

Supplementary Figures

Genetics

Improving genomic predictions with inbreeding and non-additive effects in two admixed maize hybrid populations in single and multi-environment contexts

Morgane Roth^{*,†}, Aurélien Beugnot[‡], Tristan Mary-Huard^{‡,§}, Laurence Moreau[‡], Alain Charcosset[‡], Julie B. Fievet[‡]

* Present address: INRAE, GAFL, F-84143, Montfavet, France

† Plant Breeding Research Division, Agroscope, Wädenswil, Zurich, Switzerland

‡ Université Paris-Saclay, INRAE, CNRS, AgroParisTech, GQE-Le Moulon, 91190, Gif-sur-Yvette, France.

§ Université Paris-Saclay, INRAE, AgroParisTech, UMR MIA-Paris Paris, 75005, Paris, France

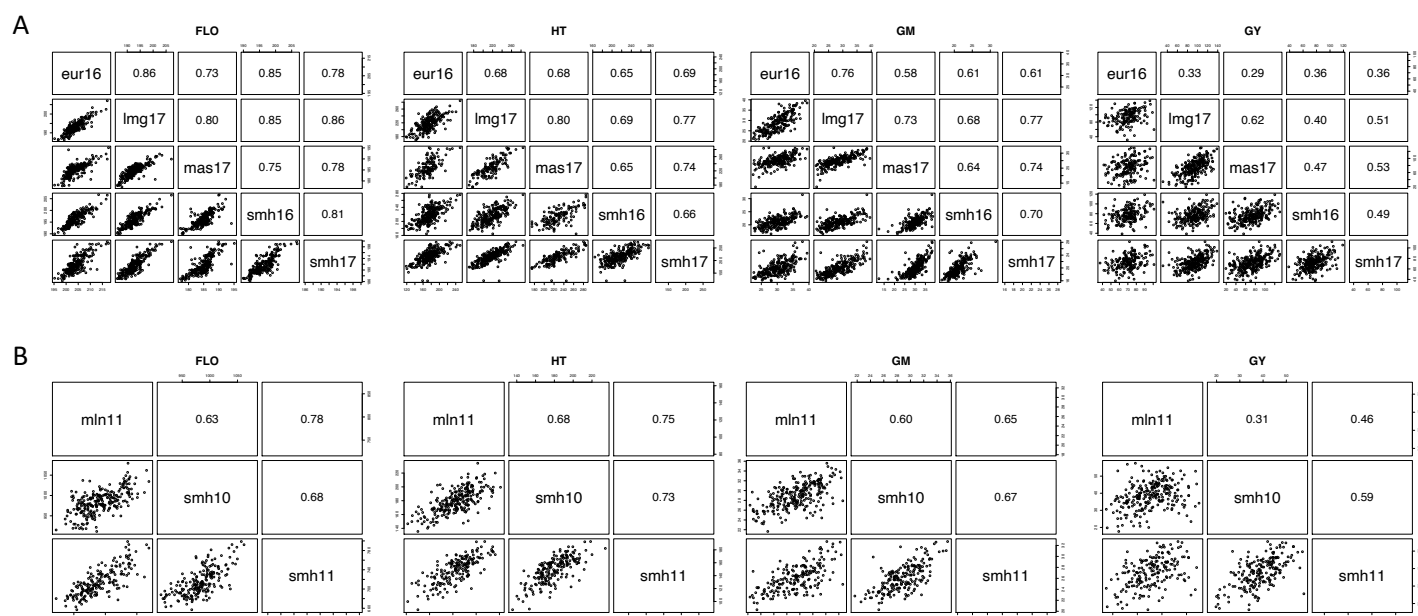


Figure S1. Correlation plots for each trait in (A) the Het2 population and (B) the iF2 population based on the mean corrected field observations per hybrid

