

**Table S6 – Prediction accuracy from GWAS models**

<b>Validation scheme</b>	<b>Baseline model</b>	<b>Trait</b>	<b>Prediction accuracy (p-value)</b>	<b>Difference in prediction accuracy by QTL effects (p-value)</b>
<b>Ames-H ⇒ NAM-H</b>	DGBLUP	DTS	0.319 ( $2.9 \times 10^{-11}$ )	-0.059 (0.061)
		PH	0.259 ( $8.0 \times 10^{-10}$ )	No QTL
		GY	-0.011 (0.71)	No QTL
<b>NAM-H ⇒ Ames-H</b>	GBLUP	DTS	0.497 ( $4.8 \times 10^{-9}$ )	-0.027 (0.075)
		PH	0.052 (0.079)	No QTL
		GY	0.254 ( $2.7 \times 10^{-6}$ )	-0.041 (0.11)

Validation scheme: training panel ⇒ validation panel; Baseline model: DGBLUP in Ames-H

(polygenic additive and dominance effects), GBLUP in NAM-H (polygenic additive effects

only); Prediction accuracy: average correlation between observed and predicted phenotypes in

validation sets, from the baseline model; Difference in prediction accuracy: difference in

prediction accuracy between baseline model and GWAS model (including fixed additive and

dominance effects of QTL in Ames-H, only additive effects of QTL in NAM-H). Significance of

average prediction accuracies (non-zero mean) and estimated differences in prediction accuracy

(non-zero difference, paired by validation set) was assessed by t-tests.