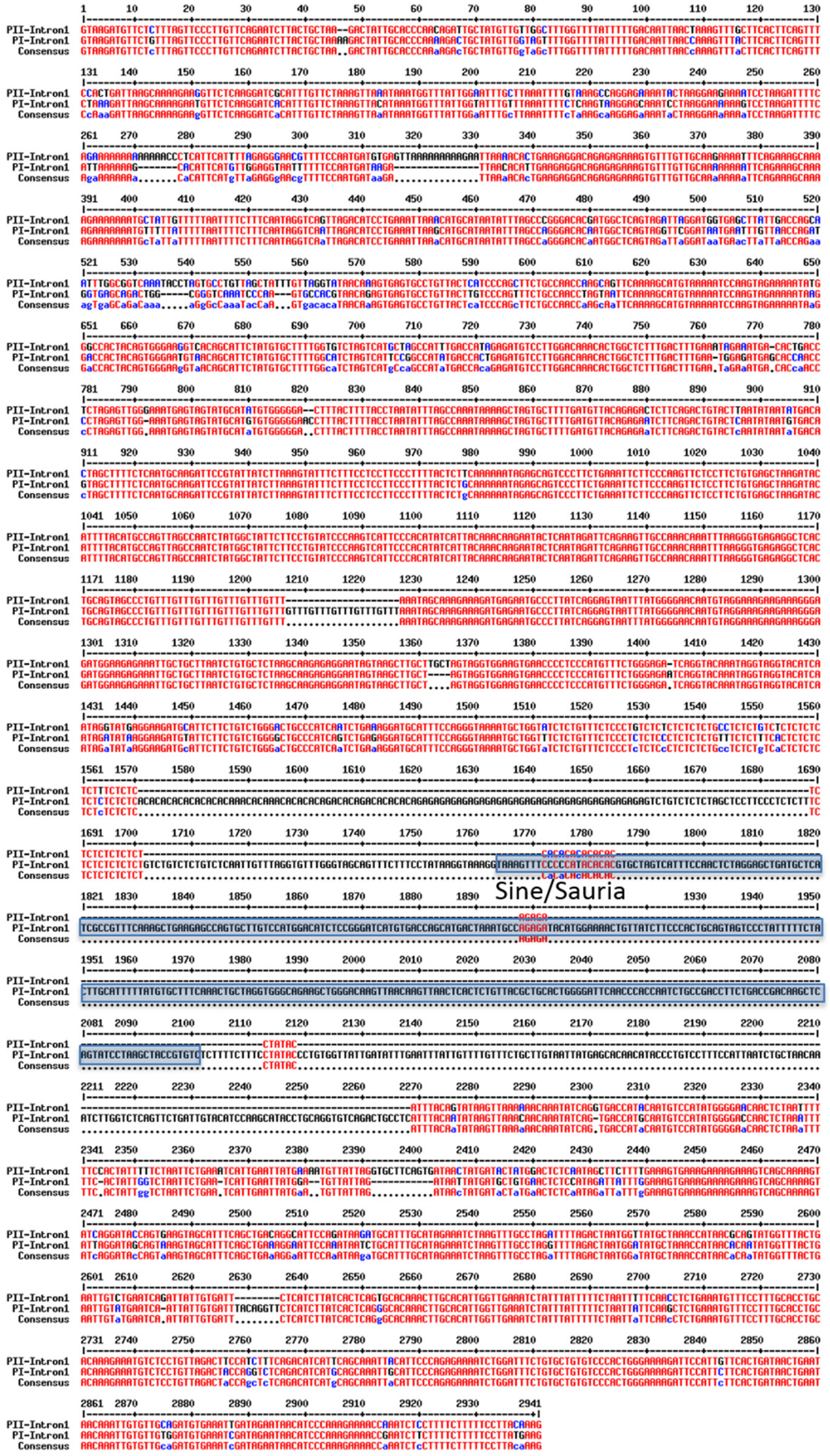
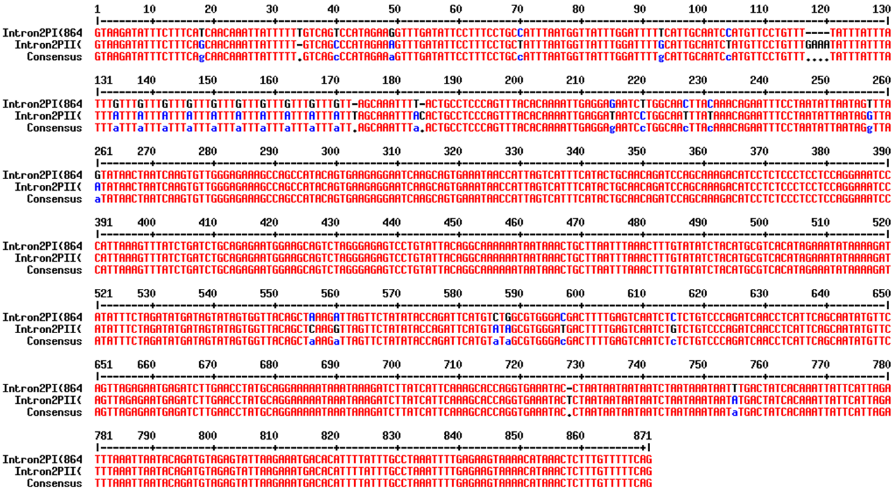
Supplementary Materials: Insights into the Evolution of a Snake Venom Multi-Gene Family from the Genomic Organization of *Echis ocellatus* SVMP Genes

