTGACACAGACATTATCAGTGAGAGTCAAGCGGAG 780
W L V D G S T K S D T D I I S E S Q G E

781 TCCACTGTTAGCAACTGACTATTTCTGTAGAAGCTGGCAAAAATCAAACACAATAACC 840
S T V S K L T I S V E D W T K S N T I T

841 TGCAGGCGCAACATCATTGTTGAGATCTCTAGATGTTTCAAACTACAGAAACT 900
C R A E H P L L R S S R C S F K T T E T

901 GTGCAGAAACGCTACAGTGGAGATCAGAAGGACTTGAAGACGTAGGGAAGAGAGAC 960
V Q K R P T V E I R R S L E D V G K R D

961 AGTCAGTCTGGAGTGTGCAAGCGCTGCTCCTCGTGAAGTCTCTGTCACTCTC 1020
S A V L E C A A S G L P P G E L S V T F

1021 CAGGCCAATAATGTGAATTTCCAGAAGCTCAGTATGTTAATCTACAAAAGGCCAGGAC 1080
Q A N N V N F P E A Q Y V N L P K G Q D

1081 ACACTAGTTGCACTTTTCACTAATCTTGGAAACACCGAAGCAAGCATCGTTCACT 1140
T L V A L F T I P G T H R T E Q H R F T

1141 TGTGAGATTCAGACAAGCGTTCCTTAAAAATGGAGTCCAATTTATAGAAAACCTTTTT 1200
C E I Q T S R S L K W R S N F I G N L F

1201 AGTGATCTTTAGTGGAACTTTCACTGTTGATCCAGTGAAGATAAATCTGCATCAACCGCA 1260
S D P L V E L S V V S S E D K S A S T A

1261 CAAAAACTTCTTTCATGGAAGTGGCTTAAACCCAGAGATCAAGTGGCTCCCGAATCT 1320
Q K L L C Y G T G L N P E I K W L P E S

1321 GTGGAAATAAATAAAGTGAATGAACAAATGAATGAAGTGAAGTCAAGTCTGCAAGC 1380
V G N N K S E V T M N E D G R V K V S S

1381 GAGCTTTCAGTTACAGAACAAGAGTGAACCGTGAACCTACATTCACCTGCCAAGTCA 1440
E L S V T E Q E W N R G T T F T C Q V S

1441 GATCAGGCTCGTCTCAACACTGTTCCAGAAGAGCATCAGTTTCTGCACTCTCACTGAGAT 1500
D Q G R L N T V Q K S I S F C A V T P D

1501 CATGCTCGGAGTGCACAGGTTTACCTTTGGGTCCCTCCATCAGTAAATGCGCAGAGGAG 1560
H A R S A Q V Y L L G P S I S N M P E E

1561 GATCCTGCTCTGTACATGCTGCTGTGGGCAATAGCTCCAGACTTCTCAGTTAAT 1620
D P V S V T C L L L G H R L Q D F S V N

1621 TGCAAGTAGGACCGCAATTTGCTTCAAATGTGATCAAACCTGAAATCCACGGCAAT 1680
C K V G T D N L S S N V I K T E I H G N

1681 GGAACAGAGAAATGTAAGGGTTATAAGGGTTCAGCTGAAAGTGGAAAAACCATGAA 1740
G T E N V Q R V I R V P A E K W K N H E

1741 AATGTTCCGTGAGTGAACACCCCTGCTGTGGCCGACATCCCTGCAAAATCTCTG 1800
N V S C E V K H P C I V V P D I P A K S L

1801 CTCTAACAGCTCGAGCCAAACAGAAATAGAAAATGGAACAGCTACCTCATCTGCTTA 1860
L L T A P S Q T E L E N G T A T F I C L

1861 GCTTCAGAAATTTACCTAAAACGTCACATTTAAGTGGACCGTGGAGGAACAAGCATC 1920
A S E F S P K T S T F K W T R G G T S I

1921 GATAATAAGCCAAAGCCCAATTTAATCGCGGAAAACCTACTTACAGTTCTTTAGT 1980
D N K A K D P I L I A G K P T Y S S F S

1981 ATTTGGTACTCACTGCTGCCGAATGGACTGGCTCAACTTCTCCAGTTAAGTGGAGTTC 2040
I L V L T A A E W T G S T S P V K C E F

2041 CAGCAGAAGTACAGACTCTGCAAGGAGGCAAGTTATCATTATGTGACCCGGGAGCAG 2100
Q Q K S Q T L S K E A S Y H Y V T R E Q

2101 CCAACAATTACAATAATCCACCTTCCAACAATGACATGTTATCAAAGATCTGGCGAC 2160
P T I T I I P P S N N D M L I K R S G D

2161 CTCGTGTCAAGGCTGAAGGACATTGGGTTTCACTGGAATTAAGTGGGTTGCTAACGGT 2220
L V C K A E G P L G F T G I K W V A N G

2221 AAAGAGGTTGTTCCCTATCTGAAAAGTTGTCTACGAAGCAGCGATCTCACTACC 2280
K E V V S L S E K V V S T K A A I S L T

2281 ACCTCAATCTCTACGAAGTGGCATAAGGGCAATAAATACCTGTGAGGTGCATCAT 2340
T S I S Y E E W H K G M K F T C E V H H

2341 TCCTCATTTGCTCAGGGTTTATAACAGAAGTCTACAAAAGAGAAAATATGCCTTAACA 2400
S S F A Q G F I T E V Y K R E N Y A L T

2401 TTTGATTTCTCTCTACCTCCTGTTCTACAGCATCGGGTGAAGTTTATGTTGACCGGAGTG 2460
F V F L F L I T L F Y S I G V T V I K V

2461 AAATGGAAACAACATATGGAACGATTTTGAATTTTCTCTCTGTTTTTTTTTCTTCAGTA 2520
K W E T T N G T I L I F S L F F F S S V


2521 TAAGTTGTTGTTGTTTTTTTTTATTTAGTGTCTGAGTTACCTTTCTGTATCATC 2580
*

2581 TAGAAGATCTTACATCACGGCAAACTTTTGGACATTTAATGTTGGACATTTTTTCT 2640
2641 ATGCATTTACTCAAATCTCAAATAAATGCTTTACAAAGTATCAAATAAAAAAAAAAAAAA 2700
2701 AAAAAAAAAAAAAAAAAAAAAA 2724

Supplementary Fig. 5. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the bighead catfish (*Cm_mIgM 3*, GenBank accession number MN934746). The sequence was consisted of seven CH and two TM domains: C μ 1-C δ 2-C δ 3-C δ 4-C δ 5-C μ 2-C μ 3-TM1-TM2. The atypical polyadenylation signal (AATTTAAA) in the 3'-UTR was bold.