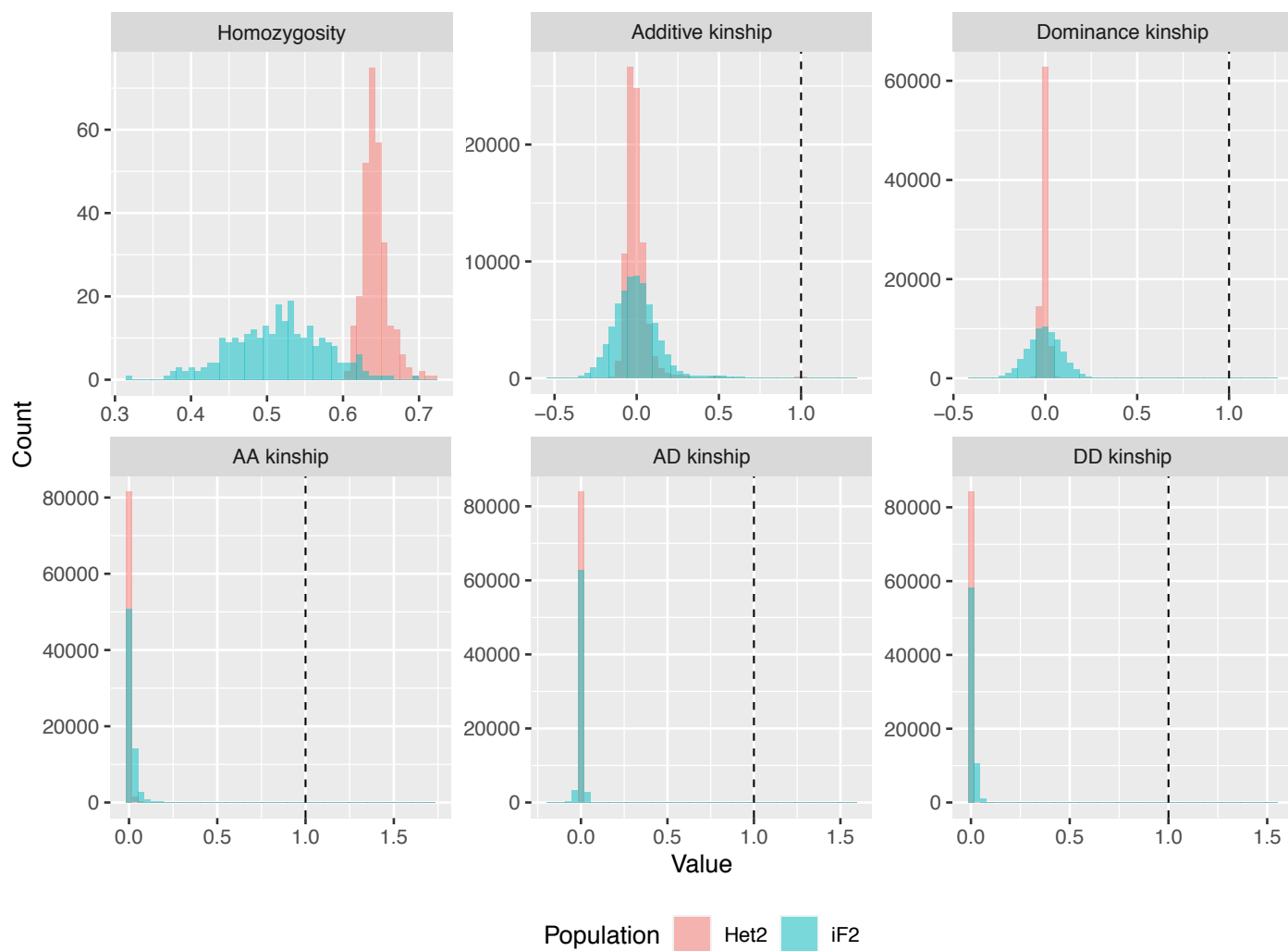


Figure S2. Distribution of homozygosity proportions and of kinship values in Het2 and iF2 populations.