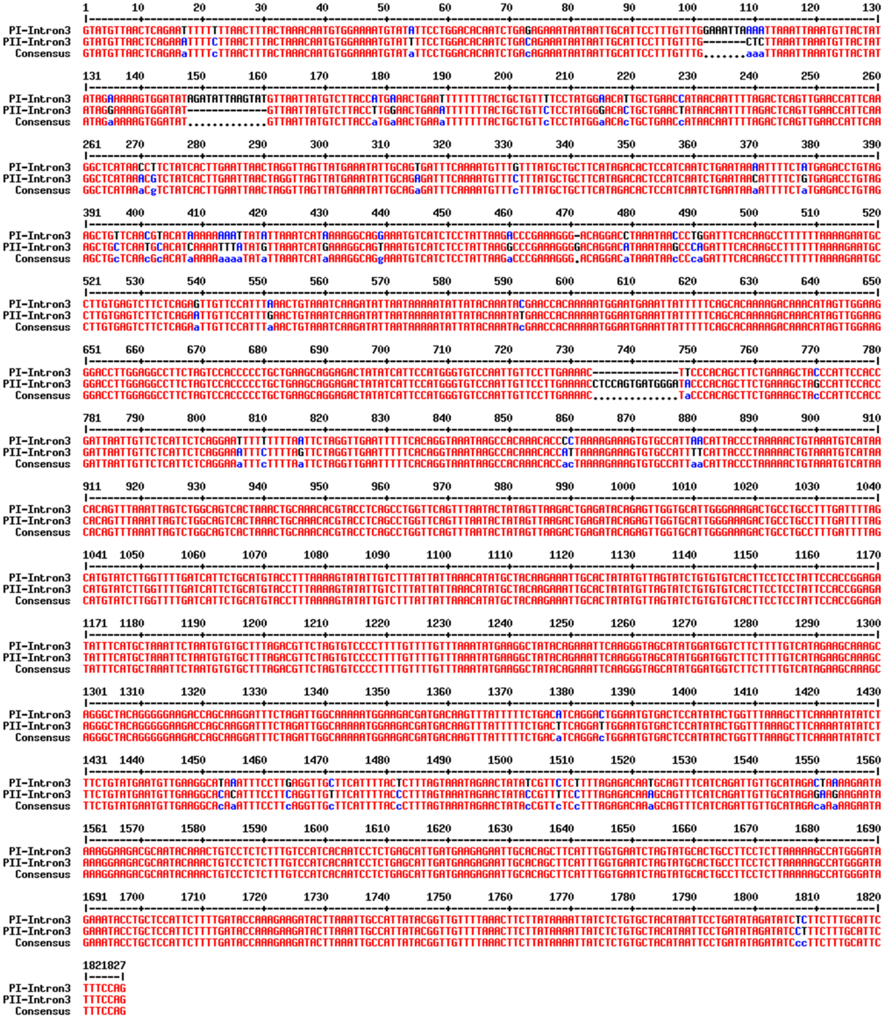
Libia Sanz and Juan J. Calvete



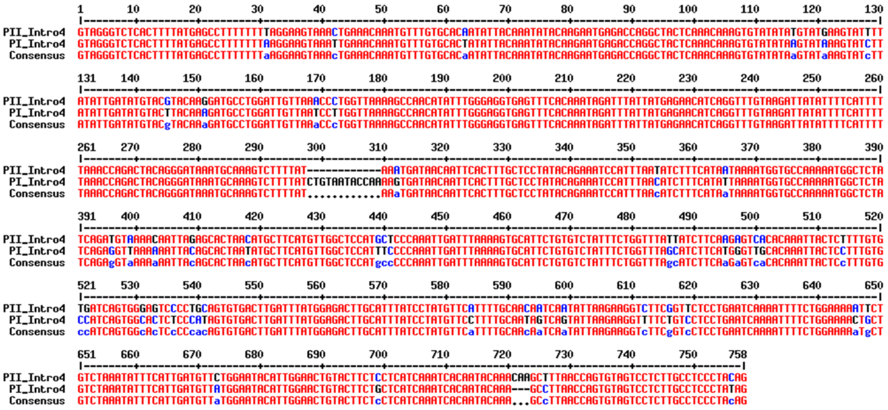
(**A**)


