

Supplementary Material

Enhancing the Potential of Phenomic and Genomic Prediction in Winter Wheat Breeding Using High-Throughput Phenotyping and Deep Learning

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Supplementary Tables and Figures

Supplementary Table 1: List of vegetation indices and equations extracted from multispectral images used in this study.

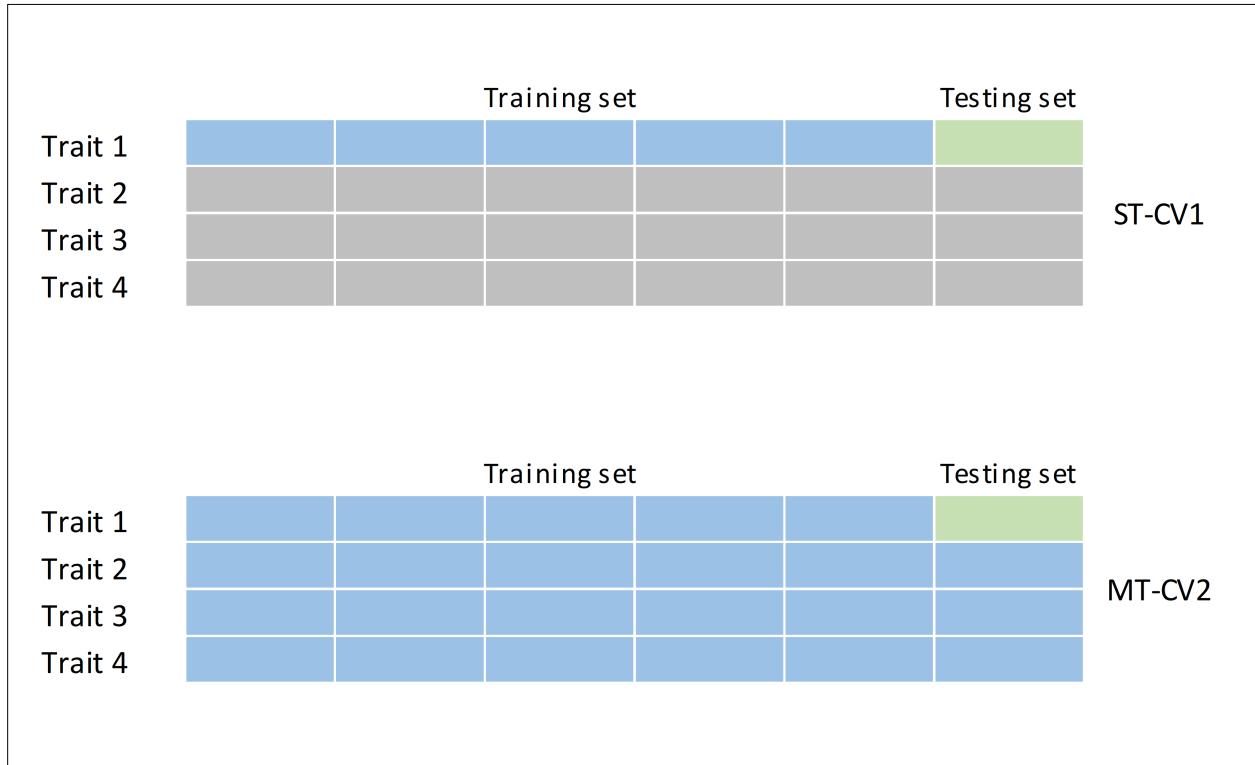
Spectral feature name	Formulation	Ref.
5 original reflectance bands: Blue (B), Green (G), Red (R), Red edge (RE), Near Infrared (NIR)	The reflectance value of each band	-
Normalized difference vegetation index	$NDVI = (NIR - R) / (NIR + R)$	(Rouse Jr et al., 1974)
Green Normalized Difference Vegetation Index (GNDVI)	$GNDVI = (NIR - G) / (NIR + G)$	(Gitelson & Merzlyak, 1997)
Ratio Vegetation Index 1	$RVI_1 = NIR / R$	(Richardson & Wiegand, 1977)
Green Chlorophyll Index	$GCI = (NIR / G) - 1.0$	(Gitelson et al., 1997)
Rice Growth Vegetation Index	$RGVI = R / G$	(Nuarsa et al., 1997)
Difference Vegetation Index	$DVI = NIR - R$	(Tucker, 1979)
Soil-Adjusted Vegetation Index	$SAVI = ((NIR - R) / (NIR + R + L)) * (1.0 + L)$, L =	(Huete, 1988)
Modified Soil Adjusted Vegetation Index	$MSAVI = 0.5 * ((2.0 * NIR) + 1.0 - \sqrt{(2.0 * NIR + 1.0)^2 - 1.0})$	(Qi et al., 1994)
Optimized Soil Adjusted Vegetation Index	$OSAVI = (NIR - R) / (NIR + R + 0.16)$	(Rondeaux et al., 1996)
Renormalized Difference Vegetation Index	$RDVI = \sqrt{(NIR - R)^2} / (NIR + R)$	(Roujean & Breon, 1995)
Triangular Vegetation Index	$TVI = 60.0 * (NIR - G) - 100.0 * (R - G)$	(Deering, 1975)
Transformed Soil Adjusted Vegetation Index	$TSAVI = (a * (NIR - a * R - b)) / (a * NIR + R - a * b)$, a, b = 0.96916, 0.084726	(Baret & Guyot, 1991)
Perpendicular Vegetation Index	$PVI = (NIR - a * R - b) / \sqrt{1 + a^2}$, a, b =	(Richardson & Wiegand, 1977)
Soil-Adjusted Vegetation Index 2	$SAVI_2 = NIR / (R - (b/a))$, a, b = 0.96916, 0.084726	(Huete, 1988)
Adjusted Transformed Soil Adjusted Vegetation Index	$ATSAVI = (a * (-a * R - b)) / (a * NIR + R - a * b + X * (1 + \sqrt{1 + a^2}))$, a, b, X = 0.96916, 0.084726, 0.08	(Baret & Guyot, 1991)
Normalized Difference Water Index	$NDWI = (G - NIR) / (G + NIR)$	(McFeeters, 1996)
Kawashima index	$IKAW = (R - B) / (R + B)$	(Kawashima & Nakatani, 1998)
Simple Ratio Pigment Index	$SRPI = B / R$	(Peñuelas et al., 1995)

