

AAAAGGCTTTTGTGTTTTAAGGTTTTGACTGCCACTATACTGGACTTTTAGAGTTTTTCTTTGTAATTAAAGGTTTTGT
TTTTCCGAAAACAAAATTCCAAAAGTACGGTGATATGACCTGAAAATCTCAAAAAAGAAACATTAATTTCCAAAACA

880

ITPR1

ITPR1-237

CATGTCATCATAAAGATAGTGTTGATCTTGAATAGTGCTTTTTTTGAAGTGTATCAAGCTGTGATTGCTTTAAATCCACC
GTACAGTAGTATTTCTATCACAAGTAACTTATCAGCAAAAAAACTTCACATAGTTTCGACACTAACGAAATTTAGGTGG

960

ITPR1

ITPR1-237

TTCAGTGCGTTGATACTGTAATCCAATAGCCAGAGAGATTTTATTCTGTTCTCTCTCCCATCTTCAGATGAGGATACAT
AAGTCACGCAACTATGACATTAGGTTATCGGTCTCTCTAAAATAAGACAAGGAGAGAGGGTAGAAGTCTACTCCTATGTA

1040

ITPR1

ITPR1-237

CTGGGTCTGTGGGGTGTGTCAAGACACTTTGCTTGTACATGAGGAAACAACTAGTTACTCTTGGAAATTGCTGGATTAGA
GACCCAGACACCCACACAGTTCTGTGAAACGAACATGTACTCCTTTGTTTGATCAATGAGAACCTTAACGACCTAATCT

1120

ITPR1

ITPR1-237

CATCTTTGCTTAGTTGTTTTCGGATCCTTTACCAGTTGGCAGATGATAAGTTCCTACACAATGCCTCCTTATAGAATACA
GTAGAAACGAATCAACAAAAGCCTAGGAAATGGTCAACCGTCTACTATTCAAGGATGTGTTACGGAGGAATATCTTATGT

1200

ITPR1

ITPR1-237

GGCTGAAAACCATGGCCTGTTTTCAATTATGTTAATCCTAAATAGTTAACCGGGATTTAGGAATTAATGGGAAAAAAATTA
CCGACTTTTGGTACCGGACAAAAGTAATACAATTAGGATTTATCAATTGGCCCTAAATCCTTAATTACCCTTTTTTTAAT

1280

ITPR1

ITPR1-237

AAGCAAGTTTCAAGGGCCACTTGAATTTGAGCAAGCAGTCTATCTTGGCCAGGGAAGCATCTTTGAACAGAAACAAACA
TTCGTTCAAAGTTCCCGGTGAACCTAAAACCTCGTTTCGTAGATAGAACCGGTCCCTTCGTAGAAACTTGTCTTTGTTGT

1360

ITPR1

ITPR1-237

GGTATTTGTAAGAGATTTCTTGAGTTCACAAATATTTCTATGGAATGTGATAGCTGATCCCAAAAGAGAGAAACCAGAG
CCATAAACATTCTCTAAAGGAACTCAAGTGTGTTATAAGATACCTTACACTATCGACTAGGGTTTTCTCTCTTTGGTCTC

1440

ITPR1

ITPR1-237

ATGTATTCATGAGTTCATGCATATGATGGATTTCTTAGGTATTTATTCCTGACCTTCTTATGCTACTCATTGACTTTA
TACATAAGTACTCAAGGTACGTATACTACCTAAAAGAATCCATAAATAAGGACTGGAAGAATACGATGAGTAACTGAAAT

1520

ITPR1

ITPR1-237

PCR Forward

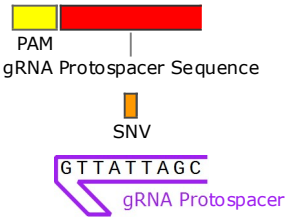
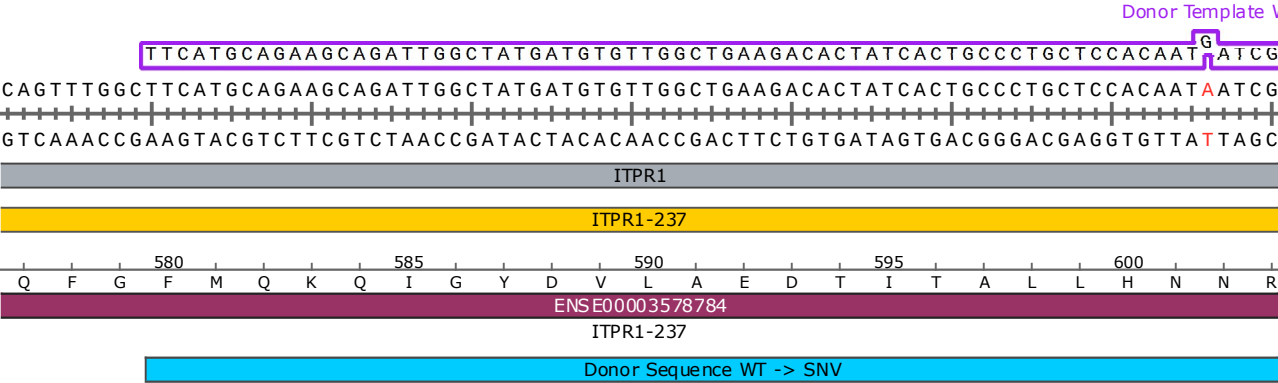
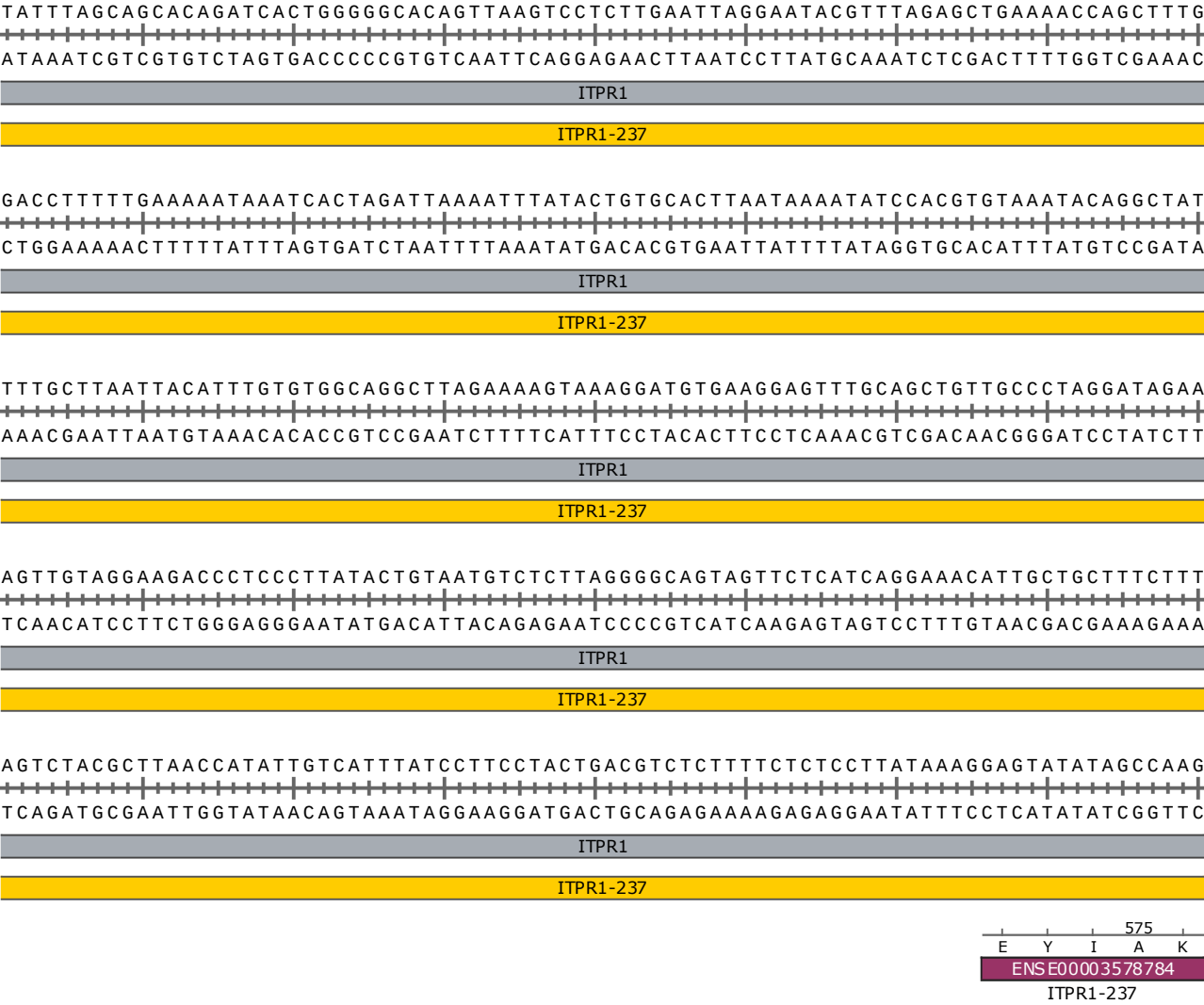
AACATTGTTCCAGATCTCCAGGTAG

AAAAAGTATTTTTACCACAAATAAAGGAAATGAAACAGGGTAACATTGTTCCAGATCTCCAGGTAGGCTTTATCTGTGTT
TTTTTCATAAAAATGGTGTTTATTTCTTTACTTTGTCCATTGTAACAAGGTCTAGAGGTCCATCCGAAATAGACACAA

1600

ITPR1

ITPR1-237



Donor Template WT -> SNV

GAAACTCCTGGAAAAACACATTACCGCGG

GAAACTCCTGGAAAAACACATTACCGCGGCAGAGATTGACACATTTGTCAGCCTGGTGCGAAAGAACAGGGAGCCCAGGT
CTTTGAGGACCTTTTGTGTAATGGCGCCGTCTCTAACTGTGTAACAGTCGGACCACGCTTTCTTGTCCTCGGGTCCA

2160

ITPR1

ITPR1-237

605 610 615 620 625
K L L E K H I T A A E I D T F V S L V R K N R E P R

ENSE00003578784

ITPR1-237

Donor Sequence WT -> SNV

gRNA Protospacer Sequence

CTTTGAGGACC

gRNA Protospacer

GAGGCGGGAGTGGGGTCCATGCAGGATGGTGTCTCTGCCTGTAAGATGCAGGGACTTAGCTGGTGCTTTTTACTACGTTT
CTCCGCCCTCACCCAGGTACGTCCTACCACAGAGACGGACATTCTACGTCCTGAATCGACCACGAAAAATGATGCAAA

2240

ITPR1

ITPR1-237

ITPR1-237

CTACGTCCTGAATCGACCA

Sanger Sequencing Primer

CCTTGCTGCTAGTGACAAGTTTTGATTAGTTAGGTCTGGAGAGGCTTTTTGATGAGTAGTGGCAAGAACTTGGTGTTA
GGAACACGACGATCACTGTTCAAACTAATCAATCCAGACCTCTCCGAAAACTACTCATCACCGTTCTTGAACCACAA

2320

ITPR1

ITPR1-237

ITPR1-237

AAATGAGACCTGGGGGTGCATTCTAGCTCCAGTGTGTCCACCTGGATGAGCTTGGGTTTTTCTGAACTTTAATTTT
TTTACTCTGGACCCCACTAAGGATCGAGGTACACAGGGTGGACCTACTCGAACCCAAAAAGGACTTGAAATTAAAG

2400

ITPR1

ITPR1-237

ITPR1-237

CTTATCTGCTAAATGGGTAGTTATGAAAATTAATGAGAATAAACGCAGGTGACGTGCAGGCACTTAGTGGATGCAGAGG
GAATAGACGATTTACCCATCAATACTTTTAATTTACTCTTATTTGCGTCCACTGCACGTCCGTGAATCACCTACGTCTCC

2480

ITPR1

ITPR1-237

ITPR1-237

CACCTACGTCTCC

PCR Reverse

AAATGACAAATTGTTGGCCACTCATTCACTTTTTAAAAAATGTTCTTAATTTTAATTTTAAATTTTGTGGGTACGTAGT
TTTACTGTTTAACAACCGGTGAGTAAGTGAAAAATTTTTTACAAGAATTAAAATTAAAAATTAAAAACACCCATGCATCA

2560

ITPR1

ITPR1-237

ITPR1-237

TTTACTGTTTAA

PCR Reverse

AGGTGTATATATTTATGGGGTACATGAGATGTTTTGATGTAGGCATGCAATGTGTAATAATCACATTGTAGAGAATGGGG
TCCACATATATAAATACCCCATGTACTCTACAAACTACATCCGTACGTTACACATTATTAGTGTAACATCTCTTACCCC

2640

ITPR1

ITPR1-237

ITPR1-237

TATCCATCCCCTCAAACATTTATTTTTGTTACAAAGAATTCAGTTCTATTCTTTTAGTTATTTTAAAATGTACAATTAA
ATAGGTAGGGGAGTTTGTAATAAAAAACAATGTTTCTTAAGTCAAGATAAGAAAATCAATAAAATTTTACATGTTAATT

2720

ITPR1

ITPR1-237

ITPR1-237

ATTATTGACTGTAATTACCCATTTACCTACAAACAGTAGGTCTTATTCATTCTGTAATTACCCAATTTACCTACAAACA
TAATAACTGACATTAATGGGGTAAATGGATGTTTGTCATCCAGAATAAGTAAGACATTAATGGGTAAATGGATGTTTGT

2800

ITPR1

ITPR1-237

ITPR1-237

GTAGGTCTTATTCGTTCTTTCTATTTTTTTTTTTTTTTTTTTTACCTGTTAACATCCCCACCTCCCCCCTGCCCTCCAC
CATCCAGAATAAGCAAGAAAGATAAAAAAAAAAAAAAAAAAAAAATGGACAATTGTAGGGGTGGAGGGGGGACGGGAGGGTG

2880

ITPR1

ITPR1-237

ITPR1-237

TATCTTTCCAGCCTCTGGTAACCATCCTTCTACTCTGTGTCCATGAGTTCAATTGTTTTGATTTTTAGATCCTACAAAT
ATAGAAAGGGTCGGAGACCATTGGTAGGAAGATGAGACACAGGTACTCAAGTTAACAAAACATAAAATCTAGGATGTTTA

2960

ITPR1

ITPR1-237

ITPR1-237

AAGTGAGAAGATGCGATGTTTGTCTTTCTGTGCTTGGCTTATTTCACTTAGCATTATGACCTCCTCCAGTTCCATCCATG
TTCACTCTTCTACGCTACAAACAGAAAGACACGAACCGAATAAAGTGAATCGTAATACTGGAGGAGGTCAAGGTAGGTAC

3040

ITPR1

ITPR1-237

ITPR1-237

TTGTTGCAAATGACTGGATCTCACTCTTTTCATTCCCTTTTTCTTTTTTTTTTTAAGATGGAGTCTCGCTCTGTCAACCA
AACAACGTTTACTGACCTAGAGTGAGAAAAGTAAGGGGAAAAAGAAAAAAATTTCTACCTCAGAGCGAGACAGTGGGT

3120

ITPR1

ITPR1-237

ITPR1-237

GGCTGGAGGGCAGTGGCGAGATCTCAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCAATTGTTCTGCCTCAGGCTCC
CCGACCTCCCGTCAACCGCTCTAGAGTCGAGTGACGTTGGAGGCGGAGGGCCCAAGTTCGTTAACAAGACGGAGTCCGAGG

3200

ITPR1

ITPR1-237

ITPR1-237

CCAGTAGCTGCGACTACAGGCACGTGCCACCACACCCAGCTAATTTTTGTGTTTTTAATAGAGACGGGGTTTTACCATAT
GGTCATCGACGCTGATGTCCGTGCACGGTGGTGTGGGTCGATTAAAAACACAAAAATTATCTCTGCCCCAAAGTGGTATA

3280

ITPR1

ITPR1-237

ITPR1-237

TGGCCAGGCTGGTCTTGAACCTCCTGACCTCGTGATCTGTCCGCCTTTGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGC
ACCGGTCCGACCAGAACTTGAGGACTGGAGCACTAGACAGGCGGAAACGGAGGGTTTCACGACCCTAATGTCCGCACTCG

3360

ITPR1

ITPR1-237

ITPR1-237

CACCGCGCTCGGCCTCATTCACTTTTTAGCACCTCTTGCTTATCAGTTAAACACTCCCCTCCCTCAGTATAATCAGTAAG
GTGGCGCGAGCCGGAGTAAGTGAAAAATCGTGGAGAACGAATAGTCAATTTGTGAGGGGAGGGAGTCATATTAGTCATTC

3440

ITPR1

ITPR1-237

ITPR1-237

AGTCTTGCAAGTTCAGTTGTTGGTTGAGCGTTTTTATTATAGATTAGTGAATTCTATTGATTGTATCTCATTACACAGA
TCAGAACGTTCAAGTCAACAACCAACTCGCAAAAATAATATCTAATCACTTAAGATAACTAACATAGAGTAAGTGTGTCT

3520

ITPR1

ITPR1-237

ITPR1-237

TCTGCTCCTCTTTCGTACACCCTCTCCCATTTCTTTCCCTTCTCTTGTCCTTCTAATTAAGACCCATATTTTCAGTTG
AGACGAGGAGAAAGCATGTGGGAGAGGGGTAAAGAAAGGGGAAGAGAACAGGAAGATTAATTCTGGGTATAAAAGTCAAC

3600

ITPR1

ITPR1-237

ITPR1-237

AAGCGGGAAGCAATTTACAATGTGGGTGTCACAAATGATTACAATGGAGCACGGACACAGTTGCTGTAAAAACACCTACT
TTCGCCCTTCGTTAAATGTTACACCCACAGTGTTTACTAATGTTACCTCGTGCCTGTGTCAACGACATTTTGTGGATGA

3680

ITPR1

ITPR1-237

ITPR1-237

ACCACCCTTGAAAATAACCCGCATTTTCTGGAGCCTGCTCAAGGGCTCAGGTAGTGAGCAATGGAAGCACTTCCGTTAAT
TGGTGGGAACTTTTATTGGGCGTAAAAGACCTCGGACGAGTTCCTCGAGTCCATCACTCGTTACCTTCGTGAAGGCAATTA

3760

ITPR1

ITPR1-237

ITPR1-237

TATCTCATTTAATCCGCAGGACAGCCCTCAGAAGTGACACATTATCCTTTTCTGTAGACGAGCATCAATTAAAGCACAGT
ATAGAGTAAATTAGGCGTCCTGTCTGGGAGTCTTCACTGTGTAATAGGAAAAGACATCTGCTCGTAGTTAATTTCTGTGTCA

3840

ITPR1

ITPR1-237

ITPR1-237

GAAATTAGTAATTTCCCAATGAACGCTCCATAGCAGAACTCCGCTAATAAGATCCTAACTGGGCTTCCAACACACGTA
CTTTAATCATTAAGGGGTTTACTTGCGAGGTATCGTCTTGAGGCGATTATTCTAGGATTGACCCGAAGGTTGTGTGCAT

3920

ITPR1

ITPR1-237

ITPR1-237

GCCAAACATCAGGGCGTTGCCTCTCACCCTGTGGTTCCCCTGTGTCTCCACCACACCTTCCTTATGTGAGCTGCTTTCT
CGGTTTGTAGTCCCGCAACGGAGAGTGGTGACACCAAGGGGACACAGAGGTGGTGTGGAAGGAATACACTCGACGAAAGA

4000

ITPR1

ITPR1-237

ITPR1-237

TGTCTTGTTCTTTCTTCTCATCTTTGCCTCATCACCTCTTCCTTGACCACAGCCACTCCTGTCTTTCTTCTTGTTCCT
ACAGAACAAGGAAGAAGAGTAGAAACGGAGTAGTGGAGAAGGAACTGGTGTGCGGTGAGGACAGAAAGGAAGAACAAGGA

4080

ITPR1

ITPR1-237

ITPR1-237

CTTCCTTCTTTCTGGCATGTGGCTTTCTGGTGATGCCATAAACATTGGCATCAAGACTTAGAATGCTGCTGACATGTCTT
GAAGGAAGAAAGACCGTACACCGAAAGACCACTACGGTATTTGTAACCGTAGTTCTGAATCTTACGACGACTGTACAGAA

4160

ITPR1

ITPR1-237

ITPR1-237

GGTAAAGGTATGTTGGACCTGTGCACTTAAGGAAGAATTGGGGTCCAGGAGCCTAACCTCTGCTCTATCTACAGAAAATG
CCATTTCCATACAACCTGGACACGTGAATTCCTTCTTAACCCAGGTCTCGGATTGGAGACGAGATAGATGTCTTTTAC

4240

ITPR1

ITPR1-237

ITPR1-237

TTTTGTTTCTGTTTCTGTTTAGATTCTTAGATTACCTCTCCGACCTCTGTGTCTCCATGAACAAATCAATTCCAGTGACC
AAAACAAAGACAAAGACAAATCTAAGAATCTAATGGAGAGGCTGGAGACACAGAGGTACTTGTTTAGTTAAGGTCACCTGG

4320

ITPR1

ITPR1-237

630 635 640 645
F L D Y L S D L C V S M N K S I P V T
ENSE00003462468

ITPR1-237

CAGGAACTGATATGTAAAGCTGTGCTGAACCCACCAACGCTGACATCCTGATTGAGACCAAGTGAGTGGGGAGCCAGGG
GTCCTTGACTATACATTTGACACGACTTGGGGTGGTTGCGACTGTAGGACTAACTCTGGTTCACCTCACCCCTCGGTCCC

4400

ITPR1

ITPR1-237

650 655 660 665
Q E L I C K A V L N P T N A D I L I E T K
ENSE00003462468

ITPR1-237

TTTAGATGGAAAACATGGGGTTCATTTCAGTGTTGGTGCTCATGAGGAATAAAACCTAGCCCTATCATTTTTTGAGTTGAT
AAATCTACCTTTTGTACCCCAAGTAAGTCACAACCACGAGTACTCCTTATTTTGATCGGGATAGTAAAAAACTCAACTA

4480

ITPR1

ITPR1-237

ITPR1-237

CTAAAGTCAGTGTGGCTGGCATTGATCTTCTTATTGGAAAAGTCTTGATTAGGAGAATTCCTGAATTTGATTTTGGTGT
GATTTTCAGTCACACCGACCGTAAACTAGAGAATAACCTTTTCAGAACTAATCCTCTTAAGGGCTTAAACTAAAACCACA

4560

ITPR1

ITPR1-237

ITPR1-237

CACCTCCTCTTCATAGTGGTGTCACTTATTTTGCATACAAGTTTAGAAGTCATGTAAACTCACCGGGGAGCATTTTATAC
GTGGAGGAGAAGTATCACCACAGTGAATAAACGTATGTTCAAATCTTCAGTACATTGAGTGGCCCTCGTAAATATG

4640

ITPR1

ITPR1-237

ITPR1-237

AGCTACATTTTAAGAGTTTAAACTCTTTGTAAGTGTGACCATCAATTTAAAATTTCAAATGACATAATGAATATTCAGT
TCGATGTAAATTTCTCAAATTTTGAGAAACATTCACACTGGTAGTTAAATTTAAAGTTTACTGTATTACTTATAAGTCA

4720

ITPR1

ITPR1-237

ITPR1-237

GTTAAGATTAAGTCAGTGTTGGGAGGAGTTTTAAATTATTACTGTTCAGAACATGTTTATTGGTCTGCAGAAATTTTGT
CAATTCTAATTCAGTCACAACCCTCCTCAAAATTTAATAATGACAAGTCTTGTACAAATAACCAGACGTCTTAAAAACAA

4800

ITPR1

ITPR1-237

ITPR1-237

ACCAGTAGTAATTCATTTTTGGCAAAGGAGCAGTTTTCTGAGAAGTACAGTGCCGGTAATATGGACAGCCTTAAAAAAC
TGGTCATCATTAAGTAAAAACCGTTTTCTCGTCAAAAGGACTCTTCATGTCTACGGCCATTATACCTGTCTGGAATTTTTTG

4880

ITPR1

ITPR1-237

ITPR1-237

ATACTAAATTACGTCCTGAGCTAGTGATACTTCATTGATTCACATGTATAACTCAGTTTTGGGCTTGGGCTAATGCAGGG
TATGATTTAATGCAGGACTCGATCACTATGAAGTAACTAAGTGTACATATTGAGTCAAAACCCGAACCCGATTACGTCCC

4960

ITPR1

ITPR1-237

ITPR1-237

TTTTTCAGTTTAGGTATTTTCACATTTGGGGCTTGGTAATTCTTTGTTGTGGGGCTGTGCTAGGCACTGTAAATGTTCA
AAAAAGTCAAATCCATAAAAGTGTAAGCCCGAACCATTAGAAACAACACCCCGACACGATCCGTGACATTTTACAAGT

5040

ITPR1

ITPR1-237

ITPR1-237

GCAGCATCCCTGGCCCCCTACCCACTTAGATGCCAGTAGCACCTCTCCATTTGGGTTGTGACAACCAAAACCTGTCCAGA
CGTCGTAGGGACCGGGGATGGGTGAATCTACGGTCATCGTGGAGAGGTAAAGCCAACACTGTTGGTTTTTGGACAGGTCT

5120

ITPR1

ITPR1-237

ITPR1-237

GACATTGCCTGGTGTCCACTGGGGGCGAGCAGCACCATAGTCGAGAACCCTGGGTTACAGTATATGAAGATGTTAATGTC
CTGTAACGGACCACAGGTGACCCCCGTCGTCGTGGTATCAGCTCTTGGTGACCCAATGTCATATACTTCTACAATTACAG

5200

ITPR1

ITPR1-237

ITPR1-237

AGGCTCTCTGCGGCTCTGCCCTTGGGGGAAATACAAAACAAAAGTGTCCTTCCATGTGTCTTTATGCTGAAAGTAAAGC
TCCGAGAGACGCCGAGACGGGAACCCCTTTATGTTTTGTTTTTCACAGAAAGGTACACAGAAATACGACTTTCATTTCG

5280

ITPR1

ITPR1-237

ITPR1-237

TAGATCTCAAAGTATTTTTAAAAATAGTAACTTTCCCTCCTCCTCTTGTTTTCTAGGTTGGTTCTTTCTCGTTTTGAAT
ATCTAGAGTTTCATAAAAAATTTTTATCATTGAAAAGGGAGGAGGAGAACAAAAGATCCAACCAAGAAAGAGCAAAACTTA

5360

ITPR1

ITPR1-237

670 L V L S R 675 F E

ENSE00003513138

ITPR1-237

TTGAAGGTGTCTCTTCCACTGGAGAGAATGCTCTGGAGGCAGGAGAAGACGAGGAAGAGGTGTGGCTGTTTTGGAGGGAC
AACTTCCACAGAGAAGGTGACCTCTCTTACGAGACCTCCGTCCTCTTCTGCTCCTTCTCCACACCGACAAAACCTCCCTG

5440

ITPR1

ITPR1-237

680 F E G V S S T G 685 E N A L E 690 A G E D E 695 E E V W L 700 F W R D

ENSE00003513138

ITPR1-237

AGCAACAAAGAGATTTCGCAGCAAGAGTGTGAGGGAATTGGCTCAGGATGCTAAAGAAGGGCAGAAGGAGGACCGAGACGT
TCGTTGTTTCTCTAAGCGTCGTTCTCACACTCCCTTAACCGAGTCCTACGATTTCTTCCCGTCTTCTCCTCTGGCTCTGCA

5520

ITPR1

ITPR1-237

705 S N K E I R 710 S K S V R 715 E L A Q D 720 A K E G Q 725 K E D R D 730 V

ENSE00003513138

ITPR1-237

TCTCAGCTACTACAGGTGCGTGGGACACGTGTGGGGCTCAGATTGGGGTGCCCCAAAACAGTGGCACTTAGGAATTTGTT
AGAGTCGATGATGTCCACGCACCCTGTGCACACCCCGAGTCTAACCCACGGGGTTTTGTCAACGTCGAATCCTTAAACAA

5600

ITPR1

ITPR1-237

735 L S Y Y R

ENSE00003513138

ITPR1-237

GCTCGTTTGTTGATTACTTCAAGGAATCACAAGGAGTCATCTTGTAAGATTGTCTAGAAAAAAGCCAGATGTGTGTTTTA
CGAGCAAACAATAATGAAGTTCCTTAGTGTTCTCAGTAGAACATTCTAACAGATCTTTTTTCGGTCTACACACAAAAAT

5680

ITPR1

ITPR1-237

ITPR1-237

GGAGTTTGGAGTGTAAGATTTAGTTAGTTGACATCTGGATGTGGCTGGTTCCCAAAAAGGATGAGTGCTTGCTCAGTC
CCTCAAACCTCACATTCTAAAGTCAATCAACTGTAGACCTACACCGACCAAGGGTTTTCTACTCACGAACGGAGTCAG

5760

ITPR1

ITPR1-237

ITPR1-237

CCTGGTGATAGTTTATCCTTCAGCAGCATGGCCCATAGATATGGTGGTAGGTACGTAAGAGGCAGGCTGTGGGGTCACAT
GGACCACTATCAAATAGGAAGTCGTCGTACCGGGTATCTATACCACCATCCATGCATTCTCCGTCCGACACCCCAAGTGA

5840

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

CCCTACCTCTCCGCTTACCAGTTTTTTGACATTGGCCAAGTTTGATTTTATGCTCTAATTTCTTTATCTGCAAAATGAAG
GGGATGGAGAGGCGAATGGTCAAAAAACTGTAACCGGTTCAAACATAAAATACGAGATTAAGAGAAATAGACGTTTTACTTC

5920

ITPR1

ITPR1-237

ITPR1-237

GTGATAGTGCCAATCTCACCAAATGTTTATAGACAGAGACAGAAGATGTGTGTGTTTGTATACACATATATCTACACATT
CACTATCACGGTTAGAGTGGTTTACAAATATCTGTCTCTGTCTTCTACACACACAAACATATGTGTATATAGATGTGTAA

6000

ITPR1

ITPR1-237

ITPR1-237

CATCCATGTATCTTTCTATAACTACACAAATATATAATAAAAAGCATGTACTTACACTAATACTTCCAATTCCATTCCAA
GTAGGTACATAGAAAGATATTGATGTGTTTATATATTATTTTCGTACATGAATGTGATTATGAAGGTTAAGGTAAGGTT

6080

ITPR1

ITPR1-237

ITPR1-237

CACCATAGGATTTATTCTAGCCTTCACCTTTTCCATTTTCATGACTCCCTCCAGCTGCCACGATTCCCTGTATGTTTACCC
GTGGTATCCTAAATAAGATCGGAAGTGGAAGGTAAGTACTGAGGGAGGTCGACGGTGCTAAGGGACATACAAATGGG

6160

ITPR1

ITPR1-237

ITPR1-237

ATCTGCCCGTTTTCCCTGTGTGTACCTGTCTCACCTCTGCCACCCACCTCCACGGTCCCCAGTGTCTCCTTGGCTCCAGCT
TAGACGGGCAAAGGGACACACATGGACAGAGTGGAGACGGTGGGTGGAGGTGCCAGGGGTCACAGAGGAACCGAGGTCGA

6240

ITPR1

ITPR1-237

ITPR1-237

GTAAGACCTGCCAGTCCTGCCACCTGAAGGGAAGGGAAGGGAAGAAAGAAAGGAAGTGAACCAATTAATACTTTTAAAA
CATTCTGGACGGTCAGGACGGTGGACTTCCCTTCCCTTCCCTTCTTTCTTTCTTTCACTTGGTTAATTATGAAAATTTT

6320

ITPR1

ITPR1-237

ITPR1-237

GAAAAGGAAAGGGAAGATAAAGCAAGGCTTTTATTATTTTTTAATAAAATAAATAAAACTGCAGATAAAATGCCTTTTCT
CTTTTCTTTCCCTTCTATTTTCGTTCCGAAAATAATAAAAAATTATTTTATTTATTTTGACGTCTATTTTACGGAAAAGA

6400

ITPR1

ITPR1-237

ITPR1-237

TGCCTCCTGTATTCTGTTCTTTTCATTCATGTGTGATGTACGCATCCTATCCACATTCTCTGTGTGCTGCATTTGTATGCA
ACGGAGGACATAAGACAAGAAAGTAAGTACACACTACATGCGTAGGATAGGTGTAAGAGACACACGACGTAAACATACGT

6480

ITPR1

ITPR1-237

ITPR1-237

TCTGTAAATCATATGTAGTATTTTATCTCTACTTAAAATTTTATATAAATGGGACTGTACTCCAAATACCATTCTAAAAC
AGACATTTAGTATACATCATAAAATAGAGATGAATTTTAAAATATATTTACCCTGACATGAGGTTTATGGTAAGATTTTG

6560

ITPR1

ITPR1-237

ITPR1-237

TTGCCTTATTTATTCAATACGGGTACTGAAGCCATATTGAATATATCTGCGTTAATAGAGATTAATCCATTTCTGTAATT
AACGGAATAAATAAGTTATGCCCATGACTTCGGTATAACTTATATAGACGCAATTATCTCTAATTAGGTAAAGACATTAA

6640

ITPR1

ITPR1-237

ITPR1-237

TGGACTGTTGGATGATATTCTGTTTTATTGATTTATCACATTTTCATCGCTGTTTGATATTTGATCACATGCTGCAGTTC
ACCTGACAACCTACTATAAGACAAAATAACTAAATAGTGTAAGAGTAGCGACAACTATAAACTAGTGACGACGTCAAG

6720

ITPR1

ITPR1-237

ITPR1-237

TTCATGTCAGGAAACATCTTCATTCAAATTTTCTGAGTATATGTATGAATTTCCATTCCACACTGGGAGGTGGGCTTG
AAGTACAGTCCTTTGTAGAAGTAAGTTTAAAAAGACTCATATACATACTTAAAGGTAAGGTGTGACCCTCCACCCGAACC

6800

ITPR1

ITPR1-237

ITPR1-237

AGGATATTCATATTTTAAGCTTTACTAAGCAATTCTAAATTGGATGTGTGTCAGTGTACACACCCACCAGTTGTAGACGACA
TCCTATAAGTATAAAATTCGAAATGATTTCGTTAAGATTTAACCTACACAGTCACATGTGTGGGTGGTCAACATCTGCTGT

6880

ITPR1

ITPR1-237

ITPR1-237

AGCTTTGTTTCTTCATGTCTTTGTTAACCTTGAATATCATGATGCTTTTAAATTTTGGTAATTTTATAAGTGTGAAATA
TCGAAACAAAGAAGTACAGAAACAATTGGAACCTATAGTACTACGAAAAATTAAAAACCATTAATTAATTCACACTTTAT

6960

ITPR1

ITPR1-237

ITPR1-237

GACTCATGTCTACACTTGCATTTCCCGACATCTAATGAGGCTGAGAATGTCTTCAAATCATGATTATTAGAAATACATA
CTGAGTACAGATGTGAACGTAAAGGGGCTGTAGATTACTCCGACTCTTACAGAAGTTTAGTACTAATAATCTTTATGTAT

7040

ITPR1

ITPR1-237

GAGTTTTTAATTCAGAAGGCAGTATTTTGAAAGCCTGTGGCTTTCTCGTTATTTACATTTCAAGTATGTTTACTCTTTC
CTCAAAAATTAAGTCTTCCGTCATAAACTTTTCGGACACCGAAAGAGCAATAAAGTGTAAGTTTCATACAAATGAGAAAG

7120

ITPR1

ITPR1-237

AGTGTTTGATGAATCTTCTCCCAAGTGAATGAGAAAGAGTGCCTTAATTGGTCAGGTTCCAGTTAACAACATTCAC TTGC
TCACAAACTACTTAGAAGAGGGTTCAC TTACTCTTCTCACGGAATTAACCAGTCCAAGGTCAATTGTTGTAAGTGAACG

7200

ITPR1

ITPR1-237

AATTGGATGAAGATGAAAAGTGAGGAGTCTCCTACTTTTGTAATGAAATGTTTTTTTACACGTGTAGGAATTAGAGTGA
TTAACCTACTTCTACTTTTCACTCCTCAGAGGATGAAAACATTTACTTTACAAAAAAATGTGCACATCCTTAATCTCACT

7280

ITPR1

ITPR1-237

CTTACATGATATAAGATCTTTAAAATGTTATAAAATTTCTAATTAGGCTGAATATGTGTGATATCTTGAACATTTCTTAC
GAATGTACTATATTCTAGAAATTTACAATATTTTAAAGATTAATCCGACTTATACACACTATAGAACTTGTAAGGATG

7360

ITPR1

ITPR1-237

ATGGTCTTTACTGTATAAAACACAGCTGAAGGGAAAGAAATAGACAACCATCTTAGGCCTTAGCATTCCCCCGTTTATT
TACCAGAAATGACATATTTTGTGTCGACTTCCCTTTCTTTATCTGTTGGTAGAATCCGGAATCGTAAGGGGGGCAAATAA

7440

ITPR1

ITPR1-237

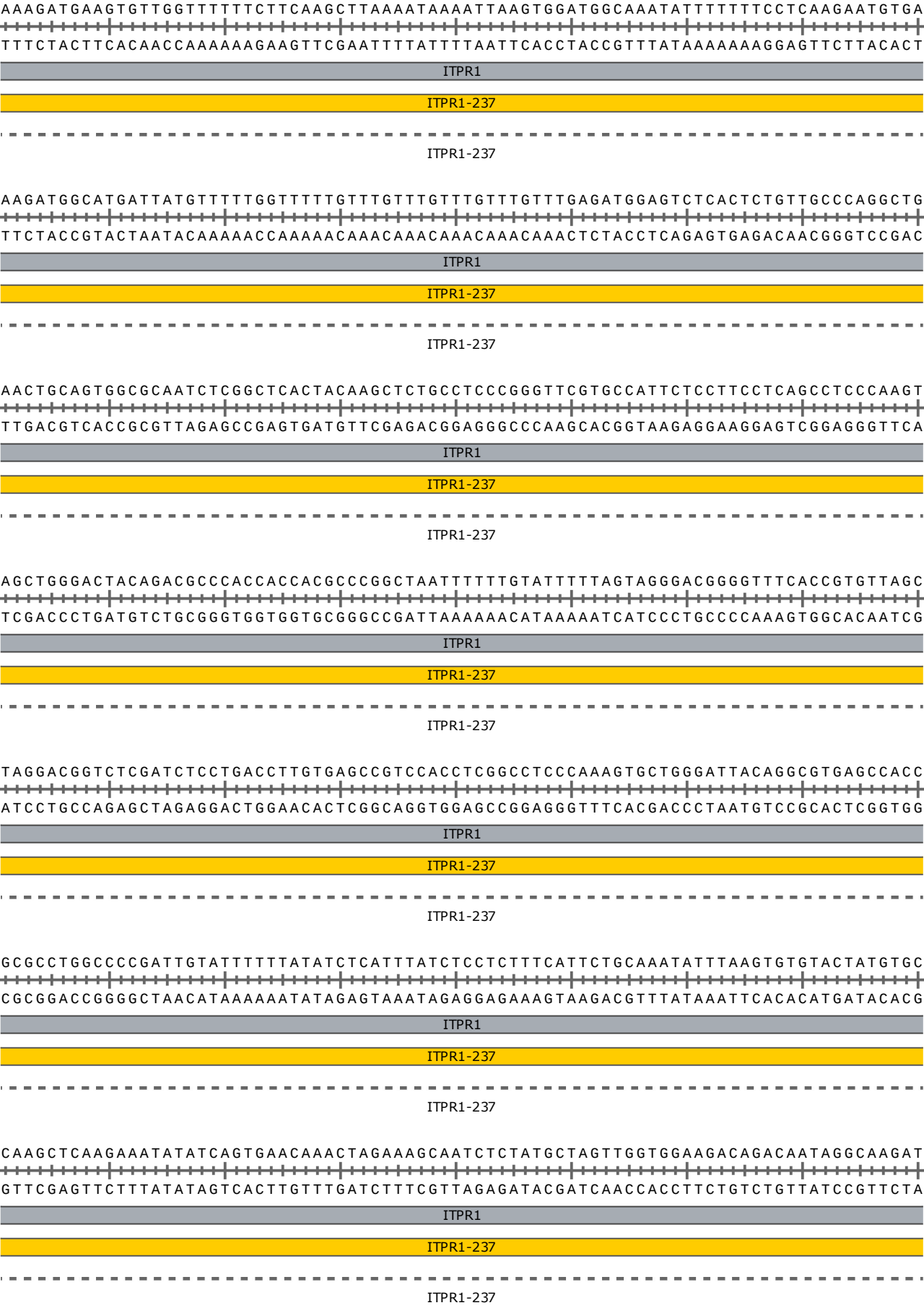
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ITPR1

ITPR1-237

ITPR1-237



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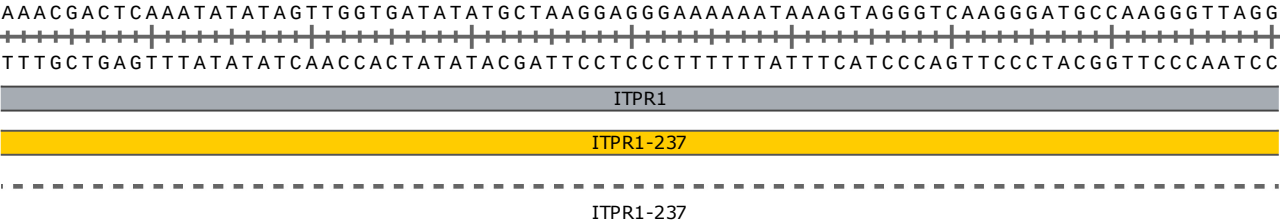
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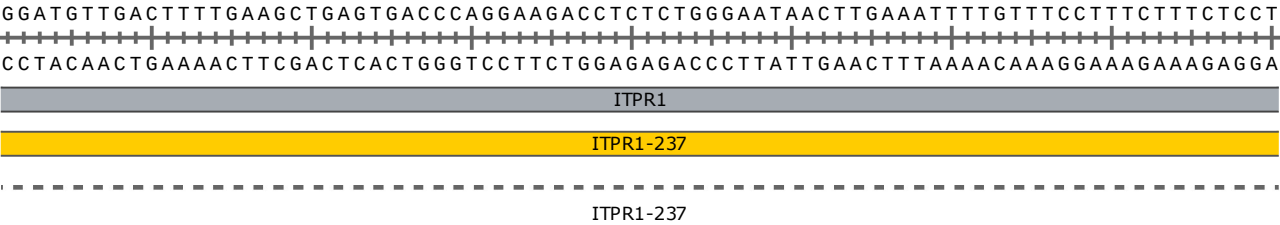
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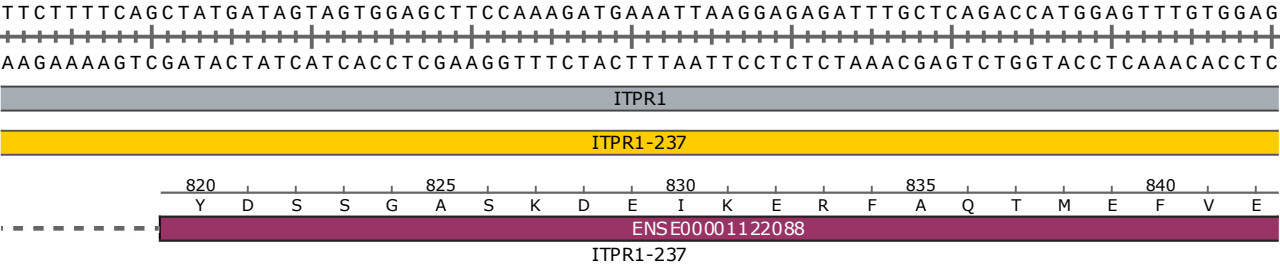
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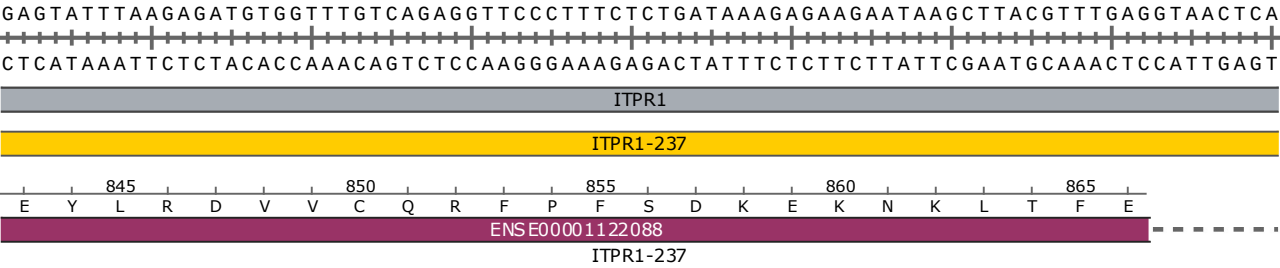
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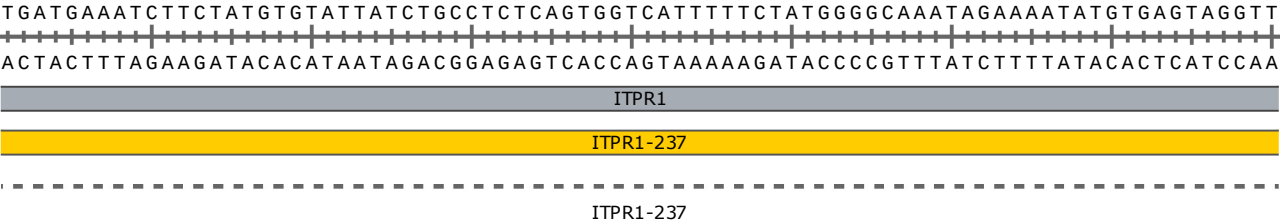
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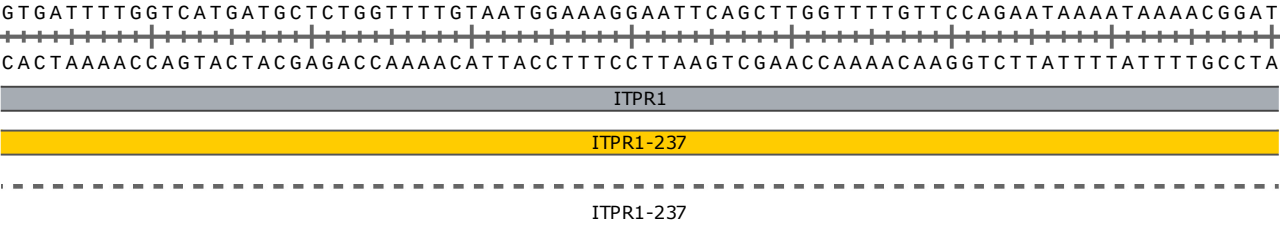
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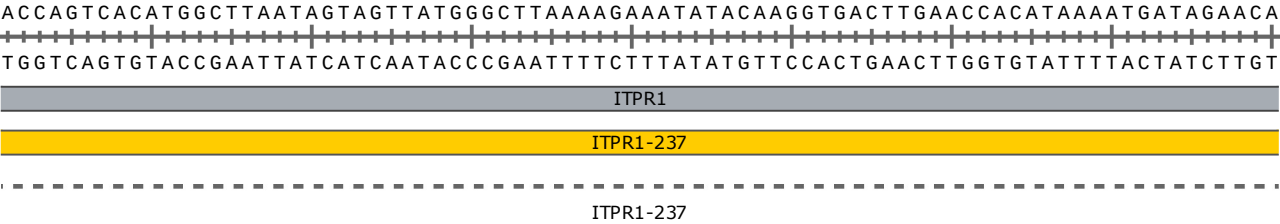
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9200

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ITPR1

ITPR1-237

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ITPR1

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ITPR1

ITPR1-237

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9600

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ITPR1-237

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9680

ITPR1

ITPR1-237

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ENS...