Intron2PI(864
Intron2PII(
Consensus

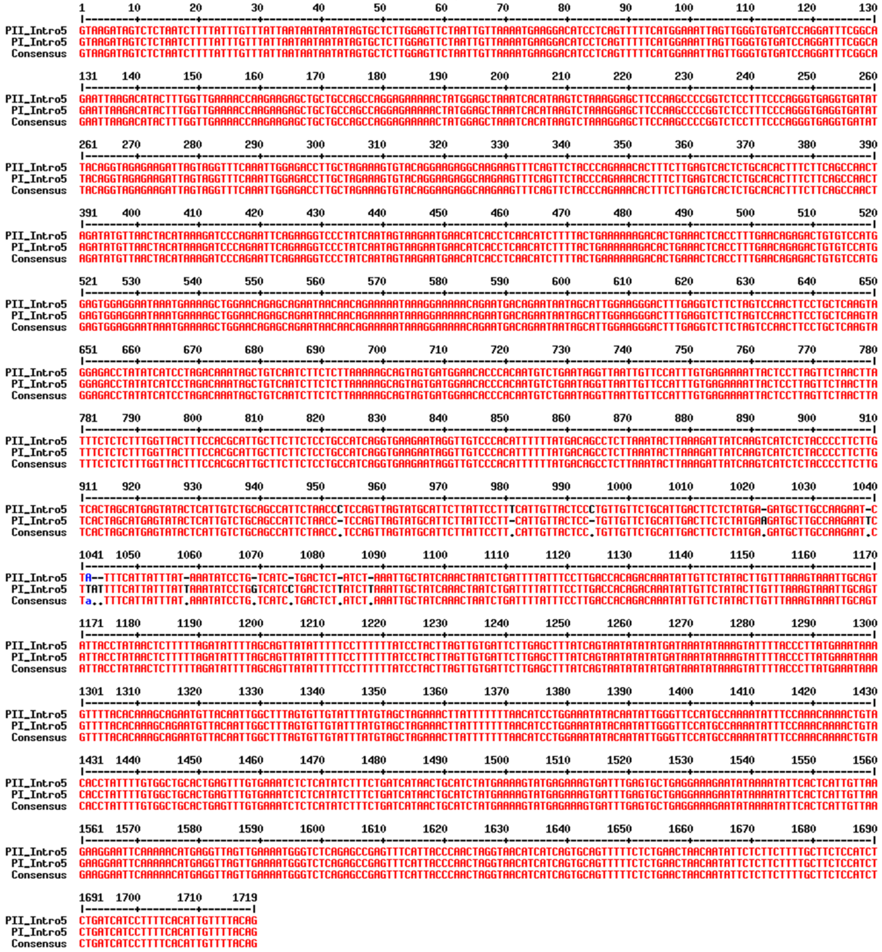
(**B**)


PI-Intron3
PII-Intron3
Consensus

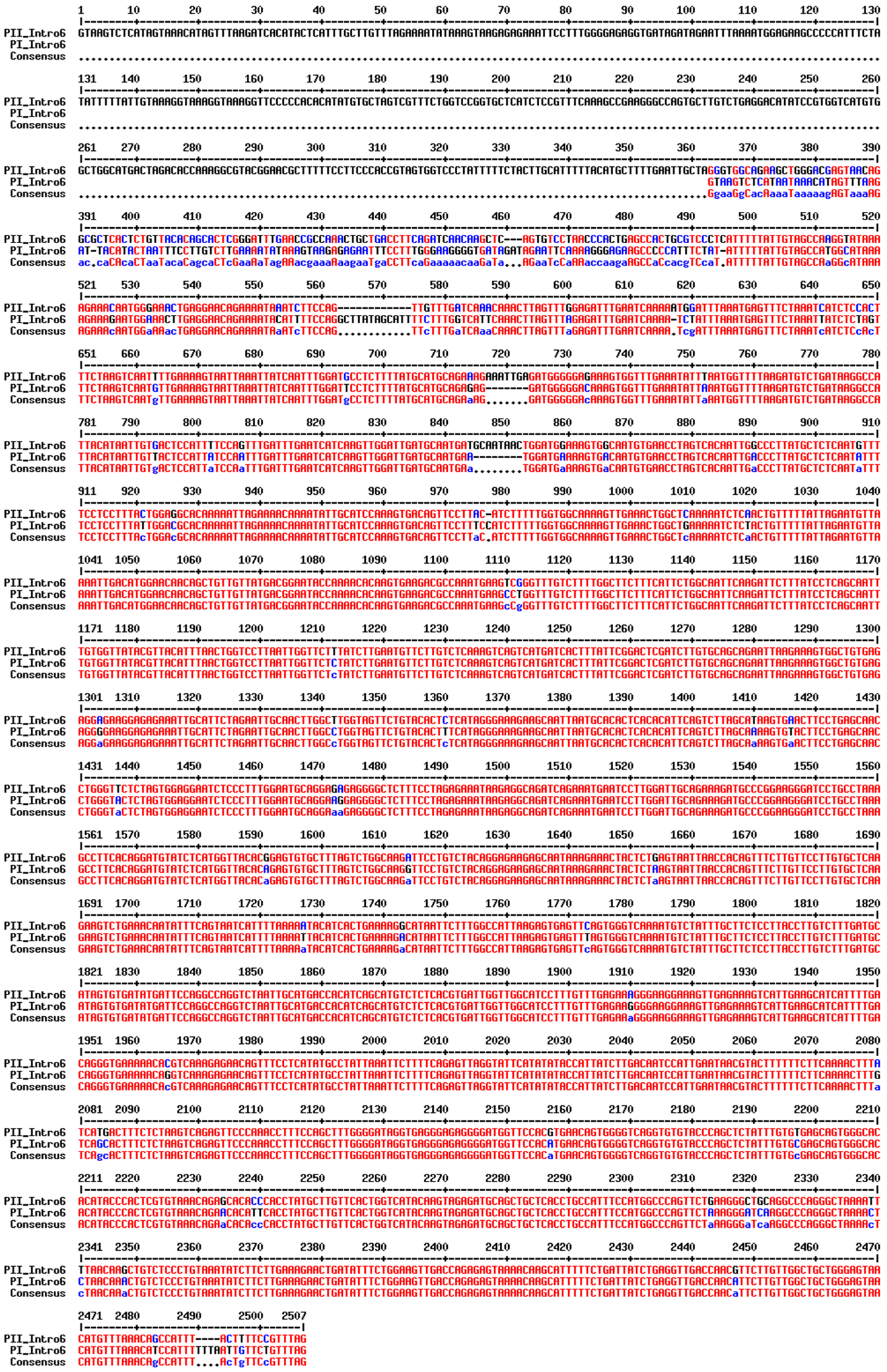
(**C**)


