

Supplementary Information

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1      GGGGGGGGCGGTGTATCCTGACGTGATTCCCGGGAGTCTGCAGAAGCTCAGCCAAAAG
61     GCAGAGGATAATGCATAAAAGAGCAGCACTTTGCATTTAGGATTACATTTAGAATCAAGA
121    TGAATAATAATTACCGTGGTCGTTTTGCCTGTATTGGAGCTGTCAAAGTCTTTGCACAAT
1      M K I I T V V V L P V L E L S N C F A Q
181    CAGGAGACAGCTTTTTATTATACAATGTGGACTCTAATAAATGCCTGACTAGCACTTTGA
21     S G D S F L L Y N V D S N K C L T S T L
241    ACAGGCTTGTACCTGTGACCCACACAGTGCCCAACAAAAGTTCCGCTGGACTTCAAGTA
41     N R L V T C D P H S A Q Q K F R W T S S
301    ACCGCATTTTGAACACTTTCACAAAGACGTGTCTTGGAGTGGGAAGTAAAGCGGTGGGCA
61     N R I L N T F T K T C L G V G S K A V G
361    AAAGTCTGCAGCCCTTAAAGTGCAACGATGACAATGCTCTGCAGAAGTGGGAATGCCATG
81     K T L Q P L K C N D D N A L Q K W E C H
421    GGAACACATTGCTTGGACTAAAGAATGAGACTCTGTTCTGCTGTAGATTTTAGGGGT
101    G N T L L G L K N E T L F L A V D F R G
481    TACCTGAGATTTCTAATAAGACTGGAATCAGAAGCAAATGGACAATTCATGGCACACAGG
121    L P E I S N K T G I R S K W T I H G T Q
541    ACAGCATTTGCTCTCGGCCTTATGAAGAAATCTACAGCATTGATGGAATGGATTTGGGC
141    D S I C S R P Y E E I Y S I D G N G F G
601    AGACATGCAAGTTTCCTTTTTTGTATGAGAAAAAGTGGTATGCAGATTGTACCACAGTTG
161    Q T C K F P F L Y E K K W Y A D C T T V
661    ATGAACCGGACCAGCGTCTGTGGTGCACAACCAAGACTGACTACAGTTTATATGAGCAGT
181    D E P D Q R L W C A T K T D Y S L Y E Q
721    GGGGATACTGTCCAACACGTGATAGTAAATACTGGACAAAACATCCTCTAACAAACGTCT
201    W G Y C P T R D S K Y W T K H P L T N V
781    ACTACCAGCTGAATGACAGGTCAACTCTGACATGGTACCAGGCTAGAAAGAGCTGTGAGC
221    Y Y Q L N D R S T L T W Y Q A R K S C Q
841    AGCAAGGCGCTGAATTGCTGAGCATATCTGAACCTCACGAACAATCCTTCATAGCAGGAA
241    Q Q G A E L L S I S E P H E Q S F I A G
901    TGTTTCAGAAGTCACAAGGCTCACTATGGATAGGACTGAACAAGTTAGATGTGTCCAGTG
261    M F Q K S Q G S L W I G L N K L D V S S
961    GATGGCAGTGGAGCAATGGACAGCCTTTACGCTATTTGAAATGGCTCAGTGGATTCCCAA
281    G W Q W S N G Q P L R Y L K W L S G F P
1021   GCTCACAACCAGGCTACAATTGTGGCGTCTTGAAAAATGGCTATAATTGAGAATGGTCAA
301    S S Q P G Y N C G V L K N G Y N S E W S
1081   ATGATGCTTGCTCTGAAAAACGTGGATACATCTGCCAACGAGGTCAATCTGTTCTACTG
321    N D A C S E K R G Y I C Q R G H S V P T
1141   TTCCACCAGAAGTGACGACTGGATTTTGCCAAAGCCCCTGGATTCCACATTCTGGCAACT
341    V P P E V T T G F C Q S P W I P H S G N
1201   GTTATTTTCTACACCGCACTAAGCAAACATGGCTGGAGGCACGGGACATCTGTCTGCGGG
361    C Y F L H R T K Q T W L E A R D I C L R
1261   AAGGAGGAGACCTGCTAAGTATTCTCAGCACAGAAGAGCAAAGCTTTGCCATCACACAGC
381    E G G D L L S I L S T E E Q S F A I T Q
1321   TTGGATACTCAAAGACTGATCAGCTGTGGATTGGTTTCAATGACCGCAAAACACAGATGT
401    L G Y S K T D Q L W I G F N D R K T Q M
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Figure S1. Cont.