ITPR1-237

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9760

ITPR1

ITPR1-237

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ITPR1-237

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ITPR1

ITPR1-237

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ENSE00001258258

ITPR1-237

9840

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ITPR1

ITPR1-237

925
V E K L K

ENSE00001258258

ITPR1-237

9920

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ITPR1

ITPR1-237

ITPR1-237

10,000

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ITPR1

ITPR1-237

ITPR1-237

10,080

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ITPR1

ITPR1-237

ITPR1-237

10,160

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ITPR1-237

10,240

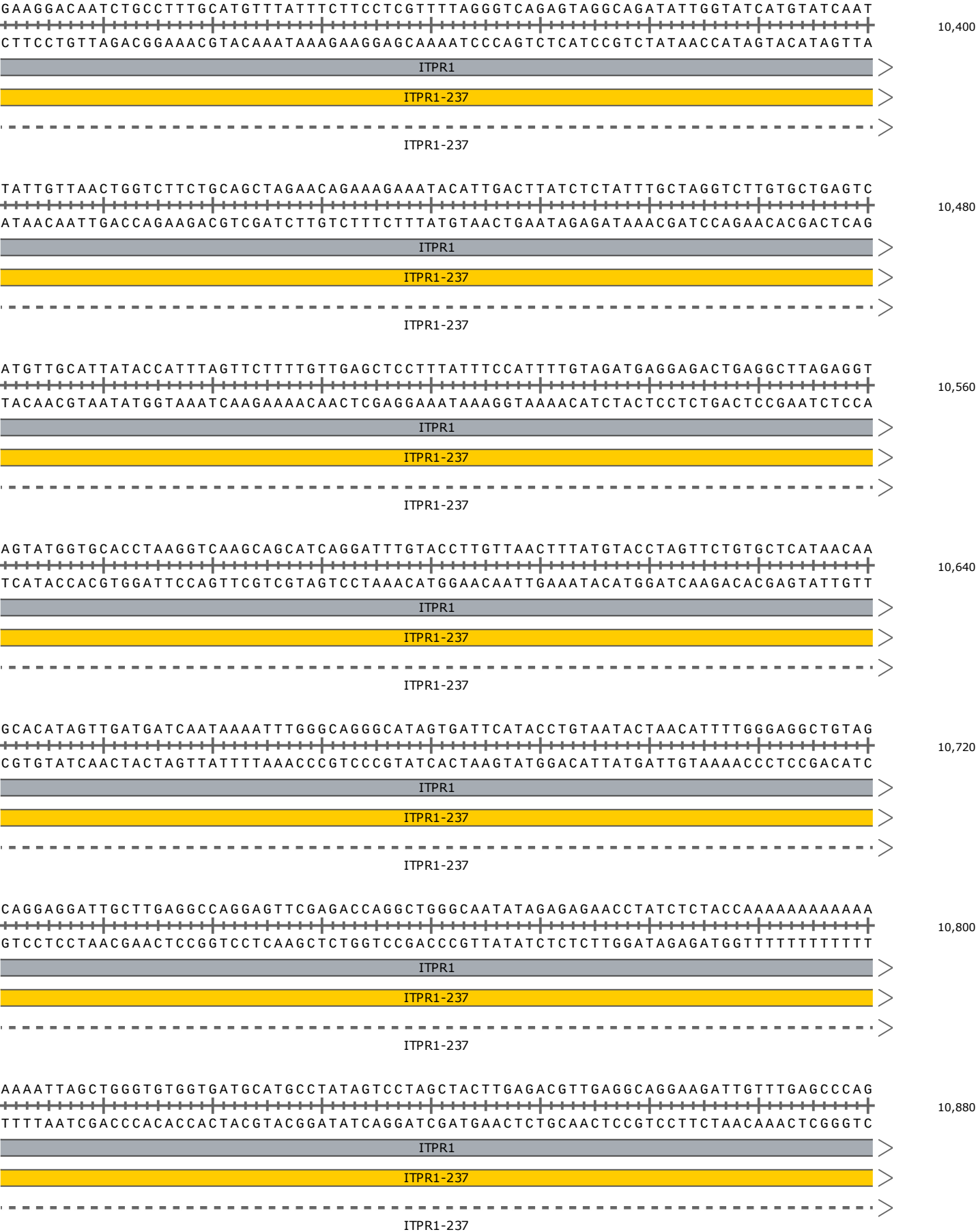
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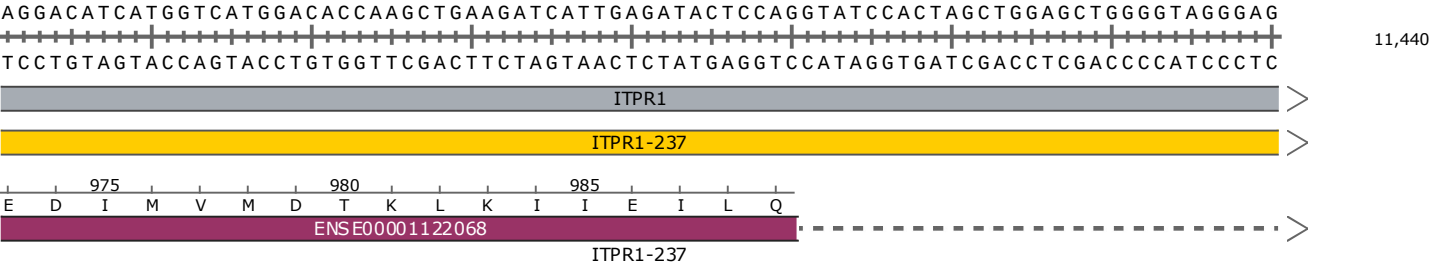
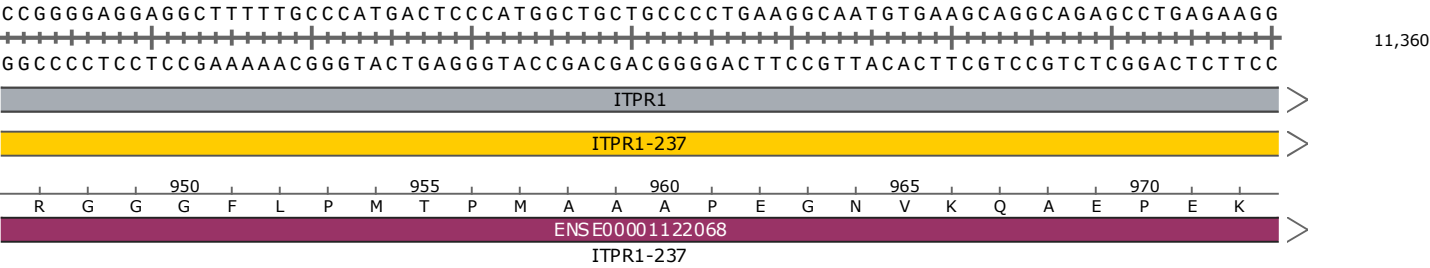
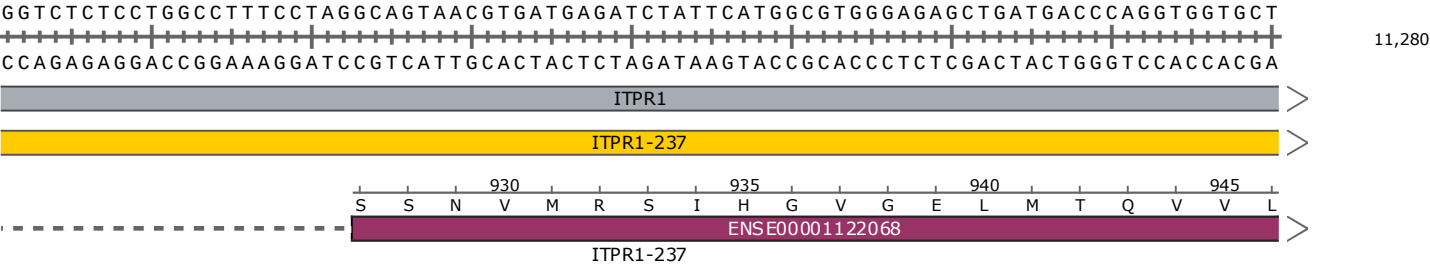
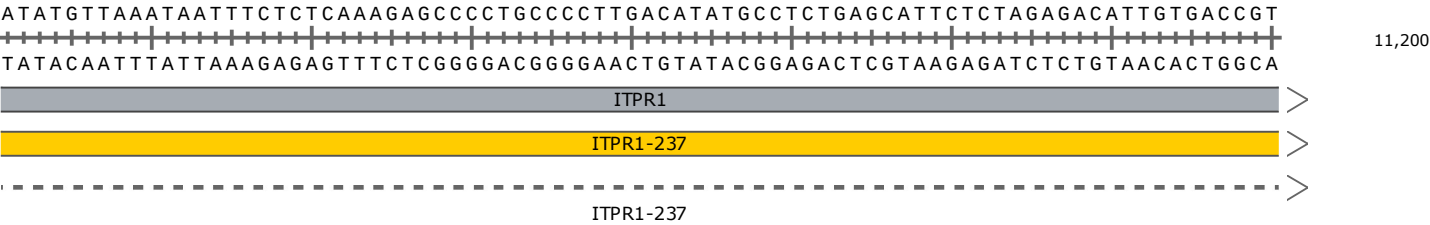
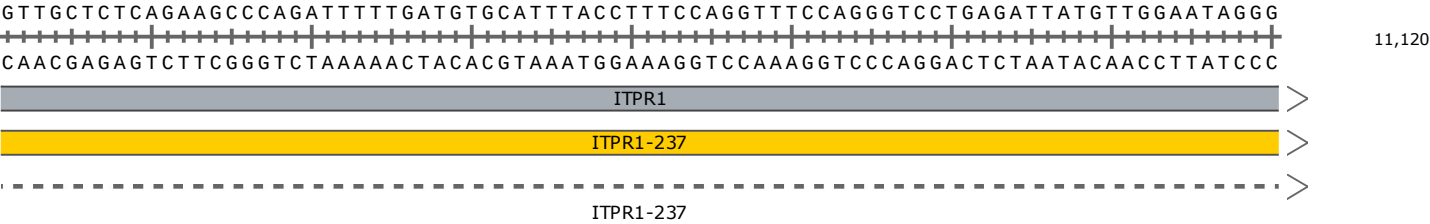
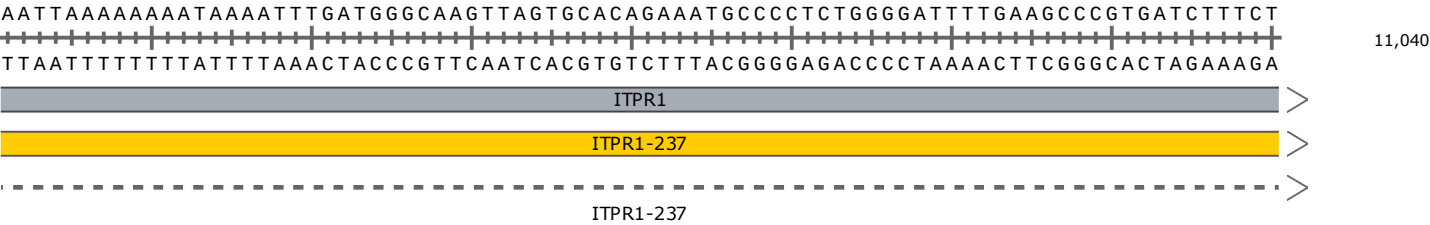
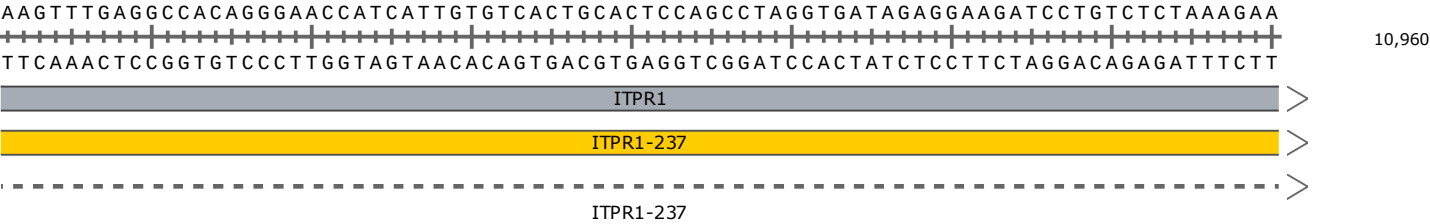
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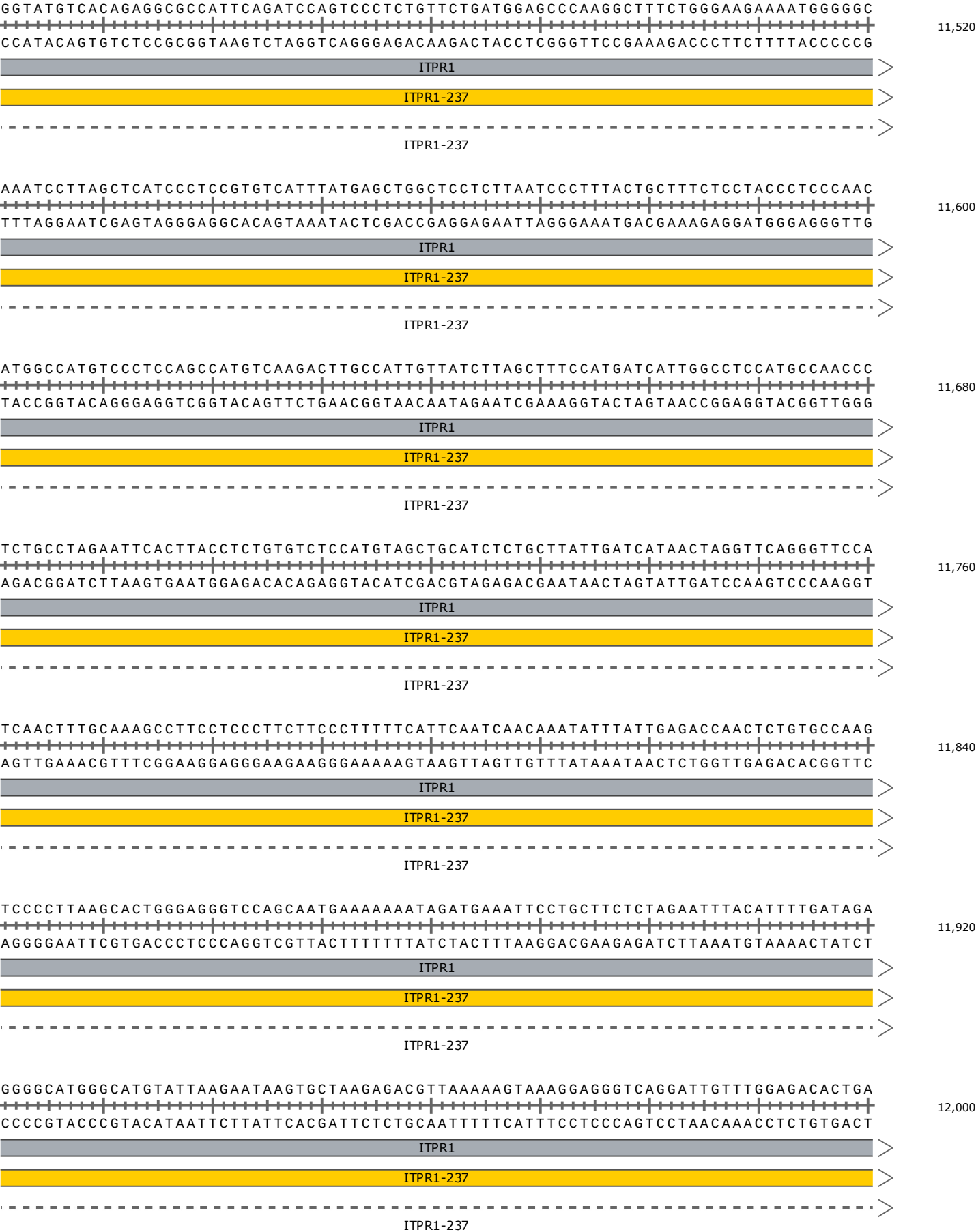
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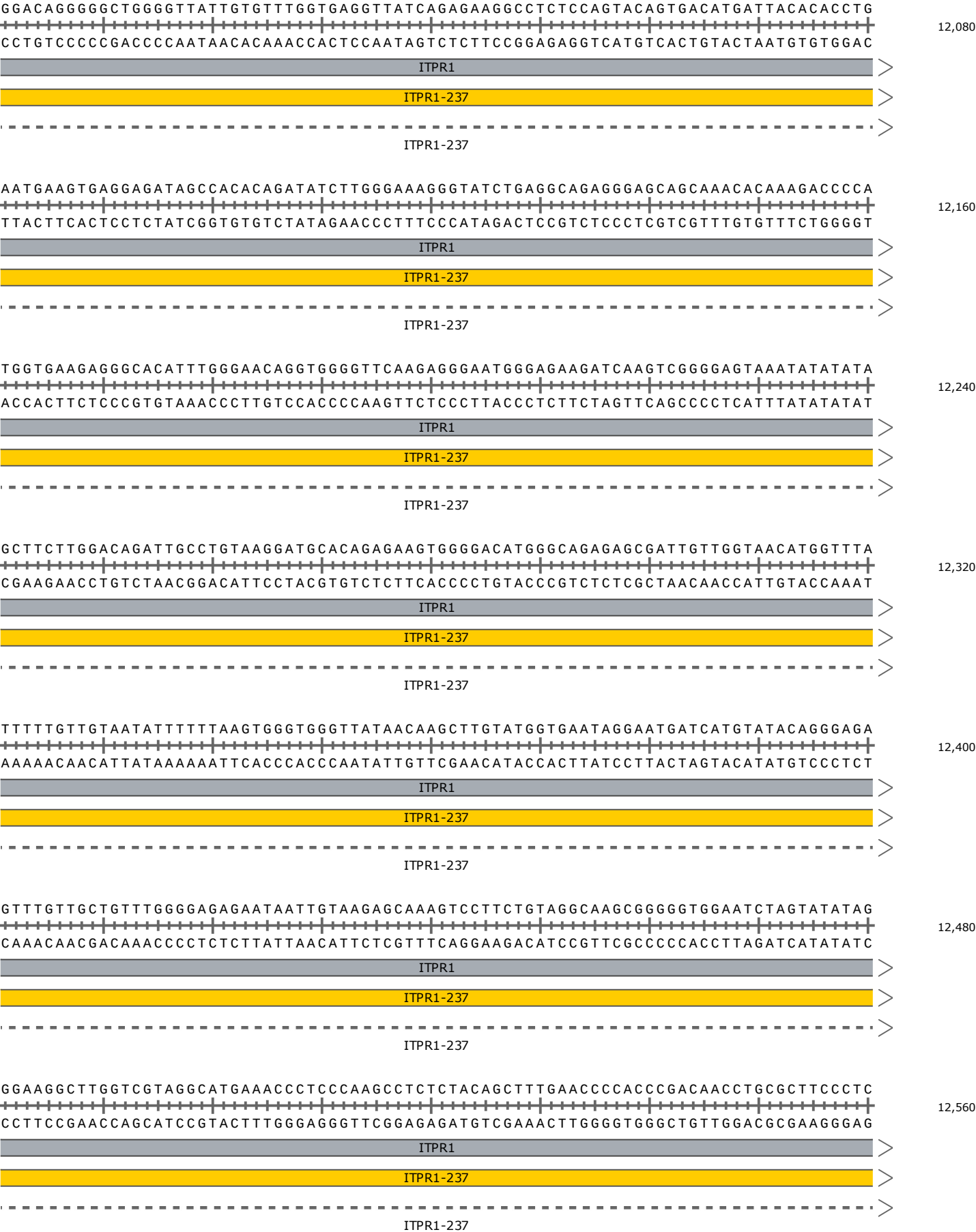
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10,320









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ITPR1-237

ITPR1-237

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ITPR1-237

ITPR1-237

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12,800

ITPR1

ITPR1-237

ITPR1-237

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12,880

ITPR1

ITPR1-237

ITPR1-237

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12,960

ITPR1

ITPR1-237

ITPR1-237

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13,040

ITPR1

ITPR1-237

ITPR1-237

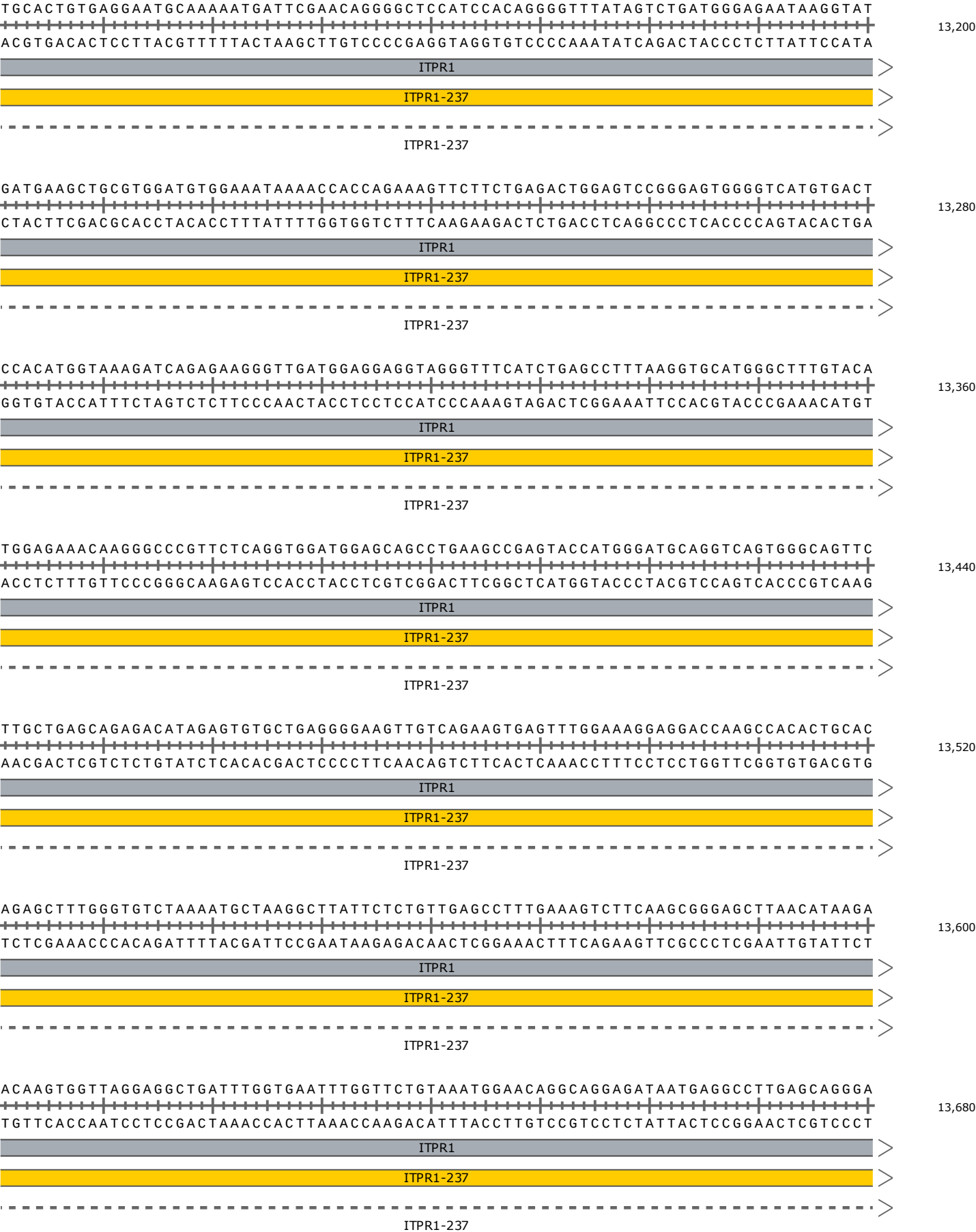
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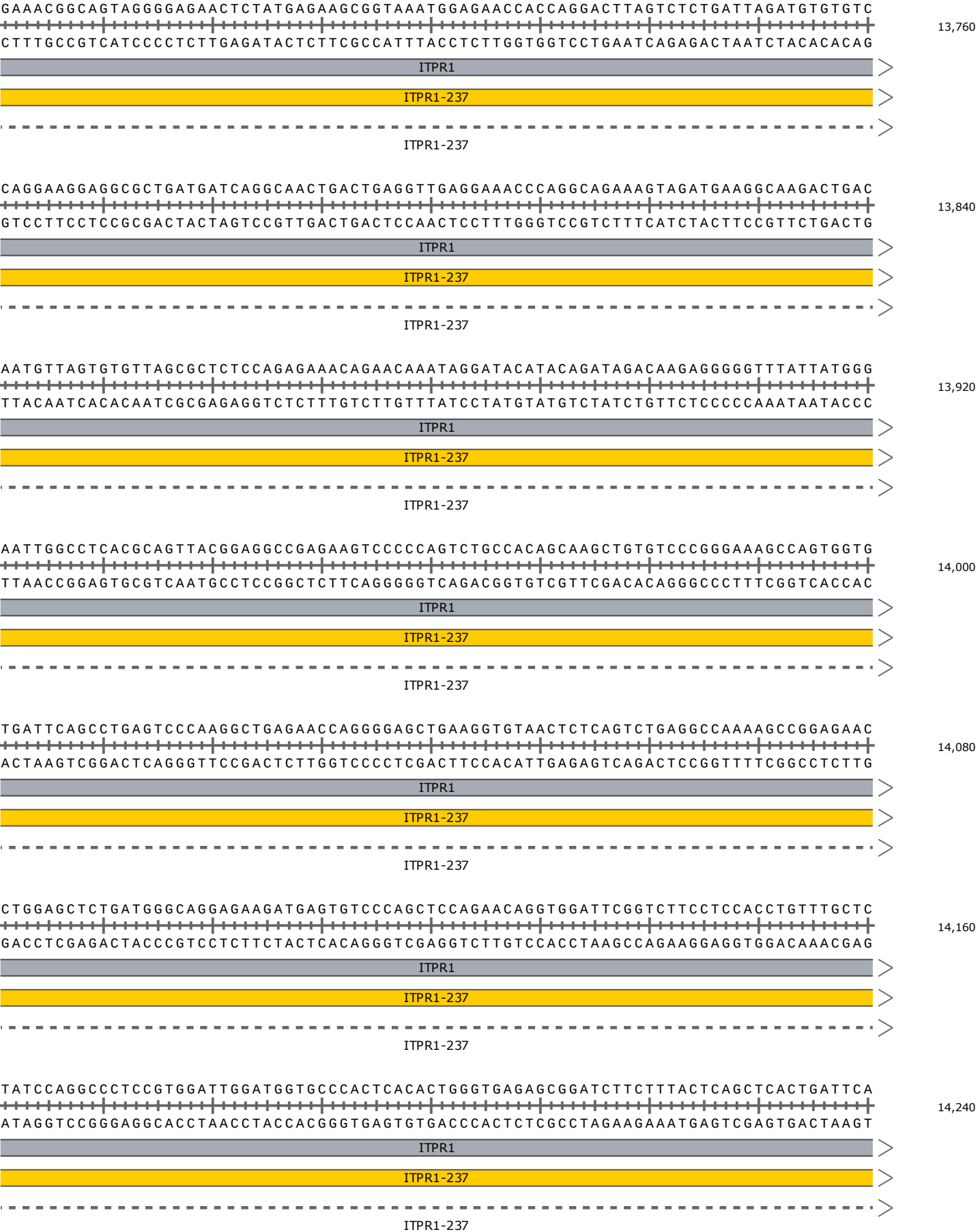
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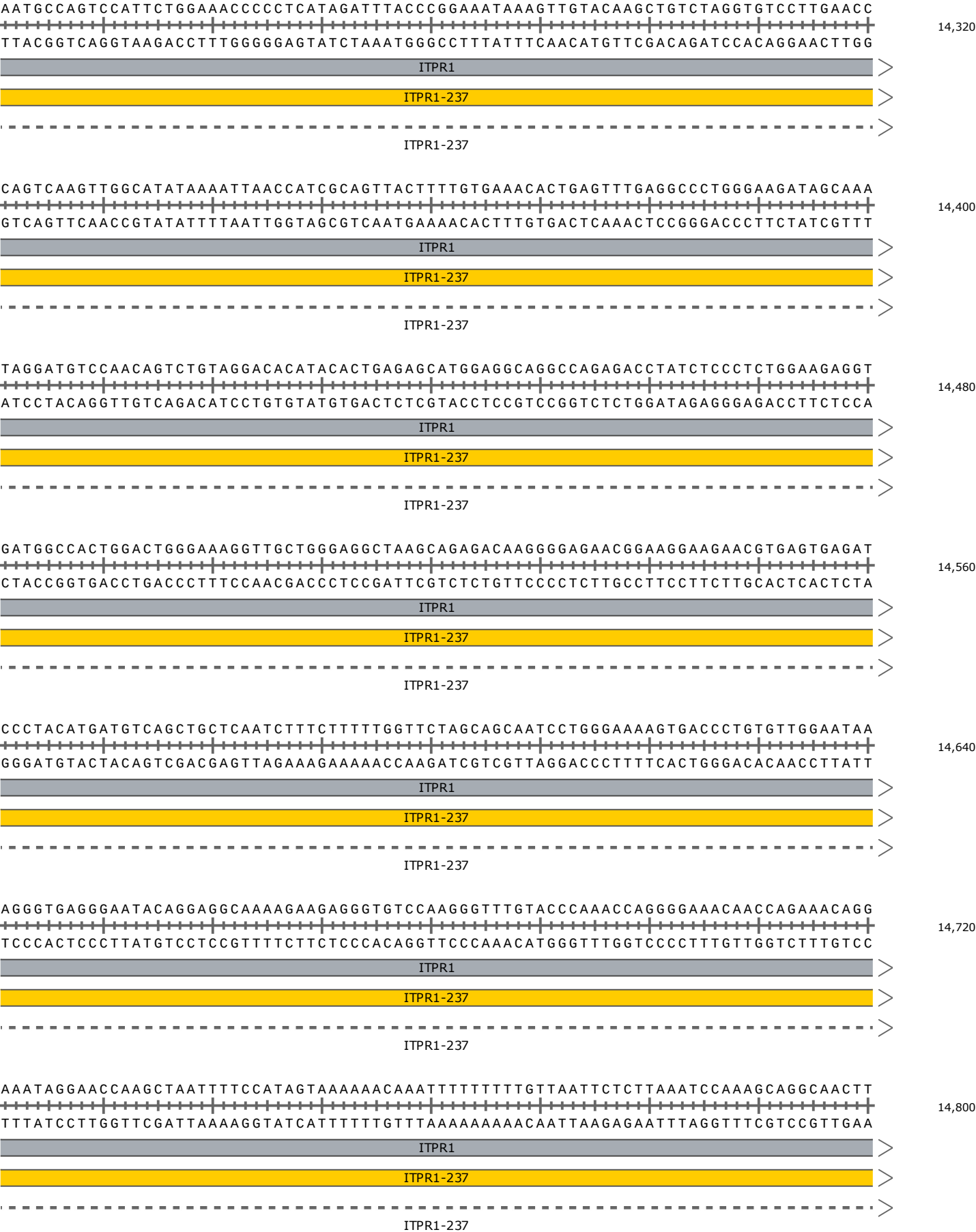
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ITPR1-237

ITPR1-237







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14,880

ITPR1

ITPR1-237

ITPR1-237

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14,960

ITPR1

ITPR1-237

ITPR1-237

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15,040

ITPR1

ITPR1-237

ITPR1-237

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15,120

ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ENSE00001122057

ITPR1-237

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15,280

ITPR1

ITPR1-237

ENSE00001122057

ITPR1-237

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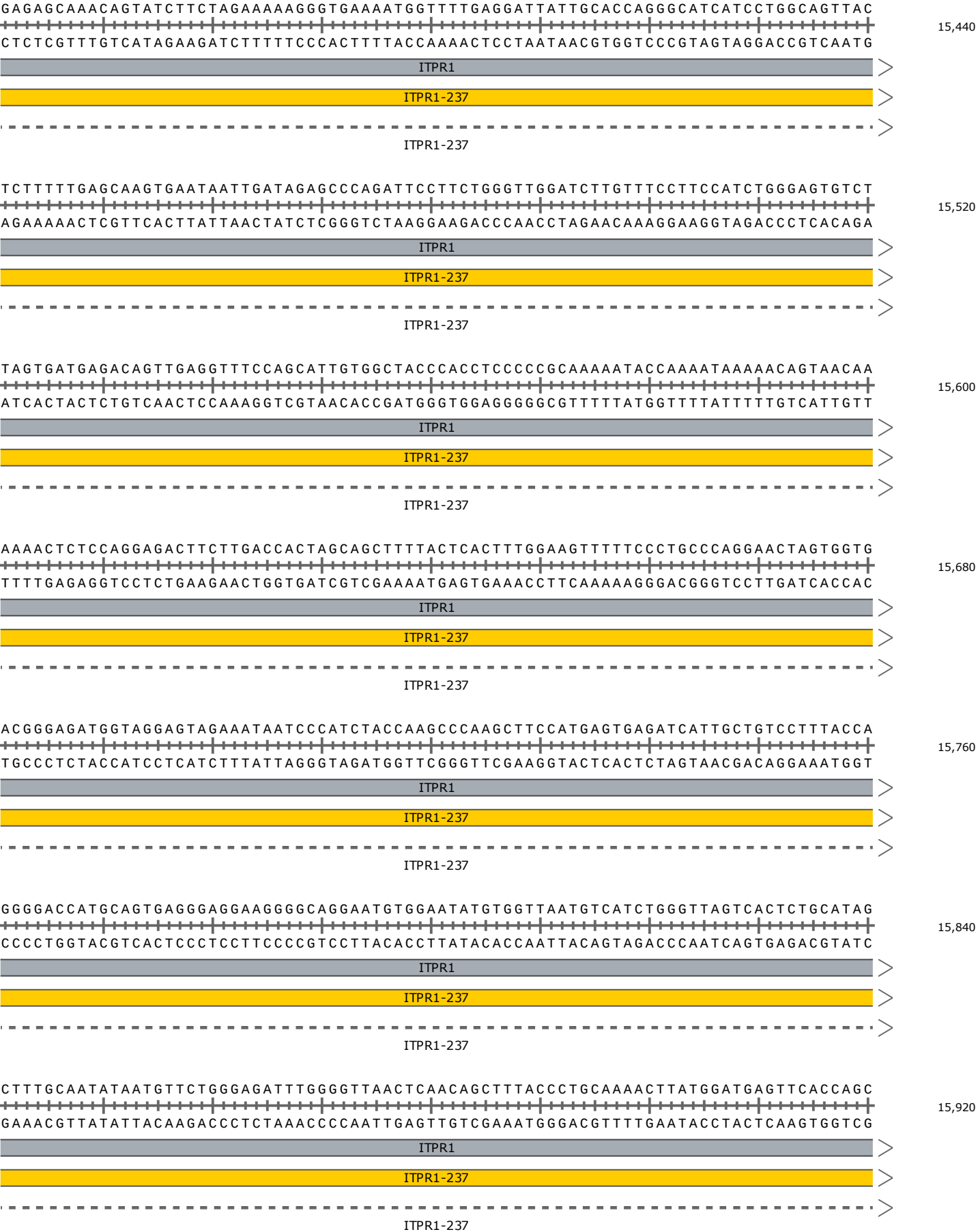
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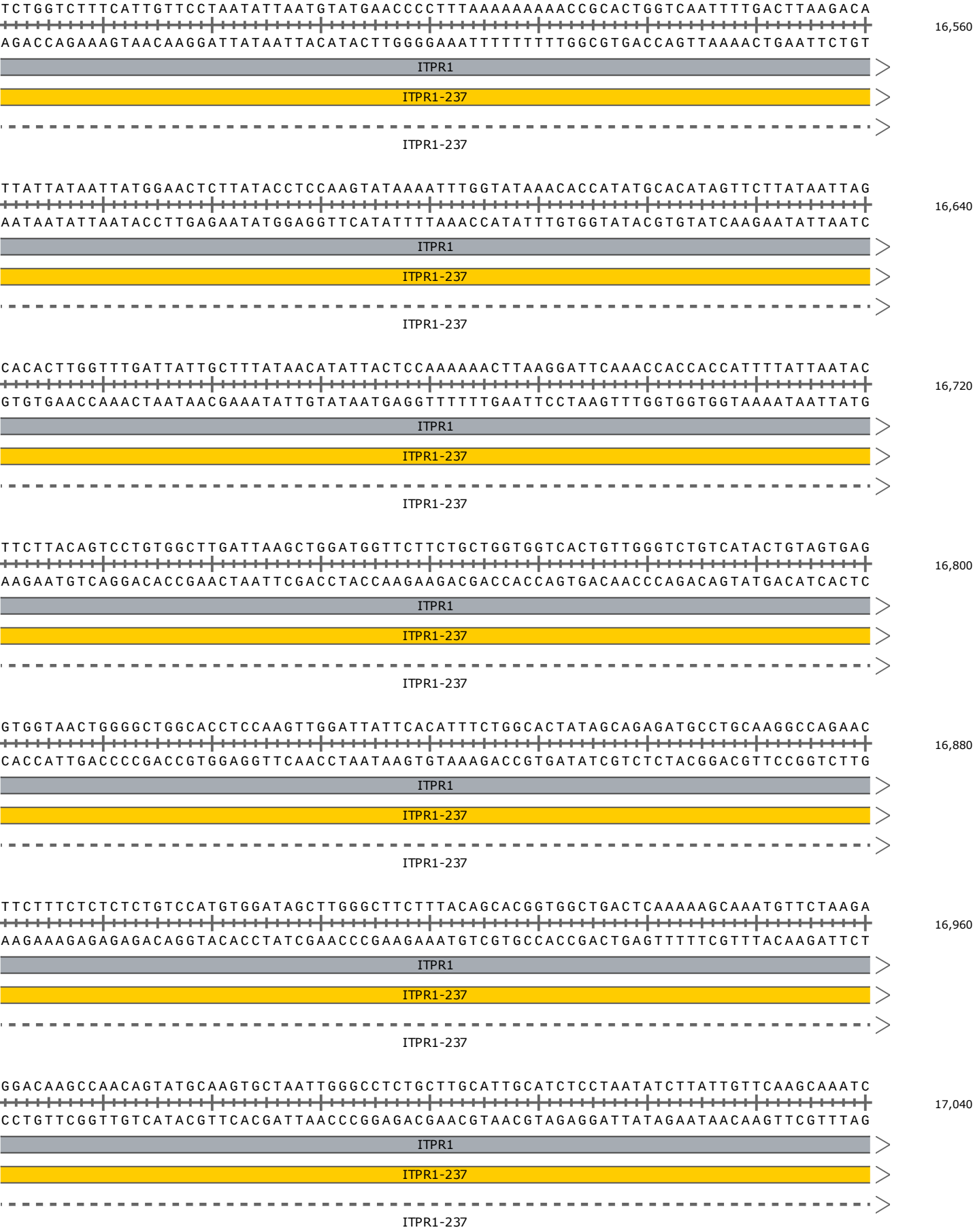
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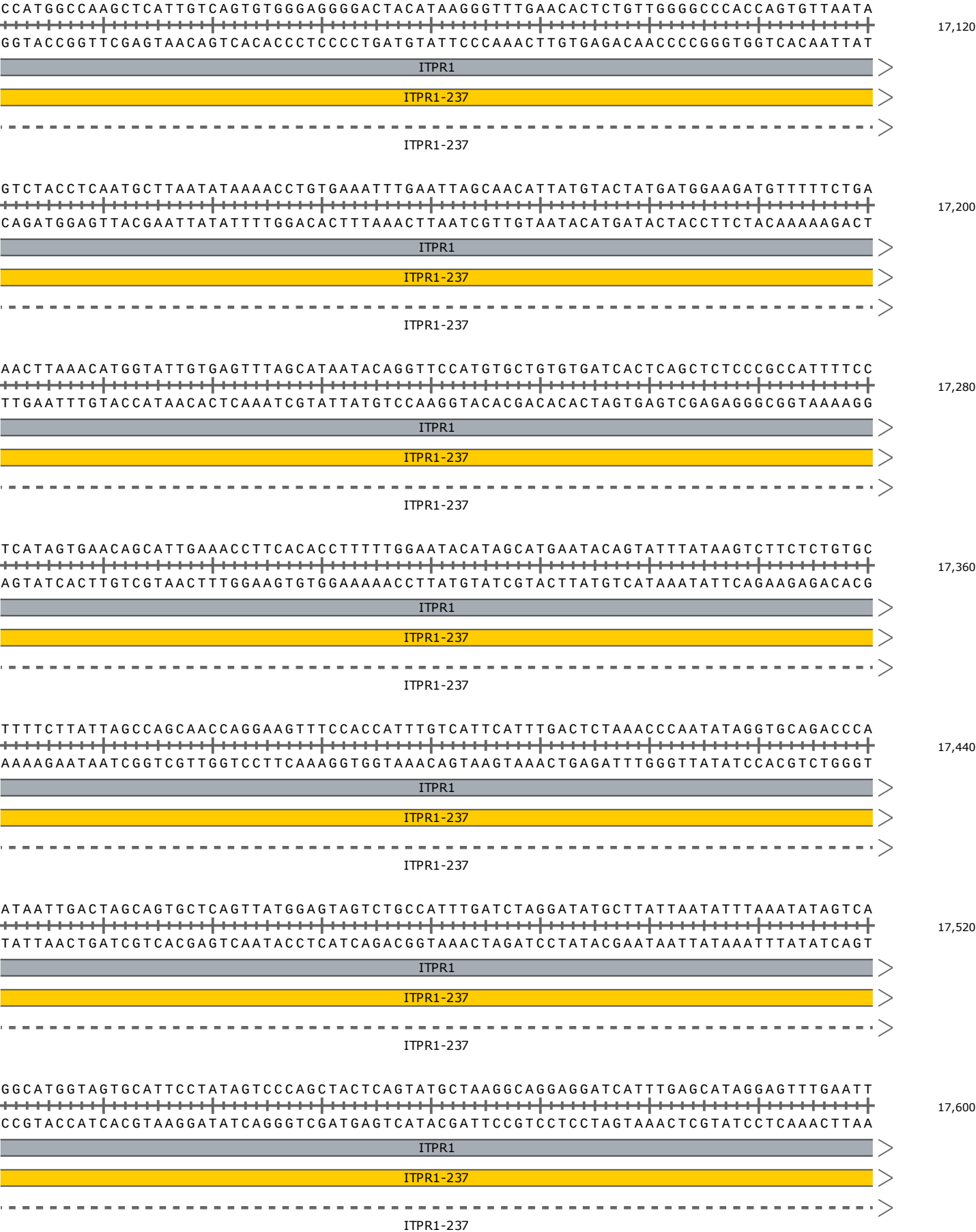
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ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

17,840

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ITPR1

ITPR1-237

ITPR1-237

17,920

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ITPR1-237

ITPR1-237

ENSE00001122044

18,000

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ITPR1-237

ITPR1-237

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18,080

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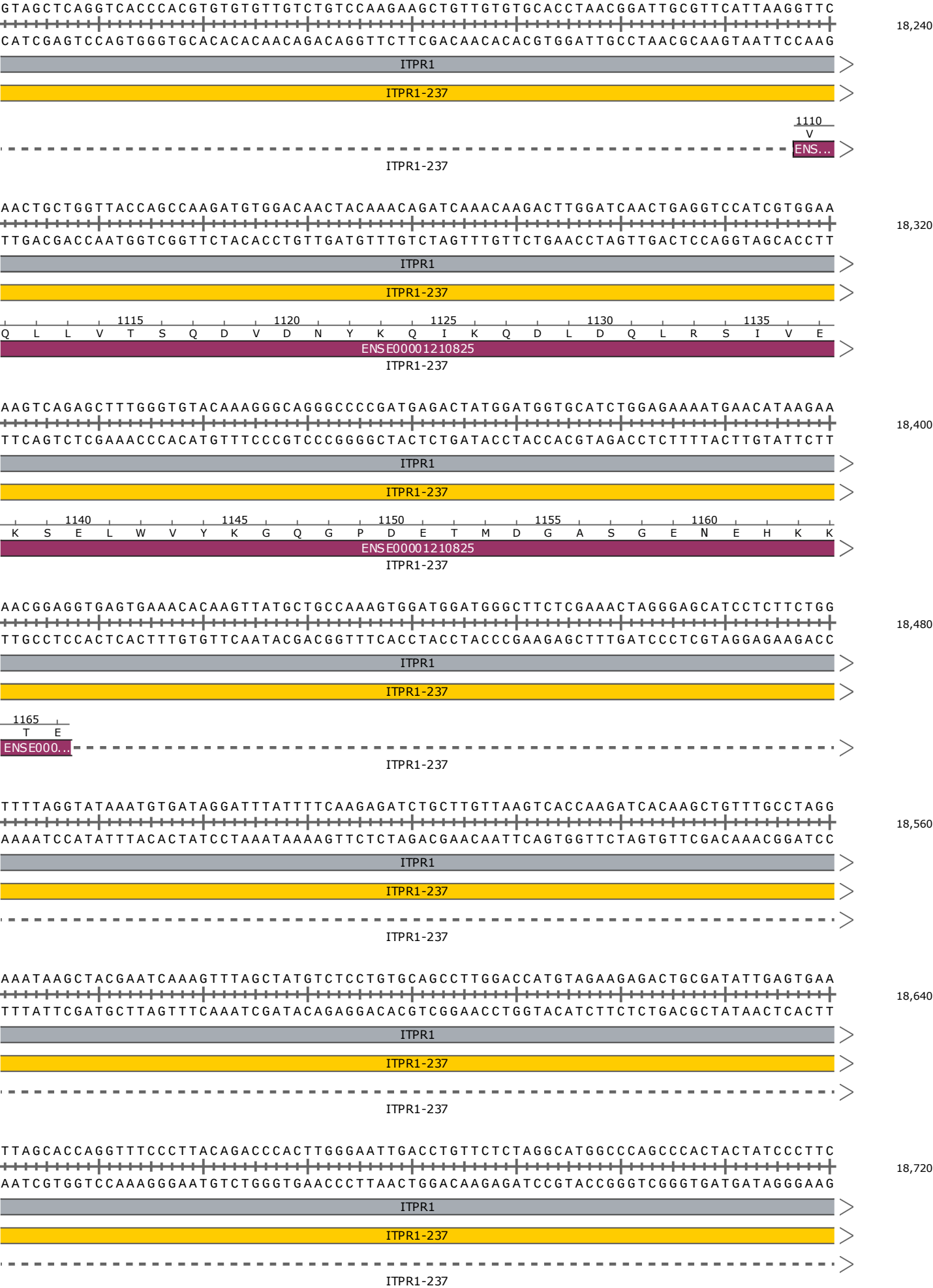
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ITPR1-237

ENSE00001122044

18,160



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ITPR1-237

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18,880

ITPR1

ITPR1-237

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18,960

ITPR1

ITPR1-237

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ENSE00001122034

ITPR1-237

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19,040

ITPR1

ITPR1-237

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19,120

ITPR1

ITPR1-237

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ITPR1-237

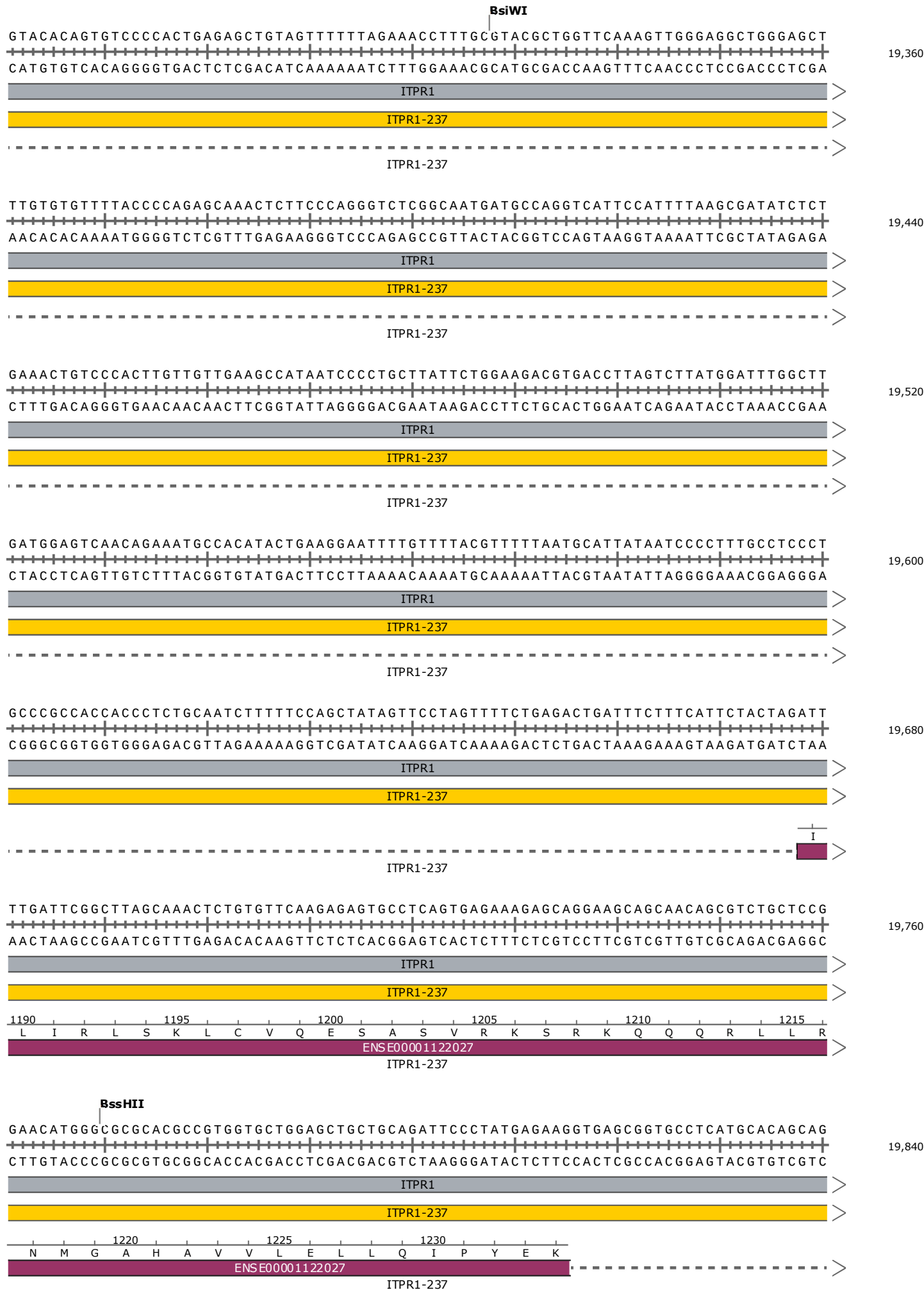
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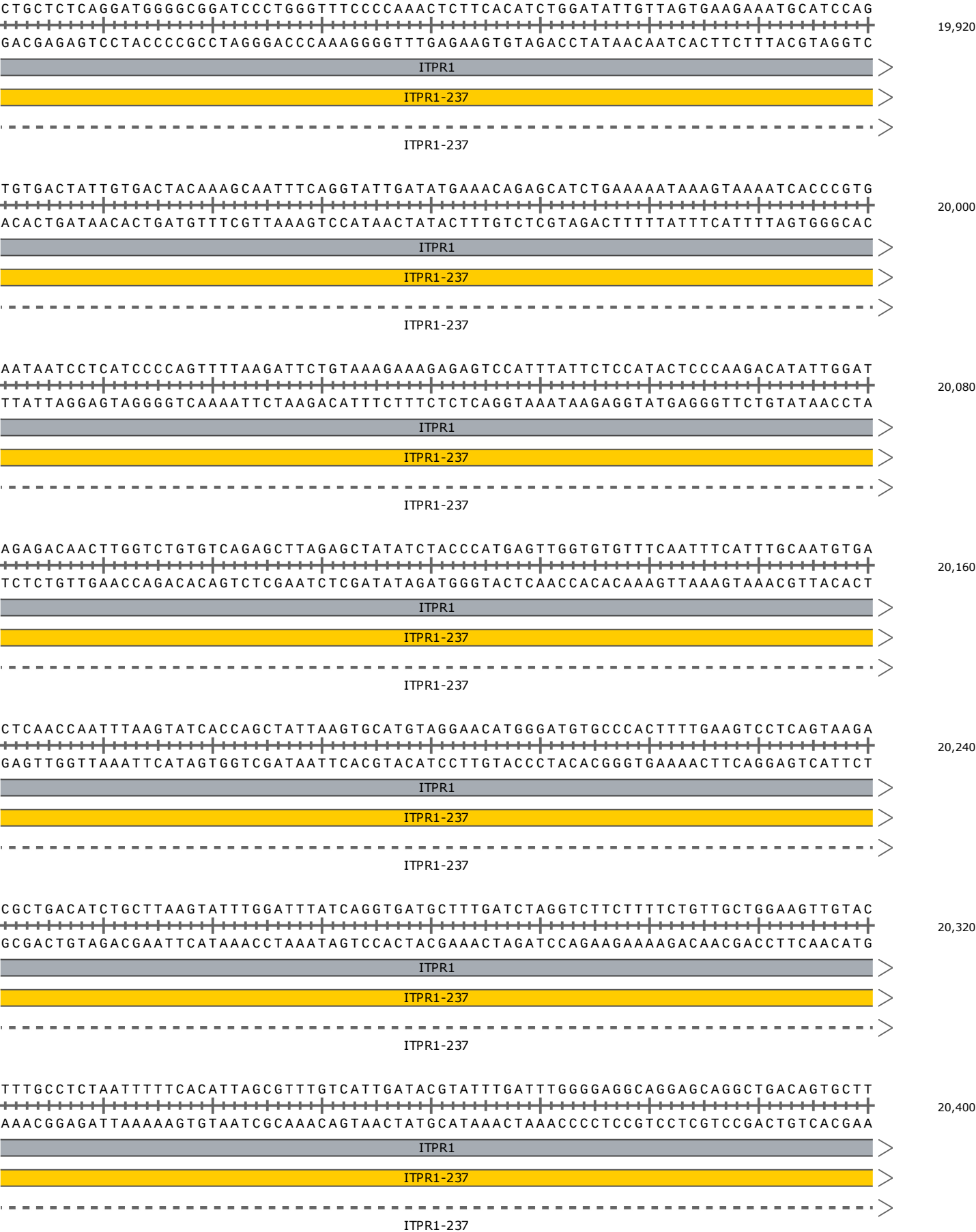
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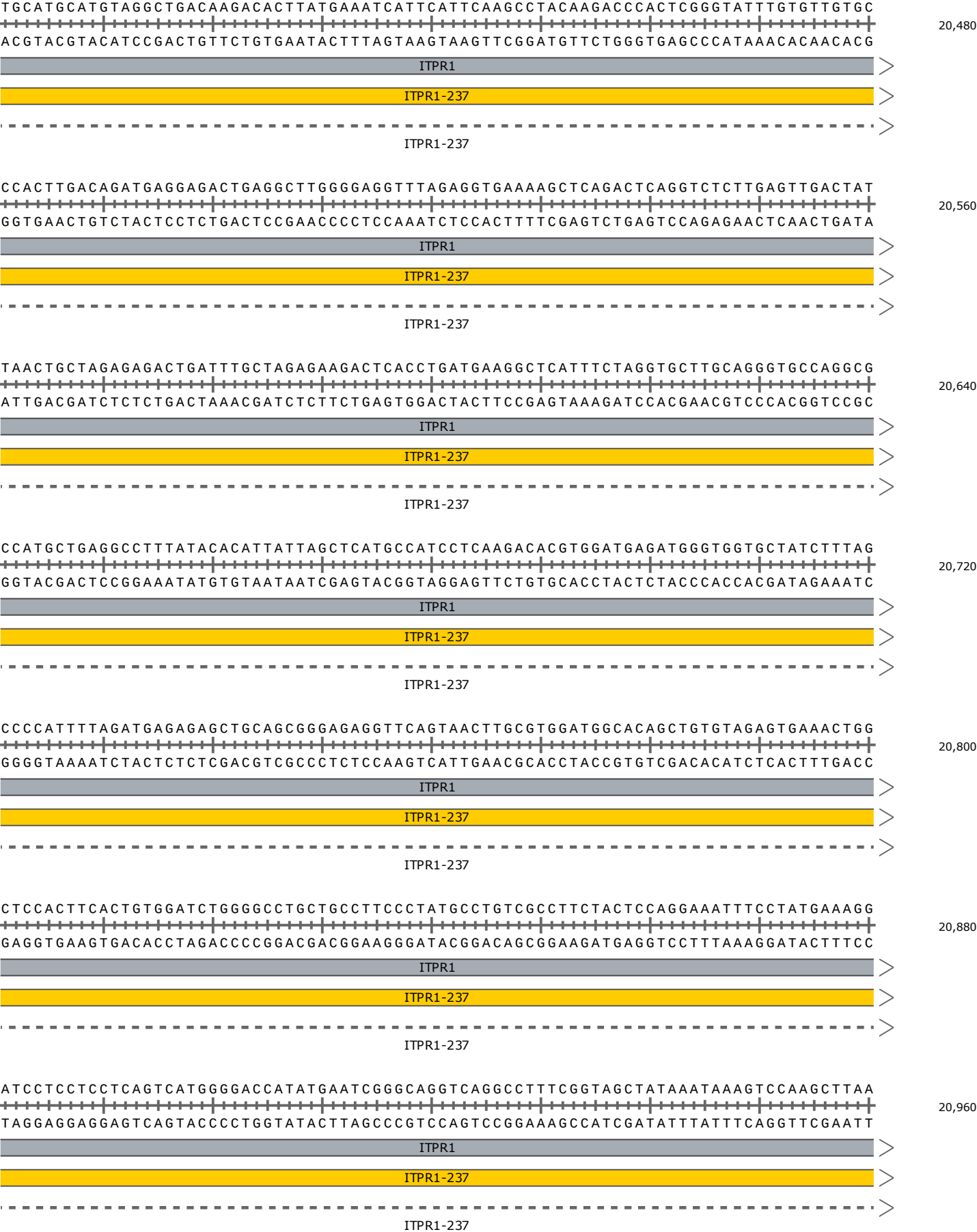
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ITPR1-237

