

ERRATUM

In the March 2007 issue of the *Journal*, the report entitled “No Gene Is an Island: The Flip-Flop Phenomenon” by Ping-I Lin et al. (80:531–538), the figure 3 legend and a table 2 footnote and corresponding text contained typographical errors, and a figure 2 panel was incorrect.

In the figure 3 legend, incomplete subscripts were shown in the formulas, and the explanatory text was incomplete. The correct legend should be

Directions of allelic association for the A allele in different situations. We used the statistic $\chi = (P_{A\text{-case}} - P_{A\text{-control}}) / \sqrt{P(1-P)/N}$, where $P_{A\text{-case}}$ and $P_{A\text{-control}}$ are the A allele frequency in affected and unaffected individuals, respectively, $P = (P_{A\text{-case}} + P_{A\text{-control}}) / 2$ and N is the sample size (cases + controls), to demonstrate how direction of allelic association varies depending on θ_2 , given the same frequency of the A (and B) allele (~50%) in the population. θ_1 is fixed at 0.1 for all models. Panel A indicates the situation where A is a risk allele and B is also a risk allele; panel B indicates the situation where the A allele is a risk allele and the B allele is a protective allele.

In the table 2 footnote c and the corresponding text in the last paragraph of p. 535, the wrong genotype was given. Footnote c should read “The genotype at *rs3741916* in the *GAPDH* gene was coded as 1 for GG + GC [not CC] and 0 for CC [not GC + CC].” The text should be “...the C [not G] allele at *rs3741916* was positively associated with

AD in the earlier-onset subset ($P = .007$) but that the G [not C] allele was positively associated with AD in the later-onset subset ($P = .047$).”

In figure 2, the original bottom-right graph in panel A (Model I: $P_A = 0.5$, $P_B = 0.5$) was derived by the set of penetrance values using $\theta_1 = 0$, not 0.1 as shown in the original legend. The corrected figure panel, with use of $\theta_1 = 0.1$, is shown here.

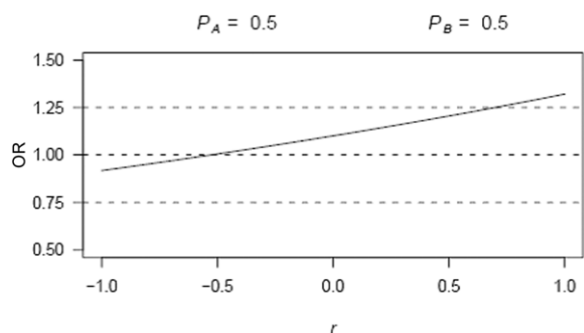


Figure 2A. ORs corresponding to the effect size of allele A under model I. $f = 0.001$, $\theta_1 = 0.1$.

The authors regret the errors.