→ *Cm_ighu1*
1 | GCAACACAAGAAGCCCCGAAGTCCTGTTTCCCGTGTGGCAGTGGCGGCTCGTCCCCTGAT 60
| A T Q E A P K S L F P V W Q C G S S P D
61 | GGTTTTGTCACTCTGGGCTGCGTCACCCGCGACTTGGCAACCCCTGATGGACTGAGCTAC 120
| G F V T L G C V T R D L A T P D G L S Y
121 | GTTTGGAAGGATGCGAGCGGCACCCGCGTACTACTAACGTTGTACAATACCCGGCGGTG 180
| V W K D A S G T A L T T N V V Q Y P A V
181 | ATCGAGGGCGAAAGTACTCCTCAGTGAGTCAGGCGCGCTCAGTGCTAACGACTGGAAC 240
| I E G G K Y S S V S Q A R V S A N D W N
241 | GCGAACAAGAAGTTCACCTTGCAGTCACTAATCCCGGGGAACGAAAACGGCAGAGCTG 300
| A N K K F T C E V T N P R G T K T A E L
→ *Cm_ighu2*
301 | AAAAAAGCCAGTTGTGCCCCGACATCCCTGCAAAATCTCTGCTTCTAACAGCTCCGAGCCAA 360
| K K P V V P D I P A K S L L L T A P S Q
361 | ACAGAATTAGAAAATGGAACAGCTACCTTCATCTGCTTAGCTTCAAGATTTTCACCTAAA 420
| T E L E N G T A T F I C L A S E F S P K
421 | ACGTCCACATTTAAGTGGACCCGTGGAGGAACAAGCATCGATAATAAGGCCAAAGACCCC 480
| T S T F K W T R G G T S I D N K A K D P
481 | ATTTTAATCGCGGGAAAACCTACTTACAGTTCCTTTAGTATTTTGGTACTCACTGCTGCC 540
| I L I A G K P T Y S S F S I L V L T A A
541 | GAATGGACTGGCTCAACTTCTCCAGTTAAGTGGGAGTTCAGCAGAAGTCACAGACTCTG 600
| E W T G S T S P V K C E F Q Q K S Q T L
→ *Cm_ighu3*
601 | TCCAAGGAGGCAAGTTATCATTATGTGACCCCGGAGCAGCCAACAATTACAATAATCCCA 660
| S K E A S Y H Y V T R E Q P T I T I I P
661 | CCTTCCAACAATGACATGCTTATCAAAAGATCTGGCGACCTCGTGTGCAAGGCTGAAGGA 720
| P S N N D M L I K R S G D L V C K A E G
721 | CCATTGGGTTTCACTGGAATTAAGTGGGTTGCTAACGGTAAAGAGGTTGTTTCCCTATCT 780
| P L G F T G I K W V A N G K E V V S L S
781 | GAAAAGTTGTGTCTACGAAGGAGCAGTCTCACTCACCACCTCAATCTTTACGAAGAG 840
| E K V V S T K A A I S L T T S I S Y E E
841 | TGGCATAAGGGCATGAAATTTACCTGTGAGGTGCATCATTCTCATTTGCTCAGGGGTTT 900
| W H K G M K F T C E V H H S S F A Q G F
→ *Cm_ighu4*
901 | ATAACAGAAGTCTACAAAAGAGAAAATGGCCGAACGCCTAACTGCCAGGGGTTTCTTGT 960
| I T E V Y K R E N G R T P N C P G V F L
961 | CTCCCGCCACCAGAGAGCTCAAAATGGGGATTTGAAGACCTGACTTGCTATATAAAAAAC 1020
| L P P P E S S N G D L K T L T C Y I K N
1021 | TTTTACCCTAAGGAGTTGCTGTGTCTTGGCTTATTTGGTGATAAAACAAGTGGACAATGAG 1080
| F Y P K E V A V S W L I G D K Q V D N E
1081 | AGCATCACTAAAGTTATTGAGAAAAATGGCAACTTTTCAGCATAACAGTCAGCTGATTGTC 1140
| S I T K V I E K N G N F S A Y S Q L I V
1141 | AATCAGGACTCCTGGGGAAATGGCACAGAGTTCCACCTGCAATGTTTATCATGAGTCCATC 1200
| N Q D S W G N G T E F T C N V Y H E S I
1201 | ATGGATAATCTTCGCCACCTTTCCAGAACCATTACTGGCACTTCAAATCCACCTCCATA 1260
| M D N L R H L S R T I T G T S N P P S I
1261 | GTGAATCTCAGCCTAAATGTTCCCAAAACTGCCCAAATCCTGGTCTGTAAGATGTAGAG 1320
| V N L S L N V P Q N C P N P G L *
1321 | ATCCTGGTGTGACCAACCTTTTCTACAATGAGACAGAACTTGATGATGACAACGTGGCA 1380
1381 | ACCACTGCCTTAACATTTGTATTTCTTCTCCTCATCACCCTGTTCTACAGCATCGGGGTG 1440
1441 | ACTGTTATCAAGGTGAAATGAGAAACAATAATGAACGATTTTGATTTTCTCTCTGTTT 1500
1501 | TTTTCTTCTCAGTATAATGTTCTGAGTTACCTTTCTGTTAAACTATCTTCTCTTAGCT 1560
1561 | ACTTTCATGTATTTTATATCTGTAATACTTTTTTGTGATTTAAATGTTGGATTTTTTT 1620
1621 | TTCATGCTTTTACTCAAATCTCA**AATAAA**TGTCAAACATAGTAAACATTTATCAGATAA 1680
1681 | TGTA

Supplementary Fig. 6. Nucleotide and translated amino acid sequences of the secreted IgM constant domain of the bighead catfish (*Cm_slgM 1*, GenBank accession number MN934747). The sequence was consisted of three CH and two TM domains: C μ 1-C μ 2-C μ 3-C μ 4. The atypical polyadenylation signal (AATAAA) in the 3'-UTR was bold.


1  *Cg_ighu1*
GCAACGCAAGAACCCCGAAGTCTCTGTTTCCCGTGTGGCAGTGC GGCTCGTCCCCTGAT 60
A T Q E A P K S L F P V W Q C G S S P D

61 GGTTCGTCACTCTGGGCTGCCTCACCCGCGACTTGGCAACCGGCGATGGACTGAGCTAC 120
G F V T L G C L T R D L A T G D G L S Y

121 GTTTGGAAGGATGCGAGCGGCACCCGCGCTGACTACCGTTGTACAATACCCGGCAGTGCTG 180
V W K D A S G T A L T T V V Q Y P A V L

181 GACAACGGAAAGTACTCCTCAGTGAGTCAGGCGCGCTCACTGCTACCGAGTGGGACGCG 240
D N G K Y S S V S Q A R V T A T E W D A

241 AACAAAGCCGTTCACTTGCCAAGTCACTAATTCCATTGGAACCGCAACGGCGAACGTGCAA 300
N K P F T C Q V T N S I G T A T A N V Q


301 AAACCACCTCTCGTCATCCCAGCAAAATCTCTGCTTCTAACAGCTCCGAGCCAAACAGAA 360
 *Cg_ighu2*
K P P L V I P A K S L L L T A P S Q T E

361 ATAGACAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTCACCTAAAAACGCAC 420
I D N G T A T F I C L A S E F S P K T H

421 ACATTTAAGTGGACCCGCGTAAAAGACAAGCCTCGATAGTAAGGCAAAAGCCCCAATTTTA 480
T F K W T R E K T S L D S K A K A P I L

481 ATCCCGGGACAAAAAATTTACAGTGCCTTAAGCATTTTGGAACTCACTGCCAGCGAATGG 540
I P G Q K I Y S A L S I L E L T A S E W

541 ATGGGCTCAACTTCTCCAGTTAAGTGTGAGTTCAGCACAAGGAACAGACTCTGTCCCAG 600
M G S T S P V K C E F Q H K E Q T L S Q


601 GAAGCAAGTCATGGGACATGTGAGGAGCAGCCAAAAATGACAATAAGTCCACCTTCCAAT 660
 *Cg_ighu3*
E A S H G T C E E Q P K M T I S P P S N


661 GGCATTCTTATCAATAGATCTGCTGATATTGTGTGCAAGGCTGAAGGACCAATGGGTTTC 720
G I L I N R S A D I V C K A E G P M G F

721 ACCGCCATTAAATGGGTTGTTAACGGTAAAGAGGTTGCTTCCCTACCTCAAAGCGATGTG 780
T A I K W V V N G K E V A S L P Q S D V

781 TCTTCGAAGACAGCGATCTCACTCACCACCACAATCTCTTATGAAGAGTGGCATACTGGC 840
S S K T A I S L T T T I S Y E E W H T G

841 ACCAAATTTACCTGTGAGGTGTATCATTAGCTCAGGGATTTATACAAGAAGAC 900
T K F T C E V Y H S A L A Q G F I Q E D

901 TACCAAAGAGTAAACTATGCCTTAACATTTGTATTTCTCTTCCCTCATCACTCTGTTCTAC 960
 *Cg_ighutm1*
Y Q R V N Y A L T F V F L F L I T L F Y

961 AGCATCGGGTGTGAAATGGGAAACAATAATGGAACGATTTTGATTTTCTCTCTGTTT 1020
 *Cg_ighutm2*
S I G V V K W E T T N G T I L I F S L F






1021 TTTTTTCTTCTTTCAGTATAAAGCTGATGCCGGGTTACTACATTGAGACAGAACTGATG 1080
F F S S S V

1081 ATGAAAACGTGGCAAAACTGCCTTAACATTTGTATTTCTCTTCCCTCATCACTCTGTTCT 1140


1141 ACAGCATCGGGTACTGTTATCAAGGTGAAAT**AATAAA**CATTTAAAAGCCAAAAA 1200

1201 AAAAAAAAAAAAAAAAAA 1219

Supplementary Fig. 7. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the north African catfish (*Cg_mIgM* 1.1, GenBank accession number MN934748). The sequence was consisted of three CH and two TM domains: C_μ1-C_μ2-C_μ3-TM1-TM2. The atypical polyadenylation signal (AATAAA) in the 3'-UTR was bold.