PII_Intro4
PI_Intro4
Consensus

(**D**)


PII_Intro5
PI_Intro5
Consensus

(**E**)



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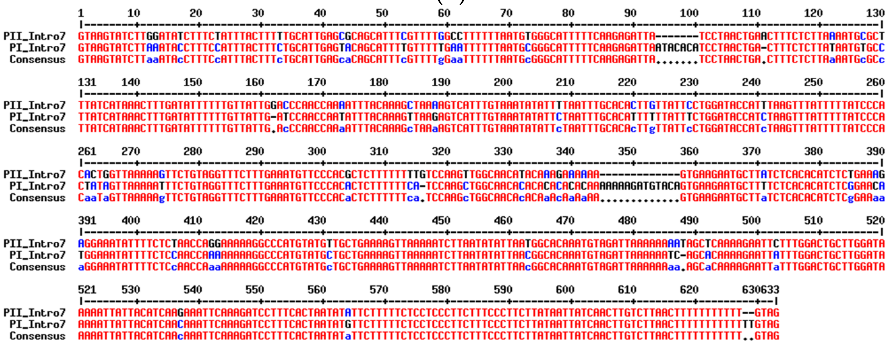

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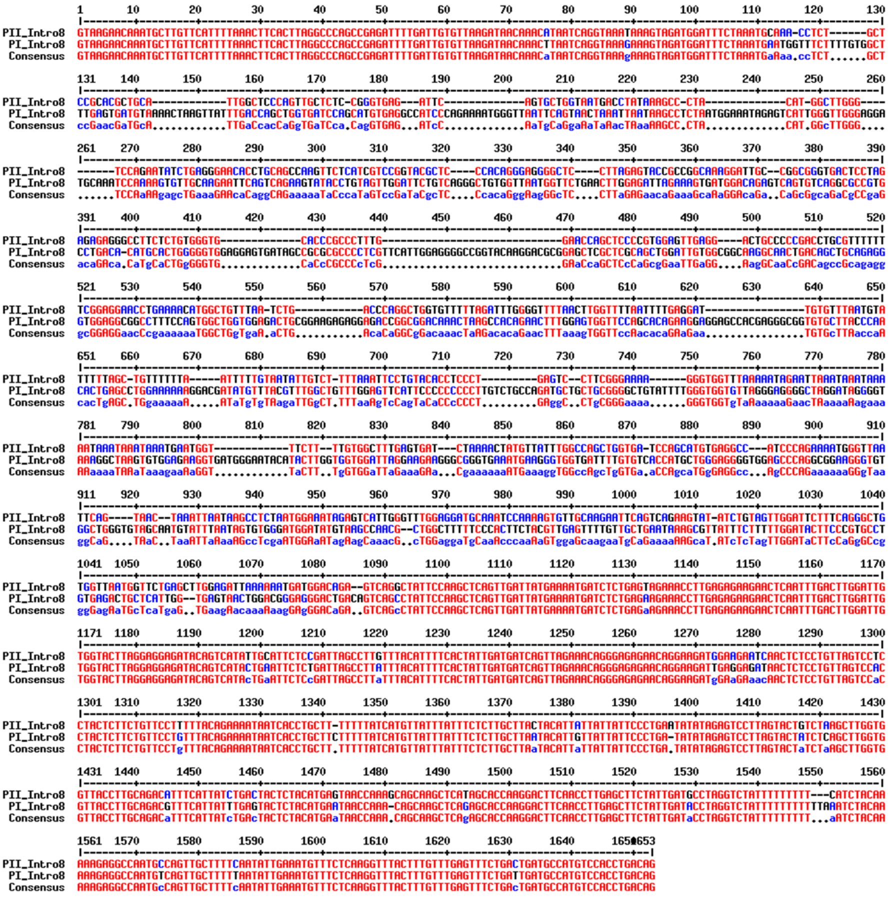
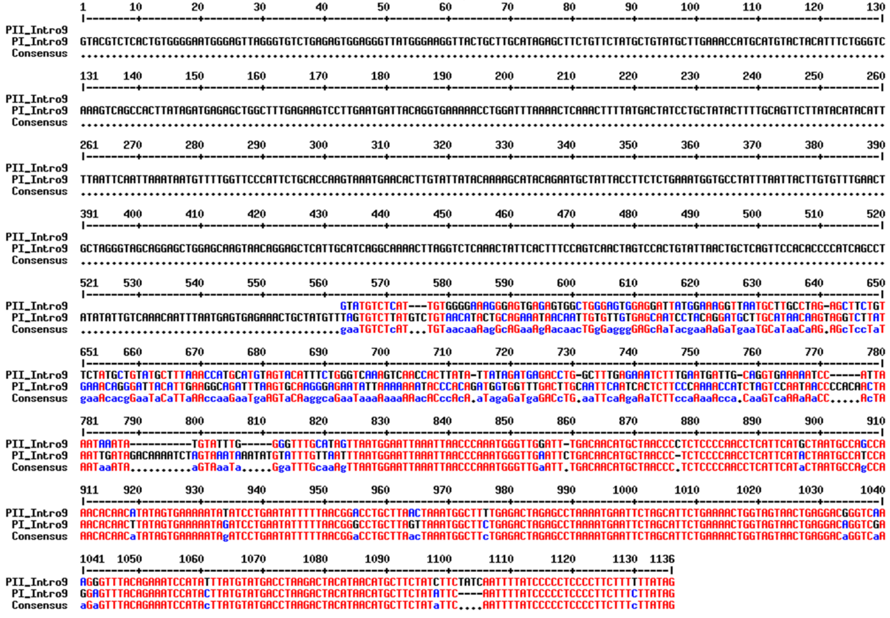
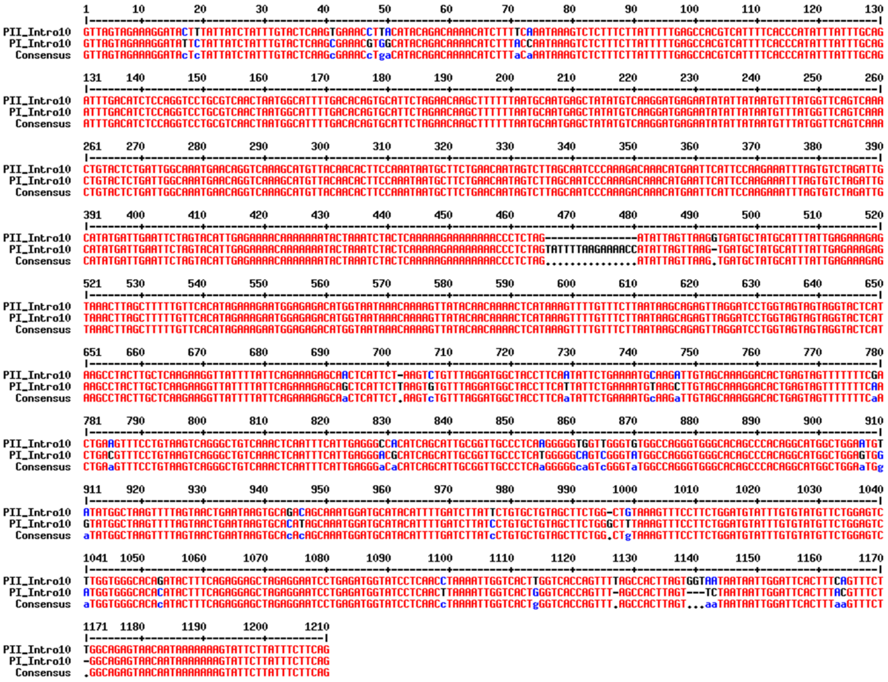


