

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

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(A)

Intron2PII(864) 1 10 20 30 40 50 60 70 80 90 100 110 120 130
Intron2PII Consensus
131 140 150 160 170 180 190 200 210 220 230 240 250 260
Intron2PII(864) 261 270 280 290 300 310 320 330 340 350 360 370 380 390
Intron2PII(864) 391 400 410 420 430 440 450 460 470 480 490 500 510 520
Intron2PII(864) 521 530 540 550 560 570 580 590 600 610 620 630 640 650
Intron2PII(864) 651 660 670 680 690 700 710 720 730 740 750 760 770 780
Intron2PII(864) 781 790 800 810 820 830 840 850 860 871
Intron2PII(864) 871
Intron2PII Consensus

(B)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
PI-Intron3
PII-Intron3
Consensus
131 140 150 160 170 180 190 200 210 220 230 240 250 260
PI-Intron3
PII-Intron3
Consensus
261 270 280 290 300 310 320 330 340 350 360 370 380 390
PI-Intron3
PII-Intron3
Consensus
391 400 410 420 430 440 450 460 470 480 490 500 510 520
PI-Intron3
PII-Intron3
Consensus
521 530 540 550 560 570 580 590 600 610 620 630 640 650
PI-Intron3
PII-Intron3
Consensus
651 660 670 680 690 700 710 720 730 740 750 760 770 780
PI-Intron3
PII-Intron3
Consensus
781 790 800 810 820 830 840 850 860 870 880 890 900 910
PI-Intron3
PII-Intron3
Consensus
911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
PI-Intron3
PII-Intron3
Consensus
1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
PI-Intron3
PII-Intron3
Consensus
1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
PI-Intron3
PII-Intron3
Consensus
1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
PI-Intron3
PII-Intron3
Consensus
1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
PI-Intron3
PII-Intron3
Consensus
1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
PI-Intron3
PII-Intron3
Consensus
1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
PI-Intron3
PII-Intron3
Consensus
1821827
PI-Intron3
PII-Intron3
Consensus

(C)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 PII_Intr04 GTAGGGTCTACCTTTATGAGCCTTTTTTAGGAGTAAATGAAACAAATGTTTGGCCACATATTACAAATACAGAAATGAGCCAGGCTACCAACAAAGTGTATATATATGAGATCTTT
 PI_Intr04 GTAGGGTCTACCTTTATGAGCCTTTTTTAGGAGTAAATGAAACAAATGTTTGGCCACATATTACAAATACAGAAATGAGCCAGGCTACCAACAAAGTGTATATATATGAGATCTTT
 Consensus GTAGGGTCTACCTTTATGAGCCTTTTTTAGGAGTAAATGAAACAAATGTTTGGCCACATATTACAAATACAGAAATGAGCCAGGCTACCAACAAAGTGTATATATATGAGATCTTT

131 140 150 160 170 180 190 200 210 220 230 240 250 260
 PII_Intr04 ATATGATATGACACACAGGATGCTGGATGTTAAACCTGGTAAAGCCACATATTGGAGGTGAGTTCCACAAATGATTTATGAGAACATCAGGTTTGTAGATATATATATATAT
 PI_Intr04 ATATGATATGACACACAGGATGCTGGATGTTAAACCTGGTAAAGCCACATATTGGAGGTGAGTTCCACAAATGATTTATGAGAACATCAGGTTTGTAGATATATATATATAT
 Consensus ATATGATATGACACACAGGATGCTGGATGTTAAACCTGGTAAAGCCACATATTGGAGGTGAGTTCCACAAATGATTTATGAGAACATCAGGTTTGTAGATATATATATATAT

261 270 280 290 300 310 320 330 340 350 360 370 380 390
 PII_Intr04 TAAACCGATACAGGATAAATGCAAGCTTTTAT...AATGATACAAATTCCTTGCCTATACAGAAATCATTATATCTTCATATAAATGGTCCCAAAATGGCTCTA
 PI_Intr04 TAAACCGATACAGGATAAATGCAAGCTTTTAT...AATGATACAAATTCCTTGCCTATACAGAAATCATTATATCTTCATATAAATGGTCCCAAAATGGCTCTA
 Consensus TAAACCGATACAGGATAAATGCAAGCTTTTAT...AATGATACAAATTCCTTGCCTATACAGAAATCATTATATCTTCATATAAATGGTCCCAAAATGGCTCTA