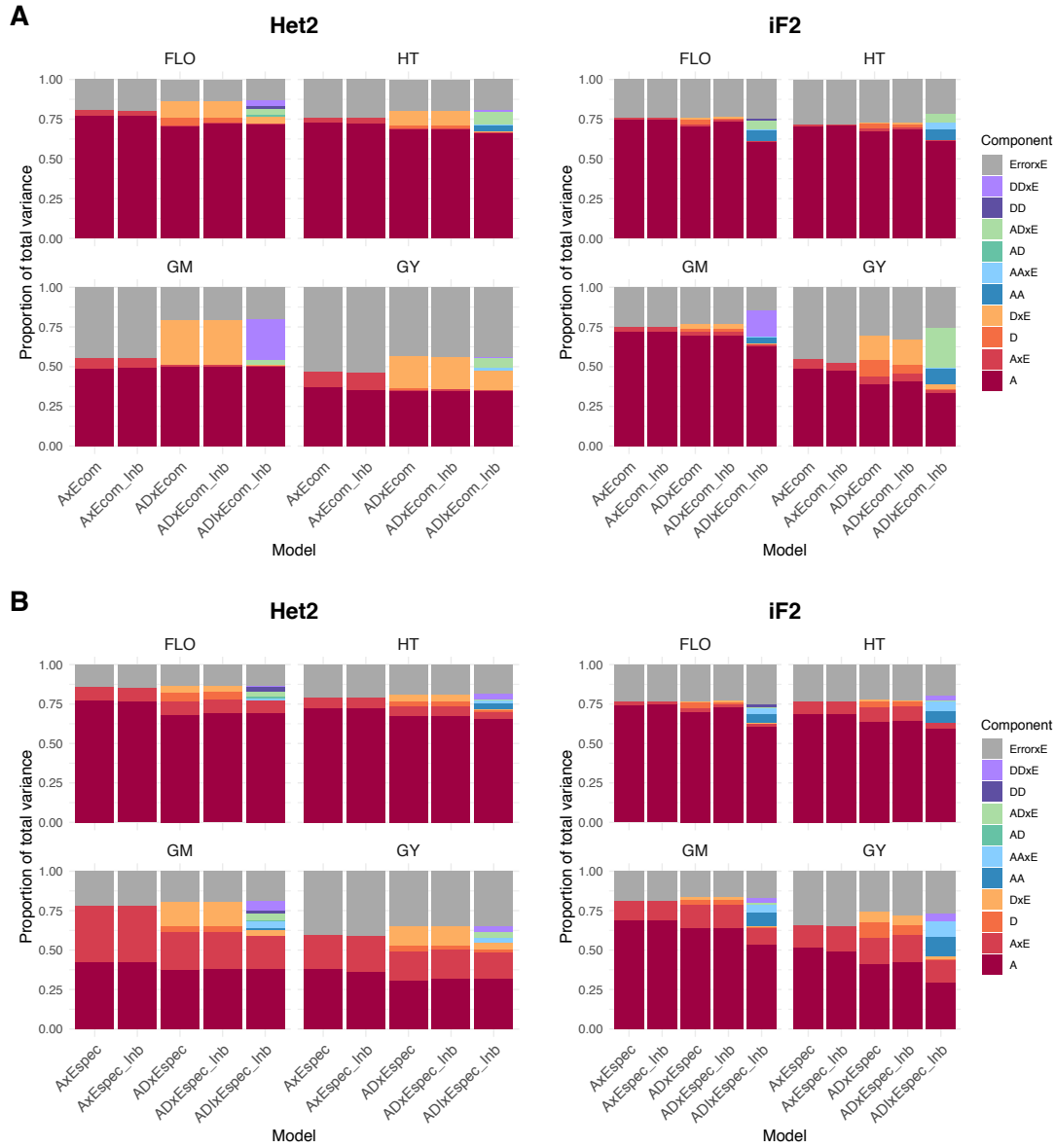
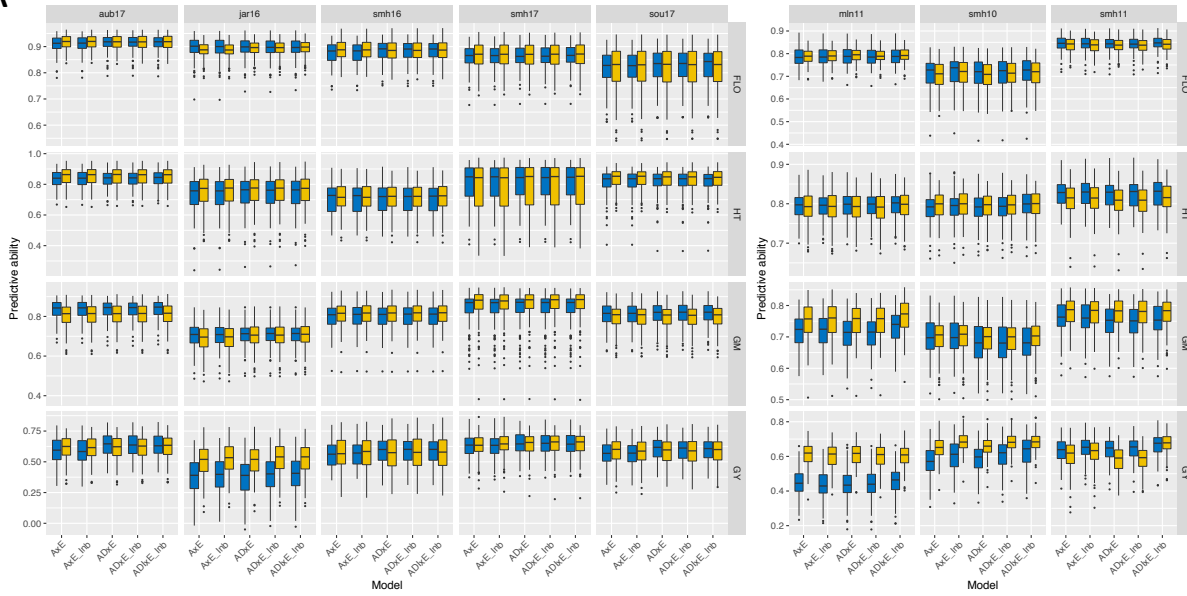