(H)



(I)



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            1       10        20        30        40        50        60        70        80        90       100       110       120       130
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 GTTAGTAGAAAGGATACTTTATTATCTATTTGTACTCAAGTGAAACCTTACATACAGACAAAACATCTTTTCAAATAAAGTCTCTTTCTTATTTTTGAGCCACGTCATTTTCACCCATATTTATTTGCAG
 PI_Intro10 GTTAGTAGAAAGGATATTCTATTATCTATTTGTACTCAAGCGAAACGTGGCATACAGACAAAACATCTTTACCAATAAAGTCTCTTTCTTATTTTTGAGCCACGTCATTTTCACCCATATTTATTTGCAG
  Consensus GTTAGTAGAAAGGATAcTcTATTATCTATTTGTACTCAAGcGAAACcTgaCATACAGACAAAACATCTTTaCaAATAAAGTCTCTTTCTTATTTTTGAGCCACGTCATTTTCACCCATATTTATTTGCAG

            131    140       150       160       170       180       190       200       210       220       230       240       250       260
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 ATTTGACATCTCCAGGTCCTGCGTCAACTAATGGCATTTTGACACAGTGCATTCTAGAACAAGCTTTTTTAATGCAATGAGCTATATGTCAAGGATGAGAATATATTATAATGTTTATGGTTCAGTCAAA
 PI_Intro10 ATTTGACATCTCCAGGTCCTGCGTCAACTAATGGCATTTTGACACAGTGCATTCTAGAACAAGCTTTTTTAATGCAATGAGCTATATGTCAAGGATGAGAATATATTATAATGTTTATGGTTCAGTCAAA
  Consensus ATTTGACATCTCCAGGTCCTGCGTCAACTAATGGCATTTTGACACAGTGCATTCTAGAACAAGCTTTTTTAATGCAATGAGCTATATGTCAAGGATGAGAATATATTATAATGTTTATGGTTCAGTCAAA

            261    270       280       290       300       310       320       330       340       350       360       370       380       390
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 CTGTACTCTGATTGGCAAATGAACAGGTCAAAGCATGTTACAACACTTCCAAATAATGCTTCTGAACAATAGTCTTAGCAATCCCAAAGACAAACATGAATTCATTCCAAGAAATTTAGTGTCTAGATTG
 PI_Intro10 CTGTACTCTGATTGGCAAATGAACAGGTCAAAGCATGTTACAACACTTCCAAATAATGCTTCTGAACAATAGTCTTAGCAATCCCAAAGACAAACATGAATTCATTCCAAGAAATTTAGTGTCTAGATTG
  Consensus CTGTACTCTGATTGGCAAATGAACAGGTCAAAGCATGTTACAACACTTCCAAATAATGCTTCTGAACAATAGTCTTAGCAATCCCAAAGACAAACATGAATTCATTCCAAGAAATTTAGTGTCTAGATTG

