

## Corrigendum

In the article by G. de los Campos, H. Naya, D. Gianola, J. Crossa, A. Legarra, E. Manfredi, K. Weigel, and J. M. Cotes (*GENETICS* 182: 375–385) entitled “Predicting Quantitative Traits with Regression Models for Dense Molecular Markers and Pedigree,” File S1 of the supporting information contains a mistake in the fully conditional density of the residual variance. This mistake has been corrected in the new version of File S1 that is available online at <http://www.genetics.org/content/182/1/375/suppl/DC1>. Importantly, the R-program used for analysis in the article, which is provided in File S2 (BRL.rda), as well as the BLR program of R (<http://cran.r-project.org/web/packages/BLR/index.html>), do not suffer from that mistake. We thank Rohan

Fernando and Rob Tempelman for pointing out the mistake in File S1.

Corrected text now shown on page 5SI (first 3 lines):

$$\begin{aligned}
 p(\sigma_e^2 | else) &\propto \left[ \prod_{i=1}^n N(y_i | \mu + \mathbf{x}'_i \boldsymbol{\beta}_r + \mathbf{x}'_i \boldsymbol{\beta}_l + u_i, \sigma_e^2) \right] \left[ \prod_{j=1}^p N(\beta_{lj} | 0, \sigma_e^2 \tau_j^2) \right] \chi^{-2}(\sigma_e^2 | S_e, df_e) \\
 &\propto \left[ \prod_{i=1}^n N(\varepsilon_i | \sigma_e^2) \right] \left[ \prod_{j=1}^p N(\tilde{\beta}_{lj} | 0, \sigma_e^2) \right] \chi^{-2}(\sigma_e^2 | S_e, df_e) \\
 &= \chi^{-2}(\sigma_e^2 | S = S_e + \boldsymbol{\varepsilon}' \boldsymbol{\varepsilon} + \tilde{\boldsymbol{\beta}}' \tilde{\boldsymbol{\beta}}, df = df_e + n + p)
 \end{aligned}
 \tag{14}$$

where  $\boldsymbol{\varepsilon} = (\varepsilon_1, \dots, \varepsilon_n)'$  =  $\mathbf{y} - \mathbf{1}\mu - \mathbf{X}_r \boldsymbol{\beta}_r - \mathbf{X}_l \boldsymbol{\beta}_l - \mathbf{u}$ ,  $\tilde{\beta}_{lj} = \left( \frac{\beta_{lj}}{\tau_j} \right)$  and  $\tilde{\boldsymbol{\beta}} = (\tilde{\beta}_{11}, \dots, \tilde{\beta}_{lp})'$ .