S5 Figure

SelPa2\_iso1 1 CACACTCAGCAGATCGAGCCTGCTGCAAGGCACCGTGATGAAGGCGGGGCTCAGCCTGCTCCTGGCTCTCTGCCTGCTCCCTGGGGGCGG  
SelPa2\_iso2 1 CACACTCAGCAGATCGAGCCTGCTGCAAGGCACCGTGATGAAGGCGGGGCTCAGCCTGCTCCTGGCTCTCTGCCTGCTCCCTGGGGGCGG  
  
SelPa2\_iso1 91 AGCAGAGAGTGAGGGGGAGGGGACCCGCTGTAAGCCACCACCTGGTTGGAGCATTGGGGAGGTGGAGCCAATGAAGGGGGTTATGGGCCA  
SelPa2\_iso2 91 AGCAGAGAGTGAGGGGGAGGGGACCCGCTGTAAGCCACCACCTGGTTGGAGCATTGGGGAGGTGGAGCCAATGAAGGGGGTTATGGGCCA  
  
SelPa2\_iso1 181 GGTCACGGTGGTGGCCCTCCTCCAGGCCAGCTGATCGTTCTGCTTGGTGCAGGCATCCTTATTGGATGAGCTGCGCCTGAAGCTGGAGGG  
SelPa2\_iso2 181 GGTCACGGTGGTGGCCCTCCTCCAGGCCAGCTGATCGTTCTGCTTGGTGCAGGCATCCTTATTGGATGAGCTGCGCCTGAAGCTGGAGGG  
  
SelPa2\_iso1 271 CCAGGGTCTGGACAATGTGACCTATATGGTGGTGAACCACCAGGGGGAGCAGGCCCAGCACCTTCACACCTTGCTGAGCCAGAAACTGTC  
SelPa2\_iso2 271 CCAGGGTCTGGACAATGTGACCTATATGGTGGTGAACCACCAGGGGGAGCAGGCCCAGCACCTTCACACCTTGCTGAGCCAGAAACTGTC  
  
SelPa2\_iso1 361 TGAGAACATCATATTGTACAAACAGGTACCCAAACAGGATGACGTGTGGCAGGCCCTGGCTGGAAAGAAGGATGACTTCCTCATCTATGA  
SelPa2\_iso2 361 TGAGAACATCATATTGTACAAACAGGTACCCAAACAGGATGACGTGTGGCAGGCCCTGGCTGGAAAGAAGGATGACTTCCTCATCTATGA  
  
SelPa2\_iso1 451 CAGGTGTGGTCGTCTGACCCACCATATCTTCCTCCCCTTTTCCATCCTGGGTACTCCCTACGTAGAGAACGCCATTAAGGAGACCTACTG  
SelPa2\_iso2 451 CAGGTGTGGTCGTCTGACCCACCATATCTTCCTCCCCTTTTCCATCCTGGGTACTCCCTACGTAGAGAACGCCATTAAGGAGACCTACTG  
  
SelPa2\_iso1 541 CCAACGCATCTGTGGGGACTGCACGTATGAGAACACAGAGATCCCAGCAGAGTGCAACAGGATGGTAGAGGTAAAGCCTGAGGGAGAAGA  
SelPa2\_iso2 541 CCAACGCATCTGTGGGGACTGCACGTATGAGAACACAGAGATCCCAGCAGAGTGCAACAGGATGGTAGAGGTAAAGCCTGAGGGAGAAGA  
  
SelPa2\_iso1 631 GAAGCCAGTCACTGGAGGGGATACACCTCACGGTGGACGCGGCCATCATCACCATGGCAATGGGCACGGTCACCATGGCAAAAGCCATGG  
SelPa2\_iso2 631 GAAGCCAGTCACTGGAGGGGATACACCTCACGGTGGACGCGGCCATCATCACCATGGCAATGGGCACGGTCACCATGGCAAAAGCCATGG  
  
SelPa2\_iso1 721 TCACGGTCACCATGGGGAGAGTGATGTGGGGCGCGAACACGGTCGTGGCCATGGGGTGGAGCAGCAGCAGCACCAAAATGGCGCTGAGAG  
SelPa2\_iso2 721 TCACGGTCACCATGGGGAGAGTGATGTGGGGCGCGAACACGGTCGTGGCCATGGGGTGGAGCAGCAGCAGCACCAAAATGGCGCTGAGAG  
  
SelPa2\_iso1 811 GCTCCACCATGGCCAGGCCCATGGCCAAGTGCACGTTGGTCAGGAGCATATGGGTCAGCAGCCCAAGGAGGTGCAGGAAGGGCATATTAT  
SelPa2\_iso2 811 GCTCCACCATGGCCAGGCCCATGGCCAAGTGCACGTTGGTCAGGAGCATATGGGTCAGCAGCCCAAGGAGGTGCAGGAAGGGCATATTAT  
  