Ratio Vegetation Index 2	$RVI_2 = NIR/G$	(Pearson & Miller, 1972)
Modified Chlorophyll Absorption in Reflective	$MCARI = (RE-R-0.2*(RE-G))*(RE/R)$	(Daughtry et al., 2000)
Modified Chlorophyll Absorption in Reflective	$MCARI_1 = 1.2*(2.5*(NIR-R)-1.3*(NIR-G))$	(Haboudane et al., 2004)
Modified Chlorophyll Absorption in Reflective	$MCARI_2 = 1.5*(2.5*(NIR-R)-1.3*(NIR-G))*(np.square(2.0*NIR+1))-(6.0*NIR-$	(Haboudane et al., 2004)
Modified Triangular Vegetation Index	$MTVI_1 = 1.2*(1.2*(NIR-G)-2.5*(R-G))$	(Haboudane et al., 2004)
Modified Triangular Vegetation Index 2	$MTVI_2 = 1.5*(1.2*(NIR-G)-2.5*(R-G))*(np.square(2*NIR+1))-(6.0*NIR-$	(Haboudane et al., 2004)
Modified chlorophyll absorption ratio index/Second modified	$R_MCARI_MTVI2 = ((RE-R-0.2*(RE-G))*(RE/R))/((1.5*(1.2*(NIR-G)-2.5*(R-G))*(np.square(2*NIR+1))-(6.0*NIR-$	(Eitel et al., 2007)
Enhanced Vegetation Index	$EVI = (NIR-R)/(NIR+6.0*R-7.5*B+1.0)$	(Huete et al., 1997)
Datt Index	$DATT = (NIR-RE)/(NIR+R)$	(Datt, 1999)
Double-peak Canopy Nitrogen Index	$DNCI = (RE-G)/(RE+G)$	(Chen et al., 2010)
Plant Senescence Reflectance Index	$PSRI = (R-G)/RE$	(Merzlyak et al., 1999)
Structure Intensive Pigment Vegetation Index	$SIPI = (NIR-B)/(NIR+R)$	(Peñuelas et al., 1995)
Spectral Polygon Vegetation Index	$SPVI = 0.4*3.7*(NIR-R)-1.2*np.absolute(G-R)$	(Vincini et al., 2006)
Transformed Chlorophyll Absorption Reflectance Index	$TCARI = 3.0*((RE-R)-0.2*(RE-G))*(RE/R)$	(Haboudane et al., 2002)
Transformed Chlorophyll Absorption in the Reflectance Index/Optimized Soil-Adjusted Vegetation Index	$R_TCARI_OSAVI = (3.0*((RE-R)-0.2*(RE-G))*(RE/R))/((NIR-R)/(NIR+R+0.16))$	(Haboudane et al., 2002)
Red edge relative index	$RERI = (RE-R)/NIR$	(Haboudane et al., 2002)
Normalized difference red edge index	$NDRE = (NIR-RE)/(NIR+RE)$	(Fitzgerald et al., 2010)
MERIS Terrestrial Chlorophyll Index	$MTCI = (NIR-RE)/(RE-R)$	(Dash & Curran, 2004)
Enhanced Vegetation Index 2	$EVI_2 = 2.5*((NIR-R)/(NIR+2.4*R+1.0))$	(Huete et al., 1997)
Red-Edge Chlorophyll Index	$RECI = (NIR/RE)-1$	(Haboudane et al., 2002)