391 400 410 420 430 440 450 460 470 480 490 500 510 520
 PII_Intr04 TCAGATGTAAGACATAGAGCTAATGCTCATGTTGGCCACCTCCAAATGATTTAAAGTGCATCTGTGCTATTTCGGTTTATATCTTCAGAGGTCACACAAATTTACTTTTGTG
 PI_Intr04 TCAGATGTAAGACATAGAGCTAATGCTCATGTTGGCCACCTCCAAATGATTTAAAGTGCATCTGTGCTATTTCGGTTTATATCTTCAGAGGTCACACAAATTTACTTTTGTG
 Consensus TCAGATGTAAGACATAGAGCTAATGCTCATGTTGGCCACCTCCAAATGATTTAAAGTGCATCTGTGCTATTTCGGTTTATATCTTCAGAGGTCACACAAATTTACTTTTGTG

521 530 540 550 560 570 580 590 600 610 620 630 640 650
 PII_Intr04 TGATCTGAGGAGTCCCTGACGTGACTGATTTATGGAGACTGCATTTATCTATGTTCTTTGCACAAATCATTATAGAGGCTTCGGTTCTCTCAATCAAAATTTCTGGAAATTTCT
 PI_Intr04 TGATCTGAGGAGTCCCTGACGTGACTGATTTATGGAGACTGCATTTATCTATGTTCTTTGCACAAATCATTATAGAGGCTTCGGTTCTCTCAATCAAAATTTCTGGAAATTTCT
 Consensus TGATCTGAGGAGTCCCTGACGTGACTGATTTATGGAGACTGCATTTATCTATGTTCTTTGCACAAATCATTATAGAGGCTTCGGTTCTCTCAATCAAAATTTCTGGAAATTTCT

651 660 670 680 690 700 710 720 730 740 750 758
 PII_Intr04 GCTAATATTTATGATGTTTGGAAATCATTGAACTGACTCTCTCTCAATCAAAATCAAAACAGCTTTACCCAGTGTAGCTCTTGCCTCCCTACAG
 PI_Intr04 GCTAATATTTATGATGTTTGGAAATCATTGAACTGACTCTCTCTCAATCAAAATCAAAACAGCTTTACCCAGTGTAGCTCTTGCCTCCCTACAG
 Consensus GCTAATATTTATGATGTTTGGAAATCATTGAACTGACTCTCTCTCAATCAAAATCAAAACAGCTTTACCCAGTGTAGCTCTTGCCTCCCTACAG

(D)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 PII_Intr05 GTAGATAGCTCTAATCTTTATTTGTTATATATATATATAGTCTTGGACTCAATTTAAATGAGGACATCCAGTTTTCATGAAATATAGTGGGTGATCCAGGATTCGGCA
 PI_Intr05 GTAGATAGCTCTAATCTTTATTTGTTATATATATATATATAGTCTTGGACTCAATTTAAATGAGGACATCCAGTTTTCATGAAATATAGTGGGTGATCCAGGATTCGGCA
 Consensus GTAGATAGCTCTAATCTTTATTTGTTATATATATATATATAGTCTTGGACTCAATTTAAATGAGGACATCCAGTTTTCATGAAATATAGTGGGTGATCCAGGATTCGGCA

