

Table 5 Prediction accuracies of genomic selection for each trait based on genomic best linear unbiased prediction (GBLUP) and vBayesB-based method

Trait	GBLUP	vBayesB
SUC	0.71	0.69
FRU	0.65	0.60
GLU	0.74	0.75
SOR	0.62	0.58
TSC	0.56	0.39
HarT	0.72	0.65
FruW	0.56	0.46
FruH	0.56	0.41
SSC	0.59	0.45
Aci	0.65	0.66

Values indicate Pearson's correlation coefficient (r) between predicted genotypic values and phenotypic values