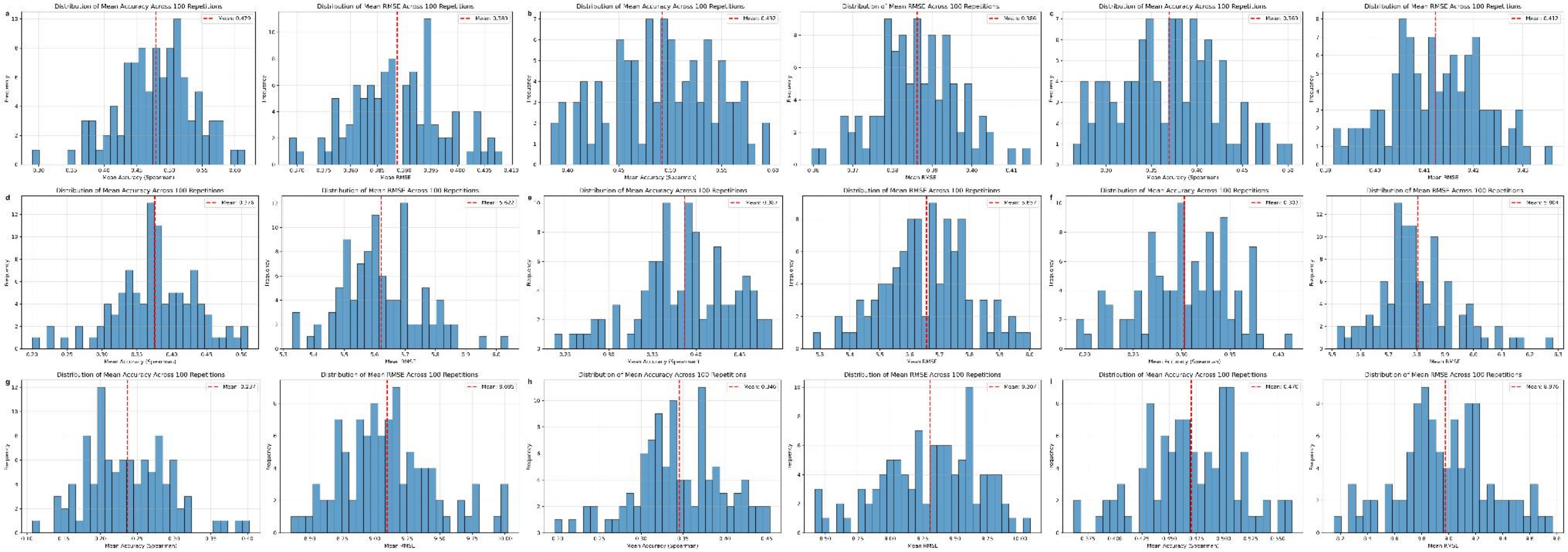

Figure S5. Prediction accuracy of spring green-up using random forest genomic selection model and 5-fold cross validation based on 19K (a), 609 (b), and 153 (c) SNP markers, spring green-up percent green cover based on 19K (d), 609 (e), and 153 (f) SNP markers, and winterkill based on 19K (g), 609 (h), and 153 (i) SNP markers. Left side of image is the distribution of prediction accuracy of each replication. Right side of image is the distribution of root mean square error (RMSE) of each replication. Red dash line is the mean of prediction accuracy and RMSE of 100 replications.