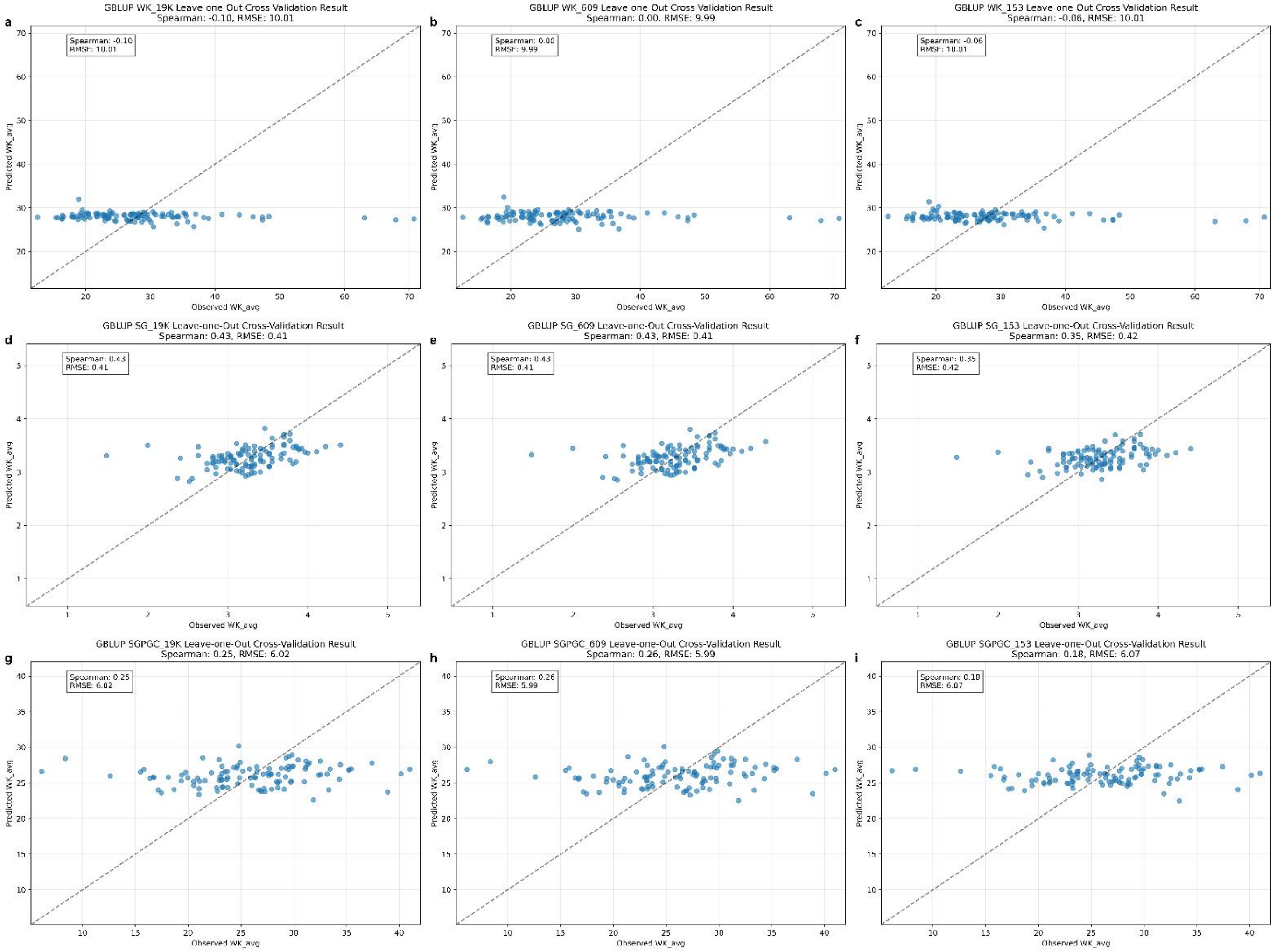

Figure S4. Scatter plots of predicted and actual value, prediction accuracy based on Spearman correlation, and root mean square error of winterkill using genomic best linear unbiased prediction genomic selection model and leave-one-out cross validation based on 19K (a), 609 (b), and 153 (c) SNP markers, 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.