Figure S3. Variance decomposition across environments using 10 models derived from model *M4* in Het2 and iF2 populations. A, ADI×Ecom_Inb model and submodels B, ADI×Espec_Inb model and submodels. In both A and B, the error variance terms $\sigma\epsilon(e)^2$ are environment specific and represented by their average value. In B, G×E variance terms $\sigma AE(e)^2 \dots \sigma DDE(e)^2$ are environment specific and represented by their average value. FLO, flowering time; HT, plant height; GM, grain moisture; GY, grain yield.

Het2

iF2

A



B

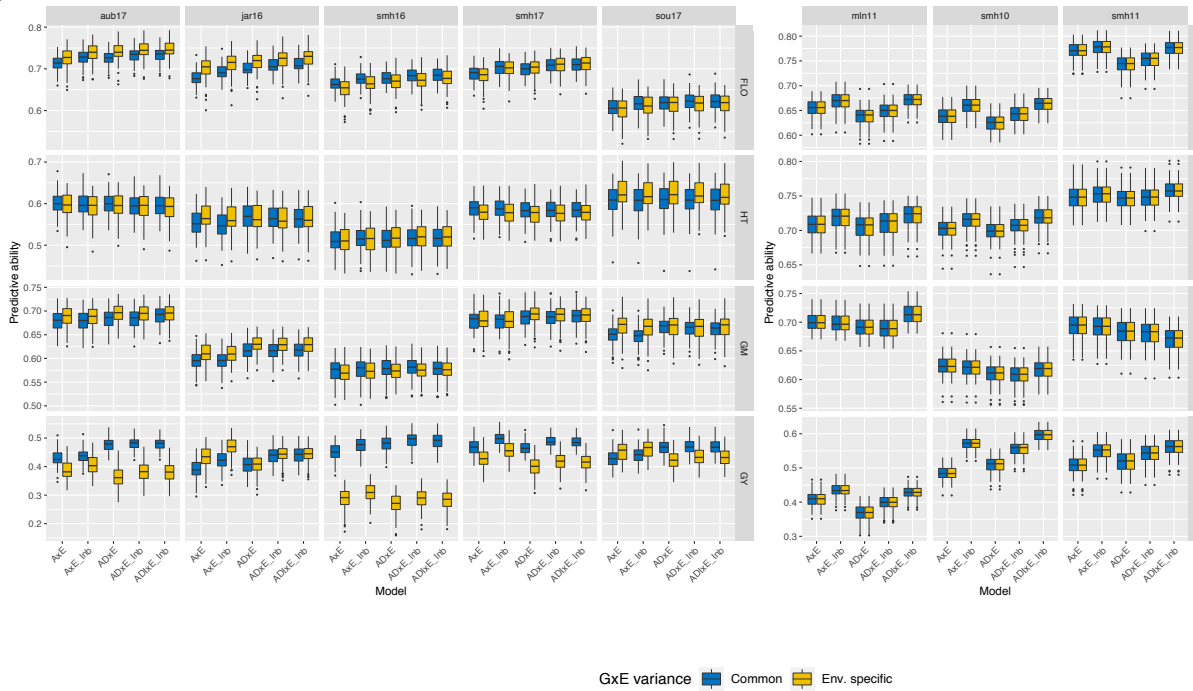


Figure S4. Boxplot representing the distribution of predictive ability in scenario « $G \times E_{\text{new_env}}$ » (A) and « $G \times E_{\text{new_hyb}}$ » (B) obtained with 100 cross-validations in Het2 (a) and in iF2 (b) populations using M4 and submodels. Environment names refers to performances of the validation set. The color legend indicates whether results are obtained with ADI×Ecom_Inb models and submodels (“Common”) or with ADI×Espe_Inb models and submodels (“Environment specific”). FLO, flowering time; HT, plant height; GM, grain moisture; GY, grain yield. Each column represents a single environment.

