Errata

Zinman B, Tildesley H, Chiasson J-L, Tsui E, Strack T: Insulin lispro in CSII: results of a double-blind crossover study. *Diabetes* 46:440–443

The authors would like to make two corrections. On page 441, column 1, in the second sentence under the subheading Materials, the pH of the U-100 insulin lispro formulation was given incorrectly. The corrected text reads: "The pH of this formulation was ~7.4."

On page 443, column 1, the corrected text of the sentence beginning on line 4 reads: "On a cautionary note, it is important to keep in mind that the interruption of CSII [continuous subcutaneous insulin injection] insulin delivery with insulin lispro might result in more rapid onset and/or greater degree of hyperglycemia compared with human regular insulin (27)."

Kaisaki PJ, Menzel S, Lindner T, Oda N, Rjasanowski I, Sahm J, Meincke G, Schulze J, Schmechel H, Petzold C, Ledermann HM, Sachse G, Boriraj VV, Menzel R, Kerner W, Turner RC, Yamagata K, Bell GI: Mutations in the hepatocyte nuclear factor-1α gene in MODY and early-onset NIDDM: evidence for a mutational hotspot in exon 4. *Diabetes* 46:528–535, 1997

The authors have found an error in Fig. 1, page 530. The polymorphism Ala (GCC) to Val (GTC) in the line labeled 991 was incorrectly placed. The true location is at nucleotide position 1007 (in codon 98), not at nucleotide position 1019 as shown in the original figure. The corrected line of the figure is shown below.

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                    Val
    SerProGluGluAlaAlaHisGlnLysAlaValValGluThrLeuLeuGl(n)109
991 AGCCCTGAGGAGGCGGCCCACCAGAAAGCCGTGGTGGAGACCCTTCTGCA gtaaggagccctgccccgtccccgctcccaggagagccta
                     T
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FIG. 1. Partial sequence of the human HNF-1α gene. The nucleotide and predicted amino acid sequences are shown. Exon and intron sequences are in uppercase and lowercase letters, respectively. The approximate sizes of the gaps in those introns, the complete sequence of which was not determined, are noted. In the promoter region, potential binding sites for transcription factors that may regulate expression of this gene are indicated, with sites identified by DNase footprinting in italics, those identified by sequence homology in normal type. The minimal promoter region is shown in boldface type. The polymorphisms and mutations in the HNF-1α gene identified to date are also shown in boldface type, with the designation of mutations noted. The asterisk notes the predicted transcriptional start site based on studies of the rat HNF-1α gene (21). The number of characters per line are indicated for the purpose of discussion; they include both characters and spaces. The letter "n" indicates that the sequence was ambiguous at this site.