

Additional file 2: Supplementary Figures for “FSBLUP: A novel strategy of fusion similarity matrix construction via optimally integrating intermediate omics data to enhance genomic prediction”

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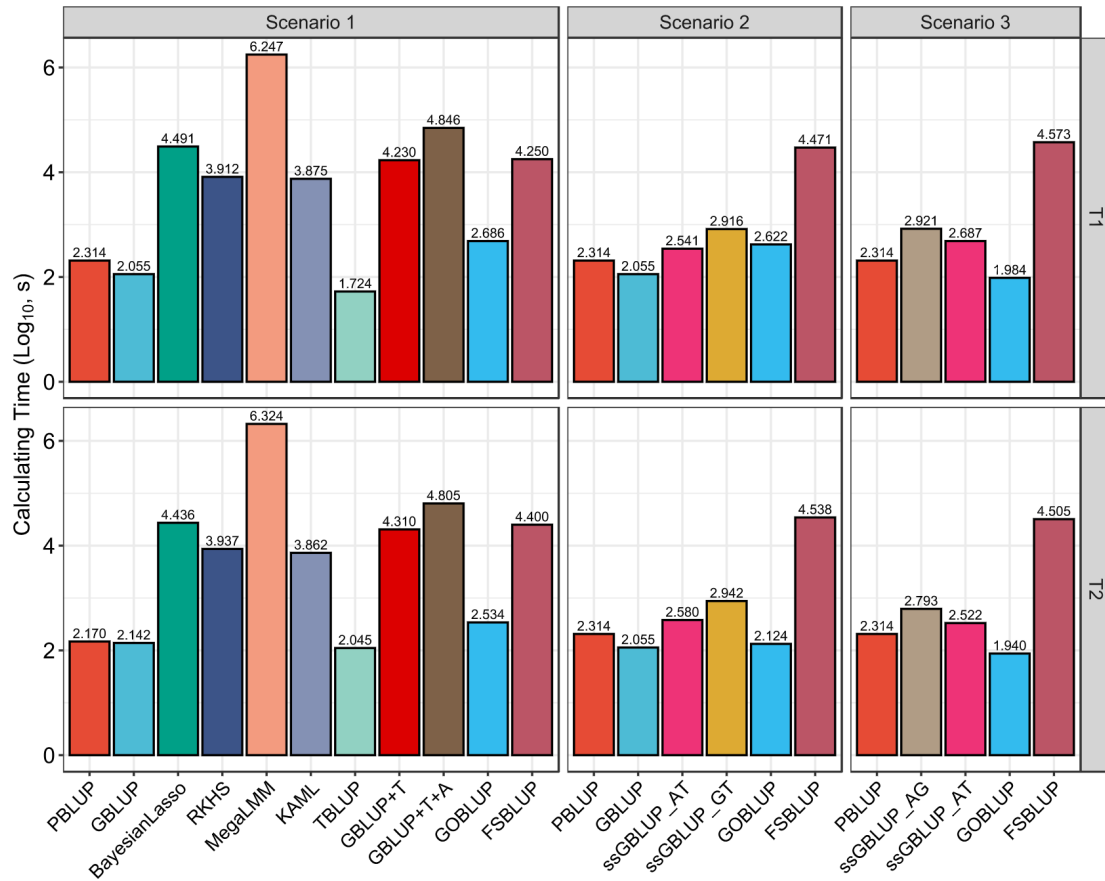


Fig. S1 The computing time of prediction performances on simulation dataset.

The x-axis indicates the methods compared. The y-axis represents the computing time on a log₁₀ scale. Computing performance tests were performed on a Red Hat Enterprise Linux server with 2.60GHz Intel(R) Xeon(R) Ice Lake 6348 CPU, and 256 GB memory.