            391    400       410       420       430       440       450       460       470       480       490       500       510       520
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 CATATGATTGAATTCTAGTACATTGAGAAAACAAAAAAATACTAAATCTACTCAAAAAGAAAAAAAACCCTCTAG---------------ATATTAGTTAAGGTGATGCTATGCATTTATTGAGAAAGAG
 PI_Intro10 CATATGATTGAATTCTAGTACATTGAGAAAACAAAAAAATACTAAATCTACTCAAAAAGAAAAAAAACCCTCTAGTATTTTAAGAAAACCATATTAGTTAAG-TGATGCTATGCATTTATTGAGAAAGAG
  Consensus CATATGATTGAATTCTAGTACATTGAGAAAACAAAAAAATACTAAATCTACTCAAAAAGAAAAAAAACCCTCTAG...............ATATTAGTTAAG.TGATGCTATGCATTTATTGAGAAAGAG

            521    530       540       550       560       570       580       590       600       610       620       630       640       650
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 TAAACTTAGCTTTTTGTTCACATAGAAAGAATGGAGAGACATGGTAATAAACAAAAGTTATACAACAAAACTCATAAAGTTTTGTTTCTTAATAAGCAGAGTTAGGATCCTGGTAGTAGTAGGTACTCAT
 PI_Intro10 TAAACTTAGCTTTTTGTTCACATAGAAAGAATGGAGAGACATGGTAATAAACAAAAGTTATACAACAAAACTCATAAAGTTTTGTTTCTTAATAAGCAGAGTTAGGATCCTGGTAGTAGTAGGTACTCAT
  Consensus TAAACTTAGCTTTTTGTTCACATAGAAAGAATGGAGAGACATGGTAATAAACAAAAGTTATACAACAAAACTCATAAAGTTTTGTTTCTTAATAAGCAGAGTTAGGATCCTGGTAGTAGTAGGTACTCAT

            651    660       670       680       690       700       710       720       730       740       750       760       770       780
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 AAGCCTACTTGCTCAAGAAGGTTATTTTATTCAGAAAGAGCAACTCATTCT-AAGTCTGTTTAGGATGGCTACCTTCAATATTCTGAAAATGCAAGATTGTAGCAAAGGACACTGAGTAGTTTTTTTCGA
 PI_Intro10 AAGCCTACTTGCTCAAGAAGGTTATTTTATTCAGAAAGAGCAGCTCATTCTTAAGTGTGTTTAGGATGGCTACCTTCATTATTCTGAAAATGTAAGCTTGTAGCAAAGGACACTGAGTAGTTTTTTTCAA
  Consensus AAGCCTACTTGCTCAAGAAGGTTATTTTATTCAGAAAGAGCAaCTCATTCT.AAGTcTGTTTAGGATGGCTACCTTCAaTATTCTGAAAATGcAAGaTTGTAGCAAAGGACACTGAGTAGTTTTTTTCaA

            781    790       800       810       820       830       840       850       860       870       880       890       900       910
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 CTGAAGTTTCCTGTAAGTCAGGGCTGTCAAACTCAATTTCATTGAGGGCCACATCAGCATTGCGGTTGCCCTCAAGGGGGTGGTTGGGTGTGGCCAGGGTGGGCACAGCCCACAGGCATGGCTGGAATGT
 PI_Intro10 CTGACGTTTCCTGTAAGTCAGGGCTGTCAAACTCAATTTCATTGAGGGACGCATCAGCATTGCGGTTGCCCTCATGGGGGCAGTCGGGTATGGCCAGGGTGGGCACAGCCCACAGGCATGGCTGGAGTGG
  Consensus CTGAaGTTTCCTGTAAGTCAGGGCTGTCAAACTCAATTTCATTGAGGGaCaCATCAGCATTGCGGTTGCCCTCAaGGGGGcaGTcGGGTaTGGCCAGGGTGGGCACAGCCCACAGGCATGGCTGGAaTGg

            911    920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 ATATGGCTAAGTTTTAGTAACTGAATAAGTGCAGACAGCAAATGGATGCATACATTTTGATCTTATTCTGTGCTGTAGCTTCTGG-CTGTAAAGTTTCCTTCTGGATGTATTTGTGTATGTTCTGGAGTC
 PI_Intro10 GTATGGCTAAGTTTTAGTAACTGAATAAGTGCACATAGCAAATGGATGCATACATTTTGATCTTATCCTGTGCTGTAGCTTCTGGGCTTTAAAGTTTCCTTCTGGATGTATTTGTGTATGTTCTGGAGTC
  Consensus aTATGGCTAAGTTTTAGTAACTGAATAAGTGCAcAcAGCAAATGGATGCATACATTTTGATCTTATcCTGTGCTGTAGCTTCTGG.CTgTAAAGTTTCCTTCTGGATGTATTTGTGTATGTTCTGGAGTC

            1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
PII_Intro10 TTGGTGGGCACAGATACTTTCAGAGGAGCTAGAGGAATCCTGAGATGGTATCCTCAACCTAAAATTGGTCACTTGGTCACCAGTTTTAGCCACTTAGTGGTAATAATAATTGGATTCACTTTCAGTTTCT
 PI_Intro10 ATGGTGGGCACACATACTTTCAGAGGAGCTAGAGGAATCCTGAGATGGTATCCTCAACTTAAAATTGGTCACTGGGTCACCAGTTT-AGCCACTTAGT---TCTAATAATTGGATTCACTTTACGTTTCT
  Consensus aTGGTGGGCACAcATACTTTCAGAGGAGCTAGAGGAATCCTGAGATGGTATCCTCAACcTAAAATTGGTCACTgGGTCACCAGTTT.AGCCACTTAGT...aaTAATAATTGGATTCACTTTaaGTTTCT

