Errata

Groves CJ, Zeggini E, Minton J, Frayling TM, Weedon MN, Rayner NW, Hitman GA, Walker M, Wiltshire S, Hattersley AT, McCarthy MI: Association analysis of 6,736 U.K. subjects provides replication and confirms *TCF7L2* as a type 2 diabetes susceptibility gene with a substantial effect on individual risk. *Diabetes* 55:2640–2644, 2006

In the above article, which reported polymorphisms in the TCF7L2 gene, the amino acid corresponding to nucleotide substitution c.A879G should have read as p.Thr293Thr, c.C1429A should have read as p.Pro477Thr, and c.A1579C should have read as c.C1579A p.Pro527Thr.

The final sentence of the last complete paragraph on p. 2642 should therefore read as follows: "Numbered with respect to adenine thymine guanine translation-initiation site, these were: c.A879G p.Thr293Thr (exon 8; in a single Asian subject), c.C1429A p.Pro477Thr (exon 14; in three subjects of Vietnamese, Chilean, and Swedish origin), c.C1579A p.Pro527Thr (exon 14; one Syrian subject), and c.T1735C p.Ser579Pro (exon 14; one Brazilian subject)."

Cauchi S, Meyre D, Choquet H, Dina C, Born C, Marre M, Balkau B, Froguel P, for the DESIR Study Group: *TCF7L2* variation predicts hyperglycemia incidence in a French population: the Data from an Epidemiological Study on the Insulin Resistance Syndrome (DESIR) Study. *Diabetes* 55:3189–3192, 2006

In this study, a Cox analysis, adjusted for BMI, age, and sex, has been preferred over a log-rank analysis. Therefore, the log-rank P value presented in the seventh sentence of the abstract ($P = 0.028$) should be replaced by the Cox analysis result (hazard ratio 1.21 [95% CI 1.05–1.39], $P = 0.008$).