Erratum to: Interaction between prenatal growth and high-risk genotypes in the development of type 2 diabetes

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Owing to a mistake in the designated risk allele in the rs13266634 polymorphism in the *SLC30A8* gene, several corrections are required (corrections shown in red font).

Abstract:

Pooling across all nine genes, each risk allele increased the risk of type 2 diabetes by **14%**.

Results: Effect of genetic variants on risk of type 2 diabetes

Considering the combined genetic profile, high-risk genotypes were associated with increased risk of type 2 diabetes compared with low-risk genotypes, each risk allele increasing the odds **14%** ($p<0.001$) (ESM Table 1).

The online version of the original article can be found at <http://dx.doi.org/10.1007/s00125-009-1291-1>

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Table 1 Effect of genetic variants on birthweight

Chr	Gene	SNP	Genotype ^a (n)	Birthweight increase (g) per risk allele (95% CI) ^b
10	<i>TCF7L2</i>	rs7903146	CC; CT; TT (1,028; 525; 67)	2 (−33, 36)
10	<i>HHEX</i>	rs1111875	AA; AG; GG (352; 807; 452)	−24 (−52, 4)
3	<i>PPARG</i>	rs1801282	GG; CG; CC (59; 445; 1,156)	−14 (−50, 22)
11	<i>KCNJ11</i>	rs5219	CC; CT; TT (465; 744; 380)	−9 (−36, 18)
8	<i>SLC30A8</i>	rs13266634	TT; CT; CC (198; 769; 673)	7 (−22, 36)
3	<i>IGF2BP2</i>	rs4402960	CC; AC; AA (814; 592; 153)	23 (−7, 53)
6	<i>CDKAL1</i>	rs7754840	GG; CG; CC (687; 712; 179)	−9 (−39, 21)
9	<i>CDKN2A/2B</i>	rs10811661	GG; AG; AA (34; 386; 1,158)	48 (8, 88)
7	<i>JAZF1</i>	rs864745	GG; AG; AA (406; 829; 390)	4 (−23, 32)
–	Combined risk	–	Per each risk allele	3 (−9, 14)

^a Ordered by increasing risk of type 2 diabetes

^b Linear regression, adjusted for gestational age, sex, maternal age, maternal BMI and parity

Chr, chromosome

The corrected version of Fig. 1 is shown below.

Fig. 1 Effect size of the interaction between birthweight and genotype

Corrections have also been made to ESM Tables 1 and 3, and ESM Fig. 1 has been redrawn.