1  GC AACGCAAGAAGCCCCGAAGTCTCTGTTTCCCGTGTGGCAGTGGCGGCTCGTCCCCTGAT 60
 A T Q E A P K S L F P V W Q C G S S P D
 61 GGTTCGTCACTCTGGGCTGCCTCACCCGCGACTTGGCAACCGGGATGGACTGAGCTAC 120
 G F V T L G C L T R D L A T G D G L S Y
 121 GTTTGGAAGGATGCGAGCGGCACCGCGCTGACTACCGTTGTACAATACCCGGCAGTGCTG 180
 V W K D A S G T A L T T V V Q Y P A V L
 181 GACAACGGAAAGTACTCCTCAGTGAGTCAGGCGCGCTCACTGCTACCGAGTGGGACGCG 240
 D N G K Y S S V S Q A R V T A T E W D A
 241 AAC AAGCCGTTCACTTGCCAAGTCACTAATTCATTGGAACCGCAACGGCGAACGTGCAA 300
 N K P F T C Q V T N S I G T A T A N V Q
 301 AAACCACCTCTCGTCATCCAGCAAAAATCTCTGCTTCTAACAGCTCCGAGCCAAACAGAA 360
 K P P L V I P A K S L L L T A P S Q T E 
 361 ATAGACAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTCACCTAAAACGCAC 420
 I D N G T A T F I C L A S E F S P K T H
 421 ACATTTAAGTGGACCCGTGAAAAGACAAGCCTCGATAGTAAGGCAAAGCCCAATTTTA 480
 T F K W T R E K T S L D S K A K A P I L
 481 ATCCCGGGACAAAAATTTACAGTGCCTTAAGCATTTTGGAACTCACTGCCAGCGAATGG 540
 I P G Q K I Y S A L S I L E L T A S E W
 541 ATGGGCTCAACTTCTCCAGTTAAGTGTGAGTTCCAGCACAAGGAACAGACTCTGTCCCAG 600
 M G S T S P V K C E F Q H K E Q T L S Q
 601 GAAGCAAGTCATGGGACATGTGAGGAGCAGCCAAAAATGACAATAAGTCCACCTTCCAAT 660
 E A S H G T C E E Q P K M T I S P P S N 
 661 GGCATTCCTTATCAATAGATCTGCTGATATGTGTGCAAGGCTGAAGACCAATGGGTTTC 720
 G I L I N R S A D I V C K A E G P M G F
 721 ACCGCCATTAATGGGTTGTTAACGGTAAAAGAGGTTGCTTCCCTACCTCAAAGCGATGTG 780
 T A I K W V V N G K E V A S L P Q S D V
 781 TCCTCGAAGACAGCGATCTCACTCACCACCACAATCTCTTATGAAGAGTGGCATACTGGC 840
 S S K T A I S L T T T I S Y E E W H T G
 841 ACCAAATTTACCTGTGAGGTGTATCATT CAGCATTAGCTCAGGGATTTATACAAGAAGAC 900
 T K F T C E V Y H S A L A Q G F I Q E D
 901 TACCAAAGAGTAAACTATGCCTTAACATTTGTATTTCTCTTCTCATCACTCTGTTCTAC 960
 Y Q R V N Y A L T F V F L F L I T L F Y 
 961 AGCATCGGGGTGGTGAATGGGAAACAATAATGGAACGATTTTGATTTTCTCTCTGTTT 1020
 S I G V V K W E T T N G T I L I F S L F 
 1021 TTTTTTTCTTCTT CAGTATAAAGCTGATGCCGGGTTACTACATTGAGACAGAAACTGATG 1080
 F F S S S V *
 1081 ATGAAAACGTGGCAAACACTGCCTTAACATTTGTATTTCTTCTTCTCATCACTCTGTTCT 1140
 1141 ACAGCATCGGGGTGACTGTTATCAAGGTGAAATAATAAACATAAACAACTGATGGAATGA 1200
 1201 GTTCGATCTTCTCTGTTTCGCCAGTATAATGTTCTGAGTTAACTTTCTGTTAAACTA 1260
 1261 TCTTGCTCTCAGCTACTTTTCATGTGTTTATATCTGTAAATACTTTTTGTCAATTAAATG 1320
 1321 TTGATTTCTTTTCATGCTTTTACTCAAATCTCA**AATAAA**TGCAATTAAAAGCCAAAAAAA 1380
 1381 AAAAAAAAAAAAAAAAAAAAAA 1402

Supplementary Fig. 8. Nucleotide and translated amino acid sequences of the membrane-bound IgM constant domain of the north African catfish (*Cg_mIgM* 1.2, GenBank accession number MN934749). The sequence consisted of three CH and two TM domains: C μ 1-C μ 2-C μ 3-TM1-TM2. The atypical polyadenylation signal (AATAAA) in the 3'-UTR was bold.


1  GCAACGCAAGAACCCCGAAGTCTCTGTTTCCCGTGTGGCAGTGC GGCTCGTCCCCTGAT 60
A T Q E A P K S L F P V W Q C G S S P D

61 GGTTCGTCCTCTGGGCTGCCTCACCCGCGACTTGGCAACCGCGATGGACTGAGCTAC 120
G F V T L G C L T R D L A T G D G L S Y

121 GTTTGGAAGGATGCGAGCGGCACCCGCGTACTACCGTTGTACAATACCCGGCAGTGCTG 180
V W K D A S G T A L T T V V Q Y P A V L

181 GACAACGGAAGTACTCCTCAGTGAGTCAGGCGCGCTCACTGTACCGAGTGGGACGCG 240
D N G K Y S S V S Q A R V T A T E W D A

241 AACAGCCGTTCACTTGCCAAGTCACTAATTCATTGGAACCGCAACGGCGAACGTGCAA 300
N K P F T C Q V T N S I G T A T A N V Q


301  AAACCACCTCTCGTCATCCCAGCAAAATCTCTGCTTCTAACAGCTCCGAGCCAAACAGAA 360
K P P L V I P A K S L L L T A P S Q T E

361 ATAGACAATGGAACAGCTACCTTCATCTGCTTAGCTTCAGAATTTTCACCTAAAACGCAC 420
I D N G T A T F I C L A S E F S P K T H

421 ACATTTAAGTGGACCCGTGAAAAGACAAGCCTCGATAGTAAGGCAAAAGCCCCAATTTTA 480
T F K W T R E K T S L D S K A K A P I L

481 ATCCCGGGACAAAAATTTACAGTGCCTTAAGCATTTTGGAACTCACTGCCAGCGAATGG 540
I P G Q K I Y S A L S I L E L T A S E W

541 ATGGGCTCAACTTCTCCAGTTAAGTGTGAGTTCAGCACAAGGAACAGACTCTGTCCCAG 600
M G S T S P V K C E F Q H K E Q T L S Q


601  GAAGCAAGTCATGGGACATGTGAGGAGCAGCCAAAAATGACAATAAGTCCACCTTCCAAT 660
E A S H G T C E E Q P K M T I S P P S N

661 GGCATTCTTATCAATAGATCTGCTGATATTGTGTGCAAGGCTGAAGGACCAATGGGTTTC 720
G I L I N R S A D I V C K A E G P M G F

721 ACCGCCATTAATGGGTTGTTAACGGTAAAGAGGTTGCTTCCCTACCTCAAAGCGATGTG 780
T A I K W V V N G K E V A S L P Q S D V

781 TC'TTCGAAGACAGCGATCTCACTCACCCACAATCTCTTATGAAGAGTGGCATACTGGC 840
S S K T A I S L T T T I S Y E E W H T G

841 ACCAAATTTACCTGTGAGGTGTATCATTCAGCATTAGCTCAGGGATTTATACAAGAAGAC 900
T K F T C E V Y H S A L A Q G F I Q E D

901  TACCAAAGAGTAAACGGCCAAACGCAATGCCAGAGCTTTTCTTGTCTCCCTCCACCAGAG 960
Y Q R V N G Q T Q C P E L F L L P P P E

961 AGCTCAAAGGGGATTCATGACCCTGACTTGCTATATTAAGGACTTCTACCCTAAGGAG 1020
S S K G D S M T L T C Y I K D F Y P K E

1021 GTTGTGTGTCTTGGCTTGTGGTGATAAACTAGTGGACAATGAGAGCACTGTTAAAGTT 1080
V A V S W L V G D K L V D N E S T V K V

1081 ATTGAGAAAAATGGCATCTTTTTCAGCATAAGTCAAGTCAATTTGTCGATAGGGCAGACTGG 1140
I E K N G I F S A Y S Q L I V D R A D W

1141 GAAAAATGGCACTGTGTTCACTGCAATGTTTATCATGAGTCCATCGTAGAGAGTGTGGCG 1200
E N G T V F T C N V Y H E S I V E S V R

1201 CACCTTTCTAGATCCGTTGCTGGTAATTCAAATCCACCCTCCGTAGTGAATCTCAGCTTA 1260
H L S R S V A G N S N P P S V V N L S L

1261 AATGTTCCCCAAACTGCCCAATGCTCTGTAAGACTGATGCCGGGTTACTACATTGAGA 1320
N V P Q N C P N A L *

1321 CAGAACTGATGATGAAAACGTGGCAAACTGCCTTAACATTTGTATTTCTTCTCTCA 1380
1381 TCACTCTGTCTACAGCATCGGGTGACTGTTATCAAGGTGAAAT**AATTAAT**GCAATTAA 1440
1441 AAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Supplementary Fig. 9. Nucleotide and translated amino acid sequences of the secreted IgM constant domain of the north African catfish (*Cm_slgM* 1.1, GenBank accession number MN934750) and hybrid catfish (hybrid:*Cg_slgM* 1.1, GenBank accession number MN934752). The sequence was consisted of four CH domains: C μ 1-C μ 2-C μ 3-C μ 4. The atypical polyadenylation signal (AATTA) in the 3'-UTR was bold.