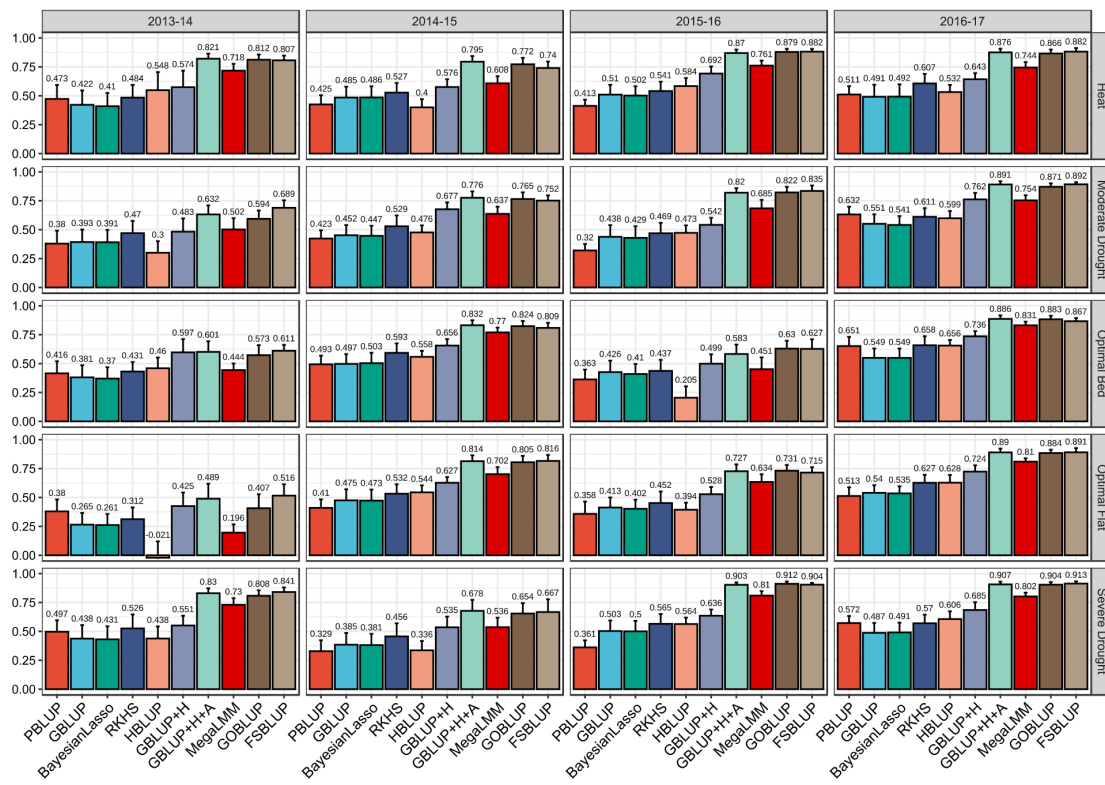


Fig. S2 The comparison of prediction performances on wheat yield across 20 experiments. Genetic value prediction accuracy was estimated using two-fold cross-validation, and 50% of the yield values were masked during model training. The bars represent average estimates ($\pm$ standard deviation) over 20 replicate cross-validation runs for each method.

