

Polymorphisms around the *SHOX* gene of the Xp/Yp pseudoautosomal region

Six non-contiguous regions were analysed (5'→3': SEQ-6, -2, -4, -1, -35, & -7). The relevant sequences, and coordinates shown to the left, are taken from Genbank entry U82668. Exons are delineated by "+", Alu repeats are shown in yellow, other dispersed repeats in magenta, inverted repeats in green and tandem repeats in blue. The locations of PCR primers used for amplification of genomic DNA and for resequencing for SNP discovery are indicated. The alternative allele at each SNP is shown above the top strand of the sequence.

SEQ-6:

U82668

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-----> SEQ6A
4261  GGATCCTCAAGCCGTAGACATTTTCACGTACAATCAAAATCAACTGAAAAGGCAGGCGACG
-----+-----+-----+-----+-----+-----+
4321  TTTCTGAGGAACTTTGCTGAAAGAAAAGTCATGAGCCATAACAAACCTGGAACCGGC
-----+-----+-----+-----+-----+-----+
4381  TTCTTAACCCACCACGCAAACCTCCCAAGCTTCGGCGTGTGTTGAAAAACCAGAAAGACAG
-----+-----+-----+-----+-----+-----+
4441  CCTTCTCTAAATAGGATCCACATCTTCATCTTTCTCTCAGGACCCCAAAGACACCTCCTG
-----+-----+-----+-----+-----+-----+
4501  GCTGTTTCTTGCTGGAGAGAAAGCATTTCACGTGCAGTACACCCTGTTTGAACATCGCT
-----+-----+-----+-----+-----+-----+
          G +6/610
4561  TGGGTATTTGATAACATTGTTTTGTTGTAGTCAGAAACAGCGCATCAGAAAACACAGTTG
-----+-----+-----+-----+-----+-----+
4621  TACAAATACTCTTTTAAATGGTACTCGGTGGGGGCTGTGTGTGTGTTTTAAATAACAAA
-----+-----+-----+-----+-----+-----+
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ACTGCTAAACTCCATGGGAATTACTCAAATGAATATCAGGGAAAGGTTTCCTTCGTTAC
 4681 -----+-----+-----+-----+-----+-----+-----+

TTAAACAGATGCCTTTGCAACCTACTATTTTATTTTATTATGTCATTTCTATGGGAAGAG
 4741 -----+-----+-----+-----+-----+-----+-----+

ATTATTTAAAAGAAGAAAAGGGGCCCCAGGTTTTCTCTCCTAAATTTCTAGCCCCAAACC
 4801 -----+-----+-----+-----+-----+-----+-----+

TTCGTGATATTGAAAAGCAAGTATATCACAAAAGACTGTCTTCTACAAATTATATTTTAA
 4861 -----+-----+-----+-----+-----+-----+-----+

ATTGCAGTGTGCGTGTGTGTTTTAAATAACAAAAGCTGCTAAACTCCATGGGAATTAGTC
 4921 -----+-----+-----+-----+-----+-----+-----+

AAAATGAATATCGGGGAAGGGTTTCCTTCGATACTTAAATAGGTACCTTTGCAACCTACT
 4981 -----+-----+-----+-----+-----+-----+-----+

A +6/1127
 ATTTTATTTTATTATGTCATTTCTATGGGAGGAGATTATTTAAAAGGAGGAGCTCACGTT
 5041 -----+-----+-----+-----+-----+-----+-----+

TTTTCGTACGAAATTTCTAGCCCCAACCCCTCCATGATACTGAAAAGCAAGTATATCAGAAA
 5101 -----+-----+-----+-----+-----+-----+-----+

AGACTGTGTTCTACAAATTATGTTTTTAATTGCACTGTGTGTGTGTGTGTGTGTGTGTGT
 5161 -----+-----+-----+-----+-----+-----+-----+

GTTTTAAATAACAAAAGCTGCTAAACTCCATGGGAATTACTCAAATGAATATCAGGGAA
 5221 -----+-----+-----+-----+-----+-----+-----+

C +6/1323
 AGGTTTCCTTCGTTACTTAAACAGATGCCTTTGCAACCTACTATTTTATTTTATTATGTC
 5281 -----+-----+-----+-----+-----+-----+-----+

ATTTCTATGGGAGGAGATTATTTAAAAGGAGGAGCCCACTTTCTTGCTTTTAAATTTCCA
 5341 -----+-----+-----+-----+-----+-----+-----+

GCCCAACCCTTCTGGACATAACTCGTCTTCCTCTGCAGATTGGAACAGATGATTTTGCC
 5401 -----+-----+-----+-----+-----+-----+-----+

GTCCAAGCATCCACCGGTGCTGTAGGAGAAGACGCACCGTGTAGGTAGGTCAGCTGGCT
 5461 -----+-----+-----+-----+-----+-----+-----+

CTGAGTTGAAAGTGTACCCAAACCCAGGAGATCCAGGGCAGAAATTGTTTTAGTTCCAC
 5521 -----+-----+-----+-----+-----+-----+-----+

-----< SEQ6C

5581 AGAGCAGCCACGGGTGCACCGTCTGTGTATCTCTGTCAGTGATGCAATCCAATGCATCTG
 -----+-----+-----+-----+-----+-----+-----+
 5641 GCAAAGGGAACGCAGGGGGCTGCGAGGAAGGCCATTTCGAGTGGCCTGTAAAAATGCTGA
 -----+-----+-----+-----+-----+-----+-----+
 5701 AAGCTCCATACACCTTCCCTGTCTCTGGGATTCTCAGCATCCTGCTCTGCCCTCCAAGTA
 -----+-----+-----+-----+-----+-----+-----+
 T +6/1808
 5761 CAGGTGCTGACCCACCTCCCACCCCTGCCACCTCCAATCACATGCCTTGCACCCCTTC
 -----+-----+-----+-----+-----+-----+-----+
 5821 CTACCATTAGGCCTGCCGCTAAGGACCTGATTAGCTATAAATTTATGGCAATCCGCAACC
 -----+-----+-----+-----+-----+-----+-----+
 5881 ACCGGCCTTCCCTCCTGATGTTTTCTGACACATTTTCAGGAGACGCAGAATACAGGCTCG
 -----+-----+-----+-----+-----+-----+-----+
 5941 CTGGTCCACCCGAGACCCCTGGCTGCAGAAACAGCCCGGCTCGTGAACACAGTTGCCGTG
 -----+-----+-----+-----+-----+-----+-----+
 6001 GTAACATGCCCCCAGCTGTAGCCGGCCTAGGAAAACACTACGTGGACAAGGATGATTTTTTT
 -----+-----+-----+-----+-----+-----+-----+
 6061 CACAAGTTTTATTTTTTATTTATTTACTTGGGACCTTTTGTGGCAGCCGGACGGTGCA
 -----+-----+-----+-----+-----+-----+-----+
 6121 GCTTTTTCTCTGCACGGAGTCTGGTTGTGTCTACACACACAGGCAACACGCATAGATGGA
 -----+-----+-----+-----+-----+-----+-----+
 6181 CATAAACTATCCCCTCCCAAGACTTGCAAAGGATGCACGTTTTTTCAGGCTGCAGCCAGG
 -----+-----+-----+-----+-----+-----+-----+
 <----- SEQ6B

SEQ-2:

U82668

-----> SEQ2A
 13161 AAGGGAGATGCCTCCAAAAGGAGGAAGTACTCTCTTTGACCAACGTACATGATAGCAA
 -----+-----+-----+-----+-----+-----+-----+
 13221 CCTGCCAGGAACCAGGAACCAGAGACACGTATCCAACAAAAGGCACCTGCCTCTTCCCC
 -----+-----+-----+-----+-----+-----+-----+

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AGCTCCTGCTGGTTTTGTGGGGCAACCCTGGGAGTCCTTGTCTTGCAAATGTGTTGTCTAG
13281 -----+-----+-----+-----+-----+-----+
CTCTCCTCCTGAATGAGGCATCACCTGCATTCTCCACCTGCGTTCTTTGGAAGAGCTTTG
13341 -----+-----+-----+-----+-----+-----+
CAGCCTCTCAGGAGAGCTGCTCACCTGTCCCCCTGCCTGCTCATTGCCCTGTGCAAACC
13401 -----+-----+-----+-----+-----+-----+
AGAGTCCTGAGACACTCCCCAAAGGTTGGTCCCTACCAACCCAGGTTGCCTCTTATTTCT
13461 -----+-----+-----+-----+-----+-----+
TGCAACAAGACAGCAAAGACGCTGCAGAAGGATCGCTTACCTTGTTTGGAAAGAGAGCC
13521 -----+-----+-----+-----+-----+-----+
CACCCTTTCACCTCGCTGGCAAACATTTTCTTGTGTCCTAATGAGAACCCCAAGGAATAC
13581 -----+-----+-----+-----+-----+-----+
-----+-----+-----+-----+-----+-----+
CCC GGGATGTGAGGAGAGGGAGCGTCCGCCCGGCGGCCCGCCCAAGGAGCCTGAGGCTG
13641 -----+-----+-----+-----+-----+-----+
> SEQ2C
TCCTGCACACATCACACACACTCTCTGCATTGCAGTCCCATGTTTATAGAGAAGATT
13701 -----+-----+-----+-----+-----+-----+
ACAGGTGAGTTTCCAAAATCCCAGCCCATGCTGCCCTACCTGACGATGTTTGATTTCGG
13761 -----+-----+-----+-----+-----+-----+
AATTCCTTTAATTTTCAGCAAATGGATATTGGCTGTGGGTCAGCATAGATTTTTTCCGGTT
13821 -----+-----+-----+-----+-----+-----+
ATTTAAACAACATTTTCAGATGCTTTTCTGGCATCATTAGCTGAATGCTTCTACTGACAG
13881 -----+-----+-----+-----+-----+-----+
CTGGAATCATTCAAACATCTGAGACAAGAGAGTGAACAGGACGTTCACTTGTTACCGTGT
13941 -----+-----+-----+-----+-----+-----+
CTCCTCGCTTCTCAACCACCACCCCTGAAATTGCGAGACTGTCACTCTGGGGAGCCTGTG
14001 -----+-----+-----+-----+-----+-----+
AACGTGGCTGAACGCAAACGGATTTAAACTTGACAGGTGTTTCCAGCATGGAAAGGAAC
14061 -----+-----+-----+-----+-----+-----+
AAGGACTATAACGGCGAATAATAATAATAATAATAAAAAGACAAATTAGGGATCAAGATCC
14121 -----+-----+-----+-----+-----+-----+
AGTCTGTTTTTGTCTCATTATAGTCTTTTCTCCAAGAGGTTGTAGGCTGGTACCATTTC
14181 -----+-----+-----+-----+-----+-----+