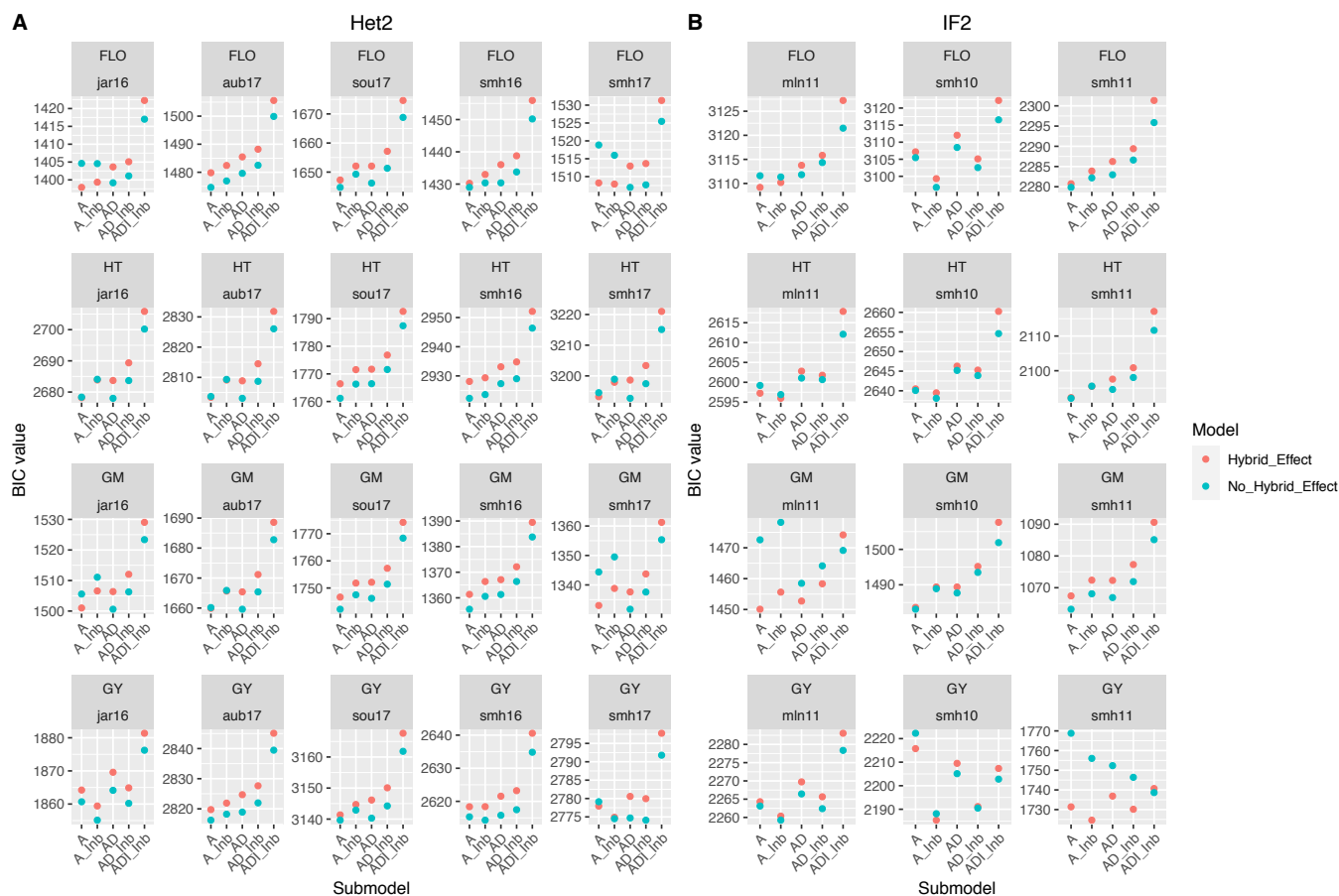


Figure S5. BIC values obtained for each trait and environment in variance decompositions using model *M3* and submodels with and without the inclusion of a residual hybrid permanent effect.