ITPR1-237







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21,040

ITPR1

ITPR1-237

ITPR1-237

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21,120

ITPR1

ITPR1-237

ITPR1-237

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21,200

ITPR1

ITPR1-237

ITPR1-237

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21,280

ITPR1

ITPR1-237

ITPR1-237

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21,360

ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

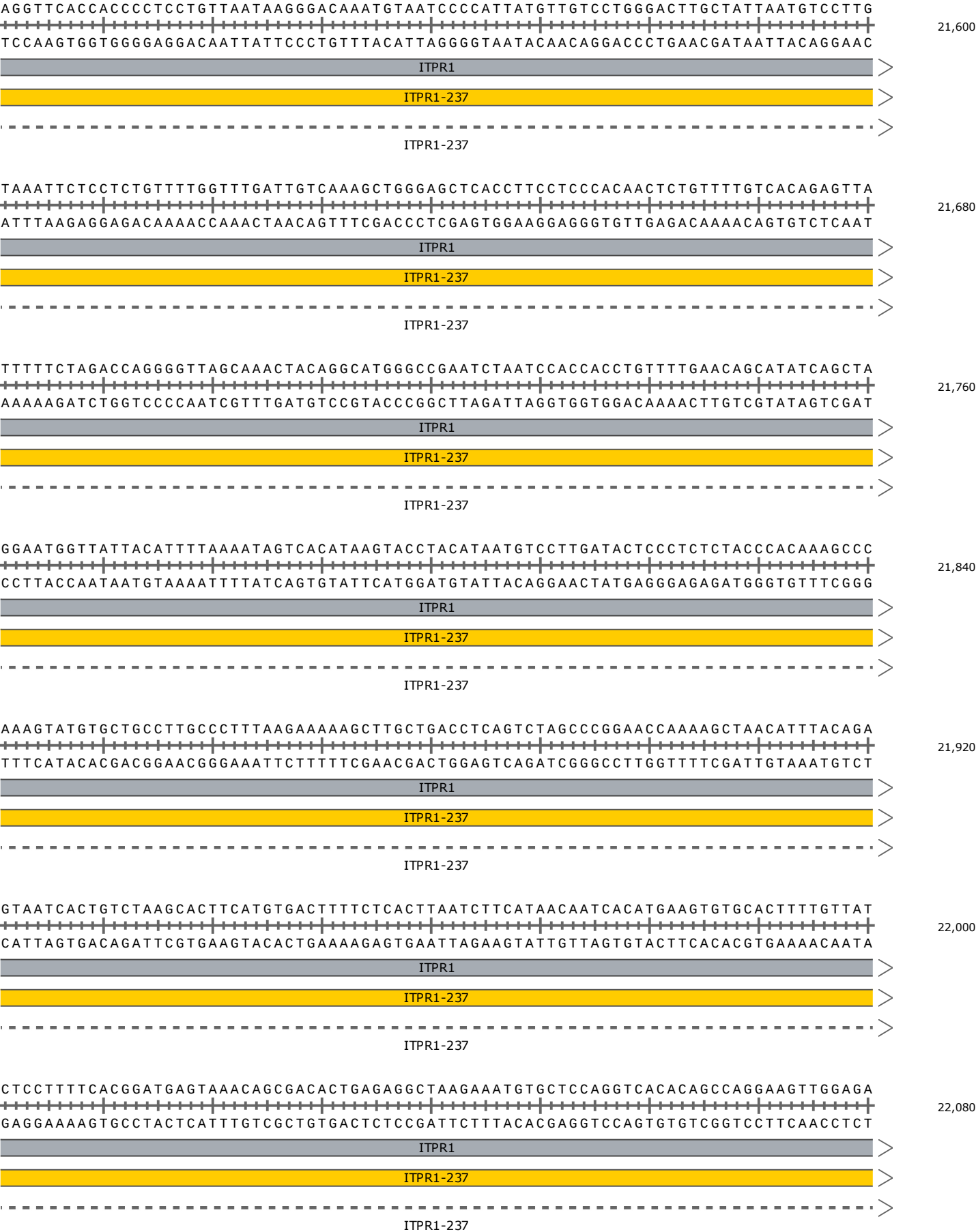
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21,520

ITPR1

ITPR1-237

ITPR1-237



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22,160

ITPR1

ITPR1-237

ITPR1-237

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22,240

ITPR1

ITPR1-237

ITPR1-237

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22,320

ITPR1

ITPR1-237

ITPR1-237

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22,400

ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

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22,560

ITPR1

ITPR1-237

ITPR1-237

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22,640

ITPR1

ITPR1-237

ITPR1-237

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23,280

ITPR1

ITPR1-237

1270 1275
K H I N L F L N P G

ENSE00001122020

ITPR1-237

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23,360

ITPR1

ITPR1-237

ITPR1-237

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23,440

ITPR1

ITPR1-237

ITPR1-237

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23,520

ITPR1

ITPR1-237

ITPR1-237

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23,600

ITPR1

ITPR1-237

ITPR1-237

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23,680

ITPR1

ITPR1-237

ITPR1-237

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23,760

ITPR1

ITPR1-237

ITPR1-237

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23,840

ITPR1

ITPR1-237

ITPR1-237

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23,920

ITPR1

ITPR1-237

ITPR1-237

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24,000

ITPR1

ITPR1-237

ITPR1-237

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24,080

ITPR1

ITPR1-237

ITPR1-237

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24,160

ITPR1

ITPR1-237

ITPR1-237

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24,240

ITPR1

ITPR1-237

ITPR1-237

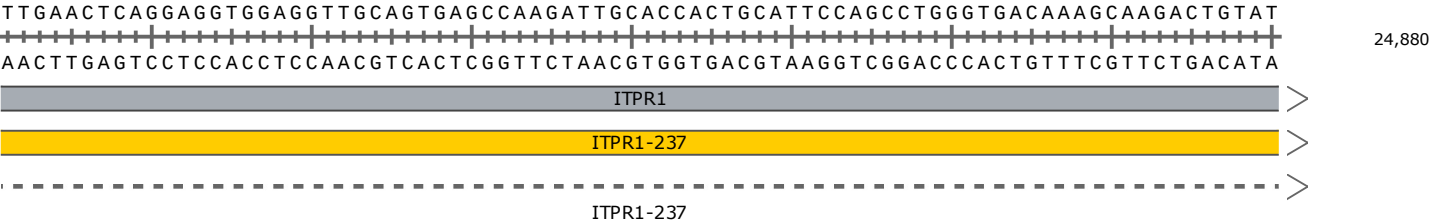
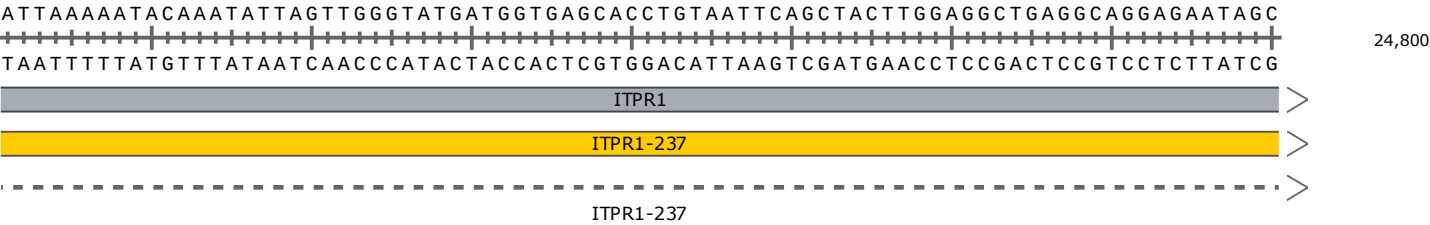
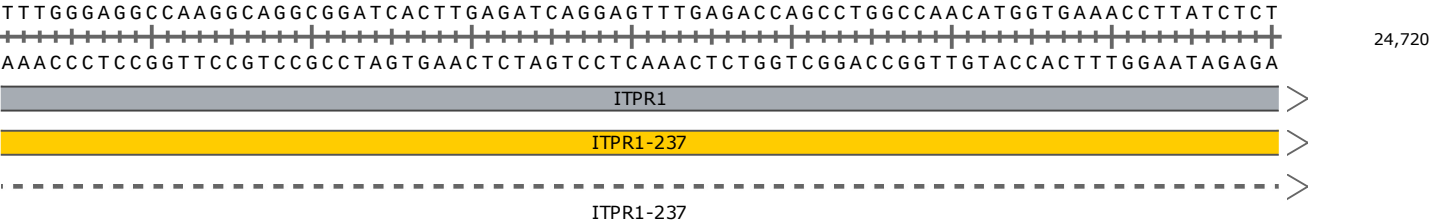
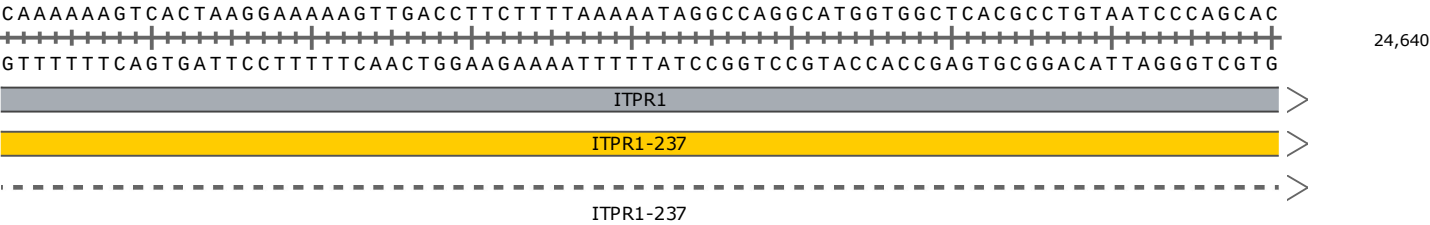
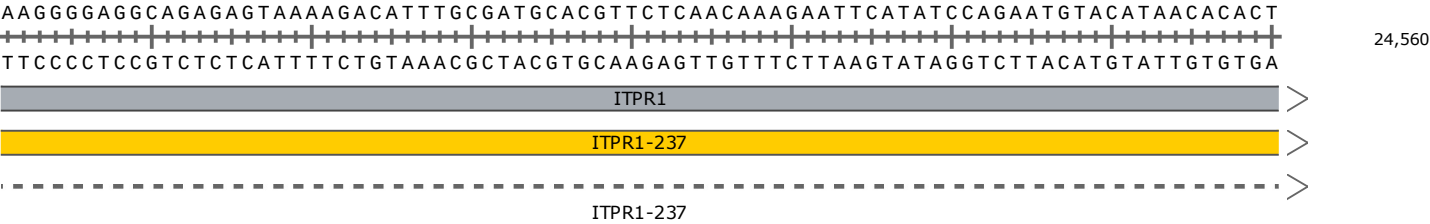
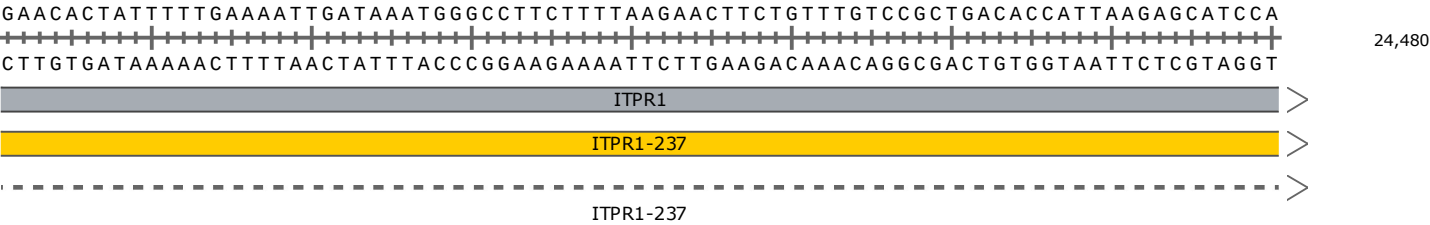
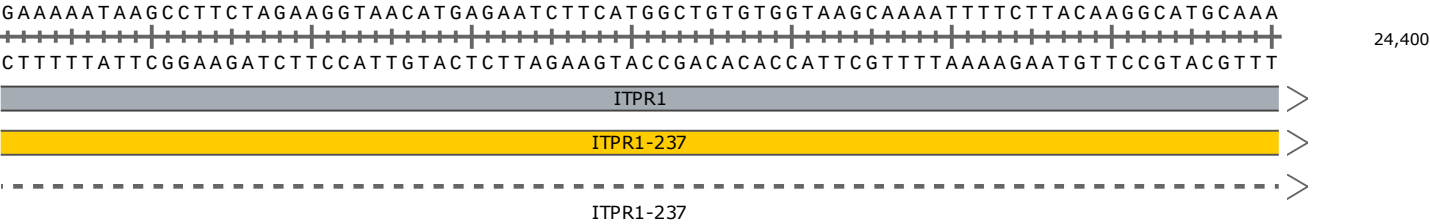
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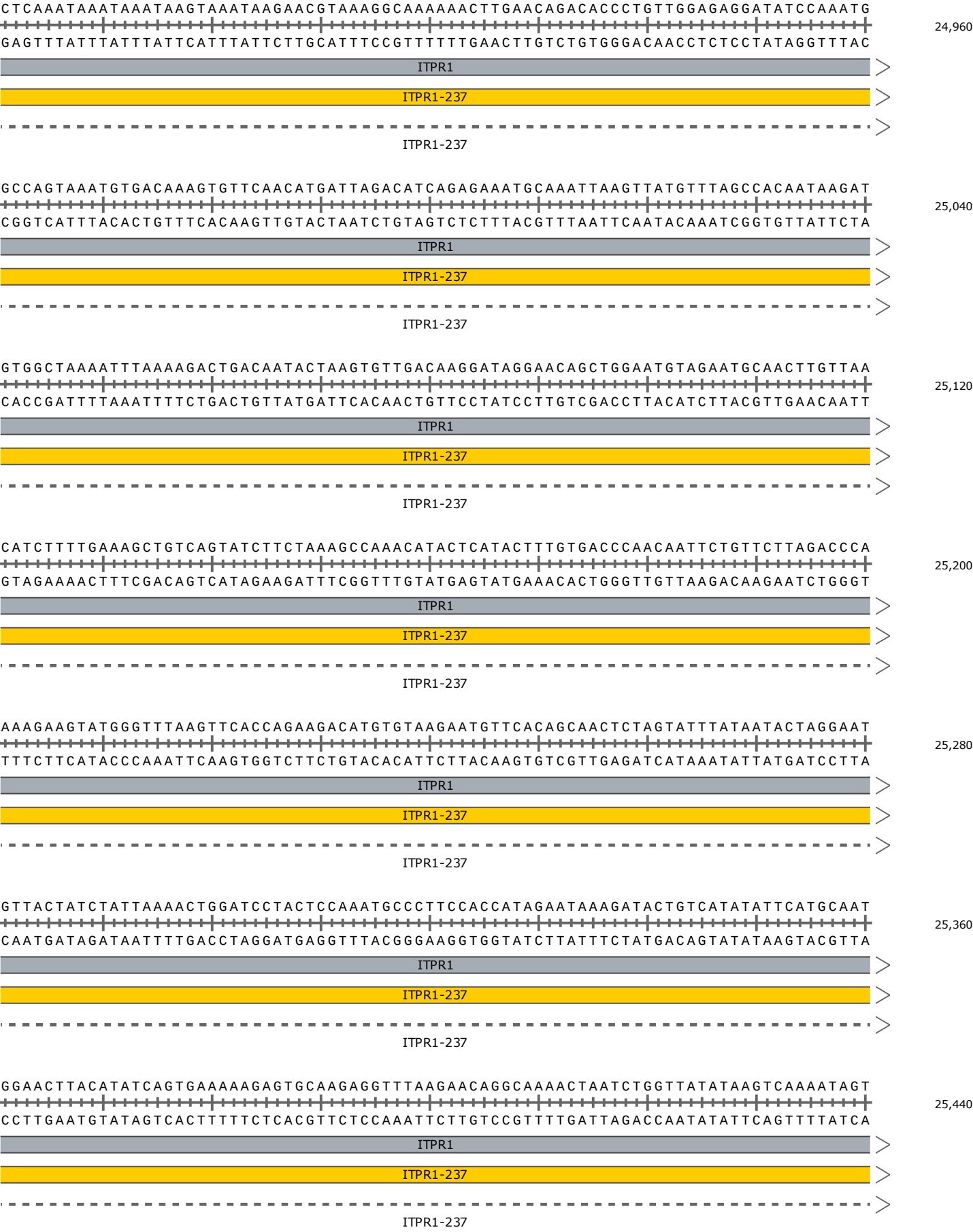
24,320

ITPR1

ITPR1-237

ITPR1-237





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25,520

ITPR1

ITPR1-237

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25,600

ITPR1

ITPR1-237

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25,680

ITPR1

ITPR1-237

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25,760

ITPR1

ITPR1-237

ITPR1-237
ENSE0000...

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25,840

ITPR1

ITPR1-237

1280 1285 1290 1295 1300 1305
A V T M Q H I F M N N F Q L C S E I N E R V V Q H F
ENSE00001122015

ITPR1-237

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25,920

ITPR1

ITPR1-237

1310 1315 1320 1325 1330
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ENSE00001122015

ITPR1-237

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26,000

ITPR1

ITPR1-237

1335 1340
I K K C Q D M V M A E
ENSE00001122015

ITPR1-237

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26,080

ITPR1

ITPR1-237

ITPR1-237

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26,160

ITPR1

ITPR1-237

ITPR1-237

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26,240

ITPR1

ITPR1-237

ITPR1-237

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26,320

ITPR1

ITPR1-237

ITPR1-237

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26,400

ITPR1

ITPR1-237

ITPR1-237

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26,480

ITPR1

ITPR1-237

ITPR1-237

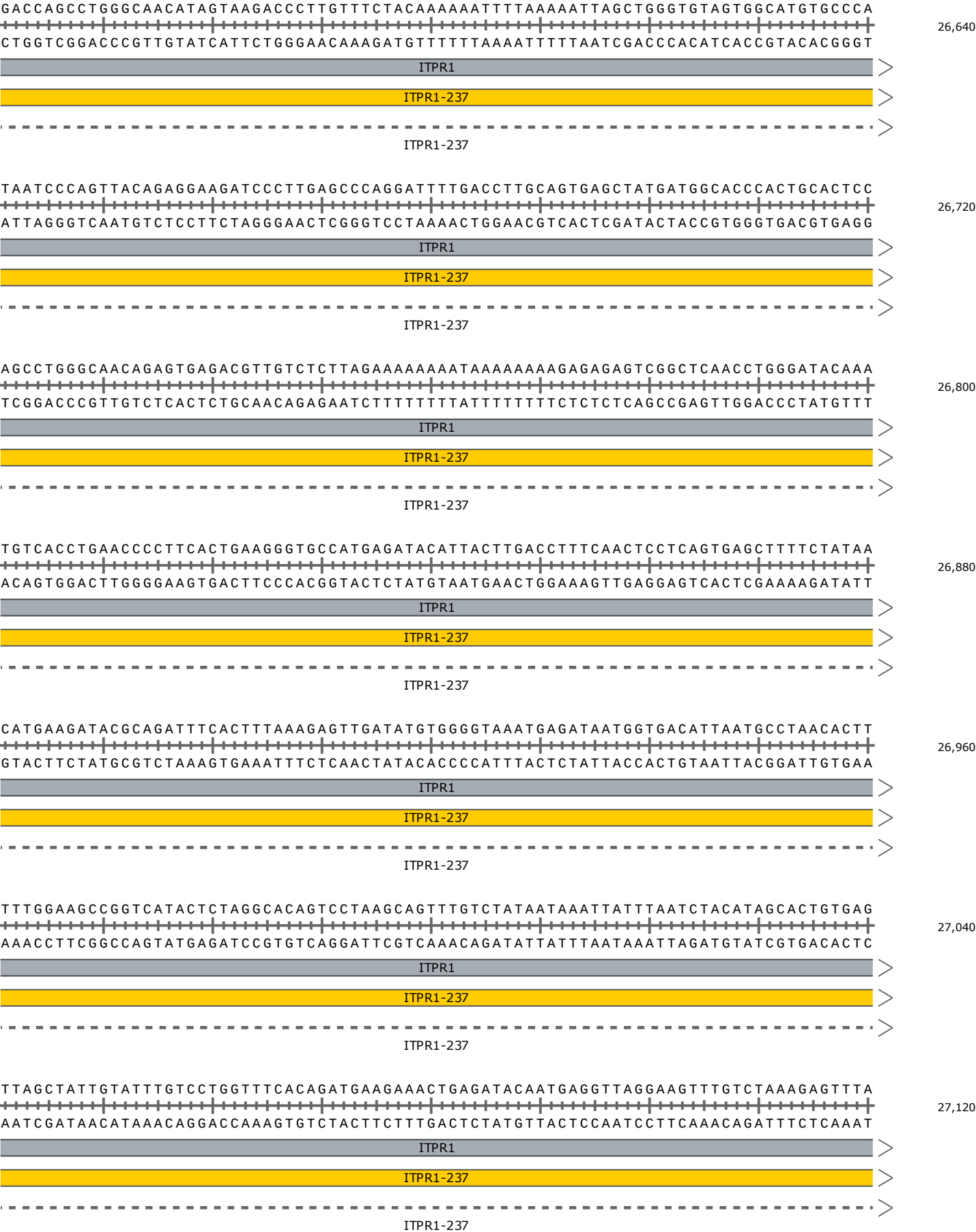
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26,560

ITPR1

ITPR1-237

ITPR1-237



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27,200

ITPR1

ITPR1-237

ITPR1-237

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27,280

ITPR1

ITPR1-237

ITPR1-237

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27,360

ITPR1

ITPR1-237

ITPR1-237

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27,440

ITPR1

ITPR1-237

ITPR1-237

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27,520

ITPR1

ITPR1-237

ITPR1-237

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27,600

ITPR1

ITPR1-237

ITPR1-237

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27,680

ITPR1

ITPR1-237

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

27,760

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ITPR1

ITPR1-237

ITPR1-237

27,840

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ITPR1

ITPR1-237

ITPR1-237

27,920

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ITPR1

ITPR1-237

ITPR1-237

28,000

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ITPR1

ITPR1-237

ITPR1-237

28,080

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ITPR1

ITPR1-237

ITPR1-237

1345 1350 1355 1360
L V N S G E D V L V F Y N D R A S F Q T L

ENSE00001122009

ITPR1-237

28,160

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ITPR1

ITPR1-237

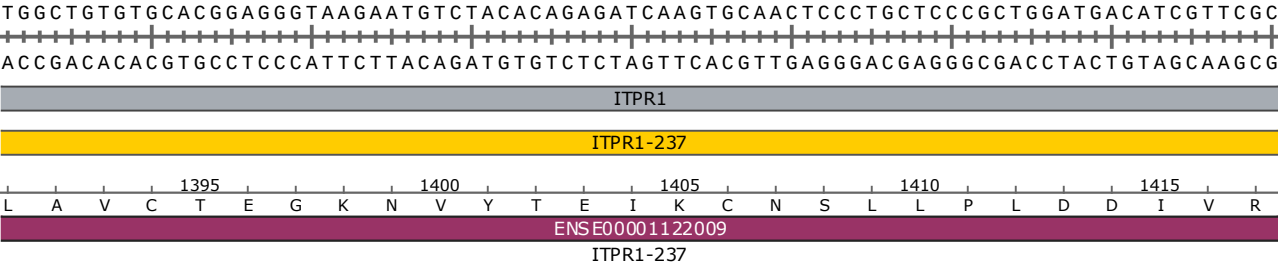
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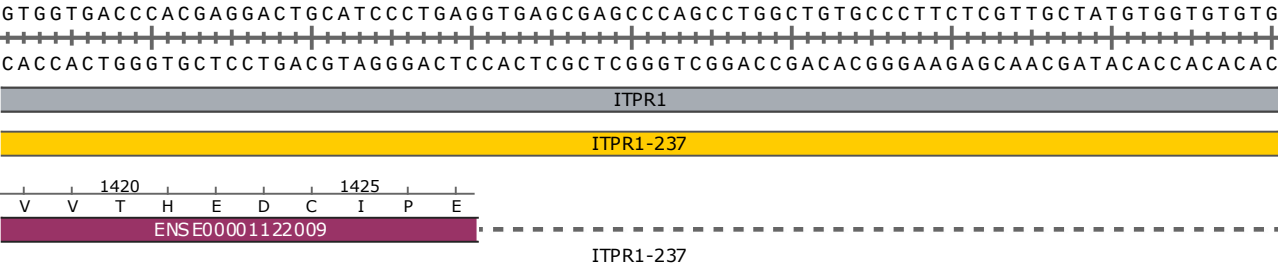
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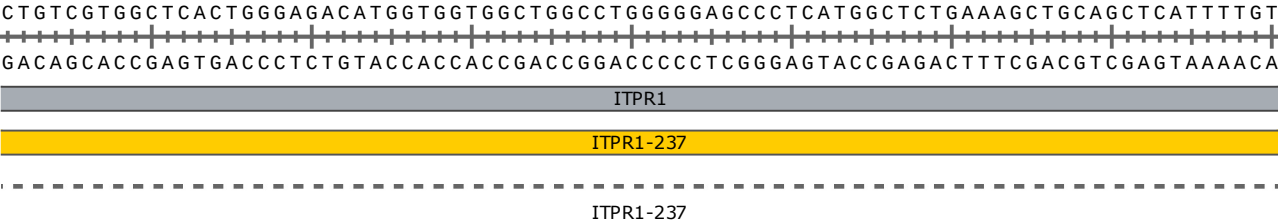
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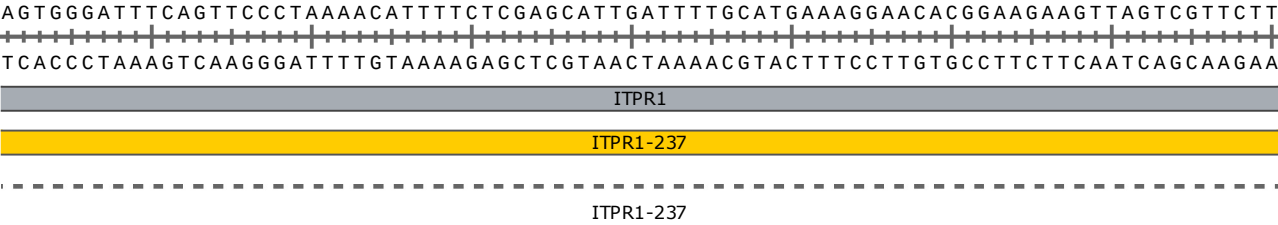
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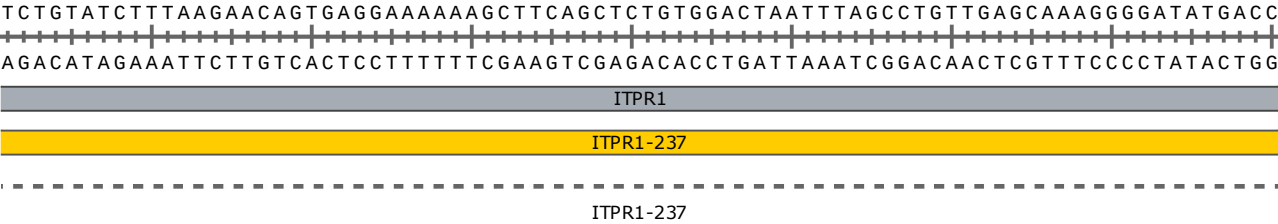
28,400



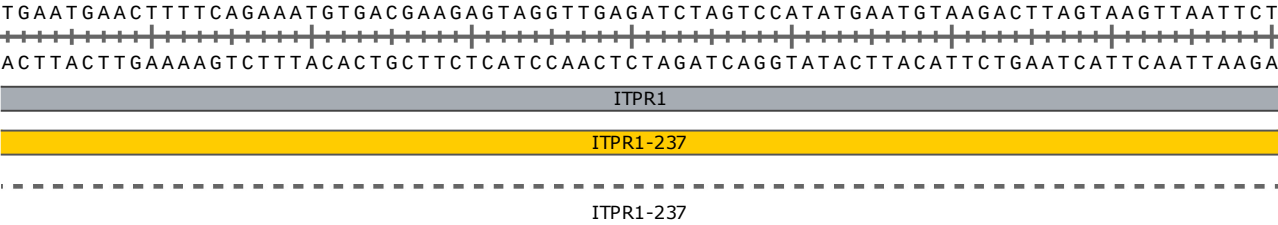
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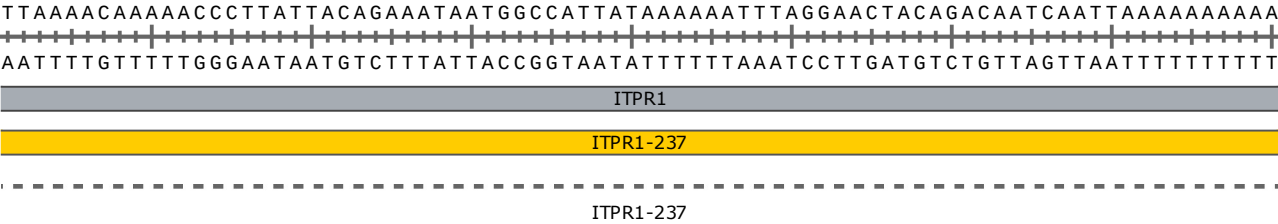
28,560



28,640



28,720



28,800

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28,880

ITPR1

ITPR1-237

ITPR1-237

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28,960

ITPR1

ITPR1-237

ITPR1-237

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29,040

ITPR1

ITPR1-237

ITPR1-237

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29,120

ITPR1

ITPR1-237

ITPR1-237

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29,200

ITPR1

ITPR1-237

ITPR1-237

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29,280

ITPR1

ITPR1-237

ITPR1-237

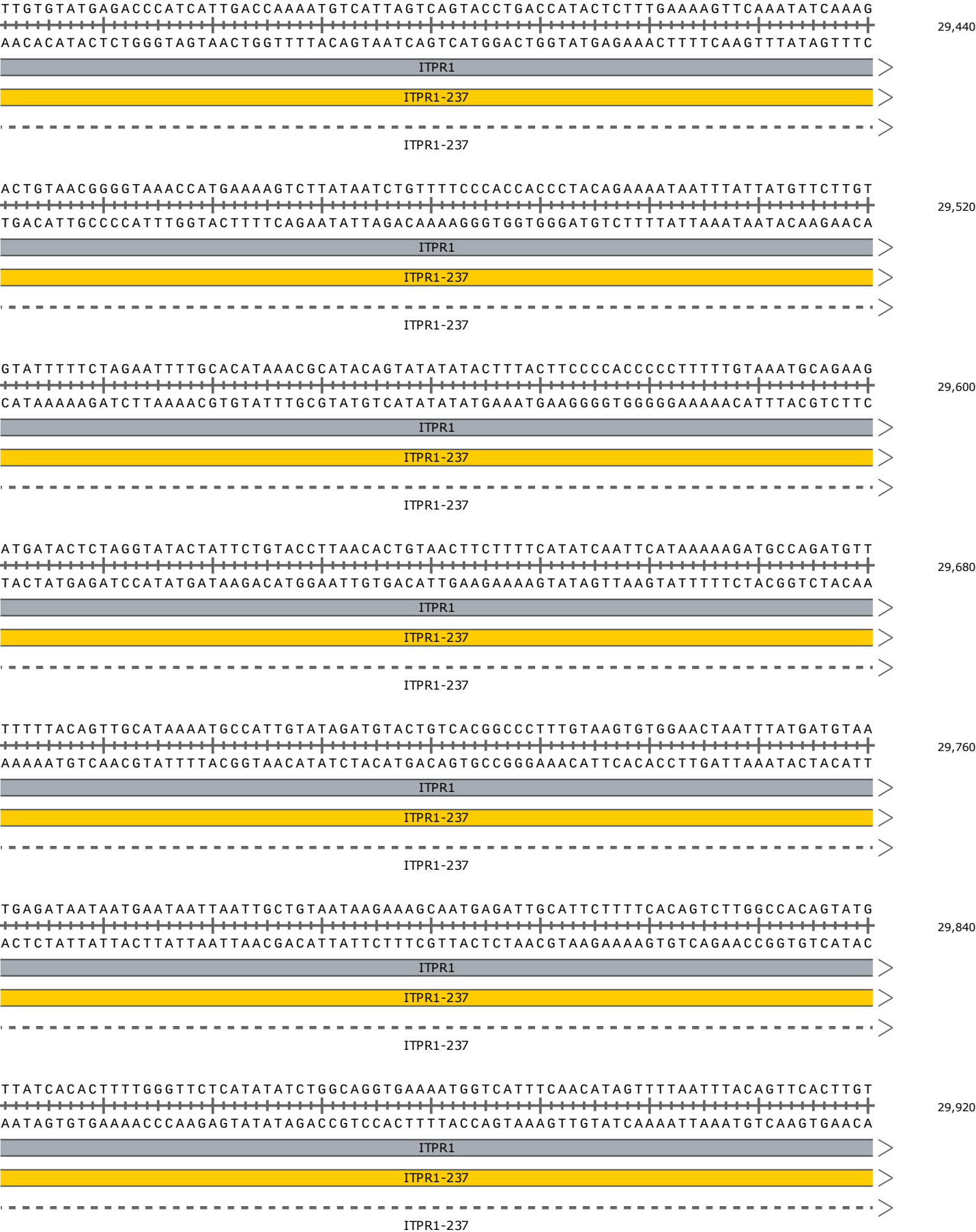
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29,360

ITPR1

ITPR1-237

ITPR1-237



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30,000

ITPR1

ITPR1-237

ITPR1-237

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30,080

ITPR1

ITPR1-237

ITPR1-237

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30,160

ITPR1

ITPR1-237

ITPR1-237

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30,240

ITPR1

ITPR1-237

ITPR1-237

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30,320

ITPR1

ITPR1-237

ITPR1-237

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30,400

ITPR1

ITPR1-237

ITPR1-237

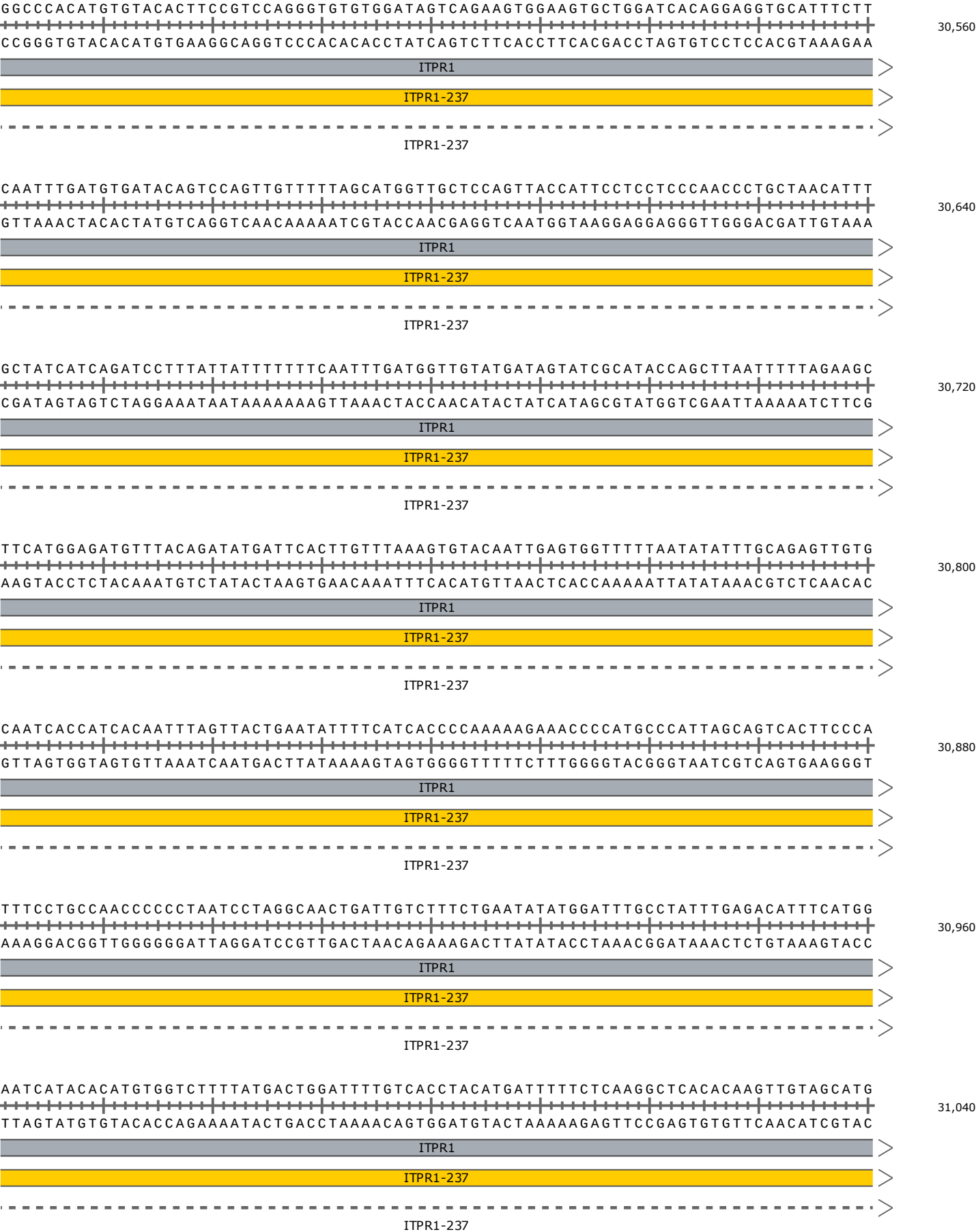
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30,480

ITPR1

ITPR1-237

ITPR1-237



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31,120

ITPR1

ITPR1-237

ITPR1-237

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31,200

ITPR1

ITPR1-237

ITPR1-237

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31,280

ITPR1

ITPR1-237

ITPR1-237

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31,360

ITPR1

ITPR1-237

ITPR1-237

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31,440

ITPR1

ITPR1-237

ITPR1-237

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31,520

ITPR1

ITPR1-237

ITPR1-237

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31,600

ITPR1

ITPR1-237

ITPR1-237

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32,240

ITPR1

ITPR1-237

ITPR1-237

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32,320

ITPR1

ITPR1-237

ITPR1-237

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32,400

ITPR1

ITPR1-237

ITPR1-237

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32,480

ITPR1

ITPR1-237

ITPR1-237

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32,560

ITPR1

ITPR1-237

ITPR1-237

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32,640

ITPR1

ITPR1-237

ITPR1-237

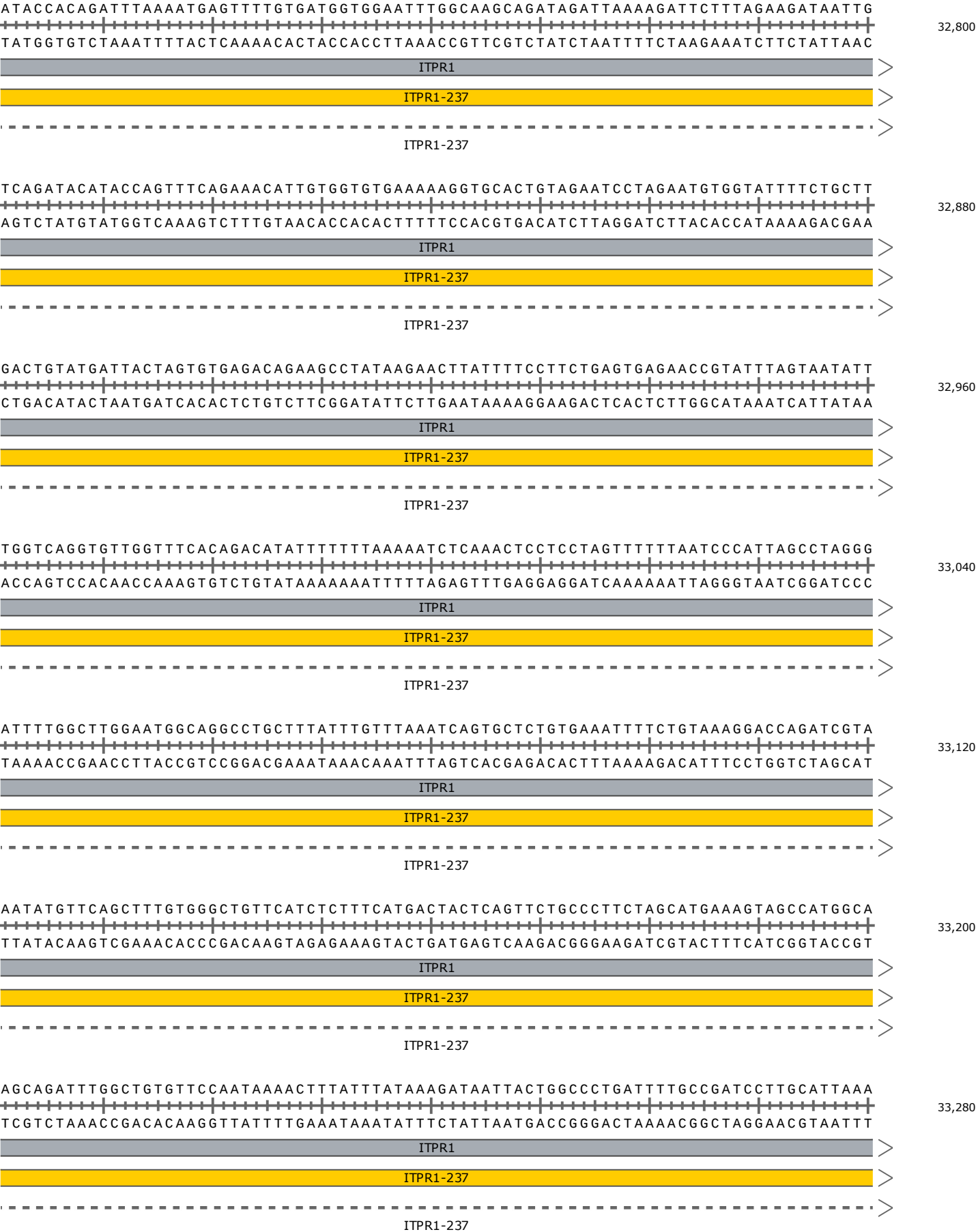
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32,720

ITPR1

ITPR1-237

ITPR1-237



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33,360

ITPR1

ITPR1-237

ITPR1-237

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33,440

ITPR1

ITPR1-237

ITPR1-237

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33,520

ITPR1

ITPR1-237

ITPR1-237

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33,600

ITPR1

ITPR1-237

ITPR1-237

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33,680

ITPR1

ITPR1-237

ITPR1-237

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33,760

ITPR1

ITPR1-237

ITPR1-237

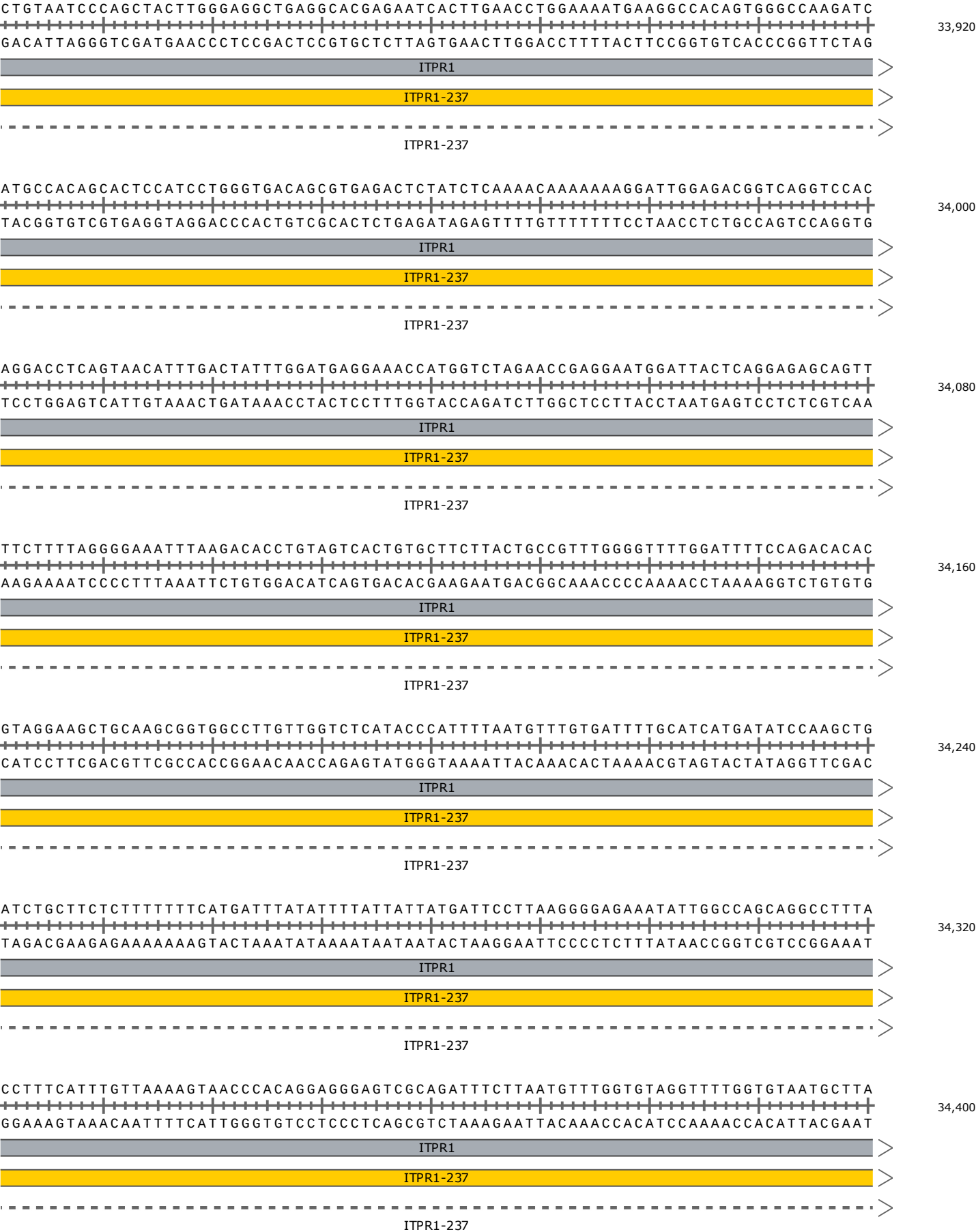
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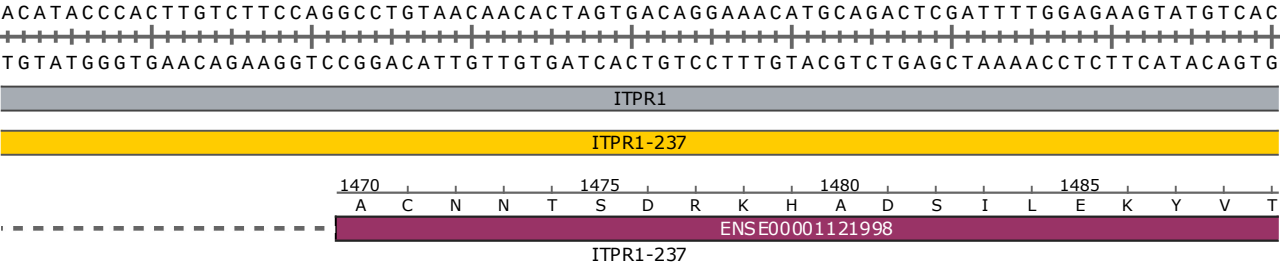
33,840

ITPR1

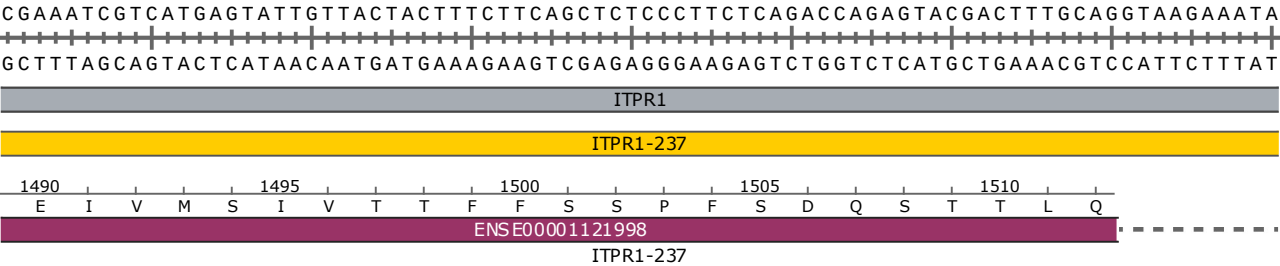
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ITPR1-237

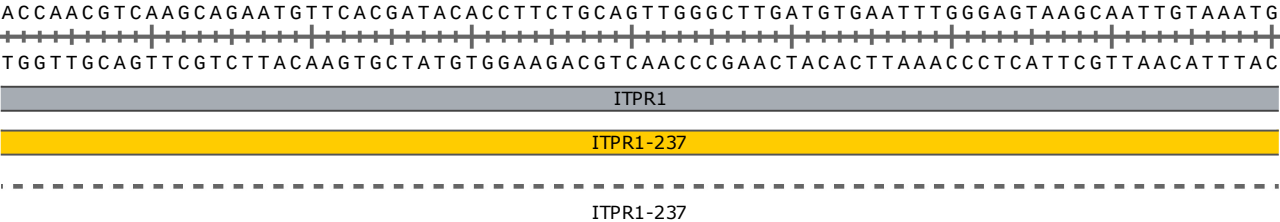




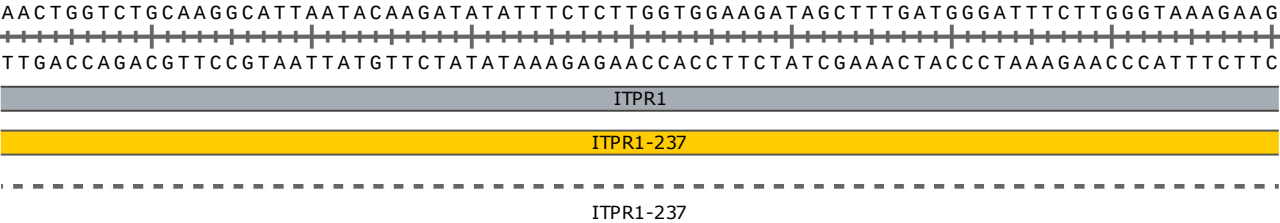
34,480



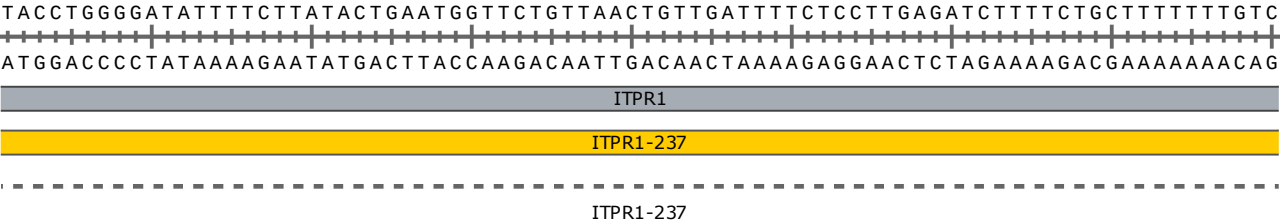
34,560



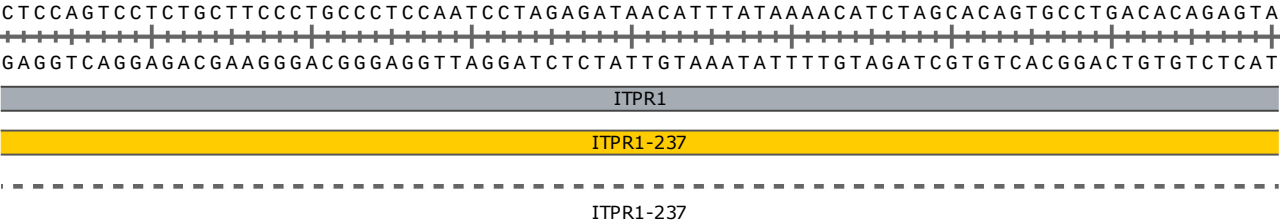
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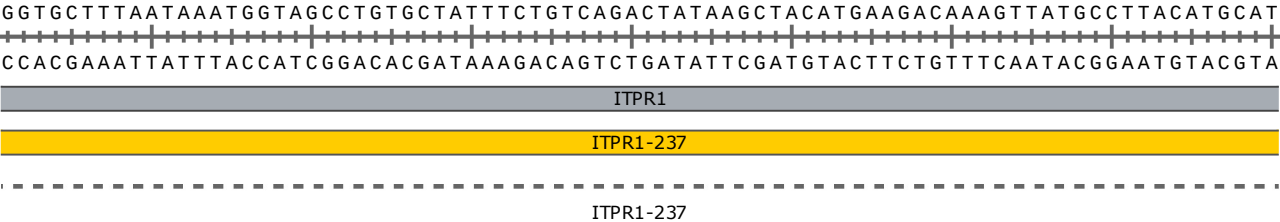
34,720