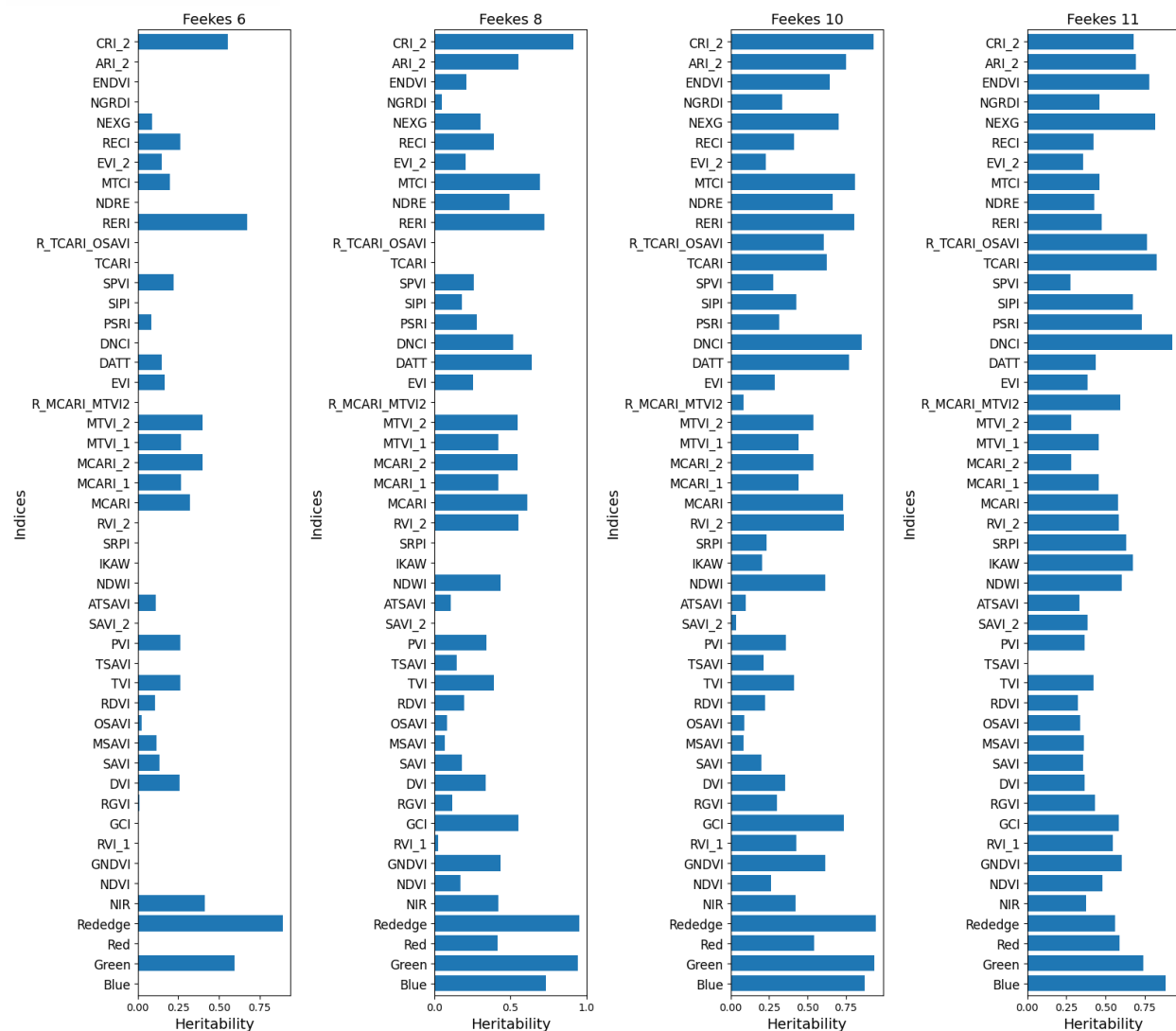
Normalized excess green vegetation index	$NEXG = (2 * G - R - B) / (G + R + B)$	(Woebbecke et al., 1995)
Normalized green–red	$NGRDI = (G - R) / (G + R)$	(Tucker, 1979)
Enhanced Normalized Difference Vegetation Index	$ENDVI = (NIR + G - 2.0 * B) / (NIR + G + 2.0 * B)$	(Anchal et al., 2022)
Anthocyanin Reflectance Index 2	$ARI_2 = NIR * (1.0 / G) - (1.0 / RE)$	(Gitelson et al., 2001)
Carotenoid Reflectance Index 2	$CRI_2 = (1.0 / G) - (1.0 / RE)$	(Gitelson et al., 2003)

Supplementary Table 2. Summary statistics and broad-sense heritability (H^2) of recorded agronomic traits.

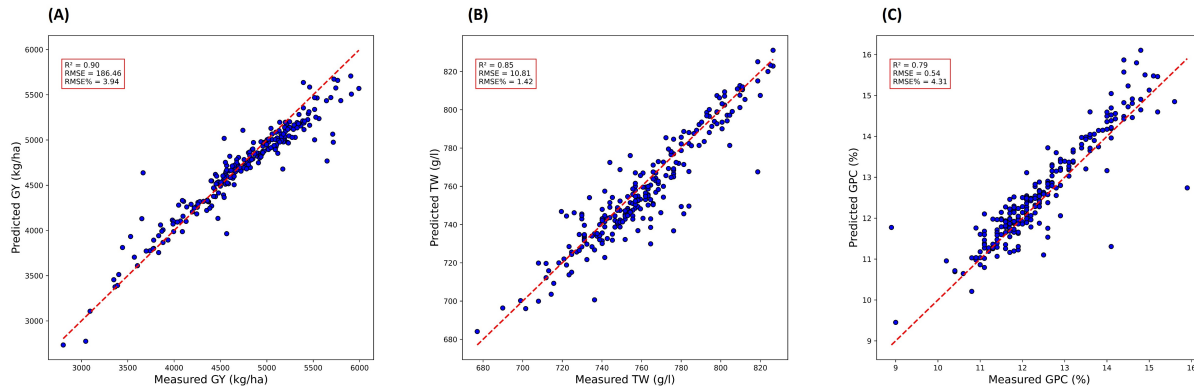
Trait	Mean	H^2
Grain Yield (GY)(kg/ha)	70.30	0.36
Grain Protein (GP)(%)	12.48	0.26
Test Weight (TW)(g/l)	58.88	0.87



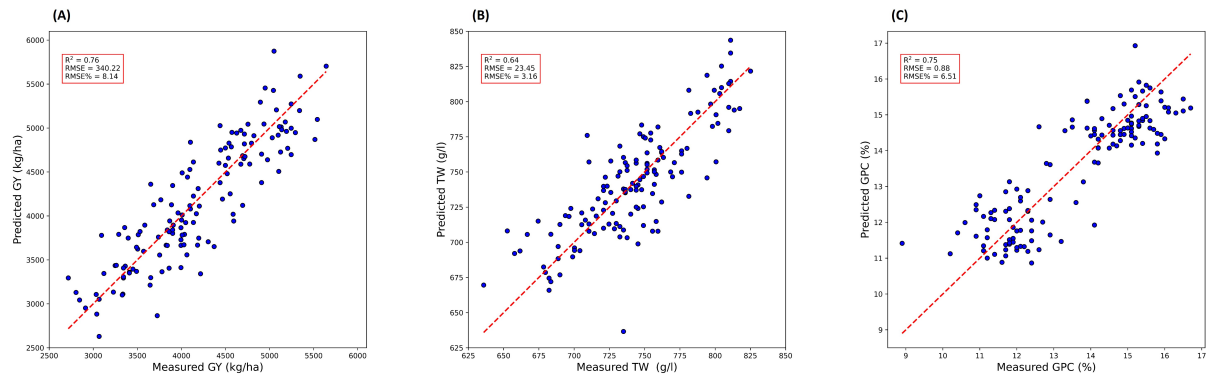
Supplementary Figure 1. Prediction accuracies were estimated for the single-trait (ST) model with cross-validation scheme 1 (ST-CV1) and multi-trait (MT) model with cross-validation scheme 2 (MT-CV2).