1 GCACACAGAAAGCCCGGAGTCCCTGTTCCCGTGGCAGTGGCGTCCGCTCCCTCGAT 60 3661 gagatcctgggtgctgaccaaccttttctacaatgagacagaacttgatgatgacaacgtg 3720

61 GATQEPKSLFPVWQCGSSPD 120 3721 gcaaccactgcttaacatttctctctcctcaccctgttctacagctcggg 3780

121 GGTTFGTCACCTGGGCTCGTCCACCCGGCCTGGCAACCCCTGATGGACTGAGCTAC 120 3781 gtgactgtatcaagtgaaatgagaacaactaatggaaactgtttgatttctctctg 3840

181 GTTTGAAGGATGCGAGCGCCCGCTGACTACTAAGCTTGTACAAATCCCGCGGTG 180 3841 ttttttttctcagataaattgctgagttacccttctgttaaacatctctctctta 3900

241 ATCGAGGGCGGAAAGTACTCTCAGTGTAGTCCAGCGCGCTCAGTGTTCACACTGGAAC 240 3901 gctactttccatgattttatctctgtaaaactttttgtcatttaaatgttgatttt 3960

301 AAAAGCCAGtagggcaaaaatcctcaaacaccattttgtgtgattttcaataagca 360 3961 tttttctgcttttactcaaatcctcaataaaaaaagaagaagaataaataaaca 4020

361 gtaaaagctgtttgttcttttctgtcccttttacgaataaacatgaaaataattg 420 4021 ttaagtatttttaaatgaagaagaatgatctaaagctcccccacaactcagcaat 4080

421 caccctaaagggcgatgcccgaagatttaatttacttaaaatgtaattgaaatcata 480 4081 gtgtgtatgtgtctgttgcattcagttactttgtcaagctttattgtgtgctctg 4140

481 accttggatggctccctattgataagagaatgtacaggttatactgtgcttactt 540 4141 tttttttcagatgattttatctctgtaaaactttttgtcatttaaatgttgatttt 4200

541 tgaactgactgtgctcaggtgatttgatattatgtgcaatgcatagtaaccaagaatac 600 4201 tctccagcaagcaagacattgagcactcgttaagtagagagttttttctaccctt 4260

601 aaatagatatacatttgccttaaacataaaataaaactacacttaaacattataa 660 4261 tttttttcagcaggttaccgatataatgttaccataaacactcaaccaaaagcttt 4320

721 attaaagaaagttcttttaagctccatttttaaatagaaaggttaaaaacaacagata 780 4321 cactactagaatgacttattgggctacacaaatagccataaacataaatgccaacaaac 4380

781 tcaactacata 840 4381 ataacagtgattgcttatacaattttaccagtaaacgtggtgacaggtcattgtgcc 4440

841 tgtgttagagtgccactaatcagactgtttcagacaatcagaaaaataaaagattcaaat 900 4441 caaggtcacaagggcagccactcgtgccaatccccaaagaaagccaaatcagcagaat 4500

901 aaagactgtttatcctcagaaacccctgagtgacatacttctgtagatgtttaaaacttt 960 4501 tctgtaaaacaccagcaacactagtgacacacactcctgcacatgtgcacaaaggtatc 4560

961 ctaaattttgggtgtaact 1020 4561 acaattttgggcaataatgtttgtgtaactgttattgtctgattgtggtgtaaccatga 4620

1021 tgagcattattcttgggaaaaatgagcaaatgacatgaaatagacggttaagcagaat 1080 4621 gggaggtgctgattgtgctggatatacagatggctgtgatacaaatcagatcaggggt 4680

1081 aatctcagatgttttaactcatttaagttgttttaataaaaaaaagaaatgctgcag 1140 4681 gcagctggagctgacaacaacagttgacccaacagttagtgatttaaacaggttaatt 4740

1141 tctttacacactgagacagctgcttgggccccataaaaagggctgactaaaattttataat 1200 4741 tttggatggaaatccagTATGCCTTAACATTGTTATTTCTTCCTCATCACCCTGCTTCT 4800

1201 tccccaaaagggaaatcccggtgaaatccccctgggaaatatttaagttaaaagcaagc 1260 4801 ACAGCTCGGGgtattggattgaaaggaagtttggtaaaatttttccaccaacccctctt 4860

1261 attttaaaatccaaagcttatttactctctgactctctctctctctctctctctctctct 1320 4861 Y S I G 4920

1321 caatgttgccttttttactgagaaatgaaatccccctgggaaatatttaagttaaaagca 1380 4921 caaagatttttgattgaggttgatttcaattggctgaaatgaaatcctcagttccagaa 4980

1381 taaaatacactcaaatgtttgctgtgcaaaaacagtaataagttgactagtaataat 1440 4981 tcactctcaaattttgactcctgatgaatcactatgcaactagaaatgctcgtggc 4980

1441 taatattaaaggtgttttaactcatttaagttgttttaataaaaaaaagaaatgctgcag 1500 4981 tcaagatttttgattgaggttgatttcaattggctgaaatgaaatcctcagttccagaa 4980

1501 taatgcaactgtttttaccataatttttttagtatagatacaaacatgatgggttctgt 1560 4981 taatcccaatctcttggctgacttgcttaaaatgggggtgtttggccacagggctgt 5040

1561 taatgcaactgtttttaccataatttttttagtatagatacaaacatgatgggttctgt 1620 5041 taatcccaatctcttggctgacttgcttaaaatgggggtgtttggccacagggctgt 5100

1621 ttgctgattacaatatttcaattgtctgaaagttgtgcaaaaaaaatatacaactaa 1680 5101 tctatgatacaactcacaacatatttgaacttaattgtcagcagactcttaagtatttt 5160

1681 tttgctgattacaatatttcaattgtctgaaagttgtgcaaaaaaaatatacaactaa 1740 5161 ctatgatacaactcacaacatatttgaacttaattgtcagcagactcttaagtatttt 5220

1741 tttgctgattacaatatttcaattgtctgaaagttgtgcaaaaaaaatatacaactaa 1800 5221 tatattttgggtgaaagctctcactacagaaatcccccaactgatagaacacatact 5280

1801 ggactatagatataatatactgtgtaaaattttactacagaaatatacaactcc 1860 5281 ttttaatttcaattgttacaactgttcaactgttcaacttaaaatgataaaagggattt 5340

1861 aactgcataagaatttttagcactcgtgataaaatttagatatttaggggtataaaaat 1920 5341 taacagcagctcagcaataattttgactcactaaacttataagttataaaaggttttag 5400

1921 agcatttttgggtgttcaataactgtggaacaacactctatttcaataactgctatgc 1980 5401 taccacaagttgattgaaatgcaacttctttaaactgaaagaaagaaaaaacaggaaga 5460

1981 ctattgctgctgcatatggatctgtttgtttgtttgcaagTTCGCGCCGACCTGCTGC 2040 5461 atgagactcactgtttttatataatagataaatgacattgtttgtggatcctcagat 5520

2041 AAAATCTCTGCTTCTAACAGCTCCGAGCCAAACAGAAATGGAACACTACTCT 2100 5521 tctgtaaacataaaatgtttaaaaggttacaattgggaaatataatgtcataagagaac 5580

2101 CATCTGCTTAGCTTTCAGAAATTTACCTAAAAGCTCCACATTTAAGTGGACCCGTTGAG 2160 5581 gaaacacactcagggaggtcctgttataagataaaagactatagaataaagat 5640

2161 AACAAAGCATCGATAAATAGGCCAAGACCCCACTTTAATCGCGGGAAAACTTACTACAG 2220 5641 caactaatacaaaaatatacaactccttcttactcttacttactatagatgataaata 5700

2221 TTCCTTTAGTATTTGGTACTACTGCTCCGCAAGTGGACTGCTCAACTCTCTCAAGTTAA 2280 5701 taatatttccccataatataatagataaaacagaaatcactatagtttaaaatt 5760

2281 GTCCGAGTTCCACGACAGACTCTGTCGAAGAGGCAAGTTATGtatgtatttaa 2340 5761 gtttctcaataaaatgtaattgtcacttcttactcactactactactactactactatt 5820

2341 gtaattcacttagttttatgtaggaaaaattctgtaacagcatttgaactttttcttac 2400 5821 gttgttgaacttaattgttttaaaatgattgctccaaataaaatgattttgatgtgct 5880

2401 accatagataaagacactgttttttaatacaagagtaacaaaactcgttaaatcttgyaa 2460 5881 tgaggtaaaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 5940

2461 actgaaattttagtactattttgaccttatttgaatgaaatgcaaggtgatttataat 2520 5941 aatatacagctcagctggtttcaatgaaataaaactcctgaaaaagtcagatattgt 6000

2521 gattattttttagtactattttgaccttatttgaatgaaatgcaaggtgatttataat 2580 6001 tgcgttggattttgtttttatgaaagaaacttaaaatcaatataaataattttgtct 6060

2581 gtttctttaaagtataaatttctttcttcaaaaacttatttctacactctctccac 2640 6121 acaacaaaaatataatgctcaactcactcaactcaactcaactcaactcaactcaactca 6120

2641 agcaactattgaccgggagcagcaacaatatacaataatccccactccaacaatgacatg 2700 6121 ttttttttctcagataaagttttgtttgtttgttttttttttttttttttttttttttt 6180

2701 cttcaaaaaattccgggattttccacagcattttagtggcgggagcggcgaactatc 2760 6181 TGACTCTTATCAAGGTGAATGGGAAACAACTAATGAGCAATTTGATTTTCTCTCTGT 6240

2761 AATAATCCACCCTTCCAACAATGACATGCTTATCAAAGATCTGGCGACCTCGTGTGCAA 2820 6241 V T V I K V K W E T N G T I L I F S L 6300

2821 GGCTGAAGGACCATTTGGTTCACGGAATTAAGTGGGTGCTAACGGTAAAGAGGTTGT 2880 6301 TTTTTCCTTCTCAGTATAAgttttgtttgtttgttttttttttttttttttttttttttt 6360

2881 ATCCCTATCTGAAAAGTTGCTACGAGGCGAGTCTCACTCACCCCAATCTC 2940 6361 accotttctgtatcactagaagatctcactacacagcggaaataactttggacatttaaa 6360

