**Supplementary Data**

**TABLES**

Table S1. Phenotypic values adjusted for spatial effects in populations Het2 and iF2

**TableS2**. Variance decompositions and BIC on replicated observations and predictive ability for each environment

Table S3. Variance decompositions and BIC on replicated observations, across environments (models including G×E interactions, 4 sheets)

Table S4. Predictive ability in 100 cross-validations on $\overbar{Y\_{..}} $values using model M2

Table S5.  Predictive ability in 100 cross-validations within environment on $\tilde{Y\_{her}}$ values using model M3

**Table S6**. Prediction accuracies in “G×E\_new\_env” scenario using models M4 and submodels, and $\tilde{Y\_{her}}$ values (100 validations each)

**Table S7**. Prediction accuracies in “G×E\_new\_hybrid” scenario using models M4 and submodels, and $\tilde{Y\_{her}}$ values ( (100 validations each)

**Table S8**. Kinship matrices for additivity, dominance and epistasis calculated in Het2 and iF2 populations

**FIGURES**

**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 $\overbar{Y}$

**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 *σε(e)2* are environment specific and represented by their average value. In B, G×E variance terms *σAE(e)2*…*σDDE(e)2* are environment specific and represented by their average value. FLO, flowering time; HT, plant height; GM, grain moisture; GY, grain yield.

**Figure S4**. Boxplot representing the distribution of predictive ability in scenario « G×E\_new\_env » (A) and « G×E\_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 hybrid permanent effect.

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

**Figure S7**. Predictive ability as a function of BIC values using model *M3* and submodels.

**Figure S8**. Difference in predictive ability between multi- and single environnement calibration (scenario GxE\_new\_hyb vs within-environment).