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ACTAGGTTAAAAGCCTACGGTGTCAAGAGGTGCTAAGCTTTGCTGCTGTCTCTTGCTTGG
 14241 -----+-----+-----+-----+-----+-----+
 CAAGACAAGCTCCGAGTCTTTCTGGAAGTACAAATTGTGTGGGGCATTTCCTTGTCTTCTG
 14301 -----+-----+-----+-----+-----+-----+
 GGGTCTTTGCATGCATAGGGGCTGATCTTTGATATCCACTCTGGACTCCTCTCTGCAAA
 14361 -----+-----+-----+-----+-----+-----+
 CCTCTGGACATGCCACAGACAGCAGCTGTAACGTAGTGGGGTCAGCCTGCTTACAACCCA
 14421 -----+-----+-----+-----+-----+-----+
 CGTACCAACCCCATGGAGGTGATTGTTCGTATGACTAACAGCAGGCAGTTAAGGAGAAAGT
 14481 -----+-----+-----+-----+-----+-----+
 CATGCTTTACAACGAGTCTGTGACTAGAAATCACAGGACCTGATGAATCCCTCAGAAAC
 14541 -----+-----+-----+-----+-----+-----+
 CCAAGAGGGATGGACTAACATTAAGGGGGTTGTGGACTGTCCAGCCGTGCAGGGACGGTC
 14601 -----+-----+-----+-----+-----+-----+
 TCCAAGAAGATGCTTTAGACACAACGGTGAATTCTGCAGGCGCTAGTTTGCATGCATATT
 14661 -----+-----+-----+-----+-----+-----+
 <----- SEQ2B

SEQ-4:

U82668

-----> SEQ4A
 AAAGTGGGCCAGTCTCAGAGTTCCTTCCTCTTCGCAGCCATCCTAAGCGGTTCTCTCGAG
 36208 -----+-----+-----+-----+-----+-----+
 TTTCCCCCAGCAGGTGCGTTCTAGAAAGCGCTGGTCAGGACGCATGGCTGCCCCATAGA
 36268 -----+-----+-----+-----+-----+-----+
 TTTCTTGGGGACGGGAGTGAGAGACGCCTGGACGCCCAAGCGCAAGCCTCCAGCCTCCAA
 36328 -----+-----+-----+-----+-----+-----+
 GGTCTACAACAGATACAGCAGCTACTGAGTCTCCTCTCTGGTTTCTTTTCCGCCCTGG
 36388 -----+-----+-----+-----+-----+-----+

GGAGAGAAAAGAGAAGGGGAGAAACGTCACCACCAGCAACTGCTCCCAGCCAGCAAGACG
 36448 -----+-----+-----+-----+-----+-----+-----+

T +4/375

CACGGCGGGGAGGCCCGGGGCTGGCCGCGTCCTGCAGCTCCTGAGCTGCGTGTCTGAGCTT
 36508 -----+-----+-----+-----+-----+-----+-----+

TTCCCAGCCCCGCCTGCGTCTCCAGGGGCGAAATAAGAAGCAAATCTTGCTGGGACCGAG
 36568 -----+-----+-----+-----+-----+-----+-----+

GGGG +4/500L

TTCAGGTCGAGGAACTCCGGGACCCTCTGCAGCCTCAGCCCTGCCGCGCTCCCCGAGCT
 36628 -----+-----+-----+-----+-----+-----+-----+

TCGGGCCTGTTGCGGGGAGTTGGGGAGGAATTCAGGGAAGGGGGGAACCAGGCCGGGATA
 36688 -----+-----+-----+-----+-----+-----+-----+

-----> OX-M

AGAGGCTNCCGGCTTGCTGTGGGCTGCATGACGGGGTGCAAAGGCGAGGAGAAGCCCCTG
 36748 -----+-----+-----+-----+-----+-----+-----+

GGATCCTTGCTTGTTTGTCTGCGGGACCCCCAGCCCCGGCGGGCGGACCGCGGAGAGCGC
 36808 -----+-----+-----+-----+-----+-----+-----+

TGTCCCGGATCCGGAGATTCGCTTTTCTTTGCGACTGCGGGGCTGGCGCGCGCGCGGA
 36868 -----+-----+-----+-----+-----+-----+-----+

GGGGTCAGCACCCCTGGGCATTGGGGTCAATGCAACCAGGGCAGGTCCCTGGGGGGCCCCC
 36928 -----+-----+-----+-----+-----+-----+-----+

† EXON I (untranslated)

AGGAGCCAATAGGGGTTTTTGTAGTCACCCTGCGGCCGCTGCTTTTCCCCGGGTCTGAG
 36988 -----+-----+-----+-----+-----+-----+-----+

AACAGGGGCTCCCCACACTTTGTTTTTTTTTTTTTGGTTTTGTTTTATTTTCGTTTCCGCGC
 37048 -----+-----+-----+-----+-----+-----+-----+

GTCTCTTCTACTGCAAACAGAAATGGGAGGGTGGACAGGCGGGTAGGAGCGGATCAGAC
 37108 -----+-----+-----+-----+-----+-----+-----+

C +4/1063

GCCCAGGACGCAGCAGCCCCGAGTCCGCACAGGGTTTGCGGGAGGTGGTGACCGCGCTGGG
 37168 -----+-----+-----+-----+-----+-----+-----+

†

GACGCCAGGACGCGAATGAACCTCCGGGGCGCGCTCGGGGCCTGCGCTCAGAGCTTGGTG
 37228 -----+-----+-----+-----+-----+-----+-----+

<-----

37288 AGCTCGGTTTTGGAACCTTCCTTTTTCTTTTCCAGAAAGCTTTGCCTTCTTTCTTTCTTC
 -----+-----+-----+-----+-----+-----+-----+
 ----- SEQ4B

SEQ-1 (recombination assay interval):