1381 TGT TTGAATGGAGTGACCAGTCTAGCGTCCCGTTTGCCTCATGGGAGGTTGGCGAGCCGA
 421 L F E W S D Q S S V P F A S W E V G E P
 1441 CTCACAGTGCTCAGCATGCCGAAGACTGCGTGTTAATGAGAGGGGAGGAGGGAAAGTGGG
 441 T H S A Q H A E D C V L M R G E E G K W
 1501 CTGATGATGTTTGTGAAAAAAATATGGCTTCATCTGTAAGAGAAAGACCAGCACTAAAG
 461 A D D V C E K K Y G F I C K R K T S T K
 1561 CCTCAAATAATGACACGGTTGTCGCAAATCCAGGATGCAAAAAGGGCTGGATCAGGTATG
 481 A S N N D T V V A N P G C K K G W I R Y
 1621 GGTACTATTGTTACATGGCAGGATCCGAGACAAAGACCTCCGAAGAGGCAAAACAGACGT
 501 G Y Y C Y M A G S E T K T S E E A K Q T
 1681 GTGAAAAGCAGAGTCTCGACTTGTAGATGTTTCATCCAGAGTAGAAAATGCATTCCTGG
 521 C E K A E S R L V D V S S R V E N A F L
 1741 TTAATCTAGTAGGAGCACGACCAGAGAAGTACTTCTGGATTGGACTGTCTAATCAGAAGG
 541 V N L V G A R P E K Y F W I G L S N Q K
 1801 ACGTACACACTTTTGAGTGGACCAACACTAAGCAAGTCCCATTCACTCACTTCAACTCTG
 561 D V H T F E W T N T K Q V P F T H F N S
 1861 GGATGCCAGGAAGAAAACAAGGCTGTGTTGCAATGACGACTGGAATAGTTGTGGGCTTT
 581 G M P G R K Q G C V A M T T G I V A G L
 1921 GGGATGTGCTTAGCTGTTCAAATAAGGAAAAATACATCTGCAAGCAAAGAGCTGATGCTC
 601 W D V L S C S N K E K Y I C K Q R A D A
 1981 TAGTAACAACCGCAGCCCCGCCAACCACCCCTTCCCTGGACTGTCCCACAGAATGGACTT
 621 L V T T A A P P T T P S L D C P T E W T
 2041 CAATTGGGACAAGAGACCTCTGTGTCAAGCATTTCATGTACCTTCACTGCAATGAAAA
 641 S I G T R D L C V K H F N V P S L Q M K
 2101 CATGGGATCAAGCCCTGGACTACTGCAGAGAACTCGGTGGTGACCTCCTGAGCATCCATC
 661 T W D Q A L D Y C R E L G G D L L S I H
 2161 ATGAATCTGATATTCCTGGAAACAAGGAGGAGGGTATCCATCTTGGATTGGTTACAGAA
 681 H E S D I P W K Q G G G Y P S W I G Y R
 2221 TGTATGATCCCTCTGTGGGTTACGTTTGGAGTGACGGCTCTTCGTCGTCCTATCAAAGCT
 701 M Y D P S V G Y V W S D G S S S S Y Q S
 2281 GGGCCAGCGATGAACCAAACAACCTAAACAACATGGAATAATGTGTTGAAATGAGAGTGT
 721 W A S D E P N N L N N M E N C V E M R V
 2341 CGCTGTGGGACGATGATGGGATGTGGAATGACGTGAACTGTAAAGACAAGAAGGACTGGT
 741 S L W D D D G M W N D V N C K D K K D W
 2401 ACTGTCAGATCCACAAAGGAAAGACTCCAGTTGAGGTGAATATTACAGAACCAGTTTATA
 761 Y C Q I H K G K T P V E V N I T E P V Y
 2461 ATGTAACAGAGGATGGCTGGATTGAATTCAGAGGTAGCCAGTATTATGGGTCCGAGTACT
 781 N V T E D G W I E F R G S Q Y Y G S E Y
 2521 CAGCGATGTCTATGCATGAAGCACGGGCGTTCTGTAAAAGAAATCATGGCGATCTTGTAG
 801 S A M S M H E A R A F C K R N H G D L V
 2581 TCATCAACGATGAGGAGGAGCGACTGTTCTCTGGCATAAGTCTAAAGAGTTGTACAACG
 821 V I N D E E E R L F L W H K S K E L Y N
 2641 ATTTTCTCATTGGCTTGACGGTTGATCTGGATGGATCTTCCAGTGGATGGATGGGTCTC
 841 D F L I G L T V D L D G S F Q W M D G S

Figure S1. Cont.