SelPa2\_iso1 901 GCAGAGGCCCTGAGTGAAGGGGAGGGCCAGGTGAAAGGCAGAGCTCAGCTGACATTTGAAGGAGGGGTCTGACATAAGTCCCTCCTCCAA  
SelPa2\_iso2 901 GCAGAGGCCCTGAGTGAAGGGGAGGGCCAGGTGAAAGGCAGAGCTCAGCTGACATTTGAAGGAGGGGTCTGACATAAGTCCCTCCTCCAA  
  
SelPa2\_iso1 991 GGTCAGCTGATGCTGACACTGACGGGGGCTGTTTGGCAATGGGGTGCGCAACGAGCCAATCGGGCTCTGACACTGTGATGAGGCGCTGCC  
SelPa2\_iso2 991 GGTCAGCTGATGCTGACACTGACGGGGGCTGTTTGGCAATGGGGTGCGCAACGAGCCAATCGGGCTCTGACACTGTGATGAGGCGCTGCC  
  
SelPa2\_iso1 1081 CGCCTCCTGACAGTGACAGGGACTGATGGGCGACTCCAACAATCACATCAGGGAGACCTGACAGTGACGCTTGCCCCCCACAGACTGACA  
SelPa2\_iso2 1081 CGCCTCCTGACAGTGACAGGGACTGATGGGCGACTCCAACAATCACATCAGGGAGACCTGACAGTGACGCTTGCCCCCCACAGACTGACA  
  
SelPa2\_iso1 1171 GCAGCCTCTGCCAGTGATGTCAGCCTGATCCCCGGGTGTTGAAACCTGAAGCTGAGAGCAGCTGTAAGCAGGGCCATGGCTCTGTGAAAG  
SelPa2\_iso2 1171 GCAGCCTCTGCCAGTGATGTCAGCCTGATCCCCGGGTGTTGAAACCTGAAGCTGAGAGCAGCTGTAAGCAGGGCCATGGCTCTGTGAAAG  
  
SelPa2\_iso1 1261 TTATCTTGCTTATAGGCCTCATATTAACATCTGTGAGACCAACACCGGGGCAAAGCGCTCATACCATCTTACCAACTAGTATTGCTCCGG  
SelPa2\_iso2 1261 TTATCTTGCTTATAGGCCTCATATTAACATCTGTGAGACCAACACCGGGGCAAAGCGCTCATACCATCTTACCAACTAGTATTGCTCCGG  
  
SelPa2\_iso1 1351 TACTGTAAAGCCACACTTGATAGAGAGGGATGGAGGAATACATTGGGTCTGGTAGAAGAATGCTAAGCCTAAACCTGTTACGATATGGGG  
SelPa2\_iso2 1351 TACTGTAAAGCCACACTTGATAGAGAGGGATGGAGGAATACATTGGGTCTGGTAGAAGAATGCTAAGCCTAAACCTGTTACGATATGGGG  
  
SelPa2\_iso1 1441 AATAGGATAGTATTTGAGATGTACCCAAAGGGATAGTATGACATCAAGGAAGGTAGCCTCCACCCTCTCTTTCTCTGTCGGTGCATTGGT  
SelPa2\_iso2 1441 AATAGGATAGTATTTGAGATGTACCCAAAGGGATAGTATGACATCAAGGAAGGTAGCCTCCACCCTCTCTTTCTCTGTCGGTGCATTGGT  
  
SelPa2\_iso1 1531 GTCACCATCCCGGGAGTGTATTGGGTGACTATTTTGATGTTTCTCCCCCTCCGTTTTGCTCCCTCCATCCAAAATGAAGGTAGGCACAGA  
SelPa2\_iso2 1531 GTCACCATCCCGGGAGTGTATTGGGTGACTATTTTGATGTTTCTCCCCCTCCGTTTTGCTCCCTCCATCCAAAATGAAGGTAGGCACAGA  
  
SelPa2\_iso1 1621 AACTACGCTGTAGTGGTGTCTGTCTGATGTCCGGCTGGGGAGAGGGGAGGGTGAGGGCCATACAATATGACCACCCCCTTAATTCAAAGT  
SelPa2\_iso2 1621 AACTACGCTGTAGTGGTGTCTGTCTGATGTCCGGCTGGGGAGAGGGGAGGGTGAGGGCCATACAATATGACCACCCCCTTAATTCAAAGT  
  