2941 S L S E K V S T K A A I S L T T S I S 3000 6361 tgttggcaatttttttctcagctcactcaaatcctcaataaaatattgacaaaaatag 6420

3001 Y E E W H K G M K F T C E V H H S S F A 3060 6421 caattaaaagctcaattttctgtactcttatttgaattatagtcagccttaagat 6480

3061 tacatatactgttttttaatttgcagtagaaaagctatatagaacttttaaaaaaagtaga 3120 6481 gttgtttagttatagcttatacactgcttcttattttatagtttttaaaaaatta 6540

3121 aaatcacattttatccaatgctactgaaatgttaagctttttttgtttgtttact 3180 6541 ttaagacgtttcagcagcagtagttttctcagtttctgtgtgaaacatagtaaaact 6600

3181 tgtgaccaatgttccccacaatacaaaaaaatgtgagagaagaaactgatcatgtttt 3240 6601 attaggttatt 6660

3241 gttgttaactatgatttcatgttcatagGGCGAAGCCCTAACTGCCAGGGGTTTCTT 3300 6661 caacotttctcaaatgagacagaacttgatgaaacagctggcaacacactgcttaac 6720

3301 G R T P N C P G V F L 3360 6721 atttgtatttctctcctcactcaactgttctcaagactcgggtgactgttatcaaggt 6780

3361 L P P P E S S N G D L K T L T C Y I K N 3420 6781 gaaatgagaaacaataaa 6798

3421 CTTTTACCTAAGGAGTGTGCTGTCTGGCTTATTGGTGATAAACAAGTGGCAATGA 3480

3421 GAGCATCAATAAGTTATTGAGAAAAATGGCAACTTTTTCAGCATACAGTCACTGATGT 3540

3481 S I T K V I E K N G N F S A Y S Q L I V 3600

3541 CAATCAGGACTCTGGGAAATGGCACAGATTCACCTGCAATGTTTATCATGATCCAT 3660

3601 N Q D S W G N G T E F T C N V Y H E S I 3660

3601 CATGGATAATCTCGCACCTTTCCAGAACCTTACTGGCACTTCAAATCCACCCTCCAT 3660

3601 M D N L R H L S R T I T G T S N P P S I 3660

3601 AGTGAATCTCAGCTAAATGTTCCCAAACTGCCAAATCTGGTCTGTAAGtagtata 3660

3601 V N L S L N V P Q N C P N P G L *

Supplementary Fig. 10. Complete nucleotide and translated amino acid sequences of the *ighu* gene of the bighead catfish and their hybrid catfish (GenBank accession number MZ559374 and MZ559376, respectively). The atypical polyadenylation signals (AATTAAA) in the 3'-UTR were bold.

1 **→Cg.ighu1**
GCAACCAAGAGCCCGAAGTCTCTGTTCCTCCGCTGGCAGTGGCGCTCGTCCCTCGAT 60
A T Q E A P K S L F P V W Q C G S S P D
61 GGTTCGTCACCTGGGCTGCCCTCACCCGCGACTGGCAACCGCGATGGACTGAGCTAC 120
G F V T L G C L T R D L A T G D G L S Y
121 GTTGGGAAGATGGAGCGGCACCGCGCTGACTCCGCTGTGACAAATACCCGGCAGTGTG 180
V W K D A S G T A L T T V V Q Y P A V L
181 GACAACGGAAAGTACTCTCAGTGTGAGTGGAGCGCGCTCAGTCTACCGAGTGGACGGC 240
D N G K Y S S V S Q A R V T A T E W D A
241 AACAAAGCCCTTCACTTGGCAAGTCAATAATTCATGGAAACCGCAACCGCGAAGCTGCAA 300
N K P F T C Q V T N S I G T A T A N V Q
301 AAACACCTGTgaaaaatactacaaaacataatTTTTGTGTCTTTTCCAAAATAAGCAGT 360
K P P
361 gaaagtcgtgattattatgtaaatattgacataatactcacacacgaacacacagaca 420
ctctcagggaaagaaaattgtaccaaaatttttgcoccttggtaggccaagacttt 480
421 attcctttattctgtaccttttacgagaaacatgaaaataatgcaacctaaaggccca 540
481 gtgcctgatatttaaatatttactcctaaagcgaattaaaataatgttaactttaaaca 600
601 agcaactatgacatcttcaaaaacagagaatgtacagtttagactgtgcttagattac 660
661 tgataacagactgtggcaggtgctttgagcaatggtaatttattattatagattatc 720
721 catagtaaacagcaattaaatagtaatacatttgcctcaactacaaaaataaaactat 780
781 acacttaccattcatgatacttttaactttaaattgtacaactatctgaattgtttatcca 840
841 acacagtttaagcttaccattaaatgacatttctgtagaaggtactcattttaaagaaga 900
901 agttaaacaacagtaagtaagtgctacatgaatgtagaggtgtagaggtgcaactaa 960
961 cacagggtttcagagaatcagagaaatacaaaatcaaaatacaacaggttttttccctaa 1020
1021 agactcagtgctgcaataaaactttaccaaaatttggtygtaactcttcttagctacat 1080
1081 gtttaagcctattagcttatcagctctctgtgtgagcataatTTTTGGGAAATGATG 1140
1141 aatgacatgaaatcagacagtaagcaaaatcaatgtctgcaattagtttttactctt 1200
1201 ttaagtccttttaaaaaaagaaatgctgcatgtcttaacacactgagacca 1260
1261 gtctgctttggccattaaaatgtctacatgaatgattttccctaaaggcttacc 1320
1321 gttgatacagcaggaattttatgcaagcattttaaactcocaagtttttactt 1380
1381 tctgactcttctctgccaatgctgcaaaagctgtttcttttcttagctgatt 1440
1441 gactttttgctggtgccaagctgatttaccagaatacactcaaatgttgcgtggc 1500
1501 aaaaaacagtaaaagttagattttaccagactgatttttaactgttcccagatagaat 1560
1561 tttacttttccatgctcaaaactactctacatttggtaaccctaaatatt 1620
1621 tttattatagaatacaacatgatgggttctgtatgagaanaaatagctataatcaagttg 1680
1681 ttgaataatgtgaaatggtttattataattttgccaactcaagtttctgctgataaaaat 1740
1741 taaatttcttgaagttaaaaaatgttaaatatatacaactaccaatattttactgagaa 1800
1801 gatttaaaacagcttcttctgtaacaggttaaaaattgtgctcctcaaaaaaacaacaa 1860
1861 aaaaaaacctgcaatattaatgcttgggaatttagtttgaataaactacacattta 1920
1921 aaaaattgtttgtttattactagtttataattatgatacaagctggtgaaattgtta 1980
1981 aatagaaataatatacaactcctaaagaaattttatggcactgataaaaatcca 2040
2041 gatataaagtttataaaaaggtattttgtgcttataatctgctgcaaacatttt 2100
2101 atttcaaacctgacagctcgtgcttattgtgctgagatggatctgtgtgtttg 2160

2161 ttttgaagctgagcag**→Cg.ighu2**CTCGTCATCCAGCAAAATCTCTGTTCTAACAGCTCCGAGCC 2220
L V T P A K S L I L I T A P S
2221 AACACGAAATAGACAATGGAAACAGCTACTCTCATCTGCTTACCTTACGAAATTTCACTA 2280
Q T E I D N G T F I C L A S E F S P
2281 AACCGCACACATTTAAGTGGCCGCGTAAAGACCAAGCCCTCGATAGTAAGGCCAAAGCCC 2340
K T H T T F K W T R E K T S L D S K A K A
2341 CAATTTTAAATCCCGGACAAAATAATTACAGTGCCTTAAGCATTTTGGAACACTACTGCCA 2400
P I L I P G Q K I Y S A L S I L E L T A
2401 GCGAATGGATGGGCTCAACTTCTCCAGTAAAGTGTGACTTCCAGCACAAGGAACAGACT 2460
S E W M G S T S P V K C E F Q H K E Q T
2461 TGTCCAGGAAGCAAGTCAATGGGACAGtatgtattaaagtatttctactttagttttatga 2520
L S Q E A S H G T
2521 ctatgatttttttcaaatgaaaatttctttaacagcatttgacttcagttgtattc 2580
2581 ttacaccatagataaagttactgttttttaagaaacaatacaaaagtaattgttaaatctt 2640
2641 gtactcaaatataatgtaataattgttcttctattgtaagtaaatgtaaatgatgtatt 2700
2701 attattttactgttaattgtgcaataaaaactcaggtatttttccagattgtaaatccaagt 2760
2761 tcttttaattacacaaaattttgtttcttgataaactatttctacacctcttttacag 2820
2821 TGTGAGGAGCAGCCAAAATGACAATAAGTCCACCTTCCAATGGCATTCTTATCAATAGA 2880
C E E Q P K M T I S P S N G I L I N R
2881 TCTGCTGATATTGTGCAAGGCTGAAGACCAATGGGTTTACCGCGCATTAATGGVTT 2940
S A D I V C K A E G P M G F T A I K W V
2941 GTTAACGGTAAAGAGGTGCTTCCCTACCTCAAGCGDGTGCTTCGAAAGACAGCGATC 3000
V N G K E V A S L P Q S D V S S K T A I
3001 TCACTCACCACCAACTCTCTTATGAAGAGTGGCATACTGGCACAATAATTACCTGTGAG 3060
S L T T T I S Y E E W H T G T K F T C E
3061 GTGTATCATTAGCATTAGCTCAGGATTATACAAGAAGACTACCAAGAGTAACGta 3120
V Y H S A L A Q G F I Q E D Y Q R V N
3121 ggaatcgtgtttactttttacatatttctgttttaatttgcagagaaagcttaaaa 3180
3181 aaaaagcaaaaatcacatttttatatccagtgctactgaaattatggaattattatatt 3240
3241 gttaaagctttttttgtgtttactgtgaccaatgttcccaaacgtacaaaaacaa 3300
3301 tttaaagaaagaaactgatcatgctttgtgttaactatgattttatgttccatag**→Cg.ighu4**GGCC 3360
G
3361 AAACGCAATGCCAGAGCTTTTCTGTCTCCCTCACCCAGAGCTCAAAGGGGATCA 3420
Q T Q C P E L F L L P P P E S S K G D S
3421 TGACCTGTACTGTCTATTTAAGGACTTCACTCCCTAAGGAGTGTGCTGCTGGCTTG 3480
M T L T C Y I K D F Y P K E V A T V T S W L