131 140 150 160 170 180 190 200 210 220 230 240 250 260
 PII_Intr05 GATTTAGACATACCTTTGGTTAAACCCAGAGAGGCTGCCCGCCAGGAAAGAAATCTGGACATCAATCAATGCTAAAGGACATCCAGGCTCCCTCCCTCCAGGCTGGGATGAT
 PI_Intr05 GATTTAGACATACCTTTGGTTAAACCCAGAGAGGCTGCCCGCCAGGAAAGAAATCTGGACATCAATCAATGCTAAAGGACATCCAGGCTCCCTCCCTCCAGGCTGGGATGAT
 Consensus GATTTAGACATACCTTTGGTTAAACCCAGAGAGGCTGCCCGCCAGGAAAGAAATCTGGACATCAATCAATGCTAAAGGACATCCAGGCTCCCTCCCTCCAGGCTGGGATGAT

261 270 280 290 300 310 320 330 340 350 360 370 380 390
 PII_Intr05 TACAGATAGAGGATAGTAGGTTCAATTTGGAGACTTCTAGAAATGACAGAGAGGACAGAGTTCCAGTCTACCCAGAAACATTTCTGAGTCACTTGCACACTTCTCCAGCACT
 PI_Intr05 TACAGATAGAGGATAGTAGGTTCAATTTGGAGACTTCTAGAAATGACAGAGAGGACAGAGTTCCAGTCTACCCAGAAACATTTCTGAGTCACTTGCACACTTCTCCAGCACT
 Consensus TACAGATAGAGGATAGTAGGTTCAATTTGGAGACTTCTAGAAATGACAGAGAGGACAGAGTTCCAGTCTACCCAGAAACATTTCTGAGTCACTTGCACACTTCTCCAGCACT

391 400 410 420 430 440 450 460 470 480 490 500 510 520
 PII_Intr05 AGATATGTTACTTACATAGAGATCCCGAATTCAGAGGCTCTCTCAATGATAGAGATGACATCACTCAACATTTTACGAAAGAACACAGAACTCACCCTTGGACAGAGCTGTGCTCATG
 PI_Intr05 AGATATGTTACTTACATAGAGATCCCGAATTCAGAGGCTCTCTCAATGATAGAGATGACATCACTCAACATTTTACGAAAGAACACAGAACTCACCCTTGGACAGAGCTGTGCTCATG
 Consensus AGATATGTTACTTACATAGAGATCCCGAATTCAGAGGCTCTCTCAATGATAGAGATGACATCACTCAACATTTTACGAAAGAACACAGAACTCACCCTTGGACAGAGCTGTGCTCATG

521 530 540 550 560 570 580 590 600 610 620 630 640 650
 PII_Intr05 GATCGAGAAATTAAGAGCTGAAACAGAGAGATACACAGAAATTAAGGAAAGACAGATGACAGAAATAGCATGAGAGGAGCTTTGAGTCTTCTAGTCAACTCTCTCCAGTA
 PI_Intr05 GATCGAGAAATTAAGAGCTGAAACAGAGAGATACACAGAAATTAAGGAAAGACAGATGACAGAAATAGCATGAGAGGAGCTTTGAGTCTTCTAGTCAACTCTCTCCAGTA
 Consensus GATCGAGAAATTAAGAGCTGAAACAGAGAGATACACAGAAATTAAGGAAAGACAGATGACAGAAATAGCATGAGAGGAGCTTTGAGTCTTCTAGTCAACTCTCTCCAGTA

651 660 670 680 690 700 710 720 730 740 750 760 770 780
 PII_Intr05 GAGAGCTATATCTCTAGACAAATAGCTCAATCTCTTAAAGACAGTAGTGGACACCCCAATGCTGATAGGTTAATTTGCCATTTGTGAAATATTTACTTACTTACTCTA
 PI_Intr05 GAGAGCTATATCTCTAGACAAATAGCTCAATCTCTTAAAGACAGTAGTGGACACCCCAATGCTGATAGGTTAATTTGCCATTTGTGAAATATTTACTTACTTACTCTA
 Consensus GAGAGCTATATCTCTAGACAAATAGCTCAATCTCTTAAAGACAGTAGTGGACACCCCAATGCTGATAGGTTAATTTGCCATTTGTGAAATATTTACTTACTTACTCTA

