

Table S5 – Prediction accuracy in NAM-H by directional effects of inbreeding in Ames-H

Trait	Prediction accuracy (p-value)	Difference in prediction accuracy (p-value)
	DGBLUP	DGBLUP + Genomic inbreeding (linear and quadratic effects)
DTS	0.319 (2.9×10^{-11})	-0.002 (0.38)
PH	0.259 (8.0×10^{-10})	+0.002 (0.52)
GY	-0.011 (0.71)	-0.000 (0.99)

Prediction accuracy: average correlation between observed and predicted phenotypes in NAM-H, over 24 populations; Difference in prediction accuracy: difference between the dominance GBLUP model (DGBLUP) and DGBLUP model incorporating F and F^2 as fixed effects (F : genomic inbreeding coefficient). Significance of average prediction accuracies (non-zero mean) and estimated differences in prediction accuracy (non-zero difference, paired by NAM-H population) was assessed by t-tests.

