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Analysis of a Tissue-Specific Enhancer: ARF6 Regulates Adipogenic Gene Expression

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Vol. 12, no. 3, p. 1205, legend to Fig. 5, lines 9 and 10: The sequence of the X oligonucleotide should read "CCATGCGACAAAGGCAGAAATGCACATTTCACCCAGAGAGAAGGGATTGATGTCAG."

Mechanism and Consequences of the Duplication of the Human C4/P450c21/Gene X Locus

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Vol. 12, no. 5, p. 2128, Fig. 3A: Figure 3A was erroneously printed backwards and should appear as shown on the following page; the legend should appear as shown below.

FIG. 3. Structure of the XA gene. (A) Nucleotide sequence of the XA gene, extending from the 5′ end of the C4B gene to the 3′ end of the P450c21A gene. The sequence is in the sense orientation with respect to XA, and thus the translated amino acid sequences for C4B and P450c21A arise from the opposite strand of DNA as represented by the inverted amino acid letter code for these two genes. The four boxed nucleotides at 1982 to 1985 are the junctional duplication boundary (II in Fig. 1); note that this seuqence is antisense to that presented in Fig. 2. The most commonly used XA cap sites are denoted with dots over the corresponding bases; the predominant cap site for the XA gene is marked by the arrow preceding nucleotide 2232. The single-letter amino acids code is aligned below the first nucleotide of each codon. The arrowhead following nucleotide 4267 denotes the site of the 121-bp deletion. XA introns are denoted by lowercase letters. The polyadenylation signal of the P450c21A pseudogene is lightly underlined at bases 6363 to 6368. The polyadenylation signal for XA is boldly underlined in the last line of sequence; the space 21 bases downstream indicates the poly(A) addition site for the XA gene.

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A
   1: GGGTCTGGTTACCTGGAGACTGAGGAGTGCGAAGTCTCTTTCTGAGCTAAGGGTGAAGTCCACCTTTGGGGAGCAGGGGACATTATTACGAGATGGTTTCTCAGGAACA
                       Q  L  S  L  L  A  F  D  R  E  S  S  L  T  F  D  V  K  P  S  P  C  P  V  N  N  R  S  P  N  R  L  F
 111: CTGATCCTTTCACTACCTGTCCTCGGGGCACATCCTGGAGCTGCACCCCCACCGATAGGGGGACCCCCAGATGAACCACAGAAGGAGAGAACAAGAGCAACCTGGGGAGA
       V  S  G  K  V  V  Q  G  R  P  V  D  Q  L  Q  V  G  V  S  L  P  V  G  L  H  V  V  S  P  S  F  L  L  L
 221: ACAGACAGGATCAGCAGTCAGACTTCGCTCTGACACCTCCACCCCTGCTCTCCCTCACTCCTGAATCGGGTCCCGATGCCAGCCCTGCGCCAATCCAAGCACCCAGCATC
 331: CCGCCTCCAGGACCTGGGCTTCTGCAGAGATAAGGTGAAGAAGCTGGATGCCCAGATCAGCCCCCAGAGCAGCCTCATGGCTGGAGGATCCAAGAGAGGTTAGATCCGTC
                       R  P  K  Q  L  S  L  T  F  F  S  S  A  W  I  L  G  W  L  I  R  M                      C4B