U82668

OX-A ----->

42331 ACCCACCCTCACTCATGTCCCCCACTGCTGTGCCATCTCACACAAGTTCACAGCTCAGC
 -----+-----+-----+-----+-----+-----+-----+

42391 TGTCACTCCTGGGTCCCCAGGCCCGCCGGGGAGGAAGATGCGCCGTGGGGTTACGGGAGG
 -----+-----+-----+-----+-----+-----+-----+

42451 AAGGGGACTCCGGGCCTCCTGGTGCCCCACTTTATTTGCAGAAGGTCCTTGGCAGGAACC
 -----+-----+-----+-----+-----+-----+-----+

Ch3 ----->

42511 GTGACGCGTTTGGTTTCCAGGACTTGGAAAACGAATTTTCAGGTCGCGATGGCGAGCACCG
 -----+-----+-----+-----+-----+-----+-----+

42571 GCTTCCCCTGAAGCACATTCAATAGCGAGAGGCCGGGAGGGAGCGAGCAGGAGCATCCCAC
 -----+-----+-----+-----+-----+-----+-----+

S1 ----->

42631 CATGAAAACCAAAAACACAAGTATTTTTTTTACCCCGGTAAATACCCAGACGCCAGGGTG
 -----+-----+-----+-----+-----+-----+-----+

42691 ACAGCGCGGCGCTAAGGGAGGAGGCCTCGCGCCGGGGTCCGCCGGGATCTGGCGCGGGCG
 -----+-----+-----+-----+-----+-----+-----+

42751 GAAAGAATATAGATCTTTACGAACCGGATCTCCCGGGACCTGGGCTTCTTTCTGCGGGC
 -----+-----+-----+-----+-----+-----+-----+

6I1 (95% homology with 6I2)
 +701 T

42811 GCTGGAGACCCGGGAGGCGGCCCGGGGATCCTCGGCCTCGCCGCGCGCTCCCAAG
 -----+-----+-----+-----+-----+-----+-----+

42871 CGCCCGCGTCCCGGTTTGGGGACACCCGGCCCTTCTTCTCACTTTGCGGGATTCTCCAG
 -----+-----+-----+-----+-----+-----+-----+

<----- S17

42931 CCGCGTTCATCTCACCAACTCTCCATCCAAGGGCGCGCCGCCACCAACTTGGAGCTCAT
 -----+-----+-----+-----+-----+-----+-----+

44671 GCCGGGCCCCCGGAGATCACGGGAAGACTCGAGGCTGCGTGGTAGGAGACGGGAAGGCC
 -----+-----+-----+-----+-----+-----+
 44731 CGGGTCAGCTCGGTTCTGTTTCCTTTAAGGAACCCCTTCATTATTATTTTCATTGTTTTCT
 -----+-----+-----+-----+-----+-----+
 44791 TGAACGTCGAGGCTTGATCTTGGCGAAAGCTGTTGGGTCCATAAAAAACCACTCCCGTGA
 -----+-----+-----+-----+-----+-----+
 OX-C ----->
 <----- OX-CR
 44851 GCGGAGGTGGCCGGGATCTGGATGGGGCGCGAGGGGCCCGGGGAAGCTGGCGGCTTCGC
 -----+-----+-----+-----+-----+-----+
 44911 GGGCGCGTCCTAAGTCAAGGTTGTCAGAGCGCAGCCGGTTGTGCGCGGCCCGGGGAGCT
 -----+-----+-----+-----+-----+-----+
 +2784 A
 <----- OX-B
 44971 CCCCTCTGGCCCTTCCTCCTGAGACCTCAGTGGTGGGTGCGTCCCGTGGTGGAAATCGGGG
 -----+-----+-----+-----+-----+-----+
 45031 AGTAAGAGGCTCAGAGAGAGGGGCTGGCCCCGGGGATCTCTGTGCACACACGACAAGTGG
 -----+-----+-----+-----+-----+-----+
 +2900 A
 45091 GCGGCATACATCTTAAGAATAAAATGGGCTGGCTGTGTGCGGGGCACAGCTGGAGACGGCT
 -----+-----+-----+-----+-----+-----+
 45151 ATGGACGCCTGTTATGTTTTTCATTACAAAGACGCAGAGAATCTAGCCTCGGCTTTTGCTG
 -----+-----+-----+-----+-----+-----+
 45211 ATTCGCAGAGTTGAGGTGCGAGGGTGAATGCCCAAAGGTAATTCTTCTAAGACTCTGG
 -----+-----+-----+-----+-----+-----+
 45271 GGCTACCTGCTCTCCGGGGCCCTGCATTTGGGGTGTGGAGTGGCCCCGGGAAATAGCCCT
 -----+-----+-----+-----+-----+-----+
 45331 TGTATTCGTAGGAGGCACCAGGCAGCTTCCCAAGGCCCTGACTTTGTGCAAGCAGAAAGC
 -----+-----+-----+-----+-----+-----+
 45391 TGTGGCTACGGTTTACAAAGCAGTCCCCGGTTTCTGACCGTCTAAGAGGCAGGAGCCCAG
 -----+-----+-----+-----+-----+-----+
 45451 CCTGCCTTTGACAGTGAGAGGAGTTCCCTCCCTACACACTGCTGCGGGCACCCGGCACTGT
 -----+-----+-----+-----+-----+-----+
 45511 AATTCATACACAGAGAGTTGGCCTTCCTGGACGCAAGGCTGGGAGCCGCTTGAGGGCCTG
 -----+-----+-----+-----+-----+-----+

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CGTGTAATTTAAGAGGGTTCGCAGCGCCCGGCGCCGCTTCTGTGGGGTTGCTTTTTTGGT
45571 -----+-----+-----+-----+-----+-----+
TGTCTTCGCAGACACCGTTTTGCTCCTCTGAACTCTCTCTTCTCCCCCTGGCCGTGGAC
45631 -----+-----+-----+-----+-----+-----+
                                +3571  C
CCGGGAGAGCAAAGTGTCTCCAGACCTTTTGAAAGTGAGAGGAAAATAAAGACCAGGCC
45691 -----+-----+-----+-----+-----+-----+
AAAGACCCAGGGCCACAGGAGAGGAGACAGAGAGTCCCCGTTACATTTTCCCCTTGGCTG
45751 -----+-----+-----+-----+-----+-----+
                                <----- S5
GGTGCAGAAAGACCCCCGGGCCAGGACTGCCACCCAGGCTACTATTTATTCATCAGATCC
45811 -----+-----+-----+-----+-----+-----+
AAGTTAAATCGAGGTTGGAGGGCAGGGGAGAGTCTGAGGTTACCGTGGAAGCCTGGAGTT
45871 -----+-----+-----+-----+-----+-----+
                                +3837  T
TTTGGGAACAGCGTGTCCCCGCCGAGCCTGGGAGCCCGTGGGTTCTGCAAAGCCTGCAGGG
45931 -----+-----+-----+-----+-----+-----+
TGTGTTGAGGACTTTGAAGACCAGTTTGTGAGTTGGGCTCAATTCTGGGGTTCAGACTTA
45991 -----+-----+-----+-----+-----+-----+
                                +3955  A
                                S6 -----
GAGAAATGAAGGAGGGAGAGCTGGGGTCGTCTCCAGGAAACGATTCACTTGGGGGGAAGG
46051 -----+-----+-----+-----+-----+-----+
                                +3983  G      A  +3990
----->
AATGGAGTGTTCTTGCAGGCACATGTCTGTTAGGAGGTGAAACAGAATGTGAAATCCACG
46111 -----+-----+-----+-----+-----+-----+
TTGGAGTAAGCGTCCAGCGCTGAATGTAGCTCGGGGTGGGGTGGGAGGGCCCTGGTGTGG
46171 -----+-----+-----+-----+-----+-----+
                                <----- S7
ATCGTGGAAGGAAGAAAGACAGAACAGGGTGCTAGTATTTACCCCGTTCCTGTAGACAC
46231 -----+-----+-----+-----+-----+-----+
CCTGGATTTGTCAGCTTTGCAAGCTTCTTGGTTGCAGCGGCCTTGCCCTGTGCCCTTTGA
46291 -----+-----+-----+-----+-----+-----+

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GACTGTTTCCAGACTAAACTTCCAAATGTCAGCCCCTTACCCTTGACAGCAAGGGACATC
 46351 -----+-----+-----+-----+-----+-----+-----+

TCATTAGGGCATCGCGTGCTTCTCATCTGTGCTCAGCAGGCCCGAGATAGGAACAGAGGG
 46411 -----+-----+-----+-----+-----+-----+-----+

GCGTTGGAGATGCCACTTCCACCAGCCCTGGGTTGAAGGGGAGCGAGGGAGACACCTTTT
 46471 -----+-----+-----+-----+-----+-----+-----+

ACTTAAACCCCTGAGCTTGGTCAGAGAGGCTGAATGTCTAAAATGAGGAAGAAAAGTTT
 46531 -----+-----+-----+-----+-----+-----+-----+

TTCACCTGGAAACGCTTGAGGGCTGAGTCTTCTGCCCTTCTGACTCCCCAGCAAATACA
 46591 -----+-----+-----+-----+-----+-----+-----+

GACAGGTCACCAACTACTGGAGATGAGAAAGTGCCATTTTTGGCACACTCTGGTGGGGTA
 46651 -----+-----+-----+-----+-----+-----+-----+

GGTGCCCCACCGCGTGTGAAAAAGTGGGAAGGAGAGATTTCTGCGCACGCGGTTTCAGCCC
 46711 -----+-----+-----+-----+-----+-----+-----+

CCAGGCGCGGTGGCGCATTTCAGGTA CT CAGACGCGGTTCTGCTGTTCTGCTGAGAAACAG
 46771 -----+-----+-----+-----+-----+-----+-----+

S20 ----->
 GCTTCGGGTAGGGGCTCCTAGCTCCGCCAGATCGCGGAGGGACCCCCAGCCCTCCTGCGC
 46831 -----+-----+-----+-----+-----+-----+-----+

TGCAGCGGTGGGGATAGCGTCTCTCCGTAGGCCTAGAATCTGCAACCCGCCCCGGGTCTT
 46891 -----+-----+-----+-----+-----+-----+-----+

CCCCCTGTCCTTCCCGGGCGTCCCGCCGGGGATCCCACAGTTGGCAGCTCTTCTCAAAT
 46951 -----+-----+-----+-----+-----+-----+-----+

TCTTTCCTTAAAAATAGGATTTGACACCCCACTCTCCTTAAAAAAAAAAAAATAAGAAAA
 47011 -----+-----+-----+-----+-----+-----+-----+

<----- S8
OX-E -----
 AAAGGTTAGGTTATGTCAACAGAGGTGAAGTGGATAATTGAGGAAACGATTCTGAGATGA
 47071 -----+-----+-----+-----+-----+-----+-----+

----->
 GGCCAAGAAAACAACGCTCGTGCAAAGCCCAGGTTTTTGGGAAAGCAGCGAGTATCCTCC
 47131 -----+-----+-----+-----+-----+-----+-----+

+6485 C
 48631 GGGAAACCCGTCAAAAATAAATGAAATTAAGATTGCCGACCAGAGAGAGAACCGTGACAAA
 -----+-----+-----+-----+-----+-----+-----+
 <----- OX-P

GCAAACGGCGTTCAAAGCAAAGAGACGAACTGAAAGCCCCTTCCCCTAGGACTGGTTATG
 48691 -----+-----+-----+-----+-----+-----+-----+
 <----- OX-J

G +6630
 48751 AGGTCAACACATTCAAACACAGCTTGCTCTGGATTTTGCTGAGCAGAGGAAGATACAGAT
 -----+-----+-----+-----+-----+-----+-----+
 GCATTTGATCCAAAGTGTGTACATCTTTCATTATATGTGTGTCTATATATATAAACATA
 48811 -----+-----+-----+-----+-----+-----+-----+
 tandem repeat/8I1
 TATAAATATATAAACATACATAAATGTATGTAAATATATATAATCTATATACATATATAA
 48871 -----+-----+-----+-----+-----+-----+-----+
 8I1 (69% homology to 8I2)
 ATATATAAACACATATATAAATATATAAATCTATAAACATATATAAATATATAAACATAAAT
 48931 -----+-----+-----+-----+-----+-----+-----+
 ATATAAACATATATAAATATATAAATATATTAACATATATAAAATATGTATAAATATATAT
 48991 -----+-----+-----+-----+-----+-----+-----+
 tandem repeat/8I1
 AAACATATAAACATATATAAATATATAAACATATAAATATATAAACATATATAAATATAT
 49051 -----+-----+-----+-----+-----+-----+-----+
 8I2
 ACAAACATATTGTATATATATAAATATATATAAAAACATATATATACATATAAAAATATA
 49111 -----+-----+-----+-----+-----+-----+-----+
 TATAAACATATATACATATAAAGAAATATATATAAACATATATACATATAAATATACATA
 49171 -----+-----+-----+-----+-----+-----+-----+
 TATAAACATATATATACATAAATATATATAAACATATATACATATAAAAATATATATAT
 49231 -----+-----+-----+-----+-----+-----+-----+
 ATTAACATATATATACATATAAAAATATATATATTAACATATATATACATATAAAAATAT
 49291 -----+-----+-----+-----+-----+-----+-----+
 ATATATATTTTGGCCCCTGATTCCCTTCGGTTCCTGTGGGATGGGTGATTGAGTCAACA
 49351 -----+-----+-----+-----+-----+-----+-----+
 CATTCAAACACAACCTTTCCATCGATGTTGCTTAGGAGATGAGGATACAGATGCGTTTGA
 49411 -----+-----+-----+-----+-----+-----+-----+

