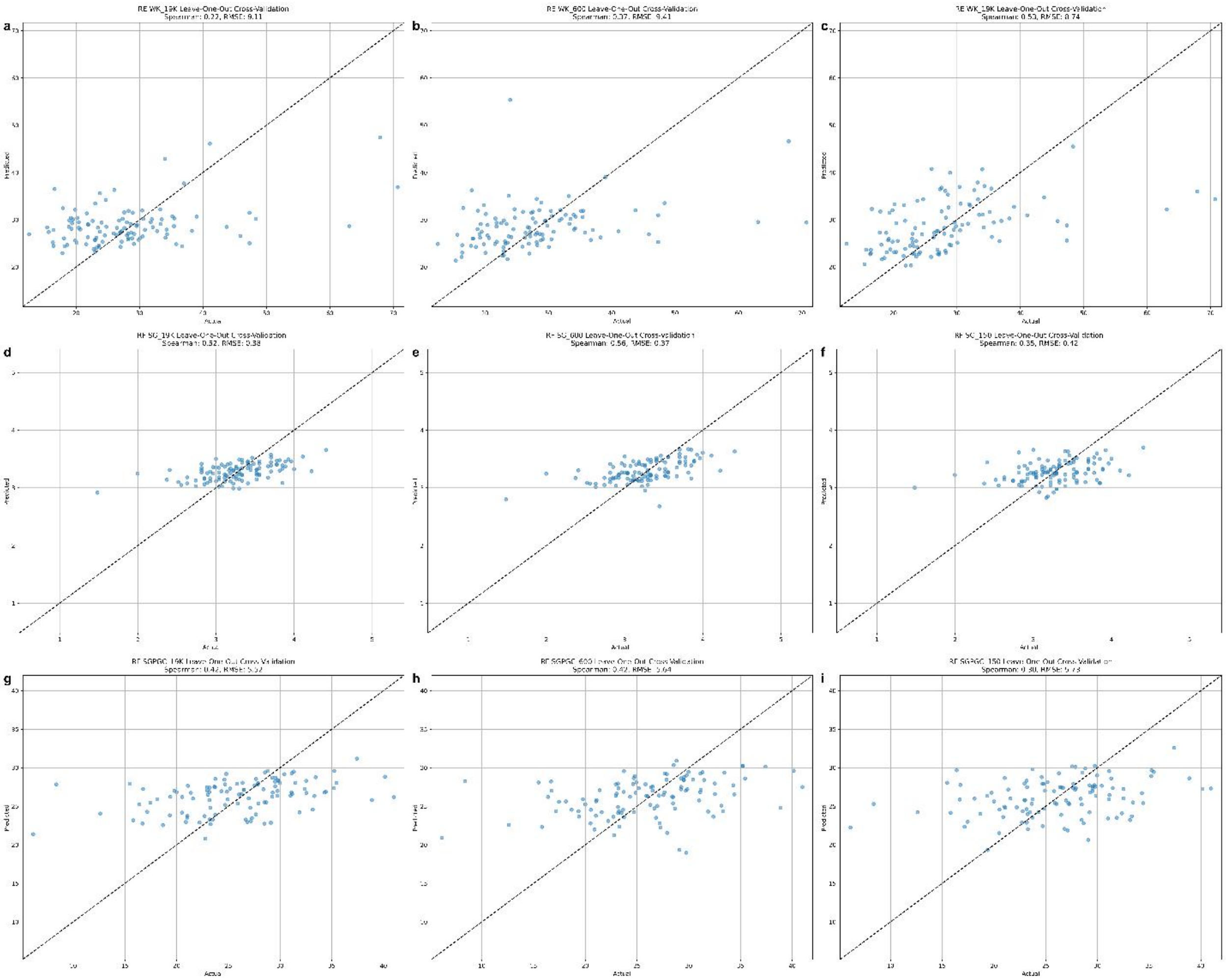

Figure S6. Scatter plots of predicted and actual value, prediction accuracy based on Spearman correlation, and root mean square error of winterkill using random forest genomic selection model and leave-one-out cross validation based on 19K (a), 609 (b), and 153 (c) SNP markers, spring green-up based on 19K (d), 609 (e), and 153 (f) SNP markers, and spring green-up percent green cover based on 19K (g), 609 (h), and 153 (i) SNP markers.