3481 TTGGTGATAAACTAGTGGACAATGAGACACTGTAAAGTTATTGAGAAAAATGGCATCT 3540
V G D K L V D N E S T V K V I E K N G I
3541 TTTTCAGCATAACAGTACAGCTAATTTGCGATAGGGGAGCAGCTGGGAAAAATGGCACTGTGTTCA 3600
F S A Y S Q L I V D R A D W E N G T V F
3601 CCTGCAAAAGTTTATCATGAGTCCATCGTAGAGACTGTGCCCACTTTCTAGATCCGTTG 3660
T C N V Y H E S I V E S V R H L S R S V
3661 TCTGGTAATTTCAATCCACCTTCCGTAGTGAATCTCAGCTTAAAGTTTCCCAAAAGTGGC 3720
A G N S N P P S V V N L S L N V P Q N C
3721 CAAATGCTCTGTAAGtagctgatgccgggttactacattgagacagaaactgatgatgaa 3780
P N A L *
3781 aacgtggcaaacactgccttaacattgtatttctctctctcatcactctgtttctacagc 3840
3841 atcggggtgactgtttatcaaggtgaaataa**→Cg.ighu1**aaacataaaacaactgatggaatgagttcg 3900
3901 atcttctctctgttttcgagcagataatgttctgagtttaactttctgttaaacatctctg 3960
3961 tctcagctacttttcatgtgttttatatctgtaaacactttttgtcattttaaagttgat 4020
4021 tcttttctcatgcttttactcaaatctcaaa**→Cg.ighu1**aaataaaaaaatgtaagaaagacaacact 4080
4081 tggataaaaacattaaatatttacaatgatacaacagagaatgctctaaagcttccccca 4140
4141 caatctgacaatgtgtgtagtctgttgcattctctgtaaatattttgtcaagctttaa 4200
4201 tttgtgtctgtgttagttacatttcaaatatttcaatgagttgcaatgtcttagttt 4260
4261 aatcactgttttctcaagcaagcagacattcagcaactctggttaagtagagaattt 4320
4321 tttctaccttctccatgaaaggtgaggtctgcaactcaatgagttgcaatgtcttagtt 4380
4381 caaagcttctacatacagaactgacatttagctacaccaattagtcataaacattaacg 4440
4441 ccaacaacacttaccacataaacatggtgattattttaccagtaaacctggtga 4500
4501 cagggctgtgaccccgctcaagggcagctcattctgttccacccacagcaagaa 4560
4561 ccaatgtagcaaaaattgctgaaaaaagtaattgctggcattgatagcccccaaac 4620
4621 cagtgcagcaactcctgacatggcctctgaggaacttaaggtcactgccccagcctct 4680
4681 agacttcccaggtctcaatagaacaaagatccaaggaatgccccagacaacagccccca 4740
4741 atccataaagggcctacccccacaacacagcaacaacaatgaatcgtgggtggctccccat 4800
4801 tccaggtatcacatcacaacactccaaggtcattggcctgaaaggggcaaacctccca 4860
4861 tttgtctttaaagggatctcccaacttggggcaaaaaggtttttgttttaagtt 4920
4921 tattggcggaaaagggggaatccccctttaaaggggtgtatccccgggttttttccc 4980

4981 tttggggccgag**→Cg.ighu1**TATGCTTAACTTTGTTTCTCTCTCTCATCACTGTCTTACAGC 5040
Y A L T F V F L F L I T L F Y S
5041 ATCGGGGtaagctgtttatcaaggtgagaactgatccccagtaaacataaacccgggtgaat 5100
I G
5101 tccaggaacaaaaaatgtgtgtgcaaacacagatgttttagtccaattctgtgagttc 5160
5161 tgttgactgtgtatgggattgctcttacatttaacataaacatagctgtaatttctaa 5220
5221 cagtaatttttttaagaaaaactcaccacttaaatatttaattgactcactatttgataa 5280
5281 ataatccacagacttaattatttgcatttttaatttagacagaaaataaaacttttt 5340
5341 gagatggcagggcagggcaatttccatgttccaaaactcactataagaaatggtaaaatcca 5400
5401 attgggtcaaaagggatcttaggaagagatttctataacagcagctctgacaataactttg 5460
5461 ctatagctctcaatagaaaggttttagtatacaatatttagtaagctcaactaatt 5520
5521 ttaacactcaaaagcagaaaaaggggggtgtagcaagagctcctgtttatgtttgtgttt 5580
5581 tttattatagactctgtagatgtggatattgtaaacataaatgtttaaaaaggttac 5640
5641 agttggaaatcctttgtaattgctatacacaataataaaacacttccagagagtg 5700
5701 cgttatga**→Cg.ighu2**aaataagaataaaaaatataagaatacaataaacttataaacataa 5760
5761 aactottaagtttttcaaacctttgtagttatactgttctattagaattataaata 5820
5821 taatattttctctacatattatagaccaatacaaaagacacacataatttaaagattg 5880
5881 cacttttaatacaaatgtaattgcaacttttactattgtactgttccataaaatgtttc 5940
5941 gacccaatgttttaataaagtagctgcaataaaataatttttaattgttagttggggat 6000
6001 aaaaagtaattgttttaaaaaaaataaaaaaacaggaataatatttaaagcttaaacg 6060
6061 aatataatagacaggttctgacagctacagtaaatagtaataacattggaaggtca 6120
6121 gaaatgtattgtgtttttgattttgttatttaattgagcagaaaactctgacaattgtg 6180
6181 taaattcaaaaactgtcccaatatttgaattccacataaaaaagagagattag**→Cg.ighu2**GTGGT 6240
V *
6241 GAAATGGGAAACAACATAAGAACAGATTTTGTATTTCTCTCTCTTTTTTTTCTTCTTCT 6300
K W E T N G T I L I F S L F F F S S S
6301 AGTATAAGtagctgatgccgggttactacattgagacagaaactgatgatgaaaactgg 6360
V *
6361 caaacactgccttaaacattgtatttctctctctcatcactctgtttctacagcagctggg 6420
6421 tgactgttatacaggtgaaata**→Cg.ighu1**aaacataaaacaactgatggaatgagttcgacttct 6480
6481 cctgtttcgcaggtataatgttctgagttaaactttctgttaaacatctctgtctcagc 6540
6541 tacttttctgtgttttatctgtaaacacttttctgacttaaatgttattttcttt 6600
6601 catgcttttactcaaatccaaat**→Cg.ighu1**gcaataaaagcc 6641

Supplementary Fig. 11. Complete nucleotide and translated amino acid sequences of the *ighu* gene of the bighead catfish and their hybrid catfish (GenBank accession number MZ559375 and MZ559377, respectively). The atypical polyadenylation signals (AATTAA) in the 3'-UTR were bold.