OX-G ----->
TGGAGAGGGTTTTACAAGCTCTTTCATTTAAATATATATATATATATATATATATTTTT
49471 -----+-----+-----+-----+-----+-----+-----+
<----- S12

OX-K ----->
GGCTCCTGATTCTCTTCCGTCTTCCCATGTGGCTGCATTTTAAAAGGCTTCCCTAAGATC
49531 -----+-----+-----+-----+-----+-----+-----+
G +7445
GTTACGATTAAATCAACCCTCCCCAGGCATCTTTACCGAGGGCTGTGGTCCCCAAAGCGA
49591 -----+-----+-----+-----+-----+-----+-----+
TACAGCCCAGGAGGGAGAGAGGCTTTGGTGACTTGGAGGAAGGACTGTGTCCCTCCTTAG
49651 -----+-----+-----+-----+-----+-----+-----+
GGCGTCTGTGGCCTCAGTGAGGGAAGGAAGCTGCATCAGACAGGGGTTTCTCGCTGTCC
49711 -----+-----+-----+-----+-----+-----+-----+
ACCCCTCTGGCAGAAGATGGATTGGGCTGCCCCGTATAAAATTAATGAAAAGATTAAAGTT
49771 -----+-----+-----+-----+-----+-----+-----+
TCGCTAAAGGGGACATCGAGTTTATGTGTCATCTCCTGGTGTCTGTGTGCCTGGGATCTG
49831 -----+-----+-----+-----+-----+-----+-----+
CAATATATCCCAGCCCTTGATGTACTGTTTCTATAAAAAATAAATTACTTGTAATTTAATT
49891 -----+-----+-----+-----+-----+-----+-----+
CCACACTATTTCTTTCCGTAGTCTATTACCGACGAGAGCACGTTAGTTCAGCTGCGGAAA
49951 -----+-----+-----+-----+-----+-----+-----+
ATTGGTTGTGGGGTGTGTGCGGACCCCGAGAACGCCCTAAAATAAAGACAAATCGGGGAC
50011 -----+-----+-----+-----+-----+-----+-----+
AAGCTGGGGGTATCGATTGCAGGGGTCGCATGAAAATTTAACGACGGTAAATAATAATA
50071 -----+-----+-----+-----+-----+-----+-----+
C +7982
AAACAACATGGGAATGCAATAAAAGACATAATTCTCCATCGCCGCGGGGGAAAGGAT
50131 -----+-----+-----+-----+-----+-----+-----+
CCTATAGTAAAGGCGAGTGCCTTTGAGGGGTCATAAAAATCAATTAGTTCCAACACCCA
50191 -----+-----+-----+-----+-----+-----+-----+
CGTCCCGCGTTGAGGGGACGGGGACGAGCAGGGACAGAAAAAGAAACCATATTTGAATCC
50251 -----+-----+-----+-----+-----+-----+-----+

S13 ----->

50311 CATCTCTCTGTGAATTCTTGGGTACATGCGTCTCAGTACAGCCCGTCCCGTGCTGTGAC
-----+-----+-----+-----+-----+-----+

50371 CGGATAGAGTTTCAATTTACTGTGGAAATTTGCTGTAAATAAATTGAGCATCCGATAGAA
-----+-----+-----+-----+-----+-----+-----<

50431 GCTGTTGCTGATTAACCTTTTATTTTTAGCGTGGCCCTGCAAAGTCGTATCACCCAGCTG
-----+-----+-----+-----+-----+-----+-----

----- S14

50491 TCAGGCTTCTAATCGAAAGTTATGAGACCACGGTGAGGGGCAGGCGGTAATTTAATTACA
-----+-----+-----+-----+-----+-----+-----

50551 ACAAATATCTTTGGGTTTATGGCGCAGAGCTAAATTAATGTCATTATTCACTGTCTGTA
-----+-----+-----+-----+-----+-----+-----

50611 ATGGAAATCAAAGGAAATCGCATTACGGCATTGGGAAAGAAAGCGGGGAGTGCTCTTT
-----+-----+-----+-----+-----+-----+-----

50671 AATGAAGAAATAACTGTCTTAAGCAGTGTACACACTTCACTTACCATATTCGGGCCTAA
-----+-----+-----+-----+-----+-----+-----

50731 TTGGAATGGATCGTGAATCACTCCAAGACTGATTTATTAGCGCTTCACGCAGCGGCTAAT
-----+-----+-----+-----+-----+-----+-----

50791 TCATCACTTGTATTCTTCATCATTTTTTTTTTTTCTCTCGCCGTGTTGAAGGGAGAGTGA
-----+-----+-----+-----+-----+-----+-----

50851 ATGAGGCTTTCACGTTTCAGGAGGATTTCTTTTTTGAAAAATGCCCTTCCAGAGGCTT
-----+-----+-----+-----+-----+-----+-----

50911 TTGGGTGGCTGGCTTGCTTTCTGGGCCCTGGAGGAGACAGGCGGAGAGTCCAGGTGGGCA
-----+-----+-----+-----+-----+-----+-----

50971 TGGAGAGGCACAGTGGCAGGTCACCTGGATGGTCAGTGGAGGTGGAGGTCTGAAGGCC
-----+-----+-----+-----+-----+-----+-----

51031 AGCTTTGAAATTATTGGTGAATTTGATGTCAGCACCAGGCAGGGGCCTTTTTGGCGGG
-----+-----+-----+-----+-----+-----+-----

+8965 C

51091 GGTGTGAGGGAGGATGACTTTGCTGGGAAACAGGATCAGGTTCTCCAGGCGCACTGCAGC
-----+-----+-----+-----+-----+-----+-----

51151 CCGGTAGGACCCACTTTGAAATGAAAAGCCAGTTCCGAAAGCTGGGCTGGAAGCTTCCG
-----+-----+-----+-----+-----+-----+-----

51211 TGTGGGTTCAAGAGCAAGTTCACGTTGCGCTGTGTAGACTCCTGGCTGCTCCCAAACCTC
 -----+-----+-----+-----+-----+-----+-----+

S15 -----> +9177 T
 51271 TGAGGGTTTTCTGAGGTTCCCTTCATAGGGGCACCGGCCCTGGGCCATGCACAGTGCCTA
 -----+-----+-----+-----+-----+-----+-----+

51331 AGGGTGGCTGTGGGCCGAGGGACCCAGCACGTGTTTTGCCACAACAGCCGGAGTGAAGT
 -----+-----+-----+-----+-----+-----+-----+

51391 GTTCACTCACCGCCTTGGCGGAGGACGCCTGTTCTCTGGACGAATCATTCTCTTGGGTG
 -----+-----+-----+-----+-----+-----+-----+

51451 GTGACTGCCTTGTGGGTCAAGGTGCAGGTTTTCTGCCACAGAAAACCTGTTAGGAGGAAT
 -----+-----+-----+-----+-----+-----+-----+

51511 TAAGCGACTAAGACTGTCAGGGAGGTGGTGGTGGGGGAGAGGAGGGGGTGGTGTCCAGAT
 -----+-----+-----+-----+-----+-----+-----+

51571 TACCAGGCATAGGCTAAACTGCCTGCACTCTCCAGCTGGTCTGTCTGTGGAGGAGGGGAT
 -----+-----+-----+-----+-----+-----+-----+

51631 TGTCAATACTGGGAGAGCAGAGGAGGCTCGTAGGAGGTGAGAGGGGGTGAATTTGCATG
 -----+-----+-----+-----+-----+-----+-----+

+9595 T
 51691 CAAATCTTACATGAGGCCTGTGTGAATTTCTCCAGCCTCCTGAGGGTCCCCTGCCTAT
 -----+-----+-----+-----+-----+-----+-----+

51751 TGCACTCAACTTCTTGATAGTTTACCCCAAGACTCAGAAGTCCTTAGAGGGGCAGAATGC
 -----+-----+-----+-----+-----+-----+-----+

s21 <-----
 +9697 T
 51811 CCCACCACAAAGCCTGCTATCCTTGGGCGTCTCAAGACCCTTGGTTCATGAATGGGACC
 -----+-----+-----+-----+-----+-----+-----+

51871 CTTTCATGTATGGGACCCTTGGTAATATGAATGGGACGCCTTCAGCTCCCCAGGGCTTC
 -----+-----+-----+-----+-----+-----+-----+

CGAGGAGGCCGAGAAGGGCAAAGACA
 51931 -----+-----+-----+-----+-----+-----+-----+

51991 CTGGGCTTGGTGTGTCAAGAGCTAGATTGGAGAAGGGGCTGGATTTGAACTCTTTAGCC
 -----+-----+-----+-----+-----+-----+-----+

52051 ATCAGCTCACCTCTCCGTTTGTGGCTAAAGTCTGAAGGTGGAAACTTCGGTTCTCCTAC
 -----+-----+-----+-----+-----+-----+-----+

52111 AGGGTCTACAGGAGTTGGGGGGCGGGGCGCCACACAGAACGCTGGAAAGTTTCGACAGTC
 -----+-----+-----+-----+-----+-----+-----+
 52171 CACTTCCACTGGCTCGGAACTCACTTTTTTCACCTTAAGTTCATCAGCGGTAACGCATAGG
 -----+-----+-----+-----+-----+-----+-----+
 52231 TCTCACTTAGGCAGGGCACGGATGATTTAACAATTTCTACTTCTAGGTCAGGTGCGGTGG
 -----+-----+-----+-----+-----+-----+-----+
 --- OX-H

