



Figure 1: **Figure S1. Actual prediction accuracy of single-trait and multi-trait prediction methods in simulated data when \mathbf{G} and \mathbf{R} are known.** 500 simulations were run for each heritability of the secondary trait ($h_2^2 = \{0.2, 0.6\}$), and each combination of genetic and non-genetic correlation between the two traits ($\rho_g = \{0, 0.3, 0.6\}$, $\rho_R = \{-0.6, -0.4, -0.2, 0, 0.2, 0.4, 0.6\}$), all with $h_1^2 = 0.2$. For each simulation, we used the 900 training individuals to fit linear mixed models (either single or multi-trait) conditioning on the true values for \mathbf{G} and \mathbf{R} , predicted the genetic values of the 100 testing individuals, and then measured the Pearson's correlation between the predicted ($\hat{\mathbf{u}}_{n1}$) and true (\mathbf{u}_{n1}) genetic values. In the CV1 method, we used only information on the testing individuals to calculate $\hat{\mathbf{u}}_{n1}$. In the CV2 method, we used the training individuals to calculate $\hat{\mathbf{u}}_o$ and combined this with the observed phenotypes for the secondary trait on the testing individuals (\mathbf{y}_{n2}). Curves show the average correlation for each method across the 500 simulations. Ribbons show $\pm 1.96 \times SE$ over the 500 simulations. Dashed lines show analytical calculations of the expected correlation given one representative training:validation data partition.