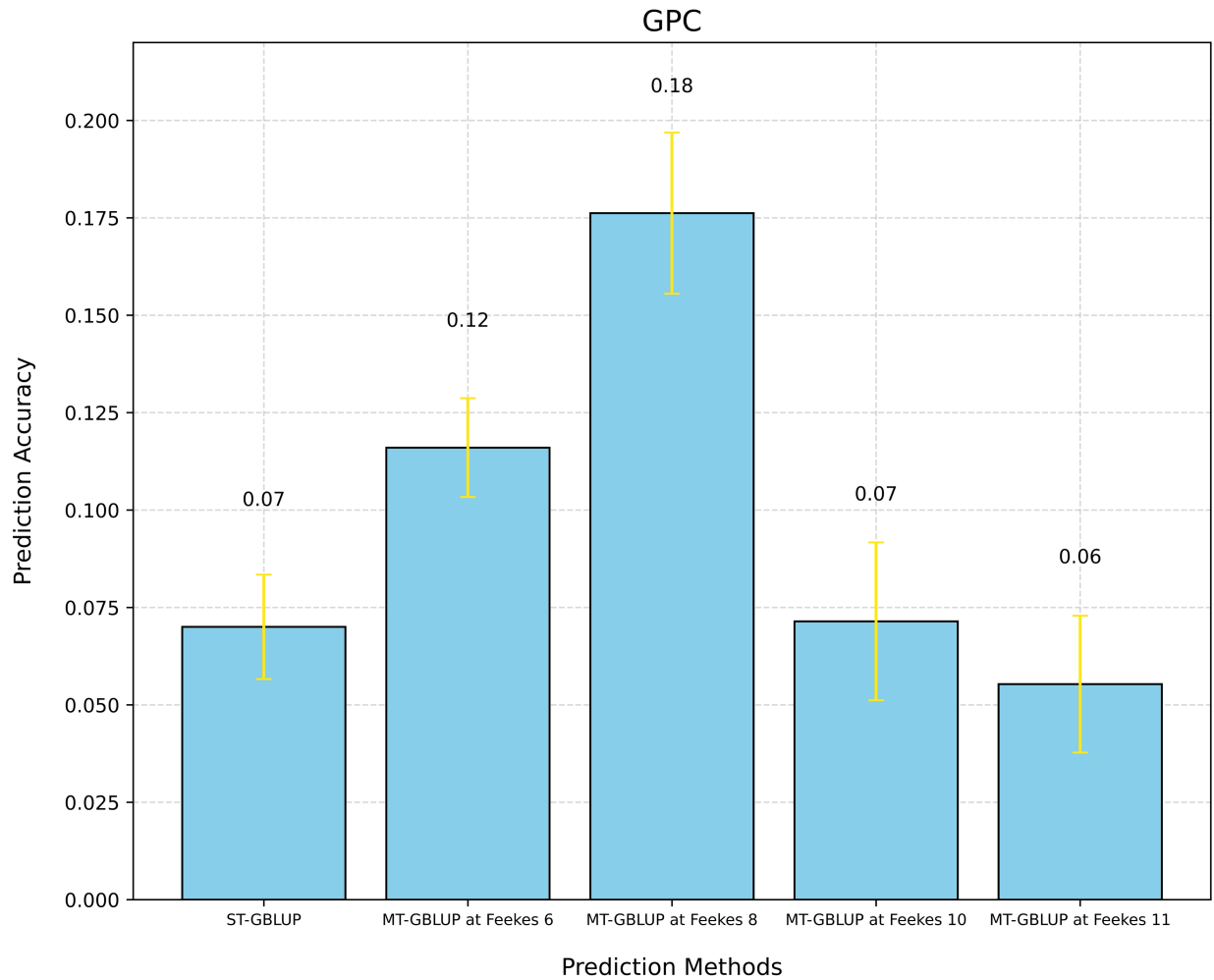
Supplementary Figure 2. Broad-sense heritability (H^2) of High-Throughput Phenotyping (HTP) based traits across various growth stages (Feekes 6: jointing, Feekes 8: Flag leaf, Feekes 10: Booting, Feekes 11: Milk ripe).