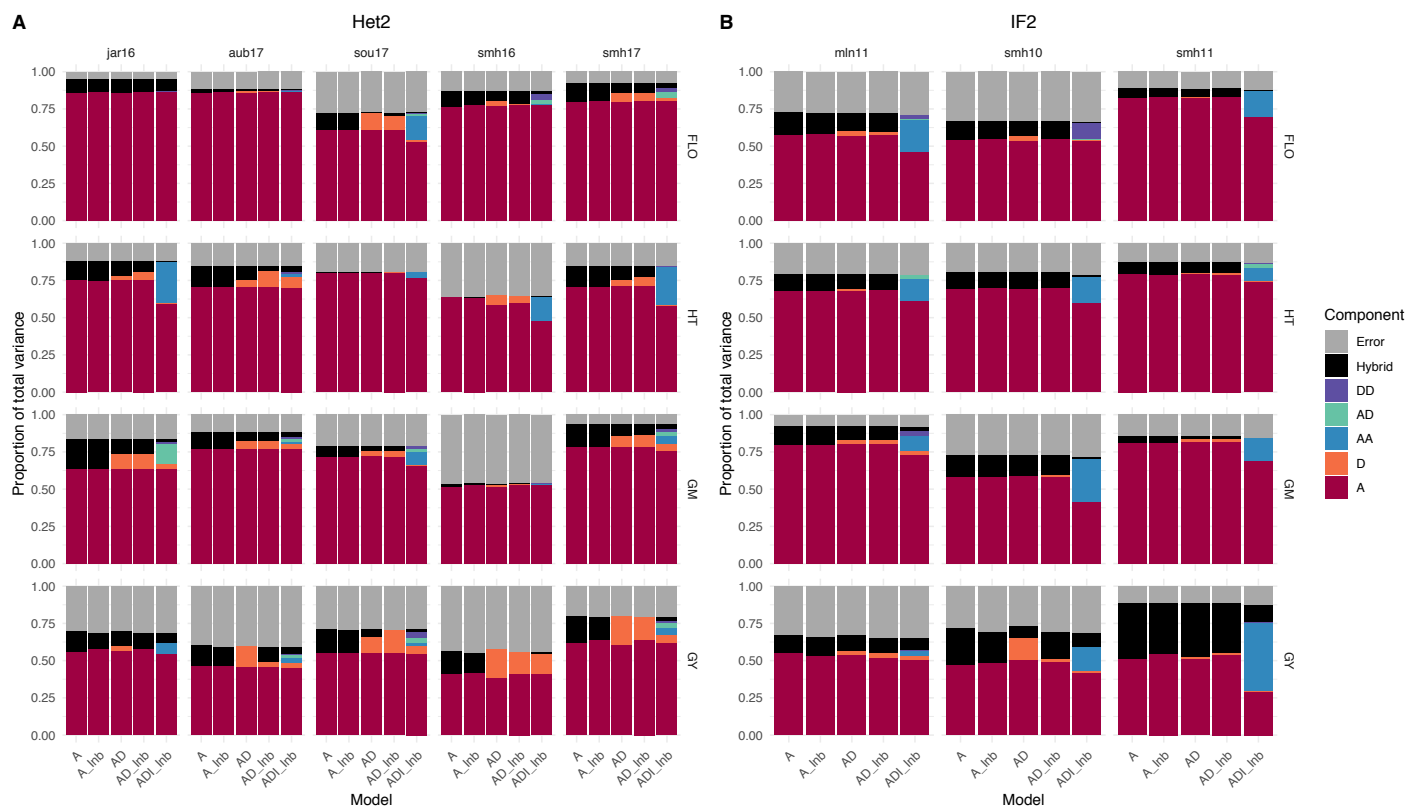


Figure S6. Variance decomposition in each environment including a random residual hybrid permanent effect with model *M3* and submodels. A, Het2 population; B, iF2 population.