SEQ-35:

U82668

-----> SEQ3A
 61282 GCGTGAACATTCAGCATGGAAACAACATACGTCTCTCCACAGGAGGTGAGAAATTGAATT
 -----+-----+-----+-----+-----+-----+-----+
 61342 TATGGGGTGGGTGTACGCTGGCGATTCTTGGTGCTTTTTGCTCAAAACAAGTTCTTTTG
 -----+-----+-----+-----+-----+-----+-----+
 61402 AAAGTCACGTTCCCTGCTTTCCCTGTGGCTTCCCGGTGAGCTCGCTCGCAGAGCAAGGAAT
 -----+-----+-----+-----+-----+-----+-----+
 A +3/341
 61462 ACCACCCAGAGAGCAACGTGGGCTGTGTTCCGTGTAACGCCGTTGCAGAGAGAGGATTT
 -----+-----+-----+-----+-----+-----+-----+
 61522 GGTGTGTGAGATCCGTACCAGCTCCAGCACACTGATAGGAACACGTTGCTGGCCGAACTG
 -----+-----+-----+-----+-----+-----+-----+
 61582 AACGATGCTGGGTTGGGTCCTGATTGATACGTATTTTTCTTCCCTCCTCTCCCCAAAACCTT
 -----+-----+-----+-----+-----+-----+-----+
 61642 GGCCAAATAGTCCGTGGAGGGTTGTCAGTCGCCGAGTTGAGCAAAAAACACTTCTTCCT
 -----+-----+-----+-----+-----+-----+-----+
 61702 TTGAGTGGCTGTTCTGGTGAAATCTGTTTCTGACATATCCACTTTTCTCTCTTTTCTC
 -----+-----+-----+-----+-----+-----+-----+
 +3/663 C
 61762 TCTCTCTGACTGCGAAGCACCCACAGGGAGAAGGAATTGGATGTATCGGATGTTGGTATT
 -----+-----+-----+-----+-----+-----+-----+
 61822 AGATTTTCTTTCTCCGTTTCGAGTCTCTGACTGGTGCATACTTTGCAAAGGTGTGTTCCCTG
 -----+-----+-----+-----+-----+-----+-----+

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GCAATTGCCAAGAGTTAGAAAAATGCACCTTCTCTGGTGGCCGTTGGGGTGTGTTTCAC
61882 -----+-----+-----+-----+-----+-----+
AGGCAGTGGTGACAGGGCCCCTTGGCTGTGGCTGTCTTCTCCAGCGCCGTGGATAAAGAG
61942 -----+-----+-----+-----+-----+-----+
      T  +3/849
ACGGGACAGATTCTGTGCCTCTGTACGATTTAGAGCGTAACTGACCGGTCCAACACCCG
62002 -----+-----+-----+-----+-----+-----+
TTTTTCCACTTACAAAGCTGGTGGTGCACGGGCTTGGTGTCTCCCGTACGGGAAGGAGG
62062 -----+-----+-----+-----+-----+-----+
CCTTTGGGCCGCTCCAAAGACGCCCTGTCGTAGGAATGGCCTCTCCATCCCGCCAAAGTC
62122 -----+-----+-----+-----+-----+-----+
      A  +3/1035
CAGCCAGGCCCCCGAAATGGTCCCATTTCTTGGGAAGCCTGAGTTTCTGTTCTGGTCTTG
62182 -----+-----+-----+-----+-----+-----+
CTGCTGTCCTTGGCCACGTCAGCACGTGGGAGCATCTGTGGATAACCGCAGAGTCTGGGGA
62242 -----+-----+-----+-----+-----+-----+
      ----->  SEQ35B
CAGCTGGGCGTTTAAACCGAAATGAAGCCGAGACGGGTTTCAGGTTTGGTGCCAAGCTCT
62302 -----+-----+-----+-----+-----+-----+
      +3/1239      G      A  +3/1248
GGTCAGGATGAAAGGGAAATACCAGAGTCCTCTGTCTCCTCGCCTCTGGGTTTCATGCTGAC
62362 -----+-----+-----+-----+-----+-----+
CTTTCTAACATTTGTTTTCCCCTAAGAACAAGCAGAAGCCTCCAGCTCCCTTTAGCTCCA
62422 -----+-----+-----+-----+-----+-----+
CAGTTTTCCCGGGACATAGCGAGGATGGCACACGGCAGCCACTCCCACGACACACATTT
62482 -----+-----+-----+-----+-----+-----+
      <-----  SEQ3B
CGGAGGCACTTTGCTGGAAGCCGCTTGTCTCCTCCAGCTTTGGGAGGTCTGGGGAGGAGA
62542 -----+-----+-----+-----+-----+-----+
      !! sequence termination !!----
GAGGCTTTCGGTGGACACGTTTGACATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAACTGG
62602 -----+-----+-----+-----+-----+-----+
      ----->  SEQ35B1
TGCCTAATTTATTAAGAGAATTAGCTTAGCGAGTATATGCTGATATTCTTCGACACACG
62662 -----+-----+-----+-----+-----+-----+

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TGGGTAAGTTGATGCCATTTATAAATGTTTTATTGAAATTTGATATTTAATGAGAAGCCG
62722 -----+-----+-----+-----+-----+-----+
GTTAAGGAATGTAGACAATATCCCGTTTCAAAGCTATGAAATGTGCTATTTATTGAAAGG
62782 -----+-----+-----+-----+-----+-----+
GGATGTGGCTTCACGAGTTCAGCCCATTGTACGTGCAGGTCCCGTGGGAAGGAGGCAAAA
62842 -----+-----+-----+-----+-----+-----+
                                     G  +35/1652          -----
GCCCCTGCTTCTTACTTTGTGATGTATGTGCATTTGTTATTTATTTTTTTTTTTCCTTGGTC
62902 -----+-----+-----+-----+-----+-----+
----->  SEQ35B2
GGACGTTCAATAATATGTACTATTTTAATTATGTTCGAGTGTAATTTGACATCGCGTTGC
62962 -----+-----+-----+-----+-----+-----+
ATTTATTTTTATATTTCTGAAAACGTTTGCTTTTTCTTTTTCCCTCCCCCATTGACGACA
63022 -----+-----+-----+-----+-----+-----+
TAGCGGCCCCCGCGTCCGGGTTACAAATACATCTACAGATATTTTCAGGGATTGCTTCAG
63082 -----+-----+-----+-----+-----+-----+
ATGAAAACAAATCACACACCGTTTCCCAAACCAACAGTCTTCACATTTCTATCCCTCTGT
63142 -----+-----+-----+-----+-----+-----+
TATTGTGCGGCAGGCGGTGAGGGGTAGAAAAAAACAAACAAACAAACAGAAAAAAAAAAC
63202 -----+-----+-----+-----+-----+-----+
----->  SEQ35B3
AAAAAAACCACCCTGAGTTTCTCTGGTGACGCCCTCATTCTCCTAACGTTCAATAATCT
63262 -----+-----+-----+-----+-----+-----+
CAATGTTGAGTTGCAGCAACAGACTGTATTTTTGTGACGCCCCGTAGTATGAATGTACAT
63322 -----+-----+-----+-----+-----+-----+
                                                    !! sequence terminati
CTTGTAAAACTGAGATATAAATAAACTTATAAATATTTGTATTCAAGTGTTAAAAA
63382 -----+-----+-----+-----+-----+-----+
                                                    !! sequence termination !!
AAAAATTCTCAACCTCTCCCCTGAGGACAGGCTTATTGGAAAAAAAAAAAAAAAAAAAA
63442 -----+-----+-----+-----+-----+-----+
TCCTGAGTCGGCCGTGGCTGAACACAGAGTGTGTTCTGCTCCGTGCATTTCCAGGGTGG
63502 -----+-----+-----+-----+-----+-----+

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64462 CGTCCGTTCTTCCTGCTGACTCCTGGTAGTTCCTGAAAGCTTCTCTTGGCCAGAGAAGGG
 -----+-----+-----+-----+-----+-----+