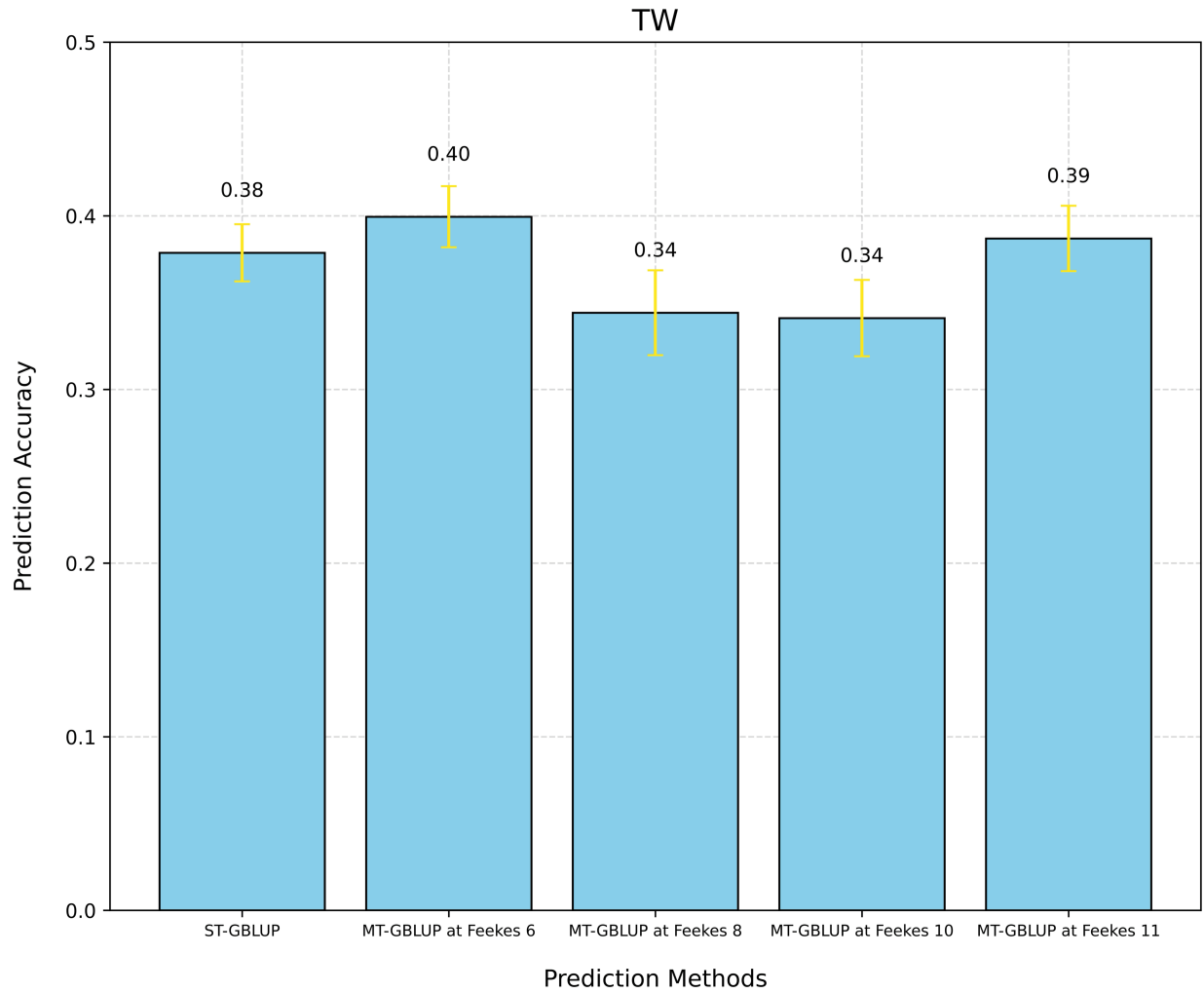
Supplementary Figure 3. Phenomic predictions for grain yield (GY), B) test weight (TW), and C) grain protein (GPC), using DNN with combined High-Throughput Phenotyping (HTP) based traits on the training set (70%) for ELITE and AYT at Brookings.



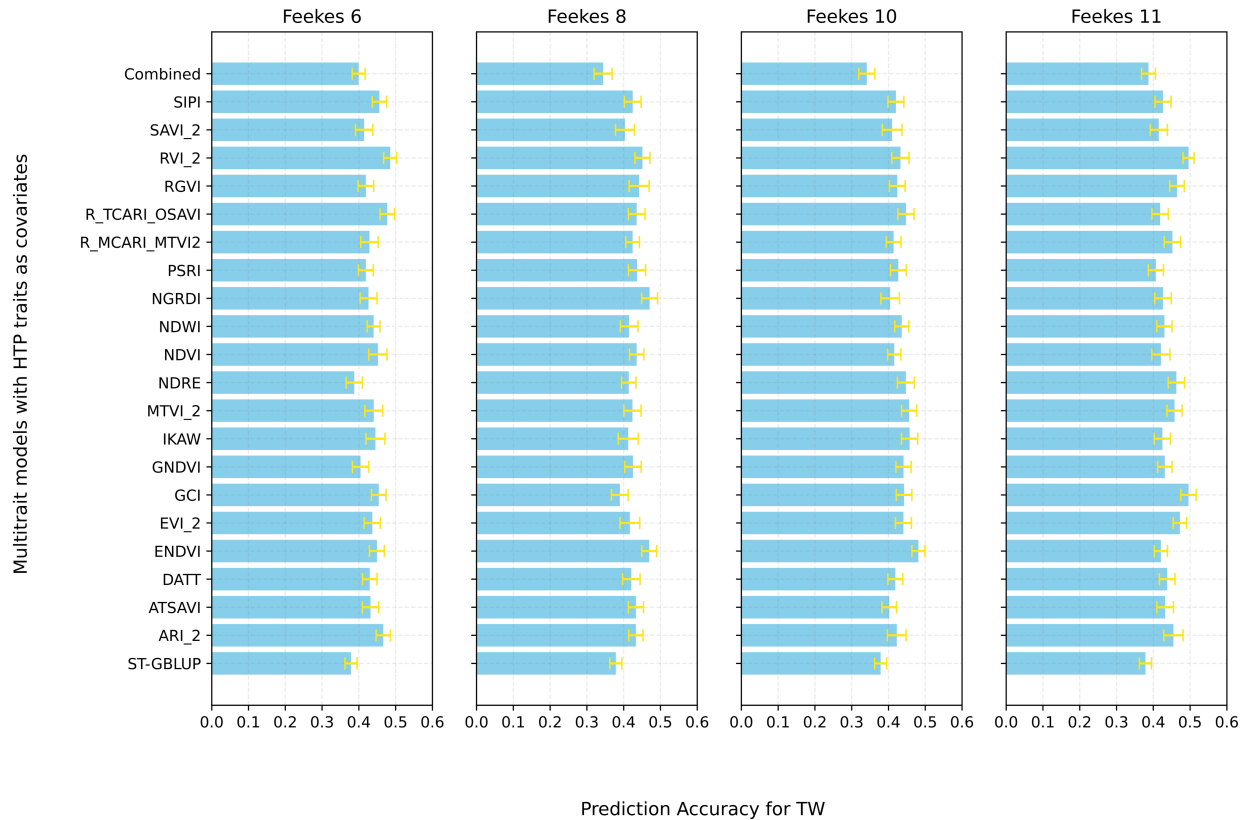
Supplementary Figure 4. A) Phenomic predictions for grain yield (GY), B) Test weight (TW), and C) grain protein content (GPC). Predictions were made on the testing set (30%) using DNN trained on ELITE and AYT at Brookings and Dakota Lakes (multi-locations).