 441: TGTCTGTCTGCTACCTTCTGGCCAAGCTAGGCCTCGGGGCAGAGTTGACTCTGGACCTTGCTCCTCCCCCAGCCCAGCTAAGCTGGGAAACCACGTGACAGCCAAGAAGT
 551: GCAACTGGCCTCAGGCCCAGAGTTGTGGGGGCACCCCGGACACCTGGGTGTCCATGGGAAACTCTGAATCTTGGCCCAGAAATAACCCTGTCCTTCCCCGTTAACTCCTC
 661: TCATTCCAGTGCCTGAGCACCTCCCCCTACCAGGTATATCTGTATCAGGGTATAGGTGCACACAAGCTCATGTATACCTGGGCGTACAAGGGCCCAACATGGCCCACGAG
 771: TACAGGATATTTAAAGGCCCTCACAAAACAATGACAGGCTTCTAAGACACTTGTCTCTTACTTTCATTCCAACACAAATTGAACTATACTAGGCTTTTGCTTTTTTAGGC
 881: CCTAACAGAAATTCCGTGGTTTAGGAGATTAGGTACACCCTCACCACTCCACAGGGAGAATGGCCTGAACGTCAGAGTGAACCCCTGACCCCTTTCCTCTCTGAATGAGG
 991: CAAAGCTCAGACTTCACCTCTACCCCTAAACAAGGCACCCAAACACACGTCACAGTAAATAAAGGACATCCAGAAAATATCACAGGCAGAGGTACTTTATTTTGGCAATT
1101: TTAACATGACACGTAGAGAAAAGAACCCTGCCCTCCTTCACCAGCCTCCCCAGAAATCCCACCTTCCTATTTCAAGACAGAGTAATAACAGCACCATTTTACACGAAAGG
1211: GAACAGCCACAGCCTTGGCACCATTTCTGGTTCCACTTTCCATGGAAGGGCAGAGAAGCATTGCTCAAACCCCACCACTGGGTCAGAAACCAGGCAAACAGCAGCAGTCA
1321: CATCTGACCTTTTGCACACACGAGAGCCCGACACTCATCCTGGCTCCCAAGCCTTCCCAAGGTGACCCTGTCTCAGCCACCATCATGCAGCTCTTCTAGTCCCCTCCCGG
1431: CCCACTCTGAGGAGCTGAGCAATGATGAGCAGAATCTTCATGTCTCTGGCAGGCGGAGGAGGGTTCCTGAAGTGGTAGAGATGCTGTGCAGGAGAAAGACAAGGCTGGAG
1541: CCAGACGCCTAGGCTCAAGCTGTGAGGAGAACTTAGAACTTGGGAAGGGGTGCTCCCGGGTTCCAGAGAAGAATGAGAGCCACTGGCCTTCACTAGGAAACTAAGCATGA
1651: GCTGGGAGGAAATCCCACTTTGGGTCATTGCTCCATAATCTGCCAGAGGCCAGGGAAAGACTCACCAGTCCACTAGCTGGGCCCCAATGAGGTCGTGCACATGGTAGGTG
1761: AGGCCAAGCCGCACCACGACAGGCACCCGCCGGCCCAGGAGCTCTGATAGGAGCAGCTCCCGGTACTTTGCCTTCCGGACCATGCCAAGGACAGCCTGGCGCCCTAGAGG
1871: AGAAGTGGCACAGGAGAGGGGAAAGGTGAATAAGGCCTAGAGGCCTGAGGAGCCACCAAAAGGTGAGGGGCTGCAGGCTTGAGCTGCAGATGGGATACCTTTAACAAAGT
1981: ACTTGTGCATTTGGTCTGAAGACAAAGATGACTGCAGGAGTGGGCAGGCCGGAGTGGGGGTGACCTGGCCTGTGCCAGGAAGGAGGAGGAGTCTGCAGCCCTGTGCGGTT
2091: CAACATCCATCAAGGAGTCCAGAGCAGGAGCCAGGCCAGGCGGAGGAAAGGCCCTGGGAGGGGCTCTCTAATCTCCCAGCCCCGACTCTGCCCCGTCACTGCCGCTGC

2201: TCCTCATTACTCGCTGGGGCTGCTGTCGCCT  CCCCGAAGGGTGGCCTTGTCCAGATAGTGGCAAACCTCCCTGCCGTGGATGAGTCAGGAGCATTTCTTAAGAGGAA   XA
2309: CATCACTGGAAAACAAAATGAGCGGGGACACAGAAACCAACAGCAGTGGCTGCATTTGTGGTACAGGCTCCTCTTCCAGAGCTCGCTGATGCCCACCTCAGACAGGCCTG
2419: ACCACGGCACGGCTGGTGGGATTTGCCAGTCACCTCAACCAGCCAGTTCCACCCTCAGCTTCTCTCAGAAGGGAGCACCACACTCCTCAAGCTCAGTGAATGTATCCCGG
2529: CATGGGTGGGGCCAGAGCCTGTGATATCTCGAGGTGGGCTCGGCAGGACACCGGGGTGTGGAAGGGGGAAGCGAGCACCTGACTCAGACAGCGCGGAGCTCGCAGGAGT
2639: CACGAGGCCACAGCGACTTCATTGTCTGACTGGGCCTGGACCTATAAACTTCCCACCTCAGCCTTGGGCCAAGCCTGGAAGATAAAAATGGAGCACCCCATGGCGCCCCT
   1:                                                                                           L  E  D  K  N  G  A  P  H  G  A  P
2749: CACTCAGATTCTCCCCTGGGCTTCTCCCACGCAGCCCCAGAAGAGGACACACCAGCCCCAGAGTTAGCCCCAGAGGCCCCTGAGCCTCCTGAAGAGCCCCGCCTAGGAGT
  13: H  S  D  S  P  L  G  F  S  H  A  A  P  E  E  D  T  P  A  P  E  L  A  P  E  A  P  E  P  P  E  E  P  R  L  G  V