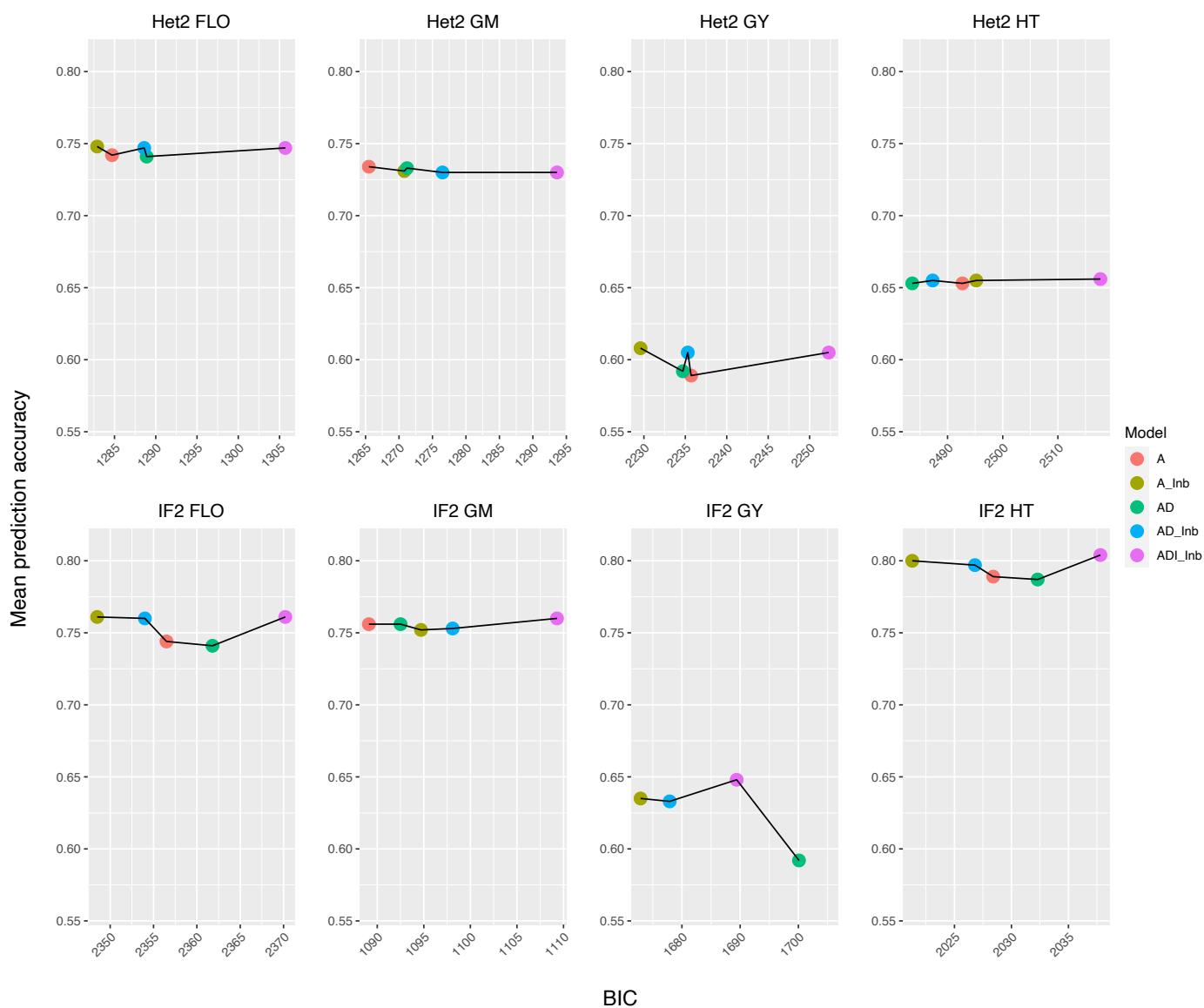


Figure S7. Predictive ability as a function of BIC values using model *M2* and submodels.