2701 CTGTTGTGTTTCAAGCTTGGGAAGCAAATCAACCTGCCTTTAAAAACAGTGAGGAAAGGT
 861 P V V F Q A W E A N Q P A F K N S E E R
 2761 GCGCAAAGATGACCATATCTCAAGGACTCTGGGAAACCGTCAACTGTGGTGATGAATATA
 881 C A K M T I S Q G L W E T V N C G D E Y
 2821 ATTATTTTGTCAAGCGAAGTGAGGCTCCTCCAGTTAATGCTACTGTGGCCCCTACACAGC
 901 N Y F C K R S E A P P V N A T V A P T Q
 2881 CACCAAAAGGAGGCTGTGCGCCTGAGTGGACACAGTTCGAGGGAAAGTGCTACAATGTGA
 921 P P K G G C A P E W T Q F E G K C Y N V
 2941 GGGGGGAAATGAAAAAATGGAGCGAAGCAAGAGAATACTGCAGAGAACACGGTGGAGATC
 941 R G E M K K W S E A R E Y C R E H G G D
 3001 TGACAGCTATTATGAGCAAATTCAGCAAACATTTTAAAGCACAATGATTGAGATAAAT
 961 L T A I M S K F Q Q T F L S T M I R D K
 3061 CCACTAACTTTTGGATTGGATTGAGCAATCTGGCAAATGGAAGGTTCAAGTGGACAGATG
 981 S T N F W I G F S N L A N G R F K W T D
 3121 GGAGTAAAGTTTCATTACAGAGTGGGCTGAAGGGGAACCTCATTCTTAGTATGGTCAC
 1001 G S K V S F T E W A E G E P H S L V W S
 3181 GTTCATACTACTGGACAAAATACTTTTCGGACGAGCCGAATGTGTTTTATGGGCAGGA
 1021 R S Y Y W T K Y F S D E P E C V F M G R
 3241 GTTCAGGATCTCACTTTAGCAAGTGGGTGGCAGACGACTGTAATTCTACTAATGGCTTCA
 1041 S S G S H F S K W V A D D C N S T N G F
 3301 TTTGCAGTCGTGATGTTGATCCAGGTATCCCCTCAGTGCCAACTGAGATTCCTAAACCT
 1061 I C S R D V D P G I P S V P T E I P K T
 3361 TTGTCAAGCTTGGAATTCATCTTTCAAAGTGATTCAAGAAAACCTAACGTGGATTGAGG
 1081 F V K L G N S S F K V I Q E N L T W I E
 3421 CAAATCGTCGCTGTAAGGCAGAAGGGGGTCTCTGGCCAGTATTCGGGACTTGATATCAC
 1101 A N R R C K A E G G H L A S I R D L I S
 3481 AAGCTTACATTGAGTTGCAGGTCTTCAGACTCAAGCAGCCTATGTGGATTGGTCTCAACA
 1121 Q A Y I E L Q V F R L K Q P M W I G L N
 3541 GTGAACAGTCAAATGGATATTTTCTGTGGGTGAATAAATGGCCAATGACCATGGAGAAAT
 1141 S E Q S N G Y F L W V N K W P M T M E K
 3601 GGGCGATATCTGAACCTAGGCCCAACAAACCTTGTGCACACATGAAAATAAATGGAGAAT
 1161 W A I S E P R P N K P C A H M K I N G E
 3661 GGAAAACGTCTCTATGCAATGAAACCTTCTACAGTGTCTGTGAGCAAACAACGGACATTC
 1181 W K T S L C N E T F Y S V C E Q T T D I
 3721 CGCCAACCCTTCCAGCACAGCAGCCCGGACACTGTCCAAAGCAAGAAAATTACAGTCCCC
 1201 P P T L P A Q Q P G H C P K Q E N Y S P
 3781 TGAGGTGGATACCTTTGAGAGACAGCTGCTATGCTTTTGTGACAGAAATGAAATCATGGA
 1221 L R W I P F R D S C Y A F V T E M K S W
 3841 GCAGAGCAGCAAGACTTTGTATGACATGGGGAGCTTCTCTTGCCAGCATCAGAGATGAAG
 1241 S R A A R L C M T W G A S L A S I R D E
 3901 CGGAGGAGAAGTTTATAGAAAGCAACCTCTTGCTCCTTGAAAGTTATAAAGAATTTTGG
 1261 A E E K F I E S N L L L L E S Y K E F W
 3961 TTGGATTGTTACACAACCATAAAGGACACTGGTTATGGGCAGACAACAGTGTGGTAGATT
 1281 I G L L H N H K G H W L W A D N S V V D

Figure S1. Cont.