2859: GCTGACCGTGACCGACACAACCCCAGACTCCATGCGCCTCTCGTGGAGCGTGGCCCAGGGCCCCTTTGATTCCTTCGTGGTCCAGTATGAGGACACGAACGGGCAGCCCC
  50:  L  T  V  T  D  T  T  P  D  S  M  R  L  S  W  S  V  A  Q  G  P  F  D  S  F  V  V  Q  Y  E  D  T  N  G  Q  P  Q
2969: AGGCCTTGCTCGTGGACGGCGACCAGAGCAAGATCCTCATCTCAGGCCTGGAGCCCAGCACCCCCTACAGGTTCCTCCTCTATGGCCTCCATGAAGGGAAGCGCCTGGGG
  87:  A  L  L  V  D  G  D  Q  S  K  I  L  I  S  G  L  E  P  S  T  P  Y  R  F  L  L  Y  G  L  H  E  G  K  R  L  G
3079: CCCCTCTCAGCTGAGGGCACCACAG  gtaccaccaggcgtctccggcctctagcctaggactcagaagggagaaacgggggctcagaaggggtggtcgcagggaaagag
 123: P  L  S  A  E  G  T  T  G
3187: cgtgaggcggtaccagggagagaggatggatgggctggatgcgagtggcctttagctctgccccacaggacccccctgtggctgcaagtccctggttacagatagagaaa
3297: cggggggcagggagggggtggaaggacgtgctctgggtcaccaagctggtgtgcttctgtctccaatcccttctcccccacccactccgtgcag  GGCTGGCTCCTGC
 132:                                                                                                    L  A  P  A
3405: TGGTCAGACCTCAGAGGAGTCAAGGCCCCGCCTGTCCCAGCTGTCTGTGACTGACGTGACCACCAGTTCACTGAGGCTCAACTGGGAGGCCCCACCGGGGGCCTTCGACT
 136:  G  Q  T  S  E  E  S  R  P  R  L  S  Q  L  S  V  T  D  V  T  T  S  S  L  R  L  N  W  E  A  P  P  G  A  F  D  S
3515: CCTTCCTGCTCCGCTTTGGGGTTCCATCACCAAGCACTCTGGAGCCGCATCCGCGTCCACTGCTGCAGCGCGAGCTGATGGTGCCGGGGACGCGGCACTCGGCCGTGCTC
 173:  F  L  L  R  F  G  V  P  S  P  S  T  L  E  P  H  P  R  P  L  L  Q  R  E  L  M  V  P  G  T  R  H  S  A  V  L
3625: CGGGACCTGCGTTCCGGGACTCTGTACAGCCTGACACTGTATGGGCTGCGAGGACCCCACAAGGCCGACAGCATCCAGGGAACCGCCCGCACCCTCAGCCCAG  gtaag
 209: R  D  L  R  S  G  T  L  Y  S  L  T  L  Y  G  L  R  G  P  H  K  A  D  S  I  Q  G  T  A  R  T  L  S  P  V
3733: gacccacacacactctgccccaaagtgggggtctttgtacttcacgggggggacctagtgcctcagccagcggtgggggtgggcgagttggtggtgggcctggaggaatc
3843: tgcagagcgacttccattcctggggactagaggaaaaggggtggtgagcctgtgctggagcagaggcgaggggggggactcgcagggaggagcctccctgcccctgcctgc
3953: gtcattgttccttgacccctctgcag  TTCTGGAGAGCCCCCGTGACCTCCAATTCAGTGAAATCAGGGAGACCTCAGCCAAGGTCAACTGGATGCCCCCACCATCCCG
 244:                              L  E  S  P  R  D  L  Q  F  S  E  I  R  E  T  S  A  K  V  N  W  M  P  P  P  S  R
4061: GGCGGACAGCTTCAAAGTCTCCTACCAGCTGGCGGACGGAG  gtggtgcctttgccatgtgctcatcgcctcgcatttcctctccccctgcactctgcccaccctcca
 271:  A  D  S  F  K  V  S  Y  Q  L  A  D  G  G
4169: gctgccctggggttccctgggtaaccctcgatccccaacgttttcag  GGGAGCCTCAGAGTGTGCAGGTGGACGGCCGGGCCCGGACCCAGAAACTCCAG▼gtggga
 285:                                                   E  P  Q  S  V  Q  V  D  G  R  A  R  T  Q  K  L  Q
4275: gtcaagaaaatggcatgggtgggagttgagagagaacgaggagggtgaaagggaggtggtggaggctccgattgcggacgggaggccagtggagtctggggaggcacgga
4385: gtagagagagccgcggggacccttctgagcccctccccttcccccag  TTCCTGACGGTCCCACACAGTTGCGTGCACTGAACTTGACCGAGGGATTCGCCGTGCTGCA
 302:                                                   F  L  T  V  P  H  S  C  V  H  *