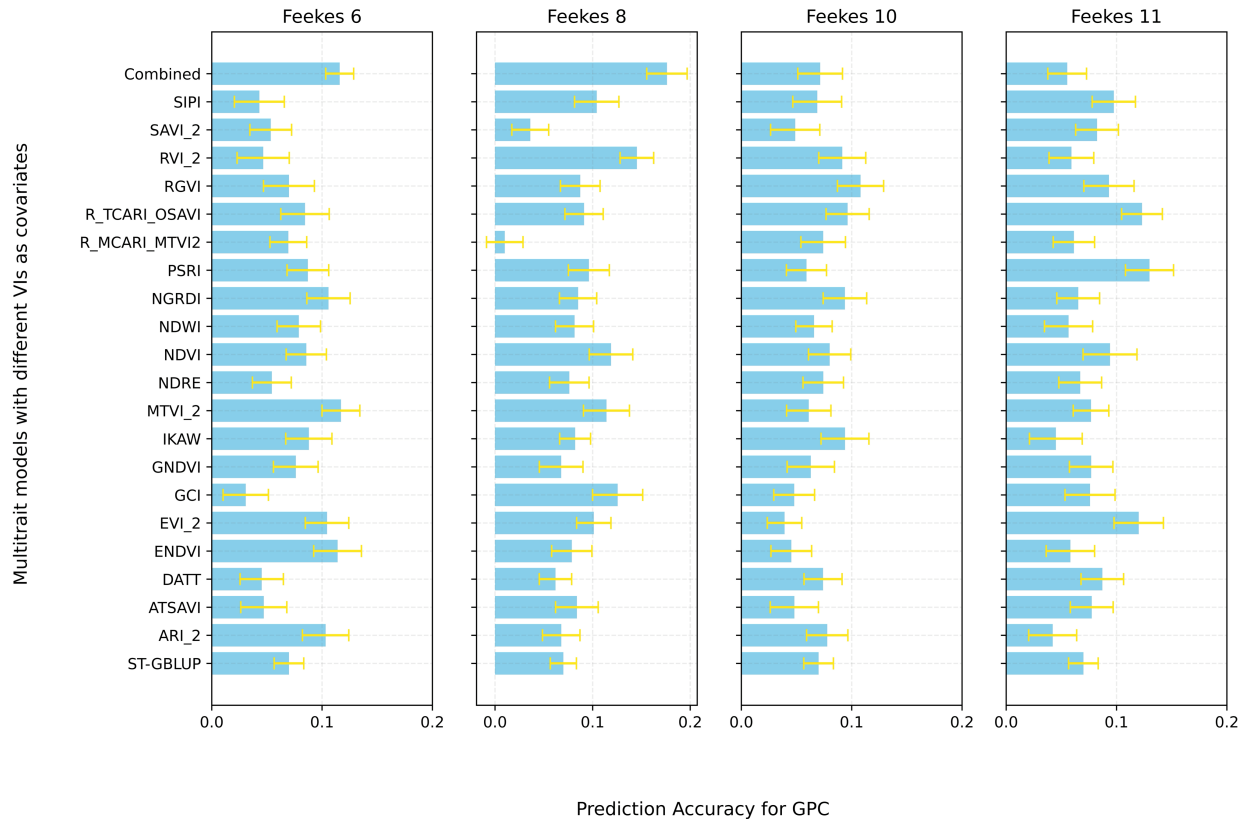
Supplementary Figure 5. Comparison of Prediction accuracy for Grain Protein (GPC) using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across different growth stages (Feekes 6: jointing, Feekes 8: Flag leaf, Feekes 10: Booting, Feekes 11: Milk ripe).