SEQ35C ----->

64522 GTTTCAGAGGCCGTGTGTCCAGGCCATTCTGCAAAGTGCAACTTGACCGTTCCTTTTCCTT
 -----+-----+-----+-----+-----+-----+

64582 TTCTGGCCTGCGTGGTCTGAAGCTCAGAGCCCTCTCTTCACCCAGCCTGTGTGTGTCTTG
 -----+-----+-----+-----+-----+-----+

C +35/3390

64642 CCGGACAGAAGAAAAATGGTGCTTTTTTGC GTGTTAGCAGAGGTGCTTTTTCATGGCTGACC
 -----+-----+-----+-----+-----+-----+

64702 TCAACGCGTCCATCTCCAGCCTTGACCAAGCTGTTTTTTAGGGGCAAACGCAGGCAAGTT
 -----+-----+-----+-----+-----+-----+

64762 CTGAATGCACACAGTTATTTTCATGGTTAAACTATTCAGCTTTGGCCGGGCGCAGTGTGGC
 -----+-----+-----+-----+-----+-----+

<----- SEQ35A

64822 TCTCACGCCTGTCATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGGTCAG
 -----+-----+-----+-----+-----+-----+

64882 GAGTTCGAGACCAGCCTGGCCAACACGGTGAAACTCTATCTCTACTAAAAATACAAAAAT
 -----+-----+-----+-----+-----+-----+

64942 TAGCCGGGCGTGGTGGTGTGTATCTGTAATCCAGCTACTCAGGAAGCTGAGGCAGGAGA
 -----+-----+-----+-----+-----+-----+

65002 ATCGCTTGGACCCAGGAGGCGGAGGTTGCACTGAGCCGAGATCGCGCCATTGCACTCCAG
 -----+-----+-----+-----+-----+-----+

65062 CCTGGGCGACAGAGCCAGACGCTGTCTCAAAAAAATGAATAATAAAATAAAATAACAGGA
 -----+-----+-----+-----+-----+-----+

65122 ACTAAATAAAATAAAACGTTTCAGCTTTGTTCTGCAAATCCACTCCTATTGTTTTACGTGG
 -----+-----+-----+-----+-----+-----+

65182 TTTGAGAGACTCTGTCCCTTAGAAATAGATGTTTGTGCAATTGTAATGAATCTGTTTC
 -----+-----+-----+-----+-----+-----+

65242 AAAAATGAACAGAATATTCAAATGGTTTGAGAGATCTTTTCCCTTAGAAATAGCTTGTG
 -----+-----+-----+-----+-----+-----+

65302 CCAATCACAAGAATGTTTTTCAAAAAATGAATGGAATCTTCCTGGATATCGCTTCCAGAT
 -----+-----+-----+-----+-----+-----+

65362 CTTCA**TTTTTTTT**GCATAGTTCAACCTGAAAAGTAAGTGTCTCAGCCCTGAATTTCTTTC
 -----+-----+-----+-----+-----+-----+-----+

65422 TGATTTTCCATGGGTTGTCTTGCAGACTTCTCTGGACTTGACCACATTT**AAAAAAAAAA**
 -----+-----+-----+-----+-----+-----+-----+

65482 AAATTAACTTTTTTCACACGGACACGGTTTTCAATAGGAATGAGATCTTTGAGTTTTTATGT
 -----+-----+-----+-----+-----+-----+-----+

65542 AACAGATTCTTACCATCAGTTCTCAGATTCCCAAATTACACACAAAAAGCCACGGACTTC
 -----+-----+-----+-----+-----+-----+-----+

65602 GCCTCCTGCTAACATGTCCTTCTGTTTTCTGAGGCTTCTGTTGGTGTTAGACTTTCATGTT
 -----+-----+-----+-----+-----+-----+-----+

65662 TAATAGCAGACAATGTAGGGATTTAAAGAAAAATGCAGAGAAAGCAAAAAACACTGACCAA
 -----+-----+-----+-----+-----+-----+-----+

65722 ACACACGGAGATAAGCTTTCTAAAGCCTTTGTTCTTGGAGTTGTCGTT**AAAAAAAAAA**G
 -----+-----+-----+-----+-----+-----+-----+

<----- SEQ35D2

-----> SEQC1

65782 TTGTTTTAACTTTGCAAGCATGCCTATATTGAACTCATAAGCAAGAGCCAAGAAAAA
 -----+-----+-----+-----+-----+-----+-----+

65842 TAGTGTCGGTCGTCTACTCTACACGTTTTCCCAAACAGACGTATTTAATTTCTTTTGT
 -----+-----+-----+-----+-----+-----+-----+

A +35/4673

65902 TTGAACTCACAGATGCTGAGAGTTAAAAGTTAAATTTTTGTCATGAACAA**TAGTGGCCAA**
 -----+-----+-----+-----+-----+-----+-----+

65962 **AACCACAGTTACTTTTGCACT**TATAGCATAATAAGAAAAATACAG**GGCTGGGCTCGGTGGCT**
 -----+-----+-----+-----+-----+-----+-----+

66022 **CACACCTGTAATCAAAGCACTTTTGGAGGCGAAACAGCCAGATCCCTTGAGCCCAGGAGA**
 -----+-----+-----+-----+-----+-----+-----+

66082 **TTGAGACCAGCCTGGGCAACATAGCGAGACCCTCATCTCTACAAAAAAGGTTTGTTACAT**
 -----+-----+-----+-----+-----+-----+-----+

66142 **ATGTAACAAACCTGCACATTGTGCACATGTACCCTAAAACCTTAAAGTATAATAA**TAAAAA
 -----+-----+-----+-----+-----+-----+-----+

66202 AATT**AAAAAAAAA**TTACCAATCAACTGCCTGCTGGTGCCTTCAAGAGACTCACCTAACA
 -----+-----+-----+-----+-----+-----+-----+

66262 CATAAGGACTTGCATAAACTTATAAAACAATTCAATGGAAGAATCCTTGAAAGTATTCTG
 -----+-----+-----+-----+-----+-----+
 66322 AGAAGACAGTATAATAAACTGATTTCTAAAAGGCTATAAAAATTGAATAAATCATTGT
 -----+-----+-----+-----+-----+-----+
 66382 TGGGCATCCTGTGCTGAAATATAATGCAGCCAATAAAAATTACAAAATGAATAAACATTT
 -----+-----+-----+-----+-----+-----+
 66442 TATAACAATAAAAAAAAGTCAAATAATTAGGCAGGCATGGTGGTGCTCTCCTACGGTTGA
 -----+-----+-----+-----+-----+-----+
 66502 AGCTATTCAGCAGGCAAGAGGATACTTTGTTTTTGTTTTTTAATTTTTTTTGAGACAGAG
 -----+-----+-----+-----+-----+-----+
 66562 TCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGTGATCTCAGCTCACTGTAATTTCTGC
 -----+-----+-----+-----+-----+-----+
 66622 CTCCCGGTTCAAGCGATTTTCTGCCCCAGCCTCCCGAGTAGCTGGGATTACAGGTGCC
 -----+-----+-----+-----+-----+-----+
 66682 CGCCACCACACCTGGCTAATTTCTTTTGTATTTTTAGTAGAGACGAGGTTTCCCATGTT
 -----+-----+-----+-----+-----+-----+
 66742 GGCCAGGCTGGTTTTGAGCTCCCGACCTCGGGTGATCCACCCGCCTCAGCCTCCCAAAGT
 -----+-----+-----+-----+-----+-----+
 66802 GCTGGGATGACAGGCGTGAGCCACCGCGCCTGGCCCAGGAGGATTATTTGATCCCAAGAG
 -----+-----+-----+-----+-----+-----+
 66862 GTGGAGGCTGCAGGAAGCCATGATTGCACCACTGCACTCCAGCCTGGCTGACAGAGTGAG
 -----+-----+-----+-----+-----+-----+
 66922 ACCACATCTCTAAATAAATGAATAAATACAGGCAGAACTTTTTTTGTTTTGTTTTGATG
 -----+-----+-----+-----+-----+-----+
 <----- SEQ35D1
 -----> SEQ35C2
 66982 GAGTCTTGCTCTGTCAAGGAGGAGTGCAGTGGTGCCATCTCAGCTCACTGCAACCTC
 -----+-----+-----+-----+-----+-----+
 67042 CACCTCCTGGGTTCAAGCAATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGT
 -----+-----+-----+-----+-----+-----+
 67102 GCCCGCCACCACGCCCGGCTAATTTTTTGTATGTTTAGTAGAGACGGGATTTACCGTGT
 -----+-----+-----+-----+-----+-----+

TAGCCAGGATGGTCTTGATCTCTTGACTTTGTGATCTGCCTGCCTCAGCCTCCCAAAGTG
 67162 -----+-----+-----+-----+-----+-----+

CTGGGATTACAGGCATGAGCCAGGAGTTCAAGACCAGCCTCAGCAACAAAGTGAGACCT
 67222 -----+-----+-----+-----+-----+-----+

TTTCTCTCCAAAAAATCAAAAATTTAGCCAGCTGTGGTGGCTCCTGCCCGTGATCCCAGT
 67282 -----+-----+-----+-----+-----+-----+

ACTGTGGGAGGCTGAGGCAGAATTGCTTGAGCCAGGAGTTCGAGACCAACCTCAGCAAA
 67342 -----+-----+-----+-----+-----+-----+

AAGGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATATATATATATATA
 67402 -----+-----+-----+-----+-----+-----+

