ERRATUM

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Mutant Insulin Syndromes

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In this article we inadvertently published a wrong Figure 5. The correct Figure 5 is as follows:

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                                                                                                HYPERVARIABLE REGION
CCCCTCCCTCACTCCCACTCTCCCACCCCCACCACCTTGGCCCATCCATGGCGGCATCTTGGGCCATCCGGGACTGGGG (ACAGGGGTCCTGGGGACAGGGGTCCGGGGACAGGGTCCTGGG   -807

GACAGGGGTGTGGGGACAGGGGTCTGGGGACAGGGGTGTGGGGACAGGGGTGTGGGGACAGGGGTCTGGGGACAGGGGTGTGGGGACAGGGGTCCGGGGACAGGGGTGTGGGGACAGGGGT   -686

CTGGGGACAGGGGTGTGGGGACAGGGGTGTGGGGACAGGGGTCTGGGGACAGGGGTGTGGGGACAGGGGTCCTGGGGACAGGGGTGTGGGGACAGGGGTGTGGGGACAGGGGTGTGGGGAC   -565

AGGGGTGTGGGGACAGGGGTCCTGGGGATAGGGGTGTGGGGACAGGGGTGTGGGGACAGGGGTCCCGGGGACAGGGGTGTGGGGACAGGGGTGTGGGGACAGGGGTCCTGGGGACAGGGGT   -444

CTGAGGACAGGGGTGTGGGCACAGGGGTCCTGGGGACAGGGGTCCTGGGGACAGGGGTCCTGGGGACAGGGGTCTGGGG) ACAGCAGCGCAAAGAGCCCCGCCCTGCAGCCTCCAGCTCTCC  -323

TGGTCTAATGTGGAAAGTGGCCCAGGTGAGGGCTTTGCTCTCCTGGAGACATTTGCCCCCAGCTGTGAGCAGGGACAGGTCTGGCCACCGGGCCCCTGGTTAAGACTCTAATGACCCGCTG   -202

GTCCTGAGGAAGAGGTGCTGACGACCAAGGAGATCTTCCCACAGACCCAGCACCAGGGAAATGGTCCGGAAATTGCAGCCTCAGCCCCCAGCCATCTGCCGACCCCCCCACCCCAGGCCCT    -81

                                                                                                EXON 1
AATGGGCCAGGCGGCAGGGGTTGACAGGTAGGGGAGATGGGCTCTGAGACTATAAAGCCAGCGGGGGCCCAGCAGCCCTC AGCCCTCCAGGACAGGCTGCATCAGAAGAGGCCATCAAGCA    41

  INTRON A
G GTCTGTTCCAAGGGCCTTTGCGTCAGGTGGGCTCAGGGTTCCAGGGTGGCTGGACCCCAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGGCTCGTGAAGCATGTGGGGGTGAGCCC   162

                                                                                  -24             -20
                                                                EXON 2            Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu
AGGGGCCCCAAGGCAGGGCACCTGGCCTTCAGCCTGCCTCAGCCCTGCCTGTCTCCCAG ATCACTGTCCTTCTGCC ATG GCC CTG TGG ATG CGC CTC CTG CCC CTG CTG    271

            -10                                     1                                                   10
Ala Leu Leu Ala Leu Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr Leu
GCG CTG CTG GCC CTC TGG GGA CCT GAC CCA GCC GCA GCC TTT GTG AAC CAA CAC CTG TGC GGC TCA CAC CTG GTG GAA GCT CTC TAC CTA    361
                                                                                         G
                                                                                         Asp
          20                                        30
Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln V  INTRON B
GTG TGC GGG GAA CGA GGC TTC TTC TAC ACA CCC AAG ACC CGC CGG GAG GCA GAG GAC CTG CAG G  GTGAGCCAACCGCCCATTGCTGCCCCTGGCCGCCCC   461
                         C   G
                        Ser Leu

CAGCCACCCCCTGCTCCTGGCGCTCCCACCCAGCATGGGCAGAAGGGGGCAGGAGGCTGCCACCCAGCAGGGGGTCAGGTGCACTTTTTTAAAAAGAAGTTCTCTTGGTCACGTCCTAAAA    582

GTGACCAGCTCCCTGTGGCCCAGTCAGAATCTCAGCCTGAGGACGGTGTTGGCTTCGGCAGCCCCGAGATACATCAGAGGGTGGGCACGCTCCTCCCTCCACTCGCCCCTCAAACAAATGC    703

CCCGCAGCCCATTTCTCCACCCTCATTTGATGACCGCAGATTCAAGTGTTTTGTTAAGTAAAGTCCTGGGTGACCTGGGGTCACAGGGTGCCCCACGCTGCCTGCCTCTGGGCGAACACCC    824

CATCACGCCCGGAGGAGGGCGTGGCTGCCTGCCTGAGTGGGCCAGACCCCTGTCGCCAGCCTCACGGCAGCTCCATAGTCAGGAGATGGGGAAGATGCTGGGGACAGGCCCTGGGGAGAAG    945

TACTGGGATCACCTGTTCAGGCTCCCACTGTGACGCTGCCCCGGGGCGGGGGAAGGAGGTGGGACATGTGGGCGTTGGGGCCTGTAGGTCCACACCCAGTGTGGGTGACCCTCCCTCTAAC   1,066

CTGGGTCCAGCCCGGCTGGAGATGGGTGGGAGTGCGACCTAGGGCTGGCGGGCAGGCGGGCACTGTGTCTCCCTGACTGTGTCCTCCTGTGTCCCTCTGCCTCGCCGCTGTTCCGGAACCT   1,187

                                EXON 3                                  50                                          60
                                al Gly Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu
GCTCTGCGCGGCACGTCCTGGCAG  TG GGG CAG GTG GAG CTG GGC GGG GGC CCT GGT GCA GGC AGC CTG CAG CCC TTG GCC CTG GAG GGG TCC CTG   1,282

                                 70                                     80                      86
Gln Lys Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn AM
CAG AAG CGT GGC ATT GTG GAA CAA TGC TGT ACC AGC ATC TGC TCC CTC TAC CAG CTG GAG AAC TAC TGC AAC TAG ACGCAGCCTGCAGGCAGCCCC   1,378
         A          T
        His        Leu

                                POLYADENYLATION SITE
ACACCCGCCGCCTCCTGCACCGAGAGAGATGGAATAAAGCCCTTGAACCAGC CCTGCTGTGCCGTCTGTGTGTCTTGGGGGCCCTGGGCCAAGCCCCACTTCCCGGCACTGTTGTGAGCCC  1,499
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Fig. 5 The sequence of the insulin gene, including the hypervariable region, the enhancer/promotor region, the exons encoding the insulin B-chain, C-peptide, the A chain, and the two introns which are present in the primary transcript of the insulin gene, but must be removed before the insulin messenger RNA can be translated. Also shown in boxes are the substitutions in the insulin gene that lead to aminoacid replacements.

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