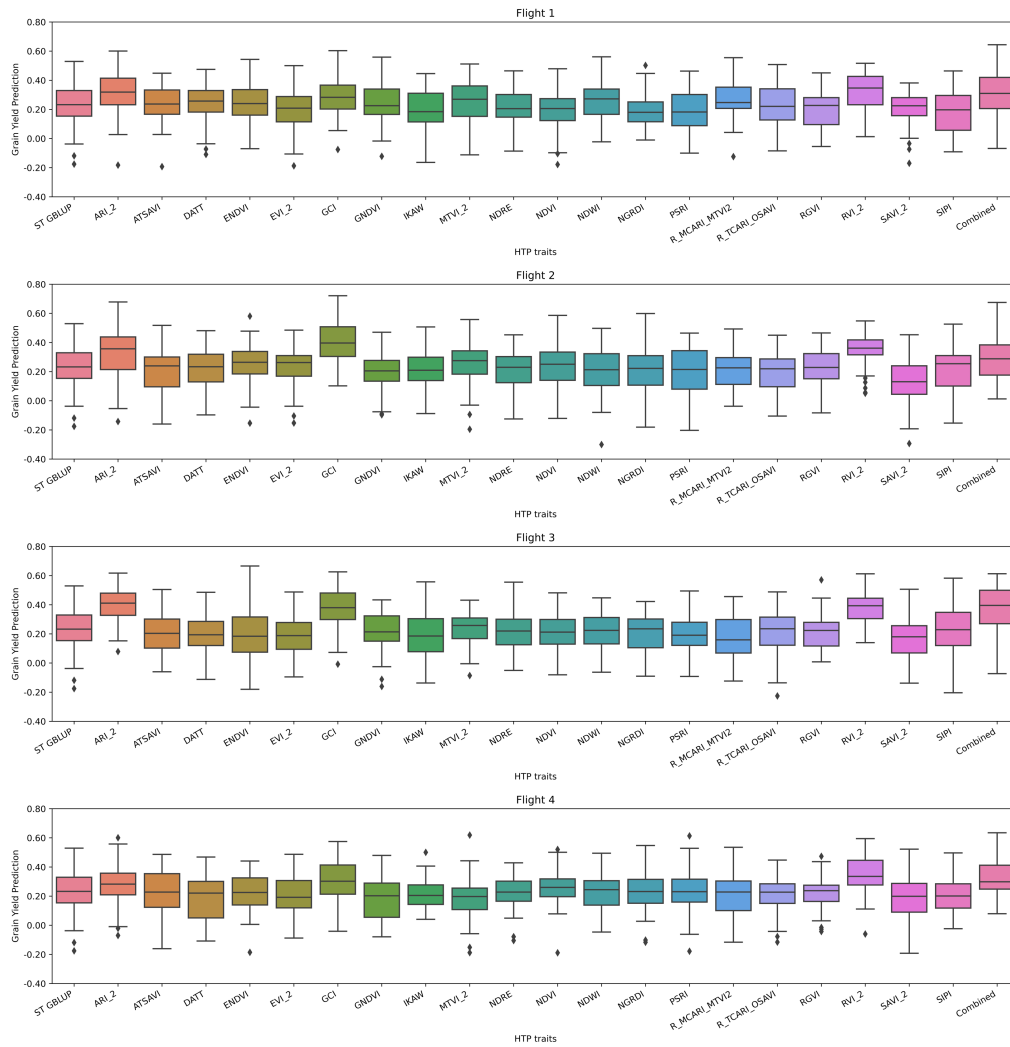
Supplementary Figure 6. Comparison of Prediction accuracy for Test Weight (TW) using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across different growth stages (Feekes 6: jointing, Feekes 8: Flag leaf, Feekes 10: Booting, Feekes 11: Milk ripe).



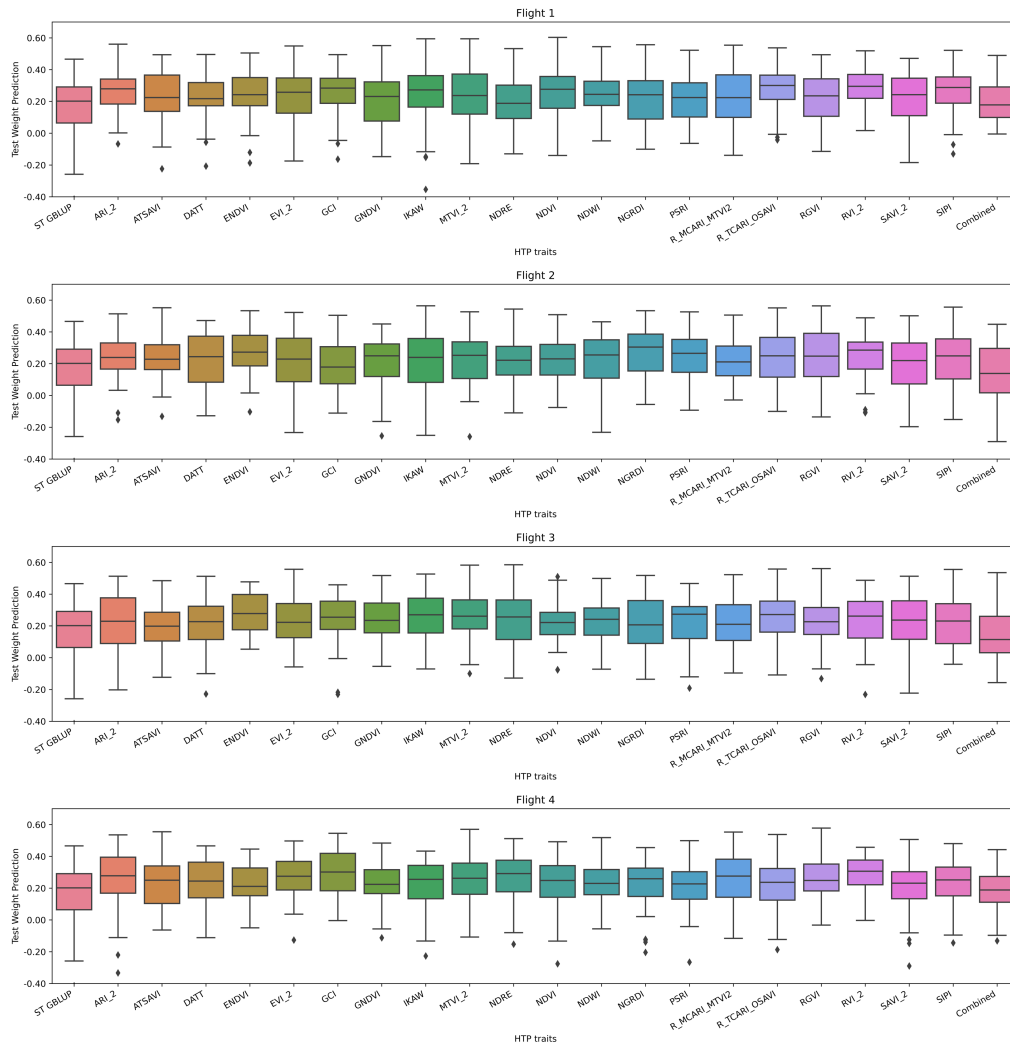
Supplementary Figure 7. Prediction accuracy for Test Weight (TW) using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across different growth stages (Feekes 6: jointing, Feekes 8: Flag leaf, Feekes 10: Booting, Feekes 11: Milk ripe).