            1171  1180      1190      1200      1210
            |--------+---------+---------+---------|
PII_Intro10 TGGCAGAGTAACAATAAAAAAAGTATTCTTATTTCTTCAG
 PI_Intro10 -GGCAGAGTAACAATAAAAAAAGTATTCTTATTTCTTCAG
  Consensus .GGCAGAGTAACAATAAAAAAAGTATTCTTATTTCTTCAG
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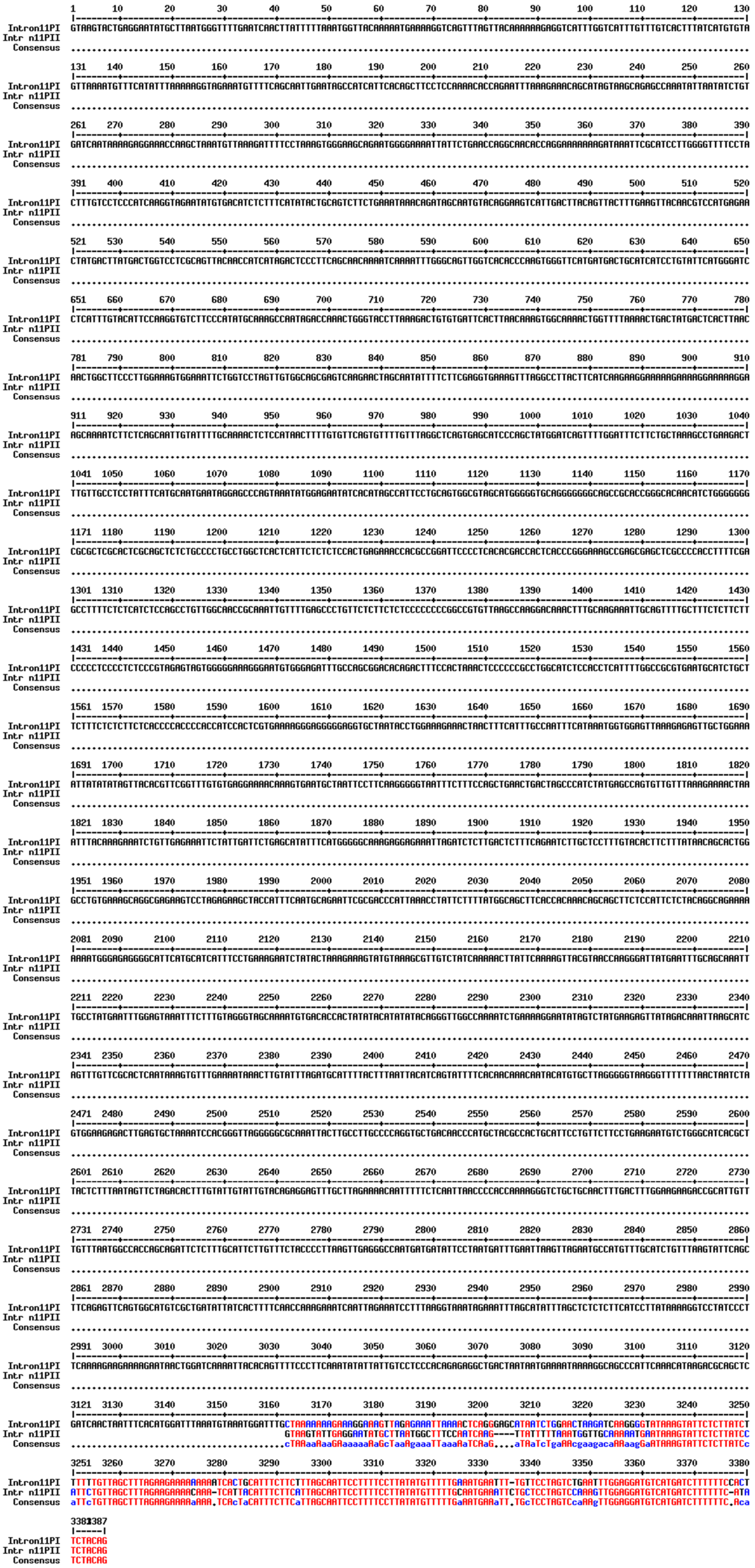