781 790 800 810 820 830 840 850 860 870 880 890 900 910
 PII_Intr05 TTTCTCTTTGGTACTTCCAGGATGCTCTCTCTCCGATCAGTAAAGATAGGTTCCCAATTTTATGACAGCTCTTAATCTTAAGATATCAGTACTCTACCCCTCTG
 PI_Intr05 TTTCTCTTTGGTACTTCCAGGATGCTCTCTCTCCGATCAGTAAAGATAGGTTCCCAATTTTATGACAGCTCTTAATCTTAAGATATCAGTACTCTACCCCTCTG
 Consensus TTTCTCTTTGGTACTTCCAGGATGCTCTCTCTCCGATCAGTAAAGATAGGTTCCCAATTTTATGACAGCTCTTAATCTTAAGATATCAGTACTCTACCCCTCTG

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
 PII_Intr05 TCACTAGCATGATATCACTTGTGACACCTTCAACCTCCAGTATGATGATCTTATCTTCAATGTTACTCCCTGTTGTTGCTGATGACTCTCTATGA...GATGCTCCAGAAAT...C
 PI_Intr05 TCACTAGCATGATATCACTTGTGACACCTTCAACCTCCAGTATGATGATCTTATCTTCAATGTTACTCCCTGTTGTTGCTGATGACTCTCTATGA...GATGCTCCAGAAAT...C
 Consensus TCACTAGCATGATATCACTTGTGACACCTTCAACCTCCAGTATGATGATCTTATCTTCAATGTTACTCCCTGTTGTTGCTGATGACTCTCTATGA...GATGCTCCAGAAAT...C

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
 PII_Intr05 TA...TTTCAATTTAT...AATATCTCTG...TCAT...TACT...ATCT...AATGCTATCAACTTACTGATTTATCTTACCCAGCAAAATTTGTTACTTCTTTAAGATATAGCAT
 PI_Intr05 TA...TTTCAATTTAT...AATATCTCTG...TCAT...TACT...ATCT...AATGCTATCAACTTACTGATTTATCTTACCCAGCAAAATTTGTTACTTCTTTAAGATATAGCAT
 Consensus TA...TTTCAATTTAT...AATATCTCTG...TCAT...TACT...ATCT...AATGCTATCAACTTACTGATTTATCTTACCCAGCAAAATTTGTTACTTCTTTAAGATATAGCAT

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
 PII_Intr05 ATACATATACCTTTTATGATATTTAGCAGTATATTTCTTTTTATCTACTAGTGTGATTTCTGAGCTTATCAGTATATATGATAAATATAGATATTTACCTTATGAAATAA
 PI_Intr05 ATACATATACCTTTTATGATATTTAGCAGTATATTTCTTTTTATCTACTAGTGTGATTTCTGAGCTTATCAGTATATATGATAAATATAGATATTTACCTTATGAAATAA
 Consensus ATACATATACCTTTTATGATATTTAGCAGTATATTTCTTTTTATCTACTAGTGTGATTTCTGAGCTTATCAGTATATATGATAAATATAGATATTTACCTTATGAAATAA

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
 PII_Intr05 GTTTTACACAGCAGATGTTACAAATGGCTTTAGTGTGATTTAGTACTAGAACTTTATTTTACATCTGGAAATACAAATTTGGTTCATGCCAAATATCCACACAAACGTA
 PI_Intr05 GTTTTACACAGCAGATGTTACAAATGGCTTTAGTGTGATTTAGTACTAGAACTTTATTTTACATCTGGAAATACAAATTTGGTTCATGCCAAATATCCACACAAACGTA
 Consensus GTTTTACACAGCAGATGTTACAAATGGCTTTAGTGTGATTTAGTACTAGAACTTTATTTTACATCTGGAAATACAAATTTGGTTCATGCCAAATATCCACACAAACGTA

