Hum Genet (2013) 132:957–958
DOI 10.1007/s00439-013-1307-2

ERRATUM

Erratum to: Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort

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Published online: 19 April 2013

Erratum to: Hum Genet (2013) 132:129–138
DOI 10.1007/s00439-012-1230-y

The sixth column of Table 1 ("Associated SNPs") has results taken from Sabatti et al. (2009), however an error was made in the processing of the results. Also, the results derived from Supplementary Table 4 of Sabatti et al. (2009), not from Supplementary Table 1 as originally stated. The corrected Table 1 is as follows:

The online version of the original article can be found under doi:10.1007/s00439-012-1230-y.

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Table 1 Heritability estimates

Trait[a]	GCTA[b]	VC IBD[c]	Zuk et al.[d]	Twin studies[e]	Associated SNPs[f]
CRP	0.02 (0.06)[g]	0.08 (0.16)	0.00 (0.21)	0.56 (0.07) [W]	0.041
Glucose	0.18 (0.07)**[h]	0.39 (0.16)**	0.51 (0.22)*	0.67 (0.06) [S]	0.0165
Insulin	0.07 (0.07)	0.04 (0.17)	0.03 (0.22)	0.49 (0.05) [S]	0.0056
Triglycerides	0.08 (0.07)	0.00 (0.17)	0.00 (0.22)	0.65 (0.05) [W]	0.0431
HDL	0.19 (0.07)**	0.46 (0.17)**	0.27 (0.22)	0.76 (0.06) [S]	0.0638
LDL	0.29 (0.07)***	0.54 (0.17)***	0.10 (0.22)	0.78 (0.05) [S]	0.06
BMI	0.16 (0.07)**	0.00 (0.16)	0.00 (0.21)	0.80 (0.03) [W]	0.0055
Diastolic	0.08 (0.07)	0.21 (0.16)	0.09 (0.21)	0.51 (0.06) [W]	0.00
Systolic	0.06 (0.06)	0.06 (0.16)	0.06 (0.21)	0.47 (0.06) [W]	0.00

[a] Traits have been transformed to adjust for covariates and achieve approximate normality, as described in Subjects and Methods. Results from the twin studies have not necessarily had the same transformations/adjustments

[b] Estimates from the GCTA software using autosomal NFBC data

[c] Variance components approach using IBD-based estimates of relatedness from the autosomal NFBC data

[d] Regression approach of Zuk et al. using autosomal NFBC data

[e] Indicative estimates of heritability from twin studies taken from previous literature. Source is denoted by [W] (Wessel et al. 2007) or [S] (Souren et al. 2007). These estimates can differ from the true narrow-sense autosomal heritability of these traits in Northern Finland due to differences in environmental variances, differences in genetic make-up, incorporation of interaction effects or shared environment into family-based estimates, and contribution of the X chromosome

[f] Estimates of the proportion of trait variation in the NFBC data explained by SNPs significantly associated in the NFBC study or from previous studies are taken from Supplementary Table 4 of Sabatti et al. (2009). These estimates include effects from the X chromosome

[g] Estimates of heritability are given with standard errors in parentheses

[h] Statistical significance of estimates from this study are indicated by * ($0.01 < p < 0.05$), ** ($0.001 < p < 0.01$), and *** ($p < 0.001$)

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