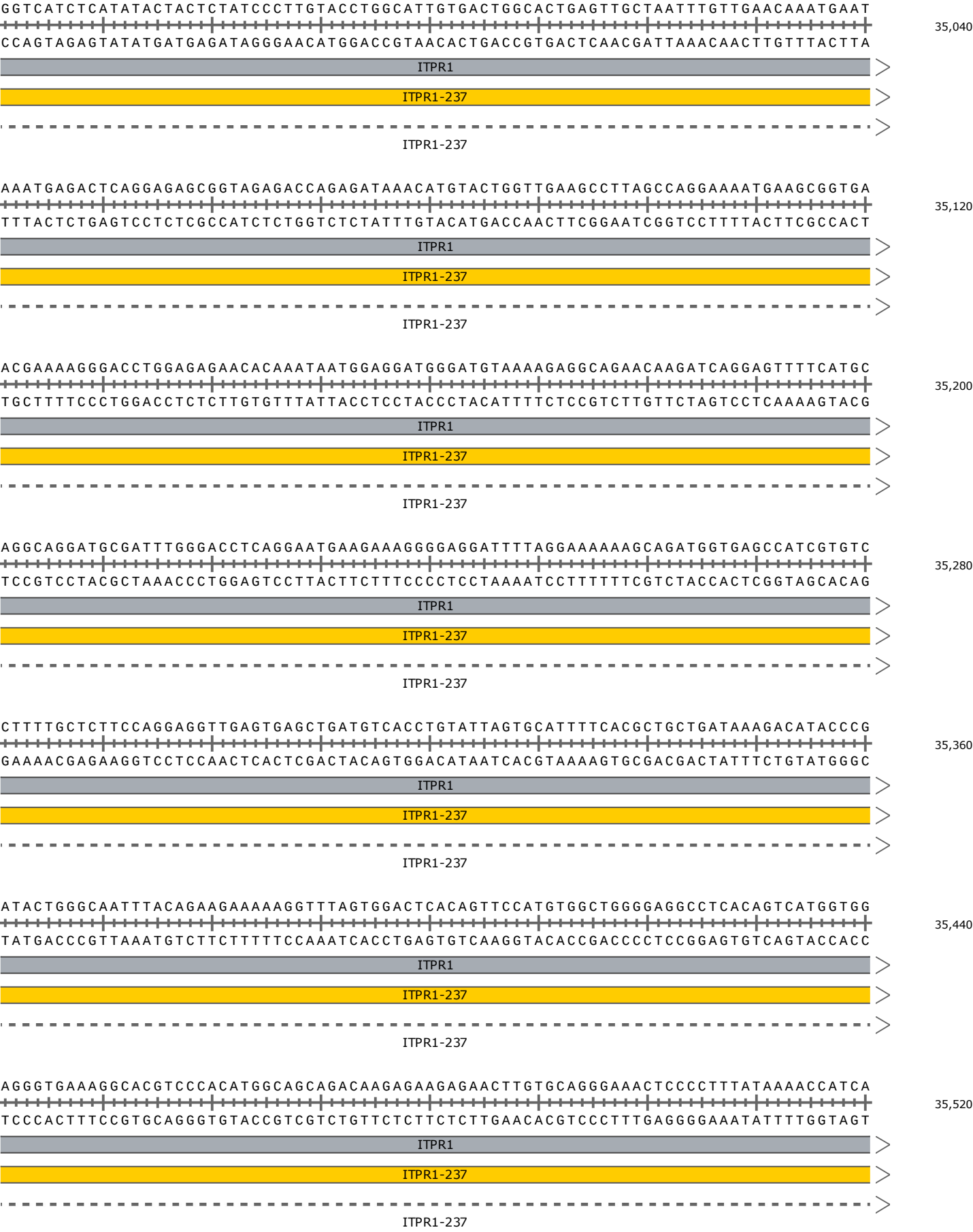
34,800

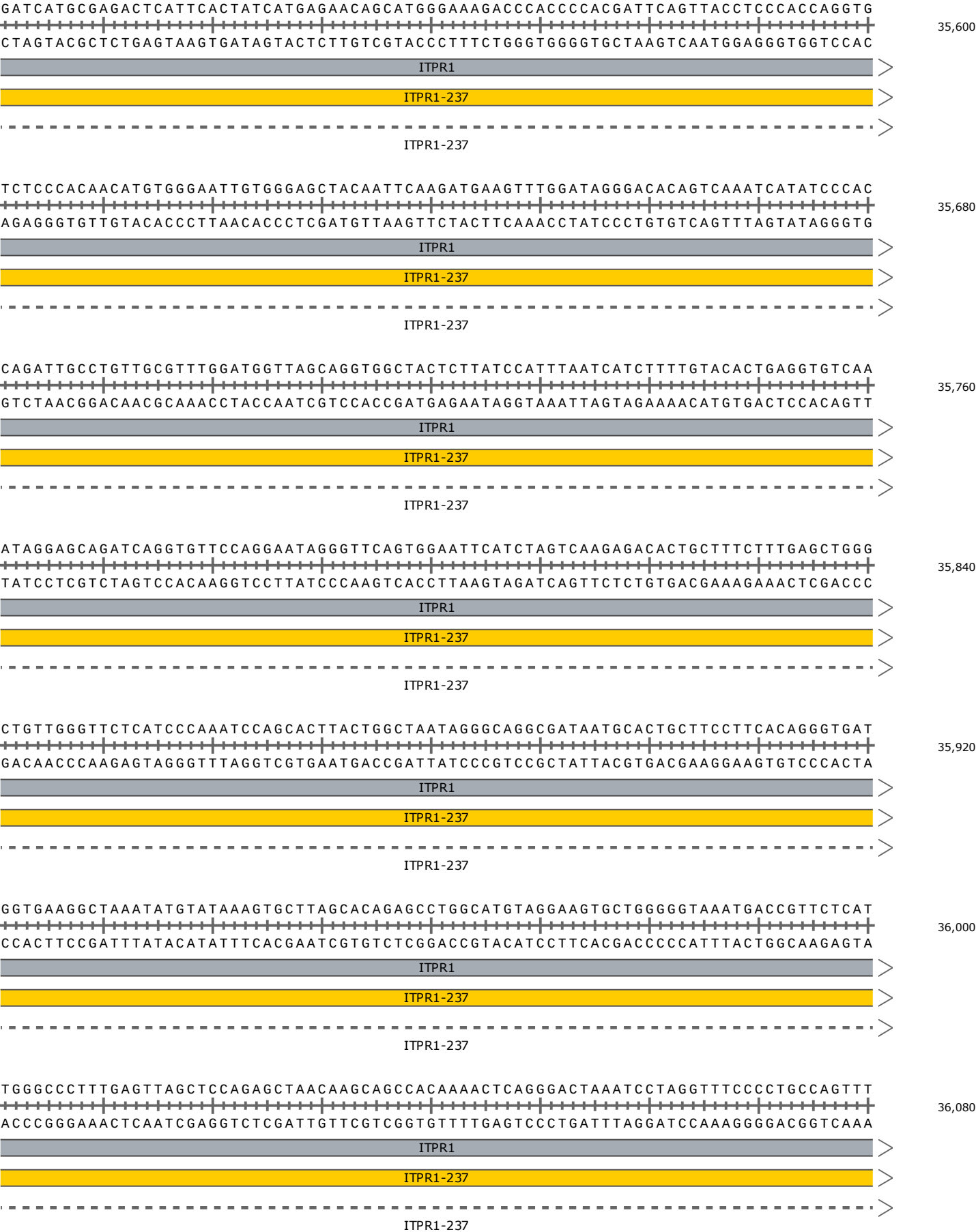


34,880



34,960





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ITPR1
ITPR1-237
ITPR1-237

36,160

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ITPR1
ITPR1-237
ITPR1-237

36,240

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ITPR1
ITPR1-237
ITPR1-237

36,320

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ITPR1
ITPR1-237
ITPR1-237

36,400

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ITPR1
ITPR1-237
ITPR1-237

36,480

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ITPR1
ITPR1-237
ITPR1-237

36,560

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ITPR1
ITPR1-237
ITPR1-237

36,640

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36,720

ITPR1

ITPR1-237

ITPR1-237

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36,800

ITPR1

ITPR1-237

ITPR1-237

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36,880

ITPR1

ITPR1-237

ITPR1-237

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36,960

ITPR1

ITPR1-237

ITPR1-237

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37,040

ITPR1

ITPR1-237

ITPR1-237

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37,120

ITPR1

ITPR1-237

ITPR1-237

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37,200

ITPR1

ITPR1-237

ITPR1-237

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37,280

ITPR1

ITPR1-237

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37,360

ITPR1

ITPR1-237

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37,440

ITPR1

ITPR1-237

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37,520

ITPR1

ITPR1-237

1515 1520 1525 1530 1535
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ENSE00001121993

ITPR1-237

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37,600

ITPR1

ITPR1-237

1540 1545 1550
A S V E S C I R V L S D V

ENSE00001121993

ITPR1-237

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37,680

ITPR1

ITPR1-237

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37,760

ITPR1

ITPR1-237

ITPR1-237

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37,840

ITPR1

ITPR1-237

ITPR1-237

CACAGCTTATTCAAGGCCCTGGGAAGTCCTCATTCAAGAACTAATTTGTTTAATCCAGCAAATGTACTTGACCATGTG
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37,920

ITPR1

ITPR1-237

ITPR1-237

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38,000

ITPR1

ITPR1-237

ITPR1-237

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38,080

ITPR1

ITPR1-237

ITPR1-237

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38,160

ITPR1

ITPR1-237

ITPR1-237

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38,240

ITPR1

ITPR1-237

ITPR1-237

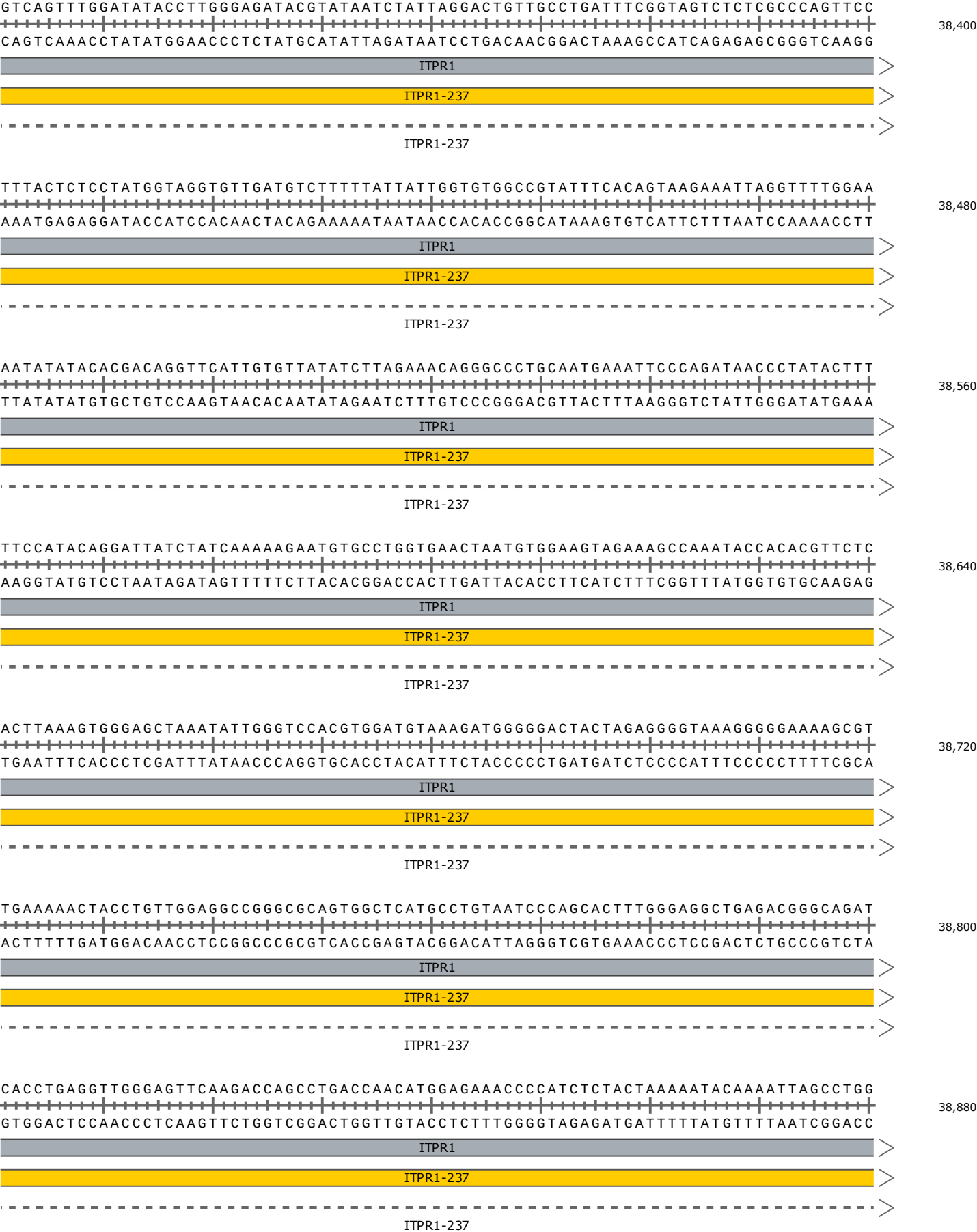
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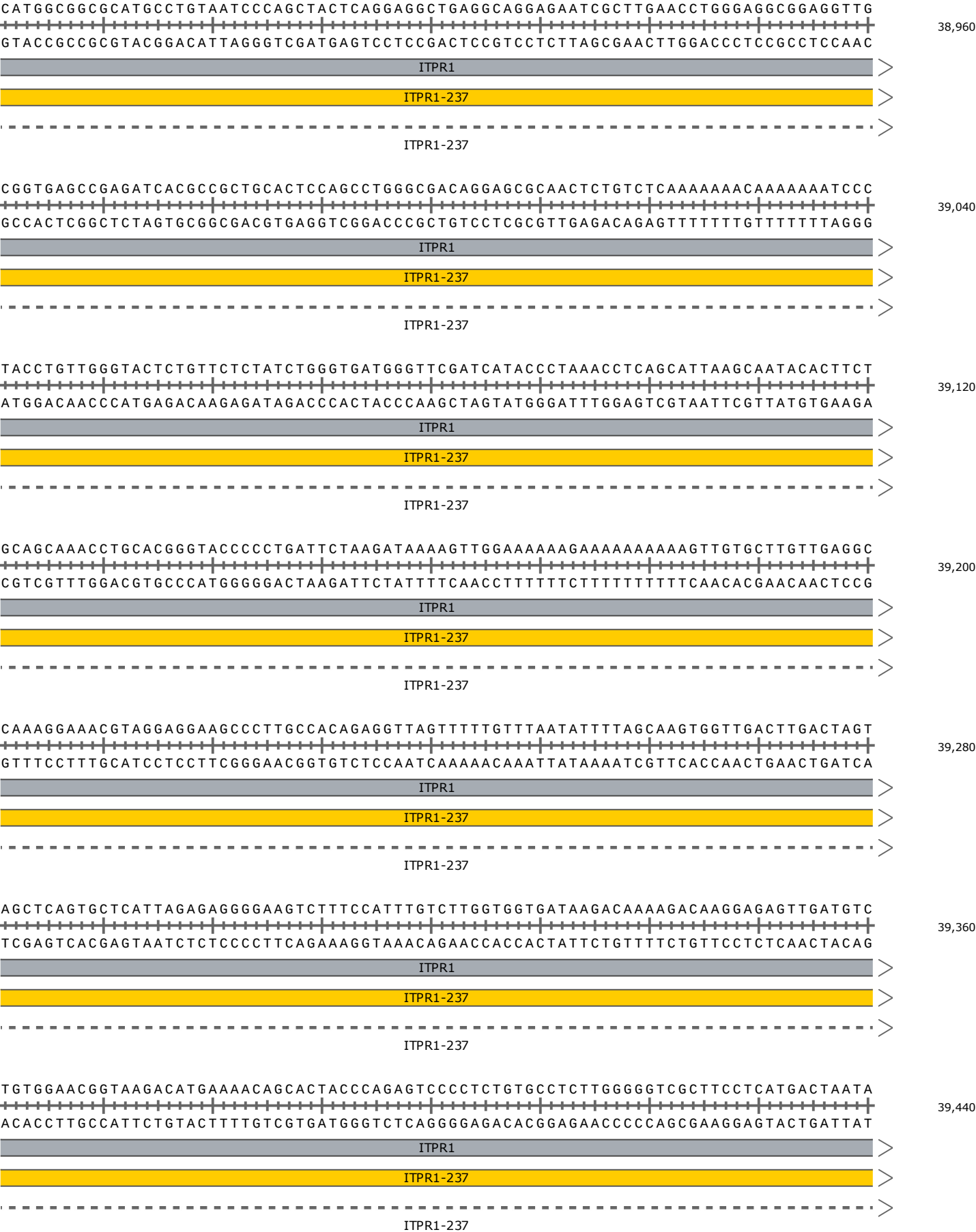
38,320

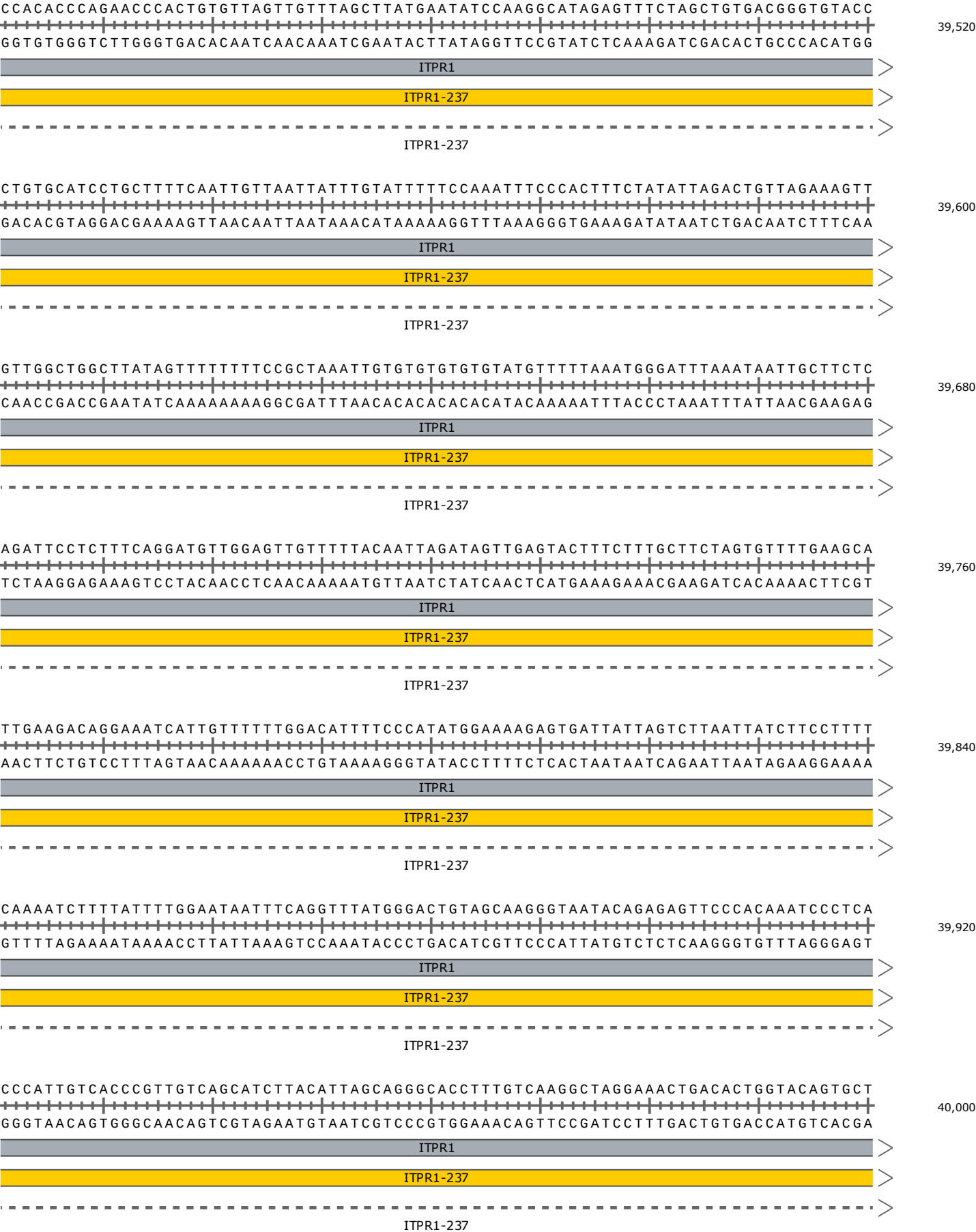
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ITPR1-237

ITPR1-237







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40,080

ITPR1

ITPR1-237

ITPR1-237

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40,160

ITPR1

ITPR1-237

ITPR1-237

CCTTGTTTCTTATGACCTTGACAGTCTTGACAAGTACTAGTCAGGAGTCTGTAGAGTGTCTCCATTATGGGTTTGACT
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40,240

ITPR1

ITPR1-237

ITPR1-237

GATGTTTGTCTCATGCTTAGACTGGAGTTCTCCTTTTTTAAGACGAAGAAAGAAGCACCTATCCAGAAAGAGGAGTTTAT
CTACAAACAGAGTACGAATCTGACCTCAAGAGGAAAAAATTCTGCTTCTTCTTCGTGGATAGGTCTTCTCCTCAAATA

40,320

ITPR1

ITPR1-237

ITPR1-237

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CGGTAACACTTACGATGGAAATCCTAATACAAACCCTATTGGGTCGTAAAAACATCTAACAACCTGTTTGGACTTTTTAT

40,400

ITPR1

ITPR1-237

ITPR1-237

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40,480

ITPR1

ITPR1-237

ITPR1-237

AAGCCATTTCATTGAGGAAACCCATTGAACTTTAACTCTGACATGCCCTGGCCTTATGACCTGAGAGCATTTTAACATTCC
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40,560

ITPR1

ITPR1-237

ITPR1-237

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40,640

ITPR1

ITPR1-237

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40,720

ITPR1

ITPR1-237

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40,800

ITPR1

ITPR1-237

ITPR1-237
ENSE00001121989

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40,880

ITPR1

ITPR1-237

V D L D S Q V N N L F L K S H S I V Q K T A M N W R
ENSE00001121989

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40,960

ITPR1

ITPR1-237

L S A R N A A R D S V L A A S R D Y R N I I E R L Q
ENSE00001121989

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41,040

ITPR1

ITPR1-237

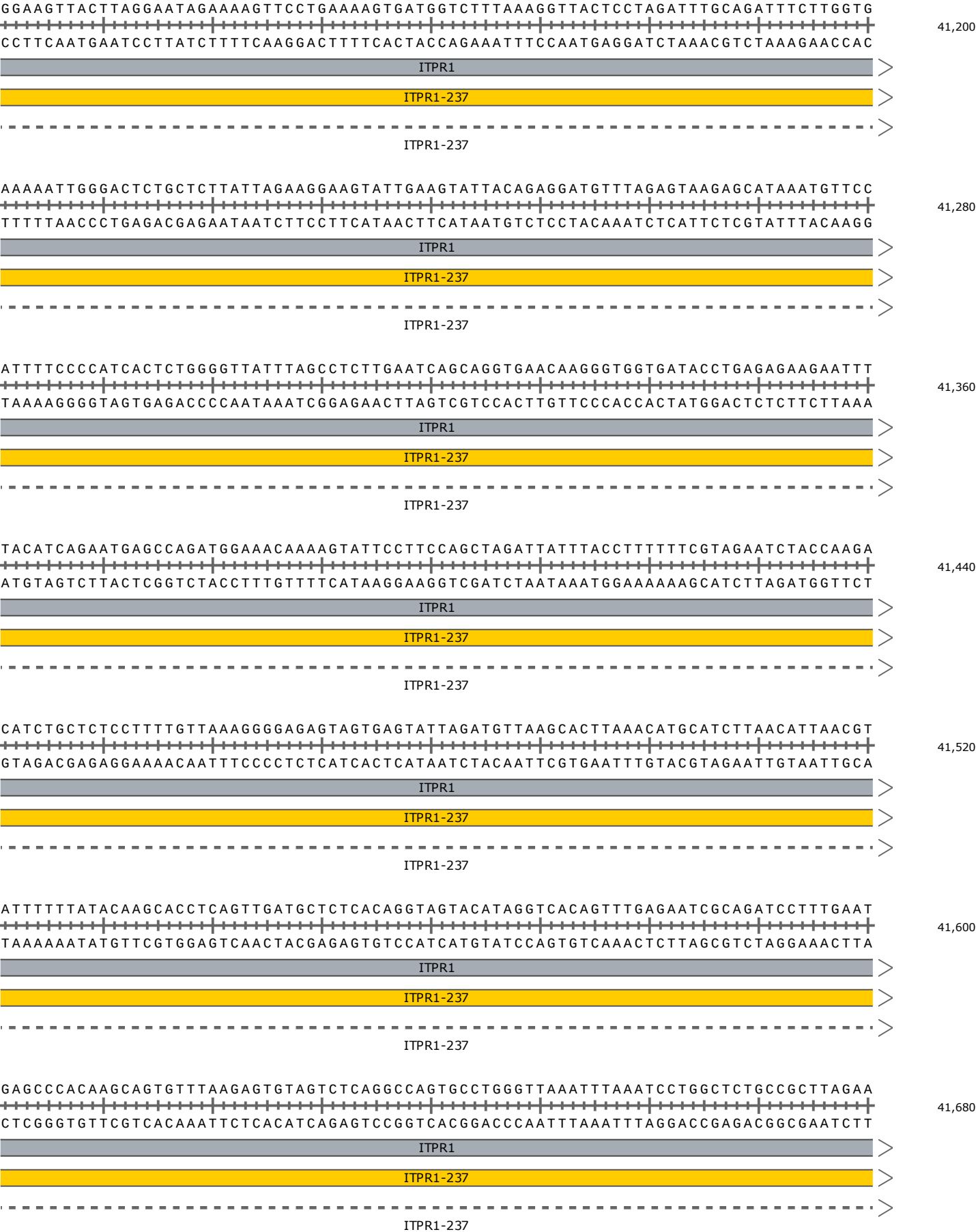
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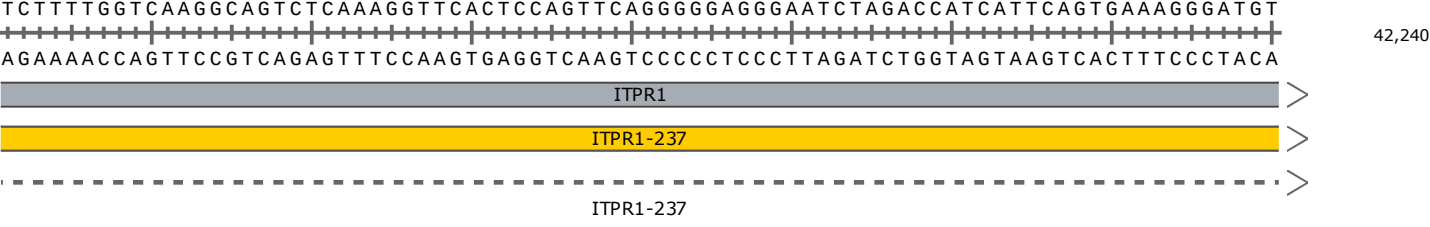
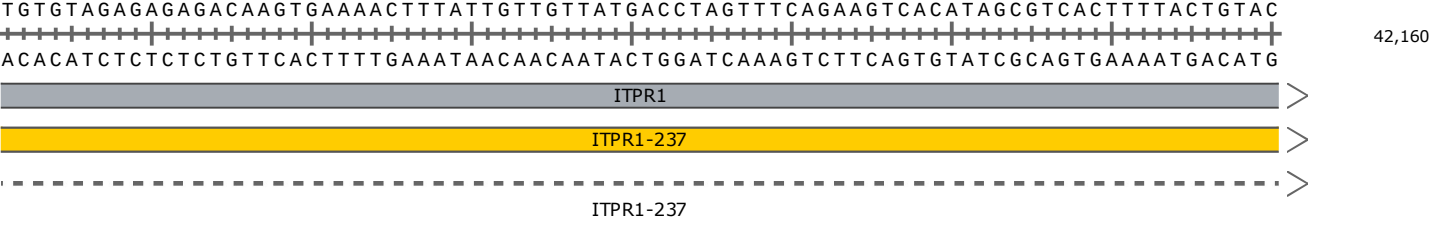
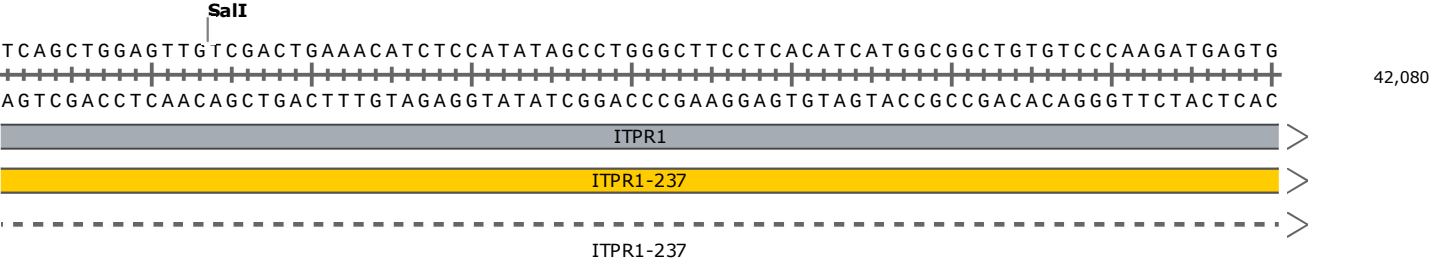
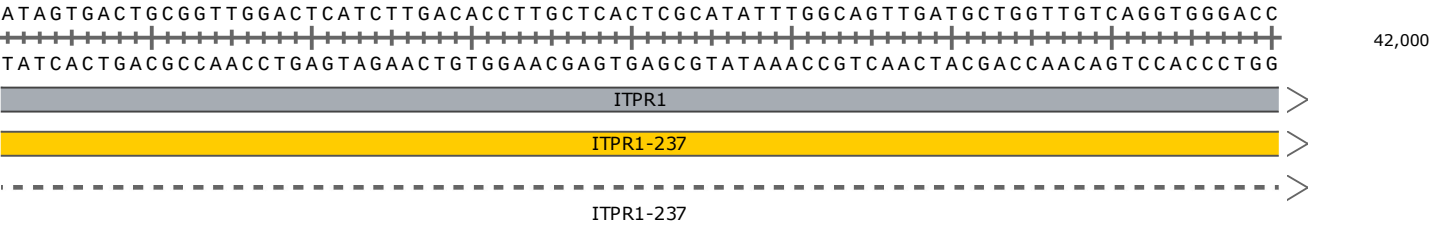
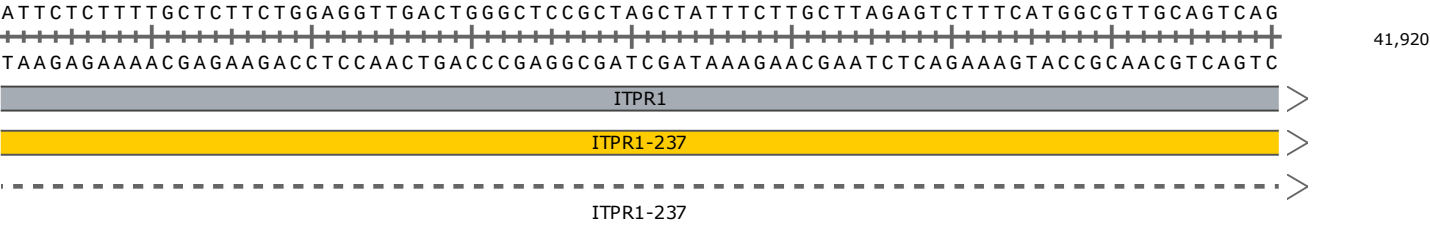
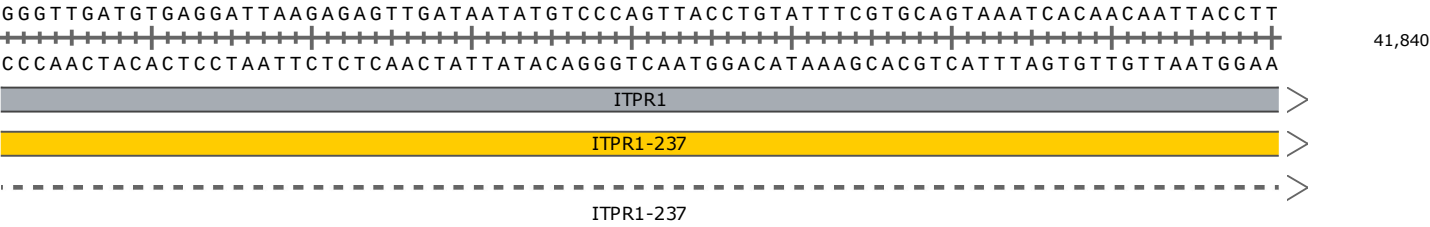
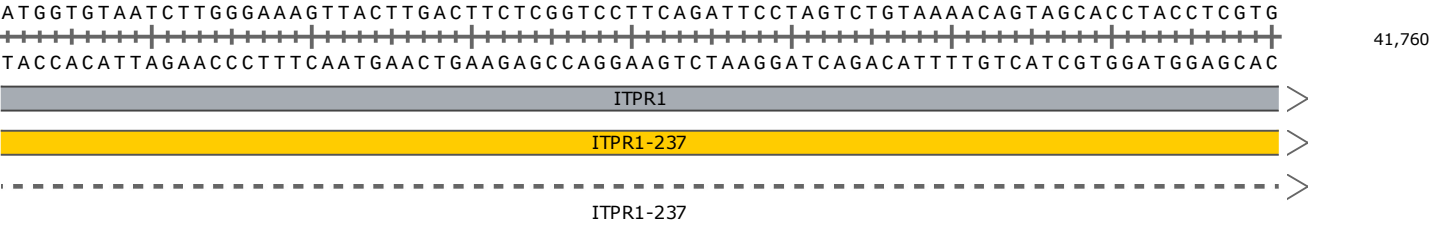
41,120

ITPR1

ITPR1-237

ITPR1-237





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42,320

ITPR1

ITPR1-237

ITPR1-237

ACACATAGAGCAGTGCCTGGCATGTAGTGAGCACTCAGTTGAGGGCTGCTATTATTATTATTACTATTATTACTGTTGTT
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42,400

ITPR1

ITPR1-237

ITPR1-237

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42,480

ITPR1

ITPR1-237

ITPR1-237

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42,560

ITPR1

ITPR1-237

ITPR1-237

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42,640

ITPR1

ITPR1-237

ITPR1-237

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CGCGAACTTTCTAAGACTACTCCTTTGATTAAACAGACTCCAATCCCTACTCCAGTTCCTTCTGGAACGACTCCTTTC

42,720

ITPR1

ITPR1-237

ITPR1-237

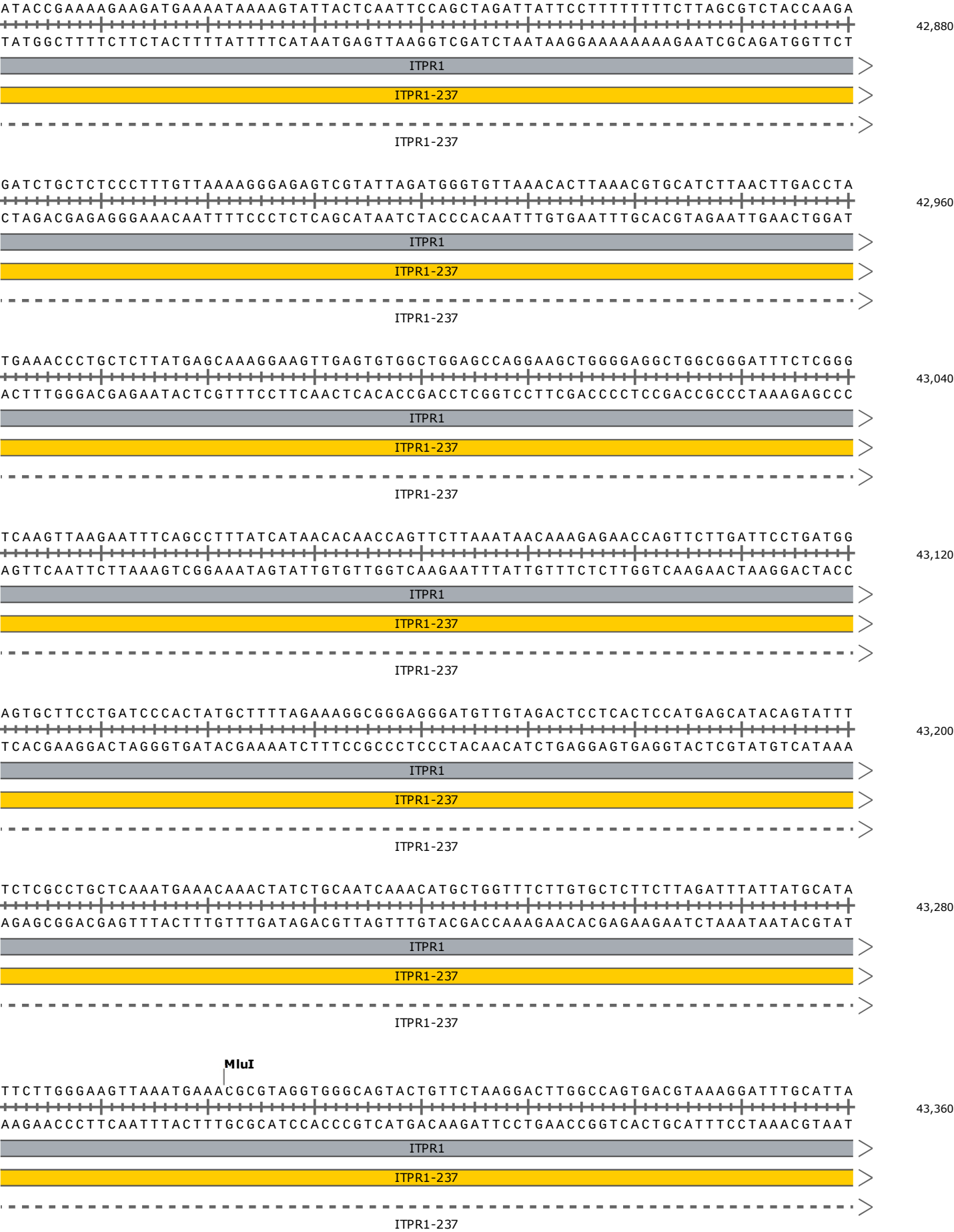
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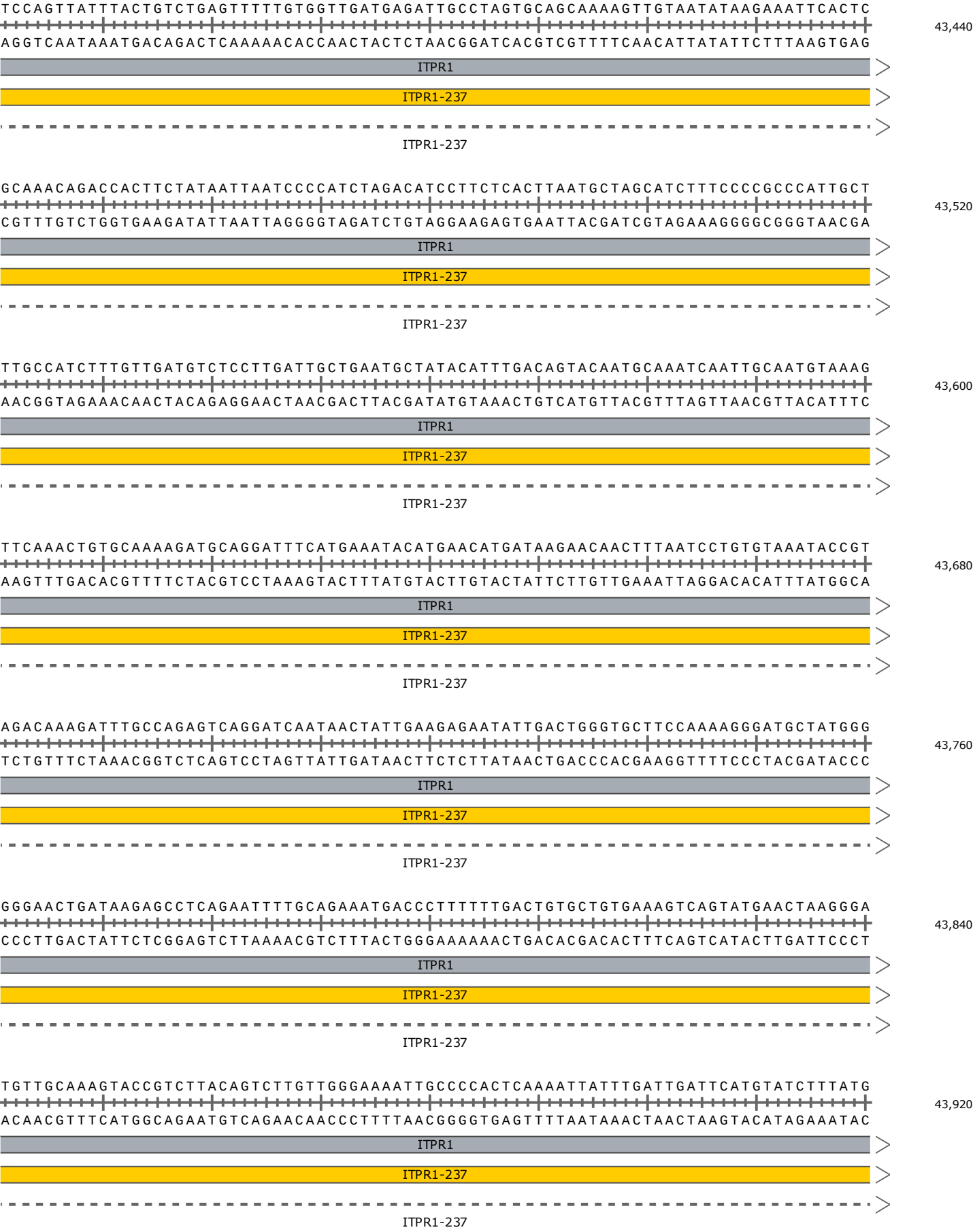
42,800

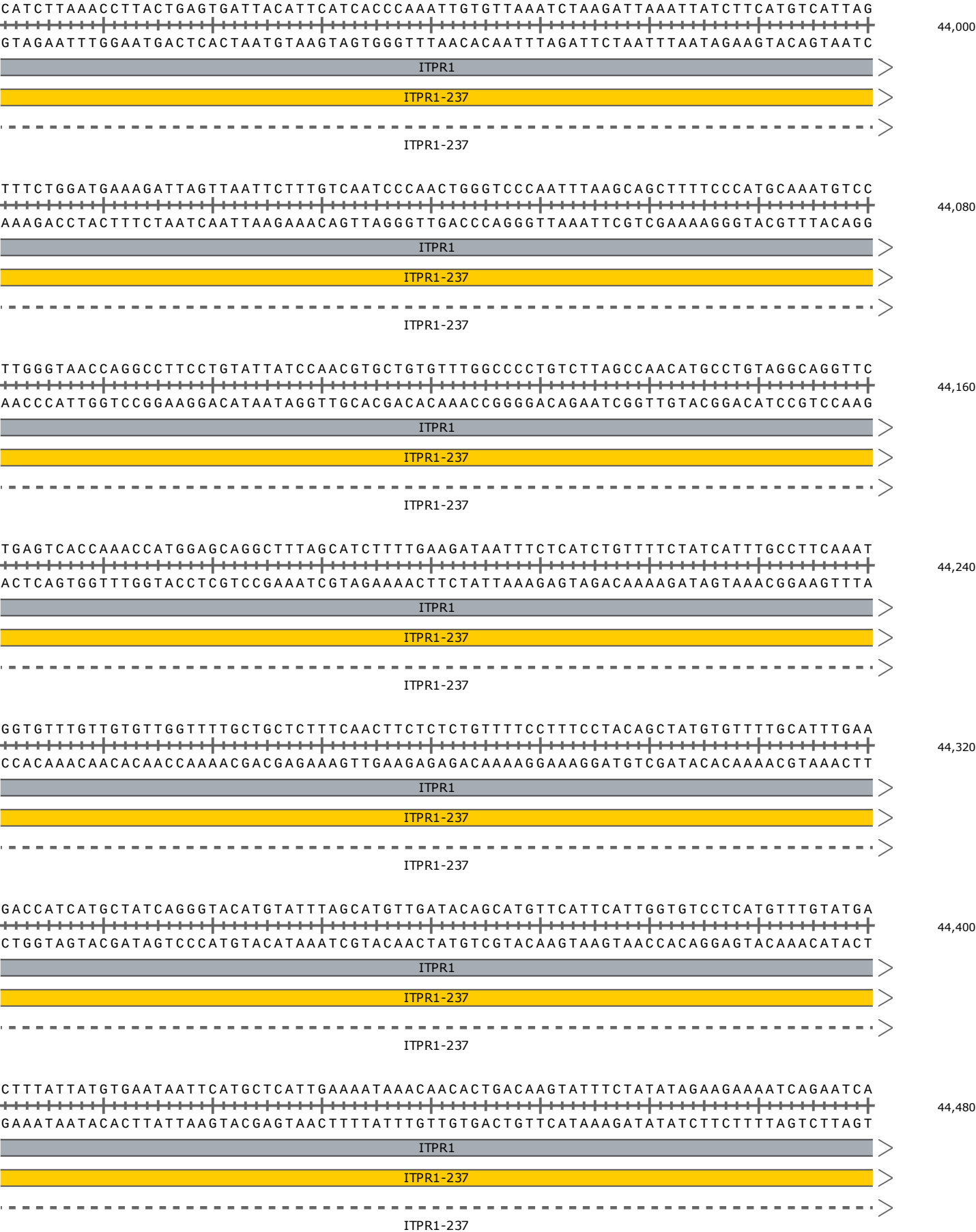
ITPR1

ITPR1-237

ITPR1-237







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ITPR1

ITPR1-237

ITPR1-237

44,560

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ITPR1

ITPR1-237

ITPR1-237

44,640

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ITPR1

ITPR1-237

ITPR1-237

44,720

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ITPR1

ITPR1-237

ITPR1-237

44,800

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ITPR1

ITPR1-237

ITPR1-237

44,880

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ITPR1

ITPR1-237

ITPR1-237

44,960

1615 1620
D I V S A L E D R
ENSE00001121982

ITPR1-237

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ITPR1

ITPR1-237

ITPR1-237

45,040

1625 1630 1635 1640 1645 1650
L R P L V Q A E L S V L V D V L H R P E L L F P E N T
ENSE00001121982

ITPR1-237

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45,120

ITPR1

ITPR1-237

1655 1660
D A R R K C E S G G F I C K

ENSE00001121982

ITPR1-237

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45,200

ITPR1

ITPR1-237

ITPR1-237

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45,280

ITPR1

ITPR1-237

ITPR1-237

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45,360

ITPR1

ITPR1-237

ITPR1-237

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45,440

ITPR1

ITPR1-237

ITPR1-237

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45,520

ITPR1

ITPR1-237

ITPR1-237

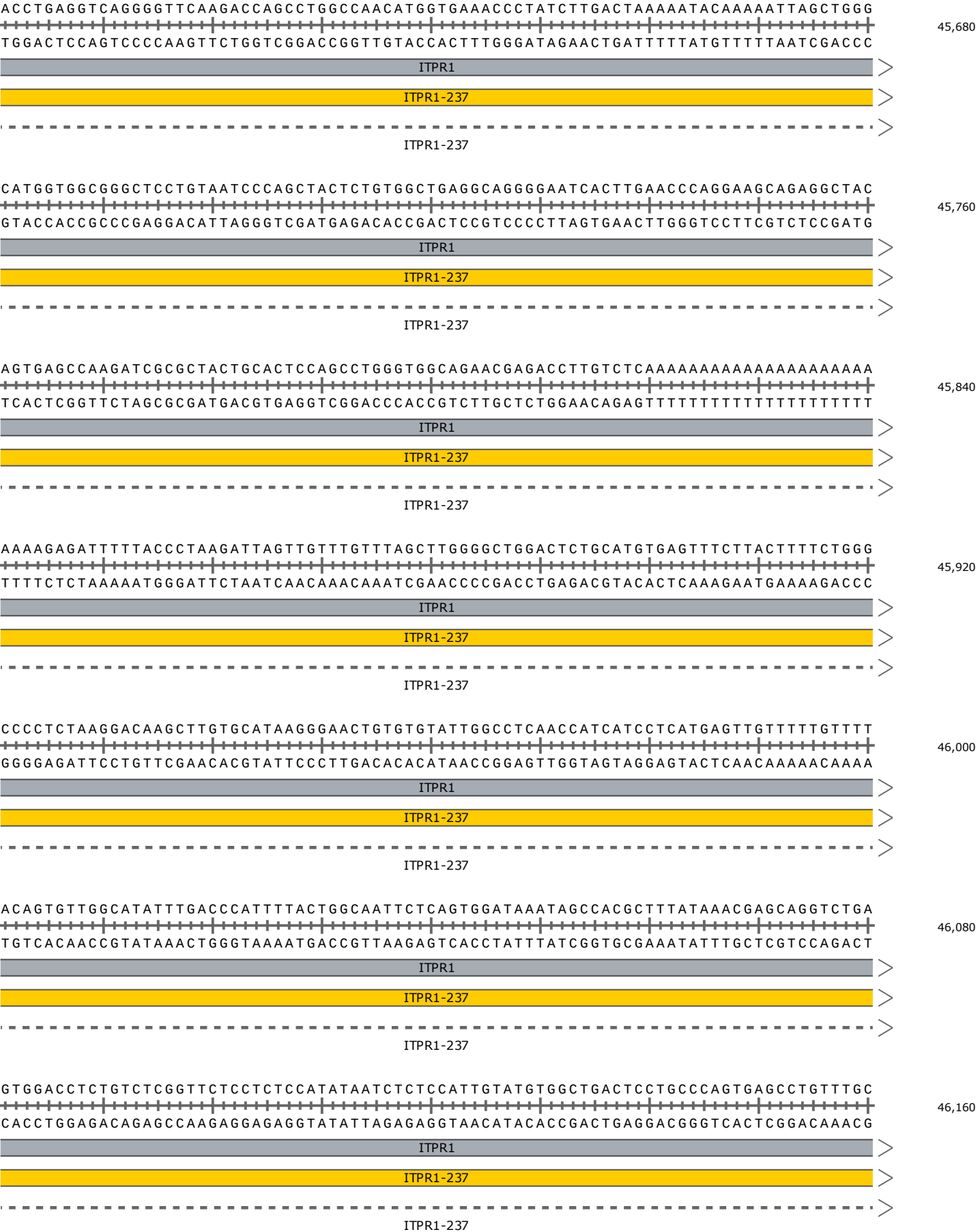
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45,600

