

Supplementary Figure 1. Nucleotide and deduced amino acid (upper case) sequences of the trout IL-17A/F2 mRNA. Position of the introns is indicated by arrows and the predicted signal peptide is highlighted in grey. Instability motifs (ATTTA) and the polyadenylation signal in the 3'-UTR are in bold. Start and stop codons for translation are boxed, and *N*-glycosylation sites are highlighted in dark grey.

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1           M E L K S N V S K Y L V V C C V S M L L G L T M A K
1  cagagatcagagatggagctcaaaagcaacgtgtcgaagtacctg▼gttggtgtgctgtgtgtctatgctgctgggcctgaccatggcgaaa

27  G M K V T K E R C N E T L I I P S D F Y K I P T E E S E G N
91  ggaatgaagggtgacaaaggagaggtgtaacgaaacactgatcatcccttcagacttctacaagattcccacagaggaatcagaggggaaat

57  G N I H T R S L S P W T W K S T T V E N R I P Q T M W E A E
181 gggaaacattcacacacgctctctgtcacccctggacctggaa▼aagcactacagtggagaaccgtattcctcagacatgtgggaggccgag

87  C S S M Y C V Y P T N R S Q Y M R Y R Q N S V P I Y Q Q V V
271 tgcagctctatgtactgtgtctacccaccaacagaagccagtacatgcgctacaggcagaactctgtacctatctaccagcaggtcgtg

117 V L Y T S A T R K C Y S A S F L S V A V G C T C A W A R T T
361 gtactctacacttcagccaccaggaagtgttacagcgctcctcctctgtctgtggccgtggggtgcacctgtgcctgggcaaggactact
   *

451 tgatgtagcctgcagtacactacatctatggccttactttggttggttattcatttaattcaatccaaatgtaatgtattttaatttaaa
541 gtaactagggagggccaacatttgtaatcccactaagcagaagaattgactgtgaatagttgagtagaattcaagaaaaagatccccat
631 tgacatatgtcctatttgagcaataaaaacatttttaaaaccccaaaaaaaaaaaaaaaaaaaaaa

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Supplementary Figure 2. Nucleotide and deduced amino acid (upper case) sequences of the trout IL-17RA mRNA.

Predicted signal peptide and transmembrane domain are highlighted in grey. Start and stop codons for translation, and upstream ATGs are boxed. Instability motif (ATTTA) and the polyadenylation signal in the 3'-UTR are in bold.

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1 agacgtcgtaccgaccttcctttacgggtagttctggggatttaccttcatgagacatttcgtggcatctatgtattgtctgtctagta
91 tagcctcgtgtattgtacagtaaatgcgcgtttgcgatttagagagttttcttctgtttcaatcgtgacgtgtgctacacattatgatt

1
181 cccaatgaacaattggaaatgtgttgtgtgtttttgagctgtgaaaatgattcgcagaaggaagctacttgcttttgactaaacgaaaatgM

2 K L L L T V G L L L A F V S T S S S L R I L E W P T L N C T
271 aagttaattctcacgggtgggattgttgttggcgtttgcctctacttcatcaagtctacggattttggaatggcccacactaaactgtact

32 Q E G L R C E A N I N N C L D P G W L K P W R Y T P S S P V
361 caagagggttgagatgtgaagccaacatcaataactgcctggatcctgggtggtgaagccttggcgctacactcctagcagcccagt

62 N L E V E L D T R K D E E G H L V P V L V A R W K A Q D D G
451 aacctagagggtggagctggacactagaaaagatgaggagggacacctggtgctgttttagtggcccagtggaagctcaggatgacgga

92 S I S S L K G T E L H V L K E A T N Q N L C V R Y E F F D K
541 agcattagttcctgaaaggaacagagcttcatgtttgaaggaagccaaaaccagaatctgtgtgttcggatgaattcttcgacaag

122 M S M R N P A Y E K W S F S L D R V V V E P G L S Y V V S V
631 atgtccatgctaatccagcatatgaaaagtgttcttccctggatcgagtggtggtgaacccggcctgtcatacgttgtctcagtc

152 S N L P K P N L K H S G Y N I D K H I T V P D C K D P K I Q
721 tccaacctccccaaaccaactcgaacactctggttacaacatcgataaacatatacctgtgcccgatgtgaagatccaagattcag

182 R S K V C L E S G S L W R P N T T L E R S T G P Q G R T T L
811 aggagcaaggtgtgtttggagagcgggagctctgtggagacctaactacgctggagcggctactggaccacaaggcagaaccacgctc

212 T V G F S T D Q H S H N Y S V S L L C S S N R Q W Q D T D M
901 actgttgggttcagtagcagaccagcactcacacaactacagtgctcactactgtgctccagcaacagacaatggcaggacacagacatg

242 T N Q T W L T V V F D L E K W P Q T C C Y F D V E I H P F F
991 accaaccagacatggctgactgtagtgtttgactggagaagtggccccagacctgttctattttgatgtggagatccatccgtttttt

272 S R C N N D C V R R R K T F N I C E T S P T V L T G D S S S
1081 agccgttgcaacaacgactgtgtacgaagaaggaaaacttcaacatatagtgagacctctccaactgtgttaacgggagattcttcatct

302 P K V Y T A I A A T V V L L V G G M V C C L V C Q L R T R R
1171 cctaaagtctacacagccatagcagccacgggtggtgctgctggtcggtggaatggtctgttctcgtctgtcaactacggacacggaga