1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
 PII_Intr05 CACCTATTGTGGCTGCACAGTTTGGAAATCTCTCATCTTTCTGATCACTGCATCTATGAAAGATGAAAGGATGTTGAGTCTGAGGAAAGATTAAGATATCACTCATGTTAA
 PI_Intr05 CACCTATTGTGGCTGCACAGTTTGGAAATCTCTCATCTTTCTGATCACTGCATCTATGAAAGATGAAAGGATGTTGAGTCTGAGGAAAGATTAAGATATCACTCATGTTAA
 Consensus CACCTATTGTGGCTGCACAGTTTGGAAATCTCTCATCTTTCTGATCACTGCATCTATGAAAGATGAAAGGATGTTGAGTCTGAGGAAAGATTAAGATATCACTCATGTTAA

1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
 PII_Intr05 GAGGAAATCAAAACATGAGGTAGTGAATGGCTCAGAGCCAGTTTCAATACCCACTAGTAACTCATCAGTGCAGTTTCTGCACTAACAATTTCTTCTTGGCTTCCACT
 PI_Intr05 GAGGAAATCAAAACATGAGGTAGTGAATGGCTCAGAGCCAGTTTCAATACCCACTAGTAACTCATCAGTGCAGTTTCTGCACTAACAATTTCTTCTTGGCTTCCACT
 Consensus GAGGAAATCAAAACATGAGGTAGTGAATGGCTCAGAGCCAGTTTCAATACCCACTAGTAACTCATCAGTGCAGTTTCTGCACTAACAATTTCTTCTTGGCTTCCACT

1691 1700 1710 1719
 PII_Intr05 CTGATCATCTTTTCAATGTTTACAG
 PI_Intr05 CTGATCATCTTTTCAATGTTTACAG
 Consensus CTGATCATCTTTTCAATGTTTACAG

(E)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 PII_Intro10 GTTAGAGAAAGGATCTTATATCTATTGTCACAGTCAGGCTTACATACAGACAAACATCTTTTCARATAGAGTCTCTTCTATTTTGGCCACGTCATTTTCACCCATTTATTTCGAG
 PII_Intro10 GTTAGAGAAAGGATCTTATATCTATTGTCACAGTCAGGCTTACATACAGACAAACATCTTTTCARATAGAGTCTCTTCTATTTTGGCCACGTCATTTTCACCCATTTATTTCGAG
 Consensus GTTAGAGAAAGGATCTTATATCTATTGTCACAGTCAGGCTTACATACAGACAAACATCTTTTCARATAGAGTCTCTTCTATTTTGGCCACGTCATTTTCACCCATTTATTTCGAG

131 140 150 160 170 180 190 200 210 220 230 240 250 260
 PII_Intro10 ATTTGACATCTCCAGGCTCGCGTCAACTGATGGCATTTGACACAGTGCATCTAGACACAGCTTTTATGACATGAGCTATATGTCAGGATGAGATATATATATGTTATGGTTCAGTCARA
 PII_Intro10 ATTTGACATCTCCAGGCTCGCGTCAACTGATGGCATTTGACACAGTGCATCTAGACACAGCTTTTATGACATGAGCTATATGTCAGGATGAGATATATATATGTTATGGTTCAGTCARA
 Consensus ATTTGACATCTCCAGGCTCGCGTCAACTGATGGCATTTGACACAGTGCATCTAGACACAGCTTTTATGACATGAGCTATATGTCAGGATGAGATATATATATGTTATGGTTCAGTCARA

261 270 280 290 300 310 320 330 340 350 360 370 380 390
 PII_Intro10 CTGACTCTGATGGCAATGACAGGTCARAGCATGTTACACACTTCCAAATATGCTTCTGACATAGTCTTAGCATCCARAGACAAACATGATTCATCCAGAAATTAGTGCTAGATGG
 PII_Intro10 CTGACTCTGATGGCAATGACAGGTCARAGCATGTTACACACTTCCAAATATGCTTCTGACATAGTCTTAGCATCCARAGACAAACATGATTCATCCAGAAATTAGTGCTAGATGG
 Consensus CTGACTCTGATGGCAATGACAGGTCARAGCATGTTACACACTTCCAAATATGCTTCTGACATAGTCTTAGCATCCARAGACAAACATGATTCATCCAGAAATTAGTGCTAGATGG