ITPR1

ITPR1-237

ITPR1-237



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46,240

ITPR1

ITPR1-237

ITPR1-237

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46,320

ITPR1

ITPR1-237

ITPR1-237

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46,400

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

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46,480

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

ITPR1-237

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46,560

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

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46,640

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

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46,720

ITPR1

ITPR1-237

ITPR1-237

ITPR1-237

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46,800

ITPR1

ITPR1-237

ITPR1-237

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46,880

ITPR1

ITPR1-237

ITPR1-237

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46,960

ITPR1

ITPR1-237

ITPR1-237

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47,040

ITPR1

ITPR1-237

ITPR1-237

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47,120

ITPR1

ITPR1-237

ITPR1-237

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47,200

ITPR1

ITPR1-237

ITPR1-237

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47,280

ITPR1

ITPR1-237

ITPR1-237

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47,360

ITPR1

ITPR1-237

ITPR1-237

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47,440

ITPR1

ITPR1-237

ITPR1-237

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47,520

ITPR1

ITPR1-237

ITPR1-237

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47,600

ITPR1

ITPR1-237

ITPR1-237

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47,680

ITPR1

ITPR1-237

ITPR1-237

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47,760

ITPR1

ITPR1-237

ITPR1-237

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47,840

ITPR1

ITPR1-237

ITPR1-237

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47,920

ITPR1

ITPR1-237

ITPR1-237

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48,000

ITPR1

ITPR1-237

ITPR1-237

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48,080

ITPR1

ITPR1-237

ITPR1-237

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48,160

ITPR1

ITPR1-237

ITPR1-237

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48,240

ITPR1

ITPR1-237

ITPR1-237

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48,320

ITPR1

ITPR1-237

ITPR1-237

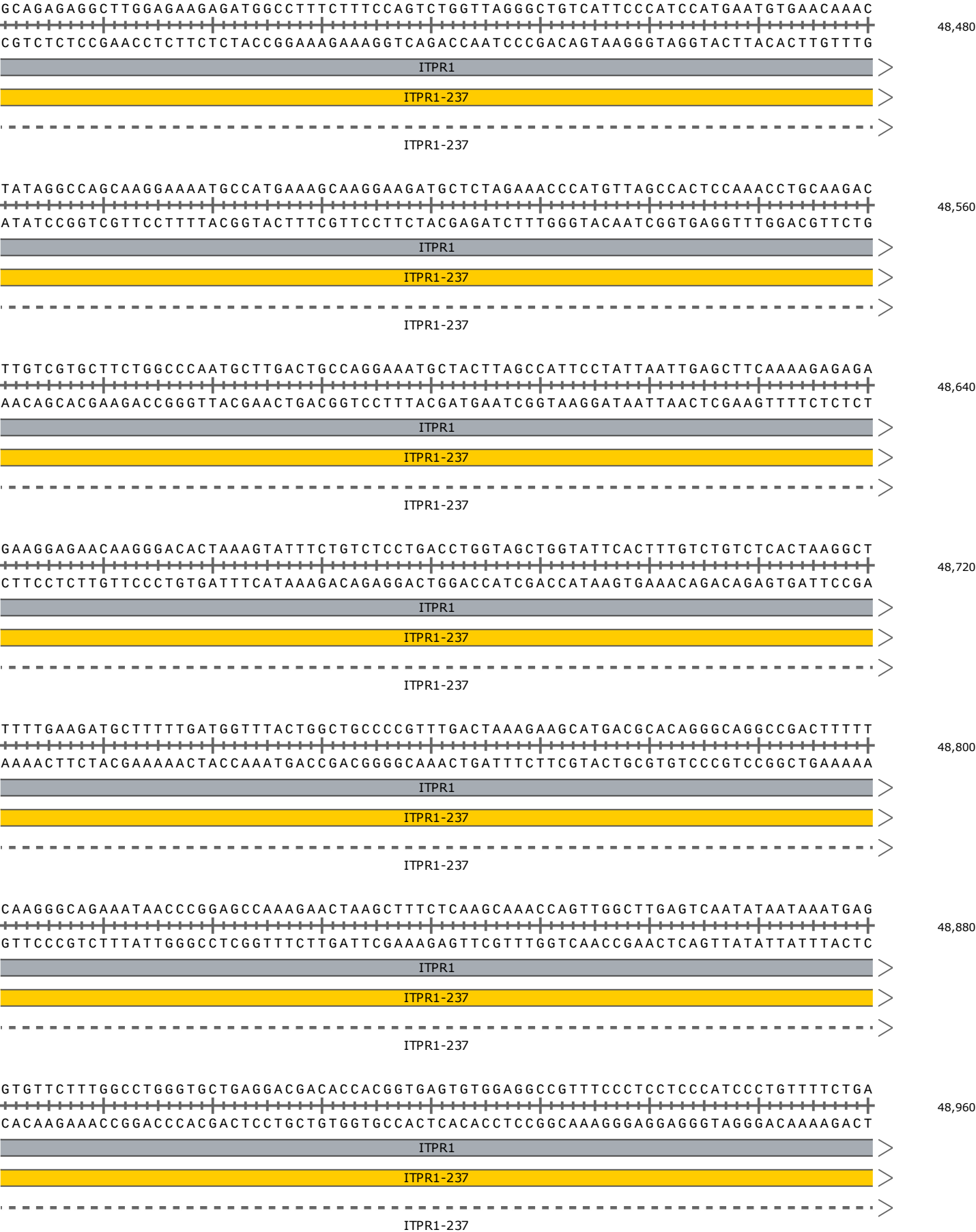
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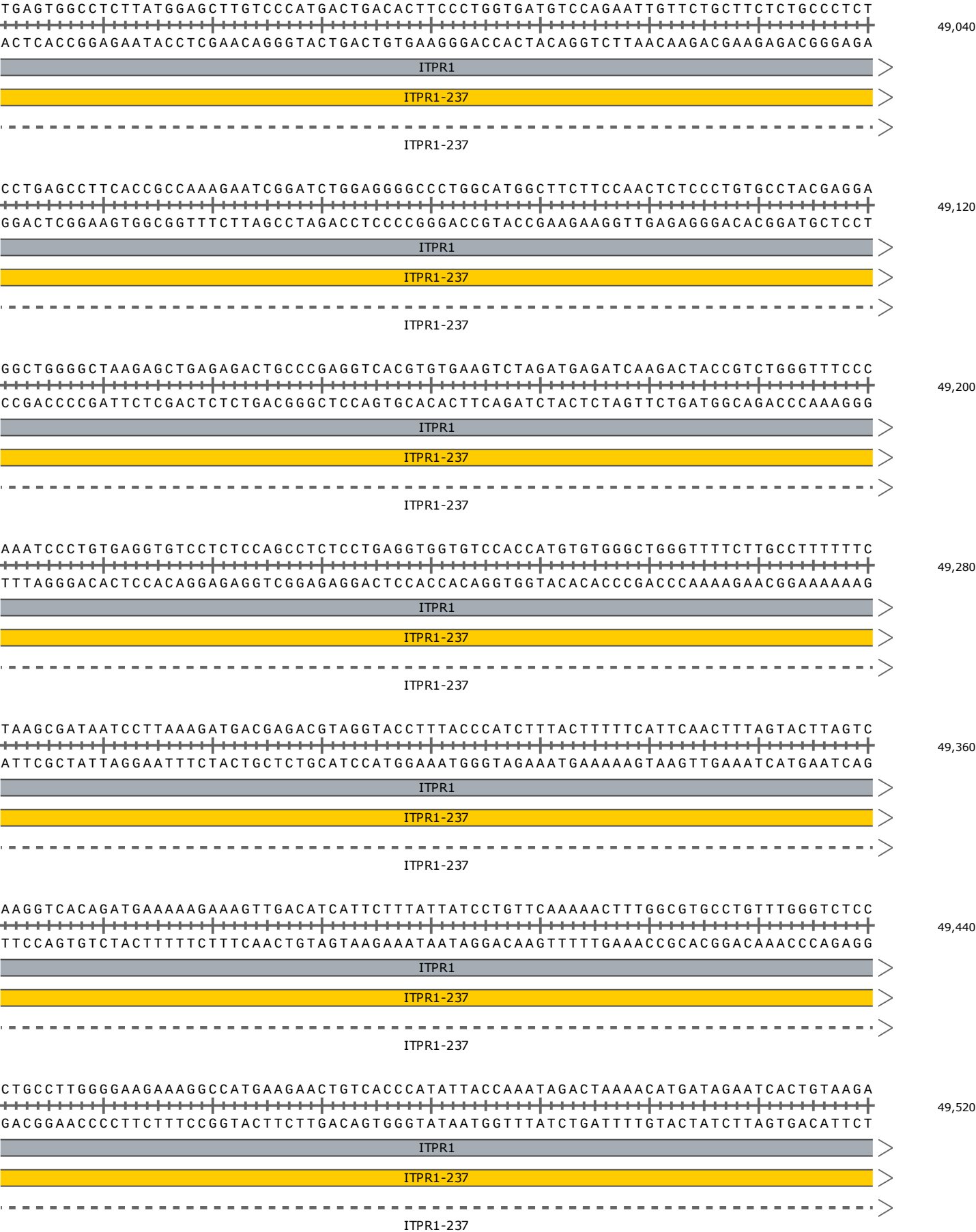
48,400

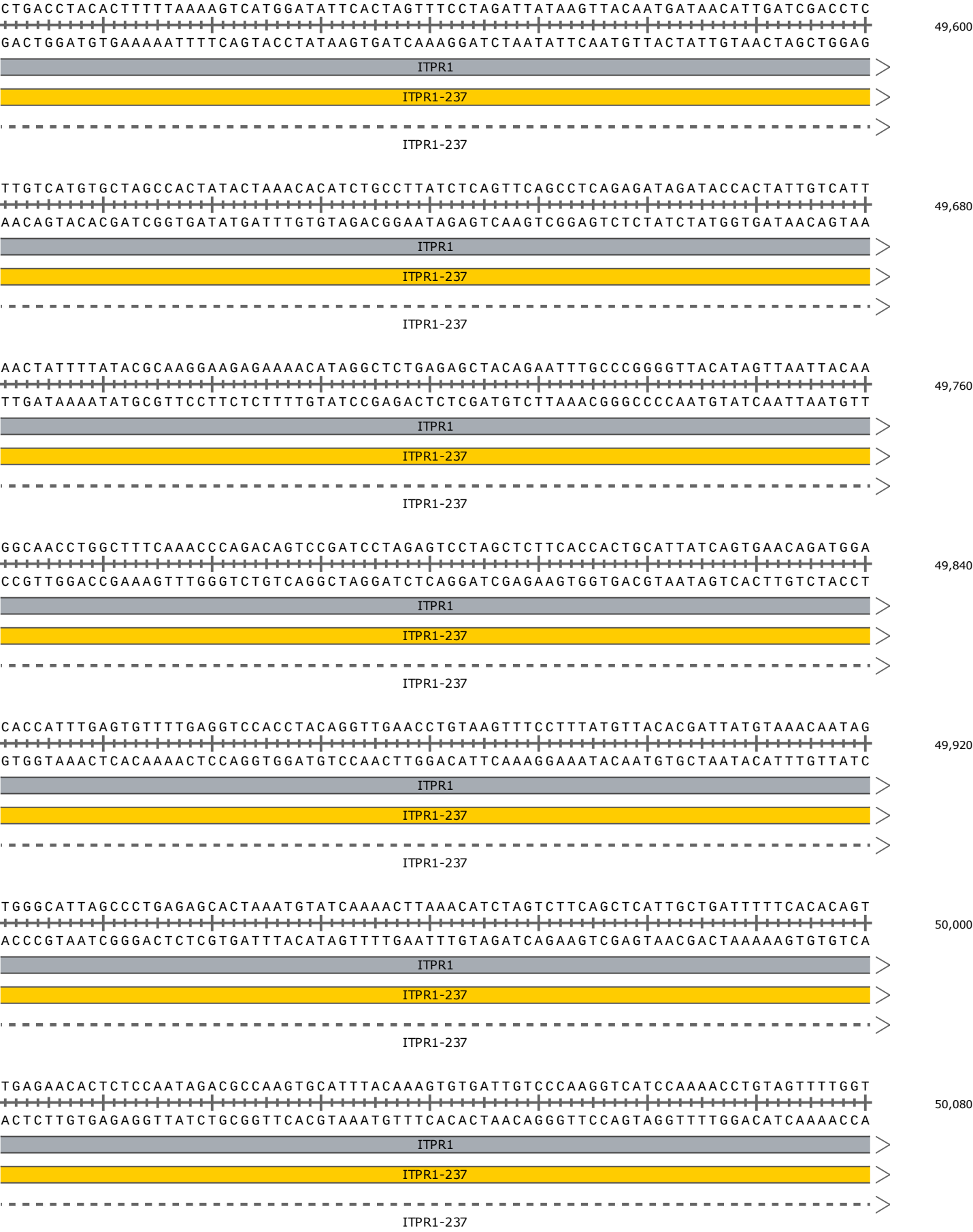
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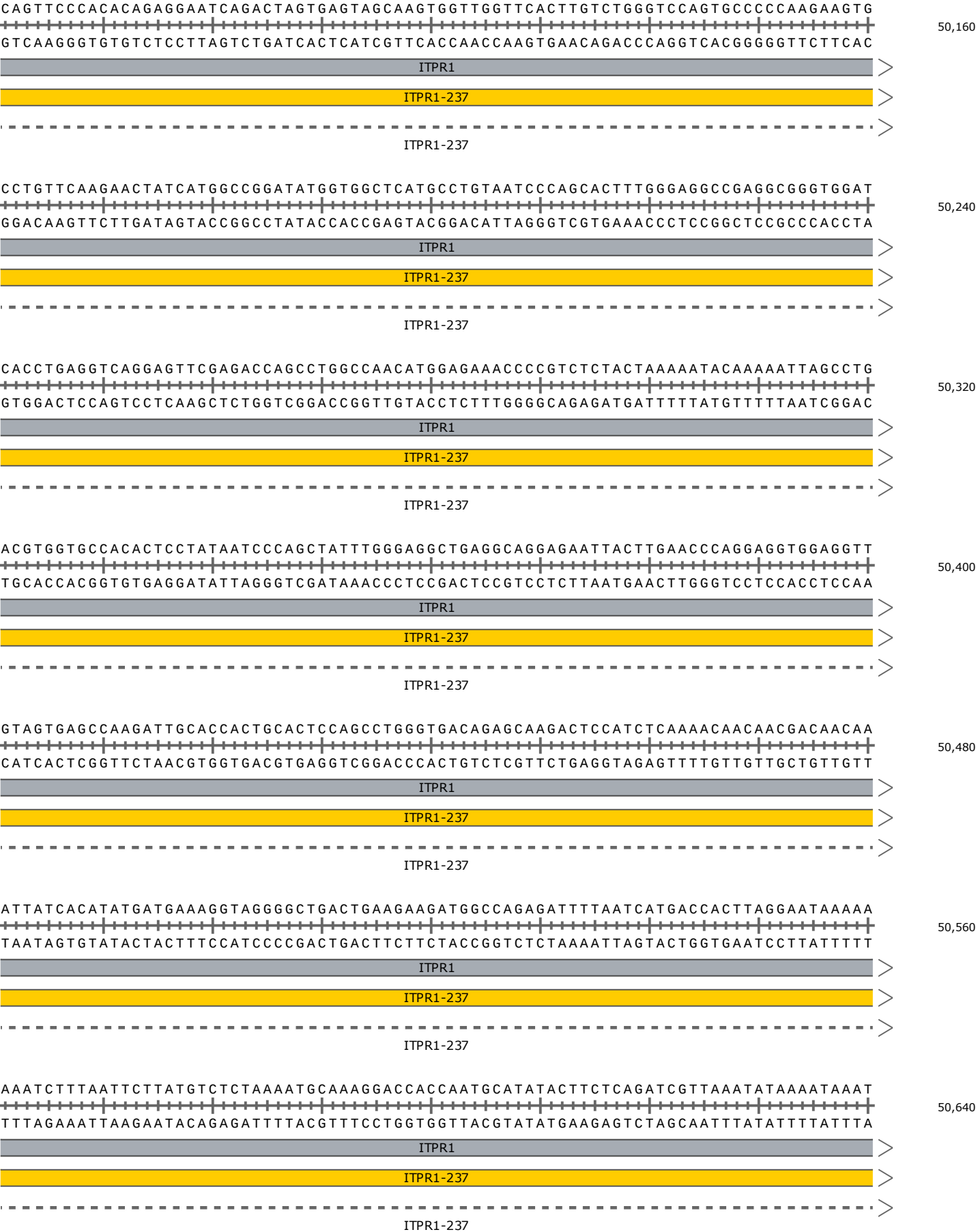
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ITPR1-237









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50,720

ITPR1

ITPR1-237

ITPR1-237

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50,800

ITPR1

ITPR1-237

ITPR1-237

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50,880

ITPR1

ITPR1-237

ITPR1-237

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50,960

ITPR1

ITPR1-237

ITPR1-237

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51,040

ITPR1

ITPR1-237

ITPR1-237

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51,120

ITPR1

ITPR1-237

ITPR1-237

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51,200

ITPR1

ITPR1-237

ITPR1-237

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51,280

ITPR1

ITPR1-237

ITPR1-237

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51,360

ITPR1

ITPR1-237

ITPR1-237

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51,440

ITPR1

ITPR1-237

ITPR1-237

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51,520

ITPR1

ITPR1-237

ITPR1-237

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51,600

ITPR1

ITPR1-237

ITPR1-237

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51,680

ITPR1

ITPR1-237

ITPR1-237

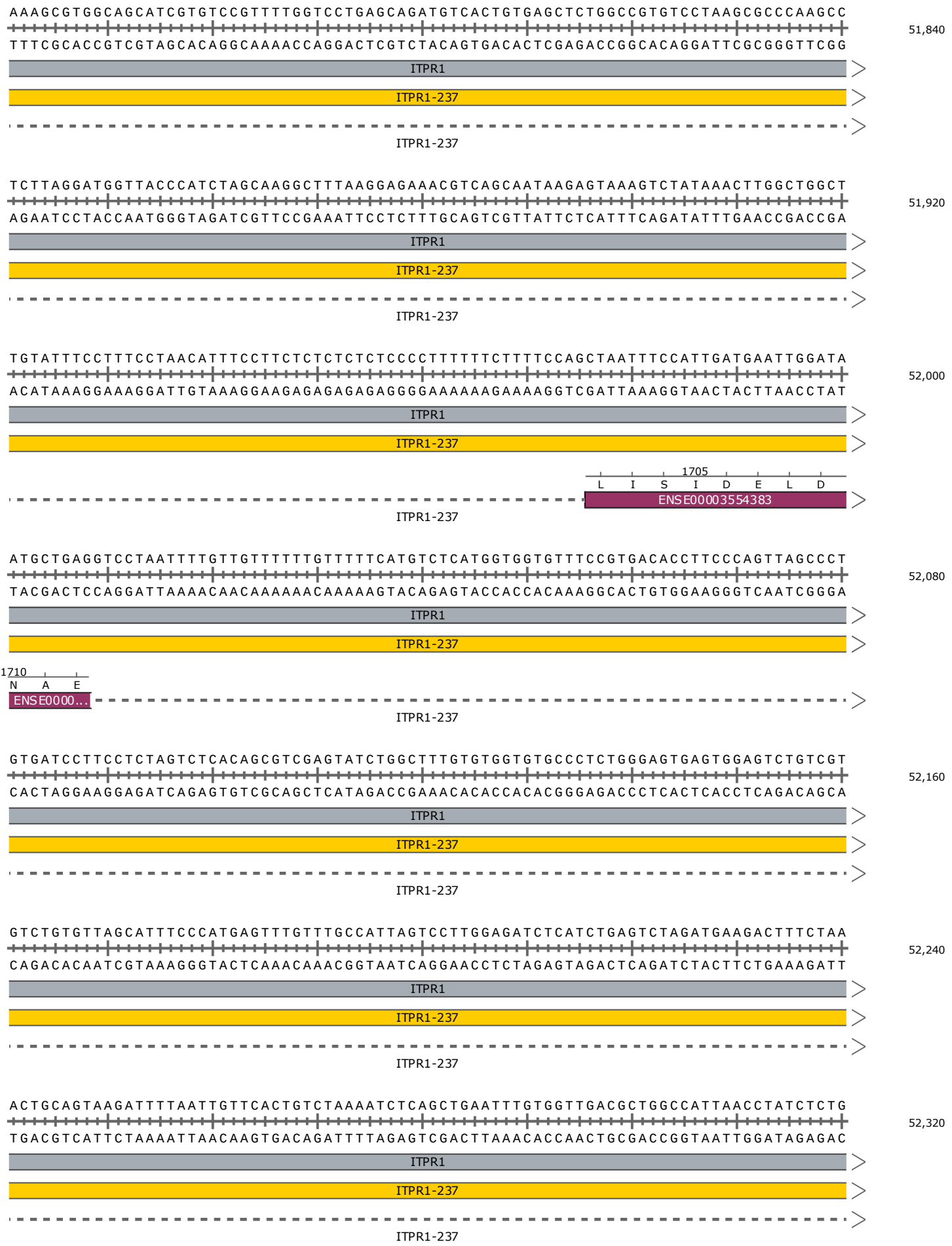
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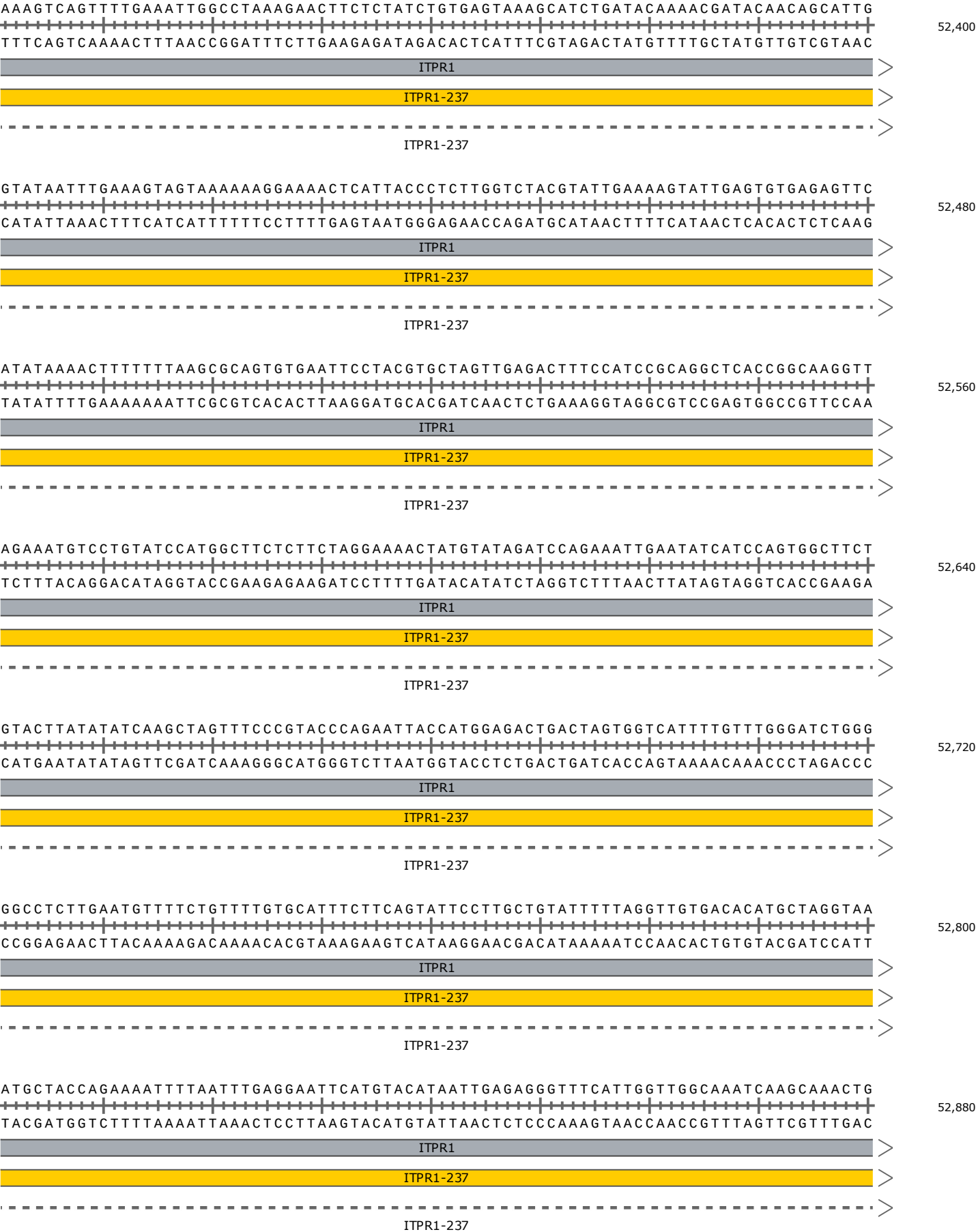
51,760

ITPR1

ITPR1-237

ITPR1-237





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52,960

ITPR1

ITPR1-237

ITPR1-237

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53,040

ITPR1

ITPR1-237

ITPR1-237

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53,120

ITPR1

ITPR1-237

ITPR1-237

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53,200

ITPR1

ITPR1-237

ITPR1-237

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53,280

ITPR1

ITPR1-237

ITPR1-237

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53,360

ITPR1

ITPR1-237

ITPR1-237

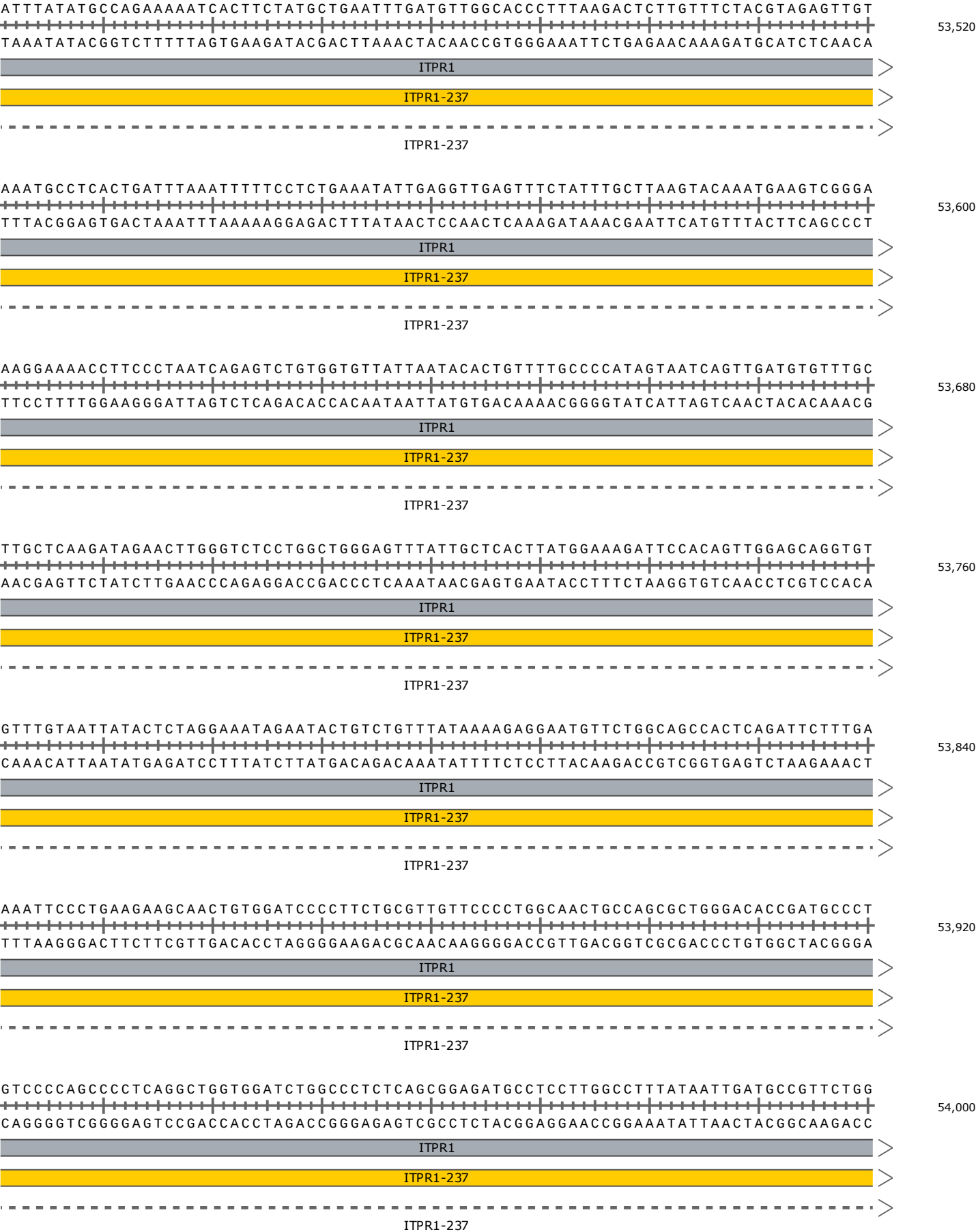
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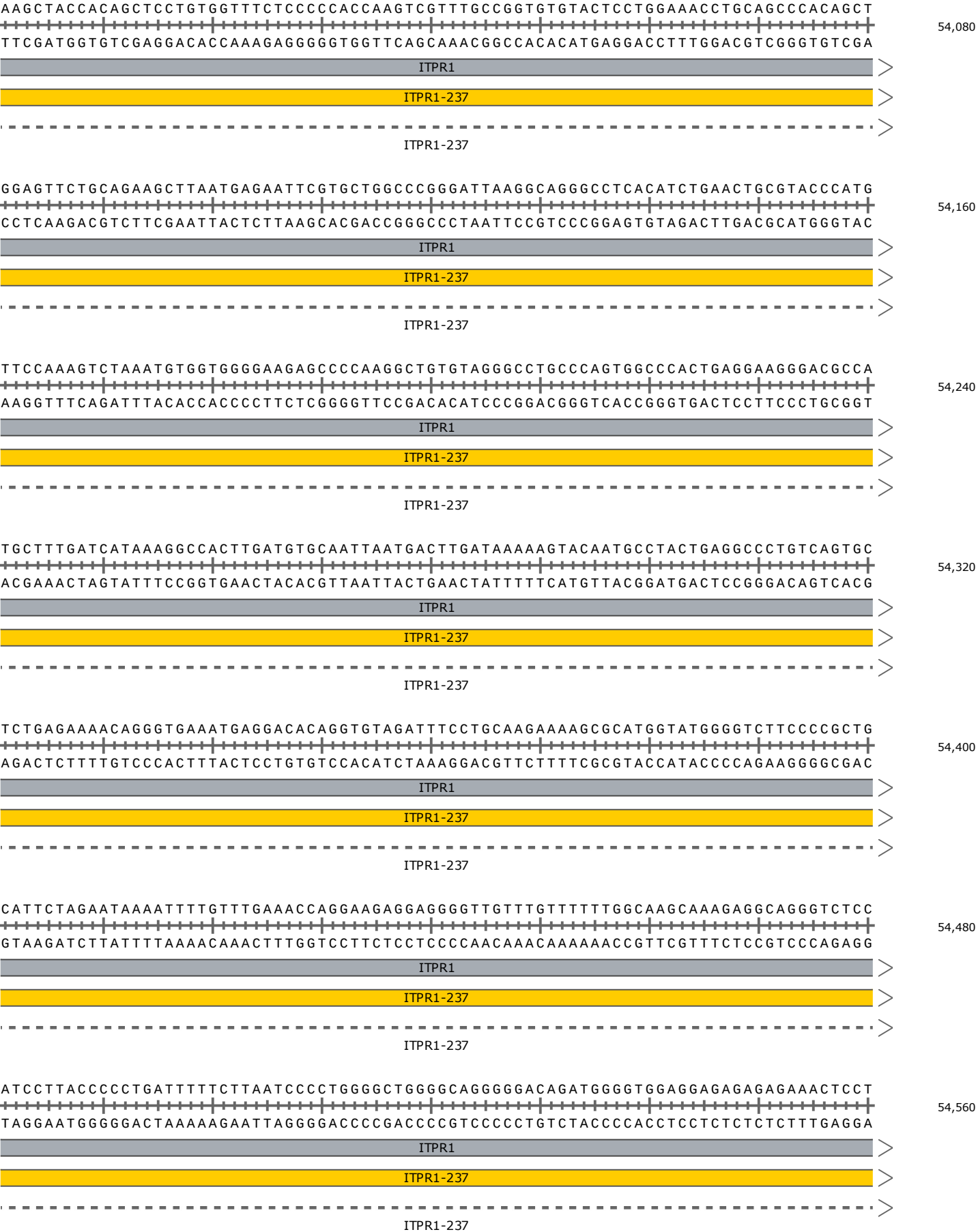
53,440

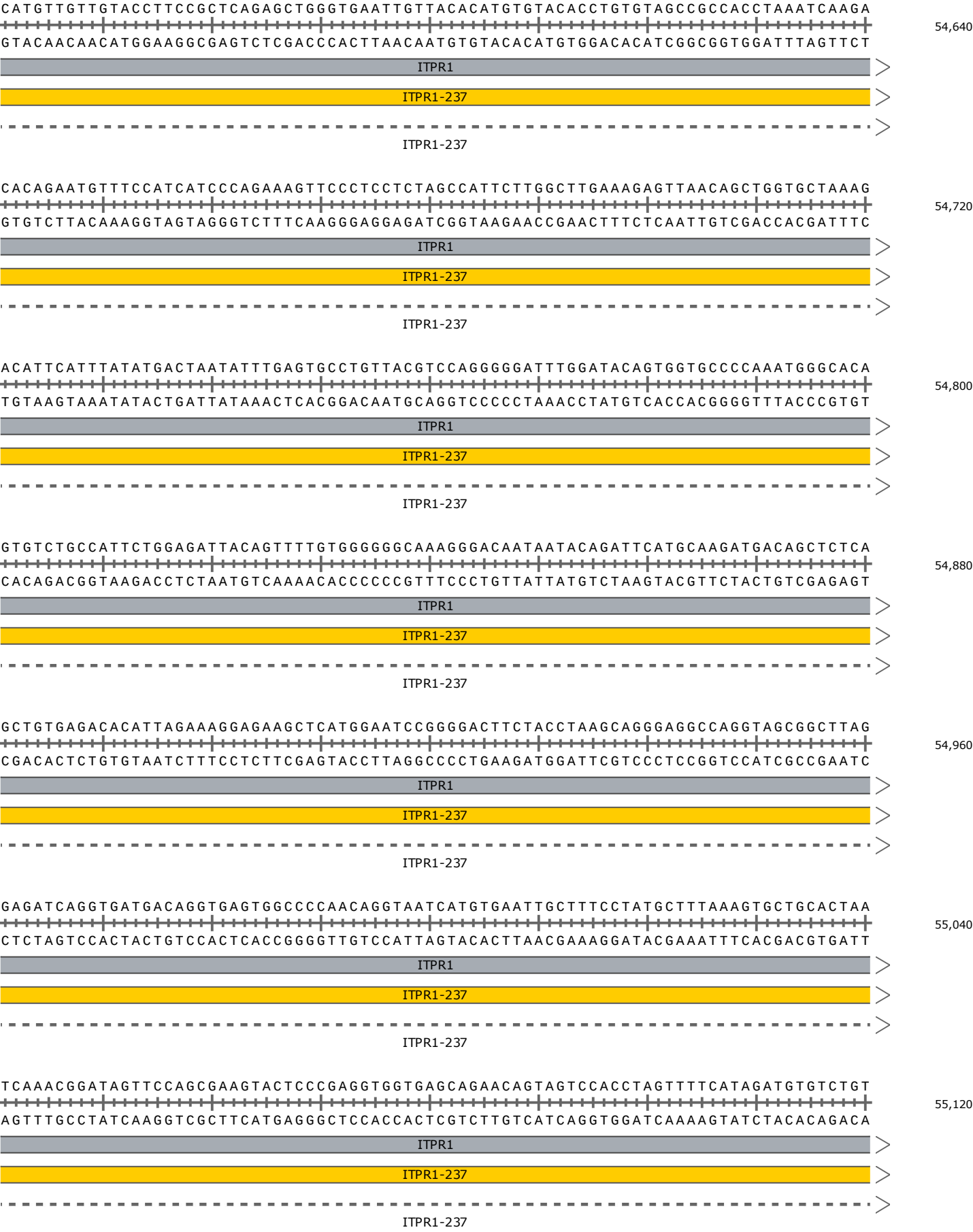
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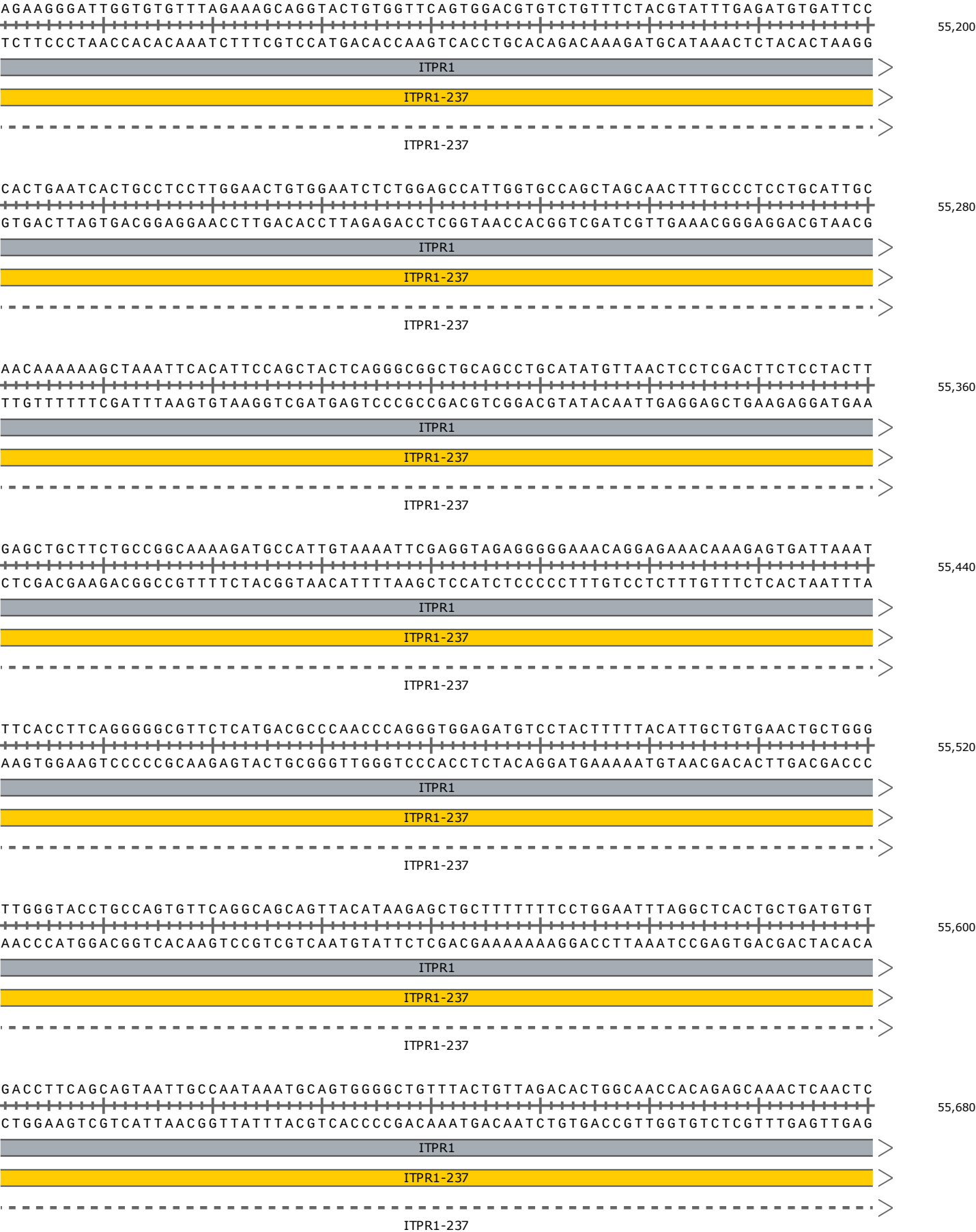
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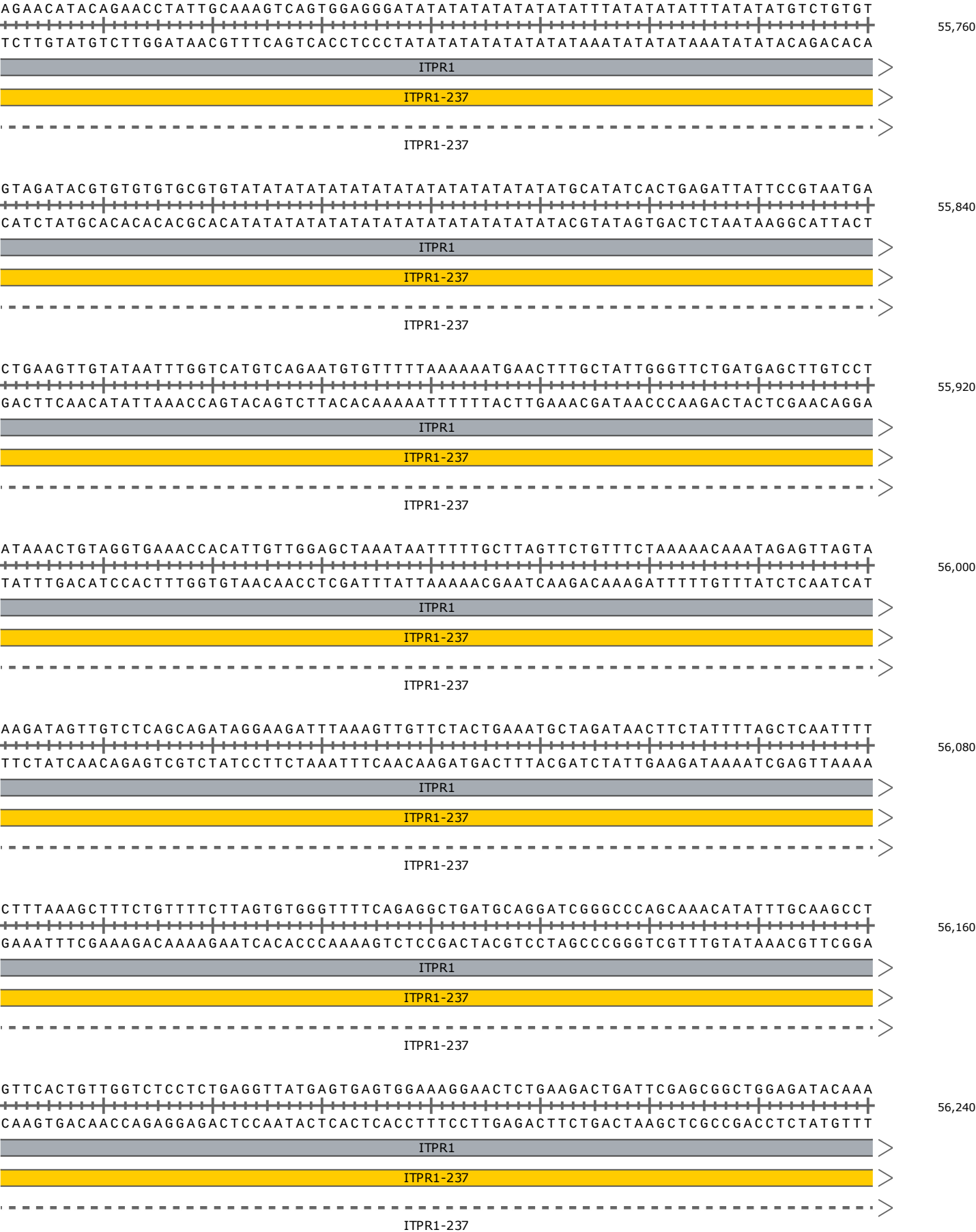
ITPR1-237











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56,320

ITPR1

ITPR1-237

ITPR1-237

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ATCTTTCTCTGTAGGGTAAAGTTTCTTTTAAGATCTTCGGGGTCCCATCCTTCCCCTAATGACGACTCCCGTCATCTTT

56,400

ITPR1

ITPR1-237

ITPR1-237

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56,480

ITPR1

ITPR1-237

ITPR1-237

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56,560

ITPR1

ITPR1-237

ITPR1-237

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AAAGTAAACATCATCTTTAAACAGGGAACATTTTACGACCCATGTAATACACAACGTTCACTCATCTAGTCACAGCGTA

56,640

ITPR1

ITPR1-237

ITPR1-237

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56,720

ITPR1

ITPR1-237

ITPR1-237

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56,800

ITPR1

ITPR1-237

ITPR1-237

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56,880

ITPR1

ITPR1-237

ITPR1-237

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56,960

ITPR1

ITPR1-237

ITPR1-237

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57,040

ITPR1

ITPR1-237

ITPR1-237

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57,120

ITPR1

ITPR1-237

ITPR1-237

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57,200

ITPR1

ITPR1-237

ITPR1-237

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57,280

ITPR1

ITPR1-237

ITPR1-237

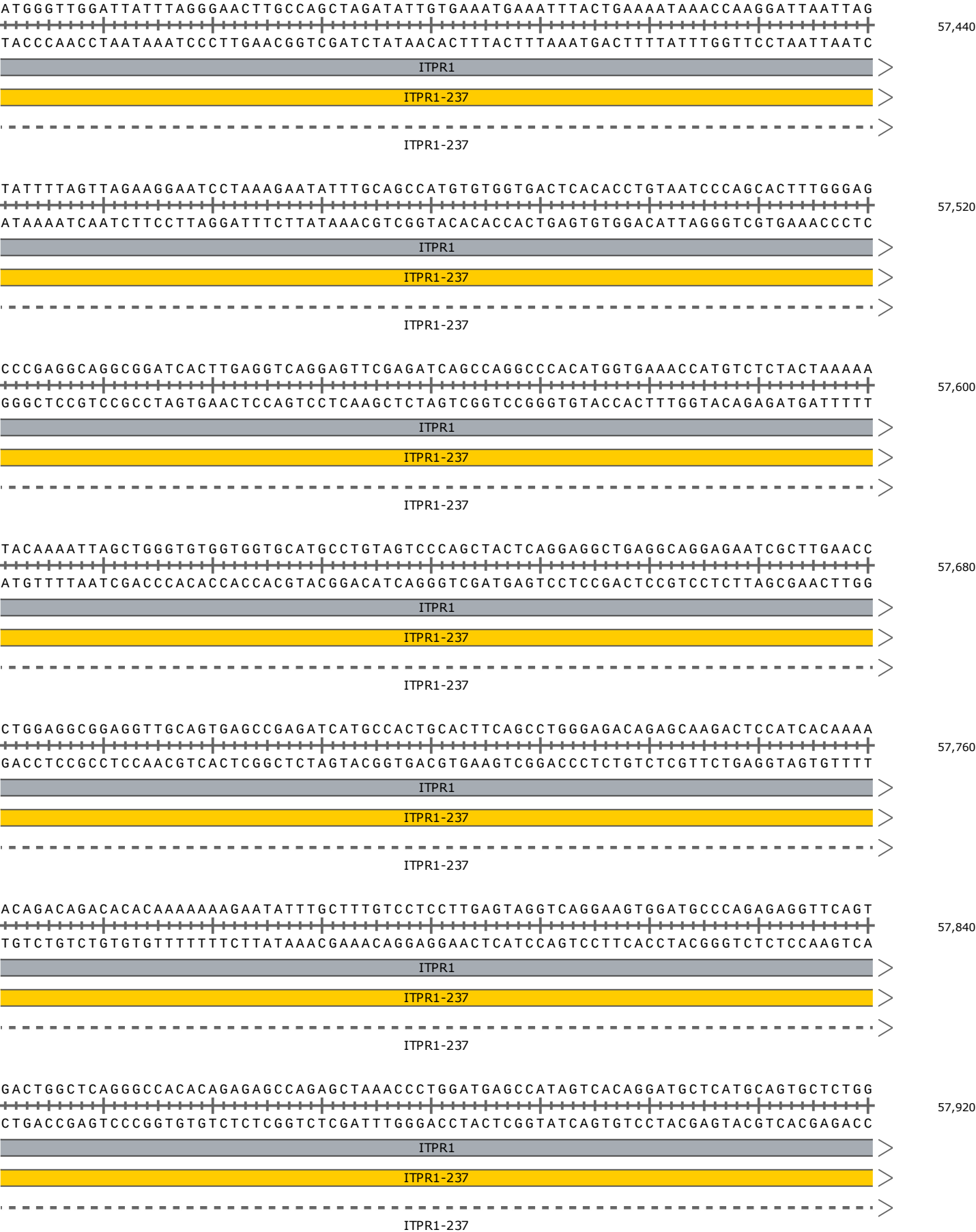
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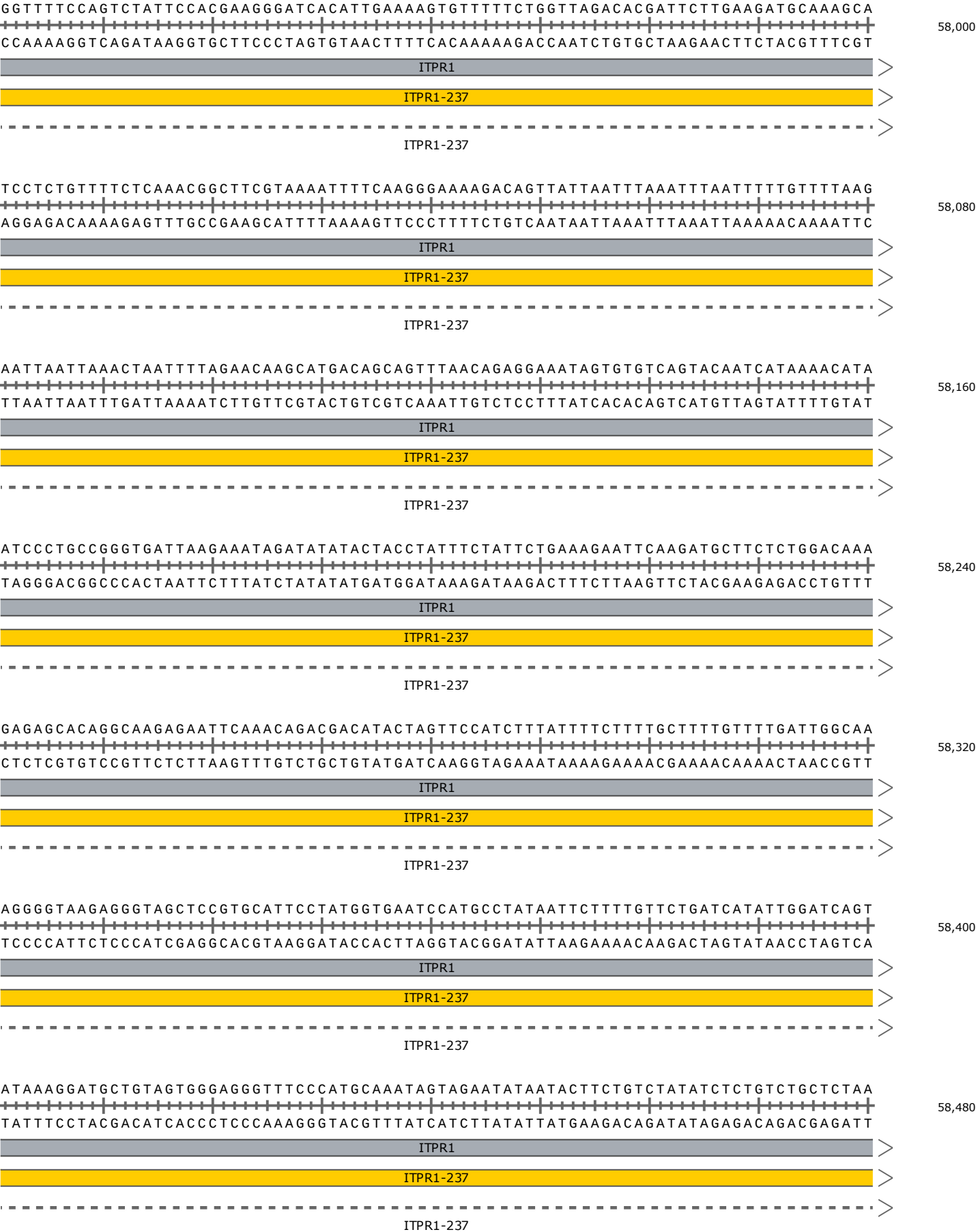
57,360

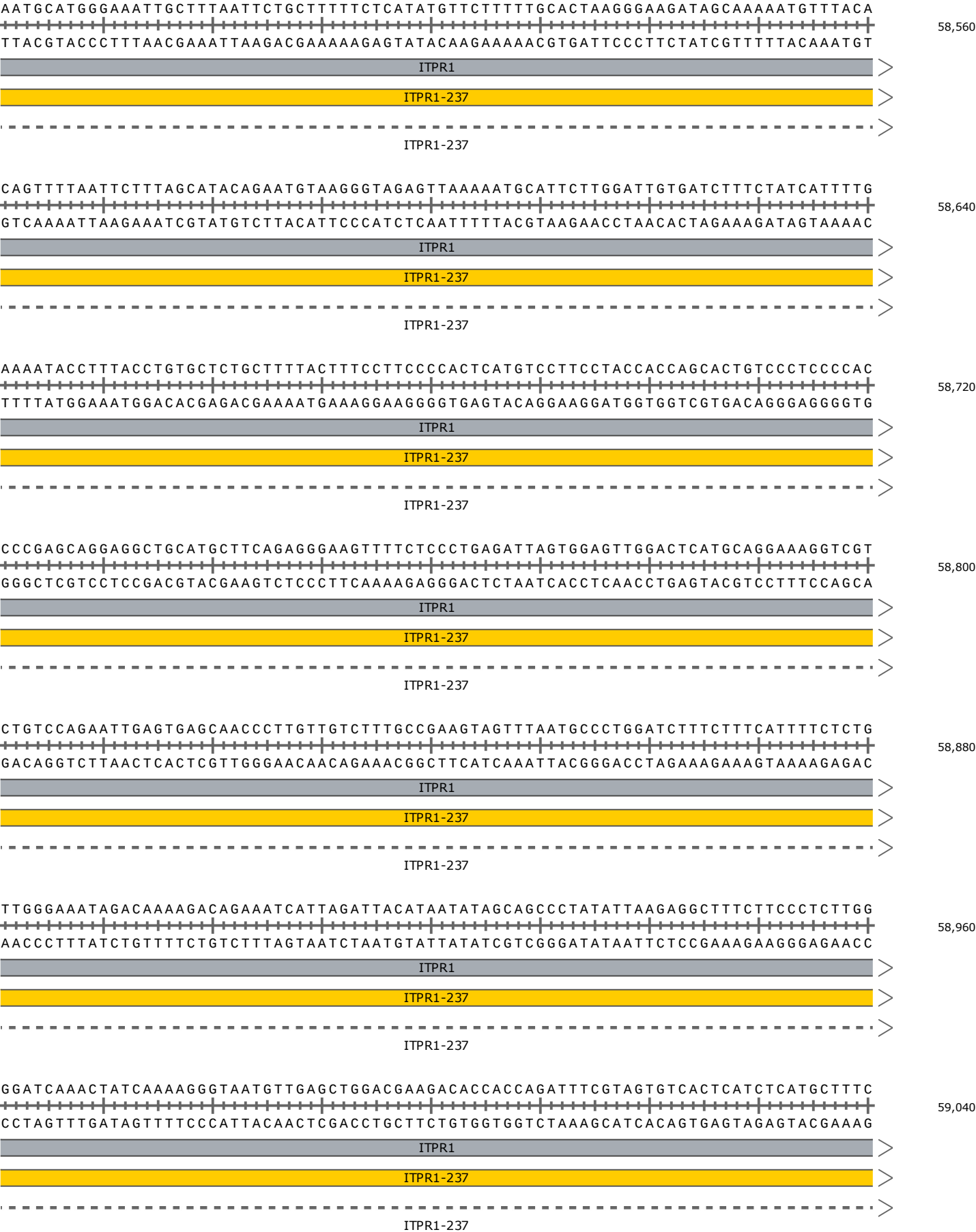
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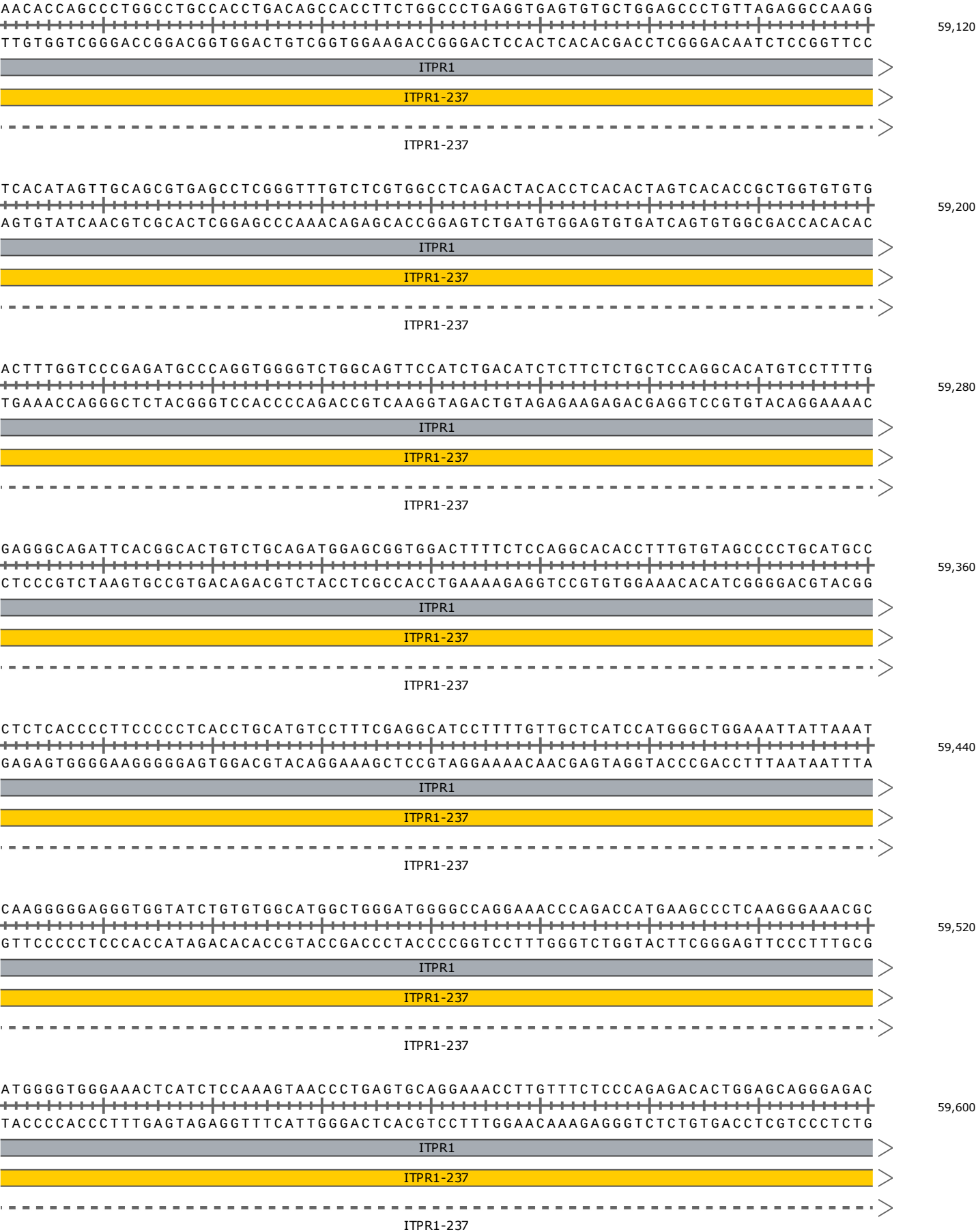
ITPR1-237

ITPR1-237









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59,680

ITPR1

ITPR1-237

ITPR1-237

GAAAGCCTAAACCCACAGGAGACATGTGGCACGTGGAACCTTCCCAAGCCTTGGGCCCTGCTTTCATCACTACCCCTGC
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59,760

ITPR1

ITPR1-237

ITPR1-237

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59,840

ITPR1

ITPR1-237

ITPR1-237

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59,920

ITPR1

ITPR1-237

ITPR1-237

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60,000

ITPR1

ITPR1-237

ITPR1-237

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60,080

ITPR1

ITPR1-237

ITPR1-237

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ACCAGAGACCTGAAGAGACACCGGGTGCTCTACGTTACGGTACTGATTGCATGAAGCAAAATGAGGGTTAATCGAAGGA

60,160

ITPR1

ITPR1-237

ITPR1-237

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ENSEO...