SelPa2\_iso1 1711 TCACAATATCGAGAGCTTTAGAAGGAGTATGAAGGAGTAGCGTCCAATGTTGAAATAAACTGAAATCATGGCCAGAAATGCAAGATTTGA  
SelPa2\_iso2 1711 TCACAATATCGAGAGCTTTAGAAGGAGTATGAAGGAGTAGCGTCCAATGTTGAAATAAACTGAAATCATGGCCAGAAATGCAAGATTTGA  
  
SelPa2\_iso1 1801 ACCAAAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTACATTCAGCGTTAGTTAGA  
SelPa2\_iso2 1801 ACCAAAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTACATTCAGCGTTAGTTAGA  
  
SelPa2\_iso1 1891 CATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACT  
SelPa2\_iso2 1891 CATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACT  
  
SelPa2\_iso1 1981 CAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTT-----  
SelPa2\_iso2 1981 CAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTA  
  
SelPa2\_iso1 2064 -------------------------------------------------------------------------AGTTAGACATTGTTATA  
SelPa2\_iso2 2071 GACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATA  
  
SelPa2\_iso1 2083 TTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGT  
SelPa2\_iso2 2161 TTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATACTCAGCGTTAGT

Figure 5 Continued,

SelPa2\_iso1 2173 TAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAAACATTGTTA  
SelPa2\_iso2 2251 TAGACATTGTTATACTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAGACATTGTTATATTCAGCGTTAGTTAAACATTGTTA  
  
SelPa2\_iso1 2263 TATTCAGTGTTAGTTAGATATTGTTATATTCAGCGTTAGTTAAACATTGTTATATTCAGTGTTAACAAAACACATTTGAATAAAATACAT  
SelPa2\_iso2 2341 TATTCAATGTTAGTTAGATATTGTTATATTCAGCGTTAGTTAAACATTGTTATATTCAGTGTTAACAAAACACATTTGAATAAAATACAT

SelPa2\_iso1 2353 TATTGATAGAGTAAGATTTTTCTATTATGACCCCATCAACCTTCTCAACTTTTTCTTCAACTAAAAATCTAATGTCACTCCTTTCAAGCA  
SelPa2\_iso2 2431 TATTGATAGAGTAAGATTTTTCTATTATGACCCCATCAACCTTTTCAACTTTTTCTTCAACTAAAAATCTAATGTCACTCCTTTCAAGCA  
  
SelPa2\_iso1 2443 ACAACATTTATTTGTACCTTTGAATTAACGCTGTGTTTATTAAAGCAGTAGTGTGTTTTGTAGACAAAATTCAATATTCATAGTGTACAG  
SelPa2\_iso2 2521 ACAACATTTATTTGTACCTTTGAATTAACGCTGTGTTTATTAAAGCAGTAGTGTGTTTTGTAGACAAAATTCAATATTCATAGCGTACAG  
  
SelPa2\_iso1 2533 CAGTGATAATGTGTGTTTAGTTTTCCATGTTTCTGTCACTGTTATTGCTGTTGGCAATATTACACATATCTATAATGCACTGTTCATGAA  
SelPa2\_iso2 2611 CTGTGATAATGTGTGTTTAGTTTTCCATGTTTCTGTCACTGTTATTGCTGTTGGCAATATT-----------------------------

SelPa2\_iso1 2623 CTAACAAAACAAAGTGACCACTTTTCAACTAACAAAATATATTACACACATATCTATAATGCACTGTTCATGAACTAACAAAACAAAGTG  
SelPa2\_iso2 2672 ---------------------------------------------ACACATATCTATAATGCACTGTTCATGAACTAACAAAACAAAGTG

SelPa2\_iso1 2713 ACCGCTTTTCAACCAACAAAAAAACAGCTGGAATGAAGGTGGGTAGAGAGAAATATTGAATATACCGTACTTAATGAAGGTCTCTGGGGA  
SelPa2\_iso2 2717 ACCGCTTTTCAACCAACAAAAAAACAGCTGGAATGAAGGTGGGTAGAGAGAAATATTGAATATACTGTACTTAATGAAGGTCTCTGGGGA

SelPa2\_iso1 2803 AGACTACGGTCACCTAGAACACCC

SelPa2\_iso2 2807 AGACTACGGTCACCTAGAACACCC

**S5 Figure: Alignment of the two trout SelPa2 cDNA sequences cloned in this study. The primer binding sites** for PCR cloning are in green. The start and stop codons of the main open reading frame (ORF) are in red. The main difference between the two cDNA sequences lies in the 3’-UTR at two repeat regions highlighted in red and blue background, respectively. The first repeat region has 29 copies of a 26 bp consensus sequence (AGTTAGACATTGTTATATTCAGCGTT) for isoform 1, but 29 copies for isoform 2.