332 K K V P P G P Y P P A V E P E V Q T P H L P R V P P K V L V
1261 aagaaagtcccaccagggcccctatccccagctgtagagccagaggtccagactcctcatctcccagggttctcccagggtgttgggt

362 I Y S Q D H P L Y R K I V L K L C A F L Q A K C G T E V V L
1351 atctactctcaggaccatcctctctacaggaagatagtcctgaagctctgtgcttctccagccaagtgtggaactgaggttgtgtt

392 D L L D T T W L G T V G R L P W L E W Q R Q Q V N K S S D K
1441 gaccttctagacacaacctggctgggcaactgtgggagactaccctggtggtgagtgggcagagacaacaggtcaacaaatcatcagacaag

422 I L V L C S R G V Q A K W R A M C G Q S R V T L R E D L R S
1531 atcctggtcctctgttctcgtggcgtccaggccaagtggagggcgatgtgtggccagagctcgtgtgacgttaagagaggacctcgggtc

452 P I D D M L T P A L N L F L P D M Q Q A A A L G K Y M V A Y
1621 cccatcgacgacatgctgacgcccgcctcaacctctcctgccgacatgcagcagggccgcccgttagggaagtacatggtggcctac

482 F D E V G S E R D V P S V F D I A V K Y K L M K H F E E L C
1711 tttgacgaggtcggcagcagcgtgacgtgcccgtctgtcctcgacatcgctgtgaagtaacaagctgatgaagcactttgaggagctctgc

512 F R I L D Q E K Y A P G Q V S H I E G I G V E E Y F T C P P
1801 ttcaggatcctggaccaggagaagtacgcaccgggacaggtcagccacatcgaggggatcggagtggaagagtacttccatgtccaccg

542 G R D L R D A I E A F Q A F Q L E N P D W F E Q E C V D I N
1891 gggagggatctgcgagacgccatcgaagccttccaggcgttccagtttagagaaccagactggtttgaacaggagtgtgttgacatcaac

572 A E E E V F A V T E Y D A L L E K P V A P V L E F V P E Y R
1981 gcagaggaggaagtgttcgcagtaacagagatgacgctctgctggaaaagccggtcgcgctgttctagagtttgtccagaatacagg

602 N G P P V L E F V P E Y R K G P P V L E F V P E F R N G P P
2071 aatgggcccactgttctagagtttgttccagagtacaggaaggggcccactgttctagagtttgttccagagttcaggaatgggcccact

632 V L E F V P E Y R N G P P V L E F F P E F R N G P P V L E F
2161 gttctagagtttgttccagaatacaggaatggaccacctgttctagagtttttccagagttcaggaatgggcccactgttctagagttt

662 V P E Y R K E P P V L E F V P E Y R K G P P V L E C V P E Y
2251 gttccagaatacaggaagggagcctcctgttttggagtttgttccagaatacaggaaggggcccactcctgttctagagttgttccagaatac
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692 R K G P P I S N Y D V E I N E N S L G V Q V S T P E V K L E
2341 aggaagggcctccaatctccaactatgatgtagagatcaatgaaaacagcctgggagtcaggtctcgactcctgaagtgaaactggaa

722 G H G T C V L E L L P R V N S D S H Q M Y P S Y P V V E A P
2431 ggtcacgggacgtgtgtgctggagcttcttccaagggttaactccgacagccaccagatgtaccatcataccagtcgttgaggcccca

752 P G V L I S D L H P N A L E S Q L C G L S D L L L S E P P L
2521 cccgggtacttatctctgatctgcacccaatgccctggagagtcactctgtgggtgtcagatcttctcctgagtgagccacccttg

782 A R E N C L R L Q E R W G T A D R C P L E N E E E E E A Y S
2611 gccagagagaactgtctccgcctacaggagaggtggggaacagcagaccgttgccctctagagaacgaggaagaggaggagccatcagt

812 P S C Q P S V D T L E Q L M S L Q L S L C G L S A I P E I T
2701 ccttctgtcaaccctccgttgacaccctggaacaactcatgtctctccagctgtcactctgtgggtctcagtgctatcccagaaatcacc

842 S V S T E N G Y L S Q P R G E M D L S L P A T M G Q S R L S
2791 tctgtgtccacggagaacggctacctatcacaaccgctggagagatggacctatcacttcctgccacgatgggccaatcacgactgtcc

872 F S S I Q V T P P V P M D S Q I Q Y L L P L P E I T H S Q P
2881 ttcagctccatccaggttaccacactgtaccgatggatagtcagattcagtacctccttcccctgcccagataaccactcccagccg

902 V E M E E G G E A M K P A A Q E K R P V S G S D L G Y I S R
2971 gtagagatggaggaggggtgggagggcgatgaagcctgtgcccaggagaagagaccctcagtggtggtcagacctgggctatatctccagg

932 S S F Q Q D S S V H Y P V R E D S D S P L V A L A R L Q Q A
3061 agctcctccagcaggactcttctgtccactaccctgtaagagaggacagcgacagtcactggtggcactggccaggctacaacaggct

962 L Y L N N *
3151 ctctacctaacaat**taa**ataactccggcttctgtataaaaaacgaggagagaacgttctagaaaacggatgtaatacatatatactctgg
3241 atcataaacacttttagttgttcagcatcgtttttcatgtgtgtataaacactattgtctataaaagttttcctgatttctgatttgaaa
3331 atgatgaacaaactggagtcactgaatcagccaatgggtttgtacagcataatccatata**atttag**ttctgacatcacttccttatatct
3421 ggttggtacagggaca**ataaaa**acgtgatcatgtccataaaaaaaaaaaaaaaaaaaaaaaaaaaaa