ITPR1-237

CCAGCTCCGGATTCTGAGAACGCCACTGAGGTGTGTTGCCCGCCTATATTTGTAGCGCCAGCGCCAGCAAATATGGATGC
GGTCGAGGCCTAAGACTCTTGCGGTGACTCCACACAACGGGCGGATATAAACATCGCGGTGCGGGTCGTTTATACCTACG

60,240

ITPR1

ITPR1-237

1715 1720
P A P D S E N A T E

ENSE00003662513

ITPR1-237

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60,320

ITPR1

ITPR1-237

ITPR1-237

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60,400

ITPR1

ITPR1-237

ITPR1-237

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60,480

ITPR1

ITPR1-237

ITPR1-237

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60,560

ITPR1

ITPR1-237

ITPR1-237

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60,640

ITPR1

ITPR1-237

ITPR1-237

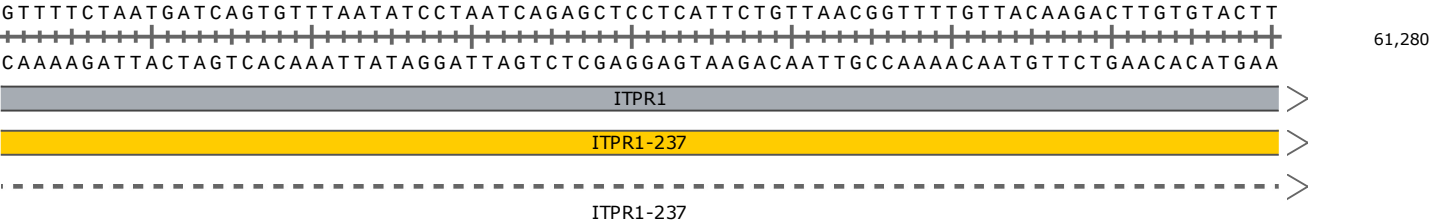
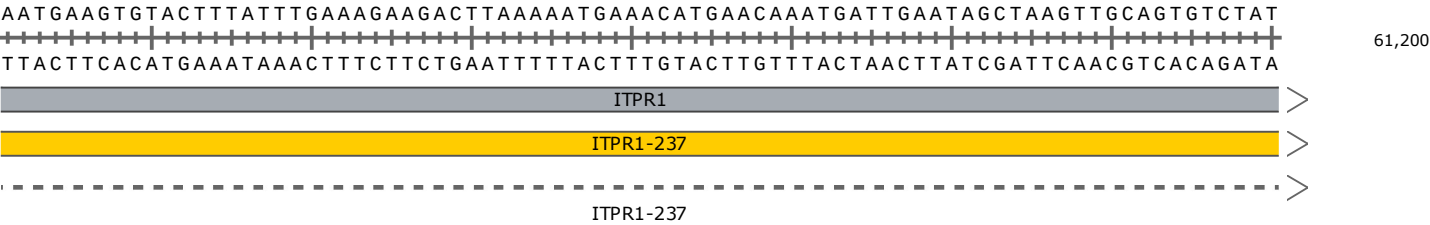
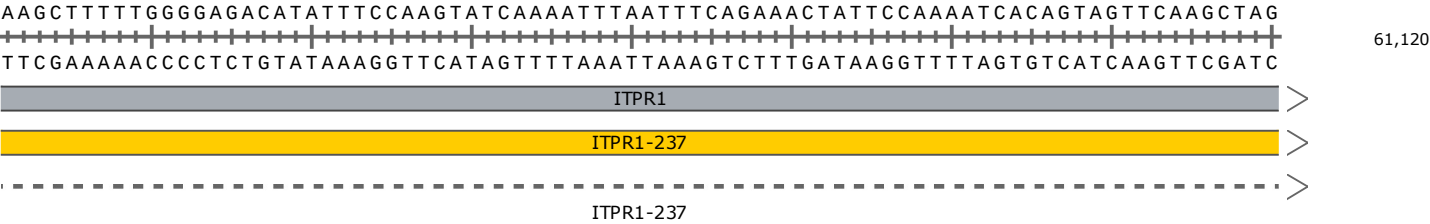
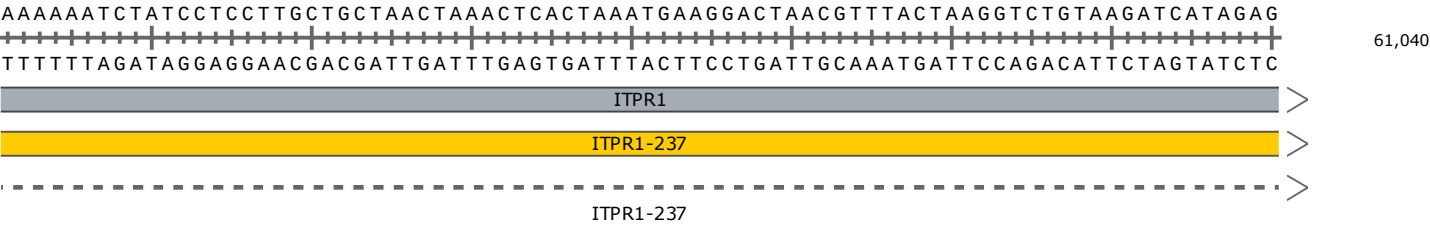
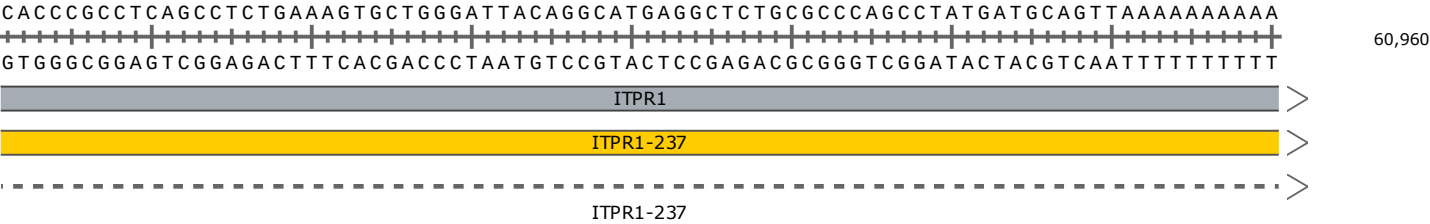
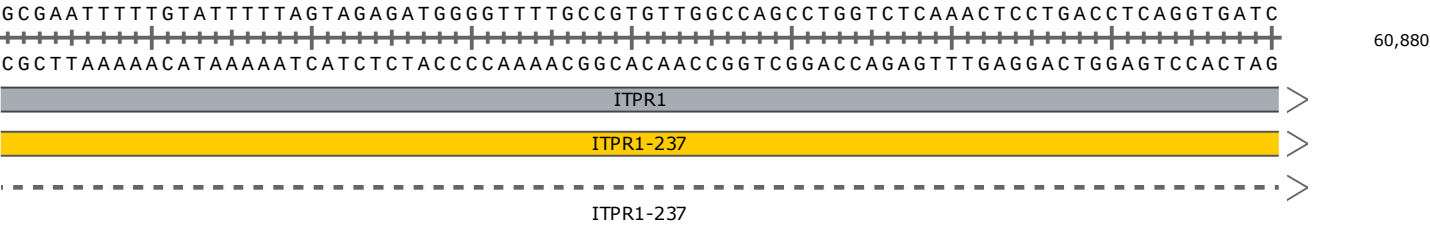
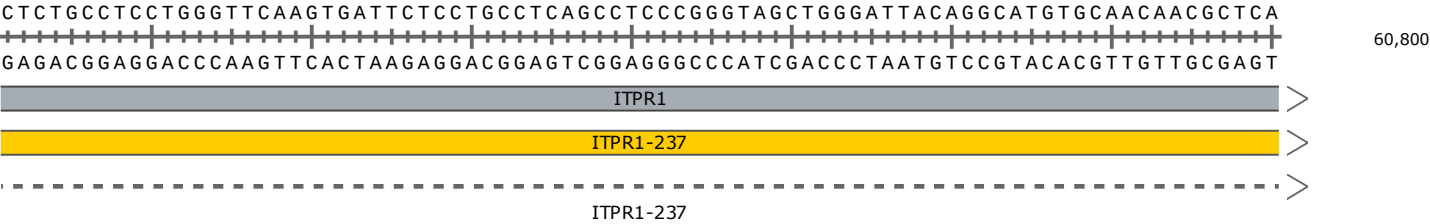
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60,720

ITPR1

ITPR1-237

ITPR1-237



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CACCCACCCCTTTCGGCACCAGGGTATAGACACAGACGAGTCTCCGCACACAGAACTACAGGAATACGTACACGACACG

61,360

ITPR1

ITPR1-237

ITPR1-237

AATGATGCATGTATGAATCATAAGGACCTGCCCGATTGAGTCTTGCATTACAACCCCTTTTGGGTTAATGTCACAGCATA
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61,440

ITPR1

ITPR1-237

ITPR1-237

TAATATAGAACTTCTTTTTCATGATCTTTGCAATAAATTATGTTGGCCAAAAAGTCATATGTCTGCCCATTTTGAACAGT
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61,520

ITPR1

ITPR1-237

ITPR1-237

GCACTAGGGTTGGGGGTATGGGACAGTCGTTAAGCAGCATCTAAAGTAATCAAGCATGGATATACGGGGGAAAAACAAAA
CGTGATCCCAACCCCATACCCTGTCAGCAATTGCTCGTAGATTTTCATTAGTTCGTACCTATATGCCCCCTTTTTGTTTT

61,600

ITPR1

ITPR1-237

ITPR1-237

ATCCAGACCTATTCTCCTTTTGTAAGTCTTGTCTATATATGAAGTCTCAATGTATTTTATATGTGACTGATGCTGCAG
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61,680

ITPR1

ITPR1-237

ITPR1-237

ATGGTAGTGTCTCCTTAGTGTTGTATTAATGGAATTTCTGCATGCCTAGCAGGAGCTTGAACCAAGTCCACCCCTGCG
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61,760

ITPR1

ITPR1-237

ITPR1-237

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61,840

ITPR1

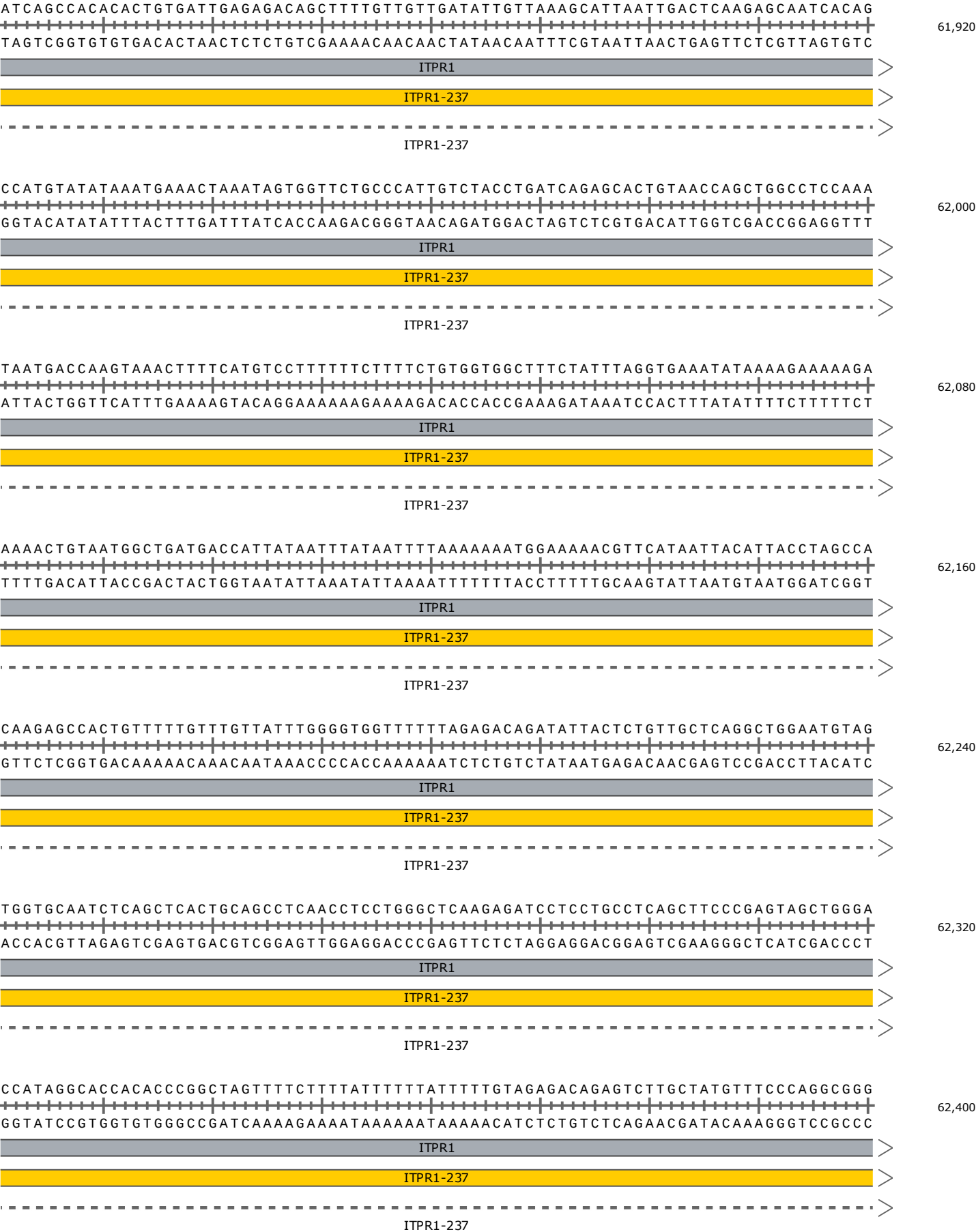
ITPR1-237

ITPR1-237

1735 1740
Q L E D H K R
ENSE00003543315

1725 1730
E L E P S P P L R
ENSE00003543315

ITPR1-237



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62,480

ITPR1

ITPR1-237

ITPR1-237

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TCGGGGTGATTACAAAATTATAAAGGAAGATGGATAAAAAATATGTGTACTCGTGTACACGGTTGTCTGTGTCCGTGTAA

62,560

ITPR1

ITPR1-237

ITPR1-237

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62,640

ITPR1

ITPR1-237

ITPR1-237

TTGAAAATCTTTGAAAGTTAACAGCTGCCTGAAGTTCCTCAAATTAACAGGTGGTTCATCACTGTTTTCTTTGATGAAG
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62,720

ITPR1

ITPR1-237

ITPR1-237

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62,800

ITPR1

ITPR1-237

ITPR1-237

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62,880

ITPR1

ITPR1-237

ITPR1-237

CCATTTTTGGGAAGATAACCAGATGTCCTGGTGACACAGGCTTCATCCGCATTTACAAGTAGGACCTTGAGACTCTGGG
GGTAAAAACCTTCTATTGGTCTACAGGACCACTGTGTCCGAAGTAGGCGTAAAGTGTTTCATCCTGGAACCTCTGAGACCC

62,960

ITPR1

ITPR1-237

ITPR1-237

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63,040

ITPR1

ITPR1-237

ITPR1-237

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63,120

ITPR1

ITPR1-237

ITPR1-237

ACAGGCACACAATGTGAAATACACACATCATGGAGAATGGGGTATCCATCCCCTCAAGCATTATCCTTTGAGTTGCAAA
TGTCCGTGTGTTACACTTTATGTGTGTAGTACCTCTTACCCCATAGGTAGGGGAGTTTCGTAATAGGAAACTCAACGTTT

63,200

ITPR1

ITPR1-237

ITPR1-237

CAATCCAATTACACTCTTTAAGTTACTTTAAAATGTACAATTATGTTATTGTTGACTGTAGTCACCCTATTGTGCTATGA
GTTAGGTTAATGTGAGAAATTCAATGAAATTTTACATGTTAATACAATAACAACCTGACATCAGTGGGATAACACGATACT

63,280

ITPR1

ITPR1-237

ITPR1-237

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63,360

ITPR1

ITPR1-237

ITPR1-237

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63,440

ITPR1

ITPR1-237

ITPR1-237

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63,520

ITPR1

ITPR1-237

ITPR1-237

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63,600

ITPR1

ITPR1-237

ITPR1-237

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CCGGGCTCCGTGGAACGTAAAGATATAAAAGGTAGGAACGGACGGGAAATCTTAACAGGATCCAGGATCCTCATCGACTA

63,680

ITPR1

ITPR1-237

ITPR1-237

AAAGGCACATAGCTGTCCCTCATGTCCTGAGCTCTCAGAGGACTTGGTATGGAATGCTGCCTATGCCTGTGAACTTTGTA
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63,760

ITPR1

ITPR1-237

ITPR1-237

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63,840

ITPR1

ITPR1-237

ITPR1-237

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63,920

ITPR1

ITPR1-237

ITPR1-237

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64,000

ITPR1

ITPR1-237

ITPR1-237

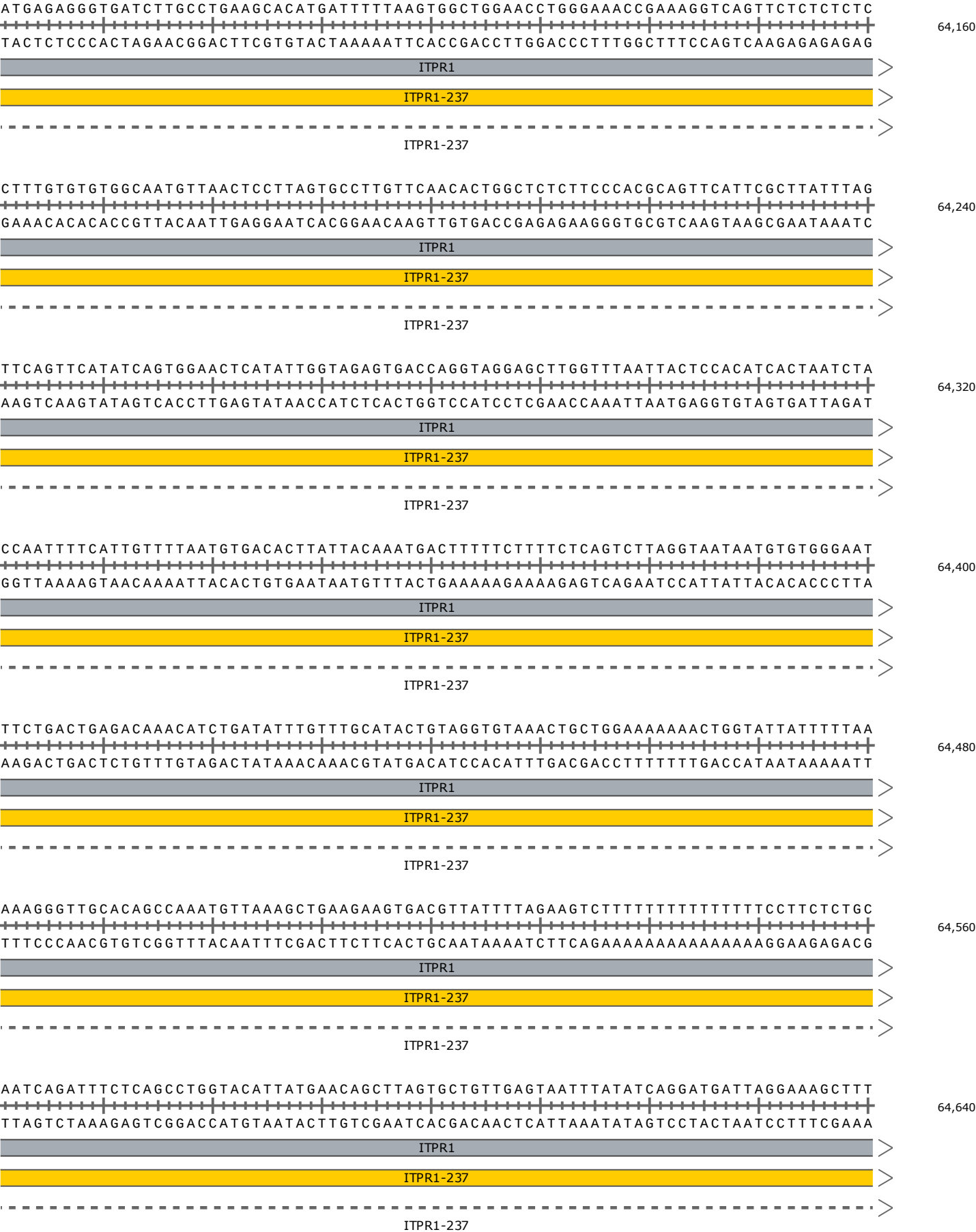
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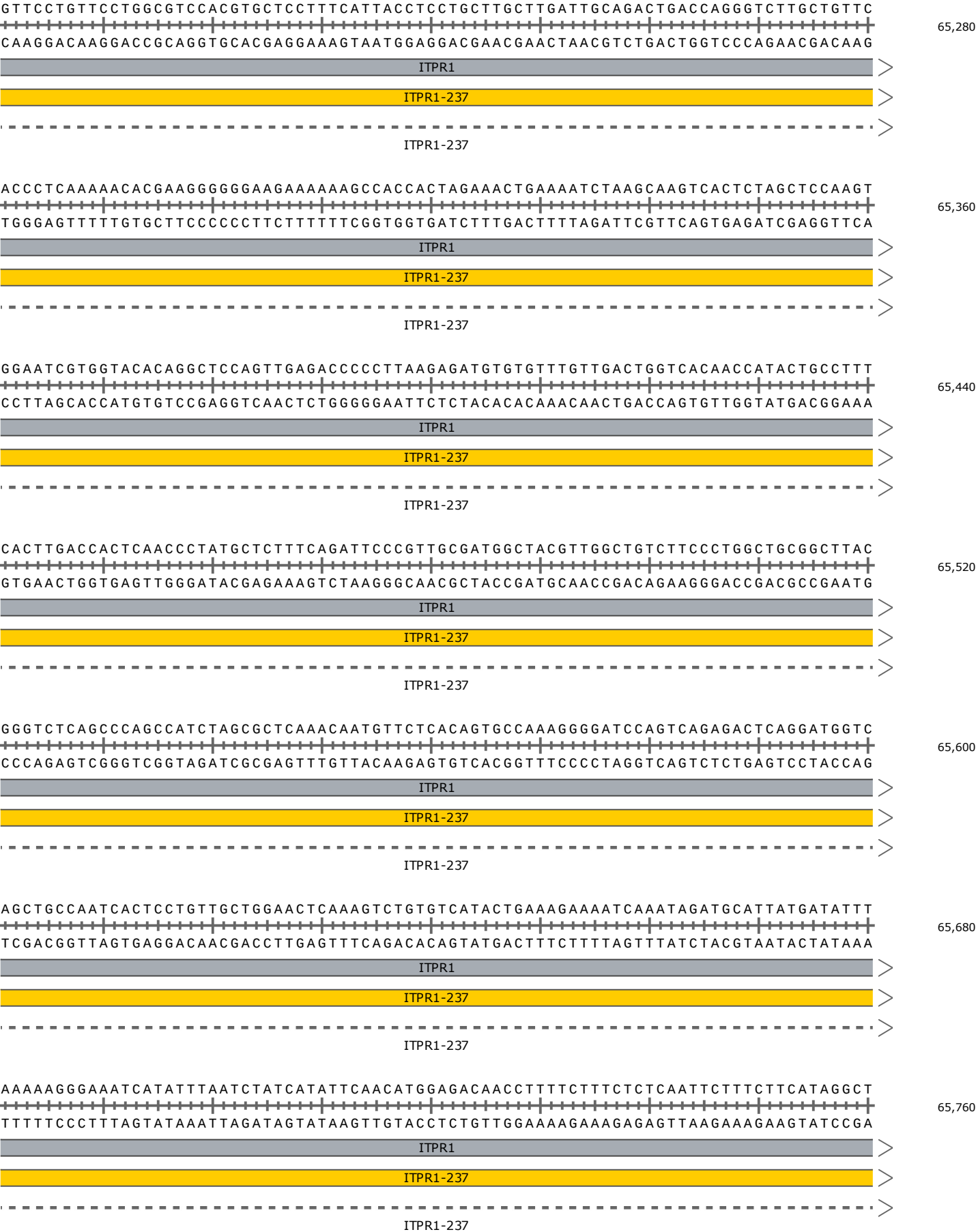
64,080

ITPR1

ITPR1-237

ITPR1-237





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AAGAACTTACATCGAAAGTTTGAACATGAAGAGAATACTTCAGTCGGAAAATTTAGTGACGCAAGGGTCACTGAAGAAGT

65,840

ITPR1

ITPR1-237

ITPR1-237

GAGAGTGCTGATGTGTTTATACTGGTGCCTGAGACTGGAATACCAGTAAAGTTGTATCTTGTTTCCAGAATGGGGTATTC
CTCTCAGGACTACACAAATATGACCACGGACTCTGACCTTATGGTCATTTCAACATAGAACAAAGGTCTTACCCCATAAAG

65,920

ITPR1

ITPR1-237

ITPR1-237

CAAGTCATTAAAGCATCTTGCAACGAAACTTTCTTCCCCACCTGTGAGCAGTTTATTTAAAAAGTACTTAAAATATCACC
GTTTCAGTAATTTCTGTAGAAGCTGGCTTTGAAAGAAGGGGTGGACACTCGTCAAATAAATTTTTCATGAATTTTATAGTGG

66,000

ITPR1

ITPR1-237

ITPR1-237

AGTAACTTACCCATTTGAAGCACTCTTGGAAATTTGAATTTACAGTCAGTCCAGTGGGAAATGAGTTTCATGAGCTGATA
TCATTGAATGGGTAAACTTCGTGAGAACCTTAAACTTAAATGTCAGTCAGGTCACCCTTTACTCAAAGTACTCGACTAT

66,080

ITPR1

ITPR1-237

ITPR1-237

GAAGTTACCCTCCTTTGCTGAACTATGAAGAGAGGCATATTTGTGGGTGGAATGGAGAGAGGAAATTTGGGATTTTTTTG
CTTCAATGGGAGGAAACGACTTGATACTTCTCTCCGTATAAACACCCACCTTACCTCTCTCTTTAAACCCTAAAAAAC

66,160

ITPR1

ITPR1-237

ITPR1-237

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66,240

ITPR1

ITPR1-237

ITPR1-237

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66,320

ITPR1

ITPR1-237

ITPR1-237

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66,400

ITPR1

ITPR1-237

ITPR1-237

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66,480

ITPR1

ITPR1-237

ITPR1-237

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66,560

ITPR1

ITPR1-237

ITPR1-237

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66,640

ITPR1

ITPR1-237

ITPR1-237

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ACTAAGGCCTTTCCTCAGGTCCCTTTTAAATATGTCGGAAGTCTGAAATCTTGGAAGTCTAATCCTCCACCAGAACCCG

66,720

ITPR1

ITPR1-237

ITPR1-237

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66,800

ITPR1

ITPR1-237

ITPR1-237

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66,880

ITPR1

ITPR1-237

ITPR1-237

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66,960

ITPR1

ITPR1-237

ITPR1-237

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67,040

ITPR1

ITPR1-237

ITPR1-237

TCCTGTATTGTTTTAAAGAAGATTCCAGACAAAATGCCATTTACCTATGTTGGGTTTTTTTTATATATTTGATATCTG
AGGACATAACAAAATTTCTTCTAAGGTCTGTTTTACGGTAAAATGGATACAACCCAAAAAAAATATATAAACTATAGAC

67,120

ITPR1

ITPR1-237

ITPR1-237

CCACTCATGCCACTAATTTATTTCCCTATAGCATTATGAGGTTTTTGTGTTGTTTTGGTTTGCTTTTTGTTTTTTAAACC
GGTGAGTACGGTGATTAAATAAAGGATATCGTAATACTCCAAAAACAACAACAAACCAACAGAAAACAAAAAATTGG

67,200

ITPR1

ITPR1-237

ITPR1-237

ATTTGGCCCATCGACTATTTTTGTAAGAAAGGCTTACTCTTGGCTTATTGTATCATCTTATTCTATTACCCTGATATCTT
TAAACCGGGTAGCTGATAAAAACATTCTTTCCGAATGAGAACCGAATAACATAGTAGAATAAGATAATGGGACTATAGAA

67,280

ITPR1

ITPR1-237

ITPR1-237

AATATTTTTTCGGACCTTGGAATAAACCTTGTGGTTGAAATAACATTTTTATATTGCTATGTGGAAGCTGACCTGTAAG
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67,360

ITPR1

ITPR1-237

ITPR1-237

CCTTTTCAATTTGTCTTAATTTATCAACTTACCCCAAAGAGATTTTTGTTTGTTATTGTTAGTTGTCCTTCAAATTAC
GGAAAAGTTAAACAGAATTAAAATAGTTGAATGGGGTTCTCTAAAAACAACAATAACAATCAACAGGAAGTTTAAATG

67,440

ITPR1

ITPR1-237

ITPR1-237

TGTTCTGTCTTATCATTGTGTGAGAGGGAACCTTCAGTCAATATTTTAGATTGCTACCGTTTTTTAAAAACATCTGGTTT
ACAAGACAGAATAGTAACACACTCTCCCTTGAAGTCAGTTATAAAATCTAACGATGGCAAAAAATTTTTGTAGACCAAA

67,520

ITPR1

ITPR1-237

TCTGAGAAAATATTGAAGTTAACTTCAGAGTTTCTAAATGCTTCCATGAATAATTTATTCTTTCGCCAAGTGAACTGGG
AGACTCTTTTATAACTTCAATTGAAGTCTCAAAGATTACGAAGGTACTTATTAAATAAGAAAGCGTTCACTTTGACCC

67,600

ITPR1

ITPR1-237

CCAATTATAACTGAGTACCCCTGTGTGTTTTGAATATTCGTCCCTCGGTGATGCATTAAATGCAGAAGCTGATTTTATTA
GGTTAATATTGACTCATGGGGACACACAAAACCTATAAGCAGGGAGCCACTACGTAATTTACGTCTTCGACTAAAATAAT

67,680

ITPR1

ITPR1-237

TCCTGTTTGAATTAAGGGTGAGGCGCTCAGGCAAGTTCTGGTCAACCGTTACTATGGAAACGTCAGACCTTCGGGACGAA
AGGACAAACTTAATTCCCACTCCGCGAGTCCGTTCAAGACCAGTTGGCAATGATACCTTTGCAGTCTGGAAGCCCTGCTT

67,760

ITPR1

ITPR1-237

G E A L R Q V L V N R Y Y G N V R P S G R
ENSE00003505787

ITPR1-237

GAGAGAGCCTTACCAGCTTTGGCAATGGCCCACTGTCTCAGCAGGAGGACCCGGCAAGCCCGGGGGAGGAGGTACGCTTTGT
CTCTCTCGGAATGGTCGAAACCGTTACCGGGTGACAGTCGTCCTCCTGGGCCGTTCTGGGCCCTCCTCCATGCGAAACA

67,840

ITPR1

ITPR1-237

R E S L T S F G N G P L S A G G P G K P G G G
ENSE00003505787

ITPR1-237

GGTGTAATTACCTTCGTGTGTGAATCAAGTGTGTTCTGTGATAGCTGCATGTTTCCTCCTAACAGGTTGAAATGCTCACA
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67,920

ITPR1

ITPR1-237

ACAGATGAATTTGTGTTGCAGGTGTATTTTTAGCAACTTGTTTTGTCTTTGGTCTACCATCAAATTGATGCCTAAACAT
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68,000

ITPR1

ITPR1-237

ITPR1-237

ATTTTCCTGCAAAC TAGCATTTCCTGCAAAC TAGATGGTGGCTAAGCCTTTTGCTCCTCCTTCCCATGCAGTGACCATCT
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68,080

ITPR1

ITPR1-237

ITPR1-237

TGGTGATGGTTGAATGATTTGAGGGATTTGATTTTATTGCACTTCGTCCCGTGGTTGTTAGGACTCTTGCTCTTCCGTAA
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68,160

ITPR1

ITPR1-237

ITPR1-237

AATAATGAGGATATTGGCACCCAGGATAGTGAAAGCTGCCATTTATTATACATTTACTGAATGCCAGGGGCTTTCCTAAG
TTATTACTCCTATAACCGTGGGTCTATCACTTTCGACGGTAAATAATATGTAAATGACTTACGGTCCCCGAAAGGATTCT

68,240

ITPR1

ITPR1-237

ITPR1-237

TGCATTGCATTCTTTGTCTCATTTTCTCCTCCCAGCTACTCATTATATGATAGGTACAGTCTATCCCAGTTCCACAGAGG
ACGTAACGTAAGAAACAGAGTAAAAGAGGAGGGTCGATGAGTAATATACTATCCATGTCAGATAGGGTCAAGGTGTCTCC

68,320

ITPR1

ITPR1-237

ITPR1-237

AAATGGAAGCTTGTTAGTGGCTGGTCTGTAATTTAGCCTGGTATATCTAATTCTAATGCCCATGCTGTGTACATCCACA
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68,400

ITPR1

ITPR1-237

ITPR1-237

AACTCCTATGGGAGTTTACAAAAAACATCCCTGTACAGAAGTGCTTACTTTAAATCAGTTTAAGCACAATTACAGGTAA
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68,480

ITPR1

ITPR1-237

ITPR1-237

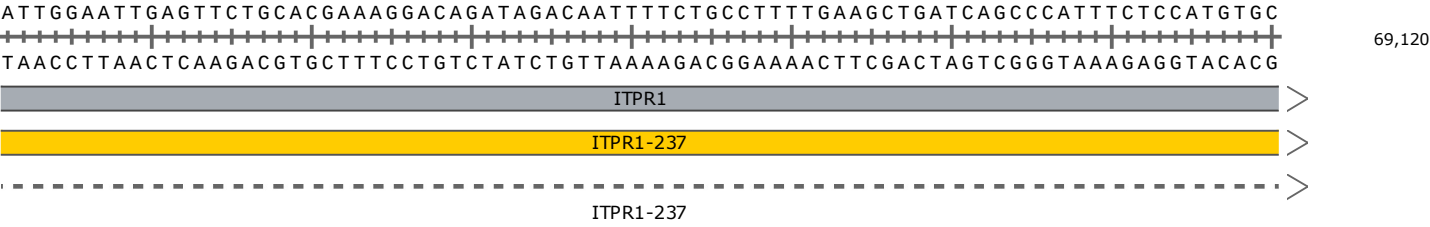
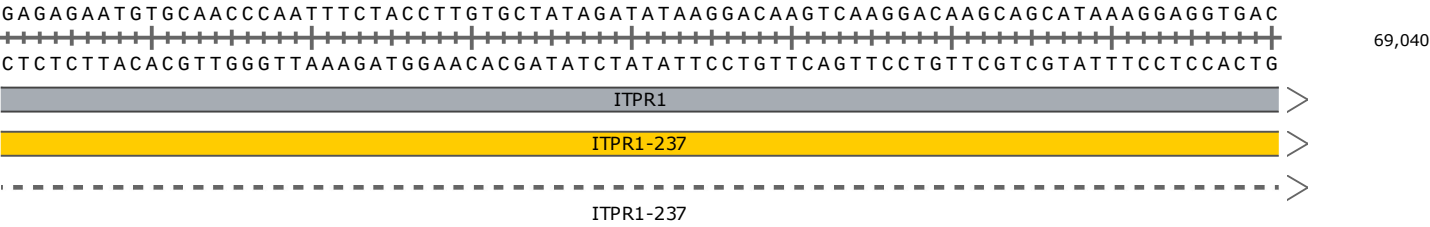
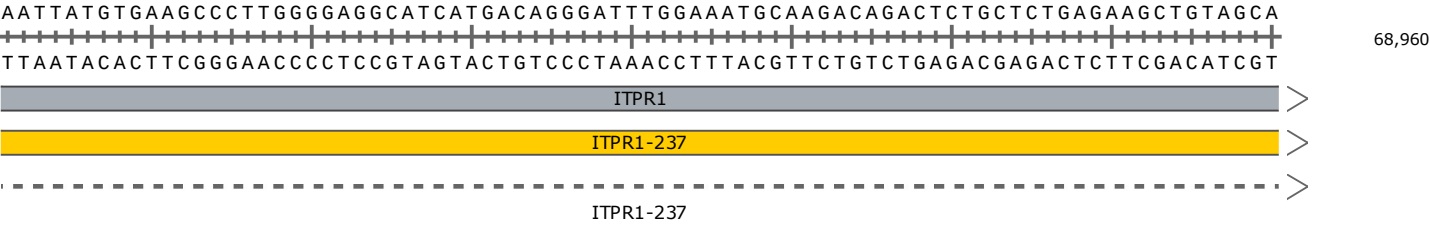
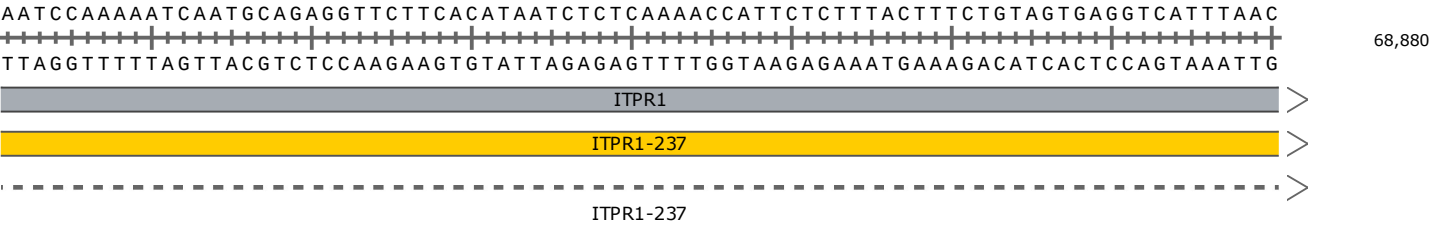
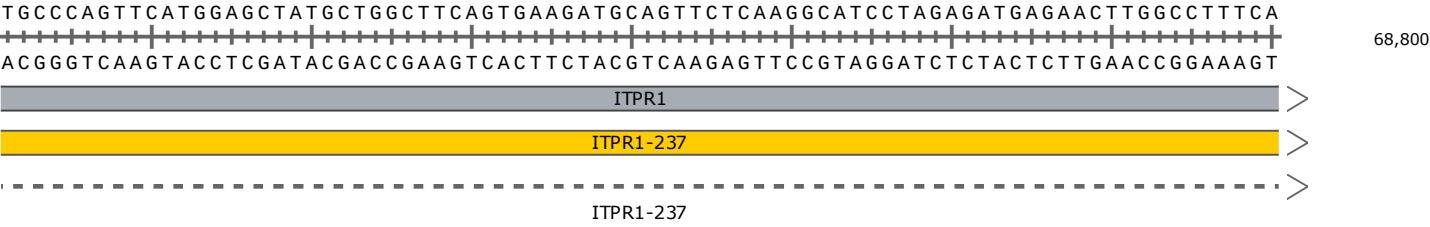
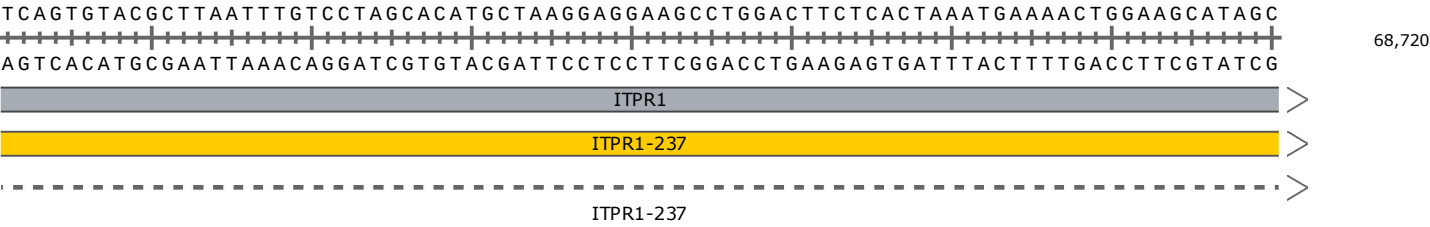
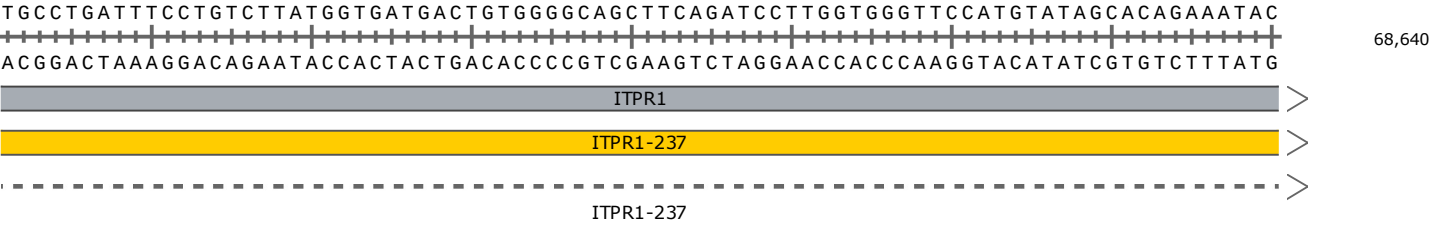
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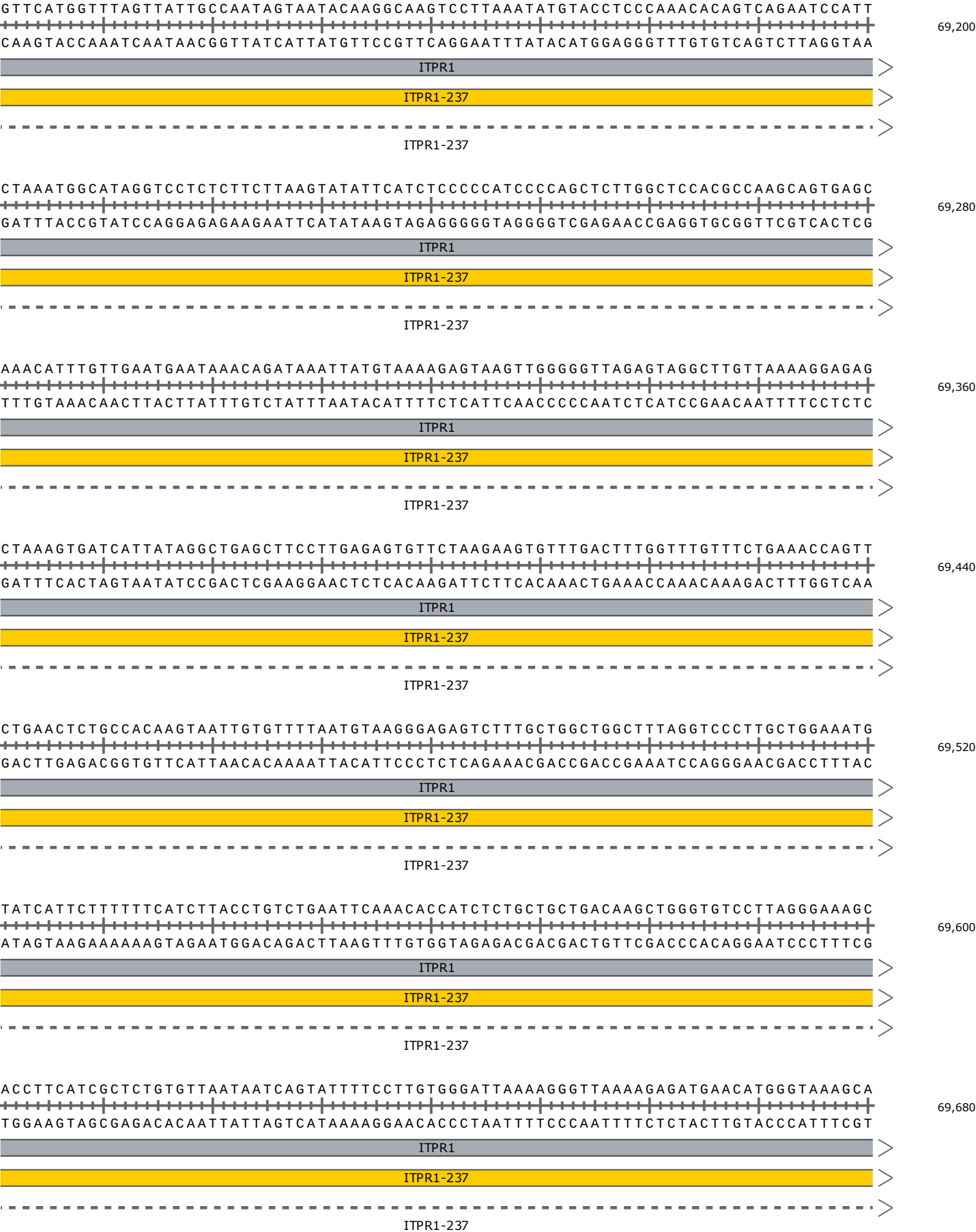
68,560