4493: CTGGAAGCCCCCCCAGAATCCTGTGGACACCTATGACGTCCAGGTCACAGCCCCTGGGG  gtgagcaggcctgaggcctctggaggggacttgttcagggtggggattg
4601: caggggggaggctggactctggccgaggatggagggggcaggccttgatgcccctctctacactcccag  CCCCGCCTCTGCAGGCGGAGACCCCAGGCAGCGCGGTGG
4709: ACTACCCCCTGCATGACCTTGTCCTCCACACCAACTACACCGCCACAGTGCGTGGCCTGCGGGGCCCCAACCTCACTTCCCCAGCCAGCATCACCTTCACCACAG  gta
4817: gggtctgtggggtgtgtgggacagggagaggaggtagagggagccaggttgggcctcatccccatctcctcttcctgctttccctcctag  GGCTAGAGGCCCCTCGGG
4925: ACTTGGAGGCCAAGGAAGTGACCCCCCGCACCGCCCTGCTCACTTGGACTGAGCCCCCAGTCCGGCCCGCAGGCTACCTGCTCAGCTTCCACACCCCTGGTGGACAGACC
5035: CAG  gtgccccggccccactgacccaactcccctccctgggtgattccaggaggtgctgctctggccctcccggagggtctccacctccctctcccctgacccccccctt
5143: gtctgtcccacag  GAGATCCTGCTCCCAGGAGGGATCACATCTCACCAGCTCCTTGGCCTCTTTCCCTCCACCTCCTACAATGCACGGCTCCAGGCCATGTGGGGCCA
5251: GAGCCTCCTGCCGCCCGTGTCCACCTCTTTCACCACGG  gtacctgacgcacgggcccggggccgggggctgggtgggcagccagggcctaaggcttggaaaaggactg
5359: gcccctgctctcctctcccag  GTGGGCTGCGGATCCCCTTCCCCAGGGACTGCGGGGAGGAGATGCAGAACGGAGCCGGTGCCTCCAGGACCAGCACCATCTTCCTCA
5467: ACGGCAACCGCGAGCGGCCCCTGAACGTGTTTTGCGACATGGAGACTGATGGGGGCGGCTGGCTG  gtgggtggcattgggaagcccaggggtctgtgcagggcaaggg
5575: gctgttggccccggagccagaggctgatggtgcccccacttgcttcccag  GTGTTCCAGCGCCACATGGATGGACAGACAGACTTCTGGAGGGACTGGGAGGACTATG
5683: CCCATGGTTTTGGGAACATCTCTGGAGAGTTCTGGCTGG  gtcagtgcctcacagggactggggaagtacggatggggatgggggccctgtggacaccaggaccctgat
5791: gagggcacgtatcccacccccag  GCAATGAGGCCCTGCACAGCCTGACACAGGCAGGTGACTACTCCATGCGCGTGGACCTGCGGGCTGGGGACGAGGCTGTGTTCGC
5899: CCAGTACGACTCCTTCCACGTAGACTCGGCTGCGGAGTACTACCGCCTCCACTTGGAGGGCTACCACGGCACCGCAG  gtaagcagaggctgtgaggctgggagggtga
6007: ggctgggaggggaggcccctcatggctccttcctccaccctgcccag  GGGACTCCATGAGCTACCACAGCGGCAGTGTCTTCTCTGCCCGTGATCGGAACCCCAACAG
6115: CTTGCTCATCTCCTGCACTGTCTCCTACCGAGGGGCCTGGTGGTACAGGAACTGCCACTACGCCAACCTCAACGGGCTCTACGGAGCACAGTGGACCATCAG  gtgag
6223: gggtggggaggcggctcagagctggggtggctggggctcggcctgcctaggtttcagccccacagtgtaacaggcaagggactgagtggctgggtgaaatggaacaatca
6333: tgccagcctcgcagagggagctggagttgatttattggctggaaaggaccagctcaggattaagcctcaatcctctgcggcagagggtcaggaagggagctctgcgggga
6443: ggttggttgagtgctgggagccacctccttaaggggaatgggaggagcagatgggacatccggctttgactctctcttgacaacccctttcccag  GGAGTGAGCTGGT
6551: ACCACTGGAAGGCTTCGAGTTCTCGGTGCCCTTCACGGAAATGAAGCTGAGACCAAGAAACTTTCGCTCCCCAGCGGGGGAGGCTGAGCTGCTGCCCACCTCTCTCGC
6661: ACCCCAGTATGACTGCCGAGCACTGAGGGGTCGCCCCGAGAGAAGAGCCAGGGTCCTTCACCACCCAGCCGCTGGAGGAAGCCTTCTCTGCCAGCGATCTCGCAGCACTG  P450
6771: TGTTTACAGGGGGGAGGGGAGGGGTTCGTACGGGAGCAATAAAGGAGAAACTGAGGTACCCGGC TGGCATCGGTCCTGCCCCATCACTGGTTCTGGCCCGGG        c21A
                                                                                                   *  Q  N  Q  G  P
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