391 400 410 420 430 440 450 460 470 480 490 500 510 520
 PII_Intro10 CATATGATGATCTAGTACATGAGAAACAAABAATCTAAATCTACAAAGAAABAABACCTCTAGTATTTAGAAABCCATATTAGTAGG-TGATGCTATGATTTAGGAAAGAG
 PII_Intro10 CATATGATGATCTAGTACATGAGAAACAAABAATCTAAATCTACAAAGAAABAABACCTCTAGTATTTAGAAABCCATATTAGTAGG-TGATGCTATGATTTAGGAAAGAG
 Consensus CATATGATGATCTAGTACATGAGAAACAAABAATCTAAATCTACAAAGAAABAABACCTCTAGTATTTAGAAABCCATATTAGTAGG-TGATGCTATGATTTAGGAAAGAG

521 530 540 550 560 570 580 590 600 610 620 630 640 650
 PII_Intro10 TAACTAGCTTTTGTTCACATGAAAGATGGAGACATGGTAAACAAAGCTATACACAAACCTAATAGTTTGTCTTATAGCAGATAGATCTGGTAGTAGGACTCAT
 PII_Intro10 TAACTAGCTTTTGTTCACATGAAAGATGGAGACATGGTAAACAAAGCTATACACAAACCTAATAGTTTGTCTTATAGCAGATAGATCTGGTAGTAGGACTCAT
 Consensus TAACTAGCTTTTGTTCACATGAAAGATGGAGACATGGTAAACAAAGCTATACACAAACCTAATAGTTTGTCTTATAGCAGATAGATCTGGTAGTAGGACTCAT

651 660 670 680 690 700 710 720 730 740 750 760 770 780
 PII_Intro10 AAGCTACTGCTCAGAGGTTATTTATCAGAAAGACACTCATCT- AAGCTCTGTTAGGATGGTACCTTCATATCTGAAATGCAAGATGAGCAGAGGACACTGATGATTTTTTTTGA
 PII_Intro10 AAGCTACTGCTCAGAGGTTATTTATCAGAAAGACACTCATCT- AAGCTCTGTTAGGATGGTACCTTCATATCTGAAATGCAAGATGAGCAGAGGACACTGATGATTTTTTTTGA
 Consensus AAGCTACTGCTCAGAGGTTATTTATCAGAAAGACACTCATCT- AAGCTCTGTTAGGATGGTACCTTCATATCTGAAATGCAAGATGAGCAGAGGACACTGATGATTTTTTTTGA

781 790 800 810 820 830 840 850 860 870 880 890 900 910
 PII_Intro10 CTGAGGTTTCTGATGTCAGGCTGTCARACTCAATTTGATGGGCTCAGATCAGATTGCGGTTGCCCTCAGGGGGTGGTGGGTTGGCCAGGGTGGCCACAGCCACAGGATGGTGAATGT
 PII_Intro10 CTGAGGTTTCTGATGTCAGGCTGTCARACTCAATTTGATGGGCTCAGATCAGATTGCGGTTGCCCTCAGGGGGTGGTGGGTTGGCCAGGGTGGCCACAGCCACAGGATGGTGAATGT
 Consensus CTGAGGTTTCTGATGTCAGGCTGTCARACTCAATTTGATGGGCTCAGATCAGATTGCGGTTGCCCTCAGGGGGTGGTGGGTTGGCCAGGGTGGCCACAGCCACAGGATGGTGAATGT

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
 PII_Intro10 ATATGCTAGCTTTAGTACTGATAGTGCAGACAGCAATGGATGATACATTTTGTCTTATCTGTCGTAGCTTCTGG-CTGTAAGTTTCTCTGAGATGATTTGATGATGTTCTGGAGTC
 PII_Intro10 ATATGCTAGCTTTAGTACTGATAGTGCAGACAGCAATGGATGATACATTTTGTCTTATCTGTCGTAGCTTCTGG-CTGTAAGTTTCTCTGAGATGATTTGATGATGTTCTGGAGTC
 Consensus ATATGCTAGCTTTAGTACTGATAGTGCAGACAGCAATGGATGATACATTTTGTCTTATCTGTCGTAGCTTCTGG-CTGTAAGTTTCTCTGAGATGATTTGATGATGTTCTGGAGTC