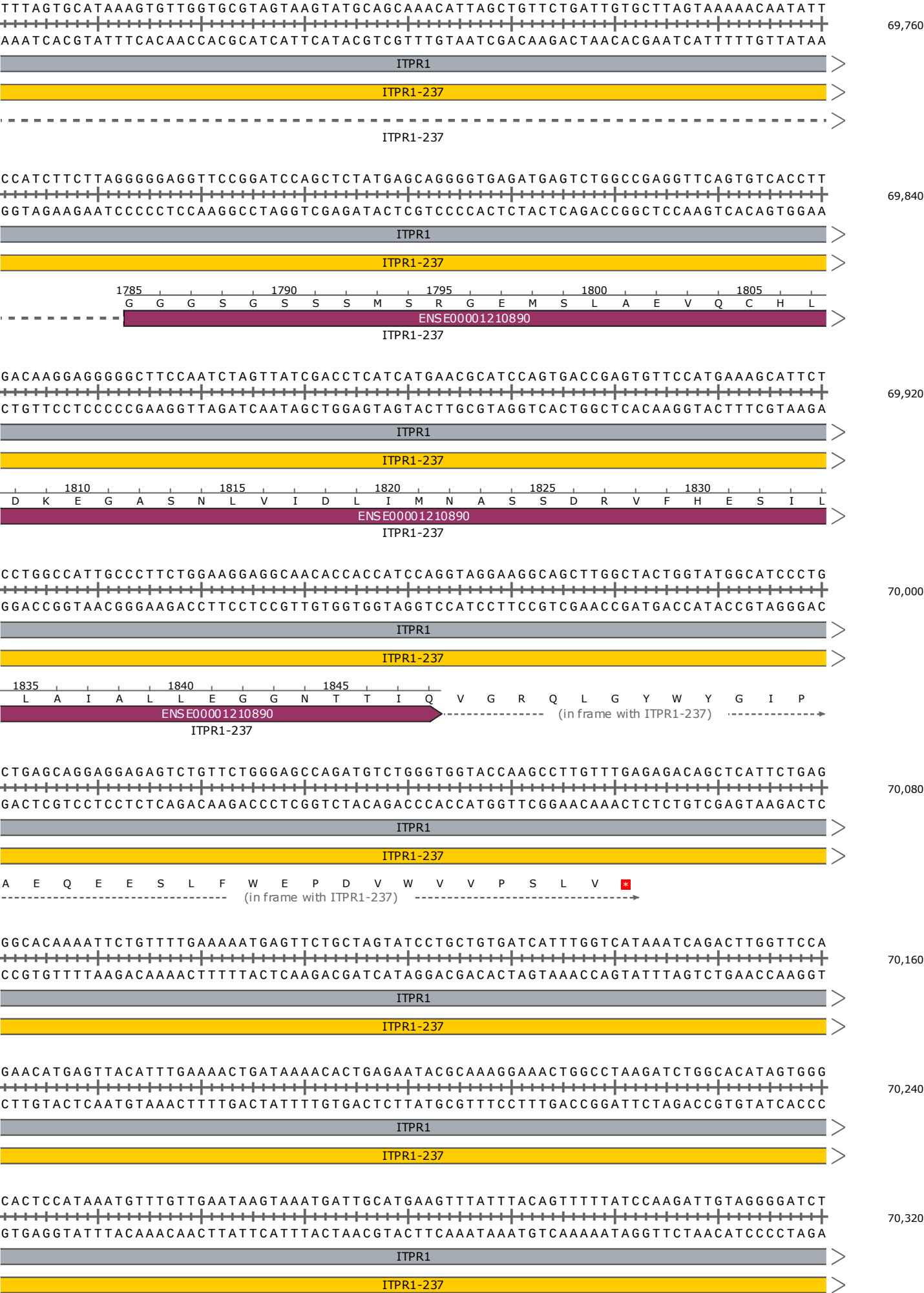
ITPR1

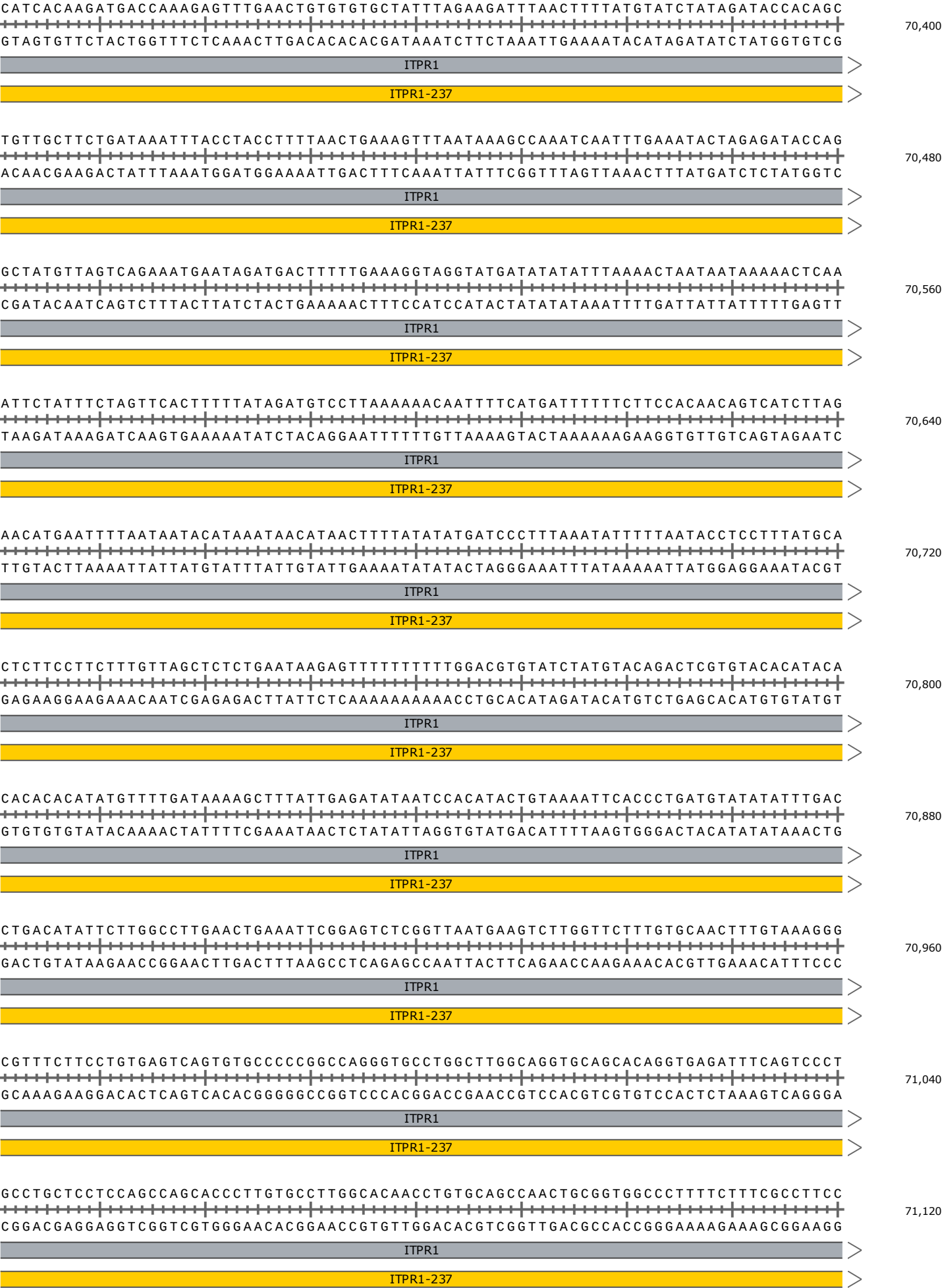
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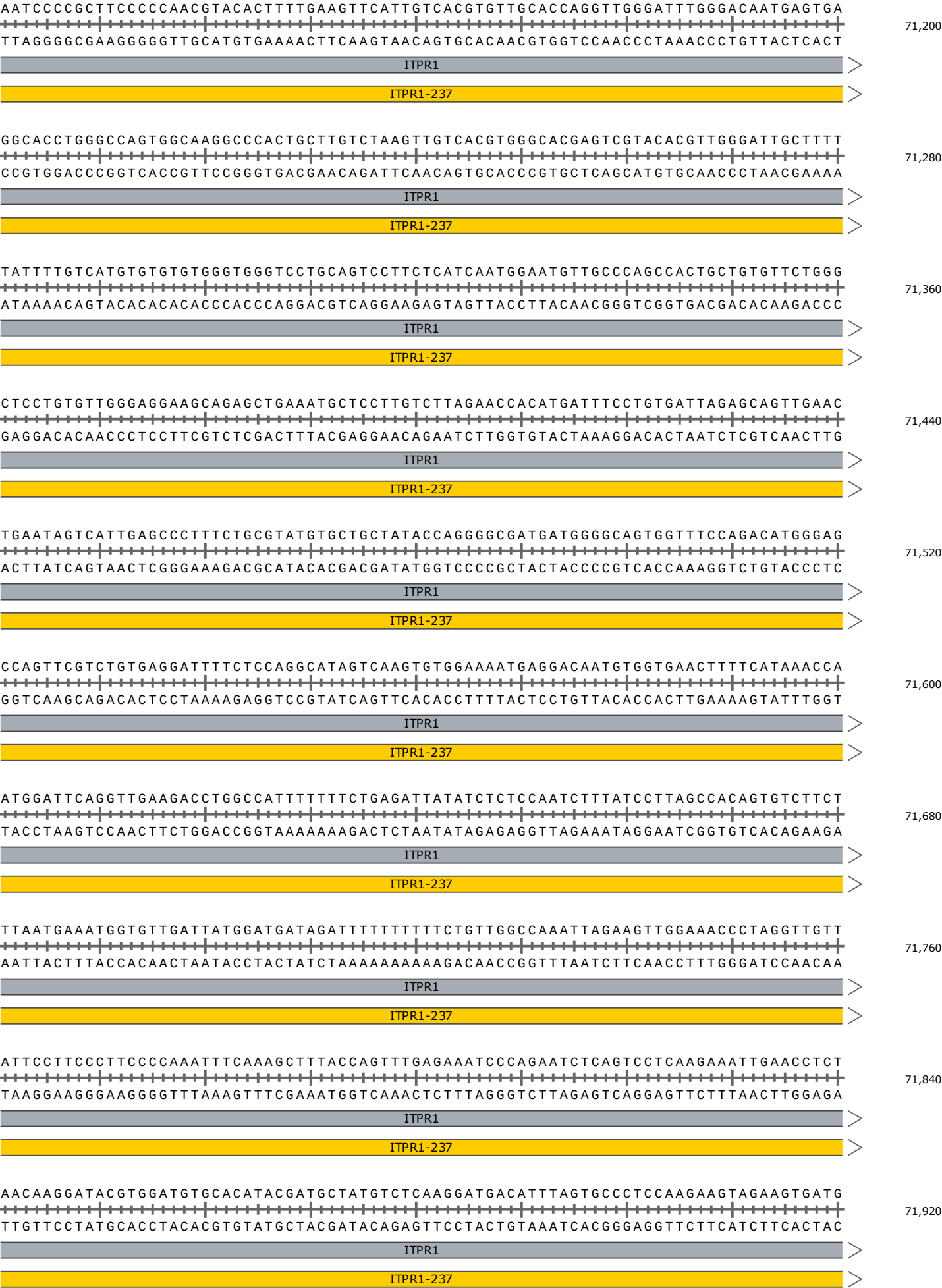
ITPR1-237











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GGCCCCTTGGTGGTTCTTCTTCTGGTCGTAGAGAGACCCCTCGGACGTCTGCCAGACACCTACTTTACCCGAAAGTTC

72,000

ITPR1

ITPR1-237

GATGGACATGGGACTGAAAGGGGGAAATTGGGCATGGACCTGGGGCATAAGGAATCTTTGTCATATTCCATGGTAGAGAG
CTACCTGTACCCTGACTTTCCCCCTTTAACCCGTACCTGGACCCCGTATTCTTAGAAACAGTATAAGGTACCATCTCTC

72,080

ITPR1

ITPR1-237

GGCCAGAGGTGTGAGAGCAGCAGTTGGGTTTCCAGAACAGCGGTTGGGTCTTTCAGACCGAGGAGTGCTATGTAGAAGT
CCGGGTCTCCACACTCTCGTCGTCAACCCAAAGGTCTTGTGCGCAACCCAGAAAGTCTGGCTCCTCACGATACATCTTCA

72,160

ITPR1

ITPR1-237

GAAGGGCCTTGGATGGGGGTTGGGGTTCATATATAGGAGCAGTGCAGCCCTCCAAGGGGCTTTGGAGCTGTAACGGAGGA
CTTCCCGGAACCTACCCCCAACCCCAAGTATATATCCTCGTCACGTGCGGAGGTTCCCCGAAACCTCGACATTGCCTCCT

72,240

ITPR1

ITPR1-237

CTATACACCTGGCAGTAGAGGACAGGTAAACTGAGGAAAGCAGGGTCCCAAGGAGGCAGTCTAAGAATTAAGGTTAAT
GATATGTGGACCGTCATCTCCTGTCCATTGACTCCTTTCGTCCAGGGTTCCTCCGTCAGATTCTTAATTTTCAATTA

72,320

ITPR1

ITPR1-237

GGGCAGTAATTTGTGGAAGAGCTGATGAGAACCTGAACTTAAATCTCTGATAAAAGAGTTCATATCTTGGGAGAGGATAT
CCCGTCATTAAACACCTTCTCGACTACTCTTGGACTTGAATTTAGAGACTATTTTCTCAAGTATAGAACCCTCTCCTATA

72,400

ITPR1

ITPR1-237

TTTCTCATAATGGCACAAGAGAGCTCTCTGGGTGCTGGAAACATATTGACCTCTTTGTTTGGGTGGTGGTTACATGACT
AAAGAGTATTACCGTGTTCTCTCGAGAGACCCACGACCTTTGTATAAGCTGGAGAAACAAACCCACCACCAATGTACTGA

72,480

ITPR1

ITPR1-237

GTGCACATGTTTTAAACTCCGTGATCGTATCCTTTGCTGGGACACGGATGGAGCTGGAGACCATTATCCTTAGCAAAATA
CACGTGTACAAATTTTGAGGCACTAGCATAGGAAACGACCCTGTGCCTACCTCGACCTCTGGTAATAGGAATCGTTTTAT

72,560

ITPR1

ITPR1-237

ACACAGGAACAGAAAATCAAATACCGCATGTTCTCAGTTATAAGTGGGAGCTAAGTGACAGGAACACATGGACACTTATA
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72,640

ITPR1

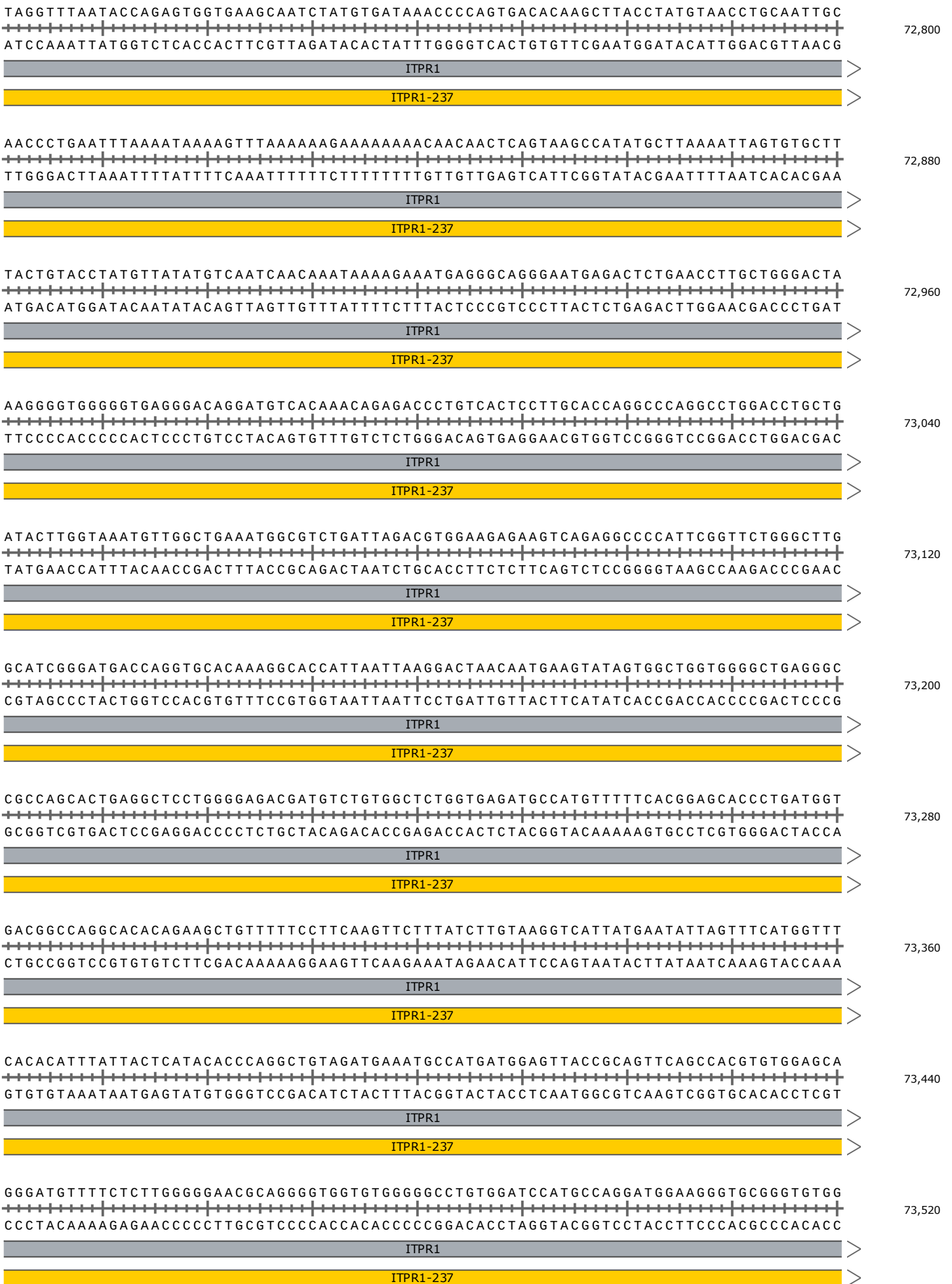
ITPR1-237

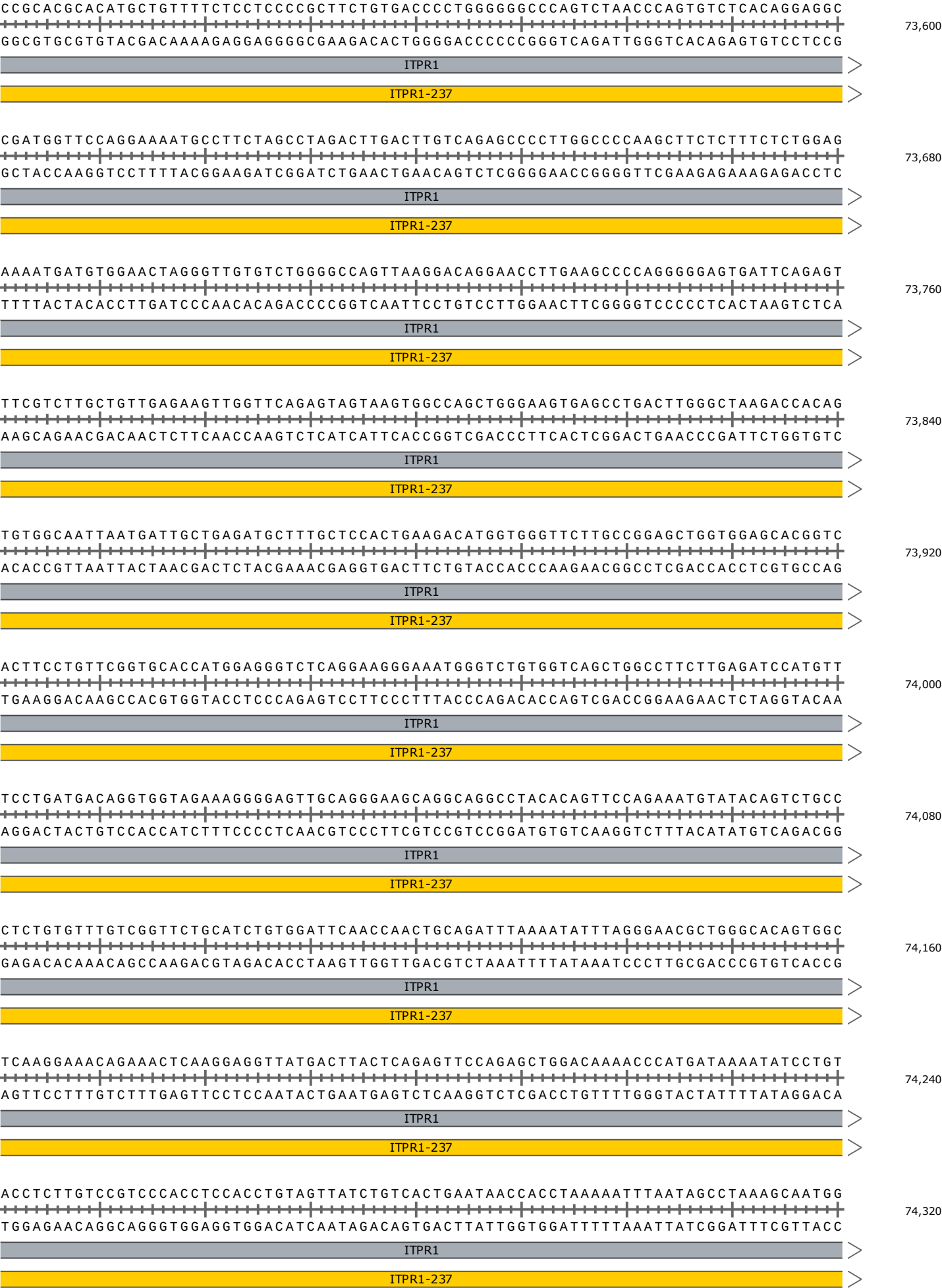
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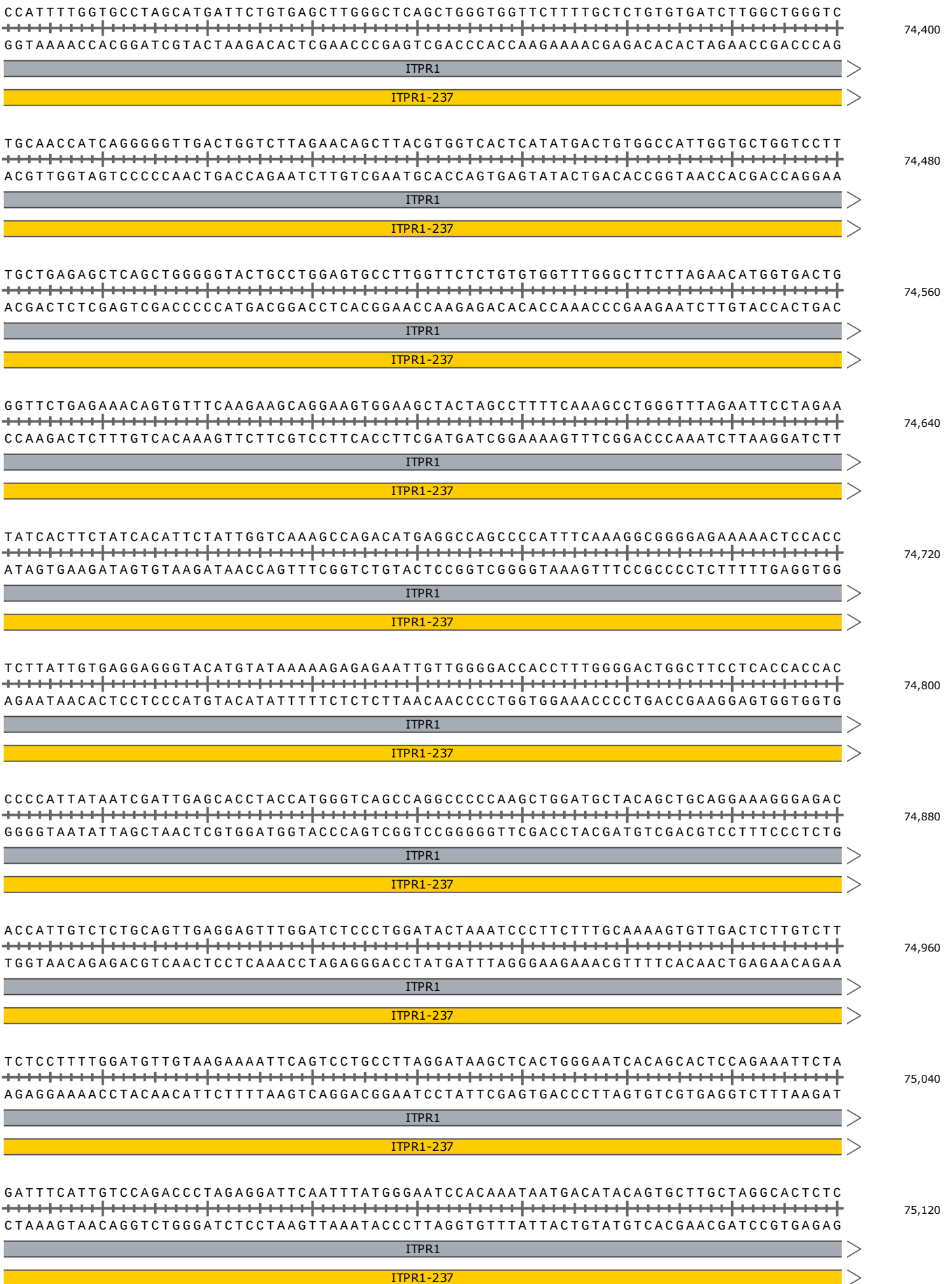
72,720

ITPR1

ITPR1-237







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75,200

ATACAGGTTACTTCCCAGTCTGGCATAATGGACTCCCAGGGGTGGTGTCCCCAGGTCTCCCAGCATCTTTTCTTCTGCC
TATGTCCAATGAAGGGTCAGACCGTATTACCTGAGGGTCCCCACCACAGGGGTCCAGAGGGTCGTAGAAAAGAAGGACGG

75,280

CCGGCTCCTGCAATGGTGATAACATCTGAGGGTAGATCGTGACTCCCAGACTTCTCCTACCTGGCTGCCATCAGAGCAGG
GGCCGAGGACGTTACCACTATTGTAGACTCCCATCTAGCACTGAGGGTCTGAAGAGGATGGACCGACGGTAGTCTCGTCC

75,360

CTTCACATTGAACCCTCCGCTTATGGGAACAAGGAGACAGTACCACAGCCCGTGGATTTTCCAGAAACGGGTGACACGTT
GAAGTGTAACCTGGGAGGCGAATACCCTTGTTCTCTGTGCATGGTGTCTGGGCACCTAAAAGGTCTTTGCCCACTGTGCAA

75,440

GTCAAGTGATAGGATCACGCTTGTCTTGAAGAGAACTTCCGGCTTTCTTTCTCCCACTCTGGTGCCACCCGCTTCTGT
CAGTCCACTATCCTAGTGCGAACAGAACTTCTCTTGAAGGCCGAAAGAAAGAGGGGTGAGACCACGGTGGGCGAAGGACA

75,520

CAGCCCCCAGAAGAAATATTTCTTGTGGCTTGATGTTTTGTAGCAAGTGGGAAACTATAAAATAAGCATTGCTTATGA
 GTCGGGGGTCTTCTTTATAAAGGAACACCGAACTACAAAACATCGTTACCCTTTGATATTTATTTCGTAAACGAATACT

75,600

ATTAAATTTTGGCACACATGGGGCTCAGCAGGGCTCACGGCACTTTCATATCCGTCCTTCGAGTCCTTGCCAATTTCTAT
TAATTAAAAACCGTGTGTACCCCGAGTCGTCCCGAGTGCCGTGAAAGTATAGGCAGGAAGCTCAGGAACGGTTAAAGATA

75,680

GTTCCTTCCTCCTAAGATGTTCCCACCAGCGCCTGGGGGAAGTTCCTTTCGCTTCCTCTTCTTTACAGAAGGACAGGGGC
CAAGGAAGGAGGATTCTACAAGGGTGGTCGCGGACCCCTTCAAGGGAAGCGAAGGAGAAGGAATGTCTTCCTGTCCCCG

75,760

TGTCTTACCTGGAATGAAGAGGAGGACAGGCTATCTTTGGACATACCTCGTTTTTTATTTTTGTTTTTTTAAGCCAAT
 ACAGGAATGGACCTTACTTCTCCTCCTGTCCGATAGAAACCTGTATGGAGCAAAAAATAAAAAACAAAAAAATTTCGGTTA

75,840

ACAGATGTTTTGGGATATATAIGCTGACATGACCATAGAGAACCTCCTAGCACATTATGGGGATAGATAGTTAAACATT
TGTCTACAAAACCTATATATACGACTGTACTGGTATCTCTTGGAGGATCGTGTAATACCCCTATCTATCAATTTGTAA

75,920

TTTTGGACTAATTGCTTCTGGTTTCAGAAGCACTGGGAATTTTCATGTATCAAATGGCTGCCACGCTCTATTCTATGCCA
+++++
AAAACCTGATTAACGAAGACCAAAGTCTTCGTGACCCTTAAAGTACATAGTTTACCGACGGGTGCAGATAAGGATACGGT

76,000

ITPR1

>

ITPR1-237

>

AAGTCTAGTCTACAGACACACCCGAAAAGGGTTTTCTTTTCTGCACGTAAGCAGCTAGAGATGGAAAATGTGAGAAGTGC
+++++
TTCAGATCAGATGTCTGTGTGGGCTTTTCCCAAAGAAAAGACGTGCATTTCGTGCATCTCTACCTTTTACACTCTTCACG

76,080

ITPR1

>

ITPR1-237

>

TCCGTCAGGAAACTGGCCTGCAAATTCAGCAGAGAGAGTGATCCCTGGTTCATGAGGCCTTTCCTACACCACACTCTTTT
+++++
AGGCAGTCCTTTGACCGGACGTTTAAGTCGTCTCTCTCACTAGGGACCAAGTACTCCGGAAGGATGTGGTGTGAGAAAA

76,160

ITPR1

>

ITPR1-237

>

TTTTTTTTTGAGGTTGGCTTAAGAAATCAGCCCAAGAACAAGTGTTAGATAGGAAATCTCACATCCCTTCCGGAAGTCAC
+++++
AAAAAAAAAACTCCAACCGAATTCTTTAGTCGGGTTCTTGTTTACAATCTATCCTTTAGAGTGTAGGGAAGGCCTTCAGTG

76,240

ITPR1

>

ITPR1-237

>

CAACACAGTGTGGGAGGGACACGTTGGTTGGGCTATCTCTGACCCCAAGTTAGCAAAGAGATGAGGGCGGAAAGGGCAATT
+++++
GTTGTGTCACACCCTCCCTGTGCAACCAACCCGATAGAGACTGGGGTCAATCGTTTCTCTACTCCGCTTTCCCGTTAA

76,320

ITPR1

>

ITPR1-237

>

TGATTTGCCTCTGCTGGAAATGGAAGGCCAGTTTGTGAGGAAGATCAGCCTTGGTTTGACAGGGCAGTCACCCTGAGGAG
+++++
ACTAAACGGAGACGACCTTTACCTTCCGGTCAAACACTCCTTCTAGTCGGAACCAAACGTGTCCTGTCAGTGGGACTCCTC

76,400

ITPR1

>

ITPR1-237

>

GAGGAAAAGATTGGTGTGTGAGCAAGTTACGTAAATGGGTGTTGTTTTGGCAGGGAAGTCAGGAATGAGTCACTTCTGA
+++++
CTCCTTTTCTAACCACACACTCGTTCAATGCATTTACCCACAACAAAACCGTCCCTTCAGTCCTTACTCAGTGAAGACT

76,480

ITPR1

>

ITPR1-237

>

GCGGTGTTTTCTAACCTCAGGTTTTATCCATGTGGGAAAGGAGTGAAGCCAGCAGTGGAGTCAGGGCAGCTCTCCTCCTG
+++++
CGCCACAAAAGATTGGAGTCCAAAATAGGTACACCCTTTCCTCACTTCGGTCGTACCTCAGTCCCGTCGAGAGGAGGAC

76,560

ITPR1

>

ITPR1-237

>

CACGTGGGGGTTTCGAGAGCTGTTGGCATTAAAGAAAGAGGGAGGCAGTGACTTGTCCCCAGCAGGCGTCCCCAGAGACAC
+++++
GTGCACCCCCAAGCTCTCGACAACCGTAATTTCTTCTCCCTCCGTCACTGAACAGGGGTCGTCCGCAGGGGTCTCTGTG

76,640

ITPR1

>

ITPR1-237

>

TGCCCTTCTGCGGAAGCTGTGAGGGGTTCAGCAAAGCCACCCAGGTTGGCTCAAGGACCAGCTTGGCTCCTTTGAGAAAT
+++++
ACGGGAAGACGCCTTCGACACTCCCCAGTCGTTTCGGTGGGGTCCAACCGAGTTCCTGGTCGAACCGAGGAAACTCTTTA

76,720

ITPR1

>

ITPR1-237

>

GGTGGCGTAAAGGTTAGGGACTCAGGGAGGACCCCTGGAAGGAGAGAGCCTATCAACTGCGGGCCTCCAGACCACAATA
CCACCGCATTTCCAATCCCTGAGTCCCTCCTGGGGGACCTTCTCTCGGATAGTTGACGCCCGGAGGTCTGGTGTTAT

76,800

ITPR1

ITPR1-237

TTTGTGCTGGAATTCCAGCTCTGCCCCTGCCAGCCTTCAGTGACCTTGGGGTTTGTGAGGGCCACTTTGAAACTCAGTTT
AAACACGACCTTAAGGTCGAGACGGGGACGGTCGGAAGTCACTGGAACCCCAAACAGTCCCGGTGAAACTTTGAGTCAAA

76,880

ITPR1

ITPR1-237

CCTCATCTGCAAAATGAGGGTTGGAAAAGCCTAGTCCCTTCTTATGGAGTTACGAAGAACATGAGGGTAAAGTGTTGG
GGAGTAGACGTTTTACTCCCAACCTTTTCGGATCAGGGAAGGAATACCTCAATGCTTCTTGTAAGTCCCATTTCACACACC

76,960

ITPR1

ITPR1-237

TCCGGTAGACAAGTGGAGCTGCTGCCAGGGCTGCTGATTCTGTGGTGTGGGTACAGCCTGGGCTCAAGCCCTGCCTCCTA
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77,040

ITPR1

ITPR1-237

TATGCCACCTCAGGACTCCTGGCGAAGTCCACCTCACTCATCCCACTGGTTCCTGACTTGGAGAATAGGATGGTGACGG
ATACGGGTGGAGTCTGAGGACCGCTTCAGGTGGAGTGAGTAGGGTGACCAAGGACTGAACCTCTTATCCTACCACTGCC

77,120

ITPR1

ITPR1-237

TTCCACCTCAGAGAACTCCTGAGATGTTTTACAGACTATTTATAGAAAGCACCTCACGTGGCATCTGGCCAATACAAA
AAGGGTGGAGTCTCTTGAGGACTCTACAAAAGTGCTGATAAATATCTTTCGTGGAGTGACCCGTAGACCGGTTATGTTT

77,200

ITPR1

ITPR1-237

GATCTCAAGATGATGTGGTTCTTATTTTTATTGTTTCATATATATTTTAAAGAGATAGGGTCTTGCTATGTTGCTGAGGC
CTAGAGTTCTACTACACCAAGAATAAAAATAACAAGTATATATAAAAATTCTCTATCCCAGAACGATACAACGACTCCG

77,280

ITPR1

ITPR1-237

TAGACTTGAACCTCCTGGGCTCAAGCATTCTCCTCCCTCAGCCTCCTGAGTAGCTGGGACTATAGGTGCGGACCACCATG
ATCTGAACCTTGAGGACCCGAGTTCGTAAGGAGGAGGGAGTCGGAGGACTCATCGACCCTGATATCCACGCCTGGTGGTAC

77,360

ITPR1

ITPR1-237

CTCGGTTCTAATTAATAATATTTTTATTTATTTTAAATACATGCTGTATTTTGTGAAATGTGTTTTCTGTCTAAATCCT
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77,440

ITPR1

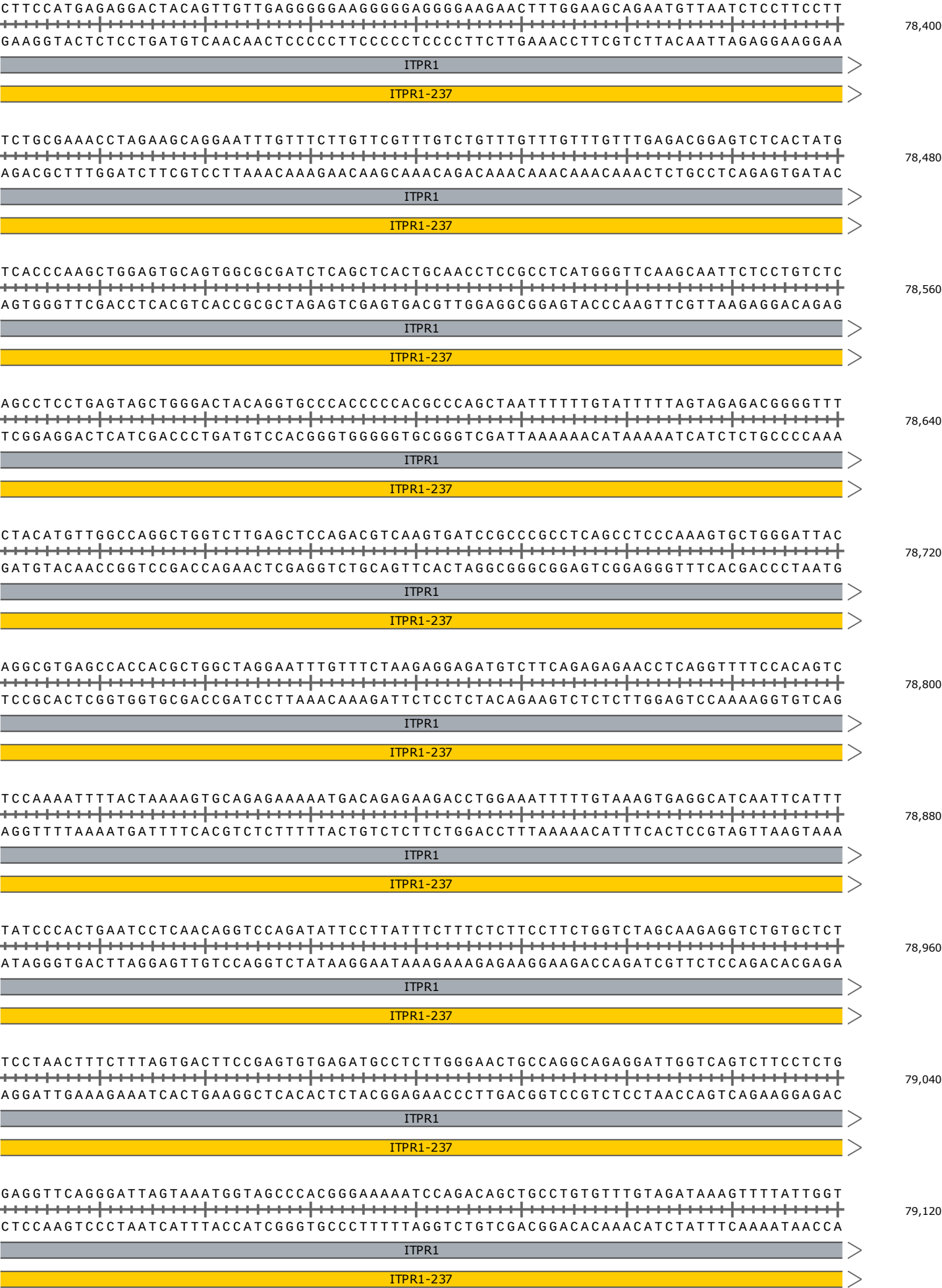
ITPR1-237

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77,520

ITPR1

ITPR1-237



GCATAGCTGCAGTTTTTCTTTGGGATTGTCTAACTGCTTTCTGCTTCAGGGGCAGAGTTGAGTAGTTGTGACAGATA
CGTATCGACGTCAAAAAGGAAACCCTAACAGGATTGACGAAAGGACGAAGTCCCCGTCTCAACTCATCAACACTGTCTAT

79,200

ITPR1

ITPR1-237

GCTGCAATGACCCTCAGCGTGTGAAATGTTTACCATTGGCCCTTTGGAAAAATGTTTGCTGACCCTAGGGTTTGTTTAA
CGACGTTACTGGGAGTCGCACACTTTACAAATGGTAAACCGGGAAACCTTTTTACAAACGACTGGGATCCCAAACAATT

79,280

ITPR1

ITPR1-237

TCTTTACTATGTAGATGTTAAACTGCCTAAGGGAAAGAACCACAGTATTTCCCTTTGTTCTGTGCTCCTCATCCCCTGG
AGAAATGATACATCTACAATTTGACGGATTCCCTTTCTTGGTGTCTATAAAGGGGAAACAAGACACGAGGAGTAGGGGACC

79,360

ITPR1

ITPR1-237

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79,440

ITPR1

ITPR1-237

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79,520

ITPR1

ITPR1-237

[illegible]

79,600

ITPR1

ITPR1-237

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AGAGAGGAAGAGAAAGGAAGGAAGGAGGAAGGGAAAGAAAAGAAGAAATAGAGAAAGAAAAGGAAAGAGAAAGACACAAA

79,680

ITPR1

ITPR1-237

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79,760

ITPR1

ITPR1-237

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AAAGGAAGGGAAGGAAAGGGAAAAGGAAGTAAAAAAGAAAGAAAAGAAAGAAGGAAAACCACTCTGCTGTCCCAAC

79,840

ITPR1

ITPR1-237

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AAAAAATTTCTGCAAAAGAAGGGATCTCAGTAGAGACGAGAGGGGTGTATCGGAGACGGTCTACATGAGGTAGTGGGG

79,920

ITPR1

ITPR1-237

ACCGCCTGCCAGCATAGGGCTGCTGAGATCTGCACCTGTCAGCCTTTTTGCCTGGATAACTGAGATAGCCTTTTAGTGGC
TGGCGGACGGTCGTATCCCGACGACTCTAGACGTGGACAGTCGGAAAAACGGACCTATTGACTCTATCGGAAAATCACCG

80,800

ITPR1

ITPR1-237

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GAGGACGGAGACCCGTAAAGAGAGAAGGTGCGCCAACAGTCACTACGGGGGGTTTACCTTGGGAGTGATGGACGAAGGGG

80,880

ITPR1

ITPR1-237

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80,960

ITPR1

ITPR1-237

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GGACCCAAAGAGGTGAGTGAGGGGATGCGAATAACAGGACGTCGACGTTGAGTACGGACGGTTAGGGGTGCCCCGGTAC

81,040

ITPR1

ITPR1-237

AACTCAGATGCCTTTGCTTCATGTGGGACGTGCCCTCATTCCCTTTGGCAGGCTCCCCAAGCCCTGATTGAAATGTCTCC
TTGAGTCTACGGAAACGAAGTACACCCTGCACGGGAGTAAGGGAAACCGTCCGAGGGGTTGCGGACTAACTTTACAGAGG

81,120

ITPR1

ITPR1-237

TACTCTAGAAACTTCCTCTTGATCCCCTGAGGCAGAGATAATGGGTTGTGCTTCATTTACTGTAGTAATGACCACACTTC
ATGAGATCTTTGAAGGAGAACTAGGGGACTCCGTCTCTATTACCCAACACGAAGTAAATGACATCATTACTGGTGTGAAG

81,200

ITPR1

ITPR1-237

AACTGGAGCTTGACTGTAAGACCCGAGGGGGCAGAGACCAAGTCTGTCTTCACTCCGAGTCCCCTCGAGGAGCCTCCACA
TTGACCTCGAACTGACATTCTGGGCTCCCCGTCTCTGGTTTCAGACAGAAGTGAGGCTCAGGGGAGCTCCTCGGAGGTGT

81,280

ITPR1

ITPR1-237

CGTGCTGGATGAAAGGTCCTCAGTGTGTACATGATGAATCAGTGTGGATACTCCTACTGTATAAACTATTCTGGGAATTC
GCACGACCTACTTTCCAGGAGTCACACATGTACTACTTAGTCACACCTATGAGGATGACATATTTGATAAGACCCTTAAG

81,360

ITPR1

ITPR1-237

ACTGAGATAATATGTGGAAGGCACTCAGCTCAGCATGGAGCTTTTAACACATCGTAACAGCTCATCCAAAGCAACTCTGC
TGACTCTATTATACACCTTCCGTGAGTCGAGTCGTACCTCGAAAATTGTGTAGCATTGTGAGTAGGTTTCGTTGAGACG

81,440

ITPR1

ITPR1-237

TTACTTTTTGGTTGTTTATCTTCCCTCACCCACTAACTCGCCCAAGGGTGCACTTTCTTCCGGGGTCAAGTCTCCATCTG
AATGAAAAACCAACAAATAGAAGGGAGTGGGTGATTGAGCGGGTCCCACGTGAAAGAAGGCCCCAGTTTCAGAGGTAGAC

81,520

ITPR1

ITPR1-237

ACTCCCCAGCACTCAGACTGTAAATGTAGAGATAGAAGTTCTGACCCAGTGTGGCCACCGTGTTACTTTAGCCTTCTTAC
TGAGGGGTCGTGAGTCTGACATTTACATCTCTATCTTCAAGACTGGGTACACCCGGTGGCACAATGAAATCGGAAGAATG

81,600

ITPR1

ITPR1-237

CATTTTTGAATAGAAACATGAGGATGTGAAATGTGAACCTTGTGTTGTTGATGATTATTGCCATTTTAAAGGGGACCTTCT
GTAAAAACTTATCTTTGTACTCCTACACTTTACACTTGAACACAACAACACTACTAATAACGGTAAAATTTCCCTGGAAGA

81,680

ITPR1

ITPR1-237

TTAGGTGTGGGAGGGAATTGATCTGAGCCCATGGGAAATACATGTCAACTTGGAGAAATAGCCTTATGATGGCAGCAGTC
AATCCACACCCTCCCTTAACTAGACTCGGGTACCCTTTATGTACAGTTGAACCTCTTTATCGGAATACTACCGTCGTCAG

81,760

ITPR1

ITPR1-237

CTCTTTTCTTCTTCTTTGTAATAATGATGGACAGTAGTGGTAACAAGTGCTCATGTACCACGGGCTAGCCAGGCGCCCTC
GAGAAAAGAAGAAGAAACATTATTACTACCTGTCATCACCATTGTTACGAGTACATGGTGCCCGATCGGTCCGCGGGAG

81,840

ITPR1

ITPR1-237

ACTGCATGGTCTCATCCATCTTCCTGGGGCGCCTATGTAGTAGGTACTGTTTTGATCCCTTCTGCTAATGAGGAAATAG
TGACGTACCAGAGTAGGTAGAAGGACCCGCGGATACATCATCCATGACAAAACAGGGAAAGACGATTACTCCTTTATC

81,920

ITPR1

ITPR1-237

AGGATCCGAGAGGTCAGGTTATATGCTCAGAGTCACAGAGCCAGCTGGTAGTTGTTCCAGGGTTTGTTTTCTGCCAGAAC
TCCTAGGCTCTCCAGTCCAATATACGAGTCTCAGTGTCTCGGTGCGACCATCAACAAGGTCCCAAACAAAAGACGGTCTTG

82,000

ITPR1

ITPR1-237

GTGAGTTTGTAACCTCTCTACCATGCCGCTCCTTACTCCACCAATTTCCAGGCACAGACATGGCCGCTTCAAGGACTT
CACTCAAACATTGGAGAGATGGTACGGCGGAGGAATGAGGTGGTTAAAAGGTCCGTGTCTGTACCGGCGAAGTTCCTGAA

82,080

ITPR1

ITPR1-237

TGCGTCTGTTTGCCAGGCAGATTGGAAGTTGTGCCTCCACATTTGTTTTCTTTGGTAGTGGAGTCTTTGTGGGAGACAC
ACGCAGACAAACGGTCCGTCTAACCTTCAACACGGAGGTGTAACAAAAGAAACCATCACCTCAGAAACACCCTCTGTG

82,160

ITPR1

ITPR1-237

TGTGCCCTCCTGATAATCAGAAGGCAGCTCGAGTGGTCAGTGTATTTGCTTTGTTTATAAGGTCTGCCCATGAATTCTGG
ACACGGGAGGACTATTAGTCTTCCGTGAGCTCACCAGTCACATAAACGAAACAAATATTCCAGACGGGTACTTAAGACC

82,240

ITPR1

ITPR1-237

AGGAGGAAATCATGAAAGACTTTTCTTTTCAGACTGGGCATCTCATTTGCCAAATGACAATTATGTGTGCTACATACATG
TCCTCCTTTAGTACTTTCTGAAAAGGAAAGTCTGACCCGTAGAGTAAACGGTTTACTGTTAATACACACGATGTATGTAC

82,320

ITPR1

ITPR1-237

TACTTCAGCAAGTTCCAGGTTCCAGGTTCTTAGGAAAGTTAATGACAGGAAGACTGTCCTACAGAACTTCCTCACTGTG
ATGAAGGTCGTTCAAGGTCCAAGGGTCCAGAATCCTTTCAATTACTGTCCTTCTGACAGGATGTCCTTGAAGGAGTGACAC

82,400

ITPR1

ITPR1-237

GAAGAGATTGACAGCAGCTCATCTAATTAGGGCCGTTATGAAAAGTTGGATTAATAGCGATTTTTGTTTTTCGTTGCGT
CTTCTCTAACTGTCGTCGAGTAGATTAATCCCGGCAATACTTTTCAACCTAATTATCGCTAAAAACAAAAGCGAACGCA

82,480

ITPR1

ITPR1-237

CTAAAGAAGCATATGTTCTTTGGCATCATGTGATGGTTATTAGATCTCAGCTTTTGCCCGTTTTGCTCAGAGAAGCTAAA
GATTTCTTCGTATACAAGAAACCGTAGTACACTACCAATAATCTAGAGTCGAAAACGGGCAAAACGAGTCTCTTCGATTT

82,560

ITPR1

ITPR1-237

TGCACCAGATACTCCCCACATCTGAGTCTTTACTGGTTGAAGAATATTCATGTTTGGGCGAAGGGAAAGGGAGGAAGGTC
ACGTGGTCTATGAGGGGTGTAGACTCAGAAATGACCAACTTCTTATAAGTACAAACCCGCTTCCCTTTCCCTCCTTCCAG

82,640

ITPR1

ITPR1-237

TTCTCATTTTATAAAGTGCCAGCACTGTGCGTGGAGCCAGTAGGTACTCTATCTGGGCTACATGGAATAGTCCCAATTG
AAGAGTAAAATATTTACGGGTCGTGACACGCACCTCGGTCATCCATGAGATAGACCCGATGTACCTTATCAGGGTTAAC

82,720

ITPR1

ITPR1-237

CAGATGAGGAAACTGAGTCTGAAAAAAGCCATGTGTCTTACCCAAAGTCACCCAGTTGGCAGAGCTGGGATTTGAACACA
GTCTACTCCTTTGACTCAGACTTTTTTTCGGTACACAGAATGGGTTTCAGTGGGTCAACCGTCTCGACCCTAAACTTGTGT

82,800

ITPR1

ITPR1-237

AGGCCCTCAGAAGTCTCTCAGCTTTCTCCCATGCTAGCCAGCCTTTAAGTTACATGAGTACAATGTGAGGGAGCTATTCA
TCCGGGAGTCTTCAGAGAGTCGAAAGAGGGTACGATCGGTCGGAAATTCAATGTACTCATGTTACACTCCCTCGATAAGT

82,880

ITPR1

ITPR1-237

GTGCCCTGTACCCACTTTGGAGCTCTGCCTACTAGAGAGCAGTGTCTATCTTGTTTTCGTTTGGGGTGGGAACAGGCTGC
CACGGGACATGGGTGAAACCTCGAGACGGATGATCTCTCGTCACAGATAGAACAAAAGCAAACCCACCCCTTGTCGGACG

82,960

ITPR1

ITPR1-237

ACTGGTTATTTGATCTGAGAAGCAAGTAGTCACTGCTTGGTTAGCCAATGAGTTTTAAAGGTAGACCTTTAAATGGAGT
TGACCAATAAACTAGACTCTTCGTTTCATCAGTGACGAACCAATCGGTTACTCAAAATTTCCATCTGGAAATTTTACCTCA

83,040

ITPR1

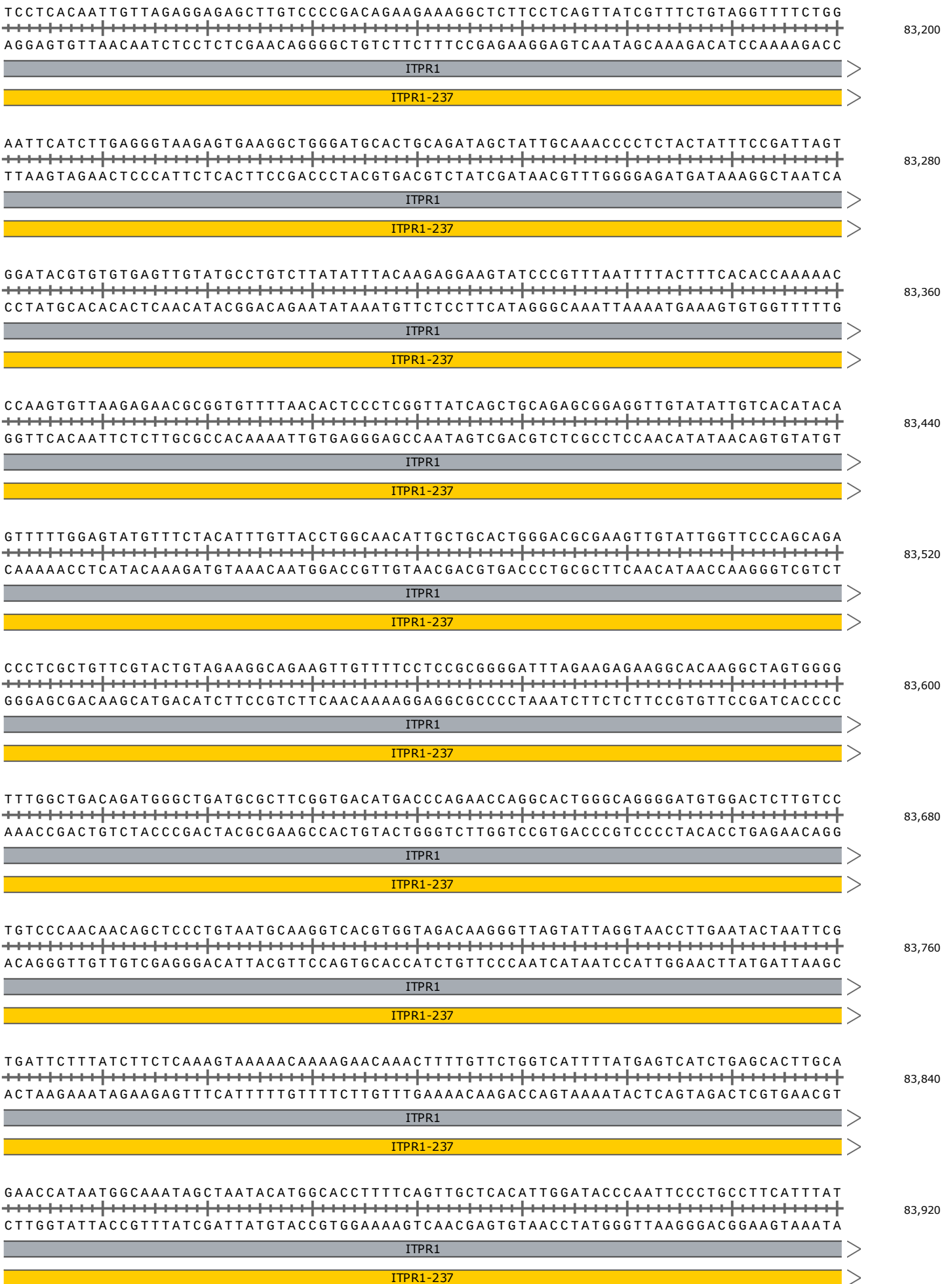
ITPR1-237

GGAATGGAAGCACATTTTTTTTTAATAACAATGCATGAGCTTTTCCTTAATTTCTGCTGGTGTCTTTCTTGTTGGGTAGCT
CCTTACCTTCGTGTAAAAAAAATTATTGTTACGTACTCGAAAAGGAATTAAGACGACCACAGAAAGAACACCCATCGA

83,120

ITPR1

ITPR1-237



GCATTATTGTGGTTTTGACCACCTACTGGTTCTGATGAGAGAGGAAATCCCGTAGTAGGAGTGATAGCCAGAGCATCTCT
CGTAATAACACCAAAACTGGTGGATGACCAAGACTACTCTCTCCTTTAGGGCATCATCTCACTATCGGTCTCGTAGAGA