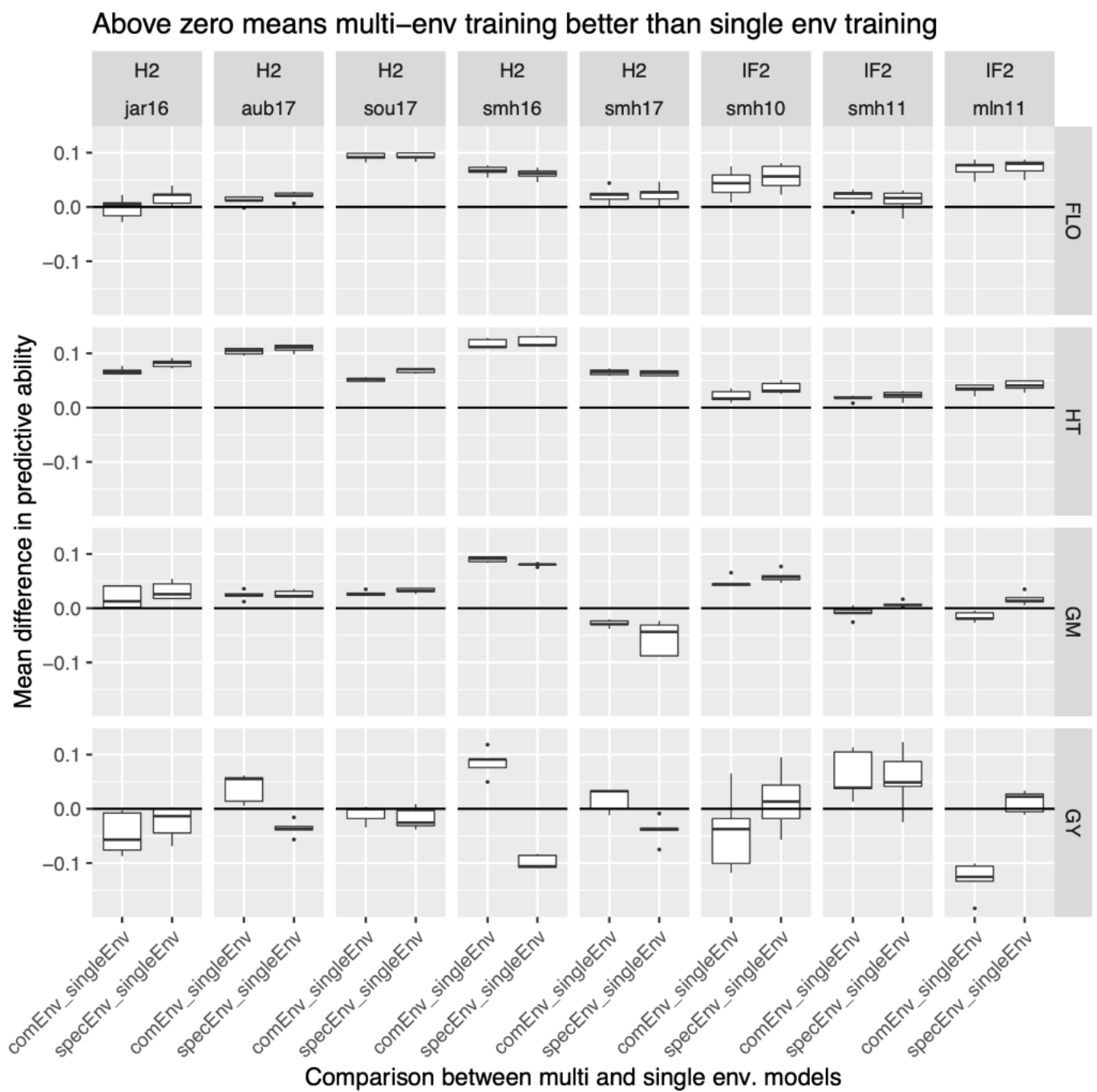


Fig. S8. Difference in predictive ability between multi- and single environment calibration (scenario GxE_new_hyb vs within-environment).