VH Number	VH	DH	JH
VH 51	GCA AAA	GAGGTTTACGGT	TAC TTT GAC TAC
VH 33	GCA AGA	TCTC <u>GGGA</u> ATTGGGT	GCT TTT GAC TAC
VH 6	GCA AGA	<u>TACGGGA</u> ATTGGGT	GCT TTT GAC TAC
VH 92	GCT CGG	GGCT <u>ACGGT</u>	GCT TTT GAC TAC
VH 94	GCC AGA	GAAGT <u>GGGGGC</u> TTCGGT	GCT TTT GAC TAC
VH 50	GCA AGT	<u>ACGGC</u> CCCCGGT	GCT TTT GAC TAC
VH 48	GCT AGA	<u>GAGGGATACCGGG</u> GTGGGGGT	GCT TTT GAC TAC
VH 75	GCG CGC	<u>TGGA</u> <u>GCAGCTC</u> CCTTTACTAC	GGC TTT GAC TAC
VH 29	GCA AGA	AGCAGCT <u>GGGCC</u>	GGC TTT GAC TAC
VH 100	GCA CGT	CGGATAGCAGCT <u>TGGGAT</u> CTAC	GGC TTT GAC TAC
VH 65	GCG CGA	CAGTCAGATAGCAGCT <u>TGGG</u> GTCCC	GGC TTT GAC TAC
VH 79	GCT CGT	CGCATG <u>AGGGATAGCAGCTGG</u>	TAC TTT GAC TAC
VH 45	GCA AAG	TT <u>GGATAGCAGCTCG</u>	TCC TTT GAC TAC
VH 10	GCA AGT	TACATCCCT <u>GGGGGG</u> GATAC	GGC TTT GAC TAC
VH 27	GCA AGA	CACGGT <u>GGGGGG</u>	GGC TTT GAC TAC
VH 49	GCA AAA	GGT <u>GGGGTGGGGGGG</u>	TAC TTT GAC TAC
VH 61	GCA AGA	<u>TGGGGGGGTACC</u>	TAC TTC GAC TAC
VH 9	GCA AGA	TAT <u>CCGGGATTACC</u>	TAC TTC GAC TAC
VH 81	GCC CGT	AAAAATAACT <u>ACGGC</u> GCCGATAATACC	TAC TTC GAC TAC
VH 63	GCA CGA	<u>GACGGGA</u> ACTAC	TAC TTT GAC AAC
VH 46	GCA AAG	TACAT <u>AGGGTCTGGAGCC</u>	TAC TTT GAC TAC
VH 18	GCA AGA	TACCAC <u>CCGGGGATAT</u>	TAC TTT GAC TAC
VH 32	GCA AGA	TACCAC <u>CCGGGGATAT</u>	TAC TTT GAC TAC
VH 68	GCA CGG	GAATAC <u>CCGGGTGGATAC</u>	GGC TTT GAC TAC
VH 91	GCT CGT	<u>ACCCGGTATAGCTATGGC</u> TATTCCTAC	GGC TTT GAC TAC
VH 83	GCC CGA	GAGATA <u>ACCGGGCGGATCTCACTAC</u>	GGC TTT GAC TAC
VH 12	GCA AGA	<u>GAGGCAGGG</u>	GCT TTT GAC TAC
VH 43	GCA AGA	GAGTATT <u>GGGGTAATGGT</u>	GCT TTT GAC TAC
VH 85	GCC CGA	GATT <u>GGG</u> GTAATAGCCACAAT	GCT TTT GAC TAC
VH 53	GCA AGA	<u>TACCGG</u> TAGCTGGTATACAT	GCT TTT GAC TAC
VH 76	GCA CGC	<u>CAGGG</u> TAGCTGGTATTAT	GCT TTT GAC TAC
VH 21	GCA AGA	<u>TCTCGAGG</u> TTAC	GGC TTT GAC TAC
VH 4	GCA AGA	<u>TACCGAGG</u> TTAC	GGC TTT GAC TAC
VH 41	GCA AGA	GATTATAGCTATGGTAGTG <u>ACCGAC</u>	TAC TTT GAC TAC
VH 14	GCA AGA	GAGT <u>ACCGGGCAGGG</u> TATAAT	TAC TTT GAC TAC
VH 23	GCA AGA	G <u>CGGG</u> GAT	TAC TTT GAC TAC
VH 88	GCC AGA	G <u>CGGGGC</u> CTACGTACGGCGAT	TAC TTT GAC TAC
VH 52	GCA AGA	GCTCC <u>CCGGATGGACT</u>	GCT TTT GAC TAC
VH 7	GCA AGA	GGGTCC <u>GGATGGACT</u>	GCT TTT GAC TAC
VH 35	GCA AGA	<u>GGGAGCACCGGT</u>	TAC TTT GAC TAC
VH 36	GCA AGA	<u>GGGAGCCCGGCCGGT</u>	TAC TTT GAC TAC
VH 34	GCA AGA	<u>GAACATTATAGCTCCAAT</u>	GCT TTT GAC TAC
VH 17	GCA AGA	GAATATTATAACT <u>ACGACGGT</u>	GCT TTT GAC TAC

Supplementary Fig. 12. Partial nucleotide sequences and V_H-D_H-J_H junction diversity of the VH domain of IgM heavy chain in bighead catfish. Core DH nucleotides are highlighted in yellow. Palindromic sequences or P-nucleotide are underlined with red. The N-diversity or N-nucleotides are non-highlighted letters which essentially observed at the VH-DH-JH junctions. The partial sequences are from a hundred unique nonredundant clones of VH domain, NCBI accession number sets are ordered from MN934442 to MN934541, respectively. Core DH segments were predicted using online tools, IgBLAST (<https://www.ncbi.nlm.nih.gov/projects/igblast/>), IMGT/HighV-QUEST (http://www.imgt.org/IMGT_vquest/input), VDJsolver 1.0 Server (<http://www.cbs.dtu.dk/services/VDJsolver/>).

VH Number	VH	DH	JH
VH 6	GCA AAG	TACATAGGGTCTGGAGCC	TAC TTT GCC TAC
VH 6	GCA AAA	CCGCTCGGCTACGCTGAC	TAC TTT GAC TAC
VH 8	GCA AGG	<u>ACCGATGAC</u>	TAC TTT GAC TAC
VH 22	GCA AGC	CCGTGGGGTAGTGGGGAC	TAC TTT GAC TAC
VH 43	GCA AAG	TACAGGGACCATAGCCACCGGTACGAC	TAC TTT GAC TAC
VH 29	GCG CGA	GGTTATACCCGGGTGGGGGACTACGGT	TAC TTT GAC TAC
VH 71	GCC CGT	CGGGTAGTGGGATACTACGT	TAC TTT GAC TAC
VH 31	GCT CGG	GAACCGGTTAGCTATGGTAGTGCTACC	TAC TTT GAC TAC
VH 72	GCA CGC	AGAACGTATAGCTCTGTCTATCACGGT	GCT TTT GAC TAC
VH 75	GCC CGA	GTCGACTATAGCTCTGTCTATT <u>CCTACAAT</u>	GCT TTT GAC TAC
VH 14	GCA AAG	<u>TACCGGGATGGA</u> TACGGT	GCT TTT GAC TAC
VH 44	GCA AGA	GACTGGATCGACGGT	GCT TTT GAC TAC
VH 53	GCC CGG	GAGATCAGTCCTGGTGT <u>CACC</u>	TAC TTC GAC TAC
VH 86	GCA AGA	<u>GACCGGG</u> TAGTGGTGAG	TAC TTC GAC TAC
VH 28	GCA AAG	TTGGATAGCAGCTCG	TCC TTT GAC TAC
VH 94	GCA CGC	TACGGGAGCTGGAGCAGCCGC	TAC TTT GAC TAC
VH 54	GGC AGG	CGAGCTGGAGCTGGC	TAC TTT GAC TAC
VH 67	GCT CGT	CGCATGAGGGATAGCAGCTGGAGT	TAC TTT GAC TAC
VH 100	GCT CGT	TTCCAGCTGGAGGC	TAC TTC GAC TAC
VH 19	GCA AGC	CTTTATGGTAGCTACGCCGGCTAC	TAC TTT GAC TAC
VH 33	GCG CGC	<u>AACATACA</u> TGGTAGC	TAC TTT GAC TAC
VH 76	GCG CGC	<u>AACAT</u> CCGTAGA	TAC TTT GAC TAC
VH 19	GCA AGC	CTTTATGGTAGCTACGCCGGCTAC	TAC TTT GAC TAC
VH 33	GCG CGC	<u>AACATACA</u> TGGTAGC	TAC TTT GAC TAC
VH 76	GCG CGC	<u>AACAT</u> CCGTAGA	TAC TTT GAC TAC
VH 66	GCA AGA	TACGAACGTTACGGGGGGG	GCT TTT CAC TAC
VH 90	GCA AGA	CACTATATACCCGGAAC	GGC TTT CAC TAC
VH 63	GCG CGA	GAGAGGCAAGAGGGGCAGCCAC	GGC TTT CAC TAC
VH 73	GCT GTC	TATTACTGCGTTCGCTACATGAGG	GGC TTT CAC TAC
VH 36	GCA AAA	<u>GGACA</u> TCCATATAGCTGGAGC	AGC TTT CCC TAC
VH 7	GCA AGA	GTCGGGCTCTACTAC	GGC TTT GAC TAC
VH 18	GCA AGA	GTCGGGCTCTACTAC	GGC TTT GAC TAC
VH 35	GCA AGA	<u>GGCCGGT</u> TATAGTGGCTATAACTATGGT	TTC TTT GAC TTC
VH 48	GCA AGA	<u>GGCCGGT</u> TATCCTGGCTATCCCTATGGT	TTC TTT GAC TAC
VH 87	GCA AGA	<u>TACAGGT</u> TATAGTGGCTATGGTGAGGGT	GCT TTC GAC TAC
VH 84	GCC AGA	GAGTACTCGGGT	CGG TTT GAC TAC
VH 1	GCA AAG	<u>TACATAGG</u> GTTGGAGCC	TAC TTT GAC TAC

Supplementary Fig. 13. Partial nucleotide sequences and V_H-D_H-J_H junction diversity of the VH domain of IgM heavy chain in north African catfish. Core DH nucleotides are highlighted in yellow. Palindromic sequences or P-nucleotide are underlined with red. The N-diversity or N-nucleotides are non-highlighted letters which essentially observed at the VH-DH-JH junctions. The partial sequences are from a hundred unique nonredundant clones of VH domain, NCBI accession number sets are ordered from MN934542 to MN934641, respectively. Core DH segments were predicted using online tools, IgBLAST (<https://www.ncbi.nlm.nih.gov/projects/igblast/>), IMGT/HighV-QUEST (http://www.imgt.org/IMGT_vquest/input), VDJsolver 1.0 Server (<http://www.cbs.dtu.dk/services/VDJsolver/>).