84,000

ITPR1

ITPR1-237

TGCTGAGGTGACCCCTGAGCTGATTATAGCCCTATGGGGTATTTTGTGCTGATACATAATACATTGAAAACACTGT
ACGACTCCACTGGGGGACTCGACTAATATCGGGATACCCATAAAACAAAACGACTATGTATTATGTAACCTTTTGTGACA

84,080

ITPR1

ITPR1-237

ATATAGAATTTTTGAATGCTTAAGTGGGGCCTCCATATACACTGAGATCATTTTATCCCCCTACCTTCCACTGCACTTC
TATATCTTAAAAAACTTACGAATTCACCCCGGAGGTATATGTGACTCTAGTAAAATAGGGGGATGGAAGGTGACGTGAAG

84,160

ITPR1

ITPR1-237

ACTGACACTTAACCCCGAAGACATTTGCATTGGAACTTCGCATTATCTGTTTGAAAGTCCTCTCAGTTCAAGCCACACA
TGACTGTGAATTGGGGCTTCTGTAAACGTAACCTTTGAAGCGTAATAGACAAACTTTCAGGAGAGTCAAGTTCGGTGTGT

84,240

ITPR1

ITPR1-237

TTCTAAGACTCAGCAAAAGCTTATTGACACCAAGGGCATTGAATTCACCAGCACCTGTAACGTTTCTTGAAGAATGCTTG
AAGATTCTGAGTCGTTTTCGAATAACTGTGGTCCCGTAACCTTAAGTGGTCGTGGACATTGCAAAGAACTTCTTACGAAC

84,320

ITPR1

ITPR1-237

CTAGGGAAAAGTTCCCATGGTAAGTGTTTTTAAAAGAGTTTTGTAGCATCAACAGGTTAGACAGGAAGTCAAAATCATGG
GATCCCTTTTCAAGGGTACCATTGACAAAAATTTCTCAAAACATCGTAGTTGTCCAATCTGTCCTTCAGTTTTAGTACC

84,400

ITPR1

ITPR1-237

AGCTCAGCAGCATCCCCTATAAGCACGTGCTCCTTTTAAACCACCCCTAACAAAGACACTGAAGCACCTGTTTCATAAGC
TCGAGTCGTCGTAGGGGATATTCGTGCACGAGGAAAAATTGGTGGGGATTGTTTCTGTGACTTCGTGGGACAAGTATTCTG

84,480

ITPR1

ITPR1-237

CCTGATGGGCACTGGAGGGTCTGGCCAGGTTGGGCTGGATTTCAAGGGGACCTGATTTGTGTTTCCCTGTGCAGTGCTCGT
GGACTACCCGTGACCTCCCAGACCGGTCCAACCCGACCTAAAGTCCCCTGGACTAAACACAAAGGGACACGTCACGAGCA

84,560

ITPR1

ITPR1-237

TTCCATCACCATCTTTAAGGAGGAGGCCTTTTCCATCCACTGGACTCTTACCATCGTGCCTGTTAAGGAACAAAAAGACA
AAGGTAGTGGTAGAAATTCCTCCTCGGAAAAGGTAGGTGACCTGAGAATGGTAGCACGGACAATTCCTTGTTTTCTGT

84,640

ITPR1

ITPR1-237

ACTGCTTAGGCCTGGAGGGTATGTGGAAACCACAGTTACCTTTGAATATACCTGTGGTGCTCGAACCTCCTTTAGAAAA
TGACGAATCCGGACCTCCCATACACCTTTGGTGGTCAATGGAAACTTATATGGACACCACGAGCTTGGAGGAAATCTTTT

84,720

ITPR1

ITPR1-237

CCCAAGATGCCATTTTAATGATGCTTTGCTCTTGGGTATCAAATTTACTCCTTAATTTACCTCAGGAGATGTTCTAAGAG
GGGTTCTACGGTAAAATTACTACGAAACGAGAACCCATAGTTTAAATGAGGAATTAATGGAGTCTCTACAAGATTCTC
ITPR1
ITPR1-237

84,800

GAAGCCACAAGATTCCATACCTGCTGTTGTTGTTTTAGAGCTGGTGGATTTTTTTTTTTTTTAAATCCGCGGAGGAGGACTT
CTTCGGTGTTCTAAGGTATGGACGACAACAACAAATCTCGACCACCTAAAAAAAAAAAAAATTAGGCGCCTCCTCCTGAA
ITPR1
ITPR1-237

84,880

GACCCTGTGGGTTCTAACTTGGATGGCCATGCAGAGCACCCTTAACTTGGAAATCTATATCCTGCTGTTTAACTTCAA
CTGGGACACCCAAGGATTGAACCTACCGGTACGTCTCGTGGGAATTGAACCTTTAGATATAGGACGACAAATTTGAAGTT
ITPR1
ITPR1-237

84,960

GATGATTCCTATCTGGATTAAAGTCTCAACCAGCAGGCCGAGGCAAACCTCTAAAGAAAAACAAGGTCATGCTGCATTTT
CTACTAAGGATAGACCTAATTTCAGGAGTTGGTCGTCCGGCTCCGTTTGAGATTTCTTTTTGTTCCAGTACGACGTA
ITPR1
ITPR1-237

85,040

TTTTTGGAAGCACAGGAATCAACAAAGAGATGTTATATAACTTCTATTTATATCCTCCTTGCTCACTATCTGCAGGCAG
AAAAACCATTCGTGTCCTTAGTTGTTTCTCTACAATATATTGAAGATAAATATAGGAGGAACGAGTGATAGACGTCCGTC
ITPR1
ITPR1-237

85,120

ACAAGAGTCGCTGAGAAGGGATTTAATGAGCTCTCTGGGTTTGCTCACCTTCCTGAGCTGGTAGGAACCAGCTTGTTCTC
TGTTCTCAGCGACTCTTCCCTAAATTACTCGAGAGACCCAAACGAGTGGAAGGACTCGACCATCCTTGGTCGAACAAGAG
ITPR1
ITPR1-237

85,200

AAATGCGTCAGTAAAGAATCTGGCTGTGGGTGGGCGGCCAGGGTAGGTGGACTGCGTTGTTGCTATGGTGTTTTTAATT
TTTACGCAGTCATTTCTTAGACCGACACCCACCCGCCGGTCCCATCCACCTGACGCAACAACGATACCACAAAAAATTAA
ITPR1
ITPR1-237

85,280

CCCCTGTCTCTCAAAGATCTCACTCCCCCTTCCCTGACTCCTTCCTTTTGCCCCCTTCCTTTCTTTCTTTCTTTTTTT
GGGGACAGAGAGTTTCTAGAGTGAGGGGGGAAGGGACTGAGGAAGGAAAACGGGGGAAGGAAAGAAAGAAAAA
ITPR1
ITPR1-237

85,360

TTTAAATCTGTAAGCTTCCTTGTTTCTCACACCTACTCATGATTCTTGGAGCTGTCTCCGGAACAGAATATTTCCCTC
AAATTTAGACATTCTGAAGGAACAAAGAGTGTGGATGAGTACTAAGAACCTCGACAGAGGCCTTGTCTTATAAAAGGGAG
ITPR1
ITPR1-237

85,440

TCCTTCCTAAGTGCTCAGCTCCCCATTGTGTAGCCCCGGGACATCAGAAGTTGTTTTCTAAGGTGTGTTTTTCCACCC
AGGAAGGATTACGAGTCGAGGGGGTAACACATCGGGGCCCTGTAGTCTTCAACAAAAGATTCCACACAAAAAAGGTGGG
ITPR1
ITPR1-237

85,520

TCCCTTATTTCTTTTCCCATGATTTTTTTATTACCAATCCCTCCATGAGAGAGACCTATCCTAGGAGTCTTCCATCTTGC
AGGGAATAAAGAAAAGGGTACTAAAAAATAATGGTTAGGGAGGTACTCTCTCTGGATAGGATCCTCAGAAGGTAGAACG

85,600

ITPR1

ITPR1-237

CTGATAGAAGTTTTCTCTGGCATATTCCAAATTCAGATTGCTCCAAAACCAGGTGAAGTCTGTTGCTAGTTGGACAGTCG
GACTATCTTCAAAGAGACCGTATAAGGTTTAAGTCTAACGAGGTTTTGGTCCACTTCAGACAACGATCAACCTGTCAGC

85,680

ITPR1

ITPR1-237

GTATGGCCTGGAGGAGAAGGGCTGTTTGATTTCCATGCATCCTCCTTTGTCCTCTTGCCCTGGGTGAAGCAATGACGTC
CATACCGGACCTCCTCTTCCCGACAAACATAAAGGTACGTAGGAGGAAACAGGAGAACGGGACCCACTTCGTTACTGCAG

85,760

ITPR1

ITPR1-237

TCTGTCTCCTCTAGTGCGTTATAAAATAGAACCGCAAGAAAACAAGAGAATGGGTTTACCCACAATCATAATTCCTGGA
AGACAGAGGAGATCACGCAATATTTTATCTTGGCGTTCTTTTGTCTCTTACCCAAATGGGGTGTTAGTATTAAGGACCT

85,840

ITPR1

ITPR1-237

GCTTGGGTAACCTCCTGTTACCTGAAGGTTGCAGGTTGAAATGACTCAGCTTGCAATTAATTAACCAACCAATGCTGCC
CGAACCCATTGAGGACAATGGACTTCCAACGTCCAACCTTACTGAGTCGAACGTAAATTAATTTTTTTTTTACGACGGG

85,920

ITPR1

ITPR1-237

CATCAGATTCTCAGCAGGGACGACGAATGCACCTTGCTGAGAACCCTATGGCTGCCCAGGGAGTGGCCCCCTGCACCCTG
GTAGTCTAAGAGTCGTCCCTGCTGCTTACGTGGAACGACTCTTGGGATACCGACGGGTCCCTCACCGGGGGACGTGGGAC

86,000

ITPR1

ITPR1-237

FseI

GCCGGCCTGGTGGTGGCCACAGAGGCTTCTGAGATGGCTCTGTGTTGTCCATCACATTCCCACCAGAGCAGAGACACTTA
CGGCCGGACCACCACCGGTGTCTCCGAAGACTCTACCGAGACACAACAGGTAGTGTAAGGGTGGTCTCGTCTCTGTGAAT

86,080

ITPR1

ITPR1-237

GAAGATGTGAGTAGGGAGGTTAGGATGAAAAGTTCTTAGAAAAGAATATGTAGTTCCATGAGGACAGGCTGAAAAAATT
CTTCTACACTCATCCCTCCAATCTACTTTCAAGAATCTTTCTTATACATCAAGGTACTCCTGTCCGACTTTTTTAAA

86,160

ITPR1

ITPR1-237

TTAAAAAGCCAAACCCACCTCTGCCTTGCCGAGAAGTTGTGCAATCCTTAATAGCAGTAGCCTGTTTGAATAATCAGAGG
AATTTTTCGGTTTGGGTGGAGACGGAACGGGTCTTCAACACGTTAGGAATTATCGTCATCGGACAAACTTATTAGTCTCC

86,240

ITPR1

ITPR1-237

CAAGCTGACTTCCCTTTATTAACCTTCTGTTAGAGACATCTGCATAAAATATCCCCGGATTCCAGACCAAGTAGGTAATT
GTTTCGACTGAAGGGAATAATTGAAGACAATCTCTGTAGACGTATTTATAGGGGCTAAGGTCTGGTTCATCCATTAAA

86,320

ITPR1

ITPR1-237

TTTTTCCCCTCTGAGTAACGGGAGGGACTTTCCCTTTGGAAATCTTCAGCAGAGTTAACTTCATGGTTGAGACTGTTT
AAAAAAGGGGAGACTCATTGCCCTCCCTGAAAGGGAAACCTTTAGAAGGTCGTCTCAATTGAAGTACCAACTCTGACAAA

86,400

ITPR1

ITPR1-237

TCTCATTATAAGGTGCCAACAGCTAGATTCTGATGCAGGGACAGTGAAGGCGCCTCATGTACACACTTGGATCCCCTGC
AGAGTAATATTCCACGGTTGTCGATCTAAGGACTACGTCCCTGTCACTTCCGCGGAGTACATGTGTGAACCTAGGGGACG

86,480

ITPR1

ITPR1-237

CTACGTCCCTG
AATCGACCA
Sanger Sequencing Primer

TTCCCTGAGAACTGACTTGATGTTACAGTTGCCTCTGGTTCTTCTGCCTTGACCCTCCTTTTACGGAGAAATCTATGC
AAGGGACTCTTGACTGAACTACAAGTGTCAACGGAGACCAAGAAGACGGAAGTGGGAGGAAAAGTGCCTCTTTAGATACG

86,560

ITPR1

ITPR1-237

CCGCTCACATTTCTGAGGTCTCTGAGTTCTCTTTGAAACTGTCAGAGGCTCTCTCAAAGTTTCTACCAATTTCTAT
GGCGAGTGTAAGGACTCCAGGAGACTCAAGGAGAACTTTGACAGTCTCCGAGAGAGTTTCAAAGATGGTTAAAGGATA

86,640

ITPR1

ITPR1-237

TCCTGGGTTTTAGACTTTTGATCAAGATGGCTCTGACACTGAAGGGGATAGTCTGTAAACCCTCTGAAGTCTTCAAGCC
AGGACCCAAAATCTGAAAAGTAGTTCTACCGAGACTGTGACTTCCCCTATCAGGACATTTGGGAGACTTCAGAAGTTCGG

86,720

ITPR1

ITPR1-237

TCGTTTTTCCCCTGGAATTCAGGACTTTAAAAATATATATATTTTATTGCTCTTCGAGGAGGATGTGTTGCAGTTGCCCT
AGCAAAAAGGGGACCTTAAGTCTGAAATTTTATATATATAAAATAACGAGAAGCTCCTCTACACAACGTCAACGGGA

86,800

ITPR1

ITPR1-237

CACCATATGGTATTTGAGAAATATGTTTTTATTAGCCTCCTTGCAACACAAACCCACAAACTGTTGAGCCCAGAGCTTGT
GTGGTATACCATAAACTCTTTATACAAAAATAATCGGAGGAACGTTGTGTTTGGGTGTTTGACAACCTCGGGTCTCGAACA

86,880

ITPR1

ITPR1-237

AGCTATCAAGTCTGGGGAGGGAGCCAGGTTTGGAGACGGAAGGTGCACAAATGATCATCCCTCCCGGGCTGTAGTTAATC
TCGATAGTTTCAGACCCCTCCCTCGGTCCAAACCTCTGCCTTCACGTGTTTACTAGTAGGGAGGGCCCGACATCAATTAG

86,960

ITPR1

ITPR1-237

ATGCAAGCTGCTGTGTCACTGGGGCCGGGGTAGTTAACAGTTAACTCGATGGATTAAGGATCCTCAGCCAGGCTGAGCCC
TACGTTTCGACGACACAGTGACCCCGGCCCCATCAATTGTCAATTGAGCTACCTAATTCCTAGGAGTCGGTCCGACTCGGG

87,040

ITPR1

ITPR1-237

ATCACAGAGTTACGTGCAAAAACGGGATAAGCCCGTAGAGGTGACAACACCACATCAGCTGCCTTTGGCTGGTCTGCGGT
TAGTGTCTCAATGCAGTTTTTGGCCTATTGCGGCATCTCCACTGTTGTGGTGTAGTCGACGGAAACCGACCAGACGCCA

87,120

ITPR1

ITPR1-237

GTGCTGCATATTTCCCACTTAGCAGGACTTTGAGCTTTCACATGCAGGCTTCTTCTGGCCATAAAGTTATACTTCAGCTGC
CACGACGTATAAGGGTGAATCGTCCTGAAACTCGAAAGTGACGTCCGAAGAAGACCGGTATTTCAATATGAAGTCGACG

87,200

ITPR1

ITPR1-237

CATGGATGCAAAGCTTGGCTTGAGTGTTTCGGAATTGCACCTCCTTCAGGATTATTGTTTCATTCATTAATATAGTAAATT
GTACCTACGTTTTCGAACCGAACTCACAAAGCCTTAACGTGGAGGAAGTCCTAATAACAAGTAAGTAATTATATCATTTAA

87,280

ITPR1

ITPR1-237

TTTTAAAAAGAGAGAAGAGGCCTTACTGTGTTGACCAAGCTGGCCTTGAACCTCTGGGCTGAAGAGATCTTCTGTCTCA
AAAATTTTTCTCTCTTCTCCGGAATGACACAACCTGGTTCGACCGGAACCTTGAGGACCCGACTTCTCTAGAAAGACAGAGT

87,360

ITPR1

ITPR1-237

GCCTCCGGAGTAGCTAGAACTACTGGCTTGTCACCACAGCCGGCTTAATATAGCAGATGTTTACTTACTGAGCACTCC
CGGAGGCCTCATCGATCTTGATGACCGAACACAGTGGTGTCGGCCGAATTATATCGTCTACAAATGAATGACTCGTGAGG

87,440

ITPR1

ITPR1-237

CTGGGTGTCAGGTGCTATACACATTGGCGTCAATACAGTCAGGGATGAGACCAACATAGCCCCTGCCCTCCAGGAGCTTA
GACCCACAGTCCACGATATGTGTAACCGCAGTTATGTCAGTCCCTACTCTGGTTGTATCGGGGACGGGAGGTCTCTGAAT

87,520

ITPR1

ITPR1-237

CAGTCTTGTTGGGAGACAGAGCTAGGAAATCAGCTCATCATCAGCTAAATCAGAGCTTCAGAGAAGTGTGATGGGGAAGCA
GTCAGAACACCCTCTGTCTCGATCCTTTAGTCGAGTAGTAGTCGATTTAGTCTCGAAGTCTCTTCACACTACCCCTTCGT

87,600

ITPR1

ITPR1-237

AACAGGCGCCACGAAGCGTGGCCAGGGAGGGCTTCTCTGGGGAGATACCGTTCAAGCTGAGACCCAACAGATGCGAAGAG
TTGTCCGCGGTGCTTCGCACCGGTCCCTCCCGAAGAGACCCTCTATGGCAAGTTCGACTCTGGGTTGTCTACGCTTCTC

87,680

ITPR1

ITPR1-237

AAGGAGCTGTGTGAAGAGTAGCAGAGGGCAAGAGTATTTCAGAAGAGGGTTGGCTTGCTGCTTGGGATGTTGGAGGAGCTG
TTCCTCGACACACTTCTCATCGTCTCCCGTTCTCATAAAGTCTTCTCCCAACCGAACACGAACCCTACAACCTCCTCGAC

87,760

ITPR1

ITPR1-237

AGTGAAGGAAGCTAACGCGGTCTACCCCATGGTGGTCGGTCAGGGGCAGAGCTGCGGAAAGTATCTGCTCCACCAGGGTG
TCACTTCCTTCGATTGCGCCAGATGGGGTACCACCAGCCAGTCCCGTCTCGACGCCTTTCATAGACGAGGTGGTCCAC

87,840

ITPR1

ITPR1-237

ATGGGCTTGTCATCAAGTCGGGGCTGGATGAGGTGATCTCTGTGGTTCCCGCCGATCCCTAGTCGGTGCTTCTAAAGGGC
TACCCGAACAGTAGTTTCAGCCCCGACCTACTCCACTAGAGACACCAAGGGCGGGCTAGGGATCAGCCACGAAGATTTC

87,920

ITPR1

ITPR1-237

ACCAAGTTGGCTTGGGCCTGTCCCCTGCTTGGATATGCGCTGCCGCCGCCAAAGCCCTAATATACAAAGCAGCTTTACCC
TGGTTCAACCGAACC CGGACAGGGGACGAACCTATACGCGACGGCGGGTTTCGGGATTATATGTTTCGTGAAATGGG

88,000

ITPR1

ITPR1-237

AGATGAGTGCTGTGTGATTTACCCCTGCCCTGCTCTAACCGCTTGGCCATCTGTACATCTTACTGTCAGCTGCCAGGGAT
TCTACTCACGACACACTAAAGTGGGACGGGACGAGATTGGCGAACCGGTAGACATGTAGAATGACAGTCGACGGTCCCTA

88,080

ITPR1

ITPR1-237

GCTCTCTGTGGCCGTGTGGAAGTTACCTGGTGGGCCAGCACACAGCAAGATGGGGATGCAGGGTGGGGAGACATGAAGAG
CGAGAGACACCGGCACACCTTCAATGGACCACCGGTCGTGTGTCGTTCTACCCCTACGTCCCACCCCTCTGTACTTCTC

88,160

ITPR1

ITPR1-237

TCCCAGAGCATTCTGCTGGGGACCAGACTCGGCTGTACCCGAGAGTCAGTTGAGTTGGGAAGGACTAGGGTTGACTGGGG
AGGGTCTCGTAAGACGACCCCTGGTCTGAGCCGACATGGGCTCTCAGTCAACTCAACCCTTCTGATCCCAACTGACCCC

88,240

ITPR1

ITPR1-237

GTGACTGCAGTCTTCATCAAGGAGGCACTTGCTTTGCTTGATGCTTTGCCACCTAAGCCAGTGTCCTTGCTCCATCCGG
CACTGACGTGAGAAGTAGTTCTCCGTGAACGAAACGAACTACGAAACGGTGGATTCCGGTCACAGGAACGGAGGTAGGCC

88,320

ITPR1

ITPR1-237

CCTGAGTGGATTTATTTTTTTCGGCTTCTATGGCCAAGTGTCTTGTGTCACAGTTTGTGTGGAGAGCAGCGAAGGGAACGT
GGACTCACCTAAATAAAAAAAGCCGAAGATACCGGTTACAGGAACAGTGTCAAACACACCTCTCGTCGCTTCCCTTGCA

88,400

ITPR1

ITPR1-237

GGCTGGTGTAGACACCCTGCCGGTACTGTGCGGGCTCTCACCTGTTTTCTCTCCTGCACTCCTTGCAATAGAATCTCAAG
CCGACCACATCTGTGGGACGGCCATGACACGCCCGAGAGTGGACAAAAGAGAGGACGTGAGGAACGTTATCTTAGAGTTC

88,480

ITPR1

ITPR1-237

TGGTTCTCCTCCTCTTTCTCCATTGCAGATGAGGGAACTGAGGATGGAAGTTAATAAATGAGCTGTCCAAACCCACCCAG
ACCAAGAGGAGGAGAAAGAGGTAACGTCTACTCCCTTGACTCCTACCTTCAATTATTTACTCGACAGGTTTGGGTGGGTC

88,560

ITPR1

ITPR1-237

TTCTAAGTCACCCCTATGCGTATGTTTCTACCTTGCTAAAGATGCAGGATAGAGATCGCTTTCACTGAGCCGTGTGACT
AAGGATTGAGTGGGGATACGCATACAAAGATGGAACGATTCTACGTCCTATCTCTAGCGAAAGTGACTCGGCACACTGA

88,640

ITPR1

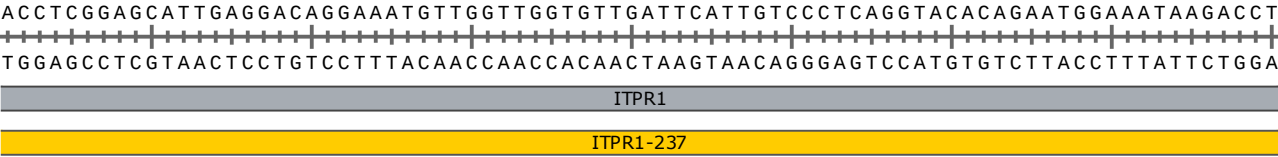
ITPR1-237

GCACAAACACAGAAAATGGGGGGGGGGTGGCAAGGATTATTCTTGGCATCTGTATAAATTTCAAGTTGAATTCCCTGGGA
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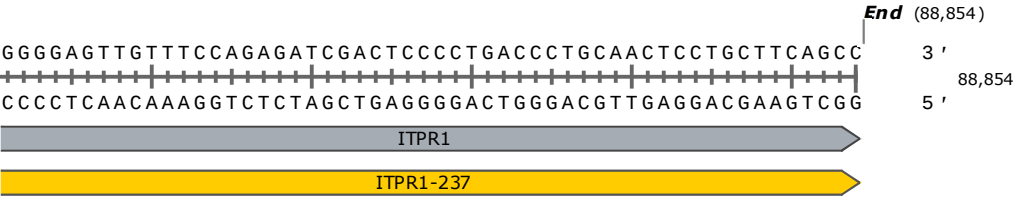
88,720

ITPR1











ITPR1-237














88,800











Feature		Location		Size	±	Type
✓	ITPR1	1	.. 88,854	88,854 bp	■ →	gene
	/note = gene ENSG00000150995 Protein coding					
	ITPR1-201	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000302640 Nonsense mediated decay					
	ITPR1-202	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000354582					
	ITPR1-203	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000357086					
	ITPR1-204	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000443694					
	ITPR1-205	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000456211					
	ITPR1-219	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000544951					
	ITPR1-230	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000648266					
	ITPR1-231	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000648309					
✓	ITPR1-237	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000649015					
	ITPR1-254	1	.. 88,854	88,854 bp	■ →	prim_transcript
	/note = primary transcript ENST00000650294					
	ITPR1-210	1	.. 8051	8051 bp	■ →	prim_transcript
	/note = primary transcript ENST00000477577 Retained intron					
	ITPR1-238	1	.. 6395	6395 bp	■ →	prim_transcript
	/note = primary transcript ENST00000649051 non_stop_decay					
	ITPR1-202	1986	.. 69,963	67,978 bp	■ →	CDS
	▶ 27 segments = 3807 bp					
	/note = coding sequence ENSP00000346595					
	/translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVCQRFPSDKEKNLTFE,,VVLARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTFIPISKMAKGEENK,,GSNMVRSIHVGELMTQVVLRGGGFLPMTPMAAAPEGNVKQAEPEKEDIMVMDTKLKIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQT SETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRFRLVLLHLMTHDYPLVSGALQLLFRHFSQRQEVQLQAFKQ,,VQLLVTSQDQVDNYKQI KQDLQDLRSIVEKSELWYKGGQGPDETMGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLELLQIPYEK ,,AEDTKMQEIMRLAHEFLQNFCAQQNQALHKKHINFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIEHGRNVQYIKFLQTIIVKAEGKFIKKQDMVMAE ,,LVNSGEDVLVFNDRASFQTLIQMRSERDRMDENSPMYHIHLVELLAVCTEGKNVYTEIKCNSLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDTEVEMKEIYT SNHMWKLFFENFLVDICR,,ACNNTSDRKHADSIKELYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQKASVESCIQVLSQV,,AKSRAIA IPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELLFPENTDARRKCESGGFICK,,LIKH TKQLLEENEEKLCKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,QELPSPLRLQLEDHQR,,GEALRQVLVNRYYGNVVRPSGRRESLTSFGNGP LSAGPGKPGGG,,GGSGSSSMRSGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLLEGNTTIQ 1269 amino acids = 144.7 kDa					
	ITPR1-203	1986	.. 69,963	67,978 bp	■ →	CDS
	▶ 24 segments = 3687 bp					
	/note = coding sequence ENSP00000349597					
	/translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVCQRFPSDKEKNLTFE,,VVLARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTFIPISKMAKGEENK,,GSNMVRSIHVGELMTQVVLRGGGFLPMTPMAAAPEGNVKQAEPEKEDIMVMDTKLKIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQT SETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRFRLVLLHLMTHDYPLVSGALQLLFRHFSQRQEVQLQAFKQ,,VQLLVTSQDQVDNYKQI KQDLQDLRSIVEKSELWYKGGQGPDETMGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLELLQIPYEK ,,AEDTKMQEIMRLAHEFLQNFCAQQNQALHKKHINFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIEHGRNVQYIKFLQTIIVKAEGKFIKKQDMVMAE ,,LVNSGEDVLVFNDRASFQTLIQMRSERDRMDENSPMYHIHLVELLAVCTEGKNVYTEIKCNSLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDTEVEMKEIYT SNHMWKLFFENFLVDICR,,ACNNTSDRKHADSIKELYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQKASVESCIQVLSQV,,AKSRAIA IPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELLFPENTDARRKCESGGFICK,,LIKH TKQLLEENEEKLCKVLQTLREMMTKDRGYGEK,,GEALRQVLVNRYYGNVVRPSGRRESLTSFGNGPLSAGPGKPGGG,,GGSGSSSMRSGEMSLAEVQCHLDKEGASNLV IDLIMNASSDRVFHESILLAIALLLEGNTTIQ 1229 amino acids = 140.2 kDa					

Feature	Location	Size			Type
ITPR1-204	1986 .. 69,963	67,978 bp			CDS
▶ 27 segments = 3831 bp					
/note	= coding sequence ENSP00000401671				
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLHMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVVCQRFPSDKEKNKLTFE,,VVLNARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENKGNNDVEKLLK,,SSNVMRSIHGVGELMTQVVLRGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIIEILQ,,FILNVRLDYRISCLLCIFKR EFDESNSQTSETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLHLLTMHDYPPPLVSGALQLLFRHFSQRQEVLAQAFKQ,,VQLLVTS QDQVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLE LLQIPYEK,,AEDTKMQEIMRLAHEFLQNFCAQNQQNALHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIETHGRNVQYIKFLQTIIVKAEGKFIK KCQDMVMAE,,LVNSGEDVLVFNDRASFQTLIQMMRSEDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDT EVEMKEIYTSNHMWKLFENFLVDICR,,ACNNTSDRKHADSILEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQSQKASVESCIRVLSDV ,,AKSRAIAPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELFPENTDARRKCESGGF ICK,,LIKHTKQLLEENEEKLCIKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,ELEPSPPLRQLEDHKKR,,GEALRQVLVNRYYGNVRPSSGRRES LTSFGNGPLSAGGPCKPGGG,,GGSGSSSSMRGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLEGNTTIQ				
	1277 amino acids = 145.6 kDa				
ITPR1-205	1986 .. 69,963	67,978 bp			CDS
▶ 24 segments = 3687 bp					
/note	= coding sequence ENSP00000397885				
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLHMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVVCQRFPSDKEKNKLTFE,,VVLNARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENK,,GSNVMRSIHGVGELMTQVVLRGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQT SETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLHLLTMHDYPPPLVSGALQLLFRHFSQRQEVLAQAFKQ,,VQLLVTSQDQVDNYKQI KQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLELLQIPYEK ,,AEDTKMQEIMRLAHEFLQNFCAQNQQNALHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIETHGRNVQYIKFLQTIIVKAEGKFIKCCQDMVMAE ,,LVNSGEDVLVFNDRASFQTLIQMMRSEDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDTDEVEMKEIYT SNHMWKLFEFENFLVDICR,,ACNNTSDRKHADSILEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQSQKASVESCIRVLSDV,,AKSRAIA IPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELFPENTDARRKCESGGFICK,,LIKH TKQLLEENEEKLCIKVLQTLREMMTKDRGYGEK,,GEALRQVLVNRYYGNVRPSSGRRESLTSFGNGPLSAGGPCKPGGG,,GGSGSSSSMRGEMSLAEVQCHLDKEGASNLV IDLIMNASSDRVFHESILLAIALLEGNTTIQ				
	1229 amino acids = 140.2 kDa				
ITPR1-230	1986 .. 69,963	67,978 bp			CDS
▶ 27 segments = 3804 bp					
/note	= coding sequence ENSP00000498014				
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLHMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVVCQRFPSDKEKNKLTFE,,VVLNARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENK,,GSNVMRSIHGVGELMTQVVLRGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQT SETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLHLLTMHDYPPPLVSGALQLLFRHFSQRQEVLAQAFKQ,,VQLLVTSQDQVDNYKQI KQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLELLQIPYEK ,,AEDTKMQEIMRLAHEFLQNFCAQNQQNALHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIETHGRNVQYIKFLQTIIVKAEGKFIKCCQDMVMAE ,,LVNSGEDVLVFNDRASFQTLIQMMRSEDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDTDEVEMKEIYT SNHMWKLFEFENFLVDICR,,ACNNTSDRKHADSILEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQSQKASVESCIRVLSDV,,AKSRAIA IPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELFPENTDARRKCESGGFICK,,LIKH TKQLLEENEEKLCIKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,ELEPSPPLRQLEDHKKR,,GEALRQVLVNRYYGNVRPSSGRRESLTSFGNGPL SAGGPCKPGGG,,GGSGSSSSMRGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLEGNTTIQ				
	1268 amino acids = 144.6 kDa				
ITPR1-231	1986 .. 69,963	67,978 bp			CDS
▶ 27 segments = 3804 bp					
/note	= coding sequence ENSP00000497026				
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCSVMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLHMHV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFVEEYLRDVVCQRFPSDKEKNKLTFE,,VVLNARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENK,,GSNVMRSIHGVGELMTQVVLRGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQT SETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLHLLTMHDYPPPLVSGALQLLFRHFSQRQEVLAQAFKQ,,VQLLVTSQDQVDNYKQI KQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHAVVLELLQIPYEK ,,AEDTKMQEIMRLAHEFLQNFCAQNQQNALHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIETHGRNVQYIKFLQTIIVKAEGKFIKCCQDMVMAE ,,LVNSGEDVLVFNDRASFQTLIQMMRSEDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDTDEVEMKEIYT SNHMWKLFEFENFLVDICR,,ACNNTSDRKHADSILEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQSQKASVESCIRVLSDV,,AKSRAIA IPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELFPENTDARRKCESGGFICK,,LIKH TKQLLEENEEKLCIKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,ELEPSPPLRQLEDHKKR,,GEALRQVLVNRYYGNVRPSSGRRESLTSFGNGPL SAGGPCKPGGG,,GGSGSSSSMRGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLEGNTTIQ				
	1268 amino acids = 144.6 kDa				

Feature	Location	Size	Icon	Type
✓ ITPR1-237	1986 .. 69,963	67,978 bp		→ CDS
▶ 27 segments = 3831 bp				
/note	= coding sequence ENSP00000497605			
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCVSMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLMHMV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFEVVEYL RDVVCQRFPSDKENKLTFE,,VVNLARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENKGNNDVEKLG,,SSNVMSRSHGVGELMTQVVL RGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIEILQ,,FILNVRLDYRISCLLCIFKR EFDESNSQTSETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLH LTMHDYPPLVSGALQLLFRHFSQRQEV LQAFKQ,,VQLLVTS QDVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESSTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHV LELLQIPYEK,,AEDTKMQEIMRLAHEFLQNFCAGNQQNQALLHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQH FVHCIETHGRNVQYIKFLTIVKAEKFIK KCQDMVMAE,,LVNSGEDVLVFNDRASFQTLIQMMRSERDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDT EVEMKEIYTSNHMWKLFENFLVDICR,,ACNNTSDRKHADSI LEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMP SQKASVESCIRVLSDV,,AKSRAIAPVDLDSQVNNFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLHRPELLFPENTDARRKCESGGF ICK,,LIKHTKQLLEENEKLCIKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,ELEPSPPLRQLEDHKR,,GEALRQVLVNRYYG NVRPSGRRES LTSFGNGPLSAGGPGKPGGG,,GGGSGSSMSRGEMLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLEGNTTIQ 1277 amino acids = 145.6 kDa			
ITPR1-254	1986 .. 69,963	67,978 bp		→ CDS
▶ 27 segments = 3834 bp				
/note	= coding sequence ENSP00000498056			
/translation	= EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPR,,FLDYLSDLCVSMNKSIPVTQELICKAVLNPTNADILIETK,,LVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLMHMV DRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEIKERFAQTMFEVVEYL RDVVCQRFPSDKENKLTFE,,VVNLARNLIYFGFYNFSDLLRLTKILLAILDCVH VTTIFPISKMAKGEENKGNNDVEKLG,,SSNVMSRSHGVGELMTQVVL RGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIEILQ,,FILNVRLDYRISCLLCIFKR EFDESNSQTSETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,EENTPLDLDDHGGRTFLRVLLH LTMHDYPPLVSGALQLLFRHFSQRQEV LQAFKQ,,VQLLVTS QDVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESSTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHV LELLQIPYEK,,AEDTKMQEIMRLAHEFLQNFCAGNQQNQALLHKKHINLFLNPG,,ILEAVTMQHIFMNNFQLCSEINERVVQH FVHCIETHGRNVQYIKFLTIVKAEKFIK KCQDMVMAE,,LVNSGEDVLVFNDRASFQTLIQMMRSERDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDT EVEMKEIYTSNHMWKLFENFLVDICR,,ACNNTSDRKHADSI LEKYVTEIVMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMP SQKASVESCIRVLSDV,,AKSRAIAPVDLDSQVNNFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLHRPELLFPENTDARRKCESGGF ICK,,LIKHTKQLLEENEKLCIKVLQTLREMMTKDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,QELPSPPLRQLEDHKR,,GEALRQVLVNRYYG NVRPSGRRE SLTSFGNGPLSAGGPGKPGGG,,GGGSGSSMSRGEMLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLAIALLEGNTTIQ 1278 amino acids = 145.7 kDa			
✓ Donor Sequence WT -> SNV	2010 .. 2109	100 bp		┼┼ misc_feature
✓ PAM	2069 .. 2071	3 bp		┼┼ misc_feature
✓ gRNA Protospacer Sequence	2072 .. 2091	20 bp		┼┼ misc_feature
✓ SNV	2076 .. 2076	1 bp		┼┼ misc_feature
/note = WT = A SNV = G				
ITPR1-227	5495 .. 88,854	83,360 bp		→ prim_transcript
/note	= primary transcript ENST00000648038			
ITPR1-227	5495 .. 69,963	64,469 bp		→ CDS
▶ 24 segments = 3306 bp				
/note	= coding sequence ENSP00000497872			
/translation	= EGQKEDRDVLSYYR,,YQLNLFARMCLDRQYLAINESGQLDVDLILRCMSDENLPYDLRASFCRLMLMHMVDRDPQEQTVPVKYARLWSEIPSEIAIDD,,YDSSGASKDEI KERFAQTMFEVVEYL RDVVCQRFPSDKENKLTFE,,VVNLARNLIYFGFYNFSDLLRLTKILLAILDCVHVTTIFPISKMAKGEENK,,GSNVMSRSHGVGELMTQVVL RGGGFLPMTMAAAPEGNVKQAEPEKEDIMVMDTKLKIIEILQ,,FILNVRLDYRISCLLCIFKREFDESNSQTSETSSGNSSQEGPSNVP,,GALDFEHIEEQAEGIFGGS,,E ENTPLDLDDHGGRTFLRVLLH LTMHDYPPLVSGALQLLFRHFSQRQEV LQAFKQ,,VQLLVTSQDVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKTE,,EGNNKPQKHESSTSSYNRVVKE,,ILIRLSKLCVQESASVRKSRKQQQRLLRNMGAAHVLELLQIPYEK,,AEDTKMQEIMRLAHEFLQNFCAGNQQNQALLHKKHINLFL NPG,,ILEAVTMQHIFMNNFQLCSEINERVVQH FVHCIETHGRNVQYIKFLTIVKAEKFIK KCQDMVMAE,,LVNSGEDVLVFNDRASFQTLIQMMRSERDRMDENSPLM YHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPE,,VKIAYINFLNHCYVDT EVEMKEIYTSNHMWKLFENFLVDICR,,ACNNTSDRKHADSI LEKYVTEI VMSIVTTFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMP SQKASVESCIRVLSDV,,AKSRAIAPVDLDSQVNNFLKSHSIVQKTAMNWRLSARNAARRDSV L AASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLHRPELLFPENTDARRKCESGGFICK,,LIKHTKQLLEENEKLCIKVLQTLREMMTKDRGYGEK,,LISIDE LDNAE,,LPPAPDSENATE,,GEALRQVLVNRYYG NVRPSGRRESLTSFGNGPLSAGGPGKPGGG,,GGGSGSSMSRGEMLAEVQCHLDKEGASNLVIDLIMNASSDRVFH ESILLAIALLEGNTTIQ 1102 amino acids = 125.5 kDa			
ITPR1-253	7903 .. 10,804	2902 bp		→ prim_transcript
/note	= primary transcript ENST00000650146 Retained intron			
ITPR1-223	9578 .. 88,854	79,277 bp		→ prim_transcript
/note	= primary transcript ENST00000647717 Retained intron			
ITPR1-233	9750 .. 88,854	79,105 bp		→ prim_transcript
/note	= primary transcript ENST00000648431			

Feature	Location	Size	Graph	Type
ITPR1-233	9750 .. 69,963	60,214 bp		→ CDS
▶ 22 segments = 2846 bp				
/note	= coding sequence ENSP00000498149			
/translation	= SFWPYWTVM*QQSSPLARWRKEKRIK,,AVT**DLFWAWES**PRWCSGEEAFCP*LPWLLPLKAM*SRQSLRRRTSWSWTPS*RSLRYSS,,LF*M*GWIIGSPASCVYLS ESLMKAIPRLQKHPPEAAKQGVYMQ,,VLLTLNLTNKNQKASLEE,,VRRTPHWMTMTAAEPFSVSCST*RCMTTHPWCGQPCSSSSGTSARGRRCSRPSNR,,FNCWLP AKMWTTTNRNKTWIN*GPSWKSQSFGCTKGRAPMRLWMVHLEKMNIRKRR,,REITSHKSMKAPAATTTTEWSKR,,F*FGLANSVFKRVQP*ERAGSSNSVCSGTWARTPWC WSCCRFPMMR,,PKIPRCKR**GWL MNFCRISAQATSRIKLCYINT*TCFSTQG,,SWRQ*PCSTSS*TISSFAVRSTRELFTSTFTA*RLTVGMSSI**SSYRQLSRQKGNLL KNAKTLWLPS,,WSIRERMSSCSTTTEPLSRL*SR*CGQNGIGWMRTALSCCTSTWSSSWLCARRVRMSTQRSSATPCSRWMTSFAW*PTRTASLR,,LKLHTLTS*ITAMWI QRWK*RRFIPAITCGNCLRISL*TSAG,,PVTTLVGTNMQTRFWRSMSPKSS*VLLLLSSALPSQTRVRLCR,,LASLSLNCCKACSGFTTATG*CQAKKPPWRAVFGCCLM *,PRAGPLPFPWTWAKSTTSFSSPTALCRKQP*TGGSQAMPAGHTLFWQLPETTGISLRDCR,,TSSPRWRTVSGPWCRQSYLCSWMFSTDPSCFSQRTQTPEGNVKVAS SFA,,S**SIQNSC*KMKRSSLRSYRP*GK**PKIEAMEKS,,*FPLMNWIMLS,,FLQLRILRTPLR,,SLNQVHPCGSWKTIKG,,VRRSGKFWSTVTMETSDLRDEER ALPALAMAHCQEDPASPGE,,GEVPDPAL*AGVR*VWPRFSVTLTRRLPI*LTSS*THPVTESCMKAFSWPLFPWKEATPPS 948 codons (42 internal stop codons)			
ITPR1-229	15,287 .. 88,854	73,568 bp		→ prim_transcript
/note	= primary transcript ENST00000648212			
ITPR1-229	15,287 .. 69,963	54,677 bp		→ CDS
▶ 20 segments = 2452 bp				
/note	= coding sequence ENSP00000498022			
/translation	= K*CTR,,CS*L*TH*RTSRRHLWRK,,*GEHPTGLG*PRRQNLSPCAPLDDA*LPTPGVRGPAAPLPALQPEAGGAPGLQT,,GSTAGYQPRCGLQTDQTRLGSTEVHRGK VRALGVQRAGPR*DYGWC IWRK*T*ENG,,GGK*QATKA*KHQQLQLQSGQR,,DFDSA*QTLCSRECLSEKEQEAATASAPHEGRARRGAGAAADSL*E,,GRRYQDARDNE VGS*IFAEFLRRQPAESSFAT*THKPVSQPR,,DPGGSNHAHLHEQFPALQ*DQRESCSALRSLHRDSRSECPVYKVLTDNCQGRREIY*KMPRHGYGR,,AGQFGRGCPRV LQRQLFPDSDPDDAVRTGSDG*EQPSHVPHPLGRAPGCVHGG*ECLHRDQVQLPAPAG*HRSRGDPRGLHP*,*G*NCIH*LPESLLCGYRGNGEGDLYQQSHVEIV*EFPC RHLQ,,GL*QH**QETCRLDFGEVCHNRNHEYCYFYFLQLSLLRPEYDFA,,DSPACLATAARRVQGLPLQLVNAKPKSLRGELYSYGA*CS,,QEPGHCHSRGPGQPSQQL SQVPQHCASHELAALSPQCRTQGLCSGSFQRLPEYH*EIA,,GHRLRAGGPSQAPGAGRVICARGCSPQTRAAPPREHRRQKEM*KWRFHLQ,,VNKAYKTAARRK*REAL H*GPTDPEGNDQ*RLWRK,,ANFH**IG*C*,ASSSSGF*ERH*,GA*TKSTPAAAGRP*K,,G*GAQASSGQPLLWKRQTFGTGREPYQLWQWPTVSRRTQRAGRR, ,GRFRIQLYEQG*DESGRGSVSP*QGGGFQSSYRPHHERIQ*PSVP*KHSPGHCPSGRRQHHPH 817 codons (47 internal stop codons)			
ITPR1-220	18,122 .. 61,478	43,357 bp		→ prim_transcript
/note	= primary transcript ENST00000647624 Retained intron			
ITPR1-226	19,782 .. 88,854	69,073 bp		→ prim_transcript
/note	= primary transcript ENST00000648016			
ITPR1-226	19,782 .. 69,963	50,182 bp		→ CDS
▶ 15 segments = 1879 bp				
/note	= coding sequence ENSP00000496893			
/translation	= GAGAAADSL*E,,GRRYQDARDNEVGS*IFAEFLRRQPAESSFAT*THKPVSQPR,,DPGGSNHAHLHEQFPALQ*DQRESCSALRSLHRDSRSECPVYKVLTDNCQGRREI Y*KMPRHGYGR,,AGQFGRGCPRVLQRQLFPDSDPDDAVRTGSDG*EQPSHVPHPLGRAPGCVHGG*ECLHRDQVQLPAPAG*HRSRGDPRGLHP*,*G*NCIH*LPESLLC GYRGNGEGDLYQQSHVEIV*EFPCRHLQ,,GL*QH**QETCRLDFGEVCHNRNHEYCYFYFLQLSLLRPEYDFA,,DSPACLATAARRVQGLPLQLVNAKPKSLRGELYSYGA *CS,,QEPGHCHSRGPGQPSQQLSQVPQHCASHELAALSPQCRTQGLCSGSFQRLPEYH*EIA,,GHRLRAGGPSQAPGAGRVICARGCSPQTRAAPPREHRRQKEM*KW RFHLQ,,VNKAYKTAARRK*REALH*GPTDPEGNDQ*RLWRK,,ANFH**IG*C*,ASSSSGF*ERH*,AGA*TKSTPAAAGRP*K,,G*GAQASSGQPLLWKRQTFGT KREPYQLWQWPTVSRRTQRAGRR,,GRFRIQLYEQG*DESGRGSVSP*QGGGFQSSYRPHHERIQ*PSVP*KHSPGHCPSGRRQHHPH 626 codons (34 internal stop codons)			
ITPR1-221	25,933 .. 48,440	22,508 bp		→ prim_transcript
/note	= primary transcript ENST00000647673 Retained intron			
ITPR1-243	34,440 .. 72,934	38,495 bp		→ prim_transcript
/note	= primary transcript ENST00000649414			
ITPR1-243	34,440 .. 71,895	37,456 bp		→ CDS
▶ 11 segments = 1227 bp				
/note	= coding sequence ENSP00000497099			
/translation	= DRKHADSILEKYVTEIVMSIVTFFSSPFSQSTTLQ,,TRQPVFVQLLQGVFRVYHCNWLMPQSQKASVESCIRVLSDV,,AKSRAIAIPVDLDSQVNNLFLKSHSIVQKTAM NWRLSARNAARRDSVLAASRDYRNIIERLQ,,DIVSALEDRLRPLVQAELSVLVDVLRPELLFPENTDARRKCESGGFICK,,LIKHTKQLLENEEKLCIKVLQTLREMMT KDRGYGEK,,LISIDELDNAE,,LPPAPDSENATE,,ELEPSPPLRQLEDHQR,,GEALRQVLVNRYYGNVVRPSGRRESLTSFGNGPLSAGGPCKPGGG,,GGSGSSSSMRG EMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHESILLALLEGNTTIQ,,LYQFEKSNLSPQEIPLTRIRGCAHTMLCLKDDI* 408 amino acids = 45.4 kDa			
ITPR1-232	40,776 .. 88,854	48,079 bp		→ prim_transcript
/note	= primary transcript ENST00000648390			
ITPR1-232	40,776 .. 46,477	5702 bp		→ CDS
▶ 3 segments = 446 bp				
/note	= coding sequence ENSP00000497404			
/translation	= PRAGPLPFPWTWAKSTTSFSSPTALCRKQP*TGGSQAMPAGHTLFWQLPETTGISLRDCR,,TSSPRWRTVSGPWCRQSYLCSWMFSTDPSCFSQRTQTPEGNVKVAVSFA ,,S**SIQNSC*KMKRSSLRSYRP*GK**PKIEAMEK 148 codons (7 internal stop codons)			

Feature	Location	Size	±	Type
ITPR1-235	40,807 .. 69,918	29,112 bp		→ CDS
▶ 6 segments = 745 bp				
/note	= coding sequence ENSP00000497186			
/translation	= PGQPSQQPLSQVPQHCAENSHLAALSPQCRTQGLCSGSFQRLPEYH*EIA,,GHRLRAGGPSQAPGAGRVICARGCSPQTRAAFPREHRRQKEM*KWRFHLQ,,VNKAYKTAARRK*REALH*GPTDPEGNDQDRLWRK,,AGA*TKSTPAAAGRP*K,,G*GAQASSGQPLLWKRQTFGTGREPYQLWQWPTVSRRTQRARGRR,,GRFRIQLYEQG*DESGRGSVSP*QGGGFQSSYRPHHERIQ*PSVP*KH 248 codons (12 internal stop codons)			
ITPR1-235	40,807 .. 69,918	29,112 bp		→ prim_transcript
/note	= primary transcript ENST00000648564			
ITPR1-244	45,042 .. 52,835	7794 bp		→ prim_transcript
/note	= primary transcript ENST00000649425 Retained intron			
ITPR1-218	46,195 .. 69,819	23,625 bp		→ prim_transcript
/note	= primary transcript ENST00000494681 Retained intron			
ITPR1-240	46,210 .. 88,854	42,645 bp		→ prim_transcript
/note	= primary transcript ENST00000649144 Retained intron			
ITPR1-214	58,986 .. 70,234	11,249 bp		→ prim_transcript
/note	= primary transcript ENST00000487016 protein_coding_CDS_not_defined			
ITPR1-247	64,992 .. 88,854	23,863 bp		→ prim_transcript
/note	= primary transcript ENST00000649694 Retained intron			
EGOT	83,801 .. 86,199	2399 bp		← gene
/note	= gene ENSG00000235947 lncRNA			
EGOT-201	83,801 .. 86,199	2399 bp		← prim_transcript
/note	= primary transcript ENST00000414938 lncRNA			
	84,942 .. 85,294	353 bp		→ gene
/note	= gene ENSG00000275981 misc_RNA			
	84,942 .. 85,294	353 bp		→ prim_transcript
/note	= primary transcript ENST00000621460 misc_RNA			
	88,855 .. 128,641	39,787 bp		← gene
/note	= gene ENSG00000235978 lncRNA			
	88,855 .. 128,641	39,787 bp		← prim_transcript
/note	= primary transcript ENST00000441894 lncRNA			
	88,855 .. 127,136	38,282 bp		← prim_transcript
/note	= primary transcript ENST00000449914 lncRNA			
	88,855 .. 109,733	20,879 bp		← prim_transcript
/note	= primary transcript ENST00000687391 lncRNA			
	88,855 .. 109,649	20,795 bp		← prim_transcript
/note	= primary transcript ENST00000686919 lncRNA			
	88,855 .. 109,629	20,775 bp		← prim_transcript
/note	= primary transcript ENST00000693140 lncRNA			
	88,855 .. 98,103	9249 bp		← prim_transcript
/note	= primary transcript ENST00000465436 lncRNA			

Primer	Length		Binding Sites		Tm	Date Added
✓ PCR Forward	25-mer		1562 .. 1586		58°C	Aug 18, 2023
/sequence = AACATTGTTCCAGATCTCCAGGTAG 44% GC / 7641.0 Da						
✓ Donor Template WT -> SNV	100-mer		2010 .. 2109		76°C	Aug 18, 2023
/sequence = TTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAGACACTATCACTGCCCTGCTCCACAATGATCGGAAACTCTGGAAAAACACATTACCGCGG 48% GC / 30,819.1 Da						
✓ gRNA Protospacer	20-mer		2072 .. 2091		54°C	Aug 18, 2023
/sequence = CCAGGAGTTTCCGATTATTG 45% GC / 6123.1 Da						
✓ Sanger Sequencing Primer	20-mer		2205 .. 2224 86,433 .. 86,443	 	58°C 43°C	Aug 18, 2023
/sequence = ACCAGCTAAGTCCCTGCATC 55% GC / 6022.0 Da						
✓ PCR Reverse	25-mer		2468 .. 2492		58°C	Aug 18, 2023
/sequence = AATTTGTCATTTCTCTGCATCCAC 40% GC / 7518.0 Da						