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
 PII_Intro10 TTGGTGGCAGACTTTCAGAGGACTAGAGATCTGAGATGATCTCAGCTAATAATGGTCACTTGGTCCAGTTTAGCCACTTAGGTTATATATATGGATCCTTTTACGTTTCT
 PII_Intro10 TTGGTGGCAGACTTTCAGAGGACTAGAGATCTGAGATGATCTCAGCTAATAATGGTCACTTGGTCCAGTTTAGCCACTTAGGTTATATATATGGATCCTTTTACGTTTCT
 Consensus TTGGTGGCAGACTTTCAGAGGACTAGAGATCTGAGATGATCTCAGCTAATAATGGTCACTTGGTCCAGTTTAGCCACTTAGGTTATATATATGGATCCTTTTACGTTTCT

1171 1180 1190 1200 1210
 PII_Intro10 TGCCAGATACAAATAAAAGATATCTTATTTCTCAG
 PII_Intro10 TGCCAGATACAAATAAAAGATATCTTATTTCTCAG
 Consensus TGCCAGATACAAATAAAAGATATCTTATTTCTCAG

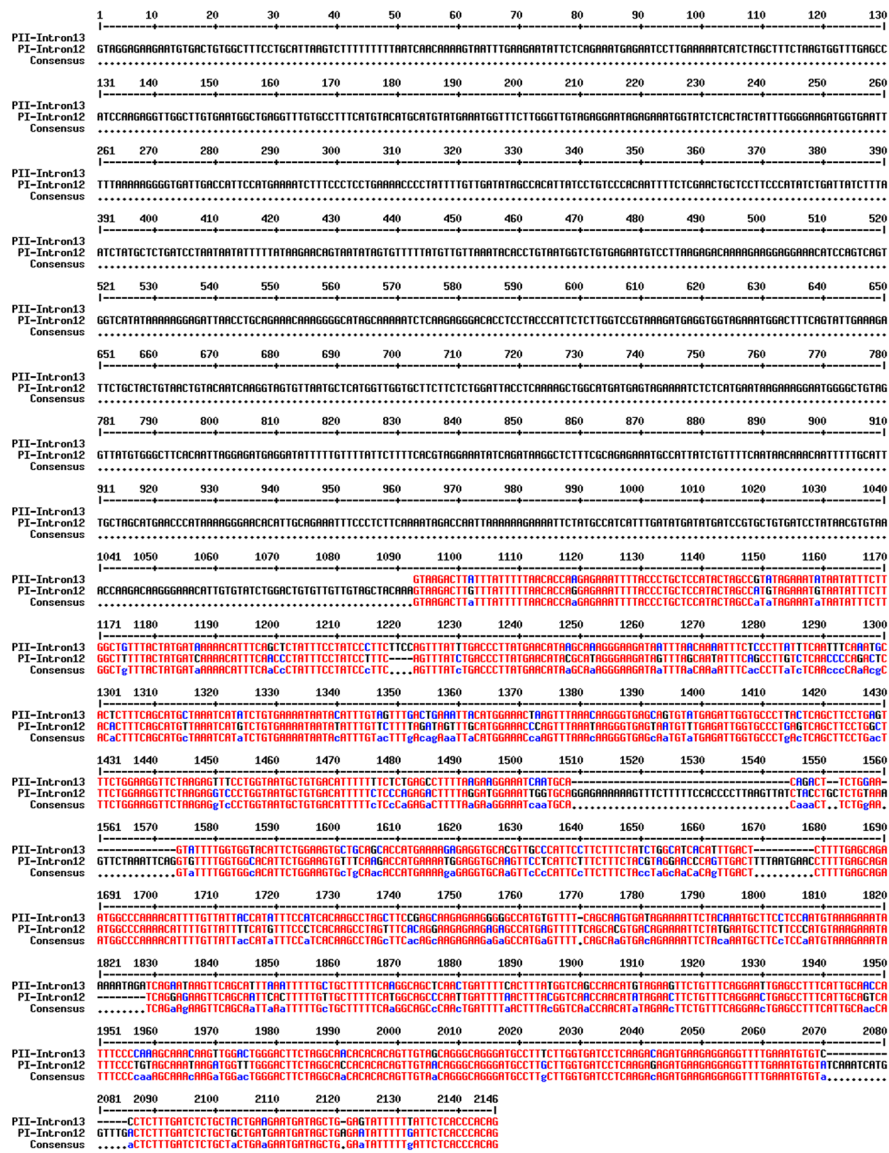
(J)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 Intron1PII
 Intron1PII
 Consensus
 131 140 150 160 170 180 190 200 210 220 230 240 250 260
 Intron1PII
 Intron1PII
 Consensus
 261 270 280 290 300 310 320 330 340 350 360 370 380 390
 Intron1PII
 Intron1PII
 Consensus
 391 400 410 420 430 440 450 460 470 480 490 500 510 520
 Intron1PII
 Intron1PII
 Consensus
 521 530 540 550 560 570 580 590 600 610 620 630 640 650
 Intron1PII
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 Consensus
 651 660 670 680 690 700 710 720 730 740 750 760 770 780
 Intron1PII
 Intron1PII
 Consensus
 781 790 800 810 820 830 840 850 860 870 880 890 900 910
 Intron1PII
 Intron1PII
 Consensus
 911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
 Intron1PII
 Intron1PII
 Consensus
 1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
 Intron1PII
 Intron1PII
 Consensus
 1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
 Intron1PII
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 Consensus
 1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
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 Intron1PII
 Consensus
 1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
 Intron1PII
 Intron1PII
 Consensus
 1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
 Intron1PII
 Intron1PII
 Consensus
 1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
 Intron1PII
 Intron1PII
 Consensus
 1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950
 Intron1PII
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 Consensus
 1951 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080
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 Consensus
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 Consensus
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 Consensus
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 Intron1PII
 Intron1PII
 Consensus
 3383387
 Intron1PII
 Intron1PII
 Consensus