T +35/6219

TATATATATGAGTTTCAAAAATTGCTGGGTGACCAGCTCATCTACTGGTTTTCCCTTGG
 67462 -----+-----+-----+-----+-----+-----+

GAAAGTGAAATTGTCATGTATTGAAGATTTCCAAGGAAGTTGTATTGAATGAGAAACAAA
 67522 -----+-----+-----+-----+-----+-----+

-----> SEQ35E

CTCAATCTGTTCTGTTTTAAAGAGCTGCAGTGCCTTGTGTTTCCATAAAACTGCA
 67582 -----+-----+-----+-----+-----+-----+

CTTCCAAAAGACACGCTGAGAAAGGAGACCAGGATTTGTAATTCAGAAATTGGAAAGCAA
 67642 -----+-----+-----+-----+-----+-----+

<-----

C +35/6445

GTTAGGCTGGACGTGGTAGCTCATGCTTGTGTAATCTCAGCACTCTGGGAGGCTGAGGC
 67702 -----+-----+-----+-----+-----+-----+

----- SEQ35D

AGGAGGATCACTTGAGCCAGGAGTTCAAGACCAGCCGTGCCACATGGTGAAACCCTGT
 67762 -----+-----+-----+-----+-----+-----+

CTCTCCAAAAAATAAAACATTTAGCCAGATGTGGTGAICTCATGCCTGTAATCCCGGTATT
 67822 -----+-----+-----+-----+-----+-----+

CTGGGAGGCTGAGGCAGAGTTGCTTGAGCCAGGAGTTCAAGACCAGCCTCGGCAACAAA
 67882 -----+-----+-----+-----+-----+-----+

GTGAGACCCTGTCTCTCCAAAAAATAAAACATTTAGCCAGCTGTGGTGAICTCATGCCTGT
 67942 -----+-----+-----+-----+-----+-----+

AATCTCAGTACTCTGGGAGGCGGCAGTGAATGGCTTGAGCCAGGAGTTCGAGACCAAC
 68002 -----+-----+-----+-----+-----+-----+

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CTCAGCAACAAAGTGAGATCTTGTCTCCAAAAAATCAAAAATTTAGCCAGCTGTGCTG
68062 -----+-----+-----+-----+-----+-----+
GCTCATGCCTGTAATCCCGGTACTCTGGGAGGCTGAGGCAGAATCGTTTGAGCCCAGGAG
68122 -----+-----+-----+-----+-----+-----+
TTCGAGACCAACCTCAGCAACAAAGTGAGATCTTGTCTCCAAAAAATCAAAAATTTA
68182 -----+-----+-----+-----+-----+-----+
      +35/6978      A      SEQ35E1 ----->
GCCAGCTGTGCTGGCTGGTGCCTGTAATCCCGGTACTCTGGGAGGCTGAGGCGGAATTGC
68242 -----+-----+-----+-----+-----+-----+
TTGAGCCCAGGAGTTCAAGACCAGCCTCAGCAACAAAGTGAGATCTTGTCTCCAAAAA
68302 -----+-----+-----+-----+-----+-----+
ATAAAACATTTAGTCAGCTGTGGTGGCTCAAGCCTGTGATCCCAGCATTTTGGGAGGCCG
68362 -----+-----+-----+-----+-----+-----+
AGGCGGGCGGATCACGAGGTCATGAGATCGAGACCATCCTGGCTAACACGGTGAAACCC
68422 -----+-----+-----+-----+-----+-----+
GTCTCTACTAAAAATACAAAGAAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTCCCA
68482 -----+-----+-----+-----+-----+-----+
GCTACTCAGGAGGCTGAGGCAGGAGAATGCCGTGAGCCTGGGAGGCGGACCATGCAGTGA
68542 -----+-----+-----+-----+-----+-----+
GTCAAGATCGCGCCACTGCCCTCCAGCCTGGGCCACAGAGCAAGACTCCGTCTCAAAAAA
68602 -----+-----+-----+-----+-----+-----+
AAAAAAAAAAAACTGCTGCCAACCTGTGTTTGCACCACTGCCCTCCAGCCTGGGCAAC
68662 -----+-----+-----+-----+-----+-----+
AGAGCAAGACTCCGTCTCAAAAAAAAAAAAAATGCTGCCCAAGCTGTGTTTGCACCACTGC
68722 -----+-----+-----+-----+-----+-----+
CCTCCAGCCTGGGCAACAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAATGCTGCC
68782 -----+-----+-----+-----+-----+-----+
CAAGCTGTGTTTGCACCACTGCCCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAA
68842 -----+-----+-----+-----+-----+-----+
AAAAAAAAAAAAATGCTGCCCAAGCTGTGTTTGCACCACTGCCCTCCGGCCTGGGCAACAGA
68902 -----+-----+-----+-----+-----+-----+
GCAAGACTCCGTCTCAAAAAAAAAAAAAATGCTGCCCAAGCTGTGTTTGCACCACTGC
68962 -----+-----+-----+-----+-----+-----+

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CCTCCAGCCTGGGCAACAAAGCAAGCCTCAGCTTTCTGCCATCTCCACAACCAAGAAAGC
 69022 -----+-----+-----+-----+-----+-----+

AATTCACACAGAAATCAGTGCATCGTGCAGTGACCTCTTCAGAAAACCAATGAGTTTTCC
 69082 -----+-----+-----+-----+-----+-----+

ACCTGAGGAAGTGTCTGAGCCCCATTGAGAAAAACACATCCCTGTAAGTGCAGGGCAG
 69142 -----+-----+-----+-----+-----+-----+

ATTTACTCACTGTATGCCTGTTTTAAATAAAGCTTCCAGCCTCTGCATGGGGTCTGTCTGG
 69202 -----+-----+-----+-----+-----+-----+

SEQ5A -----
 AAGCTCCTGTATCTGTCCCACATTCTTGGAAATCACAATGCACCCTTGGGAGGAAGATATG
 69262 -----+-----+-----+-----+-----+-----+

->
 TATTTAAAGGGAGTGGATGTTATGGTGAGAAAATGCTGCCCATCCTTCTAGAAGACAAAA
 69322 -----+-----+-----+-----+-----+-----+

GCCACACAAAATACATCACAAGAACCAGTTTTTTTTTCAGAGAAGAACCTGCACAAAGAACC
 69382 -----+-----+-----+-----+-----+-----+

<----- SEQ35F
 TGCTCCCCCACACCCCCACACACAGGTGAATTAACAGGATGTATGTTTTATCATAAAAG
 69442 -----+-----+-----+-----+-----+-----+

A +5/507
 CACAGGTTTGTTCCTATGCACTCTCTGAGGATTTGGCCATATGCAAAGATGTACAAAAA
 69502 -----+-----+-----+-----+-----+-----+

CCTTCTTTTCCCCAGGGAACCGTAACCCGTCTGAAAAGATGCCCTTCTCAGAAGCGAGT
 69562 -----+-----+-----+-----+-----+-----+

TGAACGATTGTTGGAAAAGATAAAATACGACGTGCACACACACAGTAGAGAAATGTCACC
 69622 -----+-----+-----+-----+-----+-----+

CATGCAAATTATGTGTTTGAATGGAACACATTGAGGAAGCTAAATGGGGTATGACCACAC
 69682 -----+-----+-----+-----+-----+-----+

T +5/772
 ATTTGGGTTGATTTATTTGACGAGTGAAGGGGCAGATGGAAATGAATACTGCTGTTTTTC
 69742 -----+-----+-----+-----+-----+-----+

CTTTGAAGGCCATATATGGGAATACCAAGAGGATTACTTTGGAAGTTTAGCTTCTCCAG
 69802 -----+-----+-----+-----+-----+-----+

CTCACTGCAACCTCCGCCTCCCGAGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAG
 70731 -----+-----+-----+-----+-----+-----+

CTGGGATTACAGGTGCCACCACCATGTCAAGATAATGTTTGTATTTTCAGTAGAGATGG
 70791 -----+-----+-----+-----+-----+-----+

GGTGGTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCGCCT
 70851 -----+-----+-----+-----+-----+-----+

TAGCCTCCCAAAGTGCTGGGATGACAGGCGTGAGCCCCTGCGCCCGGCCTTTGTAACCTT
 70911 -----+-----+-----+-----+-----+-----+

ATTTTAAATTTTTTTTTTTTTTTAAGAAAGACAGAGTCTTGCTCTGTCAACCAGGCTGGA
 70971 -----+-----+-----+-----+-----+-----+

GCACACTGGTGCATCATAGCTCACTGCAGCCTCAAACCTCCTGGGCTCAAGCAATCCTCC
 71031 -----+-----+-----+-----+-----+-----+

CACCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACCCACCACCACCCAGCTAATTTT
 71091 -----+-----+-----+-----+-----+-----+

TTTGATTTTTACTAGAGACGGGATCTTGCTTTGCTGCTGAGGCTGGTCTTGAGCTCCTGA
 71151 -----+-----+-----+-----+-----+-----+

GCTCCAAAGATCCTCTCACCTCCACCTCCCAAAGTGTTAGAATTACAAGCATGAACCACT
 71211 -----+-----+-----+-----+-----+-----+

†
 GCCCGTGGTCTCCAAAAACTGTTACGTGGAGGAATGTTCTAGCTTCTGTTCTCGTCTT
 71271 -----+-----+-----+-----+-----+-----+

+35/375 G ---
 TTCTTTGTTAATTGTACAGTTT**GAGGGTGTGTGTGCGTGTGCGCACGTGTGTGTG**CAG
 71331 -----+-----+-----+-----+-----+-----+

-----> SEQ35G2
 TCTCCTGATTTTATGTTAATTGTTATTACCACCACCTCCATCTCTCATTCTCTTA
 71391 -----+-----+-----+-----+-----+-----+

CCCTCACTGTGTAAGATACATGTTGTTTTTAAATTTTATGATTTTATTTATTTATTT
 71451 -----+-----+-----+-----+-----+-----+

<----- SEQ35H1
 T G +35/520 CA, TG, CG, TA
 GTATTT**CTGAGACAGAGTCTCACTCTGTTGCCAGGCTAGTGGCATGATCTCAGCTCACA**
 71511 -----+-----+-----+-----+-----+-----+

71571 GCAACCTTTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGA
 -----+-----+-----+-----+-----+-----+-----+

71631 TTACAGGCACACACCACCACACCCGGCTAGTTTTGTTTTGAGACGGAGTCTCGCTCTGTT
 -----+-----+-----+-----+-----+-----+-----+

71691 GCAGGCTGCAGTGCAGTGGCGTGATCCTGGCTCACTGCAACCTCTGCCTCCTGGATTCAA
 -----+-----+-----+-----+-----+-----+-----+

71751 GCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCACCGCCACACCT
 -----+-----+-----+-----+-----+-----+-----+

T +35/801

71811 GGCTAATTTTTTATTGGTAGTAGAGACGGGGTTTCTCCATGTTGACCAGACTGGTCTTGA
 -----+-----+-----+-----+-----+-----+-----+

71871 ACTCCCAACCTCGGGTGATCCACCCACCTGGGCCTCCCAAAGTGCTGGGATGACAGGCGA
 -----+-----+-----+-----+-----+-----+-----+

A +35/939

71931 GGGCCACCGCGTCCAGCCTTCTTCTTCTTCTTCTTTTTTTTTTTTTTTAAGATGGAGTTTC
 -----+-----+-----+-----+-----+-----+-----+

71991 ACTCTGTTGCCAGGCTGGAGTGCAGTGGTGCAATCTCGGCTCCCTGCAACCTCCACCTC
 -----+-----+-----+-----+-----+-----+-----+

72051 CCAGGTTCAAGAAATTCTTTTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGCCCGC
 -----+-----+-----+-----+-----+-----+-----+

