

Description of Additional Supplementary Files

File Name: Supplemental Data 1

Description: The weights of base learners in GEG2P (ML), GEG2P (DL), and GEG2P (SS)

File Name: Supplemental Data 2

Description: The prediction accuracy of several traits in maize using GEG2P(ML), GEG2P(DL), GEG2P(SS), and different base learners

File Name: Supplemental Data 3

Description: The prediction accuracy of GEG2P and rrBLUP in the CUBIC1404 population

File Name: Supplemental Data 4

Description: Prediction accuracy of the base learner with the highest prediction accuracy and GEG2P based on different ensemble strategies

File Name: Supplemental Data 5

Description: The prediction accuracy of various base learners and GEG2P(v3) on multiple phenotypes of different species

File Name: Supplementary Data 6

Description: The tuning range of key parameters

File Name: Supplemental Data 7

Description: Comparison of prediction accuracy for multiple traits across different species between GEG2P and six existing SOTA methods

File Name: Supplementary Data 8

Description: RMSE and SE of GEG2P and six SOTA methods across 36 traits in five species

File Name: Supplementary Data 9

Description: MAE and SE of GEG2P and six SOTA methods across 36 traits in five species

File Name: Supplementary Data 10

Description: R^2 and SE of GEG2P and six SOTA methods across 36 traits in five species

File Name: Supplemental Data 11

Description: The correlation between phenotype values predicted by the top five weighted base learners in GEG2P(v3)

File Name: Supplemental Data 12

Description: The correlation between phenotype values predicted by PCC-Top-5 base learners in GEG2P(v3)

File Name: Supplemental Data 13

Description: The average correlation and significance between the phenotype values predicted by Weight-Top-5 base learners in GEG2P(v3) and PCC-Top-5 base learners

File Name: Supplemental Data 14

Description: The method category of the Weight-Top-5 base learners in GEG2P(v3)

File Name: Supplemental Data 15

Description: SHAP values of all SNPs for Weight-Top-5 of DTA, PH, and EW in maize

File Name: Supplemental Data 16

Description: The co-localized SNPs between sQTLs and Top10% SNPs identified by Weight-Top-5 of DTA, PH, and EW in maize

File Name: Supplemental Data 17

Description: Gene Ontology enrichment results of genes of the Top10% SNPs identified by DTA-Weight-Top-5 base learners in maize

File Name: Supplemental Data 18

Description: The cloned genes of the Top10% SNPs identified by Weight-Top-5 base learners of DTA, PH, and EW in maize

File Name: Supplemental Data 19

Description: The cumulative narrow-sense heritability of the Top10% SNPs identified by Weight-Top-5 base learners of DTA, PH, and EW in maize

File Name: Supplemental Data 20

Description: Gene Ontology enrichment results of genes of chr5.s_7256657, chr1.s_253166238, chr7.s_128315768 and their potential interactive loci

File Name: Supplemental Data 21

Description: Gene Ontology enrichment results of the union of genes associated with the Top10% SNPs identified by Weight-Top-5 base learners of DTA, PH, and EW in maize

File Name: Supplemental Data 22

Description: Gene Ontology enrichment results of genes of the Top10% SNPs identified by PH-Weight-Top-5 base learners in maize

File Name: Supplemental Data 23

Description: Gene Ontology enrichment results of genes of the Top10% SNPs identified by EW-Weight-Top-5 base learners in maize

File Name: Supplemental Data 24

Description: KEGG pathway enrichment results of genes of chr5.s_7256657, chr1.s_253166238, chr7.s_128315768 and their potential interacting loci

File Name: Supplemental Data 25

Description: The base learner with the highest accuracy in predicting multiple traits of different species

File Name: Supplemental Data 26

Description: Prediction accuracy of GEG2P(v3) with different random seeds in the genetic algorithm

File Name: Supplemental Data 27

Description: Base learners removed in different crops and traits

File Name: Supplemental Data 28

Description: Gene Ontology enrichment results of genes of the Top10% SNPs identified by XGBoost for yield-related traits across multiple species

File Name: Supplemental Data 29

Description: Computational resources and running time of different methods in predicting EW of maize

File Name: Supplemental Data 30

Description: Key parameters of the genetic algorithm