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4021      A C A C T A A C T G G G C A C T A A C T G A G A C C G G T G G T G A C T A T G A A G A A T T T T C T T A T A A T C C T G
1301      Y   T   N   W   A   L   T   E   T   G   G   D   Y   E   E   F   S   Y   N   P
4081      A C T G C G C A T T T A T C T C T G C C A C G T C T A A A A A T T G G A A A A A C G C C A C T G T G A T T A C A C A G
1321      D   C   A   F   I   S   A   T   S   K   N   W   K   K   R   H   C   D   Y   T
4141      T T T T A C C G T T C A T C T G C A A A A C C G C C A A A G T G A T T A G C C C A A C T A T T A A G T C C C C A C A T C
1341      V   L   P   F   I   C   K   T   A   K   V   I   S   P   T   I   K   S   P   H
4201      A A G A T A T T A A A C C T C A T A G G G T T A A A A C T G G A T T G G C T G T A T T C T T G A C T A T T G C A G T G A
1361      Q   D   I   K   P   H   R   V   K   T   G   L   A   V   F   L   T   I   A   V
4261      T T G C C A T A C T T G G A G C T C T A G C C T A T G T T T A C T A C A G A A G G T C A C A A C A T C G C T T C C T G C
1381      I   A   I   L   G   A   L   A   Y   V   Y   Y   R   R   S   Q   H   R   F   L
4321      C T A C A T T T G A A A A T C C C A T G T A T A A T A A C G C A G A G T C T G C T T A T T C A G A T A A A G A T A A C A
1401      P   T   F   E   N   P   M   Y   N   N   A   E   S   A   Y   S   D   K   D   N
4381      A A T C A T T G C T T G A G G T T G C A G A A T A G A C C T G T A C A T G T A G T C A T C T G G C C A G T A T C A T A A
1421      K   S   L   L   E   V   A   E   *
4441      A A T A A C A A T G G C A G G G A T C A T C A A G T T T A T T T T G T G A T A T C G G C T C C C T A C T T C T T T T A
4501      C A T G G C T G G A T G C C A A A T A A A T A A T T G A T T T G G T T A G A A A A G G A A C G T A G C C A T G T A A A T
4561      C A G T T G T C A T T T A A A G A G G G A C C T A T T A T G C C C C T C T T T A C A A G A T T T A A A A T A A G T C T C
4621      T G A T G T C T C T A G A G C G T G T A T G T G A A G T T T T A T C C C A A A A T A C C T C A C C A A T A A T G A T T T
4681      A T T A C T G C C C C T T C T A G G C T T T G A T C C T A A C T G T G T T A T T T T G G T G A C T G T T G C T T T A A G
4741      T T G A A A T A A G A T T G T G C T T T T A G C C C T C T T T T C A A A A G A G T G C A G A G C T A C A A A T G C C T T
4801      T G T G T C A G C A T A G T G G C A G A T T C A A A A C A G G A C T A A C T T C T T A C G C T A A T G A G G G A G A C
4861      A T C A T C A T T A A T A G G T G G G G C T T T C C C C T T C A T G T A C A A A G G G A G A A T G T C A A T C A A A G T
4921      A T T T G T G T A G A A C T T T T T G A A G T G T G A T T A G A A A A A T T A A A G T T A T T T T T A C C A T T A G A
4981      A A C G G G T T A T A T T C A C A C A G T C G C C A C A C A A C T G T T T A A A C C C C T T A T A A A G G T G A T T T T
5041      T G C A T A A T G G A T C C C C T T T A A T T A G T T T A A A A G T C A T T A T G A T C A A A T A A A T A A T A A
5101      A A T C T G A C T G C A C A A T G G T G C A A C T G G C T A A T C A T A T C A T A C T A C A A T T G C T G G T T T T A A
5161      T T A T T T T C T C C A A A A G C T T T T G A A C A T C A G A C T T T G T T A T T A A A T G T T A A A G T T C A A A A A
5221      T A A A T G T C T C T A A T A A C C T T C A G T T T T T A C A C T A T G G T A T A T T T G C A T T G A C T G G A T T A A
5281      C A C T C A C A A T G C A A A A A G T T T T A A G G A A G G A A C A A T G T C A A C T T T T T T G T G C C A A A A A
5341      A T T G T G G A T G T A A G G T C A G C T G A C A C T T G A A A G C T G A C A G A G T T A G C A T T T G G A G A G A C T
5401      T G T G C A A A T G T T A T A T T T A T A C T G T A A A T G A A C A C T C C A A A A G T T C T T T A T A T A T T C A T A
5461      T T C T A T G A C T A A T C C A T A A T G A A T A C A G A A T A G G G G A C T T T G G G T G G G A A C G A T T C C G A A
5521      A A T C A C C A A C T G A T A A A T G T G A T G T G T G C A T T A T T G G T T T A G G A G A G C A T T T C A A T A A C A
5581      A C A A T A T A C A G T C A G A T C A A C T G A A T A C A G A A A G A A C A T C T A T A T T A C A G T G C A G C A G T A
5641      T C T G T A C T C A G A T T C A T T A A T C C A A T A T C T A C A A A G G C A T T T A T A G A G T A T A T A C A A A T G
5701      C A T A G A A A C A A T T T T C A A G C T A T A G T G T T G C C A C A A A C T A A T G C A T A G A G T A C T C A G G A A
5761      A C A T A C A G G T A T C A A A T G T A A A T A A A A G A T A T T G T T T C A G A T G C A T T G A G G A T A T G A T A T
5821      T G C C A T C T T T T G A T T A A C A G T T T C A C A A A A G T G A A A C A A A A C A T T T A C C A T G C T G T T G
5881      T A A T G A A C A A G T A T T G T A C C T A T T T T T G T C A G T A T A T T T G T G T C T T T T A A C T T T A T G
5941      A A G A T A A A A G T A A A A A A A A A A A A T C A T A C A T A C A G A T T G T A C A T A T T T C A A T A A A C A T
6001      T C T G A A A A T C A T A A A T A C A T G C A T A T G G T T G G C T A A A A A T G A T C A C G T T G T A T A T A T T A T
6061      T A A T A T G G A A A T A C A G A A C C T A A A A C A T C A A C A G T G T T C A T T T G C A A T A A C T T T G C A T G A
6121      G C A A A G T A C A C A T A A T A T G G C T C G A G A G T T G A T T T A C A T G A T T G T G G T C T T T G T A T T G A C
6181      A A A A A T G A T T C T T T A T T A A T A A A C A G G A A A T T G A A T A T C T T A A A A A A A A A A A A A A A A A A
6241      A A A A A A A A

