the Network of Applied Genetic Medicine of Québec (RMGA) and the Fonds de recherche en santé du Québec (FRSQ).

The corrected article appears in this issue and the HTML and online PDF now carry the additional text.

The authors would like to apologise for this omission.

SHAVE: shrinkage estimator measured for multiple visits increases power in GWAS of quantitative traits

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European Journal of Human Genetics (2014) **22,** 154; doi:10.1038/ejhg.2013.218

Correction to: *European Journal of Human Genetics* (2013) **21**, 673–679; doi:10.1038/ejhg.2012.215; published online 24 October 2012.

It has come to the attention of the authors that the legends for Figures 3 and 4 had been transposed. The figures with their corresponding legends appear below.

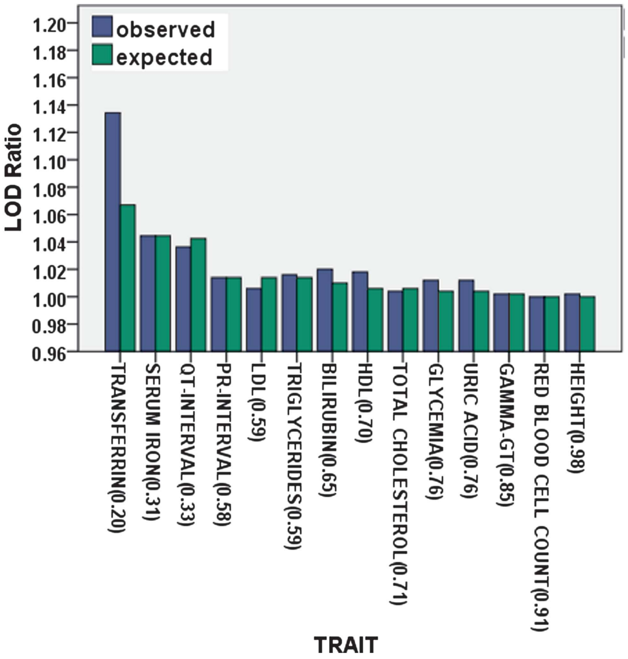

Figure 3 Observed and expected LOD ratio for SHAVE and Average for top SNPs from meta-analysis for a subset of individuals in which all individuals had visit 1 and a randomly chosen 50% of visit 2 cases were selected among the same individuals.

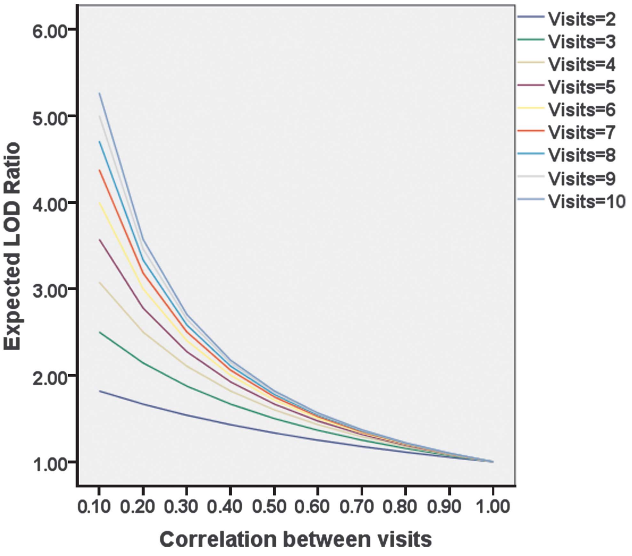

Figure 4 Expected LOD ratio between average and single visit for hypothetical datasets in which all individuals had *k* visits ranging from 2 to 10.