A +35/151

72111 CACCACCCACCTAATGTTTGTATTTTTTTGGTAGAGACGGGGCTTACCACATTGGCC
 -----+-----+-----+-----+-----+-----+-----+

72171 AGGCTGGTCTTGAACCTGACTTCAGATGATCCTCCTGCCTCAGCCTCCAGAGTGTG
 -----+-----+-----+-----+-----+-----+-----+

72231 GGATTACAGGCGTGAGCCACGGTGCCCGGCCAGACGTCATGTCTTAGGAAATCAGAAAGT
 -----+-----+-----+-----+-----+-----+-----+

A +35/329

72291 GGGTAGTTTCCGCACTCTGAGGAGAAAAAGAGACGTCCGGCGAAGAGAAAGGAGAGTGAA
 -----+-----+-----+-----+-----+-----+-----+

72351 AGGATGTCTCCTCTTGTCTGTAGCCTGTTCTCAATCGTGAGTGAGCCAATTGCCAGAAAC
 -----+-----+-----+-----+-----+-----+-----+

72411 TGAGGGTGCTTCATTTGGCCAGGCAAGCTTCTCAACAGAATGTCTAAGTACTTGTTAATG
 -----+-----+-----+-----+-----+-----+-----+

72471 CTGAGAAGCTCTCCAAGCTACTGCACTCCAGCCTGGGTGACAGAGCACGACCTTGTCTGA
 -----+-----+-----+-----+-----+-----+
 72531 AAACAAATTAATTAATCAATTAATTAATATAATGAAATCATACTGAACTCAGGAGACCATT
 -----+-----+-----+-----+-----+-----+
 72591 GGGGTGGGCAGGGCTGGGGTTGGAAAGGAACATAAAATATGGTGCAATGGACTTTGCTCC
 -----+-----+-----+-----+-----+-----+
 72651 AGTCTCCCTCCCATCTCTTCTCGCCAAGAGTCTCTGGAGGGAGCATGGGGAAGATGCTT
 -----+-----+-----+-----+-----+-----+
 <----- SEQ35H

SEQ-7:

U82668

77041 GAGCCCATGCTCACAGCCTGTCTTAAGGGAGACCTTCTCCAGATCCTGGGTGGTGCCGTT
 -----+-----+-----+-----+-----+-----+
 -> SEQ7A
 77101 TCATGGACAACAAATTCATTCTCAAAAAGCGTAGCCCCAGTGGAAGACCTTGGGTCTTTC
 -----+-----+-----+-----+-----+-----+
 77161 CACTCGGAGTGTGTCAGTTCATCACCATAACCGTTTGTGAGGTGTGTTCAAAACATCTA
 -----+-----+-----+-----+-----+-----+
 77221 TAGCCAAATTCACAGGAGGAATGGGATGAGGACTCTAAGCTTCTGGACTTGATGTAGAA
 -----+-----+-----+-----+-----+-----+
 77281 ACCGGGTCTTTGCAGATGTCTTTAAGGGAAGGATCTGAAATGAGGTCATCCTGGATTAGG
 -----+-----+-----+-----+-----+-----+
 77341 GTGGGTCTTAAATCCAATAACAGGTGTCTTGTAAAGGGACAGAAGAGGACCATAAATCTA
 -----+-----+-----+-----+-----+-----+
 77401 ATGACTACGGTCTCCTAAGAGATGGAAGAGGAGACATAGACACAGGCACAGACACAGAG
 -----+-----+-----+-----+-----+-----+
 77461 GAGAAGGCCACGTGGAGACGGAGGCAGCGACTGGAGTGATCCGGCCACAAGCCCAGGGAC
 -----+-----+-----+-----+-----+-----+
 77521 GCCTGGAGCCCCCAGGAGCTGGGAGAGGCAGGAAGGATCCTCCCCTAGAGCCTCCAGAGG
 -----+-----+-----+-----+-----+-----+

77581 GAACTTCTTATGGTTGAAGTGGATTGAACTATGGTACCCCCAAAAATATGTTTCATATTC
 -----+-----+-----+-----+-----+-----+-----+

77641 TAACCCAAGAACCTGTGAAAGGAGGTAGAGACTGGAGTGATGGGGCCACAAGCCCAGGGA
 -----+-----+-----+-----+-----+-----+-----+

77701 TACCTGGAGCACCCAGAAGCTGGGAGAGGCAGGAAGGATCCTCCCCTAGAGCCTCCAGAA
 -----+-----+-----+-----+-----+-----+-----+

-----> SEQ7C
 77761 GGAACGGGATACAACCTGAAGTGAAGTGAACCGTGGCCCCCTCAAAGACCTGTCCATGTA
 -----+-----+-----+-----+-----+-----+-----+

77821 TTGATCATCTGGAATCTGTGAATGGGACATTATTTGGAAATACGGTCTCTGCAGATGTGA
 -----+-----+-----+-----+-----+-----+-----+

77881 TTAAGTGGGAAGATCTGGAGATGAGATCATCCTAGATTAGGGTGGACCATAAATCTAATGA
 -----+-----+-----+-----+-----+-----+-----+

77941 CAGGTGTCCTTCTAAGAGACAGAAGAGGAGACACAGACACAGAGGAGGAGGCCACGTGGA
 -----+-----+-----+-----+-----+-----+-----+

78001 GACAGAGGCAGAGACTGGAGTGATGCAGCCACAAGCCCAGGGATGCC TGGAGCCCCCAGG
 -----+-----+-----+-----+-----+-----+-----+

78061 AGCTGGGAGAGGCAGGAAGGATCCTCCCTTAGAGTCTCCAGAGGGAGCACAGCCCTGAGA
 -----+-----+-----+-----+-----+-----+-----+

78121 CTCCTTGACCTCAGACTCCTGGTCTCCAGGACTGGGAGAGGCAGGAAGGACCCTCCCTTA
 -----+-----+-----+-----+-----+-----+-----+

78181 GAGCCTCTGGAGGGAGCATGGCCCTGAGACACGTTGACCTCAGACTCCTGGTCTCTATGG
 -----+-----+-----+-----+-----+-----+-----+

78241 CTGGGAGAGGCAGGAAGTCTCCTCCTCAAGAGCCTCTGGAGGGAGCATGGCCCTGAGACT
 -----+-----+-----+-----+-----+-----+-----+
 GACCCTCTCCGTCCTCAGAGGAGGAGTTCTCGGAGACCTCCCTCGTACCGGGACTCTGA

78301 CCTTGACCTCAGACTCCTGGTCTCCAGGCCTGGGAGAGGCAGGAAGGACCCTCCCTTAGA
 -----+-----+-----+-----+-----+-----+-----+

78361 GCCTCTGGAGGGAACATGGTCCTGAGACTCCTTGACCTCAGACTCCTGGTCTCCAGGACT
 -----+-----+-----+-----+-----+-----+-----+

T +7/1400
 78421 TGACGGGGATGAATTCCTGCGGCATGCATCGTCATTCTGGTCTTTGTTACGGCTGACT
 -----+-----+-----+-----+-----+-----+-----+

78481 CAGGAATCTAAGAAACTGACCTGCGGGGTTTTGCCCATCAGGATGGTGGCTTCTCCGGCT
-----+-----+-----+-----+-----+-----+-----+

78541 GTGGATTTGTTGCTTTTCCATCTTCTCTGCGGCTGACACTCTTACGGGGAGTAATGGTGC
-----+-----+-----+-----+-----+-----+-----+

T +7/1593

78601 AGAGAATTTTCGGTTGCCTCCCAGAGCTGCAGCCGGAAGACGCAAGGACCAACGAAAACAT
-----+-----+-----+-----+-----+-----+-----+

78661 TTGCATCGTGGCTCTCTGTGAGGAAGAGTCCTGCTGTGAAAGCATTTTTATTCCGAAAGA
-----+-----+-----+-----+-----+-----+-----+

78721 GGATCATCTTTGGGAGCAGAACCATGGAAAAGTCTCTTTTCGGCAGCCCACGGAATGATGG
-----+-----+-----+-----+-----+-----+-----+

<----- SEQ7D

78781 GCCGGCCACATTTTGGATACATCTCATGCTTCTTACTGTTTTCAAATGGTTTTGGCTTGA
-----+-----+-----+-----+-----+-----+-----+

78841 ATGGAATCCAAGCCATTTTTTTTTTCTCTTTCCCAAGTACTTTTTGTTCTTGAGTCT
-----+-----+-----+-----+-----+-----+-----+

78901 TGCAATCCTATGAATCCAAGGGAAGCTGAATGTCTATCTTTTTGATACGTGGACACTGT
-----+-----+-----+-----+-----+-----+-----+

78961 CATCTGCAAACAAAACCGTAGACGTCTTTGGGGGGTTCGTGAACTTGGCAGTGAAGTTC
-----+-----+-----+-----+-----+-----+-----+

A +7/1985

79021 GAAGGTCTCCAGTGCTTCTCACATCCGAAGTCAGAGCCCACATTTCTCCGTCAGTTTGTA
-----+-----+-----+-----+-----+-----+-----+

79081 ACCCTGGCAAAGAAGGTCTTCGGCTTGCTTGTTTTCTGAAAAACAGGAAGTTTTATTT
-----+-----+-----+-----+-----+-----+-----+

79141 TGCCAAGAATGAATGGAATGGGAAGCCAAAGCGTTTGATATGCACAAGGGAAAATGCAGG
-----+-----+-----+-----+-----+-----+-----+

<----- SEQ7B