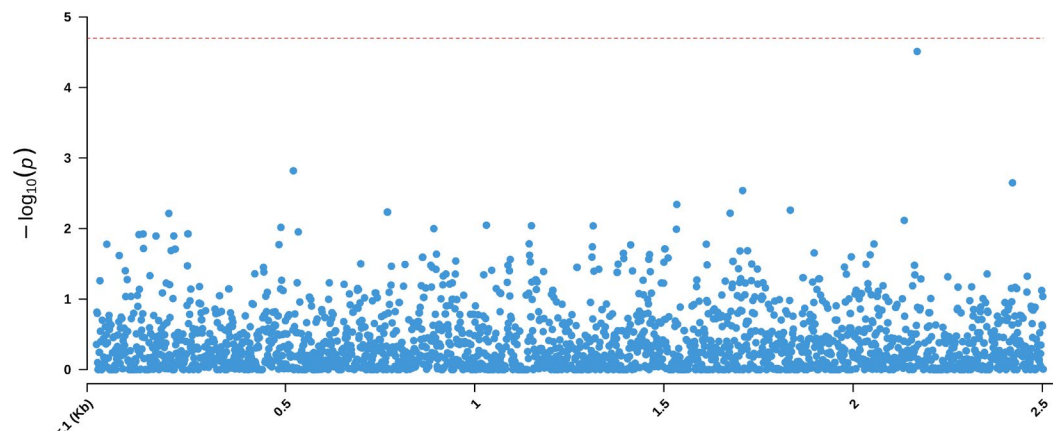


Fig. S3 Manhattan plot for grain yield. The x-axis represents the chromosomes, and the y-axis represents the $-\log_{10}(P\text{-value})$. The dashed lines represent the Bonferroni-corrected thresholds ($P=1.998\text{e-}05$).

Sensitivity of FSBLUP to change grid size

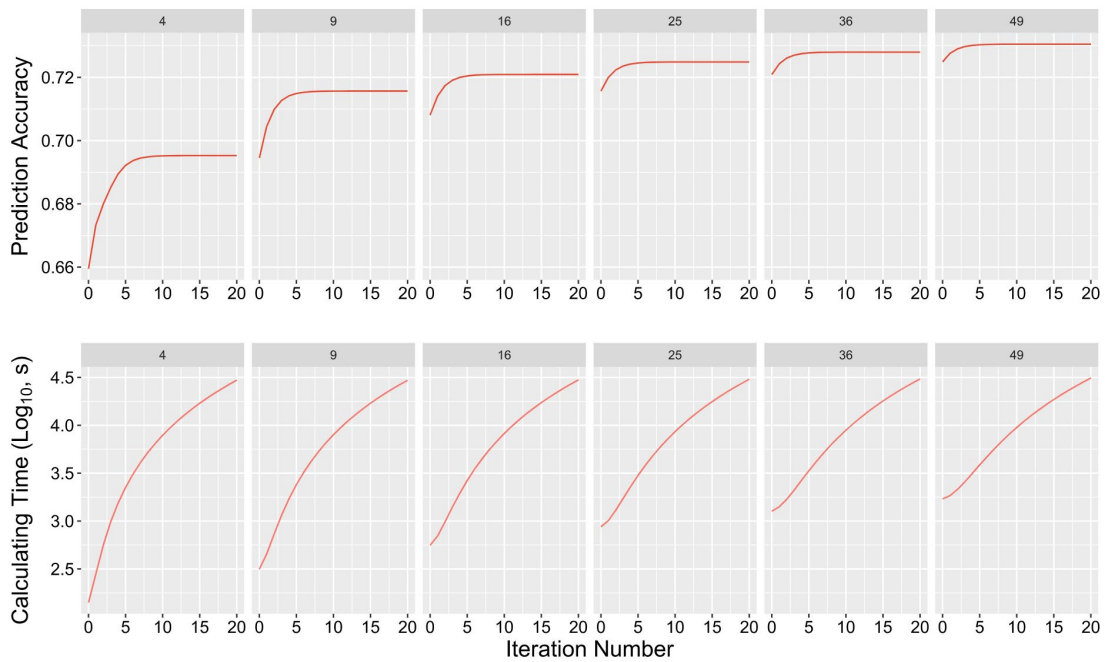


Fig. S4 Sensitivity of FSBLUP to change grid size. The prediction accuracy of each grid size was measured using the correlation method, which is the average Pearson correlation between predicted values and phenotypic values of 20 replicates. The bottom showed computing time on a log10 scale. Computing performance tests were performed on a Red Hat Enterprise Linux server with 2.60GHz Intel(R) Xeon(R) Ice Lake 6348 CPU, and 256 GB memory.