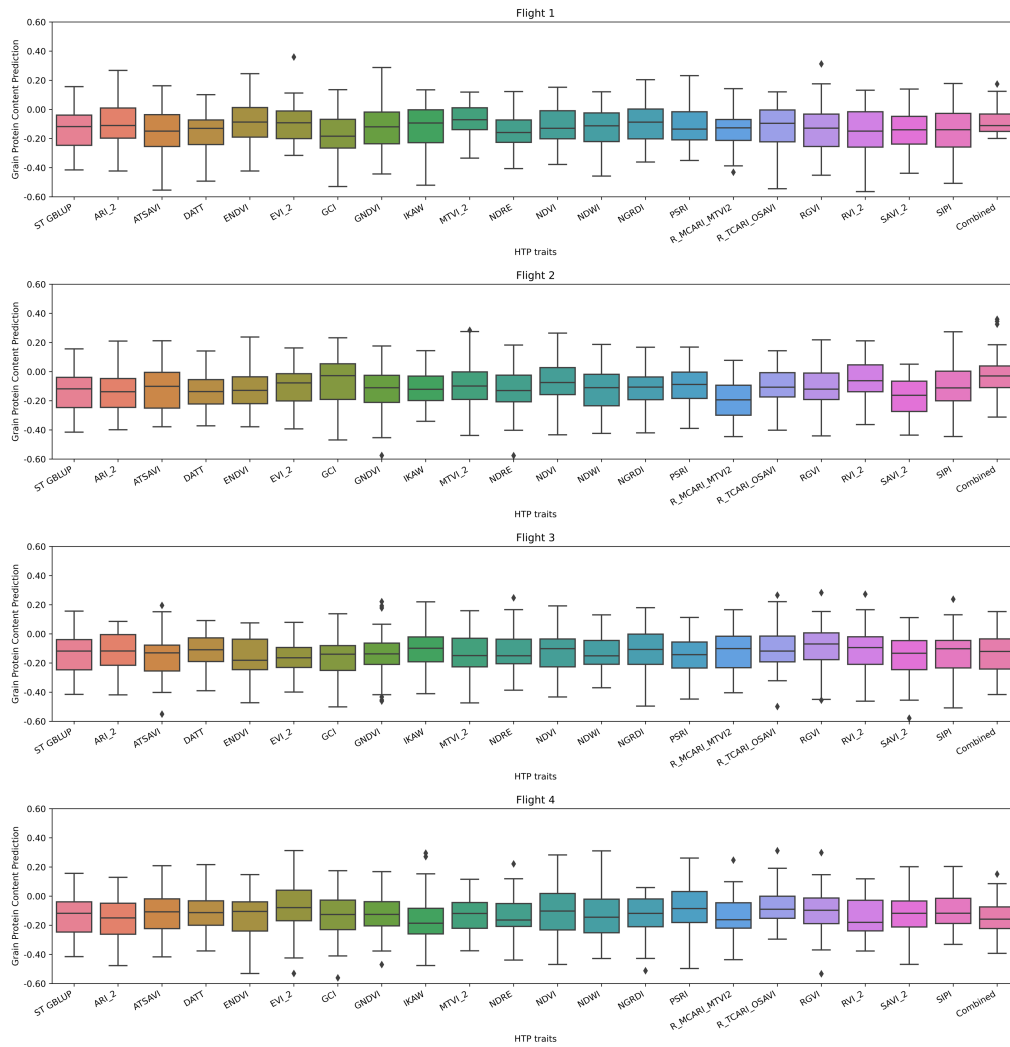
Supplementary Figure 8. Prediction accuracy for Grain Protein (GPC) using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across different growth stages (Feekes 6: jointing, Feekes 8: Flag leaf, Feekes 10: Booting, Feekes 11: Milk ripe).



Supplementary Figure 9. Distribution of prediction accuracy estimates for Grain Yield (GY) across multiple repetitions using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across flights. Each boxplot captures the variation in prediction accuracy across replicates for different prediction models.



Supplementary Figure 10. Distribution of prediction accuracy estimates for Test Weight (TW) across multiple repetitions using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across flights. Each boxplot captures the variation in prediction accuracy across replicates for different prediction models.



Supplementary Figure 11. Distribution of prediction accuracy estimates for Grain Protein Content (GPC) across multiple repetitions using Single-Trait GBLUP (ST-GBLUP) with cross-validation scheme ST-CV1 and Multi-Trait GBLUP (MT-GBLUP) incorporating High-Throughput Phenotyping (HTP) based traits with cross-validation scheme MT-CV2 across flights. Each boxplot captures the variation in prediction accuracy across replicates for different prediction models.

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