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Figure S1. Nucleotide and deduced amino acid sequences of MR from *Danio rerio*. The start codon (ATG) was shown by bold letters. The termination code (TAG) was shown by bold letters and marked with an asterisk below, and the putative signal peptide was underlined. The motif associated with mRNA instability (ATTTA) was in bold. The polyadenylation signal (AATAAA) was tagged with bold italic.

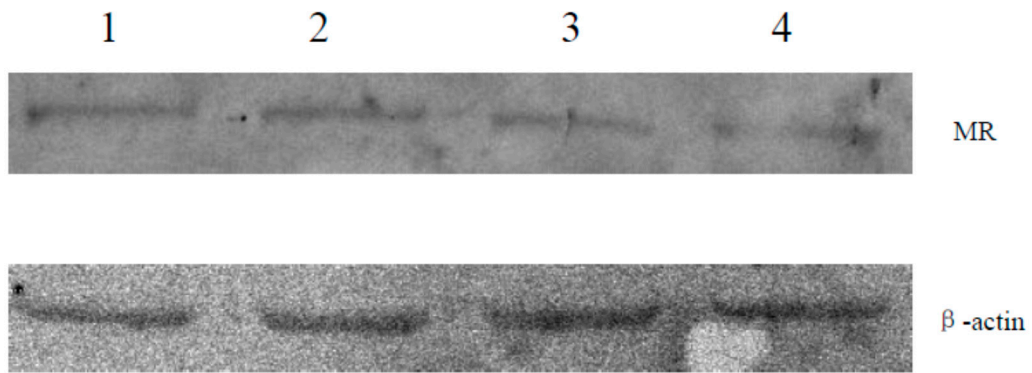


Figure S2. The expression of MR in the liver and spleen of zebra fish with or without the infection of *Aeromonas sobria*. The upper part of the figure is MR, the lower part of the figure is β -actin. Lane: 1: liver of control fish; 2: liver of infected fish; 3: spleen of control fish; 4: spleen of infected fish.