(K)

1 10 20 30 40 50 60 70 80 90 100 110 120 130
PII-Intron12
PI-Intron12
Consensus
131 140 150 160 170 180 190 200 210 220 230 240 250 260
PII-Intron12
PI-Intron12
Consensus
261 270 280 290 300 310 320 330 340 350 360 370 380 390
PII-Intron12
PI-Intron12
Consensus
391 400 410 420 430 440 450 460 470 480 490 500 510 520
PII-Intron12
PI-Intron12
Consensus
521 530 540 550 560 570 580 590 600 610 620 630 640 650
PII-Intron12
PI-Intron12
Consensus
651 660 670 680 690 700 710 720 730 740 750 760 770 780
PII-Intron12
PI-Intron12
Consensus
781 790 800 810 820 830 840 850 860 870 880 890 900 910
PII-Intron12
PI-Intron12
Consensus
911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
PII-Intron12
PI-Intron12
Consensus
1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
PII-Intron12
PI-Intron12
Consensus
1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
PII-Intron12
PI-Intron12
Consensus
1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
PII-Intron12
PI-Intron12
Consensus
1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
PII-Intron12
PI-Intron12
Consensus
1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
PII-Intron12
PI-Intron12
Consensus
1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
PII-Intron12
PI-Intron12
Consensus
1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950
PII-Intron12
PI-Intron12
Consensus
1951 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080
PII-Intron12
PI-Intron12
Consensus
2081 2090 2100 2110 2120 2130 2134
PII-Intron12
PI-Intron12
Consensus

(L)



(M)

Figure S1: Pairwise nucleotide sequence alignments of topologically equivalent paralog introns 1–12 from Pre-pro EOC0006-like PII-SVMP and 1–13 from Pre-pro EOC0028-like PI-SVMP gene sequences.