VH Number	VH	DH	JH
VH 21	GCA AGG	TTGTATAACTCTGGCTATGGTGCCGTCTAC	GGC TTT GAC TAC
VH 95	GCG CGA	CAGTCAGATAGCAGCTGGGGTCCC	GGC TTT GAC TAC
VH 67	GCA AGA	GGAGAAAACGAAATCACTACGCCTACC	TAC TTC GAC TAC
VH 71	GCA AGA	TATCCGGGATTACC	TAC TTC GAC TAC
VH 37	GCA AGA	ACGGGGGTGGCC	TAC TTC GAC TAC
VH 94	GCC CGG	GAGATCAGTAGTGGTGTCCACC	TAC TTC GAC TAC
VH 22	GCA AAA	TACTATAACTACGCC	TAC TTC GAC TAC
VH 06	GCG GGA	GAGGGGGCTCCTACC	TAC TTC GAC TAC
VH 18	GCC AAA	GGTGGTTATACT	TAC TTC GAC TAC
VH 12	GCA ATG	TATAGTTTTGGC	GTC TTC GAC TAC
VH 24	GTC CGG	GGACTTGACTAC	GTC TTC GAC TAC
VH 34	GCG AGT	ACGGCCCGGT	GGT TTT GAC TAC
VH 25	GGA AAA	GGACAATATGGGGGGTCCGAC	TAC TTT GAC TAC
VH 15	GGA AGA	TGCCCTATTGGGAGTAGTAGTAT	TAC TTT GAT TAC
VH 13	GCA AGA	ACCGCTGGACCAGCTCTC	CCT TTT GAC TAC
VH 39	GCC AGA	CATTTGACGTATCTGGGTCC	GTC TTT GAC TAC
VH 88	GCC CGA	GAGATAACCAGGGGGCGGATCTCACTAC	GGC TTT GAC TAC
VH 26	GCA AGA	GGCCGGTATAGTGGGTATAACTATGGTGCC	TTC TTT GAC TTT
VH 85	GCA AGA	GAGTACGCGGCAGGGTATAAT	TAC TTT GAC TAC
VH 43	GCA AGA	GAGTACGCGGCAGGGTATAAT	TAC TTT GAC TAC
VH 42	GCA AGA	GAGTACGCGGCAGGGTATTAT	TAC TTT CAC TAC
VH 07	GCA AGA	GCGGGAGAT	TAC TTT GAC TAC
VH 30	GCA CGA	GAGGGGAGAT	TAC TTT GAC TAC
VH 36	GCA GTA	GAGACCCCGGGGTAT	TAC TTT GAC TAC
VH 02	ACC CGA	CTGGCTGGGGGGGATGAT	TAC TTT GAC TAC
VH 01	GCA GAA	AATACGGGTCACGAA	TAC TTT GAC TAC
VH 60	GCA AGA	GGCCGTCGGGAA	TAC TTT GAC TAC
VH 27	GCA AGA	GAATATGGATCTGGTATTTGA	GAC TTT GGC TAC
VH 11	GCA AGA	GTCGGTATAATGGCGTACGGT	GCT TTT GAC TAC
VH 17	GCA AGA	GTCGGTATAATGGCGTACGGT	GCT TTT GAC TAC
VH 33	GCC AGA	GAGTATAGCTCTGTCTATGGTGCCCCAAT	GCT TTT GAC TAC
VH 38	GCA AGA	GATACCACTGTATAGCTCTGTCTATGGTGCTACGGT	GCT TTT GAC TAC
VH 98	GCA CGG	GAATACCCGGGTGGATAC	GGC TTT GAC TAC
VH 09	GCG AAA	CCTCTAACTATGCGGTAC	GGC TTT GAC TAC
VH 28	GCA AGA	GAGAGGGACAAT	GCT TTT GAC TAC
VH 86	GCA AGA	GAACATTATAGCTCCAAT	GCT TTT GAC TAC
VH 04	GCA AGA	CTGGGTAC	GCT TTT GAC TAC
VH 16	GCA AGA	CTCGCTCATTCCGGGTAGTGGTTAT	ACT TTT GAC TAC
VH 05	GCA AAA	TTAACAGCTAAT	GCT TTT GAC TAC
VH 80	GCA AGA	TACGCGGTAGCTGGTATACAT	GCT TTT GAC TAC
VH 29	GCA AGA	GACGCAAGGTGGAGCAGGGGTG	GTC TTT GAC TAC
VH 44	GCA AGA	TACGAACGTTACGGGGGG	GCT TTT GCC TAC

Supplementary Fig. 14. Partial nucleotide sequences and V_H-D_H-J_H junction diversity of the VH domain of IgM heavy chain in hybrid catfish. Core DH nucleotides are highlighted in yellow. Palindromic sequences or P-nucleotide are underlined with red. The N-diversity or N-nucleotides are non-highlighted letters which essentially observed at the VH-DH-JH junctions. The partial sequences are from a hundred unique nonredundant clones of VH domain, NCBI accession number sets are ordered from MN934642 to MN934741, respectively. Core DH segments were predicted using online tools, IgBLAST (<https://www.ncbi.nlm.nih.gov/projects/igblast/>), IMGT/HighV-QUEST (http://www.imgt.org/IMGT_vquest/input), VDJsolver 1.0 Server (<http://www.cbs.dtu.dk/services/VDJsolver/>).

<i>ighμ</i>-CH₁		1	2	3	4	5	6
Bighead catfish	1	-	100.00	82.35	82.35	72.55	38.61
Their hybrid (mlgMH)	2	100.00	-	82.35	82.35	72.55	38.61
African catfish	3	82.35	82.35	-	100.00	66.67	38.61
Their hybrid (slgMH)	4	82.35	82.35	100.00	-	66.67	38.61
Channel catfish	5	72.55	72.55	66.67	66.67	-	47.52
Zebrafish	6	38.61	38.61	38.61	38.61	47.52	-

non-<i>ighμ</i> exons		1	2	3
Bighead catfish	1	-	57.73	34.63
Channel catfish (IgDH)	2	57.73	-	36.49
Zebrafish (IgDH)	3	34.63	36.49	-

<i>ighμ</i>-CH₂		1	2	3	4	5	6
Bighead catfish	1	-	100.00	77.23	77.23	57.84	36.89
Their hybrid (mlgMH)	2	100.00	-	77.23	77.23	57.84	36.89
African catfish	3	77.23	77.23	-	100.00	57.28	33.98
Their hybrid (slgMH)	4	77.23	77.23	100.00	-	57.28	33.98
Channel catfish	5	57.84	57.84	57.28	57.28	-	34.62
Zebrafish	6	36.89	36.89	33.98	33.98	34.62	-

<i>ighμ</i>-CH₃		1	2	3	4	5	6
Bighead catfish	1	-	100.00	69.70	69.70	45.92	32.99
Their hybrid (mlgMH)	2	100.00	-	69.70	69.70	45.92	32.99
African catfish	3	69.70	69.70	-	100.00	43.75	25.00
Their hybrid (slgMH)	4	69.70	69.70	100.00	-	43.75	25.00
Channel catfish	5	45.92	45.92	43.75	43.75	-	30.85
Zebrafish	6	32.99	32.99	25.00	25.00	30.85	-

<i>ighμ</i>-CH₄		1	2	3	4	5	6
Bighead catfish	1	-	100.00	74.40	74.40	54.03	43.22
Their hybrid (mlgMH)	2	100.00	-	74.40	74.40	54.03	43.22
African catfish	3	74.40	74.40	-	100.00	57.72	44.07
Their hybrid (slgMH)	4	74.40	74.40	100.00	-	57.72	44.07
Channel catfish	5	54.03	54.03	57.72	57.72	-	42.62
Zebrafish	6	43.22	43.22	44.07	44.07	42.62	-

<i>ighμ</i>-TM		1	2	3	4	5	6
Bighead catfish	1	-	100.00	97.50	-	84.00	76.00
Their hybrid (mlgMH)	2	100.00	-	97.50	-	84.00	76.00
African catfish	3	97.50	97.50	-	-	85.71	80.95
Their hybrid (slgMH)	4	-	-	-	-	-	-
Channel catfish	5	84.00	85.71	85.71	-	-	72.00
Zebrafish	6	76.00	80.95	80.95	-	72.00	-

Overall <i>ighμ</i>-CH1-CH2-CH3-CH4		1	2	3	4	5	6
Bighead catfish	1	-	100.00	75.81	75.81	57.48	38.44
Their hybrid (mlgMH)	2	100.00	-	75.81	75.81	57.48	38.44
African catfish	3	75.81	75.81	-	100.00	56.97	36.34
Their hybrid (slgMH)	4	75.81	75.81	100.00	-	56.97	36.34
Channel catfish	5	57.48	57.48	56.97	56.97	-	39.95
Zebrafish	6	38.44	38.44	36.34	36.34	39.95	-

Supplementary Table 1. Similarity of amino acid sequences of the *ighμ* gene of the bighead catfish, north African catfish, hybrid catfish, channel catfish and zebrafish. Percent sequence similarity of *ighμ* gene determined using MATGAT version 2.0 software.