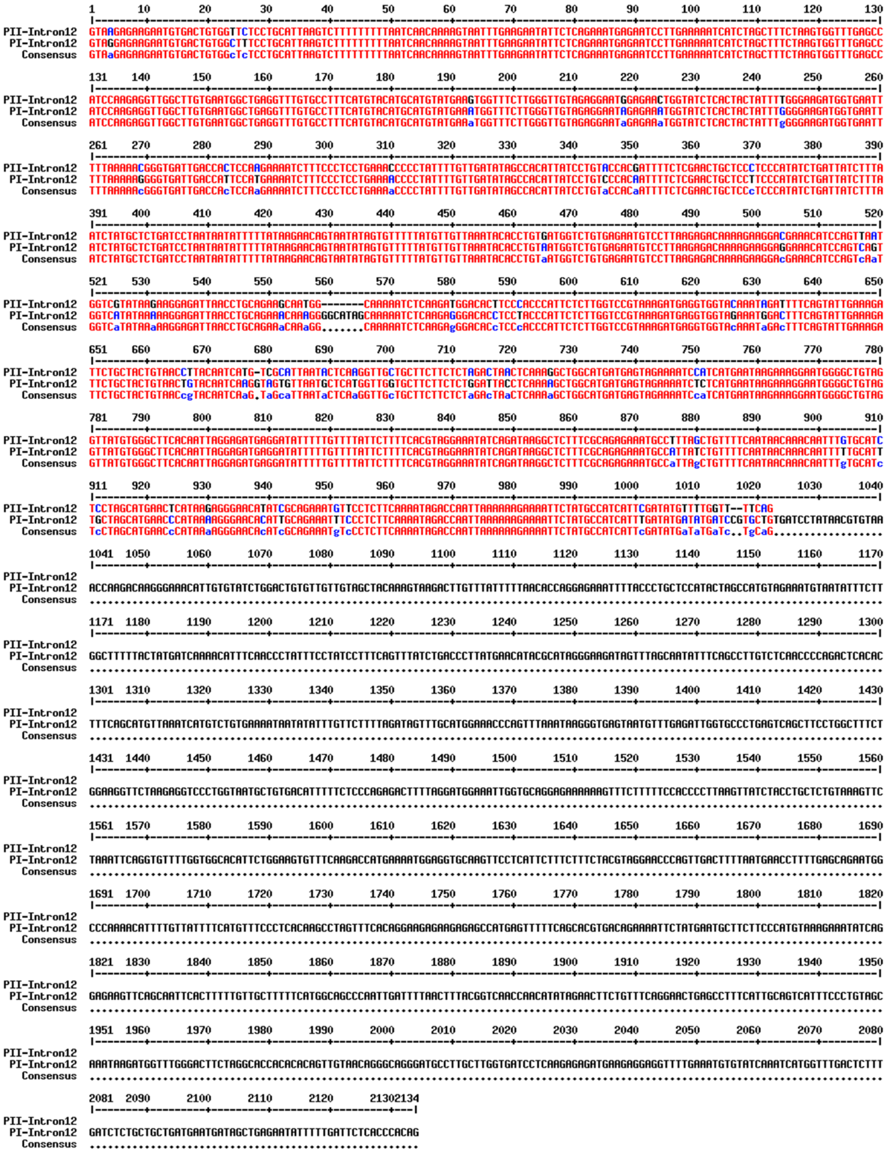
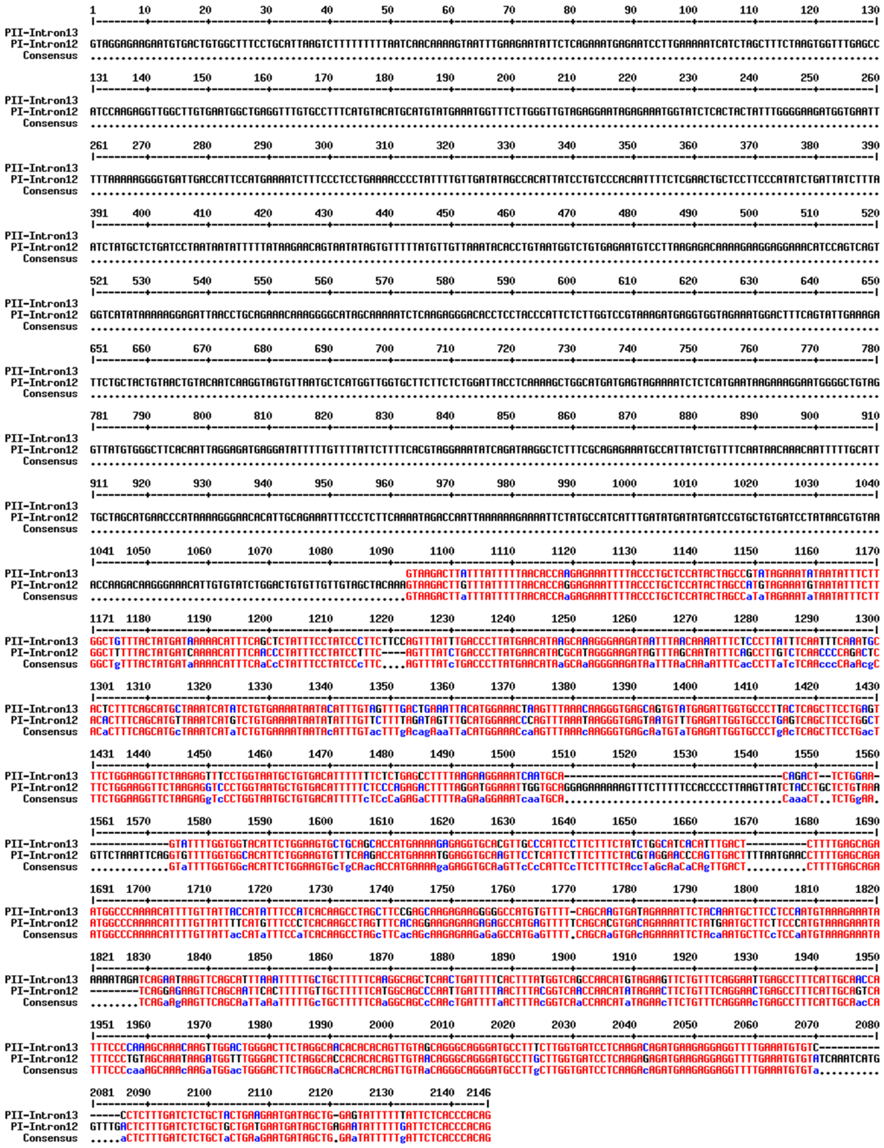
(J)



(**K**)



(**L**)



(**M**)

Figure S1: Pairwise nucleotide sequence alignments of topologically equivalent paralog introns 1–12 from Pre-pro EOC00006-like PII-SVMP and 1–13 from Pre-pro EOC00028-like PI-SVMP gene sequences.