



Figure S3: Expected error term variance in the transmissibility model versus mendelian sampling variance in the true model ($y_i = \mathbf{x}_i\boldsymbol{\beta} + a_i + epi_i + sp_i + e_i$).

Each point corresponds to different combination of H^2 from 0.1 to 0.9 and r in the true model.

Parameters in the true model : $H^2 = \frac{\sigma_a^2 + \sigma_{epi}^2 + \sigma_{sp}^2}{\sigma_a^2 + \sigma_{epi}^2 + \sigma_{sp}^2 + \sigma_e^2}$, $\Gamma = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{epi}^2 + \sigma_{sp}^2}$, $\theta = \frac{\sigma_{sp}^2}{\sigma_a^2 + \sigma_{epi}^2 + \sigma_{sp}^2}$, $\delta =$ single parent path coefficient of transmission, λ_s, λ_d : sire and dam epigenetic path coefficients of transmission.

Parameters in the transmissibility model: $\tau^2 = \frac{\sigma_e^2}{\sigma_e^2 + \sigma_e^2}$, ω_s and ω_d sire and dam path coefficient of transmission in the transmissibility model. Values in the transmissibility model have been obtained using the maximum of expected likelihood

Figure S3 confirms that the error term variance obtained with the transmissibility model is always higher than the mendelian sampling variance.